

FUNCTIONAL CHARACTERIZATION OF ESSENTIAL *BURKHOLDERIA*
PSEUDOMALLEI VIRULENCE REGULATORS

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DEDICATION

This doctoral dissertation is dedicated to my best friend and wife, Jourdan, for all of your love and support through the years; to my parents for giving me the tools to succeed; and to my brother, Cameron, for always being there for me, through thick and thin.

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ABSTRACT

Burkholderia pseudomallei (*Bp*) is a Gram-negative facultative intracellular pathogen that causes the disease melioidosis. *Bp* is endemic to tropical and subtropical regions around the globe with an expanding reach due to increased awareness and better diagnostics. Melioidosis is predicted to infect 165,000 people and cause 89,000 deaths annually marking this disease as a significant threat to public health. The CDC has classified *Bp* as a Tier 1 select agent due to potential malicious use and there is currently no licensed vaccine to protect against infection. *Bp* has one of the most complex bacterial genomes with ~7.24 mega base-pairs of genetic material across two highly plastic chromosomes. The genetic determinants encoded on the *Bp* genome allow for growth in various environments including many cell types within the human body. *Bp* has a complex intracellular lifecycle that starts by attaching to host cells, followed by invasion of the cytoplasm and replication within, and finally protrusion towards neighboring cells to continue the spread of infection. Approximately 1,953 genes are differentially regulated in a stage-specific manner indicating that a sophisticated regulation system is in place to coordinate intracellular infection. In order for *Bp* to sustain a productive infection, it relies on tight control and coordination of virulence factors and metabolic pathways by transcriptional regulators in a stage specific manner. The following dissertation investigates this hypothesis by characterizing three yet to be described transcriptional regulators: i) BP1026B_II1198; ii) BP1026B_II1561; and iii) BP1026B_II2312. Mutants of these transcriptional regulators are attenuated in cell culture and BALB/c mouse models of infection indicating a role during *Bp* pathogenesis. To characterize these transcriptional regulators I have: i) elucidated the regulation networks using an RNA-seq strategy; ii) determined the direct DNA binding sequences to discover the genes directly controlled by each transcriptional regulator with a ChIP-seq approach; and iii) determined what genes within each regulon contribute to pathogenesis. In addition to the characterization of three novel transcriptional regulators, two potential vaccine candidates were tested showing significant promise towards the development of a protective melioidosis vaccine.

TABLE OF CONTENTS

DEDICATION	i
ACKNOWLEDGEMENTS	ii
ABSTRACT	iii
TABLE OF CONTENTS	iv
LIST OF TABLES	vi
LIST OF FIGURES	vii
 Chapter 1: <i>Burkholderia pseudomallei</i> , a complex life for a complex pathogen	1
The first case of melioidosis	2
Epidemiology, global burden, and spread across the globe	3
Clinical presentation and treatment of melioidosis	5
Development of vaccines against melioidosis	7
Mechanisms of <i>Bp</i> pathogenesis	9
Regulation of virulence	12
Figures	14
References	18
 Chapter 2: BP1026B_II1198, a PadR-Type Regulator of <i>Burkholderia pseudomallei</i> Intracellular Pathogenesis	32
Abstract	33
Introduction	34
Results	37
Discussion	45
Methods and Materials	49
Figures	53
Acknowledgments	66
References	67
 Chapter 3: Identification of BP1026B_II1561, a <i>Burkholderia pseudomallei</i> Regulator of Aromatic Ring Biosynthesis and Intracellular Pathogenesis	76
Abstract	77
Introduction	78
Results	80
Discussion	90
Methods and Materials	94
Figures	98
Acknowledgments	112
References	113
 Chapter 4: Identification of BP1026B_II2312, a <i>Burkholderia pseudomallei</i> Regulator of Intracellular Pathogenesis	121
Abstract	122
Introduction	123

Results.....	125
Discussion.....	135
Methods and Materials	138
Figures	142
Acknowledgments	155
References.....	156
 Chapter 5: Live Attenuated Vaccine Candidate Provides Protection Against Lethal <i>Burkholderia pseudomallei</i> Infection in BALB/c and C57Bl/6 mice	162
Abstract.....	163
Introduction.....	164
Results.....	167
Discussion.....	174
Methods and Materials	176
Figures	178
Acknowledgments	186
References.....	187
 Chapter 6: Exploitation of <i>Burkholderia pseudomallei</i> Attachment Factors as Melioidosis Vaccines.....	193
Abstract.....	194
Introduction.....	195
Results.....	197
Discussion.....	203
Methods and Materials	206
Figures	210
Acknowledgments	218
References.....	219
 Chapter 7: Concluding remarks	225
References.....	232
Appendix A: The <i>Burkholderia pseudomallei</i> intracellular ‘TRANSITome’	238
Appendix B: The heritable natural competency trait of <i>Burkholderia pseudomallei</i> in other <i>Burkholderia</i> species through <i>comE</i> and <i>crp</i>	286
Appendix C: Current Publications	318
Appendix D: Supplemental Table 1 for Chapter 2	322
Appendix E: Supplemental Table 1 for Chapter 3	374
Appendix F: Supplemental Table 1 for Chapter 4	426

LIST OF TABLES

Chapter 2: BP1026B_II1198, a PadR-Type Regulator of *Burkholderia pseudomallei* Intracellular Pathogenesis

Supplementary table 1: Total transcriptome of BP1026B_II1198 (Appendix D)322

Chapter 3: Identification of BP1026B_II1561, a *Burkholderia pseudomallei* Regulator of Aromatic Ring Biosynthesis and Intracellular Pathogenesis

Supplementary table 1: Total transcriptome of BP1026B_II1561 (Appendix E).....374

Chapter 4: Identification of BP1026B_II2312, a *Burkholderia pseudomallei* Regulator of Intracellular Pathogenesis

Supplementary table 1: Total transcriptome of BP1026B_II2312 (Appendix F).....426

Chapter 5: Live Attenuated Vaccine Candidate Provides Protection Against Lethal *Burkholderia pseudomallei* Infection in BALB/c and C57Bl/6 mice

Table 1: Intracellular Infection Assessment of Virulence Factors178

Table 2: Conservation of Virulence Factors in Pathogenic *Burkholderia* species179

LIST OF FIGURES

Chapter 1: *Burkholderia pseudomallei*, a complex life for a complex pathogen

Figure 1: Observations from the first case of melioidosis.....	14
Figure 2: Global map of the presence or absence of <i>Bp</i> and melioidosis as of July 13, 2020 ..	15
Figure 3: Model of <i>Bp</i> intracellular infection	16
Figure 4: MNGC formation by <i>Bp</i>	17

Chapter 2: BP1026B_II1198, a PadR-Type Regulator of *Burkholderia pseudomallei* Intracellular Pathogenesis

Figure 1: BP1026B_II1198 is differentially regulated during cell infection and critical for intracellular survival.....	53
Figure 2: BP1026B_II1198 is attenuated in BALB/c mouse model	55
Figure 3: Hypothetical proteins are disproportionately controlled by BP1026B_II1198 .	56
Figure 4: Genes highly regulated by BP1026B_II1198 show involvement during <i>Bp</i> intracellular survival	57
Figure 5: ChIP-seq identifies two regions of BP1026B_II1198 binding on chromosome II	58
Figure 6: BP1026B_II1198 has direct transcriptional control of genes involved in pathogenesis of RAW264.7 murine macrophages	59
Supplemental Figure 1: WoPPER analysis reveals 21 gene clusters regulated by BP1026B_II1198 on <i>Bp</i> 1026b chromosome 1.....	61
Supplemental Figure 2: WoPPER analysis reveals 21 gene clusters regulated by BP1026B_II1198 on <i>Bp</i> 1026b chromosome 2.....	63
Supplemental Figure 3: Transposon mutants grow identical to wildtype <i>Bp</i> 1026b <i>in vitro</i>	65

Chapter 3: Identification of BP1026B_II1561, a *Burkholderia pseudomallei* Regulator of Aromatic Ring Biosynthesis and Intracellular Pathogenesis

Figure 1: Differential regulation of BP1026B_II1561 during cell infection leads to defects in pathogenesis	98
Figure 2: A BP1026B_II1561 mutant is attenuated in the BALB/c mouse infection model	100

Figure 3: BP1026B_II1561 down-regulates 83 genes and up-regulates 42 genes	101
Figure 4: General metabolic pathways controlled by BP1026B_II1561 contribute to pathogenesis in RAW264.7 cells	102
Figure 5: BP1026B_II1561 binds two regions of DNA on chromosome II	104
Figure 6: BP1026B_II1561 binds two intergenic regions controlling genes in the shikimate pathway and an outer membrane porin	105
Supplemental Figure 1: WoPPER analysis reveals 40 gene clusters regulated by BP1026B_II1561 on <i>Bp</i> 1026b chromosome I	107
Supplemental Figure 2: WoPPER analysis reveals 50 gene clusters regulated by BP1026B_II1561 on <i>Bp</i> 1026b chromosome II	109
Supplemental Figure 3: Growth analysis of transposon mutants compared to wildtype <i>Bp</i> 1026b	111
 Chapter 4: Identification of BP1026B_II2312, a <i>Burkholderia pseudomallei</i> Regulator of Intracellular Pathogenesis	
Figure 1: Differential regulation of BP1026B_II2312 during cell infection leads to defects in pathogenesis	142
Figure 2: A BP1026B_II2312 mutant is attenuated in the BALB/c mouse infection model	144
Figure 3: BP1026B_II2312 down-regulates 315 genes and up-regulates 41 genes	145
Figure 4: General metabolic pathways and hypothetical proteins controlled by BP1026B_II2312 contribute to pathogenesis in RAW264.7 cells	146
Figure 5: BP1026B_II2312 binds 11 regions of DNA on chromosome I and chromosome II	147
Figure 6: BP1026B_II2312 binds an intergenic region activating BP1026B_II2319-II2313	148
Supplemental Figure 1: WoPPER analysis reveals 45 gene clusters regulated by BP1026B_II2312 on <i>Bp</i> 1026b chromosome I	150
Supplemental Figure 2: WoPPER analysis reveals 29 gene clusters regulated by BP1026B_II2312 on <i>Bp</i> 1026b chromosome II	152
Supplemental Figure 3: Growth kinetics of transposon mutants confirms defects during intracellular pathogenesis	154
 Chapter 5: Live Attenuated Vaccine Candidate Provides Protection Against Lethal <i>Burkholderia</i>	

pseudomallei Infection in BALB/c and C57Bl/6 mice

Figure 1: Vaccination with virulence factor mutants gives partial protection against lethal <i>Bp</i> infection	180
Figure 2: Double mutant vaccinations maintains protection and eliminates persistence of LAV strain	181
Figure 3: Challenge 30 days post vaccination identifies BPSL0636/BPSS0015 as the best LAV candidate	182
Figure 4: BPSL0636/BPSS0015 gives 100% protection to BALB/c and C57Bl/6 mice from lethal challenge with virulent <i>Bp</i>	183
Figure 5: Clinical scores and weights over the course of vaccination and challenge	185
Chapter 6: Exploitation of <i>Burkholderia pseudomallei</i> Attachment Factors as Melioidosis Vaccines	
Figure 1: SR1 and SR2 are conserved in pathogenic <i>Bp</i> strains	210
Figure 2: The SR1 mutant and the SR1/SR2 double mutant as LAVs do not protect against lethal challenge in BALB/c mice	211
Figure 3: mAbs that target SR1 and SR2 reduce attachment of <i>Bp</i> to HEK293T cells	213
Figure 4: BALB/c mice are protected against a lethal <i>Bp</i> challenge when vaccinated with an SR1/SR2 based subunit vaccine	214
Supplemental Figure 1: The SR1 mutant combined with various mutants as LAVs do not protect against lethal infection in BALB/c mice	215
Supplemental Figure 2: BALB/c mice vaccinated with SR1/SR2 based subunit vaccine recover after lethal challenge	217

Chapter 1:

***Burkholderia pseudomallei*, a complex life for a complex pathogen**

The first case of melioidosis

In April 1911 a man was admitted to the Rangoon General Hospital after sustaining a high fever for seven days. The man, approximately 40 years old, had lesions from morphine injections throughout his body, a temperature fluctuating between 103-104°F, and abnormal sounds in the lungs. After three days in the hospital the man died and upon post-mortem examination, uncharacteristic ‘cheesy’ consolidations were found in his lungs (Fig. 1a)^{1, 2}. The consolidations within the lungs presented different than tuberculosis and typical pneumonia. A pure culture of non-motile Gram-negative bacilli was purified and resembled *Bacillus mallei* (now called *Burkholderia mallei*), the causative agent of glanders. While the patient had no history of contact with horses making this diagnosis odd, the pure culture was injected into a male guinea pig to confirm glanders by the observation of testicular inflammation. The guinea pig died within 36 hours and showed no inflammation in the testicles. Further confounding evidence was that motile Gram-negative bacilli were isolated from the guinea pig suggesting that what was isolated post-mortem was different than the inoculating strain. The attending pathologist and surgeon, Whitmore and Krishnaswami, hypothesized that the organism injected into the guinea pig was in-fact the motile Gram-negative bacilli that was isolated from the lungs (Fig. 1a), and that the bacilli had lost its motility after several days on artificial agar (Fig. 1b-c). This hypothesis proved to be correct leading to the conclusion that this infectious agent was unique from *B. mallei* (*Bm*) but caused a glanders-like disease^{1, 2}. Within two years, Whitmore had described 38 potential cases² of this new disease that would eventually become known as melioidosis. Thanks to this work, and the work of many others over the last century, we now know that melioidosis is caused by the Gram-negative bacillus *Burkholderia pseudomallei* (*Bp*), a truly complex pathogen.

Bp is now well established as a pathogen of humans and animals that is found within the rhizosphere and ground water of tropical regions throughout the globe³⁻⁶. *Bp* has been classified as a Tier 1 select agent by the Centers for Disease Control and Prevention (CDC) and is a major public health concern for regions with endemic presence of this organism³. *Bm* was used to intentionally infect animals in the effort of transmitting glanders to soldiers during World War I and World War II⁷. *Bm* is a clonal derivative of *Bp* that adapted from evolution within a host similar to how *Mycobacterium leprae* and *M. tuberculosis* evolved from a common ancestor^{8,9}. The observations made by Whitmore and Krishnaswami reflect this fact based on the basic microbiological test of motility^{1,2}. The genetic diversity of *Bp* is much greater than that of *Bm* allowing it to live in more diverse environments and potentially leading to more infection in humans and animals. It is therefore critical that we understand how this pathogen causes disease so that we can combat infection with *Bp*.

Epidemiology, global burden, and spread across the globe

Bp found within the environment is likely the source of infection in many cases through ingestion or inoculation of contaminated food or water^{10, 11}. Increased environmental surveillance and standardized environmental sampling protocols have helped identify that *Bp* is present in the environment globally throughout tropical and subtropical regions¹²⁻²³ and this has correlated with clinical reports²⁴⁻³¹. In recent years, this data has been continually updated and curated online (<https://www.melioidosis.info/map.aspx>) showing an ever-changing map of presence or absence of *Bp* and clinically confirmed melioidosis cases globally (Fig. 2a-b). In addition, there have been reports of *Bp* surviving in more extreme environments including distilled water for more than 16 years, low nutrient soils, and in deserts which suggests that *Bp* could be present in

obscure areas around the world^{17, 32, 33}. In 2016, a group predicted the burden of melioidosis and the distribution of *Bp* across the globe. They estimated that approximately 165,000 cases of melioidosis occurred in 2015 in South and East Asia, Pacific islands, Sub-Saharan Africa, East and North Africa, Latin America, and the Caribbean⁵. Of these, 89,000 cases are predicted to result in death, making the global predicted mortality rate in 2015 to be in excess of fifty percent⁵. The predicted annual mortality of melioidosis is comparable to other diseases considered high priority by health organizations including measles (~95,600 deaths annually), leptospirosis (~50,000 deaths annually), and dengue fever (~12,500 deaths annually)⁵. They concluded that melioidosis cases are severely underreported globally, both in countries where *Bp* is known to be endemic and countries that the environment suits *Bp* growth but has yet to be discovered⁵.

A hypothesis of the origin of this pathogen was recently made suggesting that *Bp* originated in Australia³⁴. This group analyzed the whole genome sequence of 469 *Bp* isolates from 30 countries³⁴. They tracked the movement of *Bp* from Australia to Southeast Asia, and subsequent transfer to South and East Asia³⁴. Genetic variations of *Bp* have been observed prior to this study identifying specific gene clusters and overall genetic diversity that is geographically distributed³⁵⁻³⁷. Clusters of *Bp* isolates in Africa showed strong similarity to ones found in Central and South America and the temporal occurrence of this relationship was estimated to be 1806 or 1759, correlating to the slave trade between 1650-1850³⁴. In contemporary times, transfer of *Bp* has been documented through the transport of infected animals to regions without melioidosis³⁸. The analysis looking at the origin of *Bp* and its distribution across the globe relied on the whole genome sequence of *Bp*. The *Bp* genome is large and complex including chromosome I (4.07Mb) and chromosome II (3.17 Mb). As more *Bp* strains get sequenced we

see more strain diversity that is constantly influenced by horizontal gene transfer, recombination, and mutation^{39, 40}. The large genome and the genetic heterogeneity between strains across the world could have a role in the variations we see in clinical melioidosis^{41, 42}.

Clinical presentation and treatment of melioidosis

Melioidosis is acquired through inoculation of the skin by *Bp*, ingestion of *Bp* contaminated food or water, or inhalation of *Bp*¹¹. More than 50% of melioidosis patients have diabetes mellitus making this the most important risk factor for disease potentially due to impaired *Bp*-specific cellular responses of macrophages and regulatory T cells^{3, 43-45}. Other risk factors include alcoholism, chronic kidney disease, liver disease, chronic lung disease, and exposure to soil in endemic areas^{10, 43, 44}. Infection leads to acute melioidosis in 85% of cases or chronic melioidosis, defined by symptomatic infection for greater than 2 months, in 11% of cases⁴⁶. In less than 5% of cases symptoms can develop years after exposure to *Bp*⁴⁶ with the longest suspected case occurring 62 years post-exposure⁴⁷. Case fatality rates (CFRs) can be in excess of 70% without treatment^{48, 49} and has been as high as 40% with treatment in Thailand, where there are ~2,000 culture confirmed cases annually⁴³. The mean incubation period for melioidosis is nine days (ranging from 1-21 days) but this is highly dependent on the route of infection⁵⁰. In cases where aspiration or inhalation of contaminated water is highly likely, the incubation period is much shorter⁵¹. Clinical manifestations are diverse and range from minor localized infections to sepsis and death, but also can present with non-specific symptoms making diagnosis difficult^{3, 52, 53}. Approximately 50% of cases present with bacteremia, pneumonia, or both⁵⁴. This can lead to pulmonary abscesses, pleuritis, pericarditis, or a mycotic aneurysm³. A 20 year study in Australia surveying 540 cases of melioidosis identified that 51% of cases

presented with pneumonia, 14% with gastrointestinal tract infection, 13% with skin infection, 11% with unfocused bacteremia, 4% with septic arthritis or osteomyelitis, 3% with central nervous system infection, and 4% with no central focus of infection⁴⁶. Of these patients, ~50% had bacteremia and some of those developed septic shock⁴⁶. This and other clinical reports shows how *Bp* can establish infection in many systems of the human body including, but not limited to, the gastrointestinal tract, urinary tract, skin, musculoskeletal system, and, in rare cases the central nervous system^{3, 55}. Taken together this further highlights how the large complex genome of *Bp* allows it to survive and thrive in many niches.

While diagnosis is extremely difficult and mainly relies on culturing of *Bp* from blood specimens³, it is imperative that melioidosis patients get the proper treatment due to intrinsic resistance to many antibiotics⁵⁶. Treatment consists of two phases, an intensive phase therapy that lasts approximately two to four weeks, and an eradication phase therapy that can last for more than three months⁶. Intensive phase therapy is intravenous ceftazidime, meropenem, or imipenem every six to eight hours for 10-14 days but can last up to four weeks depending on the severity of infection⁶. The introduction of ceftazidime in the 1980's reduced the mortality of melioidosis in Thailand by half⁴⁸. Although, ceftazidime therapy revolutionized the treatment of melioidosis, some cases of resistance have been reported clinically^{57, 58}. Eradication phase therapy consists of oral sulfamethoxazole-trimethoprim (co-trimoxazole) or amoxicillin-clavulanate with doxycycline for three to six months⁶. *Bp* encodes an efflux pump, BpeEF-OprC that targets trimethoprim leading to resistance⁵⁹ although clinical presence of co-trimoxazole resistance is low⁶⁰. Resistance to current antimicrobial therapy is rare in clinical cases but a reality that must be accounted for. For this reason many groups have been attempting to develop a vaccine for prevention of melioidosis.

Development of vaccines against melioidosis

Over the last decade many groups have been working towards developing a vaccine that elicits protection against infection with *Bp*. In 2015, the Steering Group on Melioidosis Vaccine Development (SGMVD) published guidelines for the development of melioidosis vaccines⁶¹. This included distinctions between what is required of a vaccine for naturally acquired melioidosis and a vaccine required for biodefense purposes. To summarize, a vaccine to protect naturally acquired melioidosis will need to protect people with diabetes mellitus from skin inoculation and therefore the vaccine candidates should be tested in a diabetic mouse model⁶¹. A vaccine for biodefense purposes will require protection of healthy individuals against inhalation melioidosis⁶¹. In both cases, the SGMVD indicates that a non-human primate model of infection will also have to be tested for protection⁶¹. Beyond this, the SGMVD recommends the use of two mouse models, BALB/c and C57Bl/6 mice for testing of potential melioidosis vaccines⁶¹. BALB/c and C57Bl/6 mice have different susceptibilities to *Bp* infection^{62, 63}. BALB/c mice are highly susceptible to infection with *Bp*, exhibiting acute forms of melioidosis, and have been extensively used to test attenuation of virulence factor mutants⁶⁴⁻⁶⁷. In general, BALB/c mice elicit a Th-2 like response during infection and have a weaker Th-1 response, making them susceptible to *Bp* infection⁶⁸. C57Bl/6 mice elicit a strong Th-1 response giving long lasting protection against *Bp* infection and have showed signs of a chronic-like melioidosis infection⁶⁸⁻⁷⁰. Preliminary testing of vaccine candidates has shifted towards the use of C57Bl/6 mice in recent years even though the mouse itself is more resistant to *Bp* infection⁷¹.

Live attenuated vaccines (LAVs) have included attenuated mutants in metabolic functions, stringent response, virulence factors, and double mutants in these processes⁷¹. A

mutant in aspartate-semialdehyde dehydrogenase (*asd*) was tested as an LAV strain giving BALB/c mice protection from acute melioidosis but no protection against chronic infection⁶⁶. A *purM* mutant of *Bp* was 100% protective for C57Bl/6 mice and ~60% protective for BALB/c mice for 60 days post challenge⁷². Although the *asd* and *purM* mutant strains have not been further developed as LAV strains, they have both been excluded from the select agent list and are valuable tools for the research community^{66, 67, 73}. Mutants in *relA* and *spoT*, required for the synthesis and degradation of hyperphosphorylated guanosine signaling molecules have also been tested as an LAV⁷⁴. A double mutant of *relA* and *spoT* showed ~60% survival of C57Bl/6 mice for ~55 days post challenge⁷⁴. More recently, a group has showed success with a double mutant of *tonB* and *hcp1* in both protection against melioidosis and glanders^{75, 76}. The TonB complex (TonB, ExbB, ExbD) is important for energy transduction across the periplasmic space allowing for iron uptake in iron-limiting conditions^{77, 78} and a *tonB* mutant was shown to be required for pathogenesis in *Bm*⁷⁹. Hcp1 forms a hexameric rings of the needle like structure of the virulence associated type VI secretion system (T6SS-1) of *Bp*⁸⁰. When mutations of *tonB* and *hcp1* are combined in LAV strains of *Bm* and *Bp*, C57Bl/6 mice are protected for 35 and 27 days against lethal challenge with their respective pathogen^{75, 76}. While these candidates have shown promise to protect against a lethal *Bp* infection and LAVs produce robust immune responses^{72, 81, 82}, persistence and reversion to virulence is a major concern for LAVs⁸³. This is an even bigger concern when considering the plasticity of the *Bp* genome and past instances of mutation during clinical infection^{39, 42, 57, 58}.

Groups have been testing other potential melioidosis vaccines as well, including subunits, outer-membrane vesicles (OMVs), and glycoconjugates⁷¹. Antigens expressed during chronic infection were purified and used in a potential subunit vaccine that gave 30% protection of

BALB/c mice for 50 days and this protection was enhanced by the addition of LolC protein or capsule polysaccharide (CPS)⁸⁴. Gram-negative bacteria can secrete OMVs that are non-infectious and comprised of numerous biologically active proteins⁸⁵. *Bp* OMVs have been tested as a potential vaccine against melioidosis in BALB/c mice giving rise to 100% protection for 21 days⁸⁶. Because OMVs are naturally multivalent and non-infectious, they have a high potential for the future development of a successful vaccine protecting against *Bp* infection. Currently, the most progress towards a melioidosis vaccine is through glycoconjugates that have achieved various levels of success⁸⁷⁻⁹³. The most recent of the glycoconjugates incorporates CPS that is conjugated to a non-toxic diphtheria toxin (CRM197) and combined with purified Hcp1 or TssM, a deubiquitinase⁹¹. The CPS-CRM197 plus Hcp1 and the CPS-CRM197 plus TssM provide 100% and 80% protection to C57Bl/6 mice, respectively⁹¹. More striking is the fact that the majority of the vaccinated mice showed sterile immunity having no detectable levels of *Bp* colonization within the lungs, liver, spleens after challenge⁹¹. All potential preclinical vaccines will need to incorporate a diabetic mouse model, incorporate both BALB/c and C57Bl/6 mouse models, and eventually add a large animal model before going to clinical trials⁶¹. As there is still no licensed vaccine to protect against naturally acquired or intentionally released melioidosis, there is much more work to be accomplished in this area of *Burkholderia* research.

Mechanisms of *Bp* pathogenesis

Bp is a facultative intracellular pathogen that has a complex lifecycle and the ability to adapt to many different host cell environments. Even with broad heterogeneity between *Bp* isolates, there are conserved mechanisms that have been studied giving a basic understanding of the intracellular lifecycle (Fig. 3). The *Bp* intracellular lifecycle can be broken down into three

discernible stages: i) attachment to host cells gaining entry into the cell via the endocytic pathway; ii) escape from the vacuole allowing replication within the cytoplasm; and iii) host cell membrane fusion allowing spread of the infection (Fig. 3). The research community has partially characterized the mechanisms that *Bp* uses to navigate this intracellular lifecycle.

Bp first attaches to various host cell types using multiple putative adhesions. CPS and type IV pili have been implied during attachment of *Bp* to human pharyngeal epithelial cells^{94, 95}. A CPS mutant did, however, increase invasion in HeLa and A549 human epithelial cell lines suggesting other attachment factors exist⁹⁶. Autotransporters BoaA and BoaB are involved in the attachment to human epithelial cells as well but a double mutant of these genes is still able to invade cells indicating other attachment proteins are present within the *Bp* genome⁹⁷. Recently, Surface Receptor 1 (SR1) and Surface Receptor 2 (SR2) were identified to be involved in attachment to multiple cell types including macrophages, epithelial cells, and neuronal cells⁹⁸. Both SR1 and SR2 are required for complete pathogenesis in BALB/c mice and are expressed on the surface of the *Bp* cell⁹⁸. After *Bp* attaches to the host cell, it gains entry through phagocytosis or an unknown mechanism^{99, 100}. In the vacuole of the host cell, the type III secretion system (T3SS-3) is used to escape into the cytoplasm before lysosomal fusion and degradation^{101, 102}. Although, *Bp* encodes three T3SSs, only one has been identified as important for mammalian virulence while the other two have been implied during plant pathogenesis¹⁰³⁻¹⁰⁶. Within the cell, *Bp* is resistant to oxidative stress using superoxide dismutase (SodC), catalase peroxidase (KatG), alkyl hydroperoxide reductase (AhpC), DNA starvation and stationary phase protection protein (DpsA)¹⁰⁷⁻¹¹⁰. *Bp* is also able to escape host cell clearance via LC3-associated phagocytosis and autophagy. T3SS effector protein BopA has been associated with the escape of early stage LC3-associated phagocytosis and autophagy^{111, 112}. Recently, another gene encoding a

hypothetical protein, BPSS0015, was identified to avoid late stage clearance by host cell autophagy⁹⁸. A mutant of BPSS0015 was identified to be encapsulated in double membrane bound vesicles during late stages of infection, indicative of autophagy⁹⁸. Taken together, *Bp* is able to efficiently attach to host cells via multiple mechanisms, invade the cytoplasm using T3SS-3, and avoid intracellular defenses using multiple factors allowing the infection to continue.

Within the cytoplasm of the host cell, *Bp* has access to the nutrients available and can transit within the cell using multiple mechanisms. BimA is an autotransporter that was identified to be critical for actin-based motility and virulence^{102, 113}. BimA uses molecular mimicry, of the host cell Ena/VASP system, to polymerize host cell actin giving *Bp* the ability to protrude towards neighboring cells¹¹⁴. *Bp* encodes a lateral flagellar locus on the second chromosome that can be used for rapid intracellular motility¹⁰². When nutrients are depleted or another unknown signal is received, *Bp* can fuse the membranes of host cells generating a multinucleated giant cell (MNGC) using T6SS-1^{115, 116}. The fusion of host cell membranes is mediated through the VgrG through several mechanisms^{117, 118}. The generation of MNGCs helps *Bp* spread the infection without leaving the intracellular milieu (Fig. 4). Many virulence factors have been described and roles assigned during intracellular pathogenesis. Our group recently identified the *Bp* intracellular ‘TRANSITome’ through the investigation of single-cell transcriptomes of *Bp*, at distinct cellular locations during infection: inside the vacuole; replicating in the host cytoplasm; and during protusion⁹⁸. This identified 1,953 genes that are differentially regulated in a stage specific manner during intracellular infection⁹⁸. This strongly suggests that many more virulence factors have yet to be described. Furthermore, this indicates that *Bp* has a sophisticated regulation system that is used to coordinate intracellular infection.

Regulation of virulence

Regulation of the *Bp* intracellular lifecycle has been partially studied but almost exclusively focuses on known virulence determinants like T3SS-3, T6SS-1, and BimA. Briefly, the transcriptional regulator BprP regulates expression of the structural components of T3SS-3 with another transcriptional regulator BsaN^{119, 120}. BsaN has a chaperone, BicA, and BsaN-BicA regulates expression of T3SS effector and accessory proteins, the two-component sensor-regulator VirAG (responsible for downstream expression of T6SS-1 and BimA), and BprC, a transcriptional regulator essential for T6SS-1 expression¹¹⁹⁻¹²¹. Global acting virulence and metabolism regulator (GvmR) was recently identified to control numerous mechanisms in virulence and metabolic functions¹²². Beyond this, the ‘TRANSITome’ data revealed that there are 33 transcriptional regulators that have no known function that are differentially expressed during intracellular infection in a stage specific manner⁹⁸.

Herein, I aim to characterize three transcriptional regulators of *Bp* virulence, BP1026B_II1198, BP1026B_II1561, and BP1026B_II2312 in chapters two, three, and four, respectively. My central hypothesis is that in order for *Bp* to sustain a productive infection it relies on tight control and coordination of specific virulence factors by various transcriptional regulators in a stage specific manner. As BP1026B_II1198, BP1026B_II1561, and BP1026B_II2312 are all differentially regulated during the intracellular infection process, the genes these transcriptional regulators control will be tied to known or unknown virulence mechanisms and comprise their regulation networks. Overall, by comprehending the regulation networks for intracellular infection, we will better understand the dynamics and pathophysiology of *Bp* association with the host environment. This can aid in vaccine development or treatment

strategies for melioidosis. Beyond the main focus of this dissertation, several promising vaccine candidates have been identified and are described in chapters five and six.



Figure 1| Observations from the first case of melioidosis^{1,2}. a) Artist illustration of the lungs of the first melioidosis patient showing ‘cheesy’ consolidations where *Bp* was isolated from ^{1,2}. Growth of *Bp* on an agar slant after 48 hours of growth (b) and one month of growth (c)^{1,2}. These illustrations are from the first publications identifying melioidosis by the pathologist Whitmore and the surgeon Krishnaswami^{1,2}.

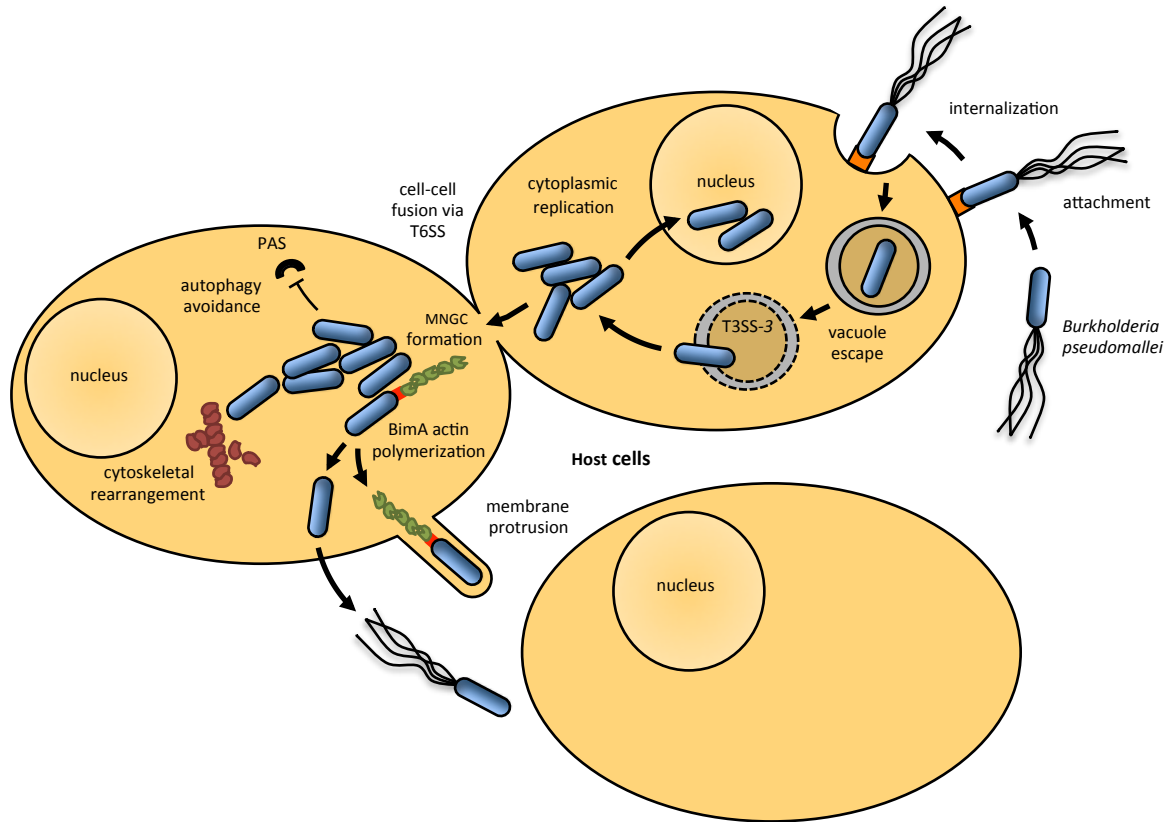


Figure 3| Model of *Bp* intracellular infection. *Bp* attaches to host cells and gets internalized via the endocytic pathway. Following cell entry, *Bp* gains entry into the cytoplasm using T3SS-3 where it can replicate freely and in some cases enter the nucleus. *Bp* can move within the cytoplasm using BimA or its lateral flagella and eventually fuse host cell membranes with T6SS-1. *Bp* avoids intracellular defenses like autophagy via various mechanisms. PAS, pre-autophagosomal structure. This is a modified version of supplemental figure 8 in appendix A (ref. 98), and was originally constructed by Ian McMillan.

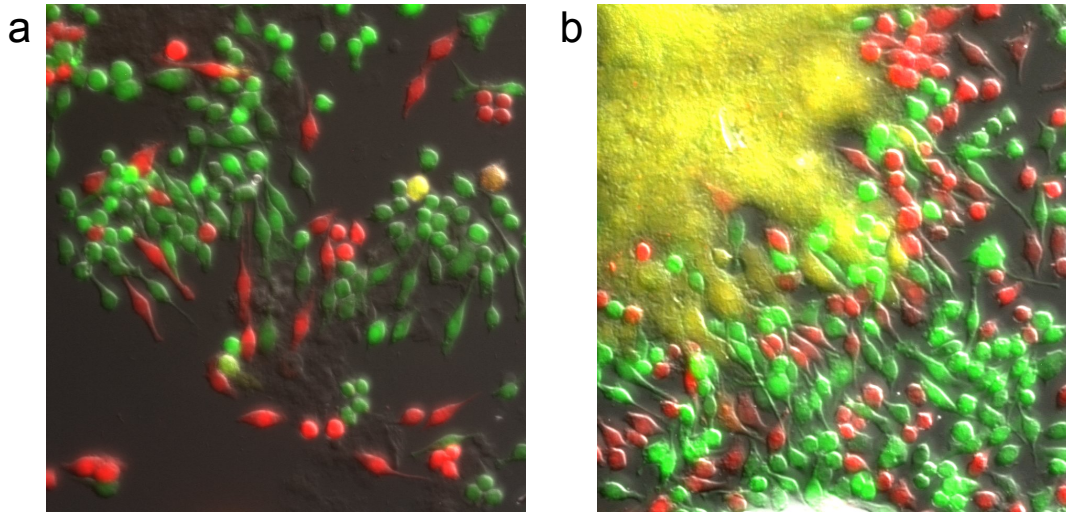


Figure 4| MNGC formation by *Bp*. a) Overlay image of uninfected RAW264.7 cells that either express GFP or RFP showing no cell membrane fusion. b) *Bp* 1026b was used to infect RAW264.7 cells generating a MNGC in the upper left corner showing the mixing of cell cytoplasm (yellow, GFP plus RFP). Cell lines were obtained from the laboratory of Jeff Miller at the University of California-Los Angeles. Infections and images carried out by Ian McMillan.

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Chapter 2:

BP1026B_II1198, a PadR-Type Regulator of *Burkholderia pseudomallei* Intracellular Pathogenesis

Abstract

Burkholderia pseudomallei (*Bp*) is the causative agent of melioidosis, a disease endemic to the tropics. Melioidosis clinically manifests in various ways ranging from acute skin lesions to pneumonia and, in rare cases, infection of the central nervous system. *Bp* can infect various cell types causing many symptoms making diagnosis difficult. The *Bp* intracellular lifecycle has been partially elucidated and is highly complex. Within the present study we have identified a transcriptional regulator, BP1026B_II1198, that is differentially expressed as *Bp* transits through host cells. A mutant of BP1026B_II1198 was attenuated during RAW264.7 cell infection and in BALB/c mouse infection. To further characterize the function of this transcriptional regulator, we endeavored to determine the regulation network controlled by BP1026B_II1198. RNA-seq analysis showed the global picture of genes controlled by BP1026B_II1198 while ChIP-seq analysis showed that BP1026B_II1198 only bound to two specific regions on chromosome II. We further characterized the genes controlled by BP1026B_II1198 and their role during pathogenesis, identifying several new virulence factors. Taken together, the data presented here sheds light on a small part of a highly complex regulation network that *Bp* uses to cause infection within the host.

Introduction

Bacteria move through various niches responding and reacting to each specific environment they encounter. For this to occur, bacteria must transduce environmental prompts through complex signaling pathways that lead to transcription of specific factors required for survival in each situation. These networks are highly complex and require the coordination of many components. The environmental signals that initiate these pathways often require transcription factors downstream that can increase or decrease RNA polymerase binding to a promoter regions leading to the activation or repression of an operon/gene¹. The transcription factor function of binding specific DNA sequences is often controlled through interactions with small ligands, other proteins, and/or by covalent modification¹⁻³. Control of transcription factors can be mediated through several mechanisms including turnover, sequestration, and synthesis that can also be coordinated by other transcription factors¹. Additionally, transcription factors can bind to several promoter regions while promoters are often controlled by several transcription factors on a local and/or global scale¹. Taken together, this highlights the highly complex landscape that bacteria use to coordinate a transcriptional response to each environment they confront. Pathogens, in particular, encounter many environments during the course of an infection allowing them to cause disease symptoms and various clinical outcomes.

Burkholderia pseudomallei (*Bp*) is a facultative intracellular pathogen that causes the disease melioidosis. *Bp* is endemic in tropical regions with increasing prevalence due to better diagnostics and rising awareness⁴⁻¹⁴, and has a predicted global mortality rate of 54 percent¹⁵. *Bp* encounters many different environments as it can cause infection in most tissues of the human body leading to the formation of localized abscesses, bacteremia, septic shock, and sometimes death^{16, 17}. *Bp* has a complex intracellular lifecycle that can be broken down into multiple initial

stages: attachment to the host cell, host cell entry and vacuole escape, cytoplasmic replication, and protrusion towards neighboring cells allowing the infection to spread¹⁸. In the vacuole, the *Burkholderia* secretion apparatus (T3SS_{Bsa}), a type III secretion system, must be expressed allowing entry into the host cell cytoplasm¹⁹. Within the cytoplasm *Bp* can use its secondary flagella or polymerize host cell actin using bacterial expressed BimA, to move freely^{19, 20}. Eventually, *Bp* will protrude towards neighboring cells and use a virulence-associated type VI secretion system (T6SS-1) to fuse host cell membranes forming multinucleated giant cells (MNGCs)²¹⁻²⁴. Although we understand the general flow of the *Bp* intracellular lifecycle, there is much more we do not know about how this pathogen transits through a host and causes the many forms of disease we cumulatively call melioidosis.

To cause such a wide array of clinical manifestations and be able to transit through the intracellular environment with such precision, *Bp* requires many virulence factors, some of which are described above, that are encoded on its 7.2Mbp genome. As demonstrated recently, *Bp* goes through drastic transcriptional changes, with 1,953 genes showing unique patterns of expression during the intracellular infection process¹⁸. This finding suggests that *Bp* has a highly complex regulatory network that is required to coordinate the differential expression of these genes during the progression of infection, from the initial stage of attachment to the eventual protrusion towards neighboring cells. The regulation of *Bp* virulence mechanisms during intracellular infection has been studied to a small extent and mainly focuses on the control of T3SS_{Bsa}, T6SS-1, and BimA. The transcriptional regulator BprP regulates expression of the structural components of the T3SS_{Bsa} and another transcriptional regulator BsaN^{25, 26}. BsaN with its chaperone, BicA, regulate expression of type III effectors and accessory proteins, the two-component sensor-regulator VirAG that is responsible for downstream expression of T6SS-1,

BimA, and BprC, a transcriptional regulator essential for T6SS-1 expression²⁵⁻²⁷. Beyond the specific control of characterized virulence pathways, the LysR type transcriptional regulator, globally acting virulence and metabolism regulator (GvmR), was identified to control a broad network of genes involved in virulence and metabolism, highlighting the tie between a expression of virulence factors and nutrient limitation within the host²⁸. Here we would like to add to understanding of *Bp* virulence regulation by describing a new transcriptional regulator that is differentially expressed throughout the intracellular lifecycle and required for complete pathogenesis.

Results

BP1026B_II1198 is differentially regulated as *Bp* transits through the host cell

To understand how intracellular pathogenesis of *Bp* is controlled, we first have to identify transcriptional regulators that control virulence mechanisms during intracellular infection. We identified BP1026B_II1198, a PadR-like transcriptional regulator that is differentially regulated during the *Bp* intracellular ‘transitome’¹⁸. BP1026B_II1198 is expressed while *Bp* is initially internalized within endocytic vesicles and later during infection as *Bp* spreads toward neighboring cells (Fig. 1a). In contrast, BP1026B_II1198 is significantly down-regulated while *Bp* replicates within the cytoplasm (Fig. 1a). Taken together, this suggests that BP1026B_II1198 plays a role during the *Bp* intracellular lifecycle.

A BP1026B_II1198 mutant is defective in plaque formation and intracellular replication

To further investigate the role of BP1026B_II1198, an in frame deletion mutant was created using modified knockout-recombineering²⁹. This mutant was used to infect RAW264.7 cells to monitor MNGC formation and intracellular replication. A mutant of BP1026B_II1198 showed a significant decrease in its ability to form MNGCs, marked by a 41% decrease in average MNGC diameter (Fig. 1b). Complementation of BP1026B_II1198 recovered this mutation beyond wildtype levels (Fig. 1b). RAW264.7 cells infected with the BP1026B_II1198 mutant also showed a significant decrease in intracellular replication at eight and 24 hours post infection further suggesting that this transcriptional regulator is important for intracellular pathogenesis (Fig. 1c). Complementation of the BP1026B_II1198 mutation recovered this defect allowing wildtype levels of intracellular replication (Fig. 1c). The BP1026B_II1198 mutant showed a similar growth pattern to wildtype *Bp* *in vitro*, indicating that the reductions in MNGC

formation and intracellular replication are due to defects in pathogenesis rather than *in vitro* fitness (Fig. 1d).

BP1026B_II1198 is required for complete pathogenesis *in vivo*

Beyond cell culture infection, we wanted to test the importance of BP1026B_II1198 during an *in vivo* infection. BALB/c mice were infected with a lethal dose (4,500CFU/mouse) of wildtype *Bp* 1026b and an equivalent dose of the BP1026B_II1198 mutant. Within four days of the initiation of infection, all mice infected with wildtype *Bp* 1026b showed significant signs of acute murine melioidosis resulting in 100% lethality (Fig. 2a). In contrast, mice infected with the BP1026B_II1198 mutant survived for the duration of the study, 62 days, indicating that this transcriptional regulator is not only important for *in vitro* cell culture infection, but is critical for *in vivo* pathogenesis of *Bp* (Fig. 2a). Even though mice challenged with the BP1026B_II1198 mutant showed no clinical symptoms 62 days post infection, there was persistent infection in the lungs and spleens of the majority of the mice and one mouse showing high levels of infection within the liver (Fig. 2b). The results taken together thus far strongly indicates that BP1026B_II1198 is a transcriptional regulator controlling *Bp* pathogenesis.

BP1026B_II1198 regulates hypothetical proteins, secondary metabolite biosynthesis, extracellular matrix, efflux, and type IV secretion

To better understand how BP1026B_II1198 controls *Bp* pathogenesis, we expressed BP1026B_II1198 *in trans*, and compared the mRNA profile to a corresponding strain with an empty vector control via RNA-seq analysis (Fig. 3b). Samples were analyzed using Rockhopper³⁰ and genes with a q-value < 0.01 and a log₂ fold-change (FC) ≥ 1 or ≤ -1 were

selected for further analysis (Table S1). There were 88 genes that were up-regulated ($\log_2FC \geq 1$) in the presence of BP1026B_II1198 while 94 genes were down-regulated ($\log_2FC \leq -1$) (Fig. 3). Genes with a $\log_2FC \geq 1$ or ≤ -1 were analyzed by COG functional predictions revealing an overabundance (57.1%) of genes annotated as hypothetical proteins, hypothetical RNA transcripts, or uncharacterized proteins that are controlled by BP1026B_II1198 (Fig. 3a). Of these proteins of unknown function, 54 genes are up-regulated and 50 genes down-regulated by BP1026B_II1198 (Fig. 3a). When we analyze the entire RNA-seq data set (Fig. 3b) using WoPPER³¹ some additional pathways that are responsible for secondary metabolite biosynthesis, components of the extracellular polymeric matrix, multidrug efflux, and type IV secretion appear to be controlled by BP1026B_II1198 (Fig. S1, Fig. S2).

Two nonribosomal peptide synthetase regions that produce the siderophores malleobactin³² and pyochelin³³ are up-regulated by BP1026B_II1198 in cluster 12 (Fig. S1) and cluster 7 (Fig. S2), respectively, suggesting the involvement of this regulator in iron acquisition during infection. BP1026B_II1198 also up-regulates the polyketide synthase cluster producing another siderophore, malleilactone (Cluster 2, Fig. S2). Malleilactone is involved in the pathogenesis of *Caenorhabditis elegans* and *Dictyostelium discoideum*³⁴. Beyond the control of secondary metabolite pathways, BP1026B_II1198 also down-regulates components of the extracellular polymeric matrix tied to contact dependent growth inhibition, BcpA (Cluster 18, Fig. S2)³⁵⁻³⁷. The genes encoding the RND efflux pump, BpeEF-OprC, responsible for multidrug efflux and clinical resistance to antimicrobials^{38, 39}, are up-regulated in the presence of BP1026B_II1198 (Cluster 3, Fig. S2). Although, we see low levels of up-regulation of *bpeEF-oprC*, we suspect that the up-regulation is indirect and could involve other known regulatory factors of this pathway including modulation of BpeT and BpeS expression⁴⁰. BP1026B_II1198

also up-regulates a type VI secretion system (T6SS-1) that is required for complete pathogenesis and allows intercellular spread and MNGC formation (Cluster 15, Fig. S2)^{19, 22, 41}. The regulation of known pathways and the numerous hypothetical proteins indicates that the BP1026B_II1198 regulation network is tied to potential and confirmed pathogenic processes, emphasizing the role of BP1026B_II1198 during pathogenesis.

Specific genes controlled by BP1026B_II1198 have potential role during pathogenesis

To further our understanding of this regulation network, we investigated individual genes that are highly regulated by BP1026B_II1198 with a \log_2 FC > 2 or < -2 (Fig. 4a). BP1026B_I0955 and BP1026B_I0956 are significantly up-regulated by BP1026B_II1198 with \log_2 FCs of 2.16 and 2.03, respectively (Fig. 4a). These genes encode putative SufC and SufB subunits of the SufBCD complex responsible for the assembly of iron-sulfur (Fe-S) clusters in proteins⁴². Genes encoding NifU and SufD are additional components of this Fe-S cluster assembly pathway that are also up-regulated to \log_2 FCs of 1.06 and 1.58 (Table S1). Another redox related protein, BP1026B_II1579, is up-regulated to a \log_2 FC of 2 and encodes a SCO1/SenC family protein predicted to be involved in the assembly of cytochrome c oxidase (Fig. 4a).

Interestingly, BP1026B_II1198 also up-regulates a putative nitrate transporter, BP1026B_I1020 (*narK-1*), with a \log_2 FC of 2.09, and a potential *Burkholderia* specific nitric oxide forming nitrite reductase, BP1026B_II1580 (*nirK*), with a \log_2 FC of 2.99 (Fig. 4a)⁴³. Other components involved in nitrogen metabolism, including *narG* and *narK-2*, are also up-regulated (\log_2 FC 1.93 and 1.42) by BP1026B_II1198 (Table S1). The regulation of these pathways by BP1026B_II1198 suggests that they play a role in *Bp* intracellular survival and virulence similar

to how nitrate transport/reduction and nitrite reduction have been tied to virulence in *Pseudomonas aeruginosa*^{44, 45}. In addition to the control of metabolic pathways, BP1026B_II1198 also up-regulates BP1026B_II1736 a type III secretion protein HrpB4 (Fig. 4a).

Many genes that showed large alterations in expression by BP1026B_II1198 are annotated as hypothetical proteins or have no known function (Fig. 3a). BP1026B_II1775 is predicted to be a lipoprotein that shows high amino acid identity to CpaD, a putative pilus assembly protein, in environmental bacteria and is up-regulated by BP1026B_II1198 (Fig. 4a). A GntR family transcriptional regulator, BP1026B_II1506 is also up-regulated and could cause downstream changes in gene expression leading to variations in pathogenesis and/or intracellular survival (Fig. 4a). BP1026B_I0528, BP1026B_I0950, BP1026B_II1464, BP1026B_II1581, and BP1026B_II1769 are hypothetical proteins that are up-regulated by BP1026B_II1198 while BP1026B_II0722 is a hypothetical protein that is down-regulated (Fig. 4a).

Mutant analysis identifies potential virulence-associated genes controlled by BP1026B_II1198

To further test the role these genes play in pathogenesis, we targeted mutants present in the sequence defined transposon mutant library of *Bp* 1026b for analysis through intracellular replication in RAW264.7 cells⁴⁶. The library lacked transposon insertions in the hypothetical proteins BP1026B_I0528, BP1026B_I0950, and BP1026B_II1464 suggesting that these genes could be essential for *Bp* growth *in vitro*⁴⁶. Transposon mutants available in the transposon library were isolated on media containing kanamycin and each insertion site sequenced confirmed to ensure that the mutants were correct (data not shown). The transposon insertion in

BP1026B_II1769 was not validated and confirmed to be present in another gene, BP1026B_II2115, a putative diguanylate cyclase. The lack of a second transposon insertion in BP1026B_II1769 suggests that this hypothetical protein is an essential gene for *Bp*.

Monolayers of RAW264.7 cells were infected with each transposon mutant present in the library and the level of intracellular replication determined at 24 hours post infection (hpi). Transposon mutants of BP1026B_II0722 and BP1026B_II1580 replicate to wildtype levels (99-100%) after 24 hours of infection indicating that these genes have no singular pathogenic function (Fig. 4b-c). In contrast, transposon mutants in BP1026B_II0956, BP1026B_II1020, BP1026B_II1581, and BP1026B_II1736 replicate between 74.9% and 82.6% of wildtype implying these genes have a small role in pathogenesis (Fig. 4b-c). BP1026B_II1736 is part of T3SS-2 that has been previously tied to virulence in *S. lycopersicum* but the T3SS-2 mutant showed wildtype levels of cytotoxicity in THP-1 cells⁴⁷. This indicates that BP1026B_II1736 and the T3SS-2 cluster could be involved in intracellular survival but does not reduce the amount cytotoxicity towards the host. Mutants of BP1026B_II0956 and BP1026B_II1020, components of the SUF pathway and nitrate transport/reduction, are also tied to a decrease in pathogenesis indicating that these genes and pathways are important for *Bp* intracellular survival (Fig. 4b-c). Transposon mutants of BP1026B_II0955, BP1026B_II1775, and BP1026B_II1506 showed the greatest decrease in intracellular survival, replicating at 61.7%, 59.3%, and 63.2% of wildtype, respectively (Fig. 4b-c). Finally, the SCO1/SenC family protein, BP1026B_II1579, replicates at 120.65% of wildtype indicating that protein is involved in reducing the intracellular survival of wildtype *Bp* within host cells (Fig. 4b-c). Transposon mutants showing a major decrease in intracellular replication were able to replicate at wildtype levels when grown *in vitro* indicating that the defects identified during RAW264.7 cell infection are not due to decreased fitness (Fig.

S3a). This data taken together suggests that BP1026B_II1198 indirectly controls several factors that contribute to the pathogenesis to some extent during *Bp* intracellular infection (Fig. 4d).

BP1026B_II1198 directly binds to two intergenic regions on chromosome II

We have shown that BP1026B_II1198 indirectly regulates numerous pathways/genes previously identified to be involved in virulence and many potential pathways/genes that have unknown functions during pathogenesis (Fig. 4, Fig. S1, Fig. S2). To determine the direct regulation network of BP1026B_II1198, we used a ChIP-seq strategy as previously described^{2,3} but modified for *Burkholderia* species. Briefly, a BP1026B_II1198-3xTY1 translational fusion was expressed in *Bp*, cellular components were cross-linked with paraformaldehyde, DNA sheared using an M220 focused-ultrasonicator (Covaris), DNA-BP1026B_II1198 complexes enriched via immunoprecipitation with a TY1 specific monoclonal antibody (Diagenode), and DNA purified for Illumina sequencing to identify regions of direct BP1026B_II1198 binding. BP1026B_II1198-enriched DNA was aligned to the *Bp* 1026b genome using Bowtie2⁴⁸ and peaks were called with MACS2⁴⁹ by comparing to an empty vector negative control. All peaks identified were plotted by genome position on each *Bp* chromosome revealing two major peaks located on chromosome II (Fig. 5a-b). When the $-\log_{10}$ of the q-value was compared to the fold-enrichment of each peak, we see the same two peaks further isolated from the background (Fig. 5c). These two peaks suggest that BP1026B_II1198 binds to two intergenic regions between divergently transcribed genes (Fig. 6a). Peak 1 is a 227bp sequence in the intergenic region between levanase, levansucrase precursor, BP1026B_II0599-0600, and a LacI family regulator protein, BP1026B_II0601 (Fig. 6a). Peak 2 is a 508bp region between BP1026B_II1006, a DNA-binding protein, and BP1026B_II1007, an oxidoreductase (Fig. 6a). By comparing the

sequences of each of these peaks using MEME⁵⁰, a 12bp conserved region was identified (Fig. 5d). The sequence, AAA AGT AXX TTA, has seven and three conserved base pairs separated by a two base pair spacer and is oriented in the same direction on both peaks suggesting that transcriptional control from each region will be in the same direction. Accentuating this point, the RNA-seq data shows that BP1026B_II1198 regulates genes in the same orientation by positively regulating BP1026B_II0600 and negatively regulating BP1026B_II1006 while showing no transcriptional control of genes in the opposite orientation, BP1026B_II0601 and BP1026B_II1007 (Fig. 6b-c).

Genes directly controlled by BP1026B_II1198 are important during intracellular infection

To investigate the role BP1026B_II0600 and BP1026B_II1006 play during intracellular pathogenesis, a RAW264.7 cell intracellular replication assay was carried out. At 24 hours post infection a transposon mutant of BP1026B_II0600, a levansucrase precursor that is up-regulated by BP1026B_II1198, replicated intracellularly at 51.62% of wildtype *Bp* 1026b (Fig. 6d-e). This is a drastic decrease indicating that BP1026B_II0600 has a role during intracellular pathogenesis. On the other hand a transposon mutant of BP1026B_II1006, a DNA-binding protein that is down-regulated by BP1026B_II1198, showed 82.89% wildtype intracellular replication at 24 hours post infection (Fig. 6d-e). Although a small decrease in the intracellular replication compared to wildtype, this decrease could be significant considering that BP1026B_II1006 is a DNA-binding protein and could contribute to downstream effects on other pathways/virulence mechanisms. Taken together, BP1026B_II1198 has direct affect on the positive transcriptional control of BP1026B_II0600 and the negative transcriptional control of BP1026B_II1006 leading to variations in the pathogenesis during RAW264.7 murine macrophage infection (Fig. 6f).

Discussion

Bacterial transcriptional networks are highly complex, dependent on many variables to properly function. When bacteria are exposed to a unique environment they sense and respond through signaling pathways that lead to the expression of proteins/factors that aid in survival. This is especially true during infection, as pathogenic bacteria encounter various immune defenses within the host. *Pseudomonas aeruginosa* (*Pa*) is a model organism for the study of biofilms and virulence factors, all of which are controlled by a complex network of transcription factors and signaling systems⁵¹. Only recently are the subtleties of the *Pa* transcription factor regulation network coming to light, highlighted by significant functional crosstalk between transcription factors and regulation systems^{52, 53}. *Mycobacterium tuberculosis* also has a well-documented, highly complex, regulatory network that it uses to navigate hypoxic environments⁵⁴. To fully understand the pathogenic processes that allow for *Bp* host colonization and infection we must understand how these pathways are regulated. Some studies have started to shed light on the intricacies of *Bp* virulence regulation^{25, 28, 55, 56}. In the present study, we add to the knowledge of the *Bp* regulatory network during intracellular infection through the identification and characterization of BP1026B_II1198.

BP1026B_II1198 is differentially expressed during the *Bp* intracellular lifecycle and is required for *in vitro* and *in vivo* pathogenesis, highlighted by the 100% attenuation of the BP1026B_II1198 mutant in the BALB/c mouse model. These two observations show that *Bp* precisely controls pathogenic function within the host. To further understand this contribution to pathogenesis we identified the genes controlled by BP1026B_II1198 using RNA-seq. We observed that 79.8% of genes differentially regulated in the presence of BP1026B_II1198 have no known function. This is a striking increase from the 26.7% of genes annotated as hypothetical

within the *Bp* 1026b genome, suggesting that many pathogenic and survival pathways are yet to be discovered. The presence of BP1026B_II1198 during the later stages of infection coincides with the expression of T6SS-1 aligning with current understanding of the *Bp* lifecycle. In addition, expression of BP1026B_II1198 leads to the up-regulation of several secondary metabolite gene clusters malleobactin³², pyochelin³³, and malleilactone³⁴, that have been previously identified to be involved in iron acquisition and pathogenesis. The regulation of these known virulence mechanisms likely contribute to the attenuation of the BP1026B_II1198 mutant, although it we believe that there are other factors that are also involved.

We probed many genes that were regulated by BP1026B_II1198 to identify contributors to pathogenesis, including genes that may have a less direct pathogenic function. Although, Fe-S clusters were first identified in 1962 to be involved during electron transport⁵⁷, their function is diverse and has been implicated in the modulation of gene expression⁵⁸. Fe-S clusters can respond to increased oxidative stress, iron levels within the host, or other environmental signals during infection leading to an adaptive response⁵⁹. The up-regulation of genes involved in Fe-S assembly (BP1026B_I0955, BP1026B_I0956, NifU, SufD) by BP1026B_II1198, could be a response to the intracellular environment, where iron-limitation, reactive-oxygen-species, and other environmental cues requires the sensitive nature of an Fe-S regulatory complexes. This result correlates with previous reports showing up-regulation of Fe-S assembly genes in *Burkholderia mallei*, a clonal derivative of *Bp*, when exposed to sub-inhibitory levels of nitric oxide⁶⁰. Genes involved in nitrogen metabolism were also up-regulated, showing that BP1026B_II1198 is partially responsible for a shift in general metabolism during infection. In addition to this, the BP1026B_I1020 mutant showed a reduction during intracellular replication in RAW264.7 cells.

Other mutants of genes regulated by BP1026B_II1198 that showed reductions in RAW264.7 pathogenesis have less indication as to their function. BP1026B_II1506 is a GntR family transcriptional regulator that could have many downstream gene expression changes that contribute to the reduction in virulence while BP1026B_II1581 is a hypothetical protein that is worth further investigation. BP1026B_II1775 is a Sec-secreted lipoprotein with cleavage site located between amino acids 28 and 29 as identified by SignalP5.0 analysis⁶¹. The function of this interesting protein should be investigated further and could potentially be manipulated as a novel therapeutic or vaccine target. BP1026B_II1736 sits within the second type III secretion system (T3SS-2) in *Bp* and encodes SctK, a cytoplasmic structural component of the type III injectasome⁶². This protein along with SctQ and SctL are referred to as the ‘sorting platform’ and play a critical role on the order in which effector proteins are secreted⁶³. Beyond the implications the specific potential function of BP1026B_II1736, it has been shown that T3SS-2 is involved in the pathogenesis of *Solanum lycopersicum* (tomato) but not mammalian cells⁴⁷.

Large numbers of genes/pathways are controlled indirectly through the expression of BP1026B_II1198 as described above. To find the direct DNA binding regions of BP1026B_II1198 we used a ChIP-seq strategy. Through this we identified two major regions of DNA binding in intergenic regions with divergently transcribed genes. BP1026B_II1198 showed up-regulation of BP1026B_II0600 and down regulation of BP1026B_II1006. Subsequent mutant analysis of these genes showed a 52% and 83% reduction in wildtype intracellular replication. BP1026B_II0600 encodes a levansucrase precursor, which to our knowledge, has yet to be described as a virulence factor during infection of mammalian cells. However, in plant pathogenesis like *Pseudomonas syringae*, levansucrase is critical for the formation of levans that contribute to exopolysaccharide production^{64, 65}. Because *Bp* is an incidental host of mammals,

and freely lives within the environment, the expression of levansucrase could indicate that this gene is used for adaptation to multiple conditions. BP1026B_II1006 is annotated as a DNA binding protein but further analysis using Phyre2⁶⁶ predicts structural similarities to an Fe-S complex containing transcriptional regulator, RrsR⁶⁷. We predict that the down-regulation of BP1026B_II1006 by BP1026B_II1198 plays a major role in the indirect gene expression changes that occur in our data set. Although outside of the scope of the present work, this data warrants further analysis of the regulation network of BP1026B_II1006.

Here we show a snapshot of what is going on during intracellular infection through the lens of the transcriptional regulator BP1026B_II1198. We believe that in the intracellular environment, many transcription factors work in unison to control how *Bp* responds to specific environments, allowing for infection to occur. The future study of many of these transcriptional regulators (i.e. BP1026B_II1006 and BP1026B_II1506) will increase the resolution of what we know about the *Bp* lifecycle and *Bp* gene expression within the host. Although the data represent the expression profile of one transcription factor, it is one step towards a better understanding of the intricacies of *Bp* intracellular pathogenesis.

Methods and Materials

Bacterial strains, media and culture conditions *Escherichia coli* strain EPMa10B (BioRad), E1869, and E1354 were used for cloning or plasmid mobilization into *Bp* as described previously^{68, 69}. *Bp* 1026b and its select agent regulation excluded analogue, *Bp*82, were used where appropriate. Luria-Bertani (LB) medium (Difco) or 1x M9 minimal medium supplemented with 20 mM glucose (MG) were used to culture all strains. MG media was supplemented with 0.3% glyphosate when appropriate. Experiments involving the manipulation of *Bp* were conducted in a CDC-approved and registered facility at the University of Hawai'i at Mānoa or Colorado State University. All work with the select agent *Bp* was approved by internal review and adhere to recommendations set forth in the BMBL, 5th edition⁷⁰ for BSL3 organisms.

Molecular methods and reagents Molecular methods and reagents were used as described previously^{29, 69, 71, 72}. An in-frame deletion mutant of BP1026B_II1198 was generated using lambda-red recombineering with minor modification⁷³. Lambda red genes were PCR amplified from pKaKa1 and co-incubated with the knockout fragment of BP1026B_II1198 and selection carried out on glyphosate. For expression of BP1026B_II1198 (complementation, RNA-seq, ChIP-seq), BP1026B_II1198 was PCR amplified from *Bp* 1026b with oligos 2778 (5'-GGT TGC CTC GCA TAT GTC CCT GCC CCA C) and 2779 (5'-TCG AAG CTT CAA GCC GAC AAC GAT CTT) digested with *Nde*I and *Hind*III and ligated into *Nde*I/*Hind*III-cut pAM3GIQ-3xTY1. Confirmation of the resulting vector, pAM3GIQ-3xTY1-BP1026B_1198, was carried out by *Eco*RV/*Phs*AI and *Nde*I/*Hind*III digests and the expression of BP1026B_II1198 confirmed via western blot analysis.

Growth analysis All strains were first grown overnight in LB broth at 37°C, harvested the following day, diluted to an OD₆₀₀ of 0.1 in 200µl of fresh LB, and placed into 96 well plate. Growth curves were carried out at 37°C shaking and data was recorded with the BioTek ELx808IU plate reader, measurements taken at an OD₆₃₀ every 30 minutes.

Cell infection assays Intracellular replication and MNGC formation assays were carried out as previously described⁷⁴ with minor modifications. Briefly, RAW264.7 murine macrophages were seeded for infection at 80-90% confluence on Corning CellBIND culture plates, allowed to attach overnight, washed twice with 1XPBS, and infected the following day. For intracellular replication assays, *Bp* 1026b, the BP1026B_II1198 mutant, or the BP1026B_II1198 complement (mutant with pAM3GIQ-3xTY1-BP1026B_II1198) were allowed to infect monolayers at an MOI of 1:1, washed with 1XPBS, and then DMEM supplemented with 10% FBS, 0.1mM IPTG to drive expression of the complement, 700 µg/mL amikacin and 700 µg/mL kanamycin were added to kill any extracellular bacteria. At 2, 8, and 24 hours post-infection, infected monolayers were lysed with 0.2% Triton X-100. Serial dilutions of lysates were plated on LB and colony-forming units (CFU) per well were determined. MNGC formation assays were carried out as intracellular replication assays, with the exception that 1.2% low-melt agarose was added to DMEM after infection allowing the formation of MNGCs. At 24 hours post-infection, monolayers were fixed with 4% paraformaldehyde, agarose plugs removed, stained with 0.05% crystal violet, and MNGC diameters measured with the Zeiss Axio Observer D1 and the AxioVision 64 bit 4.9.1 software. Cell infection assays with mutants from the *Bp* 1026b::T24 transposon mutant library were carried out as described above although kanamycin was removed

and 1,500µg/mL amikacin added to remove extracellular bacteria post infection. Monolayers were lysed at 24 hours post-infection as described above. All transposon mutants tested were confirmed to be in the gene of interest by sequencing.

Animal studies BALB/c mice between 4 and 6 weeks of age were purchased from Charles River Laboratory. All infections with *Bp* strains (wildtype and the BP1026B_II1198 mutant) were administered via the intranasal (i.n.) inoculation route. Mice were anesthetized with 100 mg of ketamine/kg of body weight plus 10 mg/kg xylazine. The challenge dose (4,500 CFU) of each *Bp* strain was suspended in 20 µl of 1XPBS and used to inoculate each mouse via the i.n. route. Each strain was used to inoculate 5 mice. Animals were monitored for disease symptoms daily and euthanized at predetermined humane end points. Lungs, liver, and spleen of surviving mice were harvested, homogenized, serially diluted, and plated on LB to determine bacterial burdens. Survival characteristics were plotted using Prism software (GraphPad, La Jolla, CA) and statistical analysis was done by Kaplan-Meier curves.

RNA-seq and ChIP-seq analysis RNA-seq and ChIP-seq analysis were carried out under the same conditions. Briefly, *Bp82* expressing BP1026B_II1198 from pAM3GIQ-3xTY1-BP1026B_II1198 was grown overnight and sub-cultured to mid-log phase in LB+adenine+0.1mM IPTG in triplicate. An empty vector (pAM3GIQ-3xTY1) was used as a control. Total RNA was harvested using RNeasy Mini Kit (Qiagen) with on-column (Qiagen) and off-column (Epicentre) DNase digestion steps. RNA samples were sent to Tufts University Genomics Core (TUCF Genomics) for library preparation and Illumina 50bp single-end reads were sequenced on the Illumina HiSeq 2500. RNA-seq data was analyzed with Rockhopper³⁰.

ChIP-seq was carried out as previously described with minor modifications^{2, 3}. Briefly, ChIP-seq samples were grown identically as RNA-seq samples, harvested, and fixed with 4% paraformaldehyde, followed by shearing of DNA-protein complexes with the Covaris M220 ultrafocused sonicator. Cell debris was removed and DNA-protein complexes were immunoprecipitated with anti-TY1-tag monoclonal antibody (Diagenode C15200054) and secondary antibodies conjugated to magnetic beads (Diagenode C03010022). DNA-protein complexes were washed, decrosslinked, treated with RNaseA and proteinase K, and purified with QIAquick PCR purification kit. Immunoprecipitated DNA was sent to TUCF Genomics where DNA libraries were prepped and 50bp single-end reads were sequenced with the Illumina HiSeq 2500. ChIP-seq data was aligned to the *Bp* 1026b genome with Bowtie2⁴⁸, peaks called with MACS2⁴⁹, and consensus binding regions determined with MEME⁵⁰.

Ethics statement All animal studies described in this manuscript were approved by the Institutional Animal Care and Use Committee at the University of Hawaii at Manoa (Protocol No. 10-1073-8), and conducted in compliance with the NIH (National Institutes of Health) Guide for the Care and Use of Laboratory Animals.

Data availability The datasets and materials generated during the current study are available from the corresponding author upon reasonable request. Any transfer of select agent materials needs additional approval from Brad Borlee and the Responsible Official at Colorado State University. Any select agent transfer must be to a select agent registered facility, approved by the CDC, and comply with all select agent regulations (selectagents.gov).

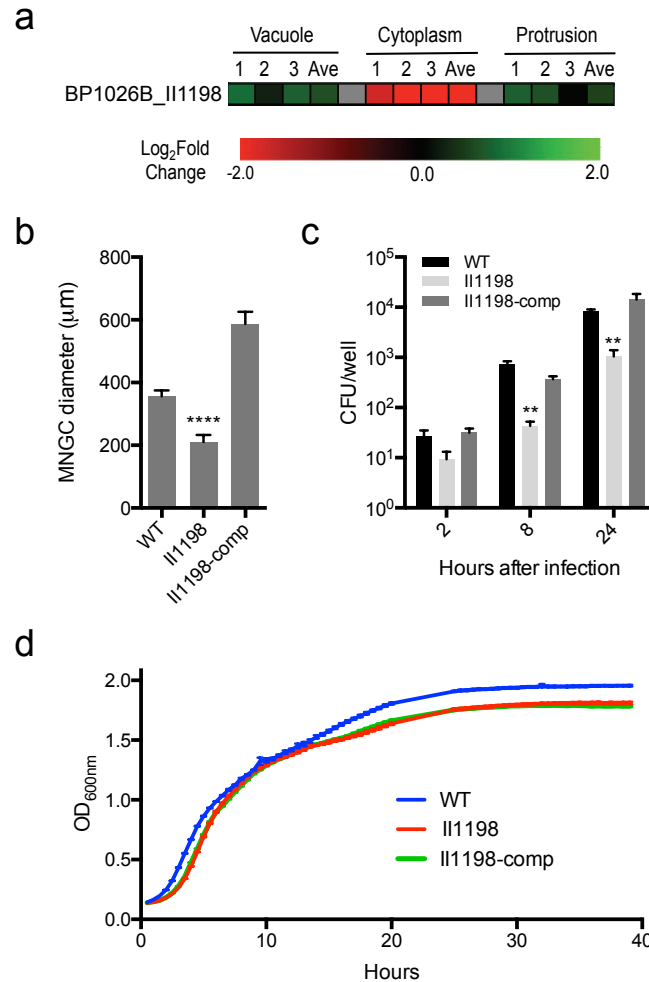


Figure 1| BP1026B_II1198 is differentially regulated during cell infection and critical for intracellular survival. a) Single cell ‘transitome’ analysis¹⁸ shows that BP1026B_II1198 is up-regulated in the vacuole and protrusion while down-regulated in the cytoplasm during infection of RAW264.7 cells. Boxes represent three biological replicates and an average (Ave)¹⁸. b) A mutant in BP1026B_II1198 shows a reduced ability to form wildtype MNGCs. When the mutant is complemented it recovers beyond wildtype levels of MNGC size. c) The BP1026B_II1198 mutant shows a significant reduction in intracellular replication at eight and 24 hours after infection compared to wildtype *Bp* 1026b. Complementation of the BP1026B_II1198 mutant recovers the intracellular replication to wildtype levels. d) The BP1026B_II1198 mutant and

complement grow to similar levels of wildtype *Bp* 1026b *in vitro*. Data in bar graphs and growth curve represent means \pm s.e.m and analyzed via unpaired t-test. P values presented are as follows: ** $p < 0.01$, **** $p < 0.0001$.

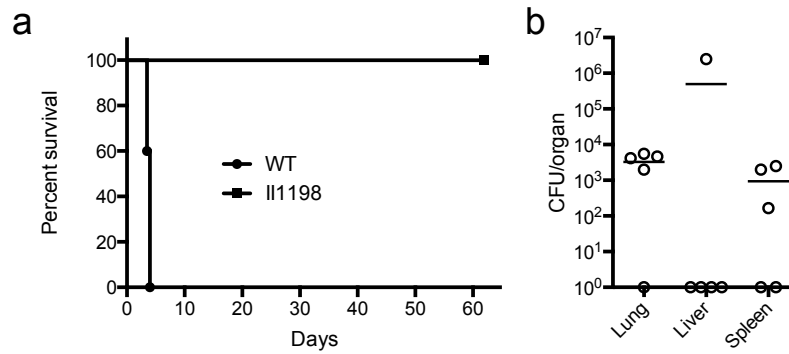


Figure 2| BP1026B_II1198 is attenuated in BALB/c mouse model. a) Mice infected with wildtype *Bp* 1026b (n=5) did not survive beyond day four post challenge while mice infected with the BP1026B_II1198 mutant (n=5) were able to survive for the duration of the study (62 days). Mice were challenged with a lethal dose (4,500CFU/mouse) via the intranasal route. b) Lungs, livers and spleens of the surviving mice were harvested, homogenized, and plated revealing persistent infection within the lungs of four mice, liver of one mouse, and spleen of three mice.

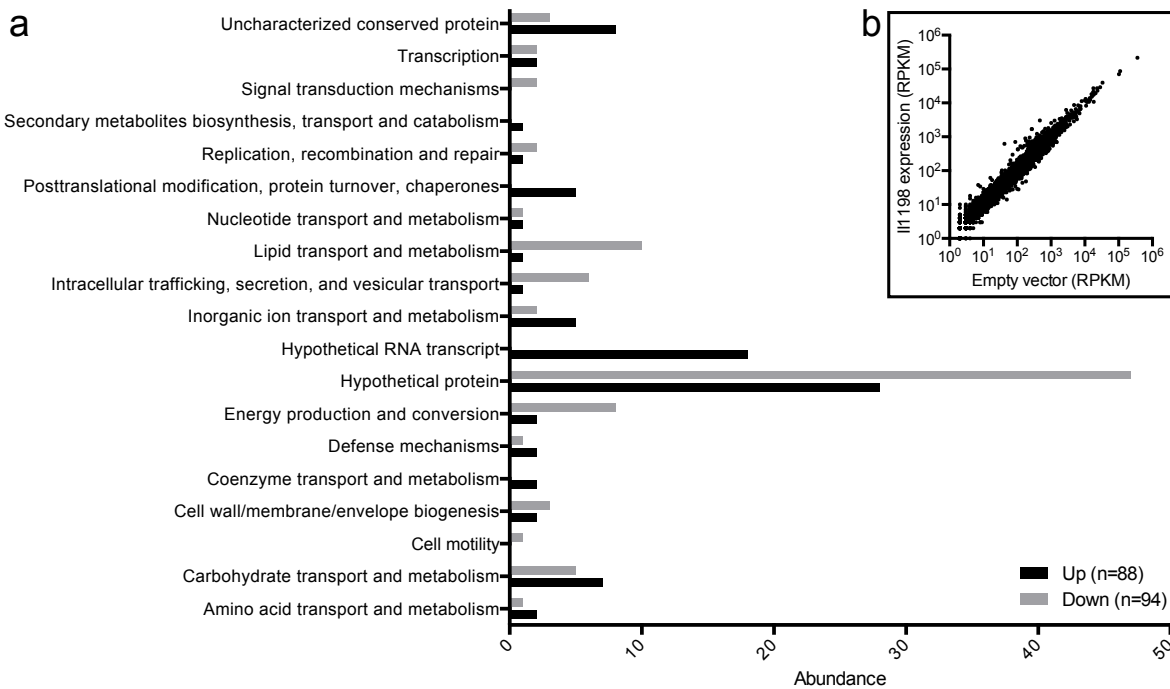


Figure 3| Hypothetical proteins are disproportionately controlled by BP1026B_II1198. a) Genes with a q-value < 0.01 and a log₂FC ≤ -1 or ≥ 1 were analyzed by COG functional predictions. There are 198 genes that are up-regulated and 94 genes that are down-regulated by BP1026B_II1198. Hypothetical proteins, hypothetical RNA transcripts and uncharacterized proteins represent 79.8% of the genes controlled by BP1026B_II1198. Of these unknown proteins 68% are up-regulated and 32% are down-regulated. b) Scatter plot showing distribution of all genes present in RNA-seq analysis.

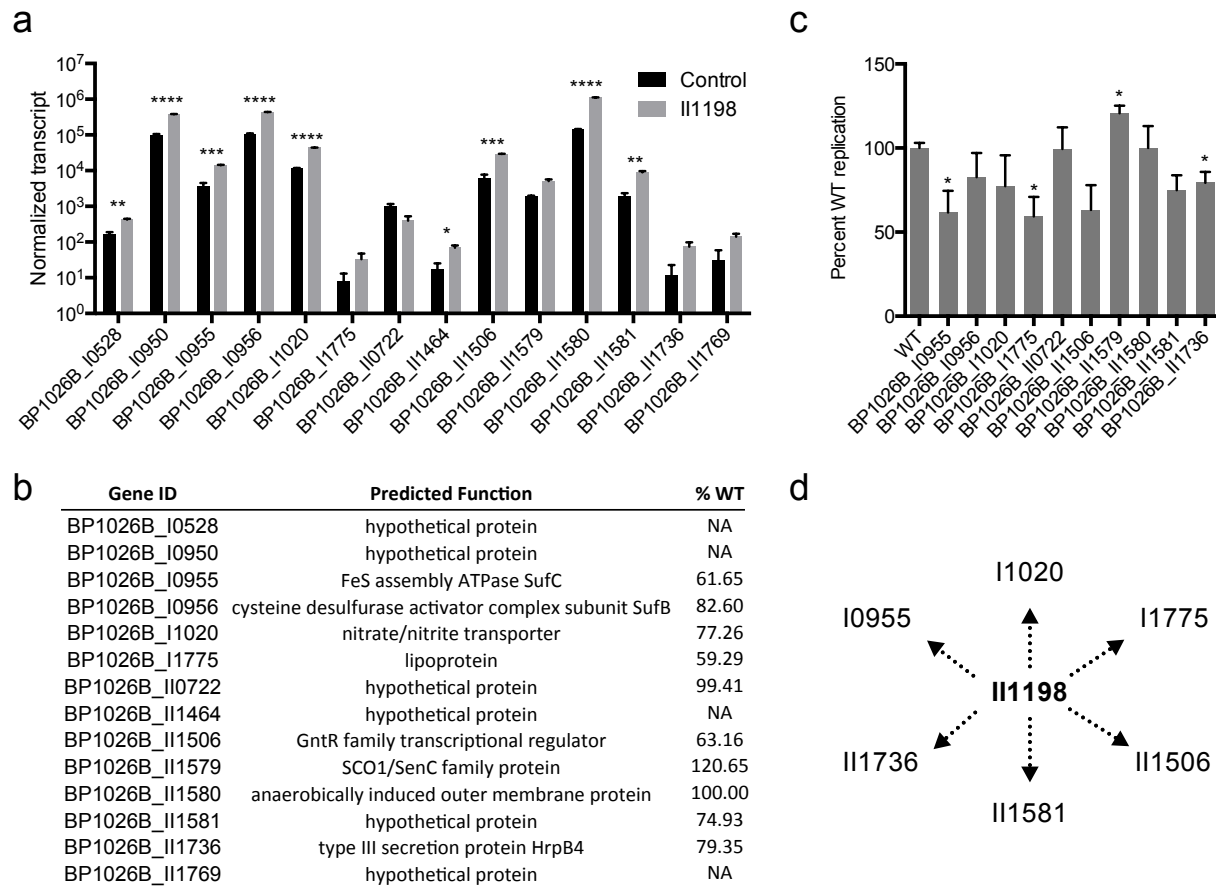


Figure 4| Genes highly regulated by BP1026B_II1198 show involvement during *Bp* intracellular survival. a) Normalized transcripts of genes showing a \log_2 FC ≤ -2 or ≥ 2 in the presence of BP1026B_II1198 compared to an empty vector control. b) Predicted functions of genes controlled by BP1026B_II1198. c) Transposon mutants present in the sequence defined transposon mutant library of *Bp* 1026b were analyzed for the ability to replicate in RAW264.7 murine macrophages for 24 hours. Intracellular replication represented as a percent of wildtype 24 hours post infection and the average of triplicates represented in (b). d) Schematic diagram showing genes involved in *Bp* intracellular survival (replicating <80% wildtype) by indirect control of BP1026B_II1198. Data in bar graphs represent means \pm s.e.m and analyzed via unpaired t-test. P values presented are as follows: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.

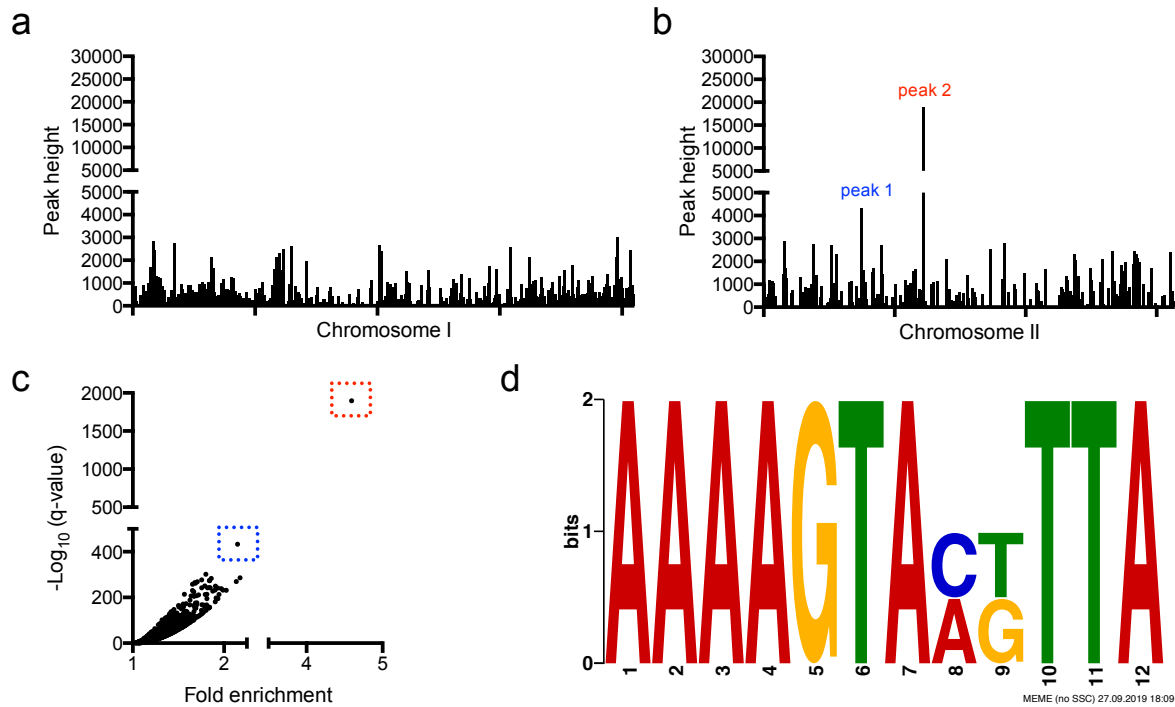


Figure 5| ChIP-seq identifies two regions of BP1026B_II1198 binding on chromosome II.

Peaks identified using MACS2⁴⁹ by comparison to an empty vector negative control are plotted by peak height and genome position on chromosome I (a) and chromosome II (b). b) Two peaks were identified on chromosome II and are labeled as peak 1 in blue and peak 2 in red. c) The two identified peaks are further isolated from background when compared by statistical ($-\log_{10} q$ -value) and fold enrichment. Blue box shows peak 1 and red box shows peak 2. d) Potential binding motif identified by analysis of peak 1 and peak 2 nucleotide sequences by MEME⁵⁰. Each peak contains the same orientation of the potential binding motif.

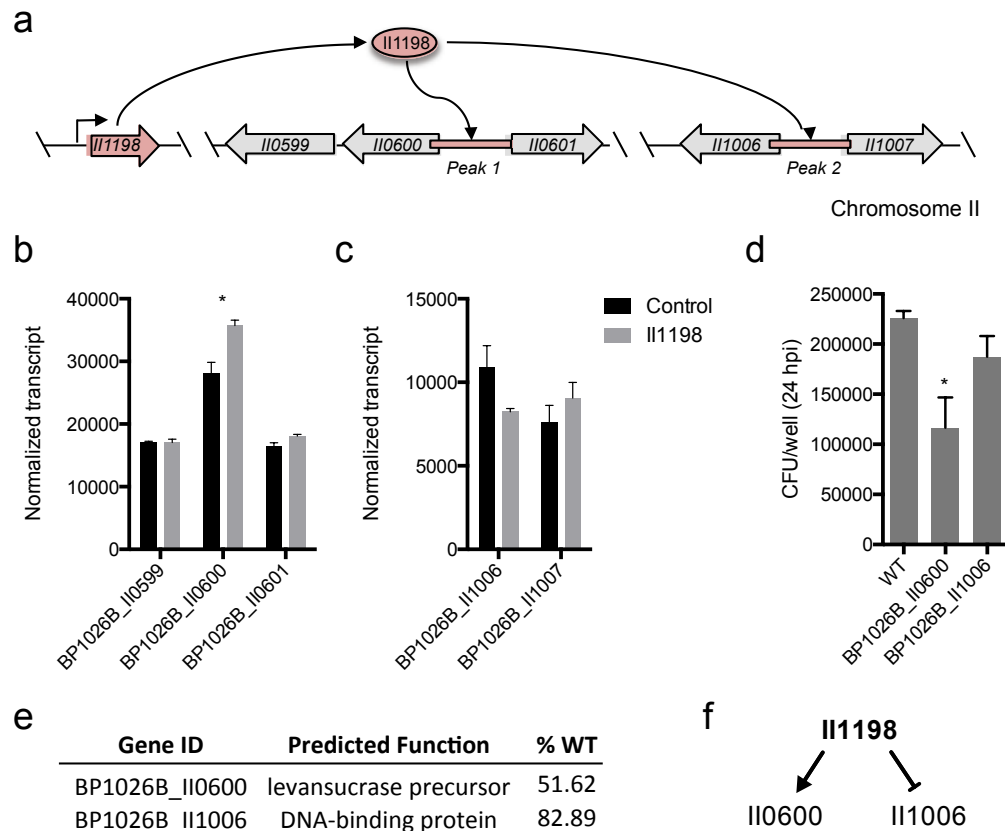
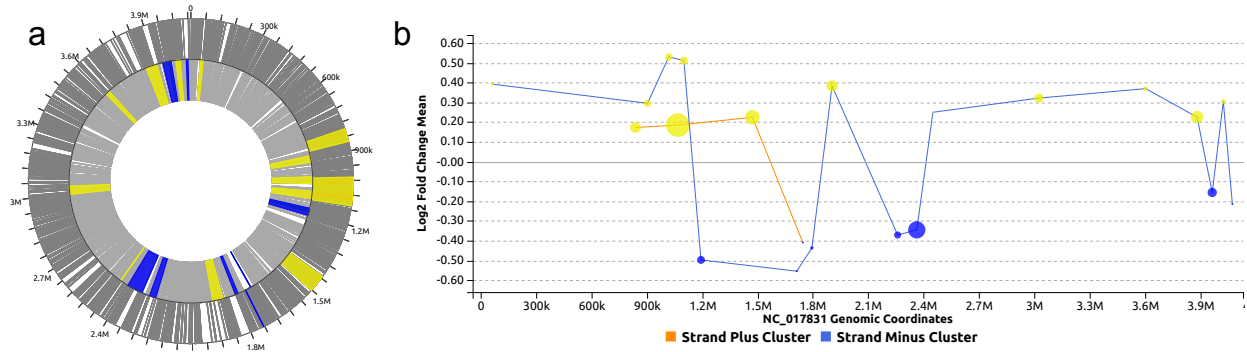


Figure 6| BP1026B_II1198 has direct transcriptional control of genes involved in pathogenesis of RAW264.7 murine macrophages. a) Schematic representation of the direct regulation network of BP1026B_II1198. BP1026B_II1198 binds to an intergenic region (peak 1) between BP1026B_II0600 and BP1026B_II0601 and an intergenic region (peak 2) between BP1026B_II1006 and BP1026B_II1007. b) Normalized transcripts of genes surrounding peak 1 identifies that BP1026B_II1198 positively regulates BP1026B_II0600. c) Normalized transcripts of genes around peak 2 identify that BP1026B_II1198 negatively regulates BP1026B_II1006. d) Infection of RAW264.7 cells by transposon mutants of BP1026B_II0600 and BP1026B_II1006 compared to wildtype *Bp* 1026b showing various levels of intracellular replication defect. e) Annotated function of BP1026B_II0600 and BP1026B_II1006 and corresponding intracellular replication when compared to wildtype *Bp* 1026b. f) Model for the direct regulation network of

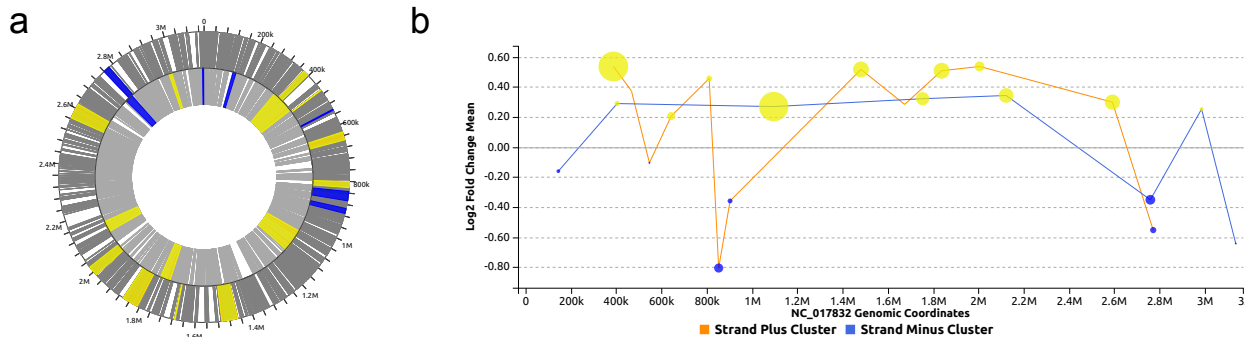
BP1026B_II1198. Data in bar graphs represent means \pm s.e.m and analyzed via unpaired t-test. P values presented are as follows: *p<0.05.



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Cluster	Start Coordinates	End Coordinates	Strand	Gene ID	Expression
1	50668	66682	-	BP10268_I0048;BP10268_I0049;BP10268_I0050;BP10268_I0051;BP10268_I0052;BP10268_I0053;BP10268_I0054;BP10268_I0055;BP10268_I0056;BP10268_I0057;BP10268_I0060;BP10268_I0061;BP10268_I0062	UP
2	809024	862500	+	BP10268_I0767;BP10268_I0769;BP10268_I0777;BP10268_I0778;BP10268_I0780;BP10268_I0785;BP10268_I0786;BP10268_I0792;BP10268_I0793;BP10268_I0794;BP10268_I0795;BP10268_I0796;BP10268_I0797;BP10268_I0798;BP10268_I0799;BP10268_I0800;BP10268_I0801;BP10268_I0802;BP10268_I0803;BP10268_I0804;BP10268_I0805;BP10268_I0806;BP10268_I0808	UP
3	885997	921194	-	BP10268_I0831;BP10268_I0832;BP10268_I0834;BP10268_I0835;BP10268_I0836;BP10268_I0837;BP10268_I0840;BP10268_I0841;BP10268_I0844;BP10268_I0845;BP10268_I0846;BP10268_I0848;BP10268_I0849;BP10268_I0852;BP10268_I0858;BP10268_I0859;BP10268_I0860;BP10268_I0861;BP10268_I0862;BP10268_I0863	UP
4	998745	1036089	-	BP10268_I0940;BP10268_I0942;BP10268_I0943;BP10268_I0944;BP10268_I0945;BP10268_I0946;BP10268_I0947;BP10268_I0949;BP10268_I0951;BP10268_I0952;BP10268_I0953;BP10268_I0954;BP10268_I0955;BP10268_I0956;BP10268_I0957;BP10268_I0958;BP10268_I0959;BP10268_I0962;BP10268_I0968;BP10268_I0969;BP10268_I0971;BP10268_I0972;BP10268_I0973;BP10268_I0974;BP10268_I0975	UP
5	1006199	1122917	-	BP10268_I0948;BP10268_I0950;BP10268_I0959;BP10268_I0960;BP10268_I0961;BP10268_I0963;BP10268_I0964;BP10268_I0965;BP10268_I0966;BP10268_I0967;BP10268_I0976;BP10268_I0977;BP10268_I0978;BP10268_I0980;BP10268_I0979;BP10268_I0981;BP10268_I0982;BP10268_I0983;BP10268_I0984;BP10268_I0985;BP10268_I0986;BP10268_I0987;BP10268_I0988;BP10268_I0989;BP10268_I0990;BP10268_I0991;BP10268_I0993;BP10268_I0994;BP10268_I0995;BP10268_I0996;BP10268_I0997;BP10268_I0998;BP10268_I0999;BP10268_I1000;BP10268_I1004;BP10268_I1005;BP10268_I1006;BP10268_I1007;BP10268_I1009;BP10268_I1010;BP10268_I1011;BP10268_I1012;BP10268_I1018;BP10268_I1019;BP10268_I1020;BP10268_I1021;BP10268_I1022;BP10268_I1023;BP10268_I1024;BP10268_I1025;BP10268_I1026;BP10268_I1027;BP10268_I1028;BP10268_I1029;BP10268_I1030;BP10268_I1033;BP10268_I1034;BP10268_I1036;BP10268_I1037;BP10268_I1038;BP10268_I1039;BP10268_I1040;BP10268_I1041;BP10268_I1042;BP10268_I1043;BP10268_I1044	UP
6	1076351	1115883	-	BP10268_I1008;BP10268_I1012;BP10268_I1013;BP10268_I1014;BP10268_I1015;BP10268_I1016;BP10268_I1017;BP10268_I1018;BP10268_I1019;BP10268_I1020;BP10268_I1021;BP10268_I1024;BP10268_I1025;BP10268_I1026;BP10268_I1027;BP10268_I1031;BP10268_I1032;BP10268_I1035	UP
7	1169046	1208323	-	BP10268_I1089;BP10268_I1125;BP10268_I1126;BP10268_I1127;BP10268_I1128;BP10268_I1129;BP10268_I1130;BP10268_I1131;BP10268_I1139	DOWN
8	1431508	1503022	+	BP10268_I1329;BP10268_I1332;BP10268_I1333;BP10268_I1334;BP10268_I1335;BP10268_I1336;BP10268_I1339;BP10268_I1340;BP10268_I1342;BP10268_I1344;BP10268_I1347;BP10268_I1351;BP10268_I1352;BP10268_I1358;BP10268_I1359;BP10268_I1360;BP10268_I1361;BP10268_I1363;BP10268_I1364;BP10268_I1365;BP10268_I1366;BP10268_I1367;BP10268_I1370;BP10268_I1371;BP10268_I1372;BP10268_I1373;BP10268_I1374;BP10268_I1375;BP10268_I1376;BP10268_I1377;BP10268_I1378;BP10268_I1379;BP10268_I1383;BP10268_I1388;BP10268_I1391;BP10268_I1392;BP10268_I1393;BP10268_I1394;BP10268_I1395;BP10268_I1396;BP10268_I1397;BP10268_I1398	UP
9	1711272	1712173	-	BP10268_I1582;BP10268_I1584	DOWN
10	1742675	1744982	+	BP10268_I1607;BP10268_I1608;BP10268_I1609	DOWN
11	1786537	1802986	-	BP10268_I1649;BP10268_I1650;BP10268_I1651;BP10268_I1658;BP10268_I1663	DOWN
12	1872678	1928301	-	BP10268_I1708;BP10268_I1711;BP10268_I1712;BP10268_I1713;BP10268_I1715;BP10268_I1722;BP10268_I1723;BP10268_I1724;BP10268_I1725;BP10268_I1726;BP10268_I1727;BP10268_I1731;BP10268_I1732;BP10268_I1733;BP10268_I1734;BP10268_I1735;BP10268_I1738;BP10268_I1739;BP10268_I1740	UP
13	2237014	2272171	-	BP10268_I2004;BP10268_I2005;BP10268_I2006;BP10268_I2008;BP10268_I2009;BP10268_I2011;BP10268_I2013;BP10268_I2014;BP10268_I2015;BP10268_I2016;BP10268_I2017;BP10268_I2018;BP10268_I2019;BP10268_I2020;BP10268_I2021;BP10268_I2022;BP10268_I2023;BP10268_I2024;BP10268_I2025;BP10268_I2026;BP10268_I2027;BP10268_I2028;BP10268_I2029;BP10268_I2030;BP10268_I2031;BP10268_I2034	DOWN
14	2315668	2401162	-	BP10268_I2063;BP10268_I2064;BP10268_I2066;BP10268_I2074;BP10268_I2080;BP10268_I2082;BP10268_I2083;BP10268_I2085;BP10268_I2087;BP10268_I2088;BP10268_I2089;BP10268_I2090;BP10268_I2091;BP10268_I2092;BP10268_I2093;BP10268_I2094;BP10268_I2095;BP10268_I2096;BP10268_I2097;BP10268_I2098;BP10268_I2099;BP10268_I2100;BP10268_I2101;BP10268_I2102;BP10268_I2103;BP10268_I2104;BP10268_I2105;BP10268_I2106;BP10268_I2107;BP10268_I2108;BP10268_I2109;BP10268_I2110;BP10268_I2111;BP10268_I2112;BP10268_I2113;BP10268_I2114;BP10268_I2115;BP10268_I2116;BP10268_I2119;BP10268_I2120;BP10268_I2121;BP10268_I2122;BP10268_I2124;BP10268_I2125;BP10268_I2126;BP10268_I2127;BP10268_I2128;BP10268_I2129;BP10268_I2130;BP10268_I2131;BP10268_I2132;BP10268_I2134;BP10268_I2135;BP10268_I2137;BP10268_I2138;BP10268_I2140;BP10268_I2144;BP10268_I2145;BP10268_I2157;BP10268_I2158;BP10268_I2159;BP10268_I2167;BP10268_I2168;BP10268_I2170;BP10268_I2172;BP10268_I2173;BP10268_I2174	DOWN
15	2445406	2447447	-	BP10268_I2215;BP10268_I2217	UP
16	2997776	3043477	-	BP10268_I2703;BP10268_I2704;BP10268_I2706;BP10268_I2707;BP10268_I2708;BP10268_I2713;BP10268_I2715;BP10268_I2718;BP10268_I2719;BP10268_I2720;BP10268_I2721;BP10268_I2722;BP10268_I2723;BP10268_I2724;BP10268_I2725;BP10268_I2730;BP10268_I2731;BP10268_I2733;BP10268_I2735;BP10268_I2736;BP10268_I2737;BP10268_I2739;BP10268_I2740;BP10268_I2741;BP10268_I2742	UP
17	3589655	3612278	-	BP10268_I3213;BP10268_I3214;BP10268_I3215;BP10268_I3223;BP10268_I3224;BP10268_I3225;BP10268_I3227;BP10268_I3228;BP10268_I3230;BP10268_I3231;BP10268_I3232;BP10268_I3233;BP10268_I3234	UP
18	3846410	3907946	-	BP10268_I3480;BP10268_I3482;BP10268_I3484;BP10268_I3489;BP10268_I3494;BP10268_I3496;BP10268_I3497;BP10268_I3499;BP10268_I3501;BP10268_I3504;BP10268_I3505;BP10268_I3506;BP10268_I3507;BP10268_I3509;BP10268_I3513;BP10268_I3515;BP10268_I3517;BP10268_I3519;BP10268_I3520;BP10268_I3523;BP10268_I3524;BP10268_I3525;BP10268_I3526;BP10268_I3527;BP10268_I3528;BP10268_I3529;BP10268_I3530;BP10268_I3531;BP10268_I3532;BP10268_I3533;BP10268_I3534;BP10268_I3535;BP10268_I3536;BP10268_I3537	UP
19	3940194	3986387	-	BP10268_I3569;BP10268_I3570;BP10268_I3571;BP10268_I3572;BP10268_I3575;BP10268_I3577;BP10268_I3578;BP10268_I3580;BP10268_I3582;BP10268_I3583;BP10268_I3584;BP10268_I3585;BP10268_I3592;BP10268_I3593;BP10268_I3622;BP10268_I3623;BP10268_I3624	DOWN
20	4010941	4034609	-	BP10268_I3653;BP10268_I3656;BP10268_I3658;BP10268_I3659;BP10268_I3660;BP10268_I3661;BP10268_I3664;BP10268_I3665;BP10268_I3666;BP10268_I3669;BP10268_I3670;BP10268_I3671;BP10268_I3672;BP10268_I3673	UP
21	4067419	4077202	-	BP10268_I3701;BP10268_I3702;BP10268_I3703;BP10268_I3704;BP10268_I3705;BP10268_I3706;BP10268_I3707;BP10268_I3708;BP10268_I3709	DOWN

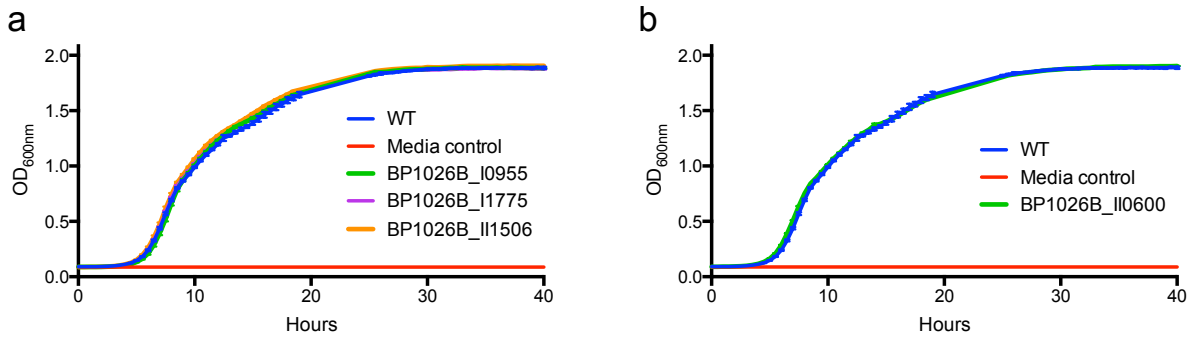
Supplemental Figure 1| WoPPER analysis reveals 21 gene clusters regulated by BP1026B_II1198 on *Bp* 1026b chromosome 1. a) Circular schematic of chromosome 1 showing up (yellow) and down (blue) regulated clusters of genes. b) Linear plot showing gene clusters that are regulated by BP1026B_II1198 and the mean of the clusters \log_2 fold change. Size of the circle represents the number of genes in each cluster; yellow is up-regulated and blue is down-regulated. c) Table listing each cluster of genes.



c

Cluster	Start Coordinates	End Coordinates	Strand	Gene ID	Expression
1	135381	148579	-	BP1026B_I10116;BP1026B_I10117;BP1026B_I10118;BP1026B_I10119;BP1026B_I10120;BP1026B_I10121;BP1026B_I10122;BP1026B_I10124;BP1026B_I10126	DOWN
2	350868	455171	-	BP1026B_I10291;BP1026B_I10292;BP1026B_I10294;BP1026B_I10296;BP1026B_I10298;BP1026B_I10300;BP1026B_I10301;BP1026B_I10304;BP1026B_I10305;BP1026B_I10306;BP1026B_I10307;BP1026B_I10308;BP1026B_I10310;BP1026B_I10311;BP1026B_I10312;BP1026B_I10314;BP1026B_I10318;BP1026B_I10319;BP1026B_I10324;BP1026B_I10325;BP1026B_I10327;BP1026B_I10328;BP1026B_I10329;BP1026B_I10330;BP1026B_I10331;BP1026B_I10332;BP1026B_I10333;BP1026B_I10334;BP1026B_I10335;BP1026B_I10336;BP1026B_I10337;BP1026B_I10338;BP1026B_I10339;BP1026B_I10340;BP1026B_I10348;BP1026B_I10349;BP1026B_I10350;BP1026B_I10356	UP
3	377577	395968	+	BP1026B_I10309;BP1026B_I10313;BP1026B_I10315;BP1026B_I10316;BP1026B_I10317;BP1026B_I10320;BP1026B_I10321;BP1026B_I10322;BP1026B_I10323	UP
4	464366	466075	+	BP1026B_I10362;BP1026B_I10363;BP1026B_I10364	UP
5	542392	546021	+	BP1026B_I10439;BP1026B_I10441;BP1026B_I10442;BP1026B_I10445	DOWN
6	627250	655441	+	BP1026B_I10509;BP1026B_I10510;BP1026B_I10511;BP1026B_I10512;BP1026B_I10513;BP1026B_I10514;BP1026B_I10525;BP1026B_I10526;BP1026B_I10527;BP1026B_I10528;BP1026B_I10529;BP1026B_I10530;BP1026B_I10531;BP1026B_I10533	UP
7	800331	820894	+	BP1026B_I10645;BP1026B_I10646;BP1026B_I10647;BP1026B_I10648;BP1026B_I10649;BP1026B_I10650;BP1026B_I10651;BP1026B_I10652;BP1026B_I10653;BP1026B_I10654	UP
8	834697	866695	+	BP1026B_I10670;BP1026B_I10681;BP1026B_I10683;BP1026B_I10682;BP1026B_I10684;BP1026B_I10685;BP1026B_I10686;BP1026B_I10690;BP1026B_I10691;BP1026B_I10694;BP1026B_I10695;BP1026B_I10696	DOWN
9	893813	911114	+	BP1026B_I10723;BP1026B_I10725;BP1026B_I10726;BP1026B_I10729;BP1026B_I10730;BP1026B_I10731;BP1026B_I10732;BP1026B_I10733;BP1026B_I10734;BP1026B_I10736;BP1026B_I10738;BP1026B_I10740;BP1026B_I10741	DOWN
10	1042707	1145759	-	BP1026B_I10850;BP1026B_I10854;BP1026B_I10863;BP1026B_I10875;BP1026B_I10876;BP1026B_I10877;BP1026B_I10878;BP1026B_I10879;BP1026B_I10880;BP1026B_I10884;BP1026B_I10885;BP1026B_I10886;BP1026B_I10891;BP1026B_I10892;BP1026B_I10898;BP1026B_I10899;BP1026B_I10907;BP1026B_I10911;BP1026B_I10912;BP1026B_I10913;BP1026B_I10916;BP1026B_I10918;BP1026B_I10920;BP1026B_I10921;BP1026B_I10922;BP1026B_I10930;BP1026B_I10932;BP1026B_I10933;BP1026B_I10934	UP
11	1452134	1507803	+	BP1026B_I1162;BP1026B_I1172;BP1026B_I1173;BP1026B_I1175;BP1026B_I1176;BP1026B_I1179;BP1026B_I1182;BP1026B_I1183;BP1026B_I1184;BP1026B_I1185;BP1026B_I1186;BP1026B_I1187;BP1026B_I1188;BP1026B_I1189;BP1026B_I1190;BP1026B_I1191;BP1026B_I1192;BP1026B_I1193;BP1026B_I1194;BP1026B_I1198;BP1026B_I1199;BP1026B_I1200;BP1026B_I1201;BP1026B_I1204;BP1026B_I1212	UP
12	1669880	1672481	+	BP1026B_I11329;BP1026B_I11332	UP
13	1728917	1775252	-	BP1026B_I11367;BP1026B_I11368;BP1026B_I11370;BP1026B_I11377;BP1026B_I11379;BP1026B_I11380;BP1026B_I11382;BP1026B_I11385;BP1026B_I11386;BP1026B_I11387;BP1026B_I11388;BP1026B_I11389;BP1026B_I11390;BP1026B_I11391;BP1026B_I11392;BP1026B_I11394;BP1026B_I11398;BP1026B_I11399;BP1026B_I1400	UP
14	1808195	1864242	+	BP1026B_I11431;BP1026B_I11438;BP1026B_I11439;BP1026B_I11440;BP1026B_I11441;BP1026B_I11442;BP1026B_I11449;BP1026B_I11452;BP1026B_I11460;BP1026B_I11464;BP1026B_I11469;BP1026B_I11470;BP1026B_I11472;BP1026B_I11471;BP1026B_I11473;BP1026B_I11476	UP
15	1985961	2020894	+	BP1026B_I11567;BP1026B_I11568;BP1026B_I11569;BP1026B_I11571;BP1026B_I11572;BP1026B_I11574;BP1026B_I11576;BP1026B_I11577;BP1026B_I11578;BP1026B_I11580;BP1026B_I11581;BP1026B_I11579;BP1026B_I11582;BP1026B_I11583;BP1026B_I11584;BP1026B_I11585;BP1026B_I11590;BP1026B_I11588;BP1026B_I11591;BP1026B_I11592;BP1026B_I11594;BP1026B_I11593;BP1026B_I11595;BP1026B_I11596	UP
16	2092808	2144294	-	BP1026B_I11663;BP1026B_I11670;BP1026B_I11671;BP1026B_I11674;BP1026B_I11677;BP1026B_I11678;BP1026B_I11679;BP1026B_I11681;BP1026B_I11682;BP1026B_I11683;BP1026B_I11684;BP1026B_I11685;BP1026B_I11686;BP1026B_I11687;BP1026B_I11688;BP1026B_I11689;BP1026B_I11693;BP1026B_I11694;BP1026B_I11699;BP1026B_I11703;BP1026B_I11704;BP1026B_I11705;BP1026B_I11706;BP1026B_I11707;BP1026B_I11708;BP1026B_I11709;BP1026B_I11710	UP
17	2563238	2616561	+	BP1026B_I12052;BP1026B_I12054;BP1026B_I12056;BP1026B_I12060;BP1026B_I12062;BP1026B_I12063;BP1026B_I12068;BP1026B_I12076;BP1026B_I12077;BP1026B_I12078;BP1026B_I12079;BP1026B_I12080;BP1026B_I12081;BP1026B_I12095;BP1026B_I12096;BP1026B_I12097;BP1026B_I12098;BP1026B_I12101	UP
18	2741722	2776012	-	BP1026B_I12207;BP1026B_I12209;BP1026B_I12210;BP1026B_I12211;BP1026B_I12213;BP1026B_I12214;BP1026B_I12217;BP1026B_I12218;BP1026B_I12220;BP1026B_I12222;BP1026B_I12223;BP1026B_I12224;BP1026B_I12225;BP1026B_I12226;BP1026B_I12227;BP1026B_I12229;BP1026B_I12230;BP1026B_I12231;BP1026B_I12232	DOWN
19	2760314	2782139	+	BP1026B_I12216;BP1026B_I12221;BP1026B_I12228;BP1026B_I12233;BP1026B_I12235;BP1026B_I12236;BP1026B_I12238;BP1026B_I12239	DOWN
20	2974712	2988613	-	BP1026B_I12408;BP1026B_I12409;BP1026B_I12410;BP1026B_I12411;BP1026B_I12412;BP1026B_I12413;BP1026B_I12414;BP1026B_I12415;BP1026B_I12416;BP1026B_I12419;BP1026B_I12422	UP
21	3131658	3136611	-	BP1026B_I12531;BP1026B_I12535;BP1026B_I12536	DOWN

Supplemental Figure 2| WoPPER analysis reveals 21 gene clusters regulated by BP1026B_II1198 on *Bp* 1026b chromosome 2. a) Circular schematic of chromosome 2 showing up (yellow) and down (blue) regulated clusters of genes. b) Linear plot showing gene clusters that are regulated by BP1026B_II1198 and the mean of the clusters \log_2 fold change. Size of the circle represents the number of genes in each cluster; yellow is up-regulated and blue is down-regulated. c) Table listing each cluster of genes.



Supplemental Figure 3| Transposon mutants grow identical to wildtype *Bp* 1026b *in vitro*.

a) Mutants controlled by BP1026B_I1198 indirectly (identified by RNA-seq) show no growth defects when grown in LB broth compared to wildtype *Bp* 1026b (WT). b) A BP1026B_I10600 mutant that is directly controlled by BP1026B_I1198 shows no defect when grown in LB broth compared to WT. Growth analysis was done in duplicate and the lines represent means \pm s.e.m.

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Chapter 3:

Identification of BP1026B_II1561, a *Burkholderia pseudomallei* Regulator of Aromatic Ring Biosynthesis and Intracellular Pathogenesis

Abstract

Burkholderia pseudomallei (*Bp*) causes the tropical disease melioidosis that afflicts an estimated 165,000 people each year. Melioidosis has many clinical presentations and can cause complications throughout the body making it difficult to diagnose and giving it the nickname ‘the great mimicker’. While originally thought to be localized in Southeast Asia and Northern Australia, increased awareness and surveillance has extended presence of *Bp* and melioidosis to tropical regions throughout the globe. *Bp* is a facultative intracellular pathogen that transits through distinct stages during its intracellular lifecycle. This includes attachment to host cells, invasion through the endocytic pathway, escape from the endosome, replication in the cytoplasm, protrusion towards neighboring cells, and host cell fusion allowing *Bp* infection to spread without exiting the intracellular environment. We previously identified 1,953 genes that are differentially regulated during the intracellular lifecycle and, in the present study, sought to characterize BP1026B_II1561, a TetR family transcriptional regulator that is up-regulated as *Bp* protrudes towards neighboring cells. A mutant of BP1026B_II1561 is attenuated in cell culture infections and in BALB/c mouse infections. We identified genes that are indirectly controlled by BP1026B_II1561 using RNA-seq and genes that are directly controlled through ChIP-seq to better understand the role of this transcriptional regulator. BP1026B_II1561 controls many pathways important for *Bp* intracellular survival including direct control of genes in the shikimate pathway that could be ideal targets for chemotherapeutic drug design to combat melioidosis.

Introduction

Burkholderia pseudomallei (*Bp*) is a Tier 1 select agent that causes the tropical disease melioidosis¹. Melioidosis is predicted to cause ~89,000 deaths annually through a wide array of clinical manifestations that are often misdiagnosed^{2, 3}. Acute, chronic, and sometimes latent forms of melioidosis are often found in patients of endemic areas with the majority of acute cases presenting with life threatening sepsis⁴. Pneumonia and localized abscesses are common presentations although many other nonspecific clinical signs can confound diagnosis making laboratory tests critical³. Treatment is broken down into an initial intensive phase that consists of intravenous ceftazidime, meropenem, or imipenem followed by an eradication phase consisting of either trimethoprim-sulfamethoxazole, or amoxicillin clavulanate and doxycycline⁵. Although modern antimicrobial treatment reduced mortality rates by half⁶, *Bp* is intrinsically resistant to antimicrobials through numerous mechanisms and resistance has developed during treatment⁷⁻⁹. Due to this and lack of a licensed vaccine, the development of novel therapeutic treatments is critical to reduce the global burden of melioidosis. Melioidosis is acquired through inhalation, ingestion, or inoculation from environments containing *Bp*⁵. *Bp* lives freely within the environment and is associated with the rhizosphere¹⁰. The global distribution of *Bp* is expanding due to better diagnostic techniques and environmental surveillance^{2, 11}. Infection is thought of as opportunistic in immunocompetent humans⁴ and intracellular virulence mechanisms could have evolved through associations with environmental eukaryotes like *Acanthamoeba* species¹².

Bp is a facultative intracellular pathogen that can infect many cell types throughout the human body including, but not limited to, cells of the lungs, liver, spleen, skin, bone/joint, gastrointestinal organs, and central nervous system¹. *Bp* requires many virulence factors to infect this variety of cell types. Described and characterized virulence factors include

lipopolysaccharide^{13, 14}, capsule polysaccharide¹⁵⁻¹⁷, type III secretion systems (T3SS)¹⁸⁻²², type VI secretion systems (T6SS)²³⁻²⁷, host cell actin polymerization through BimA^{28, 29}, and numerous others¹. The roles of these virulence factors have been assigned to specific spatial and temporal locations during infection. Briefly, *Bp* attaches to host cells, gets internalized, and uses the *Burkholderia* secretion apparatus (T3SS_{Bsa}) to escape the vacuole to gain entry into the cytoplasm²¹. Within the cytoplasm *Bp* can replicate and move freely by polymerizing host cell actin with a type 5 autotransporter BimA through molecular mimicry²⁸ or using its lateral flagella²⁰. When bacterial cell density gets high and/or nutrients become limited, *Bp* fuses host cells using T6SS-1 to generate multinucleated giant cells (MNGCs)^{20, 26, 27}. Recently, our group identified many genes that were differentially regulated through the *Bp* intracellular lifecycle indicating that many other virulence factors, some yet to be described, contribute to *Bp* intracellular pathogenesis³⁰. A refined regulatory system is critical to coordinate the expression of virulence factors and genes required for intracellular survival. Here, we present data to understand the role of a transcriptional regulator, BP1026B_II1561, and how it is involved in *Bp* pathogenesis and intracellular survival.

Results

***Bp* ‘transitome’ identifies BP1026B_II1561 as a differentially expressed gene during intracellular infection**

Recently, we reported the *Bp* ‘transitome’ that identified 1,953 differentially regulated bacterial genes during intracellular infection of RAW264.7 murine macrophages³⁰. The number of genes operating within each intracellular niche indicates to us that a sophisticated mechanism for gene regulation must exist. Although, many transcriptional regulators are encoded within the *Bp* genome, we focused on BP1026B_II1561 to understand its role during intracellular pathogenesis. BP1026B_II1561 is a TetR family regulator with 654 ortholog group members within the *Burkholderia* genus³¹. During intracellular infection, BP1026B_II1561 is highly expressed during the later stages of infection as *Bp* protrudes towards neighboring cells (Fig. 1a). This indicates that the function of this transcriptional regulator is during later stages of infection, although we recognize that the lack of BP1026B_II1561 expression is equally as important when repression is considered. We therefore wanted to test the role that BP1026B_II1561 plays in RAW264.7 murine macrophage pathogenesis.

A BP1026B_II1561 mutant is defective in multinucleated giant cell formation, intracellular replication, and *in vivo* pathogenesis

BP1026B_II1561 is annotated a TetR transcriptional regulator and is differentially regulated during the later stages of *Bp* intracellular infection (Fig. 1a). Because transcriptional regulators play an important role in many cellular processes, we hypothesized that this transcriptional regulator will be critical for late stage cell infection. To answer this we generated an in frame deletion mutant of BP1026B_II1561 to test its role during pathogenesis. When

infected with the BP1026B_II1561 mutant, RAW264.7 cells form smaller diameter multinucleated giant cells (MNGCs) when compared to cells infected with wild type *Bp* 1026b (Fig. 1b). This defect was complemented when BP1026B_II1561 was expressed *in trans* in the mutant strain. To further characterize the role of BP1026B_II1561 during RAW264.7 cell infection, the amount of intracellular bacteria were determined at various time points. At two, eight, and twenty-four hours post infection, the BP1026B_II1561 mutant showed a significant decrease in intracellular replication when compared to wildtype *Bp* 1026b (Fig. 1c). When grown in LB broth, the BP1026B_II1561 mutant and its complement showed comparable growth kinetics when compared to wildtype *Bp* 1026b indicating that the defects during intracellular infection can be tied to pathogenesis rather than fitness (Fig. 1d). Taken together, the data indicates that BP1026B_II1561 is important for intracellular replication and cell-cell spread during RAW264.7 cell infection.

We wanted to test if the role during pathogenesis carried over to a more complex infection model. We utilized the highly susceptible BALB/c mouse model to test if the BP1026B_II1561 mutant showed reduced levels of murine melioidosis. BALB/c mice were infected with 4,500 colony forming units (CFU) of either wildtype *Bp* 1026b or the BP1026B_II1561 mutant. While all mice infected with wildtype *Bp* 1026b showed significant signs of infection and 100% mortality by day four, mice infected with the BP1026B_II1561 mutant were able to survive for 62 days when the study was terminated (Fig. 2a). Upon study termination all mice infected with BP1026B_II1561 were sacrificed and lungs, liver, and spleen were harvested for bacterial burden analysis. Four mice appeared to have cleared the BP1026B_II1561 mutant and one mouse had persistent infection within the lungs (Fig. 2b). The transcriptional regulator BP1026B_II1561 is not only essential for pathogenesis in RAW264.7

cells, but is also critical for full pathogenesis in BALB/c mice. To better understand why this transcriptional regulator is critical for pathogenesis we sought to discover the regulation network of BP1026B_II1561 through RNA-seq analysis.

Hypothetical proteins and secondary metabolites are controlled by BP1026B_II1561

To further investigate the function of this transcriptional regulator, we determined how expression of BP1026B_II1561 changes the transcriptome of *Bp* 1026b. This will help us identify the pathways/genes controlled by BP1026B_II1561 to shed light on its role during pathogenesis. BP1026B_II1561 was expressed, via pAM3GIQ-3xTY1-BP1026B_II1561, under the same conditions that were used to complement the mutation during infection, followed by total RNA extraction, and Illumina sequencing. The data was analyzed by Rockhopper³² identifying the overall regulation network of BP1026B_II1561 (Fig. 3b, Table S1). We selected genes with a q-value < 0.01 and a log₂ fold-change (log₂FC) of ≥ 1 or ≤ -1 to analyze further (Fig. 3a). In total, 42 genes are up-regulated by BP1026B_II1561 while 83 genes are down-regulated (Fig. 3a). When we analyzed these genes by their COG functional groups, 76 are characterized as hypothetical proteins, hypothetical RNA transcripts, or uncharacterized conserved proteins highlighting the unknown nature of the pathways/genes controlled by BP1026B_II1561 (Fig. 3a). Of these, 42 are down-regulated and 34 are up-regulated by BP1026B_II1561. Many other general pathways are down regulated by BP1026B_II1561 including lipid, carbohydrate, and amino acid metabolism and transport, energy production and conversion, cell wall/membrane/envelope biogenesis (Fig. 3a). In addition, it appears that mechanisms of virulence are also down-regulated including COG functional categories of intracellular trafficking, secretion, and vesicular transport, secondary metabolite biosynthesis,

transport, and catabolism, and defense mechanisms (Fig. 3a). Although COG functional predictions can give us a general idea of what known pathways are being controlled by BP1026B_II1561, they are limited because much of the *Bp* genome has not been characterized.

For another perspective on what genes/pathways are being controlled by BP1026B_II1561, we analyzed the entire RNA-seq data set using WoPPER³³. WoPPER analysis will allow us to visualize regions of DNA that are being controlled by BP1026B_II1561 by comparing localized strand-separated expression across the entire data set. BP1026B_II1561 controls 40 gene clusters on chromosome I (Fig. S1) and 50 gene clusters on chromosome II (Fig. S2). In contrast to the COG analysis, WoPPER identified 53 clusters of genes that are up-regulated by BP1026B_II1561 while 37 clusters of genes are down-regulated (Fig. S1, Fig. S2). Clusters of known secondary metabolites are controlled by BP1026B_II1561 including malleobactin³⁴, malleilactone³⁵, pyochelin³⁶, and malleipeptin³⁶. Gene cluster 19 on chromosome I is up-regulated by BP1026B_II1561 and includes the non-ribosomal peptide synthase (NRPS) malleobactin, a siderophore (Fig. S1). Another siderophore, pyochelin, is located in the up-regulated gene cluster 15 on chromosome II (Fig. S2). While these gene clusters are important for iron-acquisition, they are also unnecessary for murine pathogenesis³⁷. Malleilactone on the other hand is a siderophore that has been tied to pathogenesis in *Caenorhabditis elegans* and *Dictyostelium discoideum*^{35,38}. Malleilactone is up-regulated by BP1026B_II1561 in gene cluster 6 on chromosome II (Fig. S2). Taken together, some of the genes controlled by BP1026B_II1561 appear to be critical for iron limiting environments. Other secondary metabolite gene clusters are also controlled by BP1026B_II1561. Malleipeptin is down regulated in cluster 37 on chromosome II by BP1026B_II1561 (Fig. S2). Malleipeptin is a lipopeptide encoded by five genes (BP1026B_II1742-II1746) and is required for pathogenesis in mice³⁶. While malleipeptin

has been linked to bacterial invasion³⁶, no role during later stages of infection have been identified. Our data fits into this model because we see up-regulation of BP1026B_II1561 during the later stages of infection indicating down-regulation of malleipectin (Fig. 1a). In addition to these secondary metabolites, a polyketide synthase/peptide synthetase cluster of genes around BP1026B_II1265 are down-regulated by BP1026B_II1561 (cluster 27, Fig. S2). This cluster of genes has yet to be characterized but could play a role during *Bp* intracellular survival³⁶. The variation in expression of *Bp* secondary metabolites suggests that these compounds could be critical for intracellular infection. While our COG analysis focused on single genes that fit our criteria ($q\text{-value} < 0.01$ and $\log_2\text{FC}$ of ≥ 1 or ≤ -1), WoPPER analysis does not, and will include regions of genes with minor changes in expression. Taken together, both sets of analysis help define a general regulatory role of BP1026B_II1561 within the *Bp* 1026b genome.

BP1026B_II1561 controls genes that have potential roles during intracellular pathogenesis

To better characterize the pathogenic role that BP1026B_II1561 plays during intracellular infection, genes with a $\log_2\text{FC}$ of ≥ 2 or ≤ -2 were targeted for mutant analysis (Table S1). Twelve of these genes are down-regulated and seven are up-regulated by BP1016B_II1561 (Fig. 4a). These mutants were obtained from the sequence-defined transposon mutant library of *Bp* 1026b³⁹ and the T24 transposon insertion was confirmed by sequencing (data not shown). No transposon mutants with insertions in genes BP1026B_I0528 or BP1026B_II1118 were present, indicating that these genes could be essential for *Bp* growth. To characterize the pathogenic role these genes have during infection, RAW264.7 murine macrophages were infected with the transposon mutants and wildtype *Bp* 1026b followed by determination of the intracellular bacterial burden. Transposon mutants tested were able to

replicate at 26.25-101.47% of wildtype over the course of the infection (Fig. 4b-c). Some mutants, BP1026B_I0452, BP1026B_II0231, BP1026B_II0682, BP1026B_II0683, BP1026B_II0685, and BP1026B_II0686, showed similar intracellular replication to wildtype *Bp* 1026b indicating less essential roles during infection (Fig. 4c). Interestingly, genes involved in fatty acid metabolism, BP1026B_I0063 and BP1026B_I0064, show 58.41% and 76.99% wildtype replication, respectively (Fig. 4c). These two genes encode acyl-CoA dehydrogenase and acetyl-CoA acetyltransferase and are down-regulated by BP1026B_II1561 with log₂FCs of -2.5 and -2 (Fig. 4a, Table S1). In addition to this, BP1026B_I0065, the alpha subunit of the fatty acid oxidation complex, is also down-regulated by BP1026B_II1561 (log₂FC -1.5, Table S1). Taken together, it appears that BP1026B_II1561 down-regulates fatty acid metabolism and that some of the enzymes in this pathway are important for intracellular survival.

BP1026B_I0071 encodes a transmembrane regulator protein, PrtR, that is up-regulated by BP1026B_II1561 with a log₂FC of 2 (Fig. 4a, Table S1). PrtR sits downstream from an extracytoplasmic function sigma factor (ECF), BP1026B_I0072/*prtI*, with no known function. While we see up-regulation of BP1026B_I0071, BP1026B_I0072 is only slightly up-regulated by BP1026B_II1561 with a log₂FC of 0.48 (Table S1). A transposon mutant in BP1026B_I0071 reduced intracellular replication to 38% of wildtype *Bp* 1026b, suggesting a role during intracellular replication and pathogenesis (Fig. 4b-c). BP1026B_I1775 is a potential lipoprotein up-regulated by BP1026B_II1561 and a mutant of this gene replicates at 59.29% of wildtype in RAW264.7 cells (Fig. 4a-c). The function of this lipoprotein is unknown but our results suggest that it is important for pathogenesis. Genes involved in propanoate metabolism are also controlled by BP1026B_II1561. BP1026B_II0229-II0232 are highly down-regulated with log₂FCs between -3.2 to -4.2 (Fig. 4a, Table S1). These genes catabolize propanoyl-CoA to

succinate and pyruvate that can feed into the citric acid cycle⁴⁰. Mutants of BP1026B_II0229, BP1026B_II0230, and BP1026B_II0232 showed significant decreases during intracellular replication (Fig. 4b). Strikingly, the transposon mutant of BP1026B_II0232 was reduced to replicate at 26.25% of wildtype *Bp* 1026b in RAW26.7 macrophages (Fig. 4b-c).

BP1026B_II0681-II0686 are also down-regulated by BP1026b_II1561 ranging from a log₂FC of -2.02 to -2.77 (Fig. 4a, Table S1). Some of these genes have known function in general metabolic pathways linked to BP1026B_II0229-II0232. BP1026B_II0682 encodes methylmalonate-semialdehyde dehydrogenase and catalyzes the reaction of either methylmalonate semialdehyde to propanoyl-CoA or malonate semialdehyde to acetyl-CoA⁴⁰. A transposon mutant in this gene replicates in RAW264.7 cells at 101.5% of wildtype indicating that its loss can be compensated for during intracellular infection (Fig. 4b-c). BP1026B_II0683 is an AMP-binding protein that is predicted to catalyze the reactions of acetate to acetyl-CoA or propanoate to propanoyl-CoA⁴⁰, and the mutant of this gene replicates at 87.91% of wildtype (Fig. 4b-c). BP1026B_II0684 is 3-hydroxyisobutyrate dehydrogenase that catalyzes the reaction of hydroxyl isobutyrate to methylmalonate semialdehyde that can then be converted to propanoyl-CoA by BP1026B_II0682. Propanoyl-CoA is further degraded by BP1026B_II0229-II0232 to succinate and pyruvate⁴⁰. More interesting is the fact that BP1026B_II0684 seems to be important for intracellular survival because its mutant replicates at 60.18% of wildtype in RAW264.7 cells (Fig. 4b-c). Three genes, BP1026B_II0681, BP1026B_II0685, and BP1026B_II0686, that are involved in beta-oxidation during fatty acid metabolism are also down regulated by BP1026B_II1561 (Fig. 4a). Of these genes BP1026B_II0685-II0686 show no major defect when their mutants were tested for intracellular replication while a mutant of BP1026_II0681 replicated at 61.65% of wildtype *Bp* (Fig. 4b-c). BP1026B_II1562 is a

hypothetical protein that is up-regulated by BP1026B_II1561 with a log₂FC of 2.11 (Fig. 4a, Table S1). While a mutant in BP1026B_II1562 replicates at 51% of wildtype (Fig. 4b-c), it is only found in *Bp* strain 1026b and contains regions of disorder throughout its primary sequence³¹. BP1026B_II1736 encodes a type III secretion protein HrpB4 that is up-regulated by BP1026B_II1561 (Fig. 4a) and its mutant is defective in intracellular replication (Fig. 4b-c). Transposon mutants defective in RAW264.7 cell infection were grown *in vitro* and showed similar growth kinetics to wildtype *Bp* indicating that the defects during intracellular replication were not due to decreased fitness (Fig. S3a). Taken together, we have identified genes involved in general metabolic pathways and genes with unproven function that are controlled by BP1026B_II1561 and contribute to pathogenesis in RAW264.7 macrophages (Fig. 4d).

BP1026B_II1561 binds to two regions on chromosome II

To get a better understanding of the direct role of BP1026B_II1561 on transcription, we used ChIP-seq to define the direct binding sequences within the genome. Briefly, BP1026B_II1561 was expressed from pAM3GIQ-3xTY1-BP1026B_II1561 in *Bp* 82, a select agent exempt derivative of *Bp* 1026b, and protein-DNA complexes were fixed using paraformaldehyde. Cells were lysed, DNA fragments were sheared using an M220 focused ultrasonicator, and BP1026B_II1561-DNA complexes were immunoprecipitated using an anti-TY1 monoclonal antibody. After de-crosslinking the BP1026B_II1561-DNA complexes, DNA was purified and sequenced on an Illumina HiSeq 2500. An empty vector (pAM3GIQ-3xTY1) was used as a control. Peaks were called with MACS2⁴¹ after alignment to the *Bp* 1026b genome with Bowtie2⁴². Two regions on chromosome II show high levels of enrichment for DNA sequences bound to BP1026b_II1561 while few peaks showed any enrichment on chromosome I

(Fig. 5a-b). While the peaks on chromosome I are small, we envision that the binding could be important for specific environmental niches and could involve other transcription factors. The two large peaks on chromosome II are enriched 5.9 and 6.4 fold in the BP1026B_II1561 ChIP sample compared to the empty vector control and have low false discovery rates (Fig. 5c). Using MEME⁴³ an 18bp consensus binding sequence was found, TAT XXG AAC TAA CTA GXT, with 15bp having 100% homology between both peaks (Fig. 5d). We believe that this is the region in which BP1026B_II1561 directly binds to initiate/repress transcription.

Genes directly controlled by BP1026B_II1561 are important during intracellular infection

Based on the ChIP-seq data, BP1026B_II1561 binds two peaks of 610bp and 762bps in length on chromosome II (Fig. 5a-b). These peaks overlap intergenic regions between the divergently transcribed genes BP1026B_II0369 and BP1026B_II0370, and between genes BP1026B_II0781 and BP1026B_II0782 (Fig. 6a). BP1026B_II0370-II0372 are up-regulated by BP1026B_II1561 with log₂FCs between 0.58 and 1, while BP1026B_II0369 shows no change in expression suggesting transcription in a single direction (Fig. 6b, Table S1). BP1026B_II0782 is also up-regulated by BP1026B_II1561 with a log₂FC of 0.52 (Fig. 6c, Table S1). BP1026B_II0370-II0372 encode shikimate 5-dehydrogenase, 3-dehydroquinate dehydratase, and a phthalate permease, respectively (Fig. 6e). BP1026B_II0372 is a major facilitator superfamily phthalate permease that, to our knowledge has not been characterized for its role in pathogenesis or function. BP1026B_II0370 and BP1026B_II0371 are in the shikimate pathway catalyzing the reactions generating shikimate from 3-dehydroquinate⁴⁰. Shikimate can be converted to chorismate that has many downstream products and potential applications towards pathogenesis and cell function ranging from aromatic amino acid biosynthesis, biosynthesis of

siderophore group nonribosomal peptides, and folate biosynthesis⁴⁰. BP1026B_II0782 is predicted to be an outer-membrane porin that has not been characterized for its role during intracellular infection or general function to our knowledge.

Because these genes are directly controlled by BP1026B_II1561 we wanted to determine if any had a role during pathogenesis. Transposon mutants of BP1026B_II0370-II0372 and BP1026B_II0782 were used to infect RAW264.7 cells and intracellular bacterial burdens determined at 24 hours post infection. A transposon mutant of BP1026B_II0372 replicated at wildtype levels suggesting this gene is dispensable for intracellular infection (Fig. 6d-e). Transposon mutants of BP1026B_II0370 and BP1026B_II0371 were able to replicate at 76.11% and 70.50% of wildtype in the RAW264.7 intracellular environment (Fig. 6d-e). We suspect that the pathways using shikimate as an intermediate are responsible for this decrease in intracellular replication. The BP1026B_II0782 transposon mutant showed the largest defect during RAW264.7 cell infection, replicating at 49.56% of wildtype (Fig. 6d-e). This transposon mutants grew identical to wildtype *Bp* 1026b in LB broth indicating that this defect is due to a reduction in RAW264.7 pathogenesis rather than a defect in fitness (Fig. S3b). Taken together, the data show that BP1026B_II1561 binds two regions of DNA leading to the up-regulation of four genes, and three of these genes, BP1026B_II0370, BP1026B_II0371, and BP1026B_II0782, are important for intracellular replication and pathogenesis (Fig. 6f).

Discussion

Bp encounters many environmental niches during its existence in the soil, association with the rhizosphere, and during infection of a host. During infection of a host *Bp* must navigate another complex set of environments including invasion of the host cell, escape of the vacuole, cytoplasmic replication, and spread towards neighboring cells all while avoiding host cell defenses³⁰. For *Bp* to be successful in all of these unique environments, it must encode a large number of regulated pathways and mechanisms for survival. Recently, we identified that 1,953 genes are differentially regulated during the intracellular lifecycle of *Bp*, further highlighting the importance of a sophisticated system of regulation during infection³⁰. BP1026B_II1561 was identified to be up-regulated as *Bp* protrudes towards neighboring cells indicating a role during later stages of intracellular infection. BP1026B_II1561 is critical for complete pathogenesis in RAW264.7 cell infection and BALB/c mouse infection leading us to investigate the transcriptional role of this regulator. We have identified the regulation network of BP1026B_II1561 and partially characterized the networks role during pathogenesis. The primary sequence of BP1026B_II1561 indicates it is a TetR family transcriptional regulator. This family of regulators are classically thought to control antibiotic resistance and small-molecule export but have been tied to many other functions including metabolism, antibiotic production, and quorum sensing⁴⁴. In general, we see that BP1026B_II1561 leads to variations in the expression of many known pathways and a large number of hypothetical genes that could be important for intracellular survival and pathogenesis.

Modulation of secondary metabolites expression includes the up-regulation of the siderophores malleobactin³⁴, malleilactone³⁵, and pyochelin³⁶, by BP1026B_II1561 that suggests a role in iron scavenging during intracellular infection. Although we believe the expression of

these siderophores by BP1026B_II1561 contributes to the attenuation of the BP1026B_II1561 mutant in BALB/c mice, previous studies have shown that some of these factors are dispensable³⁷. In addition, the down-regulation of malleipeptin³⁶ by BP1026B_II1561 is curious, as malleipeptin is required for pathogenesis in BALB/c mice. It is suggested that malleipeptin is required for invasion of the epithelium, which would fit with our data as BP1026B_II1561 is up-regulated during later stages of infection. In this case, BP1026B_II1561 dependent down regulation of malleipeptin could be an energy saving mechanism when there is no longer a need for this virulence-associated secondary metabolite. Considering this data together, we start to see a complex picture of the BP1026B_II1561 regulation network where many factors are controlled for various purposes.

Genes involved in propanoate and fatty acid metabolism are down-regulated by BP1026B_II1561 to potentially conserve energy during intracellular survival. During infection, *Bp* must rely on nutrients obtained from the host cell to replicate and survive. When nutrients are depleted, *Bp* will protrude towards neighboring cells to form MNGCs and gain access to additional nutrients. BP1026B_II1561 is up-regulated during protrusion and down-regulates genes that direct intermediaries into energy producing molecules like acetyl-CoA through various pathways. The energy saved doing this could allow the proper function of other virulence factors like T6SS-1 that is used for fusion of host cells into MNGCs thereby gaining access to nutrients²⁰. Transposon mutants of the genes involved in fatty acid and propanoate metabolism were showed reduced intracellular replication at various levels indicating that they are important for pathogenesis and that down-regulating energy production is critical for full infection. BP1026B_II0232 is an accessory protein for AcnD causing *trans* to *cis* isomerization of methyl aconitate⁴⁵ and its mutant replicates at 26.25% of wildtype while not showing any defect during

in vitro growth. Further investigation into this gene and its function could elucidate a better understanding of this metabolic pathway during pathogenesis.

Another potential role of BP1026B_II1561 is through the up-regulation of BP1026B_I0071, a potential transmembrane regulator PrtR. PrtR has a potential two-component regulation system with BP1026B_I0072, an ECF sigma factor PrtI. The PrtIR regulatory complex has been tied to several functions including expression of the extracellular protease, AprX in *Pseudomonas fluorescens* LS107d2⁴⁶, protease production in *P. entomophila*⁴⁷, protease/cycliclipopeptide production in *P. fluorescens* strains HCl-07 and SS101^{48, 49}, and germination arrest factor (GAF) by *P. fluorescens* WH6⁵⁰. GAF is a secondary metabolite that has been tied to herbicidal and antibacterial functions in *P. fluorescens* WH6, a rhizosphere associated bacteria⁵⁰. Recognizing that *Bp* is also a rhizosphere-associated organism, the role of *prtR* in *Bp* could be similar to *P. fluorescens*. In the same transcriptional snapshot where we see up-regulation of *prtR*, we see differential expression of various secondary metabolites that have been shown to be involved in iron acquisition and virulence. The transposon mutant in *prtR* was significantly reduced during intracellular infection of RAW264.7 cells indicating that this regulatory pathway is important for pathogenesis. These downstream virulence functions of *prtR* could be carry over from the normal *Bp* lifecycle within the rhizosphere, but still have effect on mammalian cells. Furthermore, this highlights the complexity of the BP1026B_II1561 regulation network and its role during infection.

BP1026B_II1561 up-regulates several genes in the shikimate pathway including 3-dehydroquinate dehydratase (BP1026B_II0371) and shikimate 5-dehydrogenase (BP1026B_II0370). When used to infect RAW264.7 cells, transposon mutants of BP1026B_II0370 and BP1026B_II0371 were unable to replicate to wildtype levels indicating

that these genes are important for intracellular infection. These enzymes encoded by these genes catalyze two steps in the reaction from phosphoenolpyruvate and D-erythrose 4-phosphate to chorismate, which can be shunted towards various pathways including aromatic amino acid and folate biosynthesis^{40, 51}. The shikimate pathway is absent from mammals marking this as a target for the development new chemotherapeutic interventions⁵²⁻⁵⁷. Taken together, BP1026B_II1561 appears to control the up-regulation of enzymes in the shikimate pathway and these enzymes could be a rational target for the development of new chemotherapeutic agents against *Bp* infection. Overall, the transcriptional regulator BP1026B_II1561 plays a critical role during pathogenesis, marked by attenuation of its mutant in BALB/c mice. During intracellular infection, BP1026B_II1561 has a broad affect on the transcription of many pathways and genes that are involved in pathogenesis. Although the BP1026B_II1561 regulation network is only a one part of the *Bp* pathogenic regulation story, it is nonetheless complex and plays a critical role in the sophisticated intracellular lifecycle of *Bp*.

Methods and Materials

Bacterial strains, media and culture conditions *Escherichia coli* strain EPMaX10B (BioRad), E1869, and E1354 were used for cloning or plasmid mobilization into *Bp* as described previously^{58, 59}. Luria-Bertani (LB) medium (Difco) or 1x M9 minimal medium supplemented with 20 mM glucose (MG) were used to culture all strains. MG media was supplemented with 0.3% glyphosate when appropriate. The select agent excluded analogue of *Bp* 1026b, *Bp*82, was used where appropriate. All manipulation and experiments involving *Bp* 1026b were conducted in a CDC-approved and registered facility at the University of Hawai'i at Mānoa or Colorado State University with prior approval by internal review and adhere to recommendations set forth in the BMBL, 5th edition⁶⁰ for BSL3 organisms.

Molecular methods and reagents Molecular methods and reagents were used as described previously^{59, 61-63}. An in-frame deletion mutant of BP1026B_II1561 was generated using lambda-red recombineering with minor modification⁶⁴. Lambda red genes were PCR amplified from pKaKa1 and co-incubated with the knockout fragment of BP1026B_II1561 and mutants selected for on glyphosate. For expression of BP1026B_II1561, BP1026B_II1561 was PCR amplified with oligos 2660 (5'- AAT GCG CCG CAT ATG CCG CCG TCC GAT CAC GCC AAA ATG) and 2661 (5'- ATG TCG AGC TCG ACG CCG ATG CCG) digested with *Nde*I and *Sac*I and ligated into *Nde*I/*Sac*I-cut pAM3GIQ-3xTY1. Confirmation of pAM3GIQ-3xTY1-BP1026B_II1561, was done by *Afl*II/*Sac*I, *Nde*I, and *Sal*I digests, sequencing, and expression of BP1026B_II1561 confirmed via western blot analysis.

Growth analysis All strains were first grown overnight in LB broth at 37°C, harvested the following day, diluted to an OD₆₀₀ of 0.1 in 200µl of fresh LB, and placed into 96 well plate in duplicate. Growth curves were carried out at 37°C shaking and data was recorded with the BioTek ELx808IU plate reader, measurements taken at an OD₆₃₀ every 30 minutes.

Cell infection assays Intracellular replication and MNGC formation assays were carried out as previously described⁶⁵ with minor modifications. Briefly, RAW264.7 murine macrophages were seeded for infection at 80-90% confluence on Corning CellBIND culture plates, allowed to attach overnight, washed twice with 1XPBS, and infected the following day. For intracellular replication assays, *Bp* 1026b, the BP1026B_II1561 mutant, or the BP1026B_II1561 complement (mutant with pAM3GIQ-3xTY1-BP1026B_II1561) were allowed to infect monolayers at an MOI of 1:1, washed with 1XPBS, and then DMEM supplemented with 10% FBS, 0.1mM IPTG to drive expression of the complement, 700 µg/mL amikacin and 700 µg/mL kanamycin were added to kill any extracellular bacteria. At 2, 8, and 24 hours post-infection, infected monolayers were lysed with 0.2% Triton X-100. Serial dilutions of lysates were plated on LB and colony-forming units (CFU) per well were determined. MNGC formation assays were carried out as intracellular replication assays, with the exception that 1.2% low-melt agarose was added to DMEM after infection allowing the formation of MNGCs. At 24 hours post-infection, monolayers were fixed with 4% paraformaldehyde, agarose plugs removed, stained with 0.05% crystal violet, and MNGC diameters measured with the Zeiss Axio Observer D1 and the AxioVision 64 bit 4.9.1 software. Cell infection assays with mutants from the *Bp* 1026b::T24 transposon mutant library were carried out as described above although kanamycin was removed and amikacin added a final concentration of 1,500µg/mL to remove extracellular bacteria post

infection. Monolayers were lysed at 24 hours post-infection as described above. All transposon mutants tested were confirmed to be in the gene of interest by sequencing.

Animal studies BALB/c mice between 4 and 6 weeks of age were purchased from Charles River Laboratory. All infections with *Bp* strains (wildtype and the BP1026B_II1561 mutant) were administered via the intranasal (i.n.) inoculation route. Mice were anesthetized with 100 mg of ketamine/kg of body weight plus 10 mg/kg xylazine. The challenge dose (4,500 CFU) of each *Bp* strain was suspended in 20 µl of 1XPBS and used to inoculate each mouse via the i.n. route. Each strain was used to inoculate 5 mice. Animals were monitored for disease symptoms daily and euthanized at predetermined humane end points. Lungs, liver, and spleen of surviving mice were harvested, homogenized, serially diluted, and plated on LB to determine bacterial burdens. Survival characteristics were plotted using Prism software (GraphPad, La Jolla, CA) and statistical analysis was done by Kaplan-Meier curves.

RNA-seq and ChIP-seq analysis RNA-seq and ChIP-seq analysis were carried out under the same conditions. Briefly, *Bp82* expressing BP1026B_II1561 from pAM3GIQ-3xTY1-BP1026B_II1561 was grown overnight and sub-cultured to mid-log phase in LB+adenine+0.1mM IPTG in triplicate. An empty vector (pAM3GIQ-3xTY1) was used as a control. Total RNA was harvested using RNeasy Mini Kit (Qiagen) with on-column (Qiagen) and off-column (Epicentre) DNase digestion steps. RNA samples were sent to Tufts University Genomics Core (TUCF Genomics) for library preparation and Illumina 50bp single-end reads were sequenced on the Illumina HiSeq 2500. RNA-seq data was analyzed with Rockhopper³².

ChIP-seq was carried out as previously described with minor modifications^{66, 67}. Briefly, ChIP-seq samples were grown identically as RNA-seq samples, harvested, and fixed with 4% paraformaldehyde, followed by shearing of DNA-protein complexes with the Covaris M220 ultrafocused sonicator. Cell debris was removed and DNA-protein complexes were immunoprecipitated with anti-TY1-tag monoclonal antibody (Diagenode C15200054) and secondary antibodies conjugated to magnetic beads (Diagenode C03010022). DNA-protein complexes were washed, decrosslinked, treated with RNaseA and proteinase K, and purified with QIAquick PCR purification kit. Immunoprecipitated DNA was sent to TUCF Genomics where DNA libraries were prepped and 50bp single-end reads were sequenced with the Illumina HiSeq 2500. ChIP-seq data was aligned to the *Bp* 1026b genome with Bowtie2⁴², peaks called with MACS2⁴¹, and consensus binding regions determined with MEME⁴³.

Ethics statement All animal studies described in this manuscript were approved by the Institutional Animal Care and Use Committee at the University of Hawaii at Manoa (Protocol No. 10-1073-8), and conducted in compliance with the NIH (National Institutes of Health) Guide for the Care and Use of Laboratory Animals.

Data availability The datasets and materials generated during the current study are available from the corresponding author upon reasonable request. Any transfer of select agent materials needs additional approval from Brad Borlee and the Responsible Official at Colorado State University. Any select agent transfer must be to a select agent registered facility, approved by the CDC, and comply with all select agent regulations (selectagents.gov).

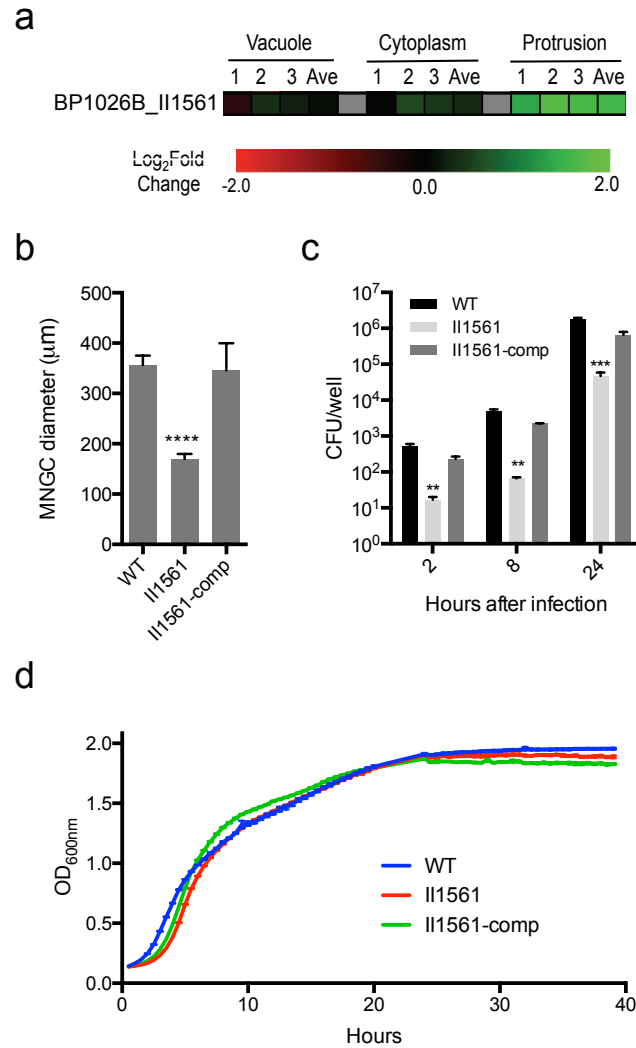


Figure 1| Differential regulation of BP1026B_II1561 during cell infection leads to defects in pathogenesis. a) BP1026B_II1561 is up-regulated while *Bp* is protruding towards neighboring cells. Expression data represents three biological replicates (1, 2, and 3) and the average (Ave) with a green-black-red color scale used to represent up- and down-regulation based on log₂FC. b) An in frame deletion mutant of BP1026B_II1561 (II1561) was unable to form MNGCs of similar diameter to wildtype *Bp* 1026b (WT) in RAW264.7 cells. Complementation of the mutant (II1561-comp) recovered this defect. c) The BP1026B_II1561 mutant was defective during intracellular replication at 2, 8, and 24 hours post infection in RAW264.7 cells and the

complement was able to recover the defect. d) The BP1026B_II1561 mutant and its complement were able to grow similar to wildtype in LB broth. Data in bar graphs and growth curve represent means \pm s.e.m and analyzed via unpaired t-test. P values presented are as follows: ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.

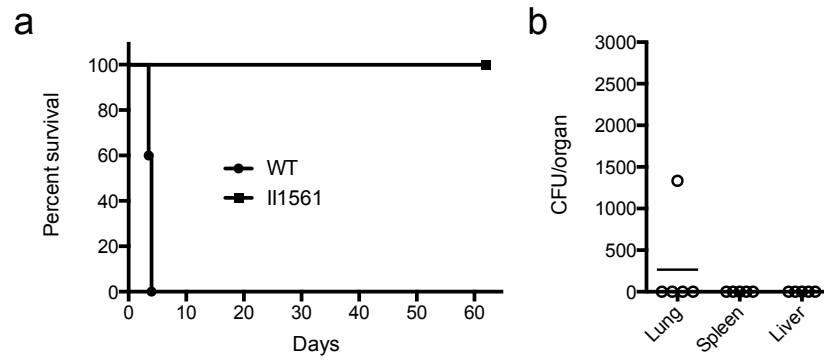


Figure 2| A BP1026B_II1561 mutant is attenuated in the BALB/c mouse infection model. a) BALB/c mice were infected with 4,500 CFU of wildtype *Bp* 1026b (WT) or the BP1026B_II1561 mutant (II1561). Mice infected with the BP1026B_II1561 mutant were able to survive for the duration of the study while mice infected with wildtype *Bp* 1026b showed 100% mortality by day five. b) Bacterial burdens from the lungs, liver, and spleen of surviving mice were determined showing significant clearance of the mutant strain with only one mouse having persistent infection in the lungs.

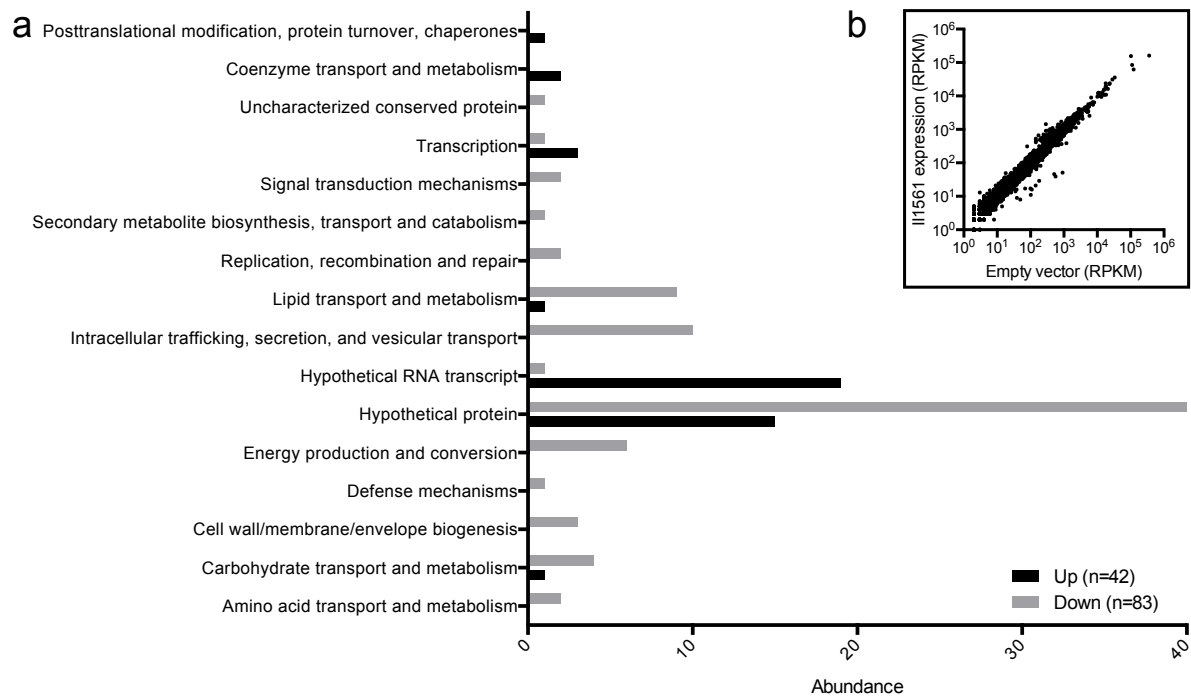


Figure 3| BP1026B_II1561 down-regulates 83 genes and up-regulates 42 genes. a) COG functional predictions of genes with a q-value of <0.01 and a \log_2FC of ≥ 1 or ≤ -1 show the general landscape of the BP1026B_II1561 regulation network. A large proportion of genes have no known function. b) Scatter plot of all *Bp* genes comparing expression of BP1026B_II1561 and the empty vector control.

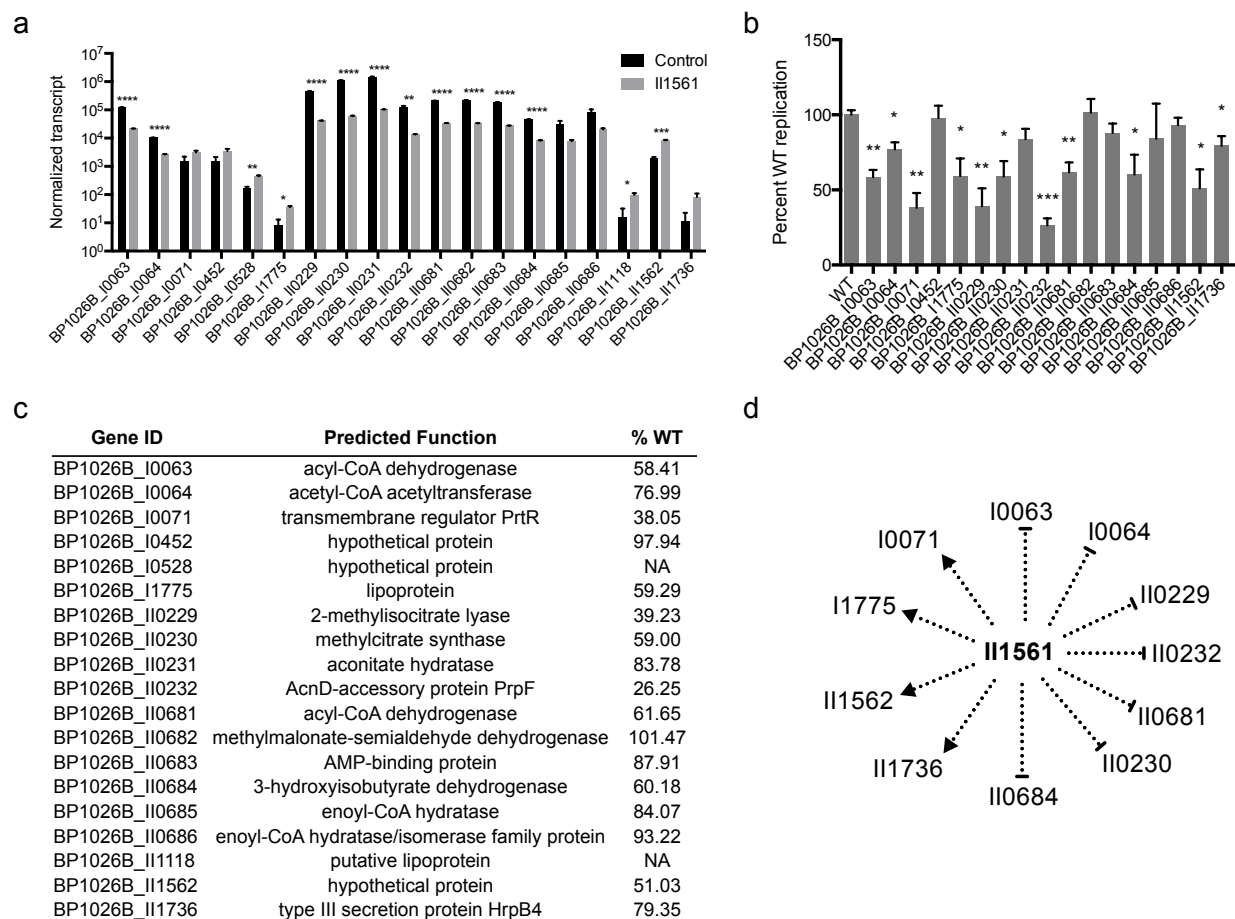


Figure 4| General metabolic pathways controlled by BP1026B_II1561 contribute to pathogenesis in RAW264.7 cells. a) BP1026B_II1561 up-regulates seven genes with a \log_2FC of ≥ 2 and down-regulates twelve genes with a \log_2FC of ≤ -2 . Black bars are normalized transcript of the empty vector control and grey bars are normalized transcript in the presence of BP1026B_II1561. b) Transposon mutants of indicated genes show various levels of intracellular replication in RW264.7 cells at 24 hours post infection when compared to wildtype *Bp* 1026b (WT). c) Predicted functions of genes controlled by BP1026B_II1561. Average percent wildtype replication (%WT) of transposon mutants identifies genes important for intracellular survival. d) Model of the genes controlled by BP1026B_II1561 that contribute to intracellular survival in RAW264.7 cells. Pointed arrows represent activation and flat arrows represent repression. Data

in bar graphs represent means \pm s.e.m and analyzed via unpaired t-test. P values presented are as follows: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.

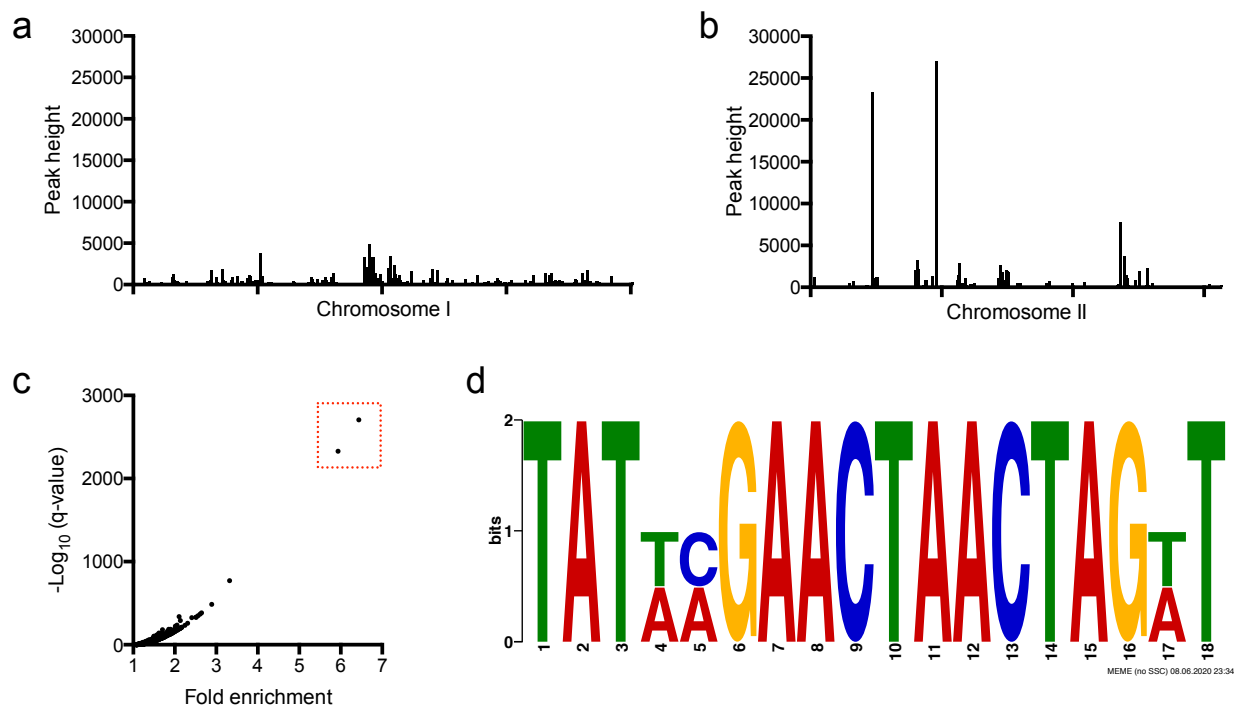


Figure 5| BP1026B_II1561 binds two regions of DNA on chromosome II. All peaks identified from ChIP-seq experiment on chromosome I (a) and chromosome II (b) show that BP1026B_II1561 binds two regions on chromosome II. c) Comparison of the $-\log_{10}$ of the q-value compared to fold enrichment further isolates two peaks (boxed in red) from the background. d) Consensus region of DNA from the two peaks identified in ChIP-seq data found using MEME⁴³. The consensus binding region shows 15 out of 18 base pairs are shared between the two peaks.

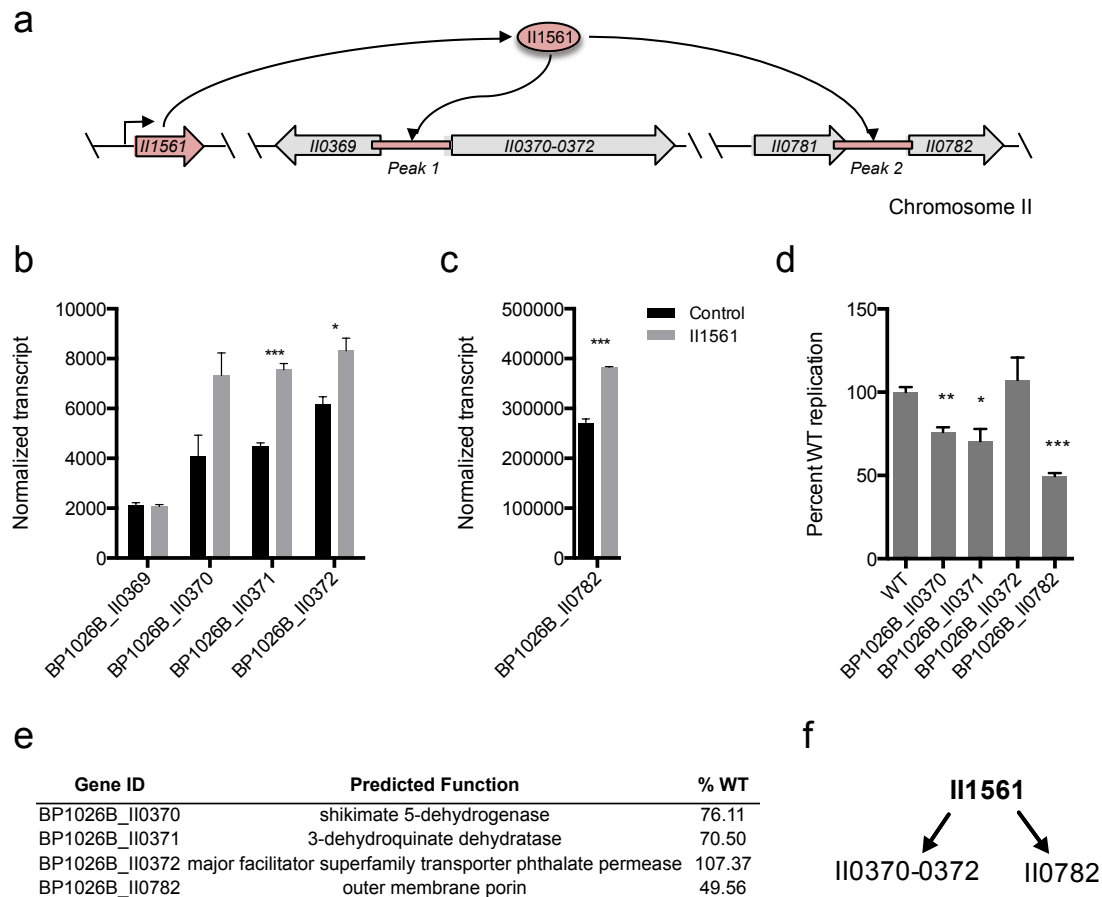
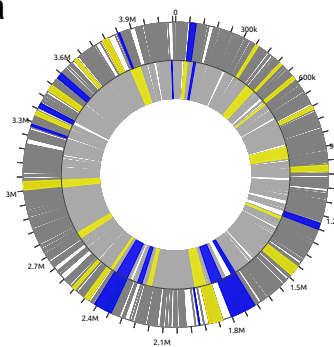


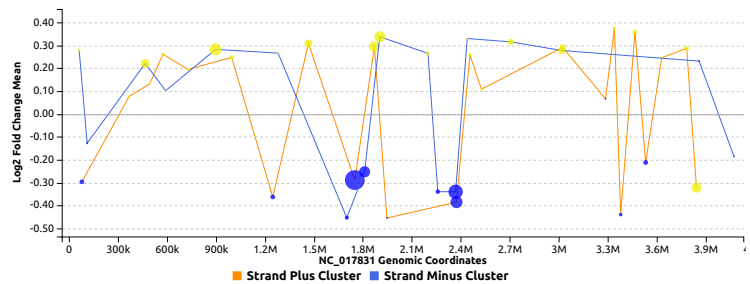
Figure 6| BP1026B_II1561 binds two intergenic regions controlling genes in the shikimate pathway and an outer membrane porin. a) Schematic representation of DNA regions on chromosome II directly bound by BP1026B_II1561. b) Normalized transcript levels of genes surrounding peak 1 comparing the level of transcription in the empty vector control (black bars) and the BP1026B_II1561 expression condition (grey bars). c) Normalized transcript levels of genes surrounding peak 2 from ChIP-seq data set comparing the level of transcription in the empty vector control (black bars) and the BP1026B_II1561 expression condition (grey bars). d) Transposon mutants were used to infect RAW264.7 cells identifying genes important for intracellular pathogenesis. e) Genes activated by BP1026B_II1561, their predicted functions, and the average wildtype replication in RAW264.7 cells (%WT). f) Schematic representation of

genes directly controlled by BP1026B_II1561 that contribute to pathogenesis. Arrows represent activation by BP1026B_II1561. Data in bar graphs represent means \pm s.e.m and analyzed via unpaired t-test. P values presented are as follows: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

a



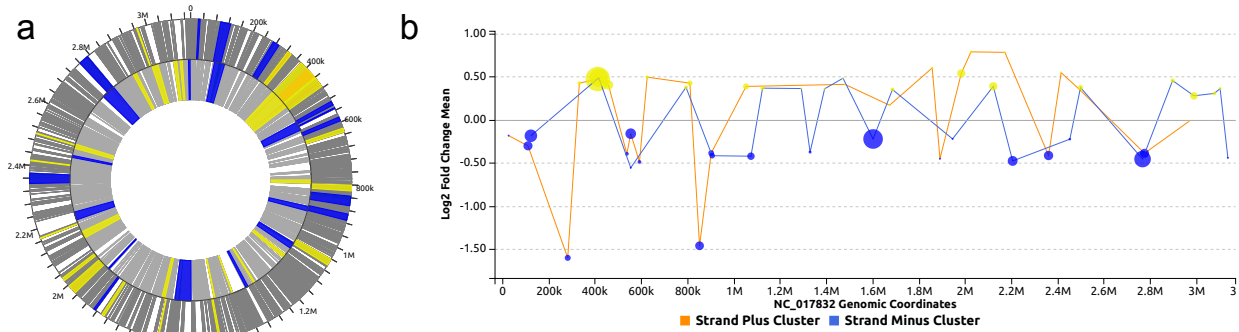
b



c

Cluster	Start Coordinates	End Coordinates	Strand	Gene ID	Expression
1	50668	66682	-	BP1026B_I0048;BP1026B_I0049;BP1026B_I0050;BP1026B_I0051;BP1026B_I0052;BP1026B_I0053;BP1026B_I0054;BP1026B_I0055;BP1026B_I0056;BP1026B_I0057;BP1026B_I0060;BP1026B_I0061;BP1026B_I0062	UP
2	61805	88125	+	BP1026B_I0059;BP1026B_I0058;BP1026B_I0063;BP1026B_I0064;BP1026B_I0065;BP1026B_I0066;BP1026B_I0069;BP1026B_I0070;BP1026B_I0073;BP1026B_I0074;BP1026B_I0078;BP1026B_I0079;BP1026B_I0080	DOWN
3	103502	114477	-	BP1026B_I0097;BP1026B_I0098;BP1026B_I0099;BP1026B_I0100;BP1026B_I0106;BP1026B_I0107;BP1026B_I0108	DOWN
4	359756	372710	+	BP1026B_I0351;BP1026B_I0352;BP1026B_I0356;BP1026B_I0357;BP1026B_I0361;BP1026B_I0364	UP
5	438386	487029	-	BP1026B_I0428;BP1026B_I0429;BP1026B_I0430;BP1026B_I0431;BP1026B_I0432;BP1026B_I0433;BP1026B_I0434;BP1026B_I0439;BP1026B_I0440;BP1026B_I0441;BP1026B_I0442;BP1026B_I0443;BP1026B_I0451;BP1026B_I0452;BP1026B_I0453;BP1026B_I0464;BP1026B_I0465;BP1026B_I0466;BP1026B_I0467;BP1026B_I0468;BP1026B_I0469	UP
6	489186	499751	+	BP1026B_I0471;BP1026B_I0476	UP
7	567168	583497	+	BP1026B_I0529;BP1026B_I0530;BP1026B_I0531;BP1026B_I0532;BP1026B_I0533;BP1026B_I0534;BP1026B_I0535;BP1026B_I0536;BP1026B_I0537;BP1026B_I0539;BP1026B_I0538;BP1026B_I0541;BP1026B_I0540;BP1026B_I0542;BP1026B_I0544;BP1026B_I0545	UP
8	584761	590384	-	BP1026B_I0547;BP1026B_I0548;BP1026B_I0549;BP1026B_I0550;BP1026B_I0551;BP1026B_I0552;BP1026B_I0553;BP1026B_I0554	UP
9	718317	733526	+	BP1026B_I0669;BP1026B_I0674;BP1026B_I0675;BP1026B_I0676;BP1026B_I0679;BP1026B_I0680;BP1026B_I0683;BP1026B_I0682;BP1026B_I0687;BP1026B_I0686	UP
10	861212	927706	-	BP1026B_I0807;BP1026B_I0809;BP1026B_I0816;BP1026B_I0819;BP1026B_I0820;BP1026B_I0823;BP1026B_I0825;BP1026B_I0827;BP1026B_I0828;BP1026B_I0829;BP1026B_I0831;BP1026B_I0832;BP1026B_I0834;BP1026B_I0835;BP1026B_I0836;BP1026B_I0837;BP1026B_I0840;BP1026B_I0841;BP1026B_I0844;BP1026B_I0845;BP1026B_I0846;BP1026B_I0848;BP1026B_I0849;BP1026B_I0852;BP1026B_I0858;BP1026B_I0859;BP1026B_I0860;BP1026B_I0861;BP1026B_I0862;BP1026B_I0863;BP1026B_I0869;BP1026B_I0871	UP
11	981465	1007411	+	BP1026B_I0924;BP1026B_I0925;BP1026B_I0926;BP1026B_I0927;BP1026B_I0928;BP1026B_I0930;BP1026B_I0939;BP1026B_I0941;BP1026B_I0948;BP1026B_I0950	UP
12	1234833	1261337	+	BP1026B_I1158;BP1026B_I1159;BP1026B_I1160;BP1026B_I1161;BP1026B_I1162;BP1026B_I1163;BP1026B_I1164;BP1026B_I1165;BP1026B_I1166;BP1026B_I1167;BP1026B_I1168;BP1026B_I1169;BP1026B_I1170;BP1026B_I1171;BP1026B_I1173;BP1026B_I1172;BP1026B_I1174;BP1026B_I1175	DOWN
13	1272459	1281740	-	BP1026B_I1184;BP1026B_I1187;BP1026B_I1193	UP
14	1444205	1488349	+	BP1026B_I1342;BP1026B_I1344;BP1026B_I1347;BP1026B_I1351;BP1026B_I1352;BP1026B_I1358;BP1026B_I1359;BP1026B_I1360;BP1026B_I1361;BP1026B_I1363;BP1026B_I1364;BP1026B_I1365;BP1026B_I1366;BP1026B_I1367;BP1026B_I1370;BP1026B_I1371;BP1026B_I1372;BP1026B_I1373;BP1026B_I1374;BP1026B_I1375;BP1026B_I1376;BP1026B_I1377;BP1026B_I1378;BP1026B_I1379;BP1026B_I1383	UP
15	1689391	1712173	-	BP1026B_I1565;BP1026B_I1568;BP1026B_I1582;BP1026B_I1584	DOWN
16	1690753	1801496	+	BP1026B_I1567;BP1026B_I1569;BP1026B_I1570;BP1026B_I1571;BP1026B_I1572;BP1026B_I1573;BP1026B_I1574;BP1026B_I1575;BP1026B_I1576;BP1026B_I1577;BP1026B_I1578;BP1026B_I1579;BP1026B_I1580;BP1026B_I1581;BP1026B_I1583;BP1026B_I1585;BP1026B_I1587;BP1026B_I1588;BP1026B_I1589;BP1026B_I1590;BP1026B_I1591;BP1026B_I1592;BP1026B_I1593;BP1026B_I1594;BP1026B_I1595;BP1026B_I1596;BP1026B_I1597;BP1026B_I1598;BP1026B_I1599;BP1026B_I1600;BP1026B_I1601;BP1026B_I1602;BP1026B_I1603;BP1026B_I1604;BP1026B_I1605;BP1026B_I1606;BP1026B_I1607;BP1026B_I1608;BP1026B_I1609;BP1026B_I1610;BP1026B_I1611;BP1026B_I1612;BP1026B_I1613;BP1026B_I1617;BP1026B_I1620;BP1026B_I1621;BP1026B_I1622;BP1026B_I1630;BP1026B_I1631;BP1026B_I1632;BP1026B_I1635;BP1026B_I1636;BP1026B_I1642;BP1026B_I1643;BP1026B_I1645;BP1026B_I1647;BP1026B_I1648;BP1026B_I1652;BP1026B_I1653;BP1026B_I1654;BP1026B_I1655;BP1026B_I1656;BP1026B_I1657;BP1026B_I1659;BP1026B_I1660;BP1026B_I1661;BP1026B_I1662	DOWN
17	1775393	1837548	-	BP1026B_I1637;BP1026B_I1638;BP1026B_I1639;BP1026B_I1640;BP1026B_I1641;BP1026B_I1644;BP1026B_I1646;BP1026B_I1649;BP1026B_I1650;BP1026B_I1651;BP1026B_I1658;BP1026B_I1663;BP1026B_I1664;BP1026B_I1665;BP1026B_I1666;BP1026B_I1667;BP1026B_I1668;BP1026B_I1669;BP1026B_I1670;BP1026B_I1671;BP1026B_I1672;BP1026B_I1673;BP1026B_I1674;BP1026B_I1675;BP1026B_I1676	DOWN
18	1842173	1900708	+	BP1026B_I1681;BP1026B_I1683;BP1026B_I1684;BP1026B_I1687;BP1026B_I1689;BP1026B_I1690;BP1026B_I1693;BP1026B_I1692;BP1026B_I1694;BP1026B_I1695;BP1026B_I1696;BP1026B_I1697;BP1026B_I1698;BP1026B_I1699;BP1026B_I1700;BP1026B_I1701;BP1026B_I1702;BP1026B_I1705;BP1026B_I1707;BP1026B_I1709;BP1026B_I1710;BP1026B_I1714;BP1026B_I1716;BP1026B_I1717;BP1026B_I1718;BP1026B_I1719;BP1026B_I1720;BP1026B_I1721;BP1026B_I1728;BP1026B_I1729;BP1026B_I1730	UP
19	1872678	1933803	-	BP1026B_I1708;BP1026B_I1711;BP1026B_I1712;BP1026B_I1713;BP1026B_I1715;BP1026B_I1716;BP1026B_I1717;BP1026B_I1718;BP1026B_I1719;BP1026B_I1720;BP1026B_I1721;BP1026B_I1722;BP1026B_I1723;BP1026B_I1724;BP1026B_I1725;BP1026B_I1726;BP1026B_I1727;BP1026B_I1728;BP1026B_I1729;BP1026B_I1730;BP1026B_I1731;BP1026B_I1732;BP1026B_I1733;BP1026B_I1735;BP1026B_I1736;BP1026B_I1739;BP1026B_I1740;BP1026B_I1741;BP1026B_I1742;BP1026B_I1743;BP1026B_I1744;BP1026B_I1745	UP
20	1942190	1944000	+	BP1026B_I1751;BP1026B_I1752;BP1026B_I1753;BP1026B_I1754	DOWN
21	2186981	2208393	-	BP1026B_I1967;BP1026B_I1968;BP1026B_I1969;BP1026B_I1970;BP1026B_I1971;BP1026B_I1973;BP1026B_I1975;BP1026B_I1976;BP1026B_I1978;BP1026B_I1981;BP1026B_I1982;BP1026B_I1983	UP
22	2242307	2267593	-	BP1026B_I2008;BP1026B_I2009;BP1026B_I2011;BP1026B_I2013;BP1026B_I2014;BP1026B_I2015;BP1026B_I2016;BP1026B_I2017;BP1026B_I2018;BP1026B_I2019;BP1026B_I2020;BP1026B_I2021;BP1026B_I2022;BP1026B_I2023;BP1026B_I2024;BP1026B_I2025;BP1026B_I2026;BP1026B_I2027;BP1026B_I2028;BP1026B_I2029;BP1026B_I2030;BP1026B_I2031	DOWN
23	2330918	2411419	+	BP1026B_I2079;BP1026B_I2081;BP1026B_I2086;BP1026B_I2117;BP1026B_I2118;BP1026B_I2123;BP1026B_I2133;BP1026B_I2136;BP1026B_I2139;BP1026B_I2141;BP1026B_I2142;BP1026B_I2143;BP1026B_I2146;BP1026B_I2148;BP1026B_I2149;BP1026B_I2150;BP1026B_I2151;BP1026B_I2152;BP1026B_I2153;BP1026B_I2154;BP1026B_I2155;BP1026B_I2156;BP1026B_I2160;BP1026B_I2161;BP1026B_I2163;BP1026B_I2165;BP1026B_I2169;BP1026B_I2171;BP1026B_I2179;BP1026B_I2184	DOWN
24	2331963	2399355	-	BP1026B_I2080;BP1026B_I2082;BP1026B_I2083;BP1026B_I2085;BP1026B_I2087;BP1026B_I2088;BP1026B_I2089;BP1026B_I2090;BP1026B_I2091;BP1026B_I2092;BP1026B_I2093;BP1026B_I2094;BP1026B_I2095;BP1026B_I2096;BP1026B_I2097;BP1026B_I2098;BP1026B_I2099;BP1026B_I2100;BP1026B_I2101;BP1026B_I2102;BP1026B_I2103;BP1026B_I2104;BP1026B_I2105;BP1026B_I2106;BP1026B_I2107;BP1026B_I2108;BP1026B_I2109;BP1026B_I2110;BP1026B_I2111;BP1026B_I2112;BP1026B_I2114;BP1026B_I2115;BP1026B_I2116;BP1026B_I2119;BP1026B_I2120;BP1026B_I2121;BP1026B_I2122;BP1026B_I2124;BP1026B_I2125;BP1026B_I2126;BP1026B_I2127;BP1026B_I2128;BP1026B_I2129;BP1026B_I2130;BP1026B_I2131;BP1026B_I2132;BP1026B_I2134;BP1026B_I2135;BP1026B_I2137;BP1026B_I2138;BP1026B_I2140;BP1026B_I2144;BP1026B_I2145;BP1026B_I2157;BP1026B_I2158;BP1026B_I2159;BP1026B_I2167;BP1026B_I2168;BP1026B_I2170;BP1026B_I2172	DOWN
25	2430474	2441381	-	BP1026B_I2201;BP1026B_I2202;BP1026B_I2203;BP1026B_I2204;BP1026B_I2205;BP1026B_I2206;BP1026B_I2207;BP1026B_I2208;BP1026B_I2209;BP1026B_I2210;BP1026B_I2211;BP1026B_I2212	UP
26	2442278	2462823	+	BP1026B_I2213;BP1026B_I2216;BP1026B_I2218;BP1026B_I2219;BP1026B_I2221;BP1026B_I2222;BP1026B_I2223;BP1026B_I2225;BP1026B_I2226;BP1026B_I2227;BP1026B_I2229	UP
27	2514959	2529685	+	BP1026B_I2270;BP1026B_I2272;BP1026B_I2276;BP1026B_I2277;BP1026B_I2278;BP1026B_I2279;BP1026B_I2280;BP1026B_I2281	UP
28	2686538	2720977	-	BP1026B_I2423;BP1026B_I2424;BP1026B_I2425;BP1026B_I2426;BP1026B_I2429;BP1026B_I2432;BP1026B_I2435;BP1026B_I2437;BP1026B_I2438;BP1026B_I2444;BP1026B_I2445;BP1026B_I2446;BP1026B_I2447;BP1026B_I2448;BP1026B_I2449;BP1026B_I2450	UP
29	2998586	3038900	-	BP1026B_I2704;BP1026B_I2706;BP1026B_I2707;BP1026B_I2708;BP1026B_I2713;BP1026B_I2715;BP1026B_I2718;BP1026B_I2719;BP1026B_I2720;BP1026B_I2721;BP1026B_I2722;BP1026B_I2723;BP1026B_I2724;BP1026B_I2725;BP1026B_I2730;BP1026B_I2731;BP1026B_I2733;BP1026B_I2735;BP1026B_I2736;BP1026B_I2737	UP
30	3003904	3040258	+	BP1026B_I2709;BP1026B_I2710;BP1026B_I2711;BP1026B_I2712;BP1026B_I2716;BP1026B_I2726;BP1026B_I2727;BP1026B_I2728;BP1026B_I2729;BP1026B_I2732;BP1026B_I2734;BP1026B_I2738	UP
31	3281284	3289470	+	BP1026B_I2939;BP1026B_I2940;BP1026B_I2941	DOWN
32	3331732	3350602	+	BP1026B_I2982;BP1026B_I2984;BP1026B_I2985;BP1026B_I2986;BP1026B_I2987;BP1026B_I2988;BP1026B_I2989;BP1026B_I2993;BP1026B_I2994;BP1026B_I2995;BP1026B_I2997;BP1026B_I2998;BP1026B_I2999;BP1026B_I3001	UP
33	3366709	3386721	+	BP1026B_I3012;BP1026B_I3013;BP1026B_I3014;BP1026B_I3015;BP1026B_I3016;BP1026B_I3017;BP1026B_I3018;BP1026B_I3019;BP1026B_I3020;BP1026B_I3021;BP1026B_I3022;BP1026B_I3024;BP1026B_I3023;BP1026B_I3025;BP1026B_I3026;BP1026B_I3027;BP1026B_I3028;BP1026B_I3029;BP1026B_I3030;BP1026B_I3031	DOWN
34	3450617	3477500	+	BP1026B_I3090;BP1026B_I3095;BP1026B_I3106;BP1026B_I3107;BP1026B_I3108;BP1026B_I3109;BP1026B_I3110;BP1026B_I3117	UP
35	3516444	3543482	+	BP1026B_I3149;BP1026B_I3157;BP1026B_I3158;BP1026B_I3159;BP1026B_I3160;BP1026B_I3161;BP1026B_I3162;BP1026B_I3166;BP1026B_I3167;BP1026B_I3168;BP1026B_I3169;BP1026B_I3171;BP1026B_I3172	DOWN
36	3620485	3634475	+	BP1026B_I3243;BP1026B_I3244;BP1026B_I3245;BP1026B_I3246;BP1026B_I3251;BP1026B_I3253;BP1026B_I3254;BP1026B_I3255;BP1026B_I3256;BP1026B_I3257	UP
37	3766881	3792553	+	BP1026B_I3390;BP1026B_I3403;BP1026B_I3405;BP1026B_I3406;BP1026B_I3411;BP1026B_I3413	UP
38	3829144	3884401	-	BP1026B_I3458;BP1026B_I3460;BP1026B_I3470;BP1026B_I3471;BP1026B_I3480;BP1026B_I3482;BP1026B_I3484;BP1026B_I3489;BP1026B_I3494;BP1026B_I3496;BP1026B_I3497;BP1026B_I3499;BP1026B_I3501;BP1026B_I3504;BP1026B_I3505;BP1026B_I3506;BP1026B_I3507;BP1026B_I3509;BP1026B_I3513;BP1026B_I3515;BP1026B_I3517	UP
39	3840193	3847401	+	BP1026B_I3472;BP1026B_I3473;BP1026B_I3474;BP1026B_I3475;BP1026B_I3476;BP1026B_I3477;BP1026B_I3478;BP1026B_I3479;BP1026B_I3481	DOWN
40	4068843	4071726	-	BP1026B_I3702;BP1026B_I3703;BP1026B_I3704	DOWN

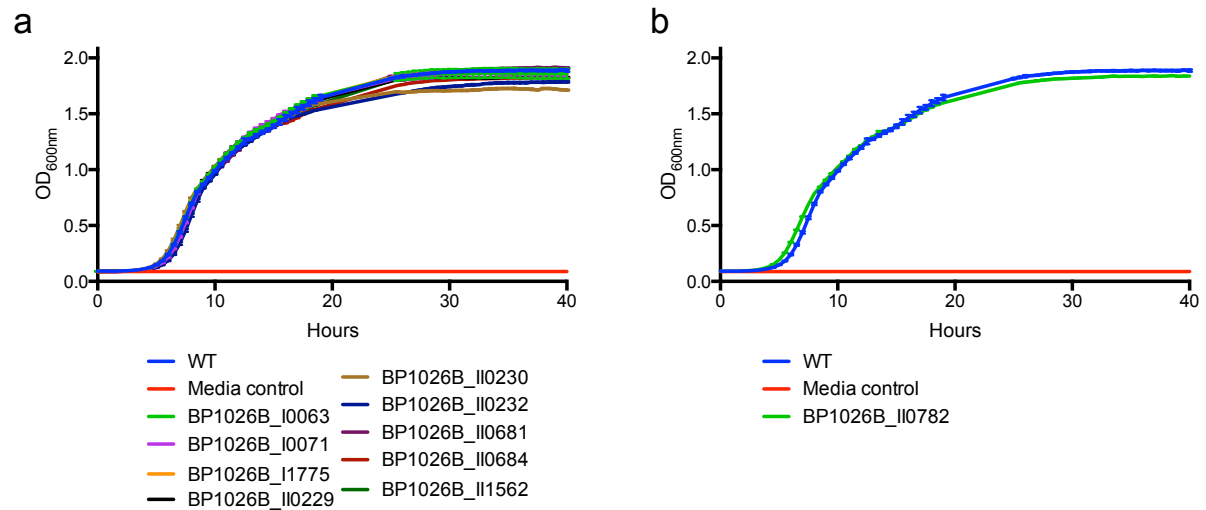
Supplemental Figure 1| WoPPER analysis reveals 40 gene clusters regulated by BP1026B_II1561 on *Bp* 1026b chromosome I. a) Circular map of *Bp* 1026b chromosome I showing up-regulated (yellow) and down-regulated (blue) gene clusters of BP1026B_II1561. Outer circle is the plus strand (dark grey) and inner circle is negative strand (light grey). b) Linear map of BP1026B_II1561 regulated gene clusters showing the mean \log_2FC of each cluster verses its position on chromosome I. The orange line represents the plus strand and the blue line represents the negative strand. Size of each gene cluster circle represents the number of genes within that given cluster. c) Table summarizing the gene clusters regulated by BP1026B_II1561.



c

Cluster	Start Coordinates	End Coordinates	Strand	Gene ID	Expression
1	24146	29691	+	BP1026B_I0026;BP1026B_I0027;BP1026B_I0028;BP1026B_I0029;BP1026B_I0031	DOWN
2	94352	125583	+	BP1026B_I0084;BP1026B_I0085;BP1026B_I0088;BP1026B_I0091;BP1026B_I0093;BP1026B_I0098;BP1026B_I0099;BP1026B_I0100;BP1026B_I0102;BP1026B_I0103;BP1026B_I0104;BP1026B_I0105;BP1026B_I0106;BP1026B_I0107;BP1026B_I0108;BP1026B_I0109;BP1026B_I0110;BP1026B_I0111	DOWN
3	99792	142814	-	BP1026B_I0090;BP1026B_I0092;BP1026B_I0094;BP1026B_I0096;BP1026B_I0097;BP1026B_I0101;BP1026B_I0116;BP1026B_I0117;BP1026B_I0118;BP1026B_I0119;BP1026B_I0120;BP1026B_I0121;BP1026B_I0122;BP1026B_I0124	DOWN
4	269328	289984	+	BP1026B_I0224;BP1026B_I0225;BP1026B_I0229;BP1026B_I0230;BP1026B_I0231;BP1026B_I0232;BP1026B_I0234;BP1026B_I0235;BP1026B_I0236;BP1026B_I0237;BP1026B_I0238	DOWN
5	323939	337210	+	BP1026B_I0265;BP1026B_I0266;BP1026B_I0274;BP1026B_I0275;BP1026B_I0276	UP
6	374520	458474	-	BP1026B_I0307;BP1026B_I0308;BP1026B_I0310;BP1026B_I0311;BP1026B_I0312;BP1026B_I0314;BP1026B_I0318;BP1026B_I0319;BP1026B_I0324;BP1026B_I0325;BP1026B_I0327;BP1026B_I0328;BP1026B_I0329;BP1026B_I0330;BP1026B_I0331;BP1026B_I0332;BP1026B_I0333;BP1026B_I0334;BP1026B_I0335;BP1026B_I0336;BP1026B_I0337;BP1026B_I0338;BP1026B_I0339;BP1026B_I0340;BP1026B_I0348;BP1026B_I0349;BP1026B_I0350;BP1026B_I0356;BP1026B_I0357;BP1026B_I0358	UP
7	377577	439709	+	BP1026B_I0309;BP1026B_I0313;BP1026B_I0315;BP1026B_I0316;BP1026B_I0317;BP1026B_I0320;BP1026B_I0321;BP1026B_I0322;BP1026B_I0323;BP1026B_I0326;BP1026B_I0341;BP1026B_I0342	UP
8	442157	474765	+	BP1026B_I0344;BP1026B_I0345;BP1026B_I0346;BP1026B_I0347;BP1026B_I0351;BP1026B_I0352;BP1026B_I0353;BP1026B_I0354;BP1026B_I0355;BP1026B_I0362;BP1026B_I0363;BP1026B_I0364;BP1026B_I0365;BP1026B_I0366;BP1026B_I0371;BP1026B_I0370;BP1026B_I0372	UP
9	529475	542392	+	BP1026B_I0429;BP1026B_I0430;BP1026B_I0431;BP1026B_I0433;BP1026B_I0435;BP1026B_I0436;BP1026B_I0439	DOWN
10	535197	571714	-	BP1026B_I0432;BP1026B_I0434;BP1026B_I0437;BP1026B_I0438;BP1026B_I0446;BP1026B_I0448;BP1026B_I0449;BP1026B_I0450;BP1026B_I0456;BP1026B_I0457;BP1026B_I0458;BP1026B_I0459	DOWN
11	551683	554448	+	BP1026B_I0452;BP1026B_I0453;BP1026B_I0454;BP1026B_I0455	DOWN
12	583763	596567	+	BP1026B_I0469;BP1026B_I0470;BP1026B_I0471;BP1026B_I0472;BP1026B_I0473;BP1026B_I0474;BP1026B_I0475;BP1026B_I0476;BP1026B_I0477;BP1026B_I0478;BP1026B_I0479;BP1026B_I0480	DOWN
13	620528	632482	+	BP1026B_I0502;BP1026B_I0504;BP1026B_I0505;BP1026B_I0506;BP1026B_I0507;BP1026B_I0508;BP1026B_I0509;BP1026B_I0510;BP1026B_I0511;BP1026B_I0512;BP1026B_I0513;BP1026B_I0514	UP
14	783879	797131	-	BP1026B_I0631;BP1026B_I0632;BP1026B_I0639;BP1026B_I0641;BP1026B_I0642;BP1026B_I0643	UP
15	800331	818579	+	BP1026B_I0645;BP1026B_I0646;BP1026B_I0647;BP1026B_I0648;BP1026B_I0649;BP1026B_I0650;BP1026B_I0651;BP1026B_I0652	UP
16	834697	864763	+	BP1026B_I0670;BP1026B_I0681;BP1026B_I0683;BP1026B_I0682;BP1026B_I0684;BP1026B_I0685;BP1026B_I0686;BP1026B_I0690;BP1026B_I0691;BP1026B_I0694	DOWN
17	891031	911114	+	BP1026B_I0720;BP1026B_I0721;BP1026B_I0722;BP1026B_I0723;BP1026B_I0725;BP1026B_I0726;BP1026B_I0729;BP1026B_I0730;BP1026B_I0731;BP1026B_I0732;BP1026B_I0733;BP1026B_I0734;BP1026B_I0736;BP1026B_I0738;BP1026B_I0740;BP1026B_I0741	DOWN
18	894813	913775	-	BP1026B_I0724;BP1026B_I0727;BP1026B_I0728;BP1026B_I0735;BP1026B_I0737;BP1026B_I0739;BP1026B_I0743	DOWN
19	1041069	1061923	+	BP1026B_I0848;BP1026B_I0849;BP1026B_I0852;BP1026B_I0853;BP1026B_I0851;BP1026B_I0855;BP1026B_I0857;BP1026B_I0859;BP1026B_I0858;BP1026B_I0860;BP1026B_I0861;BP1026B_I0862;BP1026B_I0864;BP1026B_I0865;BP1026B_I0866	UP
20	1058329	1083898	-	BP1026B_I0863;BP1026B_I0875;BP1026B_I0876;BP1026B_I0877;BP1026B_I0878;BP1026B_I0879;BP1026B_I0880;BP1026B_I0884	DOWN
21	1117827	1132188	-	BP1026B_I0907;BP1026B_I0911;BP1026B_I0912;BP1026B_I0913;BP1026B_I0916;BP1026B_I0918;BP1026B_I0920;BP1026B_I0921;BP1026B_I0922	UP
22	1288775	1294261	-	BP1026B_I1062;BP1026B_I1065;BP1026B_I1066	UP
23	1321796	1331951	-	BP1026B_I1090;BP1026B_I1091;BP1026B_I1092;BP1026B_I1093;BP1026B_I1094;BP1026B_I1095;BP1026B_I1096;BP1026B_I1097;BP1026B_I1098;BP1026B_I1099;BP1026B_I1101	DOWN
24	1391271	1393392	-	BP1026B_I1109;BP1026B_I1110;BP1026B_I1111	UP
25	1467188	1470483	-	BP1026B_I1178;BP1026B_I1180;BP1026B_I1181	UP
26	1476021	1481920	+	BP1026B_I1184;BP1026B_I1185;BP1026B_I1186;BP1026B_I1187;BP1026B_I1188;BP1026B_I1189	UP
27	1567554	1634866	-	BP1026B_I1258;BP1026B_I1259;BP1026B_I1260;BP1026B_I1261;BP1026B_I1262;BP1026B_I1263;BP1026B_I1264;BP1026B_I1265;BP1026B_I1266;BP1026B_I1267;BP1026B_I1268;BP1026B_I1269;BP1026B_I1273;BP1026B_I1278;BP1026B_I1279;BP1026B_I1280;BP1026B_I1281;BP1026B_I1282;BP1026B_I1283;BP1026B_I1284;BP1026B_I1295;BP1026B_I1300;BP1026B_I1301;BP1026B_I1304	DOWN
28	1669880	1672481	+	BP1026B_I1329;BP1026B_I1332	UP
29	1676308	1689624	-	BP1026B_I1334;BP1026B_I1335;BP1026B_I1336;BP1026B_I1339;BP1026B_I1340;BP1026B_I1345	UP
30	1852747	1860940	+	BP1026B_I1464;BP1026B_I1469;BP1026B_I1470;BP1026B_I1472;BP1026B_I1471;BP1026B_I1473	UP
31	1885275	1891541	+	BP1026B_I1492;BP1026B_I1493;BP1026B_I1494;BP1026B_I1495;BP1026B_I1496;BP1026B_I1497;BP1026B_I1498	DOWN
32	1940433	1944617	-	BP1026B_I1534;BP1026B_I1535;BP1026B_I1536;BP1026B_I1537	DOWN
33	1967614	1996059	+	BP1026B_I1553;BP1026B_I1554;BP1026B_I1558;BP1026B_I1559;BP1026B_I1560;BP1026B_I1561;BP1026B_I1562;BP1026B_I1567;BP1026B_I1568;BP1026B_I1569;BP1026B_I1571;BP1026B_I1572;BP1026B_I1574;BP1026B_I1576;BP1026B_I1577;BP1026B_I1578	UP
34	2017814	2027829	+	BP1026B_I1595;BP1026B_I1596;BP1026B_I1597;BP1026B_I1598;BP1026B_I1599;BP1026B_I1600;BP1026B_I1602	UP
35	2104407	2133113	-	BP1026B_I1677;BP1026B_I1678;BP1026B_I1679;BP1026B_I1681;BP1026B_I1682;BP1026B_I1683;BP1026B_I1684;BP1026B_I1685;BP1026B_I1686;BP1026B_I1687;BP1026B_I1688;BP1026B_I1689;BP1026B_I1693;BP1026B_I1694;BP1026B_I1699	UP
36	2168126	2170715	+	BP1026B_I1733;BP1026B_I1734;BP1026B_I1735;BP1026B_I1736;BP1026B_I1738	UP
37	2186351	2220222	-	BP1026B_I1743;BP1026B_I1744;BP1026B_I1745;BP1026B_I1746	DOWN
38	2343359	2375470	+	BP1026B_I1852;BP1026B_I1857;BP1026B_I1858;BP1026B_I1859;BP1026B_I1864;BP1026B_I1870;BP1026B_I1878;BP1026B_I1879;BP1026B_I1880	DOWN
39	2414082	2416799	+	BP1026B_I1915;BP1026B_I1916;BP1026B_I1917;BP1026B_I1918	UP
40	2448471	2457240	-	BP1026B_I1950;BP1026B_I1951;BP1026B_I1953;BP1026B_I1956;BP1026B_I1957;BP1026B_I1958;BP1026B_I1959	DOWN
41	2487404	2505816	-	BP1026B_I1984;BP1026B_I1985;BP1026B_I1986;BP1026B_I1987;BP1026B_I1988;BP1026B_I1989;BP1026B_I1992;BP1026B_I1994;BP1026B_I1996;BP1026B_I2002	UP
42	2499725	2502336	+	BP1026B_I1995;BP1026B_I1997	UP
43	2735746	2792668	-	BP1026B_I2205;BP1026B_I2207;BP1026B_I2209;BP1026B_I2210;BP1026B_I2211;BP1026B_I2213;BP1026B_I2214;BP1026B_I2217;BP1026B_I2218;BP1026B_I2220;BP1026B_I2221;BP1026B_I2223;BP1026B_I2224;BP1026B_I2245;BP1026B_I2246;BP1026B_I2247;BP1026B_I2248;BP1026B_I2250	DOWN
44	2760314	2791272	+	BP1026B_I2216;BP1026B_I2221;BP1026B_I2228;BP1026B_I2233;BP1026B_I2235;BP1026B_I2236;BP1026B_I2238;BP1026B_I2239;BP1026B_I2249	DOWN
45	2889411	2903969	-	BP1026B_I2327;BP1026B_I2328;BP1026B_I2329;BP1026B_I2332;BP1026B_I2338;BP1026B_I2339	UP
46	2967523	2970419	+	BP1026B_I2399;BP1026B_I2400;BP1026B_I2402;BP1026B_I2403	UP
47	2974712	3001078	-	BP1026B_I2408;BP1026B_I2409;BP1026B_I2410;BP1026B_I2411;BP1026B_I2412;BP1026B_I2413;BP1026B_I2414;BP1026B_I2415;BP1026B_I2416;BP1026B_I2419;BP1026B_I2422;BP1026B_I2424;BP1026B_I2425;BP1026B_I2426;BP1026B_I2427;BP1026B_I2428;BP1026B_I2429;BP1026B_I2430;BP1026B_I2431;BP1026B_I2432	UP
48	3067872	3080761	-	BP1026B_I2482;BP1026B_I2483;BP1026B_I2484;BP1026B_I2485;BP1026B_I2487;BP1026B_I2488;BP1026B_I2489;BP1026B_I2490;BP1026B_I2491;BP1026B_I2492	UP
49	3094482	3103841	-	BP1026B_I2505;BP1026B_I2506;BP1026B_I2507;BP1026B_I2508	UP
50	3129738	3136611	-	BP1026B_I2528;BP1026B_I2531;BP1026B_I2535;BP1026B_I2536	DOWN

Supplemental Figure 2| WoPPER analysis reveals 50 gene clusters regulated by BP1026B_II1561 on *Bp* 1026b chromosome II. a) Circular map of *Bp* 1026b chromosome II showing up-regulated (yellow) and down-regulated (blue) gene clusters of BP1026B_II1561. Outer circle is the plus strand (dark grey) and inner circle is negative strand (light grey). b) Linear map of BP1026B_II1561 regulated gene clusters showing the mean \log_2FC of each cluster verses its position on chromosome II. The orange line represents the plus strand and the blue line represents the negative strand. Size of each gene cluster circle represents the number of genes within that given cluster. c) Table summarizing the gene clusters regulated by BP1026B_II1561 on chromosome II.



Supplemental Figure 3| Growth analysis of transposon mutants compared to wildtype *Bp* 1026b. a) Mutants indirectly controlled by BP1026B_II1561 that show defects during intracellular replication (Fig. 4b-c) were tested for their ability to grow in LB. All mutants showed identical growth patterns to wildtype *Bp* 1026b (WT) indicating that the defects during intracellular infection were not due to a defect in fitness. b) A BP1026B_II0782 showed a significant defect during intracellular pathogenesis (Fig. 6d-e) and shows no defect in fitness.

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Chapter 4:

Identification of BP1026B_II2312, a *Burkholderia pseudomallei* Regulator of Intracellular Pathogenesis

Abstract

Burkholderia pseudomallei (*Bp*) lives a complex lifecycle within host cells leading to the disease melioidosis. Melioidosis occurs in tropical and sup-tropical regions around the world and presents diverse clinical symptoms making diagnosis difficult. The *Bp* intracellular lifecycle is partially elucidated and has been probed for novel therapeutic targets and vaccines. Recently, the ‘*Bp* intracellular TRANSITome’ identified many genes that are differentially regulated during intracellular infection, suggesting that a complex regulation system is in place. BP1026B_II2312 is a putative transcriptional regulator that is differentially regulated during infection and important for *in vitro* and *in vivo* pathogenesis. In the present study, we characterized BP1026B_II2312 and its role during *Bp* pathogenesis by looking at the transcriptional landscape through RNA-seq and the direct DNA regions through ChIP-seq. This reveals that during initial stages of infection *Bp* undergoes a stringent-like response to conserve energy and allow infection to proceed. In addition, BP1026B_II2312 up-regulates a gene encoding isochroismatase that is a rational target for development of novel therapeutics.

Introduction

Burkholderia pseudomallei (*Bp*) is a Gram-negative facultative intracellular pathogen that is found throughout the tropics and causes the disease melioidosis¹. Melioidosis presents with a diverse set of clinical manifestations that often lead to misdiagnosis^{2, 3}. *Bp* infects humans and animals through the inoculation of skin lesions, ingestion of contaminated water and food, or inhalation⁴. The global distribution of melioidosis has increased in recent years due to an increase in awareness and is now predicted to cause ~89,000 deaths annually⁵. To compound this, previous use of *Burkholderia mallei* (*Bm*), a clonal derivative of *Bp*, as a bioweapon has led to the classification of *Bp* as a Tier 1 select agent requiring strict regulations for the handling and manipulation of this pathogen^{6, 7}. For these reasons *Bp* is a major public health concern in endemic regions and for biodefense purposes. Treatment of *Bp* is through a two-phase antimicrobial therapy including an intensive intravenous phase and an oral eradication phase⁸. Although rare, antimicrobial resistance has developed during treatment^{9, 10} making the development of novel therapeutics and vaccines paramount.

In order to develop novel therapeutics and vaccines, it is critical to understand the mechanisms that *Bp* uses to cause infection. *Bp* initiates infection by attaching to host cells, gaining entry via the endocytic pathway, and escaping into host cell cytoplasm using one of its type III secretion systems (T3SS-3)¹¹⁻¹³. *Bp* encodes two other T3SSs that have been tied to pathogenesis in *Solanum lycopersicum* (tomato plant)¹⁴ but are dispensable for mammalian pathogenesis¹⁵. Following cytoplasmic entry, *Bp* is able to move freely around the cytoplasm using the Ena/VASP mimicker BimA to polymerize host cell actin¹⁶ or its secondary lateral flagella locus on chromosome II¹¹. *Bp* spreads the infection by causing host cell fusion using one of its type VI secretion systems (T6SS)^{11, 17}. While we understand some of the *Bp* intracellular

lifecycle, there is much more that is unknown about this process making development of therapeutics and vaccines difficult. Recently, our group identified 1,953 genes that are differentially regulated during the intracellular lifecycle¹⁸. This indicates that a complex regulation system is place to coordinate the drastic transcriptional changes that *Bp* undergoes during infection. We identified 33 transcriptional regulators with no known function that have distinct expression patterns during the intracellular lifecycle. Understanding the function of these transcriptional regulators could lead to the identification of genes that are required for *Bp* pathogenesis giving further insight into the mechanisms of disease and eventually identify novel targets for the development of therapeutics and vaccines. Herein, we characterize BP1026B_II2312, a putative transcriptional regulator that is differentially expressed during the *Bp* intracellular lifecycle.

Results

BP1026B_I12312 is differentially regulated during intracellular infection

BP1026B_I12312 is predicted to be a LysR family transcriptional regulator on chromosome II of the *Bp* genome. When analyzing the transcriptomes of *Bp* as it transits through its intracellular lifecycle, BP1026B_I12312 is up regulated during the early stages of infection when *Bp* is within an endocytic vacuole (Fig. 1a)¹⁸. As *Bp* escapes the vacuole and moves into the cytoplasm, BP1026B_I12312 expression is reduced. We see the same trend as *Bp* starts to protrude towards neighboring cells (Fig. 1a). This gradual decrease in the expression of BP1026B_I12312 suggests that this transcriptional regulator is important for the *Bp* intracellular lifecycle. BP1026B_I12312 is 313 amino acids with a LysR-type helix-turn-helix domain between positions six and 63 with a YidZ-like substrate-binding domain between positions 98 and 296 that has been shown to be involved in anaerobic nitric oxide production^{19, 20}. BP1026B_I12312 has 471 ortholog group members suggesting that it could have functions in other *Burkholderia* species. We wanted to investigate the role that BP1026B_I12312 has during *Bp* intracellular infection.

BP1026B_I12312 is required for multinucleated giant cell formation, intracellular replication, and *in vivo* pathogenesis

To understand the role during intracellular pathogenesis, an in-frame deletion mutant of BP1026B_I12312 was made in *Bp* 1026b using lambda-red recombineering²¹. RAW264.7 murine macrophages were infected with wildtype *Bp* 1026b, the BP1026B_I12312 mutant, and an *in trans* complemented strain of the mutant (BP1026B_I12312 expression from pAM3GIQ-3xTY1-BP1026B_I12312). When infected with wildtype *Bp* 1026b, large multinucleated giant cells

(MNGCs) were formed averaging 356 μ m in diameter (Fig. 1b). RAW264.7 cells formed much smaller MNGCs when infected with the BP1026B_II2312 mutant, averaging 199 μ m in diameter (Fig. 1b). This defect was restored to wildtype levels in the complementation strain. The reduction in MNGC formation indicated that BP1026B_II2312 does have a critical role during the intracellular lifecycle. To determine if this defect is reflected on the intracellular burden during infection in RAW264.7 cells, an intracellular replication assay was carried out. The BP1026B_II2312 mutant showed significantly reduced levels of intracellular *Bp* at two, eight, and 24 hours post infection when compared to wildtype *Bp* while the complement recovered partially (Fig. 1c). To ensure that the defects seen during MNGC formation and intracellular replication are not due to reduced fitness, all strains were grown in LB broth and showed similar growth kinetics (Fig. 1d).

After defining a clear defect during cell culture infection in RAW264.7 cells, we wanted to see if BP1026B_II2312 had a role in *Bp* pathogenesis in BALB/c mice. Five BALB/c mice were infected intranasally with 4,500 colony-forming units (CFUs) of wildtype *Bp* 1026b and five mice with 4,500 CFUs of the BP1026B_II2312 mutant. Mice infected with wildtype *Bp* 1026b showed significant clinical signs of infection and showed 100% mortality by day four (Fig. 2a). On the other hand, BALB/c mice infected with the BP1026B_II2312 mutant showed fewer signs of infection and survived the duration of the study (Fig. 2a). Lungs, livers, and spleens of the surviving mice were harvested, homogenized, serially diluted, and plated on LB to determine if the BP1026B_II2312 mutant was cleared or if persistent infection can be detected. Three mice cleared the infection while one mouse had colonization in the lungs and another mouse showed colonization in the spleen (Fig. 2b). Taken together, the BP1026B_II2312 mutant

showed attenuation in RAW264.7 murine macrophages and BALB/c mice sparking increased interest in the function of this transcriptional regulator.

General metabolic functions and hypothetical genes are down-regulated by BP1026B_II2312

To further investigate the role of this transcriptional regulator during *Bp* intracellular pathogenesis, a vector expressing BP1026B_II2312, pAM3GIQ-3xTY1-BP1026B_II2312, was used to determine what changes occur to the transcriptional landscape of *Bp* 1026b in the presence of BP1026B_II2312. A corresponding empty vector, pAM3GIQ-3xTY1, was used as a control. Briefly, mRNA from the BP1026B_II2312 expressing strain and the empty vector control were sequenced in triplicate using the Illumina HiSeq2500 and analyzed using Rockhopper²². Overall, this data set represents the total BP1026B_II2312 regulon as all genes directly and indirectly controlled will be observed (Fig. 3b, Table S1). Genes with a q-value < 0.01 and a log₂ fold-change (log₂FC) of ≥ 1 or ≤ -1 were selected for further analysis by looking at COG functional predictions (Fig. 3a). This subset of genes includes 41 that are up-regulated and 315 that are down-regulated suggesting that the main role of BP1026B_II2312 is to turn off cellular functions (Fig. 3a). Some general metabolic pathways like lipid, carbohydrate, amino acid, and nucleotide transport and metabolism are all down-regulated by BP1026B_II2312 (Fig. 3a). In addition to this, transcription, translation, and DNA repair/replication/recombination are also significantly down-regulated indicating that BP1026B_II2312 could be important for stringent-like response. This could fit into our current understanding of the overall *Bp* lifecycle as BP1026B_II2312 is up-regulated in the host cell vacuole, a nutrient limited niche, followed by down-regulation of BP1026B_II2312 during cytoplasmic replication, a nutrient rich

environment. In addition to this observation, it is interesting to note that approximately 80% of the up-regulated genes and 36% of the down-regulated genes are annotated as hypothetical or uncharacterized (Fig. 3a). The functions of these genes during pathogenesis are of great interest in the ongoing endeavor to fully understand *Bp* pathogenesis.

WoPPER²³ analysis was used to visualize broad regions of the genome that are activated and repressed by BP1026B_II2312 to gain a broader perspective. Overall, 45 and 29 gene clusters were differentially regulated on chromosomes I and II, respectively (Fig. S1, Fig. S2). BP1026B_II2312 down-regulates 27 gene clusters and up-regulates 18 gene clusters on chromosome I (Fig. S1). A similar trend is seen on chromosome II with 19 gene clusters being down-regulated while 10 gene clusters are up-regulated (Fig. S2). This coincides with the observation seen earlier where the majority of the genes controlled by BP1026B_II2312 are repressed (Fig. 3a). Some of the gene clusters regulated encode characterized or partially characterized functions. Cluster 24 on chromosome I is down-regulated by BP1026B_II2312 and encodes genes for the production of malleobactin, a siderophore that is dispensable for *in vivo* infection (Fig. S1)^{24, 25}. Another siderophore, pyochelin, is also down-regulated in cluster 10 on chromosome II (Fig. S2). An unknown non-ribosomal peptide synthase (NRPS) is down-regulated by BP1026B_II2312 on chromosome I (cluster 14, Fig. S1)²⁶. Another interesting secondary metabolite that is also down-regulated is found in clusters 22 and 23 on chromosome I (Fig. S1). This secondary metabolite is a NRPS that is required for pathogenesis but its structure has not yet been solved²⁶. One T6SS (BP1026B_II0573-II0590) that has not been connected to mammalian pathogenesis is partially up-regulated by BP1026B_II2312 (cluster 9, Fig. S2). BP1026B_II2312 appears to regulate all three T3SSs on chromosome II, through the up-regulation of T3SS-1 and T3SS-3, and down-regulation of T3SS-2 (Fig. S2). T3SS-3 is well

established as an important virulence factor for vacuole escape while T3SS-1 and T3SS-2 have only been tied to pathogenesis in plants^{11, 12, 14}. The most up-regulated gene cluster throughout the genome is cluster 26 on chromosome II, a region that includes BP1026B_II2312 suggesting localized regulation is occurring (Fig. S2).

BP1026B_II2312 controls genes that have potential roles during intracellular pathogenesis

To step beyond the broad effects of BP1026B_II2312 expression on the *Bp* genome a more targeted approach was used to identify genes that play a role in pathogenesis. Genes with a \log_2FC of ≥ 2 or ≤ -2 were targeted and T24 transposon mutants of these genes selected from the sequence-defined transposon mutant library of *Bp* 1026b²⁷. Of the 27 genes that fit this criteria, nine had no T24 mutant within the library suggesting that these genes are essential for *Bp* survival. Three genes are up-regulated and 24 genes are down-regulated by BP1026B_II2312 fitting with the trend that this transcriptional regulator is a repressor (Fig. 4a). Mutants present in the T24 library were purified and the transposon genome junction was confirmed by sequencing (data not shown). Mutants were used to infect RAW264.7 cells and compared to wildtype *Bp* 1026b intracellular replication at 24 hours to indicate any defects during pathogenesis (Fig. 4b). Eighteen T24 mutants were tested and of these, 13 showed defects during intracellular replication while five down-regulated genes, BP1026B_II0231, BP1026B_II0682, BP1026B_II0683, BP1026B_II0685, and BP1026B_II0686 replicated at 84-101% of wildtype *Bp* 1026b (Fig. 4a-c).

Genes involved in general metabolic pathways that are down-regulated by BP1026B_II2312 also showed defects during intracellular replication. BP1026B_I0064 encodes acetyl-CoA acetyltransferase that is involved in fatty acid metabolism and replicates at 77% of

wildtype *Bp* 1026b (Fig. 4b-c). Similarly, BP1026B_II0229, BP1026B_II0230, and BP1026B_II0232 are involved in propanoate metabolism, breaking down propanoyl-CoA to succinate and pyruvate, and are down regulated by BP1026B_II2312 (Fig. 4a). The mutants of BP1026B_II0229, BP1026B_II0230, and BP1026B_II0232 replicate at 26-59% of wildtype *Bp* 1026b suggesting a role for these genes in pathogenesis (Fig. 4b-c). While BP1026B_II0231 replicates at 84% of wildtype *Bp* 1026b, it is also involved in the breakdown of propanoyl-CoA to succinate and pyruvate but the data suggests that this gene is less critical during intracellular replication than the others (Fig. 4b-c). BP1026B_II0681 encodes acyl-CoA dehydrogenase, an enzyme for initial steps in β -oxidation of fatty acids, and replicates 61% of wildtype *Bp* 1026b (Fig. 4b-c). BP1026B_II0684 encodes 3-hydroxyisobutyrate dehydrogenase and is utilized in the degradation of valine, leucine, and isoleucine by breaking down 3-hydroxyisobutyrate to methylmalonate semialdehyde (Fig. 4c). This product can be further broken down into propanoyl-CoA that can feed into propanoate metabolic pathways leading to break down by BP1026B_II0229-II0232²⁸. BP1026B_II1473 is annotated as the E1 subunit beta of a pyruvate/2-oxoglutarate dehydrogenase, part of the citric acid cycle, although homologs in other *Burkholderia* species show that this protein has no known function¹⁹. A mutant of BP1026B_II1473 replicates at 62% of wildtype indicating its importance during intracellular infection (Fig. 4b-c). An ATP binding protein portion of an ABC transporter, BP1026B_II0649, replicates at 74% of wildtype *Bp* 1026b and is down-regulated by BP1026B_II2312 (Fig. 4a-c). This gene sits within the secondary metabolic gene cluster responsible for generating the siderophore pyochelin²⁶. Although pyochelin has been shown to be dispensable for mammalian pathogenesis²⁵, a role during cell culture infection has not been established to our knowledge.

Beyond the genes that have a known function or show similarity to genes that have been characterized elsewhere, several hypothetical proteins are regulated by BP1026B_II2312 and have roles in the pathogenesis of RAW264.7 murine macrophages. BP1026B_II1723 is down-regulated by BP1026B_II2312 and is annotated as a hypothetical protein (Fig. 4a, Fig. 4c). A BP1026B_II1723 mutant replicates at 70% of wildtype *Bp* 1026b suggesting that this protein is important for intracellular survival and/or pathogenesis (Fig. 4b-c). BP1026B_II0904 is down-regulated by BP1026B_II2312 and annotated as a hypothetical protein (Fig. 4a, Fig. 4c). A transposon mutant of BP1026B_II0904 was only able to replicate at 45% of wildtype *Bp* 1026b in RAW264.7 macrophages (Fig. 4b-c). BP1026B_II2312 also down-regulates the hypothetical protein BP1026B_II2475 with a putative serine hydrolase domain between amino acids eight and 181 (Fig. 4a)¹⁹. The T24 mutant of BP1026B_II2475 replicates at 61% of wildtype *Bp* 1026b further implicating its importance during intracellular pathogenesis (Fig. 4b-c). BP1026B_II2321 and BP1026B_II2323 encode a hypothetical protein and a IclR family transcriptional regulator, respectively, and are up-regulated by BP1026B_II2312 (Fig. 4a). These two genes are located close to BP1026B_II2312 on the genome and are also defective in intracellular pathogenesis, replicating at 42% and 73% of wildtype *Bp* 1026b, respectively (Fig. 4b-c). While BP1026B_II2323 likely controls the transcription of other genes, BP1026B_II2321 has no known function but does contain a putative kynurenine formamidase domain that could be involved in aerobic tryptophan degradation²⁹. All mutants tested in the intracellular replication assay showed no defect during *in vitro* growth indicating that defects in pathogenesis are not due to defects in fitness (Fig. S3a). Taken together, BP1026B_II2312 down-regulates 11 genes and up-regulates two genes that contribute to the pathogenesis of *Bp* 1026b in murine macrophages (Fig. 4d).

BP1026B_I12312 binds 11 regions on the *Bp* genome

To better understand the role of BP1026B_I12312 during pathogenesis we used a ChIP-seq approach to determine the direct DNA binding regions of this transcriptional regulator. The same conditions used for the transcriptional analysis through RNA-seq were used to allow comparisons to be made between the two data sets. The vector pAM3GIQ-3xTY1-BP1026B_I12312 was used to express BP1026B_I12312 in *Bp*, the resulting cells were fixed with paraformaldehyde, cells were lysed, and DNA-protein complexes were sheered using a Covaris M220 ultrafocused sonicator. DNA-BP1026B_I12312 complexes were enriched using an anti-TY1-tag monoclonal antibody and magnetic separation. The resulting sample was compared to an empty vector control that was treated identically after Illumina sequencing on the HiSeq 2500. Analysis was carried out by aligning the sequence reads to the *Bp* 1026b genome with Bowtie2³⁰ and subsequent peak calling with MACS2³¹. BP1026B_I12312 binds to many regions of DNA on the *Bp* 1026b genome throughout both chromosomes (Fig. 5a-b). The more significant peaks were determined by comparing the fold enrichment and the $-\log_{10}$ q-value, identifying 11 peaks of interest (Fig. 5c). A consensus DNA binding domain was determined using MEME³² (Fig. 5d). The sequence contains a total of 17 base pairs with four and two base pairs of 100% homology on the flanking regions (Fig. 5d). This region is likely responsible to be a region of direct BP1026B_I12312 binding leading to transcriptional activation or repression.

Genes directly controlled by BP1026B_I12312 contribute to intracellular pathogenesis

BP1026B_I12312 binds to many regions of DNA throughout the entire *Bp* genome. One is a 370 base pair region downstream of BP1026B_I12312 that leads to localized gene expression

(Fig. 6a). BP1026B_II2312 binds directly in front of BP1026B_II2319 and drives expression of BP1026B_II2319-II2317 with an average log₂FC of 5.7(Fig. 6b, Table S1). It is likely that BP1026B_II2312 also drives transcription of BP1026B_II2316-II2313 as well although with a different level of expression at an average log₂FC of 3.55 (Fig. 6b, Table S1). These seven genes appear to be directly controlled by BP1026B_II2312 and are highly activated as well. To determine if any of these genes have a role during pathogenesis we tested the T24 mutants in their ability to infect RAW264.7 murine macrophages.

BP1026B_II2315 encodes a putative citrate lyase and replicates at 84% of wildtype *Bp* 1026b (Fig. 6c-d). Citrate lyase is essential for citrate fermentation and has also been tied to survival of *Yersinia pestis* and *Mycobacterium tuberculosis* through reducing oxidative stress^{33, 34}. Although BP1026B_II2315 doesn't appear to be critical for pathogenesis on its own, there are other putative citrate lyases that are indirectly up-regulated by BP1026B_II2312 suggesting a duplication of function that could compensate for the mutation of BP1026B_II2315 (Table S1). BP1026B_II2319 encodes a major facilitator superfamily (MFS) transporter that sits in the cytoplasmic membrane and replicates at 73% of wildtype *Bp* 1026b (Fig. 6c-d). BP1026B_II2317 is annotated as a zinc-binding dehydrogenase that replicates at 69% of wildtype *Bp* 1026b (Fig. 6c-d). BP1026B_II2313 is annotated as a hypothetical protein but has a putative kynurenine formamidase domain similar to BP1026B_II2321 that is also up-regulated by BP1026B_II2312 (Fig. 4c). BP1026B_II2313 replicates at 64% of wildtype *Bp* 1026b in RAW264.7 cells indicating its importance during infection (Fig. 6c-d). BP1026B_II2313 and BP1026B_II2321 are 99.7% identical on the amino acid level suggesting similar functions. While single T24 mutants in both genes lead to defects during intracellular replication, it is

interesting to see that there is a 22% difference in their intracellular replication patterns (Fig. 4c, Fig. 6d).

Isochorismatases have been identified to be important for *Verticillium dahlia* virulence in *Solanum tuberosum* and in the production of phenazines in *Pseudomonas aeruginosa*^{35, 36}. The T24 mutant of BP1026B_II2318, a putative isochorismatase, replicates at 63% of wildtype *Bp* 1026b suggesting a role in pathogenesis (Fig. 6c-d). Based on what we know about isochorismatases, BP1026B_II2318 likely generates intermediates that lead to downstream products that cause this decrease in intracellular replication. BP1026B_II2314 encodes a 2-methylcitrate dehydratase (PrpD) and a citrate/2-methylcitrate dehydratase (MmgE) that is potentially involved in propanoate metabolism. As noted before, genes involved in propanoate metabolism have been tied to pathogenesis in *Bp* (Fig. 4b-c). Similarly, a mutant in BP1026B_II2314 was reduced to 51% of wildtype *Bp* 1026b replication in RAW264.7 cells indicating that propionate metabolism is critical for *Bp* pathogenesis (Fig. 6c-d). A transposon mutant in BP1026B_II2316 showed the largest decrease in intracellular replication when compared to *Bp* 1026b at 45% wildtype replication (Fig. 6c-d). This gene encodes acyl-CoA transferase/carnitine dehydratase protein likely involved in fatty acid metabolism and/or lysine degradation²⁸. The transposon mutants for BP1026B_II2313, BP1026B_II2314, BP1026B_II2316, BP1026B_II2317, and BP1026B_II2318 grow identical to wildtype *Bp* 1026b indicating that the defects during intracellular infection are due to decreased ability to survive within the host cell (Fig. S3b). Taken together, BP1026B_II2312 activates genes locally that contribute to the pathogenesis of *Bp* (Fig. 6e).

Discussion

To combat the disease melioidosis, we must first understand how *Bp* causes disease on the molecular level. Many advances in understanding the intracellular lifecycle of *Bp* have been made over the last two decades. However, the complexity that *Bp* uses to navigate the various environments within the host cell has yet to be fully characterized. The identification of 1,953 genes that are transcriptionally controlled in a stage specific manner highlights this complex nature and hints at a sophisticated regulation network that is used to coordinate infection¹⁸. In the present study, we sought to characterize a transcriptional regulator that is differentially expressed during the intracellular lifecycle. BP1026B_II2312 is up-regulated in the vacuole stage of infection and its expression decreases as *Bp* transits through the host cell. This indicates that the main function of BP1026B_II2312 is during the initial stages of infection. A mutant of BP1026B_II2312 is deficient in intracellular infection and *in vivo* pathogenesis suggesting that the genes controlled by this transcriptional regulator contribute to virulence.

The indirect and direct regulation networks of BP1026B_II2312 were determined using RNA-seq and ChIP-seq approaches, identifying a large array of repressed pathways. Although we only see slight transcriptional changes in *relA* and *spoT* (Table S1), this large down-regulation of pathways indicates a stringent-like response that *Bp* may undergo at the initial stages of infection to conserve energy. Down-regulation of lipid, carbohydrate, amino acid, nucleotide transport and metabolism, and transcription, translation, DNA repair/replication/recombination would suggest that *Bp* senses a nutrient-limited environment and is accounting for that on the transcriptional level. This fits the general trend of a stringent-like response that dictates a ‘feast or famine’ life style³⁷. In the case of *Bp* it is likely a shift in energy towards virulence mechanisms allowing successful host cell infection and thereby

gaining entry into the nutrient rich cytoplasm. In addition to this, we see that many genes that are highly regulated by BP1026B_I2312 are involved in general metabolic functions. Mutants of these genes are decreased in their ability to infect RAW264.7 cells indicating that these pathways are important during pathogenesis.

The BP1026B_I2312 regulation network also identified several genes that are up-regulated and may be good therapeutic targets. BP1026B_I2312 up-regulates a citrate lyase, BP1026B_I2315. A mutant of BP1026B_I2315 doesn't show a drastic change in intracellular replication likely due to gene duplication, as is seen in *M. tuberculosis*, but does have potential as a therapeutic target³⁴. Isochorismatase catalyzes the reaction of isochorismate to 2,3-dihydro-2,3-dihydroxybenzoate during synthesis of non-ribosomal peptides and siderophores^{28, 38, 39}. Isochorismatases have been identified as virulence factors in other organisms including PhzD in closely related *P. aeruginosa*³⁵ and no known homologs are found in humans⁴⁰. The structure of BTH_I2229 of *Burkholderia thailandensis*, a non-virulent relative of *Bp*, has been solved and is a homolog of BP1026B_I2318 with 96.9% amino acid identity and 100% coverage. Here we identified that BP1026B_I2318 is also involved during *Bp* pathogenesis. Taken together, the pathogenic role of BP1026B_I2318 combined with the structural information provided by its homolog, BTH_I2229, makes this enzyme a rational drug target for the design of novel melioidosis therapies.

In conclusion, these findings suggest an intricate role of BP1026B_I2312 during the intracellular pathogenesis of *Bp*. The loss of BP1026B_I2312 leads to a complete attenuation in BALB/c mice, and this is likely due to many transcriptional changes. This is one piece of a very large puzzle and suggests that further investigation into the transcriptional networks of regulators

should be pursued in the effort to completely understand *Bp* pathogenesis, identify novel therapeutic targets, and develop vaccines to combat melioidosis.

Methods and Materials

Bacterial strains, media and culture conditions *Escherichia coli* strains for manipulation of *Bp* were used as previously described^{41, 42}. Luria-Bertani (LB) medium (Difco) or 1x M9 minimal medium supplemented with 20 mM glucose (MG) were used to culture all strains. Glyphosate (0.3%) was used in MG media when appropriate. *Bp*82 was used where appropriate to replace *Bp* 1026b. All experiments involving *Bp* 1026b were conducted in a CDC-approved and registered facility at the University of Hawai‘i at Mānoa or Colorado State University with prior approval by internal review and adhere to recommendations set forth in the BMBL, 5th edition⁴³ for BSL3 organisms.

Molecular methods and reagents Molecular methods and reagents were used as described previously^{42, 44-46}. An in-frame deletion mutant of BP1026B_II2312 was generated using lambda-red recombineering with minor modification²¹. Lambda red genes were PCR amplified from pKaKa1 and co-incubated with the knockout fragment of BP1026B_II2312. BP1026B_II2312 was PCR amplified with oligos 2692 (5'- AAT CCA TAT GAA TCT ACG CTC GAT CGA) and 2693 (5'- ATA AGC TTG CGA TAT GCG ATA TGC GAT) digested with *NdeI* and *HindIII* and ligated into *NdeI/HindIII*-cut pAM3GIQ-3xTY1. Confirmation of pAM3GIQ-3xTY1-BP1026B_II2312, was done by *NdeI/HindIII* and *SspI* digests and expression of BP1026B_II2312 confirmed via western blot analysis.

Growth analysis All strains were grown overnight in LB broth at 37°C, harvested the following day, diluted to an OD₆₀₀ of 0.1 in 200µl of LB. Growth curves were done in 96 well plates at

37°C shaking and data was recorded with the BioTek ELx808IU plate reader, measurements taken at an OD₆₃₀ every 30 minutes.

Cell infection assays MNGC formation and intracellular replication assays were carried out as previously described with slight modification⁴⁷. RAW264.7 murine macrophages were seeded at 80-90% confluence on Corning CellBIND culture plates, incubated overnight for attachment, and washed with PBS prior to infection. Intracellular replication assays tested *Bp* 1026b, the BP1026B_II2312 mutant, or the BP1026B_II2312 complement (mutant with pAM3GIQ-3xTY1-BP1026B_II2312) for ability to infect monolayers at an MOI of 1:1 for one hour. After this cells were washed with PBS and DMEM supplemented with 10% FBS, 2.5mM IPTG (to drive expression of the complement), 700 µg/mL amikacin and 700 µg/mL kanamycin was added to monolayers. At 2, 8, and 24 hours post-infection, infected monolayers were lysed with 0.2% Triton X-100 and serial dilutions of lysates were plated on LB and colony-forming units (CFU) per well were determined. MNGC formation assays were carried out similarly, but 1.2% low-melt agarose was added to DMEM after infection. At 24 hours post-infection, monolayers were fixed with 4% paraformaldehyde, agarose plugs removed, stained with 0.05% crystal violet, and MNGC diameters measured with the Zeiss Axio Observer D1 and the AxioVision 64 bit 4.9.1 software. When mutants from the *Bp* 1026b::T24 transposon mutant library were tested for intracellular replication kanamycin was removed and amikacin added a final concentration of 1,500µg/mL. Monolayers were lysed at 24 hours post-infection as described above. All transposon mutants tested were confirmed to be in the gene of interest by sequencing.

RNA-seq and ChIP-seq analysis RNA-seq and ChIP-seq analysis were carried out under the same conditions. Briefly, *Bp*82 expressing BP1026B_I12312 was grown to mid-log phase in LB+adenine+0.1mM IPTG in triplicate. An empty vector (pAM3GIQ-3xTY1) was used as a control. Total RNA was harvested using RNeasy Mini Kit (Qiagen) with on-column (Qiagen) and off-column (Epicentre) DNase digestion steps. Library preparation and sequencing on the Illumina HiSeq2500 was carried out at Tufts University Genomics Core (TUCF Genomics). Fifty base pair single-end reads were sequenced and analyzed with Rockhopper²².

ChIP-seq was carried out as previously described but modified for *Burkholderia*^{48, 49}. Briefly, ChIP-seq samples, grown identically as RNA-seq samples, were harvested and fixed with 4% paraformaldehyde, followed by shearing of DNA-protein complexes with the Covaris M220 ultrafocused sonicator. Supernatant was used for immunoprecipitation with anti-TY1-tag monoclonal antibody targeting BP1026B_I12312-DNA complexes (Diagenode C15200054) and secondary antibodies conjugated to magnetic beads (Diagenode C03010022). DNA-BP1026B_I12312 complexes were washed, decrosslinked, treated with RNaseA and proteinase K, and purified with QIAquick PCR purification kit. The remaining DNA was sent to TUCF Genomics for library prep and sequencing. ChIP-seq data was aligned to the *Bp* 1026b genome with Bowtie2³⁰, peaks called with MACS2³¹, and consensus binding regions determined with MEME³².

Animal studies BALB/c mice between 4 and 6 weeks of age were purchased from Charles River Laboratory. Mice were infected via the intranasal (i.n.) inoculation route after being anesthetized with 100 mg of ketamine/kg of body weight plus 10 mg/kg xylazine. Mice were infected with 4,500 CFU of each *Bp* strain suspended in 20 µl of PBS. Each infection group contained five

mice. Animals were monitored daily and euthanized at predetermined humane end points. Lungs, liver, and spleen of surviving mice were harvested, homogenized, serially diluted, and plated on LB to determine bacterial burdens. Survival characteristics were plotted using Prism software (GraphPad, La Jolla, CA) and statistical analysis was done by Kaplan-Meier curves.

Ethics statement All animal studies described in this manuscript were approved by the Institutional Animal Care and Use Committee at the University of Hawaii at Manoa (Protocol No. 10-1073-8), and conducted in compliance with the NIH (National Institutes of Health) Guide for the Care and Use of Laboratory Animals.

Data availability The datasets and materials generated during the current study are available from the corresponding author upon reasonable request. Any transfer of select agent materials needs additional approval from Brad Borlee and the Responsible Official at Colorado State University. Any select agent transfer must be to a select agent registered facility, approved by the CDC, and comply with all select agent regulations (selectagents.gov).

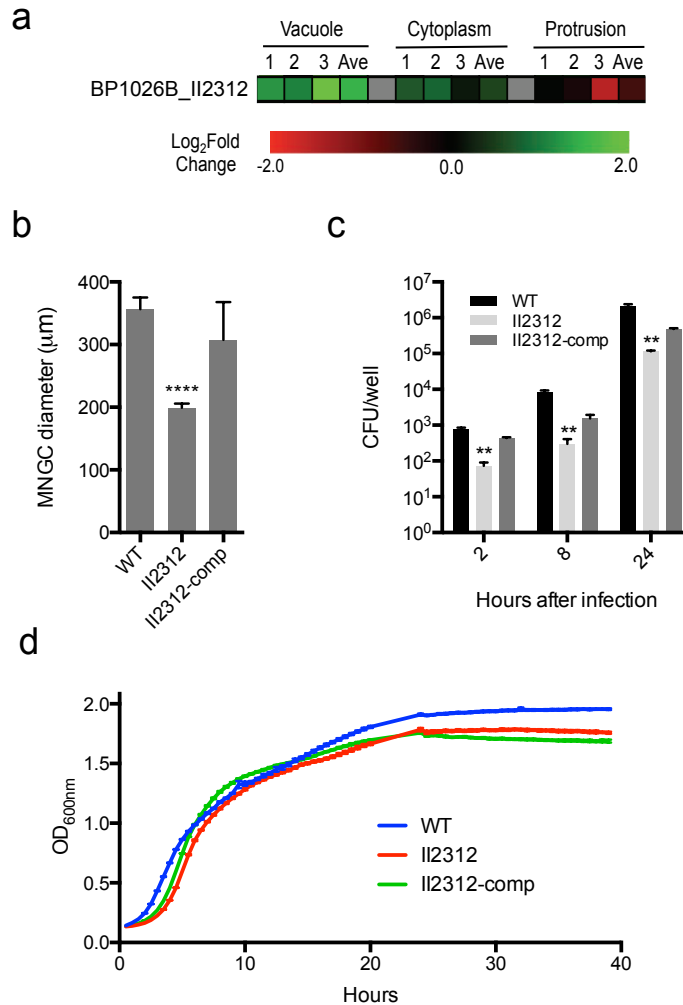


Figure 1| Differential regulation of BP1026B_II2312 during cell infection leads to defects in pathogenesis. a) BP1026B_II2312 is up-regulated in the vacuole and shows a decrease in expression throughout the cytoplasmic and protrusion stages of infection¹⁸. b) A BP1026B_II2312 mutant (II2312) is defective in the formation of MNGCs when compared to wildtype *Bp* 1026b (WT) and its complement (II2312-comp). c) Intracellular replication assays show that the BP1026B_II2312 mutant is defective at two, eight, and 24 hours after infection when compared to wildtype *Bp* 1026b and its complement. d) Growth curves indicate that the mutant and complement grow identical to wildtype *Bp* 1026b suggesting that defects during

pathogenesis are not due to fitness. Data in bar graphs and growth curve represent means \pm s.e.m and analyzed via unpaired t-test. P values presented are as follows: ** $p < 0.01$, **** $p < 0.0001$.

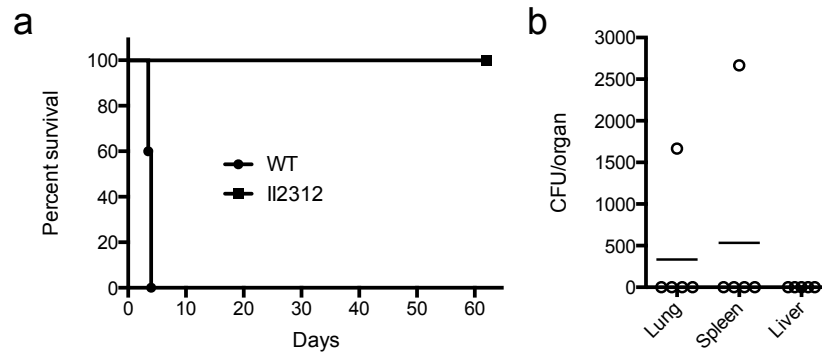


Figure 2| A BP1026B_II2312 mutant is attenuated in the BALB/c mouse infection model.

a) BALB/c mice infected with 4,500 CFU of wildtype *Bp* 1026b (WT) or the BP1026B_II2312 mutant (II2312) show drastically different survival patterns. Mice infected with wildtype *Bp* 1026b showed 100% mortality shortly after infection while mice infected with the BP1026B_II2312 mutant survived the entire length of the study. b) Sixty percent of the mice infected with BP1026B_II2312 showed complete clearance of the mutant strain while 40% of the mice had residual colonization in the lungs or spleen.

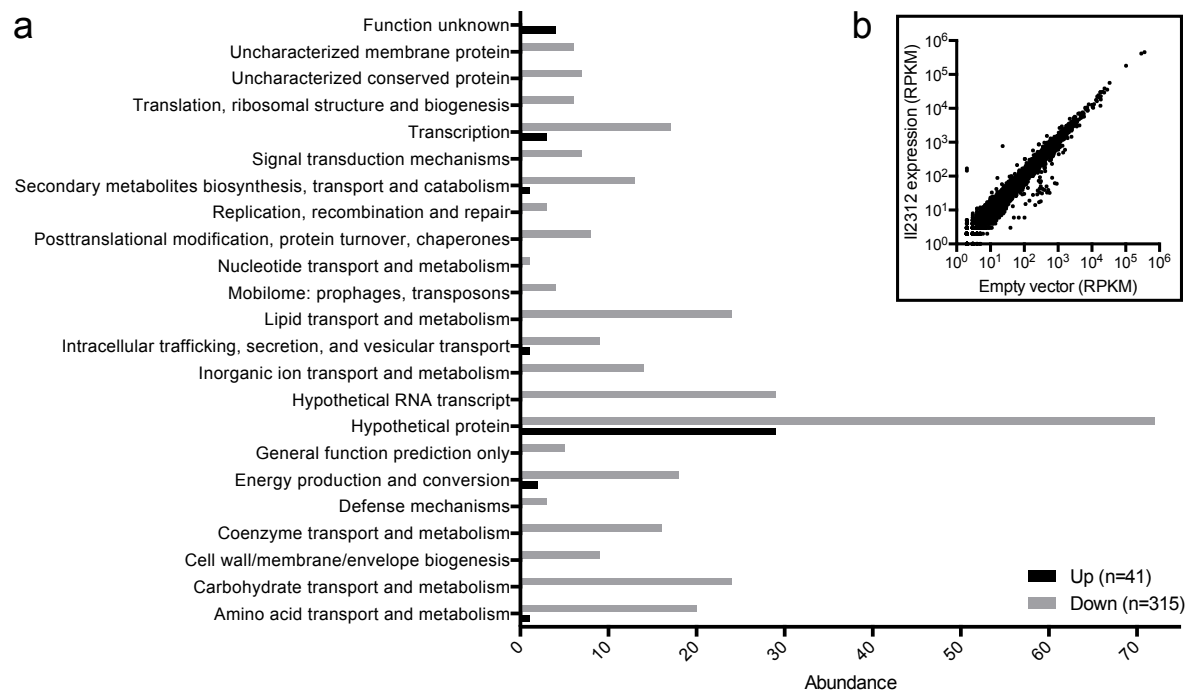


Figure 3| BP1026B_I12312 down-regulates 315 genes and up-regulates 41 genes. a) COG functional predictions of genes regulated by BP1026B_I12312 with a q-value < 0.01 and a log₂FC of ≥ 1 or ≤ -1 . Of these genes, 315 are down-regulated and 41 are up-regulated by BP1026B_I12312. b) Scatterplot showing the expression levels of all genes in the *Bp* 1026b genome comparing BP1026B_I12312 expression vs. the empty vector control.

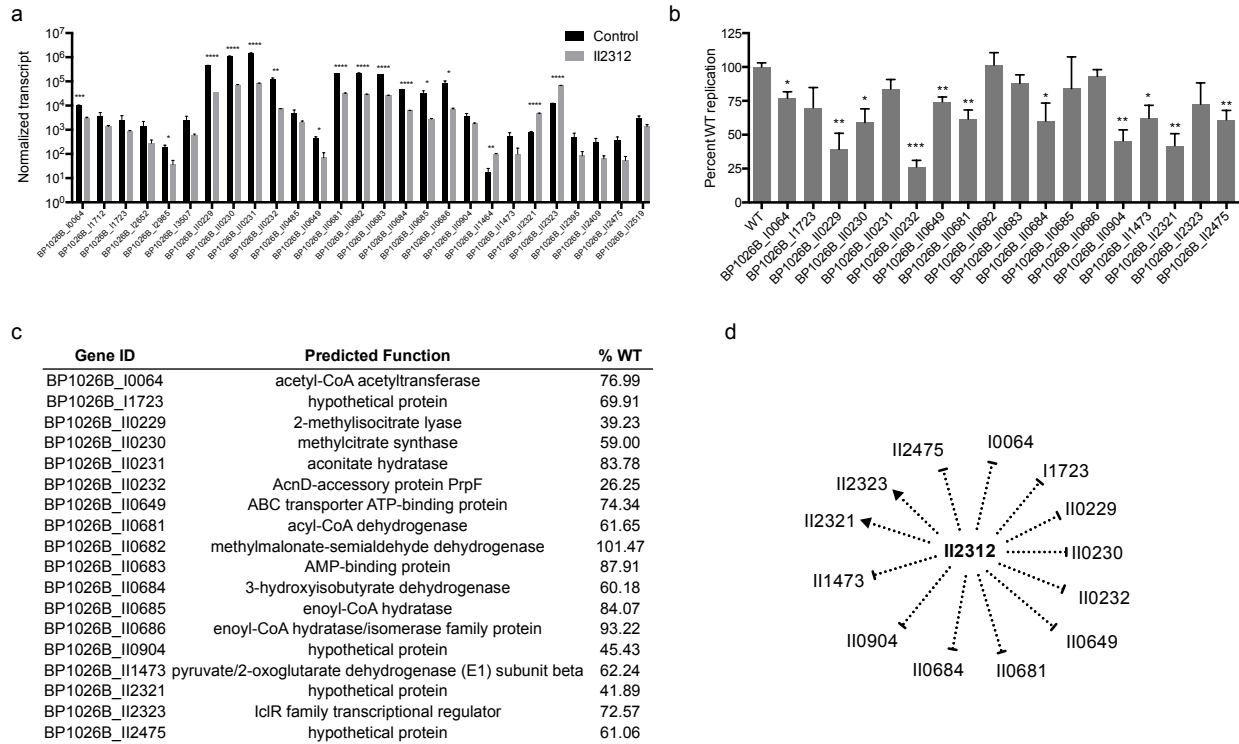


Figure 4| General metabolic pathways and hypothetical proteins controlled by BP1026B_II2312 contribute to pathogenesis in RAW264.7 cells. a) Normalized transcripts of genes controlled by BP1026B_II2312 with a \log_2FC of ≥ 2 or ≤ -2 . Twenty-four genes are down-regulated while three genes are up-regulated. b) The available T24 mutants were tested for their ability to replicate in RAW264.7 murine macrophages at 24 hours. Thirteen mutants showed defects during intracellular replication. c) Predicted functions of genes controlled by BP1026B_II2312 and the percent wildtype replication (%WT) of the corresponding T24 mutant in RAW264.7 cells. d) BP1026B_II2312 regulation map of genes that contribute to *Bp* pathogenesis. Pointed arrows represent activation and flat arrows represent repression. Data in bar graphs represent means \pm s.e.m and analyzed via unpaired t-test. P values presented are as follows: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.

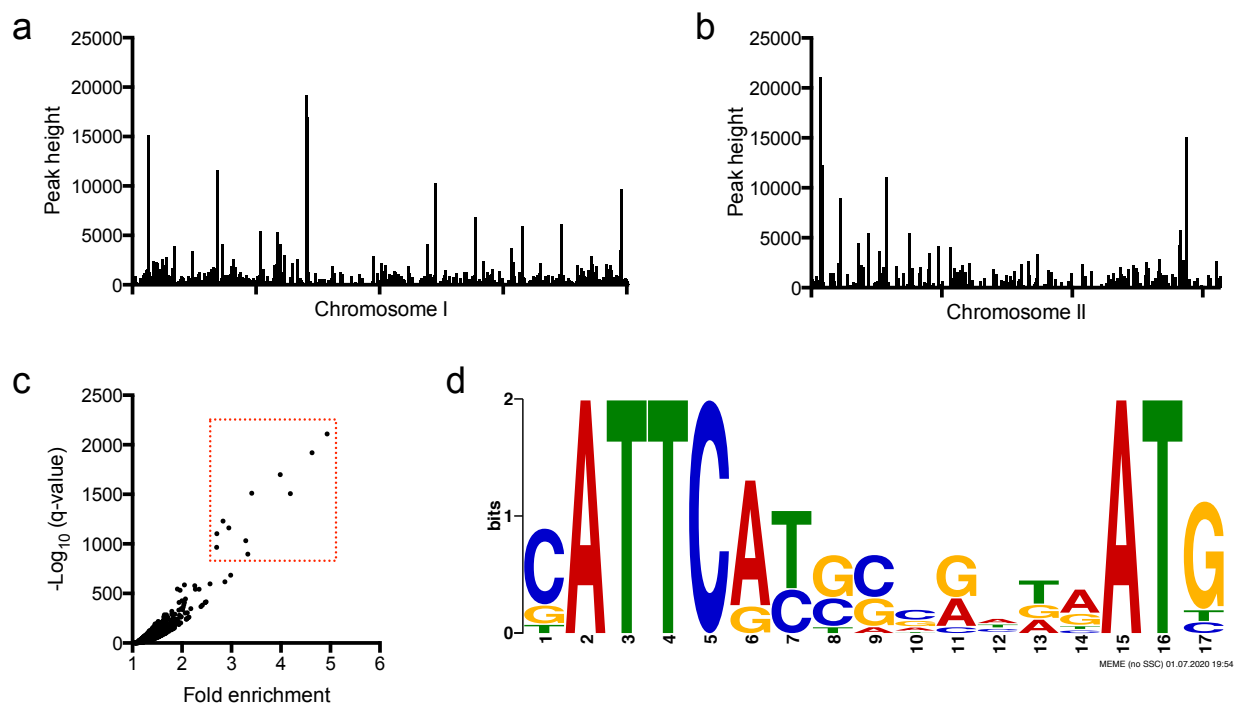


Figure 5| BP1026B_II2312 binds 11 regions of DNA on chromosome I and chromosome II.

Many regions of direct BP1026B_II2312 binding to DNA were identified through ChIP-seq on chromosome I (a) and chromosome II (b). c) Comparison of the fold enrichment and the $-\log_{10}$ of the q-value when each sample was compared to the empty vector control identified 11 peaks of interest (boxed in red). d) A 17bp consensus binding region of BP1026B_II2312 identified through MEME³² analysis of the 11 main peaks.

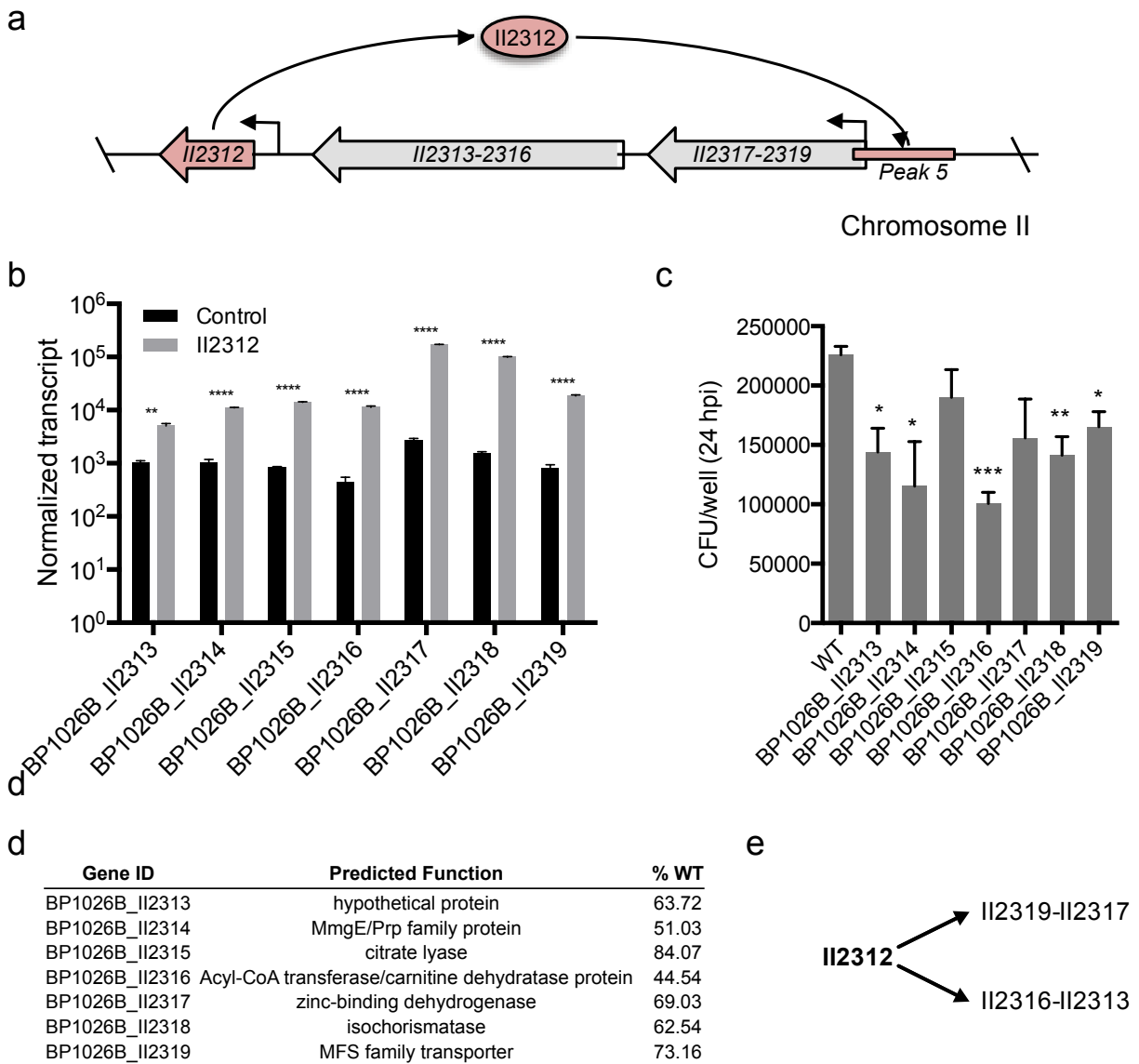
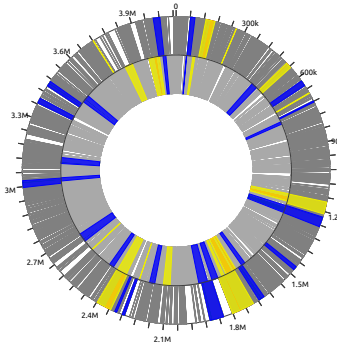


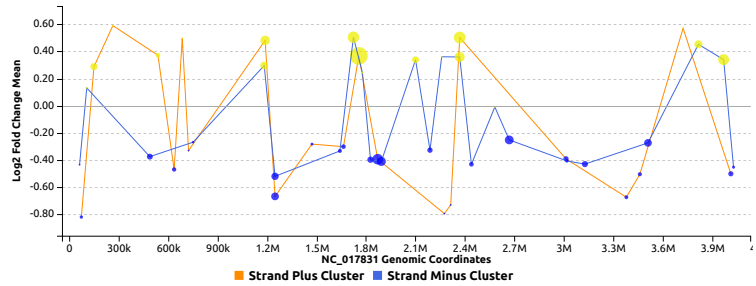
Figure 6| BP1026B_II2312 binds an intergenic region activating BP1026B_II2319-II2313. a) Schematic representation of BP1026B_II2312 regulation of BP1026B_II2319-II2313 through direct binding to ChIP-seq peak five. b) Normalized transcript of BP1026B_II2319-II2313 show that they are activated by BP1026B_II2312. c) Various levels of intracellular replication is seen when T24 mutants of genes activated by BP1026B_II2312 are tested. Infections were carried out in RAW264.7 cells and intracellular replication determined at 24 hours post infection. d) Table of annotated functions of BP1026B_II2319-II2313 and mean percent wildtype replication

(%WT) at 24 hours in RAW264.7 cells. e) Proposed mechanism of BP1026B_II2312 regulation at the local level for peak five. Arrows represent activation by BP1026B_II2312. Data in bar graphs represent means \pm s.e.m and analyzed via unpaired t-test. P values presented are as follows: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.

a



b

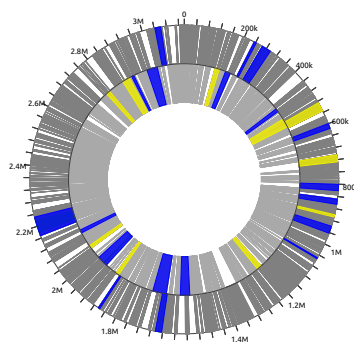


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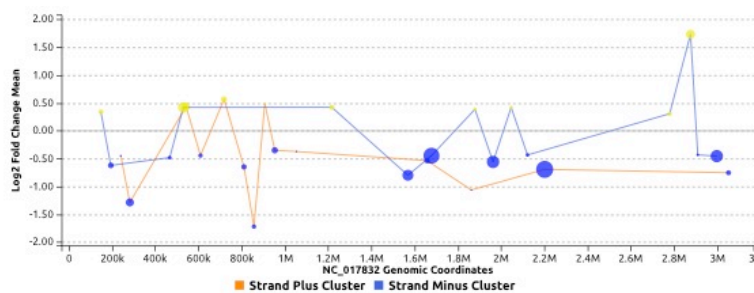
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1	57899	60067	-	BP10268_I0055;BP10268_I0056;BP10268_I0057	DOWN
2	61805	80198	+	BP10268_I0059;BP10268_I0058;BP10268_I0063;BP10268_I0064;BP10268_I0065;BP10268_I0066;BP10268_I0069;BP10268_I0070;BP10268_I0073;BP10268_I0074	DOWN
3	95564	106761	-	BP10268_I0089;BP10268_I0093;BP10268_I0097;BP10268_I0098;BP10268_I0099;BP10268_I0100	UP
4	127506	166829	+	BP10268_I0120;BP10268_I0121;BP10268_I0122;BP10268_I0123;BP10268_I0124;BP10268_I0139;BP10268_I0140;BP10268_I0141;BP10268_I0171;BP10268_I0172	UP
5	261366	262209	+	BP10268_I0261;BP10268_I0262	UP
6	469658	502363	-	BP10268_I0452;BP10268_I0453;BP10268_I0464;BP10268_I0465;BP10268_I0466;BP10268_I0467;BP10268_I0468;BP10268_I0469;BP10268_I0472;BP10268_I0473;BP10268_I0474;BP10268_I0475;BP10268_I0477	DOWN
7	521225	546935	+	BP10268_I0493;BP10268_I0496;BP10268_I0502;BP10268_I0503;BP10268_I0504;BP10268_I0505;BP10268_I0506;BP10268_I0507;BP10268_I0508;BP10268_I0510;BP10268_I0511;BP10268_I0512;BP10268_I0513;BP10268_I0514;BP10268_I0515	UP
8	619332	643231	+	BP10268_I0583;BP10268_I0585;BP10268_I0587;BP10268_I0588;BP10268_I0589;BP10268_I0590;BP10268_I0591;BP10268_I0592;BP10268_I0593;BP10268_I0594;BP10268_I0598;BP10268_I0599;BP10268_I0602	DOWN
9	679311	682034	+	BP10268_I0635;BP10268_I0636;BP10268_I0637;BP10268_I0638	UP
10	718317	723476	+	BP10268_I0669;BP10268_I0674;BP10268_I0675;BP10268_I0676	DOWN
11	740582	754438	-	BP10268_I0692;BP10268_I0693;BP10268_I0694;BP10268_I0695;BP10268_I0696;BP10268_I0697;BP10268_I0698;BP10268_I0699;BP10268_I0701;BP10268_I0702;BP10268_I0703;BP10268_I0704	DOWN
12	1156543	1199579	-	BP10268_I1076;BP10268_I1077;BP10268_I1079;BP10268_I1080;BP10268_I1082;BP10268_I1083;BP10268_I1084;BP10268_I1085;BP10268_I1086;BP10268_I1087;BP10268_I1088;BP10268_I1089;BP10268_I1100;BP10268_I1101;BP10268_I1102;BP10268_I1103;BP10268_I1104;BP10268_I1105;BP10268_I1106;BP10268_I1107;BP10268_I1108;BP10268_I1109;BP10268_I1110;BP10268_I1111;BP10268_I1112;BP10268_I1113;BP10268_I1114;BP10268_I1115;BP10268_I1116;BP10268_I1117;BP10268_I1118;BP10268_I1119;BP10268_I1120;BP10268_I1121;BP10268_I1122;BP10268_I1123;BP10268_I1124;BP10268_I1132;BP10268_I1133;BP10268_I1134;BP10268_I1135;BP10268_I1137;BP10268_I1138;BP10268_I1140;BP10268_I1141	UP
13	1158430	1210524	+	BP10268_I1153;BP10268_I1157;BP10268_I1158;BP10268_I1159;BP10268_I1160;BP10268_I1161;BP10268_I1162;BP10268_I1163;BP10268_I1164;BP10268_I1165;BP10268_I1166;BP10268_I1167;BP10268_I1168;BP10268_I1169;BP10268_I1170;BP10268_I1171;BP10268_I1173;BP10268_I1172;BP10268_I1174;BP10268_I1175;BP10268_I1176;BP10268_I1177;BP10268_I1178;BP10268_I1180	DOWN
14	1224285	1267261	+	BP10268_I1154;BP10268_I1155;BP10268_I1156;BP10268_I1179	DOWN
15	1225850	1266505	-	BP10268_I1358;BP10268_I1359;BP10268_I1360;BP10268_I1361;BP10268_I1363;BP10268_I1364;BP10268_I1365;BP10268_I1366;BP10268_I1367;BP10268_I1370;BP10268_I1371;BP10268_I1372;BP10268_I1373;BP10268_I1374	DOWN
16	1463404	1479616	+	BP10268_I1508;BP10268_I1510;BP10268_I1511;BP10268_I1513;BP10268_I1521;BP10268_I1523;BP10268_I1527	DOWN
17	1630256	1652362	-	BP10268_I1524;BP10268_I1525;BP10268_I1526;BP10268_I1528;BP10268_I1531;BP10268_I1533;BP10268_I1549;BP10268_I1548;BP10268_I1550;BP10268_I1551	DOWN
18	1650074	1675595	+	BP10268_I1548;BP10268_I1582;BP10268_I1584;BP10268_I1614;BP10268_I1615;BP10268_I1616	UP
19	1691912	1755313	-	BP10268_I1576;BP10268_I1577;BP10268_I1578;BP10268_I1579;BP10268_I1580;BP10268_I1581;BP10268_I1583;BP10268_I1585;BP10268_I1587;BP10268_I1588;BP10268_I1589;BP10268_I1590;BP10268_I1591;BP10268_I1592;BP10268_I1593;BP10268_I1594;BP10268_I1595;BP10268_I1596;BP10268_I1597;BP10268_I1598;BP10268_I1599;BP10268_I1600;BP10268_I1601;BP10268_I1602;BP10268_I1603;BP10268_I1604;BP10268_I1605;BP10268_I1606;BP10268_I1607;BP10268_I1608;BP10268_I1609;BP10268_I1610;BP10268_I1611;BP10268_I1612;BP10268_I1613;BP10268_I1617;BP10268_I1620;BP10268_I1621;BP10268_I1622;BP10268_I1630;BP10268_I1631;BP10268_I1632;BP10268_I1633;BP10268_I1635;BP10268_I1636;BP10268_I1642;BP10268_I1643;BP10268_I1645;BP10268_I1647;BP10268_I1648;BP10268_I1649;BP10268_I1653;BP10268_I1654;BP10268_I1655;BP10268_I1656;BP10268_I1657;BP10268_I1659;BP10268_I1660;BP10268_I1661;BP10268_I1662	DOWN
20	1703317	1801496	+	BP10268_I1628;BP10268_I1629;BP10268_I1633;BP10268_I1637;BP10268_I1638;BP10268_I1639;BP10268_I1640;BP10268_I1641;BP10268_I1644	UP
21	1767745	1780366	-	BP10268_I1664;BP10268_I1665;BP10268_I1666;BP10268_I1667;BP10268_I1668;BP10268_I1669;BP10268_I1670;BP10268_I1671;BP10268_I1672;BP10268_I1673;BP10268_I1674;BP10268_I1675;BP10268_I1676;BP10268_I1677;BP10268_I1678;BP10268_I1679	DOWN
22	1805168	1840163	-	BP10268_I1681;BP10268_I1683;BP10268_I1684;BP10268_I1687;BP10268_I1689;BP10268_I1690;BP10268_I1693;BP10268_I1692;BP10268_I1694;BP10268_I1695;BP10268_I1696;BP10268_I1697;BP10268_I1698;BP10268_I1699;BP10268_I1700;BP10268_I1701;BP10268_I1702;BP10268_I1705;BP10268_I1707;BP10268_I1709;BP10268_I1710;BP10268_I1714;BP10268_I1715;BP10268_I1716;BP10268_I1718;BP10268_I1719;BP10268_I1720;BP10268_I1721;BP10268_I1722;BP10268_I1723;BP10268_I1724;BP10268_I1725;BP10268_I1726;BP10268_I1727;BP10268_I1731;BP10268_I1732;BP10268_I1733;BP10268_I1734;BP10268_I1735	DOWN
23	1842173	1900708	-	BP10268_I1716;BP10268_I1717;BP10268_I1718;BP10268_I1719;BP10268_I1720;BP10268_I1721;BP10268_I1722;BP10268_I1723;BP10268_I1724;BP10268_I1725;BP10268_I1726;BP10268_I1727;BP10268_I1731;BP10268_I1732;BP10268_I1733;BP10268_I1734;BP10268_I1735	DOWN
24	1866877	1916707	-	BP10268_I1703;BP10268_I1704;BP10268_I1708;BP10268_I1711;BP10268_I1712;BP10268_I1715;BP10268_I1716;BP10268_I1717;BP10268_I1718;BP10268_I1719;BP10268_I1720;BP10268_I1721;BP10268_I1722;BP10268_I1723;BP10268_I1724;BP10268_I1725;BP10268_I1726;BP10268_I1727;BP10268_I1731;BP10268_I1732;BP10268_I1733;BP10268_I1734;BP10268_I1735	DOWN
25	2080597	2118827	-	BP10268_I1875;BP10268_I1876;BP10268_I1881;BP10268_I1882;BP10268_I1883;BP10268_I1884;BP10268_I1885;BP10268_I1887;BP10268_I1888;BP10268_I1889;BP10268_I1892;BP10268_I1896;BP10268_I1897;BP10268_I1901;BP10268_I1904;BP10268_I1905;BP10268_I1906;BP10268_I1907;BP10268_I1908;BP10268_I1909;BP10268_I1910	UP
26	2168724	2197670	-	BP10268_I1951;BP10268_I1952;BP10268_I1953;BP10268_I1954;BP10268_I1955;BP10268_I1956;BP10268_I1957;BP10268_I1958;BP10268_I1959;BP10268_I1967;BP10268_I1968;BP10268_I1969;BP10268_I1970;BP10268_I1971;BP10268_I1973;BP10268_I1975;BP10268_I1976	DOWN
27	2257640	2258001	-	BP10268_I2023;BP10268_I2024	UP
28	2269646	2279415	+	BP10268_I2032;BP10268_I2033;BP10268_I2035;BP10268_I2039;BP10268_I2040;BP10268_I2041;BP10268_I2042	DOWN
29	2305052	2313864	+	BP10268_I2058;BP10268_I2059;BP10268_I2060;BP10268_I2061;BP10268_I2062	DOWN
30	2332312	2397469	+	BP10268_I2081;BP10268_I2086;BP10268_I2117;BP10268_I2118;BP10268_I2119;BP10268_I2123;BP10268_I2133;BP10268_I2136;BP10268_I2139;BP10268_I2141;BP10268_I2142;BP10268_I2143;BP10268_I2146;BP10268_I2148;BP10268_I2149;BP10268_I2150;BP10268_I2151;BP10268_I2152;BP10268_I2153;BP10268_I2154;BP10268_I2155;BP10268_I2156;BP10268_I2160;BP10268_I2161;BP10268_I2163;BP10268_I2165;BP10268_I2169;BP10268_I2171	UP
31	2337615	2392840	-	BP10268_I2088;BP10268_I2089;BP10268_I2090;BP10268_I2091;BP10268_I2092;BP10268_I2093;BP10268_I2094;BP10268_I2095;BP10268_I2096;BP10268_I2097;BP10268_I2098;BP10268_I2099;BP10268_I2100;BP10268_I2101;BP10268_I2102;BP10268_I2103;BP10268_I2104;BP10268_I2105;BP10268_I2106;BP10268_I2107;BP10268_I2108;BP10268_I2109;BP10268_I2110;BP10268_I2111;BP10268_I2112;BP10268_I2113;BP10268_I2114;BP10268_I2115;BP10268_I2116;BP10268_I2119;BP10268_I2120;BP10268_I2121;BP10268_I2122;BP10268_I2123;BP10268_I2125;BP10268_I2126;BP10268_I2127;BP10268_I2128;BP10268_I2129;BP10268_I2130;BP10268_I2131;BP10268_I2132;BP10268_I2134;BP10268_I2135;BP10268_I2137;BP10268_I2138;BP10268_I2140;BP10268_I2144;BP10268_I2145;BP10268_I2146;BP10268_I2147;BP10268_I2148;BP10268_I2149;BP10268_I2150;BP10268_I2151;BP10268_I2152;BP10268_I2153;BP10268_I2154;BP10268_I2155;BP10268_I2156;BP10268_I2160;BP10268_I2161;BP10268_I2163;BP10268_I2165;BP10268_I2169;BP10268_I2171	UP
32	2421534	2447447	-	BP10268_I2192;BP10268_I2193;BP10268_I2195;BP10268_I2199;BP10268_I2201;BP10268_I2202;BP10268_I2203;BP10268_I2204;BP10268_I2205;BP10268_I2206;BP10268_I2207;BP10268_I2208;BP10268_I2209;BP10268_I2210;BP10268_I2211;BP10268_I2212;BP10268_I2213;BP10268_I2214;BP10268_I2215;BP10268_I2217	DOWN
33	2576521	2577955	-	BP10268_I2322;BP10268_I2323;BP10268_I2324	UP
34	2639604	2688415	-	BP10268_I2383;BP10268_I2384;BP10268_I2385;BP10268_I2386;BP10268_I2387;BP10268_I2388;BP10268_I2389;BP10268_I2400;BP10268_I2401;BP10268_I2402;BP10268_I2403;BP10268_I2411;BP10268_I2414;BP10268_I2415;BP10268_I2416;BP10268_I2417;BP10268_I2418;BP10268_I2419;BP10268_I2420;BP10268_I2423;BP10268_I2424;BP10268_I2425	DOWN
35	2996579	3025676	+	BP10268_I2702;BP10268_I2705;BP10268_I2709;BP10268_I2710;BP10268_I2711;BP10268_I2712;BP10268_I2716;BP10268_I2726;BP10268_I2727;BP10268_I2728;BP10268_I2729	DOWN
36	3009357	3027663	-	BP10268_I2713;BP10268_I2715;BP10268_I2718;BP10268_I2719;BP10268_I2720;BP10268_I2721;BP10268_I2722;BP10268_I2723;BP10268_I2724;BP10268_I2725;BP10268_I2730;BP10268_I2731	DOWN
37	3108264	3142206	-	BP10268_I2797;BP10268_I2803;BP10268_I2804;BP10268_I2805;BP10268_I2806;BP10268_I2810;BP10268_I2812;BP10268_I2813;BP10268_I2816;BP10268_I2817;BP10268_I2820	DOWN
38	3365192	3386721	+	BP10268_I3011;BP10268_I3012;BP10268_I3013;BP10268_I3014;BP10268_I3015;BP10268_I3016;BP10268_I3017;BP10268_I3018;BP10268_I3019;BP10268_I3020;BP10268_I3021;BP10268_I3022;BP10268_I3024;BP10268_I3023;BP10268_I3025;BP10268_I3026;BP10268_I3027;BP10268_I3028;BP10268_I3029;BP10268_I3030;BP10268_I3031	DOWN
39	3447766	3470406	-	BP10268_I3088;BP10268_I3090;BP10268_I3095;BP10268_I3106;BP10268_I3107;BP10268_I3108;BP10268_I3109;BP10268_I3110	DOWN
40	3484251	3526832	-	BP10268_I3122;BP10268_I3127;BP10268_I3132;BP10268_I3143;BP10268_I3144;BP10268_I3145;BP10268_I3146;BP10268_I3147;BP10268_I3148;BP10268_I3150;BP10268_I3151;BP10268_I3152;BP10268_I3153;BP10268_I3154;BP10268_I3155	DOWN
41	3721192	3722837	+	BP10268_I3340;BP10268_I3341;BP10268_I3342	UP
42	3794193	3838348	-	BP10268_I3415;BP10268_I3416;BP10268_I3417;BP10268_I3418;BP10268_I3419;BP10268_I3420;BP10268_I3421;BP10268_I3422;BP10268_I3423;BP10268_I3424;BP10268_I3425;BP10268_I3426;BP10268_I3427;BP10268_I3428;BP10268_I3429;BP10268_I3430;BP10268_I3431;BP10268_I3432;BP10268_I3433;BP10268_I3434;BP10268_I3435;BP10268_I3436;BP10268_I3437;BP10268_I3438;BP10268_I3439;BP10268_I3440;BP10268_I3441;BP10268_I3442;BP10268_I3443;BP10268_I3444;BP10268_I3445;BP10268_I3446;BP10268_I3447;BP10268_I3448;BP10268_I3449;BP10268_I3450;BP10268_I3451;BP10268_I3452;BP10268_I3453;BP10268_I3454;BP10268_I3455;BP10268_I3456;BP10268_I3457;BP10268_I3458;BP10268_I3459;BP10268_I3460;BP10268_I3461	UP
43	3936750	3990917	-	BP10268_I3566;BP10268_I3567;BP10268_I3569;BP10268_I3570;BP10268_I3571;BP10268_I3572;BP10268_I3573;BP10268_I3574;BP10268_I3575;BP10268_I3576;BP10268_I3577;BP10268_I3578;BP10268_I3579;BP10268_I3580;BP10268_I3582;BP10268_I3583;BP10268_I3584;BP10268_I3585;BP10268_I3586;BP10268_I3587;BP10268_I3588;BP10268_I3589;BP10268_I3590;BP10268_I3591;BP10268_I3592;BP10268_I3593;BP10268_I3594;BP10268_I3595;BP10268_I3596;BP10268_I3597;BP10268_I3598;BP10268_I3599;BP10268_I3600;BP10268_I3601;BP10268_I3602;BP10268_I3603;BP10268_I3604;BP10268_I3605;BP10268_I3606;BP10268_I3607;BP10268_I3608;BP10268_I3609;BP10268_I3610;BP10268_I3611;BP10268_I3612;BP10268_I3613;BP10268_I3614;BP10268_I3615;BP10268_I3616;BP10268_I3617;BP10268_I3618;BP10268_I3619;BP10268_I3620;BP10268_I3621;BP10268_I3622;BP10268_I3623;BP10268_I3624;BP10268_I3625;BP10268_I3626;BP10268_I3627;BP102	

Supplemental Figure 1| WoPPER analysis reveals 45 gene clusters regulated by BP1026B_II2312 on *Bp* 1026b chromosome I. a) Up (yellow) and down (blue) regulated gene clusters controlled by BP1026B_II2312 on a circular plot of chromosome I. The outer ring is the positive strand (dark grey) and the inner ring is the negative strand (light grey). b) A linear representation of gene clusters up and down regulated by BP1026B_II2312 and the \log_2FC mean of each cluster. The size of the circle is proportional to the number of genes within each cluster. The blue line represents the negative sense strand and the orange line represents the positive sense strand. c) A table representation of gene clusters controlled by BP1026B_II2312.

a



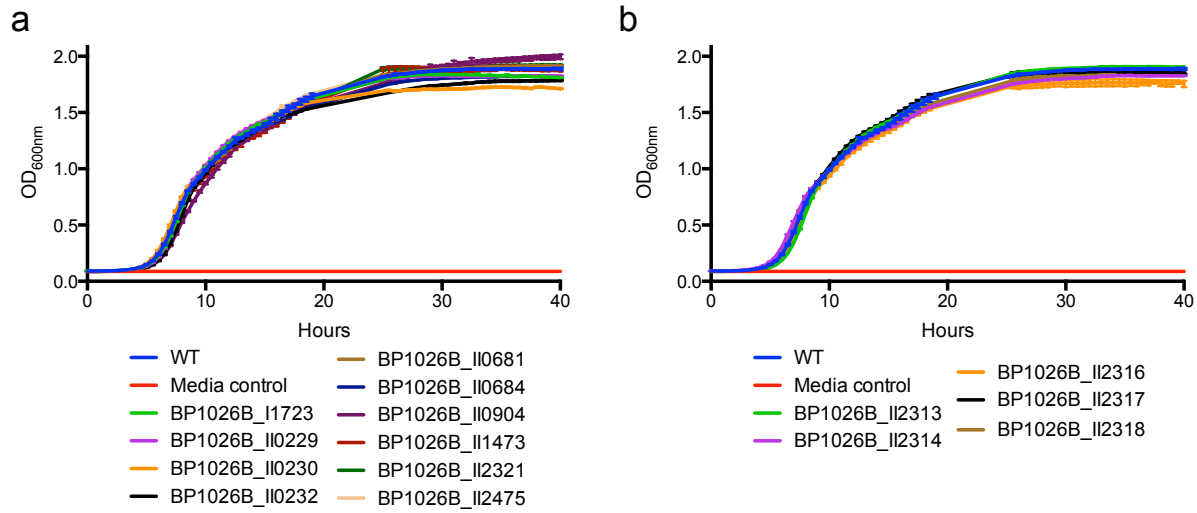
b



c

Cluster	Start Coordinates	End Coordinates	Strand	Gene ID	Expression
1	135381	154106	-	BP10268_I10116;BP10268_I10117;BP10268_I10118;BP10268_I10119;BP10268_I10120;BP10268_I10121;BP10268_I10122;BP10268_I10124;BP10268_I10126;BP10268_I10130;BP10268_I10131	UP
2	182142	204050	-	BP10268_I10133;BP10268_I10135	DOWN
3	235223	242403	+	BP10268_I10159;BP10268_I10160;BP10268_I10161;BP10268_I10162;BP10268_I10163;BP10268_I10164;BP10268_I10165;BP10268_I10166;BP10268_I10167;BP10268_I10168;BP10268_I10170	DOWN
4	264816	295250	+	BP10268_I10173;BP10268_I10174;BP10268_I10175;BP10268_I10176	DOWN
5	456965	471452	-	BP10268_I10197;BP10268_I10198;BP10268_I10199;BP10268_I10201;BP10268_I10200;BP10268_I10202;BP10268_I10203	DOWN
6	510121	549107	-	BP10268_I10222;BP10268_I10223;BP10268_I10224;BP10268_I10225;BP10268_I10229;BP10268_I10230;BP10268_I10231;BP10268_I10232;BP10268_I10234;BP10268_I10235;BP10268_I10236	UP
7	525090	554448	+	BP10268_I10237;BP10268_I10238;BP10268_I10240;BP10268_I10242	DOWN
8	599437	616330	+	BP10268_I10357;BP10268_I10358;BP10268_I10359;BP10268_I10360;BP10268_I10361;BP10268_I10367;BP10268_I10368;BP10268_I10369	DOWN
9	704422	727295	-	BP10268_I10442;BP10268_I10443;BP10268_I10444;BP10268_I10445;BP10268_I10446;BP10268_I10447;BP10268_I10448;BP10268_I10449;BP10268_I10450	UP
10	800331	820894	+	BP10268_I10442;BP10268_I10443;BP10268_I10444;BP10268_I10445;BP10268_I10446;BP10268_I10447;BP10268_I10448;BP10268_I10449;BP10268_I10450	DOWN
11	848473	865395	+	BP10268_I10483;BP10268_I10484;BP10268_I10485;BP10268_I10486;BP10268_I10487;BP10268_I10488;BP10268_I10489;BP10268_I10490;BP10268_I10491;BP10268_I10492;BP10268_I10493;BP10268_I10494;BP10268_I10495;BP10268_I10496;BP10268_I10498	DOWN
12	899706	907533	+	BP10268_I10569;BP10268_I10570;BP10268_I10571;BP10268_I10572;BP10268_I10573;BP10268_I10574;BP10268_I10575;BP10268_I10576;BP10268_I10577;BP10268_I10578;BP10268_I10579;BP10268_I10580;BP10268_I10581	UP
13	938272	962175	+	BP10268_I10582;BP10268_I10583;BP10268_I10584;BP10268_I10585;BP10268_I10586;BP10268_I10587	DOWN
14	1050082	1053560	+	BP10268_I10645;BP10268_I10646;BP10268_I10647;BP10268_I10648;BP10268_I10649;BP10268_I10650;BP10268_I10651;BP10268_I10652;BP10268_I10653;BP10268_I10654	DOWN
15	1206964	1226651	-	BP10268_I10681;BP10268_I10682;BP10268_I10683;BP10268_I10684;BP10268_I10685;BP10268_I10686;BP10268_I10687;BP10268_I10688;BP10268_I10689;BP10268_I10690;BP10268_I10691;BP10268_I10694;BP10268_I10695	DOWN
16	1545608	1586382	-	BP10268_I10730;BP10268_I10731;BP10268_I10732;BP10268_I10733;BP10268_I10734;BP10268_I10735;BP10268_I10736;BP10268_I10738	UP
17	1643043	1663808	+	BP10268_I10763;BP10268_I10765;BP10268_I10766;BP10268_I10767;BP10268_I10768;BP10268_I10769;BP10268_I10770;BP10268_I10771;BP10268_I10772;BP10268_I10778;BP10268_I10779	DOWN
18	1647963	1707016	-	BP10268_I10781;BP10268_I10782;BP10268_I10784	DOWN
19	1858707	1864242	+	BP10268_I10859;BP10268_I10858;BP10268_I10860	UP
20	1870693	1884174	-	BP10268_I10995;BP10268_I10998;BP10268_I11000;BP10268_I11002;BP10268_I11006;BP10268_I11008;BP10268_I11011;BP10268_I11012	DOWN
21	1938724	1984689	-	BP10268_I11240;BP10268_I11241;BP10268_I11246;BP10268_I11247;BP10268_I11257;BP10268_I11258;BP10268_I11259;BP10268_I11260;BP10268_I11261;BP10268_I11262;BP10268_I11263	DOWN
22	2036858	2049888	-	BP10268_I11264;BP10268_I11265	DOWN
23	2114492	2128455	-	BP10268_I11312;BP10268_I11313;BP10268_I11314;BP10268_I11321;BP10268_I11322;BP10268_I11323;BP10268_I11325	DOWN
24	2168126	2231191	+	BP10268_I11315;BP10268_I11316;BP10268_I11317;BP10268_I11318;BP10268_I11319;BP10268_I11324;BP10268_I11326;BP10268_I11327;BP10268_I11328;BP10268_I11330;BP10268_I11331	DOWN
25	2770735	2787481	-	BP10268_I11333;BP10268_I11334;BP10268_I11335;BP10268_I11336;BP10268_I11339;BP10268_I11340;BP10268_I11345;BP10268_I11346;BP10268_I11347;BP10268_I11348;BP10268_I1134	DOWN
26	2858136	2891419	-	BP10268_I11472;BP10268_I11473;BP10268_I11476	UP
27	2902815	2913068	-	BP10268_I11475;BP10268_I11480;BP10268_I11481;BP10268_I11482;BP10268_I11483;BP10268_I11484;BP10268_I11485;BP10268_I11486;BP10268_I11487;BP10268_I11488;BP10268_I11489	DOWN
28	2974712	3020504	-	BP10268_I11490;BP10268_I11491	UP
29	3042762	3062027	+	BP10268_I11533;BP10268_I11534;BP10268_I11535;BP10268_I11536;BP10268_I11537;BP10268_I11546;BP10268_I11547;BP10268_I11549;BP10268_I11550;BP10268_I11555;BP10268_I11556	DOWN
				BP10268_I11557;BP10268_I11563;BP10268_I11564;BP10268_I11565;BP10268_I11566	UP
				BP10268_I11608;BP10268_I11610;BP10268_I11611;BP10268_I11612;BP10268_I11615;BP10268_I11616;BP10268_I11617;BP10268_I11618;BP10268_I11619;BP10268_I11622;BP10268_I11623	DOWN
				BP10268_I11686;BP10268_I11687;BP10268_I11688;BP10268_I11689;BP10268_I11693;BP10268_I11694	UP
				BP10268_I11733;BP10268_I11734;BP10268_I11735;BP10268_I11736;BP10268_I11738;BP10268_I11737;BP10268_I11740;BP10268_I11739;BP10268_I11741;BP10268_I11748;BP10268_I11755	DOWN
				BP10268_I11757	UP
				BP10268_I12227;BP10268_I12229;BP10268_I12230;BP10268_I12231;BP10268_I12232;BP10268_I12234;BP10268_I12244;BP10268_I12245	DOWN
				BP10268_I12302;BP10268_I12303;BP10268_I12304;BP10268_I12305;BP10268_I12306;BP10268_I12307;BP10268_I12308;BP10268_I12311;BP10268_I12312;BP10268_I12313;BP10268_I12314	UP
				BP10268_I12315;BP10268_I12316;BP10268_I12317;BP10268_I12318;BP10268_I12319;BP10268_I12320;BP10268_I12321;BP10268_I12322;BP10268_I12323;BP10268_I12327;BP10268_I1232	DOWN
				BP10268_I12329	UP
				BP10268_I12338;BP10268_I12339;BP10268_I12340;BP10268_I12341;BP10268_I12342;BP10268_I12344;BP10268_I12346;BP10268_I12347;BP10268_I12348	DOWN
				BP10268_I12408;BP10268_I12409;BP10268_I12410;BP10268_I12411;BP10268_I12412;BP10268_I12413;BP10268_I12414;BP10268_I12415;BP10268_I12416;BP10268_I12419;BP10268_I12422	UP
				BP10268_I12424;BP10268_I12425;BP10268_I12426;BP10268_I12427;BP10268_I12428;BP10268_I12429;BP10268_I12430;BP10268_I12431;BP10268_I12432;BP10268_I12433;BP10268_I12434	DOWN
				BP10268_I12435;BP10268_I12436;BP10268_I12437;BP10268_I12438;BP10268_I12439;BP10268_I12440;BP10268_I12441;BP10268_I12442;BP10268_I12443;BP10268_I12444;BP10268_I12445;BP10268_I124	UP
				BP10268_I12447;BP10268_I12449	DOWN
				BP10268_I12464;BP10268_I12470;BP10268_I12471;BP10268_I12472;BP10268_I12473;BP10268_I12474;BP10268_I12475;BP10268_I12476;BP10268_I12477;BP10268_I12478;BP10268_I12479	DOWN

Supplemental Figure 2| WoPPER analysis reveals 29 gene clusters regulated by BP1026B_II2312 on *Bp* 1026b chromosome II. a) Up (yellow) and down (blue) regulated gene clusters controlled by BP1026B_II2312 on a circular plot of chromosome II. The outer ring is the positive strand and the inner ring is the negative sense strand. b) A linear representation of gene clusters up and down regulated by BP1026B_II2312 and the \log_2FC mean of each cluster. The size of the circle is proportional to the number of genes within each cluster. The blue line represents the negative sense strand and the orange line represents the positive sense strand. c) A table representation of gene clusters controlled by BP1026B_II2312.



Supplemental Figure 3| Growth kinetics of transposon mutants confirms defects during intracellular pathogenesis. a) Transposon mutants indirectly controlled by BP1026B_II2312 that have defects during intracellular pathogenesis in RAW264.7 cells show similar growth patterns to wildtype *Bp* 1026b (WT) during *in vitro* growth. b) Transposon mutants directly regulated by BP1026B_II2312 that have defects during intracellular pathogenesis in RAW264.7 cells show similar growth patterns to wildtype *Bp* 1026b *in vitro*.

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Chapter 5:

Live Attenuated Vaccine Candidate Provides Protection Against Lethal *Burkholderia pseudomallei* Infection in BALB/c and C57Bl/6 mice

Abstract

Burkholderia pseudomallei (*Bp*) is an environmental Gram-negative bacteria that has been classified as a Tier 1 select agent by the CDC due to its potential use as a bioweapon. *Bp* causes melioidosis, an infection in many tropical regions around the world with numerous clinical symptoms that are often misdiagnosed. The increasing awareness of melioidosis is leading us to understand its true impact making it a major public health concern for populations in endemic regions. Because *Bp* is a public health and biodefense concern the development of a vaccine is paramount. We have recently discovered several attenuated mutants in *Bp* that are completely attenuated during infection of the highly susceptible BALB/c mouse. Mutants of genes BPSL0636, BPSS0015, and BPSS1818 represent new virulence factors of unknown function, autophagy evasion, and cytoskeleton rearrangement, respectively. We tested these mutants as live attenuated vaccines (LAVs) against a lethal challenge with wildtype *Bp* 1026b showing some protection and some LAV persistence. To improve the safety and protection we constructed double mutants of these genes to reduce the possibility of LAV strain persistence within the host. The BPSL0636 and BPSS0015 double mutant protected 60% of BALB/c mice against lethal challenge with *Bp* after a single dose. When given a booster vaccination, 100% of BALB/c mice were protected against lethal *Bp* challenge. Furthermore, this LAV strain protected 100% of C57Bl/6 mice against lethal *Bp* challenge for 60 days.

Introduction

Burkholderia pseudomallei (*Bp*) is a Gram-negative saprophyte that causes melioidosis. Melioidosis is a disease with many clinical manifestations that range from acute skin lesions to infection of the central nervous system, with approximately 50% of cases presenting with pneumonia or bacteremia¹⁻³. *Bp* is endemic to tropical regions and it is predicted that there are 165,000 cases annually, with a predicted mortality rate of 54%⁴. Melioidosis is treated with antimicrobial therapy that typically involves an intensive phase of intravenous ceftazidime or meropenem followed by an eradication phase of oral trimethoprim-sufamethoxazole³. *Bp* is intrinsically resistant to many antibiotics making treatment even more difficult⁵⁻⁷. Resistance to front line antimicrobials has been reported and highlights the need for additional treatment and prevention options^{7, 8}. Although much effort has been put towards the development of a vaccine, there is still no licensed vaccine available⁹.

Clinical and environmental strains of *Bp* are genetically diverse, containing two chromosomes with a large amount of genetic information encoding many pathways and genes involved in survival in diverse environments including various virulence factors^{3, 10}. *Bp* uses known and unknown virulence pathways to undergo a sophisticated intracellular lifecycle. Briefly, *Bp* attaches to host cells, gets internalized, and escapes the endosome using a type III secretion system (T3SS-3)¹¹. Within the cytoplasm, *Bp* replicates freely and uses BimA, a mimicker of the host Ena/VASP actin polymerase¹², and its lateral flagella¹³ to move around and protrude towards neighboring cells. To spread the infection further, *Bp* encodes a type VI secretion system (T6SS-1) that allows for host cell membrane fusion leading to the formation of multinucleated giant cells (MNGCs)^{13, 14}. Beyond these major virulence factors, *Bp* encodes others including capsule polysaccharide (CPS)¹⁵, lipopolysaccharide (LPS)¹⁶, flagella¹³, and

multiple secondary metabolites¹⁷. Recently, it was identified that there are approximately 1,953 genes that are differentially expressed as *Bp* transits from the endocytic vacuole to protrusion¹⁸. This indicates that many genes are involved during the infection process, beyond what we already know and could aid in the development of novel therapies and vaccines.

Live attenuated vaccines (LAV) elicit strong immune responses that can give lasting protection^{19, 20}, although reversion to a virulent form and in host mutation by an LAV is a major safety concern²¹. Over the last decade, many attenuated *Bp* mutants have been tested as potential live attenuated vaccines against melioidosis including mutants in *purN*²², *purM*²³, *ilvI*²⁴⁻²⁶, *aroC*²⁷, *asd*²⁸, *relA/spoT*²⁹, *tonB*³⁰, and *tonB/hcp1*³¹. These mutants are defective in various processes including amino acid biosynthesis, signaling, iron transport, and in one case a secretion system. Protection given by most of these LAVs has been partial, and none have shown sterilizing immunity. The *tonB/hcp1* double mutant LAV shows exciting results, giving rise to 100% protection of C57Bl/6 mice for 27 days against lethal *Bp* challenge³¹. Even more interesting is that the same double mutant in *Burkholderia mallei* (*Bm*), the causative agent of glanders and close relative to *Bp*, protected C57Bl/6 mice for 35 days against lethal *Bm* challenge³². TonB is an inner membrane protein that transfers energy to the outer membrane for iron uptake³³⁻³⁵ while Hcp1 hexamers form the needle-like structure of the virulence secretion system, T6SS-1³⁶. In an LAV, the mutation of genes involved during intracellular processes, like iron uptake and host cell fusion, is critical to allow effective protection against subsequent infection. Recently, new virulence factors have been described that are required for full pathogenesis of *Bp* in BALB/c mice¹⁸. BPAL0636, BPSS0015, and BPSS1818 encode genes of unknown function, autophagy evasion, and host tubulin rearrangement, respectively. Here we

investigate how these recently described virulence factor mutant's function as potential LAVs against *Bp* infection.

Results

Novel virulence factors are essential for complete pathogenesis and highly conserved in pathogenic *Burkholderia* species

We recently discovered multiple hypothetical proteins involved in virulence¹⁸. Mutants in these virulence factors showed various defects in intracellular pathogenesis. Individual mutants of BPSL0636, BPSS0015, and BPSS1818 showed defects during *Bp* intracellular infection *in vitro*, including a decrease of 30-85% in intracellular replication at 24 hours post infection compared to wildtype *Bp* (Table 1)¹⁸. BPSL0636 is a hypothetical protein that is located around genes for ubiquinone biosynthesis³⁷. Although no link to this biosynthetic pathway has been determined, a mutant of this gene still shows a 29% decrease in intracellular replication and 56% decrease in cell-to-cell spread at 24 hours when compared to wildtype *Bp* (Table 1)¹⁸. BPSS0015 is annotated as a hypothetical protein but preliminary results have indicated that this protein is involved in the avoidance of autophagy and intracellular clearance¹⁸. A BPSS0015 mutant is able to replicate to wildtype levels during early stages of infection, but has an 85% decrease in intracellular replication and 38% decrease in cell-to-cell spread at 24 hours post infection indicating that this virulence factor is essential for the late stages of infection (Table 1)¹⁸. BPSS1818 is also annotated as a hypothetical protein but initial studies showed that this protein is involved in host cytoskeletal structure modifications leading to an 84% decrease in intracellular replication and 46% decrease in cell-to-cell spread of the mutant (Table 1)¹⁸. Additionally, when BALB/c mice are infected with mutants of these genes, 100% of mice survive for 60 days, while BALB/c mice infected with an equivalent dose of the wildtype strain, *Bp* 1026b, are unable to survive beyond day five¹⁸. This indicates that these novel virulence factors are essential for complete pathogenesis *in vivo*, suggesting that the mutants of these genes

allow the host to recognize *Bp* leading to a potentially protective immune response against infection. We therefore hypothesize that these mutants will serve as adequate and safe live attenuated vaccines (LAVs) against *Bp* infection.

These novel virulence factors are highly conserved in *Bp* strains as well as other *Burkholderia* pathogens, including *B. mallei* (*Bm*) and the *B. cepacia* complex (*Bcc*), causative agents of glanders and cepacia syndrome, respectively (Table 2). Within the *Burkholderia* genus, BPSL0636, BPSS0015, and BPSS1818 have 652, 642, and 638 ortholog group members, respectively³⁷. Among a small set of *Bp* strains we see conservation of all three proteins with 98-100% amino acid identity (Table 2). BPSL0636 is present in *Bm* strains Ivan and China 5 at 100% identity and shows strong conservation in *Bcc* and other pathogenic *Burkholderia* spp. as well (Table 2). BPSS1818 is absent in *Bm* but highly conserved in *Bcc* (77-80% amino acid identity) and other *Burkholderia* spp. (78-97% amino acid identity) indicating that it could play a role in the pathogenesis of multiple *Burkholderia* species (Table 2). The high level of conservation among a diverse group of pathogenic *Burkholderia* spp. suggests that these virulence factors could be important for pathogenesis of several *Burkholderia* caused diseases. All this information pushed us to investigate the potential of these attenuated mutants as LAVs to protect against melioidosis.

Vaccination with virulence factor mutants gives partial protection against challenge with virulent *Bp*

To test the efficacy of these potential LAVs we employed an acute challenge model of melioidosis using BALB/c mice as a host²⁸. Using this model, mice infected with virulent *Bp* show significant clinical symptoms leading to 100% mortality in the first week post infection²⁸.

³⁸. For our purposes, mice were first vaccinated via the intranasal route with a high dose of each attenuated mutant and monitored for 60 days. At day 60, mice were challenged intranasally with a lethal dose of wildtype *Bp* 1026b (4,500 CFU) and survival was monitored for 63 days (Fig. 1a). After challenge, control mice vaccinated with PBS showed significant signs of disease and were moribund in the first six days and had to be euthanized as expected (Fig. 1b). To contrast this, BPSL0636 vaccinated mice showed 60% survival for the duration of the study, while 40% of BPSS0015 and BPSS1818 vaccinated mice survived (Fig. 1b). One mouse vaccinated with BPSL0636 showed a delay in mortality to day 22, which would extend the potential treatment period for clinical intervention (Fig. 1b). Of the surviving mice, some showed colonization of wildtype *Bp* in the lungs combined with dissemination to the liver and/or spleen (Fig. 1c-e). One mouse in each vaccination group was able to clear the wildtype *Bp* infection in the lung but had colonization in the spleen, the liver, or the liver and spleen (Fig. 1c-e). A single mouse vaccinated with BPSL0636 showed sterile immunity with no signs of infection with wildtype *Bp* in the lungs, liver, or spleen (Fig. 1c). Although mice vaccinated with BPSL0636 showed the highest rate of survival out of all potential LAVs and one mouse with sterile immunity, another mouse did show persistence of the vaccine strain after 123 days (Fig. 1c). Persistence of an LAV strain is a great concern for vaccine safety. Although, some level of persistence of an LAV is ideal to allow the immune response to fully develop against a pathogen, persistence beyond that stage is undesirable and complete clearance is ideal. To optimize these LAVs we decided to combine mutations in a single strain to increase safety of the vaccine strains while maintaining protection against wildtype *Bp* challenge.

Optimization of LAVs allow clearance of vaccine strains and partial protection against lethal *Bp* challenge

Double mutants of these novel virulence factors were generated in a *Bp* 1026b background using λ -Red recombineering to determine if they could be completely cleared from the host and maintain protection as an LAV against lethal *Bp* infection³⁹. All combinations of these virulence factors were made because we do not know how the two mutations will affect the resulting LAV strain. BPSL0636/BPSS0015, BPSL0636/BPSS1818, and BPSS0015/BPSS1818 were used to vaccinate BALB/c mice 60 days prior to infection (Fig. 2a). Vaccinated mice were infected with 4,500 CFU of wildtype *Bp* 1026b and monitored for 63 days. Control mice vaccinated with PBS showed significant signs of murine melioidosis and 100% mortality within the first week of infection, while 20-60% of vaccinated mice were able to survive until the study was terminated (Fig. 2b). All LAV strains were completely cleared from surviving mice indicating that the vaccine strains do not persist within the host (Fig. 2c-e). Mice vaccinated with BPSL0636/BPSS1818 showed 20% survival and the surviving mouse showed significant infection (2×10^7 CFU wildtype *Bp*) in the spleen but had cleared the infection from the lungs and liver (Fig. 2b, d). Mice vaccinated with BPSS0015/BPSS1818 showed 40% survival, one mouse with sterile immunity, and one mouse with a persistent infection of wildtype *Bp* in the lungs, liver and spleen (Fig. 2b, e). This LAV strain also extended the survival of another mouse to 38 days post infection (Fig. 2b). Mice vaccinated with BPSL0636/BPSS0015 showed the highest survival at 60% and one mouse having an extended therapeutic window to 22 days post infection (Fig. 2b). Of the surviving mice, one showed sterile immunity while the others showed infection in the lungs, liver, and spleen (Fig. 2c). Creating mutants that were defective in two of

the novel virulence factors allowed complete clearance of the LAV strains from the host while maintaining various levels of vaccine efficacy.

Reduction in time between vaccination and challenge identifies BPSL0636/BPSS0015 as the most effective LAV

To further test these LAV strains we shortened the window between vaccination and challenge to determine if this would have any effect on the efficacy of our potential LAVs. As described above, BALB/c mice were vaccinated with BPSL0636/BPSS0015, BPSL0636/BPSS1818, or BPSS0015/BPSS1818 double mutants and then challenged with wildtype *Bp* 30 days post vaccination (Fig. 3a). As expected, BALB/c mice vaccinated with only PBS showed 100% mortality within the first 6 days post infection (Fig 3b). Interestingly, mice vaccinated with BPSL0636/BPSS1818 or BPSS0015/BPSS1818 also showed 100% mortality within the first week post infection (Fig. 3b). This indicates that LAVs containing a mutation in BPSS1818 in conjunction with either BPSL0636 or BPSS0015 do not provide protection immediately, requiring more than 30 days to elicit protective immunity. We suspect that at day 30 post vaccination, the host immune response is still in the process of clearing the LAV strains. Following this, the additional stress from a wildtype *Bp* infection overwhelmed the BALB/c mice leading them to succumb to infection and eventual mortality. This data suggests that BPSL0636/BPSS1818 and BPSS0015/BPSS1818 are ineffective LAVs.

BALB/c mice vaccinated with the BPSL0636/BPSS0015 double mutant showed promising results with 40% survival for the duration of the study and a mouse with an extended therapeutic window to day 62 post infection (Fig. 3b). Of the surviving mice, 100% cleared the BPSL0636/BPSS0015 double mutant indicating that this LAV strain can be cleared by the host

(Fig. 3c). One surviving mouse showed complete clearance of wildtype *Bp* while the other surviving mouse had infection in the lungs, liver and spleen (Fig. 3c). The lack of persistence of the BPSL0636/BPSS0015 LAV strain in the host after infection and the protection provided against a lethal challenge with virulent *Bp* at two time-points post-vaccination, indicates that this LAV strain is the best candidate to further test and optimize. The next step we took was to modify the vaccine schedule to see if we could provide complete protection against lethal *Bp* challenge.

***Bp* BPSL0636/BPSS0015 gives complete protection against lethal *Bp* challenge in BALB/c and C57Bl/6 mice**

To further test the most promising LAV candidate, we decided to add a homologous booster vaccination. BALB/c mice were vaccinated with a high dose of the BPSL0636/BPSS0015 LAV strain and given the same vaccination 30 days later (Fig. 4a). Thirty-three days after the booster vaccination, mice were challenged with a lethal dose of wildtype *Bp* 1026b (4,500 CFU) and monitored for 62 days (Fig. 4a). As expected BALB/c mice vaccinated with PBS-only showed rapid disease progression with an average weight loss of 17% and worsening clinical symptoms (Fig. 5a, b) leading to 100% mortality two days post challenge (Fig. 4b). Unlike PBS vaccinated mice, BPSL0636/BPSS0015 vaccinated mice lost an average 7% body weight and only showed minor clinical symptoms (Fig. 5a, b). Shortly after challenge, mice vaccinated with BPSL0636/BPSS0015 were able to recover lost weight and from clinical symptoms (Fig. 5a, b). Most significantly, BALB/c mice that were vaccinated and given a booster of BPSL0636/BPSS0015 were able to survive the entire extent of the study indicating that this LAV gave total protection against a lethal *Bp* challenge (Fig. 4b). All mice showed

some level of persistence of wildtype *Bp* 1026b in the lungs, liver, and spleen but no detectable level of the LAV strain was present in any mice (Fig. 4c).

To validate BPSL0636/BPSS0015 as an effective LAV, we decided to test it as a vaccine in another *in vivo* model. C57Bl/6 mice have been used to study the pathogenesis of *Bp*, test LAV strains, and are more resistant to *Bp* infection^{9, 23, 31}. Following the same scheme as used for the BALB/c vaccine trials, we vaccinated C57BL/6 mice with the BPSL0636/BPSS0015 LAV strain with a booster vaccination (Fig. 4a). Vaccinated and PBS vaccinated mice were challenged with a lethal dose of virulent *Bp* 1026b (12,000 CFU) and monitored for 62 days (Fig. 4a). As expected, C57Bl/6 mice vaccinated with PBS showed 14% body weight loss and rapidly increasing clinical symptoms within the first two days post challenge (Fig. 5c, d). These factors lead to 100% mortality of PBS vaccinated mice (Fig. 4d). C57Bl/6 mice vaccinated with BPSL0636/BPSS0015 were significantly protected from lethal challenge with virulent *Bp* for the duration of the study (Fig. 4d). Although all mice had some level of chronic wildtype *Bp* infection in the lungs, liver, and spleen, the LAV strain was completely cleared from the host, aligning with the results from the BALB/c vaccine trial (Fig. 4). No clinical symptoms were present in the C57Bl/6 mice at the end of the study (Fig. 5d). Taken together, the complete protection provided by the BPSL0636/BPSS0015 LAV strain in two different mouse models supports further optimization of this highly promising vaccine candidate against melioidosis.

Discussion

Bp is found in the environment of tropical regions with increasing prevalence and causes many clinical symptoms in humans that are cumulatively known as the disease melioidosis³. Infection occurs by exposure to *Bp* through inhalation, ingestion, or inoculation of the skin with contaminated soil or water⁴⁰. Due to the wide range of symptoms caused by *Bp*, it is difficult to diagnosis and has been referred to as ‘the great mimicker’^{3, 41}. Due to the high morbidity and mortality rates, ability to spread via the aerosol route, and previous use of its clonal derivative *Bm* as a bioweapon, *Bp* has been classified as a Tier 1 select agent^{40, 42-44}. Therefore, because the development of a melioidosis vaccine is important for public health and for biodefense purposes, we must pursue all potential vaccines to ensure that both military and civilian populations are protected⁴⁵. The Steering Group on Melioidosis Vaccine Development (SGMVD) have outlined critical differences between public health and biodefense that suggests that there may need to be separate vaccines for each circumstance⁴⁵. We believe that these guidelines should be followed but the development of a single vaccine for both areas of interest should not be ruled out.

Melioidosis vaccine development has included testing of subunits, glycoconjugates, nano/micro particles, whole inactivated bacteria, and LAVs⁹. In terms of LAVs against melioidosis, the *tonB/hcp1* double mutant has shown promise in the C57Bl/6 mouse model³¹. The C57Bl/6 mouse model has been the major focus of melioidosis vaccine testing in recent years because they are more resistant to acute infection, and have been suggested to develop chronic melioidosis^{9, 46}. C57Bl/6 mice are a prototypical Th1-type mouse eliciting a strong cell mediated immune response⁴⁷. Taken together, this suggests that the cell mediated skew of the C57Bl/6 mice could play a critical role in vaccine protection. On the other hand, BALB/c mice have a Th2-skewed immune response and are highly susceptible to *Bp* infection⁴⁷. The SGMVD

therefore recommends testing of vaccine candidates in both mouse models, as protection from acute forms of melioidosis is critical to extend the therapeutic window for antimicrobial intervention in both public health and biodefense scenarios⁴⁵.

In the present study we sought to test various intracellular virulence factor mutants as potential LAVs against lethal *Bp* infection. Mutants of BPSL0636, BPSS0015, and BPSS1818 represent genes of unknown function, autophagy evasion, and cytoskeletal rearrangement, respectively¹⁸. We tested single and double mutant combinations of these mutants to find a safe and protective LAV in BALB/c mice. The combinations of various virulence factors leave intracellular *Bp* arrested in unique environments allowing the immune response of the host to react in a robust and protective way before the LAV strain is cleared. Through many trials the BPSL0636/BPSS0015 double mutant showed the best protection of BALB/c mice against lethal *Bp* challenge. Furthermore, when given a booster of the LAV, BALB/c and C57Bl/6 mice were completely protected against lethal *Bp* challenge for two months. Although all mice showed persistent infection within the lungs, liver, and spleen, the extension of the therapeutic window would allow for antimicrobial intervention to help in the clearance of *Bp*. Taken together, we show that the BPSL0636/BPSS0015 double mutant is a protective LAV against melioidosis in the susceptible BALB/c mouse and the resistant C57Bl/6 mouse.

