



Supplementary Information for
Optimum growth temperature declines with body size within fish
species

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This PDF file includes:

Supplementary text
Figures S1 to S27
Tables S1 to S5
SI References

Supplementary Information Text

Literature search, selection process and criteria

This section is an overview of the literature search approach, and below we present the search terms for each rate separately (maximum consumption, metabolism and growth). In addition to search terms, we also applied filters by selecting only the following subjects: ‘marine freshwater biology’, ‘fisheries’, ‘ecology’, ‘zoology’, ‘biology’, ‘physiology’. For growth rates, we also included ‘limnology’ and for maximum consumption we included ‘limnology’ and ‘evolutionary biology’. The use of additional subjects for growth and consumption reflects the lower data availability compared to metabolism. As we suspected that relatively few studies would have considered both body size- and temperature treatments, our goal was to get an as extensive as possible list of studies. Therefore, we also evaluated articles cited by articles found in the search, from published review-type articles and reviews of applications of bioenergetics models such as the Wisconsin model (1), and if the study was found in the literature search for another rate. The source of the article (WoS search or cited in literature) is indicated in the data sets (Table S1).

Articles were filtered out at three levels of the search: title, abstract and full article. The online repository of this project (<https://github.com/maxlindmark/scaling>) contains .txt files of the complete list of articles found in the literature search. We removed studies from the lists if the titles made it clear the articles did not fulfil all of the following conditions: (1) experimental study, (2) fish as study organism in post-larval life stages, and (3) replicates across both body size and temperature (factorially). We treat data as individual-level rates (per fish); however, in some cases they were measured as averages across multiple individuals. In addition to these general criteria, we also had criteria specific for each rate (see below). When several studies were found for the same species, we did not include all but instead chose the study with the largest body size and temperature range (in that order), as there can be large differences in absolute values of some physiological parameters between studies.

For consumption and growth rate, we determined if each data point within species was below or beyond peak temperature either by using information provided by the authors (e.g. by deriving a polynomial regression of the rate as a function of temperature to find the temperature of peak rate), by fitting quadratic models or visually inspecting data for each species separately. Whether a data point was below or above peak or optimum temperatures is indicated by a separate column in the data (Table S1).

Maximum consumption rate

We used the following topic terms for maximum consumption rate (three searches in total): (consumption OR bioenerg* OR ingestion OR “food-intake”) AND (mass OR weight OR size) AND (temperature*), as well as: (feeding-rate OR bio-energ*) AND (mass OR weight OR size) AND (temperature*) and lastly: (“food intake”) AND (mass OR weight OR size) AND (temperature*). * represents any group of characters, including no character. The searches for maximum consumption rate data resulted in 15259 articles (search date: 18 December 2018), with 3449 remaining after filtering by subject categories. The second search (search date: 13 March 2019) resulted in 431 additional titles after filtering by subject categories (of which some were duplicated from the first search) and the third search (search date: 29 June 2020) yielded 626 but no additional articles as they had either been selected already or did not meet the criteria. Articles were filtered out at the abstract and whole article stage if the original reference could not be identified and evaluated, if data were normalized (i.e., using a priori defined scaling relationships to show corrected data rather than measured values), there was no acclimation, or if measurements were not maximum consumption rate. As with the growth data, definitions of ad-libitum feeding may differ between studies – the key for our purpose is that food rations led to satiation and were not limiting. Consumption rates were converted to g day⁻¹ (but note we fitted models to mass-specific rates, g g⁻¹ day⁻¹). These data were compiled in the file consumption_data.xlsx.

Metabolic rate

We used the following topic terms for metabolic rate data: (metabolism OR "oxygen-consumption" OR "oxygen consumption") AND (mass OR weight OR size) AND (temperature*). * represents any group of characters, including no character. The search for metabolic rate experiments resulted in 8405 articles (search date: 6 June 2019), which was reduced to 3458 after applying filters for subject categories. Articles were filtered out at the abstract and whole article stage if the original reference could not be identified and evaluated, if data were normalized (i.e., using a priori defined scaling relationships to normalize data for data a given size rather than measured values), if there was no acclimation or if it was not standard, routine or resting metabolic rate. The latter was defined as oxygen consumption of an unfed fish at no or little spontaneous activity. Metabolic rates were converted to mg O₂ h⁻¹, because it was the most common unit in the data set (but note models were fitted to mass-specific rates, mg O₂ g⁻¹ h⁻¹). These data were compiled in the file metabolism_data.xlsx.

