

## Methods:

### Fitting age vs. mass using GAMs, GLMS, and linear models to calculate AIM and AIM<sub>GDY</sub>

For each species, the relationship between age and predicted or observed mass was modeled using a GAM to predict mass-at-age during the pre-maturity phase of growth. As fish mass must be a positive, nonzero number, we initially assumed a Gamma error distribution for each of these GAMs, which does not allow for predicted values to be zero or negative. In order to avoid overfitting, the mass vs. age relationship was fit in iterations of GAMs, in which the flexibility (number of knots) was increased stepwise (from  $k = 1$ ) until 1000 datasets simulated with the R package DHARMA did not find significant results for uniformity and outlier tests ( $P > 0.05$ ). If no GAMs converged or passed both the uniformity and outlier tests before the maximum flexibility allowed ( $k=5$ ), a GLM with Gamma error distribution was fit to the data. If this GLM still failed the uniformity or outlier tests, a basic linear model was assumed if the linear model passed the uniformity test. For some growth curves, however, the Gamma error distribution underfits extremely young fish with mass close to zero. In these cases, and in cases where fewer than two years of data were available, the simplest linear model was assumed in order to avoid overfitting. These conservative methods were intended to avoid overfitting the data with excessively curvy fits, which can skew the value of AIM, especially in cases with limited sample size. Each fit can be seen in supplemental folder “AIM GAMs”, along with results of the DHARMA tests.

### Calculating environmental predictors for ontogenetic migrators with limited depth data

For *Alloctytus niger*, a detailed ontogenetic migration was not possible due to lack of depth-of-capture data, but it is thought that these fishes spend the first five years of life between 0-300m, and then migrate to 700-1300m (Horn et al. 2019; Horn personal comm.). As such, environmental conditions for these fish were estimated from their catch location across 0-300m for fish younger than 5 years, and across 700-1300m for older fish. Similarly, depth data was not available for *Lepidion eques*, but a temperature vs. length regression for *Lepidion eques* from Magnusson 2001 was used to predict temperature based on mean length-at-temperature. Max temperature was capped at the maximum range in the paper (7.35 degrees C). No temperatures were predicted to be lower than the minimum provided by the paper (4.09 degrees C). As most fish were taken west of 20W, only these temperature and size measurements were used.

### Adjusted metabolic rates to temperature and mass of habitat:

Metabolic rates from the literature were adjusted to both lifespan and prematurity average temperatures per work by Brown (2004) and Gillooly (2001):

$$CS_H = CS_{10}e^{E(T_H - T_A)/kT_AT_H}$$

Where  $CS_H$  is the metabolic rate at habitat temperature,  $CS_{10}$  is the metabolic rate at the assay temperature,  $E$  is the activation energy in eV (we used 0.65, the midpoint between 0.6 and 0.7 eV suggested by Brown),  $T_H$  is the average temperature in the fish habitat in Kelvin,  $T_A$  is the temperature of the assay in Kelvin (283K in all cases here), and  $k$  is Boltzmann's constant ( $8.62 \times 10^{-5} \text{ eV K}^{-1}$ ). To further adjust to lifespan and prematurity average fish masses, temperature-adjusted metabolic rates were multiplied by the  $M^{3/4}$ , where  $M$  is mass. For average masses, mass was first binned across each year of age, and these binned averages were averaged to get one average mass across the prematurity/lifespan

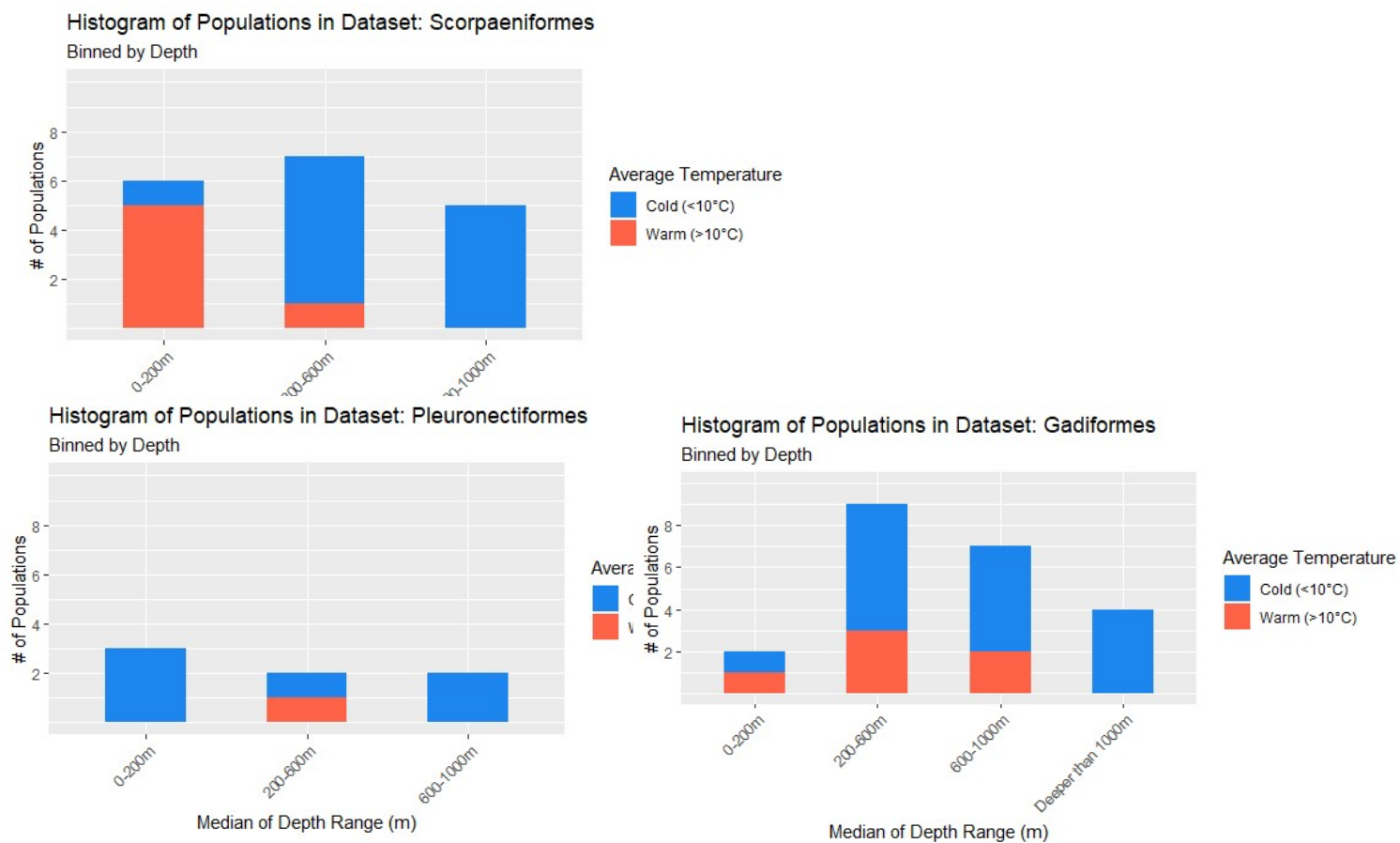
periods. This was done in order to avoid skewing the average mass by overrepresentation of large or small fish within each species' dataset.

**Quality control:** A number of studies were rejected for this analysis for using whole otoliths or scales as the primary age estimation method, listed here: Bayhan et al. 2009; Colloca et al. 1997; Consoli et al. 2010; El Serafy et al. 2015; Filiz et al. 2006; Gordo et al. 1997; İlhan et al. 2007; La Mesa et al. 2005; La Mesa et al. 2010; Massutí et al. 2000; Ordines et al. 2012; Sami et al 2016; Shahrani et al. 2015; Shakman et al. 2008; Vassilopoulou 1999.