Methods and Materials

Bacterial strains, media and culture conditions *Burkholderia pseudomallei* (*Bp*) strain 1026b was routinely grown in Luria-Bertani (LB) medium (Difco) or 1x M9 minimal medium supplemented with 20 mM glucose (MG) supplemented with 0.3% glyphosate when appropriate. Manipulation of *Bp* was conducted in a CDC-approved and registered facility at the University of Hawai'i at Mānoa or Colorado State University using institutionally approved protocols and practices based on the guidelines in the BMBL, 5th edition⁴⁸ for BSL3 organisms.

Molecular methods and reagents Molecular methods and reagents were used as described previously^{28, 39, 49, 50}. Mutants of genes BPSL0636, BPSS0015 and BPSS1818 were generated previously¹⁸. Double mutant combinations were generated by using Flp recombinase to remove the *gat* cassette, followed by PCR verification, and lambda red recombineering to generate the second in frame deletion³⁹.

Animal studies BALB/c and C57Bl/6 mice between 4 and 6 weeks of age were purchased from Charles River Laboratory. All vaccinations and challenges were administered via the intranasal (i.n.) inoculation route. Mice were anesthetized with 100 mg of ketamine/kg of body weight plus 10 mg/kg xylazine as previously described. Each LAV strain was used to vaccinate five mice with 4,500 CFU or 12,000 CFU for BALB/c and C57Bl/6 mice, respectively. Primary vaccinations were carried out 30 or 60 days prior to challenge with lethal *Bp*. Booster vaccinations were carried out 30 days prior to challenge. Vaccinated mice were challenged with 4,500 CFU (BALB/c) or 12,000CFU (C57Bl/6) of wildtype *Bp* 1026b after 30 and/or 60 days

post-vaccination. Animals were monitored for disease symptoms daily and euthanized at predetermined humane end points. Clinical scores are as follows: 1-questionable illness, 2-mild illness, 3-moderate illness, 4-severe illness-moribund (pre-determined humane end point), 5-found dead. Lungs, liver, and spleen of surviving mice were harvested, homogenized, serially diluted, and plated on LB. Survival data was plotted using Prism software (GraphPad, La Jolla, CA) and statistical analysis was done by Kaplan-Meier curves.

Ethics statement All animal studies described in this manuscript were approved by the Institutional Animal Care and Use Committee (IACUC) at the University of Hawai‘i at Mānoa or by IACUC at Colorado State University and were conducted in compliance with the NIH (National Institutes of Health) Guide for the Care and Use of Laboratory Animals.

Table 1. Intracellular Infection Assessment of Virulence Factors

Assay	% of Wildtype <i>Bp</i> 1026b in Respective Assays		
	BPSL0636	BPSS0015	BPSS1818
Attachment	60.40	52.48	45.54
Invasion	25.00	45.00	165.00
Intracellular replication (2 hours)	94.23	44.23	84.62
Intracellular replication (6 hours)	175.00	625.00	150.00
Intracellular replication (16 hours)	101.77	138.94	114.16
Intracellular replication (24 hours)	71.48	14.96	16.35
Plaque/cell-to-cell spread (24 hours)	44.33	62.29	53.84

Table 2. Conservation of Virulence Factors in Pathogenic *Burkholderia* species

<i>Genus species</i>	Strain	% Amino Acid Identity Compared to <i>Bp</i> K96243		
		BPSL0636	BPSS0015	BPSS1818
<i>Burkholderia pseudomallei</i>	K96243	100	100	100
<i>Burkholderia pseudomallei</i>	1026b	100	100	100
<i>Burkholderia pseudomallei</i>	MSHR487	100	100	100
<i>Burkholderia pseudomallei</i>	MSHR503	100	100	99.54
<i>Burkholderia pseudomallei</i>	NAU44A6	99.27	99.35	99.54
<i>Burkholderia pseudomallei</i>	MSHR840	100	99.35	98.62
<i>Burkholderia pseudomallei</i>	MSHR1655	99.27	100	99.54
<i>Burkholderia pseudomallei</i>	MSHR87	99.27	100	99.54
<i>Burkholderia mallei</i>	ATCC23344	0	100	0
<i>Burkholderia mallei</i>	Ivan	100	100	0
<i>Burkholderia mallei</i>	China 5	100	100	0
<i>Burkholderia cenocepacia</i>	J2315	83.21	68.18	77.88
<i>Burkholderia cenocepacia</i>	K56-2	83.21	68.18	77.88
<i>Burkholderia cepacia</i>	LO6	83.21	68.83	79.26
<i>Burkholderia multivorans</i>	ATCC 17616	83.94	65.58	77.42
<i>Burkholderia vietnamiensis</i>	G4	83.21	69.48	78.34
<i>Burkholderia ubonensis</i>	A21	82.48	66.23	78.34
<i>Burkholderia oklahomensis</i>	C6786	91.97	87.01	95.39
<i>Burkholderia thailandensis</i>	E264	95.62	94.07	97.24

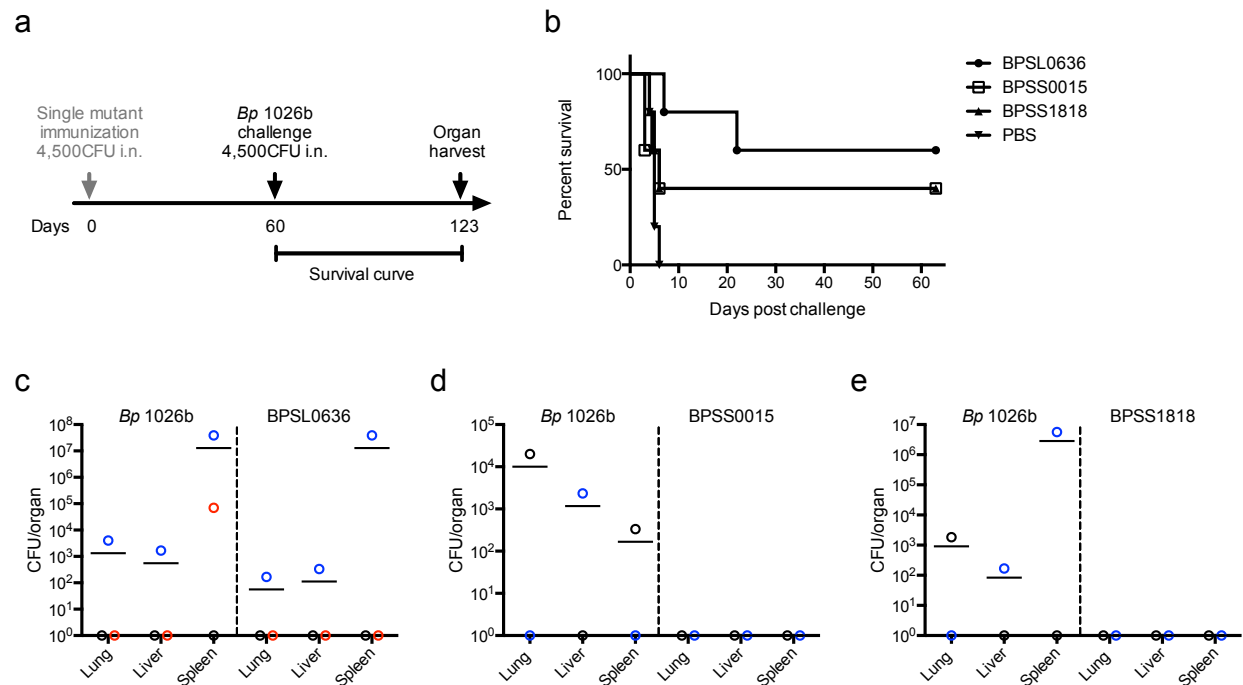


Figure 1| Vaccination with virulence factor mutants gives partial protection against lethal *Bp* infection. a) Vaccination scheme showing vaccination with mutants of BPSL0636, BPSS0015, or BPSS1818 at day 0, challenge at day 60, and organ harvest of surviving mice at day 123. b) Survival curve showing mice vaccinated with BPSL0636, BPSS0015, BPSS1818, and PBS as a control. c-e) Organ loads from vaccinated mice. Individual mice are color-coded. Left panel shows the CFU of wildtype *Bp* 1026b recovered from organs and right panel represents the CFU of the corresponding LAV strain.

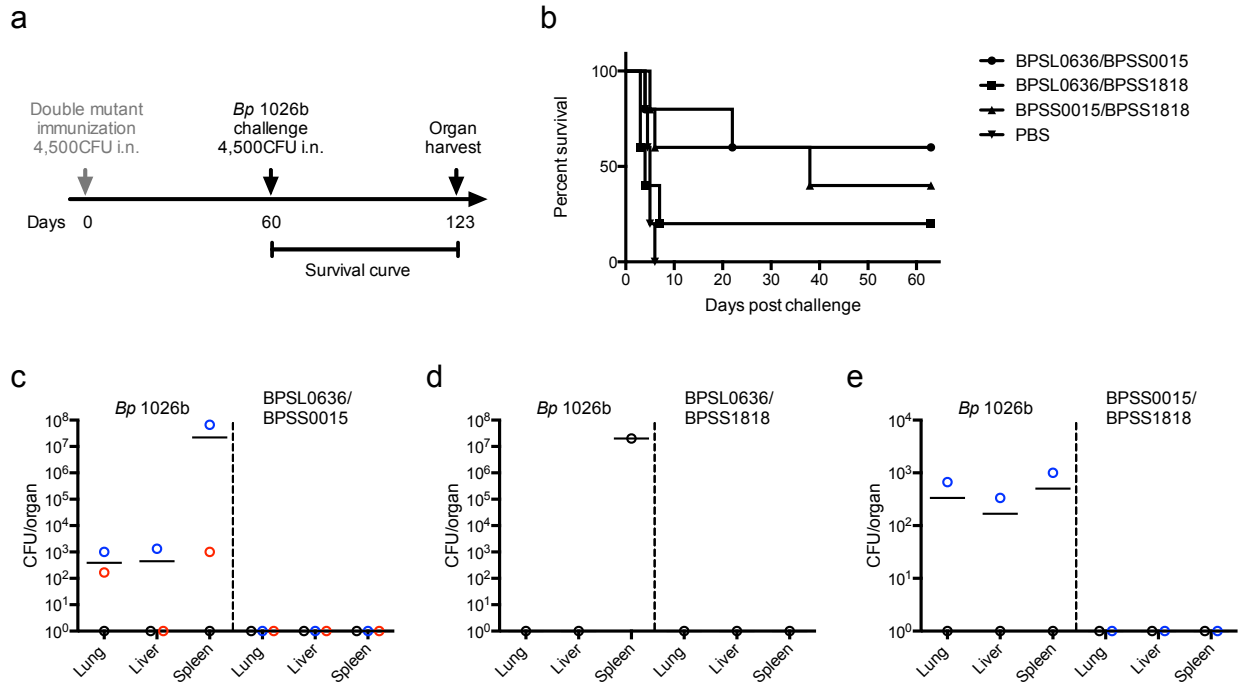


Figure 2| Double mutant vaccinations maintains protection and eliminates persistence of LAV strain. a) Vaccination scheme showing vaccination with double mutants, BPSL0636/BPSS0015, BPSL0636/BPSS1818, or BPSS0015/BPSS1818 at day 0, challenge at day 60, and organ harvest of surviving mice at day 123. b) Survival curve showing mice vaccinated with BPSL0636/BPSS0015, BPSL0636/BPSS1818, BPSS0015/BPSS1818, and PBS as a control. c-e) Organ loads from vaccinated mice. Individual mice are color-coded. Left panel shows the CFU of wildtype *Bp* 1026b recovered from organs and right panel represents the CFU of the corresponding LAV strain.

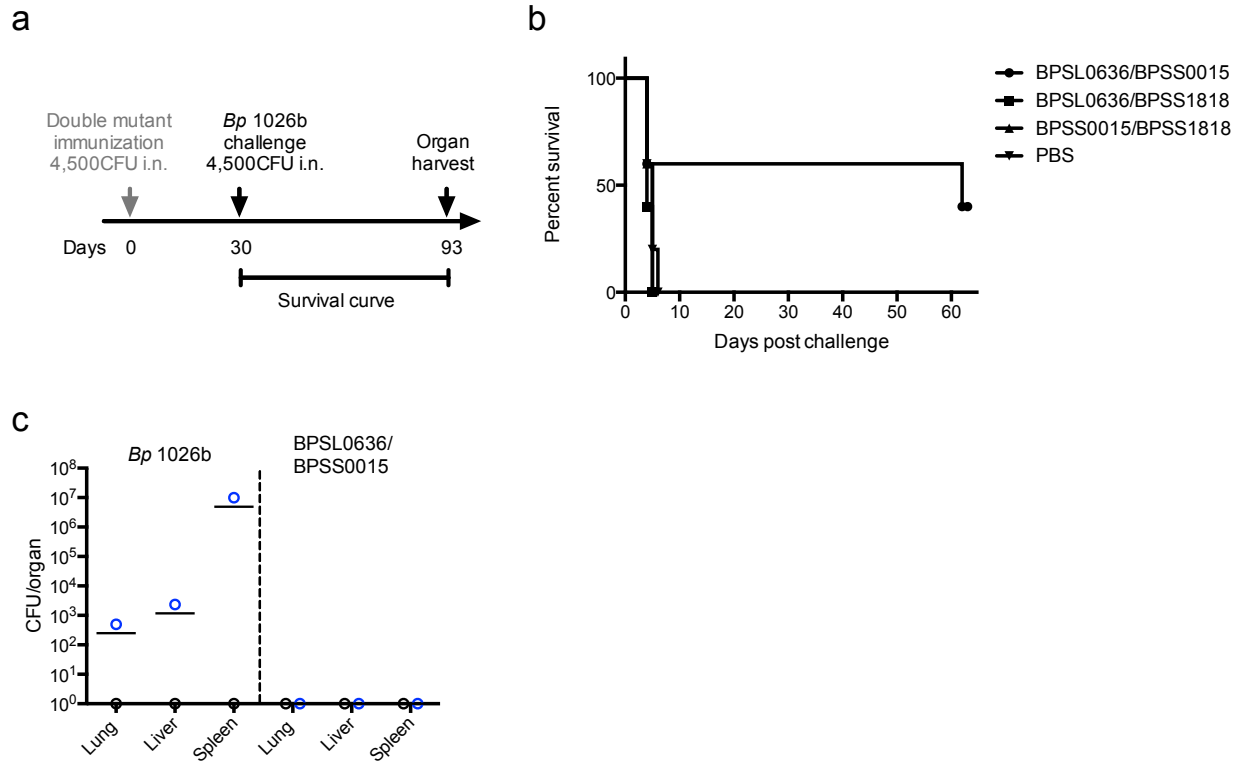


Figure 3| Challenge 30 days post vaccination identifies BPSL0636/BPSS0015 as the best LAV candidate. a) Vaccination scheme showing vaccination with double mutants, BPSL0636/BPSS0015, BPSL0636/BPSS1818, or BPSS0015/BPSS1818 at day 0, challenge at day 30, and organ harvest of surviving mice at day 93. b) Survival curve showing mice vaccinated with BPSL0636/BPSS0015, BPSL0636/BPSS1818, BPSS0015/BPSS1818, and PBS as a control. Surprisingly, BPSL0636/BPSS0015 was the only LAV strain to give protection against lethal *Bp* challenge. c) Organ loads from vaccinated mice. Individual mice are color-coded. Left panel shows the CFU of wildtype *Bp* 1026b recovered from organs and right panel represents the CFU of the BPSL0636/BPSS0015 LAV strain.

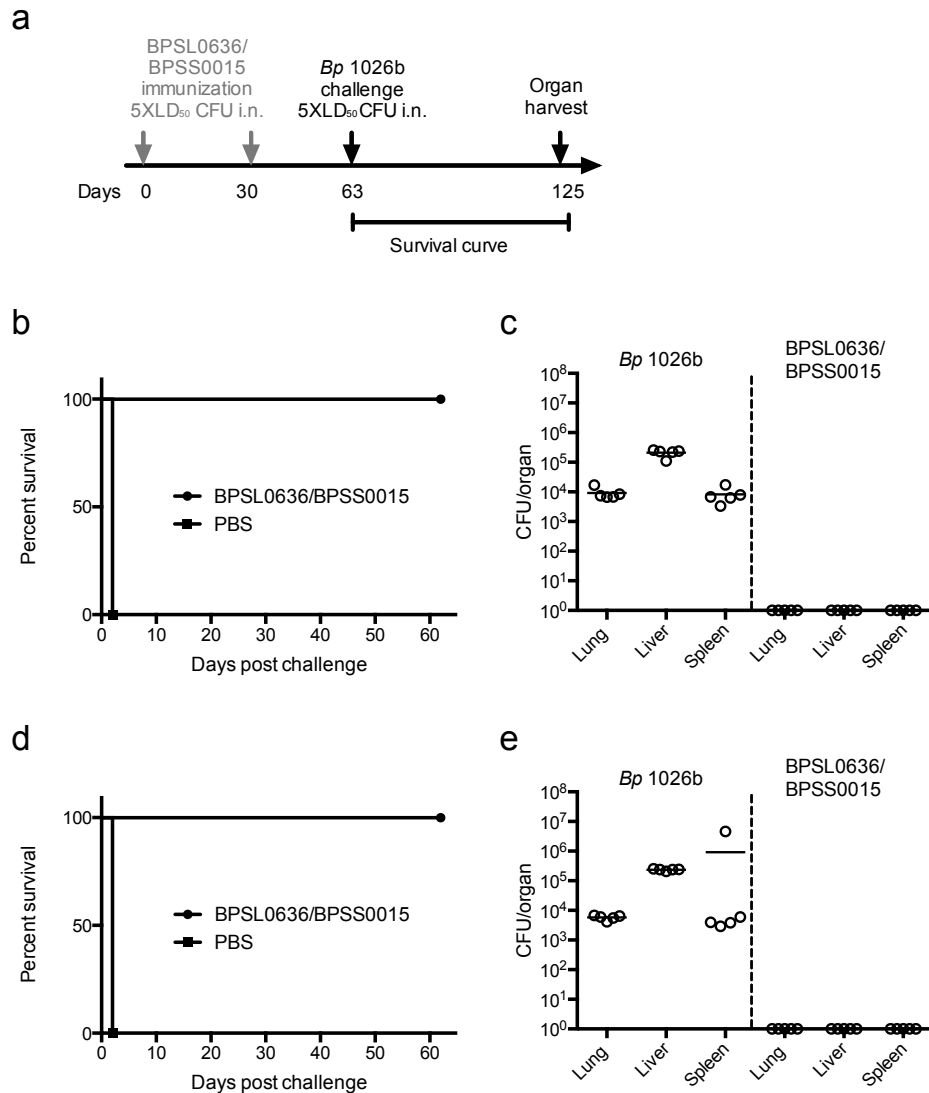


Figure 4| BPSL0636/BPSS0015 gives 100% protection to BALB/c and C57Bl/6 mice from lethal challenge with virulent *Bp*. a) Vaccination scheme showing primary and booster vaccination with BPSL0636/BPSS0015 at days 0 and 30, respectively. Mice were challenged at day 62 and organs were harvested from surviving mice at day 125. b) Survival curve for BALB/c mice vaccinated with BPSL0636/BPSS0015. c) Organ loads for BALB/c mice vaccinated with BPSL0636/BPSS0015. Left panel shows the CFU of wildtype *Bp* 1026b recovered from organs and right panel represents the CFU of the BPSL0636/BPSS0015 LAV strain. d) Survival curve for C57Bl/6 mice vaccinated with BPSL0636/BPSS0015. e) Organ loads for C57Bl/6 mice

vaccinated with BPSL0636/BPSS0015. Left panel shows the CFU of wildtype *Bp* 1026b recovered from organs and right panel represents the CFU of the BPSL0636/BPSS0015 LAV strain.

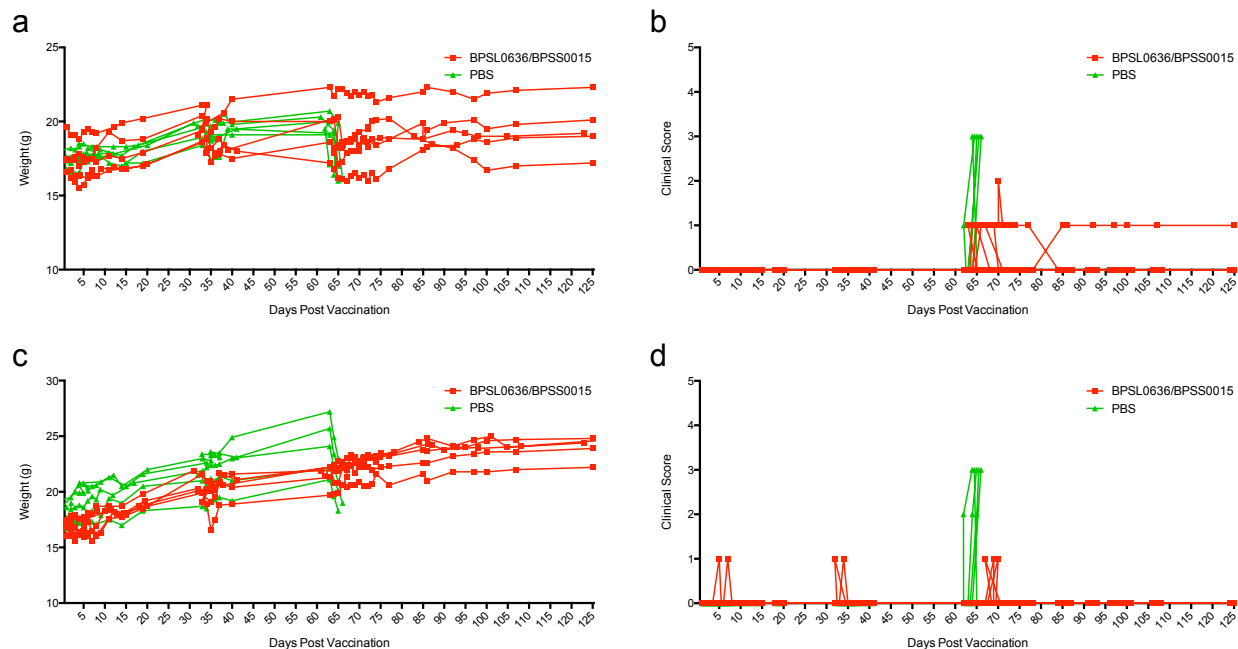


Figure 5| Clinical scores and weights over the course of vaccination and challenge. a) BALB/c mouse weights and b) clinical scores over the course of the study. c) C57Bl/6 mouse weights and d) clinical scores over the course of the study. Mice were given a booster vaccination on day 33 and challenged on day 63. Clinical scores: 1-questionable illness, 2-mild illness, 3-moderate illness, 4-severe illness-moribund, 5-found dead.

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Chapter 6:

Exploitation of *Burkholderia pseudomallei* Attachment Factors as Melioidosis Vaccines

Abstract

There has been much progress toward the development of a vaccine to prevent the tropical disease melioidosis over the last decade. The causative agent of melioidosis, *Burkholderia pseudomallei* (*Bp*) has been studied and some of its virulence mechanisms have been determined throughout its lifecycle. *Bp* is a facultative intracellular pathogen that first attaches to host cells, gains entry through the endocytic pathway, escapes into the cytoplasm where it can replicate and move freely, and finally protrudes toward neighboring cells eventually fusing the host cell membranes and spreading the infection. Surface Receptor 1 (SR1) and Surface Receptor 2 (SR2) are recently identified virulence factors that *Bp* uses for initial attachment to host cells making them attractive for vaccine development and as therapeutic targets. We used the SR1 mutant as a background strain making various double mutant strains with SR2, BPSL0636, BPSS0015, and BPSS1818, and tested them as potential live attenuated vaccines (LAVs) to no avail. Purified SR1 and SR2 were able to elicit immune responses in mice allowing the development of monoclonal antibodies (mAbs) that have neutralizing properties. These mAbs have the potential to be further developed as immunotherapies for prophylaxis or treatment of melioidosis. Finally, we combined SR1 and SR2 in a subunit vaccine that protected BALB/c mice from lethal *Bp* challenge and reduced *Bp* colonization of the lungs, livers, and spleens.

Introduction

Burkholderia pseudomallei (*Bp*) is classified a Tier 1 select agent because it causes high morbidity and mortality rates in humans, can spread via aerosols, and the precious use of *B. mallei* (*Bm*), a clonal derivative of *Bp*, as a bioweapon¹⁻⁵. *Bp* causes the tropical disease melioidosis that has an increasing global presence due to more awareness and better diagnostic and environmental surveillance⁵⁻⁷. In 2016, a group calculated the predicted global mortality rate to be ~54%, highlighting the critical need for countermeasures against melioidosis⁵. Prior to modern antimicrobial therapy treatment the mortality rate for severe melioidosis was close to 80% and the use of ceftazidime reduced it by half⁸. Currently, treatment of melioidosis patients is restricted to antimicrobial therapy through a two-stage process. Initially patients are given intravenous ceftazidime or meropenem for a minimum of approximately two weeks but can last up to eight weeks⁹. In some cases patients are given sulfamethoxazole-trimethoprim as well during the initial intensive phase therapy due to its tissue penetrating capabilities¹⁰⁻¹². Following intensive phase therapy, melioidosis patients undergo three to six months of oral eradication therapy with sulfamethoxazole-trimethoprim⁹. Even though treatment is often successful when the proper diagnosis is made and facilities are available, resistance to the frontline antibiotic ceftazidime has been observed¹³. Ceftazidime resistance is through mutation of the coding or regulatory sequences of *penA*, a class A membrane-bound β -lactamase, or deletion of the *PenA* target gene, BPSS1219¹⁴⁻²⁰. Resistance to sulfamethoxazole-trimethoprim is conferred through the expression of the BpeEF-OprC efflux pump or mutations in dihydrofolate reductase, *folA*²¹. Due to the intrinsic and adaptable nature of antimicrobial resistance in *Bp* strains and high mortality rates in endemic regions, much effort has been put towards developing vaccines to prevent melioidosis.

Over the last decade, numerous melioidosis vaccines have been tested with a wide range of outcomes. These vaccines have targeted the use of metabolic mutants, virulence factors, and surface structures of *Bp*. A *Bp* mutant in aspartate-semialdehyde dehydrogenase (*asd*) was tested as a possible live attenuated vaccine (LAV) and showed protection against acute murine melioidosis (first 30 days of challenge) but exhibited delayed symptoms leading to 100% mortality during the final 30 days of challenge in BALB/c mice²². Energy transducing inner membrane protein TonB and the monomers that form the needle like structure of the virulence-associated type VI secretion system, Hcp1, have been mutated on the genetic level and tested as a LAV showing protection for 27 days against aerosol challenge in C57Bl/6 mice²³. The *tonB/hcp1* double mutation strategy has also been successful against *Bm* infection when the mutations are made in a *Bm* background²⁴. While LAVs have been demonstrated to produce robust cellular and humoral immune responses²⁵⁻²⁷, the safety is still a major concern due to reversion back to a virulent form and the persistence of the LAV strain establishing a chronic or latent infection²⁸. Glycoconjugate vaccines have been explored extensively and utilize capsule polysaccharide (CPS) or lipopolysaccharide (LPS) and virulence-associated proteins²⁹⁻³⁵. CPS conjugated to non-toxic diphtheria toxin (CRM197) and combined with purified Hcp1 or TssM, a deubiquitinase, showed 100% and 80% protection, respectively, against a lethal *Bp* infection in C57Bl/6 mice for 35 days³⁵. Although progress has been made in the development of a melioidosis vaccine, no licensed vaccine exists. Herein, we exploit two new virulence factors, SR1 and SR2, used by *Bp* to attach to host cells, in potential LAV combinations and as a potential subunit vaccine.

Results

Surface Receptor 1 and Surface Receptor 2 are conserved among pathogenic *Bp* strains

A recent investigation into the *Bp* intracellular lifecycle identified Surface Receptor 1 (SR1) and Surface Receptor 2 (SR2) to be located on the bacterial surface, expressed during intracellular infection, and required for complete pathogenesis in cell culture and murine models of infection³⁶. SR1 and SR2 were both characterized as attachment factors for the initial stages of infection. SR1 encodes a 114 amino acid protein with a signal peptide and cleavage site between positions 22-23 while SR2 encodes a protein with 395 amino acids and an invasion/intimin cell adhesion domain between positions 65-135^{37, 38}. The proteins encoding these attachment factors are highly conserved in *Bp* strains suggesting that they might be functionally conserved (Fig. 1). SR1 is located on chromosome I and has 627 ortholog group members within the *Burkholderia* genus while SR2 is located on chromosome II and has 316 ortholog group members within the *Burkholderia* genus³⁷. A search for similar nucleotide sequences shows that SR1 is conserved in many *Burkholderia* species, with the highest abundance in the *Bp* and *B. mallei* (*Bm*) groups (Fig. 1c). While SR2 is conserved in *Bp* and *Bm*, there are no sequenced *B. cenocepacia*, *B. cepacia*, *B. ubonensis*, or *B. vietnamensis* strains that contain this gene (Fig. 1c). While there are some variations in the SR1 and SR2 conservation across the *Burkholderia* genus spectrum, the high conservation of these proteins in select agent species suggests that they could be ideal targets for vaccine development and as immunotherapeutic treatment targets.

SR1 and SR2 based live attenuated vaccines do not protect against lethal infection with *Bp*

Because SR1 is required for full pathogenesis and expressed on the surface we wanted to investigate the possibility of using the SR1 mutant strain as a potential live attenuated vaccine

(LAV). While the SR1 mutant was 100% attenuated in BALB/c mice, only 80% of mice infected with the SR2 mutant were able to survive leading us to exclude it as a single mutation LAV³⁶. We did however generate a double mutant of SR1 and SR2 to see if loss of a second attachment factor would increase protection while decreasing the likelihood of LAV reversion to a virulent state. We hypothesized that by reducing the intracellular *Bp* burden, the host will be able to develop a more robust humoral immune response leading to protection and clearance during the early stages of infection. Thirty BALB/c mice were immunized with a single dose of 4,500 colony forming units (CFU) of the SR1 mutant, the SR1/SR2 double mutant, or a PBS control (Fig. 2a). To determine if the time between immunization and challenge affects protection, half of the vaccinated mice were challenged via the intranasal route with 4,500 CFU of *Bp* 1026b after 30 days and remaining half challenged after 60 days (Fig. 2a). As expected, mice that were vaccinated with PBS alone showed significant signs of infection leading to 100% mortality within six days regardless of the time of challenge post immunization (Fig. 2b-c). Mice vaccinated with the SR1 mutant showed 80% mortality within the first 12 days when challenged 60 days after immunization (Fig. 2b). The surviving mouse showed an extension of the therapeutic window 54 days post challenge (Fig. 2b). Mice vaccinated with the SR1/SR2 double mutant and challenged after 60 days showed 100% mortality in the first nine days (Fig. 2b). Similar results were seen when mice were challenged 30 days post immunization (Fig. 2c). One mouse vaccinated with the SR1 mutant was able to survive the duration of the study but showed colonization of the lungs with wildtype *Bp* 1026b (Fig. 2d). Similarly, one mouse vaccinated with the SR1/SR2 double mutant was able to survive until the end of the study and showed colonization of wildtype *Bp* 1026b in the lungs (Fig. 2e). In both cases, the SR1 and SR1/SR2

mutants were cleared from the organs tested (Fig. 2d-e). Taken together, the SR1 and SR1/SR2 double mutants afforded little protection as LAVs against lethal *Bp* challenge in BALB/c mice.

To explore other LAV options, we generated SR1 double mutants with other virulence factors involved in autophagy avoidance, unknown processes, and tubulin rearrangement within the host. BPSS0015 is a factor involved in late stage autophagy evasion within host cells, BPSL0636 is a virulence factor with unknown function, and BPSS1818 is a factor that rearranges host cell tubulin during intracellular infection³⁶. All of these mutants are 100% attenuated in BALB/c mice suggesting that they could be used in an LAV. We generated double mutants of SR1 with BPSS0015, BPSL0636, and BPSS1818 to test them as LAVs. We hypothesize that combining an attachment deficient mutant, SR1, with other various mutations, BPSS0015, BPSL0636, or BPSS1818, in an LAV strain will shift the immune response within the host so that protection can be achieved. In addition, by mutating two different pathways in each LAV, the chance of reversion to a lethal strain is less likely. We followed the same vaccination-challenge schedule as before to test these LAVs (Fig. S1a). Mice vaccinated with SR1/BPSS1818 and the PBS control showed 100% mortality within eight days regardless of when the challenge occurred post immunization (Fig. S1b-c). Forty-percent and 20% of mice vaccinated with the SR1/BPSS0015 and SR1/BPSL0636 survived when challenged 60 days after immunization, respectively (Fig. S1b). Mice vaccinated with SR1/BPSS0015 showed 100% mortality and the therapeutic window was extended to day 43 for one mouse vaccinated with SR1/BPSL0636 when challenged 30 days after immunization (Fig. S1c). Of the surviving mice, there was significant colonization of multiple organs by *Bp* 1026b and the LAV strain (Fig. S1d-e). Because the LAV strains were not cleared and little to no protection was given, we abandoned SR1 based vaccine strains and moved towards other strategies to protect against *Bp* infection.

Monoclonal antibodies targeting SR1 and SR2 reduce *Bp* attachment to HEK293T cells

Strains lacking SR1 or SR1/SR2 gave limited protection against a lethal *Bp* challenge in BALB/c mice. We therefore shifted our focus to see if the purified SR1 and SR2 could elicit an immune response to develop monoclonal antibodies (mAbs) against each protein. This serves as both a proof-of-concept for a potential SR1/SR2 based subunit vaccine and a potential alternative therapeutic strategy utilizing mAbs to protect against *Bp* infection. SR1 and SR2 were previously purified in *E. coli* utilizing N- and C- terminal His tags, respectively³⁶. Additionally, it was shown that SR2 is immunogenic in melioidosis patient sera while SR1 was not³⁶. BALB/c mice were given an initial immunization with SR1 or SR2 with Freund's complete adjuvant (CFA) followed by subsequent boosters of SR1 or SR2 and Freund's incomplete adjuvant (IFA). Spleens were harvested and cells fused with myeloma cells to generate hybridoma cell lines. Hybridoma cell lines were diluted to purification and screened with ELISA for mAb production eventually identifying one cell line producing a mAb that targeted SR1, α SR1#140, and one cell line producing a mAb that targeted SR2, α SR2#1 (data not shown). Both mAbs were tested for their specificity against each antigen via western blot (Fig. 3a). Because each purified protein contained a His-tag for purification, we tested the specificity of each mAb against purified SR1 and SR2 to ensure that the mAbs do not bind the His-tag peptide (Fig. 3a).

To test if these mAbs are neutralizing, a *Bp* attachment assay was conducted to test each mAb. Briefly, wildtype *Bp* 1026b was incubated with α SR1#140, α SR2#1, α His-tag antibody, or PBS and then used to infect HEK293T cells for one hour, washed with PBS, and the number of attached bacteria determined by serial dilution and plating. When the mAb that targets SR1, α SR1#140, was incubated with *Bp*, attachment was reduced to 35% of wildtype attachment (Fig.

3b). When *Bp* is incubated with the mAb that targets SR2, α SR2#1, attachment was reduced to 27% of wildtype *Bp* (Fig. 3b). These reductions in attachment were comparable to mAbs that target CPS and LPS (data not shown)³⁹. Taken together, α SR1#140 and α SR2#1 reduce *Bp* attachment to HEK293T cells indicating that under the right conditions SR1 and SR2 protein can elicit an immune response with protective capabilities.

SR1 and SR2 based subunit vaccine provides protection against lethal infection with *Bp*

SR1/SR2 based LAVs showed no protection against a lethal *Bp* challenge in BALB/c mice while mAbs against SR1 and SR2 can be neutralizing. We therefore wanted to test the potential of an SR1/SR2 based subunit vaccine. To reduce the number of mice and increase the chances of success, it was decided to incorporate both SR1 and SR2 into a single vaccine. In addition to this, two adjuvants were chosen; alum, that elicits a Th2-type immune response, and monophosphoryl lipid A (MPLA), a Toll-like Receptor 4 (TLR4) agonist that elicits a strong Th1-type immune response. Cumulatively, these adjuvants are known as adjuvant system four (AS04) and have been incorporated into the licensed vaccines, Cervarix and Fendrix.

BALB/c mice were vaccinated via the intraperitoneal (IP) route with the pilot subunit vaccine, given a booster after two weeks, and bleed on week three to check if specific SR1 and SR2 antibody responses could be detected (Fig. 4a). Mice vaccinated with the SR1/SR2 based subunit vaccine showed a strong SR2 specific IgG response and a slightly smaller response to SR1 (Fig. 4b). Mice vaccinated with adjuvant only (control) showed no response to SR1 or SR2. Due to the quick and specific IgG response to the SR1/SR2 based vaccine, we decided to challenge the BALB/c mice with a lethal dose of *Bp* 1026b via the intranasal route (IN) four weeks after the initial immunization, having only given the mice a single booster vaccination

(Fig. 4a). Mice given the adjuvant control showed significant clinical signs of infection compounded by rapid weight loss within the first three days post challenge and were deemed moribund (Fig. S2a). Organs of the control mice showed significant colonization within the lungs, the initial site of infection, and disseminating infection to the liver and spleen (Fig. S2b). While vaccinated mice also showed weight loss in the first four days post challenge, fewer clinical symptoms were also observed (Fig. S2c). Vaccinated mice showed a quick recovery gaining most weight back and showing no symptoms of disease by day ten (Fig. S2c). All mice vaccinated with the SR1/SR2 based subunit vaccine survived for the duration of the study (Fig. 4c). Lungs, livers, and spleens of all vaccinated mice were harvested to determine the bacterial burden. Surprisingly, the vaccinated mice showed low levels of *Bp* colonization and one mouse showed sterile immunity (Fig. 4d). The data indicates that the pilot SR1/SR2 subunit vaccine is protective against BALB/c murine melioidosis warranting further development.

Discussion

In the present study, we examined the potential for exploiting *Bp* attachment factors SR1 and SR2 to combat and/or prevent melioidosis. We initially thought that an attachment-impaired strain of *Bp* would be a successful LAV strain. Reduced attachment would lead to a more significant humoral immune response allowing the clearance of *Bp* during early stages of infection. To our surprise this was not the case. The SR1 mutant and the SR1/SR2 double mutant showed very little protection against a lethal *Bp* challenge and only two mice were able to survive over 60 days. When we combined the SR1 mutant with other virulence factor mutants, including BPSL0636, BPSS0015, and BPSS1818 that are involved in unknown function, autophagy evasion, and host cell tubulin rearrangement, respectively, similar results were seen³⁶. It is interesting to speculate how these other virulence factors would behave in other mutant combinations as the best protection was from the SR1/BPSS0015 double mutant. However, this is beyond the scope of the current study. We believe that the failure of the SR1 based LAVs is due to the fact that these mutants elicit an immune response tailored for an extracellular pathogen. It is also plausible that the SR1 based LAVs were cleared from the system quickly leading to a weak non-protective immune response. Our data suggest that SR1 based LAVs are not effective forms of protection against *Bp* infection.

SR1 and SR2 are expressed on the surface of the cell making it a target for potential immunotherapeutic treatment³⁶. We therefore proceeded to generate mAbs that specifically target SR1 and SR2 to determine if the generated antibodies can be neutralizing. The use of mAbs targeting exotoxins and bacterial surface structures as immunotherapies have been gaining more attention recently to combat bacterial infections⁴⁰. The mAbs targeting SR1 and SR2 reduced the attachment efficiency of *Bp* to HEK293T cells. These results indicate that the

possibility of immunotherapeutic treatment using SR1 and SR2 as targets could be possible and warrant further study. Although, one mAb against each protein is a proof-of-concept, it will likely take multiple mAbs and a significant amount of screening to develop an effective immunotherapy. Because the antibodies generated from exposure to SR1 and SR2 leads to a neutralizing effect, we thought that the proteins could be incorporated into a subunit vaccine to protect against *Bp* infection.

SR1 and SR2 were combined into a single vaccine with AS04 to polarize the immune response towards a more cell-mediated immunity while maintaining the necessary humoral response²⁵. Beyond the immunological justifications for using AS04, it is also a component in two licensed vaccines, Cervarix and Fendrix, protecting against oncogenic strains of human papilloma virus and hepatitis B virus, respectively⁴¹⁻⁴⁴. We administered a primary vaccination with an identical boost and showed an antigen specific IgG response towards SR1 and SR2. The IgG response towards SR2 was larger than the IgG response towards SR1 most likely due to the large size of the SR2 protein (SR1, ~12.5kDa; SR2, ~42.5kDa). The skew of the immune response towards SR2 fits with the distribution of each protein on the surface of *Bp*. SR2 is distributed throughout the entire cell surface while SR1 is localized to the poles of the cells³⁶. Besides these observations, vaccinated mice showed complete protection against a lethal infection with *Bp* 1026b while mice given the adjuvant alone showed significant signs of disease and colonization. To compound these results, vaccinated mice showed extremely low levels of colonization in the organs tested after challenge. Although we saw complete protection and low levels of organ colonization, we believe that adjustments can be made to increase the success of this vaccine. The SR1 to SR2 ratio, the route of vaccine administration, the quantity of each antigen per dose, the ratio of antigen to adjuvant, the murine model used for efficacy testing, and

the *Bp* challenge strain are all areas that can help optimize the SR1/SR2 based subunit vaccine. The SR1/SR2 based subunit vaccine and the potential for SR1/SR2 based immunotherapies have potential for alleviating the burden on antimicrobial therapy by adding extra layers of defense against treatment and prevention of melioidosis.

Methods and Materials

Bacterial strains, media and culture conditions *Bp* strain 1026b was routinely grown in Luria-Bertani (LB) medium (Difco) or 1x M9 minimal medium supplemented with 20 mM glucose (MG) supplemented with 0.3% glyphosate (GS) when appropriate. Manipulation of *Bp* was conducted in a CDC-approved and registered facility at the University of Hawai‘i at Mānoa or Colorado State University using institutionally approved protocols and practices based on the guidelines in the BMBL, 5th edition⁴⁵ for BSL3 organisms.

Molecular methods and reagents Molecular methods and reagents were used as described previously^{22, 46-48}. Mutants of SR1 and SR2 were generated previously³⁶. Double mutants were generated by using Flp recombinase to remove the *gat* cassette⁴⁹, followed by PCR verification, and lambda red recombineering to generate the second in frame deletion in SR2, BPSL0636, BPSS0015, or BPSS1818⁴⁶.

Purification of SR1 and SR2 and subunit vaccine formulation SR1 and SR2 were purified as previously described³⁶. Equal amounts of SR1 and SR2 (50μg each) were combined with Alhydrogel® adjuvant 2% (Invivogen) and MPLA from *Salmonella minnesota* R595 (Invivogen).

Development of hybridoma cell lines Hybridoma cell line creation was done through the Monoclonal Antibody Service Facility at Kapi‘olani Community College of the University of Hawai‘i system. Briefly, BALB/c mice were vaccinated with SR1 or SR2 and Freund’s complete

adjuvant followed by subsequent boosters of SR1 or SR2 and Freund's incomplete adjuvant. SR1 and SR2 specific reactions were determined through ELISA and western blot. Spleen cells were harvested and fused with myeloma cells to generate a pool of possible hybridoma cell lines. Potential hybridoma cell lines were diluted for purification and final validation was done via western blotting.

Western blot and ELISA analysis For western blots, SR1 and SR2 were run on an SDS-PAGE gel and blotted onto a PVDF membrane overnight at 4°C. The western breeze kit (Thermo Fisher) was used and the mAbs that target SR1 and SR2 were used as primary antibodies and Goat anti-mouse-HRP used as a secondary antibody. The Novex ECL HRP chemiluminescent substrate reagent kit (Invitrogen) was used for detection. For ELISA analysis, protein was coated onto the bottom of 96-well plates at 0.5-1µg/well in PBS overnight at 4°C and blocked with BSA. Sera from mice or hybridoma cell supernatants were diluted in the wells and incubated for one hour at room temperature followed by washing with PBS. Goat anti-mouse-IgG (H+L) HRP conjugate (Invitrogen) was used as a secondary antibody. TMB substrate kit (Thermo Fisher) was via manufacturers instructions used to detect any signal with a BioTek ELx808IU.

Attachment assay Attachment assays were carried out as previously described³⁶. Briefly, HEK293T cells were washed with PBS and seeded at ~80% confluence in DMEM+FBS. *Bp* 1026b was incubated with αSR1#140, αSR2#1, αHis-tag mAb (Invitrogen), or PBS for one hour and used to infect HEK293T cells for an additional hour. HEK293T cells were washed three times with PBS, monolayers lysed with 0.2% triton X-100 in PBS, serial dilutions made, and plated on LB to enumerate the number of bacteria attached. The number of initial bacteria used

for infection was determined as well. The attachment efficiency was determined by dividing the attached number of *Bp* by the initial number of *Bp* used to infect. This experiment was done in triplicate and the error bars represent the s.e.m.

Animal studies BALB/c mice between 4 and 6 weeks of age were purchased from Charles River Laboratory. All live attenuated vaccinations were administered via the intranasal (IN) inoculation route. All challenges were administered via the IN route. LAV control mice were vaccinated with PBS. Prior to IN inoculation, mice were anesthetized with 100 mg of ketamine/kg of body weight plus 10 mg/kg xylazine as previously described²². Each LAV strain was used to vaccinate five mice with 4,500 CFU. Mice vaccinated with LAVs were challenged with 4,500 CFU of wildtype *Bp* 1026b after 30 or 60 days post-immunization. Animals were monitored for disease symptoms daily and euthanized at predetermined humane end points. Lungs, liver, and spleen of surviving mice were harvested, homogenized, serially diluted, and plated on LB and MG+0.3%GS to determine if the LAV strain had survived.

Subunit vaccinations (primary and boost) were administered via the intraperitoneal (IP) inoculation route with equal amounts of SR1 and SR2 with AS04 as the adjuvant. Control mice were vaccinated with AS04 only. Mice were bled via submandibular vein one week after the boost and IgG titers determined via ELISA. Mice were challenged with 2,075 CFU of wildtype *Bp* 1026b and clinical symptoms and weights were monitored. Clinical scores were determined with the following criteria: 0, normal ; 1, questionable illness; 2, mild but definitive illness; 3, moderate illness; 4, severe illness requiring euthanization; 5, found dead. One hundred milligrams of lungs, liver, and spleen of surviving mice were harvested, homogenized, serially diluted, and plated on LB to determine bacterial burdens. Limit of detection is ~10CFU/gram of

organ. Survival data was plotted using Prism software (GraphPad, La Jolla, CA) and statistical analysis was done by Kaplan-Meier curves.

Ethics statement Animal studies in this manuscript were approved by the Institutional Animal Care and Use Committee (IACUC) at the University of Hawai‘i at Mānoa or by IACUC at Colorado State University and were conducted in compliance with the NIH (National Institutes of Health) Guide for the Care and Use of Laboratory Animals.

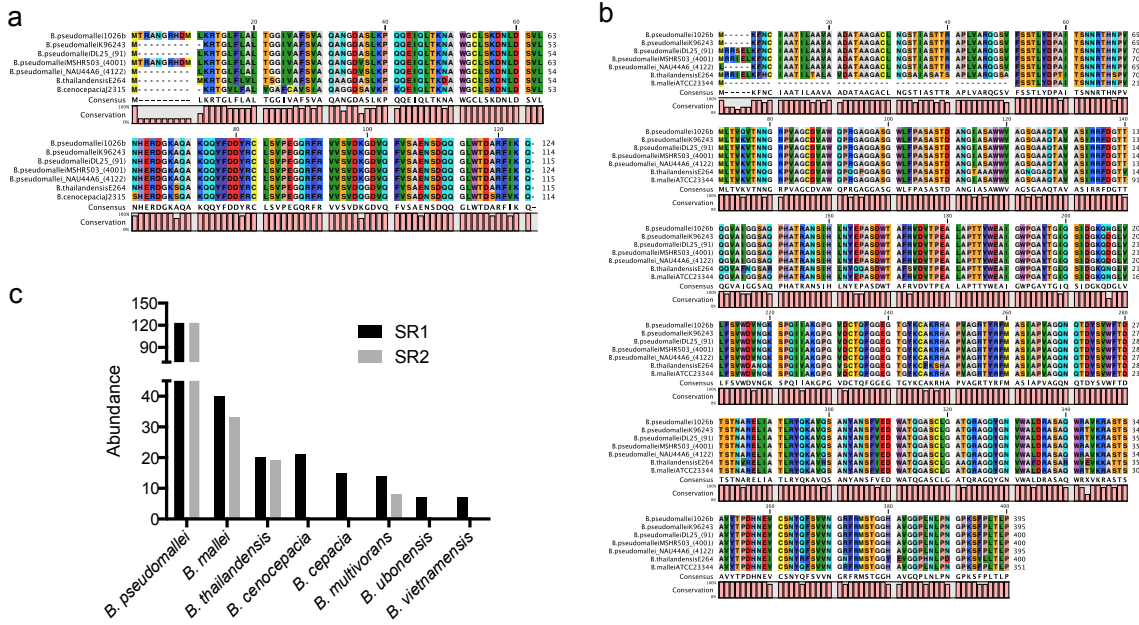


Figure 1| SR1 and SR2 are conserved in pathogenic *Bp* strains. a) Protein alignment of SR1 homologs from select *Bp* strains, *B. thailandensis* E264, and *B. cenocepacia* J2315. b) Protein alignment of SR2 homologs from select *Bp* strains, *B. thailandensis* E264, and *B. mallei* ATCC23344. c) The nucleotide sequence of SR1 and SR2 from *Bp* K96243 were used to search for homologs in each *Burkholderia* species group and the number of genomes that SR1 or SR2 are present in is plotted (abundance). Black bars represent abundance of SR1 homologs while grey bars represent SR2 homologs in each species group.

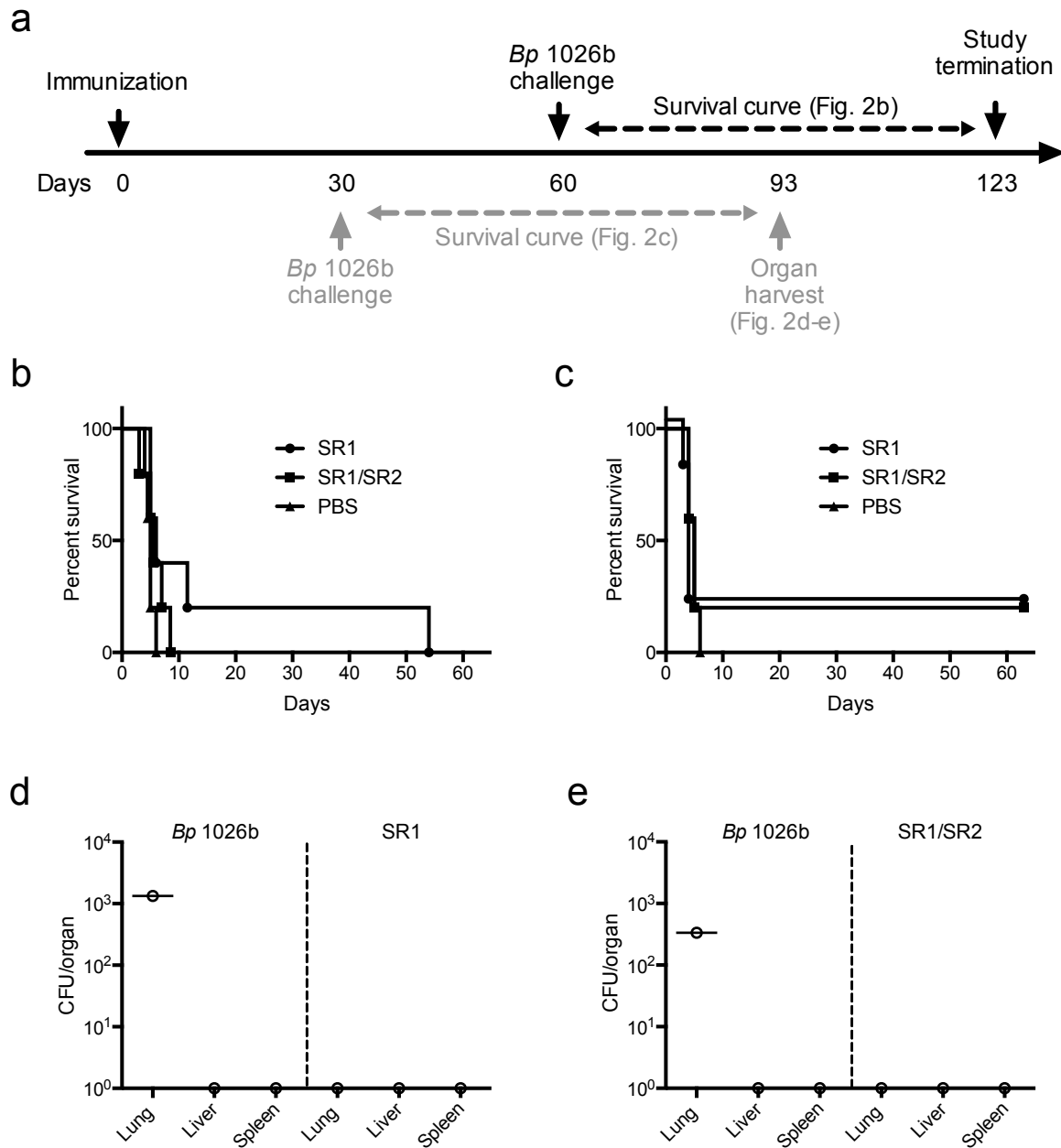


Figure 2| The SR1 mutant and the SR1/SR2 double mutant as LAVs do not protect against lethal challenge in BALB/c mice. a) An overview of the vaccination and challenge timeline. Mice were vaccinated on day zero, followed by one group of mice being challenged on day 30 and another group of mice being challenged on day 60. Mice were monitored for 63 days post challenge. b) Survival curve of mice challenged 60 days after immunization. No mice survived

the duration of the study. c) Survival curve of mice challenged 30 days after immunization. One mouse vaccinated with SR1 and one mouse vaccinated with SR1/SR2 survived to the end of the study. d) Organ loads from the surviving mouse vaccinated with SR1. *Bp* 1026b still colonized the lungs while the SR1 mutant was cleared. e) Organ loads from the surviving mouse vaccinated with the SR1/SR2 double mutant. *Bp* 1026b still colonized the lungs while the SR1 mutant was cleared.

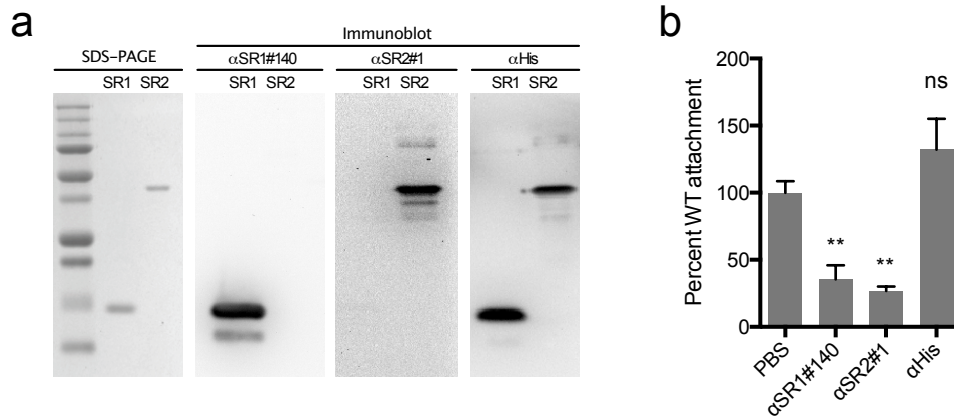


Figure 3| mAbs that target SR1 and SR2 reduce attachment of *Bp* to HEK293T cells. a) Confirmation of mAbs that target SR1 and SR2. SDS-PAGE showing purified SR1 and SR2, ~12.5kDa and ~42.5kDa, respectively. Purified SR1 and SR2 were used to generate mAbs α SR1#140 and α SR2#1. The immunoblot shows specificity of α SR1#140 towards SR1 and specificity of α SR2#1 towards SR2. Both SR1 and SR2 served as His-tag controls for the other and a α His mAb immunoblot was used as a positive control. b) α SR1#140 and α SR2#1 block *Bp* 1026b attachment to HEK293T cells while the α His mAb does not. Data in bar graphs represent means \pm s.e.m and analyzed via unpaired t-test compared to the PBS control. P values presented are as follows: ** $p < 0.01$, ns=not significant.

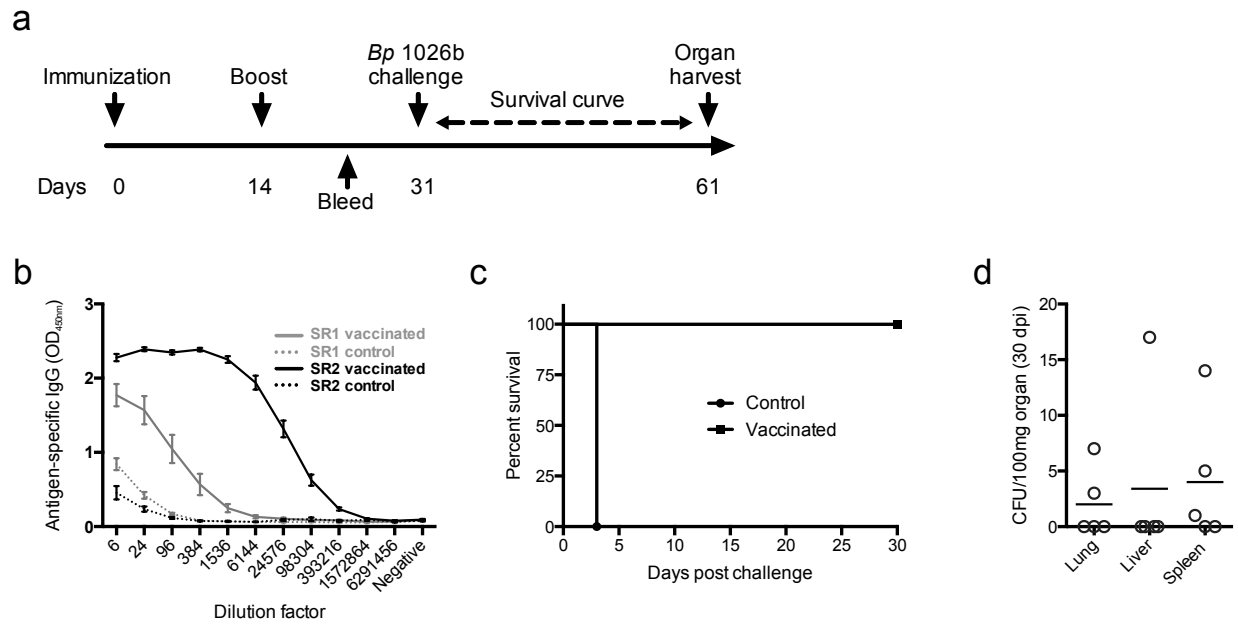
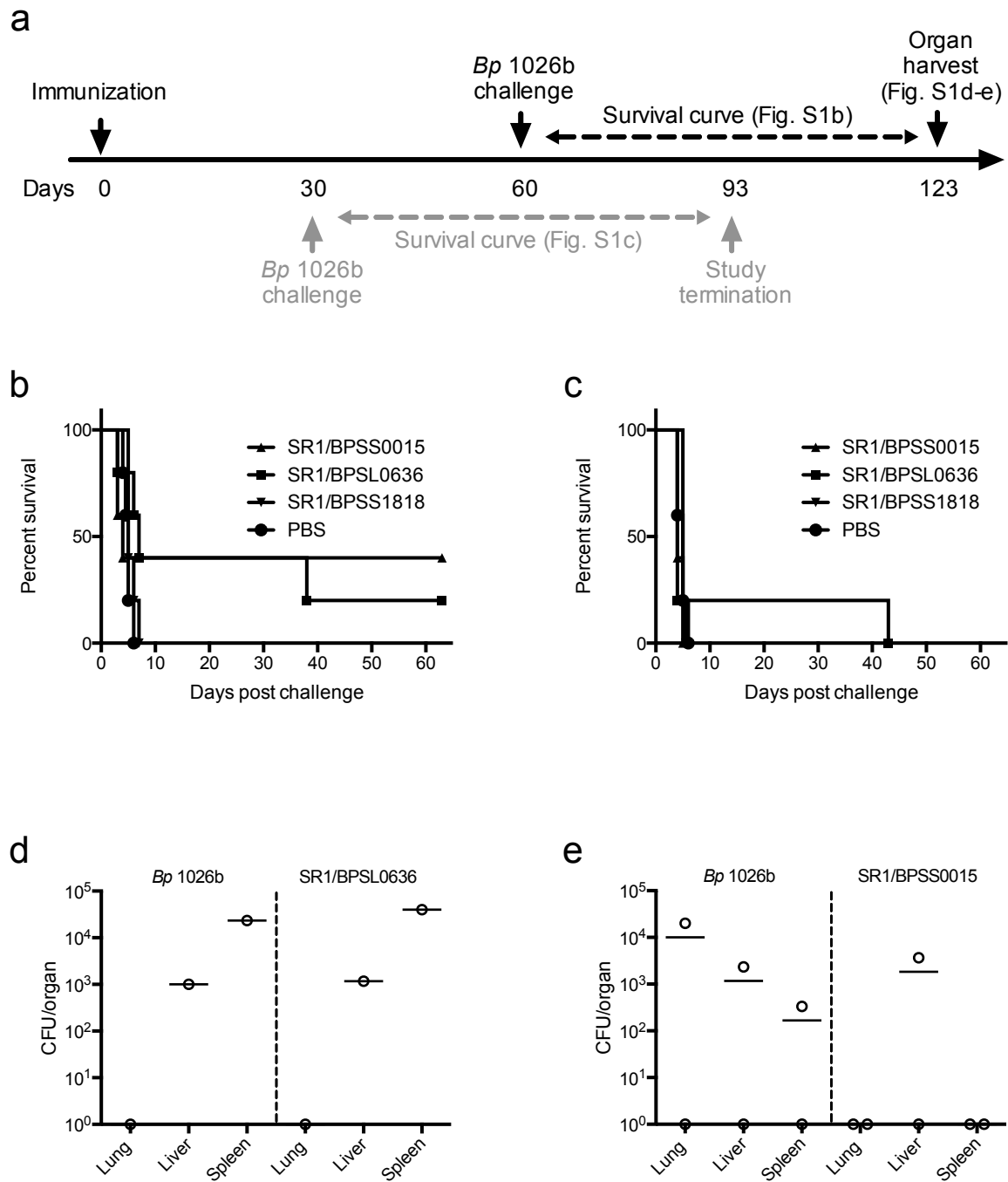
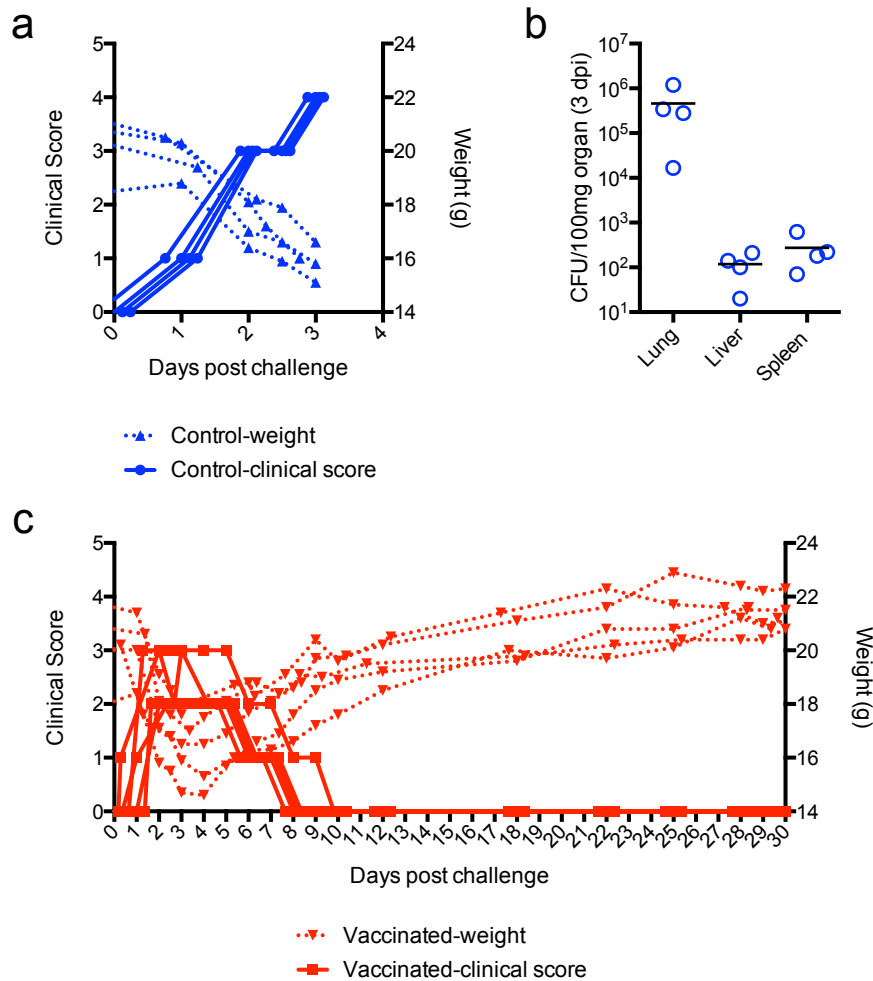


Figure 4| BALB/c mice are protected against a lethal *Bp* challenge when vaccinated with an SR1/SR2 based subunit vaccine. a) An overview of the vaccine trial. BALB/c mice were vaccinated on day zero, given an equivalent booster on day 14, bleed via the submandibular vein on day 21, challenged on day 31, and survival monitored for 30 days. b) Antigen specific IgG titers were determined for vaccinated and control mice showing that vaccinated mice had strong IgG response towards both SR1 and SR2. c) SR1/SR2 based subunit vaccine protects BALB/c mice against a lethal challenge of *Bp* 1026b. BALB/c mice given the adjuvant alone showed no protection. d) Organs from the vaccinated group showed low levels of colonization in the lungs liver and spleen at the termination of the challenge study. The limit of detection was ~10 CFU/gram of tissue.



Supplemental Figure 1| The SR1 mutant combined with various mutants as LAVs do not protect against lethal infection in BALB/c mice. a) An overview of the vaccination and challenge schedule. Mice were vaccinated on day zero, one group of mice was challenged on day 30 and another group of mice challenged on day 60. Survival was monitored for 63 days post

challenge. b) Survival curve of mice challenged 60 days post vaccination. Two mice vaccinated with the SR1/BPSS0015 mutant survived while one mouse vaccinated with SR1/BPSL0636 survived. c) Survival curve of mice challenge 30 days post vaccination. No mice survived the entire length of the study. d) Organ loads from mice vaccinated with the SR1/BPSL0636 double mutant. Wildtype *Bp* 1026b and the SR1/BPLS0636 mutant were colonizing the liver and spleen of the remaining mouse. e) Organ loads from SR1/BPSS0015 vaccinated mice. Both mice were colonized with wildtype *Bp* 1026b in various organs and one mouse had the LAV strain colonizing the liver.



Supplemental Figure 2| BALB/c mice vaccinated with SR1/SR2 based subunit vaccine recover after lethal challenge. a) BALB/c mice vaccinated with the adjuvant-only control show significant weight loss and increasing clinical scores over the first three days post challenge. b) Organ loads from control mice showing major colonization in the lungs and disseminating infection in the liver and spleen. c) BALB/c mice vaccinated with the SR1/SR2 based subunit vaccine showed weight loss and lower clinical scores that was quickly recovered over the first 10 days. Clinical scores were determined with the following criteria: 0, normal; 1, questionable illness; 2, mild but definitive illness; 3, moderate illness; 4, severe illness requiring euthanization; 5, found dead.

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Chapter 7:

Concluding remarks

Burkholderia pseudomallei (*Bp*) is a truly complex bacteria that is able to live within the rhizosphere and is a facultative intracellular pathogen of animals and humans culminating in the disease melioidosis¹. Infection with *Bp* can lead to a broad range of clinical outcomes from acute to chronic symptoms, and sometime latent onset of symptomatic melioidosis². *Bp* is classified as a Tier 1 select agent because it causes high morbidity and mortality in endemic regions, can spread via the aerosol route of infection, and has the potential to be misused as a bioweapon³⁻⁶. Case fatality rates have been reported to be ~40% with treatment⁷ and have been as high as ~70% without treatment^{8, 9}. In 2015, it was predicted that there were 165,000 cases of melioidosis worldwide and 89,000 of those cases resulted in death¹⁰. Treatment of melioidosis requires two phases of antimicrobial treatment that can last for months³. *Bp* is intrinsically resistant to many antimicrobials and has developed resistance during treatment¹¹⁻¹⁴. Due to this, the development of a melioidosis vaccine and novel therapeutic treatment is critical. In an effort to develop vaccines and therapeutics to combat melioidosis, we must first understand the mechanisms that *Bp* uses to infect and cause disease.

Windows into *Bp* pathogenesis have been opened revealing a complex lifecycle within the host cell. Briefly, *Bp* attaches to host cells, gets internalized by phagocytic or non-phagocytic cell types¹⁵, and then escapes the vacuole utilizing the a type III secretion system (T3SS-3)¹⁶⁻¹⁹. In the cytoplasm, *Bp* replicates and travels using molecular mimicry to polymerize host cell actin^{20, 21} or a lateral flagella system that is expressed in the host²². *Bp* spreads toward neighboring cells and fuses host cell membranes using VgrG and/or a type VI secretion system (T6SS-1) causing the formation of multinucleated giant cells (MNGCs)²³⁻²⁵. *Bp* encodes other virulence factors including capsule²⁶, lipopolysaccharide²⁷, and multiple T3SSs and T6SSs^{18, 20, 23}. Approximately 27% of the *Bp* genome has no known function and these genes could play an

important role during host cell infection²⁸. Recently, the transcriptional landscape of single *Bp* cells was identified at various stages of intracellular infection revealing that 1,953 genes are differentially regulated in a stage-specific manner²⁹. This result identified two areas of interest: i) many genes are required for *Bp* to maintain its normal lifecycle within the host and many of these genes have no known function; ii) a sophisticated regulation system must be in place to coordinate the expression of these genes in a stage specific manner. Within the genes that show distinct expression patterns during the *Bp* intracellular lifecycle, 33 were identified to be transcriptional regulators with no known function. The aim of this dissertation was to functionally characterize three of these transcriptional regulators, BP1026B_II1198, BP1026B_II1561, and BP1026B_II2312 in chapters two, three, and four. Furthermore, in an effort to make progress towards developing an effective vaccine against melioidosis, several vaccine trials were undertaken and described in chapters five and six.

BP1026B_II1198 is up-regulated in the vacuole, down-regulated in the cytoplasm, and up-regulated as *Bp* protrudes toward neighboring cells. A mutant of this transcriptional regulator is required for complete pathogenesis indicating that the genes that it controls play a role during the infection process. By investigating the indirect and direct transcriptional control of BP1026B_II1198 through RNA-seq and ChIP-seq, we can better understand how this regulation network contributes to pathogenesis. BP1026B_II1198 regulates genes involved in Fe-S cluster assembly and this contribution could be essential for *Bp* to rapidly react to the intracellular environment³⁰. Additionally, BP1026B_II1198 down-regulates a potential Fe-S containing transcriptional regulator, similar to RrsR³¹. This could lead to downstream transcriptional changes that should be investigated further.

BP1026B_II1561 is up-regulated as *Bp* protrudes towards neighboring cells before MNGC formation and is also required for pathogenesis in cell culture infection and a BALB/c mouse model of melioidosis. Investigation of the transcriptional network of BP1026B_II1561 showed down-regulation of propanoate and fatty acid metabolism suggesting a shift in metabolic function of *Bp* within this particular intracellular niche. In addition, broad groups of metabolism and transport were also down-regulated including amino acids, lipids, and carbohydrates. BP1026B_II1561 did however up-regulate genes in the shikimate pathway directly, and these genes were shown to be critical for pathogenesis in RAW264.7 cell infection. Enzymes of the shikimate pathway are excellent targets for drug design because this pathway is absent in mammals³²⁻³⁷. These genes that are directly controlled by BP1026B_II1561, could be excellent targets for anti-*Bp* drugs because they are expressed during infection and required for complete pathogenesis. This area of research will need to be investigated further but is an exciting avenue for melioidosis treatment research.

BP1026B_II2312 is up-regulated in the early stages of infection as *Bp* is in the vacuole. A mutant of BP1026B_II2312 is defective in intracellular pathogenesis and *in vivo* infection. Overall, BP1026B_II2312 down-regulates many pathways and genes in a stringent-like response that could be tied to the *Bp* lifecycle in an elegant way. As *Bp* begins its infection it gains entry into host cells via the endocytic pathway. Here *Bp* encounters a low nutrient environment where general metabolic pathways are not needed and specific virulence factors are required. BP1026B_II2312 down-regulates general metabolic functions including amino acid, lipid, and carbohydrate metabolism/transport, as well as transcription, translation, and DNA repair machinery. The proteins typically associated with stringent response show slight indirect control by BP1026B_II2312 through the up-regulation of *spoT*. The other gene involved, *relA*, however,

does not appear to be controlled by BP1026B_II2312. RelA/SpoT control the hyperphosphorylation of guanosine that has a direct role in the expression of genes through interaction with RNA polymerase³⁸. The small change in *spoT* regulation could have a role in this stringent-like response, but could also be due to BP1026B_II2312 on its own. In addition to this, BP1026B_II2312 regulates a citrate lyase that could be a drug target for melioidosis therapies³⁹. Isochorismatase is also up-regulated by BP1026B_II2312 and is important for the synthesis of secondary metabolites⁴⁰⁻⁴². There are no known homologs of isochorismatases in humans⁴³ and the structure of a homolog in *Burkholderia thailandensis* (96.9 % amino acid identity) has been solved⁴³ making this another excellent drug target for melioidosis treatment.

Interestingly, there is overlap between some genes and pathways controlled by several transcriptional regulators. BP1026B_II1561 and BP1026B_II2312 both down-regulate propanoate and fatty acid metabolism. This suggests that *Bp* has redundant mechanisms to control these pathways. BP1026B_II2312 is up-regulated in the vacuole and BP1026B_II1561 is up-regulated during *Bp* protrusion towards neighboring cell, both areas of critical importance to the intracellular lifecycle. *Bp* must escape the vacuole or it could be degraded by lysosomal fusion and during later stages of infection, nutrients are likely limited within the cell, due to the increase *Bp* cell density, requiring the fusion of host cell membranes to gain access to a new nutrient rich environment. The down-regulation of these metabolic pathways at early and late stages of infection suggest that *Bp* selectively shifts away from nutrient acquisition to conserve energy for expression of virulence mechanisms like T3SS-3 and T6SS-1, respectively. Overall, all three transcriptional regulators control many hypothetical proteins that require further investigation to understand their role during pathogenesis. Each transcriptional regulator controls one or more downstream transcriptional regulators that will have to be investigated as well. This

generates an even more complex picture. While the description of these transcriptional regulators gives a glimpse of the overall transcriptional network of *Bp* during pathogenesis, there is much more work to be done to fully understand how *Bp* coordinates its complex lifecycle within the host cell.

Taking several large steps forward towards translational research, within this dissertation are descriptions of two potential vaccine candidates for protecting against infection with *Bp*. A live attenuated vaccine (LAV) strain, with genetic mutations in BPSS0015 and BPSL0636, shows promise after significant optimization. C57Bl/6 and BALB/c mice vaccinated with this LAV strain were protected from a lethal infection with *Bp* 1026b but did not produce sterile immunity. The colonization within the surviving mice could eventually turn into chronic or latent melioidosis and is likely due to the large challenge dose of virulent *Bp*. To our knowledge, this is the only LAV strain, to date, that shows complete protection in both mouse models recommended for melioidosis vaccine testing⁴⁴. Testing of this LAV strain will have to be done in a diabetic mouse model and large animal model to further develop this platform. Although we see protection with this LAV strain, based on historic genome plasticity of *Bp*⁴⁵⁻⁴⁸, reversion or mutation to a virulent or persistent form is likely. For this reason, LAVs in general are not the optimal platform for a melioidosis vaccine.

A subunit vaccine incorporating two Surface Receptors (SR1 and SR2) was designed and tested in BALB/c mice. SR1 and SR2 are both expressed during infection, required for complete pathogenesis in cell culture and BALB/c mouse infection, and are conserved in *Bp* strains²⁹. These proteins were combined with an adjuvant that push a host towards a Th1 response to enhance cell-mediated immunity. BALB/c mice that were vaccinated with this pilot vaccine were protected against a lethal *Bp* challenge and showed reduced levels of organ colonization, and one

mouse with sterile immunity. This shows a major milestone in the melioidosis vaccine development as most subunit vaccine trials focus on showing protection in C57Bl/6 mice that are intrinsically more resistant to *Bp* infection^{49, 50}. While these results are exciting, optimization of this vaccine candidate will need to be undertaken.

Overall, this dissertation has delved into two regions of *Bp* research: i) virulence regulation during intracellular pathogenesis; and ii) translating the understanding of *Bp* virulence into vaccine candidates. I have described three new transcriptional regulators that control many pathways and genes important for intracellular infection. Some of the genes controlled by these transcriptional regulators are required for pathogenesis and could be potential targets for anti-*Bp* drugs. In addition this work has identified two potential vaccine candidates to protect against *Bp* infection, one an LAV and the other a highly significant subunit vaccine candidate. Taken together, this work has made a significant contribution to the overall understanding of *Bp* pathogenesis and to protection for melioidosis.

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Appendix A:

The *Burkholderia pseudomallei* intracellular ‘TRANSITome’

(As it appears when submitted to *Cell-Host and Microbe* for review in July 2020)

The *Burkholderia pseudomallei* intracellular ‘TRANSITome’

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Summary

Prokaryotic cell transcriptomics have been limited to mixed populations, sub-population dynamics, and individuality of cells within a heterogeneous population¹⁻⁴. This significantly hampers further knowledge into spatiotemporal and stage-specific processes of prokaryotic cells within complex environments. Herein, we developed a ‘TRANSITomic’ approach to profile transcriptomes of single *Burkholderia pseudomallei* (*Bp*) cells as they transit through host cell infection at defined stages, yielding pathophysiological insights. The potential bioterrorism agent, *Bp*, transits through host cells during infection in three observable stages: i) vacuole entry; ii) cytoplasmic escape and replication; and iii) membrane protrusion, promoting cell-to-cell spread⁵. The *Bp* ‘TRANSITome’ revealed dynamic global gene-expression flux as the bacterium transits through infected host cells. Some of the genes undergoing this dynamic change are required for pathogenesis. We discovered several hypothetical proteins as novel virulence determinants, and assigned them to virulence mechanisms such as attachment, cytoskeletal modulation, and autophagy evasion. Several mutants showed complete attenuation in BALB/c mice, representing potential vaccine candidates. The *Bp* ‘TRANSITome’ has provided higher resolution to the current understanding of host-pathogen interactions and opens the door for future single-cell transcriptomic analysis of other prokaryotic processes.

Prokaryotic cells undergo drastic global gene-expression changes when they encounter varying spatiotemporal niches. Such changes cannot be observed by transcriptomic analysis of mixed populations at a fixed temporal or spatial niche. We previously presented numerous potential applications for prokaryotic single-cell transcriptomics (ref 3, supplementary Figure

S1). Here we employ single-cell transcriptomic analysis to understand the ‘TRANSITome’ of *Burkholderia pseudomallei* (*Bp*), discovering novel pathophysiological processes during host cell infection.

Melioidosis, first described in 1912⁶, is an emerging tropical disease that is a significant threat to human health, caused by the facultative intracellular pathogen *Burkholderia pseudomallei* (*Bp*)⁷. Although the prevalence of *Bp* and melioidosis is expanding globally due to increasing awareness by clinicians and researchers⁸⁻¹⁶, there are still 165,000 predicted annual cases with an estimated mortality rate of 54%¹⁷. *Bp* can infect most tissues in the human body including bone, joint, skin, lung, liver, spleen, central nervous system (CNS), and genitourinary tract leading to diverse clinical manifestations, ranging from localized acute abscesses, bacteremia, septic shock, chronic infections, and, in rare cases, CNS infections, including brainstem encephalitis, making diagnosis extremely difficult^{7, 18-21}. To establish infection in a wide range of cell types, *Bp* must possess a complex network of virulence factors/pathways to survive in these different environments. The *Bp* genome contains two chromosomes, 4.07 and 3.17 megabase pairs each, that control basic metabolic pathways and accessory functions, respectively²². Thus far, only a fraction of the complex genome is understood in terms of *Bp* successfully establishing an intracellular niche.

There are a number of known virulence factors that have been characterized in *Bp*, including capsule²³, lipopolysaccharide²⁴, type III and VI secretion systems^{5, 25-29}, and BimA^{30, 31}. During its intracellular lifecycle, *Bp* attaches to host cells and gets internalized by phagocytosis or an unknown mechanism³², followed by vesicular escape using the *Burkholderia* secretion apparatus, a type III secretion system (T3SS_{Bsa}), to gain entry to the host cell cytoplasm^{5, 25, 27}. *Bp* uses Bim A, which functions through molecular mimicry as an Ena/VASP analogue, to

polymerize host cell actin^{31, 33} and its secondary flagella locus⁵ to move freely within the host cell cytoplasm. Spread to neighboring cells is then achieved by protruding and fusing host cell membranes with the virulence associated type VI secretion system leading to the formation of a multinucleated giant cell (MNGC)^{5, 26, 28, 29}. Although much of the *Bp* intracellular lifecycle has been elucidated, a large number of hypothetical/putative proteins lack characterization³⁴, suggesting a major deficiency in the current working knowledge of *Bp* pathogenesis and physiology. Due to the intricate nature of *Bp* intracellular pathogenesis, we sought to explore the transcriptomic profile of *Bp* in three distinct stages of host cell transit, the vacuole, cytoplasm, and membrane protrusion to better define this complex process.

***Bp* gene expression flux in host cells**

Bp transiting through the host experiences various environmental niches, starting from host cell entry into an intracellular vacuole, escaping from the vacuole into the host cell cytoplasm, and finally protruding towards neighboring host cells, spreading the infection⁵. Therefore, we hypothesized that, as *Bp* transits through its intracellular lifecycle, gene-expression is altered to accommodate each unique environmental niche. To probe this hypothesis, we employed our recent method of using laser capture microdissection (LCM)³⁵ and total transcript amplification³⁶ to isolate single *Bp* cells at each stage of intracellular infection and determined their transcriptional profiles, hereafter referred to as the *Bp* TRANSITome (Fig. 1a-d, Extended Data Movie 1). Comparing single *Bp* cells isolated from various stages of intracellular infection (Fig. 1a-c) to those grown *in vitro* (Fig. 1d) via microarray analysis, we show that 1,953 genes are differentially expressed in a stage-specific manner (Fig. 1e, Extended Data Fig. 1). Many genes show niche-specific expression, indicating dynamic global control of functions at

each stage of infection (Fig. 1e, Extended Data Fig. 2a). Biological triplicates from each stage of infection showed high reproducibility, supporting the validity of this approach to analyze the gene expression of intracellular pathogens (Fig. 1f). Microarray data was validated via qRT-PCR on three selected stage specific genes and three housekeeping genes (Extended Data Fig. 3a), exhibiting high correlation to validate this novel method for the investigation of intracellular pathogens (Extended Data Fig. 3b).

We observed known virulence factors that show specific expression patterns during the three defined stages of *Bp* intracellular infection (Extended data Fig. 4). For example, *Bp* uses its T3SS_{Bsa} to escape the vacuole to gain entry into the host cell cytoplasm³⁷ and this is confirmed by the up-regulation of numerous type III secretion system genes during the vacuole stage of infection (Extended Data Fig. 4a). All type VI secretion systems present in the *Bp* genome are differentially expressed compared to *Bp* grown *in vitro*, suggesting that they may be important for maintenance of intracellular infection beyond the known function of host cell membrane fusion^{26, 28, 29} (Extended Data Fig. 4b). Other significant pathways including flagella and chemotaxis genes, pilus and fimbriae genes, aerobic and anaerobic energy metabolism genes, phosphate transport genes, and potential virulence factors show significant differential regulation throughout the *Bp* TRANSITome highlighting their potential importance during infection (Extended Data Fig. 4c-g). Although the differential regulation of genes with predicted or known function is significant, it is much more intriguing that many genes of unknown functions are also differentially regulated throughout the *Bp* TRANSITome.

TRANSITome reveals uncharacterized virulence factors

The *Bp* TRANSITome consists of a large proportion of genes annotated as hypothetical or putative, having no assigned function (Extended Data Fig. 2b). We hypothesized that many of these hypothetical genes contribute to *Bp* intracellular infection in a stage-specific manner and their functions are yet to be elucidated. To investigate the function of these unknown genes in cellular pathogenesis, we targeted 206 genes and successfully created 191 in-frame deletional mutants of genes showing distinct expression patterns during the *Bp* intracellular lifecycle (Extended Data Fig. 5a). To assess their role in intracellular infection, these hypothetical/putative genes were deleted in the naturally competent prototype strain *Bp* 1026b using λ -red recombineering³⁸. Of the hypothetical genes that showed stage-specific expression, ~100 genes showed high expression in the vesicular stage of infection, while ~55 genes showed up-regulation during cytoplasmic replication, and ~74 genes were highly expressed during the process of spreading by protrusion towards neighboring cells (Extended Data Fig. 5a). The stage-specific expression of these hypothetical proteins suggests that they may contribute to different processes during intracellular infection.

The 191 mutants were screened with a qualitative cell fusion assay in RAW264.7 murine macrophages, identifying 11 mutants that showed reduced cell fusion compared to wildtype *Bp* (Extended Data Fig. 5c, Extended Data Table 1). Seven of the attenuated mutants are in genes up-regulated during the vacuole stage of infection, two mutants in genes highly expressed in the cytoplasm, and two highly expressed during the protrusion stage of infection (Extended Data Fig. 5b). The involvement of these genes during the course of host cell infection was then further assessed via a quantitative intracellular replication assay (Extended Data Fig. 5d, Extended Data Table 1). Six mutants, BPSL0097, BPSL1126, BPSL1390, BPSL1422, BPSL2714 and BPSS0015, showed defects in intracellular replication between 2 and 6 hours post-infection,

ranging from 17-75 percent wildtype replication while eight mutants, BPSL0097, BPSL0636, BPSL2714, BPSS0015, BPSS1265, BPSS1780, BPSS1818, and BPSS1860, showed 15-71 percent wildtype replication at 24 hours post-infection (Extended Data Fig. 5d, Extended Data Table 1). All 11 hypothetical genes are highly conserved in *Burkholderia* strains signifying that they may have conserved functions (data not shown). *In vitro* growth and complementation analyses show that the defects during intracellular replication are not caused by reduced *in vitro* fitness or polar effect of these mutations, which validates these genes as novel virulence factors (Extended Data Fig. 6a-b).

To further evaluate the roles of these genes in *Bp* pathogenesis, we employed multiple established infection models including HEK293T plaque formation, live cell imaging of RAW264.7 cell infection, and acute melioidosis infection in BALB/c mice^{5, 39}. Five of the mutants, BPSL1126, BPSL1390, BPSL1422, BPSL2714 and BPSS1780, showed disease progression comparable to wildtype *Bp*, indicating that even though they showed attenuation in the cell infection models (Extended Data Fig. 5c and 5d), these genes are not required for pathogenesis *in vivo* (Extended Data Fig. 6c). Mutant BPSS1265 showed delayed morbidity with 60% survival of mice over the duration of the study, suggesting that this gene could be important for acute infection but attenuation does not extend to chronic forms of murine melioidosis (Extended Data Fig. 6c). Mutant BPSL0636 showed significant attenuation in cell culture, marked by a significant reduction in plaque diameter during infection of HEK293T cells (Extended Data Fig. 7b). In RAW264.7 cells, we observed that the BPSL0636 mutant replicates to wildtype *Bp* levels during the early stages of infection, but detected a major delay in the spread and/or fusion to host cells during late stages of infection (Extended Data Table 1, Extended Data Movie 2). In addition to attenuation in two drastically different cell models, mice

infected with the BPSL0636 mutant survived the entire length of the *in vivo* study, highlighting the importance of this gene in *Bp* pathogenesis (Extended Data Fig. 7c). Eighty percent of surviving mice completely cleared the BPSL0636 mutant, while a single mouse had residual infection in the lungs (Extended Data Fig. 7c). This suggests that the BPSL0636 mutant could serve as a base strain for potential live-attenuated vaccines against melioidosis. Beyond the complete attenuation of the BPSL0636 mutant in BALB/c mice, we were unable to determine the pathogenic mechanism of this gene during infection (data not shown). As described below, several other mutants, BPSL0097, BPSS1860, BPSS1818, and BPSS0015, showed similar levels of attenuation in multiple cell lines and BALB/c mice, and additional experiments alluded to their possible pathogenic mechanisms during infection.

Hypothetical proteins aid in host cell attachment

Mutants of BPSL0097 and BPSS1860 showed an attenuated phenotype when tested in HEK293T cells (Fig. 2c and 2i, respectively, indicated by reduced plaque numbers and sizes) and the BALB/c model of melioidosis (Fig. 2f and 2m, respectively, marked by 100% and 80% survival). These genes are upregulated in the initial stage of cell infection and constitutively expressed throughout the *Bp* TRANSITome, respectively (Fig. 2a and 2g). As attachment to host cells occurs at the initial stages of infection before internalization, we investigated if these predicted outer membrane proteins have a role during this process. Mutants of BPSL0097 and BPSS1860 exhibited a significant reduction in attachment efficiency in three cell lines, RAW264.7, HEK293T, and HTB11 cells, strongly indicating an attachment function associated with these two genes (Fig. 2d and 2j, respectively). To validate that these proteins are involved in attachment, we compared wildtype *Bp* to each mutant via live-cell imaging. Wildtype *Bp* moves

through the extracellular milieu and remains in contact for an extended period of time when encountering host cells (Extended Data Movie 3). In contrast, mutants in BPSL0097 or BPSS1860 come into contact with host cells for a limited period of time, further validating these proteins as novel host cell attachment factors (Extended Data Movies 4 and 5, respectively).

To confirm the prediction that BPSL0097 and BPSS1860 are presented on the outer surface of *Bp*, we generated complemented strains expressing hemagglutinin (HA) tagged fusion proteins (BPSL0097::BPSL0097-HA or BPSS1860::BPSS1860-HA). The HA-tagged fusion strains were stained positively, via immunofluorescence (IF) with an anti-HA antibody, confirming that these proteins are located on the surface of *Bp* (Fig. 2b and 2h). Because BPSL0097-HA appears to be located on the poles of bacterium (Fig. 2b), we proceeded with immunogold labeling (IG) and transmission electron microscopy (TEM) to gain a better resolution of each protein's distribution on the bacterial surface. BPSL0097-HA showed localization limited to the poles of *Bp*, consistent with the IF result (Fig. 2e). On the contrary, BPSS1860-HA showed an even distribution across the bacterial surface via IF (Fig. 2h) and this was validated by IG TEM (Fig. 2k). Since these two surface proteins are required for full pathogenesis *in vivo* (Fig. 2f and 2m), we further evaluated their immunogenicity in clinical melioidosis via immunoblot against serum from patients with melioidosis. While BPSL0097 showed no reaction to patient sera, purified BPSS1860 was recognized specifically by pooled patient sera demonstrating its potential as a novel diagnostic target (Fig. 2l). Taken together, the data presented here highlights the discovery of these novel attachment proteins, BPSL0097 and BPSS1860, as virulence factors independently required for the progression of *Bp* infection.

BPSS1818 modulates host cell tubulin

Highly expressed in the cytoplasm (Fig. 3a), a mutant of BPSS1818 also showed interesting phenotypes during *in vitro* and *in vivo* infections (Fig. 3). The mutant of BPSS1818 was highly attenuated in RAW264.7 cells (Extended Data Fig. 5d and Table 1) as well as in HEK293T cells (Fig. 3b). More importantly, the BPSS1818 mutant was 100% attenuated in BALB/c mice, indicating that it is essential for *in vivo* pathogenesis (Fig. 3d). To better investigate the associated pathogenic function of this gene, we revisited our *in vitro* infection models. During infection of RAW264.7 cells with the BPSS1818 mutant, we noticed a major phenotypic change in the overall monolayer morphology when compared to cells infected with wildtype *Bp* (Extended Data Movie 6, Fig. 3c). Cells infected with the BPSS1818 mutant appears to be varied in overall cytoskeletal structure after extensive host cell fusion, and the ‘stretched-out’ MNGCs were unable to collapse into a spherical structure (Extended Data Movie 6, Fig. 3c). This finding suggests that BPSS1818 modulates the host cell cytoskeleton leading to this phenotype in the absence of BPSS1818. Modulation of the host cell cytoskeleton components myosin, actin, and tubulin by BPSS1818 was determined by IF. There were no morphological changes in myosin and actin filaments, between RAW264.7 macrophage cells infected with BPSS1818 and wildtype *Bp* (data not shown). On the other hand, RAW264.7 cells infected with the BPSS1818 mutant showed variations in the morphology of tubulin, as noted by elongated polymers when compared to the wildtype *Bp* infected host cells (Fig. 3e). The data support the contention that BPSS1818, which modulates host cell tubulin, is required for full pathogenesis of *Bp*. *Bp* has been shown previously to modulate host cell actin³¹, but, to our knowledge, this is the first report showing that *Bp* affects tubulin during infection of the host cell.

***Bp* evades autophagy clearance via BPSS0015**

The *Bp* TRANSITome revealed that the BPSS0015 gene was highly expressed in the protrusion stage during host cell infection, suggesting its importance for later steps of the infection lifecycle (Fig. 4a). A mutant of this gene showed a significant decrease in intracellular replication and plaque sizes in RAW264.7 and HEK293T cells, respectively (Extended Data Fig. 5d, Fig. 4b). When used to infect BALB/c mice at a lethal dose, all mice survived during the entire study period, indicating that the BPSS0015 gene is an essential virulence determinant for *Bp* pathogenesis *in vivo* (Fig. 4f). Unlike mutants of BPSS1818, BPSL0636, and BPSS1860, the BPSS0015 mutant was able to persist and disseminate to the spleen and liver of surviving mice (Fig. 4f). Upon closer examination using the cell infection model, the BPSS0015 mutant appeared to be trapped in membrane-bound structures (data not shown). To confirm this observation, RAW264.7 cells infected with wildtype *Bp* and the BPSS0015 mutant were processed for TEM. The BPSS0015 mutant was encompassed by single and double membrane-bound vacuoles, properties of autophagy clearance, while wildtype *Bp* are not associated with any membrane-bound structures within the cytoplasm (Fig. 4d). A common marker of autophagy, LC3⁴⁰, was then chosen to evaluate if BPSS0015 was linked to autophagy evasion. HEK293T cells stably expressing LC3-GFP were infected with the BPSS0015 mutant and wildtype *Bp* to assess variations in co-localization with the host cell LC3. While wildtype *Bp* does not associate with the LC3-GFP puncta, the BPSS0015 mutant shows high levels of co-localization (Fig. 4e). These data taken together imply that the BPSS0015 mutant is unable to avoid host cell autophagy clearance during the late stages of infection. To further test this hypothesis, we utilized two chemical modulators that control the level of host cell autophagy, rapamycin and 3-methyladenine⁴¹. Rapamycin, a stimulator of host cell autophagy, reduced the intracellular burden of wildtype *Bp* and the BPSS0015 mutant compared to the control infection (Fig. 4c). An

infection supplemented with 3-methyladenine, a suppressor of host cell autophagy, showed no effect on wildtype *Bp* intracellular replication, further supporting the ability of wildtype *Bp* to avoid host cell autophagy clearance (Fig. 4c). On the contrary, BPSS0015 mutant aided by 3-methyladenine was able to recover its ability to replicate within the host cells (Fig. 4c). Taken together, the data indicates that *Bp* is able to avoid host cell autophagy during the late stages of infection and that the BPSS0015 gene is involved in this autophagy evasion mechanism. Although previous studies have shown that during initial stages of infection (<6 hours post infection) *Bp* avoids LC3-associated phagocytosis^{37, 41}, this is the first investigation to identify a gene involved in *Bp* evasion of autophagy during late stages of infection.

Model of *Bp* intracellular pathogenesis

In summary, we have dissected and defined the intracellular TRANSITome of *Bp*, a globally significant pathogen. Thousands of known and unknown genes and pathways undergo dynamic gene-expression flux as *Bp* transits through distinct environmental niches in the host cells. The *Bp* TRANSITome led to the discovery of several virulence factors that are required for complete *Bp* pathogenesis. Comprehensive screens of 191 mutants and functional characterizations determined potential functions for some of these virulence factors during *Bp* infection of host cells. Based on the data presented, we suggest assigning functions to four of these virulence factors: BPSL0097 and BPSS1860 as surface attachment proteins, BPSS1818 as a modulator of host cell tubulin, and BPSS0015 as a factor involved in evasion of host cell autophagy (Extended Data Fig. 8). These virulence determinants have the potential to be exploited as therapeutic targets and vaccines against melioidosis. Beyond the findings presented in this research, the TRANSITome data (Extended Data Fig. 1) could be mined for information

about other intracellular *Bp* processes. Finally, this approach of single prokaryotic cell transcriptomics can be applied towards numerous pathogens expanding the possibilities for understanding host-pathogen interactions.

METHODS AND MATERIALS

Bacterial strains and eukaryotic cell lines, media, and culturing conditions. All manipulation of *Bp* was conducted in a CDC-approved and -registered BSL3 facility at the University of Hawaii at Manoa with all experiments approved by the Institutional Biosafety Committee (reference number: 16-07-004-585-1R) and were performed using BSL3 practices following recommendations set forth in the BMBL, 5th edition. *Escherichia coli* EPMax10B-*lacI*^q-*pir*⁴² was routinely used as a cloning strain. The *Bp* wildtype strains, K96243 and 1026b, and their derivatives were cultured in LB or 1x M9 minimal media supplemented with 20 mM glucose (MG). For selection of glyphosate resistance gene (*gat*) in *E. coli* and *Bp*, MG medium supplemented with 0.3% (w/v) glyphosate was used. Murine macrophage cell line (RAW264.7), human embryonic kidney cell line (HEK293T), and human neuroblastoma cell line (HTB-11 a.k.a. SK-N-SH cells) were used in this study for *Bp* infection. The eukaryotic cell cultures were grown in DMEM medium (Hyclone) supplemented with 10% FBS (Hyclone) at 37°C with 5% CO₂, and the Antibiotic-Antimycotic reagent (Invitrogen) was added at 1x concentration for cell culture maintenance but omitted during *Bp* infection studies.

Molecular reagents and methods. All molecular reagents and methods were used as previously described^{43, 36}.

Macrophage infection with fluorescence-tagged *B. pseudomallei*. The *Bp* wildtype strain K96243 was labeled with red- and yellow-fluorescence proteins for easy visualization during macrophage infection. Briefly, the pUC57-PS12-*yfp*⁴⁴ was digested with NcoI, blunt-ended, and the *yfp* gene was ligated with the mini-Tn7-*gat-rfp*⁴⁴ backbone digested with BamHI and blunt-ended. The *yfp* gene is in the same orientation as the *rfp* gene in the resulting plasmid and both genes are driven by a constitutive promoter in *Bp*, PC_{S12}⁴⁵. The mini-Tn7-*gat-rfp-yfp* plasmid was then conjugated into K96243 along with the helper plasmid pTNS3-*asd*_{Ec}⁴⁶. *Bp* with insertion of the mini-Tn7 plasmid at the *attTn7* site was confirmed by PCR as previously described⁴². Stable expression of the RFP and YFP proteins was confirmed and used for macrophage infection study.

The macrophage infection with *Bp* was carried as follows. First, the RAW 264.7 cells were seeded onto 0.17 mm PET membrane coated MembraneSlides (Carl Zeiss) that were pretreated with UV and then 150 µg/ml poly-L-lysine. The RFP-YFP-tagged *Bp* strain was grown to mid-log phase (OD₆₀₀ ~ 0.8) and diluted to approximately 4x10⁵ CFU/ml in DMEM medium. RAW264.7 cells were infected at a multiplicity of infection (MOI) of 0.2 for 30 minutes and extracellular *Bp* were washed away with 1x PBS. Fresh DMEM medium supplemented with 10% FBS was then added to the membrane slides. At 1, 2, 6 hours post-infection, the membrane slides were washed with 1x PBS and immediately fixed with 1% (w/v) paraformaldehyde for 5 minutes followed by 70% (v/v) ethanol for 30 minutes. To obtain the control *Bp* cells as the baseline for microarray comparison, the same diluted *Bp* culture as above was incubated in the DMEM medium for 1 hour, harvested by centrifugation and resuspended in 1% (w/v) paraformaldehyde for 5 minutes. The fixed bacteria were then smeared on to the membrane slides, treated with 70% (v/v) ethanol for 30 minutes.

To visualize *Bp* at different stages during macrophage infection, we stained the macrophage plasma and vacuolar membranes and actin with FM 4-64FX lipophilic dye and Oregon Green 488 Phalloidin (Thermo Fisher Scientific), respectively. The fluorescent images were obtained on a Zeiss PALM laser catapulting system with 100x oil immersion objective. Single *Bp* cells from the various stages (vacuole, cytoplasmic replication, and protrusion) of infection were cut by the focused laser and catapulted with unfocused low-intensity laser into the 0.2 ml PCR tube lid containing lysis buffer^{36, 43}. For the control condition (*Bp* grown in DMEM), a total of nine *Bp* cells were catapulted into the same PCR tube before processing. Single *Bp* cells and pooled control *Bp* cells were processed using previously described methods^{33, 40}.

Two-color microarray and data analysis. Transcriptomic analysis was carried out with the *B. mallei/pseudomallei* 70mer oligo arrays (kindly provided by the J. Craig Venter Institute) as previously described².

Gene assignment and pathway designation. Gene description, function prediction, and functional category assignment was assisted for some genes using Burkholderia Genome database (<http://www.burkholderia.com>)³⁴ and Kyoto Encyclopedia of Genes and Genomes (KEGG)⁴⁷.

Real-time RT-PCR. Validation of microarray data with Real-time RT-PCR was performed as previously described⁴⁸, with the exception of using Taqman probe instead of SYBR green detection. Three housekeeping genes, BPSL0602, BPSL2502, and BPSS2061, that have consistent expression levels across all conditions tested were chosen based on our microarray

data, as well as published transcriptomic data⁴⁹. Data were processed and fold-changes were calculated as previously described⁴³.

Engineering of the *Bp* 1026b virulence factor mutants. Chromosomal mutant knock-outs were attempted for 206 spatially upregulated *Bp* hypothetical genes in wildtype 1026b strain, using λ -RED recombineering as previously described³⁸. We successfully mutated 191 of the 206 genes attempted. All mutants were verified using PCR.

Growth curves of *B. pseudomallei* 1026b mutants. Growth curves were initiated by growing the 1026b wildtype and various mutant strains overnight, then diluting 200 \times into fresh LB. The 96-well plate was incubated at 37°C with shaking in the BioTek ELx808IU and measuring the OD₆₀₀ every 30 minutes for 30 h. Each growth curve was done in triplicate and average was presented with the standard error of the mean (s.e.m).

Cell infection assays. Intracellular replication assays were carried out using a modified aminoglycoside protection assay as previously described^{32, 50}. Briefly, RAW264.7 cells were seeded at ~80% confluence, infected at an MOI of 1 for 1 hour, washed with 1 \times PBS, and then fresh DMEM+FBS containing 750 μ g/ml amikacin and 750 μ g/ml kanamycin was added. At various time points post infection, monolayers were washed two times with 1x PBS, lysed with 0.2% triton X-100 in PBS, and dilutions of lysates were plated onto LB to enumerate intracellular bacteria. Attachment assays were carried out with various cell lines at an MOI of 1. For attachment efficiency test, infection was initiated similarly as the intracellular replication assay, and at 1 hour post infection (hpi) the bacteria-containing medium was removed, the

monolayers were washed 3 times with PBS, and lysed with 0.2% triton-X100 in PBS, diluted, plated onto LB to enumerate attached bacteria. The attachment efficiency was determined by dividing the attached number by the initial number of infecting bacteria. All Experiments were carried out in triplicate and error bars represent the s.e.m.

Plaque assays were carried out in confluent monolayers of HEK293T cells in 24-well plates. *Bp* 1026b strains were used to infect monolayers at an MOI of 1. After one hour, monolayers were washed with 1x PBS and overlaid with DMEM+FBS supplemented with 1.2% low-melt SeaPlaque agarose (Lonza) and 750 µg/ml amikacin and 750 µg/ml kanamycin. At 24 hpi, monolayers were fixed with 4% paraformaldehyde (PFA) in 1x PBS for 45 min. Monolayers were stained with a 1% crystal violet solution for ease of viewing. Plaques were viewed with a Zeiss AxioObserver D1 and the accompanying AxioVision 64 bit 4.9.1 software was used to measure plaque diameter. Plaque assays were carried out in triplicate and 10 to 20 plaques per replicate were measured for comparison.

Chemical modulation of autophagy was carried out as previously described with minor modifications⁴¹. Briefly, RAW264.7 cells were treated with either 4 µM rapamycin or 10 mM 3-methyladenine 1 hpi and bacterial cell counts determined at 24 hpi as described above.

Immunofluorescence and transmission electron microscopy. The BPSL0097 and BPSS1860 mutant strains were complemented with translational HA (human influenza hemagglutinin)-tagged BPSL0097, or BPSS1860, respectively. Mutants and the complemented strains were stained with primary mouse anti-HA antibody (anti-HA-Fluor 594), followed with secondary goat-anti-mouse antibody Alexa Fluor 488-10 nm colloidal gold conjugate (Thermo Fisher Scientific). Labeled bacterial cells were visualized using a Zeiss D1 observer fluorescence

microscope and a 120 kV Hitachi HT7700 digital transmission electron microscope.

For visualization of the BPSS0015 mutant infected macrophage cells, 60 mm tissue culture dishes were treated with 150 µg/ml poly-L-lysine and RAW264.7 murine macrophages were seeded and allowed to attach overnight. Wildtype *Bp* 1026b and the BPSS0015 mutant strain were used to infect the monolayers as described above. At 24 hpi, the media was removed and the monolayers were fixed for 2 hours with 2.5% glutaraldehyde in 0.1 M sodium cacodylate buffer at pH 7.4. The dishes were washed twice with 0.1 M cacodylate buffer for 20 minutes each. Samples were post-fixed in 1% osmium tetroxide in 0.1 M cacodylate buffer for 1 hour then dehydrated in a graded ethanol series. Epoxy resin was used to infiltrate samples and allowed to polymerize at 60°C for 2 days. Samples were visualized using a 120 kV Hitachi HT7700 digital transmission electron microscope. Images were captured using an AMT XR-41 2048 x 2048 pixel bottom-mount high-resolution camera.

For visualization of LC3 colocalization to the BPSS0015 mutant or wildtype *Bp*, HEK293T cells were transfected with pEGFP-LC3 (Addgene #21073) using Lipofectamine 2000 Reagent (Invitrogen) following the manufacturers protocol. Wildtype *Bp* 1026b and the BPSS0015 mutant strain were used to infect, as described above, the monolayers stably expressing LC3-GFP. At 24 hpi, monolayers were fixed with 1% PFA for 1 hour, permeablized with 0.2% triton X-100, stained with DAPI and FM 4-64FX lipophilic dyes, and visualized using Zeiss D1 observer fluorescence microscope.

For visualization of BPSS1818 mutant infected macrophage cells, the infected monolayer was stained by red plasma membrane stain (Fig. 3c), or DAPI and β -tubulin antibody conjugated with Alexa Fluor 594 (Fig. 3e). Images were captured with an AxioObserver D1 and accompanying Axiovision 4.9.1 software. Multi-color fluorescent images were captured with the

multichannel fluorescence acquisition module of the Axiovision software. Images were deconvolved using the imageJ plugin Iterative Deconvolve 3D.

Live-cell time-lapse imaging. Light microscopy of infected cell monolayers was carried out as described⁴⁴, except for a few modifications. Glass bottom 12-well plates were obtained from MatTek Corporation and treated with 150 µg/ml poly-L-lysine. Monolayers were seeded and infected with bacteria in 200 µl of DMEM+FBS at an MOI of 10. After 1 hour the medium containing bacteria was removed, the monolayers were washed two times with 1XPBS, and DMEM containing 750 µg/ml amikacin and 750 µg/ml kanamycin was added for the remainder of the experiment. Live-cell imaging was taken on an Olympus microscope equipped with the Weather Station incubation system at 37°C with 5% CO₂. Images were captured at 1 frame/5 minutes for 24 h. Images were compiled into videos using ImageJ.

Animal studies. BALB/c mice between 4 and 6 weeks of age were purchased from Charles River Laboratory. Animals were anesthetized with 100 mg/kg ketamine plus 10 mg/kg xylazine and infected with *Bp* via the intranasal (i.n.) route³⁹. Groups of mice (n=5) were challenged with a dose of 4,500 CFU (5× LD₅₀ for wildtype *Bp* 1026b), monitored daily for disease symptoms, and euthanized according to pre-determined humane endpoints. The lungs, liver, and spleen of surviving mice were removed, homogenized, and serial diluted to determine bacterial burdens. Statistical differences in survival times were determined by Kaplan-Meier curves followed by the log-rank test.

Ethics statement. The animal studies described in this manuscript were conducted in compliance with the NIH (National Institutes of Health) Guide for the Care and Use of Laboratory Animals and approved by the Institutional Animal Care and Use Committee at the University of Hawaii at Manoa (Protocol No. 10-1073).

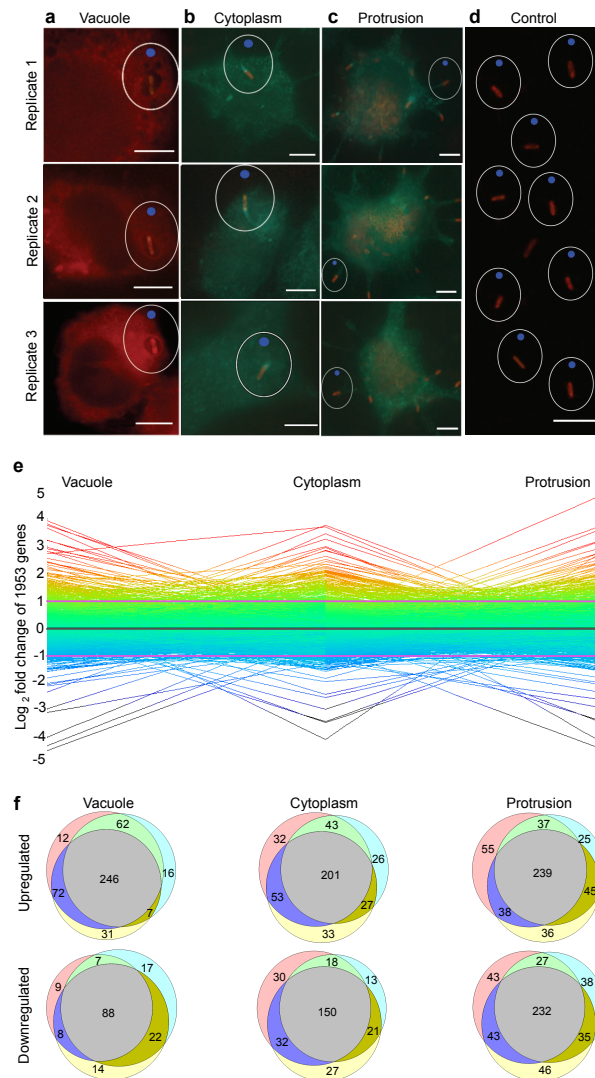


Figure 1| Single *Bp* cell isolation and the TRANSITome. a-d) YFP-RFP-tagged *Bp* infected RAW264.7 cells were fixed and stained red (plasma and vacuolar membranes) and green (actin). Single *Bp* cells were isolated from macrophage vacuoles (a), cytoplasm (b), and during membrane protrusion (c). *Bp* control cells were grown in DMEM medium and isolated as the baseline for gene expression analysis (d). Scale bars = 5 μ m. Single bacterial cells were cut with the focused laser (white circle) and catapulted using the low intensity unfocused laser (blue dot) by LCM. e) *Bp* undergoes dynamic gene expression changes relative to the control cells as it

transits through the host cell. Each line represents a single gene with \log_2FC represented in a rainbow color scheme. f) Genes up-regulated ($\log_2FC > 1$) and down-regulated ($\log_2FC < -1$) showed high reproducibility among biological triplicates. Each color circle represents a biological replicate.

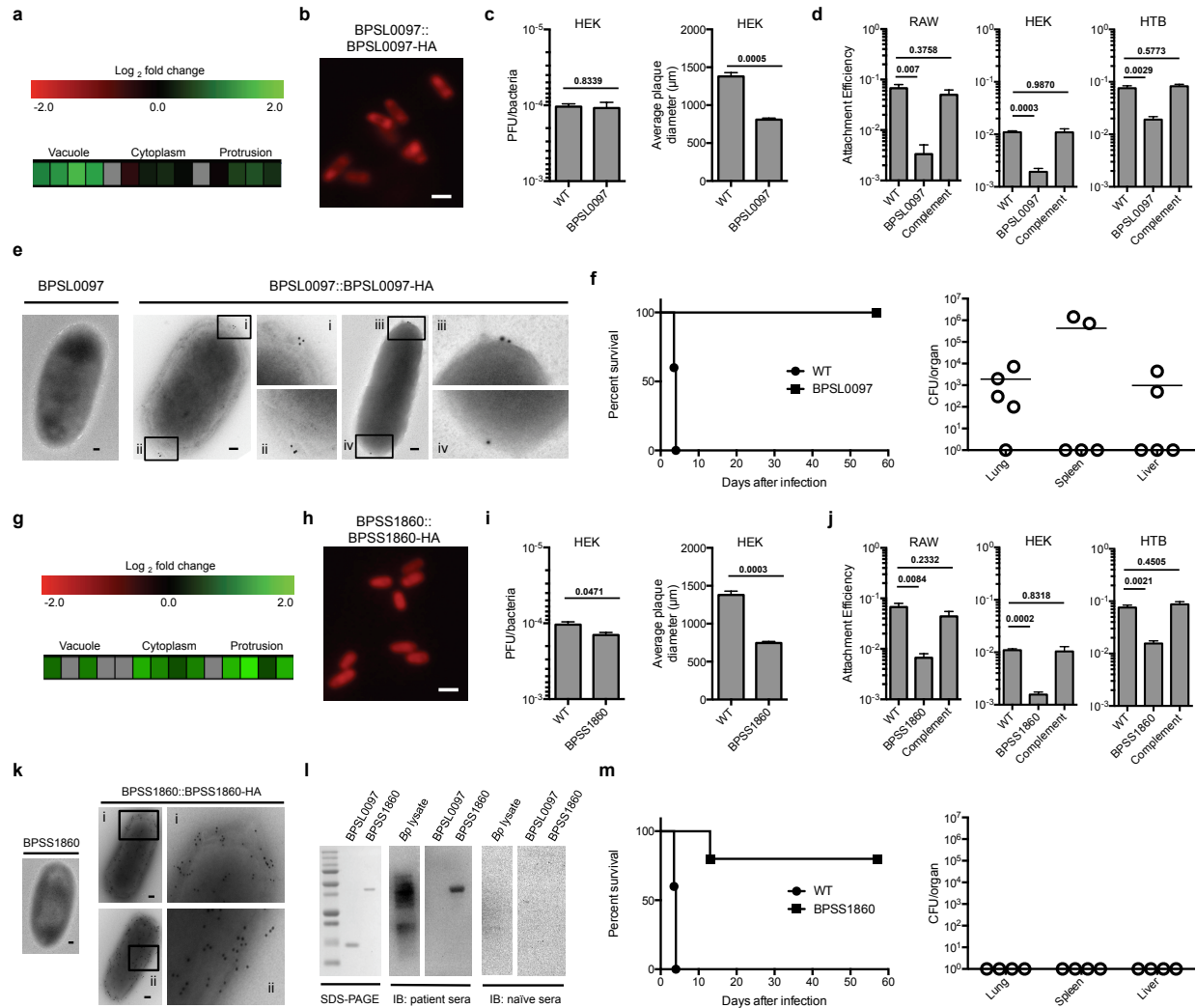


Figure 2| Characterizations of BPSL0097 and BPSS1860 mutants. BPSL0097 gene is up-regulated within the macrophage vacuole (a) and BPSS1860 gene is upregulated during cell infection relative to *in vitro* condition (g). Numbers of plaques formed by the BPSL0097 (c) and the BPSS1860 (i) mutant strains are comparable to wildtype *Bp* indicating no defect in host cell invasion; however, reduced plaque diameters indicate overall infection defects. Mutants showed reduced attachment efficiencies compared to wildtype *Bp*, suggesting that BPSL0097 and BPSS1860 play a role in attachment to host cells (d and j). Immunofluorescence (b and h; scale bars = 1 μ m) and TEM (e and k; scale bars = 100 nm) suggest BPSL0097 and BPSS1860 are

located on the surface of *Bp*. Antibodies against purified BPSS1860 were detected via immunoblot (IB) in pooled melioidosis patients' serum samples (l). BPSL0097 and BPSS1860 mutants are highly attenuated in the BALB/c mouse intranasal model when compared to wildtype *Bp* (f and m). Bacterial burdens of surviving mice suggest that the BPSL0097 mutant persists *in vivo* (f) while the BPSS1860 mutant was completely cleared in all surviving mice (m). Data in bar graphs represent means \pm s.e.m and analyzed via unpaired t-test. P-values presented above relevant comparisons.

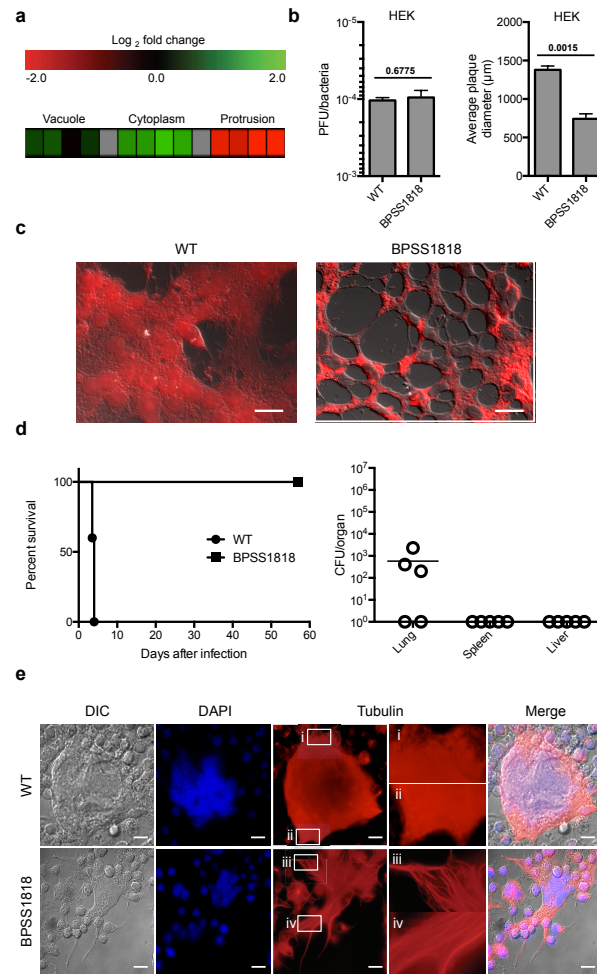


Figure 3| Characterizations of *Bp* mutant BPSS1818. a) BPSS1818 gene is up-regulated within the macrophage cytosol, then significantly down-regulated during the protrusion stage of infection. b) Number of plaques formed by the BPSS1818 mutant is comparable to wildtype *Bp*, indicating no defect in host cell invasion; however, reduced plaque diameters were observed indicating defect in infection spread. Data represents means \pm s.e.m and analyzed via unpaired t-test. P-values presented above relevant comparisons. c) Infection of RAW264.7 cells with BPSS1818 mutant shows extended host cell cytoskeleton and distended MNGCs compared to wildtype *Bp*. Scale bars = 5 μ m. d) BPSS1818 mutant is completely attenuated in BALB/c mice when compared to wildtype *Bp*. Bacterial burdens were only observed at low levels in lungs of

three mice. e) RAW264.7 cells infected with the BPSS1818 mutant showed elongated microtubules with pronounced fibers when magnified in contrast to wildtype *Bp* infected cells.

Scale bars = 10 μm .

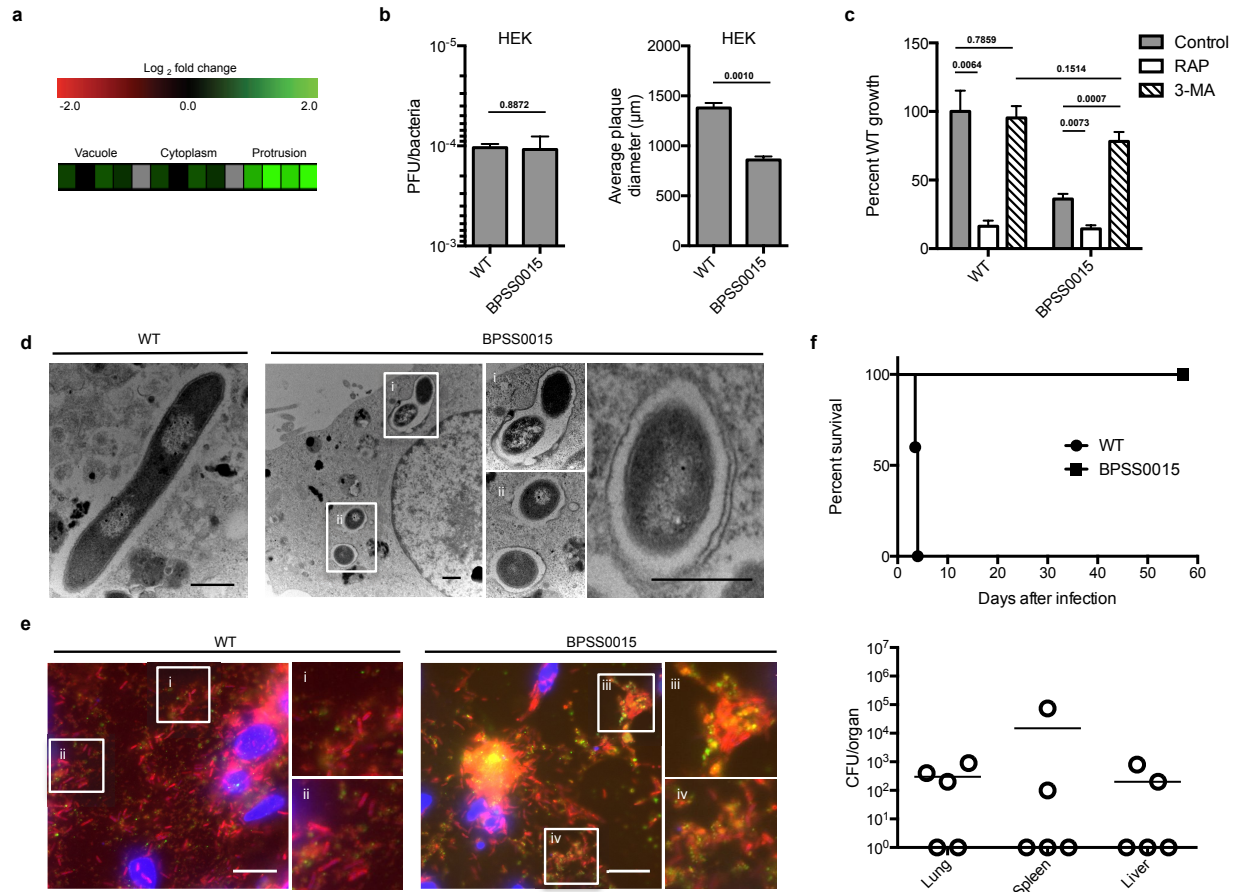


Figure 4| Characterization of *Bp* mutant BPSS0015. a) BPSS0015 gene is up-regulated at the protrusion stage during infection. b) Number of plaques formed by the BPSS0015 mutant is similar to wildtype *Bp*, indicating no defects in host cell invasion; however, reduced plaque diameters were observed, suggesting defects during the progression of infection. c) Rapamycin-induced autophagy reduced the survival of both wildtype *Bp* and the BPSS0015 mutant, whereas the inhibition of autophagy with 3-methyladenine significantly restored intracellular replication of the BPSS0015 mutant to wildtype level. d) Representative TEM images of macrophages infected with the BPSS0015 mutant show each bacterium surrounded by membrane structures. Scale bars = 1 μm. e) Infected HEK293T cells stably expressing GFP-LC3 show co-localization of the autophagy marker, LC3 (green), with the BPSS0015 mutant (red) and no co-localization

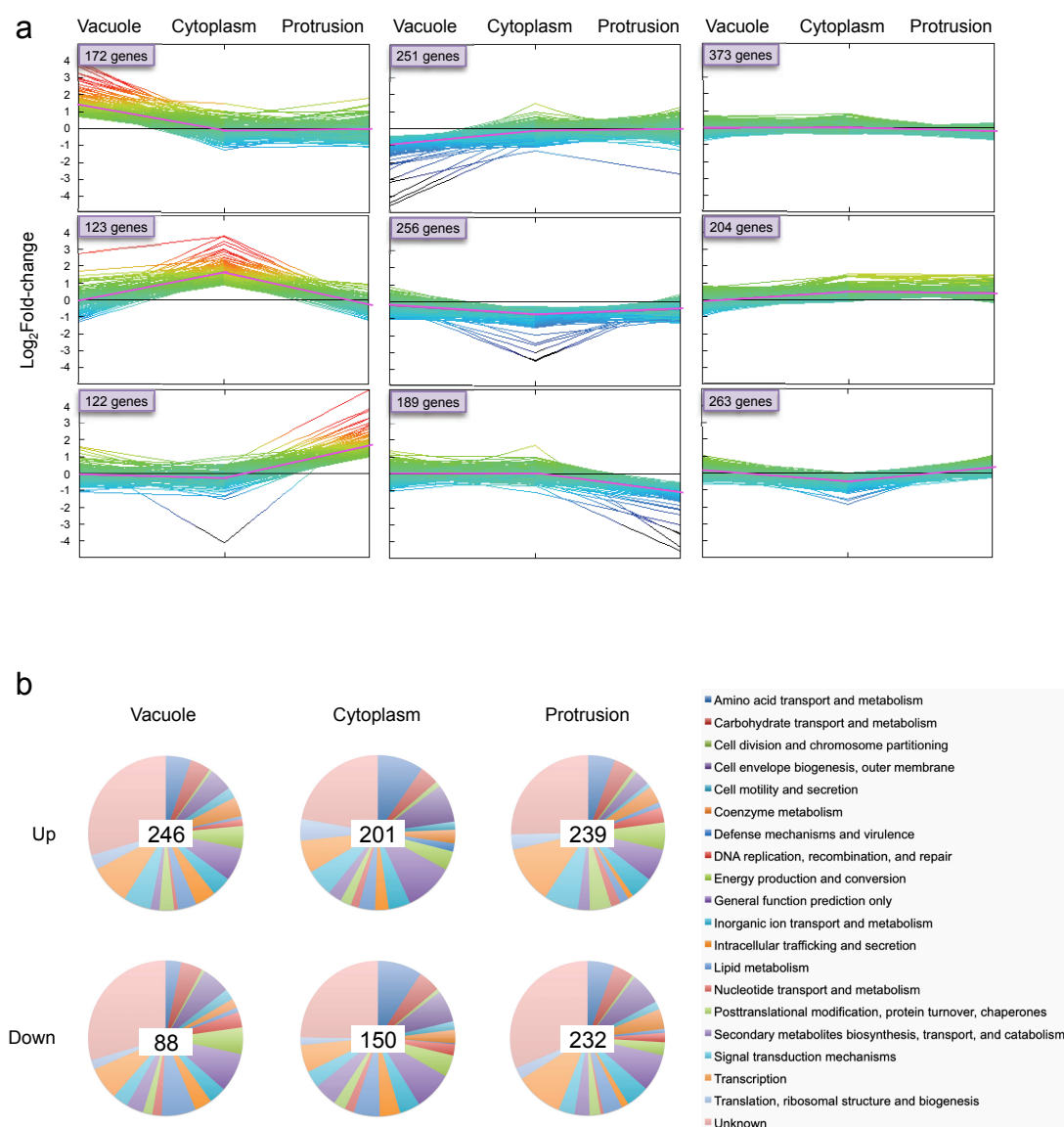
with wildtype *Bp* (red). f) The BPSS0015 mutant is completely attenuated in BALB/c mice but bacterial burdens of surviving mice suggest that this mutant persists *in vivo*. Data in bar graphs represent means \pm s.e.m and analyzed via unpaired t-test. P-values presented above relevant comparisons.

Extended Data Table 1: Characteristics and functional predictions of the 11 attenuated mutants.

Gene ID	Mutant intracellular replication (average percent of wildtype <i>Bp</i> CFU)				Annotation/functional prediction	Cellular location PSORTb 3.0
	2hpi	6hpi	16hpi	24hpi		
BPSL0097	17	50	97	16	Hypothetical protein	Unknown
BPSL0636	94	175	101	71	Hypothetical protein	Unknown
BPSL1126	37	0	93	108	Hypothetical protein	Cytoplasmic membrane
BPSL1390	71	75	107	100	Hypothetical protein	Unknown
BPSL1422	25	25	69	95	Hypothetical protein	Cytoplasm
BPSL2714	94	25	75	18	Hypothetical protein	Cytoplasmic membrane
BPSS0015	44	625	138	15	Hypothetical protein	Cytoplasmic membrane
BPSS1265	144	200	115	21	Hypothetical protein	Extracellular/unknown
BPSS1780	196	275	132	17	Hypothetical protein	Cytoplasmic membrane
BPSS1818	85	150	114	16	Hypothetical protein	Cytoplasmic membrane
BPSS1860	79	200	82	23	Hypothetical protein	Extracellular

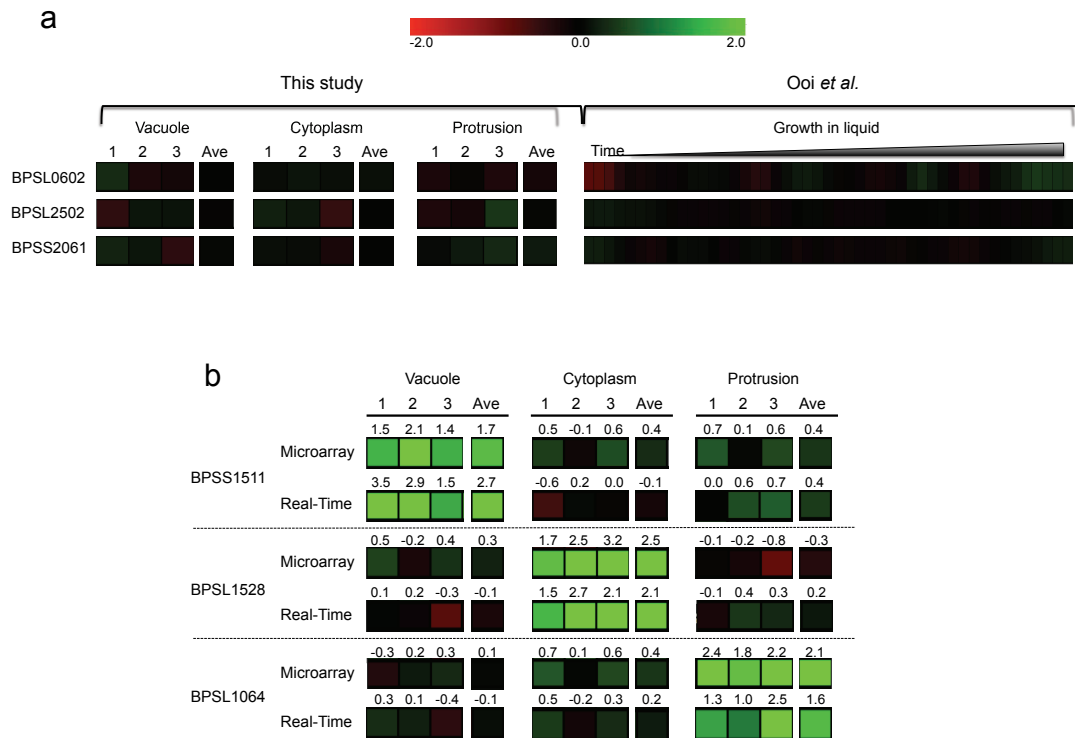
Extended Data Figure 1| Heat maps of all genes significantly and differentially expressed (fold-change above 2, $P \leq 0.05$) in three stages of intracellular infection. Heat map is presented in a green-black-red color gradient; green color indicates up-regulation and red color indicates down-regulation, when the gene expression in each infection stage was compared to the control condition. Genes were sorted according to gene ID. References for known/characterized virulence factors in *Bp* are included. The first three boxes in each heat map represent independent biological replicates and the forth box is the mean.

Due to the size and format of ‘Extended Data Figure 1’, it will only be available upon publication of this manuscript that is currently under consideration at *Cell-Host and Microbe*.



Extended Data Figure 2 | Summary of the differentially expressed genes. a) Differentially expressed genes grouped into different clusters based on their expression patterns, where each line represents one gene. The clusters of genes that were significantly up- or down-regulated at three different infection stages were shown in the left or middle panels, respectively. The clusters of genes that remained relatively unchanged between the different intracellular infection stages and the control condition were displayed in the right panels. The pink line indicates the average

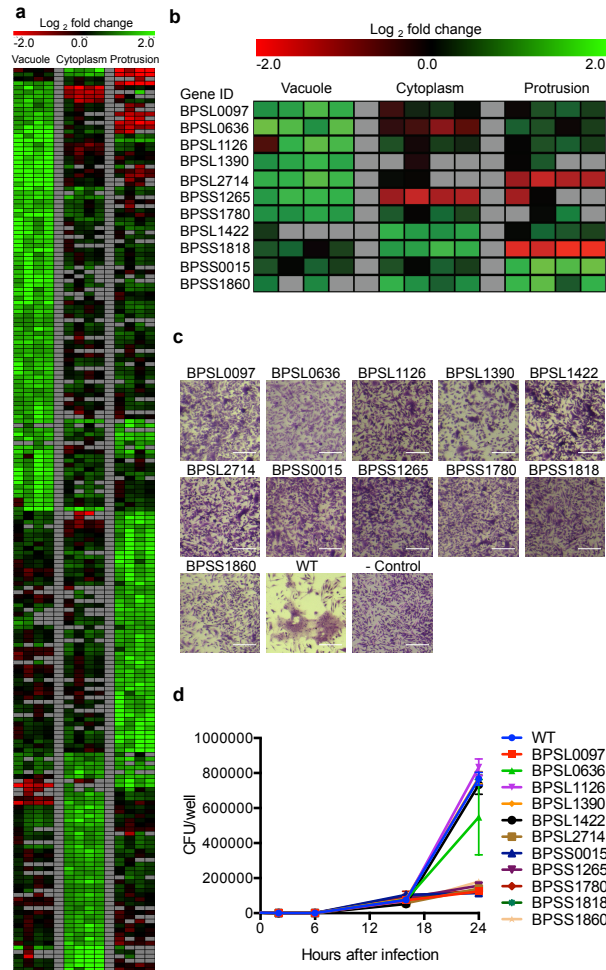
expression profile of each cluster. Number of genes in each cluster is indicated in the box at the upper left corner. b) Relative abundance of functional categories of genes differentially expressed at various stages of infection. The unknown gene (i.e., genes with neither known functions nor functional predictions) category takes up a significant portion among these functional categories, indicating that *Bp* genes possibly involved in intracellular pathogenesis are largely understudied. Total number of genes in each group is indicated in the center of the pie chart.



Extended Data Figure 3| Single-cell Real-Time RT-PCR validated microarray data. a) Three housekeeping genes, BPSL0602, BPSL2502, and BPSS2061, were chosen based on our TRANSITome data in this study, as well as previous published expression data (Ooi, *et al.*, 2013). All three housekeeping genes showed unchanged expression in the vacuole, cytoplasm, protrusion, and growth in liquid (Ooi, *et al.*). b) Three stage-specific genes were shown in a heat map format with red-black-green color gradient as indicated in (a). Real-time RT-PCR data were obtained from three single *Bp* cells and log₂fold-changes were displayed above the heat map along with averages. Real-Time RT-PCR results strongly correlated with microarray data, further validating this as a novel approach for the study of intracellular pathogens.

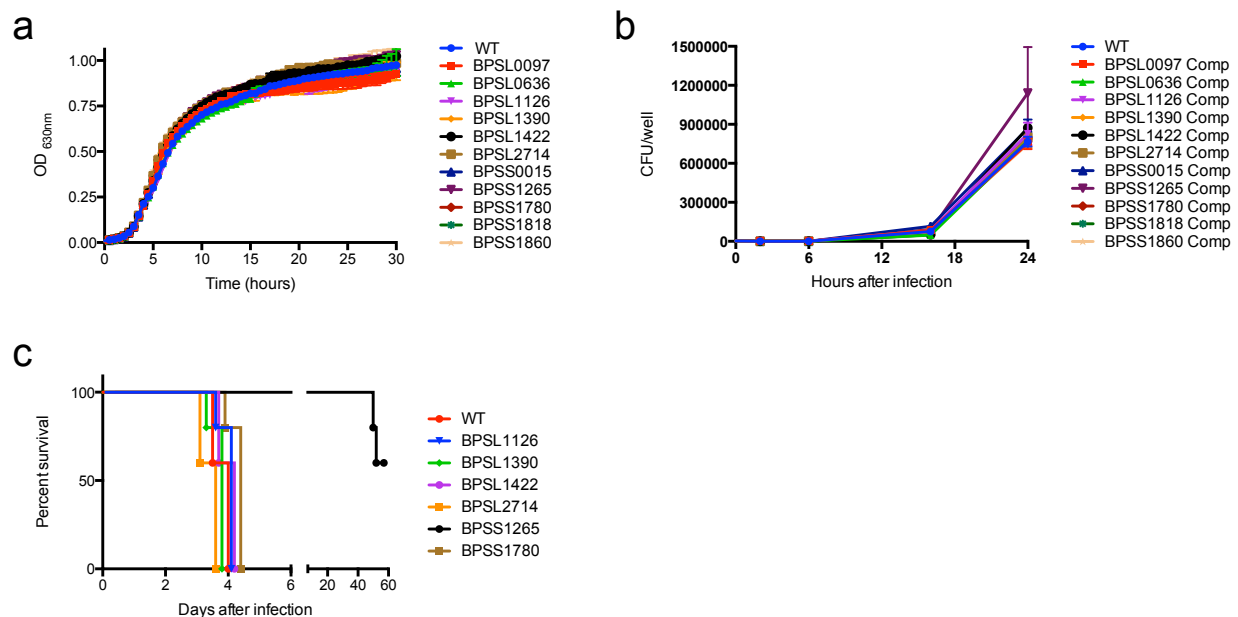
Extended Data Figure 4 | Infection stage-specific expression of genes/pathways involved in (a) type III secretion systems; (b) type VI secretion systems; (c) flagellar and chemotaxis; (d) pilus and fimbriae production; (e) energy metabolism; (f) phosphate transport; and (g) other virulence factors described in *Bp*. Genes with known functions that are differentially regulated are highlighted in orange boxes in the KEGG pathways.

Due to the size and format of ‘Extended Data Figure 4’, it will only be available upon publication of this manuscript that is currently under consideration at *Cell-Host and Microbe*.

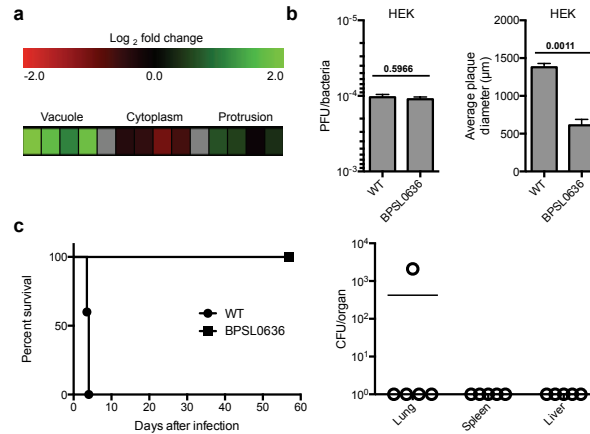


Extended Data Figure 5| TRANSITome reveals stage dependent expression of hypothetical proteins. a) Differential regulation of 206 hypothetical proteins expressed in a stage-specific manner. a) and b) First three boxes of each infection stage represent three biological replicates, the fourth represents the mean. We successfully created 191 mutants of the 206 hypothetical protein encoding genes; mutations in 15 genes were not successful because these are likely essential genes. We screened the 191 mutants for attenuation in RAW264.7 cell infection models (i.e., MNGC formation and intracellular replication assay). b) and c) Eleven of the 191 mutants showed major defects in MNGC formation in RAW264.7 cells compared to wildtype (WT) *Bp* infection. White scale bars = 100 μ m. d) Majority of the eleven mutants also showed defects

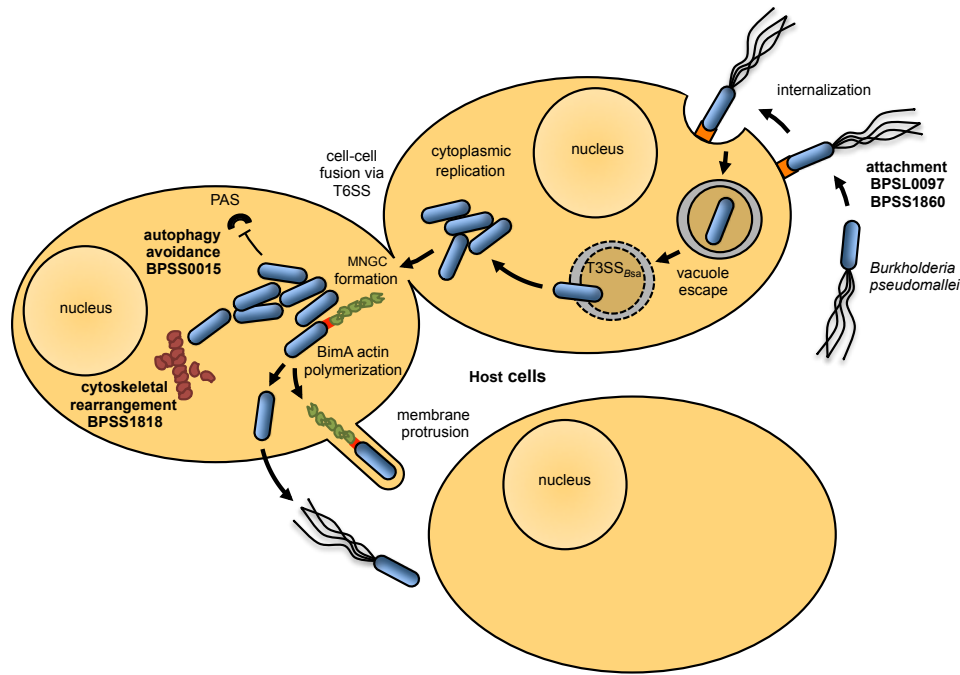
during intracellular replication in RAW264.7 cells and no apparent defects in liquid medium (Extended Data Fig. 6a). Data represents means \pm s.e.m.



Extended Data Figure 6 | Growth analysis, complementation, and *in vivo* analysis. a) Growth curves showing no growth defect of the 11 mutant strains compared to wildtype *Bp*, indicating that the defects seen during intracellular infection are not due to a reduction in mutant fitness *in vitro*. Data represents means \pm s.e.m. b) Complements of the 11 mutant strains compared to wildtype *Bp* showing similar intracellular infection capabilities. Data represents means \pm s.e.m. c) Survival curve of BALB/c mice infected with 4,500 CFU of each individual mutant; BALB/c mice data from only 6 of the 11 attenuated mutants are shown here, and the rest are shown and discussed elsewhere in this manuscript.



Extended Data Figure 7 | Characterization of *Bp* mutant BPSL0636. a) BPSL0636 is highly expressed within the macrophage vacuole. b) Equal numbers of plaques are formed by wildtype *Bp* and the BPSL0636 mutant indicating no defect in host cell invasion; however, reduced plaque diameters were observed. Data represents means \pm s.e.m and analyzed via unpaired t-test. *P*-values presented above relevant comparisons. c) The BPSL0636 mutant is highly attenuated in BALB/c mice when infected intranasally with a lethal dose (4,500 CFU). Low level of BPSL0636 mutant was recovered in lungs of only one of the infected mice, indicating the mutant was partially cleared from the lung and was unable to disseminate to other organs.



Extended Data Figure 8| Model of *Bp* intracellular pathogenesis. *Bp* attaches to host cells, using surface attachment proteins BPSL0097 and BPSS1860. After internalization, *Bp* escapes the vacuole utilizing the *Burkholderia* secretion apparatus ($T3SS_{Bsa}$)²⁵ and moves within the host cell using its secondary flagella locus⁵ or by polymerizing host cell actin (green) with bacterial BimA (red boxes on the bacterial cell pole)³¹. BPSS1818 facilitates changes in host cell cytoskeletal structure through modulation of tubulin, while BPSS0015 contributes to the autophagy evasion. PAS; pre-autophagosomal structure. Bacteria replicate intracellularly and spread to neighboring cells by actin-based membrane protrusion and by promoting cell fusion to form multinucleated giant cells (MNGC) using a Type VI Secretion System (T6SS)^{26, 28, 29}.

Due to the size and format of ‘Extended Data Movies’, they will only be available upon publication of this manuscript that is currently under consideration at *Cell-Host and Microbe*.

Extended Data Movie 1| An example of laser cutting and catapult-isolation (center panel) of a single *Bp* cell from an infected RAW264.7 macrophage cell during the protrusion stage, with fluorescent images of the same field of view before (left panel) and after (right panel) microdissection.

Extended Data Movie 2| Time-lapse of bright field microscopy showing MNGC formation of infected RAW264.7 cells. Left panel is RAW264.7 cells infected by wildtype *Bp*; right panel shows RAW cells infected by BPSL0636 mutant. RAW cells infected by BPSL0636 mutant exhibited significantly delayed MNGC formation. One frame was taken every 5 minutes for 24 hours.

Extended Data Movie 3| Time-lapse of bright field microscopy showing wildtype *Bp* attachment to RAW264.7 cells. Individual *Bp* cells were traced in the identical videos using ImageJ (left video untraced and right video shows traced wildtype *Bp* bacteria encountering host cells).

Extended Data Movie 4| Time-lapse of bright field microscopy showing the BPSL0097 mutant unable to attach to RAW264.7 cells. Individual *Bp* cells were traced in the identical videos using ImageJ (left video untraced and right video shows traced BPSL0097 mutant bacteria encountering host cells).

Extended Data Movie 5 | Time-lapse of bright field microscopy showing the BPSS1860 mutant unable to attach to RAW264.7 cells. Individual *Bp* cells were traced in the identical videos using ImageJ (left video untraced and right video shows traced BPSS1860 mutant bacteria encountering host cells).

Extended Data Movie 6 | Time-lapse of bright field microscopy showing MNGC formation of infected RAW264.7 cells. Left panel shows RAW264.7 cells infected by wildtype *Bp*; right panel shows RAW264.7 cells infected by the BPSS1818 mutant. RAW264.7 cells infected by the BPSS1818 mutant exhibited MNGC formation compared to wildtype *Bp*, but the cytoskeleton of the MNGC infected with the BPSS1818 mutant appeared to be extended as compared to wildtype *Bp* infected cells. At the end of infection, BPSS1818 infected cells showed “stretched out” phenotype. One frame was taken every 5 minutes for 24 hours.

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AUTHOR CONTRIBUTIONS

TTH, YHK, MHN, IAM, and JFM designed the experiments. YHK, MHN, IAM, ZS, JZS, and APB performed the experiments. REN and NK provided melioidosis patient sera. HPS provided unpublished *Bp* strains. IAM, YHK, DC, and TTH wrote the manuscript. MHN and IAM contributed equally to this work. All authors contributed to the editing of this manuscript.

COMPETING FINANCIAL INTERESTS

The authors declare no competing financial interests.

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Appendix B:

The heritable natural competency trait of *Burkholderia pseudomallei* in other *Burkholderia* species through *comE* and *crp*

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The heritable natural competency trait of *Burkholderia pseudomallei* in other *Burkholderia* species through *comE* and *crp*

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Abstract

Natural competency requires uptake of exogenous DNA from the environment and the integration of that DNA into recipient bacteria can be used for DNA-repair or genetic diversification. The *Burkholderia* genus is unique in that only some of the species and strains are naturally competent. We identified and characterized two genes, *comE* and *crp*, from naturally competent *B. pseudomallei* 1026b that play a role in DNA uptake and catabolism. Single-copies of rhamnose-inducible *comE* and *crp* genes were integrated into a *Tn7* attachment-site in non-naturally competent *Burkholderia* including pathogens *B. pseudomallei* K96243, *B. cenocepacia* K56-2, and *B. mallei* ATCC23344. Strains expressing *comE* or *crp* were assayed for their ability to uptake and catabolize DNA. ComE and Crp allowed non-naturally competent *Burkholderia* species to catabolize DNA, uptake exogenous *gfp* DNA and express GFP. Furthermore, we used synthetic *comE* and *crp* to expand the utility of the λ -red recombineering system for genetic manipulation of non-competent *Burkholderia* species. A newly constructed vector, pKaKa4, was used to mutate the aspartate semialdehyde dehydrogenase (*asd*) gene in four *B. mallei* strains, leading to the complete attenuation of these tier-1 select-agents. These strains have been excluded from select-agent regulations and will be of great interest to the field.

Introduction

Bacterial natural transformation, first described in 1928¹, is the process in which exogenous DNA is taken from the environment by a recipient for nutrients, DNA repair, or genetic diversification². Since then, this process has been described in 82 bacterial species including both gram-positive and gram-negative bacteria³. The molecular machinery that facilitates natural transformation is homologous to the type II secretion system (T2SS) and the type IV pilus (T4P)^{2, 3}. In gram-negative bacteria, DNA is transported across the outer membrane through the PilQ channel that houses the pseudopilus, PilE³, and is then shuttled across the periplasm by ComE⁴. An unknown nuclease generates a single-stranded DNA molecule that is transported into the cytoplasm through the ComA channel in the inner membrane³. The single-stranded DNA molecule is further broken down into nucleotide components or recombined into the chromosome of the recipient organism^{2, 5}. The ability of bacteria to be naturally transformable impart an evolutionary advantage and has driven diversification of species over time^{2, 6}.

Burkholderia pseudomallei (*Bp*) is the causative agent of the tropical disease melioidosis that presents in patients with diverse symptoms and clinical outcomes⁷. *Bp* is endemic to tropical regions around the world and readily isolated from the environment⁸. Different clinical and environmental isolates show a significant level of genetic diversity in part due to frequent recombination⁹⁻¹¹. Clinical isolates have evolved within a host by removal of virulence loci and stress response regulators leading to asymptomatic infection¹². Another example of recombination that occurred within the host is the evolution of a single *Bp* isolate into *B. mallei* (*Bm*), the causative agent of glanders¹³. Although glanders is primarily an equine disease, it also affects humans¹⁴ and is a public health concern due to its past use as a bioterrorism agent^{15, 16}.

Beyond melioidosis and glanders, other members of the *Burkholderia* genus also cause severe diseases in humans. The *Burkholderia cepacia* complex comprises of many species within the *Burkholderia* genus that cause a rapid degradation of pulmonary function leading to high mortality rates in cystic fibrosis patients¹⁷⁻¹⁹. *Burkholderia* species also encode multiple forms of antimicrobial resistance mechanisms²⁰⁻²² further complicating treatment of these diseases and highlighting the need for increased investment in basic research of these organisms at the genetic level.

Among all forms of useful genetic manipulations, techniques have been developed for the rapid generation of chromosomal deletion mutants²³⁻²⁵. Although these techniques are less cumbersome than traditional allelic-replacement strategies, they rely on the natural transformative properties of the background strain, limiting the utility of these methods²³⁻²⁵. To our knowledge, there are no naturally competent strains of *B. mallei* or within the *B. cepacia* complex yet described. Thus, the ability to make these *Burkholderia* species uptake DNA would be very significant in manipulating their genomes. Some *Bp* strains are naturally transformable (i.e., ~50% of *Bp* strains)^{5, 24}. *Bp* strain 1026b is able to naturally uptake extracellular DNA allowing for easy genetic manipulation²³⁻²⁵. Prototype strains *Bp* K96243, *Bm* ATCC23344 and *B. cenocepacia* (*Bc*) K56-2 are commonly used in the field but are non-naturally competent making genome manipulation tedious and requiring many steps. To further investigate the natural transformation mechanisms of some *Bp* strains and increase the utility of natural transformation-based genetic manipulation techniques, our lab has sought to identify specific genetic properties that confer this phenotype⁵.

Four fosmids containing genomic regions from naturally competent *Bp* 1026b were previously isolated and able to confer natural transformation to non-naturally competent

Burkholderia species⁵. The fosmids isolated encode ~30-40 genes each, which allowed the non-naturally competent *Bp* K96243, *Bm* ATCC23344 and *Bc* K56-2 to uptake *gfp* DNA and grow on DNA as a sole carbon source⁵. A bioinformatics analysis of each genomic region revealed several candidate genes for natural competency⁵. Mutation in five of these genes, in the naturally competent *Bp* 1026b background, led to a reduction in growth on DNA and *gfp* DNA uptake indicating their involvement in natural transformation⁵. In the present work, we pursued further characterization of the genetic regions of these fosmids and identified the minimal components necessary for natural competency for the purpose of creating a possible broad-species-range strategy for genome manipulation. Additionally, we exploited these genetic elements to expand the λ -Red-recombineering system for rapid chromosomal manipulation into non-naturally competent *Burkholderia* species.

Results

Downsized fosmids identify genes responsible for *Burkholderia* natural competency

We initially planned to digest each fosmid (~50 Kbp, ⁵), maintained in non-competent *Bp* K96243 or *Bc* K56-2, into smaller genetic fragments in order to identify the minimal number of genes necessary for natural competency. However, working with 50 Kbp inserts on fosmids to pinpoint a subset of genes responsible for natural competency is an arduous task. Therefore, we reintroduced and passaged the fosmid clones in the *Bc* K56-2 background, while maintaining selective pressure for DNA utilization, in anticipation that natural downsizing of the fosmid clones would occur. Upon digestion of the fosmids Bp1 and Bc17 ⁵, after passage and re-transformation into *Escherichia coli*, it was discovered that each fosmid from *E. coli* had been significantly reduced in size (data not shown). The downsized fosmids were re-introduced into

Bc K56-2 and growth on DNA was confirmed. The downsized fosmids Bp1 and Bc17 contained two open reading frames, BP1026B_I0804 and BP1026B_II2056, respectively. Interestingly, BP1026B_I0804 is highly similar to the known competence protein ComE, which has a high amino acid similarity (56%) and identity (38%) to ComEA of *Neisseria meningitidis*, a model organism for natural competency. Mutation in BP1026B_I0804 (*comE*) significantly reduced the ability of naturally competent *Bp* 1026b to grow on DNA as a sole carbon source and to uptake exogenous DNA⁵. BP1026B_II2056 (*crp*) is a putative transcriptional regulator of the Crp/Fnr family that also showed critical involvement in DNA uptake and catabolism in *Bp* 1026b⁵. Looking at the available genomes of *Bp*, both *comE* and *crp* of *Bp* 1026b exist in 99 and 198 available *Bp* genomes, respectively, even non-naturally competent strains. *Bm* ATCC23344 has *comE* and *crp* homologs to *Bp* 1026b at 100% identity while *Bc* K56-2 has homologs with 66.67% and 73.98% identity, respectively. Moving forward, the natural downsizing event of these fosmids, down to *comE* and *crp*, led us to further investigate the possible transfer of this heritable trait in other *Burkholderia* species.

***comE* and *crp* allow DNA uptake, utilization, and expression**

To further investigate the roles of *comE* and *crp* in *Burkholderia* natural transformation and competency, we constructed strains that conditionally express each of these proteins, individually and in combination, under the control of a rhamnose-inducible promoter. To reduce the chance that the introduced version of *comE*, *crp*, or *comE-crp* recombine with the native copy of *comE* or *crp*, we exchanged codons throughout each gene to ensure that the nucleotide sequence differed significantly while the amino acid sequence remained unchanged (Supplementary Figure S1). These combinations were inserted into the *attTn7* site in a diverse

group of non-naturally competent pathogenic *Burkholderia* species including *Bp* K96243, *Bm* ATCC2344, and *Bc* K56-2^{26, 27}. No growth differences were observed when these engineered strains were tested in LB or M9 minimal glucose (MG) media containing rhamnose (Fig. 1a-b). Additionally, empty vector controls (*P_{rha}*) of non-naturally competent strains *Bp* K96243, *Bm* ATCC23344, and *Bc* K56-2 were unable to grow in media containing DNA as a sole carbon source (red lines in Fig. 1c). However, single copy expression of *comE*, *crp*, or *comE-crp* enabled these non-naturally competent *Burkholderia* strains to grow in DNA to various degrees (Fig. 1c). Although the expression of *comE*, *crp*, or *comE-crp* in these strains did not allow growth to similar levels as the naturally competent *Bp* 1026b, they afforded these non-naturally competent *Burkholderia* strains the ability to significantly uptake DNA as a carbon source and sustain observable growth.

Beyond DNA catabolism, we tested DNA uptake and expression characteristics provided by *comE*, *crp*, or *comE-crp* to these non-naturally competent *Burkholderia* species. Each engineered strain was incubated with linear *gfp* DNA²⁴ and the level of GFP uptake and transient expression of GFP was quantitated using flow cytometry. To establish GFP detection parameters, an *E. coli* strain constitutively expressing GFP was compared to an *E. coli* strain with no GFP expression. The *E. coli* strain constitutively expressing GFP showed 96.8% of cells GFP+, while the *E. coli* strain that is *gfp*-, showed no GFP expression (Fig. 2a). When incubated with *gfp* DNA, 75.7% and 63.7% of naturally competent *Bp* 1026b and *Burkholderia thailandensis* (*Bt*) E264 were able to uptake and express GFP, respectively (Fig. 2a). Non-naturally competent *Bp* K96243, *Bm* ATCC23344, and *Bc* K56-2 strains displayed no GFP expression (Fig. 2b, WT and *P_{rha}* columns). In contrast, these non-naturally competent strains that express *comE*, *crp*, or *comE-crp* showed GFP expression ranging from 39.7% to 73%, demonstrating that *comE* or *crp*

is able to confer DNA uptake and subsequent expression of exogenous DNA (Fig. 2b). The capability of DNA uptake enabled by *comE* and *crp* made them promising candidates for testing in conjunction with genetic manipulation techniques that rely on natural transformation in non-naturally competent strains. In the presence of *comE-crp*, the high frequencies of cells taking up *gfp* DNA by *Bc* K56-2 (69.9% of cells) and *B. mallei* ATCC23344 (73% of cells) were comparable to wildtype *Bp* strain 1026b (75.7% of cells) and *Bt* strain E264 (63.7% of cells, Fig. 2). Because manipulating and modifying the genomes of *Bp* 1026b and *Bt* E264 has been highly dependent upon the ability to uptake DNA by natural competency^{24, 25} the high frequencies of this heritable trait (Fig. 2) indicate that genetic manipulation of the genome of *Bm* and *Bc* is very much possible. As proof-of-concept, we next utilized *comE-crp* to manipulate the genome of four different *Bm* strains. A codon-altered version of *comE-crp* was synthesized to prevent recombination between *comE-crp* on plasmid and the native genomic *comE* and *crp* copies.

Genetic manipulation of non-naturally transformable *Burkholderia* spp.

To expand the use of genetic manipulation techniques that rely on natural transformation²³⁻²⁵, we created pKaKa3, pKaKa4, and pKaKa5 where each only differ in the resistance marker (Fig. 3). These vectors expand the applicability of the λ -red recombineering system²⁴ to non-naturally competent *Burkholderia* species, including type strains *Bp* K96243, *Bm* ATCC23344, and *Bc* K56-2. Incorporation of the codon-altered version of *comE-crp* into the λ -Red-recombineering system will allow DNA uptake and rapid generation of mutants in strains that are non-naturally competent. As proof of concept, we tested this newly designed recombineering system in the non-competent select-agent *Bm* using pKaKa4. The gene encoding aspartate-semialdehyde-dehydrogenase (*asd*) was targeted to generate potentially attenuated

strains that could also be useful to the research field²⁸. The vector pKaKa4 was introduced into a variety of *Bm* strains (ATCC23344, Ivan, China 5, and 2002721278), and the chromosomal *asd* gene was deleted by incubating with a DNA fragment containing a *gat-pheS-FRT* cassette flanked by 45bp regions homologous to *Bm asd*. Glyphosate-resistant colonies of *Bm* strains were purified and their diaminopimelate (DAP) requiring phenotype verified (data not shown). The pKaKa4 plasmid with the *sacB* gene was cured by counter-selection on sucrose. Recombinant efficiencies varied among different *Bm* strains but generally, 10-50 colonies were obtained from a typical experiment when approximately 5×10^8 to 1×10^9 CFU were used. The introduction of *comE-crp* enabled *Bm* to uptake and recombine DNA, which was previously impossible. Although the focus of the present study was to conditionally attenuated *Bm* strains, we have also utilized these genetic tools successfully in non-naturally competent *Bc* K56-2 and *Bp* K96243 to manipulate their genomes with similar frequencies of recombinants.

Attenuation of *Bm* Δasd mutants in intracellular replication and acute glanders models

To determine the level of attenuation of the four *Bm* Δasd strains produced using the natural transformation properties of *comE-crp*, we first tested them in a RAW264.7 murine macrophage model of infection²⁸. RAW264.7 cells were infected with wildtype *Bm* ATCC23344, Ivan, China5, 2002721278 and the Δasd mutants of each, at an MOI of 1:1 in a modified kanamycin protection assay in order to assess each mutants ability to infect intracellularly. Wildtype *Bm* strains ATCC23344 (Fig. 4a), Ivan (Fig. 4b), China 5 (Fig. 4c), and 2002721278 (Fig. 4d) were able to replicate to high levels intracellularly, while all *Bm* Δasd strains behaved as expected, showing no replication within the intracellular environment where no DAP was present. Single-copy complementation of each *Bm* Δasd strain recovered this

defect, indicating that the defect in intracellular replication was due to the deletion of the *asd* gene (Fig. 4, triangles).

In addition to *in vitro* attenuation, we sought to test the *Bm Δasd* strains in an acute glanders model. To best mimic inhalation glanders, we infected BALB/c mice via intranasal inoculation with an intentionally high-dose of each strain that leads to acute pneumonic glanders. Groups of five mice were inoculated with 1×10^7 CFU of wildtype *Bm* strain or its *Δasd* counterpart and survival was monitored. Mice infected with wildtype *Bm* strains ATCC23344 (Fig. 5a), Ivan (Fig. 5b), China 5 (Fig. 5c), and 2002721278 (Fig. 5d) rapidly deteriorated showing severe symptoms of acute glanders and had to be euthanized within the first four days of the trial. In contrast, BALB/c mice inoculated with *Bm Δasd* strains showed no signs or symptoms of disease and survived until the study was terminated at day 63 (Fig. 5, squares). Bacterial burdens from the lungs, liver, and spleen were assessed in surviving mice to determine any level of *Bm Δasd* mutant persistence within the host. Organs were homogenized and plated onto LB agar containing DAP. *Bm Δasd* were not detected in any organ, indicating that the mutant strains were not able to persist within the host (Fig. 5).

Discussion

Natural transformation is a complex process that drives genetic diversification, DNA repair, and DNA catabolism in bacteria². The amount of bacterial species identified as naturally transformable is increasing as the molecular mechanisms that drive this activity are better understood in model organisms³. Although the exact mechanism and relationship between DNA up-take and catabolism is yet to be determined, we summarized as previously depicted that one strand of the double-stranded DNA is broken down for catabolism and the other strand can enter

the cell for transformation⁵. Only some strains of *Bp* are naturally competent,^{5, 24} a phenomenon that is not unique to *Bp*, but also found in the emerging plant pathogen *Xylella fastidiosa*²⁹. The mechanism by which certain strains of *Bp* are naturally competent is not well understood. Crp has been implicated as a regulatory factor in the process of natural competency in many organisms including *Vibrio cholerae*³⁰ and *Haemophilus influenzae*³¹. We therefore hypothesize that Crp in *Burkholderia* species plays a critical role in the regulation of competence, supported by the data presented here. The regulation network of Crp in *Burkholderia* is of critical interest for future studies and could reveal valuable insights into the complex mechanism of natural competency. ComE has been known to be involved in natural competency of many gram-negative organisms³ including *N. gonorrhoeae* and *N. meningitides*, which have shown a direct correlation with the copy number of *comE* and the level of competency³². This supports the conclusion that an additional copy of *comE* expressed in non-naturally competent *Burkholderia* would lead to increase levels of DNA uptake and catabolism above the threshold of detection. Although, no significant additive affect was observed when *comE* and *crp* were introduced in combination to the non-naturally competent backgrounds, our data did indicate that overall the *comE-crp* gave rise to a higher ability for DNA catabolism and uptake, compared to *comE* or *crp* individually (Figs. 1 and 2).

The fosmids previously isolated⁵ narrowed down the genetic elements for DNA uptake and utilization to ~50Kbp. The fosmids themselves were naturally downsized further during selection in *Burkholderia* and maintenance in *E. coli*, leading us to investigate the role of the remaining genetic elements, *comE* and *crp*. Individually and in combination, *comE* and *crp* conferred the ability for non-naturally competent *Bp* K96243 to grow on DNA as a sole carbon source. In addition to DNA catabolism, the ability to uptake and express *gfp* DNA was also

observed, solidifying the role that *comE* and *crp* play in *Burkholderia* natural transformation. To broaden the scope of these findings, we investigated a diverse range of non-naturally competent *Burkholderia* species that are of public health concern. These include the closely related but distinct *Bm*, the etiological agent of glanders, and the more distantly related *Bc*, one of the agents that cause the cepacia syndrome in cystic fibrosis patients. The expression of *comE* and *crp* in both *Bm* ATCC23344 and *Bc* K56-2 conferred the ability to catabolize DNA and uptake and express exogenous *gfp* DNA, indicating that the competence machinery in *Burkholderia* species is likely similar.

Researchers have gravitated toward utilizing *Bp* 1026b and *Bt* E264 because these are naturally competent and, therefore, easier to manipulate genetically. However, *Bp* K96243 was one of the first *Bp* genomes sequenced and is a prototype strain. The genetic manipulation of *Bp* K96243 has been limited due to its inability to uptake DNA efficiently. Likewise, the genetic manipulation of *Bm* strains and *Bc* K56-2 has been tedious because of the inefficiency in DNA uptake. We showed here *Bp* K96243, *Bc* K56-2, and *Bm* strains can inherit the high frequencies of *gfp* DNA uptake comparable to wildtype *Bp* 1026b and *Bt* E264 (Fig. 2), alleviating the difficulty in manipulating the genomes of these bacteria to knock-out and pull-out genomic sequences²⁴.

In the present study, we also developed genetic tools to expand the λ -Red recombineering system to include non-naturally competent *Burkholderia* species and strains. Three different λ -Red recombineering vectors were constructed based on various antibiotic and non-antibiotic selective markers, as well as counter-selective markers for curing of the vectors, making them broad-host-range. As a proof of concept, pKaKa4 was used successfully to mutate the *asd* gene from four strains of *Bm*. These mutants show complete attenuation in cell culture and BALB/c

models of infection and a request for the exclusion from the select-agent list has been submitted and approved by the CDC (<https://www.selectagents.gov>). The exclusion of these *Bm* strains will help accelerate the study of glanders and could be of great interest to the research field. Furthermore, development of these novel genetic tools significantly simplifies the genetic manipulation in many other non-naturally competent *Burkholderia* species/strains, allowing high-throughput targeted chromosomal manipulation.

Methods and Materials

Bacterial strains, media and culture conditions All manipulation of *Bp* and *Bm* were conducted in a CDC-approved and -registered BSL3 facility at the University of Hawaii at Manoa (UHM). All select agent experiments were approved by the Institutional Biosafety Committee of UHM (reference number: 16-07-004-585-1R) and were performed using BSL3 practices following recommendations set forth in the BMBL, 5th edition³³. *Escherichia coli* strain EPMaX10B (BioRad), E1869, and E1354 were routinely used for cloning or plasmid mobilization into *Bp*, *Bm* and *Bc* as described previously^{34, 35}. Luria-Bertani (LB) medium (Difco) or 1x M9 minimal medium supplemented with 20 mM glucose (MG) or 0.1% salmon sperm DNA was used to culture all strains. Induction of genes controlled by the rhamnose-inducible promoter (*P_{rha}*) was done as previously described²⁴. Selection of the *gat* gene in *E. coli* and *Bp* strains was performed as previously described³⁵. Fosmid downsizing: fosmids⁵ were isolated from *E. coli* and introduced into *Bc* K56-2 and selected on plates with DNA as a sole carbon source. Colonies of *Bc* K56-2 containing the fosmids from DNA plates were grown up in liquid media with DNA, fosmids were re-purified from the liquid cultures and re-transformed

into *E. coli* and tested for a downsizing event. Downsized fosmids were tested for growth on DNA in *Bc* K56-2 as previously described⁵.

Molecular methods and reagents Molecular methods and reagents were carried out as described previously^{24, 28, 35, 36}. Versions of both *comE* and *crp* genes were designed to avoid recombination between the introduced copy of *comE-crp* and the native genomic *comE* and *crp*. To achieve this, codons were swapped throughout each gene to change the nucleotide sequence without altering the amino acid sequence (Supplementary Figure S1). Newly designed *comE* and *crp* genes were synthesized through Genscript[®]. Strains conditionally expressing *comE*, *crp*, and *comE-crp* were constructed utilizing mini-Tn7 integration vectors^{26, 27, 35}. Briefly, the rhamnose inducible promoter fragment was PCR amplified from pFlpe4²³ using oligos 5'-CAT ATG CAT TTA ATC TTT CTG CGA-3' and 5'-CGA CTA GTG GAT ATC GAA CTG GCT CAT G-3', digested with *Nsi*I and *Spe*I, and cloned into mini-Tn7-*gat*³⁵ digested with the same enzymes, yielding mini-Tn7-*gat-Prha*. Newly synthesized *comE*, *crp*, and *comE-crp* were cloned into mini-Tn7-*gat-Prha* as *Bam*HI/*Hind*III, *Hind*III/*Spe*I-blunted, and *Bam*HI/*Spe*I-blunted fragments, respectively. These plasmids were conjugated into non-naturally competent *Burkholderia* strains and insertion into the *attTn7* site was screened as previously described^{26, 27}.

Growth analysis of *Burkholderia* species All strains were first grown overnight in LB at 37°C, bacteria were harvested and washed twice with 1xM9 minimal media and subcultured 1:200 into fresh LB, M9 minimal media supplemented with 20mM glucose, or minimal media supplemented with 0.1% purified salmon sperm DNA (Fig. 1). All media contained 0.2% rhamnose to express genes inserted in the *attTn7* site. Growth curves were done using the

BioTek ELx808IU by measuring OD₆₃₀ every 30 minutes for the duration of the time course. Growth analysis was done in triplicate and average ODs were shown.

Gfp uptake assays *Gfp* uptake assays were performed as previously described^{5, 24}, with the exception of the detection method. Briefly, *gfp*-DNA was amplified by PCR from pPS747³⁷ and 250 ng of the *gfp*-DNA was incubated with various strains for 30 min at room temperature⁵. After 45 min recovery in LB broth with shaking, bacteria were fixed in 1% paraformaldehyde in 1x phosphate buffered saline (PBS) for 45 min for fluorescent analysis. After fixation, bacteria were harvested and resuspended gently with 1xPBS + 0.1% Triton X-100 to reduce clumping, and then washed twice with 1xPBS to remove detergent. Fixed bacteria were analyzed using flow cytometry to detect transient expression of GFP-protein indicating that cells were able to uptake extracellular *gfp*-DNA, along with fixed *E. coli* wildtype strain DH5α and DH5α/*attB*::Gm-*gfp* as negative and positive controls, respectively.

λ-Red knockout recombineering in *Bm* with pKaKa4 Generation of mutants was done as previously described²⁴ with slight modifications. Briefly, pKaKa4 was introduced into various *Bm* strains via conjugation and selection on M9 minimal media containing 40 mM arabinose as the sole carbon source. *Bm* strains harboring pKaKa4 were streaked out on M9+arabinose plates and grown for 3 days at 37°C, then harvested from plates by gentle scraping and resuspended in fresh LB containing 0.2% rhamnose. Bacteria were then concentrated by centrifugation and resuspended in 20 μl LB + 0.2% rhamnose, and incubated with 2 μg of DNA containing a *gat-pheS-FRT* cassette flanked by 45bp regions homologous to *Bm asd*. After incubation at room temperature for 30 min, bacteria were recovered in fresh LB for 2 hours at 37°C, and selected on

MG medium containing 200 µg/ml DAP, 0.4% GS, and 1 mM each of lysine, methionine, and threonine (these 3 amino acids are required for the specific *asd* mutation).

Intracellular replication assays RAW264.7 murine macrophages were grown in Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% (v/v) fetal bovine serum (FBS) at 37°C in 5% CO₂. Antibiotic/antimycotic (Gibco) containing 100 U/mL penicillin, 100 µg/mL streptomycin and 250 ng/mL of amphotericin B was added to media at a 1X concentration during cell growth but omitted during infection trials. A modified kanamycin protection assay was used test intracellular replication³⁸. RAW264.7 cells were seeded into 24-well Corning CellBIND culture plates to 80% confluence, allowed to attach overnight, and were washed twice with 1XPBS before infection. *Bm Δasd* strains were used to infect macrophage monolayers at an MOI of 1:1. After 1 hour, infected monolayers were washed with 1XPBS and then DMEM supplemented with 10% FBS, 700 µg/mL amikacin and 700 µg/mL kanamycin were added to kill any extracellular bacteria. At 2, 6, 12, and 24 hours post-infection, infected monolayers were lysed with 0.1% Triton X-100. Serial dilutions of lysates were plated on LB and colony forming units (CFU) per well were determined.

Animal studies BALB/c mice between 4 and 6 weeks of age were purchased from Charles River Laboratory. All infections with *Bm* strains were administered via the intranasal (i.n.) inoculation route. Mice were anesthetized with 100 mg of ketamine/kg of body weight plus 10 mg/kg xylazine. The challenge dose (1×10^7 CFU) of each *Bm* strain was suspended in 20 µl of 1XPBS and used to inoculate each mouse via the i.n. route. Each strain was used to inoculate 5 mice. Animals were monitored for disease symptoms daily and euthanized at predetermined humane

end points. Lungs, liver, and spleen of surviving mice were harvested, homogenized, serially diluted, and plated on LB containing 200µg/mL DAP to determine bacterial burdens. Survival characteristics were plotted using Prism software (GraphPad, La Jolla, CA) and statistical analysis was done by Kaplan-Meier curves.

Ethics statement All animal studies described in this manuscript were approved by the Institutional Animal Care and Use Committee at the University of Hawaii at Manoa (Protocol No. 10-1073-8), and conducted in compliance with the NIH (National Institutes of Health) Guide for the Care and Use of Laboratory Animals.

Data availability The datasets and materials generated during the current study are available from the corresponding author upon reasonable request. Any transfer of select agent materials must be to a select agent registered facility, approved by the CDC, and comply with all select agent regulations (selectagents.gov).

Acknowledgements

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Author contributions

YHK and TTH designed the experiments. YHK, IAM, JZS, ZS, APB, and DC conducted the experiments. IAM and YHK analyzed the data. IAM, YHK, and TTH wrote the manuscript, and all authors contributed to editing of this manuscript.

Competing interests

The authors declare no competing interests.

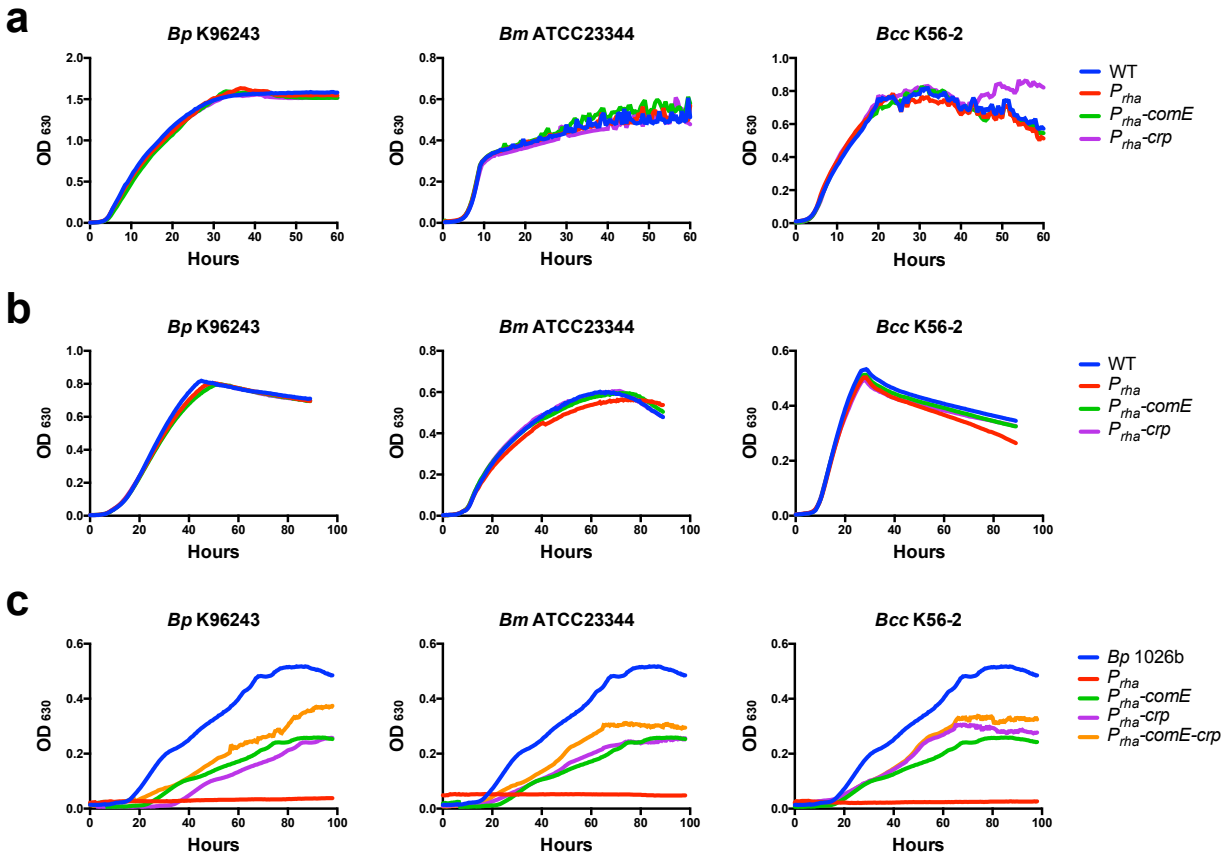


Figure 1 | *In vitro* growth characteristics of *Bp* K96243, *Bm* ATCC23344 and *Bc* K56-2. Site-specific recombination at the *attTn7* site was used to insert *comE*, *crp*, or *comE-crp* driven by the rhamnose-inducible promoter (*P_{rha}*). All strains were tested at 37°C while shaking in LB (a), M9 minimal media supplemented with 20mM glucose (b), or minimal media supplemented with 0.1% purified salmon sperm DNA (c). All media contained 0.2% rhamnose to express genes inserted in the *attTn7* site. The naturally competent *Bp* 1026b is shown as a point of reference for growth on DNA as a sole carbon source (c).

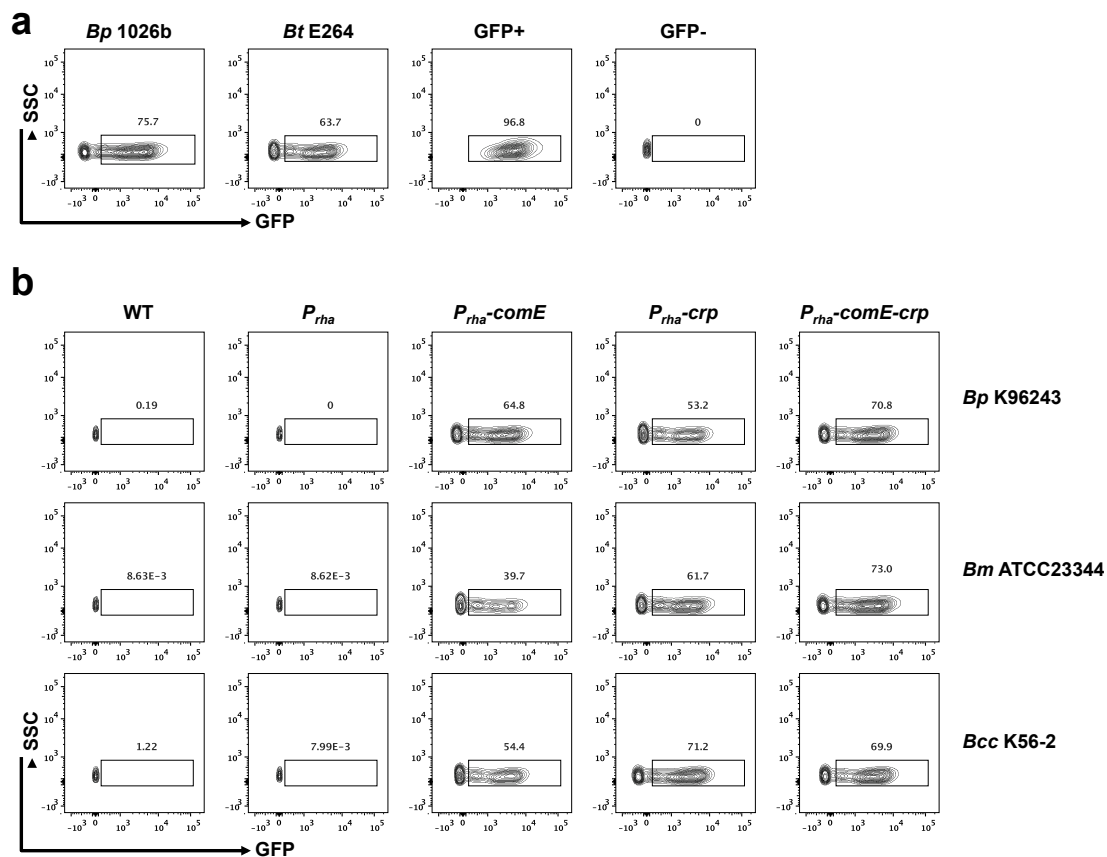


Figure 2| Linear *gfp* DNA uptake assay of strains expressing *comE*, *crp*, or *comE-crp*. For all plots side scatter (SSC) is plotted against GFP fluorescent intensity (GFP). a) Naturally competent *Bp* 1026b and *Bt* E264 show 63-75% of cells expressing GFP after incubation with *gfp*. *E. coli* constitutively expressing *gfp* (GFP+) shows 96.8% of cells expressing GFP in contrast to wildtype *E. coli* (GFP-) showing no GFP expression. b) Wildtype (WT) and *attTn7* controls (P_{rha}) of *Bp* K96243, *Bm* ATCC23344 and *Bc* K56-2 show no GFP expression indicating their inability to uptake *gfp*. However, expression of *comE*, *crp* or *comE-crp* empowered natural competency, showing 39-73% of cells expressing GFP.

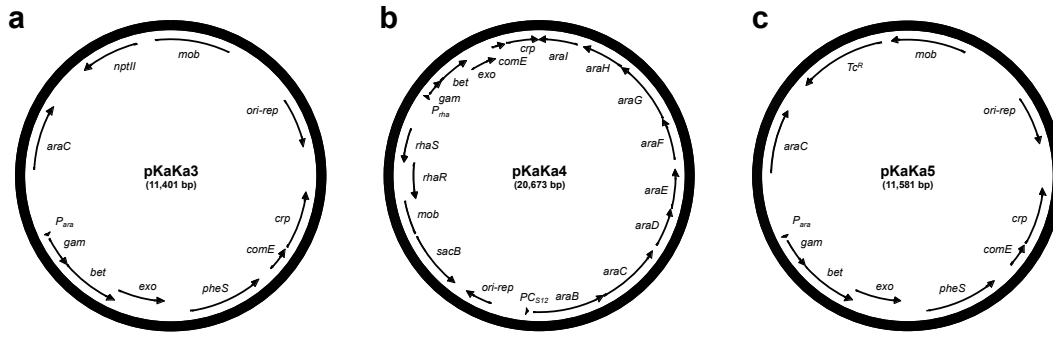


Figure 3| Plasmid maps of pKaKa3, pKaKa4, and pKaKa5 to expand the utility of λ -red recombineering to non-naturally competent *Burkholderia* species. Abbreviations: *araC* on pKaKa3 and pKaKa5, activator of the arabinose-inducible promoter (P_{ara}) from *E. coli*; *araBCDEFGHI* on pKaKa4, *B. thailandensis* arabinose utilization operon³⁹; *gam-exo-bet*, λ -red recombineering genes⁴⁰; *mob*; RP4-dependent conjugal origin of transfer of *B. bronchiseptica* cryptic plasmid pBBR1; *ori-rep*; bhr replicon of *B. bronchiseptica* pBBR1 plasmid⁴¹; *nptII*, encodes kanamycin resistance⁴²; P_{ara} , arabinose inducible promoter⁴³; P_{rha} , rhamnose inducible promoter⁴⁴; PC_{S12} , constitutive promoters of *B. pseudomallei* and *B. cenocepacia rpsL* gene⁴⁵; *pheS*, engineered gene encoding a mutant version of α -subunit of phenylalanyl tRNA synthase⁴⁶; *rhaR* and *rhaS*, regulators of the rhamnose inducible promoter⁴⁴; *sacB*, encoding for a modified levansucrase counter-selectable marker⁴⁷. Tc^R , tetracycline resistance.

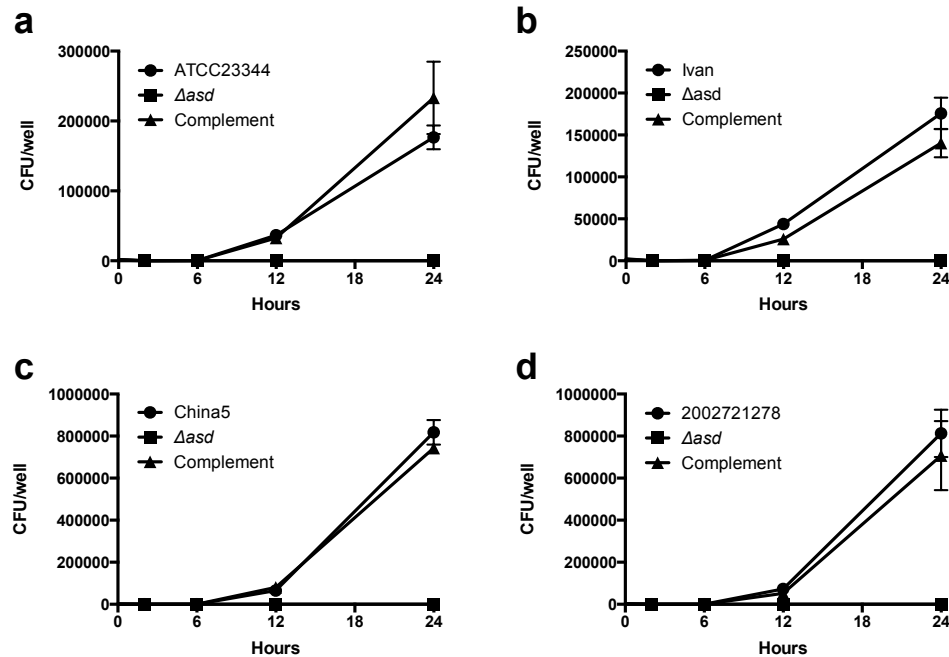


Figure 4| *In vitro* attenuation of *Bm* Δasd strains in RAW264.7 murine macrophages. *Bm* strains ATCC23344 (a), Ivan (b), China5 (c), 2002721278 (d) were able to replicate well within the intracellular environment (circles) while the Δasd counterparts showed complete abolishment of the ability to replicate intracellularly (squares). Complementation of the Δasd gene in each *Bm* strain rescued the intracellular replication defect (triangles).

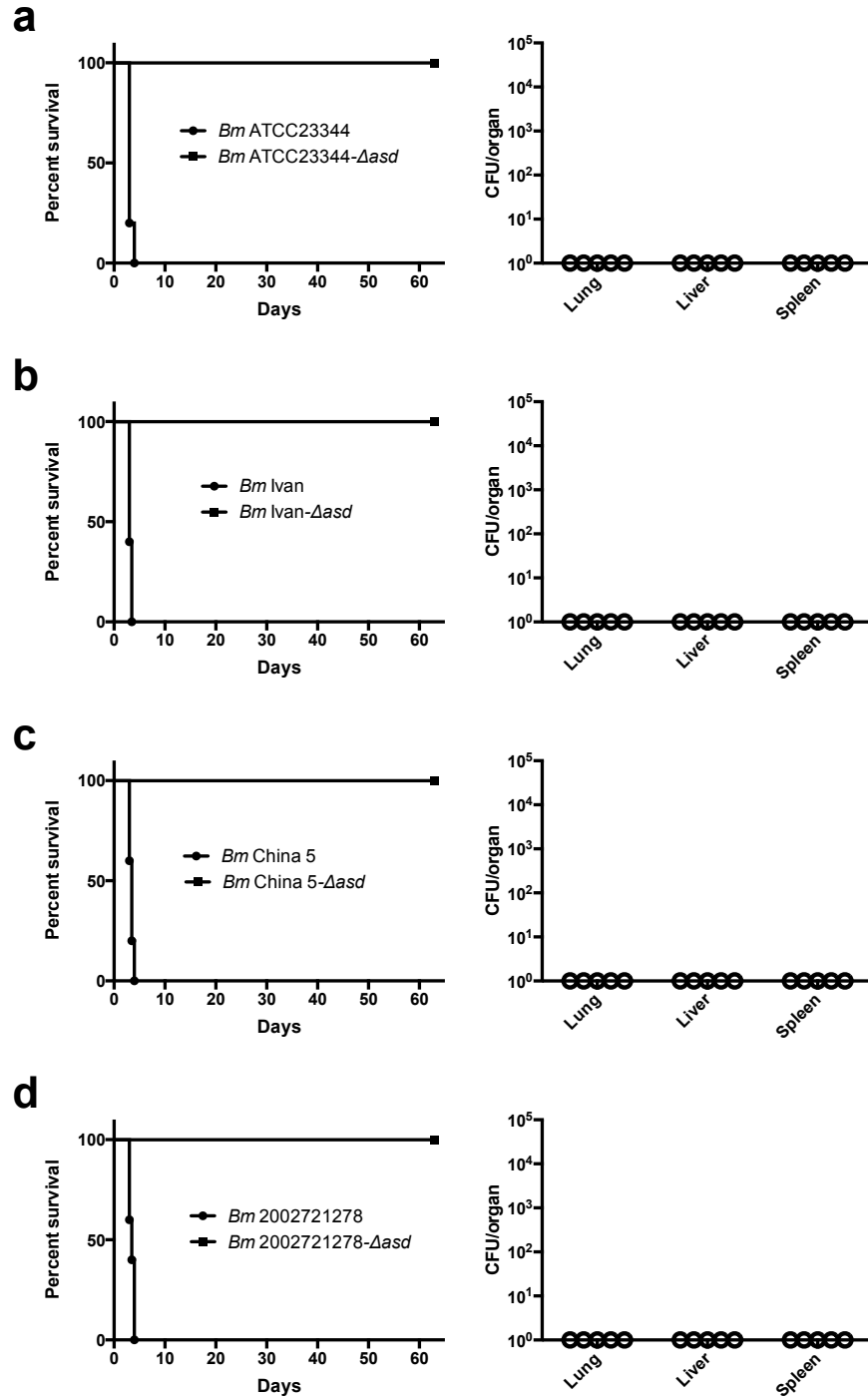
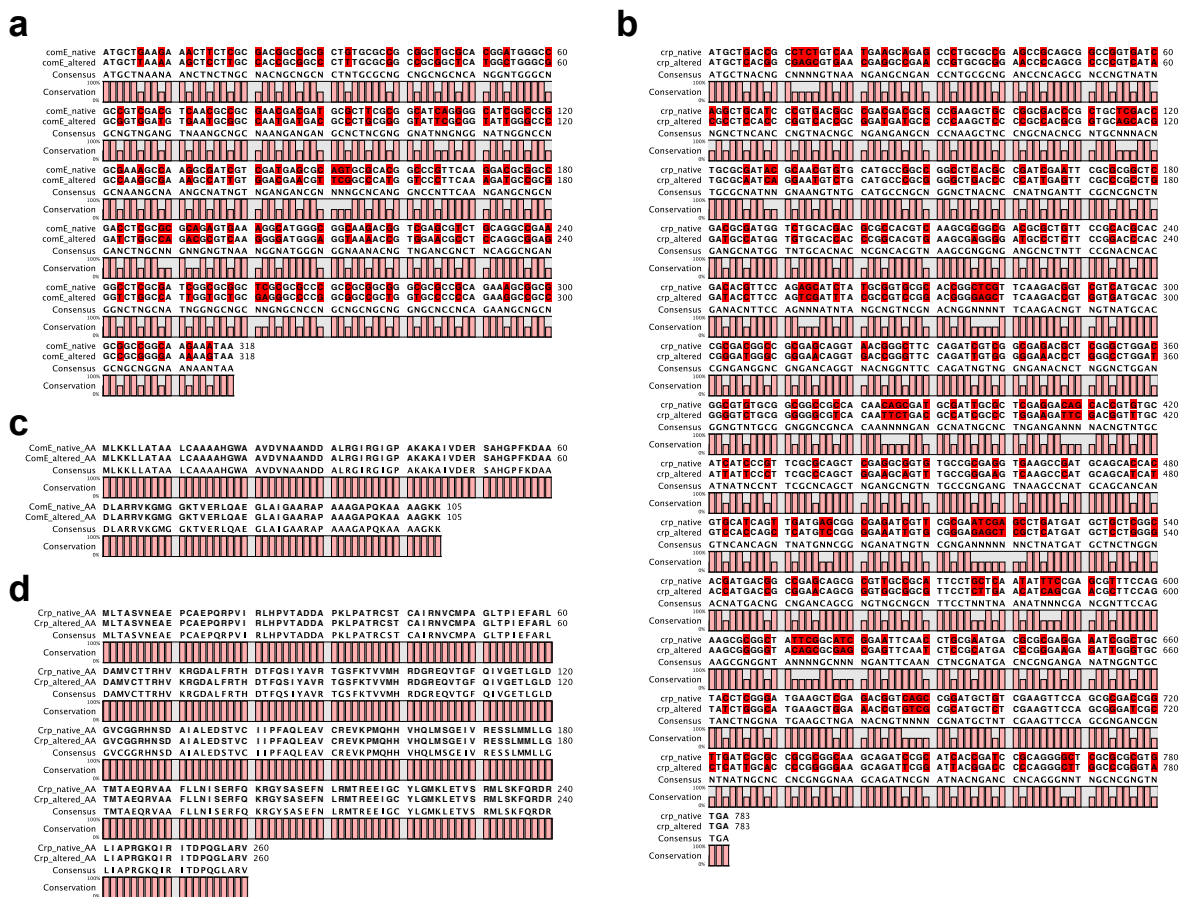


Figure 5| *In vivo* attenuation of *Bm* Δasd strains in BALB/c intranasal challenge. BALB/c mice (n=5) were challenged intranasally with 1×10^7 CFU of *Bm* strains ATCC23344 (a), Ivan (b), China5 (c), 2002721278 (d) and their Δasd counterparts. Survival was monitored for 63 days

(left panels). Surviving mice were sacrificed and bacterial burdens from the lungs, liver, and spleen were determined by serial dilution and plating (right panels).



Supplementary Figure 1| Nucleotide alignments comparing the native and altered versions of *comE* (a) and *crp* (b) showing the changes in sequence throughout the entire gene to reduce the possibility of recombination. Amino acid alignments comparing native and altered versions of *comE* (c) and *crp* (d) showing 100% identity of the protein sequence. Residues highlighted by red indicate a change in sequence. Sequence conservation is shown by pink bars below the sequence. Alignments were carried out in CLC sequence viewer.

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Appendix C:

Current Publications

Publications as of July 2020:

1. Heacock-Kang Y, **McMillan IA**, Zarzycki-Siek J, Sun Z, Bluhm AP, Cabanas D, Hoang TT. The heritable natural competency trait of *Burkholderia pseudomallei* in other *Burkholderia* species through *comE* and *crp*. *Sci Rep*. 2018;8(1):12422. doi: 10.1038/s41598-018-30853-4. PubMed PMID: 30127446; PMCID: PMC6102250.
2. Heacock-Kang Y, Zarzycki-Siek J, Sun Z, Poonsuk K, Bluhm AP, Cabanas D, Fogen D, **McMillan IA**, Chuanchuen R, Hoang TT. Novel dual regulators of *Pseudomonas aeruginosa* essential for productive biofilms and virulence. *Mol Microbiol*. 2018;109(3):401-14. doi: 10.1111/mmi.14063. PubMed PMID: 29995308; PMCID: PMC6158065.
3. Heacock-Kang Y, Sun Z, Zarzycki-Siek J, Poonsuk K, **McMillan IA**, Chuanchuen R, Hoang TT. Two Regulators, PA3898 and PA2100, Modulate the *Pseudomonas aeruginosa* Multidrug Resistance MexAB-OprM and EmrAB Efflux Pumps and Biofilm Formation. *Antimicrob Agents Chemother*. 2018;62(12). doi: 10.1128/AAC.01459-18. PubMed PMID: 30297364; PMCID: PMC6256797.
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Appendix D:

Supplemental Table 1 for Chapter 2

Supplemental Table 1: Total transcriptome of BP1026B_H11198

Synonym	Product	Empty Vector				BP1026B_H11198				pValue	qValue	Fold Change	Log2FC
		Replicate 1	Replicate 2	Replicate 3	RPKM	Replicate 1	Replicate 2	Replicate 3	RPKM				
BP1026B_0001	carboxylate-amine ligase	94552	134638	122756	105	101510	96227	87566	85	2.34E-16	1.66E-15	0.80952381	-0.30485482
BP1026B_0002	hypothetical protein	74985	79794	79007	64	74706	71938	70881	59	8.79E-10	2.86E-09	0.921875	-0.11735691
BP1026B_0003	hypothetical protein	1963125	3361208	2848114	8107	4093541	3999493	3314357	11316	0.053201209	0.06383683	1.395830764	0.481124034
predicted RNA	-	109146	152311	138284	2081	202387	176396	146961	2738	0.008370071	0.005335722	1.31571399	0.395845482
BP1026B_0004	5-methylaminomethyl-2-thiouridine methyltransferase	77169	56465	58132	32	82032	87115	94664	44	0.033731619	0.04151176	1.375	0.459431619
BP1026B_0005	DNA-binding protein HU	4277852	5543088	5491260	18294	5187363	5013987	4481769	17542	0.241101302	0.264818263	0.958895626	-0.060557314
BP1026B_0006	cobalamin synthesis protein/P47K family protein	136978	116428	116062	89	105774	106386	99400	77	9.60E-15	3.56E-14	0.865168539	-0.20804689
BP1026B_0007	HpaII	101263	149395	138058	266	74549	68336	66119	143	3.99E-45	1.35E-43	0.537592985	-0.89541099
BP1026B_0008	general secretion pathway protein D	475474	515661	516546	221	530035	531490	504013	229	3.03E-10	1.04E-09	1.036199095	0.053101229
BP1026B_0009	general secretion pathway protein E	258506	230963	234487	161	276754	279472	269800	184	2.85E-04	4.52E-04	1.142857143	0.192645078
BP1026B_0010	general secretion pathway protein F	151419	141768	144897	119	151233	162133	171966	132	2.41E-07	5.71E-07	1.09243697	0.149576556
BP1026B_0011	general secretion pathway protein G	14575	7049	6971	23	12168	14229	17238	35	0.230748501	0.254562982	1.52173913	0.605721061
BP1026B_0012	general secretion pathway protein H	196653	380039	277302	575	145694	139302	125872	302	1.39E-73	4.15E-71	0.525217391	-0.929013407
BP1026B_0013	general secretion pathway protein I	87047	72469	75208	132	88131	92381	85908	155	1.41E-04	2.31E-04	1.174242424	0.23173026
BP1026B_0014	general secretion pathway protein J	74678	67849	72461	202	78505	72054	75522	212	1.53E-06	3.34E-07	1.049580777	0.069708972
BP1026B_0015	general secretion pathway protein K	122197	107277	116232	189	122370	120579	124658	201	1.30E-08	3.63E-08	1.063492063	0.088809267
BP1026B_0016	general secretion pathway protein L	52600	52361	45967	46	46228	47960	47356	44	9.63E-13	4.48E-12	0.956521739	-0.064130337
BP1026B_0017	general secretion pathway protein M	58828	53523	59066	39	50584	57166	66293	40	2.24E-08	6.08E-08	1.025641026	0.036525876
BP1026B_0018	general secretion pathway protein N	62558	61381	63656	123	79972	78736	85255	160	0.008561475	0.011347668	1.300813008	0.37941359
BP1026B_0019	general secretion pathway protein O	107272	52821	72203	97	115523	118091	111377	145	0.050382749	0.060683846	1.494845361	0.579996248
BP1026B_0020	RND efflux system outer membrane lipoprotein	31141	32715	30137	19	32327	34351	31687	20	2.84E-07	6.68E-07	1.052631579	0.074000581
BP1026B_0021	hypothetical protein	34039	33145	32348	121	34545	33859	34019	121	3.17E-07	7.23E-07	1.049580777	0.069821449
BP1026B_0022	MarK family protein	59075	57123	59095	118	45746	49419	48719	97	2.53E-19	2.61E-18	0.82033898	-0.282730207
BP1026B_0023	hypothetical protein	4006	6470	5971	43	3135	4335	4208	30	1.15E-14	6.64E-14	0.697674419	-0.519374159
BP1026B_0024	EmrB/QacA family drug resistance transporter	40627	40383	40076	25	40727	41004	39944	25	1.06E-09	3.43E-09	1	0
BP1026B_0025	LysR family transcriptional regulator	26617	21651	22617	25	25264	27083	27512	28	2.75E-05	4.94E-05	1.12	0.163498732
BP1026B_0026	LrgA family protein	3460	875	1271	3	4027	4277	4194	8	0.002134548	0.00303813	2.666666667	1.415037499
BP1026B_0027	hypothetical protein	13765	11305	12666	16	16977	13922	13187	19	3.48E-04	5.45E-04	1.1875	0.247927513
BP1026B_0028	flagellar basal body-associated protein FliH	91983	91536	50143	86	25379	25553	26065	43	1.31E-04	2.31E-04	1.174242424	0.23173026
BP1026B_0029	flagellar motor switch protein FliM	330514	449988	410852	397	306319	285551	252959	281	5.66E-19	5.51E-18	0.707808566	-0.498568877
BP1026B_0030	flagellar motor switch protein FliN	129990	106418	104964	228	143632	154673	165836	310	0.003480537	0.004828812	1.359649123	0.443234391
BP1026B_0031	flagellar protein FliO	28025	23201	23880	37	31363	31053	30279	46	4.17E-04	6.47E-04	1.242342323	0.31410859
BP1026B_0032	flagellar biosynthesis protein FliP	62197	84026	79885	98	60981	56155	52428	74	1.35E-22	1.99E-21	0.755102041	-0.405256478
BP1026B_0033	flagellar biosynthesis protein FliQ	24535	30482	28557	102	27877	25383	23781	91	9.40E-11	3.45E-10	0.892156863	-0.164630702
BP1026B_0034	flagellar biosynthetic protein FliR	43547	37291	39866	51	45319	44342	43569	56	4.07E-07	9.34E-07	1.098093176	0.134929558
BP1026B_0035	MarK family transcriptional regulator	25104	26343	28632	65	23182	23719	23840	55	2.33E-12	0.00013467	0.846153846	-0.2410081
BP1026B_0036	aklanomic acid methyl transferase	2667	3604	3013	3	3009	3203	3118	3	0.001942067	0.002780596	1	0
BP1026B_0037	hypothetical protein	358	225	197	0	391	304	464	0	0.439833406	0.467048051	#DIV/0!	#DIV/0!
BP1026B_0038	ATP-binding cassette, ABC transporter	20071	19690	19995	19	22716	22786	21795	22	3.54E-05	6.27E-05	1.157894737	0.211504105
BP1026B_0039	ABC transporter ATP-binding protein	3832	3069	2954	3	3272	3547	3579	3	1.11E-04	1.85E-04	1	0
BP1026B_0040	ABC transporter permease	3783	2551	3526	3	3228	3513	2917	3	2.75E-06	5.61E-06	1	0
BP1026B_0041	sensor kinase protein	7245	4555	5602	4	6859	6530	6629	4	2.97E-04	4.71E-04	1	0
BP1026B_0042	DNA-binding response regulator	2585	1374	2309	3	2407	2371	2309	3	0.0068614	0.00013467	1	0
BP1026B_0043	outer membrane porin	907	778	1040	0	732	958	773	0	0.50E-05	8.78E-05	#DIV/0!	#DIV/0!
BP1026B_0044	type III DNA modification methyltransferase	30026	37920	34494	16	33172	35162	35162	16	1.59E-09	5.00E-09	1	0
BP1026B_0045	type III restriction enzyme	50960	50783	49289	16	63023	62744	65033	20	0.006327081	0.008514036	1.25	0.321928095
BP1026B_0046	outer membrane porin	1339	1637	1499	1	1563	1610	1622	1	7.13E-04	0.01078336	1	0
BP1026B_0047	AraC family transcription regulator	5695	5734	6078	6	5051	7202	5891	6	1.13E-05	2.14E-05	1	0
BP1026B_0048	branched-chain amino acid ABC transporter ATP-binding protein	1366	1125	1215	1	1600	1397	1857	2	0.120611758	0.13766619	2	1
BP1026B_0049	branched-chain amino acid ABC transporter ATP-binding protein	1324	582	543	1	1159	1570	1409	1	0.247218229	0.271346589	1	0
BP1026B_0050	protein/permease	444	437	325	0	382	508	597	0	0.3680009	0.395395821	#DIV/0!	#DIV/0!
BP1026B_0051	branched chain amino acid ABC transporter permease	1120	382	604	0	719	979	587	0	0.018149596	0.023154596	#DIV/0!	#DIV/0!
BP1026B_0052	hypothetical protein	3044	3224	2680	2	3240	3380	4351	2	0.013820326	0.017817102	1	0
BP1026B_0053	phenylacetalddehyde dehydrogenase	8802	5811	7302	4	11057	10077	9670	6	0.058804826	0.0700958	1.5	0.584962501
BP1026B_0054	hypothetical protein	2850	2408	2612	6	2340	2713	2204	6	4.81E-08	2.57E-07	1	0
BP1026B_0055	hypothetical protein	5272	5041	5041	6	6106	7232	6155	8	0.001840857	0.00264493	1.333333333	0.415037499
BP1026B_0056	short chain dehydrogenase/reductase family oxidoreductase	5872	2108	2630	3	3319	3288	3072	3	8.06E-04	0.001211404	1.333333333	0.415037499
BP1026B_0057	glucose-methanol-choline oxidoreductase	10987	8940	8722	5	10193	10370	11848	6	7.88E-05	1.33E-04	1.2	0.263034406
BP1026B_0058	PadR-like family transcriptional regulator	7509	10801	9663	28	6777	6942	6383	20	2.97E-17	2.35E-16	0.714285714	-0.485426827
BP1026B_0059	hypothetical protein	57603	45527	46584	42	63042	64288	59268	52	0.003414332	0.004744316	1.238095238	0.30122295
BP1026B_0060	fatty acid desaturase	13149	6785	8050	9	15231	18288	19801	18	0.48555421	0.512815979	2.125	1.209453366
BP1026B_0061	hypothetical protein	18890	11502	10629	16	27755	31975	33744	37	0.038308746	0.046850056	2	1
BP1026B_0062	AraC family transcription regulator	13907	10347	11254	11	12078	12611	13515	11	1.97E-08	1.36E-08	1	0
BP1026B_0063	acyl-CoA dehydrogenase	113647	126324	121742	99	35324	35553	34917	29	7.59E-239	9.51E-239	0.292929292	-4.771756263
BP1026B_0064	acetyl-CoA acetyltransferase	9421	10303	10824	8	3514	3680	4805	6	2.15E-63	3.85E-61	0.375	-4.150373499
BP1026B_0065	fatty oxidation complex subunit alpha	36826	25542	26851	14	17710	18451	20526	8	3.13E-26	6.52E-25	0.571428571	-0.807354922
BP1026B_0066	alpha-methylacyl-CoA racemase	32430	15041	19162	19	22458	24601	29752	22	7.67E-05	1.30E-04	1.157894737	0.211504105
BP1026B_0067	lipoprotein	71412	72779	75496	129	77817	76357	71214	132	3.83E-07	8.84E-07	1.023255814	0.033166864
BP1026B_0068	hypothetical protein	1996	2055	2613	4	2172	2065	2209	4	7.40E-07	1.63E-06	1	0
BP1026B_0069	hypothetical protein	158860	72364	92539	244	105027	115946	141731	274	4.18E-07	9.58E-07	1.122950802	0.167294745
BP1026B_0070	lipoprotein	127782	10797	119128	323	108674	108699	107475	286	4.46E-13	2.26E-12	0.910216718	-0.135718001
predicted RNA	-	9656	17466	16329	629	11193	10338	10845	469	4.15E-17	3.25E-16	0.745627897	-0.423472094
BP1026B_0071	transmembrane regulator PtkR	2936	671	899	1	1703	2237	3598	3	0.70148266	0.721814362	3	1.584962501
BP1026B_0072	ECF sigma factor Ptl	3805	2424	2719	5	2563	3082	2699	5	1.08E-07	2.68E-07	1	0
BP1026B_0073	catalase	3688	3070	3672	3	3031	3131	3724	3	7.46E-07	1.65E-06	1	0
BP1026B_0074	cytochrome B561	2868	3625	2892	5	2982	2459	2210	4	1.63E-11	6.58E-11	0.8	-0.321928095
BP1026B_0075													

BP1026b_10120	M48 family peptidase	449099	479416	465886	541	498056	496729	488093	576	8.20E-10	2.67E-09	1.064695009	0.090440218
BP1026b_10121	ribosomal RNA small subunit methyltransferase B	92582	43759	50154	44	71171	88046	113355	64	0.123378284	0.140618918	1.454545455	0.046568381
BP1026b_10122	hypothetical protein	320888	353231	322166	561	321211	326307	316995	544	1.46E-09	4.60E-09	0.969696967	-0.044394119
BP1026b_10123	serine kinase protein	468250	513469	513469	209	488509	481025	443565	195	1.90E-14	1.12E-13	0.931013354	-0.100280818
BP1026b_10124	DNA-binding response regulator	291769	235375	253384	397	268088	284582	269974	419	5.03E-06	9.92E-06	1.055415617	0.077811237
BP1026b_10125	Phe tRNA	9627	16515	13093	172	11256	12035	10483	148	2.11E-11	8.38E-11	0.860465116	-0.216811389
BP1026b_10126	prophage integrase	86099	139062	121397	102	127414	123331	117771	108	1.23E-08	3.46E-08	1.058823529	0.0246216
BP1026b_10127	hypothetical protein	16331	15116	16586	5	16617	17667	18234	6	1.76E-05	3.25E-05	1.2	0.263034406
BP1026b_10128	hypothetical protein	810	247	397	1	673	814	853	3	0.37013371	0.397482667	3	1.584962501
BP1026b_10129	hypothetical protein	923	1114	1245	3	1214	1016	795	2	5.40E-05	9.35E-05	0.666666667	-0.584962501
BP1026b_10130	hypothetical protein	848	1643	1335	6	753	981	915	4	1.93E-12	8.47E-12	0.666666667	-0.584962501
BP1026b_10131	hypothetical protein	2177	1800	2066	8	1246	2062	1942	7	8.53E-09	2.44E-08	0.875	-0.192645078
BP1026b_10132	putative phage-encoded membrane protein	1943	1808	1521	9	935	1062	985	5	3.44E-22	4.89E-21	0.555555556	-0.847996907
BP1026b_10133	hypothetical protein	1903	2249	2004	10	1522	1719	2099	8	5.98E-09	1.75E-08	0.8	-0.321928095
BP1026b_10134	hypothetical protein	3371	3566	3353	15	2386	2839	3091	12	6.57E-12	2.77E-11	0.8	-0.321928095
BP1026b_10135	Phage Rha protein	13455	20788	20367	33	14924	12716	13439	25	2.19E-16	1.57E-15	0.757575758	-0.40053793
BP1026b_10136	phage transcriptional activator	3170	4396	4376	15	3833	3311	3761	14	1.40E-07	3.41E-07	0.933333333	-0.099535674
BP1026b_10137	putative phage DNA-binding protein	5532	7255	7523	21	5024	4894	4942	13	3.11E-23	1.36E-22	0.714285714	-0.484260337
BP1026b_10138	hypothetical protein	5560	8992	8548	32	6809	6222	6338	27	5.52E-11	2.07E-10	0.84375	-0.245112998
BP1026b_10139	Putative phage DNA-binding protein	89966	148328	129589	267	85827	84415	86105	186	5.32E-24	9.00E-23	0.696629213	-0.32153717
BP1026b_10140	putative phage-encoded membrane protein	107249	174229	165029	205	119274	116311	116316	162	5.54E-22	7.65E-21	0.790243902	-0.339630097
BP1026b_10141	hypothetical protein	186738	331860	283593	618	177315	169348	167223	396	7.15E-41	4.57E-39	0.640776699	-0.642106408
BP1026b_10142	hypothetical protein	124489	179851	155387	139	115864	110678	93503	96	1.11E-28	2.90E-27	0.690647482	-0.533978572
BP1026b_10143	Phage-related tail protein	1466	845	857	2	999	1217	1181	2	0.008664144	0.011471613	1	0
BP1026b_10144	bacteriophage tail protein	12463	13889	12018	4	13992	13858	14151	4	2.77E-05	4.98E-05	1	0
BP1026b_10145	hypothetical protein	1079	1848	1848	12	1177	1376	1376	11	1.41E-06	0.01404218	0.916666667	-0.125530882
BP1026b_10146	putative phage tail protein	1776	1894	1941	5	1820	1732	2247	5	4.04E-05	0.09E-05	1	0
BP1026b_10147	Major tail tube protein	3071	5136	5623	9	5018	4900	4750	9	7.62E-05	1.29E-04	1	0
BP1026b_10148	Phage tail sheath monomer	2777	3093	2229	2	3486	2924	2550	2	3.66E-04	5.72E-04	1	0
BP1026b_10149	phage tail fiber assembly protein	1307	1366	977	1	1280	1318	1331	1	0.003280005	0.004567797	1	0
BP1026b_10150	Phage-related tail fiber protein	5741	6250	5385	2	5935	6232	6449	2	3.72E-05	6.56E-05	1	0
BP1026b_10151	phage tail protein I	1930	729	1178	2	1937	1907	1757	3	0.445374258	0.470780947	1.5	0.584962501
BP1026b_10152	phage baseplate assembly protein	5666	6485	3393	4	5376	6029	6382	6	0.097678753	0.12743162	1.5	0.584962501
BP1026b_10153	phage baseplate assembly protein	413	684	448	1	514	661	537	1	0.058325066	0.069603394	1	0
BP1026b_10154	baseplate assembly protein V	1190	1100	1156	1	1382	1516	1197	2	0.38193345	0.04672717	2	1
BP1026b_10157	hypothetical protein	2044941	3563938	3261699	5866	1732825	1657324	1614473	3309	0.530344448	0.52968069	0.564098193	-0.825981779
BP1026b_10158	Phage tail completion protein	13704	14994	15205	31	14452	13216	13262	29	6.70E-09	1.95E-08	0.935483871	-0.096215315
BP1026b_10159	bacteriophage tail completion protein R	1951	3021	3043	6	2607	2379	2097	5	3.61E-09	1.09E-08	0.833333333	-0.263034406
BP1026b_10160	Prophage LysC protein	275	144	274	1	251	284	415	2	0.704092099	0.724527953	2	0
BP1026b_10161	Putative phage-encoded lipoprotein	662	662	831	1	618	6049	900	0	0.013965305	0.01404218	1	0
BP1026b_10162	Putative phage-encoded peptidoglycan binding protein	1383	1413	1407	1	1196	921	1001	1	1.57E-10	2.57E-10	1	0
BP1026b_10163	Prophage membrane protein	878	424	488	2	730	608	684	2	0.054586212	0.065428249	1	0
BP1026b_10164	Prophage membrane protein	115	97	80	0	67	278	167	0	0.058571388	0.069838286	#DIV/0!	#DIV/0!
BP1026b_10165	Phage-related tail protein	137	114	173	0	211	98	247	0	0.98957125	0.991946601	#DIV/0!	#DIV/0!
BP1026b_10166	putative bacteriophage protein	143	35	32	0	26	98	54	0	0.037591425	0.046044718	#DIV/0!	#DIV/0!
BP1026b_10167	Phage head completion-stabilization protein	310	96	187	0	402	97	368	0	0.407333554	0.435044523	#DIV/0!	#DIV/0!
BP1026b_10168	phage terminase endonuclease subunit	969	969	498	1	1177	1349	93493	2	0.30871682	0.3149532	1	0
BP1026b_10169	Phage major capsid protein	2882	3327	3107	3	3409	3535	3281	3	4.37E-04	6.77E-04	1	0
BP1026b_10170	Phage capsid scaffolding protein	1049	1131	1146	1	1288	1185	845	1	9.39E-04	0.001398294	1	0
BP1026b_10171	Phage terminase, ATPase subunit	5608	4376	5798	2	5119	6083	5567	3	4.42E-05	7.74E-05	1.5	0.584962501
BP1026b_10172	Phage portal protein	8059	8977	9322	8	12233	12773	10068	11	0.014773287	0.019029379	1.375	0.459431619
BP1026b_10173	addiction module antidote protein	109035	128050	133590	346	194277	201396	175805	533	0.345669086	0.37216761	1.540462428	0.623363495
BP1026b_10174	addiction module tail protein	76383	125407	117378	333	124192	125534	125780	397	9.44E-06	1.80E-05	1.192192192	0.25361683
BP1026b_10175	ATPase	100600	171672	155017	113	108019	183039	97071	2	7.17E-24	2.30E-23	0.7256671	-0.115083135
BP1026b_10176	hypothetical protein	4231	6485	5133	44	6122	5725	6477	50	4.96E-04	7.64E-04	1.136363636	0.184425271
BP1026b_10177	phage baseplate assembly protein	4254	4359	4295	13	5608	5770	5218	16	0.01080709	0.01411553	1.230769231	-0.592660282
BP1026b_10178	phage tail protein I	2249	1380	1417	4	1957	2093	1818	4	0.003580199	0.004962684	1	0
BP1026b_10179	Phage-encoded modification methylase	4404	4302	4561	9	4478	4053	4703	9	1.23E-05	2.31E-05	1	0
BP1026b_10180	hypothetical protein	18487	31990	27700	51	18784	18360	18685	36	2.19E-19	2.26E-18	0.705882353	-0.502500341
BP1026b_10181	phage tail completion protein	32776	28341	31152	84	35564	36989	40474	102	1.14E-04	1.89E-04	1.214285714	0.280107919
BP1026b_10182	type VI secretion system	182678	175899	175899	224	185147	187612	189754	273	1.85E-07	3.73E-07	1.080337174	0.111508313
BP1026b_10183	type VI secretion system	148356	157439	160591	115	155765	145156	127045	105	9.02E-16	6.00E-15	0.913043478	-0.131244533
BP1026b_10184	type VI secretion system	23243	37319	32300	47	19818	17900	17524	28	9.57E-31	3.03E-29	0.595744681	-0.747232393
BP1026b_10185	hypothetical protein	3098	6277	5851	48	2622	2183	2510	23	1.20E-45	1.04E-43	0.479166667	-0.061400545
BP1026b_10186	lipoprotein	301862	324352	343905	481	287947	287950	278780	423	5.93E-11	2.22E-10	0.879417879	-0.185379231
BP1026b_10187	type VI secretion system	357774	402711	383194	734	402845	413111	396532	778	0.70E-09	2.05E-08	1.059945504	0.083990092
BP1026b_10188	type VI secretion system	944830	1425388	1270642	813	1196715	1149806	1028000	734	0.668080095	0.690000922	0.927429274	-0.086069239
BP1026b_10189	type VI secretion system	748634	343738	3069294	5733	3318866	3226728	2693288	593	0.175174863	0.19338002	0.19338002	-0.045399988
BP1026b_10190	type VI secretion system	204631	213068	203472	405	187710	180856	169428	371	3.10E-14	1.71E-13	0.916409383	-0.126502721
BP1026b_10191	type VI secretion system	204398	205045	199383	110	197911	198606	184793	105	2.24E-11	8.87E-11	0.954545455	-0.067114196
BP1026b_10192	type VI secretion system	64788	71260	70105	62	67825	64506	64700	59	7.22E-09	2.09E-08	0.951612903	-0.071553261
BP1026b_10193	type VI secretion system	254396	204854	216056	84	277245	285444	286004	105	0.009033755	0.011938279	1.25	0.321928095
BP1026b_10194	type VI secretion system	64298	68176	65339	58	72114	68667	69737	62	4.44E-06	8.80E-06	1.068965517	0.096215315
BP1026b_10195	type VI secretion system	125953	141056	137334	144	160012	155561	161068	170	4.08E-06	1.55E-05	1.180555556	0.239465935
BP1026b_10196	type VI secretion system	137165	151219	150468	147	178748	174327	168382	175	4.38E-05	6.66E-05	1.19047619	0.251538767
BP1026b_10197	type VI secretion system	748119	86346	837464	148	812460	789560	781451	203	0.393715239	0.424210034	0.971291866	-0.042023215
BP1026b_10198	hypothetical protein	61692	77555	74841	135	41284	42218	39130	77	8.80E-50	6.16E-48	0.57037037	-0.810029056
BP1026b_10199	hypothetical protein	130766	128477	139285	137	100183	104417	116632	110	7.54E-19	7.21E-18	0.802919708	-0.163726369
BP1026b_10200	ToIC family type I secretion outer membrane protein	16488	11707	14153	9	15496	15665						

BP1026b	10246	adenylate cyclase	21453	11666	13287	23	23044	22296	20799	34	0.039987529	0.048807849	1.47826087	0.563900885
BP1026b	10247	Indole-3-glycerol phosphate synthase	86341	84084	83373	107	108484	104173	103075	133	5.35E-04	5.52E-04	1.242990654	0.313815449
BP1026b	10248	anthranilate phosphoribosyltransferase	85158	76271	80427	78	105562	107852	108039	103	0.003292571	0.004584278	1.320512821	0.401098308
BP1026b	10249	anthranilate synthase component II	153302	80358	74094	123	86000	86972	82807	144	1.22E-04	1.22E-04	1.170731707	0.274104068
BP1026b	10250	anthranilate synthase component I	102555	136244	134711	89	160125	166046	156048	107	2.81E-05	5.04E-05	1.202247191	0.265733555
BP1026b	10251	phosphoglycolate phosphatase	53721	63554	59556	80	47970	48457	49010	66	3.46E-19	3.46E-18	0.825	-0.277533976
BP1026b	10252	ribulose-1,5-bisphosphate-3-epimerase	73542	71201	75386	105	67376	67482	63711	95	1.13E-10	4.09E-10	0.904761905	-0.144389909
BP1026b	10253	ApaC protein	73161	103236	90758	237	66737	68343	62534	175	2.99E-19	3.04E-18	0.738396624	-0.437532137
BP1026b	10255	hypothetical protein	19310	32342	30872	191	19283	16678	20828	131	2.05E-21	2.63E-20	0.685863874	-0.544005826
BP1026b	10254	membrane-bound tytic murein transglycosylase A	191739	221169	224321	189	197702	195272	192575	174	1.05E-12	4.86E-12	0.920614921	-0.119298928
BP1026b	10256	phenylacetate-CoA ligase	45203	50337	29286	37	51095	49904	45240	63	2.71E-10	9.35E-10	1.211538462	0.276840205
BP1026b	10257	phenylacetate acid degradation protein PaaI	18848	22049	21277	52	26518	25361	23175	174	4.55E-04	7.04E-04	1.031188182	-0.018179614
BP1026b	10258	enoyl-CoA hydratase	28107	22355	22762	30	22478	23014	21397	28	4.48E-10	1.50E-09	0.933333333	-0.099535674
BP1026b	10259	beta-ketoadipyl CoA thiolase	47800	32405	33740	31	38690	40146	47006	34	5.94E-07	1.33E-06	1.096774194	0.133266531
BP1026b	10260	phenylacetate acid degradation protein paaN	133920	123224	129663	75	121674	120998	116031	70	1.74E-13	8.80E-13	0.933333333	-0.099535674
BP1026b	10261	enoyl-CoA hydratase	27032	41914	34197	44	31367	33363	31960	41	2.54E-10	8.79E-10	0.931818182	-0.018179614
BP1026b	10262	hypothetical protein	98673	149493	118040	1043	142132	156295	125002	1206	1.16E-06	2.45E-06	1.156279962	0.209490749
BP1026b	10263	16S ribosomal RNA	1470237	358169	295827	466	261839	1306579	574502	3050	5.09E-06	2.01E-05	6.545043378	2.710407383
BP1026b	10264	16S rRNA	36831	54022	44410	585	51700	49062	39193	605	4.52E-09	1.33E-08	1.034188034	0.048498518
BP1026b	10265	Ala tRNA	195031	304882	242783	3257	280439	282908	214592	3412	1.27E-05	2.38E-05	1.047589807	0.067073927
BP1026b	10266	hypothetical protein	40459	61383	51609	396	73764	75165	62711	546	0.074331485	0.08714438	1.378787789	0.463400521
BP1026b	10267	23S ribosomal RNA	728539	491771	355534	182	365514	5821659	479812	771	1.39E-22	2.03E-21	4.236263736	2.08279241
BP1026b	10268	5S ribosomal RNA	3445643	4765791	3141957	33490	5803851	4875752	2795456	39749	0.124131892	0.141452096	1.186891609	0.24718819
BP1026b	10269	anaerobic dehydrogenase	122676	177422	159657	81	116222	110185	101429	58	1.58E-27	3.74E-26	0.716049383	-0.481869088
BP1026b	10270	long-chain-fatty-acid-CoA ligase	251689	280906	263615	158	291180	293024	271572	170	5.66E-06	1.11E-05	1.075393667	0.105611008
BP1026b	10271	outer membrane porin	61200	75358	72415	60	61707	59174	56131	50	1.47E-14	1.47E-14	0.833333333	-0.263034406
BP1026b	10272	hypothetical protein	81706	44744	52747	95	92550	97513	99947	154	0.55936437	0.584756077	1.621052632	0.696930932
BP1026b	10273	cell division protein MraZ	1419076	2358733	2085899	4556	2385475	2362265	2079637	5304	0.076270685	0.089184165	1.164179104	0.219313028
BP1026b	10274	S-adenosyl-methyltransferase MraW	545591	721969	683058	4900	774872	758757	739268	804	0.819565678	0.203070196	1.165217391	0.22059914
BP1026b	10275	cell division protein FtsL	40361	49314	45122	136	40998	37996	35267	115	2.79E-16	1.77E-15	0.845588235	-0.24197279
BP1026b	10276	penicillin-binding protein	313322	339297	342634	179	342876	348271	332029	184	1.47E-08	4.09E-08	1.027932961	0.039746179
BP1026b	10277	UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase	297551	164957	185317	139	277014	306505	335999	198	0.095724361	0.110569315	1.424460432	0.510415547
BP1026b	10278	UDP-N-acetylmuramoyl-tripeptide-D-alanyl-D-alanine ligase	187811	120443	130479	106	183985	199274	207964	143	0.031646823	0.039161536	1.349056604	0.319150882
BP1026b	10279	phospho-N-acetylmuramoyl-pentapeptide-transferase	191129	271686	243864	201	207373	199516	174439	164	4.02E-19	3.98E-18	0.815920398	-0.293496687
BP1026b	10280	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	215013	145309	166402	114	199388	230810	304553	160	0.311276153	0.336991673	1.403508772	0.489038081
BP1026b	10281	cell division protein FtsW	271108	289159	278189	216	307461	310605	274157	230	1.30E-06	2.78E-06	1.064814815	0.090602549
BP1026b	10282	undecaprenylidiphosphate-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	213392	117349	141916	142	184156	207281	231299	191	0.105088159	0.120917015	1.345070762	0.427681709
BP1026b	10283	UDP-N-acetylglucosamine-1-alanine ligase	325403	242775	251301	85	287244	311693	352889	228	2.55E-05	4.60E-05	1.409402949	0.2255597
BP1026b	10284	D-alanine-D-alanine ligase	204034	217990	208002	223	231501	241895	219237	245	3.18E-04	0.02E-04	0.098654709	0.135738039
BP1026b	10285	cell division protein FtsQ	132797	105767	114673	156	137607	142574	145616	188	1.19E-05	2.25E-05	1.205128205	0.269186633
BP1026b	10286	cell division protein FtsA	410504	533750	499827	390	494170	490496	444121	386	2.43E-12	1.08E-11	0.989745399	-0.014873276
BP1026b	10287	cell division protein FtsZ	1160652	1409990	1377482	1099	1351762	1356627	1396802	1143	0.150871429	0.170035737	1.040036397	0.056634017
BP1026b	10288	predicted RNA	63013	2996	5618	385	46110	75664	105385	1221	1.30E-10	4.67E-10	1.317428671	1.665132849
BP1026b	10289	predicted RNA	10049	6097	6703	229	10237	11593	12176	431	0.519036699	0.54541912	1.836005677	0.912340271
BP1026b	10290	AhpC/TSA family protein	857138	686043	720051	1490	1002313	1029710	974876	260	0.02134056	0.02134056	0.333333333	-0.449716446
BP1026b	10291	predicted RNA	95900	32487	66122	1574	99594	92707	103386	2403	0.206919945	0.29224477	1.628683609	0.610401108
BP1026b	10292	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	496524	609190	564234	587	700086	676375	617557	701	0.130774284	0.148642736	1.194207836	0.056053941
BP1026b	10293	hypothetical protein	13158	8202	8557	20	13618	13997	13014	28	0.025328793	0.031712885	1.4	0.485426827
BP1026b	10294	preprotein translocase subunit SecA	1055192	1253750	1222942	422	1409727	1383553	1311104	491	0.058362272	0.069634528	1.163507019	0.218480026
BP1026b	10295	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase	102084	124976	115788	92	126165	119990	114559	96	7.34E-09	2.12E-08	1.043478261	0.061400545
BP1026b	10296	putative ATP/GTP-binding protein	92774	122008	110813	124	125531	123389	113683	138	3.04E-07	1.75E-07	1.112903326	0.154328805
BP1026b	10297	UDP-X family pyrophosphatase	56357	70757	71787	147	83422	83071	91847	106	0.00818959	0.00818959	0.292510007	-0.087380236
BP1026b	10298	hypothetical protein	12098	43117	37962	84	35524	32076	35661	152	8.00E-15	4.73E-14	0.620806957	-0.275634443
BP1026b	10299	hypothetical protein	799969	1117708	1018576	1294	966493	962676	1261	0.32675804	0.352776782	0.974497687	0.032726932	
BP1026b	10300	dephospho-CoA kinase	45239	47038	48967	76	49703	43343	38257	71	5.96E-13	2.83E-12	0.94210526	-0.098180394
BP1026b	10301	peptidase A24 N-domain-containing protein	19257	17404	16628	19	20629	21063	17553	21	2.19E-05	4.00E-05	1.052631056	0.144389909
BP1026b	10302	type IV pilus assembly protein PilC	9750	6486	7880	6	8967	8891	10060	7	3.02E-04	4.77E-04	1.166666667	0.222392421
BP1026b	10303	type IV fimbrial biogenesis protein, PilB	7502	5192	5214	4	6994	6645	7901	5	8.99E-04	0.00134374	1.25	0.31928095
BP1026b	10304	hypothetical protein	80094	107133	988	85127	97872	69862	52855	930	9.77E-27	2.13E-25	0.941295547	-0.087380236
BP1026b	10305	Pro tRNA	12836	19503	15883	208	16745	18667	13279	120	6.31E-07	1.41E-06	1.009615383	-0.0138058
BP1026b	10306	octaprenyl-diphosphate synthase	212327	303692	279204	266	173510	166682	144042	216	5.74E-49	5.99E-47	0.690022556	-0.154323233
BP1026b	10307	50S ribosomal protein L27	472653	598524	598016	1070	636456	613962	597095	2332	5.76E-08	1.48E-07	1.106786901	0.146377474
BP1026b	10308	GTPase ObgE	382683	418536	404046	359	515719	525186	512115	462	7.78E-05	1.31E-04	1.286908078	0.363909008
BP1026b	10309	gamma-glutamyl kinase	106108	113283	107707	97	134874	143905	142194	125	2.66E-04	4.22E-04	1.288659794	0.365871442
BP1026b	10310	lipoprotein	27254	38872	35576	60	26202	24705	23682	44	1.66E-18	1.54E-17	0.314748597	-0.434758977
BP1026b	10311	diadenosine polyphosphate hydrolase	471739	769531	688743	988	651427	625342	541268	930	1.50E-12	6.81E-12	0.941295547	-0.087380236
BP1026b	10312	proH tRNA synthase	608678	674214	660282	379	649969	649365	651949	381	1.43E-06	0.02E-06	1.005277045	0.007593149
BP1026b	10313	hypothetical protein	153206	201638	183490	297	186932	172936	142843	277	9.09E-14	4.75E-13	0.932659933	-0.100576955
BP1026b	10314	hypoxanthine-guanine phosphoribosyltransferase	56060	80698	74779	127	65319	63694	58608	113	9.44E-12	3.91E-11	0.889763378	-0.168505724
BP1026b	10315	signal recognition particle protein	158971	170030	166045	120	192332	191811						

BP1026b	10364	C4-dicarboxylate transporter DctA	4561	5794	3906	3	4454	4064	3962	3	3.54E-08	9.38E-08	1	0
BP1026b	10365	allantoinase	2488	1371	1884	1	3386	2933	2776	2	0.785458051	0.801190235	2	1
BP1026b	10366	ureidoglycolate hydrolase	1765	906	688	2	2408	2967	2606	5	3.20E-05	5.69E-05	2.5	1.321928095
BP1026b	10367	ferrous uptake regulator	292200	491377	442070	952	350367	333266	333488	78	6.72E-16	4.56E-15	0.814007	0.29676563
BP1026b	10368	outer membrane lipoprotein	107173	113733	120344	144	102960	100000	88538	123	2.93E-14	1.63E-13	0.854166667	-0.227410496
BP1026b	10369	dihydrodipicolinate reductase	79484	74500	72191	93	63586	65444	62786	79	3.21E-13	1.57E-12	0.849462366	-0.235378063
BP1026b	10370	MotA/TolQ/ExbB protein channel family protein	41334	32669	33446	50	39024	35957	33183	50	6.16E-09	1.80E-08	1	0
BP1026b	10371	biopolymer ExbD/TolR family transporter	15731	15086	14818	28	12366	11924	11265	22	3.70E-15	2.28E-14	0.785714286	-0.347923303
BP1026b	10372	leucyl-tRNA synthetase	366616	391641	393565	147	442691	440756	421332	167	1.08E-07	2.68E-07	1.136054422	0.184031948
BP1026b	10373	lipoprotein	44616	77567	67425	120	69999	65202	54888	120	1.04E-07	2.59E-07	1	0
BP1026b	10374	DNA polymerase III subunit delta	148615	101463	111880	110	151063	149881	179597	151	0.010054308	0.013222666	1.372727273	0.457045026
BP1026b	10375	gamma-glutamyl phosphate reductase	149102	161856	154665	122	158565	159916	159410	122	1.51E-10	6.51E-10	1.008196721	0.011777168
BP1026b	10376	hypothetical protein	57488	61041	55983	137	59600	62510	53068	138	1.29E-08	3.61E-08	1.00729927	0.010492374
BP1026b	10377	RpR family transcriptional regulator	6058	4027	4456	4	6594	7420	7317	7	0.081188274	0.094475822	1.75	0.807354922
BP1026b	10378	phosphogluconate dehydratase	28837	17588	19598	11	33679	35991	37543	19	0.203423245	0.225566994	1.727272727	0.788495895
BP1026b	10379	KHG-KDPG aldolase	21569	14596	19095	29	25048	26274	25556	40	0.022928577	0.028869268	1.379310345	0.4639471
BP1026b	10380	GntP family high-affinity gluconate permease	181257	189426	179468	134	171004	168278	163785	123	8.38E-15	4.94E-14	0.917910448	-0.123574685
BP1026b	10381	shikimate kinase	156720	172605	151547	321	165713	167073	165703	323	2.15E-10	7.46E-10	1.066237933	0.008060868
BP1026b	10382	adenosuccinate lyase	199240	230061	222401	136	212198	204605	192670	146	2.13E-10	7.42E-10	0.935897436	-0.09557766
BP1026b	10383	nitrate transporter	3847	3841	2635	2	9173	4251	4360	2	0.001692586	0.002445194	1	0
BP1026b	10384	LysR family transcriptional regulator	22826	20642	20376	22	19006	18274	19441	19	1.11E-10	4.04E-10	0.863636364	-0.211504105
BP1026b	10385	glutamate dehydrogenase	2303325	2199232	2228183	1717	2290434	2286133	2207533	1731	0.148667278	0.167702473	1.008153757	0.011715685
BP1026b	10386	glutamate/aspartate periplasmic binding protein	3203310	4928241	4494758	4707	4188668	4162030	4212585	4683	0.224242425	0.247647162	0.994901211	-0.007374815
BP1026b	10387	glutamate/aspartate transport system permease	143469	230945	208701	262	134585	127968	116397	170	1.08E-40	6.73E-39	0.648854962	-0.624032065
BP1026b	10388	glutamate/aspartate ABC transporter, permease protein	183833	251744	213552	309	177707	167654	150379	243	1.51E-23	2.45E-22	0.786407767	-0.346650524
BP1026b	10389	Cysteine ABC transporter, ATP-binding protein	383989	569901	541241	686	382060	383384	386521	686	0.001060339	0.00165303	1.260169793	0.37767068
BP1026b	10390	hypothetical protein	36638	59215	49171	189	40731	36366	34402	145	2.22E-21	2.84E-20	0.767195767	-0.382333334
BP1026b	10391	chaperonin, 10 kDa	114141	158411	142655	435	115923	109676	98420	339	5.98E-21	7.32E-20	0.779310345	-0.359730128
BP1026b	10392	HSP20 family protein	85050	121781	115296	243	95783	95607	102667	222	1.09E-11	4.49E-11	0.913580247	-0.130396637
BP1026b	10393	HSP20 family protein	66548	54894	60080	144	75035	76398	84084	186	0.008986768	0.011878691	1.291666667	0.36923381
BP1026b	10394	hypothetical protein	29080	24549	28369	124	28381	27053	27862	126	1.91E-07	4.56E-07	0.16129032	0.023083613
BP1026b	10395	hypothetical protein	323750	476779	426331	430	387203	357000	325606	374	3.51E-14	1.93E-13	0.869767442	-0.20129839
BP1026b	10396	dehydrogenase	51162	37416	43230	41	45542	49103	46887	49	6.00E-08	1.62E-07	0.39107933	0.101879014
BP1026b	10397	hypothetical protein	11459	6008	7236	11	7878	9536	11981	14	0.001186841	0.001741479	1.272727273	0.347923303
BP1026b	10398	hypothetical protein	24316540	40353143	35961912	360686	21636714	19760833	18459023	214539	8.24E-08	2.08E-07	0.594808227	-0.749503494
BP1026b	10399	OsmC/Ohr family protein	76759	80223	76696	184	54833	55008	49963	125	3.72E-31	1.23E-29	0.679347826	-0.55777671
BP1026b	10400	50S ribosomal protein L13	784712	1336394	1229570	2068	1274550	1257896	1247084	2333	0.158286385	0.177944349	1.128143133	0.017395012
BP1026b	10401	30S ribosomal protein S9	376653	474626	432268	1088	566921	559752	540867	1414	8.62E-05	1.45E-04	1.299632353	0.378103564
BP1026b	10402	iron-sulfur cluster insertion protein EriA	488078	770057	661398	1733	704224	686474	601289	1799	0.013865192	0.017926019	0.038084247	-0.539525352
BP1026b	10403	AcuA family transcriptional regulator	157743	177443	192324	61	23576	27898	30180	29	0.001060339	0.00165303	1.260169793	0.37767068
BP1026b	10404	glutathione S-transferase	36394	50900	46143	63	42984	43147	46213	62	1.84E-10	6.46E-10	0.984126984	-0.203806313
BP1026b	10405	glutathione S-transferase-like protein	53514	59674	60940	83	55305	53119	60217	82	6.37E-09	1.86E-08	0.98795187	-0.107487427
BP1026b	10406	anhydros-N-acetylmuramic acid kinase	47237	36646	35291	34	44440	49149	46059	39	1.23E-05	2.31E-05	1.147058824	0.197939378
BP1026b	10407	tyrosyl-tRNA synthetase	186429	201139	208110	158	198593	203269	208428	163	3.27E-07	7.62E-07	1.03164557	0.044947406
BP1026b	10408	D-tyrosyl-tRNA (Tyr) deacylase	14056	7033	2622	20	11580	12135	12175	27	0.010522299	0.013800603	1.35	0.432959407
BP1026b	10409	phosphoglycerate mutase	28143	23376	6597	38	28480	26683	29278	42	5.77E-06	1.13E-05	1.105263158	-0.144389909
BP1026b	10410	hypothetical protein	53291	16903	16283	15	12626	13683	14061	16	1.40E-16	5.23E-16	0.743186882	-0.426245765
BP1026b	10411	hypothetical protein	53276	26566	33012	39	54736	57911	59369	99	0.279494833	0.29994364	1.512820513	0.59724083
BP1026b	10412	Holliday junction DNA helicase RuvB	179259	106897	122706	127	227358	244504	253344	225	0.075176499	0.088036192	0.717635543	0.058965054
BP1026b	10413	Holliday junction DNA helicase RuvA	128847	131918	124135	220	177108	168979	154062	286	0.001653171	0.002392114	1.3	0.378511623
BP1026b	10414	Holliday junction resolvase	31946	19188	23542	45	24666	26930	26757	48	1.16E-06	2.47E-06	1.066666667	0.093109404
BP1026b	10415	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclodiphosphate	231275	204489	217854	139	266093	258235	240619	161	0.002289234	0.00324429	1.158273381	0.211975805
BP1026b	10416	DNA-binding protein Fis	23034	33907	35502	134	16201	14905	13596	63	1.47E-52	7.40E-49	0.470149053	-0.108809367
BP1026b	10417	dihydrodipicolinate synthase	93775	89834	88090	89	66938	68833	67854	66	2.19E-18	2.00E-17	0.741573034	-0.43139312
BP1026b	10418	hypothetical protein	32387	12265	16900	17	25522	30540	32499	24	0.038790024	0.047401621	1.411767606	0.497496559
BP1026b	10419	aminopeptidase P	76779	39292	47852	38	54553	57136	69538	42	1.13E-05	2.13E-05	1.105263158	0.144389909
BP1026b	10420	predicted RNA	165794	162342	172173	882	152549	149644	168572	830	4.63E-14	2.50E-13	0.941043084	-0.087667319
BP1026b	10421	glutathione S-transferase	130620	154284	153732	238	98370	94673	90961	154	5.32E-31	1.73E-29	0.647058824	-0.628031223
BP1026b	10422	glutamate synthase domain-containing protein	153564	100729	109397	70	121038	129495	128662	77	7.72E-08	1.96E-07	1.1	0.137503524
BP1026b	10423	RNA-specific 2-thiouridylase MmmA	162411	129172	147664	129	161247	108479	116247	162	1.61E-24	7.40E-23	0.743186882	-0.426245765
BP1026b	10424	NUDIX domain-containing protein	10399	8806	5473	14	7057	7235	9701	15	4.69E-05	1.18E-05	0.710428571	0.099535636
BP1026b	10425	NAD(P) transhydrogenase subunit alpha	240559	228408	249229	209	198495	207134	212551	180	3.46E-13	1.68E-12	0.861244019	-0.215060630
BP1026b	10426	NAD(P) transhydrogenase subunit alpha	79463	101311	92834	276	74105	67866	61529	205	8.12E-19	7.75E-18	0.742753623	-0.429044357
BP1026b	10427	NAD(P) transhydrogenase subunit beta	563421	719136	660021	445	511924	498981	474654	340	2.51E-23	4.02E-22	0.764044944	-0.38827059
BP1026b	10428	DeoR family transcriptional regulator	36584	28092	33860	47	30248	33548	37980	49	7.33E-08	1.86E-07	1.042551911	0.060120992
BP1026b	10429	hypothetical protein	6655	6234	6894	16	6731	7638	8017	18	1.06E-04	7.6E-04	1.125	0.192652001
BP1026b	10430	N6-adenine-specific DNA methylase	58133	42186	46846	34	547591	527894	547591	43	0.061482802	0.001843260	0.743186882	-0.426245765
BP1026b	10431	hypothetical protein	60526	41223	47146	21	59374	59182	61769	29	7.59E-04	0.00114326	1.21791304	0.238739666
BP1026b	10432	hypothetical protein	48888	22141	25115	35	36730	38379	40121	49	0.007986585	0.010619395	1.4	0.485426827
BP1026b	10433	paraquat-inducible protein	178059	180285	190180	110	170244	167713	151660	98	2.21E-16	1.58E-15	0.890909091	-0.166649869
BP1026b	10434	paraquat-inducible protein	18204	19716	20056	29	13488	14048	11610	19	1.05E-21	1.40E-20	0.655172414	-0.10053482
BP1026b	10435	paraquat-inducible protein	63719	55656	53385									

BP1026b	10483	hypothetical protein	166318	125827	132337	440	157327	165703	159663	501	1.15E-06	2.46E-06	1.138636364	0.18730708
BP1026b	10484	molecular chaperone DnaK	3647305	4202833	4044280	2030	5593258	5725972	5654387	2897	0.057130965	0.068321566	1.427093596	0.513079957
BP1026b	10485	chaperone protein DnaJ	46871	39940	45875	670	75123	76492	72179	1130	0.759776666	0.77651835	1.686567164	0.754089772
BP1026b	10486	chromatin binding protein	116860	679152	679152	593	783680	806720	810720	709	0.09536888	0.110331133	1.195515514	0.257353523
BP1026b	10487	3-methyl-2-oxobutanoate hydroxymethyltransferase	338015	290188	292810	152	388832	377215	355427	186	1.43E-05	2.67E-05	1.223684211	0.291231298
BP1026b	10488	deoxymycolate kinase family protein	70412	60232	60308	78	46454	50401	51455	60	1.53E-22	2.21E-21	0.769230769	-0.378511623
BP1026b	10489	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase	31218	19863	24128	36	24000	25592	24644	36	5.15E-08	1.34E-07	1	0
BP1026b	10490	polyA polymerase	71036	68923	74038	135	67418	67325	63073	124	7.02E-10	2.31E-09	0.918518519	-0.122619287
BP1026b	10491	polyA hydrolase	170162	149419	158785	103	157726	163866	152569	102	1.48E-11	5.98E-11	0.990291262	-0.4014075185
BP1026b	10492	DnaA regulatory inactivator Hda	45715	54632	57065	76	29580	30871	30380	44	6.64E-40	4.94E-38	0.578947368	-0.788495095
BP1026b	10493	hypothetical protein	13506	7702	7006	12	9985	11521	12316	15	6.89E-04	0.001045501	1.25	-0.321928095
BP1026b	10494	tRNA delta(2)-isopentenylpyrophosphate transferase	49467	20097	33890	626	58195	58858	53584	1034	0.699501803	0.720197122	1.651757188	0.724001623
BP1026b	10495	DNA mismatch repair protein	17484	13679	16060	39	16753	17807	17425	43	2.53E-05	4.58E-05	1.102564103	0.140862536
BP1026b	10496	DcdA protein	66894	46652	51518	56	61457	61133	63293	63	4.49E-05	7.84E-05	1.125	0.169925001
BP1026b	10497	small-conductance mechanosensitive channel	155402	95844	110505	58	128441	139556	150014	67	1.14E-06	2.44E-06	1.155172414	0.208108195
BP1026b	10498	glutamine amidotransferase	63998	71841	68003	99	66039	66197	54592	91	1.16E-10	4.21E-10	0.919191919	-0.12156198
BP1026b	10499	mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase	101318	120072	121221	130	88811	85193	81212	97	5.22E-20	5.76E-19	0.746153846	-0.423454971
BP1026b	10500	capsular polysaccharide biosynthesis/export periplasmic protein WcbA	21956	28293	27057	30	19368	20480	19423	23	2.82E-16	2.00E-15	0.766666667	-0.38332864
BP1026b	10501	capsular polysaccharide glycosyltransferase biosynthesis protein WcbB	107827	164269	149884	98	123667	120653	112760	83	5.84E-18	5.02E-17	0.846938776	-0.239670413
BP1026b	10502	capsular polysaccharide export system inner membrane protein WcbC	90320	119765	111626	61	97917	87982	78488	50	4.04E-15	2.48E-14	0.819672131	-0.286881148
BP1026b	10503	capsular polysaccharide export system inner membrane protein WcbD	93465	138575	129192	104	97159	90389	81492	77	3.14E-20	3.51E-19	0.740384615	-0.433653177
BP1026b	10504	capsular polysaccharide export system inner membrane protein WcbE	209801	312748	283373	230	177078	172784	156260	144	1.71E-43	1.23E-41	0.626086957	-0.67556505
BP1026b	10505	capsular polysaccharide export system inner membrane protein WcbF	435535	743482	629727	401	434471	423535	386800	276	5.86E-30	1.71E-28	0.688279402	-0.53893297
BP1026b	10506	putative ATP-binding ABC transporter capsular polysaccharide export protein	77778	135465	120408	213	108623	108452	100028	202	4.09E-11	1.57E-10	0.948356808	-0.676498137
BP1026b	10507	Glycosyl transferase, group 1 family protein	204902	368477	313537	449	267716	272438	256438	404	8.53E-10	2.78E-09	0.899777283	-0.152360152
BP1026b	10508	Glycosyl transferase, group 2 family protein	282693	469096	393342	264	431227	452241	411265	299	1.11E-07	2.75E-07	1.132575758	-0.179607555
BP1026b	10509	hypothetical protein	326997	537332	483459	339	496897	491705	459780	344	1.32E-09	4.24E-09	1.073464313	0.102631177
BP1026b	10510	hypothetical protein	25176	41558	34741	363	35162	35414	36058	382	1.13E-07	2.78E-07	1.052341598	0.07360309
BP1026b	10511	capsular polysaccharide biosynthesis protein WcbG	137836	221755	196131	287	156374	145860	131931	224	6.51E-26	1.33E-24	0.780487805	-0.337552005
BP1026b	10512	Glycosyl transferase, group 1 family protein	303540	511746	430860	231	428561	415641	392341	229	2.98E-11	1.16E-10	0.931941391	-0.215425523
BP1026b	10513	capsular polysaccharide biosynthesis protein WcbH	213507	374679	321560	323	276909	270606	240687	280	9.91E-11	3.62E-10	0.866873065	-0.206107338
BP1026b	10514	capsular polysaccharide biosynthesis protein WcbI, NAD-dependent epimerase	100252	166896	151596	165	123223	121929	119780	144	1.14E-16	8.47E-16	0.872727272	-0.196397213
BP1026b	10515	UDP-mannose 4-epimerase	307885	517937	454044	420	377812	339644	339642	354	7.52E-16	8.05E-15	0.842772727	-0.246639068
BP1026b	10516	D-D-heptose 7-phosphate kinase	281964	478540	411125	375	333493	323408	302930	307	7.15E-15	4.20E-14	0.818666667	-0.28865194
BP1026b	10517	phosphohexose isomerase	208435	339813	302865	537	261089	249515	247772	478	1.05E-09	3.39E-09	0.890130354	-0.16791147
BP1026b	10518	D-glycero-D-manno-heptose 1-phosphatransferase	128757	197176	182190	297	160451	150555	134308	260	3.14E-18	2.82E-17	0.875420875	-0.191951308
BP1026b	10519	D-glycero-D-manno-heptose 1,7-bisphosphatransferase	123937	206698	181987	307	138194	129690	129264	238	1.70E-25	3.32E-24	0.7752443	-0.367277082
BP1026b	10520	capsular polysaccharide export protein	110547	181683	161097	125	107390	99605	95723	83	2.84E-30	8.63E-29	0.664	-0.590744853
BP1026b	10521	short chain dehydrogenase/reductase family oxidoreductase	43657	34714	39171	67	47158	42218	41919	72	8.68E-08	2.19E-07	1.074628666	0.103835811
BP1026b	10522	capsular polysaccharide biosynthesis protein WcbJ	66991	102633	91300	57	538635	57532	59368	60	5.78E-35	6.73E-34	0.631578025	-0.663965013
BP1026b	10523	capsular polysaccharide biosynthesis fatty acid synthase	655255	579749	603985	80	744148	742644	768255	98	0.138990062	0.154066127	1.225	0.92781749
BP1026b	10524	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	87673	39837	45599	62	85735	91121	113437	105	0.835964753	0.863089899	1.693548387	0.06049207
BP1026b	10525	class-I aminotransferase	112889	100881	105590	80	108981	110081	112698	83	1.19E-08	3.35E-08	1.0375	0.353111336
BP1026b	10526	acyltransferase	18812	10082	12310	19	18528	17049	17222	25	0.00559576	0.007575501	1.315789474	0.395928676
BP1026b	10527	hypothetical protein	28716	24062	22709	21	28351	29796	29927	25	7.48E-05	1.27E-04	1.19047619	0.251538767
BP1026b	10528	hypothetical protein	5540	4208	4625	3	5783	6119	6886	5	0.011397693	0.014883291	0.666666667	0.736665594
BP1026b	10529	hypothetical protein	1351	652	739	1	1092	1593	1641	2	0.603164958	0.62302481	2	1
BP1026b	10530	hypothetical protein	174	203	125	1	388	478	403	2	3.33E-06	6.73E-06	2	2
BP1026b	10531	hypothetical protein	556	518	573	1	826	869	927	2	0.065566727	0.077463217	2	1
BP1026b	10532	AraC family transcriptional regulator	12842	12860	12029	13	10620	10989	9682	11	1.19E-12	5.48E-12	0.846153846	-0.2410081
BP1026b	10533	undecaprenyl-L-phosphate galactosephosphotransferase	8740	5863	6424	6	5547	5597	5731	5	1.77E-11	7.09E-11	0.833333333	-0.263034406
BP1026b	10534	polysaccharide biosynthesis/export protein	4434	3514	3963	3	5035	5569	4705	4	0.013032819	0.016912695	1.333333333	0.415037499
BP1026b	10535	protein-tyrosine-phosphatase	1038	557	949	1	1370	1406	1081	2	0.74174848	0.75957325	2	1
BP1026b	10536	tyrosine-protein kinase Wzc	13669	13268	11789	5	10401	10789	10027	4	2.73E-13	2.73E-12	0.8	-0.32192801
BP1026b	10537	O-arabinose 5-phosphate isomerase	2583	1894	2293	1	2442	2426	2297	1	4.13E-05	7.73E-05	0.8	-0.32192801
BP1026b	10538	capsule polysaccharide biosynthesis protein	5292	6346	5261	4	4913	4816	3979	3	3.17E-10	1.08E-09	0.75	-0.415037499
BP1026b	10539	serine O-acetyltransferase	2118	4285	2963	5	2661	2521	2607	4	7.22E-11	2.67E-10	0.8	-0.321928095
BP1026b	10540	hypothetical protein	5932	6603	5838	6	6264	5922	5602	6	6.69E-07	1.49E-06	1	0
BP1026b	10541	Glycosyltransferase	29132	3593	3013	2	3358	3491	3163	3	7.06E-05	1.20E-04	1.5	0.584962105
BP1026b	10542	2-dehydro-3-deoxyphosphogluconate aldolase	20020	22682	21186	25	22727	24062	20450	26	1.94E-06	4.03E-06	1.04	0.065838228
BP1026b	10543	2-deoxy-manno-octulosonate-8-phosphatase	7769	555	5085	11	110442	106389	10639	104	0.73834489	0.747139715	1.727272727	0.884950809
BP1026b	10544	arabinose-5-phosphate isomerase	9335	7005	8036	8	9206	9951	10908	10	0.002115013	0.003011697	0.925	0.321928095
BP1026b	10545	UDP-glucose-1-phosphate uridylyltransferase	25250	31023	29687	32	27927	26056	26049	30	1.35E-09	4.29E-09	1.135	-0.093109404
BP1026b	10546	hypothetical protein	3750	2186	3236	13	3906	3262	4725	17	0.044070883	0.053437865	1.307692308	0.387023123
BP1026b	10547	regulator of flagellar biosynthesis FlhD	6152	4731	4822	22	7410	7139	6541	30	0.016669517	0.020138255	1.363636364	0.447458977
BP1026b	10548	Lys tRNA	10590	14238	12699	164	11829	9425	8526	130	3.74E-14	2.05E-13	0.792682977	-0.335184192
BP1026b	10549	hypothetical protein	2129314	2981338	2702344	3472	2997608	2974728	2810171	3903	0.131275029	0.149157769	1.124135945	-0.16816515
BP1026b	10550	OmpA family outer membrane protein	1184139	1427101	1457454	2659	1315029	1331807	1436202	2681	0.188796098	0.210206867	1.008273787	0.01887442
BP1026b	10551	translocase protein TolB	518058	623834	595581	437	420847	446313	471424	334	5.43E-24	4.71E-23	1.948728862	0.387785177
BP1026b	10552	hypothetical protein	60010	38509	42589	46	46608	48379	53283	52	1.93E-04	4.01E-06	1.130433483	0.176877762
BP1026b	10553	tolR protein	55079	49151	58299	120	47128	46184	43099	101	4.04E-18	3.56E-17	0.841666667	-0.248679113
BP1026b	1055													

BP1026810597	hypothetical protein	36182	34764	35658	24	30554	28025	30329	20	9.02E-14	4.72E-13	0.833333333	-0.263034406
BP1026810598	phospholipid-binding domain-containing protein	75296	61153	57781	175	68914	71403	64804	185	3.43E-06	6.90E-06	1.057142857	0.080170349
BP1026810599	D(-)-3-hydroxybutyrate-oligomer hydrolase	206707	174721	186242	90	223553	230267	243605	110	0.01611186	0.020685528	1.222222222	0.289506617
BP1026810600	hypothetical protein	300	494	301	495	4	5735	358	3	8.34E-05	9.45E-05	0.75	0.415037490
BP1026810601	hypothetical protein	6616	8692	6847	23	10403	9583	7419	29	0.002903125	0.004063726	1.260869565	0.334419039
BP1026810602	serine-type carboxypeptidase family protein	122954	141398	143532	74	158846	156563	158222	86	2.96E-06	6.02E-06	1.162162162	0.216811389
BP1026810603	permease	24073	16711	15781	23	25266	26036	23255	31	0.006282211	0.00845729	1.347826087	0.340634554
BP1026810604	EmrB/QacA family drug resistance transporter	24783	23073	23282	16	22736	25522	25866	17	9.03E-07	1.97E-06	1.0625	0.087462841
BP1026810605	glycerophosphoryl diester phosphodiesterase family protein	87234	73517	83135	71	73715	74310	74698	65	1.71E-10	6.03E-10	0.915429258	-0.127379306
BP1026810606	amino acid transporter LysE	8997	7522	6328	12	6996	8306	11552	14	1.64E-04	8.64E-04	1.166666667	0.22392421
BP1026810607	acyltransferase	1001	541	538	1	1245	980	1512	2	0.15566739	0.14769262	0.700082052	1
BP1026810608	DNA-binding protein	4153	2501	3056	5	4767	5317	5716	8	0.678623599	0.700082052	1.6	0.678071905
BP1026810609	metallo-beta-lactamase family protein	40976	62443	52961	42	33864	32434	33893	27	2.10E-32	7.92E-31	0.642857143	-0.637429921
BP1026810610	transcriptional regulator	11380	14722	11379	28	13192	12412	10947	27	8.25E-08	2.09E-07	0.964285714	-0.05246742
predicted RNA	-	2230872	4007535	3826378	12024	3182425	3068627	3601999	11771	0.206159666	0.228442303	0.978958749	-0.030680025
BP1026810611	lipoprotein	79249	86727	83509	52	66062	67141	66032	41	1.89E-15	1.21E-14	0.788461538	-0.342887714
BP1026810612	lipoprotein	60997	61786	58575	48	62629	66602	62384	50	2.59E-06	5.30E-06	1.041666667	0.058893689
BP1026810613	OmpW family outer membrane protein	40194	35333	41653	45	43794	44641	39085	48	4.50E-18	1.20E-07	1.066066667	-0.093109404
BP1026810614	activator protein	316074	353518	350145	658	258122	245445	263192	495	2.92E-15	1.83E-14	0.752279635	-0.110659509
BP1026810615	hypothetical protein	36462	21170	24739	26	35370	36858	37012	35	0.001887906	0.002708622	1.346153846	0.428843299
BP1026810616	zinc-binding alcohol dehydrogenase	99984	84959	87485	90	114036	110733	105158	109	6.59E-05	1.13E-04	1.211111111	0.276312228
BP1026810617	transcriptional regulator family protein	108663	175756	154048	335	180511	172426	157808	391	1.25E-05	2.35E-05	1.167164719	0.223007512
BP1026810618	hypothetical protein	258	467	427	2	302	597	403	3	0.157404526	0.177080091	1.5	0.584962501
BP1026810619	hypothetical protein	2414	3413	2642	6	3396	3385	3061	8	0.002347193	0.00322671	1.333333333	0.415037499
BP1026810620	hypothetical protein	12680	15923	13125	5	11537	12659	13031	5	5.53E-08	1.43E-07	0.333333333	0.002306207
BP1026810621	co-chaperon GroEL	3174987	5066037	4436600	14366	3883987	3670641	3301097	12306	0.009327062	0.009327062	0.856745093	-0.223062072
BP1026810622	chaperonin GroEL	30255598	43174830	40058502	23052	45252661	44567080	43817422	27145	7.18E-10	2.35E-09	1.177555093	0.235794559
BP1026810623	zinc-binding alcohol dehydrogenase	166314	159836	164748	192	174745	179712	194533	215	1.22E-06	2.60E-06	1.119791667	0.163230549
BP1026810624	rubredoxin	138008	222506	196036	1212	182475	186989	170763	1176	9.46E-12	3.92E-11	0.970297073	-0.045016319
predicted RNA	-	32847	18401	20686	319	37979	43473	49468	581	0.751623116	0.768931438	1.821316614	0.86498174
BP1026810625	hypothetical protein	111949	66766	67533	61	106228	123759	150734	95	0.098564022	0.113723528	1.557377049	0.639118271
BP1026810626	hypothetical protein	836518	1098608	1000595	1690	1222175	1186877	1058220	1994	0.145610429	0.164491204	1.179881657	0.328462163
BP1026810627	Holliday junction resolvase-like protein	192463	110757	105601	309	197906	205712	231175	479	0.991702181	0.993447341	1.550161812	0.632418818
BP1026810628	bifunctional pyrimidine regulatory protein PyrR/uracil												
BP1026810629	phosphoribosyltransferase	56591	32556	44313	85	40588	40358	40038	77	1.21E-13	6.23E-13	0.905882353	-0.142604395
BP1026810630	aspartate carbamoyltransferase catalytic subunit	78885	79073	77853	76	62526	63373	61975	60	3.09E-16	2.17E-15	0.789473684	-0.03136918
BP1026810631	dihydroorotase	264009	235707	240571	193	260149	247954	245356	196	4.55E-06	9.01E-06	1.015544041	0.022252807
BP1026810632	acyltransferase family protein	304786	260015	271961	320	342849	345243	336949	392	6.26E-05	1.07E-04	1.225	0.292781749
BP1026810633	diadenosine tetraphosphate	61809	44243	49556	61	64672	67142	62844	80	0.024704094	0.030981273	1.311475451	0.391190757
BP1026810634	dTDP-glucose 4,6-dehydratase	216103	229632	233235	213	161546	161475	157046	151	1.02E-32	1.91E-31	0.708020185	-0.496304881
BP1026810635	glucose-1-phosphate thymidyltransferase	330468	412050	389312	422	368618	352626	323340	389	1.17E-11	4.80E-11	0.921800948	-0.171472844
BP1026810636	dTDP-4-dehydrohamose 3,5-epimerase	119722	213547	178916	309	146031	138339	136121	253	4.70E-22	6.55E-21	0.81770227	-0.288469453
BP1026810637	dTDP-4-dehydrohamose reductase	147392	222722	190898	208	157841	153351	147548	170	1.39E-22	2.03E-21	0.817307697	-0.291048782
BP1026810638	ABC-2 type transport system integral membrane protein	39949	69000	56618	66	34148	32730	30512	38	9.68E-40	5.83E-38	0.575757576	-0.496466606
BP1026810639	polysaccharide ABC transporter, ATP-binding protein	190074	288599	257566	174	202618	197739	177328	136	9.95E-22	1.33E-20	0.781609195	-0.584806555
BP1026810640	O-anigen acylase WbA	156769	260270	230043	176	159512	152515	148471	123	1.13E-34	5.04E-33	0.698863636	-0.516971713
BP1026810641	NAD-dependent epimerase/dehydratase	222896	303061	303061	293	272242	258167	258167	276	0.154E-08	0.154E-08	0.941970522	-0.086232398
BP1026810642	glycosyltransferase	347412	592142	515210	524	451718	431548	408608	466	2.84E-16	2.01E-15	0.889312977	-0.169236857
BP1026810643	O-anigen methyltransferase	501928	800576	714432	389	736549	713183	642002	404	0.863456799	0.874485593	1.038560411	0.534585138
BP1026810644	glycosyl transferase family protein	274042	435725	395054	199	377544	362208	326646	192	1.74E-10	6.13E-10	0.964824171	-0.05166212
BP1026810645	glycosyl transferase WbF	68419	108708	96948	95	73523	70014	69180	74	8.47E-17	6.38E-16	0.778947368	-0.360402243
BP1026810646	UDP-glucose 4-epimerase	67696	74881	70119	73	61044	64103	59688	63	8.63E-13	4.03E-12	0.863013699	-0.212544635
BP1026810647	glycoside hydrolase family protein	40808	57493	57816	53	61491	57652	54642	37	1.36E-26	2.98E-25	0.698112008	-0.516467089
BP1026810648	polysaccharide biosynthesis protein	190547	229828	208647	96	167510	167373	163842	93	6.61E-13	1.91E-14	0.941970522	-0.413107
BP1026810649	glycosyl transferase family protein	80841	140076	93488	83	86611	82543	77296	72	1.28E-12	8.86E-12	0.867469881	-0.20511443
BP1026810650	UDP-glucose 4-epimerase	161786	148556	157411	152	156232	147708	135843	144	5.77E-14	3.09E-13	0.947368421	-0.078002512
BP1026810651	glycoside hydrolase family protein	16629	9947	10495	10	12400	14171	14064	11	2.84E-05	5.09E-05	1.1	0.137503524
BP1026810652	glycosyl transferase family protein	16635	10377	10458	14	13988	15095	16211	18	0.00117058	0.001643319	1.285714286	0.362570079
BP1026810653	hypothetical protein	19027	12016	13309	11	15776	16002	14652	11	4.03E-06	7.99E-06	1	0
BP1026810654	phosphoglucosyltransferase/phosphomannosyltransferase family protein	608559	596468	574604	411	686231	712507	719636	497	0.451747498	0.481089087	1.209245542	0.274107458
BP1026810655	hypothetical protein	55803	385519	43562	46	446188	431786	431786	46	4.35E-08	4.35E-08	0.941970522	-0.031026896
BP1026810656	hypothetical protein	287306	328456	302574	346	345991	331514	285576	362	1.26E-07	3.09E-07	1.046242757	0.065217659
BP1026810657	3-deoxy-D-manno-octulosonic-acid transferase	46964	14276	20695	19	37664	43385	52184	32	0.199798606	0.221664161	1.684210526	0.750272087
BP1026810658	urease accessory protein UreG	33295	44562	38474	59	28805	29663	29739	45	4.54E-18	3.98E-17	0.762711864	-0.390789953
BP1026810659	urease accessory protein UreE	8603	7089	6273	10	7485	7876	9035	11	5.75E-05	9.91E-05	1.1	0.137503524
BP1026810660	urease accessory protein UreF	15022	17732	17908	26	16616	15860	15674	25	2.44E-08	6.59E-08	0.961538462	-0.056583528
BP1026810661	urease subunit alpha	7700	7162	7161	4	8051	10005	9578	5	0.00404283	0.006032223	1.25	0.331928095
BP1026810662	urease, beta gamma subunit	365	59	217	0	163	0	0	0	0.066157009	0.062973962	0.910538462	-0.43197
BP1026810663	urease subunit gamma	842	924	1388	3	804	870	662	3	1.88E-09	3.85E-09	0.666666667	-0.584962501
BP1026810664	UreF-family accessory protein	10570	3599	5632	7	9550	10366	9988	11	0.183401037	0.204562695	1.571428571	0.652076697
BP1026810665	branched-chain amino acid ABC transporter ATP-binding protein	2605	2991	3136	4	3419	3277	3301	4	0.001690815	0.002443199	1	0
BP1026810666	branched-chain amino acid ABC transporter ATP-binding protein	1697	1291	1696	1	1911	1497	1718	2	0.001056993	0.001560821	2	1
BP1026810667	branched-chain amino acid transport system, permease	1208	1244	2073	1	1373	1133	1414	1	0.09E-07	1.15E-06	1	0
BP1026810668	branched-chain amino acid ABC transporter permease	3427	1700	1437	1	2174	2879	2727	1	0.002746753	0.003857772	1	0
BP1026810669	branched-chain amino acid ABC transporter substrate-binding protein	5282	5712	6883	4	6621	7453	5655	5	9.62E-06	1.83E-05	1.2	0.32192

BP1026b_0717	cell division ftsk transmembrane protein	390894	381411	388470	167	475923	474499	429335	199	1.08E-06	2.32E-06	1.191616766	0.252920328
BP1026b_0718	outer-membrane lipoprotein carrier protein	59405	53779	54592	78	62236	62483	56844	85	3.69E-06	7.40E-06	1.08974359	0.12398717
BP1026b_0719	recombination factor protein RarA	87855	53263	58558	50	80755	87629	95344	67	0.01032615	0.01566066	1.34	0.422233001
BP1026b_0720	hypothetical protein	16642	19091	19432	66	9775-05	20478	27633	76	9.77E-05	2.04E-04	1.151515152	0.20353394
BP1026b_0721	seryl-tRNA synthetase	370916	391724	375716	291	348357	348546	324053	261	2.03E-12	9.07E-12	0.896907313	-0.15699946
BP1026b_0722	Ser tRNA	24941	42025	35720	376	28632	25958	24792	290	3.13E-16	2.20E-15	0.771276596	-0.374679762
BP1026b_0723	hypothetical protein	1001737	1768776	1600447	5336	1116327	1065953	1090431	3995	0.733158521	0.751883591	0.74868156	-0.417563163
BP1026b_0725	acetyltransferase	64894	45827	52614	95	50146	48272	46827	84	4.03E-15	2.48E-14	0.884210526	-0.177538186
BP1026b_0726	septum formation inhibitor	86601	90167	92752	110	70195	67022	64535	82	1.63E-18	1.52E-17	0.745454545	-0.423807709
BP1026b_0727	septum site-determining protein MinD	208636	276459	254994	302	232027	223425	20208	267	2.05E-10	7.17E-10	0.88410596	-0.177708808
BP1026b_0728	cell division topological specificity factor MinE	26715	21990	23211	94	27006	27184	25969	103	1.14E-05	2.16E-05	0.95744681	0.131911676
BP1026b_0729	hypothetical protein	1610	1685	1665	3	1378	1901	2941	4	0.024514865	0.030773403	1.333333333	0.415037499
BP1026b_0730	hypothetical protein	2123	420	825	11	855	1241	2015	13	0.072343395	0.084940773	1.181818182	-0.2410081
BP1026b_0731	voltage gated chloride channel family protein	33995	30948	28887	18	25875	26835	23728	15	6.05E-14	3.22E-13	0.833333333	-0.263034406
BP1026b_0732	lipopolysaccharide heptosyltransferase I	43219	38645	39697	39	38836	42450	47924	42	4.03E-08	1.06E-07	0.176923077	0.106915204
BP1026b_0733	hypothetical protein	47966	25020	32194	191	48326	48570	49229	266	0.012276078	0.015970375	1.392670157	0.477853607
BP1026b_0734	metabolite proton symporter family protein	12044	8608	8714	7	13591	15258	16314	11	0.257560079	0.282104622	1.571428571	0.652076697
BP1026b_0735	TonB domain-containing protein	10412	8693	13490	20	10080	43387	8567	19	1.29E-08	3.92E-08	0.893884651	-0.16183466
BP1026b_0736	hypothetical protein	23230	2476	2569	4	1645	1849	1416	2	3.63E-18	3.22E-17	0.95	-0.074000581
BP1026b_0737	integrase	1054	2039	1434	7	1390	1519	1728	2	1.69E-04	2.75E-04	0.8	0
BP1026b_0738	Integrase	5560	5904	6037	25	4986	4652	4441	20	1.48E-10	5.26E-10	0.8	-0.321928095
BP1026b_0739	Ser tRNA	771	665	1129	9	857	641	842	8	9.04E-05	1.52E-04	0.888888889	-0.169925001
BP1026b_0740	coproporphyrinogen III oxidase	70466	61922	64409	53	76367	79083	80402	64	5.35E-04	8.21E-04	1.20754717	0.272079545
BP1026b_0741	deoxyribonucleotide triphosphate pyrophosphatase	59005	30846	37539	67	57599	64519	79139	106	0.764715726	0.780795324	1.582089552	0.661831264
BP1026b_0742	ribonuclease PH	111971	59289	74684	111	110469	112306	118679	155	0.00807502	0.01401437	1.396396396	0.81708539
BP1026b_0743	hypothetical protein	138190	145153	149992	156	190040	185312	176257	199	0.04145233	0.057564102	1.275641027	0.3122402
BP1026b_0744	guanylate kinase	120053	169049	159501	218	156123	155548	151635	225	4.43E-10	1.49E-09	1.032110092	0.045596666
BP1026b_0745	DNA-directed RNA polymerase subunit omega	55407	63395	66233	302	78631	74571	72687	399	0.001349407	0.009171242	1.221854305	0.289072267
BP1026b_0746	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphorylase	381188	514967	471359	192	618974	594642	545952	247	4.85E-05	8.45E-05	1.286458333	0.36404731
BP1026b_0747	Arg tRNA	21835	34578	25784	355	34108	34380	28202	418	5.35E-05	9.27E-05	1.177646789	0.235683918
BP1026b_0748	Arg tRNA	9627	15855	14309	172	16634	16272	13220	199	3.03E-04	4.80E-04	1.156976744	0.210359866
BP1026b_0749	transcription elongation factor GreB	564754	757635	682257	1184	620253	610774	558167	1062	7.37E-14	3.33E-13	0.896849574	-0.156885135
BP1026b_0750	outer membrane protein	6898723	957373	923239	7473	7528479	743324	788287	6686	0.61659742	0.630446459	1.294171717	0.317688777
BP1026b_0751	hypothetical protein	14283	17057	14791	58	13814	14461	12704	51	2.42E-10	8.38E-10	0.879310345	-0.185555653
BP1026b_0752	cold shock transcription regulator protein	14913593	25284887	22233287	102012	14467363	14598640	14109512	70548	7.21E-04	0.001089261	0.691565698	-0.532061782
BP1026b_0753	DNA polymerase/helicase	65085	61065	60792	54	68450	69614	71193	60	5.89E-05	1.01E-04	1.111111111	0.152003093
BP1026b_0754	chorismate mutase	10272	4422	5552	11	7129	8578	8961	13	0.001340152	0.001958636	1.181818182	0.2410081
BP1026b_0755	hypothetical protein	37987	60506	51631	340	49187	43912	35071	290	7.62E-17	5.76E-16	0.852941176	-0.229481846
BP1026b_0756	hypothetical protein	19250	8801	9871	32	18121	16876	18433	45	0.049096443	0.059178882	1.40625	0.495835096
BP1026b_0757	kinase-dependent receptor	43348	44348	44320	17	53707	53325	45434	12	5.53E-04	9.84E-04	1.294171717	0.317688777
BP1026b_0758	lipoprotein	15176	8179	8958	8	15547	15468	16450	12	0.118489996	0.134317399	1.5	0.84962501
BP1026b_0759	hypothetical protein	8628	2476	3684	9	7719	8904	9742	17	0.884947453	0.894370902	1.888888889	0.91753784
BP1026b_0760	hypothetical protein	219665	219693	218136	869	254184	249494	254762	1003	0.001741607	0.002513113	1.15420023	0.206893524
BP1026b_0761	hypothetical protein	1293	658	1265	4	1462	959	1481	5	0.087795128	0.101748137	1.25	0.321928095
BP1026b_0762	hypothetical protein	1055	680	1030	1	1075	1111	849	2	0.011964143	0.020789475	2	0
BP1026b_0763	hypothetical protein	703	183	454	1	638	1005	912	2	0.022313819	0.028213494	1.2	1
BP1026b_0764	car tRNA	701	962	1465	9	7	991	6111	513	0.100023843	0.113354437	1.285714286	0.362570079
BP1026b_0765	fructose-1,6-bisphosphatase	305064	355273	341286	328	353788	354425	320701	337	1.27E-08	3.57E-08	1.027439024	0.039052777
BP1026b_0766	transcriptional activator protein	9602	6805	9660	9	9918	8836	9006	9	0.06E-05	2.01E-05	1	0
BP1026b_0767	5-methyltetrahydropteroylriglutamate/homocysteine S-methyltransferase	12005	9805	9823	4	11502	12955	12333	5	2.37E-04	3.79E-04	1.25	0.321928095
BP1026b_0768	aminopeptidase N	205161	234582	225173	82	246139	244167	228581	88	1.79E-04	2.89E-04	1.073170732	0.101879614
BP1026b_0769	lipoprotein	251947	235496	244835	341	360382	362030	325916	489	0.020780338	0.026301887	1.434017595	0.520662726
BP1026b_0770	hypothetical protein	36840	34070	34270	58	43061	43804	44581	72	5.98E-04	1.39E-03	1.24137913	0.31944006
BP1026b_0771	guanine deaminase	11010	12952	12903	11	20149	22101	23954	6	0.032650773	0.040216955	1.454545455	0.540568381
BP1026b_0772	xanthine/uracil permease family protein	13661	16519	14688	10	14498	15454	12431	10	1.41E-08	3.93E-08	1	0
BP1026b_0773	adenosine deaminase	40210	38606	39722	38	41501	45750	42776	42	3.21E-07	7.50E-07	1.105263158	0.144389909
BP1026b_0774	xanthine dehydrogenase accessory factor	16522	10252	10392	12	12465	11929	13747	12	1.31E-06	2.78E-06	1	0
BP1026b_0775	DsbB family disulfide bond formation protein	13011	9608	10971	21	8432	8319	8899	16	1.29E-15	8.45E-15	0.761904762	-0.392317423
BP1026b_0776	amidase	17051	6993	8131	7	12389	11568	15735	9	0.001815208	0.002610899	1.285714286	0.362570079
BP1026b_0777	guanine amidotransferase	312979	320518	336801	243	316259	323657	324232	238	7.18E-09	2.38E-08	0.896849574	-0.005049935
BP1026b_0778	citrate-symporter	29177	20945	21936	17	28433	27640	31473	19	1.91E-05	3.50E-05	1.117647059	0.160464672
BP1026b_0779	hypothetical protein	29146	9257	13822	9	24399	26201	28604	14	0.102223853	0.1329849	1.555555556	0.637429921
BP1026b_0780	oxygenase	153874	77835	106744	68	169667	182565	189620	109	0.480899709	0.508157182	1.602941176	0.680721484
BP1026b_0781	NAD-dependent formate dehydrogenase subunit delta	51943	32061	35881	153	52987	55273	51677	204	0.002652368	0.007154504	1.333333333	0.401537499
BP1026b_0782	NAD-dependent formate dehydrogenase subunit alpha	251059	201356	212229	74	251771	253334	265785	86	0.001899066	0.002724009	1.162162162	0.20611389
BP1026b_0783	NAD-dependent formate dehydrogenase subunit beta	17772	12197	12117	8	20906	21076	22023	13	0.15849734	0.173146627	1.625	0.704397118
BP1026b_0784	NAD-dependent formate dehydrogenase gamma subunit	7402	7402	4619	109	109	9222	10306	99	0.41107888	0.41107888	0.750041836	0.005209949
BP1026b_0785	regulatory protein	43362	21585	26591	27	47548	54854	60485	49	0.99085554	0.99291619	1.818181815	0.598922342
BP1026b_0786	hypothetical protein	41765	70597	66729	226	41637	42967	44966	163	1.95E-27	4.55E-26	0.721238938	-0.471458088
BP1026b_0787	hypothetical protein	29050	11614	15568	29	23465	27910	34671	44	0.131517513	0.149406184	1.517241379	0.601450624
BP1026b_0788	hypothetical protein	1097	1250	1561	10	1029	1177	1747	10	3.58E-04	5.61E-04	1	0
BP1026b_0789	phosphoglycolate phosphatase	20776	7463	9827	17	14095	16744	17983	22	0.0669761	0.008981766	1.294171767	0.371968777
BP1026b_0790	3-demethylglyoxalase-9-3-methyltransferase	102065	92366	97165	119	85558	87130	76364	102	2.93E-13	1.44E-12	0.857142857	-0.222392421
BP1026b_0791	outer membrane protein A	8766036	13287637	12350959	16889	11432409	11357326	11795736	17079	0.160888443	0.18061405	1.005297549	0.00762257
BP1026b_0792	DNA gyrase subunit A	349616	943628	88421	330	943215	935311	88421	340	0.19235921	0.21218128	0.9421101	0.00849495

BP1026b	10840	prolin-rich exported protein	27700	15802	17755	7	39550	41536	46195	16	0.362311622	0.389502287	2.285714286	1.192645078
BP1026b	10841	ArsR family transcriptional regulator	2707	999	891	2	2164	3216	3314	4	0.118852416	0.135806555	2	1
BP1026b	10842	hypothetical protein	2574	716	634	9	1278	2202	2026	13	0.259264875	0.283723825	1.444444444	0.530514717
BP1026b	10843	long-chain acyl-CoA thioester hydrolase	32530	36787	32992	66	3365	34111	32362	66	0.8661-09	2.3291-08	0.2538-08	0
BP1026b	10844	fumarate hydratase	143819	128537	146007	99	148387	151393	153266	108	1.39E-08	3.86E-08	1.090909091	0.125530882
BP1026b	10845	multidrug resistance protein	37466	23781	24506	20	43574	42287	42948	30	0.04643413	0.056183772	1.5	0.584962501
BP1026b	10846	hypothetical protein	3578	2831	2290	13	3117	3427	3151	14	6.19E-04	9.43E-04	0.107692307	0.106915204
BP1026b	10847	hypothetical protein	16934	18332	17971	35	21503	23025	23283	44	0.002391284	0.003378977	1.257142857	0.330148602
BP1026b	10848	hypothetical protein	282352	325999	311876	391	395978	394869	362864	487	2.65E-05	4.77E-05	1.245524297	0.316753165
BP1026b	10849	CleA protein	26960	26802	29624	57	23904	23477	23247	49	1.97E-12	8.83E-12	0.859649123	-0.21818017
BP1026b	10850	Asn tRNA	4008	5436	4682	61	7084	7936	5912	88	0.03244614	0.069508693	1.45E-07	0.528604381
BP1026b	10851	Asn tRNA	2184	4253	3204	42	3230	3020	2727	39	1.44E-07	3.51E-07	0.928571429	-0.106915204
BP1026b	10852	ferredoxin	122685	171531	162305	469	146873	143105	130594	432	4.58E-15	2.79E-14	0.921108742	-0.11855661
BP1026b	10853	nicotinate phosphoribosyltransferase	131011	185796	168140	134	138962	138988	128920	113	3.41E-20	3.81E-19	0.843283582	-0.245910228
BP1026b	10854	hypothetical protein	130360	99171	106865	169	118333	121098	117373	179	1.54E-08	4.25E-08	1.059171598	0.082936341
BP1026b	10855	hypothetical protein	99352	99402	97776	68	97617	98320	95527	67	3.75E-09	1.13E-08	0.985294118	-0.021373651
BP1026b	10856	2-hydroxyacid dehydrogenase	33476	21639	26920	27	30922	29982	32437	31	1.79E-05	3.30E-05	1.148148148	0.199308088
BP1026b	10857	RnmC domain-containing protein	131367	101401	105214	77	139968	129323	123980	83	1.50E-19	1.45E-07	1.077923078	0.108252801
BP1026b	10858	acetyltransferase	22021	16256	14184	39	20347	21631	26341	51	0.004486294	0.006143882	1.307692308	0.387023123
BP1026b	10859	hypothetical protein	83303	118576	105082	355	91135	87392	75268	293	1.04E-14	6.06E-14	0.825352113	-0.27691836
BP1026b	10860	molybdopterin biosynthesis moeA protein	37331	13985	18826	17	27484	32264	35956	24	0.007410004	0.009877903	1.411764706	0.497499659
BP1026b	10861	molybdopterin-guanine dinucleotide biosynthesis protein MobA	15410	4715	5986	13	11063	14408	28272	27	0.160522503	0.180231754	2.076923077	1.054447784
BP1026b	10862	molybdenum cofactor biosynthesis protein A	421198	302589	360963	324	367462	373555	387585	338	6.69E-09	1.95E-08	1.043209877	0.061029433
BP1026b	10863	ribonuclease E	174494	183388	185173	355	194670	201283	208351	61	1.40E-05	2.61E-05	1.109090909	0.149377624
BP1026b	10864	hypothetical protein	108232	171664	157773	300	141463	136110	136195	283	9.58E-14	4.99E-13	0.945333333	-0.084160448
BP1026b	10865	ribosomal large subunit pseudouridine synthase C	870499	983672	950173	93	105549	105402	85402	93	1.05E-09	0.70237552	0.946236559	-0.079727192
BP1026b	10866	haloacid dehalogenase-like hydrolase	64643	54514	58073	89	67112	68270	65679	101	1.18E-04	1.94E-04	1.134831461	0.182478052
BP1026b	10867	ferredoxin, 2Fe-2S	9549	11879	9242	25	14111	14019	14306	35	0.037189206	0.045569872	1.4	0.485426827
BP1026b	10868	peptidase	229420	320721	308330	285	248185	244515	236366	242	4.82E-11	1.82E-10	0.849112807	-0.235954872
BP1026b	10869	tetrapyrrole methylase family protein	37333	15000	17587	32	29835	40013	46956	53	0.267150434	0.292098153	1.65625	0.727290455
BP1026b	10871	Ma1-like protein	30178	24909	24893	41	30213	29250	30565	46	1.46E-05	2.71E-05	1.12195122	0.166009951
BP1026b	10870	hypothetical protein	70120	88524	72711	124	61042	63667	63491	99	3.83E-16	2.66E-15	0.798387097	-0.324336969
BP1026b	10872	50S ribosomal protein L32	113214	173972	154588	818	130672	126508	108267	677	1.50E-19	1.59E-18	1.427628667	-0.272940099
BP1026b	10873	glycerol-3-phosphate acyltransferase PlxX	153766	165805	172661	148	159377	164145	149777	142	5.65E-13	2.69E-12	0.959459459	-0.059706246
BP1026b	10874	3-oxoacyl-ACP synthase	172680	169241	167658	176	132595	141311	138581	142	8.20E-23	1.23E-21	0.80681882	-0.309684499
BP1026b	10875	acyl-carrier-protein S-malonyltransferase	283757	235856	254668	276	225182	230217	258896	255	1.55E-08	4.28E-08	0.923913043	-0.11417102
BP1026b	10876	3-ketoacyl-ACP reductase	197771	213539	200995	272	197411	201040	193292	262	1.98E-10	6.93E-10	0.963235294	-0.045039894
BP1026b	10877	hypothetical protein	20322	13821	14752	115	17417	17299	20459	130	4.68E-05	8.16E-05	1.130434783	0.176877762
BP1026b	10878	acyl carrier protein	1185239	2063673	1760390	6957	1245618	1210266	1081852	4910	0.45831983	0.48552603	0.705763979	-0.02424296
BP1026b	10879	hypothetical protein	608665	983672	853310	553	130167	98670	531314	390	1.83E-27	0.70237552	0.946236559	-0.079727192
BP1026b	10880	3-oxoacyl-(acyl carrier protein) synthase II	906709	1221020	1146552	880	1030219	994184	950330	800	0.524096084	0.550090125	0.909090909	-0.137503524
BP1026b	10881	hypothetical protein	34516	41333	36181	78	40665	37225	33009	78	1.67E-09	5.08E-09	1	0
BP1026b	10882	RNA polymerase sigma factor RpoF	261913	392718	331523	547	290880	288115	232740	450	1.61E-12	7.27E-12	0.822669140	-0.281615832
BP1026b	10883	sigma E factor negative regulatory protein	176841	198963	203463	302	170705	161004	160488	256	5.01E-19	4.90E-18	0.847682119	-0.238407339
BP1026b	10884	sigma factor algU regulatory protein MucB	431133	289325	299407	322	308016	337150	334077	309	6.13E-10	2.03E-09	0.959627329	-0.05945385
BP1026b	10885	peptidase	694209	496637	562729	388	500870	526928	583166	356	4.67E-14	5.52E-13	0.917523753	-0.213479411
BP1026b	10886	hypothetical protein	245395	1352424	155620	184	233246	236434	276844	142	0.571848244	0.599024068	0.70237552	0.556216349
BP1026b	10887	GTP-binding protein LepA	189761	258657	241654	128	210344	204424	187966	111	1.36E-13	7.01E-13	0.8671875	-0.205584134
BP1026b	10888	signal peptidase I	126543	183344	161728	175	149712	136027	136027	162	3.87E-15	2.39E-14	0.925714286	-0.11361109
BP1026b	10889	ribonuclease III	217761	248321	246893	171	187764	196644	216065	144	4.73E-15	2.88E-14	0.842105263	-0.247927513
BP1026b	10890	GTP-binding protein Era	153064	222879	203510	223	154336	152468	150106	176	3.43E-25	6.44E-24	0.789237668	-0.341468281
BP1026b	10891	DNA repair protein RecO	44904	53951	51187	58	47084	44233	45104	52	4.05E-14	2.21E-13	0.896551724	-0.157541277
BP1026b	10892	pyridoxase 5-phosphate synthase	148274	119121	135636	173	113407	116405	111148	146	2.70E-17	2.15E-16	0.843906306	-0.244803669
BP1026b	10893	4-phosphatase (acyl) transferase	44101	164988	161322	23	164988	161322	44782	66	0.25E-08	0.2580668	1.64606797	0.17226997
BP1026b	10894	beta-hexosaminidase	87166	55309	64343	66	67624	69671	66858	66	7.03E-08	1.80E-07	0	0
BP1026b	10895	sigma-54 interacting response regulator protein	253974	199394	227256	162	276674	292517	312911	210	0.014018888	0.018109778	1.296296296	0.374395515
BP1026b	10896	hypothetical protein	5867	10613	8281	58	7340	7750	7805	54	3.90E-09	1.17E-08	0.931034483	-0.103093493
BP1026b	10897	elongation factor P	332308	528469	461340	789	292957	284507	253609	496	9.65E-26	1.94E-24	0.69665818	-0.29965818
BP1026b	10898	hypothetical protein	37814	26175	27989	25	34158	34237	33467	28	4.03E-16	8.03E-06	1.12	0.14698732
BP1026b	10899	excinuclease ABC subunit C	138407	146183	135069	62	126693	132377	124345	56	8.75E-15	5.14E-14	0.903225806	-0.146841388
BP1026b	10900	glycylglycylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	128511	1414576	1146469	231	87984	87157	77866	142	1.03E-33	4.20E-32	0.47470862	-0.702001323
BP1026b	10901	Gly tRNA	18071	142919	21686	296	21613	20726	16301	257	1.42E-11	5.77E-11	0.868242024	-0.203828816
BP1026b	10902	Gly tRNA	11492	18007	13679	189	16399	13630	13630	200	7.82E-06	1.51E-05	0.958521558	0.081613766
BP1026b	10903	Cys tRNA	7085	10443	8603	117	9133	9542	6477	113	5.53E-08	1.43E-07	0.965811966	-0.050185757
BP1026b	10904	hypothetical protein	37320	44314	41542	80	42533	44606	38888	81	3.21E-09	9.78E-09	1.0125	0.017921908
BP1026b	10905	LysR family transcriptional regulator	19113	11469	13471	16	16776	20892	22955	52	0.202161706	0.022728315	1.375	0.494316119
BP1026b	10906	hypothetical protein	8909	8618	9634	10	13346	11819	10814	13	0.013427862	0.01738213	1.3	0.378511623
BP1026b	10907	acetyltransferase	30819	212696	212732	41	212696	212732	22769	17	1.31E-06	1.31E-06	1.097566066	-0.143101093
BP1026b	10908	hypothetical protein	131577	149490	148167	163	134155	131814	119857	147	1.12E-15	7.35E-15	0.901840491	-0.149055809
BP1026b	10909	hypothetical protein	129322	171283	160409	343	115569	116713	110725	255	1.61E-25	3.17E-24	0.743440233	-0.427711329
BP1026b	10910	SCO1/ScmC family protein	46468	23852	29375	50	25964	31280	30459	44	1.21E-11	4.93E-11	0.88	-0.184424571
BP1026b	10911	trehalose-phosphatase	46682	20463	26877	41	33060	33152	35959	45	1.			

