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Supplementary Materials for

Respiratory capacity is twice as important as temperature in explaining patterns of metabolic rate across the vertebrate tree of life

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Supplementary Results

Is respiratory organ (i.e., lungs versus gills) a better characterization of the known difference in metabolic rate and respiratory surface area between endotherms and ectotherms?

The intercept—the metabolic rate for a given body size—did not differ significantly between organisms with lungs versus gills for all models explaining variation in metabolic rate without the inclusion of respiratory surface area (compare the overlapping 95% Bayesian Credible Intervals [BCIs] for the intercept for organisms with lungs versus gills in models "MR2_LG", "MR3_LG" in Table S6). Similarly, the body mass-scaling exponent did not differ between organisms with lungs versus gills when the body mass-scaling exponent was allowed to vary between these two groups (compare the overlapping 95% BCIs for the "mass" effect size for organisms with lungs versus gills in model "MR3_LG" in Table S6). For all models explaining variation in metabolic rate with the inclusion of respiratory surface area, neither the intercept, nor the body mass-scaling exponents (if allowed to vary, model C6_LG) differed between organisms with lungs and those with gills (models "C3_LG", "C4_LG", "C5_LG", and "C6_LG" in Table S6). Thus, the metabolic rate for a given body size and the body mass-scaling of metabolic rate did not differ between lunged- and gilled-organisms, regardless of the inclusion of respiratory surface area as a covariate (Table S6).

For the models assessing the scaling of respiratory surface area and body size—only the intercept, or respiratory surface area for a given size—was significantly different between species with lungs versus species with gills (models "RSA2_LG", "RSA3_LG" in Table S6). When the body mass-scaling exponent was allowed to vary between organisms with lungs versus gills, the difference was not significant, suggesting that the body mass-scaling of respiratory surface area does not differ between lunged- and gilled-organisms (model "RSA3_LG" in Table S6).

Supplementary Methods

Model Overview

We constructed and compared phylogenetic Bayesian multilevel linear regression models in R v.3.5.1 and v.4.0.1 in Stan using the package *rstan* (*40, 41*).

Model Parameterization

i. Metabolic Rate Models ("MR" models in Table S1)

We fitted three candidate models to examine the effects of mean body mass, mean (inverse) temperature, and thermoregulatory strategy on whole-organism metabolic rate (MR_i) (see Table S1).

General model parameterization:

$MR_i = \alpha + \Sigma_j \beta_j x_{i,j} + \varepsilon_i$

$\hat{\varepsilon} \sim$ multivariate normal $(\hat{0}, \sigma_e^2 * C_{phylo})$
$C_{phylo} = \lambda * V + (1 - \lambda) * I$
$\alpha \sim$ student-t (3, 0, 10)
$\beta_j \sim$ student-t (3, 0, 10)

σ_e^2 ~ half-Cauchy (0, 10)

Here, MR_i is the response variable (mean whole-organism metabolic rate), α is the intercept, and β_j is the slope of the *jth* predictor, and $x_{i,j}$ is species *i*'s trait value for the *j*th trait (see below for predictors in each model). The priors on the intercept, α, slope, β_j, and error, σ_e^2, are also reported (see above) and our choice of priors is explained below.

Following (*48*), we assumed the residual error, ε_i, to be distributed according to a multivariate normal distribution, where $\hat{0}$ is a vector with length N, σ_e^2 is the variation in responses to the predictors ($\beta_j x_{i,j}$), and C_{phylo} is the $N \times N$ correlation matrix resulting from the phylogeny. The strength of the phylogenetic signal, λ, in the residuals under a model of evolution of Brownian motion is estimated according to $C_{phylo} = \lambda * V + (1 - \lambda) * I$, where V is the variance covariance matrix from the phylogeny, and I is an identify matrix of $N \times N$ values with σ_e^2 on the diagonal.

Model 1: $\beta_{mass} * x_{mass} + \beta_{temp} * x_{temp}$

Model 2: $\beta_{mass} * x_{mass} + \beta_{temp} * x_{temp} + \beta_{therm} * x_{therm}$

Model 3: $\beta_{mass} * x_{mass} + \beta_{temp} * x_{temp} + \beta_{therm} * x_{therm} + \beta_{mass\_therm} * x_{therm} * x_{tmass}$,

where *mass* is the mean body mass associated with metabolic rate, *temp* is the mean inverse temperature associated with metabolic rate (for ectotherms, this is the temperature at which metabolic rate was experimentally measured and for endotherms, this is body temperature), and *therm* is thermoregulatory strategy. Following (*2*), temperature is parameterized as the Boltzmann factor (1/Boltzmann constant * temperature in Kelvin) and thus, β_{temp} is the activation energy.

ii. Respiratory Surface Models ("RSA" models in Table S1)

We fitted three candidate models to examine the effects of mean body mass and thermoregulatory strategy on whole-organism respiratory surface area (RSA_i) (see Table S1).