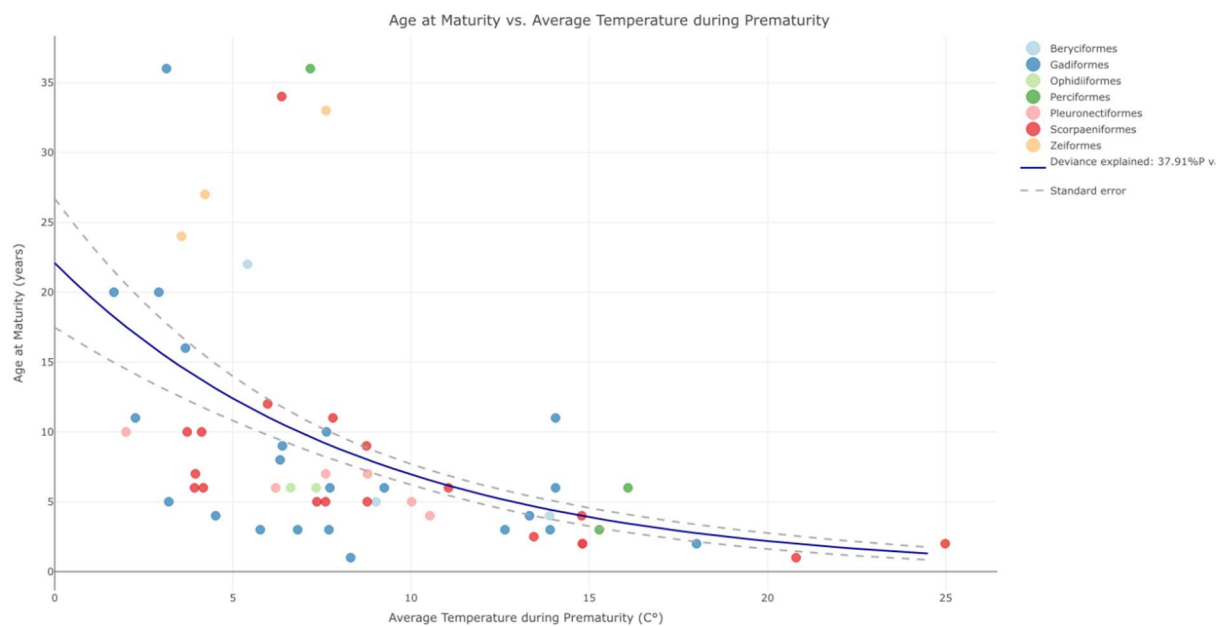
#### **Supplementary tables and figures:**

**Supp. Table 2)** P values for pairwise regressions of predictors and growth metrics, with and without *Coryphaenoides armatus*. Light blue cells indicate a P value of between 0.1 and .05. Pink cells indicate a P value below .05. Regressions were fit as generalized linear models (GLMs) with one of the following model families and link functions depending on which fit was favored by residual analysis and AICc: Gamma family with log link function, Gamma family with inverse link function.

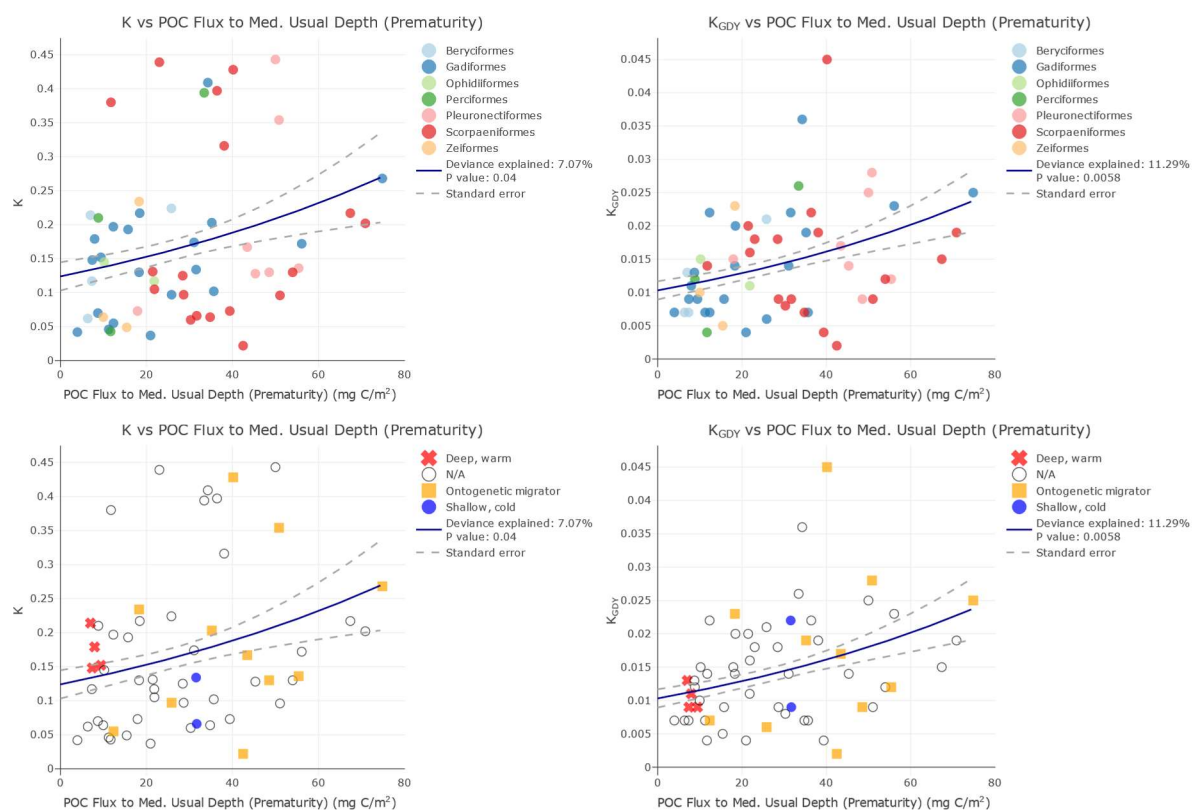
Predictor	K P	K w/o	K <sub>GDY</sub>	K <sub>GDY</sub>	AIM P	AIM	AIM <sub>GDY</sub>	AIM <sub>GDY</sub>
		CA P	P	w/o		w/o	CA P	CA P
Minimum Usual Depth (Pre-maturity)	2.1E-09	3.2E-08	1.8E-04	3.8E-04	5.0E-05	6.6E-06	3.6E-01	4.2E-02
Middle Usual Depth (Pre-maturity)	9.6E-09	3.7E-08	5.1E-04	6.7E-04	7.3E-06	8.3E-08	2.9E-01	1.4E-02
Maximum Usual Depth (Pre-maturity)	3.2E-07	6.5E-07	2.9E-03	4.0E-03	1.0E-05	3.8E-07	3.4E-01	2.4E-02
Minimum Usual Depth	7.1E-08	8.6E-07	8.0E-04	1.9E-03	6.7E-05	5.5E-05	3.6E-01	7.0E-02
Middle Usual Depth	2.3E-07	1.1E-06	3.3E-03	5.2E-03	9.9E-07	1.7E-07	2.3E-01	1.8E-02
Maximum Usual Depth	5.8E-06	1.9E-05	1.6E-02	2.6E-02	4.3E-07	1.3E-07	2.2E-01	1.9E-02
Average Oxygen Concentration (Pre-maturity)	8.6E-01	7.1E-01	4.6E-01	3.8E-01	8.8E-02	1.0E-01	3.7E-03	6.2E-03
Average Oxygen Concentration	8.6E-01	1.0E+00	9.1E-01	8.1E-01	7.6E-02	8.5E-02	4.7E-03	7.8E-03
Net Primary Production	2.8E-01	3.2E-01	2.2E-01	2.4E-01	8.8E-01	8.1E-01	3.9E-01	4.2E-01
Lutz POC Flux to Min Depth (Pre-maturity)	8.8E-02	1.3E-01	1.2E-02	1.9E-02	2.3E-01	3.4E-01	3.2E-01	2.8E-01
Lutz POC Flux to Mid Depth (Pre-maturity)	4.0E-02	6.3E-02	5.8E-03	9.8E-03	1.3E-01	2.0E-01	2.5E-01	2.1E-01
Lutz POC Flux to Max Depth (Pre-maturity)	2.4E-02	3.9E-02	5.9E-03	9.7E-03	9.0E-02	1.5E-01	2.9E-01	2.5E-01
Lutz POC Flux to Min Depth (Lifespan)	1.1E-01	1.6E-01	3.4E-02	5.0E-02	1.7E-01	2.6E-01	2.6E-01	2.2E-01
Lutz POC Flux to Mid Depth (Lifespan)	5.1E-02	7.8E-02	1.7E-02	2.7E-02	8.3E-02	1.4E-01	1.9E-01	1.5E-01
Lutz POC Flux to Max Depth (Lifespan)	2.9E-02	4.6E-02	1.6E-02	2.4E-02	5.4E-02	9.0E-02	2.2E-01	1.9E-01
Phylogenetic Order	9.3E-01	9.4E-01	9.4E-01	9.4E-01	5.1E-03	4.5E-03	1.6E-04	2.7E-04
Average Temperature (Pre-maturity)	1.0E-06	2.2E-06	7.3E-01	8.5E-01	8.2E-04	1.8E-03	4.3E-01	4.5E-01
Average Temperature (Lifespan)	3.8E-05	6.6E-05	9.0E-01	7.9E-01	4.9E-04	1.1E-03	5.3E-01	5.6E-01
Locomotory mode	7.8E-01	8.8E-01	4.6E-01	4.2E-01	1.4E-01	1.7E-01	8.4E-01	7.9E-01
CS <sub>H</sub> (Lifespan)	3.0E-02	1.9E-02	2.1E-02	1.6E-02	8.4E-02	7.4E-02	1.3E-01	1.6E-01
CS <sub>H</sub> (Pre-maturity)	7.6E-03	4.6E-03	2.7E-03	1.8E-03	9.0E-02	8.8E-02	1.3E-01	1.6E-01
CS <sub>10</sub>	4.8E-02	1.9E-02	1.3E-02	4.4E-03	3.0E-01	1.4E-01	1.2E-01	1.7E-01
SCOC (Lifespan)	8.7E-02	8.7E-02	2.4E-01	2.4E-01	1.3E-01	2.4E-01	2.8E-01	2.9E-01
SCOC (Pre-maturity)	8.3E-02	8.3E-02	1.7E-01	1.7E-01	4.1E-01	7.5E-01	8.4E-01	9.7E-01