BP1026b	I0961	cyclic nucleotide-binding domain-containing protein	464524	525113	524843	731	625964	595475	548594	855	6.00E-07	1.34E-06	1.169630643	0.226053014
BP1026b	I0962	hypothetical protein	170533	163683	167384	126	234343	237069	230613	177	0.37775303	0.404763082	1.404761905	0.490325627
BP1026b	I0963	2-nitropropane dioxygenase	984482	831266	902005	743	803676	815339	766951	652	0.66606338	0.658500295	0.877523553	-0.188490264
BP1026b	I0964	hypothetical protein	707438	619624	633914	635	561182	559293	533408	52	1.34E-17	1.10E-16	0.91025641	-0.25333046
BP1026b	I0965	U32 family peptidase	716095	883383	858027	935	807570	767605	711510	870	0.60222035	0.626005356	0.930481283	-0.103590964
BP1026b	I0966	hypothetical protein	262532	383023	353075	693	283411	271562	245063	555	2.76E-13	1.36E-12	0.800865801	-0.230367581
BP1026b	I0967	hypothetical protein	209435	235941	219699	495	224102	221411	222122	497	2.63E-06	5.39E-06	1.004040404	0.008417327
BP1026b	I0968	radical SAM domain-containing protein	123663	65599	75238	122	123989	130545	138934	182	0.036196209	0.043965225	1.491803279	0.577057303
BP1026b	I0969	hypothetical protein	142013	169059	169315	7501	228488	201221	170138	898	1.13E-04	1.88E-04	1.195739018	0.257902537
BP1026b	I0970	anaerobic ribonucleoside triphosphate reductase	483875	607153	601832	319	368651	373110	370976	210	8.07E-31	8.58E-29	0.65830721	-0.603167096
BP1026b	I0971	heme-copper membrane protein	96635	52506	44838	58	119447	122586	123101	99	0.50748634	0.586103564	1.545454555	0.731755253
BP1026b	I0972	lipoprotein	6103	2313	3090	3	6400	6296	7229	5	0.715814243	0.735541407	1.666666667	0.36965594
BP1026b	I0973	phenylacetic acid degradation protein paaD	1765	1886	2370	5	3942	3621	4346	11	0.076986718	0.089954263	2.2	1.137053524
BP1026b	I0974	nitric oxide reductase subunit B	135035	168968	155710	66	396550	375276	362484	165	2.73E-06	5.57E-06	2.5	1.321928095
BP1026b	I0975	alkane-1 monooxygenase	15292	15349	16838	13	15955	14848	15516	13	1.09E-07	2.71E-07	1	0
BP1026b	I0976	deoxyribodipyrimidine photolyase	21481	14280	15145	11	19757	20759	20896	14	4.39E-04	6.80E-04	1.272727273	0.347923303
BP1026b	I0977	adenylylsulfate kinase	82869	93580	90375	143	89593	84230	76674	134	5.73E-10	1.90E-09	0.937062917	-0.093782146
BP1026b	I0978	ATP-dependent transcription regulator LuxR	10114	10663	9931	14	10140	7804	9463	32	5.50E-09	1.43E-08	0.928571429	-0.18013504
BP1026b	I0980	alpha/beta fold family hydrolase	27327	26857	24922	26	24403	23634	23247	23	2.26E-10	7.84E-10	0.884615385	-0.176877762
BP1026b	I0979	4'-phosphopantetheinyl transferase	6999	3972	3892	6	5057	5762	8706	8	0.01162541	0.015164841	1.333333333	0.415037499
BP1026b	I0981	hypothetical protein	3555	1749	1185	4	3221	3839	3708	7	0.869542659	0.880080016	1.75	0.807354922
BP1026b	I0982	histidine ammonia-lyase	48058	28742	35212	24	54139	58842	62583	38	0.475177235	0.502449392	1.583333333	0.662965013
BP1026b	I0983	histidine utilization repressor	20940	17845	19295	27	25186	27802	29470	39	0.034723091	0.04265649	1.444444444	0.530514717
BP1026b	I0984	urocanate hydratase	135761	138393	144712	82	170035	171103	172511	101	1.79E-04	2.91E-04	1.231707317	0.30659478
BP1026b	I0985	hypothetical protein	6996	8261	3852	7	6660	6496	6985	10	0.056244448	0.067312805	1.428571429	0.34573173
BP1026b	I0986	amidoxycarboxonase	39609	1846	23446	27	34853	39416	45266	62	0.02752728	0.031131027	0.898305065	-0.540568381
BP1026b	I0987	N-formimino-L-glutamate deiminase	51930	29479	31286	27	41538	43665	53356	33	1.25E-04	2.06E-04	1.222222222	0.289506617
BP1026b	I0988	N-formylglutamate amidohydrolase	27104	20509	24011	29	25890	25834	27078	32	1.07E-05	2.03E-05	1.04248276	0.142019005
BP1026b	I0989	hypothetical protein	1731	2854	2398	16	2217	2102	2036	15	2.65E-08	7.12E-08	0.9375	-0.093109404
BP1026b	I0990	hypothetical protein	2075	392	572	10	1164	2264	3180	23	9.02E-04	0.001346805	2.3	1.201633861
BP1026b	I0991	glutamine amidotransferase	3189	2383	2581	3	4093	3036	3681	4	0.07604030	0.08893393	1.333333333	0.415037499
BP1026b	I0992	glutamine synthetase	22896	29099	25569	19	24262	24958	20946	17	2.42E-10	8.38E-10	0.894736842	-0.160466472
BP1026b	I0993	aminotransferase	15418	36635	37478	14	44073	39838	39203	28	1.63E-06	3.41E-06	0.928571429	-0.16498732
BP1026b	I0994	hypothetical protein	125234	191403	167988	351	175264	169814	158388	365	3.40E-09	1.03E-08	1.03988604	0.056425433
BP1026b	I0995	hypothetical protein	28711	43055	38481	144	54428	56698	58705	222	0.291293129	0.316836284	1.541666667	0.427490865
BP1026b	I0996	Val tRNA	3136	5306	3668	53	3244	3175	2190	38	8.91E-17	6.68E-16	0.716981312	-0.479992941
BP1026b	I0998	LysR family regulatory protein	8247	10515	9583	10	8856	9157	8067	9	4.18E-09	1.25E-08	0.9	-0.152003093
BP1026b	I0997	acyl-CoA dehydrogenase domain-containing protein	7638	4218	4046	2	6610	8860	7709	4	0.065716554	0.077610953	2	1
BP1026b	I0999	CAB/BAIF family CoA transferase	6813	3831	4688	3	6740	6523	6485	4	0.007206203	0.00962449	1.333333333	0.415037499
BP1026b	I1000	major facilitator family transporter	2916	2016	2548	1	3448	3468	3184	2	0.07133402	0.07133402	0.07133402	1
BP1026b	I1001	hypothetical protein	108550	185761	162077	551	115959	107255	98803	388	7.68E-28	1.85E-26	0.704174229	-0.50595666
BP1026b	I1002	N-acetylglutamate synthase	269042	168522	198763	154	236549	239465	242721	173	0.001027924	0.001521123	1.123376621	0.167841687
BP1026b	I1003	ATP-dependent helicase HrpA	161763	144325	155774	37	180795	180512	170787	42	8.65E-06	1.66E-05	1.135135135	0.182864057
BP1026b	I1004	hypothetical protein	130754	161893	157718	151	99495	92677	92698	95	4.23E-33	1.68E-31	0.629139073	0.668549131
BP1026b	I1005	hypothetical protein	133243	163577	146977	149	135061	139177	128487	135	1.45E-15	9.46E-15	0.906042068	-0.142352923
BP1026b	I1006	hypothetical protein	15743	15387	17089	18	12740	13304	12828	14	1.18E-13	6.09E-13	0.777777778	-0.362570079
BP1026b	I1007	hydroxyethyl-lysine binding domain-containing protein	124006	148977	148977	177	130439	131301	125459	177	0.0315016	0.0315016	0.0315016	0.154722349
BP1026b	I1008	rhodanese-like protein	34905	26937	31081	66	35246	37496	36518	78	2.56E-05	4.62E-05	1.181818182	0.2410081
BP1026b	I1009	glutamine synthetase, type I	569095	743359	688724	471	865075	832961	769829	580	0.063817011	0.075595642	1.231422255	0.30032584
BP1026b	I1010	nitrogen regulation protein	36958	39213	40245	33	54471	49352	47723	44	0.001749866	0.002523869	1.333333333	0.415037499
BP1026b	I1011	nitrogen regulation protein NR(I)	51703	38803	38727	28	58598	61660	60716	39	0.075394053	0.088224985	1.392857143	0.478047297
BP1026b	I1012	exodeoxyribonuclease III	35883	39977	44570	51	34112	32119	28614	40	2.95E-17	2.34E-16	0.784313725	-0.350497247
BP1026b	I1013	DNA-binding response regulator NarL	50625	57657	59078	79	68236	66188	71894	97	0.03055156	0.004268876	1.227484011	0.296132094
BP1026b	I1014	nitrate/nitrite sensor protein	135184	161893	160997	55	164023	178023	169229	88	0.38915641	0.416883269	0.91025641	0.678071950
BP1026b	I1015	respiratory nitrite reductase subunit gamma	11797	9532	9133	14	16937	17635	16928	25	0.950986833	0.955103679	1.78741286	0.836501268
BP1026b	I1016	nitrate reductase subunit delta	4807	9364	4522	6	5653	6532	5411	8	0.017479582	0.02233621	1.333333333	0.415037499
BP1026b	I1017	nitrate reductase subunit beta	15889	18668	17394	11	27303	23916	23304	15	0.043513746	0.052782747	1.363636364	0.447458977
BP1026b	I1018	nitrate reductase subunit alpha	55191	62630	62273	16	241124	230114	215919	61	5.04E-28	1.23E-26	3.8125	1.903737338
BP1026b	I1019	nitrate/nitrite transporter NarK	8243	9563	9262	6	23462	22589	22101	16	0.001100178	0.001621152	2.666666667	1.415037499
BP1026b	I1020	nitrate/nitrite transporter	11656	10431	12163	8	45312	42186	43375	34	7.89E-15	1.68E-14	4.25	2.087462841
BP1026b	I1021	Met tRNA	730	808	801	6	1010	1063	1027	8	0.4578465	0.48310433	1.333333333	0.415037499
BP1026b	I1022	Met tRNA	175	403	272	4	252	404	290	4	0.083359338	0.096823445	0.906823445	0
BP1026b	I1023	DNA polymerase IV	40696	30770	31949	28	32777	36516	39420	30	9.10E-08	2.29E-07	1.071428571	0.099535674
BP1026b	I1024	oligonucleotidase A	384306	395676	394603	186	586019	574390	534215	268	0.005474281	0.007427094	1.440860215	0.526930379
BP1026b	I1025	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase	72894	55003	61416	73	74481	79329	79165	90	0.001552276	0.002252886	1.232876712	0.302028573
BP1026b	I1026	LuxR family DNA-binding response regulator	361828	452369	409901	638	425753	412636	374701	632	4.47E-11	1.70E-10	0.990595611	-0.01361866
BP1026b	I1027	sensory box histidine kinase	213846	204003	204003	78	188508	191855	175148	73	0.157E-14	0.22E-13	1.784312317	0.135655011
BP1026b	I1028	pyruvate dehydrogenase subunit E1	77319	100350	960828	338	1143068	1134474	1116185	419	0.084351077	0.0979197879	1.23964497	0.309926997
BP1026b	I1029	pyruvate dehydrogenase acetyltransferase	205062	306082	276638	159	307384	299196	280314	179	2.49E-05	4.51E-05	1.125786164	0.170932822
BP1026b	I1030	pyruvate dehydrogenase, E3 component, dihydrolipoamide dehydrogenase	330224	300965	326631	180	461064	449897	444375	255	8.15E-04	0.001223252	1.416666667	0.502500341
BP1026b	I1031	phasin-like protein	1259305	1857058	1735874	2837	1295883	1259510	1165414	2175	0.815823879	0.829866967	0.766654917	-0.383350575
BP1026b	I1032	predicted RNA	5751	9743	10319	661	5393	5082	6389	432	5.17E-20	5.71E-19	0.635555219	0.361618959
BP1026b	I1033	hypothetical protein												

BP1026b.11083	hypothetical protein	2836	1756	2269	6	2365	1892	2740	7	8.35E-06	1.60E-05	1.166666667	0.222392421
BP1026b.11084	hypothetical protein	10524	12215	12021	8	11526	11020	11686	8	1.07E-07	2.65E-07	1	0
BP1026b.11085	hypothetical protein	10050	14778	12630	27	10356	9720	9951	22	8.78E-14	4.60E-13	0.814814815	-0.295455884
BP1026b.11086	hypothetical protein	4600	4015	5039	8	5332	5806	5804	6	6.23E-04	2.47E-04	0.169925001	0
BP1026b.11087	hypothetical protein	4013	2850	4145	10	4270	4823	4052	13	0.005296945	0.007195853	1.13	0.378511623
BP1026b.11088	hypothetical protein	3363	4911	4541	19	3719	3365	3304	15	1.04E-10	3.78E-10	0.789473684	-0.341036918
BP1026b.11089	putative repressor protein	113818	204618	184382	271	129657	130807	131258	211	8.08E-25	1.47E-23	0.778597786	-0.041049853
BP1026b.11090	hypothetical protein	6475	8526	7688	15	8000	8509	6814	15	1.48E-06	3.12E-06	1	0
BP1026b.11091	hypothetical protein	4148	3980	4703	12	5902	5035	5654	15	0.012281635	0.015974286	1.25	0.321928095
BP1026b.11092	hypothetical protein	2056	3390	2714	15	2556	2291	2016	12	1.17E-10	4.25E-10	0.8	-0.321928095
BP1026b.11093	hypothetical protein	8760	10705	10290	21	10014	9423	8899	19	2.70E-08	2.24E-08	0.904761905	-0.144389909
BP1026b.11094	virulence-associated protein E	51906	68862	64651	24	69230	65203	61711	26	3.37E-06	6.79E-06	1.083333333	0.154727217
BP1026b.11095	hypothetical protein	9061	11918	11581	18	12419	11649	10055	19	2.61E-06	5.34E-06	0.055555556	0.078002512
BP1026b.11096	hypothetical protein	4701	3805	4774	23	5585	6435	5051	30	0.010018156	0.013183951	1.304347826	0.38332864
BP1026b.11097	hypothetical protein	12199	20161	17343	29	17539	15800	15308	28	1.26E-07	3.09E-07	0.965517241	-0.050626073
BP1026b.11098	phage terminase large subunit (GpA)	46415	54695	52210	25	56212	54875	52009	27	7.23E-08	1.84E-07	1.08	0.11031312
BP1026b.11099	hypothetical protein	5060	4229	5307	23	6901	6905	7712	34	0.08667665	0.00470491	1.47826087	-0.593900885
BP1026b.11100	phage portal protein, lambda family	16419	6015	3764	11	17629	18731	16888	13	5.32E-08	4.14E-08	1.014027584	0.153495856
BP1026b.11101	peptidase S14, C1p	28505	22621	27189	23	31605	35576	35772	31	0.001844897	0.002605058	1.347826087	0.30634354
BP1026b.11102	hypothetical protein	8973	2366	3288	14	6506	9773	11681	27	0.66972094	0.688969854	1.928571429	0.94753258
BP1026b.11103	hypothetical protein	42824	54157	53385	48	58572	56033	53504	54	3.43E-06	6.90E-06	1.125	0.169925001
BP1026b.11104	hypothetical protein	6760	4144	3989	17	6478	6036	7038	22	0.011362336	0.014840216	1.294117647	0.371968777
BP1026b.11105	hypothetical protein	9479	7181	8488	15	11338	10597	12304	21	0.025299752	0.031682857	1.4	0.485426827
BP1026b.11106	hypothetical protein	13098	19374	16647	31	17470	16880	15577	32	8.39E-07	1.84E-06	1.032258065	0.04580369
BP1026b.11107	baseplate assembly protein V	17551	15388	16200	24	22133	23171	26643	35	0.065971638	0.07782839	1.458333333	-0.544320516
BP1026b.11108	hypothetical protein	3916	4551	5351	24	4654	4771	5577	24	1.45E-04	3.71E-04	1.014027584	0.153495856
BP1026b.11109	GPW/gp25 family protein	5701	4520	5405	15	6188	5592	6419	17	6.45E-04	9.80E-04	1.133333333	0.180572246
BP1026b.11110	hypothetical protein	14671	15132	15326	16	16935	15414	18230	18	6.54E-05	1.12E-04	1.125	0.169925001
BP1026b.11111	phage tail protein I	12835	8683	10483	18	14490	14381	16007	25	0.048803125	0.058845577	1.388888889	0.47391118
BP1026b.11112	gp26	43439	66682	58091	38	56453	53861	52835	37	6.13E-11	2.29E-10	0.97368421	-0.038474148
BP1026b.11113	hypothetical protein	14635	17704	18902	37	17541	18085	17319	38	1.29E-06	2.75E-06	1.027027027	0.038474148
BP1026b.11114	phage tail sheath protein	29993	34171	33007	27	35908	36436	38428	31	5.63E-06	1.10E-05	1.148148148	0.199380808
BP1026b.11115	phage major tail tube protein	26553	40917	37364	69	39594	35561	33488	58	1.49E-08	3.14E-08	1.014027584	0.153495856
BP1026b.11116	hypothetical protein	4551	6307	5838	18	6157	5812	6266	20	7.82E-05	1.32E-04	1.111111111	0.152003093
BP1026b.11117	hypothetical protein	3189	5763	4836	39	4322	4747	4988	40	2.26E-05	4.10E-05	1.025641026	0.036525876
BP1026b.11118	tail tape measure protein	32573	43752	40862	16	43729	44314	43572	18	1.24E-06	2.64E-06	1.125	0.169925001
BP1026b.11119	phage P2 GpU family protein	6686	5217	5626	6	8183	7716	9378	9	0.07036125	0.082737539	1.15	0.584962501
BP1026b.11120	phage Tail Protein X	1921	1790	1539	8	1824	1694	1772	8	2.94E-05	5.26E-05	1	0
BP1026b.11121	phage tail formation protein	12621	12085	12812	11	14026	13155	14327	13	4.09E-05	1.18E-05	1.181818182	0.24100681
BP1026b.11122	hypothetical protein	3624	3281	3281	6	3667	6	6282	58	0.273322974	0.292823454	0.292823454	0.054946201
BP1026b.11123	bacteriophage lysis protein	5846	6877	7416	12	5987	5987	6250	11	1.63E-08	4.51E-08	0.916666667	-0.125530882
BP1026b.11124	Site-specific DNA methylase	34227	57877	51200	60	34208	34647	32217	42	4.84E-25	8.92E-24	0.7	-0.514573173
BP1026b.11125	hypothetical protein	265395	441971	396260	494	196365	188960	190587	258	1.33E-61	2.04E-59	0.522267206	-0.937139976
BP1026b.11126	hypothetical protein	193178	245966	243315	438	120724	122999	114511	230	3.98E-68	9.58E-66	0.525114155	-0.929297009
BP1026b.11127	hypothetical protein	104181	113359	117693	235	69479	69249	63155	141	2.87E-33	1.15E-31	0.6	-0.736965594
BP1026b.11128	hypothetical protein	7821	30408	34299	67	24343	26865	26562	51	5.22E-17	4.04E-16	0.76119405	-0.39636348
BP1026b.11129	YAK motif-containing protein	3283	69413	63498	162	51080	49820	45828	38	3.85E-28	1.07E-27	0.716499371	-0.51856626
BP1026b.11130	hypothetical protein	10282	17279	15425	50	14681	13800	12206	48	1.80E-08	4.94E-08	0.96	-0.58893689
BP1026b.11131	hypothetical protein	12606	22882	20919	45	19581	19225	16488	44	6.68E-08	1.71E-07	0.977777778	-0.032421478
BP1026b.11132	gp33	15830	27160	22545	30	31506	30286	28238	41	0.012149764	0.015815902	1.366666667	0.450661409
BP1026b.11133	hypothetical protein	96829	173681	148896	227	67018	67995	69013	110	1.08E-57	1.47E-55	0.484581498	-1.045188774
BP1026b.11134	hypothetical protein	2301	3664	3533	6	3031	2468	3092	6	2.07E-08	5.64E-08	1	0
BP1026b.11135	hypothetical protein	4182	6557	5638	16	3720	3918	3573	11	3.04E-16	2.14E-15	0.6875	-0.540568381
BP1026b.11137	hypothetical protein	11676	31673	27517	62	23711	23541	24976	58	5.32E-09	2.37E-08	0.935483748	-0.096215315
BP1026b.11138	hypothetical protein	4763	5647	5230	9	5398	4982	5497	19	1.03E-05	1.96E-05	1	0
BP1026b.11139	inositol-1-monophosphatase	87035	138777	131068	149	81823	82167	83141	103	3.49E-24	6.01E-23	0.691275168	-0.532667993
BP1026b.11140	RNA methyltransferase	46246	45325	41089	48	49399	51936	61829	59	2.58E-04	4.11E-04	1.229166667	0.297680549
BP1026b.11141	serine O-acetyltransferase	27106	23500	23722	31	24339	23866	24119	30	2.41E-08	6.51E-08	0.967741935	-0.043075175
BP1026b.11142	UDP-2,3-diacylglycerol kinase	125804	155586	146147	177	173303	169211	155640	207	8.89E-06	1.70E-05	1.169491525	0.225881407
BP1026b.11143	peptidyl-prolyl cis-trans isomerase II	495964	799564	755042	1389	693468	683131	712824	1415	0.799411622	0.795411274	1.018718503	-0.607255454
BP1026b.11144	peptidyl-prolyl cis-trans isomerase A	34357	498319	46320	757	35096	32849	32849	68	0.32E-19	1.73E-18	0.723573187	-0.71856626
BP1026b.11145	hypothetical protein	45085	22396	28579	48	42520	50816	55469	50	0.7455071	0.022309371	1.416666667	0.502500241
BP1026b.11146	cysteinyl-tRNA synthetase	385407	441251	419041	297	411461	413917	375196	286	6.51E-12	2.75E-11	0.962962963	-0.55447784
BP1026b.11147	base excision DNA repair protein	137950	199771	175404	181	169448	161565	147896	170	3.87E-14	2.11E-13	0.939226519	-0.090454951
BP1026b.11148	acetyl-CoA carboxylase carboxyltransferase subunit alpha	277238	220482	220563	246	275550	300637	275470	291	8.08E-04	0.001213404	1.182926829	0.242360838
BP1026b.11149	cell cycle protein mes1	50032	18468	25004	21	35252	40182	49557	28	0.002316683	0.003280223	1.033333333	0.50137499
BP1026b.11150	aspartate kinase	188209	275688	257135	197	239508	234553	214533	188	1.73E-07	4.17E-07	0.95413721	-0.067462801
BP1026b.11151	Ser tRNA	27056	361540	361540	378	40246	33081	34076	37	3.31E-07	1.06E-07	0.666137566	-0.14378608
BP1026b.11152	hypothetical protein	46622	39620	42089	40	40198	39450	37782	37	4.72E-13	2.27E-12	0.925	-0.12474729
BP1026b.11153	outer membrane autotransporter	43179	35559	36313	20	37950	35065	33898	19	1.71E-11	6.89E-11	0.95	-0.074000581
BP1026b.11154	hypothetical protein	13684	11247	10428	9	12038	12243	10872	9	1.89E-07	4.53E-07	1	0
BP1026b.11155	AcRb/AcrD/AcrF family protein	123097	104388	108663	35	106223	109953	105638	34	5.11E-11	1.93E-10	0.971428571	-0.041820176
BP1026b.11156	multidrug efflux RND membrane fusion protein MexE	40174	32831	33053	28	30571	33269	32982	25	4.51E-11	1.71E-10	0.892857143	-0.163498732
BP1026b.11157	sulfate adenylyltransferase	79732	65635	69146	48	56492	61135	70134	42	3.05E-12	1.33E-11	0.875	-0.192645078
BP1026b.11158	peptide synthetase-domain-containing protein	52532	38877	44305	24	45984	43378	41378	24	8.01E-12	2.38E-10	1	0
BP1026b.11159	MF3 permease	52829	31952	31952	24	30768	30854	32984	24	4.30E-08	1.13E-07	1.043478261	0.061400545
BP1026b.11160	hypothetical protein	26365	12853	16386	13	19518	23673	23984	17	0			

BP1026b.11211	acyl-CoA-binding protein	111558	161353	141467	511	136084	129717	115417	470	1.90E-14	1.08E-13	0.919765166	-0.120662534
BP1026b.11212	glycoproteinase family protein	4034	869	1383	2	3039	3186	3636	4	0.706831894	0.726788409	2	1
BP1026b.11213	ribosomal-protein-alanine acetyltransferase	43301	59093	55642	105	40953	37818	35542	76	5.57E-26	1.14E-24	0.723809524	-0.466318004
BP1026b.11214	phage SPO1 DNA polymerase domain-containing protein	165407	160018	163047	214	216449	220187	211837	281	0.076419254	0.0092324	1.31308474	0.302659334
BP1026b.11215	hypothetical protein	30026	20367	24489	25	35548	36645	37018	37	0.023195904	0.029188257	1.148	0.565597176
BP1026b.11215	phosphomethylpyrimidine kinase	25021	10154	13254	19	20292	22702	26756	28	0.047679178	0.057590122	1.473684211	0.559427409
BP1026b.11216	lysophospholipid transporter	119697	143718	131553	102	120185	116347	98153	86	6.63E-17	5.06E-16	0.843137255	-0.26160587
BP1026b.11217	alanine racemase	197406	177822	176888	171	158531	168336	178038	157	8.89E-15	5.22E-14	0.918126655	-0.123231766
BP1026b.11218	DNA repair protein RadA	172097	162049	160948	179	156205	158833	164718	116	1.82E-12	8.17E-12	0.974789916	-0.36836768
BP1026b.11219	hypothetical protein	26447	16981	19640	101	27774	30479	28120	139	0.013574959	0.017568914	1.376237624	0.46072959
BP1026b.11220	ABC transporter ATP-binding protein	126401	136716	133482	68	226536	233087	117978	60	1.35E-14	7.75E-14	0.897088824	-0.156725504
BP1026b.11220	glutathione peroxidase	56196	92314	84005	162	61738	58024	53820	120	3.55E-22	5.05E-21	0.740740741	-0.432599407
BP1026b.11222	cardiolipin synthetase	74027	59227	57906	44	67299	71721	66594	47	9.01E-06	1.72E-05	1.068181818	0.095157233
BP1026b.11223	hypothetical protein	1979	731	868	4	1936	1892	2529	8	0.297525406	0.323032509	2	1
BP1026b.11224	N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase	63504	40893	51586	56	57910	58938	60152	63	2.61E-05	4.71E-05	1.125	0.169925001
BP1026b.11225	succinyl-diaminopimelate desuccinylase	40034	29564	31212	29	35412	35552	39928	32	9.55E-07	2.08E-06	1.103448276	0.142019005
BP1026b.11226	AtsC family transcription regulator	103557	90318	98826	260	100430	108392	12342	294	2.16E-06	4.27E-06	1.170369231	0.177304532
BP1026b.11227	2,3,4,5-tetrahydrodipyrroline-2,6-carboxylate N-succinyltransferase	251301	193384	203975	261	236600	244829	241093	390	5.94E-29	9.07E-04	1.111111111	0.152003093
BP1026b.11229	N-succinyl-L-L-diaminopimelate aminotransferase/alternative	46512	40015	39836	34	40352	43575	46294	35	4.06E-09	1.22E-08	1.02941765	0.041820176
BP1026b.11228	hypothetical protein	40059	25152	25656	31	37621	40839	40096	41	9.73E-04	0.001443544	1.322580645	0.403355694
BP1026b.11230	chromosome segregation protein SMC	613619	517491	542126	158	604962	627823	625804	176	7.19E-08	1.83E-07	1.113924051	0.15565087
BP1026b.11231	hypothetical protein	290250	250725	258849	209	326981	322543	309431	251	8.52E-05	1.43E-04	1.200956938	0.264184422
BP1026b.11232	NAD-dependent DNA ligase	191472	176398	168918	86	200212	199271	204722	97	2.66E-05	4.80E-05	1.127906977	0.173648087
BP1026b.11233	peptide deformylase	138530	114469	111852	227	126470	140418	138904	253	1.18E-07	2.92E-07	1.114537445	0.156448057
BP1026b.11234	pseudouridine synthase family protein	73191	59242	58229	36	84263	84595	87250	47	0.013292584	0.01724645	1.305555556	0.38466385
BP1026b.11235	PII undryltransferase	221231	195416	208085	218	840915	224606	223849	124	8.09E-05	2.02E-04	1.059811125	0.169025001
BP1026b.11236	methionine aminopeptidase	170824	253798	232184	257	170955	165017	146617	179	1.98E-29	5.53E-28	0.73540856	-0.44382125
predicted RNA	-	28381	38311	34348	590	39943	43753	44066	725	1.15E-04	1.91E-04	1.228813559	0.297266041
predicted RNA	-	6468	3974	4241	407	6618	7758	7695	613	0.138033345	0.130417884	1.506142506	0.590858279
predicted RNA	-	116160	145169	159345	655	160296	150538	153143	722	7.23E-08	1.84E-07	1.102290076	0.14050393
predicted RNA	-	281189	365686	335709	820	420741	412871	381511	1015	1.19E-05	2.24E-05	1.237804878	0.307783913
BP1026b.11237	elongation factor Ts	164007	767357	786423	820	805154	812979	855900	936	0.1771309	0.134627404	1.141461453	0.19088462
BP1026b.11238	indole kinase	104517	102102	101858	144	106338	116682	124593	131	4.29E-08	1.02E-06	1.059811125	0.169025001
BP1026b.11239	ribosome recycling factor	341452	399433	373032	661	337236	343199	332084	601	8.12E-12	3.39E-11	0.909224822	-0.137285281
BP1026b.11240	undecaprenyl diphosphate synthase	247614	211352	219950	316	297240	286181	260363	393	0.006871203	0.009020739	1.243670886	0.314604754
BP1026b.11241	phosphatidate cytidyltransferase	24779	18074	20240	25	24104	25702	28641	31	0.00119008	0.001645801	1.24	0.10340121
BP1026b.11242	1-deoxy-D-xylulose 5-phosphate reductoisomerase	134531	148971	138747	117	118276	110643	106314	93	1.38E-20	1.62E-19	0.794871795	0.321205908
BP1026b.11243	membrane-associated zinc metalloprotein	147808	87456	109096	82	135902	143636	150019	102	6.85E-05	1.17E-04	1.243902493	0.148473319
BP1026b.11244	OMP85 family outer membrane protein	139690	1598323	1549459	656	1488770	1490270	1409278	634	0.10522293	0.12102675	0.966465415	-0.409212974
BP1026b.11245	ompH/AlpC family outer membrane protein	475851	623536	606086	1067	625408	622148	566485	113	4.29E-08	1.02E-06	1.163636364	-0.18640376
BP1026b.11246	UDP-3-O-(3-hydroxymyristoyl)-glucosamine N-acyltransferase	369121	326889	331018	315	370505	383250	390624	351	2.18E-07	5.17E-07	1.114285714	0.156119202
BP1026b.11247	(3R)-hydroxymyristoyl-ACP dehydratase	87367	84096	79786	178	63180	70121	66062	141	9.59E-16	6.36E-15	0.792134831	-0.30382079
BP1026b.11248	UDP-N-acetylglucosamine acyltransferase	238222	264495	266481	324	213727	216465	205626	268	6.53E-14	3.47E-13	0.927160494	-0.273760812
BP1026b.11250	lipid-A-disaccharide synthase	155739	133132	139187	122	146023	150911	153121	128	1.33E-09	4.24E-09	1.049180328	0.069262662
BP1026b.11251	ribonuclease HII	99254	95988	98578	151	92071	91407	85314	138	5.76E-11	2.16E-10	0.913907285	-0.129880283
BP1026b.11259	RNA methyltransferase	102939	64839	82985	105	83071	86494	89808	109	3.21E-07	7.51E-07	0.103809528	0.359338807
BP1026b.11252	hypothetical protein	243467	327013	307852	358	297618	287676	259490	142	1.76E-08	4.29E-08	0.95537614	-0.086936162
BP1026b.11253	serine protease	27820	25378	25993	16	40061	40376	42679	21	0.00177556	0.002533889	1.3125	0.392317423
BP1026b.11254	primitive phytochelatin synthase	12117	8315	9498	13	12595	13719	15273	18	0.041935762	0.050106821	1.384615385	0.469485283
BP1026b.11255	phosphoenolpyruvate synthase	866537	980516	968586	391	1054178	1066092	1062058	441	0.149577222	0.168656159	1.127877238	0.173610048
BP1026b.11256	modulation efficiency protein D	10410	10219	9358	22	11056	10743	8824	23	1.02E-06	2.21E-06	1.045454545	0.064130337
BP1026b.11257	SPFH domain protein/band 7 family protein	275003	358877	332170	339	245991	237055	220934	247	8.87E-17	6.65E-16	0.788613569	-0.446774232
BP1026b.11258	SarA-binding protein	99520	148391	137641	287	108953	101570	93184	226	6.36E-19	6.18E-18	0.726456449	-0.454727964
BP1026b.11259	occlusal-dehydratase superfamily	60072	82831	82831	204	60935	57806	53532	127	1.15E-27	2.81E-27	0.686271606	-0.543142326
BP1026b.11260	TGS domain-containing protein	64325	39042	44986	152	61006	64906	71222	202	0.032496372	0.040062443	1.328947321	0.10283969
BP1026b.11261	integral membrane protein	19469	12759	14493	16	18751	19977	20389	20	0.002166062	0.003080884	1.25	0.321928095
BP1026b.11262	hypothetical protein	12987	13004	13907	19	10490	11492	11187	16	1.28E-12	5.86E-12	0.842105263	-0.247927513
BP1026b.11263	hypothetical protein	2438	664	1010	1	1211	1448	2570	1	0.051391589	0.061752718	1	0
BP1026b.11264	hypothetical protein	13065	14248	14472	18	12331	13898	13631	17	3.18E-08	8.46E-08	0.944444444	-0.084261261
BP1026b.11265	inosine 5-monophosphate dehydrogenase	400720	400439	413973	277	418153	420340	419370	286	5.12E-10	1.71E-09	1.032490975	-0.064129171
BP1026b.11266	hypothetical protein	125047	107651	107651	165	128456	128456	128456	142	2.53E-06	3.54E-06	0.945363636	-0.18640376
BP1026b.11267	GMP synthase	252445	285553	284202	169	291140	286666	266731	173	6.90E-07	1.53E-06	0.102668369	0.033748791
BP1026b.11268	Integrase	12661	21758	18925	26	15633	15822	14822	23	1.55E-11	1.50E-10	0.884613585	-0.176877762
BP1026b.11269	hypothetical protein	190908	302013	264233	215	299445	280399	244762	233	2.24E-05	4.08E-05	1.08372093	0.15993295
BP1026b.11270	hypothetical protein	89192	150607	127912	140	123471	119829	100763	131	1.10E-12	5.08E-12	0.935714286	0.095860015
BP1026b.11271	hypothetical protein	61460	104402	91124	62	55512	53524	47041	68	6.02E-43	4.15E-41	0.612903226	-0.706268797
BP1026b.11272	hypothetical protein	10746	17774	13575	150	23490	19824	18165	220	0.008666345	0.09413618	1.466666667	0.552416023
BP1026b.11273	hypothetical protein	2655	3423	34098	17	3222	3819	3819	18	2.76E-04	1.14E-03	0.105882529	0.0824621
BP1026b.11274	major facilitator superfamily transporter	1759	1231	1424	1	1973	1900	2619	0	0.416700545	0.444291441	1	0
BP1026b.11275	hypothetical protein	64308	50139	54491	111	45815	47020	45346	90	1.42E-19	1.51E-18	0.810810811	-0.30256277
predicted RNA	-	6293	2162	2843	209	5316	7533	11267	446	0.19003342	0.211433275	2.133971292	1.093540768
BP1026b.11276	hypothetical protein	40232	21336	23195	66	22765	26073	29621	61	9.91E-10	3.21E-09	0.924242424	-0.13656782
BP1026b.11277	cytidine/deoxycytidylate deaminase family protein	16290	6453	6503	18	9052	9184	10046	17	7.57E-08	1.92E-07	0.944444444	-0.08246216
BP1026b.11278	L-D-carboxypeptidase A	60625	64777	6785									

BP1026b	11329	2-dehydropantoate 2-reductase	8148	5788	5072	6	7828	8785	8712	8	0.015205391	0.019561833	1.333333333	0.415037499
BP1026b	11330	MarK family transcriptional regulator	34299	40044	40269	84	25115	26160	24903	56	2.48E-24	4.32E-23	0.666666667	-0.584962501
BP1026b	11331	glycerate kinase	3814	1900	1373	2	2015	2220	2177	1	1.23E-46	2.64E-46	0	0
BP1026b	11332	hypothetical protein	157	102	99	0	120	160	160	0	0.008287329	0.09598489	#DIV/0!	#DIV/0!
BP1026b	11333	trigger factor	596752	813856	740352	531	852167	833052	755069	602	0.131741336	0.149633314	1.133709981	0.181051626
BP1026b	11334	predicted RNA	17171	9229	12893	595	34727	34908	26555	1457	0.00592023	0.007994033	2.448739496	1.292039304
BP1026b	11334	ATP-dependent Clp protease proteolytic subunit	407645	546911	521984	752	590858	563554	554590	8470	3.03E-07	7.12E-07	1.156914894	0.210827319
BP1026b	11335	ATP-dependent protease ATP-binding subunit ClpX	1343230	1505487	1417349	1117	1711897	1811917	1710231	1371	0.037755054	0.046227063	1.227394808	0.295599385
BP1026b	11336	ATP-dependent protease La	3416901	4493626	4221420	1672	4974921	4900435	4640161	2001	0.125646851	0.142996343	1.196770335	0.219916623
BP1026b	11337	Val tRNA	22393	49744	42864	548	39479	38632	31884	482	4.73E-14	2.55E-13	0.879562044	-0.185142747
BP1026b	11338	Sigma 54 modulation protein YhhH	607192	919593	883462	2434	968317	962990	964707	2925	0.046237256	0.07600721	1.681431933	0.265107457
BP1026b	11339	hypothetical protein	817	496	741	3	613	1309	1614	65	0.144198272	0.163042956	1.666666667	0.736965594
BP1026b	11340	hypothetical protein	188532	237168	219542	434	305250	308663	280256	602	0.072684305	0.085293084	1.387096774	0.472068444
BP1026b	11341	predicted RNA	99600	121850	126714	739	145240	145204	133603	900	2.05E-05	3.74E-05	1.217861976	0.284350637
BP1026b	11342	Carboxymuconolactone decarboxylase family protein	9718	6599	7296	38	11420	11534	9175	52	0.025665405	0.032108667	1.368421053	0.452512205
BP1026b	11343	Asp tRNA	3496	7800	5986	78	6908	6273	4926	78	4.49E-05	7.84E-05	1.083333333	0.115472717
BP1026b	11344	peptidyl-prolyl cis-trans isomerase D	457918	452630	470203	237	418806	442852	446349	225	9.51E-14	4.96E-13	0.949367890	-0.479496208
BP1026b	11345	hypothetical protein	40823	14423	47089	452	44095	51121	63895	238	1.61E-04	2.5797E-05	1.681431933	0.242151573
BP1026b	11346	acyl-CoA thioesterase I	40866	35928	37981	56	37418	38774	41350	58	6.34E-09	1.86E-08	1.037514286	0.050626073
BP1026b	11347	ABC transporter ATP-binding protein	36011	29140	30476	44	33637	35060	35132	48	9.27E-07	2.02E-06	1.090909091	0.125530882
BP1026b	11348	glucose-6-phosphate isomerase	163640	125615	150744	90	171064	173390	171592	105	1.98E-05	3.62E-05	1.166666667	0.22392421
BP1026b	11349	sugar kinase	8444	3955	4198	3	6488	7640	8630	4	0.02093196	0.026477745	1.333333333	0.415037499
BP1026b	11350	D-amino acid dehydrogenase small subunit	23351	10739	13634	12	16526	17744	21272	14	1.53E-04	2.49E-04	1.166666667	0.22392421
BP1026b	11351	phosphoribosylformylglycinamide synthase	469490	416370	422169	107	579588	588480	597639	144	3.77E-04	5.89E-04	1.345794393	0.428458015
BP1026b	11352	acyltransferase	11641	2844	5218	12	11893	14167	16199	26	0.073567417	0.088210295	2.166666667	1.151477727
BP1026b	11353	peptidyl-prolyl cis-trans isomerase domain-containing protein	551222	814423	736129	906	534482	519835	476801	55	0.522632856	0.548759215	1.231841307	0.470220045
BP1026b	11354	Cell division protein BofA	11500	14329	13927	42	8102	8007	10141	27	1.02E-22	5.2E-21	0.642857143	-0.637429921
BP1026b	11355	intracellular septation protein A	88176	120779	117873	205	70163	62365	74880	128	4.28E-04	1.26E-04	0.62390244	-0.6794801
BP1026b	11356	methionine-R-sulfoxide reductase	119892	112297	121994	273	108385	113633	121255	264	2.79E-11	1.09E-10	0.967032967	0.408363022
BP1026b	11357	hypothetical protein	42368	30077	32546	22	41377	42710	43029	27	2.58E-04	4.11E-04	1.272727272	0.295455884
BP1026b	11358	long-chain-fatty-acyl-CoA ligase	63195	54429	57095	35	73503	76026	72138	45	0.005729434	0.007746421	1.285714286	0.362570079
BP1026b	11359	flavin oxidase complex subunit alpha	167443	164829	165438	79	231837	227318	217381	108	0.118641074	0.24161561	1.307886008	0.451106754
BP1026b	11360	pyrazinamide synthase	27702	18393	14997	34	37442	37892	38181	55	0.04667137	0.05196067	0.388214008	-0.175003119
BP1026b	11361	acyl-CoA acetyltransferase	46773	34913	34249	32	50287	56062	62306	47	0.095868834	0.110715778	1.46875	0.554858852
BP1026b	11362	hypothetical protein	15447	19480	18717	38	14365	14835	13064	30	1.96E-14	1.11E-13	0.789473684	-0.341036918
BP1026b	11363	stress responsive A/B barrel domain family protein	161783	98378	104456	385	142826	155957	152548	477	5.40E-05	9.35E-05	1.238961039	0.30913082
BP1026b	11364	thioesterase family protein	53443	22817	28070	72	52004	57933	64405	120	0.881315766	0.891563623	1.666666667	0.736965594
BP1026b	11365	oxoaldehyde, zinc-binding dehydrogenase family protein	94652	62406	66607	74	90595	97626	107287	98	0.005732090	0.007784313	1.324324324	0.405256092
BP1026b	11366	esterase	52688	40964	41741	47	46719	48171	48287	49	2.42E-08	6.55E-08	1.060215698	0.060120947
BP1026b	11367	acyltransferase	136367	132283	13697	34	197448	21467	21462	44	0.010667137	0.01296120	0.319	0.319280085
BP1026b	11368	hypothetical protein	17082	10763	11831	15	12744	14353	17839	17	1.24E-04	2.04E-04	1.133333333	0.180572246
BP1026b	11369	glycine cleavage I-protein, aminomethyl transferase	44428	29958	35133	34	35111	36902	39449	35	8.19E-02	2.33E-08	1.02941765	0.04182076
BP1026b	11370	hypothetical protein	27761	25835	28325	26	24215	24683	28579	25	3.81E-09	1.15E-08	0.961538462	-0.056583528
BP1026b	11371	thymidylate kinase	43266	35262	33951	60	37346	43597	51071	70	1.36E-05	2.55E-05	1.166666667	0.22392421
BP1026b	11372	DNA polymerase III subunit delta'	41785	24797	27549	30	40835	44375	47906	42	0.01289433	0.016750329	1.4	0.485426827
BP1026b	11373	phosphotriester acetyltransferase	53690	35477	41808	86	42648	44773	48153	89	4.18E-09	1.25E-08	1.034887121	0.049686676
BP1026b	11374	hypothetical protein	47434	16393	56623	66	55516	57432	46318	52	0.000190084	0.000190084	0.000190084	0.000190084
BP1026b	11375	ankyrin repeat-containing protein	268552	221438	230418	352	244824	273872	289056	372	2.03E-04	2.27E-04	1.120481928	0.164191938
BP1026b	11376	hypothetical protein	99418	82056	82471	230	93046	104420	100153	282	9.00E-06	1.72E-05	1.128	0.173767068
BP1026b	11377	predicted RNA	36709	6158	10022	383	25678	38653	44771	790	0.41162329	0.439122604	2.062663185	0.445808261
BP1026b	11377	mechanosensitive ion channel family protein	98971	67524	80779	69	85037	87930	87793	72	8.29E-07	1.82E-06	1.043478261	0.061400545
BP1026b	11378	hypothetical protein	28482	16637	18692	18	22607	23632	26787	20	6.59E-05	1.13E-04	1.111111111	0.152003093
BP1026b	11379	glycosyl transferase group I protein	96048	106001	101679	95	82940	80200	78622	75	2.86E-16	2.02E-15	0.789473684	-0.341036918
BP1026b	11380	lipoprotein	15558541	7313268	8767469	17832	14228571	16143983	17566369	27178	0.527385604	0.555396604	0.607907072	0.607907072
BP1026b	11381	hypothetical protein	5762	6381	6394	12	5716	5716	5610	12	1.06E-06	2.29E-06	0.916666667	-0.125530882
BP1026b	11382	phosphate starvation-inducible protein	1710084	2409569	2321368	7378	2070754	1997536	1852045	6781	0.189604285	0.199031292	0.919083763	-0.121731744
BP1026b	11383	asparagine family protein	112022	67487	84859	84	100186	97083	102787	95	1.14E-05	2.15E-05	1.017538186	0.177538186
BP1026b	11384	LysM domain/BON superfamily protein	381315	442331	437128	892	443980	436119	407557	911	9.12E-11	3.35E-10	1.021300448	0.030407344
BP1026b	11385	2-hydroxy-3-oxopropionate reductase	5609	3463	3655	45	5213	4817	4747	5	0.001199084	0.001759031	1.25	0.321928095
BP1026b	11386	hydroxypyruvate isomerase	18241	12169	13389	18	18587	19582	21444	25	0.017070705	0.021858319	1.388888889	0.473931188
BP1026b	11387	hydroxylase carboxylase	8682	7875	7669	4	9211-04	9669	9713	79	9.91E-04	0.001919	0.388214008	0.319280085
BP1026b	11388	LysR family transcriptional regulator	37240	28080	30903	35	33588	35578	31023	36	1.39E-07	3.39E-07	1.028571429	0.040641984
BP1026b	11389	cytochrome c oxidase family protein	994	1055	1064	2	1118	1251	882	2	0.004184547	0.005749506	0	0
BP1026b	11390	Ser/Thr protein phosphatase family protein family	2526	1240	1609	1	2311	2415	2314	2	0.04636732	0.056286173	2	1
BP1026b	11391	RNA polymerase sigma factor	8571	8095	7019	11	11334	10124	12704	16	0.085509361	0.099190859	1.454545455	0.540568381
BP1026b	11392	hypothetical protein	9951	8960	8978	9	12235	12414	10600	11	0.003718	0.005133643	1.222222222	0.286941266
BP1026b	11393	primosomal replication protein n	91872	87385	100551	437	96225	94674	105836	464	3.35E-07	7.79E-07	1.061784897	0.089491526
BP1026b	11394	SIS ribosomal protein S18	339628	339628	339628	1028	339628	339628	339628	1028	339628	339628	339628	339628
BP1026b	11395	SOS ribosomal protein L9	121270	1406910	1333897	2908	161891	1585252	1452266	3426	0.041653426	0.050693017	1.178129298	0.326497882
BP1026b	11396	replicative DNA helicase	202789	196779	209146	146	160946	160230	144950	112	4.57E-27	1.05E-25	0.767123288	-0.382469637
BP1026b	11397	hypothetical protein	205097	304689	286081	423	156460	159267	143033	243	1.43E-58	2.03E-56	0.574468085	-0.79970135
BP1026b	11398	phosphate transporter family protein	204468	203722	196692	199	188603	188342	171055	180				

BP1026b	11451	PQO repeat-containing protein	362042	211914	237021	235	367924	383333	379531	328	0.002279502	0.003231961	1.395744681	0.481035058
BP1026b	11452	GTP-binding protein EngA	200999	202398	206481	155	175149	179952	164518	133	5.32E-18	4.63E-17	0.858064516	-0.22084197
BP1026b	11453	RNA-binding protein Hfq	485807	839206	731029	2855	502261	482281	446497	1987	3.85E-30	1.15E-28	0.695971979	-0.522988873
BP1026b	11454	GTP-binding protein HfxX	261031	280922	280922	236	266643	259216	259216	226	4.35E-08	2.4E-07	0.957267191	-0.063464087
BP1026b	11455	fhlH protease activity modulator HfHK	147631	129044	134508	105	127238	135284	140020	102	4.40E-12	1.90E-11	0.971428571	-0.041820176
BP1026b	11456	HfHK protein	63932	55017	55760	64	59294	60365	60739	66	1.94E-07	4.64E-07	0.10325	0.044394119
BP1026b	11457	hypothetical protein	7266	11812	9119	47	7706	6770	5829	35	3.09E-16	2.17E-15	0.744680851	-0.425305835
BP1026b	11458	ATP phosphoribosyltransferase regulatory subunit	51804	46432	45686	41	44201	47326	49908	41	6.88E-11	2.55E-10	1	0
BP1026b	11459	adenylosuccinate synthetase	363759	463255	434734	312	419580	408823	382381	299	3.01E-12	1.32E-11	0.958333333	-0.061400545
BP1026b	11460	phosphoribosyl transferase domain-containing protein	122581	143171	136518	225	142654	139309	121590	226	4.19E-11	1.60E-10	1.004444444	0.006397771
BP1026b	11461	kup system potassium uptake protein	285855	389585	353346	181	292809	299012	240561	144	1.30E-13	7.14E-13	0.795587081	-0.339920086
BP1026b	11462	transcription accessory protein, TEX	234101	259150	253498	100	294265	289849	276233	116	1.72E-04	2.79E-04	1.16	0.21424805
BP1026b	11463	hypothetical protein	135477	184816	178495	210	166244	163266	184068	216	1.88E-09	5.85E-09	1.028571429	0.040641984
BP1026b	11464	hypothetical protein	138672	221892	207358	876	171087	166310	148260	749	6.84E-19	6.59E-18	0.855022831	-0.225965151
BP1026b	11465	ATP-dependent helicase	131406	123230	121433	55	156855	164505	165347	72	0.00100807	0.001492802	1.309090909	0.388565288
BP1026b	11466	competence lipoprotein ComL	212910	282177	251377	302	179003	174632	164880	210	9.36E-33	3.60E-31	0.695364238	-0.524159222
BP1026b	11467	ribosomal large subunit pseudouridine synthase D	31520	25804	24732	23	34146	35301	35281	29	6.71E-04	0.001019273	1.260869565	0.334419039
BP1026b	11468	poly(R)-hydroxyvalloanoic acid synthase	22472	10022	12678	17	17320	25552	33030	30	0.53244633	0.549284832	1.764705882	0.819427754
BP1026b	11469	poly(R)-hydroxyvalloanoic acid synthase	604759	625844	628453	34	752341	765580	715907	410	0.180384747	0.201377661	1.202346041	0.26585217
BP1026b	11470	acetyl-CoA acetyltransferase	626841	428937	482033	433	705562	793629	936387	686	0.00510847	0.007470233	1.584295612	0.663841551
BP1026b	11471	acetylacetyl-CoA reductase	620270	882579	821794	1045	890272	857286	800959	1146	0.142389977	0.161085573	1.096650718	0.133104102
BP1026b	11472	hypothetical protein	359942	613154	564824	993	435641	439568	426923	852	5.39E-18	4.68E-17	0.858006042	-0.220940287
BP1026b	11474	30S ribosomal protein S12 methylthiotransferase	206689	189633	187508	141	208745	205084	187611	145	9.01E-08	2.27E-07	1.028368794	0.040537738
BP1026b	11475	carbohydrate kinase	153405	92562	109433	127	132214	136223	148683	149	2.87E-06	5.84E-06	1.172228346	0.230483834
BP1026b	11476	beta-ketothiolase	262243	153649	185183	169	272206	281204	285756	236	0.144889045	0.163736468	1.396449704	0.81763613
BP1026b	11477	hypothetical protein	92272	92373	92438	161	94564	94429	101968	127	1.31E-07	8.28E-07	0.762588081	0.527821124
BP1026b	11478	cystathionine beta-lyase	177156	173638	170590	146	203777	198960	195708	168	5.14E-05	8.92E-05	1.15068492	0.20249264
BP1026b	11479	phosphoserine phosphatase	39817	42309	43391	49	47462	44601	41374	52	3.79E-08	9.99E-08	1.06122449	0.085729874
BP1026b	11480	hypothetical protein	1129	1379	1621	7	1266	1164	476	5	3.86E-12	1.67E-11	0.714285714	0.484526827
BP1026b	11481	hypothetical protein	237865	251002	249485	450	290876	305891	342479	573	0.001913987	0.002744784	1.273333333	0.348610138
BP1026b	11482	hypothetical protein	24436	20355	21111	26	21262	21626	21319	26	3.72E-08	9.81E-08	1	0
BP1026b	11483	ABC transporter ATP-binding protein	3481	1718	2171	3	2551	3240	3199	4	0.007441374	0.0091955	1.333333333	0.415037409
BP1026b	11484	AmoA family transducer	212385	237305	218703	89	26762	265738	254778	8284	0.02227786	0.023230367	1.68539382	0.324706287
BP1026b	11485	ABC transporter ATP-binding protein	144606	204404	189858	114	187112	178446	170956	113	1.19E-10	4.31E-10	0.99122807	-0.012711052
BP1026b	11486	hypothetical protein	765386	1212656	1100376	1613	757431	755827	795682	1210	0.755949444	0.772852508	0.750154901	-0.047139391
predicted RNA	-		24739	803	1840	456	12787	23879	29909	1109	0.003693714	0.00510872	2.432017544	1.282153636
BP1026b	11487	aldehyde dehydrogenase	166086	164586	162397	114	197724	193903	187095	134	5.07E-05	8.81E-05	1.175438596	0.233199176
BP1026b	11488	hypothetical protein	3754	5764	4737	45	3221	3588	3307	32	1.78E-15	1.15E-14	0.711111111	-0.491853946
BP1026b	11489	2-nitropropane dioxygenase	672939	559136	602108	526	577455	605406	608337	514	1.99E-11	7.94E-11	0.977186312	-0.03320946
BP1026b	11490	outer membrane protein W	680015	704582	759478	10853	547859	544578	516517	8284	0.86166104	0.873213067	1.26389707	0.319103124
BP1026b	11491	hypothetical protein	96017	62156	120381	591	111282	100442	79189	475	4.00E-17	1.31E-16	0.803722504	-0.315230617
BP1026b	11492	manganese transport protein	9730	1676	6976	5	8377	9919	12775	7	0.024922437	0.031235323	1.4	0.485426827
BP1026b	11493	putrescine-binding periplasmic protein	733606	1063520	981469	845	605924	592544	558882	534	4.00E-35	1.86E-33	0.631952663	-0.662115599
BP1026b	11494	putrescine ABC transporter ATP-binding protein	86111	88597	84343	74	86564	86690	81205	73	1.37E-08	3.81E-08	0.986486486	-0.019628807
BP1026b	11495	putrescine transport system permease	71389	101607	87857	100	66809	60576	51347	68	2.16E-26	4.64E-25	0.68	-0.556393349
BP1026b	11496	putrescine transport system permease	126000	141699	135533	162	128531	126439	106468	146	3.25E-15	1.02E-14	0.890234032	-0.16772446
BP1026b	11497	hypothetical protein	32231	23767	23786	16	32562	34417	31240	17	0.03462947	0.3890517	0.762588081	0.319103124
BP1026b	11498	hypothetical protein	92466	68150	75090	47	109651	115092	126519	70	0.051002865	0.061309144	1.489361702	0.574609415
BP1026b	11499	metallobeta-lactamase family protein	92992	120045	113317	122	79869	81805	85928	93	9.40E-18	8.90E-18	0.762295082	-0.391578526
BP1026b	11500	sigma-54 dependent transcriptional regulator	24065	12275	15136	12	21943	25512	24140	17	0.022912911	0.028855343	1.416666667	0.502500341
BP1026b	11501	hypothetical protein	20611	20362	21652	37	18460	19190	17987	32	1.28E-10	4.60E-10	0.864864865	-0.209453366
BP1026b	11502	transcriptional regulator	22172	29433	26640	115	28058	25604	23227	113	3.78E-08	9.97E-08	0.982608696	-0.025311089
BP1026b	11503	hypothetical protein	6696	2177	3211	8	4636	6230	7042	12	0.12431192	0.141631478	1.5	0.584962501
BP1026b	11504	MerK family transcriptional regulator	22613	18409	18460	18	18612	19213	18280	18	1.48E-07	1.04E-06	0.762588081	0.319103124
BP1026b	11505	hypothetical protein	5284	1391	1652	8	3494	5470	6484	6	0.382126282	0.409308999	2	0
BP1026b	11506	RND efflux system outer membrane lipoprotein	108154	60835	70177	41	113046	125779	134856	65	0.10270785	0.139253399	1.585368564	0.664815808
BP1026b	11507	AcrB/AcrD/AcrF family protein	485978	502191	490198	155	400651	403446	390932	125	1.83E-19	1.92E-18	0.806451613	-0.310340121
BP1026b	11508	RND family efflux transporter MFP subunit	122210	82637	104335	92	99369	98555	116717	93	8.21E-09	2.35E-08	1.010869955	-0.051968555
BP1026b	11509	TetR family transcriptional regulator	187137	230210	233232	349	181740	176214	179922	288	1.51E-19	1.60E-18	0.82521497	-0.21758225
BP1026b	11510	voltage-gated ClC-type chloride channel ClcB	37222	25300	26690	17	35543	36465	35967	20	8.70E-05	1.46E-04	1.176470888	0.244465254
BP1026b	11511	hypothetical protein	10008	48405	59446	6	7445	9345	9465	6	1.04E-05	3.94E-05	0.762588081	0.319103124
BP1026b	11512	YnfK family transcriptional regulator	13680	9769	7664	10	10780	12742	14893	14	0.063441277	0.075193123	1.4	0.485426827
BP1026b	11513	hypothetical protein	16198	8919	11285	32	17023	18524	19664	49	0.164582975	0.184394161	1.53125	0.614709844
BP1026b	11514	AP endonuclease	2538	2613	3000	2	2507	2712	2586	2	5.48E-07	1.23E-06	1	0
BP1026b	11515	2-dehydro-3-deoxygluconokinase	36597	22199	23661	27	26129	28029	32219	29	7.53E-07	1.66E-06	1.074074074	0.103093493
BP1026b	11516	major facilitator family transporter	95306	114195	103920	81	72264	70924	69683	55	2.79E-14	4.82E-23	0.679012246	-0.558490289
BP1026b	11517	2-ketoglutarate reductase	36060	15754	19240	24	33481	34658	40092	36	0.061926725	0.073523314	1.5	0.584962501
BP1026b	11518	ncd family transcriptional regulator	57267	57023	648075	651	836115	620510	620510	57	8.36E-15	4.93E-14	0.886328792	-0.740064237
BP1026b	11519	hypothetical protein	138552	94220	100508	140	103641	106819	106671	133	4.35E-11	1.66E-10	0.95	-0.470400581
BP1026b	11520	hypothetical protein	69266	96086	61017	173	62515	60918	55685	163	1.00E-10	6.70E-10	0.942196532	-0.085900073
BP1026b	11521	hypothetical protein	94811	60899	63452	167	63322	67526	67798	152	1.60E-10	5.68E-10	0.910179641	-0.135776779
BP1026b	11522	hypothetical protein	25972	18164	19097	20	29443	28122	31644	29	0.024449118	0.03		

BP1026b	11582	putative lipase	20681	35205	34097	28	15207	15863	15649	14	2.27E-41	1.48E-39	0.5	-1
BP1026b	11583	hypothetical protein	214	201	104	1	226	330	61	1	0.629452365	0.652148464	1	0
BP1026b	11584	hypothetical protein	401	616	459	3	439	449	430	2	7.10E-04	0.001074787	0.666666667	-0.584962501
BP1026b	11585	Putative baculovirus gp31 protein	1010	1757	1394	45	9289	10609	8994	2	5.57E-20	7.19E-19	0.688888889	-0.537656786
BP1026b	11587	GnRf family transcriptional regulator	31917	45883	42063	57	30244	31554	28349	42	7.41E-19	7.10E-18	0.736842105	-0.440572591
BP1026b	11588	peptide synthase	10237	14807	9114	19	14767	13760	12702	23	8.86E-04	0.001325584	1.210526316	0.275634443
BP1026b	11589	alpha/beta fold family hydrolase	6150	8886	7680	8	8230	7304	5980	8	4.02E-08	1.05E-07	1	0
BP1026b	11590	nitrilotriacetate monooxygenase	5237	8289	8666	7	8965	7308	6461	7	1.56E-06	3.28E-06	1	0
BP1026b	11591	glucose-6-phosphate dehydrogenase	6866	10783	8481	8	9072	8918	6668	7	1.54E-08	4.27E-08	0.875	-0.192645078
BP1026b	11592	aldehyde dehydrogenase	33441	47340	42250	27	59117	52798	43772	35	5.98E-04	9.11E-04	1.296296296	0.374395515
BP1026b	11593	NUP50A-P family protein	1960	2847	2411	7	2763	2204	2412	7	9.83E-06	1.97E-05	1	0
BP1026b	11594	ABC transporter substrate-binding protein	4106	5880	5221	4	4390	3308	5101	4	4.91E-09	1.46E-08	1	0
BP1026b	11595	ABC transporter permease	2779	3232	3576	3	4238	3486	3647	4	0.005043718	0.006863752	1.333333333	0.415037499
BP1026b	11596	putrescine ABC transporter permease	3204	5707	4883	5	2611	2760	3094	3	2.04E-24	3.58E-23	0.6	-0.736965594
BP1026b	11597	spermidine/putrescine ABC transporter ATP-binding protein	4332	6112	6348	5	5262	4191	4831	4	4.09E-09	1.23E-08	0.8	-0.321928095
BP1026b	11598	GnRf family transcriptional regulator	2186	3285	3105	3	2203	2628	2135	3	7.57E-12	3.18E-11	1	0
BP1026b	11599	succinate-semialdehyde dehydrogenase	5025	9267	8334	5	7342	7195	6732	4	2.92E-08	7.81E-08	0.8	-0.321928095
BP1026b	11600	outer membrane porin	1020	1263	1973	1	1165	1335	1506	1	2.36E-12	1.03E-11	1	0
BP1026b	11601	hypothetical protein	234	582	507	1	320	376	255	0	8.92E-06	1.71E-05	0	#NUM!
BP1026b	11602	hypothetical protein	203	494	447	2	267	166	140	1	1.18E-12	5.42E-12	0.5	-1
BP1026b	11603	H1-N5 histone family protein	1159	2584	1496	4	2034	1813	1394	4	2.41E-05	4.37E-05	1	0
BP1026b	11604	ompA family protein	1303	2514	1385	2	1668	1511	1762	1	3.24E-06	6.55E-06	0.5	-1
BP1026b	11605	outer membrane protein	4265	7026	6008	3	5746	5892	4872	3	5.62E-07	1.26E-06	1	0
BP1026b	11606	cable pil-associated 22 kDa adhesin protein	100815	119200	115102	11	106834	103202	101981	10	1.04E-11	4.30E-11	0.909090909	-0.137503524
BP1026b	11607	hypothetical protein	1863	2956	2446	4	1499	1657	1758	3	1.87E-17	1.52E-16	0.75	-0.415037499
BP1026b	11608	sulfotransferase domain-containing protein	2590	5477	3262	7	4082	3544	3649	2	4.89E-05	1.36E-05	0.666666667	-0.584962501
BP1026b	11609	ABC transporter ATP-binding protein/permease	17795	25622	22782	9	21584	20336	18914	8	6.34E-09	1.85E-08	0.888888889	-0.169925001
BP1026b	11610	HlyD family secretion protein	12725	18322	18453	11	19296	18548	17050	12	1.42E-05	2.65E-05	1.090909091	-0.125530882
BP1026b	11611	hypothetical protein	42503	57526	53838	11	52011	49660	47663	11	2.72E-11	1.07E-10	1	0
BP1026b	11612	hypothetical protein	9638	11164	9785	7	8409	8085	7371	5	5.93E-15	3.58E-14	0.714285714	-0.485426827
BP1026b	11613	hypothetical protein	447	472	323	3	146	328	136	1	1.31E-13	6.72E-13	0.333333333	-0.584962501
BP1026b	11614	Adenylsulfate kinase	3063	2976	3335	5	2929	2827	2360	4	1.12E-09	3.60E-09	0.8	-0.321928095
BP1026b	11615	hypothetical protein	682	682	592	6	1401	1335	1289	11	0.231767287	0.245000000	1.833333333	0.874460118
BP1026b	11616	hypothetical protein	501	910	520	4	1225	1012	947	7	0.297609112	0.323033007	1.75	0.807354922
BP1026b	11617	DNA-binding response regulator	3060	4104	2993	4	6185	6296	6329	8	0.6985319	0.691603821	2	1
BP1026b	11618	putative transposase	2056	1398	1997	3	2219	1918	2110	3	0.0015896	0.00230492	1	0
BP1026b	11619	hypothetical protein	5124	9057	8794	12	6338	6635	5978	10	2.46E-11	9.68E-11	0.833333333	-0.263034406
BP1026b	11620	hypothetical protein	2217	3639	3422	7	2454	2300	1971	5	3.83E-16	2.66E-15	0.714285714	-0.485426827
BP1026b	11621	hypothetical protein	8420	14770	13020	9	9660	9357	8741	7	2.11E-15	1.35E-14	0.777777778	-0.362570079
BP1026b	11622	phosphoglucoisomerase	2678	4087	3544	7	4336	4053	3644	6	6.68E-27	1.98E-25	0.75	-0.700439718
BP1026b	11623	outer membrane porin	3000	3269	3452	2	3685	4762	3694	3	0.018221932	0.023424146	1.5	0.584962501
BP1026b	11624	Is2000 transposase	1038	1204	1258	2	1280	924	1625	2	0.007090279	0.00937564	1	0
BP1026b	11625	phenylalanine and histidine ammonia-lyase	4388	3933	4117	2	3371	4163	4949	2	1.66E-05	3.07E-05	1	0
BP1026b	11626	major facilitator family transporter	1457	1081	1239	0	1247	1200	1379	0	5.29E-04	8.13E-04	#DIV/0!	#DIV/0!
BP1026b	11627	urocanate hydratase	6129	6492	5364	3	6945	6732	6158	4	7.37E-13	1.25E-04	1.333333333	0.415037499
BP1026b	11628	hypothetical protein	2903	1770	2170	2	2817	2453	3113	2	0.006784998	0.009097009	1	0
BP1026b	11629	LeuR family transcriptional regulator	8434	14038	12765	11	10945	10298	9920	11	8.89E-07	1.54E-06	1	0
BP1026b	11630	allantoate	9579	8316	8927	6	10800	9159	9920	7	5.67E-05	9.79E-05	1.166666667	0.22239421
BP1026b	11631	allantoate amidohydrolase	5441	5513	6348	4	5624	6311	7325	5	1.19E-04	1.96E-04	1.25	0.321928095
BP1026b	11632	hypothetical protein	11318	16446	15844	28	12337	11837	10878	22	7.02E-14	3.72E-13	0.785714286	-0.347923303
BP1026b	11633	transposase	4848	9161	6951	25	5452	5323	4848	18	1.70E-13	8.61E-13	0.72	-0.473931188
BP1026b	11635	RNA polymerase sigma factor	58932	95735	80721	149	76418	79444	77251	148	3.52E-08	9.33E-08	0.993288591	-0.009715155
BP1026b	11636	hypothetical protein	17370	14831	15085	25	16268	16131	14886	25	3.83E-07	8.84E-07	0	0
BP1026b	11637	hypothetical protein	914743	91063	109532	152	97067	10190	9385	155	3.89E-08	1.04E-07	1.019736842	0.028196982
BP1026b	11638	hypothetical protein	5277	4253	4943	8	5941	6013	5385	1	0.009855714	0.012909606	1.375	0.459431619
BP1026b	11639	hypothetical protein	5633	3352	4864	6	5451	5202	4841	6	3.29E-05	8.84E-05	1	0
BP1026b	11640	hypothetical protein	4959	7390	7208	7	6510	5916	6343	6	2.86E-07	6.74E-07	0.857142857	-0.22239421
BP1026b	11641	Putative signal peptide protein	3687	5176	4221	13	5833	5579	5032	17	0.006644479	0.00890473	1.307692308	0.387023123
BP1026b	11642	putative insertion element protein	920	2200	2129	4	1535	1679	1075	3	3.49E-09	1.06E-08	0.75	-0.415037499
BP1026b	11643	hypothetical protein	1440	2183	1725	12	2189	1898	1467	13	7.50E-05	1.27E-04	1.083333333	0.115477217
BP1026b	11644	hypothetical protein	9769	18648	17787	26	19445	19710	18727	16	6.68E-27	1.98E-25	0.615384615	-0.700439718
BP1026b	11645	recombinase	1154	2663	2642	3	1521	1654	1603	2	1.70E-13	8.62E-13	0.666666667	-0.584962501
BP1026b	11646	hypothetical protein	49	184	89	1	118	68	159	1	0.375727432	0.402846988	1	0
BP1026b	11647	hypothetical protein	709	473	361	4	508	725	522	5	0.091325732	0.105702954	1.25	0.321928095
BP1026b	11648	lipoprotein	1017	1133	1512	5	698	873	620	3	2.06E-17	1.67E-16	0.6	-0.736965594
BP1026b	11649	DNA invertase	3097	4345	3248	5	2426	2093	2027	3	4.03E-25	7.51E-24	0.6	-0.736965594
BP1026b	11650	transposase	5368	8287	6105	14	6387	6392	6222	13	2.89E-07	6.79E-07	0.928571429	-0.106915204
BP1026b	11651	hypothetical protein	34	253	116	0	764	56	50	0	7.64E-09	0.20E-08	0	#NUM!
BP1026b	11652	hypothetical protein	184	66	192	1	157	44	344	0	0.700116104	0.720711138	0	0
BP1026b	11653	hypothetical protein	202	467	460	3	234	289	324	2	2.09E-04	3.37E-04	0.666666667	-0.584962501
BP1026b	11654	hemagglutinin motif-containing protein	95377	136277	124629	23	134637	129843	108334	25	3.41E-09	1.04E-08	1.086956522	0.120294234
BP1026b	11655	hypothetical protein	956	1675	1530	13	811	896	834	8	1.28E-17	1.06E-16	0.615384615	-0.700439718
BP1026b	11656	putative HNS-like protein	844	1097	1344	3	706	913	777	2	4.67E-10	1.56E-09	0.666666667	-0.584962501
BP1026b	11657	hypothetical protein	531	692	654	6	656	421	241	4	2.24E-08	6.08E-08	0.666666667	-0.584962501
BP1026b	11658	hypothetical protein	1699	12848	1755	7	1805	2274	1770	6	8.38E-08	2.12E-07	1	0
BP1026b	11659	adactose oxidase	66626	106402	89755	37	14826	90866	74300	37	1.84E-08	4.13E-08	1	0
BP1026b	11660	hypothetical protein	728	2022	1256	9	1499	1472	1361	9	0.001641179	0.002376409	1	0
BP1026b	11661	non-ribosomal peptide synthetase	11900	12135	12635	30	15693	14660	18249	40	0.014730738	0.01892379	1.333333333	0.415037499
BP1026b	11662	hypothetical protein	2602	4368	3809	29	2448	2409	2019	18	8.43E-23	1.26E-21	0.620689655	-0.688055994
BP1026b	11663	peptidase	56926	37040	42846	19	33761	37431	41474	15	1.46E-17	1.20E-16	0.789473684	-0.341036918
BP1026b	11664	carbamoyl transferase	373759											

BP1026B.11708	MarR family transcriptional regulator	13155	8178	8888	23	15566	16840	15543	37	0.387626382	0.414916552	1.608695652	0.68589141
BP1026B.11709	major facilitator family transporter	3108	2768	2218	2	2770	4305	3294	2	0.036544345	0.044797216	1	0
BP1026B.11710	IenI protein	163972	129098	143307	92	158158	161576	159790	102	1.08E-07	2.68E-07	1.108695652	0.148863386
BP1026B.11711	precorrin-4 C(1)-methyltransferase	24616	23311	21641	32	21488	23997	23800	30	1.29E-08	3.63E-08	0.9375	-0.093109404
BP1026B.11712	cohal-precorrin-6A reductase	6652	2081	2368	5	4562	5672	6534	7	0.237295784	0.261187979	1.4	0.485426827
BP1026B.11713	cohal-precorrin-6A synthase	29614	13146	15617	17	23900	26295	30003	24	0.017084291	0.021871244	1.411764706	0.497499659
BP1026B.11715	precorrin-6Y C5,15-methyltransferase	9575	8606	10180	7	7862	7593	9210	6	6.48E-11	2.41E-10	0.857142857	-0.22329421
BP1026B.11714	hypothetical protein	1581	452	790	5	695	939	884	5	2.28E-05	4.14E-05	1	0
BP1026B.11716	precorrin-3B synthase	9371	3724	5100	4	7651	7904	10814	6	0.086249347	0.099993691	1.5	0.584962501
BP1026B.11717	precorrin-8X methylmutase	7723	5410	5947	10	7907	6381	5698	10	9.89E-06	1.88E-05	1	0
BP1026B.11718	precorrin-2 C(20)-methyltransferase	19458	12402	1346	19	15629	17440	18891	23	8.17E-04	0.001255789	1.210526616	0.375634463
BP1026B.11719	precorrin-3b C17-methyltransferase	26087	16951	17943	10	28572	30752	36672	15	0.0275735	0.034331228	1.5	0.584962501
BP1026B.11720	glycosyl hydrolase family protein	3161435	2106502	2524660	1907	3581274	3621775	3715686	2672	0.050820744	0.061113677	1.401153644	0.486615164
BP1026B.11721	hypothetical protein	33687	45381	46490	164	38023	91014	41482	155	8.01E-12	3.35E-11	0.945121951	-0.081427599
BP1026B.11722	carboxylesterase	60376	38965	41361	68	48210	49850	52630	73	6.66E-08	1.70E-07	0.173529412	0.102361718
BP1026B.11723	hypothetical protein	5227	983	1198	4	4089	5769	8801	10	3.21E-04	5.06E-04	2.5	1.321928095
BP1026B.11724	magnesium chelatase subunit ChII	25919	15429	15611	14	22490	21965	23150	17	2.59E-04	4.13E-04	1.214285714	0.280107919
BP1026B.11725	cobalochelatase subunit CobN	334060	237904	274653	71	349956	369124	372087	94	4.65E-04	7.76E-04	1.333943662	-0.404846732
BP1026B.11726	cobalamin biosynthesis protein CobW	168215	121329	120675	128	159308	183398	201260	169	0.005924429	0.007979799	1.320125	0.400879436
BP1026B.11727	high affinity nickel transporter	202844	170623	179938	173	190344	202186	203194	186	8.65E-07	8.89E-06	1.075144509	0.104530583
BP1026B.11728	predicted RNA	30077	15438	19352	441	17082	22992	36336	519	1.89E-04	2.91E-04	1.176870748	0.234955883
BP1026B.11729	cobalamin biosynthesis protein ChbG	1927	258	687	2	1387	1363	1796	3	0.633779063	0.656414029	1.5	0.584962501
BP1026B.11729	cob(ly)rimic acid a,c-diamide amidotransferase	26301	19760	21603	37	22748	22533	21041	36	3.72E-08	9.81E-08	0.972972973	-0.039528364
BP1026B.11730	cob(ly)rimic acid A,C-diamide synthase	18967	6781	10144	7	12186	14264	19062	9	0.004373241	0.005995618	1.285714286	0.362570079
BP1026B.11731	pyoverdine synthetase F	6414	8246	8465	9	6924	8559	7601	9	3.35E-07	7.79E-07	1	0
BP1026B.11732	ionB-dependent siderophore receptor	8379	9441	9441	4	10199	8579	829	4	2.46E-06	4.94E-06	1	0
BP1026B.11733	l-ornithine S5-monooxygenase	1264	1046	1177	0	1324	1828	2088	1	0.746254392	0.763813319	#DIV/0!	#DIV/0!
BP1026B.11734	pyoverdine synthetase D	4532	2292	2029	0	3635	5160	5927	0	0.971682607	0.974638888	#DIV/0!	#DIV/0!
BP1026B.11735	siderophore malleobactin non-ribosomal peptide synthetase MbaJ	5315	2473	3696	0	5146	6078	6753	0	0.287757939	0.313426488	#DIV/0!	#DIV/0!
BP1026B.11736	cyclic peptide ABC transporter ATP-binding protein	3220	3550	2928	1	3247	3526	4104	2	0.0010077	0.001492606	2	1
BP1026B.11737	hypothetical protein	9478	8095	8144	14	7656	6139	7187	12	1.63E-12	7.37E-12	0.857142857	-0.22239421
BP1026B.11738	iron compound ABC transporter substrate-binding protein	1031	632	588	0	820	1083	1251	1	0.737567716	0.757586712	#DIV/0!	#DIV/0!
BP1026B.11739	feric iron reductase protein FhuE	379	123	132	0	269	131	438	0	0.54708997	0.572601169	#DIV/0!	#DIV/0!
BP1026B.11740	iron-hydroxamate transporter permease subunit	2193	1313	1404	0	2527	2628	1986	1	0.3420807	0.368620937	#DIV/0!	#DIV/0!
BP1026B.11741	iron compound ABC transporter ATP-binding protein	1540	994	803	1	1526	1393	1199	1	0.096108441	0.110972032	1	0
BP1026B.11742	SyrP-like protein	2024	1865	1731	1	2068	1334	1807	1	4.86E-07	1.10E-06	1	0
BP1026B.11743	mbtH-like protein	259	188	328	1	109	60	254	0	6.53E-09	1.91E-08	0	#NUM!
BP1026B.11744	extracytoplasmic-function sigma-70 factor	4613	6117	5443	6	5092	6844	4785	7	1.61E-05	2.99E-05	1.166666667	0.22239421
BP1026B.11745	short chain dehydrogenase	3221	2449	2034	3	2844	2818	3285	3	0.002455225	0.003461816	1	0
BP1026B.11750	predicted RNA	5088	2342	6316	568	7456	3824	4031	386	7.45E-16	1.83E-15	0.679577465	-0.557290082
BP1026B.11746	zinc-binding dehydrogenase family oxidoreductase	16393	22150	20590	18	14553	13554	12425	12	7.66E-21	9.27E-20	0.666666667	-0.584962501
BP1026B.11747	ribiose ABC transporter permease	1931	1271	921	1	1646	1762	1692	1	0.030095058	0.037315013	1	0
BP1026B.11748	ribiose ABC transporter ATP-binding protein	6457	5163	5594	3	6116	7264	6197	4	2.27E-04	3.63E-04	1.333333333	0.415037499
BP1026B.11749	Xylose ABC transporter, periplasmicxylose-binding protein XylF	2256	1787	2306	2	1966	2470	2249	2	3.91E-05	6.88E-05	1	0
BP1026B.11750	AraC family transcriptional regulator	20300	25740	25780	24	15789	17995	14825	16	2.99E-21	3.79E-20	0.666666667	-0.584962501
BP1026B.11751	hypothetical protein	705	1006	1044	8	807	847	525	6	1.63E-07	9.94E-07	0.75	-0.415037499
BP1026B.11752	hypothetical protein	1814217	2299023	16210	22277	2371341	2990384	15257	1	0.186729271	0.200602678	0.94120913	-0.087412779
BP1026B.11753	hypothetical protein	108524	388544	129014	176	98009	93724	86668	60	6.38E-21	7.79E-20	0.738636364	-0.367306306
BP1026B.11754	asparagine synthase	125526	121708	131475	72	131202	129300	113453	71	2.96E-11	1.15E-10	0.986111111	-0.3020177882
BP1026B.11755	ABC transporter membrane protein	196856	107299	135501	85	152297	158968	166531	92	4.60E-08	1.20E-07	1.082352941	0.11417102
BP1026B.11756	hypothetical protein	47862	59957	60311	54	37356	35851	36188	35	1.54E-33	6.24E-32	0.648148148	-0.625604485
BP1026B.11757	hypothetical protein	9679	5048	5220	8	6659	8352	8357	10	3.09E-04	4.89E-04	1.25	0.321928095
BP1026B.11758	Pi-fimbriae usher protein	40757	32486	31184	14	39963	39039	41985	16	8.33E-06	1.60E-05	1.142857143	0.192645078
BP1026B.11759	Pi-fimbriae major subunit FimA	277125	178613	178331	346	209543	209544	210505	411	0.001959632	0.002803823	0.91831272	-0.24366594
BP1026B.11760	Outer membrane efflux protein	111307	59602	76790	53	110827	117820	135076	70	0.031691523	0.039209105	1.47169813	0.557481764
BP1026B.11761	multidrug efflux protein	237756	203862	207553	70	249243	254141	247614	71	0.002112669	0.003009039	1.157142857	0.10566986
BP1026B.11762	periplasmic multidrug efflux lipoprotein	38494	24928	26526	24	33702	37587	44940	32	7.17E-04	0.001084431	1.333333333	0.415037499
BP1026B.11763	Transcription repressor of multidrug effluxpump acrAB operon, TetR (AcrR) family	19282	14211	13226	23	19941	24029	27319	35	0.141391871	0.159985311	1.521739061	0.605721061
BP1026B.11764	peptidase	36248	24200	24779	20	33773	36079	36138	24	2.61E-04	4.15E-04	1.2	-0.26304406
BP1026B.11765	amino acid transport system, membrane protein	3698	433	5033	5	2938	2641	2822	3	6.73E-22	1.03E-21	0.6	-0.36965994
BP1026B.11766	binding-protein-dependent transport system inner membrane protein	807	423	668	0	390	881	481	0	0.002618802	0.003686313	#DIV/0!	#DIV/0!
BP1026B.11767	extracellular solute-binding protein	4758	4691	5234	5	5973	5541	6123	7	0.001722564	0.002487353	1.4	0.485426827
BP1026B.11768	hypothetical protein	847	434	861	0	568	881	841	0	0.012958586	0.016868222	#DIV/0!	#DIV/0!
BP1026B.11769	hypothetical protein	927	1217	945	2	873	1138	787	2	3.73E-05	6.58E-05	1	0
BP1026B.11770	hypothetical protein	515	50	8	0	304	270	201	0	0.71631628	0.735936555	#DIV/0!	#DIV/0!
BP1026B.11771	fimbriae membrane protein	495	640	655	0	613	827	965	0	0.538935934	0.564719755	#DIV/0!	#DIV/0!
BP1026B.11772	hypothetical protein	873	873	776	0	965	673	745	0	0.009136532	0.012063686	#DIV/0!	#DIV/0!
BP1026B.11773	type IV pilus protein	5017	5193	3709	2	4699	5023	5088	1	8.11E-05	1.37E-04	1.5	0.584962501
BP1026B.11774	fimbriae assembly protein	2712	2447	2897	2	2628	2563	1687	1	3.69E-10	1.25E-09	0.5	-1
BP1026B.11775	lipoprotein	1	18	5	0	21	62	16	0	3.21E-07	7.51E-07	#DIV/0!	#DIV/0!
BP1026B.11776	RhcC2	2072	1889	1593	1	1693	1589	1841	1	4.78E-07	1.09E-06	1	0
BP1026B.11777	CpaB family FliP pilus assembly protein	206	48	136	0	194	254	258	0	0.03469158	0.04263545	#DIV/0!	#DIV/0!
BP1026B.11778	fimbriae assembly protein	441	345	279	0	364	434	537	0	0.540740919	0.566326888	#DIV/0!	#DIV/0!
BP1026B.11779	fimbriae assembly protein	9752	8917	10602	50	7782	7730	6271	37	1.85E-16	3.34E-15	0.74	-0.24402824
BP1026B.11780	permease	974	436	662	0	639	662	663	0	0.02426685	0.030215666	#DIV/0!	#DIV/0!
BP1026B.11781	ABC transporter ATP-binding protein	898	763	553	0	817	746	669	0	0.002874935	0.004025166	#DIV/0!	#DIV/0!
BP1026B.11782	ABC transporter substrate binding protein	9000	6283	6355	6	9283	10351	9862	9	0.031379941	0.038854309	1.5	0.584962501
BP1026B.11783	dicarboxylic acid transporter PcaI	76501	66634	74226	55	65090	62836	61447	48	2.58E-12	1.12E-11	0.872727273	-0.196397213
BP1026B.11784	SpoVR family protein	224121	352664	310972	175	235861	218454	206473	130	3.30E-17	2.60E-16	0.742857143	-0.428843299
BP1026B.11785	hypothetical protein	151264	237602										

BP1026b	I1831	GntR family transcriptional regulator	29542	27429	30795	40	33031	34345	34049	47	1.94E-05	3.56E-05	1.175	0.232660757
BP1026b	I1832	ribose-5-phosphate isomerase A	112760	99657	104919	151	101771	99817	95654	142	6.85E-11	2.54E-10	0.940397351	-0.08865762
BP1026b	I1833	N-acetylneuraminyl-L-alanine amidase domain-containing protein	25278	21417	24622	26	21377	24045	25311	26	1.34E-07	3.28E-07		0
BP1026b	I1834	DNA methyltransferase	51415	45622	48629	65	53876	53893	51899	73	3.68E-06	2.39E-06	1.123076923	0.16745646
BP1026b	I1835	ribonuclease R	525024	56752	557640	235	690381	691365	660776	279	0.94151082	0.94619345	1.234	0.10340121
BP1026b	I1836	Leu tRNA	1280	2811	1829	22	2257	2260	1982	24	2.36E-04	3.79E-04	1.090909091	0.125530882
BP1026b	I1837	Leu tRNA	89374	141423	114386	1322	138672	129110	104488	1426	2.95E-08	7.89E-08	0.078668684	0.109251805
BP1026b	I1838	methyl-accepting chemotaxis domain-containing protein	11590	13378	12248	7	13115	13392	13302	7	9.87E-06	1.88E-05	1	0
BP1026b	I1839	phosphotransferase family protein	5530	7069	6941	4	6810	8168	6217	4	2.81E-05	5.04E-05	1	0
BP1026b	I1840	hypothetical protein	3350	2715	2362	1	2533	3593	3434	2	0.001050857	0.001552127	2	1
BP1026b	I1841	sulfate permease family protein	33888	25924	29595	17	22081	32946	30894	20	3.32E-08	2.97E-08		0
BP1026b	I1842	hypothetical protein	41299	49596	47919	73	52507	33779	28895	50	1.35E-25	2.67E-24	0.684931507	-0.545986369
BP1026b	I1843	acetyltransferase	4021	3349	2487	5	2608	3315	3450	5	4.87E-07	1.10E-06	1	0
BP1026b	I1844	major facilitator family transporter	44105	44791	45715	36	40756	38185	36651	31	9.15E-16	6.08E-15	0.861111111	-0.215728691
BP1026b	I1845	TetR family transcriptional regulator	152084	207314	183373	189	223521	215120	193806	220	7.64E-04	0.001149748	1.164021164	0.219117289
BP1026b	I1846	long-chain-fatty-acid-CoA ligase	28378	28324	27356	15	27577	26513	27630	15	1.83E-08	5.02E-08	1	0
BP1026b	I1847	hypothetical protein	22338	21490	19390	21	21526	24657	22290	23	6.68E-06	1.30E-05	1.095238095	0.131244533
BP1026b	I1848	hypothetical protein	1663	4270	3563	18	4237	4921	4084	12	7.32E-04	4.44E-04	0.737797598	-0.365780079
BP1026b	I1849	hypothetical protein	11796	8422	10126	37	9464	10848	11920	39	5.56E-06	1.09E-05	1.054054054	0.075948853
BP1026b	I1850	Hfq protein	60676	78804	72935	108	66367	67372	62704	100	6.49E-10	2.14E-09	0.925925926	-0.11031312
BP1026b	I1851	hypothetical protein	189002	208542	217554	280	177564	169852	159114	230	2.26E-20	2.58E-19	0.821428571	-0.283792966
BP1026b	I1852	sigma-54 dependent transcriptional regulator	124467	94148	100611	76	120050	124553	128180	89	3.70E-06	7.42E-06	1.171052632	0.227805918
BP1026b	I1853	hypothetical protein	28247	28977	28584	15	27707	26529	28360	15	9.97E-09	2.83E-08	1	0
BP1026b	I1854	hypothetical protein	3439	2125	1971	6	4569	5135	5465	12	0.100076473	0.115383586	2	1
BP1026b	I1855	hypothetical protein	20772	17578	20826	21	23263	25036	24803	26	9.94E-04	0.001472665	1.238095853	0.308122295
BP1026b	I1856	hypothetical protein	17531	14672	15112	15	20383	21380	20975	20	0.00739027	0.000570243	1.333333333	0.145037499
BP1026b	I1857	Flp pilus assembly protein TadB	12546	10160	10334	10	9871	9977	8943	9	7.32E-11	2.71E-10	0.9	-0.152003093
BP1026b	I1858	type II/IV secretion system protein	72863	59159	64722	48	80375	77987	78613	58	7.10E-04	0.001074787	1.208333333	0.273018494
BP1026b	I1859	fimbriae assembly protein	15553	12969	11610	10	14569	14845	14316	11	2.55E-05	4.61E-05	1.1	0.137503524
BP1026b	I1860	type II/III secretion system protein	65399	49715	50989	41	56990	61430	62439	45	4.70E-06	9.28E-06	1.097560976	0.134301092
BP1026b	I1861	CpaB family Flp pilus assembly protein	10008	7736	8334	9	7875	7802	9090	9	2.27E-08	6.16E-08	1	0
BP1026b	I1862	hypothetical protein	8903	5972	5782	14	12582	10880	11795	25	0.001720585	0.016316278	1.785714286	0.836501268
BP1026b	I1863	hypothetical protein	4025	4025	3563	11	4237	4921	4084	12	7.32E-04	4.44E-04	0.737797598	-0.365780079
BP1026b	I1864	Flp pilus assembly protein, pilin Flp	52751	86992	70447	353	73233	72746	66600	357	2.68E-07	6.31E-07	0.101313445	0.016255891
BP1026b	I1865	hypothetical protein	622	2028	1564	10	1189	1400	1269	9	8.44E-06	1.62E-05	0.9	-0.152003093
BP1026b	I1866	hypothetical protein	486	1707	1181	9	941	1018	920	7	1.58E-06	3.31E-06	0.777777778	-0.362570079
BP1026b	I1867	hypothetical protein	1906	680	905	0	1476	1726	3064	1	0.239563726	0.263406562	#DIV/0!	#DIV/0!
BP1026b	I1868	lipoprotein	1995	736	1225	1	1659	2206	2349	1	0.831187352	0.84439792	1	0
BP1026b	I1869	two-partner secretion family protein	15641	15573	14384	9	17486	18615	17519	10	2.84E-04	4.51E-04	1.111111111	0.152003093
BP1026b	I1870	hypothetical protein	60415	56337	66148	131	71439	70873	67089	14	7.23E-04	1.23E-03	0.818181818	0.176030367
BP1026b	I1871	hypothetical protein	7178	5989	6458	15	7833	8034	7804	19	8.37E-04	0.001255319	1.266666667	0.341036918
BP1026b	I1872	ATPase, AFG1 type	51720	47359	45435	43	46205	49848	44453	42	2.69E-11	1.05E-10	0.976744186	-0.033947332
BP1026b	I1873	dihydrolipamide dehydrogenase	906818	1065498	1028398	698	1157287	1128716	1095295	787	0.195826263	0.217453592	1.127507163	0.173136599
BP1026b	I1874	dihydrolipamide succinyltransferase	363785	406880	406649	309	554723	546463	502282	422	7.97E-04	0.001198036	1.365695793	0.449636161
BP1026b	I1875	predicted RNA	10455	564	1680	124	11861	16920	25217	529	1.27E-18	1.19E-17	4.266129032	2.099272602
BP1026b	I1876	2-oxoglutarate dehydrogenase E1 component	1927441	1800810	1707489	558	1916913	1838775	1824110	649	0.09090531	0.070321182	1.163082471	0.217953356
BP1026b	I1877	UTP-binding protein TtpA	90250	92728	9228	32	10236	12480	12480	32	0.00142364	0.000570243	1.326923072	0.480840739
BP1026b	I1878	RND efflux system outer membrane lipoprotein	7039	6787	7756	14	7630	6664	7639	14	1.39E-06	2.94E-06		0
BP1026b	I1879	multidrug resistance protein	26547	17520	18815	14	25531	28187	31521	18	0.011031879	0.014423646	1.285714286	0.362570079
BP1026b	I1880	EmrB_QacA family drug resistance transporter	30916	30554	29756	24	36475	34175	34848	28	1.54E-05	2.87E-05	1.166666667	0.222392421
BP1026b	I1881	EmrB_QacA family drug resistance transporter	26015	28877	31126	18	28718	26570	24802	17	1.39E-09	4.40E-09	0.944444444	-0.084426216
BP1026b	I1882	tRNA pseudouridine synthase B	44229	31555	33209	39	50032	51462	52956	56	0.026649277	0.032664555	1.435897436	0.521952703
BP1026b	I1883	ribosome-binding factor A	29422	49943	42580	97	44661	43520	38948	101	1.46E-08	4.05E-08	1.041237113	0.058298641
BP1026b	I1884	translation initiation factor IF-2	90250	92728	9228	32	10236	12480	12480	32	0.00142364	0.000570243	1.326923072	0.480840739
BP1026b	I1885	transcription elongation factor NusA	424174	559997	515012	338	523539	505534	463623	337	7.97E-12	1.34E-11	0.99704142	-0.004274655
BP1026b	I1886	hypothetical protein	63934	108781	94632	192	68649	62328	54421	142	1.44E-19	1.53E-18	0.739583333	-0.435215381
BP1026b	I1887	tRNA pseudouridine synthase family protein	111372	85568	90342	57	114181	119554	128976	72	1.80E-04	2.91E-04	1.263157593	0.33704987
BP1026b	I1888	segregation and condensation protein B	196716	186623	188238	139	183487	200679	208311	144	4.91E-08	1.28E-07	1.035971223	0.050983929
BP1026b	I1889	hypothetical protein	12990	21442	18311	183	14388	14480	11800	141	2.39E-15	1.51E-14	0.770491803	-0.376148486
BP1026b	I1890	OsmT protein	3081	37438	37117	39	30480	31016	25740	32	9.54E-15	5.58E-14	0.820512821	-0.285402219
BP1026b	I1891	hypothetical protein	22122	36952	26635	66	54381	51082	21788	52	5.83E-14	2.35E-13	0.818181818	0.120950664
BP1026b	I1892	hypothetical protein	29893	21542	22537	85	24601	27419	31754	108	3.06E-05	5.46E-05	1.136842105	0.185031894
BP1026b	I1893	hypothetical protein	154007	238704	209851	631	172320	164627	156240	516	3.19E-21	4.03E-20	0.817749604	-0.290626894
BP1026b	I1894	hypothetical protein	40889	62130	55988	623	73145	77541	72278	84	0.088582993	0.106262342	1.402889246	0.484801116
BP1026b	I1895	hypothetical protein	610461	228858	332665	540	892709	936778	1087873	1375	8.31E-09	2.38E-08	2.490740741	1.31657486
BP1026b	I1896	hypothetical protein	4121964	6996066	6396454	20925	5576086	5483876	5258316	19497	0.314150355	0.339868364	0.917562722	-0.01975469
BP1026b	I1897	hypothetical protein	190908	292754	273616	977	237055	217981	212940	863	2.76E-10	9.50E-10	0.883162274	-0.178990031
BP1026b	I1898	hypothetical protein	149989	232464	217155	687	110209	108525	107075	368	6.08E-09	1.67E-08	0.63566262	-0.900604313
BP1026b	I1899	hypothetical protein	385730	528634	495804	383	356562	349748	341218	384	1.34E-21	1.76E-20	0.74151436	-0.431453462
BP1026b	I1900	Pro tRNA	1290	945	1329	2	1091	1306	1609	2	0.010675192	0.013977718	1	0
BP1026b	I1901	hypothetical protein	9574	11376	11113	8	9102	8431	7372	6	4.84E-15	2.94E-14	0.75	-0.415037499
BP1026b	I1902	hypothetical protein	167	378	326	3	258	109	219	2	1.35E-05	2.53E-05	0.666666667	-0.584962501
BP1026b	I1903	hypothetical protein	2274	4159	3723	34	3250	2564	2443	27	1.04E-11	4.30E-11	0.79417647	-0.332575339
BP1026b	I1904	hypothetical protein	38302	64592	56294	44	37499	37908	33769	30	5.23E-29	1.42E-27	0.681818182	-0.552541023
BP1026b	I1905	hypothetical protein	26194	31226	29126	14	30864	31277	28552	15	4.96E-07	1.12E-06	1.071428571	0.099535674

BP1026b	11951	lipoprotein	13529	6479	8196	15	11224	13994	17143	22	0.180164528	0.201167665	1.466666667	0.552541023	
BP1026b	11952	sensor histidine kinase	164474	126813	126273	58	152920	158568	162379	65	7.22E-07	1.60E-06	1.120689655	0.14386818	
BP1026b	11953	LysM domain-containing protein	248861	193765	209568	172	234875	238950	237855	188	2.67E-04	4.24E-04	1.093023256	0.128324097	
BP1026b	11954	DNA-binding response regulator	196994	282435	255304	336	166809	165054	155194	221	1.70E-39	1.00E-37	0.657738095	0.664414863	
BP1026b	11955	hypothetical protein	28701	17106	18395	55	19455	23431	26019	59	4.34E-06	8.62E-06	1.072722727	0.101283336	
BP1026b	11956	hypothetical protein	101388	141597	127439	534	124831	116053	100706	492	3.58E-13	1.74E-12	0.921348315	-0.11818426	
BP1026b	11957	homoserine dehydrogenase	10337	4746	4585	6	10104	12283	14964	11	0.51158707	0.538012717	1.833333333	0.874469118	
BP1026b	11958	myo-inositol 2-dehydrogenase	18049	9698	9482	12	16099	18705	22291	18	0.19148661	0.212936646	1.5	0.584962501	
BP1026b	11959	SIS domain-containing protein	18031	22703	19184	22	20538	19052	17725	21	1.33E-08	3.70E-08	0.954545455	0.907114196	
BP1026b	11960	sugar ABC transporter periplasmic sugar-binding protein	9032	13171	11708	10	10197	11563	9886	9	4.71E-09	3.40E-08	0.9	-0.152003093	
BP1026b	11961	permease protein of sugar ABC transporter	6129	6756	6657	5	8780	9381	8472	7	0.08233394	0.03317947	1.4	0.485426827	
BP1026b	11962	sugar ABC transporter ATP-binding protein	9218	11899	10888	13	9832	10186	9234	12	1.22E-10	4.40E-10	0.923076923	-0.115472717	
BP1026b	11963	iolC protein	11080	8761	8849	4	10771	11734	11568	5	5.04E-04	7.77E-04	1.25	0.321928095	
BP1026b	11964	iolD protein	4319	4216	3599	2	4210	4682	3966	2	1.22E-04	2.01E-04	1	0	
BP1026b	11965	hypothetical protein	7191	2989	4205	5	6504	6275	8039	7	0.067452096	0.079540597	1.4	0.485426827	
BP1026b	11966	iolB protein	16047	15670	16119	19	13814	12472	14153	16	6.48E-12	2.74E-11	0.842105263	-0.247927513	
BP1026b	11967	Branched-chain amino acid transport ATP-bindingprotein LivF	9064	2069	3866	7	6974	8990	13335	13	0.53235276	0.558288576	1.857142857	0.893084796	
BP1026b	11968	ABC-transporter	75876	44373	51912	24	58852	63048	67970	28	7.50E-26	1.45E-05	1.083333333	-0.15477237	
BP1026b	11969	branched amino acid transport system, membrane protein	12837	13074	12884	13	10622	10775	8905	10	4.77E-15	9.20E-15	0.769207692	-0.378511623	
BP1026b	11970	thioesterase family protein	31903	23323	24458	50	16543	17422	16596	31	3.14E-25	5.92E-24	0.62	-0.689659879	
BP1026b	11971	alcohol dehydrogenase	132620	69254	82704	82	101390	110898	132758	100	4.46E-05	7.80E-05	1.219512195	0.286304185	
BP1026b	11972	hypothetical protein	44675	32297	33718	109	31070	31748	27333	89	6.44E-15	3.87E-14	0.816531761	-0.292450894	
BP1026b	11973	MutT/NUDIX NTP pyrophosphatase	81466	59588	67464	125	62265	64851	63112	114	1.38E-10	4.94E-10	0.912	-0.13289427	
BP1026b	11974	hypothetical protein	12004	13003	12673	18	8238	8134	7662	11	2.19E-25	4.22E-24	0.611111111	-0.710493383	
BP1026b	11975	hypothetical protein	43311	31793	32508	23	68318	69382	73305	45	0.055662885	0.066642261	1.956521739	0.96829114	
BP1026b	11976	major facilitator superfamily permease	9023	6214	6214	3	6597	6509	6214	3	1.59E-07	1.59E-07	1	0	
BP1026b	11977	hypothetical protein	4747	4672	4406	4	5529	6570	6026	6	0.013254719	0.017179301	1.5	0.584962501	
BP1026b	11978	alanine tRNA synthetase	471126	386048	410797	161	596260	623761	631912	235	0.00588096	0.00794272	1.459627329	0.546000608	
BP1026b	11979	CAI/B/BAIF family protein	117005	83138	94576	80	96062	98278	98547	79	7.32E-09	2.11E-08	0.9875	-0.018147347	
BP1026b	11981	lipoprotein	5477	6751	7110	26	4203	3540	4421	16	1.16E-19	1.24E-18	0.615384615	-0.700439718	
BP1026b	11980	glutaminyl-tRNA synthetase	378316	448122	441438	247	400220	404377	373094	229	4.09E-13	9.98E-12	0.927125506	-0.109163443	
BP1026b	11982	NUDIX family hydrolase	66645	17490	28192	77	73358	77772	86669	164	0.006566828	0.00882149	2.12987013	1.090765464	
BP1026b	11983	hypothetical protein	170711	11973	134724	364	12362	19612	25129	53	0.42385147	0.451303095	1.46458524	0.550197083	
BP1026b	11984	Beta-hexosaminidase	52323	37592	43206	21	54922	56978	60023	28	0.00414205	0.005692365	1.333333333	-0.415037499	
BP1026b	11985	hypothetical protein	31617	40931	37108	46	27400	27529	28143	35	2.09E-17	1.69E-16	0.760869565	-0.394278939	
BP1026b	11986	cytochrome c peroxidase	2799	4137	4213	2	2424	3043	2722	1	1.62E-15	1.05E-14	0.5	-1	
BP1026b	11987	acid phosphatase	9277	9137	10851	6	9306	10641	9792	6	8.85E-07	1.93E-06	1	0	
BP1026b	11988	trans-2-enoyl-CoA reductase	24298	20584	25854	19	20882	21103	22860	18	5.88E-10	1.95E-09	0.97364821	-0.078002512	
BP1026b	11989	HivD family secretion protein	890	971	815	0	1708	1186	1022	1	0.991246558	0.993149042	#DIV/0!	#DIV/0!	
BP1026b	11990	EmrL/QueA family drug resistance transporter	2471	32842	29085	1	1	0.00621383	4203	3724	0.00621383	4203	3724	2	1
BP1026b	11991	hypothetical protein	4670	2437	3192	2	4370	4681	5033	2	0.085891958	0.099702145	0	0	
BP1026b	11992	DNA-binding response regulator	6914	9044	10052	13	8909	7935	8631	13	1.55E-07	3.75E-07	1	0	
BP1026b	11993	sensor histidine kinase/response regulator	9300	9175	8855	4	8529	10004	10151	4	4.85E-06	9.56E-06	1	0	
BP1026b	11994	type 1 pilin protein CusE	10159	8679	10343	10	9528	9187	10937	10	0.90E-07	1.98E-06	1	0	
BP1026b	11995	fimbriae protein	5095	3782	3070	1	5184	4779	5231	2	0.010614294	0.01396961	2	1	
BP1026b	11996	type 1 pilus usher pathway chaperone CusC	824	486	539	0	285	406	634	0	6.09E-08	1.56E-07	#DIV/0!	#DIV/0!	
BP1026b	11997	hypothetical protein	773	497	528	0	443	583	589	0	0.047172977	0.057032462	0.057032462	0.057032462	
BP1026b	11998	hypothetical protein	14400	9841	13155	22	9708	11005	15562	21	5.86E-08	1.51E-07	0.954545455	-0.067114196	
BP1026b	11999	hypothetical protein	694	1153	1032	1	1247	599	912	1	3.23E-04	5.09E-04	1	0	
BP1026b	12000	LysR family transcriptional regulator	100541	106488	101274	114	109539	110849	101126	119	2.78E-08	7.45E-08	1.043859649	0.061927749	
BP1026b	12001	major facilitator family transporter	629769	612237	622492	493	598886	609524	586405	474	8.66E-12	2.89E-11	0.961460446	-0.056700587	
BP1026b	12002	hydrolase	153784	164239	158177	161	138285	145473	135449	142	1.65E-10	1.34E-10	0.881987578	-0.181169759	
BP1026b	12003	predicted RNA	36691	7003	12522	398	23145	32991	34859	645	0.222529621	0.297408632	1.626003051	0.69653073	
BP1026b	12004	H-NS histone family protein	52067	67831	67031	222	46033	47929	44792	165	9.97E-26	3.20E-24	0.743243243	-0.280930562	
BP1026b	12004	Manganese transport protein	16530	19678	19680	60	15075	15447	14338	40	1.39E-13	7.14E-13	0.8	-0.321928095	
BP1026b	12005	hypothetical protein	22614	24616	23426	17	22204	23386	20002	16	1.28E-09	4.10E-09	0.941176471	-0.087462841	
BP1026b	12006	hypothetical protein	33641	57213	49238	45	34248	32404	33393	32	5.73E-24	9.63E-23	0.711111111	-0.491853096	
BP1026b	12008	Transposase mutator family	10482	16528	15655	24	10735	11416	11605	19	1.69E-14	9.66E-14	0.791666667	-0.337034987	
BP1026b	12009	hypothetical protein	5958	10445	7407	26	5601	5539	5250	18	3.51E-17	2.77E-16	0.692307692	-0.530514717	
BP1026b	12011	hypothetical protein	930	2859	1998	6	1297	1890	1622	5	1.49E-09	4.68E-09	0.833333333	-0.26304406	
BP1026b	12012	hypothetical protein	1314	2273	1770	9	1218	1546	1374	7	3.05E-10	4.78E-10	0.777777778	-0.625700729	
BP1026b	12013	transposase	596	803	704	7	276	556	397	4	1.86E-13	3.38E-13	0.571428571	-0.807354922	
BP1026b	12014	integrase core subunit	9074	16783	13054	73	14804	12928	11341	73	5.15E-07	1.16E-06	1	0	
BP1026b	12015	transposase	18947	29633	25523	98	15931	16201	15193	62	1.11E-24	2.00E-23	0.632653061	-0.660513534	
BP1026b	12016	hypothetical protein	58872	103857	90020	91	51623	46448	49473	53	3.19E-48	3.07E-46	0.582417582	-0.779874186	
BP1026b	12017	hypothetical protein	105776	158763	145599	48	108582	104843	98599	36	1.26E-21	1.67E-20	0.75	-0.415037499	
BP1026b	12018	hypothetical protein	31565	45325	44237	57	28810	28042	24216	38	2.16E-24	3.79E-23	0.666666667	-0.584962501	
BP1026b	12019	Rhs element Vgr protein	63361	57477	57967	20	52383	56914	6614	20	1.61E-10	3.67E-10	0	0	
BP1026b	12020	hypothetical protein	2752	3587	3587	10	2663	2282	2560	4	1.01E-14	8.89E-14	0.8	-0.321928095	
BP1026b	12021	hypothetical protein	13796	13540	13727	51	13330	11394	10582	44	2.17E-11	8.59E-11	0.862745098	-0.212993723	
BP1026b	12022	putative lipoprotein	45950	79146	65873	94	46460	48961	41334	67	1.46E-28	3.69E-27	0.712765957	-0.488499661	
BP1026b	12023	putative lipoprotein	18352	29633	25892	110	20260	20307	17563	87	4.00E-15	2.46E-14	0.790909091	-0.338416218	
BP1026b	12024	putative lipoprotein	81258	137797	115168	226	81646	83779	84119	169	1.19E-19	1.28E-18	0.747787611	-0.419299526	
BP1026b	12025	hypothetical protein	263791	295917	282722	84	250412	255988	269545	77	6.60E-09	1.93E-08	0.916666667	-0.125530882	
BP1026b	12026	hypothetical protein	137119	215368	204920	120	134322	143802	138616	92	1.63E-27	3.83E-26	0.766666667	-0.38332864	
BP1026b	12027	hypothetical protein	400180	429918	401801	134	429918	429918	401801	134	2.61E-2				

BP1026b_12078	hypothetical protein	15313	25150	23731	60	8581	9295	9651	26	1.20E-66	2.69E-64	0.433333333	-1.206450877
BP1026b_12079	DNA-damage-inducible protein F	33033	22696	24200	19	22142	25643	23929	17	1.37E-10	4.90E-10	0.894736842	-0.160464672
BP1026b_12080	lipoprotein	6225	4910	5577	29	3736	5291	6931	27	7.26E-07	1.61E-06	0.931034483	-0.103093493
BP1026b_12081	hypothetical protein	10833	14653	12055	73	16336	12953	88	0.00133879	0.000183139	0.205470606	0.26604706	
BP1026b_12082	hypothetical protein	458531	405661	434396	528	354405	353702	340424	426	2.65E-17	2.12E-16	0.806818182	-0.309684499
BP1026b_12083	phosphohistidine phosphatase SixA	228260	183911	188303	436	210553	212465	191638	446	2.50E-07	5.90E-07	1.02293578	0.032715575
BP1026b_12084	Pro tRNA	551	971	790	10	768	617	457	7	1.01E-06	2.19E-06	0.7	-0.514573173
BP1026b_12085	putative bacteriophage protein	14634	25118	23890	38	22941	23231	21070	41	2.09E-06	4.33E-06	1.078947368	0.109624491
BP1026b_12086	hypothetical protein	22673	39677	36192	71	27977	27071	25293	57	5.36E-14	2.88E-13	0.802816901	-0.16857105
BP1026b_12087	hypothetical protein	223873	368338	326601	280	176536	164497	161195	153	1.11E-61	1.74E-59	0.546428571	-0.871895174
BP1026b_12088	putative bacteriophage protein gp29	139954	231545	199761	259	101308	95616	88841	129	2.02E-62	3.34E-60	0.498660498	1.005581032
BP1026b_12089	putative bacteriophage protein gp28	199992	347462	292591	499	135690	129232	129232	234	3.91E-95	8.88E-92	0.468937876	-1.09231286
BP1026b_12090	hypothetical protein	273334	429432	371517	457	270853	262064	247403	332	9.48E-17	7.09E-16	0.726477024	-0.461010924
BP1026b_12091	Site-specific DNA methylase	3770	6724	5671	6	3721	3717	3148	4	2.40E-18	2.18E-17	0.666666667	-0.584962501
BP1026b_12092	bacteriophage lysis protein	5513	7307	6872	12	5883	5577	4555	9	8.35E-11	3.08E-10	0.75	-0.415037499
BP1026b_12093	Glycoside hydrolase family protein gp24	1498	935	1130	2	790	1060	871	1	2.34E-09	7.23E-09	0.5	-1
BP1026b_12094	putative class II holin gp23	399	263	615	1	345	207	318	1	3.38E-06	6.80E-06	1	0
BP1026b_12095	hypothetical protein	2445	3224	3140	3	2738	2688	2978	3	3.85E-07	8.88E-07	0.8	0
BP1026b_12096	hypothetical protein	440	387	342	1	249	286	211	0	8.24E-07	8.1E-06	0	#NUM!
BP1026b_12097	gp20	5303	6578	5795	1	4149	5177	5270	1	5.81E-10	1.93E-09	1	0
BP1026b_12098	Phage tail assembly protein I	157	300	377	0	97	87	157	0	1.39E-17	1.15E-16	#DIV/0!	#DIV/0!
BP1026b_12099	Phage tail assembly protein	412	464	521	0	551	427	239	0	5.11E-04	7.87E-04	#DIV/0!	#DIV/0!
BP1026b_12100	phage minor tail protein	2523	5035	3805	5	3312	2870	2636	4	2.85E-13	1.40E-12	0.8	-0.321928095
BP1026b_12101	Phage-related tail fiber protein	7444	13841	11752	7	7291	7519	6594	5	1.44E-23	2.35E-22	0.714285714	-0.485426827
BP1026b_12102	phage minor tail protein	649	628	501	1	818	653	588	2	0.489117724	0.51639907	2	1
BP1026b_12103	hypothetical protein	11718	13633	12772	3	15101	13701	14406	3	1.10E-04	0.45E-07	0	-0.321928095
BP1026b_12104	hypothetical protein	2136	3468	2652	9	2903	2470	2303	8	1.06E-07	2.63E-07	0.888888889	-0.169925001
BP1026b_12105	Phage tail assembly chaperone	2055	2764	1789	4	2532	1582	2331	4	1.15E-06	2.46E-06	1	0
BP1026b_12106	gp11	1418	1853	2090	3	1482	1455	1363	3	9.08E-10	2.95E-09	1	0
BP1026b_12107	putative bacteriophage protein gp10	1020	1272	926	3	1343	871	1060	3	0.001804127	0.002597346	1	0
BP1026b_12108	HK97 family phage protein	3735	5334	4245	10	3890	3750	2734	8	6.48E-12	2.74E-11	0.8	-0.321928095
BP1026b_12109	putative bacteriophage protein gp8	725	2047	1340	9	1366	865	1063	7	1.94E-08	5.31E-08	0.777777778	-0.36257079
BP1026b_12110	gp7	1163	1633	2030	5	1760	1129	2062	5	2.76E-07	6.88E-07	0.8	-0.321928095
BP1026b_12111	Phage major capsid protein	42342	67463	62862	45	51888	50709	45068	39	4.91E-17	8.30E-16	0.866666667	-0.206450877
BP1026b_12112	gp4	4034	5365	5131	8	5274	4156	4162	8	7.39E-07	1.63E-06	1	0
BP1026b_12113	Phage portal protein	11748	20649	18817	12	9251	9371	9681	7	5.91E-36	2.87E-34	0.583333333	-0.777607579
BP1026b_12114	Phage terminase large subunit	1063	2022	2165	1	1730	1836	1222	0	4.84E-07	1.23E-06	0	#NUM!
BP1026b_12115	Phage terminase small subunit	206	311	328	1	253	89	142	1	3.24E-08	8.60E-08	1	0
BP1026b_12116	putative bacteriophage protein gp82	941	712	812	2	793	842	842	1	1.03E-05	1.96E-05	0.5	-1
BP1026b_12117	Phage protein	37220	63000	60141	255	59099	56906	53308	269	9.80E-08	4.54E-07	1.054901961	0.077108926
BP1026b_12118	Phage-related transcriptional regulator	39447	60646	50878	129	68073	66260	61630	168	0.017149702	0.021950497	1.302325581	0.381090167
BP1026b_12119	gp78	91014	147547	131955	89	86191	82989	81734	60	7.91E-26	1.60E-24	0.674157203	-0.568842835
BP1026b_12120	gp77	7889	12503	12397	16	13251	11795	10136	18	7.97E-06	1.54E-05	1.125	0.169925001
BP1026b_12121	gp76	942	1615	1338	6	1042	585	508	3	8.78E-22	1.18E-20	0.5	-1
BP1026b_12122	gp75	966	1717	1318	4	1094	1114	981	3	1.58E-08	4.38E-08	0.75	-0.415037499
BP1026b_12124	gp74	691	1039	972	2	494	976	754	1	1.21E-06	2.57E-06	0.5	-1
BP1026b_12125	putative bacteriophage protein gp73	1030	1430	1092	2	982	668	1040	1	9.02E-04	0.0013425	1	0
BP1026b_12123	hypothetical protein	529	299	604	2	478	336	600	2	0.043362311	0.052629629	#DIV/0!	#DIV/0!
BP1026b_12126	gp72	343	614	566	0	368	485	491	0	4.88E-04	7.53E-04	#DIV/0!	#DIV/0!
BP1026b_12127	gp60	631	1078	1182	0	475	586	651	0	1.66E-15	1.07E-14	#DIV/0!	#DIV/0!
BP1026b_12128	gp69	409	291	320	1	336	524	412	1	0.548240972	0.573798069	1	0
BP1026b_12129	gp58	1212	1727	1449	1	1695	1434	1197	1	6.53E-05	1.12E-04	1	0
BP1026b_12130	gp67	2281	2599	3075	1	2438	2639	2350	1	1.05E-07	1.61E-07	1	0
BP1026b_12131	hypothetical protein	493	912	937	1	941	974	787	2	0.048998381	0.050860401	2	1
BP1026b_12132	gp65	477	613	641	1	611	805	685	0	0.002003851	0.002259904	1	0
BP1026b_12133	gp64	65561	111723	102012	425	45554	43962	38828	195	9.19E-88	1.84E-85	0.458823529	-1.123988717
BP1026b_12134	putative bacteriophage protein	31254	53108	46364	238	24975	23205	20168	124	9.80E-45	7.58E-43	0.521008403	-0.940621453
BP1026b_12135	putative bacteriophage protein gp62	9490	13625	13399	38	11706	11600	10202	35	1.51E-09	4.77E-09	0.921052632	-0.118644496
BP1026b_12136	putative bacteriophage protein	38252	69717	57079	247	36491	35463	32251	156	7.41E-35	3.37E-33	0.631578947	-0.662650103
BP1026b_12137	gp59	25777	38401	37918	26	21792	19884	21099	16	5.80E-29	1.55E-27	0.61584615	-0.700439718
BP1026b_12138	Glycine cleavage system transcriptional activator	13687	14543	13581	23	16634	17225	16343	13	9.20E-30	0.0013425	0.61584615	-0.700439718
predicted RNA		12079	17338	15266	531	21366	20532	16747	698	0.006635065	0.00890471	1.314500942	-0.394515175
BP1026b_12139	bacteriophage protein Gp49	388	320	154	1	289	352	357	1	0.42639934	0.453674328	#DIV/0!	#DIV/0!
BP1026b_12140	bacteriophage protein	608	866	670	2	392	367	313	1	3.99E-14	3.52E-17	0.5	-1
BP1026b_12141	gp54	863	1060	836	5	499	551	625	3	2.47E-14	1.38E-13	0.6	-0.736965594
BP1026b_12142	hypothetical protein	6639	8926	7256	16	5920	6699	4421	12	4.30E-14	2.34E-13	0.75	-0.415037499
BP1026b_12144	bacteriophage protein Gp46	13072	19808	15175	62	13041	11505	11777	47	1.98E-16	1.42E-15	0.758066416	-0.399607459
BP1026b_12143	gp52	13731	21061	17301	79	13724	12343	11403	59	1.81E-16	8.74E-16	0.621137699	-0.321928095
BP1026b_12145	bacteriophage protein	28832	47085	43397	67	22245	21347	21843	36	2.78E-39	1.61E-37	0.537313433	-0.896164189
BP1026b_12146	bacteriophage protein Gp44	908	1265	992	6	1225	1290	951	7	0.061162151	0.072712035	1.166666667	0.222392421
BP1026b_12148	gp47	5759	9665	9562	11	7086	7791	5977	9	1.11E-11	4.55E-11	0.818181818	-0.289506617
BP1026b_12149	gp46	1807	1561	1639	2	1308	1392	1471	2	2.08E-08	5.67E-08	1	0
BP1026b_12150	gp45	1757	2539	1905	7	1961	1570	1620	5	5.69E-10	1.89E-09	0.714285714	-0.485426827
BP1026b_12151	gp44	1404	2140	1963	6	1476	1652	1254	5	3.85E-10	1.30E-09	0.833333333	-0.263034406
BP1026b_12152	gp43	12319	15251	14396	7	14741	13958	12857	7	2.63E-06	5.39E-06	1	0
BP1026b_12153	gp42	2427	4632	3651	13	2332	3015	2619	11	1.29E-09	4.13E-09	0.846153846	-0.24100081
BP1026b_12154	gp40	2476	2544	2305	14	2284	1473	1924	11	8.07E-13	3.78E-12	0.785714286	-0.347923303
BP1026b_12155	gp39	2758	4531	3873	10	3819	3158	2739	9	4.57E-09	1.36E-08	0.9	-0.152003093
BP1026b_12156	Bacteriophage protein gp37	12021	16674	13643	13	10936	10267	8059	9	2.05E-20	2.35E-19	0.692307692	-0.530514717
BP1026b_12157	hypothetical protein	15210	18776	16422	68	10208	11835	10347	43	3.00E-25	5.69E-24	0.632352941	-0.661198087
BP1026b_12158	gp36-related protein	15178	22496	21322	96	13416	12091	10984	57	1.26E-29	3.62E-28	0.59375	-0.752072487
BP1026b_12159	putative bacteriophage protein	81641	122941	111400	468	69996	71681	60079	298	1.65E-28	4.15E-27	0.636751277	-

BP1026b	12205	triphosphoribosyl-dephospho-CoA synthase	4662	2002	2834	4	3426	3339	3771	4	6.93E-04	0.001050705	1	0
BP1026b	12206	phosphoribosyl-dephospho-CoA transferase	11356	9064	9556	10	9526	8570	8944	9	1.15E-09	3.69E-09	0.9	-0.152003093
BP1026b	12207	malonate decarboxylase subunit gamma	16655	15168	14530	21	17526	17694	17591	24	9.25E-05	5.55E-04	1.142857143	0.192645078
BP1026b	12208	malonate decarboxylase subunit beta	20493	6305	8851	12	15987	18723	23504	20	0.57082164	0.59124006	1.666666667	0.736965504
BP1026b	12209	malonate decarboxylase subunit delta	5617	3802	3927	13	4919	5885	5596	17	0.00376653	0.005341697	1.307692308	0.387023123
BP1026b	12210	malonate decarboxylase alpha-subunit	61560	52112	56351	34	54733	52047	50242	31	3.44E-13	1.68E-12	0.911764706	-0.133266531
BP1026b	12211	malonate transporter, M subunit	2158	820	752	1	1394	1231	1526	1	0.005570418	0.007544453	1	0
BP1026b	12212	malonate transporter, L subunit	1152	859	744	2	1037	1009	956	2	0.013796047	0.017843989	1	0
BP1026b	12213	LysR family transcriptional regulator	8785	5440	5670	7	5098	6892	8047	7	1.78E-06	3.72E-06	1	0
BP1026b	12214	3-hydroxyacyl-CoA dehydrogenase	50977	41966	41552	48	48836	49019	48098	52	1.45E-07	3.54E-07	1.083333333	0.118477217
BP1026b	12215	phosphoenolpyruvate carboxykinase	504234	42670	438046	244	532366	564723	563094	296	3.04E-06	5.51E-06	1.231147574	0.278716028
BP1026b	12217	ferredoxin	127	168	223	0	206	231	167	0	0.555982319	0.581608758	#DIV/0!	#DIV/0!
BP1026b	12216	HSP20 family protein	352866	453519	441589	949	457353	458842	461058	1048	9.47E-09	2.70E-08	1.104320337	0.143158725
BP1026b	12218	heat shock protein	165787	205908	196059	470	204121	208618	248144	547	0.001792449	0.002581721	1.163829787	0.218880076
BP1026b	12219	GntR family transcriptional regulator	81669	41999	53174	39	73158	80335	85180	53	0.027254117	0.033960571	1.358974359	0.442518236
BP1026b	12220	hypothetical protein	6181	6870	7457	36	9456	7487	6408	41	1.13E-04	1.87E-04	1.138888889	0.187627003
BP1026b	12221	nitrite/sulfite reductase family protein	28956	24415	24253	14	27116	27140	29806	15	4.18E-06	8.32E-06	1.071428571	0.099535674
BP1026b	12222	hypothetical protein	5679	4004	4212	11	5964	9446	1274	14	0.012574221	0.016340053	1.272727273	0.349925303
BP1026b	12223	hypothetical protein	13630	15594	14020	10	12580	13260	12722	9	3.71E-10	1.04E-09	1.0	-0.321200393
BP1026b	12224	short chain dehydrogenase	13033	13974	13056	17	10257	11349	12230	14	4.72E-12	2.03E-11	0.825392412	-0.280107919
BP1026b	12225	LysR family transcriptional regulator	15144	6811	9816	11	9440	10556	11295	11	1.26E-07	3.11E-07	1	0
BP1026b	12226	hypothetical protein	4617	2093	2299	4	3101	3433	4957	5	0.032142163	0.039682554	1.25	0.321928095
BP1026b	12227	dioxygenase	18002	7516	7637	8	13748	14143	16339	11	0.015480651	0.019003694	1.375	0.459431619
BP1026b	12228	glucosamine-fructose-6-phosphate aminotransferase	49048	32699	35461	20	44276	46152	47681	23	1.62E-05	2.99E-05	1.15	0.201633861
BP1026b	12229	AscC family transcriptional regulator	40701	44552	42577	86	47723	49624	48302	98	2.77E-06	5.65E-06	1.139534884	0.158453889
BP1026b	12230	GntR family transcriptional regulator	22164	1358	18020	12	28730	32472	31401	10	0.295649697	0.321240012	1.583333333	0.662665039
BP1026b	12231	transcriptional regulator PaaB-like protein	4969	5456	4774	7	3917	3416	5195	6	1.50E-09	4.73E-09	0.857142857	-0.22392421
BP1026b	12232	hypothetical protein	3949	1708	1516	3	3991	3459	4386	5	0.927848965	0.933848236	1.666666667	0.666665594
BP1026b	12233	hypothetical protein	23363	26689	24566	41	31409	32281	29681	51	6.27E-04	9.54E-04	1.243902493	0.314873337
BP1026b	12234	hypothetical protein	270	692	945	3	469	559	456	2	1.47E-06	3.11E-06	0.666666667	-0.584962501
BP1026b	12235	diguanylate cyclase	161723	178368	177434	126	167407	166223	153584	118	1.03E-13	5.32E-13	0.936507797	-0.094636874
BP1026b	12236	hypothetical protein	93523	105477	107405	88	83753	87197	86760	74	5.13E-14	2.76E-13	0.940090901	-0.249978253
BP1026b	12237	Ribose ABC transport system, permease protein RbsC	1921	1358	1325	5	1968	1451	1274	9	0.45E-04	1.04E-04	#DIV/0!	#DIV/0!
BP1026b	12241	LacI family transcriptional regulator	2026	1554	1970	1	2257	2007	2791	2	0.002573975	0.028434221	1	0
BP1026b	12240	ABC transporter substrate-binding protein	36118	52658	43037	44	55473	54049	47642	52	4.21E-05	7.37E-05	1.181818182	0.2410081
BP1026b	12242	ABC transporter permease	18972	17259	18703	22	18474	19074	19223	22	9.02E-07	1.97E-06	1	0
BP1026b	12243	hypothetical protein	186461	267425	259436	1165	187337	183011	166628	877	8.43E-26	1.70E-24	0.7527897	-0.409681207
BP1026b	12244	ABC transporter permease	10426	9997	10129	11	12254	12665	11707	13	7.09E-04	0.010731011	1.181818182	0.2410081
BP1026b	12245	ABC transporter ATP-binding protein	5463	3619	4115	4	5216	4809	6326	5	0.00470805	0.00647036	1.25	0.321928095
BP1026b	12246	Sar11 protein phosphatase family protein	10896	10896	10896	15	10896	20128	23262	23	0.26324758	0.26324758	1.333333333	0.61667136
BP1026b	12247	hypothetical protein	4010	2100	2782	7	2825	3299	3676	7	4.14E-04	6.44E-04	1	0
BP1026b	12248	hypothetical protein	3076	1649	2717	3	3856	3670	3759	4	0.524575272	0.550408627	1.333333333	0.415037499
BP1026b	12249	major facilitator family transporter	12470	7085	8571	7	10335	11465	10997	9	2.64E-04	4.20E-04	1.285714286	0.362570079
BP1026b	12250	integral membrane protein	29115	12139	13246	19	19927	25018	28969	26	0.012951706	0.016814401	1.368421053	0.452512205
BP1026b	12251	oxidoreductase, molybdopterin-binding protein	8859	8057	8609	10	8228	10031	9210	11	1.74E-05	3.21E-05	1.1	0.137503524
BP1026b	12252	hypothetical protein	2951	3173	3424	2	2839	2984	3638	2	4.11E-06	8.18E-06	1	0
BP1026b	12253	hypothetical protein	796	796	796	0	2813868	895	920	1082	0.4	0.45514340	#DIV/0!	#DIV/0!
BP1026b	12255	hypothetical protein	31537	49771	45581	138	35589	34520	31092	110	1.66E-17	1.36E-16	0.797101449	-0.32716743
BP1026b	12254	hypothetical protein	1057	1371	1169	2	1287	1514	1166	3	0.006450278	0.006666782	1.5	0.584962501
BP1026b	12256	thiamine biosynthesis protein ThiC	834227	1118322	1079426	523	942760	929945	912462	480	0.442955125	0.470283204	0.917782027	-0.123776541
BP1026b	12257	lipoprotein	15895	24848	21404	97	17650	16112	16550	78	3.26E-13	1.59E-12	0.804123711	-0.34510623
BP1026b	12258	hypothetical protein	999	878	820	3	548	495	710	2	5.08E-12	2.17E-11	0.666666667	-0.584962501
BP1026b	12259	DMT1 family permease	36966	19401	22046	28	22068	26921	31320	29	3.27E-07	7.63E-07	1.035714286	0.050626073
BP1026b	12260	EAL domain-containing protein	49417	38173	37154	28	397628	391960	30180	30	9.97E-08	1.46E-04	0.780476809	-0.874250545
BP1026b	12261	peptidyl-rRNA hydrolase domain-containing protein	45916	53166	53559	125	58683	52590	55340	137	6.74E-07	1.50E-06	1.096	0.132247798
BP1026b	12262	exodeoxyribonuclease V subunit alpha	107656	43977	49807	24	100000	109141	112216	39	0.301223092	0.326729255	1.625	0.004393718
BP1026b	12263	exodeoxyribonuclease V subunit beta	274026	242406	248342	66	285469	295278	313112	78	1.28E-04	2.10E-04	1.181818182	0.2410081
BP1026b	12264	Exodeoxyribonuclease V gamma chain	164331	87899	109326	36	144412	153023	163857	45	2.60E-04	4.14E-04	1.25	0.321928095
BP1026b	12265	hypothetical protein	96280	94193	92356	41	78662	75411	70100	33	1.98E-15	1.27E-14	0.804878049	-0.33157885
BP1026b	12266	amino acid permease	26874	23098	23410	17	26532	25235	29613	19	1.38E-05	2.57E-05	1.116747059	0.160464672
BP1026b	12267	hypothetical protein	24450	36071	36071	181	302983	169871	10906	16	1.66E-34	1.29E-04	0.563535433	-0.874250545
BP1026b	12268	ABC transporter substrate-binding protein	99812	17658	23779	25	39531	42954	48641	41	0.172992707	0.193401091	1.64	0.13695815
BP1026b	12269	ABC transporter permease	16948	9202	11407	7	16389	17555	20003	10	0.069163352	0.08139005	1.428571429	0.514573173
BP1026b	12270	ABC transporter ATP-binding protein	23682	18719	22365	28	28311	27673	25238	35	0.001375821	0.002006552	1.25	0.321928095
BP1026b	12271	AscC family transcriptional regulator	44900	52819	51319	96	49096	52970	56642	102	5.44E-08	1.41E-07	1.0625	0.087462841
BP1026b	12272	cysteine dioxygenase type I family protein	3799	1922	2435	4	2791	3025	4099	5	0.009340418	0.012322742	1.25	0.321928095
BP1026b	12273	NAD-dependent epimerase/dehydratase family protein	18903	15949	17482	27	24022	25772	31657	42	0.137367302	0.155770414	1.555555556	0.637429921
BP1026b	12274	Rv2 family protein	29897	28778	27747	62	34027	31254	32581	70	9.27E-06	1.97E-05	1.129032258	0.17508667
BP1026b	12275	hypothetical protein	82	1614	1147	2	922	1260	1147	0	0.062834416	0.074530351	1	0
BP1026b	12276	exported alkaline phosphatase	5207	5298	5231	2	5525	5374	5570	2	2.32E-07	5.49E-07	1	0
BP1026b	12277	hypothetical protein	258	434	188	2	588	730	359	5	0.009814011	0.012931209	2.5	1.321928095
BP1026b	12278	IcIR family transcriptional regulator	26469	24236	25127	30	51663	49149	48103	59	0.579008699	0.603178196	1.966666667	0.975752454
BP1026b	12279	HlyD family secretion protein	37319	35997	31538	26	32419	33871	34574	25	8.13E-10	2.65E-09	0.961538462	-0.056853528
BP1026b	12280	AcrB/AcrD/AcrF family protein	126381	12943	126956	40	112090	116875	106940	40	1.23E-14	7.10E-14	0.875	-0.192645078
BP1026b	12281	multidrug resistance protein indC	108704	99642	96587	30	119578	116600	116553	35	4.21E-06	8.36E-06	1.166666667	0.325164517
BP1026b	12282	NAD-dependent epimerase/dehydratase family protein</												

BP1026b	12330	NADH-ubiquinone oxidoreductase subunit N	438012	453341	439142	304	505913	505759	454792	335	8.41E-09	2.41E-08	1.101973684	0.1400897722
BP1026b	12331	NADH-ubiquinone oxidoreductase subunit M	552630	737056	657383	435	609024	599224	532373	389	1.26E-14	7.24E-14	0.894252874	-0.161245246
BP1026b	12332	NADH-ubiquinone oxidoreductase subunit L	775936	1011740	954757	448	890734	860043	805560	417	0.405787645	0.433541499	0.930803571	-0.103451349
BP1026b	12333	NADH-ubiquinone oxidoreductase subunit K	146318	215422	171542	647	173715	169076	160483	559	1.47E-17	3.80E-16	0.862442294	-0.21350059
BP1026b	12334	NADH-ubiquinone oxidoreductase subunit J	213296	192916	214800	315	249175	249222	229161	374	0.005447843	0.007394429	1.187301587	0.247686442
BP1026b	12335	NADH-ubiquinone oxidoreductase subunit I	244161	331116	309608	603	286975	279291	262029	564	5.49E-09	1.61E-08	0.933233383	-0.09646284
BP1026b	12336	NADH-ubiquinone oxidoreductase subunit H	359552	492685	459762	610	421863	408251	375369	377	6.88E-14	3.65E-13	0.919512195	-0.121059386
BP1026b	12337	NADH-ubiquinone oxidoreductase subunit G	647630	715544	686530	292	826053	826879	797946	350	0.08499172	0.098626923	1.198630137	0.261386553
BP1026b	12338	NADH-ubiquinone oxidoreductase subunit F	455436	528972	542983	388	513254	528520	494421	390	2.74E-11	1.07E-10	1.005154639	0.007417472
BP1026b	12339	NADH-ubiquinone oxidoreductase subunit E	114327	150642	138593	265	113031	110203	100765	213	3.17E-19	2.30E-18	0.803775885	-0.315138929
BP1026b	12340	NADH-ubiquinone oxidoreductase subunit D	598232	749001	685542	336	729406	713399	663923	559	0.986502443	0.98119931	0.942010448	0.066615282
BP1026b	12341	NADH-ubiquinone oxidoreductase subunit C	115211	151810	142434	236	100497	106953	103423	171	1.12E-21	1.50E-20	0.756637168	-0.402326448
BP1026b	12342	NADH-ubiquinone oxidoreductase subunit B	138768	172137	164919	303	119902	121636	109045	223	8.04E-27	1.80E-25	0.735973597	-0.442274084
BP1026b	12343	NADH-ubiquinone oxidoreductase chain A	64446	110937	94629	250	91155	84908	81656	238	1.82E-09	5.68E-09	0.952	-0.070966521
BP1026b	12344	Leu tRNA	34722	59196	49929	564	55613	58969	52314	654	2.33E-05	4.22E-05	1.159574468	0.213595473
BP1026b	12345	preprotein translocase subunit SecEg	39813	37377	40645	103	45775	43754	40705	114	5.00E-07	1.13E-06	1.106796117	0.146389487
BP1026b	12346	triosephosphate isomerase	116443	94287	101247	129	105076	110354	122461	140	1.28E-07	1.14E-07	1.085271318	0.118055762
BP1026b	12347	oxidoreductase, zinc-binding dehydrogenase family protein	112729	149518	131266	85	108404	113116	134029	117	0.005469114	0.007445606	1.376470588	-0.066935983
BP1026b	12348	polynucleotide phosphorylase/polyadenylase	595281	707773	690621	310	821401	833964	825593	386	0.057441904	0.06865409	1.24516129	0.133126332
BP1026b	12349	30S ribosomal protein S15	495143	605349	635071	1662	590672	582980	572019	1672	1.15E-10	4.16E-10	1.006016847	0.008654465
BP1026b	12350	branched-chain amino acid ABC transporter periplasmic protein	23645	17141	18740	15	20347	22924	25411	17	9.45E-05	1.58E-04	1.133333333	0.180572246
BP1026b	12351	lipoprotein	48105	58352	58658	109	35669	35051	35281	70	7.89E-34	3.27E-32	0.642201835	-0.638901308
BP1026b	12352	hypothetical protein	796	1614	934	8	1283	1274	782	8	9.60E-04	0.00142535	1	0
BP1026b	12353	carbonic anhydrase	7107	6113	5984	10	4263	5553	7457	9	1.92E-08	5.26E-08	0.9	-0.152003093
BP1026b	12354	sulfate transporter family protein	160395	176218	174513	110	175287	171027	164095	119	1.11E-10	4.01E-10	0.990909091	-0.031375389
BP1026b	12355	phosphoenolpyruvate synthase	2312178	231684	231684	243	347043	346811	346811	221	1.15E-09	1.86E-09	0.747352496	-0.171766348
BP1026b	12356	CDP-diacetylglucosyl-serine O-phosphatidyltransferase	177203	151818	147869	182	139443	148068	141186	163	1.71E-16	2.4E-15	0.895604396	-0.159066286
BP1026b	12357	phosphatidylserine decarboxylase	246009	236846	242910	371	152141	152938	145401	230	1.21E-46	6.19E-46	0.619946692	-0.696785326
BP1026b	12358	ketol-acid reductoisomerase	148016	190567	176934	168	171200	171838	167702	167	5.21E-11	1.96E-10	0.994047619	-0.00861313
BP1026b	12359	acetylacetate synthase 3 regulatory subunit	43191	71484	61815	119	54537	53568	53356	109	2.35E-13	1.17E-12	0.915966387	-0.126633439
BP1026b	12360	acetylacetate synthase 3 catalytic subunit	323510	433551	407202	220	328597	326785	301944	180	1.15E-14	6.64E-14	0.818181818	-0.289506617
BP1026b	12361	RNA polymerase factor sigma-70	40834	453259	45435	78	35686	34426	30558	59	8.07E-20	8.78E-19	0.756410256	-0.420175077
BP1026b	12362	hypothetical protein	10795	15940	14992	23	8204	7383	6441	18	9.02E-34	2.69E-32	1.049381574	-0.830074999
BP1026b	12363	hypothetical protein	29591	36639	36955	45	24927	25650	21835	31	9.62E-21	1.15E-19	0.688888889	-0.537656786
BP1026b	12364	RDD family protein	3492	3124	2642	6	3330	2983	3171	6	1.91E-05	3.51E-05	1	0
BP1026b	12365	calcineurin-like phosphoesterase	1285	1767	1718	1	2233	2134	1681	2	0.033651651	0.041421486	2	1
BP1026b	12366	glycoside hydrolase family protein	28612	11754	13727	17	35430	39735	44952	38	0.139877813	0.158415227	2.235294118	1.160464672
BP1026b	12367	diacylglycerol kinase	8181	6811	6954	13	10357	10845	9771	18	0.063118674	0.074839178	1.384615385	0.469485283
BP1026b	12368	TerF family transcriptional regulator	366356	555395	506192	661	355809	359607	353178	494	1.28E-21	1.69E-20	0.747352496	-0.420139323
BP1026b	12369	hypothetical protein	124101	157249	152019	243	161583	150686	138051	221	1.15E-09	1.86E-09	0.747352496	-0.171766348
BP1026b	12370	glucose-1-dehydrogenase	8994	2956	4477	7	7094	9051	7677	10	0.064312592	0.070667613	1.428571429	0.154573173
BP1026b	12371	hypothetical protein	67643	64196	59530	33	71442	75701	70765	38	9.87E-05	1.65E-04	1.151515151	0.203333394
BP1026b	12372	major facilitator family transporter	13044	11321	12990	9	10111	12533	9023	8	6.19E-12	2.62E-11	0.888888889	-0.169925001
BP1026b	12373	amidase	31789	24588	26579	19	26780	25888	29137	19	3.98E-08	1.05E-07	1	0
BP1026b	12374	hypothetical protein	27164	18450	24399	36	30420	30176	30900	47	0.002788782	0.003911539	1.305555556	0.38466385
BP1026b	12375	alanine tRNA synthetase	64157	44368	53489	73	52254	55769	56784	75	3.78E-09	1.14E-08	0.10779726	-0.584963912
BP1026b	12376	hypothetical protein	9468	4948	4901	16	49145	66148	64545	10	3.43E-05	3.61E-04	0.88755102	0.093109406
BP1026b	12377	permease	66107	24351	32940	15	68452	79962	84789	29	0.137520008	0.155829473	1.933333333	0.9510904
BP1026b	12378	type IV secretory pathway protein	108299	76060	105574	156	162919	157996	176274	268	0.789797541	0.805317627	1.71794878	0.80686972
BP1026b	12379	quaternary ammonium compound-resistance protein	22254	25922	21559	72	23951	24415	19506	70	2.52E-08	6.79E-08	0.972222222	-0.40641984
BP1026b	12380	hypothetical protein	127471	86351	104911	357	128106	128680	126438	430	1.48E-05	2.75E-05	1.20481793	0.268412586
BP1026b	12381	DNA-binding response regulator KdpE	38035	22040	25396	40	129353	124535	36376	46	1.29E-05	2.42E-05	1.15	0.20133861
BP1026b	12382	two-component system, sensor kinase protein KdpD	127609	109089	111611	39	139731	144887	136970	47	1.37E-05	2.57E-05	1.205128205	0.269186633
BP1026b	12383	potassium-transporting ATPase subunit C	132781	153278	140443	35	17715	17915	14993	33	2.05E-09	3.61E-09	0.9428571	-0.06488889
BP1026b	12384	potassium-transporting ATPase subunit B	113940	101153	111153	47	85897	82153	82449	39	3.62E-18	3.22E-17	0.75	-0.415037499
BP1026b	12385	potassium-transporting ATPase subunit A	131027	122447	124990	69	96072	96650	94510	52	5.56E-20	6.09E-19	0.753623188	-0.408084739
BP1026b	12386	potassium-transporting ATPase, KdpF subunit	6791	10145	7720	88	4414	3391	2018	35	2.42E-65	4.74E-63	0.397727273	-1.330148602
BP1026b	12387	quinone oxidoreductase	115673	121606	119184	121	117626	109880	105915	113	2.61E-12	1.15E-11	0.933884298	-0.09684275
BP1026b	12388	methyglyoxal synthase	52133	36297	41728	110	45838	47449	48783	120	1.92E-07	4.59E-07	1.090909091	0.125530882
BP1026b	12389	short chain dehydrogenase/reductase family oxidoreductase	23275	35113	18461	24	14323	15460	16734	19	8.34E-13	3.91E-12	0.791666667	-0.33704987
BP1026b	12390	thiacyl phosphoribosyltransferase	12341877	128653	128653	86	108483	108483	112701	238	0.268788871	0.23200712	0.81755102	0.07304406
BP1026b	12391	hypothetical protein	214880	224377	219936	301	176872	185311	173947	245	1.74E-20	0.01E-19	0.813953488	-0.296981738
BP1026b	12392	phosphoribosylamine-glycine ligase	109249	101718	102695	81	104303	104000	100000	79	6.86E-10	2.24E-09	0.975306842	-0.306609255
BP1026b	12393	coproporphyrinogen III oxidase	51735	43377	47148	51	44517	45244	45327	48	3.25E-12	1.42E-11	0.941176471	-0.087462841
BP1026b	12394	nicotinic acid mononucleotide adenyltransferase	8586	1865	2639	5	5941	7938	11427	11	0.767214774	0.69782691	2.2	1.137503524
BP1026b	12395	ioiaph superfamily protein	29951	34764	39584	74	22719	24060	26073	52	4.75E-21	5.89E-20	0.702702703	-0.59013647
BP1026b	12396	rRNA large subunit methyltransferase	11137	5670	5894	16	10536	10525	13686	24	0.238821615	0.26236692	1.5	0.584962501
BP1026b	12397	RNA-like protein	7803	73321	73099	12	60532	60842	60842	10	3.43E-05	3.61E-04	0.88755102	0.093109406
BP1026b	12398	ribonuclease G	292675	326419	329713	215	356162	351831	337995	237	3.86E-07	8.89E-07	1.102325581	0.140550399
BP1026b	12399	xanthine/uracil permease family protein	21599	17642	18031	13	18277	17906	18108	13	1.11E-08	3.13E-08	1	0
BP1026b	12400	hypothetical protein	29686	38484	37103	25	32446	31749	31168	22	2.35E-11	9.27E-11	0.88	-0.184424571
BP1026b	124													

BP1026b_12452	integral membrane protein	4015	2130	2182	3	3409	2741	3912	3	0.008063222	0.010716746			0
BP1026b_12453	aminotransferase family protein	15971.44	1797075	1784735	1435	2691665	2452389	2041146	1990	0.023096882	0.029069494	1.386759582	0.471717694	
BP1026b_12454	L-PSP family endonuclease	204811	243931	221956	487	238946	245850	238204	525	1.59E-04	2.59E-04	1.078028747	0.10839565	
BP1026b_12455	PhaI family phenazine biosynthesis protein	313013	275458	275076	313	354296	354320	401900	411	3.23E-04	3.08E-04	1.333999040	0.392975737	
BP1026b_12456	hypothetical protein	116852	140772	130857	54	125045	117021	109108	49	2.14E-14	1.21E-13	0.907407407	-0.40177658	
BP1026b_12457	chromate transport protein	215287	259326	233938	186	337116	326559	295652	251	0.014579844	0.018799535	1.349463662	0.432384743	
BP1026b_12458	acetylphosphate aminohydrolase	27755	23142	24200	24	302766	29142	25233	27	2.31E-05	4.20E-05	1.125	0.169925001	
BP1026b_12459	allantoinase amidohydrolase	19791	16442	18423	14	24507	24954	23965	19	0.010359637	0.013601503	1.357142857	0.440572591	
BP1026b_12460	major facilitator family transporter	25922	12965	15008	13	19458	22234	20585	15	9.55E-05	1.59E-04	1.153846154	0.206450877	
BP1026b_12461	LysR family transcriptional regulator	23515	23507	23218	23	20964	20804	19593	20	1.94E-11	7.75E-11	0.869565217	-0.201633861	
BP1026b_12463	hypothetical protein	6261	6794	49638	14	8307	8253	8503	18	0.007508926	0.011018978	1.285714286	0.362570079	
BP1026b_12462	LysR family transcriptional regulator	5370	2575	3828	4	4992	5831	6540	6	0.126256883	0.143664508	1.5	0.584962501	
BP1026b_12464	integral membrane protein	11599	9378	10394	22	11873	10392	10152	23	1.37E-06	2.90E-06	1.045454545	0.064130337	
BP1026b_12465	DNA topoisomerase IV subunit A	178188	198206	202658	83	251200	245294	245845	106	0.046862827	0.056669642	1.277108434	0.352881023	
BP1026b_12466	DNA topoisomerase IV subunit B	183238	202196	199721	98	234471	226584	221801	114	0.002780925	0.00390314	1.163265306	0.21818017	
BP1026b_12467	ABC transporter ATP-binding protein	146207	124403	124904	67	167713	167797	160587	84	3.42E-04	5.38E-04	1.253731343	0.326228232	
BP1026b_12468	hypothetical protein	592389	604167	625723	1488	475046	468502	438178	1128	1.13E-24	2.03E-23	0.758064516	-0.399607459	
BP1026b_12469	Rubredoxin-NAD(+) reductase	56179	45573	49638	275	47081	43125	39018	245	6.90E-15	3.91E-14	0.890909091	-0.166649609	
BP1026b_12470	hypothetical protein	7036	9469	8950	5	10664	9944	9983	6	8.86E-04	0.001325584	1.0	0.263034406	
BP1026b_12471	alpha-beta fold family hydrolase	3832	4021	4183	4	4142	3273	3516	3	1.06E-07	2.63E-07	0.75	-0.415037499	
BP1026b_12473	translation initiation factor IF-1	18220	29383	26957	93	20531	20023	18132	73	4.04E-15	2.48E-14	0.784946237	-0.349334252	
BP1026b_12474	hypothetical protein	1486	1418	1505	6	1023	1096	1356	5	7.22E-09	2.09E-08	0.833333333	-0.263034406	
BP1026b_12475	hypothetical protein	3226	3205	2591	9	4490	5563	5273	16	0.956938871	0.960619405	1.777777778	0.830074999	
BP1026b_12476	hypothetical protein	4745	6676	6986	21	6738	6610	6331	23	2.46E-05	4.46E-05	1.095238095	0.131244533	
BP1026b_12477	Arg tRNA	4613	8703	6596	88	6042	5586	4824	72	1.02E-10	3.74E-10	0.818181818	-0.289506617	
BP1026b_12479	hemolysin activator protein	72192	109740	106344	67	10902	21690	25366	118	0.012051621	0.015694395	1.945142857	0.404872591	
BP1026b_12480	hypothetical protein	58183	97803	79283	326	68810	64693	65189	275	4.27E-13	2.06E-12	0.843558282	-0.245440446	
BP1026b_12481	Large exoproteins involved in heme utilization and/or adhesion	151050	223912	209597	21	188215	181702	170521	19	7.54E-14	3.98E-13	0.904761905	-0.144389909	
BP1026b_12482	hypothetical protein	2551	4914	3864	19	2733	3335	3316	16	1.11E-10	4.03E-10	0.842105263	-0.247927513	
BP1026b_12483	hypothetical protein	453338	703725	626993	1835	452923	459596	420721	1371	1.66E-25	3.24E-24	0.747138965	-0.202551492	
BP1026b_12484	hypothetical protein	5961	6506	7605	29	6310	4982	5974	25	1.46E-09	4.62E-09	0.862089666	-0.214124805	
BP1026b_12486	hypothetical protein	2367	1795	2938	5	1451	1794	2149	3	3.35E-13	1.64E-12	0.6	-0.36965594	
BP1026b_12485	mucon-DD-endopetidase	75499	64961	67961	105	7707	78000	79821	118	4.01E-05	1.93E-04	1.133333333	0.180572346	
BP1026b_12487	ecotin	252241	353285	345260	586	271668	215201	228143	407	1.69E-20	1.96E-19	0.694592949	-0.52587187	
BP1026b_12488	hypothetical protein	22792	12970	17205	46	23909	24488	21478	61	0.006358955	0.008535252	1.326086957	0.407175382	
BP1026b_12489	hypothetical protein	892	611	683	2	1728	1083	1176	4	0.058032683	0.069307288	2	1	
BP1026b_12491	hypothetical protein	131406	148170	153547	281	164493	157521	154315	309	9.66E-08	2.42E-07	1.099644228	0.137036708	
BP1026b_12492	major facilitator superfamily multidrug efflux transporter	17504	13082	13554	10	15200	16824	17644	12	8.69E-05	1.46E-04	1.2	0.263034406	
BP1026b_12493	hypothetical protein	18485	8830	13511	22	19286	20742	21894	33	0.160306502	0.1800215	1.0	0.584962501	
BP1026b_12494	hypothetical protein	23127	13246	13466	38	21003	21690	23506	49	0.012051621	0.015694395	1.945142857	0.404872591	
BP1026b_12496	alpha-alpha-trehalose-phosphate synthase (UDP-forming)	117022	119468	110595	82	110706	115141	109586	79	4.34E-11	1.65E-10	0.963414634	-0.053771256	
BP1026b_12497	hypothetical protein	2772	3993	3624	17	2652	2726	3475	14	4.62E-10	1.55E-09	0.823529412	-0.280107919	
BP1026b_12498	lipoprotein	44852	39797	42861	76	42290	44691	46256	80	9.70E-09	2.76E-08	1.052631579	0.074000581	
BP1026b_12499	lipoprotein	10747	5466	7982	15	9565	8473	11603	19	0.001759651	0.002537397	1.266666667	0.341036918	
BP1026b_12500	hypothetical protein	12935	12494	13341	79	15731	14658	17677	98	0.002679940	0.003755481	1.240506329	0.310929096	
BP1026b_12501	ABC transporter ATP-binding protein	384387	320444	344465	260	456726	461438	442729	338	4.48E-05	7.83E-05	1.0	0.78311623	
BP1026b_12502	ABC transporter permease	230832	280388	267389	149	21803	21523	19861	118	1.85E-05	1.07E-04	0.791946305	0.36525799	
BP1026b_12503	hypothetical protein	12165	6087	7584	31	9314	11248	11938	39	0.00318468	0.004440969	1.258064516	0.331205908	
BP1026b_12504	hypothetical protein	145651	252780	233612	789	138037	132397	127431	496	2.21E-45	1.85E-43	0.628643853	-0.66968518	
BP1026b_12505	signal transduction histidine kinase	64261	38369	45358	37	53924	58594	65955	45	5.45E-04	8.36E-04	1.216216216	0.282399731	
BP1026b_12506	DNA-binding response regulator OmpR	53044	37380	44100	61	48213	49124	50464	67	3.34E-07	7.77E-07	1.098360656	0.135315853	
BP1026b_12507	hypothetical protein	8292	10104	9594	17	7780	10010	9639	16	1.77E-07	4.25E-07	0.941176677	-0.087462841	
BP1026b_12508	hypothetical protein	4732	3210	4052	5	4200	4833	4520	6	7.35E-04	0.0010976	1.2	0.263034406	
BP1026b_12509	amino acid ABC transporter substrate-binding protein	58286	66690	66238	82	67963	67965	68021	84	9.90E-07	2.30E-06	1.024390244	0.034765418	
BP1026b_12510	histidine transport system permease	56333	29921	31104	42	30876	28688	28085	42	6.95E-08	1.78E-07	1	0	
BP1026b_12511	histidine transport system permease	32272	60602	46931	59	39005	40338	36011	53	1.78E-13	8.98E-13	0.898305085	-0.154722595	
BP1026b_12512	histidine transport ATP-binding protein	55708	69847	64618	81	61071	61847	60463	78	3.09E-09	9.45E-09	0.962962963	-0.054447784	
BP1026b_12513	porin	350376	383505	384809	338	316000	315813	308054	282	1.06E-13	5.52E-13	0.834319527	-0.261328084	
BP1026b_12514	nitrogen regulatory protein P-II	236096	380945	340462	941	301831	292445	258441	838	1.32E-10	4.75E-10	0.890541977	-0.167244479	
BP1026b_12515	NAD synthetase	98081	70073	77756	48	94797	98125	105499	58	2.48E-04	3.96E-04	1.208333333	0.173018494	
BP1026b_12516	hypothetical protein	18237	13350	14936	13	14524	14570	13234	11	1.24E-09	3.36E-09	0.846158846	-0.24100801	
BP1026b_12517	alpha-D-glucosidase	176	45	0	0	28	220	248	0	3.42E-04	3.37E-04	#DIV/0!	0	
BP1026b_12518	inorganic pyrophosphatase	645241	892649	805142	1479	383659	380885	342534	698	3.31E-68	7.79E-66	0.4719495	-1.083323111	
BP1026b_12519	aldehyde dehydrogenase family protein	95191	38566	48066	42	81410	91064	104208	64	0.256056581	0.280999864	1.523809524	0.607862577	
BP1026b_12520	3-ketoacyl-ACP reductase	12806	11293	11781	15	12309	12647	13573	17	2.94E-05	5.27E-05	1.133333333	0.180572246	
BP1026b_12521	major facilitator family transporter	51160	40721	46948	35	51179	53708	55427	40	9.54E-06	1.82E-05	1.142857143	0.192645078	
BP1026b_12522	hypothetical protein	253779	245811	251483	210	272055	257297	256925	220	9.88E-06	1.88E-05	1.047619048	0.067114196	
BP1026b_12523	bifunctional uroporphyrinogen-III synthetase/uroporphyrin-III C-methyltransferase	283458	258682	256313	134	248890	264236	274535	132	3.09E-07	7.24E-07	0.985074627	-0.021695071	
BP1026b_12524	porphobilinogen deaminase	70068	57149	62506	63	75402	72478	69787	73	1.40E-04	2.30E-04	1.158730159	0.125244635	
BP1026b_12525	phosphoenolpyruvate carboxylase	153684	109930	113795	42	200666	227769	232795	74	0.111476404	0.127915039	1.761904762	0.817135943	
BP1026b_12526	methyltransferase	8112	5995	5684	8	5922	7250	8374	9	2.96E-05	5.29E-05	1.125	0.169925001	
BP1026b_12527	DNA-binding protein	30270	15985	18760	26	31961	31905	33418	39	0.061686838	0.073266278	1.5	0.584962501	
BP1026b_12528	lipoprotein	100000	95594	97568	94	119072	118676	109796	111	1.42E-05	2.65E-05	1.180851064	0.239827015	
BP1026b_12529	spore coat protein U													

BP1026b_12580	uroporphyrin-III C-methyltransferase	18879	6873	7736	14	12843	19771	27689	25	0.973892808	0.976999415	1.785714286	0.836501268
BP1026b_12581	sulfate adenylyltransferase, subunit 1	258447	264567	265566	199	335142	332029	311977	247	2.60E-04	4.14E-04	1.24120603	0.17142611
BP1026b_12582	sulfate adenylyltransferase subunit 2	71603	75030	78778	77	85719	86030	88283	89	7.99E-05	1.35E-04	1.15584416	0.20894689
BP1026b_12583	phosphoenolpyruvate phosphosulfate reductase	20312	18155	16340	24	19483	17927	19880	25	1.41E-06	2.90E-06	1.04166667	0.05889369
BP1026b_12584	hypothetical protein	5412	8372	4850	9	8138	4471	5400	9	1.77E-06	2.90E-06	0	0
BP1026b_12585	sulfite reductase	99935	131312	121113	69	88535	85528	82339	50	2.86E-21	3.63E-20	0.724637681	-0.464668267
BP1026b_12586	transcriptional regulator CysB-like protein	50426	56327	56080	57	53595	53294	48260	54	5.77E-12	2.45E-11	0.947368421	-0.078002512
BP1026b_12587	hypothetical protein	7344	5771	6727	19	8037	7910	9278	24	0.004832796	0.006596783	1.263157895	0.337034987
BP1026b_12588	Leu tRNA	1697	2161	1891	22	2219	1832	1682	22	8.65E-06	1.66E-05	1	0
BP1026b_12589	hypothetical protein	2007	1850	2028	12	2197	1723	2035	12	1.14E-05	2.15E-05	0	0
BP1026b_12590	putative replication protein	12133	10570	16158	30	12626	10918	12933	29	2.62E-20	2.97E-19	0.7	-0.54573173
BP1026b_12592	IS407A, transposase OvrA	43607	71570	62579	224	35069	33215	30927	125	3.04E-06	8.20E-04	0.558035714	-0.84170637
BP1026b_12593	putative insertion element protein	114203	159965	172486	225	162573	152583	141287	213	5.13E-14	2.76E-13	0.946666667	-0.079071571
BP1026b_12595	hypothetical protein	1532191	2645665	2293260	1128	2127906	2046901	1954894	1069	0.17522056	0.19578694	0.947695035	-0.077505215
BP1026b_12596	hypothetical protein	937609	1559124	1293448	307	1001573	1080469	1006367	250	0.911751144	0.919491694	0.814332248	-0.296310561
BP1026b_12597	hypothetical protein	15277	25820	23610	119	20108	19023	19023	110	1.23E-09	3.94E-09	0.924369748	-0.11345805
BP1026b_12598	DeoK family transcriptional regulator	136366	212049	191933	178	177976	169085	161013	168	2.37E-13	1.18E-12	0.943820225	-0.083416008
BP1026b_12599	hypothetical protein	921	1762	1181	11	873	898	851	7	2.29E-13	1.14E-12	0.636363636	-0.650376697
BP1026b_12600	hypothetical protein	5239	2029	2847	7	4930	5785	8551	13	0.52477956	0.550293771	1.851124857	0.893084796
BP1026b_12601	DNA-binding protein	92302	112928	98126	179	115725	109091	93037	187	4.74E-08	1.24E-07	0.144692737	0.063078683
BP1026b_12602	class II aldolase/adducin domain-containing protein	23316	28303	30076	32	21284	23019	24001	27	6.41E-13	3.03E-12	0.84375	-0.245112498
BP1026b_12603	dihydrodipicolinate synthase	10946	12643	10379	12	11155	11354	11430	12	2.27E-07	5.39E-07	1	0
BP1026b_12604	MOSC domain-containing protein	18953	10805	13909	21	16609	16701	17275	24	1.66E-04	2.70E-04	1.142857143	0.192645078
BP1026b_12605	alpha/beta fold family hydrolase	10911	5678	7336	8	12377	12627	15801	15	0.833995816	0.846890617	1.875	0.968095096
BP1026b_12606	lysK family transcriptional regulator	6390	3313	4071	5	6653	6135	6169	10	0.039904154	0.039904154	1.474	0.85426827
BP1026b_12607	LyxR substrate binding domain-containing protein	9294	26075	204581	326	102739	116884	113895	120	0.036090947	0.036090947	1.428571429	0.530514713
BP1026b_12608	copper resistance protein	6125	5074	5520	14	5819	5710	6863	16	9.71E-05	1.62E-04	1.142857143	0.192645078
BP1026b_12610	ribosomal small subunit pseudouridine synthase A	20982	11764	13357	21	17449	20972	20972	26	8.40E-04	0.001271631	1.238095238	0.38122295
BP1026b_12609	hypothetical protein	83960	137488	121996	605	147002	135771	122714	715	4.34E-06	8.62E-06	1.18181818	0.2410081
BP1026b_12611	NAD-dependent epimerase/dehydratase family protein	87174	96786	97889	84	119921	115417	108014	115	5.73E-05	9.88E-05	1.223404252	0.290901199
BP1026b_12612	CDP-6-deoxy-delta-3,4-glucosone reductase	81478	75576	75476	75	76497	71178	69018	69	1.03E-09	3.33E-09	0.92	-0.120942434
BP1026b_12613	acetylformate transaminase protein	84429	71561	76437	65	87220	93966	90780	76	1.19E-04	1.96E-04	1.169230609	-0.2255597
BP1026b_12614	acetyltransferase	18475	16139	16102	36	22779	24751	25132	52	0.043105381	0.052327927	1.444444444	0.530514713
BP1026b_12615	hypothetical protein	45403	59894	53195	78	44768	46069	39945	65	7.23E-19	6.95E-18	0.833333333	-0.263044006
BP1026b_12616	branched-chain amino acid ABC transporter ATP-binding protein	66123	72757	73093	98	78486	77908	69344	104	3.09E-06	6.25E-06	1.06122449	0.085729874
BP1026b_12617	leucine/isoleucine/valine transport system ATP-binding protein	45282	51625	54223	65	51937	52677	52085	67	7.15E-09	2.07E-08	1.030769231	0.043721377
BP1026b_12618	branched-chain amino acid ABC transporter permease	66887	72127	70817	59	61877	57754	50395	48	5.23E-18	4.56E-17	0.813559322	-0.297680549
BP1026b_12619	amino-acid transport permease protein	27746	39367	36919	36	19521	17216	17082	18	3.70E-43	2.58E-41	0.5	-0.1
BP1026b_12620	hypothetical protein	11573	12723	11211	22	12201	11561	11863	22	3.34E-07	7.74E-07	0	0
BP1026b_12621	4-hydroxy-3-methylthio-2-ethyl diphosphate reductase	366075	290655	270230	326	30273	311080	31289	314	2.38E-09	3.87E-08	0.963190184	0.454107405
BP1026b_12622	FKBP-type peptidyl-prolyl cis-trans isomerase	193973	169687	198598	411	134934	133068	135325	294	3.57E-32	1.31E-30	0.715328467	-0.483322239
BP1026b_12623	DNA repair protein RadC	1401	1198	747	1	1004	943	852	1	7.79E-07	1.71E-06	1	0
BP1026b_12624	50S ribosomal protein L33	125323	221864	194714	367	151951	155065	156230	313	1.21E-19	1.29E-18	0.852861035	-0.229617406
BP1026b_12625	50S ribosomal protein L35	33125	39374	350646	1939	341905	358263	347413	2078	9.29E-08	2.33E-07	0.071686646	0.09882851
BP1026b_12626	L-aspartate oxidase	95520	82948	89279	54	95488	96533	91157	57	5.70E-07	1.28E-06	0.055555556	0.078002512
BP1026b_12627	nicotinate-nucleotide pyrophosphorylase	87184	49063	52704	79	99232	105381	111384	119	0.660829228	0.683074964	1.676065338	0.745070644
BP1026b_12628	guanine nucleotide synthetase	29667	239657	230230	240	186657	207764	200197	248	3.86E-07	1.07E-06	1.13801072	0.187527091
BP1026b_12629	fatty acid desaturase family protein	829984	1126537	1060235	842	599579	580809	533464	478	3.90E-46	3.54E-44	0.567695962	-0.816809615
BP1026b_12630	mechanosensitive ion channel family protein	81919	56126	60835	49	78960	79924	79938	58	5.64E-04	8.64E-04	1.183673469	0.243271151
BP1026b_12631	NOL1/NOP2/Sun family protein	145466	73434	93208	82	158741	173604	193360	138	0.789761523	0.805317627	1.682962892	0.750972452
BP1026b_12632	phosphoribosylglycinamide formyltransferase	19375	21113	20060	30	18617	21664	19835	30	2.96E-08	2.47E-07	1	0
BP1026b_12633	bifunctional riboflavin kinase/FMN adenylyltransferase	51407	40702	38456	41	60177	57539	51830	53	0.00261436	0.003209252	1.292682927	0.37036845
BP1026b_12634	isoleucyl-tRNA synthetase	262387	271346	273819	94	387831	386298	364675	133	0.003106201	0.003436359	1.41489361	0.50695584
BP1026b_12635	lipoprotein signal peptidase	28140	36581	35571	66	48786	47494	44082	93	0.012208278	0.015888771	1.409090909	0.494764692
BP1026b_12636	decarboxylase/phosphotransferase	89358	48318	57205	53	77374	80634	86687	67	0.002672644	0.003756213	1.264150943	0.33168736
BP1026b_12637	deoxyuridine 5'-triphosphate nucleotidohydrolase	21439	20716	20610	46	19194	21606	19745	45	1.90E-08	5.20E-08	0.978266087	-0.03170886
BP1026b_12638	hypothetical protein	4932	5291	4565	6	5708	5679	4775	6	1.38E-04	2.26E-04	1	0
BP1026b_12639	hypothetical protein	14530	7026	8409	13	14925	15679	15188	20	0.2340905	0.257980096	1.538461538	0.621488137
BP1026b_12640	amino acid permease	29845	26455	25024	19	30789	31153	32034	22	3.17E-05	5.64E-05	1.157894737	-0.21104405
BP1026b_12641	ATP-dependent Clp protease ATP-binding subunit clpA	2692746	334055	337379	1337	337649	327364	337364	1458	0.150827042	0.17633042	1.017053635	0.17053635
BP1026b_12642	ATP-dependent Clp protease adaptor protein ClpB	813797	813797	725291	2131	648160	653936	633189	2047	1.21E-09	3.87E-09	0.960581886	-0.058019198
BP1026b_12643	hypothetical protein	247637	402970	354929	1893	280726	260472	268495	1524	3.32E-13	1.02E-12	0.80073115	-0.112851501
BP1026b_12644	cold shock transcription regulator protein	856208	1379916	1185883	4636	980374	941137	890520	3810	0.762297603	0.77870714	0.821829163	-0.283089569
BP1026b_12645	multicopper oxidase domain-containing protein	148492	136371	145138	89	153738	152320	148578	94	2.22E-09	6.87E-09	1.056179775	0.078855421
BP1026b_12646	isocitrate dehydrogenase	1762183	2507299	2345714	1750	2186533	2208160	2118515	1723	0.15822213	0.177904043	0.984571429	-0.02432222
BP1026b_12647	pseudouridine synthase family protein	4159	3667	3541	6	7210	2988	3426	5	6.94E-10	2.28E-09	0.833333333	-0.263044006
BP1026b_12648	predicted RNA	4876319	7692780	659280	15849	7409719	7534808	689306	18049	0.645365128	0.66613808	1.13801072	0.187527091
BP1026b_12649	hypothetical protein	14499	20835	17428	34	10966	11866	13607	27	9.19E-21	1.10E-19	0.67407588	-0.563900885
BP1026b_12648	elongation factor G	570870	780736	716367	325	903180467	871079	871079	423	0.031080467	0.035849112	1.301538462	0.380217945
BP1026b_12651	hypothetical protein	308	394	272	0	534	690	803	1	7.78E-04	0.001171385	#DIV/0!	#DIV/0!
BP1026b_12652	hypothetical protein	3009	407	731	2	1474	2267	2838	4	0.884182528	0.89374203	2	1
BP1026b_12653	aldo/keto reductase family oxidoreductase	60695	38212	46080	57	49666	58058	61457	60	4.25E-05	7.43E-05	1.157894737	-0.21104405
BP1026b_12654	GnR family transcriptional regulator	36987	35798	32410	47	30139	31741	28670	46	2.24E-13	1.12E-12	0.85106383	-0.232660757
BP1026b_12655	hypothetical protein	210	153	327	1	143	238	185	1	0.043436983	0.05299984	1	0
BP1026b_12656	citrate synthase family protein	8274	59074	6820	5	82478							

BP1026b	12705	hypothetical protein	556	464	766	5	732	774	606	6	0.112571048	0.129123795	1.2	0.263034406
BP1026b	12706	2-dehydroantoinase 2-reductase	10582	10185	9556	10	13567	12257	12606	13	0.004239946	0.005820517	1.3	0.378511623
BP1026b	12707	aldehyde dehydrogenase family protein	23645	11481	15125	11	22958	25497	30145	18	0.194146677	0.215703225	1.636363636	0.10493383
BP1026b	12708	benzoylformate decarboxylase	26430	15263	19610	12	32096	37294	43322	23	0.336934787	0.848947805	1.916666667	0.93859045
BP1026b	12709	transcriptional regulatory protein	23222	12879	15945	18	22788	21494	24680	25	0.007176546	0.009591185	1.388888889	0.473931188
BP1026b	12710	mannitol dehydrogenase family protein	3263	2368	2482	1	3482	2832	3269	2	0.003642441	0.005046726	2	1
BP1026b	12711	xylulokinase	26296	14489	18136	13	27298	27821	30930	19	0.057653792	0.068881052	1.461538462	0.547487795
BP1026b	12712	transcriptional regulator	35074	18609	23591	27	27938	28972	31220	30	3.00E-05	5.36E-05	1.111111111	0.152003093
BP1026b	12713	major facilitator family transporter	1371	484	544	0	1208	1577	2186	1	0.003360502	0.004672628	#DIV/0!	#DIV/0!
BP1026b	12715	beta-lactamase	3698	1120	2579	2	3333	3237	3298	2	0.12057186	0.137645731	1	0
BP1026b	12716	LysR family transcriptional regulator	6351	1955	2323	4	6287	6434	8628	2	0.79366318	0.800727705	1.75	0.807354023
BP1026b	12718	ABC sugar transporter, ATP-binding protein	11436	10072	9274	9	9525	11155	10360	9	4.85E-07	1.10E-06	1	0
BP1026b	12719	HAD-superfamily hydrolase	2911	943	1761	2	2878	2781	3692	4	0.833926185	0.846890617	2	1
BP1026b	12720	binding-protein-dependent transporter inner membrane component	8413	8156	8948	9	9137	9105	7317	9	5.27E-07	1.19E-06	1	0
BP1026b	12721	mannitol ABC transporter permease	6684	7582	6673	7	6246	5949	6106	6	2.14E-09	6.63E-09	0.857142857	-0.222392421
BP1026b	12722	extracellular solute-binding protein	13780	16279	15542	11	14582	13975	14272	10	9.57E-09	2.73E-08	0.909090909	-0.137503524
BP1026b	12723	tagatose 6-phosphate kinase protein	3646	1117	2309	1	3105	3808	3419	2	0.335633531	0.362047066	2	1
BP1026b	12724	carboxylate dehydrogenase	1796	1767	1459	1	1833	1803	1868	2	0.862027998	0.87146621	3	1
BP1026b	12725	sorbitol dehydrogenase	11629	10510	12580	14	11224	11767	12384	15	6.88E-07	0.8153E-06	0.171428571	0.099535674
BP1026b	12726	transcriptional regulator np20	23439	32009	27966	59	17569	16550	14641	34	8.86E-31	2.82E-29	0.576271186	-0.795180208
BP1026b	12727	ABC transporter substrate binding protein	52670	57155	62484	59	34761	34292	37052	36	8.93E-38	4.78E-36	0.610169492	-0.712718048
BP1026b	12728	ABC transporter ATP-binding protein	27784	18279	20176	25	24299	25624	26709	29	9.06E-05	1.52E-04	1.16	0.214124805
BP1026b	12729	metal ABC transporter permease	17268	13842	11189	16	13977	14961	15700	17	9.23E-06	1.76E-05	1.0625	0.087462841
BP1026b	12730	S-formylglutathione hydrolase	49871	44136	49623	55	64386	61738	66838	74	0.042237263	0.051333763	1.345454545	0.428093652
BP1026b	12731	glutathione-dependent formaldehyde dehydrogenase	110481	117053	109596	101	97932	101470	100085	90	5.99E-13	2.84E-12	0.891089109	-0.166358667
BP1026b	12732	AraC family transcription regulator	40269	40269	2374	26	34073	34073	34073	32	3.58E-04	5.61E-04	1.230769231	0.299560282
BP1026b	12733	xylulose kinase	5031	2207	2604	2	4891	5330	5135	3	0.463683294	0.491124815	1.5	0.584962501
BP1026b	12734	permease protein	11800	9952	12070	8	16275	14054	13036	10	0.005430094	0.007371935	1.25	0.321928095
BP1026b	12735	RND efflux system outer membrane lipoprotein	399666	336150	359634	236	510032	509576	522039	332	0.001940483	0.002778964	1.406779661	0.423396382
BP1026b	12736	inner membrane protein	992259	121974	1136738	347	1333395	1327464	1263696	408	0.082694771	0.096103905	1.175792507	0.233633489
BP1026b	12737	RND family efflux transporter MFP subunit	291253	288280	301345	232	293224	309820	316493	242	2.47E-07	5.85E-07	0.043103448	0.06882424
BP1026b	12738	repressor protein	43970	44777	42058	68	69528	77882	71621	114	0.80187034	0.816336065	0.676470588	0.745427173
BP1026b	12739	hypothetical protein	26177	20520	21616	31	27465	26898	22643	35	9.12E-05	3.17E-05	0.682396984	0.510151169
BP1026b	12740	hypothetical protein	67719	64168	68740	182	88737	86647	78751	231	0.003197407	0.004457725	0.269207699	0.343954401
BP1026b	12741	hypothetical protein	51726	43791	47007	112	69104	64565	64720	156	0.104786568	0.120592148	1.392857143	0.478047297
BP1026b	12742	serine protease	595656	699056	666170	439	784067	765524	715099	507	0.200658587	0.222528256	1.548497494	0.27764807
BP1026b	12743	sensor kinase protein	44890	43406	40687	32	38119	40153	38801	29	2.20E-13	1.10E-12	0.90625	-0.142019005
BP1026b	12744	Two-component system response regulator QseB	56026	59065	54949	86	47648	46803	48020	72	3.26E-18	9.29E-17	0.837209922	-0.256339753
BP1026b	12745	peptidase	38795	19821	24749	18	29590	34768	38423	22	2.05E-04	3.31E-04	1.022222222	0.28936617
BP1026b	12746	carotol desaturase family protein	46541	65543	62919	43	61706	61436	62940	42	9.17E-32	3.17E-05	0.682396984	0.510151169
BP1026b	12747	lipase	147518	149699	147270	129	150747	154204	157875	135	8.63E-10	2.81E-09	0.046511626	0.065588342
BP1026b	12748	StuA5/Yco/YrdC/YwC family protein	40587	27460	30809	32	48957	44250	44875	44	0.010620854	0.013915296	1.375	0.459431619
BP1026b	12749	phosphoribosylaminoimidazole carboxylase ATPase subunit	43445	25312	26159	26	34436	41287	52584	35	0.003478447	0.004826981	1.346153846	0.428834299
BP1026b	12750	phosphoribosylaminoimidazole carboxylase catalytic subunit	30566	38563	36143	67	33090	34606	31173	63	2.05E-10	7.15E-10	0.940298507	-0.088809267
BP1026b	12751	phosphoribosylaminoimidazole succinocarboxamide synthase	101004	116515	112617	123	99909	95705	91401	107	2.45E-13	1.22E-12	0.869918699	-0.201047519
BP1026b	12752	fructose-1,6-bisphosphate aldolase	529175	646995	631281	565	702333	698601	661522	645	0.902262663	0.910401832	1.141599292	0.910487929
BP1026b	12753	pyruvate kinase	265126	265126	274029	169	258874	258772	286269	194	0.000793446	0.001073294	0.000793446	0.001073294
BP1026b	12754	phosphoglycerate kinase	236892	225831	236712	195	262514	258157	271276	221	4.93E-04	7.60E-04	1.133333333	0.180572246
BP1026b	12755	hypothetical protein	4519	2714	3115	10	4835	5623	5210	16	0.305853655	0.33146493	1.6	0.678071905
BP1026b	12756	A2C family protein	30232	32471	30304	41	40667	37430	34707	50	7.48E-05	1.27E-04	1.219512195	0.286304185
BP1026b	12757	branched-chain amino acid aminotransferase	307330	421779	383963	401	290834	284545	250980	298	1.86E-16	1.34E-15	0.743142145	-0.428289906
BP1026b	12758	hypothetical protein	9009	5896	5466	34	8203	9763	11453	49	0.091184692	0.105559215	1.441176471	0.52747003
BP1026b	12759	lipopolysaccharide heptosyltransferase II	43656	35681	37537	37	34447	35725	30737	32	1.57E-13	8.00E-13	0.864648665	-0.209453366
BP1026b	12760	hypothetical protein	67648	73266	73681	163	80034	84506	72966	178	0.348E-06	1.74E-06	0.10920454	0.12700527
BP1026b	12761	alpha/beta fold family hydrolase	26727	22169	21486	23	20558	24726	25476	12	1.57E-07	3.79E-07	1	0
BP1026b	12762	hypothetical protein	8668	3489	4965	9	6249	6457	7701	10	8.25E-04	0.0012379	1.111111111	0.152003093
BP1026b	12763	M48 family peptidase	31996	32275	33175	18	28344	27257	30316	16	1.89E-11	7.56E-11	0.888888889	-0.169925001
BP1026b	12764	molybdenum cofactor biosynthesis protein MoaC	30291	26987	28123	57	28900	30070	34128	62	2.67E-06	5.45E-06	1.087719298	0.121306296
BP1026b	12765	TonB domain-containing protein	11341	4481	4815	18	8398	10148	11913	27	0.123449837	0.150383501	1.5	0.584962501
BP1026b	12766	hypothetical protein	16894	16284	19245	16	14818	17408	17869	35	3.14E-08	8.37E-08	0.972222222	-0.404641984
BP1026b	12767	antigen polymerase family protein	46659	47562	47640	28	52296	54615	52996	29	5.46E-08	1.033E-08	0.050636073	0.000636073
BP1026b	12768	Type IV pilin PilA	2471	1271	1654	3	2103	2309	2390	4	0.011902208	0.015055653	0.333333333	0.415037499
BP1026b	12769	IerC family integral membrane protein	38240	22929	26831	41	34884	38381	36617	51	2.53E-04	4.04E-04	1.243902342	0.34873337
BP1026b	12770	succinyl-CoA synthetase subunit alpha	392969	382051	403730	445	434056	468196	500884	530	1.15E-06	2.46E-06	1.191011236	0.252187024
BP1026b	12771	succinyl-CoA synthetase subunit beta	469843	662607	608568	497	517222	507714	470758	427	2.59E-17	2.07E-16	0.85915493	-0.219009782
BP1026b	12772	hypothetical protein	82942	77599	82372	132	63393	64349	61990	103	5.20E-17	4.02E-16	0.78030303	0.57893592
BP1026b	12773	recombination regulator RecX	69700	43050	52586	86	77270	76507	75186	120	0.057720732	0.068947876	1.395348837	0.480625841
BP1026b	12774	recombinase A	724260	980923	930711	812	757703	765919	759396	708	0.818062654	0.83338098	0.871921182	-0.197730303
BP1026b	12775	DNA-binding response regulator	19496	23819	22105	26	23845	19438	19613	25	2.25E-11	8.90E-11	0.892857143	-0.163498732
BP1026b	12776	two-component sensor kinase transcriptional regulatory protein	12899	12533	10821	7	11960	13008	12371	7	1.40E-06	2.96E-06	1	0
BP1026b	12777	major facilitator family transporter	3320	4842	4213	2	3930	3958	3704	2	5.86E-07	1.31E-06	1	0
BP1026b	12778	Met tRNA	413	611	415	6	639	289	440	5	0.003656169	0.005063507	0.833333333	-0.263034406
BP1026b	12779	Integrase	254891	447409	399194	266	211332	215627	210254	154	2.71E-34	1.17E-32	0.578947368	-0.788495895
BP1026b	12780	plasmid recombination enzyme	3599	5738	5128	5	3552	3719	3924	4				

BP1026b	12831	glycerol-3-phosphate regulon repressor	51505	58675	61809	73	50776	49254	46908	62	4.47E-17	3.48E-16	0.849315068	-0.235628248
BP1026b	12832	hypothetical protein	22198	35935	32570	305	16616	15609	13210	152	2.52E-45	2.08E-43	0.498360656	-1.004737919
BP1026b	12833	hypothetical protein	126544	187790	177933	828	82072	78909	68767	386	2.76E-47	5.39E-45	0.466183575	-1.10102992
BP1026b	12834	hypothetical protein	190409	290133	260133	32	14002	165321	102933	41	0.004536059	0.000230339	0.28125	0.357552005
BP1026b	12835	glycerol-3-phosphate dehydrogenase	61212	31699	39636	38	81293	94445	102938	60	0.011627919	0.015164956	2.142857143	1.099535674
BP1026b	12836	glycerol kinase	71664	91612	80081	52	138917	140358	138375	89	0.530381211	0.556314117	1.711538462	0.75293713
BP1026b	12837	glycerol uptake facilitator protein	41543	26889	26833	44	73019	77247	70433	102	5.22E-04	8.03E-04	2.318181818	1.212993723
BP1026b	12838	hypothetical protein	1127	2015	2109	12	2940	4040	4517	26	0.002921439	0.004087534	2.166666667	-1.154727217
BP1026b	12839	hypothetical protein	722	1046	921	2	1369	1280	1490	3	0.717277763	0.736716066	1.5	0.584962501
BP1026b	12841	3-phosphoshikimate 1-carboxyvinyltransferase	6626	3720	4462	3	6006	5461	5521	4	5.30E-04	1.333333333	0.415037499	
BP1026b	12840	3-phosphoshikimate 1-carboxyvinyltransferase	10880	9204	9605	7	12350	13323	12953	9	0.004586637	0.006270339	1.285714286	0.362570079
BP1026b	12842	asparagine synthase	4203	3982	3709	2	4091	4168	4297	2	1.15E-04	1.90E-04	1	0
BP1026b	12843	hypothetical protein	13423	12220	11100	10	13951	11911	13100	10	6.46E-06	1.26E-05	1	0
BP1026b	12844	hypothetical protein	44984	21208	26162	35	32890	37833	38626	42	3.42E-05	6.06E-05	1.2	0.263034406
BP1026b	12845	HAD-superfamily hydrolase	30001	22793	28664	39	24281	24318	26699	36	9.64E-10	3.13E-09	0.923076923	-0.1154727217
BP1026b	12846	3,4-dihydroxy-2-butanone 4-phosphate synthase	13667	13663	11549	17	11624	12822	13826	17	1.72E-07	4.14E-07	1	0
BP1026b	12847	DNA-binding protein	125997	102535	101043	164	141937	144823	134089	209	1.95E-04	3.14E-04	1.274390240	0.349807127
BP1026b	12848	major facilitator family transporter	5220	35762	32943	4	24699	24555	5190	4	1.34E-20	2.58E-07	0.709677479	-0.449476462
BP1026b	12849	LyxR family transcriptional regulator	29328	29843	30412	32	24857	27293	25519	27	9.72E-12	4.02E-11	0.84375	-0.245112498
BP1026b	12850	(dimethylallyl)adenosine RNA methyltransferase	48609	52496	51817	37	59575	58584	56531	42	2.86E-05	5.12E-05	1.135135135	0.182864057
BP1026b	12851	PhoH family protein	69236	82233	79149	72	86888	87244	89566	82	5.10E-05	8.85E-05	1.138888889	0.187627003
BP1026b	12852	hypothetical protein	143244	118357	131670	161	135292	130385	120895	158	1.14E-11	4.67E-11	0.98136646	-0.02713613
BP1026b	12853	hypothetical protein	17026	10790	12565	21	14404	14597	17289	24	2.05E-04	3.30E-04	1.142857143	0.192645078
BP1026b	12854	magnesium and cobalt efflux protein CorC	106649	147899	135689	146	120771	114552	94427	123	8.95E-17	6.70E-16	0.842465753	-0.247310054
BP1026b	12855	apolipoprotein N-acyltransferase	72848	67990	65427	40	59188	58889	63900	35	2.95E-12	3.88E-12	0.846153846	-0.192645078
BP1026b	12856	glycyl-tRNA synthetase subunit alpha	167106	128741	118034	136	12541	90045	82053	87	6.89E-17	0.790000001	0.10277161	-0.33841621
BP1026b	12857	glycyl-tRNA synthetase subunit beta	105162	75384	79728	41	127702	136977	149963	65	0.160894951	0.180610145	1.585365854	0.664815808
BP1026b	12858	D,D-hexose 1,7-bisphosphate phosphatase	55566	32732	39840	73	71374	71870	72394	127	0.749268335	0.766727888	1.693333333	0.79865996
BP1026b	12859	phospholipid and glycerol acyltransferase	21675	30700	25747	33	17047	16550	15065	20	2.72E-26	5.67E-25	0.606060606	-0.722466024
BP1026b	12860	hypothetical protein	69188	84503	85103	87	70414	69692	71116	77	2.30E-11	9.08E-11	0.885057471	-0.176156955
BP1026b	12861	lactoylglutathione lyase	80394	111783	101562	251	76037	75092	66598	186	2.78E-19	2.85E-18	0.741035857	-0.432384743
BP1026b	12862	integral membrane protein	12424	12743	14063	13	11559	9782	10981	11	6.35E-13	3.01E-12	0.846153846	-0.2410081
BP1026b	12863	dimethyladenosine transferase	117371	134786	128238	153	115215	112729	106931	134	4.22E-15	2.58E-07	0.875816993	-0.191298652
BP1026b	12864	4-hydroxybutyronine 4-phosphate dehydrogenase	101794	92289	102907	95	110468	106726	101728	102	1.97E-07	4.49E-07	0.176848211	-0.102569734
BP1026b	12865	PtpC-type peptidyl-prolyl cis-trans isomerase	425162	348265	380920	285	425715	422898	413915	312	2.36E-08	6.40E-08	1.094736482	0.13058411
BP1026b	12866	organic solvent tolerance protein	588287	662794	643305	267	559522	562119	552785	236	2.65E-15	1.67E-14	0.883895131	-0.178052882
BP1026b	12868	hypothetical protein	5520	3079	3466	29	4222	4585	5049	33	0.00108617	0.001601641	1.137931034	0.186413124
BP1026b	12867	phosphotransferase domain-containing protein	53994	68732	62631	55	56659	59833	59041	52	1.69E-10	5.96E-10	0.945454545	-0.080919995
BP1026b	12869	nucleotidyltransferase family protein	23085	12150	15412	22	15607	20948	25027	28	0.001949139	0.002843487	1.272727273	0.347925303
BP1026b	12870	GTP-binding transmembrane ABC transporter protein	175326	275326	267540	36	136746	127640	117572	37	1.36E-06	2.44E-06	0.709677479	-0.449476462
BP1026b	12871	thioesterase superfamily protein	66596	68646	61655	156	60700	57561	55290	144	1.88E-11	5.55E-11	0.923076923	-0.1154727217
BP1026b	12872	nitrate reductase associated protein	126462	182352	166533	330	198942	178155	153528	368	1.14E-06	2.44E-06	1.115151515	0.157239742
BP1026b	12873	formate dehydrogenase family accessory protein FdhD	28883	14328	17701	24	26286	27779	29877	33	0.017326044	0.022167145	1.375	0.459431619
BP1026b	12874	enoyl-CoA hydratase	14938	14771	16381	20	19347	19113	19019	25	0.001477679	0.002149102	1.25	0.321928095
BP1026b	12875	acetyl-CoA acyltransferase	164528	180815	177372	145	242904	242259	232917	199	0.251335276	0.256722241	1.372413793	0.456715531
BP1026b	12876	3-hydroxyacyl-CoA dehydrogenase	302988	288683	291678	120	439373	446210	433373	180	0.004389434	0.006015186	1.5	0.584962501
BP1026b	12877	acyl-CoA dehydrogenase domain-containing protein	354389	456282	431941	231	648346	631352	590053	348	0.015053814	0.019378769	1.506493506	0.591194454
BP1026b	12878	putative transcriptional regulator for fatty acid degradation FadP, TetR family	1393911	1306165	1401864	2796	3175477	3118988	2842557	6228	2.65E-05	4.77E-05	2.227467811	1.155405484
BP1026b	12879	cardiolipin synthetase II	57778	72539	70854	52	60844	63909	62337	48	3.73E-10	1.26E-09	0.923076923	-0.1154727217
BP1026b	12880	dATP pyrophosphohydrolase	30434	24382	25313	55	32584	29735	30008	64	3.15E-05	5.65E-05	1.163636364	0.218640286
BP1026b	12881	aspartyl-tRNA synthetase	566465	671349	646878	349	732600	743680	722506	407	0.276712918	0.30180172	1.166189112	0.221801758
BP1026b	12882	hypothetical protein	47427	57679	54211	81	47279	43143	35148	64	2.87E-21	3.64E-20	0.790123457	-0.339850003
BP1026b	12883	regulatory protein	24439	32963	29013	93	240144	229316	21816	69	2.80E-05	5.64E-05	0.9	0.201633869
BP1026b	12884	thiohydromy 5-methyltransferase family protein	48052	38842	35647	52	44962	49828	52888	63	5.76E-05	9.92E-05	1.211538462	0.72684025
BP1026b	12885	ubiquinone biosynthesis protein UbiB	301639	340655	330375	205	322373	318944	288129	196	1.40E-09	4.44E-09	0.956097561	-0.064770255
BP1026b	12886	hypothetical protein	73848	90110	87329	129	79609	74040	80323	120	5.04E-10	1.68E-09	0.930232558	-0.10433666
BP1026b	12887	predicted RNA	62053	3845	8115	666	42623	63426	85503	1725	6.15E-05	1.06E-04	2.59009009	0.373002279
BP1026b	12888	transmembrane protein	1012711	889006	912787	919	1279232	1291931	1264002	1252	0.01912752	0.024332816	1.362350181	0.446097794
BP1026b	12887	ubiquinone/menquinone biosynthesis methyltransferase	75541	86316	84472	112	76664	78563	77345	105	1.44E-09	4.57E-09	0.9375	-0.093109606
BP1026b	12889	hypothetical protein	29758	24243	24243	60	24065	24446	31339	69	2.80E-05	5.64E-05	0.9	0.201633869
BP1026b	12890	HTI family hydrolase	160995	233104	209056	452	182073	164909	162470	382	8.18E-19	8.00E-18	0.845132742	-0.242750134
BP1026b	12891	oxidoreductase, FAD-binding protein	454735	493532	487854	118	569104	566054	550096	139	5.91E-07	1.32E-06	1.177966102	0.236298028
BP1026b	12893	7-cyano-7-deazaquinone reductase	87313	93445	97929	112	84297	81135	77561	98	1.88E-12	8.44E-12	0.875	-0.192645078
BP1026b	12894	YigF family protein	202222	182924	187368	493	202399	199300	208116	525	1.70E-06	3.56E-06	1.064908722	0.090729776
BP1026b	12895	D-aminoacylase	52564	28667	32870	25	49587	56025	61620	37	0.10288162	0.11848694	1.48	0.556597176
BP1026b	12896	transcriptional regulator	11064	5153	7440	8	9424	12289	14234	13	0.211641857	0.234351174	1.625	0.700439718
BP1026b	12897	D-serine deaminase	26389	21921	26638	13	4355	4608	5104	18	2.53E-09	1.03E-08	0.9	0.201633869
BP1026b	12898	peptidase	152217	188434	178751	297	159800	155822	161140	272	2.48E-15	5.65E-14	0.915824961	-0.12665828
BP1026b	12899	MarK family regulatory protein	34807	16869	20607	55	27974	28603	30845	66	2.93E-04	4.65E-04	1.2	0.263034406
BP1026b	12900	EmrB/QacA family drug resistance transporter	20494	9653	11167	8	19471	21956	23743	13	0.27669757	0.30180172	1.625	0.700439718
BP1026b	12901	hypothetical protein	92388	40367	51521	67	78332	86037	100766	96	0.096885733	0.111848919	1.432835821	0.51887331
BP1026b	12902	esterase	80437	50987	58714	65	78872	81661	79035	82	0.003235851	0.004508313	1.2615384	

BP1026b	12950	excinuclease ABC subunit A	270509	257384	257598	90	369865	375324	356272	126	0.00419819	0.005663056	1.4	0.485426827
BP1026b	12951	hypothetical protein	104800	103043	99903	94	112279	109380	90554	95	8.10E-09	2.32E-08	1.010638298	0.015266757
BP1026b	12952	formyltetrahydrofolate deformylase	53169	59951	56967	64	59859	60081	54653	65	5.14E-08	1.34E-07	1.015625	0.022367813
BP1026b	12953	NUDIX domain-containing protein	59903	59903	41160	51	59598	66411	74261	78	0.471954	0.50139602	1.529411765	0.129768077
BP1026b	12954	Nxf1 type translocator	8377	5236	5770	10	6429	7689	7041	11	6.09E-05	6.51E-05	1.1	0.137503254
BP1026b	12955	adenine phosphoribosyltransferase	75161	76789	80053	137	70476	66874	66262	120	1.43E-11	5.78E-11	0.875912409	-0.191141487
BP1026b	12956	potassium efflux system protein	144596	124475	132285	66	139327	144638	147400	71	7.50E-09	2.16E-08	1.075757576	0.105533
BP1026b	12957	carbohydrate isomerase KpsF/GutQ family protein	84295	59103	59106	68	69633	68984	71898	71	1.36E-06	2.88E-06	1.044117647	0.062284278
BP1026b	12958	YrbI family phosphatase	85090	59016	64959	129	60628	63562	67364	118	2.13E-10	7.42E-10	0.914728682	-0.12884206
BP1026b	12959	hypothetical protein	57669	46740	52604	85	37383	39431	41793	64	1.68E-23	2.72E-22	0.752941176	-0.409390936
BP1026b	12960	CoxA-like family protein	117284	121454	132267	185	102856	102807	99232	152	9.55E-17	7.13E-16	0.821621622	-0.284539047
BP1026b	12961	ABC transporter ATP-binding protein	307386	332599	332238	417	301720	281987	260087	361	2.94E-11	1.15E-10	0.865707434	-0.20808547
BP1026b	12962	RNA polymerase factor sigma-54	607692	945017	843296	529	1000000	998629	995522	661	0.047646074	0.05757234	1.2495274	0.321382549
BP1026b	12963	hypothetical protein	292818	301676	307241	1318	463350	481091	524185	2147	0.042546446	0.051699503	1.628983308	0.703971821
BP1026b	12964	PTS system transporter subunit IIA	1887826	2994582	2873816	7181	2816206	2747693	2784105	7729	0.147908991	0.166972783	1.076312491	0.106097004
BP1026b	12965	PTS transporter subunit IIA-like nitrogen-regulatory protein PtsN	90945	126025	112741	215	72921	68397	71405	179	6.93E-28	1.68E-26	0.646511628	-0.629251777
BP1026b	12966	HPr kinase/phosphorylase	93592	115435	107302	108	106836	105146	92718	104	3.34E-10	1.14E-09	0.962962963	-0.054477784
BP1026b	12967	hypothetical protein	104076	91498	99751	110	110777	109372	100731	119	3.75E-07	8.66E-07	1.081818182	0.11345805
BP1026b	12968	ATP-dependent protease La	116276	122026	113449	185	124364	128495	117420	194	5.58E-09	1.64E-08	0.486486489	0.068513382
BP1026b	12969	A/G-specific adenine glycosylase	67923	46687	56392	51	58369	59024	56245	52	1.95E-08	5.32E-08	0.109607843	0.028014376
BP1026b	12970	formamidopyrimidine-DNA glycosylase	30118	14227	16218	24	25573	28249	32117	34	0.031979074	0.039513177	1.416666667	0.502500341
BP1026b	12971	hypothetical protein	465984	481227	479752	262	544210	552425	539245	301	1.51E-07	3.67E-07	1.148854962	0.200196675
BP1026b	12972	outer membrane lipoprotein LolB	26182	23795	25227	39	22620	20081	20616	33	1.10E-12	5.08E-12	0.846153846	-0.2410081
BP1026b	12973	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	124661	180552	161545	176	125331	119547	109304	132	2.31E-25	4.44E-24	0.75	0.415037499
BP1026b	12974	Gln (RNA)	42147	67980	58215	728	47458	45568	40397	577	1.96E-21	2.52E-20	0.792581418	-0.33567132
BP1026b	12975	ribose-phosphate phosphokinase	125400	143841	138859	142	120531	128429	118231	19	0.03014108	0.039384234	1.5	0.534962835
BP1026b	12976	50S ribosomal protein L25/general stress protein Ctc	624733	949055	872816	1127	1085848	1077357	1048173	1480	0.036054546	0.044231429	1.31320941	0.39310966
BP1026b	12977	peptidyl-rRNA hydrolase	16179	9257	9561	19	15983	19205	16753	28	0.127254555	0.144720867	1.477684211	0.599427409
BP1026b	12978	histidinol-phosphate aminotransferase	92093	88408	87438	83	75026	80215	86666	75	3.82E-11	1.47E-10	0.903614458	-0.146220741
BP1026b	12979	ferredoxin	31027	51631	50384	166	37894	34603	31229	129	3.28E-19	3.30E-18	0.777108434	-0.363812176
BP1026b	12980	phosphopantetheine adenylyltransferase	301000	348592	331523	652	375995	357113	288272	679	3.07E-08	8.19E-08	1.041411043	0.05833961
BP1026b	12981	methyltransferase	4842	2746	3203	5	4914	3941	4058	6	5.86E-04	1.96E-04	0.0068427	0.263034406
BP1026b	12982	signal recognition particle-docking protein FtsY	135972	58055	57564	68	115739	128617	123888	93	0.0042673	0.008384234	0.928571429	0.45169597
BP1026b	12983	maleylacetoacetate isomerase	70369	74878	74943	113	62242	60366	57529	93	6.55E-16	4.46E-15	0.82300885	-0.281020151
BP1026b	12984	nitrite reductase (NAD(P)H) large subunit	10572	10469	10619	4	10992	10845	11005	4	1.60E-06	3.35E-06	1	0
BP1026b	12985	nitrite reductase (NAD(P)H) small subunit	240	96	226	0	248	296	163	0	0.924572835	0.930813925	#DIV/0!	#DIV/0!
BP1026b	12986	molybdopterin oxidoreductase family protein	5077	3456	4664	1	5089	4520	4883	1	2.47E-04	3.95E-04	1	0
BP1026b	12987	glycosyl transferase family protein	28879	14852	18960	21	21385	20915	24770	22	3.74E-06	7.49E-06	1.047619048	0.067114196
BP1026b	12988	acetyltransferase	49888	30049	36343	47	31242	31923	31169	38	1.03E-15	8.83E-15	0.808510638	-0.30663138
BP1026b	12989	2-isopropylmalate synthase	24525	24525	20756	12	30849	30841	28730	10	0.0320108	0.039384234	1.5	0.534962835
BP1026b	12990	hypothetical protein	284995	202805	238158	625	235064	240018	225334	603	3.38E-07	7.86E-07	0.9648	-0.051698188
BP1026b	12991	hypothetical protein	118384	154443	141388	242	98722	95807	96249	170	3.04E-25	5.74E-24	0.702479339	-0.509472301
BP1026b	12992	hypothetical protein	12747	19721	15387	132	20480	18052	15147	149	4.39E-05	7.67E-05	1.128787879	0.17474401
BP1026b	12993	hypothetical protein	31065	53378	44883	342	31984	29956	31067	246	4.87E-22	6.77E-21	0.719298284	-0.47533801
BP1026b	12994	RNA polymerase factor sigma-32	816263	1017694	938025	987	801377	791214	735837	829	0.840655137	0.85304778	0.839918946	-0.251677983
BP1026b	12996	hypothetical protein	1020	1075	823	10	8177	942	774	8	6.44E-06	1.26E-05	0.931292805	0.10691534
BP1026b	12995	hypothetical protein	4375	4375	4434	14	3776	4177	3406	10	0.0042673	0.008384234	0.928571429	0.45169597
BP1026b	12997	cytochrome d ubiquinol oxidase subunit I	91011	112264	114213	66	130183	118702	109888	74	7.84E-07	1.72E-06	1.121212121	0.165059246
BP1026b	12998	cytochrome d ubiquinol oxidase, subunit II	43376	42174	47781	39	68838	68412	67746	60	0.566060273	0.591163979	1.538461538	0.621488377
BP1026b	12999	hypothetical protein	2780	2214	1617	22	3751	4089	3438	37	0.706102955	0.726277325	1.681881818	0.750021747
BP1026b	13001	hypothetical protein	1103	253	443	1	829	1225	1105	2	0.113015519	0.129567474	2	1
BP1026b	13002	hypothetical protein	656	339	226	0	356	459	331	0	0.006688636	0.008971652	#DIV/0!	#DIV/0!
BP1026b	13003	chitinase	92805	51089	58377	26	74245	79962	90933	32	7.37E-04	0.001112367	1.230769231	-0.295052682
BP1026b	13004	PTS system, glucose-glycoside (Glc) family EHA:phosphocarrier	56473	52257	57495	31	62038	57944	57012	33	7.54E-07	1.66E-06	1.064516129	0.909197809
BP1026b	13005	HPH/phosphoenolpyruvate-carboxy phosphotransferase component	21757	14582	14972	6	22828	24901	27189	9	0.06151347	0.073091063	1.5	0.584962501
BP1026b	13006	SIS domain-containing protein	7353	4850	4743	5	8722	8685	7970	8	0.130580796	0.148449747	1.6	0.678071905
BP1026b	13007	N-acetylglucosamine-6-phosphate deacetylase	8371	4736	5793	5	7429	8137	8429	7	0.003776539	0.005212922	1.4	0.485426827
BP1026b	13008	GntR family transcriptional regulator	3253	3059	3319	4	2847	3551	3910	4	1.77E-04	2.87E-04	1	0
BP1026b	13009	hypothetical protein	102	73	157	-1	33	65	78	0	1.39E-06	2.95E-06	0	#NUM!
BP1026b	13010	UvrX family regulatory protein	130043	124066	122806	136	119998	126232	132136	78	7.89E-11	2.91E-10	1.046153846	0.065095028
BP1026b	13011	AMP-binding domain-containing protein	127277	106753	112157	15	123012	122601	115317	16	3.88E-09	1.17E-08	0.928571429	0.45169597
BP1026b	13012	hypothetical protein	24119	23279	20612	20	17900	19279	19237	16	5.38E-13	2.57E-12	0.8	-0.321928095
BP1026b	13013	acyl carrier protein	27811	43906	40124	149	21914	20549	20564	84	2.53E-36	1.26E-34	0.563758389	-0.826851098
BP1026b	13014	hypothetical protein	15306	11677	12028	14	11250	11364	13011	13	1.55E-09	4.87E-09	0.928571429	-0.106915204
BP1026b	13015	hypothetical protein	10090	5465	5563	12	6908	7033	8324	13	6.81E-06	1.32E-05	1.083333333	0.115472717
BP1026b	13016	hypothetical protein	50587	51088	48223	50	39077	40268	38595	39	1.93E-20	2.22E-19	1.78	-0.35843971
BP1026b	13017	hypothetical protein	38123	28769	30663	30	32306	32476	33466	32	1.08E-06	2.31E-06	1.066666667	0.931094666
BP1026b	13018	pyridoxal-dependent decarboxylase family protein	46710	23079	25278	23	21785	22992	23428	16	5.32E-07	1.20E-06	1.043478262	0.061400545
BP1026b	13019	AMP-binding domain-containing protein	24873	25160	25789	16	26554	22244	24641	32	2.34E-07	3.74E-07	1	0
BP1026b	13020	hypothetical protein	10470	3892	6999	6	8046	8878	13124	9	0.058475488	0.069743042	1.5	0.584962501
BP1026b	13021	acyl-CoA dehydrogenase domain-containing protein	109799	80287	93014	50	107591	106836	111594	58	6.73E-06	1.31E-05	1.16	0.214124805
BP1026b	13022	hypothetical protein	19976	17890	16876	15	19344	20043	19139	16	4.10E-06	8.17E-06	1.066666667	0.093109404
BP1026b	13024	ubiE/COQ5 methyltransferase family protein	5290	2367	2243	4	2900	3492	3791	5	3.34E-05	5.92E-05	1.25	0.321928095
BP1026b	13023	SyrP-like protein	3											

BP1026b_13075	acetyltransferase	6032	5054	5219	11	5939	7215	8287	15	0.009395757	0.01239314	1.363636364	0.447458977
BP1026b_13076	thioesterase domain-containing protein	69126	58883	63730	81	53668	54288	54897	69	1.24E-16	9.13E-16	0.851851852	-0.231325546
BP1026b_13077	hypothetical protein	7554	5294	4455	8	5290	6351	6420	10	9.72E-04	0.004442244	1.25	0.31928095
BP1026b_13078	RNA domain-containing protein	137993	20193	185077	325	131483	129402	103832	239	3.81E-32	2.90E-30	0.701538383	-0.511408904
BP1026b_13079	C4-dicarboxylate transport transcriptional regulatory protein	183781	95148	117876	97	169061	183454	197067	134	0.019740888	0.025036833	1.381443299	0.466176348
BP1026b_13080	C4-dicarboxylate transport sensor protein	63173	42279	45733	26	57391	61761	68644	33	0.003166174	0.004417129	1.269230769	0.343954401
BP1026b_13081	C4-dicarboxylate transporter DctA	132466	127153	131779	103	90145	82638	79048	66	9.63E-30	2.77E-28	0.640776699	-0.462106408
BP1026b_13082	acetate permease	22229	29531	28601	15	14983	17150	17075	9	1.80E-27	4.23E-26	0.6	-0.736965594
BP1026b_13083	hypothetical protein	10120	10795	9963	33	8272	8995	6870	26	8.95E-15	4.10E-14	0.787878788	-0.439544401
BP1026b_13084	CAIB/BAIF family protein	108785	42232	57772	57	80941	91338	101818	75	0.007891883	0.010497951	1.315789474	0.395928676
BP1026b_13085	acyl-CoA dehydrogenase domain-containing protein	76929	72224	74632	65	65870	16659	83290	64	2.45E-08	6.61E-08	0.984615385	-0.023267913
BP1026b_13086	acyl-CoA dehydrogenase domain-containing protein	28533	31261	33101	25	39395	37795	38794	31	2.16E-04	3.47E-04	1.111111124	0.310340121
BP1026b_13087	enoyl-CoA hydratase/isomerase/3-hydroxyacyl-CoA dehydrogenase	47555	30228	33829	17	51377	53723	53697	24	0.033932721	0.041751044	1.411764706	0.497496659
BP1026b_13088	LysR family transcriptional regulator	12987	12314	10449	13	11675	12885	12365	13	1.55E-06	3.26E-06	1	0
BP1026b_13089	hypothetical protein	4888	3786	3957	10	3509	4768	3907	10	2.81E-06	5.71E-06	1	0
BP1026b_13090	hypothetical protein	14552	6693	8369	5	15115	14866	19595	8	0.69248007	0.713671464	1.6	0.678071905
BP1026b_13092	lipovI synthase	323449	374362	355188	354	222960	234884	228427	231	1.36E-22	1.99E-21	0.652542373	-0.618586509
BP1026b_13093	lipote-protein ligase B	137489	127963	134710	174	96862	99302	92020	125	2.64E-23	4.30E-22	0.718390805	-0.477159211
BP1026b_13094	hypothetical protein	3453	4277	3400	11	2588	2508	3390	8	6.49E-14	3.45E-13	0.727272727	-0.459431619
BP1026b_13095	DNA-binding transcriptional activator GcvA	33703	22113	26317	28	31959	32557	31670	33	4.61E-05	8.04E-05	1.178571429	0.237039197
BP1026b_13096	hypothetical protein	152179	213475	196914	606	175965	172533	154386	542	5.97E-16	4.09E-15	0.894389439	-0.161024942
BP1026b_13097	D-amino acid aminotransferase	243468	280706	270684	279	240959	236324	228696	248	1.03E-09	3.34E-09	0.888888889	-0.169925001
BP1026b_13098	penicillin-binding protein 6	279335	331758	326341	237	220999	223035	230472	172	1.02E-17	8.52E-17	0.725738397	-0.462478494
BP1026b_13099	esterase/lipase-thioesterase family protein	67541	73899	70954	109	59377	61859	65501	96	3.90E-12	1.69E-11	0.880733945	-0.183221824
BP1026b_13100	ferredoxin, 2Fe-2S	19490	18619	19152	60	12805	13830	13863	42	3.02E-19	3.25E-18	0.7	-0.354573173
BP1026b_13101	hypothetical protein	13315	96139	10242	9	13743	12042	12102	10	7.02E-05	0.000111111	1.111111111	0.15200309
BP1026b_13102	hypothetical protein	29660	15235	19591	33	25229	25869	30480	42	0.001783956	0.002570669	1.272727273	0.347923303
BP1026b_13103	ABC transporter substrate-binding protein	190822	171222	162550	188	164484	164159	150920	171	2.22E-15	1.41E-14	0.909574668	-0.136736337
BP1026b_13104	ABC transporter ATP-binding protein	170768	125550	136869	171	154003	153951	138823	176	2.84E-10	9.75E-10	1.029239766	-0.54179104
BP1026b_13105	ABC transporter permease	102442	102873	91550	87	89625	94332	95068	82	2.99E-10	1.02E-09	0.942528736	-0.085391491
BP1026b_13106	2',3'-cyclic-nucleotide 2'-phosphodiesterase	27652	25582	27145	13	27428	26025	27071	13	1.02E-07	2.55E-07	1	0
BP1026b_13107	hypothetical protein	1719	282	160	0	1053	1302	1575	1	0.060437279	0.071904865	#DIV/0!	#DIV/0!
BP1026b_13108	biotin-protein ligase	8786	9029	6080	7	8079	8034	7722	8	2.16E-04	4.38E-04	1.142857143	0.192645078
BP1026b_13109	type III pantothenate kinase	25496	14780	17003	24	16148	15707	19196	21	3.99E-10	3.35E-09	0.875	-0.192645078
BP1026b_13110	hypothetical protein	1704	870	1078	2	1437	1677	1994	4	0.311149905	0.336913225	2	1
BP1026b_13111	bifunctional ADP-lyase synthase	35864	32234	32523	70	45175	48533	45535	95	0.003748171	0.005176045	1.357142857	0.440572591
BP1026b_13112	hypothetical protein	361993	549856	488020	538	362345	346688	316101	394	6.15E-22	8.44E-21	0.732342007	-0.449410543
BP1026b_13113	patatin	135161	76541	94704	82	127137	140686	153344	112	0.003368387	0.004682551	1.365853659	0.449802917
BP1026b_13114	hypothetical protein	89970	95159	89778	115	115887	113512	105135	140	7.03E-05	2.00E-04	1.217913091	-0.083792966
BP1026b_13115	enoyl-CoA hydratase	56280	36280	30749	46	57943	64904	70762	78	0.699165022	0.023442803	1.698963171	0.718400263
BP1026b_13116	fumarylacetoacetate (FAA) hydrolase family protein	54538	34588	40881	43	59649	63104	61755	61	0.117468374	0.134421245	1.418604651	0.504472583
BP1026b_13117	IcIR family transcriptional regulator	15595	10577	11159	13	14037	16309	18016	16	0.008496205	0.01263541	1.230769231	0.299626282
BP1026b_13118	hypothetical protein	9600	7302	8182	6	8171	8689	8378	6	6.37E-07	1.42E-06	1	0
BP1026b_13119	hypothetical protein	480733	795260	721185	2580	857910	826563	796623	3204	0.058409515	0.069677624	1.241860465	0.312503082
BP1026b_13120	5-methyltetrahydrofolate--homocysteine methyltransferase	91316	94269	93535	86	71255	71925	65845	64	1.70E-18	1.57E-17	0.744186047	-0.426264755
BP1026b_13121	methionine synthase	562623	637376	617707	223	592728	591719	550772	213	3.01E-12	1.32E-11	0.955156951	-0.066190208
BP1026b_13122	hypothetical protein	349952	367387	30749	1076	317865	307585	303530	128	0.001839793	0.023442803	1.34375	0.426264755
BP1026b_13123	arginyl-tRNA synthetase	154457	127637	138786	78	156451	172131	167450	92	1.56E-05	2.89E-05	1.179487179	0.238159737
BP1026b_13124	sporulation repeat-containing protein	91768	103780	105450	118	84780	83548	82351	98	2.37E-14	1.33E-13	0.830508475	-0.267933205
BP1026b_13125	thiol:disulfide interchange protein	412820	592124	544475	808	366786	363410	357394	567	9.20E-26	1.85E-24	0.701732673	-0.511006558
BP1026b_13126	short chain dehydrogenase	166772	229782	212461	260	159054	154714	141415	194	2.42E-29	6.66E-28	0.746153846	-0.422454971
BP1026b_13127	short chain dehydrogenase	131427	85944	100714	148	115725	127497	146212	181	3.30E-05	1.222927972	0.290325221	0
BP1026b_13128	MarK family regulatory protein	28887	13263	16418	39	26196	27560	31792	58	0.0559876	0.067018216	1.487179487	0.27578776
BP1026b_13129	acetyl-CoA acetyltransferase	1970	1023	1471	15	4392-05	13727	1510	237	8.76E-15	5.14E-15	0.877777778	-0.188072348
BP1026b_13130	peptide ABC transporter periplasmic peptide-binding protein	355386	478851	452074	270	381353	377501	379987	237	6.26E-04	4.27E-04	1.2	0.263034406
BP1026b_13131	peptide ABC transporter ATP-binding protein	10286	7549	10124	5	10069	11337	11209	6	2.69E-04	1.27E-04	1.2	0.263034406
BP1026b_13132	metallo-beta-lactamase family protein	55536	67825	62282	57	51002	51665	44874	45	4.24E-21	5.30E-20	0.789473684	-0.341036918
BP1026b_13133	bifunctional isocitrate dehydrogenase kinase/phosphatase protein	437372	557651	523291	279	580026	594672	561610	319	1.84E-07	4.42E-07	1.143369176	0.193291302
BP1026b_13134	carbonic anhydrase	158261	121141	125623	175	157902	159507	156824	205	4.97E-06	9.79E-06	1.171428571	0.228268988
BP1026b_13135	acetyl-CoA acetyltransferase	471505	364963	414728	349	623614	636786	646069	532	0.020881439	0.026424511	1.524355301	0.608199209
BP1026b_13136	short chain dehydrogenase	72809	61955	61304	96	85995	83538	80838	129	0.001839793	0.023442803	1.34375	0.426264755
BP1026b_13137	hypothetical protein	9992	7312	8233	18	7013	8614	9711	18	3.18E-07	7.43E-07	1	0
BP1026b_13138	hypothetical protein	91742	65508	73858	57	67013	70894	70041	52	9.96E-11	3.64E-10	0.912280702	-0.132450296
BP1026b_13139	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	31296	29723	33557	23	25986	24539	22412	18	4.29E-16	2.96E-15	0.782606860	-0.353636955
BP1026b_13140	8-amino-7-oxononanoate synthase	18866	7775	10109	10	14818	16110	18614	13	0.021536322	0.027187327	1.3	0.378511623
BP1026b_13141	dithiobiotin synthetase	9224	2571	3389	6	8626	9272	10334	3	0.798501882	0.813711157	2.166666667	0.174172717
BP1026b_13142	biotin synthase	84600	74090	74975	77	72350	76512	71538	72	2.05E-09	6.36E-09	0.995064935	-0.096861539
BP1026b_13143	Cu/Cu ⁺ family protein	18707	85073	80441	15	132698	138113	131313	18	0.001421988	0.000300874	0.3	0.263034406
BP1026b_13144	hypothetical protein	14386	7075	9216	12	10430	12588	11332	13	5.23E-05	9.07E-05	1.083333333	0.115477217
BP1026b_13145	alkaline phosphatase family protein	4794	3541	4004	2	3849	4347	4257	2	2.04E-05	3.72E-05	1	0
BP1026b_13146	alkaline phosphatase family protein subfamily	2700	3217	2943	1	2796	2845	2789	1	3.48E-07	8.08E-07	1	0
BP1026b_13147	hypothetical protein	3921	4932	5253	12	514E-05	5004	4005	13	3.14E-05	5.59E-05	1.083333333	0.115477217
BP1026b_13148	EAL domain-containing protein	6403	4178	5689	4	6077	6846	7479	5	0.00335682	0.004668544	1.25	0.321928095
BP1026b_13149	Na ⁺ /H ⁺ antiporter	22154	20911	18236	12	16981	18089	19489	10	1.81E-10	6.34E-10	0.833333333	-0.263034406
BP1026b_13150	2-oxoacid ferredoxin oxidoreductase	43029	33655	34629	10	38782	41447	41817					

BP1026B_13199	CzcA family heavy metal efflux protein	11654	9582	10579	3	12611	13754	13128	4	0.00214202	0.003145784	1.333333333	0.415037499
BP1026B_13200	RND family efflux transporter MFP subunit	16973	11169	13626	8	17751	17518	16192	11	0.001963977	0.002808756	1.375	0.459431619
BP1026B_13201	outer membrane efflux protein	10272	9124	10407	7	10340	10405	11247	8	9.56E-06	1.79E-05	1.142857143	0.192645078
BP1026B_13202	hypothetical protein	74964	17494	718	718	39955	23501	21084	775	8.44E-05	1.24E-04	1.078908187	0.10312466
BP1026B_13203	hypothetical protein	595291	568701	570243	1160	548580	562602	542661	1106	1.36E-12	6.20E-12	0.953448276	-0.06877342
BP1026B_13204	lipoprotein	412734	450864	423832	505	477807	463266	414151	531	2.77E-10	9.53E-10	1.051485149	0.072428473
BP1026B_13205	LemA family protein	533069	636678	604890	876	414695	448289	440098	643	2.39E-26	5.06E-25	0.734018265	-0.46112132
BP1026B_13207	copper-translocating P-type ATPase	311480	212829	223177	102	297548	321121	355868	134	0.002803768	0.00365636	1.31372549	0.393663848
BP1026B_13208	heavy metal binding protein	19312	11586	13064	72	24624	25922	25524	126	0.721889752	0.741054966	1.75	0.807354922
BP1026B_13209	hypothetical protein	38596	26279	32268	45	44106	42013	45681	62	0.004052229	0.005575041	1.377777778	0.462343214
BP1026B_13210	hypothetical protein	11643	13063	9234	20	14327	14305	17015	30	0.11048853	0.126851201	1.5	0.584962501
BP1026B_13211	argininosuccinate synthase	282400	407336	385336	267	324699	330149	323680	243	1.95E-11	7.79E-11	0.91011236	-0.35883428
BP1026B_13212	glutathione-disulfide reductase	174205	140328	138205	110	174728	184606	196392	136	2.83E-04	4.49E-04	1.236363636	0.306103128
BP1026B_13213	hypothetical protein	27027	15607	16008	86	247178	30745	40396	141	0.267456977	0.292382287	1.639534884	0.713286598
BP1026B_13214	manganese/iron transporter	11774	11113	11904	6	22722	22506	19560	13	0.758640846	0.775477523	2.166666667	1.154772717
BP1026B_13215	hypothetical protein	3017	4301	3971	26	3532	4260	4396	28	2.52E-04	4.02E-04	1.076923077	0.106915204
BP1026B_13216	hypothetical protein	257	391	303	2	374	108	239	2	5.90E-04	0.02E-04		0
BP1026B_13217	hypothetical protein	68370	17089	97324	0	219	261	1701	0	0.01695542	0.02176877	#DIV/0!	#DIV/0!
BP1026B_13218	carbohydrate porin	13984	11992	12991	8	22032	22449	26112	15	0.8979084	0.906154055	1.875	0.906890596
BP1026B_13219	glycoyl transferase family protein	5581	3445	3993	3	5188	5328	6198	4	0.01025201	0.013474317	1.333333333	0.415037499
BP1026B_13220	hypothetical protein	3832	2383	2562	2	2536	3594	2842	2	1.60E-05	2.97E-05	1	0
BP1026B_13221	hypothetical protein	5985	6628	5395	10	5773	6727	4085	9	9.68E-08	2.42E-07	0.9	-0.152003093
BP1026B_13222	hypothetical protein	18757	24968	23872	27	19811	19097	17684	22	1.18E-12	5.42E-12	0.81481481	-0.295455884
BP1026B_13223	outer membrane porin protein	140749	196369	187615	154	142763	147069	143393	127	6.27E-22	8.58E-21	0.824675325	-0.278101854
BP1026B_13224	hypothetical protein	54160	68759	64207	84	78754	68732	68732	101	7.57E-04	0.001141625	1.202380952	0.265898046
BP1026B_13225	alkyl-ubiquitin utilization operon protein PhnA	68370	81225	79048	244	90987	91253	133808	83	0.000801207	0.001405217	1.234606571	0.302872339
BP1026B_13226	hypothetical protein	16082	15444	15306	46	17437	16187	15208	48	3.01E-06	6.11E-06	1.043478261	0.601400545
BP1026B_13227	chromate transporter	25008	22103	22094	43	36373	36094	33523	66	0.073412655	0.080699396	1.534883721	0.68129365
BP1026B_13228	chromate transporter	7262	1954	2748	6	7019	8384	9745	13	0.288809064	0.314420216	2.166666667	1.154772717
BP1026B_13229	DNA-binding transcriptional activator GcvA	47626	29605	32508	46	62339	70954	70883	86	0.165784715	0.185674138	1.869565217	0.90270729
BP1026B_13230	uracil permease	103067	77952	80431	66	99703	99540	91346	74	6.17E-06	1.20E-05	1.121212121	0.165059246
BP1026B_13231	flagellar hook-associated protein FlgI	1142833	1158732	1165175	937	1343815	1427407	1624109	1188	0.019657706	0.024941436	1.267876201	0.342413883
BP1026B_13232	flagellar hook-associated protein FlgK	163941	1407564	1408749	754	1607367	1674918	1819435	848	0.063569172	0.073100557	1.124668435	0.160499741
BP1026B_13233	YcgR protein superfamily protein	192589	132289	137250	202	158834	178978	199193	235	1.51E-05	2.80E-05	1.163366337	0.218305644
BP1026B_13234	flagellar body rod assembly protein/muramidase FlgJ	205781	211189	201266	220	250770	248111	229617	259	0.004383887	0.006000899	1.177272727	0.235448571
BP1026B_13235	flagellar basal body P-ring protein	224382	182115	201393	169	252989	253271	263503	214	0.027954713	0.034785125	1.266272189	0.34085755
BP1026B_13236	flagellar basal body L-ring protein	127541	159308	150640	201	205417	208761	216397	290	0.014407124	0.043894635	1.44278609	0.528857399
BP1026B_13237	flagellar basal body rod protein FlgG	237760	281058	285074	339	346022	342543	345704	436	4.18E-04	6.48E-04	1.286135693	0.340324862
BP1026B_13238	flagellar basal body rod protein FlgF	225953	177783	187104	260	382308	394889	410533	519	0.232195722	0.250024292	1.996153864	0.997229315
BP1026B_13239	flagellar basal body rod protein FlgE	645409	1097341	994721	568	1008612	102726	1047471	838	0.008012207	0.011405217	1.234606571	0.302872339
BP1026B_13240	flagellar basal body rod modification protein	232670	247421	256079	291	277650	271278	270003	323	9.99E-05	1.66E-04	1.109965366	0.150515012
BP1026B_13241	flagellar basal body rod protein FlgC	87356	123114	118904	257	89458	84309	85886	203	7.00E-17	5.32E-16	0.789883268	-0.30288632
BP1026B_13242	flagellar basal body rod protein FlgB	98170	79985	87613	180	78853	81320	74196	158	6.03E-12	2.56E-11	0.877777778	-0.180727348
BP1026B_13243	flagellar basal body P-ring biosynthesis protein FlgA	31456	12745	17581	13	27709	29632	38366	20	0.125414114	0.142783353	1.538461538	0.681483777
BP1026B_13244	negative regulator of flagellin synthesis	164673	167180	172960	487	208521	190146	175349	554	5.84E-06	1.14E-05	1.137577002	0.185964204
BP1026B_13245	flagella synthase protein FlgN	477782	456101	429657	974	529740	568037	636290	1189	4.51E-06	8.95E-06	1.22073922	0.287755038
BP1026B_13246	RebH protein	6545	10519	10596	41	7357	6900	6164	30	3.27E-16	2.29E-15	0.731707317	-0.450664091
BP1026B_13247	multifunctional tRNA nucleotidyl transferase/2'3'-cyclic phosphodiesterase/2' nucleotidase/phosphatase	67399	50411	50354	45	59008	66569	72520	53	5.54E-04	8.49E-04	1.177777778	0.236067358
BP1026B_13248	glutathione S-transferase domain-containing protein	21565	12411	13102	24	15753	17160	17465	25	9.04E-06	1.73E-05	0.041666667	0.058893689
BP1026B_13249	nucleoside-diphosphate-sugar epimerase	34130	21430	21787	27	30748	31914	34387	34	5.06E-04	8.58E-04	1.259259259	0.332575319
BP1026B_13250	soluble lytic murein transglycosylase	518839	475958	495603	253	493142	504579	505082	256	2.37E-11	9.35E-11	1.011857708	0.017060425
BP1026B_13251	5-formyltetrahydrofolate cyclo-lyase	10433	3893	5241	10	9967	10605	12553	18	0.697768543	0.718885223	1.8	0.847996607
BP1026B_13252	hypothetical protein	70690	9839	97324	173	68344	68326	66853	18	0.063569172	0.073100557	1.124668435	0.160499741
BP1026B_13253	hypothetical protein	16288	17614	7848	16	8871	12357	16426	19	4.11E-04	6.38E-04	1.1875	0.247927513
BP1026B_13254	urea amidolase-like protein	127041	51016	65884	75	81341	100659	127838	95	9.51E-04	0.001413485	1.266666667	0.341036918
BP1026B_13255	LamB-YcsF family protein	166565	121130	132729	183	134085	148631	148504	187	1.70E-10	5.99E-10	1.021857923	0.03194622
BP1026B_13256	hypothetical protein	8442	4357	6186	8	5595	6695	9341	9	1.53E-04	2.50E-04	1.125	0.169925001
BP1026B_13257	hypothetical protein	62197	66544	65244	67	57743	53654	50459	56	1.28E-17	1.06E-16	0.835820896	-0.258734268
predicted RNA	CumX family protein	20064222	24675389	24467680	111444	1956788	18507787	15794675	86747	2.03E-04	3.27E-04	0.737990941	-0.361433175
BP1026B_13258	dipeptide transport ATP-binding subunit	60101	33667	44141	49	173578	173578	173578	48	1.73E-04	4.31E-04	0.933333333	0.230334406
BP1026B_13259	peptide ABC transporter ATP-binding protein	452002	338325	356884	376	490904	525259	527892	508	6.00E-04	9.19E-04	1.3106383	0.343095835
BP1026B_13260	peptide ABC transporter ATP-binding protein	1140893	1318446	1242585	1242	1108695	1075040	996819	1067	0.796665682	0.811431343	0.859098229	-0.21914909
BP1026B_13261	dipeptide transport system permease	70785	53156	59806	66	62402	64993	65160	69	1.70E-06	3.55E-06	1.045454545	0.064130337
BP1026B_13262	dipeptide ABC transporter permease	89703	104182	102797	97	75821	72713	69482	71	9.54E-20	1.03E-18	0.731958763	-0.450165723
BP1026B_13263	dipeptide ABC transporter substrate-binding protein	1438149	2099451	1948486	1135	1296046	1279531	1232030	787	0.61014791	0.633510112	0.69339207	-0.258955672
BP1026B_13264	major facilitator family transporter	39157	37418	38364	30	39621	34589	34023	28	4.15E-11	1.59E-10	0.933333333	-0.209935674
BP1026B_13265	high potential iron-sulfur protein	1386326	832678	832678	2583	93725509	8405777	8405777	243	0.137255609	0.153818473	1.093480808	0.230334406
BP1026B_13266	oxidoreductase, FAD-binding family protein	136679	124714	117752	112	164342	162258	155563	146	0.001324921	0.001972723	303571429	0.332469637
BP1026B_13267	ATP-dependent protease	135891	164090	154328	154	237504	228559	223916	234	0.012294248	0.019782902	1.51948051	0.603578179
BP1026B_13268	hypothetical protein	44174	41879	48573	79	44462	44582	52292	83	1.37E-08	3.81E-08	1.050632911	0.071258683
BP1026B_13269	endonuclease/exonuclease/phosphatase family protein	87022	55732	60327	83	85493	84989	85565	104	0.002671716	0.003755751	1.253012048	0.325400287
BP1026B_13270	LysE type translocator	31133	16193	21980	35	30392	28173	25814	43	4.54E-04	7.02E-04	1.228514729	0.296981738
BP1026B_13271	ferredoxin-NADP reductase	265060	382982	361026	436	277057	264585	243442	339	3.62E-14	1.98E-13	0.7775229	

BP1026b	13320	major facilitator superfamily mureopeptide transporter	105759	103921	102193	79	94178	98853	83424	70	3.07E-12	1.34E-11	0.886075949	-0.174497731
BP1026b	13321	M48 family peptidase	63369	49825	48395	51	52867	56213	65807	55	1.48E-06	3.12E-06	1.078431373	0.108934372
BP1026b	13322	AraC family transcriptional regulator	10513	8639	9417	10	10795	10670	12210	11	3.85E-04	6.00E-04	1.1	0.137503524
BP1026b	13323	NAD(P)-dependent alcohol dehydrogenase	12745	12745	12078	11	16272	15325	13880	13	6.62E-04	0.001905985	1.181818181	0.2410081
BP1026b	13324	exodeoxyribonuclease III	82584	125858	110881	138	94911	92722	84015	117	9.65E-14	5.02E-13	0.847826087	-0.238159737
BP1026b	13325	hypothetical protein	56480	54379	55097	65	70809	72847	71443	85	0.012946446	0.016811057	1.307692308	0.387023123
BP1026b	13326	aspartyl/glutamyl-L-lysine amidotransferase subunit B	149058	194532	177979	118	207656	208076	203066	140	9.28E-04	0.001382042	1.186440678	0.246639968
BP1026b	13327	aspartyl/glutamyl-L-lysine amidotransferase subunit A	92460	100000	96166	64	107630	109397	100372	70	8.80E-07	1.92E-06	1.09375	0.129283017
BP1026b	13328	aspartyl/glutamyl-L-lysine amidotransferase subunit C	10882	11999	11492	38	10823	10537	9373	34	3.35E-10	1.14E-09	0.894736842	-0.160464672
BP1026b	13329	rod shape-determining protein MreB	187348	269547	246571	224	173092	174294	158112	161	4.13E-30	1.22E-28	0.71875	-0.476438044
BP1026b	13330	rod shape-determining protein MreC	13288	13805	13451	12	13667	14901	13574	12	7.12E-07	1.58E-06	1	0
BP1026b	13331	rod shape-determining protein MreD	21207	17381	19205	37	21069	19998	16817	37	1.71E-07	4.11E-07	1	0
BP1026b	13332	penicillin-binding protein 2	66084	76910	75247	30	76469	75717	68361	30	1.85E-07	4.44E-07	1	0
BP1026b	13333	rod shape-determining protein RodA	59158	66762	62462	54	65516	66479	57488	54	1.19E-07	2.92E-07	1	0
BP1026b	13334	hypothetical protein	9269	3491	5280	7	7389	8278	9602	10	0.042092621	0.05117783	1.428571429	0.514573173
BP1026b	13335	Hspc1/Hspal aldolase family protein	15665	6051	8353	12	15050	19143	27552	26	0.204702003	0.226907334	2.166666667	1.115472721
BP1026b	13336	6-pyruvyl-tetrahydropterin synthase	49278	78960	69586	145	57480	59872	65349	134	1.07E-10	3.88E-10	0.924137931	-0.1138199
BP1026b	13337	hypothetical protein	46237	31711	24966	66	32793	31085	34242	51	4.03E-18	3.35E-17	0.722992723	-0.573949599
BP1026b	13338	hypothetical protein	211767	198533	202362	277	193873	179816	163069	243	1.77E-16	2.29E-15	0.877256138	-0.188929662
BP1026b	13340	hypothetical protein	298357	522930	491304	923	286403	267355	272144	580	1.57E-25	3.09E-24	0.628385699	-0.670277748
BP1026b	13341	predicted RNA	11220	19082	15979	593	10157	10301	10155	485	1.71E-21	2.23E-20	0.682967696	-0.550110197
BP1026b	13342	hypothetical protein	125003	206798	185658	245	85102	81105	79587	116	4.49E-66	9.38E-64	0.473469388	1.078656944
BP1026b	13343	hypothetical protein	298744	533280	503033	1246	318274	306824	346371	907	4.85E-21	6.00E-20	0.727929374	-0.458129612
BP1026b	13344	hypothetical protein	121966	122913	124854	451	182673	182827	169817	653	0.074343887	0.08714438	1.44789357	0.533955558
BP1026b	13345	hypothetical protein	46622	75290	66640	193	73152	67544	64125	210	1.47E-05	7.73E-05	1.088082902	0.12178848
BP1026b	13346	Phage portal protein	57488	6444	4720	64	6474	6474	5860	64	1.77E-07	4.11E-07	1	0
BP1026b	13347	Trf RNA	18908	32552	28313	349	28190	24949	24326	339	1.88E-08	5.15E-08	0.971346705	-0.041941763
BP1026b	13348	ClpXP protease specificity-enhancing factor	109017	171810	154736	278	94212	90891	95039	178	3.07E-31	1.03E-29	0.64028777	-0.643207642
BP1026b	13349	stringent starvation protein A	338338	590981	463718	714	264206	259741	249272	421	1.33E-28	3.42E-27	0.589635854	-0.267103841
BP1026b	13350	cytochrome c1	1844099	2329057	2256160	2821	1852055	1797921	1665364	2334	0.241153755	0.264829439	0.827366182	-0.273401081
BP1026b	13351	ubiquinol-cytochrome c reductase, cytochrome b	1470086	2216392	2028251	1377	1078637	1037081	971548	744	0.121429639	0.138574469	0.54035011	-0.888154033
BP1026b	13352	ubiquinol-cytochrome c reductase, iron-sulfur subunit	327064	336364	323783	529	260441	272942	252726	421	2.27E-13	1.14E-12	0.7958412	-0.383647889
BP1026b	13353	hypothetical protein	156660	119334	120118	168	166933	171311	177892	224	0.004883517	0.006463395	1.333323233	-0.415037499
BP1026b	13354	DcpG protease	263043	256744	280591	220	256537	257556	250408	210	7.73E-08	1.96E-07	0.954545455	-0.067114196
BP1026b	13355	twin arginine translocase protein C	158595	172721	159266	208	149041	147438	131230	182	3.42E-18	3.05E-17	0.875	-0.192645078
BP1026b	13356	twin arginine translocase protein B	154177	175554	178333	320	199649	188200	172482	353	4.57E-07	1.04E-06	1.10325	0.141596278
BP1026b	13357	twin arginine translocase protein A	284918	369881	372820	1463	331377	321169	302288	1360	1.34E-10	4.78E-10	0.929596719	-0.105232118
BP1026b	13358	predicted RNA	17884	4974	10254	478	15534	18762	30858	944	0.407952745	0.435631775	1.97489397	0.981776241
BP1026b	13359	Mta/Hcf106 family protein	180636	239983	221843	590	221879	202669	170554	533	2.23E-13	1.12E-12	0.903389831	-0.146579241
BP1026b	13360	phosphoribosyl-ATP pyrophosphatase	190947	289391	273682	632	198312	178285	182965	496	1.78E-22	5.87E-21	0.76792308	-0.331399903
BP1026b	13361	phosphoribosyl-AMP cyclohydrolase	34265	44213	37468	104	39868	40798	35269	104	1.28E-09	4.08E-09	1	0
BP1026b	13362	imidazole glycerol phosphate synthase subunit HisF	81709	90448	92056	212	76034	72275	74963	179	2.51E-13	1.24E-12	0.844339623	-0.244104677
BP1026b	13363	imidazole-4-carboxamide isomerase	92224	55196	65553	91	78610	89703	98715	114	0.001931683	0.002768259	1.252747253	0.325095374
BP1026b	13364	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	357253	483610	441297	653	335893	321309	302892	489	3.36E-19	3.38E-18	0.748851455	-0.417284527
BP1026b	13365	imidazole glycerol phosphate synthase subunit HisH	25549	44555	40214	593	25961	23919	21533	392	2.45E-24	4.28E-23	0.661045331	-0.071778453
BP1026b	13366	hypothetical protein	65380	72802	73802	114	72802	59701	58717	97	1.21E-14	9.87E-14	0.850877193	-0.232971732
BP1026b	13367	imidazoleglycerol-phosphate dehydratase	17986	62317	55245	88	46069	43787	40976	70	1.85E-21	2.40E-20	0.795454545	-0.330148602
BP1026b	13368	histidinol-phosphate aminotransferase	18782	16530	15107	15	16464	17795	17365	16	1.00E-06	2.17E-06	1.066666667	0.093109404
BP1026b	13369	histidinol dehydrogenase	116986	79966	88754	71	133747	140962	140681	103	0.01837947	0.023428776	1.450704225	-0.536753408
BP1026b	13370	ATP phosphoribosyltransferase catalytic subunit	56329	43556	45575	73	59440	60885	57537	90	9.24E-04	0.001377267	1.232876712	0.302028537
BP1026b	13371	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	87575	68251	78772	57	88552	90443	92507	67	7.42E-05	1.26E-04	0.175438596	-0.233199176
BP1026b	13372	BoA-like protein	19032	19032	28664	109	15380	15653	15653	74	2.57E-21	3.35E-20	0.785870812	-0.538730967
BP1026b	13373	ABC transporter permease	15463	52275	49109	60	33528	30469	30043	56	3.20E-25	6.02E-24	0.683333333	-0.549338591
BP1026b	13374	ABC transporter ATP-binding protein	60188	68713	69985	71	52936	53927	50712	76	5.81E-21	7.12E-20	0.788732940	-0.34292197
BP1026b	13375	hypothetical protein	24104	24170	25337	90	26924	26787	23697	95	1.35E-06	2.86E-06	1.055555556	0.78002512
BP1026b	13376	hypothetical protein	289872	348200	360092	525	289632	284177	270321	444	4.51E-12	1.95E-11	0.845714286	-0.24157746
BP1026b	13377	lipoprotein VacJ	167950	176503	180525	182	176485	176615	167525	180	6.43E-11	2.40E-10	0.989010989	-0.015941544
BP1026b	13378	ABC transporter substrate-binding protein	110390	145962	126181	227	103336	101521	88423	174	8.64E-20	9.37E-19	0.766519824	-0.383646991
BP1026b	13379	ABC transporter permease	104226	114571	114571	146	93624	79824	77586	146	5.96E-24	9.94E-23	0.93123076	-0.531613076
BP1026b	13380	ABC transporter ATP-binding protein	85873	104088	98222	117	74610	74679	67495	88	1.81E-18	1.67E-17	0.75213652	-0.410933101
BP1026b	13381	thiamine-phosphate pyrophosphorylase	64951	28286	33871	38	47880	54747	63557	50	0.003710778	0.00512893	1.315789474	0.392952876
BP1026b	13382	thiazole synthase	212601	180851	179605	234	198284	209159	209749	252	6.29E-06	1.23E-05	1.076923077	0.106915204
BP1026b	13383	sulfur carrier protein ThiS	2938	3477	3727	17	2768	2541	2061	12	3.85E-16	2.67E-15	0.705882353	-0.502500341
BP1026b	13384	oxidoreductase, FAD-binding protein	212419	176981	176218	166	193564	195214	193061	171	7.12E-09	2.06E-08	1.030120482	0.042813084
BP1026b	13385	ABC transporter ATP-binding protein	131850	141140	137765	77	122717	115389	104563	64	3.47E-08	0.08E-07	0.331168831	-0.266786541
BP1026b	13386	2,5 RNAse ligase	9534	20666	20666	8	92319	11855	135	5.62E-33	1.08E-32	0.585790674	-0.875	
BP1026b	13387	amino acid carrier protein	50533	27085	35303	24	53443	58004	60794	37	0.281529463	0.306855848	1.541666667	0.624490865
BP1026b	13388	glutamate synthase subunit beta	165779	175358	174038	112	204475	209596	206474	135	0.001944039	0.002872783	1.205357143	-0.392646075
BP1026b	13389	glutamate synthase, large subunit	460269	458495	458617	97	620933	628102	613488	131	3.62E-04	5.66E-04	1.350515464	0.433510159
BP1026b	13390	transposase	268649	391365	207375	311	192378	195930	180790	265	2.89E-17	2.30E-16	0.852090032	-0.203922221
BP1026b	13391	OmpW family outer membrane protein	351689	402829	424249	536	500962	482199	436770	646	2.28E-06	4.71E-06	1.205233881	0.269301164
BP1026b	13392	glycerophosphodiester phosphodiesterase												

BP1026b	13442	50S ribosomal protein L4	324141	527744	468484	708	537161	508379	470654	813	1.38E-07	3.37E-07	1.148305085	0.199505992
BP1026b	13443	50S ribosomal protein L3	300963	438081	412075	570	453994	428336	402799	637	5.92E-08	1.52E-07	1.11754386	0.160331453
BP1026b	13444	30S ribosomal protein S10	195994	209276	209602	656	255679	254286	244120	805	0.013044304	0.016924092	1.227134146	0.295299968
BP1026b	13445	elongation factor Tu	651835	232706	217174	177	205110	242496	225822	200	0.87494667	0.08823574	1.1832807	0.24189688
BP1026b	13446	elongation factor G	798198	1195648	1078576	486	1291554	1255637	1208340	595	0.078094855	0.091096127	1.224279835	0.291933555
BP1026b	13447	30S ribosomal protein S7	294710	496674	430609	864	437997	423220	381150	879	1.73E-10	6.11E-10	1.01736111	0.024813853
BP1026b	13448	30S ribosomal protein S12	287644	471858	406403	1020	372887	347409	330376	919	1.41E-12	6.41E-12	0.90080392	-0.150432386
BP1026b	13449	ATP-dependent DNA helicase RecQ	329436	319572	318140	174	318177	334674	339672	179	2.32E-08	6.29E-08	1.028735632	0.040872281
predicted RNA	-		6613	169	531	162	6526	8755	9132	542	2.57E-11	1.01E-10	3.345679012	1.742299038
BP1026b	13450	DNA-directed RNA polymerase beta prime subunit	1356907	1836938	1681323	383	2274252	2176577	1987684	506	0.02918964	0.036249783	1.321148825	0.401792993
BP1026b	13451	DNA-directed RNA polymerase subunit beta	651832	182482	807100	190	1057324	1023006	941834	245	0.03064999	0.04305627	1.289173684	0.366782331
BP1026b	13452	50S ribosomal protein L7/L12	986740	1104691	1140399	2881	1506445	1466614	1341338	3940	0.01155674	0.01457623	1.330787921	0.412280677
BP1026b	13453	50S ribosomal protein L7/L12	795144	812065	892079	2776	1178854	1158723	1096533	3815	0.028693072	0.035675547	1.374279539	0.458675489
BP1026b	13454	50S ribosomal protein L10	470387	772575	696423	1164	715394	690809	646030	1232	0.012306909	0.538425247	1.058419244	0.081911198
predicted RNA	-		25220	36845	29102	844	44401	36825	32918	1056	2.48E-04	3.96E-04	1.251184834	0.323294931
BP1026b	13455	50S ribosomal protein L1	672861	759768	762630	1046	1018292	974338	873139	1366	0.02981074	0.03697124	1.305927342	0.385074632
BP1026b	13456	50S ribosomal protein L11	307136	485164	412295	929	487899	459641	388717	1011	1.97E-08	5.38E-08	1.109795479	0.150293831
BP1026b	13457	transcription antitermination protein NusG	315194	530799	465229	783	39392	382936	340415	672	9.80E-14	6.49E-15	0.858297548	-0.20551075
BP1026b	13458	preprotein translocase subunit SecE	204592	323293	300008	732	264312	250936	224216	646	7.06E-10	3.32E-09	0.882513661	-0.180309484
BP1026b	13459	Trp tRNA	52838	73045	62187	824	96007	89679	74541	1141	0.040643947	0.049541484	1.384708738	0.469582549
BP1026b	13460	elongation factor Tu	1919107	2804822	2569766	2041	2925559	2848640	2587294	2340	0.114828717	0.131496724	1.146496815	0.197232347
BP1026b	13461	Thr tRNA	72815	119870	95899	1282	107117	100316	71938	1241	2.50E-09	7.70E-09	0.968018721	-0.046893146
BP1026b	13462	Gly tRNA	113756	190463	187796	2216	124780	129763	137315	1765	3.44E-23	5.40E-22	0.796480144	-0.328289698
BP1026b	13463	Tyr tRNA	13099	22858	19942	216	15375	14833	14929	174	2.30E-13	1.14E-12	0.805555556	0.311940066
BP1026b	13464	5S ribosomal RNA	1842276	2541390	1679461	17885	3068278	2585105	1468152	21007	0.076330548	0.089237505	1.174386867	0.20028
BP1026b	13465	23S ribosomal RNA	407475	287313	21356	104	20722	318832	274738	301	0.34603382	0.819422	4.086338812	2.30879313
BP1026b	13466	hypothetical protein	30372	45181	38892	295	54052	51867	43621	386	0.001929087	0.002765172	1.308474576	0.37885893
BP1026b	13467	Ala tRNA	106256	167474	137033	1801	157623	156463	118280	1896	1.48E-09	4.67E-09	1.052748473	0.08160783
BP1026b	13468	Ile tRNA	19951	28936	22969	311	27304	26234	19832	317	3.42E-07	7.93E-07	1.019292605	0.26756826
BP1026b	13469	16S ribosomal RNA	846448	220308	175908	272	157411	7214478	323976	1688	3.37E-62	5.41E-60	6.205882353	2.633636347
BP1026b	13470	hypothetical protein	54937	82314	67560	583	81113	86467	69377	675	1.26E-04	2.08E-04	1.15780446	0.213191619
BP1026b	13471	lipase acylhydrolase	14887	13372	6752	10	12114	12329	13068	99	1.03E-09	3.34E-09	0.661971831	-0.351003093
BP1026b	13472	phenylacetate-CoA oxygenase subunit PaaA	118939	180646	148924	94	96643	92458	81858	301	5.65E-23	8.19E-22	0.661971831	-0.351003093
BP1026b	13473	phenylacetate acid degradation protein PaaB	24361	27067	24458	88	18848	20432	24783	74	1.32E-12	6.02E-12	0.840090991	-0.49978253
BP1026b	13474	phenylacetate-CoA oxygenase subunit PaaC	74355	81445	73198	99	58252	57765	56117	71	9.25E-25	1.67E-23	0.717171717	-0.249696501
BP1026b	13475	phenylacetate acid degradation protein PaaD	24209	8425	12931	24	13943	14594	15701	23	7.50E-08	1.90E-07	0.958333333	-0.061400545
BP1026b	13476	phenylacetate-CoA oxygenase/reductase subunit PaaK	152922	166155	162761	147	120230	115179	106434	105	9.55E-29	2.49E-27	0.714285714	-0.485426827
BP1026b	13477	hypothetical protein	62777	36257	45882	59	43590	48090	52200	59	1.77E-10	6.23E-10	0.717171717	-0.249696501
BP1026b	13478	TerF family transcriptional regulator	57643	64733	55579	99	46056	47042	50782	79	2.44E-20	7.78E-19	0.797979798	-0.325575072
BP1026b	13479	acyltansferrase	110441	142380	135589	199	20722	318832	274738	301	0.34603382	0.819422	4.086338812	2.30879313
BP1026b	13480	transcriptional regulator	52835	89877	74837	160	45471	43896	38107	94	2.44E-47	2.28E-45	0.5875	-0.767339243
BP1026b	13481	4-hydroxyphenylpyruvate dioxygenase	25624	31111	30794	28	32451	31291	28767	28	3.14E-08	8.37E-08	1	0
BP1026b	13482	outer membrane protein	268	97	100	0	261	496	167	1	0.006137359	0.008274734	#DIV/0!	#DIV/0!
BP1026b	13483	indolepyruvate ferredoxin oxidoreductase	89279	85717	84201	24	97089	102659	99353	27	2.62E-05	4.73E-05	1.125	0.169925001
BP1026b	13484	malic enzyme	272913	252839	262863	113	370805	381928	387884	163	0.00272107	0.009704005	1.442477876	0.528549192
BP1026b	13485	orotate phosphoribosyltransferase	103445	125673	115889	167	123386	125389	117607	177	1.18E-08	3.33E-08	1.05988024	0.063901258
BP1026b	13486	phosphatidylcholine-binding protein	15300	89867	89657	21	10512	10512	10512	30	0.0545475	0.06030486	0.661971831	-0.351003093
BP1026b	13487	flavodoxin domain-containing protein	11977	15150	15399	24	11555	12191	12112	20	4.59E-12	1.98E-11	0.833333333	-0.263044066
BP1026b	13488	N-acetyl-gamma-glutamyl-phosphate reductase	138565	84205	97955	113	137164	141769	148211	150	0.001081848	0.001596395	1.327433628	-0.403639728
BP1026b	13489	hypothetical protein	912	1252	1882	7	2888	3021	3155	16	0.001365313	0.001989529	2.285714286	1.192645078
BP1026b	13490	lipoprotein	3868	3196	4009	2	4532	4792	4375	3	0.010928834	0.014296195	0.5	0.584962501
BP1026b	13491	lipoprotein	3923	2437	2170	2	2665	2903	2941	2	4.19E-06	8.34E-06	1	0
BP1026b	13492	OmpW family outer membrane protein	16894	21211	21631	23	34426	36108	33999	41	0.570687348	0.595669126	1.782086896	0.833990049
BP1026b	13493	Islm1, transposase	68536	99075	88239	69	76137	71347	63870	57	8.16E-14	0.036046957	-0.275444343	0
BP1026b	13494	transcriptional regulator	10067	4588	4588	6	8605	11436	11655	11	0.867837956	0.87863859	1.833333333	0.874469118
BP1026b	13495	MFS permease	1567	483	807	0	1171	1155	1686	1	0.674937763	0.69662385	#DIV/0!	#DIV/0!
BP1026b	13496	amino acid transporter LysE	62356	54110	57310	86	61673	59774	60679	90	6.33E-07	1.41E-06	1.046511628	0.065588342
BP1026b	13497	dehydrogenase	68373	66122	68729	77	54147	55867	54100	62	3.43E-19	3.44E-18	0.805194805	-0.31259023
BP1026b	13498	hypothetical protein	31626	17411	19535	30	32566	33803	32768	43	0.027091465	0.033791269	1.433333333	0.519374159
predicted RNA	-		60408	7777	6078	557	26137	43302	62138	1044	0.954919661	0.95881776	1.87432675	0.963972479
BP1026b	13499	hypothetical protein	1255605	1360632	181108	6580	1365048	1306408	1373577	503	0.57878708	0.60030486	0.661971831	-0.351003093
predicted RNA	-		82103	190865	127662	1519	91505	87926	83263	1174	3.68E-18	1.26E-17	0.772876893	-0.371689461
BP1026b	13500	hypothetical protein	19773	9014	11273	35	12703	13314	14450	36	7.43E-07	1.64E-06	1.028571429	0.040641984
BP1026b	13501	hypothetical protein	72233	97739	92646	275	67838	64677	62835	204	4.34E-19	4.27E-18	0.741818182	-0.403624646
BP1026b	13502	amino acid permease	40968	52544	47250	33	31659	32007	27643	21	7.96E-29	2.10E-27	0.636363636	-0.650276697
BP1026b	13503	Ala tRNA	1679	2831	2546	30	1937	1934	2119	26	4.63E-10	1.55E-09	0.866666667	-0.206450877
BP1026b	13504	cytochrome c family protein	25972	31654	30515	87	24869	25797	23966	74	1.64E-12	7.40E-12	0.850574713	-0.2349013
BP1026b	13505	phospholipid-binding domain-containing protein	51835	67376	67376	79	46236	46236	46236	57	7.62E-34	3.76E-32	0.741818182	-0.567403059
BP1026b	13506	phosphohexose isomerase	12885	9813	11640	19	10903	10413	9479	13	4.03E-10	1.36E-09	0.894736842	-0.160464672
BP1026b	13507	hypothetical protein	4862	1157	1271	5	2850	3694	5943	9	0.65763215	0.679882454	1.8	0.847996907
BP1026b	13508	hypothetical protein	18905	8667	10848	12	13046	13919	19116	15	9.39E-04	0.001398294	1.25	0.321928095
BP1026b	13509	rare lipoprotein A family protein	26604	30152	29951	45	23212	26133	26133	39	5.62E-12	2		

BP1026b	13558	hypothetical protein	516095	339241	389376	177	607420	630415	618322	265	0.011767792	0.015337796	1.497175141	0.582242999
BP1026b	13559	aminotransferase	202297	276757	259082	214	301575	300323	272055	253	4.25E-04	6.60E-04	1.182242991	0.241526588
BP1026b	13560	3-oxoacyl-(acyl-carrier-protein) synthase III	51418	34860	40412	40	68977	75333	74260	70	0.57169963	0.59645676	1.75	0.80734922
BP1026b	13561	hypothetical protein	42721	49283	45923	204	57945	56108	49734	244	7.04E-05	3.37E-04	1.19607833	0.258311996
BP1026b	13562	3-oxoacyl-ACP synthase	125657	98076	107414	103	137880	141651	117008	136	7.47E-04	0.001126017	1.32038835	0.400962314
BP1026b	13563	short chain dehydrogenase/reductase family oxidoreductase	85230	48941	55226	83	86405	88633	92215	117	0.060467145	0.071926737	1.409638554	0.495325288
BP1026b	13564	hexapeptide transferase family protein	232722	185424	205157	328	242747	241379	237308	379	0.002445574	0.003451797	1.155487803	0.208502034
BP1026b	13565	Rieske (2Fe-2S) domain-containing protein	260055	275439	263053	249	268750	271178	259326	350	5.42E-07	1.22E-06	1.004016064	0.005782553
BP1026b	13566	hypothetical protein	273475	472460	419921	260	263200	255579	238991	270	6.37E-22	8.70E-21	0.649122807	0.234346649
BP1026b	13567	putative outer membrane protein	196889	340648	312893	705	141340	127626	127708	328	3.09E-97	1.61E-94	0.465248227	1.103927443
BP1026b	13568	LysC family protein	10619	12478	11589	18	8508	8608	8498	13	4.00E-17	3.31E-16	0.722222222	0.469485383
BP1026b	13569	acid phosphatase	109231	100962	104483	63	119493	126626	128493	75	9.91E-06	1.88E-05	1.19047619	0.251538767
BP1026b	13570	lipoprotein	39084	30525	33799	51	52062	53741	56462	80	0.270712196	0.295682859	1.586627451	0.649502753
BP1026b	13571	hypothetical protein	17978	14809	17197	38	20606	20942	22165	49	0.002370559	0.003353474	1.289473684	0.366782331
BP1026b	13572	CsgG family protein	46408	68728	62007	86	63297	53745	51714	82	1.16E-10	4.20E-10	0.953488372	-0.06871275
BP1026b	13573	putative lipoprotein	11222	15337	15193	29	14018	14159	12684	28	1.32E-07	3.24E-07	0.965517241	-0.050626073
BP1026b	13574	3-oxoadipate enol-lactone hydrolase family protein	185282	114501	124821	167	165174	186135	183870	211	8.00E-04	0.001202078	1.263473054	0.337394886
BP1026b	13575	methyl-accepting chemotaxis protein	503748	432168	433641	251	553465	553424	539838	298	1.10E-06	2.37E-06	1.187250996	0.247624967
BP1026b	13576	hypothetical protein	1810	261	2883	12	1451	1926	2002	8	1.85E-14	0.05E-13	0.666666667	-0.584962501
BP1026b	13577	hexose oxidase	14824	19430	19354	10	15850	15308	16648	9	4.74E-10	1.58E-09	0.9	-0.152003093
BP1026b	13578	chitin binding domain-containing protein	13614	19659	19451	31	23258	22418	20694	39	0.0016672	0.002410188	1.258064516	0.331205908
BP1026b	13580	hypothetical protein	58625	53404	51481	218	43711	46447	46335	182	2.06E-18	1.89E-17	0.834862385	-0.260389685
BP1026b	13582	gp30	221335	369557	325516	282	164806	158401	140116	143	2.23E-80	7.76E-78	0.507092199	-0.979680016
BP1026b	13583	gp29	121631	204005	176334	292	84681	83539	74274	141	7.10E-63	1.20E-60	0.482876712	-1.050273206
BP1026b	13584	hypothetical protein	46599	75913	67916	69	36643	37837	36128	40	1.29E-45	1.11E-43	0.579710145	-0.786596362
BP1026b	13585	site-specific recombinase, phage integrase family	3971	4664	4564	4	4987	4798	3325	12	8.79E-12	5.14E-11	0.415017499	
BP1026b	13587	transposase	186014	318167	288177	907	204123	205494	205225	704	1.45E-18	1.35E-17	0.776185226	-0.36527122
BP1026b	13589	Helix-turn-helix domain protein	22530	37579	32096	65	2308	20776	19566	43	2.67E-23	4.23E-22	0.661538462	-0.596103058
BP1026b	13590	SMF family protein	91311	152265	142815	343	114455	109281	106236	293	2.98E-16	2.10E-15	0.854227405	-0.227307912
BP1026b	13591	hypothetical protein	55946	95826	91890	576	66843	65075	67190	470	1.91E-14	1.08E-13	0.815972222	-0.293408055
BP1026b	13592	Phage portal protein	2129	2589	3078	2	3246	3283	2707	2	0.003346115	0.00465469	1	0
BP1026b	13593	Phage terminase, ATPase subunit	2723	2603	2674	1	3241	2674	2614	1	8.11E-05	1.37E-04	1	0
BP1026b	13594	Phage capsid scaffolding protein	1912	1946	1650	2	1813	2153	2080	2	1.87E-04	9.14E-04	0.5	-1
BP1026b	13595	Phage major capsid protein	2444	3020	3300	2	2253	2532	2415	2	1.91E-11	7.65E-11	1	0
BP1026b	13596	Phage terminase, endonuclease subunit	798	551	475	0	962	443	1056	1	0.5339714	0.559892342	#DIV/0!	#DIV/0!
BP1026b	13597	Phage head completion-stabilization protein	444	150	221	0	432	641	496	1	0.007259142	0.009691233	#DIV/0!	#DIV/0!
BP1026b	13598	putative bacteriophage protein	162	121	142	0	178	242	219	0	0.383500934	0.410641	#DIV/0!	#DIV/0!
BP1026b	13599	Phage-related tail protein	320	91	226	1	131	127	0	0	2.80E-15	1.76E-14	0	#NUM!
BP1026b	13600	Prophage membrane protein	203	148	29	0	167	262	174	0	0.195530294	0.217163433	#DIV/0!	#DIV/0!
BP1026b	13601	Prophage membrane protein	721	515	512	1	1876	1573	174	0	1.87E-15	3.20E-14	0.5	-1
BP1026b	13602	Putative phage-encoded peptidoglycan binding protein	938	1409	1293	2	1099	932	1386	1	6.25E-05	1.07E-04	1	0
BP1026b	13603	Putative phage-encoded lipoprotein	224	305	380	0	274	183	510	0	0.182246459	0.203347314	#DIV/0!	#DIV/0!
BP1026b	13604	Prophage LysC protein	116	83	0	0	201	240	140	1	5.07E-07	1.15E-06	#DIV/0!	#DIV/0!
BP1026b	13605	bacteriophage tail completion protein R	1409	2299	2074	4	2091	1705	1480	4	1.71E-07	4.12E-07	1	0
BP1026b	13606	Phage tail completion protein	3454	5351	6511	10	5092	4650	5301	10	3.63E-06	7.29E-06	1	0
BP1026b	13607	hypothetical protein	1649	1386	1586	2	1650	2188	1901	0	1.86E-05	3.41E-05	#DIV/0!	#DIV/0!
BP1026b	13609	baseplate assembly protein V	1649	1386	1586	2	1650	2188	1901	0	0.01349884	0.01713455	0.625	-0.678071905
BP1026b	13610	Phage baseplate assembly protein	697	599	749	1	768	721	857	2	0.057627134	0.068862336	2	1
BP1026b	13611	Phage baseplate assembly protein	3707	2126	2291	2	4149	3667	3575	4	0.564461907	0.589691359	2	1
BP1026b	13612	phage tail protein I	1350	679	783	1	1085	1280	921	1	0.064071989	0.075840313	1	0
BP1026b	13613	Phage-related tail fiber protein	7483	7750	8364	3	7677	8397	7883	3	8.38E-07	1.84E-06	1	0
BP1026b	13614	phage tail fiber assembly protein	1361	797	1211	1	1390	1255	1004	1	1.39E-04	2.28E-04	1	0
BP1026b	13615	Phage tail sheath monomer	2818	2928	2790	2	3024	2630	2266	2	8.69E-08	2.19E-07	1	0
BP1026b	13616	Major tail tube protein	5244	7469	6190	12	7644	7414	6682	14	2.17E-04	9.84E-04	1.166666667	0.222392421
BP1026b	13617	putative phage tail protein	1812	1836	1860	5	1729	1763	2204	4	4.93E-05	5.57E-05	1	0
BP1026b	13618	hypothetical protein	978	1369	1494	11	869	1113	1059	8	1.15E-08	3.26E-08	0.727272727	-0.459431619
BP1026b	13619	bacteriophage tail protein	9087	10557	11186	3	10067	11130	9981	3	5.42E-07	1.22E-06	1	0
BP1026b	13620	Phage-related tail protein	1003	1005	775	2	1169	1232	1611	3	0.85263005	0.86435906	1.5	0.584962501
BP1026b	13621	hypothetical protein	43771	65473	55846	50	53397	51945	43747	45	2.37E-14	1.33E-13	0.9	-0.152003093
BP1026b	13622	hypothetical protein	124138	208635	178479	189	112721	108717	103719	120	8.15E-38	4.40E-36	0.634920635	-0.655518329
BP1026b	13623	gp22, putative phage-encoded membrane protein	86445	148635	129989	162	94531	94280	92866	124	4.45E-19	4.37E-18	0.358359949	-0.385512893
BP1026b	13624	putative phage DNA-binding protein	383236	592548	532529	1164	483078	471628	448066	1082	1.00E-14	8.85E-14	0.925919125	-0.103590559
BP1026b	13625	hypothetical protein	3317	4802	5065	18	3902	3402	2893	14	5.12E-12	1.11E-11	0.777777778	-0.362570079
BP1026b	13626	hypothetical protein	3492	5079	4965	15	3419	3710	2793	11	2.45E-14	1.37E-13	0.733333333	-0.447458977
BP1026b	13627	phage transcriptional activator	1616	2162	2074	7	1431	886	1319	4	8.8E-18	5.05E-17	0.571428571	-0.807354922
BP1026b	13629	hypothetical protein	2183	1646	2321	9	1249	1899	1230	6	3.48E-14	1.91E-13	0.666666667	-0.584962501
BP1026b	13628	hypothetical protein	1892	1480	1888	8	1376	1661	2003	8	4.10E-06	8.17E-06	0.625	-0.678071905
BP1026b	13630	putative phage-encoded membrane protein	1198	1041	1293	960	8	1078	1072	3	1.07E-17	8.90E-17	0.625	-0.678071905
BP1026b	13631	hypothetical protein	2150	1811	1929	7	1709	1287	1796	6	3.95E-09	1.19E-08	0.857142857	-0.22392421
BP1026b	13632	hypothetical protein	729	1708	1143	5	555	943	852	3	8.58E-14	4.50E-13	0.6	-0.736965594
BP1026b	13633	hypothetical protein	1082	884	1233	2	1264	1054	870	2	9.04E-04	0.001348613	1	0
BP1026b	13634	hypothetical protein	908	515	660	2	899	561	920	3	0.050670867	0.060956849	1.5	0.584962501
BP1026b	13635	hypothetical protein	17525	16303	16137	5	17046	17741	19384	6	1.01E-05	1.91E-05	1.2	0.263034406
BP1026b	13636	Phage integrase	42954	59621	55107	53	47614	46281	43331	46	2.84E-16	2.01E-15	0.867924528	-0.204358499
BP1026b	13638	Arg tRNA	4017	5292	5222	66	5181	4869	4414	63	4.36E-06	8.64E-06	0.76537369	-0.25270077
BP1026b	13639	nitrochromosome c family protein	82739	82476	89023	49	4956	46611	45002	52	7.59E-54	4.50E-52	0.553191925	0.85419134
BP1026b	13641	ATP-dependent DNA helicase Rep	136402	168586	160753	73	163579	158469	152047	75	3.13E-10	1.07E-09	0.102739726	-0.038994132
BP1026b	13642	hypothetical protein	17332	4338	6704	1								

BP1026b	13687	F0F1 ATP synthase subunit gamma	593112	842339	752659	832	868594	837067	762076	939	0.130808968	0.148655184	1.128605769	0.17454163
BP1026b	13688	F0F1 ATP synthase subunit alpha	1991829	2418665	2408475	1474	2718399	2641966	2435221	1685	0.102373784	0.117988847	1.143147897	0.193012067
BP1026b	13689	F0F1 ATP synthase subunit delta	352115	409794	399247	716	318380	323418	314637	590	1.38E-14	7.89E-14	0.82402346	-0.29244633
BP1026b	13690	F0F1 ATP synthase subunit epsilon	486644	683296	676643	1251	661939	463276	438144	964	1.01E-28	2.99E-27	0.713455427	-0.486922623
BP1026b	13691	F0F1 ATP synthase subunit C	479434	796055	752703	2503	438885	425116	399256	1559	1.18E-38	6.60E-37	0.622852577	-0.683037363
BP1026b	13692	F0F1 ATP synthase subunit A	192370	286930	254025	286	166588	158317	146513	184	2.14E-43	1.52E-41	0.643356643	-0.636309381
BP1026b	13693	ATP synthase protein I	244621	320154	315516	949	205763	192418	175167	618	1.78E-36	8.92E-35	0.651211802	-0.618801249
BP1026b	13694	hypothetical protein	2615	3299	4350	23	3485	2664	3203	21	4.85E-08	1.26E-07	0.913043478	-0.131244533
BP1026b	13695	transporter	47119	33208	32716	33	42154	42123	41904	37	1.08E-06	2.33E-06	1.121212321	0.165059246
BP1026b	13696	chromosome partitioning protein ParB	147146	151285	150113	168	156802	160262	155166	177	3.08E-09	9.39E-09	1.053571429	0.075288127
BP1026b	13697	chromosome partitioning protein ParA	63537	86631	85429	101	56683	57671	48443	69	3.87E-31	1.28E-29	0.683168317	-0.549687026
BP1026b	13698	16S rRNA methyltransferase Grib	73209	74962	72688	105	67771	66653	59492	92	8.40E-12	3.50E-11	0.876190476	-0.190683562
BP1026b	13699	tRNA uridine 5-carboxymethylaminomethyl modification protein	288002	447258	407152	192	275933	260646	247440	132	2.27E-19	2.34E-18	0.6875	-0.540568381
BP1026b	13700	branched-chain amino acid ABC transporter ATP-binding protein	19817	29143	27771	33	23208	19934	20096	27	1.86E-13	9.38E-13	0.818181818	-0.289506617
BP1026b	13701	branched-chain amino acid ABC transporter permease/ATP-binding protein	17845	23422	22737	11	14899	15612	13366	8	1.05E-20	1.24E-19	0.727272727	-0.459431619
BP1026b	13702	branched-chain amino acid ABC transporter permease	76871	111631	99233	90	117505	120232	103566	109	4.08E-05	7.91E-05	1.211111111	0.213545228
BP1026b	13703	branched-chain amino acid ABC transporter substrate-binding protein	51752	75504	60952	48	50082	48900	47973	42	7.92E-17	5.97E-16	0.875	-0.192645078
BP1026b	13704	hypothetical protein	61879	46684	59354	48	49909	50846	51990	44	5.50E-14	2.95E-13	0.916666667	-0.125530882
BP1026b	13705	branched-chain amino acid ABC transporter integral membrane subunit	21545	24705	25788	24	21259	22515	21062	22	1.64E-10	5.81E-10	0.916666667	-0.125530882
BP1026b	13706	branched-chain amino acid ABC transporter permease	3442	3869	3585	4	2926	3030	2632	3	1.40E-12	6.36E-12	0.75	-0.415037499
BP1026b	13707	branched-chain amino acid ABC transporter, periplasmic branched-chain amino acid-binding protein	18970	27821	26112	20	18801	18790	16514	15	2.78E-17	2.21E-16	0.75	-0.415037499
BP1026b	13708	branched-chain amino acid ABC transporter ATP-binding protein	6059	5448	62375	6	6401	5546	6010	8	4.09E-06	1.81E-06	0	0
BP1026b	13709	branched-chain amino acid ABC transporter ATP-binding protein	8152	8686	9414	11	6279	6917	6732	8	8.50E-15	5.00E-14	0.727272727	-0.459431619
BP1026b	13710	oxidoreductase, GMC family protein	86497	64351	70098	43	61111	68655	67226	38	3.91E-11	1.50E-10	0.88372093	-0.178372741
BP1026b	13711	methylmalonate-semialdehyde dehydrogenase	466362	483446	481774	312	365465	361239	358523	236	3.28E-21	4.13E-20	0.756410256	-0.40275917
BP1026b	13712	LysR family transcriptional regulator	37547	18622	21252	28	35405	38932	37172	41	0.016654167	0.021359889	1.464285714	0.550197083
BP1026b	13713	hypothetical protein	7139	5611	3875	16	7610	9710	7810	25	0.212923425	0.235645289	1.5625	0.64385619
BP1026b	13714	adenylate cyclase	360530	321692	351228	648	341240	339012	336838	638	1.36E-09	4.31E-09	0.984567301	-0.243273389
BP1026b	13715	NotC family transcriptional regulator	84891	123901	121939	24	78084	74023	70813	156	3.72E-23	5.79E-22	0.69428571	-0.51952703
BP1026b	13716	phenylalanine 4-monooxygenase	67059	79425	73844	82	49847	49120	47340	54	1.33E-34	8.53E-33	0.658536585	-0.602664502
BP1026b	13717	pterin-4-alpha-carbolamine dehydratase	128013	195399	171779	539	121011	117948	95843	364	6.95E-33	2.70E-31	0.675324675	-0.566346823
BP1026b	13718	hypothetical protein	98631	158190	132715	562	110764	101123	87863	432	4.95E-20	5.48E-19	0.768683274	-0.537938818
BP1026b	13719	DNA-binding response regulator	529949	641989	627769	852	430393	404738	386032	587	1.77E-29	5.00E-28	0.689897162	-0.357492927
BP1026b	13720	predicted RNA	28945	2399	2552	251	12115	15168	16256	322	0.005798266	0.007826771	1.282868526	0.359373234
BP1026b	13721	sensor histidine kinase	59654	41887	45406	121	56766	49785	51949	54	6.32E-09	1.98E-08	1.0625	0.087462841
BP1026b	13722	SET domain-containing protein	118978	183061	163086	302	109264	109823	108733	102	4.00E-30	1.00E-29	0.682118205	-0.519045212
BP1026b	13723	oxidoreductase FADFMN-binding protein	175321	107696	130944	123	181729	187341	171965	162	0.003517737	0.004878261	1.317037131	0.397335498
BP1026b	13724	glutamine amidotransferase	275200	248900	239064	357	296144	290429	295756	413	1.11E-04	1.84E-04	1.156862745	0.210217707
BP1026b	13724	MarK family transcriptional regulator	297326	436372	408420	667	312793	305210	285460	528	3.05E-15	1.90E-14	0.791604198	-0.337148832
Synonym		Product	Normalized Co	Normalized Co	Normalized Co	Expression Em	Normalized Co	Normalized Co	Normalized Co	Expression BPS	pValue Em	qValue Em	#VALUE!	#VALUE!
BP1026b	10001	hypothetical protein	55027	80260	73177	58	59774	58978	56912	49	3.46E-15	2.15E-14	0.844827586	-0.243271151
BP1026b	10002	chase integrase family protein	58885	73562	73652	67	68545	65993	63038	63	1.47E-09	6.43E-09	0.940298507	-0.088809267
BP1026b	10003	hypothetical protein	21217	17117	21103	52	21926	20906	17923	53	4.72E-07	1.07E-06	0.919230769	0.027480736
BP1026b	10004	DNA-binding protein	21873	28273	25759	41	32222	33871	32312	53	0.001491808	0.002167637	1.292682927	0.37036845
BP1026b	10005	2-amino-3-ketobutyrate coenzyme A ligase	213996	200161	207824	172	251717	252553	238570	207	0.0076332	0.010162458	1.20348872	0.267222203
BP1026b	10006	L-chreonine 3-dehydrogenase	256792	336399	308446	291	332794	323303	288228	305	1.73E-07	4.16E-07	1.048109966	0.067790909
BP1026b	10007	hypothetical protein	15503	12792	14057	21	11937	11421	12110	18	5.92E-12	1.14E-11	0.857142857	-0.222392421
BP1026b	10008	Teir family transcriptional regulator	34275	27414	27454	48	45300	44957	46249	73	0.09222481	0.092342691	1.520833333	0.604862058
BP1026b	10009	hypothetical protein	41111	47311	483283	95	51862	50590	48321	67	0.2909791	0.393207	1.094736842	0.13058421
BP1026b	10010	succinylglutamate desuccinylase	47484	17725	19109	20	27724	29702	29052	28	0.024470188	0.030730003	0.682118205	0.4485426827
BP1026b	10012	tartate dehydrogenase	23053	21685	21734	18	18667	20882	18748	16	3.74E-11	1.44E-10	0.888888889	-0.169925001
BP1026b	10011	LysR family transcriptional regulator	19955	10769	12164	15	15885	18004	18212	18	0.001124044	0.001652819	1.2	0.263044406
BP1026b	10013	hypothetical protein	25386	27378	25180	38	29966	29486	29224	43	2.66E-05	4.80E-05	1.131578947	0.178337241
BP1026b	10014	hypothetical protein	387	421	351	2	348	511	294	2	0.025440599	0.031846055	0	0
BP1026b	10015	glutathione S-transferase	97635	117747	116307	177	86656	78842	75766	128	5.64E-21	5.93E-20	0.723163842	-0.467605555
BP1026b	10016	hypothetical protein	1024	784	1024	1	957	1024	957	1	0.2909791	0.393207	1.094736842	0.13058421
BP1026b	10017	petatin-like phospholipase	66561	58625	63987	50	76400	79368	77927	62	0.00176852	0.002549599	1.24	0.10340121
BP1026b	10018	3-hydroxybutyrate dehydrogenase	121658	140839	140198	170	133846	129279	134607	168	1.22E-11	5.06E-11	0.988235294	-0.017073513
BP1026b	10019	acetoacetate decarboxylase	19636	27964	25540	32	16704	14902	13569	20	5.19E-27	1.18E-25	0.625	-0.678017905
BP1026b	10020	PAP2 family protein	10561	6722	7620	13	10736	11731	11889	19	0.034373981	0.042260769	1.461538462	0.547487795
BP1026b	10021	hypothetical protein	25709	28174	27048	113	35713	36546	31712	146	8.47E-04	0.001269501	0.926035398	0.366645596
BP1026b	10022	siderophore-interacting protein	10517	10609	10145	12	8578	9944	10812	11	2.89E-08	7.75E-08	1.192266371	-0.125530882
BP1026b	10023	PaikR-like family regulatory protein	3544	3544	4312	6	30978	40813	4313	63	6.49E-06	6.49E-06	0.919230769	0.027480736
BP1026b	10024	cytochrome monooxygenase protein	30155	34861	36031	28	26463	27715	26406	22	6.34E-15	3.82E-14	0.785714286	-0.347923303
BP1026b	10025	hypothetical protein	54505	99441	84623	395	71050	75676	68486	356	9.76E-11	3.57E-10	0.901265823	-0.149975412
BP1026b	10026	hypothetical protein	6505	8428	8217	9	6922	6321	6417	7	1.08E-10	3.94E-10	0.777777778	-0.362570079
BP1026b	10027	hypothetical protein	8822	8583	8842	10	5495	6053	6272	7	1.07E-18	1.01E-17	0.7	-0.514573173
BP1026b	10028	radical SAM domain/B12 binding domain-containing protein	35122	24884	29421	15	29371	29548	30611	15	5.16E-08	1.34E-07	1	0
BP1026b	10029	hypothetical protein	10399	8977	9506	9	8439	8968	9967	9	2.63E-08	7.07E-08	1	0
BP1026b	10030	LysE family protein	40556	4296	2877	6	4096	3261	3231	5	8.53E-07	1.87E-06	0.833333333	-0.263044406
BP1026b	10031	chromosome replication initiation inhibitor protein	33053	32471	34221	38	34212	34221	34212	38	3.42E-13	3.42E-13	0.67368421	-0.087462841
BP1026b	10032	CypENR family transcriptional regulator	1091924	1223802	1129969	1519	1405653	1405806	1404505	1858	0.027320058	0.034055812	1.22317314	0.290628632
BP1026b	10033	universal stress protein	354006	407474	422939	843	344927	335529	318754					

BP1026b	BP0081	H-NS histone family protein	19202	31452	25091	82	24571	23665	19363	73	9.25E-11	3.39E-10	0.890243902	-0.167727446
BP1026b	BP0082	Rhs element Vgr protein	97938	83994	86011	32	101290	106524	110000	38	4.04E-05	7.09E-05	1.1875	0.247927513
BP1026b	BP0083	hypothetical protein	135359	184038	170997	72	185925	179558	179160	80	7.56E-07	1.67E-06	1.111111111	0.152003093
BP1026b	BP0084	hypothetical protein	492247	753043	704107	467	534509	530853	530853	383	6.54E-19	6.31E-18	0.83012848	-0.286878158
BP1026b	BP0085	PAAR motif-containing protein	57079	45582	45714	187	71830	75988	74860	281	0.341012514	0.367531102	1.502673797	-0.58753186
BP1026b	BP0086	hypothetical protein	36917	40977	39746	93	36847	37011	33792	85	4.04E-12	7.5E-11	0.913978495	-0.129767875
BP1026b	BP0087	thioredoxin	13687	12736	13939	41	13173	14472	13993	42	2.04E-06	4.22E-06	1.024390244	0.034765418
BP1026b	BP0088	hypothetical protein	31638	38753	38294	51	41775	39218	39179	56	7.17E-07	1.59E-06	1.098039216	0.13492958
BP1026b	BP0089	hypothetical protein	1761	2349	1930	3	1719	1712	1801	3	7.64E-09	2.20E-08	1	0
BP1026b	BP0090	cytochrome c oxidase polypeptide I	20027	26913	26405	15	23952	25261	21340	14	1.25E-08	3.45E-08	0.933333333	-0.099535674
BP1026b	BP0091	hypothetical protein	436	499	521	1	314	375	517	0	2.33E-08	6.31E-08	0	#NUM!
BP1026b	BP0092	hypothetical protein	4822	6785	6189	4	7041	4916	5667	4	1.60E-06	0.35E-06	1	0
BP1026b	BP0093	hypothetical protein	1070	1752	1435	3	801	863	584	1	2.14E-24	3.76E-23	0.333333333	-1.584962501
BP1026b	BP0094	hypothetical protein	101	307	145	1	372	300	306	1	0.045261106	0.054827996	1	0
BP1026b	BP0096	hypothetical protein	17621	25419	21656	14	17364	17733	15610	11	1.78E-14	1.01E-13	0.785714286	-0.347923303
BP1026b	BP0097	hypothetical protein	3132	3619	3874	7	1987	2461	2269	4	3.42E-23	5.38E-22	0.571428571	-0.807354922
BP1026b	BP0098	frimbrin protein	5979	9507	9790	15	6795	6175	6096	11	1.19E-14	6.85E-14	0.733333333	-0.447458977
BP1026b	BP0099	chaperone protein EcpD precursor	1281	1834	1381	2	1099	963	1001	1	2.42E-24	9.52E-11	0.5	0
BP1026b	BP0100	outer membrane usher protein	2393	3005	3037	1	2935	2542	2643	3	6.63E-07	1.47E-06	0	0
BP1026b	BP0101	hypothetical protein	142	305	273	1	223	366	129	1	0.131909117	0.149796721	1	0
BP1026b	BP0102	major fibrillar subunit protein	892	1143	1608	2	1136	785	1151	2	4.81E-07	1.09E-06	1	0
BP1026b	BP0103	type VI secretion system	664	588	724	0	325	480	537	0	2.53E-09	7.80E-09	#DIV/0!	#DIV/0!
BP1026b	BP0104	type VI secretion system	4169	4546	3584	2	3188	3135	3066	1	1.87E-13	9.42E-13	0.5	-1
BP1026b	BP0105	type VI secretion system	825	1454	969	2	1285	1038	914	1	9.01E-04	0.001345817	0.5	-1
BP1026b	BP0106	type VI secretion system	3982	5107	5654	3	5860	6079	5612	3	0.001362698	0.001988803	0	0
BP1026b	BP0107	type VI secretion system	3403	6292	5605	10	6432	7024	5653	13	0.001948484	0.002312047	1.3	0.78511623
BP1026b	BP0108	type VI secretion system	299	376	181	0	162	197	127	0	2.08E-08	5.67E-08	#DIV/0!	#DIV/0!
BP1026b	BP0109	type VI secretion system	2166	1548	1623	1	1985	1994	1596	1	9.26E-05	1.55E-04	1	0
BP1026b	BP0110	type VI secretion system	864	746	917	0	801	1248	630	0	0.00719825	0.009616088	#DIV/0!	#DIV/0!
BP1026b	BP0111	type VI secretion system	12650	13891	12070	3	13751	15021	14270	3	6.21E-05	1.07E-04	1	0
BP1026b	BP0112	hypothetical protein	2365	2169	2254	3	1959	2679	2247	4	6.67E-06	1.29E-05	1.333333333	0.415037499
BP1026b	BP0113	type VI secretion system	12799	14725	13176	5	11671	11607	12129	4	5.00E-11	1.89E-10	0.8	-0.321928095
BP1026b	BP0114	Rhs family protein	768	1088	1038	3	899	863	1061	3	2.17E-06	4.49E-06	1.5	0
BP1026b	BP0115	Rhs1 protein	78399	110602	104319	28	87194	82415	76787	23	5.87E-14	3.13E-13	0.821428571	-0.283792966
BP1026b	BP0116	hypothetical protein	16511	21621	19394	14	17275	16758	15238	12	2.95E-11	1.15E-10	0.857142857	-0.222392421
BP1026b	BP0117	hypothetical protein	7933	13100	11866	10	8149	8206	8694	8	7.50E-16	5.05E-15	0.8	-0.321928095
BP1026b	BP0118	type VI secretion system	6503	7725	6440	6	5536	6750	6146	5	6.55E-09	1.91E-08	0.833333333	-0.263034406
BP1026b	BP0119	type VI secretion system	5490	3458	4027	4	5376	7157	5632	5	0.048167061	0.058100996	1.25	0.321928095
BP1026b	BP0120	type VI secretion system	7792	8283	8652	4	7650	8102	8908	4	3.53E-07	8.19E-07	0	0
BP1026b	BP0121	type VI secretion system	2637	3095	2084	4	2226	2034	1961	5	9.00E-08	2.04E-07	0.75	-0.415037499
BP1026b	BP0122	type VI secretion system	4092	6249	6038	6	4972	4935	4907	5	8.86E-08	2.23E-07	0.833333333	-0.263034406
BP1026b	BP0124	type VI secretion system	2229	3015	3946	5	2018	1827	1890	3	4.43E-23	6.81E-22	0.6	-0.736965594
BP1026b	BP0123	hypothetical protein	3849	3023	3003	7	2473	3113	2521	5	2.27E-11	8.97E-11	0.714285714	-0.485426827
BP1026b	BP0125	type VI secretion system	10130	8830	9260	3	11041	12800	10313	4	9.58E-04	0.001423365	1.333333333	0.415037499
BP1026b	BP0126	two-component system sensor protein	28109	41853	39533	11	33723	30588	30334	10	5.10E-13	2.44E-12	0.909090909	-0.137503524
BP1026b	BP0128	hypothetical protein	1303	1762	2231	5	1414	1681	1507	4	5.51E-18	1.43E-07	0.8	-0.321928095
BP1026b	BP0129	hypothetical protein	517	788	761	2	526	531	561	0	2.26E-11	5.98E-10	0	-1
BP1026b	BP0130	hypothetical protein	358	357	336	1	178	118	268	0	1.60E-10	5.68E-10	0	#NUM!
BP1026b	BP0131	hypothetical protein	649	989	672	2	509	823	986	2	0.002196635	0.003121534	1	0
BP1026b	BP0132	hypothetical protein	2612	4997	2938	8	3782	3201	2527	7	3.42E-08	9.07E-08	0.875	-0.192645078
BP1026b	BP0133	DNA-binding response regulator	1305	2454	1976	2	1696	1245	1509	2	4.31E-11	1.64E-10	1	0
BP1026b	BP0134	hypothetical protein	171	607	132	2	123	109	224	1	2.21E-11	8.76E-11	0.5	-1
BP1026b	BP0135	fimbrial usher protein	6851	9671	9391	3	7172	6460	5918	2	6.89E-15	4.12E-14	0.666666667	-0.584962501
BP1026b	BP0136	periplasmic chaperone protein	6809	6084	6084	7	3312	2943	3502	4	5.98E-24	6.03E-23	0.571428571	-0.807354922
BP1026b	BP0137	hypothetical protein	409	647	775	4	869	867	815	6	0.720062406	0.739030265	1.5	0.584962501
BP1026b	BP0138	hypothetical protein	820	1335	1465	1	1078	1157	967	0	2.95E-06	5.99E-06	1	0
BP1026b	BP0139	hypothetical protein	6393	10500	8926	13	6324	6163	5737	9	4.38E-17	3.41E-16	0.692307692	-0.530514717
BP1026b	BP0140	DNA-binding response regulator	1320	2395	2611	3	1693	1976	1476	2	1.26E-10	4.53E-10	0.666666667	-0.584962501
BP1026b	BP0141	H-NS histone family protein	1332	1831	1949	5	1001	1041	1188	3	1.13E-16	8.38E-16	0.6	-0.736965594
BP1026b	BP0142	MSF transporter	8075	8162	6863	5	10539	10058	9873	7	0.013642753	0.017649616	1.4	0.485426827
BP1026b	BP0143	glycerate kinase	4658	4658	3795	4	4564	4073	5024	4	0.001832136	0.002381337	1.333333333	0.415037499
BP1026b	BP0144	pyruvate kinase	15457	12884	11798	9	15470	16894	15764	11	9.85E-04	0.001460857	1.222222222	0.289506617
BP1026b	BP0145	transcriptional regulator	6012	5271	4734	4	4974	5437	5876	4	9.61E-06	1.83E-05	0	0
BP1026b	BP0146	hypothetical protein	4778	5842	6318	11	5824	5357	4567	10	2.23E-07	5.30E-07	0.909090909	-0.137503524
BP1026b	BP0147	peptide synthase protein	76569	65859	68877	25	141501	147788	145387	51	0.178275731	0.199129668	2.04	1.028569152
BP1026b	BP0149	dehydratase	43451	25530	32559	34	65358	67294	74597	30	0.024018134	0.030192572	2.058823529	1.041820176
BP1026b	BP0148	hypothetical protein	22336	8040	10467	34	30549	34159	41511	89	0.001033057	0.001528358	2.617647059	1.38827059
BP1026b	BP0150	methytransferase	33231	35381	35381	35	50940	50445	50445	28	0.45418725	0.481333333	0.7	0.678017905
BP1026b	BP0151	LysR family transcriptional regulator	15946	8569	10223	12	15215	19138	20452	19	0.288847461	0.314462017	1.583333333	0.662965013
BP1026b	BP0152	hypothetical protein	7572	9184	7240	20	7940	7963	8150	20	4.28E-07	8.79E-07	1	0
BP1026b	BP0153	hypothetical protein	9389	10098	10629	7	8364	9018	9759	6	1.10E-09	3.53E-09	0.857142857	-0.222392421
BP1026b	BP0154	hypothetical protein	1332	1770	2152	6	2104	2031	2288	7	0.010016351	0.013183951	1.666666667	0.222392421
BP1026b	BP0155	hypothetical protein	242	193	279	1	241	344	448	1	0.510727636	0.537228869	1	0
BP1026b	BP0156	lipoprotein	655	850	672	4	555	690	557	3	7.45E-06	1.44E-05	0.75	-0.415037499
BP1026b	BP0157	mercaptan reductase	19154	17629	16119	12	19467	20545	18885	14	1.94E-05	3.56E-05	1.666666667	0.222392421
BP1026b	BP0158	sugar ABC transporter substrate-binding protein	36324	34204	36919	38	26910	26910	26910	17	3.81E-17	6.24E-15	0.440457259	0.440457259
BP1026b	BP0159	ABC transporter permease	12351	4422	9636	9	8206	8546	10340	8	4.73E-09	1.40E-08	0.888888889	-0.169925001
BP1026b	BP0160	ribose ABC transporter ATP-binding protein	21925	16120	17784	12	17887	18514	17597	11	3.75E-08	9.88E-08	0.916666667	-0.125530882
BP1026b	BP0161	ROK family transcriptional regulator	23655	8224	13409	12	16217	15731	19947	13	1.32E-04	2.18E-04	1.083333333	0.115472717
BP1026b	BP0162	hypothetical protein	745	89	271	2	620	712	701	3	0.06214406	0.032753378	1.5	0.