General model parameterization:

$$RSA_i = \alpha + \Sigma_j \beta_j x_{i,j} + \varepsilon_i$$

$\hat{\varepsilon}$ ~ multivariate normal ($\hat{0}, \sigma_e^2 * C_{phylo}$)
$C_{phylo} = \lambda * V + (1 - \lambda) * I$
α ~ student-t (3, 0, 10)
β_j ~ student-t (3, 0, 10)
σ_e^2 ~ half-Cauchy (0, 10)

Here, RSA_i is the response variable (mean whole-organism respiratory surface area), α is the intercept, and β_j is the slope of the *jth* predictor, and $x_{i,j}$ is species *i*'s trait value for the *j*th trait (see below for predictors in each model). The priors on the intercept, α, slope, β_j, and error, σ_e^2, are also reported and our choice of priors is explained below.

The parameterization of the phylogenetic components is the same as above for the Metabolic Rate models.

Model 1: $\beta_{mass} * x_{mass}$

Model 2: $\beta_{mass} * x_{mass} + \beta_{therm} * x_{therm}$

Model 3: $\beta_{mass} * x_{mass} + \beta_{therm} * x_{therm} + \beta_{mass\_therm} * x_{therm} * x_{mass}$,

where *mass* is the mean body mass associated with respiratory surface area and *therm* is as defined above. For the models with respiratory organ, "*organ*" replaced "*therm*" and was designated as either lung or gill.

iii. Combined Models ("C" models in Table S1)

We fitted six candidate models to examine the effects of mean body mass, mean temperature, residual respiratory surface area, and thermoregulatory strategy on whole-organism metabolic rate (MR_i) (see Table S1). The first level of the model regressed mean whole-organism respiratory surface (RSA_i) against mean body mass associated with respiratory surface area. The residuals from this model indicate whether a species had a higher respiratory surface area (positive residual) or lower respiratory surface area (negative residual) than would be expected based on its body mass. The second level modeled metabolic rate as a function of different combinations of covariates (body mass associated with metabolic rate, temperature, thermoregulatory strategy, as well as respiratory surface area, see Table S1). The entire posterior distribution of residual respiratory surface area estimated in the first level of the model was included as the respiratory surface area covariate in the second level of the model. Importantly, each iteration of both models happens in succession so estimates and uncertainty of residual respiratory surface area are propagated across levels of the model.

General model parameterization:

First level of the model:

$RSA_i = \alpha + \Sigma_j \beta_j x_{i,j} + \varepsilon_\mathrm{i}$

$\hat{\varepsilon} \sim$ multivariate normal $(\hat{0}, \sigma_e^2 * C_{phylo})$
$C_{phylo} = \lambda * \mathrm{V} + (1 - \lambda) * \mathrm{I}$
$\alpha \sim$ student-t (3, 0, 10)
$\beta_{mass} \sim$ student-t (3, 0, 10)
$\sigma_e^2 \sim$ half-Cauchy (0, 10)

Here, RSA_i is the response variable (mean whole-organism respiratory surface area), α is the intercept, and β_{mass} is the slope of the body mass associated with respiratory surface area, x_{mass}. The priors on the intercept, α, slope, β_{mass}, and error, σ_e^2, are also reported and our choice of priors is explained below.

Second level of the model:

$MR_i = \alpha + \Sigma_j \beta_j x_{i,j} + \varepsilon_\mathrm{i}$

$\hat{\varepsilon} \sim$ multivariate normal $(\hat{0}, \sigma_e^2 * C_{phylo})$
$C_{phylo} = \lambda * \mathrm{V} + (1 - \lambda) * \mathrm{I}$
$\alpha \sim$ student-t (3, 0, 10)
$\beta_j \sim$ student-t (3, 0, 10)
$\sigma_e^2 \sim$ half-Cauchy (0, 10)

Here, MR_i is the response variable (mean whole-organism metabolic rate), α is the intercept, and β_j is the slope of the *jth* predictor, and $x_{i,j}$ is species *i*'s trait value for the *j*th trait (see below for predictors in each model). The priors on the intercept, α, slope, β_j, and error, σ_e^2, are also reported and our choice of priors is explained below.

The parameterization of the variance and phylogeny is the same as above in the "Metabolic Rate Models" and "Respiratory Surface Area Models".