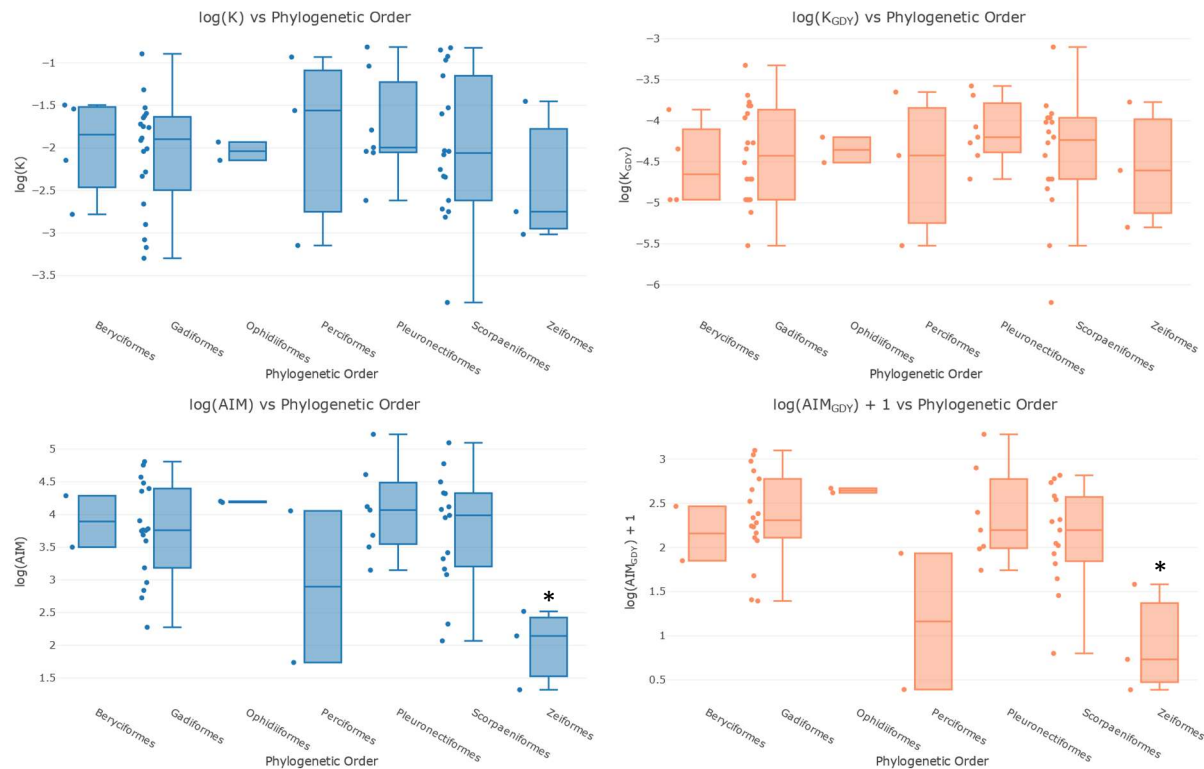
**Supp. Figure 1.)** Stacked histograms of populations in the dataset, separated into the three most populous orders. Histograms are binned by depth category and colored by temperature.



**Supp. Figure 2)** Regression of age at maturity vs. average temperature during prematurity. Smallest age of maturity between the sexes was used. The dashed grey line represents the standard error, and the blue line represents the fit curve.



**Supplementary Figure 3.** K and  $K_{GDY}$  vs. average Lutz POC flux to median usual depth. For ontogenetic migrators, Lutz POC flux concentrations to **average prematurity depth** were averaged. The blue lines show best-fit regression, and grey bands show the standard error. Rate of increase in fish length increases as the K coefficients increase. **Top row:** values of K (left) and  $K_{GDY}$  (right) vs. Lutz POC flux, colored by phylogenetic order. **Bottom row:** values of K (left) and  $K_{GDY}$  (right) vs. Lutz POC flux, with unique thermal situations for some species are highlighted with shape and color: species that ontogenetically migrate to deeper waters are shown as yellow squares, species that live in cold, shallow water ( $< 300\text{m}$  maximum usual depth and  $< 4^\circ\text{C}$  average temperature of habitat) are shown as blue circles, and species that live in deep, warm water ( $\geq 300\text{m}$  minimum usual depth and  $> 10^\circ\text{C}$  average temperature of habitat) are denoted with a red X.