BP1026b	BP1026b	LysR family transcriptional regulator	28780	33807	32152	35	39534	42338	38645	44	4.18E-04	6.48E-04	1.257142857	0.330148602
BP1026b	BP1026b	quinone reductase	8047	10240	10889	12	8400	8740	7518	10	7.50E-12	3.15E-11	0.833333333	-0.263034406
BP1026b	BP1026b	AraC/XyS family transcriptional regulator	1181	406	381	2	554	1019	889	2	0.16860007	0.239747809		0
BP1026b	BP1026b	O-acetylcholine sulfolipase	113798	96378	103498	81	110396	114775	11889	82	5.68E-08	1.84E-07	0.107407407	0.103094393
BP1026b	BP1026b	glyoxalase family protein	15472	10378	12462	32	18458	18688	17616	46	0.061504309	0.073091063	1.4375	0.523561956
BP1026b	BP1026b	hypothetical protein	8878	9388	7209	10	11152	12516	12436	14	0.062079878	0.073670622	1.4	0.485426827
BP1026b	BP1026b	hypothetical protein	3468	4957	4403	12	6395	6166	4774	17	0.027140354	0.033839008	1.416666667	0.502500341
BP1026b	BP1026b	hypothetical protein	2200	2491	2500	1	2544	1948	2790	1	6.23E-06	1.22E-05	1	0
BP1026b	BP1026b	urea amidolyase-like protein	7024	2612	3736	4	6481	6265	5677	6	0.034781231	0.042719536	1.5	0.584962501
BP1026b	BP1026b	allophanate hydrolase, subunit I	6088	5035	6471	6	5772	5750	5989	6	2.59E-06	8.31E-06	1	0
BP1026b	BP1026b	acetyl-CoA carboxylase biotin carboxylase subunit	2963	1744	1834	1	2473	2996	2474	1	0.005752809	0.00777467	1	0
BP1026b	BP1026b	hypothetical protein	1095	391	451	2	703	929	1032	3	0.627345075	0.650287862	1.5	0.584962501
BP1026b	BP1026b	hypothetical protein	2458	3072	1890	3	1828	2165	2613	2	7.01E-09	2.03E-08	0.666666667	-0.584962501
BP1026b	BP1026b	LysR family transcriptional regulator	12939	11834	11252	13	11285	11673	9560	11	5.16E-10	1.72E-09	0.846153846	-0.2410081
BP1026b	BP1026b	penicillin acylase	57421	48320	49996	20	63803	63437	63315	25	0.002431397	0.003434108	1.25	0.321928095
BP1026b	BP1026b	proline iminopeptidase	30813	25451	27461	27	28592	29501	29541	28	6.60E-07	1.47E-06	1.037037037	0.05246742
BP1026b	BP1026b	hypothetical protein	12966	12802	11694	15	12875	11895	12637	15	3.22E-07	5.2E-07	1	0
BP1026b	BP1026b	lipoprotein	6060	2476	4737	3	5690	7151	7151	3	0.020385499	0.02533682	1.5	0.584962501
BP1026b	BP1026b	methyl-accepting chemotaxis protein I	106651	93217	95102	60	81735	89301	97858	55	4.29E-11	1.64E-10	0.916666667	-0.125530882
BP1026b	BP1026b	propanate catabolism operon regulatory protein PprR	42675	19346	22668	13	39254	42085	49142	20	0.077685201	0.09065203	1.538461538	0.621488377
BP1026b	BP1026b	2-methylisocitrate lyase	466991	451789	461029	514	208193	213786	220357	239	1.42E-58	2.03E-56	0.464980545	-1.104757741
BP1026b	BP1026b	methylcitrate synthase	952777	1145722	1121699	915	554855	525098	492594	446	2.16E-68	5.63E-66	0.487431694	0.36728033
BP1026b	BP1026b	aconitate hydratase	1559198	1371483	1443237	561	959521	972611	1005135	377	0.593136704	0.617074957	0.67201426	-0.573436247
BP1026b	BP1026b	AcnD-accessory protein PprP	156711	99537	109558	102	69061	73074	80845	62	5.54E-33	2.18E-31	0.607843137	-0.18229032
BP1026b	BP1026b	hypothetical protein	41755	41840	40857	93	30139	29080	28756	66	4.90E-22	6.80E-21	0.709574719	-0.594764692
BP1026b	BP1026b	N-acetylglucosamine 2-epimerase	67888	181871	170280	366	238145	234982	22844	506	1.36E-15	3.30E-14	1.382151088	0.46273736
BP1026b	BP1026b	hypothetical protein	41211	36824	39835	61	36490	36609	37294	57	1.66E-11	6.66E-11	0.93442623	-0.097847323
BP1026b	BP1026b	hypothetical protein	77778	92559	92049	147	70218	67861	64938	114	7.58E-17	5.73E-16	0.77510204	-0.36782331
BP1026b	BP1026b	heme biosynthesis protein	39787	34354	34343	24	33861	34901	35849	23	9.80E-10	3.17E-09	0.958333333	-0.061400545
BP1026b	BP1026b	methyl-accepting chemotaxis protein	189543	167884	173620	109	175428	184135	192444	114	4.31E-09	1.29E-08	1.04587156	0.064705689
BP1026b	BP1026b	RemM protein	11453	5720	8021	4	13751	14354	13256	8	0.577099536	0.601489433	2	1
BP1026b	BP1026b	LysR family transcriptional regulator	32161	17765	18083	25	23631	26080	27935	29	5.14E-05	8.92E-05	1.16	0.24124805
BP1026b	BP1026b	N-acetylglucosamine 2-epimerase	36096	2676	27730	27	34918	34388	42844	33	1.41E-06	2.32E-06	1.222222222	0.28930617
BP1026b	BP1026b	MgtC family protein	46272	41116	42617	62	48779	49844	48816	70	2.28E-06	4.71E-06	1.129032258	0.175086707
BP1026b	BP1026b	hypothetical protein	54679	40632	46558	164	58534	60053	58965	205	0.00228911	0.003165964	1.25	0.321928095
BP1026b	BP1026b	hypothetical protein	722744	1190739	1037015	6304	1370813	1337350	1265130	8489	0.016604805	0.021300942	1.34660533	0.42932708
predicted RNA	-		7051	184	585	173	4832	11714	23794	896	1.15E-41	7.69E-40	5.179190751	2.327276694
predicted RNA	-		375516	127054	177853	1267	530688	524892	555137	2999	0.008977795	0.011869335	2.367008682	1.243064998
predicted RNA	-		41777	43167	38272	127	77545	66345	54644	1002	0.015025588	0.027866422	1.610932476	0.687896023
BP1026b	BP1026b	acetyltransferase	155665	181871	170280	366	238145	234982	22844	506	1.36E-15	3.30E-14	1.382151088	0.46273736
BP1026b	BP1026b	Putative exported protein precursor	246746	343678	322671	685	329830	336608	315383	737	3.16E-07	7.41E-07	0.075912409	0.105560631
BP1026b	BP1026b	hypothetical protein	303183	135572	189462	260	227328	259933	325451	336	0.032421796	0.039978372	1.292307692	0.36994961
predicted RNA	-		45403	22388	30415	17	35974	34563	37573	679	1.24E-06	2.64E-06	1.100486224	0.138141085
predicted RNA	-		34148	27113	26912	576	30809	28472	26882	563	1.80E-08	4.95E-08	0.977430556	-0.032933889
BP1026b	BP1026b	hypothetical protein	80717	32530	37547	35	59108	65395	82003	48	0.06785739	0.079973413	1.317428571	0.455679484
BP1026b	BP1026b	hypothetical protein	381436	288274	314490	83	364052	371972	379646	94	6.22E-07	1.39E-06	1.13253012	0.17954442
predicted RNA	-		14050	493	1116	200	18008	19863	20249	590	1.33E-06	2.34E-06	1.044444444	0.067235735
BP1026b	BP1026b	hypothetical protein	4530	7991	6210	27	5518	4500	4459	21	3.20E-11	1.24E-10	0.777777778	-0.362570079
BP1026b	BP1026b	type I phosphodiesterase/nucleotide pyrophosphatase family protein	19562	10997	13998	8	16243	17689	18637	10	3.76E-04	5.87E-04	1.225	0.321928095
BP1026b	BP1026b	glyoxalase/bleomycin resistance protein/dioxygenase family protein	30300	29089	35276	80	38170	38407	37247	97	5.27E-05	9.14E-05	1.2125	0.277984747
BP1026b	BP1026b	hypothetical protein	17686	12690	14087	52	17565	18274	17816	62	7.10E-04	0.001074405	1.192307692	0.253765692
BP1026b	BP1026b	squalene:phytyl synthase family protein	30147	24311	25794	25	22381	23218	24320	22	1.88E-11	7.52E-11	0.88	-0.184424571
BP1026b	BP1026b	LysR family transcriptional regulator	10207	8398	8999	12	9689	12306	12332	15	0.00263954	0.00371286	1.25	0.321928095
BP1026b	BP1026b	hypothetical protein	21613	22879	22879	45	26134	25824	22561	47	0.010797164	0.01415116	0.964444444	0.07970135
BP1026b	BP1026b	hypothetical protein	11146	14462	14942	29	13906	13727	16292	85	1.59E-05	2.94E-05	0.197594967	0.105610188
BP1026b	BP1026b	cyamide-insensitive terminal oxidase	98896	100344	106390	101	115204	117058	115745	115	1.64E-06	3.43E-06	1.138613861	0.187278568
BP1026b	BP1026b	ubiquinol oxidase family protein	128809	51927	146513	100	129199	123229	123011	88	1.53E-16	1.12E-15	0.88	-0.184424571
BP1026b	BP1026b	L-allo-threonine aldolase	152384	126482	126907	133	116925	124489	122403	119	3.17E-15	1.98E-14	0.894736842	-0.160464672
BP1026b	BP1026b	chromosome replication initiation inhibitor protein	57483	47703	47150	50	52971	53184	47887	51	9.11E-10	2.96E-09	1.02	0.028569152
BP1026b	BP1026b	IA family penicillin-binding protein	77058	75541	70564	34	116573	109518	101545	50	0.05040143	0.060683846	1.47058821	0.53639349
BP1026b	BP1026b	hypothetical protein	61748	47148	47148	82	87992	87992	87992	82	0.63213469	0.645017041	1.47058821	0.53639349
BP1026b	BP1026b	hemin importer ATP-binding subunit	18097	19650	19026	23	26473	25245	28565	32	0.031975143	0.03951317	1.391304348	0.476438044
BP1026b	BP1026b	hemABC transporter, permease protein	6243	3326	4044	4	6907	6614	6781	6	0.113141837	0.129683526	1.5	0.584962501
BP1026b	BP1026b	hemABC transporter periplasmic hemin-binding protein	2643	1804	2127	2	2542	2415	2925	2	0.003805971	0.005251234	1	0
BP1026b	BP1026b	hemABC transporter protein HmuS	2607	1711	1857	1	3382	2909	2798	2	0.031660238	0.037349184	2	1
BP1026b	BP1026b	TonB-dependent heme/hemoglobin receptor family protein	46891	43033	43080	19	67925	70340	58542	28	0.32373296	0.349873251	1.473684211	0.559427409
BP1026b	BP1026b	hypothetical protein	6266	7510	6584	29	11178	9955	9287	44	0.160134684	0.178607096	1.517241379	0.601450624
BP1026b	BP1026b	LysR family transcriptional regulator	1819	1799	1804	1	1161	1658	2127	1	0.010797164	0.01415116	0.964444444	0.07970135
BP1026b	BP1026b	ABC transporter membrane protein	2388	1210	1737	2	2373	2587	2766	1	0.30472516	0.33036249	1.5	0.584962501
BP1026b	BP1026b	ABC transporter ATP-binding protein	333	156	116	0	341	327	360	0	0.092756436	0.107259796	#DIV/0!	#DIV/0!
BP1026b	BP1026b	ABC transporter substrate-binding protein	1029	1520	1495	1	1069	1249	1594	1	7.26E-05	1.24E-04	1	0
BP1026b	BP1026b	ABC transporter membrane protein	671	1248	977	1	794	999	1084	1	0.00103445	0.001529697	1	0
BP1026b	BP1026b	hypothetical protein	250	194	214	0	196	473	367	0	0.235979036	0.259875647	#DIV/0!	#DIV/0!
BP1026b	BP1026b	outer membrane porin	12264	995	12315	9	12977	13133	10741	10	1.10E-05	2.09E-05	1.111111111	0.152003093
BP1026b	BP1026b	PTS system mannitol-specific transporter subunit IIBC	26007	16218	15163	16	19397	19478	19					

BP1026b	II030	hypothetical protein	55849	67805	63553	144	64721	66239	63436	149	1.19E-06	2.54E-06	1.034722222	0.049243519
BP1026b	II031	fatty-acid-CoA ligase	296222	332364	323290	170	373213	351861	324685	188	3.82E-07	8.82E-07	1.105882353	0.145197916
BP1026b	II032	diaminopimelate decarboxylase	96518	47356	53755	52	94408	112798	135385	90	0.761236784	0.77775032	1.730769231	0.791433578
BP1026b	II033	FhlM domain-containing protein	46680	31345	31345	22	59812	59812	59812	43	0.198971343	0.22883877	1.954545454	0.96683136
BP1026b	II034	ketol-acid reductoisomerase	68552	61149	59298	59	78844	84676	81887	77	0.007952625	0.010576484	1.305084766	0.384143491
BP1026b	II035	polyketide non-ribosomal peptide synthase	779706	525370	592185	51	932938	986656	1039427	79	0.004017733	0.005528851	1.549019608	0.631355406
BP1026b	II036	gamma-aminobutyraldehyde dehydrogenase	182000	101094	117434	94	202769	226211	240168	156	0.343423384	0.369940512	1.659574468	0.730813367
BP1026b	II037	hypothetical protein	187660	119027	133409	103	200115	204557	209720	144	0.166669298	0.186564775	1.398058252	0.483424474
BP1026b	II038	peptide synthase regulatory protein	100733	52589	62389	70	91604	96211	107811	96	0.017387858	0.022232608	1.371428571	0.455679484
predicted RNA	-	-	59493	62115	56919	531	70063	69666	68223	618	3.41E-04	3.53E-04	1.163841808	0.218894977
predicted RNA	-	-	1169831	997196	1033359	2094	134566	129950	1233599	2538	0.063504566	0.077272577	1.21204384	0.27430627
BP1026b	II039	hypothetical protein	259222	324095	320427	580	302140	299203	263404	549	5.36E-09	1.58E-08	0.946551724	-0.09246751
BP1026b	II040	thiotemplate mechanism natural product synthetase	1484893	977806	1077952	139	1464442	1572588	1714142	186	0.015386505	0.019790774	1.338129496	0.420217738
predicted RNA	-	-	26066	41905	35097	687	42913	41181	39200	821	3.65E-05	6.46E-05	1.195050946	0.257072123
BP1026b	II041	ATP-dependent transcription regulator LuxR	56637	57952	59620	80	45911	43786	42204	61	2.55E-24	4.42E-23	0.7625	-0.391190757
BP1026b	II042	D-methionine-binding lipoprotein MetQ	5158	6344	5806	6	5907	5959	4498	6	3.84E-07	8.84E-07	1	0
BP1026b	II043	monooxygenase	8044	7701	6644	5	8028	8311	7572	5	9.87E-06	1.88E-05	1	0
BP1026b	II044	ABC transporter ATP-binding protein	2511	2354	2840	2	3011	2481	3149	2	5.17E-04	7.96E-04	1	0
BP1026b	II045	ABC transporter permease	1452	1020	905	1	1270	1607	1624	2	0.242193356	0.26391072	2	1
BP1026b	II046	hypothetical protein	898	501	630	1	785	873	957	1	0.303670247	0.32936598	1	0
BP1026b	II047	monooxygenase	30721	9768	15562	15	20243	25765	36938	22	0.077319343	0.090292388	1.466666667	0.552541023
BP1026b	II048	hypothetical protein	6347	2268	3150	5	5230	5725	5706	7	0.071588051	0.084085422	1.4	0.485426827
BP1026b	II049	hypothetical protein	18207	23735	22209	37	17745	16874	14383	28	2.05E-15	1.31E-14	0.756756757	-0.402098444
BP1026b	II050	GntR family transcriptional regulator	22868	15834	15524	25	23509	25669	30182	36	0.06383549	0.07603234	1.44	0.526068812
BP1026b	II051	hypothetical protein	11453	5676	6458	10	10376	12612	13843	15	0.200226072	0.22312422	1.15737353	0.6262501
BP1026b	II052	iron-sulfur cluster binding protein	47906	48912	48844	33	60950	61027	60950	43	0.01002623	0.012877094	1.303030303	0.381970653
BP1026b	II053	hypothetical protein	8804	3326	3808	7	10527	10975	12238	15	0.17393749	0.194422633	2.142857143	1.099535674
BP1026b	II054	glycolate permease	11937	8478	10266	5	12791	13048	12783	7	0.003473695	0.004821454	1.4	0.485426827
BP1026b	II055	hypothetical protein	3783	3899	3312	8	3554	2814	3250	7	5.94E-09	1.74E-08	0.875	-0.192645078
BP1026b	II056	major facilitator family transporter	2238	1516	1743	1	2274	2078	1971	1	0.001637659	0.00237186	1	0
BP1026b	II057	major facilitator family transporter	35771	30872	32038	25	36346	34490	32033	26	1.07E-07	2.67E-07	0.04	0.05683528
BP1026b	II058	malate-L-lactate dehydrogenase family protein	1271	583	316	0	1246	1314	1730	1	0.01023415	0.01345362	#DIV/0!	#DIV/0!
BP1026b	II059	alkaldehyde dehydrogenase family protein	577	2354	907	0	392	691	425	0	0.375897395	0.402787094	#DIV/0!	#DIV/0!
BP1026b	II060	amino acid permease	6455	5122	5312	3	6696	6998	7439	4	0.002870363	0.004019664	1.333333333	0.415037499
BP1026b	II061	hypothetical protein	8597	10979	8952	10	10990	12226	9664	11	1.70E-04	2.76E-04	1.1	0.137503524
BP1026b	II062	hydroxyproline-2-epimerase	2995	2809	2672	3	3409	2910	2190	3	5.65E-06	1.11E-05	1	0
BP1026b	II063	oxidoreductase, FAD-binding family protein	1278	654	878	0	1431	1954	1826	1	0.064972977	0.076819691	#DIV/0!	#DIV/0!
BP1026b	II064	2Fe-2S iron-sulfur cluster binding domain-containing protein	435	275	437	1	423	407	515	1	0.253614918	0.277977926	1	0
BP1026b	II065	oxidoreductase	1559	768	880	0	1008	1247	1332	0	0.020968138	0.026518382	#DIV/0!	#DIV/0!
BP1026b	II066	AraC family transcriptional regulator	29226	19922	22885	25	19873	2194	23047	23	0.173E-09	2.43E-09	0.92	-0.120294234
BP1026b	II067	hypothetical protein	12676	7003	10001	36	10955	11314	9891	39	1.40E-05	2.61E-05	1.083333333	0.115472717
BP1026b	II068	transposase	3828	3934	3979	4	4009	3614	3228	3	2.69E-07	6.34E-07	0.75	-0.415037499
BP1026b	II069	amino acid dioxygenase	2289	1978	2108	1	2015	2060	2000	0	4.70E-07	1.07E-06	0	#NUM!
BP1026b	II071	3-dehydroquinate dehydratase	4739	4421	4225	9	4194	3419	4503	8	1.49E-07	3.63E-07	0.888888889	-0.169925001
BP1026b	II070	shikimate 5-dehydrogenase	5765	3209	3239	4	4432	5930	5799	6	0.021204332	0.026795226	1.5	0.584962501
BP1026b	II072	major facilitator family transporter phthalate permease	6461	5593	6464	4	6657	7599	6937	5	2.00E-04	3.23E-04	1.25	0.312928095
BP1026b	II073	2-aminoethylphosphonate-pyruvate transaminase	1992	1992	2556	2	2475	3566	3285	2	0.233962033	0.25245844	2	1
BP1026b	II074	ABC transporter substrate-binding protein	891	1291	1568	1	962	1200	1141	1	3.88E-06	7.75E-06	#DIV/0!	#DIV/0!
BP1026b	II075	ABC transporter ATP-binding protein	185	164	150	0	477	327	267	0	0.14E-04	0.001362605	#DIV/0!	#DIV/0!
BP1026b	II076	2-aminoethylphosphonate ABC transporter permease	1835	624	809	1	1768	2004	2054	2	0.18804899	0.2094068	2	1
BP1026b	II077	ABC transporter membrane protein	362	357	151	0	493	580	651	0	0.003687039	0.005101748	#DIV/0!	#DIV/0!
BP1026b	II078	phosphonoacetate hydrolase	33767	25054	32027	24	43192	45317	50185	37	0.080157399	0.093380313	1.541666667	0.624490865
BP1026b	II079	alkaldehyde dehydrogenase family protein	38182	25182	31150	21	37065	39246	37864	26	6.17E-05	1.06E-04	1.238095238	0.38122295
BP1026b	II080	hypothetical protein	6715	6880	7023	12	6035	6365	5649	10	2.77E-09	8.49E-09	0.833333333	-0.26304406
BP1026b	II081	hypothetical protein	0	0	0	0	0	0	0	0	0	0	#DIV/0!	#DIV/0!
BP1026b	II082	16S ribosomal RNA	0	44	0	0	0	0	0	0	0.00252579	0.003557802	#DIV/0!	#DIV/0!
BP1026b	II083	Ile tRNA	0	0	0	0	0	0	0	0	0	1	#DIV/0!	#DIV/0!
BP1026b	II084	Ala tRNA	0	0	0	0	0	0	0	0	0	1	#DIV/0!	#DIV/0!
BP1026b	II085	hypothetical protein	0	0	0	0	0	0	0	0	0	1	#DIV/0!	#DIV/0!
BP1026b	II086	23S ribosomal RNA	179115	240211	187011	70	233864	565281	217613	117	0.794606634	0.809598886	1.671428571	0.741081703
BP1026b	II087	35S ribosomal RNA	3199	4205	4204	128	4306	4123	3490	30	0.00810366	0.008655	1.177353535	0.160446793
BP1026b	II088	Cu/I-dependent transcriptional regulator	120230	189086	158459	358	143254	152701	135512	330	3.93E-15	2.42E-14	0.92178709	-0.117493563
BP1026b	II089	hypothetical protein	2690102	4191280	3531150	23611	3522523	3604329	3065477	23111	0.211014523	0.233697838	0.97882343	0.008782343
BP1026b	II090	hypothetical protein	110242	123821	134806	440	141747	135680	122787	478	2.38E-08	6.44E-08	1.086363636	0.119507094
BP1026b	II091	hypothetical protein	88804	116214	110594	116	98879	98835	91125	106	2.07E-11	8.26E-11	0.913793105	0.13060541
BP1026b	II092	aldo-keto reductase family oxidoreductase	69090	89478	85377	86	87085	86777	86777	84	1.74E-08	4.80E-08	0.976744186	-0.033947332
BP1026b	II093	3-hydroxybutyrate dehydrogenase	278261	389003	366568	436	320413	319179	325262	407	1.41E-10	5.04E-10	0.933486239	-0.099299241
BP1026b	II094	aromatic amino acid aminotransferase	384441	398076	409576	331	384711	368719	364567	34	1.05E-11	2.76E-11	0.346746683	-0.760660568
BP1026b	II095	excystase ABC subunit B	327849	431354	417666	186	447047	435443	409702	205	2.44E-08	6.60E-08	1.102150358	0.140321288
BP1026b	II096	19 kDa periplasmic protein	13816	16910	17666	29	12711	10738	11218	1	3.71E-18	2.87E-17	0.724137931	-0.465663572
BP1026b	II098	hypothetical protein	4385	4320	3265	12	3164	4686	4577	12	5.50E-05	9.52E-05	1	0
BP1026b	II097	FTR1 family iron permease	13812	16082	17096	18	13737	14021	13762	16	1.67E-10	5.91E-10	0.888888889	-0.169925001
BP1026b	II099	nitrogen fixation protein VnfA	14737	10737	10521	8	13818	15119	15525	10	0.002485965	0.003504859	1.25	0.321928095
BP1026b	II040	glcG protein	77255	48780	55171	146	70011	77764	78887	183	0.003159655	0.004049999	1.253424658	0.325875279
BP1026b	II0401	hypothetical protein	2692	3085	3503	21	2863	2727	2036	17	2.94E-11	1.15E-10	0.80959281	-0.304854582
BP1026b	II0402	hypothetical protein	713	1105	832	9	1105	832	656	6	5.90E-04	6.56E-04	0.888888889	-0.169925001
BP1026b	II0403	hypothetical protein	7133	2242	2348	9	1652	1341	1405	6	7.19E-14	3.81E-13	0.75	-0.415037499
BP1026b	II0404	hypothetical protein	85661	94411	97693	190	79519	82025	71209	158				

BP1026b	II0454	hypothetical protein	8246	14627	13592	59	9286	10810	10180	49	1.50E-12	6.81E-12	0.830508475	-0.267933205
BP1026b	II0455	integrase core subunit	3209	4405	3615	21	2765	2397	2433	14	2.61E-19	2.68E-18	0.666666667	-0.584962501
BP1026b	II0456	hypothetical protein	10372	12751	11715	16	8507	8659	7465	11	2.04E-19	2.12E-18	0.6875	-0.540568381
BP1026b	II0457	LysM domain-containing protein	14041	16842	16342	12	143437	14360	13859	11	2.10E-16	1.50E-15	0.916666667	-0.125330882
BP1026b	II0458	hypothetical protein	48424	61933	56324	15	55747	54775	50490	14	3.05E-11	1.19E-10	0.933333333	-0.099535674
BP1026b	II0459	hypothetical protein	65307	114599	99724	134	82488	80909	81014	117	2.28E-12	1.02E-11	0.873134328	-0.195724471
BP1026b	II0461	hypothetical protein	41402	78299	64016	150	58909	55593	49677	134	3.58E-14	1.96E-13	0.833333333	-0.1627295
BP1026b	II0462	acetyltransferase large subunit	33279	31600	32660	18	35591	34293	34785	20	4.54E-07	1.04E-06	1.111111111	0.152003093
BP1026b	II0463	hypothetical protein	139344	143209	141935	47	140796	135555	125166	44	1.47E-13	7.50E-13	0.936170213	-0.095157233
BP1026b	II0464	lipoprotein	40695	28173	30440	48	31779	37910	39354	53	1.01E-06	1.19E-06	1.104166667	0.142957954
BP1026b	II0466	hypothetical protein	9784	3949	5246	27	6724	8194	12328	38	0.06786162	0.07997343	1.444444444	0.530514717
BP1026b	II0465	hypothetical protein	22959	12502	14175	47	16612	18705	16031	58	9.54E-04	0.001417383	1.234042553	0.30392143
BP1026b	II0467	hypothetical protein	35754	45678	45831	50	37168	36519	30899	123	1.42E-16	1.04E-15	0.82	-0.286304185
predicted RNA	-	-	14780	2253	5011	1306	10710	13407	18179	587	0.384159296	0.41127565	1.918300654	0.93982885
BP1026b	II0468	capsule polysaccharide export system periplasmic protein	475966	516187	498511	194	430967	423568	422101	166	9.91E-18	8.31E-17	0.855670103	-0.224873411
BP1026b	II0469	transport-related membrane protein	118743	135720	124811	103	115561	119643	113872	95	1.60E-13	8.16E-13	0.922330097	-0.116644919
BP1026b	II0470	glucose-1-phosphate cytidylyltransferase	200515	192088	189967	249	158319	165764	155625	205	2.10E-21	2.69E-20	0.823291173	-0.280521833
BP1026b	II0471	UDP-glucose-6-dehydrogenase	225829	208223	198571	196	208513	218581	218546	200	2.42E-06	4.97E-06	1.020408163	0.029146346
BP1026b	II0472	CDP-4-deoxy-D-xylulose-3-dehydrogenase	229123	225295	235577	169	179744	184464	172356	132	2.03E-23	1.23E-22	0.781065089	-0.336485317
BP1026b	II0473	peroxamine synthetase	510212	525712	505930	289	545038	544448	497381	297	1.97E-10	6.88E-10	1.027681661	0.039393438
BP1026b	II0474	hypothetical protein	116755	73334	83165	67	84554	89699	90407	65	4.24E-09	1.27E-08	0.970149254	-0.043721377
BP1026b	II0475	glycosyl transferase family protein	148971	139064	139874	136	128222	130515	121150	121	4.02E-16	2.78E-15	0.889705882	-0.168599604
BP1026b	II0476	ADP-heptose-lipooligosaccharideheptosyltransferase II	71975	107494	99375	72	63194	66714	61232	50	8.82E-23	1.26E-21	0.694444444	-0.526068812
BP1026b	II0477	ADP-heptose-LPS heptosyltransferase II	72887	93951	92206	73	55262	55020	49992	45	2.09E-40	1.28E-38	0.616483356	-0.697971463
BP1026b	II0478	galactoside O-acetyltransferase	8649	10317	10027	18	6490	6729	8078	13	7.91E-17	5.97E-16	0.722222222	-0.69485283
BP1026b	II0479	Rhamnosyl transferase	33801	35725	33982	31	37482	37469	33856	31	1.74E-39	1.23E-38	0.548387097	-0.866733469
BP1026b	II0480	hypothetical protein	22181	30776	29490	26	16536	16469	12252	14	3.12E-36	1.54E-34	0.538461538	-0.893048796
BP1026b	II0481	hypothetical protein	3023	1089	1615	9	2038	2238	2225	11	9.03E-04	0.001348613	1.222222222	0.289506617
BP1026b	II0482	LysR family transcriptional regulator	32468	21549	22714	26	28943	30253	36296	32	4.53E-04	7.01E-04	1.230769231	0.299560282
BP1026b	II0483	hypothetical protein	12104	10811	10948	15	12738	13456	13254	18	2.62E-04	4.17E-04	1.2	0.263034406
BP1026b	II0484	hypothetical protein	2392	1590	1330	2	2400	2842	2490	3	0.329714659	0.35785121	1.5	0.584962501
BP1026b	II0485	cyclic nucleotide-binding domain-containing protein	8590	1910	3042	4	5758	7790	7820	6	0.239832078	0.263655342	1.5	0.584962501
BP1026b	II0486	AraC family transcriptional regulator	11769	12795	11670	12	11216	12182	12343	12	3.12E-07	2.32E-07	1.25	0.331928095
BP1026b	II0487	AraC family transcriptional regulator	9232	9010	9664	10	9336	8383	7343	9	6.91E-10	2.27E-09	0.9	-0.152003093
BP1026b	II0488	major facilitator family transporter	2646	1742	2505	1	3084	2547	2707	2	0.00468169	0.006396097	0.2	0.1
BP1026b	II0489	LysR family transcriptional regulator	23109	13279	15148	18	20187	19113	19588	21	6.45E-05	1.10E-04	1.166666667	0.222392421
BP1026b	II0490	isochorismatase superfamily hydrolase	45237	59293	56076	77	56807	58008	50302	78	7.68E-10	2.51E-09	1.012987013	0.018615678
BP1026b	II0491	hypothetical protein	438	280	445	1	209	136	204	0	7.39E-15	4.39E-14	0	#NUM!
BP1026b	II0492	amylodolase	22026	26352	25993	13	26675	25441	24693	13	5.66E-07	1.27E-06	0	0
BP1026b	II0493	hypothetical protein	5340	6187	5187	4	5300	5330	5828	5	0.0232004	0.0232869	1.25	0.331928095
BP1026b	II0494	hypothetical protein	4978	3144	3209	2	4551	4446	4370	3	0.00314817	0.004613201	1.5	0.584962501
BP1026b	II0495	hypothetical protein	461	113	61	0	376	288	419	0	0.089343251	0.10348486	#DIV/0!	#DIV/0!
BP1026b	II0496	non-heme chloroperoxidase	7640	7697	6812	8	8637	8476	9664	10	0.001451849	0.002113006	1.25	0.331928095
BP1026b	II0498	hypothetical protein	3151	1874	2649	4	2661	2335	1987	3	1.93E-08	5.43E-08	0.75	-0.415037499
predicted RNA	-	-	25423	27662	28681	556	37049	35876	30691	704	5.61E-04	8.60E-04	1.26618705	0.340490546
BP1026b	II0499	NAD(PH)-flavin oxidoreductase	22771	20940	22538	36	20150	19779	19499	32	1.26E-10	4.52E-10	0.888888889	-0.095725001
BP1026b	II0500	hypothetical protein	39075	65157	65157	149	33876	33876	32547	89	2.34E-39	1.54E-38	0.597315351	-0.143435089
BP1026b	II0501	GntR family transcriptional regulator	6445	1656	3074	2	5541	6545	8371	5	0.888639362	0.897812413	2.5	1.331928095
BP1026b	II0502	DJ-1/Pip1 family protein	5561	2951	4068	6	4969	5189	6218	8	0.014509329	0.018716318	1.333333333	0.415037499
BP1026b	II0503	peptidase	71242	63025	65395	99	71569	72563	66608	62	3.07E-06	6.22E-06	1.050847458	0.071552361
BP1026b	II0504	hypothetical protein	16274	13281	18542	104	22943	22905	28228	161	0.157486858	0.177140902	1.548076923	0.630477116
BP1026b	II0505	hypothetical protein	271	303	467	1	310	450	294	2	0.059942122	0.071369978	0	1
BP1026b	II0506	DNA polymerase X family/PHP domain-containing protein	146793	98255	109145	60	146499	158324	166935	80	0.002035886	0.002904302	1.333333333	0.415037499
BP1026b	II0507	hypothetical protein	5892	1244	2134	8	4193	4858	5858	12	0.7233860	0.2973805	1.5	0.584962501
BP1026b	II0508	hypothetical protein	838	199	320	1	618	755	863	3	0.284679196	0.310234948	2	1
BP1026b	II0509	copper tolerance protein	6385	5974	6523	3	5272	5094	6255	3	8.06E-09	2.31E-08	1	0
BP1026b	II0510	multicopper oxidase	3592	5684	5244	3	4753	4055	3054	3	4.11E-10	1.38E-09	1	0
BP1026b	II0511	RND family efflux transporter MFP subunit	1395	1888	2466	4	2438	2149	2198	5	0.002795528	0.003920123	1.25	0.331928095
BP1026b	II0512	hypothetical protein	732	559	492	1	973	1082	730	2	0.468643727	0.49604331	0	1
BP1026b	II0513	copper-resistance membrane protein	842	203	340	0	1111	1295	1470	1	4.12E-10	1.38E-09	#DIV/0!	#DIV/0!
BP1026b	II0514	methyl-accepting chemotaxis protein	157380	138792	136400	79	166788	170000	180771	95	9.46E-05	0.000331646	0.2067486	0.26607486
BP1026b	II0515	oxidoreductase	25745	22130	22967	18	25708	26438	26073	20	1.27E-05	2.39E-05	1.111111111	0.152003093
BP1026b	II0516	oxidoreductase	6134	2922	3504	3	4435	5014	6467	4	0.008712955	0.011530623	1.333333333	0.415037499
BP1026b	II0517	hypothetical protein	30157	34164	30439	20	32065	33115	27429	19	8.03E-09	2.31E-08	0.95	-0.074000581
BP1026b	II0518	putrescine transport system permease	900	1280	1549	1	1247	859	846	1	1.60E-08	4.41E-08	1	0
BP1026b	II0519	putrescine ABC transport system, permease protein	613	955	543	0	640	621	626	0	1.21E-04	2.00E-04	#DIV/0!	#DIV/0!
BP1026b	II0520	putrescine ABC transport system, ATP-binding protein	1498	1358	1357	1	1612	1904	1246	1	0.003648516	0.00509383	1	0
BP1026b	II0521	putrescine ABC transport system, binding exported protein	1908	1360	1820	1	1756	1820	1504	0	3.11E-05	1.95E-05	1	0
BP1026b	II0522	aminotransferase	200	360	187	0	440	466	260	0	0.248195739	0.272371778	#DIV/0!	#DIV/0!
BP1026b	II0523	glutamine synthetase	2176	2954	2436	1	2191	2585	1946	1	5.52E-09	1.57E-08	1	0
BP1026b	II0524	glutamine amidotransferase	1132	494	559	0	984	515	1613	1	0.862347876	0.87364501	#DIV/0!	#DIV/0!
BP1026b	II0525	hypothetical protein	3921	5862	5590	12	5699	5671	5377	13	1.07E-04	1.78E-04	1.083333333	0.115472717
BP1026b	II0526	aldehyde dehydrogenase-like protein	24562	35702	31612	55	30003	26776	23491	48	1.57E-11	6.32E-11	0.872727273	-0.196397213
BP1026b	II0527	aldehyde dehydrogenase family protein	27822	16739	17783	13	28892	31570	33064	20	0.076503625	0.089406475	1.538461538	0.621488377
BP1026b	II0528	agmatinase	13670	18278	18371	17	15758	15416	13676	15	5.32E-10	1.19E-09	0.882352941	-0.180572246
BP1026b	II0529	hypothetical protein	4484	6513	6057	12	6309	5450	5250	12	6.45E-05	0.000333333	0.154477217	0.154477217
BP1026b	II0530	co-chaperonin GroES	2923	4230										

BP1026b	II0579	type VI secretion system	1962	1088	1914	0	2048	2043	2021	0	0.015684193	0.020152981	#DIV/0!	#DIV/0!
BP1026b	II0580	type VI secretion system	4072	5604	6087	2	4727	4965	5017	2	4.23E-07	9.71E-07	1	0
BP1026b	II0581	type VI secretion system	6355	8652	8965	3	7357	6922	6023	2	5.40E-11	2.03E-10	0.666666667	-0.584962501
BP1026b	II0582	type VI secretion system	8966	8216	8661	3	9147	8378	8879	3	1.53E-06	3.25E-06	1	0
BP1026b	II0583	type VI secretion system	3046	2886	1609	2	2777	3280	2369	1	3.80E-04	6.93E-04	1	0
BP1026b	II0584	type VI secretion system	1273	1016	737	1	1035	966	784	1	7.14E-05	1.22E-04	1	0
BP1026b	II0586	type VI secretion system	6236	8062	6865	18	7759	8156	8330	20	1.73E-04	2.81E-04	1.111111111	0.152003093
BP1026b	II0585	type VI secretion system	1241	532	848	1	1265	1671	1743	2	0.118351465	0.1532535	2	1
BP1026b	II0587	type VI secretion system	2579	2702	2781	1	3120	2992	4107	2	0.027806566	0.034607767	2	1
BP1026b	II0588	type VI secretion system	3752	1826	3590	1	4215	4528	4548	2	0.377890405	0.404841029	2	1
BP1026b	II0589	type VI secretion system	1013	8292	10251	2	12905	14748	15953	3	0.055227226	0.06333669	1	0.584962501
BP1026b	II0590	hypothetical protein	10824	16555	14701	38	17305	16533	15369	45	4.03E-04	6.26E-04	1.184210526	0.243925583
BP1026b	II0591	hypothetical protein	1802	2280	2682	7	2270	2532	2915	8	8.42E-04	0.001262852	1.142857143	0.192645078
BP1026b	II0592	hypothetical protein	10748	16407	15265	38	12311	12791	11551	32	3.31E-11	1.28E-10	0.842105263	-0.249272513
BP1026b	II0593	rhamnosyltransferase 1, subunit A	33685	43248	42159	44	40920	40739	41076	45	6.92E-09	2.01E-08	1.022727273	0.032421478
BP1026b	II0594	rhamnosyltransferase 1, subunit B	15115	9990	10856	8	15862	20591	24589	14	0.635822865	0.658421959	1.75	0.807354922
BP1026b	II0595	multidrug resistance protein	12562	8388	8193	6	11233	13116	15813	8	0.062626562	0.044475335	1.333333333	0.415037499
BP1026b	II0596	rhamnosyltransferase 1	11614	10623	10597	10	11845	12102	12903	12	5.90E-05	1.02E-04	1.2	0.263034406
BP1026b	II0597	RND efflux system outer membrane lipoprotein	17250	10153	12809	8	15179	17352	20151	11	0.010087947	0.013264253	1.375	0.459436169
BP1026b	II0598	multidrug resistance protein	6413	6773	6889	4	5908	8000	8601	5	7.49E-05	1.27E-04	1.25	0.321928095
BP1026b	II0599	levansucrase	16672	16975	17454	10	17853	16114	17218	10	3.59E-07	8.30E-07	1	0
BP1026b	II0600	levansucrase precursor	31115	24866	28139	18	37226	35639	34332	24	5.70E-04	8.73E-04	1.333333333	0.415037499
BP1026b	II0601	LacI family regulatory protein	15238	17310	16647	14	17572	18364	18312	16	2.04E-05	3.72E-05	1.142857143	0.192645078
BP1026b	II0603	hypothetical protein	163	550	270	1	202	115	228	0	9.74E-10	3.16E-09	0	#NUM!
BP1026b	II0602	glutathione-independent formaldehyde dehydrogenase	2222	2169	2077	1	3178	2836	2210	2	0.018491051	0.02556629	2	1
BP1026b	II0604	AraC family transcriptional regulator	1653	6033	2353	3	2117	2275	1689	1	4.34E-07	1.04E-06	1	0
BP1026b	II0605	serine hydroxymethyltransferase	1872	1565	1109	1	1162	1172	1514	1	1.88E-07	4.50E-07	1	0
BP1026b	II0606	renal dipeptidase family protein	686	1165	1077	1	639	819	458	0	1.13E-12	5.20E-12	0	#NUM!
BP1026b	II0607	V4R domain-containing protein	418	276	448	0	462	526	368	0	0.297505515	0.323032509	#DIV/0!	#DIV/0!
BP1026b	II0608	NADH:flavin oxidoreductase	3027	1683	1357	0	2041	2593	2801	1	0.006965513	0.00932108	#DIV/0!	#DIV/0!
BP1026b	II0609	iron-sulfur cluster binding protein	671	891	458	0	721	810	1021	0	0.24786871	0.264612098	#DIV/0!	#DIV/0!
BP1026b	II0610	electron transfer flavoprotein subunit alpha	785	389	257	0	645	704	1048	0	0.226770898	0.25030712	#DIV/0!	#DIV/0!
BP1026b	II0611	electron transfer flavoprotein subunit beta	165	134	124	0	306	0	144	0	0.47759491	0.50484707	#DIV/0!	#DIV/0!
BP1026b	II0613	iron-sulfur Rieske protein	2919	3374	2744	2	3206	2700	3040	2	3.01E-06	6.10E-06	1	0
BP1026b	II0612	iron-sulfur cluster-binding protein	5050	6706	6595	5	5978	5187	6508	5	5.52E-07	1.24E-06	1	0
BP1026b	II0614	ABC transporter, periplasmic glycine/betaine-binding protein	2997	3047	2947	3	4027	4114	4211	4	0.135266719	0.15338717	1.333333333	0.415037499
BP1026b	II0615	hypothetical protein	29880	32163	29574	18	33302	34984	31245	20	1.34E-06	2.86E-06	1.111111111	0.152003093
BP1026b	II0616	formyltetrahydrofolate deformylase	6102	5182	6838	6	4942	5665	5483	6	1.75E-08	4.83E-08	1	0
BP1026b	II0617	LysR family regulatory protein	2605	1616	1980	2	1988	1755	1943	2	9.01E-08	2.27E-07	1	0
BP1026b	II0618	cholesterol oxidase	5298	6073	5854	3	6476	6885	5427	3	3.47E-06	1.04E-06	1	0
BP1026b	II0619	glycine betaine ABC transporter substrate-binding protein	1315	1406	1757	1	1447	1544	1990	1	0.001961993	0.00280656	1	0
BP1026b	II0620	outer membrane porin	2943	4124	3433	3	3164	2683	3431	2	7.29E-09	2.10E-08	0.666666667	-0.584962501
BP1026b	II0621	aminopeptidase	4614	4540	4587	3	7194	8361	7948	6	0.54361624	0.569243084	2	1
BP1026b	II0622	metallopeptidase domain-containing protein	29344	34702	34183	19	42999	45236	43242	25	0.002617851	0.003685822	1.315789474	0.395928676
BP1026b	II0623	AraC family transcriptional regulator	7080	6414	7388	7	5515	5783	5221	5	7.96E-12	3.33E-11	0.714285714	-0.485426827
BP1026b	II0624	hypothetical protein	823	728	1036	3	849	743	407	2	1.01E-07	2.52E-07	1	0
BP1026b	II0625	ABC transporter, periplasmic glycine/betaine-binding protein	4972	6293	5754	5	5326	5399	5749	5	1.34E-09	3.54E-09	1	0
BP1026b	II0626	hypothetical protein	6935	5599	5663	6	7516	6144	7254	7	2.44E-04	3.90E-04	1.166666667	0.22392421
BP1026b	II0628	3-hydroxybutyryl-CoA dehydrogenase	8926	8319	10531	9	8528	8397	8527	8	2.99E-09	9.17E-09	0.888888889	-0.169925001
BP1026b	II0627	hypothetical protein	9951	7777	7737	17	9930	9977	9099	19	9.18E-05	1.54E-04	1.117647059	0.160464672
BP1026b	II0629	lipase	8324	3869	4917	5	7258	7462	7618	7	0.007221275	0.009642734	1.4	0.485426827
BP1026b	II0630	hypothetical protein	101851	102771	125710	356	119144	108381	107010	360	1.68E-09	5.28E-09	1.011235955	0.161196665
BP1026b	II0631	short chain dehydrogenase/reductase family oxidoreductase	17239	9361	11477	12	16699	16961	18545	17	0.029275225	0.03641659	1.416666667	0.502500341
BP1026b	II0632	hypothetical protein	45923	57863	56261	183	37874	35824	39691	129	2.28E-27	5.28E-26	0.704918033	-0.504472583
BP1026b	II0634	leucine-, isoleucine-, valine-, threonine-, and alanine-binding protein precursor	302209	426590	383782	332	346201	343444	324818	323	9.96E-12	4.12E-11	0.912650602	-0.131865448
BP1026b	II0635	high-affinity branched-chain amino acid transport system permease	14746	15952	16519	16	13290	12283	12198	13	5.36E-14	2.88E-13	0.8125	-0.299560282
BP1026b	II0636	leucine/isoleucine/valine transporter permease subunit	85421	86030	81219	66	86408	85270	72212	63	5.13E-09	1.51E-08	0.954545455	-0.067114196
BP1026b	II0637	leucine/isoleucine/valine transporter ATP-binding subunit	59886	52406	52017	67	56718	57678	53867	72	3.42E-07	7.94E-07	0.107462866	0.103835811
BP1026b	II0638	Branched-chain amino acid transport ATP-binding protein LivF	51788	70702	73618	96	69099	68714	61710	94	3.62E-08	9.56E-08	0.979166667	-0.303736649
BP1026b	II0639	hypothetical protein	808	868	733	2	785	808	838	2	1.58E-08	3.3E-08	1	0
BP1026b	II0640	hypothetical protein	47789	46018	46366	37	62790	60590	72517	52	0.112833805	0.129401493	0.140540540	0.490986353
BP1026b	II0641	salicylelate biosynthesis isochorismate synthase	6744	1345	2622	2	8590	8066	10348	5	0.048268484	0.058212126	2.5	1.321928095
BP1026b	II0642	isochorismate-pyruvate lyase	115	57	111	0	209	153	173	0	0.02047399	0.0259351	#DIV/0!	#DIV/0!
BP1026b	II0643	pyochelin biosynthetic protein	4283	4068	4412	6	3865	3840	4070	5	3.06E-07	7.19E-07	0.833333333	-0.263034406
BP1026b	II0644	salicyl-AMP lyase	2647	1796	1310	1	0.9181238	2363	2784	1	0.001981238	0.002832148	1	0
BP1026b	II0645	AraC family transcriptional regulator	2973	1343	1444	2	3586	4016	4361	4	0.021674923	0.027345764	2	1
BP1026b	II0646	pyochelin synthetase	4005	4095	3254	0	4091	4051	4610	0	0.0355366494	0.06382386	#DIV/0!	#DIV/0!
BP1026b	II0647	pyochelin synthetase	7500	5711	6238	1	7875	8455	8766	1	0.006936897	0.00928477	1	0
BP1026b	II0648	pyochelin biosynthetic protein	554	305	45	0	257	620	290	0	0.807351952	0.821840008	#DIV/0!	#DIV/0!
BP1026b	II0649	ABC transporter ATP-binding protein	549	291	461	0	500	577	943	0	0.504593012	0.531043452	#DIV/0!	#DIV/0!
BP1026b	II0650	ABC transporter	2694	1230	1456	1	2622	2539	3710	1	0.889901705	0.898797852	1	0
BP1026b	II0651	Fe(III)-pyochelin receptor precursor	3662	3363	3871	1	3878	3083	3544	1	2.52E-06	5.17E-06	1	0
BP1026b	II0652	hypothetical protein	105	41	57	0	124	43	103	0	0.936322825	0.941735095	#DIV/0!	#DIV/0!
BP1026b	II0653	iron-regulated membrane protein	378	48	329	0	771	320	331	0	0.077461982	0.090425244	#DIV/0!	#DIV/0!
BP1026b	II0654	hypothetical protein	543	403	456	0	745	584	686	0	0.29730463	0.3284578	#DIV/0!	#DIV/0!
BP1026b	II0655	2Fe-2S iron-sulfur	1605	1119	1149	4	1180	956	1246	4	1.86E-05	4.42E-05	1	0
BP1026b	II0656	sigma-54 activated regulatory protein	50935	40846	41060	22	57102	55550	55930	28	0.001576659	0.002286685	1.272727273	0.347923303
BP1026b	II0657	hypothetical protein	17430	7133	8962	57	27495	32978	29499	153	2.41E-04	3.86E-04	2.684210526	1.424497829
BP1026b	II0658	hypothetical protein	37338	47188	45723	150	81690	83570	79343	283	0.169976929	0.190131336	1.886666667	0.915839552
BP1026b	II0659	hypothetical protein	668	495	320	3	1357	901	836	6	0.00149			

BP1026B_I0705	glyoxalase/biomycin resistance protein/dioxygenase superfamily protein	11519	12187	11924	24	12104	13046	9521	24	5.78E-08	1.49E-07	1	0	0
BP1026B_I0706	glutathione S-transferase-like protein	3052	1259	1695	3	3027	3122	2797	4	0.37507893	0.402448515	1.333333333	0.415037499	
BP1026B_I0707	hypothetical protein	13723	8169	9399	14	9751	11845	1197	15	2.15E-05	1.144E-05	1.071428571	0.099535674	
BP1026B_I0709	hypothetical protein	1361	2153	2258	3	1450	1295	1714	3	2.09E-11	1.05E-10	1	0	0
BP1026B_I0710	sensor kinase protein	15999	13042	15593	10	13415	13944	15662	10	4.81E-08	1.25E-07	1	0	0
BP1026B_I0711	response regulator protein	10046	11665	10157	16	7651	7743	9525	12	9.00E-15	5.28E-14	0.75	-0.415037499	
BP1026B_I0712	DNA-binding protein	24553	29762	27582	31	20286	17569	18181	21	1.12E-21	1.50E-20	0.677419355	-0.561878888	
BP1026B_I0713	hypothetical protein	729219	1137535	977723	3511	885267	830130	705412	2988	0.699284099	0.720091335	0.851039595	-0.232701848	
BP1026B_I0714	hypothetical protein	36307	41262	40772	120	37615	32599	32741	104	1.11E-13	5.84E-13	0.866666667	-0.206450877	
BP1026B_I0715	rhodanese-related sulfurtransferase	1347	813	1303	2	2005	1643	2168	4	0.5515454	0.577901756	1.388888889	0.473931188	
BP1026B_I0716	transcriptional activator FurA	23959	13659	14572	18	21161	24738	26117	25	0.019413906	0.024657077	1	0	0
BP1026B_I0717	hypothetical protein	3645	2955	3600	7	3549	3658	2782	7	3.62E-06	1.26E-06	1	0	0
BP1026B_I0718	M20/M25/M40 family peptidase	237029	220912	234616	158	238567	240749	241459	165	2.98E-05	5.34E-05	1.044303797	0.062541466	
BP1026B_I0719	hypothetical protein	37527	23699	28375	82	39644	34906	38115	103	3.01E-04	4.77E-04	1.256097561	0.328948523	
BP1026B_I0720	hypothetical protein	62727	41633	43550	85	45375	47114	41822	77	3.91E-14	2.13E-13	0.905882353	-0.142604395	
BP1026B_I0721	insertion element membrane protein	29274	41806	35559	133	18417	19263	18189	69	1.84E-42	1.26E-40	0.518796692	-0.946757979	
BP1026B_I0722	hypothetical protein	5514	3259	1081	4	299	465	239	1	5.02E-37	2.40E-35	1.725	0.169925001	
BP1026B_I0723	x-prolyl-dipeptidyl aminopeptidase	43381	66286	61836	29	39807	40151	37037	19	5.57E-32	9.98E-30	0.655172414	-0.4610053482	
BP1026B_I0724	hypothetical protein	4362	6158	6871	26	4128	3774	3978	18	4.27E-16	2.94E-15	0.692307692	-0.350514717	
BP1026B_I0725	serine-type carboxypeptidase family protein	27084	47451	43763	22	24496	23460	24490	13	7.43E-30	2.14E-28	0.590909091	-0.7589919	
BP1026B_I0726	hypothetical protein	21460	32931	28317	69	23766	22005	22682	57	2.56E-13	1.27E-12	0.826066957	-0.275634443	
BP1026B_I0727	hypothetical protein	6702	10468	9796	39	8163	7745	7978	34	2.11E-10	7.35E-10	0.871794872	-0.197939378	
BP1026B_I0728	transposase B	2224	3461	3143	13	2505	1892	1493	9	1.42E-19	1.51E-18	0.692307692	-0.550514717	
BP1026B_I0729	hypothetical protein	4899	3188	7544	17	5532	6193	6365	14	1.34E-09	4.26E-09	0.825259412	-0.280107919	
BP1026B_I0730	hypothetical protein	1536	28209	21745	10	20757	17890	20409	10	1.61E-18	1.38E-17	0.73684105	-0.152003093	
BP1026B_I0731	hypothetical protein	1378	2966	2526	5	1427	923	1277	2	1.81E-27	4.24E-26	0.4	-1.321928095	
BP1026B_I0732	transposase	5496	8133	7286	26	7503	7546	6988	27	7.05E-06	1.37E-05	1.038461538	0.054447784	
BP1026B_I0733	integrase core subunit	1123	1853	1455	8	1752	1934	1766	10	0.022468129	0.028312283	1.25	0.321928095	
BP1026B_I0734	hypothetical protein	2139	3691	2497	7	2227	2118	2324	5	3.62E-12	1.57E-11	0.714285714	-0.485426827	
BP1026B_I0735	hypothetical protein	3238	5206	3849	6	3219	3158	3479	5	1.70E-11	6.85E-11	0.833333333	-0.263034406	
BP1026B_I0736	response regulator protein	2299	3351	2843	3	1948	1732	1855	2	2.69E-20	3.05E-19	0.666666667	-0.584962501	
BP1026B_I0737	hypothetical protein	2897	974	3431	6	299	2231	1671	4	1.48E-18	1.38E-17	0.666666667	-0.584962501	
BP1026B_I0738	alpha-ketoglutarate-dependent taurine dioxygenase	8159	14771	15162	14	9371	8435	6842	9	2.55E-24	4.42E-23	0.642857143	-0.637429921	
BP1026B_I0739	peptidase	21401	32584	32471	15	18493	15761	16473	9	1.04E-30	3.28E-29	0.6	-0.736965594	
BP1026B_I0740	acetyltransferase	18571	27698	27869	40	21768	21088	17020	32	3.81E-14	2.09E-13	0.8	-0.321928095	
BP1026B_I0741	hypothetical protein	34361	50358	49622	204	36713	35430	32407	159	1.91E-19	2.00E-18	0.779411765	-0.359542387	
BP1026B_I0743	EmrB/QacA family drug resistance transporter	23187	27511	24798	18	21420	20916	20450	14	4.21E-13	2.03E-12	0.777777778	-0.362570079	
BP1026B_I0744	trehalase	11865	11877	11973	7	11807	13037	11823	7	1.12E-06	2.40E-06	1	0	0
BP1026B_I0745	hypothetical protein	1542	974	2395	2	182	1575	1098	2	1.47E-09	1.38E-09	1	0	0
BP1026B_I0746	cytochrome c oxidase, subunit III family protein	821	1509	1198	1	775	876	1098	1	8.86E-09	2.53E-08	1	0	0
BP1026B_I0748	LuxR family transcriptional regulator	18657	20104	20027	21	19499	17551	17242	20	2.26E-09	6.98E-09	0.952380952	-0.070389328	
BP1026B_I0749	hypothetical protein	11978	7259	8403	11	7453	7743	7432	9	5.68E-13	2.70E-12	0.818181818	-0.289506617	
BP1026B_I0750	asparagine synthase	42537	28648	36872	18	43584	43797	42068	21	3.81E-05	6.71E-05	1.166666667	0.223924241	
BP1026B_I0751	two-component system response regulator	2185	3232	2617	5	2413	2972	1693	4	3.02E-09	9.24E-09	0.8	-0.321928095	
BP1026B_I0752	isoquinoline 1-oxidoreductase subunit beta	61929	37372	44524	21	62209	69604	72223	30	0.153945731	0.173320492	1.428571428	0.514537333	
BP1026B_I0753	isoquinoline 1-oxidoreductase subunit alpha	1542	974	2395	2	182	1575	1098	2	1.47E-09	1.38E-09	1	0	0
BP1026B_I0754	AraC family transcription regulator	63860	47318	50740	55	57514	64357	63654	63	1.01E-04	1.68E-04	1.145454545	0.1959201	
BP1026B_I0755	hypothetical protein	16066	15766	15926	39	16822	16434	16628	41	3.06E-06	6.20E-06	1.051282051	0.072149786	
BP1026B_I0756	hypothetical protein	489079	587664	569654	1537	520995	493516	427794	1346	6.93E-17	5.28E-16	0.875731945	-0.191438755	
BP1026B_I0757	acyl-CoA dehydrogenase domain-containing protein	3857	3808	3797	3	4165	3184	3916	3	5.27E-06	1.04E-05	1	0	0
BP1026B_I0758	acyl-CoA dehydrogenase domain-containing protein	2787	631	1235	1	2371	3035	4112	2	0.017637505	0.022524227	2	1	0
BP1026B_I0759	monooxygenase	10629	6598	9023	6	11544	13186	12814	9	0.075213453	0.088063004	1.5	0.584962501	
BP1026B_I0760	sensor kinase protein	56314	30669	37218	32	43998	32457	39245	36	8.7E-07	1.81E-06	1	0	0
BP1026B_I0761	response regulator protein	43037	53831	51703	48	39993	40571	59455	5	1.74E-19	1.82E-18	0.808823529	-0.306103128	
BP1026B_I0762	MipA family MipA-interacting protein	196285	144149	153637	220	160020	170832	170177	223	3.64E-10	1.23E-09	1.013636364	0.019540186	
BP1026B_I0763	NAD-dependent epimerase/dehydratase family protein	36424	20990	25391	22	34615	30491	36282	28	1.86E-04	3.00E-04	1.21791304	0.283792966	
BP1026B_I0764	homoproteotecheute degradation operon regulator HpaR	64615	88837	78518	176	89182	81613	69712	183	4.77E-07	1.09E-06	1.039772727	0.05262822	
BP1026B_I0765	4-hydroxyphenylacetate degradation bifunctional isomerase/decarboxylase, subunit A	4084	2731	2308	4	3809	4415	6065	6	0.582189989	0.606290622	1.5	0.584962501	
BP1026B_I0766	4-hydroxyphenylacetate degradation bifunctional isomerase/decarboxylase, subunit B	9201	7398	6937	10	8605	7810	9332	11	3.47E-05	6.15E-05	1.1	0.137305324	
BP1026B_I0767	5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase	30892	31214	34246	21	37934	37474	37122	25	1.58E-05	2.93E-05	1.190476199	0.25138767	
BP1026B_I0768	3,4-dihydroxyphenylacetate 2,3-dioxygenase	10266	10884	10589	12	12720	11002	10939	13	1.77E-05	3.26E-05	1.083333333	0.115477217	
BP1026B_I0769	5-carboxymethyl-2-hydroxymuconate delta-isomerase	4120	5737	4891	12	4474	4536	3739	10	2.12E-08	5.76E-08	0.833333333	-0.263034406	
BP1026B_I0770	2-oxo-hepta-3-ene-1,7-dioic acid hydratase	26578	28738	29007	34	29494	28295	30874	36	7.51E-07	1.66E-06	1.058823529	0.08426216	
BP1026B_I0771	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase	7564	4532	3804	6	6192	6873	7232	8	0.00531846	0.0072678	1.333333333	0.415037499	
BP1026B_I0773	AraC family transcription regulator	3599	3599	3463	4	35554	4668	4	5.25E-04	8.07E-04	1	0	0	
BP1026B_I0774	zinc-binding dehydrogenase family oxidoreductase	28820	10252	15196	20	15246	18754	22716	21	1.54E-06	2.24E-06	1.05	0.70789328	
BP1026B_I0776	outer membrane porin protein	24270	21734	23279	21	16899	17633	17052	15	8.82E-17	6.63E-16	0.714285714	-0.485426827	
BP1026B_I0775	ABC transporter ATP-binding protein	1236	376	723	0	1008	1171	1155	1	0.876189159	0.886520577	#DIV/0!	#DIV/0!	
BP1026B_I0776	transmembrane ABC transporter protein	1409	1073	951	0	1202	1140	1288	0	0.0037909	0.005231592	#DIV/0!	#DIV/0!	
BP1026B_I0777	periplasmic solute-binding protein	3355	4880	4020	3	3193	3150	3281	2	2.74E-12	1.21E-11	0.666666667	-0.584962501	
BP1026B_I0778	DNA-binding response regulator TctD	598	466	408	0	553	633	519	0	0.12323839	0.140485036	#DIV/0!	#DIV/0!	
BP1026B_I0779	sensor histidine kinase	1835	678	1220	0	1708	1459	1972	1	0.263849571	0.260742656	#DIV/0!	#DIV/0!	
BP1026B_I0780	MORC domain-containing protein	37983	30285	30890	37	28387	30068	33692	35	3.02E-10	6.43E-09	0.945945946	-0.4080170349	
BP1026B_I0781	hypothetical protein	1395	2755	1982	4	1806	1716	1990	4	1.43E-07	3.48E-07	1	0	0
BP1026B_I0782	outer membrane porin	285889	253425	268936	223	260317	261583	254357	215	8.08E-08	2.04E-07	0.964125561	-0.05270705	
BP1026B_I0783	hypothetical protein	18616	17963	15908	41	17156	18252	20520	44	3.96E-06	7.90E-06	1.073170732	0.101879	

BP1026b	II0831	outer membrane porin OpcP	2139	2185	2623	2	2419	2458	2621	2	1.09E-04	1.81E-04	1	1	0	
BP1026b	II0832	glyoxalase family protein	5599	2867	3713	9	3660	4570	4832	10	1.70E-04	2.77E-04	1.111111111	0.152003093		
BP1026b	II0833	cytosine permease	82935	70992	75271	60	73688	69746	67617	55	5.37E-10	1.79E-09	0.916666667	-0.125530882		
BP1026b	II0834	DNA-binding protein	75325	93590	88279	69	96503	83330	84599	73	1.03E-06	2.32E-06	1.057971014	0.081300103		
BP1026b	II0835	cytosine deaminase	67645	66790	63960	52	86753	88144	81471	67	0.006048367	0.00816002	1.288461538	0.365649472		
BP1026b	II0836	membrane protein	7741	6850	7722	5	8575	9618	9349	6	0.002712263	0.003810185	1.2	0.263034406		
BP1026b	II0837	hypothetical protein	12053	12019	11056	12	10009	10918	9901	11	8.71E-11	3.20E-10	0.916666667	-0.125530882		
BP1026b	II0838	short chain dehydrogenase	3222	2456	2391	3	2319	2502	2641	3	6.72E-08	1.72E-07	1	0		
BP1026b	II0839	GntR family transcriptional regulator	5600	6168	6966	8	4601	3932	4191	5	7.22E-16	4.88E-15	0.625	-0.678071905		
BP1026b	II0840	voltage gated chloride channel family protein	18801	17980	16609	13	10895	12981	13355	9	2.87E-20	3.23E-19	0.692307692	-0.530514717		
BP1026b	II0841	cytochrome c peroxidase	657844	1043392	938608	2715	644555	623964	604162	1926	7.78E-26	1.58E-24	0.709392265	-0.495344405		
BP1026b	II0842	twi-arginine translocation pathway signal sequence domain-containing protein	23132	15327	16239	11	17997	16932	18215	10	5.50E-08	1.42E-07	0.909090909	-0.137503524		
BP1026b	II0844	containing protein	2990	652	1965	1	2174	2211	2847	2	0.030101991	0.037316222	2	1		
BP1026b	II0845	hypothetical protein	62	7	38	0	39	116	50	0	0.019178668	0.024392929	#DIV/0!	#DIV/0!		
BP1026b	II0846	GerF family regulatory protein	978	780	669	1	473	706	801	1	1.77E-06	3.68E-06	1	0		
BP1026b	II0847	LigA protein	386	615	500	1	620	307	560	1	0.007720704	0.010274589	1	0		
BP1026b	II0848	hypothetical protein	2404	2392	2370	11	2328	27901	2393	10	1.40E-07	3.42E-07	0.909090909	-0.137503524		
BP1026b	II0849	MarK family regulatory protein	22204	7831	8922	26	13735	17849	25061	39	0.0994497	0.114703171	1.5	0.584962501		
BP1026b	II0850	galactose-binding protein regulator	672	702	855	1	490	822	1118	1	0.017042976	0.021827274	1	0		
BP1026b	II0852	sugar ABC transporter permease	469	145	574	1	620	617	648	1	0.347809986	0.374408275	1	0		
BP1026b	II0853	senescence marker protein-30 family protein	4748	1179	1637	2	2904	3768	4277	4	0.488553943	0.515897151	1	0		
BP1026b	II0851	hypothetical protein	10354	10921	9290	19	8833	8691	7291	15	2.62E-13	1.30E-12	0.789473684	-0.341036918		
BP1026b	II0854	hypothetical protein	24820	21064	22497	51	24842	28388	28007	61	2.15E-04	3.46E-04	1.196078431	0.258311996		
BP1026b	II0855	hypothetical protein	6422	7896	5963	13	8962	7609	8462	16	0.002142103	0.00304819	1.230769231	0.299526282		
BP1026b	II0856	Leu tRNA	31349	50515	40933	481	30727	34657	28407	363	3.74E-19	8.93E-14	0.754677755	-0.460667346		
BP1026b	II0857	p-hydroxycinnamoyl CoA hydratase/lyase	3822	3458	3271	4	3602	3371	3650	4	1.83E-05	3.37E-05	0	0		
BP1026b	II0859	aldehyde dehydrogenase	894	323	253	0	660	853	1147	0	0.063849207	0.075605186	#DIV/0!	#DIV/0!		
BP1026b	II0858	feruloyl-CoA synthase	1273	1018	889	0	1876	1500	1395	0	0.93813771	0.943257563	#DIV/0!	#DIV/0!		
BP1026b	II0860	3-hydroxyphenylpropionic transporter MhpT	184	102	33	0	199	86	266	0	0.063915466	0.07566934	#DIV/0!	#DIV/0!		
BP1026b	II0861	porin	2919	1727	2045	1	2796	2893	2370	2	0.00438134	0.005950092	2	1		
BP1026b	II0862	chloronate esterase	7552	5801	5163	3	5918	6450	6406	3	2.69E-04	3.25E-04	1	0		
BP1026b	II0863	ICR family transcriptional regulator	32603	20261	20478	25	32874	37901	42891	38	0.069164533	0.08139085	1.52	0.604071324		
BP1026b	II0864	sugar ABC transporter periplasmic sugar-binding protein	3	4122	3716	3685	3	3645	3736	3783	3	2.55E-06	5.23E-06	1	0	
BP1026b	II0865	sugar ABC transporter ATP-binding protein	916	1273	1047	0	1130	1435	1061	0	0.021069175	0.026635179	#DIV/0!	#DIV/0!		
BP1026b	II0866	sugar ABC transporter permease	2732	764	1136	1	2540	2654	1961	2	0.706651502	0.726722214	2	1		
BP1026b	II0867	dehydratase, D-galactarate dehydratase, altronate dehydratase	203	0	26	0	216	160	54	0	0.047447732	0.057343737	#DIV/0!	#DIV/0!		
BP1026b	II0868	UxaA family hydrolase	4393	2324	2944	2	4129	5284	5958	3	0.578099975	0.602431916	1.5	0.584962501		
BP1026b	II0869	amidoaldehyde	3405	631	1355	0	367	583	357	0	0.580550995	0.64480265	#DIV/0!	#DIV/0!		
BP1026b	II0870	short chain dehydrogenase/reductase family oxidoreductase	1405	1340	1465	71	1	174E-14	1.83E-14	10	0.001440333	0.00139085	1.52	0.604071324		
BP1026b	II0871	fumarylacetoacetate (FAA) hydrolase family protein	1711	1392	1250	1	2052	2477	1939	2	0.469278902	0.496631702	1	0		
BP1026b	II0872	short chain dehydrogenase	1026	1150	1540	1	1496	1269	1162	1	0.001838547	0.002642648	1	0		
BP1026b	II0873	putative alternative L-fucose mutarotase	2624	2452	3134	8	2740	3065	2451	8	5.38E-06	1.06E-05	1	0		
BP1026b	II0875	hypothetical protein	0	0	45	0	58	32	36	0	0.00488266	0.006663395	#DIV/0!	#DIV/0!		
BP1026b	II0876	H-N5 histone family protein	1020	1154	1418	3	1238	1335	1725	4	0.031701779	0.039209105	1.333333333	0.415037499		
BP1026b	II0877	ICR family transcriptional regulator	2228	1736	2422	2	2498	2333	2262	3	2.48E-04	3.97E-04	1.5	0.584962501		
BP1026b	II0878	hypothetical protein	3067	3067	2823	6	3140	3770	2790	6	9.01E-06	0.001340134	1.666666667	-0.22392421		
BP1026b	II0879	EAL domain-containing protein	1919	1644	1998	1	1586	1964	1872	1	4.79E-06	4.64E-06	1	0		
BP1026b	II0880	TeR family transcriptional regulator	15133	16631	16518	26	16639	17802	18583	28	1.98E-05	3.62E-05	0.076923077	0.106915204		
BP1026b	II0881	thioesterase (4HBT) superfamily protein	43037	48950	48397	106	37955	31827	30253	76	4.35E-24	7.43E-23	0.716981132	-0.479992941		
BP1026b	II0882	putative extracellular ligand binding protein	1030142	1164790	1136652	971	1268187	1281530	1319029	1128	0.10238726	0.117988847	1.16168898	0.216223867		
BP1026b	II0883	hemolysin III	81197	56881	60235	106	74716	76413	65550	116	1.48E-05	2.75E-05	0.094339623	0.130606541		
BP1026b	II0884	hypothetical protein	4093	3484	4107	7	4255	4268	3989	7	1.89E-04	3.05E-04	0.909090909	-0.137503524		
BP1026b	II0885	EAL/GED/EF domain-containing protein	2255	2392	2097	11	21042	23636	22655	10	0.000499232	0.005950092	1.52	0.604071324		
BP1026b	II0886	AacX family transcriptional regulator	11873	23448	25659	47	26705	24084	21047	48	2.20E-07	5.23E-07	1.021276596	0.030373649		
BP1026b	II0887	aromatic amino acid transport protein	29167	33684	32746	22	32908	34249	29768	23	4.27E-08	1.12E-07	0.045454545	0.064130337		
BP1026b	II0888	aromatic amino acid aminotransferase	89749	85536	83831	71	119431	115809	111726	96	0.002372776	0.003355852	1.352112676	0.435215381		
BP1026b	II0889	hypothetical protein	24130	23219	25175	61	30321	31206	29012	77	7.04E-04	0.00106607	1.262295082	0.336049203		
BP1026b	II0890	acetyltransferase	40857	56410	51801	80	32934	32643	31119	52	2.35E-10	7.20E-09	0.65	-0.42188377		
BP1026b	II0891	2OG-Fc(II) oxygenase	26508	26915	27190	41	28978	27528	24860	41	1.48E-07	3.60E-07	0.909090909	-0.137503524		
BP1026b	II0892	hypothetical protein	38621	39471	40822	30	38802	38044	37455	28	3.56E-10	1.00E-09	0.966666667	-0.048906		
BP1026b	II0893	hypothetical protein	110962	141933	134246	268	18117	175419	167845	364	0.010607924	0.01390417	1.35208955	0.44170545		
BP1026b	II0894	hypothetical protein	1612	875	1133	3	1441	2145	2134	5	0.99796633	0.998233877	1.666666667	0.736965594		
BP1026b	II0895	sensor histidine kinase	7513	8041	7608	5	7304	7075	7170	5	1.30E-08	3.63E-08	1	0		
BP1026b	II0896	response regulator	3435	4095	3937	10	2796	3355	2703	7	2.24E-13	1.12E-12	0.7	-0.514573173		
BP1026b	II0897	CheC family protein	6413	3986	5085	8	5760	5847	7848	10	0.004099232	0.005950092	1.25	0.321928095		
BP1026b	II0898	penicillin-binding protein 1C	51555	37780	41286	16	55202	57219	60613	21	0.014819304	0.013672796	1.3125	0.392317423		
BP1026b	II0899	alpha-2-macroglobulin family protein	20703	101506	124257	23	110306	225346	26885	38	0.33078539	0.33252555	1.652173931	0.23465557		
BP1026b	II0900	hypothetical protein	11445	17776	14500	26	12999	4464	11888	9	1.06E-11	4.36E-11	0.046153846	-0.2410081		
BP1026b	II0901	hypothetical protein	4596	2264	3620	7	4104	4664	3786	9	0.004904217	0.006687519	1.285714286	0.362570079		
BP1026b	II0902	leucyl-tRNA synthetase	9177	5185	5869	3	8428	8518	8798	3	0.005481576	0.007406849	1	0		
BP1026b	II0903	hypothetical protein	1463	1041	680	1	1023	1351	1053	1	0.010303831	0.013539584	1	0		
BP1026b	II0904	hypothetical protein	5792	2416	2746	4	4292	4887	5547	5	0.051991682	0.062425895	1.25	0.321928095		
BP1026b	II0905	hypothetical protein	3957	1988	2306	1	2422	2821	3276	1	2.46E-05	4.39E-05	1	0		
BP1026b	II0906	TauD/TIDA family dioxygenase	9001	4038	5285	6	8601	8061	9171	9	0.050505045	0.060792391	1.5	0.584962501		
BP1026b	II0907	hypothetical protein	9223	12642	14555	12	10670	12401	14401	14	0.003406836	0.004308881	1.666666667	-0.22392421		
BP1026b	II0908	aminotransferase class-V	87907	87317	85955	76	104444	106807	98221	90	5.57E-05	9.63E-05	1.184210526	0.243925583		
BP1026b	II0909															

BP1026b	II0956	AraC family transcription regulator	16850	15815	16234	17	15988	16418	15587	17	146E-07	3.56E-07	1		0	
BP1026b	II0958	outer membrane porin	429	828	563	0	747	700	619	0	0.055141096	0.066042797	#DIV/0!	#DIV/0!	0	
BP1026b	II0959	hypothetical protein	1256	2320	1556	5	1690	1571	2010	5	7.28E-05	1.24E-04			0	
BP1026b	II0960	LysR family protein	11517	11376	12903	19	10877	10671	8645	16	8.22E-12	0.842105263	0.247927313		0	
BP1026b	II0961	acetyltransferase	33591	37665	35969	74	41182	38578	36003	80	2.19E-07	5.21E-07	1.081081081	0.112474729	0	
BP1026b	II0962	N-ethylmaleimide reductase	22168	18408	20616	19	25243	26979	24312	24	0.001391127	0.000207328	1.263157895	0.337034987	0	
BP1026b	II0963	ArS family transcriptional regulator	18607	13518	14012	50	22733	21305	20177	69	0.02417827	0.030387778	1.38	0.464668267	0	
BP1026b	II0964	outer membrane porin	26295152	35292283	33891742	28290	34424285	32878230	30776159	29060	1.55E-06	3.25E-06	1.027218098	0.038742526	0	
BP1026b	II0966	regulator of nucleoside diphosphate kinase	58261	68506	64631	159	71679	79011	75665	189	3.87E-04	6.03E-04	1.188679245	0.249359469	0	
BP1026b	II0965	hypothetical protein	6138	10331	9537	74	9868	10741	11539	91	0.00194712	0.002771966	1.22972973	0.298412175	0	
BP1026b	II0967	hypothetical protein	206527	208321	22323	618	351293	344034	325104	994	0.452478593	0.473990031	1.608418239	0.685639014	0	
BP1026b	II0968	predicted RNA	71878	46860	45957	603	80468	89631	86814	941	0.447587918	0.474799445	1.56053068	0.642036721	0	
BP1026b	II0968	hypothetical protein	220050	353267	312996	635	288631	267849	244982	574	1.23E-09	3.94E-09	0.903937008	-0.145705855	0	
BP1026b	II0969	GTP cyclohydrolase II	109470	87548	96282	147	72248	74965	70562	109	3.43E-19	3.44E-18	0.741496599	-0.43148802	0	
BP1026b	II0970	hypothetical protein	176429	218386	202420	242	127112	126537	117218	150	2.91E-45	2.34E-43	0.619834711	-0.690044547	0	
BP1026b	II0971	N-acetylhomoserine lactone synthase	204233	267500	249774	392	126849	127808	128065	208	2.49E-69	6.79E-67	0.530612245	-0.914270126	0	
BP1026b	II0972	hypothetical protein	19190	14197	14447	74	6224	5856	5824	28	1.33E-82	4.91E-80	0.378378378	-1.402098444	0	
BP1026b	II0973	hypothetical protein	148373	88541	107367	258	115337	118291	125340	269	3.66E-09	0.004253528	1.042635659	0.06027107	0	
BP1026b	II0974	Transcriptional regulator RhlR	18515	25410	21864	30	21133	21104	22242	29	3.84E-08	1.01E-07	0.966666667	-0.0489096	0	
BP1026b	II0975	MgC ²⁺ family protein	6882	7640	7890	10	7875	7056	6962	10	1.82E-07	4.38E-07			0	
BP1026b	II0976	calcineurin-like phosphoesterase	15609	9085	11699	10	12616	11931	14507	10	1.07E-05	2.03E-05			0	
BP1026b	II0977	hypothetical protein	15687	16931	16056	27	11238	10113	10762	18	1.30E-23	2.14E-22	0.666666667	-0.584962501	0	
BP1026b	II0978	2OG-Fe(II) oxygenase	78369	48689	50717	94	99202	108315	116489	172	0.689551999	0.71088771	1.829787234	0.871675903	0	
BP1026b	II0979	IcIR family transcriptional regulator	69673	46401	47746	57	59403	61376	66121	65	8.99E-05	1.51E-04	1.140350877	0.189477799	0	
BP1026b	II0980	outer membrane porin protein	5701	4317	3855	3	5516	5581	4858	4	1.33E-04	0.001078336	1.333333333	0.415037499	0	
BP1026b	II0981	Rieske (2Fe-2S) domain-containing protein	250	145	398	0	14527	13194	1253	0	0.5895277	0.6131896	#DIV/0!	#DIV/0!	0	
BP1026b	II0982	hypothetical protein	1	350	632	398	1	905	964	784	2	0.019417867	0.02465711		1	0
BP1026b	II0983	Rieske family iron-sulfur cluster-binding protein	3020	4288	3156	3	3916	3980	3019	3	7.98E-07	1.63E-06			0	
BP1026b	II0984	short chain dehydrogenase	501	128	285	0	829	761	1243	1	2.71E-14	1.50E-13	#DIV/0!	#DIV/0!	0	
BP1026b	II0985	hypothetical protein	1106	1138	1265	2	979	1110	852	1	5.06E-07	1.15E-06	0.5		-1	
BP1026b	II0986	alpha/beta fold family hydrolase	556	532	680	0	534	673	656	0	0.017008745	0.021787889	#DIV/0!	#DIV/0!	0	
BP1026b	II0987	IcIR family transcriptional regulator	1345	731	993	1	2933	1244	1017	1	0.01278328	0.01661712			0	
BP1026b	II0988	short chain dehydrogenase	255371	43030	2156	2	2180	2438	2478	2	0.003043472	0.004253528	1.125	-0.169925001	0	
BP1026b	II0989	hypothetical protein	3119	2459	2623	1	2910	2878	3519	1	9.03E-04	0.001348613			0	
BP1026b	II0990	L-aspartate dehydrogenase	815	193	468	0	648	597	844	0	0.914565337	0.921924247	#DIV/0!	#DIV/0!	0	
BP1026b	II0991	aldehyde dehydrogenase family protein	1379	1157	786	0	1744	1980	2323	1	0.140034742	0.158564285	#DIV/0!	#DIV/0!	0	
BP1026b	II0992	glyoxalase/bleomycin resistance protein/dioxygenase superfamily													0	
BP1026b	II0993	pyridine nucleotide-disulfide oxidoreductase, class I	1666	602	692	1	1041	1847	1752	1	0.719294877	0.738633297			0	
BP1026b	II0994	major facilitator family transporter	910	260	458	0	733	871	1411	0	0.034020086	0.041842101	#DIV/0!	#DIV/0!	0	
BP1026b	II0995	hypothetical protein	1727	1171	1581	1	1569	1427	974	0	1.12E-06	1.24E-06	0	4NUN1	0	
BP1026b	II0995	hypothetical protein	575	944	736	4	975	938	851	6	0.149566565	0.168656159	1.5	0.584962501	0	
BP1026b	II0996	membrane-anchored cell surface protein	15080	8094	10588	4	17138	19068	21743	8	0.71077723	0.730725188	2		0	
BP1026b	II0997	OmpA family protein	9234	8317	7406	10	11231	11058	10154	13	0.008179858	0.010857943	1.3	0.378511623	0	
BP1026b	II0998	UspA family protein	4147	6026	6879	13	4235	3672	4504	9	2.01E-13	1.01E-12	0.692307692	-0.530514717	0	
BP1026b	II0999	amidase	99056	76684	82476	59	97904	98078	105626	69	4.11E-05	7.20E-05	1.164941528	0.225881407	0	
BP1026b	II1000	AacN ₁ family transcriptional regulator	47460	56367	52001	107	48594	51736	48101	102	4.89E-12	2.10E-11	0.951271025	-0.069091644	0	
BP1026b	II1001	methionine gamma-lyase	443071	43030	2156	341	30954	31390	29044	23	1.27E-22	0.004253528	1.125	-0.169925001	0	
BP1026b	II1002	hypothetical protein	38778	58270	55943	226	30619	30539	30803	136	1.09E-35	5.21E-34	0.601769912	-0.732716121	0	
BP1026b	II1002	predicted RNA	31025	50756	45211	682	25059	23373	22005	378	1.42E-38	7.86E-37	0.554252199	-0.851385505	0	
BP1026b	II1003	hypothetical protein	17001	16453	15464	23	9804	9458	9030	13	3.82E-32	1.39E-30	0.565217391	-0.823122238	0	
BP1026b	II1004	N-hydroxyarylamine O-acetyltransferase	21621	27310	24098	27	20857	19555	20664	23	7.30E-13	3.43E-12	0.851851852	-0.231255546	0	
BP1026b	II1005	hypothetical protein	6086	4111	4585	8	8444	5288	4443	9	2.00E-05	3.67E-05	1.125	0.169925001	0	
BP1026b	II1006	DNA-binding protein	8337	13090	10997	23	8607	8129	7963	17	3.50E-16	2.44E-15	0.739130435	-0.436099115	0	
BP1026b	II1007	oxidoreductase	94999	94999	9231	699	8	80320	10859	9	7.93E-04	0.001078336	1.333333333	0.415037499	0	
BP1026b	II1008	LysR family regulatory protein	37904	52729	51765	49	47357	46209	42065	47	4.40E-12	1.90E-11	0.959183673	-0.060120992	0	
BP1026b	II1009	hypothetical protein	12856	13173	14778	9	18002	17355	17518	12	0.00751156	0.000106093	1.333333333	0.415037499	0	
BP1026b	II1010	major facilitator family transporter	3121	3343	3272	2	2778	2767	2274	2	5.13E-12	2.19E-11			0	
BP1026b	II1011	alpha/beta fold family hydrolase	1612	972	1131	1	1400	1605	2358	1	0.426369855	0.453674328			0	
BP1026b	II1012	hypothetical protein	3034	5559	4896	4	4502	4040	4096	4	1.12E-06	2.41E-06			0	
BP1026b	II1013	short chain dehydrogenase	1890	2536	2942	2	1880	2152	1894	2	9.31E-12	3.86E-11			0	
BP1026b	II1014	flavin-binding monooxygenase-like protein	6780	10144	8233	5	8732	9126	7786	5	1.33E-06	2.83E-06			0	
BP1026b	II1015	hypothetical protein	1200	1376	1171	1	948	1117	1176	1	1.38E-06	2.92E-06			0	
BP1026b	II1016	aliphatic compound ABC transporter, periplasmic substrate-binding protein	50355	42409	47588	47	40322	43227	46260	43	4.10E-13	1.98E-12	0.914893617	-0.128324097	0	
BP1026b	II1017	MerR family transcriptional regulator	605580	395374	436197	558	442862	474618	506591	553	2.82E-12	1.24E-11	0.991039427	-0.012985642	0	
BP1026b	II1018	phosphothioric N-acetyltransferase	16075	16577	14839	27	12763	10587	11208	20	2.72E-18	2.46E-17	0.740740741	-0.432959407	0	
BP1026b	II1019	hypothetical protein	39184	52547	46863	57	31656	33813	31135	40	7.34E-25	3.34E-23	0.701754386	-0.010961919	0	
BP1026b	II1020	EmrR/QacA family drug resistance transporter	66989	44481	50265	35	65960	68124	64124	43	0.00174598	0.000105236	1.228517429	0.296987191	0	
BP1026b	II1021	hypothetical protein	183	241	351	1	227	518	256	0	0.00375615	0.005341442			0	
BP1026b	II1022	methy-accepting chemotaxis protein	1542675	825107	1006913	722	1043674	1135013	1265135	737	0.42081118	0.448140306	1.02075623	0.902665782	0	
BP1026b	II1023	hypothetical protein	118947	79096	85015	56	113686	115596	117722	69	6.97E-05	1.19E-04	1.232142857	0.301169535	0	
BP1026b	II1024	hypothetical protein	2769	1666	1633	3	2688	2380	3254	5	0.091335736	0.105702954	1.666666667	0.73695594	0	
BP1026b	II1025	hypothetical protein	22670	24391	23778	27	19015	19411	18927	22	5.78E-14	3.09E-13	0.814814815	-0.295455884	0	
BP1026b	II1026	agaF protein	129407	93483	101955	81	128188	135717	133565	99	2.88E-05	5.17E-05	1.222222222	-0.295906617	0	
BP1026b	II1027	TKA domain-containing protein	42102	42469	40705	37	39224	37290	34538	33	1.40E-13	7.16E-13	0.931891892	-0.105959246	0	
BP1026b	II1028	alpha/beta fold family hydrolase	35588	27208	22972	31	24675	22772	22144	26	2.45E-07	2.39E-07</				

BP1026B_I1078	histidine transport ATP-binding protein	4894	6073	6284	7	2946	4176	4355	4	2.47E-17	1.97E-16	0.571428571	-0.807354922
BP1026B_I1079	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	167890	119992	137096	108	142341	139984	135059	106	4.10E-12	1.77E-11	0.981481481	-0.026967048
BP1026B_I1080	hypothetical protein	26515	27738	28757	55	25996	25293	24864	51	5.40E-10	1.80E-09	0.927272727	-0.108934372
BP1026B_I1081	hypothetical protein	34474	23232	27905	38	34351	31923	29508	42	4.33E-06	9.33E-06	1.105263158	0.144389909
BP1026B_I1082	hypothetical protein	947423	1502830	1338420	3660	847897	815113	720881	2303	0.362997785	0.390145506	0.629234973	-0.668329237
BP1026B_I1083	hypothetical protein	9512	9397	10415	7	8568	8159	8900	6	1.21E-10	4.37E-10	0.857142857	-0.222392421
BP1026B_I1084	hypothetical protein	1719	954	779	2	1074	1448	1405	2	0.01733357	0.022172244	1	0
BP1026B_I1086	hypothetical protein	4654	5756	5641	40	3795	4480	4434	32	1.22E-10	4.38E-10	0.8	-0.321928095
BP1026B_I1085	histidine kinase	20025	11323	13442	14	13096	13122	14348	13	1.01E-09	3.28E-09	0.928571429	-0.106915204
BP1026B_I1087	response regulator	10161	7352	8848	28	9606	8605	8650	29	1.37E-06	2.90E-06	1.035714286	0.030626073
BP1026B_I1088	catalse	13151	10340	17484	10	12855	12484	12536	8	3.05E-15	1.91E-14	1.105263158	0.4321928095
BP1026B_I1089	hypothetical protein	25510	21190	22625	15	20959	22105	20878	14	9.07E-10	2.95E-09	0.933333333	-0.099535674
BP1026B_I1090	AraC family transcriptional regulator	13322	10248	11058	7	13610	14163	12459	8	2.48E-04	3.96E-04	1.142857143	0.192645078
BP1026B_I1091	Rieske family iron-sulfur cluster-binding protein	14109	19913	16057	16	14902	14138	13095	13	4.60E-12	1.98E-11	0.8125	-0.299560282
BP1026B_I1092	hypothetical protein	17041	20072	19715	11	16078	14434	15446	9	2.91E-13	1.43E-12	0.818181818	-0.289506617
BP1026B_I1093	polyketide beta-ketoacyl:acyl carrier protein synthase	9623	9092	8858	7	9200	9476	8984	7	5.97E-07	1.33E-06	1	0
BP1026B_I1094	acyl carrier protein	3177	6545	5188	20	2963	3298	2727	12	1.44E-25	2.85E-24	0.6	-0.736965594
BP1026B_I1095	polyketide biosynthesis enoyl-CoA hydratase	10997	23023	23738	28	17483	17063	14314	20	3.57E-14	3.68E-16	0.714285714	-0.485426327
BP1026B_I1096	polyketide biosynthesis enoyl-CoA hydratase	21969	24544	21293	29	19897	18485	17041	23	1.38E-14	9.90E-14	0.793103448	-0.33419039
BP1026B_I1097	hydroxymethylglutaryl-coenzyme A synthase	49434	65986	60676	46	39533	36526	36687	29	7.64E-36	3.68E-34	0.630434783	-0.665580961
BP1026B_I1098	hypothetical protein	1924	2280	2290	6	2898	3380	3233	9	0.308417819	0.334128194	1.5	0.584962501
BP1026B_I1099	hypothetical protein	53	171	89	0	58	85	73	0	0.001397722	0.002036124	#DIV/0!	#DIV/0!
BP1026B_I1100	Cys tRNA	558	500	556	7	807	1052	581	10	0.70119286	0.72170758	1.428571429	0.514573173
BP1026B_I1101	malonyl CoA:acyl carrier protein transacylase	18569	16562	17380	14	17505	17376	17216	14	1.94E-07	4.65E-07	1	0
BP1026B_I1102	sodium/hydrogen exchanger	21295	22852	23581	18	18121	16786	16339	13	3.99E-16	2.76E-15	0.722222222	-0.469485283
BP1026B_I1103	polyketide synthase	46702	40511	41486	3	50063	51584	52304	1	1.17E-04	1.90E-04	1	0
BP1026B_I1104	beta-ketoacyl synthase domain-containing protein	46754	38437	39695	2	50972	49043	49361	2	3.99E-05	7.01E-05	1	0
BP1026B_I1105	polyketide synthase	47559	35313	37961	2	49667	50399	52841	3	3.06E-04	4.84E-04	1.5	0.584962501
BP1026B_I1106	polyketide synthase	15341	16522	15460	3	16083	16400	15764	3	1.06E-06	2.29E-06	1	0
BP1026B_I1107	halogenase PtnC	18065	21269	18585	11	20568	21445	21051	12	8.60E-06	1.65E-05	1.090909091	0.125530882
BP1026B_I1108	EmrB/QacA family drug resistance transporter	5147	5419	5180	3	6346	4825	5007	3	1.50E-05	2.78E-05	1	0
BP1026B_I1109	voltage-gated chloride channel/CBS domain-containing protein	8036	3677	4845	2	6659	7960	8432	4	0.146671614	0.165600114	2	1
BP1026B_I1110	Mark family transcriptional regulator	8096	8906	1402	3	7039	1409	9242	4	0.054699031	0.065500916	1.333333333	0.415037499
BP1026B_I1111	HPP family protein	1681	1274	1529	1	1600	1094	1734	1	5.97E-05	1.03E-04	1	0
BP1026B_I1112	transcriptional regulator	53162	47094	46452	50	36998	38269	37112	38	1.04E-21	1.40E-20	0.76	-0.395928676
BP1026B_I1113	calcium/proton exchanger	56790	39818	43662	43	46099	44223	45629	41	2.24E-11	8.87E-11	0.953488372	-0.06871275
BP1026B_I1114	membrane efflux protein	20436	23127	22707	32	19658	17905	17772	27	1.79E-12	5.37E-12	0.84375	-0.245112498
BP1026B_I1115	CAAX protease family protein	12923	13660	11004	14	13036	12937	12665	14	1.53E-06	3.22E-06	1	0
BP1026B_I1116	fumarylacetoacetate (FAA) hydrolase	21910	11504	14098	22	16368	19711	24878	28	0.000229906	0.004225728	1.272727273	0.347923303
BP1026B_I1117	AraC family transcriptional regulator	12649	10511	10160	18	8666	8146	9461	13	1.47E-14	1.96E-13	0.727272727	-0.45943519
BP1026B_I1118	putative lipoprotein	0	48	0	0	71	65	0	0	0.001607492	0.002329785	#DIV/0!	#DIV/0!
BP1026B_I1120	ECF subfamily RNA polymerase sigma factor	652	361	559	1	413	380	761	0	0.006335025	0.008522895	0	#NUM!
BP1026B_I1119	hypothetical protein	591	132	170	0	446	612	801	0	8.13E-04	0.001221541	#DIV/0!	#DIV/0!
BP1026B_I1121	hypothetical protein	2112	752	1087	1	2011	2122	2873	2	0.392263191	0.419664668	2	1
BP1026B_I1122	lipoprotein	1503	777	792	2	1349	1756	2036	4	0.289306775	0.314839756	2	1
BP1026B_I1125	ECF subfamily RNA polymerase sigma factor	803	346	532	1	677	500	688	1	0.243562118	0.30060656	1	0
BP1026B_I1124	FeoB family protein	699	738	752	0	655	9	724	0	0.060962056	0.07248791	#DIV/0!	#DIV/0!
BP1026B_I1126	TonB-dependent siderophore receptor	70443	63614	62105	24	70037	74057	76902	27	5.55E-05	9.60E-05	1.125	0.169925001
BP1026B_I1127	ribosome ABC transporter permease	1906	1137	1184	1	1649	2391	2519	2	0.734310555	0.752941777	2	1
BP1026B_I1128	sugar ABC transporter permease	3868	3236	3863	3	4146	3490	5064	3	0.00278592	0.003909275	1	0
BP1026B_I1129	ABC transporter ATP-binding protein	9324	3937	5288	3	7573	7344	9461	4	0.009335444	0.012318774	1.333333333	0.415037499
BP1026B_I1130	Ribose transport ATP-binding protein rbsA	5941	5486	6016	5	4662	4963	4123	4	4.61E-11	1.75E-10	0.8	-0.321928095
BP1026B_I1131	hypothetical protein	241759	231483	244413	345	210317	205458	180584	286	1.29E-16	5.52E-16	0.828985507	-0.270587215
BP1026B_I1133	hypothetical protein	12330	4230	6791	30	8880	10321	1452	44	0.07545617	0.087809571	1.466666667	0.552541023
BP1026B_I1134	acyl-CoA dehydrogenase-family protein	2315	1074	1476	1	1813	1473	2341	0	0.003697168	0.00511247	1	0
BP1026B_I1135	hypothetical protein	4155	2499	2545	2	2564	3124	3148	2	6.40E-07	1.42E-06	1	0
BP1026B_I1136	hypothetical protein	1347	1741	1731	6	1100	1050	894	4	1.65E-16	1.20E-15	0.666666667	-0.584962501
BP1026B_I1137	hypothetical protein	45995	27568	29203	125	36099	35165	40358	136	4.35E-07	9.94E-07	1.088	0.121678557
BP1026B_I1138	Signal transduction histidine kinase	143844	105830	118560	87	135737	136239	130281	96	3.66E-08	9.67E-08	1.103448276	0.142019005
BP1026B_I1139	DNA-binding response regulator IrIR	25652	29945	28463	40	18515	17340	16679	25	1.42E-26	3.11E-25	0.625	-0.678071905
BP1026B_I1140	heavy metal efflux pump CzcA	61785	53133	57041	17	56444	55783	53343	17	8.66E-11	1.34E-10	1	0
BP1026B_I1141	heavy metal resistance protein CzcB	11666	4041	6850	5	7993	11376	11631	7	0.035491802	0.04355812	1.4	0.485426827
BP1026B_I1142	heavy metal resistance protein CzcC	10015	3240	3226	3	7017	8450	9275	5	0.124952366	0.142309385	1.666666667	-0.69635594
BP1026B_I1143	hypothetical protein	14310	4225	7004	29	8627	8229	8084	29	1.19E-07	2.94E-07	1	0
BP1026B_I1145	bacteriophage protein	8372	8506	8836	60	5991	5202	4516	37	6.84E-23	1.03E-21	0.616666667	-0.67347323
BP1026B_I1147	hypothetical protein	14899	19664	17557	35	16317	15186	13993	31	1.39E-10	4.98E-10	0.885714286	-0.175086707
BP1026B_I1146	hypothetical protein	13338	13051	15258	55	15602	14906	13373	54	8.42E-08	2.12E-07	0.981818182	-0.206472211
BP1026B_I1148	hypothetical protein	11985	13508	13230	27	15688	13655	13539	26	1.57E-05	2.30E-05	0.704074074	-0.3003489
BP1026B_I1149	YnfK _{proh} -tRNA synthetase associated domain-containing protein	139786	183620	162573	333	142419	140977	14319	292	7.96E-18	6.73E-17	0.876786877	-0.189533808
BP1026B_I1150	alanine dehydrogenase	46804	31506	36948	34	38283	39485	47295	37	2.00E-07	4.76E-07	1.088325994	0.121995524
BP1026B_I1151	H-Ns histone family protein	338097	557130	470828	1379	369824	363908	300590	1044	2.70E-20	3.05E-19	0.757070431	-0.401500745
BP1026B_I1152	ProQ protein	176083	207018	199942	359	113502	113769	106522	206	1.49E-51	1.67E-49	0.573816156	-0.801339507
BP1026B_I1153	hydratase/decarboxylase family protein	6523	1355	2513	4	3521	4463	5592	5	0.04048751	0.049369419	1.25	0.321928095
BP1026B_I1154	hypothetical protein	7330	4929	5397	10	5437	6743	9191	12	0.001108712	0.001632291	1.2	0.263034406
BP1026B_I1155	heat shock protein 70	49113	25380	28701	18	57210	63158	67039	33	0.34481784	0.369940521	1.833333333	0.87469118
BP1026B_I1156	heat shock protein 70	58663	38823	42331	16	59822087	80267	80267	27	0.94921827	0.94921827	1.6875	0.5488702
BP1026B_I1157	polyglutamate synthase	54887	63464	59727	54	51764	52637	53980	48	7.92E-15	1.469E-14	0.888888889	-0.169925001
predicted RNA	-	85119	99010	95726	1277	98793	96562	99474	1346	2.60E-07	6.14E-07	1.05403289	0.075919885
BP1026B_I1158	hypothetical protein	50674	63929	65361	229	53243	48818	49098	193	6.37E-18	5.45E-17	0.84279467	-0.246746751
predicted RNA	-	81603	9282	14633	19	60702	85262	132326	5769	2.			

BP1026B_I1203	hypothetical protein	14837	16686	17419	63	55993	54934	46630	203	2.54E-08	6.85E-08	3.22222222	1.688055994
BP1026B_I1204	universal stress protein	976270	537716	684438	773	929020	927038	916485	974	0.041035757	0.049688334	1.260025873	0.333453358
BP1026B_I1205	hypothetical protein	181941	207380	183880	458	170047	182241	167778	415	6.80E-15	4.08E-14	0.906113537	-0.142236262
BP1026B_I1206	Ni-Fe-hydrogenase H ₂ small subunit	22813	15147	17973	34	19039	19046	87995	37	6.65E-06	1.29E-05	0.120252294	0.131090924
BP1026B_I1207	hydrogenase subunit	110420	96143	94562	56	92293	91682	93205	52	8.51E-11	3.13E-10	0.928571429	-0.106915204
BP1026B_I1208	hydrogenase 4 subunit F	122847	113046	112189	79	111833	112569	98950	73	3.25E-12	1.42E-11	0.924050633	-0.11396189
BP1026B_I1209	hydrogenase 4 membrane component	61542	92155	84888	120	71319	64470	53022	95	1.93E-16	1.39E-15	0.79166667	-0.337034987
BP1026B_I1210	formate hydrogen-lyase subunit 4	70532	60599	62774	67	71339	71192	76003	76	6.10E-05	1.05E-04	1.134328358	0.18183823
BP1026B_I1211	hydrogenase 4 component B / Formatehydrogen-lyase subunit 3	259702	123903	153875	89	229783	251375	250775	121	0.19766651	0.219491638	1.359550556	0.443129806
BP1026B_I1212	hypothetical protein	40184	33863	37881	48	38211	37779	38162	49	6.57E-09	1.92E-08	1.020833333	0.029747343
BP1026B_I1213	hypothetical protein	3383	2644	373	1	11332	10051	365	38	7.42E-04	0.00169073	1.04964539	0.069902013
BP1026B_I1214	phosphocarrier HPr protein	23719	21056	23411	87	20734	20220	20891	78	3.22E-10	1.10E-09	0.896551724	-0.157541277
BP1026B_I1216	transferase	58460	31209	37209	50	38885	39424	43102	48	1.93E-11	7.71E-11	0.96	-0.058893689
BP1026B_I1217	hypothetical protein	8530	2616	3047	45	3274	4633	6657	46	2.36E-05	4.28E-05	1.022222222	0.03170886
BP1026B_I1218	proline dehydrogenase	22640	34134	32383	135	23593	23206	20633	102	5.77E-17	4.45E-16	0.755555556	-0.404390255
BP1026B_I1219	hypothetical protein	8750	1546	2219	12	5693	6601	10107	22	0.794853357	0.809718886	1.833333333	0.874469118
BP1026B_I1220	nitrate/nitrite transporter	13688	11034	11227	8	4558	9289	3617	46	4.53E-15	2.30E-14	1.22380606	0.347019076
BP1026B_I1221	peptidyl-prolyl cis-trans isomerase C	5614	13890	14780	18	14770	15326	14052	18	3.25E-07	5.59E-07	0.75	-0.415037496
BP1026B_I1222	respiratory nitrate reductase subunit gamma	20135	20111	19540	29	21705	20289	17491	28	1.15E-07	2.86E-07	0.965517241	-0.050626073
BP1026B_I1223	nitrate reductase 1 subunit delta	18616	15634	18292	25	21078	20826	20484	30	2.51E-04	4.00E-04	1.2	0.263034406
BP1026B_I1224	nitrate reductase subunit beta	65670	70290	69188	44	63485	63606	55325	39	4.18E-12	1.81E-11	0.886363636	-0.1740294
BP1026B_I1225	nitrate reductase subunit alpha	195087	163786	170724	46	191883	201792	213049	53	8.40E-05	1.41E-04	1.152137913	0.204358499
BP1026B_I1226	hypothetical protein	1552	1335	2378	3	1489	1066	1062	2	1.44E-13	7.35E-13	0.666666667	-0.584962501
BP1026B_I1227	sensor histidine kinase/response regulator	169139	133406	138434	71	167382	170527	166319	82	3.59E-06	7.21E-06	1.154595577	0.307804885
BP1026B_I1228	LuxS family auto-inducer binding response regulator	176499	163840	170630	114	173443	166519	182907	142	0.001853463	0.002463706	1.271929825	0.347019076
BP1026B_I1229	response regulator	459950	440563	497901	1134	311304	319764	311966	764	8.96E-25	1.63E-23	0.67372134	-0.569726097
BP1026B_I1230	Cys/FNR family transcriptional response regulator	559647	565485	573388	725	557385	533031	504477	681	2.67E-13	1.32E-12	0.939130345	-0.090326197
BP1026B_I1231	hydroxylase CooC/NonD family protein subfamily	30102	35886	32821	19	33044	32465	30383	18	3.22E-09	9.80E-09	0.47368421	-0.078002512
BP1026B_I1232	TauD/TigA family dioxygenase	3032360	4765900	4325868	4777	2537227	2503561	2271495	2881	0.764531308	0.780734286	0.60398179	-0.729535216
BP1026B_I1233	transport/efflux protein	256465	237299	230790	193	194218	193496	183933	152	8.67E-22	1.17E-20	0.787564767	-0.344529524
BP1026B_I1234	thioesterase	82828	66529	73300	34	69679	68445	73470	80	5.40E-09	2.70E-08	0.952380952	-0.073893238
BP1026B_I1235	acetyltransferase	373016	232184	247227	335	450355	485350	529607	577	0.12448156	0.141717346	1.22380606	0.784410223
BP1026B_I1236	polyketide synthase	1214459	1205952	1199704	757	1587285	1614735	1607382	1006	0.017586528	0.022463706	1.328929987	-0.4102651
BP1026B_I1237	polyketide synthase	960850	749496	833332	343	1250217	1303998	1409224	535	0.002420849	0.003419982	1.559766764	0.641330315
BP1026B_I1238	non-ribosomal peptide synthase/polyketide synthase	1576889	1489607	1533648	441	224617	2223772	2347383	653	0.010922641	0.014286631	1.480725624	0.566304336
BP1026B_I1239	TubD protein	1870475	1548291	1591205	418	2392462	2555429	2736281	631	0.00326364	0.013566066	1.533492962	0.616821415
BP1026B_I1240	TubF protein	2171772	1424256	1637723	379	2609128	2769083	3027007	610	0.008099126	0.01057617	1.609496881	0.686611394
BP1026B_I1241	non-ribosomal peptide/polyketide synthase	3971183	3168942	3266605	754	4235983	4379606	4505299	947	0.0091750873	0.106136189	1.25596871	0.732879902
BP1026B_I1242	sluagelipase	4940401	6338404	596318	299	532629	537878	526607	284	8.85E-13	4.21E-12	0.940932776	-0.407425455
BP1026B_I1243	hypothetical protein	34239	57229	51626	230	33849	33243	35952	165	5.14E-24	8.72E-23	0.717391304	-0.479167837
BP1026B_I1244	hypothetical protein	77012	132485	111849	965	82827	78081	73528	77	1.52E-18	1.42E-17	0.76062167	-0.394748879
BP1026B_I1245	N-acyl-homoserine lactone dependent regulatory protein	153918	179059	172066	265	126161	125095	123402	197	8.06E-28	1.94E-26	0.734936226	-0.42779673
BP1026B_I1246	hypothetical protein	567870	483555	513620	608	470377	470077	450946	540	1.50E-16	1.10E-15	0.888157895	-0.171119116
BP1026B_I1247	predicted RNA	14677	1517	2286	293	4937	8492	14982	450	0.226369495	0.249908092	1.535836177	0.619204337
BP1026B_I1248	sodium/hydrogen exchanger	593443	380296	408783	373	433915	449648	444680	359	2.54E-13	1.26E-12	0.962664688	-0.095197786
BP1026B_I1249	hypothetical protein	70593	44876	20593	116	104544	10023	10454	13	1.04E-14	1.04E-14	0.75	-0.407425455
BP1026B_I1249	hypothetical protein	12999	11095	10308	28	8408	9237	9479	22	2.84E-14	1.57E-13	0.787514286	-0.347923303
BP1026B_I1251	N-acyl-homoserine lactone synthase	382704	487806	462988	715	272759	260645	221065	404	2.06E-31	7.04E-30	0.565034965	-0.283587949
BP1026B_I1250	nonribosomal peptide synthetase	1465602	1178443	1213887	847	1205425	1281784	1391694	851	0.314505901	0.34019426	1.00472255	0.00679162
BP1026B_I1252	acyl carrier protein	1317548	216443	1874659	7439	2039810	2003237	1741583	8034	0.093751238	0.108370133	1.079983869	0.11009764
BP1026B_I1253	deoxygenase	3639626	5830454	5330149	5339	4531797	4373798	4254983	4747	0.28830036	0.313962701	0.899117812	-0.169553498
BP1026B_I1254	hypothetical protein	75077	38300	46361	179	83344	85728	94836	296	0.865530748	0.876444327	1.653631285	0.732675588
BP1026B_I1255	shikimate transferase	22943	16073	12026	46	20650	23704	25740	46	7.22E-04	2.30E-04	1.17913043	0.231255466
BP1026B_I1256	hypothetical protein	17653	26373	25372	26	16878	16851	15740	18	7.18E-19	9.91E-18	0.692307692	-0.530514717
BP1026B_I1257	hypothetical protein	6397	6461	5674	22	4270	5100	5758	18	1.97E-10	8.89E-10	0.818181818	-0.289506617
BP1026B_I1258	peptide synthetase NRPS-4-3	56367	55779	53540	30	40649	38321	36543	21	5.49E-29	1.48E-27	0.7	-0.514573173
BP1026B_I1259	luciferase-like monooxygenase	14520	11692	12627	14	13301	13416	10956	14	7.07E-08	1.80E-07	1	0
BP1026B_I1260	L-aminocyclopropane-1-carboxylate deaminase	29258	9402	12353	15	21832	24443	30449	24	0.10343181	0.119076799	1.6	0.678071905
BP1026B_I1261	hypothetical protein	71189	69529	73495	54	68313	68964	77570	54	1.51E-07	3.67E-07	0.75	-0.407425455
BP1026B_I1262	hypothetical protein	135787	67988	896065	20	116151	123414	128414	37	7.93E-05	0.000136746	1.333333333	0.415037499
BP1026B_I1263	nonribosomal peptide synthetase	71793	4026	53740	26	78824	85575	102452	36	0.047762696	0.057646537	1.384611535	0.469485283
BP1026B_I1264	Syr-like protein	126646	90625	103068	100	115429	123600	124422	114	8.82E-07	1.93E-06	1.1	0.189033824
BP1026B_I1265	polyketide synthase peptide synthetase fusion protein	460379	327538	364380	40	423062	437087	455452	46	1.53E-07	3.71E-07	1.15	0.20163861
BP1026B_I1266	hypothetical protein	445854	493547	491910	682	419490	421793	413829	598	1.90E-16	1.37E-15	0.876832845	-0.189626255
BP1026B_I1267	hypothetical protein	792122	1368596	1231480	4959	883327	878377	868065	3844	0.91790753	0.924995619	0.715756282	-0.367440889
BP1026B_I1268	predicted RNA	211713	35806	313983	1912	263900	227924	209811	1516	1.54E-13	7.86E-13	0.792882757	-0.334817277
BP1026B_I1269	hypothetical protein	1792	3278	3090	24	1978	21416	1416	13	2.95E-20	3.36E-19	0.625	-0.678071905
BP1026B_I1270	GntR family transcriptional regulator	2295	2974	2201	9	3694	2555	2145	9	2.16E-06	4.47E-06	0.75	-0.407425455
BP1026B_I1272	carboxymuconalactone decarboxylase family protein	14987	6740	7743	6	13396	14589	16789	10	0.215382477	0.238240479	1.666666667	0.736965594
BP1026B_I1272	carboxymuconalactone decarboxylase family protein	13899	10339	11042	26	12311	13321	13424	29	3.80E-05	6.69E-05	1.115384615	0.157541277
BP1026B_I1271	cupin domain-containing protein	16098	7881	10693	25	15887	16385	19118	38	0.126735635	0.144183076	1.52	0.604071324
BP1026B_I1273	entericidin EcnAB	95037	60024	71105	558	88493	89633	74907	624	2.12E-05	3.88E-05	1.11827957	0.161280997
BP1026B_I1274	aspartate carbamoyltransferase	68880	60260	60731	49	61465	62715	59529	47	2.20E-09	6.82E-09	0.959183673	-0.060120992
BP1026B_I1275	outer membrane ferric siderophore receptor	13794	16705	17195									

BP1026b	II1454	dihydroneopterin aldolase	778	361	128	0	735	985	936	1	0.001482303	0.002154826	#DIV/0!	#DIV/0!
BP1026b	II1455	sarcosine oxidase gamma subunit	1111	748	645	1	1324	1093	1328	1	0.841108635	0.853231497	1	0
BP1026b	II1456	sarcosine oxidase alpha subunit	6522	4731	5930	1	9007	8284	8251	2	0.118073698	0.134996627	2	-1
BP1026b	II1457	sarcosine oxidase subunit delta	9587	6828	856	1	10022	9122	910	3	0.031903123	0.03943974	1.5	0.584962501
BP1026b	II1458	sarcosine oxidase, beta subunit	1939	3233	2760	2	3354	2958	2946	2	0.002179262	0.003097548	0	0
BP1026b	II1459	L-serine ammonia-lyase	2791	2336	3245	1	2280	2725	2489	1	9.98E-09	2.84E-08	1	0
BP1026b	II1460	AraC/XyIS family transcriptional regulator	14490	5791	7934	7	11489	14736	14843	11	0.06265087	0.122159021	1.571428571	0.652076697
BP1026b	II1461	hypothetical protein	19791	26433	22823	91	22579	19977	18404	80	5.14E-11	1.94E-10	0.879120879	-0.185866545
BP1026b	II1462	hypothetical protein	32823	29468	34708	45	30020	30319	28386	41	1.85E-10	6.47E-10	0.911111111	-0.134301092
BP1026b	II1463	glutathione S-transferase	32473	40248	38843	47	32582	32636	31449	41	3.91E-13	1.89E-12	0.872340426	-0.197036847
BP1026b	II1465	hypothetical protein	22	4804	4137	7	2798	2705	2456	4	7.02E-21	8.55E-20	0.571428571	-0.807354922
BP1026b	II1464	hypothetical protein	22	0	28	0	53	68	88	0	2.97E-09	9.10E-09	#DIV/0!	#DIV/0!
BP1026b	II1466	cytochrome d ubiquinol oxidase, subunit II	1233	869	902	0	1030	1292	1455	1	0.190228962	0.211613252	#DIV/0!	#DIV/0!
BP1026b	II1467	ubiquinol oxidase subunit I, cyanide insensitive	1714	1456	1720	1	2210	2071	1717	1	0.015174035	0.019525504	1	0
BP1026b	II1468	hypothetical protein	1030	729	813	2	585	690	917	1	6.56E-06	1.28E-05	0.5	-1
BP1026b	II1469	MgtC family membrane protein	951	548	961	1	726	932	663	1	3.05E-04	4.82E-04	1	0
BP1026b	II1470	hypothetical protein	34	49	0	0	88	0	73	0	0.023496133	0.031271308	#DIV/0!	#DIV/0!
BP1026b	II1472	phospholipase D	1144	1215	1177	0	1644	1568	1363	0	0.070216386	0.0808205	#DIV/0!	#DIV/0!
BP1026b	II1471	endonuclease/exonuclease/phosphatase family protein	1212	340	858	0	1280	1085	1480	1	0.465533509	0.492834528	#DIV/0!	#DIV/0!
BP1026b	II1473	pyruvate-2-oxoglutarate dehydrogenase complex, dehydrogenase (E1)	918	143	532	1	791	876	1321	2	0.026527377	0.033134096	2	1
BP1026b	II1474	rotamase	8035	16506	12971	17	11462	9813	10592	14	7.26E-12	3.05E-11	0.823529412	-0.280107919
BP1026b	II1475	hypothetical protein	8673	9821	9683	7	8268	8813	8777	6	3.56E-09	1.08E-08	0.877142857	-0.222392421
BP1026b	II1476	hypothetical protein	291	277	356	2	251	149	239	1	3.46E-05	6.12E-05	0.5	-1
BP1026b	II1477	ATP/GTP binding protein	14186	25698	22900	26	16472	14863	14863	20	3.99E-15	2.46E-14	0.769230769	-0.378511623
BP1026b	II1478	hypothetical protein	12434	22591	19155	5	17454	16814	16814	6	4.41E-08	1.69E-07	0.75	-0.415037499
BP1026b	II1479	hypothetical protein	1695	3084	3052	5	2695	2506	1990	4	3.76E-08	9.91E-08	0.8	-0.321928095
BP1026b	II1480	hypothetical protein	18616	28438	26465	13	35431	34182	27075	17	0.002461878	0.003473245	1.307692308	-0.387023123
BP1026b	II1481	hypothetical protein	4951	5190	4300	3	3961	4773	4883	3	1.06E-06	2.30E-06	1	0
BP1026b	II1482	Ysc/Hrc family type III secretion outer membrane protein	5408	7548	6634	3	5692	6170	5344	3	6.07E-09	1.50E-08	1	0
BP1026b	II1483	hypothetical protein	3367	3428	3709	2	2594	2621	3424	1	3.64E-11	1.40E-10	0.5	-1
BP1026b	II1484	type III secretion protein SpaR/YscI/HrcT	289	631	408	0	534	320	333	0	0.001346072	0.001966829	#DIV/0!	#DIV/0!
BP1026b	II1485	type III secretion protein HrpB7	231	627	365	0	241	174	221	0	0.27000182	0.29500938	#DIV/0!	#DIV/0!
BP1026b	II1486	type III secretion system ATPase	545	1017	722	0	427	606	670	0	5.33E-08	1.38E-07	#DIV/0!	#DIV/0!
BP1026b	II1487	type III secretion system protein HrpB	1305	1382	1086	1	1073	1253	957	1	2.08E-06	4.31E-06	1	0
BP1026b	II1488	type III secretion protein HrpB4	566	1059	536	2	511	618	258	1	3.96E-11	1.52E-10	0.5	-1
BP1026b	II1489	lipoprotein transmembrane protein	1987	2237	2599	2	1818	1748	1880	2	1.37E-11	5.57E-11	1	0
BP1026b	II1490	type III secretion protein HrpB2	260	467	472	1	344	506	257	0	0.005785897	0.0078177	0	#NUM!
BP1026b	II1491	type III secretion protein HrpB1/HrpK	794	887	940	1	960	990	883	1	0.001499217	0.00217393	1	0
BP1026b	II1492	type III secretion system protein HrcU	6943	9942	10341	8	7297	6979	6494	6	4.99E-14	2.69E-13	0.75	-0.415037499
BP1026b	II1493	type III secretion protein	2723	4313	4625	1	3874	3518	3366	1	2.55E-07	6.02E-07	1	0
BP1026b	II1494	type III secretion protein HrpA	444	217	310	1	353	305	328	1	0.08802502	0.101995695	1	0
BP1026b	II1495	Type III secretion inner membrane protein SctQ	8311	11946	9592	7	12057	10253	10334	8	2.02E-05	3.69E-05	1.142857143	0.192645078
BP1026b	II1496	type III secretion system protein	6308	9286	7404	10	8293	7105	5131	9	1.77E-09	5.53E-09	0.9	-0.152003093
BP1026b	II1497	type III secretion inner membrane protein SctS	628	608	980	2	554	596	443	2	1.34E-08	3.75E-08	1	0
BP1026b	II1498	hypothetical protein	995	1337	1905	2	991	1090	659	1	2.42E-15	1.53E-14	0.5	-1
BP1026b	II1499	secretion-associated protein	7140	6681	6788	6	7868	6171	6942	6	1.59E-04	6.66E-04	0.8	0.321928095
BP1026b	II1500	hypothetical protein	825	736	504	2	516	601	781	2	3.12E-04	4.92E-04	1	0
BP1026b	II1501	hypothetical protein	22329	39684	38611	116	29942	26803	28720	98	9.73E-13	4.52E-12	0.844827586	-0.243271151
BP1026b	II1502	hypothetical protein	1993	3540	2663	5	2701	2402	2130	5	3.11E-09	9.48E-09	1	0
BP1026b	II1503	hypothetical protein	4616	6867	6186	5	5616	5080	4469	4	4.19E-09	1.25E-08	0.8	-0.321928095
BP1026b	II1504	cupin domain-containing protein	13286	20732	21430	38	16227	16452	13774	32	5.03E-12	2.15E-11	0.842105263	-0.247927513
BP1026b	II1505	HAD-superfamily hydrolase	16281	6309	7236	16	17489	22065	26320	35	0.052597046	0.063140647	2.1875	1.129283017
BP1026b	II1506	GntR family transcriptional regulator	9236	9781	5142	2	6238	5966	29923	38	6.44E-13	2.49E-04	5.428571429	2.440572591
BP1026b	II1507	6-phosphogluconate dehydrogenase	7957	6217	6857	7	14079	14219	12039	15	0.29240766	0.318116369	2.142857143	1.099535674
BP1026b	II1508	type III effector Hop protein	11364	6987	6953	6	11566	12483	15267	9	0.300000283	0.325515637	1.5	0.584962501
BP1026b	II1509	aldolase	4727	1769	2508	4	4951	5809	6334	8	0.371191782	0.398550793	2	1
BP1026b	II1510	major facilitator family transporter	5126	7012	5988	4	5306	5686	4580	3	3.48E-09	1.06E-08	0.75	-0.415037499
BP1026b	II1511	hydroxyprolyl isomerase	4458	5262	5495	6	4104	3689	4134	5	3.33E-11	1.29E-10	0.833333333	-0.263034406
BP1026b	II1512	NAD-dependent epimerase/dehydratase family protein	4640	2811	4102	3	4365	4286	4466	4	0.001891946	0.001596395	1.333333333	-0.415037499
BP1026b	II1513	asparaginyl beta-hydroxylase	24806	12119	15179	23	27073	23485	23485	3	0.261367253	0.2391588	1.666666667	0.736965504
BP1026b	II1514	predicted RNA	36557	39063	36089	721	36625	33195	32688	698	1.93E-09	4.00E-09	0.968099891	-0.406772223
BP1026b	II1514	hypothetical protein	94807	101596	98606	109	71743	75522	79416	83	1.10E-17	9.14E-17	0.761466986	-0.393144893
BP1026b	II1515	glycine betaine/L-proline ABC transporter, periplasmic glycine	6631	9075	8578	8	6803	6783	5408	6	3.05E-13	1.49E-12	0.75	-0.415037499
BP1026b	II1516	betaine/L-proline-binding protein	836	466	679	0	542	836	1030	0	0.125355054	0.142742057	#DIV/0!	#DIV/0!
BP1026b	II1517	glycine betaine/L-proline ABC transporter permease	1997	2063	2001	2	2506	2373	2069	2	8.59E-04	0.01287267	1	0
BP1026b	II1518	glycine betaine/L-proline ABC transporter ATP-binding protein	2272	3233	3642	2	3231	3232	4289	3	0.005577891	0.007525942	1.5	0.584962501
BP1026b	II1519	NADPH-dependent FMN reductase family protein	1322	1105	1108	1	1408	1382	1108	1	0.002807125	0.003934623	1	0
BP1026b	II1520	hypothetical protein	1551	2317	1744	8	2242	2452	1921	10	0.003065272	0.004281129	1.25	0.321928095
BP1026b	II1521	hypothetical protein	41519	50053	47814	51	30482	28932	30879	33	1.26E-28	3.25E-27	0.647058824	-0.628031223
BP1026b	II1522	arsenical resistance transcriptional regulator	6947	10624	10585	27	7989	7963	7239	23	6.36E-13	3.01E-12	0.851851852	-0.231325546
BP1026b	II1523	glyoxalase	9921	13618	11813	24	11854	10323	9697	22	4.87E-10	1.63E-09	0.916666667	-0.125530882
BP1026b	II1524	arsenate reductase	8915	4465	5703	12	7742	7842	7909	15	0.001454252	0.002116013	1.25	0.321928095
BP1026b	II1525	sodium bile acid symporter family protein	23319	23106	23832	21	20748	22121	21108	19	3.72E-10	1.26E-09	0.904761905	-0.13458909
BP1026b	II1527	thiazole protein ser motif family	3353	4994	5505	5	4062	4314	323	82	2.98E-08	7.9E-08	0.8	-0.321928095
BP1026b	II1526	membrane-anchored cell surface protein	38532	46424	42631	7	40584	37823	37891	6	3.76E-13	1.82E-12	0.871428571	-0.22392421
BP1026b	II1528	lipoprotein	497	97	360	0	446	704	467	1	0.095537892	0.110374282	#DIV/0!	#DIV/0!
BP1026b	II1529	hypothetical protein	23995	1723	21319	11	25184	24532	25374	13	2.99E-04	4.73E-04	1.181818182	-0.2410081
BP1026b	II1530	membrane-anchored cell surface protein	40129	47827	46053	9	29617	32281	33491	6	3.44E-23	5.40E-22	0.666666667	-0.584962501
BP1026b	II1531	hypothetical protein	103849	109077	99704	90	77591	80182	76468	67	3.81E-19	3.78E-18	0.744444444	-0.425763906
BP1026b	II1532	hypothetical protein	121189	149714	141651	119	109166	105931	91529	88	9.63E-23	1.43E-21	0.739459798</	

predicted RNA	-	19369	5216	11505	802	18233	19861	27417	1455	0.927079344	0.933187371	1.814214464	0.859345011
BP1026b.II1578	hypothetical protein	820278	765420	771843	1781	846545	820925	743536	1822	0.271629483	0.296581328	1.023020775	0.032835443
BP1026b.II1580	anaerobically induced outer membrane protein	126031	151952	138875	88	1047397	1106932	1136744	701	2.17E-240	3.40E-237	7.965909091	0.2993839015
BP1026b.II1581	hypothetical protein	2738	1426	1603	2	7244	8425	10540	10	4.76E-34	2.03E-32	5	2.321928095
BP1026b.II1579	SCO1/ScnF family protein	1688	2122	1711	2	1160	4883	4209	8	1.79E-07	4.31E-07	1	2
BP1026b.II1582	N-acetylmuramoyl-L-alanine amidase domain-containing protein	1757	2182	1856	1	1778	2031	2796	2	9.18E-04	0.00136878	2	1
BP1026b.II1583	hypothetical protein	2586	2572	2655	1	3085	3082	3688	2	0.02247679	0.028317501	2	1
BP1026b.II1584	intracellular motility protein A	9535	8523	8960	6	11633	10471	11461	7	0.002167476	0.003081495	1.166666667	0.222392421
BP1026b.II1585	hypothetical protein	235	226	328	0	601	221	428	1	0.232697286	0.256532172	#DIV/0!	#DIV/0!
BP1026b.II1586	type VI secretion system	10797	7376	8555	4	9881	12742	11169	5	0.003677918	0.005091377	1.25	0.331928095
BP1026b.II1587	DNA-binding response regulator	11639	8995	9963	14	11819	13303	10786	16	2.77E-05	2.31E-04	1.142857143	0.192645078
BP1026b.II1589	sensor histidine kinase	6401	2971	2854	2	4886	6188	5786	3	0.042119333	0.051200369	1	0.584962501
BP1026b.II1590	type VI secretion system	4210	4792	3596	8	5562	5111	3842	9	0.001034187	0.001529669	1.125	0.169925001
BP1026b.II1588	type VI secretion system	23321	30385	30126	18	28448	25908	26516	17	1.19E-08	3.34E-08	0.944444444	-0.08246216
BP1026b.II1591	type VI secretion system	5358	8937	8529	14	12239	11893	9341	21	0.119177946	0.136153684	1.5	0.584962501
BP1026b.II1592	type VI secretion system	704	372	468	1	622	375	560	1	0.010445187	0.013705206	1	0
BP1026b.II1594	type VI secretion system	1365	588	549	0	960	1367	1177	0	0.751747648	0.768933257	#DIV/0!	#DIV/0!
BP1026b.II1593	type VI secretion system	735	398	724	0	539	868	1272	0	0.106387284	0.12227055	#DIV/0!	#DIV/0!
BP1026b.II1595	type VI secretion system	4638	2814	3215	1	4207	4466	5969	1	0.074881752	0.091513346	0.75	-0.415037499
BP1026b.II1596	type VI secretion system	2214	1039	2129	0	2793	2009	1974	0	0.019197936	0.024412479	#DIV/0!	#DIV/0!
BP1026b.II1597	type VI secretion system	686	316	182	0	632	643	733	0	0.143364125	0.162129063	#DIV/0!	#DIV/0!
BP1026b.II1598	type VI secretion system	87	495	53	0	316	313	221	0	0.762938658	0.779234918	#DIV/0!	#DIV/0!
BP1026b.II1599	type VI secretion system	0	0	0	0	0	28	0	0	1	1	#DIV/0!	#DIV/0!
BP1026b.II1600	type VI secretion system	510	315	369	1	453	457	442	1	0.142753535	0.161467703	1	0
BP1026b.II1602	type VI secretion system	285	145	135	0	422	422	589	0	2.79E-06	2.49E-06	#DIV/0!	#DIV/0!
BP1026b.II1601	type VI secretion system	810	380	195	0	628749477	0.651527994	0	0.028749477	0.051527994	#DIV/0!	#DIV/0!	
BP1026b.II1603	type VI secretion system	460	243	452	0	646	262	220	0	0.019560078	0.024827625	#DIV/0!	#DIV/0!
BP1026b.II1604	type VI secretion system	3368	2036	2805	0	3872	3335	4010	0	0.12548249	0.142835239	#DIV/0!	#DIV/0!
BP1026b.II1605	hypothetical protein	5590	7505	7002	5	5767	5484	5904	4	9.69E-10	3.14E-09	0.8	-0.321928095
BP1026b.II1606	hypothetical protein	899	1543	1438	4	864	1176	1041	3	1.12E-08	3.95E-08	0.75	-0.415037499
BP1026b.II1608	hypothetical protein	3640	5085	5523	10	3921	3357	2859	7	2.75E-15	1.73E-14	0.7	-0.514573173
BP1026b.II1607	GTP cyclohydrolase I	4704	6787	7034	9	4912	4193	3710	6	3.65E-15	2.26E-14	0.666666667	-0.584962501
BP1026b.II1609	hypothetical protein	275	253	719	4	569	657	605	1	2.93E-07	6.89E-07	0.75	-0.415037499
BP1026b.II1610	hypothetical protein	29252	53936	46774	40	33135	31589	32411	30	1.70E-20	9.97E-19	0.75	-0.415037499
BP1026b.II1611	hypothetical protein	2938	5442	5891	10	2911	3016	2678	6	2.83E-25	5.39E-24	0.6	-0.736965594
BP1026b.II1612	transposase	2723	4670	3829	12	2701	2766	2781	9	1.62E-15	1.05E-14	0.75	-0.415037499
BP1026b.II1615	AraC family transcriptional regulator	5347	4009	5785	5	7069	7071	7791	7	0.063077285	0.074804263	1.4	0.485426827
BP1026b.II1616	hypothetical protein	26230	23488	24302	55	22456	24453	23397	52	5.92E-09	1.74E-08	0.945454545	-0.080919995
BP1026b.II1617	DNA-binding response regulator	5203	3578	4044	6	6310	5163	7393	9	0.101872399	0.117432592	1.5	0.584962501
BP1026b.II1618	chaperone	2303	2808	2141	5	3907	4249	1824	4	3.94E-10	1.51E-10	0.8	-0.321928095
BP1026b.II1619	BopA protein	4740	6918	6239	3	5982	6134	6101	3	5.18E-06	1.02E-05	#DIV/0!	#DIV/0!
BP1026b.II1620	hypothetical protein	102	0	38	0	75	117	0	0.868646212	0.879314782	#DIV/0!	#DIV/0!	
BP1026b.II1621	type III secretion target BopE	25948	27598	25676	33	28469	28761	30012	36	7.38E-06	1.43E-05	1.090909091	0.125530882
BP1026b.II1622	BapC protein	5029	2916	3475	6	4811	5060	5618	9	0.045424943	0.055015824	1.5	0.584962501
BP1026b.II1623	acyl carrier protein	1291	1490	1581	5	2168	1333	1859	6	0.022184825	0.027966541	1.2	0.263034406
BP1026b.II1624	hypothetical protein	7562	5831	4949	2	9199	7893	9176	3	0.065008084	0.076909051	1.5	0.584962501
BP1026b.II1625	type III effector protein IpaD/SipD/SspD	10713	22107	21071	21	20687	20688	20707	21	1.03E-07	2.56E-07	0	0
BP1026b.II1626	HNS-like transcription regulator protein	4386	2368	2315	10	3693	4739	5784	16	0.590661625	0.614602063	1.6	0.678071905
BP1026b.II1627	cell invasion protein	35907	41198	41195	31	51763	50174	55040	41	0.003912204	0.005387128	1.322580645	0.403356694
BP1026b.II1628	BipB protein	16573	22307	19463	10	21373	22976	22684	11	7.77E-05	1.31E-04	1.1	0.137503524
BP1026b.II1629	type III secretion low calcium response chaperone LcrH/SycD	5472	6719	6470	12	4927	5368	4922	9	1.71E-10	6.02E-10	0.75	-0.415037499
BP1026b.II1630	surface presentation of antigens protein SpaS	2765	2562	3019	2	2060	2770	2649	2	1.07E-08	3.02E-08	1	0
BP1026b.II1631	type III secretion protein SpaR/VscI/HrcI	1917	1446	1898	2	2196	1577	2029	2	5.75E-04	8.80E-04	1	0
BP1026b.II1632	type III secretion system protein BsaX	7813	1263	1265	5	1574	1574	1269	5	9.90E-04	1.53E-04	1	0
BP1026b.II1633	surface presentation of antigens protein SpaP	3732	5618	5409	7	5478	4816	4148	7	3.85E-06	7.70E-06	1	0
BP1026b.II1634	type III secretion system apparatus protein YscQ/HrcQ	1054	510	362	0	1047	688	1232	1	0.644580481	0.666939566	#DIV/0!	#DIV/0!
BP1026b.II1635	BsaI protein	356	455	272	0	1101	768	1264	0	8.78E-12	3.65E-11	#DIV/0!	#DIV/0!
BP1026b.II1636	surface presentation of antigens protein	300	204	0	0	253	262	349	0	0.064274731	0.076037188	#DIV/0!	#DIV/0!
BP1026b.II1637	ATP synthase SpaL	6163	3932	4730	3	7738	7871	8950	6	0.425914443	0.453266747	1	0
BP1026b.II1638	surface presentation of antigens protein	4780	7574	5956	14	5844	5568	5388	13	7.29E-08	1.85E-07	0.928571429	-0.106915204
BP1026b.II1639	type III secretion system protein BsaQ	8230	1313	8769	4	9144	7869	7869	4	1.59E-06	3.94E-06	1	0
BP1026b.II1640	type III secretion system protein	4350	4253	4441	4	4761	4056	3668	3	2.45E-06	5.03E-06	1	0
BP1026b.II1641	YscC/HrcC family type III secretion outer membrane protein	10666	10236	11213	5	12224	11219	9917	5	1.68E-06	3.52E-06	1	0
BP1026b.II1642	type III secretion system transcriptional regulator BsaN	3570	5575	5034	6	4510	4428	4774	6	3.05E-06	6.18E-06	1	0
BP1026b.II1643	type III secretion system protein PrgH/EprH	4690	5413	4869	3	6034	5248	5485	4	2.67E-04	4.24E-04	1.333333333	0.415037499
BP1026b.II1644	MxiI protein	9460	16007	14627	49	15963	15691	14838	57	3.10E-04	4.90E-04	1.163265000	0.21818017
BP1026b.II1645	type III secretion system protein	1010	1155	823	3	1460	1200	789	4	0.04774152	0.057643192	1.333333333	0.415037499
BP1026b.II1646	type III secretion system protein	4594	4594	5111	3	5150	4742	4781	3	5.33E-05	1.31E-04	21	0
BP1026b.II1647	type III secretion apparatus protein OrgA/MxiK	3203	1784	2506	4	3293	3714	3160	5	0.104256601	0.120004291	1.25	0.321928095
BP1026b.II1648	type III secretion system protein	8404	3639	5420	7	8020	9210	9155	11	0.161978926	0.18167162	0.714285714	0.652076697
BP1026b.II1649	hypothetical protein	3293	2184	2363	13	2920	3526	3367	16	0.018098256	0.023098507	1.230769231	0.299560282
BP1026b.II1650	hypothetical protein	17006	20551	20773	39	17552	17522	17403	35	5.98E-10	1.98E-09	0.897435897	-0.156119202
BP1026b.II1651	hypothetical protein	15462	19747	21627	20	11758	11860	10282	12	2.03E-30	6.36E-29	0.6	-0.736965594
BP1026b.II1652	hypothetical protein	16712	20908	18665	38	11017	12172	9595	22	2.81E-32	1.05E-30	0.578947368	-0.788495895
BP1026b.II1653	hypothetical protein	9645	11333	12204	17	11452	9810	12520	18	6.12E-07	1.36E-06	0.058825786	0.08246216
BP1026b.II1654	thermolytic metalloproteinase	47421	57202	54476	40	46782	46462	47812	27	4.47E-15	1.08E-14	0.8	-0.152080903
BP1026b.II1655	MarR family transcriptional regulator	49637	50838	48133	77	60339	62613	57489	94	8.48E-04	0.00120703	1.220779221	0.087802311
BP1026b.II1656	glyoxalase	8981	11189	9080	21	9948	8376	8530	19	3.89E-09	1.17E-08	0.904761905	-0.144389909
BP1026b.II1657	alpha-ketoglutarate permease	2756	2771	2226	1	2904	2399	2936	2	5.95E-05	1.02E-04	2	1
BP1026b.II1659	LysR family transcriptional regulator	18356	16352	17456	19	19390	20983	18816	22	4.87E-05	8.48E-05	1.157894737	0.211504015
BP1026b.II1660	L(+)-mandelate dehydrogenase	23238	14499	13421	13	19784	19979	25869	17	0.002830059	0.003965881	1.307692308	0.387023123
BP1026b.II1661	serine-type carboxypeptidase family protein	521201	628132	589271	348	488410	489070	491750	294	2.87E-18	2.59E-17	0.844827586	-0.24327151

BP1026b	II1707	Integral membrane protein	64408	47166	48935	49	81818	82132	86243	77	0.464902195	0.492249383	1.571428571	0.652076697
BP1026b	II1708	type II/IV secretion system protein	102748	66781	72815	50	105567	113981	120390	70	0.011823166	0.015406764	1.4	0.485426827
BP1026b	II1709	hypothetical protein	1608	1071	894	2	1678	2248	1626	3	0.917494497	0.924728162	1.5	0.584962501
BP1026b	II1710	type IV pilus biosynthesis protein	68525	37361	48779	39	74731	79777	82320	61	0.49898947	0.447244857	1.564102564	0.64535119
BP1026b	II1711	PilN	104264	67024	78314	47	113147	12170	115557	64	0.005179302	0.007042141	1.361702128	0.445411148
BP1026b	II1712	PilL domain protein	24466	12882	14680	29	17019	17103	17434	29	1.94E-07	1.64E-07	1	0
BP1026b	II1713	twitching motility protein	345540	402727	387449	341	287264	289436	285315	259	3.60E-16	2.51E-15	0.759530792	0.396819641
BP1026b	II1714	type III secretion system family protein	17680	15587	11298	8	15836	17453	18130	9	1.90E-04	3.06E-04	1.125	0.169925001
BP1026b	II1715	DNA-binding response regulator	27213	14117	15720	25	21784	24429	28931	34	0.00619217	0.008343246	1.36	0.443606651
BP1026b	II1716	sensor histidine kinase	35446	23215	21234	24	25902	32440	38047	29	1.42E-04	2.33E-04	1.208333333	0.273018494
BP1026b	II1717	hypothetical protein	3108	5082	3935	1	321	3246	2910	5	5.32E-15	1.59E-14	0.714285714	-0.485426827
BP1026b	II1718	hypothetical protein	755	410	407	1	321	652	636	1	0.013365893	0.017312645	1	0
BP1026b	II1719	hypothetical protein	1151	678	726	1	1494	732	1399	1	0.833124662	0.84622878	1	0
BP1026b	II1720	hypothetical protein	271	277	291	0	239	247	284	0	0.040487022	0.049369419	#DIV/0!	#DIV/0!
BP1026b	II1721	AraC family transcription regulator	1167	424	632	0	1339	1230	1431	0	0.079229646	0.092342691	#DIV/0!	#DIV/0!
BP1026b	II1722	hypothetical protein	4060	4444	4349	9	3329	3169	2529	6	5.84E-17	4.50E-16	0.666666667	-0.584962501
BP1026b	II1723	hypothetical protein	62852	105826	97283	484	76346	75196	72283	407	1.61E-13	8.20E-13	0.840090909	-0.249978253
BP1026b	II1724	type III secretion protein	38	151	214	0	180	225	108	0	0.35822453	0.35209632	#DIV/0!	#DIV/0!
BP1026b	II1725	secretion-associated protein	991	547	691	0	719	1593	1698	1	0.081605958	0.09408971	#DIV/0!	#DIV/0!
BP1026b	II1726	type III secretion protein	355	232	135	0	167	262	477	0	0.990533895	0.917590646	#DIV/0!	#DIV/0!
BP1026b	II1727	type III secretion inner membrane protein SctS	949	791	593	2	1006	515	584	2	8.37E-05	1.41E-04	1	0
BP1026b	II1728	type III secretion system protein	1712	1791	2083	2	1938	1611	1788	2	1.98E-06	4.10E-06	1	0
BP1026b	II1729	type III secretion inner membrane protein SctQ	2775	2832	1915	1	2177	2197	3082	2	6.18E-05	1.06E-04	2	1
BP1026b	II1730	type III secretion inner membrane protein HspA	752	265	684	0	650	682	529	1	0.038491865	0.047055628	#DIV/0!	#DIV/0!
BP1026b	II1731	type III secretion inner membrane protein SctV	7699	7011	7591	3	6913	7605	6459	3	5.12E-09	1.75E-08	1	0
BP1026b	II1732	type III secretion system protein HspB7	1709	1580	1774	1	1987	1633	2086	12	1.15E-13	0.90E-05	0.857142857	0.22392421
BP1026b	II1733	type III secretion protein HspB1/HspK	267	248	180	0	333	230	507	0	0.297247162	0.322845781	#DIV/0!	#DIV/0!
BP1026b	II1734	type III secretion protein HspB2	542	886	504	1	244	379	363	1	7.74E-16	5.19E-15	0	#NUM!
BP1026b	II1735	lipoprotein transmembrane protein	1034	743	760	0	734	1326	814	1	0.035134507	0.043128072	#DIV/0!	#DIV/0!
BP1026b	II1736	type III secretion protein HspB4	34	0	0	0	117	32	73	0	8.96E-20	9.71E-19	#DIV/0!	#DIV/0!
BP1026b	II1738	type III secretion system protein HspB	275	48	0	0	188	460	221	0	8.36E-08	2.11E-07	#DIV/0!	#DIV/0!
BP1026b	II1737	type III secretion system ATPase	3498	2117	1856	1	2488	3517	3467	2	0.021759514	0.026994815	#DIV/0!	2
BP1026b	II1740	type III secretion system protein HspB7	52	151	8	0	207	149	40	0	0.027149	0.030384	#DIV/0!	#DIV/0!
BP1026b	II1739	Flagellar biosynthesis protein FliR	1972	2121	2017	2	2012	2501	1728	2	1.25E-05	2.34E-05	1	0
BP1026b	II1741	hypothetical protein	1973	1393	1435	0	1408	1593	2315	1	0.001247177	0.001825734	#DIV/0!	#DIV/0!
BP1026b	II1742	SyrP-like protein	5207	3983	3399	4	4362	4951	4673	4	4.03E-04	6.27E-04	1	0
BP1026b	II1743	hypothetical protein	126907	133054	129951	7	116952	111926	113519	6	1.84E-15	1.19E-14	0.857142857	-0.222392421
BP1026b	II1744	hypothetical protein	146305	176269	167041	12	127384	130341	127661	9	9.32E-24	1.56E-22	0.75	-0.415037499
BP1026b	II1745	non-ribosomal peptide synthetase	104159	134076	121256	12	94160	99578	92145	9	2.17E-17	1.75E-16	0.75	-0.415037499
BP1026b	II1746	diaminopyruvate-2-oxoglutarate aminotransferase	42813	37441	40148	13	36807	33545	33520	13	1.54E-13	3.90E-03	0.857142857	0.22392421
BP1026b	II1747	hypothetical protein	7525	9444	7507	15	4946	5032	5195	10	2.35E-18	2.13E-17	0.666666667	-0.584962501
BP1026b	II1748	hypothetical protein	13078	21933	18260	81	8512	10527	9567	43	1.11E-38	6.26E-37	0.530864198	-0.913585248
BP1026b	II1749	hypothetical protein	1117	507	470	3	483	971	800	3	0.015625478	0.020085777	1	0
BP1026b	II1750	pyruvate dehydrogenase	43836	38825	38018	23	37742	38243	38628	22	2.39E-11	9.41E-11	0.956521739	-0.064130337
BP1026b	II1751	acetyl-CoA hydrolase/transferase family protein	79428	107356	97462	71	81578	79696	70552	58	5.39E-15	3.26E-14	0.816901408	-0.291761624
BP1026b	II1752	MotC domain-containing protein	32947	50400	43128	79	31642	28326	32223	58	4.50E-21	5.61E-20	0.734177215	-0.445799753
BP1026b	II1753	diolate lyase subunit beta	11527	15201	10201	12	11467	12723	15258	49	3.14E-08	1.01E-08	0.616666667	-0.25530882
BP1026b	II1754	LysR family transcriptional regulator	26673	27884	25243	29	20027	22969	19485	22	1.98E-15	1.27E-14	0.758620699	-0.398549376
BP1026b	II1755	hypothetical protein	2255	996	1722	10	2119	2086	3245	15	0.496843857	0.523503771	1.5	0.584962501
BP1026b	II1756	LysR family transcriptional regulator	13218	8909	7840	10	9818	8831	9156	10	6.80E-09	1.97E-08	1	0
BP1026b	II1757	EmrB_QacA family drug resistance transporter	809	916	498	0	474	688	625	0	2.01E-06	4.16E-06	#DIV/0!	#DIV/0!
BP1026b	II1758	hypothetical protein	1659	1798	2128	4	1627	1604	1328	3	1.08E-09	3.49E-09	0.75	-0.415037499
BP1026b	II1759	sensor box sensor histidine kinase	4570	4993	5654	4	4741	5669	4726	4	5.93E-06	1.6E-05	0.75	-0.415037499
BP1026b	II1760	hypothetical protein	6124	4747	4747	4	6180	6519	6073	3	0.0041626	0.00732612	0.000232612	0.321928085
BP1026b	II1761	response regulator	7177	3553	4801	3	6423	6187	7187	4	0.005340352	0.007512262	1.333333333	0.415037499
BP1026b	II1762	hypothetical protein	137	206	225	3	239	98	73	0	3.01E-04	7.77E-04	#DIV/0!	#DIV/0!
BP1026b	II1763	lectin repeat-containing protein	4799	4417	4226	1	5077	4765	5082	2	3.15E-04	4.97E-04	2	1
BP1026b	II1764	hypothetical protein	336	563	585	1	415	390	534	0	9.05E-04	0.001350492	0	#NUM!
BP1026b	II1765	hypothetical protein	1372	1412	1558	2	1754	1705	1980	2	0.033615929	0.041385691	1	0
BP1026b	II1766	patatin-like phospholipase	7013	6450	6269	6	7512	6908	6329	6	9.06E-06	1.75E-05	1	0
BP1026b	II1767	4-hydroxybenzoate transporter	1069	689	699	1	1169	1130	1273	1	0.010995276	0.014337081	1	0
BP1026b	II1768	cytochrome P450	6185	8856	6611	3	8472	8173	7891	1	1.27E-04	2.09E-04	1	0
BP1026b	II1769	hypothetical protein	89	0	0	0	132	196	96	1	2.87E-23	4.54E-22	#DIV/0!	#DIV/0!
BP1026b	II1770	hypothetical protein	4939	3548	3550	3	3483	3774	3956	2	3.63E-07	8.40E-07	0.666666667	-0.584962501
BP1026b	II1771	beta-glucosidase	5715	4890	4741	2	5116	5465	5651	2	4.36E-05	7.63E-05	1	0
BP1026b	II1772	hypothetical protein	107295	127962	161428	299	127939	119915	116392	246	1.01E-19	1.09E-18	0.822742745	-0.281487169
BP1026b	II1773	glutaryl-tRNA(Gln) amidotransferase subunit A	7545	8341	8927	28	8915	8845	6960	28	3.40E-07	7.89E-07	1	0
BP1026b	II1774	hypothetical protein	65388	109092	109092	197	67619	53611	5588	15	1.52E-31	1.53E-30	0.634517267	-0.65636785
BP1026b	II1775	hypothetical protein	66785	59724	55879	17	33591	33769	59827	112	6.28E-32	2.22E-32	0.636363636	-0.652076697
BP1026b	II1776	selenocysteine-specific translation elongation factor	41599	26307	28111	16	35273	39454	39377	19	3.14E-05	5.60E-05	1.1875	0.247927513
BP1026b	II1777	selenocysteine synthase	41058	16066	22237	18	32046	36613	43531	25	0.010338161	0.013576152	1.388888889	0.473931188
BP1026b	II1778	formate dehydrogenase accessory protein FdhE	54897	68546	59233	62	63862	68729	68223	69	2.66E-05	4.79E-05	1.112903226	0.154328146
BP1026b	II1779	formate dehydrogenase subunit gamma	134113	160335	147207	234	154987	141432	121640	222	9.28E-14	4.84E-13	0.948717949	-0.075948853
BP1026b	II1780	formate dehydrogenase subunit beta	236101	226808	256604	262	264476	259023	244282	279	3.99E-05	7.01E-05	1.064858966	0.09069831
BP1026b	II1781	formate dehydrogenase subunit alpha	460485	529234	543557	218	461738	449666	419811	182	1.96E-19	2.05E-18	0.834862385	-0.390389683
BP1026b	II1782	formate dehydrogenase-O ₂ major subunit	188835	212154	221727	351	168259	15870	150017	268	9.40E-27	1.50E-26	0.763532764	-0.389238083
BP1026b	II1783	hypothetical protein	8754	9221	9619	18	6699	8906	7467	16	1.56E-09	4.90E-09	0.888888889	-0.169925001
BP1026b	II1784	hypothetical protein	24484	21382	21351	29	25647	23857	22294	30	8.78E-07	1.92E-06	1.034482759	0.0489096
BP1026b	II1785	cystine-binding periplasmic protein FliY	1267	400	800	0	1132	974	1149	1	0.416784371	0.444305191	#DIV/0!	#DIV/0!
BP1026b	II1786													

BP1026b	II1832	hypothetical protein	6914	6162	6634	14	5048	6077	7118	13	5.68E-08	1.47E-07	0.928571429	-0.106915204
BP1026b	II1833	glyoxalase	12084	18681	14207	38	11410	10747	9480	27	7.56E-20	8.24E-19	0.710526316	-0.493040011
BP1026b	II1834	AraC family transcriptional regulator	16485	11419	12633	13	17911	19134	19206	19	0.032353194	0.039094993	1.461538462	0.547887795
BP1026b	II1835	IpsE1 citrate synthase	984904	1490653	1347439	978	128859	1244883	1134534	938	0.55013597	0.582126	0.959106204	0.660246452
BP1026b	II1836	hypothetical protein	74241	65748	59985	244	91954	103935	103662	365	0.13438093	0.152491203	1.495901639	0.581015316
BP1026b	II1837	succinate dehydrogenase iron-sulfur subunit	341050	426840	417908	563	515917	502468	498214	720	5.52E-05	9.54E-05	1.278862233	0.354861984
BP1026b	II1838	succinate dehydrogenase flavoprotein subunit	713382	758044	768489	420	826600	860758	878230	481	0.102605726	0.118190928	1.145238095	0.195467566
BP1026b	II1839	succinate dehydrogenase, hydrophobic membrane anchor protein	144618	224469	206335	519	134293	131931	127913	356	4.48E-36	2.19E-34	0.685934489	0.543857297
BP1026b	II1840	succinate dehydrogenase cytochrome b subunit	223678	391488	362289	782	195322	191452	189892	460	4.67E-46	4.12E-44	0.588232494	-0.765534746
BP1026b	II1841	hypothetical protein	10375	14718	14366	63	12654	16148	13901	68	1.81E-05	3.33E-05	1.079365079	0.110182918
BP1026b	II1842	GntR family transcriptional regulator	57395	62141	62852	75	53732	58843	58957	71	3.30E-11	1.24E-10	0.946666667	-0.079071571
BP1026b	II1843	malate dehydrogenase	943387	1022777	1008447	1007	107390	1067876	985579	1059	0.246809136	0.270945045	1.05163857	0.072638906
BP1026b	II1844	lyase	22310	16599	16586	18	19536	20498	22268	20	3.16E-05	5.62E-05	1.111111111	0.152003093
BP1026b	II1845	hypothetical protein	116506	124278	118806	235	109593	105968	105944	210	9.95E-14	5.17E-13	0.893617021	-0.162271429
BP1026b	II1846	2-methylcitrate dehydratase	191748	169815	166825	124	199321	210020	219535	148	0.001665158	0.002408346	1.193548387	0.255257055
BP1026b	II1847	aconitate hydratase	1561335	1927356	1850298	654	2473795	2448200	2392965	897	0.026637397	0.033258253	1.371559633	0.455817349
BP1026b	II1848	hemagglutinin, homolog	60780	74591	72509	25	77002	74028	72812	27	5.77E-06	1.13E-05	1.08	0.111031312
BP1026b	II1849	hypothetical protein	2074	3969	3471	15	2650	3030	2902	13	3.12E-10	1.07E-09	0.866666667	-0.308450973
BP1026b	II1850	HydV family hemolysin activator protein	39872	55084	51984	29	36198	33346	31950	20	1.19E-26	2.62E-25	0.69655172	-0.5360529
BP1026b	II1851	transposase	42332	49876	45795	168	40761	41406	35088	143	1.92E-16	1.38E-15	0.851190476	-0.232446086
BP1026b	II1852	hypothetical protein	188025	280800	247687	380	208580	212177	185106	322	6.84E-15	4.09E-14	0.847368421	-0.23893873
BP1026b	II1853	cytochrome c family protein	1187792	1152440	1139998	556	1164295	1185452	1156179	560	0.471614652	0.499019287	1.007194245	-0.010341944
BP1026b	II1854	hypothetical protein	17076	8033	8808	30	14478	14628	17546	41	0.032239844	0.039797121	1.566666667	0.450661409
BP1026b	II1855	tyrosinase	12285	16754	16588	9	12748	13028	12245	7	1.99E-12	8.93E-12	0.777777778	-0.362570079
BP1026b	II1856	hypothetical protein	7943	6174	5257	10	10294	9793	11586	16	0.490680495	0.517793568	0.517793568	0.678071905
BP1026b	II1857	hypothetical protein	6234	7943	8530	14	4953	6173	6801	11	1.14E-12	3.84E-07	0.785714286	-0.479233063
BP1026b	II1858	hypothetical protein	38604	51010	44541	331	33679	30740	31354	236	4.75E-23	2.29E-22	0.712990937	-0.48804357
BP1026b	II1859	sedolisin	52576	60095	59002	32	73522	76443	72289	42	0.010789252	0.014124111	1.3125	0.032717423
BP1026b	II1860	polyamine ABC transporter permease	9581	8083	8262	10	8165	8482	7171	9	2.36E-09	7.29E-09	0.9	-0.152003093
BP1026b	II1861	spermidine/putrescine ABC transporter permease	5416	6262	5802	4	3783	3873	4552	3	4.70E-15	2.86E-14	0.75	-0.415037499
BP1026b	II1862	spermidine/putrescine ABC transporter periplasmic												
BP1026b	II1863	spermidine/putrescine-binding protein	17464	22923	21856	19	19322	18964	17263	17	1.83E-10	6.41E-10	0.894736842	-0.160464672
BP1026b	II1864	GntR family transcriptional regulator	17695	19557	20740	17	19159	18240	17780	17	1.55E-07	7.35E-07	1	0.10893437
BP1026b	II1865	lipase chaperone	39098	36792	37059	24	60304	64899	63858	41	8.20483967	0.834247431	1.708333333	0.772589504
BP1026b	II1866	lipase precursor	6458	5118	4474	5	5941	7932	8368	7	0.02690472	0.03365626	1.4	0.485426827
BP1026b	II1867	TonB-dependent copper receptor	15643	16950	16041	14	16980	17458	19976	16	3.63E-05	6.42E-05	1.142857143	0.192645078
BP1026b	II1868	hypothetical protein	103649	117991	111899	49	105818	102454	101061	45	1.02E-11	4.21E-11	0.918367347	-0.122856748
BP1026b	II1869	hypothetical protein	70887	22325	26673	100	42336	73687	89065	172	0.584525073	0.608621187	1.1	0.72
BP1026b	II1870	cytochrome b5L1	104975	153616	140789	247	111648	102610	91494	189	8.69E-21	1.04E-19	0.765182187	-0.386124807
BP1026b	II1871	integral membrane protein	130074	121260	127405	198	18953	187983	134348	284	0.05723196	0.066525287	1.035483333	0.503050683
BP1026b	II1872	peptidase	51565	40063	43865	43	40905	41503	42490	40	4.74E-13	2.28E-12	0.930235558	-0.10433666
BP1026b	II1873	DSBII domain-containing protein	57574	43895	53282	165	54733	54598	51477	171	1.05E-08	2.99E-08	1.036363636	-0.05130301
BP1026b	II1874	6-phosphogluconate dehydrogenase	167420	207961	211076	587	238558	247960	254761	742	0.032572041	0.040147829	1.264054514	0.338058684
BP1026b	II1875	hypothetical protein	143784	170229	165505	112	159214	160633	160376	113	5.19E-11	1.96E-10	1.008928571	0.01282404
BP1026b	II1876	NAD-dependent deacetylase	8682	5473	4817	10	5112	7719	8658	11	1.33E-04	2.18E-04	1.1	0.137503524
BP1026b	II1877	histone/purines/uracil/thiamine/allantoin permease family protein	30892	19735	22505	25	26226	27670	32686	30	1.45E-04	2.37E-04	1.2	0.26304406
BP1026b	II1878	hypothetical protein	2167	2348	23185	102	47648	44663	43901	16	4.08E-08	1.84E-07	0.941766667	-0.087462831
BP1026b	II1879	hypothetical protein	2373	3607	3309	20	3109	3614	3327	21	2.28E-04	3.65E-04	1.05	0.070389328
BP1026b	II1880	Acyltransferase family protein	296811	511776	479597	437	180808	179381	188922	186	7.26E-07	5.05E-104	0.425629291	-1.232330658
BP1026b	II1881	Met tRNA	168630	288515	260870	196	107250	98681	101290	84	5.94E-09	3.38E-06	0.428571429	-1.222392421
BP1026b	II1882	RNA polymerase sigma factor RpoD	1039	2342	2167	24	1332	1684	928	17	1.48E-13	2.37E-12	0.708333333	-0.49749659
BP1026b	II1883	DNA primase	721962	902881	870318	407	852135	842278	800347	407	0.27264212	0.302312102	1	0
BP1026b	II1884	GntR family transcriptional regulator	375147	471438	457767	231	538079	540573	547825	289	1.29E-05	2.41E-05	1.051282521	0.323176641
BP1026b	II1885	30S ribosomal protein S21	40572	44663	44663	102	47648	44663	43901	16	4.08E-08	1.84E-07	0.941766667	-0.087462831
BP1026b	II1886	hypothetical protein	24554	23864	21455	19	23674	22967	23916	19	1.97E-07	4.71E-07	1	0
BP1026b	II1887	DNA-binding iron metalloprotein/AP endonuclease	17728	12146	13425	13	21072	23158	24049	21	0.261489169	0.286058008	1.615384615	0.691877705
BP1026b	II1888	GTP cyclohydrolase	84848	93200	87706	109	79636	80534	71530	95	2.53E-12	1.14E-11	0.871559633	-0.108328716
BP1026b	II1889	1-deoxy-D-xylulose-5-phosphate synthase	726620	887562	720439	373	824522	804497	756326	417	0.165965355	0.185843222	1.117962466	-0.16871753
BP1026b	II1890	geranyltransferase	2998959	2454349	254434	102	26479	284366	267444	93	1.53E-06	2.36E-06	0.930235558	-0.0503050683
BP1026b	II1891	ribosephosphatase VII small subunit	88979	104095	114875	360	84393	86991	85085	290	7.99E-16	3.53E-15	0.805555556	-0.31194006
BP1026b	II1892	XsdE family iron-sulfur cluster-binding protein	388252	488637	461429	387	362188	358816	327752	304	1.04E-18	9.83E-18	0.785529716	-0.34826227
BP1026b	II1893	rhodanese domain-containing protein	238966	204899	234848	260	329495	334627	327158	379	0.09056621	0.104862614	1.457692308	0.64866225
BP1026b	II1894	carboxymethylglutaminolase	84426	95685	95631	104	95781	93560	86992	105	2.88E-08	7.71E-08	1.009615385	0.0138058
BP1026b	II1895	NADH dehydrogenase	135857	106946	119407	61	131601	125668	140097	69	1.47E-07	3.57E-07	1.13147541	0.17787119
BP1026b	II1896	NADH dehydrogenase	103170	105235	102369	74	127498	128856	130506	63	7.41E-05	2.66E-04	1.25676757	0.339770549
BP1026b	II1897	DNA polymerase I	193824	2063803	214809	72	3483603	234809	231490	64	0.00236031	0.003790036	1.166666667	-0.23442321
BP1026b	II1898	decarboxylase family protein	109489	20142	141124	182	134544	128532	116051	171	2.89E-13	1.42E-12	0.933555556	-0.089942725
BP1026b	II1899	hypothetical protein	3093	2038	2362	8	3465	3446	4360	13	0.478370325	0.505569717	1.625	0.70439718
BP1026b	II1900	hypothetical protein	7461	6517	5935	13	8921	9185	7644	17	0.008086921	0.010745963	1.307692308	0.387023123
BP1026b	II1901	hypothetical protein	6076	6725	5572	11	5692	5764	5841	11	2.14E-07	5.09E-07	1	0
BP1026b	II1902	hypothetical protein	15120	23759	20313	16	21071	22642	19376	17	3.28E-06	6.63E-06	1.0625	0.087462841
BP1026b	II1903	hypothetical protein	560	1253	535	8	780	809	873	8	0.006384959	0.008584543	1	0
BP1026b	II1904	hypothetical protein	1228	978	1251	4	1090	1244	1575	4	0.01497126	0.019276459	1	0
BP1026b	II19													

BP1026B	II1955	hypothetical protein	47889	18420	24493	39	33065	37784	46116	50	6.31E-04	9.60E-04	1.282051282	0.358453971
BP1026B	II1956	HepII protein	5667	3921	3855	3	5645	5630	5547	4	0.00561958	0.007606104	1.333333333	0.415037499
BP1026B	II1957	glycosyltransferase	2961	2501	3716	2	2925	3124	2620	2	2.45E-07	3.80E-07	1	0
BP1026B	II1958	hypothetical protein	3648	3454	3442	2	4184	4340	3940	2	0.00568974	0.00089749	1	0
BP1026B	II1959	glycosyltransferase family protein	3229	3111	2761	2	2482	2880	2790	2	9.66E-09	2.75E-08	1	0
BP1026B	II1960	glycosyltransferase	3145	1296	1478	2	2206	1883	2044	2	2.85E-05	5.12E-05	1	0
BP1026B	II1961	Tyrosine-protein kinase Wzc	7305	7753	7208	3	7147	7512	8153	3	1.58E-06	3.32E-06	1	0
BP1026B	II1962	capsular polysaccharide biosynthesis/export periplasmic protein	5004	4496	4986	4	5057	4583	4300	3	2.28E-06	4.71E-06	0.75	-0.415037499
BP1026B	II1963	hypothetical protein	1135	743	1236	2	810	601	675	1	3.56E-12	1.55E-11	0.5	-1
BP1026B	II1964	UDP-glucose 6-dehydrogenase 2	7565	6187	5667	4	6530	5720	5668	4	5.69E-08	1.47E-07	1	0
BP1026B	II1965	calanin biosynthesis UDP-glucose lipid carrier transferase	7240	10184	8089	6	5385	6635	5700	4	1.67E-17	1.36E-16	0.666666667	-0.584962501
BP1026B	II1966	mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase	319845	448086	401424	253	458280	447843	364180	275	1.29E-08	3.61E-08	1.086956522	0.120294234
BP1026B	II1967	hypothetical protein	192586	127263	149186	177	126546	134034	136905	150	3.22E-19	3.25E-18	0.847457627	-0.23878686
BP1026B	II1968	hypothetical protein	13922	4755	6321	396	9496	12316	11915	535	0.020535754	0.026008079	1.351010101	0.434038461
BP1026B	II1969	hypothetical protein	72872	117672	108886	282	776E-31	66293	24251	535	0.020535754	0.026008079	1.351010101	0.434038461
BP1026B	II1970	ferredoxin	6142	6721	6805	11	8890	7734	6853	13	5.76E-04	8.81E-04	1.181818182	0.2410081
BP1026B	II1971	rubredoxin	9078	8093	8156	6	11187	10991	9750	7	0.003614862	0.005009624	1.166666667	0.223392321
BP1026B	II1972	N-acetylmutamoyl-L-alanine amidase domain-containing protein	2854	3332	2844	7	2370	2262	1921	5	4.63E-16	3.17E-15	0.714285714	-0.485426827
BP1026B	II1973	ECF subfamily RNA polymerase sigma factor	26277	27630	27935	26	27779	27080	30223	27	5.82E-07	1.30E-06	1.038461538	0.054447784
BP1026B	II1974	hypothetical protein	4040	2077	2195	2	2744	4013	4068	2	0.053898529	0.064653463	1	0
BP1026B	II1975	DGPF domain-containing protein	5019	3352	3185	7	4288	4298	4346	7	7.47E-04	0.001126022	1	0
BP1026B	II1976	DGPF domain-containing protein	6767	7302	7252	17	8258	7519	9517	20	6.90E-04	0.001045917	1.176470588	0.234465254
BP1026B	II1977	extracellular nuclease	24549	22728	23295	66	27776	26675	24573	74	2.21E-05	4.03E-05	1.121212121	0.165059246
BP1026B	II1978	transmembrane protein	9649	7331	7327	4	11603	12855	12925	6	0.25801919	0.282489249	1.086121212	0.388662501
BP1026B	II1979	lipoprotein	29351	29977	32420	79	31373	30017	26397	82	1.06E-06	2.90E-06	1.075949367	0.105610188
BP1026B	II1980	PerM family permease	225375	218461	220027	378	252575	255856	260711	438	0.001862141	0.002674106	1.158730159	0.212544635
BP1026B	II1981	hypothetical protein	68300	77465	76870	70	61660	57986	51445	53	1.03E-20	1.22E-19	0.757142857	-0.401362562
BP1026B	II1982	TonB-dependent receptor	56501	43052	49130	115	50523	56563	61829	131	1.00E-05	1.90E-05	1.139130435	0.187932951
BP1026B	II1983	major facilitator family transporter	11285	6214	7468	4	11061	11556	11590	5	0.0292228	0.03628377	1.25	0.321928095
BP1026B	II1984	oxidoreductase, zinc-binding dehydrogenase family protein	3038	1117	1355	1	2061	2477	3136	2	0.159617242	0.179343929	2	1
BP1026B	II1985	short chain dehydrogenase	11080	6169	6774	7	6258	10793	12791	10	0.070991562	0.083431734	1.428571429	0.154573713
BP1026B	II1986	short chain dehydrogenase	39943	33065	35889	45	39175	40929	41310	50	3.17E-07	1.94E-06	1.111111111	0.132003093
BP1026B	II1987	phosphoglycerate mutase family protein	22793	26962	25694	32	24826	24634	22212	30	5.91E-09	1.74E-08	0.9375	-0.093109404
BP1026B	II1988	phosphotransferase enzyme family protein	2282	493	435	1	1695	2032	3906	3	1.96E-05	3.60E-05	3	1.584962501
BP1026B	II1989	acyl-CoA dehydrogenase domain-containing protein	15238	10674	10644	11	18446	19240	22912	18	0.502426884	0.529119368	1.636363636	0.710493383
BP1026B	II1990	hydrolase	21083	9626	13714	12	22336	23622	27005	19	0.419653713	0.04705967	1.583333333	0.626965013
BP1026B	II1991	hypothetical protein	15876	17944	17790	42	19954	20300	21991	51	4.28E-04	6.64E-04	1.212425874	0.280107919
BP1026B	II1992	hypothetical protein	126912	125688	129444	107	141671	138977	134167	116	1.89E-08	5.19E-08	1.08411215	0.116514009
BP1026B	II1993	CtAAX amino terminal protease family protein	153879	159379	13220	144	137147	14979	16397	165	3.17E-07	1.94E-06	1.131044444	0.178803153
BP1026B	II1994	ABC transporter, permease protein/ATP-binding protein	31501	22460	25173	13	35433	36087	37907	18	0.00615339	0.008294563	1.384615385	0.469485283
BP1026B	II1995	DJ-1/Pip1 family protein	24835	18798	19568	30	23647	27363	26573	36	7.58E-04	0.001142507	1.2	0.263034406
BP1026B	II1996	AraC family transcriptional regulator	13229	5900	7181	7	8102	11707	13221	9	0.002895309	0.004174102	1.285714286	0.362570079
BP1026B	II1997	tryptophan-tRNA synthetase II	8855	5920	6622	6	9909	8938	9714	9	0.020010573	0.025368595	1.5	0.584962501
BP1026B	II1998	SlyB protein	4719	3284	3847	6	4027	3753	4604	6	6.64E-05	1.13E-04	1	0
BP1026B	II1999	AraC/XyS family transcriptional regulator	1353	832	1206	3	1382	1699	1987	5	0.745410474	0.771507282	1.666666667	0.736965594
BP1026B	II2000	CtAAX amino terminal protease family protein	23944	20038	22088	25	26142	25675	25933	26	1.22E-08	2.39E-08	1	0.1103131
BP1026B	II2001	voltage-gated chloride channel	24462	18482	18604	15	26254	25568	25566	20	0.001641903	0.002376907	1.333333333	0.415037499
BP1026B	II2002	haloacid dehalogenase	36840	21478	22398	37	30875	34272	37546	47	6.62E-04	0.001066601	1.27027027	0.345135486
BP1026B	II2003	chemotaxis-specific methyltransferase	52651	26369	31865	35	55932	61584	63022	58	8.82645199	0.839859712	1.657142857	0.728697978
BP1026B	II2004	chemotaxis histidine kinase	110418	92655	91210	37	114135	118856	124685	45	3.65E-05	6.46E-05	1.216216216	0.282399731
BP1026B	II2005	chemotaxis protein cheW	49335	31137	34302	52	47088	51756	49400	67	0.001211629	0.001757751	1.288461538	0.365649472
BP1026B	II2006	CheR methyltransferase SAM binding/TPR domain-containing protein	71615	45236	49239	26	72674	76504	76234	36	0.038211926	0.046740774	1.384615385	0.469485283
BP1026B	II2007	cheW domain-containing protein	19288	11512	13318	28	21309	24755	24837	45	0.327517549	0.33533669	1.607142857	0.684498174
BP1026B	II2008	methyl-accepting chemotaxis transducer	156162	133461	139549	85	133187	138725	141993	82	7.23E-13	3.41E-12	0.964705882	-0.051838932
BP1026B	II2009	sensor histidine kinase/response regulator	66133	62579	61186	57	62462	65012	69946	59	1.33E-06	2.83E-06	1.03587719	0.049753035
BP1026B	II2010	hypothetical protein	6924	3862	3691	14	9562	10303	8454	9	0.540070477	0.565813927	2.071428571	1.050626073
BP1026B	II2011	hypothetical protein	1829	2458	2268	9	1856	1507	2130	7	4.78E-10	1.60E-09	0.777777778	-0.362570079
BP1026B	II2012	Acyl dehydratase	4422	5794	4717	15	4058	3546	3846	12	4.97E-12	2.13E-11	0.8	-0.331928095
BP1026B	II2013	aldehyde dehydrogenase	3928	3928	3911	28	530815	3911	3801	20	5.30E-15	3.40E-14	0.742857143	-0.448426827
BP1026B	II2014	aldehyde dehydrogenase	36596	36502	38197	25	43386	40137	41394	29	1.48E-06	3.12E-06	1.16	0.214124805
BP1026B	II2015	acetylacetylase	43687	54434	51831	30	46212	45878	44348	27	2.20E-14	1.24E-13	0.9	-0.152003093
BP1026B	II2016	Na+/H+ antiporter	47241	47973	48896	30	43792	41848	37818	26	2.06E-16	1.48E-15	0.866666667	-0.206450877
BP1026B	II2017	hypothetical protein	48373	57275	54565	41	41165	43858	43300	33	1.81E-20	2.09E-19	0.804878049	-0.313157885
BP1026B	II2018	phospholipase D	74506	71549	70019	43	79900	76575	74762	46	3.42E-06	6.88E-06	1.069767442	0.097297201
BP1026B	II2019	III family protein	158932	209218	200552	454	145675	145294	150036	352	1.50E-26	3.26E-25	0.775330396	0.367116869
BP1026B	II2020	ferredoxin	1805	1015	1437	1	1791	2581	1892	1	0.426437157	0.453743728	1	0
BP1026B	II2021	RcsK family non-sulfur cluster-binding protein	523	535	400	1	635	591	558	1	0.189278577	0.210662627	1	0
BP1026B	II2022	ortho-haloacetate 1,2-dioxygenase beta-ISP protein OhbA	424	388	416	0	457	428	167	0	0.001107586	0.0016313	0.75330396	0.367116869
BP1026B	II2023	ortho-haloacetate 1,2-dioxygenase alpha-ISP protein OhbB	1875	2386	2054	1	2115	3034	2370	1	0.003262835	0.004544896	1	0
BP1026B	II2024	AraC family transcriptional regulator	9945	8871	9017	9	6541	7328	8895	7	4.96E-13	2.38E-12	0.777777778	-0.362570079
BP1026B	II2025	transcriptional regulator CatR	9017	5884	5322	7	6635	8811	10838	9	0.009826313	0.012944695	1.285714286	0.362570079
BP1026B	II2026	muconate cycloisomerase	16094	19797	20073	16	19044	17497	16885	15	1.91E-08	5.23E-08	0.9375	-0.093109404
BP1026B	II2027	catechol 1,2-dioxygenase	6533	4960	4969	6	6217	7459	7704	7	0.006832769	0.009157138	1.166666667	0.222392321
BP1026B	II2028	muconolactone delta-isomerase	2447	1865	2087	8	2385	2958	1854	6	3.78E-06	1.85E-06	1	0
BP1026B	II2029	ubiquinol oxidase subunit IV	1787	1579	1545	4	2410	2089	1857	6	0.407018695	0.056847154	1.5	0.584962501
BP1026B	II2030	ubiquinol oxidase subunit III	4486	3637										

BP1026b	I12202	IS element transposase	25617	32238	30794	40	28144	28983	25974	37	1.79E-09	5.58E-09	0.925	-0.112474729
BP1026b	I12205	hypothetical protein	1004	1204	880	4	671	562	548	2	6.39E-17	4.89E-16	0.5	-1
BP1026b	I12206	hypothetical protein	1964	3967	3606	8	2348	2572	2610	6	1.16E-12	5.37E-12	0.75	-0.415037499
BP1026b	I12207	adhesin hemolysin	51757	69020	69020	6	61184	61077	58728	10	6.05E-10	1.89E-09	0	0
BP1026b	I12209	Integrase	2131	2307	2038	13	2161	1991	1682	10	6.11E-11	2.28E-10	0.769230769	-0.378511623
BP1026b	I12210	RhsD protein	89965	146133	127046	26	113792	108873	97001	23	2.64E-14	1.47E-13	0.884615385	-0.176877762
BP1026b	I12211	hypothetical protein	9396	7644	8128	6	8023	10330	9100	7	3.09E-05	5.52E-05	1.166666667	0.222392421
BP1026b	I12213	hypothetical protein	10315	14995	16253	15	10488	11479	8977	11	6.05E-17	4.65E-16	0.733333333	-0.447458977
BP1026b	I12214	diaminopimelate decarboxylase	1028	799	1280	2	1045	1178	1131	2	0.010371454	0.013614163	1	0
BP1026b	I12216	hypothetical protein	46898	64600	59724	55	62818	58774	51620	56	1.47E-08	4.07E-08	1.018181818	0.025995209
BP1026b	I12217	Aerobic C4-dicarboxylate transporter for formate, L-malate, D-malate, succinate	11659	19745	17595	27	12056	10308	11651	18	9.84E-21	1.17E-19	0.666666667	-0.584962501
BP1026b	I12218	endoribonuclease L-PSP	8613	16134	13811	31	8758	10315	8566	22	2.56E-18	2.32E-17	0.709677419	-0.494764692
BP1026b	I12220	GntR family transcriptional regulator	8011	10716	9475	21	8156	8383	7851	18	4.09E-11	1.57E-10	0.857142857	-0.222392421
BP1026b	I12221	senescence marker protein-30	57956	95823	89663	91	61169	57923	60228	67	1.45E-21	1.90E-20	0.736263736	-0.44170545
BP1026b	I12222	Polypeptide-transport-associated domain protein ShlR-type transposase B	16405	22976	23497	61	16927	16303	14782	46	2.07E-15	1.32E-14	0.754098361	-0.407175382
BP1026b	I12223	transposase	565	386	534	0	630	345	447	0	0.003869761	0.005335722	#DIV/0!	#DIV/0!
BP1026b	I12224	hypothetical protein	24859	44578	37330	18	25502	26432	27074	13	2.07E-18	1.87E-17	0.722222222	-0.469485283
BP1026b	I12226	alpha-galactosidase	15553	25336	21680	9	14133	15333	12931	6	1.91E-21	2.47E-20	0.666666667	-0.584962501
BP1026b	I12227	ABC transporter permease	2009	3312	2760	8	1225	955	1082	3	3.75E-52	4.27E-50	0.375	-1.415037499
BP1026b	I12228	hypothetical protein	498	990	564	3	367	281	365	1	9.45E-18	7.94E-17	0.333333333	-1.584962501
BP1026b	I12229	ABC transporter permease	4055	6923	6826	6	3925	4047	4002	4	1.17E-16	8.64E-16	0.666666667	-0.584962501
BP1026b	I12230	ABC transporter substrate-binding protein	4156	6122	5407	4	4097	3585	3575	3	2.25E-14	1.27E-13	0.75	-0.415037499
BP1026b	I12231	maltose/maltodextrin import ATP-binding protein malK	3460	7033	6407	4	4442	3557	3481	3	7.14E-17	5.41E-16	0.75	-0.415037499
BP1026b	I12232	hypothetical protein	11776	20700	18026	8	12982	14003	13224	6	4.60E-14	2.49E-13	0.75	-0.415037499
BP1026b	I12233	hypothetical protein	2175	3827	2712	13	1365	1152	1332	6	3.62E-44	2.74E-42	0.461538462	-1.15477217
BP1026b	I12234	LacI family regulatory protein	17654	29934	27564	21	12870	12968	12202	10	5.43E-45	4.31E-43	0.476190476	-1.070389328
BP1026b	I12235	transposase	300	967	328	2	257	424	193	1	1.63E-11	6.58E-11	0.55	-0.862496476
BP1026b	I12236	hypothetical protein	11633	19424	18106	20	8462	9696	9302	11	7.08E-35	3.26E-33	0.5	-0.862496476
BP1026b	I12238	transposase	1349	2586	2142	6	2433	2180	1816	7	4.88E-05	8.48E-05	1.166666667	0.222392421
BP1026b	I12239	transposase B	579	554	559	0	423	478	505	0	3.91E-04	6.10E-04	#DIV/0!	#DIV/0!
BP1026b	I12244	Integrase	4058	6489	5764	6	4637	5902	4045	6	1.47E-08	1.07E-08	0.833333333	-0.263034406
BP1026b	I12245	transposase	3120	4935	4012	13	4442	4512	4016	13	1.86E-04	3.00E-04	0	0
BP1026b	I12246	IssoR-transposase orb protein	34608	53847	50914	52	44320	39511	35906	44	4.61E-16	3.17E-15	0.846153846	-0.2410081
BP1026b	I12247	transposase	18128	24053	25369	76	28312	30368	30463	101	0.004323535	0.005931368	1.328947368	0.410283969
BP1026b	I12248	hypothetical protein	855	1092	1217	7	1430	1312	1400	9	0.268829591	0.29383154	1.285714286	0.362570079
BP1026b	I12249	transposase	43457	72887	64753	52	81894	84769	76482	70	0.021980555	0.027714612	1.346153846	0.428843299
BP1026b	I12250	hypothetical protein	13891	25648	20164	26	15447	15921	15427	21	3.92E-13	1.90E-12	0.807692308	-0.308122295
BP1026b	I12252	YjD repeat/RHS repeat protein	13909	23922	18593	9	14532	13641	11557	6	5.93E-18	4.07E-17	0.666666667	-0.584962501
BP1026b	I12253	hypothetical protein	5783	8898	5374	8	6311	5619	5171	8	4.11E-06	8.18E-06	1	0
BP1026b	I12254	type VI secretion system	4995	6701	5486	2	4947	5087	5497	2	5.91E-08	1.52E-07	1	0
BP1026b	I12255	type VI secretion system	3913	2982	3020	1	3802	4189	4169	1	0.011421613	0.014911418	1	0
BP1026b	I12256	type VI secretion system	616	748	600	0	730	907	589	0	0.046515315	0.056271134	#DIV/0!	#DIV/0!
BP1026b	I12257	type VI secretion system	4851	3202	4197	2	5388	5627	5346	2	0.02450773	0.030764813	1	0
BP1026b	I12258	type VI secretion system	947	657	731	1	1120	928	735	1	0.093515019	0.108117032	1	0
BP1026b	I12259	type VI secretion system	2516	2075	2539	4	1430	3011	3045	6	0.061204478	0.072855524	0.5	0.584962501
BP1026b	I12260	type VI secretion system	4798	4767	4650	3	5495	5339	4763	3	1.84E-04	2.97E-04	1	0
BP1026b	I12261	type VI secretion system	1120	1375	1082	2	1069	1398	777	1	1.64E-05	3.03E-05	0.5	-1
BP1026b	I12262	type VI secretion system	1026	704	639	0	1491	1335	1478	1	0.076991939	0.089954263	#DIV/0!	#DIV/0!
BP1026b	I12263	type VI secretion system	13281	14456	14537	5	14605	15175	14067	5	2.68E-06	5.48E-06	1	0
BP1026b	I12264	type VI secretion system	974	545	238	0	453	976	1121	0	0.993524065	0.995112687	#DIV/0!	#DIV/0!
BP1026b	I12265	type VI secretion system	8932	5436	6058	1	10435	10971	12468	3	0.58955177	0.62292134	3	1.584962501
BP1026b	I12266	type VI secretion system	507	707	336	0	630	331	331	0	0.031465048	0.03481989	#DIV/0!	#DIV/0!
BP1026b	I12267	type VI secretion system	1666	1196	1063	0	1261	1320	1640	0	0.001632937	0.002365568	#DIV/0!	#DIV/0!
BP1026b	I12268	type VI secretion system	384	653	569	0	604	456	239	0	2.53E-05	4.58E-05	#DIV/0!	#DIV/0!
BP1026b	I12269	type VI secretion system	111	548	135	0	213	196	117	0	8.27E-06	1.59E-05	#DIV/0!	#DIV/0!
BP1026b	I12270	type VI secretion system	4670	4824	5677	3	5300	4904	3828	3	3.63E-07	8.39E-07	1	0
BP1026b	I12271	hypothetical protein	13123	7786	8942	5	12334	13177	15928	7	0.041034022	0.049968334	1.4	0.485426827
BP1026b	I12272	hypothetical protein	10258	13167	11771	9	17694	16970	16146	14	0.081700338	0.095001098	1.555555556	0.637429921
BP1026b	I12273	isomerase lyase superfamily protein	389	1913	204	0	213	504	586	1	0.129652572	0.147676499	#DIV/0!	#DIV/0!
BP1026b	I12274	hypothetical protein	399	173	332	1	354	426	348	2	0.691818002	0.713107286	2	1
BP1026b	I12275	short chain dehydrogenase/reductase family oxidoreductase	5558	2975	3245	5	5495	5173	5932	7	0.066109358	0.078030717	1.4	0.485426827
BP1026b	I12276	LysR family transcriptional regulator	5761	3996	4978	5	4838	5293	6290	5	2.44E-04	3.90E-04	1	0
BP1026b	I12277	D-serine dehydratase	3241	1094	1761	1	3026	4019	3708	2	0.481195525	0.508384005	2	1
BP1026b	I12278	LysR family transcriptional regulator	17529	10542	11664	14	17328	20855	24612	22	0.295316761	0.320934107	1.571428571	0.652076697
BP1026b	I12279	hypothetical protein	5612	9651	8240	25	6740	6102	4765	19	3.00E-14	1.66E-13	0.76	-0.395928676
BP1026b	I12280	AcrR family transcriptional regulator	73438	10775	71363	98	52121	51023	4383	73	2.41E-25	4.63E-24	0.744897969	-0.248653385
BP1026b	I12281	metallo-beta-lactamase family protein	6828	8171	6633	7	6562	5823	6891	6	7.28E-06	1.41E-05	1.142857143	0.192645078
BP1026b	I12282	major facilitator family transporter	9426	10144	10667	6	8475	8315	7561	6	4.27E-12	1.85E-11	0.75	-0.415037499
BP1026b	I12283	cysteine desulfurase	11279	12353	12546	10	9677	10677	10200	9	5.47E-12	2.33E-11	0.9	-0.152003093
BP1026b	I12284	hypothetical protein	335	163	371	0	351	416	294	0	0.066609982	0.030036238	#DIV/0!	#DIV/0!
BP1026b	I12285	major facilitator family transporter	18349	16877	16427	12	12428	11895	13159	9	3.48E-18	3.09E-17	0.75	-0.415037499
BP1026b	I12286	LysR family transcriptional regulator	5519	1733	1890	3	2828	4159	4729	4	0.034073513	0.041899585	1.333333333	-0.415037499
BP1026b	I12287	L-lactate dehydrogenase	10169	9474	8926	9	10446	11541	10325	9	2.01E-05	1.87E-05	1	0
BP1026b	I12288	flumarylacetoacetate hydrolase family protein	19477	10687	12459	16	18105	18371	20813	22	0.02059597	0.020218751	1.375	0.459431619
BP1026b	I12289	IcR family transcriptional regulator	5548	3829	4241	5	4084	4053	5235	5	6.26E-06	1.22E-05	0	0
BP1026b	I12290	indole acetamide hydrolase	34430	21737	24842	19	28673	32581	32493	22	3.41E-05	6.05E-05	1.157894737	0.211504105
BP1026b	I12291	hypothetical protein	16875	19139	18040	32	12670	13990	13515	24	7.16E-17	5.43E-16	0.75	-0.415037499
BP1026b	I12292	acetyltransferase	67877	55681	58004	25	75528	76506	80516	32	0.006297027	0.008475415	1.28	0.35614381
BP1026b	I12293	hypothetical protein	1516	2234	1369	3	1720	1639	1389	3	1.53E-06	3.21E-06	1	0
BP1026b	I12294	hypothetical protein	3054	4529	4402	8	4							

BP1026b	I2337	hypothetical protein	19464	29842	23810	52	18471	16327	14103	34	6.06E-22	8.33E-21	0.653846154	-0.612976877
BP1026b	I2338	hypothetical protein	5179	4559	5767	24	7173	6663	6604	32	0.011177454	0.014601788	1.333333333	0.415037499
BP1026b	I2339	carbon starvation protein A	35584	34924	31467	16	34136	32248	29249	15	1.29E-09	4.13E-09	0.9375	-0.093109404
BP1026b	I2340	cytochrome P450	2839	2078	1803	4	2073	3283	3283	6	0.119974747	0.127380076	1.5	0.584962501
BP1026b	I2341	epoxide hydrolase	9990	6098	7003	7	10111	11386	10204	10	0.033009795	0.040655398	1.428571429	0.514573173
BP1026b	I2342	hypothetical protein	22935	14849	14332	11	18344	19784	19284	12	1.54E-05	1.86E-05	1.090909091	0.22530882
BP1026b	I2343	LysR family transcriptional regulator	15933	20278	18285	18	21456	21451	19295	21	5.98E-05	1.03E-04	1.166666667	0.222392421
BP1026b	I2344	cysteine transferase	3989	5447	5066	12	4083	4558	3225	10	4.60E-10	1.54E-09	0.833333333	-0.263034406
BP1026b	I2345	hypothetical protein	1041	1324	765	2	1034	1297	1212	2	0.10700269	0.122961815	1	0
BP1026b	I2346	hypothetical protein	4447	178	216	0	448	323	407	1	0.7352579	0.753789768	#DIV/0!	#DIV/0!
BP1026b	I2347	Genetic methyltransferase	1734	658	1040	1	1553	1236	2051	2	0.521474141	0.547310548	1	0
BP1026b	I2348	glycosyl transferase family protein	11882	14316	13399	12	11821	11357	11490	10	7.43E-11	2.75E-10	0.833333333	-0.263034406
BP1026b	I2349	hypothetical protein	1953	559	672	0	1511	1917	1666	1	0.662830551	0.684917613	#DIV/0!	#DIV/0!
BP1026b	I2350	hypothetical protein	8060	6477	7031	5	7028	6660	7250	5	2.14E-07	5.09E-07	1	0
BP1026b	I2351	hypothetical protein	459	683	488	0	534	499	660	0	0.015990835	0.020538567	#DIV/0!	#DIV/0!
BP1026b	I2352	pilus subunit protein	799	1477	1361	7	1302	934	596	5	8.44E-09	2.41E-08	0.714285714	-0.485426827
BP1026b	I2353	pilus subunit protein	333	326	725	2	186	129	200	0	2.66E-26	5.57E-25	0	#NUM!
BP1026b	I2354	type IV prepilin peptidase-like protein	108	54	119	1	170	120	148	0	0.416419188	0.444083688	#DIV/0!	#DIV/0!
BP1026b	I2355	hypothetical protein	2491	1366	1762	1	2761	2645	2592	2	0.211855226	0.234545977	1	0
BP1026b	I2356	pilus assembly transmembrane protein	697	585	596	0	482	362	633	0	2.45E-06	5.04E-06	#DIV/0!	#DIV/0!
BP1026b	I2357	phospholipid-binding domain-containing protein	3703	2858	3409	1	4002	4419	4684	2	0.050874689	0.061166805	2	1
BP1026b	I2359	tRNA delta(2)-isopentenylpyrophosphatetransferase	312	554	334	1	470	261	234	1	4.33E-04	6.71E-04	1	0
BP1026b	I2360	hypothetical protein	3468	3975	3964	3	3528	4598	3517	3	2.83E-05	5.08E-05	1	0
BP1026b	I2358	hypothetical protein	2394	1545	1847	3	2502	2435	2706	5	0.051476046	0.061842338	1.666666667	0.736965594
BP1026b	I2361	hypothetical protein	842	1047	834	1	634	1088	800	1	1.10E-04	1.82E-04	1	0
BP1026b	I2362	Flp pilus assembly protein, ATPase	2002	348	1303	1	2696	3024	2608	0	0.852495531	0.863268238	1	0
BP1026b	I2364	type II secretion system protein	7177	6925	7095	5	9316	8048	7969	6	8.87E-04	0.001326106	1.2	0.263034406
BP1026b	I2363	Flp pilus assembly protein TadB	4520	6813	5664	5	4389	4254	3617	4	7.62E-14	4.02E-13	0.8	-0.321928095
BP1026b	I2365	type II secretion system protein	5623	4174	5310	5	5270	5424	5643	5	9.22E-05	1.54E-04	1	0
BP1026b	I2366	transcription regulator AscC	39523	51977	46564	96	36068	32499	31034	69	3.59E-23	5.60E-22	0.71875	-0.476438044
BP1026b	I2367	aromatic amino acid aminotransferase	1270	899	862	0	1482	878	1207	0	0.068182848	0.080501816	#DIV/0!	#DIV/0!
BP1026b	I2368	translation initiation inhibitor	43	61	45	0	106	65	46	0	0.649546147	0.671706181	#DIV/0!	#DIV/0!
BP1026b	I2369	outer membrane porin protein	1821	1356	1115	1	1886	2140	2537	2	0.642966351	0.665379353	2	1
BP1026b	I2370	amino acid transporter	55931	58334	58912	40	42800	44114	41654	29	2.20E-25	4.24E-24	0.725	-0.4639471
BP1026b	I2371	GntR family transcriptional regulator	80970	70423	76063	97	50431	47156	49772	63	6.90E-37	3.51E-35	0.649484536	-0.622632919
BP1026b	I2372	hypothetical protein	644476	362113	411734	307	540321	580149	622507	377	6.14E-06	1.20E-05	1.228013029	0.296325868
BP1026b	I2373	major facilitator family transporter	461140	478522	459050	356	391219	416102	398986	307	1.27E-16	9.31E-16	0.862359551	-0.213638586
BP1026b	I2374	LysR family transcriptional regulator	163715	104565	108769	137	158800	168252	151689	174	3.61E-04	5.65E-04	1.270072993	0.344911413
BP1026b	I2375	hypothetical protein	161240	153928	160527	74	180797	180997	174063	83	2.18E-06	5.52E-06	1.121621622	0.165586066
BP1026b	I2377	hypothetical protein	722	348	221	1	645	320	678	0	0.3454568	0.37245969	1	0
BP1026b	I2376	hypothetical protein	720	4153	4372	10	3638	3957	3550	9	1.28E-07	3.13E-07	0.9	-0.152003093
BP1026b	I2378	Na ⁺ /H ⁺ antiporter-like protein	4330	4667	5650	3	4462	3444	4474	3	4.63E-09	1.38E-08	1	0
BP1026b	I2379	ATP-dependent DNA ligase	7209	5176	6273	1	5852	7752	8318	2	4.13E-04	6.42E-04	2	1
BP1026b	I2380	Ku70/Ku80 beta-barrel domain-containing protein	2837	3739	3207	2	2670	2890	2506	2	3.34E-11	1.29E-10	1	0
BP1026b	I2381	hypothetical protein	193	145	169	0	213	263	252	0	0.473193636	0.500436424	#DIV/0!	#DIV/0!
BP1026b	I2382	hydroperoxidase II	3102	3168	2972	1	3179	2851	3069	1	2.75E-06	5.62E-06	#DIV/0!	#DIV/0!
BP1026b	I2383	hypothetical protein	205	48	45	0	156	168	163	0	1.30E-04	1.25E-05	#DIV/0!	#DIV/0!
BP1026b	I2384	hypothetical protein	176	74	264	1	143	199	36	0	6.35E-04	9.67E-04	0	#NUM!
BP1026b	I2385	hypothetical protein	35	212	160	0	142	196	110	0	0.352033304	0.378824362	#DIV/0!	#DIV/0!
BP1026b	I2386	RNA polymerase factor sigma-54	2953	1407	2199	1	2385	2520	2394	1	2.98E-04	4.71E-04	1	0
BP1026b	I2388	lipoprotein	2475	2329	1901	2	2352	2777	2336	3	3.33E-04	5.23E-04	1.5	0.584962501
BP1026b	I2389	Manganese catalase	1153	776	1267	1	1675	1602	2142	1	0.359253217	0.386328266	1	0
BP1026b	I2390	hypothetical protein	2835	3644	2852	6	2859	2811	3048	5	1.40E-07	3.41E-07	0.833333333	-0.263034406
BP1026b	I2391	hypothetical protein	6251	6571	1110	2	1524	1916	1916	2	0.4402773	0.4336676	1.5	0.584962501
BP1026b	I2392	hypothetical protein	9106	15585	13572	36	10455	9681	8637	27	2.33E-16	2.01E-15	0.75	-0.415037499
BP1026b	I2393	hypothetical protein	20265	34534	31401	81	18850	19623	19902	55	1.97E-22	2.84E-21	0.679012346	-0.558490289
BP1026b	I2394	hypothetical protein	14122	9540	11156	13	11617	12541	11189	13	5.64E-07	1.26E-06	1	0
BP1026b	I2395	lipoprotein	976	242	224	1	883	888	1156	3	0.003885188	0.00535228	3	1.584962501
BP1026b	I2396	hypothetical protein	4070	3916	3163	11	3593	2754	3342	10	5.67E-08	1.46E-07	0.909090909	-0.137503524
BP1026b	I2397	hypothetical protein	243	445	399	1	146	261	270	0	4.16E-07	5.54E-07	0	#NUM!
BP1026b	I2398	hypothetical protein	886	665	888	0	902	1072	1072	3	0.1105172	0.12384376	1.5	0.584962501
BP1026b	I2399	hypothetical protein	539	249	654	1	609	550	550	2	0.031622198	0.03917682	1	0
BP1026b	I2400	hypothetical protein	578	607	644	5	643	765	554	5	0.019663615	0.024943881	1	0
BP1026b	I2401	hypothetical protein	98520	58735	67908	116	101329	106318	109401	163	0.021265759	0.026867429	1.405172414	0.490747159
BP1026b	I2402	hypothetical protein	1748	907	1513	3	1419	1394	1249	3	3.98E-05	1.19E-04	1	0
BP1026b	I2403	PRC-barrel domain-containing protein	10416	9227	7790	18	11403	9432	9848	20	6.22E-05	1.07E-04	1.111111111	0.152003093
BP1026b	I2405	CheY-like domain-containing protein	347	436	555	0	580	666	673	1	0.971372198	0.974483576	#DIV/0!	#DIV/0!
BP1026b	I2404	hypothetical protein	0	0	0	0	35	32	36	0	0	0	#DIV/0!	#DIV/0!
BP1026b	I2406	DNA glycosylase	376	48	361	0	319	131	405	0	0.340909294	0.367485083	#DIV/0!	#DIV/0!
BP1026b	I2407	NRAMP family Mn ²⁺ /Fe ²⁺ transporter	9172	5432	6558	4	9118	10506	10369	6	0.070949963	0.083398493	1.5	0.584962501
BP1026b	I2408	glutathione-dependent formaldehyde dehydrogenase	1429	853	1031	0	1933	2021	2253	1	0.077958372	0.090953853	#DIV/0!	#DIV/0!
BP1026b	I2409	oxido-reductase, zinc-binding dehydrogenase family	500	17	380	0	241	432	224	0	0.103084074	0.11869828	#DIV/0!	#DIV/0!
BP1026b	I2410	hypothetical protein	3128	3049	2804	4	3222	3143	3637	5	6.94E-04	0.001051896	1.25	0.321928095
BP1026b	I2411	hypothetical protein	827	425	440	0	1085	999	1278	1	0.005499979	0.007457114	#DIV/0!	#DIV/0!
BP1026b	I2412	short chain dehydrogenase/reductase family oxidoreductase	1270	2212	1759	2	1501	1162	1865	1	2.45E-08	6.63E-08	0.5	-1
BP1026b	I2413	hypothetical protein	962	1023	1160	1	1567	690	915	1	1.50E-07	1.65E-07	1	0
BP1026b	I2414	hypothetical protein	1901	1309	1628	5	2097	1901	2194	6	0.040335577	0.049203906	1.2	0.263034406
BP1026b	I2415	short chain dehydrogenase	9755	9920	10796	9	10275	9558	10404	9	2.33E-07	5.51E-07	1	0
BP1026b	I2416	osmotically inducible protein Y	454	357	687	0	648	543	457	1	0.05441591	0.065236605	#DIV/0!	#DIV/0!
BP1026b	I2417	glycoside hydrolase family protein	1488	789	927	0	1485	1462	1261	1	0.258633067	0.283081868	#DIV/0!	#DIV/0!
BP1026b	I2418	NAD-dependent epimerase/dehydratase family protein	7771	5900	6413	6	6689	5956	7234	6	8.51E-07	1.86E-06	1	0
BP1026b	I2419	sensory box histidine kinase-response regulator	28175	16950	14781	7	23718	25071	32489	10	0.085444846	0.099180371	1.571428571	0.625079627
BP1026b	I2420													

BP1026B	I2461	hypothetical protein	72884	78690	69338	43	77981	76091	76631	44	9.11E-07	1.98E-06	1.02325814	0.03166864
BP1026B	I2462	hypothetical protein	645635	487564	529602	537	888538	924205	940216	889	0.002042073	0.002912465	1.655493482	0.727261331
BP1026B	I2463	sulfate transporter family protein	193546	84002	104420	69	228182	237059	244103	128	0.024524736	0.030773827	1.855072464	0.891475543
BP1026B	I2465	hypothetical protein	38493	41077	33661	88	45933	44037	41281	94	4.31E-08	2.01E-07	1.068181818	0.095157233
BP1026B	I2464	nitroreductase family protein	455853	255471	330262	530	500645	530273	582524	822	0.024601723	0.030864249	1.550943396	0.633146034
BP1026B	I2466	HSP20/alpha crystallin family protein	3547101	4846765	4742764	10066	5142909	5134011	5054375	11748	0.140742528	0.159308131	1.167097159	0.222924668
BP1026B	I2467	porin protein	16739	15800	15080	13	16557	16500	15581	14	1.13E-06	2.42E-06	1.076923077	0.106915204
BP1026B	I2468	medium-chain-fatty-acid--CoA ligase	5542	5694	5502	3	5656	5031	4409	2	6.61E-08	1.69E-07	0.666666667	-0.584962501
BP1026B	I2469	GerE family regulatory protein	45232	24521	28005	12	44083	48496	53205	18	0.065157859	0.077009213	1.5	0.584962501
BP1026B	I2470	hypothetical protein	15888	22729	21521	18	13665	13540	13113	12	4.66E-22	6.51E-21	0.666666667	-0.584962501
BP1026B	I2471	quinone oxidoreductase	12369	8883	19932	10	10780	10862	10993	11	4.37E-07	9.97E-07	1.5	0.137503524
BP1026B	I2472	taurine catabolism dioxygenase TauD, TtdA family protein	15177	13379	13600	16	12488	15973	14756	16	1.47E-06	3.10E-06	1	0
BP1026B	I2473	hypothetical protein	23622	24101	23745	22	19774	21364	21349	19	2.16E-11	8.57E-11	0.863636364	-0.211504105
BP1026B	I2474	major facilitator family transporter	3072	2325	3380	2	2381	2005	1650	1	3.21E-18	2.87E-17	0.5	-1
BP1026B	I2475	hypothetical protein	627	328	159	0	551	385	177	0	0.034631701	0.042560913	#DIV/0!	#DIV/0!
BP1026B	I2476	DSBA-like thioresdoxin domain-containing protein	1309	639	499	1	796	1136	1373	1	0.540514372	0.064184285	1	0
BP1026B	I2477	molybdopterine oxidoreductase family protein	27902	33946	35786	11	26204	26929	26585	9	6.01E-14	3.20E-13	0.818181818	-0.289506617
BP1026B	I2478	iron-sulfur cluster-binding protein	5140	8264	7453	8	7297	5836	6589	8	8.80E-08	2.22E-07	1	0
BP1026B	I2479	DMSO reductase subunit C	3197	2568	1887	2	2697	2583	2674	3	0.002119042	0.003016745	1.5	0.584962501
BP1026B	I2480	polysaccharide deacetylase family protein	238368	375685	290865	1839	334948	348757	287852	1974	3.52E-07	8.17E-07	1.073409462	0.10220051
BP1026B	I2481	hypothetical protein	22256	19747	20457	23	19918	19719	21419	22	4.02E-08	1.06E-07	0.956521739	-0.064130337
BP1026B	I2482	penicillin-binding protein	114491	98166	104362	75	110303	114164	110211	80	3.02E-08	8.08E-08	1.066666667	0.093109404
BP1026B	I2483	hypothetical protein	69215	46634	57219	22	50743	53199	53460	20	7.33E-14	3.87E-13	0.909090909	-0.137503524
BP1026B	I2484	outer membrane porin	29997	24543	24355	16	27742	27776	31020	18	6.55E-06	1.27E-05	1.125	0.169925001
BP1026B	I2485	amidase	15747	13638	12574	11	14440	14971	14925	12	8.25E-06	1.59E-05	1.090909091	0.125530882
BP1026B	I2486	hypothetical protein	22099	14343	12086	10	21070	24036	28227	15	0.115405024	0.132211409	0.875	-0.584962501
BP1026B	I2487	acetyltransferase	47669	23250	30212	104	33928	39641	41860	118	4.54E-06	8.99E-06	1.134615385	0.182203331
BP1026B	I2488	acetyltransferase	8063	2831	3770	8	5829	7620	10731	13	0.395483512	0.42289326	1.625	0.700439718
BP1026B	I2489	hypothetical protein	6562	4595	4763	10	6474	6717	6884	12	0.004074307	0.005602955	1.2	0.263034406
BP1026B	I2490	TldD/PmbA family protein	48886	28366	30928	26	45498	51776	59952	38	0.053349593	0.064019512	1.461538462	0.54787795
BP1026B	I2491	ABC transporter ATP-binding protein	120675	95114	99208	73	119647	119882	116296	82	8.39E-07	1.84E-06	1.123287671	0.167727446
BP1026B	I2492	ABC transporter ATP-binding protein	28452	11647	14874	43	18378	19971	29624	54	9.83E-04	0.00457929	1.255813953	0.328622747
BP1026B	I2493	sensor kinase protein	1425	2403	1753	19	1176	1240	1240	11	6.60E-18	5.63E-17	0.578947368	-0.784805995
BP1026B	I2494	LuxR family DNA-binding response regulator	87119	80700	84724	60	70267	70788	80728	52	7.76E-12	3.25E-11	0.866666667	-0.206450877
BP1026B	I2495	hypothetical protein	81887	65666	69069	111	74047	75147	80741	118	2.30E-06	4.74E-06	1.063063063	0.088227183
BP1026B	I2496	hypothetical protein	170918	155705	154819	268	114443	117005	110965	191	5.05E-29	1.38E-27	0.712686567	-0.488660362
BP1026B	I2497	hypothetical protein	3348	2779	3492	11	2477	3178	3070	10	2.61E-08	7.02E-08	0.909090909	-0.137503524
BP1026B	I2498	sensor box protein	35409	47108	41766	55	35522	36146	35377	48	1.19E-14	6.85E-14	0.872727273	-0.196397213
BP1026B	I2499	permease	58728	63632	59880	25	50706	48713	46165	20	7.51E-21	9.10E-20	0.8	-0.321928095
BP1026B	I2500	4'-phosphopantetheinyl transferase	9015	10815	9634	8	8734	8789	8789	15	1.52E-11	1.63E-11	0.875	-0.924645078
BP1026B	I2501	hypothetical protein	1276	176	314	0	1245	1579	1881	2	1.79E-08	4.91E-08	#DIV/0!	#DIV/0!
BP1026B	I2502	hypothetical protein	6301	6834	5695	15	5632	6346	6287	15	6.09E-07	1.36E-06	1	0
BP1026B	I2503	hypothetical protein	10747	5812	5957	5	10160	11507	10869	8	0.091559693	0.105934599	1.6	0.678071905
BP1026B	I2504	permease	3454	3663	4011	4	4044	3619	3746	4	3.83E-05	6.75E-05	1	0
BP1026B	I2505	ABC-transporter ATP binding protein	4034	3405	3709	2	4733	4380	4391	3	0.006802161	0.009118069	1.5	0.584962501
BP1026B	I2506	flavin-binding monooxygenase-like protein	1358	1193	1137	1	1921	2014	2152	2	0.752665374	0.76974627	2	1
BP1026B	I2507	cytochrome P450 family protein	5125	5037	5268	3	5169	5286	4849	3	4.94E-06	9.75E-06	1	0
BP1026B	I2508	beta keto-acyl synthase	9103	6679	6073	1	9725	9949	11589	2	0.080466086	0.093722493	2	1
BP1026B	I2509	acyl transferase domain-containing protein	63725	51229	54203	8	76242	77699	78129	11	0.04510332	0.054657999	1.375	0.459431619
BP1026B	I2510	hypothetical protein	10644	11909	11272	6	10812	12448	13790	7	2.17E-05	3.96E-05	1.666666667	0.222392421
BP1026B	I2511	hypothetical protein	267	765	626	4	179	427	521	2	3.60E-08	9.52E-08	0.5	-1
BP1026B	I2512	lipoprotein VacJ	57150	46180	47368	19	53372	54949	56503	27	5.91E-07	1.32E-06	1.052631579	0.074000581
BP1026B	I2513	hypothetical protein	36411	41988	41336	40	40282	39492	37776	39	2.46E-10	8.52E-10	0.975	-0.036525876
BP1026B	I2514	hypothetical protein	2603	2732	2918	5	3437	2699	3602	5	0.003723368	0.00514279	1	0
BP1026B	I2515	hypothetical protein	5501	4858	4559	3	6062	5706	6178	4	0.001679914	0.002428007	1.333333333	0.415037499
BP1026B	I2516	glutamine ABC transporter ATP-binding protein	2157	847	1281	1	1417	2103	1953	1	0.050598976	0.060882056	1	0
BP1026B	I2517	glutamine ABC transporter permease	6471	9341	9218	11	7555	6146	6642	9	2.10E-12	9.38E-12	0.818181818	-0.289506617
BP1026B	I2518	glutamine ABC transporter periplasmic protein	1581	2644	2335	3	2115	1879	1463	2	2.90E-10	9.96E-10	0.666666667	-0.584962501
BP1026B	I2519	hypothetical protein	2895	4660	3996	5	4161	4634	4010	5	5.93E-04	9.05E-04	1	0
BP1026B	I2520	hypothetical protein	4573	1994	2030	4	6136	5721	6259	8	0.071193549	0.083653422	2	1
BP1026B	I2521	squalene-hopene cyclase	131708	97746	100000	55	151595	161503	168172	81	0.04850719	0.052038949	1.472727273	0.558490289
BP1026B	I2522	squalene hydroxylase synthase	104367	90105	106438	118	78370	75314	76722	90	5.79E-18	4.16E-17	0.762711864	-0.390789953
BP1026B	I2523	esterase EstC	43004	32354	36670	41	36979	38979	38511	42	7.34E-09	2.12E-08	1.024390244	0.034765418
BP1026B	I2524	diguanylate cyclase	181174	161636	167336	181	144238	137585	134147	148	2.19E-22	3.15E-21	0.817679558	-0.290392521
BP1026B	I2525	response regulator	131445	127018	122714	203	114633	113698	105208	178	3.27E-15	2.03E-14	0.876847291	-0.189602486
BP1026B	I2526	response regulator	159528	219761	201994	525	158255	150449	125358	392	1.81E-29	5.08E-28	0.746666667	-0.421463768
BP1026B	I2527	hypothetical protein	1241	1879	1549	5	1191	1963	1854	6	5.87E-04	8.98E-04	1.2	0.263034406
BP1026B	I2528	sensor histidine kinase/response regulator	196502	174811	178086	80	161730	166847	150490	69	5.55E-18	4.80E-17	0.8625	-0.213403638
BP1026B	I2529	NADPH-dependent FMN reductase domain-containing protein	195027	307469	283064	469	246321	234440	224264	421	2.13E-09	6.62E-09	0.897654584	-0.155767689
BP1026B	I2530	RNA polymerase sigma factor	83055	134632	121720	186	100006	103993	102990	168	1.33E-12	6.07E-12	0.903225806	-0.146841388
BP1026B	I2531	hypothetical protein	22421	30768	31724	142	31459	30691	27288	150	7.35E-07	1.63E-06	1.056338028	0.079071571
BP1026B	I2532	arsenate reductase	12562	23607	19904	52	13178	13414	12968	36	2.17E-19	2.25E-18	0.692307692	-0.530514717
BP1026B	I2533	hypothetical protein	192	437	212	2	329	280	580	4	0.687667869	0.70906198	2	1
BP1026B	I2534	ParA family protein	72120	128210	115609	158	62219	58578	57596	89	8.36E-44	6.16E-42	0.563291139	-0.828047317
BP1026B	I2535	parB family protein	128348	208338	191156	164	155021	153220	153619	144	3.16E-18	2.84E-17	0.87804878	-0.187672003
BP1026B	I2536	plasmid replication protein	171596	247659	220214	154	113388	113413	107134	80	3.03E-65	3.75E-63	0.519408519	-0.944858446
BP1026B	I2537													

Appendix E:

Supplemental Table 1 for Chapter 3

Supplemental Table 1: Total transcriptome of BP1026B_H11561

Synonym	Product	Empty Vector				BP1026B_H11561				pValue	qValue	Fold Change	Log2FC
		Replicate 1	Replicate 2	Replicate 3	RPKM	Replicate 1	Replicate 2	Replicate 3	RPKM				
BP1026B_0001	carboxylate-amine ligase	94552	134638	122576	105	81129	9048	88792	78	1.33E-12	2.28E-11	0.742857143	-0.428843299
BP1026B_0002	hypothetical protein	74985	79794	79007	64	75130	67802	70909	58	2.15E-06	9.05E-06	0.90625	-0.142019005
BP1026B_0003	hypothetical protein	1963125	3361208	2848114	8107	1869900	2328933	2252416	6400	7.08E-04	0.001592175	0.789441224	-0.341096238
predicted RNA	-	108337	151673	137578	2137	104109	112415	117533	1796	8.19E-10	7.72E-09	0.84043051	-0.250799558
BP1026B_0004	5-methylaminomethyl-2-thiouridine methyltransferase	77169	56465	58132	32	94754	74354	75984	41	0.102189522	0.13553289	1.28125	0.357552005
BP1026B_0005	DNA-binding protein HU	4277852	5543088	5491260	18294	4663314	5788048	5502786	19061	0.075168072	0.102931524	1.041926315	0.095253253
BP1026B_0006	cobalamin synthase protein P47K family protein	126978	116428	116962	88	136993	130752	132982	99	0.003496828	0.006555969	1.112329551	0.153633189
BP1026B_0007	HspH1	101263	149395	138058	266	95211	117157	114378	224	1.00E-09	9.24E-09	0.842105263	-0.247927513
BP1026B_0008	general secretion pathway protein D	475474	515661	516546	221	493994	539719	514580	226	0.58238651	0.632336915	1.02262434	0.032276403
BP1026B_0009	general secretion pathway protein E	258506	230963	234487	161	260498	240950	254989	168	6.81E-04	0.00153775	1.043478261	0.061400545
BP1026B_0010	general secretion pathway protein F	151419	141768	144897	119	177189	170001	160304	138	0.030829338	0.046191679	1.159663866	0.213706693
BP1026B_0011	general secretion pathway protein C	14575	7049	6971	23	16618	12303	13318	34	0.458135089	0.512461022	1.47826087	0.563900885
BP1026B_0012	general secretion pathway protein G	196653	308039	277302	575	198980	235454	221423	182	7.89E-09	5.89E-08	0.83826087	-0.254523881
BP1026B_0013	general secretion pathway protein H	87047	72469	75208	132	97437	99042	94447	164	0.039144118	0.05724224	1.24242392	0.31157885
BP1026B_0014	general secretion pathway protein I	74678	67849	72461	202	81107	77084	78951	113	0.002932965	0.005605877	1.079603692	0.142688417
BP1026B_0015	general secretion pathway protein J	122197	107277	116232	189	134498	121296	125023	208	0.001922129	0.003827783	1.005291001	0.138197294
BP1026B_0016	general secretion pathway protein K	52600	52361	45967	46	54943	51360	53733	49	0.001406751	0.00290568	1.065217391	0.091147888
BP1026B_0018	general secretion pathway protein L	58828	53523	59066	39	66643	61638	57132	43	0.002554115	0.00496036	1.102564103	0.140862536
BP1026B_0017	general secretion pathway protein M	62558	61381	63656	123	67422	68893	64762	132	0.001686035	0.003409574	1.073170732	0.101879614
BP1026B_0019	general secretion pathway protein N	107272	52821	72203	97	107715	95263	98544	126	0.088730068	0.119442858	1.298969072	0.377367081
BP1026B_0020	RND efflux system outer membrane lipoprotein	31141	32715	30137	19	29164	29995	32821	18	7.31E-05	2.08E-04	0.947368421	-0.078002512
BP1026B_0021	hypothetical protein	34039	33145	32348	121	32937	31562	34572	113	1.17E-05	4.08E-05	0.933884298	-0.09684275
BP1026B_0022	MarR family protein	59075	57123	59095	118	72707	64148	67752	138	0.01982921	0.031088427	1.169491525	0.225881407
BP1026B_0023	hypothetical protein	4006	6470	5971	43	3855	4360	4226	32	1.92E-07	1.04E-06	0.744186047	-0.426264755
BP1026B_0024	EmrB/QacA family drug resistance transporter	40627	40383	40076	25	38659	39066	41189	25	3.30E-04	8.10E-04	1	0
BP1026B_0025	LysR family transcriptional regulator	26617	21651	22617	25	33277	29381	28972	33	0.090035024	0.121017721	1.32	0.40053793
BP1026B_0027	LrgA family protein	3460	875	1271	3	3708	2290	2908	6	0.670802436	0.714300404	1	1
BP1026B_0028	hypothetical protein	13765	11305	12666	16	14377	12546	14607	18	0.001161413	0.002454489	1.125	0.16992500
BP1026B_0029	flagellar body-associated protein FliH	39183	51556	50143	86	57637	38042	35450	65	2.29E-10	0.05724224	0.75813929	-0.431396942
BP1026B_0030	flagellar motor switch protein FliM	330514	449988	410852	397	285201	317565	313063	305	2.67E-06	1.09E-05	0.768261965	-0.380327665
BP1026B_0031	flagellar motor switch protein FliN	129990	106418	104964	238	154668	121732	131858	273	0.028001427	0.042387295	1.197368421	0.259867127
BP1026B_0032	flagellar protein FliO	28025	23201	23880	37	27532	23572	27879	39	6.90E-04	0.00156826	1.054054054	0.075948853
BP1026B_0033	flagellar biosynthesis protein FliP	62197	84026	79885	98	58028	69787	69664	86	2.26E-07	1.21E-06	0.87755102	-0.188445089
BP1026B_0034	flagellar biosynthesis protein FliQ	24535	30482	28557	102	20736	22460	22044	79	1.64E-09	1.43E-08	0.774509804	-0.368644594
BP1026B_0035	flagellar biosynthetic protein FliR	53457	37291	39866	51	41343	39875	42629	52	0.001331171	0.002367795	1.019607843	0.028014376
BP1026B_0036	MarR family protein	53104	33124	32348	121	32937	31562	34572	113	1.17E-05	4.08E-05	0.933884298	-0.09684275
BP1026B_0037	hypothetical protein	2667	2360	3013	65	3098	3581	2708	3	0.03526442	0.049836818	1	0
BP1026B_0038	ATP-binding cassette, ABC transporter	358	225	197	0	314	445	272	0	0.686877617	0.729931101	#DIV/0!	#DIV/0!
BP1026B_0039	ABC transporter ATP-binding protein	20071	19690	19995	19	20020	21414	21558	20	0.001157834	0.002448784	1.052631579	0.074000581
BP1026B_0040	ABC transporter permease	3832	3069	2954	3	3341	3059	3821	3	0.003692173	0.006893155	1	0
BP1026B_0041	sensor kinase protein	3783	2551	3526	3	3211	4064	3473	4	0.016100904	0.025785287	1.333333333	0.415037499
BP1026B_0042	DNA-binding response regulator	7245	4555	5602	4	7881	6478	6614	5	0.036601899	0.053214842	1.25	0.321928095
BP1026B_0043	outer membrane porin	2585	1374	1040	0	2369	2366	2366	4	0.23691754	0.23691754	1.333333333	0.333333333
BP1026B_0044	type III DNA modification methyltransferase	30026	37920	34494	16	35750	34918	31920	16	5.25E-04	0.00121069	1	0
BP1026B_0045	type III restriction enzyme	50960	50783	49289	16	57944	55989	54628	18	0.007165719	0.012472407	1.125	0.169925001
BP1026B_0046	outer membrane porin	1339	1637	1499	1	1883	2054	2218	1	0.326890158	0.380089335	1	0
BP1026B_0047	AraC family transcriptional regulator	5695	5734	6078	6	5972	6334	6738	6	0.005980043	0.010593846	1	0
BP1026B_0048	branched-chain amino acid ABC transporter ATP-binding protein	1366	1125	1215	1	1926	1173	1243	1	0.047993539	0.068767353	1	0
BP1026B_0049	branched chain amino acid ABC transporter ATP-binding protein	1324	582	543	1	1180	840	1094	1	0.490586162	0.543794678	1	0
BP1026B_0050	protein/permease	444	437	325	0	749	587	607	0	0.20140831	0.248053392	#DIV/0!	#DIV/0!
BP1026B_0051	branched chain amino acid ABC transporter permease	1120	382	604	0	946	889	1082	1	0.977483435	0.9821354	#DIV/0!	#DIV/0!
BP1026B_0052	hypothetical protein	3044	3224	2680	2	3528	3575	3704	2	0.126214614	0.163515959	1	0
BP1026B_0053	phenylacetaldehyde dehydrogenase	8802	5811	7302	4	8731	7842	7804	5	0.004247652	0.00780478	1.25	0.321928095
BP1026B_0054	hypothetical protein	2520	2408	2612	6	2956	2552	2800	7	0.001395873	0.002804859	1.166666667	0.222392421
BP1026B_0055	short chain dehydrogenase/reductase family oxidoreductase	5672	5683	5941	5	5809	5633	4648	7	7.54E-05	2.14E-04	0.833333333	-0.26304406
BP1026B_0056	glucose-methanol-choline oxidoreductase	3873	2108	2630	3	3067	2927	2760	3	5.92E-04	0.00131801	0	0
BP1026B_0057	glucose-methanol-choline oxidoreductase	10987	8940	8772	5	11835	9524	9933	6	9.12E-04	0.001982905	1.2	0.26304406
BP1026B_0058	hypothetical protein	7509	10801	9663	28	8320	10046	8704	27	1.81E-05	6.05E-05	0.964285714	-0.05246742
BP1026B_0059	fatty acid desaturase	57603	45527	46584	42	63244	64123	64207	53	0.169283429	0.212966709	1.261904762	0.335603032
BP1026B_0060	hypothetical protein	13149	6785	8050	9	16717	10635	12440	13	0.278427972	0.33156227	1.444444444	0.530514717
BP1026B_0061	hypothetical protein	18890	11502	10629	16	24626	17793	19130	24	0.617162301	0.665656566	1.5	0.584962501
BP1026B_0062	AraC family transcriptional regulator	10609	11263	11511	11	11546	15363	15248	13	0.022408170	0.034716327	1.524088	0.214008
BP1026B_0063	acyl-CoA dehydrogenase	113647	126324	121742	99	19758	22520	22520	0	0	0	0	0
BP1026B_0064	acyl-CoA acyltransferase	9421	10303	10824	8	2374	2495	2914	2	9.58E-157	5.01E-154	0.25	-2
BP1026B_0065	fatty oxidation complex subunit alpha	36826	25542	26851	14	13539	12444	11895	5	2.33E-51	8.59E-49	0.357142857	-1.485426827
BP1026B_0066	alpha-methylacyl-CoA racemase	32430	15041	19162	19	32884	21924	23729	23	0.015769243	0.025318777	1.210526316	0.275634443
BP1026B_0067	lipoprotein	71412	72779	75496	129	81658	89123	80823	147	0.004322699	0.012883482	1.139548884	0.188445089
BP1026B_0068	hypothetical protein	1996	2055	2613	4	2197	2259	2660	5	9.53E-04	0.002064238	1.25	0.321928095
BP1026B_0069	hypothetical protein	158860	72664	62539	244	185331	165927	155783	383	0.515748417	0.657993927	1.569672181	0.650462444
BP1026B_0070	lipoprotein	12782	11077	119244	323	131754	129884	129416	32	0.005755502	0.00532869	1.092879229	0.128134018
predicted RNA	-	9656	17466	16329	629	10967	13499	11820	525	5.88E-09	4.53E-08	0.834568188	-0.260742594
BP1026B_0071	transmembrane regulator PrtR	2936	671	899	1	3867	2212	3278	4	0.004609537	0.00386202	1	0
BP1026B_0072	ECF sigma factor PrtI	3805	2424	2719	5	5085	3566	3139	7	0.3973634	0.451568951	1.4	0.485426827
BP1026B_0073	catalase	3688	3070	3672	3	3735	3300	3308	3	0.001286346	0.002685274	1	0
BP1026B_0074	cytochrome B561	2868	3625	2892	5	2361	3045	2704	5	3.98E-07	1.98E-0		

BP1026b_1019	homoserine/homoserine lactone efflux protein	41898	46465	48949	71	48602	55974	53924	83	0.019970766	0.031295682	1.169014085	0.225292312
BP1026b_1020	M48 family peptidase	449099	479416	465886	541	540095	556590	550228	639	0.819221373	0.846758226	1.181146026	0.240187337
predicted RNA	-	7028	257	576	145	14429	4201	6180	459	4.49E-10	4.56E-09	3.165517241	1.662441253
BP1026b_1021	ribosomal RNA small subunit methyltransferase B	92582	4759	50154	44	117400	8120	9309	9	0.92960855	0.935043388	1.568181818	0.649928338
BP1026b_1022	hypothetical protein	320888	353231	322166	561	339398	316216	338616	560	0.019828598	0.031088427	0.998217469	-0.002573944
BP1026b_1023	sensor kinase protein	468250	530023	513469	209	452380	499402	493105	199	0.303965888	0.356407071	0.95215311	-0.070734512
BP1026b_1024	DNA-binding response regulator	291769	253575	253384	397	297533	301501	305098	460	0.085408774	0.115542212	1.158690176	0.212494854
BP1026b_1025	Phe tRNA	9627	16515	13093	172	9316	11847	10875	140	1.37E-09	1.21E-08	0.813953488	-0.296981738
BP1026b_1026	prophage integrase	86099	139062	121397	102	77715	97916	89928	78	9.87E-12	1.41E-10	0.764705882	-0.387023123
BP1026b_1027	hypothetical protein	16331	15116	16586	5	17258	15264	17242	5	4.01E-04	9.53E-04	1	0
BP1026b_1028	hypothetical protein	810	247	397	1	1009	824	748	3	0.04628669	0.04609314	1	0
BP1026b_1029	hypothetical protein	923	1114	1245	3	652	1245	898	2	1.80E-05	6.01E-05	0.666666667	-0.584962501
BP1026b_1030	hypothetical protein	848	1643	1315	6	664	957	575	3	7.30E-17	3.12E-15	0.5	-1
BP1026b_1031	hypothetical protein	2177	1800	2066	8	2009	1910	1680	7	4.31E-06	1.67E-05	0.875	-0.192645078
BP1026b_1032	putative phage-encoded membrane protein	1943	1808	1521	9	1430	1493	1497	7	5.62E-07	2.70E-06	0.777777778	-0.362570079
BP1026b_1033	hypothetical protein	1903	2249	2004	10	1999	1533	1942	9	5.85E-07	2.80E-06	0.9	-0.152003093
BP1026b_1034	hypothetical protein	3371	3566	3353	15	2817	3324	2890	13	3.22E-06	1.29E-05	0.866666667	-0.206450877
BP1026b_1035	Phage Rha protein	13455	20788	20367	15	12704	14399	13907	25	1.01E-11	1.43E-10	1.086666667	-0.40657393
BP1026b_1036	Phage transcriptional activator	3170	4396	4376	15	3480	3561	3124	13	3.76E-06	1.48E-05	0.866666667	-0.206450877
BP1026b_1037	putative phage DNA-binding protein	5532	7255	6243	21	3936	4520	5257	15	1.06E-08	7.69E-08	0.714285714	-0.485426827
BP1026b_1038	hypothetical protein	5560	8992	8548	32	5463	6231	6071	24	2.83E-08	1.86E-07	0.75	-0.415037499
BP1026b_1039	Putative phage DNA-binding protein	89966	148328	129589	267	90026	122806	110016	234	2.27E-08	1.53E-07	0.876404494	-0.190331212
BP1026b_1040	putative phage-encoded membrane protein	107249	174229	165029	205	112659	148704	137093	183	1.36E-07	7.62E-07	0.892682927	-0.163780261
BP1026b_1041	hypothetical protein	186738	331860	283593	618	237088	318286	276962	642	6.12E-04	0.001394541	1.038834951	0.054966549
BP1026b_1042	hypothetical protein	124489	179851	155387	139	128212	144863	148722	126	4.22E-07	2.08E-06	0.90647482	-0.141661469
BP1026b_1043	Phage-related tail fiber protein	1466	845	1456	2	1456	1408	1406	3	0.24720002	0.24720002	1	0
BP1026b_1044	bacteriophage tail protein	12463	13889	12018	4	9885	12690	11129	3	9.29E-08	5.45E-07	0.75	-0.415037499
BP1026b_1045	hypothetical protein	1079	1427	1848	12	1079	1227	703	8	1.18E-10	1.35E-09	0.666666667	-0.584962501
BP1026b_1046	putative phage tail protein	1776	1894	1941	5	2215	2166	2282	6	0.024763479	0.037897365	1.2	0.263034406
BP1026b_1047	Major tail tube protein	3071	5136	5623	9	3663	4119	3736	7	7.35E-06	2.68E-05	0.777777778	-0.362570079
BP1026b_1048	Phage tail sheath monomer	2777	3093	2229	2	2289	2994	2827	2	2.18E-04	5.56E-04	1	0
BP1026b_1049	phage tail fiber assembly protein	1307	1366	977	1	1434	1474	1778	2	0.184900485	0.23408816	2	0
BP1026b_1050	Phage-related tail fiber protein	5741	6250	5385	1	5817	4051	4987	1	0.081E-04	0.00152175	1	0
BP1026b_1051	phage tail protein I	1930	729	1178	2	1989	1287	1773	3	0.206994145	0.253955461	1.5	0.584962501
BP1026b_1052	phage baseplate assembly protein	5666	3538	3392	4	6184	4369	4140	5	0.039384994	0.057575311	1.25	0.321928095
BP1026b_1053	Phage baseplate assembly protein	413	684	448	1	834	472	389	1	0.11971332	0.146821941	1	0
BP1026b_1054	baseplate assembly protein V	1190	1100	1156	1	1488	1038	932	1	0.004003155	0.007405424	1	0
BP1026b_1057	hypothetical protein	2044941	3563938	3261699	5866	1131387	1435824	1310468	2564	7.56E-10	7.23E-09	0.437095124	-1.193980809
BP1026b_1058	Phage tail completion protein	13704	44994	15205	31	10900	12360	12033	25	5.39E-10	5.35E-09	0.806451613	-0.310340121
BP1026b_1059	bacteriophage tail completion protein R	1951	30123	3043	6	24053	2407	2636	743	0.801E-07	1.90E-06	0.833333333	-0.263034406
BP1026b_1060	Prophage LysC protein	275	144	274	1	305	309	471	2	0.148750175	0.189521744	1	0
BP1026b_1061	Putative phage-encoded lipoprotein	662	539	831	1	610	624	570	1	6.96E-04	0.00158013	1	0
BP1026b_1062	Putative phage-encoded peptidoglycan binding protein	1383	1413	1407	1	1220	1482	1464	1	7.47E-04	0.001664246	1	0
BP1026b_1063	Prophage membrane protein	878	424	488	2	566	541	588	2	0.005430199	0.009702158	1	0
BP1026b_1064	Prophage membrane protein	115	97	80	0	148	161	208	0	0.058776179	0.082483886	#DIV/0!	#DIV/0!
BP1026b_1065	Phage-related tail protein	137	114	173	0	128	190	234	0	0.899579137	0.915635231	#DIV/0!	#DIV/0!
BP1026b_1066	putative bacteriophage protein	143	33	35	0	128	143	142	0	0.199269923	0.24597014	#DIV/0!	#DIV/0!
BP1026b_1067	Phage head completion-stabilization protein	310	96	187	0	395	256	442	0	0.017828499	0.02097484	#DIV/0!	#DIV/0!
BP1026b_1068	Phage terminase, endonuclease subunit	969	713	495	1	1034	699	1020	1	0.433210346	0.487186995	1	0
BP1026b_1069	Phage major capsid protein	2882	3327	3107	3	3308	3336	4246	3	0.073443848	0.100922948	1	0
BP1026b_1070	Phage capsid scaffolding protein	1049	1131	1146	1	1006	873	842	1	3.19E-06	1.28E-05	1	0
BP1026b_1071	Phage terminase, ATPase subunit	5608	4376	5798	2	5425	5872	5292	3	0.004064245	0.007496327	1.125	0.584962501
BP1026b_1072	Phage portal protein	8059	8977	9322	8	9291	10157	10509	9	0.003196461	0.00606632	1	0
BP1026b_1073	addiction module holin protein	13590	13980	13590	346	10708	126120	13228	346	6.39E-15	1.26E-14	1.008666667	0.169952501
BP1026b_1074	addiction module killer protein	76383	125407	117378	33	75671	100000	87597	278	5.23E-09	4.10E-08	0.834834835	-0.260437294
BP1026b_1075	ATPase	100600	171672	155017	113	92700	125533	108430	86	3.49E-13	6.70E-12	0.761061947	-0.393914208
BP1026b_1076	hypothetical protein	4231	6485	5133	44	5044	6494	5725	47	0.008029887	0.013834518	1.068181818	0.095157233
BP1026b_1077	phage baseplate assembly protein	4254	4359	4295	13	4040	3938	4353	12	7.52E-04	0.00167377	0.923076923	-0.115477217
BP1026b_1078	phage tail protein I	2249	1380	1417	4	2101	2036	2076	5	0.060718515	0.085038456	1.25	0.321928095
BP1026b_1079	Phage-encoded modification methylase	4404	4302	4361	9	5121	5432	5444	11	0.008622927	0.08181736	1.222222222	0.289506617
BP1026b_1080	hypothetical protein	18087	30930	29080	431	33912	30788	30788	743	0.081E-04	0.00393866	0.557883529	0.082426146
BP1026b_1081	phage tail completion protein	32776	28341	31152	84	34091	39278	35988	99	0.046432693	0.066729045	1.178571429	0.237039197
BP1026b_1082	type VI secretion system	172678	181056	175989	224	162525	185405	168748	219	3.93E-05	1.20E-04	0.977678571	-0.032567862
BP1026b_1083	type VI secretion system	148356	157439	160591	115	140016	159238	158136	113	4.82E-05	1.44E-04	0.982608696	-0.025311089
BP1026b_1084	type VI secretion system	23243	37319	32300	47	23070	29054	27582	40	2.13E-07	1.14E-06	0.85106383	-0.232660757
BP1026b_1085	hypothetical protein	3098	6277	5851	48	2966	4503	3786	35	3.60E-08	2.31E-07	0.729166667	-0.455679484
BP1026b_1086	lipoprotein	301862	324352	343905	481	311317	337744	325714	483	0.018089802	0.028677616	1.004158004	0.009596295
BP1026b_1087	type VI secretion system	35774	402711	383190	734	421912	438312	438312	743	0.04429167	0.04429167	1.01226188	0.01752148
BP1026b_1088	type VI secretion system	944830	1425388	1270642	813	8990435	1040800	1005724	63	0.20244935	0.249061536	0.808888889	-0.309595337
BP1026b_1089	type VI secretion system	2482174	3435758	3059294	5733	2382825	2715688	2680660	4967	0.003004129	0.005272993	0.866387581	-0.206915532
BP1026b_1090	type VI secretion system	170463	213068	203472	405	156317	181685	173536	353	6.50E-08	3.95E-07	0.871604938	-0.198253725
BP1026b_1091	type VI secretion system	204398	205045	199383	110	186466	190291	190911	102	4.53E-06	1.74E-05	0.927272727	-0.108934372
BP1026b_1092	type VI secretion system	64788	71260	70105	62	57537	57149	56435	51	9.44E-09	6.96E-08	0.822580645	-0.281770968
BP1026b_1093	type VI secretion system	254396	204854	216056	84	231378	206565	217095	81	5.14E-05	1.52E-04	0.964285714	-0.05246742
BP1026b_1094	type VI secretion system	64298	68176	65539	58	59941	64202	58751	54	4.63E-06	1.77E-05	0.931034483	-0.103093493
BP1026b_1095	type VI secretion system	125953	141056	137316	144	116234	128760	122373	131	2.19E-07	1.20E-06	0.909722222	-0.136501
BP1026b_1096	type VI secretion system	137165	151219	150468	147	145159	149165	142593	147	7.80E-05	2.20E-04	0.907222222	-0.136501
BP1026b_1097	type VI secretion system	748119	863467	837708	209	791308	800400	791786	204	0.854864344	0.877980032	0.976076555	-0.0349379
BP1026b_1098	hypothetical protein	61692	77555	74841	135	65066	72828	73603					

BP1026b	10243	peptidase	137180	122372	127773	70	136590	128872	125055	71	7.51E-05	2.13E-04	1.014285714	0.020464103
BP1026b	10244	acyl carrier protein phosphodiesterase	48553	52846	49172	84	51813	50411	48232	84	1.85E-04	4.79E-04	1	0
BP1026b	10245	uracil-DNA glycosylase	19695	11978	12965	18	22142	17493	19134	24	0.131993218	0.170228918	1.333333333	0.415037499
BP1026b	10246	adenylate cyclase	216663	116666	13287	23	23164	20343	20890	24	0.25913907	0.308699473	1.431786604	0.520832163
BP1026b	10247	Indole-3-glycerol phosphate synthase	86341	84084	83373	107	97754	94236	94263	121	0.003737413	0.00635659	1.13084121	0.177296251
BP1026b	10248	anthranilate phosphoribosyltransferase	85158	76271	80427	78	93995	91651	92735	89	0.006577631	0.011548134	1.141025641	0.19031212
BP1026b	10249	anthranilate synthase component II	65302	80186	74094	123	67219	75824	72684	121	5.65E-05	1.66E-04	0.983739837	-0.023651268
BP1026b	10250	anthranilate synthase component I	130255	136244	134711	89	153341	152775	152585	102	0.01403917	0.02335378	1.146066714	0.196691191
BP1026b	10251	phosphoglycolate phosphatase	53721	63554	59556	80	60915	64036	58077	83	9.95E-04	0.001357855	1.0375	0.053111336
BP1026b	10252	ribulose-phosphate 3-epimerase	73542	71201	75386	105	79299	83099	79677	115	0.002472668	0.004823087	1.095238095	0.131244533
BP1026b	10253	APG protein	73161	103236	90758	72495	89941	81594	82246	288	1.15E-06	5.31E-06	0.911582669	-0.13385745
BP1026b	10255	hypothetical protein	19130	32342	30872	191	21306	27315	25006	170	1.48E-06	6.45E-06	0.890523256	-0.168037892
BP1026b	10254	membrane-bound lytic murein transglycosylase A	191739	221169	224321	189	201809	230078	216780	193	3.74E-04	8.97E-04	1.021164021	0.030214613
BP1026b	10256	phenylacetate-CoA ligase	45203	51937	49286	37	35722	38263	39179	29	1.04E-09	9.52E-09	0.783783784	-0.351472371
BP1026b	10257	phenylacetic acid degradation protein PaaI	18848	22049	21277	52	14827	17914	19171	44	7.55E-08	4.51E-07	0.846153846	-0.2410081
BP1026b	10258	enoyl-CoA hydratase	28107	22355	22762	30	20845	19343	19627	25	2.99E-08	1.95E-07	0.833333333	-0.263034406
BP1026b	10259	beta-ketoadipyl CoA thiolase	47800	32405	33740	31	43552	32716	35481	30	3.41E-04	8.26E-04	0.967741955	-0.047305715
BP1026b	10260	phenylacetic acid degradation protein paaN	133920	123224	129663	75	100312	98384	96219	57	9.26E-13	1.62E-11	0.84558206	-0.395926676
BP1026b	10261	enoyl-CoA hydratase	27032	41914	34197	44	29781	32836	32734	40	1.14E-05	4.00E-05	0.909090909	-0.137503524
BP1026b	10262	hypothetical protein	98673	144993	118040	1043	103856	142927	136480	1091	3.27E-04	7.95E-04	1.046021093	0.064911944
BP1026b	10263	16S ribosomal RNA	1470237	358169	295827	466	590527	2505052	691736	831	0.011939292	0.019750838	1.783261803	0.834518522
BP1026b	10264	Ile tRNA	36831	54022	44410	585	36729	49256	48012	580	2.42E-04	6.08E-04	0.991452991	-0.012387324
BP1026b	10265	Ala tRNA	195031	304882	242783	3257	207377	261738	281136	3290	1.55E-04	4.07E-04	1.010132023	0.014543864
BP1026b	10266	hypothetical protein	40459	61383	51609	396	53949	73206	69394	507	0.163369818	0.206116296	1.2803003	0.356485317
BP1026b	10267	23S ribosomal RNA	728539	491771	255334	382	802504	1549893	653260	313	0.011443459	0.03903097	1.7197802	0.78230420
BP1026b	10268	SS ribosomal RNA	344564	476391	314195	33490	347569	123516	446943	3559	0.08076893	0.10987483	1.062014303	0.02292825
BP1026b	10269	anaerobic dehydrogenase	122676	174222	159657	81	122040	137024	144473	69	7.19E-09	5.43E-08	0.851851852	-0.231325546
BP1026b	10270	long-chain-fatty-acyl-CoA ligase	251689	280906	263615	158	235524	246380	252899	146	2.01E-06	8.50E-06	0.924050685	-0.113956189
BP1026b	10271	outer membrane porin	61200	75358	72615	60	61241	70892	66460	57	1.54E-05	5.24E-05	0.95	-0.074000581
BP1026b	10272	hypothetical protein	81706	44744	52747	95	101197	88933	97064	152	0.735415022	0.771964263	1.6	0.678071905
BP1026b	10273	cell division protein MraZ	1419076	2358733	2085899	4556	1392882	1701176	1612996	3657	0.007473727	0.01294386	0.802677788	-0.31710712
BP1026b	10274	S-adenosyl-methyltransferase MraW	545591	721969	683058	690	523102	604112	564876	598	0.22649619	0.274572331	0.866666667	-0.206408077
BP1026b	10275	cell division protein FtsI	40378	40378	45122	136	38195	38195	38195	15	3.48E-07	8.88E-08	0.84558206	-0.24297229
BP1026b	10276	penicillin-binding protein	313322	339297	342634	179	319846	360839	338416	184	0.035292851	0.052165895	1.027952961	0.039746179
BP1026b	10277	UDP-N-acetylmuramoylalanine-D-glutamate-2,6-diaminopimelate ligase	297551	164957	185317	139	329185	262921	276048	187	0.652194262	0.698278649	1.345323741	0.427953387
BP1026b	10278	UDP-N-acetylmuramoyl-tripeptide-D-alanyl-D-alanine ligase	187811	120443	130479	106	190843	167659	167659	125	0.048922908	0.069987092	1.179245283	0.273866383
BP1026b	10279	phospho-N-acetylmuramoyl-pentapeptide-transferase	191129	271686	243864	201	2000515	243585	234111	193	2.50E-05	8.03E-05	0.960199045	-0.058944654
BP1026b	10280	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	215013	145309	166402	114	284594	207007	211771	153	0.430609805	0.484696808	1.342105263	0.424497829
BP1026b	10281	cell division protein FtsW	271108	289159	278189	216	255707	267344	284448	208	1.75E-05	5.86E-05	0.962962963	-0.05447784
BP1026b	10282	undecaprenyl-diphosphate-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	213392	117349	141916	142	229459	169282	187508	177	0.164466578	0.207418344	1.246477873	0.317858431
BP1026b	10283	UDP-N-acetylmuramate-L-alanine ligase	325403	242775	251301	195	340854	281120	280767	215	0.029738087	0.044733577	1.102564013	0.140862536
BP1026b	10284	D-alanine-D-alanine ligase	204034	217990	208002	223	206699	208993	220323	225	2.61E-04	6.52E-04	1.00896661	0.012881291
BP1026b	10285	cell division protein FtsQ	132797	105767	114673	156	139585	128751	130464	176	0.005392102	0.009639401	1.128205131	0.1740294
BP1026b	10286	cell division protein FtsA	410504	533750	499827	390	376166	422618	405508	325	0.001585412	0.003521318	0.833333333	-0.263034406
BP1026b	10287	cell division protein FtsZ	1160637	1409967	1377483	1099	1440571	1145280	1145280	115	0.04444872	0.058933857	1.22987444	0.1608438
BP1026b	10288	predicted RNA	63013	2996	5618	385	94552	40242	55483	1022	3.38E-07	1.72E-06	2.654545455	1.408464845
BP1026b	10289	AhpC/TSA family protein	857138	689646	720051	1490	835536	817852	781333	1600	0.750973157	0.786059055	1.073825503	0.102759574
BP1026b	10290	predicted RNA	98053	33499	68140	1512	94510	101572	86554	2141	0.404085868	0.458212338	1.416002591	0.501826656
BP1026b	10291	UDP-N-acetylglucosamine deacetylase	496524	609190	564234	587	598613	622164	621272	647	0.943596943	0.952862786	1.1102214651	0.140405209
BP1026b	10292	hypothetical protein	31518	8202	8557	20	11972	11843	11361	24	0.06882711	0.01202653	1.2	0.263034406
BP1026b	10293	preprotein translocase subunit SecA	1055192	1253570	1222942	422	1147280	1244780	1180796	427	0.539747426	0.591102585	1.011848341	0.016995071
BP1026b	10294	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase	102084	124976	115788	92	111956	117084	117525	93	4.16E-05	1.26E-04	1.010806955	0.01596855
BP1026b	10295	putative ATP/GTP-binding protein	92774	122008	110813	124	97685	110233	107580	120	6.55E-06	2.42E-05	0.967741935	-0.047305715
BP1026b	10296	NUDIX family pyrophosphatase	56357	70635	71787	147	62975	72878	63919	147	1.66E-04	4.33E-04	1	0
BP1026b	10297	32098	43117	37962	184	28784	29530	30190	144	4.36E-10	4.43E-09	0.78260669	-0.353636955	
BP1026b	10298	799969	1117708	1018576	1294	774662	902261	847720	1113	0.457629401	0.511986666	0.860123648	-0.217384025	
BP1026b	10299	dephospho-CoA kinase	45239	47038	48967	76	42191	42734	46416	72	4.47E-05	7.95E-05	0.947368421	0.078002512
BP1026b	10300	type IV pilus assembly protein PilQ	17404872	17404872	17404872	19	21549	20339	22343	23	0.04444872	0.058933857	1.22987444	0.1608438
BP1026b	10301	type IV pilus assembly protein PilQ	9750	6486	7880	6	9118	8139	10364	7	0.004576775	0.00834113	1.166666667	0.222924221
BP1026b	10302	type IV fibrillogenesis protein, PilB	7502	5922	5214	4	7359	6369	6884	5	0.015885929	0.025493076	1.25	0.321928095
BP1026b	10303	hypothetical protein	80094	111498	102713	81	68120	78334	81600	62	6.76E-11	8.13E-10	0.765432099	-0.385653692
BP1026b	10304	Pro tRNA	12836	19503	15883	208	15184	21180	19181	240	0.010194565	0.017135721	1.153846154	0.206450877
BP1026b	10305	octaprenyl-diphosphate synthase	212327	300692	279204	266	212114	246205	239616	234	1.29E-07	7.25E-07	0.879699248	-0.184917716
BP1026b	10306	50S ribosomal protein L27	472653	598524	598016	2107	641150	717170	679844	2573	0.71216777	0.659207473	1.221167537	0.288261143
BP1026b	10307	GTPase ObgG	318263	418536	408466	339	403618	478069	430618	365	0.142380801	0.162496953	1.067617012	0.29781883
BP1026b	10308	gamma-glutamyl kinase	106108	113283	107707	97	117816	119516	115814	115	0.03E-04	0.001375628	0.082474227	0.11432675
BP1026b	10309	lipoprotein	27254	38872	35576	60	26568	32491	32360	54	1.97E-06	8.33E-06	0.9	-0.152003093
BP1026b	10310	dinucleoside polyphosphate hydrolase	474179	769531	686874	988	401989	493011	484916	706	0.006993414	0.012202973	0.714574899	-0.484842858
BP1026b	10311	prolyl-tRNA synthetase	608678	674214	660282	379	620798	638341	610790	365	0.487693528	0.541277689	0.963060686	-0.054301384
BP1026b	10312	hypothetical protein	153206	201638	183490	297	141832	150975	157804	249	1.60E-0			

BP1026b	10359	cyanate hydratase	2739	4071	4103	7	3194	3811	3393	7	4.26E-04	0.001006213	1	0
BP1026b	10360	carbonic anhydrase	5977	3988	5366	7	6588	6729	6108	9	0.009084171	0.122110335	1.285714286	0.362570079
BP1026b	10361	DNA-binding transcriptional regulator CynR	54318	48711	49380	54	67066	58510	65064	67	0.110529432	0.145143631	1.240740741	0.311201688
BP1026b	10362	hypothetical protein	26352	30150	36551	73	37014	51574	37043	90	0.117320004	0.153070591	1.232876712	0.302036337
BP1026b	10363	GntR family transcriptional regulator	32555	41824	39722	54	63079	33737	35356	49	6.76E-06	2.50E-05	0.907407407	-0.140177658
BP1026b	10364	C4-dicarboxylate transporter DctA	4561	5794	3906	3	4028	4519	4312	3	1.40E-04	3.70E-04	1	0
BP1026b	10365	allantoicase	2488	1371	1884	1	30719	2653	2423	2	0.47071755	0.524850905	2	1
BP1026b	10366	ureidoglycolate hydrolase	1765	906	688	2	2306	1285	2232	3	0.233284575	0.282290535	1.5	0.584962501
BP1026b	10367	ferric uptake regulator	292300	491317	442070	952	264579	324679	295105	687	1.04E-08	7.58E-08	0.721638655	-0.470651474
BP1026b	10368	outer membrane lipoprotein	107173	113733	120344	144	100051	118590	121227	144	2.02E-08	6.64E-05	1	0
BP1026b	10369	dihydroxydipicolinate reductase	79484	74590	72191	73	8842	79744	83995	104	0.003352401	0.006318994	1.11827957	0.161289091
BP1026b	10370	MetA/TotQ/ExbB protein channel family protein	41334	32669	33446	50	43705	41022	44444	60	0.072507767	0.09978965	1.2	0.263034406
BP1026b	10371	biopolymer ExbD/TolR family transporter	15731	15086	14818	28	14708	14718	15642	28	5.10E-05	1.51E-04	1	0
BP1026b	10372	leucyl-tRNA synthetase	366616	391641	393565	147	402215	406367	404489	155	0.175126538	0.219450414	1.054421769	0.07645206
BP1026b	10373	lipoprotein	44616	77567	67425	120	44241	53451	54500	96	9.77E-10	9.07E-09	0.8	-0.321928695
BP1026b	10374	DNA polymerase III subunit delta	148615	101033	111890	110	193442	158241	157057	155	0.776674319	0.809315283	1.409090909	0.494764692
BP1026b	10375	gamma-glutamyl phosphate reductase	149102	161856	154665	122	160243	155412	160432	124	4.06E-04	9.65E-04	0.161394344	0.023458973
BP1026b	10376	hypothetical protein	57488	61641	55983	137	33140	56163	55498	129	0.0814085	0.79E-05	0.941608539	-0.066104828
BP1026b	10377	RpiR family transcriptional regulator	6058	4027	4456	4	8355	6369	7124	4	0.546985285	0.597985133	1.75	0.07354922
BP1026b	10378	phosphoglucomate dehydratase	28837	17588	19598	11	40753	34997	34269	19	0.537569363	0.589231629	1.727272727	0.788495895
BP1026b	10379	KHG/KDPG aldolase	21569	14596	19095	29	29263	24554	27168	43	0.477695118	0.530915014	1.482758621	0.56828376
BP1026b	10380	GntP family high-affinity gluconate permease	181257	189426	179468	134	239969	253580	243116	179	0.393926574	0.447906724	1.335820886	0.417726587
BP1026b	10381	shikimate kinase	156720	172605	171547	321	193458	206035	194391	381	0.055531176	0.078509593	1.186915891	0.2472717
BP1026b	10382	adenylosuccinate lyase	199240	230061	222401	156	212775	221567	224621	158	2.90E-04	7.16E-04	0.101282051	0.018378529
BP1026b	10383	nitrile hydratase	3847	3841	2635	2	4728	3309	3596	2	0.035294685	0.012678611	1.363636364	0.231325546
BP1026b	10384	lysate transcriptional regulator	22826	20320	142655	22	27084	2001495	173451	53	2.40E-09	2.12E-08	0.446464646	-0.19592103
BP1026b	10385	glutamate dehydrogenase	2303325	2193923	2228183	1717	2307307	2323573	2305148	1771	0.062000447	0.086698351	1.031450204	0.044674173
BP1026b	10386	glutamate/aspartate periplasmic binding protein	3203310	4928241	4494758	4707	3275850	3783689	3389428	3877	8.55E-04	0.001872791	0.82366679	-0.2796711
BP1026b	10387	glutamate/aspartate transport system permease	143469	230945	208701	262	158801	185740	168547	230	1.20E-07	6.82E-07	0.877862595	-0.17372951
BP1026b	10388	glutamate/aspartate ABC transporter, permease protein	183833	231744	213352	309	185538	212128	204982	296	2.45E-05	7.89E-05	0.957928803	-0.062009662
BP1026b	10389	Cystine ABC transporter, ATP-binding protein	383989	569901	541241	686	410069	534777	545824	642	0.224801187	0.273184395	0.935608605	-0.095635279
BP1026b	10390	hypothetical protein	36638	59215	497171	189	45520	53589	52265	197	0.006403	0.002148246	1.043230402	0.05908905
BP1026b	10391	chaperonin 10.4/14	114141	15841	142655	435	163029	173451	173451	53	0.1884067	0.14294287	1.225876035	0.291120332
BP1026b	10392	HSP20 family protein	85050	121781	115296	243	106245	135253	116538	270	0.001741292	0.003508873	1.111111111	0.152003093
BP1026b	10393	HSP20 family protein	66548	54864	60080	144	90608	90527	86254	212	0.699279224	0.741226525	1.472222222	0.557995453
BP1026b	10394	hypothetical protein	29080	24549	28369	124	34176	35840	34592	159	0.130423788	0.168412603	1.282258065	0.358666645
BP1026b	10395	hypothetical protein	323750	476779	426331	430	282726	335839	333144	333	1.60E-05	5.41E-05	0.774418605	-0.368814483
BP1026b	10396	dihydroorotase	51162	37416	43230	11	49096	53551	54931	52	0.15881087	0.200974292	1.268292683	0.342887714
BP1026b	10397	hypothetical protein	11459	5608	39216	11	50031	8606	9941	15	0.12552336	0.16287611	1.363636364	0.047458977
BP1026b	10398	hypothetical protein	2431640	40353143	35961912	360686	9143935	16894125	14594983	16102	2.49E-09	2.12E-08	0.446464646	-0.19592103
BP1026b	10399	predicted RNA	17145556	21840312	19409099	123196	9134933	9876899	10506398	62293	1.32E-06	5.79E-06	0.50564147	-0.983813456
BP1026b	10400	OsmC/Otr family protein	76759	80223	76696	184	70024	70791	76120	170	4.32E-06	1.67E-05	0.923913043	-0.11417102
BP1026b	10401	SOS ribosomal protein L13	784712	1336394	1229570	2068	1066317	1367310	1213344	2251	0.797919038	0.828288288	1.088491296	0.122329871
BP1026b	10402	SOS ribosomal protein S9	376653	474626	432268	1088	512635	560303	531756	1361	0.548955629	0.600034615	1.250911918	0.32298851
BP1026b	10403	iron-sulfur cluster insertion protein ErpA	488078	770057	661398	1733	560373	693042	682636	1748	0.622141914	0.670796876	1.009651001	0.01243533
BP1026b	10404	AraC family transcriptional regulator	27743	18538	19124	23	29560	22996	24312	27	0.01408327	0.022828713	1.173913043	0.231325546
BP1026b	10405	glutathione S-transferase	36494	59684	46143	58	59684	40961	37714	58	0.0014084	0.0014084	0.0014084	0.0014084
BP1026b	10406	glutathione S-transferase-like protein	53514	59674	60940	83	55906	55710	54167	79	1.60E-05	5.42E-05	0.951807229	-0.071258683
BP1026b	10407	anhydride-N-acetylmuramic acid kinase	47237	36646	35291	34	49390	43168	46244	39	0.033260256	0.049949783	1.147058824	0.197939378
BP1026b	10408	tyrosyl-tRNA synthetase	186429	201139	201810	158	197567	210063	203940	164	7.15E-04	0.001601253	1.037974684	0.053771256
BP1026b	10409	D-tyrosyl-tRNA (Tyr) deacylase	14056	7023	6262	20	15992	11196	13418	30	0.474393189	0.528198167	1.5	0.584962501
BP1026b	10410	phosphoglycerate mutase	28143	23376	25937	38	36283	32270	32092	50	0.146577912	0.187249311	1.315789474	0.359298308
BP1026b	10411	lipoprotein	15291	19908	16283	15	15916	17624	15092	14	1.35E-05	4.64E-05	0.933333333	-0.099535674
BP1026b	10412	hypothetical protein	265376	25666	33012	39	4275388	493370	439370	47	0.023253888	0.023253888	1.205129305	0.04686633
BP1026b	10413	Holliday junction DNA helicase RuvB	179259	106897	122706	127	172610	148745	163872	151	0.048960525	0.070024937	1.189767378	0.249720053
BP1026b	10414	Holliday junction DNA helicase RuvA	128847	131918	124135	220	98341	96791	100107	169	2.57E-12	4.17E-11	0.768181818	-0.380480277
BP1026b	10415	Holliday junction resolvase	31946	19188	23542	45	28097	24712	26059	48	8.12E-04	0.001792408	1.066666667	0.093109404
BP1026b	10416	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	231275	204489	217854	139	233534	227512	230592	147	0.001591671	0.003242791	1.057553957	0.080731272
BP1026b	10417	DNA-binding protein Fis	23034	37907	33502	34	17888	22947	22829	90	3.70E-14	8.65E-13	0.671641391	-0.57426094
BP1026b	10418	dihydroxydipicolinate synthase	82375	88824	89862	80	88962	92370	99362	92	2.05E-04	2.46E-04	0.937078635	0.04828525
BP1026b	10419	hypothetical protein	32387	12265	16900	17	37331	25419	27097	25	0.466419688	0.520706657	1.074058235	0.556393499
BP1026b	10420	aminopeptidase P	76779	39292	47852	38	89542	65052	67641	52	0.33358944	0.386604888	1.368421053	0.452512205
BP1026b	10421	predicted RNA	165794	162342	172173	882	180434	171447	167209	915	7.08E-04	0.001592175	1.037414966	0.052993088
BP1026b	10422	glutathione S-transferase	130620	154284	153732	238	138846	151080	144769	236	6.20E-05	1.80E-04	0.991596639	-0.012174714
BP1026b	10423	glutamate synthase domain-containing protein	135564	100729	109397	70	161721	159571	157412	97	0.589270073	0.638757762	1.385714286	0.470629825
BP1026b	10424	(RNA-specific 2-thiohydriylase MmmA	129172	164371	147464	129	129418	139802	136255	119	0.907E-07	4.16E-06	0.92248062	-0.116409492
BP1026b	10425	NAD(P) transhydrogenase subunit alpha	54073	58068	58068	133	58068	58068	58068	133	0.555680838	0.606676123	1.037611111	0.584962501
BP1026b	10426	NAD(P) transhydrogenase subunit alpha	240559	228408	249229	209	229402	258219	229762	209	1.27E-04	3.41E-04	0	0
BP1026b	10427	NAD(P) transhydrogenase subunit beta	79463	101311	92834	276	61868	67641	66574	198	1.81E-13	3.64E-12	0.717391304	-0.479167837
BP1026b	10428	NAD(P) transhydrogenase subunit beta	563421	719136	660021	445	435855	495928	477704	323	0.012480318	0.020521373	0.725842697	-0.462271171
BP1026b	10429	DeoR family transcriptional regulator	36584	28092	33860	47	40537	36936	34921	54	0.			

BP1026b	10590	hypothetical protein	21296	14612	15295	42	28695	19567	20778	56	0.177668238	0.222457656	1.333333333	0.415037499
predicted RNA	-	-	63096	37160	43283	520	71574	60774	57083	686	0.292062889	0.34516023	1.319230769	0.399669053
BP1026b	10591	TonB-dependent siderophore receptor family protein	49832	22197	28003	15	51821	43157	44789	22	0.576791845	0.62696504	1.466666667	0.552541023
BP1026b	10592	iron chelate uptake ABC transporter, ATP-binding component	9174	58986	6495	8	10469	80938	80938	24	0.02507378	0.07500833	0.07500833	0.459831610
BP1026b	10593	periplasmic binding protein	26301	22642	24894	23	25422	23860	26612	24	3.59E-04	8.66E-04	1.043777778	0.61400545
BP1026b	10594	FecD-family membrane transporter protein	6239	1885	2766	3	7833	4946	5296	5	0.731456671	0.768431274	1.666666667	0.736965594
BP1026b	10595	LysR family regulatory protein	23580	10058	13301	16	28075	20576	23521	25	0.715094782	0.754929244	1.5625	0.64385619
BP1026b	10596	DSBA-like thioresoxin domain-containing protein	79939	75480	71971	118	90701	83029	81659	133	0.004058755	0.007488071	1.127118644	0.172639386
BP1026b	10597	hypothetical protein	36182	34764	35658	24	38032	35567	35104	25	0.001211995	0.002558592	1.041666667	0.058891689
BP1026b	10598	phospholipid-binding domain-containing protein	75296	61153	57781	175	72957	67706	69759	190	0.002116453	0.004178945	1.085714286	0.118644496
BP1026b	10599	D-2,3-hydroxybutyrate-oligomer hydrolase	26707	174721	186242	90	22873	212898	208136	103	0.01785942	0.028362667	0.977777778	0.144444444
BP1026b	10600	hypothetical protein	300	874	301	4	246	301	338	2	6.16E-08	3.76E-07	0.5	0.194647431
BP1026b	10601	hypothetical protein	6616	8692	6847	23	5937	9406	7642	24	8.52E-04	0.001866846	1.043478261	0.061400545
BP1026b	10602	serine-type carboxypeptidase family protein	122954	141398	143532	74	112969	136309	120563	67	2.03E-07	1.10E-06	0.905405405	-0.143364175
BP1026b	10603	permease	24073	16711	15781	23	25621	23132	23455	30	0.007786879	0.106258637	1.304347826	0.38332864
BP1026b	10604	EmrB/QacA family drug resistance transporter	24783	20733	23282	16	27563	24994	26243	18	0.003260459	0.006164214	1.125	0.169925001
BP1026b	10605	glycerophosphoryl diester phosphodiesterase family protein	87234	73517	83135	71	95948	90340	91243	81	0.004767343	0.008655728	1.14084507	0.190102883
BP1026b	10606	amino acid transporter LysT	8906	7532	6188	12	71953	25931	7926	14	0.014038402	0.02280313	0.977777778	-0.032424781
BP1026b	10607	acetyltransferase	1001	541	538	1	1458	939	967	2	0.09292706	0.23949212	1.225	1
BP1026b	10608	DNA-binding protein	4153	2501	3056	5	5209	4572	5900	8	0.730645366	0.767985654	1.6	0.678071905
BP1026b	10609	metallo-beta-lactamase family protein	40976	62443	52961	42	45128	52080	45697	38	3.78E-06	1.49E-05	0.904761905	-0.144389999
BP1026b	10610	transcriptional regulator	11380	14722	11379	28	10662	12352	12676	27	4.24E-06	1.64E-05	0.964285714	-0.05246742
predicted RNA	-	-	2229975	406275	3825314	12107	2284037	3394394	2582804	9941	8.87E-04	0.001933514	0.821095234	-0.284378533
BP1026b	10611	lipoprotein	79249	86727	83509	52	75544	81223	75228	48	4.07E-06	1.59E-05	0.923076923	-0.115477217
BP1026b	10612	lipoprotein	60997	61786	58575	48	58931	60450	58175	47	6.46E-05	1.86E-04	0.979166667	-0.030373649
BP1026b	10613	OmpW family outer membrane protein	45024	40714	41653	45	37624	39067	39548	199	7.12E-06	2.81E-05	0.80625	-0.142090046
BP1026b	10614	activator protein	316074	335518	350145	658	214831	229651	216767	427	1.26E-17	5.97E-16	0.64893617	-0.623851514
BP1026b	10615	hypothetical protein	36462	21170	24739	26	36621	31340	31505	32	0.041017798	0.059685605	0.239769231	-0.299560282
BP1026b	10616	zinc-binding alcohol dehydrogenase	99984	84959	87485	90	103003	96507	101996	99	0.001512245	0.003102694	1.1	0.137503524
BP1026b	10617	transcriptional regulator family protein	108663	175756	154048	335	116461	145548	142698	310	1.12E-06	5.02E-06	0.925373134	-0.11189288
BP1026b	10618	hypothetical protein	258	467	247	2	650	589	615	4	0.171317028	0.215235673	2	1
BP1026b	10619	hypothetical protein	2414	2413	2642	6	2195	2663	1793	5	6.12E-10	6.00E-09	0.833333333	-0.263034406
BP1026b	10620	hypothetical protein	12630	12923	11215	5	11733	12361	11035	5	6.12E-06	1.23E-05	0.833333333	0
BP1026b	10621	co-chaperonin GroES	3174987	5060037	4436660	14366	3448999	4311290	3878998	12993	0.007492118	0.012971958	0.904427212	-0.144923842
BP1026b	10622	chaperonin GroEL	30255598	43174830	40058502	23052	34685947	40762772	36861782	22813	0.200814912	0.247536243	0.989632136	-0.015035746
BP1026b	10623	hydroxymethylpyrimidine kinase	166314	159836	164748	192	182311	165487	166331	201	0.001094344	0.002326268	1.046875	0.06608919
BP1026b	10624	rubredoxin	138008	222506	196036	1212	142851	197030	171504	114	1.59E-06	6.87E-06	0.919141914	-0.121640466
BP1026b	10625	hypothetical protein	111949	66766	67533	61	160831	99899	116536	94	0.802532363	0.890990794	1.549806047	-0.628515114
BP1026b	10626	hypothetical protein	836518	1098608	1000595	1690	827707	903079	903103	1516	0.596684537	0.646216427	1.04936702	0.156753493
BP1026b	10627	Holliday junction resolvase-like protein	192463	110757	105601	309	213645	150788	174284	107	0.392155828	0.446784146	1.317152014	0.397421956
BP1026b	10628	bifunctional pyrimidine regulatory protein Pyr/Ruracil phosphoribosyltransferase	56591	32556	44313	85	60298	58676	54664	111	0.240069197	0.289885289	1.305882353	0.0282493
BP1026b	10629	aspartate carboxyltransferase catalytic subunit	78885	79073	77853	76	84089	81160	82023	79	4.77E-04	0.00100665	1.039473684	0.055853235
BP1026b	10630	dihydroorotase	264009	235707	240571	193	254746	235856	245565	192	8.51E-05	2.39E-04	0.994818653	-0.044945377
BP1026b	10631	acetyltransferase family protein	304786	260015	271961	320	301906	285146	289902	339	0.008091523	0.013917775	1.059375	0.083213368
BP1026b	10632	condensin tetraphosphatase	61809	44243	49356	61	67924	49983	54624	67	0.000034629	0.01066645	1.093636676	0.135351853
BP1026b	10633	gDTP-glucose 4-6-dehydratase	216180	228418	23215	213	217146	232784	212783	199	7.12E-06	2.81E-05	0.80625	-0.142090046
BP1026b	10634	glucose-1-phosphate thymidyl synthase	330468	412050	389312	422	300437	340931	320717	358	4.48E-04	0.001048838	0.848341232	-0.237283411
BP1026b	10635	gDTP-4-dehydrohamose 3,5-epimerase	119722	213547	178916	309	110785	141783	128777	239	1.91E-14	4.80E-13	0.74433657	-0.425972977
BP1026b	10636	gDTP-4-dehydrohamose reductase	147392	222722	190898	208	136088	155888	147474	163	5.28E-12	8.12E-11	0.783653846	-0.357171564
BP1026b	10637	ABC-2 type transport system integral membrane protein	39949	69000	56618	66	43711	53650	51969	59	1.46E-06	6.38E-06	0.893939394	-0.16175107
BP1026b	10638	polysaccharide ABC transporter, ATP-binding protein	190074	288599	257566	174	165167	211411	196246	135	2.05E-11	2.68E-10	0.775862069	-0.366127899
BP1026b	10639	O-antigen acetylase WbIA	165769	260270	230043	176	146337	193457	169891	137	1.51E-11	2.03E-10	0.734000991	-0.361399536
BP1026b	10640	NAD-dependent epimerase/dehydratase	222686	321459	303621	293	254409	270248	233208	239	0.234E-06	0.995E-06	0.816096959	-0.203890046
BP1026b	10641	glycosyltransferase	447412	592142	515210	249	293932	364611	444096	284	2.76E-07	1.44E-06	0.68891298	-0.537567975
BP1026b	10642	O-antigen methyl transferase	501928	800576	714432	389	435624	532824	505596	364	0.01880514	0.029631912	0.730077121	-0.453879225
BP1026b	10643	glycosyl transferase family protein	274042	435725	395054	199	217696	266941	253005	133	1.74E-15	5.37E-14	0.668341709	-0.581342185
BP1026b	10644	glycosyl transferase WbfI	68419	108708	96948	95	59703	77074	70615	72	1.55E-11	2.08E-10	0.757894377	-0.399930607
BP1026b	10645	UDP-glucose 4-epimerase	67696	74881	70119	73	99619	64040	65936	65	7.47E-07	3.48E-06	0.890410959	-0.167456746
BP1026b	10646	glycoside hydrolase family protein	480808	57493	57816	53	93538	468440	442227	44	5.09E-08	3.16E-07	0.830186676	-0.268488836
BP1026b	10647	polysaccharide biosynthesis protein	121288	108138	200947	96	159260	172922	152731	87	6.31E-07	1.99E-06	0.97106676	-0.124090046
BP1026b	10648	glycosyl transferase family protein	80841	104076	93488	83	78636	83137	90432	75	7.59E-07	3.53E-06	0.903614458	-0.146220741
BP1026b	10649	UDP-glucose 4-epimerase	161786	148556	157411	152	161181	171233	166964	162	0.002507018	0.004881297	1.065780474	0.091922489
BP1026b	10650	glycoside hydrolase family protein	16629	9947	10495	10	17056	14165	13854	13	0.018644351	0.029422896	1.3	0.378511623
BP1026b	10651	glycosyl transferase family protein	16635	10377	10458	14	195172	16520	19139	21	0.491805182	0.544877059	1.5	0.584962501
BP1026b	10652	hypothetical protein	19027	12016	13309	11	20483	17920	19816	14	0.127626244	0.165063778	1.272727273	0.347333033
BP1026b	10653	phosphoglucomutase/phosphomannomutase family protein	608559	569468	574604	411	719721	665598	653688	479	0.874359555	0.894413904	1.165450102	0.220887262
BP1026b	10654	phosphoglucomutase heptosyltransferase I	121288	108138	200947	96	159260	172922	152731	87	0.125006761	0.16215037	1.260069655	-0.124090046
BP1026b	10655	hypothetical protein	287306	328456	302877	346	275586	284872	299825	323	6.53E-05	8.8E-04	0.93352601	-0.099237873
BP1026b	10656	3-deoxy-D-manno-oxulosonic-acid transferase	46964	14276	20695	19	53200	33965	41202	30	0.833481318	0.858808854	1.578947368	0.658963082
BP1026b	10657	urease accessory protein UreG	33295	44562	38474	59	30257	34032	31451	49	2.88E-08	1.88E-07	0.830504875	-0.267933205
BP1026b	10658	urease accessory protein	8603	7089	6273	10	8877	6195	74					

BP1026b	10709	glucose-6-phosphate 1-dehydrogenase	192461	158114	170642	118	198193	185881	187720	129	0.005133614	0.009229912	1.093322060	0.128584266
BP1026b	10710	maltose ABC transporter, periplasmic maltose-binding protein	508866	585131	567436	443	497722	531099	509136	410	0.295628223	0.348389225	0.925507901	-0.111682789
BP1026b	10711	ABC transporter permease	103042	98374	94185	104	93014	100436	102435	105	4.01E-05	1.22E-04	1.009615385	0.0138058
BP1026b	10712	ABC transporter permease	133728	164980	158545	177	124018	129066	129085	149	1.79E-09	1.55E-08	0.84180791	-0.24843703
BP1026b	10713	ABC transporter ATP-binding protein	387030	512178	465812	406	351041	382603	379304	331	1.90E-04	4.90E-04	0.815270936	-0.29464851
BP1026b	10714	hypothetical protein	32501	19674	20675	39	41788	29218	32988	55	0.50763488	0.559903055	1.41025641	0.495957495
BP1026b	10715	Snr domain-containing protein	46527	36540	37294	54	50809	50725	45740	66	0.086390449	0.116744353	1.222222222	0.28906617
BP1026b	10716	thioredoxin-disulfide reductase	318947	276296	296027	308	386673	399028	379576	403	0.609943898	0.658668611	1.308441558	0.387849488
BP1026b	10717	cell division flsk transmembrane protein	390894	381411	388470	167	393634	404409	421226	176	0.187551257	0.233434332	1.053891222	0.075727326
BP1026b	10718	outer-membrane lipoprotein carrier protein	59405	53779	54592	78	61885	63516	68843	91	0.017606516	0.02800467	1.166666667	0.222392421
BP1026b	10719	recombination factor protein RarA	87855	53263	59858	50	98779	92660	86574	68	0.206479247	0.247219641	0.797872937	0.443696651
BP1026b	10720	hypothetical protein	16642	17091	19432	66	15077	18826	19914	63	2.94E-05	9.30E-05	0.954545455	-0.067114196
BP1026b	10721	seryl-tRNA synthetase	370916	393724	375716	291	377704	387390	383781	294	0.038501644	0.05639057	1.010309278	0.014797002
BP1026b	10722	Ser tRNA	24941	42025	35720	376	19528	27340	22360	253	2.22E-14	5.55E-13	0.67287234	-0.571595277
BP1026b	10723	hypothetical protein	1001737	1768776	1600447	5336	819087	1085064	932737	3463	0.019457143	0.035055904	0.648988006	-0.623736279
BP1026b	10725	acetyltransferase	64894	45827	52614	95	65524	66143	68943	116	0.067915997	0.094047914	1.221052632	0.288125387
BP1026b	10726	septum formation inhibitor	86601	90167	92752	110	97556	101206	97528	121	0.001313121	0.002734692	1.1	0.137053524
BP1026b	10727	septum site-terminating protein MinD	208636	276459	254994	302	194666	224554	213081	258	3.06E-08	1.99E-07	0.854304636	-0.227177484
BP1026b	10728	cell division topological specificity factor MinE	26715	21990	23211	94	23825	25868	26869	100	0.001087466	0.002314	0.063829787	0.089267338
BP1026b	10729	hypothetical protein	1610	1685	1665	3	3447	1771	2264	5	0.90179969	0.91727998	1.666666667	0.736955954
BP1026b	10730	hypothetical protein	2123	420	825	11	1796	1165	1452	14	0.349466662	0.403008471	1.272727273	0.347923303
BP1026b	10731	voltage gated chloride channel family protein	33995	30948	28887	18	34103	29393	32555	19	5.51E-04	0.001267011	1.055555556	0.078002521
BP1026b	10732	lipopolysaccharide heptosyltransferase I	43219	38645	39697	39	41191	33854	35856	36	1.70E-05	5.72E-05	0.923076923	-0.115477217
BP1026b	10733	hypothetical protein	47966	25020	32194	191	41675	41709	41005	226	0.05590161	0.077956368	1.183246073	0.242750134
BP1026b	10734	metalloprotein symporter family protein	12044	8608	8714	14	19095	14312	15773	12	0.731524928	0.768431274	1.714285714	0.07677579
BP1026b	10735	TonB domain-containing protein	10412	8625	14908	20	11084	10924	10940	30	0.011E-05	0.000000000	0.927872937	0.443696651
BP1026b	10736	hypothetical protein	2320	2476	2569	4	2190	2370	1635	3	3.26E-08	2.11E-07	0.75	-0.415037499
BP1026b	10737	integrase	1054	2039	1434	7	917	1170	1216	5	3.90E-09	3.14E-08	0.714285714	-0.485426827
BP1026b	10738	Integrase	5560	5904	6037	25	4347	5649	5935	23	9.03E-05	2.52E-04	0.92	-0.120294234
BP1026b	10739	Ser tRNA	771	665	1129	9	646	601	688	7	5.51E-07	2.64E-06	0.777777778	-0.362570079
BP1026b	10740	coproporphyrinogen III oxidase	70466	61922	64409	53	78404	76523	80472	64	0.02670674	0.040593986	1.2057417	0.272079545
BP1026b	10741	deoxyribonucleotide triphosphate pyrophosphatase	59005	30846	37539	67	82259	57676	61204	106	0.528199086	0.580128938	1.58208952	0.661831264
BP1026b	10742	ribonuclease HI	111971	59249	74684	50	139016	139016	139016	13	0.948670254	1.02773	1.576576577	0.659792345
BP1026b	10743	hypothetical protein	138190	145150	149992	156	167258	175592	167995	184	0.04716952	0.068402295	1.19487179	0.238159373
BP1026b	10744	guanylate kinase	120053	169049	159501	218	152075	175148	162084	238	0.005303601	0.009070698	1.09174319	0.126633439
BP1026b	10745	DNA-directed RNA polymerase subunit omega	55407	63395	66233	302	60412	61398	64072	303	1.82E-04	4.71E-04	1.00331258	0.046792944
BP1026b	10746	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	381188	514967	471359	192	390111	435330	418484	174	0.030300205	0.04551561	0.90625	-0.142019005
BP1026b	10747	Arg tRNA	21835	34578	25784	355	24827	30277	28687	362	2.40E-04	6.04E-04	1.01971831	0.028170673
BP1026b	10748	Arg tRNA	9627	15855	14309	172	10463	12617	11780	150	8.74E-08	5.14E-07	0.407393023	-0.194746064
BP1026b	10749	transcription elongation factor GreB	16134	68257	68257	1184	498232	55824	548672	93	0.08783218	0.11838464	0.797872937	0.443696651
BP1026b	10750	outer membrane protein	6989723	9451373	9207339	7473	6599596	7701848	6804584	6171	4.37E-04	0.00102693	0.825727282	-0.276183228
BP1026b	10751	hypothetical protein	14283	17057	14791	58	12736	13985	15960	53	2.48E-06	1.02E-05	0.913793103	-0.130600541
BP1026b	10752	cold shock transcription regulator protein	14913593	25284887	22233287	102012	26383372	37534720	31952387	156651	0.957792961	0.965454579	1.53613457	0.618815108
BP1026b	10753	DNA polymerase/helicase	65085	61065	60792	54	74384	73420	73110	64	0.022919186	0.035420561	1.18158185	0.182512498
BP1026b	10754	chorismate mutase	10272	4422	5552	11	11906	7890	8856	16	0.26436676	0.315880173	1.545454555	0.540568381
BP1026b	10755	hypothetical protein	37987	60506	51631	340	29780	34563	35836	227	1.80E-15	5.44E-14	0.667647059	-0.582842449
BP1026b	10756	hypothetical protein	19250	8801	8801	192	14949	15996	15996	16	0.06868397	0.084132	0.927872937	0.443696651
BP1026b	10757	TonB-dependent receptor	43348	40772	41230	17	39286	38028	39937	16	4.63E-05	1.39E-04	0.94117674	-0.087462841
BP1026b	10758	lipoprotein	15176	8179	8958	8	15560	13586	13962	11	0.007101041	0.133705896	1.375	0.459431619
BP1026b	10759	hypothetical protein	8628	2476	3684	9	8378	6362	7523	14	0.551062247	0.602323313	1.555555556	0.637429921
BP1026b	10760	hypothetical protein	219665	219693	218316	869	228201	221434	222542	889	4.51E-04	0.001055718	1.02301496	0.032872422
BP1026b	10761	hypothetical protein	1293	658	1265	4	1183	963	1327	4	0.02988734	0.044927698	1	0
BP1026b	10762	hypothetical protein	1055	680	1030	1	1297	1150	900	2	0.288607075	0.34165544	2	1
BP1026b	10763	hypothetical protein	451	183	451	1	1210	109	652	1	0.046472344	0.06677031	2	1
BP1026b	10764	The tRNA	701	632	465	7	396	534	556	6	1.39E-04	3.68E-04	0.857142857	-0.222392421
BP1026b	10765	fructose 1,6-bisphosphatase	305064	355273	341286	328	298106	319177	323118	308	0.00270923	0.005224408	0.939024927	-0.090765464
BP1026b	10766	transcriptional activator protein	9602	6805	9660	9	9598	9327	8584	9	4.09E-04	9.72E-04	1	0
BP1026b	10767	5-methyltetrahydropteroyltylgutamate/homocysteine S-methyltransferase	12005	9805	9823	4	11436	10054	10504	4	5.39E-05	1.59E-04	1	0
BP1026b	10768	aminopectidase N	205161	254852	225173	82	204378	222132	215991	79	4.20E-08	1.27E-04	0.963414634	-0.053771256
BP1026b	10769	lipoprotein	251047	235496	244851	341	223877	237720	237447	324	1.17E-05	4.04E-05	0.963414634	-0.053771256
BP1026b	10770	hypothetical protein	36849	29972	34070	58	32478	34588	35333	59	8.22E-04	0.001730726	1.017243179	0.024662505
BP1026b	10771	guanine deaminase	21010	12952	12903	11	22010	18290	20040	15	0.09150973	0.12276316	0.26636364	-0.44758977
BP1026b	10772	xanthine/uracil permease family protein	13661	16519	14688	10	14607	14612	16287	11	1.38E-04	3.67E-04	1.1	0.137053524
BP1026b	10773	adenosine deaminase	40210	38606	39722	38	43235	43104	42345	41	0.006641276	0.011643578	1.07894788	0.109624491
BP1026b	10774	xanthine dehydrogenase accessory factor	16522	10252	10392	12	17108	14181	15537	15	0.042060924	0.061047734	1.25	0.321928905
BP1026b	10775	DsbB family disulfide bond formation protein	13011	9608	10971	21	13845	13202	12744	26	0.0071545	0.012456336	1.238095238	0.308122295
BP1026b	10776	amidase	19051	69059	69059	146	12952	14688	14688	10	0.187235284	0.23087306	1.272727273	0.423871429
BP1026b	10777	glutamine amidotransferase	312979	320518	336801	243	303116	321282	309796	234	0.003957033	0.007335245	0.962962963	-0.054447784
BP1026b	10778	citrate-proton symporter	29177	20945	21936	17	29031	29694	28286	21	0.022740688	0.035162025	1.23529418	0.304854582
BP1026b	10779	hypothetical protein	29146	9257	13822	9	32779	23851	26257	14	0.907263883	0.921801885	1.555555556	0.637429921
BP1026b	10780	oxygenase	153874	77835	106744	68	149310	123830	132417	82	0.02818873	0.042619404	1.205883333	0.27089163
BP1026b	10781	NAD-dependent formate dehydrogenase subunit delta	51943	30361	35881	153	52674	43851	47085	183	0.05771827	0.081199082	1.196074831	0.258311996
BP1026b	1													

BP1026b	10832	hypothetical protein	113698	70788	85631	178	115589	110600	113172	224	0.039383973	0.057575311	1.258426966	0.331621491
BP1026b	10833	pmbA protein	188115	185210	183556	135	209975	197532	201671	148	0.004637018	0.008433752	1.096296296	0.132637769
BP1026b	10834	dihydrofolate reductase	9028	6127	5341	13	10084	7742	10000	18	0.154314036	0.195874535	1.384615385	0.469485283
BP1026b	10835	sigma-54 dependent DNA-binding transcriptional regulator	10290	10290	10290	6	16318	12381	12487	7	0.013401027	0.020439101	1.166666667	0.222392421
BP1026b	10836	hypothetical protein	5799	6099	5221	4	5308	6334	6363	4	0.00138421	0.002867619	1	0
BP1026b	10837	hypothetical protein	297	88	129	1	483	247	266	2	0.00442221	0.008087616	1	0
BP1026b	10838	sigma-54 dependent DNA-binding transcriptional regulator	100175	77891	86284	63	97256	95347	95493	69	0.00110698	0.002349149	1.095238095	0.131244533
BP1026b	10839	thymidylate synthase	110577	122721	129057	124	110964	129605	120511	123	2.69E-05	8.60E-05	0.991935484	-0.011681805
BP1026b	10840	prolin-rich exported protein	27700	15802	17755	7	10016	25030	25070	10	0.113957302	0.149207713	1.428571429	0.514573173
BP1026b	10841	Arsk family transcriptional regulator	2707	999	891	2	3579	2446	2087	3	0.211369794	0.258868161	1.5	0.584962501
BP1026b	10842	hypothetical protein	2574	716	634	9	2814	1697	2493	16	0.224972685	0.273339851	1.777777778	0.830074990
BP1026b	10843	long-chain acyl-CoA thioester hydrolase	32530	36527	32292	66	35718	37030	34904	70	0.003834917	0.007125721	1.060660661	0.084888898
BP1026b	10844	fumarate hydratase	143819	128537	146007	99	152501	155639	152941	110	0.005044265	0.009090111	1.111111111	0.152003093
BP1026b	10845	multidrug resistance protein	37466	23781	24506	20	42733	38465	37768	28	0.470148045	0.524588881	1.4	0.485426827
BP1026b	10846	hypothetical protein	3578	2831	2290	13	3633	4152	4283	18	0.65393132	0.699662722	1.384615385	0.469485283
BP1026b	10847	hypothetical protein	16934	18332	17971	35	19651	18998	16947	36	8.44E-04	0.001853902	1.028571429	0.040641984
BP1026b	10848	hypothetical protein	282352	325999	317876	391	262665	278314	281036	347	8.75E-07	4.02E-06	0.887468031	-0.172323945
BP1026b	10849	CrcA protein	26640	28032	29604	139	29912	31582	28164	62	0.003574544	0.00531306	1.087179298	0.12136296
BP1026b	10850	Asn tRNA	4008	5436	4682	61	5402	6378	7644	85	0.255978787	0.306417325	1.393442622	0.478653599
BP1026b	10851	Asn tRNA	2184	4253	3204	42	2796	3261	3320	41	2.11E-04	5.38E-04	0.976190476	-0.034765418
BP1026b	10852	ferredoxin	122685	171531	162305	469	99583	117899	115531	342	2.52E-15	7.46E-14	0.729211087	-0.455591598
BP1026b	10853	nicotinate phosphoribosyltransferase	131011	185796	168140	134	118939	143516	134452	110	2.05E-10	2.23E-09	0.820895522	-0.284729477
BP1026b	10854	hypothetical protein	103060	99771	106865	169	115946	129444	124944	187	0.001899489	0.003788224	1.106508876	0.146015024
BP1026b	10855	hypothetical protein	99352	99402	97776	68	121458	123414	124677	85	0.043190008	0.062556204	1.25	0.321928095
BP1026b	10856	2-hydroxyacid dehydrogenase	33476	21639	26920	27	25419	29425	32993	32	0.029129244	0.045355501	1.183185185	0.245112688
BP1026b	10857	RnuC domain-containing protein	131367	101081	105214	77	131245	120874	120874	139	0.00315324	0.00591068	1.116883117	0.159478214
BP1026b	10858	acetyltransferase	22021	16256	14184	39	32202	20440	24000	57	0.455531535	0.110007479	1.461538462	0.547487795
BP1026b	10859	hypothetical protein	83303	118576	105082	355	85208	99596	103030	333	2.40E-06	9.95E-06	0.938028169	-0.092266847
BP1026b	10860	molybdopterin biosynthesis moeA protein	37331	13985	18826	17	47533	32294	35668	29	0.583713859	0.633501217	1.705882353	0.770518154
BP1026b	10861	molybdopterin-guanine dinucleotide biosynthesis protein MobA	15410	4715	5986	13	26427	12503	14453	27	0.036574642	0.053882745	2.076923077	0.105447784
BP1026b	10862	molybdenum cofactor biosynthesis protein A	421198	302589	360963	324	454674	457590	436758	404	0.719017021	0.758304265	1.24691358	0.31836148
BP1026b	10863	ribonuclease E	174486	183388	185173	355	216629	214610	22188	65	0.47092949	0.06756889	1.181818181	0.2410081
BP1026b	10864	hypothetical protein	108232	17164	157214	300	90841	16217	109175	24	1.91E-15	2.80E-14	0.72	-0.47391188
BP1026b	10865	ribosomal large subunit pseudouridine synthase C	87049	99787	95012	93	89551	87971	90487	88	6.43E-06	2.39E-05	0.946236559	-0.079727192
BP1026b	10866	haloacid dehalogenase-like hydrolase	64643	54514	58073	89	66851	61892	63172	95	0.001699142	0.00343276	1.06741573	0.094122177
BP1026b	10867	ferredoxin, 2Fe-2S	9549	11879	9242	25	12030	11766	11232	29	0.002993188	0.005712282	1.16	0.214124805
BP1026b	10868	peptidase	229420	320721	308330	285	232489	259320	253347	247	8.61E-08	5.07E-07	0.866666667	-0.206450877
BP1026b	10869	tryptophan methylase family protein	37333	15000	17587	32	47053	27189	35290	50	0.906960184	0.921801885	1.5625	0.64385619
BP1026b	10871	Mal-f like protein	30178	24909	24893	41	30766	29610	27057	44	0.001936649	0.008542551	1.073170732	0.101879614
BP1026b	10870	hypothetical protein	70120	88524	7721	124	90814	78391	77044	139	1.02E-04	7.90E-04	1.0	0.47391188
BP1026b	10872	S0S ribosomal protein L32	113214	17972	154588	818	127004	151323	145244	784	1.10E-05	3.88E-05	0.958435208	-0.061247189
BP1026b	10873	phosphatidyl-3-phosphate acyltransferase PlxX	153766	165805	172661	148	185742	188728	178728	171	0.031283707	0.046746711	1.155405501	-0.08399149
BP1026b	10874	3-oxoacyl-ACP synthase	172680	169241	167658	176	193436	185302	187115	195	0.007932055	0.013677236	1.107954545	0.147898695
BP1026b	10875	acyl-carrier-protein S-malonyltransferase	283757	235856	254668	276	333663	298402	296151	331	0.200420303	0.247195549	1.199275362	0.26216295
BP1026b	10876	predicted RNA	82793	34222	55397	1793	87244	101242	83019	1885	0.779234138	0.81143731	1.580052093	0.65997048
BP1026b	10877	3-ketoacyl-ACP reductase	91171	21359	200995	272	214427	214958	210056	284	9.55E-04	0.00260744	1.044117647	0.062284278
BP1026b	10878	hypothetical protein	20122	13821	11824	115	21864	11864	11864	14	0.0387578	0.04589813	1.20094354	0.20911021
BP1026b	10878	acyl carrier protein	1185239	206367	1760390	6957	1255289	1596743	1430452	5947	0.040424065	0.058917323	0.854822481	-0.226303145
BP1026b	10879	hypothetical protein	608665	985962	835101	5551	626533	762838	715420	4772	0.22840612	0.255334902	0.85964295	-0.21815363
BP1026b	10880	3-oxoacyl-(acyl carrier protein) synthase II	906709	1221020	1146552	880	888519	1006769	926720	759	0.407946295	0.46191743	0.8625	-0.21303638
BP1026b	10881	hypothetical protein	34516	41333	36181	78	30374	29132	31239	63	5.42E-09	4.23E-08	0.807692308	-0.308122295
BP1026b	10882	RNA polymerase sigma factor RpoE	261913	392718	331523	347	216754	270018	274287	422	1.28E-10	1.46E-09	0.771480804	-0.342978734
BP1026b	10883	sigma factor negative regulatory protein	176841	189863	203463	302	151605	168458	163772	252	2.70E-09	2.28E-08	0.834437086	-0.261124816
BP1026b	10884	sigma factor algU regulatory protein MucB	431133	283032	298620	322	461259	430162	437627	444	0.02393055	0.078517455	1.248103436	0.190197486
BP1026b	10885	peptidase	694209	498637	562279	388	769196	669905	667808	466	0.70812032	0.749205191	2.01030992	0.264273302
BP1026b	10886	hypothetical protein	245395	130328	155620	694	247970	207905	207905	856	0.114363057	0.149614068	1.233429395	0.302675134
BP1026b	10887	GTP-binding protein LepA	189761	258657	241654	128	198543	237573	218784	121	1.72E-05	5.76E-05	0.9453125	-0.081136763
BP1026b	10888	signal peptidase I	126543	183344	161728	175	149448	160931	153491	170	2.40E-05	7.75E-05	0.971428571	-0.041820176
BP1026b	10889	ribonuclease III	217761	248321	246893	171	216704	220614	220806	153	8.05E-07	3.72E-06	0.894736842	-0.160464672
BP1026b	10890	GTP-binding protein Era	153064	222879	203510	223	139463	169248	153889	178	4.88E-11	6.08E-10	0.798206058	-0.325166469
BP1026b	10891	DNA repair protein RecQ	41133	44004	51882	41	53924	40817	40817	44	0.02E-08	4.02E-08	1.0	0.47391188
BP1026b	10892	pyridoxal 5-phosphate synthase (UDP-forming)	148274	119312	135636	173	156693	145916	142532	191	0.040432812	0.007931895	1.104041642	0.1428006
BP1026b	10893	4'-phosphopantetheinyl transferase	44101	16498	16122	59	52607	34262	41100	98	0.495720678	0.548730512	1.601016949	0.732066795
BP1026b	10894	beta-hexosaminidase	87166	55309	64343	66	82676	71949	73199	73	0.003077584	0.005855532	1.106060606	0.14543044
BP1026b	10895	sigma-54 interacting response regulator protein	253974	199394	227256	162	270498	256638	249480	185	0.014818574	0.023957967	1.141975309	0.191531458
BP1026b	10896	hypothetical protein	5867	10613	8281	58	5172	6636	5564	41	1.35E-10	1.54E-09	0.706896552	-0.500428991
BP1026b	10897	elongation factor P	332308	528469	461340	789	358321	429612	410509	715	0.00926564	0.015734531	0.906210393	-0.142082058
BP1026b	10898	hypothetical protein	37814	26175	27989	25	38044	35628	34453	29	0.038572031	0.056480475	1.16	0.214124805
BP1026b	10899	resuscitane ABC subunit C	138407	146183	135069	62	119411	121466	119979	53	5.27E-09	4.12E-08	0.85483871	-0.226275856
BP1026b	10900	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	128511	142876	141469	231	128084	133363	148282	231	6.31E-05	1.82E-04	1	0
BP1026b	10901	Gly tRNA	18071	27919	21686	296	13588	18412	17861	218	1.79E-11	2.36E-10	0.736468486</	

BP1026b_10953	cysteine desulfurase SufS	13324	8551	8962	8	22099	17460	19320	15	0.157262913	0.199214509	1.875	0.906890596
BP1026b_10954	SuflD domain-containing protein	6322	2535	2843	3	11223	8480	9576	7	0.001775808	0.003566968	2.333333333	1.222392421
BP1026b_10955	FeS assembly ATPase SufC	5546	2302	2576	4	8598	6836	8088	10	0.0111054	0.018527706	2.5	1.321928095
BP1026b_10956	cysteine desulfurase activator complex subunit SufB	9210	11266	10897	73	14380	1303	10894	101	0.26328582	0.10713505	1.38356364	0.46838604
BP1026b_10957	heme/copper membrane protein	200467	148669	152092	136	214908	206619	225058	176	0.296208456	0.348941905	1.294117647	0.371968777
BP1026b_10958	hypothetical protein	389	387	333	1	417	434	296	1	0.154391472	0.195933179	1	0
BP1026b_10959	methyl-accepting chemotaxis protein I	1713827	1235346	1367575	762	2271508	2107491	2074459	1139	0.6361251	0.6813343	1.494750656	0.57990484
BP1026b_10960	coproporphyrinogen III oxidase	915668	1024205	1024026	680	1071088	1185577	1127522	776	0.825283993	0.852603176	1.141176471	0.190521906
BP1026b_10961	cyclic nucleotide-binding domain-containing protein	464524	525113	524843	731	493353	503286	513722	729	0.46341586	0.51813982	0.997260402	0.003952592
BP1026b_10962	hypothetical protein	170533	163683	167384	126	190659	191357	194932	146	0.024305969	0.037301537	1.158730159	0.212544635
BP1026b_10963	2-nitropropane dioxygenase	984482	831266	902005	73	990489	949142	982151	797	0.890133455	0.830037667	1.075120521	0.09853293
BP1026b_10964	hypothetical protein	770438	610624	653914	635	685736	699252	686815	667	0.767917455	0.803158583	1.050393701	0.07029017
BP1026b_10965	U32 family peptidase	716095	883383	858027	935	657218	744095	722611	808	0.230646832	0.279206402	0.86417123	-0.210611072
BP1026b_10966	hypothetical protein	262532	383023	353075	693	243660	295491	279854	568	1.75E-08	1.22E-07	0.81962482	-0.286964423
BP1026b_10967	hypothetical protein	209435	235941	219699	495	210663	202324	205324	461	6.39E-06	2.37E-05	0.931313131	-0.102661775
BP1026b_10968	radical SAM domain-containing protein	123663	65599	75238	122	130014	104519	111086	160	0.090824669	0.121983842	1.311475451	0.391190757
BP1026b_10969	hypothetical protein	142013	169059	169315	751	140240	167436	160444	732	3.96E-05	1.21E-04	0.974700399	-0.03669259
BP1026b_10970	anaerobic ribonucleoside triphosphate reductase	483833	607133	601882	319	453544	522267	482459	275	0.11084245	0.168857584	0.862064966	-0.267124805
BP1026b_10971	heme/copper membrane protein	96515	52506	46438	58	110539	103463	103678	86	0.613960412	0.662544928	1.562758621	0.56828376
BP1026b_10972	lipoprotein	6103	2313	3090	3	7730	5716	6508	5	0.624915812	0.673556167	1.666666667	0.736955994
BP1026b_10973	phenylacetic acid degradation protein paaD	1765	1886	2370	5	2685	3345	2477	8	0.474970901	0.528653737	1.6	0.678071905
BP1026b_10974	nitric oxide reductase subunit B	135035	168968	155710	66	188412	206721	200740	86	0.36196814	0.415598528	1.303030303	0.381870635
BP1026b_10975	alkane-1 monooxygenase	15292	15349	16838	13	11972	14101	13749	11	6.99E-09	7.13E-08	0.846153846	-0.2410081
BP1026b_10976	deoxyribodipyrimidine photolase	21481	14280	15145	11	24077	19918	21411	14	0.087349979	0.117863287	1.272727273	0.347923303
BP1026b_10977	adenylylsulfate kinase	82869	93880	90375	143	72615	76788	76632	121	2.61E-08	1.73E-07	0.96153846	-0.2410081
BP1026b_10978	ATP-dependent transcription regulator LuxR	10114	11933	9931	14	111E-04	10649	11882	9	1.11E-04	1.02E-04	0.931313131	0.098536714
BP1026b_10980	alpha/beta fold family hydrolase	27327	26857	24922	26	27692	24731	23371	24	2.87E-05	9.11E-05	0.923076923	-0.115477217
BP1026b_10979	4'-phosphopantetheinyl transferase	6999	3972	3892	6	9655	5475	5964	8	0.331950918	0.384974692	1.333333333	0.415037499
BP1026b_10981	hypothetical protein	3555	1749	1185	4	3981	3201	3394	7	0.40781199	0.524588881	1.75	0.807354922
BP1026b_10982	histidine ammonia-lyase	48058	28742	35212	24	47003	35063	38429	26	0.006358214	0.0119111	1.083333333	0.115477217
BP1026b_10983	histidine utilization repressor	20940	17845	19295	27	18470	19627	20249	27	2.70E-04	6.71E-04	1	0
BP1026b_10984	uracilate hydratase	135761	138393	144712	82	120971	123505	116840	71	6.05E-09	4.65E-08	0.865853659	-0.207804885
BP1026b_10985	hypothetical protein	6996	3996	3725	72	33344	6207	6207	9	0.15344245	0.230916475	1.287142427	0.08572591
BP1026b_10986	imidazolepropiolonase	39699	18461	22846	22	40350	37917	33986	30	0.423778183	0.47769282	1.362636364	0.447458977
BP1026b_10987	N-formimino-L-glutamate deiminase	51930	29479	31286	27	47975	38512	41010	31	0.020573519	0.032095918	1.148148148	0.199308878
BP1026b_10988	N-formylglutamate amidohydrolase	27104	20509	24011	29	2634	21393	21299	27	1.03E-05	3.66E-05	0.931043835	-0.10393493
BP1026b_10989	hypothetical protein	1731	2854	2398	16	1619	2004	1884	13	4.52E-10	4.58E-09	0.8125	-0.299560282
BP1026b_10990	hypothetical protein	2075	392	572	2	3083	1365	1270	20	0.03966431	0.050407244	1	1
BP1026b_10991	glutamine amidotransferase	3189	2383	2581	3	3835	2817	3250	4	0.094721381	0.126369099	1.333333333	0.415037499
BP1026b_10992	glutamine synthetase	220896	240999	254507	19	19271	19748	20088	14	1.16E-09	1.05E-08	0.738462161	0.08572591
BP1026b_10993	amino transferase	35418	36636	37578	25	30619	33838	29378	21	2.15E-07	1.15E-06	0.84	-0.25138767
BP1026b_10994	hypothetical protein	125234	191403	167988	351	134411	165800	164240	337	1.54E-05	5.23E-05	0.96011396	-0.960722439
BP1026b_10995	hypothetical protein	28711	43055	38481	144	26595	35718	32076	123	2.30E-07	1.22E-06	0.854166667	-0.227410496
BP1026b_10996	Val tRNA	3136	5306	3668	53	2956	4497	4471	52	0.001495061	0.003071902	0.981132075	-0.027480736
BP1026b_10998	LysR family regulatory protein	8247	10515	9583	10	9103	10007	9045	10	4.17E-05	1.26E-04	1	0
BP1026b_10997	acyl-CoA dehydrogenase domain-containing protein	7638	4218	4046	2	8889	6310	6651	4	0.225978288	0.274404333	1	0
BP1026b_10999	CAIIR-BAIF family CoA transferase	6913	6913	7376	3	7376	6469	6864	4	0.194748652	0.23419053	1.333333333	0.415037499
BP1026b_11000	major facilitator family transporter	2916	1699	2548	1	3198	2736	2540	2	0.025348163	0.03868328	2	1
BP1026b_11001	hypothetical protein	108550	185761	162077	551	108978	140062	126217	453	2.46E-10	2.65E-09	0.822141561	-0.282541269
BP1026b_11002	N-acetylglutamate synthase	269042	146522	198763	154	291455	251415	257822	193	0.136490868	0.175452298	1.253246753	0.325670497
BP1026b_11003	ATP-dependent esterase HrpA	161763	168325	155774	37	166327	158262	157462	38	9.93E-04	0.002135508	1.027027027	0.038474148
BP1026b_11004	hypothetical protein	130754	161893	157718	151	131918	146311	137152	139	1.22E-06	5.43E-06	0.920529801	-0.119463667
BP1026b_11005	hypothetical protein	133243	163577	146977	149	128680	129715	133680	132	6.35E-08	3.86E-07	0.88590604	-0.174774401
BP1026b_11006	hypothetical protein	15748	15089	15879	18	15327	18346	18346	17	0.001491457	0.005698976	1.055555556	0.08572591
BP1026b_11007	polyketide binding domain-containing protein	124006	162716	148977	177	101724	114410	113900	134	1.21E-13	2.52E-12	0.757062142	0.40151636
BP1026b_11008	rhodanese-like protein	34905	26937	31081	66	37903	31375	32490	72	0.002104901	0.01958771	1.090909091	0.125530882
BP1026b_11009	glutamine synthetase, type I	569995	743359	688724	471	598836	678399	647523	453	0.470566603	0.524775875	0.961783439	-0.05621601
BP1026b_11010	nitrogen regulation protein	36958	39213	40245	33	38919	42670	42188	36	0.00420196	0.007729882	1.090909091	0.125530882
BP1026b_11011	nitrogen regulation protein NR(I)	51703	38803	38727	28	56774	46209	49608	33	0.036798843	0.054149458	1.178571429	0.23709197
BP1026b_11012	exodeoxyribonuclease III	35883	39977	44570	31	36743	40550	37819	49	1.24E-04	3.32E-04	0.960784314	0.075175498
BP1026b_11013	DNA-binding response regulator NarL	50525	37657	50073	78	56057	54937	54937	81	4.64E-07	6.43E-08	1.025316456	0.0606925
BP1026b_11014	nitrate/nitrite sensor protein	135134	88053	96697	55	137011	135561	133328	50	0.508313426	0.561038499	1.381818182	0.4665678
BP1026b_11015	respiratory nitrate reductase subunit gamma	11797	9532	9133	14	15068	14269	15789	21	0.46666499	0.524148805	1.5	0.584962501
BP1026b_11016	nitrate reductase subunit delta	4807	3964	4522	61	5601	6123	6526	8	0.268483535	0.320267015	1.333333333	0.415037499
BP1026b_11017	nitrate reductase subunit beta	15889	18668	17394	11	17796	20979	18856	12	0.004498118	0.008214468	1.090909091	0.125530882
BP1026b_11018	nitrate reductase subunit alpha	55191	62630	62273	16	63525	66645	63963	17	0.0017269	0.004276121	1.0625	0.087462841
BP1026b_11019	nitrate/nitrite transporter NarX	8243	9563	9262	6	16910	14600	17428	11	0.31427386	0.366916048	1.833333333	0.87469118
BP1026b_11020	nitrate/nitrite transporter	11656	10431	12163	8	9585	10078	10163	7	5.01E-08	3.61E-07	0.875	-0.192645078
BP1026b_11021	hypothetical protein	730	801	602	6	602	730	962	6	0.00874495	0.014921197	1	0
BP1026b_11022	Met tRNA	175	403	372	4	322	247	212	3	0.09395524	0.015924919	0.875	-0.415037499
BP1026b_11023	DNA polymerase IV	40696	30770	31949	28	41916	34823	34833	30	0.006515735	0.01144587	1.071428571	0.099535674
BP1026b_11024	oligopeptidase A	384306	395676	394603	186	480278	482647	483332	229	0.600123961	0.649401002	1.231182796	0.300044977
BP1026b_11025	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/5,10-methylene-tetrahydrofolate cyclohydrolase	72894	55003	61416	73	78921	72552	72916	87	0.02382185	0.036628147	1.191780822	0.253118937
BP1026b_11026	LuxR family DNA-binding response regulator	361828	452369	409901	638	350214	375697	367142	570	0.00320569	0.006122466	0.893416928	-0.16

BP1026b	I1076	putative lipoprotein	1651645	1987828	1931957	7282	1546809	1613055	1709384	6365	0.02691181	0.040875021	0.874073057	-0.194174227
BP1026b	I1077	cupin superfamily protein family	77129	82517	79920	65	72934	81616	77733	63	2.73E-05	8.72E-05	0.969230769	-0.04508789
BP1026b	I1078	kRb-type peptidyl-prolyl cis-trans isomerase	443070	724108	632851	1098	412888	521134	470772	857	0.03385857	0.050299589	0.780510018	-0.357510945
BP1026b	I1079	hypothetical protein	91587	82330	86801	76	106775	89719	92331	84	0.00183275	0.0043135	1.105263158	0.144389909
BP1026b	I1080	DNA mismatch repair protein MutS	138667	135256	139405	51	134937	138490	139275	51	6.59E-05	1.89E-04	0	0
BP1026b	I1081	Phage integrase	59872	98973	85375	62	53515	67542	65210	47	3.32E-11	4.21E-10	0.758064516	-0.399607459
BP1026b	I1082	hypothetical protein	5298	8427	7470	14	5882	6997	7186	14	1.05E-04	2.88E-04	1	0
BP1026b	I1083	hypothetical protein	2836	1756	2269	6	2528	2940	2651	8	0.021512529	0.033419722	1.333333333	0.415037499
BP1026b	I1084	hypothetical protein	10524	12215	12021	8	11880	13083	11944	9	2.66E-04	6.62E-04	1.125	0.169925001
BP1026b	I1085	hypothetical protein	10050	14778	12630	27	11115	13871	12724	27	2.44E-05	1.28E-04	1	0
BP1026b	I1086	hypothetical protein	4600	4915	5039	8	6145	6058	4979	9	0.037106816	0.054577036	1.125	0.169925001
BP1026b	I1087	hypothetical protein	4013	2850	4145	10	4272	4683	4772	13	0.146852879	0.187504195	1.3	0.378511623
BP1026b	I1088	hypothetical protein	3363	4911	4541	19	3570	4512	3767	18	2.70E-04	6.72E-04	0.947368421	-0.078002512
BP1026b	I1089	putative repressor protein	113818	204618	184382	271	93462	123372	105492	173	2.28E-22	2.50E-20	0.638376384	-0.647520814
BP1026b	I1090	hypothetical protein	6475	8526	7688	15	8498	9253	9807	18	0.020349507	0.031793888	1.2	0.263034406
BP1026b	I1091	hypothetical protein	4148	3980	4703	12	5342	5800	5290	15	0.131450209	0.169598346	1.25	0.321928095
BP1026b	I1092	hypothetical protein	2056	3390	2714	15	1944	2841	2728	13	4.55E-06	1.75E-05	0.866666667	-0.206450877
BP1026b	I1093	hypothetical protein	8760	10360	10280	9297	9297	11377	10672	2	2.80E-04	6.93E-04	1.047619648	0.067401356
BP1026b	I1094	virulence-associated protein E	51906	68862	64651	24	57275	67553	62417	25	2.25E-04	5.71E-04	1.041666667	0.058893689
BP1026b	I1095	hypothetical protein	9061	11918	11581	18	9622	12167	10510	18	2.42E-05	7.79E-05	1	0
BP1026b	I1096	hypothetical protein	4701	3805	4774	23	5404	4784	4533	25	0.015988311	0.025631146	1.086956522	0.120294234
BP1026b	I1097	hypothetical protein	12199	20161	17343	29	15095	19352	17346	30	5.89E-04	0.001346109	1.034827599	0.04809096
BP1026b	I1098	phage terminase large subunit (GpA)	46415	54695	52210	25	49804	53300	51878	26	2.57E-04	6.43E-04	1.04	0.056583528
BP1026b	I1099	hypothetical protein	5060	4229	5307	23	7715	8016	6681	36	0.640648566	0.687099215	1.565217391	0.646363045
BP1026b	I1100	phage portal protein, lambda family	16419	17097	15874	11	20440	20981	19813	13	0.045345284	0.063011299	1.181818182	0.2410081
BP1026b	I1101	peptidase S14, ClpP	2865	22621	27384	23	36617	35424	32424	36	0.006704419	0.010738826	1.347836083	0.430643541
BP1026b	I1102	hypothetical protein	8973	2366	3288	14	13390	7414	9317	29	0.109368482	0.143785826	2.071428571	1.050626073
BP1026b	I1103	hypothetical protein	42824	54157	53385	48	56147	55652	52089	53	0.00343073	0.006445334	1.104166667	0.142957954
BP1026b	I1104	hypothetical protein	6760	4144	3989	17	7965	6179	6823	24	3.06E-179676	0.359434435	1.411764706	0.497499659
BP1026b	I1105	hypothetical protein	9479	7181	8488	15	13980	13789	12562	25	0.9165178	0.929708305	1.666666667	0.736965594
BP1026b	I1106	hypothetical protein	13098	19374	16647	31	15594	18479	15888	32	2.29E-04	5.80E-04	1.032258065	0.04580369
BP1026b	I1107	basplate assembly protein V	17551	15388	16200	24	24637	22109	22904	34	0.327160098	0.380332709	1.416666667	0.502500341
BP1026b	I1108	hypothetical protein	3916	6015	5351	24	5012	5578	5323	36	0.006704419	0.010738826	1.347836083	0.430643541
BP1026b	I1109	GPW/gp25 family protein	5701	4520	5405	15	6253	5735	5972	17	0.02157998	0.032925855	1.333333333	0.180572246
BP1026b	I1110	hypothetical protein	14671	15132	15326	16	17940	16554	17243	19	0.007880046	0.013591292	1.1875	0.247927513
BP1026b	I1111	phage tail protein I	12835	8683	10483	18	15237	16492	16064	27	0.503600029	0.556438775	1.5	0.584962501
BP1026b	I1112	gp26	43439	66682	58091	38	50593	60381	54466	37	6.90E-05	1.98E-04	0.973684211	-0.038474148
BP1026b	I1113	hypothetical protein	14635	17704	18902	37	16688	19901	17145	39	8.51E-04	0.001865772	1.054054054	0.075948853
BP1026b	I1114	phage tail sheath protein	29993	34717	33007	27	38008	40532	35728	32	0.046226571	0.066539532	1.181818182	0.2410081
BP1026b	I1115	phage mouth tail tube protein	26153	40817	37364	69	31044	34097	34097	69	6.40E-04	0.001666667	1.032258065	0.04580369
BP1026b	I1116	hypothetical protein	4551	6307	5838	18	5904	6976	6661	21	0.024673241	0.037777701	1.166666667	0.222392421
BP1026b	I1117	hypothetical protein	3189	5763	4836	39	4786	5444	5052	43	0.014887734	0.024057381	1.102564103	0.140862536
BP1026b	I1118	tail tape measure protein	32573	43752	40622	16	39978	44638	42644	17	0.007018979	0.012237369	1.0625	0.087462841
BP1026b	I1119	phage P2 gpI family protein	6686	5217	5626	6	7973	8506	8268	10	0.526152389	0.578435671	1.666666667	0.736965594
BP1026b	I1120	phage Tail Formation X	1921	1790	1539	8	2346	1774	1693	9	0.004264129	0.007832762	1.125	0.169925001
BP1026b	I1121	phage tail formation protein	12621	12085	12812	11	15596	16355	14581	14	0.031051782	0.046461022	1.272727273	0.347923403
BP1026b	I1122	gp24	3629	2828	3015	6	6069	4230	4541	9	0.38636904	0.943121	1.0	0.584962501
BP1026b	I1123	bacteriophage lysis protein	5846	6877	7416	12	5578	6534	5422	11	1.15E-05	4.03E-05	0.916666667	-0.125330882
BP1026b	I1124	Site-specific DNA methylase	34227	57877	51200	60	35764	47306	41656	52	9.69E-07	4.41E-06	0.866666667	-0.206450877
BP1026b	I1125	hypothetical protein	265395	441971	396260	494	232899	303754	268618	360	8.52E-12	1.23E-10	0.728744939	-0.456514135
BP1026b	I1126	hypothetical protein	193178	245966	243315	438	183419	213440	198082	382	1.47E-07	8.18E-07	0.872146119	-0.197358232
BP1026b	I1127	hypothetical protein	104181	113359	117693	235	97258	120743	107108	228	5.94E-06	2.22E-05	0.970212766	-0.043626932
BP1026b	I1128	hypothetical protein	37821	30408	34299	67	40098	37293	38805	76	0.022475911	0.034804095	1.134328558	0.181838323
BP1026b	I1129	PAAR motif-containing protein	73323	60133	65488	126	66370	66453	62268	158	4.77E-05	0.001266667	0.973503333	0.087088888
BP1026b	I1130	hypothetical protein	10282	12739	15425	40	7700	10517	9834	3	3.5E-17	1.05E-15	0	0.59946207
BP1026b	I1131	hypothetical protein	12606	22882	20919	45	11759	15256	14421	33	2.01E-12	3.35E-11	0.733333333	-0.447458977
BP1026b	I1132	gp33	15830	27160	22545	30	14853	20122	17802	24	1.12E-08	8.11E-08	0	0.321928095
BP1026b	I1133	hypothetical protein	96829	173681	148896	227	133111	178387	154020	252	0.006605765	0.011587797	1.110132159	0.150771436
BP1026b	I1134	hypothetical protein	2301	3664	3533	6	2030	3470	2548	5	1.28E-07	7.24E-07	0.833333333	-0.263034406
BP1026b	I1135	hypothetical protein	4182	6557	5638	16	4180	5025	4128	13	3.54E-06	1.40E-05	0.8125	-0.299560282
BP1026b	I1136	hypothetical protein	16736	31067	27517	37	37529	43075	38168	64	5.57E-07	3.10E-06	0.873292421	0.137333374
BP1026b	I1137	hypothetical protein	4763	5647	5230	19	3551	3801	4436	14	1.26E-07	1.12E-07	0.736842105	-0.044725991
BP1026b	I1138	inositol-1-monophosphatase	87055	138777	131068	149	91141	110379	97647	125	2.26E-09	1.93E-08	0.838926174	-0.253384236
BP1026b	I1140	RNA methyltransferase	46246	45325	41089	48	55976	48884	46405	55	0.015634588	0.025128304	1.145833333	0.196397213
BP1026b	I1141	serine O-acetyltransferase	27106	23500	27272	31	30245	27758	26809	35	0.006288935	0.011084712	1.129032258	0.175086707
BP1026b	I1142	UDP-2,3-diacylglycerolamine hydrolase	125804	155586	146147	177	140549	142946	142299	177	6.93E-05	1.98E-04	1	0
BP1026b	I1143	peptidyl-prolyl cis-trans isomerase B	495964	799564	755042	1389	566286	717250	605308	1279	0.357156694	0.610471383	0.920806135	-0.119030335
BP1026b	I1144	peptidyl-prolyl cis-trans isomerase A	34737	490715	464300	49	37529	43075	38168	700	0.038573871	0.029333381	0.937333333	0.137333374
BP1026b	I1145	hypothetical protein	55085	22396	28579	49	67712	50291	53848	9	0.398441021	0.4524657	0.645833333	0.718818247
BP1026b	I1146	cysteine ly-RNA synthase	385407	441251	419041	297	391662	405986	414663	289	0.035499668	0.0759112	0.973063973	-0.039393438
BP1026b	I1147	base excision DNA repair protein	137950	197971	175404	181	120399	136690	139660	140	1.57E-12	2.67E-11	0.773480663	-0.37056287
BP1026b	I1148	acetyl-CoA carboxylase carboxyltransferase subunit alpha	277238	220482	220563	246	302264	276973	298528	301	0.187056142	0.232910516	1.223577236	0.291105171
BP1026b	I1149	cell cycle protein mefJ	50032	18468	25004	21	57250	43430	47457	33	0.650077663	0.696250159	1.571428571	0.652076697
BP1026b	I1150	aspartate kinase	188209	275688	257135	197	225290	274559	249960	205	5.83E-04	0.00133141	1.0406091	

BP1026b	11203	hypothetical protein	44288	42875	45088	108	36253	43930	38968	97	7.87E-06	2.86E-05	0.898148148	-0.15497466
BP1026b	11204	malate synthase	409315	503632	511035	297	381313	436363	420057	258	0.011291073	0.018812458	0.868686869	-0.203091865
BP1026b	11205	balacofal dehalogenase	20390	6541	8911	14	24641	15991	18687	34	0.847192839	0.870791526	1.714285714	0.777607579
BP1026b	11206	lysR family transcriptional regulator	32308	33027	28831	30	42003	3712	37926	338	0.23981916	0.2781189	0.333333333	-0.43037499
BP1026b	11207	universal stress protein family protein	8141	4689	4862	13	7045	5731	7348	25	0.013311616	0.021751436	1.15386454	0.206450877
BP1026b	11208	isocitrate lyase	363909	440767	441862	317	333747	374956	353183	270	9.64E-04	0.002083425	0.851735016	-0.231523433
BP1026b	11209	ATP-dependent RNA helicase	19744	18154	18392	12	23246	21728	22197	14	0.023211797	0.035811019	1.166666667	0.222392421
BP1026b	11211	acyl-CoA-binding protein	111558	161353	141467	511	98510	111746	112140	398	2.02E-12	3.35E-11	0.778864971	-0.36055486
BP1026b	11212	glycoprotease family protein	4034	869	1383	2	5412	3248	3432	5	0.034045007	0.050499959	2.5	1.321928095
BP1026b	11210	ribosomal-protein-alanine acetyltransferase	43301	59093	55642	105	40924	47574	42836	87	3.37E-08	2.18E-07	0.828571429	-0.271302022
BP1026b	11213	phage SPO1 DNA polymerase domain-containing protein	165407	160018	162047	214	135991	159486	149311	198	2.18E-06	1.70E-06	0.925233645	-0.43101366
BP1026b	11214	hypothetical protein	30026	20367	24489	25	33450	31484	32968	33	0.143029212	0.183218755	1.32	0.40053793
BP1026b	11215	phosphomethylpyrimidine kinase	25021	10154	13254	19	26964	20884	20759	28	0.328171669	0.381296699	1.473684211	0.559427409
BP1026b	11216	lysophospholipid transporter	119697	143718	131553	102	105830	108542	116513	85	7.12E-10	6.85E-09	0.833333333	-0.263034406
BP1026b	11217	alanine racemase	197406	177822	176888	171	216940	194566	192242	187	0.004557227	0.008312732	1.093567521	0.129041945
BP1026b	11218	DNA repair protein RadA	172097	162049	160948	179	187236	172103	175655	129	0.003313897	0.006250172	1.084031613	0.116409492
BP1026b	11219	hypothetical protein	22805	35405	33317	598	19640	28746	22023	460	4.95E-10	4.97E-09	0.769230769	-0.37811623
BP1026b	11220	ABC transporter ATP-binding protein	26439	16980	19640	105	22951	23352	21687	109	0.002038468	0.004039657	1.07920792	0.10997343
BP1026b	11221	glutathione peroxidase	56196	93214	84005	162	49237	61095	57747	116	1.51E-13	3.10E-12	0.716049383	-0.481869008
BP1026b	11222	cardiolipin synthase	74027	59227	57906	44	75031	67261	73228	49	0.006833397	0.011947018	1.113636364	0.155278225
BP1026b	11223	hypothetical protein	1979	731	868	4	2369	1499	2381	8	0.244951104	0.295098801	2	1
BP1026b	11224	N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase	63504	40893	51586	56	66381	62593	62769	69	0.075601603	0.10345743	1.232142857	0.301169535
BP1026b	11225	succinyl-L-diaminopimelate desuccinylase	40034	29564	31212	29	46442	481821	40446	37	0.19499512	0.241549049	1.275862069	0.351472731
BP1026b	11226	OMP5L family protein	136530	114369	118452	240	130599	125190	127450	328	0.057001902	0.000235416	0.333333333	-0.43037499
BP1026b	11227	2,3,4,5-tetrahydrodipyrindine-2,6-carboxylate N-succinyltransferase	251361	193334	203975	261	306311	282777	287493	352	0.762342161	0.796190612	1.348659004	0.433152622
BP1026b	11229	N-succinyl-L-L-diaminopimelate aminotransferase/alternative	46512	40015	39823	34	59872	51993	49066	43	0.161893232	0.204378395	1.264705882	0.33801913
BP1026b	11228	hypothetical protein	40059	25152	25656	31	41270	33287	38052	39	0.106569782	0.14047326	1.258064516	0.331205908
BP1026b	11230	chromosome segregation protein SMC	613619	517491	542126	158	632246	589019	591123	171	0.879075258	0.897970867	1.082278481	0.114071767
BP1026b	11231	hypothetical protein	290250	250725	258449	209	297043	276799	278083	223	0.002949132	0.005633345	1.066956466	0.093540768
BP1026b	11232	NAD-dependent DNA ligase	191472	176398	168818	86	170747	188610	192664	93	0.006969635	0.010767475	1.04651163	0.143590824
BP1026b	11233	peptide deformylase	138530	114369	118452	227	136099	124032	126487	34	5.52E-04	0.001259506	0.96524009	-0.07918192
BP1026b	11234	peptidoglycan synthase family protein	73191	54242	59522	36	73563	67650	69310	40	0.006908161	0.012064281	1.111111111	0.152003093
BP1026b	11235	Pil uridylyl-transferase	221231	195416	200805	80	231842	228908	224155	88	0.004966202	0.008972634	1.1	0.137503524
BP1026b	11236	methionine aminopeptidase	170824	253798	232184	257	155437	184861	175596	202	4.03E-11	5.07E-10	0.785992218	-0.347413066
BP1026b	11237	predicted RNA	29736	39446	35592	582	37269	50519	46211	744	0.199539894	0.24625492	1.278350151	0.354283468
BP1026b	11238	predicted RNA	20046	13325	13994	367	28956	23842	24861	602	0.903023261	0.918405291	1.640326975	0.173983424
BP1026b	11239	predicted RNA	417196	519895	507668	723	582940	658854	619797	931	0.51761033	0.569569128	1.26769018	0.364785521
BP1026b	11240	elongation factor Ts	616407	703757	786423	820	809538	784850	784850	94	0.43675296	0.48092075	0.93435112	-0.07780874
BP1026b	11241	uridylic kinase	104517	102102	101858	144	135995	123774	120376	177	0.03826783	0.056113628	1.229166667	0.297680549
BP1026b	11242	ribosome recycling factor	341452	399433	373032	661	401151	408985	399332	718	0.252404444	0.273373725	1.08623298	0.119333572
BP1026b	11243	undecaprenyl diphosphate synthase	247614	211352	219950	316	270315	267609	268586	376	0.040532918	0.059048536	1.189873418	0.250808104
BP1026b	11244	phosphatidate cytidylyltransferase	24779	18074	20240	25	35375	26165	27408	36	0.321780105	0.374574942	1.44	0.526068812
BP1026b	11245	1-deoxy-D-xylulose 5-phosphate reductoisomerase	134531	148971	138747	117	129121	119334	120381	102	1.84E-08	1.28E-07	0.871794872	-0.19739378
BP1026b	11246	membrane-associated zinc metalloprotein	147808	87456	100906	82	158368	133049	138567	102	0.087148269	0.117660565	1.241902439	0.314873337
BP1026b	11247	OMP5L family protein	136530	114369	118452	240	130599	125190	127450	328	0.057001902	0.000235416	0.333333333	-0.43037499
BP1026b	11248	OmpH/HlpA family outer membrane protein	475851	628536	600606	1067	490349	567253	524173	987	0.320470298	0.373166564	0.92502343	-0.112438186
BP1026b	11249	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	369121	326889	331018	315	401898	360797	369644	347	0.11362329	0.148832484	1.101587302	0.139583834
BP1026b	11250	(3R)-hydroxymyristoyl-ACP dehydratase	87367	84096	79786	178	82753	90096	84108	183	1.70E-04	4.43E-04	1.028088908	0.039666407
BP1026b	11251	UDP-N-acetylglucosamine acyltransferase	238222	264495	266481	324	228320	252675	239073	304	4.52E-06	1.74E-05	0.938271605	-0.091922489
BP1026b	11252	lipid-A-disaccharide synthase	155739	133132	139187	122	164232	154372	156081	135	0.007314945	0.012704029	1.066557377	0.146078259
BP1026b	11253	ribonuclease HII	99254	59598	98578	151	96056	93183	94690	146	1.07E-05	3.79E-05	0.848888889	-0.169925001
BP1026b	11254	RNA methyltransferase	82939	83807	84338	105	96837	97226	96127	125	0.0108373	0.018117065	0.944176712	0.533676
BP1026b	11255	hypothetical protein	243467	327013	307852	358	257988	290109	280370	320	3.56E-05	5.28E-05	0.944176712	-0.08293641
BP1026b	11256	serine protease	37820	25378	29593	16	40749	36198	37468	38	0.01827574	0.13726246	1.25	0.321928095
BP1026b	11257	primitive phytochelatin synthase	12117	8315	9498	13	14592	12986	12531	18	0.109338127	0.143785826	1.384615385	0.469485283
BP1026b	11258	phosphoenolpyruvate synthase	866537	980516	968586	391	874832	917402	891555	372	0.81511476	0.842791312	0.95140665	-0.071865986
BP1026b	11259	modulation efficiency protein D	10410	10219	9358	22	11506	10626	11354	25	0.001734306	0.003498042	1.136363636	0.18442457
BP1026b	11260	SPFH domain protein/band 7 family protein	275003	358877	332170	339	310348	337560	332776	344	0.022972946	0.035460616	0.147490249	0.021123292
BP1026b	11261	SarA-binding protein	99120	143261	137641	237	94380	107595	107595	236	1.72E-10	2.99E-09	0.948717949	-0.075948853
BP1026b	11262	cysteine dehydratase superfamily	60072	101881	92431	104	42281	68792	58244	144	4.05E-14	9.28E-13	0.705882353	-0.502500341
BP1026b	11263	TGS domain-containing protein	64325	39042	44986	152	68499	56536	52696	182	0.047837485	0.06859411	1.197368221	0.086971227
BP1026b	11264	integral membrane protein	19469	12759	14493	16	18984	17316	19066	19	0.019569492	0.030719191	1.1875	0.247927513
BP1026b	11265	hypothetical protein	12987	13004	13907	19	9994	10512	10103	14	1.90E-11	2.49E-10	0.736842105	-0.440572591
BP1026b	11266	hypothetical protein	2438	664	1010	1	2400	1606	1385	1	0.15851548	0.200639145	1	0
BP1026b	11267	hypothetical protein	13065	14248	14472	18	13353	12388	12375	16	7.09E-07	3.32E-06	0.888888889	-0.169925001
BP1026b	11268	inosine 5'-monophosphate dehydrogenase	409720	4106639	413073	277	4106639	4007232	381435	272	0.06667283	0.06667283	0.981940438	-0.02679325
BP1026b	11269	hypothetical protein	105047	112438	107651	165	102434	95149	96654	149	3.11E-07	1.59E-06	0.903030303	-0.147153694
BP1026b	11270	GMP synthase	252445	285535	284202	169	245522	264431	255959	157	3.20E-06	1.28E-05	0.928940303	-0.106258687
BP1026b	11271	Integrase	12661	21758	18925	26	11592	13420	12834	19	5.22E-14	1.16E-12	0.730769231	-0.455212205
BP1026b	11272	hypothetical protein	109098	302013	264233	215	161927	200906	198843	160	2.42E-13	4.78E-12	0.744186047	-0.426264755
BP1026b	11273													

BP1026b	I1321	hypothetical protein	279619	490180	452907	1061	290461	397197	331289	884	4.98E-04	0.001152184	0.833176249	-0.263306382	
BP1026b	I1322	hypothetical protein	1444	2627	2851	10	1448	1634	1798	7	7.17E-13	1.28E-11	0.7	-0.514573173	
BP1026b	I1323	exported avidin family protein	4881	9358	8561	16	4380	6385	5080	11	2.87E-10	3.03E-09	0.6875	-0.540668381	
BP1026b	I1324	endomembrane protein	3220	2761	3397	5	3108	3517	3256	5	0.004992344	0.0034999	1	0	
BP1026b	I1325	histone deacetylase family protein	1135	823	1078	0	1198	1142	1294	1	0.201834482	0.248451276	#DIV/0!	0	
BP1026b	I1326	transporter	630	242	542	0	583	677	926	0	0.405815907	0.459841616	#DIV/0!	#DIV/0!	
BP1026b	I1328	LuxR family transcriptional regulator	11107	9183	10199	8	11586	9690	9869	9	8.50E-05	2.39E-04	1.125	0.169925001	
BP1026b	I1329	2-dehydropanthoate 2-reductase	8148	5788	5072	6	8691	6765	6590	7	0.015720402	0.025246821	1.166666667	0.222392421	
BP1026b	I1330	MarR family transcriptional regulator	34299	40044	40269	84	28182	29452	29053	64	4.21E-11	5.28E-10	0.761904762	-0.392317423	
BP1026b	I1331	glycerate kinase	3814	1900	1373	2	3089	2328	2425	2	0.003850626	0.007150673	1	0	
BP1026b	I1332	hypothetical protein				0	96	1134	119	0	0.00102451	0.002340331	#DIV/0!	#DIV/0!	
BP1026b	I1333	trigger factor	596752	813586	740352	531	741047	847350	802979	590	0.66308990	0.708301187	1.111111111	0.152003093	
BP1026b	I1334	predicted RNA	16667	8895	12480	603	15990	18014	19728	852	0.307760955	0.360490818	1.412935323	0.498695428	
BP1026b	I1335	ATP-dependent Clp protease proteolytic subunit	407645	546911	521984	752	435028	498064	466650	713	0.251321733	0.301961546	0.948138298	-0.076830585	
BP1026b	I1336	ATP-dependent protease ATP-binding subunit ClpX	1343230	1505487	1417349	1117	1410562	1435321	1434676	1121	0.256962547	0.307736933	1.003581021	0.005157092	
BP1026b	I1337	ATP-dependent protease La	3416901	4493626	4221420	1672	3860853	4322528	4119476	1696	0.04527229	0.065272186	1.014354067	0.020561322	
BP1026b	I1338	Val RNA	32393	49744	42864	548	32652	40905	45748	523	1.03E-04	2.83E-04	0.954379562	-0.067364947	
BP1026b	I1339	Sigma 54 modulation protein YbhI	607192	919752	883462	2434	718635	908381	773435	2416	0.93737991	0.94740191	0.992604996	-0.217708713	
BP1026b	I1340	hypothetical protein	817	496	741	3	1400	757	914	4	0.539971475	0.591247371	1.333333333	0.415073499	
BP1026b	I1341	predicted RNA	188532	237168	219542	434	170077	181218	178197	356	1.23E-09	1.10E-08	0.820276498	-0.288817801	
BP1026b	I1342	Carboxymuconolactone decarboxylase family protein	-	45627	74256	72741	987	50112	62002	49731	829	1.59E-08	1.12E-07	0.839918946	-0.251677983
BP1026b	I1343	Asp RNA	30830	16642	24871	588	32086	34138	31045	790	0.208413022	0.255496362	1.343537415	0.42606498	
BP1026b	I1344	Asp RNA	9718	6999	7296	38	9499	10864	11092	51	0.103413262	0.136801222	1.342105263	0.424497829	
BP1026b	I1345	Asp RNA	3496	7380	5986	72	5358	5658	5000	69	3.26E-04	7.94E-04	0.958333333	-0.061400545	
BP1026b	I1346	peptidyl-polyol cis-trans isomerase D	457918	452630	470203	237	607800	626067	589997	314	0.417696991	0.471518834	1.324884515	0.4058775	
BP1026b	I1347	phosphoribosylformylglycinamide synthase	40822	46423	47085	452	59673	56473	51485	125	0.84163573	0.865780986	1.085274299	0.234312988	
BP1026b	I1348	acyl-CoA thioesterase I	40866	35928	37981	56	41642	38835	39093	59	0.002503292	0.004878271	0.053571429	0.075288127	
BP1026b	I1349	ABC transporter ATP-binding protein	36011	29140	30476	44	38884	38458	36644	52	0.058501988	0.082149083	1.181818181	0.2140081	
BP1026b	I1350	glucose-6-phosphate isomerase	163640	125615	150744	90	180811	167809	171732	106	0.052657701	0.074818066	1.177777778	0.236607358	
BP1026b	I1351	sugar kinase	8444	3955	4198	3	8581	6087	6582	4	0.09323934	0.124683517	1.333333333	0.415037499	
BP1026b	I1352	D-amino acid dehydrogenase small subunit	23351	10739	13634	12	30273	20982	23643	19	0.828000994	0.855391551	1.583333333	0.662965031	
BP1026b	I1353	phosphoribosylformylglycinamide synthase	469490	416370	422169	107	531591	505910	498276	125	0.84163573	0.865780986	1.085274299	0.234312988	
BP1026b	I1354	acetyltransferase	11641	2845	3218	9	15445	9605	11485	22	0.29137999	0.34548024	1.234313327	0.290956708	
BP1026b	I1355	peptidyl-polyol cis-trans isomerase domain-containing protein	551222	814782	756129	906	554675	667686	627745	790	0.235946147	0.285456158	0.87196468	-0.19768397	
BP1026b	I1356	Clp division protein BOLA	11500	14329	13927	42	13443	13103	12878	41	2.98E-05	9.40E-05	0.976190476	-0.034765418	
BP1026b	I1357	intracellular septation protein A	88176	120779	117873	205	92181	106250	106691	191	1.27E-06	5.61E-06	0.931707317	-0.102051271	
BP1026b	I1358	methylthionine-R-sulfoxide reductase	119892	112297	121994	273	138206	150051	139965	330	0.043692716	0.063196774	1.208791209	0.273565073	
BP1026b	I1359	hypothetical protein	42368	30077	32546	62	46275	40012	42636	37	0.00634303	0.140467181	1.227272727	0.295455884	
BP1026b	I1360	long-chain-fatty-acid-CoA ligase	63195	54429	57095	35	64839	63560	61038	28	0.003645185	0.006815572	0.887514286	0.118644946	
BP1026b	I1361	fatty-oxoaldehyde reductase, subunit alpha	161439	164329	164838	79	161358	156475	156475	72	0.14E-05	9.81E-05	0.734531327	0.290956708	
BP1026b	I1362	pyrazinamidase/nicotinamidase	27702	14442	13429	27	32643	22596	25652	42	0.728458257	0.766200309	1.555555556	0.637429921	
BP1026b	I1363	acetyl-CoA acetyltransferase	46773	34193	34429	32	49019	41198	41990	37	0.022687558	0.035097177	1.15625	0.209453366	
BP1026b	I1364	hypothetical protein	15447	9480	18717	38	10905	15112	13045	28	5.40E-13	9.84E-12	0.736842015	-0.440572591	
BP1026b	I1365	stress responsive A/B barrel domain family protein	161783	19378	104456	385	192902	164072	17820	560	0.95571898	0.963547619	1.454545455	-0.50668381	
BP1026b	I1366	thioesterase family protein	53443	22817	28070	72	78318	52790	58518	130	0.051791212	0.073770725	1.805555556	0.852442814	
BP1026b	I1367	oxoaldehyde, zinc-binding dehydrogenase family protein	94652	62406	66607	74	103325	92911	94326	99	0.14381942	0.18410256	1.783783838	0.419903252	
BP1026b	I1368	esterase	40984	40984	40984	47	56371	51479	51479	35	0.031180858	0.031180858	1.000000000	0.64466467	
BP1026b	I1369	acetyltransferase	23283	10411	13697	34	21430	18425	19788	43	0.063053479	0.088053088	1.264705882	0.338801913	
BP1026b	I1370	hypothetical protein	17082	10763	11831	15	20607	17194	16496	21	0.17793114	0.266020495	1.15625	0.485426827	
BP1026b	I1371	glycine cleavage T-protein, aminomethyl transferase	44428	29958	35133	34	42940	41981	40232	39	0.026811886	0.040743934	1.147058824	0.197939378	
BP1026b	I1372	hypothetical protein	27761	25835	28325	26	37134	36900	34070	35	0.226050893	0.274437247	1.346153846	0.428843299	
BP1026b	I1373	thymidylate kinase	43266	35262	33951	60	56145	42214	43807	76	0.163320941	0.20609782	1.266666667	0.341036918	
BP1026b	I1374	DNA polymerase III subunit delta'	41785	24797	27549	30	50849	38634	42512	42	0.07070542	0.102160622	1.4	0.485426827	
BP1026b	I1375	rhomboid protease family protein	53690	35647	41808	86	33860	36610	34918	100	0.02765396	0.04195346	1.627890000	0.5914533	
BP1026b	I1376	hypothetical protein	47434	56605	56622	66	51381	57265	48465	85	0.86E-04	1.71E-04	0.969696969	-0.044394119	
BP1026b	I1377	ankyrin repeat-containing protein	268552	221438	230418	332	290593	241898	250258	360	0.002582452	0.005007642	0.848337349	0.116813665	
BP1026b	I1378	hypothetical protein	99418	82056	82471	250	116420	96458	105428	302	0.015366276	0.024750751	1.208	0.272620455	
BP1026b	I1379	predicted RNA	36709	6158	10022	383	49187	31285	39687	870	0.001537704	0.00314715	2.27154047	1.183671009	
BP1026b	I1380	mechanosensitive ion channel family protein	98971	67254	80779	69	95768	87620	90560	76	0.00230156	0.004510367	1.014492575	0.139403075	
BP1026b	I1381	thymidylate kinase	28482	16637	18692	18	25178	21509	21612	19	0.00369875	0.00321906	0.555555556	0.078002512	
BP1026b	I1382	glycosyl transferase group I protein	101636	96478	101636	95	91545	90569	90569	85	0.61E-07	9.82E-06	0.969696969	-0.044394119	
BP1026b	I1383	lipoprotein	15558541	7131268	8767469	17832	15952023	12474262	13453234	2374	0.35746814	0.407240551	1.3317057	0.412912183	
BP1026b	I1384	hypothetical protein	5762	6381	5394	12	5647	5540	5334	11	2.28E-04	5.79E-04	0.916666667	-0.125530882	
BP1026b	I1385	phosphate starvation-inducible protein	1710084	2409569	2321368	7378	1705426	2039311	1897696	6463	0.012495858	0.020541541	0.875986291	-0.191025797	
BP1026b	I1386	asparaginase family protein	112022	67487	84859	84	114204	108454	107843	105	0.034950265	0.051713615	1.25	0.321928095	
BP1026b	I1387	LysM domain BON superfamily protein	381315	442331	437128	892	401515	436278	415831	887	0.145781979	0.186440349	0.994391699	-0.008109606	
BP1026b	I1388	2-hydroxy-3-oxopropionate reductase	5609	3463	3655	4	5403	4799	5872	5	0.113118481	0.164264152	1.25	0.321928095	
BP1026b	I1389	hydroxypyruvate isomerase	18241	12169	13389	18	19869	17903	17180	22	0.04741643	0.06456506	1.222222222	0.289506617	
BP1026b	I1390	glyoxylate carboxylase	8682	723	787	4	8285	8451	9458	0	0.001917875	0.003820254	1.000000000	0.000000000	
BP1026b	I1391	LysR family transcriptional regulator	37240	28080	30903	35	37126	37022	35542	40	0.022185785	0.034380294	1.000000000	0.192645078	
BP1026b	I1392	cytochrome c oxidase family protein	994	1055	1064	2	1201	1000	1077	2	0.019090727	0.03005927	1	0	
BP1026b	I1393	Ser/Thr protein phosphatase family protein family	2526	1240	1609	1	2807	1775	1931	2	0.041221653	0.059940527	2	1	
BP1026b	I1394	RNA polymerase sigma factor	8571</												

BP1026b	11442	endonuclease/exonuclease/phosphatase family protein	111258	81701	85475	107	93376	87041	87396	103	1.11E-05	3.88E-05	0.962616822	-0.054966459
BP1026b	11443	23S rRNA 5-methyluridine methyltransferase	81207	64653	68600	51	88105	80400	79793	59	0.009998128	0.01682808	1.158662745	0.210217707
BP1026b	11444	hypothetical protein	867770	1051964	1072176	1426	848654	959791	947704	1314	0.65731396	0.702939547	0.921458626	-0.118008706
BP1026b	11445	nucleoside diphosphate kinase	481741	563999	546373	1246	60976866	736374	763741	1698	0.30156404	0.54408738	1.367058239	0.045532301
BP1026b	11445	radical SAM protein	313936	365801	345216	305	449750	450243	475652	403	0.483572229	0.536940918	1.32111475	0.401970596
BP1026b	11447	hypothetical protein	111281	57243	60879	70	161542	114764	122353	122	0.279075168	0.332063454	1.74285714	0.801454321
BP1026b	11448	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	245742	190303	211685	165	289842	268190	265826	147	0.190306053	0.23694034	1.272727273	0.347923303
BP1026b	11449	histidyl-tRNA synthetase	169368	193473	196983	139	193266	202597	193397	146	0.00114033	0.002415021	1.050359712	0.070883486
BP1026b	11450	hypothetical protein	82923	77164	80362	127	121179	96742	98742	167	0.015314788	0.13905276	1.131496063	0.395019606
BP1026b	11451	PQO repeat-containing protein	562042	211914	237021	235	388784	332732	357179	313	0.712540336	0.752807473	1.331914894	0.41350159
BP1026b	11452	GTP-binding protein EngA	200999	202398	204681	155	218561	230433	229057	173	0.00826218	0.01418844	1.116705409	0.15803823
BP1026b	11452	predicted RNA	18867	25268	25741	1294	23236	24612	24612	1488	0.008454537	0.014486564	1.14992272	0.201536909
BP1026b	11453	RNA-binding protein Hfq	485807	839206	731029	2855	616788	791685	723118	2960	0.78267368	0.814349311	1.03677583	0.05210643
BP1026b	11454	GTP-binding protein HflX	261031	285257	280992	236	282817	300609	285620	248	0.00368762	0.006851486	1.050847458	0.071553261
BP1026b	11455	f1aH protease activity modulator HfK	147631	129044	134508	105	180323	152805	150599	123	0.039573643	0.057812172	1.171428571	0.228268988
BP1026b	11456	hHc protein	63932	55017	55760	64	70165	59723	61373	70	0.003658275	0.006835971	1.09375	0.129283017
BP1026b	11457	hypothetical protein	7266	11182	9119	47	6071	7679	7019	36	1.00E-09	9.24E-09	0.765957547	-0.38466385
BP1026b	11458	ATP phosphoribosyltransferase regulatory subunit	51804	88032	45680	74	52160	53318	51293	44	0.00254266	0.004944236	1.073170732	0.101789614
BP1026b	11459	adenylsuccinate synthetase	363759	463285	434734	312	373479	418129	394158	293	0.015611299	0.02510422	0.939102564	-0.090643669
BP1026b	11460	phosphoribosyl transferase domain-containing protein	122581	143171	136518	225	125339	139600	135784	224	5.07E-05	1.50E-04	0.995555556	-0.006426209
BP1026b	11461	kup system potassium uptake protein	285855	389585	353346	181	310981	363586	374123	184	0.037780635	0.055477042	1.016574586	0.012716069
BP1026b	11462	transcription accessory protein, TEX	234101	259150	253498	100	286119	295872	292345	118	0.069262773	0.095764905	1.18	0.23878686
BP1026b	11463	hypothetical protein	135477	184816	178495	210	152135	178662	148070	202	1.85E-05	6.16E-05	0.961904762	-0.056034035
BP1026b	11464	hypothetical protein	138672	212892	207358	876	11813	139676	137627	600	1.38E-18	7.99E-17	0.684931507	-0.545968369
BP1026b	11465	ATP-dependent helicase	131406	125230	121433	55	158145	143999	149512	66	0.046091696	0.067310533	0.657603223	-0.263053465
BP1026b	11466	competence lipoprotein ComL	212480	251375	251375	302	237859	207831	257714	135	0.010051002	0.010051002	1.039734009	0.016321601
BP1026b	11467	ribosomal large subunit pseudouridine synthase D	31520	25804	24732	23	36176	30276	31799	27	0.032155411	0.047992123	1.17931304	0.231325546
BP1026b	11468	hypothetical protein	22472	10022	12678	17	32239	15393	18800	26	0.046555837	0.049461063	1.52941765	0.612967787
BP1026b	11469	poly(R)-hydroxylalkanoic acid synthase	604759	625844	628453	341	539894	576289	561871	300	0.30858489	0.361215342	0.903225806	-0.14648138
BP1026b	11470	acetyl-CoA acetyltransferase	626841	428937	482033	433	662711	587306	559476	518	0.831725022	0.857497465	1.178299099	0.236130222
BP1026b	11471	acetylacetyl-CoA reductase	620270	882579	821794	1045	515494	643338	591388	783	0.049460012	0.070723195	0.749282297	-0.41641873
BP1026b	11472	hypothetical protein	559942	613154	564824	993	298312	378203	335832	653	4.02E-08	2.56E-07	0.657603223	-0.604710726
BP1026b	11474	Sds ribonucleoside synthetase S12 methyltransferase	189633	189633	187500	141	189633	190290	190290	39	6.77E-05	4.26E-05	0.864444444	0.118645846
BP1026b	11475	carbohydrate kinase	153405	92562	109433	127	150768	120144	127690	143	0.004411005	0.008069476	1.125984252	-0.1178665
BP1026b	11476	beta-ketothiolase	262243	153649	185183	169	260638	241822	243948	209	0.01971833	0.144190724	1.236686391	0.306479696
BP1026b	11477	hypothetical protein	92272	93737	95438	161	88917	84834	85027	148	1.48E-06	6.45E-06	0.919254658	-0.12146512
BP1026b	11478	cystathionine beta-lyase	177156	173638	170590	146	181130	165990	170223	145	9.05E-05	2.52E-04	0.993150685	-0.009915469
BP1026b	11479	phosphoserine phosphatase	39817	42039	43391	49	47018	48350	45232	55	0.012315923	0.020314958	1.12244898	0.166649869
BP1026b	11480	hypothetical protein	1129	1379	1621	4	894	1398	1054	6	1.14E-06	5.12E-06	0.857142857	-0.239234241
BP1026b	11481	hypothetical protein	227465	251063	249485	450	225867	204752	207483	39	6.77E-05	4.26E-05	0.864444444	0.118645846
BP1026b	11482	hypothetical protein	24436	20055	21111	26	25131	22616	25807	29	0.005020729	0.00906054	1.115384613	0.157541277
BP1026b	11483	ABC transporter ATP-binding protein	3481	1718	2173	3	4088	3101	2504	4	0.258617805	0.309482924	1.333333333	0.415037499
BP1026b	11484	AsmA family protein	212385	237681	218703	89	222275	224910	220018	89	1.70E-04	4.44E-04	1	0
BP1026b	11485	ABC transporter ATP-binding protein	144606	203404	189585	114	150409	182749	164159	105	2.24E-06	9.36E-06	0.921025632	-0.118644496
BP1026b	11486	hypothetical protein	765386	1212656	1100376	1613	550479	622428	563532	910	1.75E-04	4.56E-04	0.56416615	-0.825807988
BP1026b	11486	predicted RNA	24739	803	1840	456	31960	12255	21831	1100	3.49E-04	8.44E-04	2.412280072	1.27039794
BP1026b	11487	aldehyde dehydrogenase	166866	166866	163397	114	145167	148855	15109	105	1.78E-05	1.19E-06	0.97170526	-0.118645846
BP1026b	11488	hypothetical protein	3754	5764	4737	45	3067	3495	3456	31	1.69E-10	1.88E-09	0.688888889	-0.537656786
BP1026b	11489	2-nitropropane dioxygenase	672939	559136	602108	526	789700	711126	749888	646	0.470961623	0.525021361	1.228136882	0.296471365
BP1026b	11490	outer membrane protein W	6380015	7043820	7597658	10863	7120007	8991634	8218452	12574	0.054192444	0.076824678	1.157507914	0.21021086
BP1026b	11491	hypothetical protein	96017	145756	120381	591	103253	116547	123836	561	1.89E-06	8.01E-06	0.949238579	-0.07515736
BP1026b	11492	manganese transport protein	9730	6216	6976	5	15944	9345	10666	9	0.77696091	0.809422965	1.8	0.84799607
BP1026b	11493	putrescine-binding periplasmic protein	733606	1063520	981469	845	755809	919684	846625	768	0.648180594	0.69436897	0.90887574	-0.13784503
BP1026b	11494	putrescine ABC transporter ATP-binding protein	861411	843087	848741	84	859104	968070	884	8.89E-04	0.00490788	1.081087329	0.18772739	
BP1026b	11495	putrescine transport system permease	71389	101607	87857	100	105828	74234	77949	84	4.42E-08	1.01E-07	0.84	-0.25153767
BP1026b	11496	putrescine transport system permease	126000	141699	135533	164	119619	130910	129571	156	2.93E-06	9.92E-06	0.93902429	-0.090765464
BP1026b	11497	hypothetical protein	32231	22579	23786	32	47328	27533	32623	44	0.342819816	0.396115068	1.375	0.459431619
BP1026b	11498	hypothetical protein	92466	68150	75090	47	115051	97432	95628	61	0.069909726	0.1291494	1.29787234	0.376148486
BP1026b	11499	metallo-beta-lactamase family protein	92592	120045	113317	122	91385	101116	94063	107	6.86E-08	4.14E-07	0.87706918	-0.29720351
BP1026b	11500	sigma-54 dependent transcriptional regulator	24065	12275	15136	12	26447	21963	24191	17	0.309437098	0.326054269	0.974193548	-0.10719666
BP1026b	11501	hypothetical protein	20861	20861	21655	37	19630	20938	20938	8	8.73E-05	2.40E-04	0.9616088	0.502500341
BP1026b	11502	transcriptional regulator	22172	29433	26640	115	22007	26073	29067	115	1.30E-04	3.47E-04	0.945945946	-0.080170349
BP1026b	11503	hypothetical protein	6696	2177	3211	8	9235	5681	6094	14	0.686945962	0.729931101	1.75	0.807354922
BP1026b	11504	MerR family transcriptional regulator	21613	18400	18060	18	22466	18950	17982	19	4.75E-04	0.00110446	1.055555556	0.078002152
BP1026b	11505	hypothetical protein	5284	1391	1652	8	7305	3376	4063	15	0.211563787	0.259004613	1.875	0.906890596
BP1026b	11506	RND efflux system outer membrane lipoprotein	108154	60835	70177	41	124231	92573	103016	55	0.173499132	0.176603615	1.341463451	0.423807709
BP1026b	11507	AcrlA/AcrF family protein	485978	502191	490198	155	487102	481090	477745	151	0.363187387	0.416555903	0.974193548	-0.10719666
BP1026b	11508	RND family efflux transporter ATP subunit	122508	126377	126377	137	142715	124476	124730	130	0.161030991	0.2461026	1.306167226	0.306167226
BP1026b	11509	[YerK] family transcriptional regulator	187137	230210	233232	349	189584	222369	212419	335	2.97E-05	9.37E-05	0.959833333	-0.059065941
BP1026b	11510	voltage-gated ClC-type chloride channel ClcB	37222	25300	26690	17	94400	33675	34286	20	0.057169675	0.008553768	1.176470588	0.234465254
BP1026b	11511	hypothetical protein												