Model 1: $\beta_{Rrsa} * x_{Rrsa} + \beta_{mass} * x_{mass} + \beta_{temp} * x_{temp}$

Model 2: $\beta_{Rrsa} * x_{Rrsa} + \beta_{mass} * x_{mass} + \beta_{mass\_Rrsa} * x_{mass} * x_{Rrsa} + \beta_{temp} * x_{temp}$

Model 3: $\beta_{Rrsa} * x_{Rrsa} + \beta_{mass} * x_{mass} + \beta_{temp} * x_{temp} + \beta_{therm} * x_{therm}$

Model 4: $\beta_{Rrsa} * x_{Rrsa} + \beta_{mass} * x_{mass} + \beta_{mass\_Rrsa} * x_{mass} * x_{Rrsa} + \beta_{temp} * x_{temp} + \beta_{therm} * x_{therm}$

Model 5: $\beta_{Rrsa} * x_{Rrsa} + \beta_{mass} * x_{mass} + \beta_{therm} * x_{therm} + \beta_{mass\_\_therm} * x_{mass} * x_{therm} + \beta_{temp} * x_{temp}$

Model 6: $\beta_{Rrsa} * x_{Rrsa} + \beta_{mass} * x_{mass} + \beta_{therm} * x_{therm} + \beta_{mass\_\_therm} * x_{mass} * x_{therm} +$
$\beta_{mass\_Rrsa} * x_{mass} * x_{Rrsa} + \beta_{temp} * x_{temp}$

Choice of Priors

We used weakly informative regularizing priors based on recommendations for Stan (https://github.com/stan-dev/stan/wiki/Prior-Choice-Recommendations). As λ (phylogenetic signal) has an equal chance of taking any value within the bounds of zero to one, we used a prior with a uniform distribution from zero to one. As σ_e^2 (variation in responses to the predictors ($\beta_j x_{i,j}$) can only be positive, we used a half-Cauchy prior with a location of zero and a scale of ten. Priors are also shown below for each set of models.

Supplementary Tables

Table S1: Comparison of all models using Pareto-smoothing importance sampling leave-one-out cross validation (PSIS-LOO) using the *loo* package in R v.5.3.1 and v.4.0.1. Values reported are for the first model run and include the LOO information criterion value (similar to Akaike Information Criterion [AIC]) *looic*, the effective number of parameters (p_{loo}), the expected log predictive density ($elpd_{loo}$), the standard error of the expected log predictive density (se_{elpd_loo}), the difference in the expected log predictive density ($elpd_{diff}$) for a given model compared to the best model, and the Bayesian stacking weight (similar to Akaike weight). The model with the lowest $elpd_{loo}$ has the most support and is emboldened and highlighted in grey for each group. Any model with $elpd_{diff}$ < 2 is also highlighted in grey.

	model	**looic**	**p_{loo}**	**$elpd_{loo}$**	**se_{elpd_loo}**	**$elpd_{diff}$**	**weight**
	Metabolic rate:						
MR1	MR ~ $mass_{MR}$ + temperature	299.5	11.6	-149.7	5.9	-9.8	0.230
MR2	MR ~ $mass_{MR}$ + temperature + thermoregulatory strategy	285.9	8.4	-142.9	13.1	-3.0	0
MR3	**MR ~ $mass_{MR}$ * thermoregulatory strategy + temperature**	**279.9**	**9.9**	**-140.0**	**13.9**	**0.0**	**0.770**
	Respiratory surface area:						
RSA1	RSA ~ $mass_{RSA}$	346.4	3.0	-173.2	5.6	-46.3	0
RSA2	**RSA ~ $mass_{RSA}$ + thermoregulatory strategy**	**253.8**	**3.2**	**-126.8**	**7.3**	**0.0**	**1.00**
RSA3	RSA ~ $mass_{RSA}$ * thermoregulatory strategy	255.7	4.0	-127.8	7.2	-0.9	0
	Combined:						
C1	MR ~ residual RSA + $mass_{MR}$ + temperature	277.9	10.6	-139.0	13.5	-7.2	0
C2	MR ~ residual RSA * $mass_{MR}$ + temperature	278.6	12.6	-139.3	12.6	-7.6	0.071
C3	MR ~ residual RSA + $mass_{MR}$ + temperature + thermoregulatory strategy	271.6	11.2	-135.8	13.9	-4.1	0.118
C4	MR ~ residual RSA * $mass_{MR}$ + temperature + thermoregulatory strategy	270.0	12.2	-135.0	14.1	-3.3	0
C5	**MR ~ residual RSA + $mass_{MR}$ * thermoregulatory strategy + temperature**	**263.4**	**11.7**	**-131.7**	**14.6**	**0.0**	**0.811**
C6	MR ~ residual RSA * $mass_{MR}$ * thermoregulatory strategy + temperature	267.5	13.5	-133.7	14.8	-2.0	0