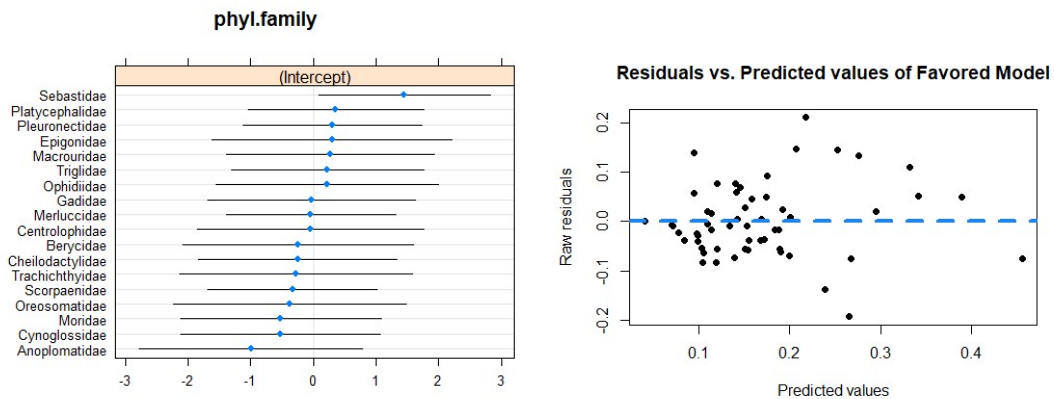


**Supp. Figure 4)** Boxplots of log transformed growth metrics across phylogenetic order. Variables are log transformed to create normal distribution. 1 was added to all values of  $\log(\text{AIM}_{GDY})$  to shift values above 0. **Top row:** log transformations of K (left) and  $K_{GDY}$  (right) across order. **Bottom Row:** log transformations AIM (left) and  $\text{AIM}_{GDY} + 1$  (right) across order. Middle bars of each box represent the median, and box upper and lower bounds represent Q1 and Q3. Whiskers represent min and max values for each order. Asterisks denote orders found to be significantly different from the rest when tested with Anova (P value  $> .05$ ).

### Supplementary GLMM figures

**Supp. Table 2)** Results of dredge analysis of K vs. pre-maturity predictors with phylogenetic family as a random effect. Global model call: `glmer(formula = K ~ scale(min depth) + scale(Lutz POC flux to max depth) + scale( $\text{O}_2$ ) + locomotory mode + (1 | phyl.family), data = meta.sub, family = Gamma, na.action = "na.fail")`. Predictors removed: NPP.

Models	Loc. mode	Min. Depth	Lutz POC flux	Temp	R <sup>2</sup>	AICc	Δ	Weight
<b>1</b>		<b>3.345</b>		<b>-0.6743</b>	<b>0.472</b>	<b>-127.9</b>	<b>0</b>	<b>0.205</b>
<b>2</b>		3.881			0.4461	-127.7	0.26	0.18
<b>3</b>	+	3.61		-0.7151	0.4916	-127.5	0.4	0.168
<b>4</b>	+	2.835	-0.7975	-1.027	0.5144	-127.5	0.45	0.164
<b>5</b>		2.641	-0.7279	-0.9488	0.49	-127.3	0.57	0.154
<b>6</b>	+	4.144			0.4631	-127	0.93	0.129



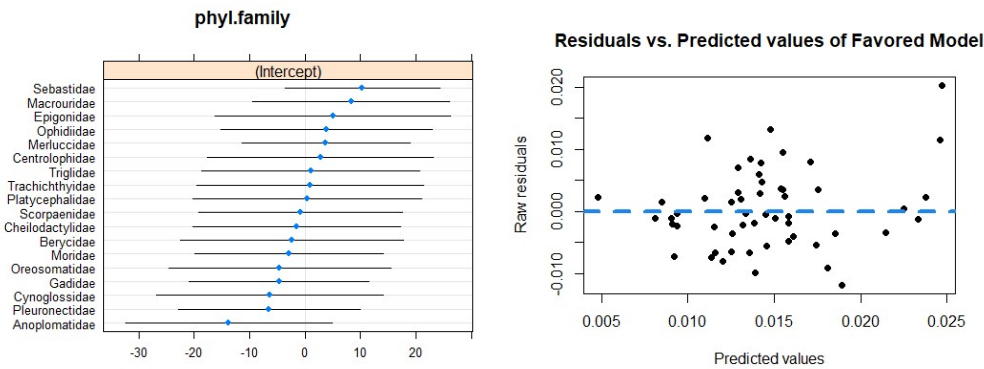
**Supp. Figure 5) Left)** Dotplot of random effect intercepts for each phylogenetic family produced by GLMM analysis of K vs. prematurity predictors. Blue dots represent the random effect intercept for each family, and the bars represent confidence intervals for each intercept. **Right)** Residuals of best model returned by GLMM analysis, plotted against the model's fitted values.

**Supp. Table 3)** Results of dredge analysis of K vs. pre-maturity predictors when phylogenetic family is **not** included as a random effect. Global model call: `glm(formula = K ~ scale(min depth) + scale(Lutz POC flux to max depth) + scale(O2) + locomotory mode, data = meta.sub, family = Gamma, na.action = "na.fail")`. Predictors removed: NPP.

Model	(Int)	Loc. mode	Min. Depth	Lutz POC flux	Temp	R <sup>2</sup>	AICc	Δ	weight
<b>1</b>	<b>8.24</b>	<b>+</b>	<b>3.511</b>		<b>-0.9149</b>	<b>0.4845</b>	<b>-129.3</b>	<b>0</b>	<b>0.364</b>
2	7.207		3.225		-0.8095	0.4588	-128.9	0.31	0.311
3	8.27	+	2.879	-0.4983	-1.168	0.495	-127.9	1.36	0.184
4	7.207		2.664	-0.4519	-1.041	0.4668	-127.4	1.89	0.141

**Supp. Table 4)** Results of dredge analysis of  $K_{GDY}$  vs. pre-maturity predictors with phylogenetic family as a random effect. Global model: Global model call: `glmer(formula =  $K_{GDY} \sim \text{scale}(\text{min depth}) + \text{scale}(\text{Lutz POC flux to mid depth}) + \text{scale}(\text{O}_2) + \text{locomotory mode} + (1 | \text{phyl.family})$ , data = meta.sub, family = Gamma, na.action = "na.fail")`. Predictors removed: NPP.

Model	(Int)	Loc. mode	Min. depth	Lutz POC flux	R <sup>2</sup>	AICc	Δ	weight
1	92.19	+	26.97		0.2732	-399.2	0	0.644
2	92.23	+	22.82	-5.888	0.2902	-398	1.19	0.356

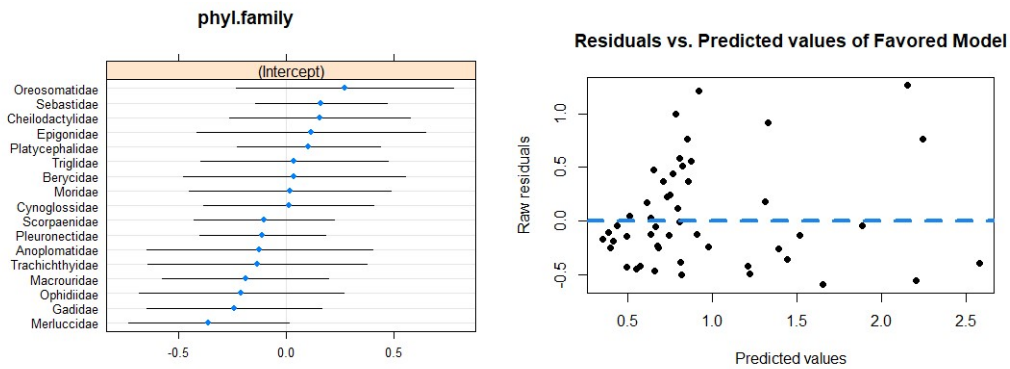


**Supp. Figure 6) Left)** Dotplot of random effect intercepts for each phylogenetic family produced by GLMM analysis of  $K_{GDY}$  vs. pre-maturity predictors. Blue dots represent the random effect intercept for each family, and the bars represent confidence intervals for each intercept. **Right)** Residuals of best model returned by GLMM analysis, plotted against the model's fitted values.