BP1026b	1573	hypothetical protein	749	952	858	1	733	473	693	1	3.02E-07	1.55E-06	#DIV/0!	1	0
BP1026b	1574	hypothetical protein	149	86	77	0	95	63	76	0	0.003360694	0.00632892	#DIV/0!	#DIV/0!	0
BP1026b	1575	outer membrane protein	37860	43650	42198	11	30706	35393	32032	9	3.42E-09	2.81E-08	0.818181818	-0.289506617	0
BP1026b	1576	hypothetical protein	3856	4936	3052	12	3052	3512	3357	8	1.47E-09	3.90E-08	0.666666667	-0.584962501	0
BP1026b	1577	DNA-binding response regulator	28638	42092	38034	54	29034	30830	28711	44	4.16E-09	3.31E-08	0.814814815	-0.295458884	0
BP1026b	1578	two-component regulatory system, sensor kinase protein	112506	103034	109954	33	112098	109400	113582	34	8.37E-05	2.36E-04	1.03030303	0.043068722	0
BP1026b	1579	EAL domain-containing protein	53541	77741	72344	90	40322	47121	47268	60	1.24E-16	4.92E-15	0.666666667	-0.160464672	0
BP1026b	1580	hypothetical protein	1798	1239	1426	3	1209	1271	1140	2	9.40E-07	4.29E-06	0.666666667	-0.584962501	0
BP1026b	1581	H-NS histone family protein	3065	5928	4597	14	2314	3322	3470	9	3.30E-14	7.84E-13	0.642857143	-0.637429921	0
BP1026b	1582	putative lipase	20681	35205	34097	28	17319	23219	20030	18	3.95E-14	9.07E-13	0.642857143	-0.637429921	0
BP1026b	1583	hypothetical protein	214	201	459	1	36	229	230	1	0.01260007	0.026020159	0.571428571	-0.584962501	0
BP1026b	1584	hypothetical protein	401	216	459	3	283	472	339	2	6.33E-05	1.83E-04	0.666666667	-0.584962501	0
BP1026b	1585	Putative bacteriophage gp31 protein	10104	17555	13794	45	8377	10519	10863	32	1.18E-13	2.47E-12	0.711111111	-0.491853096	0
BP1026b	1587	GntR family transcriptional regulator	31917	45883	42063	57	30831	40935	36649	51	1.12E-05	3.93E-05	0.894736842	-0.160464672	0
BP1026b	1588	peptide synthase	10237	14807	9114	19	10311	13148	12722	20	2.47E-04	6.18E-04	1.052631579	0.074000581	0
BP1026b	1589	alpha/beta fold family hydrolase	6150	8886	7680	8	6742	6510	7026	7	9.48E-06	3.39E-05	0.875	-0.192645078	0
BP1026b	1590	nitrilotriacetate monooxygenase	5237	8289	8666	7	6232	6808	6986	6	1.70E-05	5.71E-05	0.857142857	-0.222392421	0
BP1026b	1591	alucose-6-phosphate dehydrogenase	6866	10783	8481	8	5922	7178	6768	6	3.31E-09	3.32E-08	0.571428571	-0.415037499	0
BP1026b	1592	aldehyde dehydrogenase	33441	47340	42250	27	28933	36141	40028	23	5.89E-07	2.81E-06	0.851851852	-0.231255446	0
BP1026b	1593	NIPSNAP family protein	1960	2847	2411	7	1770	2281	2102	6	7.06E-08	4.24E-07	0.857142857	-0.222392421	0
BP1026b	1594	ABC transporter substrate-binding protein	4106	5880	5221	4	3646	3969	4686	3	3.34E-06	1.33E-05	0.75	-0.415037499	0
BP1026b	1595	ABC transporter permease	2779	3232	3576	3	2867	3295	3460	3	8.43E-04	0.00185182	1	0	0
BP1026b	1596	putrescine ABC transporter permease	3204	5707	4883	5	3251	4362	4023	4	1.27E-05	4.39E-05	0.8	-0.321928095	0
BP1026b	1597	spermidine/putrescine ABC transporter ATP-binding protein	4332	6112	6348	5	3382	4284	4236	3	6.15E-09	4.72E-08	0.6	-0.736965594	0
BP1026b	1598	GntR family transcriptional regulator	2186	3285	3105	3	1779	1832	2446	2	1.94E-13	3.88E-12	0.666666667	-0.584962501	0
BP1026b	1599	succinyl-semialdehyde dehydrogenase	5025	9259	8334	5	5149	6347	6613	4	2.00E-07	1.60E-06	0.8	-0.321928095	0
BP1026b	1600	outer membrane porin	1020	2452	1973	1	938	1282	1168	0	3.91E-14	9.01E-13	0	#NUM!	0
BP1026b	1601	hypothetical protein	234	582	507	1	331	266	569	1	0.0601166	0.01063784	1	0	0
BP1026b	1602	hypothetical protein	203	494	447	2	533	325	256	1	0.066211632	0.092012754	0.5	-1	0
BP1026b	1603	H-NS histone family protein	1159	2584	1496	4	1199	1571	1595	4	4.90E-07	2.39E-06	1	0	0
BP1026b	1604	ompA family protein	1303	2514	1385	2	1597	1883	1474	1	5.71E-05	1.67E-04	0.5	-1	0
BP1026b	1605	outer membrane protein	4265	7026	6008	3	4273	4648	4615	2	6.25E-07	2.97E-06	0.666666667	-0.584962501	0
BP1026b	1606	cable pilus-associated 22 kDa adhesin protein	100815	119200	115102	11	99025	103716	101569	10	3.37E-09	3.32E-08	0.909090909	-0.571428571	0
BP1026b	1607	hypothetical protein	1863	2956	2446	4	1457	1654	1769	3	1.29E-14	3.38E-13	0.75	-0.415037499	0
BP1026b	1608	sulfotransferase domain-containing protein	2590	3477	3262	3	2398	2265	2176	1	3.62E-12	5.70E-11	0.666666667	-0.584962501	0
BP1026b	1609	ABC transporter ATP-binding protein/permease	17795	23622	22782	9	15604	17098	17057	7	6.15E-10	6.02E-09	0.777777778	-0.362570079	0
BP1026b	1610	HlyD family secretion protein	12725	18932	18453	11	11605	14516	13512	9	2.43E-10	2.62E-09	0.818181818	-0.289506617	0
BP1026b	1611	hypothetical protein	42503	57526	53838	11	35896	44404	42629	9	5.66E-09	4.39E-08	0.818181818	-0.289506617	0
BP1026b	1612	hypothetical protein	9638	11164	9785	7	7328	7868	6932	5	1.73E-11	2.28E-10	0.714285714	-0.485426827	0
BP1026b	1614	hypothetical protein	3216	472	338	1	192E-10	3.32E-09	3.32E-09	0	1.92E-10	3.32E-09	0.333333333	-0.584962501	0
BP1026b	1613	Adenylsulfate kinase	3063	2976	3335	5	2494	102	2766	4	1.62E-07	8.92E-07	0.8	-0.321928095	0
BP1026b	1615	hypothetical protein	682	929	872	6	588	1085	1004	7	0.039716836	0.058003178	1.166666667	0.222392421	0
BP1026b	1616	hypothetical protein	501	910	520	4	431	981	741	5	0.078464631	0.106955374	1.25	0.321928095	0
BP1026b	1617	DNA-binding response regulator	3060	4104	2993	4	2981	3227	3882	4	0.001013418	0.002176367	1	0	0
BP1026b	1618	putative transposase	2056	1398	1997	3	1885	1990	1990	3	0.001830251	0.003662253	1	0	0
BP1026b	1619	hypothetical protein	5124	9057	8794	12	4955	5515	4533	8	7.90E-12	1.15E-10	0.666666667	-0.584962501	0
BP1026b	1620	hypothetical protein	6129	9629	8362	3	5508	5508	5508	2	6.35E-05	3.98E-04	1	0	0
BP1026b	1623	hypothetical protein	2903	1770	2170	2	3331	2700	2977	2	0.2089939	0.256115096	0	0	0
BP1026b	1629	LysR family transcriptional regulator	8434	11456	10765	11	7289	9314	8314	8	1.41E-10	1.59E-09	0.727272727	-0.459431619	0
BP1026b	1630	allantoinase	9579	8316	8927	6	8538	8945	9538	6	8.90E-05	2.48E-04	1	0	0
BP1026b	1631	allantoate amidohydrolase	5441	5513	6348	4	5344	5302	4434	3	2.61E-05	8.35E-05	0.75	-0.415037499	0
BP1026b	1632	hypothetical protein	11318	16446	15844	28	10101	11441	12450	22	6.94E-11	8.30E-10	0.785714286	-0.347923303	0
BP1026b	1633	transposase	4848	9161	6951	25	4613	5281	5760	18	2.61E-08	1.73E-07	0.72	-0.473931188	0
BP1026b	1635	RNA polymerase sigma factor	8023	95758	83428	149	67634	83828	84248	155	3.47E-04	8.98E-04	1.040263846	-0.655855885	0
BP1026b	1636	hypothetical protein	17370	14831	15085	25	2137	15635	10729	9	0.01352321	0.02519174	1.16	0.214228085	0
BP1026b	1637	hypothetical protein	94743	9863	100552	152	98924	10014591	105239	163	4.95E-04	0.001145901	0.07236481	0.100800641	0
BP1026b	1638	hypothetical protein	5277	3253	4943	8	5142	4627	5921	10	0.034459248	0.051041998	1.25	0.321928095	0
BP1026b	1639	hypothetical protein	5633	4352	4864	6	5237	4229	5165	6	0.001195609	0.002516797	1	0	0
BP1026b	1640	hypothetical protein	4959	7390	7208	7	4544	5527	5428	5	4.99E-07	2.42E-06	0.714285714	-0.485426827	0
BP1026b	1641	Putative signal peptide protein	3687	5176	4221	13	4281	4894	4647	14	0.006895783	0.012046017	0.1076923077	-0.06915204	0
BP1026b	1642	putative insertion element protein	120	2300	2129	4	1054	1480	1054	3	1.11E-10	1.28E-09	0.75	-0.415037499	0
BP1026b	1643	hypothetical protein	1440	1231	1725	9	977	1350	1256	8	1.00E-11	1.43E-10	0.666666667	-0.584962501	0
BP1026b	1644	hypothetical protein	9769	18629	17787	26	8173	10735	11017	17	6.52E-18	3.25E-16	0.653846154	-0.612976877	0
BP1026b	1645	recombinase	1154	2663	2642	3	928	1376	1321	1	2.62E-19	1.71E-17	0.333333333	-1.584962501	0
BP1026b	1646	hypothetical protein	49	184	89	1	80	45	132	0	0.02443027	0.037478866	0	#NUM!	0
BP1026b	1647	hypothetical protein	709	473	361	4	629	652	767	6	0.760075936	0.794659391	1.5	0.584962501	0
BP1026b	1648	lipoprotein	1017	1133	1512	5	527	867	1475	4	1.96E-07	1.06E-06	0.8	-0.321928095	0
BP1026b	1649	DNA invertase	3097	4545	3248	5	3425	3599	3445	5	0.001014207	0.002177317	0	0	0
BP1026b	1650	transposase	5368	8287	6105	14	5117	5785	6105	12	8.70E-06	6.15E-05	0.857142857	-0.222392421	0
BP1026b	1651	hypothetical protein	34	253	165	1	85	85	32	0	1.96E-10	2.16E-09	0	#NUM!	0
BP1026b	1652	hypothetical protein	184	66	192	1	126	209	166	1	0.35681163	0.410392254	1	0	0
BP1026b	1653	hypothetical protein	202	467	460	3	337	967	202	5	0.966863776	0.973380913	1.666666667	0.736965594	0
BP1026b	1654	hemagglutinin motif-containing protein	95377	136277	124629	23	77067	84773	89520	16	1.02E-14	2.75E-13	0.695652174	-0.523561956	0
BP1026b	1655	hypothetical protein	956	1675	1530	13	892	954	996	9	3.08E-11	3.93E-10	0.692307692	-0.530514717	0
BP1026b	1656	putative HNS-like protein	844	1087	1344	3	937	1102	965	3	3.11E-04	7.60E-04	1	0	0
BP1026b	1657	hypothetical protein	531	692	654	4	654	800	484	4	2.36E-08	9.80E-08	0.666666667	-0.584962501	0
BP1026b	1658	hypothetical protein	1699	2948	1755	7	1630	1467	1564	5	4.80E-11				

BP1026B	I1700	ornithine carbamoyltransferase	1011057	1400676	1337722	1236	1477792	1676328	1565742	1556	0.946832247	0.955822126	1.258899676	0.332163317
BP1026B	I1701	carbamate kinase	772519	457706	559724	635	1238525	1036887	1041371	1177	0.004014123	0.007423524	1.853543307	0.890285823
BP1026B	I1703	short-chain dehydrogenase	85163	55196	63126	85	133897	107701	112369	148	0.337405916	0.390723151	1.741176471	0.800662429
BP1026B	I1704	Pdlt protein	24616	12541	1525	4	2174	2471	2369	0	0.04081194	0.05861821	1.75417657	0.321928095
BP1026B	I1702	LYR family transcriptional regulator	20632	12354	10451	4	2174	18897	21257	22	0.721216929	0.760113205	1.571428571	0.652076697
BP1026B	I1705	glutathione S-transferase	66598	74462	76921	103	64968	67686	64598	93	1.55E-06	6.72E-06	0.902912621	-0.147341716
BP1026B	I1707	putative extracellular ligand binding protein	5031	2595	3382	3	5375	3789	4054	3	0.091921438	0.123131151	1	0
BP1026B	I1708	MarR family transcriptional regulator	13155	8178	8888	23	12273	9541	10901	25	6.60E-04	0.001494494	1.086956522	0.120294234
BP1026B	I1709	major facilitator family transporter	3108	2768	2218	2	2976	2683	2376	2	1.52E-04	3.98E-04	1	0
BP1026B	I1710	fenI protein	163972	129098	143307	92	150269	145142	149270	94	2.33E-04	5.88E-04	1.02173913	0.031026896
BP1026B	I1711	precursor-C-G(11)-methyltransferase	24616	12541	1525	4	2174	2471	2369	32	2.74E-04	6.39E-04	1	0
BP1026B	I1712	cobalt-precorrin-6A reductase	6652	2081	2368	5	7526	3854	4920	7	0.65078236	0.69685925	1.4	0.485426827
BP1026B	I1713	cobalt-precorrin-6A synthase	29614	13146	15617	17	33547	22624	25628	24	0.292946916	0.346009416	1.411764706	0.497499659
BP1026B	I1715	precorrin-6Y C5,15-methyltransferase	9575	8606	10180	7	11908	9068	10628	8	0.001772215	0.003563175	1.142857143	0.192645078
BP1026B	I1714	hypothetical protein	1581	452	790	5	1046	1160	795	6	0.029444194	0.044362992	1.2	0.263034406
BP1026B	I1716	precorrin-3B synthase	9371	3724	5100	4	13712	9101	10643	7	0.365205624	0.418588504	1.75	0.807354922
BP1026B	I1717	precorrin-8X methyltransferase	7723	5410	5947	10	7953	7344	7735	12	0.030721493	0.046071222	1.2	0.263034406
BP1026B	I1718	precorrin-2 C20-methyltransferase	19458	12402	13146	19	20604	16136	16456	24	0.03964453	0.058320559	1.263157895	0.337034983
BP1026B	I1719	precorrin-3b C17-methyltransferase	26087	14951	17943	10	26823	22699	27998	13	0.027848254	0.042175784	1.3	0.378511623
BP1026B	I1720	glycosyl hydrolase family protein	3161435	2106502	2524660	1907	3324519	3146084	3090745	2340	0.25417179	0.305035324	1.227058207	0.295203686
BP1026B	I1721	hypothetical protein	33687	45381	46490	164	39080	40893	37525	153	4.72E-05	1.41E-04	0.932926829	-0.100164162
BP1026B	I1722	carboxylesterase	60376	38965	41361	68	51390	45303	46103	69	4.51E-04	0.001055532	1.014705882	0.021061616
BP1026B	I1723	hypothetical protein	5227	983	1198	4	8274	3570	5119	9	0.001090109	0.002318052	2.25	1.169925001
BP1026B	I1724	magnesium chelatase subunit ChII	25919	15429	15611	14	26753	23678	25702	19	0.157100616	0.199049114	1.357142857	0.440572591
BP1026B	I1725	cobaltchelatase subunit CobN	334060	237094	264655	71	381934	323086	328706	89	0.426687616	0.480454391	1.253521127	0.32505311
BP1026B	I1726	cobalamin biosynthesis protein CobW	16832	12139	12675	128	20231	16917	171763	167	0.33944302	0.39292394	1.3046875	0.383708292
BP1026B	I1727	high affinity nickel transporter	202844	170623	179938	173	274337	257553	261839	249	0.854310442	0.877709718	1.439306358	0.525373704
BP1026B	I1728	predicted RNA	30951	15904	19902	436	46388	44866	34168	819	0.110107618	0.13411886	1.878440367	0.909535317
BP1026B	I1728	cobalamin biosynthesis protein ChbG	1927	258	687	2	2337	1304	1789	4	0.020094907	0.031460733	2	1
BP1026B	I1729	cobD lyrimic acid a,c-diamide adenosyltransferase	26301	19760	21603	37	28355	26886	25646	44	0.021566428	0.033494975	1.189189189	0.249978253
BP1026B	I1730	cobrinic acid a,c-diamide synthase	18967	6781	10144	7	20661	14903	15690	10	0.318441035	0.371228851	1.428571429	0.514573173
BP1026B	I1731	pyoverdine synthetase F	6430	8246	8465	9	8275	8135	8028	9	8.70E-04	0.001900846	1	0
BP1026B	I1732	iron-dependent siderophore receptor	83739	9214	9441	4	9031	9196	9328	4	1.22E-04	9.32E-04	1	0
BP1026B	I1733	l-ornithine 5-monooxygenase	1264	1046	1177	0	2055	1714	1440	1	0.907042082	0.921801885	#DIV/0!	#DIV/0!
BP1026B	I1734	pyoverdine synthetase D	4532	2292	2029	0	6243	3609	4766	0	0.487382791	0.541028535	#DIV/0!	#DIV/0!
BP1026B	I1735	siderophore malleobactin non-ribosomal peptide synthetase MbaJ	5315	2473	3696	0	6859	5550	4731	0	0.656751487	0.702558335	#DIV/0!	#DIV/0!
BP1026B	I1736	cyclic peptide ABC transporter ATP-binding protein	3220	3550	2928	1	3712	3648	3228	2	0.16753399	0.026782383	2	1
BP1026B	I1737	hypothetical protein	9478	8095	8144	14	8074	8648	9209	15	1.16E-04	3.13E-04	1.071428571	0.099535674
BP1026B	I1738	iron compound ABC transporter substrate-binding protein	1031	632	588	0	1247	983	1264	1	0.349116268	0.047796827	1	0
BP1026B	I1739	feric iron reductase protein FhuF	152	192	155	0	319	203	112	0	0.021639287	0.033599813	1	0
BP1026B	I1740	iron-hydroxamate transporter permease subunit	2193	1313	1404	0	3010	2277	2934	1	0.386357845	0.440979396	#DIV/0!	#DIV/0!
BP1026B	I1741	iron compound ABC transporter ATP-binding protein	1540	994	803	1	16847	1219	1140	1	0.60426237	0.202776414	1	0
BP1026B	I1742	SyrP-like protein	2024	1865	1731	1	2371	2017	2238	2	0.02038389	0.031385971	2	1
BP1026B	I1743	mbfH-like protein	259	188	328	1	200	261	324	1	0.23928076	0.289100194	1	0
BP1026B	I1744	extracytoplasmic-function sigma-70 factor	4613	6117	5443	6	6031	5927	5438	7	0.00597007	0.010582157	1.166666667	0.222392421
BP1026B	I1745	short chain dehydrogenase	3221	2349	2034	3	3439	2486	1956	3	5.80E-04	0.001327524	1	0
BP1026B	I1746	predicted RNA	5088	7347	426	568	4236	4485	4386	43	7.48E-08	4.38E-07	0.7447181	-0.42533266
BP1026B	I1746	zinc-binding dehydrogenase family oxidoreductase	16933	22150	20590	18	14208	16412	15520	14	5.18E-10	5.15E-09	0.777777778	-0.362570079
BP1026B	I1747	ribose ABC transporter permease	1931	1271	921	1	1492	1233	1237	1	4.36E-04	0.001025008	1	0
BP1026B	I1748	ribose ABC transporter ATP-binding protein	6457	5163	5594	3	5723	5029	4668	3	6.18E-05	1.79E-04	1	0
BP1026B	I1749	Xylose ABC transporter, periplasmicxylose-binding protein XylF	2256	1787	2306	2	2316	1857	2332	2	2.34E-04	5.90E-04	1	0
BP1026B	I1750	AraC family transcriptional regulator	20300	25740	25780	24	16566	18380	17258	17	1.04E-11	1.47E-10	0.708333333	-0.497499659
BP1026B	I1751	hypothetical protein	705	1006	1044	8	439	641	479	4	1.88E-14	4.77E-13	0.5	1
BP1026B	I1752	hypothetical protein	181437	138151	229024	16210	126453	173616	1649574	10760	1.31E-04	3.02E-04	0.663787785	-0.591206013
BP1026B	I1753	hypothetical protein	108524	138154	129014	76	90867	108617	101459	141	0.07E-11	8.45E-10	0.801136363	-0.319802660
BP1026B	I1754	asparagine synthase	125526	121708	131475	72	120683	119227	116672	68	1.46E-06	6.35E-06	0.944444444	-0.08246216
BP1026B	I1755	ABC transporter membrane protein	196856	107299	135501	85	190015	162252	172120	101	0.064436138	0.089843942	1.188235294	0.24820547
BP1026B	I1756	hypothetical protein	47862	59957	60311	54	45744	46155	45195	44	6.30E-09	4.82E-08	0.814814815	-0.295455884
BP1026B	I1757	hypothetical protein	9679	5048	5220	8	11446	8437	9613	13	0.433434912	0.448227606	1.625	0.700437581
BP1026B	I1758	Pi-fimbriae usher protein	40757	32486	31184	14	48445	43144	49100	19	0.393001765	0.474792199	1.357142857	0.440572591
BP1026B	I1759	type 1 fimbriae subunit FimA	117759	17863	19693	346	198235	190360	203760	393	0.03560493	0.080969491	1.15379019	0.34561709
BP1026B	I1760	Outer membrane efflux protein	111307	59462	76790	53	130260	108193	111211	75	0.32985246	0.392849482	1.4150994	0.50089236
BP1026B	I1761	multidrug efflux protein	237756	203862	207553	70	265562	267920	257076	34	0.017392934	0.084957124	1.214285714	0.280107919
BP1026B	I1762	periplasmic multidrug efflux lipoprotein	38494	24928	26526	24	52988	34390	38880	35	0.553959231	0.60512138	1.458333333	0.544320516
BP1026B	I1763	Transcription repressor of multidrug effluxpump acrAB operon, TetR (AcrR) family	19282	14211	13226	23	20822	16425	16995	26	0.012064724	0.019926807	1.130434783	0.176877762
BP1026B	I1764	peptidase	36248	24200	24779	20	42335	30506	32065	24	0.089649467	0.120602853	1.2	0.263034406
BP1026B	I1765	amino acid transport system, membrane protein	3698	4331	5033	5	3036	3387	2767	4	1.57E-11	2.09E-10	0.8	-0.321928095
BP1026B	I1766	binding-protein-dependent transport system inner membrane protein	807	423	568	0	644	956	384	0	0.077829018	0.106227466	#DIV/0!	#DIV/0!
BP1026B	I1767	extracellular solute-binding protein	4758	4691	5234	5	5171	5168	4788	6	0.003234872	0.006125162	1.2	0.263034406
BP1026B	I1768	hypothetical protein	847	434	861	0	737	684	733	0	0.010174144	0.017110565	#DIV/0!	#DIV/0!
BP1026B	I1769	hypothetical protein	927	1217	945	2	766	862	678	1	7.13E-08	4.27E-07	0.5	-1
BP1026B	I1770	hypothetical protein	515	50	8	0	213	164	130	0	0.014280142	0.023171063	#DIV/0!	#DIV/0!
BP1026B	I1771	fimbriae membrane protein	495	640	655	0	585	620	486	0	0.004960493	0.008969491	#DIV/0!	#DIV/0!
BP1026B	I1772	hypothetical protein	776	837	856	0	786	800	760	0	0.01536124	0.02475339	#DIV/0!	#DIV/0!
BP1026B	I1773	type IV pilus protein	5017	5193	3709	2	5099	4387	5364	3	0.011973465	0.019796929	1.5	0.584962501
BP1026B	I1774	fimbriae assembly protein	2712	2447	2897	2	2969	1992	2772	2	3.78E-05	1.16E-04	1	0
BP1026B	I1775	lipoprotein	1	18	5	0	30</							

BP10268	I1823	Met tRNA	757	1054	672	10	576	779	910	9	5.77E-04	0.001322855	0.9	-0.152003093
BP10268	I1825	mutT/ndix family protein	34724	46836	43817	76	31808	36049	34620	62	3.69E-08	2.36E-07	0.815789474	-0.293731203
BP10268	I1824	leucyl-phenylalanyl-tRNA-protein transferase	26952	22127	23283	31	28684	26659	28776	36	0.01089763	0.016973206	1.161290323	0.215728691
BP10268	I1826	arylsulfatase protein transferase	108627	170472	162792	171	102556	119232	111801	133	9.36E-14	1.24E-13	0.751412429	0.415322115
BP10268	I1827	dihydroorotate dehydrogenase 2	18011	15125	17240	17	21993	20305	21495	21	0.066995744	0.09287609	1.235294118	0.304854582
BP10268	I1828	amino acid ABC transporter substrate-binding protein	74258	80385	80683	98	85296	85817	84132	107	0.001373038	0.002846353	1.091836735	0.126575742
BP10268	I1829	amino acid ABC transporter permease	19144	21300	19500	28	20460	20649	21750	30	8.87E-04	0.0021245	1.071428571	0.09953564
BP10268	I1830	Glo/ldh/MocA family oxidoreductase	12560	4751	6270	7	13276	11697	11060	12	0.604565237	0.653417942	1.714285714	0.77607579
BP10268	I1831	GntR family transcriptional regulator	29542	27429	30795	40	31999	38754	36968	50	0.00038894	0.108935557	1.25	0.321928095
BP10268	I1832	ribose-5-phosphate isomerase A	112760	99657	104919	151	136088	142085	137868	199	0.182008438	0.227031007	1.317880795	0.398219881
BP10268	I1833	N-acetylglucosyl-L-alanine amidase domain-containing protein	25278	21417	24622	26	26407	28986	25361	29	0.00563386	0.010933924	1.171412429	0.165412775
BP10268	I1834	RNA methyltransferase	51415	45418	48629	65	44981	53129	49784	70	0.003304336	0.006234015	1.076923077	0.106915204
BP10268	I1835	ribonuclease R	525024	567755	557640	225	527071	562410	544951	223	0.528155008	0.580128938	0.991111111	-0.012881291
BP10268	I1836	Leu tRNA	1280	2811	1829	22	1584	2053	1725	20	2.07E-06	8.73E-06	0.909090909	-0.137503524
BP10268	I1837	Leu tRNA	89374	141423	114386	1322	100128	128566	132268	1382	2.09E-04	5.33E-04	1.045385779	0.064035439
BP10268	I1838	methyl-accepting chemotaxis domain-containing protein	11590	13378	12248	7	13451	14082	13527	8	0.00117668	0.00248028	1.142857143	0.192645078
BP10268	I1839	phosphoesterase family protein	5530	7069	6941	4	4943	5419	5809	3	2.53E-06	1.04E-05	0.75	-0.415037499
BP10268	I1840	hypothetical protein	3350	2715	2362	21	4209	3601	2271	2	0.214504422	0.263398874	0.2	-0.415037499
BP10268	I1841	sulfate permease family protein	33888	25924	29955	17	32566	25775	29665	17	6.93E-05	1.98E-04	0	0
BP10268	I1842	hypothetical protein	41299	49596	47919	73	37786	41572	40938	63	1.05E-06	4.72E-06	0.863013699	-0.212544635
BP10268	I1843	acetyltransferase	4021	3349	2487	5	4719	3829	3684	7	0.168836637	0.212502453	1.4	0.485426827
BP10268	I1844	major facilitator family transporter	44105	44791	45715	36	33251	35074	36525	28	1.84E-09	1.59E-08	0.777777778	-0.362570079
BP10268	I1845	TetR family transcriptional regulator	152084	207314	183573	189	141001	157165	155094	157	1.30E-09	1.15E-08	0.83068731	-0.267621675
BP10268	I1846	long-chain-fatty-acyl-CoA ligase	28378	28324	27356	15	22325	22287	22620	12	6.51E-09	4.97E-08	0	-0.321928095
BP10268	I1847	hypothetical protein	22338	21490	19390	21	17997	19152	17995	19	9.83E-07	4.47E-06	0.904761905	-0.14438899
BP10268	I1848	hypothetical protein	1962	14663	1962	18	8805	1595	1368	8	0.26E-09	6.83E-09	0.357142857	0.405714196
BP10268	I1849	hypothetical protein	11796	8422	10126	37	10988	10110	10792	38	2.42E-04	6.07E-04	0.127027027	0.038474148
BP10268	I1850	Hfq protein	60676	78804	72935	108	70041	72117	70028	108	1.15E-04	3.13E-04	1	0
BP10268	I1851	hypothetical protein	189002	208542	217554	280	185343	218494	208363	278	1.38E-04	3.67E-04	0.992857143	-0.010341944
BP10268	I1852	sigma-54 dependent transcriptional regulator	124467	94148	100611	76	120111	111742	110160	81	4.06E-04	9.65E-04	1.065789474	0.091922489
BP10268	I1853	hypothetical protein	28247	28977	28584	15	26821	25167	24854	14	1.67E-06	7.17E-06	0.933333333	-0.099535674
BP10268	I1854	hypothetical protein	3439	2125	1971	6	4498	2602	5210	8	0.490357542	0.54357275	1.313333333	0.0537499
BP10268	I1855	hypothetical protein	20772	15758	20824	21	21650	20924	21771	19	0.027604028	0.02856088	0.047149848	0.067114196
BP10268	I1856	hypothetical protein	17531	14672	15122	15	20073	16219	16788	17	0.004932924	0.008917646	1.333333333	0.180572246
BP10268	I1857	Flp pilus assembly protein TadB	12546	10160	10334	10	11321	9680	10540	10	4.70E-06	1.79E-05	1	0
BP10268	I1858	type II/IV secretion system protein	72863	59159	64272	48	66848	65405	62492	48	1.03E-04	2.82E-04	1	0
BP10268	I1859	fimbriae assembly protein	15553	12969	11610	10	13450	10098	12269	9	2.27E-07	1.21E-06	0.9	-0.152003093
BP10268	I1860	type III secretion system protein	65399	49715	50989	41	62432	57209	57276	44	0.001621077	0.003294143	1.073170732	0.101879614
BP10268	I1861	CpaB family Flp pilus assembly protein	100008	7736	8334	9	10909	9404	8340	10	0.001654005	0.002461477	1.131111111	0.152003093
BP10268	I1862	hypothetical protein	8903	5972	5972	14	8800	8800	8800	10	0.096524658	0.12856088	0.047149848	0.067114196
BP10268	I1863	hypothetical protein	4025	4270	3563	11	4476	4691	5606	14	0.104490837	0.138052026	0.272727272	0.347923303
BP10268	I1864	Flp pilus assembly protein, pilin Flp	52751	86992	70447	353	49969	64803	61126	296	1.79E-08	1.24E-07	0.83855261	-0.254071008
BP10268	I1865	hypothetical protein	622	2028	1564	10	1084	1790	1564	10	0.003002829	0.005727196	1	0
BP10268	I1866	hypothetical protein	486	1707	1181	9	1080	1725	1372	11	0.144706754	0.185178594	1.222222222	0.289506617
BP10268	I1867	hypothetical protein	1906	680	905	0	2128	1472	1628	1	0.19551088	0.29262581	#DIV/0!	#DIV/0!
BP10268	I1868	lipoprotein	1995	736	1225	1	2298	1573	2188	1	0.920266328	0.923606925	1.111111111	0.152003093
BP10268	I1869	two-purine secretion family protein	15441	15441	1476	9	1718	1629	16746	10	0.00323661	0.004553451	1.111111111	0.152003093
BP10268	I1870	hypothetical protein	60415	56337	66148	131	51772	62525	60537	126	2.14E-05	6.98E-05	0.961832061	-0.056143078
BP10268	I1871	hypothetical protein	7178	5989	6458	15	7833	6883	6030	16	0.002324271	0.004553451	1.066666667	0.093109404
BP10268	I1872	ATPase, AFG1 type	51720	47359	45435	43	51158	51623	54350	47	0.00353855	0.00628046	1.093023256	0.128342097
BP10268	I1873	diacylglycerol dehydrogenase	906818	1065498	1028398	698	1032333	1081316	1049756	737	0.972174378	0.977787774	1.05873892	0.09347583
BP10268	I1874	diacylglycerol dehydrogenase	363785	406880	406649	309	403226	451441	432923	336	0.500501257	0.552796627	1.083736192	0.120845395
BP10268	I1875	2-oxoglutarate dehydrogenase E1 component	1292741	1800810	1707489	558	1424323	1706452	1562709	545	0.139854852	0.179025506	0.976702509	-0.03408892
BP10268	I1876	GTP-binding protein Tpa	90250	10327	9728	52	114190	123605	12373	63	0.01593265	0.02937913	1.211538462	0.27640205
BP10268	I1877	Marr family transcriptional regulator	7039	6787	7756	74	7469	6644	7469	1	3.97E-05	9.48E-04	0	0
BP10268	I1878	RND efflux system outer membrane lipoprotein	26547	17520	18815	14	31705	26297	28572	19	0.22997403	0.278445684	1.357142857	0.440572591
BP10268	I1879	multidrug resistance protein	30916	30554	29756	24	38350	41261	38711	31	0.224501089	0.27287257	1.291666667	0.36923381
BP10268	I1880	EmrB/QacA family drug resistance transporter	26015	28877	31126	18	31663	33897	32387	20	0.011060769	0.018463066	1.111111111	0.152003093
BP10268	I1881	(RNA pseudouridylation synthase B	44229	31555	33209	39	56369	45140	49764	55	0.563286148	0.614307025	1.41025641	0.499597495
BP10268	I1882	ribosome-binding factor A	29422	49643	42580	97	31065	40077	36658	86	4.19E-06	1.63E-05	0.886597938	-0.173648087
BP10268	I1883	translation initiation factor IF-2	70263	83278	79646	267	75510	82063	79646	267	0.82063639	0.92481324	1.018722727	0.10934669
BP10268	I1884	transcription elongation factor NusA	424174	559997	515012	338	451309	504507	490700	338	0.328193867	0.381296699	1.624E-07	-0.052151282
BP10268	I1885	hypothetical protein	63934	108781	94632	192	66453	88926	78523	168	1.62E-07	8.92E-07	0.875	-0.192645078
BP10268	I1887	RNA pseudouridylation synthase family protein	111372	85568	90342	57	117919	100657	103304	64	0.00181793	0.003641084	1.122807018	0.167109986
BP10268	I1888	segregation and condensation protein B	196716	186623	188238	139	229495	218321	208721	159	0.019298888	0.030327185	1.143884892	0.193441883
BP10268	I1886	hypothetical protein	12990	21442	18311	183	12838	14957	14528	146	1.23E-09	1.10E-08	0.797814208	-0.325875279
BP10268	I1889	OsmT protein	32081	37438	37117	39	34582	34958	35509	38	2.44E-04	6.12E-04	0.974358974	-0.03744705
BP10268	I1890	hypothetical protein	26398	109823	109823	2	21081	20826	20144	2	0.44E-08	0.00000000	0.803030303	0.10934669
BP10268	I1891	hypothetical protein	28993	21542	22537	95	29324	24333	25154	101	0.001661341	0.002266096	0.063157895	0.088355874
BP10268	I1892	hypothetical protein	154007	238704	209851	631	128540	151772	147095	448	2.18E-16	8.13E-15	0.709984152	-0.494141273
predicted RNA	-		39612	60306	54240	626	42980	55891	51872	612	7.14E-05	2.04E-04	0.977635783	-0.032631004
BP10268	I1893	hypothetical protein	610461	228858	332665	540	648041	533164	537315	792	0.103051618	0.136380338	1.466666667	0.552541023
BP10268	I1894	hypothetical protein	4121964	6996066	6396454	20925	4068990	4941679	4623861	16311	4.36E-04	0.001025008	0.779498208	-0.359382389
BP10268	I1895	hypothetical protein	190098	292754										

BP1026B	11944	Fusaric acid resistance protein fusE	17045	15706	15913	18	16654	15548	15680	18	5.86E-05	1.71E-04	1	0
BP1026B	11945	methyl-accepting chemotaxis protein	232414	160617	183849	114	242656	202256	205751	129	0.011562107	0.019207918	1.131578947	0.178337241
BP1026B	11946	fosmidomycin resistance protein	16343	16393	16915	13	17653	16397	17713	13	5.89E-04	0.001346109	0.001346109	0.001346109
BP1026B	11947	5-methylthioadenosine S-adenosylhomocysteine nucleosidase	12835	67589	63864	83	71623	61333	63333	84	2.37E-04	6.97E-04	0.1204881	0.017277991
BP1026B	11948	DNA helicase II	159103	174731	176646	71	158008	157780	152148	65	1.14E-06	5.11E-06	0.915492958	-0.127379306
BP1026B	11949	valyl-L-glutamine synthetase	341909	394959	390522	131	355880	377374	369065	128	0.022544507	0.034901702	0.977099237	-0.033423002
BP1026B	11950	UTP-glucose-1-phosphate uridylyltransferase	338484	456296	421291	459	316832	341032	336190	375	2.32E-04	5.87E-04	0.816993464	-0.291603558
BP1026B	11951	lipoprotein	13529	6479	8196	15	16927	11505	10705	21	0.196240258	0.242803775	1.14	0.485426827
BP1026B	11952	sensor histidine kinase	164474	126813	126273	58	175760	151853	154965	67	0.04641537	0.038028876	1.1551724	0.208108195
BP1026B	11953	LysM domain-containing protein	248861	193765	209568	172	256507	239403	234222	193	0.009205516	0.013649478	1.122093023	0.166192283
BP1026B	11954	DNA-binding response regulator	196984	28225	255704	336	168110	196619	190947	254	2.43E-12	2.45E-11	0.759582333	-0.403637346
BP1026B	11955	hypothetical protein	28701	17106	18395	55	27441	19651	22915	60	0.002619855	0.005069673	0.090909091	0.125330882
BP1026B	11956	hypothetical protein	101388	141597	127439	534	94784	106011	107906	445	1.02E-09	9.42E-09	0.833333333	-0.263034406
BP1026B	11957	homoserine dehydrogenase	10337	4746	4585	6	12915	8268	9551	9	0.723760122	0.76228127	1.5	0.584962501
BP1026B	11958	myo-inositol 2-dehydrogenase	18049	9698	9482	12	20719	15213	16004	16	0.247903987	0.298197835	1.333333333	0.415037499
BP1026B	11959	SIS domain-containing protein	18031	22703	19184	22	19295	22499	22309	24	0.001744106	0.003512288	1.090909091	0.125530882
BP1026B	11960	sugar ABC transporter periplasmic sugar-binding protein	9032	13171	11708	10	8812	10419	10232	8	4.62E-08	2.91E-07	0.8	-0.321928095
BP1026B	11961	permease protein of sugar ABC transporter	9032	6756	6667	5	6597	6805	6234	5	5.09E-04	0.015990352	0.1631862	0.415037499
BP1026B	11962	sugar ABC transporter ATP-binding protein	9218	13189	10888	13	8633	9086	8731	11	4.81E-10	4.85E-09	0.846153846	-0.2410081
BP1026B	11963	uAC protein	11080	8761	8849	4	12633	10044	11291	5	0.008972719	0.015286764	1.25	0.321928095
BP1026B	11964	iolD protein	4319	4216	3599	2	3623	3539	3320	1	1.36E-05	4.65E-05	0.5	-1
BP1026B	11965	hypothetical protein	7191	2989	4205	5	6692	5873	5798	6	0.10996391	0.144416169	1.2	0.263034406
BP1026B	11966	iolF protein	16047	15670	16119	19	14177	13659	14820	17	4.38E-07	2.15E-06	0.894736842	-0.160464672
BP1026B	11967	Branched-chain amino acid transport ATP-bindingprotein LrvF	9064	2069	3866	7	12369	6676	6631	12	0.826002233	0.852783411	1.714285714	0.77607579
BP1026B	11968	ABC transporter	75876	42657	51912	24	69178	58028	57839	26	0.02104281	0.004157529	1.083333333	0.115477217
BP1026B	11969	branched amino acid transport system, membrane protein	12837	13074	134724	13	12626	104236	102846	2	2.25E-04	0.1940377	1.631862	0.923073002
BP1026B	11970	thioesterase family protein	31903	23323	24458	50	25740	23393	24873	46	8.55E-06	3.08E-05	0.92	-0.120294234
BP1026B	11971	alcohol dehydrogenase	132620	69254	82704	82	139657	95078	102512	97	0.009309747	0.015792332	1.182926829	0.24236038
BP1026B	11972	hypothetical protein	44675	32297	33718	109	41989	39112	43476	123	0.018901766	0.029769214	1.128440367	0.173401811
BP1026B	11973	Mut/NUDIX NTP pyrophosphatase	81466	59588	67464	125	77834	80604	0.019132676	133	8.86E-04	0.019132676	1.064	0.089498151
BP1026B	11974	hypothetical protein	12004	13003	12673	18	10083	12060	11273	16	1.48E-07	8.22E-07	0.888888889	-0.169925001
BP1026B	11975	hypothetical protein	43374	31793	32508	23	40377	37466	40898	26	0.021072585	0.013400173	1.130434783	0.17687762
BP1026B	11976	major facilitator superfamily permease	9023	60196	6314	3	9299	8061	8234	4	0.0107916	0.01809661	0.1331862	0.415037499
BP1026B	11977	hypothetical protein	4747	4672	4406	4	6123	6192	5302	6	0.11281316	0.147892453	1.5	0.584962501
BP1026B	11978	alanyl-tRNA synthetase	471126	386048	410797	161	543334	519752	501792	198	0.596970349	0.646322921	1.229813665	0.298439742
BP1026B	11979	CAIB/BAIF family protein	117005	83138	94576	80	99318	97674	94854	79	2.72E-05	8.69E-05	0.9875	-0.018147347
BP1026B	11981	lipoprotein	5477	6751	7110	26	5723	6311	5894	24	9.46E-05	2.62E-04	0.923076923	-0.115477217
BP1026B	11982	glutamyl-tRNA synthetase	378316	448122	441438	247	334058	376189	361664	248	7.38E-04	0.00164782	0.842105263	-0.247927513
BP1026B	11983	NUDX family hydrolase	66645	17490	28192	77	77965	62467	66327	102	0.033260949	0.034997833	1.844155844	0.882960579
BP1026B	11984	hypothetical protein	170731	117973	124722	364	26978	210237	218774	59	0.1537104	0.1940377	1.631862	0.923073002
BP1026B	11985	Beta-hexosaminidase	52323	37592	43206	21	63216	59664	57685	29	0.439605984	0.493759774	1.380952381	0.465663572
BP1026B	11986	hypothetical protein	31617	40931	37108	46	37079	37025	37992	42	0.001403765	0.002902067	1.0217391	0.031026896
BP1026B	11987	cytochrome c peroxidase	2799	4137	4213	2	2880	3717	3464	2	4.17E-05	1.26E-04	1	0
BP1026B	11988	acid phosphatase	9277	9137	10851	6	8987	8909	9474	5	3.66E-06	1.45E-05	0.833333333	-0.263034406
BP1026B	11989	trans-2-enoyl-CoA reductase	24298	20584	25854	19	28584	29014	27818	23	0.02335919	0.035985314	1.210526316	0.275634443
BP1026B	11990	HVD family secretion protein	890	971	815	0	1217	1139	652	0	0.093190794	0.124645171	#DIV/0!	#DIV/0!
BP1026B	11991	EmrB/OacA family drug resistance transporter	9023	3286	3440	1	3460	3367	3405	0	0.0289168	0.0455346	0.1	0
BP1026B	11992	hypothetical protein	4670	2437	3192	2	5636	3706	3954	2	0.247208253	0.297465877	1	0
BP1026B	11993	DNA-binding response regulator	6914	9044	10052	13	7828	7071	7420	12	7.07E-06	2.59E-05	0.923076923	-0.115477217
BP1026B	11994	sensor histidine kinase/response regulator	9300	9175	8855	4	10537	10420	9276	4	0.001463201	0.003090397	1	0
BP1026B	11995	type I pili protein CsuE	10159	8679	10343	10	10659	12181	12380	12	0.01350222	0.022011286	1.2	0.263034406
BP1026B	11996	fimbriae protein	5095	3782	3070	1	5074	4750	4928	2	0.027515781	0.124190378	2	1
BP1026B	11997	type I pili usher pathway chaperone CsuC	824	486	539	0	665	430	721	0	0.00928572	0.016728964	#DIV/0!	#DIV/0!
BP1026B	11998	hypothetical protein	9023	273	295	0	564	392	302	0	0.20426089	0.59853381	#DIV/0!	#DIV/0!
BP1026B	11999	hypothetical protein	14400	9841	13155	22	16399	13469	13831	25	0.006871458	0.010210214	1.136363636	0.184424571
BP1026B	12000	hypothetical protein	694	1153	1032	1	733	618	792	1	9.87E-08	5.76E-07	1	0
BP1026B	12001	LysR family transcriptional regulator	100541	106488	101274	114	101728	108108	110256	119	1.26E-04	3.39E-04	1.043859649	0.061927749
BP1026B	12002	major facilitator family transporter	629769	612237	622492	493	688320	709148	702308	555	0.937991122	0.947812228	1.125766094	0.170900125
BP1026B	12003	hydroxylase	153784	164239	158177	161	160687	157845	158024	161	1.53E-04	4.02E-04	1	0
BP1026B	12004	predicted RNA	93237	7429	13314	144	64055	34316	36571	749	0.055603152	0.07859364	1.950520833	0.96389408
BP1026B	12005	H-NS histone family protein	68233	67031	58863	232	7341-04	67033837	67033837	232	7.34E-04	0.004937594	1.04504504	0.06365128
BP1026B	12006	lipoprotein	16530	19678	19680	60	17689	18136	17542	57	3.75E-05	1.16E-04	0.95	-0.074000581
BP1026B	12007	Manganese transport protein	22614	24616	23426	17	23948	24546	23481	18	2.97E-04	7.30E-04	1.058823529	0.08246216
BP1026B	12008	hypothetical protein	33641	57213	49238	45	35276	45827	40112	39	8.91E-07	4.09E-06	0.866666667	-0.206450877
BP1026B	12009	Transposase mutator family	10482	16528	15655	24	8581	11064	10157	17	1.06E-14	2.84E-13	0.708333333	-0.497499659
BP1026B	12010	hypothetical protein	5958	10445	7407	26	6066	8365	7832	24	2.44E-05	7.88E-05	0.923076923	-0.115477217
BP1026B	12011	Rhs element Vgr protein	930	2859	1998	6	1564	2039	1283	5	1.67E-07	9.17E-07	0.833333333	-0.263034406
BP1026B	12012	hypothetical protein	1314	2273	1401	9	1214	1054	2056	8	3.58E-08	1.32E-05	0.888888889	-0.169925001
BP1026B	12013	transposase	596	803	704	7	272	860	924	7	0.005275279	0.009452107	0.009452107	0.009452107
BP1026B	12014	integrase core subunit	9074	16783	13054	73	8007	10495	11193	55	1.32E-11	1.79E-10	0.75324658	-0.408464845
BP1026B	12015	transposase	18947	29633	25523	98	15648	19394	16332	67	2.09E-13	4.14E-12	0.683673469	-0.548620654
BP1026B	12016	hypothetical protein	58872	103857	90020	91	54152	72714	60964	67	4.28E-12	6.69E-11	0.732623736	-0.44170545
BP1026B	12017	hypothetical protein	105776	158763	145599	48	85834	103326	97432	33	4.48E-16	1.54E-14	0.6875	-0.540568381
BP1026B	12018	hypothetical protein	31565	45325	44237	57	20331	26306	25205	33	8.73E-21	7.02E-19	0.578947368	-0.788495895
BP1026B	12019	Rhs element Vgr protein	63361	57647	57967	2								

BP1026b	I2071	hypothetical protein	106670	178945	153895	205	94652	123615	110440	153	3.68E-14	8.63E-13	0.746341463	-0.422092257
BP1026b	I2072	Integrase	5803	6146	6164	24	4637	5551	6824	23	1.85E-04	4.78E-04	0.958333333	-0.061400545
BP1026b	I2073	Arg tRNA	3505	3127	3884	45	5134	5641	6931	76	0.62919559	0.677156313	1.688888889	0.756074417
BP1026b	I2074	undecaprenyl pyrophosphate phosphatase	19415	19697	18570	23	23899	24933	24852	29	0.06203887	0.08670789	0.240864655	0.33419030
BP1026b	I2075	aldose 1-epimerase	17046	16859	15316	18	14518	14833	14376	16	4.22E-07	2.08E-06	0.888888889	-0.169925001
BP1026b	I2076	peptidase	11485	11122	11898	16	12687	11774	12493	17	3.55E-04	8.57E-04	1.0625	0.087462841
BP1026b	I2077	acetyl-coenzyme A synthetase	31319	21974	24875	16	26063	26684	25584	16	1.46E-04	3.85E-04	1	0
BP1026b	I2078	hypothetical protein	15313	25150	23731	60	11195	15772	14292	39	9.90E-17	4.01E-15	0.65	-0.62148377
BP1026b	I2079	DNA-damage-inducible protein F	33033	22696	24200	19	3292	29229	30844	22	0.009443988	0.015985466	1.157894737	0.211504105
BP1026b	I2080	lipoprotein	6225	4910	5577	29	8118	5080	6463	34	0.026812061	0.040743934	1.172413793	0.229481846
BP1026b	I2081	hypothetical protein	10833	14685	12055	73	7492	9286	9468	53	3.37E-14	7.94E-13	0.69064965	-0.517399217
BP1026b	I2082	hypothetical protein	458531	405661	434396	528	39352	398202	402980	486	0.011655767	0.019373907	0.920454545	-0.119581616
BP1026b	I2083	phosphohistidine phosphatase SixA	228260	183911	188303	436	157760	146486	157859	335	1.95E-12	3.26E-11	0.768348624	-0.380167039
BP1026b	I2084	Pro tRNA	551	971	790	10	537	846	613	8	1.31E-04	3.50E-04	0.8	-0.321928095
BP1026b	I2085	putative bacteriophage protein	14634	25118	23890	38	12156	14485	13960	24	3.43E-18	1.86E-16	0.631578947	-0.662965031
BP1026b	I2086	hypothetical protein	22673	39677	36192	71	21786	26643	27234	54	3.51E-10	3.66E-09	0.76056338	-0.394859617
BP1026b	I2087	hypothetical protein	232873	368338	326601	280	167722	210516	201792	177	2.37E-20	1.81E-18	0.632142857	-0.661677467
BP1026b	I2088	putative bacteriophage protein gp29	139054	231545	199762	259	107087	134031	123436	165	3.01E-23	5.01E-21	0.637065637	-0.650486073
BP1026b	I2089	putative bacteriophage protein gp28	199992	347462	292591	499	163388	210561	192358	336	1.72E-17	8.06E-16	0.673346693	-0.570578583
BP1026b	I2090	hypothetical protein	273334	429432	371517	457	273950	342722	318075	397	3.94E-04	9.40E-04	0.868708972	-0.203055158
BP1026b	I2091	Site-specific DNA methylase	3770	6724	5671	6	3493	4286	4149	5	4.97E-08	3.10E-07	0.833333333	-0.263034406
BP1026b	I2092	bacteriophage lysis protein	5513	7307	6872	12	4904	5048	5477	9	3.07E-07	1.58E-06	0.75	-0.415037499
BP1026b	I2093	Glycoside hydrolase family protein gp24	1498	935	1130	2	1145	1517	990	2	0.005869257	0.010429985	1	0
BP1026b	I2094	putative class II holin gp23	399	263	615	1	247	573	405	1	0.029482422	0.044044138	1	0
BP1026b	I2095	gp22	2445	3224	3140	3	1860	2467	2636	3	9.14E-10	8.54E-09	1	0
BP1026b	I2096	hypothetical protein	34072	387	342	1	1578	158	1331	0	9.57E-08	9.04E-08	0	#NUM!
BP1026b	I2097	gp20	5303	6578	5795	1	3682	4881	5540	1	1.17E-06	5.23E-06	1	0
BP1026b	I2098	Phage tail assembly protein I	157	300	377	0	95	237	238	0	1.21E-05	4.21E-05	#DIV/0!	#DIV/0!
BP1026b	I2099	Phage tail assembly protein	412	464	521	0	352	506	709	0	0.159372352	0.201601686	#DIV/0!	#DIV/0!
BP1026b	I2100	phage minor tail protein	2523	5035	3805	5	2668	3363	3564	4	1.16E-06	5.19E-06	0.8	-0.321928095
BP1026b	I2101	Phage-related tail fiber protein	7444	13841	11752	7	5654	8198	7125	5	8.37E-16	2.69E-14	0.714285714	-0.485426827
BP1026b	I2102	phage minor tail protein	649	628	501	1	612	651	683	1	0.064674235	0.090171703	0.666666667	-0.584962501
BP1026b	I2103	hypothetical protein	11718	13633	12733	3	10621	10872	10572	2	2.31E-18	3.24E-16	0.627423441	-0.672425341
BP1026b	I2104	hypothetical protein	2136	3468	2652	9	1772	2424	1835	7	2.94E-12	4.68E-11	0.777777778	-0.362570079
BP1026b	I2105	Phage tail assembly chaperone	2055	2764	1789	4	2111	1661	1804	3	3.09E-08	2.01E-07	0.75	-0.415037499
BP1026b	I2106	gp11	1418	1853	2090	3	1496	1472	1205	3	2.17E-08	1.47E-07	1	0
BP1026b	I2107	putative bacteriophage protein gp10	1020	1272	926	3	1182	1260	1015	3	0.026917993	0.040875471	1	0
BP1026b	I2108	HK97 family phage protein	3735	5334	4245	10	2032	3579	3422	7	8.30E-13	1.47E-11	0.7	-0.514573173
BP1026b	I2109	putative bacteriophage protein gp8	7125	2047	1349	9	483	802	1380	6	7.32E-13	1.31E-11	0.666666667	-0.584962501
BP1026b	I2110	gp4	1163	2272	1044	3	879	1393	1454	1	8.79E-13	1.55E-11	0.6	-0.73065594
BP1026b	I2111	Phage major capsid protein	42342	67463	62862	45	39182	46008	41064	33	4.70E-12	7.26E-11	0.733333333	-0.447458977
BP1026b	I2112	gp4	4034	5365	5131	8	3306	4110	3551	6	8.84E-08	5.19E-07	0.75	-0.415037499
BP1026b	I2113	Phage portal protein	11748	20649	18817	12	8925	11932	9483	7	1.62E-22	1.89E-20	0.583333333	-0.777607579
BP1026b	I2114	Phage terminase large subunit	1063	2022	2165	1	1160	1597	1476	0	1.29E-07	7.29E-07	0	#NUM!
BP1026b	I2115	Phage terminase small subunit	206	311	328	1	131	210	246	1	1.99E-05	6.55E-05	1	0
BP1026b	I2116	putative bacteriophage protein gp82	947	712	812	2	693	614	486	1	2.04E-07	1.10E-06	0.5	0
BP1026b	I2117	Phage protein	37220	63650	66041	258	2918	3716	3446	160	2.31E-18	3.24E-16	0.627423441	-0.672425341
BP1026b	I2118	Phage-related transcriptional regulator	39447	60464	50878	129	35466	40777	38827	99	3.74E-10	3.87E-09	0.76744186	-0.381870635
BP1026b	I2119	gp78	91014	147547	131955	89	70272	95397	79840	59	1.76E-17	8.17E-16	0.662921348	-0.593090382
BP1026b	I2120	gp77	7889	12503	12397	16	7642	8177	8167	12	7.52E-12	1.10E-10	0.75	-0.415037499
BP1026b	I2121	gp76	942	1615	1338	6	982	687	916	4	7.06E-12	1.04E-10	0.666666667	-0.584962501
BP1026b	I2122	gp75	966	1717	1318	4	742	1003	784	2	1.53E-13	3.12E-12	0.5	-1
BP1026b	I2124	gp74	691	1039	972	2	503	935	780	1	1.11E-08	3.91E-05	0.5	-1
BP1026b	I2125	putative bacteriophage protein gp73	1030	610	1092	2	560	767	787	1	8.61E-07	3.97E-06	0.5	-1
BP1026b	I2126	hypothetical protein	529	299	504	2	248	389	318	2	6.10E-05	1.77E-04	1	0
BP1026b	I2126	gp72	343	614	566	0	576	576	173	0	2.93E-06	1.19E-05	#DIV/0!	#DIV/0!
BP1026b	I2127	gp60	631	1078	1182	0	640	694	924	0	9.87E-07	4.48E-06	#DIV/0!	#DIV/0!
BP1026b	I2128	gp69	409	291	320	1	253	388	409	1	0.187728612	0.233608726	1	0
BP1026b	I2129	gp58	1212	1727	1449	1	979	1545	1416	1	3.78E-05	1.16E-04	1	0
BP1026b	I2130	gp67	2281	2599	3075	1	2108	2457	2761	1	4.17E-06	1.62E-05	1	0
BP1026b	I2131	hypothetical protein	443	912	937	1	634	931	716	1	0.003983314	0.00373245	0	0
BP1026b	I2132	gp55	477	953	641	1	397	531	720	1	2.04E-05	6.70E-05	1	0
BP1026b	I2133	gp64	65561	111723	102012	425	63562	78146	73685	327	5.88E-11	7.20E-10	0.769411765	-0.378172206
BP1026b	I2134	putative bacteriophage protein	31254	53108	46364	238	29330	35421	31642	175	1.10E-11	1.54E-10	0.735294118	-0.443606651
BP1026b	I2135	putative bacteriophage protein gp62	9490	13625	13399	38	8704	10938	10698	32	3.38E-09	2.78E-08	0.842105263	-0.247927513
BP1026b	I2136	putative bacteriophage protein	38252	69717	57079	247	41367	54684	47596	215	2.52E-07	1.33E-06	0.870445344	-0.200174382
BP1026b	I2137	gp59	87777	38401	37918	26	26398	31340	31178	23	3.73E-07	1.87E-06	0.884615385	-0.17687762
BP1026b	I2138	Glycine cleavage system transcriptional activator	25990	13860	13633	13	6718	10112	8108	9	1.38E-15	4.37E-14	0.693207692	-0.530514717
BP1026b	I2139	predicted RNA	7423	10726	9508	576	7627	10844	10660	606	3.20E-04	7.82E-04	1.052083333	0.073249882
BP1026b	I2139	Bacteriophage protein Gp49	888	320	154	1	366	479	470	1	0.22858091	0.277047107	1	0
BP1026b	I2140	bacteriophage protein	608	866	670	2	523	719	833	2	0.003962794	0.007343754	1	0
BP1026b	I2141	gp54	863	1060	836	5	512	541	615	3	2.35E-12	3.86E-11	0.6	-0.736965594
BP1026b	I2142	hypothetical protein	6639	8926	7256	16	5029	5730	5348	11	6.21E-10	6.07E-09	0.6875	-0.540568381
BP1026b	I2144	bacteriophage protein Gp46	13072	19808	15175	62	9735	11959	11829	43	1.06E-14	2.83E-13	0.693548387	-0.527931556
BP1026b	I2143	gp52	13731	21061	17201	79	10918	12499	13267	56	4.34E-14	9.89E-13	0.708860759	-0.49642626
BP1026b	I2145	bacteriophage protein	28832	47085	43397	67	25077	32980	30900	52	1.63E-07	1.46E-06	0.746268657	-0.22233401
BP1026b	I2146	bacteriophage protein Gp44	908	1285	792	6	587	943	670	4	6.50E-08	3.95E-07	0.666666667	-0.584962501
BP1026b	I2148	gp47	5759	9665	9562	11	5381	6470	6062	8	3.57E-10	3.72E-09	0.727272727	-0.459431619
BP1026b	I2149	gp46	1807	1561	1639	2	1114	1396	911	1	6.04E-11	7.36E-10	0.5	-1
BP1026b	I2150	gp45	1757	2539	1905	7	1765	1555	1620	5	3.76E-09	3.03E		

BP1026b	12197	RNase H	24988	33507	28111	65	23812	25910	25033	56	3.01E-07	1.55E-06	0.861538462	-0.215012891	
BP1026b	12198	DNA polymerase III subunit epsilon	55358	53438	59290	77	50560	55695	52541	73	1.17E-05	4.09E-05	0.948051948	-0.070661982	
BP1026b	12199	hypothetical protein	11672	6208	7019	18	11512	10619	13141	25	0.254641211	0.305481797	1.388888889	0.473931188	
BP1026b	12200	proline-beta-transporter	7214	4803	4212	3	10058	8952	80655	25	0.872478783	0.883123273	1.666666667	0.73665594	
BP1026b	12201	glutathione S-transferase domain-containing protein	42845	55319	50168	78	42733	45844	46829	71	5.46E-06	2.06E-05	0.91025609	-0.135655099	
BP1026b	12202	alpha/beta fold family hydrolase	48752	20092	25646	35	45632	29668	36132	42	0.045227347	0.065250954	1.2	0.263034406	
BP1026b	12203	hypothetical protein	9903	2353	2668	9	15900	6903	9072	21	0.052697142	0.07485715	2.333333333	1.222392421	
BP1026b	12204	acyl-carrier-protein S-malonyltransferase	2551	1047	1473	1	2939	1801	1904	2	0.181151238	0.22618647	2	1	
BP1026b	12205	triphosphoribosyl-dephospho-CoA synthase	4662	2002	2834	4	3989	4248	4112	5	0.317694573	0.370427148	1.25	0.321928095	
BP1026b	12206	phosphoribosyl-dephospho-CoA transferase	11356	9064	9556	10	11731	9533	9460	10	1.01E-04	2.78E-04	1	0	
BP1026b	12207	malonate decarboxylase subunit gamma	16653	15168	14530	21	16310	14681	15361	21	9.55E-05	2.40E-04	1	0	
BP1026b	12208	malonate decarboxylase subunit beta	20993	6116	8851	12	26940	14980	16865	20	0.837134672	0.862148382	1.666666667	0.736965594	
BP1026b	12209	malonate decarboxylase subunit delta	5617	3802	3927	13	6886	5672	6042	19	0.308021494	0.360690467	1.461538462	0.547487795	
BP1026b	12210	malonate decarboxylase alpha-subunit	61560	52112	56351	34	58483	54660	59440	34	2.71E-04	6.72E-04	1	0	
BP1026b	12211	malonate transporter, M subunit	2158	820	752	1	1833	1374	1589	2	0.1718838	0.215818069	2	1	
BP1026b	12212	malonate transporter, L subunit	1152	859	744	2	1263	1056	1207	2	0.53853219	0.590080774	1	0	
BP1026b	12213	LysR family transcriptional regulator	8785	5440	5670	7	8385	6348	6729	8	0.003351005	0.006318261	1.142857143	0.192645078	
BP1026b	12214	3-hydroxyacyl-CoA dehydrogenase	50977	41966	41532	48	46890	42509	40148	47	9.37E-05	5.07E-04	0.979166667	-0.030373640	
BP1026b	12215	phosphoenolpyruvate carboxykinase	504234	426270	438046	244	481526	454908	447106	247	0.415083036	0.468987011	0.012259082	0.017623890	
BP1026b	12217	ferredoxin	127	168	223	0	191	174	229	0	0.444957486	0.499234182	#DIV/0!	#DIV/0!	
BP1026b	12216	HSP20 family protein	352866	453519	441589	949	418747	468702	421188	995	0.439166315	0.493442647	1.048472076	0.062888438	
BP1026b	12218	heat shock protein	165787	205908	196059	470	249358	222328	214760	569	0.067017924	0.092886309	1.210638298	0.275767896	
BP1026b	12219	GntR family transcriptional regulator	81669	41999	53174	39	88887	73392	80626	54	0.347570279	0.401234516	1.384615385	0.469485283	
BP1026b	12220	hypothetical protein	6181	6870	7457	36	6580	6420	5908	33	5.85E-05	1.71E-04	0.916666667	-0.125530882	
BP1026b	12221	nitrite/sulfite reductase family protein	28956	24415	24553	14	32427	28858	29415	16	0.011491591	0.019100887	1.142857143	0.192645078	
BP1026b	12222	hypothetical protein	5679	4013	4257	11	40013	39413	5760	14	0.147920143	0.181011454	1.272727273	0.347923503	
BP1026b	12223	hypothetical protein	13630	15594	14020	10	13998	14337	13984	10	2.60E-05	8.34E-05	1	0	
BP1026b	12224	short chain dehydrogenase	13033	13974	13056	17	11510	12408	11391	15	1.16E-07	6.64E-07	0.882352941	-0.180572246	
BP1026b	12225	LysR family transcriptional regulator	15144	6811	9816	11	14189	11959	12708	14	0.015849022	0.025440357	1.272727273	0.347923303	
BP1026b	12226	hypothetical protein	4617	2093	2299	4	5540	4249	4310	6	0.759264729	0.794075966	1.5	0.584962501	
BP1026b	12227	dioxigenase	18002	7516	7637	8	18611	13058	15623	11	0.291999394	0.345150217	1.375	0.459431619	
BP1026b	12228	glucosaminyl-fructose-6-phosphate aminotransferase	49048	32699	35461	20	51242	43195	46657	24	0.066774592	0.092610439	1.2	0.263034406	
BP1026b	12229	AsnC family transcriptional regulator	40791	44532	42573	86	40005	39513	49156	47	9.20E-05	5.98E-04	0.918604651	-0.121484005	
BP1026b	12230	GntR family transcriptional regulator	22164	15984	18020	12	25545	21022	21322	14	0.029721242	0.04472088	1.166666667	0.222392421	
BP1026b	12231	transcriptional regulator PailB-like protein	4969	5456	4774	7	5987	4451	4112	7	5.65E-04	0.001296206	1	0	
BP1026b	12232	hypothetical protein	3949	1708	1516	3	4633	3650	4283	5	0.195534721	0.241978557	1.666666667	0.736965594	
BP1026b	12233	hypothetical protein	23363	26689	24566	41	21769	23823	22702	37	5.61E-06	2.11E-05	0.902439024	-0.148098639	
BP1026b	12234	hypothetical protein	270	692	945	3	452	789	527	3	0.00261929	0.005069673	1	0	
BP1026b	12235	diguanylate cyclase	161723	17858	177434	126	129809	139753	131773	98	1.52E-12	2.58E-11	0.777777778	-0.362570079	
BP1026b	12236	hypothetical protein	9236	10547	10740	88	106693	108854	107700	82	2.01E-04	5.13E-04	1.045454545	0.064130337	
BP1026b	12237	Ribose ABC transport system, permease proteinRbsC	5	1921	1558	5	1660	1446	1069	5	6.04E-06	2.26E-05	1	0	
BP1026b	12241	LacI family transcriptional regulator	5	2026	1554	1970	1	3053	1973	2428	2	0.244904249	0.295098801	1	0
BP1026b	12240	ABC transporter substrate-binding protein	36118	52658	43037	44	39849	47327	45012	44	4.10E-04	9.73E-04	1	0	
BP1026b	12242	ABC transporter permease	18972	17259	18703	22	18927	20945	19360	23	0.002190961	0.004304832	1.045454545	0.064130337	
BP1026b	12243	hypothetical protein	186461	267425	259436	1165	166518	206985	196660	931	2.15E-10	2.33E-09	0.799141631	-0.323476882	
BP1026b	12244	ABC transporter permease	10426	9997	10129	11	11256	11087	11121	12	9.17E-04	0.001993574	1.090909091	0.035250882	
BP1026b	12245	ABC transporter ATP-binding protein	3619	3463	3619	4	4182	4182	4182	4	0.0872124	0.1182353	1	0	
BP1026b	12246	Ser/Thr protein phosphatase family protein	19896	7921	10077	15	25675	14278	18209	23	0.716209778	0.755851941	1.533333333	0.61667136	
BP1026b	12247	hypothetical protein	4010	2100	2782	7	3120	3578	3177	8	0.017066657	0.027227655	1.142857143	0.192645078	
BP1026b	12248	hypothetical protein	3076	1649	2717	3	3526	3445	3324	4	0.542356477	0.593545391	1.333333333	0.415037499	
BP1026b	12249	major facilitator family transporter	12470	7085	8571	7	14646	12112	13954	11	0.353237008	0.406728295	1.571428571	0.652076697	
BP1026b	12250	integral membrane protein	29115	12139	13246	19	40706	29494	33230	36	0.142936092	0.183174281	1.894736842	0.921974888	
BP1026b	12251	oxodoreductase, molybdopterin-binding protein	8859	8057	8609	10	8913	8363	10349	11	8.97E-04	0.001952079	1.1	0.375035524	
BP1026b	12252	hypothetical protein	2951	3173	3434	2	3465	3265	3465	3	0.036180744	0.053337659	1.5	0.01963501	
BP1026b	12253	hypothetical protein	796	572	449	0	1127	1080	980	1	0.052124937	0.04178705	#DIV/0!	#DIV/0!	
BP1026b	12255	hypothetical protein	31537	49771	45581	138	24933	33084	31460	97	7.29E-14	1.59E-12	0.702898551	-0.508611615	
BP1026b	12254	hypothetical protein	1057	1371	1169	2	950	1073	905	2	1.69E-06	7.23E-06	1	0	
BP1026b	12256	thiamine biosynthesis protein ThiC	834227	1118322	1079426	523	926285	1058371	967389	509	0.773457733	0.806393616	0.973231358	-0.03914529	
BP1026b	12257	lipoprotein	15895	24848	21404	97	14123	17208	18712	75	3.81E-10	3.94E-09	0.773195876	-0.371094152	
BP1026b	12258	hypothetical protein	999	878	820	3	671	803	805	3	3.82E-05	1.17E-04	1	0	
BP1026b	12259	DMT family permease	3046	3046	2345	28	41986	33171	33206	3	0.301357083	0.332156	1.357142857	-0.440759759	
BP1026b	12260	DMT family permease	34947	38133	37154	28	61913	32686	31184	24	6.33E-07	3.00E-06	0.857142857	-0.222392421	
BP1026b	12261	peptidyl-RNA hydrolase domain-containing protein	45916	53166	53559	125	41864	46611	43892	108	4.11E-07	2.04E-06	0.864	-0.210896782	
BP1026b	12262	exodeoxyribonuclease V subunit alpha	107656	43977	49807	24	108935	81587	87871	34	0.299755312	0.352444135	1.416666667	0.502500341	
BP1026b	12263	exodeoxyribonuclease V subunit beta	274026	242406	248342	66	287018	248117	248942	68	2.33E-04	5.87E-04	1.03030303	0.034068722	
BP1026b	12264	Exodeoxyribonuclease V gamma chain	164331	87899	109326	36	174557	140650	152189	46	0.222737754	0.271104471	1.277777778	0.353636955	
BP1026b	12265	hypothetical protein	96280	94193	92356	41	97640	94438	101165	42	1.70E-04	4.44E-04	1.024390244	0.034765418	
BP1026b	12266	amino acid permease	26874	23088	23562	17	33862	29628	29628	16	0.100630222	0.135291734	1.352941176	0.073901175	
BP1026b	12267	hypothetical protein	24450	38295	35071	181	156640	31521	25724	153	1.00E-07	5.94E-07	0.845304869	-0.242458044	
BP1026b	12268	ABC transporter substrate-binding protein	39812	17658	23779	25	56394	42964	47852	46	0.155824822	0.1975923	1.84	0.879705766	
BP1026b	12269	ABC transporter permease	16948	9202	11407	7	21113	16291	19442	11	0.035544801	0.06313443	1.571428571	0.652076697	
BP1026b	12270	ABC transporter ATP-binding protein	23682	18719	22365	28	24783	25067	24585	32	0.609287951	0.015763884	1.142857143	0.192645078	
BP1026b	12271	AsnC family transcriptional regulator	44900	52819	51319	96	44295	49990	45301	90	1.55E-05	5.26E-05	0.9375	-0.093109404	
BP1026b	12272	cysteine dioxygenase type I family protein	3799	1922	2435	4	4063	3049	2412	4	0.036692806	0.054018768	1	0	
BP1026b	12273	NAD-dependent epimerase/dehydratase family protein	19803	15949	17482	27	26389	20050	22015	35	0.088708539	0.1194393			

BP1026b	12322	lipoprotein	28595	29113	26639	22	31691	30925	30147	24	0.002954004	0.005640933	1.090909091	0.125530882
BP1026b	12323	MaoC-like domain-containing protein	12950	11400	10227	23	13397	12207	11712	25	4.54E-04	0.001059664	1.086956522	0.120294244
BP1026b	12324	MaoC domain-containing protein	34018	47360	46089	92	30154	38334	33149	73	7.17E-09	5.43E-08	0.793478261	-0.333737397
BP1026b	12325	acyl-CoA dehydrogenase domain-containing protein	29814	29408	29408	25	26381	27892	26381	23	0.88E-06	2.93E-05	0.842553191	0.126294234
BP1026b	12326	acyl-CoA dehydrogenase family protein	45357	40181	39406	34	49272	43069	43640	37	0.005640648	0.010049157	1.088235294	0.121990524
BP1026b	12327	hypothetical protein	43936	57222	50700	119	33430	35490	39718	85	2.39E-12	3.91E-11	0.714285714	-0.485426827
BP1026b	12328	MutT/NUDIX NTP pyrophosphatase	65977	88102	87356	136	69431	81173	77571	128	9.11E-06	3.27E-05	0.941176471	-0.408746281
BP1026b	12329	hypothetical protein	77006	11171	10038	315	86402	103669	99822	315	5.44E-05	1.34E-04	1	0
BP1026b	12330	NADH-ubiquinone oxidoreductase subunit N	438012	453341	439142	304	537729	540629	550607	372	0.652951498	0.698850835	1.222682111	0.291231298
BP1026b	12331	NADH-ubiquinone oxidoreductase subunit M	552630	757056	657383	435	645162	689025	690699	452	0.709916674	0.750726112	1.039080846	0.053073752
BP1026b	12332	NADH-ubiquinone oxidoreductase subunit L	775936	1013740	954757	442	901748	1005939	976387	471	0.87337260	0.893608662	0.951330218	0.072232328
BP1026b	12333	NADH-ubiquinone oxidoreductase subunit K	146318	236381	211542	647	169551	212908	194839	632	4.79E-05	1.43E-04	0.976816074	-0.035841154
BP1026b	12334	NADH-ubiquinone oxidoreductase subunit J	213296	192916	214800	315	275561	287092	273224	424	0.49136604	0.544828292	1.346011746	0.428712436
BP1026b	12335	NADH-ubiquinone oxidoreductase subunit I	244161	331116	309608	603	272810	330669	306712	620	0.008416883	0.014433872	1.028192371	0.040110213
BP1026b	12336	NADH-ubiquinone oxidoreductase subunit H	359552	492685	459762	410	409122	490124	458075	424	0.470954121	0.525021361	1.034146341	0.048440355
BP1026b	12337	NADH-ubiquinone oxidoreductase subunit G	647630	713544	686530	292	701042	674588	686864	294	0.610392561	0.659034486	1.006849315	0.099847786
BP1026b	12338	NADH-ubiquinone oxidoreductase subunit F	455436	528972	542983	388	510918	554462	533012	406	0.680133657	0.722886891	1.046391753	0.065423075
BP1026b	12339	NADH-ubiquinone oxidoreductase subunit E	141437	150642	138593	265	125916	140288	136959	113	0.132E-04	7.86E-04	1	0
BP1026b	12340	NADH-ubiquinone oxidoreductase subunit D	598232	735614	685542	536	638941	694688	684716	536	0.568235011	0.619058393	1	0
BP1026b	12341	NADH-ubiquinone oxidoreductase subunit C	115211	151810	142434	226	120997	146808	135304	222	3.02E-05	9.50E-05	0.982300885	-0.025763096
BP1026b	12342	NADH-ubiquinone oxidoreductase subunit B	138768	172137	164919	303	137445	161310	152268	288	7.48E-06	2.73E-05	0.95045095	-0.073248982
BP1026b	12343	NADH ubiquinone oxidoreductase chain A	64446	110937	94629	250	73360	95678	84891	235	4.82E-06	1.84E-05	0.94	-0.089267338
BP1026b	12344	Leu tRNA	34722	59196	49929	564	55414	50595	45138	501	2.40E-06	9.95E-06	0.888297982	-0.170884559
BP1026b	12345	treponeme translocase subunit SecG	39813	37377	40645	103	45825	53381	52308	133	0.206917611	0.25391818	1.291262136	0.368781908
BP1026b	12346	triisopropylphosphite isomerase	116443	94287	101247	29	142974	137546	128392	170	0.17062557	0.214530825	1.317829457	0.398163681
BP1026b	12347	oxidoreductase, zinc-binding dehydrogenase family protein	16807004	691129	81206	85	116800	127477	108804	117	0.4407705	0.16607604	1.329411765	0.01878602
BP1026b	12348	polynucleotide phosphorylase/polyadenylase	595281	707773	690621	310	753381	817784	767743	363	0.526285218	0.578435671	1.170967472	0.227013333
BP1026b	12349	30S ribosomal protein S15	495143	605349	635071	1662	713462	866044	775405	2255	0.195160399	0.214706058	1.356799037	0.402700751
BP1026b	12350	branched-chain amino acid ABC transporter periplasmic protein	23645	17141	18740	15	36219	26815	30487	24	0.919771861	0.932255434	1.6	0.678071905
BP1026b	12351	lipoprotein	48105	58352	58658	109	50090	51477	53544	103	9.72E-06	3.46E-05	0.944954128	-0.081683798
BP1026b	12352	hypothetical protein	796	614	934	8	911	1110	1636	9	0.03150056	0.051968158	1.125	0.169925001
BP1026b	12353	carbonic anhydrase	7107	1613	5984	10	9391	76148	7162	11	0.021396393	0.033263834	1	0.137503524
BP1026b	12354	sulfate permease	160198	171184	174513	1010	171566	175589	171056	112	1.23E-04	7.86E-04	1.018181818	0.05999209
BP1026b	12355	2-isopropylmalate synthase	281278	347904	331684	206	315489	347873	329750	213	0.034097825	0.050554398	0.139080583	0.048209903
BP1026b	12356	CDP-diacylglycerol--serine O-phosphatidyltransferase	177203	151818	147869	182	204749	186069	194072	223	0.128479236	0.166076064	1.225274725	0.29105026
BP1026b	12357	phosphatidylserine decarboxylase	246009	236846	242910	371	285473	281121	289921	438	0.062578948	0.087429341	1.180592992	0.239511683
BP1026b	12358	ketol-acyl reductoisomerase	148016	190567	176934	188	187904	200169	194428	190	0.01708697	0.022318883	1.130952381	0.177538186
BP1026b	12359	acetylactate synthase 3 regulatory subunit	43191	71484	61815	119	48045	59331	52714	108	1.44E-06	6.30E-06	0.907563025	-0.139902601
BP1026b	12360	acetylactate synthase 3 catalytic subunit	235510	433551	407202	220	281356	326331	315236	174	1.37E-05	4.68E-05	0.790909901	-0.384616218
BP1026b	12361	RNA polymerase factor sigma-70	453146	40834	42435	78	39917	47117	44201	17	0.40E-05	8.25E-04	0.987179448	0.01878602
BP1026b	12362	hypothetical protein	10795	15040	14992	32	9830	13026	10776	26	2.60E-09	2.21E-08	0.8125	-0.299560282
BP1026b	12363	hypothetical protein	29591	36639	36955	45	27507	31731	31622	40	6.52E-07	3.08E-06	0.888888889	-0.169925001
BP1026b	12364	RDD family protein	3492	3124	2642	6	3788	2625	3970	6	0.027934646	0.042296412	1	0
BP1026b	12365	calcineurin-like phosphoesterase	1285	1767	1718	1	1616	1872	2008	1	0.01269768	0.020849423	1	0
BP1026b	12366	glycoside hydrolase family protein	28612	11574	13727	17	37892	22528	27601	28	0.936176524	0.946741147	1.647058824	0.719892801
BP1026b	12367	diacylglycerol kinase	8181	6811	6954	13	9607	7690	8241	15	0.010435329	0.017502893	1.133666154	0.206450877
BP1026b	12368	TeKt family transcriptional regulator	323636	55458	508123	661	341181	401331	371634	89	0.104196483	0.137721121	1.333333333	0.415037499
BP1026b	12369	hypothetical protein	124101	153726	152019	243	107814	124899	120154	200	1.37E-10	1.56E-09	0.823045267	-0.280956314
BP1026b	12370	glucose-1-dehydrogenase	8994	2956	4477	7	10062	7944	8691	11	0.889300602	0.906644349	1.571428571	0.652076697
BP1026b	12371	hypothetical protein	67643	64196	59530	33	80240	72107	76544	39	0.028492393	0.034068141	1.181818182	0.2410081
BP1026b	12372	major facilitator family transporter	13044	11321	12990	9	13014	12341	12388	9	4.35E-05	1.31E-04	1	0
BP1026b	12373	amidase	31789	24588	26579	19	30093	25977	27745	20	1.79E-04	4.63E-04	0.105261579	0.074000581
BP1026b	12374	hypothetical protein	27164	18450	24199	36	28499	27915	25784	42	0.013333806	0.021776351	1.166666667	0.222392421
BP1026b	12375	adenylyl-RNA synthetase	64157	44658	53459	73	70249	63792	70249	89	0.056867844	0.079813335	1.210710889	0.295908782
BP1026b	12376	hypothetical protein	9468	4992	4901	15	9188	7845	7865	2	0.104196483	0.137721121	1.333333333	0.415037499
BP1026b	12377	permease	66107	24351	32940	15	68265	53460	53381	80	0.76739799	0.764775514	1.466666667	0.552541023
BP1026b	12378	type IV secretory pathway protein	108299	76660	105574	156	99443	129142	105986	180	0.004402674	0.008056585	1.153846154	0.206450877
BP1026b	12379	quaternary ammonium compound-resistance protein	22254	25922	21559	72	26272	25017	27951	82	0.00636145	0.01193654	1.138888889	0.187627003
BP1026b	12380	hypothetical protein	127471	86351	104911	357	125057	125090	130176	426	0.018505952	0.029241269	1.193277311	0.254295956
BP1026b	12381	DNA-binding response regulator KdpE	38035	22040	25396	40	34612	28791	30106	44	0.002782488	0.005349924	1.133333333	0.254295956
BP1026b	12382	two-component system, sensor kinase protein KdpD	101038	101038	101038	37	101038	101038	101038	36	1.75E-06	7.47E-06	1.05240693	0.1547721
BP1026b	12383	potassium-transporting ATPase subunit C	23278	18658	20443	35	12629	12915	13422	22	4.59E-18	2.40E-16	0.628571429	-0.669851398
BP1026b	12384	potassium-transporting ATPase subunit B	113940	111533	111153	52	71779	70926	68832	33	6.18E-18	3.15E-16	0.634615825	-0.650455999
BP1026b	12385	potassium-transporting ATPase subunit A	131027	122447	124990	69	89158	79942	79636	45	5.38E-18	2.77E-16	0.652173913	-0.61667136
BP1026b	12386	potassium-transporting ATPase, KdpF subunit	6791	10145	7720	88	3901	3858	4400	43	1.33E-22	1.59E-20	0.488636364	-0.103166684
BP1026b	12387	quinoxidoreductase	115673	121606	119184	121	100508	97872	96152	100	1.04E-09	9.52E-09	0.826446281	-0.275007704
BP1026b	12388	methylglyoxal synthase	52133	32697	41728	110	53077	46701	48024	125	0.014572135	0.023601329	1.136363636	0.184424571
BP1026b	12389	short-chain dehydrogenase/reductase family oxidoreductase	151315	184618	184618	24	136066	232610	236649	102	0.173215841	0.217346066	0.923076923	0.1547721
BP1026b	12390	uracil ribophosphotransferase	131877	123649	128863	196	118676	120964	112148	180	0.62E-07	3.37E-06	0.918367373	-0.122586748
BP1026b	12391	hypothetical protein	214880	224377	219936	301	204247	227380	219301	297	1.12E-04	3.04E-04	0.986710963	-0.019300556
BP1026b	12392	phosphoribosylamine-glycine ligase	109249											

BP10263	12444	sodium solute symporter family protein	5708	6629	6260	3	5492	6653	5924	3	3.93E-04	9.39E-04	1	0	
BP10263	12445	hypothetical protein	481	965	673	2	483	854	676	2	0.002728705	0.005255502	1	0	
BP10263	12446	hypothetical protein	24957	21691	22699	24	29942	28150	32675	32	0.109190042	0.143625316	1.333333333	0.415037499	
BP10263	12447	hypothetical protein	52325	47528	47154	104	73481	69288	73329	150	0.730235167	0.767777739	1.447206673	0.528378973	
BP10263	12448	chormate lyase family protein	22049	4536	6974	18	44370	18466	25660	49	4.13E-05	1.26E-04	2.722222222	1.444784843	
BP10263	12449	heat shock protein 90	4051649	5065585	4982893	2475	5749177	6436153	5917348	3177	0.392979917	0.447479219	1.283636364	0.360326563	
BP10263	12450	GntR family transcriptional regulator	123580	91785	105738	73	137815	128470	130715	90	0.051160376	0.072954999	1.23287612	0.302028537	
BP10263	12451	hypothetical protein	4532	2407	2192	4	8141	4379	4831	8	0.116662222	0.15220926	2	1	
BP10263	12452	integral membrane protein	4015	2130	2182	3	5517	4599	5093	5	0.142948591	0.183174281	1.666666667	0.736965594	
BP10263	12453	aminotransferase family protein	1597144	1797075	1784735	1435	1943138	2103126	2170246	1722	0.430709434	0.484721974	1.2	0.263044066	
BP10263	12454	L-PSR family endonuclease	204813	243931	221956	487	288800	274977	269277	604	0.137885959	0.176972363	1.442067913	0.310636773	
BP10263	12455	PhzF family phenazine biosynthesis protein	113103	257548	275076	313	368065	335923	322258	380	0.307736064	0.364908018	1.240570508	0.279836761	
BP10263	12456	hypothetical protein	116852	140772	130857	54	108859	123588	117759	49	1.02E-07	5.93E-07	0.907407407	-0.140177658	
BP10263	12457	chromate transport protein	215287	259326	233938	186	214833	215577	217696	170	2.25E-06	9.42E-06	0.913978495	-0.129767875	
BP10263	12458	acetylpolymine aminohydrolase	27755	23142	24200	24	30918	30340	31768	30	0.044601101	0.064409932	1.25	0.321928095	
BP10263	12459	allantoate amidohydrolase	19791	16442	18423	14	28422	23903	23102	19	0.240272774	0.290075272	1.357142857	0.440572591	
BP10263	12460	major facilitator family transporter	25922	12965	15008	13	34526	25594	29235	22	0.814731401	0.842533808	1.692307692	0.7589919	
BP10263	12461	LysR family transcriptional regulator	23515	23507	23218	23	21806	20334	19648	20	8.51E-06	5.68E-06	0.688965217	-0.525410263	
BP10263	12463	hypothetical protein	6261	6704	6494	14	5462	8287	7616	15	0.005204471	0.009338572	1.071428571	0.099535674	
BP10263	12462	LysR family transcriptional regulator	5370	2575	3828	4	6879	5556	5048	6	0.587813725	0.637289232	1.5	0.584962501	
BP10263	12464	integral membrane protein	11599	9378	10194	22	13054	13013	12163	27	0.014567607	0.023600877	1.227272727	0.295455884	
BP10263	12465	DNA topoisomerase IV subunit A	178188	198206	202658	83	197887	205362	188008	84	3.53E-04	8.52E-04	1.012048193	0.017277991	
BP10263	12466	DNA topoisomerase IV subunit B	183238	202196	199721	98	212765	219970	210852	108	0.005462555	0.009754229	1.102040816	0.140177658	
BP10263	12467	ABC transporter ATP-binding protein	146207	124403	124904	67	166384	149577	155496	80	0.048267032	0.069111867	1.194029851	0.255838904	
BP10263	12468	hypothetical protein	592389	604167	625723	1488	545442	542233	563506	1349	0.308813482	0.361415458	0.906586022	-0.141484178	
BP10263	12469	Rubredoxin (NADH)- reductase	56179	45273	49618	275	61144	72239	74883	30	0.575747095	0.660490918	1.403636364	0.489169222	
BP10263	12470	hypothetical protein	5	7036	9469	8950	5	8031	9179	8770	5	1.74E-04	4.52E-04	1	0
BP10263	12471	alpha/beta fold family hydrolase	3832	4021	4183	4	4043	3780	3769	4	7.75E-04	0.00119027	1	0	
BP10263	12473	translation initiation factor IF-1	18220	29383	26957	93	13553	14906	14893	54	1.32E-22	1.59E-20	0.580645161	-0.784271309	
BP10263	12474	hypothetical protein	1486	1418	1505	6	1109	1269	1244	5	1.69E-06	7.24E-06	0.833333333	-0.263034406	
BP10263	12475	hypothetical protein	3226	3205	2591	9	4761	4301	3845	14	0.77932144	0.811437131	1.555555556	0.637429921	
BP10263	12476	hypothetical protein	4745	6676	6986	21	4994	6694	5320	19	1.10E-04	2.98E-04	0.904761905	-0.144389909	
BP10263	12477	Ara (R)-ALA	730	8781	8564	8	18053	14363	14893	40	8.51E-10	5.68E-06	0.688965217	-0.525410263	
BP10263	12479	hemolysin activator protein	72192	109871	106254	67	57892	71365	64550	45	4.05E-16	1.39E-14	0.671641791	-0.572326094	
BP10263	12480	hypothetical protein	58183	97803	79283	326	67398	92362	76052	327	1.02E-04	2.80E-04	1.003067485	0.004418671	
BP10263	12481	Large exoproteins involved in heme utilization/or adhesion	151050	223912	209597	21	122415	153225	143104	15	2.06E-15	6.20E-14	0.714285714	-0.485426827	
BP10263	12482	hypothetical protein	2551	4914	3864	19	2292	3592	2929	15	3.62E-09	2.94E-08	0.789473684	-0.341036918	
BP10263	12483	hypothetical protein	453338	703725	626993	1835	399671	460261	446346	1343	0.003119025	0.005923599	0.731880109	-0.450320758	
BP10263	12484	hypothetical protein	5961	6506	7605	29	5334	5486	5349	23	7.8E-07	3.61E-06	0.739104448	-0.334419039	
BP10263	12486	hypothetical protein	293428	1795	1795	5	2239	2026	2029	0	0.001247091	0.0026	0	0	
BP10263	12485	murein-DG-endopeptidase	75499	64961	67961	105	80544	72483	76556	116	0.003024365	0.005763015	1.104761905	0.143735477	
BP10263	12487	ecotin	252241	353285	345260	586	219558	260917	231952	439	7.63E-12	1.11E-10	0.749146758	-0.416697925	
BP10263	12488	hypothetical protein	22792	12970	17205	46	20289	21626	22115	56	0.030231549	0.045434237	1.217391304	0.283792966	
BP10263	12489	hypothetical protein	892	611	683	2	1226	800	1148	3	0.691061485	0.733755703	1.5	0.584962501	
BP10263	12491	hypothetical protein	131406	148170	153547	281	137325	166553	150994	295	8.84E-04	0.001928674	1.049821064	0.070144824	
BP10263	12492	major facilitator superfamily multidrug efflux transporter	17504	13082	13554	10	22731	16038	18749	13	0.114103012	0.149316356	1.3	0.387011623	
BP10263	12493	hypothetical protein	18485	13511	13511	22	18053	14363	14893	40	8.51E-10	5.68E-06	0.688965217	-0.525410263	
BP10263	12495	hypothetical protein	23127	14217	13546	28	22122	16127	19850	32	0.008913313	0.05193496	1.142857143	0.192645078	
BP10263	12496	alpha alpha-trehalose-phosphate synthase (UDP-forming)	117022	119468	110595	82	96891	89008	92144	65	1.98E-10	2.17E-09	0.792682927	-0.33814192	
BP10263	12497	hypothetical protein	2772	3993	3624	17	2167	2857	2644	12	1.41E-11	1.91E-10	0.705882353	-0.502500341	
BP10263	12498	lipoprotein	44852	39797	42861	76	48931	40928	45759	81	0.002806379	0.005390206	1.065789474	0.091922489	
BP10263	12499	lipoprotein	10747	5466	7982	15	12237	10244	10468	21	0.146563704	0.187249311	1.4	0.485426827	
BP10263	12500	hypothetical protein	12935	12494	13341	79	12316	12299	11235	73	1.18E-06	5.25E-06	0.924050633	-0.113956189	
BP10263	12501	ABC transporter ATP-binding protein	38483	304444	3446024	2260	35480	364024	359724	269	0.3792921	0.364908018	1.036153855	0.04909455	
BP10263	12502	ABC transporter permease	238321	280156	267389	149	243027	266823	264919	146	4.39E-05	1.32E-04	0.979865772	-0.029343962	
BP10263	12503	hypothetical protein	12165	6087	7584	31	12592	11619	11762	43	0.200639009	0.247368023	1.387096774	0.472684444	
BP10263	12504	hypothetical protein	145651	252780	233612	789	152225	196692	176488	655	2.95E-09	2.46E-08	0.830167466	-0.268530394	
BP10263	12505	signal transduction histidine kinase	64261	38369	45358	37	72103	56719	58724	47	0.146369553	0.187269933	1.27027027	0.345135486	
BP10263	12506	DNA-binding response regulator OmpR	53044	37380	44100	61	54021	49701	51604	71	0.020857441	0.032506517	1.163944262	0.219009782	
BP10263	12507	hypothetical protein	8292	10104	9594	17	7383	7502	7398	13	9.93E-09	7.28E-08	0.764705882	-0.387021323	
BP10263	12508	hypothetical protein	3210	18053	14363	40	8.51E-10	5.68E-06	0.688965217	0	0.035887421	0.42873687	1.4	0.485426827	
BP10263	12509	amino acid ABC transporter substrate-binding protein	58286	66670	66238	82	72571	71894	70347	92	0.006219601	0.010971755	1.12195122	0.166099551	
BP10263	12511	histidine transport system permease	26333	29921	31104	42	30061	35563	34041	48	0.013239042	0.021649768	1.142857143	0.192645078	
BP10263	12510	histidine transport system permease	32272	48602	46931	59	35811	41654	40645	55	2.68E-05	8.55E-05	0.93223039	-0.101283336	
BP10263	12512	histidine transport ATP-binding protein	55708	69847	64618	81	62140	68628	65138	83	4.42E-04	0.001037651	1.024691358	0.035189428	
BP10263	12513	porin	350376	383505	384809	338	322877	360425	348100	312	0.006828347	0.011941517	0.923076923	-0.115477217	
BP10263	12514	nitrogen regulatory protein P-II	236096	380945	340462	941	214114	254773	245796	702	5.74E-12	8.72E-11	0.746014878	-0.387021323	
BP10263	12515	NAD synthetase	98803	70073	77356	48	109903	105327	98147	61	0.059528734	0.07042399	1.270833333	0.345747833	
BP10263	12516	hypothetical protein	18237	13350	14936	13	18372	14628	138	3	4.45E-04	0.00104413	1	0	
BP10263	12517	beta-glucosidase	176	2	45	0	328	145	138	0	4.85E-06	1.85E-05	#DIV/0!	#DIV/0!	
BP10263	12518	inorganic pyrophosphatase	645241	892649	805142	1479	707519	756288	753223	1399	0.577530491	0.627659177	0.945909398	-0.08022609	
BP10263	12519	aldehyde dehydrogenase family protein	95191	38566	48066	42	97816	69913	75916	56	0.23855635	0.288336027	1.333333333	0.415037499	
BP10263	12520	3-ketoacyl-ACP reductase	12806	11293	11781	15	12219	12282	12244	16	7.56E-05	2.14E-04	0.10666666		

BP1026b	12572	dihydroxy-acid dehydratase	214399	253398	249405	142	249706	272341	256284	154	0.002589481	0.005018169	1.084507042	0.117039421
BP1026b	12573	cytochrome C552	54891	42829	45379	106	57968	57835	58619	130	0.07144523	0.09847856	1.226415094	0.294447358
BP1026b	12574	hypothetical protein	45951	31297	36139	53	48260	40454	39616	60	0.020461745	0.031875123	1.12075472	0.178970141
BP1026b	12575	DNA polymerase III subunit chi	55921	34731	42429	108	54911	52975	51001	135	0.171488508	0.215497971	1.285730070	0.362570070
BP1026b	12576	leucyl aminopeptidase	515849	420316	447550	305	551494	519059	522336	351	0.937606219	0.947575933	1.50819672	0.202661788
BP1026b	12577	permease	81326	105735	99216	86	87635	102705	107007	90	1.733E-04	4.51E-04	1.046511628	0.06588342
BP1026b	12578	hypothetical protein	60110	72280	66181	57	61714	69125	68456	57	1.56E-04	4.08E-04	1	0
BP1026b	12579	sirohdrochlorin cobaltochelatase	20172	9967	12415	36	24570	18018	20307	54	0.535659672	0.58734668	1.5	0.584962501
BP1026b	12580	urophyllin-III C-methyltransferase	18879	6873	7736	14	30458	51500	17686	27	0.218607775	0.266639426	1.928571429	0.94753258
BP1026b	12581	sulfate adenylyltransferase, subunit I	258447	264567	265366	199	272478	277086	268517	207	4.15E-04	9.83E-04	1.040201005	0.056862337
BP1026b	12582	sulfate adenylyltransferase subunit 2	71603	75030	78778	105	70756	76523	71055	75	3.64E-05	1.33E-04	0.974092924	-0.03796785
BP1026b	12583	phosphoadenosine phosphosulfate reductase	20312	18246	16340	24	20730	19350	20547	26	0.004080906	0.007539946	0.833333333	0.115477217
BP1026b	12584	hypothetical protein	5412	5372	4850	9	5974	5036	5632	10	0.005315593	0.009518903	1.111111111	0.152003093
BP1026b	12585	sulfite reductase	99935	131312	121113	69	74894	87689	85345	49	9.12E-15	2.48E-13	0.710144928	-0.493814613
BP1026b	12586	transcriptional regulator CysB-like protein	50426	56327	56080	57	44705	50764	49947	51	9.87E-07	4.48E-06	0.894736842	-0.160464672
BP1026b	12587	hypothetical protein	7344	5771	6727	19	7236	6816	6468	20	0.001341881	0.002788214	1.052631579	0.074000581
BP1026b	12588	Leu tRNA	1697	2161	1891	22	1489	2164	1991	22	6.25E-05	1.81E-04	1	0
BP1026b	12589	hypothetical protein	20184	1850	5208	12	6462	5955	6736	9	0.12E-08	8.07E-09	1	0
BP1026b	12590	putative replication protein	12133	19570	16158	30	7903	10276	8857	17	8.74E-25	1.44E-22	0.566666667	-0.81942754
BP1026b	12592	IS407A, transposase OrfA	43607	71570	62579	224	41788	50819	48476	178	7.63E-10	7.26E-09	0.794642857	-0.331621491
BP1026b	12593	putative insertion element protein	114203	195965	172486	225	94095	118925	114693	152	5.57E-19	3.46E-17	0.675555556	-0.565853678
BP1026b	12595	hypothetical protein	1532191	2645665	2293260	1128	1432780	1830096	1632502	833	0.001784383	0.0035819	0.752602964	-0.403149421
BP1026b	12596	hypothetical protein	937069	1559124	1293448	307	787496	1139467	991739	236	0.03276431	0.171063166	0.768729642	-0.379451796
BP1026b	12597	hypothetical protein	15277	25820	23610	19	13098	16316	14654	81	7.94E-15	2.19E-13	0.680672269	-0.55496776
BP1026b	12598	DeoR family transcriptional regulator	136366	212049	191933	178	107408	137566	121352	121	1.74E-19	1.16E-17	0.67975281	-0.55687034
BP1026b	12599	hypothetical protein	17621	17543	16740	11	805	814	724	11	0.02E-10	2.75E-09	0.233636364	0.18705553
BP1026b	12600	hypothetical protein	5239	2029	2847	7	5832	3676	5264	10	0.707789809	0.74898203	1.428571429	0.514573173
BP1026b	12601	DNA-binding protein	92302	112928	98126	179	81274	90906	95288	158	1.35E-07	7.55E-07	0.882681564	-0.180035029
BP1026b	12602	class II aldolase/alducin domain-containing protein	23316	28303	30076	32	19321	22466	17989	22	1.59E-12	2.69E-11	0.6875	-0.540568381
BP1026b	12603	dihydropicolinate lyase	10946	12643	10379	12	7022	10610	10488	11	3.09E-07	1.59E-06	0.916666667	-0.125530882
BP1026b	12604	MOSC domain-containing protein	18953	10805	13909	21	14777	11892	13744	19	1.86E-06	7.93E-06	0.904761905	-0.144389099
BP1026b	12605	alpha/beta fold family hydrolase	10911	3678	7336	8	13743	9613	9821	12	0.193548578	0.240089031	1.95	0.584962501
BP1026b	12606	LysR family transcriptional regulator	6390	3313	4028	15	6649	5955	6736	9	0.32129601	0.74570492	1.38463638	0.48542682
BP1026b	12607	LysR substrate binding domain-containing protein	92941	74560	77762	84	101145	90313	92251	98	0.007125596	0.012412903	1.166666667	0.222392421
BP1026b	12608	copper resistance protein	6125	5074	5575	14	7216	6407	6279	17	0.032261858	0.048139542	1.214285714	-0.280107919
BP1026b	12610	ribosomal small subunit pseudouridine synthase A	20982	11764	13357	21	26231	18143	21375	30	0.360167206	0.413796499	1.428571429	0.514573173
BP1026b	12609	hypothetical protein	83960	137348	121996	605	70900	86124	86124	427	1.59E-14	4.13E-13	0.705785124	-0.502699073
BP1026b	12611	NAD-dependent epimerase/dehydratase family protein	87174	96876	97889	94	78288	83851	86976	83	2.09E-07	1.12E-06	0.882978723	-0.17954492
BP1026b	12612	CDF-6-deoxy-delta-3,4-glucosene reductase	81478	75576	75476	75	88112	88678	88668	85	0.005862458	0.010420855	1.133333333	0.180572246
BP1026b	12613	acetylcholinesterase	84920	70471	70437	65	85594	89072	85594	74	0.00510034	0.00979792	1.133463636	0.180572246
BP1026b	12614	acetyltransferase	18475	16139	16102	36	18155	16985	17090	37	4.27E-04	0.001007255	1.027777778	0.039523664
BP1026b	12615	hypothetical protein	45403	59894	53195	78	38869	43398	39193	60	3.22E-10	3.38E-09	0.769230769	-0.37851623
BP1026b	12616	branched-chain amino acid ABC transporter ATP-binding protein	66123	72757	73093	98	57244	60659	60370	82	2.62E-08	1.73E-07	0.836734694	-0.257157839
BP1026b	12617	leucine/isoleucine/valine transport system ATP-binding protein	45282	51625	54223	65	42328	43878	41145	54	1.15E-07	6.59E-07	0.830769231	-0.267480311
BP1026b	12618	branched-chain amino acid ABC transporter permease	66887	72127	70817	59	59243	64399	64778	53	1.11E-06	4.97E-06	0.893305085	-0.154272595
BP1026b	12619	amino acid transport permease protein	11776	39367	36919	36	25722	31658	29943	30	4.44E-08	2.80E-07	0.833333333	0.106344006
BP1026b	12620	hypothetical protein	11530	17543	16740	11	805	814	724	11	0.12E-10	2.75E-09	0.954545455	0.114194
BP1026b	12621	4-hydroxy-3-methyl-2-oxylidiphosphate reductase	366975	299608	294381	326	380696	340299	352176	364	0.126322448	0.163621869	1.116564417	0.159066486
BP1026b	12622	FKBP-type peptidyl-prolyl cis-trans isomerase	193973	169687	198598	411	164991	191505	178714	391	1.04E-05	0.9513382	-0.071967876	
BP1026b	12623	DNA repair protein RadC	1401	1198	747	1	1282	1131	915	1	0.003932418	0.007293926	1	0
BP1026b	12624	SOS ribosomal protein L28	125323	221864	194714	367	157379	214885	183239	376	3.61E-04	8.68E-04	1.024523161	0.034952599
BP1026b	12625	SOS ribosomal protein L33	233125	393874	350646	1939	339162	455334	389324	2348	0.393838731	0.447888027	1.210933471	0.276119605
BP1026b	12626	L-asparagine oxidase	95824	82948	89279	54	104393	99868	103836	64	0.004326157	0.007930445	1.148148148	0.199380808
BP1026b	12627	nicotinamide nucleotide pyrophosphorylase	180934	240094	232148	19	29635	29635	29635	19	0.01040887	0.01732184	1.157894737	0.211504371
BP1026b	12628	quinolinate synthetase	299667	250535	270230	240	314756	313190	303191	272	0.081380947	0.110690087	1.133333333	0.180572246
BP1026b	12629	fatty acid desaturase family protein	829984	1126337	1060235	842	875209	1030651	991771	808	0.749977803	0.785541954	0.96919952	-0.05946494
BP1026b	12630	mechanosensitive ion channel family protein	81919	56126	60835	49	95963	80059	88112	65	0.17628536	0.220858411	1.326530612	0.407657969
BP1026b	12631	NOL1/NOP2/Sun family protein	145466	73434	93208	82	170313	139030	143754	119	0.78694121	0.817975512	1.451219512	0.537265759
BP1026b	12632	phosphoribosylglycinamide formyltransferase	19375	21113	20060	30	20937	22797	23060	33	0.003822711	0.007105145	1.1	0.137053524
BP1026b	12633	bifunctional riboflavin kinase/FMN adenylyltransferase	51407	40702	38456	41	62211	55387	62692	57	554896753	0.559990577	1.390243902	0.47533801
BP1026b	12634	isoleucyl-tRNA synthetase	262387	271346	273819	194	314485	319819	313144	111	0.159749204	0.020376763	1.180876106	0.239827015
BP1026b	12635	lipoprotein signal peptidase	28140	36581	35571	66	35225	39869	36083	73	0.012549645	0.020619152	1.106060606	0.14545044
BP1026b	12636	bifunctional phosphatantennoloyl-cysteine decarboxylase/phosphopantothetate synthase	89358	48318	57205	53	110485	91918	91214	81	0.788094102	0.818902485	1.528301887	0.611929548
BP1026b	12637	deoxyuridine 5'-triphosphate nucleotidohydrolase	21439	20716	20610	46	22096	22096	22504	51	0.003101581	0.005897611	1.108695652	0.148863386
BP1026b	12638	hypothetical protein	4932	5291	4565	6	5032	5844	5261	6	0.099708728	0.016398183	1	0
BP1026b	12639	hypothetical protein	14530	7026	8409	13	16306	13071	13421	19	0.298263172	0.35090114	1.461538462	0.547487795
BP1026b	12640	amino acid permease	29845	29845	29845	19	29845	29845	29845	19	0.06400887	0.07321384	1.157894737	0.211504371
BP1026b	12641	ATP-dependent Clp protease ATP-binding subunit clpA	269274	3348906	3132479	1337	2514566	2631573	2561507	1123	0.001704618	0.003442714	0.839940165	-0.251641538
BP1026b	12642	ATP-dependent Clp protease adaptor protein ClpS	475307	813797	725291	2131	452280	593939	537780	1676	0.072294506	0.099539824	0.786485218	-0.366508444
BP1026b	12643	hypothetical protein	247637	402970	354299	1893	282454	369615	336236	1861	0.014627894	0.023667986	0.983095615	-0.024596356
BP1026b	12644	cold shock transcription regulator protein	856208	1379916	1185883	4636	911338	1162590	1115651	4321	0.47042808	0.524714677	0.932053494	-0.101515335
BP1026b	12645													

BP1026b	12697	peptide methionine sulfoxide reductase	81964	110824	111870	181	81347	92764	86845	155	2.84E-08	1.86E-07	0.856353591	-0.223721482
BP1026b	12698	flavin reductase domain-containing protein	66846	60752	63773	123	67233	65514	66992	129	6.89E-04	0.001553026	1.048780488	0.06871275
BP1026b	12699	transcription regulator AsnC	81364	103007	102091	189	88516	100747	91104	185	1.98E-05	6.54E-05	0.978815599	-0.030606964
BP1026b	12700	cyclase	198673	15114	18189	24	20964	194131	148	27	0.005810345	0.10331148	0.98813277	0.166925001
BP1026b	12701	xyreninase	45425	30911	31805	28	42650	33555	35518	29	0.001912771	0.003811567	1.035714286	0.050626073
BP1026b	12702	tryptophan 2,3-dioxygenase family protein	70932	70687	76322	76	64947	67482	64140	69	1.30E-06	5.74E-06	0.907894737	-0.139403057
BP1026b	12703	4-hydroxybenzoate transporter	12152	8323	9527	7	12310	9169	9757	7	1.77E-04	4.60E-04	1	0
BP1026b	12704	hypothetical protein	275	194	95	0	128	468	438	1	0.01459984	0.023628688	#DIV/0!	#DIV/0!
BP1026b	12705	hypothetical protein	556	464	766	5	638	541	512	5	0.005252607	0.009414173	1	0
BP1026b	12706	2-dehydropanoate 2-reductase	10882	10185	9556	10	11024	9183	9284	10	1.30E-05	4.49E-05	1	0
BP1026b	12707	aldehyde dehydrogenase family protein	28645	11493	15325	11	27270	18696	20230	15	0.1283931	0.1659762	1.363636364	0.447458971
BP1026b	12708	benzoylformate decarboxylase	26430	15775	19610	12	29861	20823	27265	16	0.062502552	0.08734206	1.333333333	0.415037499
BP1026b	12709	transcriptional regulatory protein	23222	12879	15945	18	24885	21475	22816	25	0.146124121	0.186789377	1.388888889	0.473931188
BP1026b	12710	mammotil dehydrogenase family protein	3263	2368	2482	1	4404	3028	4060	2	0.761582757	0.795816173	2	1
BP1026b	12711	xylokisase	26296	14489	18136	13	31799	26645	29306	19	0.553281379	0.604552184	1.461538462	0.547487795
BP1026b	12712	transcriptional regulator	35074	18609	23591	27	37850	30589	31366	35	0.129990661	0.167783262	1.296296296	0.374395515
BP1026b	12713	major facilitator family transporter	1371	484	544	0	1984	1405	1916	1	1.10E-04	2.98E-04	#DIV/0!	#DIV/0!
BP1026b	12714	beta-lactamase transporter	13098	49871	44136	22	52703	2886	15464	2	0.300781228	0.53333454	1	0
BP1026b	12716	LysR family transcriptional regulator	6351	2267	3283	4	7933	6389	5828	7	0.809123	0.837838986	1.75	0.807354922
BP1026b	12718	ABC sugar transporter, ATP-binding protein	11436	10072	9274	9	9977	9082	7867	8	1.34E-07	7.52E-07	0.888888889	-0.169925001
BP1026b	12719	HAD-superfamily hydrolase	2911	943	1761	2	2998	1845	2740	3	0.262277895	0.313623568	1.5	0.584962501
BP1026b	12720	binding-protein-dependent transporter inner membrane component	8413	8156	8948	9	6613	7574	8641	8	3.05E-06	1.23E-05	0.888888889	-0.169925001
BP1026b	12721	mammotil ABC transporter permease	6684	7582	6673	7	5221	6287	6744	6	9.33E-06	3.34E-05	0.857142857	-0.222392421
BP1026b	12722	extracellular solute-binding protein	13780	16279	15542	11	12893	12483	13132	9	1.22E-08	6.74E-08	0.818181818	0.459506617
BP1026b	12723	magasin 6-phosphate kinase protein	23075000	1117	117	1	4861	2792	3761	2	0.502423112	0.5624111	2	1
BP1026b	12724	carbohydrate kinase	1796	767	1159	1	2241	1637	1697	1	0.803438708	0.832640181	1	0
BP1026b	12725	sorbitol dehydrogenase	11629	10510	12580	14	11569	11308	11118	14	1.36E-05	4.65E-05	1	0
BP1026b	12726	transcriptional regulator np20	23439	32009	27966	59	20994	22373	21618	46	1.49E-09	1.32E-08	0.779661017	-0.359081093
BP1026b	12727	ABC transporter substrate binding protein	52670	57155	62484	59	58059	59456	54914	59	1.51E-04	3.98E-04	1	0
BP1026b	12728	ABC transporter ATP-binding protein	27784	18279	20176	25	31666	25849	25688	32	0.054671715	0.077416629	1.28	0.35614381
BP1026b	12729	metal ABC transporter permease	17268	13482	11189	16	17983	14310	15992	19	0.00717921	0.012492422	1.70125373	0.24767513
BP1026b	12730	S-form lyphatase hydrolase	49871	44136	49633	22	52703	2886	15464	2	0.300781228	0.53333454	1.032530325	0.44670101
BP1026b	12731	glutathione-dependent formaldehyde dehydrogenase	110481	117053	109596	101	111096	120989	112279	103	6.32E-05	1.83E-04	0.10909108	0.02829044
BP1026b	12732	AraC family transcriptional regulator	40269	18958	22374	26	48864	33241	38488	38	0.799549065	0.829568522	1.461538462	0.547487795
BP1026b	12733	xylosylase kinase	5031	2207	2604	2	5881	4197	4948	3	0.963872698	0.97058666	1.5	0.584962501
BP1026b	12734	permease protein	11800	9952	12070	8	10847	10947	12456	8	5.11E-05	1.51E-04	1	0
BP1026b	12735	RND efflux system outer membrane lipoprotein	399966	336150	339634	236	477170	461286	453150	300	0.558182015	0.609164193	1.271186441	0.346175641
BP1026b	12736	inner membrane protein	992259	1211974	1136738	247	1109796	1206677	1157484	361	0.711066875	0.751653279	1.040329422	0.24767513
BP1026b	12737	RND family efflux transporter MFP subunit	291253	288260	301341	232	35236	370152	340943	282	0.28681552	0.342780838	1.208693652	0.218640286
BP1026b	12738	repressor protein	43970	44777	42058	68	47918	47173	46547	34	0.004571208	0.007714019	1.088252594	0.121990524
BP1026b	12739	hypothetical protein	26177	20520	21616	31	26468	23697	26344	34	0.004587137	0.008355143	1.096774194	0.12366531
BP1026b	12740	hypothetical protein	67719	64168	68740	182	64633	70430	71161	187	3.65E-04	8.78E-04	1.027472527	0.03909892
BP1026b	12741	hypothetical protein	51726	43791	47007	112	46816	45517	45399	108	7.40E-05	2.10E-04	0.964285714	-0.05246742
BP1026b	12742	serine protease	595656	698056	666170	439	508125	525254	527732	349	0.07903292	0.10825356	0.79498861	-0.330993903
BP1026b	12743	sensor kinase protein	44890	43406	40687	32	48664	41822	43373	33	0.001299592	0.002709318	1.01325	0.044394119
BP1026b	12745	two-component system response regulator QseB	56126	56126	59061	86	54948	52485	54707	86	0.68E-05	2.46E-05	0.9883781	0.016871861
BP1026b	12744	peptidase	38795	19821	24749	18	15152	36984	41250	28	0.863000014	0.884172347	1.555555556	0.637429921
BP1026b	12746	serine desaturase family protein	46541	65633	62819	63	42143	47503	49488	50	0.96E-01	9.02E-09	0.793650794	-0.333423734
BP1026b	12747	lipase	147518	149699	147270	129	175492	173896	162734	149	0.027413823	0.041598188	1.15503876	0.207941265
BP1026b	12748	Sua5/YcoO/YrdC/YwC family protein	40587	27460	30809	32	49537	37673	40286	41	0.223020613	0.271283363	1.28125	0.357552005
BP1026b	12749	phosphoribosylaminoimidazole carboxylase subunit	43445	25312	26159	26	55250	37059	38621	36	0.487991472	0.541276619	1.384615385	0.469485283
BP1026b	12750	phosphoribosylaminoimidazole carboxylase catalytic subunit	30566	38563	36143	67	36494	34274	36192	68	0.001036779	0.002212123	1.04025373	0.21373651
BP1026b	12751	phosphoribosylaminoimidazole succinocarboxamide synthase	26159	11653	12127	123	11809	11659	11659	127	0.33E-05	9.42E-06	0.9883781	0.016871861
BP1026b	12752	fructose-1,6-bisphosphate aldolase	529175	646995	631287	565	581047	640067	612006	573	0.66136406	0.706769463	1.014159292	0.020284271
BP1026b	12753	pyruvate kinase	265126	207308	224929	169	304838	281641	275451	120	0.19046628	0.240654845	1.24260355	0.313366081
BP1026b	12754	phosphoglycerate kinase	236892	225831	236712	195	269123	239052	240540	209	0.001982769	0.003934802	1.071794872	0.100028818
BP1026b	12755	hypothetical protein	4519	2714	3115	10	4008	3510	4048	11	0.030552389	0.045861482	1.1	0.137035254
BP1026b	12756	AzC family peptidase	30232	32471	30304	41	26579	27567	30100	37	2.49E-06	1.03E-05	0.902439024	-0.148098639
BP1026b	12757	branched-chain amino acid aminotransferase	307330	421779	383963	401	310714	337366	330320	352	0.001442138	0.002097087	0.877805486	-0.188026808
BP1026b	12758	hypothetical protein	9009	9009	9009	34	9009	9009	9009	34	0.90090798	0.9167633	1.92	0.42466
BP1026b	12759	heptoyl-acyltransferase II	43656	35071	37573	37	46558	45621	48460	45	0.074652164	0.102272857	1.216216216	0.282399731
BP1026b	12760	hypothetical protein	67648	77366	73681	163	56666	67828	66357	142	2.33E-07	1.24E-06	0.871165644	-0.198881035
BP1026b	12761	alpha/beta fold family hydrolase	26727	22169	21486	22	28458	26102	26532	26	0.008652924	0.01479708	1.181818182	0.2410081
BP1026b	12762	hypothetical protein	8668	3489	4965	9	7800	5455	5937	10	0.011144723	0.018588366	1.111111111	0.152003093
BP1026b	12763	M48 family peptidase	31996	32275	33175	18	31267	32401	31644	18	1.08E-04	2.94E-04	1	0
BP1026b	12764	molybdenum cofactor biosynthesis protein McoC	30291	26987	28123	57	32613	30520	28617	61	0.001424613	0.0020939671	1.070175439	0.097847323
BP1026b	12765	TonB domain-containing protein	11341	12341	12341	11806	9265	9265	9265	27	0.43323884	0.466891919	0.9883781	0.016871861
BP1026b	12766	hypothetical protein	16894	16284	19245	37	18625	19174	19174	40	0.002864623	0.005493666	1.111111111	0.152003093
BP1026b	12767	Q-antigen polymerase family protein	60659	47862	47640	28	78403	65445	73604	40	0.45459027	0.548537677	1.428571429	0.514573173
BP1026b	12768	Type IV pilin PilA	2471	1271	1764	3	2848	2472	2124	5	0.277796121	0.30729752	1.666666667	0.736965594
BP1026b	12769	TerC family integral membrane protein	38240	22929	26831	41	43340	40312	42188	58	0.444800101	0.691187804	1.414634146	0.500428991
BP1026b	12770	succinyl-CoA synthetase subunit alpha	392969	382051	403730	445	508379	521921	486929	573	0.409783215	0.463584328	1.287640499	0.364729803
BP1026b	12771	succinyl-CoA synthetase subunit beta	469843	662607	608568	497	521691	605764	568254	484	0.509794287	0.562225661	0.973843058	-0.038238804
BP1026b	12772	hypothetical protein	82942											

BP10268	12819	EAL/GGDEF domain-containing protein	103726	92233	97109	51	106497	102410	96736	54	1.77E-04	4.60E-04	1.058823529	0.08246216
BP10268	12820	Ser/Thr protein phosphatase family protein	30257	29404	34030	18	26880	32661	29760	17	2.09E-05	6.85E-05	0.944444444	-0.08246216
BP10268	12821	hypothetical protein	23179	15183	15579	37	27230	23516	24071	52	0.255367918	0.306010226	1.405405405	0.490986353
BP10268	12822	hypothetical protein	22978	33823	31533	84	6.32E-09	4.33E-08	31338	67	6.32E-09	4.33E-08	0.797619048	0.32629233
BP10268	12823	galactonate dehydratase	49610	21296	37440	36	0.001726163	0.003482863	41349	37	0.001726163	0.003482863	1.027777778	0.039528364
BP10268	12824	transmembrane transporter protein	29139	8365	12305	17	34984	21281	24525	29	0.967610344	0.973507569	1.705882353	0.770518154
BP10268	12825	cytochrome c	88200	93372	92919	121	91860	95219	93452	124	1.18E-04	3.18E-04	1.024793388	0.035333073
BP10268	12826	cytochrome C	738913	9117172	910017	658	736397	836318	816319	613	0.690254365	0.733022792	0.91610942	-0.10220051
BP10268	12827	ATP-dependent RNA helicase	64953	60967	61084	42	63903	63628	63683	43	3.52E-04	8.50E-04	1.023809524	0.03947332
BP10268	12828	hypothetical protein	109385	125373	124444	238	115780	108931	106175	220	3.74E-07	1.87E-06	0.923469748	-0.11345805
BP10268	12829	hypothetical protein	387193	661222	644289	164	517940	599592	563820	671	0.22319169	0.25680629	0.897619048	0.17207460
BP10268	12830	gamma-glutamyl transferase 2	367736	207522	244813	164	348529	291832	305883	189	0.122769874	0.159646646	1.152429024	0.20469042
BP10268	12831	glycerol-3-phosphate regulon repressor	51505	58675	61809	73	43654	48384	44614	58	1.09E-09	9.95E-09	0.794520548	-0.331843564
BP10268	12832	hypothetical protein	22198	35935	32570	305	14277	19358	19936	180	4.63E-20	3.38E-18	0.590163934	-0.760812336
BP10268	12833	hypothetical protein	126544	187790	177933	828	92384	115979	109247	534	9.57E-22	9.25E-20	0.644927536	-0.632791026
BP10268	12834	hypothetical protein	19049	8070	9013	32	20211	15134	15988	45	0.300832137	0.353333454	1.40625	0.491853096
BP10268	12835	glycerol-3-phosphate dehydrogenase	61212	31699	39636	28	77241	56784	62781	42	0.95546987	0.963456437	1.5	0.584962501
BP10268	12836	glycerol kinase	71664	91812	80801	52	80374	88609	83600	34	3.90E-04	9.33E-04	1.038461538	-0.48944784
BP10268	12837	glycerol uptake facilitator protein	41543	26889	21893	44	47281	44406	50107	65	0.949436522	0.957988628	1.472722722	0.562936194
BP10268	12838	hypothetical protein	1127	2015	2109	12	1413	2045	1523	11	4.61E-05	1.38E-04	0.916666667	-0.125530882
BP10268	12839	hypothetical protein	722	1046	921	2	797	800	971	2	0.002210197	0.00434536	1	0
BP10268	12841	3-phosphoshikimate 1-carboxyvinyltransferase	6626	3720	4462	3	5843	5521	5486	4	0.020091136	0.031460733	1.333333333	0.415037499
BP10268	12840	3-phosphoshikimate 1-carboxyvinyltransferase	10880	9204	9605	7	10199	9204	10176	7	3.69E-05	1.14E-04	1	0
BP10268	12842	asparagine synthase	4203	3982	3709	2	3365	3592	3876	2	1.17E-04	3.16E-04	1	0
BP10268	12843	hypothetical protein	13423	17520	11100	10	12442	11861	12821	10	4.65E-05	1.39E-04	1	0
BP10268	12844	hypothetical protein	140844	261823	261823	35	449986	387401	387401	49	0.542487937	0.593593701	1	0.485426827
BP10268	12845	HAD-superfamily hydrolase	30001	22793	28664	39	30655	29158	27550	42	0.00112058	0.002374796	1.076923077	0.106915204
BP10268	12846	3,4-dihydroxy-2-butanone 4-phosphate synthase	13667	13673	11549	17	12876	10860	12146	16	1.08E-06	4.86E-06	0.941176471	-0.08462841
BP10268	12847	DNA-binding protein	125997	102535	101043	164	128911	112988	119674	180	0.001198237	0.002520444	1.097560976	0.134301092
BP10268	12848	major facilitator family transporter	5220	5122	5543	4	5528	5086	5363	4	0.0015627	0.003193365	1	0
BP10268	12849	LysR family transcriptional regulator	29328	29843	30412	32	33095	33165	29233	34	0.001689716	0.003415916	1.0625	0.087462841
BP10268	12850	(dimethylallyl)adenosine (RNA methyl)transferase	48609	52496	51817	37	57608	59101	56926	42	0.011922858	0.019739268	1.135151515	0.182864057
BP10268	12851	Pho1 family protein	52236	92233	79149	72	85434	89841	87868	103	0.022476014	0.308278319	1.102982863	0.167621028
BP10268	12852	hypothetical protein	143244	118357	131670	161	162688	157350	156204	195	0.071336474	0.098415153	2.11180124	0.276413436
BP10268	12853	hypothetical protein	17026	10790	12565	21	19350	15538	17227	27	0.086792936	0.117237745	1.285714286	0.362570079
BP10268	12854	magnesium and cobalt efflux protein CorC	106649	147899	135689	146	83564	99714	101476	106	4.98E-14	1.11E-12	0.726027397	-0.461904104
BP10268	12855	apolipoprotein N-acyltransferase	72848	67090	65427	40	66082	64094	67721	38	3.00E-05	9.44E-05	0.95	-0.074000581
BP10268	12856	glycyl-L-RNA synthetase subunit alpha	86706	128741	118036	110	88545	101652	96643	94	1.88E-08	1.29E-07	0.854545455	-0.226770862
BP10268	12857	glycyl-tRNA synthetase subunit beta	105162	75384	79728	41	143006	111898	115352	57	0.252839528	0.303494519	1.390243902	0.47533801
BP10268	12858	2-D-lysine peptidyl cys-trans isomerase	55564	92233	39842	35	59834	58321	58321	103	0.022476014	0.308278319	1.386666667	0.071621028
BP10268	12859	phospholipid and glycerol acyltransferase	21675	30700	25747	33	23993	28050	26244	33	1.48E-04	3.89E-04	1	0
BP10268	12860	hypothetical protein	69188	84503	85103	87	74795	74496	73367	81	4.96E-06	1.89E-05	0.931034483	-0.10309349
BP10268	12861	lactoylglutathione lyase	80394	111783	101562	251	82339	97249	92443	232	1.71E-06	7.31E-06	0.924302789	-0.113562559
BP10268	12862	integral membrane protein	12424	12743	14063	13	11015	14004	13029	13	1.04E-05	3.67E-05	1	0
BP10268	12863	dimethyladenosine transferase	117377	134786	128238	153	108645	116269	117819	137	9.67E-08	5.66E-07	0.895424837	-0.15935576
BP10268	12864	4-hydroxythreonine-4-phosphate dehydrogenase	101794	92289	102907	95	109991	99647	102552	97	8.04E-05	2.71E-04	1.02105623	0.059057234
BP10268	12865	Pro-type peptidyl-prolyl cis-trans isomerase	125163	348233	380149	258	425724	428632	428632	197	0.003666864	0.00846245	0.96997561	-0.05742828
BP10268	12866	organic solvent tolerance protein	588287	662794	643305	267	589609	630019	605064	257	0.497596626	0.550321516	0.962548616	-0.055071382
BP10268	12868	hypothetical protein	5520	3079	3466	29	5109	6047	5444	40	0.300635399	0.353287051	1.379310345	0.4639471
BP10268	12867	phosphotransferase domain-containing protein	53994	68732	62631	55	54752	57395	56384	50	1.72E-06	7.34E-06	0.909090909	-0.137503524
BP10268	12869	nucleotidyltransferase family protein	23085	12150	13412	22	32361	19574	21312	33	0.597151339	0.646407308	1.5	0.584962501
BP10268	12870	ATP-binding transmembrane ABC transporter protein	67526	67205	69549	36	69025	67844	66822	36	1.19E-04	3.20E-04	1	0
BP10268	12871	thioesterase superfamily protein	56596	68646	61655	156	55891	46395	48766	117	1.56E-11	2.08E-10	0.75	-0.415037499
BP10268	12872	nitrate reductase associated protein	1264872	183123	166333	330	102434	116766	119643	235	1.35E-16	5.37E-15	0.712121212	0.415037499
BP10268	12873	formate dehydrogenase family accessory protein FdhD	28883	14328	17701	24	27616	29441	23526	29	0.036509071	0.053798778	1.1	0.321928095
BP10268	12874	acetyl-CoA hydratase	14938	14716	16381	20	16073	17077	17369	22	0.002266842	0.004446498	1.1	0.137503524
BP10268	12875	acetyl-CoA acetyltransferase	164528	180815	177372	145	174454	183701	173704	142	2.70E-04	6.72E-04	1.013793103	0.019763255
BP10268	12876	3-hydroxyacyl-CoA dehydrogenase	302988	288683	291678	120	298246	296073	302812	127	0.004323657	0.007928179	1.016666667	0.023846742
BP10268	12877	acyl-CoA dehydrogenase domain-containing protein	354389	456282	431941	231	350496	380488	378464	206	0.002965743	0.005661627	0.891774892	-0.165248514
BP10268	12878	putative transcriptional regulator for fatty acid degradation FadP, TetR family	1393911	1306165	1401864	2796	1387493	1560025	1570288	3079	0.458690454	0.512899325	1.012146023	0.139097507
BP10268	12879	cardiolipin synthase II	57778	72539	70854	52	61411	68504	63600	50	2.84E-05	9.02E-05	0.961538062	-0.056833528
BP10268	12880	GATP pyrophosphohydrolase	30434	24882	25313	55	32148	34882	32954	69	0.075340649	0.103145328	1.254545455	0.327164743
BP10268	12881	aspartyl-tRNA synthetase	566465	671349	646878	349	621721	639292	619897	348	0.602656797	0.651804498	0.99713467	-0.00413973
BP10268	12882	hypothetical protein	47427	57679	54211	81	52572	55141	56997	84	5.22E-04	0.001204735	1.037037037	0.05246742
BP10268	12883	regulatory protein	24439	38761	32913	93	32936	31941	33496	95	7.11E-04	0.00159608	1.021505376	0.036096797
BP10268	12884	thioesterase S-methyltransferase family protein	48052	38842	35647	52	47844	38020	45992	56	0.004564017	0.008322697	1.076923077	0.106915204
BP10268	12885	ubiquitinon biosynthesis protein UbIB	37848	34085	33025	205	302477	315366	315366	197	0.003666864	0.00846245	0.96997561	-0.05742828
BP10268	12886	hypothetical protein	73848	90110	87359	129	47148	77349	77388	129	4.35E-06	1.68E-05	0.930232558	-0.10433666
BP10268	12887	predicted RNA	62053	3845	8115	666	76940	33513	45917	1401	0.007584823	0.013114552	2.103603661	0.072862873
BP10268	12888	transmembrane protein	1012711	889006	912787	919	1035157	977977	1005013	986	0.86599114	0.887007848	1.072905332	0.101522785
BP10268	12889	ubiquitinon/menagubiquinon biosynthesis methyltransferase	75541	86316	84472	912	71761	79713	70976	101	1.04E-06	4.71E-06	0.901785714	-0.149143439
BP10268	12890	HIT family hydrolase	29758	21690	24243	60	29938	28147	26366	68	0.0038413			

BP1026B_12942	putative ATP binding protein	228239	390527	348108	210	219420	296644	250301	166	7.03E-10	6.78E-09	0.79047619	-0.339206086
predicted RNA	-	22240	37670	34710	671	26315	37366	32091	679	3.74E-04	8.97E-04	1.011922504	-0.017098808
predicted RNA	-	41889	73419	66984	660	49916	67933	58793	640	4.12E-05	1.25E-04	0.96969697	-0.044394119
predicted RNA	-	18923	32966	23554	3768	28205	37688	28205	635	7.74E-04	0.00136334	0.95789693	-0.145908053
BP1026B_12943	hypothetical protein	144800	239098	210021	111	125447	153721	141158	79	1.36E-16	5.28E-15	0.711711712	-0.490631118
BP1026B_12944	hypothetical protein	123519	197604	176948	522	108919	127423	123541	377	5.32E-16	1.77E-14	0.722222222	-0.469485283
BP1026B_12945	hypothetical protein	19389	26119	23548	91	17672	15970	16001	65	2.70E-12	4.34E-11	0.714285714	-0.485426827
BP1026B_12946	hypothetical protein	87770	104929	101328	61	88744	96389	95199	59	6.08E-06	2.27E-05	0.967213115	-0.048094288
BP1026B_12947	dienelactone hydrolase family protein	24109	25708	25114	36	20940	22102	24053	32	2.30E-06	9.55E-06	0.888888889	-0.169925001
BP1026B_12948	single-stranded DNA-binding protein	92202	141342	120837	211	108747	129613	126061	617	1.11E-04	3.01E-04	1.028436019	0.040452044
predicted RNA	-	5387	14534	50791	270	8122	7675	7974	225	0.00292148	0.00375973	2.31067383	1.210086783
BP1026B_12949	major facilitator family transporter	68943	64605	65650	55	87574	84857	83392	71	0.10232307	0.13659048	2.90909091	0.36837406
BP1026B_12950	excinuclease ABC subunit A	270509	257384	257598	90	320617	324257	322203	111	0.342459443	0.395844497	2.33333333	0.30256277
BP1026B_12951	hypothetical protein	104800	103043	99903	94	96338	103343	111172	95	4.57E-05	1.37E-04	0.101063829	0.015266757
BP1026B_12952	formyltetrahydrofolate deformylase	53169	59951	56967	64	57380	59637	60413	67	7.81E-04	0.00129677	1.046875	0.06608919
BP1026B_12953	NUDX domain-containing protein	59903	31641	41160	51	71083	65845	64926	78	0.784611923	0.816095273	1.529411765	0.612976877
BP1026B_12954	LysK type translocator	8377	5236	5770	10	9825	7811	9174	14	0.198937658	0.245656679	1.4	0.485426827
BP1026B_12955	adenine phosphoribosyltransferase	67923	76799	80053	137	78739	80780	82333	146	8.46E-04	0.00356946	0.065092333	0.27927476
BP1026B_12956	potassium efflux system protein	144596	124475	132285	66	170400	153157	155974	79	0.054481012	0.077181434	0.19969697	0.259386629
BP1026B_12957	carbohydrate isomerase KpsF/GutQ family protein	84295	59103	59106	68	91877	80982	84472	87	0.08337234	0.11312853	1.279411765	0.355480655
BP1026B_12958	YrbI family phosphatase	85090	59016	64959	129	90299	76776	80095	152	0.018068068	0.028650403	1.178294574	0.270020258
BP1026B_12959	hypothetical protein	57669	46740	52604	85	60409	59515	58724	96	0.01243408	0.020472175	1.129411765	0.175571565
BP1026B_12960	OstA-like family protein	117284	121454	132267	185	120936	133348	129077	191	1.96E-04	5.04E-04	0.032432432	0.040647368
BP1026B_12961	ABC transporter ATP-binding protein	307386	332599	332238	471	320035	321976	323373	414	0.012954697	0.02124015	0.992807555	-0.010416616
BP1026B_12962	RNA polymerase factor sigma-54	607692	945017	845296	529	525051	673393	586328	394	0.046524641	0.066827869	0.744801532	-0.425072093
BP1026B_12964	hypothetical protein	29226	301676	307241	1318	309962	294994	284603	1287	0.0046104	0.00389793	0.976479514	0.33433317
predicted RNA	-	32604	32237	34804	2767	40691	41728	38074	3347	0.082459666	0.112000101	1.2096133	0.274545907
BP1026B_12963	PTS system transporter subunit IIA	1887826	2994582	2873816	7181	1965988	2455799	2204026	6135	0.003262343	0.006165917	0.854337836	-0.22121419
BP1026B_12965	PTS transporter subunit IIA-like nitrogen-regulatory protein PtsN	90945	126025	112741	215	84802	97858	89729	178	2.08E-09	1.78E-08	0.827906977	-0.272459491
BP1026B_12966	HPr kinase/phosphorylase	93592	115435	107302	108	84167	93205	93789	93	2.40E-08	1.60E-07	0.861111111	-0.27278691
BP1026B_12967	hypothetical protein	104076	91498	99751	110	90635	95077	98337	107	1.31E-05	4.50E-05	0.972727272	-0.039892727
BP1026B_12968	ATP-dependent protease La	116276	122026	113449	51	103225	110393	113398	170	4.05E-07	2.01E-06	0.918918919	-0.121990524
BP1026B_12969	Ac-g-specific adenine glycosylase	62473	46637	50303	151	67537	68423	65271	60	0.0251198	0.03839793	1.176470538	0.234665254
BP1026B_12970	formamidopyrimidine-DNA glycosylase	30118	14227	16218	24	40422	25652	31784	99	0.829725838	0.855782668	1.625	0.700439718
BP1026B_12971	hypothetical protein	465984	481227	479572	262	457791	473993	467572	257	0.335236349	0.38849762	0.980916031	-0.027798452
BP1026B_12972	outer membrane lipoprotein LoIB	26182	23795	25227	39	25689	25401	26888	41	4.59E-04	0.001070987	0.151208251	0.072149786
BP1026B_12973	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	124661	180552	161545	176	116445	137706	130880	145	3.89E-10	4.01E-09	0.823863636	-0.279522529
BP1026B_12974	Gln tRNA	42147	67980	58215	728	38811	48395	47366	158	1.97E-09	1.69E-08	0.799450549	-0.322919297
BP1026B_12975	ribose-phosphate pyrophosphokinase	125400	143848	138859	42	133464	129513	135175	138	1.85E-05	6.16E-05	0.971830996	-0.041226663
BP1026B_12976	SOS ribonucleotide isomerase	62473	949057	872643	1127	983738	1041716	904564	1287	0.57608978	0.6212138	0.9637124	0.26173124
BP1026B_12977	peptidyl-L-lysine hydrolase	16179	9257	9561	19	18054	16140	15704	92	0.30102214	0.335378096	1.421052632	0.506959899
BP1026B_12978	histidinol-phosphate aminotransferase	92093	88408	87438	83	109164	92354	95751	92	0.007138832	0.003505043	1.08433735	0.148522525
BP1026B_12979	ferredoxin	31027	51631	50384	166	30826	37125	35436	129	1.47E-09	1.29E-08	0.777108434	-0.363812176
BP1026B_12980	phosphatantetheine adenyltransferase	301000	348592	331523	652	270975	326302	325958	614	0.001760948	0.003542793	0.941717791	-0.068663309
BP1026B_12981	hypothetical protein	4842	2746	3203	5	6068	4894	5352	8	0.813233841	0.841123806	1.6	0.678071905
BP1026B_12982	signal recognition particle-docking protein PisY	135972	58055	75764	68	149916	122878	130297	101	0.797937399	0.828283888	1.828494118	0.570748642
BP1026B_12983	molybdoxide dehydrogenase	103269	74168	79850	113	79750	84952	82714	130	0.00195781	0.00295781	1.088493575	0.122335353
BP1026B_12984	nitrite reductase (NAD(P)H) large subunit	10732	10469	10619	4	11962	12606	11035	4	0.001785515	0.003583026	0.299050003	0.33331
BP1026B_12985	nitrite reductase (NAD(P)H) small subunit	240	96	226	0	303	194	224	0	0.874489494	0.894413904	#DIV/0!	0
BP1026B_12986	molybdopterine oxidoreductase family protein	5077	3456	4664	1	5354	4557	5091	1	0.024302787	0.037301537	1	0
BP1026B_12987	glycosyl transferase family protein	28879	14852	18960	21	33724	24585	26316	28	0.178605492	0.223363687	1.333333333	0.415037499
BP1026B_12988	acylttransferase	49888	30049	36343	47	54978	47023	51000	62	0.294592268	0.347364154	1.319148996	0.399607459
BP1026B_12989	2-isopropylmalate synthase	245525	17888	207556	12	29821	26386	28356	17	0.158402751	0.200536924	0.918696667	0.502500341
BP1026B_12990	hypothetical protein	202805	230858	230858	625	280565	297336	303326	757	0.160980794	0.20280793	1.339393939	0.47916783
BP1026B_12991	hypothetical protein	118384	154443	141388	242	115290	123762	119253	67	7.52E-09	5.66E-08	0.863636363	-0.211504105
BP1026B_12992	hypothetical protein	12747	19721	18327	132	11102	13695	14541	109	2.80E-09	2.35E-08	0.825757576	-0.276209795
BP1026B_12993	hypothetical protein	31065	53378	44883	342	24457	32989	28794	228	3.78E-16	1.34E-14	0.666666667	-0.58496201
BP1026B_12994	RNA polymerase factor sigma-32	816263	1017694	935285	987	782007	843520	809726	667	0.5061159	0.558950353	0.878419453	-0.17818091
BP1026B_12996	hypothetical protein	1020	1075	823	10	1222	1531	892	12	0.393278923	0.447657174	1.2	0.263034406
BP1026B_12995	hypothetical protein	4375	3554	4434	14	4799	6313	5074	18	0.176967339	0.2216243	1.285714286	0.263570079
BP1026B_12997	cytochrome d ubiquinol oxidase subunit I	910101	11864	11423	66	136285	151028	92	0.535897948	0.57502243	1.393939393	0.47916783	
BP1026B_12998	cytochrome d ubiquinol oxidase, subunit II	43376	42174	4731	39	80931	73337	73688	66	0.18186186	0.226928422	0.692307692	0.7589199
BP1026B_12999	hypothetical protein	2780	2214	1617	22	4383	3522	3954	39	0.134452155	0.173079903	1.727227272	0.8259706
BP1026B_13001	hypothetical protein	1103	253	443	1	1439	1029	1033	2	0.004382351	0.008024077	2	1
BP1026B_13002	hypothetical protein	656	339	226	0	320	384	122	0	2.35E-05	7.60E-05	#DIV/0!	0
BP1026B_13003	chitinase	92805	51089	58377	26	108196	96138	93378	39	0.599352001	0.648677554	1.5	0.584962501
BP1026B_13004	PTS system, N-acetylglucosamine-specific IIABIC component	56473	52257	57495	31	50322	53843	52109	29	9.86E-06	3.51E-05	0.935483871	-0.096215315
BP1026B_13005	PTS system, glucose-glucoside (Glc) family EIIA phosphocarrier	21757	14582	14972	6	22501	18235	17988	7	0.009438054	0.015979734	1.166666667	0.222392421
BP1026B_13006	hypophosphorylative protein phosphotransferase component	7353	4850	4743	5	7410	6798	7252	7	0.077973722	0.106201784	1.4	0.485426827
BP1026B_13007	N-acetylglucosamine-6-phosphate deacetylase	8371	4736	5793	5	8292	7605	8052	7	0.06455562	0.089995034	1.4	0.485426827
BP1026B_13008	GntR family transcriptional regulator	3253	3059	3319	4	2813	3086	3839	4	0.001262598	0.002640093	1	0
BP1026B_13009	hypothetical protein	102	73	157	1	81	92	94	0	0.026477815	0.040265535	0	#NUM!
BP1026B_13010	LysK family regulatory protein	130043	124969	122906	136	105761	100683	101854	111	2.01E-10	2.20E-09	0.816176471	-0.293046975
BP1026B_13011	AMP-binding domain-containing protein	127277	106753	112157	65	104115	99692	97064	56	2.35E-08	1.57E-07	0.861538462	-0.25012891

BP1026b	I3184	sodium/bile acid symporter family protein	425082	194935	217091	268	410238	335698	378306	359	0.711033088	0.751653279	1.339552239	0.421750843
BP1026b	I3185	methyl-accepting chemotaxis protein 1	3431	2790	2845	1	2716	2697	1	1	2.54E-06	1.04E-05	1	0
BP1026b	I3186	LacI family transcriptional regulator	51359	28397	33827	37	54955	44931	49028	48	0.281046435	0.3338391	1.297297297	0.375509135
BP1026b	I3187	N-acetylglucosamine 2-epimerase (GlcNAc 2-epimerase) family protein	128372	105237	112213	77	97600	101733	97432	67	1.74E-08	1.22E-07	0.87012987	-0.20069735
BP1026b	I3188	fructokinase	49056	38412	38365	46	48208	36981	40270	46	4.43E-04	0.001039213	1	0
BP1026b	I3189	hypothetical protein	264155	410940	393460	1583	204950	257628	246787	1050	4.67E-16	1.59E-14	0.663297536	-0.592271928
BP1026b	I3190	hypothetical protein	73003	39134	41801	263	69865	49558	61872	309	0.030948541	0.046323121	1.174904943	0.232544039
BP1026b	I3191	hypothetical protein	154618	115883	131161	112	143877	131233	138212	115	2.47E-04	6.20E-04	0.026785714	0.038135129
BP1026b	I3192	hypothetical protein	3160	1771	1821	2	3990	2830	2680	3	5.03744462	0.55643875	1.5	0.584962501
BP1026b	I3193	divalent cation-dependent protein kinase	17333	21808	22008	47	18821	19332	19240	44	2.39E-05	1.73E-05	0.936107012	-0.095157233
BP1026b	I3194	C32 tRNA thiolase	78726	101381	93432	91	78487	86542	85736	83	1.43E-06	6.27E-06	0.912087912	-0.132755209
BP1026b	I3195	UDP-N-acetylglucosamine pyrophosphorylase	113195	105635	112403	78	134543	125798	124265	91	0.009787621	0.016513649	1.166666667	0.222392421
BP1026b	I3196	glucosamine-fructose-6-phosphate aminotransferase	203199	186012	187830	104	211541	204027	202366	112	0.002258743	0.004433385	0.076923077	0.106915204
BP1026b	I3197	avidin family protein	13844	20382	17870	45	14390	15616	14647	38	8.60E-08	5.07E-07	0.844444444	-0.243925853
BP1026b	I3198	hypothetical protein	7265	8617	7488	22	6688	8508	7620	22	1.32E-04	3.52E-04	1	0
BP1026b	I3199	CzxA family heavy metal efflux protein	11654	9582	10579	3	13646	11286	11448	3	0.00284593	0.005439401	1	0
BP1026b	I3200	RND family efflux transporter MFP subunit	17333	21808	22008	47	18821	19332	19240	44	2.39E-05	1.73E-05	0.936107012	-0.095157233
BP1026b	I3201	outer membrane efflux protein	10272	9124	10407	2	12503	10673	11304	8	0.00459965	0.008370643	1.142857143	0.192645078
BP1026b	I3202	hypothetical protein	261579	177809	174864	718	254668	195549	238640	805	0.009722611	0.016417211	1.121169916	0.165004939
BP1026b	I3203	hypothetical protein	595291	568701	570243	1160	557360	538313	538043	1093	0.392898794	0.447468072	0.942241379	-0.085831404
BP1026b	I3204	lipotein	412734	450864	423832	505	392590	397557	399990	467	0.011930663	0.01947177	0.924752475	-0.112860838
BP1026b	I3205	LemA family protein	533069	636678	604890	876	558152	529252	525460	796	0.298970777	0.35160174	0.908675799	-0.138162439
BP1026b	I3207	copper-translocating P-type ATPase	311480	212829	223177	102	342945	273338	286812	124	0.191920637	0.238210953	1.215686275	0.281770968
BP1026b	I3208	chevry metal binding protein	198312	11586	13064	72	22692	21934	22851	110	0.677903017	0.721090759	1.527777778	0.611474712
BP1026b	I3209	hypothetical protein	38596	182615	182615	45	43362	38042	36215	55	0.08200705	0.11484704	1.222222222	0.289506615
BP1026b	I3210	hypothetical protein	11643	10362	9224	20	16418	11767	13544	27	0.102231254	0.13538038	1.35	0.432959407
BP1026b	I3211	argininosuccinate synthase	282400	407336	385336	267	343044	307781	367149	276	0.005768861	0.072495575	1.033707865	0.047828525
BP1026b	I3212	glutathione-disulfide reductase	174205	140328	138205	110	199645	173935	178985	135	0.113530405	0.148741903	1.272727272	0.295455884
BP1026b	I3213	hypothetical protein	27027	15607	16008	86	41001	30110	30832	151	0.39351342	0.447657174	1.75813953	0.812139985
BP1026b	I3214	manganese/iron transporter	11774	11113	11904	6	24601	24342	25805	15	0.02498842	0.037024131	2.5	1.321928095
BP1026b	I3215	hypothetical protein	3017	4301	3971	26	3301	4617	3628	27	0.004242045	0.00776631	1.03846158	0.05447784
BP1026b	I3216	hypothetical protein	257	391	303	2	313	177	215	1	0.15151518	0.192670647	#DIV/0!	#DIV/0!
BP1026b	I3217	hypothetical protein	372	141	231	0	192	258	279	0	0.15151518	0.192670647	#DIV/0!	#DIV/0!
BP1026b	I3218	carbohydrate porin	13984	11992	12991	8	24550	21791	22627	15	0.466226666	0.520583815	1.875	0.906809596
BP1026b	I3219	glycosyl transferase family protein	5581	3445	3993	3	6014	4302	4490	3	0.025082196	0.038338357	1	0
BP1026b	I3220	hypothetical protein	3832	2383	2562	2	3358	3136	3795	3	0.061810691	0.086471558	1.5	0.584962501
BP1026b	I3221	hypothetical protein	5985	6628	5395	10	5476	6739	7854	11	0.008688574	0.01484298	1	0.137053524
BP1026b	I3222	hypothetical protein	17460	24968	23872	27	15568	18203	19719	21	4.13E-09	3.29E-08	0.777777778	-0.362570079
BP1026b	I3223	outer membrane porin protein	140740	187611	182615	154	21716	155508	141844	123	1.77E-10	1.96E-09	0.8116827	-0.01002245
BP1026b	I3224	hypothetical protein	54160	68759	64207	84	55774	60494	61425	79	1.68E-05	5.66E-05	0.94047619	-0.08536675
BP1026b	I3225	alkylphosphonate utilization operon protein PtnA	68370	81228	79048	244	89619	79965	80628	267	0.001923308	0.002828916	1.094262295	0.129958594
BP1026b	I3226	hypothetical protein	16082	15444	15306	46	16235	18172	18887	52	0.007200586	0.012519201	1.130434783	0.17687762
BP1026b	I3227	chromate transporter	25008	22103	22094	43	29377	28110	29882	54	0.055763821	0.078749763	1.25813953	0.328622747
BP1026b	I3228	chromate transporter	17062	1964	2748	6	10380	6150	6787	12	0.244686523	0.294893094	2	1
BP1026b	I3229	DNA-binding transcriptional activator GcvA	47626	29505	32508	46	57880	45952	47935	64	0.542787047	0.593890408	1.391304348	0.476438044
BP1026b	I3230	uracil nucleoside phosphorylase	107924731	806158	806158	158	67924731	106915005	106915005	66	0.001944731	0.001944731	1	0.8706317
BP1026b	I3231	flagellar hook-associated protein FlgK	1142833	1158732	1161575	937	1305468	1182535	1140720	980	0.640547777	0.687099215	1.04589142	0.064372701
BP1026b	I3232	flagellar hook-associated protein FlgJ	1635947	1402564	1498749	754	1718655	1677680	1599572	830	0.371071124	0.424613127	1.100795756	0.138546813
BP1026b	I3233	YcgR protein superfamily protein	192589	132289	137520	202	242002	168114	186598	262	0.342237705	0.39579008	1.297027903	0.375125119
BP1026b	I3234	flagellar rod assembly protein/muramidase FlgJ	205781	211189	201266	220	206071	200676	215563	221	2.31E-04	5.84E-04	1.005454545	0.006542846
BP1026b	I3235	flagellar basal body P-ring protein	224382	182115	201393	169	248706	242068	237924	303	0.05248899	0.074613007	1.201183432	0.264456481
BP1026b	I3236	flagellar basal body L-ring protein	127541	159308	150640	201	133210	139325	133028	186	1.44E-06	6.31E-06	0.925373134	-0.1189288
BP1026b	I3237	flagellar basal body rod protein FlgG	237760	281058	285074	339	251665	285074	285074	339	1.31E-05	0.159019777	0.986703337	-0.02143717
BP1026b	I3238	flagellar basal body rod protein FlgG	229953	177873	187104	240	288113	240429	239498	322	0.108153211	0.142440708	1.238461538	0.308549065
BP1026b	I3239	flagellar hook protein FlgE	645469	728809	697341	568	695792	734546	683781	580	0.70304619	0.744590368	1.02126761	0.030161971
BP1026b	I3240	flagellar basal body rod modification protein	232670	247421	256079	291	230074	251799	227758	280	2.36E-05	7.64E-05	0.962199312	-0.055923226
BP1026b	I3241	flagellar basal body rod protein FlgC	87356	123114	118904	257	84848	91918	89525	208	5.53E-10	5.48E-09	0.809338821	-0.055184831
BP1026b	I3242	flagellar basal body rod protein FlgB	98170	79985	87613	180	94048	93826	96777	192	6.34E-04	0.001442283	1.066666667	0.093109404
BP1026b	I3243	flagellar basal body P-ring biosynthesis protein FlgA	31456	12745	17581	13	41254	29072	32543	202	0.587138988	0.693740818	1.69207692	0.7589919
BP1026b	I3244	negative regulator of flagellin synthesis	166733	176680	176680	47	138442	153656	145266	47	0.18E-08	0.18E-08	0.986703337	-0.02143717
BP1026b	I3245	flagellin synthesis protein FlgN	47782	456101	486517	974	511947	544775	485101	105	0.786755896	0.817918418	0.85215606	0.117981699
BP1026b	I3246	RebB protein	6545	10519	10596	41	4980	6711	6208	26	2.18E-13	4.31E-12	0.634146341	-0.657112286
BP1026b	I3247	multifunctional tRNA nucleotidyl transferase/2'-3'-cyclic phosphodiesterase/2'-nucleotidase/phosphatase	67399	50411	50354	45	75191	57898	60116	51	0.01481009	0.023466641	1.133333333	0.180572246
BP1026b	I3248	glutathione S-transferase domain-containing protein	21565	12411	13102	24	21380	17600	18991	29	0.042518951	0.061683945	1.208333333	0.273018494
BP1026b	I3249	nucleoside-diphosphate-sugar epimerase	34130	21430	21787	27	35119	25912	29789	32	0.012976367	0.02127012	1.185185185	0.231212498
BP1026b	I3250	soluble lytic transglycosylase	50839	495368	495368	253	57280	556366	546630785	285	0.977988558	0.986330785	1.226832313	0.00634343
BP1026b	I3251	5-formyltetrahydrofolate cyclo-ligase	10433	3893	5241	10	11498	8435	10412	6	0.67642416	0.7197996	1	0.678071905
BP1026b	I3252	hypothetical protein	706959	98579	97524	173	70261	85780	75292	150	1.03E-07	5.95E-07	0.867052023	-0.205809731
BP1026b	I3253	hypothetical protein	16288	7774	7848	16	25890	11340	15252	26	0.877210428	0.89649994	1.625	0.700439718
BP1026b	I3254	urea amidolyase-like protein	127041	51016	65884	75	149130	99432	110906	110	0.574206044	0.624803906	1.466666667	0.525541023
BP1026b	I3255	Lamb/YesF family protein	166565	121130	132729	183	176535	149306	152106	208	0.015415689	0.02483323	1.136612022	0.18473988
BP1026b	I3256	hypothetical protein	8442	4357	6186	8	10307	7847	9925	12	0.421852341	0.475864006	1.5	0

BP1026b	13306	site-specific tyrosine recombinase XerC	27130	24143	27758	28	28921	27472	25787	29	4.75E-04	0.001104434	1.035714286	0.050626073
BP1026b	13307	SAM-dependent methyltransferase	20224	12302	14232	12	21039	19912	20396	16	0.12248627	0.159310879	1.333333333	0.415037499
BP1026b	13308	cobalamin synthesis protein P47K family protein	305373	437049	398831	351	363931	425422	395722	364	0.092757402	0.124190378	1.037037037	0.05246742
predicted RNA	-		39202	32922	40571	725	34608	46038	39168	97	0.0345844	0.09008064	1.0298396	0.140214506
BP1026b	13309	DnaK suppressor protein	349497	522450	488683	1087	364936	433703	394714	369	0.001586347	0.003232993	0.863845446	-0.21154877
BP1026b	13310	ATP-dependent protease peptidase subunit	83637	50113	62618	121	119383	109349	105908	207	0.451553907	0.50582101	1.710743802	0.77462372
BP1026b	13311	ATP-dependent protease ATP-binding subunit HslU	1614949	2261123	2089544	1479	2074204	2351738	2168372	1635	0.164508362	0.207429338	1.054767731	0.144668583
BP1026b	13312	response regulator protein	620110	603917	632723	1139	717179	701707	682224	1289	0.918521999	0.931139059	1.131694469	0.174884517
BP1026b	13313	sensor kinase protein	102183	45613	57862	53	108442	86380	95751	75	0.379828501	0.433842715	1.41509434	0.500898236
BP1026b	13314	hypothetical protein	20002	18253	15684	71	18781	16588	19615	72	4.02E-04	9.56E-04	0.140484507	0.020177882
BP1026b	13316	acetylglutamate kinase	442054	639917	569344	518	433609	510749	407333	455	0.147337081	0.188045982	0.87038378	-0.187085553
BP1026b	13315	HAO-superfamily hydrolase	14839	15520	14701	23	12454	13500	13539	21	1.34E-06	5.86E-06	0.913043478	-0.13124533
BP1026b	13317	TetR family transcriptional regulator	84229	74306	75516	112	68138	71967	65820	99	3.09E-07	1.59E-06	0.883928571	-0.177998302
BP1026b	13318	homoserine O-acetyltransferase	81166	80299	80892	70	93778	94853	92112	81	0.007576972	0.013104589	1.157142857	0.210566986
BP1026b	13319	methionine biosynthesis protein MetW	46215	62203	54847	88	47063	51602	48000	79	1.30E-06	5.74E-06	0.897727273	-0.15565807
BP1026b	13320	major facilitator superfamily muropetide transporter	105759	103921	102193	79	11675	119303	124828	90	0.004598209	0.008370449	1.139240506	0.188072348
BP1026b	13321	M48 family peptidase	63369	49825	48395	51	85414	61373	68620	68	0.270471216	0.32286099	1.333333333	0.415037499
BP1026b	13322	AraC family transcriptional regulator	105748	10327	8639	140	15246	12320	12853	14	0.26186122	0.313310354	1.333333333	0.021698237
BP1026b	13323	NADP-dependent alcohol dehydrogenase	12751	12412	12078	11	15286	4915	16128	14	0.032421797	0.048355191	1.272727273	0.347923303
BP1026b	13324	exodexyribonuclease III	82584	125858	110881	138	84364	100172	95524	121	7.60E-08	4.53E-07	0.876811594	-0.18966122
BP1026b	13325	hypothetical protein	56480	54379	55907	65	63959	66010	62101	76	0.017908675	0.028433591	1.169230769	0.2255597
BP1026b	13326	aspartyl/glutamyl-tRNA amidotransferase subunit B	149058	194532	177979	118	166576	183243	171880	118	1.30E-04	3.47E-04	1	0
BP1026b	13327	aspartyl/glutamyl-tRNA amidotransferase subunit A	92460	100000	96166	64	102751	101613	101008	68	3.03E-04	7.43E-04	1.0625	0.087462841
BP1026b	13328	aspartyl/glutamyl-tRNA amidotransferase subunit C	10882	11999	11492	38	13047	12844	12847	43	0.001786809	0.003584475	1.131578947	0.178337241
BP1026b	13329	rod shape-determining protein MreB	187548	269547	246571	224	207451	233113	229922	211	1.17E-05	4.07E-05	0.941964286	-0.086255733
BP1026b	13330	rod shape-determining protein MreC	1276316	138051	128451	12	137316	17118	18375	95	0.09187402	0.03276316	1.333333333	0.415037499
BP1026b	13331	rod shape-determining protein MreD	21207	17381	19205	37	18535	18162	18036	35	3.05E-05	9.58E-05	0.945945946	-0.080170349
BP1026b	13332	penicillin-binding protein 2	66084	76910	75247	30	66934	72492	69703	28	2.11E-05	6.91E-05	0.933333333	-0.099535674
BP1026b	13333	rod shape-determining protein RodA	59158	66762	62462	54	55484	57894	57901	49	1.77E-06	7.56E-06	0.907407407	-0.140177658
BP1026b	13334	hypothetical protein	9269	3491	5280	7	9267	6422	7399	9	0.081799609	0.11123541	1.285714286	0.362570079
BP1026b	13335	HpHc/HpaI aldolase family protein	15665	6051	8353	12	21481	13967	14224	21	0.82932804	0.855560893	1.75	0.807354922
BP1026b	13336	6-pyruvoyl-tetrahydropterin synthase	49278	78960	69586	145	54161	74759	60368	139	2.34E-05	7.59E-05	0.95862069	-0.060968017
BP1026b	13337	hypothetical protein	105748	10327	8639	140	15246	12320	12853	14	0.26186122	0.313310354	1.333333333	0.021698237
BP1026b	13338	hypothetical protein	211767	198533	202362	277	199328	192873	199246	265	1.93E-05	6.38E-05	0.9566787	-0.063893617
BP1026b	13340	hypothetical protein	298357	522930	491304	923	259934	351617	293832	636	4.49E-09	3.56E-08	0.689057421	-0.537303882
predicted RNA	-		11220	19082	15979	593	10121	12763	12292	450	1.11E-11	1.55E-10	0.758853288	-0.398107103
BP1026b	13341	hypothetical protein	125003	206798	185658	245	117822	150707	135506	191	2.87E-12	4.57E-11	0.779591837	-0.259209111
BP1026b	13342	hypothetical protein	298744	332800	503033	1246	355966	520335	422464	1212	0.180644337	0.225643553	0.972712681	-0.03991437
BP1026b	13343	hypothetical protein	121966	122913	124854	451	144480	172453	165709	589	0.289057478	0.342656682	1.305986661	0.385140201
BP1026b	13344	hypothetical protein	66402	75290	66640	193	47161	64067	54393	167	0.73E-08	4.60E-07	0.865284974	-0.208752474
BP1026b	13345	Phage portal protein	5748	5	6444	5	4943	6990	6615	5	0.002539367	0.004939364	1	0
BP1026b	13347	The tRNA	18908	32552	28313	349	19009	23438	22661	231	0.82932804	0.855560893	1.75	0.807354922
BP1026b	13348	ClnXP protease specificity-enhancing factor	109017	171810	154736	278	119105	147626	130634	253	4.96E-07	2.41E-06	0.910071942	-0.135947498
predicted RNA	-		16066	28644	26029	785	16142	21107	19341	628	9.84E-09	7.22E-08	0.8	-0.321928095
BP1026b	13349	stringent starvation protein A	338338	309081	463718	714	344909	433638	389006	635	0.003027618	0.00576746	0.889355742	-0.169167462
BP1026b	13350	cytochrome c	1844099	2329057	2251610	2821	1664287	1980076	1848875	2386	0.008427159	0.014447546	0.94779962	-0.241612623
BP1026b	13351	ubiquitin-cytochrome c reductase, cytochrome b	1470062	2026403	1841408	1377	1623083	14064532	14064532	995	0.020831507	0.02664532	1.906209	0.021698237
BP1026b	13352	ubiquitin-cytochrome c reductase, iron-sulfur subunit	327064	336364	322783	529	297338	281912	293164	468	2.66E-05	8.52E-05	0.884886091	-0.176759193
BP1026b	13353	hypothetical protein	156660	111934	120118	168	160361	147418	147186	197	0.026013728	0.039636657	1.172619049	0.229734397
BP1026b	13354	DeqQ protease	263043	256744	280591	220	271357	305677	291570	239	0.008715576	0.014885055	1.086363636	0.119507094
BP1026b	13355	twin arginine translocase protein C	158595	172217	159266	208	151187	147116	156365	193	2.19E-06	9.19E-06	0.927884615	-0.139286281
BP1026b	13356	twin arginine translocase protein B	154177	175554	178333	230	161362	170921	168712	316	7.47E-05	2.12E-04	0.9875	-0.018147347
BP1026b	13357	twin arginine translocase protein A	2849178	369881	372820	1463	285560	334693	322965	1343	0.001792033	0.003592696	0.91797676	-0.123470465
BP1026b	13358	predicted RNA	18574	15474	89648	43	431391	570821	451460	9	0.146321	0.18697821	1.906209	0.021698237
BP1026b	13358	Mta/Hctf06 family protein	186036	239983	221843	590	190017	208222	216747	560	1.71E-05	5.74E-05	0.949152542	-0.075288127
BP1026b	13359	hypothetical protein	190947	295891	273862	650	197679	246149	231168	576	2.83E-07	1.47E-06	0.886153846	-0.174370906
BP1026b	13360	phosphoribosyl-ATP pyrophosphatase	34265	44213	37468	104	34883	38251	35949	98	6.63E-05	1.90E-04	0.942307692	-0.085729874
BP1026b	13361	phosphoribosyl-AMP cyclohydrolase	81709	90448	92056	212	82829	95927	88576	215	9.77E-05	2.70E-04	0.941450309	0.020272395
BP1026b	13362	imidazole glycerol phosphate synthase subunit HslF	92224	55196	65553	91	121581	88886	96378	132	0.445893708	0.500105709	1.450549451	0.536599470
BP1026b	13363	1-(5-phosphoribosyl)-5-(4-(5-phosphoribosyl)amino)methylimidazole-4-carboxamide isomerase	357253	483610	441297	653	345088	401917	363644	566	0.001251848	0.002619361	0.86676786	-0.206280939
BP1026b	13364	imidazole glycerol phosphate synthase subunit HslH	65380	70911	72902	114	65964	70673	65041	100	7.06E-05	9.20E-05	0.964912281	-0.051530301
BP1026b	13365	hypothetical protein	47986	62317	55245	88	49638	54450	54317	85	2.14E-05	6.97E-05	0.965909091	-0.050040682
BP1026b	13366	imidazoleglycerol-phosphate dehydratase	93054	112447	112962	180	97254	117223	105222	181	3.12E-05	9.77E-05	1.005555556	0.007992791
BP1026b	13367	histidinol-phosphate aminotransferase	18782	16530	15107	15	22434	17803	18033	18	0.011676269	0.01936168	1.2	0.263044066
BP1026b	13368	histidinol dehydrogenase	116986	79966	88754	71	133572	112723	122340	91	0.080681943	0.116377593	1.28169041	0.358047521
BP1026b	13369	ATP phosphoribosyltransferase catalytic subunit	36329	43556	45575	73	60226	58521	58333	98	0.057299708	0.080770373	1.219178082	0.285187082
BP1026b	13370	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	78253	78253	78253	57	78253	78253	78253	57	0.99849	1.00000	1.00000	0.99849
BP1026b	13371	HoA-like protein	19032	30178	28664	109	23221	27644	26137	106	4.89E-05	1.46E-04	0.77407204	-0.04026387
BP1026b	13372	ABC transporter permease	35463	52275	49109	60	38797	42436	42424	54	7.35E-06	2.68E-05	0.9	-0.152003093
BP1026b	13373	ABC transporter ATP-binding protein	60188	68713	69985	71	69911	76878	76265	80	0.005331678	0.005942259	1.126760653	0.172180975

BP1026b	13425	50S ribosomal protein L15	388925	477068	449069	1007	487333	550191	539261	1208	0.741432405	0.778020321	1.199602781	0.262556771
BP1026b	13426	50S ribosomal protein L30	169959	143552	162087	825	219444	250243	249917	1249	0.525239281	0.577533043	1.51393994	0.598307452
BP1026b	13427	50S ribosomal protein L18	246467	414627	386771	1041	440070	473018	447184	1238	0.847012601	0.870748942	1.189241114	0.250041246
BP1026b	13428	50S ribosomal protein L6	517944	809334	785253	1376	708583	899601	776558	1497	0.921266678	0.163072387	1.147126437	0.198340415
BP1026b	13429	50S ribosomal protein S8	243380	306737	295250	721	313599	361379	357201	868	0.328855054	0.381949223	1.220815752	0.287845483
BP1026b	13430	50S ribosomal protein S14	204482	262910	264458	797	314241	401462	342755	1153	0.6096254	0.658433219	1.446675031	0.532740884
BP1026b	13431	50S ribosomal protein L5	320553	463310	410731	737	429571	532033	509427	908	0.593552466	0.643288635	1.23202171	0.301027678
BP1026b	13432	50S ribosomal protein L24	149151	245205	222097	664	232155	298368	268100	861	0.226964145	0.275226383	1.296686477	0.374829996
BP1026b	13433	50S ribosomal protein L14	126551	210024	188140	473	195183	248606	220222	599	0.19197201	0.237453978	1.266384778	0.340715819
BP1026b	13434	50S ribosomal protein S17	574632	986089	897242	3001	805096	1055994	900583	3372	0.57071755	0.621439194	1.12625458	0.168162127
BP1026b	13435	50S ribosomal protein L29	320863	547627	519624	2372	428328	551520	483244	2501	0.628462892	0.676732412	1.053391743	0.076400485
BP1026b	13436	50S ribosomal protein L16	350744	447799	430556	982	407942	576230	512682	1267	0.470242382	0.46191743	1.290024033	0.367621595
BP1026b	13437	50S ribosomal protein S3	589569	924274	806571	965	756095	898554	864450	1048	0.677868995	0.721090759	1.086010363	0.119037869
BP1026b	13438	50S ribosomal protein L22	352206	581614	511202	1459	480968	609649	543387	1650	0.991903605	0.994281131	1.130911583	0.177486141
BP1026b	13439	50S ribosomal protein S19	260249	432893	384778	1301	371805	512264	397904	1548	0.858641185	0.880553352	1.189853958	0.250784509
BP1026b	13440	50S ribosomal protein L2	545374	596934	602833	702	736910	814562	761724	931	0.25277054	0.30346978	1.326210826	0.407310137
BP1026b	13441	50S ribosomal protein L23	291599	517630	449865	1332	398276	490015	451573	1417	0.568653704	0.619387553	1.063813814	0.089254676
BP1026b	13442	50S ribosomal protein L4	324141	527744	468484	708	459613	545077	501677	803	0.980248864	0.994466293	1.133498091	0.181630623
BP1026b	13443	50S ribosomal protein L3	400963	438081	412075	570	415166	502565	473124	689	0.40769994	0.764036233	1.208717913	0.275542064
BP1026b	13444	50S ribosomal protein S10	195994	209276	209602	656	248505	284420	274781	862	0.285805659	0.338978804	1.314020493	0.393992054
BP1026b	13445	elongation factor Tu	1631535	2332706	2171774	1717	1945547	2301971	2169872	1796	0.092832671	0.124219143	1.046010483	0.064897311
BP1026b	13446	elongation factor G	798198	1195648	1078576	486	1001828	1203500	1102760	524	0.969561346	0.975314035	1.0781893	0.108610498
BP1026b	13447	50S ribosomal protein S7	294710	496674	430609	864	401183	482878	447292	942	0.67239384	0.711835486	1.090277778	0.124695747
BP1026b	13448	30S ribosomal protein S12ase RecQ	287644	471858	406403	1020	369839	449601	419463	1083	0.27803451	0.330950755	1.061764706	0.086464091
BP1026b	13449	ATP-dependent DNA helicase RecQ	29436	195722	318140	174	248476	344559	342019	186	0.069468833	0.096026455	1.068965517	0.096215315
BP1026b	13450	DNA-directed RNA polymerase beta prime subunit	1356070	1836938	161123	1412002	15045605	1538723	1408664	558	0.09259509	0.00832073	1.053391743	0.07578253
BP1026b	13451	DNA-directed RNA polymerase subunit beta	651821	882482	807100	190	683324	777272	756359	179	0.57955615	0.629642489	0.942105263	0.086039831
BP1026b	13453	50S ribosomal protein L7/L12	996079	1104691	1140399	2881	1373074	1637287	1541983	4046	0.678768966	0.541277689	1.404373478	0.094926659
BP1026b	13452	50S ribosomal protein L7/L12	795144	812065	892079	2776	1110397	1336366	1235747	4091	0.138927649	0.178219452	1.47370317	0.559445969
BP1026b	13454	50S ribosomal protein L10	470387	772575	696423	1164	633566	787537	728324	1290	0.936934099	0.947545446	1.108247423	0.148280007
BP1026b	13455	50S ribosomal protein L1	672861	759768	762630	1046	838069	881542	889992	1244	0.399815615	0.53862351	1.189292543	0.250103634
BP1026b	13456	50S ribosomal protein L11	307736	485164	412595	929	471063	478561	465578	1045	0.08488192	0.089841558	1.124865457	0.16973441
BP1026b	13457	predicted RNA	280938	467237	411118	929	471063	478561	465578	1045	0.08488192	0.089841558	1.124865457	0.16973441
BP1026b	13457	transcription antitermination protein NusG	315194	530799	465229	783	387603	472412	445377	779	0.250405665	0.301033847	0.994891437	-0.00738879
BP1026b	13458	preprotein translocase subunit SecE	204592	332395	300008	732	228239	278192	265267	675	2.00E-06	8.49E-06	0.922131148	-0.116956146
BP1026b	13459	Trp tRNA	52838	73045	62187	824	59985	70808	65788	862	7.46E-04	0.001661323	1.046116505	0.065043532
BP1026b	13460	elongation factor Tu	1919107	2804822	2569766	2041	2274575	2711269	2585312	2118	0.053392813	0.075776722	1.037726605	0.053426407
BP1026b	13461	Gly tRNA	72815	119870	95899	1282	77260	93050	98876	1196	2.54E-06	1.04E-05	0.932917317	-0.100178872
BP1026b	13462	Gly tRNA	119586	190463	187796	2216	131571	194390	152998	2156	3.81E-05	1.17E-04	0.97924188	-0.039600703
BP1026b	13463	Ile tRNA	134099	228458	199412	216	123146	199412	146300	207	0.00564033	0.00832073	1.053391743	0.07578253
BP1026b	13464	5S ribosomal RNA	1842276	2541390	1679461	17885	1841090	2202577	2372865	18927	0.105762089	0.141481578	1.058261113	0.081695638
BP1026b	13465	23S ribosomal protein L7/L12	407475	287313	210156	104	276176	844495	559371	171	0.057400141	0.080824037	1.644230769	0.171412797
BP1026b	13466	hypothetical protein	30372	45181	38892	295	30641	40282	37732	280	9.48E-05	2.62E-04	0.949152542	-0.075288127
BP1026b	13467	Ala tRNA	106256	167474	137033	1801	116880	144737	153700	1821	1.19E-04	3.21E-04	1.011104942	0.015932741
BP1026b	13468	Ile tRNA	19951	28936	22969	311	20916	26319	26974	321	4.34E-04	0.00122414	1.032154341	0.045687177
BP1026b	13469	16S ribosomal RNA	846448	220308	175908	272	345382	393790	390342	467	0.015185606	0.02449455	1.176911765	0.779818898
BP1026b	13470	hypothetical protein	54740	87564	75640	383	57224	79634	73335	599	9.43E-06	2.42E-05	0.93575849	0.07578253
BP1026b	13471	lipase/acylhydrolase	14887	13372	13192	10	16915	16445	16985	13	0.026515206	0.040312625	1.3	0.378511623
BP1026b	13472	phenylacetate-CoA oxygenase subunit PaaA	118939	159646	148924	142	78752	87194	87194	86	3.46E-23	4.43E-21	0.605633803	-0.723482365
BP1026b	13473	phenylacetate-CoA degradation protein PaaB	24361	27067	24458	88	17341	16114	15288	57	9.21E-17	3.80E-15	0.647727273	-0.626541604
BP1026b	13474	phenylacetate-CoA oxygenase subunit PaaI	74355	81445	83918	99	48081	49238	47530	60	9.43E-22	9.25E-20	0.606060606	-0.72246024
BP1026b	13475	phenylacetate-CoA degradation protein PaaD	24209	8425	12931	24	14897	10311	12890	22	7.58E-07	3.52E-06	0.916666667	-0.125530882
BP1026b	13476	phenylacetate-CoA oxygenase/reductase subunit PaaK	152922	166155	162761	147	96110	101806	101074	91	2.66E-23	3.63E-21	0.619047619	-0.691877705
BP1026b	13477	hypothetical protein	62767	134737	126597	50	60232	72667	59332	30	0.313335594	0.366036989	1.133498091	0.181630623
BP1026b	13478	tetR family transcriptional regulator	57643	64733	55979	99	59516	71800	60086	100	0.07E-04	7.53E-04	1.0101001	0.01449957
BP1026b	13479	acyltransferase	110461	142382	135589	199	100120	111762	110411	165	4.31E-10	4.39E-09	0.829145729	-0.27032406
BP1026b	13480	transcriptional regulator	52835	89387	74837	160	54632	67375	65288	138	1.27E-07	7.18E-07	0.8625	-0.213403638
BP1026b	13481	4-hydroxyphenylpyruvate dioxygenase	25624	36111	30794	28	25121	30687	27971	25	2.55E-06	1.05E-05	0.892857143	-0.163498732
BP1026b	13482	outer membrane protein	268	97	100	0	411	251	616	2	4.36E-08	2.76E-07	#DIV/0!	#DIV/0!
BP1026b	13483	indolepyruvate ferredoxin oxidoreductase	89279	85717	84201	24	80826	77075	77630	21	1.23E-06	5.46E-06	#DIV/0!	0.875
BP1026b	13484	nucleic enzyme	26861	2530934	262639	113	312271	301231	308128	19	0.012352	0.10182352	1.0182352	0.1323157
BP1026b	13485	rotamase phosphoribosyltransferase	103445	125673	115899	167	132346	139250	134340	196	0.018315298	0.02898382	1.176526926	0.231005552
BP1026b	13486	phosphatidylethanolamine-binding protein	15300	6677	8967	21	19112	12744	13035	31	0.62992377	0.16498187	1.616190476	0.561878888
BP1026b	13487	flavodoxin domain-containing protein	11977	15150	15399	24	11383	14760	13713	23	3.11E-06	1.25E-05	0.958333333	-0.061400545
BP1026b	13488	N-acetyl-gamma-glutamyl-phosphate reductase	138565	84205	97955	113	167699	146128	154302	165	0.891196894	0.908282391	1.460176991	0.546143252
BP1026b	13489	hypothetical protein	912	1252	1882	7	1286	2476	1667	9	0.027494638	0.265499473	1.285714286	0.362570079
BP1026b	13490	lipoprotein	3668	3196	4009	2	3994	3440	4318	2	0.21704037	0.03919824	1	0
BP1026b	13491	lipoprotein	24123	21700	2771	2	2431	2365	2421	0	6.53E-06	2.42E-05	1	0
BP1026b	13492	CmpW family outer membrane protein	16894	21211	2163	23	16567	20380	19300	22	3.09E-05	9.69E-05	0.95652179	-0.064130337

BP1026B 13547	glycoside hydrolase family protein	25913	32210	32027	28	25275	25753	24879	23	8.44E-08	4.99E-07	0.821428571	-0.283792966
BP1026B 13549	H-NS histone family protein	38830	56467	48808	161	41558	44260	44244	145	4.44E-06	1.71E-05	0.900621118	-0.151007788
BP1026B 13548	hypothetical protein	14853	26130	21500	100	12526	16844	16793	74	1.18E-11	1.62E-10	0.74	-0.434402824
BP1026B 13550	hypothetical protein	945	928	928	4	928	928	928	0	0.7823436	0.8134893	0.25	0.321928095
BP1026B 13551	aquaporin Z	75632	41630	51041	79	73146	62319	67588	96	0.044629961	0.064418717	1.215189973	0.281811753
BP1026B 13552	cof family hydrolase	122847	106468	109545	135	111757	108509	116346	135	1.78E-05	5.96E-05	1	0
BP1026B 13553	BadF/BadG/BerA/BerD family ATPase	22753	13318	16180	18	21890	14925	16305	18	3.12E-04	7.63E-04	1	0
BP1026B 13554	DNA-3-methyladenine glycosylase I	128274	121907	125736	205	107207	108736	114412	180	2.09E-08	1.42E-07	0.87804878	-0.187627003
predicted RNA	-	118914	121763	122700	708	165115	192704	179639	1047	0.812884349	0.840964732	1.478813559	0.564440177
predicted RNA	-	21539	36034	34476	639	31170	42779	34936	756	0.043399446	0.064102728	1.183098592	0.242570303
BP1026B 13555	flagellin	12186143	19424603	12864003	10567	13594313	14539364	13740960	1980	0.12023196	0.156542722	1.131825494	0.17865154
predicted RNA	-	79945	95514	89250	5410	85255	93853	90901	5625	2.70E-04	6.71E-04	1.03974122	0.056224502
BP1026B 13556	flagellar hook-associated protein	1050682	990376	1017265	670	1207710	1138882	1086654	752	0.928663933	0.940204786	1.12238806	0.166571566
BP1026B 13557	hypothetical protein	260244	291683	277054	877	270942	266899	265152	849	2.07E-05	6.78E-05	0.968072976	-0.046812289
BP1026B 13558	hypothetical protein	516095	339241	389376	177	511626	492419	506082	215	0.668410733	0.712479274	1.214689266	0.2805873
BP1026B 13559	aminotransferase	202297	276757	259082	214	206081	234288	224223	192	7.63E-07	3.54E-06	0.897196262	-0.156504486
BP1026B 13560	3-oxoacyl-(acyl-carrier-protein) synthase III	51418	34860	40412	40	56135	54418	53604	52	0.216809736	0.264909909	1.3	0.378511623
BP1026B 13561	hypothetical protein	42741	47458	45923	204	41187	47077	46190	201	2.08E-04	5.32E-04	0.98329496	-0.021373651
BP1026B 13562	3-oxoacyl-ACP synthase	125657	98076	107414	103	138847	126209	121916	121	0.01925957	0.019739268	1.174757282	0.23236271
BP1026B 13563	short chain dehydrogenase/reductase family oxidoreductase	85230	48941	55226	83	93055	79838	80584	111	0.215908678	0.263963192	1.337349398	0.149376435
BP1026B 13564	hexapeptide transferase family protein	327272	185424	205157	328	226270	227413	230581	360	0.005165285	0.009276218	1.097566097	0.413310192
BP1026B 13565	Rieske (2Fe-2S) domain-containing protein	260055	275439	263053	249	276185	274634	286348	262	0.001499984	0.00224414	1.052208835	0.073421069
BP1026B 13566	hypothetical protein	273475	472460	419921	570	320835	419485	375993	546	0.015223938	0.024543758	0.957894737	-0.062060968
predicted RNA	-	10281	10331	10311	542	10053	11775	11896	591	7.79E-04	0.001727756	1.090405904	0.124865279
BP1026B 13567	putative outer membrane protein	196889	340648	312893	705	208959	255899	238102	585	4.93E-09	3.88E-08	0.829787234	-0.286916633
BP1026B 13568	LysE family protein	158045	12473	11589	18	11210	11210	12960	201	1.12E-05	9.93E-06	0.9	0
BP1026B 13569	acid phosphatase	109231	100962	104483	63	134973	131450	128644	79	0.068666944	0.095024871	1.259368354	0.326500825
BP1026B 13570	lipoprotein	39084	30525	33799	51	54396	51962	49612	77	0.895002405	0.91156845	1.509803922	0.594361199
BP1026B 13571	hypothetical protein	17978	14809	17197	38	28833	28257	26556	64	0.780113988	0.811955376	1.684210526	0.752072487
BP1026B 13572	CsgG family protein	46408	68728	60207	86	61148	69032	67767	97	0.008595207	0.0147035	1.127906977	0.173648087
BP1026B 13573	putative lipoprotein	11222	15337	15193	29	11449	12712	13906	27	1.06E-06	4.80E-06	0.931034483	-0.10393493
BP1026B 13574	5-oxoadipate enol-lactone hydrolase family protein	185582	114501	124821	167	188892	144925	169737	199	0.052948478	0.075180127	1.191616766	0.252502328
BP1026B 13575	methylenetetrahydropterin chemotaxis protein	503748	43718	11589	251	520034	475899	489041	201	0.759063685	0.793998078	1.083665238	-0.408497397
BP1026B 13576	hypothetical protein	1810	2617	2883	12	2020	2401	1576	9	7.77E-09	5.81E-08	0.75	-0.415037499
BP1026B 13577	hexose oxidase	14824	19430	19354	10	14574	14917	11972	8	1.67E-11	2.22E-10	0.8	-0.321928095
BP1026B 13578	chitin binding domain-containing protein	13614	19659	19451	31	11414	11988	10749	20	7.87E-18	3.86E-16	0.64516129	-0.632268215
BP1026B 13580	hypothetical protein	58625	53404	51481	218	74931	76034	77143	305	0.473591108	0.527492369	1.399082569	0.484811108
BP1026B 13582	gp30	221335	369557	325516	282	194744	241854	230504	205	3.86E-13	7.35E-12	0.726950355	-0.460071253
BP1026B 13583	gp29	121631	204005	176334	292	99609	124712	114508	196	9.59E-20	6.61E-18	0.671232877	-0.575114715
BP1026B 13584	hypothetical protein	46159	75913	67917	69	57587	55787	48868	62	3.67E-11	4.43E-10	0.753623188	-0.408497397
BP1026B 13585	site-specific recombinase, phage integrase family	3971	5987	5464	8	4096	4977	4368	4	4.11E-05	1.25E-04	0.875	-0.192645078
BP1026B 13587	transposase	186014	318167	288177	907	169524	220854	189177	663	8.15E-14	1.75E-12	0.730981257	-0.45209368
BP1026B 13589	Helix-turn-helix domain protein	22530	37579	32096	65	20675	28715	24373	52	5.21E-09	4.09E-08	0.8	-0.321928095
BP1026B 13590	SMF family protein	91311	152265	142815	343	79417	105668	94080	248	2.38E-14	5.92E-13	0.723032037	-0.467868456
BP1026B 13591	hypothetical protein	55946	95826	91890	576	39875	54792	46804	334	5.51E-24	8.43E-22	0.579861111	-0.786220709
BP1026B 13592	Phage portal protein	2129	2589	3078	2	2793	2852	2336	2	4.21E-04	9.96E-04	1	0
BP1026B 13593	Phage terminase, ATPase subunit	10619	26083	26133	1	19133	2448	2246	1	1.57E-08	1.07E-07	1	0
BP1026B 13594	Phage capsid scaffolding protein	1912	1946	1650	2	2382	2011	2071	2	0.019321432	0.030361558	1	0
BP1026B 13595	Phage major capsid protein	2444	3020	3300	2	2655	2941	3207	2	4.46E-04	0.001045153	1	0
BP1026B 13596	Phage terminase, endonuclease subunit	798	551	475	0	612	972	366	0	0.04534431	0.065359571	#DIV/0!	#DIV/0!
BP1026B 13597	Phage head completion-stabilization protein	444	150	221	0	666	770	787	1	6.92E-10	6.68E-09	#DIV/0!	#DIV/0!
BP1026B 13598	putative bacteriophage protein	162	121	142	0	233	95	159	0	0.406337804	0.460266771	#DIV/0!	#DIV/0!
BP1026B 13599	Phage-related tail protein	320	91	226	1	239	136	265	0	0.126350272	0.163624123	1	0
BP1026B 13600	Prophage membrane protein	303	248	261	0	272	266	241	0	0.001203	0.00238961	#DIV/0!	#DIV/0!
BP1026B 13601	Prophage membrane protein	721	611	512	2	4440	479	580	1	7.18E-05	2.05E-04	0.5	-1
BP1026B 13602	Putative phage-encoded peptidoglycan binding protein	938	1409	1293	1	1386	1168	1222	1	0.006279884	0.01107187	1	0
BP1026B 13603	Putative phage-encoded lipoprotein	224	305	380	0	193	290	415	0	0.15124163	0.192402909	#DIV/0!	#DIV/0!
BP1026B 13604	Prophage LysC	116	83	0	0	28	106	274	1	0.015521154	0.024977988	#DIV/0!	#DIV/0!
BP1026B 13605	bacteriophage tail completion protein R	1490	2299	2074	4	1466	2006	1532	4	4.84E-07	2.36E-06	1	0
BP1026B 13606	phage tail completion protein	3454	5351	6511	10	4287	4846	4884	9	1.71E-04	4.46E-04	0.9	-0.152003093
BP1026B 13607	hypothetical protein	78	13	78	0	36	105	64	0	0.16E-05	5.31E-04	#DIV/0!	#DIV/0!
BP1026B 13609	basalplate assembly protein V	1649	1596	1486	2	1842	1811	1275	2	0.001270917	0.002654832	1	0
BP1026B 13610	phage baseplate assembly protein	697	599	749	1	973	515	720	2	0.044218996	0.063928501	2	1
BP1026B 13611	phage baseplate assembly protein	3707	2126	2291	2	3854	3177	3447	3	0.287720081	0.340798351	1.5	0.584962501
BP1026B 13612	phage tail protein I	1350	679	783	1	1332	1020	1058	2	0.295840747	0.348574193	2	1
BP1026B 13613	Phage-related tail fiber protein	7483	7750	8364	3	7436	6931	6286	2	3.16E-06	1.27E-05	0.666666667	-0.584962501
BP1026B 13614	phage tail fiber assembly protein	1361	797	1211	1	1160	1178	1563	1	0.076411041	0.104519507	1	0
BP1026B 13615	Phage tail sheath monomer	2818	2928	2849	2	2849	2849	2849	2	2.67E-08	2.09E-05	1	0
BP1026B 13616	Major tail tube protein	5244	7469	6190	12	4975	6762	6140	1	1.83E-04	4.72E-04	0.916666667	-0.125530882
BP1026B 13617	putative phage tail protein	1812	1836	1860	5	1695	2142	1523	5	6.83E-05	1.96E-04	1	0
BP1026B 13618	hypothetical protein	978	1369	1494	11	931	1127	1044	9	8.91E-07	4.09E-06	0.818181818	-0.289506617
BP1026B 13619	bacteriophage tail protein	9087	10557	11186	3	9053	9555	9184	3	4.98E-07	2.41E-06	1	0
BP1026B 13620	Phage-related tail protein	1003	1005	775	2	1195	1114	1090	2	0.327851806	0.380995624	1	0
BP1026B 13621	hypothetical protein	43771	65473	55846	50	43692	51100	52692	44	9.31E-07	4.26E-06	0.88	-0.184424571
BP1026B 13622	hypothetical protein	124138	208635	178479	189	140989	179565	166841	180	1.28E-05	4.43E-05	0.952388982	-0.070382388
BP1026B 13623	gp22, putative phage-encoded membrane protein	148263	148683	129912	162	102661	129912	90154	121	4.28E-13	0.00351879	0.740707407	-0.035949407
BP1026B 13624	putative phage DNA-binding protein	383236	593548	532529	1164	403695	505703	476444	1069	0.177813004	0.222594487	0.918348488	-0.12829205
BP1026B 13625	hypothetical protein	3317	4802	5065	18	2603	3321	3156	12	2.83E-12	4.52E-11	0.666666667	-0.584962501
BP1026B 1													

BP1026b	13675	long-chain fatty acid CoA ligase (AMP-binding)	6720	5989	4706	3	5955	4706	5664	3	2.04E-04	5.23E-04	1	0
BP1026b	13676	putative extracellular ligand binding protein	1993922	228611	2315342	1928	1897018	2108202	1933962	1736	0.01492561	0.024106166	0.900414938	-0.151338104
BP1026b	13677	trifunctional transcriptional regulator/proline dehydrogenase/proline-5-carboxylate dehydrogenase	499111	440198	437257	116	432297	405126	414149	106	0.034945642	0.051713615	0.913793103	-0.130060541
BP1026b	13678	hypothetical protein	62625	83219	72168	424	61494	66865	67380	381	1.047E-06	4.68E-06	0.898584906	-0.154273267
BP1026b	13679	primosome assembly protein PriA	96090	48575	54377	29	102096	80320	86708	39	0.239846213	0.289671794	1.344827586	0.427421224
BP1026b	13680	uroporphyrinogen decarboxylase	165363	161909	158608	147	181104	173110	169512	159	0.003232008	0.006123342	1.081632653	0.11321061
BP1026b	13681	cyclohexadienyl dehydratase	36899	56204	51811	61	35860	43855	40067	50	6.91E-08	4.17E-07	0.91867231	-0.286881148
BP1026b	13683	CoA-binding domain-containing protein	2068	1110	1057	4	2241	1993	2348	6	0.987386641	0.990815784	1.5	0.58462501
BP1026b	13682	hypothetical protein	1056	2402	1557	4	1070	1423	1644	3	6.25E-07	2.97E-06	0.75	-0.451503749
BP1026b	13684	AMP-binding protein	11420	1547	1646	6	9283	9664	9788	8	3.57E-09	2.91E-08	0.833333333	-0.36304406
BP1026b	13685	F0F1 ATP synthase subunit epsilon	273643	383070	354247	791	318023	362462	345777	803	0.032479229	0.048429334	1.015170067	-0.021722293
predicted RNA			101080	159262	135704	1783	99173	113566	121372	1505	1.13E-09	1.02E-08	0.844083006	-0.244543216
BP1026b	13686	F0F1 ATP synthase subunit beta	1301748	1918975	1767115	1191	1449953	1706083	1599252	1136	0.09892158	0.131582216	0.953820319	-0.068210578
predicted RNA			38064	4431	7976	317	57788	42555	45124	914	4.40E-08	2.78E-07	2.883280757	1.527711325
BP1026b	13687	F0F1 ATP synthase subunit gamma	593112	842339	752659	832	721798	851294	783877	896	0.797764173	0.828264591	1.076923077	0.106915204
BP1026b	13688	F0F1 ATP synthase subunit alpha	1991829	2418665	2408475	1474	2347154	2704732	2519988	1636	0.124784303	0.161896987	1.109905002	0.150436224
BP1026b	13689	F0F1 ATP synthase subunit delta	352115	407999	399247	758	469007	449283	457499	849	0.23701817	0.857497465	1.18355419	0.245804966
BP1026b	13690	F0F1 ATP synthase subunit B	496644	683296	676043	1351	735865	824485	769889	1649	0.412808556	0.473218349	1.22057735	0.287563724
BP1026b	13691	F0F1 ATP synthase subunit C	479434	796055	752703	2503	591101	722562	679893	2461	0.514894374	0.567152311	0.983220136	-0.024413633
BP1026b	13692	F0F1 ATP synthase subunit A	192370	286930	254025	286	221282	267596	257340	291	2.27E-04	5.75E-04	1.017482517	0.025004006
BP1026b	13693	ATP synthase protein I	244621	320154	315516	949	227014	268993	260347	815	5.65E-08	3.47E-07	0.858798736	-0.219680828
BP1026b	13694	hypothetical protein	2615	3299	4350	23	2995	4060	3864	25	0.0106603	0.017856358	1.086956522	0.120294234
BP1026b	13695	transporter	47119	33208	32716	33	47917	40651	45116	39	0.050593202	0.072261192	1.181818182	0.2410081
BP1026b	13696	chromosome partitioning protein ParB	147146	151285	150113	168	140973	150862	148329	165	4.12E-05	1.25E-04	0.982124857	-0.025094209
BP1026b	13697	chromosome partitioning protein ParA	63637	86631	85429	101	55116	65699	64920	80	3.90E-10	4.02E-09	0.792079208	-0.33633388
BP1026b	13698	16S rRNA methyltransferase GidB	73209	74962	72688	105	60440	65183	67695	92	2.64E-07	1.38E-06	0.876190476	-0.190683562
BP1026b	13699	tRNA uridine 5-carboxymethylaminomethyl modification protein GidA	288002	447258	407152	192	230609	291488	269884	133	1.36E-13	2.80E-12	0.692708333	-0.529680065
BP1026b	13700	branched-chain amino acid ABC transporter ATP-binding protein	19817	29143	27771	33	14515	17063	17321	21	4.18E-17	1.81E-15	0.636363636	-0.652076697
BP1026b	13701	branched-chain amino acid ABC transporter permease/ATP-binding protein	17845	23422	22737	11	12651	14973	16657	8	3.40E-14	8.02E-13	0.727272727	-0.459431619
BP1026b	13702	branched-chain amino acid ABC transporter permease	76871	111631	97223	90	67232	83030	78980	72	8.17E-10	7.71E-09	0.8	-0.321928095
BP1026b	13703	branched-chain amino acid ABC transporter substrate-binding protein	51752	57504	60952	48	42114	47596	44909	38	9.17E-10	8.56E-09	0.791666667	-0.337034987
BP1026b	13704	hypothetical protein	61879	46684	59354	48	62480	59567	57808	52	0.00195607	0.003886736	1.083333333	0.115477217
BP1026b	13705	branched-chain amino acid ABC transporter integral membrane subunit	21545	24705	25788	24	20157	20002	21874	21	4.34E-07	2.13E-06	0.875	-0.192645078
BP1026b	13706	branched-chain amino acid ABC transporter permease	3442	3869	3585	4	3309	3085	3085	3	3.38E-06	1.34E-05	0.75	-0.415037499
BP1026b	13707	branched-chain amino acid ABC transporter, periplasmic branched-chain amino acid-binding protein	18970	27821	26112	20	13198	17087	12873	12	1.21E-21	1.15E-19	0	-0.736965594
BP1026b	13708	branched-chain amino acid ABC transporter ATP-binding subunit	6059	5448	6275	8	4349	4830	4672	6	4.62E-07	2.26E-06	0.75	-0.415037499
BP1026b	13709	branched-chain amino acid ABC transporter ATP-binding protein	8152	8686	9414	11	6329	6546	6356	8	5.10E-10	5.10E-09	0.727272727	-0.459431619
BP1026b	13710	oxidoreductase, GMC family protein	86497	64351	70098	43	71186	63220	64847	39	1.26E-06	5.56E-06	0.906976744	-0.140862536
BP1026b	13711	methylmalonate-semialdehyde dehydrogenase	466362	483446	481774	312	342496	342431	334069	222	1.38E-06	6.02E-06	0.711538462	-0.490986353
BP1026b	13712	LysR family transcriptional regulator	37547	18622	21252	28	37966	30041	32072	37	0.132601869	0.17087361	1.321428571	-0.020984444
BP1026b	13713	hypothetical protein	71139	1406368	13815	16	28750231	7928	8528	3	0.28750231	0.28750231	0.7928	-0.36333388
BP1026b	13714	adenylate cyclase	360530	321692	351228	648	353443	373103	362532	684	0.065005041	0.090536551	1.055555556	0.078002512
BP1026b	13715	AsnC family transcriptional regulator	84891	123901	121939	224	84095	99263	83332	182	7.47E-10	7.18E-09	0.8125	-0.299560282
BP1026b	13716	phenylalanine 4-monooxygenase	67059	79425	73844	82	50139	49402	50308	55	7.64E-16	2.47E-14	0.670731907	-0.576192291
BP1026b	13717	pterin-4-alpha-carbinolamine dehydratase	128013	195399	171779	539	111828	137554	131014	414	5.12E-13	9.37E-12	0.768089054	-0.360645405
predicted RNA			14763	24655	21640	881	12632	15470	14316	403	2.64E-14	6.46E-13	0.69361607	-0.527758325
BP1026b	13718	hypothetical protein	98631	158190	132715	562	77430	92848	96988	385	2.35E-16	8.62E-15	0.68053381	-0.545711685
BP1026b	13719	DNA-binding response regulator	529949	618989	627699	582	513018	545371	526291	762	0.03708848	0.036337901	0.894666667	-0.10652433
predicted RNA			31485	2380	2787	245	55116	65699	64920	80	0.020936858	0.040894218	0.222222222	1.099535674
BP1026b	13720	sensor histidine kinase	59654	41887	45406	32	53798	50333	50432	34	0.02148645	0.002614402	1.0625	0.06262841
BP1026b	13721	SET domain-containing protein	118978	183606	162986	302	158538	227761	184530	370	0.128051989	0.165588564	1.225165563	0.292976721
BP1026b	13722	oxidoreductase FAD/FMN-binding protein	175321	107696	130944	123	171543	162390	168752	150	0.088615309	0.11936522	1.219512195	0.263048185
BP1026b	13723	glutamine amidotransferase	275200	248090	239064	357	276696	259148	260474	373	4.73E-04	0.0010035	1.044817927	0.063251556
BP1026b	13724	Marr family transcriptional regulator	297326	436372	408420	667	304401	346699	239316	572	8.14E-04	0.001794986	0.857571212	-0.221671614
Synonym	Product	Normalized Co	Normalized Co	Normalized Co	Expression	Em	Normalized Co	Normalized Co	Normalized Co	Expression	BP's Value Empty	qValue Empty	qValue	BP's Value
BP1026b	II0001	hypothetical protein	55027	80260	73177	58	61147	71262	67125	55	2.17E-05	7.06E-05	0.948275862	-0.076621282
BP1026b	II0002	phage integrase family protein	58885	78986	73562	67	56655	63140	63133	58	1.42E-07	7.92E-07	0.865671642	-0.208108195
BP1026b	II0003	hypothetical protein	21217	17117	21103	52	19522	20832	21928	54	9.82E-04	0.00211508	1.038461538	0.054447784
BP1026b	II0004	DNA-binding protein	21873	28273	25759	41	24497	28824	25298	43	4.45E-04	0.001044143	1.048780488	0.06871275
BP1026b	II0005	2-amino-3-ketobutyrate coenzyme A ligase	213996	206161	207824	172	244401	259411	255626	210	0.076871393	0.105080044	1.220930763	0.07890763
BP1026b	II0006	3-chloro-3-dehydrogenase	256792	33599	308446	291	301663	329790	31279	312	0.04811043	0.04811043	0.707169048	-0.10652433
BP1026b	II0007	hypothetical protein	15503	12792	14057	21	14049	15205	16762	24	0.004891754	0.008855981	1.142857143	0.19245078
BP1026b	II0008	YerR family transcriptional regulator	34275	27414	27454	48	43250	33716	34775	50	0.231485484	0.160410943	1.25	0.321928095
BP1026b	II0009	hypothetical protein	41111	47731	48283	95	48098	56119	50088	107	0.016068851	0.017784426	1.126315789	0.17611378
BP1026b	II0010	succinylglutamate desuccinylase	24784	17725	19109	20	28526	28348	29489	108	0.290469531	0.343656667	1.5	0.485426827
BP1026b	II0012	tartrate dehydrogenase	23053	21685	21734	18	21881	20754	21294	17	5.27E-05	1.55E-04	0.944444444	-0.08246216
BP1026b	II0011	LysR family transcriptional regulator	19955	10769	12164	15	20646	16550	17706	19	0.084193701	0.114070645	1.266666667	0.341036918
BP1026b	II0013	hypothetical protein	25386	27378	25180	38	26864	25677	27430	39	3.20E-04	7.82E-04	1.026315789	0.03747405
BP1026b	II0014	hypothetical protein	421	536	2	2	536	2	474	2	0.365019452	0.41845376	0.40109	-0.36333388
BP1026b	II0015	glutathione S-transferase	97635	117747	116307	177	89219	101716	91500	150	1.03E-08	7.53E-08	0.847457627	-0.23878686
BP1026b	II0016	hypothetical protein	1024	786	701	1	1229	1063	918	2	0.528923623	0.80668164	2	1
BP1026b	II0017	patatin-like phospholipase	66561	58625	63987	50	75823	7477						

BP1026b	II0064	hypoethetical protein	2414	4622	4362	18	3064	3734	3103	16	7.03E-06	2.58E-05	0.88888889	-0.169925001
BP1026b	II0065	hypoethetical protein	3876	6553	6598	21	3263	3971	4908	15	9.19E-09	6.81E-08	0.714285714	-0.485426827
BP1026b	II0067	hypoethetical protein	1130	1492	1530	5	1418	1603	1484	5	0.000603163	0.010713865		0
BP1026b	II0068	IL-N5 histone family protein	106846	149313	139371	429	129766	16800	142486	491	0.011899448	0.019705713	1.144522145	0.194745377
BP1026b	II0069	alpha-ketoglutarate permease	3570	4350	4444	3	2957	4021	3831	2	3.01E-05	9.47E-05	0.666666667	-0.584962501
BP1026b	II0070	C4-dicarboxylate transport sensor protein	13370	12995	13424	6	14209	13611	12494	6	7.19E-05	2.05E-04	1	0
BP1026b	II0071	C4-dicarboxylate transport transcriptional response regulator	21091	23761	20990	16	19125	20184	20555	14	6.25E-06	2.32E-05	0.875	-0.192645078
BP1026b	II0072	hypoethetical protein	259845	451335	418641	1630	224720	321009	258740	1160	1.50E-12	2.56E-11	0.711656441	-0.490747159
BP1026b	II0073	hypoethetical protein	4108	2510	2700	7	4833	3996	4840	11	0.857267928	0.879849757	1.571428571	0.652076697
BP1026b	II0074	hypoethetical protein	37725	32022	33752	17	33340	32767	32520	16	6.02E-05	1.75E-04	0.941176471	-0.087462841
BP1026b	II0075	Arac family transcription regulator	2949	1746	1678	5	1587	1982	1743	4	2.38E-08	1.59E-07	0.8	-0.321928095
BP1026b	II0076	phospholipase C	3250	3110	2779	1	3404	3355	3563	1	0.030737823	0.04608409	1	0
BP1026b	II0077	transposase	3028	3556	3162	8	2404	3020	3083	7	1.02E-06	4.61E-06	0.875	-0.192645078
BP1026b	II0078	hypoethetical protein	189893	334457	286176	265	210457	280317	250130	242	1.22E-06	5.43E-06	0.913207547	-0.130985312
BP1026b	II0079	ABC transporter membrane protein	52316	87366	76553	128	51135	64394	60499	104	3.14E-09	2.61E-08	0.8125	-0.299560282
BP1026b	II0080	ABC transport system, exported substrate-binding protein	261850	622551	563154	499	366113	480074	428233	411	0.011294729	0.018813551	0.823647295	-0.279901422
BP1026b	II0081	predicted RNA	11481	19983	16501	571	10097	12882	11985	416	4.09E-13	7.70E-12	0.72854641	-0.456097217
BP1026b	II0082	IL-N5 histone family protein	19202	31452	25991	82	17431	19933	19789	62	2.50E-10	2.68E-09	0.857142857	-0.403356694
BP1026b	II0083	Rhs element Vgr protein	97938	83994	86011	32	104532	99143	100492	36	0.003288506	0.006207883	1.125	0.169925001
BP1026b	II0083	hypoethetical protein	135359	184038	170997	72	136232	152698	143673	64	7.64E-08	4.55E-07	0.888888889	-0.169925001
BP1026b	II0084	hypoethetical protein	492247	753031	704107	467	510487	625360	556510	406	0.228199179	0.276507997	0.869379015	-0.201942823
BP1026b	II0085	PAAR motif-containing protein	57079	45588	45714	187	62321	58399	58360	227	0.06307292	0.088060634	1.213903743	0.279654027
BP1026b	II0086	hypoethetical protein	36917	40917	39746	93	32439	36497	36040	83	5.84E-06	2.19E-05	0.892473118	-0.16411938
BP1026b	II0087	thioredoxin	13687	12736	13939	41	15101	14228	14911	45	0.001458069	0.003000536	1.097560976	0.134301092
BP1026b	II0088	hypoethetical protein	31638	38753	38294	51	29573	31764	32170	42	6.06E-07	1.37E-06	0.843137255	-0.246160587
BP1026b	II0089	hypoethetical protein	1761	2349	1931	3	1271	1449	2361	3	1.27E-06	5.64E-06	1	0
BP1026b	II0090	cytochrome c oxidase polypeptide I	20027	26915	26405	15	19195	21778	20643	12	1.26E-07	7.14E-07	0.8	-0.321928095
BP1026b	II0091	hypoethetical protein	436	499	821	1	427	435	307	0	3.21E-07	1.64E-06	0	#NUM!
BP1026b	II0092	hypoethetical protein	4822	6785	6189	4	4596	5691	5352	3	2.97E-05	9.37E-05	0.75	-0.415037499
BP1026b	II0093	hypoethetical protein	1070	1752	1435	3	888	1079	783	1	4.40E-13	8.19E-12	0.333333333	-1.584962501
BP1026b	II0094	hypoethetical protein	101	307	145	1	85	200	108	0	1.87E-04	4.83E-04	0	#NUM!
BP1026b	II0096	hypoethetical protein	17621	2419	21656	14	16174	17191	17176	11	1.15E-09	1.04E-08	0.785714286	-0.347923303
BP1026b	II0097	hypoethetical protein	3132	3619	3874	7	2613	3452	3315	4	5.36E-06	2.03E-05	0.857142857	-0.222392421
BP1026b	II0098	fibrinogen	9799	9507	9790	15	6636	9491	7672	14	1.73E-05	5.81E-05	0.933333333	-0.099535674
BP1026b	II0099	chaperone protein EcpD precursor	1281	1834	1581	2	1256	1200	1289	1	3.38E-07	1.72E-06	0.5	-1
BP1026b	II0100	outer membrane usher protein	2393	3005	3037	1	2104	2450	2254	0	3.47E-09	2.84E-08	0	#NUM!
BP1026b	II0101	hypoethetical protein	142	305	273	1	113	266	128	0	4.95E-05	1.47E-04	0	#NUM!
BP1026b	II0102	major fibrin subunit protein	892	1143	1608	2	618	784	683	1	7.40E-17	3.14E-15	0.5	-1
BP1026b	II0103	type VI secretion system	664	588	724	0	193	651	424	0	1.25E-08	8.90E-08	#DIV/0!	#DIV/0!
BP1026b	II0104	type VI secretion system	4169	4546	3874	2	3514	4390	3632	2	3.62E-04	8.73E-04	1	0
BP1026b	II0105	type VI secretion system	825	1454	969	2	642	1152	795	1	1.28E-06	5.64E-06	0.5	-1
BP1026b	II0106	type VI secretion system	3982	5107	5654	3	3236	4155	4484	2	2.43E-06	1.01E-05	0.666666667	-0.584962501
BP1026b	II0107	type VI secretion system	3403	6792	5605	10	3694	5715	5344	10	2.65E-04	6.62E-04	1	0
BP1026b	II0108	type VI secretion system	299	376	181	0	209	290	111	0	6.36E-05	1.84E-04	#DIV/0!	#DIV/0!
BP1026b	II0109	type VI secretion system	2166	1548	1623	1	1400	1861	1988	1	1.23E-04	3.31E-04	1	0
BP1026b	II0110	type VI secretion system	864	746	917	0	648	538	376	0	2.57E-11	3.32E-10	#DIV/0!	#DIV/0!
BP1026b	II0111	type VI secretion system	12650	13891	13914	3	12478	13509	12912	3	0.00303024	0.0031301	1	0
BP1026b	II0112	hypoethetical protein	2365	2169	2254	3	2716	2291	2296	4	0.001946879	0.003872153	1.333333333	0.415037499
BP1026b	II0113	type VI secretion system	12799	14725	13176	5	11626	12019	11136	4	2.27E-08	1.53E-07	0.8	-0.321928095
BP1026b	II0114	Rhs family protein	768	1088	1038	3	906	949	777	3	4.10E-04	9.73E-04	1	0
BP1026b	II0115	Rhs1 protein	78399	110602	104319	28	70055	85203	82070	22	1.20E-09	1.08E-08	0.785714286	-0.347923303
BP1026b	II0116	hypoethetical protein	16511	21621	19394	14	15643	17284	18312	12	1.60E-06	6.92E-06	0.857142857	-0.222392421
BP1026b	II0117	hypoethetical protein	7933	13100	11866	10	7819	8763	8608	8	7.58E-11	9.04E-10	0.8	-0.321928095
BP1026b	II0118	type VI secretion system	6503	8725	6440	6	7533	6237	6323	6	5.36E-04	0.0031372	1	0
BP1026b	II0119	type VI secretion system	5490	3458	4027	4	5332	4230	4916	4	0.018479213	0.029206375	1	0
BP1026b	II0120	type VI secretion system	7792	8283	8652	4	7082	7817	7785	4	9.62E-06	3.44E-05	1	0
BP1026b	II0121	type VI secretion system	2637	1993	2084	4	2366	2686	2183	4	0.00197687	0.002520325	1	0
BP1026b	II0122	type VI secretion system	4092	6249	6038	6	5160	4955	5915	6	7.62E-04	0.001693982	1	0
BP1026b	II0124	type VI secretion system	2229	3015	3946	5	2469	2581	3098	4	1.60E-06	6.90E-06	0.8	-0.321928095
BP1026b	II0123	hypoethetical protein	3849	3023	3003	7	3500	2962	3179	6	3.31E-04	8.05E-04	0.857142857	-0.222392421
BP1026b	II0125	type VI secretion system	88130	82601	8621	3	88343	90621	90602	3	3.31E-04	8.05E-04	0.857142857	-0.222392421
BP1026b	II0126	two-component system sensor protein	28109	41853	39533	11	28460	35179	31754	10	6.85E-07	3.21E-06	0.909090909	-0.137503524
BP1026b	II0128	hypoethetical protein	1303	1762	2231	5	1395	1649	1820	5	1.45E-05	4.94E-05	1	0
BP1026b	II0129	hypoethetical protein	517	788	761	2	590	603	513	2	8.25E-05	2.32E-04	1	0
BP1026b	II0130	hypoethetical protein	358	357	336	1	236	269	265	1	4.58E-04	0.001688847	1	0
BP1026b	II0131	hypoethetical protein	649	989	672	2	520	892	768	2	0.001678889	0.003398409	1	0
BP1026b	II0132	hypoethetical protein	2612	4997	2938	8	2949	3366	3151	7	1.16E-05	4.04E-05	0.875	-0.192645078
BP1026b	II0133	DNA-binding response regulator	1305	2454	1816	2	1544	1844	1900	2	2.40E-06	1.03E-05	1	0
BP1026b	II0134	hypoethetical protein	128	607	138	2	194	209	128	1	0.004980018	0.008989827	0.5	-1
BP1026b	II0135	fibrinogen	6851	9671	9391	3	5484	6672	6071	2	3.89E-10	4.01E-09	0.666666667	-0.584962501
BP1026b	II0136	periplasmic chaperone protein	4079	6080	6004	7	4151	5445	5181	7	1.41E-04	3.72E-04	1	0
BP1026b	II0137	hypoethetical protein	409	641	775	4	477	772	811	4	0.101616223	0.134708066	1	0
BP1026b	II0138	hypoethetical protein	820	1335	1465	1	698	1202	1073	1	2.53E-06	1.04E-05	1	0
BP1026b	II0139	hypoethetical protein	6393	10500	8926	13	6074	7226	7230	10	2.85E-08	1.87E-07	0.769230769	-0.378511623
BP1026b	II0140	DNA-binding response regulator	1320	2395	2611	3	1479	2741	2284	3	2.68E-04	6.67E-04	1	0
BP1026b	II0141	IL-N5 histone family protein	1432	1831	1949	5	1719	1439	936	3	5.71E-13	1.83E-12	0.6	-0.736965594
BP1026b	II0142	MFS transporter	8075	862	6863	5	7746	7501	7029	5	8.47E-05	2.38E-04	1	0
BP1026b	II0143	glycerate kinase	4458	3093	3795	3	4869	3449	4328	3	0.027483862	0.041694381	1	0
BP1026b	II0144	pyruvate kinase	15457	12884	11798	9	15416	13190	13511	9	3.03E-04	7.43E-04	1	0
BP1026b	II0145	transcriptional regulator	6012	5271	4734	4	5219	4858	5257	4	4.80E-04	0.00113588	1	0
BP1026b	II0146	hypoethetical protein	4778	5842	6318	11	5336	6521	6050	12				

BP1026b	II0192	type VI secretion system	2493	2725	2439	5	2467	2842	3090	5	0.004223089	0.007766473	1	0
BP1026b	II0193	type VI secretion system	7606	9515	9604	5	6637	7731	7392	4	4.95E-08	3.09E-07	0.8	-0.321928095
BP1026b	II0194	type VI secretion system	1294	974	820	1	1204	968	1180	1	0.039466326	0.057668825	1	0
BP1026b	II0195	type VI secretion system	3336	2035	2926	0	2926	2927	3270	0	7.05E-04	0.005864085	#DIV/0!	#DIV/0!
BP1026b	II0196	hypothetical protein	411	1081	757	2	534	561	440	1	1.86E-08	1.28E-07	0.5	-1
BP1026b	II0197	type VI secretion system	401	320	276	0	401	376	577	0	0.750048777	0.785541954	#DIV/0!	#DIV/0!
BP1026b	II0198	type VI secretion system	2280	1113	1948	1	2562	1608	1956	2	0.01244975	0.020481846	2	1
BP1026b	II0199	type VI secretion system	2117	1688	1674	3	1804	1756	1895	3	1.50E-04	3.95E-04	1	0
BP1026b	II0201	type VI secretion system	4927	4600	5025	2	6235	5448	5784	3	0.047195329	0.06770096	1.5	0.584962501
BP1026b	II0200	type VI secretion system	3734	2567	2561	2	3712	2909	3704	3	0.058145027	0.081726138	1.5	0.584962501
BP1026b	II0202	type VI secretion system	3328	1690	2091	2	4435	2837	3941	3	0.975781781	0.980919815	1.5	0.584962501
BP1026b	II0203	type VI secretion system	8688	10524	8849	4	7644	7194	7944	3	2.38E-08	1.59E-07	0.75	-0.415037499
BP1026b	II0204	type VI secretion system	14859	13240	15126	5	10772	13134	12355	4	7.46E-09	5.62E-08	0.8	-0.321928095
BP1026b	II0205	type VI secretion system	5874	5569	4855	5	5979	4532	5289	4	6.11E-04	0.001392529	0.8	-0.321928095
BP1026b	II0206	type VI secretion system	3484	2849	3025	4	3006	2930	2496	4	4.38E-06	1.69E-05	1	0
BP1026b	II0207	type VI secretion system	6152	5161	6886	15	5552	6421	5896	15	5.61E-04	0.001289316	1	0
BP1026b	II0208	hypothetical protein	46599	54710	50826	26	45988	50629	48276	25	2.67E-05	8.53E-05	0.961538462	-0.056583528
BP1026b	II0209	LysR family transcriptional regulator	38780	33807	32152	3	31895	30615	30852	34	1.37E-04	3.63E-04	0.971428571	-0.041820176
BP1026b	II0210	quinone reductase	8047	10240	10889	12	7706	9646	10184	11	5.23E-06	1.98E-05	0.916666667	-0.125530882
BP1026b	II0211	AraC/XylS family transcriptional regulator	1181	406	381	2	1265	675	722	2	0.809773251	0.838259446	1	0
BP1026b	II0212	O-acetylhomoserine sulphydrilase	113295	99939	103498	81	109978	105416	105629	82	4.60E-05	1.38E-04	1.012345679	0.017720202
BP1026b	II0213	glyoxalase family protein	15472	10378	12462	32	15839	15437	15501	39	0.023348386	0.035977505	1.21875	0.285402219
BP1026b	II0214	hypothetical protein	8878	9388	7209	10	5998	6782	6637	7	5.26E-09	4.11E-08	0.7	-0.514573173
BP1026b	II0215	hypothetical protein	3688	4957	4403	12	3472	3727	4164	11	6.14E-05	1.78E-04	0.916666667	-0.125530882
BP1026b	II0216	hypothetical protein	2200	2491	2500	1	2480	2257	1580	1	2.56E-07	1.88E-06	1	0
BP1026b	II0217	area amblyase-like protein	373032	7024	2612	6	7621	4953	5918	6	0.28621067	0.33937397	1.5	0.584962501
BP1026b	II0218	allophanate hydrolase, subunit 1	6088	5035	6471	6	5179	4645	4581	5	3.07E-06	1.24E-05	0.833333333	-0.263034406
BP1026b	II0219	acyl-CoA carboxylase biotin carboxylase subunit	2963	1744	1834	1	3076	2223	2839	1	0.061831417	0.086481267	1	0
BP1026b	II0220	hypothetical protein	1095	391	451	2	1217	1162	884	4	0.11537949	0.146314837	2	1
BP1026b	II0221	hypothetical protein	2458	3072	1890	3	2911	2296	2876	3	0.002697905	0.005205769	1	0
BP1026b	II0222	LysR family transcriptional regulator	12939	11834	11252	13	11287	11119	12377	12	7.47E-06	2.73E-05	0.923076923	-0.115477217
BP1026b	II0223	penicillin acylase	57421	48320	49996	20	55380	51847	53672	21	5.26E-04	0.001213778	1.605	0.070389328
BP1026b	II0224	proline imine peptidase	28780	17483	25451	27	31899	30531	30852	30	0.000198278	0.000198278	1.148148148	0.199308805
BP1026b	II0225	hypothetical protein	12966	12802	11694	15	12053	12212	13920	15	6.88E-05	1.97E-04	1	0
BP1026b	II0226	lipoprotein	6060	4716	4773	2	8148	6105	6008	3	0.126750028	0.164107931	1.5	0.584962501
BP1026b	II0227	methyl-accepting chemotaxis protein 1	106651	93217	95102	60	120617	103593	102937	66	0.001290695	0.002692561	1	0.137503524
BP1026b	II0228	propionate catabolism operon regulatory protein PprR	42675	19346	22668	13	50814	34371	36362	19	0.64611651	0.692362294	1.461538462	0.54787795
BP1026b	II0229	2-methylisocitrate lyase	469991	451789	461029	514	41679	42247	41319	46	0	0	0.089494163	-3.482062593
BP1026b	II0230	methylcitrate synthase	952777	1145722	1121699	915	56465	61959	62894	51	0	0	0.053737705	-4.165202591
BP1026b	II0231	acetylhydrolase	1550198	1371483	1441321	561	106646	100351	101117	39	0	0	0.060518717	-3.846454742
BP1026b	II0232	AcdD-accessory protein PrpF	156711	99537	109558	102	14527	12284	13294	11	0	0	0.107843137	-3.219937223
BP1026b	II0233	hypothetical protein	41755	41840	40857	93	18797	19239	19351	43	1.20E-37	3.41E-35	0.462365591	-1.128945061
BP1026b	II0234	hypothetical protein	6788	6375	6727	34	2511	3335	3505	16	3.35E-31	8.09E-29	0.470588235	-1.087462841
BP1026b	II0235	hypothetical protein	41211	36824	39835	61	25562	22019	21752	36	6.07E-21	5.06E-19	0.590163934	-0.760812336
BP1026b	II0236	hypothetical protein	77778	92559	92049	147	38857	46789	41385	71	5.08E-37	1.39E-34	0.486993197	-1.049925225
BP1026b	II0237	heme biosynthesis protein	39787	34354	33433	24	26592	24016	23637	16	8.82E-14	1.88E-12	0.666666667	-0.584962501
BP1026b	II0238	methyl-accepting chemotaxis protein	1618938	1678843	173620	109	227330	206460	20357	131	0.004660781	0.000198278	1.20183867	0.23623467
BP1026b	II0239	RemN protein	11453	5720	8021	4	14248	11894	11692	7	0.502960808	0.555911803	1.75	0.807354922
BP1026b	II0240	LysR family transcriptional regulator	32161	17765	18083	25	33300	25380	29561	32	0.058402568	0.082051357	1.28	0.35614381
BP1026b	II0241	N-acylglycosaminic 2-epimerase	36096	26293	27770	27	44560	36932	39056	36	0.329278437	0.382370166	1.333333333	0.415037499
BP1026b	II0242	MgtC family protein	46272	41116	42617	62	44081	4194	44314	62	4.34E-04	0.01022141	1	0
BP1026b	II0243	hypothetical protein	54679	40632	46558	164	52921	51272	52841	181	0.006310289	0.011116103	1.103658537	0.142293882
BP1026b	II0244	hypothetical protein	722744	1190739	1037015	6304	809009	1018393	951206	5937	0.731386433	0.768431274	0.941782995	-0.086533422
predicted RNA	-		79124	9051	58057	667	1206	1807	6962	667	1.20E-18	5.81E-16	3.855491329	1.046014724
predicted RNA	-		372281	126950	177460	1326	424590	315687	366549	21	0.087034889	0.117539259	0.636500728	0.710614267
predicted RNA	-		37271	39057	34421	683	40124	39014	45414	768	0.018733274	0.029555792	1.124450952	0.169220732
BP1026b	II0245	acetyltransferase	155665	181871	170280	366	138186	139507	145987	305	1.09E-09	9.95E-09	0.833333333	-0.263034406
BP1026b	II0246	putative exported protein precursor	246746	343678	322671	685	244595	287577	268472	601	2.40E-07	1.27E-06	0.877372263	-0.187388997
BP1026b	II0248	hypothetical protein	303183	135572	189462	260	316978	302928	257757	363	0.992602668	0.994822901	1.396153846	0.481457925
predicted RNA	-		45403	22388	30415	617	40886	33821	34730	668	0.013491321	0.021999236	1.115072934	0.157138076
predicted RNA	-		24148	27113	26122	376	24817	26844	23240	489	0.000198278	0.000198278	0.848991403	0.23623467
BP1026b	II0250	hypothetical protein	80717	32530	37547	35	98621	66149	72159	55	0.669835877	0.713513407	1.571428571	0.652076697
BP1026b	II0251	hypothetical protein	381436	288274	314090	83	414813	366258	378908	145	0.002547551	0.30564394	1.80722892	0.239670413
predicted RNA	-		13645	482	1089	202	18296	8965	11377	515	4.26E-04	0.001005291	2.54950495	1.350217139
BP1026b	II0252	hypothetical protein	4530	7591	6210	27	3902	4352	4565	19	3.18E-09	2.64E-08	0.703703704	-0.50695989
BP1026b	II0253	type I phosphodiesterase/nucleotide pyrophosphatase family protein	19562	10997	13998	8	18699	15615	15692	10	0.004175424	0.007690087	1.25	0.321928095
BP1026b	II0254	glyoxalase/bleomycin resistance protein/dioxygenase family protein	30300	29089	35276	80	36781	35084	33662	90	0.011665276	0.019348566	1.125	0.169925001
BP1026b	II0256	hypothetical protein	17686	12690	14087	52	26692	22154	22113	82	0.948912515	0.957613932	1.576923077	0.657112286
BP1026b	II0255	squalene/phytoene synthase family protein	30147	24131	25794	25	32357	29026	30400	29	0.00779337	0.013432365	1.16	0.214124805
BP1026b	II0257	LysR family transcriptional regulator	10207	8398	8999	12	11593	11465	10552	15	0.017968602	0.028559053	1.25	0.321928095
BP1026b	II0259	hypothetical protein	21613	24269	22879	45	26453	23372	27355	51	0.004795655	0.008702095	1.133333333	0.180572246
BP1026b	II0260	hypothetical protein	11146	14682	14942	79	14216	14216	12399	79	4.64E-05	1.39E-04	1	0
BP1026b	II0261	cyanide-insensitive terminal oxidase	98896	100434	106390	01	106093	112574	107000	107	3.21E-04	7.82E-04	1.05949046	0.28535504
BP1026b	II0262	ribonucleoside diphosphate kinase	12862	12827	144523	100	146004	156324	145344	107	0.001828075	0.000198278	1.166666667	0.08046262
BP1026b	II0263	allo-threonine aldolase	152384	126482	126907	133	156308	142461	143344	145	0.002730484	0.005257513	1.090225564	1.124626655
BP1026b	II0264	chromosome replication initiation inhibitor protein	57483	47703	47150	50	62440	56317	57745	58	0.020707006	0.032296133	1.16	0.214124805
BP1026b	II0265	1A family penicillin-binding protein												

BP1026b	II0310	C4-dicarboxylate anaerobic carrier family protein	11614	12046	12611	7	12552	12850	12505	8	1.62E-04	4.24E-04	1.142887143	0.192645078	
BP1026b	II0311	IcR family transcriptional regulator	2477	1413	1651	2	2666	2243	2030	3	0.077648318	0.10602697	1.5	0.584962501	
BP1026b	II0312	N-formylglutamate amidohydrolase	4967	1999	5687	3	8338	5531	6047	7	0.251081521	0.301730724	2.333333333	1.222392421	
BP1026b	II0313	outer membrane porin protein	834	543	545	1	1274	1298	1019	3	0.02547298	0.020516851	3	1.584963501	
BP1026b	II0314	hypothetical protein	609	255	247	0	699	595	568	0	0.08459732	0.11449832	#DIV/0!	#DIV/0!	
BP1026b	II0315	selenophosphate synthetase	41222	32491	35148	34	49583	39198	42360	41	0.074444835	0.102097169	1.205882353	0.270089163	
BP1026b	II0316	hypothetical protein	1682	1589	1659	3	2599	2413	2444	4	0.916635446	0.929708305	1.333333333	0.415037499	
BP1026b	II0317	lipoprotein	169512	188966	198741	174	207489	223479	206292	200	0.017582109	0.027977283	1.149425287	0.200912694	
BP1026b	II0318	hypothetical protein	426	39	118	0	749	339	257	1	3.52E-05	1.09E-04	#DIV/0!	#DIV/0!	
BP1026b	II0319	LysR family transcriptional regulator	18296	22252	25634	21	20732	22062	21234	21	1.98E-04	5.08E-04	1	0	
BP1026b	II0320	lysine-dependent protein LysE	1434	970	1269	1	1226	1827	1388	2	0.8058931	0.363157541	2	0	
BP1026b	II0321	RND family efflux transporter MFP subunit	9958	7823	7299	6	15229	12805	12556	11	0.951931535	0.960197222	1.833333333	0.874469118	
BP1026b	II0322	multidrug-efflux transporter protein	38815	44101	43401	13	52836	54374	55527	17	0.196657185	0.243271647	1.307692308	0.387023123	
BP1026b	II0323	RND efflux system outer membrane lipoprotein	9889	7274	7746	5	14522	11748	12207	8	0.664087303	0.708955012	1.6	0.678071905	
BP1026b	II0324	sodium dicarboxylate symporter family protein	250633	215878	232323	191	239982	236021	249505	199	6.44E-04	0.001462491	1.041884817	0.059195793	
BP1026b	II0325	GntR family transcriptional regulator	71854	107261	98783	140	68997	83734	77602	116	6.69E-09	5.08E-08	0.828571429	-0.271302022	
BP1026b	II0326	acetyltransferase	54619	41713	44465	99	64005	53412	53607	121	0.066502818	0.092356696	1.222222222	0.289066177	
BP1026b	II0327	auxin efflux carrier	260327	266651	11465	13350	19	32084	24234	27832	31	0.837609671	0.862399733	1.631578947	0.706265797
BP1026b	II0328	AMP-binding domain-containing protein	230210	168103	178624	103	303884	264101	266907	149	0.92714087	0.994822901	0.446601942	0.532667993	
BP1026b	II0329	malonyl CoA-acyl carrier protein transacylase	103842	92124	95866	108	134321	125903	129207	144	0.189852203	0.235876979	1.333333333	0.415037499	
BP1026b	II0330	hypothetical protein	55849	67805	63353	144	74462	77806	72544	173	0.033344483	0.049601598	1.201388889	0.264703226	
BP1026b	II0331	fatty-acid-CoA ligase	296222	323264	323290	170	367706	398475	398627	208	0.364577973	0.418098286	1.232529412	0.291048782	
BP1026b	II0332	diaminopimelate decarboxylase	96518	47356	53755	52	155309	98402	116469	97	0.840176373	0.114696546	1.865384615	0.899473124	
BP1026b	II0333	Fkfh domain-containing protein	46680	24161	31345	22	65830	50203	54598	38	0.279992674	0.332965696	1.727272727	0.788495895	
BP1026b	II0334	ketol-acid reductoisomerase	68552	61449	59298	59	98540	90108	90383	89	0.77370529	0.806505297	1.508474576	0.593903823	
BP1026b	II0335	polyketide non-ribosomal peptide synthase	729106	523928	592185	51	1159606	1007980	104217863	238	0.014975349	0.06580818	1.68627451	0.7134839413	
BP1026b	II0336	gamma-aminobutyraldehyde dehydrogenase	182000	101094	117434	94	278992	222598	236141	174	0.007193522	0.012599916	1.85106383	0.888354644	
BP1026b	II0337	hypothetical protein	187660	119027	133409	103	270284	238332	248204	177	0.045693732	0.0658481	1.718446602	0.781105023	
BP1026b	II0338	peptide synthase regulatory protein	100733	52589	62389	70	150936	132276	132199	134	0.034722851	0.050789887	1.914285714	0.936806174	
predicted RNA	-		62999	64111	59014	508	93191	80218	78857	689	0.266028677	0.31768473	1.356299213	0.439675486	
predicted RNA	-		1170358	997605	1031983	2091	1522489	1408703	1476879	2881	0.519617014	0.571852198	1.37780996	0.462376599	
BP1026b	II0339	hypothetical protein	259222	324095	320427	580	329688	382566	359244	688	0.253518475	0.293780708	1.186208966	0.264355665	
BP1026b	II0340	thiol template mechanism natural product synthetase	1484893	977803	1073552	139	219394	1778934	1849136	238	0.11840104	0.154097800	1	0	
predicted RNA	-		23141	37333	31431	712	21089	27618	30020	610	1.96E-07	1.06E-06	0.856471573	-0.223067999	
BP1026b	II0341	ATP-dependent transcription regulator LuxR	56637	57952	59620	80	72465	73660	73660	102	0.106661215	0.140562444	1.275	0.350497247	
BP1026b	II0342	D-methionine-binding lipoprotein MetQ	5158	6344	5806	6	5836	6593	7767	8	0.021769958	0.033785984	1.333333333	0.415037499	
BP1026b	II0343	monooxygenase	8044	7701	6644	5	8291	9637	9282	6	0.008413716	0.014432387	1.2	0.263034406	
BP1026b	II0344	ABC transporter ATP-binding protein	2511	2354	2840	2	3287	3303	3108	2	0.147911593	0.188663974	1	0	
BP1026b	II0345	ABC transporter permease	1452	1020	905	1	1537	1432	1069	2	0.17344702	0.153057991	2	1	
BP1026b	II0346	hypothetical protein	898	501	501	1	1094	502	628	0	0.18404104	0.154097800	1	0	
BP1026b	II0347	monooxygenase	30721	9768	15562	15	47614	29883	30224	29	0.088018788	0.118612644	1.933333333	0.9510094	
BP1026b	II0348	hypothetical protein	6347	2268	3150	5	6719	5416	6352	8	0.84612015	0.870117562	1.6	0.678071905	
BP1026b	II0349	hypothetical protein	18207	23735	22209	37	15691	17796	18040	30	7.96E-09	5.93E-08	0.810810811	-0.30256277	
BP1026b	II0350	GntR family transcriptional regulator	22868	15834	15524	25	28243	23437	22556	34	0.216449285	0.264558501	1.36	0.443606651	
BP1026b	II0351	hypothetical protein	11433	5676	7238	10	13768	11844	12002	15	0.661539817	0.706836871	1.5	0.584962501	
BP1026b	II0352	iron-sulfur cluster binding protein	47906	48919	48844	33	55276	51016	50868	36	0.02727177	0.005254172	1.090909091	0.125350882	
BP1026b	II0353	hypothetical protein	8804	3326	3326	1	11011	8908	8246	2	0.807753498	0.8858818	1.714285714	0.7134839413	
BP1026b	II0354	glycolate permease	11937	8478	10266	5	12709	11674	12957	7	0.014571648	0.023601329	1.4	0.485426827	
BP1026b	II0355	hypothetical protein	3783	3899	3312	8	3610	2998	3419	7	5.56E-05	1.63E-04	0.875	-0.192645078	
BP1026b	II0356	major facilitator family transporter	2238	1516	1743	1	2574	1850	2114	1	0.027703734	0.041997468	1	0	
BP1026b	II0357	major facilitator family transporter	35771	30872	32038	25	38197	36184	39272	29	0.030439533	0.045713955	1.16	0.214124805	
BP1026b	II0358	malate/L-lactate dehydrogenase family protein	1271	583	316	0	2136	1061	1224	1	0.001505409	0.003090128	#DIV/0!	#DIV/0!	
BP1026b	II0359	aldehyde dehydrogenase family protein	577	97	307	0	650	327	473	0	0.388295525	0.442624984	#DIV/0!	#DIV/0!	
BP1026b	II0360	amino acid permease	5123	5123	5123	3	29688	29688	29688	4	0.091522331	0.12276316	1.333333333	0.415037499	
BP1026b	II0361	hypothetical protein	8597	10979	8952	10	8359	8886	9002	9	2.48E-06	0.102E-05	0.9	-0.152003093	
BP1026b	II0362	hydroxyproline-2-epimerase	2995	2809	2672	3	3180	2945	2863	3	0.002906548	0.005567239	1	0	
BP1026b	II0363	oxidoreductase, FAD-binding family protein	1278	654	878	0	2438	1406	1283	1	0.040087267	0.0584944	#DIV/0!	#DIV/0!	
BP1026b	II0364	2Fe-2S iron-sulfur cluster binding domain-containing protein	435	275	437	1	444	324	574	1	0.428425083	0.482324218	1	0	
BP1026b	II0365	oxidoreductase	1559	768	880	0	1633	875	1233	0	0.113302113	0.148473815	#DIV/0!	#DIV/0!	
BP1026b	II0366	AraC family transcriptional regulator	25926	19292	22685	25	24409	23468	21890	26	4.29E-04	0.001011744	1.04	0.056853528	
BP1026b	II0367	hypothetical protein	12676	7003	10001	36	11678	11522	13129	42	0.0065982	0.011577665	1.166666667	0.222392421	
BP1026b	II0368	transposase	3828	3934	2905	4	1357	1037	1037	1	1.84E-07	1.01E-06	0.75	-0.415037499	
BP1026b	II0369	amino acid dioxygenase	2289	1978	2108	1	1945	2058	2208	1	3.76E-05	1.16E-04	1	0	
BP1026b	II0371	3-dehydroquinate dehydratase	4739	4421	4225	9	8033	7213	7422	16	0.843938471	0.868217656	1.777777778	0.830074999	
BP1026b	II0370	shikimate 5-dehydrogenase	5765	3209	3239	4	8966	5875	7144	8	0.532474194	0.584055013	1.5	0.584962501	
BP1026b	II0372	major facilitator superfamily transporter phthalate permease	6461	5593	6464	4	9321	7852	7770	6	0.148794244	0.189521744	1.5	0.584962501	
BP1026b	II0373	2-aminooethylphosphonate-pyruvate transaminase	3610	1435	856	1	3288	2193	2732	2	0.742266963	0.778723824	2	1	
BP1026b	II0374	ABC transporter substrate-binding protein	891	1291	1561	1	1487	1400	1100	0	0.003458591	0.004931387	1	0	
BP1026b	II0375	ABC transporter ATP-binding protein	185	164	150	0	357	347	348	0	0.001673701	0.003900997	#DIV/0!	#DIV/0!	
BP1026b	II0376	2-aminooethylphosphonate ABC transporter permease	1835	624	809	1	2325	1348	1972	1	0.212390128	0.259965517	1	0	
BP1026b	II0377	ABC transporter membrane protein	362	357	151	0	771	350	576	0	0.002710597	0.005225438	#DIV/0!	#DIV/0!	
BP1026b	II0378	phosphonoacetate hydrolase	33767	25054	32027	24	41064	35044	34612	29	0.078163191	0.106590804	1.208333333	0.273018494	
BP1026b	II0379	aldehyde dehydrogenase family protein	38182	25182	31150	21	36362	33905	36576	24	0.016883932	0.026977306	1.142857143	0.192645078	
BP1026b	II0380	hypothetical protein	6715	6880	7023	12	5677	5774	5726	10	3.29E-06	1.31E-05	0.833333333	-0.263034406	
BP1026b	II0381	hypothetical protein	0	0	0	0	0	0	0	0	1	1	#DIV/0!	#DIV/0!	
BP1026b	II0382	16S ribosomal RNA	0	0	0	0	0	0	0	0	1	1	#DIV/0!	#DIV/0!	

BP1026b	II0430	hypotheical protein	2954	4933	3707	13	2533	3556	2880	10	3.68E-09	2.97E-08	0.769230769	-0.378511623
BP1026b	II0431	hypotheical protein	4135	6777	5674	10	3347	3620	3002	6	1.17E-15	3.73E-14	0.6	-0.73696594
BP1026b	II0432	XRE family transcriptional regulator	5946	10123	8903	33	5381	6466	6368	24	8.11E-10	7.66E-09	0.727272727	-0.459431619
BP1026b	II0433	hypotheical protein	14388	26328	22971	36	16851	21266	16858	31	2.30E-07	1.22E-06	0.861111111	-0.215728691
BP1026b	II0434	hypotheical protein	6968	12284	10585	12	6264	7923	8457	9	3.70E-10	3.84E-09	0.75	-0.415037499
BP1026b	II0435	IS407A, transposase OrfA	5221	7141	7155	24	4380	4809	4926	17	1.04E-08	7.59E-08	0.708333333	-0.497499659
BP1026b	II0436	IS407A, transposase OrfB	692	973	773	0	704	719	815	0	7.25E-04	0.001621033	#DIV/0!	#DIV/0!
BP1026b	II0437	hypotheical protein	15391	24755	22155	18	14243	16499	15608	13	2.07E-11	2.70E-10	0.722222222	-0.469485283
BP1026b	II0438	Integrase	29490	49994	45874	57	24986	31959	30441	39	2.91E-14	7.00E-13	0.684210526	-0.547487795
BP1026b	II0439	Integrase	8456	15029	12860	7	7960	9087	9008	5	3.05E-13	5.88E-12	0.714285714	-0.485426827
BP1026b	II0441	IS407A, transposase OrfA	0	0	0	0	0	0	0	0	1	1	#DIV/0!	#DIV/0!
BP1026b	II0442	IS407A, transposase OrfB	0	0	0	0	0	0	0	0	1	1	#DIV/0!	#DIV/0!
BP1026b	II0445	hypotheical protein	245180	378109	353179	1142	284991	354682	310956	1111	0.007130387	0.0124178	0.972854641	-0.039703834
BP1026b	II0446	hypotheical protein	1475	2246	2534	10	1339	1679	1313	7	2.02E-12	3.35E-11	0.7	-0.514573173
BP1026b	II0448	IS407A, transposase OrfB	1101	2480	2038	2	1409	1125	1550	1	3.34E-10	3.50E-09	0.5	-1
BP1026b	II0449	IS407A, transposase OrfA	8627	13943	12005	43	7076	8124	9820	31	1.31E-12	2.26E-11	0.720910233	-0.472068444
BP1026b	II0450	transposase	850	1282	1498	6	509	729	629	3	8.78E-21	7.02E-19	0.5	-1
BP1026b	II0451	Ser/Thr protein phosphatase family protein	3547	3019	3054	2	3996	3199	3136	2	0.01031868	0.017349434	1	0
BP1026b	II0452	cytochrome c peroxidase	10790	11414	12155	9	13351	16385	12062	11	0.015046507	0.024288918	1.222222222	0.289506617
BP1026b	II0453	glycerophosphoryl diester phosphodiesterase family protein	10432	18003	14892	15	9518	12409	12030	12	1.07E-10	1.24E-09	0.8	-0.321928095
BP1026b	II0454	hypotheical protein	8246	14627	13592	59	9461	13559	11564	56	3.54E-06	1.40E-05	0.949152542	-0.075288127
BP1026b	II0455	integrase core subunit	3209	4405	3615	21	2151	2835	2964	14	8.40E-13	1.49E-11	0.666666667	-0.584962501
BP1026b	II0456	hypotheical protein	10372	12751	11715	16	7451	9264	7879	11	2.62E-13	5.14E-12	0.6875	-0.540568381
BP1026b	II0457	LysM domain-containing protein	140411	168626	163642	12	109066	110819	110916	8	2.13E-17	9.62E-16	0.666666667	-0.584962501
BP1026b	II0458	48458	48424	61933	56324	15	34136	37968	37146	10	5.21E-16	1.75E-14	0.666666667	-0.584962501
BP1026b	II0459	hypotheical protein	72124	114599	99724	134	44458	58224	38711	75	1.90E-26	2.94E-21	0.733333333	-0.433458977
BP1026b	II0461	hypotheical protein	41402	78299	64016	150	36117	45089	41461	100	1.64E-15	5.09E-14	0.666666667	-0.584962501
BP1026b	II0462	acetylactate synthase large subunit	33279	31600	32660	18	32832	29746	30391	18	2.96E-05	9.36E-05	1	0
BP1026b	II0463	hypotheical protein	139344	143209	141935	47	127225	130795	127658	43	3.13E-07	1.61E-06	0.914893617	-0.128324097
BP1026b	II0464	lipoprotein	40695	28175	30440	48	46337	35638	41246	60	0.126099454	0.164246545	1.25	0.321928095
BP1026b	II0466	hypotheical protein	9784	3949	5246	27	13325	9147	7905	43	0.846653339	0.07822274	1.592592593	0.671377253
BP1026b	II0465	hypotheical protein	22559	12502	14175	47	27710	20966	17541	63	0.15435821	0.194918377	1.340425532	-0.422691072
BP1026b	II0467	hypotheical protein	35754	45678	45831	150	27571	33367	32853	119	6.37E-12	2.98E-11	0.733333333	-0.447458977
BP1026b	II0468	predicted RNA	14780	2253	5011	306	18743	13669	15139	660	0.009692882	0.016380239	2.158662745	1.108943772
BP1026b	II0468	capsule polysaccharide export system periplasmic protein	475966	516187	498511	194	437186	433150	447256	172	0.068009448	0.094156337	0.886597938	-0.175648087
BP1026b	II0469	transport-related membrane protein	118743	135720	124811	103	106115	106025	103892	86	7.58E-10	7.24E-09	0.834951456	-0.260235772
BP1026b	II0470	glucose-1-phosphate cytidylyltransferase	200515	192088	189967	249	154109	161808	158618	203	3.40E-10	3.55E-09	0.815261044	-0.294666015
BP1026b	II0471	CDP-glucose 4,6-dehydratase	225829	208223	198571	196	197074	161571	172446	164	6.14E-09	4.71E-08	0.836734694	-0.257157839
BP1026b	II0472	CDP-4-deoxy-D-xylulose-3-dehydrase	2529123	225295	235577	169	179255	199554	91163	139	1.52E-09	1.17E-08	0.824852457	-0.281938364
BP1026b	II0473	arsonium synthase	510212	525712	509425	289	36134	387738	387511	218	6.10E-06	2.94E-05	0.740484421	-0.433458977
BP1026b	II0474	hypotheical protein	16755	73334	83165	67	90092	80883	83599	62	3.04E-06	1.23E-05	0.925373134	-0.11189288
BP1026b	II0475	glycosyl transferase family protein	148971	139064	139874	136	106779	106332	115966	105	5.52E-13	1.00E-11	0.772058842	-0.373217324
BP1026b	II0476	ADP-heptose-lipopoligosaccharideheptosyltransferase II	71975	107494	92935	72	49721	56453	59640	43	1.25E-21	1.17E-19	0.597222222	-0.74660247
BP1026b	II0477	ADP-heptose-LPS heptosyltransferase II	72887	93951	92206	73	46501	52452	50165	42	7.70E-25	1.31E-22	0.575342466	-0.797507136
BP1026b	II0478	galactoside O-acetyltransferase	8649	10317	10027	18	6845	7578	5516	12	3.20E-12	5.05E-11	0.666666667	-0.584962501
BP1026b	II0479	Rhamnosyl transferase	30201	35725	33982	31	17553	18899	18642	17	1.02E-23	1.52E-21	0.548387097	-0.866733469
BP1026b	II0480	hypotheical protein	22181	30776	29490	26	14034	16007	15153	13	7.76E-23	6.90E-21	0.5	-1
BP1026b	II0481	hypotheical protein	3023	1089	1615	9	1982	1671	1904	9	4.13E-05	1.26E-04	0.1	-1
BP1026b	II0482	LysR family transcriptional regulator	32468	21549	22714	26	35902	26874	29456	31	0.023258103	0.035873636	1.192307692	0.253765692
BP1026b	II0483	hypotheical protein	12104	10811	10948	15	12286	10623	11420	15	5.34E-05	1.58E-04	1	0
BP1026b	II0484	hypotheical protein	2392	1590	1330	2	3089	2395	2596	3	0.990497894	0.993189464	1.5	0.584962501
BP1026b	II0485	cyclic nucleotide-binding domain-containing protein	8590	1910	3013	4	7710	4881	6748	6	0.386224344	0.440907245	1.5	0.584962501
BP1026b	II0486	AraC family transcriptional regulator	11769	12292	11670	12	11960	12571	11329	12	3.55E-05	1.10E-04	0.9	-0.152003093
BP1026b	II0487	AraC family transcriptional regulator	9010	9010	8428	10	8428	8647	9174	8	9.71E-06	2.96E-05	0.9	-0.152003093
BP1026b	II0488	major facilitator family transporter	2646	1742	2505	1	3731	2709	2764	2	0.267943197	0.31972754	1	0
BP1026b	II0489	LysR family transcriptional regulator	21309	13279	15148	18	19609	15275	15994	18	9.19E-05	2.56E-04	1	0
BP1026b	II0490	isochorismatase superfamily hydrolase	45237	59293	56076	77	40642	46609	44304	63	1.31E-08	9.31E-08	0.818181818	-0.289506617
BP1026b	II0491	hypotheical protein	438	280	445	1	459	236	436	1	0.060156852	0.084308297	1	0
BP1026b	II0492	amidohydrolase	22026	26352	25993	13	19836	20271	19262	10	7.96E-09	5.93E-08	0.769230769	-0.378511623
BP1026b	II0493	hypotheical protein	5360	3271	3187	4	6669	4947	4782	6	0.335611271	0.38886027	1.5	0.584962501
BP1026b	II0494	hypotheical protein	4978	7144	3209	18	2778	4278	3977	3	0.031778129	0.047474209	0.4478	1.5
BP1026b	II0495	hypotheical protein	461	113	0	0	360	281	456	0	0.038579303	0.056480745	#DIV/0!	#DIV/0!
BP1026b	II0496	non-heme chloroperoxidase	7640	7697	6812	8	8310	8281	7994	9	0.001677686	0.003397071	1.125	0.169925001
BP1026b	II0498	hypotheical protein	3151	1874	2649	4	2745	2589	2716	4	8.97E-04	0.001952212	1	0
BP1026b	II0499	predicted RNA	23692	25868	26819	565	28439	31484	30473	669	0.015218214	0.024540838	1.184070796	0.243755343
BP1026b	II0500	NAD(P)H-flavin oxidoreductase	22771	20940	22858	36	23682	23232	23528	38	0.001070549	0.002281873	1.055555556	0.078002512
BP1026b	II0501	hypotheical protein	39075	65331	65157	149	29758	38677	33344	89	7.28E-21	5.93E-19	0.597315456	-0.743435089
BP1026b	II0501	GntR family transcriptional regulator	6445	1656	2012	2	8645	5808	6078	4	0.448938875	0.03315175	0.4	0.169925001
BP1026b	II0502	DI-1/PIIa family protein	5561	2951	4068	6	2222	6275	6602	11	8.77971332	0.89723391	1.833333333	0.87469118
BP1026b	II0503	peptidase	71242	63025	65395	59	65571	71479	66493	60	2.77E-04	6.85E-04	0.101694913	0.024247546
BP1026b	II0504	hypotheical protein	16274	13281	18542	104	16699	22627	19824	128	0.041190846	0.059909616	1.230769231	0.299560282
BP1026b	II0505	hypotheical protein	271	303	467	1	397	325	377	2	0.226547783	0.274774602	1	0
BP1026b	II0506	DNA polymerase X family/PHP domain-containing protein	146793	98255	109145	60	158886	139967	142587	74	0.093167149	0.12464012	1.233333333	0.30256277
BP1026b	II0507	hypotheical protein	5892	1894	2134	8	7443	6340	6711	16	0.052295935	0.074353382	0.7	-1
BP1026b	II0508	hypotheical protein	638	199	320	1	986	705	1094	3	0.001350438	0.002804371	3	1.584962501
BP1026b	II0509	copper tolerance protein	6385	5912	6323	3	6679	6640	6447	4	0.004980242	0.003420482	0	0
BP1026b</														

BP1026b	II0559	hypothetical protein	22802	18437	19760	18	28917	24988	27688	25	0.160257681	0.202558218	1.388888889	0.473931188
BP1026b	II0561	AraC family transcriptional regulator	12070	8811	10512	10	12514	12336	11880	12	0.005305339	0.009503253	1.2	0.263034406
BP1026b	II0560	DJ1/Plp1 family protein	4745	3147	3789	5	6833	5310	5834	8	0.764908529	0.798514096	1.6	0.678071905
BP1026b	II0562	2-aminooxyisovalerate-pyruvate transaminase	13374	10689	11918	112	13722	13612	12912	124	0.003030746	0.005710667	1.07142857	0.146841388
BP1026b	II0563	3-phosphonopyruvate decarboxylase	66174	36967	44744	41	85569	60550	64713	99	0.686977415	0.729931101	1.43902439	0.525091045
BP1026b	II0564	phosphoenolpyruvate phosphomutase	262533	281769	273522	161	283240	288045	271274	166	7.12E-04	0.001597304	1.031055901	0.044122553
BP1026b	II0565	ADP-glucose pyrophosphorylase	91346	69284	78449	103	107990	95878	89370	127	0.028776754	0.043456085	1.233009709	0.30218416
BP1026b	II0566	hypothetical protein	35496	17218	21210	24	44313	29769	32092	3	0.555595174	0.606763323	1.458333333	0.544320516
BP1026b	II0567	ZOG-Fet(II) oxygenase	202338	210033	217084	272	200959	207637	207434	266	6.85E-05	1.96E-04	0.977941176	-0.032180406
BP1026b	II0568	CDP-alcohol phosphatidyltransferase	69005	41442	46556	75	71365	64186	70101	90	0.221771734	0.270026026	1.32	0.40053793
BP1026b	II0569	acetyl-CoA hydrolase	58734	668905	669784	423	577051	623530	608197	397	0.423686678	0.477675509	0.938534279	-0.091516666
BP1026b	II0570	hypothetical protein	1109	2168	1569	11	1099	1637	1337	9	1.75E-06	7.49E-06	0.818181818	-0.289506617
BP1026b	II0572	type VI secretion system	2716	4720	3537	3	2960	3434	3782	3	1.27E-04	3.41E-04	1	0
BP1026b	II0573	type VI secretion system	2738	3468	2772	5	2521	2881	2972	5	1.99E-05	6.55E-05	1	0
BP1026b	II0574	type VI secretion system	6457	7628	7783	4	6509	7310	5963	4	2.16E-05	7.03E-05	1	0
BP1026b	II0575	type VI secretion system	6692	10107	8147	15	6413	8201	8624	14	1.42E-05	4.86E-05	0.933333333	-0.099535674
BP1026b	II0576	type VI secretion system	426	460	465	1	423	373	669	1	0.110017456	0.144531833	1	0
BP1026b	II0577	type VI secretion system	1839	855	1268	0	2180	1599	1659	0	0.281735604	0.334519266	#DIV/0!	#DIV/0!
BP1026b	II0578	type VI secretion system	621	486	814	0	722	788	784	0	0.223261687	0.271523956	#DIV/0!	#DIV/0!
BP1026b	II0579	type VI secretion system	1962	1088	1914	0	2078	1362	1510	0	0.322E-04	7.84E-04	#DIV/0!	#DIV/0!
BP1026b	II0580	type VI secretion system	4072	5604	6087	2	3770	4626	4622	1	6.69E-06	2.47E-05	0.5	-1
BP1026b	II0581	type VI secretion system	6355	8652	8965	3	5621	6731	6729	2	7.52E-08	4.49E-07	0.666666667	-0.584962501
BP1026b	II0582	type VI secretion system	8966	8216	8661	3	8279	7348	8022	3	5.63E-06	2.12E-05	1	0
BP1026b	II0583	type VI secretion system	3046	2886	1609	2	2374	2662	2274	2	3.31E-05	2.26E-06	0.875	-0.192645078
BP1026b	II0584	type VI secretion system	1273	1016	1297	1	1110	865	963	1	0.002566379	0.004981094	1	0
BP1026b	II0586	type VI secretion system	6246	8062	6865	18	6718	7672	7852	18	0.001663922	0.002770063	1	0
BP1026b	II0585	type VI secretion system	1241	532	848	1	1868	1390	1565	2	0.028874652	0.043572455	2	1
BP1026b	II0587	type VI secretion system	2579	2702	2781	1	3135	3512	3018	2	0.067715967	0.093791623	2	1
BP1026b	II0588	type VI secretion system	3752	1826	3390	1	3287	3729	3048	1	0.024542081	0.037613603	1	0
BP1026b	II0589	type VI secretion system	11013	8292	10251	2	12546	11694	11489	3	0.01369332	0.022299636	1.5	0.584962501
BP1026b	II0590	hypothetical protein	10824	16555	14701	38	10698	13976	13078	34	3.17E-07	1.62E-06	0.894736842	-0.160464672
BP1026b	II0591	hypothetical protein	1802	2280	2682	0	2044	2412	2320	7	1.02E-04	2.80E-04	1	0
BP1026b	II0592	hypothetical protein	10748	16407	15365	38	12518	17331	1731	36	1.30E-05	4.48E-06	0.947368421	-0.078002512
BP1026b	II0593	thiaminoyltransferase I, subunit A	33685	43248	42159	44	34397	39609	34751	40	1.78E-05	5.96E-05	0.909090909	-0.137503524
BP1026b	II0594	thiaminoyltransferase I, subunit B	15115	9990	10986	8	13301	11170	12270	8	6.91E-05	1.98E-04	1	0
BP1026b	II0595	multidrug resistance protein	12562	8388	8193	6	8738	8885	9000	5	1.52E-06	6.61E-06	0.833333333	-0.263034406
BP1026b	II0596	thiaminoyltransferase II	11614	10622	10597	10	9301	8307	7497	8	7.60E-11	9.05E-10	0.321928095	0
BP1026b	II0597	RND efflux system outer membrane lipoprotein	17250	10153	12809	8	14037	10689	11692	7	4.64E-07	2.26E-06	0.875	-0.192645078
BP1026b	II0598	multidrug resistance protein	6413	6773	6889	4	6835	7594	5897	4	7.82E-04	0.001730856	1	0
BP1026b	II0599	levansucrase	16752	16975	15461	10	16631	17331	1731	36	1.45E-04	0.00104232	1	0
BP1026b	II0600	levansucrase precursor	31115	24866	28139	18	33032	36594	37443	24	0.135853355	0.174704046	1.333333333	0.415037499
BP1026b	II0601	LactI family regulatory protein	15238	17310	16647	14	16747	17420	17116	15	5.60E-04	0.001286367	1.071428571	0.099535674
BP1026b	II0603	hypothetical protein	163	550	270	1	108	93	136	0	2.03E-25	3.64E-23	0	#NUM!
BP1026b	II0602	glutathione-independent formaldehyde dehydrogenase	2222	2160	2077	1	2174	2161	2562	1	9.67E-04	0.002087692	1	0
BP1026b	II0604	AraC family transcriptional regulator	2026	2013	2353	1	2282	2376	2319	2	0.001906389	0.003800057	2	1
BP1026b	II0605	serine hydroxymethyltransferase	1872	1565	1109	1	1302	1456	1430	1	6.07E-05	1.77E-04	1	0
BP1026b	II0606	renal dipeptidase family protein	686	1165	1165	1	499	614	499	1	2.06E-12	3.30E-11	1	#NUM!
BP1026b	II0607	VAR domain-containing protein	418	276	448	0	192	246	584	0	0.020281282	0.031695187	#DIV/0!	#DIV/0!
BP1026b	II0608	NADH:flavin oxidoreductase	3027	1683	1357	0	2266	2013	2262	1	0.001362025	0.002826325	#DIV/0!	#DIV/0!
BP1026b	II0609	iron-sulfur cluster binding protein	671	891	458	0	899	671	791	0	0.180196237	0.225128659	#DIV/0!	#DIV/0!
BP1026b	II0610	electron transfer flavoprotein subunit alpha	785	389	257	0	405	606	442	0	0.037187042	0.054682211	#DIV/0!	#DIV/0!
BP1026b	II0611	electron transfer flavoprotein subunit beta	165	134	124	0	251	224	330	0	0.010625608	0.017807577	#DIV/0!	#DIV/0!
BP1026b	II0613	iron-sulfur Rieske protein	2919	3374	2744	2	2720	2832	2348	2	6.28E-07	2.98E-06	1	0
BP1026b	II0612	iron-sulfur cluster-binding protein	6052	5906	6595	5	6463	6598	4659	6	2.03E-07	1.81E-06	0.8	-0.321928095
BP1026b	II0614	ABC transporter, periplasmic glycine/betaine-binding protein	2997	3047	2967	3	2166	2885	2968	3	1.89E-06	8.04E-06	1	0
BP1026b	II0615	hypothetical protein	29880	32163	29574	18	30408	33770	34748	19	0.003356141	0.006322243	1.055555556	0.078002512
BP1026b	II0616	formyltetrahydrofolate deformylase	6102	5182	6838	6	6145	6256	5188	6	4.30E-04	0.001012723	1	0
BP1026b	II0617	LysR family regulatory protein	2605	1616	1980	2	3089	1887	2050	2	0.005680157	0.010111311	1	0
BP1026b	II0618	choline sulfatase	5298	6975	5854	3	6601	6400	6602	4	0.00477347	0.008664351	1.333333333	0.415037499
BP1026b	II0619	glycine betaine ABC transporter substrate-binding protein	1315	1406	1757	1	1544	1546	1385	1	6.11E-04	0.001395259	1	0
BP1026b	II0620	outer membrane porin	2043	4124	2434	3	2267	3228	2727	2	2.35E-05	4.31E-05	0.666666667	-0.584962501
BP1026b	II0621	aminopeptidase	4614	4540	4587	3	6387	7010	6896	5	0.496443578	0.549433763	0.666666667	0.736965994
BP1026b	II0622	metallopeptidase domain-containing protein	29344	34702	34183	19	40993	43229	39941	24	0.16745357	0.210888626	2.63157895	0.337034987
BP1026b	II0623	AraC family transcriptional regulator	7080	6414	7388	7	6935	6938	8080	7	0.001578512	0.003220165	1	0
BP1026b	II0624	hypothetical protein	823	728	1036	3	499	513	937	2	4.81E-07	2.34E-06	0.666666667	-0.584962501
BP1026b	II0625	ABC transporter, periplasmic glycine/betaine-binding protein	4972	6384	5754	5	3704	4714	4368	4	1.01E-07	5.87E-07	0.8	-0.321928095
BP1026b	II0626	hypothetical protein	6935	5599	5663	6	7268	6180	7053	7	0.01033008	0.017349434	1.166666667	0.222392421
BP1026b	II0628	3-hydroxybutyryl-CoA dehydrogenase	8926	8319	10531	9	8958	10618	10618	7	7.08E-04	0.003217575	1.111111111	0.153003093
BP1026b	II0627	hypothetical protein	9951	7777	7737	17	12528	8627	10264	21	0.023487653	0.036156376	1.235294118	0.304854582
BP1026b	II0629	lipase	8324	3869	4917	5	9866	7296	7964	8	0.393464686	0.447657174	1.6	0.678071905
BP1026b	II0630	hypothetical protein	101851	102771	125710	356	94428	113727	105503	338	2.49E-06	1.03E-05	0.949438202	-0.45835995
BP1026b	II0631	short chain dehydrogenase/reductase family oxidoreductase	17239	9361	11477	12	18426	16415	16076	17	0.136195359	0.175108318	1.416666667	0.502500341
BP1026b	II0632	hypothetical protein	45923	57863	56261	183	42103	50563	46323	159	2.86E-07	1.48E-06	0.868852459	-0.202816883
BP1026b	II0634	leucine-, isoleucine-, valine-, threonine-, and alanine-binding protein precursor	302209	426590	383782	332	319263	349835	336974	300	0.003855184	0.007157019	0.903614475	-0.146220741
BP1026b	II0635	high-affinity branched-chain amino acid transport system permease	14746	15952	16519	16	18653	17170	17135	19	0.004901763	0.008866424	1.1875	0.247927513
BP1026b	II0636	leucine/isoleucine/valine transporter permease subunit	85421	86030	81219	67	86940	95097	97771	73	0.002051802	0.004062801	1.06060606	0.14543044
BP1026b	II0637	leucine/isoleucine/valine transporter ATP-binding subunit	51986	52406	52017	67	55524	60171	53470	72	0.002595858	0.005028974	1.074626866	0.03353811
BP1026b	II0638	Branched-chain amino acid transport ATP-binding protein LivF	59788	70702	73618	96	67166	72493	68593	98	2.76E-04	6.83E-04	1.0208333	

BP1026b	II0686	enoyl-CoA hydratase/isomerase family protein	127571	48132	63370	69	24010	17846	19033	17	3.37E-166	1.92E-163	0.246376812	-2.021061616
BP1026b	II0687	outer membrane efflux protein	65557	49016	52667	40	67986	65916	63493	47	0.028032855	0.042414399	1.175	0.232660757
BP1026b	II0688	macrolide-specific ABC-type efflux carrier	231146	195400	206230	107	220669	224968	224580	113	0.001626138	0.00302287	1.050474766	0.078711976
BP1026b	II0689	macrolide-binding protein MacA	130345	143222	143516	115	132028	134749	137156	111	1.31E-05	4.90E-05	0.965217391	-0.051074185
BP1026b	II0690	luciferase-like monooxygenase	5585	4706	4697	4	4514	5096	4339	4	2.90E-04	7.15E-04	1	0
BP1026b	II0691	ribonuclease T2 family protein	4395	5180	3976	6	3703	4372	4637	5	4.56E-04	0.001063822	0.833333333	-0.263034406
BP1026b	II0692	hypothetical protein	2459	2000	1611	4	2486	2218	2693	5	0.033641186	0.049995536	1.25	0.321928095
BP1026b	II0693	glutaminase	23734	22473	21177	24	24451	22915	25154	26	0.001664585	0.003374901	1.083333333	0.115477217
BP1026b	II0694	hypothetical protein	15536	23846	23701	68	15173	19673	16620	55	1.88E-08	1.29E-07	0.808823529	-0.306103128
BP1026b	II0695	DNA-binding response regulator	54727	57448	56363	79	55906	61916	56411	81	5.44E-04	0.001252075	1.025316456	0.036069525
BP1026b	II0696	serine histidine kinase	34581	27906	30971	27	34905	32611	37320	31	0.03001724	0.03306133	1.148787143	0.195298808
BP1026b	II0697	putative retinol-like phospholipase	93033	117708	115290	46	93100	110905	100908	43	1.39E-06	6.08E-06	0.934782699	-0.092792201
BP1026b	II0698	rod shape-determining protein MreB	332973	245928	269838	265	370393	300752	321708	310	0.188994843	0.234904824	1.169811321	0.226275856
BP1026b	II0699	cytochrome c4 family protein	9573	5325	8177	31	10373	9529	9205	39	0.040203921	0.058637339	1.258064516	0.331205908
BP1026b	II0700	IHD domain-containing protein	6356	5975	6154	10	5421	5982	5540	9	8.61E-05	2.41E-04	0.9	-0.152003093
BP1026b	II0701	amylol-alpha-1,6-glucosidase family	57929	34723	38255	18	57952	44510	48828	21	0.022085978	0.034251011	1.166666667	0.222392421
BP1026b	II0702	hypothetical protein	427847	167104	207780	1013	443272	334305	361727	1438	0.963778783	0.97058666	1.419545903	0.505429502
BP1026b	II0703	terpene cyclase	16031	12291	13800	58	16859	11907	14468	58	1.94E-04	3.37E-04	1	0
BP1026b	II0704	terpene cyclase	35755	22533	25500	51	36559	28678	31696	59	0.014445739	0.023415534	1.156862475	0.210217707
BP1026b	II0705	glyoxalase/bleomycin resistance protein/dioxygenase superfamily protein	11519	12187	11924	24	9914	10939	10386	21	7.32E-08	4.38E-07	0.875	-0.192645078
BP1026b	II0706	glutathione S-transferase-like protein	3052	1259	1695	3	3688	2615	3728	5	0.361966986	0.415559828	1.666666667	0.736965594
BP1026b	II0707	hypothetical protein	12373	8160	9399	14	10338	9488	11038	14	1.29E-04	3.44E-04	1	0
BP1026b	II0709	hypothetical protein	1361	2153	2258	3	1610	1629	1732	3	3.95E-07	1.96E-06	1	0
BP1026b	II0710	sensor kinase protein	15999	13042	15593	10	18506	15441	14652	11	0.001665164	0.00374984	1	0
BP1026b	II0711	response regulator protein	34645	29963	34000	16	34986	30811	34488	14	1.22E-07	0.01323938	1.142878743	0.192645078
BP1026b	II0712	DNA-binding protein	24553	29762	27582	31	25699	24987	24856	29	6.15E-06	2.29E-05	0.935483871	-0.096215315
BP1026b	II0713	hypothetical protein	729219	1137333	977223	3511	622980	713070	704188	2518	0.017033406	0.027195357	0.717174594	-0.479603713
predicted RNA	-	-	5182	2099	2637	330	9501	3801	5170	615	0.223340366	0.271566992	1.863636364	0.898120386
BP1026b	II0714	hypothetical protein	36307	41262	40772	120	34185	38175	37820	112	4.22E-05	1.28E-04	0.933333333	-0.099535674
BP1026b	II0715	Rhodanese-related sulfurtransferase	1347	812	1303	2	1867	1346	2312	3	0.702309659	0.743935915	1.5	0.584962501
BP1026b	II0716	transcriptional activator FtrA	23959	13659	14572	18	33302	21775	25896	28	0.072929906	0.8068301	1.555555556	0.637429921
BP1026b	II0717	hypothetical protein	34645	29963	34000	16	34986	30811	34488	14	1.22E-07	0.01323938	1.142878743	0.192645078
BP1026b	II0718	M20/M25/M40 family peptidase	237029	220912	234616	158	236227	228226	230348	159	1.99E-04	5.11E-04	1.006329114	0.009102207
BP1026b	II0719	hypothetical protein	37527	23699	28375	82	36907	34207	34120	96	0.033835773	0.050249007	1.170731707	0.227410496
predicted RNA	-	-	6428	6671	6918	606	5476	6298	6632	557	6.20E-05	1.80E-04	0.919149194	-0.121640466
BP1026b	II0720	hypothetical protein	62727	41633	43550	85	52147	47764	50560	86	3.79E-04	9.08E-04	0.911764706	0.016873819
BP1026b	II0721	insertion element membrane protein	29274	41806	35559	133	20232	22587	25424	85	1.47E-16	5.61E-15	0.639097744	-0.645891499
BP1026b	II0722	hypothetical protein	714	1239	1081	2	391	725	536	2	1.46E-16	5.61E-15	0.75	0
BP1026b	II0723	L-prolyl-dipeptidyl aminopeptidase	45381	66286	61834	29	42452	50748	50328	24	1.17E-07	8.30E-08	0.827582697	-0.273018494
BP1026b	II0724	hypothetical protein	4362	6158	6871	26	3146	4116	3961	17	1.22E-11	1.68E-10	0.653846154	-0.612967877
BP1026b	II0725	serine-type carboxypeptidase family protein	27084	47451	43763	22	23284	28753	24818	14	1.65E-16	6.23E-15	0.636363636	-0.630766977
BP1026b	II0726	hypothetical protein	21460	32931	28317	69	14814	21418	17106	44	5.23E-16	1.75E-14	0.637681159	-0.649092838
BP1026b	II0727	hypothetical protein	6702	10468	9796	39	6187	7709	6100	29	6.30E-10	6.15E-09	0.743589744	-0.427421224
BP1026b	II0728	transposase B	2224	3461	3143	13	2382	2247	2424	10	2.07E-09	1.78E-08	0.769230949	-0.378511623
BP1026b	II0729	hypothetical protein	4899	8438	7544	17	5117	6703	5599	14	2.13E-06	8.98E-06	0.823529612	-0.280107919
BP1026b	II0730	hypothetical protein	15326	21456	21745	10	15132	16444	14	4.38E-05	1.31E-04	0.8	0	
BP1026b	II0731	hypothetical protein	1378	2966	2526	5	1727	2387	2272	4	4.41E-06	1.70E-05	0.8	-0.321928095
BP1026b	II0732	transposase	5496	8133	7286	26	4870	5575	5104	19	2.13E-08	1.44E-07	0.730769231	-0.455212205
BP1026b	II0733	integrase core subunit	1123	1853	1455	8	726	1013	937	5	1.99E-15	6.04E-14	0.625	-0.678071905
BP1026b	II0734	hypothetical protein	2139	3691	2497	7	2000	2695	2321	5	4.69E-08	2.95E-07	0.714285714	-0.485426827
BP1026b	II0735	hypothetical protein	3238	5206	3849	6	2933	3817	3604	5	4.19E-06	1.63E-05	0.933333333	-0.263034406
BP1026b	II0736	response regulator protein	2299	3351	2843	3	2264	3201	2466	3	1.32E-05	4.54E-05	1	0
BP1026b	II0737	hypothetical protein	2897	2687	2987	6	1439	2650	2431	4	3.94E-16	1.37E-14	0.666666667	-0.584962501
BP1026b	II0738	alpha-tetraglutamate-dependent taurine dioxygenase	8159	14771	15162	14	8141	8686	8121	9	2.45E-16	8.95E-15	0.642857143	-0.637429921
BP1026b	II0739	peptidase	21401	32584	32471	15	15094	20533	19183	9	1.32E-16	5.20E-15	0.6	-0.736965594
BP1026b	II0740	acetyltransferase	18571	27698	27869	40	20512	23750	21041	35	1.16E-06	5.17E-06	0.875	-0.192645078
BP1026b	II0741	hypothetical protein	34361	50358	49622	204	37812	42501	40473	183	6.67E-06	2.47E-05	0.897058824	-0.156725504
BP1026b	II0743	EmrB/QacA family drug resistance transporter	23187	27511	24798	18	22809	25666	25906	17	8.51E-05	2.39E-04	0.944444444	-0.08246216
BP1026b	II0744	trehalase	11865	18777	19737	7	11804	11620	12255	7	2.97E-08	9.37E-05	1	0
BP1026b	II0745	hypothetical protein	1576	1988	2265	2	1646	1580	1896	2	1.30E-07	7.44E-07	1	0
BP1026b	II0746	cytochrome c oxidase, subunit III family protein	921	1509	1198	1	846	890	816	1	2.10E-08	1.43E-07	1	0
BP1026b	II0748	LuxR family transcriptional regulator	18657	20104	20027	21	22488	20754	23064	24	0.006683145	0.01710439	1.142857143	0.192645078
BP1026b	II0749	hypothetical protein	11978	7259	8403	11	10615	9646	10957	12	0.002658636	0.005134737	1.090909091	0.125530882
BP1026b	II0750	asparagine synthase	42537	28648	36872	18	38868	38662	40079	19	0.008720872	0.014890046	0.555555556	0.078002512
BP1026b	II0751	two-component system response regulator	1185	3232	2617	5	1952	2499	2449	4	1.27E-07	7.18E-07	0.8	-0.321928095
BP1026b	II0752	isooquinoline-1-oxidoreductase subunit beta	61929	37372	44524	21	63281	51561	51312	24	0.01963135	0.030718284	1.142857143	0.192645078
BP1026b	II0753	isooquinoline-1-oxidoreductase subunit alpha	9714	9714	9714	19	8161	78746	78746	17	4.33E-06	1.87E-05	0.894736842	0.16046673
BP1026b	II0754	AraC family transcription regulator	63860	47318	50740	55	59834	49725	56723	36	0.00E-04	9.53E-04	0.018181818	0.025959209
BP1026b	II0755	hypothetical protein	16066	15766	15926	39	17278	14460	14076	38	1.79E-05	5.99E-05	0.974358974	-0.037474705
BP1026b	II0756	hypothetical protein	489079	587664	569654	1537	423992	473609	465205	1272	0.050344222	0.071921956	0.827582697	-0.273018494
BP1026b	II0757	acyl-CoA dehydrogenase domain-containing protein	3857	3808	3797	3	3933	4042	4052	3	0.037964512	0.03725655	1	0
BP1026b	II0758	acyl-CoA dehydrogenase domain-containing protein	2787	631	1235	1	4116	2334	3202	2	0.003576971	0.006069013	1.2	1
BP1026b	II0759	monooxygenase	10629	6598	9023	6	14192	10877	12007	9	0.245305663	0.295468976	1.5	0.584962501
BP1026b	II0760	senior kinase protein	56414	35060	37218	32	67186	53188	58257	44	0.531473069	0.58305886	1.375	0.459431619
BP1026b	II0761	response regulator protein	92831	62033	61701	6	50646	45056	48454	40	0.50E-04	0.00345404	1.027477227	0.10616169
BP1026b	II0762	MjA family MjLA-interacting protein	196285</											

BP1026b	II089	hypothetical protein	1739	668	1382	0	2180	1358	1476	1	0.229375199	0.277881542	#DIV/0!	#DIV/0!
BP1026b	II0810	DNA-binding protein	15868	25806	22624	64	11777	15262	15528	42	3.40E-16	1.22E-14	0.65625	-0.607682577
BP1026b	II0811	hypothetical protein	5180	2086	2176	6	5246	4233	4536	9	0.897578062	0.913895014	1.5	0.584962501
BP1026b	II0812	cupin domain-containing protein	13762	9270	10540	23	11026	10540	10633	22	2.89E-06	1.17E-05	0.956521739	-0.064130337
BP1026b	II0813	hypothetical protein	991	1307	1542	1	103E-09	1033	906	10	1.03E-09	9.46E-09	1	0
BP1026b	II0814	LysR family regulatory protein	36285	30488	34579	35	35857	30370	32260	34	1.26E-04	3.38E-04	0.971428571	-0.041820176
BP1026b	II0815	beta alanine--pyruvate transaminase	21314	14625	17107	11	21842	18937	19418	13	0.007870587	0.01357871	1.181818182	0.2410081
BP1026b	II0816	methylmalonate-semialdehyde dehydrogenase	24342	21474	22743	15	27059	24594	25045	16	0.00454496	0.008141915	1.066666667	0.093109404
BP1026b	II0817	putative TIS1421-transposase orfA protein	2100	2436	2087	6	2570	2562	2384	7	0.005928847	0.01051503	1.166666667	0.222392421
BP1026b	II0818	hypothetical protein	3516	5712	4820	6	3763	3970	3530	5	1.47E-06	6.40E-06	0.833333333	-0.26304406
BP1026b	II0819	secretory lipase family protein	10940	15326	15227	11	8336	9970	11069	7	2.80E-14	2.98E-13	0.636363636	-0.652076697
BP1026b	II0820	hypothetical protein	81	121	88	0	906	85	110	0	0.192291835	0.239817975	#DIV/0!	#DIV/0!
BP1026b	II0821	outer membrane porin protein	2007	2701	2041	2	2126	2220	2528	2	1.88E-04	4.85E-04	1	0
BP1026b	II0822	hypothetical protein	7641	6446	7714	19	7628	7183	6351	18	1.74E-04	4.52E-04	0.947368421	-0.078002512
BP1026b	II0823	LuxR family transcriptional regulator	3376	4450	4436	4	4052	4082	4052	4	0.001960622	0.003894547	1	0
BP1026b	II0824	amino acid permease	3528	1669	2117	1	3666	3143	3157	2	0.424187309	0.47806809	2	1
BP1026b	II0825	peptidase	1123	818	664	0	1119	1239	1228	1	0.987012846	0.990645054	#DIV/0!	#DIV/0!
BP1026b	II0826	lipoprotein	5178	4804	4177	2	5530	5915	6024	3	0.01243303	0.135618913	1.5	0.584962501
BP1026b	II0827	hypothetical protein	163	315	112	0	250	203	144	0	0.118962698	0.154987801	#DIV/0!	#DIV/0!
BP1026b	II0828	fusaric acid resistance domain-containing protein	731	896	663	0	669	795	690	0	0.001611541	0.003276886	#DIV/0!	#DIV/0!
BP1026b	II0829	LysR family transcriptional regulator	6050	4199	4555	4	5949	5423	5053	5	0.013111943	0.021464306	1.25	0.321928095
BP1026b	II0830	hypothetical protein	490	160	312	1	192	434	511	1	0.669715294	0.713506121	1	0
BP1026b	II0831	outer membrane porin OpcP	2139	2185	2623	2	2431	2468	2448	2	7.42E-04	0.00165392	1	0
BP1026b	II0832	glyoxalase family protein	5599	2867	3713	9	6614	5117	5382	13	0.360828773	0.414404777	1.444444444	0.530514717
BP1026b	II0833	cytosine permease	82935	2992	75271	60	93027	90744	93991	72	0.019633779	0.030806076	1.2	0.26304406
BP1026b	II0834	DNA-binding protein	75325	9352	88279	69	93925	93157	94654	69	7.31E-05	2.68E-04	1	0
BP1026b	II0835	cytosine deaminase	67645	66790	63960	52	77432	80231	76040	61	0.018755583	0.029583549	1.173076923	0.230297619
BP1026b	II0836	membrane protein	7741	6850	7722	5	8451	8137	8144	6	0.003422249	0.006431327	1.2	0.26304406
BP1026b	II0837	hypothetical protein	12053	12019	11056	12	12062	11719	11884	12	5.48E-05	1.61E-04	1	0
BP1026b	II0838	short chain dehydrogenase	3222	2456	2391	3	4212	2858	3009	4	0.160756729	0.203066243	1.333333333	0.415037499
BP1026b	II0839	GntR family transcriptional regulator	5600	6168	6966	8	6262	7252	7836	9	0.011856061	0.019639046	1.125	0.169925001
BP1026b	II0840	voltage gated chloride channel family protein	18801	17980	16699	13	18389	17953	17538	13	2.51E-04	6.28E-04	1	0
BP1026b	II0841	hypothetical protein	65744	1043392	938497	2715	453465	554564	513301	156	1.71E-04	4.40E-05	0.576427256	-0.794789541
BP1026b	II0842	cytochrome c peroxidase	23132	15327	16239	11	22557	20644	20060	13	0.012166302	0.020084003	1.181818182	0.2410081
BP1026b	II0844	twin-arginine translocation pathway signal sequence domain-containing protein	2990	652	1965	1	4094	2381	2960	3	0.330245045	0.383279772	3	1.584962501
BP1026b	II0845	hypothetical protein	62	7	38	0	0	44	0	0	9.46E-05	2.62E-04	#DIV/0!	#DIV/0!
BP1026b	II0846	GerE family regulatory protein	978	780	669	1	1236	592	1108	1	0.263983426	0.315542689	1	0
BP1026b	II0847	Lga protein	886	615	500	1	271	492	375	0	9.95E-05	2.74E-04	0	#N/M!
BP1026b	II0848	hypothetical protein	2444	2892	2370	11	2616	2460	3082	12	0.001594229	0.003245894	1.090909091	0.125330882
BP1026b	II0849	MarR family regulatory protein	22204	7383	8922	26	33232	19881	20680	50	0.18151419	0.226594729	1.923076923	0.943416472
BP1026b	II0850	galactose-binding protein regulator	672	702	855	1	833	909	835	1	0.136588197	0.175541438	1	0
BP1026b	II0852	sugar ABC transporter permease	469	145	574	1	449	506	680	1	0.858366827	0.800553352	1	0
BP1026b	II0853	senescence marker protein-30 family protein	4748	1179	1637	2	5020	3119	3362	4	0.83541276	0.806657619	2	1
BP1026b	II0851	hypothetical protein	10354	10921	9290	19	10165	10801	10179	19	7.74E-05	2.19E-04	1	0
BP1026b	II0854	hypothetical protein	24820	21064	22497	51	27210	25364	26400	59	0.009589207	0.016218144	1.158662745	0.210217707
BP1026b	II0853	hypothetical protein	6422	7896	6961	13	6961	6535	6515	13	1.04E-04	6.96E-05	1	0
BP1026b	II0856	Leu tRNA	31349	50515	40933	481	35844	47013	41727	488	8.78E-04	0.001916323	1.014555015	0.020844254
BP1026b	II0857	p-hydroxycinnamoyl CoA hydratase/lyase	3822	3458	3271	4	3315	3561	3968	4	0.004670325	0.00848492	1	0
BP1026b	II0859	aldehyde dehydrogenase	894	323	253	0	935	890	611	0	0.150369703	0.191410135	#DIV/0!	#DIV/0!
BP1026b	II0858	feruloyl-CoA synthase	1273	1018	889	0	1447	1581	1712	0	0.87649149	0.897681777	#DIV/0!	#DIV/0!
BP1026b	II0860	3-hydroxyphenylpropionic transporter MhpT	184	102	33	0	456	132	226	0	6.29E-07	2.98E-06	#DIV/0!	#DIV/0!
BP1026b	II0861	porin	2919	1277	2045	1	2759	1950	1953	1	8.52E-05	2.39E-04	1	0
BP1026b	II0862	chitinase esterase	37395	3801	6013	3	6013	6367	6367	3	0.0047249	0.0071333	1	0
BP1026b	II0861	ICR family transcriptional regulator	32662	20631	20478	25	35970	27553	29562	31	0.063452833	0.08855164	1.24	0.310340121
BP1026b	II0864	sugar ABC transporter periplasmic sugar-binding protein	4122	3716	3685	3	3611	3891	4233	3	0.003464905	0.006816756	1	0
BP1026b	II0865	sugar ABC transporter ATP-binding protein	916	1273	1047	0	1615	1066	1038	0	0.088138578	0.118748561	#DIV/0!	#DIV/0!
BP1026b	II0866	sugar ABC transporter permease	2732	764	1136	1	2714	1878	2310	2	0.77356288	0.806393616	2	1
BP1026b	II0867	dehydratase, D-galactarate dehydratase, altronate dehydratase	203	0	26	0	567	179	117	0	0.01646215	0.026320206	#DIV/0!	#DIV/0!
BP1026b	II0868	UxaA family lysozyme	4393	2324	2944	2	5309	4686	5016	3	0.915847307	0.929625821	1.5	0.584962501
BP1026b	II0869	amidohydrolase	6405	6305	576	0	576	576	576	0	0.449957683	0.504526708	#DIV/0!	#DIV/0!
BP1026b	II0870	short chain dehydrogenase/reductase family oxidoreductase	1340	1118	1465	1	1085	1019	889	1	2.59E-07	1.36E-06	1	0
BP1026b	II0871	fumarylacetoacetate (FAA) hydrolase family protein	1711	1392	1250	1	1755	1756	1760	2	0.040814222	0.059416945	2	1
BP1026b	II0872	short chain dehydrogenase	1026	1150	1540	1	1686	1459	1119	1	0.033835787	0.050249007	1	0
BP1026b	II0873	putative alternative L-fucose mutarotase	2624	2452	3134	8	2514	3056	3148	8	0.002150473	0.004235454	1	0
BP1026b	II0875	hypothetical protein	0	0	45	0	0	0	0	0	1	1	#DIV/0!	#DIV/0!
BP1026b	II0876	H-NS histone family protein	1020	1154	1418	3	1217	1334	1036	3	0.00291644	0.005584002	1	0
BP1026b	II0877	ICR family transcriptional regulator	1736	1736	2441	2	2510	2410	2312	3	0.041001333	0.04651549	1.5	0.584962501
BP1026b	II0878	hypothetical protein	3067	2680	2823	6	2839	2468	2468	6	2.74E-05	8.74E-05	1	0
BP1026b	II0879	EAL domain-containing protein	1919	1644	1998	1	1655	1466	1692	1	9.37E-07	4.28E-06	1	0
BP1026b	II0880	TerR family transcriptional regulator	15133	16631	16518	26	17127	18695	18807	29	0.006707545	0.01174663	1.115384615	0.157541277
BP1026b	II0881	thioesterase (4HBT) superfamily protein	43037	48950	48397	106	45833	53194	49037	112	0.001570604	0.003206512	1.056603774	0.079434467
BP1026b	II0882	putative extracellular ligand binding protein	1030142	1164790	1136652	971	912978	1014976	895488	823	0.358523977	0.412059529	0.847579815	-0.238578865
BP1026b	II0883	hemolysin III	81197	56881	60235	106	75901	72363	80341	122	0.011275298	0.018791165	1.150943963	0.202816883
BP1026b	II0884	hypothetical protein	4093	3484	4107	1	4075	3670	4088	7	0.003175208	0.006026651	1	0
BP1026b	II0885	EAL/GDFE1 domain-containing protein	22255	23299	23977	11	23977	24460	24065	12	2.46E-06	2.40E-05	0.909090909	-0.137053241
BP1026b	II0886	AsnC family transcriptional regulator	21873	23448	25659	47	18637	21226	21478	41	5.47E-07	2.63E-06	0.872340426	-0.170306847
BP1026b	II0887	aromatic amino acid transport protein	29167	33684	32746	22	28189	30449	32964	22	3.14E-05	9.81E-05	1	0
BP1026b	II0888	aromatic amino acid aminotransferase	89749	85536	83831	71	89996	96807	91209	77	7.40E-04	0.001650835	1.084507042	0.117039421
BP1026b	II0889	hypothetical protein	24130	23219	25175	61	25606	27103	25203	66	0.001386066	0.002869569	1.081967213	0.113656782
BP1026b	II0890	acetyltransferase	40857	56410	51801	80	31088	33697	31784					

BP1026b	II0936	nitrilotriacetate monooxygenase component A	5123	2145	2545	2	6506	4218	4887	3	0.829092627	0.85551579	1.5	0.584962501
BP1026b	II0937	inosine-uridine preferring nucleoside hydrolase	39848	28472	30355	33	46229	33425	34915	39	0.036328484	0.035370423	1.181818182	0.2410081
BP1026b	II0938	ribokinase	57231	38636	43170	49	62207	59374	57968	64	0.217461548	0.265449473	1.306122449	0.385290156
BP1026b	II0939	hypothetical protein	4617	2418	2983	6	4874	4743	4937	6	0.89763977	0.9399014	1.666666667	0.73065594
BP1026b	II0940	hypothetical protein	24377	14868	17937	11	25403	22318	22846	13	0.043610988	0.063093111	1.181818182	0.2410081
BP1026b	II0941	hypothetical protein	43149	22652	25047	13	50086	38249	42352	19	0.696235203	0.738499057	1.461538462	0.547487795
BP1026b	II0942	L-2-amino-thiazoline-4-carboxylic acid hydrolase	6320	6673	5462	5	6946	6226	6101	5	0.602187772	0.004303509	1	0
BP1026b	II0943	L-2-Amino-thiazoline-4-carboxylic acid hydrolase	1500	332	223	2	2335	799	852	5	0.005149905	0.009253896	2.5	1.321928095
BP1026b	II0944	N-carbamoyl-L-cysteine amidohydrolase	5041	2146	3363	6	6477	3569	4159	9	0.35443065	0.407952929	1.5	0.584962501
BP1026b	II0945	flagellar hook-associated protein 2	1546469	1656484	1676031	1067	1785273	1912760	1844354	1212	0.36099999	0.42266598	1.135895033	0.183829523
predicted RNA			1250	1512	3594	211	17143	10599	12247	476	0.00806578	0.013893923	2.255924171	1.173718575
BP1026b	II0946	LysR family transcriptional regulator	16453	12042	13639	15	20177	17907	20133	21	0.262024151	0.313395642	1.4	0.485426827
BP1026b	II0947	protein-disulfide isomerase	3442	3143	3518	4	3106	2936	2571	4	3.43E-07	1.74E-06	1	0
BP1026b	II0948	aldo/keto reductase family oxidoreductase	274168	355800	340258	341	295927	332952	322878	334	0.008437592	0.01446148	0.979472141	-0.029923637
BP1026b	II0949	hypothetical protein	2585	3574	2623	10	2550	2769	2886	9	1.97E-05	6.51E-05	0.9	-0.152003093
BP1026b	II0951	MoaF protein precursor	9017	8055	9270	10	9673	9688	10256	11	0.002388926	0.004668452	1.1	0.137503524
BP1026b	II0950	3-ketoacyl-ACP reductase	1632	1167	1037	1	1877	1199	1556	1	0.064004665	0.089310833	1	0
BP1026b	II0952	LuxR family transcriptional regulator	1626	1678	1552	2	1633	1483	1493	2	8.36E-04	0.00144051	1	0
BP1026b	II0953	phenylacetaldehyde dehydrogenase	3840	3423	4542	2	2664	4599	4328	2	0.00996215	0.01678103	0.83171521	-0.26983479
BP1026b	II0954	hypothetical protein	8102	7335	7058	5	8855	8157	6875	5	0.001260191	0.002635937	1	0
BP1026b	II0955	amino acid permease	3912	3258	3179	2	407E-06	3320	2793	2	4.07E-06	1.59E-05	1	0
BP1026b	II0957	hypothetical protein	1719	866	768	1	1680	1562	1326	2	0.527082609	0.5790524	2	1
BP1026b	II0956	AraC family transcription regulator	16850	15815	16234	17	16210	16456	16586	17	1.42E-04	3.75E-04	1	0
BP1026b	II0958	outer membrane porin	429	828	563	0	1134	457	711	0	0.449916275	0.504256708	#DIV/0!	0
BP1026b	II0959	hypothetical protein	1256	2320	1556	5	1459	1366	1360	4	2.94E-07	1.52E-06	0.8	-0.321928095
BP1026b	II0960	LysR family protein	11376	20812	12903	618	10763	12643	1400E-04	59	1.68E-05	1.40E-04	1	0
BP1026b	II0961	acetyltransferase	33591	37665	35969	74	33271	35159	32815	70	5.47E-05	1.61E-04	0.945945946	-0.080170349
BP1026b	II0962	N-ethylmaleimide reductase	22168	18408	20616	19	25975	22649	24175	22	0.020717188	0.032030983	1.157894737	0.211504105
BP1026b	II0963	AraR family transcriptional regulator	18607	13518	14012	50	18305	17426	18688	59	0.017180979	0.027396106	1.18	0.23878686
BP1026b	II0964	outer membrane porin	26295152	35292283	33891742	28290	32730288	37210218	35143204	31135	0.336854425	0.390156538	1.100655571	0.138245102
BP1026b	II0965	regulator of nucleoside diphosphate kinase	58261	68506	64631	159	83540	81997	82224	206	0.126816469	0.164160072	1.295597484	0.373617572
BP1026b	II0966	hypothetical protein	6138	10331	5537	74	9720	13436	14824	93	0.034910946	0.056174461	1.253756577	0.329705445
BP1026b	II0967	hypothetical protein	20637	20812	22122	618	16339	182643	181703	59	2.98E-09	6.48E-05	0.83171521	-0.26983479
BP1026b	II0968	hypothetical protein	220050	353267	312996	635	179638	217787	210390	435	5.10E-16	1.72E-14	0.68503937	-0.545741191
BP1026b	II0969	GTP cyclohydrolase II	109470	87548	96282	147	101924	110548	111638	162	0.001161204	0.002454489	1.1402040816	0.140177658
BP1026b	II0970	hypothetical protein	176429	218386	202420	242	153895	158634	169091	191	3.87E-11	4.87E-10	0.789256198	-0.341434409
BP1026b	II0971	N-acylhomoserine lactone synthase	204233	267500	249774	392	194755	219671	207923	338	6.49E-08	3.95E-07	0.86224498	-0.213830408
BP1026b	II0972	hypothetical protein	19190	14977	14447	74	17155	14638	16325	75	1.30E-04	3.46E-04	0.103513514	0.019365325
BP1026b	II0973	hypothetical protein	148373	88541	107767	258	146109	141187	143825	323	0.091096714	0.122235227	1.251937984	-0.041027268
BP1026b	II0974	transcriptional regulator RhlR	186435	25412	21864	30	21810	20614	20414	24	2.07E-05	1.28E-05	0.933333333	0.133333333
BP1026b	II0975	MgtC family protein	6882	7640	7890	10	7387	7517	8991	11	0.001431356	0.002950672	1.1	0.137503524
BP1026b	II0976	calcineurin-like phosphoesterase	15609	9085	11699	10	19988	16129	16904	14	0.14503936	0.170253633	1.4	0.485426827
BP1026b	II0977	hypothetical protein	15687	16931	16056	27	19002	20196	19525	33	0.028582285	0.043193609	1.222222222	0.289506617
BP1026b	II0978	ZOG-Fc (I) oxygenase	78369	48689	50717	94	88657	70708	75365	124	0.022819801	0.249468355	1.319148936	0.399607459
BP1026b	II0979	IcIR family transcriptional regulator	69673	46401	47746	57	617921	58312	60121	65	0.01120034	0.019594893	1.140350877	0.189477799
BP1026b	II0980	outer membrane porin protein	5701	4317	3855	3	5296	5070	6051	4	0.041620919	0.060451036	1.333333333	0.415037499
BP1026b	II0981	Rieske (2Fe-2S) domain-containing protein	13601	1458	1458	0	2382	1409191	1409191	1	0.001409191	0.001409191	#DIV/0!	#DIV/0!
BP1026b	II0982	hypothetical protein	350	632	398	1	686	807	1021	2	0.029736811	0.044733577	1	1
BP1026b	II0983	Rieske family iron-sulfur cluster-binding protein	3020	4288	3156	3	3423	2884	3136	2	1.42E-05	4.86E-05	0.666666667	-0.584962501
BP1026b	II0984	short chain dehydrogenase	501	128	285	0	927	560	608	0	9.48E-06	3.39E-05	#DIV/0!	#DIV/0!
BP1026b	II0985	hypothetical protein	1106	1138	1265	2	1357	1246	1588	2	0.09084555	0.121983842	1	0
BP1026b	II0986	alpha/beta fold family hydrolase	556	532	680	0	434	607	668	0	0.00932193	0.015808723	#DIV/0!	#DIV/0!
BP1026b	II0987	ICR family transcriptional regulator	1345	731	914	1	914	1132	1061	1	0.015697147	0.02521593	1	0
BP1026b	II0988	short chain dehydrogenase	2233	2338	2576	2	2333	2178	1973	2	0.00180326	0.0036104	1	0
BP1026b	II0989	hypothetical protein	3119	2459	2623	1	3035	2656	2158	1	1.64E-05	1.12E-04	1	0
BP1026b	II0990	L-aspartate dehydrogenase	815	193	468	0	974	657	680	1	0.333498516	0.386626337	#DIV/0!	#DIV/0!
BP1026b	II0991	aldehyde dehydrogenase family protein	1379	1157	786	0	1818	1774	2112	1	0.241180091	0.291058621	#DIV/0!	#DIV/0!
BP1026b	II0992	glyoxalase/bleomycin resistance protein/dioxygenase superfamily	1666	602	692	1	1890	1109	1452	1	0.666263331	0.710886291	1	0
BP1026b	II0993	pyridine nucleotide-disulfide oxidoreductase, class I	1717	260	458	0	852	810	976	0	0.202893089	0.249468355	#DIV/0!	#DIV/0!
BP1026b	II0994	major facilitator family transporter	1137	1191	1581	1	2080	1651	2053	1	0.1159433	0.14635193	4	1
BP1026b	II0995	hypothetical protein	575	944	736	4	713	820	844	9	9.20E-04	0.00199308	1	0
BP1026b	II0996	membrane-anchored cell surface protein	15080	8094	10588	4	20889	15454	16237	7	0.760799732	0.79283573	1.75	0.807354922
BP1026b	II0997	OmpA family protein	9234	8317	7406	10	10163	9076	10119	11	0.007834888	0.013520839	1.1	0.137503524
BP1026b	II0998	UspA family protein	4147	6026	6879	13	5048	4815	4693	11	1.47E-05	5.00E-05	0.846153846	-0.2410081
BP1026b	II0999	amidase	99056	76684	82476	59	96504	94147	89420	64	0.001050087	0.00224414	1.084745763	0.117356951
BP1026b	II1000	AscC family transcriptional regulator	47460	56367	52001	107	51185	50078	49888	104	4.90E-05	1.46E-04	0.971962617	-0.041027268
BP1026b	II1001	methionine gamma-lyase	4438071	438120	452971	241	275247	280494	276499	21	2.17E-17	9.73E-16	0.618786667	-0.69252874
BP1026b	II1002	hypothetical protein	38778	58270	55943	226	24095	29404	28748	12	1.39E-28	3.12E-26	0.33539832	-0.901315725
predicted RNA			31025	50756	45211	682	7006	24233	21672	338	4.70E-32	1.18E-29	0.495601173	-0.102748493
BP1026b	II1003	hypothetical protein	17001	16453	15464	23	9997	9726	11183	14	4.14E-19	2.65E-17	0.60869562	-0.71620734
BP1026b	II1004	N-hydroxyarylamine O-acetyltransferase	21621	27310	24098	27	23100	22601	19984	25	2.92E-06	1.19E-05	0.925925926	-0.11031312
BP1026b	II1005	hypothetical protein	6086	4111	4585	8	6428	5745	5701	10	0.051261746	0.073082939	1.25	0.321928095
BP1026b	II1006	DNA-binding protein	8537	13090	10997	23	8340	9836	8703	19	4.01E-09	3.21E-08	0.826086957	-0.275634443
BP1026b	II1007	oxidoreductase	9499	6144	7251	8	12064	10840	10840	11	0.184589089	0.203607029	1.375	0.459431619
BP1026b	II1008	LysR family regulatory protein	37904	52929	51765	35	71311	42852	40425	44	0.047300592	0.067836445	0.857142857	-0.223292421
BP1026b	II1009	hypothetical protein	12856	13173	14778	9	15855	14380	12899	9	1.68E-05	5.68E-05	1	0
BP1026b	II1010	major facilitator family transporter	3121	3343	3272	2								

BP1026B	II1056	solute-binding family 5 protein	232925	254414	255540	155	200517	199596	198104	125	4.18E-10	4.27E-09	0.806451613	-0.310340121
BP1026B	II1057	cupin family protein	54934	57892	58577	45	35719	42078	39203	31	2.53E-14	6.28E-13	0.688888889	-0.537656786
BP1026B	II1059	manganese/iron transporter	8984	4996	5962	5	8365	5940	7540	5	0.004582345	0.00834838	1	0
BP1026B	II1058	ATPase	90474	23248	2648	17	4988	10914	10914	37	0.01202462	0.04662483	2.176470588	1.121990524
BP1026B	II1060	YuaAB two helix domain-containing protein	44932	45549	48468	102	58135	66307	64764	139	0.455755409	0.510163041	1.362745098	0.446515731
BP1026B	II1061	hypothetical protein	7829	7879	6387	8	9538	8310	7855	9	0.009878716	0.016658384	1.125	0.169925001
BP1026B	II1062	oxidoreductase alpha (molybdopterin) subunit	10773	6880	7556	3	8751	9827	10164	3	0.003586807	0.006711075	1	0
BP1026B	II1063	GntR family transcriptional regulator	35024	32179	36261	24	33010	36437	33606	24	4.50E-04	0.010513777	1	0
BP1026B	II1064	hypothetical protein	4613	2002	3098	7	5378	4389	3792	10	0.559852288	0.610880745	1.428571429	0.514573173
BP1026B	II1065	hypothetical protein	4865	2917	3652	5	6336	5566	6468	8	0.974171312	0.97948018	1.6	0.678071905
BP1026B	II1066	magnesium-translocating P-type ATPase	94074	9633	11221	3	11682	11713	11108	4	0.004889402	0.00854277	1.333333333	0.415037499
BP1026B	II1067	hypothetical protein	229	135	19	0	828	165	139	2	6.64E-10	6.44E-09	#DIV/0!	0
BP1026B	II1068	peptidase	347639	320748	333783	197	459662	422030	418851	256	0.744004069	0.780495964	1.299492386	0.377948181
BP1026B	II1069	hypothetical protein	8546	7472	9732	51	7691	7594	8053	46	4.28E-06	1.66E-05	0.901960784	-0.148863386
BP1026B	II1070	Tat pathway signal sequence domain-containing protein	3824	5016	5278	9	4030	4333	3450	7	1.01E-05	3.59E-05	0.777777778	-0.362570079
BP1026B	II1071	glucose dehydrogenase	35878	46421	44458	26	34944	37088	36608	22	7.18E-07	3.36E-06	0.846153846	-0.2410081
BP1026B	II1072	cytochrome c family protein	22045	19887	20223	15	21989	19087	19885	14	1.17E-04	3.17E-04	0.933333333	-0.099535674
BP1026B	II1073	DoxD-like family protein	88413	8410	9145	21	9003	7631	7902	18	3.90E-07	1.95E-06	0.857142857	-0.222392421
BP1026B	II1074	outer membrane porin protein	77736	89015	95342	79	71616	80375	78140	70	2.17E-07	1.16E-06	0.886075949	-0.174497731
BP1026B	II1075	hypothetical protein	27577	38572	36154	42	30098	32173	30507	38	3.39E-06	1.35E-05	0.904761905	-0.144389999
BP1026B	II1077	histidine ABC transporter permease	2092	2325	1614	2	1271	1721	1642	2	1.10E-09	1.00E-08	1	0
BP1026B	II1076	histidine transport system permease	2176	1653	2146	2	2267	1859	1888	2	1.61E-04	4.21E-04	1	0
BP1026B	II1078	histidine transport ATP-binding protein	4894	6073	6284	7	4520	4877	5011	6	6.79E-06	2.50E-05	0.857142857	-0.222392421
BP1026B	II1079	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	167890	119992	137096	108	160640	147236	150228	117	0.002326793	0.004556969	1.083333333	0.115477217
BP1026B	II1080	hypothetical protein	26515	27738	28757	55	26202	25189	24316	50	3.86E-06	1.51E-05	0.909090909	-0.137503524
BP1026B	II1081	hypothetical protein	34474	23248	27905	38	33412	36853	34843	19	1.20E-04	3.41E-04	1	0
BP1026B	II1082	hypothetical protein	947423	1502830	1338420	3660	666734	738310	753205	2085	2.32E-04	5.87E-04	0.569672131	-0.811796265
BP1026B	II1083	hypothetical protein	9512	9397	10415	7	9040	8122	7600	6	5.81E-08	3.55E-07	0.857142857	-0.222392421
BP1026B	II1084	hypothetical protein	1719	954	779	2	2102	1293	1008	2	0.226097839	0.274441127	1	0
BP1026B	II1086	hypothetical protein	4654	5756	5641	40	3446	4991	4988	33	9.65E-06	3.44E-05	0.825	-0.277533976
BP1026B	II1085	hypothetical protein	20025	11323	13442	14	16793	15945	15751	15	0.001405977	0.002905037	1.071482571	0.099535674
BP1026B	II1087	response regulator	10161	7352	8848	28	8667	7411	8406	26	7.31E-06	2.67E-05	0.928571429	-0.106915204
BP1026B	II1088	catalase	13121	18240	14843	10	18240	14843	14843	10	3.32E-06	1.33E-05	0.909090909	-0.137503524
BP1026B	II1089	hypothetical protein	25510	21190	22625	15	26386	24560	23372	16	0.001393525	0.002884059	1.066666667	0.093109404
BP1026B	II1090	AraC family transcriptional regulator	13322	10248	11058	7	12432	11999	12833	7	4.16E-04	9.86E-04	1	0
BP1026B	II1091	Rieske family iron-sulfur cluster-binding protein	14109	19913	16057	16	11255	11965	11132	11	2.15E-15	6.45E-14	0.6875	-0.540568381
BP1026B	II1092	hypothetical protein	17041	20072	19715	11	11965	14706	14964	8	1.75E-12	2.95E-11	0.727272727	-0.459431619
BP1026B	II1093	polyketide beta-ketoacyl:acyl carrier protein synthase	9623	9092	8858	7	10145	8263	8548	7	2.82E-05	8.97E-05	1	0
BP1026B	II1094	acyl carrier protein	3577	6545	5188	20	2614	3101	2816	11	1.65E-21	1.50E-19	0.55	-0.862496476
BP1026B	II1095	polyketide biosynthesis enoyl-CoA hydratase	273143	23023	23835	28	137335	160132	14948	19	1.27E-15	1.21E-13	0.678514286	-0.159274409
BP1026B	II1096	polyketide biosynthesis enoyl-CoA hydratase	21969	24544	23293	29	17397	18522	17849	23	7.77E-10	7.37E-09	0.793103448	-0.33419039
BP1026B	II1097	hydroxymethylglutaryl-coenzyme A synthase	49434	65986	60676	46	39866	45331	43988	34	4.44E-12	6.89E-11	0.739130435	-0.436099115
BP1026B	II1098	hypothetical protein	1924	2280	2290	6	1309	2081	1910	5	6.73E-09	5.11E-08	0.833333333	-0.263034406
BP1026B	II1099	hypothetical protein	53	171	89	0	108	64	0	0	6.48E-05	1.87E-04	#DIV/0!	0
BP1026B	II1100	Cys tRNA	558	500	556	7	434	572	877	8	0.223858738	0.272144557	1.142857143	0.192645078
BP1026B	II1101	malonyl-CoA:acyl carrier protein transacylase	18369	16562	17380	14	20108	19772	19495	16	0.007326592	0.012571349	1.142857143	0.192645078
BP1026B	II1102	sodium/hydrogen exchanger	21495	23823	23981	18	23908	23088	2337	9	7.24E-04	0.8345782	2	0
BP1026B	II1103	polyketide synthase	46702	40511	41486	3	48308	44642	44440	3	0.002999984	0.00572351	1.055555556	0.078002513
BP1026B	II1104	beta-ketoacyl synthase domain-containing protein	46754	38437	39695	2	45951	43821	43532	2	0.031369859	0.006391338	1	0
BP1026B	II1105	polyketide synthase	47559	35313	39761	2	48008	42420	45031	2	0.008842241	0.015080853	1	0
BP1026B	II1106	polyketide synthase	15341	16522	15460	3	13805	13498	13072	2	2.90E-08	1.90E-07	0.666666667	-0.584962501
BP1026B	II1107	halogenase PrnC	18065	21269	18585	11	17482	15961	15137	9	8.47E-08	5.00E-07	0.818181818	-0.289506617
BP1026B	II1108	EmrB/OacA family drug resistance transporter	5147	5419	5180	3	4234	5244	4465	3	6.13E-05	1.78E-04	1	0
BP1026B	II1109	voltage-gated chloride channel/CBS domain-containing protein	6813	48469	8986	2	8986	7573	7669	4	0.80563176	0.8345782	2	0
BP1026B	II1110	MarR family transcriptional regulator	806	1924	1402	3	1171	1527	1716	3	0.004509347	0.008232576	1	0
BP1026B	II1111	HPP family protein	1681	1274	1529	1	2147	1742	1666	1	0.056960001	0.080294401	1	0
BP1026B	II1112	transcriptional regulator	53162	47094	46452	50	42137	42838	41443	43	4.64E-07	2.26E-06	0.86	-0.217591433
BP1026B	II1113	calcium/proton exchanger	56790	39818	43662	43	58593	54130	57519	52	0.065185046	0.090746959	1.209302326	0.274174965
BP1026B	II1114	membrane efflux protein	20436	23127	22707	32	20066	23532	22841	32	2.16E-04	5.52E-04	1	0
BP1026B	II1115	CAAX protease family protein	12923	13660	11004	14	13986	12713	12238	14	1.32E-04	3.51E-04	1	0
BP1026B	II1116	fumaroylacetate (FAA) hydrolase	12110	15046	14381	22	28066	18788	19552	30	0.22096108	0.26917347	1.363636364	0.447458977
BP1026B	II1117	AraC family transcriptional regulator	12649	10568	10160	11	11087	10951	12444	11	1.34E-04	3.56E-04	1	0
BP1026B	II1118	putative lipoprotein	0	48	0	0	123	71	98	0	0.02E-02	3.00E-18	#DIV/0!	0
BP1026B	II1120	ECF subfamily RNA polymerase sigma factor	652	361	559	1	463	312	451	0	1.32E-04	3.53E-04	0	#NUM!
BP1026B	II1119	hypothetical protein	591	132	170	0	829	584	552	0	5.27E-05	1.56E-04	#DIV/0!	0
BP1026B	II1121	hypothetical protein	2112	752	1087	1	2778	1679	2430	2	0.317414503	0.370225457	2	1
BP1026B	II1122	lipoprotein	1503	776	732	2	2024	1584	1600	4	0.148735142	0.189521744	2	1
BP1026B	II1125	ECF subfamily RNA polymerase sigma factor	803	347	507	1	832	524	612	1	0.12373553	0.164781736	1	0
BP1026B	II1124	FecR family protein	699	738	352	0	796	526	428	0	0.010816264	0.018093447	#DIV/0!	#DIV/0!
BP1026B	II1126	TonB-dependent siderophore receptor	70443	63614	62105	24	62964	58012	59748	22	4.02E-06	1.57E-05	0.916666667	-0.125530882
BP1026B	II1127	ribose ABC transporter permease	1906	1137	1184	1	2853	1746	1728	2	0.57672783	0.79276053	2	1
BP1026B	II1128	sugar ABC transporter permease	3868	3236	3863	3	3783	3864	3266	3	0.002109712	0.004166947	1	0
BP1026B	II1129	ABC transporter ATP-binding protein	9324	3937	5288	3	10461	7021	7661	4	0.160133739	0.202423551	1.333333333	0.415037499
BP1026B	II1130	Ribose transport ATP-binding protein rbsA	5941	5486	6016	5	5696	4993	4935	4	5.79E-05	1.69E-04	0.8	-0.321928095
BP1026B	II1131	hypothetical protein	241759	231483	244413	345	159454	211085	21003	297	7.03E-08	4.23E-07	0.860869565	-0.216133431
BP1026B	II1230	hypothetical protein	579785	12240	4293	30	13619	8309	10837	15	0.237551689	0.28273507	1.433333333	0.519374159
BP1026B	II1134	acyl-CoA dehydrogenase-family protein	2315	1074	1476	1	2204	1810	1869	1	0.037410851	0.054985536	1	0
BP1026B	II1135	sugar transport protein	4155	2499	2545	2	3764	2893	3015	2	0.003634586	0.006797		