Table S2: Coefficient means and 95% Bayesian Credible Intervals (BCI, in parentheses) for all models examined. Model names correspond to those in Table S1. Intercepts are back transformed from the natural log scale. Pagel's λ indicates the strength of the phylogenetic signal in the residuals of the response variable. The models with the most support from each group are highlighted in grey (see Table S1). The coefficient means reported here are from the first model run.

model		intercept	mass	temp	residual RSA	mass: residual RSA	sigma	Pagel's λ
MR1		0.18 (0.10 to 0.38)	0.89 (0.82 to 0.96)	-1.60 (-2.00 to -1.17)	NA	NA	1.37 (0.90 to 2.24)	0.33 (0.03 to 0.72)
MR2	*ectotherm*	0.12 (0.07 to 0.21)	0.84 (0.77 to 0.90)	-0.53 (-1.00 to -0.06)	NA	NA	0.95 (0.65 to 1.50)	0.29 (0.02 to 0.68)
	endotherm	0.81 (0.28 to 2.61)						
MR3	*ectotherm*	0.13 (0.07 to 0.22)	0.93 (0.84 to 1.02)	-0.59 (-1.05 to -0.14)	NA	NA	0.89 (0.59 to 1.43)	0.31 (0.02 to 0.70)
	endotherm	0.95 (0.32 to 3.01)	0.74 (0.53 to 0.95)					
RSA1		1597.59 (787.52 to 3201.40)	1.05 (0.97 to 1.13)	NA	NA	NA	1.74 (1.18 to 2.86)	0.26 (0.01 to 0.70)
RSA2	*ectotherm*	1002.16 (679.33 to 1524.50)	0.92 (0.87 to 0.98)	NA	NA	NA	0.70 (0.49 to 1.09)	0.22 (0.01 to 0.63)
	endotherm	9407.04 (4428.47 to 20574.87)						
RSA3	*ectotherm*	1005.28 (673.15 to 1611.09)	0.93 (0.86 to 1.00)	NA	NA	NA	0.71 (0.49 to 1.11)	0.23 (0.01 to 0.62)
	endotherm	9615.49 (4404.45 to 22723.31)	0.91 (0.74 to 1.10)					
C1		0.18 (0.10 to 0.32)	0.93 (0.86 to 1.00)	-0.75 (-1.14 to -0.34)	0.63 (0.47 to 0.79)	NA	0.77 (0.55 to 1.19)	0.21 (0.01 to 0.58)
C2		0.18 (0.10 to 0.32)	0.96 (0.88 to 1.04)	-0.81 (-1.21 to -0.40)	0.60 (0.44 to 0.76)	0.05 (-0.10 to 0.01)	0.75 (0.53 to 1.13)	0.21 (0.01 to 0.57)
C3	*ectotherm*	0.14 (0.08 to 0.26)	0.90 (0.83 to 0.97)	-0.45 (-0.90 to 0.00)	0.46 (0.27 to 0.66)	NA	0.75 (0.53 to 1.17)	0.25 (0.01 to 0.63)
	endotherm	0.37 (0.11 to 1.31)						
C4	*ectotherm*	0.14 (0.09 to 0.26)	0.92 (0.84 to 1.00)	-0.51 (-0.94 to -0.06)	0.42 (0.22 to 0.61)	-0.05 (-0.10 to 0.00)	0.73 (0.51 to 1.12)	0.25 (0.01 to 0.62)
	endotherm	0.37 (0.12 to 1.33)						
C5	*ectotherm*	0.15 (0.09 to 0.26)	0.96 (0.88 to 1.04)	-0.51 (-0.92 to -0.07)	0.45 (0.26 to 0.64)	NA	0.69 (0.48 to 1.07)	0.24 (0.01 to 0.62)
	endotherm	0.44 (0.14 to 1.52)	0.80 (0.60 to 1.01)					
C6	*ectotherm*	0.15 (0.09 to 0.28)	0.98 (0.89 to 1.08)	-0.50 (-0.91 to -0.08)	0.45 (0.27 to 0.66)	0.02 (-0.06 to 0.09)	0.70 (0.48 to 1.08)	0.24 (0.02 to 0.61)
	endotherm	0.45 (0.14 to 1.57)	0.77 (0.49 to 1.05)					