**Supp. Table 5)** Results of dredge analysis of AIM vs. pre-maturity predictors with phylogenetic family as a random effect when *C. armatus* is included. Global model call: `glmer(formula = AIM ~ scale(med. depth) + scale(Lutz POC flux to max depth) + scale(O2) + scale(temperature) + locomotory mode + (1 | phyl.family)`, data = meta.sub, family = Gamma, na.action = "na.fail"). Predictors removed: NPP.

Model	(Int)	Med. Depth	O <sub>2</sub>	Lutz POC flux	Temp.	R <sup>2</sup>	AICc	delta	weight
1	1.361		-0.3944	-0.3187	-0.3689	0.3799	81.2	0	0.367
2	1.337	0.5791	-0.2696		-0.1653	0.3687	82.1	0.87	0.237
3	1.377	0.3014	-0.3561	-0.2198	-0.2738	0.4012	82.2	1.02	0.22
4	1.292	0.7638	-0.2156			0.3261	82.7	1.47	0.176





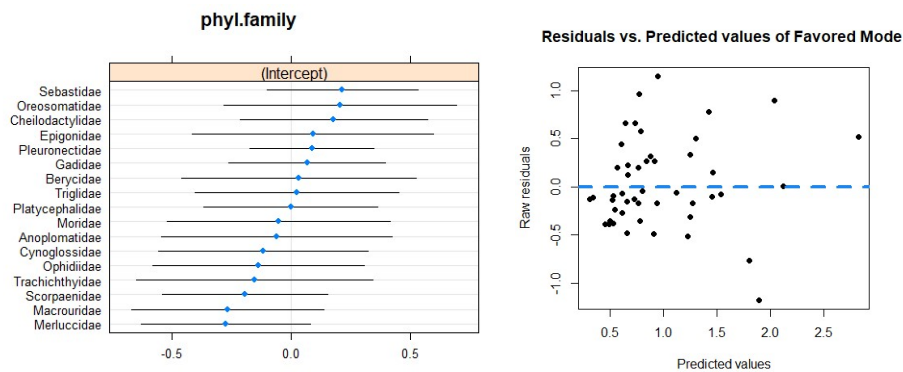
**Supp. Figure 7)** Random effects intercept and residuals for GLMM analysis of AIM vs. prematurity predictors when *C. armatus* is **included**. **Left)** Dotplot of random effect intercepts for each phylogenetic family produced by GLMM analysis of AIM vs. prematurity predictors. Blue dots represent the random effect intercept for each family, and the bars represent confidence intervals for each intercept. **Right)** Residuals of best model returned by GLMM analysis, plotted against the model's fitted values.

**Supp. Table 6)** Results of dredge analysis of AIM vs. pre-maturity predictors **without phylogenetic family as a random effect** when *C. armatus* is **included**. Global model call: `glm(formula = AIM ~ scale(med. depth) + scale(Lutz POC flux to max depth) + scale(O2) + scale(temperature) + locomotory mode, data = meta.sub, family = Gamma, na.action = "na.fail")`. Predictors removed: NPP.

Model	(Int)	Med. Depth	O <sub>2</sub>	Lutz POC flux	Temp.	R <sup>2</sup>	AICc	Δ	weight
1	1.249	0.5516	-0.2339		-0.1316	0.3821	78.4	0	0.338
2	1.219		-0.3446	-0.2599	-0.3041	0.379	78.7	0.24	0.299
3	1.248	0.3136	-0.294	-0.1532	-0.2146	0.4011	79.5	1.07	0.197
4	1.24	0.7233	-0.1784			0.3308	79.8	1.42	0.166

**Supp. Table 7)** Results of dredge analysis of AIM vs. pre-maturity predictors **with phylogenetic family as a random effect** when *C. armatus* is **excluded**. Global model call: `glmer(formula = AIM ~ scale(med. depth) + scale(Lutz POC flux to max depth) + scale(O2) + scale(temperature) + locomotory mode + (1 | phyl.family), data = meta.sub, family = Gamma, na.action = "na.fail")`. Predictors removed: NPP.

Model	(Int)	Med. Depth	O <sub>2</sub>	Temp.	R <sup>2</sup>	AICc	Δ	weight
1	1.307	0.5934	-0.2306		0.3741	76.3	0	0.603
2	1.373	0.5093	-0.2779	-0.1431	0.3975	77.2	0.84	0.397



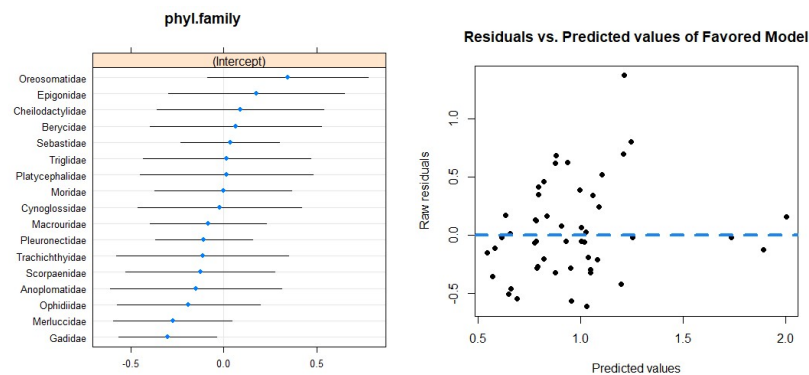
**Supp. Figure 8)** Random effects intercept and residuals for GLMM analysis of AIM vs. prematurity predictors when *C. armatus* is excluded. **Left)** Dotplot of random effect intercepts for each phylogenetic family produced by GLMM analysis of AIM vs. prematurity predictors. Blue dots represent the random effect intercept for each family, and the bars represent confidence intervals for each intercept. **Right)** Residuals of best model returned by GLMM analysis, plotted against the model's fitted values.

**Supp. Table 8)** Results of dredge analysis of AIM vs. pre-maturity predictors **without phylogenetic family as a random effect** when *C. armatus* is excluded. Global model call: `glm(formula = AIM ~ scale(med. depth) + scale(Lutz POC flux to max depth) + scale(O2) + scale(temperature) + locomotory mode, data = meta.sub, family = Gamma, na.action = "na.fail")`. Predictors removed: NPP.

Model	(Int)	Loc. mode	Med. Depth	O <sub>2</sub>	Temp.	R <sup>2</sup>	AICc	Δ	weight
1	1.227		0.517	-0.1682		0.3672	74.3	0	0.263
2	1.236		0.4258	-0.214	-0.1009	0.3993	74.4	0.07	0.255
3	1.208		0.5295			0.3216	75.2	0.88	0.17
4	1.208		0.4501		-0.08454	0.3428	76.1	1.78	0.108
5	1.355	+	0.4491	-0.2146	-0.1124	0.4104	76.2	1.83	0.105
6	1.324	+	0.5423	-0.1683		0.3747	76.3	1.95	0.099

**Supp. Table 9)** Results of dredge analysis of AIM<sub>GDY</sub> vs. pre-maturity predictors **with phylogenetic family as a random effect** when ***C. armatus* is included**. Global model call: glmer(formula = AIM ~ scale(med. depth) + scale(Lutz POC flux to max depth) + scale(O<sub>2</sub>) + locomotory mode + (1 | phyl.family), data = meta.sub, family = Gamma, na.action = "na.fail"). Predictors removed: NPP.