Growth rates & optimum temperature for growth over body mass

Growth rates were taken from data found in the literature search for optimum growth temperatures. Therefore, articles in which growth rates were measured at sub-optimum temperatures only were not included (note this is in contrast to consumption data where "optimum" was not included in the search terms). We used the following topic terms for growth rate data: (growth) AND (mass OR weight OR size) AND (temperature*) AND (optimum), as well as: (growth) AND (mass OR weight OR size) AND (temperature*) AND (optim*). * represents any group of characters, including no character. The two searches for growth rates resulted in 3313 articles (search date: 22 March 2019), and 3747 articles (search date: 5 May 2019), respectively. After applying additional filters by subject category, we acquired 566 and 893 studies, respectively (of which some are duplicates due to similar search-strings). We removed studies at the abstract and whole article stage where the original reference could not be identified and evaluated, if we could not extract actual growth rates, if there was not a controlled temperature for each growth trial, or if there were not multiple defined size-classes. We used only one observation (data point) per size class and temperature treatment, and in cases where there were two, we used the mean value. In addition, we ensured that no other treatment (e.g., food limitation) confounded the response variable and thus only used data from experiments with satiating food levels. Body mass is either the geometric mean of the initial and final mass of the growth trial or the size class, depending on data availability (see Table S1). It is important to control for feeding ratios as it affects the temperature optimum for growth (2). This was achieved in different ways in the different experimental studies, but commonly involved excess feeding ratios once or several times per day. The key description we looked for in the study was that food was not limiting. We treat data as individual-level growth (per fish); however, these were commonly measured as averages for multiple individuals. In the case growth was length-based, we converted it to mass using weight-length relationships from FishBase (3, 4). We compiled two separate data sets: raw growth rates (growth_data.xlsx) and temperature at optimum growth (growth_data_Topt.xlsx). In the latter, we defined optimum temperature for growth as the fitted optimum temperature by size-class (usually estimated in the original study). Therefore, the optimum temperature may not always correspond to an actual experimental temperature but could be an estimation. If the optimum temperature (by size group) was not estimated in the original study, we used the temperature where growth rate was maximized. All growth rates were expressed in unit % day⁻¹.

Supplementary methods and analysis

At below peak temperatures, the intraspecific mass- and temperature dependence of specific growth (% increase in size day⁻¹) can be described by the equation: $\ln(G) = 0.5 - 0.36 \times \ln(m) - 0.74 \times t_A + 0.0046 \times t_A \times \ln(m)$ (Fig. S12), based on posterior medians of the global parameters, thus representing an average (unmeasured) fish. (see SI Appendix Fig S15, S19, S23 and S27 for the full posteriors distributions of parameters for all models). The mass exponent of growth is estimated to be -0.36 [-0.5, -0.23] and the activation energy ($-\mu_{\beta_2}$) of growth 0.74 [0.95, 0.53]. This is similar to the predicted mass scaling of net energy at sub-optimum temperatures, defined

as the difference between consumption and metabolism (Fig. 3; see also methods on 'Net energy gain'), which scales with a mass-specific exponent of -0.38. The estimated temperature-mass interaction coefficient is both small and uncertain (0.0046 [-0.064, 0.075]), where Bayesian 95% credible intervals are indicated in square brackets.

Model validation and fit

Figures showing convergence of species-level parameters can be found on:
<https://github.com/maxlindmark/scaling>, in this section only global parameters are visualized (Fig. S8-S27).