Table S3: Comparison of the best models with and without respiratory surface area that explained variation in metabolic rate across 109 vertebrate species (i.e., "best metabolic rate model" and "best combined model"). Model names correspond to those in Table S1. Each model was run a total of four times to ensure the robustness of results. All model comparison was conducted using Pareto-smoothing importance sampling leave-one-out cross validation (PSIS-LOO) using the *loo* package in R v.5.3.1 and v.4.0.1. Values reported are the LOO information criterion value (similar to Akaike Information Criterion [AIC]) *looic,* the effective number of parameters (p_{loo}), the expected log predictive density ($elpd_{loo}$), the standard error of the expected log predictive density (se_{elpd_loo}), the difference in the expected log predictive density ($elpd_{diff}$) for a given model compared to the best model, the Bayesian stacking weight (similar to Akaike weight), and the evidence ratio (weight of evidence of the best model divided by the weight of evidence of the other model(s) of interest).

model	**model run**	**looic**	$\mathbf{p_{loo}}$	$\mathbf{elpd_{loo}}$	$\mathbf{se_{elpd\_loo}}$	$\mathbf{elpd_{diff}}$	**weight**	**evidence ratio**
MR3	1	279.9	9.9	-140.0	13.9	-8.2	0.043	22.3
C5		263.4	11.7	-131.7	14.6	0	0.957	
MR3	2	279.6	9.6	-139.8	13.8	-8.0	0.054	17.5
C5		263.6	11.8	-131.8	14.7	0	0.946	
MR3	3	279.6	9.7	-139.8	14	-7.8	0.044	21.7
C5		264	12	-132	14.9	0	0.956	
MR3	4	279.7	9.7	-139.8	13.9	-8.1	0.075	12.3
C5		263.4	11.7	-131.7	14.8	0	0.925	
							average	18.5

Table S4: Standardized coefficient means (i.e., effect sizes) and 95% Bayesian Credible Intervals (BCIs, in parentheses) for the top model that explains metabolic rate as a function of body mass, temperature, respiratory surface area, thermoregulatory strategy, and the interaction of body mass and thermoregulatory strategy, while accounting for evolutionary history. The model name corresponds to that in Table S1. Intercepts are back transformed from the natural log scale. Pagel's λ indicates the strength of the phylogenetic signal in the residuals of the response variable.

model		**intercept**	**mass**	**temp**	**residual RSA**	**sigma**	**Pagel's λ**
C5	*ectotherm*	0.15 (0.10 to 0.25)	2.66 (2.42 to 2.90)	-0.25 (-0.47 to -0.04)	0.52 (0.29 to 0.75)	0.69 (0.48 to 1.09)	0.24 (0.01 to 0.61)
	endotherm	0.44 (0.14 to 1.41)	2.17 (1.61-0. to 2.73)				

Table S5: Comparison of models using thermoregulatory strategy *or* respiratory organ to characterize the differences in metabolic rate and respiratory surface area between endotherms and ectotherms using Pareto-smoothing importance sampling leave-one-out cross validation (PSIS-LOO) with the *loo* package in R v.5.3.1 and v.4.0.1. Values reported are the LOO information criterion value (similar to Akaike Information Criterion [AIC]) *looic*, the effective number of parameters (p_{loo}), the expected log predictive density ($elpd_{loo}$), the standard error of the expected log predictive density (se_{elpd_loo}), and the difference in the expected log predictive density ($elpd_{diff}$) for a given model compared to the best model. The model with the lowest $elpd_{loo}$ of each group has the most support and is highlighted in grey.

	model	**looic**	$\mathbf{p_{loo}}$	$\mathbf{elpd_{loo}}$	$\mathbf{se_{elpd\_loo}}$	$\mathbf{elpd_{diff}}$
MR2	MR ~ mass_{MR} + temperature + thermoregulatory strategy	286.8	8.5	-143.3	13	0
MR2_LG	MR ~ mass_{MR} + temperature + respiratory organ	302.8	6.9	-151.4	11.7	-8.0
MR3	MR ~ mass_{MR} * thermoregulatory strategy + temperature	281.3	9.9	-140.7	13.9	0
MR3_LG	MR ~ mass_{MR} * respiratory organ + temperature	304.1	8.3	-152.1	12.0	-11.4
RSA2	RSA ~ mass_{RSA} + thermoregulatory strategy	253.7	3.2	-126.8	7.3	0
RSA2_LG	RSA ~ mass_{RSA} + respiratory organ	269.3	2.7	-134.7	5.8	-7.8
RSA3	RSA ~ mass_{RSA} * thermoregulatory strategy	255.6	4.0	-127.8	5.8	0
RSA3_LG	RSA ~ mass_{RSA} * respiratory organ	272.3	4.0	-136.2	5.8	-8.4
C3	MR ~ residual RSA + mass_{MR} + temperature + thermoregulatory strategy	271.6	11.2	-135.8	13.9	0
C3_LG	MR ~ residual RSA + mass_{MR} + temperature + respiratory organ	283.3	11.4	-141.6	13.6	-5.9
C4	MR ~ residual RSA * mass_{MR} + temperature + thermoregulatory strategy	270.0	12.2	-135.0	14.1	0
C4_LG	MR ~ residual RSA * mass_{MR} + temperature + respiratory organ	284.3	13.8	-142.2	14.4	-7.2
C5	MR ~ residual RSA + mass_{MR} * thermoregulatory strategy + temperature	263.4	11.7	-131.7	14.6	0
C5_LG	MR ~ residual RSA + mass_{MR} * respiratory organ + temperature	283.9	12.9	-142.0	13.9	-10.2
C6	MR ~ residual RSA * mass_{MR} * thermoregulatory strategy + temperature	267.5	11.7	-133.7	14.8	0
C6_LG	MR ~ residual RSA * mass_{MR} * respiratory organ + temperature	294.0	17.2	-147.0	14.7	-13.3