Model	(Int)	Loc. Mode	O2	Lutz POC flux	R <sup>2</sup>	AICc	Δ	weight
1	1.176		-0.2506	-0.1428	0.217	73.3	0	0.401
2	1.204		-0.2006		0.176	73.3	0.02	0.398
3	1.343	+	-0.2493	-0.1635	0.2362	74.7	1.39	0.201



**Supp. Figure 9)** Random effects intercept and residuals for GLMM analysis of AIM<sub>GDY</sub> vs. prematurity predictors when ***C. armatus* is included**. **Left)** Dotplot of random effect intercepts for each phylogenetic family produced by GLMM analysis of AIM vs. prematurity predictors. Blue dots represent the random effect intercept for each family, and the bars represent confidence intervals for each intercept. **Right)** Residuals of best model returned by GLMM analysis, plotted against the model's fitted values.

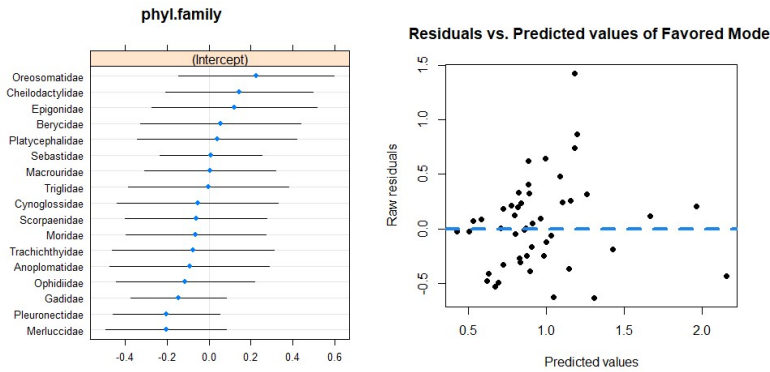
**Supp. Table 10)** Results of dredge analysis of AIM<sub>GDY</sub> vs. pre-maturity predictors **without phylogenetic family as a random effect** when ***C. armatus* is included**. Global model call: glm(formula = AIM ~ scale(med. depth) + scale(Lutz POC flux to max depth) + scale(O<sub>2</sub>) + locomotory mode, data = meta.sub, family = Gamma, na.action = "na.fail"). Predictors removed: NPP.

Model	(Int)	Loc. Mode	O2	POC flux	R <sup>2</sup>	AICc	Δ	weight
1	1.069		-0.2761	-0.1611	0.2032	71.7	0	0.505
2	1.227	+	-0.282	-0.19	0.2254	72.8	1.1	0.292
3	1.047		-0.2333		0.1321	73.5	1.81	0.204

**Supp. Table 11)** Results of dredge analysis of AIM<sub>GDY</sub> vs. pre-maturity predictors **with phylogenetic family as a random effect** when ***C. armatus* is excluded**. Global model call: glmer(formula = AIM ~ scale(med. depth) + scale(Lutz POC flux to max depth) +

scale(O<sub>2</sub>) + locomotory mode + (1 | phyl.family), data = meta.sub, family = Gamma, na.action = "na.fail"). Predictors removed: NPP.

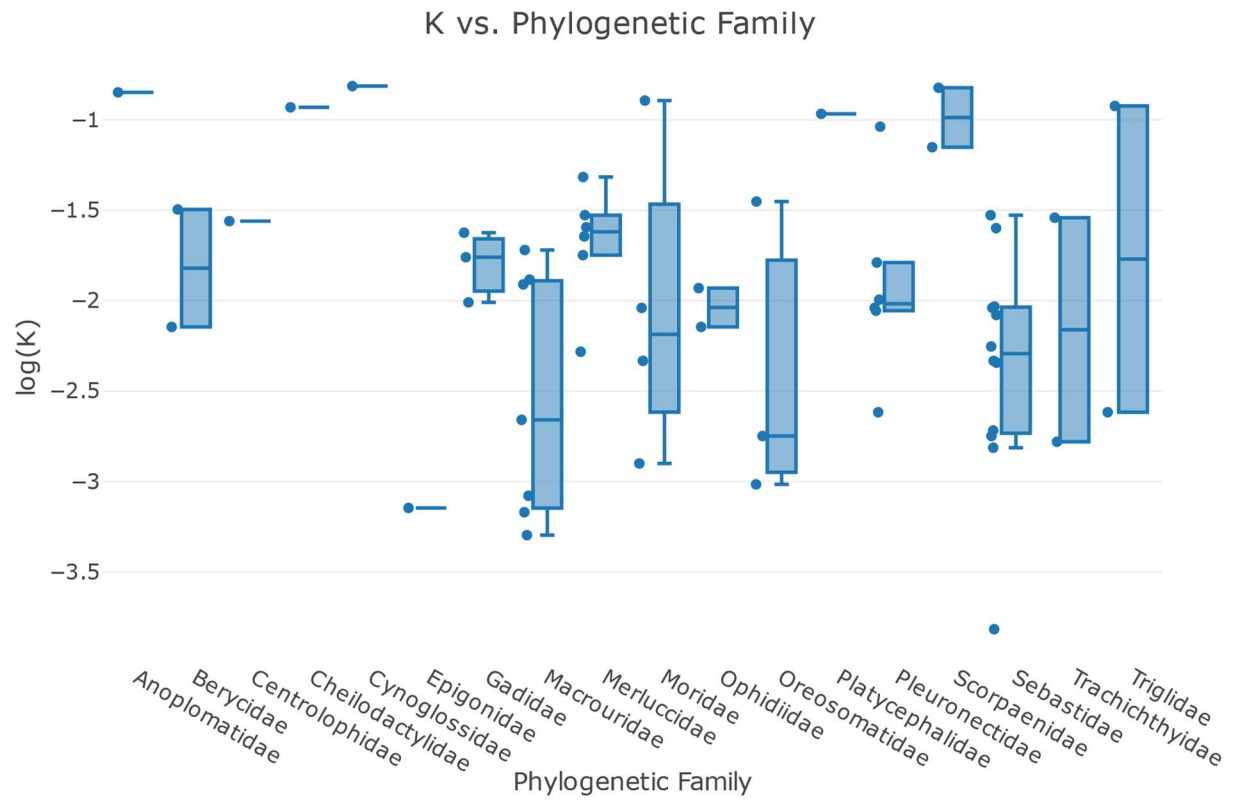
Model	(Int)	Loc. Mode	Med. Depth	O <sub>2</sub>	Lutz POC flux	R <sup>2</sup>	AICc	Δ	weight
1	1.439	+	0.2573	-0.2168		0.283	70.4	0	0.329
2	1.184		0.1922	-0.2157		0.2409	70.4	0.04	0.322
3	1.174			-0.2442	-0.1478	0.222	71.6	1.2	0.18
4	1.213			-0.1892		0.1769	71.7	1.34	0.168