BP1026b	II182	RND family efflux transporter MFP subunit	8342	3738	4797	5	10601	7782	6969	7	0.4946481	0.547736546	1.4	0.485426827
BP1026b	II183	hydrophobe/amphiphile efflux family protein	55978	60998	60467	19	57367	56273	55020	18	1.51E-05	5.15E-05	0.947368421	-0.078002512
BP1026b	II184	RND efflux system outer membrane lipoprotein	2895	1498	2296	1	2544	2522	2236	1	0.001772813	0.003563234	1	0
BP1026b	II185	KTIP cyclohydrolase II	26186	30730	32460	47	33942	34483	34483	55	0.02633266	0.040064138	1.17021276	0.23670865
BP1026b	II186	WD domain-containing protein	33401	27141	27713	17	41922	37981	41005	23	0.424654336	0.47842253	1.352941176	0.436099115
BP1026b	II187	hypothetical protein	4244	2756	2865	4	5334	4949	4736	7	0.935553062	0.946263199	1.75	0.807354922
BP1026b	II188	hypothetical protein	15392	17436	16605	16	21972	19220	22082	21	0.082233458	0.11728499	1.3125	0.392317423
BP1026b	II189	riboflavin biosynthesis protein RibD	2076	1873	2007	1	4175	3144	2426	2	0.476427346	0.52971082	2	1
BP1026b	II190	O-methyltransferase	12953	13464	13812	12	18226	18804	18052	17	0.225415049	0.273771268	1.416666667	0.502500341
BP1026b	II191	glyoxylase/bioleumycin resistance protein/dioxygenase superfamily protein	56933	16573	18964	35	72377	51392	50608	67	0.038290099	0.056133161	1.914285714	0.936806174
BP1026b	II192	major facilitator superfamily transporter	81672	58744	69261	49	78788	72382	77513	54	0.002324852	0.004906613	1.02040816	0.140177658
BP1026b	II193	hypothetical protein	21430	28347	27876	51	18862	20486	18748	38	1.39E-10	1.57E-09	0.745098039	-0.424497829
BP1026b	II194	hypothetical protein	24832	16207	16864	13	26369	18576	21048	15	0.008519919	0.01458266	1.153846154	0.206450877
BP1026b	II195	LuxR family transcriptional regulator	94704	133020	123374	145	87579	101702	97472	118	5.92E-10	5.84E-09	0.813793103	-0.297266041
BP1026b	II196	predicted RNA	60242	35170	34117	324	101757	55619	69396	568	0.11626496	0.151785659	1.75308642	0.809897117
BP1026b	II197	hypothetical protein	31245	29624	31113	69	32300	34258	38709	79	0.020406528	0.031867102	1.144927536	0.195262691
BP1026b	II198	2,4-dienoyl-CoA reductase	46786	28767	32863	18	56142	50739	50804	25	0.747266632	0.762946441	1.388388889	0.392991188
BP1026b	II199	PadR-like family regulatory protein	28643	20899	21712	42	30436	28071	28667	42	0.037077419	0.04604809	1.238095238	0.390812295
BP1026b	II200	hydroxyethylthiazole kinase	9968	6084	6816	9	13088	9796	9772	13	0.298848576	0.35152393	1.444444444	0.530514717
BP1026b	II201	hypothetical protein	14218	14041	14031	16	15273	15333	15564	18	0.001570286	0.003206512	1.125	0.169925001
BP1026b	II202	hypothetical protein	4634	3870	4997	5	6844	6373	6240	7	0.411472499	0.46532666	1.4	0.485426827
BP1026b	II203	hypothetical protein	3344	1177	1688	3	5666	4439	4300	7	2.92E-04	7.19E-04	2.333333333	1.222392421
BP1026b	II204	universal stress protein	14837	16686	17419	63	19980	22345	21744	82	0.116629879	0.152198717	1.301587020	0.380272081
BP1026b	II205	hypothetical protein	97620	537716	684438	773	969756	873950	894233	962	0.294366192	0.347228116	1.24450194	0.31566848
BP1026b	II206	hypothetical protein	18105	20730	18380	458	171695	181735	183515	429	0.571E-05	0.755E-05	0.926666667	-0.084369951
BP1026b	II207	Ni,Fe-hydrogenase III small subunit	22813	13477	17972	34	24845	19548	20248	41	0.022676183	0.035088233	1.205882353	0.27089163
BP1026b	II208	hydrogenase 4 subunit F	110420	96143	94562	56	93321	82265	88222	49	1.03E-07	5.97E-07	0.875	-0.192645078
BP1026b	II209	hydrogenase 4 membrane component	122847	113046	112189	79	106810	101240	108583	72	2.35E-07	1.24E-06	0.911392405	-0.133857547
BP1026b	II210	formate hydrogenlyase subunit 4	61542	92153	84888	120	48869	56273	60214	83	3.84E-15	1.09E-13	0.691666667	-0.531851164
BP1026b	II211	Hydrogenase-4 component B / Formatehydrogenlyase subunit 3	70532	60599	62774	67	69868	60098	65024	68	1.77E-04	4.59E-04	1.014925373	0.021373651
BP1026b	II212	hypothetical protein	259702	123903	153575	89	243755	230139	246811	119	0.433666266	0.487837488	1.337078652	0.419044332
BP1026b	II213	hypothetical protein	40184	33865	3738	3	3380	39070	37789	42	0.007608	0.00232835	0.00232835	0
BP1026b	II214	hypothetical protein	383	646	473	4	472	380	227	3	2.38E-05	7.70E-05	0.75	-0.415037499
BP1026b	II215	phosphocarrier HPr protein	66383	58833	64176	141	70594	68341	69860	155	0.003720497	0.006941903	1.09929078	0.136573053
BP1026b	II216	transferase	23719	21056	23411	87	22333	24751	22068	88	2.84E-04	7.03E-04	1.011494253	0.016488123
BP1026b	II217	hypothetical protein	58460	31209	37209	50	61260	46284	49846	63	0.101586534	0.134697174	1.26	0.333423734
BP1026b	II218	proline dehydrogenase	8530	2616	3047	45	11958	6435	80843	84	0.409634973	0.463499312	1.866666667	0.900464326
BP1026b	II219	hypothetical protein	22640	34134	32353	15	20610	26864	25643	111	2.14E-08	1.45E-07	0.222222222	-0.232399731
BP1026b	II220	hypothetical protein	8750	15748	15446	12	10364	7168	7168	23	0.9874544	0.42378421	1.916666667	0.091447301
BP1026b	II221	nitrate/nitrite reductase	11868	11104	11227	8	9344	10484	8949	16	8.14E-09	6.05E-08	0.875	-0.192645078
BP1026b	II222	peptidyl-prolyl cis-trans isomerase C	15614	13890	14780	18	12764	13205	13256	16	1.88E-07	1.02E-06	0.888888889	-0.169925001
BP1026b	II223	respiratory nitrate reductase subunit gamma	20135	20111	19540	29	17296	17147	18664	25	1.85E-06	7.88E-06	0.862066666	-0.214124805
BP1026b	II224	nitrate reductase 1 subunit delta	18616	15634	18292	25	21542	19691	20401	29	0.016044264	0.026244312	1.16	0.214124805
BP1026b	II225	nitrate reductase subunit beta	65670	70290	69188	44	52019	59889	59566	37	1.41E-08	9.98E-08	0.840909091	-0.249978253
BP1026b	II226	nitrate reductase subunit alpha	195087	163786	170724	46	191143	181554	186867	49	0.00144001	0.002960264	1.065217391	0.091147888
BP1026b	II227	hypothetical protein	1351	1351	1353	3	1353	1353	1353	3	1.11E-07	1.11E-07	0.666666667	-0.57419406
BP1026b	II228	sensory box histidine kinase/response regulator	169139	133406	138344	71	185467	175882	176065	87	0.105227243	0.13986642	1.225532103	0.291963676
BP1026b	II229	LuxR family DNA-binding response regulator	76369	76144	70656	114	84586	78563	80069	125	0.001844871	0.003685629	1.096491228	0.13289427
BP1026b	II230	response regulator	459950	440563	497901	1134	512909	553402	517604	1284	0.9873409	0.990815784	1.132275132	0.179224642
BP1026b	II231	Crp/FNR family transcriptional regulator	559647	565485	573388	725	590695	618696	606794	776	0.835414279	0.860657619	1.070344828	0.098075657
BP1026b	II232	hydrolyase Cdc/NonD family protein subfamily	30102	35886	32821	19	28483	31142	28508	17	1.10E-06	4.95E-06	0.894736842	-0.160464672
BP1026b	II233	predicted RNA	31483	51714	54008	1429	25604	41311	29208	1001	1.14E-13	2.39E-12	0.704889853	-0.513563942
BP1026b	II234	IauD/IDA family dioxygenase	3032340	476930	4386304	4773	371644	337286	342604	3638	0.23E-04	1.32E-04	0.767329326	0.093993334
BP1026b	II235	transport/efflux protein	26465	237299	230790	193	202286	187466	195387	136	6.02E-10	5.93E-09	0.808290155	-0.307054818
BP1026b	II236	thioesterase	82828	66329	73300	84	68538	57588	61799	71	3.60E-08	2.31E-07	0.845238095	-0.242570303
BP1026b	II237	acetyltransferase	373016	232182	247360	335	311346	238113	260944	319	1.07E-05	3.76E-05	0.952238806	-0.076046672
BP1026b	II238	polyketide synthase	1214459	1205952	1199704	757	1016802	1022344	1002190	636	0.25019701	0.300840684	0.84015852	-0.251266535
BP1026b	II239	polyketide synthase	960850	1489603	833332	343	847279	762318	741425	317	0.636456233	0.683282916	0.924198251	-0.113725736
BP1026b	II240	non-ribosomal peptide synthase/polyketide synthase	1576889	449607	1533648	441	1378835	1307475	1300893	382	0.079139794	0.107805414	0.862613152	-0.207206018
BP1026b	II241	TubP protein	1870478	1590753	1591205	418	1833585	1873033	1873033	418	0.146029581	0.16730134	0.892352326	0.091447301
BP1026b	II242	TubP protein	171772	1424256	1637723	379	2274575	1935681	1984084	449	0.387294542	0.41727203	1.18469657	0.244517597
BP1026b	II243	non-ribosomal peptide/polyketide synthase	3971183	3168942	3266605	754	4052190	3522000	3681463	815	0.054942998	0.126166294	1.080901851	0.112235536
BP1026b	II244	oligopeptidase A	494041	633894	596518	299	551086	554653	531731	283	0.406686618	0.460578653	0.946488294	-0.079343431
BP1026b	II245	hypothetical protein	34239	57229	51626	230	37482	32888	43904	216	2.57E-05	8.25E-05	0.939130435	-0.090602549
BP1026b	II246	N-acetyl-homoserine lactone dependent regulatory protein	77012	132485	111849	605	81592	119307	102686	911	2.39E-06	9.92E-06	0.940441451	-0.083077888
BP1026b	II247	N-acyl-homoserine lactone dependent regulatory protein	153918	179059	172066	265	157184	161344	161579	253	1.39E-05	4.75E-05	0.94716981	-0.066848975
BP1026b	II248	hypothetical protein	59270	483205	513200	968	50213	502416	507446	49	0.37373257	0.4323480	0.965452326	0.091447301
BP1026b	II249	predicted RNA	17400	1684	2409	278	25301	12401	12401	605	0.007492014	0.012971958	1.12625899	1.121850259
BP1026b	II250	sodium/hydrogen exchanger	593443	380296	408783	373	582234	457281	521533	426	0.975759548	0.980919815	1.142095133	0.1916778
BP1026b	II251	hypothetical protein	14876	22050	20593	116	12016	14364	14284	82	7.36E-14	1.60E-12	0.706896552	-0.500428991
BP1026b	II252	hypothetical protein	12999	11095	10308	28	11622	13542	12845	31	9.67E-04	0.002087692	1.107142857	0.146841388
BP1026b	II253	N-acetylhomoserine lactone synthase	382704	487806	462988	715	309638	367170	356815	554	4.18E-05	1.27E-04	0.774825151	-0

BP1026b	II1301	CorA family protein	45159	47565	47387	45	42366	40693	43240	41	5.52E-06	2.08E-05	0.911111111	-0.134301092
BP1026b	II1302	DeoR family transcriptional regulator	3547	3468	3979	4	4328	3638	3161	4	0.003405728	0.00646037	1	0
BP1026b	II1303	transporter	6453	2846	3500	3	7450	5172	6319	5	0.529449058	0.580939993	1.666666667	0.736965594
BP1026b	II1304	hypothetical protein	4728	4728	6201	13	7229	6500	6000	14	0.00507718	0.009138924	1.076923077	0.196915204
BP1026b	II1305	hypothetical protein	1599	1191	1341	2	2939	1281	1539	3	0.348269064	0.401967219	1.5	0.584962501
BP1026b	II1306	transporter periplasmic binding protein	8377	9612	10123	7	7480	8413	8596	6	3.69E-07	1.86E-06	0.857142857	-0.222392421
BP1026b	II1308	sugar ABC transporter permease	1509	1061	1011	1	1364	1647	1952	1	0.459404018	0.513605669	1	0
BP1026b	II1307	ABC transporter permease	895	663	502	0	972	693	668	0	0.108814213	0.143191012	#DIV/0!	#DIV/0!
BP1026b	II1310	zinc-binding dehydrogenase family oxidoreductase	774	598	678	0	690	764	471	0	0.0024605	0.004083833	#DIV/0!	#DIV/0!
BP1026b	II1311	sugar ABC transporter ATP-binding protein	1731	1433	1530	1	1621	1929	1648	1	0.005606863	0.009997683	1	0
BP1026b	II1309	AsnC family transcriptional regulator	10869	1265	12362	12	10335	12829	11746	11	4.05E-07	0.0101E-06	0.916666667	-0.12530883
BP1026b	II1312	xylokinase	15043	7047	10291	7	11201	10886	11803	8	0.002470833	0.004822506	1.428571429	0.148245078
BP1026b	II1313	peptidase	15739	21972	20951	19	20480	22344	20730	21	0.002547306	0.004948669	1.105263158	0.144389999
BP1026b	II1314	penicillin-binding protein	5871	2716	4156	2	7177	4834	7326	3	0.635426724	0.683124565	1.5	0.584962501
BP1026b	II1315	hypothetical protein	5076	2875	2673	16	3240	2571	2853	13	3.68E-08	2.35E-07	0.8125	-0.299560282
BP1026b	II1316	Assimilatory nitrate reductase large subunit	332088	260701	274958	68	226408	205664	206640	50	4.97E-13	9.14E-12	0.735294118	-0.443606651
BP1026b	II1317	nitrite reductase (NAD(P)H) small subunit	33944	25814	29629	84	21516	22585	22987	63	1.22E-10	4.11E-09	0.75	-0.415037499
BP1026b	II1318	nitrite reductase (NAD(P)H) large subunit	233308	183470	190562	79	183121	169577	168348	67	2.40E-08	1.60E-07	0.848107566	-0.237691558
BP1026b	II1319	nitrate transporter	852	521	640	0	730	903	853	0	0.34887529	0.402592843	#DIV/0!	#DIV/0!
BP1026b	II1321	uroporphyrin-III C-methyltransferase	549	96	407	0	735	578	652	0	0.009220727	0.015666744	#DIV/0!	#DIV/0!
BP1026b	II1323	response regulator NasI	7551	5090	5915	10	8357	6284	7424	12	0.02551948	0.03893086	1.2	0.263034406
BP1026b	II1322	nitrate transporter ATP-binding protein	14374	8408	9134	10	16672	11758	12963	12	0.057914875	0.081439142	1.2	0.263034406
BP1026b	II1324	GTP cyclohydrolase I	2773	1882	2427	3	2078	2078	2252	1	8.99E-05	2.51E-04	1	0
BP1026b	II1325	lipotein	77380	63350	68546	31	76844	68662	69987	32	3.57E-04	8.61E-04	1.032258065	0.04580369
BP1026b	II1326	predicted RNA	134568	12497	125799	791	13042	120663	122092	767	8.49E-06	3.06E-05	0.96965866	-0.04431117
BP1026b	II1327	acetylpolymine aminohydrolase	146084	22915	23245	263	371813	32715	32501	30	0.121770488	0.15847831	1.153695181	0.213764443
BP1026b	II1327	allantoate amidohydrolase	415263	202752	236831	206	458662	362125	377320	289	0.908912332	0.929299955	1.402912621	0.488425155
BP1026b	II1328	major facilitator family transporter	349477	248208	263776	217	358360	320705	353293	260	0.268466352	0.320267051	1.198156682	0.260816581
BP1026b	II1329	LysR family transcriptional regulator	103757	104703	99156	105	99502	104599	104557	105	3.53E-05	1.09E-04	1	0
BP1026b	II1330	hypothetical protein	17883	13792	16257	44	20002	18189	192157	52	0.024560901	0.037633251	1.181818182	0.2410081
BP1026b	II1331	LysR family transcriptional regulator	12436	10984	11304	11	14808	11825	12272	12	0.00153416	0.003140923	1.090909091	0.125530882
BP1026b	II1332	short chain dehydrogenase	9003	7351	6718	10	9871	9550	9629	13	0.038478852	0.056274455	1.3	0.378511623
BP1026b	II1333	CAIB/BAIF family CoA transferase	11394	4417	4926	5	11926	9774	9501	0	0.19834895	0.245578125	1.5	0.584962501
BP1026b	II1334	zinc-containing alcohol dehydrogenase	10059	5277	6712	7	11442	9548	10339	10	0.291309271	0.34446429	1.428571429	0.514573173
BP1026b	II1335	iron-containing alcohol dehydrogenase	6032	2985	3802	3	7891	6673	7574	6	0.693133673	0.735582394	1.2	0
BP1026b	II1336	hypothetical protein	15323	14946	14031	91	13959	13522	13608	84	2.20E-06	9.24E-06	0.923076923	-0.115477217
BP1026b	II1339	hypothetical protein	514	389	617	1	490	462	244	1	2.20E-04	5.59E-04	1	0
BP1026b	II1338	hypothetical protein	34815	37056	35631	18	38685	39225	40870	20	0.01267403	0.020812616	1.111111111	0.152003093
BP1026b	II1340	hypothetical protein	8787	3221	4737	16	11500	13107	10872	35	0.045249113	0.056267445	2.1875	0.192583017
BP1026b	II1341	hypothetical protein	2679	2774	4818	4	4188	4275	4250	0	0.92927186	0.82498381	1	0
BP1026b	II1342	Methyl-accepting chemotaxis protein	53603	36805	40338	15	69956	60881	62884	22	0.966904908	0.973380913	1.466666667	0.552541023
BP1026b	II1343	hypothetical protein	16677	9267	10155	18	21187	15505	18140	28	0.636150258	0.684333905	1.555555556	0.57429921
BP1026b	II1344	hypothetical protein	6652	9440	7864	23	7994	9467	9088	26	0.002126699	0.004197854	1.130434783	0.176877762
BP1026b	II1345	nonribosomal peptide synthetase DhhI	4848	3370	3660	1	4754	3625	4944	1	0.023277504	0.035894735	1	0
BP1026b	II1346	MBH-like protein	248	246	266	1	831	209	269	1	0.82183086	0.88348955	1	0
BP1026b	II1347	major facilitator superfamily transporter	1350	1027	879	0	1912	1235	1244	1	0.529530068	0.580939929	#DIV/0!	#DIV/0!
BP1026b	II1348	ribosephosphate mechanism natural product synthetase	34119	2451	2451	2	36511	31986	31727	22	0.08423404	0.070861727	1	0
BP1026b	II1349	AMP-binding domain-containing protein	3957	2237	2193	3	3669	3321	3174	4	0.102642148	0.135867011	1.333333333	0.415037499
BP1026b	II1350	phosphopantetheine attachment site domain-containing protein	1403	2045	2244	5	1258	1164	1141	4	1.50E-10	1.68E-09	0.8	-0.321928095
BP1026b	II1351	acyl-CoA dehydrogenase domain-containing protein	5618	3902	5055	2	5940	5647	5184	3	0.024678552	0.037777701	1.5	0.584962501
BP1026b	II1352	acyl-CoA dehydrogenase domain-containing protein	7803	6365	7764	4	9694	7444	8602	3	0.01236326	0.020381682	1	0
BP1026b	II1353	AMP-binding domain-containing protein	6059	6225	6062	3	6479	5958	5497	3	4.86E-04	0.001126931	1	0
BP1026b	II1354	ECF subfamily RNA polymerase sigma factor	2428	3367	2936	5	2034	2796	2080	4	9.86E-10	9.12E-09	0.8	-0.321928095
BP1026b	II1355	hypothetical protein	12873	8043	10198	17	15893	11569	12038	22	0.0361277	0.0276187	1.294114767	0.371968777
BP1026b	II1356	membrane protein	9557	5149	6033	6	9852	8008	7995	3	0.039087474	0.057195177	1.333333333	0.415037499
BP1026b	II1357	hypothetical protein	1268	1089	1013	5	1684	799	1146	5	0.01888925	0.029756972	1	0
BP1026b	II1358	oxidoreductase	2510	1448	1176	1	1735	1989	1814	1	0.002195833	0.00431666	1	0
BP1026b	II1359	TerR family transcriptional regulator	8370	4207	3997	7	9645	5358	6053	9	0.08306957	0.113620281	1.285714286	0.362570079
BP1026b	II1360	threonine dehydratase	9228	6434	7019	4	8060	6632	7292	2	1.16E-04	3.13E-04	1	0
BP1026b	II1361	hypothetical protein	19996	29600	26939	98	18337	18388	19128	71	1.60E-11	2.12E-10	0.724489796	-0.464967225
BP1026b	II1362	phosphatase kinase 2 family protein	245342	347646	319578	328	190099	226777	245332	226	2.21E-15	6.75E-14	0.689024581	-0.37370447
BP1026b	II1363	lipotein	5097	3675	4172	2	5499	4941	5225	3	0.05561441	0.07859364	1.5	0.584962501
BP1026b	II1364	secretion protein	9533	13990	11876	9	8222	9149	7899	6	3.54E-13	6.78E-12	0.686666667	-0.584962501
BP1026b	II1365	hypothetical protein	3615	3005	3868	3	3602	3055	3800	3	0.00169736	0.00383157	1	0
BP1026b	II1366	peptidase	19557	21231	20137	9	17135	18664	18612	8	2.67E-06	1.09E-05	0.888888889	-0.169925001
BP1026b	II1367	hypothetical protein	4569	8540	7475	36	4423	6239	5495	28	2.41E-07	1.27E-06	0.777777778	-0.362570079
BP1026b	II1368	hypothetical protein	59822	45261	46146	289	107059	98643	94190	574	0.011820247	0.019594893	1.98615917	0.98981244
BP1026b	II1369	outer membrane protein TolC	40369	14218	19028	26	42021	42021	42021	27	0.064918637	0.064918637	1.038461538	0.2781784
BP1026b	II1370	gamma-glutamyl transferase	421456	418105	431955	246	392341	421586	393720	23	0.030824898	0.046191679	0.947154476	-0.07832836
BP1026b	II1372	hypothetical protein	1408	580	680	1	1533	1604	2	0.14575421	0.185201541	1	0	
BP1026b	II1373	hypothetical protein	4170	3888	4420	8	6170	4344	3275	8	0.016857714	0.026942278	1	0
BP1026b	II1374	DEAD/DEAH box helicase	64267	55886	57763	12	73400	67965	65523	14	0.017581133	0.027977283	1.166666667	0.222392421
BP1026b	II1375	amino acid permease	2066	811	996	0	2694	1343	1621	1	0.607840776	0.656731862	#DIV/0!	#DIV/0!
BP1026b	II1377	DGPF domain-containing protein	3087	2512	3067	6	2131	2356	2301	5	5.16E-10	5.14E-09	0.833333333	-0.263034406
BP1026b	II1378	phospho-2-dehydro-3-deoxyheptonate aldolase	61094	37848	46255	43	68539	61253	60316	56	0.255760743	0.306414656	1.302225581	0.381900167
BP1026b	II1379	O-methyltransferase family protein	746215	275142	27142	34055	1375049	34055	34055	10	0.03379946	0.056190171	1.25	0.321928095
BP1026b	II1380	diguanylate cyclase	13889	11792	12486	8	18859	14833	14008	10	0.33578413	0.3662		

BP1026B	II1429	serine acetyltransferase	1407	1356	1222	1	1736	1228	1223	1	0.00401694	0.007424357	#DIV/0!	1	0
BP1026B	II1430	rhodanese-like domain-containing protein	180	494	112	0	224	144	224	0	3.05E-04	7.48E-04	#DIV/0!	#DIV/0!	0
BP1026B	II1431	prolyl oligopeptidase family protein	151373	127665	144657	67	143427	144779	147207	69	2.96E-04	7.27E-04	1.029850746	0.042435266	
BP1026B	II1432	multidrug resistance protein	8001	7286	8001	5	4292-07	6023	6259	4	4.29E-07	2.11E-06	0	0	0.321928095
BP1026B	II1433	RND efflux system outer membrane lipoprotein	18271	13315	14192	9	15697	12944	12903	8	8.56E-07	3.95E-06	0.888888889	-0.169925001	
BP1026B	II1434	thiamosyltransferase II	13365	10532	11410	11	10000	7790	8530	8	4.56E-12	7.06E-11	0.727272727	-0.459431619	
BP1026B	II1435	multidrug resistance protein	12324	8063	10036	6	10624	9162	9778	6	1.24E-05	4.31E-05	1	0	
BP1026B	II1436	thiamosyltransferase I, subunit B	20186	12564	15201	11	17538	14876	15893	11	1.39E-04	3.68E-04	1	0	
BP1026B	II1437	thiamosyltransferase I, subunit A	36481	47268	41689	46	36081	37477	36686	40	2.65E-06	1.09E-05	0.869565217	-0.201633861	
BP1026B	II1438	transcriptional regulator Btf1	15375	10097	9886	20	21700	14264	18134	31	0.669213189	0.13213444	1.355	0.63268215	
BP1026B	II1439	lysine aldehyde dehydrogenase	192349	162105	170357	118	227478	203615	209454	145	0.096234298	0.128251062	1.238815559	0	0.297260411
BP1026B	II1440	choline dehydrogenase	212492	279002	265293	148	237521	252062	251847	8	3.95E-05	1.21E-04	0.97972973	-0.02544276	
BP1026B	II1441	hypothetical protein	1703213	1400452	1523680	456	1893870	1781185	1738053	534	0.496898595	0.549646427	1.171052632	0.227805189	
BP1026B	II1442	major facilitator family transporter	9634	8632	8841	6	10680	9524	10024	7	0.001859458	0.003713587	1.166666667	0.222392421	
BP1026B	II1443	sensory box histidine kinase/response regulator	28974	33366	35172	21	22162	25266	25838	16	8.49E-11	1.00E-09	0.761904762	-0.392317423	
BP1026B	II1444	response regulator	19583	26730	23357	51	16840	17916	17916	37	3.06E-11	3.92E-10	0.725490196	-0.462971976	
BP1026B	II1445	sensory box histidine kinase	17711	14897	15330	7	16110	15232	15216	7	3.17E-05	9.88E-05	1	0	
BP1026B	II1446	OsmC-like protein	6351	6585	3358	12	6283	3549	5431	11	1.99E-04	5.11E-04	0.916666667	-0.125530883	
BP1026B	II1447	2-hydroxyacid dehydrogenase	4602	3821	3633	4	6286	4698	4968	5	0.203570906	0.250146972	1.25	0.321928095	
BP1026B	II1448	hypothetical protein	4605	5116	4709	18	4473	4915	4438	17	6.61E-04	0.001496377	0.944444444	-0.08246216	
BP1026B	II1449	hypothetical protein	4143	4398	4518	9	2641	4507	3920	8	1.18E-05	4.11E-05	0.888888889	-0.169925001	
BP1026B	II1450	hypothetical protein	4753	7616	6147	29	5243	5991	4889	25	1.86E-05	6.17E-05	0.862068966	-0.214124805	
BP1026B	II1451	cold shock transcription regulator protein	38705	71539	63626	284	41548	51984	47251	230	3.09E-09	2.57E-08	0.809859155	-0.304257069	
BP1026B	II1452	30S ribosomal protein S21	4275	6997	7006	28	5381	5959	4953	25	4.08E-05	1.25E-04	0.892857143	-0.163498732	
BP1026B	II1453	thymidylate synthase	1778	361	128	0	870	742	716	1	0.021846124	0.033958004	#DIV/0!	#DIV/0!	0
BP1026B	II1454	sarcosine oxidase gamma subunit	1111	548	645	1	1060	983	1231	1	0.63820518	0.60855007	1.155555556	0.208586623	
BP1026B	II1455	sarcosine oxidase alpha subunit	6522	4731	5930	1	6851	7044	6086	2	0.02087204	0.032521188	2	1	
BP1026B	II1456	sarcosine oxidase subunit delta	587	998	856	2	848	950	1318	3	0.51107796	0.563777123	1.5	0.584962501	
BP1026B	II1457	sarcosine oxidase, beta subunit	1939	3233	2760	2	2205	2810	3238	2	2.92E-04	0.002016296	1	0	
BP1026B	II1458	L-serine ammonia-lyase	2791	2336	3245	1	2871	2730	3064	1	9.88E-04	0.0021245	1	0	
BP1026B	II1459	AraC/XylS family transcriptional regulator	14490	5791	7934	7	15151	12240	13102	11	0.317403556	0.70225457	1.571428571	0.652076697	
BP1026B	II1460	hypothetical protein	19791	26433	22823	91	18067	19742	18070	73	1.91E-08	1.31E-07	0.802197802	-0.002197081	
BP1026B	II1461	hypothetical protein	32823	29448	34708	13	32940	30959	36884	42	0.029440959	0.043454992	1.155555556	0.208586623	
BP1026B	II1462	glutathione S-transferase	32473	40248	38843	47	33341	36429	35777	45	7.76E-05	2.20E-04	0.957446809	-0.062735755	
BP1026B	II1463	hypothetical protein	3207	4804	4117	7	2363	3017	2765	4	1.71E-14	4.39E-13	0.571428571	-0.807354922	
BP1026B	II1464	hypothetical protein	22	0	28	0	0	21	44	0	0.867086583	0.888038226	#DIV/0!	#DIV/0!	0
BP1026B	II1465	cytochrome d ubiquinol oxidase, subunit II	1233	869	902	0	1308	679	971	0	0.003988011	0.007379585	#DIV/0!	#DIV/0!	0
BP1026B	II1466	ubiquinol oxidase subunit I, cytochrome insensitive	1714	1456	1720	1	2144	2177	2405	1	0.34974748	0.403154345	1	0	
BP1026B	II1467	hypothetical protein	1030	729	813	2	451	812	832	1	1.00E-05	3.57E-05	0.5	-1	
BP1026B	II1468	Mgc family membrane protein	951	647	961	1	963	892	901	1	0.094457167	0.136000001	1	0	
BP1026B	II1469	hypothetical protein	34	49	0	0	0	134	40	0	0.004643619	0.00844331	#DIV/0!	#DIV/0!	0
BP1026B	II1470	phospholipase D	1144	1215	1177	0	1867	1314	1289	0	0.184000594	0.12736655	#DIV/0!	#DIV/0!	0
BP1026B	II1471	endonuclease/exonuclease/phosphatase family protein	1212	340	858	0	2305	1272	1189	1	0.004655999	0.008463367	#DIV/0!	#DIV/0!	0
BP1026B	II1472	pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) subunit beta	918	143	532	1	1289	660	660	0	0.176294934	0.220858411	1	0	
BP1026B	II1473	rotamase	8035	16506	12971	17	8680	11808	11220	14	1.01E-08	7.40E-08	0.823529412	-0.280107919	
BP1026B	II1474	hypothetical protein	8673	9823	8082	7	9462	8707	9503	6	1.02E-07	3.90E-07	0.857142857	-0.222392421	
BP1026B	II1475	hypothetical protein	291	277	356	2	128	294	224	1	4.24E-05	1.28E-04	0.5	-1	
BP1026B	II1476	ATP/GTP binding protein	14186	25698	22200	26	11415	17424	14995	18	1.82E-13	3.64E-12	0.692307692	-0.530514717	
BP1026B	II1477	hypothetical protein	12434	22591	19155	5	11858	15784	14008	4	6.26E-11	7.59E-10	0.8	-0.321928095	
BP1026B	II1478	hypothetical protein	1695	3084	3052	5	1325	1696	1424	3	2.36E-21	2.12E-19	0.6	-0.736965594	
BP1026B	II1479	hypothetical protein	18616	28438	26465	13	16218	19063	18759	9	3.31E-11	4.21E-10	0.692307692	-0.530514717	
BP1026B	II1480	hypothetical protein	4951	5190	4300	3	4570	4274	4652	3	2.39E-04	6.01E-04	1	0	
BP1026B	II1481	YscJ/HrcF family type III secretion outer membrane protein	5408	75448	6709	3	44739	5344	45445	2	1.82E-08	1.38E-07	0.666666667	-0.584962501	
BP1026B	II1482	YscJ/HrcF family type III secretion outer membrane protein	3367	3428	3709	2	2637	2938	2974	1	2.99E-08	1.95E-07	1	0	
BP1026B	II1483	type III secretion protein SpaR/YscT/HrcT	289	631	408	0	286	490	285	1	8.89E-04	0.001936033	#DIV/0!	#DIV/0!	0
BP1026B	II1484	type III secretion protein HrpB7	231	97	265	0	320	328	204	0	0.367470164	0.421030199	#DIV/0!	#DIV/0!	0
BP1026B	II1485	type III secretion system ATPase	545	1017	722	0	551	686	611	0	2.07E-05	6.78E-05	#DIV/0!	#DIV/0!	0
BP1026B	II1486	type III secretion system protein HrpB	1305	1382	1086	1	1025	1457	1459	1	0.00546831	0.009761727	1	0	
BP1026B	II1487	type III secretion protein HrpB4	566	1059	536	2	834	609	427	2	2.35E-04	5.92E-04	1	0	
BP1026B	II1488	lipoprotein transmembrane protein	1987	2237	2569	2	1158	1518	1318	1	0.20E-13	3.80E-15	0.5	-1	
BP1026B	II1489	type III secretion protein HrpB2	260	487	472	1	514	496	504	1	0.668033053	0.712439875	1	0	
BP1026B	II1490	type III secretion protein HrpB1/HrpK	943	467	940	1	643	986	777	1	7.86E-04	0.001729292	1	0	
BP1026B	II1491	type III secretion system protein HrcU	6943	9642	10341	8	6793	7557	7433	6	3.43E-08	2.21E-07	0.75	-0.415037499	
BP1026B	II1492	type III secretion protein	2723	4313	4625	1	2840	3364	2232	1	1.15E-11	1.60E-10	1	0	
BP1026B	II1493	type III secretion protein HrpA	444	217	310	1	315	180	256	0	0.00217253	0.00427621	0	#NUM!	
BP1026B	II1494	type III secretion inner membrane protein SctQ	8311	11946	9592	7	7498	7994	8083	6	2.43E-09	2.07E-08	0.857142857	-0.222392421	
BP1026B	II1495	type III secretion system protein	6308	9286	7482	10	4282	4266	5352	6	4.80E-13	3.80E-13	0.6	-0.736965594	
BP1026B	II1496	type III secretion inner membrane protein SctS	628	608	980	2	433	1303	684	2	3.11E-05	1.80E-04	1	0	
BP1026B	II1497	hypothetical protein	995	1337	1905	2	629	978	979	1	6.49E-15	1.81E-13	0.5	-1	
BP1026B	II1498	secretion-associated protein	7140	6081	6788	6	5487	6237	5830	5	1.52E-05	5.18E-05	0.833333333	-0.263034406	
BP1026B	II1499	hypothetical protein	825	736	504	2	876	534	373	2	3.07E-04	7.53E-04	1	0	
BP1026B	II1500	hypothetical protein	22329	39684	38611	116	19847	26529	23597	80	2.96E-13	5.75E-12	0.68955172	-0.5360529	
BP1026B	II1501	hypothetical protein	1993	3540	2663	5	2194	2128	2098	4	4.11E-10	4.21E-09	0.8	-0.321928095	
BP1026B	II1502	hypothetical protein	4616	6867	6186	5	4155	4623	4396	3	7.82E-08	4.65E-07	0.6	-0.736965594	
BP1026B	II1503	cupin domain-containing protein	13286	23732	21438	38	11806	12399	12399	27	1.73E-15	1.60E-14	0.710526316	-0.493040011	
BP1026B	II1504	HAD-superfamily hydrolase	16281	6809	7236	16	18792	15147	15926	27	0.745947427	0.782103996	1.6875	0.754887502	
BP1026B	II1505	GntR family transcriptional regulator	9236	3781	5142	7	11109	9138	8856	12	0.831743523	0.857497465	1.714285714	0.77607579	
BP1026B	II1														

BP1026b	II1552	Tat pathway signal sequence domain-containing protein	3071	2448	3414	6	3859	3623	3219	7	0.10640367	1.140313269	1.166666667	0.222392421
BP1026b	II1553	sulfite reductase (NADPH) flavoprotein alpha-component	6814	4393	5124	2	7637	5152	5592	2	0.013469807	0.021696865	1	0
BP1026b	II1554	ApbE family protein	28000	10681	14202	14	24629	15275	18099	15	0.003419605	0.006428284	1.071428571	0.099535674
BP1026b	II1555	apoptosis-inducing factor dehydrogenase	21429	15820	18320	123	146107	13019	122487	90	1.86E-15	1.90E-13	0.7370700	0.46189241
BP1026b	II1556	aminoimidazole transferase family protein	23601	9553	12157	12	10776	7072	8076	7	1.51E-23	2.15E-21	0.583333333	-0.777607579
BP1026b	II1557	hypothetical protein	40976	34248	34548	35	14955	15959	14538	14	8.63E-52	3.38E-49	0.4	-1.321928095
BP1026b	II1558	LysR family transcriptional regulator	19691	11377	13605	16	21815	17150	155807922	21	0.119619154	0.155807922	1.3125	0.392317423
BP1026b	II1559	prevent-host-death family protein subfamily	10948	7684	7763	17	14220	12404	11672	25	0.350404521	0.403763299	1.470588235	0.556393349
BP1026b	II1560	FAD-dependent oxidoreductase	19491	13857	14754	12	18696	16559	16340	13	0.001330413	0.002766136	1.083333333	0.115477271
BP1026b	II1561	family transcriptional regulator	161236	225659	218294	288	916770	1087213	101346	1438	6.73E-58	3.01E-55	4.990555556	2.319922959
BP1026b	II1562	hypothetical protein	2245	1437	2075	3	8226	7326	9023	13	4.29E-28	8.96E-26	1.25	0.215477271
BP1026b	II1563	phospholipase D	30588	12140	15417	10	30783	26638	27518	15	0.458567841	0.51285364	1.5	0.584962501
BP1026b	II1564	DeoR family transcriptional regulator	21232	10159	11986	19	27215	17770	19283	28	0.544727052	0.595827863	1.473684211	0.559427409
BP1026b	II1565	membrane transport protein	9829	7103	8412	6	7725	8195	8643	6	3.97E-05	1.21E-04	1	0
BP1026b	II1566	mannitol dehydrogenase family protein	11472	4926	6732	5	11659	11197	10484	7	0.331631799	0.384675716	1.4	0.485426827
BP1026b	II1567	GntR family transcriptional regulator	2397	1741	2220	2	3275	3081	3215	4	0.93475306	0.945588546	2	1
BP1026b	II1568	starvation sensing protein RspA	10202	9384	7639	7	10777	10446	9996	8	0.00401524	0.007423524	1.142857143	0.192645078
BP1026b	II1569	dehydrogenase	5826	3916	3956	4	6630	4247	4827	5	0.05390283	0.17460667	1.25	0.321928095
BP1026b	II1570	hypothetical protein	10837	15604	13499	71	10991	14674	15288	82	0.006483835	0.011396217	1.154929577	0.207804885
BP1026b	II1572	hypothetical protein	4586	2320	2203	3	5772	5208	5557	6	0.207382835	0.254382582	2	1
BP1026b	II1574	NAD synthetase	34878	22236	23772	31	42771	30032	34740	41	0.245607529	0.295775778	1.322580645	0.403555694
BP1026b	II1575	family transcriptional regulator	111987	128823	129184	120	93712	97647	95746	93	1.09E-11	1.53E-10	0.775	-0.367731785
BP1026b	II1576	hypothetical protein	784770	677416	720264	597	776926	736997	719746	611	0.874309909	0.894413904	1.023450586	0.033441449
BP1026b	II1577	hypothetical protein	863884	583738	595015	807	951450	730114	777200	972	0.393629623	0.447731392	1.204460967	0.26838764
BP1026b	II1578	predicted RNA	13317	3608	7909	752	14903	16543	13612	1365	0.327380901	0.380518879	1.815159574	0.86096384
BP1026b	II1578	hypothetical protein	820678	765420	771483	1781	770831	825590	770831	1835	0.901025599	0.912813775	1.030230045	0.043092547
BP1026b	II1580	anaerobically induced outer membrane protein	126031	151952	138875	88	193989	180827	176132	117	0.421710947	0.475790067	1.329545455	0.410933101
BP1026b	II1581	hypothetical protein	2738	1426	1603	2	3612	3857	3908	4	0.013161889	0.021529213	2	1
BP1026b	II1579	SCO1/SenC family protein	1688	2122	1711	2	22625	2670	2418	3	0.198641809	0.245436295	1.5	0.584962501
BP1026b	II1582	N-acetylmutamoyl-L-alanine amidase domain-containing protein	1757	2182	1856	1	1804	1917	2139	1	1.65E-04	4.33E-04	1	0
BP1026b	II1583	hypothetical protein	2586	2572	2655	1	3008	2358	2799	7	0.001002358	0.002153353	1	0
BP1026b	II1584	intracellular motility protein A	9535	8523	8960	6	10512	10421	10308	7	0.005026298	0.009056545	1.166666667	0.222392421
BP1026b	II1585	hypothetical protein	2245	1437	2075	3	8226	7326	9023	13	4.29E-28	8.96E-26	1.25	0.215477271
BP1026b	II1586	type VI secretion system	10797	7376	8555	4	10159	9617	8859	5	5.84E-04	0.00135986	1.25	0.321928095
BP1026b	II1587	DNA-binding response regulator	11639	8495	9863	14	10819	9916	11802	15	7.13E-04	0.001599996	1.071428571	0.099535674
BP1026b	II1589	sensor histidine kinase	6401	2971	2854	2	6820	4598	4894	2	0.219688945	0.267801934	1	0
BP1026b	II1590	type VI secretion system	4210	4792	3596	8	3161	4259	3520	7	2.68E-05	8.55E-05	0.875	-0.192645078
BP1026b	II1588	type VI secretion system	23321	30385	30126	18	21568	23160	22588	14	8.27E-09	6.14E-08	0.777777778	-0.362570079
BP1026b	II1591	type VI secretion system	5588	8937	8529	14	5443	6135	6080	11	4.45E-08	2.80E-07	0.777777778	-0.347923303
BP1026b	II1592	type VI secretion system	460901	372	468	0	346	454	450	0	0.005044418	0.009090151	1	0
BP1026b	II1594	type VI secretion system	1365	588	549	0	1725	920	1008	0	0.663023206	0.708301187	#DIV/0!	#DIV/0!
BP1026b	II1593	type VI secretion system	755	678	724	0	888	928	697	0	0.157754806	0.199797273	#DIV/0!	#DIV/0!
BP1026b	II1595	type VI secretion system	4638	2814	3215	1	4644	4086	3464	1	0.046377035	0.066672688	1	0
BP1026b	II1596	type VI secretion system	2214	1039	2129	0	2386	1815	2394	0	0.051410711	0.073262015	#DIV/0!	#DIV/0!
BP1026b	II1597	type VI secretion system	686	316	182	0	629	640	705	0	0.114892255	0.150181104	#DIV/0!	#DIV/0!
BP1026b	II1598	type VI secretion system	87	495	53	0	160	112	176	0	0.979E-05	2.70E-04	#DIV/0!	#DIV/0!
BP1026b	II1599	type VI secretion system	0	0	0	0	36	0	0	0	0	0	#DIV/0!	#DIV/0!
BP1026b	II1600	type VI secretion system	510	315	369	1	433	441	395	1	0.148478309	0.189271374	1	0
BP1026b	II1602	type VI secretion system	285	145	135	0	359	447	448	0	2.71E-04	6.72E-04	#DIV/0!	#DIV/0!
BP1026b	II1601	type VI secretion system	810	389	595	0	1166	978	955	0	0.073540464	0.101001175	#DIV/0!	#DIV/0!
BP1026b	II1603	type VI secretion system	460	243	452	0	400	359	611	0	0.457037287	0.51141543	#DIV/0!	#DIV/0!
BP1026b	II1604	type VI secretion system	3368	2036	2805	0	4401	3170	3680	0	0.581804476	0.631866253	#DIV/0!	#DIV/0!
BP1026b	II1605	hypothetical protein	5590	7505	7002	5	5733	5879	7464	5	1.48E-04	3.91E-04	1	0
BP1026b	II1606	hypothetical protein	5590	7505	7002	5	5733	5879	7464	5	1.48E-04	3.91E-04	1	0
BP1026b	II1607	GTP cyclohydrolase I	3640	5083	5523	10	3710	3724	3432	3	1.12E-03	1.39E-03	0.75	-0.415037499
BP1026b	II1608	hypothetical protein	4704	6787	7034	9	4558	4919	4286	7	4.97E-08	3.10E-07	0.777777778	-0.514573173
BP1026b	II1609	hypothetical protein	275	1253	719	4	301	465	504	2	2.48E-12	4.04E-11	0.5	-1
BP1026b	II1610	hypothetical protein	29252	53936	46774	40	28014	36262	33239	30	4.99E-11	6.17E-10	0.75	-0.415037499
BP1026b	II1611	hypothetical protein	2738	5442	5891	10	2964	3798	2872	7	3.14E-12	4.97E-11	0.75	-0.415037499
BP1026b	II1612	transposase	2723	4670	3829	12	3070	3432	3154	11	3.16E-06	1.27E-05	0.916666667	-0.125350882
BP1026b	II1615	Arac family transcriptional regulator	4087	2789	2803	5	4868	4453	4868	4	3.32E-04	8.8E-04	0.8	-0.321928095
BP1026b	II1616	hypothetical protein	26230	23488	24302	55	24284	23476	20279	51	6.96E-06	2.56E-05	0.927272727	-0.10894372
BP1026b	II1617	DNA-binding response regulator	5203	3578	4044	6	5751	4989	6294	8	0.19828779	0.245143734	1.333333333	0.415037499
BP1026b	II1618	chaperone	2303	2806	2141	5	2462	1616	2852	5	1.75E-05	5.86E-05	1	0
BP1026b	II1619	BopA protein	4740	6918	6239	3	5824	6176	5683	3	6.95E-04	0.00156497	1	0
BP1026b	II1620	hypothetical protein	102	0	38	0	64	31	40	0	0.444361623	0.498654823	#DIV/0!	#DIV/0!
BP1026b	II1621	type III secretion target BopE	25948	27598	25676	33	32508	30032	29792	39	0.011826696	0.019555579	1.181818182	0.2410081
BP1026b	II1622	BapC protein	5020	2916	3155	6	4657	4748	4263	7	0.4046245	0.4732663	1.166666667	0.222392421
BP1026b	II1623	acyl carrier protein	1291	1490	1583	5	1305	1429	1573	5	5.28E-04	0.00116634	1	0
BP1026b	II1624	hypothetical protein	7562	5831	4949	2	8670	5662	6828	2	0.015551343	0.025020153	1	0
BP1026b	II1625	type III effector protein IspD/SipD/SspD	14073	24857	22107	21	14525	19128	16409	17	2.08E-08	1.41E-07	0.8095328	-0.304854582
BP1026b	II1626	HNS-like transcription regulator BsaN	4386	2368	2315	10	4201	2958	2833	11	0.01397897	0.022723523	1.1	0.137053524
BP1026b	II1627	cell invasion protein	35907	41198	41195	31	39733	40276	40740	31	0.002149046	0.002614402	1	0
BP1026b	II1628	BipB protein	16573	22307	19463	10	17253	17063	16464	9	4.97E-07	2.41E-06	0.9	-0.152003093
BP1026b	II1629	type III secretion low calcium response chaperone LerH/YscD	5472	6719	6470	12	4447	4968	4304	8	3.06E-08	1.99E-07	0.666666667	-0.584962501
BP1026b	II1630	surface presentation of antigens protein SpaP	2765	2562	2018	2	2865	2388	2288	1	2.90E-07	2.32E-06	2	0.5
BP1026b	II1631	type III secretion protein SpaR/YscI/HrcI	1917	1446	1898	2	1856	1525	1774	2	2.25E-04	5.71E-04	1	0
BP1026b	II1632	type III secretion system protein BsaX	1723	1285	1265	5	1456	1160	1179	4	3.34E-05	1.04E-04	0.8	-0.321928095
BP1026b	II1633	surface presentation of antigens protein SpaP	3732	5618	5409	7	4129	4654	4112	6	5.10E-05	1.51E-04	0.857142857	-0.222392

BP1026b	II1682	hypothetical protein	38889	33635	32913	22	39410	41146	35541	24	0.011570556	0.019214269	1.090909091	0.125530882
BP1026b	II1683	glycosyl transferase family protein	35634	22303	27389	11	40945	31029	34478	13	0.084001491	0.113834814	1.181818182	0.2410081
BP1026b	II1684	hypothetical protein	7475	3472	3091	5	7964	4457	6656	7	0.229665968	0.278180076	1.4	0.485426827
BP1026b	II1685	hypothetical protein	3410	1640	1645	3	1645	1088	1285	9	0.013039043	0.019876342	1	0.075396637
BP1026b	II1686	hypothetical protein	29498	18831	20068	10	33369	28101	29872	13	0.152966001	0.194431986	1	0.378511623
BP1026b	II1687	cellulose synthase operon protein C	41286	25422	26996	7	53635	43130	46516	11	0.881199668	0.899408643	1.571428571	0.652076697
BP1026b	II1688	endo-1,4-D-glucanase	32452	14087	18925	16	44338	31765	32998	27	0.53861578	0.590080774	1.6875	0.794887502
BP1026b	II1689	cellulose synthase regulator protein	68911	41381	52232	25	81735	70083	71280	34	0.394410668	0.44829464	1.36	0.443606651
BP1026b	II1690	predicted RNA	8253	8423	9198	574	9121	9725	8939	617	6.87E-04	0.00155053	1.074912892	0.104219752
BP1026b	II1692	HspB domain-containing protein	20494	13605	19184	43	22957	23663	21923	56	0.089657181	0.120602853	1.302325581	0.381090167
BP1026b	II1691	hspA protein	12316	58458	65817	58	113669	80543	92910	70	0.023408202	0.036051965	1.208686552	0.271302023
BP1026b	II1693	hypothetical protein	254515	171775	190679	453	227480	205729	222786	482	0.001805168	0.003616678	1.06401766	0.089522096
BP1026b	II1694	LysR family transcriptional regulator	85261	55925	58880	72	77248	64321	71343	77	0.001160923	0.002454489	1.069444444	0.096861539
BP1026b	II1695	agmatinase	4010	1215	1677	2	3118	2962	3220	3	0.297306565	0.349972618	1.5	0.584962501
BP1026b	II1696	hypothetical protein	1154460	1303448	1257882	884	1191921	1146591	1091804	816	0.319984764	0.372820287	0.923076923	-0.115477217
BP1026b	II1697	hypothetical protein	31073	30522	28335	99	33661	28695	31177	103	6.63E-04	0.001499684	1.04040404	0.057143907
BP1026b	II1698	hypothetical protein	48087	43096	47665	115	46691	50397	46940	120	9.67E-04	0.002087692	1.043478261	0.061400545
BP1026b	II1699	hypothetical protein	51303	60905	59017	162	48823	54821	52372	148	2.03E-06	8.57E-06	0.913500247	-0.130366637
BP1026b	II1701	hypothetical protein	218262	178266	186136	242	249381	222488	229552	291	0.059275016	0.083128141	1.202479319	0.266012106
BP1026b	II1700	hypothetical protein	16240	14637	15076	66	13237	13691	12462	56	3.17E-08	2.05E-07	0.848484848	-0.237039197
BP1026b	II1702	hypothetical protein	10201	7488	8190	13	8286	6851	7694	11	1.65E-06	7.12E-06	0.846153846	-0.2410081
BP1026b	II1703	VscC/HrcC family type III secretion outer membrane protein	15248	16322	16003	8	12357	13744	16516	7	5.40E-07	2.60E-06	0.875	-0.192645078
BP1026b	II1704	type IV prepilin	37197	32909	31809	20	44158	39272	41560	24	0.105399946	0.139135914	1.2	0.263034406
BP1026b	II1705	hypothetical protein	2435	1351	2078	4	2717	2400	2548	5	0.146956453	0.187598256	1.25	0.321928095
BP1026b	II1706	major pilin subunit	25155	36172	34883	57	23983	31790	29868	49	7.21E-07	6.88E-07	0.859649123	-0.21818017
BP1026b	II1707	integral membrane protein	64408	71791	68935	49	67569	66186	65819	5	0.215073114	0.035624372	1.326530612	0.407657969
BP1026b	II1708	type II/IV secretion system protein	102748	66781	72815	50	109739	89844	94966	60	0.022921935	0.035420561	1.2	0.263034406
BP1026b	II1709	hypothetical protein	1608	1071	894	2	2514	1326	1699	3	0.192649596	0.292625821	1.5	0.584962501
BP1026b	II1710	type IV pilus biosynthesis protein	68525	37361	48779	39	74758	67851	63562	52	0.294500452	0.347321176	1.333333333	0.415037499
BP1026b	II1711	PilN	104264	67024	78314	47	117542	98455	105514	60	0.067678618	0.093760594	1.276595745	0.352301744
BP1026b	II1712	PilL domain protein	24466	12882	14680	29	27912	22811	24459	43	0.40060603	0.460035139	1.482758621	0.56828376
BP1026b	II1713	switching motility protein	345540	407277	387499	341	323940	335310	322868	295	0.001052401	0.00247774	0.865102639	-0.209056785
BP1026b	II1714	type II secretion system family protein	17480	15587	11293	8	19231	15984	16374	9	0.15223151	0.035624372	1.1	0.169256001
BP1026b	II1715	DNA-binding response regulator	27213	14117	15720	25	33755	21096	25324	36	0.302983421	0.35552095	1.44	0.526068812
BP1026b	II1716	sensor histidine kinase	35446	23215	21234	24	49210	31691	36758	36	0.766757665	0.800311286	1.5	0.584962501
BP1026b	II1717	hypothetical protein	3108	5082	3935	7	2585	3428	2832	5	4.90E-11	6.08E-10	0.714285714	-0.485426827
BP1026b	II1718	hypothetical protein	755	410	407	1	882	571	579	1	0.614059195	0.662544928	1	0
BP1026b	II1719	hypothetical protein	1151	678	726	1	1072	1194	1003	1	0.534758438	0.586457987	1	0
BP1026b	II1720	hypothetical protein	271	277	291	0	282	189	407	0	0.316535564	0.563157541	#DIV/0!	#DIV/0!
BP1026b	II1721	AcrC family transcription regulator	1167	4224	632	0	1763	1287	1490	0	0.015980001	0.035624372	#DIV/0!	#DIV/0!
BP1026b	II1722	hypothetical protein	4060	4444	4349	9	3121	3442	3798	7	6.78E-07	3.19E-06	0.777777778	-0.362570079
BP1026b	II1723	hypothetical protein	62852	105826	97283	484	70653	87223	84724	441	1.29E-06	5.69E-06	0.911157025	-0.134228392
BP1026b	II1724	type III secretion protein	88	151	214	0	64	143	108	0	4.75E-04	0.001104446	#DIV/0!	#DIV/0!
BP1026b	II1725	secretion-associated protein	991	547	691	0	979	811	1214	1	0.809662679	0.838259446	#DIV/0!	#DIV/0!
BP1026b	II1726	type III secretion protein	355	232	135	0	295	246	126	0	0.054349708	0.077032102	#DIV/0!	#DIV/0!
BP1026b	II1727	type III secretion inner membrane protein SctS	949	791	593	2	674	981	894	3	0.051559822	0.073458716	2.15	0.584962501
BP1026b	II1728	type III secretion inner membrane protein SctB	1712	1791	1693	2	17816	16045	1893	1	1.24E-04	1.00E-05	1	0
BP1026b	II1729	type III secretion inner membrane protein SctQ	2775	2832	1915	1	2313	2662	2750	3	3.75E-04	9.00E-04	1	0
BP1026b	II1730	type III secretion protein HspA	752	265	684	0	647	562	843	1	0.291252737	0.344462372	#DIV/0!	#DIV/0!
BP1026b	II1731	type III secretion inner membrane protein SctV	7699	7731	7591	3	6702	6869	6788	3	5.91E-06	2.21E-05	1	0
BP1026b	II1732	type III secretion system protein HrcU	1709	1586	1774	1	1576	2000	2208	1	0.010267039	0.017248296	1	0
BP1026b	II1733	type III secretion protein HspB1/HspK	267	248	180	0	353	240	371	0	0.477683137	0.503915014	#DIV/0!	#DIV/0!
BP1026b	II1734	type III secretion protein HspB2	542	886	504	1	563	439	316	1	1.67E-07	9.14E-07	#DIV/0!	#DIV/0!
BP1026b	II1735	hypothetical transmembrane protein	1034	743	760	0	648	732	1164	0	0.008170521	0.014648908	#DIV/0!	#DIV/0!
BP1026b	II1736	type III secretion protein HspB4	34	0	0	0	32	93	122	0	1.13E-24	1.81E-22	#DIV/0!	#DIV/0!
BP1026b	II1738	type III secretion system protein HspB	275	48	0	0	256	203	244	0	2.55E-04	6.37E-04	#DIV/0!	#DIV/0!
BP1026b	II1737	type III secretion system ATPase	3498	2117	1856	1	3301	3500	2851	2	0.202107734	0.248738829	2	1
BP1026b	II1740	type III secretion protein HspB7	52	20	8	0	78	65	0	0	0.040325088	0.058786725	#DIV/0!	#DIV/0!
BP1026b	II1739	Flagellar biosynthesis protein FlhR	2172	2121	2017	2	2006	1709	1874	1	2.28E-06	9.49E-06	0.5	-1
BP1026b	II1741	hypothetical protein	1973	1393	1435	0	1931	1520	1308	0	3.28E-04	7.97E-04	#DIV/0!	#DIV/0!
BP1026b	II1742	Syrf-like protein	2907	3983	5340	4	3083	3461	3083	4	0.005656178	0.00988412	0.3083412	0
BP1026b	II1743	hypothetical protein	126007	133054	129951	7	90618	92414	95292	5	7.44E-15	2.05E-13	0.714285714	-0.485426827
BP1026b	II1744	hypothetical protein	146305	176269	167041	12	100427	108397	102964	7	2.62E-22	2.78E-20	0.583333333	-0.77707579
BP1026b	II1745	non-ribosomal peptide synthetase	104159	134076	121256	12	73648	86345	81448	8	1.02E-16	4.12E-15	0.666666667	-0.584962501
BP1026b	II1746	diaminobutyrate-2-oxoglutarate aminotransferase	42813	37441	40168	14	34676	36105	34550	12	2.12E-06	8.93E-06	0.857142857	-0.222392421
BP1026b	II1747	hypothetical protein	7525	7944	7507	15	7367	8893	7804	16	7.47E-04	0.001664246	1.066666667	0.093109044
BP1026b	II1748	hypothetical protein	13078	21933	18260	81	10409	14715	14048	59	1.25E-12	2.16E-11	0.728395062	-0.457206954
BP1026b	II1749	hypothetical protein	4701	5071	747	3	4607	4747	4701	3	0.057672437	0.081171011	0.782068096	-0.35365955
BP1026b	II1750	pyruvate dehydrogenase	43836	38825	38018	23	34265	30792	31032	3	3.48E-09	2.84E-08	0.782068096	-0.35365955
BP1026b	II1751	acetyl-CoA hydrolase/transferase family protein	79428	107356	97462	71	59894	65317	64826	47	2.32E-16	8.56E-15	0.661971831	-0.595158268
BP1026b	II1752	Moac domain-containing protein	32947	50400	43128	79	21735	27020	24547	46	2.43E-22	2.63E-20	0.582278481	-0.780218792
BP1026b	II1753	citrate lyase subunit beta	15287	7579	10201	12	10697	10155	10473	11	3.33E-06	1.33E-05	0.916666667	-0.125530882
BP1026b	II1754	LysR family transcriptional regulator	26673	27884	25243	29	27373	28898	31601	32	0.002357824	0.004611983	1.103448276	0.142019005
BP1026b	II1755	hypothetical protein	2255	996	1722	10	2965	2115	1927	14	0.471219406	0.525130455	1.4	0.485426827
BP1026b	II1756	LysR family transcriptional regulator	13218	8909	7840	10	12307	10305	11460	12	0.002625997	0.00507952	1.2	0.263034406
BP1026b	II1757	EmmB/ClaB family drug resistance transporter	916	916	916	0	1045	1045	1045	0	0.03419712	0.05609237	#DIV/0!	#DIV/0!
BP1026b	II1758	hypothetical protein	1659	1798	2128	4	1657	1556	1466	3	2.35E-07			

BP1026B	II1807	oxidoreductase Rmd	6989	6435	6307	6	9376	7492	8000	8	0.054463256	0.077173708	1.333333333	0.415037499
BP1026B	II1808	cupin domain-containing protein	27441	41787	38615	94	34086	40870	40133	100	0.005138395	0.00923586	1.063829787	0.089267338
BP1026B	II1809	D-succinylthiosuccinyl sulfhydrylase	115938	127500	120539	101	148274	155564	150308	127	0.106629566	0.140152703	1.257425743	0.330473204
BP1026B	II1810	amidophosphotransferase	310323	373426	363494	227	301533	329267	317276	205	0.001420754	0.003923673	0.803808737	0.147693380
BP1026B	II1811	CyA family protein	122907	213554	118295	244	128086	118222	124625	249	1.04E-04	2.85E-04	1.020491803	0.029264953
BP1026B	II1812	sporeulation repeat-containing protein	80277	58111	58108	80	94716	73559	78923	100	0.073419672	0.100911833	1.25	0.321928095
BP1026B	II1813	bifunctional poly(poly)glutamate synthase/dihydrofolate synthase	92027	83190	84328	65	89952	87465	85123	66	1.03E-04	2.82E-04	1.015384615	0.02026306
BP1026B	II1814	acetyl-CoA carboxylase subunit beta	280466	261636	271906	310	276835	276915	276119	316	3.04E-04	7.47E-04	1.019354859	0.027656343
BP1026B	II1815	tryptophan synthase subunit alpha	64240	36997	48904	61	70882	63659	64930	81	0.298120299	0.350798843	1.327868852	0.409112665
BP1026B	II1816	DNA methylase	27111	36346	35041	38	24108	27741	25153	30	1.08E-09	9.85E-09	0.789473684	-0.341036918
BP1026B	II1817	tryptophan synthase subunit beta	18061	136654	146628	108	115559	117522	114616	96	5.27E-08	3.36E-07	0.88889807	-0.169925001
BP1026B	II1818	N ⁴ -C-phosphorylchrysoylanthranilate isomerase	50329	57793	54732	71	22275	47914	49376	65	3.70E-06	1.46E-05	0.915492958	-0.127379306
BP1026B	II1819	RNA pseudouridine synthase A	69495	57570	63876	78	71937	67730	68708	85	0.002734012	0.005260876	1.08974359	0.123988717
BP1026B	II1820	hypothetical protein	94592	50470	57592	25	114862	86618	91132	36	0.493946371	0.547056071	1.44	0.526668812
BP1026B	II1821	aspartate-semialdehyde dehydrogenase	167682	204354	192238	167	200715	220790	209942	187	0.009428201	0.015967362	1.119760479	0.163190167
BP1026B	II1822	hypothetical protein	25245	44057	38341	221	28600	38942	32224	205	2.15E-05	7.00E-05	0.92760181	-0.10842246
BP1026B	II1823	3-isopropylmalate dehydrogenase	61997	58281	60392	56	60975	62344	61252	57	3.63E-04	8.73E-04	1.017857143	0.025355092
BP1026B	II1824	isopropylmalate isomerase small subunit	44209	51074	45987	75	45987	46751	2280	72	5.37E-05	1.58E-04	0.96	-0.05893689
BP1026B	II1825	Entereidin	2559	960	971	10	3655	1701	2280	17	0.387656676	0.4419782	1.7	0.76534746
BP1026B	II1826	isopropylmalate isomerase large subunit	110215	97312	101133	72	108141	102625	102056	73	5.08E-05	1.51E-04	1.013888889	0.01899557
BP1026B	II1827	nitrotriacetate monooxygenase	16074	22968	20895	15	19186	21020	20495	15	3.50E-04	8.46E-04	1	0
BP1026B	II1828	hypothetical protein	6992	9028	7103	8	7070	8899	7908	8	5.02E-04	0.001160429	1	0
BP1026B	II1829	bkd operon transcriptional regulator	32474	34333	35491	64	36619	37094	36217	69	0.0055998	0.009987929	1.078125	0.108524457
BP1026B	II1830	2-oxoacid dehydrogenase subunit E1	203233	164408	172412	66	226558	184368	186322	70	0.001525144	0.003125523	1.060606061	0.084888898
BP1026B	II1831	hypothetical protein	57619	47500	48229	41	50413	47831	50640	40	1.54E-04	4.05E-04	0.95626391	-0.05562391
BP1026B	II1832	hypothetical protein	664283	566347	566347	14	55420	566347	566347	14	0.28E-04	0.00578814	1.167262138	-0.216254943
BP1026B	II1833	glyoxalase	12084	18681	14207	38	11682	13646	13344	33	3.53E-08	2.27E-07	0.868421053	-0.20535394
BP1026B	II1834	AraC family transcriptional regulator	16485	11419	12633	13	19831	15445	16296	17	0.066634035	0.09249357	1.307692308	0.387023123
BP1026B	II1835	type II citrate synthase	984904	1490682	1347439	978	1119969	1315376	1267212	947	0.33764432	0.390938769	0.968302658	-0.046470039
BP1026B	II1836	predicted RNA	11796	20133	19036	679	14967	20800	16282	693	3.25E-04	7.92E-04	1.020618557	0.029443778
BP1026B	II1837	hypothetical protein	74241	65748	59985	244	100022	86891	95540	344	0.3939862	0.447906724	1.409836066	0.495527177
BP1026B	II1838	succinate dehydrogenase iron-sulfur subunit	341050	425480	417908	563	399000	469773	426092	614	0.580269159	0.630307954	1.099586146	0.12537433
BP1026B	II1839	succinate dehydrogenase flavoprotein subunit	713382	78504	768499	420	89327	88589	88589	512	0.34223082	0.39579098	1.21904766	0.285754483
BP1026B	II1839	succinate dehydrogenase, hydrophobic membrane anchor protein	144618	224469	206335	519	183775	221482	207313	535	0.001834948	0.003668141	1.065510597	0.091544942
BP1026B	II1840	succinate dehydrogenase cytochrome B subunit	223678	393488	362289	782	266313	347462	306118	733	0.001496203	0.003072237	0.939897698	-0.089424358
BP1026B	II1841	hypothetical protein	10375	14718	14366	63	10446	12551	11861	56	1.33E-07	7.43E-07	0.888888889	-0.169925001
BP1026B	II1842	GntR family transcriptional regulator	57395	62111	62852	75	67080	66778	62780	81	0.002150648	0.004235454	1.08	0.111031312
BP1026B	II1843	malate dehydrogenase	943387	1022777	1008447	1007	1007238	1057008	1041951	1052	0.967116821	0.973380913	1.04668719	0.063071021
BP1026B	II1844	lyase	22530	16599	16586	18	24864	20134	21517	21	0.023309529	0.038638763	1.066666667	0.222392421
BP1026B	II1845	hypothetical protein	116586	12478	118801	235	139676	140121	138738	235	0.0161408	0.02517518	1.167262138	0.173414892
BP1026B	II1846	2-methylcitrate hydratase	191748	169815	166825	124	238104	189516	201877	148	0.055128574	0.07988382	1.195348387	0.255257055
BP1026B	II1847	aconitate hydratase	1561335	1972356	1850298	654	1722709	1897178	1760300	659	0.123490999	0.160410943	1.00764526	0.01098783
BP1026B	II1848	hemagglutinin, homolog	60780	74591	72509	25	60835	66308	63008	23	2.77E-06	1.13E-05	0.92	-0.120294234
BP1026B	II1849	hypothetical protein	2074	3969	3471	15	1888	2376	2174	10	3.00E-15	8.66E-14	0.666666667	-0.584962501
BP1026B	II1850	HLyB family hemolysin activator protein	39872	55084	51984	29	32123	38029	39159	21	6.00E-11	7.32E-10	0.724137931	-0.465663572
BP1026B	II1851	transposase	42332	49876	45795	168	39016	39861	43568	149	3.19E-06	1.28E-05	0.886904762	-0.117418902
BP1026B	II1852	hypothetical protein	188052	246808	246808	13	196844	179316	188052	13	1.03E-14	1.03E-14	0.723626138	-0.13444343
BP1026B	II1853	cytochrome c family protein	118792	1152440	1139998	556	1159852	1143886	1155476	553	0.54059173	0.59182058	0.99460317	-0.007805402
BP1026B	II1854	hypothetical protein	17076	8033	8808	30	18583	11858	13834	39	0.069664773	0.096278281	1.3	0.378511623
BP1026B	II1855	tyrosinase	12285	16754	16588	9	9721	11741	12971	7	6.44E-12	9.61E-11	0.777777778	-0.362570079
BP1026B	II1856	hypothetical protein	7943	6174	5257	10	7372	6526	6960	10	0.003528648	0.00613448	1	0
BP1026B	II1857	hypothetical protein	6224	8125	8530	14	3847	5014	42705	8	9.47E-16	3.03E-14	0.571482571	-0.807354922
BP1026B	II1858	hypothetical protein	38604	51010	44541	331	32940	43511	37400	281	4.30E-07	2.11E-06	0.848942598	-0.236261087
BP1026B	II1859	sedolisin	52576	60095	59003	32	59423	60646	57140	31	5.14E-05	1.93E-04	0.96875	-0.045803661
BP1026B	II1860	polymaline ABC transporter permease	9581	8083	8262	10	8575	9283	8826	10	9.99E-05	5.11E-04	1	0
BP1026B	II1861	spermidine/putrescine ABC transporter permease	5416	6262	5802	4	5551	5338	6368	4	1.49E-04	0.001667468	1	0
BP1026B	II1862	spermidine/putrescine ABC transporter periplasmic	17464	22923	21856	19	16190	18721	18272	16	2.92E-07	1.51E-06	0.842105263	-0.247927513
BP1026B	II1863	spermidine/putrescine ABC transporter ATP-binding protein	17695	19557	20740	17	15185	17205	18244	15	5.62E-07	2.70E-06	0.885232941	-0.180572246
BP1026B	II1864	GntR family transcriptional regulator	39908	36792	37059	24	39477	42143	38739	26	0.004849504	0.008797354	1.083333333	0.074717217
BP1026B	II1865	lipase chaperone	1473	5118	4469	5	8469	66330	66330	6	0.145660093	0.186653942	1.2	0.26304406
BP1026B	II1866	lipase rescuer	15643	16950	16041	14	15049	15895	15764	14	2.09E-05	6.86E-05	0.8	0
BP1026B	II1867	iron-binding copper receptor	103649	117991	111989	49	113210	114335	110102	50	4.04E-05	1.23E-04	1.020408103	0.029146346
BP1026B	II1868	hypothetical protein	70887	22325	26673	100	105308	50546	66253	186	0.029485817	0.044404138	1.86	0.895302621
BP1026B	II1869	cytochrome b561	104975	153616	140789	247	101081	117003	113885	206	3.70E-10	3.84E-09	0.834008097	-0.261866704
BP1026B	II1870	integral membrane protein	130074	121260	127805	198	48734	54860	54563	82	4.88E-57	2.04E-54	1.014141414	-0.127180615
BP1026B	II1871	peptidase	51565	40063	43865	43	51810	44607	46644	46	0.00184375	0.003684563	1.069767442	0.097297201
BP1026B	II1872	DSBH domain-containing protein	57572	43854	43854	195	528326	563268	563268	174	0.001094368	0.02517358	1.05313283	0.0513283
BP1026B	II1873	hypothetical protein	167420	207961	210706	587	196400	214294	198342	690	7.41E-04	0.001652044	1.037478705	0.053081725
BP1026B	II1874	5-phosphogluconate dehydrogenase	143784	170229	165505	112	152385	161372	154854	114	4.53E-05	1.36E-04	0.982142857	-0.025952909
BP1026B	II1875	hypothetical protein	8682	5473	4817	10	11934	7778	7829	14	0.349428196	0.403008471	1.4	0.485426827
BP1026B	II1876	NAD-dependent deacetylase	30892	19735	22505	25	30852	25556	30796	30	0.01716934	0.027384508	1.2	0.26303406
BP1026B	II1877	cytosine/purines/uracil/thiamine/allantoin permease family protein	26491	23346	23185	17	22660	23763	23167	16	7.81E-05	2.21E-04	0.941176471	-0.0874

BP1026B	II1927	alpha amylase family protein	13093	6299	7595	5	13052	11366	13011	7	0.191478405	0.23770909	1	0.485426827
BP1026B	II1928	hypothetical protein	5179	3258	3139	5	4906	4541	4975	6	0.117314788	0.15299702	1.2	0.263034406
YbaK/prolyl-tRNA synthetase associated domain-containing protein														
BP1026B	II1929	853103	1339096	1081664	2259	496659	567737	580280	1135	3.83E-06	1.50E-05	0.502434706	-0.992991973	
BP1026B	II1930	97455	88629	73	90588	92390	94848	74	1.26E-04	3.37E-04	1.01369863	0.019628807		
BP1026B	II1931	6313	6517	6643	15	5010	4443	4616	11	1.02E-08	7.44E-08	0.733333333	-0.447458977	
BP1026B	II1932	4888	7395	6753	12	4369	5029	5326	9	2.31E-07	1.23E-06	0.75	-0.415037499	
BP1026B	II1933	70724	96994	90275	110	54731	61701	60920	76	3.34E-15	9.58E-14	0.690909091	-0.5343322	
BP1026B	II1934	1916	1502	1806	1	1576	1735	1997	1	3.93E-04	9.39E-04	1	0	
BP1026B	II1935	7249	7223	7392	12	5278	6447	5645	9	6.91E-08	4.17E-07	0.75	-0.415037499	
BP1026B	II1936	3640	4794	4379	10	2954	3627	3369	7	3.44E-09	2.92E-08	0.7	-0.514573173	
BP1026B	II1937	6087	6239	5934	5	6378	5829	5000	5	1.94E-04	4.98E-04	1	0	
BP1026B	II1938	5116	7418	6272	7	4280	5260	5023	5	2.65E-07	1.38E-06	0.714285714	-0.485426827	
BP1026B	II1939	5776	4481	4161	5	4842	3896	4315	5	1.51E-04	3.98E-04	1	0	
BP1026B	II1940	5749	6971	7275	7	4853	5786	6211	5	4.06E-06	1.58E-05	0.714285714	-0.485426827	
BP1026B	II1941	5405	5179	6176	8	5363	4740	4667	7	4.22E-05	1.28E-04	0.875	-0.192645078	
BP1026B	II1942	16921	14599	15054	19	14510	14632	14268	18	3.73E-06	1.47E-05	0.947366124	-0.078002512	
BP1026B	II1943	83567	127177	107340	116	59957	73679	72341	75	6.75E-18	5.30E-18	0.646551724	-0.629162305	
BP1026B	II1944	18910	28772	24180	91	13386	17801	17948	62	3.69E-14	8.65E-13	0.681318681	-0.55359833	
BP1026B	II1945	12313	12923	12761	7	10629	12281	10992	7	2.04E-07	1.10E-06	1	0	
BP1026B	II1946	9997	7176	7828	22	12607	9267	10413	29	0.059105698	0.08291765	1.318181818	0.398549376	
BP1026B	II1947	84481	68657	76801	165	91348	97797	93233	203	0.032550322	0.048523805	1.23030303	0.299013703	
BP1026B	II1948	7683	6816	7864	11	8190	8092	8942	12	0.004851896	0.008799058	1.090909091	0.125530882	
BP1026B	II1949	16598	9523	10739	16	17685	14251	13882	20	0.030664958	0.040608439	1.25	0.321928095	
BP1026B	II1950	69577	62031	64618	92	60657	58597	62507	85	5.26E-06	3.99E-05	0.923913043	-0.11417102	
BP1026B	II1951	49254	58139	53612	127	43059	43660	45079	104	1.21E-08	8.67E-08	0.818897638	-0.28824969	
BP1026B	II1952	0	240	247	1	38	140	79	0	2.30E-07	1.22E-06	0	#N/IM!	
BP1026B	II1953	15092	20360	19754	20	15072	18129	15435	17	6.67E-07	3.14E-06	0.85	-0.234465254	
BP1026B	II1954	37812	35881	40954	111	46826	52476	47147	142	0.191206181	0.237453978	1.279279279	0.355331253	
BP1026B	II1955	47889	18420	24493	39	57126	42341	43803	62	0.705394821	0.746825605	1.589745939	0.668794092	
BP1026B	II1956	5667	3921	3855	3	4508	4637	3892	3	0.001042319	0.002292725	1	0	
BP1026B	II1957	2961	2501	3716	2	2210	2552	2284	1	1.23E-10	1.41E-09	0.5	-1	
BP1026B	II1958	3648	3434	3442	1	2711	9748	3302	1	9.74E-08	5.70E-07	0.5	-1	
BP1026B	II1959	3229	3111	2761	2	2400	2706	2322	2	7.70E-09	5.78E-08	1	0	
BP1026B	II1960	3145	1296	1478	2	2858	2263	2587	2	0.137935767	0.176983241	1	0	
BP1026B	II1961	7305	7735	7208	3	7482	7215	5957	3	3.94E-05	1.21E-04	1	0	
BP1026B	II1962	5004	4496	4986	4	4943	3976	3801	3	6.30E-05	1.82E-04	0.75	-0.415037499	
BP1026B	II1963	1135	743	1236	2	534	771	484	1	7.96E-15	2.19E-13	0.5	-1	
BP1026B	II1964	7565	6187	5667	4	4943	4628	4564	3	1.45E-08	1.02E-07	0.75	-0.415037499	
BP1026B	II1965	7240	10184	8089	6	4732	5292	5080	3	1.98E-15	6.03E-14	0.5	-1	
mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase														
BP1026B	II1966	319845	448086	401424	253	222131	255424	268899	161	2.85E-17	1.26E-15	0.636363636	-0.652076697	
BP1026B	II1967	192586	127263	149186	177	155159	126460	136279	157	1.51E-07	8.36E-07	0.88700565	-0.172984801	
predicted RNA	-	13922	4755	6321	396	11408	8723	9614	472	0.010236516	0.017261624	1.191919192	0.253286429	
BP1026B	II1968	72872	117672	108886	382	46040	66076	56765	215	2.67E-26	5.08E-24	0.562827225	-0.526235978	
BP1026B	II1969	6142	6721	6805	11	5372	6733	4644	9	6.42E-06	2.38E-05	0.818181818	-0.289506617	
BP1026B	II1970	81594	8093	7914	6	7914	8854	8624	6	3.88E-01	2.38E-01	0.5	-1	
BP1026B	II1971	2854	3332	2844	7	1780	2203	1923	4	9.33E-17	3.80E-15	0.571428571	-0.807354922	
BP1026B	II1972	26277	27630	27935	26	31421	32981	30610	30	0.013350536	0.021797999	1.153846154	0.206450877	
BP1026B	II1973	4040	2077	2195	2	5317	2706	3296	2	0.557394665	0.608410776	1	0	
BP1026B	II1974	5019	3352	3185	7	4424	3142	3986	7	0.002237178	0.004393806	1	0	
BP1026B	II1975	6767	7302	7252	17	7812	8085	7490	18	0.003695463	0.00897244	1.058823529	0.08246216	
BP1026B	II1976	24549	22728	25295	66	22772	22561	24306	65	1.07E-04	2.93E-04	0.984848485	-0.022630606	
BP1026B	II1977	9649	7331	7314	6	6365	7196	5194	6	0.44765196	0.5394193	1.428571429	0.54863501	
BP1026B	II1978	29351	28977	32420	79	30271	23893	23469	67	8.88E-07	1.02E-06	0.848012667	-0.237691558	
BP1026B	II1979	225375	218461	220027	378	211723	197152	198384	346	2.64E-06	1.08E-05	0.915343915	-0.127614197	
BP1026B	II1980	68300	77465	76870	70	75041	82925	76697	73	6.75E-04	0.001525537	1.042857143	0.060541542	
BP1026B	II1981	56501	43052	49130	115	68187	73159	64685	160	0.509537223	0.562040971	1.391304348	0.476438044	
BP1026B	II1982	11285	6214	7468	4	12644	9849	9966	5	0.06639675	0.09249357	1.25	0.321928095	
BP1026B	II1983	3038	1117	1355	1	3291	2159	2964	2	0.951074671	0.9594872	2	-1	
BP1026B	II1984	6108	6169	6109	7	12389	9810	9638	0	0.251783363	0.3491058	1.428571429	0.514573173	
BP1026B	II1985	39943	33065	35899	45	43570	42159	40668	52	0.036705629	0.05402968	1.155555556	0.208586622	
BP1026B	II1986	22793	26662	25694	32	24023	26114	23984	32	7.78E-05	2.20E-04	1	0	
BP1026B	II1987	2282	493	435	1	3747	1311	1722	3	0.001515212	0.0031072	3	1.584962501	
BP1026B	II1988	15238	10674	10644	11	17927	13120	14706	14	0.03481346	0.05154494	1.272727273	0.347923303	
BP1026B	II1989	21083	9626	13714	12	24397	19541	21466	17	0.007798846	0.06061631	1.146666667	0.502500341	
BP1026B	II1991	15876	17944	17790	42	18964	20719	19246	48	0.00931631	0.015374605	1.042857143	0.542645078	
BP1026B	II1992	126012	12568	129346	107	143316	141879	141321	119	0.005223305	0.009169687	1.131240393	0.15330777	
BP1026B	II1994	153879	193399	132220	144	173225	147233	157918	141	0.041353443	0.060090375	1.1875	0.247927513	
BP1026B	II1995	31501	22460	25173	13	36424	32495	31232	16	0.089739858	0.120672697	1.23076621	0.299560282	
BP1026B	II1996	24835	18798	19568	30	25076	23272	23723	34	0.008041631	0.013850948	1.133333333	0.180572246	
BP1026B	II1997	13229	5900	7181	7	13911	8839	10160	9	0.032134949	0.047984417	1.285714286	0.362570079	
BP1026B	II2000	8855	5920	6622	6	8920	8407	8995	8	0.031801071	0.047497172	1.333333333	0.415037499	
BP1026B	II2001	4719	3284	3847	2	4516	3977	3773	6	0.05119657	0.009210096	1	0	
BP1026B	II2002	13553	832	1206	2	4701	2767	1346	4	0.671628662	0.71505478	1.333333333	0.415037499	
BP1026B	II2003	200384	200384	200384	25	32114	34336	34336	34	0.29696601	0.3491058	1.428571429	0.514573173	
BP1026B	II2004	28954	18482	18604	15	26327	24125	24040	19	0.029266324	0.044118477	1.266666667	0.341036918	
BP1026B	II2005	36840	21478	22398	37	35676	30452	31268	44	0.035432835	0.052333666	1.189189189	0.249978253	
BP1026B	II2006	52651	26369	31865	35	57405	50376	52298	51	0.825615169	0.852664464	1.457142857	0.543142325	
BP1026B	II2007	110418	92655	91210	37	119375	98383	98751	40	4.86E-04	0.00112674	1.081081081	0.112474729	
BP1026B	II2008	49335	31137	34302	52	50414	44144	48072	64	0.122190152	0.158958694	1.23076621	0.299560282	

BP10268	BP10253	hypothetical protein	11320	16849	14618	16	9595	12681	11441	12	1.51E-10	1.68E-09	0.75	-0.415037499
BP10268	BP10252	hypothetical protein	1455	2983	2233	11	1545	2454	1943	10	6.06E-07	2.89E-06	0.909090909	-0.137503524
BP10268	BP10254	metallo-beta-lactamase family protein	250516	253737	250841	178	246763	244079	241730	176	7.68E-05	2.18E-04	0.988764045	-0.016301812
predicted RNA	-	-	82815	131388	127332	1650	78860	94271	92140	129	7.75E-11	3.45E-10	0.773636363	-0.345195540
BP10268	BP10255	acetoacetyl-CoA reductase	878167	975121	975317	1262	815430	888357	828426	179	0.992996949	0.64659157	0.894611727	-0.160666424
predicted RNA	-	-	141186	70646	86053	878	139187	124219	137702	1183	0.240546108	0.290349381	1.3473804	0.430157229
BP10268	BP10256	Crp/FNR family transcriptional regulator	476373	479523	472296	608	420673	420491	421548	537	0.027759208	0.042071397	0.883236841	-0.179149235
BP10268	BP10257	zinc-containing alcohol dehydrogenase	527922	399828	418684	454	502869	449458	463754	478	0.596665957	0.646216427	1.052863436	0.074318321
BP10268	BP10258	hypothetical protein	318011	329307	338261	1440	301093	328520	324279	1394	0.006808804	0.011910659	0.968055556	-0.046883825
BP10268	BP10260	hypothetical protein	694685	488504	464140	1464	671403	468667	532799	1486	0.624360123	0.67301466	1.015027322	0.021583862
predicted RNA	-	-	979804	625364	630415	329	900294	521973	514234	370	0.04186222	0.50533994	0.832610497	-0.271047553
BP10268	BP10261	hypothetical protein	120379	161798	137065	465	117203	117797	125975	401	5.65E-09	4.99E-08	0.862365591	-0.21263848
BP10268	BP10262	decarboxylase family protein	143326	127631	126582	139	127586	118252	124089	130	9.38E-07	4.28E-06	0.935251799	-0.09657326
BP10268	BP10263	hypothetical protein	116631	78734	88077	335	83014	84456	90444	304	8.72E-07	4.01E-06	0.907462687	-0.140089772
predicted RNA	-	-	128580	153155	132289	1069	126233	114005	117020	923	6.19E-09	4.74E-08	0.863423761	-0.2118593
predicted RNA	-	-	31640	2649	4792	283	33990	20603	23020	562	0.101616381	0.134708066	1.985865724	0.989768077
BP10268	BP10264	OsmY domain-containing protein	660527	519501	512341	866	619846	550638	559308	885	0.668235837	0.712439875	1.021939594	0.03131043
BP10268	BP10265	adenylate kinase	15946	14295	18209	13	15282	13019	14308	13	1.85E-05	1.61E-05	0.907462687	-0.140089772
BP10268	BP10266	adenylate kinase	4691	3829	3650	5	6044	5294	5412	7	0.003408547	0.04972618	1.4	0.485426827
BP10268	BP10267	methyl-accepting chemotaxis protein	106407	96710	102352	60	118777	120682	118936	71	0.00868496	0.01484048	1.183333333	0.242856524
predicted RNA	-	-	16057	3909	7116	300	19436	21611	21199	691	0.0017059	0.003444193	2.303333333	1.20372321
BP10268	BP10268	polysaccharide deacetylase domain-containing protein	86793	54615	63519	81	98373	78041	81068	102	0.065734206	0.091470869	1.259259259	0.332575339
BP10268	BP10269	ABC-type export system, outer membrane channel protein	74508	53030	59145	41	86539	70034	77048	52	0.074414209	0.102081669	1.268292683	0.342887714
BP10268	BP10270	ABC-type export system, membrane fusion protein	156110	114084	121823	120	182648	168655	167628	159	0.04126176	0.455205726	1.325	0.40599236
BP10268	BP10271	ABC transporter ATP-binding protein	192660	214934	203402	291	218673	216188	223674	314	0.002942941	0.005623251	1.079037801	0.109745406
BP10268	BP10272	ABC transporter permease	276384	294932	278055	248	342536	345329	342476	300	0.29247518	0.34053456	0.90677419	0.113780633
BP10268	BP10273	hypothetical protein	144323	91476	102223	448	175110	155445	173073	666	0.857102234	0.879823648	1.486607143	0.572023445
BP10268	BP10274	universal stress protein	378885	397281	379740	818	523131	547054	548884	1145	0.174820626	0.219154634	1.399755501	0.48517485
BP10268	BP10275	TerF family transcriptional regulator	169095	60807	76068	117	225083	149847	171551	210	0.054541147	0.077249179	1.794871795	0.843880798
BP10268	BP10276	RND efflux system, outer membrane protein	482890	366264	391852	271	601897	565867	582257	383	0.183314801	0.228696618	1.413284133	0.499051541
BP10268	BP10277	efflux transporter	650527	402135	451405	466	858067	724533	781939	732	0.051867689	0.073862885	1.570815451	0.651513694
BP10268	BP10278	RND efflux system, cytoplasmic membrane extrusion protein	1275860	1126511	1131406	359	1483701	1376023	1453657	439	0.962617537	0.969728571	1.22841226	0.290237066
BP10268	BP10279	ABC transporter permease	358604	378556	374349	248	342536	345329	342476	300	0.29247518	0.34053456	0.90677419	0.113780633
BP10268	BP10280	sensory box histidine kinase/response regulator	322567	336518	331784	176	300420	299703	312088	165	0.001098135	0.00232748	0.9375	-0.093109404
predicted RNA	-	-	22716	33949	34778	622	19268	22158	22526	435	7.97E-13	1.42E-11	0.699356913	-0.5189917
BP10268	BP10282	methyl-accepting chemotaxis transducer transmembrane protein	41967	32384	35194	23	39184	41091	40688	25	0.012893507	0.021145352	1.086956522	0.120294234
BP10268	BP10281	hypothetical protein	98832	140758	125814	238	870181	96618	96770	183	5.96E-12	8.66E-11	0.768907563	-0.379117925
BP10268	BP10283	hypothetical protein	177696	186999	188849	409	156473	170054	165963	362	1.52E-07	8.41E-07	0.885085575	-0.176111146
predicted RNA	-	-	22784	18552	1129	246	37933	11908	19752	702	1.34E-07	7.50E-07	2.853658537	1.512812715
BP10268	BP10284	zinc-containing alcohol dehydrogenase	1510070	1697606	1611449	1553	1745400	151828	151828	146	0.108826333	0.143976503	1.1671875	0.741460986
BP10268	BP10285	hypothetical protein	22947	18989	19926	104	25006	20553	21360	112	0.002281234	0.004471931	0.107922307	0.106915204
BP10268	BP10286	ATP synthase subunit gamma	302514	256486	249674	317	330972	264535	279324	343	0.009703734	0.016394162	1.02018927	0.113725736
BP10268	BP10287	FOF1 ATP synthase subunit alpha	424276	252128	286216	158	479054	361618	384652	202	0.794271119	0.824911047	1.274881013	0.354430735
BP10268	BP10288	ATP synthase F0 subunit B	325619	333762	323202	436	303169	319433	324349	420	0.054422848	0.009721806	0.963302752	-0.053938807
BP10268	BP10289	FOF1 ATP synthase subunit C	91023	101942	95571	386	85347	89695	91644	357	1.69E-06	7.23E-06	0.924870466	-0.112676773
BP10268	BP10290	FOF1 ATP synthase subunit A	133446	133044	123104	184	141213	127465	125345	187	9.48E-05	2.62E-04	0.16304348	0.023332504
BP10268	BP10291	FOF1 ATP synthase subunit D	16743	121318	12615	34	17595	15096	14601	50	0.003427	0.003427	0.940451449	-0.083062351
BP10268	BP10292	FOF1-ATPase subunit	49867	42198	46315	93	49077	46739	48483	97	0.00168832	0.002465394	1.043071053	0.060754031
BP10268	BP10293	FOF1 ATP synthase subunit epsilon	52816	19224	23367	70	55380	41731	42528	102	0.805523805	0.83196692	1.457142857	0.451423235
BP10268	BP10294	FOF1 ATP synthase subunit beta	854421	599591	631808	438	1013860	762059	841912	549	0.273801398	0.326354462	1.25342658	0.328575279
BP10268	BP10295	poly-beta-hydroxybutyrate polymerase	1263067	1453932	1446200	773	1239620	1317119	1254885	708	0.181906553	0.246949046	0.915912031	-0.126719054
BP10268	BP10296	bifunctional enoyl-CoA hydratase/phosphate acetyltransferase	752311	536213	572541	441	867117	636558	671577	516	0.780599073	0.749585481	1.170068027	0.22659241
BP10268	BP10297	acetate kinase	699157	273066	366706	378	680773	515505	574343	500	0.390324538	0.444859343	1.322751323	0.40354186
BP10268	BP10298	hypothetical protein	146086	131366	136508	128	138506	123246	131803	146	0.50297182	0.51283803	1.1371875	0.16992504
BP10268	BP10299	delta-phosphofructokinase	60450	43722	46432	53	67992	51268	56857	70	0.02616551	0.039906922	1.16981133	0.236275856
BP10268	BP10300	OsmY domain-containing protein	540409	522855	524702	816	498888	490489	509201	214	0.311867821	0.364514038	0.943627451	-0.083710706
BP10268	BP10301	hypothetical protein	1435	1397	1620	5	1333	1622	1580	5	0.001015344	0.002179012	1	0
BP10268	BP10302	cytidine deaminase	28716	38835	33060	85	30514	33947	33265	82	1.11E-04	3.02E-04	0.964705882	-0.051838932
BP10268	BP10303	thymidine phosphorylase	51906	24310	27796	26	63528	43638	49671	39	0.893643242	0.910331935	1.5	0.584962501
BP10268	BP10304	hypothetical protein	247619	382911	341196	1799	209607	267735	260071	1365	2.75E-11	3.55E-10	0.758748564	-0.398294235
BP10268	BP10305	deoxyribose-phosphate aldolase	23005	16123	19219	24	25738	19219	24637	29	0.026421459	0.040189576	1.208333333	0.1371875
BP10268	BP10306	nucleoside transporter	60028	33577	49155	35	60401	52291	61767	40	0.280123214	0.333057794	1.314285714	0.394278939
BP10268	BP10307	pyruvate decarboxylase	4857	5654	4500	4	3793	4379	4394	3	1.22E-05	4.25E-05	0.75	-0.415037499
BP10268	BP10308	glutathione S-transferase	2936	2768	2723	4	2594	2813	2457	4	1.30E-05	4.49E-05	1	0
BP10268	BP10309	LysR family transcriptional regulator	25249	9537	15454	18	28667	22786	23519	27	0.55352808	0.64552184	1.5	0.584962501
BP10268	BP10310	TerF family transcriptional regulator	9469	9992	7543	13	11471	10113	10846	16	0.013082446	0.021421609	1.27069231	0.299560282
BP10268	BP10311	short chain dehydrogenase/reductase family oxidoreductase	10682	10802	12387	12	13299	12377	11396	13	7.16E-04	0.004603295	1.083333333	0.115477217
BP10268	BP10312	monoxxygenase flavin-binding family protein	14668	13136	11633	8	11633	14068	14068	9	0.002471859	0.0130008	1.3	1.125
BP10268	BP10314	hypothetical protein	12428	9676	7965	10	14483	12143	12109	13	0.05192469	0.073927277	1	0
BP10268	BP10315	diacylglycerol cyclase	67291	65950	64832	43	67802	65902	68258	44	2.84E-04	7.01E-04	0.023258814	0.033166684
BP10268	BP10316	hypothetical protein	8528	3435	4637	12	8577	8622	8679	19	0.668121965	0.712		

BP1026b	BP12173	hypothetical protein	2764	3210	4075	10	2565	2748	2478	8	5.01E-10	5.02E-09	0.8	-0.321928095
BP1026b	BP12174	hypothetical protein	3940	2203	2264	9	4633	3832	4492	13	0.761032711	0.795394567	1.444444444	0.530514717
BP1026b	BP12175	pyridoxal-dependent decarboxylase domain-containing protein	28446	30085	28152	20	26628	28012	27670	19	1.93E-05	6.38E-05	0.95	-0.074000581
BP1026b	BP12176	ectin	21469	34633	33537	34	22631	28647	26168	29	1.12E-07	1.85E-07	0.852941367	-0.229481846
BP1026b	BP12177	hypothetical protein	1919	995	1009	3	1606	837	946	4	0.077471564	0.105837749	1.333333333	0.415037499
BP1026b	BP12178	alcohol dehydrogenase	4932	3883	4032	3	4095	3863	3356	3	4.89E-05	1.46E-04	1	0
BP1026b	BP12179	pyridoxal-dependent decarboxylase domain-containing protein	61368	63967	63684	44	59335	57510	58039	40	4.57E-06	1.75E-05	0.909090909	-0.137035254
BP1026b	BP12180	xylulose kinase	16943	15267	15347	9	15116	14458	16372	9	2.41E-05	7.76E-05	1	0
BP1026b	BP12181	hypothetical protein	18417	23794	21689	56	19512	21485	19088	53	2.52E-05	8.11E-05	0.946428571	-0.079434467
BP1026b	BP12182	Acyclic terpenes utilization regulator AtuR, TetR family	53937	53257	40079	63	57056	51829	52584	79	0.113813332	0.149050319	1.253968254	0.326500825
BP1026b	BP12183	acyl-CoA dehydrogenase	4873	3564	4554	3	3969	4217	4214	3	7.36E-04	0.00142428	1	0
BP1026b	BP12184	short chain dehydrogenase/reductase family oxidoreductase	3136	2089	2910	3	3049	3132	2779	3	0.003818472	0.007099371	1	0
BP1026b	BP12185	acetyl-CoA carboxylase carboxyltransferase	9141	7167	6911	4	9461	7859	8984	5	0.004178273	0.007693076	1.25	0.321928095
BP1026b	BP12186	acyl-CoA dehydrogenase	5010	5545	5842	4	5645	4880	4624	4	1.76E-04	4.57E-04	1	0
BP1026b	BP12188	enoyl-CoA hydratase	643	360	346	0	433	357	376	0	0.003617612	0.006768052	#DIV/0!	#DIV/0!
BP1026b	BP12187	carbamoyl-phosphate synthase L subunit	3149	1746	2969	1	3764	2766	3223	1	0.12523863	0.162419253	1	0
BP1026b	BP12189	hypothetical protein	7657	6526	4147	6	5782	5207	6342	6	2.08E-04	5.32E-04	1	0
BP1026b	BP12190	AMP-activated acetyl-CoA synthetase	50960	44632	42068	28	30306	27913	30831	17	1.44E-18	8.30E-17	0.607142857	-0.719892300
BP1026b	BP12191	hypothetical protein	8766	13792	69933	22	7451	8693	7929	17	4.88E-11	6.08E-10	0.727272727	-0.371968777
BP1026b	BP12192	hypothetical protein	23055	26138	24632	23	18855	18373	19139	18	4.65E-10	4.70E-09	0.782608696	-0.355636955
BP1026b	BP12193	polyketide synthase subunit	37083	59359	51864	183	30373	36388	32999	123	4.04E-15	1.15E-13	0.672131148	-0.573185333
BP1026b	BP12194	cyclopropane-fatty-acyl-phospholipid synthase	74640	75456	81673	82	67663	69942	72792	74	1.57E-06	6.80E-06	0.902439024	-0.14809639
BP1026b	BP12195	hypothetical protein	13110	9479	12580	11	10208	10115	9910	10	5.41E-07	2.60E-06	0.909090909	-0.137035254
BP1026b	BP12196	amidohydrolase	13918	13702	11851	12	11750	11129	11842	11	1.01E-07	5.89E-07	0.916666667	-0.125530882
BP1026b	BP12197	sulfamycin Mx1 synthetase B	63599	66970	63404	34	56726	57248	53813	30	1.16E-07	6.65E-07	0.87325841	-0.180572246
BP1026b	BP12198	thioesterase family protein	31469	28870	32140	74	24884	25493	25872	74	1.56E-08	1.10E-07	0.810810811	-0.30256277
BP1026b	BP12199	hydrolase alpha-beta fold domain-containing protein	34720	23111	27585	29	27830	26763	27362	28	2.91E-05	9.21E-05	0.965517241	-0.050626073
BP1026b	BP12200	hypothetical protein	17260	24196	22224	35	16110	17139	17432	28	3.88E-09	3.13E-08	0.8	-0.321928095
BP1026b	BP12201	Beta-phosphoglucosyltransferase	32120	43232	45073	60	27724	34925	30673	46	3.14E-10	3.31E-09	0.766666667	-0.38332864
BP1026b	BP12202	IS element transposase	25617	32338	30794	40	22582	27078	25404	34	1.11E-07	6.39E-07	0.85	-0.234465254
BP1026b	BP12205	hypothetical protein	1004	1204	880	4	734	950	639	3	1.16E-07	6.65E-07	0.75	-0.415037499
BP1026b	BP12206	hypothetical protein	1964	3967	3606	8	2545	3567	3236	8	2.71E-04	6.72E-04	1	0
BP1026b	BP12207	adhesin/mucolin	51207	69430	69933	6	45287	53133	51769	5	6.32E-10	6.30E-09	0.833333333	-0.263034406
BP1026b	BP12209	Integrase	2131	2307	2038	13	1204	1710	1652	9	2.75E-12	4.40E-11	0.692307692	-0.530514717
BP1026b	BP12210	RhsD protein	89965	146133	127046	26	79752	95536	90438	19	1.76E-13	3.56E-12	0.730769231	-0.455212205
BP1026b	BP12211	hypothetical protein	9396	7644	8128	6	8573	8753	8392	6	1.91E-04	4.91E-04	1	0
BP1026b	BP12213	hypothetical protein	10315	14995	16253	15	7417	10296	10516	10	1.19E-15	3.76E-14	0.666666667	-0.584962501
BP1026b	BP12214	diaminopimelate decarboxylase	1028	799	1280	2	611	995	824	1	8.04E-07	3.72E-06	0.5	-1
BP1026b	BP12216	Aerobic C4-dicarboxylate transporter for formate, L-malate, D-malate, succinate	46898	64600	59724	55	39657	49747	50259	45	5.42E-09	4.23E-08	0.818181818	-0.289506617
BP1026b	BP12217	malate, succinate	11659	19745	17595	27	8096	12282	10685	17	5.69E-19	3.50E-17	0.629629629	-0.667424661
BP1026b	BP12218	endonuclease L-PSF	8613	16134	13811	31	6339	9389	8100	19	2.25E-18	1.24E-16	0.612903226	-0.70626797
BP1026b	BP12220	GntR family transcriptional regulator	8011	10716	9475	21	7775	8565	8347	19	4.12E-07	2.04E-06	0.904761905	-0.144389909
BP1026b	BP12221	senescence marker protein-30	57956	95823	89663	91	49972	65060	59812	65	1.76E-13	3.56E-12	0.714285714	-0.485426827
BP1026b	BP12222	Polyketide transport-associated domain protein ShIB-type	16405	22976	23497	61	13574	17151	16553	46	5.43E-11	6.70E-10	0.754098361	-0.407175382
BP1026b	BP12223	transposase B	565	386	534	0	533	491	504	0	0.041944029	0.060892129	#DIV/0!	#DIV/0!
BP1026b	BP12224	transposase	3	3	0	0	0	0	0	0	0	0	0	0
BP1026b	BP12225	hypothetical protein	24859	44578	37530	18	20742	29788	25557	12	1.04E-12	1.80E-11	0.666666667	-0.584962501
BP1026b	BP12226	alpha-galactosidase	15553	25336	21680	9	13081	16191	14368	6	5.71E-14	1.26E-12	0.666666667	-0.584962501
BP1026b	BP12227	ABC transporter permease	2009	3312	2760	8	1232	1988	1456	4	5.32E-21	4.51E-19	0.5	-1
BP1026b	BP12228	hypothetical protein	498	990	564	3	400	510	568	2	4.97E-07	2.41E-06	0.666666667	-0.584962501
BP1026b	BP12229	ABC transporter permease	4055	6923	6826	6	3895	4705	4570	5	5.20E-08	3.22E-07	0.833333333	-0.263034406
BP1026b	BP12230	ABC transporter substrate-binding protein	4156	6122	5407	4	2778	3415	3284	2	1.46E-16	5.61E-15	0.5	-1
BP1026b	BP12231	malolase/malolacton import ATP-binding protein malK	41601	50633	46933	38	34047	39646	38414	3	2.43E-10	2.90E-09	0.35	-0.415037499
BP1026b	BP12232	hypothetical protein	11776	20700	18026	6	9705	12668	11350	5	1.90E-16	7.14E-15	0.625	-0.678071905
BP1026b	BP12233	hypothetical protein	2175	3827	2712	13	1776	2308	2863	10	1.61E-09	1.40E-08	0.769230769	-0.378511623
BP1026b	BP12234	Lact family regulatory protein	17654	29934	27564	21	16278	20849	20579	16	7.69E-10	7.29E-09	0.761904762	-0.392317423
BP1026b	BP12235	transposase	300	967	328	2	363	293	213	1	2.87E-10	3.03E-09	0.5	-1
BP1026b	BP12236	hypothetical protein	11633	19424	18106	20	9663	13860	10810	14	1.06E-14	2.84E-13	0.7	-0.514573173
BP1026b	BP12238	transposase	1349	2586	2142	6	1610	2072	2219	6	2.98E-08	9.40E-05	1	0
BP1026b	BP12239	transposase B	5799	5548	5548	0	5414	5600	5414	0	0.033744809	0.050125785	#DIV/0!	#DIV/0!
BP1026b	BP12244	Integrase	4058	6489	5764	6	3498	4900	4264	5	5.92E-07	2.82E-06	0.833333333	-0.263034406
BP1026b	BP12245	transposase	3120	4935	4012	13	2816	3450	3732	10	8.84E-07	4.06E-06	0.769230769	-0.378511623
BP1026b	BP12246	Irsso8-transposase orfB protein	34608	53847	50914	52	32025	38680	36952	40	1.10E-09	1.00E-08	0.769230769	-0.378511623
BP1026b	BP12247	transposase	18128	24053	25369	76	18384	23857	22948	73	5.73E-05	1.68E-04	0.960526316	-0.058102955
BP1026b	BP12248	hypothetical protein	855	1092	1217	7	839	975	503	5	2.29E-08	1.54E-07	0.714285714	-0.485426827
BP1026b	BP12249	hypothetical protein	43457	72887	64753	52	35246	50966	40590	36	9.67E-14	2.05E-12	0.692307692	-0.530514717
BP1026b	BP12250	predicted RNA	91667	16184	19947	568	7137	99437	9188	392	1.39E-14	3.04E-13	0.690142857	-0.672712765
BP1026b	BP12250	transposase	13891	23648	20164	26	11953	18016	14047	20	6.65E-11	8.03E-10	0.769230769	-0.378511623
BP1026b	BP12252	YD repeat/RHS repeat protein	13909	22097	18293	9	10791	14046	13173	6	1.60E-14	4.15E-13	0.666666667	-0.584962501
BP1026b	BP12253	hypothetical protein	5783	5898	5374	8	4997	4811	4877	7	1.93E-05	6.40E-05	0.875	-0.192645078
BP1026b	BP12254	type VI secretion system	4995	6701	5486	2	4623	4787	4892	2	6.16E-06	2.29E-05	1	0
BP1026b	BP12255	type VI secretion system	3913	2982	3020	1	4126	3061	3884	1	0.028849754	0.043543558	1	0
BP1026b	BP12256	type VI secretion system	616	748	600	0	833	692	576	0	0.039137876	0.057242224	#DIV/0!	#DIV/0!
BP1026b	BP12257	type VI secretion system	4851	5202	4197	2	5741	4084	4773	2	0.055630539	0.07589693	1	0
BP1026b	BP12258	type VI secretion system	947	6357	6357	1	779	1086	1061	1	0.3394143	0.39144115	1	0
BP1026b	BP12259	type VI secretion system	2516	6075	2539	4	1361	2391	2420	4	3.00E-04	3.47E-04	1	0
BP1026b	BP12260	type VI secretion system	4798	4767	4650	3	4080	5434	5877	3	0.009209984	0.015652731	1	0
BP1026b	BP12261	type VI secretion system	1120	1375	1082	2	1114	1051	1157	1	3.48E-04	8.41E-0		

BP1026B	I2307	oligopeptide ABC transporter periplasmic oligopeptide-binding protein	42620	53985	52300	30	43048	48671	45036	27	6.91E-06	2.54E-05	0.9	-0.152003093
BP1026B	I2308	DNA-binding protein	72945	102574	98495	150	67535	78224	73476	120	7.55E-10	7.23E-09	0.8	-0.321928095
BP1026B	I2309	amino acid permease transporter	74730	79173	79176	150	84576	87188	87188	57	0.001264001	0.00261253	1.07547	0.110490565
BP1026B	I2310	hypothetical protein	4640	5975	5500	26	5139	4663	4745	23	9.94E-05	2.74E-04	0.884615385	-0.176877763
BP1026B	I2311	hypothetical protein	9373	8142	8840	5	9897	9324	9707	5	0.001209394	0.002539849	1	0
BP1026B	I2312	LysR family transcriptional regulator	20516	24022	22613	23	16993	18499	18435	19	1.04E-08	7.59E-08	0.826086957	-0.275634443
BP1026B	I2313	hypothetical protein	907	1202	993	1	1091	990	974	1	0.003471506	0.006514135	1	0
BP1026B	I2314	MmgE/Prp family protein	1343	824	856	0	1016	946	1096	0	0.007799118	0.013462814	#DIV/0!	#DIV/0!
BP1026B	I2315	citrate lyase	878	862	760	0	1471	1134	924	1	0.859903891	0.881257492	#DIV/0!	#DIV/0!
BP1026B	I2316	Acyl-CoA transferase/carnitine dehydratase protein	12200	12609	11645	16	11814	11288	11362	15	0.646504726	0.602659974	0.9375	-0.091109404
BP1026B	I2317	zinc-binding dehydrogenase	2577	3142	2416	2	2931	3395	2897	2	0.017239555	0.027498146	1	0
BP1026B	I2318	isochorismatase	1469	1491	1729	2	2092	2119	1503	3	0.042543579	0.061705403	1.5	0.584962501
BP1026B	I2319	MFS family transporter	1022	511	829	0	886	754	633	0	0.002799369	0.005378589	#DIV/0!	#DIV/0!
BP1026B	I2320	MFS transporter	9199	11804	11630	7	8315	8796	8801	5	6.03E-10	5.93E-09	0.714285714	-0.485426827
BP1026B	I2321	hypothetical protein	651	923	743	0	1112	1005	1244	1	0.695667954	0.737510365	#DIV/0!	#DIV/0!
BP1026B	I2322	Acyl-CoA transferase/carnitine dehydratase protein	14667	8175	10989	8	15791	12709	12942	10	0.017291128	0.027557736	1.25	0.321928095
BP1026B	I2323	IGR family transcriptional regulator	12200	12609	11645	16	11814	11288	11362	15	2.73E-06	1.13E-05	0.9375	-0.091109404
BP1026B	I2324	citrate lyase subunit beta	1202	195	543	0	701	374	693	0	0.001618228	0.003289418	#DIV/0!	#DIV/0!
BP1026B	I2325	porin	12214	7403	8029	8	13694	10537	11860	11	0.071424088	0.098471056	1.375	0.459431619
BP1026B	I2326	MmgE/PrpD family protein	8843	5631	6429	4	9166	8359	7361	5	0.018774743	0.029598885	1.25	0.321928095
BP1026B	I2327	hypothetical protein	4840	3490	3509	3	5056	3939	4440	4	0.028103992	0.042511778	1.333333333	0.415037499
BP1026B	I2328	rarD protein	9847	5828	6150	8	13789	8114	9240	11	0.01727598	0.036249017	1.375	0.459431619
BP1026B	I2329	acylphosphatase	8687	3121	4031	17	13954	7682	9440	34	0.198458809	0.245258493	2	1
BP1026B	I2330	thiolaldehyde-4-reductase family protein	38196	11160	14887	21	48603	31891	33004	37	0.237976453	0.287690555	1.761904762	0.817135943
BP1026B	I2331	hypothetical protein	35194	32894	39201	24	39929	36408	36408	24	0.017483621	0.027102331	1.666666667	0.125330883
BP1026B	I2332	glycosyl transferase family protein	22501	16562	18004	15	27831	22362	26180	21	0.160610214	0.202922029	4	0.485426827
BP1026B	I2333	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	245495	176544	197029	219	301091	277348	283520	305	0.880357489	0.898841558	1.392694064	0.477878373
BP1026B	I2334	radical SAM domain-containing protein	377341	510252	465032	388	378121	440269	439256	361	0.056520603	0.079764621	0.930412371	-0.104057815
BP1026B	I2335	DOPA 4.5-dioxygenase	3555	4235	5694	12	3859	5132	4169	12	0.001204305	0.002530008	1	0
BP1026B	I2336	aminotransferase	55681	46931	46311	36	56801	48548	51816	38	0.001271378	0.002654911	1.055555556	0.078002512
BP1026B	I2337	hypothetical protein	19464	29842	23810	52	17081	21017	20397	41	9.42E-09	6.96E-08	0.788461538	-0.342887714
BP1026B	I2338	hypothetical protein	5179	4559	5761	24	5847	5362	5362	24	0.017483621	0.027102331	1.666666667	0.125330883
BP1026B	I2339	carbon starvation protein A	33584	34924	31467	16	47481	43598	46145	22	0.479595944	0.532983878	1.375	0.459431619
BP1026B	I2340	cytochrome P460	2839	2078	1803	4	3417	2350	2585	5	0.061593651	0.086187145	1.25	0.321928095
BP1026B	I2341	epoxide hydrolase	9990	6098	7003	7	10713	8673	9656	9	0.037574548	0.055213198	1.285714286	0.362570079
BP1026B	I2342	hypothetical protein	22935	14849	14332	11	22931	17580	19205	13	0.009885456	0.016665268	1.181818182	0.2410081
BP1026B	I2343	LysR family transcriptional regulator	15933	20278	18285	18	16954	17102	16594	17	9.19E-06	3.30E-05	0.944444444	-0.08246216
BP1026B	I2344	cysteine transferase	3989	5447	5066	12	2512	4158	3396	8	1.07E-10	1.24E-09	0.666666667	-0.584962501
BP1026B	I2345	hypothetical protein	1041	1324	765	2	1097	1168	1019	2	0.1686101	0.028122924	1	0
BP1026B	I2346	hypothetical protein	447	178	216	0	511	461	367	1	0.13521767	0.1719881	#DIV/0!	#DIV/0!
BP1026B	I2347	Generic methyltransferase	1734	656	1040	1	2014	1059	1628	2	0.492879056	0.54597039	2	1
BP1026B	I2348	glycosyl transferase family protein	11882	14316	13399	12	10744	11084	11472	10	8.86E-09	6.57E-08	0.833333333	-0.263034406
BP1026B	I2349	hypothetical protein	1953	559	672	0	1876	1232	1728	1	0.779908651	0.811437131	#DIV/0!	#DIV/0!
BP1026B	I2350	hypothetical protein	8060	6477	7031	5	7999	8051	6272	6	9.68E-04	0.00208819	1.2	0.263034406
BP1026B	I2351	hypothetical protein	459	683	488	0	512	811	390	0	0.055381384	0.078315469	#DIV/0!	#DIV/0!
BP1026B	I2352	pilus subunit	799	1671	1367	1	771	1261	1367	1	0.771E-04	0.647E-04	0.857142857	-0.222392421
BP1026B	I2353	pilus subunit	333	326	725	2	280	190	239	1	1.17E-11	1.61E-10	0.5	1
BP1026B	I2354	type IV prepilin peptidase-like protein	108	54	138	0	306	114	208	0	0.00176148	0.003542793	#DIV/0!	#DIV/0!
BP1026B	I2355	hypothetical protein	2491	1366	1762	1	4036	2462	3412	2	0.14815134	0.188892959	2	1
BP1026B	I2356	pilus assembly transmembrane protein	697	585	596	0	515	609	484	0	3.08E-04	7.53E-04	#DIV/0!	#DIV/0!
BP1026B	I2357	phospholipid-binding domain-containing protein	3703	2858	3409	1	3900	4244	4408	2	0.196934245	0.243518336	2	1
BP1026B	I2358	RNA delta(2)-isopentenylpyrophosphatetransferase	312	554	334	1	391	355	413	1	0.045559442	0.064571124	1	0
BP1026B	I2359	hypothetical protein	3975	3975	3892	3	3892	3726	4419	3	0.099305461	0.14789331	1	0
BP1026B	I2360	hypothetical protein	2394	1545	1847	3	2369	2242	2284	4	0.022587349	0.034959397	1.333333333	0.415037499
BP1026B	I2361	hypothetical protein	842	1047	833	1	865	760	761	1	9.01E-05	2.51E-04	1	0
BP1026B	I2362	flp pilus assembly protein, ATPase	2002	1801	1303	1	2505	2219	2586	2	0.556312854	0.607335631	2	1
BP1026B	I2364	type II secretion system protein	7177	6925	7095	5	8039	6780	7272	5	0.001214592	0.002549535	1	0
BP1026B	I2363	flp pilus assembly protein TadB	4520	6813	5664	5	3909	4497	4363	4	1.27E-07	7.19E-07	0.8	-0.321928095
BP1026B	I2365	type II secretion system protein	5623	4174	5310	5	5368	4975	5228	5	0.003603907	0.008533047	1	0
BP1026B	I2366	transcription regulator AsnC	39523	51976	46564	96	34845	38807	40880	80	1.21E-07	6.98E-07	0.833333333	-0.263034406
BP1026B	I2367	aromatic amino acid aminotransferase	1270	899	862	0	1183	900	1100	0	0.020250887	0.031655104	#DIV/0!	#DIV/0!
BP1026B	I2368	translation initiation inhibitor	43	61	45	0	86	66	0	0	0.498636354	0.551374202	#DIV/0!	#DIV/0!
BP1026B	I2369	outer membrane porin protein	1821	1356	1115	1	2203	1675	1788	1	0.16958775	0.213276655	1	0
BP1026B	I2370	amino acid transporter	55931	58334	58912	40	41216	42933	41540	29	2.64E-12	4.27E-11	0.725	-0.4369471
BP1026B	I2371	GntR family transcriptional regulator	80970	70432	76063	97	54719	49206	50493	66	5.04E-16	1.71E-14	0.680412371	-0.555518723
BP1026B	I2372	hypothetical protein	644476	362113	411734	307	557718	457856	487576	325	0.670227128	0.71380896	1.058611922	0.082201063
BP1026B	I2373	major facilitator family transporter	461340	437223	437223	336	382087	398574	398574	298	6.50E-04	0.00575456	0.837078652	-0.25656911
BP1026B	I2374	LysR family transcriptional regulator	163715	104565	108769	137	149208	132863	146394	136	0.09005186	0.015337349	1.13886131	0.187370136
BP1026B	I2375	hypothetical protein	161240	153928	160327	74	158358	149307	156186	72	3.97E-05	1.21E-04	0.972972973	-0.039528364
BP1026B	I2377	hypothetical protein	722	348	221	1	568	450	428	1	0.189044622	0.23492015	1	0
BP1026B	I2376	hypothetical protein	3700	4153	4372	10	2391	3662	2704	7	1.02E-11	1.44E-10	0.7	-0.514573173
BP1026B	I2378	Na ⁺ /H ⁺ antiporter-like protein	4330	4667	5650	3	4041	4083	4440	3	2.89E-05	9.15E-05	1	0
BP1026B	I2379	ATP-dependent DNA ligase	7209	5176	6273	1	6719	6182	5505	1	5.70E-04	0.001308469	1	0
BP1026B	I2380	Ku/Okazaki beta-barrel domain-containing protein	2837	3739	3207	2	3284	2637	2158	2	2.83E-08	1.86E-07	1	0
BP1026B	I2381	hypothetical protein	193	145	169	0	301	307	307	0	0.03083972	0.04271007	#DIV/0!	#DIV/0!
BP1026B	I2382	hydroxylase II	3102	3168	2972	1	3313	3070	3359	1	0.026023934	0.039642579	1	0
BP1026B	I2383	hypothetical protein	205	48	45	0	420	182	310	0	6.29E-11	7.61E-10	#DIV/0!	#DIV/0!
BP1026B	I2384	hypothetical protein	176	74	264	1	142	164	140	0	0.014026511	0.022794898	0	#NUM!
BP1026B	I2385	hypothetical protein	35	212	160	0	332	107	152	1	0.56516816	0.616252367	#DIV/0!	#DIV/0!

BP1026b	I2432	ATP-binding transmembrane ABC transporter protein	2622	1609	1584	0	2487	2269	1942	0	0.01018388	0.017122347	#DIV/0!	#DIV/0!
BP1026b	I2433	hypothetical protein	247	48	181	0	287	140	416	0	0.029860135	0.044897562	#DIV/0!	#DIV/0!
BP1026b	I2434	phosphatidylserine decarboxylase	3419	2626	3160	2	3225	2994	3356	2	0.00231569	0.004564897	1	0
BP1026b	I2435	succinate dehydrogenase iron-sulfur subunit	1170	1411	1166	1	1363	1245	1245	1	0.00207372	0.004008246	1	0
BP1026b	I2436	hypothetical protein	1232	553	1086	3	865	1082	1549	4	0.01269753	0.355723852	1.333333333	0.415037499
BP1026b	I2437	2-hydroxy-3-oxopropionate reductase	45398	33663	36494	43	49429	46545	47784	53	0.123251848	0.160140605	1.23255814	0.3016557
BP1026b	I2438	nitriltransferase	29339	26896	28661	20	29371	29343	29255	21	3.98E-04	9.49E-04	1.05	0.070389328
BP1026b	I2439	4'-phosphopantetheinyl transferase	30850	16663	18377	26	31172	22830	23900	31	0.016947964	0.027072721	1.192307692	0.253756592
BP1026b	I2440	oxalate-formate antiporter	76377	75926	79048	61	69742	74524	68470	56	2.83E-06	1.15E-05	0.918032787	-0.123824216
BP1026b	I2441	flavin reductase domain-containing protein	3133	1348	1049	2	3588	1773	2211	3	0.329592874	0.382664464	1.5	0.584962501
BP1026b	I2442	hypothetical protein	1134	255	397	2	1162	930	1192	4	0.018444682	0.02875735	1.22	1
BP1026b	I2443	hypothetical protein	455	145	360	0	779	648	807	0	4.25E-06	1.65E-05	#DIV/0!	#DIV/0!
BP1026b	I2444	hypothetical protein	24136	8502	12403	33	28089	31803	29502	65	0.100558702	0.133588466	1.96969697	0.977973694
BP1026b	I2445	dihydropyrimidine dehydrogenase	45615	28363	32723	25	33149	26639	26520	20	5.05E-09	3.98E-08	0.8	-0.321928095
BP1026b	I2446	branched-chain alpha-keto acid dehydrogenase subunit E2	106651	95569	100562	69	78104	74697	76945	52	1.36E-11	1.84E-10	0.753623188	-0.408084739
BP1026b	I2447	2-oxoisovalerate dehydrogenase, E1 component, beta subunit	66668	59659	61583	62	38276	37132	36251	37	4.55E-21	3.91E-19	0.596774194	-0.744742945
BP1026b	I2449	2-oxoisovalerate dehydrogenase subunit alpha	156740	185614	195768	145	79469	92028	82234	68	5.49E-45	1.64E-42	0.468965517	-1.092466249
BP1026b	I2448	hypothetical protein	1899	2035	1641	9	556	986	636	4	4.88E-28	9.87E-26	1.066251674	0.02512139
BP1026b	I2450	hypothetical protein	1647	1623	1213	1	2266	1975	1541	2	0.116010966	0.151493428	1.444444444	-1.169925001
BP1026b	I2451	hypothetical protein	1751	1808	1489	3	1589	1893	1487	3	2.02E-04	5.17E-04	1	0
BP1026b	I2452	hypothetical protein	29475	21840	25598	22	24820	25317	24520	22	4.91E-05	1.46E-04	1	0
BP1026b	I2453	LysR family regulatory protein	41728	40811	39814	43	31583	32028	32508	34	1.29E-09	1.15E-08	0.790697674	-0.338801913
BP1026b	I2454	hypothetical protein	1966	833	632	1	2161	1973	1780	3	0.263995967	0.315542689	1	1.584962501
BP1026b	I2455	GMC oxidoreductase family protein	36352	31722	31331	19	22802	33325	35928	20	0.001089564	0.00211679	1.052631579	0.074000581
BP1026b	I2456	oxidoreductase	586748	490206	508015	232	587127	540557	543208	244	0.74484771	0.78121219	1.051724138	0.072756342
BP1026b	I2457	C4-type zinc finger DksA/TrA family protein	68392	52417	52417	151	69033	62038	63874	161	0.018330082	0.02134599	1.066251674	0.02512139
predicted RNA			46214	48248	47846	790	52119	58579	46630	874	0.006003752	0.010629843	1.063219014	0.145780626
BP1026b	I2458	hypothetical protein	5002	4878	4956	9	4262	3788	4251	7	8.39E-06	3.03E-05	0.777777778	-0.362570079
predicted RNA			29607	3178	7266	310	25826	23478	27917	598	0.157064181	0.199047203	1.29303258	0.94787269
BP1026b	I2459	intracellular polyhydroxyalkanoate depolymerase	44806	24449	25884	24	48343	32376	38060	31	0.135098483	0.17340571	1.291666667	0.36923381
BP1026b	I2460	ribonucleotide reductase-like protein	575886	204335	246438	195	539319	379975	417791	249	0.6630889	0.708301187	1.276923077	0.352671618
BP1026b	I2461	hypothetical protein	72884	78690	69388	43	92902	60573	61627	35	5.85E-09	4.31E-08	0.13953488	-0.29698738
BP1026b	I2462	hypothetical protein	64546	487564	529402	537	626842	568766	571276	161	0.780385604	0.61876549	1.066251674	0.075879965
BP1026b	I2463	sulfate transporter family protein	193546	84002	104420	69	224898	171180	186152	105	0.521618853	0.573752399	1.52172913	0.605721061
BP1026b	I2465	hypothetical protein	38493	41917	38461	88	39879	43954	41072	92	0.00284319	0.00545423	1.045454545	0.064130337
BP1026b	I2464	nitriltransferase family protein	455853	255471	330262	530	519046	442462	450548	719	0.362917119	0.416498187	1.356603774	0.439999411
BP1026b	I2466	HSP20/alpha crystallin family protein	3547101	4846765	4742764	10066	3835490	4547243	4042860	9521	0.017338418	0.027619069	0.945857342	-0.080305489
BP1026b	I2467	porin	16739	15800	15800	13	14945	16725	16230	14	1.26E-04	3.39E-04	1.076923077	0.106915204
BP1026b	I2468	medium-chain fatty-acyl-CoA ligase	5542	5694	5502	3	3498	4650	4407	2	2.85E-08	1.87E-07	0.666666667	-0.584962501
BP1026b	I2469	GlcF family nucleovir protein	45432	45432	28005	12	45432	34046	34046	12	0.047010021	0.061876549	1.066251674	0.02512139
BP1026b	I2470	hypothetical protein	15888	22729	21521	18	10490	12909	12266	11	2.24E-22	2.50E-20	0.611111111	-0.710493383
BP1026b	I2471	quinone oxidoreductase	12369	8888	10932	10	8554	8052	8858	8	8.40E-11	9.93E-10	0.8	-0.321928095
BP1026b	I2472	taurine catabolism dioxygenase TauD, TrdA family protein	15177	13379	13600	16	10896	10879	11475	13	1.58E-10	1.76E-09	0.8125	-0.299560282
BP1026b	I2473	hypothetical protein	23622	24101	23745	22	14498	15667	14607	14	2.22E-18	1.24E-16	0.636363636	-0.652076697
BP1026b	I2474	major facilitator family transporter	3072	2325	3380	2	1862	1967	2010	1	3.85E-16	1.35E-14	0.5	-1
BP1026b	I2475	hypothetical protein	627	328	159	0	172	140	269	0	3.99E-12	6.26E-11	#DIV/0!	#DIV/0!
BP1026b	I2476	DSXA-like thoredoxin domain-containing protein	134306	6139	1492	1	1492	952	1036	1	0.386867358	0.43000316	1.066251674	0.02512139
BP1026b	I2477	mol/hydropterin oxidoreductase family protein	27902	33946	35786	11	26007	28139	26444	9	2.61E-08	1.73E-07	0.818181818	-0.289506617
BP1026b	I2478	iron-sulfur cluster-binding protein	5140	8264	7453	8	4773	5797	6000	6	3.48E-07	1.76E-06	0.75	-0.415037499
BP1026b	I2479	DMSO reductase subunit C	3197	2568	1887	2	3006	2173	3085	2	0.002618482	0.005069673	1	0
predicted RNA			238368	375685	290865	1839	215660	280798	271610	1561	3.30E-08	2.13E-07	0.848830886	-0.236450942
BP1026b	I2480	polysaccharide deacetylase family protein	22256	19747	20457	23	22853	20069	21021	23	4.75E-04	0.001104446	1	0
BP1026b	I2481	hypothetical protein	114491	98166	104362	75	104318	100569	104372	74	1.01E-05	3.60E-05	0.986666667	-0.019365325
BP1026b	I2482	penicillin-binding protein	69215	46634	46634	25	69215	61820	61820	25	0.00906583	0.013790865	1.136363636	0.18424571
BP1026b	I2483	hypothetical protein	29997	24543	24355	16	33175	26460	29104	16	0.004231102	0.00777829	1.066251674	0.169925001
BP1026b	I2484	outer membrane porin	15747	13638	12374	11	17231	16658	16998	14	0.029333357	0.044211472	1.272727272	0.347923303
BP1026b	I2485	amidase	22099	14343	12086	10	35875	25115	25248	18	0.462546444	0.516934588	1.8	0.847996697
BP1026b	I2486	hypothetical protein	47669	23250	30212	104	53765	45335	48035	151	0.838938649	0.863722656	1.451923077	0.537965021
BP1026b	I2487	acetyltransferase	8063	2831	3770	8	12295	5973	7752	15	0.636908476	0.683689601	1.875	0.906890596
BP1026b	I2488	acyltransferase	6562	4595	4763	10	8893	5183	6235	12	0.094302754	0.12594447	1.2	0.263034406
BP1026b	I2489	hypothetical protein	48886	26388	30288	26	55753	44800	44800	34	0.280980378	0.33823847	1.307692308	0.28703121
BP1026b	I2490	TldD/PmhA family protein	120675	95114	99208	73	117258	105136	113029	77	3.11E-04	7.61E-04	1.054794521	0.076961982
BP1026b	I2491	ABC transporter ATP-binding protein	28452	11647	14874	43	31999	21905	22142	60	0.248459044	0.298808202	1.395348837	0.480625841
BP1026b	I2492	hypothetical protein	1425	2403	1753	19	1068	1676	1113	13	3.08E-11	3.93E-10	0.684210526	-0.547487795
BP1026b	I2493	sensor kinase protein	87119	80700	84724	60	95902	81587	81647	61	1.68E-04	4.38E-04	1.016666667	0.023846742
BP1026b	I2494	LuxR family DNA-binding response regulator	81887	65666	69069	111	77200	75761	73726	116	5.77E-04	0.001322256	1.045045045	0.063565129
BP1026b	I2496	hypothetical protein	170918	155705	154819	268	156926	151508	148716	255	8.72E-06	3.14E-05	0.951492537	-0.071735754
BP1026b	I2495	hypothetical protein	3248	2779	3984	3	3984	3326	3326	13	0.137685023	0.176769988	1.181818181	0.2410081
BP1026b	I2497	hypothetical protein	35409	47108	41766	55	36043	40971	39633	55	5.45E-05	1.60E-04	1.904545454	-0.080919995
BP1026b	I2498	sensory box protein	58728	63632	59880	25	55520	54072	56194	22	7.40E-06	7.30E-06	0.88	-0.184424571
BP1026b	I2499	lipase	9015	10815	9634	8	8973	11686	10223	9	2.36E-04	5.93E-04	1.125	0.169925001
BP1026b	I2500	4'-phosphopantetheinyl transferase	1276	176	314	0	1564	1036	1141	1	2.43E-04	6.09E-04	#DIV/0!	#DIV/0!
BP1026b	I2501	hypothetical protein	6301	6834	5695	15	6017	6044	5383	14	1.06E-04	2.89E-04	0.933333333	-0.099555674
BP1026b	I2502	hypothetical protein	10747	5812	5957	5	13068	9723	9908	8	0.373135831	0.426897879	1.6	0.678071905
BP1026b	I2503	hypothetical protein	3454	3663	4011	4	3669	4064	4015	5	0.009522384	0.01010947	1.25	0.321928095
BP1026b	I2504	permease	4034	3405	3709									

Appendix F:

Supplemental Table 1 for Chapter 4

Supplemental Table 1: Total transcriptome of BP1026B_H2312

Synonym	Product	Empty Vector				BP1026B_H2312				pValue	qValue	Fold Change	Log2FC
		Normalized Transcripts			Expression	Normalized Transcripts			Expression				
		Replicate 1	Replicate 2	Replicate 3	RPKM	Replicate 1	Replicate 2	Replicate 3	RPKM				
BP1026B_00001	carboxylate-amine ligase	94552	134638	122576	105	133393	144294	143329	125	4.58E-06	7.15E-06	1.19047619	0.251538767
BP1026B_00002	hypothetical protein	74985	79794	79007	64	83892	78253	83735	67	4.63E-12	1.18E-11	1.046875	0.06608919
BP1026B_00003	hypothetical protein	1963125	3361208	2848114	8107	4032751	4883053	4370120	13180	0.367905698	0.392390997	1.62575552	0.701110322
BP1026B_00004	5-methylaminomethyl-2-thiouridine methyltransferase	77169	56465	58132	32	59241	56644	61664	29	6.96E-17	2.76E-16	0.90625	-0.142019005
BP1026B_00005	DNA-binding protein HU	4277852	5543088	5491260	18294	6280854	5778394	7071318	22856	0.194438994	0.214122098	1.249371379	0.321202385
BP1026B_00006	cobalamin synthesis protein/P47K family protein	126978	116428	116962	89	111322	107017	113247	82	2.96E-16	1.11E-15	0.921348315	-0.118181426
BP1026B_00007	HpaI	101263	149395	138058	266	169511	182178	180267	364	0.009146633	0.011273172	1.368421053	0.452512205
BP1026B_00008	general secretion pathway protein D	475474	515661	516546	221	526197	511124	541146	231	0.005866589	0.007341731	1.045248869	0.063846482
BP1026B_00009	general secretion pathway protein E	258506	230963	234487	161	209153	211233	239064	147	1.95E-16	7.45E-16	0.913043478	-0.131244533
BP1026B_00010	general secretion pathway protein F	151419	141768	144897	119	132563	134814	127155	107	2.31E-17	9.54E-17	0.899159664	-0.153350777
BP1026B_00011	general secretion pathway protein C	14575	7049	6971	23	6407	5733	6303	14	3.22E-30	3.59E-29	0.608695652	-0.716207034
BP1026B_00012	general secretion pathway protein G	196653	308039	277302	575	326559	344530	339230	743	1.67E-04	2.33E-04	1.292173913	0.369800255
BP1026B_00013	general secretion pathway protein H	87047	72469	75208	132	63894	59037	57790	101	1.01E-28	1.03E-27	0.765151515	-0.386182637
BP1026B_00014	general secretion pathway protein I	74678	67849	72461	202	55929	53573	57856	157	6.91E-27	6.17E-26	0.772227223	-0.363590734
BP1026B_00015	general secretion pathway protein J	122197	107277	116232	189	98428	80600	96059	150	7.71E-27	6.87E-26	0.793650794	-0.332437334
BP1026B_00016	general secretion pathway protein K	52600	52361	45967	46	51614	50349	53344	48	6.76E-11	1.54E-10	1.043478261	0.061400545
BP1026B_00018	general secretion pathway protein L	58828	53523	59066	39	52576	49316	50390	35	1.15E-17	4.86E-17	0.897435897	-0.156119202
BP1026B_00017	general secretion pathway protein M	62558	61381	63656	123	51144	47837	52445	99	2.42E-23	1.63E-22	0.804878049	-0.213157885
BP1026B_00019	general secretion pathway protein N	107272	52821	72203	97	47419	37253	52626	57	1.04E-50	3.46E-49	0.587628866	-0.767022828
BP1026B_00020	RND efflux system outer membrane lipoprotein	31141	32715	30137	19	30514	30932	28975	18	3.57E-10	7.70E-10	0.947368421	-0.078002512
BP1026B_00021	hypothetical protein	34039	33145	32348	121	47185	43081	34844	152	1.92E-04	2.67E-04	1.256198347	0.329064276
BP1026B_00022	MarK family protein	59075	57123	59095	118	67424	75611	66353	141	2.01E-07	3.45E-07	1.194915254	0.256908303
BP1026B_00023	hypothetical protein	4006	6470	5971	43	5631	8909	4746	51	4.14E-06	6.48E-06	1.186046512	0.246160587
BP1026B_00024	EmrB/QacA family drug resistance transporter	40627	40383	40076	25	52072	49337	48732	32	3.47E-05	5.09E-05	1.28	0.35614381
BP1026B_00025	LysR family transcriptional regulator	26617	21651	22617	25	22693	21569	23521	24	4.53E-12	1.15E-11	0.96	-0.058993689
BP1026B_00027	LrgA family protein	3460	875	1271	3	698	1486	1288	2	3.88E-13	1.09E-12	0.666666667	-0.584962501
BP1026B_00026	hypothetical protein	13765	11305	12666	16	14082	11968	14282	17	3.29E-09	6.53E-09	1.0625	0.087462841
BP1026B_00028	flagellar basal body-associated protein FIL	39183	51556	50143	86	45850	46057	45994	84	5.89E-12	1.48E-11	0.976744186	-0.033947332
BP1026B_00029	flagellar motor switch protein FlIM	330514	449988	410852	397	460342	482179	491070	478	2.08E-05	3.10E-05	1.204030227	0.267871611
BP1026B_00030	flagellar motor switch protein FlIN	129990	106418	104964	228	117460	121009	115088	236	4.09E-11	9.47E-11	1.035087719	0.049753035
BP1026B_00031	flagellar protein FlO	28025	23201	23880	37	24384	22700	24939	36	2.67E-11	6.31E-11	0.972972973	-0.039528364
BP1026B_00032	flagellar biosynthesis protein FlP	62197	84026	79885	98	91409	102857	99269	128	4.15E-05	6.03E-05	1.306122449	0.385290156
BP1026B_00033	flagellar biosynthesis protein FlQ	24535	30482	28557	102	33393	33656	34457	123	7.93E-05	1.13E-04	1.205882353	0.270089163
BP1026B_00034	flagellar biosynthetic protein FlR	43547	37291	39866	51	36475	34539	39633	47	1.62E-12	4.29E-12	0.921568627	-0.11783649
BP1026B_00035	MerK family transcriptional regulator	25104	30424	28632	65	37201	43027	29022	84	8.08E-04	0.00107437	1.292307027	0.36949661
BP1026B_00036	aklanonic acid methyl transferase	2667	2360	3013	3	3053	1774	2642	2	4.74E-06	7.39E-06	0.666666667	-0.584962501
BP1026B_00037	hypothetical protein	358	225	197	0	77	175	228	0	0.003660025	0.004654702	#DIV/0!	#DIV/0!
BP1026B_00038	ATP-binding cassette, ABC transporter	20071	19690	19995	19	22108	21347	20450	21	4.04E-09	7.94E-09	1.105263158	0.144389909
BP1026B_00039	ABC transporter ATP-binding protein	3832	3069	2954	3	2125	2066	2967	2	8.18E-13	2.24E-12	0.666666667	-0.584962501
BP1026B_00040	ABC transporter permease	3783	2551	3526	3	2687	1992	2592	2	2.11E-12	5.53E-12	0.666666667	-0.584962501
BP1026B_00041	sensor kinase protein	7245	4555	5602	4	4119	4593	5429	3	7.55E-14	2.26E-13	0.75	-0.415037499
BP1026B_00042	DNA-binding response regulator	2585	1374	2209	3	20188	1871	1854	2	6.31E-05	9.09E-05	0.666666667	-0.584962501
BP1026B_00043	outer membrane porin	907	778	1040	0	1466	1217	1219	1	0.652692301	0.674879531	#DIV/0!	#DIV/0!
BP1026B_00044	type III DNA modification methyltransferase	30026	37920	34494	16	39109	41842	37029	19	5.61E-06	8.71E-06	1.1875	0.247927513
BP1026B_00045	type III restriction enzyme	50960	50783	49289	16	48263	48324	51714	16	1.81E-12	4.78E-12	1	0
BP1026B_00046	outer membrane porin	1339	1637	1499	1	1708	1529	1675	1	0.00889104	0.045823854	1	0
BP1026B_00047	AraC family transcription regulator	5695	5734	6078	6	5080	4609	6057	5	2.05E-11	4.90E-11	0.833333333	-0.263034406
BP1026B_00048	branched-chain amino acid ABC transporter ATP-binding protein	1366	1125	1215	1	983	1174	522	1	6.09E-07	1.01E-06	1	0
BP1026B_00049	branched-chain amino acid ABC transporter ATP-binding protein	1324	582	543	1	749	646	715	0	0.003664083	0.004657972	0	#NUM!
BP1026B_00050	branched-chain amino acid ABC transporter ATP-binding protein/permease	444	437	325	0	351	482	285	0	0.076259037	0.087500298	#DIV/0!	#DIV/0!
BP1026B_00051	branched-chain amino acid ABC transporter permease	1120	382	604	0	442	1016	788	0	0.174507837	0.193021378	#DIV/0!	#DIV/0!
BP1026B_00052	hypothetical protein	3044	3224	2680	2	3035	2126	2289	1	1.23E-08	2.31E-08	0.5	-1
BP1026B_00053	phenylacetalddehyde dehydrogenase	8802	5811	7302	4	4360	4395	5604	3	3.39E-24	2.46E-23	0.75	-0.415037499
BP1026B_00054	hypothetical protein	2850	2408	2612	6	2464	2187	1853	5	4.57E-08	8.23E-08	0.833333333	-0.263034406
BP1026B_00055	hypothetical protein	5272	5683	5041	6	4327	4430	4837	5	5.47E-12	1.38E-11	0.833333333	-0.263034406
BP1026B_00056	short chain dehydrogenase/reductase family oxidoreductase	3873	2108	2630	3	1798	1823	1861	2	3.17E-15	1.08E-14	0.666666667	-0.584962501
BP1026B_00057	glucose-methanol-choline oxidoreductase	10987	8940	8772	5	6778	8011	6708	4	1.37E-22	8.68E-22	0.8	-0.321928095
BP1026B_00059	PadR-like family transcriptional regulator	7509	10801	9663	28	10501	11213	11894	33	6.63E-06	1.02E-05	1.178571429	0.237039197
BP1026B_00058	hypothetical protein	57603	45527	46584	42	39070	34016	37231	30	3.54E-24	2.56E-23	0.714285714	-0.485426827
BP1026B_00060	fatty acid desaturase	13149	6785	8050	9	8339	6668	6173	7	6.79E-22	4.07E-21	0.777777778	-0.362570079
BP1026B_00061	hypothetical protein	18890	11502	10629	16	10462	9617	11575	12	1.78E-20	9.44E-20	0.75	-0.415037499
BP1026B_00062	AraC family transcription regulator	13907	10699	11254	11	11861	9532	9711	9	5.07E-15	1.70E-14	0.818181818	-0.289506617
BP1026B_00063	acyl-CoA dehydrogenase	113647	126324	121742	99	35307	39537	34397	30	8.75E-230	1.57E-227	0.303030303	-1.722466024
BP1026B_00064	acetyl-CoA acetyltransferase	9421	10303	10824	8	3575	2909	2537	2	1.25E-129	1.78E-127	0.25	-2
BP1026B_00065	fatty oxidation complex subunit alpha	36826	25542	26851	14	10027	9805	10882	4	4.55E-151	7.50E-149	0.285714286	-1.807354922
BP1026B_00066	alpha-methylacyl-CoA racemase	32430	15041	19162	19	11265	10058	12686	9	2.58E-60	1.29E-58	0.473684211	-1.078002512
BP1026B_00067	lipoprotein	71412	72779	75496	129	70960	70193	68710	123	7.62E-16	2.76E-15	0.953488372	-0.06871275
BP1026B_00068	hypothetical protein	1996	2055	2613	4	2231	2163	1605	4	9.81E-06	1.50E-05	1	0
BP1026B_00069	hypothetical protein	158860	72364	92539	244	60885	51040	61243	130	3.34E-72	2.33E-70	0.532786885	-0.908369525
BP1026B_00070	lipoprotein	127782	110797	119128	323	95637	83219	91494	244	3.48E-31	4.12E-30	0.755417957	-0.404653017
predicted RNA	-	11892	21432	20054	593	23851	28758	21212	820	0.004204132	0.005315394	1.382799325	0.467591805
BP1026B_00071	transmembrane regulator PrtR	2936	671	899	1	1285	1138	616	1	9.58E-10	2.00E-09	1	0
BP1026B_00072	ECF sigma factor PrtI	3805	2424	2719	5	1334	1913	1632	3	1.46E-21	8.49E-21	0.6	-0.736965594
BP1026B_00073	catalase	3688	3070	3672	3	2104	2233	2017	1	3.88E-19	1.86E-18	0.333333333	-1.584962501
BP1026B_00074													

BP1026B_10094	O6-methylguanine-DNA methyltransferase	20124	20063	16798	17	14864	16032	16175	14	7.40E-21	4.04E-20	0.823529412	-0.280107919
BP1026B_10095	DNA-3-methyladenine glycosylase II	15006	5308	7480	9	4127	3528	5159	4	6.88E-53	2.49E-51	0.444444444	-1.169925001
BP1026B_10096	glutamate-cysteine ligase	259855	225670	250445	151	214180	197697	235303	133	1.74E-18	7.88E-18	0.880794702	-0.183122304
BP1026B_10097	RNA polymerase sigma factor	292518	235329	239398	176	299207	260396	301912	198	1.60E-07	2.77E-07	1.125	0.169925001
BP1026B_10098	hypothetical protein	47986	32267	37657	71	33176	29912	34079	58	2.53E-16	9.56E-16	0.816901408	-0.291766124
predicted RNA	-	25492	22983	25204	599	24360	20619	26592	581	5.46E-11	1.25E-10	0.969949917	-0.044017839
BP1026B_10099	hypothetical protein	387877	427893	428903	727	484402	513458	433330	836	1.95E-06	3.12E-06	1.149931224	0.201547578
BP1026B_10100	LysR family transcriptional regulator	62457	55646	52364	58	52720	53763	58737	56	5.06E-14	1.54E-13	0.965517241	-0.050626073
BP1026B_10101	ABC transporter substrate-binding protein	21252	28554	26794	23	34420	37523	31696	31	0.002804934	0.003600106	1.347826087	0.430634354
BP1026B_10102	histone deacetylase family protein	19951	20091	18946	17	17758	16952	19984	16	1.57E-15	5.52E-15	0.941176471	-0.087462841
BP1026B_10103	carbon-nitrogen family hydrolase	21760	18803	18601	22	19100	15868	17345	19	1.07E-17	4.57E-17	0.863636364	-0.211504105
predicted RNA	-	5909	9739	9111	550	12579	13420	10425	809	0.005087007	0.006395503	1.470909091	0.556708084
BP1026B_10106	hypothetical protein	28283	40683	40058	127	41808	44850	45894	155	3.20E-05	4.71E-05	1.220472441	0.287439719
BP1026B_10107	hypothetical protein	66782	111449	103950	194	123149	149255	120369	271	0.002099817	0.002717691	1.396907216	0.482236199
BP1026B_10108	hypothetical protein	105623	186406	156098	148	187180	215723	187934	195	0.001626637	0.002119905	1.317567568	0.397876948
BP1026B_10109	Lys tRNA	3544	5514	3708	55	6061	6740	7185	87	0.030416241	0.036096244	1.581818182	0.661583782
BP1026B_10110	thioesterase family protein	19460	29693	26037	61	29258	32474	30479	75	1.06E-04	1.50E-04	1.229508197	0.298081353
BP1026B_10111	putatin-like phospholipase family protein	54372	46891	50517	58	41786	36822	43047	46	2.48E-20	1.30E-19	0.793103448	-0.334419039
BP1026B_10112	D-isomer specific 2-hydroxyacid dehydrogenase	65066	73648	67302	67	72793	70708	71407	70	5.01E-12	1.27E-11	1.044776119	0.063193826
BP1026B_10113	LysR family transcriptional regulator	408074	394343	419465	385	423544	402477	433376	397	9.16E-09	1.75E-08	1.031168831	0.044280562
BP1026B_10114	DNA topoisomerase III	499105	664673	635211	220	666809	704932	698782	253	0.921404116	0.931212611	1.15	0.201633861
BP1026B_10115	thioredoxin	11887	13465	11460	32	13197	13454	13508	35	1.25E-08	2.35E-08	1.09375	0.129283017
BP1026B_10116	SMF family protein	5463	2418	3588	3	2606	2053	2314	1	9.39E-21	5.08E-20	0.333333333	-1.584962501
BP1026B_10117	peptide deformylase	68666	80922	81215	152	119434	126546	122491	243	0.091414097	0.104145588	1.598684211	0.67688499
BP1026B_10118	methionyl-tRNA formyltransferase	28784	18638	21015	23	23732	24757	24234	24	2.75E-08	5.04E-08	1.043478261	0.061400545
BP1026B_10119	homoserine/homoserine lactone efflux protein	41898	46465	48949	71	52916	41254	52442	76	3.46E-09	6.86E-09	1.070422535	0.098180394
BP1026B_10120	M48 family peptidase	449099	479416	465886	541	677639	716681	721511	822	0.135660682	0.152038962	1.519408503	0.6035098
predicted RNA	-	19814	1101	2133	334	906	514	725	31	0	0.092814371	-3.429507982	
BP1026B_10121	ribosomal RNA small subunit methyltransferase B	92582	43759	50154	44	46997	50892	37338	31	1.70E-29	1.82E-28	0.704545455	-0.505235308
BP1026B_10122	hypothetical protein	320888	353231	322166	561	369584	390710	374686	640	9.86E-07	1.62E-06	1.140819964	0.190071134
BP1026B_10123	sensor kinase protein	468250	530023	513469	209	542593	513507	569590	224	0.079822643	0.09147196	1.071703355	0.09999579
BP1026B_10124	DNA-binding response regulator	291769	253573	253384	397	265625	260366	272965	407	1.84E-10	4.03E-10	1.025188917	0.035887887
BP1026B_10125	Phe tRNA	9627	16515	13093	172	17663	17558	19452	239	6.20E-04	8.32E-04	1.389534884	0.474602503
BP1026B_10126	prophage integrase	86099	139062	121397	102	152098	165425	156062	139	0.006137527	0.007670073	1.362745098	0.446515731
BP1026B_10127	hypothetical protein	16331	15116	16586	5	14969	15521	14981	5	5.45E-14	1.65E-13	1	0
BP1026B_10128	hypothetical protein	810	247	397	1	334	363	469	1	0.003849732	0.004882093	1	0
BP1026B_10129	hypothetical protein	923	1114	1245	3	870	842	1211	2	0.001161849	0.001526556	0.666666667	-0.584962501
BP1026B_10130	hypothetical protein	848	1643	1315	6	1111	727	1084	4	3.73E-06	5.87E-06	0.666666667	-0.584962501
BP1026B_10131	hypothetical protein	2177	1800	2066	8	1203	1295	1404	5	1.76E-12	4.66E-12	0.625	-0.678071905
BP1026B_10132	putative phage-encoded membrane protein	1943	1808	1521	9	1569	1298	1645	7	1.84E-05	2.74E-05	0.777777778	-0.362570079
BP1026B_10133	hypothetical protein	1903	2249	2004	10	2375	2289	2006	11	0.00343722	0.004381127	1.1	0.137503524
BP1026B_10134	hypothetical protein	3371	3566	3353	15	3821	3207	3165	15	7.69E-06	1.18E-05	1	0
BP1026B_10135	Phage Rha protein	13455	20788	20367	33	17896	18323	17524	32	5.49E-13	1.52E-12	0.969696967	-0.044394119
BP1026B_10136	phage transcriptional activator	3170	4396	4376	15	5200	4678	4586	19	1.95E-04	2.73E-04	1.266666667	0.341036918
BP1026B_10137	putative phage DNA-binding protein	5532	7255	6243	21	8223	8507	7849	27	7.90E-05	1.13E-04	1.285714286	0.362570079
BP1026B_10138	hypothetical protein	5560	8992	8548	32	10112	10818	9559	42	3.30E-04	4.52E-04	1.3125	0.392317423
BP1026B_10139	Putative phage DNA-binding protein	89966	148328	129589	267	206049	241574	203276	472	0.770371697	0.788878747	1.767790262	0.821947118
BP1026B_10140	putative phage-encoded membrane protein	107249	174229	165029	205	224029	257177	227809	326	0.43165309	0.457035867	1.590243902	0.669248055
predicted RNA	-	16588	27008	23783	440	37806	45439	39629	803	0.637438936	0.660197087	1.825	0.867896464
BP1026B_10141	hypothetical protein	186738	331860	283593	618	370459	444990	390928	930	0.024017832	0.028731526	1.504854369	0.589623878
BP1026B_10142	hypothetical protein	124489	179851	155387	139	167278	184658	206327	169	4.78E-05	6.93E-05	1.215827338	0.281938364
BP1026B_10143	Phage-related tail protein	1466	845	857	2	525	653	420	1	7.88E-14	2.35E-13	0.5	-1
BP1026B_10144	bacteriophage tail protein	12463	13889	12018	4	14924	14646	14542	4	1.34E-07	2.32E-07	1	0
BP1026B_10145	hypothetical protein	1079	1427	1848	12	2373	2104	1581	17	0.771057487	0.789451995	1.416666667	0.502500341
BP1026B_10146	putative phage tail protein	1776	1894	1941	5	2103	2858	2141	6	0.114664863	0.129387724	1.2	0.263034406
BP1026B_10147	Major tail tube protein	3071	5136	5623	9	6014	6749	6500	12	0.002009008	0.002603069	1.333333333	0.415037499
BP1026B_10148	Phage tail sheath monomer	2777	3093	2229	2	2588	2327	2182	2	3.84E-07	6.48E-07	1	0
BP1026B_10149	phage tail fiber assembly protein	1307	1366	977	1	1387	1052	949	1	0.00246965	0.003182811	1	0
BP1026B_10150	Phage-related tail fiber protein	5741	6250	5385	2	6413	5043	4659	2	1.17E-10	2.61E-10	1	0
BP1026B_10151	phage tail protein I	1930	729	1178	2	1056	646	783	1	4.75E-09	9.28E-09	0.5	-1
BP1026B_10152	phage baseplate assembly protein	5666	3538	3392	4	2794	3780	3553	3	1.46E-11	3.54E-11	0.75	-0.415037499
BP1026B_10153	Phage baseplate assembly protein	413	684	448	1	752	406	471	1	0.258985278	0.280955982	1	0
BP1026B_10154	baseplate assembly protein V	1190	1100	1156	1	1137	978	1254	1	0.09060356	0.011824701	1	0
BP1026B_10157	hypothetical protein	204491	356398	3261699	5866	2664367	3237209	2766575	5732	0.899992211	0.91089504	0.977156495	-0.033338461
predicted RNA	-	26222	45295	47432	3304	41171	53108	28902	3421	5.66E-09	1.10E-08	1.035411622	0.050204417
BP1026B_10158	Phage tail completion protein	13704	14994	15205	31	19616	18731	16571	39	6.72E-06	1.04E-05	1.258064516	0.331205908
BP1026B_10159	bacteriophage tail completion protein R	1951	3021	3043	6	4513	3117	3570	8	0.17936568	0.198219639	1.333333333	0.415037499
BP1026B_10160	Prophage LysC protein	275	144	274	1	84	130	115	0	6.57E-05	9.45E-05	0	#NUM!
BP1026B_10161	Putative phage-encoded lipoprotein	662	539	831	1	371	624	756	1	0.007415305	0.009193569	1	0
BP1026B_10162	Putative phage-encoded peptidoglycan binding protein	1383	1413	1407	1	1260	1290	1518	1	0.003239058	0.004139494	1	0
BP1026B_10163	Prophage membrane protein	878	424	488	2	538	777	865	2	0.735261316	0.754898805	1	0
BP1026B_10164	Prophage membrane protein	115	97	80	0	144	102	17	0	0.809099373	0.82543417	#DIV/0!	#DIV/0!
BP1026B_10165	Phage-related tail protein	137	114	173	0	65	58	259	0	0.493017831	0.518330491	#DIV/0!	#DIV/0!
BP1026B_10166	putative bacteriophage protein	143	35	32	0	46	58	50	0	0.267861979	0.290334399	#DIV/0!	#DIV/0!
BP1026B_10167	Phage head completion-stabilization protein	310	96	187	0	154	235	95	0	0.186915858	0.206163486	#DIV/0!	#DIV/0!
BP1026B_10168	Phage terminase, endonuclease subunit	969	713	495	1	995	510	664	1	0.069677099	0.080227252	1	0
BP1026B_10169	Phage major capsid protein	2882	3327	3107	3	3315	3473	2957	3	1.30E-04	1.84E-04	1	0
BP1026B_10170	Phage capsid scaffolding protein	1049	1131	1146	1	878	1186	1111	1	0.005544937	0.006951696	1	0
BP1026B_10171	Phage terminase, ATPase subunit	5608	4376	5798	2	5334	3944						

BP1026B_10192	type VI secretion system	64788	71260	70105	62	74013	80468	71976	68	2.86E-10	6.19E-10	1.096774194	0.133266531
BP1026B_10193	type VI secretion system	254396	204854	216056	84	194008	181619	190025	70	1.75E-20	9.28E-20	0.833333333	-0.263034406
BP1026B_10194	type VI secretion system	64298	68176	65539	58	59201	54624	58772	51	6.90E-20	3.51E-19	0.879310345	-0.185555653
BP1026B_10195	type VI secretion system	125953	141056	137334	144	134418	144375	124397	144	2.70E-12	7.01E-12	1	0
BP1026B_10196	type VI secretion system	137165	151219	150468	147	144508	131104	151371	143	6.25E-13	1.72E-12	0.972789116	-0.039801008
BP1026B_10197	type VI secretion system	748119	863467	837708	209	790956	800812	793912	204	0.586653401	0.611032282	0.976076555	-0.03493379
BP1026B_10198	hypothetical protein	61692	77555	74841	135	95349	105315	99044	189	0.001305399	0.001708717	1	0
BP1026B_10199	hypothetical protein	130766	128477	139285	137	118265	121188	106381	118	1.51E-19	7.47E-19	0.861313869	-0.215389034
BP1026B_10200	ToIC family type I secretion outer membrane protein	16488	11707	14153	9	10580	9203	10454	7	5.72E-25	4.39E-24	0.777777778	-0.362570079
BP1026B_10201	colicin V processing peptidase	10548	12582	10719	4	9028	10233	11585	4	4.07E-13	1.14E-12	1	0
BP1026B_10202	secretion protein	2740	2804	2205	2	2712	3116	3008	2	0.004122436	0.005215261	1	0
BP1026B_10203	hypothetical protein	814	758	735	4	1018	1145	894	5	0.873782419	0.887377737	1.25	0.321928095
BP1026B_10204	hypothetical protein	123632	132546	124461	549	165105	170164	181083	745	0.006691395	0.008342277	1.35701275	0.440434276
BP1026B_10205	hypothetical protein	51697	53000	51266	219	62336	63846	55704	255	1.15E-07	2.00E-07	1.164383562	0.219566377
BP1026B_10206	peptidase	236377	339243	312176	136	261287	277125	264312	123	3.32E-15	1.13E-14	0.904411765	-0.144948336
BP1026B_10207	hypothetical protein	1744	1445	2174	15	2534	2203	2458	21	0.289332971	0.312417783	1.4	0.485426827
BP1026B_10208	lipoprotein	34308	30450	31460	63	30284	28124	30177	58	1.36E-11	3.29E-11	0.920634921	-0.119298928
BP1026B_10209	acyltransferase family protein	4627	4536	4529	4	3703	5353	4876	4	2.09E-07	3.58E-07	1	0
BP1026B_10210	methyltransferase small domain-containing protein	27074	9759	13389	14	9789	7818	10169	8	2.77E-48	8.26E-47	0.571428571	-0.807354922
BP1026B_10211	hypothetical protein	116579	143520	142064	148	162126	158014	160423	177	2.22E-05	3.29E-05	1.195945946	0.258152184
BP1026B_10212	hypothetical protein	54484	67718	65385	100	72840	76112	74484	119	1.18E-07	2.06E-07	1.19	0.250961574
BP1026B_10213	TetR family transcriptional regulator	17348	25056	22140	33	23442	24913	24296	37	6.29E-07	1.05E-06	1.121212121	0.165059246
BP1026B_10214	hypothetical protein	233	23	73	0	117	136	47	0	0.818032499	0.834275983	#DIV/0!	#DIV/0!
BP1026B_10215	monocarboxylate MFS permease	14323	12089	13602	10	9451	9305	9014	7	2.90E-27	2.69E-26	0.7	-0.514573173
BP1026B_10216	predicted RNA	20758	8330	13374	416	10439	5373	10115	254	1.30E-38	2.38E-37	0.610576923	-0.711755031
BP1026B_10217	nitroreductase family protein	176021	149537	166107	270	138374	136652	129658	222	6.73E-23	4.40E-22	0.822222222	-0.283299731
BP1026B_10218	molecular chaperone, Hsp70 class	35123	31449	29384	25	30501	35751	31934	25	1.95E-08	3.61E-08	1	0
BP1026B_10219	cold shock transcription regulator protein	68169	118552	101043	470	180285	208413	208447	975	0.068574124	0.078986298	2.074468085	1.052741462
BP1026B_10220	amino acid permease	105162	120540	118357	71	112531	118170	113720	71	2.02E-12	5.32E-12	1	0
BP1026B_10221	class III extradiol-type catechol dioxygenase family protein	3887	3998	2980	4	3842	4259	3343	4	2.49E-05	3.69E-05	1	0
BP1026B_10222	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	139163	96731	113529	195	104187	94231	105721	169	1.39E-19	6.94E-19	0.866666667	-0.206450877
BP1026B_10223	glutaredoxin-like protein	326581	551969	495888	1482	646110	765331	678791	2254	0.144700121	0.161620491	1.520917679	0.604942068
BP1026B_10224	protein methyltransferase HemK	8686	3894	4544	6	3542	4580	4527	4	4.61E-19	2.19E-18	0.666666667	-0.584962501
BP1026B_10225	peptide chain release factor 1	33383	36751	35305	32	38405	38123	37845	35	2.89E-07	4.91E-07	1.09375	0.129283017
BP1026B_10226	glutamyl-tRNA reductase	485808	409195	405780	333	459959	459610	458162	353	2.18E-08	4.03E-08	1.0600006	0.084146006
BP1026B_10227	hypothetical protein	3818	3177	3860	15	3593	3318	3549	14	1.31E-06	2.12E-06	0.933333333	-0.099535674
BP1026B_10228	peptidase, M24 family protein	130646	101081	101300	61	95094	80362	91493	49	1.14E-26	1.00E-25	0.803278689	-0.316027493
BP1026B_10229	isochorismatase family protein	10762	9122	8822	17	9942	8765	8965	16	1.67E-11	4.01E-11	0.941176471	-0.087462841
BP1026B_10230	hydrolase	52226	65454	63860	96	64388	69167	61277	104	7.01E-11	1.59E-10	1.083333333	0.115477217
BP1026B_10231	ABC transporter ATP-binding protein	340972	457203	429185	245	455287	484598	486955	285	3.72E-06	5.86E-06	1.163265306	0.21818017
BP1026B_10232	hypothetical protein	1676	1214	957	4	1051	591	926	2	1.48E-08	2.77E-08	0.5	-1
BP1026B_10233	glycophosphoryl diester phosphodiesterase family protein	29494	12634	16772	20	12210	10224	12006	11	2.54E-43	5.96E-42	0.55	-0.862496476
BP1026B_10234	hypothetical protein	25727	27080	26929	155	24926	25477	21213	139	1.20E-13	3.53E-13	0.896774194	-0.157183333
BP1026B_10235	GABA permease	195552	215143	213890	148	188610	187073	199105	136	1.76E-15	6.17E-15	0.918918919	-0.121990524
BP1026B_10236	AraC/XyIS family transcriptional regulator	32942	15140	17763	26	11930	11700	13586	14	2.96E-49	9.14E-48	0.538461538	-0.893084796
BP1026B_10237	NADH dehydrogenase subunit B	39677	31981	33629	69	33017	29999	29570	61	2.64E-13	7.55E-13	0.884057971	-0.177787119
BP1026B_10238	hypothetical protein	11323	9494	9482	35	9403	9442	11243	35	2.72E-10	5.89E-10	1	0
BP1026B_10239	GTP-dependent nucleic acid-binding protein EngD	162235	173898	167494	153	190261	189911	196479	175	6.93E-07	1.15E-06	1.14379085	0.193823269
BP1026B_10240	hypothetical protein	274454	409638	377563	966	452108	515818	434232	1277	6.53E-04	8.75E-04	1.32194617	0.402663431
BP1026B_10241	putative lipoprotein	906	1664	1180	9	1126	1454	1481	10	0.0558977	0.064934184	1.111111111	0.152003093
BP1026B_10242	ubiquinone biosynthesis hydroxylase family protein	295142	174613	210954	193	158961	131108	156784	126	2.24E-41	4.72E-40	0.652849741	-0.615177114
BP1026B_10243	thiol disulfide interchange protein DsbC	395763	480492	469378	615	569012	631182	598941	822	0.563153026	0.588217514	1.336585366	0.418551983
BP1026B_10244	peptidase	137180	122372	127773	70	116022	109975	119045	62	4.97E-18	2.17E-17	0.885714286	-0.175086707
BP1026B_10245	acyl carrier protein phosphodiesterase	48553	52846	49172	84	50023	50022	50724	84	8.48E-12	2.10E-11	1	0
BP1026B_10246	uncH-DNA glycosylase	19695	11978	12965	18	10502	9836	10470	13	2.71E-27	2.52E-26	0.722222222	-0.469485283
BP1026B_10247	adenylate cyclase	21453	11666	13287	23	11690	9741	11111	16	1.35E-26	1.19E-25	0.695652174	-0.523561956
BP1026B_10248	Indole-3-glycerol phosphate synthase	86341	84084	83373	107	89778	91624	92775	116	1.12E-10	2.49E-10	1.08411215	0.116514009
BP1026B_10249	anthranilate phosphoribosyltransferase	85158	76271	80427	78	80137	78836	77987	76	5.08E-15	1.70E-14	0.974358974	-0.037474705
BP1026B_10250	anthranilate synthase component II	65302	80186	74094	123	89198	96763	85301	152	1.23E-06	1.99E-06	1.235772358	0.305413008
BP1026B_10251	anthranilate synthase component I	130255	136244	134711	89	146645	152242	143271	98	4.96E-08	8.89E-08	1.101123596	0.138976413
BP1026B_10252	phosphoglycolate phosphatase	53721	63554	59556	80	67002	66357	65369	90	3.20E-09	6.36E-09	1.125	0.169925001
BP1026B_10253	ribulose-phosphate 3-epimerase	73542	71201	75386	105	83508	84448	82160	119	2.82E-09	5.64E-09	1.133333333	0.180572246
BP1026B_10254	ApaG protein	73161	103236	90758	237	100970	110119	98783	275	1.17E-07	2.04E-07	0.37033553	0.21454456
BP1026B_10255	hypothetical protein	19310	32342	30872	191	42737	49274	33859	291	0.048197575	0.056344403	1.523560209	0.607446515
BP1026B_10256	membrane-bound lytic murein transglycosylase A	191739	221169	224321	189	194974	175147	194701	168	3.04E-17	1.25E-16	0.888888889	-0.169925001
BP1026B_10257	phenylacetate-CoA ligase	45203	51937	49286	37	51382	55619	54299	41	1.09E-08	2.06E-08	1.108108108	0.148098639
BP1026B_10258	phenylacetic acid degradation protein Paal	18848	22049	21277	52	25712	26586	27970	68	4.64E-04	6.29E-04	1.307692308	0.387023123
BP1026B_10259	enoyl-CoA hydratase	28107	22355	22762	30	18258	16671	20116	23	3.30E-27	3.03E-26	0.766666667	-0.383328664
BP1026B_10260	beta-ketoadipyl CoA thiolase	47800	32405	33740	31	26660	27758	25719	22	4.27E-25	3.31E-24	0.709677419	-0.494764692
BP1026B_10261	phenylacetic acid degradation protein paaN	133920	123224	129663	75	105008	107273	107045	62	1.32E-22	8.42E-22	0.766666667	-0.27462238
BP1026B_10262	enoyl-CoA hydratase	27032	41914	34197	44	40286	45460	41918	54	9.15E-05	1.30E-04	1.227272727	0.295455884
BP1026B_10263	hypothetical protein	98673	149493	118040	1043	216130	233381	221542	1911	0.459058057	0.48474179	1.832214765	0.873558862
BP1026B_10264	16S ribosomal RNA	1470237	358169	295827	466	5544830	1230315	257158	1543	1.82E-14	5.77E-14	3.311158798	1.727336202
BP1026B_10265	16S ribosomal RNA	36831	54022	44410	585	77275	82340	72686	1005	0.412500186	0.437866536	1.717948718	0.780666972
BP1026B_10266	Ala tRNA	195031	304882	242783	3257	396210	428516	432916	5515	0.367001632	0.391493399	1.693276021	0.759817166
BP1026B_10267													

BP1026B_10288	AhpC/TSA family protein	857138	689646	720051	1490	642471	610704	623453	1233	0.101021406	0.114632403	0.827516779	-0.273139531
predicted RNA	-	132343	51281	94997	1407	41102	18751	39448	501	1.16E-147	1.82E-145	0.356076759	-1.48973982
BP1026B_10289	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	496524	609190	564234	587	781095	779230	829234	840	0.042058826	0.049416246	1.43100051	0.517028825
BP1026B_10290	hypothetical protein	13158	8202	8557	20	8199	5369	8554	15	1.35E-23	9.31E-23	0.75	-0.415037499
BP1026B_10291	preprotein translocase subunit SecA	1055192	1253750	1222942	422	1375846	1421069	1392804	90	0.082948791	0.094846191	1.187203791	0.247567604
BP1026B_10292	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase	102084	124976	115788	92	116218	111511	120995	93	8.68E-12	2.15E-11	1.010869565	0.015596855
BP1026B_10293	putative ATP/GTP-binding protein	92774	122008	110813	124	131359	132799	135817	153	1.03E-05	1.57E-05	1.233870968	0.303191532
BP1026B_10294	NUDIX family pyrophosphatase	56357	70635	71787	147	74667	72190	66894	158	6.93E-11	1.57E-10	1.074829932	0.104108403
BP1026B_10295	hypothetical protein	32098	43117	37962	184	53089	55090	63977	281	0.044079377	0.051732792	1.527173913	0.610864364
BP1026B_10296	hypothetical protein	799699	1117708	1018576	1294	1239667	1309331	1264811	1681	0.045685598	0.053537676	1.299072643	0.377482107
BP1026B_10297	dephospho-CoA kinase	45239	47038	48967	76	44798	42322	53355	76	1.78E-11	4.27E-11	1	0
BP1026B_10298	peptidase A24 N-domain-containing protein	19257	17404	16628	19	16254	15362	16034	17	9.45E-17	3.70E-16	0.894736842	-0.160464672
BP1026B_10299	type IV pilus assembly protein PilC	9750	6486	7880	6	6999	5998	6398	5	5.61E-18	2.43E-17	0.833333333	-0.263034406
BP1026B_10300	type IV fimbrial biogenesis protein, PilB	7502	5192	5214	4	4005	4971	4063	3	2.33E-17	9.63E-17	0.75	-0.415037499
BP1026B_10301	hypothetical protein	80094	111498	102713	81	121433	127148	134590	105	1.16E-04	1.64E-04	1.296296296	0.374395515
BP1026B_10302	Pro tRNA	12836	19503	15883	208	26464	28825	29606	367	0.618383608	0.641628033	1.764423077	0.819196535
BP1026B_10303	octaprenyl-diphosphate synthase	212327	303692	279204	266	318187	351290	347431	341	9.93E-05	1.41E-04	1.281954587	0.358345494
BP1026B_10304	50S ribosomal protein L27	472653	598524	598016	2107	622575	624397	630754	2370	0.8602107	0.874823935	1.124822022	0.169696745
BP1026B_10305	GTPase OhgE	382683	418536	404046	359	479659	423259	473076	409	2.15E-06	3.43E-06	1.139275766	0.188116999
BP1026B_10306	gamma-glutamyl kinase	106108	113283	107707	97	122837	119578	120875	108	9.61E-09	1.83E-08	1.113402062	0.15497466
BP1026B_10307	lipoprotein	27254	38872	35576	60	48690	50266	44978	85	0.007306395	0.009067512	1.416666667	0.502500341
BP1026B_10308	dimucopeptide polyphosphate hydrolase	474179	769531	668874	988	870120	1013248	911069	1430	0.011672601	0.014296427	1.447368421	0.5334322
BP1026B_10309	prolyl-tRNA synthetase	608678	674214	660282	379	661862	647304	659380	384	0.588754067	0.612908315	1.031392612	0.018908463
BP1026B_10310	hypothetical protein	153206	201638	183490	297	195524	209873	220320	345	7.32E-07	1.21E-06	1.161616162	0.216133431
BP1026B_10311	hypoxanthine-guanine phosphoribosyltransferase	56600	80698	74779	127	92289	94602	92917	168	6.40E-05	9.21E-05	1.322834646	0.403632736
BP1026B_10312	signal recognition particle protein	158971	170030	166045	120	174015	166104	174909	125	1.55E-09	3.16E-09	1.041666667	0.058893689
BP1026B_10313	cytochrome C assembly family protein	44145	45942	45218	50	59923	56956	61233	65	2.01E-04	2.80E-04	1.3	0.378511623
BP1026B_10314	hypothetical protein	24140	21099	19590	67	25869	27409	28751	85	2.35E-04	3.26E-04	1.268656716	0.343301746
BP1026B_10315	N-acetyl-anhydromuramyl-L-alanine amidase	38038	38154	35549	63	42423	43126	45752	74	6.22E-06	9.63E-06	1.174603175	0.232173442
BP1026B_10316	ribonucleotide-diphosphate reductase subunit alpha	188047	220731	216042	69	246638	250740	256955	84	2.30E-05	3.41E-05	1.217391304	0.283792966
BP1026B_10317	ribonucleotide-diphosphate reductase subunit beta	737307	1120662	990871	783	1180651	1277706	1232452	1015	0.04740516	0.055428388	1.296296296	0.374395515
BP1026B_10318	HcbB	6776623	9600537	8908081	14117	9407945	9866121	9785805	16225	0.001773629	0.002307153	1.149323511	0.200784944
BP1026B_10319	outer membrane lipoprotein	309934	196527	231419	519	197131	172143	201049	401	2.88E-26	2.44E-25	0.772639692	-0.372132302
BP1026B_10320	sugar kinase	583940	563319	588071	616	566020	542948	570937	596	0.086912081	0.099292092	0.967532468	-0.04761802
BP1026B_10321	thiol peroxidase	148751	129272	144791	279	126975	118360	115813	238	1.23E-20	6.57E-20	0.853046595	-0.229303549
BP1026B_10322	hypothetical protein	55663	58304	56627	39	62118	54746	56698	40	2.62E-12	6.82E-12	1.025641026	0.036525876
BP1026B_10323	acetyl-CoA carboxylase biotin carboxylase subunit	192011	254888	239234	167	244636	257375	249733	183	5.97E-08	1.07E-07	1.095808383	0.131995546
BP1026B_10324	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	41717	57131	53590	107	57834	68667	67799	136	1.99E-05	2.97E-05	1.271028037	0.345995855
BP1026B_10325	3-dehydroquinate dehydratase	132016	130408	134563	292	130010	120718	145079	291	2.02E-12	5.30E-12	0.996575342	-0.004994192
BP1026B_10326	thioredoxin	70847	112138	96207	165	130369	146531	137341	246	0.022468674	0.026950365	1.490900901	0.576192291
BP1026B_10327	hypothetical protein	95184	70442	72833	120	99450	88756	92242	142	8.38E-08	1.48E-07	1.183333333	0.242856524
BP1026B_10328	UDP-N-acetylmuramate L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase	192503	243873	230899	146	262751	282028	274729	180	7.40E-05	1.06E-04	1.232876712	0.302028537
BP1026B_10329	esterase	19437	14103	13618	27	16587	14613	15507	27	2.25E-12	5.89E-12	1	0
BP1026B_10331	ribonuclease II (RNB) family protein	134816	130625	132656	63	129121	124876	126088	60	1.58E-14	5.03E-14	0.952380952	-0.070389328
BP1026B_10330	shikimate 5-dehydrogenase	20956	19169	19509	22	20022	21678	17470	22	2.98E-12	7.69E-12	1	0
BP1026B_10332	monofunctional biosynthetic peptidoglycan transglycosylase	18309	16398	17155	22	18068	15762	16279	21	1.59E-13	4.62E-13	0.954545455	-0.067114196
BP1026B_10333	hypothetical protein	2507	2677	2084	12	3488	3745	3148	17	0.314049943	0.337478467	1.416666667	0.502500341
BP1026B_10334	hypothetical protein	455	782	537	3	713	1233	802	4	0.233270689	0.254691434	1.333333333	0.415037499
BP1026B_10335	serine-type carboxypeptidase family protein	246080	314714	308753	177	314939	316896	308436	191	1.08E-08	2.04E-08	1.079096045	0.109823278
BP1026B_10336	hypothetical protein	14441	16969	16991	40	15976	19703	14067	41	3.14E-11	7.36E-11	1.025	0.03562391
BP1026B_10337	transcriptional regulator	37282	19867	22600	29	19744	19385	19664	21	1.74E-27	1.65E-26	0.724137931	-0.465663572
BP1026B_10338	2-dehydro-3-deoxygalactonokinase	4894	2890	3094	3	2781	2669	2111	2	4.33E-15	1.45E-14	0.666666667	-0.584962501
BP1026B_10339	2-dehydro-3-deoxy-6-phosphogalactonate aldolase	9251	5142	5344	9	4661	3401	4102	5	4.19E-25	3.25E-24	0.555555556	-0.847996907
BP1026B_10340	short chain dehydrogenase	12526	4616	5963	9	4118	4274	4969	5	2.10E-31	2.51E-30	0.555555556	-0.847996907
BP1026B_10341	L-arabinose ABC transporter periplasmic L-arabinose-binding protein	15327	18240	15672	16	16039	16395	15469	16	3.87E-13	1.09E-12	1	0
BP1026B_10342	L-arabinose transporter ATP-binding protein	44099	37635	40844	27	33071	30743	34716	22	1.12E-17	4.75E-17	0.814814815	-0.295455884
BP1026B_10343	L-arabinose transporter permease	21392	16494	15530	17	15657	15522	18388	16	3.32E-15	1.13E-14	0.941176471	-0.087462841
BP1026B_10344	short chain dehydrogenase/reductase family oxidoreductase	8663	7652	8528	10	7893	9718	7294	10	8.23E-11	1.85E-10	1	0
BP1026B_10345	aldose 1-epimerase	11693	4448	6739	7	4902	4114	5303	4	3.99E-27	3.65E-26	0.571428571	-0.807354922
BP1026B_10346	orotidine 5'-phosphate decarboxylase	86228	97421	100176	114	89631	88123	93484	109	6.01E-16	2.20E-15	0.956140351	-0.064706689
BP1026B_10347	competence/damage-inducible protein ClnA	28677	17975	23902	46	18497	13492	17963	33	1.45E-31	1.76E-30	0.173991304	-0.479167837
BP1026B_10348	phosphatidylglycerophosphatase A	30605	41142	37978	59	39104	40054	44138	66	1.04E-06	1.70E-06	1.118644068	0.16175107
BP1026B_10349	thiamine monophosphate kinase	5880	5241	6620	7	6696	6806	5254	6	3.05E-12	7.86E-12	0.857142857	-0.222392421
BP1026B_10350	malic enzyme	584141	617494	607743	261	604589	613501	614837	264	0.469860658	0.495314078	1.011494253	0.016488123
BP1026B_10351	ribonuclease SA	93474	85406	82872	201	86054	86988	82865	197	3.66E-15	1.24E-14	0.980099502	-0.028999872
BP1026B_10352	barstar family protein	116176	173282	164182	257	181510	205685	214201	355	0.008852755	0.01092386	1.381322957	0.466050665
BP1026B_10353	16S ribosomal RNA methyltransferase RsmE	13659	5098	5958	10	5629	3661	4368	5	1.08E-35	1.71E-34	0.5	-1
BP1026B_10354	glyoxalase/bleomycin resistance protein/dioxigenase family protein	35978	35426	33129	83	32679	35765	38470	85	1.22E-08	2.30E-08	1.024096386	0.034351505
BP1026B_10355	spermidine synthase	41212	31945	33446	41	32956	32552	35361	39	7.34E-11	1.66E-10	0.951219512	-0.072149786
BP1026B_10356	transketolase	568823	533919	538016	263	564315	543594	556061	267	0.10424677	0.118142568	1.015209125	0.021776942
BP1026B_10357	glyceraldehyde-3-phosphate dehydrogenase, type I	1294335	1750096	1665010	1552	1923386	1967056	1877877	1901	0.087111554	0.099442703	1.224871134	0.292629974
BP1026B_10358	MFS transporter	3520	3708	2637	2	3083	3298	2942	2	1.57E-06	2.53E-06	1	0
BP1026B_10359	cyanate hydratase	2739	4071	4103	7	4325	4697	4287	9</				

BP1026B_10385	glutamate dehydrogenase	2303225	2193923	2228183	1717	2056873	2050973	2052838	1573	0.670492751	0.692142929	0.91613279	-0.126371369
BP1026B_10386	glutamate/aspartate periplasmic binding protein	3203310	4928241	4494758	4707	5062623	5653725	4916197	5815	0.366791355	0.391335711	1.235394094	0.304971339
BP1026B_10387	glutamate/aspartate transport system permease	1434669	230945	208701	262	212103	244004	235410	311	3.89E-06	6.11E-06	1.187022901	0.247347769
BP1026B_10388	glutamate/aspartate ABC transporter, permease protein	183833	231744	213352	309	207978	204673	223159	312	1.23E-11	3.00E-11	1.009708738	0.013939191
BP1026B_10389	Cystine ABC transporter, ATP-binding protein	383989	569901	541241	686	581128	632658	559532	814	0.860164421	0.874823935	1.186588921	0.246820218
BP1026B_10390	hypothetical protein	36638	59215	49171	189	60432	67801	65436	253	2.45E-04	3.39E-04	1.338624339	0.42075115
BP1026B_10391	chaperonin, 10 kDa	114141	15841	142655	435	181904	191660	186343	586	0.004939475	0.006219513	1.347126437	0.429885264
BP1026B_10392	HSP20 family protein	85500	121781	115296	243	157178	159938	133013	340	0.008155046	0.010086758	1.399176955	0.484578433
BP1026B_10393	HSP20 family protein	66548	54894	60080	144	63790	60408	58582	145	3.40E-13	9.60E-13	1.006944444	0.009984089
BP1026B_10394	hypothetical protein	29080	24549	28369	124	27906	26918	27343	125	3.33E-09	6.60E-09	1.008064516	0.011587974
BP1026B_10395	hypothetical protein	323750	476779	426331	430	502836	540100	520229	547	0.134194251	0.150503164	1.272093023	0.347204173
BP1026B_10396	dihydroorotase	51162	37416	43230	41	37876	33625	36313	33	1.38E-17	5.80E-17	0.804878049	-0.313157885
BP1026B_10397	hypothetical protein	11459	5608	7236	11	4948	5070	6669	7	4.12E-24	2.97E-23	0.636363636	-0.652076697
BP1026B_10398	hypothetical protein	24316540	40353143	35961912	360686	40945630	47308272	38297997	453591	0.156010273	0.17329558	1.257578614	0.330648589
BP1026B_10399	OsmC/Ohr family protein	76759	80223	76696	184	86673	92716	97500	218	1.16E-07	2.03E-07	1.184782609	0.244622369
BP1026B_10400	50S ribosomal protein L13	784712	1336394	1229570	2068	1770369	2061334	1753390	3447	0.00166839	0.002173549	1.666827853	0.737105113
BP1026B_10401	30S ribosomal protein S9	376653	474626	432268	1088	554119	616241	610340	1510	0.413459266	0.438810257	1.387867647	0.472869993
BP1026B_10402	iron-sulfur cluster insertion protein ErpA	488078	770057	661398	1733	1061309	1167249	1082405	2990	8.26E-04	0.001096726	1.725331795	0.78687383
BP1026B_10403	AraC family transcriptional regulator	27743	18538	19324	23	22701	21769	20783	23	3.54E-11	8.24E-11	1	0
BP1026B_10404	glutathione S-transferase	36394	50900	46143	63	47716	47957	45805	66	3.22E-09	6.40E-09	1.047619048	0.067114196
BP1026B_10405	glutathione S-transferase-like protein	53514	59674	60940	83	58915	56380	56257	81	1.31E-13	3.84E-13	0.975903614	-0.035189428
BP1026B_10406	anhydro-N-acetylmuramic acid kinase	47237	36646	35291	34	34884	35572	37390	30	7.02E-13	1.93E-12	0.882352941	-0.180572246
BP1026B_10407	tyrosyl-tRNA synthetase	186429	201139	201810	158	208074	212550	219158	171	4.82E-09	9.42E-09	1.082278481	0.114071767
BP1026B_10408	D-tyrosyl-tRNA(Tyr) deacylase	14056	7023	6262	20	6821	5922	7033	15	7.55E-24	5.30E-23	0.75	-0.415037499
BP1026B_10409	phosphoglycerate mutase	28143	23376	25937	38	23814	23959	23293	35	5.80E-13	1.60E-12	0.92102632	-0.11864496
BP1026B_10410	lipoprotein	15291	19908	16283	15	18442	18950	17550	16	4.46E-10	9.53E-10	1.066666667	0.093109404
BP1026B_10411	hypothetical protein	53276	26566	33012	39	21022	18648	24363	22	7.77E-50	2.50E-48	0.564102564	-0.8259706
BP1026B_10412	Holliday junction DNA helicase RuvB	179259	106897	122706	127	109966	101254	112119	100	1.33E-25	1.07E-24	0.787401575	-0.344828497
BP1026B_10413	Holliday junction DNA helicase RuvA	128847	131918	124135	220	131468	120942	137017	223	6.82E-12	1.70E-11	1.013636364	0.019540186
BP1026B_10414	Holliday junction resolvase	31946	19188	23542	45	16116	14943	16833	29	3.85E-40	7.58E-39	0.644444444	-0.63872101
BP1026B_10415	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	231275	204489	217854	139	200276	179145	204630	124	4.04E-17	1.64E-16	0.892086331	-0.164744762
BP1026B_10416	DNA-binding protein Fy1	23034	37907	33502	134	39311	45166	42278	180	0.001851048	0.002404367	1.343283582	0.425763906
BP1026B_10417	dihydrodiphenyl synthase	93375	89834	88900	89	110954	109833	109420	108	2.78E-06	4.42E-06	1.213483146	0.279154071
BP1026B_10418	hypothetical protein	32387	12265	16900	17	11133	8137	10899	8	1.73E-64	1.01E-62	0.470588235	-1.087462841
BP1026B_10420	aminopeptidase P	76779	39292	47852	38	38655	33212	37422	25	6.75E-32	8.36E-31	0.657894737	-0.604071324
BP1026B_10421	predicted RNA	159476	159044	167494	925	154512	143038	156111	864	2.07E-14	6.53E-14	0.934054054	-0.098422053
BP1026B_10419	glutathione S-transferase	130620	154284	153732	238	165484	161949	170329	271	1.25E-06	2.03E-06	1.138655462	0.18731278
BP1026B_10421	glutamate synthase domain-containing protein	135564	100729	109397	70	97182	91793	92140	57	6.51E-25	4.98E-24	0.814285714	-0.296393003
BP1026B_10422	tRNA-specific 2-thiouridylylase MmaA	129172	164371	147464	129	157181	157879	164760	141	6.38E-08	1.14E-07	1.09302256	0.128324097
BP1026B_10424	NUDIX domain-containing protein	10399	5806	5473	14	5981	5768	5155	11	1.67E-17	7.00E-17	0.785714286	-0.347923303
BP1026B_10423	NAD(P) transhydrogenase subunit alpha	240559	228408	249229	209	215071	214146	189235	180	1.09E-19	5.46E-19	0.861244019	-0.215506036
BP1026B_10426	NAD(P) transhydrogenase subunit alpha	79463	101311	92834	276	82593	90513	101915	277	1.72E-13	4.95E-13	1.006231842	0.005217709
BP1026B_10425	NAD(P) transhydrogenase subunit beta	563421	719136	660021	445	644709	679100	647590	451	0.595527807	0.619760378	1.013483146	0.019322097
BP1026B_10427	DeoR family transcriptional regulator	36584	28092	33860	47	27447	22622	24018	35	1.49E-21	8.64E-21	0.744680851	-0.425305835
BP1026B_10428	hypothetical protein	6655	6234	6894	16	7343	7184	7474	17	1.21E-07	2.12E-07	1.0625	0.087462841
BP1026B_10429	N6-adenine-specific DNA methylase	58133	33769	42186	34	32272	27443	32340	23	4.37E-27	3.96E-26	0.676470588	-0.563900885
BP1026B_10430	hypothetical protein	60526	41223	47146	23	36617	33039	38798	17	1.07E-24	7.97E-24	0.739130435	-0.436099115
BP1026B_10431	hypothetical protein	34888	22141	25115	35	20406	20225	23744	27	9.75E-22	5.76E-21	0.771428571	-0.374395515
BP1026B_10432	paraquat-inducible protein	178059	180285	190180	110	178402	170267	177430	105	4.53E-13	1.27E-12	0.954545455	-0.067114196
BP1026B_10433	paraquat-inducible protein	18204	19716	20056	29	16681	18045	17721	26	1.31E-16	5.06E-16	0.896551724	-0.157541277
BP1026B_10434	paraquat-inducible protein	63719	55656	53385	87	59497	56127	58438	88	9.40E-13	2.55E-12	1.011494922	0.016488123
BP1026B_10435	cytochrome B561	17246	18883	18522	32	22780	22005	23105	40	4.18E-05	6.67E-05	1.25	0.321928095
BP1026B_10436	YceI, base-induced periplasmic protein	117949	153798	140157	244	154913	154760	152988	274	3.79E-07	6.40E-07	1.12295082	0.167294745
BP1026B_10437	hypothetical protein	506721	636440	595695	1001	641781	668798	662277	1135	0.972548075	0.977383519	1.133866134	0.181250323
BP1026B_10438	major facilitator family transporter	10983	9728	8135	17	8554	9172	8661	16	9.17E-13	4.27E-13	0.941176471	-0.087462841
BP1026B_10439	preprotein translocase subunit SecF	266730	378669	341221	345	402937	454871	442635	455	5.36E-04	7.23E-04	1.31884058	0.399270183
BP1026B_10440	preprotein translocase subunit SecD	310052	216233	222615	123	203237	194660	206386	99	6.39E-24	4.51E-23	0.804878049	-0.313157885
BP1026B_10441	preprotein translocase subunit YajC	278952	442474	392655	1135	566351	647295	607946	1856	0.042756557	0.050208506	1.635242291	0.709504413
BP1026B_10442	queuine tRNA-ribosyltransferase	52475	64313	58528	48	65310	68399	63139	54	2.83E-09	5.65E-09	1.125	0.169925001
BP1026B_10443	S-adenosylmethionine-tRNA ribosyltransferase-isomerase	41516	27696	33931	31	27988	24791	26067	24	4.58E-20	2.36E-19	0.774193548	-0.36923381
BP1026B_10444	ATP-dependent DNA helicase RecG	92400	63399	67339	27	56527	52356	55696	20	6.86E-31	7.98E-30	0.740740741	-0.432959407
BP1026B_10445	oxidative stress regulatory protein	416134	396439	427457	430	409651	390407	431422	427	7.64E-10	1.60E-09	0.993023256	-0.01010059
BP1026B_10446	catalase/peroxidase HPI	364144	401998	393784	176	409054	413401	403114	186	5.17E-08	9.25E-08	1.056818182	0.079272192
BP1026B_10447	hypothetical protein	225	77	66	0	360	326	171	1	8.51E-06	1.30E-05	#DIV/0!	#DIV/0!
BP1026B_10448	Non-specific DNA-binding protein Dps /Iron-binding ferritin-like antioxidant protein	656328	809745	816630	1556	960875	1070263	910978	2005	0.034551538	0.040841339	1.288560411	0.365760176
BP1026B_10449	predicted RNA	45079	2281	6203	350	2582	814	3091	42	0	0	0.12	-3.058893689
BP1026B_10450	transcriptional regulator	17274	8029	9029	24	6330	6270	6924	13	8.11E-43	1.86E-41	0.541666667	-0.884522783
BP1026B_10450	4-hydroxybenzoate octaprenyltransferase	82518	87330	84986	101	84383	80981	88951	100	3.35E-14	1.04E-13	0.99009091	-0.014355293
BP1026B_10451	phosphate metabolism protein/1,5-bisphosphokinase PhnN	12591	7118	10146	17	9238	6065	8809	14	2.95E-19	1.42E-18	0.823299412	-0.280170919
BP1026B_10452	hypothetical protein	2761	886	1003	1	1053	1205	1105	1	3.92E-08	7.10E-08	1	0
BP1026B_10453	phosphonates metabolism transcriptional regulator PhnF	16170	12070	14062	18	12341	11663	12098	15	1.57E-16	6.04E-16	0.833333333	-0.263034406
BP1026B_10454	alkylphosphonate utilization operon protein PhnG	515	436	386	0	358	465	414	0	0.05850482	0.06783701	#DIV/0!	#DIV/0!
BP1026B_10455	carbon-phosphorus lyase complex subunit	1085	1019	951	1	581	984	1080	1	0.00101497	0.001339187	1	0
BP1026B_													

BP1026b_10480	ferrochelatase	95751	72325	83331	75	78934	67320	67142	64	2.07E-22	1.29E-21	0.853333333	-0.22881869
BP1026b_10481	heat shock protein 15	58589	36934	44291	114	35747	32594	33825	83	1.10E-23	7.67E-23	0.728070175	-0.457850583
BP1026b_10482	heat shock protein GrpE	570220	486997	502413	931	637644	599939	648567	1126	0.879502348	0.892174472	1.209452202	0.274353755
BP1026b_10483	hypothetical protein	166318	125827	132337	440	136871	122120	136668	410	1.47E-15	5.19E-15	0.931818182	-0.101879614
BP1026b_10484	molecular chaperone DnaK	3647305	4202833	4044280	2030	5419434	5435332	5175149	2735	0.599971029	0.623866324	1.34729064	0.430061106
BP1026b_10485	chaperone protein DnaJ	40794	34862	39867	770	40869	25526	39633	706	3.41E-12	8.76E-12	0.916883117	-0.125190262
BP1026b_10486	chorismate binding protein	616860	717860	67651	593	890871	973179	882335	809	0.024338166	0.029098063	1.364249578	0.448107598
BP1026b_10487	3-methyl-2-oxobutanoate hydroxymethyltransferase	338015	290188	292810	152	306616	279474	320917	150	1.62E-11	3.91E-11	0.986842105	-0.019108823
BP1026b_10488	deoxynucleoside kinase family protein	70412	60232	60308	78	51842	53078	51249	63	1.01E-22	6.50E-22	0.807692308	-0.308122295
BP1026b_10489	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase	31218	19863	24128	36	21745	20829	19419	30	1.11E-19	5.58E-19	0.833333333	-0.263034406
BP1026b_10490	polyA polymerase	71036	68923	74038	135	80477	74831	72031	143	1.73E-11	4.16E-11	1.059259259	0.08305574
BP1026b_10491	HAD family hydrolase	170162	149419	158785	103	146882	140876	140611	92	4.57E-17	1.85E-16	0.893203883	-0.162938571
BP1026b_10492	DnaA regulatory inactivator Hda	45715	54638	57865	76	67200	74821	63349	99	4.02E-05	5.86E-05	1.302631579	0.381429107
BP1026b_10493	predicted RNA	13506	7702	7006	12	7140	6023	7291	9	4.91E-24	3.50E-23	0.75	-0.415037499
BP1026b_10494	hypothetical protein	49467	20097	33890	626	21709	16140	20878	355	5.30E-53	1.93E-51	0.567092652	-0.818343633
BP1026b_10495	tRNA delta(2)-isopentenylpyrophosphate transferase	17484	13679	16060	39	14534	14092	14901	36	7.38E-15	2.43E-14	0.923076923	-0.115477217
BP1026b_10496	DNA mismatch repair protein	66894	46652	51518	56	43259	35562	42241	41	2.75E-26	2.34E-25	0.732142857	-0.449802917
BP1026b_10497	DedA protein	155402	95844	110505	58	89396	76249	86596	40	2.20E-39	4.17E-38	0.689655172	-0.5360529
BP1026b_10498	small-conductance mechanosensitive channel	63998	71841	68003	99	74911	71453	82000	111	1.30E-09	2.66E-09	1.121212121	0.165059246
BP1026b_10499	glutamine amidotransferase	101318	120072	121221	130	123899	127094	131351	145	1.75E-08	3.27E-08	1.15384615	0.157541277
BP1026b_10500	mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase	21956	28293	27057	30	29217	31816	29013	35	1.31E-05	1.98E-05	1.166666667	0.222392421
BP1026b_10501	capsular polysaccharide biosynthesis/export periplasmic protein WcbA	107827	164269	149884	98	164008	177699	164319	118	3.14E-05	4.62E-05	1.204081633	0.267933205
BP1026b_10502	capsular polysaccharide biosynthesis/export periplasmic protein WcbB	90320	149419	111626	61	122626	121255	121074	70	4.32E-08	7.79E-08	1.147540984	0.198545871
BP1026b_10503	capsular polysaccharide biosynthesis/export periplasmic protein WcbC	93465	138575	129192	104	167471	185185	169196	150	0.044885726	0.052629857	1.442307692	0.528378972
BP1026b_10504	capsular polysaccharide export inner-membrane protein	209801	312748	283373	230	317453	344637	326542	283	1.33E-05	2.01E-05	1.230434783	0.299168192
BP1026b_10505	putative ATP-binding ABC transporter capsular polysaccharide export protein	435535	743482	629727	401	749608	883187	815126	543	0.052315543	0.060919753	1.354114713	0.437349961
BP1026b_10506	Glycosyl transferase, group 1 family protein	77778	135465	120408	213	165977	187928	174191	337	0.304094764	0.327173385	1.582159624	0.661895161
BP1026b_10507	Capsular polysaccharide biosynthesis protein WcbF	204902	368477	313537	449	396759	457503	390771	631	0.003193269	0.004082641	1.405345212	0.49092456
BP1026b_10508	phosphohexose isomerase	282693	469996	393342	264	546912	618945	544841	395	0.230988909	0.252244075	1.496212121	0.581314724
BP1026b_10509	hypothetical protein	326997	537732	483459	339	621374	711187	616415	491	0.24888889	0.27075966	1.448377581	0.534437751
BP1026b_10510	capsular polysaccharide biosynthesis protein	25176	41558	34741	363	45183	51975	48029	520	0.010040673	0.012348352	1.432506887	0.518542075
BP1026b_10511	Glycosyl transferase, group 1 family protein	137836	221755	196131	287	224994	250749	236846	368	3.21E-04	4.40E-04	1.282229965	0.358655029
BP1026b_10512	capsular polysaccharide biosynthesis protein	303540	511746	430860	231	530901	623011	551036	316	0.598940843	0.622898476	1.367965368	0.452031707
BP1026b_10513	capsular polysaccharide biosynthesis protein WcbJ, NAD-dependent epimerase	213507	374679	321560	323	373912	435854	416477	436	9.37E-04	0.001239912	1.349845201	0.43279397
BP1026b_10514	GDP-mannose 4,6-dehydratase	100252	166896	151596	165	171711	189561	175454	212	7.16E-04	9.55E-04	1.284848485	0.36159824
BP1026b_10515	D,D-heptose 7-phosphate kinase	307885	517937	454844	420	494021	575912	541773	529	0.406231857	0.431432003	1.25952381	0.332878394
BP1026b_10516	D-glycero-D-manno-heptose 1-phosphatransferase	281964	478540	411125	375	443615	515021	465386	455	3.50E-05	5.13E-05	1.213333333	0.27897595
BP1026b_10517	D-glycero-D-manno-heptose 1,7-bisphosphatransferase	208435	339813	302865	337	342590	391225	340635	678	5.81E-05	8.39E-05	1.262569832	0.336363185
BP1026b_10518	phosphohexose isomerase	128757	197176	182190	297	183137	211249	204641	350	2.89E-06	4.58E-06	1.178451178	0.236891991
BP1026b_10519	capsular polysaccharide export protein	123937	206698	181987	307	192925	232296	194342	372	1.05E-05	1.59E-05	0.711726384	0.277063966
BP1026b_10520	short chain dehydrogenase/reductase family oxidoreductase	110547	181683	161097	125	170988	196338	177950	151	3.30E-05	4.84E-05	1.208	0.272620451
BP1026b_10521	undecaprenyl-phosphate galactosephosphotransferase	43657	34714	39171	67	35904	33600	34356	59	1.40E-13	4.09E-13	0.880597015	-0.183446445
BP1026b_10522	capsular polysaccharide biosynthesis protein WcbQ	66991	105053	91630	57	109088	122677	109272	74	6.57E-05	9.45E-05	1.298245614	0.376563351
BP1026b_10523	capsular polysaccharide biosynthesis fatty acid synthase	652525	579749	603985	80	526962	524318	551272	69	6.00E-04	8.07E-04	0.8625	-0.21340368
BP1026b_10524	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	87673	39837	45399	62	36220	31048	30703	35	2.20E-46	6.03E-45	0.564516129	-0.824913293
BP1026b_10525	class-4 aminotransferase	112889	100881	105590	80	97530	88498	98223	71	5.14E-19	2.43E-18	0.8875	-0.172180975
BP1026b_10526	acetyltransferase	18812	10082	12310	19	11435	10008	11090	15	1.93E-19	9.45E-19	0.789473684	-0.341036918
BP1026b_10527	hypothetical protein	28716	24062	22709	21	19543	18853	19919	16	1.49E-24	1.10E-23	0.761904762	-0.392317423
BP1026b_10528	hypothetical protein	5540	4208	4625	3	4441	3819	4261	3	1.36E-10	3.00E-10	1	0
BP1026b_10529	PAP2 family protein	1351	652	739	1	595	887	588	1	8.68E-05	1.24E-04	1	0
BP1026b_10530	hypothetical protein	174	203	125	1	213	231	150	2	0.64967632	0.672093747	2	1
BP1026b_10531	hypothetical protein	556	518	373	1	808	875	757	2	0.048605044	0.056799554	2	1
BP1026b_10532	AraC family transcriptional regulator	12842	12860	12029	13	10881	13599	14392	13	4.13E-10	8.84E-10	1	0
BP1026b_10533	undecaprenyl-phosphate galactosephosphotransferase	8740	5863	6424	6	4826	4071	6653	4	7.16E-19	3.36E-18	0.666666667	-0.584962501
BP1026b_10534	polysaccharide biosynthesis/export protein	4434	3514	3963	3	4224	3123	3437	2	1.23E-08	2.32E-08	0.666666667	-0.584962501
BP1026b_10535	protein-tyrosine-phosphatase	1038	557	939	1	906	518	652	1	0.001069693	0.001408721	1	0
BP1026b_10536	Tyrosine-protein kinase Wzc	13659	13120	11789	5	11681	12400	12558	5	2.48E-12	6.47E-12	1	0
BP1026b_10537	O-antigen transferase	2583	1894	2293	1	1961	1693	2055	1	7.31E-07	1.21E-06	1	0
BP1026b_10538	capsule polysaccharide biosynthesis protein	5292	6346	5261	4	6037	5581	5449	4	9.74E-09	1.86E-08	1	0
BP1026b_10539	serine O-acetyltransferase	2118	4285	2963	5	2976	2835	3395	5	1.38E-05	2.08E-05	1	0
BP1026b_10540	hypothetical protein	5932	6603	5838	6	6624	7254	6611	7	2.24E-07	3.83E-07	1.166666667	0.222392421
BP1026b_10541	Glycosyltransferase	2932	3593	3013	2	3157	2997	3099	2	6.85E-06	1.06E-05	1	0
BP1026b_10542	2-dehydro-3-deoxyphosphocetate aldolase	20100	22682	21186	25	19667	20286	21224	24	2.71E-13	7.71E-13	0.96	-0.058893689
BP1026b_10543	3-deoxy-manno-octulosonate-8-phosphatase	7769	5135	5685	11	4636	4467	3954	7	5.06E-19	2.39E-18	0.636363636	-0.652076697
BP1026b_10544	arabinose-5-phosphate isomerase	9335	7008	8036	8	5799	7442	6652	6	1.30E-17	5.51E-17	0.75	-0.415037499
BP1026b_10545	UTP-glucose-1-phosphate uridylyltransferase	25250	31023	29687	32	31276	33685	30223	35	1.51E-06	2.43E-06	1.09375	0.129283017
BP1026b_10546	hypothetical protein	3750	2186	3236	13	1942	2506	1650	8	1.37E-14	4.39E-14	0.615384615	-0.700439718
BP1026b_10547	regulator of flagellar biosynthesis FlhD	6152	4731	4822	22	4244	3527	5176	18	1.46E-12	3.89E-12	0.818181818	-0.289506617
BP1026b_10548	Lys tRNA	10590	14238	12699	164	15477	15556	20305	225	2.93E-04	4.04E-04	1.37195122	0.456229187
BP1026b_10549	hypothetical protein	2129314	2981338	2702344	3472	2955266	3048861	3025330	4013	0.682494127	0.703951967	1.155817972	0.208914208
BP1026b_10550	OmpA family outer membrane protein	1184139	1427121	1457454	2659	1494948	1550243	1327522	2857	0.167534703	0.185504939	1.074464084	0.103617259
BP1026b_10551	translocation protein TolB	518058	632838	595581	437	664122	689821	625591	495	0.972651142	0.977383519	1.132723112	0.179795245
BP1026b_10552	TolA protein	50010	38509	42589	46	44506	44166	37639	44	9.09E-12	2.24E-11	0.956521739	-0.064130337
BP1026b_10553	TolR protein	55079	49151	58299	120	42778	40727	42186	93				

BP1026b_10573	FAD-dependent oxidoreductase	12047	12444	13022	7	12992	12449	13242	7	4.66E-10	9.94E-10	1	0
BP1026b_10574	hypothetical protein	685	927	834	3	1136	1217	936	4	0.954456115	0.961051264	1.333333333	0.415037499
BP1026b_10575	4-hydroxybenzoate transporter	7637	3415	3983	3	3161	2713	2768	2	6.24E-26	5.15E-25	0.666666667	-0.584962501
BP1026b_10577	homogenisate 1,2-dioxygenase	14957	14476	14813	11	13596	12130	12481	9	1.47E-16	5.68E-16	0.818181818	-0.289506617
BP1026b_10576	fumarylacetoacetase	15410	10034	10570	9	10619	8532	8915	7	3.04E-20	1.58E-19	0.777777778	-0.362570079
BP1026b_10578	major facilitator superfamily transporter	11860	5030	7365	6	5283	4845	4662	4	1.09E-29	1.19E-28	0.666666667	-0.584962501
BP1026b_10579	major facilitator superfamily transporter	36122	21466	27137	25	20009	16912	16879	16	1.22E-41	2.63E-40	0.64	-0.64385619
BP1026b_10580	nitroreductase family protein	3296	2526	2618	4	2984	1734	3215	4	5.18E-06	8.06E-06	1	0
BP1026b_10581	D-lactate dehydrogenase	189972	244066	240116	223	230104	241449	232608	233	7.38E-10	1.55E-09	1.044843049	0.063286245
BP1026b_10582	LysR family transcriptional regulator	1594817	2017172	1927784	1882	2011851	2063070	2085961	2093	0.250317631	0.272118368	1.112114772	0.153305684
BP1026b_10583	alanine-glyoxylate aminotransferase	318590	247618	271321	229	253537	240254	257313	206	4.01E-16	1.49E-15	0.899563319	-0.152703261
BP1026b_10584	AraC family transcriptional regulator	41880	22329	25685	31	25890	24051	23492	25	2.53E-17	1.04E-16	0.806451613	-0.310340121
BP1026b_10585	membrane protein	15782	15676	13965	16	17324	14768	14992	17	8.69E-11	1.95E-10	1.0625	0.087462841
BP1026b_10586	major facilitator superfamily transporter	23676	13219	14061	13	14885	14362	16469	12	2.39E-16	9.04E-16	0.923076923	-0.115477217
BP1026b_10587	xanthine dehydrogenase subunit A	24136	14866	18978	12	11940	12002	10524	7	1.29E-41	2.76E-40	0.583333333	-0.777607579
BP1026b_10588	xanthine dehydrogenase, subunit B	28988	25193	25107	11	14717	14962	16206	6	3.54E-51	1.19E-49	0.545454545	-0.874469118
BP1026b_10589	solute-binding periplasmic protein	14909	9915	9780	14	9189	6594	9014	10	4.04E-26	3.39E-25	0.714285714	-0.485426827
BP1026b_10590	hypothetical protein	21296	14612	15295	42	11331	11119	11019	27	3.57E-32	4.52E-31	0.642857143	-0.637429921
BP1026b_10591	predicted RNA	61676	35976	42082	523	34197	33143	29067	361	4.42E-27	3.84E-26	0.690248566	-0.534812109
BP1026b_10592	TonB-dependent siderophore receptor family protein	49832	22197	28003	15	20562	21704	22119	10	5.36E-36	8.61E-35	0.666666667	-0.584962501
BP1026b_10593	iron chelate uptake ABC transporter, ATP-binding component	9174	5096	6495	8	4258	4100	4963	5	3.50E-24	2.53E-23	0.625	-0.678071905
BP1026b_10594	periplasmic binding protein	26301	22642	24894	23	22683	22101	24739	22	2.67E-12	6.93E-12	0.956521739	-0.064130327
BP1026b_10595	FecCD-family membrane transporter protein	6239	1885	2766	3	1675	1119	1619	1	1.73E-43	4.09E-42	0.333333333	-1.584962501
BP1026b_10596	LysR family regulatory protein	23580	10058	13301	16	10715	11172	9898	11	7.24E-29	7.53E-28	0.6875	-0.540568381
BP1026b_10597	DSBA-like thiorodoxin domain-containing protein	79939	75480	71971	118	80168	84440	73637	124	3.70E-12	9.45E-12	1.050847458	0.071552361
BP1026b_10598	hypothetical protein	36182	34764	35658	24	34984	35764	34849	24	1.55E-09	3.16E-09	1	0
BP1026b_10599	phospholipid-binding domain-containing protein	75296	61153	57781	175	57219	58918	60094	159	6.74E-18	2.91E-17	0.908571429	-0.138328157
BP1026b_10600	D-(-)-3-hydroxybutyrate-oligomer hydrolase	206707	174721	186242	90	165285	159898	151027	75	3.56E-20	1.84E-19	0.833333333	-0.263034406
BP1026b_10601	hypothetical protein	300	874	301	4	495	546	566	4	0.372220982	0.396723366	1	0
BP1026b_10602	hypothetical protein	6616	8692	6847	23	9197	11826	10052	33	0.002550941	0.003284874	1.434782609	0.520832163
BP1026b_10603	serine-type carboxypeptidase family protein	122954	141398	143532	74	113974	104205	111644	60	4.87E-24	3.48E-23	0.810810811	-0.302562777
BP1026b_10604	permease	24073	16711	15781	23	19288	16698	19579	23	4.49E-13	1.28E-12	1	0
BP1026b_10605	EmrB-QacA family drug resistance transporter	24783	23073	23282	16	24075	23788	22075	16	7.91E-11	1.79E-10	1	0
BP1026b_10606	glycerophosphoryl diester phosphodiesterase family protein	87234	73517	83135	71	65527	57572	62983	54	8.39E-30	9.17E-29	0.76056338	-0.394859617
BP1026b_10607	amino acid transporter LysE	8997	7522	6328	12	6308	7459	7340	11	6.28E-13	1.73E-12	0.916666667	-0.125530882
BP1026b_10608	acetyltransferase	1001	541	538	1	605	464	667	1	0.003385423	0.004319499	1	0
BP1026b_10609	DNA-binding protein	4153	2501	3056	5	2091	2409	2307	3	1.10E-13	3.26E-13	0.6	-0.736965594
BP1026b_10610	metallo-beta-lactamase family protein	40976	62443	52961	42	54388	58538	47596	43	2.77E-11	6.52E-11	1.023809524	0.033947332
BP1026b_10611	transcriptional regulator	11380	14722	11379	28	16669	16952	18670	39	6.05E-04	8.13E-04	1.392857143	0.478047297
BP1026b_10612	lipoprotein	79249	86727	83509	52	59969	56408	62539	37	1.28E-34	1.91E-33	0.711538462	-0.490986353
BP1026b_10613	lipoprotein	60997	61726	58575	48	45587	40422	40453	33	2.86E-31	3.40E-30	0.6875	-0.540568381
BP1026b_10614	OmpW family outer membrane protein	40194	38123	41653	45	25753	23717	24785	48	4.71E-36	7.61E-35	0.622222222	-0.68498174
BP1026b_10615	activator protein	316074	353518	350145	658	237867	226962	221344	443	2.25E-36	3.71E-35	0.67325228	-0.570780885
BP1026b_10616	hypothetical protein	36462	21170	24739	26	16563	14400	16795	15	1.91E-51	6.56E-50	0.576923077	-0.793549123
BP1026b_10617	zinc-binding alcohol dehydrogenase	99984	84959	87485	90	66522	57828	69211	64	2.85E-36	4.67E-35	0.711111111	-0.491853096
BP1026b_10618	transcriptional regulator family protein	108663	175756	154048	335	190888	212683	198074	461	0.007065675	0.008782686	1.376119403	0.466065655
BP1026b_10619	hypothetical protein	258	467	427	2	588	621	548	4	0.125285988	0.140738975	2	1
BP1026b_10620	hypothetical protein	2414	3413	2642	6	3934	4810	3181	9	0.153590719	0.170880583	1.5	0.584962501
BP1026b_10621	hypothetical protein	12680	12923	13125	5	12599	11921	12783	5	5.16E-12	1.30E-11	1	0
BP1026b_10622	co-chaperonin GroES	3174987	5060037	4436660	14366	6249497	6675226	6735607	22290	0.789625388	0.807143994	1.55158012	0.633738196
BP1026b_10623	chaperonin GroEL	3025598	43174830	40058502	23052	47610802	49655052	46962068	29296	0.150347659	0.16754018	1.270865868	0.345811771
BP1026b_10624	bifunctional pyrimidine regulatory protein PyrR/uracil phosphoribosyltransferase	166314	159836	164748	192	173753	171800	164733	200	1.52E-09	3.11E-09	1.041666667	0.058893689
BP1026b_10625	rubredoxin	138008	222596	196036	1212	296963	343961	273252	1991	0.508498635	0.533621244	1.642739274	0.716103522
BP1026b_10626	hypothetical protein	111949	66766	67533	61	66979	64309	70566	50	1.14E-24	8.53E-24	0.819672311	-0.286881148
BP1026b_10627	Holliday junction resolvase-like protein	836518	1098608	1000595	1690	1319070	1410908	1433701	2397	0.010141047	0.012464457	1.818343195	0.504206662
BP1026b_10628	hypothetical protein	192463	110757	105601	309	111260	105283	125541	258	9.91E-22	5.85E-21	0.834951456	-0.260235772
BP1026b_10629	aspartate carbamoyltransferase catalytic subunit	56591	32556	44313	85	33254	28511	28422	57	3.92E-28	3.83E-27	0.670588235	-0.576500922
BP1026b_10630	acyltransferase family protein	78885	79073	77853	76	87648	88359	84793	84	4.09E-10	8.77E-10	1.05263158	0.144389909
BP1026b_10631	dihydroorotase	264009	235707	240571	193	229017	211025	236414	176	3.59E-16	1.34E-15	0.911917098	-0.133025419
BP1026b_10632	acyltransferase family protein	304786	260015	271961	320	253915	251336	259815	293	4.47E-15	1.50E-14	0.9156625	-0.12717124
BP1026b_10633	diadenosine tetraphosphatase	61809	44243	49356	61	48619	48039	48523	57	1.48E-14	4.73E-14	0.9442623	-0.097847323
BP1026b_10634	dTDP-glucose 4,6-dehydratase	216180	228418	233235	213	221918	238185	223598	215	2.34E-11	5.56E-11	1.09389671	0.013483229
BP1026b_10635	glucose-1-phosphate thymidyllyltransferase	330468	412050	389312	422	430820	437270	428073	483	3.51E-06	5.53E-06	1.144549763	0.19478019
BP1026b_10636	dTDP-4-dehydroammonase 3,5-epimerase	119722	213547	178916	309	226238	268170	242048	444	0.037460508	0.044188167	1.436893204	0.522952838
BP1026b_10637	dTDP-4-dehydroammonase reductase	147392	222722	190898	208	241908	271566	243292	281	0.003631486	0.004619551	1.350961538	0.433986602
BP1026b_10638	ABC-2 type transport system integral membrane protein	39949	69000	56618	66	81435	92621	85196	103	0.033964513	0.040162603	1.560660601	0.642106408
BP1026b_10639	polysaccharide ABC transporter, ATP-binding protein	190074	288599	257566	174	297135	336671	328244	227	4.36E-04	5.92E-04	1.304597701	0.383604991
BP1026b_10640	O-antigen acetylase WbIA	165769	260270	230043	176	274165	306976	287967	233	0.001905622	0.002471668	1.32363636	0.404754526
BP1026b_10641	NAD-dependent epimerase/dehydratase	222896	321459	303061	293	308723	345846	308053	333	2.16E-07	3.69E-07	1.136518771	0.184621513
BP1026b_10642	glycosyltransferase	347412	592142	515210	524	557422	619466	581090	634	0.897551988	0.908572013	1.209923664	0.274916029
BP1026b_10643	O-antigen methyl transferase	501928	800576	714432	389	797660	895301	859802	493	0.070355439	0.080919086	1.267352185	0.341817491
BP1026b_10644	glycosyl transferase family protein	274042	435725	395054	199	431987	480431	464071	249	1.03E-04	1.46E-04	1.251256281	0.323377312
BP1026b_10645	glycosyl transferase WbIF	68419	108708	96948	95	120292	135774	118370	130	7.95E-04	0.001057463	1.368421053	0.452512205
BP1026b_10646	UDP-glucose 4-epimerase	67696	74881	70119	73	66527	67682	73385	71	8.69E-15	2.85E-14	0.97260274	-0.040077439
BP1026b_10647	glycoside hydrolase family protein	40808	57493	57816</									

BP1026B_10670	Rhodanese-related sulfurtransferase	168472	190333	174007	548	177901	175269	175152	543	1.27E-11	3.09E-11	0.990875912	-0.013223695
BP1026B_10671	protein-L-isoaspartate(D-aspartate) O-methyltransferase	261162	190920	215557	340	203031	209825	212235	318	4.79E-15	1.61E-14	0.935294118	-0.096507981
BP1026B_10672	hypothetical protein	50137	34589	39814	160	37377	34503	34624	137	2.72E-15	9.33E-15	0.85625	-0.223896012
BP1026B_10673	coproporphyrinogen III oxidase	792626	769836	787842	561	699548	668094	669110	486	0.200292101	0.219976132	0.86631016	-0.207044557
BP1026B_10674	proteinase inhibitor	1413	326	248	2	322	314	214	1	1.22E-14	3.93E-14	0.5	-1
BP1026B_10675	hypothetical protein	18364	17033	15924	29	16491	15825	16511	27	4.51E-14	1.38E-13	0.931034483	-0.103093493
BP1026B_10676	undecaprenyl pyrophosphate phosphatase	242288	227136	223617	277	266497	268058	281604	327	6.94E-06	1.07E-05	1.180505415	-0.239404659
BP1026B_10677	tRNA (guanine-N(7)-)-methyltransferase	34757	28959	32824	40	31852	26828	30101	37	1.20E-11	2.92E-11	0.925	-0.112474729
BP1026B_10678	Gly tRNA	244	470	521	5	836	912	855	11	1.34E-04	1.89E-04	2.2	1.137503524
BP1026B_10679	Sir2 family transcriptional regulator	33010	36338	33207	40	29642	29791	32255	36	1.23E-12	3.31E-12	0.9	-0.152003093
BP1026B_10680	methyl transferase	24210	23785	24442	33	26377	24397	22628	33	1.69E-09	3.43E-09	1	0
BP1026B_10681	hypothetical protein	121708	125914	125904	101	122456	114861	124710	98	7.35E-14	2.20E-13	0.97029703	-0.043501639
BP1026B_10683	Integral membrane protein possibly involved in chromosome condensation	36340	26786	28018	78	24769	20177	26650	61	1.28E-19	6.39E-19	0.782051282	-0.354664881
BP1026B_10682	hypothetical protein	21268	26480	20823	64	26578	26393	31560	78	1.01E-04	1.44E-04	1.21875	0.285402219
BP1026B_10684	hypothetical protein	53684	73016	64120	112	75140	73432	77677	133	7.99E-08	1.41E-07	1.1875	0.247927513
BP1026B_10685	hypothetical protein	17566	5389	8535	9	5728	5009	6657	5	2.47E-42	5.54E-41	0.555555556	-0.847996907
BP1026B_10687	hypothetical protein	5356	2777	3692	14	3274	2742	2885	10	2.86E-13	8.13E-13	0.714285714	-0.485426827
BP1026B_10686	serine/threonine dehydratase	47897	26284	27967	34	23238	22259	22922	23	7.32E-31	8.50E-30	0.676470588	-0.563900885
BP1026B_10688	LysE family protein	18007	13839	15385	23	15693	15990	14655	22	1.10E-12	2.98E-12	0.956521739	-0.064130337
BP1026B_10689	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	48300	51711	51037	32	49441	46143	49735	31	3.46E-13	9.76E-13	0.96875	-0.045803069
BP1026B_10690	transglycosylase	34368	32328	33504	30	37704	35313	37376	33	8.42E-07	1.39E-06	1.1	0.137503524
BP1026B_10691	aminotransferase	42520	23622	27727	25	23617	20724	25246	18	2.25E-23	1.52E-22	0.72	-0.473931188
BP1026B_10692	Transcription termination protein NusB	529263	468836	517826	1153	372901	348701	370531	831	9.15E-25	6.90E-24	0.720728534	-0.472472131
BP1026B_10693	6,7-dimethyl-8-ribityllumazine synthase	242428	305334	298661	540	332328	325006	303053	613	1.95E-07	3.35E-07	1.135185185	0.182927667
BP1026B_10694	bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II-like protein	180779	220714	213597	180	194885	192798	202542	173	9.77E-14	2.89E-13	0.961111111	-0.057224869
BP1026B_10695	riboflavin synthase subunit alpha	168559	206665	186267	304	203395	207996	207973	335	1.62E-08	3.04E-08	1.101973684	0.140089772
BP1026B_10696	riboflavin biosynthesis protein RibD	104647	40176	52130	57	42000	35192	37923	33	2.08E-46	5.73E-45	0.578947368	-0.788495895
BP1026B_10697	glutamate-1-semialdehyde aminotransferase	243108	118309	140915	130	120628	111557	125787	92	3.81E-35	5.90E-34	0.707692308	-0.498805857
BP1026B_10698	hypothetical protein	18442	20251	21385	43	17957	15968	18397	37	1.72E-18	7.80E-18	0.860465116	-0.216811389
BP1026B_10699	hypothetical protein	7953	10517	9528	17	14513	15108	14101	27	0.015027398	0.018259033	1.588235294	0.667424661
BP1026B_10700	major facilitator superfamily transporter	17024	20235	18508	15	18063	19414	19700	15	2.77E-11	6.52E-11	1	0
BP1026B_10701	hypothetical protein	5695	2446	3055	9	2491	1676	3155	6	1.50E-17	6.29E-17	0.666666667	-0.584962501
BP1026B_10702	D-cysteine desulfhydrase	4409	1567	2171	2	1693	1428	1592	1	4.13E-18	1.81E-17	0.5	-1
BP1026B_10703	Cystine ABC transporter, ATP-binding protein	9505	8248	7872	11	7030	7412	6466	9	5.11E-18	2.22E-17	0.818181818	-0.289506617
BP1026B_10704	His/Glu/Gln/Arg/opine ABC transporter permease	3826	3833	3907	5	2970	3341	3386	4	3.86E-10	8.30E-10	0.8	-0.321928095
BP1026B_10705	ABC transporter substrate-binding protein	11512	9300	8768	12	7719	5495	7494	8	2.30E-26	1.97E-25	0.666666667	-0.584962501
BP1026B_10706	hypothetical protein	1222	2431	1818	11	3133	4363	3078	22	0.051184426	0.059669138	2	1
BP1026B_10707	bifunctional glucokinase/RpiI family transcriptional regulator	171509	180424	176693	91	141786	153256	144909	76	1.89E-21	1.08E-20	0.835164835	-0.259867127
BP1026B_10708	6-phosphogluconolactonase	19888	6994	8812	17	6448	4919	5430	8	5.23E-61	2.71E-59	0.470588235	-1.087462841
BP1026B_10709	glucose-6-phosphate 1-dehydrogenase	192461	158114	170642	118	130357	127191	141164	90	8.91E-29	9.16E-28	0.762711864	-0.390789953
predicted RNA	-	19315	29424	26756	535	39326	44294	34765	839	0.083644068	0.095588861	1.568224299	0.649131919
BP1026B_10710	maltose ABC transporter, periplasmic maltose-binding protein	508866	585131	567346	443	423911	437570	403422	337	1.69E-20	8.99E-20	0.760722348	-0.394558107
BP1026B_10711	ABC transporter permease	103042	98374	94185	104	83313	88510	86427	91	4.00E-21	2.24E-20	0.875	-0.192645078
BP1026B_10712	ABC transporter permease	133728	164900	158545	177	134355	130917	143139	158	1.47E-17	6.18E-17	0.892655367	-0.163824802
BP1026B_10713	ABC transporter ATP-binding protein	387300	512178	465812	406	409031	421984	429049	375	1.90E-12	5.02E-12	0.92364532	-0.114589132
BP1026B_10714	hypothetical protein	32501	19674	20675	39	17563	16051	16883	27	2.54E-33	3.54E-32	0.692307692	-0.530514717
BP1026B_10715	Smr domain-containing protein	46527	36540	37294	54	37473	35558	34174	48	1.70E-13	4.92E-13	0.888888889	-0.169925001
BP1026B_10716	thioredoxin-disulfide reductase	318947	276296	296027	308	290063	285792	288712	299	3.80E-12	9.72E-12	0.970779221	-0.042784866
BP1026B_10717	cell division ftsK transmembrane protein	390894	381411	388470	167	421252	394556	438751	181	1.88E-07	3.22E-07	1.083832335	0.116141595
BP1026B_10718	outer-membrane lipoprotein carrier protein	59405	53779	54592	78	55349	54300	60757	79	3.18E-12	8.19E-12	1.017820513	-0.018785229
BP1026B_10719	recombination factor protein RarA	87855	53263	58858	50	54438	51767	53978	40	2.35E-24	1.71E-23	0.8	-0.321928095
BP1026B_10720	hypothetical protein	16642	17091	19432	66	13883	13660	16981	55	1.30E-19	6.47E-19	0.833333333	-0.263034406
BP1026B_10721	seryl-tRNA synthetase	370916	393724	375716	291	385504	384226	390072	296	3.96E-09	7.79E-09	1.017182131	0.024578023
BP1026B_10722	Ser tRNA	24941	42025	35720	376	41782	41809	47808	481	3.03E-04	4.16E-04	1.279255319	0.355304232
BP1026B_10723	hypothetical protein	1001737	1768776	1600447	5336	1620398	1897931	1645156	6304	0.081193893	0.092992311	1.181409295	0.240508868
BP1026B_10725	acetyltransferase	64894	45827	52614	95	46402	33933	49708	75	5.68E-22	3.43E-21	0.789473684	-0.341036918
BP1026B_10726	septum formation inhibitor	86601	90167	92752	110	90724	96224	88758	113	9.93E-13	2.69E-12	0.102727272	0.038819249
BP1026B_10727	septum site-determining protein MinD	208636	276459	254994	302	260536	266230	271408	326	1.41E-08	2.66E-08	0.107947019	-0.110323415
BP1026B_10728	cell division topological specificity factor MinE	26715	21990	23211	94	21505	19607	22117	82	2.65E-16	1.00E-15	0.872340426	-0.197036847
BP1026B_10729	hypothetical protein	1610	1685	1665	3	1979	2470	1915	5	0.230435108	0.251814856	1.666666667	0.736965594
BP1026B_10730	hypothetical protein	2123	420	825	11	235	470	408	3	4.23E-35	6.52E-34	0.272727273	-1.87469118
BP1026B_10731	voltage gated chloride channel family protein	33995	30948	28887	18	31231	27573	28450	17	2.81E-11	6.61E-11	0.944444444	-0.08246216
BP1026B_10732	lipopolysaccharide heptosyltransferase I	43219	38645	39697	39	36469	35317	41250	36	4.03E-12	1.03E-11	0.923076923	-0.115477217
BP1026B_10733	hypothetical protein	47966	25020	32194	191	24707	20932	22094	123	1.92E-34	2.84E-33	0.643979058	-0.634914323
BP1026B_10734	metabolite proton symporter family protein	12044	8608	8714	7	7962	7325	7846	5	2.13E-20	1.12E-19	0.714285714	-0.485426827
BP1026B_10735	TonB domain-containing protein	10412	8688	11490	20	9546	6559	8289	16	6.64E-20	3.38E-19	0.8	-0.321928095
BP1026B_10736	hypothetical protein	2320	2476	2569	4	2766	2453	2699	4	0.001068268	0.001407141	1	0
BP1026B_10737	integrase	1054	2039	1434	7	1821	2597	2494	10	0.76786519	0.786697724	1.428571429	0.514573173
BP1026B_10738	Integrase	5560	5904	6037	25	10628	12902	9412	48	0.586377965	0.610846937	1.92	0.941106311
BP1026B_10739	Ser tRNA	771	665	1129	9	1359	1818	1209	16	0.062390914	0.072102816	1.777777778	0.830074999
BP1026B_10740	coproporphyrinogen III oxidase	70466	61922	64409	53	68372	70029	70667	57	2.68E-11	6.33E-11	1.075471698	0.10496956
BP1026B_10741	deoxycarbonyl triphosphate pyrophosphatase	59005	30846	37539	67	31942	26624	29068	46	1.23E-26	1.08E-25	0.686567164	-0.542527234
BP1026B_10742	ribonuclease PH	111971	59289	74684	111	61935	51252	64406	80	6.72E-34	9.60E-33	0.720720721	-0.472487771
BP1026B_10743	hypothetical protein	138190	145150	149992	156	167410	148397	171614	175	6.67E-07	1.11E-06	1.121794872	0.165808893
BP1026B_10744	guanylate kinase	120053	169049	159501	218	193963	198498	184355	281	6.45E-04	8.64E-04	1.288990826	0.366241995
BP1026B_10745													

BP1026B_10767	5-methyltetrahydropteroyltrimethylglutamate/homocysteine S-methyltransferase	12005	9805	9823	4	9571	9595	10478	4	3.63E-12	9.31E-12	1	0
BP1026B_10768	aminopeptidase N	205161	234852	225173	82	256721	271371	267221	98	1.73E-05	2.59E-05	1.195121951	0.257157839
BP1026B_10769	lipoprotein	251947	235496	244835	341	252477	240132	267786	354	7.16E-10	1.51E-09	1.038123167	0.053977621
BP1026B_10770	hypothetical protein	36840	29972	34070	58	29317	23056	27729	46	5.43E-18	2.36E-17	0.793103448	-0.334419039
BP1026B_10771	guanine deaminase	21010	12952	12903	11	12139	10337	11630	8	1.31E-24	9.70E-24	0.727272727	-0.459431619
BP1026B_10772	xanthine/uracil permease family protein	13661	16519	14688	10	13045	16254	15370	10	5.69E-12	1.43E-11	1	0
BP1026B_10773	adenosine deaminase	40210	38606	39722	38	32459	29867	30729	30	1.42E-18	6.51E-18	0.789473684	-0.341036918
BP1026B_10774	xanthine dehydrogenase accessory factor	16522	10252	10392	12	9008	8440	9234	8	2.11E-25	1.67E-24	0.666666667	-0.584962501
BP1026B_10775	DsbB family disulfide bond formation protein	13011	9608	10971	21	12994	11257	13525	24	1.22E-07	2.12E-07	1.142857143	0.192645078
BP1026B_10776	amidase	17051	6993	8131	7	6179	4318	5900	3	2.28E-49	7.10E-48	0.428571429	-1.222392421
BP1026B_10777	glutamine amidotransferase	312979	320518	336801	243	341769	370602	327018	260	1.46E-08	2.74E-08	1.069958848	0.097555309
BP1026B_10778	citrate-proton symporter	29177	20945	21936	17	22700	19132	20081	15	1.11E-17	4.73E-17	0.882352941	-0.180572246
BP1026B_10779	hypothetical protein	29146	9257	13822	9	8998	7592	8142	4	6.18E-73	4.50E-71	0.444444444	-1.169925001
BP1026B_10780	oxygenase	153874	77835	106744	68	84047	71648	89256	49	1.36E-35	2.16E-34	0.720588235	-0.472752997
BP1026B_10781	NAD-dependent formate dehydrogenase subunit delta	51943	32061	35881	153	35758	36329	39229	142	4.60E-12	1.17E-11	0.928104575	-0.107640723
BP1026B_10782	NAD-dependent formate dehydrogenase subunit alpha	251059	201356	212229	74	187925	177316	187549	62	9.92E-21	5.35E-20	0.837837838	-0.255257055
BP1026B_10783	NAD-dependent formate dehydrogenase subunit beta	17772	12197	12117	8	10778	9841	9883	6	5.05E-24	3.60E-23	0.75	-0.415037499
BP1026B_10784	NAD-dependent formate dehydrogenase gamma subunit	7402	2602	4619	10	3278	2159	2730	5	2.50E-27	2.34E-26	0.5	-1
BP1026B_10785	regulatory protein	43362	21585	26591	27	27188	24079	28004	23	3.37E-14	1.04E-13	0.851851852	-0.231325546
BP1026B_10786	hypothetical protein	41765	70597	66729	226	81986	94716	69564	310	2.43E-04	3.37E-04	1.371681416	0.455945443
BP1026B_10787	hypothetical protein	29050	11614	15568	29	12893	11458	11733	18	3.66E-35	5.67E-34	0.620689655	-0.688055994
BP1026B_10788	hypothetical protein	1097	1250	1561	10	2534	2366	1424	16	0.278251401	0.301230697	1	0.678071905
predicted RNA	-	85364855	128560674	98428656	288415	143134869	154279902	149125062	412317	0.003914422	0.004962122	1.429596622	0.515607747
BP1026B_10789	phosphoglycolate phosphatase	20776	7463	9827	17	6464	5390	6395	8	9.26E-62	5.00E-60	0.470588235	-1.087462841
BP1026B_10790	3-demethylubiquinone-9 3-methyltransferase	102065	92366	97165	119	98621	92210	103227	121	1.03E-12	2.79E-12	1.016806723	0.024045474
BP1026B_10791	outer membrane protein A	87660363	13287637	12350795	16989	14605481	16261265	14186987	22248	0.002824557	0.003623066	1.30955324	0.389074174
BP1026B_10792	DNA gyrase subunit A	739616	936288	884821	320	1000792	1026635	1038758	383	0.067859902	0.078249935	1.196875	0.259272487
BP1026B_10793	hypothetical protein	2282406	331541	3087684	447	3398263	3490906	3418967	5755	0.919697946	0.929638221	1.187332371	0.247272346
BP1026B_10794	phosphoserine aminotransferase	230494	293488	278490	246	331664	320383	340575	305	2.01E-05	3.00E-05	1.239837398	0.310150927
BP1026B_10795	chorismate mutase/prephenate dehydratase	191057	158351	170807	160	168664	150988	168303	150	6.39E-14	1.92E-13	0.9375	-0.093109404
BP1026B_10796	bifunctional prephenate dehydrogenase/3-phosphohikimate 1-carboxyvinyltransferase	89922	72990	77465	35	73492	65665	73120	31	4.97E-20	2.55E-19	0.885714286	-0.175086707
BP1026B_10797	cytidylate kinase	28508	25402	24065	37	28554	28196	24310	39	2.58E-08	4.74E-08	1.054054054	0.059488553
predicted RNA	-	428267	598732	570217	940	630433	648261	612112	1113	0.950053654	0.957079774	1.184042553	0.243720931
BP1026B_10798	integration host factor subunit beta	613202	822663	748670	3034	895623	917736	1058775	3989	0.030503837	0.036179641	1.314765985	0.394806038
BP1026B_10799	hypothetical protein	69404	72348	73940	244	76071	77365	83668	268	2.48E-10	5.38E-10	1.098360656	0.133531853
BP1026B_10800	hypothetical protein	126522	134973	132914	112	140140	139082	138040	118	8.60E-10	1.79E-09	1.053571429	0.075288127
BP1026B_10801	UDP-glucose 6-dehydrogenase	238367	305485	287633	197	314263	339427	313724	230	8.05E-07	1.33E-06	1.16751269	0.223438231
BP1026B_10802	bifunctional ADP-heptose synthase	200838	73522	86263	121	71041	61286	74811	69	5.80E-63	3.34E-61	0.570247934	-0.81033878
BP1026B_10803	ADP-L-glycero-D-manno-heptose-6-epimerase	154532	176597	169433	168	177282	185399	194303	186	1.52E-07	2.62E-07	1.107142857	0.146841388
BP1026B_10804	competence protein ComE	40074	23336	30406	98	25719	19616	24156	72	2.13E-23	1.44E-22	0.734693878	-0.444784843
BP1026B_10805	hypothetical protein	1293	1070	1196	3	996	1462	1132	3	0.018263251	0.022066627	1	0
BP1026B_10806	cysteine synthase B	391826	496128	464952	499	572222	587887	579438	642	0.854251012	0.869091872	1.286573146	0.363533482
BP1026B_10807	murein transglycosylase domain-containing protein	376518	512864	465732	348	518756	528086	526181	404	0.034531273	0.040825087	1.16091954	0.215267987
BP1026B_10808	histone deacetylase family protein	155153	138795	143988	157	128467	111751	127534	132	8.76E-22	5.19E-21	0.840764331	-0.25022663
BP1026B_10809	alpha/beta fold family hydrolase	22192	7007	12945	15	8016	5826	7283	7	1.70E-60	8.60E-59	0.466666667	-1.099535674
BP1026B_10810	DL-methionine transporter ATP-binding subunit	43584	36132	37273	37	40888	43395	44748	41	1.99E-07	3.41E-07	1.108108108	0.148098639
BP1026B_10811	ABC transporter permease	20205	16255	15091	26	20044	17672	20106	29	2.34E-08	4.30E-08	1.115384615	0.157541277
BP1026B_10812	D-methionine ABC transporter substrate-binding protein	34364	38186	38335	46	42663	33926	39618	48	3.08E-08	5.63E-08	1.043478261	0.061400545
BP1026B_10813	electron transfer flavoprotein subunit beta	748705	939173	909844	1154	1368772	1422583	1423051	1873	0.001293869	0.001694333	1.6205062	0.698707676
BP1026B_10814	electron transfer flavoprotein subunit alpha	271634	265294	255680	282	287071	280152	293084	306	1.46E-08	2.73E-08	1.085106583	0.11783649
BP1026B_10815	Acyl-CoA dehydrogenase	241469	225115	240747	131	242201	234736	233321	132	2.37E-11	5.62E-11	1.007633588	0.010971118
BP1026B_10816	D-amino acid dehydrogenase small subunit	730133	633728	638406	518	564274	553791	566774	436	0.014260619	0.017357622	0.841698842	-0.248623963
BP1026B_10817	leucine-responsive regulatory protein	206084	294176	265305	521	330571	381411	340086	717	0.00209964	0.002717691	1.376199616	0.460689746
BP1026B_10818	radical SAM domain-containing protein	71303	72727	76308	64	81403	77798	88461	71	2.42E-10	5.25E-10	1.109375	0.14974712
BP1026B_10819	hypothetical protein	12125	19560	18348	35	24046	26801	19970	50	0.006937335	0.00863172	1.428571429	0.514573173
BP1026B_10820	hypothetical protein	118098	52167	67806	70	47755	40365	50156	41	2.87E-53	1.08E-51	0.585714286	-0.771731012
BP1026B_10821	16S rRNA-processing protein RimM	244795	220314	230856	336	239485	227846	235994	339	3.84E-11	8.92E-11	1.008928571	0.01282404
BP1026B_10822	RNA (guanine-N(1)-)-methyltransferase	202093	264440	253395	301	287526	283102	288665	360	1.02E-05	1.55E-05	1.196013289	0.25823342
predicted RNA	-	7474	1093	1890	268	1116	359	1392	73	1.28E-95	1.41E-93	0.27238806	-1.876264632
BP1026B_10823	acetyltransferase	11962	10230	9696	17	9412	8637	9226	15	5.14E-16	1.89E-15	0.882352941	-0.180572246
BP1026B_10825	hypothetical protein	1010	821	1135	4	1077	963	1195	5	0.098367126	0.111701415	1.25	0.321928095
BP1026B_10824	MutT/NUDIX NTP pyrophosphatase	43326	37116	36673	57	42576	42080	44383	62	1.84E-07	3.17E-07	1.087719298	0.121306296
BP1026B_10826	CobD/CbiB family protein	158272	166490	170762	175	195017	195548	193130	207	4.07E-06	6.38E-06	1.182857143	0.242275846
BP1026B_10827	lipoprotein	16268	3295	6185	26	4309	2556	3680	11	7.13E-62	3.89E-60	0.423076923	-1.2410081
BP1026B_10828	ribosome-associated GTPase	70822	70813	72521	75	80250	75365	77274	82	1.05E-10	2.35E-10	1.093333333	0.128733314
BP1026B_10829	peptidase	144867	144050	153958	117	155104	148002	153930	120	5.74E-10	1.22E-09	0.025641026	0.05525876
BP1026B_10830	oligonucleotidase	39306	54644	49321	78	66313	78622	67898	117	0.014228001	0.017324651	1.5	0.584962501
BP1026B_10831	molybdenum cofactor biosynthesis protein MogA	76000	95070	86575	146	92264	93656	86096	154	1.35E-11	3.27E-11	1.054794521	0.076961982
BP1026B_10832	hypothetical protein	113698	70788	85631	178	60822	50392	60575	113	1.94E-46	5.39E-45	0.634831461	-0.655554469
BP1026B_10833	pmbA protein	188115	185210	183556	135	183797	178797	191478	134	9.34E-12	2.30E-11	0.992592593	-0.010726407
BP1026B_10834	dihydrofolate reductase	9028	6127	5341	13	7965	7748	8090	15	7.56E-07	1.25E-06	1.153846154	0.206450877
BP1026B_10835	sigma-54 dependent DNA-binding transcriptional regulator	13972	10290	10737	6	10929	9194	10023	5	2.76E-15	9.46E-15	0.833333333	-0.263034406
BP1026B_10836	hypothetical protein	5799	6698	5221	4	7325	6615	8411	5	3.58E-05	5.24E-05	1.25	0.321928095
BP1026B_10837	hypothetical protein	297	88	129	1	163	48	154	0	0.074440325	0.08549		

BP1026B_10862	molybdenum cofactor biosynthesis protein A	421198	302589	360963	324	367302	311850	333846	303	1.36E-12	3.62E-12	0.935185185	-0.096676019
BP1026B_10863	ribonuclease E	174494	183388	185173	55	177671	187442	180375	55	2.97E-11	6.98E-11	1	0
BP1026B_10864	hypothetical protein	108232	171664	157773	300	198176	205074	178430	398	0.002497591	0.003217497	1.326666667	0.40780593
BP1026B_10865	ribosomal large subunit pseudouridine synthase C	87049	99787	95012	93	133594	137352	143327	136	0.017242439	0.02084931	1.462365591	0.54830403
BP1026B_10866	haloacid dehalogenase-like hydrolase	64643	54514	58073	89	59800	64882	55851	91	1.32E-12	3.53E-12	1.02247191	0.032061209
BP1026B_10867	ferredoxin, 2Fe-2S	9549	11879	9242	25	13139	12814	12849	32	2.85E-05	4.20E-05	1.28	0.35614381
BP1026B_10868	peptidase	229420	320721	308330	285	370669	380391	349880	366	1.15E-04	1.63E-04	1.284210526	0.360881729
BP1026B_10869	tetrapyrrole methylase family protein	37333	15000	17587	32	14618	13292	14720	19	7.49E-44	1.82E-42	0.59375	-0.752072487
BP1026B_10871	Mal-like protein	30178	24909	24893	41	23152	22394	20392	33	1.35E-18	6.18E-18	0.804878049	-0.313157885
BP1026B_10870	hypothetical protein	70120	88524	77211	124	91092	90817	86388	141	4.51E-09	8.83E-09	1.137096774	0.185355042
BP1026B_10872	50S ribosomal protein L32	113214	173972	154588	818	239427	254945	232731	1346	0.750091867	0.769621032	1.654476773	0.718505662
BP1026B_10873	glycerol-3-phosphate acyltransferase PlxX	153766	165805	172661	148	184985	179666	182577	164	1.83E-07	3.14E-07	1.108108108	0.148098639
BP1026B_10874	3-oxoacyl-ACP synthase	172680	169241	167658	176	158486	167216	166362	170	1.48E-12	3.95E-12	0.965909091	-0.050040682
BP1026B_10875	acyl-carrier-protein S-malonyltransferase	283757	235856	254668	276	234397	214630	230113	242	2.18E-18	9.77E-18	0.876811594	-0.18966122
BP1026B_10876	3-ketoacyl-ACP reductase	197771	213539	200995	272	196739	185141	208519	262	1.61E-13	4.66E-13	0.963235294	-0.05403984
BP1026B_10877	hypothetical protein	20322	13821	14752	115	13913	16410	15697	108	2.90E-14	9.03E-14	0.939130435	-0.090602549
BP1026B_10878	acyl carrier protein	1185239	2063637	1760390	6957	2266209	2559859	2386699	10017	0.05145309	0.059948878	1.439844761	0.525913273
BP1026B_10879	hypothetical protein	608665	985962	853510	5551	1037586	1089582	1062854	7233	0.028462792	0.033822843	1.303008467	0.381846459
BP1026B_10880	3-oxoacyl-(acyl carrier protein) synthase II	906709	1221020	1146552	880	1265936	1389245	1310463	1066	0.084640586	0.096692418	1.211363636	0.276622009
BP1026B_10881	hypothetical protein	34516	41333	36181	78	39563	40676	47911	90	1.88E-06	3.01E-06	1.153846154	0.206450877
BP1026B_10882	RNA polymerase sigma factor RpoI	261913	392718	331523	547	463892	484747	492148	800	0.008890693	0.010968514	1.462522852	0.548459167
BP1026B_10883	sigma E factor negative regulatory protein	176841	198963	203463	302	223686	226437	225548	352	1.14E-06	1.86E-06	1.05626914	0.221026879
BP1026B_10884	sigma factor algU regulatory protein MucB	431133	289325	299407	322	306705	310060	308542	292	3.16E-14	9.82E-14	0.906832298	-0.141092319
BP1026B_10885	peptidase	694209	498637	562279	388	427030	379303	410490	269	5.64E-26	4.68E-25	0.693298969	-0.52845048
BP1026B_10886	hypothetical protein	245395	130328	155620	694	115103	84616	107271	401	5.16E-61	2.69E-59	0.577809798	-0.791333426
BP1026B_10887	GTP-binding protein LepA	189761	258657	241654	128	261263	274923	267445	149	3.78E-06	5.94E-06	1.1640625	0.21916852
BP1026B_10888	signal peptidase I	126543	183344	161728	175	222924	245061	239700	263	0.134541376	0.150865473	1.502857143	0.587707877
BP1026B_10889	ribonuclease III	217761	248321	246893	171	285071	319967	287628	214	1.13E-04	1.60E-04	1.251461988	0.323614472
BP1026B_10890	GTP-binding protein Era	153064	222879	203510	223	236545	251497	219323	272	2.52E-05	3.73E-05	1.219730942	0.286562941
BP1026B_10891	DNA repair protein RecO	44904	53951	51187	58	57465	58359	48550	63	5.50E-09	1.07E-08	1.086206897	0.119298928
BP1026B_10892	pyridoxine 5'-phosphate synthase	148274	119312	135636	173	105162	101559	94426	129	2.19E-30	2.47E-29	0.74566474	-0.423400972
BP1026B_10893	4'-phosphopantetheinyl transferase	44101	16498	16122	59	12959	9202	14331	28	3.86E-74	2.91E-72	0.474576271	-1.075288127
BP1026B_10894	beta-hexosaminidase	87166	55309	64343	66	43606	37756	44364	40	1.33E-44	3.31E-43	0.606060606	-0.722466024
BP1026B_10895	sigma-54 interacting response regulator protein	253974	199394	227256	162	218934	205332	204480	149	1.07E-15	3.83E-15	0.919753086	-0.120681482
BP1026B_10896	hypothetical protein	5867	10613	8281	58	11359	13205	11514	85	0.00409379	0.005180066	1.465517241	0.551409941
BP1026B_10897	elongation factor P	332308	528469	461340	789	530965	594134	582263	1019	0.925013542	0.934408328	1.291508238	0.369056846
BP1026B_10898	hypothetical protein	37814	26175	27989	25	28071	22693	25300	20	2.09E-16	7.95E-16	0.8	-0.321928095
BP1026B_10899	exonuclease ABC subunit C	138407	146183	135069	62	140042	136589	139941	61	2.71E-12	7.02E-12	0.983870968	-0.023458973
BP1026B_10900	CDP-diacylglycerol-3-phosphate 3-phosphatidyltransferase	128511	142876	141469	231	180093	189021	193265	315	0.007007825	0.008715965	1.363636364	0.447458977
BP1026B_10901	Gly tRNA	18071	27919	21686	296	31395	36703	35166	452	0.050020817	0.058366935	1.527027002	0.610725597
BP1026B_10902	Gly tRNA	11492	18007	13679	189	28499	32687	33164	463	0.118825067	0.133817015	2.185185185	1.127755547
BP1026B_10903	Cys tRNA	7085	10443	8603	117	16262	17711	20494	245	0.955946705	0.962397502	2.094017094	1.066273219
BP1026B_10904	hypothetical protein	37320	44314	41542	80	39937	42278	36361	77	3.53E-11	8.22E-11	0.9625	-0.055141554
BP1026B_10905	LysR family transcriptional regulator	19113	11469	13471	16	11120	8859	11049	11	6.14E-26	5.08E-25	0.6875	-0.540568381
BP1026B_10906	hypothetical protein	8909	8618	9634	10	8513	9198	10071	10	9.62E-10	2.00E-09	1	0
BP1026B_10907	acetyltransferase	20819	20260	22172	41	21525	20669	24269	43	2.60E-09	5.20E-09	1.048780488	0.06871275
BP1026B_10908	hypothetical protein	131577	149490	148167	163	131548	141521	137953	156	5.59E-14	1.69E-13	0.957055215	-0.063325935
BP1026B_10909	hypothetical protein	129322	171283	160409	343	159407	165843	151085	355	1.08E-09	2.23E-09	1.034985423	0.049610448
BP1026B_10910	SCO1/SenC family protein	46468	23852	29375	50	20875	17105	21349	29	9.20E-47	2.57E-45	0.58	-0.785875195
BP1026B_10911	trehalose-phosphatase	46682	20463	26877	41	19476	19112	20513	26	6.78E-41	1.39E-39	0.634146341	-0.657112286
BP1026B_10912	alpha-alpha-trehalose-phosphate synthase (UDP-forming)	159161	150606	156801	112	151023	145879	153969	109	9.47E-13	2.57E-12	0.973214286	-0.039170597
BP1026B_10913	ABC transporter ATP-binding protein	88562	82501	85700	45	85743	86333	86446	46	8.53E-14	2.54E-13	1.022222222	0.03170886
BP1026B_10914	hypothetical protein	82443	130614	107546	791	135993	158091	166415	1137	0.022014173	0.026430506	1.437420986	0.523482654
BP1026B_10915	glycosyl transferase group 1 protein	247096	258179	262436	240	268946	260103	274477	251	1.15E-09	2.38E-09	1.045833333	0.064652958
BP1026B_10916	hypothetical protein	44196	44044	45507	53	42241	41396	39533	48	2.45E-13	7.01E-13	0.905660377	-0.142957954
BP1026B_10917	hypothetical protein	32290	39911	39004	80	43402	44780	44410	95	1.21E-05	1.83E-05	1.1875	0.247927513
BP1026B_10918	oxidoreductase, FAD-binding family protein	16815	8091	10031	9	8883	7516	8873	7	2.10E-25	1.67E-24	0.777777778	-0.362570079
BP1026B_10919	periplasmic ligand binding lipoprotein	10187	10098	11733	9	9569	7926	9747	7	3.15E-16	1.18E-15	0.777777778	-0.362570079
BP1026B_10920	non-hemolytic phospholipase C	65119	63323	62166	30	61537	61274	58292	28	8.79E-16	3.17E-15	0.933333333	-0.099535674
BP1026B_10922	pyridoxal kinase	91146	85555	89433	102	75965	80300	84181	92	3.35E-19	1.62E-18	0.901960784	-0.148863386
BP1026B_10921	alpha/beta fold family hydrolase	38983	44226	43730	41	41462	42188	41070	40	6.79E-11	1.54E-10	0.975609756	-0.03562391
BP1026B_10923	luciferase-like monooxygenase	11921	5862	7714	8	5826	5380	4593	4	6.57E-30	7.23E-29	0.5	-0.514573173
BP1026B_10924	syl transferase, group 2 family protein	62584	27066	32146	33	31840	28408	35425	26	1.10E-18	5.11E-18	0.787878788	-0.343954401
BP1026B_10925	Fe-S oxidoreductase	242552	345739	321947	209	365291	396046	353167	256	1.89E-05	2.82E-05	1.224880833	0.292640868
BP1026B_10926	YdcJ-like family protein	25918	13455	15539	20	16059	11059	12902	15	5.87E-27	5.27E-26	0.75	-0.415037499
BP1026B_10927	hypothetical protein	62442	29110	37037	40	25445	21331	28803	24	4.95E-41	1.02E-39	0.6	-0.736965594
BP1026B_10928	lipoprotein	14839	11909	13036	23	9872	7653	10377	16	1.57E-26	1.37E-25	0.695652174	-0.523561956
BP1026B_10930	histidine transport system permease	12674	12822	12919	16	13550	15513	14225	19	4.71E-08	8.46E-08	1.1875	0.247927513
BP1026B_10929	histidine transport system permease	14058	18373	17259	23	18270	18645	18746	25	1.32E-08	2.48E-08	1.086956522	0.120294234
BP1026B_10931	histidine transport ATP-binding protein	71702	93181	91667	107	93780	100382	86966	117	5.55E-10	1.18E-09	1.093457944	0.128897733
BP1026B_10932	AraC family transcription regulator	41253	38674	37952	40	34422	38630	35461	37	3.15E-12	8.11E-12	0.925	-0.112472429
BP1026B_10933	hypothetical protein	4035	7043	4850	21	5327	5212	4469	20	1.06E-09	2.20E-09	0.952380952	-0.070389328
BP1026B_10934	bifunctional N-succinyl-diaminopimelate-aminotransferase/acetylornithine transaminase protein	128277	91937	111835	89	100545	84766	98668	76	1.99E-21	1.14E-20	0.853932584	-0.227805918
BP1026B_10935	argin												

BP1026B.10959	methyl-accepting chemotaxis protein I	1713827	1235346	1367575	762	1242678	1147139	1279103	648	0.89505859	0.906194397	0.850393701	-0.233797185
BP1026B.10960	coproporphyrinogen III oxidase	915668	1024205	1024026	680	1034389	1034634	1032277	711	0.223148993	0.244236086	1.045588235	0.064314813
BP1026B.10961	cyclic nucleotide-binding domain-containing protein	464524	525113	524843	731	521574	495446	536647	750	4.17E-04	5.67E-04	1.025991792	0.037019189
BP1026B.10962	hypothetical protein	170533	163683	167384	126	169932	176147	176180	132	1.50E-09	3.08E-09	1.047619048	0.067114196
BP1026B.10963	2-nitropropane dioxygenase	984482	831266	902005	743	776626	715146	802583	627	0.731162668	0.751059882	0.843876178	-0.244896768
BP1026B.10964	hypothetical protein	707438	610624	653914	635	602253	579387	604371	575	0.158423305	0.175882429	0.905511811	-0.143194636
BP1026B.10965	U32 family peptidase	716095	883383	858027	935	888759	882977	892250	1013	0.195999795	0.215613539	1.08342246	0.115595904
BP1026B.10966	hypothetical protein	262532	383023	353075	693	395162	411893	401938	839	2.15E-05	3.20E-05	1.120678211	0.275815458
BP1026B.10967	hypothetical protein	209435	235941	219699	495	240871	234144	256545	545	6.66E-08	1.19E-07	1.010101011	0.138827705
BP1026B.10968	radical SAM domain-containing protein	123663	65599	75238	122	67549	54170	65994	86	3.07E-36	5.02E-35	0.704918033	-0.504472583
BP1026B.10969	hypothetical protein	142013	169059	169315	751	195774	184579	193449	897	1.31E-05	1.98E-05	1.194407457	0.256295077
BP1026B.10970	anaerobic ribonucleoside triphosphate reductase	483875	607153	601832	319	669378	705018	631041	378	0.867848764	0.881923509	1.184952978	0.24482981
BP1026B.10971	heme/copper membrane protein	96515	52506	64638	58	52004	48612	53312	41	5.25E-32	6.57E-31	0.706896552	-0.500428991
BP1026B.10972	lipoprotein	6103	2313	3090	3	2394	2343	2187	2	2.65E-21	1.50E-20	0.666666667	-0.584962501
BP1026B.10973	phenylacetic acid degradation protein paaD	1765	1886	2370	5	2002	1481	1522	4	1.59E-06	2.56E-06	0.8	-0.321928095
BP1026B.10974	nitric oxide reductase subunit B	135053	168968	155710	66	118697	118257	124507	52	2.22E-26	1.90E-25	0.787878788	-0.343954401
BP1026B.10975	alkane-1 monoxygenase	15292	15349	16838	13	15856	15942	15918	13	6.52E-12	1.63E-11	1	0
BP1026B.10976	deoxyribodipyrimidine photolyase	21481	14280	15145	11	15593	12110	15285	9	7.72E-19	3.61E-18	0.818181818	-0.289506617
BP1026B.10977	adenylsulfate kinase	82869	93880	90375	143	95892	92145	95306	152	4.65E-11	1.07E-10	1.062937063	0.088056177
BP1026B.10978	ATP-dependent transcription regulator LuxR	10114	11965	9931	14	11449	11588	10034	15	2.77E-09	5.54E-09	1.071428571	0.099535674
BP1026B.10980	alpha/beta fold family hydrolase	27327	26857	24922	26	21743	21365	23628	22	2.95E-17	1.21E-16	0.846153846	-0.2410081
BP1026B.10979	4'-phosphopantetheinyl transferase	6999	3972	3892	6	3274	2779	2792	3	6.88E-24	4.85E-23	0.5	-1
BP1026B.10981	hypothetical protein	3555	1749	1185	4	1219	1067	1806	2	1.53E-13	4.45E-13	0.5	-1
BP1026B.10982	histidine ammonia-lyase	48058	28742	35212	24	24194	17642	25617	14	4.39E-41	9.15E-40	0.583333333	-0.777607579
BP1026B.10983	histidine utilization repressor	20940	17845	19295	27	16023	14836	13486	21	3.55E-25	2.77E-24	0.777777778	-0.362570079
BP1026B.10984	urocanate hydratase	135761	138393	144712	82	114111	111960	111743	66	2.96E-24	2.15E-23	0.804878049	-0.313157885
BP1026B.10985	hypothetical protein	6996	3261	3852	7	2734	2817	2890	4	1.92E-23	1.31E-22	0.571428571	-0.807354922
BP1026B.10986	imidazolonepropionase	39699	18461	22846	22	15648	14955	13681	12	3.60E-58	1.62E-56	0.545454545	-0.874469118
BP1026B.10987	N-formimino-L-glutamate deiminase	51930	29479	31286	27	24014	19919	26963	17	2.03E-35	3.20E-34	0.629629693	-0.667424661
BP1026B.10988	N-formylglutamate amidohydrolase	27104	20509	24011	29	18706	17918	21630	24	1.74E-21	1.00E-20	0.827586207	-0.273018494
BP1026B.10989	hypothetical protein	1731	2854	2398	16	2659	3156	2710	20	0.026940588	0.032062626	1.25	0.321928095
BP1026B.10990	hypothetical protein	2075	392	572	10	389	376	463	4	2.87E-22	1.76E-21	0.4	-1.321928095
BP1026B.10991	glutamine amidotransferase	3189	2383	2581	3	2039	1879	1948	2	2.68E-11	6.33E-11	0.666666667	-0.84962501
BP1026B.10992	glutamine synthetase	22896	29099	25569	19	22295	26441	22525	17	7.02E-13	1.93E-12	0.894736842	-0.160464672
BP1026B.10993	aminotransferase	35418	36636	37578	25	24106	27286	28314	18	5.84E-23	3.84E-22	0.72	-0.473931188
BP1026B.10994	hypothetical protein	125234	191403	167988	351	215340	233377	218443	484	0.007593303	0.009408669	1.378917379	0.463536017
BP1026B.10995	hypothetical protein	28711	43055	38481	144	54673	53540	48181	218	0.040983278	0.048198427	1.513888889	0.598259323
BP1026B.10996	Val tRNA	3136	5306	3668	53	8235	8850	9337	117	0.5827165	0.607335593	2.2054717	1.14244265
BP1026B.10998	LysR family regulatory protein	8247	10515	9583	10	11081	12169	10781	12	6.28E-06	9.71E-06	1.2	0.263034406
BP1026B.10997	acyl-CoA dehydrogenase domain-containing protein	7638	4218	4046	2	4094	4443	4080	2	1.32E-13	3.87E-13	1	0
BP1026B.10999	CAIB/BAIF family CoA transferase	6813	3831	4688	3	3925	2871	3553	2	3.17E-18	1.41E-17	0.666666667	-0.584962501
BP1026B.11000	major facilitator family transporter	2916	1699	2548	1	3207	2236	2191	1	9.79E-04	0.001292793	1	0
BP1026B.11001	hypothetical protein	108550	185761	162077	551	208631	232973	216622	794	0.038959447	0.045895826	1.441016334	0.527086689
BP1026B.11002	N-acetylglutamate synthase	269042	168522	198763	154	149316	122877	147584	101	1.92E-42	4.35E-41	0.655844156	-0.608575058
BP1026B.11003	ATP-dependent helicase HrpA	161763	144325	155774	37	140037	134638	134739	33	4.97E-18	2.17E-17	0.891891892	-0.16059246
BP1026B.11004	hypothetical protein	130754	161893	157718	151	150394	139897	137242	143	4.82E-14	1.48E-13	0.947019688	-0.078533403
BP1026B.11005	hypothetical protein	133243	163577	146977	149	153001	163638	162799	161	3.77E-08	6.84E-08	1.080536913	0.111748358
BP1026B.11006	hypothetical protein	15743	15387	17089	18	15761	14642	17677	17	3.30E-12	8.50E-12	0.944444444	-0.08246216
BP1026B.11007	molybdopterin binding domain-containing protein	124006	162716	148977	177	148530	160381	146906	185	1.74E-09	3.52E-09	1.04519774	0.06377591
BP1026B.11008	rhodosome-like protein	34905	26937	31081	66	25020	23334	26480	53	8.87E-18	3.79E-17	0.803030303	-0.316473665
BP1026B.11009	glutamine synthetase, type I	569095	743359	688724	471	785873	807363	806930	565	0.165084841	0.183051073	1.199575372	0.262523808
BP1026B.11010	nitrogen regulation protein	36958	39213	40245	33	36098	29960	36705	29	1.48E-13	4.30E-13	0.878787879	-0.186413124
BP1026B.11011	nitrogen regulation protein NR(I)	51703	38803	38727	28	32524	33790	37594	22	3.77E-18	1.66E-17	0.785714286	-0.347923303
BP1026B.11012	exodeoxyribonuclease III	35883	39977	44570	51	43046	37522	40540	51	8.23E-10	1.72E-09	1	0
BP1026B.11013	DNA-binding response regulator NarL	50525	57657	59078	79	70686	69753	67656	98	3.04E-06	4.82E-06	1.240506329	0.310929096
BP1026B.11014	nitrate/nitrite sensor protein	135134	88053	96907	55	93482	83027	93824	46	7.30E-23	4.75E-22	0.836363636	-0.257797757
BP1026B.11015	respiratory nitrate reductase subunit gamma	11797	9532	9133	14	9211	6807	10874	13	8.36E-15	2.74E-14	0.987271429	-0.106915204
BP1026B.11016	nitrate reductase subunit delta	4807	3964	4522	6	4453	5017	3834	6	1.66E-07	2.86E-07	1	0
BP1026B.11017	nitrate reductase subunit beta	15889	18668	17394	11	20417	23086	22408	14	8.00E-05	1.14E-04	1.272727273	0.347923303
BP1026B.11018	nitrate reductase subunit alpha	55191	62630	62273	16	63383	65282	66838	17	1.91E-10	4.17E-10	1.0625	0.087462841
BP1026B.11019	nitrate/nitrite transporter NarK	8243	9563	9262	6	10295	10191	10913	7	1.58E-06	2.54E-06	1.166666667	0.222392421
BP1026B.11020	nitrate/nitrite transporter	11656	10431	12163	8	9957	10773	10250	8	2.18E-13	6.25E-13	1	0
BP1026B.11021	hypothetical protein	730	800	801	6	1020	1464	1312	10	0.160148094	0.177022844	1.666666667	0.736965594
BP1026B.11022	Met tRNA	175	403	372	4	219	450	372	4	0.654302821	0.67621004	1	0
BP1026B.11023	DNA polymerase IV	40696	30770	31949	28	31156	26701	26959	23	3.09E-16	1.16E-15	0.821428571	-0.283792966
BP1026B.11024	oligonucleotide phosphatase A	384306	395676	394603	186	461019	448970	479663	220	1.25E-05	1.89E-05	1.182795699	0.242200902
BP1026B.11025	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase	72894	55093	61416	73	58477	55137	53228	64	6.33E-19	2.97E-18	0.876712329	-0.189824559
BP1026B.11026	LuxR family DNA-binding response regulator	361828	452369	409001	638	424289	432954	448299	681	6.69E-08	1.19E-07	1.067398119	0.094098374
BP1026B.11027	sensory box histidine kinase	208460	213561	204903	78	213606	222892	214364	81	1.45E-10	3.19E-10	1.038461538	0.054447784
BP1026B.11028	pyruvate dehydrogenase subunit E1	773819	1003650	960828	338	1009011	1022639	979365	372	0.147956283	0.165022084	1.100591716	0.138279375
BP1026B.11029	dihydropyrimidine acetyltransferase	205062	306082	276638	159	301644	300860	291899	181	2.60E-07	4.43E-07	1.13836478	0.186962932
BP1026B.11030	pyruvate dehydrogenase, E3 component, dihydrolipoamide dehydrogenase	330224	300965	326631	180	282199	274446	294282	160	1.71E-15	5.98E-15	0.888888889	-0.169925001
BP1026B.11031	phasin-like protein	1259305	1857058	1735874	2837	1831194	1903160	1866987	3275	0.130955223	0.146923084	1.154388438	0.207128756
BP1026B.11032	predicted RNA	6641	11290	11912	621	15604	19216	9840	930	0.00513193	0.0064481	1.497584541	0.582637448
BP1026B.11033	hypothetical protein	5694	7708	6006	31	7734	7414	7083					

BP1026B.11056	DNA internalization-related competence protein	22726	16027	16299	7	16717	14737	12196	5	1.42E-22	8.97E-22	0.714285714	-0.485426827
BP1026B.11057	hydrolase	191938	194509	185838	230	197181	198850	213503	245	1.05E-09	2.19E-09	1.065217391	0.091147888
BP1026B.11058	CTP synthetase	769272	973183	943871	538	1024930	1081957	1011172	625	0.092480814	0.105265174	1.161710037	0.216250017
BP1026B.11059	2-dehydro-3-deoxyphosphocetate aldolase	171221	176555	168799	201	177582	180437	199404	217	1.24E-08	2.34E-08	1.07960199	0.110499517
BP1026B.11060	phosphopyruvate hydratase	845553	1033256	1001281	747	969620	994881	997665	768	0.249675581	0.271514611	1.02811245	0.039998068
BP1026B.11061	cell division protein FtsB	71681	85069	82870	184	87360	100272	90368	214	3.06E-08	5.61E-08	1.163043478	0.21790503
BP1026B.11062	lipoprotein	32354	33824	35900	97	37864	40033	41143	114	9.83E-06	1.50E-05	1.175257732	0.232977172
BP1026B.11063	chaperonin HSP33	217856	232118	232168	239	258401	246698	265440	270	5.56E-07	9.30E-07	1.129707113	0.175948789
BP1026B.11064	hexapeptide repeat-containing transferase	75752	96049	94765	169	124855	117098	113898	225	2.84E-04	3.91E-04	1.331360947	0.412901755
BP1026B.11065	hypothetical protein	22658	14451	16632	21	15174	12993	14568	17	3.77E-22	2.30E-21	0.80952381	-0.304854582
BP1026B.11066	alpha/beta fold family hydrolase	31820	24271	27310	30	27044	27496	27291	30	7.76E-10	1.63E-09	1	0
BP1026B.11067	hypothetical protein	1729	384	597	4	368	474	428	2	2.61E-15	8.98E-15	0.5	-1
BP1026B.11068	metal-dependent phosphoesterase	63295	56231	60098	72	62171	58835	54354	70	3.26E-14	1.01E-13	0.972222222	-0.040641984
BP1026B.11069	Sua5/YciO/YrdC/YwIC family protein	18800	12280	13847	23	13155	12410	15036	21	3.82E-15	1.30E-14	0.913043478	-0.131244533
BP1026B.11071	membrane metalloprotease	28661	28179	30227	43	33370	29610	36229	49	5.62E-06	8.72E-06	1.139534884	0.188445089
BP1026B.11070	tryptophanyl-tRNA synthetase	409545	438973	443657	366	439105	432472	447311	373	2.92E-09	5.83E-09	1.019125683	0.027331982
BP1026B.11072	methyltransferase	12403	4731	6567	13	5281	4155	5393	8	6.67E-28	6.44E-27	0.615384615	-0.700439718
BP1026B.11073	dihydrodipicolinate synthase	328389	375733	363304	394	407653	410862	427663	460	6.60E-06	1.02E-05	1.16751269	0.223438231
BP1026B.11074	lipoprotein	276864	300371	296500	254	285164	272988	283286	245	1.62E-12	4.30E-12	0.964566929	-0.052046748
BP1026B.11075	metallo-beta-lactamase family protein	116262	121863	116867	152	128502	127661	132207	166	4.86E-09	9.49E-09	1.092105263	0.127111918
BP1026B.11076	putative lipoprotein	1651645	1987828	1931957	7282	2369789	2557448	2805263	10107	0.108311216	0.122571443	1.387942873	0.472948188
BP1026B.11077	cupin superfamily protein family	77129	82517	79920	65	77898	77234	77982	3	2.65E-15	9.10E-15	0.969230769	-0.04508789
BP1026B.11078	FkpP-type peptidyl-prolyl cis-trans isomerase	443070	724108	632851	1098	904070	1014682	935715	1742	0.003702409	0.004702878	1.586520947	0.66586657
BP1026B.11079	hypothetical protein	91597	82430	86801	76	84590	73624	84690	71	1.50E-17	6.28E-17	0.934210526	-0.098180394
BP1026B.11080	DNA mismatch repair protein MutS	138667	135256	139405	51	139519	143446	138151	52	3.93E-11	9.11E-11	1.019607873	0.028014376
BP1026B.11081	Phage integrase	59872	98973	85375	62	114566	121634	113817	89	0.004361632	0.005508967	1.435483871	0.521537121
BP1026B.11082	hypothetical protein	5298	8427	7470	14	11822	11563	12089	24	0.11769982	0.132621304	1.714285714	0.777607579
BP1026B.11083	hypothetical protein	2836	1756	2269	6	3130	2209	2902	8	0.020743126	0.024942704	1.333333333	0.415037499
BP1026B.11084	hypothetical protein	10524	12215	12021	8	15332	16795	17135	12	9.18E-04	0.001215089	1	0.584962501
BP1026B.11085	hypothetical protein	10050	14778	12630	27	22236	21890	19748	47	0.22018529	0.241076538	1.740740741	0.79970135
BP1026B.11086	hypothetical protein	4600	4915	5039	8	7037	7020	5882	10	0.01030903	0.001359351	1.25	0.321928095
BP1026B.11087	hypothetical protein	4013	2850	4145	10	4525	3854	4420	12	3.23E-04	4.42E-04	1.2	0.263034406
BP1026B.11088	hypothetical protein	3363	4911	4541	19	7133	6410	5724	29	0.014348041	0.017453859	1.526315789	0.610053482
BP1026B.11089	putative repressor protein	113818	204618	184382	271	212753	254185	203754	361	0.001904983	0.002471351	1.332103321	0.413705986
BP1026B.11090	hypothetical protein	6475	8526	7688	15	11118	12503	10736	21	0.014809138	0.01800428	1.533333333	0.61667136
BP1026B.11091	hypothetical protein	4148	3980	4703	12	4660	5984	6066	15	6.90E-04	9.23E-04	1.25	0.321928095
BP1026B.11092	hypothetical protein	2056	3390	2714	15	3993	4206	4116	22	0.391471016	0.416319991	1.466666667	0.552541023
BP1026B.11093	hypothetical protein	8760	10706	10280	21	12210	13260	15083	28	3.73E-04	5.08E-04	1.333333333	0.415037499
BP1026B.11094	virulence-associated protein E	51906	68862	64651	24	87169	94386	94687	36	0.007116243	0.008840281	1.5	0.584962501
BP1026B.11095	hypothetical protein	9061	11918	11581	18	14166	16652	14293	25	4.62E-04	6.26E-04	1.388888889	0.473931188
BP1026B.11096	hypothetical protein	4701	3805	4774	23	6949	7799	7403	39	0.082711146	0.094608988	1.695652174	0.761840263
BP1026B.11097	hypothetical protein	12199	20161	17343	29	27901	33030	31073	53	0.977237991	0.98115258	1.827586207	0.869939459
BP1026B.11098	phage terminase large subunit (GpA)	46415	54695	52210	25	69645	67531	69826	34	3.01E-04	4.14E-04	1.36	0.443606651
BP1026B.11099	hypothetical protein	5060	4229	5307	23	6832	7084	7952	35	0.008947534	0.011036466	1.52173913	0.605721061
BP1026B.11100	phage portal protein, lambda family	16419	17097	15874	11	21769	23602	22053	15	0.00194471	0.002079716	1.363636364	0.447458977
BP1026B.11101	peptidase S14, ClpP	28505	22621	27189	23	29826	24741	33631	26	2.72E-06	4.32E-06	1.130434783	0.176877762
BP1026B.11102	hypothetical protein	8973	2366	3288	14	4327	3018	4211	11	5.35E-13	1.49E-12	0.785714286	-0.347923303
BP1026B.11103	hypothetical protein	42824	54157	53385	48	75888	82135	82215	78	0.080747187	0.092497601	1.625	0.700439718
BP1026B.11104	hypothetical protein	6760	4144	3989	17	4122	3598	5061	14	3.56E-11	8.28E-11	0.823529412	-0.280107919
BP1026B.11105	hypothetical protein	9479	7181	8488	15	12394	11291	9011	20	1.58E-04	2.21E-04	1.333333333	0.415037499
BP1026B.11106	hypothetical protein	13098	19374	16647	31	22365	24300	23297	45	0.007724707	0.009565813	1.451612903	0.537656786
BP1026B.11107	baseplate assembly protein V	17551	15388	16200	24	20930	17998	17048	27	4.12E-08	7.46E-08	1.125	0.169925001
BP1026B.11108	hypothetical protein	3916	6015	5351	24	7656	7616	8579	38	0.020694517	0.024893807	1.583333333	0.662965013
BP1026B.11109	GPW/gp25 family protein	5701	4520	5405	15	6756	6831	6344	19	9.19E-05	1.31E-04	1.266666667	0.341036918
BP1026B.11110	hypothetical protein	14671	15132	15326	16	19357	18462	20363	21	4.16E-05	6.05E-05	1.3125	0.392317423
BP1026B.11111	phage tail protein I	12835	8683	10483	18	11139	10452	12316	19	1.08E-08	2.05E-08	1.055555556	0.078002512
BP1026B.11112	gp26	43439	66682	58091	38	93936	104406	95253	66	0.452823461	0.478561613	1.736842105	0.796466666
BP1026B.11113	hypothetical protein	14635	17704	18902	37	23902	22246	20905	49	3.34E-04	4.57E-04	1.324324324	0.405256478
BP1026B.11114	phage tail sheath protein	29993	34171	33007	27	50816	58099	45298	43	0.113628857	0.12833425	1.592592593	0.671377253
BP1026B.11115	phage major tail tube protein	26553	40517	37364	69	55306	55499	56117	110	0.13678637	0.153138244	1.594202899	0.672835257
BP1026B.11116	hypothetical protein	4551	6307	5838	18	9651	11045	9793	33	0.426785013	0.452187164	1.833333333	0.874469118
BP1026B.11117	hypothetical protein	3189	5763	4836	39	9188	10387	8009	78	0.888830022	0.900033762	2	1
BP1026B.11118	tail tape measure protein	32573	43752	40862	16	68932	67853	63995	27	0.43824967	0.463550377	1.6875	0.754887502
BP1026B.11119	phage P2 GpU family protein	6686	5217	5626	6	7006	6608	7195	7	4.15E-06	6.50E-06	1.166666667	0.222392421
BP1026B.11120	phage Tail Protein X	1921	1790	1539	8	2538	2457	2102	11	0.336975425	0.360876434	1.375	0.459431619
BP1026B.11121	phage tail formation protein	12621	12085	12812	11	13769	17441	15660	14	7.28E-06	1.12E-05	1.272727273	0.347923303
BP1026B.11122	gp24	3629	2869	3281	6	4948	5822	4696	10	0.292041447	0.315233713	1.666666667	0.736965594
BP1026B.11123	bacteriophage lysis protein	5846	6877	7416	12	11096	10390	10692	20	0.058610494	0.067946966	1.666666667	0.736965594
BP1026B.11124	Site-specific DNA methylase	34227	57877	51200	60	71126	80966	73580	95	0.067954726	0.078330448	1.583333333	0.662965013
BP1026B.11125	hypothetical protein	265395	441971	396260	494	474345	546612	472191	668	0.007349452	0.009113727	1.35226721	0.435337061
BP1026B.11126	hypothetical protein	193178	245966	243315	438	250794	269753	245521	492	3.56E-07	6.02E-07	1.123287671	0.167727446
BP1026B.11127	hypothetical protein	104181	113359	117693	235	111282	101257	109036	226	2.55E-14	7.97E-14	0.961702128	-0.056337984
BP1026B.11128	hypothetical protein	37821	34048	34299	67	32751	29783	32243	62	1.72E-11	4.13E-11	0.925373134	-0.1189288
BP1026B.11129	PAAR motif-containing protein	73283	69413	65498	162	75250	74708	70589	172	1.74E-11	4.17E-11	1.061728395	0.086414752
BP1026B.11130	hypothetical protein	10282	12729	15425	50	18114	21995	20829	72	0.002443083	0.003149868		

BP1026B.1156	multidrug efflux RND membrane fusion protein MexE	40174	32381	33053	28	20771	19149	18315	15	2.67E-57	1.16E-55	0.535714286	-0.900464326
BP1026B.1157	sulfate adenylyltransferase	79732	65635	69146	48	43764	50899	51930	33	4.41E-36	7.16E-35	0.6875	-0.540568381
BP1026B.1158	peptide synthetase-domain-containing protein	52232	38877	44505	24	21380	20314	21008	11	6.61E-85	5.92E-83	0.458333333	-1.125550882
BP1026B.1159	MFS permease	32829	27912	31952	23	18335	16993	18600	13	9.60E-52	3.32E-50	0.565217391	-0.823122238
BP1026B.1160	hypothetical protein	26365	12853	16386	13	8773	6881	7747	5	1.32E-96	1.47E-94	0.384615385	-1.378511623
BP1026B.1161	nonribosomal peptide synthetase	175301	122618	137521	16	88561	76761	84279	9	9.03E-66	5.60E-64	0.5625	-0.830074999
BP1026B.1162	hypothetical protein	19108	17872	17341	22	10685	9999	10288	12	2.10E-44	5.15E-43	0.545454545	-0.874469118
BP1026B.1163	dioxigenase, Taud/TidA	26139	20152	21012	25	12252	11670	11539	13	6.62E-57	2.84E-55	0.52	-0.943416472
BP1026B.1164	hypothetical protein	30969	24973	21908	30	15716	16101	17215	19	3.85E-42	8.50E-41	0.633333333	-0.658963082
BP1026B.1165	hypothetical protein	69579	77375	77436	95	49574	48272	46028	61	3.30E-42	7.33E-41	0.642105263	-0.639118271
BP1026B.1166	hypothetical protein	32942	14922	17405	21	8480	8591	8975	8	8.52E-110	1.07E-107	0.380952381	-1.392317423
BP1026B.1167	transketolase	9482	6733	6510	9	4644	3656	4399	5	5.76E-33	7.81E-32	0.555555556	-0.847996907
BP1026B.1168	transketolase	26648	16037	17288	21	9708	7498	11067	10	1.58E-71	1.09E-69	0.476190476	-1.070389328
BP1026B.1169	hypothetical protein	31440	16684	18712	19	11265	10174	10962	9	4.88E-67	3.06E-65	0.473684211	-1.078002512
BP1026B.1170	acyltransferase family protein	19788	24865	21040	19	19016	17999	18492	16	4.75E-20	2.44E-19	0.842105263	-0.247927513
BP1026B.1171	phosphoserine aminotransferase	57283	66899	63932	57	45475	45949	46948	42	8.71E-29	8.97E-28	0.736842105	-0.440572591
BP1026B.1173	glycosyl transferase family protein	39703	30532	33271	42	22459	21345	20420	26	1.29E-39	4.47E-38	0.619047619	-0.691877705
BP1026B.1172	sulfate adenylyltransferase subunit 2	72583	77585	77079	78	74689	67220	68686	72	2.24E-17	9.26E-17	0.923076923	-0.114772717
BP1026B.1174	kinase	32886	39718	39892	31	33768	32813	32049	27	1.31E-13	3.84E-13	0.870967742	-0.199308808
BP1026B.1175	cysteine synthase/cystathionine beta-synthase family protein	27417	24462	26197	25	19330	19328	19637	19	8.90E-27	7.90E-26	0.76	-0.395928676
BP1026B.1176	argininosuccinate lyase	40256	23576	24982	10	18590	16959	19008	6	3.69E-45	9.61E-44	0.6	-0.736965594
BP1026B.1177	hypothetical protein	18876	9060	10349	64	9486	8211	8717	44	3.31E-28	3.24E-27	0.6875	-0.540568381
BP1026B.1178	methionine aminopeptidase	46479	34710	37245	51	31435	29710	30156	39	1.79E-19	8.82E-19	0.764705882	-0.387023123
BP1026B.1179	TetR family transcriptional regulator	29163	21487	23525	27	22964	24239	23021	25	5.69E-12	1.43E-11	0.925925926	-0.110131312
BP1026B.1180	ferredoxin	3668	1506	1654	6	1728	2001	1829	5	1.63E-07	2.80E-07	0.833333333	-0.263034406
BP1026B.1182	ferredoxin--NADP reductase	4401	4492	5096	6	4711	4978	6102	6	5.95E-06	9.23E-06	1	0
BP1026B.1183	molybdopterin oxidoreductase family protein	26912	33112	33519	13	35283	37580	33777	15	5.20E-06	8.09E-06	1.153846154	0.206450877
BP1026B.1184	hypothetical protein	2322	1698	1665	8	1400	1664	1083	6	7.45E-09	1.43E-08	0.75	-0.415037499
BP1026B.1185	hypothetical protein	5458	1838	2719	9	2284	2281	2128	6	1.73E-15	6.06E-15	0.666666667	-0.584962501
BP1026B.1187	enoyl-ACP reductase	170239	148565	162403	202	143274	123349	146875	174	7.65E-20	3.88E-19	0.861386139	-0.215267987
BP1026B.1186	ABC transporter substrate-binding protein	167652	130354	137407	74	127926	120030	124528	63	1.32E-20	7.09E-20	0.851351351	-0.232173442
BP1026B.1188	ABC transporter membrane protein	51146	60509	58585	54	66870	66829	68420	64	1.64E-07	2.83E-07	1.185185185	-0.245112498
BP1026B.1189	ABC transporter permease	47876	36860	38969	37	39232	34656	38550	34	5.41E-13	1.50E-12	0.918918919	-0.121990524
BP1026B.1190	ABC transporter ATP-binding protein	81998	51886	61153	39	53302	49649	53721	31	3.55E-24	3.79E-23	0.794871795	-0.331205908
BP1026B.1191	hypothetical protein	7592	12524	12910	107	15392	18598	12989	153	0.001058615	0.001394718	1.429906542	0.515920856
BP1026B.1192	NLP/P60 family protein	226178	275544	249851	355	288167	320969	301595	430	1.30E-05	1.96E-05	1.211267606	0.276517635
BP1026B.1193	patatin-like phospholipase	18898	19029	18544	20	18716	16600	17667	18	2.19E-15	7.61E-15	0.9	-0.152003093
BP1026B.1194	glutamyl-tRNA synthetase	94912	104068	100357	65	112314	112459	108699	73	1.14E-08	2.15E-08	1.123076923	0.167456746
BP1026B.1195	tRNA	25698	39798	34856	440	68911	65079	923	0.16614364	0.184127352	2.097727273	1.068827124	
BP1026B.1196	Glu tRNA	61092	104993	86935	1109	194717	206491	204641	2657	6.38E-04	8.56E-04	2.395852119	1.260538862
BP1026B.1197	Asp tRNA	36562	56452	45949	601	90382	100805	106872	1290	0.052635214	0.061269228	2.146422629	1.10193417
BP1026B.1198	Glu tRNA	24459	37110	28334	394	66272	70176	86128	976	0.002230961	0.002882904	2.47715736	1.308685518
BP1026B.1199	Asp tRNA	7934	14542	10725	143	21920	22874	25166	302	0.414452672	0.439790083	2.11888112	1.078533403
BP1026B.1200	acetyltransferase	20195	29361	29136	56	28013	32686	31338	61	1.61E-05	2.41E-05	1.160714286	0.215012891
BP1026B.1201	AraC family transcriptional regulator	11314	7736	9265	10	9358	7892	10040	10	1.39E-11	3.36E-11	1	0
BP1026B.1202	ribonuclease activity regulator protein RraA	24290	27021	27970	53	38588	40188	36787	77	0.019137018	0.023060107	1.452830189	0.538866086
BP1026B.1203	hypothetical protein	44288	42875	45088	108	36782	31792	35014	84	1.50E-19	7.45E-19	0.777777778	-0.362570079
BP1026B.1204	malate synthase	409315	503632	511035	297	504787	531896	504144	322	5.01E-04	6.77E-04	1.084175084	0.116597757
BP1026B.1205	haloacid dehalogenase	20390	6541	8911	14	7164	6056	6979	8	1.44E-44	3.58E-43	0.571428571	-0.807354922
BP1026B.1206	LysR family transcriptional regulator	32308	30367	28831	30	30853	30236	27900	30	7.41E-10	1.56E-09	1	0
BP1026B.1207	universal stress protein family protein	8141	4689	4862	13	3584	3971	3853	8	1.56E-21	9.01E-21	0.615384615	-0.700439718
BP1026B.1208	isocitrate lyase	363990	440767	441862	317	539901	537241	553373	415	0.759113054	0.778239921	1.309148265	0.388628496
BP1026B.1209	ATP-dependent RNA helicase	19744	18154	18392	12	22846	23072	22457	14	1.56E-05	2.34E-05	1.166666667	0.222392421
BP1026B.1211	acyl-CoA-binding protein	111558	161353	141467	511	193243	189761	205444	726	0.023396594	0.028015107	1.42074364	0.506646257
BP1026B.1212	glycoprotease family protein	4034	869	1383	2	932	597	1105	1	1.21E-31	1.47E-30	0.5	-1
BP1026B.1210	ribosomal-protein-alanine acetyltransferase	43301	59093	55642	105	54116	62679	54317	114	1.01E-09	2.09E-09	1.085714286	0.118644496
BP1026B.1213	phage SPO1 DNA polymerase domain-containing protein	165407	166018	162047	214	160169	155443	165116	211	1.38E-11	3.34E-11	0.985981308	-0.020367798
BP1026B.1214	hypothetical protein	30026	20367	24489	25	18984	13857	18970	17	1.53E-33	2.15E-32	0.68	-0.556393349
predicted RNA	-	50918	74502	62708	1161	70051	73158	74146	1341	1.67E-08	3.12E-08	1.15503876	0.207941265
BP1026B.1215	phosphomethylpyrimidine kinase	25021	10154	13254	19	10786	8030	10198	11	3.11E-39	5.83E-38	0.578947368	-0.788495895
BP1026B.1216	lysophospholipid transporter	119697	143718	131553	102	152746	149380	164937	121	9.43E-06	1.44E-05	1.18627451	0.246437895
BP1026B.1217	alanine racemase	197406	177822	176888	171	172413	162105	162449	154	4.91E-16	1.82E-15	0.900584795	-0.15056974
BP1026B.1218	DNA repair protein RadA	172097	162049	160948	119	160600	150549	163002	114	6.07E-13	1.68E-12	0.957983193	-0.061927749
BP1026B.1219	hypothetical protein	26447	16981	19640	101	18021	15804	18045	83	1.49E-21	8.63E-21	0.821782178	-0.283172051
BP1026B.1220	ABC transporter ATP-binding protein	126401	136716	133482	68	144099	150537	148231	76	1.29E-07	2.24E-07	1.117647059	0.160464672
BP1026B.1221	glutathione peroxidase	56196	93214	84005	162	93165	102290	99860	205	1.18E-05	1.79E-05	1.265432099	0.339630097
BP1026B.1222	cardiolipin synthetase	74027	59227	57906	44	55014	50263	56366	37	5.27E-21	2.92E-20	0.840909091	-0.249978253
BP1026B.1223	hypothetical protein	1979	731	868	4	684	679	510	2	1.61E-13	4.66E-13	0.5	-1
BP1026B.1224	N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase	63504	40893	51586	56	34948	32114	36765	37	4.33E-31	5.10E-30	0.660714286	-0.597901556
BP1026B.1225	succinyl-diaminopimelate decarboxylase	40034	29564	31212	29	27414	25311	27602	23	8.50E-18	3.64E-17	0.793103448	-0.334419039
BP1026B.1226	ArsC family transcription regulator	103557	90318	98826	260	92169	79252	71752	216	2.00E-24	1.46E-23	0.830769231	-0.267480311
BP1026B.1227	2,3,4,5-tetrahydropyridine-2,6-carboxylate L-n-succinyltransferase	251361	193334	203975	261	187888	179579	193462	225	1.47E-18	6.69E-18	0.862068966	-0.214124805
BP1026B.1229	N-succinyl-L,L-diaminopimelate aminotransferase/alternative	46512	40015	39823	34	36798	38658	33259	29	3.78E-15	1.28E-14	0.852941176	-0.229481846
BP1026B.1228	hypothetical protein	40059	25152	25656	31	26233	25174	26231	27	7.23E-15	2.39E-14	0.870967742	-0.199308808
BP1026B.1230	chromosome segregation protein SMC	613619	517491	542126	158	508048	464518	486097	138	1.23E-14	3.95E-14	0.873417722	-0.195256291
BP1026B.1231	hypothetical protein	290250	250725	258849	209	233385	212577	241995					

BP1026B_11251	RNA methyltransferase	102939	64839	82985	105	61297	50312	66265	75	1.56E-35	2.47E-34	0.714285714	-0.485426827
BP1026B_11252	hypothetical protein	243467	327013	307852	358	373777	379692	369331	458	1.10E-04	1.55E-04	1.279329609	0.355388011
BP1026B_11253	serine protease	37820	25378	29593	16	25050	20597	23933	12	1.09E-22	7.00E-22	0.75	-0.415037499
BP1026B_11254	primitive phytocyclin synthase	12117	8315	9498	13	7784	6283	7373	9	3.01E-25	2.35E-24	0.692307692	-0.530514717
BP1026B_11255	phosphoenolpyruvate synthase	866537	980516	968586	391	1058728	1065934	1091110	446	0.112470579	0.12707188	1.140664962	0.189875103
BP1026B_11256	modulation efficiency protein D	10410	10219	9358	22	10197	10193	13669	26	4.92E-07	8.25E-07	1.181818182	0.2410081
BP1026B_11257	SPFH domain protein/band 7 family protein	275003	358877	332170	339	339907	353299	348864	366	2.23E-08	4.11E-08	1.079646018	0.110558375
BP1026B_11258	SsrA-binding protein	99520	148391	137641	287	200803	213444	195712	454	0.29767366	0.320705494	1.581881533	0.661641561
BP1026B_11259	cyclase/dehydrase superfamily	60072	101881	92431	204	139690	148313	136632	341	0.031192313	0.0355168755	1.671568627	0.741202587
BP1026B_11260	TGS domain-containing protein	64325	39042	44986	152	39615	36248	43536	122	9.71E-20	4.90E-19	0.802631579	-0.317190176
BP1026B_11261	integral membrane protein	19469	12759	14493	16	15622	14724	14847	15	4.17E-13	1.17E-12	0.9375	-0.093109404
BP1026B_11262	hypothetical protein	12987	13004	13907	19	12680	12308	12583	18	7.56E-13	2.07E-12	0.947368421	-0.078002512
BP1026B_11263	hypothetical protein	2438	664	1010	1	1005	616	1364	0	1.51E-07	2.60E-07	0	#NUM!
BP1026B_11264	hypothetical protein	13065	14248	14472	18	13338	11367	13438	16	3.62E-14	1.12E-13	0.888888889	-0.169925001
BP1026B_11265	inosine 5'-monophosphate dehydrogenase	400720	400639	413973	277	449683	428374	426222	297	9.89E-08	1.73E-07	1.072202166	0.100576955
BP1026B_11266	hypothetical protein	105047	112438	107651	165	115079	121639	122305	182	6.68E-09	1.29E-08	1.103030303	0.141472426
BP1026B_11267	GMP synthase	252445	285535	284202	169	287182	291354	288133	178	1.82E-09	3.69E-09	1.053254438	0.074853995
BP1026B_11268	Integrase	12661	21758	18925	26	22201	23020	23043	34	1.62E-04	2.27E-04	1.307692308	0.387023123
BP1026B_11269	hypothetical protein	190908	302013	264233	215	323595	361476	338693	291	0.001250123	0.001638075	1.353488372	0.436682493
BP1026B_11270	hypothetical protein	89192	150607	127912	140	153979	178233	170447	191	0.008218823	0.010161631	1.364285714	0.448145811
BP1026B_11271	hypothetical protein	61460	104402	91124	62	104988	122029	111885	82	1.64E-04	2.29E-04	1.322580645	0.403355694
BP1026B_11272	hypothetical protein	10746	17774	13575	150	20396	23980	22697	240	0.092186528	0.104968342	1.6	0.678071905
BP1026B_11273	hypothetical protein	2555	3632	3498	17	4068	4483	4707	23	0.04361298	0.052034424	1.32941176	0.436099151
BP1026B_11274	major facilitator superfamily transporter	1759	1231	1424	1	1418	1073	1560	1	5.69E-04	7.66E-04	1	0
BP1026B_11275	hypothetical protein	64308	50139	54491	111	54877	54809	57548	109	3.51E-13	9.90E-13	0.981981982	-0.026231542
BP1026B_11276	hypothetical protein	40232	21336	23195	66	24140	22921	21262	53	4.78E-19	2.27E-18	0.803030303	-0.316473665
BP1026B_11277	cytidine/deoxycytidylate deaminase family protein	16290	6453	6503	18	6209	3785	5859	10	1.75E-41	3.70E-40	0.555555556	-0.847969607
BP1026B_11278	L,D-carboxypeptidase A	60625	64777	67855	68	59556	53367	59482	61	1.44E-18	6.57E-18	0.897058824	-0.156725504
BP1026B_11279	GnR family transcriptional regulator	12123	8242	10299	14	6199	6483	7223	9	3.19E-31	3.79E-30	0.642857143	-0.637429921
BP1026B_11280	NCS1 nucleoside transporter family protein	10114	9032	8627	6	8701	7814	8275	5	7.96E-15	2.62E-14	0.833333333	-0.263034406
BP1026B_11281	racemase	2015	1052	1060	1	828	669	760	0	1.75E-13	5.03E-13	0	#NUM!
BP1026B_11283	polysaccharide deacetylase family protein	88244	78479	87615	88	63739	54226	66445	64	4.82E-34	6.93E-33	0.727272727	-0.459431619
BP1026B_11282	chitinoglycosaccharide deacetylase	25478	14661	15036	35	10979	12451	12277	22	3.80E-34	5.51E-33	0.628571429	-0.669851398
BP1026B_11284	allantoicase	39366	38952	41258	39	30915	32827	29166	30	3.76E-19	1.81E-18	0.769230769	-0.378511623
BP1026B_11285	ureidoglycolate hydrolase	27817	27131	29246	54	21458	20846	20339	40	1.90E-25	1.51E-24	0.740740741	-0.432959407
BP1026B_11286	hypothetical protein	74813	76920	79339	64	72340	73626	77191	61	1.68E-15	5.90E-15	0.953125	-0.069262662
BP1026B_11287	Transthyretin family protein	9056	8345	9924	25	8481	8018	8026	23	1.19E-14	3.83E-14	0.92	-0.120294234
BP1026B_11288	translthyretin family protein	2158	1243	1611	3	952	1018	1598	2	8.78E-09	1.68E-08	0.666666667	-0.584962501
BP1026B_11289	hydroxydechlorotrazine ethylaminohydrolase	32316	24173	25050	18	20582	20582	22141	14	1.39E-22	8.82E-22	0.777777778	-0.362570079
BP1026B_11290	LysR family regulatory protein	50826	62757	58319	56	61752	67204	64534	63	3.79E-09	7.47E-09	1.125	0.169925001
BP1026B_11291	hypothetical protein	17842	27247	26985	114	34684	38416	36690	174	0.048862559	0.057089837	1.526315789	0.610053482
BP1026B_11292	6-phosphogluconate dehydrogenase	9058	6718	7269	8	6437	6217	5687	6	1.05E-17	4.48E-17	0.75	-0.415037499
BP1026B_11293	hypothetical protein	49538	39966	42192	89	47777	49777	43705	97	7.75E-09	1.49E-08	1.078651685	0.109229097
BP1026B_11294	large-conductance mechanosensitive channel	400738	656597	567782	1253	725406	817321	766784	1782	0.070196434	0.080780689	1.422186752	0.508110922
BP1026B_11295	hypothetical protein	130855	104772	107874	94	112885	100746	95573	84	1.43E-17	6.02E-17	0.893617021	-0.162271429
BP1026B_11296	PspA/IM30 family protein	431576	369512	414655	595	419070	350490	414490	579	1.86E-10	4.07E-10	0.973109244	-0.03932632
BP1026B_11297	1A family penicillin-binding protein	187213	195467	197508	76	189010	184807	185064	73	3.59E-13	1.01E-12	0.960526136	-0.058102955
BP1026B_11298	hypothetical protein	30119	19174	20051	50	18700	16981	16831	38	9.49E-27	8.40E-26	0.76	-0.359528676
BP1026B_11299	threonine dehydratase catabolic	163392	144159	153363	148	149253	140235	143359	139	1.94E-14	6.15E-14	0.939189189	-0.090512293
BP1026B_11300	acetylornithine deacetylase	133355	101213	110264	94	94662	89204	99426	77	4.67E-24	3.34E-23	0.819148936	-0.287802311
BP1026B_11301	transcription-repair coupling factor	343737	339753	351834	97	366129	347928	380442	103	1.50E-08	2.81E-08	1.06185567	0.086587685
BP1026B_11302	2-C-methyl-D-erythritol 4-phosphate cytidyllyltransferase	14058	9189	10689	15	9329	8583	8502	12	8.93E-21	4.84E-20	0.8	-0.321928095
BP1026B_11303	2-C-methyl-D-erythritol 4-cyclo diphosphate synthase	23885	23464	23274	48	20688	20567	22536	43	4.99E-15	1.67E-14	0.895833333	-0.158697746
BP1026B_11304	alkyl hydroperoxide reductase D	209180	199808	195248	381	201506	204204	201773	383	6.59E-12	1.65E-11	1.005249344	0.007553394
BP1026B_11305	anti-oxidant AhpCTSA family protein	5384322	8542629	7864899	13231	9165213	10060944	9759249	17598	0.011691312	0.014313748	1.330658197	0.141489372
BP1026B_11306	hypothetical protein	58815	96680	93221	112	117833	145222	101935	112	0.009631411	0.011856664	0.78098296	0.553832603
BP1026B_11307	sensor histidine kinase RtsA	149815	164129	150710	813	167030	174929	169180	1295	1.53E-07	2.64E-07	1.106194949	0.145605322
BP1026B_11308	osmolarity response regulator	163146	184509	182872	243	180062	179647	179785	258	2.49E-09	4.99E-09	1.061728395	0.086414752
BP1026B_11309	hypothetical protein	4540	8105	6483	39	10485	9485	8591	57	0.007613222	0.009431484	1.46138462	0.547487795
BP1026B_11310	hypothetical protein	54633	62746	57573	200	69165	66734	77495	244	7.32E-07	1.21E-06	1.22	0.286881148
BP1026B_11311	hypothetical protein	180699	158587	173834	116	141209	134007	147914	96	1.77E-22	1.11E-21	0.827586207	-0.273018494
BP1026B_11312	twin-arginine translocation pathway signal sequence domain-containing protein	43104	37433	37924	31	32368	30620	35138	26	4.00E-16	1.48E-15	0.838709677	-0.253756592
BP1026B_11313	phytoene synthase	21401	21736	20129	25	19848	19603	18301	22	7.42E-16	2.69E-15	0.88	-0.184424571
BP1026B_11314	Leu tRNA	2416	3874	3623	37	8514	9036	7985	97	0.002973936	0.003813893	2.621621622	1.390459477
BP1026B_11315	hypothetical protein	88354	147331	138342	261	152710	182484	156162	343	0.001850487	0.002404136	1.314176245	0.39415877
BP1026B_11316	hypothetical protein	41113	37615	42180	85	38571	39608	34977	79	7.07E-12	1.76E-11	0.929411765	-0.105610188
BP1026B_11317	hypothetical protein	18048	12603	12518	28	15274	14658	12417	27	3.35E-12	8.62E-12	0.964285714	-0.05246742
BP1026B_11318	PAAR motif-containing protein	26712	23664	26544	60	29042	24628	23375	60	1.69E-09	3.43E-09	1	0
BP1026B_11319	transposase B	140161	187179	169915	193	179139	190827	189805	218	3.25E-07	5.50E-07	1.129533679	0.175727288
BP1026B_11320	transposase	185855	319324	282056	901	361973	408545	328293	1258	0.0030455	0.003900879	1.396226415	0.481532911
BP1026B_11321	hypothetical protein	279619	490180	452907	1061	460821	536667	442230	1249	6.63E-06	1.02E-05	1.177191329	0.235348821
BP1026B_11322	hypothetical protein	1444	2627	2851	10	2590	3437	3547	14	0.225554231	0.246739318	1.4	0.485426827
BP1026B_11323	exported avidin family protein	4881	9358	8561	16	8879	11432	9991	21	4.35E-04	5.92E-04	1.3125	0.392317423
BP1026B_11324	endonuclease Nuc	3220	2761	3397	5	3673	3674	3766	5	0.003795273	0.004814979	1	0
BP1026B_11325	histone deacetylase family protein	1135	823	1078	0	688	577	1007	0	2.			