Table S6: **Coefficient means and 95% Bayesian Credible Intervals (BCIs, in parentheses) for all models that included respiratory organ (i.e., lungs or gills) in place of thermoregulatory strategy (i.e., ectotherm or endotherm)**. Model names correspond to Table S5. Intercepts are back transformed from the natural log scale. Pagel's λ indicates the strength of the phylogenetic signal in the residuals of the response.

model		**intercept**	**mass**	**temp**	**residual RSA**	**mass: residual RSA**	**sigma**	**Pagel's λ**
MR2_LG	*gills*	0.14 (0.07 to 0.27)	0.89 (0.82 to 0.97)	-1.23 (-1.71 to -0.75)	NA	NA	1.24 (0.84 to 2.00)	0.30 (0.02 to 0.68)
	lungs	0.26 (0.09 to 0.82)						
MR3_LG	*gills*	0.14 (0.08 to 0.29)	0.94 (0.82 to 1.07)	-1.31 (-1.81 to -0.80)	NA	NA	1.27 (0.85 to 2.05)	0.31 (0.02 to 0.70)
	lungs	0.26 (0.09 to 0.84)	0.86 (0.58 to 1.15)					
RSA2_LG	*gills*	820.00 (395.54 – 1671.05)	1.02 (0.96 to 1.07)	-0.59 (-1.05 to -0.14)	NA	NA	1.17 (0.75 to 1.85)	0.49 (0.11 to 0.77)
	lungs	4147.50 (1432.91 – 11917.25)						
RSA3_LG	*gills*	825.27 (403.64 – 1706.42)	1.02 (0.93 to 1.12)	NA	NA	NA	1.19 (0.76 to 1.89)	0.49 (0.10 to 0.78)
	lungs	4175.97 (1454.04 – 12183.13)	1.01 (0.79 to 1.23)					
C3_LG	*gills*	0.19 (0.10 to 0.38)	0.93 (0.86 to 1.00)	-0.80 (-1.20 to -0.39)	0.67 (0.48 to 0.86)	NA	0.79 (0.55 to 1.21)	0.23 (0.01 to 0.59)
	lungs	0.15 (0.05 to 1.48)						
C4_LG	*gills*	0.19 (0.10 to 0.37)	0.96 (0.88 to 1.05)	-0.86 (-1.27 to -0.44)	0.64 (0.45 to 0.83)	-0.05 (-0.10 to 0.01)	0.76 (0.54 to 1.17)	0.22 (0.01 to 0.58)
	lungs	0.16 (0.05 to 0.48)						
C5_LG	*gills*	0.19 (0.10 to 0.37)	0.95 (0.85 to 1.06)	-0.84 (-1.27 to -0.39)	0.66 (0.48 to 0.85)	NA	0.79 (0.55 to 1.20)	0.22 (0.01 to 0.59)
	lungs	0.15 (0.05 to 0.48)						
C6_LG	*gills*	0.18 (0.10 to 0.36)	0.92 (0.80 to 1.04)	-0.80 (-1.23 to -0.37)	0.63 (0.45 to 0.82)	-0.07 (-0.14 to 0.01)	0.77 (0.54 to 1.17)	0.22 (0.01 to 0.58)
	lungs	0.16 (0.05 to 0.49)	1.00 (0.70 to 1.29)					

Table S7: Model comparison for the three additional runs per model. Model names correspond to those in Table S1. All model comparison was conducted using Pareto-smoothing importance sampling leave-one-out cross validation (PSIS-LOO) using the *loo* package in R v.5.3.1 and v.4.0.1. Values reported are the LOO information criterion value (similar to Akaike Information Criterion [AIC]) *looic*, the effective number of parameters (p_{loo}), the expected log predictive density ($elpd_{loo}$), the standard error of the expected log predictive density (se_{elpd_loo}), the difference in the expected log predictive density ($elpd_{diff}$) for a given model compared to the best model, and the Bayesian stacking weight (similar to Akaike weight). The grey shading serves as a visualization tool for separating models being compared.