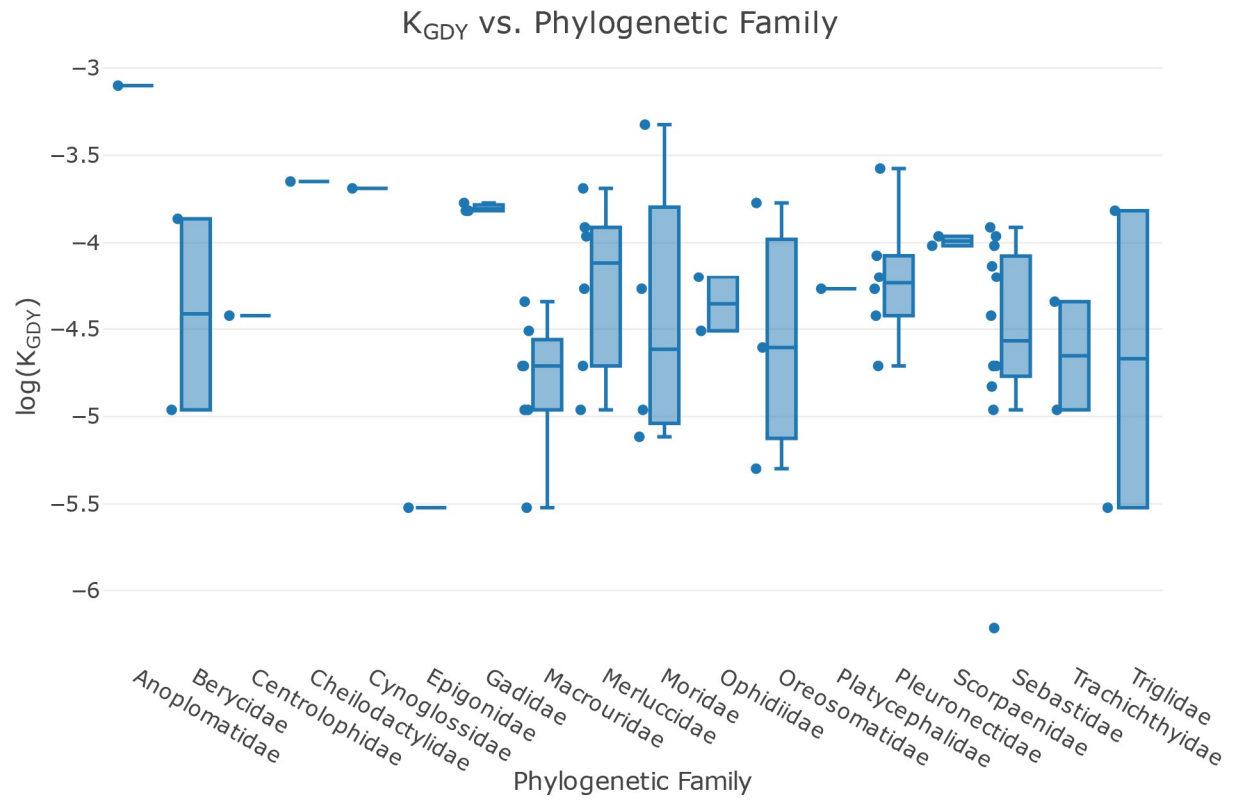
**Supp. Figure 10)** Random effects intercept and residuals for GLMM analysis of AIM<sub>GDY</sub> vs. prematurity predictors when *C. armatus* is **excluded**. **Left)** Dotplot of random effect intercepts for each phylogenetic family produced by GLMM analysis of AIM vs. prematurity predictors. Blue dots represent the random effect intercept for each family, and the bars represent confidence intervals for each intercept. **Right)** Residuals of best model returned by GLMM analysis, plotted against the model's fitted values.

**Supp. Table 12)** Results of dredge analysis of AIM<sub>GDY</sub> vs. pre-maturity predictors **without phylogenetic family as a random effect** when *C. armatus* is **excluded**. Global model call: glm(formula = AIM ~ scale(med. depth) + scale(Lutz POC flux to max depth) + scale(O<sub>2</sub>) + locomotory mode, data = meta.sub, family = Gamma, na.action = "na.fail"). Predictors removed: NPP.

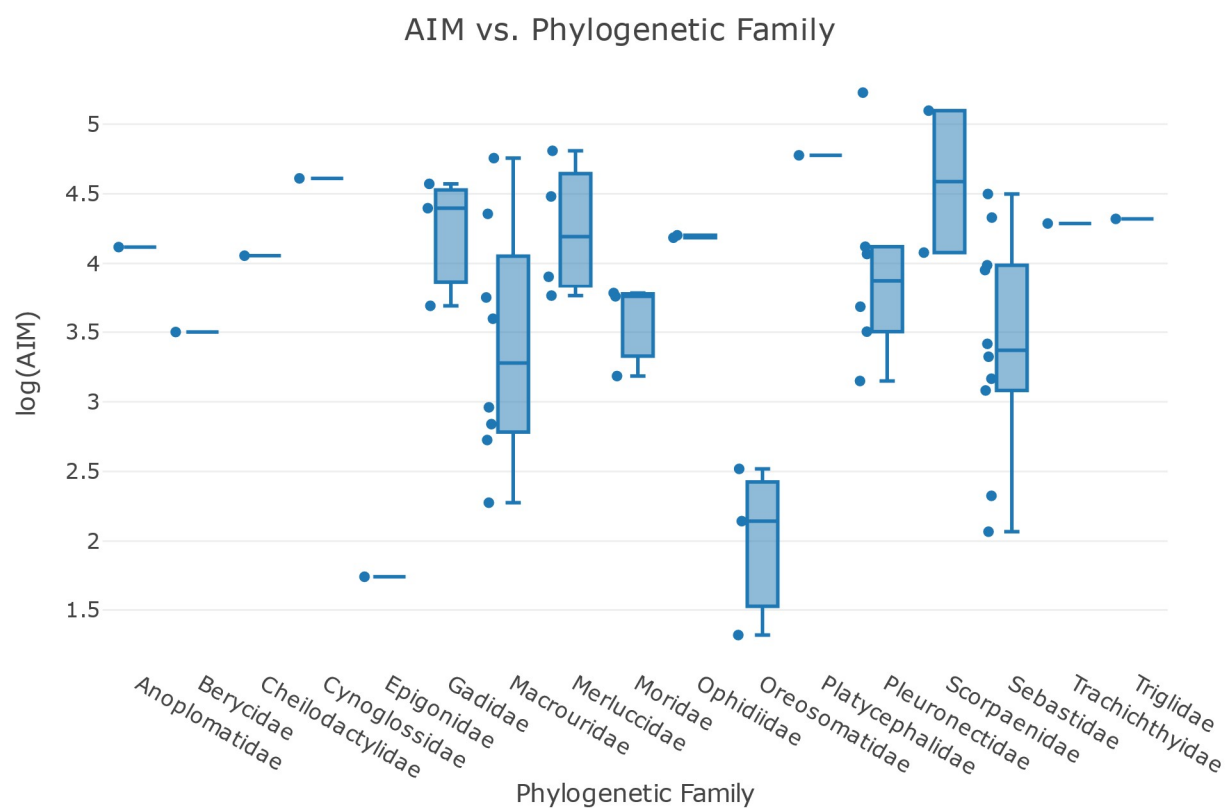
Model	(Int)	Loc. Mode	Med. Depth	O <sub>2</sub>	R <sup>2</sup>	AICc	Δ	weight
1	1.32	+	0.2825	-0.2332	0.2926	67.1	0	0.563
2	1.088		0.2228	-0.2372	0.2458	67.6	0.5	0.437