BP1026B_11349	sugar kinase	8444	3955	4198	3	2979	2372	3309	1	8.99E-33	1.20E-31	0.333333333	-1.584962501
BP1026B_11350	D-amino acid dehydrogenase small subunit	23351	10739	13634	12	11942	12152	12114	9	8.47E-23	5.48E-22	0.75	-0.415037499
BP1026B_11351	phosphoribosylformylglycinamide synthase	469490	416370	422169	107	427529	420020	423606	104	1.13E-10	2.52E-10	0.971962617	-0.041027268
BP1026B_11352	acetyltransferase	11641	2844	5218	12	2831	3063	3392	5	1.73E-42	3.95E-41	0.416666667	-1.26304406
BP1026B_11353	peptidyl-prolyl cis-trans isomerase domain-containing protein	551222	814782	756129	906	750656	778005	738323	968	0.575769435	0.600794551	1.068432671	0.095495997
BP1026B_11354	Cell division protein BoA	11500	14329	13927	42	16154	17574	15294	51	3.70E-06	5.83E-06	1.214285714	0.280107919
BP1026B_11355	intracellular septation protein A	88176	120779	117873	205	158702	176095	166458	314	0.154552163	0.171858714	1.531707317	0.615140649
BP1026B_11356	methionine-R-sulfoxide reductase	119892	112297	121994	273	127636	131775	117910	291	5.00E-10	1.06E-09	1.065934066	0.092118202
BP1026B_11357	hypothetical protein	42368	30077	32546	22	37189	31107	35198	21	1.26E-09	2.59E-09	0.954545455	-0.067114196
BP1026B_11358	long-chain-fatty-acid--CoA ligase	63195	54429	57095	35	52463	49644	53125	31	7.49E-18	3.22E-17	0.885714286	-0.175086707
BP1026B_11359	fatty oxidation complex subunit alpha	167443	164829	165438	79	168933	153115	164467	77	5.81E-12	1.46E-11	0.974683544	-0.036994207
BP1026B_11360	pyrazinamidase/nicotinamidase	27702	11442	13429	27	10746	8117	9868	14	2.10E-49	6.58E-48	0.518518519	-0.947532558
BP1026B_11361	acetyl-CoA acetyltransferase	46773	34913	34249	32	34060	33259	32703	28	2.12E-14	6.68E-14	0.875	-0.192645078
BP1026B_11362	hypothetical protein	15447	19480	18717	38	23033	23105	20607	47	3.85E-05	5.62E-05	1.23684105	0.306661338
BP1026B_11363	stress responsive A/B barrel domain family protein	161783	98378	104456	385	101941	98539	111037	329	1.59E-20	8.50E-20	0.854545455	-0.226770862
BP1026B_11364	thioesterase family protein	53443	22817	28070	72	22365	19306	22772	44	6.32E-40	1.23E-38	0.611111111	-0.710493383
BP1026B_11365	oxaloductase, zinc-binding dehydrogenase family protein	94652	62406	66607	74	52705	42803	50521	48	1.38E-40	2.77E-39	0.648648649	-0.624490865
BP1026B_11366	esterase	52688	40964	41741	47	40500	39852	40668	42	1.88E-14	5.96E-14	0.893617021	-0.162271429
BP1026B_11367	acetyltransferase	23283	10411	13697	34	10093	8018	9006	19	8.48E-45	2.14E-43	0.558823259	-0.839535328
BP1026B_11368	hypothetical protein	17082	10763	11831	15	10572	7680	9626	10	2.19E-26	1.88E-25	0.666666667	-0.584962501
BP1026B_11369	glycine cleavage I-protein, aminomethyl transferase	44428	29958	35133	34	28085	27562	26263	26	4.01E-21	2.24E-20	0.764705882	-0.387023123
BP1026B_11370	hypothetical protein	27761	25835	28325	26	36080	33863	32109	33	2.06E-04	2.87E-04	1.269230769	0.343954401
BP1026B_11371	thymidylate kinase	43266	35262	33951	60	38600	38759	35889	60	2.55E-09	5.12E-09	1	0
BP1026B_11372	DNA polymerase III subunit delta'	41785	24797	27549	30	27131	27045	26085	25	9.02E-15	2.95E-14	0.833333333	-0.26304406
BP1026B_11373	phosphothioric acetyltransferase	53690	35647	41808	86	37528	36547	32503	70	7.79E-18	3.35E-17	0.813953488	-0.296981738
BP1026B_11374	hypothetical protein	47434	56605	56622	66	60659	56996	47208	67	1.74E-11	4.17E-11	1.015151515	0.021695071
BP1026B_11375	ankyrin repeat-containing protein	268552	221438	230418	332	208587	187198	210302	279	4.50E-21	2.51E-20	0.840361446	-0.25091812
BP1026B_11376	hypothetical protein	99418	82056	82471	250	97576	90951	102528	276	1.58E-09	3.22E-09	1.104	0.142740172
BP1026B_11377	mechanosensitive ion channel family protein	98971	67254	80779	69	70815	62120	72443	57	9.94E-24	6.94E-23	0.826086957	-0.275634443
BP1026B_11378	hypothetical protein	28482	16637	18692	18	15903	14476	15697	13	1.51E-29	1.63E-28	0.722222222	-0.469485283
BP1026B_11379	glycosyl transferase group 1 protein	96048	106001	101679	95	94343	92272	96556	88	1.17E-16	4.54E-16	0.926315789	-0.11042399
BP1026B_11380	lipoprotein	15558541	7131268	8767469	17832	7200314	6399763	7389836	11899	1.23E-07	2.15E-07	0.667283535	-0.583628188
BP1026B_11381	hypothetical protein	5762	6381	5394	12	6106	6100	6100	12	2.50E-08	4.60E-08	1	0
BP1026B_11382	phosphate starvation-inducible protein	1710084	2409569	2321368	7378	2605019	2647422	2499832	8880	0.318835601	0.342386269	1.203578205	0.267329888
BP1026B_11383	asparaginase family protein	112022	67487	84859	84	59992	5184	56178	53	2.37E-46	6.42E-45	0.630952381	-0.664369668
BP1026B_11384	LysM domain/BON superfamily protein	381315	442331	437128	892	459713	452170	474528	981	2.19E-07	3.75E-07	1.099775501	0.137209426
BP1026B_11385	2-hydroxy-3-oxopropionate reductase	5609	3463	3655	4	2724	2888	3079	3	6.27E-17	2.50E-16	0.75	-0.415037499
BP1026B_11386	hydroxypyruvate isomerase	18241	12169	13389	18	12339	10352	12751	14	6.19E-19	2.91E-18	0.777777778	-0.362570079
BP1026B_11387	glyoxylate carboligase	8682	7223	7875	4	9588	7861	9085	4	1.08E-07	1.89E-07	1	0
BP1026B_11388	LysR family transcriptional regulator	37240	28080	30903	35	26906	24743	25026	28	4.37E-18	1.92E-17	0.8	-0.321928095
BP1026B_11389	cytochrome c oxidase family protein	994	1055	1064	2	996	1015	678	2	8.25E-04	0.001095892	1	0
BP1026B_11390	Ser/Thr protein phosphatase family protein family	2526	1240	1609	1	1135	971	1192	1	2.49E-13	7.12E-13	1	0
BP1026B_11391	RNA polymerase sigma factor	8571	8095	7019	11	9143	9846	7750	12	2.16E-07	3.70E-07	1.090909091	0.125530882
BP1026B_11392	hypothetical protein	9951	8960	8978	9	6644	7440	7762	7	2.55E-20	1.34E-19	0.777777778	-0.362570079
BP1026B_11393	primosomal replication protein n	91872	87385	100551	437	92400	89532	79073	408	2.01E-17	8.35E-17	0.933638444	-0.099064128
BP1026B_11394	30S ribosomal protein S18	206628	335999	308737	1028	379656	441115	387498	1459	0.00446429	0.005631818	1.4192607	0.505139619
BP1026B_11395	50S ribosomal protein L9	1212070	1406910	1333897	2908	1532693	1508060	1579158	3399	0.078107319	0.089588223	1.168844567	0.225083093
BP1026B_11396	replicative DNA helicase	202789	196779	209146	146	160894	153953	162994	113	2.01E-24	1.47E-23	0.787671233	-0.344345058
BP1026B_11397	hypothetical protein	205097	304689	286081	423	340795	366661	335465	554	2.80E-04	3.86E-04	1.309692671	0.389228313
BP1026B_11398	phosphate transporter family protein	204468	203722	196692	199	209619	210461	229826	214	2.40E-09	4.83E-09	1.075376884	0.104842366
BP1026B_11399	NLP/P60 family lipoprotein	60962	45239	45834	41	49900	44898	50970	39	1.46E-13	4.24E-13	0.951219512	-0.072149786
BP1026B_11400	PhoH family protein	481586	550953	522254	289	544065	582084	531390	309	0.154595837	0.171876777	1.069204152	0.096537345
BP1026B_11401	anti-oxidant AhpCTSA family protein	56709	92810	84530	168	109490	116185	113763	244	0.006267913	0.007828332	1.452380952	0.538419915
BP1026B_11402	polysaccharide deacetylase family protein	89535	58890	65069	79	57374	52310	56164	61	6.39E-27	5.72E-26	0.772151899	-0.373043411
BP1026B_11403	NAD-dependent epimerase/dehydratase family protein	437252	666101	615069	542	663958	724982	661384	647	0.825344414	0.841322009	1.193726937	0.255472861
BP1026B_11404	formyltransferase	76845	31525	42866	53	33735	23151	29611	30	1.09E-43	2.60E-42	0.566037736	-0.821029859
BP1026B_11405	glycosyl transferase family protein	104423	127278	129841	119	129972	136679	118755	127	5.89E-10	1.25E-09	1.067226891	0.093866923
BP1026B_11406	aminotransferase	118616	103013	105245	94	104562	110700	101989	91	7.34E-14	2.20E-13	0.968085106	-0.046794211
BP1026B_11407	drug/metabolite exporter (DME) family protein	59896	82635	71608	191	88912	90850	83716	236	7.46E-07	1.23E-06	0.305214221	0.305214221
BP1026B_11408	dolichyl-phosphate-mannose-protein mannosyltransferase family protein	35316	28889	27634	17	28139	27042	29051	16	8.05E-12	2.00E-11	0.941176471	-0.087462841
BP1026B_11409	hypothetical protein	12477	9289	9845	28	10976	9023	10056	26	1.17E-11	2.86E-11	0.928571429	-0.106915204
BP1026B_11410	aminotransferase AlaT	146221	180473	162270	131	205519	201275	213002	166	1.80E-04	2.51E-04	1.267175573	0.34161643
BP1026B_11411	homoserine dehydrogenase	90941	87575	86923	66	87930	84466	87095	65	4.26E-15	1.43E-14	0.948484848	-0.020206306
BP1026B_11412	threonine synthase	167001	184151	178492	121	191861	193054	209666	136	9.24E-08	1.63E-07	1.123966942	0.168599604
BP1026B_11413	molybdopterin biosynthesis moeA protein	402111	238184	304701	242	237370	197882	205550	163	4.65E-38	8.23E-37	0.673553719	-0.570135083
BP1026B_11414	molybdopterin converting factor subunit 1	16242	21655	22177	77	22839	24891	24124	92	1.12E-05	1.70E-05	1.194805195	0.256775415
BP1026B_11415	molybdopterin converting factor subunit 2	139695	90118	101236	225	87987	75052	85439	169	2.53E-32	3.25E-31	0.751111111	-0.412901755
BP1026B_11416	hypothetical protein	45891	33641	38788	72	34480	29732	37670	62	1.30E-14	4.18E-14	0.861111111	-0.215728691
BP1026B_11417	transcriptional regulator	126870	158015	147498	289	210249	203223	232815	432	0.097374085	0.110608519	1.494809689	0.57996182
BP1026B_11418	CtpB heat-shock protein	2355275	2759543	2727938	1006	3532439	3624791	3487936	1365	0.557709168	0.582822823	1.356858847	0.440270646
BP1026B_11419	ISBma2, transposase	162815	252482	226597	146	280002	284427	266751	189	7.92E-04	0.001054721	1.294520548	0.372417865
BP1026B_11420	hypothetical protein	79289	100724	96579	217	99284	96919	100227	233	2.25E-10	4.90E-10	1.073732719	0.102634912
BP1026B_11421	hypothetical protein	86191	60550	66817	116	55655	56981	48461	88	8.32E-29	8.60E-28	0.75862069	-0.398549376
BP1026B_11422	MerR family transcriptional regulator	18889	17872	17377	36	16016	15534	18623	33	2.83E-15	9.70E-15	0	

BP1026B	I1447	hypothetical protein	111281	57243	60879	70	66320	60643	55479	56	1.84E-26	1.60E-25	0.8	-0.321928095
BP1026B	I1448	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	245742	190303	211685	165	204690	189292	188978	148	9.75E-17	3.82E-16	0.896696997	-0.156868849
BP1026B	I1449	histidyl-tRNA synthetase	169368	193473	196983	139	213076	209070	210031	157	8.93E-08	1.57E-07	1.129496406	0.175679676
BP1026B	I1450	hypothetical protein	82923	77164	80362	127	81072	73354	78119	123	1.35E-15	4.78E-15	0.968503937	-0.046170181
BP1026B	I1451	PQQ repeat-containing protein	362042	211914	237021	235	197204	156693	207707	163	2.59E-35	4.03E-34	0.693617021	-0.527788792
BP1026B	I1452	GTP-binding protein EngA	200999	202398	204681	155	192890	188561	194192	147	3.49E-14	1.08E-13	0.948387097	-0.07645206
BP1026B	I1453	RNA-binding protein Hfq	485807	839206	731029	2855	1156775	1373403	1202951	5184	3.65E-04	4.98E-04	1.815761821	0.860574973
BP1026B	I1454	GTP-binding protein HflX	261031	285257	280992	236	285327	271251	301322	245	5.70E-10	1.21E-09	1.038135593	0.053994989
BP1026B	I1455	HflH protease activity modulator HflK	147631	129044	134508	105	127167	131194	125327	98	1.16E-15	4.16E-15	0.933333333	-0.099535674
BP1026B	I1456	HflC protein	63932	55017	55760	64	57085	57237	50922	61	3.84E-15	1.30E-14	0.953125	-0.069262662
BP1026B	I1457	hypothetical protein	7266	11182	9119	47	11428	13558	12173	64	3.44E-04	4.71E-04	1.361702128	0.445411148
BP1026B	I1458	ATP phosphoribosyltransferase regulatory subunit	51804	46432	45686	41	48760	49405	48332	42	6.55E-11	1.49E-10	1.024390244	0.034765418
BP1026B	I1459	adenylosuccinate synthetase	363759	463285	434734	312	516517	524550	512220	384	0.042649987	0.050092749	1.230769231	0.299560282
BP1026B	I1460	phosphoribosyl transferase domain-containing protein	122581	143171	136518	225	151041	156991	168853	267	1.33E-05	2.00E-05	1.186666667	0.24691474
BP1026B	I1461	kup system potassium uptake protein	285855	389585	353346	181	405746	430267	441801	225	7.60E-05	1.09E-04	1.243093923	0.313935304
BP1026B	I1462	transcription accessory protein, TEX	234101	259150	253498	100	282998	281524	286027	114	5.11E-07	8.57E-07	1.14	0.189033824
BP1026B	I1463	hypothetical protein	135477	184816	178495	210	218604	258509	182998	278	0.00134378	0.001758221	1.323809534	0.404695555
BP1026B	I1464	hypothetical protein	138672	221892	207358	876	269463	298795	281900	1311	0.091059697	0.103760695	1.496575342	0.581664911
BP1026B	I1465	ATP-dependent helicase	131406	123230	121433	55	126524	128808	131912	57	3.41E-11	7.95E-11	1.036363636	0.051530301
BP1026B	I1466	competence lipoprotein ComL	212910	282177	251377	302	296205	315835	282681	362	8.20E-06	1.26E-05	1.198675483	0.261441148
BP1026B	I1467	ribosomal large subunit pseudouridine synthase D	31520	25804	24732	23	28178	26840	27281	23	3.44E-09	6.81E-09	1	0
BP1026B	I1468	hypothetical protein	22472	10022	12678	17	10886	11808	9749	12	5.85E-25	4.49E-24	0.705882353	-0.502500341
BP1026B	I1469	poly(R)-hydroxyalkanoic acid synthase	604759	625844	628453	341	605580	582539	590235	326	0.245205082	0.267163109	0.95601173	-0.064899775
BP1026B	I1470	acetyl-CoA acetyltransferase	626841	428937	482033	433	392792	378635	349241	316	9.30E-24	6.51E-23	0.729792148	0.145442467
BP1026B	I1471	acetylacetyl-CoA reductase	620270	882579	821794	1045	887664	931124	913474	1229	0.097712562	0.11018479	1.176076555	0.233981973
BP1026B	I1472	hypothetical protein	359942	613154	564824	993	644769	768507	639134	1325	0.481616624	0.50710969	1.334340583	0.416126737
BP1026B	I1474	30S ribosomal protein S12 methyltransferase	206689	189633	187508	141	189854	191043	195691	139	2.63E-12	6.85E-12	0.985815603	-0.020610028
BP1026B	I1475	carbohydrate kinase	153405	92562	109433	127	90877	69618	94625	91	2.20E-36	3.64E-35	0.716535433	-0.480890047
BP1026B	I1476	beta-ketothiolase	262243	153649	185183	169	142543	122214	137240	113	1.03E-41	2.22E-40	0.668639053	-0.580700474
BP1026B	I1477	hypothetical protein	92272	93737	95438	161	89361	89876	82012	149	1.15E-17	4.88E-17	0.925465839	-0.111748358
BP1026B	I1478	cystathionine beta-lyase	177156	173638	170590	146	188318	177487	198680	158	1.34E-08	2.52E-08	1.082191781	0.113956189
BP1026B	I1479	phosphoserine phosphatase	39817	42039	43391	49	46034	48587	50293	57	9.19E-07	1.51E-06	1.163265306	0.21818017
BP1026B	I1480	hypothetical protein	1129	1379	1621	7	1656	1764	2015	10	0.564322841	0.589242946	1.428571429	0.514573173
BP1026B	I1481	hypothetical protein	237865	251002	249485	450	242714	258237	234048	448	1.18E-11	2.87E-11	0.995555556	-0.006426269
BP1026B	I1482	hypothetical protein	24436	20055	21111	26	21565	20609	23035	26	3.24E-11	7.59E-11	1	0
BP1026B	I1483	ABC transporter ATP-binding protein	3481	1718	2173	3	1287	1337	1259	1	1.42E-21	8.24E-21	0.333333333	-1.584962501
BP1026B	I1484	AsmA family protein	212385	237681	218703	89	249837	248131	253873	100	3.61E-07	6.10E-07	1.123595506	0.168122759
BP1026B	I1485	ABC transporter ATP-binding protein	144606	203404	189858	114	236611	256345	224770	152	0.002122503	0.002745584	1.333333333	0.415037499
BP1026B	I1486	hypothetical protein	765386	1212656	1100376	1613	1107364	1279819	1098471	1826	0.150479867	0.16765769	1.132062077	0.178940327
predicted RNA	-		24739	803	1840	456	1053	628	1378	50	0	0	0.109649123	-1.890338224
BP1026B	I1487	aldehyde dehydrogenase	166086	164586	162397	114	169192	159948	165172	114	6.55E-11	1.49E-10	1	0
BP1026B	I1488	hypothetical protein	3754	5764	4737	45	6049	6475	6581	60	6.58E-04	8.81E-04	1.333333333	0.415037499
BP1026B	I1489	2-nitropropane dioxygenase	672939	559136	602108	526	543822	484628	550522	453	4.24E-05	6.17E-05	0.86121673	-0.215551747
BP1026B	I1490	outer membrane protein W	638001	7043820	7597658	10863	6695860	6701689	6735244	10404	9.55E-04	0.001261769	0.957746479	-0.062284278
BP1026B	I1491	hypothetical protein	96017	145756	120381	591	161602	169540	179505	834	0.022384302	0.026859448	1.411167513	0.496889253
BP1026B	I1492	manganese transport protein	9730	6216	6976	5	5207	4821	5917	4	1.61E-22	1.02E-21	0.8	-0.321928095
BP1026B	I1493	putrescine-binding periplasmic protein	733606	1063520	981469	845	1014941	1046698	1003745	933	0.14621598	0.161561585	1.104142012	0.14292574
BP1026B	I1494	putrescine ABC transporter ATP-binding protein	86111	88597	84343	74	95458	89003	96627	80	2.50E-10	5.42E-10	1.081081081	0.112474729
BP1026B	I1495	putrescine transport system permease	71389	101607	87857	100	103873	112959	110159	126	1.35E-05	2.04E-05	1.26	0.333423734
BP1026B	I1496	putrescine transport system permease	126000	141699	135533	164	124449	124634	146545	161	4.23E-13	1.19E-12	0.981707317	-0.026651527
BP1026B	I1497	hypothetical protein	32231	22579	23786	32	24457	24569	25571	30	2.37E-11	5.61E-11	0.9375	-0.093109404
BP1026B	I1498	hypothetical protein	92466	68150	75909	47	73288	64428	63642	40	5.29E-22	3.20E-21	0.85106383	-0.232660757
BP1026B	I1499	metallo-beta-lactamase family protein	92992	120045	113317	122	140693	157171	125419	159	2.56E-04	3.53E-04	1.303278689	0.382145618
BP1026B	I1500	sigma-54 dependent transcriptional regulator	24065	12275	15136	12	12106	9078	11323	8	9.53E-35	1.44E-33	0.666666667	-0.584962501
BP1026B	I1501	hypothetical protein	20611	20362	21652	37	20644	21742	20145	36	1.64E-11	3.94E-11	0.972972973	-0.039528364
BP1026B	I1502	transcriptional regulator	22172	29433	26640	115	28425	30730	30001	132	4.76E-06	7.43E-06	1.147826087	0.198904068
BP1026B	I1503	hypothetical protein	6696	2177	3211	8	2529	1905	2806	5	3.32E-22	2.04E-21	0.625	-0.678071905
BP1026B	I1504	MerR family transcriptional regulator	21613	18400	18060	18	19519	18300	18249	18	9.81E-14	2.90E-13	1	0
BP1026B	I1505	hypothetical protein	5284	1391	1652	8	1570	1448	1310	4	6.55E-23	4.29E-22	0.5	-1
BP1026B	I1506	RND efflux system outer membrane lipoprotein	108154	60835	70177	41	58536	54207	56493	29	6.59E-35	1.00E-33	0.707317073	-0.499571009
BP1026B	I1507	AcrB/AcrD/AcrF family protein	485978	502191	490198	155	484848	465868	485429	150	4.12E-11	9.52E-11	0.967741935	-0.047305715
BP1026B	I1508	RND family efflux transporter MFP subunit	122210	82637	104335	92	93502	73420	75012	72	8.93E-29	9.17E-28	0.782608696	-0.353636955
BP1026B	I1509	TerR family transcriptional regulator	187137	230210	233232	349	288901	284389	273914	454	9.87E-04	0.001303416	1.300859599	0.379465261
BP1026B	I1510	voltage-gated CIC-type chloride channel ClcB	37222	25300	26690	17	28108	25343	28417	15	6.72E-12	1.68E-11	0.882352941	-0.180572246
BP1026B	I1511	hypothetical protein	10008	4906	5946	6	3667	2557	4103	3	7.58E-39	1.40E-37	0.5	-1
BP1026B	I1512	LysR family transcriptional regulator	13680	5769	7664	10	5650	5655	4811	5	1.48E-33	2.09E-32	0.5	-1
BP1026B	I1513	hypothetical protein	16198	8919	11285	32	10597	8627	9767	25	6.82E-19	3.20E-18	0.78125	-0.35614381
BP1026B	I1514	AP endonuclease	2538	2613	3000	2	3284	4166	3005	3	0.04661582	0.054566548	1.5	0.584962501
BP1026B	I1515	2-dehydro-3-deoxygluconokinase	36597	22199	23661	27	25113	25045	22807	24	4.99E-14	1.52E-13	0.888888889	-0.169925001
BP1026B	I1516	major facilitator family transporter	95306	114195	1103920	81	115304	120282	122825	93	7.49E-08	1.33E-07	1.148148148	0.199308808
BP1026B	I1517	2-ketoglutarate reductase	36060	15754	19240	24	12393	9908	10957	11	9.21E-74	6.79E-72	0.458333333	-1.125530882
BP1026B	I1518	LacI family transcriptional regulator	822697	570142	648975	651	445632	365634	450301	402	3.31E-34	4.85E-33	0.617511521	-0.695462042
BP1026B	I1519	hypothetical protein	138552	94220	100508	140	88491	80385	86705	107	1.92E-30	2		

BP1026B.11549	ApbE family protein	86394	36779	39864	51	36730	37624	36741	34	2.46E-30	2.76E-29	0.666666667	-0.584962501
BP1026B.11548	ABC transporter ATP-binding protein	52797	29707	34920	38	28254	23749	32838	28	3.14E-23	2.11E-22	0.736842105	-0.440572591
BP1026B.11550	ABC transporter membrane protein	14977	17370	15190	21	19824	18226	19738	25	2.34E-06	3.72E-06	1.19047619	0.251538767
BP1026B.11552	hypothetical protein	660	287	568	4	348	419	253	3	6.12E-05	8.83E-05	0.75	-0.415037499
BP1026B.11551	methyl-accepting chemotaxis transmembrane protein	77738	33647	48249	34	37669	32958	34803	22	4.77E-32	5.99E-31	0.647058824	-0.628031223
BP1026B.11554	dihydroxyacetone kinase	21548	13251	14203	9	12788	11521	12913	7	4.28E-23	2.84E-22	0.777777778	-0.362570079
BP1026B.11555	hypothetical protein	24837	20203	20945	21	20954	18196	22971	19	1.04E-13	3.06E-13	0.904761905	-0.144389909
BP1026B.11556	Rieske (2Fe-2S) domain-containing protein	2353	1314	1471	1	1329	965	1242	1	9.93E-10	2.07E-09	1	0
BP1026B.11557	sodium/hydrogen exchanger	3005	2487	2408	1	2615	3087	2246	1	9.99E-05	1.42E-04	1	0
BP1026B.11558	alkylhalidase	16346	18409	16674	11	16134	18508	15565	11	4.16E-13	1.17E-12	1	0
BP1026B.11559	hypothetical protein	19965	32274	28189	38	28254	30758	34376	44	1.25E-05	1.89E-05	1.157894737	0.211504105
BP1026B.11560	hypothetical protein	7377	7129	8204	14	7353	10221	7010	15	1.40E-08	2.63E-08	1.071428571	0.099535674
BP1026B.11562	Alcohol dehydrogenase	1930	1209	1201	4	1087	1312	1106	4	1.09E-05	1.65E-05	1	0
BP1026B.11564	hypothetical protein	7885079	13078253	11453937	18283	10133424	11350259	11017732	18331	1.37E-04	1.93E-04	1.006262539	0.003782673
BP1026B.11565	polyhydroxyalkanoate depolymerase domain-containing protein	1518954	2204158	2059273	1769	1652782	1735539	1618928	1532	0.582172095	0.606869131	0.866026003	-0.207517751
BP1026B.11567	hypothetical protein	66002	86280	83640	168	74443	79699	76003	163	3.91E-15	1.32E-14	0.970238095	-0.043589269
BP1026B.11568	hypothetical protein	219	214	261	2	608	562	331	5	3.34E-05	4.90E-05	2.5	1.321928095
BP1026B.11569	fimbrial subunit	16809	21149	19225	35	22540	25316	21889	43	2.28E-05	3.39E-05	1.228571429	0.296981738
BP1026B.11570	fimbrial chaperone protein	18326	28582	25982	31	28575	30496	27308	37	2.37E-05	3.51E-05	1.193548387	0.252527055
BP1026B.11571	outer membrane usher protein	81521	69604	75015	29	65244	64693	67629	25	1.42E-20	7.62E-20	0.862068966	-0.214124805
BP1026B.11572	type-1 fimbrial protein, A subunit	9818	8283	9900	9	9796	10252	9929	10	2.62E-08	4.82E-08	1.111111111	0.152003093
BP1026B.11573	hypothetical protein	749	952	858	1	823	757	655	1	0.004081732	0.005165852	1	0
BP1026B.11574	hypothetical protein	149	86	77	0	181	110	47	0	0.674188324	0.695614036	#DIV/0!	#DIV/0!
BP1026B.11575	outer membrane protein	37860	43650	42198	11	49224	51407	47746	14	6.26E-06	9.69E-06	1.272727273	0.347923303
BP1026B.11576	hypothetical protein	3856	5629	4936	12	5428	6471	5267	14	2.35E-05	3.49E-05	1.166666667	0.222392421
BP1026B.11577	DNA-binding response regulator	28638	42492	38034	54	46416	48814	50031	72	9.15E-04	0.00121104	1.333333333	-0.415037499
BP1026B.11578	two-component regulatory system, sensor kinase protein	112506	103034	109954	33	113878	102054	111663	33	2.97E-12	7.66E-12	1	0
BP1026B.11579	EAL domain-containing protein	53541	77741	72434	90	81412	87080	88724	114	3.02E-06	4.79E-06	1.266666667	0.341036918
BP1026B.11580	hypothetical protein	1798	1239	1426	3	1970	1912	1762	3	0.300870857	0.323982951	1	0
BP1026B.11581	H-NS histone family protein	3065	5928	4597	14	4934	4962	4533	15	1.07E-06	1.75E-06	1.071428571	0.099535674
BP1026B.11582	putative lipase	20681	35205	34097	28	37493	44215	34151	36	6.09E-04	8.18E-04	1.285714286	0.362570079
BP1026B.11583	hypothetical protein	214	201	104	1	284	234	441	2	0.005252027	0.006592388	2	1
BP1026B.11584	hypothetical protein	401	616	459	3	1068	832	543	5	0.066135677	0.076374152	1.666666667	0.736965594
BP1026B.11585	Putative bacteriophage gp31 protein	10104	17555	13794	45	18952	22617	18058	64	0.003372163	0.004303457	1.422222222	0.508146904
BP1026B.11587	GntR family transcriptional regulator	31917	45883	42063	57	50784	55965	50128	74	3.45E-04	4.72E-04	1.298245614	0.376563351
BP1026B.11588	peptide synthase	10237	14807	9114	19	14726	14451	16226	25	1.00E-04	1.42E-04	1.31579474	0.395928676
BP1026B.11589	alpha/beta fold family hydrolase	6150	8886	7680	8	9293	7927	9897	10	4.17E-06	6.53E-06	1.25	0.321928095
BP1026B.11590	nitrilotriacetate monooxygenase	5237	8289	8666	7	10173	10322	11430	11	0.005073011	0.006379187	1.571428571	0.652076697
BP1026B.11591	glucose-6-phosphate dehydrogenase	6866	10783	8481	8	13605	13034	12955	12	0.008169134	0.01010219	1.5	0.584962501
BP1026B.11592	aldehyde dehydrogenase	33441	47340	42250	27	64019	68192	68721	45	0.184469897	0.203573155	1.666666667	0.736965594
BP1026B.11593	NIPSNAP family protein	1960	2847	2411	7	3053	3439	2824	9	0.072227716	0.082996308	1.285714286	0.362570079
BP1026B.11594	ABC transporter substrate-binding protein	4106	5880	5221	4	4547	5369	5700	5	7.87E-08	1.39E-07	1.25	0.321928095
BP1026B.11595	ABC transporter permease	2779	3232	3576	3	3045	4054	3277	3	3.10E-04	4.26E-04	1	0
BP1026B.11596	putrescine ABC transporter permease	3204	5707	4883	5	4910	5677	5234	6	1.15E-05	1.74E-05	1.2	0.263034406
BP1026B.11597	spermidine/putrescine ABC transporter ATP-binding protein	4332	6112	6348	5	5444	7044	6701	6	1.32E-06	2.14E-06	1.2	0.263034406
BP1026B.11598	GntR family transcriptional regulator	2186	3285	3105	3	3031	2954	3504	4	0.001226902	0.001608319	1.333333333	-0.415037499
BP1026B.11599	succinate-semialdehyde dehydrogenase	5025	9267	8334	5	8420	9098	8967	6	1.42E-06	2.29E-06	1.2	0.263034406
BP1026B.11600	outer membrane porin	1020	2452	1973	1	1681	2600	2670	1	0.151424933	0.168620692	1	0
BP1026B.11601	hypothetical protein	234	582	507	1	704	646	473	1	0.495113241	0.520184367	1	0
BP1026B.11602	hypothetical protein	203	494	447	2	449	818	498	3	0.100989884	0.11461739	1.5	0.584962501
BP1026B.11603	H-NS histone family protein	1159	2584	1496	4	2529	2236	2564	6	0.490670035	0.516121948	1.5	0.584962501
BP1026B.11604	ompA family protein	1303	2514	1385	2	2827	3105	2752	3	0.456712613	0.482346407	1.5	0.584962501
BP1026B.11605	outer membrane protein	4265	7026	6008	3	7443	9011	7991	4	0.001587026	0.002070437	1.333333333	-0.415037499
BP1026B.11606	cable pili-associated 22 kDa adhesin protein	100815	119200	115102	11	119294	113394	114989	11	5.03E-11	1.16E-10	1	0
BP1026B.11607	hypothetical protein	1863	2956	2446	4	2674	3529	3201	6	0.076156692	0.08739887	1.5	0.584962501
BP1026B.11608	sulfotransferase domain-containing protein	2590	3477	3262	3	3581	3125	3196	3	2.02E-04	2.82E-04	1	0
BP1026B.11609	ABC transporter ATP-binding protein/permease	17795	23622	22782	9	19243	20008	23249	9	2.07E-12	5.43E-12	1	0
BP1026B.11610	HlyD family secretion protein	12725	18932	18453	11	18147	19442	19460	13	4.80E-08	8.62E-08	1.181818182	0.2410081
BP1026B.11611	hypothetical protein	42503	57526	53838	11	56836	59349	58956	13	3.58E-08	6.51E-08	1.181818182	0.2410081
BP1026B.11612	hypothetical protein	9638	11164	9785	7	10131	11576	10168	7	5.81E-09	1.13E-08	1	0
BP1026B.11614	hypothetical protein	447	472	323	3	633	218	511	3	0.468764925	0.494325314	1	0
BP1026B.11613	Adenylsulfate kinase	3063	2976	3335	5	3749	5483	4823	7	0.199579805	0.219282317	1.4	0.485426827
BP1026B.11615	hypothetical protein	682	929	872	6	877	1578	901	8	0.993271716	0.996292712	1.333333333	-0.415037499
BP1026B.11616	hypothetical protein	501	910	520	4	713	835	762	5	0.579390809	0.604070351	1.25	0.321928095
BP1026B.11617	DNA-binding response regulator	3060	4104	2993	4	5506	6198	4640	7	0.277885801	0.300886889	1.75	0.807354922
BP1026B.11618	putative transposase	2056	1398	1997	3	1573	1185	1322	2	3.98E-08	7.21E-08	0.666666667	-0.584962501
BP1026B.11619	hypothetical protein	5124	9057	8794	12	9367	12679	10266	17	0.002384162	0.003075167	1.416666667	0.502500341
BP1026B.11620	hypothetical protein	2217	3639	3422	7	5027	5606	5606	12	0.992790868	0.999843933	1.714285714	0.777607579
BP1026B.11621	hypothetical protein	8420	14770	13020	9	15766	16732	16923	13	2.61E-04	3.60E-04	1.444444444	0.530514717
BP1026B.11622	integrase catalytic subunit	2678	5087	3544	7	6150	6031	4819	11	0.042144509	0.049508341	1.571428571	0.652076697
BP1026B.11623	outer membrane porin	3000	3269	3452	2	3988	4526	4055	3	0.015545798	0.018863279	1.5	0.584962501
BP1026B.11624	Is2000 transposase	1038	1204	1258	2	2037	1903	1443	3	0.393565116	0.418475991	1.5	0.584962501
BP1026B.11625	phenylalanine and histidine ammonia-lyase	4388	3933	4117	2	3651	3599	3632	2	1.52E-09	3.11E-09	1	0
BP1026B.11626	major facilitator family transporter	1457	1081	1239	0	1413	1115	1769	1	0.132395975	0.148512921	#DIV/0!	#DIV/0!
BP1026B.11627	urocanate hydratase	6129	6492	5364	3	6580	5842	6921	3	5.78E-08	1.03E-07	1	0
BP1026B.11628	hypothetical protein	2903	1770	2170	2	2206	1808	2113	1	6.10E-06	9.45E-06	0.5	-1
BP1026B.11629	LysR family transcriptional regulator	8434	11456	10765	11	12788	12154	12477	13	7.74E-06	1.19E-05	1.181818182	0.2410081
BP1026B.11630	allantoase	9579	8316	8927	6	7472	9393	8512	6	1.31E-12	3.50E-12	1	0
BP1026B.11631	allantoate amidohydrolase	5441	5513	6348	4	5160	4643	5086	3	2.40E-12	6.28E-12	0.75	-0.415037499
BP1026B.11632	hypothetical protein	11318	16446	15844	28	21021	19041	21778	40	0.002767622	0.00355544		

BP1026B	I1652	hypothetical protein		184	66	192	1	103	274	391	2	0.019078018	0.022997857	2	1
BP1026B	I1653	hypothetical protein		202	467	460	3	644	1200	482	7	1.29E-04	1.82E-04	2.333333333	1.222392421
BP1026B	I1654	hemagglutinin motif-containing protein		95377	136277	124629	23	138730	143655	156658	29	3.92E-05	5.72E-05	1.260869565	0.334419039
BP1026B	I1655	hypothetical protein		956	1675	1530	13	1829	2707	2699	23	0.126744314	0.142351653	1.769230769	0.823122238
BP1026B	I1656	putative HNS-like protein		844	1097	1344	3	1808	1920	1655	5	0.150994881	0.168171689	1.666666667	0.736965594
BP1026B	I1657	hypothetical protein		531	692	654	6	746	999	687	7	0.960214719	0.966383782	1.166666667	0.222392421
BP1026B	I1658	hypothetical protein		1699	2848	1755	7	2703	4135	2593	11	0.646588785	0.669120615	1.571428571	0.652076697
BP1026B	I1659	galactose oxidase		66526	106402	89755	37	111237	117596	123129	50	3.40E-04	4.66E-04	1.351351351	0.434402824
BP1026B	I1660	hypothetical protein		728	2022	1256	9	1608	2891	2192	15	0.20265894	0.22243141	1.666666667	0.736965594
BP1026B	I1661	non-ribosomal peptide synthetase		11900	12135	12635	30	16188	14672	14202	37	3.57E-06	5.63E-06	1.233333333	0.30256277
BP1026B	I1662	hypothetical protein		2602	4368	3809	29	4365	5245	4174	37	0.004024908	0.005095994	1.275862069	0.351472371
BP1026B	I1663	peptidase		56926	37040	42846	19	27527	24354	23326	10	6.66E-49	2.03E-47	0.526315789	-0.925999419
BP1026B	I1664	carbamoyl transferase		373759	437697	425208	239	298864	307008	296339	174	3.26E-25	2.54E-24	0.728033473	-0.457923312
BP1026B	I1665	hypothetical protein		1327623	988638	1075270	60	730587	688388	729579	38	0.007187655	0.008925455	0.633333333	-0.658963082
BP1026B	I1666	ribosomal-protein-serine acetyltransferase		169382	148202	161848	278	111679	90734	99818	175	2.13E-48	6.39E-47	0.629496403	-0.667729961
BP1026B	I1667	Beta-eliminating lyase		117792	75157	80131	84	59573	57372	57605	54	3.09E-46	8.32E-45	0.642857143	-0.637429921
BP1026B	I1668	argininosuccinate lyase		326989	194381	232188	93	147291	131786	153831	53	4.06E-60	1.19E-58	0.569992473	-0.811238357
BP1026B	I1669	cysteine synthase		350520	208574	259282	251	146334	121153	145785	127	3.06E-85	2.82E-83	0.505976096	-0.982858867
BP1026B	I1670	hypothetical protein		55159	36230	43230	70	28054	25198	28948	42	1.18E-36	1.96E-35	0.6	-0.736965594
BP1026B	I1671	hypothetical protein		231666	256333	241605	197	190822	210467	204194	163	5.50E-22	3.33E-21	0.827411168	-0.273323665
BP1026B	I1672	kinase		350564	338257	357407	394	260543	238896	252461	283	2.22E-28	2.20E-27	0.718274112	-0.477393577
BP1026B	I1673	argininosuccinate lyase		769353	803558	854932	577	612782	563600	576208	416	0.004426897	0.005568895	0.702970537	-0.471987791
BP1026B	I1674	argininosuccinate synthase		705358	860297	818294	654	610132	608565	657695	514	0.056494756	0.065603436	0.785932722	-0.347522276
BP1026B	I1675	nonribosomal peptide synthetase		195113	254805	249747	284	206919	228147	204098	260	2.71E-16	1.02E-15	0.915492958	-0.127379306
BP1026B	I1676	hypothetical protein		525922	489785	749641	643	678637	758269	721522	653	0.88286962	0.894738752	1.0155521	0.022264254
BP1026B	I1677	histidinol-phosphate aminotransferase		464953	625478	575670	549	468010	496177	498458	482	2.86E-14	8.94E-14	0.877959927	-0.13773003
BP1026B	I1678	JmjC domain-containing protein		713847	1221365	1099975	1143	1037429	1204564	1017055	1227	0.195120435	0.214780378	1.073490814	0.102309845
BP1026B	I1679	mbtH-like protein		116928	207387	191596	764	212125	238787	191789	952	5.68E-05	8.20E-05	1.246073298	-0.317388935
BP1026B	I1681	syringopeptin synthetase C		57314	35895	40467	23	34358	29324	31823	16	1.64E-24	1.21E-23	0.695652174	-0.523561956
BP1026B	I1682	outer membrane protein		9640	10592	10760	8	9508	7691	10168	7	1.13E-14	3.66E-14	0.875	-0.192645078
BP1026B	I1683	AraC family transcriptional regulator		21454	17787	18227	23	15537	14237	17333	19	2.99E-21	1.69E-20	0.826086957	-0.275634443
BP1026B	I1684	transmembrane protein		954	383	1069	0	311	289	613	0	1.18E-12	3.17E-12	#DIV/0!	#DIV/0!
BP1026B	I1685	chemotaxis protein CheW2		17129	16441	16577	32	13946	14114	16462	28	1.22E-16	4.75E-16	0.875	-0.192645078
BP1026B	I1686	methyl-accepting chemotaxis protein		41140	39302	39000	23	34774	33671	39876	20	7.93E-13	2.17E-12	0.869565217	-0.201633861
BP1026B	I1687	hypothetical protein		1682	2039	1962	4	1899	2482	2309	5	0.025922276	0.03089178	1.25	0.321928095
BP1026B	I1688	hypothetical protein		1623	2868	2987	13	2816	3689	2635	16	0.022856705	0.02740006	1.230762931	0.299560282
BP1026B	I1689	AMP-binding protein		70810	40852	47430	26	31878	25406	31354	14	6.20E-47	1.76E-45	0.538461538	-0.893084796
BP1026B	I1690	EmrB/QacA family drug resistance transporter		56413	35078	38330	30	27633	25316	28608	19	5.16E-34	7.40E-33	0.633333333	-0.658963082
BP1026B	I1691	predicted RNA		143996	203476	179505	738	189258	215808	248454	915	4.16E-05	6.05E-05	1.29837398	0.310150927
BP1026B	I1692	ubiquinone/menaquinone biosynthesis methyltransferase		440063	564832	578276	684	576816	627169	565216	764	0.633156593	0.656195702	1.116959064	0.159576313
BP1026B	I1693	ABC transporter substrate-binding protein		107328	100284	107870	111	80758	70473	78453	81	1.31E-34	1.95E-33	0.729729793	-0.454565863
BP1026B	I1692	ABC transporter permease		25286	9994	13064	13	8857	8818	8282	7	3.44E-53	1.28E-51	0.538461538	-0.893084796
BP1026B	I1694	ABC transporter ATP-binding protein		52389	17934	26737	34	18117	15753	17614	18	1.32E-64	7.82E-63	0.529411765	-0.917533784
BP1026B	I1695	ABC transporter permease		37398	25406	29817	37	24474	20483	24648	28	1.49E-22	9.40E-22	0.756756757	-0.402098444
BP1026B	I1696	hypothetical protein		63798	35349	35537	94	39339	30208	34395	73	1.99E-20	1.05E-19	0.767595745	-0.364764293
BP1026B	I1697	hypothetical protein		636122	771951	662250	2072	913478	991204	937681	2845	0.019917491	0.023977522	1.373069498	0.45740465
BP1026B	I1698	arginine/ornithine antiporter		416733	432278	430985	292	588501	597256	610502	409	0.356149888	0.380565348	1.400649392	0.486132474
BP1026B	I1699	arginine deiminase		736205	863519	820611	641	1056946	1085125	1129650	867	0.019196029	0.023122322	1.352574103	0.435707637
BP1026B	I1700	ornithine carbamoyltransferase		1011057	1400676	1337722	1236	1850677	1895005	1795349	1826	0.010285325	0.012629404	1.477346278	0.563008022
BP1026B	I1701	carbamate kinase		772519	457706	559724	635	562308	491852	539077	565	4.64E-04	6.28E-04	0.88976304	-0.168505724
BP1026B	I1703	short-chain dehydrogenase		85163	55196	63126	85	63987	57871	66763	79	3.05E-17	1.25E-16	0.929411765	-0.105610188
BP1026B	I1704	PduO protein		2339	1824	1521	4	2180	1954	1611	4	0.001396538	0.001825345	1	0
BP1026B	I1702	LysR family transcriptional regulator		20632	13254	10451	14	12577	13242	13171	12	6.02E-16	2.20E-15	0.857142857	-0.222392421
BP1026B	I1705	glutathione S-transferase		66598	74462	76921	103	70377	73507	69517	100	1.06E-14	3.45E-14	0.970873786	-0.042644337
BP1026B	I1707	putative extracellular ligand binding protein		5031	2595	3382	3	2587	1995	2134	1	5.97E-20	3.05E-19	0.333333333	-1.584962501
BP1026B	I1708	MarK family transcriptional regulator		13155	8178	8888	23	7089	6682	8616	17	1.33E-23	9.23E-23	0.739130435	-0.436099115
BP1026B	I1709	major facilitator family transporter		3108	2768	2218	2	1606	2177	1097	1	1.52E-16	5.83E-16	0.5	-1
BP1026B	I1710	fen1 protein		163972	129098	143307	92	127482	109582	120847	76	2.80E-23	1.88E-22	0.826086957	-0.275634443
BP1026B	I1711	precorrin-4 C(11)-methyltransferase		24616	23541	21641	32	22833	23834	21741	31	3.85E-11	8.93E-11	0.96875	-0.04580369
BP1026B	I1712	cobalt-precorrin-6x reductase		6652	2081	2368	5	1416	1582	1106	1	2.27E-53	8.58E-52	0.2	-2.321928095
BP1026B	I1713	cobalt-precorrin-6A synthase		29614	13146	15617	17	10126	9587	10782	9	4.27E-55	1.73E-53	0.529411765	-0.91753784
BP1026B	I1715	precorrin-6Y C5,15-methyltransferase		9575	8606	10180	7	10457	9603	8672	7	7.25E-10	1.52E-09	1	0
BP1026B	I1714	hypothetical protein		1581	452	790	5	651	473	571	3	1.07E-08	2.02E-08	0.6	-0.736965594
BP1026B	I1716	precorrin-3B synthase		9371	3724	5100	4	4177	4322	2808	2	1.96E-23	1.34E-22	0.5	-1
BP1026B	I1717	precorrin-8X methylmutase		7723	5410	5947	10	5241	4444	6122	8	3.13E-14	9.74E-14	0.8	-0.321928095
BP1026B	I1718	precorrin-2 C(20)-methyltransferase		19458	12402	11346	19	13763	12463	10446	16	6.44E-17	2.56E-16	0.842105263	-0.247927513
BP1026B	I1719	precorrin-3b C17-methyltransferase		26087	16951	17943	10	13841	13846	15699	7	5.27E-30	5.83E-29	0.7	-0.51473173
BP1026B	I1720	glycosyl hydrolase family protein		3161435	2106502	2524660	1907	1934585	1599595	1910109	1332	0.744176837	0.763677049	0.698479287	-0.517710761
BP1026B	I1721	hypothetical protein		33687	45381	46490	164	49843	52255	38006	183	1.34E-07	2.32E-07	1.115853659	0.158147834
BP1026B	I1722	carboxylesterase		60376	38965	41361	68	36893	30019	34311	49	1.19E-24	8.84E-24	0.720588235	-0.472752997
BP1026B	I1723	hypothetical protein		5227	983	1198	4	771	890	968	1	1.21E-47	3.50E-46	0.25	-2
BP1026B	I1724	magnesium chelatase subunit ChII		25919	15429	15611	14	14110	11920	14545	10	7.39E-29	7.67E-28	0.714285714	-0.485426827
BP1026B	I1														

BP1026B_11750	AraC family transcriptional regulator	20300	25740	25780	24	28527	33654	32992	32	0.001477643	0.001929743	1.333333333	0.415037499
BP1026B_11751	hypothetical protein	705	1006	1044	8	1012	1805	1122	11	0.662913782	0.684770484	1.375	0.459431619
BP1026B_11752	hypothetical protein	1814217	2889661	2299022	16210	2948099	3114248	2964853	20896	0.366395293	0.390979719	1.289080814	0.366342711
BP1026B_11753	hypothetical protein	108524	138154	129014	176	123700	134439	126888	180	2.01E-11	4.80E-11	1.022727273	0.032421478
BP1026B_11754	asparagine synthase	125526	121708	131475	72	106286	92269	110219	59	1.53E-23	1.06E-22	0.819444444	-0.287281952
BP1026B_11755	ABC transporter membrane protein	196856	107299	135501	85	91870	76764	93752	50	4.42E-59	2.07E-57	0.588235294	-0.765534746
BP1026B_11756	hypothetical protein	47862	59957	60311	54	57348	61397	59768	57	7.99E-11	1.80E-10	1.055555556	0.078002512
BP1026B_11757	hypothetical protein	9679	5048	5220	8	4033	5697	4635	6	4.47E-19	2.13E-18	0.75	-0.415037499
BP1026B_11758	Pi-fimbriae usher protein	40757	32486	31184	14	31143	30965	28302	12	7.12E-14	2.13E-13	0.857142857	-0.222392421
BP1026B_11759	type I fimbriae major subunit FimA	177125	178613	176931	346	185614	175833	178255	350	8.00E-11	1.81E-10	1.011560694	0.016582884
BP1026B_11760	Outer membrane efflux protein	111307	59462	76790	53	59890	49298	60263	36	4.10E-38	7.32E-37	0.679245283	-0.557995453
BP1026B_11761	multidrug efflux protein	237756	203862	207553	70	213139	195002	207538	66	1.88E-14	5.96E-14	0.942857143	-0.084888898
BP1026B_11762	periplasmic multidrug efflux lipoprotein	38494	24928	26526	24	28532	23807	23555	21	1.45E-15	5.13E-15	0.875	-0.192645078
BP1026B_11763	Transcription repressor of multidrug efflux pump acrAB operon, TetR (AcrR) family	19282	14211	13226	23	18642	18158	18083	27	2.21E-07	3.79E-07	1.173913043	0.231325546
BP1026B_11764	peptidase	36248	24200	24779	20	23899	22534	22792	16	1.89E-18	8.51E-18	0.8	-0.321928095
BP1026B_11765	amino acid transport system, membrane protein	3698	4331	5033	5	5031	5708	4875	6	6.40E-05	9.20E-05	1.2	0.263034406
BP1026B_11766	binding-protein-dependent transport system inner membrane protein	807	423	568	0	507	541	713	0	0.083255778	0.095179841	#DIV/0!	#DIV/0!
BP1026B_11767	extracellular solute-binding protein	4758	4691	5234	5	4555	6545	5366	6	2.93E-06	4.65E-06	1.2	0.263034406
BP1026B_11768	hypothetical protein	847	434	861	0	620	529	759	0	0.011526477	0.014120216	#DIV/0!	#DIV/0!
BP1026B_11769	hypothetical protein	927	1217	945	2	803	703	1061	1	3.59E-04	4.90E-04	0.5	-1
BP1026B_11770	hypothetical protein	515	50	8	0	193	58	9	0	1.22E-04	1.72E-04	#DIV/0!	#DIV/0!
BP1026B_11771	fimbriae membrane protein	495	640	655	0	466	425	598	0	0.005029955	0.006327584	#DIV/0!	#DIV/0!
BP1026B_11772	hypothetical protein	776	837	676	0	1044	1241	965	1	0.730019354	0.750008406	#DIV/0!	#DIV/0!
BP1026B_11773	type IV pilus protein	5017	5193	3709	2	4347	5122	4385	2	7.39E-08	1.31E-07	1	0
BP1026B_11774	fimbriae assembly protein	2712	2447	2897	2	2034	1674	2096	1	3.64E-11	8.45E-11	0.5	-1
BP1026B_11775	lipoprotein	1	18	5	0	23	16	0	0	0.050308248	0.058691395	#DIV/0!	#DIV/0!
BP1026B_11776	RhcC2	2072	1889	1593	1	1398	942	1119	0	6.47E-13	1.78E-12	0	#NUM!
BP1026B_11777	CpaB family Pil pilus assembly protein	206	48	136	0	125	0	71	0	0.002531148	0.003260056	#DIV/0!	#DIV/0!
BP1026B_11778	fimbriae assembly protein	441	345	279	0	394	396	288	0	0.288865931	0.311967239	#DIV/0!	#DIV/0!
BP1026B_11779	fimbriae assembly protein	9752	8917	10602	50	9436	7416	9036	44	5.52E-15	1.84E-14	0.88	-0.184424571
BP1026B_11780	permease	974	436	362	0	360	235	285	0	3.59E-10	7.72E-10	#DIV/0!	#DIV/0!
BP1026B_11781	ABC transporter ATP-binding protein	898	763	553	0	1318	972	845	1	0.727021589	0.747173573	#DIV/0!	#DIV/0!
BP1026B_11782	ABC transporter substrate binding protein	9000	6283	6355	6	7677	5801	6609	6	2.07E-12	5.44E-12	1	0
BP1026B_11783	dicarboxylic acid transporter PcaT	76501	66634	74226	55	56180	59058	58896	44	2.44E-25	1.93E-24	0.8	-0.321928095
BP1026B_11784	SpoVR family protein	224121	352664	310972	175	374583	401775	374857	228	2.10E-04	2.92E-04	1.302857143	0.381678902
BP1026B_11785	hypothetical protein	151264	237602	208553	157	258941	289774	267225	214	0.00602665	0.007534327	1.363057325	0.446846238
BP1026B_11786	protein kinase	872429	1429515	1277894	620	1600203	1788001	1636367	870	0.013445821	0.016400918	1.403258606	0.488747185
BP1026B_11788	methyl-accepting chemotaxis protein I	175502	143969	154365	83	142866	136958	142803	74	2.11E-17	8.76E-17	0.891566265	-0.165586066
BP1026B_11789	ribokinase	45902	15738	23534	29	14248	12556	14377	14	6.73E-76	5.41E-74	0.482758621	-1.050626073
BP1026B_11790	ribose operon repressor RbsR	66975	63474	65091	63	71777	66319	70921	67	4.66E-11	1.07E-10	1.063492063	0.088892667
BP1026B_11791	membrane protein component of ABC ribose transporter	29212	25393	26525	26	27488	25639	24276	25	6.74E-11	1.53E-10	0.961538462	-0.056583528
BP1026B_11792	ABC transporter ATP-binding protein	227330	148549	170510	115	144363	126156	145916	88	9.97E-29	1.02E-27	0.765217391	-0.386058432
BP1026B_11793	ribose ABC transporter periplasmic ribose-binding protein	71361	63233	63224	68	57589	52488	51566	55	3.64E-23	2.43E-22	0.808823529	-0.306103128
BP1026B_11794	transcriptional regulator CysB-like protein	15122	14462	15325	16	15904	16725	14764	17	3.31E-10	7.14E-10	1.0625	0.087462841
BP1026B_11795	sulfate ABC transporter ATP-binding protein	8673	4841	5505	6	4795	3413	4317	3	1.02E-21	6.02E-21	0.65	-1
BP1026B_11796	sulfate transport system permease	4572	4402	4192	5	4548	3518	4050	4	6.51E-09	1.26E-08	0.8	-0.321928095
BP1026B_11797	sulfate ABC transporter, permease protein CysT	4976	5976	5600	6	5467	5458	5485	6	5.78E-09	1.12E-08	1	0
BP1026B_11798	sulfate ABC transporter substrate-binding protein	22850	23221	24964	22	22479	21321	22002	21	1.43E-13	4.18E-13	0.954545455	-0.067114196
BP1026B_11800	LexA repressor	72521	45395	51467	79	40028	33588	46155	56	8.50E-29	8.77E-28	0.708860759	-0.496425826
BP1026B_11799	hypothetical protein	14480	11828	12905	39	10085	9618	9558	29	2.34E-22	1.45E-21	0.743589744	-0.427421224
BP1026B_11801	hypothetical protein	34796	47941	45076	57	57724	61669	54333	78	9.33E-04	0.001234332	1.368421053	0.452512205
BP1026B_11802	DNA binding protein	61849	86566	79834	154	91991	89749	86121	181	4.03E-08	7.29E-08	1.175324675	0.233059346
BP1026B_11803	modulation ABC transporter NodJ	19720	22658	20940	23	21287	22962	21616	23	1.11E-09	2.29E-09	1	0
BP1026B_11804	ABC transporter permease NodJ	25572	26338	28107	31	26530	28859	30641	34	2.66E-07	4.52E-07	1.096774194	0.133266531
BP1026B_11805	hypothetical protein	21215	20184	18728	47	21799	22483	22119	52	5.99E-08	1.07E-07	1.106382979	0.145850866
BP1026B_11806	hypothetical protein	47882	35237	36805	37	36038	29976	33802	31	5.13E-16	1.89E-15	0.837837838	-0.255257055
BP1026B_11807	aldo/keto reductase family oxidoreductase	45267	53538	46503	45	53182	52018	54426	30	1.05E-08	2.00E-08	1.111111111	0.152003093
BP1026B_11808	thioesterase family protein	8531	6393	7184	16	7182	7402	7839	17	3.87E-10	8.31E-10	1.0625	0.087462841
BP1026B_11809	transcriptional regulator	43154	37495	42085	85	38701	35032	37324	77	4.35E-13	1.22E-12	0.905882553	-0.142604395
BP1026B_11810	sodium dicarboxylate symporter family protein	40094	41558	40965	31	39930	37321	42933	30	1.17E-10	2.60E-10	0.967741935	-0.047305715
BP1026B_11811	tRNA-dihydrouridine synthase A	20083	20145	18591	20	22280	24431	22538	23	3.70E-06	5.83E-06	1.15	0.201633661
BP1026B_11812	His tRNA	2200	2475	2265	30	5028	5179	4114	62	0.062242259	0.07194429	2.066666667	1.047305715
BP1026B_11813	hypothetical protein	82405	93046	89812	346	107193	124731	95778	428	6.14E-06	9.52E-06	1.23699422	0.306838759
BP1026B_11814	hypothetical protein	103337	179023	157263	740	202991	231213	197481	1063	0.032321738	0.038285068	1.436486486	0.522544421
BP1026B_11815	molybdenum-pterin-binding protein	966	1304	1087	5	1402	1367	1156	6	0.223776477	0.244837332	1.2	0.263034406
BP1026B_11816	aliphatic sulfonates ABC transporter ATP-binding protein	2462	504	1081	1	672	802	792	0	1.10E-12	2.98E-12	0	#NUM!
BP1026B_11817	aliphatic sulfonates ABC transporter permease	2233	1199	2012	2	1626	1508	1890	2	1.71E-04	2.39E-04	1	0
BP1026B_11818	alkanesulfonate monooxygenase	6113	5877	6162	5	5762	4716	4704	4	1.70E-13	4.92E-13	0.8	-0.321928095
BP1026B_11819	hypothetical protein	7714	6542	7196	15	5887	5411	6334	12	1.05E-15	3.78E-15	0.8	-0.321928095
BP1026B_11820	3-hydroxyisobutyryl-CoA hydrolase	58488	36487	39311	39	35292	34124	36276	30	1.72E-19	8.50E-19	0.769230769	-0.378511623
BP1026B_11821	SMR family multidrug efflux pump	5575	4438	4215	13	3923	3115	3105	9	9.04E-16	3.25E-15	0.692307692	-0.530514717
BP1026B_11822	hypothetical protein	9658	2816	4140	12	2724	2387	2946	6	2.80E-38	5.04E-37	0.5	-1
BP1026B_11823	Met tRNA	757	1054	672	10	1819	1409	1349	19	0.013655131	0.016640033	1.9	0.925999419
BP1026B_11825	mutT/nudix family protein	34724	46836	43817	76	50869	52915	50552	94	1.92E-05	2.86E-05	1.236842105	0.306661338
BP1026B_11824	leucyl/phenylalanyl-tRNA--protein transferase	26952	22127	23283	31	21257	22224	24725	29	1.86E-12	4.90E-12	0.935483871	-0.096215315
BP1026B_11826	arginyl-tRNA-protein transferase	108627	170472	162782	177	190664	216311	186147	237	0.003306506	0.004223107	1.338983051	0.421137699
BP1026B_11827	dihydroxotrate dehydrogenase 2	18011	15125	17340	17	17607	14775	15692	16	5.68E-14	1.72E-13	0.941176471	-0.087462841
BP1026B_11828	amino acid ABC transporter substrate-binding protein	74258	80385	80683	98	75137	80219	78569	98	2.51E-14	7.87E-14	1	0
BP1026B_11829	amino acid ABC transporter permease	19144	21300	19500	28								

BP1026B.11849	hypothetical protein	11796	8422	10126	37	9549	9246	11279	36	2.40E-10	5.21E-10	0.972972973	-0.039528364
BP1026B.11850	Hfq protein	60676	78804	72935	108	97092	107621	102826	157	0.004939083	0.006219513	1.453703704	0.539733247
BP1026B.11851	hypothetical protein	189002	208542	217554	280	193068	182730	182931	254	5.94E-16	2.18E-15	0.907142857	-0.1405983
BP1026B.11852	sigma-54 dependent transcriptional regulator	124467	94148	100611	76	89936	84794	93695	64	2.73E-23	1.84E-22	0.842105263	-0.247927513
BP1026B.11853	hypothetical protein	28247	28977	28584	15	27996	25420	27476	14	4.41E-11	1.02E-10	0.933333333	-0.099535674
BP1026B.11854	hypothetical protein	3439	2125	1971	6	2365	2911	2760	6	7.23E-04	9.65E-04	1	0
BP1026B.11855	hypothetical protein	20772	17578	20826	21	19439	15521	18557	19	1.19E-16	4.64E-16	0.904761905	-0.144389909
BP1026B.11856	hypothetical protein	17531	14672	15122	15	15348	15677	16674	15	8.31E-12	2.06E-11	1	0
BP1026B.11857	Flp pilus assembly protein TadB	12546	10160	10334	10	10484	11223	12365	11	1.90E-09	3.85E-09	1.1	0.137503524
BP1026B.11858	type II/IV secretion system protein	72863	59159	64272	48	62140	59035	62792	45	1.46E-16	5.62E-16	0.9375	-0.093109404
BP1026B.11859	fimbriae assembly protein	15553	12969	11610	10	12833	11107	12264	9	3.36E-14	1.04E-13	0.9	-0.152003093
BP1026B.11860	type II/III secretion system protein	65399	49715	50989	41	50726	51064	55393	39	1.07E-14	3.48E-14	0.951219512	-0.072149786
BP1026B.11861	CpaB family Flp pilus assembly protein	10008	7736	8334	9	7352	8301	6135	8	3.06E-17	1.25E-16	0.888888889	-0.169925001
BP1026B.11862	hypothetical protein	8903	5972	5782	14	7364	5762	6433	13	1.45E-11	3.51E-11	0.928571429	-0.106915204
BP1026B.11863	hypothetical protein	4025	4270	3563	11	5572	5471	6894	17	0.023086087	0.027659162	1.545454545	0.628031223
BP1026B.11864	Flp pilus assembly protein, pilin Flp	52751	86992	70447	353	123672	122834	122873	621	0.516151293	0.541289373	1.759206799	0.814925085
BP1026B.11865	hypothetical protein	622	2028	1564	10	2937	3312	1961	19	0.011914671	0.014575816	1.9	0.925999419
BP1026B.11866	hypothetical protein	486	1707	1181	9	2396	2643	1530	17	0.004747304	0.005981622	1.888888889	0.91753784
BP1026B.11867	hypothetical protein	1906	680	905	0	1027	1077	792	0	1.02E-04	1.44E-04	#DIV/0!	#DIV/0!
BP1026B.11868	lipoprotein	1995	736	1225	1	902	1104	492	0	7.76E-10	1.63E-09	0	#NUM!
BP1026B.11869	two-partner secretion family protein	15641	15573	14384	9	15564	16129	15673	9	9.54E-11	2.14E-10	1	0
BP1026B.11870	hypothetical protein	60415	56337	66148	131	74884	71874	74600	159	3.53E-07	5.97E-07	1.213740458	0.279459954
BP1026B.11871	hypothetical protein	7178	5989	6458	15	7102	5911	6628	15	6.23E-10	1.32E-09	1	0
BP1026B.11872	ATPase, AFG1 type	51720	47359	45435	43	46857	43502	50611	42	2.78E-12	7.20E-12	0.97644186	-0.033947332
BP1026B.11873	dihydropyrimidine dehydrogenase	906818	1065498	1028398	698	1174152	1164994	1139500	810	0.121828767	0.137051895	1.160458453	0.214694872
BP1026B.11874	dihydropyrimidine succinyltransferase	363785	406880	406649	399	470695	494292	497001	384	9.56E-05	1.36E-04	1.242718447	0.313499473
BP1026B.11875	2-oxoglutarate dehydrogenase E1 component	1292741	1800810	1707489	558	2038427	2098497	1975297	711	0.079254796	0.090854474	1.274193588	0.349584438
BP1026B.11876	GTP-binding protein TypA	90250	101027	97228	52	110187	109513	104273	59	1.74E-08	3.24E-08	1.134615385	0.182203331
BP1026B.11877	MarR family transcriptional regulator	7039	6787	7756	14	9586	10940	12200	21	0.019177306	0.02310421	1.5	0.584962501
BP1026B.11878	RND efflux system outer membrane lipoprotein	26547	17520	18815	14	18384	15439	18473	11	5.95E-21	3.28E-20	0.785714286	-0.347923303
BP1026B.11879	multidrug resistance protein	30916	30554	29756	24	34199	34533	31953	27	1.21E-06	1.97E-06	1.125	0.169925001
BP1026B.11880	EmrB QacA family drug resistance transporter	26015	28877	31126	18	33792	29107	33123	20	2.17E-06	3.47E-06	1.111111111	0.152003093
BP1026B.11881	tRNA pseudouridine synthase B	44229	31555	33209	39	28889	26089	32357	32	2.51E-17	1.04E-16	0.820512821	-0.285402219
BP1026B.11882	ribosome-binding factor A	29422	49643	42580	97	59099	65487	61993	149	0.043424297	0.05098307	1.536082474	0.619256788
BP1026B.11883	translation initiation factor IF-2	702651	852578	796464	267	911279	958889	926160	318	0.082417426	0.094307449	1.191011236	0.252187024
BP1026B.11884	transcription elongation factor NusA	424174	559997	515012	338	595609	580107	591908	399	0.822476785	0.838535557	1.180473733	0.2393655
BP1026B.11885	hypothetical protein	63934	108781	94632	192	129049	139898	122486	282	0.01107475	0.013622909	1.46875	0.554588852
BP1026B.11887	RNA pseudouridylation synthase family protein	111372	85568	90342	57	71411	63451	77184	42	6.40E-33	8.61E-32	0.736842105	-0.440572591
BP1026B.11888	segregation and condensation protein B	196716	186623	188238	139	204448	209174	203401	150	2.97E-09	5.91E-09	1.079136691	0.109877618
BP1026B.11886	hypothetical protein	12990	21442	18311	183	29372	33815	30559	325	0.671958853	0.693542114	1.775956284	0.82859607
BP1026B.11889	Osm1 protein	33081	37438	37117	39	32057	33044	33593	36	7.34E-12	1.83E-11	0.923076923	-0.115472717
BP1026B.11890	hypothetical protein	22122	30983	26635	66	40018	44274	39404	103	0.067565365	0.077953338	1.560606061	0.642106408
predicted RNA	-	10736	18123	15216	473	26233	33337	21088	867	0.884882224	0.896615785	1.832980973	0.87419181
predicted RNA	-	21126	37178	34250	390	46492	56964	42352	615	0.093593505	0.106475705	1.576923077	0.657112286
BP1026B.11891	hypothetical protein	29893	21542	22537	95	24413	25268	28044	100	3.45E-08	6.28E-08	1.052631579	0.074000581
BP1026B.11892	hypothetical protein	154007	238704	209851	631	291981	324361	303905	964	0.12461894	0.140039864	1.527733756	0.611393141
predicted RNA	-	46429	70055	63011	592	96908	101366	89671	950	0.075678311	0.08686578	1.60472973	0.682330338
BP1026B.11893	hypothetical protein	610461	228858	332665	540	279312	205997	282605	354	4.43E-35	6.82E-34	0.655555556	-0.609210047
BP1026B.11894	hypothetical protein	4121964	6996066	6396544	20925	8215548	9356985	8015831	30571	0.140835218	0.157500714	1.460979689	0.546936122
BP1026B.11895	hypothetical protein	190098	292754	273616	977	347728	396689	346205	1409	0.010837569	0.013297084	1.442169908	0.528241144
BP1026B.11896	lipoprotein	149989	232404	217715	687	304529	338772	304995	1086	0.24062039	0.262350333	1.580786026	0.660642099
BP1026B.11897	hypothetical protein	385730	528634	495804	383	618837	644034	609775	508	0.541748481	0.56680514	1.326370757	0.407484105
BP1026B.11898	hypothetical protein	1290	945	1329	2	1384	690	749	1	2.13E-05	3.17E-05	0.5	-1
BP1026B.11899	hypothetical protein	9574	11376	11113	8	12230	11487	11460	9	6.00E-08	1.07E-07	1.125	0.169925001
BP1026B.11900	Pro tRNA	167	378	326	3	559	494	469	6	0.009243323	0.01387861	2	1
BP1026B.11901	hypothetical protein	2274	4159	3723	34	6645	5700	7200	65	0.825449901	0.841322009	1.911764706	0.934904972
BP1026B.11902	hypothetical protein	38302	64592	56294	44	72297	89789	85055	69	0.029686131	0.035249819	1.568181818	0.649092838
BP1026B.11903	hypothetical protein	26194	31226	29126	14	34170	39154	33037	18	1.21E-04	1.71E-04	1.285714286	0.362570079
BP1026B.11904	MerK family transcriptional regulator	87505	133403	114320	275	137818	154602	151114	365	0.001035639	0.001365309	1.327272727	0.408464845
BP1026B.11905	integration host factor subunit alpha	47018	50768	46313	121	55687	56122	62340	146	2.41E-06	3.83E-06	1.20661157	0.270961322
BP1026B.11906	phenylalanyl-tRNA synthetase subunit beta	155995	152929	154229	64	169810	159840	164561	68	1.72E-08	3.21E-08	1.0625	0.087462841
BP1026B.11907	phenylalanyl-tRNA synthetase subunit alpha	61262	80363	75035	70	85976	90859	88564	86	6.16E-07	1.03E-06	1.228571429	0.296981738
predicted RNA	-	27838	44339	38482	1024	48684	54705	50579	1425	0.009629193	0.005019633	1.391601563	0.476746204
BP1026B.11908	50S ribosomal protein L20	712549	1162801	1057256	2715	1384011	1589424	1492708	4135	0.003408205	0.004345912	1.523020258	0.60695131
BP1026B.11909	50S ribosomal protein L35	271132	476433	461345	2035	651674	767306	560691	3332	0.035668644	0.042122074	1.637346437	0.711359606
predicted RNA	-	30769	45505	41209	1350	53279	61114	45350	1836	0.001551662	0.002024722	1.36	0.443606651
BP1026B.11910	translation initiation factor IF-3	274194	455681	407899	1118	581788	669290	625991	1845	0.030482561	0.036161251	1.650268336	0.722700628
BP1026B.11911	threonyl-tRNA synthetase	188746	269654	227426	119	299496	320056	338685	167	0.009418192	0.01160102	1.403361345	0.488886529
BP1026B.11912	Val tRNA	1067	2090	1480	20	1915	2118	2862	29	9.57215193	0.963519743	1.45	0.5360529
BP1026B.11913	GTP pyrophosphokinase	180584	157582	158884	74	156446	147887	150632	67	2.10E-15	7.29E-15	0.905405405	-0.143364175
BP1026B.11914	L-PSP family endoribonuclease	36970	46756	47568	123	57453	65521	57961	170	0.001298926	0.0017006	1.382113821	0.466876431
BP1026B.11915	alpha/beta fold family hydrolase	61911	44419	47701	56	40575	37353	40579	43	1.93E-22	1.20E-21	0.767857143	-0.381090167
BP1026B.11916	LysR family transcriptional regulator	19893	8523	11180	14	7809	7111	8816	8	1.17E-40	2.38E-39	0.571428571	-0.807354922
BP1026B.11917	hypothetical protein	1455	1882	2402	3	1593	1759	2257	3	5.45E-04	7.35E-04	1	0
BP1026B.11918	polysaccharide deacetylase family protein	7940	9677	8810	8	9399	8247	8868	8	1.52E-10	3.34E-10	1	0
BP1026B.11919	short chain dehydrogenase	1403	258	743									

BP1026B_11943	hypothetical protein	5378	8823	6252	33	7971	8669	8236	40	6.99E-06	1.08E-05	1.21212121	0.27753976
BP1026B_11944	Fusaric acid resistance protein fusE	17045	15706	15913	18	15081	14112	16145	17	1.28E-14	4.13E-14	0.94444444	-0.08246216
BP1026B_11945	methyI-accepting chemotaxis protein	232414	160617	183849	114	140543	138178	141745	83	2.02E-32	2.62E-31	0.728070175	-0.457850583
BP1026B_11946	fosmidomycin resistance protein	16343	16393	16915	13	17286	16766	16292	13	1.06E-11	2.60E-11	1	0
BP1026B_11947	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	65395	67589	63575	83	73135	74762	71989	92	1.53E-09	3.13E-09	1.108433735	0.148522525
BP1026B_11948	DNA helicase II	159103	174731	176646	71	185506	180247	173076	75	3.28E-09	6.51E-09	1.056338028	0.079071571
BP1026B_11949	valyl-tRNA synthetase	341909	394959	390522	131	443004	434853	448381	154	1.15E-05	1.74E-05	1.175572519	0.233635359
BP1026B_11950	UTP-glucose-1-phosphate uridylyltransferase	338484	456296	421291	459	467961	515258	518169	567	8.79E-04	0.001164997	1.235294118	0.304854582
BP1026B_11951	lipoprotein	13529	6479	8196	15	6551	4885	6085	9	5.77E-32	7.20E-31	0.6	-0.736965594
BP1026B_11952	sensor histidine kinase	164474	126813	126273	58	120907	114201	121509	49	1.43E-20	7.64E-20	0.844827586	-0.243271151
BP1026B_11953	LysM domain-containing protein	248861	193765	209568	172	172170	147569	171702	130	3.12E-27	2.88E-26	0.755813953	-0.403896942
BP1026B_11954	DNA-binding response regulator	196984	282215	255704	336	283798	308689	288893	403	1.03E-05	1.56E-05	1.199404762	0.262318606
BP1026B_11955	hypothetical protein	28701	17106	18395	55	15245	15615	13098	37	2.72E-33	3.78E-32	0.672727273	-0.571906348
BP1026B_11956	hypothetical protein	101388	141597	127439	534	123784	114087	126706	526	3.62E-13	1.02E-12	0.985018727	-0.021776942
BP1026B_11957	homoserine dehydrogenase	10337	4746	4585	6	3562	4078	3623	3	1.49E-28	1.50E-27	0.85	-1
BP1026B_11958	myo-inositol 2-dehydrogenase	18049	9698	9482	12	9316	9604	7997	8	6.74E-25	5.15E-24	0.666666667	-0.584962501
BP1026B_11959	SIS domain-containing protein	18031	22703	19184	22	20726	19526	17738	21	2.28E-13	6.54E-13	0.954545455	-0.067114196
BP1026B_11960	sugar ABC transporter periplasmic sugar-binding protein	9032	13171	11708	10	11755	10181	11028	9	4.41E-11	1.02E-10	0.9	-0.152003903
BP1026B_11961	permease protein of sugar ABC transporter	6129	6756	6667	5	8186	7804	7134	6	2.00E-06	3.20E-06	1.2	0.26304406
BP1026B_11962	sugar ABC transporter ATP-binding protein	9218	13189	10888	13	11600	11744	10868	14	1.42E-09	2.91E-09	1.076923077	0.106915204
BP1026B_11963	ioiC protein	11080	8761	8849	4	7812	6838	6879	3	1.67E-22	1.05E-21	0.75	-0.415037499
BP1026B_11964	ioiD protein	4319	4216	3599	2	2605	2735	3516	1	2.29E-14	7.20E-14	0.5	-1
BP1026B_11965	hypothetical protein	7191	2989	4205	5	3031	2246	3185	3	2.14E-24	1.57E-23	0.6	-0.736965594
BP1026B_11966	ioiB protein	16047	15670	16119	19	13397	12769	14334	16	3.76E-18	1.66E-17	0.842105263	-0.247927513
BP1026B_11967	Branched-chain amino acid transport ATP-binding protein LivF	9064	2069	3866	7	2631	2192	2115	3	1.24E-40	2.50E-39	0.68871429	-1.222392421
BP1026B_11968	ABC-transporter	75876	44467	51912	24	42041	36261	38257	16	7.03E-32	8.67E-31	0.426666667	-0.584962501
BP1026B_11969	branched amino acid transport system, membrane protein	12837	13074	12884	13	10871	12580	13219	13	1.48E-12	3.94E-12	1	0
BP1026B_11970	thioesterase family protein	31903	23323	24458	50	23490	24248	26205	46	8.33E-12	9.79E-12	0.92	-0.120294234
BP1026B_11971	alcohol dehydrogenase	132620	69254	82704	82	63236	58650	63295	53	2.70E-45	7.09E-44	0.646341463	-0.62963155
BP1026B_11972	hypothetical protein	44675	32297	33718	109	32524	31717	34361	97	5.73E-13	1.59E-12	0.889908257	-0.168271483
BP1026B_11973	MutT/NUDIX NTP pyrophosphatase	81466	59588	67464	125	55885	49624	59220	99	1.22E-25	9.84E-25	0.792	-0.336427665
BP1026B_11974	hypothetical protein	12004	13003	12673	18	14585	14154	12583	20	1.30E-08	2.44E-08	1.111111111	0.152003903
BP1026B_11975	hypothetical protein	43311	31793	32508	23	34473	32380	37150	22	2.98E-10	6.45E-10	0.956521739	-0.064130337
BP1026B_11976	major facilitator superfamily permease	9023	6064	6214	3	7536	9047	8925	4	3.78E-06	5.94E-06	1.333333333	0.415037499
BP1026B_11977	hypothetical protein	4747	4672	4406	4	4296	4525	4274	4	1.10E-08	2.09E-08	1	0
BP1026B_11978	alanyl-tRNA synthetase	471126	386048	410797	161	440417	405848	430028	162	1.55E-09	3.17E-09	1.00621118	0.008933125
BP1026B_11979	CAIB/BAIF family protein	117005	83138	94576	80	71612	63644	65663	54	1.73E-40	3.46E-39	0.675	-0.567040593
BP1026B_11981	lipoprotein	5477	6751	7110	26	6150	8344	6913	29	1.14E-07	1.99E-07	1.115384615	0.157541277
BP1026B_11980	glutaminyI-tRNA synthetase	378316	448122	441438	247	520336	529097	544910	310	0.282797324	0.305835007	1.255060729	0.327757174
BP1026B_11982	NUDIX family hydrolase	66645	17490	28192	77	18129	12418	17064	32	9.91E-11	1.29E-10	0.415584416	-1.266786541
BP1026B_11983	hypothetical protein	170711	117973	134724	364	122355	127171	114267	313	2.81E-20	1.47E-19	0.85989011	-0.217775793
BP1026B_11984	Beta-hexosaminidase	52323	37592	43206	21	40971	40197	40573	20	1.59E-13	4.61E-13	0.952380952	-0.070389328
BP1026B_11985	hypothetical protein	31617	40931	37108	46	48751	46667	49976	61	8.06E-04	0.001072326	1.326086957	0.407175382
BP1026B_11986	cytochrome c peroxidase	2799	4137	4213	2	3053	4660	5551	3	4.75E-04	6.43E-04	1.5	0.584962501
BP1026B_11987	acid phosphatase	9277	9137	10851	6	8273	6742	9448	5	1.37E-17	5.78E-17	0.833333333	-0.26304406
BP1026B_11988	trans-2-enoyl-CoA reductase	24298	20584	25854	19	21830	19172	19614	16	4.00E-18	1.76E-17	0.842105263	-0.247927513
BP1026B_11989	HlyD family secretion protein	890	971	815	0	518	821	1091	0	0.006769115	0.008434138	#DIV/0!	#DIV/0!
BP1026B_11990	EmrB/QacA family drug resistance transporter	3471	3286	2895	1	4079	3669	4800	2	0.018692215	0.022554481	2	1
BP1026B_11991	hypothetical protein	4670	2437	3192	2	1938	1736	1782	1	8.91E-25	6.72E-24	0.65	-1
BP1026B_11992	DNA-binding response regulator	6914	9044	10052	13	9577	10909	10486	16	5.23E-06	8.14E-06	1.230769231	0.299560282
BP1026B_11993	sensor histidine kinase/response regulator	9300	9175	8855	4	8629	9967	8334	4	5.28E-11	1.21E-10	1	0
BP1026B_11994	type 1 pilI protein CsuE	10159	8679	10343	10	10042	10463	9949	10	6.44E-09	1.24E-08	1	0
BP1026B_11995	fimbriae protein	5095	3782	3070	1	3311	2953	3597	1	9.42E-11	2.11E-10	1	0
BP1026B_11996	type 1 pilI usher pathway chaperone CsuC	824	486	539	0	465	319	285	0	4.08E-08	7.39E-08	#DIV/0!	#DIV/0!
BP1026B_11997	hypothetical protein	773	195	258	0	143	286	37	0	2.23E-11	5.32E-11	#DIV/0!	#DIV/0!
BP1026B_11998	hypothetical protein	14400	9841	13155	22	10222	8527	9346	16	3.33E-22	2.04E-21	0.727272727	-0.459431619
BP1026B_11999	hypothetical protein	694	1153	1032	1	889	777	1328	1	0.04827903	0.0564291	1	0
BP1026B_12000	LysR family transcriptional regulator	100541	106488	101274	114	126238	130382	127673	143	1.49E-05	2.24E-05	1.254385965	0.326981323
BP1026B_12001	major facilitator family transporter	629769	612237	622492	493	638166	664351	657817	518	0.709210981	0.729946782	1.050709399	0.071364451
BP1026B_12002	hydrolase	153784	164239	158177	161	162567	162195	159490	164	2.71E-10	5.86E-10	1.01863354	0.026635127
BP1026B_12003	predicted RNA	36691	7003	12522	398	10186	5615	9176	177	3.19E-85	2.90E-83	0.444723618	-1.16901907
BP1026B_12004	H-NS histone family protein	52067	68733	67031	222	100889	109922	100791	368	0.184421668	0.203555781	1.657657658	0.72914609
BP1026B_12003	lipoprotein	16530	19678	19680	60	18905	22258	19627	65	5.84E-09	1.13E-08	1.083333333	0.115477217
BP1026B_12005	Manganese transport protein	22614	24616	23426	17	25141	26367	25046	19	1.54E-07	2.66E-07	1.117647059	0.160464672
BP1026B_12006	hypothetical protein	33641	57213	49238	45	60365	71711	54515	60	2.56E-04	3.54E-04	1.333333333	0.415037499
BP1026B_12008	Transposase mutator family	10482	16528	15655	24	16713	16088	13380	26	2.36E-09	4.74E-09	1.083333333	0.115477217
BP1026B_12009	hypothetical protein	5958	10445	7407	26	13266	13049	10587	40	0.018745897	0.0226149	1.538461538	0.621488377
BP1026B_12011	hypothetical protein	930	2859	1998	6	2507	2010	2665	8	0.071598273	0.08228811	1.333333333	0.415037499
BP1026B_12012	hypothetical protein	1314	2273	1770	9	1834	3014	2249	12	0.253027747	0.274873762	1.333333333	0.415037499
BP1026B_12013	transposase	596	803	704	7	857	1499	898	11	0.294189609	0.317333808	1.571428571	0.652076697
BP1026B_12014	integrase core subunit	9074	16783	13054	73	14629	17382	17087	92	1.08E-05	1.65E-05	1.260273973	0.333737397
BP1026B_12015	transposase	18947	29633	25523	98	28540	33379	29566	121	1.31E-04	1.85E-04	1.234693878	0.304153393
BP1026B_12016	hypothetical protein	58872	103857	90020	91	97514	107784	87355	105	5.75E-08	1.03E-07	1.153846154	0.206450877
BP1026B_12017	hypothetical protein	105776	158763	145599	48	158287	182834	172421	60	2.66E-04	3.68E-04	1.25	0.321928095
BP1026B_12018	hypothetical protein	31565	45325	44237	57	43953	46754	44884	64	2.60E-07	4.43E-07	1.122807018	0.167109986
BP1026B_12019	Rhs element Vgr protein	63361	57647	57967	20	52438	50223	47757	17	1.19E-20	6.38E-20	0.85	-0.234465254
BP1026B_12020	hypothetical protein	2752	3677	3587	10	3936	3978	3727	12	0.001148339	0.001510414	1.2	0.263034406
BP1026B_12021	hypothetical protein	13796	13540	13727	51								

BP1026B_12044	hypothetical protein	4380	3004	3776	2	4238	3266	2944	2	2.49E-07	4.25E-07	1	0
BP1026B_12045	OmpA family protein	1532	825	1483	1	1592	1292	986	1	0.012539002	0.015321643	1	0
BP1026B_12046	hemagglutinin	7216	4970	5137	1	5974	4267	5307	1	2.36E-11	5.60E-11	1	0
BP1026B_12047	DNA-binding response regulator	477	392	408	0	574	294	442	0	0.240774928	0.262473155	#DIV/0!	#DIV/0!
BP1026B_12048	Fels-1 prophage	6689	8393	8215	20	8262	10250	10408	25	2.90E-05	4.27E-05	1.25	0.321928095
BP1026B_12049	hypothetical protein	3216	3585	3211	15	3457	4226	4643	19	0.004377311	0.005526542	1.266666667	0.341036918
BP1026B_12050	DNA-binding response regulator	6876	10798	10006	11	8459	9174	8384	11	9.85E-13	2.67E-12	1	0
BP1026B_12051	LysR family transcriptional regulator	136966	126299	137864	143	156924	140904	169649	167	4.09E-06	6.41E-06	1.167832168	0.223832956
BP1026B_12052	hypothetical protein	2898	1505	1493	1	1894	1647	1873	1	6.70E-05	9.63E-05	1	0
BP1026B_12053	hypothetical protein	165	145	240	0	296	377	91	1	0.254229302	0.276035489	#DIV/0!	#DIV/0!
BP1026B_12054	hypothetical protein	23665	42410	38635	159	47366	53913	48652	228	0.010029723	0.012337307	1.433962264	0.520007059
BP1026B_12055	poly(3-hydroxybutyrate) depolymerase	23655	21702	22971	15	20812	17719	18508	12	2.07E-20	1.09E-19	0.8	-0.321928095
BP1026B_12056	alpha amylase domain-containing protein	7612	5629	6163	1	5516	5590	5166	1	4.40E-14	1.35E-13	1	0
BP1026B_12057	Trehalose synthase	14817	16325	16251	4	15574	17484	17443	4	4.70E-10	1.00E-09	1	0
BP1026B_12058	glycogen branching protein	1208	629	724	0	828	294	620	0	4.00E-06	6.27E-06	#DIV/0!	#DIV/0!
BP1026B_12059	glycogen debranching protein GlgX	2814	2947	2302	1	1551	1823	2189	0	2.74E-12	7.10E-12	0	#NUM!
BP1026B_12060	malto-oligosyltrehalose trehalohydrolase	843	123	680	0	362	353	429	0	7.19E-05	1.03E-04	#DIV/0!	#DIV/0!
BP1026B_12061	4-alpha-glucanotransferase	978	583	647	0	256	234	190	0	1.59E-26	1.38E-25	#DIV/0!	#DIV/0!
BP1026B_12062	malto-oligosyltrehalose synthase	13078	8303	12223	4	9263	8183	9148	3	7.57E-20	3.84E-19	0.75	-0.415037499
BP1026B_12063	Multimeric flavodoxin WrbA	531	760	403	1	718	598	648	1	0.563165826	0.588217514	1	0
BP1026B_12064	hypothetical protein	2853	2896	2987	7	3393	3505	3632	9	0.00899688	0.012184531	1.285714286	0.362570079
BP1026B_12065	GntR family transcriptional regulator	177369	121623	130040	97	137958	124493	132364	90	3.39E-16	1.27E-15	0.927835052	-0.108059746
BP1026B_12066	MerR family transcriptional regulator	43773	35153	38859	20	39841	38377	35204	19	8.03E-11	1.81E-10	0.95	-0.074000581
BP1026B_12068	PAAR motif-containing protein	52083	49406	49111	118	58268	56288	51356	130	7.20E-09	1.39E-08	1.101694915	0.139724764
BP1026B_12067	hypothetical protein	30906	25061	26000	53	28511	24187	27694	52	6.83E-10	1.44E-09	0.981132075	-0.027480736
BP1026B_12069	hypothetical protein	33674	34247	38505	74	40382	38661	39631	83	1.00E-06	1.64E-06	1.121621622	0.165586066
BP1026B_12070	hypothetical protein	72098	105090	98550	152	125318	133647	120820	209	0.001134015	0.001492175	1.375	0.459431619
BP1026B_12071	hypothetical protein	106670	178945	153895	205	198683	234345	221141	305	0.091790218	0.104536079	1.487804878	0.573185333
BP1026B_12072	Integrase	5803	6146	6164	24	7996	6818	7238	309	9.00E-06	1.38E-05	1.208333333	0.273018494
BP1026B_12073	Arg tRNA	3505	3127	3884	45	4208	5166	5677	65	0.045136677	0.052904306	1.444444444	0.530514717
BP1026B_12074	undecaprenyl pyrophosphate phosphatase	19415	19697	18570	23	18349	17197	17210	21	4.24E-16	1.57E-15	0.913043478	-0.131244533
BP1026B_12075	aldose 1-epimerase	17046	16859	15316	18	18868	17689	20918	21	2.46E-07	4.19E-07	1.166666667	0.222392421
BP1026B_12076	peptidase	11485	11122	11898	16	13282	13881	12558	18	2.69E-07	4.57E-07	1.125	0.169925001
BP1026B_12077	acetyl-coenzyme A synthetase	31319	21974	24875	16	20785	15842	19687	11	5.02E-30	5.57E-29	0.6875	-0.540568381
BP1026B_12078	hypothetical protein	15313	25150	23731	60	27540	32459	27360	82	0.00302094	0.003881845	1.366666667	0.450661409
BP1026B_12079	DNA-damage-inducible protein F	33033	22696	24200	19	20296	20775	21096	14	7.54E-23	4.90E-22	0.736842105	-0.440572591
BP1026B_12080	lipoprotein	6225	4910	5577	29	6479	7348	6502	35	1.34E-05	2.02E-05	1.206896552	0.271302022
BP1026B_12081	hypothetical protein	10833	14685	12055	73	18851	22321	21389	121	0.136490614	0.152859729	1.657534247	0.729038678
BP1026B_12082	hypothetical protein	458531	405661	434396	528	440882	436980	415384	526	6.14E-10	1.30E-09	0.996212121	-0.00547513
predicted RNA	-	3789	6416	6070	452	8974	10865	6707	737	0.062177862	0.071883115	1.630530973	0.705341847
BP1026B_12083	phosphohistidine phosphatase SixA	228260	183911	188303	436	151724	145756	159736	332	3.03E-27	2.80E-26	0.76146789	-0.393144893
BP1026B_12084	Pro tRNA	551	971	790	10	1827	1916	991	2	7.66E-04	0.001020409	2	1
BP1026B_12085	putative bacteriophage protein	14634	25118	23890	38	32522	32418	31924	59	0.049800502	0.05813151	1.552631579	0.634715536
BP1026B_12086	hypothetical protein	22673	39677	36192	71	45610	47805	47007	101	0.009111773	0.011234626	1.422535211	0.508464363
BP1026B_12087	hypothetical protein	223873	368338	326601	280	345860	397263	360419	336	7.86E-06	1.21E-05	1.2	0.263034406
BP1026B_12088	putative bacteriophage protein gp29	139954	231545	199761	259	228088	257151	244040	330	2.97E-04	4.08E-04	1.274131274	0.349513927
BP1026B_12089	putative bacteriophage protein gp28	199992	347462	292591	499	337307	389514	346544	637	9.18E-05	1.31E-04	1.276553106	0.352253557
BP1026B_12090	hypothetical protein	273334	429432	371517	457	419244	470091	441161	566	7.77E-05	1.11E-04	1.238512035	0.308607888
BP1026B_12091	Site-specific DNA methylase	3770	6724	5671	6	7950	9758	8611	11	0.059280853	0.068660596	1.833333333	0.874469118
BP1026B_12092	bacteriophage lysis protein	5513	7307	6872	12	9819	9492	11099	18	0.029492209	0.03502619	1.5	0.584962501
BP1026B_12093	Glycoside hydrolase family protein gp24	1498	935	1130	2	794	793	845	1	1.52E-07	2.63E-07	0.5	-1
BP1026B_12094	putative class II holin gp23	399	263	615	1	559	1088	695	3	0.006758771	0.008422924	3	1.584962501
BP1026B_12095	gp22	2445	3224	3140	3	3810	4956	4267	5	0.237998491	0.259717615	1.666666667	0.736965594
BP1026B_12096	hypothetical protein	440	387	342	1	636	666	286	1	0.473050721	0.498509219	1	0
BP1026B_12097	gp20	5303	6578	5795	1	7951	7922	7594	2	2.09E-04	2.91E-04	2	1
BP1026B_12098	Phage tail assembly protein I	157	300	377	0	176	58	273	0	0.002087563	0.002703176	#DIV/0!	#DIV/0!
BP1026B_12099	Phage tail assembly protein	412	464	521	0	587	647	899	0	0.184649558	0.20373554	#DIV/0!	#DIV/0!
BP1026B_12100	phage minor tail protein	2523	5035	3805	5	4578	5010	5620	7	0.004701595	0.005927604	1.4	0.485426827
BP1026B_12101	Phage-related tail fiber protein	7444	13841	11752	7	14586	14176	14176	9	4.38E-06	6.84E-06	1.285714286	0.362570079
BP1026B_12102	phage minor tail protein	649	628	501	1	1068	868	1169	3	0.0388392	0.04577138	3	1.584962501
BP1026B_12103	hypothetical protein	11718	13633	12772	3	14781	15286	15507	3	8.90E-07	1.47E-06	1	0
BP1026B_12104	hypothetical protein	2136	3468	2652	9	3285	1915	2532	9	5.18E-06	8.06E-06	1	0
BP1026B_12105	Phage tail assembly chaperone	2055	2764	1789	4	2771	1768	2344	4	7.84E-04	0.001043794	1	0
BP1026B_12106	gp11	1418	1853	2090	3	2477	2228	2239	5	0.188914167	0.208294241	1.666666667	0.736965594
BP1026B_12107	putative bacteriophage protein gp10	1020	1272	926	3	1638	810	1015	3	0.074594035	0.085652597	1	0
BP1026B_12108	HK97 family phage protein	3735	5334	4245	10	4935	5307	5384	12	3.23E-05	4.74E-05	1.2	0.263034406
BP1026B_12109	putative bacteriophage protein gp8	725	2047	1349	9	1953	2662	1810	14	0.486471132	0.511963069	1.555555556	0.637429921
BP1026B_12110	gp7	1163	2272	2030	5	2633	2730	2233	6	0.42897128	0.454349905	1.2	0.263034406
BP1026B_12111	Phage major capsid protein	42342	67463	62862	45	68763	81287	74630	59	2.45E-05	3.63E-05	1.311111111	0.390789953
BP1026B_12112	gp4	4034	5365	5131	8	7051	7052	7204	12	0.005858637	0.007001321	1.5	0.584962501
BP1026B_12113	Phage portal protein	11748	20649	18817	12	21597	23616	21362	16	2.42E-04	3.35E-04	1.333333333	0.415037499
BP1026B_12114	Phage terminase large subunit	1063	2022	2165	1	2708	3126	3141	1	0.354132991	0.378539291	1	0
BP1026B_12115	Phage terminase small subunit	206	311	328	1	220	137	179	1	0.003690128	0.00469013	1	0
BP1026B_12116	putative bacteriophage protein gp82	941	712	812	2	1273	890	1174	3	1	1	1.5	0.584962501
BP1026B_12117	Phage protein	37220	63650	60141	255	66872	80405	73948	351	4.57E-04	6.19E-04	1.376470588	0.460973783
BP1026B_12118	Phage-related transcriptional regulator	39447	60464	50878	129	67988	75115	71959	185	0.002996337	0.00384105	1.434108527	0.520154205
BP1026B_12119	gp78	91014	147547	131955	89	144192	175496	151002	113	3.70E-04	5.04E-04	1.269662921	0.344445531
BP1026B_12120	gp77	7889	12503	12397	16	14880	14892	13423	22	8.38E-05	1.20E-04	1.375	0.459431619
BP1026B_12121	gp76	942	1615	1338	6	1236	1548	1726	8	0.155217148	0.172506323	1.333333333	0.415037499
BP1026B_12122	gp75	966	1717	1318	4	2090	1970	1788	5	0.795191227	0.812568205	1.25	

BP1026B_12141	gp54		863	1060	836	5	982	1538	1155	6	0.92760675	0.936645657	1.2	0.263034406
BP1026B_12142	hypothetical protein		6639	8926	7256	16	8348	9228	10187	19	1.11E-05	1.69E-05	1.1875	0.247927513
BP1026B_12144	bacteriophage protein Gp46		13072	19808	15175	62	21097	23086	24587	89	0.007786979	0.009641021	1.435483871	0.521537121
BP1026B_12143	gp52		13731	21061	17201	79	23431	24902	25438	112	0.009173568	0.011304145	1.417721519	0.503574174
BP1026B_12145	bacteriophage protein		28832	47085	43397	67	50000	58035	50305	89	6.03E-04	8.11E-04	1.328358209	0.409644241
BP1026B_12146	bacteriophage protein Gp44		908	1265	792	6	1472	1070	1713	9	0.636879431	0.659726651	1.5	0.584962501
BP1026B_12148	gp47		5759	9665	9562	11	12756	15248	13640	19	0.061932496	0.071612663	1.727272727	0.788495895
BP1026B_12149	gp46		1807	1561	1639	2	2633	2720	2189	3	0.976578575	0.980647653	1.5	0.584962501
BP1026B_12150	gp45		1757	2539	1905	7	2243	2941	3268	9	0.226681525	0.24788594	1.285714286	0.362570079
BP1026B_12151	gp44		1404	2140	1963	6	2341	3051	2859	9	0.830090707	0.845747702	1.5	0.584962501
BP1026B_12152	gp43		12319	15251	14396	7	16764	18530	18713	9	2.58E-05	3.81E-05	1.285714286	0.362570079
BP1026B_12153	gp41		2427	4331	3651	13	3671	4399	5236	17	0.006503872	0.008111716	1.307692308	0.387023123
BP1026B_12154	gp40		2476	2544	2305	14	3515	4043	3865	23	0.699621073	0.720905384	1.642857143	0.716207034
BP1026B_12155	gp39		2758	4531	3873	10	5697	6343	4789	16	0.053536763	0.062249278	1.6	0.678071905
BP1026B_12156	Bacteriophage protein gp37		12021	16674	13643	13	17442	18625	16904	17	6.97E-06	1.07E-05	1.307692308	0.387023123
BP1026B_12157	hypothetical protein		15210	18776	16422	68	18989	18278	20069	77	4.84E-08	8.68E-08	1.132352591	0.179323699
BP1026B_12158	gp36-related protein		15178	22496	23122	96	31148	36183	39845	170	0.493415963	0.518662041	1.770833333	0.824428435
BP1026B_12159	putative bacteriophage protein		81641	122941	111400	468	161218	174840	162119	738	0.253875643	0.275699269	1.576923077	0.657112286
BP1026B_12160	gp34		2088	3593	2362	11	4203	5803	4036	20	0.806771591	0.823461604	1.818181818	0.862496476
BP1026B_12161	Phage integrase		29254	46702	43733	36	60899	65807	61538	56	0.082927061	0.09483865	1.555555556	0.637429921
BP1026B_12163	hypothetical protein		33827	51384	45609	167	52715	59966	55109	214	8.76E-05	1.25E-04	1.281437126	0.357762694
BP1026B_12165	hypothetical protein		1007274	1680505	1417230	5303	1838059	2008626	2043932	7610	0.018604436	0.022457214	1.435036772	0.521087705
BP1026B_12167	hypothetical protein		53034	73509	65461	112	78350	86103	78689	142	3.43E-06	5.42E-06	1.267857143	0.342392197
BP1026B_12168	PAP2 family protein		25783	17162	19121	19	20012	18553	18257	17	6.67E-16	2.43E-15	0.894736842	-0.160464672
BP1026B_12169	hypothetical protein		21918	17649	18121	43	18846	15250	17641	38	5.65E-17	2.27E-16	0.88372093	-0.178337241
BP1026B_12170	exopolyphosphatase		124978	105620	103233	73	107003	107104	117922	73	1.01E-12	2.74E-12	1	0
BP1026B_12171	polyphosphate kinase		173311	206456	197939	93	211661	210717	212625	102	1.32E-08	2.49E-08	1.096774194	0.133266531
BP1026B_12172	phosphate regulon sensor protein PhoR		125924	137527	139767	102	137816	128264	143260	104	1.79E-11	4.28E-11	1.019607843	0.028014376
BP1026B_12173	phosphate regulon transcriptional regulatory protein PhoB		24895	32416	33708	43	28972	27975	30782	41	3.79E-10	8.14E-10	0.953488372	-0.06871275
BP1026B_12174	phosphate transport system regulatory protein PhoU		25851	33263	31365	42	30363	36300	30171	45	2.64E-07	4.49E-07	1.071428571	0.099535674
BP1026B_12175	phosphate transporter ATP-binding protein		28138	38706	37447	40	34288	40933	36830	43	1.92E-07	3.30E-07	1.075	0.10433666
BP1026B_12176	phosphate transporter permease subunit PtsA		15538	13954	13470	16	12921	10653	12279	13	1.83E-17	7.65E-17	0.8125	-0.299560282
BP1026B_12177	phosphate transporter permease subunit PtsC		18856	18466	19604	19	17544	17471	17308	17	7.46E-16	2.70E-15	0.894736842	-0.160464672
BP1026B_12178	phosphate ABC transporter substrate-binding protein		210857	226899	235534	220	184088	185404	181190	179	1.02E-21	6.02E-21	0.813636364	-0.297543936
BP1026B_12179	hypothetical protein		19608	22463	23093	108	18157	21349	19775	98	1.07E-15	3.83E-15	0.907407407	-0.140177658
BP1026B_12180	phosphoglucosamine mutase		99385	79432	81932	63	70722	74417	74752	53	5.77E-23	3.79E-22	0.841269841	-0.249359469
BP1026B_12181	dihydropterotease synthase		21423	13245	13815	20	11191	11459	11139	13	2.06E-27	1.94E-26	0.65	-0.621488377
BP1026B_12182	cell division protein FtsH		3058410	3586256	3397635	1773	4016267	4287594	4192264	2207	0.83607608	0.851569037	1.244783459	0.315894093
predicted RNA	-		61829	40477	47376	519	65920	67528	52710	646	6.42E-06	9.92E-06	1.244701349	0.315799626
BP1026B_12183	ribosomal RNA large subunit methyltransferase j		99279	161002	138401	209	219835	250298	218125	362	0.905966739	0.916330118	1.732057416	0.792486755
BP1026B_12184	RNA-binding protein		42080	44425	41247	76	39603	39067	43004	73	7.69E-12	1.91E-11	0.960526316	-0.058102955
BP1026B_12185	hypothetical protein		96945	31679	46075	115	30126	24915	32952	58	8.32E-61	4.27E-59	0.504347826	-0.987509056
BP1026B_12186	transcription elongation factor GreA		379275	462551	444254	898	462297	470857	503727	1004	3.54E-07	5.98E-07	1.118040089	0.160971919
BP1026B_12187	carbamoyl phosphate synthase large subunit		486407	560260	490360	152	539921	514370	575650	166	0.10870747	0.122997654	1.092105263	0.127111918
BP1026B_12188	leucine export protein LeuE		27012	30805	27404	42	29936	30803	34422	47	2.22E-06	3.54E-06	1.119047619	0.162271429
BP1026B_12189	carbamoyl phosphate synthase small subunit		103181	72341	72551	72	75305	73242	72930	64	1.55E-19	7.67E-19	0.888888889	-0.169925001
BP1026B_12190	AraC family transcriptional regulator		40647	27424	26601	30	26574	25481	28424	26	6.94E-15	2.29E-14	0.866666667	-0.206450877
BP1026B_12191	hypothetical protein		4632	3156	4167	3	3679	3995	4598	3	1.40E-06	2.26E-06	1	0
BP1026B_12192	major facilitator family transporter		18804	19602	17915	15	19059	21657	21017	16	1.24E-08	2.34E-08	1.066666667	0.093109404
BP1026B_12193	exported transglycosylase protein		411543	381709	394187	245	325490	305239	319293	196	1.51E-19	7.49E-19	0.8	-0.321928095
BP1026B_12194	hypothetical protein		4095	6817	5228	57	7342	8803	7802	85	0.006142584	0.007674862	1.49122807	0.576500922
BP1026B_12195	hydroxyacylglutathione hydrolase		27656	21368	21249	29	24303	21604	22990	28	4.65E-11	1.07E-10	0.965517241	-0.050626073
BP1026B_12196	hypothetical protein		35300	38466	40166	46	40051	35720	41335	48	7.31E-09	1.40E-08	1.043478261	0.061400545
BP1026B_12197	RNase H		24988	33507	28111	65	35927	33575	30683	75	1.09E-05	1.66E-05	1.153846154	0.206450877
BP1026B_12198	DNA polymerase III subunit epsilon		55358	53438	59290	77	52091	53143	51528	72	2.18E-15	7.57E-15	0.935064935	-0.096861539
BP1026B_12199	hypothetical protein		11672	6208	7019	18	5164	6939	6768	13	1.48E-20	7.89E-20	0.722222222	-0.469485283
BP1026B_12200	proline/betaine transporter		7214	4825	4459	3	6299	4060	5544	3	1.73E-09	3.51E-09	1	0
BP1026B_12201	glutathione S-transferase domain-containing protein		42845	55319	50168	78	50831	53895	55616	84	2.66E-09	5.33E-09	1.076923077	0.106915204
BP1026B_12202	alpha/beta fold family hydrolase		48752	20092	25646	35	18970	18330	18330	21	4.58E-50	1.49E-48	0.6	-0.736965594
BP1026B_12203	hypothetical protein		9903	2353	2668	9	1877	2327	1969	4	1.44E-49	4.55E-48	0.444444444	-0.169925001
BP1026B_12204	acyl-carrier-protein S-malonyltransferase		2551	1047	1473	1	573	176	708	0	2.74E-55	1.13E-53	0	#NUM!
BP1026B_12205	triphosphoribosyl-dephospho-CoA synthase		4662	2002	2834	4	1872	1583	1975	2	3.01E-20	1.57E-19	0.5	-1
BP1026B_12206	phosphoribosyl-dephospho-CoA transferase		11356	9064	9556	10	10149	9280	8614	9	2.09E-12	5.49E-12	0.9	-0.152003093
BP1026B_12207	malonate decarboxylase subunit gamma		16655	15168	14530	21	12704	11920	12469	17	4.51E-20	2.33E-19	0.80952581	-0.304854582
BP1026B_12208	malonate decarboxylase subunit beta		20493	6116	8851	12	6815	5408	6051	6	6.23E-52	2.18E-50	0.5	-1
BP1026B_12209	malonate decarboxylase subunit delta		5617	3802	3927	13	3843	3405	2866	10	1.65E-13	4.79E-13	0.769230769	-0.378511623
BP1026B_12210	malonate decarboxylase alpha-subunit		61560	52112	56351	34	48436	39793	47459	27	1.34E-22	8.53E-22	0.794117647	-0.332575339
BP1026B_12211	malonate transporter, M subunit		2158	820	752	1	1171	723	1017	1	8.03E-06	1.23E-05	1	0
BP1026B_12212	malonate transporter, L subunit		1152	859	744	2	729	650	1189	2	0.009119471	0.011241905	1	0
BP1026B_12213	LysR family transcriptional regulator		8785	5440	5670	7	3776	4095	4419	4	4.93E-25	3.06E-24	0.571428571	-0.807354922
BP1026B_12214	3-hydroxyacyl-CoA dehydrogenase		50977	41966	41552	48	38750	32851	38988	40	1.46E-17	6.14E-17	0.833333333	-0.263034406
BP1026B_12215	phosphoenolpyruvate carboxykinase		504234	426270	438046	244	444214	414366	446893	233	2.29E-11	5.45E-11	0.954918033	-0.066551193
BP1026B_12216	ferredoxin		127	168	223	0	263	136	74	0	0.484228002	0.509773632	#DIV/0!	#DIV/0!
BP1026B_12217	HSP20 family protein		352866	453519	441589	949	580779	624919	561013	1344	0.339114158	0.362918756	1.416227608	0.502053146
BP1026B_12218	heat shock protein	</												

BP1026B_12245	ABC transporter ATP-binding protein	5463	3619	4115	4	3356	4151	3686	3	1.51E-10	3.32E-10	0.75	-0.415037499
BP1026B_12246	Ser/Thr protein phosphatase family protein	19896	7921	10077	15	9807	9116	7367	10	7.31E-28	7.02E-27	0.666666667	-0.584962501
BP1026B_12247	hypothetical protein	4010	2100	2782	7	1876	1223	1708	3	6.91E-22	4.14E-21	0.428571429	-1.222392421
BP1026B_12248	hypothetical protein	3076	1649	2717	3	1996	3030	2937	3	8.82E-04	0.001169316	1	0
BP1026B_12249	major facilitator family transporter	12470	7085	8571	7	7187	5558	6994	5	1.18E-25	9.55E-25	0.714285714	-0.485426827
BP1026B_12250	integral membrane protein	29115	12139	13246	19	10882	10652	10903	11	2.61E-40	5.18E-39	0.578947368	-0.788495895
BP1026B_12251	oxidoreductase, molybdopter-in-binding protein	8859	8057	8609	10	9902	9773	8180	11	4.43E-08	7.99E-08	1.1	0.137503524
BP1026B_12252	hypothetical protein	2951	3173	3424	2	2472	2090	2149	2	1.99E-13	5.73E-13	1	0
BP1026B_12253	hypothetical protein	796	572	449	0	457	274	553	0	7.22E-05	1.03E-04	#DIV/0!	#DIV/0!
BP1026B_12255	hypothetical protein	31537	49771	45581	138	56583	62292	60268	195	0.003481022	0.004435154	1.413043478	0.498805857
BP1026B_12254	hypothetical protein	1057	1371	1169	2	960	1018	1431	2	0.004267803	0.005394806	1	0
BP1026B_12256	thiamine biosynthesis protein ThiC	834227	1118322	1079426	523	1033946	1086606	1007293	539	0.248851721	0.27075966	1.030592734	0.043474327
BP1026B_12257	lipoprotein	15895	24848	21404	97	27761	33371	25931	136	0.006890997	0.008577471	1.402061856	0.487549999
BP1026B_12258	hypothetical protein	999	878	820	3	1180	1239	776	4	0.316661247	0.340167902	1.333333333	0.415037499
BP1026B_12259	DMT family permease	36966	19401	22046	28	18250	17850	14462	18	7.46E-40	1.45E-38	0.642857143	-0.637429921
BP1026B_12260	EAL domain-containing protein	34947	38133	37154	28	43424	44855	41764	33	8.54E-06	1.31E-05	1.178571429	0.237059197
BP1026B_12261	peptidyl-rRNA hydrolase domain-containing protein	45916	53166	53559	125	53718	48448	50769	125	6.84E-12	1.71E-11	1	0
BP1026B_12262	exodeoxyribonuclease V subunit alpha	107656	43977	49807	24	35540	34464	40482	13	1.95E-53	7.42E-52	0.541666667	-0.884522783
BP1026B_12263	exodeoxyribonuclease V subunit beta	274026	242406	248342	66	227249	205619	216854	56	1.45E-20	7.74E-20	0.848484848	-0.237039197
BP1026B_12264	exodeoxyribonuclease V gamma chain	164331	87899	109326	36	86045	64730	82870	23	1.27E-47	3.64E-46	0.638888889	-0.646363045
BP1026B_12265	hypothetical protein	96280	94193	92356	41	97191	92926	105162	43	2.39E-11	5.67E-11	1.048780488	0.06871275
BP1026B_12266	amino acid permease	26874	23098	23410	17	22826	22708	20141	16	5.59E-15	1.86E-14	0.941176471	-0.087462841
BP1026B_12267	hypothetical protein	24450	38295	35071	181	40566	47800	37155	232	4.11E-04	5.59E-04	1.281767956	0.358135108
BP1026B_12268	ABC transporter substrate-binding protein	39812	17658	23779	25	19936	16118	16856	16	4.05E-39	7.58E-38	0.64	-0.64385619
BP1026B_12269	ABC transporter permease	16948	9202	11407	7	7985	7364	8113	4	1.17E-36	1.94E-35	0.571428571	-0.807354922
BP1026B_12270	ABC transporter ATP-binding protein	23682	18719	22365	28	20930	19275	19916	25	1.13E-14	3.68E-14	0.892857143	-0.163498732
BP1026B_12271	AsnC family transcriptional regulator	44900	52819	51319	96	64296	75360	63162	131	5.00E-04	6.76E-04	1.364583333	0.448460501
BP1026B_12272	cysteine dioxygenase type I family protein	3799	1922	2435	4	2756	2079	2847	3	7.19E-06	1.11E-05	0.75	-0.415037499
BP1026B_12273	NAD-dependent epimerase/dehydratase family protein	19803	15949	17482	27	16574	17538	17588	26	2.20E-13	6.32E-13	0.962969629	-0.054447784
BP1026B_12274	RcT2 family protein	29897	28778	27747	62	29408	27862	31816	64	2.78E-08	5.10E-08	1.032258065	0.04580369
BP1026B_12275	hypothetical protein	1614	582	657	2	461	353	586	1	6.22E-14	1.87E-13	0.5	-1
BP1026B_12276	exported alkaline phosphatase	5207	5298	5231	2	5129	4970	5874	2	3.20E-08	5.84E-08	1	0
BP1026B_12277	hypothetical protein	258	434	188	2	362	526	683	5	0.005685365	0.007123475	2.5	1.321928095
BP1026B_12278	IcIR family transcriptional regulator	26469	24236	25127	30	24147	22885	25945	29	4.66E-11	1.07E-10	0.966666667	-0.0489096
BP1026B_12279	HydD family secretion protein	37319	35997	31538	26	34959	30414	31216	24	1.23E-11	2.98E-11	0.923076923	-0.115477217
BP1026B_12280	AcrB/AcrD/AcrF family protein	126381	124943	126956	40	119183	121986	125590	39	7.06E-14	2.12E-13	0.975	-0.036525876
BP1026B_12281	multidrug resistance protein mdrC	108704	99642	95287	30	98942	90068	102462	29	6.38E-15	2.11E-14	0.966666667	-0.0489096
BP1026B_12282	NAD-dependent epimerase/dehydratase family protein	239700	187354	194766	314	186117	181771	175514	274	9.01E-18	3.85E-17	0.872611465	-0.196588666
BP1026B_12283	AhpC/TSA family protein	53245	72435	67422	117	72376	78945	85282	143	5.28E-07	8.84E-07	1.222222222	0.289506617
BP1026B_12284	EAL domain-containing protein	476395	393611	406363	231	395454	399025	390410	215	3.66E-12	9.38E-12	0.930735931	-0.103556192
BP1026B_12285	hypothetical protein	913124	686135	708569	528	659331	631250	699319	455	0.187382665	0.206641988	0.861742424	-0.214671384
predicted RNA	-	157349	254842	217330	1925	255247	279644	263932	2442	3.21E-04	4.40E-04	1.268571429	0.343204755
BP1026B_12286	cytochrome c protein	1132522	1333899	1219067	1557	1189922	1258462	1266847	1569	0.424151631	0.449549073	1.007707129	0.011076408
BP1026B_12287	cytochrome c oxidase subunit I	2258141	2703082	2613302	1573	2454761	2563537	2560723	1574	0.784768305	0.802571927	1.006635728	0.00091687
BP1026B_12288	cytochrome c oxidase subunit II	422979	519461	517360	849	582623	610604	568232	1024	0.906002291	0.911365303	1.206124853	0.270379256
BP1026B_12289	hypothetical protein	108925	97174	99489	556	97576	96798	93860	525	7.32E-16	2.66E-15	0.944244604	-0.08276746
BP1026B_12290	cytochrome C	1334914	1164742	1283301	984	997502	923966	909235	736	0.838024985	0.853415335	0.74796748	-0.418952459
BP1026B_12291	cytochrome c	170766	164312	167745	235	192684	193792	169633	260	6.99E-08	1.70E-07	1.106382979	0.145850866
BP1026B_12292	hypothetical protein	2622	3206	2488	18	3054	3087	3461	21	0.004411023	0.005567983	1.166666667	0.222392421
BP1026B_12293	hypothetical protein	94349	77205	76328	72	73552	68390	74716	63	1.12E-20	6.00E-20	0.875	-0.192645078
BP1026B_12294	two-component hybrid sensor and regulator	163149	165933	161421	94	175091	186826	171844	102	4.86E-08	8.72E-08	1.085106383	0.11783649
BP1026B_12295	ABC-type transporter periplasmic sulfonate-binding protein	19019	11690	13925	14	14855	11632	13541	13	2.32E-15	8.03E-15	0.928571429	-0.106915204
BP1026B_12296	hypothetical protein	39035	36429	37816	81	40874	39552	34443	82	3.59E-09	7.10E-09	1.012345679	0.017702002
predicted RNA	-	30868	55447	45394	593	71414	85272	62212	986	0.24652789	0.268371049	1.662731872	0.733555542
BP1026B_12297	D-3-phosphoglycerate dehydrogenase	36700	30732	34263	28	31251	28701	31007	25	1.28E-12	3.44E-12	0.892857143	-0.163498732
BP1026B_12298	AraC family transcriptional regulator	80590	108356	99567	92	112949	117528	112643	109	7.85E-07	1.30E-06	1.184782609	0.244622369
BP1026B_12299	hypothetical protein	18800	23330	24523	20	26436	27973	30751	26	3.82E-04	5.21E-04	1.3	0.378511623
BP1026B_12300	M24 family metalloproteinase	195677	195229	195437	105	231324	239529	254082	130	5.89E-05	8.50E-05	1.238095238	0.308122295
BP1026B_12301	5S ribosomal RNA	1840403	2541837	1678548	17878	3056600	3044717	4096971	30083	0.067612639	0.077993519	1.682682627	0.705763093
BP1026B_12302	23S ribosomal RNA	405869	284178	214921	104	1823596	610699	344249	321	3.15E-12	8.13E-12	3.086538462	1.625899769
BP1026B_12303	hypothetical protein	29169	45566	39363	294	62063	70099	60181	497	0.335845156	0.359850504	1.69047619	0.757429697
BP1026B_12304	Ala tRNA	107961	168966	136304	1812	220109	236583	237041	3042	0.847144585	0.862001944	1.678807947	0.747437198
BP1026B_12305	Ile tRNA	20497	29480	22643	314	41336	44817	39719	344	0.365821269	0.390433669	1.732480492	0.792842004
BP1026B_12306	16S ribosomal RNA	831341	219735	173745	268	3098957	681585	152584	863	2.48E-14	7.77E-14	3.220149254	1.687127559
BP1026B_12307	hypothetical protein	53426	84432	66715	582	119320	133574	131126	1094	0.927527338	0.936645657	1.879725086	0.91052168
BP1026B_12308	hypothetical protein	3904	3552	4240	22	3725	3882	3454	21	1.16E-07	2.03E-07	0.954545455	-0.067114196
BP1026B_12309	hypothetical protein	78556	90593	90038	70	108469	114162	106775	90	2.76E-05	4.07E-05	1.285714286	0.362570079
BP1026B_12310	DNA-binding response regulator	47266	59779	56411	64	63734	67992	64780	80	2.98E-06	4.72E-06	1.25	0.321928095
BP1026B_12311	hypothetical protein	72991	50739	54975	88	51412	45015	52532	73	4.68E-21	2.60E-20	0.829545455	-0.26960706
BP1026B_12312	hypothetical protein	171447	201309	200821	307	209806	193532	200186	323	3.97E-10	8.51E-10	1.052117264	0.073295509
BP1026B_12313	peptidase	165085	194921	192527	159	196112	193360	195353	168	1.01E-09	2.09E-09	1.056603774	0.079434467
BP1026B_12314	hypothetical protein	22509	20056	21104	27	23517	19021	24856	28	5.44E-09	1.06E-08	1.037037037	0.05246742
BP1026B_12315	hypothetical protein	15417	14075	14071	21	12812	12129	11398	18	1.16E-17	4.90E-17	0.857142857	-0.222392421
BP1026B_12316	aminotransferase	158148	198564	185997	153	182496	184560	185384	156	8.92E-11	2.00E-10	1.019607843	0.028014376
BP1026B_12317	glutathione S-transferase domain-containing protein	483318	701530	631277	921	704447	754452	759798	1125	0.357922114	0.381720782	1.221498371	0.28865194
BP1026B_12318													

BP1026B_12342	NADH-ubiquinone oxidoreductase subunit B	138768	172137	164919	303	193943	205092	204358	385	2.25E-04	3.12E-04	1.270627068	0.345540652
BP1026B_12343	NADH ubiquinone oxidoreductase chain A	64446	110937	94629	250	181912	208296	176654	524	0.054310101	0.063136752	2.096	1.067638717
BP1026B_12344	Leu tRNA	34722	59196	49929	564	69354	79765	66620	846	0.018966796	0.022868183	1	0.584962501
BP1026B_12345	preprotein translocase subunit SecE	39813	37377	40645	103	39839	37834	39589	103	6.73E-10	1.42E-09	1	0
BP1026B_12346	triosephosphate isomerase	116443	94287	101247	129	110021	114593	100877	135	6.84E-11	1.55E-10	1.046511628	0.065588342
BP1026B_12347	oxidoreductase, zinc-binding dehydrogenase family protein	110729	69118	81206	85	68675	61761	61970	62	7.00E-33	9.39E-32	0.729411765	0.455194626
BP1026B_12348	polynucleotide phosphorylase/polyadenylase	595281	707773	690621	310	749232	768712	697906	344	0.603473575	0.627092109	1.109677419	0.150140349
BP1026B_12349	30S ribosomal protein S15	495143	605349	635071	1662	720600	640617	715661	1989	0.783820011	0.801863868	1.196750903	0.259122894
BP1026B_12350	branched-chain amino acid ABC transporter periplasmic protein	23645	17141	18740	15	17438	15817	15724	12	2.63E-21	1.49E-20	0.8	0.321928095
BP1026B_12351	lipoprotein	48105	58352	58658	109	76265	78613	69469	149	2.32E-04	3.22E-04	1.366972477	0.450984196
BP1026B_12352	hypothetical protein	796	1614	934	8	1650	1645	1553	11	0.641444604	0.664235976	1.375	0.459431619
BP1026B_12353	carbonic anhydrase	7107	6113	5984	10	6041	6560	7091	10	2.85E-09	5.69E-09	1	0
BP1026B_12354	sulfate transporter family protein	160395	176218	174513	110	188836	184016	188390	120	4.62E-08	8.31E-08	1.090906991	0.125530882
BP1026B_12355	2-isopropylmalate synthase	281278	347904	331684	206	369252	360182	356529	233	4.11E-07	6.91E-07	1.131067961	0.177685617
BP1026B_12356	CDP-diacylglycerol--serine O-phosphatidyltransferase	177203	151818	147869	182	132679	124952	132848	149	1.83E-23	1.25E-22	0.818681319	0.28862612
BP1026B_12357	phosphatidylserine decarboxylase	246009	236846	242910	371	215837	205424	218840	327	2.88E-18	1.28E-17	0.881401617	0.182128551
BP1026B_12358	ketol-acid reductoisomerase	148016	190567	176934	168	199291	206649	196470	197	1.45E-06	2.34E-06	1.172619048	0.229734397
BP1026B_12359	acetolactate synthase 3 regulatory subunit	43191	71484	61815	119	89307	103981	91087	192	0.082619816	0.094521776	1.613445378	0.69014737
BP1026B_12360	acetolactate synthase 3 catalytic subunit	32510	433551	407202	220	460312	490490	483713	271	6.21E-05	8.96E-05	1.231818182	0.300789328
BP1026B_12361	RNA polymerase factor sigma-70	40834	45329	45435	78	49577	53635	55893	94	5.76E-06	8.94E-06	1.205128205	0.269186633
BP1026B_12362	hypothetical protein	10795	15040	14992	32	19600	20546	14305	42	1.19E-04	1.68E-04	1.3125	0.392317423
BP1026B_12363	hypothetical protein	29591	36639	36955	45	39185	43080	37953	53	8.71E-06	1.34E-05	1.177777778	0.236067358
BP1026B_12364	RDD family protein	3492	3124	2642	6	3066	2259	2560	5	2.53E-08	4.65E-08	0.833333333	0.263034406
BP1026B_12365	calciuretin-like phosphoesterase	1285	1767	1718	1	2162	1256	2306	2	0.113040241	0.127692473	2	1
BP1026B_12366	glycoside hydrolase family protein	28612	11754	13727	17	17331	14757	12550	14	2.00E-20	1.06E-19	0.823529412	0.280107919
BP1026B_12367	diacylglycerol kinase	8181	6811	6954	13	8108	8460	8069	15	1.31E-07	2.28E-07	1.153846154	0.206450877
BP1026B_12368	TetR family transcriptional regulator	366356	555395	506192	661	603973	680298	590160	867	0.58516594	0.609787092	1.311649017	0.391381722
BP1026B_12369	hypothetical protein	124101	153726	152019	243	145291	139489	150397	246	3.97E-11	9.19E-11	1.012345679	0.017702002
BP1026B_12370	glucose-1-dehydrogenase	8994	2956	4477	7	4049	2193	3331	4	1.28E-25	1.03E-24	0.571428571	0.807354922
BP1026B_12371	hypothetical protein	67643	64196	59530	33	65069	67495	64323	34	1.62E-12	4.30E-12	1.03030303	0.043068722
BP1026B_12372	major facilitator family transporter	13044	11321	12990	9	11749	9473	9668	7	5.33E-17	2.15E-16	0.777777778	0.362570079
BP1026B_12373	amidase	31789	24588	26579	19	23538	18920	20511	15	4.52E-24	3.24E-23	0.789473684	0.341036918
BP1026B_12374	hypothetical protein	27164	18450	24399	36	17430	17986	16532	26	3.73E-28	3.65E-27	0.722222222	0.469485283
BP1026B_12375	alanine tRNA synthetase	64157	44368	53489	73	38455	33238	35728	48	1.24E-32	1.63E-31	0.657534247	0.604862058
BP1026B_12376	hypothetical protein	9468	4592	4901	15	4825	4219	5869	12	1.24E-15	4.40E-15	0.8	0.321928095
BP1026B_12377	permease	66107	24351	32940	15	21116	15435	22806	7	1.39E-79	1.21E-77	0.466666667	0.1099535674
BP1026B_12378	type IV secretory pathway protein	108299	76606	105574	156	77949	57717	78317	115	6.26E-33	8.43E-32	0.737179487	0.439912168
BP1026B_12379	quaternary ammonium compound-resistance protein	22254	25922	21559	72	30229	32360	39918	106	0.022946585	0.027497285	1.472222222	0.557995453
BP1026B_12380	hypothetical protein	127471	86351	104911	357	94268	84027	94653	306	6.38E-22	3.83E-21	0.857142857	0.222392421
BP1026B_12381	DNA-binding response regulator KdpE	38035	22040	25396	40	21343	19656	21271	29	5.21E-27	4.69E-26	0.725	0.4639471
BP1026B_12382	two-component system, sensor kinase protein KdpD	127609	109989	111611	39	108852	100146	106830	35	3.26E-17	1.33E-16	0.897435897	0.156119202
BP1026B_12383	potassium-transporting ATPase subunit C	23278	18658	20443	35	14437	13630	14947	24	2.31E-32	2.98E-31	0.685714286	0.544320516
BP1026B_12384	potassium-transporting ATPase subunit B	113940	101153	111153	52	90298	80657	79878	40	2.78E-30	3.11E-29	0.769230769	0.378511623
BP1026B_12385	potassium-transporting ATPase subunit A	131027	122447	124990	69	97572	97110	106614	55	1.98E-25	1.58E-24	0.797101449	0.327164743
BP1026B_12386	potassium-transporting ATPase, KdpF subunit	6791	10145	7720	88	9140	11399	10205	110	3.64E-05	5.32E-05	1.25	0.321928095
BP1026B_12387	quinone oxidoreductase	115673	121606	119184	121	106146	100000	101484	105	5.86E-20	3.00E-19	0.867768595	0.20461772
BP1026B_12388	methylglyoxal synthase	52133	36297	41728	110	36660	35995	36211	92	1.52E-16	5.85E-16	0.836363636	0.257797757
BP1026B_12389	short chain dehydrogenase/reductase family oxidoreductase	23275	15115	18461	24	14773	13840	13878	18	4.25E-26	3.56E-25	0.75	0.415037499
BP1026B_12390	uracil phosphoribosyltransferase	131877	123649	128863	196	137372	149658	135191	216	1.84E-08	3.43E-08	1.102040816	0.140177658
BP1026B_12391	hypothetical protein	214880	224377	219936	301	235467	226036	235855	318	1.75E-09	3.55E-09	1.056478405	0.079263279
BP1026B_12392	phosphoribosylamine--glycine ligase	109249	101718	102695	81	96165	93150	95438	74	6.69E-18	2.89E-17	0.913580247	0.130396637
BP1026B_12393	coproporphyrinogen III oxidase	51735	43377	47148	51	44609	37892	42223	44	9.44E-16	3.39E-15	0.862745094	0.212993723
BP1026B_12394	nicotinic acid mononucleotide adenylyltransferase	8586	1865	2639	5	1720	1159	1652	2	7.39E-65	4.45E-63	0.4	0.321928095
BP1026B_12395	iojap superfamily protein	29951	34764	39584	74	33058	31784	30160	68	5.10E-12	1.29E-11	0.91818919	0.121990524
BP1026B_12396	rRNA large subunit methyltransferase	11137	5670	5894	16	5553	4820	4701	10	2.82E-24	2.05E-23	0.625	0.678071905
BP1026B_12397	Maf-like protein	7303	8324	7309	12	8086	6951	6872	11	5.63E-12	1.42E-11	0.916666667	0.125530882
BP1026B_12398	ribonuclease G	292675	326419	329713	215	338602	327226	328511	225	2.28E-09	4.59E-09	1.046511628	0.065588342
BP1026B_12399	xanthine/uracil permease family protein	21599	17642	18031	13	16071	13368	16398	11	1.75E-22	1.10E-21	0.846153846	0.24100881
BP1026B_12400	hypothetical protein	29686	38484	37103	25	40440	42902	44406	30	3.78E-05	5.52E-05	1.2	0.263034406
BP1026B_12401	phospholipase C accessory protein	55724	32126	44888	64	35619	28399	35852	48	1.35E-21	7.86E-21	0.75	0.415037499
BP1026B_12402	hypothetical protein	2771	1714	1368	3	1419	1193	1896	2	8.92E-08	1.57E-07	0.666666667	0.584962501
BP1026B_12403	hypothetical protein	314	177	296	0	190	46	0	0	3.45E-12	8.87E-12	#DIV/0!	#DIV/0!
BP1026B_12404	hypothetical protein	5147	6088	5693	19	5204	5028	4517	16	7.55E-12	1.87E-11	0.842105263	0.247927513
BP1026B_12405	hypothetical protein	681	409	395	3	455	411	1043	3	0.869782241	0.883745017	1	0
BP1026B_12406	ECF subfamily RNA polymerase sigma factor	6175	4078	4126	5	3994	4376	4157	4	1.38E-10	3.06E-10	0.8	0.321928095
BP1026B_12407	carboxymuconolactone decarboxylase family protein	478	1274	658	1	903	1559	1029	2	0.600672044	0.624491626	2	1
BP1026B_12408	hypothetical protein	11966	7733	8232	9	7806	8090	7077	7	2.89E-18	1.28E-17	0.777777778	0.362570079
BP1026B_12409	major facilitator superfamily protein	45297	30750	38495	30	30084	27436	30706	23	1.98E-19	9.73E-19	0.766666667	0.38332864
BP1026B_12410	hypothetical protein	40834	29000	33378	57	28395	26275	28888	46	7.00E-17	2.78E-16	0.807017544	0.309328058
predicted RNA	-	11691	4526	7056	408	3791	2172	4459	182	1.12E-49	3.57E-48	0.446078431	0.164630702
BP1026B_12411	hypothetical protein	931915	862081	878916	2338	888280	910671	929136	2386	0.284897371	0.307840477	1.020530368	0.029319113
BP1026B_12412	lipopolysaccharide core biosynthesis glycosyltransferase	27446	27279	25526	34	25514	23029	25498	32	2.37E-12	6.19E-12	0.941176471	0.087462841
BP1026B_12413	hypothetical protein	16988	7530	10334	43	5733	4296	8138	22	2.96E-50	9.70E-49	0.511627909	0.966833136
BP1026B_12414	lipopolysaccharide core biosynthesis heptosyltransferase	59827	47127	47649	43	43923	42027	45572	37	3.50E-18	1.55E-17	0.860465116	0.216811389
BP1026B_12415	glycoside hydrolase family protein	86152	72966	74542	61	77410	76071	78436	61	2.29E-14	7.20E-14	1	0
BP1026B_12416	lipoprotein												

BP1026B_12439	hypothetical protein	113502	129050	122625	103	137619	137667	130616	115	2.66E-08	4.87E-08	1.116504854	0.158989524
BP1026B_12441	benzoate transport protein	20682	11163	14458	12	12803	8847	11960	9	1.30E-24	9.67E-24	0.75	-0.415037499
BP1026B_12442	transaldolase B	178038	228721	214724	217	218009	222859	224272	232	2.17E-09	4.38E-09	1.069124424	0.096429763
predicted RNA	-	5159	8177	8143	550	9345	8999	7367	659	3.92E-06	6.15E-06	1.198181818	0.260846847
predicted RNA	-	12669	23746	20548	513	23587	30343	22149	685	0.001404902	0.001835895	1.335282651	0.417145162
BP1026B_12443	glyoxalase family protein	43149	52540	56543	116	52305	51216	57327	123	3.94E-10	8.46E-10	1.060344828	0.08453351
BP1026B_12444	sodium:solute symporter family protein	5708	6629	6260	3	6711	5182	7391	4	7.60E-09	1.46E-08	1.333333333	0.415037499
BP1026B_12445	hypothetical protein	481	965	673	2	945	1875	1293	5	0.003394522	0.004329345	2.5	1.321928095
BP1026B_12446	hypothetical protein	24957	21691	22699	24	21932	23127	25667	25	1.34E-09	2.74E-09	1.041666667	0.058893689
BP1026B_12447	hypothetical protein	50674	52328	47154	104	56989	51364	65132	121	1.29E-07	2.24E-07	1.163461538	0.218423519
BP1026B_12448	chorismate lyase family protein	22049	4536	6974	18	5246	5396	6041	9	4.92E-53	1.80E-51	0.5	-1
BP1026B_12449	heat shock protein 90	4051649	5065585	4982893	2475	6099668	6213337	6080794	3228	0.312217296	0.335566652	1.304242424	0.383212053
BP1026B_12450	GntR family transcriptional regulator	123580	91745	105738	73	95084	80629	97110	62	2.12E-22	1.31E-21	0.849315068	-0.235628248
BP1026B_12451	hypothetical protein	4532	2407	2192	4	3040	3406	3432	4	4.22E-04	5.73E-04	1	0
BP1026B_12452	integral membrane protein	4015	2130	2182	3	3144	2081	2602	2	5.39E-06	8.38E-06	0.666666667	-0.584962501
BP1026B_12453	aminotransferase family protein	1597144	1797075	1784735	1435	1739708	1486619	1926253	1427	0.302683693	0.325767094	0.994425087	-0.008065402
BP1026B_12454	L-PSP family endonuclease	204811	243931	221956	487	280871	282924	289212	619	3.64E-04	4.97E-04	1.271047228	0.346017637
BP1026B_12455	PhuT family phenazine biosynthesis protein	313013	257548	275076	313	226596	218871	200135	239	1.05E-27	1.00E-26	0.763578275	-0.389152039
BP1026B_12456	hypothetical protein	116852	140772	130857	54	130814	133864	139103	57	1.27E-10	2.82E-10	1.055555556	0.078002512
BP1026B_12457	chromate transport protein	215287	259326	233938	186	320619	330172	324615	256	0.004455519	0.005621886	1.376344086	0.460841189
BP1026B_12458	acetylpolymine aminohydrolase	27755	23142	24200	24	22077	22147	27131	23	1.01E-11	2.50E-11	0.958333333	-0.061400545
BP1026B_12459	allantoin amidohydrolase	19791	16442	18423	14	15642	14945	16489	12	1.53E-18	6.98E-18	0.857142857	-0.222392421
BP1026B_12460	major facilitator family transporter	25922	12965	15008	13	10003	7896	10362	7	5.88E-55	2.36E-53	0.538461538	-0.893084796
BP1026B_12461	LysR family transcriptional regulator	23515	23507	23218	13	20016	23491	21335	22	1.97E-12	5.18E-12	0.956521739	-0.064130337
BP1026B_12463	hypothetical protein	6261	6704	6494	14	7730	8628	7340	17	6.99E-06	1.08E-05	1.214285714	0.280107919
BP1026B_12462	LysR family transcriptional regulator	5370	2575	3828	4	3304	2915	2286	3	1.21E-14	3.89E-14	0.75	-0.415037499
BP1026B_12464	integral membrane protein	11599	9378	10394	22	11286	12805	12402	26	9.50E-07	1.56E-06	1.181818182	0.2140081
BP1026B_12465	DNA topoisomerase IV subunit A	178188	198206	202658	83	191728	195673	200988	84	2.67E-11	6.31E-11	1.012048193	0.017277991
BP1026B_12466	DNA topoisomerase IV subunit B	183238	202196	199721	98	201218	200367	203543	101	8.88E-11	2.00E-10	1.030612245	0.043501639
BP1026B_12467	ABC transporter ATP-binding protein	146207	124403	124904	67	116989	103028	113388	57	3.32E-21	1.87E-20	0.850746269	-0.233199176
BP1026B_12468	hypothetical protein	592389	604167	625723	1488	585769	518730	660111	1441	0.246391503	0.268269185	0.968413978	-0.046304191
BP1026B_12469	Rubredoxin-NAD(+) reductase	56179	45273	49618	275	55280	51628	58169	300	4.26E-09	8.35E-09	1.090909091	0.125530882
BP1026B_12470	hypothetical protein	7036	9469	8950	5	8267	7984	9676	5	3.34E-10	7.21E-10	1	0
BP1026B_12471	alpha/beta fold family hydrolase	3832	4021	4183	4	5437	5066	4692	5	5.20E-04	7.03E-04	1.25	0.321928095
BP1026B_12473	translation initiation factor IF-1	18220	29383	26957	93	28503	37585	33245	124	0.00178554	0.002321684	1.333333333	0.415037499
BP1026B_12474	hypothetical protein	1486	1418	1505	6	1590	1520	1565	7	0.021828411	0.02622255	1.166666667	0.222392421
BP1026B_12475	hypothetical protein	3226	3205	2591	9	3510	3510	3952	12	0.014265888	0.017360663	1.333333333	0.415037499
BP1026B_12476	hypothetical protein	4745	6676	6986	21	6651	6027	6023	21	3.37E-09	6.67E-09	1	0
BP1026B_12477	Arg tRNA	4613	8703	6560	88	10181	13473	13754	166	0.538023867	0.563002263	1.886363636	0.915607813
BP1026B_12479	hemolysin activator protein	72192	109871	106254	67	95487	114258	99840	72	4.89E-10	1.04E-09	1.074626866	0.108335811
BP1026B_12480	hypothetical protein	58183	97803	79283	326	105285	126798	112026	477	0.008373309	0.010342431	1.463190184	0.549117302
BP1026B_12481	Large exoproteins involved in heme utilization or adhesion	151050	223912	209597	21	242070	261836	241642	26	3.21E-04	4.40E-04	1.238095238	0.308122295
BP1026B_12482	hypothetical protein	2551	4914	3864	19	6762	6467	5476	32	0.159628426	0.177157584	1.684210526	0.752072487
BP1026B_12483	hypothetical protein	453338	703725	626993	1835	720219	763765	723241	2270	0.357369334	0.381738194	1.237057221	0.306912234
BP1026B_12484	hypothetical protein	5961	6506	7605	29	9737	7380	7648	36	1.29E-05	1.95E-05	1.24137931	0.311944066
BP1026B_12486	hypothetical protein	2367	1795	2930	5	2477	3503	3364	6	0.106382307	0.120453837	1.2	0.263034406
BP1026B_12485	murcin-DD-endopeptidase	75499	64961	67961	105	66053	60325	68044	98	6.11E-17	2.44E-16	0.933333333	-0.099535674
BP1026B_12487	ecotin	252241	353285	345260	586	420555	464276	387045	785	8.09E-04	0.001074775	1.339590444	0.421791989
BP1026B_12488	hypothetical protein	22792	12970	17205	46	15236	12318	16409	38	5.99E-20	3.06E-19	0.826086957	-0.275634443
BP1026B_12489	hypothetical protein	892	611	683	2	1011	652	643	2	0.140018126	0.156637202	1	0
BP1026B_12491	hypothetical protein	131406	148170	153547	281	172000	183394	155262	331	1.26E-05	1.91E-05	1.177935943	0.236261087
BP1026B_12492	major facilitator superfamily multidrug efflux transporter	17504	13082	13554	10	12868	12085	12737	9	8.55E-17	2.34E-16	0.9	-0.152003093
BP1026B_12493	hypothetical protein	18485	8830	13511	22	10262	9440	10962	16	6.99E-22	4.18E-21	0.727272727	-0.459431619
BP1026B_12495	hypothetical protein	23127	14217	13546	28	11647	10319	11857	18	5.75E-31	6.71E-30	0.642857143	-0.637429921
BP1026B_12496	alpha.alpha.-trehalose-phosphate synthase (UDP-forming)	117022	119468	110595	82	106308	104714	109275	75	3.62E-16	1.35E-15	0.914634146	-0.128733314
BP1026B_12497	hypothetical protein	2772	3993	3624	17	3959	5892	3919	23	0.013398715	0.016349824	1.352941176	0.436099115
BP1026B_12498	lipoprotein	44852	39797	42614	76	36019	36632	37431	66	4.12E-15	1.39E-14	0.868421053	-0.203533394
BP1026B_12499	lipoprotein	10747	5466	7982	15	5094	4623	5706	10	2.20E-27	2.06E-26	0.666666667	-0.584962501
BP1026B_12500	hypothetical protein	12935	12494	13341	79	14036	11163	10796	74	4.95E-13	1.38E-12	0.936708861	-0.094327383
BP1026B_12501	ABC transporter ATP-binding protein	384387	320444	344465	260	305394	289994	323817	228	1.37E-15	4.85E-15	0.876923077	-0.189477799
BP1026B_12502	ABC transporter permease	238321	280156	267389	149	272264	269930	287991	157	2.30E-09	4.62E-09	1.053691275	0.075452228
BP1026B_12503	hypothetical protein	12165	6087	7584	31	5164	4392	6051	18	1.51E-31	1.83E-30	0.580645161	-0.784271309
BP1026B_12504	hypothetical protein	145651	252780	233612	789	338299	402965	337322	1346	0.70533186	0.72667041	1.705956907	0.770581205
BP1026B_12505	signal transduction histidine kinase	64261	38369	45358	37	39168	31784	38299	27	6.46E-24	4.56E-23	0.72972973	-0.454565863
BP1026B_12506	DNA-binding response regulator OmpR	53044	37380	44100	61	40833	33578	42863	53	2.99E-15	1.02E-14	0.868852459	-0.202816883
BP1026B_12507	hypothetical protein	8292	10104	9594	17	9697	14565	10304	21	1.90E-05	2.83E-05	1.235294118	0.304854582
BP1026B_12508	hypothetical protein	4732	3210	4052	5	3505	3241	3573	4	9.63E-10	2.00E-09	0.8	-0.321928095
BP1026B_12509	amino acid ABC transporter substrate-binding protein	58286	66670	66238	82	65485	66595	64003	84	1.23E-12	3.31E-12	1.024390244	0.034765418
BP1026B_12511	histidine transport system permease	26333	29921	31104	42	32589	35803	32003	48	8.10E-06	1.24E-05	1.142857143	0.192645078
BP1026B_12510	histidine transport system permease	32272	48602	46931	59	53707	55596	49035	73	2.21E-05	3.28E-05	1.237288136	0.30718151
BP1026B_12512	histidine transport ATP-binding protein	55708	69847	64618	81	72490	79200	68494	94	1.81E-08	3.36E-08	1.160493827	0.214738849
BP1026B_12513	porin	350376	383505	384809	338	324456	330348	312654	292	8.75E-16	3.16E-15	0.863905325	-0.211054877
BP1026B_12514	nitrogen regulatory protein P-II	236096	380945	340462	941	409943	446634	433280	1268	0.001004891	0.001326168	1.347502657	0.430288117
BP1026B_12515	NAD synthetase	98081	70073	77756	48	65833	63309	67543	38	2.08E-26	1.79E-25	0.791666667	-0.337034987
BP1026B_12516	hypothetical protein	18237	13350	14936	13	13556	11417	14448	11	7.79E-18	3.35E-17	0.846153846	-0.2410001
BP1026B_12517	beta-glucosidase	176	2	45	0	153							

BP1026B_12540	methionyl-tRNA synthetase	181637	212337	200149	90	212027	207959	210070	96	7.43E-10	1.56E-09	1.066666667	0.093109404
BP1026B_12541	O-methyltransferase family protein	22601	16281	19208	19	16330	15050	16655	15	6.40E-21	3.51E-20	0.789473684	-0.341036918
BP1026B_12542	hypothetical protein	18200	13356	13242	21	14652	14813	13428	20	3.38E-13	9.56E-13	0.952380952	-0.070389328
BP1026B_12543	hypothetical protein	188038	149251	145225	39	146269	147969	154876	36	1.31E-14	4.20E-14	0.923076923	-0.115472717
BP1026B_12544	OMP85 family outer membrane protein	106023	105403	106202	61	110580	101185	105087	61	1.04E-12	2.82E-12	1	0
BP1026B_12545	hypothetical protein	194569	161637	186039	956	193144	194275	169761	982	1.88E-10	4.11E-10	1.027196653	0.038712406
BP1026B_12546	segregation and condensation protein A	127029	133904	132272	149	152437	159585	155714	177	1.34E-05	2.02E-05	1.187919463	0.248437303
BP1026B_12547	pantoate-β-alanine ligase	59691	68832	67689	77	63265	68948	62577	77	4.89E-14	1.49E-13	1	0
BP1026B_12548	aspartate alpha-decarboxylase	69414	79817	82492	199	84597	87945	80920	218	1.44E-10	3.17E-10	1.095477387	0.131559704
BP1026B_12549	ParA family protein	109230	140346	133839	206	118836	116425	113697	188	7.33E-17	2.90E-16	0.912621359	-0.131911676
BP1026B_12550	hypothetical protein	14897	15312	16346	37	17200	16212	19237	42	2.30E-08	4.23E-08	1.135135135	0.182864057
BP1026B_12552	cobryic acid synthase	23811	12909	16090	10	13854	11526	11407	7	9.03E-29	9.24E-28	0.7	-0.514573173
BP1026B_12551	cobinamide kinase	9472	2141	3184	8	13671	2149	2313	3	3.36E-49	1.03E-47	0.375	-1.415037499
BP1026B_12554	cobalamin biosynthesis protein	5693	1153	2146	3	1434	1476	2330	1	7.18E-19	3.37E-18	0.333333333	-1.584962501
BP1026B_12555	threonine-phosphate decarboxylase	9830	3491	5369	5	2637	2224	2989	2	6.47E-54	2.47E-52	0.4	-1.321928095
BP1026B_12556	iron chelate uptake transporter, periplasmic binding protein	12230	7359	7182	9	6268	5274	6089	6	8.24E-28	7.90E-27	0.666666667	-0.584962501
BP1026B_12557	hypothetical protein	105305	153308	143052	159	125945	136153	141904	160	6.07E-12	1.52E-11	1.006289308	0.00904514
BP1026B_12558	phosphoglycerate mutase family protein	13705	15071	15193	24	15429	15561	17808	27	9.28E-09	1.77E-08	1.125	0.169925001
BP1026B_12559	cobalamin synthase	13423	10129	10356	14	11606	12858	11271	16	3.35E-08	6.11E-08	1.142857143	0.192645078
BP1026B_12560	nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase	30094	14664	17211	19	12062	12108	12651	11	7.38E-45	1.89E-43	0.578947368	-0.788495895
BP1026B_12561	iron compound ABC transporter ATP-binding protein	14272	4690	5926	9	3651	2996	3583	3	9.13E-61	4.65E-59	0.333333333	-1.584962501
BP1026B_12562	transmembrane ABC transporter permease	11718	4296	5015	6	3589	4246	4972	4	9.29E-27	8.23E-26	0.666666667	-0.584962501
BP1026B_12563	outer membrane receptor for transport of vitamin B	94933	102155	97706	47	102106	98512	102420	49	9.49E-12	2.34E-11	1.042553191	0.060120992
BP1026B_12564	hypothetical protein	6358	7026	7104	14	7207	7105	7167	15	4.90E-09	9.56E-09	1.071428571	0.099535674
BP1026B_12565	hypothetical protein	66058	80895	84708	220	94542	94864	88924	264	3.01E-07	5.11E-07	1.2	0.263034406
BP1026B_12566	hypothetical protein	76422	74214	80901	245	81062	79364	90692	265	7.16E-11	1.62E-10	1.081632653	0.11321061
BP1026B_12567	hypothetical protein	29844	38416	37202	76	44166	44853	45731	97	2.50E-04	3.46E-04	1.276315789	0.351985329
BP1026B_12568	hypothetical protein	506689	311124	395811	548	313495	273254	296237	398	1.88E-25	1.50E-24	0.726277372	-0.461407462
BP1026B_12569	prolipoprotein diacylglycerol transferase	148657	142264	142900	162	129435	120348	147434	148	2.00E-16	7.62E-16	0.913580247	-0.130396637
BP1026B_12570	isoleucine biosynthesis transcriptional activator	61143	42307	45412	47	44524	40963	44728	41	1.78E-16	6.82E-16	0.872340426	-0.197036847
BP1026B_12571	hypothetical protein	3845	5855	5531	24	7826	9047	6303	36	0.011714027	0.014338757	1.5	0.584962501
BP1026B_12572	dihydroxy-acid dehydratase	214399	253398	249405	142	272213	276955	247268	158	1.40E-07	2.43E-07	1.112676056	0.154033629
BP1026B_12573	cytochrome C552	54891	42829	45379	106	41153	34319	42690	88	4.07E-18	1.79E-17	0.830188679	-0.268488836
BP1026B_12574	hypothetical protein	45951	31297	36139	53	30451	29744	29078	42	2.70E-18	1.21E-17	0.79245283	-0.335603032
BP1026B_12575	DNA polymerase III subunit chi	55219	34731	42429	105	35562	32987	35527	83	2.32E-19	1.13E-18	0.79047619	-0.339206086
BP1026B_12576	leucyl aminopeptidase	515849	420316	447550	305	409590	409514	396676	268	3.07E-14	9.54E-14	0.878688525	-0.186576242
BP1026B_12577	permease	81326	105735	99216	86	113241	116814	111797	103	1.01E-06	1.66E-06	1.197674419	0.260235772
BP1026B_12578	hypothetical protein	60110	72280	66181	57	69131	71933	74327	62	1.40E-10	3.09E-10	1.087719298	0.121306296
BP1026B_12579	Sirohydrochlorin cobaltochelatease	20172	9967	12415	36	10371	10563	12191	28	2.52E-20	1.32E-19	0.777777778	-0.362570079
BP1026B_12580	uroporphyrin-III C-methyltransferase	18879	6873	7736	14	6807	7055	5188	8	5.14E-42	1.13E-40	0.571428571	-0.807354922
BP1026B_12581	sulfate adenylyltransferase, subunit 1	258447	264567	265566	199	264833	254095	263593	198	1.19E-11	2.91E-11	0.994974874	-0.007268
BP1026B_12582	sulfate adenylyltransferase, subunit 2	71603	75030	78778	77	75647	73487	72030	76	9.83E-15	3.21E-14	0.987012987	-0.018859027
BP1026B_12583	phosphodenosine phosphosulfate reductase	20312	18246	16340	24	16150	13396	14792	19	1.44E-21	8.35E-21	0.791666667	-0.337034987
BP1026B_12584	hypothetical protein	5412	5372	4850	9	5406	3205	2844	7	1.13E-15	4.03E-15	0.777777778	-0.362570079
BP1026B_12585	sulfite reductase	99935	131312	121113	69	117013	117871	122394	70	6.18E-12	1.55E-11	1.04492754	0.02075886
BP1026B_12586	transcriptional regulator CysB-like protein	50426	56327	56080	57	55925	52013	56311	58	3.62E-12	9.28E-12	1.0175486	0.025090981
BP1026B_12587	hypothetical protein	7344	5771	6727	19	4986	4313	5602	14	1.33E-17	5.62E-17	0.736842105	-0.440572591
BP1026B_12588	Leu tRNA	1697	2161	1891	22	4181	5960	4692	58	9.88E-06	1.51E-05	2.636363636	1.398549376
BP1026B_12589	hypothetical protein	2007	1850	2028	12	2898	1887	2813	5	0.129979655	0.145854677	1.25	0.321928095
BP1026B_12590	putative replication protein	12133	19570	16158	30	20234	23562	20925	41	7.93E-04	0.001055494	1.366666667	0.450661409
BP1026B_12592	IS407A, transposase OrfA	43607	71570	62579	224	74745	90199	86026	316	7.49E-04	9.98E-04	1.410714286	0.496425826
BP1026B_12593	putative insertion element protein	114203	195965	172486	225	205887	226645	215379	302	0.002721924	0.003500016	1.342222222	0.424623548
BP1026B_12595	hypothetical protein	1532191	2645665	2293260	1128	2697974	3159549	2791469	1508	0.230504002	0.251846241	1.336879433	0.418869361
BP1026B_12596	hypothetical protein	937609	1559124	1293448	307	1604712	1770774	1488865	394	0.00336963	0.039474062	1.283387622	0.359569714
BP1026B_12597	hypothetical protein	12727	25820	23610	119	29550	29264	28476	161	0.002327601	0.003004687	1.352941176	0.436099115
BP1026B_12598	DeoR family transcriptional regulator	136366	212049	191933	178	264473	294326	266658	272	0.161892181	0.179542726	1.528089888	0.61172941
BP1026B_12599	hypothetical protein	921	1762	1181	11	1226	1916	1753	14	0.456315123	0.482007849	1.272727273	0.347923303
BP1026B_12600	hypothetical protein	5239	2029	2847	7	2905	2556	2982	6	2.67E-09	5.34E-09	0.857142857	-0.222924221
BP1026B_12601	DNA-binding protein	92302	112928	98126	179	132338	127830	143292	238	4.46E-04	6.06E-04	1.329608939	0.411001986
BP1026B_12602	class II aldolase/adducin domain-containing protein	23316	28303	30076	32	23682	23804	21517	27	1.12E-16	4.36E-16	0.84375	-0.245112498
BP1026B_12603	dihydrodipicolinate synthase	10946	12643	10379	12	10986	12113	13104	13	8.32E-09	1.59E-08	0.383333333	0.115477217
BP1026B_12604	MOSC domain-containing protein	18953	10805	13909	21	6968	5256	9079	10	6.80E-65	4.14E-63	0.476190476	-1.070389328
BP1026B_12605	alpha/beta fold family hydrolase	10911	5678	7336	8	5331	5203	6037	6	1.84E-23	1.26E-22	0.75	-0.415037499
BP1026B_12606	LysR family transcriptional regulator	6390	3313	4071	5	3806	2120	3542	3	5.56E-17	2.24E-16	0.6	-0.736965594
BP1026B_12607	LysR substrate binding domain-containing protein	92941	74560	77762	84	69683	67161	76778	73	7.57E-21	4.13E-20	0.869047619	-0.202492864
BP1026B_12608	copper resistance protein	6125	5074	5520	14	4719	5226	4613	13	9.32E-12	2.30E-11	0.928571429	-0.106915204
BP1026B_12610	ribosomal small subunit pseudouridine synthase A	20982	11764	13357	21	11473	8354	9838	13	1.10E-32	1.46E-31	0.619047619	-0.691877705
BP1026B_12609	hypothetical protein	83960	137348	121996	605	173202	191058	173388	948	0.260964894	0.283005543	1.566942149	0.647951917
BP1026B_12611	NAD-dependent epimerase/dehydratase family protein	87174	96876	97889	94	105615	104611	109244	107	2.98E-08	5.46E-08	1.138297872	0.186878135
BP1026B_12612	CDP-6-deoxy-δ-3,4-glucosone reductase	81478	75576	75476	75	73361	72210	75111	71	2.76E-16	1.04E-15	0.946666667	-0.079071571
BP1026B_12613	acetylornithine transaminase protein	84429	71561	76437	65	70561	65607	68638	57	3.97E-20	2.05E-19	0.876923077	-0.189477799
BP1026B_12614	acetyltransferase	18475	16139	16102	36	16952	14537	15856	34	9.50E-15	3.10E-14	0.944444444	-0.08246216
BP1026B_12615	hypothetical protein	45403	59894	53195	78	57194	59243	55924	85	1.30E-09	2.66E-09	1.08974359	0.123988717
BP1026B_12616	branched-chain amino acid ABC transporter ATP-binding protein	66123	72757	73093	98	62889	60128	69237	89	2.14E-18	9.60E-18	0.908163265	-0.138976413
BP1026B_12617	leucine/isoleucine/valine transport system ATP-binding protein	45282	51625	54223	65	48687	52008	49119					

BP1026B	I2641	ATP-dependent Clp protease ATP-binding subunit clpA	2692746	3348906	3132479	1337	3510793	3641503	3525270	1556	0.941770419	0.949498543	1.163799551	0.218842595
BP1026B	I2642	ATP-dependent Clp protease adaptor protein ClpS	475307	813797	725291	2131	1090726	1255172	1036201	3578	0.0016239482	0.001624471	1.679023932	0.747622794
BP1026B	I2643	hypothetical protein	247637	402970	354929	1893	504682	586930	455664	2913	0.598359027	0.62239669	1.538827258	0.62183129
BP1026B	I2644	cold shock transcription regulator protein	856208	1379916	1185883	4636	1638865	1832172	1664824	6959	0.005989021	0.007490461	1.501078516	0.585999441
BP1026B	I2645	multicopper oxidase domain-containing protein	148492	136371	145138	89	123728	121143	131666	78	3.66E-19	1.76E-18	0.876404494	-0.190331212
BP1026B	I2646	isocitrate dehydrogenase	1762183	2507299	2345714	1750	2531056	2852915	2532374	2094	0.355112334	0.379521386	1.196571429	0.25890652
BP1026B	I2647	pseudouridine synthase family protein	4159	3667	3541	6	2944	1924	2260	4	2.06E-19	1.01E-18	0.666666667	-0.584962501
BP1026B	I2648	predicted RNA	4876319	7692727	6593280	15849	9639823	10507948	9326907	24379	0.081240106	0.093011237	1.538240303	0.621247134
BP1026B	I2649	hypothetical protein	14499	20835	17428	34	20669	23349	19688	41	5.46E-06	8.49E-06	1.205882353	0.270089163
BP1026B	I2650	elongation factor G	570870	780736	716367	325	877392	944398	853760	421	0.046293449	0.054229716	1.295384615	0.373380515
BP1026B	I2651	hypothetical protein	308	394	272	0	326	530	333	0	0.882389197	0.894455679	#DIV/0!	#DIV/0!
BP1026B	I2652	hypothetical protein	3009	407	731	2	262	117	453	0	2.45E-90	2.43E-88	0	#NUM!
BP1026B	I2653	aldo/keto reductase family oxidoreductase	60695	38212	46080	57	32631	30043	36042	38	2.07E-28	2.06E-27	0.666666667	-0.584962501
BP1026B	I2654	GntR family transcriptional regulator	36987	35798	34219	47	35714	31549	33854	45	6.59E-11	1.50E-10	0.957446809	-0.062735755
BP1026B	I2655	hypothetical protein	210	153	237	1	36	70	134	0	3.94E-06	6.19E-06	0	#NUM!
BP1026B	I2656	citrate synthase family protein	8274	5901	6820	5	4983	4604	4458	3	1.33E-22	8.50E-22	0.6	-0.736965594
BP1026B	I2658	hypothetical protein	2067	1376	1642	5	2184	1771	1785	5	0.030421174	0.036096244	1	0
BP1026B	I2657	MFS transporter	55663	53625	49652	37	51878	45389	52271	35	1.55E-14	4.94E-14	0.945945946	-0.080170349
BP1026B	I2659	EAL domain-containing protein	184024	142127	160425	127	136400	122440	135885	103	4.61E-24	3.30E-23	0.811023622	-0.30218416
BP1026B	I2660	methyltransferase	47604	63010	62538	95	64721	64241	51536	99	1.22E-11	2.96E-11	1.021052623	0.059501012
BP1026B	I2661	2-dehydropanotate 2-reductase	4648	5142	4252	4	3571	3588	2960	3	2.42E-15	8.33E-15	0.75	-0.415037499
BP1026B	I2662	PRS2-like protein	6119	6219	5662	11	7157	7435	7297	13	8.81E-06	1.35E-05	1.181818182	0.2410081
BP1026B	I2663	cyclic nucleotide-binding protein	36551	31296	32216	43	30439	24344	28984	36	2.18E-15	7.55E-15	0.837209302	-0.256339753
BP1026B	I2664	chromate transport protein	2700	1691	1922	1	1866	1768	1898	1	6.96E-06	1.07E-05	1	0
BP1026B	I2666	lipoprotein	20916	26561	26189	19	26630	26594	25102	20	6.80E-08	1.21E-07	1.052631579	0.074000581
BP1026B	I2667	superoxide dismutase	824854	1137911	1102272	1764	1241744	1394495	1204356	2211	0.066925962	0.077244074	1.253401361	0.325848464
BP1026B	I2668	exodeoxyribonuclease VII large subunit	44145	23181	29752	21	17502	13501	17607	10	8.49E-74	6.33E-72	0.476190476	-1.070389328
BP1026B	I2669	3-deoxy-manno-oxulosonate cytidyltransferase	15091	17634	17795	16	18708	20624	15766	17	2.11E-09	4.26E-09	1.0625	0.087462841
BP1026B	I2670	tetraacyldisaccharide-1-P 4-kinase	31274	46809	43655	196	55003	60277	57399	278	0.005104767	0.006415257	1.418367347	0.504231229
BP1026B	I2671	3-deoxy-manno-oxulosonate cytidyltransferase	28086	16359	19129	26	15864	15392	16240	19	2.74E-27	2.55E-26	0.730769231	-0.452512205
BP1026B	I2672	adenylate kinase	289469	286335	294375	437	264784	247002	261691	388	3.10E-16	1.16E-15	0.887871854	-0.171576627
BP1026B	I2673	ISBma2, transposase	162174	240654	210564	139	259648	276295	263750	182	0.001002375	0.001323127	1.369355167	0.388853657
BP1026B	I2674	3-hydroxyacyl-CoA dehydrogenase	35133	24054	208381	38	18052	18746	19338	24	3.03E-40	5.99E-39	1.031578947	-0.662965013
BP1026B	I2675	hypothetical protein	67308	63755	69563	79	59288	49319	58591	66	3.20E-22	1.97E-21	0.835443038	-0.259386629
BP1026B	I2676	integral membrane protein MvN	30634	29045	30652	19	30998	28553	32387	19	1.44E-08	2.70E-08	1	0
BP1026B	I2677	30S ribosomal protein S20	134862	202993	186428	626	278649	291211	264149	996	0.374928935	0.399473679	1.591054313	0.66983085
BP1026B	I2678	PhnO-like protein	39740	57295	53278	154	87631	90604	85304	271	0.49999275	0.525046853	1.75974026	0.815325201
BP1026B	I2679	ornithine carbamoyltransferase	388071	493771	488184	491	570360	603345	551084	618	0.993861965	0.996725204	1.258655804	0.33188314
BP1026B	I2680	UDP-N-acetylenolpyruvoglucosamine reductase	53827	34130	42215	41	35685	33405	34672	33	1.43E-18	6.51E-18	0.804878049	-0.313178885
BP1026B	I2681	nucleotide-binding protein	322758	515914	472649	899	586480	648705	589637	1251	0.377750841	0.402411896	1.391546162	0.476688769
BP1026B	I2682	glycerol-3-phosphate acyltransferase PlsY	54139	73442	68612	106	71180	77528	77087	122	1.02E-08	1.95E-08	1.150943396	0.202816883
BP1026B	I2684	ybaK/ebcC protein	50561	40322	41749	89	38083	39581	45732	83	6.42E-13	1.77E-12	0.93258427	-0.100694
BP1026B	I2683	AMP-binding domain-containing protein	76511	46523	56981	38	48667	40157	46948	28	1.51E-26	1.32E-25	0.736842105	-0.440572591
BP1026B	I2685	site-specific tyrosine recombinase XerD	90841	66534	71356	83	66793	60094	71752	72	6.01E-21	3.31E-20	0.86746988	-0.20511443
BP1026B	I2686	methylated-DNA--protein-cysteine methyltransferase	74188	70611	69565	152	79624	76816	82072	169	6.34E-10	1.34E-09	1.11842105	0.152951923
BP1026B	I2687	iron-sulfur cluster-binding protein	78993	67096	74389	59	90437	87690	78561	69	1.76E-08	3.28E-08	1.169491525	0.225881407
BP1026B	I2688	hypothetical protein	26493	20039	21159	40	23857	25052	22908	43	1.94E-08	3.61E-08	1.075	0.10433666
BP1026B	I2689	N-acetylmuramoyl-L-alanine amidase, AMIC protein	266449	348843	330584	202	335893	345284	337653	218	1.57E-08	2.94E-08	1.079207921	0.109972842
BP1026B	I2691	Permease of the drug/metabolite transporter(DMT) superfamily	16146	10478	12245	14	11831	9926	10113	12	1.80E-17	7.50E-17	0.857142857	-0.222394221
BP1026B	I2690	Pirin-like protein	25748	16773	21072	24	17033	14481	16036	17	3.07E-27	2.83E-26	0.708333333	-0.497499659
BP1026B	I2692	thioredoxin	165181	142227	159050	183	173121	153170	169245	194	1.17E-08	2.21E-08	1.06010929	0.084213004
BP1026B	I2693	HesA/MoeB/ThiF family protein	77249	87245	79894	93	92147	90409	94963	106	6.51E-09	1.26E-08	1.139784946	0.188761643
BP1026B	I2694	pyridoxamine 5'-phosphate oxidase	555169	674463	643152	967	663372	684725	685055	1050	0.844342434	0.859290188	1.085832472	0.118801533
BP1026B	I2695	cyclopropane fatty acid synthase family protein	1267091	1869977	1749718	1334	2039445	2195704	2032056	1710	0.08409566	0.096091881	1.28185907	0.358237659
BP1026B	I2696	hypothetical protein	180122	114096	130630	91	106802	96933	98814	65	9.95E-35	1.50E-33	0.714285714	-0.485426827
BP1026B	I2697	peptide methionine sulfoxide reductase	81964	110824	111870	181	116090	120441	112977	208	8.63E-08	1.52E-07	1.149171271	0.209593831
BP1026B	I2698	flavin reductase domain-containing protein	66846	60752	63773	123	68207	64571	71121	131	3.37E-11	7.87E-11	1.06504065	0.090908496
BP1026B	I2699	transcription regulator AnS	81364	103007	102091	189	116359	119114	117997	233	6.39E-06	9.88E-06	1.232804233	0.30194372
BP1026B	I2700	cyclase	19673	15814	18189	24	12006	14460	12960	18	3.64E-26	3.07E-25	0.75	-0.415037499
BP1026B	I2701	kymureninase	45425	30911	31805	28	24763	24717	25140	19	6.33E-27	5.67E-26	0.678571429	-0.559427409
BP1026B	I2702	tryptophan 2,3-dioxygenase family protein	70932	70687	76322	76	64927	57978	64798	65	2.50E-21	1.43E-20	0.855263158	-0.2255597
BP1026B	I2703	4-hydroxybenzoate transporter	12152	8323	9527	7	8860	8533	7747	6	2.05E-17	8.50E-17	0.857142857	-0.222394221
BP1026B	I2704	hypothetical protein	275	194	95	0	311	58	244	0	0.99620169	0.998911792	#DIV/0!	#DIV/0!
BP1026B	I2705	hypothetical protein	556	464	766	5	680	203	355	4	4.03E-05	5.87E-05	0.8	-0.321928095
BP1026B	I2706	2-dehydropanotate 2-reductase	10582	10185	9556	10	8806	7738	9706	9	9.42E-16	3.39E-15	0.9	-0.152003093
BP1026B	I2707	aldehyde dehydrogenase family protein	23645	11481	15125	11	11029	10475	10930	7	7.70E-33	1.03E-31	0.636363636	-0.652076697
BP1026B	I2708	benzoylformate decarboxylase	26430	15775	19610	12	13728	17992	16709	10	2.98E-20	1.55E-19	0.833333333	-0.263034406
BP1026B	I2709	transcription regulatory protein	23222	12879	15945	18	13471	11577	13001	13	6.73E-26	5.55E-25	0.722222222	-0.469485283
BP1026B	I2710	mannitol dehydrogenase family protein	3263	2368	2482	1	2503	2117	1647	1	1.28E-09	2.63E-09	1	0
BP1026B	I2711	xylulokinase	26296	14489	18136	13	14791	12278	14608	9	7.45E-30	8.16E-29	0.692307692	-0.530514717
BP1026B	I2712	transcriptional regulator	35074	18609	23591	27	16888	14225	20402	18	8.97E-37	1.51E-35	0.666666667	-0.584962501
BP1026B	I2713	major facilitator family transporter	1371	484	544	0	462	471	190	0	9.35E-15	3.06E-14	#DIV/0!	#DIV/0!
BP1026B	I2715	beta-lactamase	3698	1120	2379	2	1424	1525	1388	1	1.51E-15	5.32E-15	0.5	-1
BP1026B	I2716	LysR family transcriptional regulator	6351	2267	3283	4								

BP1026B_12743	sensor kinase protein	44890	43406	40687	32	42255	39191	47381	32	1.36E-10	3.01E-10	1	0
BP1026B_12745	Two-component system response regulator QseB	56026	59065	54949	86	59655	63912	61484	94	3.77E-10	8.10E-10	1.093023256	0.128324097
BP1026B_12744	peptidase	38795	19821	24749	18	19967	17546	17045	11	1.33E-38	2.42E-37	0.611111111	-0.710493383
BP1026B_12746	sterol desaturase family protein	46541	65633	62819	63	84045	92456	83597	94	0.00571287	0.007156402	1.492063492	0.577308928
BP1026B_12747	lipase	147518	149699	147270	129	131240	124758	116994	109	7.88E-22	4.70E-21	0.84496124	-0.243042931
BP1026B_12748	Sua5/YciO/YrdC/YwIc family protein	40587	27460	30809	32	26359	23424	28154	25	1.70E-18	7.73E-18	0.78125	-0.35614381
BP1026B_12749	phosphoribosylaminoimidazole carboxylase ATPase subunit	43445	25312	26159	26	23825	24489	21623	19	1.12E-23	7.79E-23	0.730769231	-0.452512205
BP1026B_12750	phosphoribosylaminoimidazole carboxylase catalytic subunit	30566	38563	36143	67	38974	41420	40790	77	4.58E-06	7.15E-06	1.149253731	0.20069735
BP1026B_12751	phosphoribosylaminoimidazolesuccinocarboxamide synthase	101004	116515	112617	123	116653	101029	106710	121	2.82E-13	8.02E-13	0.983739837	-0.023651268
BP1026B_12752	fructose-1,6-bisphosphate aldolase	529175	646995	631281	565	689598	699318	696062	652	0.888471236	0.899870032	1.153982301	0.206621097
BP1026B_12753	pyruvate kinase	265126	207308	224929	169	194325	175065	186646	135	1.48E-23	1.02E-22	0.798816568	-0.324063839
BP1026B_12754	phosphoglycerate kinase	236892	225831	236712	195	235284	224869	238923	195	1.23E-11	3.01E-11	1	0
BP1026B_12755	hypothetical protein	4519	2714	3115	10	3462	2914	3688	10	3.43E-06	5.42E-06	1	0
BP1026B_12756	AzIc family protein	30232	32471	30304	41	37295	36781	36139	48	2.75E-05	4.05E-05	1.170731707	0.227410496
BP1026B_12757	branched-chain amino acid aminotransferase	307330	421779	383963	401	411684	410641	400751	441	3.98E-07	6.70E-07	1.099750623	0.137176419
BP1026B_12758	hypothetical protein	9009	5896	5466	34	5564	5466	5464	27	1.40E-15	4.96E-15	0.794117647	-0.332575339
BP1026B_12759	lipopolysaccharide heptosyltransferase II	43656	35071	37537	37	35117	32257	34529	32	8.13E-14	2.42E-13	0.864864865	-0.209453366
BP1026B_12760	hypothetical protein	67648	77366	73681	163	95906	95334	90131	209	1.72E-05	2.58E-05	1.282208589	0.358630978
BP1026B_12761	alpha/beta fold family hydrolase	26727	22169	21486	22	21234	22787	20997	20	7.56E-14	2.26E-13	0.909090909	-0.137503524
BP1026B_12762	hypothetical protein	8668	3489	4965	9	3291	3084	3760	5	5.68E-25	4.37E-24	0.555555556	-0.847996907
BP1026B_12763	M48 family peptidase	31996	32275	33175	18	30640	29023	27886	16	1.84E-12	4.86E-12	0.888888889	-0.169925001
BP1026B_12764	molybdenum cofactor biosynthesis protein MoaC	30291	26987	28123	57	25754	26508	24432	51	4.87E-13	1.36E-12	0.894736842	-0.160464672
BP1026B_12765	TonB domain-containing protein	11341	4481	4815	18	4237	3170	5327	11	8.30E-26	6.77E-25	0.611111111	-0.710493383
BP1026B_12766	hypothetical protein	16894	16284	19245	36	17110	15721	17054	35	4.08E-14	1.25E-13	0.972222222	-0.040641984
BP1026B_12767	O-antigen polymerase family protein	60659	47862	47640	28	45772	42054	44431	24	1.80E-18	8.14E-18	0.857142857	-0.222392421
BP1026B_12768	Type IV pilin PilA	2471	1271	1764	3	1240	706	954	1	5.62E-19	2.65E-18	0.333333333	-1.584962501
BP1026B_12769	TerC family integral membrane protein	38240	22929	26831	41	25778	22159	26582	34	1.44E-15	5.07E-15	0.829268293	-0.270089163
BP1026B_12770	succinyl-CoA synthetase subunit alpha	392969	382051	403730	445	437940	452799	389094	483	2.30E-07	3.93E-07	1.085392258	0.118217853
BP1026B_12771	succinyl-CoA synthetase subunit beta	469843	662607	608568	497	657653	703013	699347	588	0.843362487	0.859432317	1.183098592	0.242570303
BP1026B_12772	hypothetical protein	82942	77599	82372	132	98634	99283	87015	155	9.16E-08	1.61E-07	1.174242424	0.231730286
BP1026B_12773	recombination regulator RecX	69700	43050	52856	86	44244	39324	44399	67	1.17E-23	8.11E-23	0.79969767	-0.360175564
BP1026B_12774	recombinase A	724260	981982	903711	812	937651	978900	913178	880	0.172582874	0.190925898	1.083734842	0.116025796
BP1026B_12776	DNA-binding response regulator	19496	23519	22105	28	25343	24569	25866	33	4.07E-06	6.39E-06	1.178571429	0.237039197
BP1026B_12775	two-component sensor kinase transcriptional regulatory protein	12899	12533	10821	7	10322	9896	9369	6	1.08E-17	4.59E-17	0.857142857	-0.222392421
BP1026B_12777	major facilitator family transporter	3320	4842	4213	2	5277	5388	3642	2	4.06E-05	5.92E-05	1	0
BP1026B_12778	Met tRNA	413	611	415	6	542	1025	846	10	0.052130218	0.060715232	1.666666667	0.736965594
BP1026B_12779	Integrase	254981	447409	399194	266	461389	533180	461355	351	7.55E-04	0.001005394	1.319548872	0.400044785
BP1026B_12780	plasmid recombination enzyme	3599	5738	5128	5	7093	7346	6531	8	0.004285069	0.005415539	1.6	0.678071905
predicted RNA	-	73671	124458	112822	660	168135	194720	168336	1127	0.807005378	0.823566075	1.707575758	0.771949586
BP1026B_12781	XRE family transcriptional regulator	24079	38123	36361	150	56463	63305	59075	272	0.797329407	0.814354697	1.813333333	0.858644151
BP1026B_12782	IS407A, transposase OrfB	61593	99543	93653	98	101071	109555	112717	125	2.44E-05	3.61E-05	1.275510204	0.351074441
BP1026B_12783	IS407A, transposase OrfA	41541	69905	64136	221	77608	90721	82290	316	0.001202742	0.001578961	1.429864253	0.515878189
BP1026B_12784	hypothetical protein	70712	127240	111737	111	149149	175475	155489	172	0.16552918	0.183511296	1.54954955	0.631848888
BP1026B_12785	hypothetical protein	31873	45366	41066	84	53232	60798	54142	120	0.006372098	0.007952115	1.428571429	0.514573173
BP1026B_12786	hypothetical protein	5963	7511	6828	30	9456	8873	9298	41	8.25E-04	0.001095892	1.366666667	0.450661409
BP1026B_12787	two-component transcriptional response regulator	28540	34175	32876	33	32758	32243	32148	33	1.33E-08	2.51E-08	1	0
BP1026B_12788	hypothetical protein	39002	49028	52925	93	66789	65613	68620	133	0.003791773	0.004811512	1.430107527	0.516123624
BP1026B_12789	two-component regulator histidine sensor kinase	69573	85967	79929	43	95755	99830	99830	53	3.21E-06	5.07E-06	1.23255814	0.3016557
BP1026B_12790	LysR family transcriptional regulator	80694	88069	85035	86	92333	92063	102081	97	7.25E-09	1.39E-08	1.127906977	0.173648087
BP1026B_12791	peptidase	52217	34131	43086	18	35178	28239	33196	13	9.27E-22	5.48E-21	0.722222222	-0.469485283
BP1026B_12792	hypothetical protein	30208	28234	27967	15	28532	27362	24368	14	1.36E-11	3.31E-11	0.933333333	-0.099535674
BP1026B_12793	glucose dehydrogenase	4580	3011	3875	2	3207	2295	3853	1	1.03E-10	2.31E-10	0.5	-1
BP1026B_12794	hypothetical protein	1059	485	317	0	775	294	619	0	0.022593324	0.027094693	#DIV/0!	#DIV/0!
BP1026B_12795	hypothetical protein	155	241	270	0	51	5	266	0	1.30E-04	1.82E-04	#DIV/0!	#DIV/0!
BP1026B_12797	mandelate racemase	678	389	271	0	207	412	95	0	5.92E-07	9.88E-07	#DIV/0!	#DIV/0!
BP1026B_12796	thiamine pyrophosphate protein	5288	3126	4548	2	4972	4616	3718	2	5.60E-07	9.35E-07	1	0
BP1026B_12798	cytochrome oxidase subunit II	1645	1556	1494	1	860	1134	1117	0	1.93E-10	4.21E-10	0	#NUM!
BP1026B_12799	cytochrome C oxidase subunit I	3498	4528	4073	1	5623	5710	5798	2	0.006152376	0.007685564	2	1
BP1026B_12800	hypothetical protein	1546	1021	1533	2	985	1056	1100	1	1.42E-06	2.29E-06	0.5	-1
BP1026B_12801	cytochrome c family protein	1670	534	632	0	294	293	452	0	7.55E-26	6.19E-25	#DIV/0!	#DIV/0!
BP1026B_12802	hypothetical protein	130100	141500	141969	44	176023	182193	185346	58	0.002038139	0.002639723	1.318181818	0.398549376
BP1026B_12803	phosphoribosyl transferase protein	11611	6933	8101	12	7260	7002	7595	10	4.31E-18	1.89E-17	0.833333333	-0.263034406
BP1026B_12804	nicotinate phosphoribosyltransferase	76986	55215	58864	46	55209	44548	46443	35	1.23E-26	1.08E-25	0.760869565	-0.394278939
BP1026B_12805	hypothetical protein	33875	9883	13054	27	9166	5976	9640	12	2.26E-89	2.18E-87	0.444444444	-1.169925001
BP1026B_12806	hypothetical protein	33320	14070	19058	55	15159	14676	15960	38	3.54E-33	4.87E-32	0.690909091	-0.5334322
BP1026B_12807	hypothetical protein	76693	66778	68949	156	72046	62138	62879	145	3.11E-17	1.27E-16	0.929487179	-0.105493129
BP1026B_12808	transmembrane transporter	75092	62402	63100	38	62285	59848	63264	35	2.63E-17	1.08E-16	0.921052632	-0.118644496
BP1026B_12809	ATP-binding transmembrane ABC transporter	37488	31432	32080	25	25981	25330	32090	21	5.60E-16	2.06E-15	0.84	-0.251538767
BP1026B_12810	hypothetical protein	11320	2645	4587	36	3535	2809	3959	20	2.03E-29	2.17E-28	0.555555556	-0.847996907
BP1026B_12811	hypothetical protein	33600	31160	36466	175	36892	31781	35127	180	1.78E-08	3.31E-08	1.028571429	0.040641984
predicted RNA	-	16830	20105	18569	637	20944	18608	22828	717	6.99E-08	1.24E-07	1.125588697	0.170679746
predicted RNA	-	103965	64418	83573	1134	65060	48437	54582	757	1.35E-40	2.71E-39	0.667548501	-0.583055435
BP1026B_12812	tRNA 2-selenouridine synthase	112678	76879	80999	83	84189	85189	90715	80	6.81E-16	2.48E-15	0.963855422	-0.053111336
BP1026B_12813	LysR family transcriptional regulator	6453	4480	3851	6	3724	3403	2748	4	1.80E-18	8.13E-18	0.666666667	-0.584962501
BP1026B_12814	cholesterol oxidase	17920	16826	15474	9	13204	15937	12846	7	3.77E-19	1.81E-18	0.777777778	-0.362570079
BP1026B_12815	methyl-accepting chemotaxis protein	48548	48273	46306	27	48314	46327	45809	26	5.28E-12	1.33E-11	0.962962963	-0.054447784
BP1026B_12816	hypothetical protein	13461	16697	15991	26	20446	2066						

BP1026B 12839	hypothetical protein	722	1046	921	2	1164	1436	765	2	0.57620252	0.60104631	1	0
BP1026B 12841	3-phosphoshikimate 1-carboxyvinyltransferase	6626	3720	4462	3	3282	3726	5640	3	3.14E-11	7.36E-11	1	0
BP1026B 12840	3-phosphoshikimate 1-carboxyvinyltransferase	10880	9204	9605	7	9847	7301	9294	6	1.56E-14	4.99E-14	0.857142857	-0.222392421
BP1026B 12842	asparagine synthase	4203	3982	3709	2	4495	4473	3997	2	1.03E-05	1.57E-05	1	0
BP1026B 12843	hypothetical protein	13423	12220	11100	10	11714	11720	10196	9	3.38E-13	9.56E-13	0.9	-0.152003093
BP1026B 12844	hypothetical protein	44984	21208	26162	35	19221	19304	22865	23	1.73E-34	2.57E-33	0.657142857	-0.605721061
BP1026B 12845	HAD-superfamily hydrolase	30001	22793	28664	39	22494	20599	22605	31	1.03E-19	5.18E-19	0.794871795	-0.331205908
BP1026B 12846	3,4-dihydroxy-2-butanone 4-phosphate synthase	13667	13663	11549	17	12145	13799	12294	17	1.80E-11	4.32E-11	1	0
BP1026B 12847	DNA-binding protein	125997	102535	101043	164	150603	147474	165385	230	0.012884609	0.015728611	1.402439024	0.487938046
BP1026B 12848	major facilitator family transporter	5220	5122	5543	4	6419	6734	6379	5	2.68E-05	3.96E-05	1.25	0.321928095
BP1026B 12849	LysR family transcriptional regulator	29328	29843	30412	32	29669	28757	26327	30	8.91E-11	2.00E-10	0.9375	-0.093109404
BP1026B 12850	(dimethylallyl)adenosine tRNA methyltransferase	48609	52496	51817	37	74071	78226	70520	54	0.005522415	0.006924845	1.459459459	0.545434137
BP1026B 12851	PhoH family protein	69236	82233	79149	72	91574	101217	94308	89	3.71E-06	5.84E-06	1.236111111	0.30580843
BP1026B 12852	hypothetical protein	143244	118357	131670	161	110505	88949	102473	123	3.27E-28	3.20E-27	0.763975155	-0.388402373
BP1026B 12853	hypothetical protein	17026	10790	12565	21	10397	7604	9557	14	1.60E-28	1.61E-27	0.666666667	-0.584962501
BP1026B 12854	magnesium and cobalt efflux protein CorC	106649	147899	135689	146	174962	188211	190035	207	0.026318466	0.031351998	1.417808219	0.503662399
BP1026B 12855	apolipoprotein N-acyltransferase	72848	67090	65427	40	63789	59323	64572	36	5.70E-18	2.47E-17	0.9	-0.152003093
BP1026B 12856	glycyl-tRNA synthetase subunit alpha	86706	128741	118036	110	149778	165595	157167	156	0.018527015	0.022372379	1.418181818	0.504042505
BP1026B 12857	glycyl-tRNA synthetase subunit beta	105162	75384	79728	41	79524	70995	76419	36	4.45E-21	2.54E-20	0.87804878	-0.187627003
BP1026B 12858	D,D-heptose 1,7-bisphosphate phosphatase	55566	32732	39840	75	37268	34236	36822	64	5.49E-16	2.02E-15	0.853333333	-0.22881869
BP1026B 12859	phospholipid and glycerol acyltransferase	21675	30700	25747	33	34016	34635	29811	42	3.02E-04	4.16E-04	1.272727273	0.347923303
BP1026B 12860	hypothetical protein	69188	84503	85103	87	84680	81337	83203	91	2.30E-12	6.01E-12	1.045977011	0.064851144
BP1026B 12861	lactoylglutathione lyase	80394	111783	101562	251	117466	127014	122065	313	1.19E-05	1.81E-05	1.247011952	0.318475293
BP1026B 12862	integral membrane protein	12424	12743	14063	13	11869	9295	11668	11	1.13E-16	4.42E-16	0.846153846	-0.2410081
BP1026B 12863	dimethyladenosine transferase	117377	134786	128238	153	136212	147871	138783	170	4.67E-08	8.40E-08	1.111111111	0.152003093
BP1026B 12864	4-hydroxythreonine-4-phosphate dehydrogenase	101794	92289	102907	95	97543	97694	96115	93	6.05E-14	1.82E-13	0.978947368	-0.030696797
BP1026B 12865	PpiC-type peptidyl-prolyl cis-trans isomerase	425162	348265	380920	285	319674	282728	316145	228	1.22E-19	6.08E-19	0.8	-0.321928095
BP1026B 12866	organic solute tolerance protein	588287	662794	643305	267	626283	611352	622552	262	0.418058833	0.443316407	0.981273408	-0.02727293
BP1026B 12868	hypothetical protein	5520	3079	3466	29	3981	4430	3860	29	9.28E-07	1.53E-06	1	0
BP1026B 12867	phosphotransferase domain-containing protein	53994	68732	62631	55	78229	83212	70456	70	2.05E-06	3.27E-06	1.272727273	0.347923303
BP1026B 12869	nucleotidyltransferase family protein	23085	12150	13412	22	13510	14648	12957	19	2.13E-18	9.57E-18	0.863636364	-0.211504105
BP1026B 12870	ATP-binding transmembrane ABC transporter protein	67526	67205	69549	36	62448	61758	64231	33	1.77E-17	7.37E-17	0.916666667	-0.125530882
BP1026B 12871	thioesterase superfamily protein	56596	68646	61655	156	80876	80157	79535	200	8.88E-06	1.36E-05	1.282051282	0.358453971
BP1026B 12872	nitrate reductase associated protein	126462	182352	166533	330	213309	240745	251814	490	0.10104432	0.114637644	1.484848484	0.570315725
BP1026B 12873	formate dehydrogenase family accessory protein FdhD	28883	14328	17701	24	15004	10414	14953	16	1.12E-34	1.67E-33	0.666666667	-0.584962501
BP1026B 12874	enoyl-CoA hydratase	14938	14771	16381	20	16042	12743	13768	18	1.34E-14	4.28E-14	0.9	-0.152003093
BP1026B 12875	acetyl-CoA acyltransferase	164528	180815	177372	145	181666	185592	176050	150	7.49E-10	1.57E-09	1.04484729	0.0489096
BP1026B 12876	3-hydroxyacyl-CoA dehydrogenase	302988	288683	291678	120	287028	283462	291576	117	5.85E-12	1.47E-11	0.975	-0.036525876
BP1026B 12877	acyl-CoA dehydrogenase domain-containing protein	354389	456082	431941	231	523545	557059	543671	302	0.70778859	0.728722199	1.307359307	0.38665698
BP1026B 12878	putative transcriptional regulator for fatty acid degradation FadP, TetR family	1393911	1306165	1401864	2796	1870918	1897893	2083700	3989	0.019227045	0.023155231	1.426680973	0.512662763
BP1026B 12879	cardiolipin synthetase II	57778	72539	70854	52	79642	84641	76687	62	1.22E-07	2.13E-07	1.192307692	0.253756592
BP1026B 12880	dATP pyrophosphohydrolase	30434	24382	25313	55	27901	27534	26026	56	7.20E-09	1.39E-08	1.018181818	0.025995209
BP1026B 12881	aspartyl-tRNA synthetase	566465	671349	646878	349	700567	702446	681406	386	0.963377178	0.969099598	1.106017192	0.145373811
BP1026B 12882	hypothetical protein	47427	57679	54211	81	70748	65933	72485	87	6.80E-05	9.76E-05	1.320987654	0.401616984
BP1026B 12883	regulatory protein	24439	38761	32913	93	46944	56970	47663	147	0.099888097	0.113408012	1.580645161	0.660513534
BP1026B 12884	thiopurine S-methyltransferase family protein	48052	38842	35647	52	37253	38706	33360	46	1.43E-13	4.17E-13	0.884615385	-0.176877762
BP1026B 12885	ubiquinone biosynthesis protein UbiB	301639	340665	330375	205	341592	352721	339171	218	8.80E-09	1.68E-08	1.063414634	0.088704225
BP1026B 12886	hypothetical protein	73848	90110	87329	129	106019	115841	92650	161	1.06E-05	1.62E-05	1.248062016	0.319689623
BP1026B 12887	transmembrane protein	1012711	889006	912787	919	914261	888359	934036	894	0.387983557	0.412821357	0.972796518	-0.03979003
BP1026B 12888	ubiquinone/menaquinone biosynthesis methyltransferase	75541	86316	84472	112	92905	101989	87943	128	1.94E-08	3.59E-08	1.142857143	0.192645078
BP1026B 12889	hypothetical protein	29758	21690	24243	60	23071	22668	21517	54	6.40E-15	2.12E-14	0.9	-0.152003093
BP1026B 12890	HIT family hydrolase	160995	233104	209056	452	231001	236773	229532	523	8.73E-07	1.44E-06	1.157079646	0.210488174
BP1026B 12891	oxidoreductase, FAD-binding protein	454735	493352	487854	118	527694	526582	533599	131	0.028767707	0.034172219	1.110164992	0.150779952
BP1026B 12893	7-cyano-7-deazaguanine reductase	87313	93445	79529	112	88172	76845	92416	104	5.84E-18	2.52E-17	0.928571429	-0.106915204
BP1026B 12894	YjgF family protein	202222	182924	187368	493	168060	157144	178287	433	2.94E-17	1.21E-16	0.878296146	-0.187220622
BP1026B 12895	D-aminoacylase	52564	28667	32870	25	26171	23823	22993	16	2.60E-33	3.61E-32	0.64	-0.64385619
BP1026B 12896	transcriptional regulator	11064	5153	7440	8	4727	3953	5790	5	5.87E-29	6.14E-28	0.625	-0.678071905
BP1026B 12897	D-serine deaminase	21921	28561	26638	20	27099	29790	27188	21	4.51E-07	7.57E-07	1.05	0.070389328
BP1026B 12898	peptidase	152217	188434	178751	297	199784	213964	220367	363	1.73E-05	2.59E-05	1.222222222	0.289506617
BP1026B 12899	MarK family regulatory protein	34807	16869	20607	55	15698	13896	16144	35	4.48E-41	9.29E-40	0.636363636	-0.652076697
BP1026B 12900	EmrB-QacA family drug resistance transporter	20494	9653	11167	8	11155	9095	11715	6	2.15E-20	1.13E-19	0.75	-0.415037499
BP1026B 12901	hypothetical protein	92388	40367	5121	67	37006	31030	35292	37	7.63E-49	2.31E-47	0.552238806	-0.856635825
BP1026B 12902	esterase	80437	50987	58724	65	50682	47671	57992	53	1.82E-22	1.14E-21	0.815384615	-0.294447358
BP1026B 12903	hypothetical protein	17760	12143	15339	162	14871	13823	15155	157	7.04E-13	1.93E-12	0.969135802	-0.045229254
BP1026B 12904	hypothetical protein	37732	28701	33391	77	33351	33153	30425	74	6.47E-10	1.37E-09	0.961038961	-0.057333175
BP1026B 12905	hypothetical protein	474	602	626	1	822	828	1107	1	0.117337499	0.132260617	1	0
BP1026B 12906	hypothetical protein	18707	19029	19634	21	21771	20897	20502	23	2.25E-08	4.14E-08	1.095238095	0.131244533
BP1026B 12907	glycosyl transferase group 1 protein	2075	1461	1189	1	1410	1727	1493	1	0.002353268	0.003037195	1	0
BP1026B 12908	capsular polysaccharide biosynthesis/export periplasmic protein	3226	2566	3384	2	3658	3062	3070	2	2.62E-04	3.61E-04	1	0
BP1026B 12909	colanic biosynthesis UDP-glucose lipid carrier transferase	3365	3010	3126	2	2845	3392	4371	2	8.24E-04	0.00109408	1	0
BP1026B 12910	hypothetical protein	1452	2187	2145	2	2023	2119	1582	2	6.79E-04	9.09E-04	1	0
BP1026B 12911	hypothetical protein	10	252	213	1	157	181	132	1	0.740948298	0.760488458	1	0
BP1026B 12912	hypothetical protein	124	126	164	1	85	92	174	1	0.384903746	0.409892399	1	0
BP1026B 12913	hypothetical protein	242	242	339	1	422	724	275	2	0.010953279	0.01346422	2	1
BP1026B 12914	cyclic nucleotide-binding domain-containing protein	4028	3881	4091	5	4053	4019	4632	5	3.72E-06	5.86E-06	1	0
BP1026B 12915	acyl carrier protein	3851	6179	5154	20	6847	7096	5980	26	2.48E-04			

BP1026b_12937	hypothetical protein	4802	4068	4207	11	3331	2522	3038	7	3.34E-17	1.36E-16	0.636363636	-0.652076697
BP1026b_12938	hypothetical protein	21350	25200	28582	73	20170	22282	17090	58	1.39E-22	8.84E-22	0.794520548	-0.331843564
BP1026b_12939	hypothetical protein	5330	5970	6259	1	6158	6051	5329	1	3.26E-09	6.48E-09	1	0
BP1026b_12940	FG-GAP/YD repeat-containing protein	7758	4502	5707	0	4973	4977	5030	0	1.86E-13	5.35E-13	#DIV/0!	#DIV/0!
BP1026b_12941	carboxymuconolactone decarboxylase family protein	41582	54492	45912	134	57272	62777	64381	175	7.86E-05	1.12E-04	1.305970149	0.385121921
BP1026b_12942	putative ATP binding protein	228239	390527	348108	210	434478	512604	439016	301	0.005679143	0.007117102	1.433333333	0.519374159
predicted RNA	-	24419	41367	37992	652	49198	57030	43875	944	0.013445959	0.016400918	1.447852761	0.533914895
predicted RNA	-	77184	137430	122267	558	168269	200727	164305	884	0.306892414	0.330070007	1.584229391	0.663781248
BP1026b_12943	hypothetical protein	144800	239098	210021	111	253766	290073	274658	154	0.008371048	0.010341678	1.387387387	0.472370674
BP1026b_12944	hypothetical protein	123519	197604	176948	522	192734	217485	197518	637	2.25E-05	3.35E-05	1.220306513	0.287243566
BP1026b_12945	hypothetical protein	19389	26119	23548	91	30787	36210	32120	131	0.013060856	0.015940655	1.43956044	0.525628361
BP1026b_12946	hypothetical protein	87770	104929	101328	61	109920	102401	106844	67	1.40E-09	2.86E-09	1.098360656	0.135351853
BP1026b_12947	dienelactone hydrolase family protein	24109	25708	25114	36	24523	25596	22990	35	1.21E-10	2.68E-10	0.972222222	-0.040641984
BP1026b_12948	single-stranded DNA-binding protein	92202	141342	120837	211	155394	168517	166448	292	0.011137911	0.013657564	1.383886256	0.46872537
BP1026b_12949	major facilitator family transporter	68943	64605	65650	55	73145	68272	63883	57	1.80E-12	4.77E-12	1.036363636	0.051530301
BP1026b_12950	exonuclease ABC subunit A	270509	257384	257598	90	276367	267835	276611	94	9.67E-10	2.01E-09	1.044444444	0.062735755
BP1026b_12951	hypothetical protein	104800	103043	99903	94	103133	101008	112250	97	1.65E-11	3.98E-11	1.031914894	0.045323991
BP1026b_12952	formyltetrahydrofolate deformylase	53169	59951	56967	64	62535	63723	61833	71	1.14E-09	2.36E-09	1.109375	0.14974712
BP1026b_12953	NUDIX domain-containing protein	59903	31641	41160	51	30801	24970	27615	32	5.43E-34	7.77E-33	0.62745098	-0.672425342
BP1026b_12954	LysE type translocator	8377	5236	5770	10	4828	5994	4738	8	2.92E-15	9.98E-15	0.8	-0.321928095
BP1026b_12955	adenine phosphoribosyltransferase	75161	76789	80053	137	80416	72940	78941	138	5.29E-14	1.61E-13	1.00729927	0.010492374
BP1026b_12956	potassium efflux system protein	144596	124475	132285	66	117542	117685	114522	58	2.76E-19	1.34E-18	0.878787879	-0.186413124
BP1026b_12957	carbohydrate isomerase KpsF/GutQ family protein	84295	59103	59106	68	58729	49557	54794	55	3.70E-24	2.67E-23	0.808823529	-0.306103128
BP1026b_12958	YrbI family phosphatase	85090	59016	64959	129	58714	47699	51882	97	2.60E-28	2.57E-27	0.751937984	-0.411314413
BP1026b_12959	hypothetical protein	57669	46740	52604	85	52853	42911	43578	75	1.14E-16	4.43E-16	0.882352941	-0.180572246
BP1026b_12960	OstA-like family protein	117284	121454	132267	185	125513	127058	117536	185	1.35E-12	3.62E-12	1	0
BP1026b_12961	ABC transporter ATP-binding protein	307386	332599	332328	417	315907	290335	312888	394	8.30E-13	2.27E-12	0.944844125	-0.081851754
BP1026b_12962	RNA polymerase factor sigma-54	607692	945017	843296	529	1034767	1165338	979160	702	0.023282703	0.027884063	1.327023136	0.408203308
BP1026b_12964	hypothetical protein	292818	301676	307241	1318	325750	332956	319335	1429	1.57E-08	2.94E-08	1.084218513	0.116655546
BP1026b_12963	PTS system transporter subunit IIA	1887826	2994582	2873816	7181	3712901	4166492	3658559	10683	0.421954674	0.447296226	1.487675811	0.573060174
BP1026b_12965	PTS transporter subunit IIA-like nitrogen-regulatory protein PtsN	90945	126025	112741	215	154726	168288	141296	303	0.01350874	0.016471252	1.409302326	0.494981134
BP1026b_12966	HPr kinase/phosphorylase	93592	115435	107302	108	118539	127394	118996	125	1.33E-07	2.31E-07	1.157407407	0.210896782
BP1026b_12967	hypothetical protein	104076	91498	99751	110	104529	93201	105329	112	8.63E-12	2.13E-11	1.018181818	0.025995209
BP1026b_12968	ATP-dependent protease La	116276	122026	113449	185	124872	135533	129646	205	1.43E-08	2.69E-08	1.108108108	0.148098639
BP1026b_12969	A/G-specific adenine glycosylase	67923	46687	56392	51	44400	35279	42505	36	1.74E-28	1.75E-27	0.705882353	-0.502500341
BP1026b_12970	formamidopyrimidine-DNA glycosylase	30118	14227	16218	24	14412	13059	14867	16	4.82E-31	5.66E-30	0.666666667	-0.584962501
BP1026b_12971	hypothetical protein	465984	481227	479752	262	487399	453794	478158	261	2.35E-10	5.12E-10	0.996183206	-0.005517005
BP1026b_12972	outer membrane lipoprotein LolB	26182	23795	25227	39	27152	22865	26869	41	2.99E-08	5.48E-08	1.051282051	0.072149786
BP1026b_12973	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	124661	180552	161545	176	239594	261397	253900	285	0.617560934	0.640880559	1.619318182	0.69538649
BP1026b_12974	Gln tRNA	42147	67980	58215	728	88196	107671	98846	1275	0.07715278	0.503044844	1.751373626	0.808486892
BP1026b_12975	ribose-phosphate pyrophosphokinase	125400	143848	138859	128	182328	211842	206690	209	0.4661613001	0.071282693	1.173130986	0.557612013
BP1026b_12976	50S ribosomal protein L25/general stress protein Ctc	624733	949055	872816	1127	1087806	1169995	1066813	1532	0.018573965	0.022381289	1.359361136	0.442928782
BP1026b_12977	peptidyl-tRNA hydrolase	16179	9257	9561	19	10789	10151	9490	16	6.59E-15	2.18E-14	0.842105263	-0.247927513
BP1026b_12978	histidinol-phosphate aminotransferase	92093	88408	87438	83	82482	85101	82340	77	1.65E-17	6.92E-17	0.927710843	-0.108252891
BP1026b_12979	ferredoxin	31027	51631	50384	166	58714	63085	56560	222	4.38E-04	5.95E-04	1.337439987	0.419376435
BP1026b_12980	phosphopantetheine adenylyltransferase	301000	348592	331523	652	407120	392035	450181	831	1.56E-04	2.19E-04	1.337439987	0.349976513
BP1026b_12981	methyltransferase	4842	2746	3203	5	2434	2514	2624	4	1.17E-14	3.78E-14	0.8	-0.321928095
BP1026b_12982	signal recognition particle-docking protein FtsY	135972	58055	75764	68	54295	42807	58254	39	2.29E-57	1.01E-55	0.573529412	-0.802066022
BP1026b_12983	maleylacetate isomerase	70369	74878	74943	113	60140	56999	58635	90	9.83E-26	8.00E-25	0.796460177	-0.328325866
BP1026b_12984	nitrite reductase (NAD(P)H) large subunit	10572	10469	10619	4	11101	9433	10690	4	1.69E-10	3.71E-10	1	0
BP1026b_12985	nitrite reductase (NAD(P)H) small subunit	240	96	226	0	51	58	0	0	2.10E-26	1.81E-25	#DIV/0!	#DIV/0!
BP1026b_12986	molybdopterine oxidoreductase family protein	5077	3456	4664	1	2805	3021	3044	1	1.08E-17	4.60E-17	1	0
BP1026b_12987	glycosyl transferase family protein	28879	14852	18960	21	14185	12213	14092	13	4.35E-37	7.43E-36	0.619047619	-0.691877705
BP1026b_12988	acetyltransferase	49888	30049	36343	47	27383	24179	25841	31	2.69E-29	2.86E-28	0.659574468	-0.600392541
BP1026b_12989	2-isopropylmalate synthase	24525	17888	20756	12	17513	15885	19360	10	9.62E-21	5.20E-20	0.833333333	-0.263034406
BP1026b_12990	hypothetical protein	284995	202805	238158	625	210300	201651	184784	513	1.77E-22	1.11E-21	0.8208	-0.284897364
BP1026b_12991	hypothetical protein	118384	154443	141388	242	155723	127912	163394	287	1.75E-05	2.62E-05	1.185950413	0.246043689
BP1026b_12992	hypothetical protein	12747	19721	15387	132	24639	28496	32865	638	0.756619428	0.775937371	1.803030303	0.850423644
BP1026b_12993	hypothetical protein	31065	53378	44883	342	75705	87771	68761	214	0.755368127	0.774780927	1.79521637	0.84424233
BP1026b_12994	RNA polymerase factor sigma-32	816263	1017694	938025	987	1188807	1292951	1225686	1320	0.032570438	0.038565073	1.337386018	0.41941594
BP1026b_12996	hypothetical protein	1020	1075	823	10	2207	2728	1749	23	7.01E-06	1.08E-05	2.3	1.20163861
BP1026b_12995	hypothetical protein	4375	3554	4434	14	4990	6017	5698	19	0.002036521	0.002638172	1.357142857	0.440572591
BP1026b_12997	cytochrome d ubiquinol oxidase subunit I	91011	112264	114213	66	157563	168405	171296	103	0.223406568	0.244475298	1.560600601	0.642106408
BP1026b_12998	cytochrome d ubiquinol oxidase, subunit II	43376	42174	47781	39	58779	59599	68201	54	0.002095562	0.002712973	1.384615385	0.469485283
BP1026b_12999	hypothetical protein	2780	2214	1617	22	2594	3040	2178	26	0.016218339	0.0196527	1.181818182	0.2410081
BP1026b_13001	hypothetical protein	1103	253	443	1	455	293	512	0	5.62E-05	8.13E-05	0	#NUM!
BP1026b_13002	hypothetical protein	656	339	226	0	328	284	190	0	3.02E-04	4.15E-04	#DIV/0!	#DIV/0!
BP1026b_13003	chitinase	92805	51089	58377	26	56506	54066	44530	20	4.11E-27	3.75E-26	0.769230769	-0.378511623
predicted RNA	-	14894	11372	11324	783	13132	12689	12249	793	1.68E-10	3.68E-10	1.012771392	0.018308558
BP1026b_13004	PTS system, N-acetylglucosamine-specific IIABC component	56473	52257	57495	31	45898	43237	44142	25	5.28E-22	3.20E-21	0.806451613	-0.310340121
BP1026b_13005	PTS system, glucose-glucoside (Glc) family EIIA/phosphocarrier HPr/phosphoenolpyruvate-protein phosphotransferase component	21757	14582	14972	6	13808	10906	12394	4	3.15E-26	2.67E-25	0.666666667	-0.584962501
BP1026b_13006	SIS domain-containing protein	7353	4850	4743	5	4236	4716	3873	4	1.59E-15	5.58E-15	0.8	-0.321928095
BP1026b_13007	N-acetylglucosamine-6-phosphate deacetylase	8371	4736	5793	5	4822	4270	4089	3	1.75E-19	8.60E-19	0.6	-0.736965594
BP1026b_13008	GntR family transcriptional regulator	3253	3059	3319	4	3298	2969	3551	4	4.00E-05	5.83E-05	1	0
BP1026b_13009	hypothetical protein	102	73	157	1	268	220	46	1				

BP1026B_13033	hypothetical protein	3945	3345	3193	2	2530	2984	3121	1	8.07E-10	1.69E-09	0.5	-1
BP1026B_13034	hypothetical protein	1981	1041	1240	1	979	1006	708	1	1.24E-10	2.75E-10	1	0
BP1026B_13035	ABC transporter ATP-binding protein	10490	7047	7633	10	6677	5909	7978	8	7.89E-18	3.39E-17	0.8	-0.321928095
BP1026B_13036	branched chain amino acid ABC transporter permease	4348	4586	4521	5	4504	4019	4573	4	4.86E-08	8.72E-08	0.8	-0.321928095
BP1026B_13037	hypothetical protein	151547	156708	158559	160	154695	165125	137662	156	5.06E-12	1.28E-11	0.975	-0.036525876
BP1026B_13038	hypothetical protein	1500	717	667	8	645	460	1234	6	3.92E-04	5.34E-04	0.75	-0.415037499
BP1026B_13039	D-methionine ABC transporter substrate-binding protein	716449	870504	846788	990	874043	873259	861599	1061	0.22579639	0.246961106	1.071717172	0.099924226
BP1026B_13040	methyl-accepting chemotaxis protein	1021275	1002287	1067352	627	905337	842500	858432	529	0.842528303	0.857722558	0.843700159	-0.245197721
BP1026B_13041	hypothetical protein	22694	17611	18288	66	19726	17309	17457	61	2.00E-15	6.98E-15	1.14754098	-0.1563656782
BP1026B_13042	SCO1/SenC family protein	50633	60636	58297	91	65933	61709	60008	101	1.22E-09	2.52E-09	1.10989011	0.150416843
BP1026B_13043	protoheme IX farnesyltransferase	151904	169747	165534	179	200357	202210	207520	225	1.03E-04	1.46E-04	1.25698324	0.329965414
BP1026B_13044	cytochrome c assembly family protein	92992	118891	110792	96	119048	119037	126695	109	3.47E-08	6.31E-08	1.135416667	0.183221824
BP1026B_13045	hypothetical protein	39775	44817	45403	67	48702	47282	48506	75	7.25E-08	1.29E-07	1.119402985	0.1627295
BP1026B_13046	SURF1 family protein	164497	138956	150141	211	140569	118706	140249	186	1.61E-18	7.31E-18	0.881516588	-0.181940378
BP1026B_13046	hypothetical protein	52315	79934	74120	327	100000	113188	99701	496	0.0218918	0.026293659	1.516819572	0.601049485
BP1026B_13048	cytochrome c oxidase subunit III	342195	455117	418972	472	467237	516897	480410	568	2.48E-05	3.67E-05	1.20338931	0.26710407
BP1026B_13049	hypothetical protein	39330	24972	27571	152	27838	25746	30537	139	6.77E-12	1.69E-11	0.914473684	-0.128986441
BP1026B_13050	cytochrome C oxidase assembly protein	402042	491541	441926	734	555539	581964	577189	943	0.932599017	0.941160483	1.284741144	0.361477708
BP1026B_13051	hypothetical protein	13606	24967	22212	143	25031	25090	24256	175	4.13E-05	6.02E-05	1.223762224	0.29139775
BP1026B_13052	cytochrome c oxidase polypeptide I	1217051	1687485	1512678	915	1545645	1644411	1733336	1020	0.119560394	0.134594265	1.114754098	-0.1563656782
predicted RNA	-	23057	30273	26798	763	26329	25825	25930	743	3.24E-10	7.00E-10	0.97378768	-0.038320846
BP1026B_13053	cytochrome c oxidase subunit II	637933	749229	703885	448	731855	779452	723305	479	0.665246404	0.686953521	1.069196429	0.096526924
BP1026B_13054	hypothetical protein	114599	130940	121631	256	120218	116850	137848	261	1.28E-11	3.10E-11	1.01953125	0.027905997
BP1026B_13055	hypothetical protein	66930	45740	51896	59	38456	34807	38405	40	8.67E-31	1.00E-29	0.677966102	-0.560714954
BP1026B_13056	ComF family protein	6029	5321	7306	8	5714	4177	6139	6	4.57E-13	1.28E-12	0.75	-0.415037499
BP1026B_13057	RNA methyltransferase	8776	9438	10388	20	10810	8724	9141	20	3.60E-10	7.75E-10	1	0
BP1026B_13058	Appr-1-p processing enzyme family protein	9333	4927	5103	12	5556	4437	5644	9	4.22E-15	1.42E-14	0.75	-0.415037499
BP1026B_13059	NAD(PH)-dependent glycerol-3-phosphate dehydrogenase	93107	69730	71050	77	66898	61807	64459	63	4.08E-24	2.94E-23	0.818181818	-0.289506617
BP1026B_13060	preprotein translocase subunit SecB	189248	307165	272653	534	347505	380507	338563	740	0.002762267	0.003548251	1.38576779	0.470685529
BP1026B_13061	glutaredoxin 3	175965	217291	231882	798	275696	285159	246777	1031	6.97E-04	9.32E-04	1.29197995	0.369583681
BP1026B_13062	rhodanese-like domain-containing protein	25465	23509	27054	62	27823	26310	27716	66	1.97E-07	3.38E-07	1.064516129	0.090197809
BP1026B_13063	phosphoglyceromutase	216404	283872	273032	343	300919	297717	293552	396	7.31E-07	1.21E-06	1.15481895	0.207291854
BP1026B_13064	carboxy-terminal protease	701401	973437	903604	541	993002	1074638	972840	638	0.078570004	0.090085937	1.179297597	0.23792783
BP1026B_13065	molybdopterin biosynthesis protein MoeB	89788	64797	69804	98	62550	62688	63380	82	6.97E-23	4.55E-22	0.836734694	-0.257157839
predicted RNA	-	11960	15921	17807	525	20700	22099	15897	674	3.96E-05	5.77E-05	1.283809524	0.360431169
BP1026B_13066	phosphoenolpyruvate-protein phosphotransferase	863741	841111	823910	478	861345	893472	830762	489	0.316296977	0.339834853	1.023012552	0.032823847
BP1026B_13067	phosphocarrier protein HPr	19072	29058	24196	101	36054	38464	36645	156	0.056765223	0.065905297	1.544554455	0.627190736
BP1026B_13068	PTS system fructose-specific transporter subunit IIA	114976	96753	105084	222	108127	98632	105610	219	2.96E-13	8.40E-13	0.986486484	-0.019628807
BP1026B_13069	glutathione synthetase	91059	92829	96208	97	100010	104835	104465	107	3.73E-09	7.35E-09	1.103092784	0.141554144
BP1026B_13070	glutamate--cysteine ligase	301329	316058	316631	241	322223	311144	336778	250	1.05E-09	2.17E-09	1.037344398	0.052894948
BP1026B_13071	ammonium transporter	13660	17038	13806	9	14870	15638	15677	10	1.11E-10	2.47E-10	1.111111111	0.152003093
BP1026B_13072	nitrogen regulatory protein P-II	1019	1171	1312	3	2750	2970	1724	7	3.06E-04	4.21E-04	2.333333333	1.222392421
BP1026B_13073	hypothetical protein	104834	142941	137995	510	136296	136839	156415	568	6.62E-08	1.18E-07	1.11372549	0.155393683
BP1026B_13074	Mg chelatase-like protein	14181	5332	7504	5	6164	4627	6503	3	1.88E-29	2.01E-28	0.6	-0.736965594
BP1026B_13075	acetyltransferase	6032	5054	5219	11	5208	5276	5751	11	8.55E-09	1.64E-08	1	0
BP1026B_13076	thioesterase domain-containing protein	69126	58883	63730	81	62528	56623	57124	75	3.21E-17	1.31E-16	0.925925926	-0.110313112
BP1026B_13077	hypothetical protein	7554	3294	4455	8	4289	3111	5108	7	1.51E-12	4.02E-12	0.875	-0.192645078
BP1026B_13078	resA domain-containing protein	137993	201481	185077	325	192972	197642	200515	366	1.38E-07	2.38E-07	1.126153846	0.17140393
BP1026B_13079	C4-dicarboxylate transport transcriptional regulatory protein	183781	95148	117876	97	81312	68187	85969	57	1.51E-59	7.20E-58	0.587628866	-0.767022828
BP1026B_13080	C4-dicarboxylate transport sensor protein	63173	42279	45733	26	40461	34321	39337	20	4.76E-23	3.15E-22	0.769230769	-0.378511623
BP1026B_13081	C4-dicarboxylate transporter DctA	132466	127153	131779	103	68058	65912	76124	55	8.65E-75	6.61E-73	0.533980583	-0.905140814
BP1026B_13082	acetate permease	22229	29531	28601	15	23002	23957	21327	13	1.36E-16	5.24E-16	0.866666667	-0.206450877
BP1026B_13083	hypothetical protein	10120	10795	9963	33	9757	10981	11174	34	3.46E-09	6.86E-09	1.03030303	0.043068722
BP1026B_13084	CAIB/BAIF family protein	108785	42232	57772	57	33045	29345	33356	26	2.02E-78	1.68E-76	0.456140351	-1.132450296
BP1026B_13085	acyl-CoA dehydrogenase domain-containing protein	76929	72224	76432	65	75871	73980	68221	64	5.58E-15	1.86E-14	0.984615385	-0.022367813
BP1026B_13086	acyl-CoA dehydrogenase domain-containing protein	28533	31261	33101	25	37972	38226	38423	31	1.33E-04	1.88E-04	1.24	0.31040121
BP1026B_13087	enoyl-CoA hydratase/isomerase/3-hydroxyacyl-CoA dehydrogenase	47555	30228	33829	17	28117	26326	31576	13	2.26E-19	1.10E-18	0.764705882	-0.387023123
BP1026B_13088	LysR family transcriptional regulator	12987	12314	10449	13	10773	9076	12159	11	7.72E-14	2.31E-13	0.846153846	-0.2410081
BP1026B_13089	hypothetical protein	4888	3786	3957	10	2682	2140	2830	6	7.80E-21	4.26E-20	0.6	-0.736965594
BP1026B_13090	hypothetical protein	14552	6693	8369	5	7369	6394	6222	3	1.95E-28	1.95E-27	0.6	-0.736965594
BP1026B_13092	lipoyl synthase	323449	374362	355188	354	337437	357123	328516	344	2.79E-11	6.57E-11	0.971751412	-0.041340795
BP1026B_13093	lipote-protein ligase B	137489	127963	134719	174	131839	129209	127830	169	1.18E-13	3.48E-13	0.971264368	-0.04206406
BP1026B_13094	hypothetical protein	3453	4277	3400	11	3991	4488	4289	13	1.94E-04	2.71E-04	1.181818182	0.2410081
BP1026B_13095	DNA-binding transcriptional activator GcvA	33703	22113	26317	28	23417	21347	23953	23	3.37E-17	1.37E-16	0.821428571	-0.283792966
BP1026B_13096	hypothetical protein	152179	213475	196914	606	201183	207558	202098	658	4.90E-09	9.56E-09	1.085808881	0.11876979
BP1026B_13097	D-amino acid aminotransferase	243468	280706	270684	279	267860	259846	269037	280	3.15E-11	7.38E-11	1.003584229	0.005161705
BP1026B_13098	penicillin-binding protein 6	279335	331758	326341	237	300542	332554	282538	232	9.65E-12	2.38E-11	0.978902954	-0.030762254
BP1026B_13099	esterase/lipase/thioesterase family protein	67541	73889	70954	109	69909	67246	61607	102	8.05E-17	3.18E-16	0.935779817	-0.095758993
BP1026B_13100	ferredoxin, 2Fe-2S	19490	18619	19152	60	22118	24663	19776	69	1.19E-06	1.94E-06	1.15	0.201633861
BP1026B_13101	hypothetical protein	13315	9619	11242	9	11348	9181	12190	9	1.48E-11	3.57E-11	1	0
BP1026B_13102	hypothetical protein	29660	15235	15991	33	15231	11112	12897	20	2.67E-42	5.98E-41	0.606060606	-0.722466024
BP1026B_13103	ABC transporter substrate-binding protein	190822	171222	162550	188	158969	153568	168394	172	4.14E-15	1.40E-14	0.914893617	-0.128324097
BP1026B_13104	ABC transporter ATP-binding protein	170768	125350	136869	171	119095	102981	126487	137	1.75E-24	1.29E-23	0.801169591	-0.319820432
BP1026B_13105	ABC transporter permease	102442	102873	91550	87	100535	103251	97281	89	2.76E-12	7.16E-12	1.022988506	0.032789935
BP1026B_13106	2',3'-cyclic-nucleotide 2'-phosphodiesterase	27652	25582	27145	13	24035	22553	22719	11	1.09E-1			

BP1026B_13131	peptide ABC transporter ATP-binding protein	10286	7549	10124	5	8682	8530	8848	5	5.23E-13	1.45E-12	1	0
BP1026B_13132	metallo-beta-lactamase family protein	55536	67825	62282	57	62252	59618	66583	58	5.52E-13	1.53E-12	1.01754386	0.025090981
BP1026B_13133	bifunctional isocitrate dehydrogenase kinase/phosphatase protein	437372	557651	523291	279	721009	779482	732900	410	0.087095574	0.099442578	1.46953405	0.55538788
BP1026B_13134	carbonic anhydrase	158261	121141	125623	175	122099	120549	139074	165	3.57E-15	1.21E-14	0.942857143	-0.08488898
BP1026B_13135	acetyl-CoA acetyltransferase	471505	364963	414728	349	350432	327626	337024	283	1.35E-18	6.18E-18	0.810888252	-0.302424983
BP1026B_13136	short chain dehydrogenase	72808	61979	61304	96	56674	56723	56503	83	4.66E-20	2.40E-19	0.864583333	-0.209923069
BP1026B_13137	hypothetical protein	9992	7312	8233	18	7959	7030	5915	15	7.36E-18	3.17E-17	0.833333333	-0.263034406
BP1026B_13138	hypothetical protein	91742	65508	73858	57	52983	44810	51399	37	3.72E-42	8.24E-41	0.649122807	-0.623436649
BP1026B_13139	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	31296	29723	33557	23	29595	26008	28733	20	7.87E-13	2.15E-12	0.869565217	-0.201633861
BP1026B_13140	8-amino-7-oxononanoate synthase	18866	7775	10109	10	7061	6089	5993	5	3.05E-52	1.09E-50	0.5	-1
BP1026B_13141	dithiobiotin synthetase	9224	2517	3389	6	2513	2363	2729	3	1.86E-34	2.75E-33	0.5	-1
BP1026B_13142	biotin synthase	84600	74090	74975	77	69807	67756	71392	68	2.89E-19	1.40E-18	0.883116883	-0.179323699
BP1026B_13143	CutC family protein	15507	8435	8441	15	5919	4626	6769	8	1.05E-45	2.80E-44	0.533333333	-0.906890596
BP1026B_13144	hypothetical protein	14386	7075	9216	12	7098	5814	6003	7	2.65E-34	3.89E-33	0.583333333	-0.777607579
BP1026B_13145	alkaline phosphatase family protein	4794	3541	4004	2	3521	3684	3576	2	1.69E-09	3.43E-09	1	0
BP1026B_13146	alkaline phosphatase family protein subfamily	2700	3217	2943	1	2543	2260	2466	1	5.89E-09	1.14E-08	1	0
BP1026B_13147	hypothetical protein	3921	4932	5253	12	4505	4676	4659	12	3.56E-08	6.48E-08	1	0
BP1026B_13148	EAL domain-containing protein	6403	4178	5689	4	4196	3282	3823	2	8.96E-18	3.83E-17	0.5	-1
BP1026B_13149	Na+/H+ antiporter	22154	20911	18236	12	19698	20562	18314	11	9.07E-14	2.69E-13	0.916666667	-0.125530882
BP1026B_13150	2-oxoacid ferredoxin oxidoreductase	43029	33655	34629	10	32275	26426	33819	8	1.05E-15	3.77E-15	0.8	-0.321928095
BP1026B_13151	inward rectifier potassium channel	15378	15044	13590	14	10994	10233	14499	11	7.27E-19	3.41E-18	0.785714286	-0.347923303
BP1026B_13152	hypothetical protein	3796	3054	3978	8	2973	2973	3534	7	4.99E-08	8.95E-08	0.875	-0.192645078
BP1026B_13153	serine-type carboxypeptidase family protein	48678	57866	54078	31	49692	50790	50304	29	1.13E-14	3.66E-14	0.935483871	-0.096215315
BP1026B_13154	sulfate-binding protein	154346	192242	185223	174	167253	177406	173397	170	2.65E-12	6.89E-12	0.977011494	-0.033552526
BP1026B_13155	Fis family regulatory protein	16208	21624	18244	41	17396	16921	16230	37	1.34E-16	5.18E-16	0.90249024	-0.148098639
BP1026B_13156	hypothetical protein	332416	567576	521077	848	426246	486900	433193	804	1.11E-11	2.72E-11	0.948113208	-0.076868763
BP1026B_13157	hypothetical protein	8437	15014	12523	102	13957	17737	13480	128	9.73E-06	1.49E-05	1.254901961	0.327574658
BP1026B_13158	hypothetical protein	466622	825720	721333	1183	575234	662759	585467	1071	0.196011006	0.215613539	0.905325444	-0.143491594
BP1026B_13159	putative transposase	16661	21409	20496	38	14073	15688	20000	32	1.48E-19	7.35E-19	0.842105263	-0.247927513
BP1026B_13160	dihydrodipicolinate synthase	26279	16056	18303	22	19588	16787	19303	20	6.16E-16	2.25E-15	0.909090909	-0.137503524
BP1026B_13161	kelch repeat-containing protein	6239	8457	7663	2	8727	9849	8221	3	4.88E-06	7.61E-06	1.5	0.584962501
BP1026B_13162	SCO1/SenC family protein	1852	3333	3405	4	3465	5198	4702	7	0.443588955	0.468881307	1.75	0.807354922
BP1026B_13163	lactonase	26365	8926	12135	21	8280	6485	9011	10	2.79E-63	1.62E-61	0.476190476	-0.1070389328
BP1026B_13164	hypothetical protein	50292	53628	57284	177	59595	56294	59733	193	9.79E-10	2.04E-09	1.09039548	0.124851487
BP1026B_13165	azalucine resistance protein AzlC	26195	28203	28007	37	30360	31149	32230	42	5.02E-06	7.82E-06	1.135135135	0.182864057
BP1026B_13166	transcription regulator AsnC	19951	24140	21201	47	21279	22512	22268	47	1.58E-10	3.47E-10	1	0
BP1026B_13167	lipoprotein	905	574	751	2	638	495	653	2	0.001015766	0.001339956	1	0
BP1026B_13168	non-hemolytic phospholipase C	53496	54005	51457	25	47517	47207	45060	21	3.11E-17	1.27E-16	0.84	-0.251538767
BP1026B_13169	MutT/NUDIX family protein	5073	1772	2310	7	1636	1930	1534	4	6.89E-21	3.77E-20	0.571428571	-0.807354922
BP1026B_13170	alpha/beta hydrolase	4226	1970	2551	4	1707	1055	1827	2	4.91E-23	3.24E-22	0.5	-1
BP1026B_13171	glyoxalase/bleomycin resistance protein/dioxygenase superfamily protein	39124	33414	34292	81	41571	36642	38514	88	3.67E-07	6.20E-07	1.086419753	0.119581616
BP1026B_13172	hypothetical protein	36079	24056	24897	30	25993	27130	27577	28	7.30E-11	1.65E-10	0.933333333	-0.099535674
BP1026B_13173	hydroxymethylglutaryl-CoA lyase	105866	100068	105703	110	96913	87578	88917	97	2.11E-20	1.11E-19	0.881818182	-0.181446871
BP1026B_13174	hypothetical protein	15732	9927	12086	24	8841	6752	9204	16	1.91E-32	2.49E-31	0.666666667	-0.584962501
BP1026B_13175	ISBma1, transposase	54834	81165	73639	57	92224	96876	98719	78	4.55E-04	6.17E-04	1.368421053	0.452512205
BP1026B_13176	hypothetical protein	12425	8822	10936	11	9902	9406	10213	10	6.47E-13	1.78E-12	0.909090909	-0.137503524
BP1026B_13177	transcription regulator AsnC	6889	6838	5836	13	7220	8596	8299	16	1.18E-05	1.78E-05	1.230769231	0.299560282
BP1026B_13178	hydrolase	143465	168278	166478	178	248118	254991	226958	272	0.206986697	0.227141619	1.528089888	0.61172941
BP1026B_13179	2-nitropropane dioxygenase	104215	114425	115953	116	150150	147013	149957	155	0.001629063	0.002122626	1.336206897	0.41814341
BP1026B_13180	LysR family regulatory protein	70323	44402	50096	56	41155	34851	40447	39	2.74E-28	2.71E-27	0.696428571	-0.521952703
BP1026B_13181	hypothetical protein	507	1061	715	7	1302	1424	1059	12	0.119558199	0.134594265	1.714285714	0.77607579
BP1026B_13182	outer membrane porin protein	9538	11682	11108	9	14257	12552	12767	11	5.82E-06	9.02E-06	1.222222222	0.289506617
BP1026B_13183	hypothetical protein	3236	5308	4023	8	6254	6572	4851	12	0.004311886	0.005447447	1.5	0.584962501
BP1026B_13184	sodium/bile acid symporter family protein	425082	194935	217091	268	156091	134911	182008	151	1.63E-59	7.67E-58	0.563432836	-0.827684451
BP1026B_13185	methyl-accepting chemotaxis protein I	3431	2790	2845	1	3053	1559	1900	1	2.54E-12	6.61E-12	1	0
BP1026B_13186	LacI family transcriptional regulator	51359	28397	33827	37	23155	19348	21265	20	2.67E-51	9.11E-50	0.540540541	-0.887525271
BP1026B_13187	N-acetylglucosamine 2-epimerase (GlcNAc 2-epimerase) family protein	128372	105237	112213	77	72414	73223	73420	49	2.56E-49	7.94E-48	0.636363636	-0.652076697
BP1026B_13188	fructokinase	49056	38412	38365	46	29510	30370	32558	33	1.89E-22	1.18E-21	0.717391304	-0.479167837
BP1026B_13189	hypothetical protein	264155	410940	393460	1583	425731	459494	380839	1875	1.30E-05	1.96E-05	1.184459886	0.24224934
BP1026B_13190	hypothetical protein	73003	39134	41801	263	37861	33507	42496	194	2.15E-24	1.57E-23	0.737642586	-0.439006147
BP1026B_13191	hypothetical protein	154618	115883	131161	112	116557	104927	119674	95	8.78E-21	4.77E-20	0.848214286	-0.237499314
BP1026B_13192	hypothetical protein	3160	1771	1821	2	2927	3149	2781	3	0.10950715	0.123857726	1.5	0.584962501
BP1026B_13193	dihydroneopterin aldolase	17333	21808	22008	47	29318	28695	25834	64	0.003630911	0.004619551	1.361702128	0.445411148
BP1026B_13194	C32 (RNA thiolase	78726	101381	93432	91	103119	107122	105711	105	9.65E-08	1.69E-07	1.153846154	0.206450877
BP1026B_13195	UDP-N-acetylglucosamine pyrophosphorylase	113195	105635	112403	78	107078	97023	99744	71	1.08E-16	4.24E-16	0.91025641	-0.136550999
BP1026B_13196	glucosamine-fructose-6-phosphate aminotransferase	203199	186012	187830	104	185428	190393	194971	103	3.33E-12	8.56E-12	0.990384615	-0.013939191
BP1026B_13197	avidin family protein	13844	20382	17870	45	20842	22275	22379	56	5.05E-05	7.32E-05	1.244444444	0.315501826
BP1026B_13198	hypothetical protein	7265	8617	7488	22	9982	8070	7641	25	3.80E-08	6.89E-08	1.136363636	-0.18442571
BP1026B_13199	CzcA family heavy metal efflux protein	11654	9582	10579	3	7886	8560	9603	2	2.52E-18	1.13E-17	0.666666667	-0.584962501
BP1026B_13200	RND family efflux transporter MFP subunit	16973	11169	13626	8	11389	10948	12868	7	7.13E-17	2.82E-16	0.875	-0.192645078
BP1026B_13201	outer membrane efflux protein	10272	9124	10407	7	10027	11214	9028	7	1.20E-09	2.48E-09	1	0
BP1026B_13202	hypothetical protein	261579	177809	174864	718	177919	173208	182907	624	5.77E-18	2.50E-17	0.86908078	-0.202437815
BP1026B_13203	hypothetical protein	595291	568701	570243	1160	537514	533075	527998	1070	0.001598265	0.00208423	0.922413793	-0.116514009
BP1026B_13204	lipoprotein	412734	450864	423832	505	447544	402624	451709	511	1.75E-09	3.55E-09	1.011881188	0.017039903
BP1026B_13205	LeuA family protein	533069	636678	604890	876	657121	710191	662714	1002	0.975476907	0.979855451	1.143835616	0.193879734
BP1026B_13207	copper-translocating P-type ATPase	311480	212829	223177	102	219701	211912	215020	88	1.99E-19	9.73E-19	0.862745098	-0.212993723
BP102													

BP1026B_13230	uracil permease	103067	77952	80431	66	69232	60314	70627	51	9.95E-30	1.09E-28	0.772727273	-0.371968777
BP1026B_13231	flagellar hook-associated protein FlgL	1142833	1158732	1165175	937	1241370	1249018	1128460	978	0.322543473	0.346190031	1.04375667	0.061785417
BP1026B_13232	flagellar hook-associated protein FlgK	1635947	1402564	1498749	754	1447900	1302367	1286013	671	0.641535692	0.664235976	0.889920424	-0.168251757
BP1026B_13233	YcgR protein superfamily protein	192589	132289	137250	202	135105	133440	143655	181	1.34E-17	5.67E-17	0.89603604	-0.158365596
BP1026B_13234	flagellar rod assembly protein/muramidase FlgJ	205781	211189	201266	220	225447	228689	237962	246	9.55E-08	1.68E-07	1.118181818	0.161515492
BP1026B_13235	flagellar basal body P-ring protein	224382	182115	201393	169	185311	165062	178382	147	6.10E-18	2.64E-17	0.869822485	-0.201207091
BP1026B_13236	flagellar basal body L-ring protein	127541	159308	150640	201	177055	180511	164934	240	2.61E-05	3.86E-05	1.194029851	0.255838904
BP1026B_13237	flagellar basal body rod protein FlgG	237760	281058	285074	339	300504	299064	286233	374	3.71E-08	6.74E-08	1.103244838	0.141752997
BP1026B_13238	flagellar basal body rod protein FlgF	229953	177873	187104	260	193815	194370	190973	253	5.67E-13	1.57E-12	0.973076923	-0.039374238
BP1026B_13239	flagellar hook protein FlgE	645469	728809	697341	568	762026	762669	758942	626	0.453994852	0.479637791	1.102112676	0.140271727
BP1026B_13240	flagellar basal body rod modification protein	232670	247421	256079	291	257342	238993	231393	287	5.76E-12	1.45E-11	0.986254296	-0.019968416
BP1026B_13241	flagellar basal body rod protein FlgC	87356	123114	118904	257	126652	132451	125878	301	3.98E-07	6.71E-07	1.171206226	0.227995128
BP1026B_13242	flagellar basal body rod protein FlgB	98170	79985	87613	180	75353	69886	79633	152	6.79E-23	4.43E-22	0.844444444	-0.243925583
BP1026B_13243	flagellar basal body P-ring biosynthesis protein FlgA	31456	12745	17581	13	15546	15386	11887	9	6.67E-32	8.28E-31	0.692307692	-0.530514717
BP1026B_13244	negative regulator of flagellin synthesis	164673	167180	172960	487	165997	159909	172261	481	1.35E-11	3.28E-11	0.987679671	-0.017884878
BP1026B_13245	flagella synthesis protein FlgN	477782	456101	486517	974	502292	498171	425573	978	4.23E-10	9.05E-10	1.004106776	0.005912693
BP1026B_13246	RebB protein	6545	10519	10596	41	14180	16449	10923	62	0.006086104	0.007607327	1.512195122	0.596644306
BP1026B_13247	multifunctional tRNA nucleotidyl transferase/2'-3'-cyclic phosphodiesterase/2'-nucleotidase/phosphatase	67399	50411	50354	45	47690	47334	46396	37	6.37E-20	3.25E-19	0.822222222	-0.282399731
BP1026B_13248	glutathione S-transferase domain-containing protein	21565	12411	13102	24	14101	12392	12642	20	1.01E-18	4.68E-18	0.833333333	-0.263044006
BP1026B_13249	nucleoside-diphosphate-sugar epimerase	34130	21430	21787	27	20375	19752	21807	21	3.03E-21	1.72E-20	0.777777778	-0.362570079
BP1026B_13250	soluble lytic murein transglycosylase	518839	475958	495603	253	429972	385085	412377	209	6.09E-17	2.43E-16	0.826086957	-0.275634443
BP1026B_13251	5-formyltetrahydrofolate cyclo-ligase	10433	3893	5241	10	5574	3699	4827	7	8.72E-19	4.06E-18	0.7	-0.514573173
BP1026B_13252	hypothetical protein	70690	98579	97524	173	115781	129505	115704	234	4.94E-04	6.68E-04	1.326011156	0.435736492
BP1026B_13253	hypothetical protein	16288	7774	7848	16	7135	6903	6874	10	3.60E-31	4.26E-30	0.625	-0.678071905
BP1026B_13254	urea amidolyase-like protein	127041	51016	65884	75	47169	40452	46537	41	5.00E-60	2.43E-58	0.546666667	-0.871266686
BP1026B_13255	LamB/VcsF family protein	166565	121130	132729	183	117890	111516	116988	150	7.86E-23	5.09E-22	0.819672131	-0.286881148
BP1026B_13256	hypothetical protein	8442	4357	6186	8	4335	3763	3241	5	6.76E-26	5.57E-25	0.625	-0.678071905
BP1026B_13257	hypothetical protein	62197	66544	65244	67	54851	50194	55485	55	2.57E-22	1.59E-21	0.820895522	-0.284729477
BP1026B_13258	GumN family protein	60101	33665	44141	40	34371	29977	32539	28	7.94E-26	6.50E-25	0.7	-0.514573173
BP1026B_13259	dipeptide transporter ATP-binding subunit	452042	338325	356884	376	337749	344002	361199	341	2.66E-13	7.59E-13	0.906914894	-0.140960921
BP1026B_13260	peptide ABC transporter ATP-binding protein	1140893	1318446	1242585	1242	1351175	1323179	1382443	1361	0.19322158	0.212856262	1.095813205	0.132001893
BP1026B_13261	dipeptide ABC transporter permease	70785	53156	59806	66	52501	54395	52232	57	1.71E-19	8.43E-19	0.863636364	-0.211504105
BP1026B_13262	dipeptide ABC transporter permease	89703	104182	102797	97	105271	109583	102809	104	4.46E-10	9.52E-10	1.072164948	0.100526876
BP1026B_13263	dipeptide ABC transporter substrate-binding protein	1438149	2099451	1948486	1135	1634962	1728189	1623128	1031	0.46815882	0.493935539	0.908370044	-0.138647965
BP1026B_13264	major facilitator family transporter	39157	37418	38364	30	39231	35729	35764	29	1.18E-10	2.63E-10	0.966666667	-0.0480906
BP1026B_13265	high potential iron-sulfur protein	57141	12073	26275	663	12921	7208	13268	231	9.03E-149	1.45E-146	0.34841629	-1.521116019
BP1026B_13266	oxidoreductase, FAD-binding family protein	798326	778299	864584	2583	771243	668907	804234	2375	0.875283371	0.888757998	0.919473818	-0.121120131
BP1026B_13267	ATP-dependent protease	136679	124714	117752	112	134188	132175	146444	123	7.31E-09	1.41E-08	1.089285714	0.123824216
BP1026B_13268	hypothetical protein	135891	164090	154328	154	165609	153076	156458	161	2.89E-09	5.77E-09	1.045454545	0.064130337
BP1026B_13269	hypothetical protein	44174	41879	48573	79	57599	58839	48145	97	9.30E-06	1.42E-05	1.227848101	0.296132094
BP1026B_13270	endonuclease/exonuclease/phosphatase family protein	87022	55732	60327	83	70825	55116	68647	79	1.22E-15	4.36E-15	0.951807229	-0.071258683
BP1026B_13271	LysE type translocator	31133	16193	21980	35	17449	16794	17905	26	3.69E-27	3.38E-26	0.742857143	-0.428843299
BP1026B_13272	ferredoxin--NADP reductase	265600	382982	361026	436	468106	479282	463112	609	0.00303913	0.003893495	1.396788991	0.482114093
BP1026B_13273	sensor kinase protein	5983	9612	7935	67	11434	13568	9615	98	0.006483815	0.008088311	1.462686567	0.548620654
BP1026B_13274	LuxR family DNA-binding response regulator	64754	78104	80986	87	100122	110739	96469	120	6.90E-04	9.23E-04	1.379310345	0.4639471
BP1026B_13275	amino acid permease	555153	674514	660663	967	690416	666885	689506	1048	0.840532394	0.855829701	1.083764219	0.116050922
BP1026B_13276	lipoprotein	41056	44054	45329	30	41914	40472	45338	10	1.11E-10	2.48E-10	0.7	0
BP1026B_13277	PepSY-associated TM helix family protein	65383	43345	49078	51	39114	34013	38615	36	2.41E-27	2.26E-26	0.705882353	-0.502500341
BP1026B_13278	flagellar biosynthetic protein FlhB domain-containing protein	12151	13299	12958	16	13516	15023	14854	18	5.27E-08	9.43E-08	1.125	0.169925001
BP1026B_13279	hypothetical protein	34028	23408	25885	87	24783	19779	20682	68	1.76E-21	1.01E-20	0.781609195	-0.355480655
BP1026B_13280	hypothetical protein	38993	31415	32498	22	31708	35325	28724	20	2.91E-11	6.85E-11	0.909090909	-0.137503524
BP1026B_13281	flagellar biosynthesis protein FlhI	380005	210655	251969	858	197988	167929	199047	575	2.04E-38	3.68E-37	0.67016317	-0.577415692
BP1026B_13282	flagellar protein FlhS	280160	369627	358270	772	391266	397516	369088	887	1.82E-06	2.92E-06	1.148963731	0.200333257
BP1026B_13283	predicted RNA	3086	5154	4922	438	6431	7908	4970	643	0.007845151	0.00970927	1.46803653	0.553887868
BP1026B_13284	flagellar hook-basal body complex protein	35316	48455	45271	125	47165	52316	53287	148	2.28E-06	3.64E-06	1.184	0.243669081
BP1026B_13285	flagellar MS-ring protein	213514	216519	218909	120	199688	190424	197532	109	1.71E-16	6.56E-16	0.908333333	-0.138706271
BP1026B_13286	flagellar motor switch protein G	402332	335856	466606	489	544514	579832	558613	586	0.588748029	0.612908315	1.198364008	0.261066199
BP1026B_13287	flagellar assembly protein H	50018	42106	44035	66	42391	42841	45085	63	2.63E-12	6.83E-12	0.954545455	-0.067114196
BP1026B_13288	flagellar protein export ATPase FlhI	89038	54452	57614	42	49493	42903	49486	30	1.25E-32	1.63E-31	0.714285714	-0.485426827
BP1026B_13289	flagellar export protein FljI	16199	20473	19080	41	19238	19166	18547	41	1.93E-11	4.61E-11	1	0
BP1026B_13290	flagellar hook-length control protein	59441	45959	53500	37	49927	45794	45651	33	1.01E-16	3.95E-16	0.891891892	-0.165059246
BP1026B_13291	GMC family oxidoreductase	25789	28702	26853	16	29089	29063	26903	17	5.16E-08	9.23E-08	1.0625	0.087462841
BP1026B_13292	Acyl-CoA dehydrogenase	60444	63411	59056	35	86696	86208	93381	52	0.002661665	0.003423936	1.485714286	0.571156701
BP1026B_13293	comiferyl aldehyde dehydrogenase	22964	17718	20678	14	17800	14199	17707	11	2.72E-22	1.68E-21	0.785714286	-0.347923303
BP1026B_13294	hypothetical protein	968	732	724	2	371	529	712	1	1.98E-06	3.16E-06	0.5	-1
BP1026B_13295	serine/threonine protein kinase	53105	29826	33443	39	29677	26669	28182	28	6.93E-23	4.52E-22	0.717948718	-0.478047297
BP1026B_13296	hypothetical protein	44967	74567	67503	292	90993	97331	94995	443	0.013967193	0.017013692	1.517122288	0.60133833
BP1026B_13297	major facilitator family transporter	20944	21926	17856	15	23921	19781	23239	17	5.96E-08	1.06E-07	1.133333333	0.180572246
BP1026B_13298	hypothetical protein	5587	6234	7014	7	6311	6372	6471	7	2.50E-09	5.02E-09	1	0
BP1026B_13299	hypothetical protein	11521	9730	11829	59	8548	8579	8372	45	1.42E-21	8.26E-21	0.762711864	-0.390789953
BP1026B_13300	aldo/keto reductase family oxidoreductase	263880	229348	238002	233	219363	217552	219991	209	3.21E-17	1.31E-16	0.896995708	-0.156827013
BP1026B_13301	Hemin uptake protein	63770	80119	73087	349	83423	86960	86024	412	5.10E-08	9.12E-08	1.180515759	0.239417301
BP1026B_13302	phytanoyl-CoA dioxygenase	291551	258693	293565	364	251122	230202	237785	326	3.59E-16	1.34E-15	0.895604396	-0.159066486
BP1026B_13303	predicted RNA	30310											

BP1026B 13324	exodeoxyribonuclease III	82584	125858	110881	138	124879	132391	122637	164	1.08E-06	1.76E-06	1.188405797	0.249027548
BP1026B 13325	hypothetical protein	56480	54379	55097	65	58185	58161	59101	69	7.48E-11	1.69E-10	1.061538462	0.086156644
BP1026B 13326	aspartyl/glutamyl-tRNA amidotransferase subunit B	149058	194532	177979	118	194890	196281	189665	131	7.50E-08	1.33E-07	1.110169492	0.150779952
BP1026B 13327	aspartyl/glutamyl-tRNA amidotransferase subunit A	92460	100000	96166	64	101407	100080	115483	70	3.07E-09	6.11E-09	1.09375	0.129283017
BP1026B 13328	aspartyl/glutamyl-tRNA amidotransferase subunit C	10882	11999	11492	38	13948	13231	14826	46	3.80E-06	5.97E-06	1.210526316	0.275634443
BP1026B 13329	rod shape-determining protein MreB	187348	269547	246571	224	310184	339785	325800	311	0.009575266	0.007474749	1.388392857	0.473415848
BP1026B 13330	rod shape-determining protein MreC	13288	13805	13451	12	16591	12278	14855	13	2.93E-09	5.85E-09	1.083333333	0.115477217
BP1026B 13331	rod shape-determining protein MreD	21207	17381	19205	37	17733	16851	16959	33	3.36E-17	1.57E-16	0.891891892	-0.165059246
BP1026B 13332	penicillin-binding protein 2	66084	76910	75247	30	78865	83206	77899	33	2.43E-10	5.27E-10	1.478330658	0.137503524
BP1026B 13333	rod shape-determining protein RodA	59158	66762	62462	54	60769	59062	63575	53	1.03E-14	3.37E-14	0.981481481	-0.026967048
BP1026B 13334	hypothetical protein	9269	3491	5280	7	3343	2902	2915	3	2.37E-35	3.72E-34	0.428571429	-1.222392421
BP1026B 13335	HpcH/HpaI aldolase family protein	15665	6051	8353	12	6121	4702	5814	7	7.09E-41	1.45E-39	0.583333333	-0.777607579
BP1026B 13336	6-pyruvoyl-tetrahydropterin synthase	49278	78960	69586	145	88992	103972	79780	200	3.32E-04	4.54E-04	1.379310345	0.4639471
BP1026B 13337	hypothetical protein	46237	37171	41966	66	44542	39373	42007	66	3.42E-10	7.37E-10	1	0
BP1026B 13338	hypothetical protein	211767	198533	202362	277	203477	189041	217392	276	2.67E-12	6.93E-12	0.996389892	-0.005217709
predicted RNA	-	10819	19657	15625	426	24562	25778	29922	743	0.531535744	0.556584722	1.744131455	0.80250878
BP1026B 13340	hypothetical protein	298357	522930	491304	923	587107	712979	572704	1317	0.28124809	0.304264595	1.426868906	0.512852793
predicted RNA	-	10458	17056	14168	578	18789	21584	21470	858	0.01072739	0.013164479	1.484429066	0.569908155
BP1026B 13341	hypothetical protein	125003	206798	185658	245	244809	299494	259591	381	0.254586333	0.276375253	1.555102041	0.637009248
BP1026B 13342	hypothetical protein	298744	533280	503033	1246	637408	741376	594921	1842	0.195339363	0.214962495	1.478330658	0.563968993
BP1026B 13343	hypothetical protein	121966	122913	124854	451	147172	147035	144643	535	5.28E-06	8.22E-06	1.186252772	0.246414558
BP1026B 13344	hypothetical protein	46622	75290	66640	193	91263	101377	93292	294	0.015174727	0.018430867	1.523316062	0.607215308
BP1026B 13345	Phage portal protein	5748	6444	4720	5	5427	6019	7105	5	2.65E-07	4.51E-07	1	0
BP1026B 13347	Thr tRNA	18908	32552	28313	349	39320	43779	45780	565	0.135696227	0.152051602	1.618911175	0.695023831
BP1026B 13348	ClpXP protease specificity-enhancing factor	109017	171810	154736	278	201454	226734	192788	396	0.024791272	0.029588973	1.424460432	0.510415547
BP1026B 13349	stringent starvation protein A	338338	509081	463718	714	592705	661618	616834	1019	0.280207246	0.303243282	1.427170868	0.513158072
BP1026B 13350	cytochrome c1	1844099	2329057	2251610	2821	2218432	2342996	2275455	3002	0.43659495	0.461745	1.064161645	0.089717311
BP1026B 13351	ubiquinol-cytochrome c reductase, cytochrome b	1470086	2216392	2028251	1377	1792558	2005998	1847086	1360	0.386822188	0.411725468	0.987654321	-0.017921908
BP1026B 13352	ubiquinol-cytochrome c reductase, iron-sulfur subunit	327064	336364	322783	529	278960	286232	287244	457	1.32E-16	5.10E-16	0.86389414	-0.211073557
BP1026B 13353	hypothetical protein	156660	111934	120118	168	132034	125912	131957	169	3.19E-12	8.21E-12	1.005952281	0.008562014
BP1026B 13354	DegQ protease	263043	256744	280591	220	283937	266337	272358	226	2.61E-10	5.65E-10	1.027272727	0.038819249
BP1026B 13355	twin arginine translocase protein C	158595	172217	159266	208	177946	192132	192245	239	1.25E-06	2.02E-06	1.149038462	0.20042709
BP1026B 13356	twin arginine translocase protein B	154177	175554	178333	320	200730	204747	184895	372	1.28E-06	2.08E-06	1.1625	0.217230716
BP1026B 13357	twin arginine translocase protein A	284918	369881	372820	1463	483786	546311	482485	2155	0.10532718	0.119280699	1.473000684	0.5587581
predicted RNA	-	43595	14541	27689	621	18167	13319	15019	336	2.89E-60	1.44E-58	0.541062802	-0.886132035
BP1026B 13358	MtaA/Hcf106 family protein	186036	239983	221843	590	276392	273436	297753	771	0.00195585	0.001569894	1.306796631	0.386015906
BP1026B 13359	hypothetical protein	190947	295891	273682	650	348346	394016	341027	925	0.007291358	0.009050643	1.423076923	0.509013647
BP1026B 13360	phosphoribosyl-ATP pyrophosphatase	34265	44213	37468	104	46277	46903	51639	130	6.34E-05	9.13E-05	1.25	0.321928095
BP1026B 13361	phosphoribosyl-AMP cyclohydrolase	81709	90448	92056	212	91718	87367	84999	212	3.92E-14	1.21E-13	1	0
BP1026B 13362	imidazole glycerol phosphate synthase subunit HisF	92224	55196	65553	91	50896	44490	51748	63	4.48E-35	6.88E-34	0.692307692	-0.530514717
[1-(5-phosphoribosyl)-5-[(S-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase													
BP1026B 13363	imidazole glycerol phosphate synthase subunit HisH	357253	483610	441297	653	463672	454895	461529	703	6.25E-08	1.11E-07	1.076569678	0.106441698
BP1026B 13364	imidazole glycerol phosphate synthase subunit HisI	65380	70911	72902	114	84971	81120	75825	132	1.08E-08	2.05E-08	1.157894737	0.211504105
BP1026B 13365	hypothetical protein	47986	62317	55245	88	64136	63409	66299	104	7.79E-08	1.38E-07	1.181818182	0.2410081
BP1026B 13366	imidazoleglycerol-phosphate dehydratase	93054	112447	112962	180	127722	129158	125897	216	1.99E-06	3.18E-06	1.2	0.263034406
BP1026B 13367	histidinol-phosphate aminotransferase	18782	16330	15107	15	14106	11693	14634	12	5.68E-21	3.14E-20	0.8	0.321928095
BP1026B 13368	histidinol dehydrogenase	116986	79966	88754	71	77581	66672	77145	55	4.64E-29	4.87E-28	0.774647887	-0.368387406
BP1026B 13369	ATP phosphoribosyltransferase catalytic subunit	56329	43556	45575	73	41179	35957	40623	59	3.66E-19	1.76E-18	0.808219178	-0.30718151
BP1026B 13370	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	87575	68251	78772	57	61561	58106	63692	45	8.63E-28	8.26E-27	0.789473684	-0.341036918
BP1026B 13371	BoA-like protein	19032	30178	28664	109	31063	36113	29408	135	1.75E-04	2.44E-04	1.23853211	0.308631272
BP1026B 13372	ABC transporter permease	35463	52275	49109	60	59118	58643	60572	78	1.21E-04	1.71E-04	1.3	0.378511623
BP1026B 13373	ABC transporter ATP-binding protein	60188	68713	69985	71	78325	84994	74619	85	1.14E-07	2.00E-07	1.197183009	0.259643817
BP1026B 13374	hypothetical protein	24104	24170	25337	90	24503	24313	26880	93	6.62E-09	1.28E-08	1.033333333	0.047305715
BP1026B 13375	hypothetical protein	289872	348820	360092	525	372464	384121	370466	593	5.91E-07	9.86E-07	1.12952381	0.175714682
BP1026B 13376	lipoprotein VacJ	167950	176503	180525	182	173073	154828	179836	176	1.48E-12	3.95E-12	0.967032967	-0.048363022
BP1026B 13377	ABC transporter substrate-binding protein	110390	145962	126181	227	153148	173377	167845	293	9.98E-04	0.001317482	1.290748899	0.368208367
BP1026B 13378	ABC transporter permease	104226	119185	114971	146	120961	130899	126079	164	1.74E-08	3.24E-08	1.12328767	0.167727446
BP1026B 13379	ABC transporter ATP-binding protein	85873	104088	98222	117	112890	116813	117944	141	1.84E-06	2.96E-06	1.205128205	0.269186633
BP1026B 13380	thiamine-phosphate pyrophosphorylase	64951	28286	33871	38	25755	23438	26208	22	4.16E-40	8.15E-39	0.578947368	-0.788495895
BP1026B 13381	thiazole synthase	212601	180851	179605	234	149876	143259	154586	182	1.15E-25	9.30E-25	0.777777778	-0.362570079
BP1026B 13382	sulfur carrier protein ThiS	2938	3477	3727	17	4027	4541	2576	18	2.43E-04	3.37E-04	1.058823529	0.08246216
BP1026B 13383	oxidoreductase, FAD-binding protein	212419	176981	177628	166	154031	144736	144695	130	1.02E-25	8.31E-25	0.78132523	-0.352671618
BP1026B 13384	ABC transporter ATP-binding protein	131850	141140	137765	77	126478	120471	131986	71	3.02E-16	1.14E-15	0.922077922	-0.117039421
predicted RNA	-	13221	996	2758	282	653	425	955	33	0	0	0.117021277	-0.095157233
BP1026B 13385	2'-5' RNA ligase	9534	1477	2666	8	1635	1759	2420	3	8.25E-45	2.10E-43	0.375	-1.415037499
BP1026B 13386	amino acid carrier protein	50533	27085	35303	24	28697	26254	28505	18	8.21E-22	4.87E-21	0.75	-0.415037499
BP1026B 13387	glutamate synthase subunit beta	165779	175358	174038	112	182821	177369	182252	118	2.39E-09	4.80E-09	1.053571429	0.075288127
BP1026B 13388	glutamate synthase, large subunit	460269	458495	458617	97	477038	464434	478256	102	2.56E-09	5.13E-09	1.030927835	0.043943348
BP1026B 13389	transposase	268649	191365	207375	311	166959	162535	179139	237	2.80E-26	2.38E-25	0.762057878	-0.392027521
BP1026B 13390	OmpW family outer membrane protein	351689	402829	424249	536	442914	412287	461460	599	9.45E-07	1.55E-06	1.117537313	0.160323002
BP1026B 13391	glycerophosphodiester phosphodiesterase	56388	56849	60860	76	48034	47927	46811	62	1.34E-21	7.84E-21	0.815789474	-0.293731203
BP1026B 13392	glycerol-3-phosphate transporter ATP-binding subunit	150872	169517	161318	148	139799	126850	148386	127	1.10E-19	5.51E-19	0.858108108	-0.220768679
BP1026B 13393	glycerol-3-phosphate transporter membrane protein	65649	62869	59554	74	60716	62555	62591	73	3.95E-14	1.21E-13	0.986486486	-0.019628807
BP1026B 13394	binding-protein-dependent transporter inner membrane component</												

predicted RNA	-	13814	22163	21236	762	28255	32084	23472	1117	0.023473771	0.020896781	1.465879265	0.551766283
BP1026B 13420	30S ribosomal protein S11	229533	221981	21710	554	256558	267472	28164	668	2.72E-05	4.02E-05	1.205776173	0.269962126
BP1026B 13421	30S ribosomal protein S13	375306	574975	511524	1331	738534	818903	746626	2098	0.024473975	0.029243693	1.576258452	0.656504107
BP1026B 13422	50S ribosomal protein L36	163477	262352	227551	1544	314968	362359	368214	2471	0.276326698	0.299250448	1.600388601	0.678422258
BP1026B 13423	translation initiation factor IF-1	352691	616663	548831	2309	718253	843227	720892	3473	0.049325017	0.057608678	1.504114335	0.588914238
BP1026B 13424	preprotein translocase subunit SecY	1461829	2276916	2073957	1438	2469517	2805064	2638317	1958	0.141456303	0.158166523	1.361613352	0.445317089
BP1026B 13425	50S ribosomal protein L15	388925	477068	449609	1007	507960	486749	555680	1188	0.012743117	0.015564985	1.179741807	0.238471153
BP1026B 13426	50S ribosomal protein L30	169599	143552	162087	825	148016	133619	169770	783	1.38E-13	4.04E-13	0.949090909	-0.075381812
predicted RNA	-	23074	22001	20077	1034	22532	20295	25865	1090	6.16E-09	1.19E-08	1.054158607	0.076091949
BP1026B 13427	50S ribosomal protein L18	342647	414627	386771	1041	481534	504533	505856	1358	0.002618412	0.003369679	1.30451489	0.383513411
BP1026B 13428	50S ribosomal protein L6	517994	803934	758253	1305	991602	1084747	918766	1880	0.010126581	0.012449119	1.440613027	0.526682855
BP1026B 13429	30S ribosomal protein S8	243380	360737	295250	711	336266	342016	370279	882	2.38E-05	3.53E-05	1.240506329	0.310929096
BP1026B 13430	30S ribosomal protein S14	204482	262910	264458	797	322441	366753	296403	1073	0.001471906	0.001922652	1.34629862	0.428998447
BP1026B 13431	50S ribosomal protein L5	320553	463310	410731	737	493626	514764	557030	966	0.229197451	0.250549761	1.310719132	0.39035857
BP1026B 13432	50S ribosomal protein L24	149151	245205	222097	664	322997	368160	320410	1091	0.431545115	0.456998765	1.643072289	0.716395955
BP1026B 13433	50S ribosomal protein L14	126551	210024	188140	473	298763	337954	299522	845	0.706563279	0.727699787	1.786469345	0.837111158
BP1026B 13434	30S ribosomal protein S17	574632	986689	897242	3001	1247751	1462848	1263815	4852	0.001729474	0.002251119	1.616794402	0.693136232
BP1026B 13435	50S ribosomal protein L29	320863	547627	519624	2372	679235	785676	670048	3649	0.10453078	0.118456948	1.53836425	0.621397141
BP1026B 13436	50S ribosomal protein L16	350744	447799	430556	982	545222	626276	518258	1350	0.615968844	0.639334235	1.374745418	0.459164478
BP1026B 13437	30S ribosomal protein S3	589569	924274	806571	965	1072795	1161625	1182927	1422	0.00734644	0.009111796	1.473575713	0.559320617
BP1026B 13438	50S ribosomal protein L22	352206	581614	511202	1459	702870	795303	710622	2231	0.068925893	0.079376888	1.529129541	0.612710663
BP1026B 13439	30S ribosomal protein S19	260249	432893	384778	1301	533187	608340	506161	1989	0.37438208	0.398958863	1.528823982	0.612422314
BP1026B 13440	50S ribosomal protein L2	545374	969394	602833	702	668554	634698	664231	792	0.948450676	0.955727264	1.128205128	0.1740294
BP1026B 13441	50S ribosomal protein L23	291599	517630	449865	1332	600363	683974	643693	2040	0.11038496	0.124805514	1.531531532	0.614975707
BP1026B 13442	50S ribosomal protein L4	324141	527744	468484	708	596935	674370	640623	1026	0.238750519	0.26400222	1.449152542	0.535209466
BP1026B 13443	50S ribosomal protein L3	300963	438081	412075	570	529074	555460	555402	813	0.367407167	0.379306284	1.426315789	0.512293433
BP1026B 13444	50S ribosomal protein S10	195994	209276	209602	656	262464	293812	262845	875	0.002466704	0.003179668	1.333841463	0.415587202
BP1026B 13445	elongation factor Tu	1631535	2332706	2171774	1717	2574394	2693888	2640416	2213	0.215882762	0.236531104	1.288875946	0.366113412
BP1026B 13446	elongation factor G	798198	1195648	1078576	486	1304357	1423241	1305012	639	0.031622325	0.037484958	1.314814815	0.394859617
BP1026B 13447	30S ribosomal protein S7	294710	496674	430609	864	555914	635901	605856	1272	0.195105317	0.214780378	1.472222222	0.557995453
BP1026B 13448	30S ribosomal protein S12	287644	471858	406403	1020	544827	619826	553935	1503	0.251328848	0.273122886	1.473529412	0.559275857
BP1026B 13449	ATP-dependent DNA helicase RecQ	329436	319572	318140	174	305780	310571	304202	166	1.51E-12	4.03E-12	0.954022989	-0.067904065
BP1026B 13450	DNA-directed RNA polymerase beta prime subunit	1356907	1836938	1681323	383	1928392	2012487	2027670	469	0.102830508	0.116660789	1.292454301	0.292243531
BP1026B 13451	DNA-directed RNA polymerase subunit beta	651821	882482	807100	190	940740	986001	959953	234	0.054778232	0.063657344	1.231578947	0.300509111
BP1026B 13453	50S ribosomal protein L7/L12	966079	1104691	1140399	2881	1267021	1262973	1392806	3486	0.089180768	0.101767746	1.209965329	0.25002909
BP1026B 13452	50S ribosomal protein L7/L12	795144	812065	892079	2776	944285	930446	899944	3182	0.107085472	0.121206514	1.146255602	0.196926268
BP1026B 13454	50S ribosomal protein L10	470387	772575	696423	1164	1012718	1144863	1012657	1904	0.001841022	0.002392335	1.635738832	0.70994242
BP1026B 13455	50S ribosomal protein L1	672861	759768	762630	1046	786568	778501	843675	1148	0.291871022	0.315104036	1.09751434	0.13423979
BP1026B 13456	50S ribosomal protein L11	307136	485164	412295	929	571107	600480	634155	1393	0.14700961	0.164053823	1.499461787	0.58444756
predicted RNA	-	28958	46727	41118	927	61979	74013	55707	1521	0.207955857	0.228125245	1.640776699	0.714378909
BP1026B 13457	transcription antitermination protein NusG	315194	530799	465229	783	654552	754214	690223	1253	0.066681264	0.076978929	1.600255428	0.678302202
BP1026B 13458	preprotein translocase subunit SecE	204592	332395	300008	732	412416	497268	466536	1204	0.117216434	0.132147926	1.644808743	0.717919838
BP1026B 13459	Trp tRNA	52838	73045	62187	824	71178	72035	89002	1018	9.19E-07	1.51E-06	1.235436893	0.305021319
BP1026B 13460	elongation factor Tu	1919107	2804822	2569766	2041	3099373	3281991	3129573	2661	0.437008096	0.462315167	1.30377266	0.382692328
BP1026B 13461	Thr tRNA	72815	119870	95899	1282	193653	207393	260894	2941	0.001934031	0.002507996	2.294071763	1.197910522
BP1026B 13462	Gly tRNA	113756	190463	187796	2216	378960	437410	273319	4908	0.001689291	0.002199729	2.214801444	1.147177368
BP1026B 13463	Tyr tRNA	13099	22858	19942	216	37509	45003	30285	437	0.547056917	0.572072537	2.023148148	1.016601967
BP1026B 13464	5S ribosomal RNA	1842276	2541390	1679461	17885	3066810	3074622	4061434	30096	0.067862343	0.078249935	1.682750909	0.750821636
BP1026B 13465	23S ribosomal RNA	407475	287313	210156	104	1826110	606838	342503	321	3.49E-12	8.96E-12	3.086538462	1.625899769
BP1026B 13466	hypothetical protein	30372	45181	38892	295	60418	68802	61182	491	0.266227032	0.288612211	1.66440678	0.73500807
BP1026B 13467	Ala tRNA	106256	1674474	137033	1801	224355	238955	237702	3074	0.982560194	0.986338061	1.706829539	0.771318984
BP1026B 13468	Ile tRNA	19951	28936	22969	311	41941	44244	39236	543	0.399895079	0.425062352	1.75980707	0.804037618
BP1026B 13469	16S ribosomal RNA	846448	220308	175908	272	3091798	680024	154345	861	1.41E-13	4.11E-13	3.165441176	1.662406586
BP1026B 13470	hypothetical protein	54937	82314	67560	583	121184	132828	124898	1079	0.935459739	0.943591552	1.85077187	0.888127076
BP1026B 13471	lipase/acylhydrolase	14887	13372	13192	10	13033	10766	11899	9	5.13E-16	1.89E-15	0.9	-0.152003093
BP1026B 13472	phenylacetate-CoA oxygenase subunit PaaA	118939	159646	148924	142	125364	116647	115123	119	4.88E-22	2.96E-21	0.838028169	-0.254929356
BP1026B 13473	phenylacetic acid degradation protein PaaB	24361	27067	24458	88	22491	26503	21259	82	8.77E-13	2.39E-12	0.931818182	-0.101879614
BP1026B 13474	phenylacetate-CoA oxygenase subunit PaaC	74355	81445	83918	99	55038	52706	56015	67	1.00E-37	1.75E-36	0.67676677	-0.56326743
BP1026B 13475	phenylacetic acid degradation protein PaaD	24209	8425	12931	24	5413	4274	5819	8	1.62E-125	2.20E-123	0.333333333	-1.584962501
BP1026B 13476	phenylacetate-CoA oxygenase/reductase subunit PaaK	152922	166155	162761	147	118673	112391	122107	108	2.93E-32	3.72E-31	0.734693878	-0.444784843
BP1026B 13477	hypothetical protein	62777	36257	45882	59	36373	35346	34801	43	7.70E-24	5.40E-23	0.728813559	-0.456378295
BP1026B 13478	TetR family transcriptional regulator	57643	64733	55979	99	62485	69188	60105	106	9.43E-11	2.11E-10	1.070770701	0.098563834
BP1026B 13479	acetyltransferase	110461	142382	135589	199	214037	217370	213710	331	0.652157186	0.674437519	1.663166583	0.663462786
BP1026B 13480	transcriptional regulator	52835	89387	74837	160	90761	97089	89949	205	1.13E-05	1.72E-05	1.28125	0.357552005
BP1026B 13481	4-hydroxyphenylpyruvate dioxygenase	25624	36111	30794	28	37865	41412	38713	35	4.19E-04	5.70E-04	1.25	0.321928095
BP1026B 13482	outer membrane protein	268	97	100	0	22	72	255	0	0.145947369	0.162922213	#DIV/0!	#DIV/0!
BP1026B 13483	indolepyruvate ferredoxin oxidoreductase	89279	85717	84201	24	86261	86477	86066	24	3.77E-14	1.16E-13	-1	0
BP1026B 13484	malic enzyme	272913	252839	262863	113	266179	254658	263621	112	1.42E-11	3.44E-11	0.991150442	-0.01282404
BP1026B 13485	orotate phosphoribosyltransferase	103445	125673	115889	167	136004	152468	145054	210	8.55E-05	1.22E-04	1.25748503	0.330541225
BP1026B 13486	phosphatidylethanolamine-binding protein	15300	6677	8967	21	7354	6459	7587	15	1.48E-27	1.41E-26	0.714285714	-0.485426827
BP1026B 134													

BP1026B 13516	hypothetical protein	31201	49343	44137	166	62310	69487	56301	251	0.026694728	0.031782095	1.512048193	0.596504123
BP1026B 13517	pyridoxamine 5'-phosphate oxidase family protein	38918	23618	26498	34	26616	28009	25349	30	9.62E-13	2.61E-12	0.882352941	-0.180572246
BP1026B 13518	amino acid ABC transporter permease	10946	7827	8205	7	7647	6326	6390	5	1.05E-21	6.15E-21	0.714285714	-0.485426827
BP1026B 13519	putative extracellular ligand binding protein	110167	92471	88835	85	73758	75935	79328	66	3.08E-28	3.03E-27	0.764705888	-0.364996817
BP1026B 13520	2-nitropropane dioxygenase	17747	8514	9300	10	8704	7621	7281	7	1.41E-31	1.71E-30	0.7	-0.514573173
BP1026B 13522	diene lactone hydrolase	202455	206096	233073	308	209301	187905	193962	284	1.15E-15	4.11E-15	0.922077922	-0.117039421
BP1026B 13521	6-aminohexanoate-cyclic-dimer hydrolase	106428	108579	108024	72	99905	103146	102316	68	3.17E-15	1.08E-14	0.944444444	-0.08246216
BP1026B 13523	5,10-methylenetetrahydrofolate reductase	376931	304556	321509	402	307985	282663	316168	363	2.00E-14	6.33E-14	0.902985075	-0.147225953
BP1026B 13524	hypothetical protein	148387	222519	198425	536	256029	291382	277140	776	0.039591875	0.046605803	1.447761194	0.533823652
BP1026B 13525	S-adenosyl-L-homocysteine hydrolase	1279793	1677153	1600955	1068	1930470	1962221	1955919	1370	0.059146877	0.068518087	1.282771536	0.359264246
BP1026B 13526	flagellar biosynthesis sigma factor	174058	165214	168567	231	177424	168653	186785	242	2.25E-09	4.52E-09	1.047619048	0.067114196
BP1026B 13527	flagellar biosynthesis protein FlhG	57919	39363	42399	57	36771	33131	45485	47	9.11E-18	3.89E-17	0.824561404	-0.278301162
BP1026B 13528	flagellar biosynthesis regulator FlhF	203162	201388	215092	117	209233	200854	216197	119	1.09E-11	2.67E-11	1.017094017	0.024453044
BP1026B 13529	flagellar biosynthesis protein FlhA	253927	252155	256571	120	252916	248929	260338	120	2.11E-11	5.02E-11	1	0
BP1026B 13530	flagellar biosynthesis protein FlhB	81045	75734	71901	63	80351	86232	80758	68	5.39E-11	1.24E-10	1.079365079	0.110182918
BP1026B 13531	DNA binding protein	73883	71882	69438	143	75657	71267	74872	147	1.33E-12	3.57E-12	1.027972028	0.039801008
predicted RNA	-	77334	2618	9447	805	2631	1088	3188	62	0	0	0.077018634	-3.698648663
BP1026B 13532	lipoprotein	406957	343512	351904	281	299857	268950	299671	221	8.91E-21	4.83E-20	0.786476868	-0.346523761
BP1026B 13533	hypothetical protein	121715	106313	109920	223	109684	105059	116613	219	2.61E-13	7.46E-13	0.98206278	-0.02611284
BP1026B 13534	chemotaxis regulator CheZ	239222	142832	162349	255	140476	128177	147605	195	1.82E-28	1.82E-27	0.764705882	-0.387025123
BP1026B 13535	chemotaxis protein CheY	348965	460152	407752	1024	562457	598775	525886	1420	0.57773183	0.602440946	1.3861875	0.47165214
predicted RNA	-	28132	1786	2790	242	1223	915	1867	29	0	0	0.119834711	-3.060882242
predicted RNA	-	641578	283977	375199	2477	315894	223979	224893	1456	2.24E-46	6.10E-45	0.587807832	-0.766583513
BP1026B 13536	chemotaxis-specific methyltransferase	554098	465442	478701	456	486477	490917	482080	444	6.16E-11	1.41E-10	0.973684211	-0.038474148
BP1026B 13537	chemoreceptor glutamine deamidase CheD	282333	281944	284238	401	280699	249231	259685	373	3.86E-14	1.19E-13	0.930174564	-0.104426606
BP1026B 13538	chemotaxis protein methyltransferase	716389	851855	800206	836	870834	853122	871752	915	0.197717929	0.217274735	1.094497608	0.130268801
BP1026B 13539	methyl-accepting chemotaxis protein I	1875793	1227368	1359441	731	1187652	1068397	1156953	559	0.875920102	0.889116371	0.764705882	-0.387023123
BP1026B 13540	chemotaxis protein CheW	739800	925942	892412	1614	1043365	1049426	1060082	1990	0.051342757	0.059831452	1.232961586	0.302127852
BP1026B 13541	chemotaxis protein CheA	1823130	2008750	1966704	841	2036201	1949925	2162027	891	0.332191906	0.356179754	1.059453032	0.083319631
BP1026B 13542	chemotaxis two-component response regulator CheY1	160897	159829	165724	474	180360	191911	175415	533	4.56E-07	7.66E-07	1.124472574	0.169248474
BP1026B 13543	flagellar motor protein MotB	714481	842476	792023	765	889548	922246	882093	877	0.12437651	0.139817583	1.146405229	0.197117095
BP1026B 13544	flagellar motor protein MotA	433866	459993	442491	541	625905	658243	598873	763	0.32203104	0.345710737	1.140351201	0.496054463
BP1026B 13545	transcriptional activator FlhC	336454	485183	456073	771	613007	666104	633947	1155	0.153356137	0.170649895	1.498054475	0.583090086
BP1026B 13546	transcriptional activator FlhD	516279	745756	695295	2032	803664	879961	853321	2634	0.058855492	0.068205754	1.296259483	0.374354943
BP1026B 13547	glycoside hydrolase family protein	25913	32210	32027	28	38260	37890	40228	36	6.45E-04	8.64E-04	1.285714286	0.362570079
BP1026B 13549	H-NS histone family protein	38830	56467	48808	161	60305	68600	52990	203	1.64E-05	2.45E-05	1.260869565	0.334419039
BP1026B 13548	hypothetical protein	14853	26130	21500	100	28187	29928	25010	133	0.001389436	0.001816442	1.33	0.411426246
BP1026B 13550	hypothetical protein	467	945	425	4	1686	1990	1232	11	1.85E-09	3.74E-09	2.75	1.459431619
BP1026B 13551	aquaporin Z	75632	41630	51041	79	41344	34968	45376	57	1.85E-27	1.74E-26	0.721518987	-0.470890734
BP1026B 13552	cof family hydrolase	122847	106468	109545	135	112475	106906	115164	134	5.50E-13	1.52E-12	0.992592593	-0.010726407
BP1026B 13553	BadF/BadG/BcrA/BcrD family ATPase	22753	13318	16180	18	10355	9630	11543	11	1.23E-38	2.26E-37	0.611111111	-0.710493383
BP1026B 13554	DNA-3-methyladenine glycosylase I	128274	121907	125736	205	105616	101327	123933	181	1.26E-18	5.78E-18	0.882926829	-0.179634212
predicted RNA	-	148884	179972	173811	646	247662	258799	234468	953	0.080641383	0.092393291	1.475232198	0.560942049
BP1026B 13555	flagellin	12186143	11944666	12860403	10567	13079583	12916902	12759854	11070	8.48E-05	1.21E-04	1.047601022	-0.067089372
predicted RNA	-	74945	95514	89250	5410	94582	82602	98321	5739	2.61E-11	6.16E-11	1.060813309	0.08517078
BP1026B 13556	flagellar hook-associated protein	1050682	990376	1017265	670	1033480	1011082	951277	656	0.34536891	0.36936023	0.979104478	-0.030465281
BP1026B 13557	hypothetical protein	260244	291683	277054	877	342398	362064	342566	1107	5.29E-05	7.67E-05	1.262256797	0.336006474
BP1026B 13558	hypothetical protein	516095	339241	389376	177	382843	349692	373118	158	5.15E-14	1.57E-13	0.892655367	-0.163824802
BP1026B 13559	aminotransferase	202297	276757	259082	214	318371	327660	307806	276	2.78E-04	3.83E-04	1.289719626	0.36705747
BP1026B 13560	3-oxoacyl-(acyl-carrier-protein) synthase III	51418	34860	40412	40	37731	35331	37967	35	1.78E-14	5.66E-14	0.875	-0.192645078
BP1026B 13561	hypothetical protein	42741	47458	45923	204	47316	40226	49926	206	1.01E-10	2.25E-10	1.009803922	0.014075185
BP1026B 13562	3-oxoacyl-ACP synthase	125657	98076	107414	103	96350	93301	92056	88	7.39E-22	4.41E-21	0.854368932	-0.227068909
BP1026B 13563	short chain dehydrogenase/reductase family oxidoreductase	85230	48941	55236	83	47000	37238	46322	57	5.73E-33	7.78E-32	0.686746988	-0.542149417
BP1026B 13564	hexapeptide transferase family protein	232722	185424	205157	328	194474	183902	199066	304	3.18E-15	1.08E-14	0.926829268	-0.109624491
BP1026B 13565	Rieske (2Fe-2S) domain-containing protein	260055	275439	263053	249	280711	290399	310190	275	4.27E-08	7.72E-08	1.104417621	-0.123258576
BP1026B 13566	hypothetical protein	273475	472460	419921	570	493313	578199	507408	772	0.494500947	0.519628196	1.354385965	0.437638928
predicted RNA	-	32676	42142	38357	739	40373	37915	47366	821	4.27E-07	7.19E-07	1.110960758	0.515807858
BP1026B 13567	putative outer membrane protein	196889	340648	312893	705	398299	453313	401854	1039	0.012432816	0.015194856	1.473758865	0.559500492
BP1026B 13568	LysE family protein	10619	12478	11589	18	12018	13207	12808	10	2.81E-08	5.14E-08	1.111111111	0.152003093
BP1026B 13569	acid phosphatase	109231	100962	104483	63	95826	94978	97679	57	3.01E-17	1.23E-16	0.904761905	-0.144389909
BP1026B 13570	lipoprotein	39084	30525	33799	51	28419	27936	30614	42	4.30E-15	1.44E-14	0.823529412	-0.280107919
BP1026B 13571	hypothetical protein	17978	14809	17197	38	18943	17240	16377	40	1.48E-10	3.25E-10	1.052631579	0.074000581
BP1026B 13572	CsgG family protein	46408	68728	60207	86	72168	76391	76145	110	1.02E-05	1.55E-05	1.279069767	0.355094959
BP1026B 13573	putative lipoprotein	11222	15337	15193	29	19376	19659	20006	41	0.001764295	0.002295966	1.413793103	0.499571009
BP1026B 13574	3-oxoadipate enol-lactone hydrolase family protein	185382	114501	124821	167	106403	97807	118380	127	1.11E-28	1.13E-27	0.60479042	-0.395019606
BP1026B 13575	methyl-accepting chemotaxis protein	503748	432718	433641	251	450117	439773	449353	245	1.17E-10	2.60E-10	0.976095618	-0.034905615
BP1026B 13576	hypothetical protein	1810	2617	2883	12	3454	4823	3173	18	0.72585048	0.746692373	1.5	0.584962501
BP1026B 13577	hexose oxidase	14824	19430	19354	10	19448	20165	18629	11	2.98E-09	5.93E-09	1.1	0.137503524
BP1026B 13578	chitin binding domain-containing protein	13614	19659	19451	31	25043	26270	24911	45	0.016607117	0.020100482	1.451612903	0.537656786
BP1026B 13580	hypothetical protein	58625	53404	51481	218	76749	81424	71671	807	9.64E-04	0.001273659	1.408256881	0.493910521
BP1026B 13582	gp30	221335	369557	325516	282	416288	469882	438420	408	0.007008044	0.008715965	1.446808511	0.53287399
BP1026B 13583	gp29	121631	204005	176334	292	250664	274533	256879	454	0.293731388	0.316894091	1.554794521	0.636723928
BP1026B 13584	hypothetical protein	46599	75913	67916	69	85118	105409	87412	100	0.003605324			

BP1026B 13613	Phage-related tail fiber protein	7483	7750	8364	3	7920	7248	6408	3	1.79E-13	5.15E-13	1	0
BP1026B 13614	phage tail fiber assembly protein	1361	797	1211	1	826	366	967	1	3.31E-08	6.04E-08	1	0
BP1026B 13615	Phage tail sheath monomer	2818	2928	2790	2	2765	2008	2191	1	7.90E-09	1.52E-08	0.5	-1
BP1026B 13616	Major tail tube protein	5244	7469	6190	12	9360	9895	9111	18	0.013413208	0.016364323	1.5	0.584962501
BP1026B 13617	putative phage tail protein	1812	1836	1860	5	2166	2334	2691	6	0.191280631	0.210866367	1.2	0.263034406
BP1026B 13618	hypothetical protein	978	1369	1494	11	1949	1961	1111	14	0.614641329	0.638062055	1.272727273	0.347923303
BP1026B 13619	bacteriophage tail protein	9087	10557	11186	3	11674	11352	12041	3	4.38E-07	7.36E-07	1	0
BP1026B 13620	Phage-related tail protein	1003	1005	775	2	694	684	478	1	1.10E-06	1.79E-06	0.5	-1
BP1026B 13621	hypothetical protein	43771	65473	55846	50	71757	80054	77980	69	6.05E-04	8.13E-04	1.38	0.464668267
BP1026B 13622	hypothetical protein	124138	208635	178479	189	223997	265133	235703	268	0.023219689	0.027813911	1.417989418	0.503846766
BP1026B 13623	gp22, putative phage-encoded membrane protein	86485	148683	127999	162	182557	206507	181240	255	0.274461	0.297281353	1.574074074	0.654503434
BP1026B 13624	putative phage DNA-binding protein	383236	593548	532529	1164	743470	861913	775052	1836	0.015954252	0.01933643	1.577319588	0.657475001
BP1026B 13625	hypothetical protein	3317	4802	5065	18	5850	6824	5888	26	0.003318405	0.004237442	1.444444444	0.530514717
BP1026B 13626	hypothetical protein	3492	5079	4965	15	5153	6522	6061	19	5.40E-04	7.29E-04	1.266666667	0.341036918
BP1026B 13627	phage transcriptional activator	1616	2162	2074	7	2527	2779	2648	10	0.268501753	0.290977513	1.428571429	0.514573173
BP1026B 13629	hypothetical protein	2183	1646	2321	9	1745	1475	1329	6	6.57E-09	1.27E-08	0.666666667	-0.584962501
BP1026B 13628	hypothetical protein	1892	1480	1888	8	1349	1788	1797	8	3.38E-04	4.63E-04	1	0
BP1026B 13630	putative phage-encoded membrane protein	1198	1414	2393	8	2175	2402	1599	10	0.135958352	0.152290854	1.25	0.321928095
BP1026B 13631	hypothetical protein	2150	1611	1929	7	1121	1308	1431	5	9.07E-11	2.03E-10	0.714285714	-0.485426827
BP1026B 13632	hypothetical protein	729	1708	1143	5	1148	1358	775	5	0.001601929	0.002088139	1	0
BP1026B 13633	hypothetical protein	1082	884	1233	2	927	1815	843	3	0.142896724	0.159720099	1.5	0.584962501
BP1026B 13634	hypothetical protein	908	515	660	2	365	370	348	1	6.08E-11	1.39E-10	0.5	-1
BP1026B 13635	hypothetical protein	17525	16303	16137	5	14466	15870	16248	5	1.05E-14	3.41E-14	1	0
BP1026B 13636	Phage integrase	42954	59621	55107	53	61854	65128	63339	64	7.44E-07	1.23E-06	1.20754717	0.272079545
BP1026B 13638	Arg tRNA	4017	5192	5522	64	6385	7198	6376	87	7.05E-04	9.42E-04	1.539375	0.442943496
BP1026B 13639	cytochrome c family protein	82789	82478	89023	94	78691	78110	75438	86	1.66E-18	7.53E-18	0.914893617	-0.128324097
BP1026B 13641	ATP-dependent DNA helicase Rep	136402	165856	160753	73	168316	164146	165806	79	3.20E-08	5.83E-08	1.082191781	0.113956189
BP1026B 13642	hypothetical protein	17332	4338	6704	11	4051	3212	4037	4	3.10E-09	2.07E-07	0.363636364	-1.459431619
BP1026B 13643	GDSL-like lipase/acylhydrolase domain-containing protein	9404	3056	4198	7	2139	2007	2626	3	1.24E-54	4.87E-53	0.428571429	-1.222394221
BP1026B 13644	Gfo/Idh/MocA family oxidoreductase	65919	47400	52374	50	46541	42922	44519	40	1.55E-21	8.94E-21	0.8	-0.321928095
BP1026B 13645	lipoprotein	14316	9912	10659	32	8304	8980	10543	25	4.07E-19	1.94E-18	0.78125	-0.35614381
BP1026B 13646	hypothetical protein	70222	84273	84506	169	93877	103238	86685	200	1.93E-07	3.32E-07	1.183431953	0.242976753
BP1026B 13647	glycine cleavage system aminomethyltransferase T	176021	192864	186128	174	187374	181235	179546	172	5.27E-12	1.33E-11	0.988505747	-0.016678741
BP1026B 13648	glycine cleavage system H protein	192017	242566	232027	583	246462	233816	236088	626	9.38E-09	1.79E-08	1.073756432	0.102666774
BP1026B 13649	hypothetical protein	6847	6793	4915	57	6263	8321	7047	66	1.43E-06	2.30E-06	1.157894737	0.211504105
BP1026B 13650	glycine dehydrogenase	476669	433446	436408	154	403976	400470	398280	138	1.25E-13	3.67E-13	0.896103896	-0.158262084
BP1026B 13651	hypothetical protein	72344	65160	66778	60	59793	56195	59119	52	4.85E-21	2.69E-20	0.866666667	-0.206450877
BP1026B 13652	L-serine ammonia-lyase	154036	109039	122881	92	108076	103933	97463	74	9.96E-25	7.46E-24	0.804347826	-0.31410859
BP1026B 13653	hypothetical protein	34227	29852	31675	27	33181	35748	36179	29	8.51E-07	1.40E-06	1.074074074	0.103093493
BP1026B 13654	thiamine pyrophosphate protein	100996	109412	100104	60	109006	112766	103782	63	9.77E-11	2.19E-10	1.05	0.070389328
BP1026B 13655	hypothetical protein	90059	89788	89580	84	75638	73364	79994	71	1.09E-22	7.00E-22	0.845238095	-0.242570303
BP1026B 13656	AraC family transcriptional regulator	6796	6614	6738	6	5659	7074	5727	5	3.68E-12	9.41E-12	0.833333333	-0.263034406
BP1026B 13657	acetaldehyde dehydrogenase	42702	43299	42301	26	27377	26403	29631	17	5.20E-31	6.09E-30	0.653846154	-0.612976877
BP1026B 13658	hypothetical protein	956	110	634	2	444	351	195	1	2.65E-07	4.50E-07	0.5	-1
BP1026B 13659	ethanolamine ammonia-lyase small subunit	11475	4388	5247	8	3471	3632	4140	4	4.25E-34	6.16E-33	0.5	-1
BP1026B 13660	ethanolamine ammonia-lyase, large subunit	46173	45834	46992	33	49582	48300	48922	35	1.45E-09	2.97E-09	1.060606061	0.084888898
BP1026B 13661	ethanolamine permease	25676	24373	24412	17	23721	21784	23203	16	3.91E-13	1.10E-12	0.941176471	-0.087462841
BP1026B 13662	acyltransferase family protein	21689	8759	11559	11	8566	7882	7896	6	2.36E-44	5.78E-43	0.545454545	-0.874469118
BP1026B 13663	hypothetical protein	281	143	215	1	51	116	0	0	1.99E-14	6.27E-14	0	#NUM!
BP1026B 13664	hypothetical protein	223988	194649	201031	136	183992	182244	207410	126	3.42E-15	1.16E-14	0.926470588	-0.110182918
BP1026B 13665	hypothetical protein	8974	2446	3572	12	2689	1618	2664	5	4.09E-40	8.03E-39	0.416666667	-1.263034406
BP1026B 13666	cadmium-translocating P-type ATPase	119389	80617	90485	38	91146	86594	85130	34	4.94E-19	2.34E-18	0.894736842	-1.60464672
BP1026B 13667	Cd(II)/Pb(II)-responsive transcriptional regulator	29977	42714	43172	89	51479	56413	47170	119	9.27E-04	0.001226092	1.337078652	0.419084332
BP1026B 13668	PadR transcriptional regulator	15041	20364	18414	27	20820	24636	23924	36	2.43E-04	3.37E-04	1.333333333	0.415037499
BP1026B 13669	oxidoreductase	2366	1562	1786	8	1288	1134	1346	5	1.66E-11	3.99E-11	0.625	-0.678071905
BP1026B 13670	hypothetical protein	689	863	411	2	465	471	419	1	2.62E-05	3.87E-05	0.5	-1
BP1026B 13671	lysine-arginine-ornithine-binding periplasmic protein	10328	11394	12166	14	8795	9816	8935	11	3.05E-18	1.35E-17	0.785714286	-0.347923303
BP1026B 13672	aminotransferase	15410	7286	9185	9	6054	4560	6770	5	1.11E-43	2.65E-42	0.555555556	-0.847996907
BP1026B 13673	TetR family transcriptional regulator	11284	12895	14537	23	13406	12109	12206	22	1.14E-11	2.79E-11	0.956521739	-0.064130337
BP1026B 13674	acyl-CoA dehydrogenase	19046	22647	21399	12	19085	23524	18583	12	9.11E-13	2.48E-12	1	0
BP1026B 13675	long-chain fatty acid CoA ligase (AMP-binding)	6720	5989	4706	3	4777	4933	5656	3	8.25E-12	2.04E-11	1	0
BP1026B 13676	putative extracellular ligand binding protein	1993922	2286111	2315342	1928	2168710	2156515	2128706	1887	0.56480258	0.589645613	0.97873444	-0.031010629
predicted RNA	-	12164	19299	18600	667	22923	28693	17873	926	0.00344037	0.004384251	1.388305847	0.473325432
BP1026B 13677	trifunctional transcriptional regulator/proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase	499111	440198	437257	116	403172	385466	402565	101	6.27E-15	2.08E-14	0.870689655	-0.199769512
BP1026B 13678	hypothetical protein	62625	83219	72168	424	92745	96056	91854	547	1.72E-05	2.58E-05	1.29009434	0.367476568
BP1026B 13679	primosome assembly protein PriA	96900	48575	54377	29	43387	41106	45189	19	4.47E-38	7.93E-37	0.655172414	-0.610053482
BP1026B 13680	uroporphyrinogen decarboxylase	165363	161909	158608	147	181127	179028	163201	159	2.67E-08	4.89E-08	1.081632653	0.11321061
BP1026B 13681	cyclohexadienyl dehydratase	36899	56204	51811	61	54404	51960	56081	68	3.68E-08	6.68E-08	1.114754098	0.156725504
BP1026B 13683	CoA-binding domain-containing protein	2068	1110	1057	4	1140	1022	1267	3	1.36E-05	2.05E-05	0.75	-0.415037499
BP1026B 13682	hypothetical protein	1056	2402	1557	4	2485	3038	2511	6	0.635920185	0.658841911	1.5	0.584962501
BP1026B 13684	AMP-binding protein	11420	11547	11646	6	12455	12101	13747	7	4.30E-08	7.77E-08	1.166666667	0.222924221
BP1026B 13685	F0F1 ATP synthase subunit epsilon	273643	383070	354247	791	405860	411321	428584	974	5.00E-05	7.25E-05	1.231352718	0.300244078
BP1026B 13686	F0F1 ATP synthase subunit beta	1301748	1918975	1767115	1191	2000824	2084385	2075067	1471	0.111163043	0.12566257	1.235096558	0.304623833
BP1026B 13687	F0F1 ATP synthase subunit gamma	593112	842339	752659	832	900607	934844	949211	1059	0.046319472	0.054250058	1.272836538	0.348047156
BP1026B 13688	F0F1 ATP synthase subunit alpha	1991829	2418665	2408475	1474	2540547	2529648	2550116	1647	0.468392453	0.494015672	1.117367707	0.160104031
BP1026B 13689	F0F1 ATP synthase subunit delta	352115	409794	399247	716	424155	434255	439863	801	1.08E-06	1.76E-06	1.118715084	0.161842655
BP1026B 13690	F0F1 ATP synthase subunit B	549644	683296	676043	1351	768945	746293	761505	1611	0.295366088	0.318548005	1.192450037	0.253928819
BP1													

BP1026B_I3711	methylmalonate-semialdehyde dehydrogenase	466362	483446	481774	312	321500	322613	321402	210	1.07E-30	1.23E-29	0.673076923	-0.571156701
BP1026B_I3712	LysR family transcriptional regulator	37547	18622	21252	28	17964	15929	15142	18	1.54E-41	3.27E-40	0.642857143	-0.637429921
BP1026B_I3713	hypothetical protein	7139	5161	3875	16	3459	3750	3600	11	4.89E-19	2.32E-18	0.6875	-0.540568381
BP1026B_I3714	adenylate cyclase	360530	321692	351228	648	340072	329433	327676	625	1.10E-11	2.70E-11	0.964506173	-0.052137623
BP1026B_I3715	AsnC family transcriptional regulator	84891	123901	121939	224	132694	149506	119967	272	6.37E-06	9.85E-06	1.214285714	0.280107919
BP1026B_I3716	phenylalanine 4-monooxygenase	67059	79425	73844	82	63771	65484	66351	72	1.13E-19	5.67E-19	0.87804878	-0.187627003
BP1026B_I3717	pterin-4-alpha-carbinolamine dehydratase	128013	195399	171779	539	233873	257403	249665	807	0.123514542	0.138898442	1.497217069	0.582283401
predicted RNA	-	36178	60079	51514	623	69156	75546	80068	948	0.024677549	0.02948132	1.521669342	0.605654896
BP1026B_I3718	hypothetical protein	98631	158190	132715	562	179084	192416	194707	817	0.050929216	0.05938267	1.453736655	0.539765948
BP1026B_I3719	DNA-binding response regulator	529949	614989	627769	852	484064	463053	476526	684	4.13E-18	1.81E-17	0.802816901	-0.316875105
predicted RNA	-	28945	2399	2552	251	1756	1425	1998	38	0	0.151394422	-2.723616041	
BP1026B_I3720	sensor histidine kinase	59654	41887	45406	32	43636	36584	40881	27	1.26E-18	5.79E-18	0.84375	-0.245112498
BP1026B_I3721	SET domain-containing protein	118978	183606	162986	302	201022	208508	194256	392	6.90E-04	9.23E-04	1.298013245	0.376305105
BP1026B_I3722	oxidoreductase FAD/FMN-binding protein	175321	107696	130944	123	99727	94095	104382	89	8.15E-34	1.16E-32	0.723577236	-0.466781074
BP1026B_I3723	glutamine amidotransferase	275200	248090	239064	357	215450	202591	233684	305	3.61E-20	1.87E-19	0.854341737	-0.227114832
BP1026B_I3724	MarR family transcriptional regulator	297326	436372	408420	667	445108	480227	429836	792	1.60E-05	2.41E-05	1.187406297	0.247813669
												#DIV/0!	
Synonym	Product	Normalized Co	Normalized Co	Normalized Co	Expression Em	Normalized Co	Normalized Co	Normalized Co	Expression BP	pValue Empty	qValue Empty	#VALUE!	#VALUE!
BP1026B_I0001	hypothetical protein	55027	80260	73177	58	106706	110732	94572	87	0.014942073	0.01815885	1.5	0.584962501
BP1026B_I0002	phage integrase family protein	58885	78986	73562	67	88153	88440	94285	86	9.40E-06	1.44E-05	1.28358209	0.360175564
BP1026B_I0003	hypothetical protein	21217	17117	21103	52	16292	15503	22276	47	2.09E-16	7.95E-16	0.903846154	-0.145850866
BP1026B_I0004	DNA-binding protein	21873	28273	25759	41	35023	32002	32612	54	0.001156317	0.001519925	1.317073171	0.397335498
BP1026B_I0005	2-amino-3-ketobutyrate coenzyme A ligase	213996	200161	207824	172	224586	228631	248696	194	2.08E-07	3.56E-07	1.127996977	0.173648087
BP1026B_I0006	L-threonine 3-dehydrogenase	256792	336399	308446	291	331185	358166	342888	333	4.67E-07	7.84E-07	1.144329897	0.194503024
BP1026B_I0007	hypothetical protein	15503	12792	14057	21	12891	12023	12423	19	2.00E-15	6.96E-15	0.904761905	-0.144389909
BP1026B_I0008	TetR family transcriptional regulator	34275	27414	27454	48	32233	30844	36361	53	2.05E-06	3.28E-06	1.104166667	0.142957954
BP1026B_I0009	hypothetical protein	41111	47731	48283	95	53581	54476	54770	113	1.73E-06	2.78E-06	1.189473684	0.250323354
BP1026B_I0010	succinylglutamate desuccinylase	24784	17725	19109	20	19093	18476	17981	18	8.80E-17	3.46E-16	0.9	-0.152003093
BP1026B_I0012	tartrate dehydrogenase	23053	21685	21734	18	21789	20701	22999	18	1.87E-11	4.47E-11	1	0
BP1026B_I0011	LysR family transcriptional regulator	19955	10769	12164	15	8801	9038	12736	11	4.28E-25	3.31E-24	0.733333333	-0.447458977
BP1026B_I0013	hypothetical protein	25386	27378	25180	38	30750	32098	33568	47	1.54E-04	2.16E-04	1.236842103	0.306661338
BP1026B_I0014	hypothetical protein	387	421	351	2	551	222	331	2	0.125029133	0.140475623	1	0
BP1026B_I0015	glutathione S-transferase	97635	117747	116307	177	125078	128451	121545	200	3.93E-08	7.12E-08	1.129943503	0.176256064
BP1026B_I0016	hypothetical protein	1024	786	701	1	818	514	638	1	3.40E-04	4.66E-04	1	0
BP1026B_I0017	patatin-like phospholipase	66561	58625	63987	50	59985	53024	61628	46	7.09E-17	2.81E-16	0.92	-0.120294234
BP1026B_I0018	3-hydroxybutyrate dehydrogenase	121658	140839	140198	170	137163	145535	134152	176	1.36E-10	3.01E-10	1.035294118	0.050040682
BP1026B_I0019	acetate decarboxylase	19636	27964	25540	32	30676	36133	29440	43	0.001213746	0.001591407	1.34375	0.426264755
BP1026B_I0020	PAP2 family protein	10561	6722	7620	13	6667	6412	8048	11	2.68E-16	1.01E-15	0.846153846	-0.2410081
BP1026B_I0021	hypothetical protein	25709	28174	27048	113	24614	20423	25185	98	2.87E-15	9.82E-15	0.867256637	-0.205469118
BP1026B_I0022	siderophore-interacting protein	10517	10069	10145	12	9961	10266	9655	12	5.91E-11	1.35E-10	0.666666667	-0.584962501
BP1026B_I0023	PadR-like family regulatory protein	5564	3627	4312	6	3623	3446	3007	4	4.93E-14	1.51E-13	0.666666667	-0.584962501
BP1026B_I0024	cytochrome monooxygenase protein	30155	34861	36031	28	39826	39897	38383	33	1.15E-05	1.74E-05	1.178571429	0.237039197
BP1026B_I0025	hypothetical protein	54505	99441	84623	395	107142	118980	109399	556	0.002144757	0.002773225	1.407594937	0.493232223
BP1026B_I0026	hypothetical protein	6505	8428	8217	9	9023	8472	8844	10	3.10E-07	5.25E-07	1.111111111	0.152003093
BP1026B_I0027	hypothetical protein	8822	8583	8842	10	9727	9256	9452	11	3.42E-08	6.22E-08	1.1	0.137503524
BP1026B_I0028	radical SAM domain/B12 binding domain-containing protein	35122	24884	29421	15	26669	24594	26068	13	2.18E-14	6.87E-14	0.866666667	-0.206450877
BP1026B_I0029	hypothetical protein	10399	8977	9506	9	7812	7587	7572	7	7.03E-20	3.57E-19	0.777777778	-0.362570079
BP1026B_I0030	LysE family protein	4056	4296	2877	6	4505	3198	4354	6	2.41E-05	3.57E-05	1	0
BP1026B_I0031	chromosome replication initiation inhibitor protein	35033	33477	34321	38	36223	33247	37195	39	3.19E-08	5.82E-08	1.026315789	0.037474705
BP1026B_I0032	Crp/FNR family transcriptional regulator	1091924	1223802	1129669	1519	1197504	1268295	1319838	1669	0.233618903	0.255027186	1.098749177	0.135862085
BP1026B_I0033	universal stress protein	354006	407474	422939	843	396497	365264	428756	847	1.93E-09	3.89E-09	1.004744958	0.006829338
BP1026B_I0034	hypothetical protein	43073	58538	53928	224	55572	54253	55674	238	4.27E-10	9.13E-10	1.0625	0.087462841
BP1026B_I0035	NAD-dependent aldehyde dehydrogenase	30572	22975	25454	16	17002	15726	18191	10	5.91E-40	1.15E-38	0.625	-0.678071905
BP1026B_I0036	gluconolactonase	79615	82913	83072	86	68918	74094	68137	74	1.35E-21	7.88E-21	0.860465116	-0.216811389
BP1026B_I0037	hypothetical protein	11823	9095	8868	24	9757	8436	9668	22	1.90E-12	5.02E-12	0.916666667	-0.125530882
BP1026B_I0038	hypothetical protein	20040	33678	29905	117	35028	41605	32960	154	0.00109538	0.001442247	1.316239316	0.396421821
BP1026B_I0039	serine O-acetyltransferase	99831	84942	98397	102	77569	69861	77930	84	3.76E-27	3.44E-26	0.794117647	-0.332575339
BP1026B_I0040	pteridine reductase 1	45649	47871	45168	47	46236	46280	49162	58	1.67E-10	3.66E-10	1.01754386	0.025090981
BP1026B_I0041	GTP cyclohydrolase I	30135	34683	35081	46	35463	39901	36284	51	1.72E-06	2.76E-06	1.108095652	0.148863386
BP1026B_I0042	LysR family transcriptional regulator	17374	16642	18192	18	18602	16326	18238	19	1.11E-11	2.72E-11	1.055555556	0.078002512
BP1026B_I0043	4-hydroxybenzoate 3-monooxygenase	20899	16985	19238	15	15745	14147	14147	11	1.88E-26	1.63E-25	0.733333333	-0.447458977
BP1026B_I0044	3-oxoadipate CoA-transferase subunit A	39330	34233	35500	50	24863	22168	25964	34	1.28E-29	1.39E-28	0.68	-0.556393349
BP1026B_I0045	3-oxoadipate CoA-succinyl transferase subunit beta	49646	49295	49678	75	40179	38556	41850	61	1.99E-19	9.77E-19	0.813333333	-0.298081353
BP1026B_I0046	3-carboxy-cis-cis-muconate cycloisomerase	61372	37002	37223	33	30686	26357	33340	22	3.08E-29	3.25E-28	0.666666667	-0.584962501
BP1026B_I0047	3-oxoadipate enol-lactonase	85578	59506	70733	91	51757	50402	53729	66	6.05E-32	7.54E-31	0.725274725	-0.463400521
BP1026B_I0048	4-carboxymuconolactone decarboxylase	59411	62270	65443	161	53376	46061	52281	130	4.50E-23	2.98E-22	0.807453416	-0.308549065
BP1026B_I0049	4-hydroxybenzoate transporter	24183	10023	12665	11	11667	11340	11478	8	4.72E-24	3.37E-23	0.727272727	-0.459431619
BP1026B_I0050	hypothetical protein	12499	12876	11601	49	12883	12369	12701	50	5.36E-10	1.14E-09	1.020408163	0.029146346
BP1026B_I0051	LysE family protein	8648	12134	11178	17	13385	14305	14559	22	1.06E-04	1.50E-04	1.294176647	0.371968777
BP1026B_I0052	hypothetical protein	9063	12454	10147	10	13391	14225	13576	13	6.10E-05	8.80E-05	1.3	0.378511623
BP1026B_I0053	hypothetical protein	7181	8006	9114	8	9895	11483	9917	11	1.23E-04	1.73E-04	1.375	0.459431619
BP1026B_I0054	major facilitator family transporter	2365	1776	1877	1	2154	1663	1730	1	6.34E-05	9.13E-05	1	0
BP1026B_I0055	hypothetical protein	5156	8372	6406	15	8757	9851	9901	22	0.004068707	0.005150408	1.466666667	0.552541023
BP1026B_I0056	chromate resistance transport protein	19175	18959	18688	15	18875	14926	17441	14	1.22E-16	4.72E-16	0.933333333	-0.099535674
BP1026B_I0057	chromate resistance exported protein	6301	3613	5078	5	3804	3410	3213	3	6.64E-17	2.64E-16	0.6	-0.736965594
BP1026B_I0058	hypothetical protein	815	992	1143	2	469	798	1108	1	2.69E-04	3.71E-04	0.5	-1
BP1026B_I0059	hypothetical protein	5945	7621	7202	12	6496	7674	7321	13	2.21E-			

BP1026b_I0081	H-NS histone family protein	19202	31452	25091	82	31255	33993	33179	107	8.34E-04	0.001107092	1.304878049	0.383914982
BP1026b_I0082	Rhs element Vgr protein	97938	83994	86011	32	88301	89528	80585	30	9.20E-16	3.31E-15	0.9375	-0.093109404
BP1026b_I0083	hypothetical protein	135359	184038	170997	72	186554	201286	188563	85	4.33E-06	6.77E-06	1.180555556	0.239465935
BP1026b_I0084	hypothetical protein	492247	753031	704107	467	812971	917113	794573	605	0.060813217	0.070370382	1.29530212	0.373512592
BP1026b_I0085	PAAR motif-containing protein	57079	45588	45714	187	45779	41620	43245	164	3.57E-16	1.33E-15	0.877005348	-0.189342455
BP1026b_I0086	hypothetical protein	36917	40917	39746	93	42609	42543	39040	98	2.03E-08	3.75E-08	1.053763441	0.075551033
BP1026b_I0087	thioredoxin	13687	12736	13939	41	12335	11221	14015	38	3.02E-13	8.56E-13	0.926829268	-0.109624491
BP1026b_I0088	hypothetical protein	31638	38753	38294	51	47192	49562	52615	70	0.002743993	0.003526222	1.37254902	0.456857675
BP1026b_I0089	hypothetical protein	1761	2349	1930	3	1791	1694	1814	3	1.13E-05	1.71E-05	1	0
BP1026b_I0090	cytochrome c oxidase polypeptide I	20027	26915	26405	15	31361	34567	32160	20	0.002008226	0.002602595	1.333333333	0.415037499
BP1026b_I0091	hypothetical protein	436	499	821	1	1000	559	405	1	0.395063832	0.419998298	1	0
BP1026b_I0092	hypothetical protein	4822	6785	6189	4	6947	8145	6607	4	1.07E-05	1.62E-05	1	0
BP1026b_I0093	hypothetical protein	1070	1752	1435	3	1641	1688	1643	3	0.128550234	0.144302358	1	0
BP1026b_I0094	hypothetical protein	101	307	145	1	33	266	253	1	0.712661302	0.733257097	1	0
BP1026b_I0096	hypothetical protein	17621	25419	21656	14	24739	26395	26865	17	2.97E-05	4.37E-05	1.214285714	0.280107919
BP1026b_I0097	hypothetical protein	3132	3619	3874	7	4453	4547	4777	10	0.006539566	0.008154611	1.428571429	0.514573173
BP1026b_I0098	fimbrial protein	5979	9507	9790	15	12327	13903	11367	22	0.006019808	0.007527463	1.466666667	0.552541023
BP1026b_I0099	chaperone protein EcpD precursor	1281	1834	1581	2	2031	2590	2134	3	0.786583467	0.80416577	1.5	0.584962501
BP1026b_I0100	outer membrane usher protein	2393	3005	3037	1	3439	3850	2828	1	0.010268142	0.012610776	1	0
BP1026b_I0101	hypothetical protein	142	305	273	1	129	294	143	0	0.095475187	0.108555166	0	#NUM!
BP1026b_I0102	major fimbrial subunit protein	892	1143	1608	2	1350	1682	1824	3	0.778731836	0.796887664	1.5	0.584962501
BP1026b_I0103	type VI secretion system	664	588	724	0	924	1186	933	1	0.30765526	0.330833681	#DIV/0!	#DIV/0!
BP1026b_I0104	type VI secretion system	4169	4546	3584	2	4828	5865	4144	2	1.37E-04	1.93E-04	1	0
BP1026b_I0105	type VI secretion system	825	1454	969	2	1501	1309	1270	2	0.529313541	0.554535805	1	0
BP1026b_I0106	type VI secretion system	3982	5107	5654	3	6617	6541	6245	4	3.34E-04	4.57E-04	1.333333333	0.415037499
BP1026b_I0107	type VI secretion system	3403	6792	5605	10	7952	7986	8282	16	0.01358408	0.015566671	1.6	0.678071905
BP1026b_I0108	type VI secretion system	299	376	181	0	71	294	94	0	1.67E-04	2.34E-04	#DIV/0!	#DIV/0!
BP1026b_I0109	type VI secretion system	2166	1548	1623	1	2506	2408	2317	1	0.329304971	0.353265699	1	0
BP1026b_I0110	type VI secretion system	864	746	917	0	451	907	1118	0	0.03005687	0.03567652	#DIV/0!	#DIV/0!
BP1026b_I0111	type VI secretion system	12650	13891	12070	3	11426	11205	13869	3	1.66E-12	4.40E-12	1	0
BP1026b_I0112	hypothetical protein	2365	2169	2254	3	2119	1413	2099	3	3.75E-07	6.33E-07	1	0
BP1026b_I0113	type VI secretion system	12799	14725	13176	5	14487	15446	14261	5	4.19E-09	8.23E-09	1	0
BP1026b_I0114	Rhs family protein	768	1088	1038	3	985	1284	1044	4	0.207874049	0.228075431	1.333333333	0.415037499
BP1026b_I0115	Rhs1 protein	78399	110602	104319	28	119352	125197	124760	35	1.94E-05	2.90E-05	1.25	0.321928095
BP1026b_I0116	hypothetical protein	16511	21621	19394	14	21541	24852	24963	17	5.76E-05	8.33E-05	1.214285714	0.280107919
BP1026b_I0117	hypothetical protein	7933	13100	11866	10	13301	13741	16086	13	6.69E-05	9.61E-05	1.3	0.378511623
BP1026b_I0118	type VI secretion system	6503	7725	6440	6	7595	7345	8912	7	5.68E-07	9.50E-07	1.166666667	0.223924221
BP1026b_I0119	type VI secretion system	5490	3458	4027	4	4718	4133	3494	3	3.21E-08	5.85E-08	0.75	-0.415037499
BP1026b_I0120	type VI secretion system	7792	8283	8652	4	9777	10810	9769	5	1.91E-05	2.85E-05	1.25	0.321928095
BP1026b_I0121	type VI secretion system	2637	1993	2084	4	2380	2564	2797	4	0.009059669	0.011172581	1	0
BP1026b_I0122	type VI secretion system	4092	6249	6038	6	6056	4772	5253	6	4.44E-09	8.68E-09	1	0
BP1026b_I0124	type VI secretion system	2229	3015	3946	5	2833	3537	2828	5	3.07E-05	4.51E-05	1	0
BP1026b_I0123	hypothetical protein	3849	3023	3003	7	3901	2567	2951	6	2.37E-06	3.77E-06	0.857142857	-0.222392421
BP1026b_I0125	type VI secretion system	10130	8830	9260	3	11275	9248	9931	3	4.27E-08	7.72E-08	1	0
BP1026b_I0126	two-component system sensor protein	28109	41853	39533	11	50463	55913	48678	16	0.006878794	0.008565684	1.454545455	0.540568381
BP1026b_I0128	hypothetical protein	1303	1762	2231	5	2974	3460	3016	9	0.200465285	0.220100837	1.8	0.847996907
BP1026b_I0129	hypothetical protein	517	788	761	2	1350	667	781	3	0.905947188	0.916330118	1.5	0.584962501
BP1026b_I0130	hypothetical protein	358	357	336	1	500	285	461	2	0.934538549	0.942814128	2	1
BP1026b_I0131	hypothetical protein	649	989	672	2	1296	1739	1709	5	7.10E-04	9.49E-04	2.5	1.321928095
BP1026b_I0132	hypothetical protein	2612	4997	2938	8	6560	7079	5652	14	0.765978933	0.784893539	1.75	0.807354922
BP1026b_I0133	DNA-binding response regulator	1305	2454	1976	2	3150	3953	2656	4	0.453109916	0.478783597	2	1
BP1026b_I0134	hypothetical protein	171	607	132	2	335	221	364	2	0.417306466	0.442668413	1	0
BP1026b_I0135	fimbrial usher protein	6851	9671	9391	3	12000	12322	14085	5	0.005046916	0.006347647	1.666666667	0.736965594
BP1026b_I0136	periplasmic chaperone protein	4079	6080	6004	7	6622	7369	7344	10	2.34E-04	3.25E-04	1.428571429	0.514573173
BP1026b_I0137	hypothetical protein	409	641	775	4	1455	1448	1012	9	1.49E-04	2.09E-04	2.25	1.169925001
BP1026b_I0138	hypothetical protein	820	1335	1465	1	1882	2250	1887	3	0.15088521	0.168079417	3	1.584962501
BP1026b_I0139	hypothetical protein	6393	10500	8926	13	13339	13030	12246	19	0.006286102	0.007849485	1.461538462	0.547487795
BP1026b_I0140	DNA-binding response regulator	1320	2395	2611	3	2749	3101	2851	4	0.255390898	0.277200652	1.333333333	0.415037499
BP1026b_I0141	H-NS histone family protein	1332	1831	1949	5	1617	2077	2287	6	0.054899895	0.063786898	1.2	0.263034406
BP1026b_I0142	MFS transporter	8075	8162	6863	5	8174	7279	8704	6	1.61E-09	3.27E-09	1.2	0.263034406
BP1026b_I0143	glycerate kinase	4458	3093	3795	3	2637	2266	3100	2	5.70E-15	1.90E-14	0.666666667	-0.584962501
BP1026b_I0144	pyruvate kinase	15457	12884	11798	9	10800	9523	10108	6	2.24E-21	1.28E-20	0.666666667	-0.584962501
BP1026b_I0145	transcriptional regulator	6012	5271	4734	4	4965	3727	3990	3	9.35E-14	2.77E-13	0.75	-0.415037499
BP1026b_I0146	hypothetical protein	4778	5842	6318	11	6341	7510	6681	14	1.10E-05	1.67E-05	1.272727273	0.347923303
BP1026b_I0147	peptide synthase protein	76569	65859	68877	25	51489	47390	50676	17	3.65E-33	5.02E-32	0.68	-0.556393349
BP1026b_I0149	dehydratase	43451	25530	32559	34	18149	16231	17997	17	2.16E-49	1.45E-47	0.5	-1
BP1026b_I0148	hypothetical protein	22336	8040	10467	34	7561	4127	6654	15	1.24E-72	8.80E-71	0.441176471	-1.180572246
BP1026b_I0150	methyltransferase	43231	31965	35381	35	24065	22042	20400	21	1.06E-41	2.29E-40	0.6	-0.736965594
BP1026b_I0151	LysR family transcriptional regulator	15946	8569	10223	12	6911	5990	7014	7	1.96E-42	4.43E-41	0.583333333	-0.777607579
BP1026b_I0152	hypothetical protein	7572	9184	7240	20	6409	7182	7311	17	3.86E-15	1.31E-14	0.85	-0.234465254
BP1026b_I0153	hypothetical protein	9389	10098	10629	7	10173	9535	9213	6	2.00E-11	4.77E-11	0.857142857	-0.222392421
BP1026b_I0154	hypothetical protein	1332	1770	2152	6	1622	1873	1762	6	0.001934255	0.002507996	1	0
BP1026b_I0155	hypothetical protein	242	193	279	1	543	264	282	1	0.111737208	0.126288843	1	0
BP1026b_I0156	lipoprotein	655	850	672	4	705	1257	943	5	0.965913487	0.97149501	1.25	0.321928095
BP1026b_I0157	mercuric reductase	19154	17629	16119	12	15153	13548	12776	10	1.31E-22	8.39E-22	0.833333333	-0.263034406
BP1026b_I0158	sugar ABC transporter substrate-binding protein	34204	36136	38899	38	20920	19785	19426	21	2.98E-56	1.26E-54	0.552631579	-0.855610091
BP1026b_I0159	ABC transporter permease	12351	7422	9636	9	3832	5662	4390	4	9.51E-53	3.42E-51	0.444444444	-1.169925001
BP1026b_I0160	ribiose ABC transporter ATP-binding protein	21925	16120	17784	12	8803	8354	9194	5	1.20E-72	8.64E-71	0.416666667	-1.263034406
BP1026b_I0161	ROK family transcriptional regulator	23655	8224	13409	12	4798	4961	7311	4	2.00E-105	2.46E-103	0.333333333	-1.584962501
BP1026b_I0162	hypothetical protein	745	89	271	2	165	107	203	0	0.227E-08	4.18E-08	0	#NUM!
BP1026b_I0163	hypothetical protein	12741	4494	6939	22	4943	3011	4772	11	2.88E-38	5.17E-37	0.5	-1
BP1026b_I0164	amylase	564419	572195	564586	214	491597	476165	471982	181	6.83E-16	2.49E-15	0.845794393	-0.241621099
BP1026b_I0165	ATP-dependent RNA helicase DbpA</												