Model	Model run	**looic**	**p_{loo}**	**$elpd_{loo}$**	**se_{elpd_loo}**	**$elpd_{diff}$**	**weight**
MR1	1	306.5	14.8	-153.2	6.2	-13.4	0.207
MR2		286.7	8.8	-143.4	13.3	-3.5	0
MR3		279.6	9.6	-139.8	13.8	0	0.793
MR1	2	305.4	14.4	-152.7	6.2	-12.9	0.208
MR2		286.4	8.7	-143.2	13.2	-3.4	0
MR3		279.6	9.7	-139.8	14	0	0.792
MR1	3	302.8	13.1	-151.4	6.1	-11.6	0.219
MR2		285.9	8.4	-143	13.2	-3.1	0
MR3		279.7	9.7	-139.8	13.9	0	0.781
RSA1	1	346.5	3.1	-173.2	5.6	-46.3	0
RSA2		253.9	3.3	-127	7.3	0	1
RSA3		255.8	4.1	-127.9	7.3	-0.9	0
RSA1	2	346.5	3.2	-173.3	5.6	-46.3	0
RSA2		253.9	3.3	-126.9	7.3	0	1
RSA3		255.9	4.1	-128	7.2	-1	0
RSA1	3	346.3	3.1	-173.2	5.6	-46.3	0
RSA2		253.7	3.2	-126.8	7.2	0	1
RSA3							0
		255.6	4	-127.8	7.2	-0.9	
C1	1	276.5	10	-138.2	13.2	-6.5	0.002
C2		277.4	12	-138.7	14	-6.9	0.08
C3		271.7	11.4	-135.8	14	-4.1	0.108
C4		270.7	12.7	-135.4	14.2	-3.6	0
C5		263.6	11.8	-131.8	14.7	0	0.809
C6		267.2	13.3	-133.6	14.8	-1.8	267.2
C1	2	276.6	9.9	-138.3	13.3	-6.3	0
C2		275.8	11.2	-137.9	13.3	-5.9	0.118
C3		270.8	11	-135.4	13.9	-3.4	0.138
C4		269.1	11.7	-134.5	13.7	-2.6	0
C5		264	12	-132	14.9	0	0.744
C6		266.8	13.1	-133.4	14.6	-1.4	0
C1	3	278.1	10.5	-139.1	13.3	-7.1	0
C2		277.3	11.8	-138.7	13.8	-7	0.069
C3		270.8	10.8	-135.4	13.8	-3.7	0.14
C4		271.9	13.3	-136	14.8	-4.3	0
C5		263.4	11.7	-131.7	14.8	0	0.791
C6		267	13.3	-133.5	14.6	-1.8	0

Table S8: The corresponding species identity to the species code (number) along the y-axis in Figure 1.

Species code	Scientific name	Common name
1	*Seriola lalandi*	Yellowtail
2	*Euthynnus affinis*	Mackerel Tuna
3	*Ctenopharyngodon idella*	Grass Carp
4	*Sebastes diploproa*	Rockfish
5	*Carcharodon carcharias*	White Shark
6	*Morone saxatilis*	Striped Bass
7	*Pagrus auratus*	Silver Seabream
8	*Cirrhinus mrigala*	Mrigal Carp
9	*Brevoortia tyrannus*	Menhaden
10	*Carassius auratus*	Goldfish
11	*Conger conger*	Conger Eel
12	*Isurus oxyrinchus*	Shortfin Mako
13	*Hoplias malabaricus*	Wolf Fish
14	*Sander lucioperca*	Pikeperch
15	*Cottus gobio*	European Bullhead
16	*Varanus exanthematicus*	Savannah Monitor Lizard
17	*Tinca tinca*	Tench
18	*Labeo rohita*	Rohu Carp
19	*Pseudopleuronectes americanus*	Winter Flounder
20	*Carcharhinus plumbeus*	Sandbar Shark
21	*Anguilla anguilla*	European Eel
22	*Thunnus albacares*	Yellowfin Tuna
23	*Scomber scombrus*	Atlantic Mackerel
24	*Merlangius merlangus*	Whiting
25	*Pomatomus saltatrix*	Bluefish
26	*Oncorhynchus mykiss*	Rainbow Trout
27	*Hoplerythrinus unitaeniatus*	Trahira
28	*Catostomus commersonii*	White Sucker
29	*Misgurnus fossilis*	Weatherfish
30	*Gekko gecko*	Tokay Gecko
31	*Centropristis striata*	Black Sea Bass
32	*Gymnocephalus cernua*	Ruffe
33	*Scomber japonicus*	Chub Mackerel
34	*Seriola quinqueradiata*	Amberjack
35	*Platichthys flesus*	European Flounder
36	*Trachemys scripta*	Pond Slider Turtle
37	*Sander vitreus*	Walleye