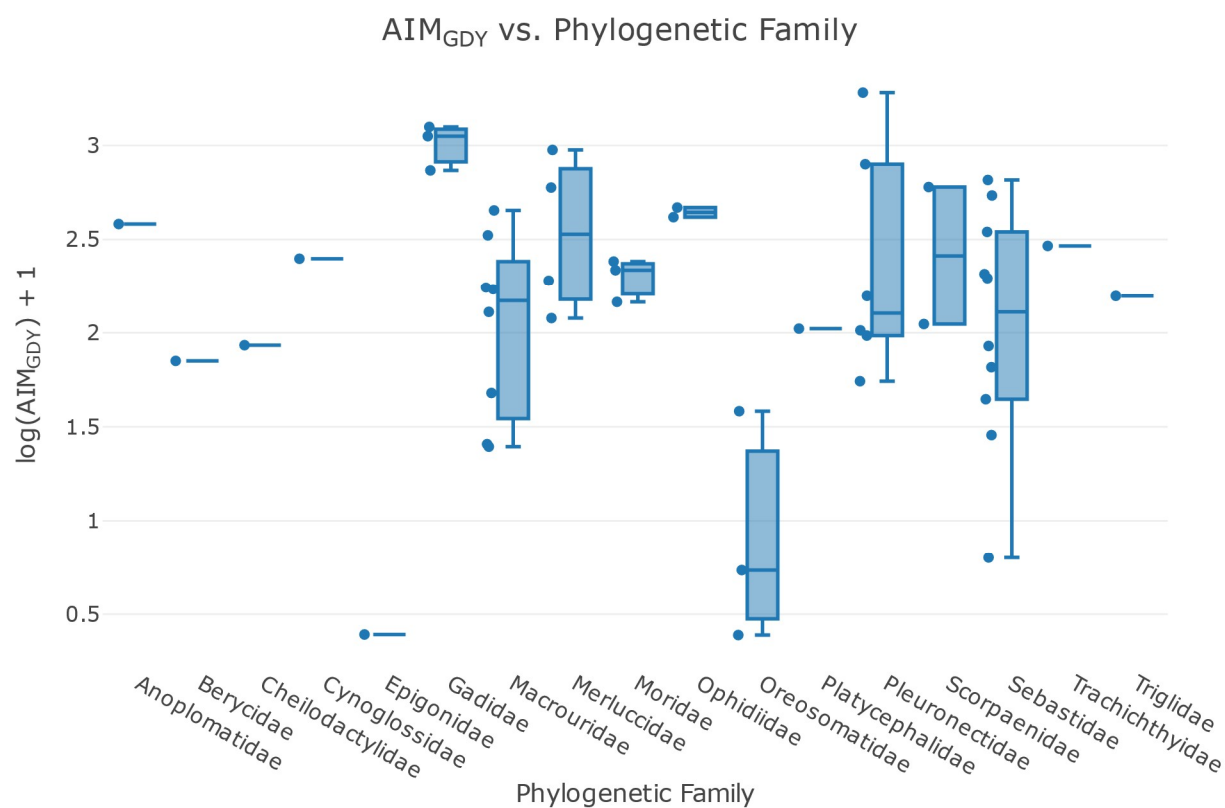
**Supp. Figure 11)** Boxplots of log transformed K across phylogenetic family. Middle bars of each box represent the median, and box upper and lower bounds represent Q1 and Q3. Whiskers represent min and max values for each family.



**Supp. Figure 12)** Boxplots of log transformed K<sub>GDY</sub> across phylogenetic family. Middle bars of each box represent the median, and box upper and lower bounds represent Q1 and Q3. Whiskers represent min and max values for each family.

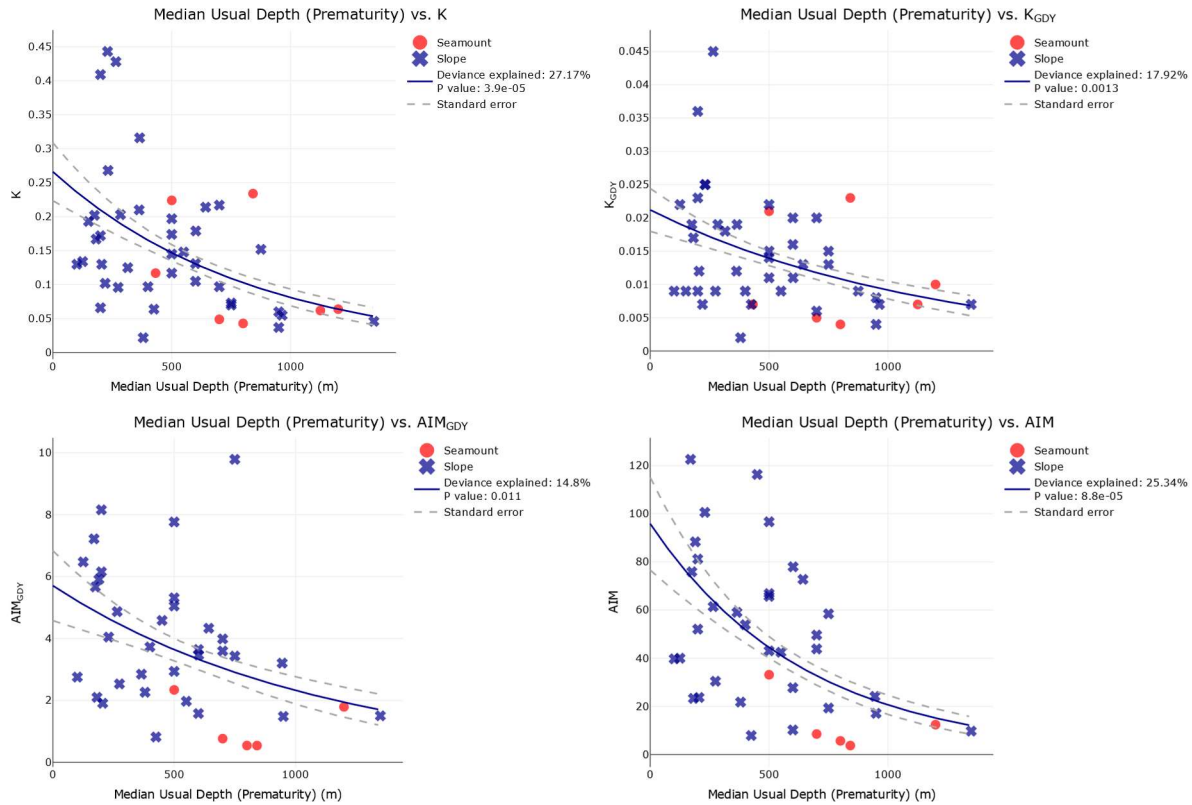


**Supp. Figure 13)** Boxplots of log transformed AIM across phylogenetic family. Middle bars of each box represent the median, and box upper and lower bounds represent Q1 and Q3. Whiskers represent min and max values for each family.



**Supp. Figure 14)** Boxplots of log transformed AIM<sub>GDY</sub> across phylogenetic family. Middle bars of each box represent the median, and box upper and lower bounds represent Q1 and Q3. Whiskers represent min and max values for each family. 1 was added to all values of log(AIM<sub>GDY</sub>) to shift values above 0.





**Supplementary Figure 15:** Pairwise regressions of growth rates vs. median of species' depth range for fishes that inhabit continental slopes and seamounts. For ontogenetic migrators, the average pre-maturity depth is used. The blue lines show best-fit regression, and grey bands show the standard error. **Top row:** regressions of  $K$  (left) and  $K_{GDY}$  (right) against median usual depth range during pre-maturity, colored by whether species primarily inhabit continental slopes or seamounts. **Bottom row:** regressions of  $AIM$  (left) and  $AIM_{GDY}$  (right) against median usual depth range during pre-maturity, colored by whether species primarily inhabit continental slopes or seamounts.