BP1026B_I0182	pyoverdine chromophore biosynthetic protein PvcC	17100	17890	16945	11	21679	20699	22444	14	3.22E-05	4.74E-05	1.272727273	0.347923303
BP1026B_I0183	asparagine synthase	16991	13197	14764	8	16119	14920	17590	8	1.63E-09	3.32E-09	1	0
BP1026B_I0184	quinone oxidoreductase	6703	3996	3996	5	3922	4835	4400	4	3.56E-10	7.67E-10	0.8	-0.321928095
BP1026B_I0185	dioxygenase	17885	13711	14650	16	17519	14275	17659	17	6.72E-10	1.42E-09	1.0625	0.087462841
BP1026B_I0186	LysR family regulatory protein	43970	40293	41522	43	47303	40948	49390	47	4.41E-08	7.95E-08	1.093023256	0.128324097
BP1026B_I0188	type VI secretion system	7622	5432	5249	1	4815	4949	4933	1	1.17E-14	3.79E-14	1	0
BP1026B_I0189	type VI secretion system	3398	2138	2442	2	3160	2953	2524	2	9.01E-04	0.001194119	1	0
BP1026B_I0190	type VI secretion system	1785	1872	1528	1	1069	1942	2205	1	0.00238277	0.003074004	1	0
BP1026B_I0191	type VI secretion system	3142	3565	3926	7	3565	2161	3788	6	5.92E-08	1.06E-07	0.857142857	-0.222392421
BP1026B_I0192	type VI secretion system	2493	2725	2439	5	2319	2149	2827	5	1.59E-05	2.38E-05	1	0
BP1026B_I0193	type VI secretion system	7606	9515	9604	5	9764	10714	10100	6	8.40E-07	1.39E-06	1.2	0.263034406
BP1026B_I0194	type VI secretion system	1294	974	820	1	1174	1028	1079	1	0.06177986	0.071449354	1	0
BP1026B_I0195	type VI secretion system	3336	2035	3014	0	2550	1931	3229	0	2.17E-06	3.46E-06	#DIV/0!	#DIV/0!
BP1026B_I0196	hypothetical protein	411	1081	757	2	978	1194	803	3	0.88075997	0.893305596	1.5	0.584962501
BP1026B_I0197	type VI secretion system	401	320	276	0	301	116	253	0	0.003435713	0.004380097	#DIV/0!	#DIV/0!
BP1026B_I0198	type VI secretion system	2280	1113	1948	1	672	530	906	0	1.87E-30	2.12E-29	0	#NUM!
BP1026B_I0199	type VI secretion system	2117	1688	1674	3	1145	1607	1336	2	3.44E-08	6.26E-08	0.666666667	-0.584962501
BP1026B_I0201	type VI secretion system	4927	4600	5025	2	4758	4131	4962	2	6.46E-09	1.25E-08	1	0
BP1026B_I0200	type VI secretion system	3734	2567	2561	2	2709	1918	2468	2	1.69E-09	3.43E-09	1	0
BP1026B_I0202	type VI secretion system	3328	1690	2091	2	1375	2044	1502	1	2.49E-11	5.89E-11	0.5	-1
BP1026B_I0203	type VI secretion system	6888	10524	8849	4	10945	9913	9569	4	5.42E-08	9.69E-08	1	0
BP1026B_I0204	type VI secretion system	14859	13240	15126	5	12587	10688	13946	5	1.94E-16	7.42E-16	1	0
BP1026B_I0205	type VI secretion system	5874	5569	4855	5	4593	4606	3914	4	1.72E-13	4.98E-13	0.8	-0.321928095
BP1026B_I0206	type VI secretion system	3484	2849	3025	4	2954	2931	3203	4	8.02E-06	1.23E-05	1	0
BP1026B_I0207	type VI secretion system	6152	5161	6886	15	5654	6284	5242	15	1.29E-10	2.85E-10	1	0
BP1026B_I0208	hypothetical protein	46599	54710	50826	26	54133	49397	51741	26	3.25E-11	7.60E-11	1	0
BP1026B_I0209	LysR family transcriptional regulator	28780	33807	32152	35	35634	37360	39727	42	3.15E-05	4.64E-05	1.2	0.263034406
BP1026B_I0210	quinone reductase	8047	10240	10889	12	10180	11759	10202	13	1.30E-07	2.26E-07	1.083333333	0.115477217
BP1026B_I0211	AraC/XylS family transcriptional regulator	1181	406	381	2	423	191	340	1	1.10E-11	2.69E-11	0.5	-1
BP1026B_I0212	O-acetylhomoserine sulphydrylase	113295	99939	103498	81	96538	95721	95254	73	8.26E-18	3.54E-17	0.901234568	-0.150025444
BP1026B_I0213	glyoxalase family protein	15472	10378	12462	32	10185	9654	11039	26	3.25E-18	1.44E-17	0.8125	-0.299560282
BP1026B_I0214	hypothetical protein	8878	9388	7209	10	8513	9687	9078	10	1.23E-08	2.32E-08	1	0
BP1026B_I0215	hypothetical protein	3468	4957	4403	12	7324	8991	8483	25	0.597687694	0.621904864	2.083333333	1.058893689
BP1026B_I0216	hypothetical protein	2200	2491	2500	1	1816	2260	2884	1	4.93E-05	7.15E-05	1	0
BP1026B_I0217	urea amidolyase-like protein	7024	2612	3736	4	2574	2329	2410	2	8.86E-28	8.46E-27	0.5	-1
BP1026B_I0218	allophanate hydrolase, subunit I	6088	5035	6471	6	4798	4144	5365	5	6.32E-14	1.90E-13	0.833333333	-0.263034406
BP1026B_I0219	acetyl-CoA carboxylase biotin carboxylase subunit	2963	1744	1834	1	1178	1397	1602	0	4.18E-13	1.17E-12	0	#NUM!
BP1026B_I0220	hypothetical protein	1095	391	451	2	394	203	170	1	2.12E-16	8.03E-16	0.5	-1
BP1026B_I0221	hypothetical protein	2458	3072	1890	3	3426	4017	2629	4	0.148044671	0.165091282	1.333333333	0.415073499
BP1026B_I0222	LysR family transcriptional regulator	12939	11834	11252	13	10297	13029	11863	12	3.22E-11	7.54E-11	0.923076923	-0.115477217
BP1026B_I0223	penicillin acylase	57421	48320	49996	20	45500	39300	41736	16	3.38E-20	1.75E-19	0.8	-0.321928095
BP1026B_I0224	proline iminopeptidase	30813	25451	27461	27	23142	28779	22825	24	1.96E-13	5.64E-13	0.888888889	-0.169925001
BP1026B_I0225	hypothetical protein	12966	12802	11694	15	10512	8008	10683	11	5.51E-20	2.82E-19	0.733333333	-0.447458977
BP1026B_I0226	lipoprotein	6060	4716	4773	2	3900	3413	4227	1	3.23E-15	1.10E-14	0.5	-1
BP1026B_I0227	methyl-accepting chemotaxis protein I	106651	93217	95102	60	98737	96167	89228	58	5.23E-15	1.75E-14	0.966666667	-0.0489096
BP1026B_I0228	propionate catabolism operon regulatory protein PrpR	42675	19346	22668	13	18494	14903	20582	8	2.77E-41	5.80E-40	0.615384615	-0.700439718
BP1026B_I0229	2-methylisocitrate lyase	466991	451789	461029	514	35568	34987	35183	39	0	0	0.075875486	-3.72022233
BP1026B_I0230	methylcitrate synthase	952777	1145722	1121699	915	66198	69060	77903	60	0	0	0.06557377	-3.930737338
BP1026B_I0231	aconitate hydratase	1559198	1371483	1443237	561	85528	80462	85742	32	0	0	0.057040998	-4.131856961
BP1026B_I0232	AcnD-accessory protein PrpF	156711	99537	109558	102	6970	7271	7733	6	0	0	0.058823529	-4.087462841
BP1026B_I0233	hypothetical protein	41755	41840	40857	93	20812	20727	21018	46	6.51E-69	4.25E-67	0.494623656	-1.015596855
BP1026B_I0234	hypothetical protein	6788	6375	6727	34	4452	5226	5564	26	6.02E-17	2.41E-16	0.764705882	-0.38702123
BP1026B_I0235	hypothetical protein	41211	36824	39835	61	24306	21733	27290	38	8.51E-36	1.36E-34	0.62295082	-0.682809824
BP1026B_I0236	hypothetical protein	77778	92559	92049	147	61545	65178	58278	104	9.72E-37	1.63E-35	0.707482993	-0.499232627
BP1026B_I0237	heme biosynthesis protein	39787	34354	33433	24	24594	22110	22672	15	1.04E-33	1.48E-32	0.625	-0.678071905
BP1026B_I0238	methyl-accepting chemotaxis protein	189543	167884	173620	109	163562	156565	155421	98	2.25E-16	8.50E-16	0.899082569	-0.153474481
BP1026B_I0239	RemN protein	11453	5720	8021	4	7144	6243	7982	4	1.97E-16	7.52E-16	1	0
BP1026B_I0240	LysR family transcriptional regulator	32161	17765	18083	25	20092	17972	23352	23	1.43E-15	5.06E-15	0.92	-0.120294234
BP1026B_I0241	N-acetylglucosamine 2-epimerase	36096	26293	27770	27	30312	28992	25605	25	6.49E-11	1.48E-10	0.925925926	-0.111031312
BP1026B_I0242	MgtC family protein	46272	41116	42617	62	39796	37394	40513	56	1.40E-13	4.09E-13	0.903225806	-0.146841388
BP1026B_I0243	hypothetical protein	54679	40632	46558	164	45338	39483	45356	150	4.08E-14	1.25E-13	0.914634146	-0.128733314
BP1026B_I0244	hypothetical protein	722744	1190739	1037015	6304	1584171	1765379	1515056	10394	0.00110463	0.00145412	1.648794416	0.721411524
predicted RNA	-	28765	886	2925	472	843	538	909	33	0	0	0.069915254	-3.83824893
predicted RNA	-	370309	126696	177047	1353	143686	110372	141484	794	6.27E-59	2.91E-57	0.58684405	-0.768950927
predicted RNA	-	34799	36509	32133	703	39433	32434	44934	794	2.29E-06	3.65E-06	1.129445235	0.175614318
BP1026B_I0245	acetyltransferase	155665	181871	170280	366	205525	198362	211111	443	1.26E-05	1.91E-05	1.210382514	0.27546305
BP1026B_I0246	Putative exported protein precursor	246746	343678	322671	685	388195	418283	372865	885	2.03E-04	2.82E-04	1.291970803	0.369573467
BP1026B_I0248	hypothetical protein	303183	135572	189462	260	122259	100721	109965	138	4.64E-76	3.78E-74	0.530769231	-0.131843356
predicted RNA	-	45403	22388	30415	617	18786	12537	16552	301	1.48E-78	1.26E-76	0.487844408	-1.035507002
predicted RNA	-	34148	27113	26912	576	23117	21106	24083	446	3.59E-21	2.02E-20	0.774305556	-0.369025102
BP1026B_I0250	hypothetical protein	80717	32530	37547	35	29029	23782	28239	18	3.18E-51	1.08E-49	0.514285714	-0.959358016
BP1026B_I0251	hypothetical protein	381436	288274	314090	83	287812	269591	292434	72	1.17E-16	4.56E-16	0.86746988	-0.20511443
predicted RNA	-	9046	336	769	211	354	86	265	14	0	0	0.066350711	-3.913744267
BP1026B_I0252	hypothetical protein	4530	7591	6210	27	6621	8884	7511	34	2.72E-05	4.02E-05	1.259259259	0.332575339
BP1026B_I0253	type I phosphodiesterase/nucleotide pyrophosphatase family protein	19562	10997	13998	8	13054	12753	13775	7	1.13E-15	4.04E-15	0.875	-0.192645078
BP1026B_I0254	glyoxalase/bleomycin resistance protein/dioxygenase family protein	30300	29089	35276	80	33022	30590	34666	83	4.66E-08	8.38E-08	1.0375	0.053111336
BP1026B_I0256	hypothetical protein	17686	12690	14087	52	14331	14622	16269	52	2.96E-11	6.94E-11	1	0
BP1026B_I0255	squalene/phytoene synthase family protein	30147	24131	25794	25	24950	23951	22479	22	5.26E-14	1.60E-13	0.88	-0.184424571
BP1026B_I0257	LysR family transcriptional regulator	10207	8398	8999	12	10749	8412	9747	13	5.84E-09	1.13E-08	1.083333333	0.115477217
BP1026B_I0259	hypothetical protein	21613	24269	22879	45	26885	29129	29545	56	1.46E-04	2.05E-04	1.244444444	0.315501826
BP1026B_I0260	hypothetical protein	11146	14682	14942	79	16315	19072	13187	94	6.80E-07	1.13E-06	1.189873418	0.258088104
BP1026B_I0261	cyanide-insensitive terminal oxidase	98896	100										

BP1026B_I0279	outer membrane porin	12264	9595	12315	9	9576	9775	11097	8	6.11E-14	1.84E-13	0.888888889	-0.169925001
BP1026B_I0280	PTS system manniitol-specific transporter subunit IIBC	20607	16218	15163	16	16258	15236	14721	15	7.45E-17	2.95E-16	0.9375	-0.093109404
BP1026B_I0281	ribose 5-phosphate isomerase B	1453	606	825	1	1000	899	914	1	0.015924755	0.019304414	1	0
BP1026B_I0283	ribose ABC transport system, ATP-binding protein	7142	4765	4505	3	4670	3708	4954	2	2.65E-13	7.57E-13	0.666666667	-0.584962501
BP1026B_I0282	sugar ABC transporter permease	7322	5489	6471	6	5174	5994	5385	5	2.32E-13	6.67E-13	0.833333333	-0.263034406
BP1026B_I0284	LacI family transcriptional regulator	6537	9498	8078	7	7787	8162	7494	7	1.00E-11	2.47E-11	1	0
BP1026B_I0285	short chain dehydrogenase	2756	1856	1737	2	1434	1351	1446	1	1.05E-11	2.57E-11	0.5	-1
BP1026B_I0286	zinc-binding dehydrogenase family oxidoreductase	4996	5029	3987	4	4221	3534	3076	3	3.32E-13	9.41E-13	0.75	-0.415037499
BP1026B_I0287	kinase	7044	7515	7848	7	6309	7088	6353	6	3.23E-14	1.00E-13	0.857142857	-0.222392421
BP1026B_I0288	dihydroxyacetone kinase family protein	4684	3018	3727	5	2650	2538	2025	3	2.86E-19	1.39E-18	0.6	-0.736965594
BP1026B_I0289	Aminoglycoside 6'-N-acetyltransferase	4060	1632	2604	5	2122	2291	2038	4	1.19E-09	2.46E-09	0.8	-0.321928095
BP1026B_I0290	hypothetical protein	55630	65306	63903	160	57732	47453	70817	152	2.03E-15	7.08E-15	0.95	-0.074000581
BP1026B_I0291	hypothetical protein	23448	31372	30147	108	34420	40889	36375	142	0.001204589	0.001580723	1.314814815	0.394859617
BP1026B_I0292	outer membrane porin	1237067	1407970	1363142	1178	1454070	1454833	1418143	1271	0.16766875	0.185620563	1.078947368	0.109624491
BP1026B_I0293	D-methionine-binding lipoprotein metQ	40954	50739	48515	57	55538	55934	56813	69	2.35E-06	3.75E-06	1.210526316	0.275644443
BP1026B_I0294	succinylglutamate desuccinylase	160884	182371	179104	156	188846	186516	179065	165	3.47E-09	6.87E-09	1.057692908	0.080919995
BP1026B_I0295	O-antigen acetylase	6003	5023	5625	2	4603	5563	3468	2	3.21E-13	9.09E-13	1	0
BP1026B_I0296	lysine-arginine-ornithine transport system, binding exported protein	167689	211405	203025	251	179917	185542	176825	234	1.64E-14	5.23E-14	0.932270916	-0.101178834
BP1026B_I0298	LysR family transcriptional regulator	13422	2836	4677	7	3935	2381	2858	3	1.92E-50	6.32E-49	0.428571429	-1.222392421
BP1026B_I0297	peptidase	7970	7796	8301	6	6549	6833	6534	5	5.97E-17	2.39E-16	0.833333333	-0.263034406
BP1026B_I0299	major facilitator family transporter	3007	2445	2346	1	2036	2646	2286	1	1.32E-06	2.13E-06	1	0
BP1026B_I0300	TetR family transcriptional regulator	24051	26038	2441	34	23651	23130	25260	33	4.69E-11	1.08E-10	0.970588235	-0.043068722
BP1026B_I0301	IcIR family transcriptional regulator	54745	60467	62005	75	51374	50129	54150	66	1.75E-18	7.90E-18	0.88	-0.184424571
BP1026B_I0302	beta-ketoadipyl CoA thiolase	5743	4108	4098	3	2310	3327	3491	2	4.87E-19	2.31E-18	0.666666667	-0.584962501
BP1026B_I0303	aerotaxis receptor	1461062	1464245	1506163	956	1622723	1629775	1554331	1037	0.14369695	0.160585605	1.084728033	0.117333371
BP1026B_I0304	O-methyltransferase family protein	394627	420422	425428	406	501482	491475	509249	492	4.56E-04	6.19E-04	1.21182266	0.277178588
BP1026B_I0305	hypothetical protein	34473	41844	37850	36	43230	42588	44063	41	1.19E-06	1.94E-06	1.138888889	0.187627003
BP1026B_I0306	Rieske iron-sulfur protein	18317	10503	10943	13	9200	7450	7886	8	5.69E-38	9.98E-37	0.615384615	-0.700439718
BP1026B_I0307	succinate-semialdehyde dehydrogenase	611054	614190	613368	416	634438	591996	619630	418	0.463029322	0.488770508	1.004807692	0.006919414
BP1026B_I0308	4-aminobutyrate transaminase	202305	149545	164470	134	146262	129864	143171	108	1.06E-23	7.34E-23	0.805970149	-0.312101688
BP1026B_I0309	GntR family transcriptional regulator	45760	29780	32963	21	33612	29235	33304	19	4.41E-13	1.23E-12	0.904761905	-0.144389909
BP1026B_I0310	C4-dicarboxylate anaerobic carrier family protein	11614	12046	12611	7	12405	12341	13223	8	1.61E-09	3.28E-09	1.142857143	0.192645078
BP1026B_I0311	IcIR family transcriptional regulator	2477	1413	1651	2	1646	1626	1735	2	7.56E-05	1.08E-04	1	0
BP1026B_I0312	N-formylglutamate amidohydrolase	4967	1999	3687	3	2392	1861	3151	2	7.81E-15	2.57E-14	0.666666667	-0.584962501
BP1026B_I0313	outer membrane porin protein	834	139	545	1	520	27	207	0	6.46E-09	1.25E-08	0	#NUM!
BP1026B_I0314	hypothetical protein	609	255	247	0	155	175	450	0	0.002553991	0.003288126	#DIV/0!	#DIV/0!
BP1026B_I0315	selenophosphate synthetase	41222	32491	35148	34	38445	34633	38770	35	1.16E-08	2.20E-08	0.129411765	0.041820176
BP1026B_I0316	hypothetical protein	1682	1589	1659	3	1455	2850	1132	3	0.024046621	0.028760474	1	0
BP1026B_I0317	lipoprotein	169512	188966	198741	174	172352	169731	168397	160	3.51E-15	1.19E-14	0.91954023	-0.121015401
BP1026B_I0318	hypothetical protein	426	39	118	0	85	174	83	0	0.006383091	0.007964247	#DIV/0!	#DIV/0!
BP1026B_I0319	LysR family transcriptional regulator	18296	22252	23634	21	21906	23661	23418	22	2.20E-08	4.06E-08	1.047619048	0.067114196
BP1026B_I0320	lipase-like protein LlpE	1421	970	1269	1	943	502	1228	1	1.04E-06	1.70E-06	1	0
BP1026B_I0321	RND family efflux transporter MFP subunit	9958	7823	7399	6	7658	7347	6570	5	4.56E-16	1.69E-15	0.833333333	-0.263034406
BP1026B_I0322	multidrug-efflux transporter protein	38815	44101	43401	13	41820	42209	44139	13	5.45E-10	1.16E-09	1	0
BP1026B_I0323	RND efflux system outer membrane lipoprotein	9889	7274	7746	5	6660	6762	6560	4	1.90E-18	8.54E-18	0.8	-0.321928095
BP1026B_I0324	sodium.dicarboxylate symporter family protein	250633	215878	233223	191	182302	169652	202294	152	5.55E-24	3.93E-23	0.795811518	-0.329501315
BP1026B_I0325	GntR family transcriptional regulator	71854	107261	98783	140	113335	125383	115331	178	3.37E-05	4.94E-05	1.271428571	0.346450414
BP1026B_I0326	acetyltransferase	54619	41713	44465	99	49466	50406	49056	105	1.32E-09	2.72E-09	1.060606061	0.084888898
BP1026B_I0327	auxin efflux carrier	26861	11465	15350	19	10798	7449	10943	10	6.69E-50	2.16E-48	0.526315789	-0.925999419
BP1026B_I0328	AMP-binding domain-containing protein	230210	168103	178624	103	192400	187552	204998	104	2.40E-11	5.69E-11	1.009708738	0.013939191
BP1026B_I0329	malonyl CoA-acyl carrier protein transacylase	103842	92124	95866	108	103060	89911	89358	104	6.24E-15	2.07E-14	0.962692963	-0.054447784
BP1026B_I0330	hypothetical protein	55849	67805	63353	144	87663	92736	87215	206	0.001387441	0.001814591	1.430555556	0.516755526
BP1026B_I0331	fatty-acyl-CoA ligase	296222	332364	323290	170	376224	354664	396131	201	4.91E-06	7.66E-06	1.182352941	0.241660755
BP1026B_I0332	diaminopimelate decarboxylase	96518	47356	53755	52	58539	56004	55417	44	1.68E-20	8.95E-20	0.846153846	-0.2410081
BP1026B_I0333	FkhH domain-containing protein	46680	24161	31345	22	27579	20445	26740	16	4.96E-23	3.28E-22	0.727272727	-0.459431619
BP1026B_I0334	ketol-acyl reductoisomerase	68552	61149	59298	59	75942	80034	75967	47	6.33E-07	1.05E-06	1.237288136	0.30718151
BP1026B_I0335	polyketide non-ribosomal peptide synthase	779706	523570	592185	51	616735	531166	598787	73	0.134945523	0.151264516	0.921568627	-0.11783649
BP1026B_I0336	gamma-aminobutyraldehyde dehydrogenase	182000	101094	117434	94	109494	93145	110800	73	1.77E-26	1.54E-25	0.776595745	-0.364764293
BP1026B_I0337	hypothetical protein	187660	119027	133409	103	126992	115101	129301	87	1.85E-21	1.06E-20	0.844660101	-0.243557031
BP1026B_I0338	peptide synthase regulatory protein	100733	52589	62389	70	55332	48250	52714	50	1.03E-31	1.26E-30	0.714285714	-0.485426827
predicted RNA	-	59071	61847	56655	533	70603	80041	76767	682	8.83E-06	1.35E-05	1.279549719	0.355636206
predicted RNA	-	1169831	997196	1031539	2094	1005137	924406	1085126	1974	0.4354909	0.460685728	0.94269431	-0.085139452
BP1026B_I0339	hypothetical protein	259222	324095	320427	580	377889	377927	384519	732	7.30E-05	1.05E-04	1.262089696	0.335790748
BP1026B_I0340	thiotemplate mechanism natural product synthetase	1484893	977806	1077952	139	1097504	1018203	1043416	124	0.603695766	0.622718981	0.892086361	-0.164744762
predicted RNA	-	32093	53307	45147	630	62600	69175	59465	923	0.010187291	0.012513932	1.465079635	0.550978819
BP1026B_I0341	ATP-dependent transcription regulator LuxR	56637	57952	59620	80	52988	52286	55520	74	3.85E-16	1.43E-15	0.925	-0.112474729
BP1026B_I0342	D-methionine-binding lipoprotein MetQ	5158	6344	5806	6	6510	5848	5582	7	2.05E-08	3.80E-08	1.166666667	0.222392421
BP1026B_I0343	monooxygenase	8044	7701	6644	5	6095	5567	6166	4	2.81E-17	1.16E-16	0.6	-0.321928095
BP1026B_I0344	ABC transporter ATP-binding protein	2511	2354	2840	2	2109	2511	1950	1	2.25E-07	3.85E-07	0.5	-1
BP1026B_I0345	ABC transporter permease	1452	1020	905	1	1010	704	579	1	3.09E-07	5.23E-07	1	0
BP1026B_I0346	hypothetical protein	898	501	630	1	925	791	285	1	0.072292326	0.08305532	1	0
BP1026B_I0347	monooxygenase	30721	9768	15562	15	10501	9096	9261	7	2.61E-57	1.15E-55	0.466666667	-1.099535674
BP1026B_I0348	hypothetical protein	6347	2268	3150	5	2456	1630	2162	2	2.37E-27	2.22E-26	0.4	-1.321928095
BP1026B_I0349	hypothetical protein	18207	23735	22209	37	26578	28760	27976	48	6.23E-04	8.36E-04	1.297297297	0.375509135
BP1026B_I0350	GntR family transcriptional regulator	22868	15834	15524	25	15049	14329	14574	20	2.59E-21	1.48E-20	0.8	-0.321928095
BP1026B_I0351	hypothetical protein	11433	5676	7238	10	7425	6400	5807	8	5.22E-18	2.27E-17	0.8	-0.321928095
BP1026B_I0352	iron-sulfur cluster binding protein	47906	48919	48844	33	55761	46900	48719	35	2.39E-10	5.20E-10	1.060606061	0.084888898
BP1026B_I0353	hypothetical protein	8804	3326	3808	7	3368	2824	2912	4	1.45E-26	1.27E-25	0.57142857	

BP1026B_I0375	ABC transporter ATP-binding protein	185	164	150	0	0	58	146	0	1.68E-05	2.52E-05	#DIV/0!	#DIV/0!
BP1026B_I0376	2-aminoethylphosphonate ABC transporter permease	1835	624	809	1	530	646	638	0	2.90E-11	6.81E-11	0	#NUM!
BP1026B_I0377	ABC transporter membrane protein	362	357	151	0	134	229	292	0	0.034668165	0.040971468	#DIV/0!	#DIV/0!
BP1026B_I0378	phosphoacetate hydrolase	33767	25054	32027	24	24602	20683	23425	18	1.95E-22	1.22E-21	0.75	-0.415037499
BP1026B_I0379	aldehyde dehydrogenase family protein	38182	25182	31150	21	28393	21651	26770	17	4.03E-17	1.64E-16	0.80952381	-0.304854582
BP1026B_I0380	hypothetical protein	6715	6880	7023	12	6356	6062	7279	11	2.52E-11	5.96E-11	0.916666667	-0.125530882
BP1026B_I0381	hypothetical protein	0	0	0	0	0	0	0	0	1	1	#DIV/0!	#DIV/0!
BP1026B_I0382	16S ribosomal RNA	0	44	0	0	0	0	0	0	1	1	#DIV/0!	#DIV/0!
BP1026B_I0383	Ile tRNA	0	0	0	0	0	0	0	0	1	1	#DIV/0!	#DIV/0!
BP1026B_I0384	Ala tRNA	0	0	0	0	0	0	0	0	1	1	#DIV/0!	#DIV/0!
BP1026B_I0385	hypothetical protein	0	0	0	0	0	0	0	0	1	1	#DIV/0!	#DIV/0!
BP1026B_I0386	23S ribosomal RNA	179115	240211	187011	70	469192	387214	345367	139	0.201960273	0.221703411	1.985714286	0.989658056
BP1026B_I0387	5S ribosomal RNA	3199	4205	4204	34	8268	8835	6386	69	0.96748265	0.972760957	2.029411765	1.021061616
BP1026B_I0388	Cu(I)-responsive transcriptional regulator	120230	189086	158459	358	191274	211622	191237	455	2.84E-04	3.91E-04	1.270949721	0.345906958
BP1026B_I0389	hypothetical protein	2690102	4191280	3531150	23611	5476945	6053138	5472634	38554	0.692025377	0.71319589	1.632882978	0.707421403
BP1026B_I0390	hypothetical protein	110242	123821	134806	440	147541	122813	159398	513	1.31E-06	2.12E-06	1.165909091	0.221455302
BP1026B_I0391	hypothetical protein	88804	116214	110594	116	135017	151019	137639	155	0.001045439	0.001377649	1.336206897	0.41814341
BP1026B_I0392	aldo/keto reductase family oxidoreductase	69900	89478	85377	86	97503	111376	95350	107	7.33E-06	1.13E-05	1.244186047	0.31502232
BP1026B_I0393	3-hydroxybutyrate dehydrogenase	278261	389003	366568	436	409655	449066	376418	521	1.54E-05	2.32E-05	1.194954128	0.256955238
BP1026B_I0394	aromatic amino acid aminotransferase	384341	398949	409576	331	411437	416063	414962	345	2.08E-08	3.84E-08	1.042296073	0.059765145
BP1026B_I0395	exicuclease ABC subunit B	327849	431354	413000	186	521848	518347	521253	248	0.253525296	0.275366529	1.333333333	0.415037499
BP1026B_I0396	19 kDa periplasmic protein	13816	16910	17666	29	20651	19290	20577	36	1.61E-05	2.42E-05	1.24137931	0.311944006
BP1026B_I0398	hypothetical protein	4385	4320	3265	12	3161	2546	2757	8	1.79E-15	6.26E-15	0.666666667	-0.584962501
BP1026B_I0397	FTR1 family iron permease	13812	16082	17096	18	14897	16996	15673	18	1.20E-11	2.92E-11	1	0
BP1026B_I0399	nitrogen fixation protein VnfA	14737	10737	10251	8	11353	10508	11944	8	4.71E-12	1.20E-11	1	0
BP1026B_I0400	glcG protein	77255	48780	55171	146	48394	47890	48871	117	2.74E-23	1.84E-22	0.801369863	-0.319459839
BP1026B_I0401	hypothetical protein	2692	3085	3503	21	4879	6258	5748	38	0.880987243	0.893305596	1.80952381	0.855610091
BP1026B_I0402	hypothetical protein	713	1101	832	9	1699	1444	1209	15	0.117453294	0.132367327	1.666666667	0.736965594
BP1026B_I0403	hypothetical protein	1533	2242	2348	8	2430	2923	3306	11	0.369859515	0.394407713	1.375	0.459431619
BP1026B_I0404	hypothetical protein	85661	94411	97693	190	127386	116904	123691	252	2.10E-04	2.92E-04	1.326315789	0.407424315
BP1026B_I0405	Pilin-like protein	18249	16103	16878	19	17685	16812	18323	20	3.15E-11	7.39E-11	1.052631579	0.074000581
BP1026B_I0406	LysR family transcriptional regulator	72696	58824	61067	66	66674	67449	72100	70	5.22E-11	1.20E-10	1.060606061	0.084888989
BP1026B_I0407	predicted RNA	1126755	429229	514503	4286	514949	468450	533503	3140	2.45E-15	8.43E-15	0.732617825	-0.448867291
BP1026B_I0407	biopolymer ExbD/TolR family transporter	93145	101373	99531	228	95269	99423	104129	232	2.96E-12	7.66E-12	1.01754386	0.025090981
BP1026B_I0408	MotA/TolQ/ExbB proton channel family protein	96810	104581	108274	141	94972	84412	99302	127	1.11E-18	5.13E-18	0.90070922	-0.150866666
BP1026B_I0409	siderophore-mediated iron transport protein	39254	30783	33540	49	26064	23920	25705	36	5.49E-23	3.62E-22	0.734693878	-0.444784843
BP1026B_I0410	bacterioferritin-associated ferredoxin	1434	3030	2038	9	1702	2617	2278	9	4.69E-04	6.35E-04	1	0
BP1026B_I0411	glutamate racemase	45127	24484	26176	36	23079	22099	23250	26	4.68E-26	3.90E-25	0.722222222	-0.469485283
BP1026B_I0412	predicted RNA	6658	11390	9616	709	11005	12642	12126	917	9.67E-05	1.37E-04	1.293370945	0.371136106
BP1026B_I0412	bacterioferritin	391202	708388	628445	1207	907469	1089129	899948	2024	0.001794921	0.002332914	1.676884368	0.747583614
BP1026B_I0413	tartrate/fumarate family Fe-S type hydro-lyase	544760	534885	540763	351	553180	531532	530956	350	0.018778036	0.022649311	0.997150997	-0.004116108
BP1026B_I0414	hypothetical protein	21806	30893	28716	51	36905	39964	36876	71	0.006861322	0.008545626	1.392156863	0.477321778
BP1026B_I0415	hypothetical protein	29743	20318	22806	26	22673	21158	24500	25	1.20E-12	3.25E-12	0.961538462	-0.056835328
BP1026B_I0415	predicted RNA	151459	37039	71724	1606	36438	14541	46086	599	1.22E-130	1.78E-128	0.372976339	-1.422843985
BP1026B_I0416	acetyl-CoA synthetase	674701	712069	718384	353	723258	700294	737564	363	0.931917839	0.940624546	1.028328612	0.040301365
BP1026B_I0417	hypothetical protein	2608	901	1571	4	1579	838	1162	3	4.35E-09	8.52E-09	0.75	-0.415037499
BP1026B_I0418	sodium:solute symporter family protein	20575	18606	18668	9	17875	16887	17304	8	8.62E-17	3.40E-16	0.888888889	-0.169925001
BP1026B_I0419	Ser tRNA	1190	1250	1387	14	2288	2394	1878	24	0.110221182	0.124642831	1.714285714	0.777607579
BP1026B_I0420	hypothetical protein	9609	15050	14160	67	17004	19328	16757	92	3.03E-04	4.16E-04	1.373134328	0.457472766
BP1026B_I0421	hypothetical protein	57773	99080	86061	65	109789	126838	117630	96	0.007716397	0.009557411	1.476923077	0.562594688
BP1026B_I0422	site-specific recombinase, DNA invertase	68714	112051	101369	155	120033	130008	122699	206	1.96E-04	2.73E-04	1.329032258	0.410376122
BP1026B_I0423	hypothetical protein	64305	117483	102838	241	139042	134683	1372	372	0.089384925	0.101982145	1.543568465	0.626269475
BP1026B_I0424	hypothetical protein	218034	358967	310385	313	386342	437143	426340	440	0.003557899	0.004529418	1.405750799	0.491340867
BP1026B_I0425	hypothetical protein	24417	40528	37679	101	48251	53100	47998	148	0.015794867	0.019150665	1.465346535	0.551241883
BP1026B_I0426	hypothetical protein	13225	15336	13175	82	17515	17782	17483	104	1.15E-05	1.75E-05	1.268292683	0.342887714
BP1026B_I0427	transposase	50	79	55	0	74	142	81	0	0.04089418	0.051734887	#DIV/0!	#DIV/0!
BP1026B_I0428	transposase B	36	58	108	0	43	157	119	0	0.061623662	0.071282693	#DIV/0!	#DIV/0!
BP1026B_I0429	hypothetical protein	248235	426409	378796	160	431309	512416	460725	214	8.68E-04	0.001150904	1.3375	0.419538892
BP1026B_I0430	hypothetical protein	2954	4933	3707	13	4743	5166	5696	17	0.003511417	0.004472061	1.307692308	0.387023123
BP1026B_I0431	hypothetical protein	4135	6777	5674	10	7482	7050	6650	13	7.44E-05	1.07E-04	1.3	0.378511623
BP1026B_I0432	XRE family transcriptional regulator	5946	10123	8903	33	10783	13508	10550	46	0.001325663	0.00173488	1.393939394	0.479167837
BP1026B_I0433	hypothetical protein	14388	26328	22971	36	26589	29194	27319	48	7.34E-04	9.79E-04	1.333333333	0.415037499
BP1026B_I0434	hypothetical protein	6968	12284	10585	12	14261	16017	15685	19	0.011493856	0.014083008	1.583333333	0.662965013
BP1026B_I0435	IS407A, transposase OrfA	5221	7141	7155	24	9266	8716	9725	34	0.002988167	0.003831359	1.416666667	0.502500341
BP1026B_I0436	IS407A, transposase OrfB	692	973	773	0	941	709	1626	1	0.946263775	0.953721862	#DIV/0!	#DIV/0!
BP1026B_I0437	hypothetical protein	15391	24755	22155	18	27312	30805	29933	26	0.008783557	0.010840609	1.444444444	0.530514717
BP1026B_I0438	Integrase	29490	49994	45874	57	50407	60158	58323	77	7.71E-04	0.001026769	1.350877193	0.433896527
BP1026B_I0439	Integrase	8456	15029	12860	77	18982	20175	18106	11	0.026357809	0.031386931	1.571428571	0.652076697
BP1026B_I0441	IS407A, transposase OrfA	0	0	0	0	0	0	0	0	1	1	#DIV/0!	#DIV/0!
BP1026B_I0442	IS407A, transposase OrfB	0	0	3	0	3	3	0	0	1	1	#DIV/0!	#DIV/0!
BP1026B_I0445	hypothetical protein	245180	378109	353179	1142	458571	485253	418525	1593	0.002808619	0.003604097	1.394921191	0.480183616
BP1026B_I0446	hypothetical protein	1475	2246	2534	10	3057	3062	2655	14	0.33231637	0.356268612	1.4	0.485426827
BP1026B_I0448	IS407A, transposase OrfB	1101	2480	2038	2	2330	2178	3051	2	0.259105819	0.281038093	1	0
BP1026B_I0449	IS407A, transposase OrfA	8627	13943	12005	43	14870	16189	18984	63	0.001870511	0.002428139	1.465116279	0.551015169
BP1026B_I0450	transposase	850	1282	1498	6	1647	1699	1736	9	0.922336916	0.932005017	1.5	0.584962501
BP1026B_I0451	Ser/Thr protein phosphatase family protein	3547	3019	3036	2	2613	2878	2858	1	4.49E-08	8.10E-08	0.5	-1
BP1026B_I0452	cytochrome c peroxidase	10790	11414	12155	9	13421	12678	11103	9	1.65E-08	3.08E-08	1	0
BP1026B_I0453	glycerophosphoryl diester phosphodiesterase family protein	10432	18003	14892	15	18616	20062	18567	20	1.06E-04	1.50E-04	1.333333333	0.415037499
BP1026B_I0454	hypothetical protein	8246	14627	13592	59	16291							

BP1026B_I0475	glycosyl transferase family protein	148971	139064	139874	136	116796	107868	123159	111	9.34E-24	6.53E-23	0.816176471	-0.293046975
BP1026B_I0476	ADP-heptose--lipooligosaccharideheptosyltransferase II	71975	107494	92935	72	98737	16105	96952	80	3.66E-09	7.23E-09	1.111111111	0.152003093
BP1026B_I0477	ADP-heptose--L-PS heptosyltransferase II	72887	93951	92206	73	69970	73290	75268	62	6.25E-23	4.10E-22	0.849315068	-0.235628248
BP1026B_I0478	galactoside O-acetyltransferase	8649	10137	10027	18	8387	7765	7654	15	1.94E-18	8.71E-18	0.833333333	-0.263044006
BP1026B_I0479	Rhamnosyl transferase	30201	35725	33982	31	26359	25893	25542	24	3.93E-19	1.88E-18	0.774193548	-0.36923381
BP1026B_I0480	hypothetical protein	22181	30776	29490	26	26917	30157	32041	28	3.74E-07	6.31E-07	1.076923077	0.106915204
BP1026B_I0481	hypothetical protein	3023	1089	1615	9	758	1274	1344	5	6.53E-15	2.16E-14	0.555555556	-0.847996907
BP1026B_I0482	LysR family transcriptional regulator	32468	21549	22714	26	25204	23752	25536	25	1.21E-10	2.69E-10	0.961538462	-0.056835328
BP1026B_I0483	hypothetical protein	12104	10811	10948	15	9360	8679	9263	12	1.04E-18	4.86E-18	0.8	-0.321928095
BP1026B_I0484	hypothetical protein	2392	1590	1330	2	1397	1200	1808	2	5.55E-06	8.61E-06	1	0
BP1026B_I0485	cyclic nucleotide-binding domain-containing protein	8590	1910	3013	4	2508	1848	1910	1	4.87E-38	8.59E-37	0.25	-2
BP1026B_I0486	AraC family transcriptional regulator	11769	12292	11670	12	9692	9246	10470	10	2.49E-17	1.03E-16	0.833333333	-0.263034406
BP1026B_I0487	AraC family transcriptional regulator	9232	9010	9664	10	8424	9031	8216	9	1.50E-13	4.37E-13	0.9	-0.152003093
BP1026B_I0488	major facilitator family transporter	2646	1742	2505	1	2152	1483	1736	1	1.94E-08	3.60E-08	1	0
BP1026B_I0489	LysR family transcriptional regulator	23109	13279	15148	18	10929	9268	11494	11	7.61E-37	1.28E-35	0.611111111	-0.710493383
BP1026B_I0490	isochorismatase superfamily hydrolase	45237	59293	56076	77	60222	63695	58998	88	1.82E-08	3.38E-08	1.142857143	0.192645078
BP1026B_I0491	hypothetical protein	438	280	445	1	255	258	173	0	6.23E-05	8.98E-05	0	#NUM!
BP1026B_I0492	amidohydrolase	22026	26352	25993	13	24903	25697	22569	12	2.15E-10	4.69E-10	0.923076923	-0.115477217
BP1026B_I0493	hypothetical protein	5360	3271	3187	4	1871	2046	2116	2	1.91E-29	2.04E-28	0.5	-1
BP1026B_I0494	hypothetical protein	4978	3144	3209	2	2476	2349	2954	1	6.39E-16	2.33E-15	0.5	-1
BP1026B_I0495	hypothetical protein	461	113	61	0	316	332	165	0	0.514337374	0.5394774	#DIV/0!	#DIV/0!
BP1026B_I0496	non-heme chloroperoxidase	7640	7697	6812	8	7481	6801	7395	8	4.21E-11	9.74E-11	1	0
BP1026B_I0498	hypothetical protein	3151	1874	2649	4	1918	1416	1860	2	1.71E-12	4.53E-12	0.5	-1
predicted RNA	-	16319	20152	20020	607	18056	13089	15207	498	4.02E-21	2.25E-20	0.820428336	-0.285550774
BP1026B_I0499	NAD(P)H-flavin oxidoreductase	22771	20940	22858	36	20745	22021	21005	35	9.25E-13	2.51E-12	0.972222222	-0.040641984
BP1026B_I0500	hypothetical protein	39075	65331	65157	149	59006	69257	57668	163	6.65E-10	1.40E-09	1.09359732	0.129559634
BP1026B_I0501	GntR family transcriptional regulator	6445	1656	3074	2	1712	1639	1964	1	2.14E-32	2.77E-31	0.5	-1
BP1026B_I0502	DJ-1/Pip1 family protein	5561	2951	4068	6	3410	2935	3429	5	1.51E-12	4.03E-12	0.833333333	-0.263034406
BP1026B_I0503	peptidase	71242	63025	65395	59	64324	61244	64806	56	7.11E-16	2.58E-15	0.949152542	-0.075288127
BP1026B_I0504	hypothetical protein	16274	13281	18542	104	12734	9990	12663	77	2.24E-24	1.63E-23	0.740384615	-0.433653177
BP1026B_I0505	hypothetical protein	271	303	467	1	306	480	416	2	0.806113293	0.822960796	2	1
BP1026B_I0506	DNA polymerase X family/PHP domain-containing protein	146793	98255	109145	60	105491	105395	107584	54	1.62E-17	6.79E-17	0.9	-0.152003093
BP1026B_I0507	hypothetical protein	5892	1894	2134	8	2558	1838	2918	5	1.79E-12	4.73E-12	0.625	-0.678071905
BP1026B_I0508	hypothetical protein	838	199	320	1	198	170	439	0	9.07E-06	1.39E-05	0	#NUM!
BP1026B_I0509	copper tolerance protein	6385	5974	6523	3	6557	6529	6336	3	4.19E-09	8.23E-09	1	0
BP1026B_I0510	multicopper oxidase	3592	5684	5244	3	5963	5413	5947	4	2.39E-05	3.54E-05	1.333333333	0.415037499
BP1026B_I0511	RND family efflux transporter MFP subunit	1395	1888	2466	4	2751	2980	2783	7	0.68485631	0.706155939	1.75	0.807354922
BP1026B_I0512	hypothetical protein	732	539	492	1	1006	728	711	2	0.62016584	0.64326422	2	1
BP1026B_I0513	copper-resistance membrane protein	842	203	330	0	402	473	671	0	0.499418394	0.524531622	#DIV/0!	#DIV/0!
BP1026B_I0514	methyl-accepting chemotaxis protein	157380	138463	136400	79	145623	134007	139293	76	2.91E-13	8.28E-13	0.962025316	-0.055853235
BP1026B_I0515	oxidoreductase	25745	22130	22967	18	22619	18660	20892	16	1.24E-16	4.83E-16	0.888888889	-0.169925001
BP1026B_I0516	oxidoreductase	6134	2922	3504	3	3689	3260	2310	2	3.74E-14	1.15E-13	0.666666667	-0.584962501
BP1026B_I0517	hypothetical protein	30157	34164	30439	20	32570	33130	35764	21	2.43E-07	4.14E-07	1.05	0.070389328
BP1026B_I0518	putrescine transport system permease	900	1280	1549	1	1023	1590	1436	1	0.058781353	0.068132437	1	0
BP1026B_I0519	putrescine ABC transport system, permease protein	613	955	543	0	532	1078	763	0	0.295550005	0.318691504	#DIV/0!	#DIV/0!
BP1026B_I0520	putrescine ABC transport system, ATP-binding protein	1498	1358	1357	1	1761	2500	2895	2	0.192869564	0.212505836	2	1
BP1026B_I0521	putrescine ABC transport system, binding exported protein	1318	1590	1820	1	1873	1654	2411	1	0.212083996	0.232490958	1	0
BP1026B_I0522	aminotransferase	200	360	187	0	259	242	161	0	0.250977974	0.272788895	#DIV/0!	#DIV/0!
BP1026B_I0523	glutamine synthetase	2176	2954	2436	1	2690	3274	3132	2	0.014794045	0.017989421	2	1
BP1026B_I0524	glutamine amidotransferase	1132	494	559	0	699	475	537	0	6.31E-04	8.46E-04	#DIV/0!	#DIV/0!
BP1026B_I0525	hypothetical protein	3921	5862	5590	12	7443	7415	6729	17	0.001598997	0.002084751	1.416666667	0.502500341
BP1026B_I0526	aldehyde dehydrogenase-like protein	24562	35702	31612	55	21369	37018	40514	65	2.81E-05	4.15E-05	1.181818182	0.2410081
BP1026B_I0527	aldehyde dehydrogenase family protein	27822	16739	17783	13	14513	14481	13759	9	1.01E-32	1.34E-31	0.692307692	-0.530514717
BP1026B_I0528	agmatinase	13670	18278	18371	17	14798	13033	14745	14	1.15E-18	5.31E-18	0.823529412	-0.280107919
BP1026B_I0529	hypothetical protein	4484	5513	6057	12	5196	5644	4447	12	1.53E-09	3.13E-09	1	0
BP1026B_I0530	co-chaperonin GroES	2923	4230	3400	12	4818	5083	5105	17	0.038003087	0.044811318	1.416666667	0.502500341
BP1026B_I0531	chaperonin GroEL	38197	34939	34933	21	30093	29308	32952	18	1.88E-14	5.97E-14	0.857142857	-0.222392421
BP1026B_I0532	hypothetical protein	5875	5097	5789	12	5832	6411	5752	13	1.36E-07	2.35E-07	1.083333333	0.115477217
BP1026B_I0533	ribonucleotide reductase, coenzyme B12-dependent	582807	557550	571856	225	557369	583826	554822	223	0.14514975	0.161471262	0.991111111	-0.012881291
BP1026B_I0535	2-aminobenzoate-CoA ligase	457541	405461	406019	260	426746	391402	446155	259	7.97E-10	1.67E-09	0.996153846	-0.005559525
BP1026B_I0536	hypothetical protein	164398	87836	88770	127	95048	87238	91126	102	2.44E-26	2.09E-25	0.803149606	-0.316259345
BP1026B_I0537	beta-oxoacyl-ACP synthase	571626	474499	485697	452	529125	502349	498017	451	6.90E-06	1.06E-05	0.997787611	-0.003195339
BP1026B_I0538	3-oxoacyl-ACP synthase	483770	453099	463620	467	488412	411377	474781	458	1.18E-10	2.63E-10	0.980728051	-0.00274952
BP1026B_I0539	metallobeta-lactamase-related protein	189304	184322	198745	214	191781	178520	182657	206	5.58E-13	1.55E-12	0.962616822	-0.054966459
BP1026B_I0540	polyketide synthase	1076733	834713	920251	246	965949	936556	948142	247	0.296229292	0.31934902	1.004065041	0.005852726
BP1026B_I0541	hypothetical protein	646483	486889	511177	256	562260	513741	583916	259	0.090800733	0.10348443	1.01171875	0.016808288
BP1026B_I0542	hypothetical protein	86561	80422	83813	224	97093	98799	98079	263	1.35E-07	2.34E-07	1.174107143	0.231564067
predicted RNA	-	78008	130601	120334	929	154928	172675	153404	1358	0.046572674	0.054526229	1.461786688	0.547732978
predicted RNA	-	18682	27196	22809	532	34018	35790	36770	826	0.069741753	0.080286942	1.552631579	0.634715536
predicted RNA	-	5131	8370	6693	420	9650	11856	9482	65	0.026133188	0.031137204	1.535714286	0.618909833
BP1026B_I0544	hypothetical protein	48874	79954	67411	138	81194	96043	86006	186	7.66E-05	1.10E-04	1.347826087	0.430634354
BP1026B_I0545	transposase B	4043	5720	5860	21	7540	8421	7869	33	0.012112957	0.014812605	1.571428571	0.652076697
BP1026B_I0546	alkyl hydroperoxide reductase subunit	34931	34546	37548	22	37265	35506	38938	23	3.29E-08	6.00E-08	1.045454545	0.064130337
BP1026B_I0547	alkyl hydroperoxide reductase protein	67682	88293	89624	145	104328	110170	106605	189	9.81E-05	1.39E-04	1.303448276	0.382333334
BP1026B_I0548	chitin binding domain-containing protein	612544	789669	733267	648	680065	717715	645448	620	0.42800608	0.453404243	0.956790123	-0.063725598
BP1026B_I0549	hypothetical protein	316	369	481	0	423	226	463	0	0.124433435	0.139856485	#DIV/0!	#DIV/0!
BP1026B_I0550	nitroreductase family protein	1655	412	905	1	752	375	288	0	3.66E-15	1.24E-14	0	#NUM!
BP1026B_I0551	hypothetical protein	25918	29964	28357	19	29561	28351	26944	19	5.82E-09	1.13E-08	1	0
BP1026B_I0553	hypothetical protein	10793	14945	13269	13	16509	15984	14595	16	1.36E-06	2.20E-06	1.230769231	0.299560282
BP1026B_I0552	transglutaminase-like superfamily protein	8953	4349	6166	6	4361	4526	37					

BP1026B_I0574	type VI secretion system	6457	7628	7783	4	16469	12992	13369	9	0.708827193	0.729671626	2.25	1.169925001
BP1026B_I0575	type VI secretion system	6692	10107	8147	15	21321	22355	24424	42	0.003049918	0.00390574	2.8	1.485426827
BP1026B_I0576	type VI secretion system	426	460	465	1	1553	1100	1518	3	1.40E-14	4.48E-14	3	1.584962501
BP1026B_I0577	type VI secretion system	1839	855	1268	0	1921	1373	1397	0	0.200154414	0.219875098	#DIV/0!	#DIV/0!
BP1026B_I0578	type VI secretion system	621	486	814	0	1055	1043	1078	1	0.117812103	0.132723954	#DIV/0!	#DIV/0!
BP1026B_I0579	type VI secretion system	1962	1088	1914	0	2010	1964	1394	0	0.015453796	0.018762543	#DIV/0!	#DIV/0!
BP1026B_I0580	type VI secretion system	4072	5604	6087	2	7070	8981	8767	3	0.025765602	0.030716755	1.5	0.584962501
BP1026B_I0581	type VI secretion system	6355	8652	8965	3	12362	12118	10609	5	0.005274239	0.006618943	1.666666667	0.736965594
BP1026B_I0582	type VI secretion system	8966	8216	8661	3	9438	9361	10913	4	9.63E-07	1.58E-06	1.333333333	0.415037499
BP1026B_I0583	type VI secretion system	3046	2886	1609	2	1301	1716	2409	1	9.01E-11	2.02E-10	0.5	-1
BP1026B_I0584	type VI secretion system	1273	1016	737	1	1272	1364	986	1	0.352102588	0.376433171	1	0
BP1026B_I0586	type VI secretion system	6236	8062	6865	18	10312	10620	9765	26	0.006789674	0.008458071	1.444444444	0.530514717
BP1026B_I0585	type VI secretion system	1241	532	848	1	1199	997	1004	1	0.434768491	0.460178947	1	0
BP1026B_I0587	type VI secretion system	2579	2702	2781	1	2933	3071	2846	2	0.001347641	0.001762906	2	1
BP1026B_I0588	type VI secretion system	3752	1826	3390	1	2850	2399	1	8.46E-07	1.40E-06	1	0	
BP1026B_I0589	type VI secretion system	11013	8292	10251	2	10527	11335	9963	3	3.79E-08	6.89E-08	1.5	0.584962501
BP1026B_I0590	hypothetical protein	10824	16555	14701	38	20268	25745	24043	64	0.237277759	0.259976213	1.684210526	0.752072487
BP1026B_I0591	hypothetical protein	1802	2280	2682	7	3841	4159	2470	11	0.771678836	0.789959089	1.571428571	0.652076697
BP1026B_I0592	hypothetical protein	10748	16407	15265	38	24225	27879	24674	68	0.778070431	0.796887664	1.789473684	0.839535328
BP1026B_I0593	rhamnosyltransferase I, subunit A	33685	43248	42159	44	49430	54501	48628	56	1.55E-04	2.17E-04	1.272727273	0.347925303
BP1026B_I0594	rhamnosyltransferase I, subunit B	15115	9990	10856	8	10917	9441	7706	6	3.63E-20	1.88E-19	0.75	-0.415037499
BP1026B_I0595	multidrug resistance protein	12562	8388	8193	6	9730	8705	8139	5	1.24E-13	3.64E-13	0.833333333	-0.263034406
BP1026B_I0596	rhamnosyltransferase II	11614	10622	10597	10	11107	10386	10203	10	3.42E-11	7.97E-11	1	0
BP1026B_I0597	RND efflux system outer membrane lipoprotein	17250	10153	12809	8	11474	11416	10796	7	9.10E-17	3.57E-16	0.875	-0.192645078
BP1026B_I0598	multidrug resistance protein	6413	6773	6889	4	8237	7234	5772	5	1.00E-08	1.90E-08	1.25	0.321928095
BP1026B_I0599	levansucrase	16672	16975	17454	10	14114	13468	15523	8	6.27E-19	2.95E-18	0.8	-0.321928095
BP1026B_I0600	levansucrase precursor	31115	24866	28139	18	29591	30639	29744	20	2.25E-07	3.84E-07	1.111111111	0.152003093
BP1026B_I0601	LacI family regulatory protein	15238	17310	16647	14	17201	17143	16036	15	2.23E-11	5.55E-11	1.071428571	0.099535674
BP1026B_I0603	hypothetical protein	163	550	270	1	441	444	314	1	0.906052343	0.916330118	1	0
BP1026B_I0602	glutathione-independent formaldehyde dehydrogenase	2222	2160	2077	1	2432	2739	3232	2	0.106397495	0.120453837	2	1
BP1026B_I0604	AraC family transcriptional regulator	2026	2013	2353	1	2425	2135	2241	2	0.001769338	0.00230205	2	1
BP1026B_I0605	serine hydroxymethyltransferase	1872	1565	1109	1	1137	1150	1085	0	1.73E-07	2.97E-07	0	#NUM!
BP1026B_I0606	renal dipeptidase family protein	686	1165	1077	1	1472	1053	1421	1	0.974513514	0.979044681	1	0
BP1026B_I0607	V4R domain-containing protein	418	276	448	0	206	747	333	0	0.649827702	0.672139383	#DIV/0!	#DIV/0!
BP1026B_I0608	NADH:flavin oxidoreductase	3027	1683	1357	0	1668	1867	2277	0	1.77E-04	2.47E-04	#DIV/0!	#DIV/0!
BP1026B_I0609	iron-sulfur cluster binding protein	671	891	458	0	432	831	474	0	0.007147404	0.008877232	#DIV/0!	#DIV/0!
BP1026B_I0610	electron transfer flavoprotein subunit alpha	785	389	257	0	185	293	381	0	6.54E-06	1.01E-05	#DIV/0!	#DIV/0!
BP1026B_I0611	electron transfer flavoprotein subunit beta	165	134	124	0	134	145	76	0	0.346160902	0.370144064	#DIV/0!	#DIV/0!
BP1026B_I0613	iron-sulfur Rieske protein	2919	3374	2744	2	3539	3630	3756	2	0.007828238	0.00969019	1	0
BP1026B_I0612	iron-sulfur cluster-binding protein	5050	6706	6595	5	8352	7248	6641	6	7.07E-06	1.09E-05	1.2	0.263034406
BP1026B_I0614	ABC transporter, periplasmic glycine/betaine-binding protein	2997	3047	2947	3	2121	3163	3225	3	3.94E-06	6.19E-06	1	0
BP1026B_I0615	hypothetical protein	29880	32163	29574	18	41611	41056	36782	24	8.51E-04	0.001129058	1.333333333	0.415037499
BP1026B_I0616	formyltetrahydrofolate deformylase	6102	5182	6838	6	6345	5652	6972	7	1.68E-08	3.14E-08	1.666666667	0.222392421
BP1026B_I0617	LysR family regulatory protein	2605	1616	1980	2	1582	1055	1511	1	1.58E-11	3.80E-11	0.5	-1
BP1026B_I0618	choline sulfatase	5298	6975	5854	3	7179	6418	6550	4	2.23E-07	3.81E-07	1.333333333	0.415037499
BP1026B_I0619	glycine betaine ABC transporter substrate-binding protein	1315	1406	1757	1	1034	1030	1196	1	6.52E-08	1.16E-07	1	0
BP1026B_I0620	outer membrane porin	2943	4124	3433	3	3497	3963	3358	3	2.37E-05	3.51E-05	1	0
BP1026B_I0621	aminopeptidase	4614	4540	4587	3	6014	5648	4906	4	5.34E-05	7.73E-05	1.333333333	0.415037499
BP1026B_I0622	metallopeptidase domain-containing protein	29344	34702	34183	19	36897	37443	34126	21	1.04E-06	1.70E-06	1.105263158	0.144389909
BP1026B_I0623	AraC family transcriptional regulator	7080	6414	7388	7	7117	5428	5165	6	1.74E-14	5.55E-14	0.857142857	-0.222392421
BP1026B_I0624	hypothetical protein	823	728	1036	3	531	1294	1396	4	0.522909621	0.548098079	1.333333333	0.415037499
BP1026B_I0625	ABC transporter, periplasmic glycine/betaine-binding protein	4972	6384	5754	5	6270	5999	5767	6	4.71E-08	8.46E-08	1.2	0.263034406
BP1026B_I0626	hypothetical protein	6935	5599	5663	6	4986	4704	5243	5	5.08E-14	1.55E-13	0.833333333	-0.263034406
BP1026B_I0628	3-hydroxybutyryl-CoA dehydrogenase	8926	8319	10531	9	9633	10269	9159	9	5.87E-09	1.14E-08	1	0
BP1026B_I0627	hypothetical protein	9951	7777	7737	17	6905	6110	7618	14	3.09E-18	1.37E-17	0.823529412	-0.280107919
BP1026B_I0629	lipase	8324	3869	4917	5	2885	2237	2741	2	2.90E-43	6.77E-42	0.4	-1.321928095
BP1026B_I0630	hypothetical protein	101851	102771	125710	356	101335	97275	98368	320	5.81E-18	2.52E-17	0.898876404	-0.153805336
BP1026B_I0631	short chain dehydrogenase/reductase family oxidoreductase	17239	9361	11477	12	10123	10438	10904	10	4.39E-17	1.78E-16	0.833333333	-0.263034406
BP1026B_I0632	hypothetical protein	45923	57863	56261	183	73398	79428	63850	248	2.64E-04	3.64E-04	1.355191257	0.438496472
BP1026B_I0634	leucine-, isoleucine-, valine-, threonine-, and alanine-binding protein precursor	302209	426590	383782	332	392164	408470	385978	354	7.16E-08	1.27E-07	1.06626506	0.092566119
BP1026B_I0635	high-affinity branched-chain amino acid transport system permease	14746	15952	16519	16	14744	14587	15206	16	5.07E-14	1.54E-13	1	0
BP1026B_I0636	leucine/isoleucine/valine transporter permease subunit	85421	86030	81219	66	69971	66513	74372	55	1.76E-23	1.21E-22	0.833333333	-0.263034406
BP1026B_I0637	leucine/isoleucine/valine transporter ATP-binding subunit	51986	52406	52017	67	49220	49652	49584	63	5.45E-14	1.65E-13	0.940298507	-0.088809267
BP1026B_I0638	Branched-chain amino acid transport ATP-binding protein LivF	59788	70702	73618	96	69620	67902	65313	96	5.27E-14	1.60E-13	1	0
BP1026B_I0639	hypothetical protein	868	1293	733	2	1931	2181	1047	4	0.02676655	0.031861551	2	1
BP1026B_I0640	hypothetical protein	47789	46018	46366	37	40833	36749	40798	31	6.33E-17	2.52E-16	0.837837838	-0.255257055
BP1026B_I0641	salicylate biosynthesis isochorismate synthase	6744	1345	2622	2	1734	1464	1239	1	2.74E-41	5.77E-40	0.5	-1
BP1026B_I0642	isochorismate-pyruvate lyase	115	57	111	0	77	176	130	0	0.180898026	0.199807339	#DIV/0!	#DIV/0!
BP1026B_I0643	pyochelin biosynthetic protein	4283	4068	4412	6	3218	3358	3888	5	4.34E-11	1.00E-10	0.833333333	-0.263034406
BP1026B_I0644	salicyl-AMP ligase	2647	1796	1310	1	1086	1177	1042	0	5.03E-16	1.86E-15	0	#NUM!
BP1026B_I0645	AraC family transcription regulator	2973	1343	1444	2	1518	1089	1273	1	5.39E-11	1.24E-10	0.5	-1
BP1026B_I0646	pyochelin synthetase	4005	2794	3254	0	3159	3343	3053	0	1.72E-06	2.76E-06	#DIV/0!	#DIV/0!
BP1026B_I0647	pyochelin synthetase	7500	5711	6238	1	5535	5719	4562	0	5.98E-15	1.99E-14	0	#NUM!
BP1026B_I0648	pyochelin biosynthetic protein	554	305	45	0	102	147	104	0	1.64E-08	3.07E-08	#DIV/0!	#DIV/0!
BP1026B_I0649	ABC transporter ATP-binding protein	549	291	461	0	153	9	47	0	1.11E-49	3.54E-48	#DIV/0!	#DIV/0!
BP1026B_I0650	ABC transporter	2694	1230	1456	1	847	411	715	0	2.38E-35	3.72E-34	0	#NUM!
BP1026B_I0651	Fe(III)-pyochelin receptor precursor	3662	3363	3871	1	3092	2452	3233	1	1.33E-10	2.94E-10	1	0
BP1026B_I0652	hypothetical protein	105	41	57	0	151	70	68	0	0.136763734	0.153138234	#DIV/0!	#DIV/0!
BP1026B_I0653	iron-regulated membrane protein	378	48	329	0	320	242	286	0	0.940030729	0.947897095	#DIV/0!	#DIV/0!
BP1026B_I0654	hypothetical protein	543	406	455	0	423	235	358	0	5.66E-04	7.62E-04	#DIV/0!	#DIV/0!
BP1026B_I0655	2Fe-2S iron-sulfur	1605	1119	1149	4	1392	1401	936	4	0.00438878	0.005481333	1	0
BP1026B_I0656	sigma-54 activated regulatory protein	50935	40846	41060	22	42724	37613	39844	20	8.02E-14	2.39E-13	0.909090909	-0.137503524
BP1026B_I0657	hypothetical protein	17430	7133	8962	57	9360	9487	9212	47	9.00E-17	3.54		

BP1026B_II0675	hypothetical protein	4582	2949	3019	3	3954	3511	4176	4	1.56E-04	2.18E-04	1.33333333	0.415037499
BP1026B_II0676	short chain dehydrogenase	8635	4554	5931	3	5975	4495	5111	2	1.03E-14	3.36E-14	0.666666667	-0.584962501
BP1026B_II0677	Xaa-Pro aminopeptidase	5798	5480	5766	6	11784	10739	10502	12	0.758970373	0.778220972	0.778220972	1
BP1026B_II0678	hypothetical protein	11330	11243	11223	14	8858	8656	10400	12	2.01E-17	8.35E-17	0.857142857	-0.222392421
BP1026B_II0679	modulation efficiency protein D	1294	557	942	0	853	914	562	0	9.52E-04	0.001258373	#DIV/0!	#DIV/0!
BP1026B_II0680	AraC family transcription regulator	14209	9222	10974	10	10036	9647	9177	8	1.48E-16	5.69E-16	0.8	-0.321928095
BP1026B_II0681	acyl-CoA dehydrogenase	196617	214444	208756	182	32770	34053	29229	28	0	0	0.153846154	-2.700439718
BP1026B_II0683	AMP-binding protein	191428	179444	188010	109	27252	26056	26869	15	0	0	0.137614679	-2.861293729
BP1026B_II0682	methylmalonate-semialdehyde dehydrogenase	227906	208942	217466	142	27900	28510	31036	19	0	0	0.133802817	-2.901819606
BP1026B_II0684	3-hydroxyisobutyrate dehydrogenase	48286	40598	44218	49	6042	6406	6379	6	0	0	0.12244898	-3.029747343
BP1026B_II0685	enoyl-CoA hydratase	50185	19379	23840	39	2494	2831	3054	3	0	0	0.076923077	-3.700439718
BP1026B_II0686	enoyl-CoA hydratase/isomerase family protein	127571	48132	63370	69	6959	5589	8432	6	0	0	0.086956522	-3.523561956
BP1026B_II0687	outer membrane efflux protein	65557	49016	52667	40	46683	43075	43677	32	2.47E-22	1.53E-21	0.8	-0.321928095
BP1026B_II0688	macrolide-specific ABC-type efflux carrier	231146	195400	206230	107	182366	180628	182139	92	1.50E-18	6.83E-18	0.859813084	-0.21790503
BP1026B_II0689	macrolide efflux protein MacA	130345	144822	142514	115	148592	144311	135486	118	9.63E-11	2.16E-10	1.026086957	0.037152998
BP1026B_II0690	luciferase-like monooxygenase	5585	4706	4697	4	4403	4168	4445	3	5.58E-11	1.28E-10	0.75	-0.415037499
BP1026B_II0691	ribonuclease T2 family protein	4395	5180	3976	6	4933	4703	4955	6	1.81E-06	2.91E-06	1	0
BP1026B_II0692	hypothetical protein	2459	2000	1611	4	1917	1515	1764	4	4.27E-06	6.68E-06	1	0
BP1026B_II0693	glutaminase	23734	22473	21177	24	20719	19319	22093	22	1.57E-14	5.01E-14	0.916666667	-0.125530882
BP1026B_II0694	hypothetical protein	15536	23846	23701	68	36955	40825	32672	119	0.438663227	0.463831215	1.75	0.807354922
BP1026B_II0695	DNA-binding response regulator	54727	57448	56363	79	66564	67482	69709	95	5.21E-07	8.72E-07	1.202531646	0.26607486
BP1026B_II0696	sensor histidine kinase	34581	27906	30971	27	29487	24941	28120	24	2.99E-13	8.49E-13	0.888888889	-0.169925001
BP1026B_II0697	putative patatin-like phospholipase	93033	117708	115290	46	127661	132800	125355	54	9.01E-07	1.48E-06	1.173913003	0.231325546
BP1026B_II0698	rod shape-determining protein MreB	332973	245928	269838	265	231949	208294	226393	208	2.74E-25	2.15E-24	0.78490566	-0.349408831
BP1026B_II0699	cytochrome c4 family protein	9573	5325	8177	31	5939	6552	6209	25	1.74E-17	7.28E-17	0.806451613	-0.310340121
BP1026B_II0700	HD domain-containing protein	6356	5975	6154	10	5094	5352	5090	8	3.35E-13	9.49E-13	0.8	-0.321928095
BP1026B_II0701	amylase-1,6-glucosidase family	57929	34723	38255	18	32614	31308	33943	14	8.84E-22	5.24E-21	0.777777778	-0.362570079
BP1026B_II0702	hypothetical protein	427847	167104	207780	1013	175050	124254	179306	604	8.60E-52	2.99E-50	0.596248766	-0.746013719
BP1026B_II0703	terpene cyclase	16031	12291	13980	58	16057	14017	15652	62	2.42E-09	4.85E-09	1.068965517	0.096215315
BP1026B_II0704	terpene cyclase	35755	22533	25500	51	25233	25955	27743	48	3.34E-11	7.80E-11	0.941176471	-0.087462841
BP1026B_II0705	glyoxalase/bleomycin resistance protein/dioxygenase superfamily protein	11519	12187	11924	24	13405	13805	13552	28	1.65E-07	2.84E-07	1.166666667	0.222392421
BP1026B_II0706	glutathione S-transferase-like protein	3052	1259	1695	3	1424	1074	1359	1	1.26E-12	3.39E-12	0.333333333	-1.584962501
BP1026B_II0707	hypothetical protein	12373	8160	9399	14	8371	7123	7541	10	1.27E-21	7.44E-21	0.714285714	-0.485426827
BP1026B_II0709	hypothetical protein	1361	2153	2258	3	2858	2670	3078	5	0.71842375	0.738700889	1.666666667	0.736965594
BP1026B_II0710	sensor kinase protein	15999	13042	15593	10	13343	11555	11636	8	1.17E-18	5.39E-18	0.8	-0.321928095
BP1026B_II0711	response regulator protein	10046	11665	10157	16	11887	12696	10448	17	7.18E-08	1.27E-07	1.0625	-0.087462841
BP1026B_II0712	DNA-binding protein	24553	29762	27582	31	37332	43308	36360	45	0.01820046	0.01446288	1.451612903	0.537656786
BP1026B_II0713	hypothetical protein	729219	1137353	977723	3511	1130479	1218341	1339277	4553	0.046774979	0.054742626	1.296781544	0.374935463
predicted RNA	-	53917	10264	12045	403	11315	10348	10775	171	7.89E-92	8.10E-90	0.424317618	-1.236783514
BP1026B_II0714	hypothetical protein	36307	41262	40772	120	46304	39550	43889	132	1.24E-07	2.16E-07	1.1	0.137503524
BP1026B_II0715	Rhodanese-related sulfurtransferase	1347	812	1303	2	1481	1106	1449	2	0.200281492	0.219976132	1	0
BP1026B_II0716	transcriptional activator FtrA	23959	13659	14572	18	11628	10285	13799	12	1.40E-29	1.51E-28	0.666666667	-0.584962501
BP1026B_II0717	hypothetical protein	3645	2955	3600	7	2636	2347	2613	5	2.63E-12	6.85E-12	0.714285714	-0.485426827
BP1026B_II0718	M20/M25/M40 family peptidase	237029	220912	234616	158	210395	207303	205312	143	4.31E-17	1.74E-16	0.905063291	-0.143909411
BP1026B_II0719	hypothetical protein	37527	23699	28375	82	20074	19236	21378	55	3.42E-33	4.72E-32	0.670731707	-0.576192291
BP1026B_II0720	hypothetical protein	62727	41633	43550	85	37634	34739	38482	63	4.17E-23	2.77E-22	0.741176471	-0.432111013
BP1026B_II0721	insertion element membrane protein	29274	41806	35559	133	35477	43038	36077	143	1.61E-07	2.77E-07	1.07518797	0.104588901
BP1026B_II0722	hypothetical protein	714	1239	1081	4	895	1417	1170	4	0.21222208	0.232601636	1	0
BP1026B_II0723	x-prolyl-dipeptidyl aminopeptidase	45381	66286	61836	29	55243	56977	53692	28	1.17E-14	3.79E-14	0.965517241	-0.050626073
BP1026B_II0724	hypothetical protein	4362	6158	6871	26	5188	5822	4455	23	1.29E-11	3.14E-11	0.884615385	-0.176877762
BP1026B_II0725	serine-type carboxypeptidase family protein	27084	47451	43763	22	35933	40474	33567	20	6.22E-12	1.56E-11	0.909090909	-0.137503524
BP1026B_II0726	hypothetical protein	21460	32931	28317	69	29683	35533	30377	80	1.06E-05	1.62E-05	1.15942029	0.213403638
BP1026B_II0727	hypothetical protein	6702	10468	9796	39	10937	12231	11901	51	1.25E-04	1.76E-04	1.307692308	0.387023123
BP1026B_II0728	transposase B	2224	3461	3143	13	3318	3036	2999	14	2.94E-04	4.04E-04	1.076923077	0.106915204
BP1026B_II0729	hypothetical protein	4899	8438	7544	17	10751	11619	9654	26	0.025602883	0.030528576	1.529411765	0.612976877
BP1026B_II0730	hypothetical protein	15326	28206	21745	10	30182	34471	30362	15	0.018366703	0.022183069	1.5	0.584962501
BP1026B_II0731	hypothetical protein	1378	2966	2526	5	3945	4001	3028	8	0.928713778	0.937541571	1.6	0.678071905
BP1026B_II0732	transposase	5496	8133	7286	26	11452	11619	10433	42	0.059102543	0.068479389	1.615384615	0.691877705
BP1026B_II0733	integrase core subunit	1123	1853	1455	8	1371	1237	1944	8	0.011347066	0.013911974	1	0
BP1026B_II0734	hypothetical protein	2139	3691	2497	7	3523	4601	3923	10	0.230885223	0.252174797	1.428571429	0.514573173
BP1026B_II0735	hypothetical protein	3238	5206	2843	6	5517	6626	6486	9	0.020079857	0.024168341	1.5	0.584962501
BP1026B_II0736	response regulator protein	2299	3351	3849	3	3771	4607	3761	5	0.180848874	0.199782666	1.666666667	0.736965594
BP1026B_II0737	hypothetical protein	2897	2687	3431	6	3895	4809	3104	8	0.036747215	0.043371265	1.333333333	0.415037499
BP1026B_II0738	alpha-ketoglutarate-dependent taurine dioxygenase	8159	14771	15162	14	15925	18251	17637	19	2.42E-04	3.35E-04	1.357142857	0.440572591
BP1026B_II0739	peptidase	21401	32584	32471	15	30582	34320	33420	17	5.19E-06	8.08E-06	1.133333333	0.180572246
BP1026B_II0740	acetyltransferase	18571	27698	27869	40	27632	32254	28786	48	3.74E-05	5.46E-05	1.2	0.263034406
BP1026B_II0741	hypothetical protein	34361	50358	49622	204	46380	49777	45513	215	2.12E-09	4.28E-09	1.053921569	0.07567508
BP1026B_II0743	EmrB/QacA family drug resistance transporter	23187	27511	24798	18	37227	40241	37949	27	0.052887182	0.061539663	1.5	0.584962501
BP1026B_II0744	trehalase	11865	11877	11973	7	13305	13776	10393	7	2.20E-09	4.43E-09	1	0
BP1026B_II0745	hypothetical protein	1562	1988	2295	2	2783	2306	2504	3	0.045654878	0.162628914	1.5	0.584962501
BP1026B_II0746	cytochrome c oxidase, subunit III family protein	821	1509	1198	1	1279	1153	1035	1	0.010520176	0.012915248	1	0
BP1026B_II0748	LuxR family transcriptional regulator	18657	20104	20027	21	20053	20431	18751	22	1.12E-11	2.75E-11	1.047619048	0.067114196
BP1026B_II0749	hypothetical protein	11978	7259	8403	11	7513	6649	7191	8	7.34E-21	4.02E-20	0.727272727	-0.459431619
BP1026B_II0750	asparagine synthase	42537	28648	36872	18	27284	21695	25814	12	9.63E-27	8.52E-26	0.666666667	-0.584962501
BP1026B_II0751	two-component system response regulator	2185	3232	2617	5	3528	3367	3886	7	0.103457699	0.117269526	1.4	0.485426827
BP1026B_II0752	isoquinoline 1-oxidoreductase subunit beta	61929	37372	44524	21	34423	28875	35597	14	1.15E-27	1.09E-26	0.666666667	-0.584962501
BP1026B_II0753	isoquinoline 1-oxidoreductase subunit alpha	7588	9714	9391	19	7991	7564	8551	17	1.95E-14	6.15E-14	0.894736842	-0.160464672
BP1026B_II0754	AraC family transcription regulator	63860	47318	50740	55								

BP1026B_I0774	outer membrane porin protein	24270	21734	23279	21	18065	16197	18368	16	1.57E-26	1.37E-25	0.761904762	-0.392317423
BP1026B_I0775	ABC transporter ATP-binding protein	1236	376	723	0	512	412	333	0	1.11E-10	2.47E-10	#DIV/0!	#DIV/0!
BP1026B_I0776	transmembrane ABC transporter protein	1409	1073	951	0	1018	823	1381	0	0.003256072	0.004160388	#DIV/0!	#DIV/0!
BP1026B_I0777	periplasmic solute-binding protein	3355	4880	4020	3	4361	5074	3886	4	7.01E-06	1.08E-05	1.333333333	0.415037499
BP1026B_I0778	DNA-binding response regulator TctD	598	466	408	0	81	442	265	0	1.43E-07	2.48E-07	#DIV/0!	#DIV/0!
BP1026B_I0779	sensor histidine kinase	1835	678	1220	0	414	530	1192	0	2.55E-11	6.02E-11	#DIV/0!	#DIV/0!
BP1026B_I0780	MOSC domain-containing protein	37983	30295	30890	37	32435	33219	28804	36	1.80E-10	3.94E-10	0.972972973	-0.039528364
BP1026B_I0781	hypothetical protein	1395	2715	1902	4	2619	2707	2986	6	0.30772621	0.330853197	1.5	0.584962501
BP1026B_I0782	outer membrane porin	285889	253425	268936	223	209615	194409	214573	171	7.24E-28	6.98E-27	0.766816143	-0.383047385
BP1026B_I0783	hypothetical protein	18616	17963	15908	41	19532	21025	18254	46	2.75E-08	5.04E-08	1.12195122	0.166009951
BP1026B_I0784	enoyl-CoA hydratase	22330	17094	17374	24	15713	14715	12019	18	4.44E-26	3.71E-25	0.75	-0.415037499
BP1026B_I0785	alanine racemase	70440	52948	56807	53	44173	40160	46211	38	7.39E-29	7.67E-28	0.716981132	-0.479992941
BP1026B_I0786	hypothetical protein	39658	39385	40701	104	42271	38415	34818	101	7.06E-11	1.60E-10	0.971153846	-0.042228235
BP1026B_I0787	hypothetical protein	28162	26203	32332	23	22928	20702	20947	17	1.20E-24	8.93E-24	0.739130435	-0.436099115
BP1026B_I0788	hypothetical protein	36578	24457	29632	30	19443	16809	22902	19	3.37E-37	5.76E-36	0.633333333	-0.658963082
BP1026B_I0789	hypothetical protein	5399	2547	2863	7	2435	1514	2065	4	2.25E-23	1.52E-22	0.571428571	-0.807354922
BP1026B_I0790	hydrolase alpha/beta fold domain-containing protein	30643	16942	21629	28	16289	14862	17771	19	1.35E-31	1.64E-30	0.678571429	-0.559427409
BP1026B_I0791	hypothetical protein	29361	14944	19698	16	12093	9837	13144	9	2.13E-51	7.30E-50	0.5625	-0.830074999
BP1026B_I0792	TetR family transcriptional regulator	289800	436254	365120	563	408989	446215	446729	672	1.99E-05	2.96E-05	1.193605684	0.255326311
BP1026B_I0793	peptidase	28935	25436	25457	39	28209	25387	26034	38	1.83E-09	3.71E-09	0.974358974	-0.037474705
BP1026B_I0794	NADH:flavin oxidoreductase	20443	14964	16266	15	13674	14415	13905	12	1.20E-20	6.44E-20	0.8	-0.321928095
BP1026B_I0795	enoyl-ACP reductase	196753	188867	196419	254	196891	181581	217285	260	4.06E-11	9.41E-11	1.023622047	-0.033683126
BP1026B_I0796	hypothetical protein	121228	101281	105268	172	110354	110695	105713	172	1.28E-12	3.43E-12	1	0
BP1026B_I0797	hypothetical protein	26298	20127	19337	20	19444	18530	18387	17	3.54E-19	1.71E-18	0.85	-0.234465254
BP1026B_I0798	osmotically-inducible lipoprotein OsmE	49921	69322	59847	150	77095	78358	81911	199	4.53E-05	6.58E-05	1.326666667	-0.487080593
BP1026B_I0799	D-beta-hydroxybutyrate dehydrogenase	39726	40418	37712	49	42499	47304	43110	55	5.34E-07	8.93E-07	1.12244898	0.166649869
BP1026B_I0800	GntR family transcriptional regulator	15253	6636	8097	6	7667	6832	7154	4	7.60E-25	5.76E-24	0.666666667	-0.584962501
BP1026B_I0801	hypothetical protein	5966	5518	5950	8	5301	5231	4423	6	1.77E-12	4.68E-12	0.75	-0.415037499
BP1026B_I0803	cyclic nucleotide-binding domain-containing protein	103414	113730	116737	121	128907	123733	131766	139	1.58E-07	2.72E-07	1.148760331	0.200077835
BP1026B_I0804	acyl-CoA synthetase	1136292	894264	913278	590	664426	650563	688243	401	0.007494696	0.009290161	0.679661017	-0.557112718
BP1026B_I0805	methyl-accepting chemotaxis protein II	121199	60133	74166	41	59470	51126	57485	27	4.08E-42	8.97E-41	0.658536585	-0.602664502
BP1026B_I0806	outer membrane efflux protein	6203	4923	5723	3	3887	3469	3811	2	7.98E-20	4.03E-19	0.666666667	-0.584962501
BP1026B_I0807	beta 1,3 glucan synthase catalytic subunit	2427	2361	2361	1	2071	3120	1587	1	2.63E-05	3.89E-05	1	0
BP1026B_I0808	hypothetical protein	485	383	234	0	259	232	176	0	2.43E-04	3.36E-04	#DIV/0!	#DIV/0!
BP1026B_I0809	hypothetical protein	1739	668	1382	0	880	587	533	0	1.13E-13	3.34E-13	#DIV/0!	#DIV/0!
BP1026B_I0810	DNA-binding protein	15868	25806	22624	64	30488	32788	29543	93	0.015097931	0.018341146	1.453125	0.539158811
BP1026B_I0811	hypothetical protein	5180	2086	2176	6	5418	2118	1760	5	8.40E-11	1.89E-10	0.833333333	-0.263034406
BP1026B_I0812	cupin domain-containing protein	13762	9270	11445	23	8355	7044	9032	16	3.97E-26	3.34E-25	0.695652174	-0.523561956
BP1026B_I0813	hypothetical protein	991	1307	1542	1	1607	2190	1096	2	0.489308776	0.514776492	2	1
BP1026B_I0814	LysR family regulatory protein	36285	30488	34579	35	32656	32164	33163	34	4.66E-10	9.94E-10	0.971428571	-0.041820176
BP1026B_I0815	beta alanine-pyruvate transaminase	21314	14625	17107	11	16042	14607	11907	9	1.39E-21	8.09E-21	0.818181818	-0.289506617
BP1026B_I0816	methylmalonate-semialdehyde dehydrogenase	24342	21474	22743	15	21979	20865	23835	14	1.09E-11	2.67E-11	0.933333333	-0.099535674
BP1026B_I0817	putative TIS1412-transposase orfA protein	2100	2436	2087	6	2147	2773	2337	6	0.002797657	0.003591502	1	0
BP1026B_I0818	hypothetical protein	3516	5712	4820	6	4851	4874	4617	7	1.78E-07	3.06E-07	1.166666667	0.222392421
BP1026B_I0819	secretory lipase family protein	10940	15328	15227	11	17361	19496	17843	14	7.62E-05	1.09E-04	1.272727273	0.347923303
BP1026B_I0820	hypothetical protein	81	121	88	0	29	92	4	0	3.59E-04	4.90E-04	#DIV/0!	#DIV/0!
BP1026B_I0821	outer membrane porin protein	2007	2701	2041	2	2311	2248	2811	2	0.002479986	0.003195475	1	0
BP1026B_I0822	hypothetical protein	7641	6446	7714	19	7581	8599	5910	19	4.18E-10	8.94E-10	1	0
BP1026B_I0823	LuxR family transcriptional regulator	3376	4450	4436	4	4361	3958	5203	5	1.10E-05	1.67E-05	1.25	0.321928095
BP1026B_I0824	amino acid permease	3528	1669	2117	1	2575	1600	2757	1	2.07E-05	3.08E-05	1	0
BP1026B_I0825	peptidase	1123	818	664	0	759	1118	788	0	0.050849741	0.059312077	#DIV/0!	#DIV/0!
BP1026B_I0826	lipoprotein	5178	4464	4177	2	4172	4579	6009	2	1.11E-06	1.81E-06	1	0
BP1026B_I0827	hypothetical protein	163	315	112	0	219	218	208	0	1	1	#DIV/0!	#DIV/0!
BP1026B_I0828	fusaric acid resistance domain-containing protein	731	896	663	0	622	396	572	0	1.26E-05	1.91E-05	#DIV/0!	#DIV/0!
BP1026B_I0829	LysR family transcriptional regulator	6050	4199	4555	4	5294	4330	4961	4	2.17E-08	4.00E-08	1	0
BP1026B_I0830	hypothetical protein	490	160	312	1	592	176	715	1	0.082219549	0.094115399	1	0
BP1026B_I0831	outer membrane porin OpcP	2139	2185	2623	2	2279	1471	2145	1	7.28E-07	1.21E-06	0.5	-1
BP1026B_I0832	glyoxalase family protein	5599	2867	3713	9	2619	2757	3889	7	4.94E-13	1.38E-12	0.777777778	-0.362570079
BP1026B_I0833	cytosine permease	82935	70992	75271	60	67178	66260	68858	53	5.09E-20	2.61E-19	0.883333333	-0.178970141
BP1026B_I0834	DNA-binding protein	75325	93550	88279	69	82463	84267	86029	68	6.70E-15	2.22E-14	0.985507246	-0.021061616
BP1026B_I0835	cytosine deaminase	67645	66790	63960	52	59508	55930	56303	45	3.35E-20	1.74E-19	0.865384615	-0.208586622
BP1026B_I0836	membrane protein	7741	6850	7722	5	7007	7053	7470	5	1.69E-11	4.05E-11	1	0
BP1026B_I0837	hypothetical protein	12053	12019	11056	12	10757	11826	12100	12	8.07E-11	1.82E-10	1	0
BP1026B_I0838	short chain dehydrogenase	3222	2456	2391	3	2268	2131	2151	2	1.46E-08	2.74E-08	0.666666667	-0.584962501
BP1026B_I0839	GntR family transcriptional regulator	5600	6168	6966	8	5809	5994	6142	8	1.52E-10	3.34E-10	1	0
BP1026B_I0840	voltage gated chloride channel family protein	18801	17980	16699	13	15817	19330	16442	12	1.16E-13	3.42E-13	0.923076923	-0.115477217
BP1026B_I0841	hypothetical protein	657844	1043392	938608	2715	917095	988370	892827	2878	0.208569885	0.228758778	1.060036832	0.084114394
BP1026B_I0842	cytochrome c peroxidase	23132	15327	16239	11	15024	13602	14713	8	1.66E-22	1.04E-21	0.727272727	-0.459431619
BP1026B_I0844	twin-arginine translocation pathway signal sequence domain-containing protein	2990	652	1965	1	771	1264	924	1	3.81E-19	1.83E-18	1	0
BP1026B_I0845	hypothetical protein	62	7	38	0	0	35	0	0	1.83E-04	2.55E-04	#DIV/0!	#DIV/0!
BP1026B_I0846	GerE family regulatory protein	978	780	669	1	783	884	652	1	0.024370543	0.029131214	1	0
BP1026B_I0847	LigA protein	386	615	500	1	324	589	461	0	0.049443672	0.052687941	0	#NUM!
BP1026B_I0848	hypothetical protein	2404	2892	2370	11	3756	3594	4226	17	0.467333519	0.493147833	1.545454545	0.628031223
BP1026B_I0849	MarR family regulatory protein	22204	7383	8922	26	5505	3394	5326	9	6.92E-97	7.89E-95	0.346153846	-1.530514717
BP1026B_I0850	galactose-binding protein regulator	672	702	855	1	691	530	515	1	4.77E-04	6.46E-04	1	0
BP1026B_I0852	sugar ABC transporter permease	469	145	574	1	258	235	480	1	0.017012523	0.020575269	1	0
BP1026B_I0853	senescence marker protein-30 family protein	4748	1179	1637	2	816	919	1199	1	9.89E-42	2.14E-40	0.5	-1
BP1026B_I0851	hypothetical protein	10354	10921	9290	19	11048	12247	12823	22	2.21E-06	3.52E-06	1.157894737	0.211504105
BP1026B_I0854	hypothetical protein	24820	21064	22497	51	18846	18241	18309	41	2.04E-22	1.27E-21	0.803921569	-0.314873337
BP1026B_I0855	hypothetical protein	6422	7896	5963	13	10119	12404	10696	21	0.090311772	0.102964622	1.615384615	0.691877705
BP1026B_I0856	Leu tRNA	31349	50515	40933	481	75123	77865	80945	917	0.707192521	0.728228157	1.906444906	0.93088484
BP1026B_I0857	p												

BP1026B_I0875	hypothetical protein	0	0	45	0	51	0	28	0	0.139673431	0.156284593	#DIV/0!	#DIV/0!
BP1026B_I0876	H-NS histone family protein	1020	1154	1418	3	1310	1127	936	3	0.003293999	0.004207991	1	0
BP1026B_I0877	IcIR family transcriptional regulator	2228	1736	2442	2	2171	1457	2145	2	1.51E-05	2.28E-05	1	0
BP1026B_I0878	hypothetical protein	3067	2680	2823	6	3669	2652	3510	7	0.003204185	0.004095762	1.166666667	0.222392421
BP1026B_I0879	EAL domain-containing protein	1919	1644	1998	1	1291	1550	1322	1	3.78E-08	6.87E-08	1	0
BP1026B_I0880	TetR family transcriptional regulator	15133	16631	16518	26	17993	20112	13899	28	9.40E-10	1.96E-09	1.076923077	0.106915204
BP1026B_I0881	thioesterase (4HBT) superfamily protein	43037	48950	48397	106	45263	44738	48682	105	1.28E-11	3.11E-11	0.990566038	-0.013674937
BP1026B_I0882	putative extracellular ligand binding protein	1030142	1164790	1136652	971	1084834	1120523	1061390	952	0.371449924	0.396036281	0.980432544	-0.028509722
BP1026B_I0883	hemolysin III	81197	56881	60235	106	67042	65649	71688	109	1.75E-12	4.64E-12	1.028301887	0.04026387
BP1026B_I0884	hypothetical protein	4093	3484	4107	7	4860	3893	4333	8	3.37E-05	4.94E-05	1.142857143	0.192645078
BP1026B_I0885	EAL/GGDEF domain-containing protein	22555	23299	23097	11	21175	21866	20380	10	2.21E-14	6.96E-14	0.909090909	-0.137503524
BP1026B_I0886	AsnC family transcriptional regulator	21873	23448	22659	47	25961	24488	28908	53	1.04E-06	1.70E-06	1.127659574	0.173331603
BP1026B_I0887	aromatic amino acid transport protein	29167	33684	32746	22	40317	44173	41419	30	0.001016934	0.001341215	1.363636364	0.447458977
BP1026B_I0888	aromatic amino acid aminotransferase	89749	85536	83831	71	83795	82656	81212	68	2.85E-16	1.07E-15	0.957746479	-0.062284278
BP1026B_I0889	hypothetical protein	24130	23219	25175	61	21864	22225	20927	55	4.69E-15	1.58E-14	0.901639344	-0.149377624
BP1026B_I0890	acetyltransferase	40857	56410	51801	80	51510	51662	46540	81	1.35E-11	3.27E-11	1.0125	0.017921908
BP1026B_I0891	ZOG-Fe(II) oxygenase	26508	26915	27190	41	23306	22587	26123	36	7.98E-14	2.38E-13	0.87804878	-0.187627003
BP1026B_I0892	hypothetical protein	38621	39473	40622	30	36314	34254	34320	26	1.09E-13	3.21E-13	0.866666667	-0.206450877
BP1026B_I0893	hypothetical protein	110962	141935	134246	268	156998	166054	169248	341	4.90E-04	6.63E-04	1.27238806	0.347538739
BP1026B_I0894	hypothetical protein	1612	875	1133	3	530	414	765	1	5.22E-17	2.10E-16	0.333333333	-1.584962501
BP1026B_I0895	sensor histidine kinase	7513	8041	7608	5	8400	8121	9537	6	1.56E-07	2.68E-07	1.2	0.263034406
BP1026B_I0896	response regulator	3435	4095	3937	10	3378	3179	2918	8	2.10E-10	4.59E-10	0.8	-0.321928095
BP1026B_I0897	CheC family protein	6413	3986	5085	8	4392	4041	4626	7	6.81E-12	1.70E-11	0.875	-0.192645078
BP1026B_I0898	penicillin-binding protein 1C	51555	37780	41286	16	34259	29603	32503	11	1.76E-22	1.10E-21	0.6875	-0.540568381
BP1026B_I0899	alpha-2-macroglobulin family protein	205673	101596	124257	23	98011	82251	95492	14	1.20E-48	3.61E-47	0.608095652	-0.716207034
BP1026B_I0900	hypothetical protein	11445	17776	14500	26	25543	32062	27780	51	0.629948883	0.652979272	1.961338462	0.971985624
BP1026B_I0901	hypothetical protein	4596	2564	3620	7	2213	2177	2803	5	1.96E-16	7.49E-16	0.714285714	-0.485426827
BP1026B_I0902	leucyl-tRNA synthetase	9177	5185	5869	3	5233	4466	6203	2	2.16E-16	8.18E-16	0.666666667	-0.584962501
BP1026B_I0903	hypothetical protein	1463	1041	680	1	636	881	618	0	4.24E-07	7.12E-07	0	#NUM!
BP1026B_I0904	hypothetical protein	5792	2416	2746	4	1793	2000	1617	1	1.24E-29	1.35E-28	0.25	-2
BP1026B_I0905	hypothetical protein	3957	1988	2306	1	2433	1822	2524	1	1.77E-08	3.30E-08	1	0
BP1026B_I0906	TauD/TtdA family dioxygenase	9001	4038	5285	6	5342	3038	4359	4	3.47E-19	1.68E-18	0.666666667	-0.584962501
BP1026B_I0907	hypothetical protein	9923	7264	8355	12	8306	8315	9740	12	9.63E-10	2.00E-09	1	0
BP1026B_I0908	aminotransferase class-V	87907	87317	85955	76	104778	102120	105980	91	9.34E-07	1.54E-06	1.197368421	0.259867127
BP1026B_I0909	hypothetical protein	7863	7506	9209	29	7424	7306	9828	29	6.35E-11	1.45E-10	1	0
BP1026B_I0910	peptidase	958088	1208174	1128950	565	1256976	1335528	1209195	651	0.154068808	0.171351642	1.152212389	0.204406676
BP1026B_I0911	hypothetical protein	54527	33378	37545	129	35051	32806	36065	106	1.32E-16	5.11E-16	0.821705426	-0.283306801
BP1026B_I0912	monooxygenase	70128	67027	63192	57	59908	52739	55833	48	1.03E-21	6.04E-21	0.842105263	-0.247927513
BP1026B_I0913	DNA-binding protein	15234	19528	18911	24	16200	17036	16137	22	1.43E-15	5.04E-15	0.916666667	-0.125530882
BP1026B_I0914	hypothetical protein	105391	136693	122135	642	155469	162950	171647	864	0.004468423	0.005635898	1.345794933	0.428458015
BP1026B_I0916	hypothetical protein	51976	35224	35683	91	37326	35036	36375	80	6.31E-14	1.90E-13	0.879120879	-0.185866545
BP1026B_I0915	hypothetical protein	1104488	1286668	1220990	4137	1326256	1257011	1520693	4700	0.13586491	0.152213397	1.136088953	0.184075799
BP1026B_I0917	hypothetical protein	82625	56954	56026	275	62018	65737	57188	260	3.67E-16	1.37E-15	0.945454545	-0.080919995
BP1026B_I0918	LuxR family DNA-binding response regulator	281243	266358	272518	421	236782	226580	241241	362	4.56E-19	2.17E-18	0.859857482	-0.217830536
BP1026B_I0919	universal stress protein	430555	154435	203848	572	141081	115781	143538	290	2.47E-85	2.31E-83	0.506993007	-0.979962247
BP1026B_I0920	universal stress protein family protein	143558	55069	69904	106	54999	42798	53228	60	3.32E-60	1.64E-58	0.566037736	-0.821029859
BP1026B_I0921	universal stress protein	108908	59519	63041	155	54105	42895	50478	99	2.22E-43	5.23E-42	0.638709677	-0.646767785
BP1026B_I0922	universal stress protein family protein	819189	571959	615531	796	573758	519975	536997	647	7.27E-04	9.70E-04	0.81281407	-0.299002719
BP1026B_I0923	zinc-containing alcohol dehydrogenase	720040	612698	659074	637	626262	568397	625957	582	0.210402797	0.230688351	0.913657771	-0.130274129
BP1026B_I0924	dedA family protein	114901	81581	86145	82	82771	71756	76405	67	2.01E-25	1.60E-24	0.817031701	-0.291462814
BP1026B_I0925	major facilitator superfamily protein	5488	3387	3349	3	3527	3383	4084	3	6.82E-09	1.31E-08	1	0
BP1026B_I0926	short chain dehydrogenase/reductase family oxidoreductase	1544	1531	1547	1	1678	1784	1842	2	0.07029439	0.08086331	2	1
BP1026B_I0927	methyltransferase CmcJ	9452	8855	8805	10	8899	10285	9840	11	2.07E-08	3.83E-08	1.1	0.137503524
BP1026B_I0929	amino acid permease	85391	85658	82045	57	81736	86987	90285	59	4.28E-13	1.20E-12	1.035087719	0.049753035
BP1026B_I0930	DNA-binding protein	24477	40689	39218	143	51685	67051	43920	223	0.08230211	0.094192698	1.559405559	0.641028563
BP1026B_I0931	H-NS histone family protein	60681	89435	86342	270	105691	120314	103779	377	0.001519068	0.001982603	1.396296296	0.481605116
BP1026B_I0932	acyl-CoA dehydrogenase domain-containing protein	23227	154435	13220	11	8578	8827	9074	6	3.30E-43	7.69E-42	0.545454545	-0.874469118
BP1026B_I0933	hypothetical protein	2158	2821	2447	4	2741	3852	2918	6	0.057031858	0.066190335	1.5	0.584962501
BP1026B_I0934	hypothetical protein	2967	4786	4047	4	4580	4348	5600	5	3.47E-04	4.74E-04	1.25	0.321928095
BP1026B_I0935	hypothetical protein	353	634	271	1	366	333	354	1	0.015474916	0.018780907	1	0
BP1026B_I0936	nitrotriacetate monooxygenase component A	5123	2145	2545	2	2218	1827	3092	1	9.78E-13	2.65E-12	0.5	-1
BP1026B_I0937	inosine-uridine preferring nucleoside hydrolase	39848	28472	30355	33	25343	26206	23077	25	4.36E-21	2.44E-20	0.757575758	-0.40053793
BP1026B_I0938	ribokinase	57231	38636	43170	49	31265	28168	33795	33	5.56E-29	5.82E-28	0.673469388	-0.570315725
BP1026B_I0939	hypothetical protein	4001	2418	2987	6	2117	3109	2812	5	2.55E-08	4.68E-08	0.833333333	-0.263034406
BP1026B_I0940	hypothetical protein	24377	14868	17937	11	16381	16870	17942	10	5.53E-17	2.23E-16	0.909090909	-0.137503524
BP1026B_I0941	hypothetical protein	43149	22652	25047	13	18196	15355	20955	8	6.41E-48	1.90E-46	0.615384615	-0.700439718
BP1026B_I0942	L-2-amino-thiazoline-4-carboxylic acid hydrolase	6320	6673	5462	5	4865	4408	5236	4	2.31E-15	7.98E-15	0.8	-0.321928095
BP1026B_I0943	L-2-Amino-thiazoline-4-carboxylic acid hydrolase	1500	332	223	2	310	231	270	1	3.01E-17	1.24E-16	0.5	-1
BP1026B_I0944	N-carbamoyl-L-cysteine amidohydrolase	5041	2146	3363	6	2074	2692	2538	4	6.22E-15	2.06E-14	0.666666667	-0.584962501
BP1026B_I0945	flagellar hook-associated protein 2	1546469	1656484	1676031	1067	1872974	1790109	1830638	1201	0.149794019	0.166952922	1.125885754	0.17675975
BP1026B_I0946	LysR family transcriptional regulator	16453	12042	13639	15	15086	15743	13030	16	2.39E-10	5.19E-10	1.066666667	0.093109404
BP1026B_I0947	protein-disulfide isomerase	3442	3143	3518	4	2530	2910	3579	4	9.40E-08	1.65E-07	1	0
BP1026B_I0948	aldo/keto reductase family oxidoreductase	274168	355800	340258	341	362169	351630	363776	378	1.55E-07	2.67E-07	1.108504399	0.148614495
BP1026B_I0949	hypothetical protein	2585	3574	2623	10	3532	3380	2736	11	8.66E-04	0.00148411	1.1	0.137503524
BP1026B_I0951	MoaF protein precursor	9017	8055	9270	10	7324	7749	8662	9	1.77E-14	5.63E-14	0.9	-0.152003093
BP1026B_I0950	3-ketoacyl-ACP reductase	1632	1167	1037	1	859	751	784	0	1.01E-09	2.09E-09	0	#NUM!
BP1026B_I0952	LuxR family transcriptional regulator	1626	1076	1672	2	1113	1047	1227	1	1.84E-06	2.95E-06	0.5	-1
BP1026B_I0953	phenylacetaldehyde dehydrogenase	3840	3423	4542	2	4238	4284	4713	2	2.82E-05	4.15E-05	1	0
BP1026B_I0954	hypothetical protein	8102	7335	7058	5	6286							

BP1026B_I0975	MgtC family protein	6882	7640	7890	10	9095	8599	8973	12	3.40E-06	5.37E-06	1.2	0.263034406
BP1026B_I0976	calcineurin-like phosphoesterase	15609	9085	11699	10	7403	7534	7038	6	5.13E-39	9.56E-38	0.6	-0.736965594
BP1026B_I0977	hypothetical protein	15687	16931	16056	27	18759	19431	18780	32	2.49E-07	4.25E-07	1.185185185	0.245112498
BP1026B_I0978	2OG-Fe(II) oxygenase	78369	48689	50717	94	68640	67126	61733	104	1.18E-09	2.44E-09	1.106382979	0.145850866
BP1026B_I0979	IcIR family transcriptional regulator	69673	46401	47746	57	46004	38095	42217	44	1.48E-23	1.02E-22	0.771929825	-0.373458396
BP1026B_I0980	outer membrane porin protein	5701	4317	3855	3	4864	4875	5260	4	1.60E-06	2.58E-06	1.333333333	0.415037499
BP1026B_I0981	Rieske (2Fe-2S) domain-containing protein	250	145	143	0	237	117	311	0	0.527864183	0.55320237	#DIV/0!	#DIV/0!
BP1026B_I0982	hypothetical protein	350	632	398	1	479	590	641	1	0.963014636	0.968890448	1	0
BP1026B_I0983	Rieske family iron-sulfur cluster-binding protein	3020	4288	3156	3	4297	2885	3971	3	6.80E-05	9.77E-05	0	0
BP1026B_I0984	short chain dehydrogenase	501	128	285	0	259	183	218	0	0.016939729	0.020491186	#DIV/0!	#DIV/0!
BP1026B_I0985	hypothetical protein	1106	1138	1265	2	1883	1794	1258	3	0.8676235	0.881837608	1.5	0.584962501
BP1026B_I0986	alpha/beta fold family hydrolase	556	532	680	0	674	791	595	0	0.557764922	0.582822823	#DIV/0!	#DIV/0!
BP1026B_I0987	IcIR family transcriptional regulator	1345	731	914	1	727	657	581	0	3.33E-07	5.64E-07	0	#NUM!
BP1026B_I0988	short chain dehydrogenase	2233	1578	2156	2	1831	1707	2304	2	3.97E-04	5.41E-04	1	0
BP1026B_I0989	hypothetical protein	3119	2459	2623	1	2608	2116	2110	1	3.57E-08	6.49E-08	1	0
BP1026B_I0990	L-aspartate dehydrogenase	815	193	468	0	155	222	47	0	1.62E-21	9.36E-21	#DIV/0!	#DIV/0!
BP1026B_I0991	aldehyde dehydrogenase family protein	1379	1157	786	0	1465	1290	898	0	0.106627424	0.11422671	#DIV/0!	#DIV/0!
BP1026B_I0992	glyoxalase/bleomycin resistance protein/dioxygenase superfamily protein	1666	602	692	1	1408	694	1193	1	0.137934552	0.154394052	1	0
BP1026B_I0993	pyridine nucleotide-disulfide oxidoreductase, class I	910	260	458	0	541	613	568	0	0.261254348	0.283270418	#DIV/0!	#DIV/0!
BP1026B_I0994	major facilitator family transporter	1727	1191	1581	1	1759	1434	1343	1	0.00674569	0.008408294	1	0
BP1026B_I0995	hypothetical protein	575	944	736	4	677	909	704	4	0.072223635	0.088590864	1	0
BP1026B_I0996	membrane-anchored cell surface protein	15080	8094	10588	4	8727	7909	6381	3	2.17E-29	2.31E-28	0.75	-0.415037499
BP1026B_I0997	OmpA family protein	9234	8317	7406	10	5811	6529	7809	8	3.27E-18	1.45E-17	0.8	-0.321928095
BP1026B_I0998	UspA family protein	4147	6026	6879	13	7805	7789	5916	16	4.35E-05	6.32E-05	1.230769231	0.299560282
BP1026B_I0999	amidase	99056	76684	82476	59	66539	58855	69649	44	7.87E-31	9.12E-30	0.745762712	-0.423211431
BP1026B_I1000	AsnC family transcriptional regulator	47460	56367	52001	107	81755	90382	82054	175	0.114834016	0.129555266	1.635514019	0.709744125
BP1026B_I1001	methionine gamma-lyase	443071	438130	452971	341	384696	362135	395641	292	1.70E-15	5.94E-15	0.856304985	-0.22380337
BP1026B_I1002	hypothetical protein	38778	58270	55943	226	55717	62207	53126	253	1.39E-08	2.61E-08	1.119469027	0.162814612
BP1026B_I1003	predicted RNA	39700	62935	56038	645	64198	81086	69361	872	2.62E-04	3.62E-04	1.351937984	0.435028974
BP1026B_I1004	hypothetical protein	17001	16453	15464	23	13140	15492	16795	21	8.99E-15	2.94E-14	0.913043478	-0.131244533
BP1026B_I1005	N-hydroxyarylamine O-acetyltransferase	21621	27310	24098	27	25576	28794	26189	30	6.09E-07	1.01E-06	1.111111111	0.152003093
BP1026B_I1006	hypothetical protein	6086	4111	4585	8	4277	3795	3951	7	2.20E-12	5.76E-12	0.875	-0.192645078
BP1026B_I1007	DNA-binding protein	8537	13090	10997	23	12756	11507	11993	26	9.19E-08	1.62E-07	1.130434783	0.176877762
BP1026B_I1008	oxidoreductase	9499	6144	7231	8	5217	6109	5338	6	1.09E-20	5.84E-20	0.75	-0.415037499
BP1026B_I1009	LysR family regulatory protein	37904	52729	51765	49	53896	56210	55464	57	3.90E-07	6.57E-07	1.163265306	0.21818017
BP1026B_I1010	hypothetical protein	12856	13173	14778	9	13450	11174	12825	8	8.96E-14	2.66E-13	0.888888889	-0.169925001
BP1026B_I1011	major facilitator family transporter	3121	3343	3372	2	4008	4440	4176	3	0.016309592	0.019748001	1.5	0.584962501
BP1026B_I1012	alpha/beta fold family hydrolase	1612	972	1131	1	1843	2117	1451	1	0.712539909	0.733252598	1	0
BP1026B_I1013	hypothetical protein	3034	5559	4896	4	9357	12172	10225	11	0.186039547	0.205233604	2.75	1.459431619
BP1026B_I1014	short chain dehydrogenase	1890	2536	2942	2	4721	5137	4031	4	0.316711511	0.340167902	2	1
BP1026B_I1015	flavin-binding monooxygenase-like protein	6780	10144	8233	5	19257	20505	17744	11	0.342369006	0.366276967	2.2	1.137503524
BP1026B_I1016	hypothetical protein	1200	1376	1177	1	1465	1843	1494	2	0.530180441	0.555258339	2.2	1
BP1026B_I1017	aliphatic compound ABC transporter, periplasmic substrate-binding protein	50355	42409	47588	47	49097	40252	43263	44	4.91E-13	1.37E-12	0.936170213	-0.095157233
BP1026B_I1018	predicted RNA	8231	9786	11789	662	12542	10433	10271	738	2.20E-07	3.77E-07	1.114803625	0.156789599
BP1026B_I1019	MerR family transcriptional regulator	605580	395374	436197	558	387465	361210	383691	439	2.04E-19	9.96E-19	0.786738351	-0.346044182
BP1026B_I1020	phosphotriothrin N-acetyltransferase	16075	16577	14839	27	17611	16202	18657	30	5.03E-09	9.81E-09	1.111111111	0.152003093
BP1026B_I1021	hypothetical protein	39184	52547	46863	57	48935	53570	54005	65	9.71E-08	1.70E-07	1.140350877	0.189477799
BP1026B_I1022	EmrB/QacA family drug resistance transporter	66989	44958	50285	35	43845	38654	42229	27	1.57E-23	1.08E-22	0.771428571	-0.374395515
BP1026B_I1023	hypothetical protein	183	441	351	1	340	563	325	2	0.735120977	0.754878407	2	1
BP1026B_I1024	methyl-accepting chemotaxis protein	1542675	825107	1006913	722	699624	574287	683115	418	1.81E-04	2.52E-04	0.578947368	-0.788495895
BP1026B_I1025	hypothetical protein	118947	79096	85015	56	75049	72231	81898	45	4.97E-26	4.13E-25	0.803571429	-0.315501826
BP1026B_I1026	hypothetical protein	2769	1666	1633	3	1682	1293	1780	2	1.20E-07	0.666666667	0.584962501	0.584962501
BP1026B_I1027	hypothetical protein	22670	24391	23778	27	27988	27449	27863	32	1.42E-05	2.13E-05	1.185185185	0.245112498
BP1026B_I1028	agaE protein	129407	93483	101955	81	84918	71817	86732	61	2.12E-32	2.75E-31	0.75308642	-0.409112665
BP1026B_I1029	TrkA domain-containing protein	42102	42469	40705	37	40181	42267	42680	37	2.46E-10	5.33E-10	1	0
BP1026B_I1030	alpha/beta fold family hydrolase	25588	30799	27308	31	34211	31546	33603	37	3.24E-05	4.76E-05	1.193548387	0.255257055
BP1026B_I1031	4-carboxymuconolactone decarboxylase	12310	9950	9981	26	10659	7701	9702	23	4.18E-15	1.41E-14	0.884615385	-0.176877762
BP1026B_I1032	ornithine cyclodeaminase	19764	6919	9404	12	7793	5209	6992	6	3.06E-46	8.26E-45	0.5	-1
BP1026B_I1033	esterase	24156	15865	19197	23	15327	14694	15878	18	1.54E-24	1.14E-23	0.782086966	-0.353636955
BP1026B_I1034	hypothetical protein	14320	11690	11771	10	11150	9962	10556	9	1.84E-16	7.05E-16	0.9	-0.152003093
BP1026B_I1035	outer membrane porin	781950	987590	916347	775	932565	979422	950402	826	0.194986879	0.214687715	1.065806452	0.091945471
BP1026B_I1036	LysR family transcriptional regulator	46173	39896	38536	45	32858	34694	37126	38	5.77E-16	2.12E-15	0.844444444	-0.243925583
BP1026B_I1037	hypothetical protein	3709	4813	3886	39	5895	8130	5805	62	0.04733428	0.055366175	1.58974359	0.668794092
BP1026B_I1038	peptidase	29562	23647	25010	27	24942	27100	23120	26	6.76E-11	1.54E-10	0.962962963	-0.054447784
BP1026B_I1039	beta-lactamase	125296	102128	109111	126	102256	111272	94239	115	8.34E-17	3.29E-16	0.912698413	-0.131789873
BP1026B_I1040	LysR family transcriptional regulator	84028	97657	93275	107	117192	116318	111339	134	1.49E-05	2.24E-05	1.252336449	0.324622204
BP1026B_I1041	hypothetical protein	191373	180284	192675	559	194085	212921	202644	604	3.32E-09	6.60E-09	1.080500894	0.111700266
BP1026B_I1042	ABC transporter ATP-binding protein	9710	7464	8337	11	6136	5298	5303	7	4.66E-27	4.20E-26	0.636363636	-0.652076697
BP1026B_I1043	ABC transporter ATP-binding protein	9473	8177	8397	9	6971	6084	6748	7	4.47E-21	2.49E-20	0.777777778	-0.362570079
BP1026B_I1044	dipeptide transport system permease	5225	2066	3660	3	2122	1327	1871	1	1.29E-30	1.48E-29	0.333333333	-1.584962501
BP1026B_I1045	ABC transporter permease	5583	6264	5596	5	5547	6020	7193	5	8.42E-08	1.49E-07	1	0
BP1026B_I1046	periplasmic solute-binding protein	25711	28158	25362	16	25560	20249	21839	14	1.60E-16	6.14E-16	0.875	-0.192645078
BP1026B_I1047	D-alanyl-D-alanine dipeptidase	18665	5059	8301	18	4656	3848	5384	8	8.11E-65	4.84E-63	0.444444444	-1.169925001
BP1026B_I1048	hypothetical protein	16120	14082	13495	16	11841	10449	12721	13	2.66E-19	1.29E-18	0.8125	-0.299560282
BP1026B_I1049	hypothetical protein	25469	20939	21630	19	16559	15369	17416	14	1.23E-29	1.34E-28	0.736842105	-0.440572591
BP1026B_I1050	hypothetical protein	16	97	71	0	36	121	61	0	0.481050167	0.506598378	#DIV/0!	#DIV/0!
BP1026B_I1051	Rhs element Vgr protein	45602	53147	54916	25	50271	51432	52974	26	9.28E-12	2.29E-11	1.04	0.056583528
BP1026B_I1052	hypothetical protein	10219	9718	11248	23	10571	9682	10972	23	4.66E-10	9.94E-10	1	0
BP1026B_I1053	YD repeat-containing protein	115542	136088	133707	27	119673	121946	125781	26	1.14E-14	3.69E-14	0.962962963	-0.054447784
BP1026B_I1054	hypothetical protein	50301	88635	75089	148	84870	92489	89765	185	1.92			

BP1026B_II1071	glucose dehydrogenase	35878	46421	44458	26	50655	46898	51147	30	1.69E-06	2.71E-06	1.153846154	0.206450877
BP1026B_II1072	cytochrome c family protein	22045	19887	20223	15	19432	19286	19085	14	4.86E-15	1.63E-14	0.933333333	-0.099535674
BP1026B_II1073	DoxD-like family protein	8841	8410	9145	21	8681	8510	8383	20	8.32E-12	2.06E-11	0.952380952	-0.070389328
BP1026B_II1074	outer membrane porin protein	77736	89015	95242	79	76654	75184	73623	68	7.94E-22	4.73E-21	0.860759494	-0.216317907
BP1026B_II1075	hypothetical protein	27577	38572	36154	42	42701	44964	41619	53	2.01E-04	2.80E-04	1.261904762	0.335603032
BP1026B_II1077	histidine ABC transporter permease	2092	2325	1614	2	1417	2371	2116	2	3.57E-04	4.87E-04	1	0
BP1026B_II1076	histidine transport system permease	2176	1653	2146	2	1962	2188	1944	2	0.001155543	0.001519226	1	0
BP1026B_II1078	histidine transport ATP-binding protein	4894	6073	6284	7	6107	7067	5250	7	7.36E-08	1.30E-07	1	0
BP1026B_II1079	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	167890	119992	137096	108	92573	86789	99978	71	8.29E-45	2.10E-43	0.657407407	-0.605140383
BP1026B_II1080	hypothetical protein	26515	27738	28757	55	24866	21666	25520	48	6.28E-15	2.08E-14	0.872727273	-0.196397213
BP1026B_II1081	hypothetical protein	34474	23282	27905	38	23989	17029	21471	27	7.90E-27	7.03E-26	0.710526316	-0.493400011
BP1026B_II1082	hypothetical protein	947423	1502830	1338420	3660	1307067	1451921	1403723	4021	0.169165525	0.187211441	1.09863388	0.135710688
BP1026B_II1083	hypothetical protein	9512	9397	10415	7	8695	8413	9843	7	2.96E-13	8.41E-13	1	0
BP1026B_II1084	hypothetical protein	1719	954	779	2	880	817	866	1	4.19E-06	6.56E-06	0.5	-1
BP1026B_II1086	hypothetical protein	4654	5756	5641	40	6851	5686	7904	51	7.70E-05	1.10E-04	1.275	0.350497247
BP1026B_II1085	histidine kinase	20025	11323	13442	14	9158	7326	10438	8	1.26E-39	2.42E-38	0.571428571	-0.807354922
BP1026B_II1087	response regulator	10161	7352	8848	28	7597	7056	8237	24	7.76E-16	2.81E-15	0.857142857	-0.222392421
BP1026B_II1088	catalase	13121	18240	17484	10	16511	19595	18241	11	7.59E-09	1.46E-08	1.1	0.137503524
BP1026B_II1089	hypothetical protein	25510	21190	22625	15	20821	16225	19206	12	2.11E-22	1.31E-21	0.8	-0.321928095
BP1026B_II1090	AraC family transcriptional regulator	13322	10248	11058	7	10145	11052	11432	6	4.50E-12	1.14E-11	0.857142857	-0.222392421
BP1026B_II1091	Rieske family iron-sulfur cluster-binding protein	14109	19913	16057	16	14504	16828	15948	15	2.96E-14	9.21E-14	0.9375	-0.093109404
BP1026B_II1092	hypothetical protein	17041	20072	19715	11	14651	16451	18229	9	2.16E-18	9.70E-18	0.818181818	-0.289506617
BP1026B_II1093	polyketide beta-ketoacyl:acyl carrier protein synthase	9623	9092	8858	7	7643	5779	7072	5	1.30E-22	8.29E-22	0.714285714	-0.485426827
BP1026B_II1094	acyl carrier protein	3377	6545	5188	20	5614	5285	6573	24	6.01E-06	9.31E-06	1.2	0.263044006
BP1026B_II1095	polyketide biosynthesis enoyl-CoA hydratase	19597	23023	23738	28	20095	19253	19870	25	1.38E-16	5.32E-16	0.892857143	-0.163498732
BP1026B_II1096	polyketide biosynthesis enoyl-CoA hydratase	21969	24544	23293	29	20055	20563	21358	26	3.57E-16	1.33E-15	0.896551724	-0.157541277
BP1026B_II1097	hydroxymethylglutaryl-coenzyme A synthase	49434	65986	60676	46	53850	58586	56806	44	1.22E-14	3.93E-14	0.956521739	-0.064130337
BP1026B_II1098	hypothetical protein	1924	2280	2290	6	2785	2961	2662	8	0.097089476	0.110370583	1.333333333	0.415037499
BP1026B_II1099	hypothetical protein	53	171	89	0	160	147	157	1	0.067974746	0.078339113	#DIV/0!	#DIV/0!
BP1026B_II1100	Cys tRNA	558	500	556	7	332	467	488	5	0.002821617	0.003620035	0.714285714	-0.485426827
BP1026B_II1101	malonyl CoA-acyl carrier protein transacylase	18569	16562	17380	14	15963	16401	17268	13	2.05E-14	6.48E-14	0.928571429	-0.106915204
BP1026B_II1102	sodium/hydrogen exchanger	21495	22852	23581	18	22897	25383	20864	18	6.86E-10	1.44E-09	1	0
BP1026B_II1103	polyketide synthase	46702	40511	41486	3	41544	39901	43130	3	1.22E-10	2.71E-10	1	0
BP1026B_II1104	beta-ketoacyl synthase domain-containing protein	46754	38437	39695	2	38009	37271	37381	2	2.49E-13	7.12E-13	1	0
BP1026B_II1105	polyketide synthase	47559	35313	39761	2	38405	31621	34296	2	2.37E-15	8.19E-15	1	0
BP1026B_II1106	polyketide synthase	15341	16522	15460	3	17760	17993	16342	3	4.04E-09	7.94E-09	1	0
BP1026B_II1107	halogenase PnxC	18065	21269	18585	11	21563	22211	21299	13	1.24E-07	2.15E-07	1.181818182	0.2410081
BP1026B_II1108	EmrB/QacA family drug resistance transporter	5147	5419	5180	3	4515	4836	4022	3	7.23E-12	1.80E-11	1	0
BP1026B_II1109	voltage-gated chloride channel/CBS domain-containing protein	6513	3677	4845	2	4410	3703	4262	2	3.16E-12	8.16E-12	1	0
BP1026B_II1110	MarR family transcriptional regulator	806	1924	1402	3	2383	2803	1895	5	0.154893998	0.172177717	1.666666667	0.736965594
BP1026B_II1111	HPP family protein	1681	1274	1529	1	1359	1577	945	1	8.13E-05	1.16E-04	1	0
BP1026B_II1112	transcriptional regulator	53162	47094	46452	50	43103	48837	45288	47	6.88E-14	2.06E-13	0.94	-0.089267338
BP1026B_II1113	calcium/proton exchanger	56790	39818	43662	43	35175	33676	36148	32	1.92E-22	1.20E-21	0.744186047	-0.426264755
BP1026B_II1114	membrane efflux protein	20436	23127	22707	32	20391	18712	21933	30	8.48E-15	2.78E-14	0.9375	-0.093109404
BP1026B_II1115	CAAX protease family protein	12923	13660	11004	14	11215	8344	12765	12	1.88E-15	6.56E-15	0.857142857	-0.222392421
BP1026B_II1116	fumarylacetoacetate (FAA) hydrolase	21910	11504	14098	22	10481	10178	7739	13	1.33E-39	2.55E-38	0.590909091	-0.7589919
BP1026B_II1117	AraC family transcriptional regulator	12649	10368	10160	11	10166	9478	10166	9	1.16E-13	3.42E-13	0.818181818	-0.289506617
BP1026B_II1118	putative lipoprotein	0	48	0	0	0	0	47	0	0.914568718	0.924602708	#DIV/0!	#DIV/0!
BP1026B_II1120	ECF subfamily RNA polymerase sigma factor	652	361	559	1	600	586	333	0	0.089657629	0.102274659	0	#NUM!
BP1026B_II1119	hypothetical protein	591	132	170	0	89	64	237	0	5.14E-07	8.61E-07	#DIV/0!	#DIV/0!
BP1026B_II1121	hypothetical protein	2112	752	1087	1	594	646	765	0	3.35E-15	1.14E-14	0	#NUM!
BP1026B_II1122	lipoprotein	1503	776	732	2	1108	1030	1216	3	0.138902075	0.15544926	1.5	0.584962501
BP1026B_II1125	ECF subfamily RNA polymerase sigma factor	803	347	592	1	382	546	615	1	0.01863368	0.022488181	1	0
BP1026B_II1124	FecR family protein	699	738	352	0	354	525	784	0	0.037930076	0.044733645	#DIV/0!	#DIV/0!
BP1026B_II1126	TonB-dependent siderophore receptor	70443	63614	62105	24	80530	69530	68263	27	9.94E-10	2.07E-09	1.125	0.169925001
BP1026B_II1127	ribosome ABC transporter permease	1906	1137	1184	1	877	1119	1237	1	1.00E-06	1.65E-06	1	0
BP1026B_II1128	sugar ABC transporter permease	3868	3236	3863	3	2587	2675	2620	2	5.24E-14	1.59E-13	0.666666667	-0.584962501
BP1026B_II1129	ABC transporter ATP-binding protein	9324	3937	5288	3	3880	3092	4094	2	1.50E-25	1.20E-24	0.666666667	-0.584962501
BP1026B_II1130	Ribose transport ATP-binding protein rbsA	5941	5486	6016	5	6352	5842	6584	5	8.97E-08	1.58E-07	1	0
BP1026B_II1131	hypothetical protein	241759	231483	244413	345	220914	212954	239572	323	8.90E-15	2.91E-14	0.936231884	-0.095062197
BP1026B_II1133	hypothetical protein	12230	4293	6791	30	5254	4093	4925	18	1.32E-28	1.34E-27	0.6	-0.736965594
BP1026B_II1134	acyl-CoA dehydrogenase-family protein	2315	1074	1476	1	1570	1028	1695	1	9.38E-05	1.33E-04	1	0
BP1026B_II1135	sugar transport protein	4155	2499	2545	2	2273	2641	2427	1	8.57E-10	1.79E-09	0.5	-1
BP1026B_II1136	hypothetical protein	1347	1741	1731	6	2611	3305	2027	10	0.438482416	0.463718281	1.666666667	0.736965594
BP1026B_II1137	hypothetical protein	45995	27568	29203	125	31354	30210	30508	112	1.48E-12	3.93E-12	0.896	-0.158429363
BP1026B_II1138	Signal transduction histidine kinase	143844	105830	118560	87	105716	93792	110511	74	1.89E-21	1.08E-20	0.850574713	-0.23349013
BP1026B_II1139	DNA-binding response regulator IIR	25652	29945	28463	40	30127	30400	29097	43	1.89E-07	3.24E-07	1.075	0.10433666
BP1026B_II1140	heavy metal efflux pump CzcA	61785	53123	57041	17	55218	48292	53590	16	1.89E-16	7.20E-16	0.941176471	-0.087462841
BP1026B_II1141	heavy metal resistance protein CzcB	11666	4041	6850	5	6098	4731	5245	3	2.76E-21	1.57E-20	0.6	-0.736965594
BP1026B_II1142	heavy metal resistance protein CzcC	10015	3240	3226	3	3026	2824	3000	2	1.26E-30	1.44E-29	0.666666667	-0.584962501
BP1026B_II1143	hypothetical protein	14310	4225	7004	29	3776	2272	3910	11	1.26E-68	8.13E-67	0.379310345	-1.398549376
BP1026B_II1145	bacteriophage protein	8372	8506	8836	60	6675	7655	5976	48	2.40E-19	1.17E-18	0.8	-0.321928095
BP1026B_II1147	hypothetical protein	14899	19364	17557	35	18971	18089	20018	39	5.94E-09	1.15E-08	1.114285714	0.156119202
BP1026B_II1146	hypothetical protein	13338	16501	15258	55	16657	16385	17624	62	1.73E-08	3.22E-08	1.127272727	0.172836597
BP1026B_II1148	hypothetical protein	11985	15090	13520	27	15995	16957	17661	34	6.24E-06	9.65E-06	1.259259259	0.332575339
BP1026B_II1149	YbaK/prolyl-tRNA synthetase associated domain-containing protein	139786	183620	162573	333	230898	242959	213029	471	0.020657938	0.024854578	1.414414414	0.500204883
BP1026B_II1150	alanine dehydrogenase	46804	31506	36948	34	30480	27912	27259	25	1.95E-21	1.12E-20	0.735294118	-0.443606651
BP1026B_II1151	H-NS histone family protein	338097	557130	470828	1379	582087	655454	608856	1865	0.48471044	0.510195803	1.352429297	0.435553174
BP1026B_II1152	ProQ protein	176083	207018	199942	359	188113	160398	190623	332	6.78E-15	2.24E-14	0.924791086	-0.112806062
BP1026B_II1153	hydratase/decarboxylase family protein	6523	1355	2513	4	1639	1418	1					

BP1026B_II1171	hypothetical protein	2748	2317	2426	14	3367	3707	3141	20	0.15318506	0.170520085	1.428571429	0.514573173
BP1026B_II1172	phosphoethanolamine N-methyltransferase	15701	16394	16533	20	21858	23185	21238	27	0.001280433	0.00167744	1.35	0.432959407
BP1026B_II1173	gamma-butyrolactamase, 2-oxoglutarate dioxygenase	27784	24804	28573	23	26746	26195	23938	22	3.36E-11	7.84E-11	0.956211791	-0.064130337
BP1026B_II1174	integral membrane protein	23792	11416	11370	18	10418	9399	10226	11	1.81E-32	2.36E-31	0.611111111	-0.710493383
BP1026B_II1175	amino acid permease	286257	202049	219863	158	216502	194892	238949	145	5.23E-16	1.92E-15	0.917721519	-0.123871658
BP1026B_II1176	peptidase	21277	14519	16422	28	18542	17688	17262	29	1.79E-11	4.28E-11	1.035714286	0.050626073
BP1026B_II1177	FtsH-2 protease	2156112	1044031	1251648	741	941959	827310	969776	456	0.308852822	0.332007511	0.615384615	-0.700439718
BP1026B_II1178	hypothetical protein	78782	21655	36865	89	23135	14432	23477	39	3.50E-95	3.79E-93	0.438202247	-1.190312122
BP1026B_II1180	thymidylate synthase	966	717	635	1	886	859	826	1	0.192234086	0.211880173	1	0
BP1026B_II1179	hypothetical protein	21811	10615	14652	8	14521	10671	13973	7	1.11E-18	5.14E-18	0.875	-0.192645078
BP1026B_II1181	transcriptional regulator	16100	9650	11563	18	10710	10467	9948	15	1.19E-16	4.63E-16	0.833333333	-0.263034406
BP1026B_II1182	RND family efflux transporter MFP subunit	8342	3738	4797	5	4573	3654	5527	4	1.79E-13	5.16E-13	0.8	-0.321928095
BP1026B_II1183	hydrophobe/amphiphile efflux family protein	55978	60998	60467	19	63528	60135	64577	20	3.36E-11	7.84E-11	1.052631579	0.074000581
BP1026B_II1184	RND efflux system outer membrane lipoprotein	2895	1498	2296	1	2262	1816	1803	1	4.17E-06	6.53E-06	1	0
BP1026B_II1185	GTP cyclohydrolase II	26186	33749	32460	47	30312	31075	30711	47	4.08E-09	8.02E-09	1	0
BP1026B_II1186	WD domain-containing protein	33401	27141	27713	17	22946	17779	22201	12	2.88E-28	2.83E-27	0.705882353	-0.502500341
BP1026B_II1187	hypothetical protein	4244	2756	2865	4	2162	1517	2547	2	4.02E-17	1.63E-16	0.5	-1
BP1026B_II1188	hypothetical protein	15392	17436	16605	16	12380	12094	12067	12	1.55E-24	1.14E-23	0.75	-0.415037499
BP1026B_II1189	riboflavin biosynthesis protein RibD	2076	1873	2007	1	994	1168	937	0	1.84E-20	9.72E-20	0	#NUM!
BP1026B_II1190	O-methyltransferase	12953	13464	13812	12	9240	9553	10525	9	9.42E-24	6.58E-23	0.75	-0.415037499
BP1026B_II1191	glyoxylase/bleomycin resistance protein/dioxygenase superfamily protein	56933	16573	18964	35	17041	16749	13878	18	1.63E-68	1.04E-66	0.514285714	-0.959358016
BP1026B_II1192	major facilitator superfamily transporter	81672	58744	69261	49	53777	48773	55316	37	9.57E-29	9.78E-28	0.755102041	-0.405256478
BP1026B_II1193	hypothetical protein	21430	28347	27876	51	25378	28642	23701	51	1.80E-09	3.64E-09	1	0
BP1026B_II1194	hypothetical protein	24832	16207	16864	13	13662	14406	13030	9	2.40E-29	2.56E-28	0.692307692	-0.530514717
BP1026B_II1195	LuxR family transcriptional regulator	94704	133020	123374	145	138667	145987	149345	179	3.93E-05	5.74E-05	1.234482759	0.303906687
BP1026B_II1196	predicted RNA	59402	38236	37348	338	50281	59261	48807	396	1.03E-06	1.69E-06	1.171597633	0.228477184
BP1026B_II1197	hypothetical protein	31245	29624	31113	69	30254	28896	32551	69	3.99E-09	7.85E-09	1	0
BP1026B_II1197	2,4-dienoyl-CoA reductase	46786	28767	34462	18	34084	29965	30139	15	1.98E-14	6.26E-14	0.833333333	-0.263034406
BP1026B_II1198	PadR-like family regulatory protein	28643	20809	21712	42	20846	15958	19142	33	4.19E-24	3.02E-23	0.785714286	-0.347923303
BP1026B_II1199	hydroxyethylthiazole kinase	9968	6084	6816	9	7389	5354	6714	7	1.67E-15	5.87E-15	0.777777778	-0.362570079
BP1026B_II1200	hypothetical protein	14218	14041	14031	16	18486	20514	19448	23	7.34E-04	9.79E-04	1.4375	0.523561956
BP1026B_II1201	hypothetical protein	4634	3870	4997	5	4046	5101	5055	5	8.51E-07	1.40E-06	1	0
BP1026B_II1202	hypothetical protein	3344	1177	1688	3	1553	1220	1194	2	5.43E-13	1.51E-12	0.666666667	-0.584962501
BP1026B_II1203	hypothetical protein	14837	16686	17419	63	12371	10783	12764	46	9.50E-25	7.13E-24	0.73015873	-0.453717967
BP1026B_II1204	universal stress protein	976270	537716	684438	773	509044	397443	545219	510	1.59E-29	1.71E-28	0.659767141	-0.599971167
BP1026B_II1205	hypothetical protein	181941	207380	183880	458	209694	210896	219652	511	4.35E-08	7.85E-08	1.115720524	-0.157975693
BP1026B_II1206	Ni,Fe-hydrogenase III small subunit	22813	13477	17972	34	13827	14312	11491	25	1.19E-26	1.05E-25	0.735294118	-0.443606651
BP1026B_II1207	hydrogenase subunit	110420	96143	94562	56	87841	89064	91389	50	1.05E-19	5.30E-19	0.892857143	-0.163498732
BP1026B_II1208	hydrogenase 4 subunit F	122847	113046	112189	79	104463	101648	112416	72	1.25E-16	4.85E-16	0.911392405	-0.133855747
BP1026B_II1209	hydrogenase 4 membrane component	61542	92153	84888	120	93668	102321	94639	146	1.21E-06	1.216666667	0.282933963	-0.282933963
BP1026B_II1210	formate hydrogenlyase subunit 4	70532	60599	62774	67	64166	62600	67533	68	1.31E-13	3.84E-13	1.014925373	0.021373651
BP1026B_II1211	hydrogenase-4 component B / Formatehydrogenlyase subunit 3	259702	123903	153875	89	301095	114251	141448	64	1.01E-34	1.52E-33	0.719101124	-0.475733431
BP1026B_II1212	hypothetical protein	40184	33865	37881	48	33884	34753	32745	43	1.89E-12	4.98E-12	0.895833333	-0.158697746
BP1026B_II1213	hypothetical protein	383	646	473	4	624	304	386	4	0.02178662	0.026177366	1	0
BP1026B_II1214	hypothetical protein	66383	58833	64176	141	67107	60080	63879	142	2.70E-13	7.69E-13	1.007092199	0.010195767
BP1026B_II1215	phosphocarrier HPI protein	23719	21056	23411	87	24060	19081	20029	80	3.82E-14	1.18E-13	0.91954023	-0.121015401
BP1026B_II1216	transferase	58460	31209	37209	50	30326	26526	31092	35	4.36E-26	3.65E-25	0.7	-0.514573173
BP1026B_II1217	hypothetical protein	8530	2616	3047	45	2775	2388	2303	23	9.62E-31	1.11E-29	0.511111111	-0.96829114
BP1026B_II1218	proline dehydrogenase	22640	34134	32383	135	36193	41491	36211	173	4.67E-04	6.32E-04	1.281481481	-0.357812631
BP1026B_II1219	hypothetical protein	8750	1546	2219	12	1687	1297	1704	4	1.61E-54	6.30E-53	0.333333333	-1.584962501
BP1026B_II1220	nitrate/nitrite transporter	11868	11104	11227	8	14393	13058	11130	10	1.18E-07	2.06E-07	1.25	0.321928095
BP1026B_II1221	peptidyl-prolyl cis-trans isomerase C	15614	13890	14780	18	13403	11566	14426	16	1.65E-15	5.78E-15	0.888888889	-0.169925001
BP1026B_II1222	respiratory nitrate reductase subunit gamma	20135	20111	19540	29	19073	19075	21424	29	5.06E-12	1.28E-11	1	0
BP1026B_II1223	nitrate reductase 1 subunit delta	18616	15634	18292	25	14259	14546	15999	21	1.07E-18	4.98E-18	0.84	-0.251538767
BP1026B_II1224	nitrate reductase subunit beta	65670	70290	69188	44	71365	66610	74204	46	2.47E-12	6.45E-12	1.045454545	0.064130337
BP1026B_II1225	nitrate reductase subunit alpha	195087	163786	170724	46	169436	163686	163635	43	5.97E-14	1.80E-13	0.934782609	-0.097297201
BP1026B_II1226	hypothetical protein	1552	1335	2378	3	3070	3043	2558	6	0.55058036	0.575564983	2	1
BP1026B_II1227	sensory box histidine kinase/response regulator	169139	133406	138434	71	119358	111096	125046	58	1.94E-24	1.43E-23	0.816901408	-0.291766124
BP1026B_II1228	LuxR family DNA-binding response regulator	76369	76144	70656	114	70237	71281	74064	110	2.41E-15	8.32E-15	0.964912281	-0.051530301
BP1026B_II1229	response regulator	459950	440563	497901	1134	312708	259420	317558	721	4.64E-36	7.52E-35	0.635802469	-0.653349476
BP1026B_II1230	Crp/FNR family transcriptional regulator	559647	565485	573388	725	499710	477511	501680	632	1.17E-13	3.44E-13	0.871724138	-0.198056437
BP1026B_II1231	hydrolase CooC/NonD family protein subfamily	30102	35886	32821	19	33138	36106	29038	19	3.21E-09	6.38E-09	1	0
BP1026B_II1232	predicted RNA	18683	30540	33196	1056	40101	49614	22618	1440	0.003484018	0.004438068	1.363636364	0.447458977
BP1026B_II1233	TauD/TidA family dioxygenase	3032360	4765930	4325868	4777	4196488	4672735	4330060	5200	0.293560105	0.31676384	1.088549299	0.122406746
BP1026B_II1234	transport/efflux protein	256465	237299	230790	193	178451	186910	197373	149	1.15E-25	9.30E-25	0.772020725	-0.73288517
BP1026B_II1234	thioesterase	82828	66329	73300	84	48872	45722	50755	55	2.33E-40	4.63E-39	0.654761905	-0.610957709
BP1026B_II1235	acetyltransferase	373016	232182	247360	335	174657	168966	177863	205	6.71E-48	1.97E-46	0.611940299	-0.708537186
BP1026B_II1236	polyketide synthase	1214459	1205952	1199704	757	984669	1036034	996968	631	0.796911302	0.814060355	0.833553501	-0.262653295
BP1026B_II1237	polyketide synthase	960850	749496	833332	343	636660	593989	603217	247	0.01206486	0.014756669	0.720116618	-0.473697535
BP1026B_II1238	non-ribosomal peptide synthase/polyketide synthase	1576889	1489607	1533648	441	1317753	1324867	1301486	378	0.796732874	0.814010792	0.857142857	-0.222392421
BP1026B_II1239	TubD protein	1870475	1548291	1591205	418	1414363	1420443	1392584	353	0.706337648	0.727586997	0.844497608	-0.243834759
BP1026B_II1240	TubF protein	2171772	1442426	1637723	379	1230385	1094268	1180116	254	0.463258471	0.488930028	0.670184697	-0.577369351
BP1026B_II1241	non-ribosomal peptide/polyketide synthase	3971183	3168942	3266605	754	2741693	2611429	2834414	593	0.417977385	0.443305059	0.786472149	-0.346532419
BP1026B_II1242	oligopeptidase A	499401	633894	596518	299	640216	726731	611447	342	0.99768072	1	1.143812709	0.193850841
BP1026B_II1243	hypothetical protein	34239	57229	51626	230	69774	81488	63470	345	0.01984313	0.023892593	1.5	0.584962501
BP1026B_II1244	hypothetical protein	77012	132485	111849	965	166675							

BP1026B_II1267	hypothetical protein	792122	1368596	1231480	4959	1286725	1507561	1274747	5948	0.083528514	0.09547422	1.19943537	0.262355422
BP1026B_II1268	hypothetical protein	1792	3328	3090	24	2873	4307	3024	30	0.024415199	0.029179027	1.25	0.321928095
BP1026B_II1269	hypothetical protein	2295	2974	2201	9	3995	3559	3528	13	0.425420758	0.450817939	1.444444444	0.530514717
BP1026B_II1270	GntR family transcriptional regulator	14987	6740	7743	6	6983	5992	6248	4	3.51E-30	3.91E-29	0.666666667	-0.584962501
BP1026B_II1272	carboxymuconolactone decarboxylase family protein	13899	10339	11042	26	11117	11749	9837	24	1.28E-12	3.43E-12	0.923076923	-0.115477217
BP1026B_II1271	cupin domain-containing protein	16098	7881	10693	25	7860	5736	6693	15	1.04E-40	2.13E-39	0.6	-0.736965594
BP1026B_II1273	entericidin EcnAB	95037	60024	71105	558	64237	59785	66506	470	9.16E-23	5.92E-22	0.842293907	-0.247604365
BP1026B_II1274	aspartate carbamoyltransferase	68880	62060	60731	49	56739	54441	58490	43	8.36E-19	3.90E-18	0.87755102	-0.188445089
BP1026B_II1275	outer membrane ferric siderophore receptor	13794	16705	17195	7	18072	20122	15831	8	2.40E-08	4.41E-08	1.142857143	0.192645078
BP1026B_II1276	hypothetical protein	3174	980	1436	2	1088	1761	1310	1	2.58E-08	4.74E-08	0.5	-1
BP1026B_II1277	hydroxylase	2396	2085	2585	3	2537	2233	2119	3	7.28E-05	1.04E-04	1	0
BP1026B_II1278	transposase	1505	2118	1704	9	2158	1882	2089	11	0.033185936	0.039264176	1.222222222	0.289506617
BP1026B_II1279	transposase	41363	69659	62294	157	76131	85141	73998	214	1.60E-04	2.25E-04	1.363057325	0.446846238
BP1026B_II1280	PAAR motif-containing protein	55505	43918	46848	184	43732	40078	41215	157	4.11E-17	1.67E-16	0.85326087	-0.228941207
BP1026B_II1281	hypothetical protein	395521	572963	545705	425	576192	668211	560879	507	0.951774517	0.958505163	1.192941176	0.254522906
BP1026B_II1282	hypothetical protein	153799	206589	196499	82	209481	233759	208099	96	1.08E-06	1.76E-06	1.170371707	0.227410496
BP1026B_II1283	Rhs element Vgr protein	98948	90970	96908	34	96565	92940	87400	33	3.29E-15	1.12E-14	0.970588235	-0.043068722
BP1026B_II1284	H-NS histone family protein	20831	35277	29517	93	34512	38478	34668	117	2.75E-04	3.80E-04	1.258064516	0.331205908
BP1026B_II1285	predicted RNA	198799	339999	276677	1006	290016	331360	290401	1125	8.67E-08	1.53E-07	1.118290258	0.161294966
BP1026B_II1286	transcriptional regulator	166777	297708	267647	350	382648	431566	354085	559	0.16175312	0.17942026	1.597142857	0.675493361
BP1026B_II1287	sugar transporter	129881	236734	215364	190	229444	265064	205164	228	9.44E-06	1.44E-05	1.2	0.263034406
BP1026B_II1287	dGTP-pyrophosphohydrolase, thiamine phosphate synthase	62056	107383	91809	149	97391	116735	106162	183	3.74E-06	5.89E-06	1.228187919	0.296531318
BP1026B_II1288	hypothetical protein	5912	9927	9363	54	14890	16095	13674	97	0.166587684	0.184521553	1.796296296	0.84502534
BP1026B_II1289	hypothetical protein	1885	515	586	1	490	205	447	0	9.29E-25	6.99E-24	0	#NUM!
BP1026B_II1290	hypothetical protein	1105	483	630	4	274	522	522	2	3.80E-08	6.90E-08	0.5	-1
BP1026B_II1291	methyl-accepting chemotaxis protein	59252	63512	62846	40	62489	59480	56282	39	3.97E-15	1.34E-14	0.975	-0.036525876
BP1026B_II1292	penicillin-binding protein	240880	237763	239348	134	223065	206382	222375	121	1.28E-16	4.96E-16	0.902985075	-0.147225953
BP1026B_II1293	L-arabinose ABC transporter periplasmic L-arabinose-binding protein	11816	12744	13108	12	14705	14896	12678	14	4.36E-08	7.88E-08	0.702394221	0.222392421
BP1026B_II1294	short chain dehydrogenase	13433	9009	8555	13	10351	8726	9186	12	2.67E-13	7.60E-13	0.923076923	-0.115477217
BP1026B_II1295	potassium-efflux system protein	162690	161981	169293	94	165175	166782	153846	92	1.03E-11	2.52E-11	0.978723240	-0.031026896
BP1026B_II1296	hypothetical protein	4457	3908	3958	4	4160	5399	5550	5	2.06E-04	2.87E-04	1.25	0.321928095
BP1026B_II1297	hypothetical protein	8032	8876	10052	4	11128	11129	11291	5	2.78E-05	4.10E-05	1.25	0.321928095
BP1026B_II1298	hypothetical protein	697	179	295	1	273	302	324	0	0.007324024	0.009087591	0	#NUM!
BP1026B_II1299	hypothetical protein	6413	5198	4440	20	4302	4555	4867	17	7.39E-12	1.84E-11	0.85	-0.234465254
BP1026B_II1300	3-demethylubiquinone-9 3-methyltransferase	63353	55451	60089	125	51452	45241	52519	104	4.81E-21	2.67E-20	0.832	-0.265344567
BP1026B_II1301	CoA family protein	45159	47565	47387	45	46860	44319	48459	45	2.52E-11	5.96E-11	1	0
BP1026B_II1302	DeoR family transcriptional regulator	3547	3468	3979	4	3035	3358	3098	3	6.17E-09	1.19E-08	0.75	-0.415037499
BP1026B_II1303	transporter	6453	2846	3500	3	1980	1963	2083	1	7.54E-36	1.21E-34	0.333333333	-1.584962501
BP1026B_II1304	hypothetical protein	7367	4728	6291	13	4705	4362	4560	9	4.27E-17	1.73E-16	0.692307692	-0.530514717
BP1026B_II1305	hypothetical protein	1599	1191	1341	2	881	850	1070	1	6.71E-09	1.29E-08	0.5	-1
BP1026B_II1306	transporter periplasmic binding protein	8377	9612	10123	7	10354	10712	9381	7	5.11E-08	9.14E-08	1	0
BP1026B_II1308	sugar ABC transporter permease	1509	1061	1011	1	1183	1242	1611	1	0.118310022	0.133260938	1	0
BP1026B_II1307	ABC transporter permease	895	663	502	0	722	909	840	1	0.532298211	0.55728999	#DIV/0!	#DIV/0!
BP1026B_II1310	zinc-binding dehydrogenase family oxidoreductase	774	598	678	0	250	176	520	0	3.41E-13	9.64E-13	#DIV/0!	#DIV/0!
BP1026B_II1311	sugar ABC transporter ATP-binding protein	1731	1433	1530	1	1693	1187	1348	1	2.35E-04	3.26E-04	1	0
BP1026B_II1309	AraC family transcriptional regulator	10869	14365	13382	12	13708	17368	16220	15	2.73E-06	4.34E-06	1.25	0.321928095
BP1026B_II1312	xylulokinase	15043	7047	10291	7	7173	5523	7238	4	1.17E-35	1.85E-34	0.571428571	-0.807354922
BP1026B_II1313	peptidase	15739	21972	20951	19	20210	21719	19648	20	5.38E-10	1.14E-09	1.052631579	0.074000581
BP1026B_II1314	penicillin-binding protein	5871	2716	4156	2	2741	2233	2758	1	6.13E-22	3.69E-21	0.5	-1
BP1026B_II1315	hypothetical protein	5076	2875	2673	16	2058	1676	1899	8	2.46E-25	1.94E-24	0.5	-1
BP1026B_II1316	Assimilatory nitrate reductase large subunit	332088	260701	274958	68	195634	176965	188685	44	5.14E-42	1.13E-40	0.647058824	-0.628031223
BP1026B_II1317	nitrite reductase (NAD(P)H) small subunit	33944	25814	29629	84	20444	20738	21058	59	2.64E-30	2.96E-29	0.702380952	-0.509674373
BP1026B_II1318	nitrite reductase (NAD(P)H) large subunit	233258	183470	190562	79	137136	125754	131292	51	2.14E-45	5.62E-44	0.64556962	-0.631355406
BP1026B_II1319	nitrate transporter	852	521	640	0	914	463	1054	0	0.57695098	0.601726837	#DIV/0!	#DIV/0!
BP1026B_II1321	uroporphyrin-III C-methyltransferase	549	96	407	0	155	235	291	0	0.001157632	0.001521334	#DIV/0!	#DIV/0!
BP1026B_II1323	response regulator NstI	7551	5090	5915	10	3809	3834	3951	6	1.68E-23	1.16E-22	0.6	-0.736965594
BP1026B_II1322	nitrate transport ATP-binding protein	14374	8408	9134	10	7064	6199	7153	6	8.71E-33	1.16E-31	0.6	-0.736965594
BP1026B_II1324	GTP cyclohydrolase I	2773	1882	2427	3	1350	2186	1563	2	2.62E-10	5.69E-10	0.666666667	-0.584962501
BP1026B_II1325	lipoprotein	77380	63350	68546	31	50321	49548	53207	23	1.13E-30	1.30E-29	0.741935484	-0.430634354
BP1026B_II1326	predicted RNA	130761	119719	126680	816	108949	91993	120736	696	1.66E-20	8.84E-20	0.852941176	-0.229481846
BP1026B_II1327	acyl/polyamine aminohydrolase	346084	229155	232436	263	220657	225440	216027	215	1.20E-22	7.67E-22	0.817490494	-0.29072614
BP1026B_II1327	allantoinase amidohydrolase	415263	202752	236831	206	177938	164634	180833	126	1.03E-47	3.00E-46	0.611650485	-0.709220604
BP1026B_II1328	major facilitator family transporter	349477	248208	263776	217	195599	172346	211317	146	1.88E-38	3.40E-37	0.67281106	-0.571726674
BP1026B_II1329	LysR family transcriptional regulator	103757	104703	99156	105	124865	121857	126573	128	2.93E-06	4.65E-06	1.219047619	0.285754482
BP1026B_II1330	hypothetical protein	17883	13792	16257	44	15321	14008	16025	41	5.53E-14	1.67E-13	0.931818182	-0.101879614
BP1026B_II1331	LysR family transcriptional regulator	12436	10994	11304	11	10589	10878	11056	10	2.92E-12	7.54E-12	0.909090909	-0.137503524
BP1026B_II1332	short chain dehydrogenase	9003	7351	6718	10	6028	6389	4724	7	4.19E-20	2.16E-19	0.7	-0.514573173
BP1026B_II1333	CAIB/BAIF family CoA transferase	11394	4411	6411	5	4697	3177	4629	2	4.13E-32	5.22E-31	0.4	-1.321928095
BP1026B_II1334	zinc-containing alcohol dehydrogenase	10059	5277	6712	7	5379	6215	5862	5	3.05E-17	1.25E-16	0.714285714	-0.485426827
BP1026B_II1335	iron-containing alcohol dehydrogenase	6032	2985	3802	3	3701	2862	3846	2	2.25E-11	5.35E-11	0.666666667	-0.584962501
BP1026B_II1336	hypothetical protein	15323	14946	14031	91	12729	12936	18546	90	8.12E-12	2.01E-11	0.989010989	-0.015941544
BP1026B_II1339	hypothetical protein	514	389	617	1	403	352	266	0	5.65E-05	8.16E-05	0	#NUM!
BP1026B_II1338	hypothetical protein	34815	37056	35631	18	38567	36280	37867	19	4.17E-08	7.54E-08	1.055555556	0.078002512
BP1026B_II1340	hypothetical protein	8787	3221	4737	16	3805	1852	3455	9	7.11E-30	7.80E-29	0.5625	-0.830074999
BP1026B_II1341	hypothetical protein	3679	2774	3412	4	2575	2241	2458	3	1.95E-12	5.14E-12	0.75	-0.415037499
BP1026B_II1342	Methyl-accepting chemotaxis protein	53603	36805	40338	15	36091	33702	35513	12	3.36E-18	1.49E-17	0.8	-0.321928095
BP1026B_II1343	hypothetical protein	16677	9267	10155	18	10492	8917	10292	15	2.56E-17	1.06E-16	0.833333333	-0.263034406
BP1026B_II1344	hypothetical protein	6652	9440	7864	23	10824	9438	12226	32	6.97E-04	9.32E-04	1.391304348	0.476438044
BP1026B_II1345	nonribosomal peptide synthetase DhhB	4848	3370	366									

BP1026B_II1366	peptidase	19557	21231	20137	9	24445	22404	26136	11	1.40E-05	2.10E-05	1.22222222	0.289506617
BP1026B_II1367	hypothetical protein	4569	8540	7475	36	11593	13738	11512	66	0.304652823	0.327717526	1.83333333	0.874469118
BP1026B_II1368	hypothetical protein	59822	45261	46146	289	55841	56984	50518	312	1.86E-09	3.76E-09	1.079584775	0.110476536
BP1026B_II1369	outer membrane protein TolC	40547	44218	39640	26	42684	45609	41989	27	4.68E-09	9.15E-09	1.038461538	0.054447784
BP1026B_II1370	gamma-glutamyltransferase	421456	418105	431955	246	328978	333291	324798	191	3.59E-21	2.02E-20	0.776422764	-0.365085677
BP1026B_II1372	hypothetical protein	1408	580	680	1	552	494	214	0	5.80E-15	1.93E-14	0	#NUM!
BP1026B_II1373	hypothetical protein	4170	3888	4420	8	4588	5158	3318	8	1.72E-06	2.77E-06	1	0
BP1026B_II1374	DEAD/DEAH box helicase	64267	55886	57763	12	56842	54879	54107	11	6.55E-16	2.39E-15	0.916666667	-0.125530882
BP1026B_II1375	amino acid permease	2066	811	996	0	804	877	892	0	1.06E-08	2.01E-08	#DIV/0!	#DIV/0!
BP1026B_II1377	DGPF domain-containing protein	3087	2512	3067	6	2640	3063	2183	6	1.10E-06	1.80E-06	1	0
BP1026B_II1378	phospho-2-dehydro-3-deoxyheptonate aldolase	61094	37848	46255	43	37417	34500	32976	31	7.43E-25	5.64E-24	0.720930233	-0.472068444
BP1026B_II1379	O-methyltransferase family protein	46236	27511	27142	50	27900	27275	28687	41	1.18E-15	4.22E-15	0.82	-0.286304185
BP1026B_II1380	diguanylate cyclase	13889	11792	12486	8	11935	9823	10643	7	5.19E-16	1.91E-15	0.875	-0.192645078
BP1026B_II1381	hypothetical protein	40086	46986	46173	66	44479	45582	48573	68	1.02E-09	2.12E-09	1.03030303	0.043068722
BP1026B_II1382	pca operon transcription factor PcaQ	14495	11159	12116	12	14480	13082	13018	13	4.44E-09	8.68E-09	1.083333333	0.115477217
BP1026B_II1383	protocatechuate 3,4-dioxygenase subunit beta	3785	2740	3323	4	2486	2993	3781	4	1.42E-06	2.29E-06	1	0
BP1026B_II1384	protocatechuate 3,4-dioxygenase subunit alpha	876	780	701	1	779	462	624	1	5.48E-04	7.39E-04	1	0
BP1026B_II1385	peptidase	14623	8364	9074	12	7009	7023	7201	8	1.36E-30	1.55E-29	0.666666667	-0.584962501
BP1026B_II1386	aminopeptidase DmpA	9244	3772	3841	4	2486	3026	2777	2	1.92E-37	3.33E-36	0.5	-1
BP1026B_II1387	ABC transport system permease	10977	7663	7943	9	6833	5679	5570	6	3.89E-26	3.28E-25	0.666666667	-0.584962501
BP1026B_II1388	ABC transporter permease	7577	6002	6306	7	4869	4575	5690	5	3.38E-17	1.37E-16	0.714285714	-0.485426827
BP1026B_II1389	ABC transporter substrate-binding protein	38989	43873	41709	26	42027	37969	42425	26	1.03E-10	2.31E-10	1	0
BP1026B_II1390	ATP-binding ABC transporter protein	33999	27697	29118	15	27669	24130	27370	13	6.30E-14	1.90E-13	0.866666667	-0.206450877
BP1026B_II1391	asparaginase	9537	3779	6450	6	4360	3961	4755	4	4.19E-22	2.55E-21	0.666666667	-0.584962501
BP1026B_II1392	transcriptional regulator	6029	4006	4301	5	3326	3645	3380	3	2.17E-15	7.55E-15	0.6	-0.736955994
BP1026B_II1393	choline/carnitine/betaine transporter	19041	16162	15728	8	16669	15643	17095	8	2.60E-13	7.43E-13	1	0
BP1026B_II1394	beta-lactamase	14927	13301	15940	12	14257	13088	12778	11	7.98E-15	2.62E-14	0.916666667	-0.125530882
BP1026B_II1395	hypothetical protein	507	161	147	0	273	72	220	0	0.016465132	0.01993248	#DIV/0!	#DIV/0!
BP1026B_II1396	phosphoesterase family protein	43488	38749	41155	29	41726	41604	38212	29	1.42E-10	3.13E-10	1	0
BP1026B_II1397	hypothetical protein	15662	12180	13307	21	11078	9986	11743	17	5.40E-19	2.55E-18	0.80952381	-0.304854582
BP1026B_II1398	hypothetical protein	16200	11924	12292	38	11078	10962	12054	32	1.54E-16	5.91E-16	0.842105263	-0.247927513
BP1026B_II1399	isoleucyl-tRNA synthetase	11438	8391	8465	3	7922	7318	8765	2	5.77E-17	2.31E-16	0.666666667	-0.584962501
BP1026B_II1400	DMT family permease	1304	502	684	0	791	552	816	0	0.003921474	0.004970055	#DIV/0!	#DIV/0!
BP1026B_II1401	alanine-tRNA synthetase	2128	1200	1534	2	1288	1043	1044	1	2.93E-09	5.84E-09	0.5	-1
BP1026B_II1402	D-lactate dehydrogenase	3309	1932	2693	1	2319	2014	2306	1	7.15E-08	1.27E-07	1	0
BP1026B_II1403	hypothetical protein	845	290	497	1	276	48	339	0	6.70E-13	1.84E-12	0	#NUM!
BP1026B_II1404	hypothetical protein	4705	4737	4483	5	4340	4267	4832	5	2.18E-08	4.03E-08	1	0
BP1026B_II1405	hypothetical protein	6724	8612	8451	8	9416	8855	8614	9	2.42E-07	4.13E-07	1.125	0.169925001
BP1026B_II1406	transcriptional regulator	14547	17283	15537	18	17152	17663	17200	19	3.63E-09	7.17E-09	1.055555556	0.078002512
BP1026B_II1407	hypothetical protein	1369	1020	966	1	1547	1352	1117	1	0.296806979	0.319881756	1	0
BP1026B_II1408	1-aminocyclopropane-1-carboxylate deaminase	21474	19258	23321	20	18894	19338	17785	18	3.55E-18	1.57E-17	0.9	-0.152003093
BP1026B_II1409	Lip regulator	3272	3633	3694	6	3781	4309	4347	8	7.23E-04	9.65E-04	1.333333333	0.415037499
BP1026B_II1411	hypothetical protein	55666	53331	53747	38	58336	61413	58874	41	1.35E-09	2.77E-09	1.078947368	0.109624491
BP1026B_II1412	major facilitator family transporter	4538	3354	3511	3	5401	4658	5062	3	0.003660191	0.004654702	1	0
BP1026B_II1413	transcriptional regulator	5225	5219	4429	6	8904	8286	9501	12	0.284187138	0.307231989	2	1
BP1026B_II1414	major facilitator family transporter	6571	4038	5670	3	4863	3648	4379	3	6.66E-14	2.00E-13	1	0
BP1026B_II1415	hydrolase	1827	803	726	1	891	317	627	0	7.40E-12	1.84E-11	0	#NUM!
BP1026B_II1416	Ser/Thr protein phosphatase family protein	6268	6360	8007	4	7218	7583	7086	4	8.83E-09	1.69E-08	1	0
BP1026B_II1417	cytochrome c peroxidase	1836	1312	1541	0	1162	1059	1001	0	1.68E-09	3.42E-09	#DIV/0!	#DIV/0!
BP1026B_II1418	MerR family transcriptional regulator	22280	8432	10608	15	9324	7388	7945	9	2.91E-41	6.08E-40	0.6	-0.736955994
BP1026B_II1419	hypothetical protein	8720	2950	4452	19	2986	1928	2670	9	1.77E-40	3.53E-39	0.473684211	-1.078002512
BP1026B_II1420	hypothetical protein	133032	192066	186944	801	182244	192866	194398	891	9.64E-08	1.69E-07	1.11259551	0.153623189
BP1026B_II1421	acetyltransferase	51666	57071	59152	144	61124	63118	52243	152	3.93E-11	9.12E-11	1.055555556	0.078002512
BP1026B_II1422	YeeE/YeeF family protein	29663	20539	19545	54	21016	22515	24348	53	1.84E-11	4.40E-11	0.981481481	-0.026967048
BP1026B_II1423	YeeE/YeeF family protein	25966	16082	18164	46	15973	13252	16501	35	7.32E-26	6.01E-25	0.760869565	-0.394278939
BP1026B_II1424	ArsR family transcriptional regulator	80493	97045	100374	296	121145	102397	122043	369	9.67E-06	1.48E-05	1.246621622	0.31802364
BP1026B_II1425	cytochrome b561 family protein	7613	7084	6839	13	6865	7242	7202	13	1.23E-10	2.72E-10	1	0
BP1026B_II1426	selenocysteine lyase	8021	4172	6204	3	5055	4023	5422	2	3.02E-15	1.03E-14	0.666666667	-0.584962501
BP1026B_II1427	major membrane protein I	1007	1574	1401	1	1057	1946	1157	1	0.024836098	0.029636829	1	0
BP1026B_II1428	transcriptional regulator	607	532	396	1	602	303	366	1	0.007049046	0.008763755	1	0
BP1026B_II1429	serine acetyltransferase	1407	1356	1222	1	1036	765	1471	1	2.79E-05	4.12E-05	1	0
BP1026B_II1430	rhodanese-like domain-containing protein	180	494	112	0	134	176	81	0	5.23E-05	7.58E-05	#DIV/0!	#DIV/0!
BP1026B_II1431	prolyl oligopeptidase family protein	151373	127665	144657	67	119158	107348	122867	55	7.76E-23	5.03E-22	0.820895522	-0.284729477
BP1026B_II1432	multidrug resistance protein	8401	7286	7929	5	8802	7522	4930	5	5.78E-14	1.75E-13	1	0
BP1026B_II1433	RND efflux system outer membrane lipoprotein	18271	13315	14192	9	15237	15303	11448	8	8.83E-15	2.89E-14	0.888888889	-0.169925001
BP1026B_II1434	rhannosyltransferase II	13365	10532	11410	11	10085	9253	9466	9	7.99E-18	3.43E-17	0.818181818	-0.289506617
BP1026B_II1435	multidrug resistance protein	12324	8063	10036	6	9790	8946	8722	5	8.48E-14	2.52E-13	0.833333333	-0.263034406
BP1026B_II1436	rhannosyltransferase I, subunit B	20186	12564	15201	11	15253	14158	14175	10	1.92E-15	6.71E-15	0.909090909	-0.137503524
BP1026B_II1437	rhannosyltransferase I, subunit A	36481	47268	41689	46	51685	50006	51707	56	1.41E-05	2.12E-05	1.217391304	0.283792966
BP1026B_II1438	transcriptional regulator BclI	15375	10927	9886	20	13315	11914	11942	21	2.75E-09	5.50E-09	1.05	0.070389238
BP1026B_II1439	betaine aldehyde dehydrogenase	192249	162105	170357	118	169382	158541	174845	114	5.85E-13	1.62E-12	0.966101695	-0.049753035
BP1026B_II1440	choline dehydrogenase	212492	279002	265293	148	309824	339543	311591	188	9.98E-05	1.42E-04	1.27027027	0.345135486
BP1026B_II1441	hypothetical protein	1703213	1400452	1523680	456	1502107	1476480	1492716	441	0.321986573	0.345710737	0.967105263	-0.048255169
BP1026B_II1442	major facilitator family transporter	9634	8632	8841	6	9502	8663	9695	6	1.33E-09	2.73E-09	1	0
BP1026B_II1443	sensory box histidine kinase/response regulator	28974	33366	35172	21	33590	30767	35510	22	1.95E-08	3.61E-08	1.047619048	0.067114196
BP1026B_II1444	response regulator	19583	26730	23357	51	28667	31698	25230	62	9.16E-05	1.31E-04	1.215686275	0.281770968
BP1026B_II1445	sensory box histidine kinase	17711	14897	15330	7	13769	10974	13212	5	5.93E-21	3.26E-20	0.714285714	-0.485426827
BP1026B_II1446	OsmC-like protein	6351	6585	5358	12	6420	6753	6149	13	2.21E-08	4.07E-08	1.083333333	0.115477217
BP1026B_II1447	2-hydroxyacid dehydrogenase	4602	3821	3633	4	3354	2883	2739	3	1.05E-13	3.10E-13	0.75	-0.415037499
BP1026B_II1448	hypothetical protein	4605	5116	4709	18	4188	2930	4862	15	1.09E-11	2.67E-11	0.833333333	-0.263034406
BP1026B_II1449	hypothetical protein	4143	4398	4518									

BP1026B_I11469	MgtC family membrane protein	951	548	961	1	624	302	591	0	7.82E-08	1.38E-07	0	#NUM!
BP1026B_I11470	hypothetical protein	34	49	0	0	12	55	35	0	0.36509644	0.38972614	#DIV/0!	#DIV/0!
BP1026B_I11472	phospholipase D	1144	1215	1177	0	1030	883	807	0	9.25E-06	1.41E-05	#DIV/0!	#DIV/0!
BP1026B_I11471	endonuclease/exonuclease/phosphatase family protein	1212	340	858	0	518	411	142	0	2.14E-16	8.10E-16	#DIV/0!	#DIV/0!
BP1026B_I11473	pyruvate/2-oxoglutarate dehydrogenase complex,dehydrogenase (E1) subunit beta	918	143	532	1	250	0	47	0	2.11E-42	4.75E-41	0	#NUM!
BP1026B_I11474	rotamase	8035	16506	12971	17	14565	16036	16332	21	7.52E-06	1.16E-05	1.23529418	0.304854582
BP1026B_I11475	hypothetical protein	8673	9821	9683	7	9286	10255	10390	8	1.63E-08	3.05E-08	1.142857143	0.192645078
BP1026B_I11476	hypothetical protein	291	277	356	2	201	325	233	2	0.060287405	0.069080066	1	0
BP1026B_I11477	ATP/GTP binding protein	14186	25698	22200	26	25829	29707	25853	34	8.15E-04	0.001082549	1.307692308	0.387023123
BP1026B_I11478	hypothetical protein	12434	22591	19155	5	24363	27224	26319	8	0.014737931	0.017924665	1.6	0.678071905
BP1026B_I11479	hypothetical protein	1695	3084	3052	5	3466	3779	4054	7	0.283333295	0.306361764	1.4	0.485426827
BP1026B_I11480	hypothetical protein	18616	28438	26465	13	30638	31193	34861	17	0.001209919	0.001586721	1.307692308	0.387023123
BP1026B_I11481	hypothetical protein	4951	5190	4300	3	6093	4475	5344	4	1.94E-06	3.11E-06	1.333333333	0.415037499
BP1026B_I11482	Ysc/Hrc family type III secretion outer membrane protein	5408	7548	6634	3	6398	7331	8032	4	1.18E-07	2.06E-07	1.333333333	0.415037499
BP1026B_I11483	hypothetical protein	3367	3428	3709	2	4928	5885	4184	3	0.043688054	0.05128313	1.5	0.584962501
BP1026B_I11484	type III secretion protein SpaR/YscT/HrcT	289	631	408	0	723	954	1014	1	6.22E-04	8.35E-04	#DIV/0!	#DIV/0!
BP1026B_I11485	type III secretion protein HrpB7	231	97	265	0	50	563	408	0	0.020697126	0.024893807	#DIV/0!	#DIV/0!
BP1026B_I11486	type III secretion system ATPase	545	1017	722	0	1064	294	809	0	0.027925124	0.033202813	#DIV/0!	#DIV/0!
BP1026B_I11487	type III secretion system protein HrpB	1305	1382	1086	1	1186	1441	857	1	0.001900213	0.002466184	1	0
BP1026B_I11488	type III secretion protein HrpB4	566	1059	536	2	752	580	679	2	0.02503371	0.029866951	1	0
BP1026B_I11489	lipoprotein transmembrane protein	1987	2237	2599	2	2841	2202	3920	3	0.109308961	0.123655885	1.5	0.584962501
BP1026B_I11490	type III secretion protein HrpB2	260	467	472	1	809	636	537	1	0.041767148	0.049101867	1	0
BP1026B_I11491	type III secretion protein HrpB1/HrpK	794	887	940	1	1404	1510	1238	2	0.212354253	0.232705797	2	1
BP1026B_I11492	type III secretion system protein HrcU	6943	9642	10341	8	10171	9455	10525	9	2.80E-07	4.75E-07	1.125	0.169925001
BP1026B_I11493	type III secretion protein	2723	4313	4625	1	4304	4907	3876	2	3.64E-05	5.32E-05	2	1
BP1026B_I11494	type III secretion protein HpaP	444	217	310	1	347	473	365	1	0.876945554	0.890013094	1	0
BP1026B_I11495	Type III secretion inner membrane protein SetQ	8311	11946	9592	7	11379	13079	13145	9	2.90E-05	4.28E-05	1.285714286	0.362570079
BP1026B_I11496	type III secretion system protein	6308	9286	7404	10	10446	11459	12399	16	0.009986672	0.012289176	1.6	0.678071905
BP1026B_I11497	type III secretion inner membrane protein SetS	628	608	980	2	589	1179	1399	5	0.015463876	0.018771144	2.5	1.321928095
BP1026B_I11498	hypothetical protein	995	1337	1905	2	1540	1928	1821	3	0.303101313	0.32616054	1.5	0.584962501
BP1026B_I11499	secretion-associated protein	7140	6081	6788	6	6505	6267	7143	6	3.73E-10	8.01E-10	1	0
BP1026B_I11500	hypothetical protein	825	736	504	2	444	385	765	2	5.12E-04	6.92E-04	1	0
BP1026B_I11501	hypothetical protein	22329	39684	38611	116	40402	48262	39479	148	2.86E-04	3.95E-04	1.275862069	0.351472371
BP1026B_I11502	hypothetical protein	1993	3540	2663	5	4271	4079	3037	8	0.148258747	0.165271181	1.6	0.678071905
BP1026B_I11503	hypothetical protein	4616	6867	6186	5	7518	7350	6501	6	7.98E-06	1.23E-05	1.2	0.263034406
BP1026B_I11504	cupin domain-containing protein	13286	20732	21430	38	23236	25403	24039	50	6.13E-04	8.24E-04	1.315789474	0.359528676
BP1026B_I11505	HAD-superfamily hydrolase	16281	6309	7236	16	6450	4333	6701	9	1.00E-36	1.68E-35	0.5625	-0.830074999
BP1026B_I11506	GntR family transcriptional regulator	9236	3781	5142	7	4733	2738	5428	5	2.41E-18	1.08E-17	0.714285714	-0.485426827
BP1026B_I11507	6-phosphogluconate dehydrogenase	7957	6217	6857	7	5880	5190	6269	6	2.06E-15	7.18E-15	0.857142857	-0.222392421
BP1026B_I11508	type III effector Hop protein	11364	6987	6953	6	5126	5153	4930	3	2.24E-31	2.68E-30	0.5	-1
BP1026B_I11509	aldolase	4727	1769	2508	4	1204	1146	2007	2	1.47E-27	1.40E-26	0.5	-1
BP1026B_I11510	major facilitator family transporter	5126	7012	5988	4	6880	5171	7765	4	1.02E-07	1.79E-07	1	0
BP1026B_I11511	hydroxypyruvate isomerase	4458	5262	5495	6	4551	5514	4413	6	3.43E-09	6.79E-09	1	0
BP1026B_I11512	NAD-dependent epimerase/dehydratase family protein	4640	2811	4102	3	2230	2233	2511	2	3.66E-21	2.05E-20	0.666666667	-0.584962501
BP1026B_I11513	asparaginyl beta-hydroxylase	24806	12119	15179	21	17664	16553	18625	22	8.31E-12	2.06E-11	1.047619048	0.06714196
BP1026B_I11514	predicted RNA	28647	42138	38845	702	49138	48954	53189	969	0.003109419	0.003979497	1.38034188	0.465025635
BP1026B_I11515	hypothetical protein	94807	101596	98606	109	119942	121585	116488	132	2.64E-06	4.20E-06	1.211009174	0.276209795
BP1026B_I11516	glycine betaine/L-proline ABC transporter, periplasmic glycine betaine/L-proline-binding protein	6631	9075	8578	8	8305	7239	9380	8	4.46E-10	9.53E-10	1	0
BP1026B_I11517	AraC family transcriptional regulator	836	486	679	0	465	425	243	0	6.68E-09	1.29E-08	#DIV/0!	#DIV/0!
BP1026B_I11518	glycine betaine/L-proline ABC transporter permease	1997	2063	2001	2	2054	1724	2140	2	3.10E-04	4.26E-04	1	0
BP1026B_I11519	glycine betaine/L-proline ABC transporter ATP-binding protein	2572	3235	3642	2	3413	4315	3520	3	0.004005907	0.005073987	1.5	0.584962501
BP1026B_I11520	NADPH-dependent FMN reductase family protein	1322	1105	1219	1	880	1103	976	1	3.62E-05	5.30E-05	1	0
BP1026B_I11521	hypothetical protein	1551	2317	1744	8	2895	2253	2525	11	0.326348496	0.350154055	1.375	0.459431619
BP1026B_I11522	hypothetical protein	41519	50053	47814	51	57700	59845	53034	63	6.48E-06	1.00E-05	1.23529418	0.304854582
BP1026B_I11523	arsenical resistance transcriptional regulator	6947	10624	10585	27	12109	14786	11245	37	3.71E-04	5.06E-04	1.37037037	0.454565863
BP1026B_I11524	glyoxalase	9921	13618	11813	24	13068	12848	13535	27	5.10E-08	9.13E-08	1.125	0.169925001
BP1026B_I11525	arsenate reductase	8915	4465	5703	12	5192	3850	5727	9	3.46E-16	1.29E-15	0.75	-0.415037499
BP1026B_I11526	sodium bile acid symporter family protein	23319	23106	23832	21	28814	26578	28089	25	2.22E-05	3.30E-05	1.19047619	0.251538767
BP1026B_I11527	tash protein pest motif family	4994	4665	5505	5	7036	7964	6278	7	3.62E-05	5.30E-05	1.4	0.485426827
BP1026B_I11528	membrane-anchored cell surface protein	38532	46424	42631	7	49676	47588	48398	8	3.79E-07	6.40E-07	1.142857143	0.192645078
BP1026B_I11529	lipoprotein	497	97	360	0	311	58	238	0	0.00211396	0.002731779	#DIV/0!	#DIV/0!
BP1026B_I11530	hypothetical protein	23995	17623	21319	11	17669	17568	19175	10	6.11E-19	2.88E-18	0.909090909	-0.137503524
BP1026B_I11531	membrane-anchored cell surface protein	40129	47827	46053	9	50961	47780	49903	10	4.76E-08	8.55E-08	1.111111111	0.152003093
BP1026B_I11532	hypothetical protein	103849	109077	99704	90	94564	100732	103930	86	8.68E-15	2.84E-14	0.955555556	-0.065588342
BP1026B_I11533	hypothetical protein	121189	149174	141651	119	142197	144628	145641	125	7.70E-04	1.54E-09	1.050420168	0.070966521
BP1026B_I11534	hypothetical protein	114141	138231	130636	111	113972	126932	124172	106	1.23E-14	3.95E-14	0.954954955	-0.066495412
BP1026B_I11535	biotin carboxylase	77846	51416	57710	31	31472	32455	30087	15	5.12E-62	2.84E-60	0.483870968	-1.047305715
BP1026B_I11536	enoyl-CoA hydratase	27626	9934	13385	21	7252	4341	6947	7	1.15E-121	1.54E-119	0.333333333	-1.584962501
BP1026B_I11537	carboxyl transferase domain-containing protein	239348	188290	190939	128	118238	106509	112304	69	5.83E-71	3.97E-69	0.5390625	-0.891475543
BP1026B_I11538	isovaleryl-CoA dehydrogenase	482636	590473	544708	456	404429	426187	424137	353	1.31E-19	6.50E-19	0.774122807	-0.369365641
BP1026B_I11539	TetR family transcriptional regulator	26822	19930	20158	29	14938	12064	14311	18	6.69E-42	1.45E-40	0.620689655	-0.688055994
BP1026B_I11540	multicopper oxidase domain-containing protein	14715	15747	15143	10	12431	12121	16303	9	1.40E-15	4.95E-15	0.9	-0.152003093
BP1026B_I11541	Rieske family iron-sulfur cluster-binding protein /carboxynorspermidine decarboxylase	109907	132672	128778	36	151297	165484	137277	44	4.11E-05	5.98E-05	1.222222222	0.289506617
BP1026B_I11542	hypothetical protein	8061	5765	6612	4	5355	5047	6282	4	2.16E-15	7.51E-15	1	0
BP1026B_I11543	JmjC domain-containing protein	8527	8613	8988	10	8998	7485	9732	11	1.37E-10	3.03E-10	1.1	0.137503524
BP1026B_I11544	hypothetical protein	3516	3680	4048	5	3936	2953	2460	4	4.71E-10	1.00E-09	0.8	-0.321928095
BP1026B_I11545	hypothetical protein	18886	14332	14176	15	11868	9613	10806	10	1.47E-28	1.49E-27	0.666666667	-0.584962501
BP1026B_I11546	major facilitator family transporter	66643	57717	59797	43	56278	55358	58444	39	1.31E-16	5.07E-16	0.906976744	-0.140862536
BP1026B_I11547	acetyltransferase	75739	46819	56995	82	38324	29295	39414	48	1.57E-42	3.60E-41	0.585365854	-0.772589504
BP1026B_I11548	hypothetical protein	1831	282	728	2	473	523	514	1	9.83E-12	2.42E-11	0.5	-1
BP1026B_I11549	sensor histidine kinase	31353	20756	21038	17	19512	19071	22143					

BP1026B	II1566	mannitol dehydrogenase family protein	11472	4926	6732	5	5231	4519	4804	3	4.28E-27	3.89E-26	0.6	-0.736965594
BP1026B	II1567	GntR family transcriptional regulator	2397	1741	2220	2	2383	1875	2312	3	9.10E-04	0.001205251	1.5	0.584962501
BP1026B	II1568	starvation sensing protein RspA	10202	9384	7639	7	8305	8041	6816	6	8.75E-17	3.44E-16	0.857142857	-0.222392421
BP1026B	II1569	dehydrogenase	5246	3916	3956	4	4028	3349	3744	3	1.56E-10	3.42E-10	0.75	-0.415037499
BP1026B	II1571	hypothetical protein	10837	15604	13499	71	19473	21365	18345	106	0.007501979	0.00929735	1.492957746	0.578173335
BP1026B	II1572	hypothetical protein	4586	2320	2203	3	1724	1693	1377	1	2.05E-23	1.39E-22	0.333333333	-1.584962501
BP1026B	II1574	NAD synthetase	34878	22236	23772	31	23198	22300	21094	25	1.75E-18	7.92E-18	0.806451613	-0.310340121
BP1026B	II1575	family transcriptional regulator	111987	128823	129184	120	136459	142560	134384	134	4.92E-08	8.82E-08	1.116666667	0.159198595
BP1026B	II1576	hypothetical protein	784770	677416	720264	597	713225	688986	662113	564	0.408434631	0.433697915	0.944723618	-0.082035769
BP1026B	II1577	hypothetical protein	863884	583738	595015	807	564549	533752	570189	659	0.004953152	0.006234723	0.816604709	-0.292290208
BP1026B	II1578	predicted RNA	46651	13514	28106	1050	15363	9146	12803	444	1.16E-99	1.37E-97	0.422857143	-1.241757746
BP1026B	II1578	hypothetical protein	820278	765420	771843	1781	760714	702558	806553	1715	0.88800435	0.893305596	0.962942167	-0.05447894
BP1026B	II1580	anaerobically induced outer membrane protein	126031	151952	138875	88	43637	49110	46297	29	3.53E-210	6.15E-208	0.329545455	-1.601450624
BP1026B	II1581	hypothetical protein	2738	1426	1603	2	1394	1352	1156	1	7.02E-11	1.59E-10	0.5	-1
BP1026B	II1579	SCO1/SenC family protein	1688	2122	1711	2	1249	1123	1667	2	9.94E-09	1.89E-08	1	0
BP1026B	II1582	N-acetylmuramoyl-L-alanine amidase domain-containing protein	1757	2182	1856	1	2024	1413	1954	1	1.16E-04	1.64E-04	1	0
BP1026B	II1583	hypothetical protein	2586	2572	2655	1	3729	2022	2484	1	4.52E-04	6.13E-04	1	0
BP1026B	II1584	intracellular motility protein A	9535	8523	8960	6	8999	7593	9098	5	2.12E-12	5.55E-12	0.833333333	-0.263034406
BP1026B	II1585	hypothetical protein	235	226	328	0	473	597	458	1	7.20E-04	9.60E-04	#DIV/0!	#DIV/0!
BP1026B	II1586	type VI secretion system	10797	7376	8555	4	9182	8411	8213	4	7.30E-12	1.82E-11	1	0
BP1026B	II1587	DNA-binding response regulator	11639	8495	9863	14	9655	9553	8557	13	7.83E-13	2.14E-12	0.928571429	-0.106915204
BP1026B	II1589	sensor histidine kinase	6401	2971	2854	2	3069	2501	3560	1	1.18E-13	3.48E-13	0.5	-1
BP1026B	II1590	type VI secretion system	4210	4792	3596	8	5147	4250	6129	10	2.01E-04	2.80E-04	1.25	0.321928095
BP1026B	II1588	type VI secretion system	23321	30385	30126	18	32062	32273	30604	21	4.17E-06	6.53E-06	1.166666667	0.222392421
BP1026B	II1591	type VI secretion system	5358	8937	8529	14	11302	12562	9852	22	0.008419401	0.010397313	1.571428571	0.652076697
BP1026B	II1592	type VI secretion system	704	372	468	1	394	365	597	0	0.02239498	0.026867116	0	#NUM!
BP1026B	II1594	type VI secretion system	1365	588	549	0	217	429	459	0	4.92E-17	1.99E-16	#DIV/0!	#DIV/0!
BP1026B	II1593	type VI secretion system	755	678	724	0	724	706	857	0	0.155939656	0.173247852	#DIV/0!	#DIV/0!
BP1026B	II1595	type VI secretion system	4638	2814	3213	1	3005	2001	2919	0	9.52E-13	2.58E-12	0	#NUM!
BP1026B	II1596	type VI secretion system	2214	1039	2129	0	1492	1639	1768	0	1.20E-04	1.69E-04	#DIV/0!	#DIV/0!
BP1026B	II1597	type VI secretion system	686	316	182	0	292	684	166	0	0.134878606	0.151216559	#DIV/0!	#DIV/0!
BP1026B	II1598	type VI secretion system	87	495	53	0	51	58	169	0	3.87E-05	5.65E-05	#DIV/0!	#DIV/0!
BP1026B	II1599	type VI secretion system	0	0	0	0	0	0	0	0	1	1	#DIV/0!	#DIV/0!
BP1026B	II1600	type VI secretion system	510	315	369	1	196	339	231	0	2.23E-04	3.10E-04	0	#NUM!
BP1026B	II1602	type VI secretion system	285	145	135	0	49	353	0	0	0.056907781	0.066058569	#DIV/0!	#DIV/0!
BP1026B	II1601	type VI secretion system	810	389	595	0	1005	750	826	0	0.501501393	0.526454637	#DIV/0!	#DIV/0!
BP1026B	II1603	type VI secretion system	460	243	452	0	604	584	330	0	0.60462141	0.628076551	#DIV/0!	#DIV/0!
BP1026B	II1604	type VI secretion system	3368	2036	2805	0	2535	1647	2489	0	1.13E-08	2.15E-08	#DIV/0!	#DIV/0!
BP1026B	II1605	hypothetical protein	5590	7505	7002	5	6238	6838	6297	5	6.22E-11	1.42E-10	1	0
BP1026B	II1606	hypothetical protein	899	1543	1438	4	1719	1633	1534	5	0.421690259	0.447091567	1.25	0.321928095
BP1026B	II1608	hypothetical protein	3640	5085	5523	10	8444	10519	8059	19	0.544844234	0.569888591	1.9	0.925999419
BP1026B	II1607	GTP cyclohydrolase I	4704	6787	7034	9	10502	12962	10205	17	0.402584608	0.427776014	1.888888889	0.91753784
BP1026B	II1609	hypothetical protein	275	1253	719	4	760	1045	1635	7	0.339687316	0.363470069	1.75	0.807354922
BP1026B	II1610	hypothetical protein	29252	53936	46774	40	77031	82226	71952	72	0.67752413	0.698940763	1.8	0.847996907
BP1026B	II1611	hypothetical protein	2938	5442	5891	10	9243	9577	9157	21	0.769955619	0.788581547	2.1	1.070389328
BP1026B	II1612	transposase	2723	4670	3829	12	7242	6538	5785	22	0.337355643	0.361221883	1.833333333	0.874469118
BP1026B	II1615	AraC family transcriptional regulator	5347	4009	5785	5	4013	3424	5141	4	4.55E-12	1.16E-11	0.8	-0.321928095
BP1026B	II1616	hypothetical protein	26230	23488	24302	55	31099	33269	34325	74	0.001859275	0.002414552	1.345454545	0.428093652
BP1026B	II1617	DNA-binding response regulator	5203	3578	4044	6	4269	3787	3420	5	2.71E-09	5.41E-09	0.833333333	-0.263034406
BP1026B	II1618	chaperone	2303	2806	2141	5	3424	3685	3361	7	0.363024082	0.38758032	1.4	0.485426827
BP1026B	II1619	BopA protein	4740	6918	6239	3	9953	10901	8098	6	0.067844144	0.078246164	2	1
BP1026B	II1620	hypothetical protein	102	0	38	0	0	58	47	0	0.258557166	0.280540122	#DIV/0!	#DIV/0!
BP1026B	II1621	type III secretion target BopE	25948	27598	25676	33	40281	41895	36399	50	0.033753564	0.039920693	1.515151515	0.59946207
BP1026B	II1622	BapC protein	5029	2916	3475	6	3264	2531	4281	5	8.80E-09	1.68E-08	0.833333333	-0.263034406
BP1026B	II1623	acyl carrier protein	1291	1490	1581	5	1356	1516	1640	5	0.013846818	0.016870341	1	0
BP1026B	II1624	hypothetical protein	7562	5831	4949	2	5418	6005	5759	2	7.56E-11	1.71E-10	1	0
BP1026B	II1625	type III effector protein IpaD/SipD/SspD	14073	24857	22107	21	31033	36113	32193	35	0.172020426	0.190337275	1.666666667	0.736965594
BP1026B	II1626	HNS-like transcription regulator protein	4386	2368	2315	10	2109	3145	2416	8	2.21E-08	4.08E-08	0.8	-0.321928095
BP1026B	II1627	cell invasion protein	35907	41198	41195	31	53679	54084	48824	41	5.74E-04	7.72E-04	1.32258064	0.403355694
BP1026B	II1628	BipB protein	16573	22307	19463	10	25766	28713	23485	13	0.001493108	0.001949128	1.3	0.378511623
BP1026B	II1629	type III secretion low calcium response chaperone LcrH/SycD	5472	6719	6470	12	9016	9442	9823	18	0.016799281	0.020329142	1.5	0.584962501
BP1026B	II1630	surface presentation of antigens protein SpaS	2765	2562	3019	2	3364	3259	3085	2	0.005160034	0.006480812	1	0
BP1026B	II1631	type III secretion protein SpaR/YscT/HrcT	1917	1446	1898	2	1657	1074	1130	1	1.83E-08	3.39E-08	0.5	-1
BP1026B	II1632	type III secretion system protein BsaX	1723	1285	1265	5	1208	1492	1384	5	0.002203056	0.002847431	1	0
BP1026B	II1633	surface presentation of antigens protein SpaP	3732	5618	5409	7	6559	7458	6024	9	7.54E-04	0.001005036	1.285714286	0.362570079
BP1026B	II1634	type III secretion system apparatus protein YscQ/HrcQ	1054	510	362	0	404	448	305	0	1.25E-07	2.17E-07	#DIV/0!	#DIV/0!
BP1026B	II1635	BsaU protein	356	455	272	0	309	235	143	0	5.95E-04	8.00E-04	#DIV/0!	#DIV/0!
BP1026B	II1636	surface presentation of antigens protein	300	204	0	0	130	76	55	0	0.002770574	0.003557463	#DIV/0!	#DIV/0!
BP1026B	II1637	ATP synthase SpaL	6163	3932	4730	3	3108	2305	3382	2	5.19E-24	3.69E-23	0.666666667	-0.584962501
BP1026B	II1638	surface presentation of antigens protein	4780	7574	5956	14	8592	9867	7329	21	0.00169772	0.002210246	1.5	0.584962501
BP1026B	II1639	type III secretion system protein BsaQ	8330	7811	8769	4	8411	8591	8707	4	7.43E-10	1.56E-09	1	0
BP1026B	II1640	type III secretion system protein	4350	4253	4441	3	3679	3900	4924	3	3.85E-08	6.97E-08	1	0
BP1026B	II1641	YscR/HrcC family type III secretion outer membrane protein	10666	10236	11213	5	10133	10207	10175	5	1.12E-11	2.75E-11	1	0
BP1026B	II1642	type III secretion system transcriptional regulator BsaN	3570	5575	5034	6	5729	7194	7467	8	0.003748667	0.004759705	1.333333333	0.415037499
BP1026B	II1643	type III secretion system protein PrgH/EprH	4690	5413	4869	3	7002	9011	6663	5	0.01066517	0.013090686	1.666666667	0.736965594
BP1026B	II1644	MxiH protein	9460	16007	14627	49	23554	26222	22196	88	0.647667322	0.670126063	1.795918367	0.844721775
BP1026B	II1645	type III secretion system protein	1010	1155	823	3	1120	920	994	3	0.02777825	0.03303445	1	0
BP1026B	II1646	type III secretion system protein	4594	4552	5111	4	4765	5319	5993	5	4.81E-06	7.50E-06	1.25	0.321928095
BP1026B	II1647	type III secretion apparatus protein OrgA/MxiK	3203	1784	2506	4	2074	1702	1751	3	4.00E-10	8.57E-10	0.75	-0.415037499
BP1026B	II1648	type III secretion system protein	8404	3639	5420	7	3216	3975	2919	4	2.24E-26	1.92E-25	0.571428571	-0.807354922
BP1026B														

BP1026B	II1669	AMP-binding domain-containing protein	26149	19164	19322	13	19995	20093	21227	12	1.37E-13	4.00E-13	0.923076923	-0.115477217
BP1026B	II1671	hypothetical protein	3401	4472	5007	15	8121	8924	6024	28	0.245315571	0.267237025	1.866666667	0.900464326
predicted RNA	-		3476	5988	5902	394	7750	10647	6093	627	0.032496787	0.038485138	1.591370558	0.670269813
BP1026B	II1672	LuxR family transcriptional regulator	523823	702895	690651	917	732025	733666	720352	1051	0.605638341	0.62902865	1.14612688	0.19676903
BP1026B	II1674	hypothetical protein	24088	20992	24477	85	19156	16398	17659	65	4.19E-26	3.51E-25	0.764750882	-0.387023123
BP1026B	II1673	N-acylhomoserine lactone synthase	89548	67392	72141	125	53160	46753	56829	85	5.93E-37	1.00E-35	0.68	-0.556393349
BP1026B	II1675	NADH:flavin oxidoreductase	47154	46617	45450	34	50669	50955	47465	37	3.68E-09	7.26E-09	1.088235294	0.121990524
BP1026B	II1676	hypothetical protein	1966	2509	1526	12	2839	2952	1509	15	0.044518008	0.052208467	1.25	0.321928905
BP1026B	II1677	permease component of taurine ABC transporter	2979	2276	2574	3	2251	2492	2871	2	3.30E-05	4.85E-05	0.666666667	-0.584962501
BP1026B	II1678	taurine ABC transporter ATP-binding protein	618	310	339	0	518	361	522	0	0.500610473	0.525607444	#DIV/0!	#DIV/0!
BP1026B	II1679	taurine ABC transporter substrate-binding protein	1939	1481	1836	1	1552	1681	1731	1	4.14E-04	5.63E-04	1	0
BP1026B	II1680	taurine dioxygenase	5155	4767	4581	5	4877	5354	5150	6	4.95E-07	8.30E-07	1.2	0.263034406
BP1026B	II1681	hypothetical protein	5453	3135	3549	21	2879	2982	2184	14	7.40E-18	3.19E-17	0.666666667	-0.584962501
BP1026B	II1682	hypothetical protein	38889	33635	32913	22	31010	31293	27599	19	1.65E-14	5.26E-14	0.863636364	-0.211504105
BP1026B	II1683	glycosyl transferase family protein	35634	23203	27389	11	21356	20720	22343	8	1.47E-24	1.09E-23	0.727272727	-0.459431619
BP1026B	II1684	hypothetical protein	7475	3472	3091	5	2206	3443	2743	3	2.11E-23	1.43E-22	0.6	-0.736965594
BP1026B	II1685	hypothetical protein	1410	304	426	3	200	147	308	1	9.95E-26	8.09E-25	0.333333333	-1.584962501
BP1026B	II1686	hypothetical protein	29498	18831	20068	10	21282	17558	19333	8	3.78E-19	1.81E-18	0.8	-0.321928095
BP1026B	II1687	cellulose synthase operon protein C	41286	25422	26996	7	23990	24311	25145	6	2.50E-19	1.21E-18	0.857142857	-0.222392421
BP1026B	II1688	endo-1,4-D-glucanase	32452	14087	18925	16	12470	11420	10910	8	3.86E-55	1.57E-53	0.5	-1
BP1026B	II1689	cellulose synthase regulator protein	68911	41381	52232	25	38292	32973	41312	17	3.65E-29	3.84E-28	0.68	-0.556393349
BP1026B	II1692	HipB domain-containing protein	20494	13605	19184	43	15735	11058	16739	35	9.83E-21	5.31E-20	0.813953488	-0.296981738
BP1026B	II1691	hipA protein	112316	58458	65817	58	59310	49578	55255	40	2.72E-36	4.48E-35	0.689655172	-0.5360529
BP1026B	II1693	hypothetical protein	254515	171775	190679	453	149314	145833	147008	325	6.12E-33	8.28E-32	0.717439294	-0.479071332
BP1026B	II1694	LysR family transcriptional regulator	85261	55925	58880	72	63281	59801	63166	67	5.75E-17	2.31E-16	0.930555556	-0.103835811
BP1026B	II1695	agmatinase	4010	1215	1677	2	1266	587	1194	1	4.66E-31	5.48E-30	0.5	-1
BP1026B	II1696	hypothetical protein	1154460	1303448	1257882	884	1307271	1428785	1243277	946	0.2486019	0.270575566	1.070135747	0.097793814
BP1026B	II1697	hypothetical protein	31073	30522	28335	99	25812	21127	33552	89	5.48E-13	1.52E-12	0.898989899	-0.153623189
BP1026B	II1698	hypothetical protein	48087	43096	47665	115	41528	45033	36357	102	4.42E-15	1.48E-14	0.886956522	-0.173064709
BP1026B	II1699	hypothetical protein	51303	60905	59017	162	51662	51254	54364	149	3.30E-16	1.24E-15	0.919753086	-0.120681482
BP1026B	II1701	hypothetical protein	218262	178266	186136	242	174305	190410	165411	220	1.40E-15	4.96E-15	0.909090909	-0.137503524
BP1026B	II1700	hypothetical protein	16240	14637	15076	66	15666	14664	15944	66	1.02E-11	2.52E-11	1	0
BP1026B	II1702	hypothetical protein	10201	7488	8190	13	8087	6320	8762	11	1.16E-14	3.76E-14	0.846153846	-0.2410081
BP1026B	II1703	YscH/HrcC family type III secretion outer membrane protein	15248	16322	16003	8	15838	16125	12725	8	3.28E-14	1.02E-13	1	0
BP1026B	II1704	type IV prepilin	37197	32099	31809	20	30184	31258	29666	18	1.25E-12	3.35E-12	0.9	-0.152003093
BP1026B	II1705	hypothetical protein	2435	1351	2078	4	2089	1308	1548	3	3.78E-06	5.94E-06	0.75	-0.415037499
BP1026B	II1706	major pilin subunit	25155	36172	34883	57	42266	43271	36990	73	3.41E-04	4.66E-04	1.280701754	0.356934545
BP1026B	II1707	Integral membrane protein	64408	47166	48935	49	45431	41605	51610	42	4.30E-18	1.89E-17	0.857142857	-0.222392421
BP1026B	II1708	type II/IV secretion system protein	102748	66781	72815	50	54748	52338	59718	34	2.66E-37	4.59E-36	0.68	-0.556393349
BP1026B	II1709	hypothetical protein	1608	1071	894	2	1341	885	947	2	6.06E-04	8.15E-04	1	0
BP1026B	II1710	type IV pilus biosynthesis protein	68525	37361	48779	39	39655	34970	39493	29	1.14E-24	8.53E-24	0.743589744	-0.427421224
BP1026B	II1711	PilN	104264	67024	78314	47	62380	55376	66789	34	2.49E-32	3.20E-31	0.723404255	-0.46712601
BP1026B	II1712	PilL domain protein	24466	12882	14680	29	11716	11566	11699	20	1.32E-30	1.50E-29	0.689655172	-0.5360529
BP1026B	II1713	twiching motility protein	345540	402727	387449	341	422673	410261	415708	375	4.60E-07	7.73E-07	1.099706745	0.137118856
BP1026B	II1714	type II/III secretion system family protein	17680	15587	11298	8	16166	14889	18604	9	1.13E-08	2.13E-08	1.125	0.169925001
BP1026B	II1715	DNA-binding response regulator	27213	14117	15720	25	12946	12516	12582	17	6.21E-33	8.38E-32	0.68	-0.556393349
BP1026B	II1716	sensor histidine kinase	35446	23215	21234	24	21037	19449	21758	19	9.94E-23	6.42E-22	0.791666667	-0.337034987
BP1026B	II1717	hypothetical protein	3108	5082	3935	7	5223	5496	4731	9	6.08E-04	8.17E-04	1.285714286	0.362570079
BP1026B	II1718	hypothetical protein	755	410	407	1	416	463	365	0	0.00235754	0.00304208	0	#NUM!
BP1026B	II1719	hypothetical protein	1151	678	726	1	413	412	572	0	1.91E-10	4.17E-10	0	#NUM!
BP1026B	II1720	hypothetical protein	271	277	291	0	249	218	176	0	0.050880933	0.059337415	#DIV/0!	#DIV/0!
BP1026B	II1721	AraC family transcription regulator	1167	424	632	0	355	466	846	0	1.68E-04	2.35E-04	#DIV/0!	#DIV/0!
BP1026B	II1722	hypothetical protein	4060	4444	4349	9	5019	4572	4955	10	1.52E-05	2.29E-05	1.111111111	0.152003093
BP1026B	II1723	hypothetical protein	62852	105826	97283	484	122394	140778	127005	710	0.011677836	0.014300043	1.466942149	0.55281977
BP1026B	II1724	type III secretion protein	88	151	214	0	195	174	216	0	0.390244169	0.415085718	#DIV/0!	#DIV/0!
BP1026B	II1725	secretion-associated protein	991	547	691	0	616	373	564	0	1.62E-05	2.43E-05	#DIV/0!	#DIV/0!
BP1026B	II1726	type III secretion protein	355	232	135	0	155	235	88	0	0.014324841	0.01742902	#DIV/0!	#DIV/0!
BP1026B	II1727	type III secretion inner membrane protein SctS	949	791	593	2	778	870	411	2	0.007114377	0.008839715	1	0
BP1026B	II1728	type III secretion system protein	1712	1791	2083	2	1671	2013	1816	2	8.42E-04	0.00117288	1	0
BP1026B	II1729	type III secretion inner membrane protein SctQ	2775	2832	1915	1	2834	4233	3208	2	0.15578095	0.173102222	2	1
BP1026B	II1730	type III secretion protein HpaP	752	265	684	0	776	450	532	0	0.192532876	0.212172178	#DIV/0!	#DIV/0!
BP1026B	II1731	type III secretion inner membrane protein SctV	7699	7731	7591	3	7318	7305	7475	3	6.85E-12	1.71E-11	1	0
BP1026B	II1732	type III secretion system protein HrcU	1709	1586	1774	1	1657	885	1123	1	1.54E-08	2.88E-08	1	0
BP1026B	II1733	type III secretion protein HrpB1/HrpK	267	248	180	0	81	129	54	0	4.50E-07	7.57E-07	#DIV/0!	#DIV/0!
BP1026B	II1734	type III secretion protein HrpB2	542	886	504	1	730	686	1066	1	0.887304887	0.89892521	1	0
BP1026B	II1735	lipoprotein transmembrane protein	1034	743	760	0	1033	815	1000	1	0.177508473	0.196236431	#DIV/0!	#DIV/0!
BP1026B	II1736	type III secretion protein HrpB4	34	0	0	0	0	58	0	0	0.103316909	0.11713113	#DIV/0!	#DIV/0!
BP1026B	II1738	type III secretion system protein HrpB	275	48	0	0	0	234	95	0	0.860239273	0.874823935	#DIV/0!	#DIV/0!
BP1026B	II1737	type III secretion system ATPase	3498	2117	1856	1	1393	1172	1188	0	4.96E-24	3.54E-23	0	#NUM!
BP1026B	II1740	type III secretion protein HrpB7	52	20	8	0	0	0	0	0	1	1	#DIV/0!	#DIV/0!
BP1026B	II1739	Flagellar biosynthesis protein FlhR	1972	2121	2017	2	2121	2650	2651	2	0.03893157	0.045918271	1	0
BP1026B	II1741	hypothetical protein	1973	1393	1435	0	1590	438	1125	0	8.20E-11	1.85E-10	#DIV/0!	#DIV/0!
BP1026B	II1742	SyrP-like protein	5207	3983	3399	4	3585	3825	3859	3	3.55E-09	7.02E-09	0.75	-0.415037499
BP1026B	II1743	hypothetical protein	126907	133054	129951	7	107714	107514	106594	5	1.26E-22	8.06E-22	0.714285714	-0.485426827
BP1026B	II1744	hypothetical protein	146305	176269	167041	12	129709	132401	131426	9	8.41E-25	6.35E-24	0.75	-0.415037499
BP1026B	II1745	non-ribosomal peptide synthetase	104159	134076	121256	12	98643	106364	103162	10	2.35E-20	1.24E-19	0.833333333	-0.263034406
BP1026B	II1746	diaminobutyrate-2-oxoglutarate aminotransferase	42813	37441	40168	14	27065	24314	26313	9	7.01E-32	8.66E-31	0.642857143	-0.637429921
BP1026B	II1747	hypothetical protein	7525	7944	7507	15	7356	6129	6915	13	3.48E-14	1.08E-13	0.866666667	-0.206450877
BP1026B	II1748	hypothetical protein	13078	21933	18260	81	24332	27071	22818	112				

BP1026B	II1769	hypothetical protein	89	0	0	0	51	16	64	0	0.059284372	0.068660596	#DIV/0!	#DIV/0!
BP1026B	II1770	hypothetical protein	4939	3548	3550	3	3063	2485	2520	2	2.28E-17	9.44E-17	0.666666667	-0.584962501
BP1026B	II1771	beta-glucosidase	5715	4890	4741	2	3377	4556	4134	1	1.60E-13	4.63E-13	0.5	-1
BP1026B	II1772	hypothetical protein	107295	172962	161428	299	149762	174363	141064	315	3.98E-09	7.83E-09	1.05311706	0.075206344
BP1026B	II1773	glutamyl-tRNA(Gln) amidotransferase subunit A	7545	8341	8927	28	9159	8761	11179	33	2.29E-06	3.65E-06	1.178571429	0.237039197
BP1026B	II1774	hypothetical protein	65388	119114	100992	197	133005	151826	140638	293	0.030793513	0.036516304	1.487309645	0.572705035
BP1026B	II1775	hypothetical protein	36755	59724	55879	176	66507	76840	75047	252	0.003321947	0.0042411	1.431818182	0.517848305
BP1026B	II1776	selenocysteine-specific translation elongation factor	41599	26307	28111	16	27496	28481	25117	14	4.07E-15	1.38E-14	0.875	-0.192645078
BP1026B	II1777	selenocysteine synthase	41058	16066	22237	18	16898	13138	14694	10	3.87E-54	1.49E-52	0.555555556	-0.847996907
BP1026B	II1778	formate dehydrogenase accessory protein FdhE	54897	68546	59233	62	71925	78939	66621	74	1.35E-07	2.34E-07	1.193548387	0.255257055
BP1026B	II1779	formate dehydrogenase subunit gamma	134413	160335	147207	234	151936	144956	167837	247	3.54E-09	7.01E-09	1.055555556	0.078002512
BP1026B	II1780	formate dehydrogenase subunit beta	236101	228608	256664	262	231350	222524	246189	255	5.70E-13	1.58E-12	0.973282443	-0.039069565
BP1026B	II1781	formate dehydrogenase subunit alpha	460485	592934	543557	218	577081	594416	599909	242	0.614466688	0.637986457	1.110091743	0.150678912
BP1026B	II1782	formate dehydrogenase-O ₂ major subunit	188535	212779	221727	351	215580	186235	218611	349	2.54E-12	6.62E-12	0.994301994	-0.008243994
BP1026B	II1783	hypothetical protein	8754	9221	9619	18	10333	6427	8601	17	1.20E-13	3.53E-13	0.944444444	-0.08246216
BP1026B	II1784	hypothetical protein	24484	21382	21351	29	21214	19778	20675	26	7.43E-15	2.44E-14	0.896551724	-0.157541277
BP1026B	II1785	cystine-binding periplasmic protein FliY	1267	400	800	0	574	450	694	0	1.02E-05	1.55E-05	#DIV/0!	#DIV/0!
BP1026B	II1786	amino acid ABC transporter, ATP-binding/permease protein	3812	7036	5341	2	6105	6761	7811	3	8.33E-05	1.19E-04	1.5	0.584962501
BP1026B	II1787	nitrilotriacetate monoxygenase component A	3478	2276	2442	2	2286	2151	3152	1	3.49E-06	5.51E-06	0.5	-1
BP1026B	II1788	luciferase-like monoxygenase superfamily protein	1051	631	679	0	692	529	348	0	2.18E-06	3.48E-06	#DIV/0!	#DIV/0!
BP1026B	II1789	cystine-binding periplasmic protein FliY	5898	5200	5206	5	5178	4367	4815	5	2.72E-11	6.41E-11	1	0
BP1026B	II1790	N-acetyltransferase GCN5	1100	514	813	1	425	937	726	1	0.003690613	0.00469013	1	0
BP1026B	II1791	succinylglutamate desuccinylase/aspartoacylase family protein	21261	21201	16954	19	21154	21019	19866	20	4.25E-10	9.09E-10	1.052631579	0.074000581
BP1026B	II1792	hypothetical protein	44790	43268	46110	191	45913	44288	51528	201	2.43E-09	4.88E-09	1.052356021	0.073622863
BP1026B	II1793	ribonuclease	57982	45736	47085	54	44729	43686	51225	50	1.43E-14	4.58E-14	0.92529296	-0.11031312
BP1026B	II1794	outer membrane porin	669224	673211	690813	586	658230	633826	668970	565	0.434486943	0.45958639	0.964163823	-0.052649797
BP1026B	II1795	hypothetical protein	35543	25183	26937	62	22520	18518	23496	45	1.80E-25	1.43E-24	0.725806452	-0.462343214
BP1026B	II1797	DNA-binding protein BplH2	4702713	5345316	5339520	11552	5793299	5882213	5923529	13212	0.120569951	0.135684503	1.143680661	0.193706227
BP1026B	II1796	acyltransferase family protein	13315	20770	21721	13	25247	35050	28544	21	0.14001356	0.156637202	1.615384615	0.691877705
BP1026B	II1798	hypothetical protein	1953	1326	1961	3	1740	1913	1428	3	8.99E-04	0.00119077	1	0
BP1026B	II1799	UTP-glucose-1-phosphate uridylyltransferase	42276	56938	53386	57	55764	65123	71538	72	1.11E-05	1.68E-05	1.263157895	0.337034987
BP1026B	II1800	hypothetical protein	16460	26568	21994	150	22369	27933	23962	171	1.69E-06	2.71E-06	1.14	0.189033824
BP1026B	II1801	O-antigen acetylase	9160	14915	12586	10	14358	16415	13692	12	2.00E-06	3.21E-06	1.2	0.263034406
BP1026B	II1802	glycoside hydrolase family protein	8175	6690	6574	2	6158	6099	5246	2	7.10E-16	2.58E-15	1	0
BP1026B	II1803	polysaccharide biosynthesis family protein	4960	3957	3378	2	3393	2933	4139	2	5.01E-10	1.07E-09	1	0
BP1026B	II1804	hypothetical protein	4426	3695	3529	1	2180	2484	3354	1	4.07E-16	1.51E-15	1	0
BP1026B	II1805	acyltransferase family protein	1366	1615	1874	1	1714	1119	1701	1	5.64E-04	7.60E-04	1	0
BP1026B	II1806	GDP-mannose 4-6-dehydratase	14772	19323	21899	17	17824	16411	19429	17	4.52E-14	1.38E-13	1	0
BP1026B	II1807	oxidoreductase Rmd	6989	6435	6307	6	6074	5225	6282	6	1.23E-12	3.32E-12	1	0
BP1026B	II1808	cupin domain-containing protein	27441	41787	38615	94	46236	47892	47766	124	6.44E-04	8.63E-04	1.319148936	0.399607459
BP1026B	II1809	O-succinylhomoserine sulphydrylase	115938	127500	120539	101	124813	125460	127850	105	5.77E-11	1.32E-10	1.03960996	0.056034035
BP1026B	II1810	amidophosphoribosyltransferase	313083	373426	363419	227	375738	376979	386633	247	1.05E-07	1.84E-07	1.088105727	0.121818744
BP1026B	II1811	CvpA family protein	122907	121354	118295	244	121087	108500	127901	240	4.39E-13	1.23E-12	0.983606557	-0.023846742
BP1026B	II1812	sporulation repeat-containing protein	80277	58111	58108	80	72425	74129	71542	89	8.33E-10	1.74E-09	1.1125	0.153805336
BP1026B	II1813	bifunctional folylpolyglutamate synthase/dihydrofolate synthase	92027	83190	84328	65	83149	81557	81479	62	1.17E-16	4.56E-16	0.953846154	-0.068171503
BP1026B	II1814	acetyl-CoA carboxylase subunit beta	280466	261636	271906	310	233944	222161	251417	270	2.12E-18	9.56E-18	0.870967742	-0.199308808
BP1026B	II1815	tryptophan synthase subunit alpha	64240	36997	48904	61	31233	28855	36246	39	4.36E-33	5.98E-32	0.639344262	-0.64535119
BP1026B	II1816	DNA methylase	27111	36346	35041	38	38902	39242	43118	47	9.52E-05	1.35E-04	1.236842105	0.306661338
BP1026B	II1817	tryptophan synthase subunit beta	118061	136654	134628	108	139371	138719	147068	118	1.39E-08	2.61E-08	1.092592593	0.127555447
BP1026B	II1818	N-(5'-phosphoribosyl)anthranilate isomerase	50329	57793	54732	71	64949	63921	68769	86	8.16E-07	1.35E-06	1.211267606	0.276517635
BP1026B	II1819	tRNA pseudouridine synthase A	69495	57570	63876	78	58929	51991	63298	71	1.71E-17	7.16E-17	0.91025641	-0.135655099
BP1026B	II1820	hypothetical protein	94592	50470	57592	25	49770	47902	47563	18	1.15E-31	1.41E-30	0.72	-0.473931188
BP1026B	II1821	aspartate-semialdehyde dehydrogenase	167682	204354	192238	167	269966	278913	273450	244	0.04715412	0.055176034	1.461077844	0.547033045
BP1026B	II1822	hypothetical protein	25245	44057	38341	221	62094	74799	60852	406	0.970525163	0.975507005	1.837104072	0.877433358
BP1026B	II1823	3-isopropylmalate dehydrogenase	61997	58281	60392	56	58006	58174	59960	54	2.43E-14	7.63E-14	0.964285714	-0.05246742
BP1026B	II1824	isopropylmalate isomerase small subunit	44209	51074	48501	75	57126	59825	54843	90	1.41E-06	2.28E-06	1.2	0.263034406
BP1026B	II1825	Entericidin	2559	960	971	10	697	380	880	4	1.05E-22	6.74E-22	0.4	-1.321928095
BP1026B	II1826	isopropylmalate isomerase large subunit	110215	97312	101133	72	92543	87796	89124	63	8.10E-21	4.41E-20	0.875	-0.192645078
BP1026B	II1827	nitrilotriacetate monoxygenase	16074	22968	20895	15	23497	24075	23268	18	8.06E-06	1.24E-05	1.2	0.263034406
BP1026B	II1828	hypothetical protein	6992	9028	7103	8	10438	11758	10241	11	0.002141135	0.002769113	1.375	0.459431619
BP1026B	II1829	bkd operon transcriptional regulator	32474	34333	35491	64	36077	35065	33771	66	1.70E-08	3.17E-08	1.03125	0.043941919
BP1026B	II1830	2-oxoacid dehydrogenase subunit E1	203233	164408	172412	66	156635	149964	155295	56	3.19E-19	1.54E-18	0.848484848	-0.237039197
BP1026B	II1831	hypothetical protein	57619	47500	482929	41	46849	45244	45180	36	4.74E-16	1.75E-15	0.87804878	-0.187627003
BP1026B	II1832	hypothetical protein	6914	6162	6634	14	6204	6120	5636	12	4.59E-12	1.17E-11	0.857142857	-0.222392421
BP1026B	II1833	glyoxalase	12084	18881	14207	38	19010	19176	19085	48	2.07E-05	3.07E-05	1.263157895	0.337034987
BP1026B	II1834	AraC family transcriptional regulator	16485	11419	12633	13	10832	10032	11923	11	2.82E-18	1.26E-17	0.846153846	-0.2410081
BP1026B	II1835	type II citrate synthase	984904	1490682	1347439	978	1607472	1795779	1707093	308	0.024684416	0.029483902	1.337423313	0.419456171
BP1026B	II1836	hypothetical protein	74241	65748	59985	244	78358	79970	79970	1305	1.58E-06	2.55E-06	1.25	0.321928095
BP1026B	II1837	succinate dehydrogenase iron-sulfur subunit	341050	426840	417908	563	498996	522209	469255	707	7.15E-04	9.54E-04	1.255772647	0.328575293
BP1026B	II1838	succinate dehydrogenase flavoprotein subunit	713382	758044	768489	420	839192	827871	769451	457	0.284188479	0.307231989	1.088095238	0.121804837
BP1026B	II1839	succinate dehydrogenase, hydrophobic membrane anchor protein	144618	224469	206335	519	273301	299588	298096	786	0.113945208	0.12666835	1.514450867	0.598794774
BP1026B	II1840	succinate dehydrogenase cytochrome B subunit	223678	393488	362289	782	567806	695287	565790	1461	0.008037556	0.00945364	1.868286445	0.901715665
BP1026B	II1841	hypothetical protein	10375	14718	14366	63	14505	16956	15730	75	8.37E-07	1.38E-06	1.19047619	0.251538767
BP1026B	II1842	GntR family transcriptional regulator	57395	62111	62852	75	57628	59369	55273	71	1.31E-15	4.65E-15	0.946666667	-0

BP1026B	II1867	TonB-dependent copper receptor	103649	117991	111989	49	113546	120966	115336	51	1.20E-10	2.66E-10	1.040816327	0.057715498
BP1026B	II1868	hypothetical protein	70887	22325	26673	100	32106	39668	22387	79	1.22E-18	5.64E-18	0.79	-0.340075442
BP1026B	II1869	cytochrome b561	104975	153616	140789	247	183958	195574	193548	355	0.034863881	0.041194998	1.437246964	0.523307983
BP1026B	II1870	integral membrane protein	130074	121260	127805	198	136481	126015	150787	216	8.10E-09	1.55E-08	1.090909091	0.125530882
BP1026B	II1871	peptidase	51565	40063	43865	43	37541	36401	41335	37	3.01E-16	1.13E-15	0.860465116	-0.216811389
BP1026B	II1872	DSBH domain-containing protein	57574	43895	53282	165	41665	36940	41284	128	3.37E-22	2.06E-21	0.775757576	-0.366322214
BP1026B	II1873	hypothetical protein	167420	207961	211076	587	230995	242593	218640	692	2.89E-06	4.58E-06	1.178875639	0.237411535
BP1026B	II1874	6-phosphogluconate dehydrogenase	143784	170229	165505	112	173768	191899	170662	126	3.72E-07	6.28E-07	1.125	0.169925001
BP1026B	II1875	hypothetical protein	8682	5473	4817	10	5385	3468	4032	6	1.69E-20	8.99E-20	0.6	-0.736965594
BP1026B	II1876	NAD-dependent deacetylase	30892	19735	22505	25	16393	14781	17221	17	3.30E-37	5.67E-36	0.68	-0.556393349
BP1026B	II1877	cytosine/purines/uracil/thiamine/allantoin permease family protein	26491	23346	23185	17	21738	16263	18066	13	1.52E-25	1.22E-24	0.764705882	-0.387023123
BP1026B	II1878	hypothetical protein	2373	3607	3309	20	3981	5210	4005	28	0.104626953	0.118530553	1.4	0.485426827
BP1026B	II1879	hypothetical protein	296811	511776	479597	437	513037	612136	498049	551	0.491641448	0.516970182	1.260869565	0.334419039
BP1026B	II1880	Acyltransferase family protein	168630	288515	260870	196	265399	328168	273599	237	1.98E-05	2.95E-05	1.209183673	0.274033405
BP1026B	II1881	Met tRNA	1039	2342	2167	24	3011	3924	3509	45	0.091522082	0.104249657	1.875	0.906890596
BP1026B	II1882	RNA polymerase sigma factor RpoD	721962	902881	870318	407	945454	973871	956914	469	0.101300972	0.114980018	1.152334152	0.204559128
BP1026B	II1883	DNA primase	375147	471438	457767	231	515575	538670	477485	272	0.002613166	0.003363619	1.177489177	0.2357138
BP1026B	II1884	GatB/Yqey domain-containing protein	49572	43176	44663	102	53284	53238	60151	124	4.93E-06	7.69E-06	1.215686275	0.281770968
BP1026B	II1885	predicted RNA	22461	15963	20694	1791	16353	8827	21538	1415	1.88E-23	1.28E-22	0.790061418	-0.339963284
BP1026B	II1886	30S ribosomal protein S21	481720	804538	697800	3104	1173679	1305598	1124663	5639	3.72E-04	5.08E-04	1.816688144	0.861310785
BP1026B	II1886	hypothetical protein	24554	23864	21455	19	23192	24733	23644	19	2.20E-09	4.43E-09	1	0
BP1026B	II1887	DNA-binding/iron metalloprotein/AP endonuclease	17728	12146	13425	13	13646	11504	14303	12	1.52E-14	4.85E-14	0.923076923	-0.115477217
BP1026B	II1888	GTP cyclohydrolase	84848	93200	87706	109	90154	78864	101665	111	4.63E-13	1.29E-12	1.018348624	0.026231542
BP1026B	II1889	1-deoxy-D-xylulose-5-phosphate synthase	726620	687562	720439	373	680907	657433	696716	356	0.415385691	0.44070551	0.954423592	-0.067298389
BP1026B	II1890	geranyltransferase	299859	245492	254434	310	245987	237375	259738	288	1.34E-14	4.31E-14	0.929032258	-0.106199404
BP1026B	II1891	exodeoxyribonuclease VII small subunit	98979	104095	114875	360	112729	86195	113928	354	2.38E-13	6.82E-13	0.983333333	-0.024247546
BP1026B	II1892	Rieske family iron-sulfur cluster-binding protein	388522	488637	461429	387	502758	526198	525245	449	0.011447346	0.014028764	1.160206718	0.214381879
BP1026B	II1893	rhodanese domain-containing protein	238966	204989	234848	260	202738	175861	219133	229	3.99E-18	1.75E-17	0.880769231	-0.183164025
BP1026B	II1894	carboxymethylglutaminase	84426	95685	95631	104	90812	88013	88356	101	2.30E-15	7.97E-15	0.971153846	-0.042228235
BP1026B	II1895	hypothetical protein	135857	106946	119407	61	104584	98777	107431	53	2.88E-20	1.50E-19	0.868852459	-0.202816883
BP1026B	II1896	NADH dehydrogenase	103170	105235	102369	74	103654	102549	105812	75	1.73E-12	4.58E-12	1.013513514	0.019365325
BP1026B	II1897	DNA polymerase I	193842	206389	205192	72	217681	223589	209748	78	2.54E-09	5.10E-09	1.083333333	0.115477217
BP1026B	II1898	decarboxylase family protein	109489	151492	141124	182	165612	173292	181915	236	0.001178017	0.001547151	1.296703297	0.374848409
BP1026B	II1899	hypothetical protein	3093	2038	2362	8	2628	2761	2164	8	1.25E-04	1.77E-04	1	0
BP1026B	II1900	hypothetical protein	7461	6517	5935	13	6951	6344	5997	13	9.32E-11	2.09E-10	1	0
BP1026B	II1901	hypothetical protein	6076	6725	5572	11	7401	8755	7779	15	1.06E-04	1.51E-04	1.363636364	0.447458977
BP1026B	II1902	hypothetical protein	15120	23759	20313	16	25993	32415	28290	23	0.02276431	0.027294521	1.4375	0.523561956
BP1026B	II1903	hypothetical protein	560	1253	535	8	1102	1212	1023	11	0.716918259	0.73727389	1.375	0.459431619
BP1026B	II1904	hypothetical protein	1228	978	1251	4	1461	800	1468	4	0.064039392	0.073980611	1	0
BP1026B	II1905	site-specific recombinase, phage integrase family protein	1369	2245	1508	3	3067	3429	2252	5	0.335309242	0.35937373	1.666666667	0.736965994
BP1026B	II1906	site-specific recombinase, phage integrase family protein	2696	5333	3829	16	5365	7353	5940	26	0.044335516	0.052013919	1.625	0.700439718
BP1026B	II1907	AMP nucleosidase	104782	94250	94865	64	99014	100159	104992	66	1.96E-11	4.69E-11	1.03125	0.044394119
BP1026B	II1908	hypothetical protein	23423	23612	22010	57	32734	35318	31894	83	0.016256539	0.019691373	1.456140351	0.542149417
BP1026B	II1909	homoserine kinase	25881	33152	29561	29	38854	41671	39273	40	0.002626369	0.003379225	1.379310345	0.4639471
BP1026B	II1910	hypothetical protein	22726	15689	15979	22	18397	15273	20568	22	1.76E-12	4.66E-12	1	0
BP1026B	II1911	MarK family transcriptional regulator	163806	177790	171759	358	173466	175787	177429	368	3.49E-10	7.51E-10	1.027932961	0.039746179
BP1026B	II1912	organic hydroperoxide resistance protein	67934	75829	77272	175	77487	81648	69567	181	1.51E-12	4.03E-12	1.04285714	0.048634775
BP1026B	II1913	hypothetical protein	460501	750074	664533	3931	1114934	1217993	998764	6984	5.22E-04	7.05E-04	1.776647164	0.829157195
BP1026B	II1914	polyhydroxybutyrate depolymerase domain-containing protein	26395	24275	21690	20	23180	23048	25471	20	2.36E-10	5.13E-10	1	0
BP1026B	II1915	PAP2 family protein	23186	14414	15043	25	15500	15085	16746	22	1.93E-16	7.37E-16	0.88	-0.184424571
BP1026B	II1916	molybdenum ABC transporter periplasmic molybdate-binding protein	33810	19994	22943	31	19883	18579	18713	23	2.49E-27	2.33E-26	0.741935484	-0.430634354
BP1026B	II1917	molybdate ABC transporter permease	14652	4560	7047	12	4599	3786	5417	6	1.20E-40	2.43E-39	0.5	-1
BP1026B	II1918	molybdenum ABC transporter ATP-binding protein	51729	40749	42179	63	44315	38508	40934	58	1.74E-13	5.02E-13	0.920634921	-0.119298928
BP1026B	II1919	transcriptional regulator ModE	72677	66210	69203	81	69616	72607	66800	82	1.54E-13	4.48E-13	1.012345679	0.017702002
BP1026B	II1920	hypothetical protein	123417	49311	61953	40	49804	39915	45989	23	3.19E-53	1.19E-51	0.575	-0.798366139
BP1026B	II1921	tautomerase enzyme family protein	31770	39664	37216	94	44260	36474	51196	114	3.10E-05	4.57E-05	1.212765957	0.278301162
BP1026B	II1922	LysR family transcriptional regulator	1390	452	478	0	726	263	342	0	4.94E-09	9.64E-09	#DIV/0!	#DIV/0!
BP1026B	II1924	hypothetical protein	7073	6905	6179	7	7550	5416	8184	7	5.86E-09	1.14E-08	1	0
BP1026B	II1923	sensor histidine kinase	14450	7118	8774	12	7550	6975	9376	10	1.63E-20	8.68E-20	0.833333333	-0.263034406
BP1026B	II1925	hypothetical protein	118712	112137	114086	85	109487	103036	118316	82	2.89E-14	9.01E-14	0.964705882	-0.05183932
BP1026B	II1926	dGTP-pyrophosphohydrolase, thiamine phosphate synthase	41006	14928	24647	45	15860	10945	15938	24	1.16E-61	6.23E-60	0.533333333	-0.906890596
BP1026B	II1927	alpha amylase family protein	13093	6299	7595	5	6438	5454	6038	3	1.51E-27	1.43E-26	0.6	-0.736965594
BP1026B	II1928	hypothetical protein	5179	3258	3139	5	2941	2909	1785	3	1.29E-17	5.43E-17	0.6	-0.736965594
BP1026B	II1929	YbaK/prolyl-tRNA synthetase associated domain-containing protein	853103	1339096	1081664	2259	1124073	1220553	1363816	2559	0.181027857	0.199915501	1.132802125	0.179895877
BP1026B	II1930	FMN-dependent dehydrogenase	97455	86029	88253	73	91229	98829	91392	75	4.75E-12	1.20E-11	1.02739726	0.038994132
BP1026B	II1931	transposon protein	6313	6517	6643	15	5754	6719	5888	14	3.37E-11	7.86E-11	0.933333333	-0.099535674
BP1026B	II1932	amino acid transporter LysE	4888	7395	6753	12	8310	6627	7866	14	3.83E-06	6.01E-06	1.166666667	0.222392421
BP1026B	II1933	AraC family transcriptional regulator	70724	96994	90275	110	96315	94039	99601	124	6.21E-09	1.20E-08	1.127272727	-0.459431619
BP1026B	II1934	hypothetical protein	1916	1502	1806	1	1774	1803	1973	1	0.008092938	0.010011915	1	0
BP1026B	II1935	hypothetical protein	7249	7723	7392	12	6572	5322	5702	9	1.20E-17	5.07E-17	0.75	-0.415037499
BP1026B	II1936	hypothetical protein	3640	4794	4379	10	3559	4970	4911	10	1.38E-06	2.23E-06	1	0
BP1026B	II1937	4-hydroxy-2-ketovale aldolase	6087	6239	5934	5	5290	5234	4683	4	1.17E-13	3.43E-13	0.8	-0.321928095
BP1026B	II1938	acetaldehyde dehydrogenase	5116	7418	6272	7	6638	5249	5624	6	3.51E-11	8.17E-11	0.857142857	-0.222392421
BP1026B	II1939	Thioesterase	5776	4481	4161	5	2535	2034	2336	2	2.67E-37	4.60E-36	0.4	-0.321928095
BP1026B														

BP1026B II1965	colanic biosynthesis UDP-glucose lipid carrier transferase mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase	7240	10184	8089	6	8699	7789	8156	5	5.15E-12	1.30E-11	0.833333333	-0.263034406
BP1026B II1966	hypothetical protein	319845	448086	401424	253	359125	368308	400871	244	8.18E-11	1.84E-10	0.964426877	-0.052256237
BP1026B II1967	hypothetical protein	192586	127263	149186	177	94751	90134	88756	103	6.07E-62	3.34E-60	0.581920904	-0.781105023
BP1026B II1968	hypothetical protein	72872	117672	108886	382	107732	124587	100453	424	9.45E-09	1.80E-08	1.109947644	0.150491627
BP1026B II1969	hypothetical protein	6142	6721	6805	11	6324	5059	6004	9	7.84E-13	2.14E-12	0.818181818	-0.289506617
BP1026B II1970	ferredoxin	9078	8093	8156	6	8022	7154	6015	5	5.67E-17	2.28E-16	0.833333333	-0.263034406
BP1026B II1971	rubrerythrin	2854	3332	2844	7	3165	2151	2056	5	8.83E-09	7.55E-09	0.714285714	-0.485426827
BP1026B II1972	N-acetylglucosyl-L-alanine amidase domain-containing protein	26277	27630	27935	26	25827	27432	24735	25	6.71E-11	1.53E-10	0.961538462	-0.05683528
BP1026B II1973	ECF subfamily RNA polymerase sigma factor	4040	2077	2195	2	2258	1745	2251	1	2.15E-10	4.68E-10	0.5	-1
BP1026B II1974	hypothetical protein	5019	3352	3185	7	2634	2842	3600	5	7.23E-12	1.80E-11	0.714285714	-0.485426827
BP1026B II1975	DGPF domain-containing protein	6767	7302	7252	17	9015	8369	8748	21	1.20E-05	1.81E-05	1.235294118	0.304854582
BP1026B II1976	DGPF domain-containing protein	24549	22728	23295	66	19406	18438	22140	56	1.17E-18	5.39E-18	0.848484848	-0.237039197
BP1026B II1977	extracellular nuclease	9649	7331	7327	4	7766	7587	7769	4	2.02E-12	5.31E-12	1	0
BP1026B II1978	transmembrane protein	29351	28977	32420	79	37110	41508	27811	93	1.85E-05	2.76E-05	1.17721519	0.235378063
BP1026B II1979	lipoprotein	225375	218461	220027	378	232846	237279	215179	390	1.82E-10	3.98E-10	1.031746032	0.04508789
BP1026B II1980	PerM family permease	68300	77465	76870	70	72182	71037	78697	69	5.28E-14	1.60E-13	0.985714286	-0.02075856
BP1026B II1981	hypothetical protein	56501	43052	49130	115	43226	43431	40873	99	3.45E-17	1.40E-16	0.860689565	-0.216134341
BP1026B II1982	TonB-dependent receptor	11285	6214	7468	4	7354	4642	6479	3	1.62E-21	9.33E-21	0.75	-0.415037499
BP1026B II1983	major facilitator family transporter	3038	1117	1355	1	1189	906	989	0	8.93E-17	3.51E-16	0	#NUM!
BP1026B II1984	oxidoreductase, zinc-binding dehydrogenase family protein	11080	6169	5774	7	4595	4843	6091	5	6.99E-24	4.91E-23	0.714285714	-0.485426827
BP1026B II1985	short chain dehydrogenase	39943	33065	35889	45	32237	28583	32162	38	1.62E-14	5.16E-14	0.844444444	-0.243925583
BP1026B II1986	short chain dehydrogenase	22793	26962	25694	32	29625	30345	31196	39	5.82E-05	8.41E-05	1.21875	0.285402219
BP1026B II1987	phosphoglycerate mutase family protein	2282	493	435	1	562	365	406	0	4.60E-21	2.56E-20	0	#NUM!
BP1026B II1988	phosphotransferase enzyme family protein	15238	10674	10644	11	12932	12133	14325	12	7.04E-09	1.36E-08	1.090909091	0.125530882
BP1026B II1989	acyl-CoA dehydrogenase domain-containing protein	21083	9626	13714	12	12408	10382	10257	8	6.51E-23	4.27E-22	0.666666667	-0.584962501
BP1026B II1991	hydrolase	15876	17944	17790	42	19998	22604	16550	49	1.19E-07	2.07E-07	1.166666667	0.223924221
BP1026B II1992	hypothetical protein	126912	125688	129344	107	133352	131038	136570	112	2.63E-10	5.71E-10	1.046728972	0.065887936
BP1026B II1994	dyp-type peroxidase family protein	153879	119389	132220	144	108332	94679	104843	109	5.76E-29	6.03E-28	0.756944444	-0.401740677
BP1026B II1995	predicted RNA	2547	4626	4045	373	6556	7212	6477	674	0.489069686	0.51461136	1.806970509	0.853572961
BP1026B II1995	ABC transporter, permease protein/ATP-binding protein	31501	22460	25173	13	24653	20182	24554	11	5.66E-15	1.89E-14	0.846153846	-0.2410081
BP1026B II1996	DJ-1/Pip1 family protein	24835	18798	19588	30	21068	18824	21897	29	2.27E-12	5.95E-12	0.966666667	-0.0489096
BP1026B II1997	AraC family transcriptional regulator	13229	5900	7188	7	5909	4346	4580	4	5.21E-36	8.39E-35	0.571428571	-0.807354922
BP1026B II2000	tryptophanyl-RNA synthetase II	8855	5920	6622	6	7170	5806	6584	6	9.40E-13	2.55E-12	1	0
BP1026B II2001	SlyB protein	4719	3284	3847	6	4408	3117	3879	5	1.57E-07	2.71E-07	0.833333333	-0.263034406
BP1026B II2002	AraC/XyS family transcriptional regulator	1353	832	1206	3	1173	514	717	2	1.24E-06	2.01E-06	0.666666667	-0.584962501
BP1026B II2003	CAAX amino terminal protease family protein	28954	20038	22088	25	17611	13971	19295	17	9.98E-31	1.15E-29	0.68	-0.556393349
BP1026B II2004	voltage-gated chloride channel	24462	18482	18604	15	16902	15097	17998	12	3.76E-22	2.30E-21	0.8	-0.321928095
BP1026B II2005	haloacid dehalogenase	36840	21478	22398	37	20721	17446	20803	27	4.64E-28	4.51E-27	0.729729723	-0.454565863
BP1026B II2006	chemotaxis-specific methyltransferase	52651	26369	31865	35	25586	23882	29011	25	9.42E-25	7.08E-24	0.714285714	-0.485426827
BP1026B II2007	chemotaxis histidine kinase	110418	92655	91210	37	91737	85345	89927	34	9.34E-19	4.35E-18	0.918918919	-0.121990524
BP1026B II2008	chemotaxis protein cheW	49335	31137	34302	52	29427	26810	28059	38	3.55E-22	2.17E-21	0.730769231	-0.452512205
BP1026B II2009	CheR methyltransferase SAM binding/TPR domain-containing protein	71615	45236	49239	26	40311	34967	38900	18	4.22E-30	4.70E-29	0.692307692	-0.530514717
BP1026B II2010	cheW domain-containing protein	19288	11512	13318	28	11961	10877	12612	22	2.64E-19	1.28E-18	0.785714286	-0.347923303
BP1026B II2011	hypothetical protein	156162	133461	139549	85	125849	117775	123872	73	1.57E-20	8.35E-20	0.858823529	-0.219566377
BP1026B II2012	sensor histidine kinase/response regulator	66133	62579	61186	57	67884	66802	66633	61	2.37E-11	5.61E-11	1.070175439	0.097847323
BP1026B II2013	hypothetical protein	6924	3862	3691	14	4190	3059	3589	11	2.52E-14	7.90E-14	0.785714286	-0.347923303
BP1026B II2015	hypothetical protein	1829	2458	2268	9	2819	3008	2310	11	0.046546784	0.054060101	1.222222222	0.289506617
BP1026B II2014	Acyl dehydratase	4422	5794	4717	15	4562	4735	4822	15	3.38E-09	6.71E-09	1	0
BP1026B II2016	hypothetical protein	3928	4951	3911	28	3379	3038	4139	23	6.03E-11	1.38E-10	0.821428571	-0.283792966
BP1026B II2017	aldehyde dehydrogenase	36596	36502	38197	25	37179	35621	36189	25	4.97E-10	1.06E-09	1	0
BP1026B II2018	acetylactate synthase	43687	54434	51831	30	62116	62820	59278	37	3.41E-06	5.38E-06	1.233333333	0.30256277
BP1026B II2019	Na ⁺ /H ⁺ antiporter	47241	47973	48896	30	44149	49788	48922	30	9.41E-12	2.32E-11	1	0
BP1026B II2020	hypothetical protein	48373	57275	54565	41	65957	64345	56007	48	6.80E-08	1.21E-07	1.170371707	0.227410496
BP1026B II2022	phospholipase D	74506	71549	70019	43	70306	70716	70775	42	1.20E-14	3.88E-14	0.976474186	-0.033947332
BP1026B II2023	HIT family protein	158932	209218	200552	454	218629	253603	207681	543	5.51E-06	8.57E-06	1.196035242	0.258259901
BP1026B II2024	ferredoxin reductase	1805	1015	1437	1	1243	781	533	0	1.07E-11	2.63E-11	0	#NUM!
BP1026B II2025	Rieske family iron-sulfur cluster-binding protein	533	559	400	1	538	355	749	1	0.40333559	0.428501324	1	0
BP1026B II2026	ortho-halobenzoyl 1,2-dioxygenase beta-ISP protein OhbA	424	388	416	0	440	382	348	0	0.104675086	0.118563646	#DIV/0!	#DIV/0!
BP1026B II2027	ortho-halobenzoyl 1,2-dioxygenase alpha-ISP protein OhbB	1875	2386	2054	1	2493	3272	2594	2	0.148181058	0.165213969	2	1
BP1026B II2028	AraC family transcriptional regulator	9945	8871	9017	9	7972	8250	6290	7	6.03E-19	2.84E-18	0.777777778	-0.362570079
BP1026B II2029	transcriptional regulator CatR	9017	5884	5322	7	4634	4529	4359	5	4.89E-22	2.97E-21	0.714285714	-0.485426827
BP1026B II2030	muconate cycloisomerase	16094	19797	20073	16	18957	18334	18963	16	4.25E-12	1.08E-11	1	0
BP1026B II2031	catechol 1,2-dioxygenase	6533	4960	4999	6	4906	4380	4884	5	5.55E-12	1.40E-11	0.833333333	-0.263034406
BP1026B II2032	muconolactone delta-isomerase	2447	2306	2967	8	1914	2143	1854	6	1.75E-09	3.55E-09	0.75	-0.415037499
BP1026B II2033	ubiquinol oxidase subunit IV	1787	1579	1545	4	1734	1831	1844	5	0.023589371	0.028229756	1.25	0.321928095
BP1026B II2034	ubiquinol oxidase subunit III	4486	3637	3772	6	4076	4025	4237	6	2.13E-06	4.23E-06	1	0
BP1026B II2035	ubiquinol oxidase, subunit I	35032	46319	43658	20	42521	49188	46684	22	9.30E-08	1.64E-07	1.1	0.137503524
BP1026B II2036	ubiquinol oxidase polypeptide II precursor	19408	22837	23504	24	23823	22600	26181	27	2.33E-07	3.98E-07	1.125	0.169925001
BP1026B II2037	2,4-dienyl-CoA reductase	44073	54300	53996	24	63317	65507	58513	30	2.84E-06	4.50E-06	1.25	0.321928095
BP1026B II2038	AraC family transcriptional regulator	21762	15143	16370	15	12959	13511	11938	11	5.04E-27	4.53E-26	0.733333333	-0.447458977
BP1026B II2039	LysR family transcriptional regulator	35459	17863	20499	25	15602	13737	16136	15	8.66E-44	2.09E-42	0.6	-0.736965594
BP1026B II2040	NAD-dependent epimerase/dehydratase family protein	14282	9270	10365	10	9634	9652	7102	8	8.35E-21	4.54E-20	0.8	-0.321928095
BP1026B II2041	transcriptional regulator CatR	148980	164281	167765	175	163352	161871	167311	179	5.16E-10	1.10E-09	1.022857143	0.032604665
BP1026B II2043	Benzoate 1,2-dioxygenase alpha subunit	7136	8528	7291	5	8937	10097	7964	6	1.93E-06	3.09E-06	1.2	0.263034406
BP1026B II2042	benzoate 1,2-dioxygenase subunit beta	6097	6692	7408	13	7227	7809	8273	15	5.90E-07	9.85E-07	1.153846154	0.206450877
BP1026B II2044	benzoate 1,2-dioxygenase ferredoxin reductase subunit	1180	539	788	0	311	328	375	0	8.72E-20	4.40E-19	#DIV/0!	#DIV/0!
BP1026B II2045	1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase	3886	4044	3686	4	3161	3706	4167	4	1.51E-07	2.60E-07	1	0
BP1026B II2046	carboxylesterase family protein	1816	1284	778	1	899	509	1242	0				

predicted RNA	-	30048	2517	4553	287	1795	1096	2780	43	0	0	0.149825784	-2.738642172
BP1026B_I22064	OsmY domain-containing protein	660527	519501	512341	866	501833	493131	478537	754	4.85E-14	1.48E-13	0.149669746	-0.199802501
BP1026B_I22065	sulfotransferase domain-containing protein	15946	14995	18209	13	19012	18490	17683	15	1.50E-08	2.81E-08	1.153846154	0.206450877
BP1026B_I22066	adenylsulfate kinase	4691	3829	3650	5	3044	2505	3599	4	1.97E-13	5.66E-13	0.8	-0.321928095
BP1026B_I22067	methyl-accepting chemotaxis protein	106407	96710	102352	60	104585	102345	111487	63	5.60E-11	1.28E-10	1.05	0.070389328
predicted RNA	-	9172	2293	4030	322	2609	1617	2156	132	3.59E-51	1.20E-49	0.409937888	-1.286522759
BP1026B_I22068	polysaccharide deacetylase domain-containing protein	86793	54615	63519	81	58619	46224	54714	63	2.54E-26	2.17E-25	0.777777778	-0.362570079
BP1026B_I22069	ABC-type export system, outer membrane channel protein	74508	53030	59145	41	56108	47892	56890	36	7.73E-20	3.91E-19	0.87804878	-0.187627003
BP1026B_I22070	ABC-type export system, membrane fusion protein	156110	114084	121823	120	111276	92128	123033	100	4.94E-22	3.00E-21	0.833333333	-0.263034406
BP1026B_I22071	ABC transporter ATP-binding protein	192660	214934	203402	291	230870	250889	241822	345	5.89E-06	9.13E-06	1.18556701	0.245577209
BP1026B_I22072	ABC transporter permease	276384	294993	277085	248	335490	337835	372895	306	1.82E-05	2.72E-05	1.233870968	0.303191532
BP1026B_I22073	hypothetical protein	144323	91476	103223	448	98990	89158	105177	387	2.91E-20	1.52E-19	0.863839286	-0.211165166
BP1026B_I22074	universal stress protein	378885	397281	379740	818	460188	434087	494040	982	2.46E-05	3.65E-05	1.200488998	0.263622181
BP1026B_I22075	TetR family transcriptional regulator	169095	60807	76068	117	62671	52493	64242	68	2.51E-58	1.14E-56	0.581196581	-0.782901878
BP1026B_I22076	RND efflux system, outer membrane protein	482890	366264	391852	271	416244	383631	386295	259	4.50E-11	1.04E-10	0.955719557	-0.065340754
BP1026B_I22077	efflux transporter	650527	402135	451405	466	429384	401706	439585	394	8.28E-16	2.99E-15	0.845493562	-0.242134325
BP1026B_I22078	RND efflux system, cytoplasmic membrane extrusion protein	1272680	1126511	1131406	359	1189558	1137567	1230600	362	0.387668885	0.412556595	1.008356546	0.012005853
BP1026B_I22079	ABC transporter permease	358604	378556	374345	329	401808	384503	411596	354	1.36E-07	2.36E-07	1.075987842	0.105661776
BP1026B_I22080	sensory box histidine kinase/response regulator	322567	336518	313784	176	335687	335186	366173	188	1.10E-08	2.09E-08	1.068181818	0.095157233
predicted RNA	-	24183	36136	36927	611	47082	50643	48635	920	0.036584875	0.043187797	1.505728314	0.590461481
BP1026B_I22082	methyl-accepting chemotaxis transducer transmembrane protein	41967	32384	35194	23	30901	29865	31601	19	5.03E-15	1.68E-14	0.826086957	-0.275634443
BP1026B_I22081	hypothetical protein	98832	140758	125814	238	139271	151607	156656	292	3.78E-05	5.52E-05	1.226890756	0.295006796
BP1026B_I22083	hypothetical protein	177696	189999	188849	409	198164	202849	200819	442	4.09E-09	8.02E-09	1.080684597	0.111945526
predicted RNA	-	27961	821	1612	273	870	348	722	17	0	0	0.062271062	-4.0052943
BP1026B_I22084	zinc-containing alcohol dehydrogenase	1510070	1667698	1611149	1555	1537207	1513769	1556132	1496	0.323702148	0.34737415	0.962058788	-0.055804405
BP1026B_I22085	hypothetical protein	22947	18989	19926	104	17675	16771	18492	89	2.12E-19	1.03E-18	0.855769231	-0.224706287
BP1026B_I22086	ATP synthase subunit gamma	302514	256486	249674	317	247343	235037	267986	294	1.28E-14	4.13E-14	0.927444795	-0.108666685
BP1026B_I22087	FOF1 ATP synthase subunit alpha	424276	251218	286216	158	247941	230684	253139	120	2.89E-25	2.26E-24	0.759493013	-0.396890153
BP1026B_I22088	ATP synthase F0 subunit B	325619	333762	323202	436	341949	327662	344908	450	1.20E-09	2.48E-09	1.032110092	0.045596866
BP1026B_I22089	FOF1 ATP synthase subunit C	91023	101942	95571	386	107133	109645	115535	444	9.92E-08	1.74E-07	1.150259067	0.201958829
BP1026B_I22090	FOF1 ATP synthase subunit A	133446	133044	123104	184	143430	146639	154885	211	6.22E-07	1.04E-06	1.14673913	0.197537233
BP1026B_I22091	hypothetical protein	16743	12218	12605	44	14369	12404	16425	46	2.58E-10	5.60E-10	1.045454545	0.064130337
BP1026B_I22092	FOF1-ATPase subunit	49867	42198	46315	93	46023	45980	48346	95	1.02E-10	2.28E-10	1.021505376	0.030696797
BP1026B_I22093	FOF1 ATP synthase subunit epsilon	52816	19824	23367	70	21502	21440	19971	45	4.77E-35	7.29E-34	0.642857143	-0.637429921
BP1026B_I22094	FOF1 ATP synthase subunit beta	854421	999591	631808	438	620624	561581	598529	374	0.081197559	0.092992311	0.853881279	-0.2278926
BP1026B_I22095	poly-beta-hydroxybutyrate polymerase	1263067	1453932	1446620	773	1434570	1495431	1415243	807	0.20968885	0.229945805	1.043984476	0.062100259
BP1026B_I22096	bifunctional enoyl-CoA hydratase/phosphate acetyltransferase	752311	536213	572541	441	490046	435198	473564	332	2.87E-21	1.63E-20	0.752834467	-0.409595414
BP1026B_I22097	acetate kinase	699157	273066	366706	378	266887	199877	275502	209	7.48E-55	2.99E-53	0.552910053	-0.854883292
BP1026B_I22098	hypothetical protein	146096	31222	59293	128	31895	22608	29161	45	1.67E-145	2.55E-143	0.3515625	-1.508146904
BP1026B_I22099	6-phosphofructokinase	60450	43784	46432	53	41825	43631	39923	44	1.24E-18	5.70E-18	0.830188679	-0.268488836
BP1026B_I22100	OsmY domain-containing protein	540409	522855	524702	816	544007	518464	567553	838	0.049514907	0.057808907	1.026960784	0.038381092
BP1026B_I22101	hypothetical protein	1435	1397	1620	5	1760	1508	1273	5	0.009525734	0.011731181	1	0
BP1026B_I22102	cytidine deaminase	28716	38835	33060	85	42422	39752	40515	104	6.04E-05	8.72E-05	1.223529412	0.291048782
BP1026B_I22103	thymidine phosphorylase	51906	24310	27796	26	20858	20121	22831	16	5.93E-41	1.22E-39	0.615384615	-0.700439718
BP1026B_I22104	hypothetical protein	247619	382911	341196	1799	512037	592726	523841	3015	0.241542339	0.263263924	1.675931073	0.744962816
BP1026B_I22105	deoxyribose-phosphate aldolase	23901	16312	17659	24	19667	21049	20178	25	5.65E-10	1.20E-09	1.041666667	0.058893689
BP1026B_I22106	nucleoside transporter	60028	33577	39155	35	27677	24889	31103	22	1.06E-33	1.50E-32	0.628571429	-0.669851398
BP1026B_I22108	pyridoxamine 5'-phosphate oxidase family protein	4857	5654	4500	4	4718	4346	4912	3	1.51E-09	3.09E-09	0.75	-0.415037499
BP1026B_I22109	glutathione S-transferase	2936	2768	2723	4	1831	2968	1700	3	5.62E-10	1.19E-09	0.75	-0.415037499
BP1026B_I22110	LysR family transcriptional regulator	25249	9537	15454	18	10878	9331	9813	11	2.35E-39	4.45E-38	0.611111111	-0.710493383
BP1026B_I22111	TetR family transcriptional regulator	9469	9992	7543	13	9982	10198	10013	15	2.57E-07	4.38E-07	1.153846154	0.206450877
BP1026B_I22112	short chain dehydrogenase/reductase family oxidoreductase	10682	10802	12387	12	12904	14464	12023	14	4.98E-07	8.35E-07	1.166666667	0.222392421
BP1026B_I22113	monooxygenase flavin-binding family protein	14685	13136	11984	8	15120	12780	14658	8	2.14E-09	4.31E-09	1	0
BP1026B_I22114	hypothetical protein	12428	9676	7965	10	10122	9596	11434	10	4.16E-09	8.17E-09	1	0
BP1026B_I22115	diguanylate cyclase	67291	65950	64832	43	64115	53226	60420	38	1.57E-18	7.14E-18	0.88372093	-0.178337241
BP1026B_I22116	hypothetical protein	8528	3435	4637	12	5522	4993	5335	11	1.01E-09	2.11E-09	0.916666667	-0.125530882
BP1026B_I22117	sedolisin-B	19460	16467	16584	9	14868	12511	16417	7	1.07E-19	5.38E-19	0.777777778	-0.362570079
BP1026B_I22118	hypothetical protein	1758	2196	1851	4	3205	4540	3635	7	0.060657147	0.070202748	1.75	0.807354922
BP1026B_I22119	lipoprotein	6551	5956	6877	3	6113	4813	6448	3	2.51E-12	6.53E-12	1	0
BP1026B_I22120	hypothetical protein	6281	7765	7873	5	8713	7844	8692	6	5.58E-07	9.33E-07	1.2	0.263034406
BP1026B_I22121	hypothetical protein	3295	2329	2925	2	2073	1647	1842	1	1.78E-14	5.66E-14	0.5	-1
BP1026B_I22122	hypothetical protein	1973	1748	2095	1	1638	823	1393	0	1.46E-11	3.53E-11	0	#NUM!
BP1026B_I22123	exopolysaccharide tyrosine-protein kinase	8673	10140	8848	3	9754	10292	9323	4	1.45E-08	2.72E-08	1.333333333	0.415037499
BP1026B_I22124	hypothetical protein	1855	3205	2354	2	2595	2648	3351	2	0.006897184	0.008583467	1	0
BP1026B_I22125	hypothetical protein	4974	4965	5442	14	3686	3681	5210	11	1.44E-12	3.84E-12	0.785714286	-0.347923303
BP1026B_I22126	hypothetical protein	2395	3619	3685	11	3461	4800	3769	14	0.007105985	0.00883104	1.272727273	0.347923303
BP1026B_I22127	Cu/Zn/Cd efflux system protein	19226	19922	19812	15	19039	19327	21552	15	2.93E-11	6.88E-11	1	0
BP1026B_I22128	hypothetical protein	2427	2755	2158	11	2831	1878	2573	11	8.97E-05	1.28E-04	1	0
BP1026B_I22129	deoxyribonuclease	1684	3257	2407	2	3043	2685	3616	2	0.053331119	0.06203319	1	0
BP1026B_I22130	hypothetical protein	2175	2835	2548	0	2617	2884	2756	0	0.001388387	0.001815449	#DIV/0!	#DIV/0!
BP1026B_I22132	hypothetical protein	2055	1753	1576	2	1763	1848	2180	2	0.00866112	0.01069371	1	0
BP1026B_I22131	hypothetical protein	541	554	452	0	180	339	195	0	0.34E-10	7.20E-10	#DIV/0!	#DIV/0!
BP1026B_I22133	phosphatase	3877	2857	3531	2	2482	2305	2855	1	2.41E-12	6.30E-12	0.5	-1
BP1026B_I22134	hypothetical protein	4115	3368	3619	3	3437	3130	3786	3	2.24E-07	3.83E-07	1	0
BP1026B_I22135	hypothetical protein	3115	3281	3304	2	4475	3711	4620	3	0.023408253	0.028023713	1.5	0.584962501
BP1026B_I22136	aldolase II superfamily protein	11862	19460	17387	21	16628	19019	18220	23	5.29E-09	1.03E-08	1.095238095	0.131244533
BP1026B_I22137	uracil-DNA glycosylase	20667	19963	16204	35	20425	19017	17616	36	4.31E			

BP1026B_I2161	outer membrane protein	15246	16299	14496	7	17625	14416	16393	7	2.23E-10	4.85E-10	1	0
BP1026B_I2162	hypothetical protein	177	153	237	0	185	116	182	0	0.273833569	0.296653033	#DIV/0!	#DIV/0!
BP1026B_I2163	hypothetical protein	944	2187	1689	1	2561	1125	1797	1	0.047310494	0.055348684	1	0
BP1026B_I2164	hypothetical protein	1830	756	1213	1	1162	791	1043	1	9.34E-06	1.43E-05	1	0
BP1026B_I2165	inner membrane glycosyltransferase	1372	1306	1363	0	1125	1142	1607	0	0.003147963	0.004027181	#DIV/0!	#DIV/0!
BP1026B_I2166	hypothetical protein	348	62	90	0	242	0	47	0	0.013548662	0.016516715	#DIV/0!	#DIV/0!
BP1026B_I2167	UDP-N-acetylglucosamine 2-epimerase	6221	4858	5751	4	4603	5299	4667	3	5.77E-12	1.45E-11	0.75	-0.415037499
BP1026B_I2168	Val tRNA	1230	1978	1316	19	2297	3108	2505	34	0.157870121	0.17529934	1.789473684	0.839535328
BP1026B_I2170	LysR family transcriptional regulator	13429	5673	8027	10	5467	4116	4265	5	1.14E-43	2.69E-42	0.5	-1
BP1026B_I2171	TerC family membrane protein	2520	2392	2586	3	2720	2945	2191	3	4.24E-04	5.76E-04	1	0
BP1026B_I2172	hypothetical protein	495	845	740	3	839	776	764	3	0.357633488	0.381955247	1	0
BP1026B_I2173	hypothetical protein	2764	3210	4075	10	4084	4525	3523	12	0.002728515	0.00350777	1.2	0.263034406
BP1026B_I2174	hypothetical protein	3940	2203	2264	9	1832	1539	1685	5	6.61E-17	2.63E-16	0.555555556	-0.847996907
BP1026B_I2175	pyridoxal-dependent decarboxylase domain-containing protein	28446	30085	28152	20	26542	22955	28689	18	1.02E-12	2.77E-12	0.9	-0.152003093
BP1026B_I2176	lectin	25455	34633	33537	34	36039	38155	35673	40	1.81E-05	2.71E-05	1.176470588	0.234465254
BP1026B_I2177	hypothetical protein	1019	995	1009	3	794	1036	586	3	1.74E-04	2.43E-04	1	0
BP1026B_I2178	alcohol dehydrogenase	4932	3883	4032	3	2820	3037	4172	2	1.67E-12	4.44E-12	0.666666667	-0.584962501
BP1026B_I2179	pyridoxal-dependent decarboxylase domain-containing protein	61368	63967	63684	44	54567	54334	59117	39	1.75E-18	7.90E-18	0.886363636	-0.1740294
BP1026B_I2180	xylulose kinase	16943	15267	15347	9	18264	17539	16818	10	5.74E-09	1.12E-08	1.111111111	0.152003093
BP1026B_I2181	hypothetical protein	18417	23794	21689	56	24765	23400	23066	63	2.92E-07	4.96E-07	1.125	0.169925001
BP1026B_I2182	Acyclic terpenes utilization regulator AtuR, TetR family	53937	35257	40079	63	42431	37781	39631	59	9.15E-13	2.49E-12	0.936507937	-0.094658874
BP1026B_I2183	acyl-CoA dehydrogenase	4873	3564	4554	3	3926	4098	3969	3	8.76E-09	1.68E-08	1	0
BP1026B_I2184	short chain dehydrogenase/reductase family oxidoreductase	3356	2089	2910	3	2420	1606	2044	2	2.87E-11	6.75E-11	0.666666667	-0.584962501
BP1026B_I2185	acetyl-CoA carboxylase carboxyltransferase	9141	7167	6911	4	6977	6390	7361	4	4.27E-14	1.31E-13	1	0
BP1026B_I2186	acyl-CoA dehydrogenase	5010	5545	5842	4	6179	6466	5481	5	5.09E-07	8.53E-07	1.25	0.321928095
BP1026B_I2188	enoyl-CoA hydratase	643	360	346	0	378	183	165	0	6.57E-07	1.09E-06	#DIV/0!	#DIV/0!
BP1026B_I2187	carbamoyl-phosphate synthase L subunit	3149	1746	2969	1	1965	1405	1764	0	1.07E-13	3.15E-13	0	#NUM!
BP1026B_I2189	hypothetical protein	7657	6526	4147	6	5181	3945	5863	5	3.68E-14	1.14E-13	0.833333333	-0.263034406
BP1026B_I2190	AMP-binding acetyl-CoA synthetase	50968	46522	42308	28	29020	29277	29525	17	4.47E-34	6.45E-33	0.607142857	-0.719892081
BP1026B_I2191	hypothetical protein	8766	13792	9493	22	13882	15482	15165	31	5.37E-04	7.25E-04	1.409090909	0.494764692
BP1026B_I2192	hypothetical protein	23055	26318	24632	23	27902	28437	26026	26	1.07E-06	1.75E-06	1.130434783	0.176877762
BP1026B_I2193	polyketide synthase subunit	37083	59359	51864	183	59830	62362	64355	230	1.24E-05	1.88E-05	1.256830601	0.329790213
BP1026B_I2194	cyclopropane-fatty-acyl-phospholipid synthase	74640	75456	81673	82	70521	79371	74604	79	2.24E-15	7.75E-15	0.963414634	-0.053771256
BP1026B_I2195	hypothetical protein	13110	9479	12580	11	11366	10710	10548	10	1.33E-12	3.55E-12	0.909090909	-0.137503524
BP1026B_I2196	amidohydrolase	13918	13702	11851	12	12388	13122	13876	12	3.91E-11	9.08E-11	1	0
BP1026B_I2197	saframycin Mx1 synthetase B	63299	66970	63400	34	65957	55444	66349	33	4.87E-15	1.63E-14	0.970588235	-0.043068722
BP1026B_I2198	thioesterase family protein	31369	29870	32144	74	28267	26417	26676	64	7.64E-14	2.29E-13	0.864864865	-0.209453366
BP1026B_I2199	hydrolase alpha/beta fold domain-containing protein	34720	23111	27585	29	18310	18034	20641	19	3.98E-36	6.49E-35	0.655172414	-0.610053482
BP1026B_I2200	hypothetical protein	17260	24196	22224	35	20059	23626	22495	36	1.09E-09	2.25E-09	1.028571429	0.040641984
BP1026B_I2201	Beta-phosphoglucomutase	32120	43232	45073	60	43537	52401	47252	71	5.30E-06	8.25E-06	1.183333333	0.242856524
BP1026B_I2202	IS element transposase	25617	32238	30794	40	34608	33248	32189	45	3.64E-06	5.74E-06	1.125	0.169925001
BP1026B_I2205	hypothetical protein	1004	1204	880	4	1625	1883	1899	7	0.042009653	0.049368433	1.75	0.807354922
BP1026B_I2206	hypothetical protein	1964	3967	3606	8	5892	5845	5868	16	0.877434807	0.89022126	2	1
BP1026B_I2207	adhesin/hemolysin	51657	69403	69893	6	71664	71127	69551	7	1.05E-09	2.17E-09	1.166666667	0.222392421
BP1026B_I2209	Integrase	2131	2307	2038	13	2388	2402	1730	13	3.96E-04	5.39E-04	1	0
BP1026B_I2210	RhsD protein	89965	146133	127046	26	157199	175157	157256	35	0.004767278	0.006005582	1.346153846	0.428843299
BP1026B_I2211	hypothetical protein	9396	7644	8128	6	7763	7053	8358	6	1.35E-13	3.96E-13	1	0
BP1026B_I2213	hypothetical protein	10315	14995	16253	15	18627	19172	18336	20	2.30E-04	3.20E-04	1.333333333	0.415037499
BP1026B_I2214	diaminopimelate decarboxylase	1028	799	1280	2	1448	888	1147	2	0.152030743	0.169265216	1	0
BP1026B_I2216	hypothetical protein	46898	64600	59724	55	60268	64398	63772	61	7.97E-10	1.67E-09	1.109090909	0.149377624
BP1026B_I2217	Aerobic C4-dicarboxylate transporter for formate, L-malate, D-malate, succinate	11659	19745	17595	27	20471	23778	20557	36	3.52E-04	4.81E-04	1.333333333	0.415037499
BP1026B_I2218	endoribonuclease L-PSP	8613	16134	13811	31	14226	18410	14889	38	3.75E-06	5.89E-06	1.225806452	0.293731203
BP1026B_I2220	GntR family transcriptional regulator	8011	10716	9475	21	10811	11507	11385	26	5.29E-06	8.23E-06	1.238095238	0.308122295
BP1026B_I2221	senescence marker protein-30	57956	95823	89663	91	111596	130323	111793	132	0.006887873	0.008575286	1.450549451	0.536599479
BP1026B_I2222	Polypeptide-transport-associated domain protein ShlB-type	16405	22976	23497	61	23983	28637	26198	76	1.47E-04	2.06E-04	1.245901639	0.37190176
BP1026B_I2223	transposase B	565	386	534	0	694	847	998	0	0.039965593	0.047036891	#DIV/0!	#DIV/0!
BP1026B_I2224	transposase	5	3	0	0	0	0	4	0	1	1	#DIV/0!	#DIV/0!
BP1026B_I2225	hypothetical protein	24859	44578	37530	18	48429	55006	44970	25	0.003775498	0.004791831	1.388888889	0.473931188
BP1026B_I2226	alpha-galactosidase	15553	25336	21680	9	25037	26954	25100	11	6.74E-05	9.68E-05	1.222222222	0.289506617
BP1026B_I2227	ABC transporter permease	2009	3312	2760	8	2763	4240	2309	9	0.00470358	0.005928914	1.125	0.169925001
BP1026B_I2228	hypothetical protein	498	990	564	3	885	740	1232	4	0.762527886	0.781485072	1.333333333	0.415037499
BP1026B_I2229	ABC transporter permease	4055	6923	6826	6	6773	8175	7404	8	2.94E-05	4.33E-05	1.333333333	0.415037499
BP1026B_I2230	ABC transporter substrate-binding protein	4156	6122	5407	4	5887	6429	6628	5	1.73E-05	2.59E-05	1.25	0.321928095
BP1026B_I2231	maltose/maltodextrin import ATP-binding protein malK	3460	7033	5062	4	5374	5131	5274	4	3.65E-08	6.63E-08	1	0
BP1026B_I2232	hypothetical protein	11776	20700	18026	8	20817	25569	23425	11	0.003124145	0.003997528	1.375	0.459431619
BP1026B_I2233	hypothetical protein	2175	3827	2712	13	4661	4084	4053	20	0.228176593	0.249477322	1.538461538	0.621488377
BP1026B_I2234	Lael family regulatory protein	17654	29934	27564	21	27988	32145	31901	26	1.03E-04	1.46E-04	1.238095238	0.308122295
BP1026B_I2235	transposase	300	967	328	2	447	184	322	1	1.50E-06	2.42E-06	0.5	-1
BP1026B_I2236	hypothetical protein	11633	19424	18106	20	17666	20555	17612	23	3.29E-08	5.99E-08	1.15	0.201633861
BP1026B_I2238	transposase	1349	2586	2142	6	2193	3146	2527	9	0.114194195	0.128926275	1.5	0.584962501
BP1026B_I2239	transposase B	579	554	459	0	678	790	1224	1	0.052329977	0.060925238	#DIV/0!	#DIV/0!
BP1026B_I2244	Integrase	4058	6489	5764	6	6317	7391	7088	8	7.63E-05	1.09E-04	1.333333333	0.415037499
BP1026B_I2245	transposase	3120	4935	4012	13	5710	6355	5152	18	0.007239736	0.008988347	1.384615385	0.469485283
BP1026B_I2246	IsrS8-transposase orb protein	34608	53847	50914	52	54174	56539	55962	62	2.07E-06	3.31E-06	1.192307692	0.253756592
BP1026B_I2247	transposase	18128	24053	25369	76	30674	33073	28840	104	0.003818663	0.004843673	1.368421053	0.452512205
BP1026B_I2248	hypothetical protein	855	1092	1217	7	1370	1145	1456	8	0.5342401	0.559229614	1.142857143	0.192645078
BP1026B_I2249	hypothetical protein	43457	72887	64753	52	73844	90021	77568	69	5.74E-05	8.30E-05	1.326923077	0.408084739
predicted RNA	-	9367	16184	11997	568	14161	16721	17791	737	3.47E-05	5.08E-05	1.297535211	0.37577369
BP1026B_I2250	transposase	13891	23648	20164	26	25816	33237	21002	36	0.005089058	0.006396798	1.384615385	0.469485283
BP1026B_I2252	YD repeat/RHS repeat protein	13909	22097	18293	9	23320	24601	23242	12	5.49E-04	7.40E-04	1.333333333	0.415037499
BP1026B_I2253	hypothetical protein												

BP1026B_I2271	hypothetical protein	13123	7786	8942	5	7834	5849	7589	3	1.79E-25	1.43E-24	0.6	-0.736965594
BP1026B_I2272	hypothetical protein	10258	13167	11771	9	12647	13021	11689	10	4.62E-09	9.03E-09	1.111111111	0.152003093
BP1026B_I2273	chorismate lyase superfamily protein	389	193	204	0	226	58	143	0	3.44E-04	4.71E-04	#DIV/0!	#DIV/0!
BP1026B_I2274	hypothetical protein	399	173	232	1	196	117	351	1	0.119198792	0.13421377	1	0
BP1026B_I2275	short chain dehydrogenase/reductase family oxidoreductase	5558	2975	3245	5	3314	3521	2936	4	1.58E-10	3.47E-10	0.8	-0.321928095
BP1026B_I2276	LysR family transcriptional regulator	5761	3996	4978	5	4714	4406	4457	4	1.25E-09	2.58E-09	0.8	-0.321928095
BP1026B_I2277	D-serine dehydratase	3241	1094	1761	1	1427	941	1336	0	2.00E-14	6.32E-14	0	#NUM!
BP1026B_I2278	LysR family transcriptional regulator	17529	10542	11664	14	12796	12876	14255	14	5.45E-11	1.25E-10	1	0
BP1026B_I2279	hypothetical protein	5612	9651	8240	25	12072	13213	10706	39	0.015706207	0.019050541	1.56	0.641546029
BP1026B_I2280	ArsR family transcriptional regulator	54338	73197	71763	98	84035	90425	94421	132	1.17E-04	1.65E-04	1.346938776	0.429684275
BP1026B_I2281	metallo-beta-lactamase family protein	6828	5171	6633	7	7091	5763	7751	8	1.46E-07	2.52E-07	1.142857143	0.192645078
BP1026B_I2282	major facilitator family transporter	9426	10144	10667	8	11934	10753	10758	9	1.34E-07	2.33E-07	1.125	0.169925001
BP1026B_I2283	cysteine desulfurase	11279	12353	12546	10	11965	11496	11152	10	8.36E-12	2.07E-11	1	0
BP1026B_I2284	hypothetical protein	335	163	371	0	265	515	540	1	0.101364758	0.114959561	#DIV/0!	#DIV/0!
BP1026B_I2285	major facilitator family transporter	18349	16877	16427	12	11746	10037	11802	8	1.08E-32	1.43E-31	0.666666667	-0.584962501
BP1026B_I2286	LysR family transcriptional regulator	5519	1733	1890	3	1623	1155	1727	1	6.64E-27	5.93E-26	0.333333333	-1.584962501
BP1026B_I2287	L-lactate dehydrogenase	10169	9474	9926	9	10642	10746	10218	9	2.64E-08	4.84E-08	1	0
BP1026B_I2288	flumarylacetoacetate hydrolase family protein	19477	10061	12459	16	8655	8118	9703	10	2.37E-35	3.72E-34	0.625	-0.678071905
BP1026B_I2289	IclR family transcriptional regulator	5548	3829	4241	5	5183	3313	3594	4	7.91E-10	1.66E-09	0.8	-0.321928095
BP1026B_I2290	indole acetamide hydrolase	34430	21737	24842	19	20928	17491	18695	13	1.96E-31	2.36E-30	0.684210526	-0.547487795
BP1026B_I2291	hypothetical protein	16875	19139	18040	32	18848	19552	20796	35	6.50E-09	1.26E-08	1.09375	0.129283017
BP1026B_I2292	acetyltransferase	67877	55681	58004	25	59049	51354	53333	23	1.73E-17	7.22E-17	0.92	-0.120294234
BP1026B_I2293	hypothetical protein	1516	2234	1369	3	2438	2454	2423	5	0.628829491	0.651926801	1.666666667	0.736965594
BP1026B_I2294	hypothetical protein	3054	5329	4402	8	6121	6694	6837	12	0.02164294	0.026009716	1.5	0.584962501
BP1026B_I2295	H-NS histone family protein	504671	767912	693975	2252	949492	1102507	899944	3381	0.006353881	0.00793096	1.50132149	0.586243189
BP1026B_I2296	hypothetical protein	13286	22935	19028	61	23098	28628	25476	85	0.006324154	0.007895428	1.393442623	0.478653599
BP1026B_I2297	hypothetical protein	4484	6578	5818	16	6753	7706	5273	18	2.81E-06	4.46E-06	1.125	0.169925001
BP1026B_I2298	sigma-54 dependent DNA-binding transcriptional regulator	80963	67787	74763	48	58195	43373	59602	35	1.59E-32	2.08E-31	0.729166667	-0.455679484
BP1026B_I2299	YsjC protein	112314	104133	102051	75	84737	87358	88647	61	2.47E-25	1.95E-24	0.813333333	-0.298081353
BP1026B_I2300	hypothetical protein	291713	469106	444569	1471	560127	633723	499052	2067	0.49353571	0.518700899	1.405166553	0.490741142
BP1026B_I2301	integral-membrane protein	32653	21146	25650	26	22536	19155	23013	21	1.42E-19	7.08E-19	0.807692308	-0.308122295
BP1026B_I2302	OptD family outer membrane porin	18655	24077	23459	15	24069	26512	22493	16	2.43E-07	4.15E-07	1.066666667	0.093109404
BP1026B_I2303	oligopeptide ABC transport system ATP-binding protein Oppf	9352	9276	9361	8	7231	7905	8799	7	1.33E-16	5.13E-16	0.875	-0.192645078
BP1026B_I2304	oligopeptide ABC transporter ATP-binding protein	34352	32997	34451	34	25121	23677	26990	25	7.22E-22	4.31E-21	0.735294118	-0.443606651
BP1026B_I2305	oligopeptide transport system permease	13090	10313	10607	12	7625	7182	7516	8	6.13E-32	7.63E-31	0.666666667	-0.584962501
BP1026B_I2306	oligopeptide ABC transporter permease	19038	23077	23053	23	20293	20366	21939	22	7.33E-13	2.01E-12	0.956521739	-0.064130337
BP1026B_I2307	oligopeptide ABC transporter periplasmic oligopeptide-binding protein	42620	53985	52300	30	38994	36626	37344	22	1.44E-22	9.14E-22	0.733333333	-0.447458977
BP1026B_I2308	DNA-binding protein	72945	102574	98495	150	89609	92365	98328	154	1.45E-12	3.87E-12	1.026666667	0.03796785
BP1026B_I2309	amino acid/petide transporter	74703	85113	97176	53	68426	71117	72067	46	7.11E-20	3.61E-19	0.867924528	-0.204358499
BP1026B_I2310	hypothetical protein	4640	5975	5500	26	6720	7200	6863	33	1.16E-04	1.64E-04	1.269230769	0.343954401
BP1026B_I2311	hypothetical protein	9373	8142	8840	5	10105	8075	7192	4	4.83E-12	1.22E-11	0.8	-0.321928095
BP1026B_I2312	LysR family transcriptional regulator	20516	24022	22613	23	708722	717053	757170	772	0	0	33.56521739	5.068895081
BP1026B_I2313	hypothetical protein	907	1202	993	1	5922	5098	4132	4	2.32E-56	9.88E-55	4	2
BP1026B_I2314	MmgE/Prp family protein	1343	824	856	0	11308	10399	11239	7	0	0	#DIV/0!	#DIV/0!
BP1026B_I2315	citrate lyase	878	862	760	0	14430	14150	13693	16	0	0	#DIV/0!	#DIV/0!
BP1026B_I2316	Acyl-CoA transferase/carnitine dehydratase protein	631	416	284	0	12249	10131	11670	9	0	0	#DIV/0!	#DIV/0!
BP1026B_I2317	zinc-binding dehydrogenase	2577	3142	2416	2	170910	174620	166986	146	0	0	73	6.189824559
BP1026B_I2318	isochorismatase	1469	1491	1729	2	104116	95171	98949	169	0	0	84.5	6.400879436
BP1026B_I2319	MFS family transporter	1022	511	829	0	18862	16791	19802	12	0	0	#DIV/0!	#DIV/0!
BP1026B_I2320	MFS transporter	9199	11804	11630	7	20288	22008	21362	14	0.926914903	0.936178076	2	1
BP1026B_I2321	hypothetical protein	651	923	743	0	4652	4809	4971	4	6.62E-98	7.68E-96	#DIV/0!	#DIV/0!
BP1026B_I2322	Acyl-CoA transferase/carnitine dehydratase protein	14667	8175	10989	8	22975	18947	23619	17	0.942943644	0.950528454	2.125	1.087462841
BP1026B_I2323	IclR family transcriptional regulator	12200	12699	11645	16	67998	62857	70625	89	1.17E-44	2.92E-43	5.5625	2.475733431
BP1026B_I2324	citrate lyase subunit beta	1202	195	543	0	1486	1648	1904	1	1.06E-08	2.02E-08	#DIV/0!	#DIV/0!
BP1026B_I2325	porin	12214	7403	8029	8	7749	7983	8483	7	1.24E-15	4.40E-15	0.875	-0.192645078
BP1026B_I2326	MmgE/PrpD family protein	8843	5631	6429	4	4506	4478	4139	2	2.99E-25	2.34E-24	0.5	-1
BP1026B_I2327	hypothetical protein	4840	3490	3509	3	3413	3237	4091	3	1.54E-08	2.89E-08	1	0
BP1026B_I2328	rarD protein	9847	5828	6150	8	5604	4831	4992	5	4.82E-21	2.68E-20	0.625	-0.678071905
BP1026B_I2329	acylphosphatase	8687	3121	4031	17	3118	3144	2035	9	4.27E-32	5.37E-31	0.529411765	-0.91753784
BP1026B_I2330	dihydroflavonol-4-reductase family protein	38196	11160	14887	21	8730	6928	9975	8	4.31E-110	5.51E-108	0.380952381	-1.392317423
BP1026B_I2331	hypothetical protein	32894	35166	39201	22	34137	34266	36449	22	6.14E-10	1.30E-09	1	0
BP1026B_I2332	glycosyl transferase family protein	22501	16562	18004	15	17302	19900	15965	14	2.69E-15	9.25E-15	0.933333333	-0.099535674
BP1026B_I2333	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	245495	176544	197029	219	175585	145982	173788	175	5.63E-23	3.71E-22	0.79906758	-0.325579548
BP1026B_I2334	radical SAM domain-containing protein	377341	510252	465032	388	510858	525972	561263	458	0.127616288	0.143279638	1.180412371	0.239290946
BP1026B_I2335	DOPA 4,5-dioxygenase	3555	4235	5694	12	4242	4430	3533	11	2.20E-09	4.44E-09	0.916666667	-0.125530882
BP1026B_I2336	aminotransferase	55681	46931	46311	36	42573	41707	40264	30	3.20E-18	1.42E-17	0.833333333	-0.263034406
BP1026B_I2337	hypothetical protein	19464	29842	23810	52	34239	33767	38393	75	0.018188848	0.021980968	1.442307692	0.528378972
BP1026B_I2338	hypothetical protein	5179	4559	5767	24	4043	4601	3526	19	1.11E-13	3.26E-13	0.791666667	-0.337034987
BP1026B_I2339	carbon starvation protein A	33584	34924	31467	16	29277	28915	30619	14	7.26E-13	1.99E-12	0.875	-0.192645078
BP1026B_I2340	cytochrome P460	2839	2078	1803	4	1682	1225	1565	2	4.80E-12	1.22E-11	0.5	-1
BP1026B_I2341	epoxide hydrolase	9990	6098	7003	7	5022	4435	5277	4	2.18E-26	1.88E-25	0.571428571	-0.807354922
BP1026B_I2342	hypothetical protein	22935	14849	14332	11	14486	13182	12915	8	8.83E-23	5.71E-22	0.727272727	-0.459431619
BP1026B_I2343	LysR family transcriptional regulator	15933	20278	18285	18	20721	23036	21367	22	4.07E-06	6.38E-06	1.222222222	0.289506617
BP1026B_I2344	cysteine transferase	3989	5447	5066	12	5094	4799	5181	12	2.32E-07	3.96E-07	1	0
BP1026B_I2345	hypothetical protein	1041	1324	765	2	981	1648	1404	2	0.667533863	0.689429182	1	0
BP1026B_I2346	hypothetical protein	447	178	216	0	158	86	232	0	5.53E-04	7.45E-04	#DIV/0!	#DIV/0!
BP1026B_I2347	Generic methyltransferase	1734	656	1040	1	574	383	746	0	7.36E-15	2.43E-14	0	#NUM!
BP1026B_I2348	glycosyl transferase family protein	11882	14316	13399	12	12395	13235	13729	12	2.75E-41	6.48E-41	1	0
BP1026B_I2349	hypothetical protein	1953	559	672	0	421	262	307	0	5.67E-37	9.63E-36	#DIV/0!	#DIV/0!
BP1026B_I2350	hypothetical protein	8060	6477	7031	5	7087	4987	6541	5	2.30E-14	7.21E-14	1	0
BP1026B_I2351	hypothetical protein	459	683	488	0	842	695	514	0	0.988733537	0.992058342	#DIV/0!	#DIV/0!
BP1026B_I2352	pilus subunit protein	79											

BP1026B_I2370	amino acid transporter	55931	58334	58912	40	45758	41190	47330	31	2.23E-24	1.63E-23	0.775	-0.367731785
BP1026B_I2371	GntR family transcriptional regulator	80970	70432	76063	97	49488	41952	53434	62	4.55E-43	1.05E-41	0.639175258	-0.645716532
BP1026B_I2372	hypothetical protein	644476	362113	411734	307	323130	313600	328166	208	4.59E-30	5.10E-29	0.67752443	-0.561655127
BP1026B_I2373	major facilitator family transporter	461140	478522	459050	356	517943	553927	518708	405	0.052912298	0.061557457	1.137640449	0.186044667
BP1026B_I2374	LysR family transcriptional regulator	163715	104565	108769	137	108962	101000	112565	117	2.62E-20	1.37E-19	0.854014599	-0.227667363
BP1026B_I2375	hypothetical protein	161240	153928	160327	74	145076	142258	147626	68	8.89E-16	3.20E-15	0.918918919	-0.121990524
BP1026B_I2377	hypothetical protein	722	348	221	1	354	369	435	1	0.039997649	0.047065779	1	0
BP1026B_I2376	hypothetical protein	3700	4153	4372	10	4619	4924	4957	12	9.18E-05	1.31E-04	1.2	0.263034406
BP1026B_I2378	Na ⁺ /H ⁺ antiporter-like protein	4330	4667	5650	3	5116	5479	5195	3	7.82E-07	1.29E-06	1	0
BP1026B_I2379	ATP-dependent DNA ligase	7209	5176	6273	1	5643	5788	4455	1	2.85E-13	8.12E-13	1	0
BP1026B_I2380	Ku70/Ku80 beta-barrel domain-containing protein	2837	3739	3207	2	3310	3380	2666	2	3.07E-06	4.86E-06	1	0
BP1026B_I2381	hypothetical protein	193	145	169	0	306	117	188	0	0.586275697	0.610841955	#DIV/0!	#DIV/0!
BP1026B_I2382	hydroperoxidase II	3102	3168	2972	1	2485	2766	3285	1	1.07E-06	1.74E-06	1	0
BP1026B_I2383	hypothetical protein	205	48	45	0	206	117	95	0	0.129238792	0.145049305	#DIV/0!	#DIV/0!
BP1026B_I2384	hypothetical protein	176	74	264	1	97	122	84	0	0.012810648	0.01564442	0	#NUM!
BP1026B_I2385	hypothetical protein	35	212	160	0	382	361	167	1	6.28E-05	9.06E-05	#DIV/0!	#DIV/0!
BP1026B_I2386	RNA polymerase factor sigma-54	2953	1407	2199	1	1435	1174	1715	0	3.76E-12	9.62E-12	0	#NUM!
BP1026B_I2388	lipoprotein	2475	2329	1901	2	936	1704	1669	1	4.98E-13	1.39E-12	0.5	-1
BP1026B_I2389	Manganese catalase	1153	776	1267	1	1313	1295	1240	1	0.33674865	0.360695221	1	0
BP1026B_I2390	hypothetical protein	2835	3644	2852	6	3562	2764	3261	6	6.86E-05	9.84E-05	1	0
BP1026B_I2391	hypothetical protein	1651	621	1110	2	784	445	693	1	6.19E-11	1.41E-10	0.5	-1
BP1026B_I2392	hypothetical protein	9106	15585	13572	36	17756	22515	20586	58	0.049803871	0.05813151	1.611111111	0.688055994
BP1026B_I2393	hypothetical protein	20265	34534	31401	81	42371	54345	41665	131	0.124172367	0.139613144	1.617283951	0.693572999
BP1026B_I2394	hypothetical protein	14122	9540	11156	13	9827	6471	8316	9	4.63E-27	4.18E-26	0.692307692	-0.530514717
BP1026B_I2395	lipoprotein	976	242	224	1	136	114	0	0	4.19E-45	1.09E-43	0	#NUM!
BP1026B_I2396	hypothetical protein	4070	3916	3163	11	3303	3422	3775	11	3.31E-07	5.60E-07	1	0
BP1026B_I2397	hypothetical protein	243	445	399	1	497	365	566	1	0.544786572	0.569888591	1	0
BP1026B_I2398	hypothetical protein	886	665	888	2	821	1064	973	3	0.297519754	0.320594802	1.5	0.584962501
BP1026B_I2399	hypothetical protein	539	249	654	1	293	615	474	1	0.090372045	0.103014596	1	0
BP1026B_I2400	hypothetical protein	578	607	644	5	544	1196	783	7	0.715270992	0.735700597	1.4	0.485426827
BP1026B_I2401	hypothetical protein	98520	58735	67908	116	51478	47488	46445	75	1.24E-41	2.64E-40	0.646551724	-0.629162305
BP1026B_I2402	hypothetical protein	1748	907	1513	3	1380	1448	1564	3	0.02554326	0.030463279	1	0
BP1026B_I2403	PRC-barrel domain-containing protein	10416	9227	7790	18	8263	7595	8763	16	1.20E-14	3.87E-14	0.888888889	-0.169925001
BP1026B_I2405	CheY-like domain-containing protein	347	436	555	0	225	309	591	0	0.012272549	0.015001911	#DIV/0!	#DIV/0!
BP1026B_I2404	hypothetical protein	0	0	0	0	0	0	0	0	1	1	#DIV/0!	#DIV/0!
BP1026B_I2406	DNA glycosylase	376	48	361	0	155	176	143	0	0.002733432	0.003513372	#DIV/0!	#DIV/0!
BP1026B_I2407	NRAMP family Mn2+/Fe2+ transporter	9172	5432	6558	4	5162	4935	5712	3	1.32E-18	6.06E-18	0.75	-0.415037499
BP1026B_I2408	glutathione-dependent formaldehyde dehydrogenase	1429	853	1031	0	1055	493	662	0	2.14E-07	3.67E-07	#DIV/0!	#DIV/0!
BP1026B_I2409	oxido-reductase, zinc-binding dehydrogenase family	500	17	380	0	43	43	104	0	7.06E-25	5.39E-24	#DIV/0!	#DIV/0!
BP1026B_I2410	hypothetical protein	3128	3049	2804	4	3624	3306	4226	6	0.014893471	0.018103296	1.5	0.584962501
BP1026B_I2411	hypothetical protein	827	425	440	0	576	218	502	0	9.74E-04	0.001286501	#DIV/0!	#DIV/0!
BP1026B_I2412	short chain dehydrogenase/reductase family oxido-reductase	1270	2272	1759	2	1759	1715	2148	2	0.006976093	0.00867822	1	0
BP1026B_I2413	hypothetical protein	962	1021	769	1	672	725	856	1	7.05E-04	9.42E-04	1	0
BP1026B_I2414	hypothetical protein	1901	1309	1628	5	1498	1444	1332	4	1.04E-04	1.48E-04	0.8	-0.321928095
BP1026B_I2415	short chain dehydrogenase	9755	9920	10796	9	10628	9324	9045	9	1.04E-11	2.56E-11	1	0
BP1026B_I2416	osmotically inducible protein Y	454	357	687	0	319	534	368	0	0.004841615	0.006098002	#DIV/0!	#DIV/0!
BP1026B_I2417	glycoside hydrolase family protein	1488	789	927	0	1125	860	631	0	1.59E-04	2.23E-04	#DIV/0!	#DIV/0!
BP1026B_I2418	NAD-dependent epimerase/dehydratase family protein	7771	5900	6413	6	7022	6936	6156	6	5.12E-10	1.09E-09	1	0
BP1026B_I2419	sensory box histidine kinase/response regulator	28175	11690	14781	7	9796	8571	8961	3	2.36E-62	1.32E-60	0.428571429	-1.222392421
BP1026B_I2420	hypothetical protein	8288	9625	9438	13	9364	9148	8574	13	8.23E-11	1.85E-10	1	0
BP1026B_I2421	glycosyl transferase family protein	7403	4165	5686	6	3366	3549	3152	3	6.81E-26	5.60E-25	0.5	-1
BP1026B_I2422	sigma-54 interacting response regulator	137561	121844	128263	94	121369	116289	118481	86	2.05E-16	7.81E-16	0.914893612	-0.128324097
BP1026B_I2423	sigma-54 interacting transcriptional regulator	57577	65485	64690	64	65222	70340	64394	68	3.35E-11	7.82E-11	1.0625	0.087462841
BP1026B_I2424	glycosyltransferase	4499	3715	4893	4	3462	3659	3945	3	1.28E-10	2.84E-10	0.75	-0.415037499
BP1026B_I2425	ADP-heptose-LPS heptosyltransferase II	1442	872	533	0	331	794	764	0	7.25E-07	1.20E-06	#DIV/0!	#DIV/0!
BP1026B_I2426	glycosyl transferase family protein	674	395	235	0	383	153	362	0	4.43E-04	6.01E-04	#DIV/0!	#DIV/0!
BP1026B_I2427	carbamoyltransferase family protein	6117	3765	3573	2	3791	2253	3885	1	2.08E-14	6.56E-14	0.5	-1
BP1026B_I2428	heptosyltransferase family protein	2871	1928	1811	1	2366	2101	1980	1	1.29E-04	1.82E-04	1	0
BP1026B_I2429	HAD-superfamily hydrolase	1088	1163	1095	1	1395	1353	1335	2	0.386322702	0.411263685	2	1
BP1026B_I2430	short chain dehydrogenase/reductase family oxido-reductase	1601	502	408	1	302	0	675	0	4.84E-21	2.69E-20	0	#NUM!
BP1026B_I2431	hypothetical protein	702	380	358	0	431	361	140	0	4.10E-05	5.97E-05	#DIV/0!	#DIV/0!
BP1026B_I2432	ATP-binding transmembrane ABC transporter protein	2622	1609	1584	0	1086	1758	1333	0	2.70E-09	5.40E-09	#DIV/0!	#DIV/0!
BP1026B_I2433	hypothetical protein	247	48	181	0	207	235	380	0	0.010909512	0.023019339	#DIV/0!	#DIV/0!
BP1026B_I2434	phosphatidylserine decarboxylase	3419	2626	3160	2	2931	3588	2998	2	9.33E-05	1.33E-04	1	0
BP1026B_I2435	succinate dehydrogenase iron-sulfur subunit	1170	1411	1166	1	518	565	760	0	7.50E-16	2.72E-15	0	#NUM!
BP1026B_I2436	hypothetical protein	1232	553	1086	3	518	334	804	2	1.07E-09	2.22E-09	0.666666667	-0.584962501
BP1026B_I2437	2-hydroxy-3-oxopropionate reductase	45398	33663	36494	43	28470	23219	28467	30	4.52E-26	3.77E-25	0.697674419	-0.519374159
BP1026B_I2438	nitroflavonoid monoxygenase	29339	26896	28661	20	20266	17923	19260	14	1.05E-34	1.58E-33	0.7	-0.514573173
BP1026B_I2439	4'-phosphopantetheinyl transferase	30850	16663	18377	26	13978	11811	13411	16	1.06E-44	2.66E-43	0.615384615	-0.700439718
BP1026B_I2440	oxalate/formate antiporter	76377	75926	79048	61	63749	59669	62158	49	5.42E-26	4.50E-25	0.803278689	-0.316027493
BP1026B_I2441	flavin reductase domain-containing protein	3133	1348	1049	2	685	643	1021	1	1.93E-27	1.81E-26	0.5	-1
BP1026B_I2442	hypothetical protein	1134	255	397	2	309	291	507	1	8.60E-07	1.42E-06	0.5	-1
BP1026B_I2443	hypothetical protein	455	145	360	0	479	483	425	0	0.196432945	0.215938392	#DIV/0!	#DIV/0!
BP1026B_I2444	hypothetical protein	24136	8502	12403	33	9407	8606	7863	19	5.65E-45	1.45E-43	0.575757576	-0.796466606
BP1026B_I2445	dihydropyrimidine dehydrogenase	45615	28363	32723	25	19054	18238	19806	13	1.49E-62	8.43E-61	0.52	-0.943416472
BP1026B_I2446	branched-chain alpha-keto acid dehydrogenase subunit E2	106651	95569	100562	69	67282	61578	64702	44	1.05E-47	3.04E-46	0.637681159	-0.649092838
BP1026B_I2447	2-oxoisovalerate dehydrogenase, E1 component, beta subunit	66668	59659	61583	62	37537	43527	41329	40	1.35E-36	2.24E-35	0.64516129	-0.632268215
BP1026B_I2449	2-oxoisovalerate dehydrogenase subunit alpha	156740	185614	195768	145	133953	138021	122249	106	1.11E-32	1.46E-31	0.731034483	-0.451988635
BP1026B_I2448	hypothetical protein	899	2075	1641	9	1582	2474	1756	11	0.255571224	0.277348336	1.222222222	0.289506617
BP1026B_I2450	hypothetical protein	1647	1623	1213	1	1622	1761	1462	1	0.028105892	0.033411405	1	0
BP1026B_I2451	hypothetical protein	1751	1808	1489	3	2754	2578	1915	5	0.672791634	0.694287282	1.666666667	0.736965594
BP1026B_I2452	hypothetical protein	29475	21840	25598	22	22336	22533	18794	19	5.01E-19	2.37E-18	0.863636364	-0.211504105
BP1026B_I2453	LysR family regulatory protein	41728	40811	39814	43	40104	38999	45402	44	1.23E-09	2.53E-09	1.023255814	0.033166864
BP1026B_I2454	hypothetical protein	1966	833	632	1	796	705	858	1	3.77E-07	6.37E-07	1	0
BP													

BP1026B_I2468	medium-chain-fatty-acid-CoA ligase	5542	5694	5502	3	6250	6652	4215	3	1.80E-08	3.35E-08	1		0
BP1026B_I2469	GerE family regulatory protein	45232	24521	28005	12	22747	20147	21633	7	1.13E-33	1.60E-32	0.583333333	-0.777607579	7
BP1026B_I2470	hypothetical protein	15888	22729	21521	18	17920	17590	18492	16	4.79E-17	1.94E-16	0.888888889	-0.169925001	0
BP1026B_I2471	quinone oxidoreductase	12369	8888	10932	10	7743	6886	6337	7	1.11E-31	1.36E-30	0	-0.514573173	7
BP1026B_I2472	taurine catabolism dioxygenase TauD, TfdA family protein	15177	13379	13600	16	11770	10080	9929	12	7.98E-22	4.74E-21	0.75	-0.415037499	0
BP1026B_I2473	hypothetical protein	23622	24101	23745	22	18561	18749	19523	17	3.58E-23	2.39E-22	0.727272727	-0.371968777	0
BP1026B_I2474	major facilitator family transporter	3072	2325	3380	2	981	824	1100	0	4.53E-61	2.39E-59	0	#NUM!	0
BP1026B_I2475	hypothetical protein	627	328	159	0	82	0	76	0	1.64E-55	6.79E-54	#DIV/0!	#DIV/0!	0
BP1026B_I2476	DSBA-like thioredoxin domain-containing protein	1309	639	499	1	633	403	482	0	1.16E-07	2.03E-07	0	#NUM!	0
BP1026B_I2477	molybdopterin oxidoreductase family protein	27902	33946	35786	11	29490	32609	29207	10	4.80E-11	1.10E-10	0.909090909	-0.137503524	0
BP1026B_I2478	iron-sulfur cluster-binding protein	5140	8264	7453	8	7850	7060	6342	8	9.07E-10	1.89E-09	1	0	0
BP1026B_I2479	DMSO reductase subunit C	3197	2568	1887	2	1269	1000	1362	1	2.96E-27	2.74E-26	0.5	-1	0
predicted RNA	-	239399	377292	292210	1814	446765	475384	461556	2761	0.022899583	0.02744621	1.522050717	0.606016432	0
BP1026B_I2480	polysaccharide deacetylase family protein	22256	19747	20457	23	23309	22901	20257	24	5.74E-09	1.12E-08	1.043478261	0.061400545	0
BP1026B_I2481	hypothetical protein	114491	98166	104362	75	93596	85528	87317	63	2.31E-23	1.56E-22	0.84	-0.251538767	0
BP1026B_I2482	penicillin-binding protein	69215	46634	57219	22	39068	34491	41466	14	3.50E-33	4.84E-32	0.636363636	-0.652076697	0
BP1026B_I2483	hypothetical protein	29997	24543	24355	16	23227	28191	24298	16	7.33E-11	1.66E-10	1	0	0
BP1026B_I2484	outer membrane porin	15747	13638	12374	11	12929	12971	13786	11	6.95E-13	1.91E-12	1	0	0
BP1026B_I2485	amidase	22099	14343	12086	10	16296	14059	13754	9	1.66E-15	5.81E-15	0.9	-0.152003093	0
BP1026B_I2486	hypothetical protein	47669	23250	30212	104	24247	24127	22212	72	4.40E-27	3.98E-26	0.692307692	-0.530514717	0
BP1026B_I2487	acetyltransferase	8063	2831	3770	8	2290	2395	2321	4	1.11E-37	1.93E-36	0.5	-1	0
BP1026B_I2488	acetyltransferase	6562	4595	4763	10	3238	4315	4200	7	1.21E-15	4.30E-15	0.7	-0.514573173	0
BP1026B_I2489	hypothetical protein	48886	28366	30928	26	27204	27518	27213	20	2.17E-20	1.14E-19	0.769230769	-0.378511623	0
BP1026B_I2490	TldD/PmbA family protein	120675	95114	99208	73	92118	90042	100607	65	1.14E-18	5.29E-18	0.890410959	-0.167456746	0
BP1026B_I2491	ABC transporter ATP-binding protein	28452	11647	14874	43	12534	11966	11046	28	3.79E-34	5.51E-33	0.651162791	-0.618909833	0
BP1026B_I2492	hypothetical protein	1425	2403	1753	19	3748	2713	2676	31	0.626063135	0.649166242	1.631578947	0.706268797	0
BP1026B_I2493	sensor kinase protein	87119	80700	84724	60	91287	93244	80487	63	5.78E-12	1.45E-11	1.05	0.070389328	0
BP1026B_I2494	LuxR family DNA-binding response regulator	81887	65666	69069	111	66789	68544	61886	101	2.84E-18	1.27E-17	0.909090909	-0.136204384	0
BP1026B_I2496	hypothetical protein	170918	155705	154819	268	174784	177350	188354	301	4.50E-07	7.57E-07	1.123134328	0.167530486	0
BP1026B_I2495	hypothetical protein	3348	2779	3492	11	3770	3744	3043	12	4.60E-04	6.24E-04	1.090909091	0.125530882	0
BP1026B_I2497	hypothetical protein	35409	47108	41766	55	43611	46281	45888	61	4.96E-08	8.89E-08	1.109090909	0.149377624	0
BP1026B_I2498	sensory box protein	58728	63632	59880	25	56155	58783	55761	23	5.85E-16	2.14E-15	0.92	-0.120294234	0
BP1026B_I2499	lipase	9015	10815	9634	8	9168	8314	10288	8	3.36E-12	8.64E-12	1	0	0
BP1026B_I2500	4'-phosphopantetheinyl transferase	1276	176	314	0	174	412	95	0	2.41E-15	8.32E-15	#DIV/0!	#DIV/0!	0
BP1026B_I2501	hypothetical protein	6301	6834	5695	15	7584	7280	6845	18	8.12E-07	1.34E-06	1.2	0.263034406	0
BP1026B_I2502	hypothetical protein	10747	5812	5957	5	5306	4452	5241	3	5.35E-24	3.79E-23	0.6	-0.736965594	0
BP1026B_I2503	hypothetical protein	3454	3663	4011	4	3783	5166	4435	5	6.64E-04	8.88E-04	1.25	0.321928095	0
BP1026B_I2504	permease	4034	3405	3709	2	2578	2720	3426	2	1.52E-11	3.67E-11	1	0	0
BP1026B_I2505	ABC-transporter ATP binding protein	1358	1193	1137	1	878	580	1277	1	1.55E-06	2.51E-06	1	0	0
BP1026B_I2506	flavin-binding monooxygenase-like protein	5125	5037	5268	3	4880	5852	5820	3	3.53E-07	5.97E-07	1	0	0
BP1026B_I2507	cytochrome P450 family protein	9103	6679	6073	1	5558	6381	6078	1	7.80E-16	2.82E-15	1	0	0
BP1026B_I2508	beta keto-acyl synthase	63725	51229	54203	8	47747	42159	47416	6	1.11E-21	6.50E-21	0.75	-0.415037499	0
BP1026B_I2509	acyl transferase domain-containing protein	10644	11909	11272	6	12925	14999	12726	8	2.09E-06	3.34E-06	1.333333333	0.415037499	0
BP1026B_I2510	hypothetical protein	267	765	626	4	1078	1639	729	8	3.08E-04	4.23E-04	2	1	0
BP1026B_I2511	hypothetical protein	57150	46180	47368	19	48437	52160	54280	19	6.12E-11	1.40E-10	1	0	0
BP1026B_I2512	lipoprotein VacJ	36411	41988	41336	40	43625	47819	46092	46	1.08E-06	1.76E-06	1.15	0.201633861	0
BP1026B_I2513	hypothetical protein	2603	2732	2918	5	3425	3408	3238	6	0.016237274	0.019671841	1.2	0.263034406	0
BP1026B_I2514	hypothetical protein	5501	4858	4559	3	3366	3147	3848	2	5.86E-17	2.34E-16	0.666666667	-0.584962501	0
BP1026B_I2515	hypothetical protein	2157	847	1281	1	1117	395	846	0	8.15E-14	2.43E-13	0	#NUM!	0
BP1026B_I2516	glutamine ABC transporter ATP-binding protein	6471	9341	9218	11	12466	10832	11446	15	0.001122832	0.001477771	1.363636364	0.447458977	0
BP1026B_I2517	glutamine ABC transporter permease	1581	2644	2335	3	2102	2509	2100	3	5.23E-04	7.06E-04	1	0	0
BP1026B_I2518	glutamine ABC transporter periplasmic protein	2895	4660	3996	5	5232	6199	5623	7	0.022007903	0.026428042	1.4	0.485426827	0
BP1026B_I2519	hypothetical protein	4573	1994	2030	4	956	1873	1215	1	2.80E-29	2.96E-28	0.25	-2	0
BP1026B_I2520	squalene-hopene cyclase	131708	97746	100000	55	96057	88292	100034	48	8.73E-21	4.74E-20	0.872727273	-0.196397213	0
BP1026B_I2521	squalene/phytoene synthase	104367	90105	106438	118	99042	99849	96712	116	1.01E-13	3.00E-13	0.983050847	-0.024662054	0
BP1026B_I2522	esterase EstC	43004	32354	36670	41	28181	22705	27879	28	3.93E-25	3.06E-24	0.682926829	-0.550197083	0
BP1026B_I2523	diguanylate cyclase	181174	161636	167336	181	138701	135306	149250	150	4.88E-22	2.96E-21	0.828729282	-0.271027197	0
BP1026B_I2524	response regulator	131445	127018	122714	203	114072	100214	124547	181	4.40E-18	1.92E-17	0.891625616	-0.165499003	0
BP1026B_I2525	response regulator	159528	219761	201994	525	197758	198732	219168	556	6.14E-10	1.30E-09	1.059047619	0.08276746	0
BP1026B_I2526	hypothetical protein	1241	1879	1549	5	1609	1751	2026	6	0.071543993	0.082240811	1.2	0.263034406	0
BP1026B_I2527	sensor histidine kinase/response regulator	196502	174811	178086	80	155280	144205	161183	67	1.86E-20	9.86E-20	0.8375	-0.255838904	0
BP1026B_I2528	NADPH-dependent FMN reductase domain-containing protein	195027	307469	283064	469	319240	368212	328992	607	1.71E-04	2.39E-04	1.29424307	0.372108594	0
BP1026B_I2529	RNA polymerase sigma factor	83055	134632	121720	186	156699	179510	153511	269	0.036816753	0.043445156	1.446236559	0.532303551	0
BP1026B_I2530	hypothetical protein	22421	30768	31724	142	36414	34094	38075	182	4.97E-04	6.71E-04	1.281690141	0.358047521	0
BP1026B_I2531	arsenate reductase	12562	23607	19904	52	26017	29916	27267	77	0.032932077	0.038978541	1.480769231	0.566346823	0
BP1026B_I2532	hypothetical protein	192	437	212	2	619	611	156	4	0.0272551	0.032424617	2	1	0
BP1026B_I2533	ParA family protein	72120	128210	115609	158	196204	227973	195265	311	0.196768533	0.216269361	1.96835443	0.976990022	0
BP1026B_I2534	parB family protein	128348	208338	191156	164	243830	281797	234689	237	0.038031497	0.044836381	1.445121951	0.531191244	0
BP1026B_I2535	plasmid replication protein	171596	247659	220214	154	230466	248794	244087	175	3.50E-07	5.93E-07	1.136363636	0.184424571	0
BP1026B_I2536	hypothetical protein	1156	2323	1723	3	2810	2173	2339	4	0.527977283	0.55322837	1.333333333	0.415037499	0
BP1026B_I2537	hypothetical protein	766	1826	1356	9	1523	1883	1637	12	0.477894456	0.503359667	1.333333333	0.415037499	0
BP1026B_I2538	hypothetical protein	2434	3796	3732	32	6438	7134	4286	58	0.810592395	0.826822717	1.8125	0.857980995	0