38	*Coryphaena hippurus*	Dolphinfish
39	*Salmo trutta*	Brown Trout
40	*Struthio camelus*	Common Ostrich
41	*Rhinoptera bonasus*	Cownose Ray
42	*Pollachius virens*	Coalfish Pollock
43	*Callionymus lyra*	Dragonet
44	*Channichthys rhinoceratus*	Unicorn Icefish
45	*Sebastolobus altivelis*	Longspine Thornyhead
46	*Bos taurus*	Cow
47	*Mus musculus*	Mouse
48	*Equus caballus*	Horse
49	*Heteropneustes fossilis*	Stinging Catfish
50	*Connochaetes taurinus*	Blue Wildebeest
51	*Limanda limanda*	Common Dab
52	*Ameiurus nebulosus*	Brown Bullhead Catfish
53	*Scyliorhinus stellaris*	Nursehound
54	*Notophthalmus viridescens*	Eastern Newt
55	*Camelus dromedarius*	Camel
56	*Katsuwonus pelamis*	Skipjack Tuna
57	*Rutilus rutilus*	Common Roach
58	*Sorex minutus*	Pygmy Shew
59	*Anguilla rostrata*	American Eel
60	*Taurotragus oryx*	Eland Antelope
61	*Perca flavescens*	Yellow Perch
62	*Opsanus tau*	Oyster Toadfish
63	*Bufo bufo*	Common Toad
64	*Larus argentatus*	Herring Gull
65	*Anabas testudineus*	Climbing Perch
66	*Oryctolagus cuniculus*	Rabbit
67	*Esox lucius*	Northern Pike
68	*Cavia porcellus*	Guinea Pig
69	*Perca fluviatilis*	European Perch
70	*Lipophrys pholis*	Shanny Blenny
71	*Phyllotis darwini*	Darwin’s Mouse
72	*Scyliorhinus canicula*	Lesser Spotted Dogfish
73	*Oreochromis niloticus*	Nile Tilapia
74	*Pleuronectes platessa*	European Plaice
75	*Channa striata*	Snakehead Murrel
76	*Zoarces viviparus*	Eelpout
77	*Ambystoma opacum*	Marbled Salamander
78	*Taricha granulosa*	Rough Skinned Newt

79	*Dasyuroides byrnei*	Kowari Rat
80	*Dromaius novaehollandiae*	Emu
81	*Gallus gallus*	Chicken
82	*Echeneis naucrates*	Sharksucker
83	*Dicamptodon ensatus*	Giant California Salamander
84	*Vulpes lagopus*	Arctic Fox
85	*Amphiuma means*	Two Toed Amphiuma Salamander
86	*Setonix brachyurus*	Quokka
87	*Torpedo marmorata*	Marbled Electric Ray
88	*Spheniscus humboldti*	Chilean Penguin
89	*Balistes capriscus*	Grey Triggerfish
90	*Hyla arborea*	European Tree Frog
91	*Channa punctata*	Spotted Snakehead
92	*Rhyacotriton olympicus*	Olympic Torrent Salamander
93	*Myoxocephalus scorpius*	Shortfin Sculpin
94	*Cyprinus carpio*	Common Carp
95	*Dasyatis sabina*	Atlantic Stingray
96	*Clarias batrachus*	Walking Catfish
97	*Homo sapiens*	Human
98	*Bagre cavasius*	Gangetic Catfish
99	*Python regius*	Ball Python
100	*Gadus morhua*	Cod
101	*Chaenocephalus aceratus*	Blackfin Icefish
102	*Madoqua kirkii*	Dik Dik Antelope
103	*Pipistrellus pipistrellus*	Bat
104	*Anas platyrhynchos*	Mallard Duck
105	*Rana temporaria*	Common Frog
106	*Mugil cephalus*	Grey Mullet
107	*Cynopterus brachyotis*	Fruit Bat
108	*Rana arvalis*	Moor Frog
109	*Suncus etruscus*	Shrew

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