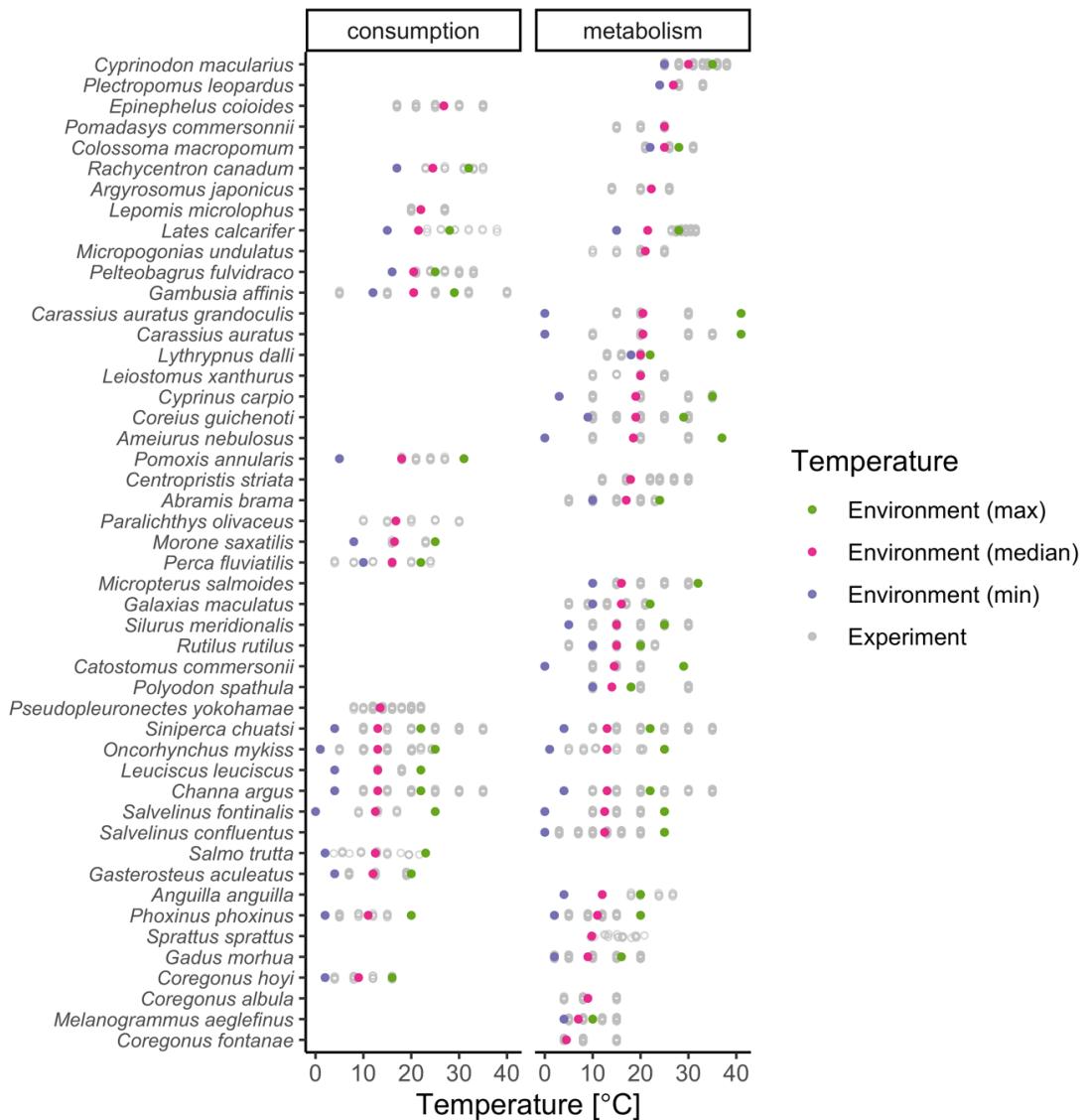


Fig. S1. Experimental temperatures (gray) and environmental (min, median and max) temperatures (purple, pink and green, respectively) of species represented in the consumption (left) and metabolism (right) data sets. Missing temperatures means information was not available on FishBase. Experimental temperatures are jittered vertically for visibility.

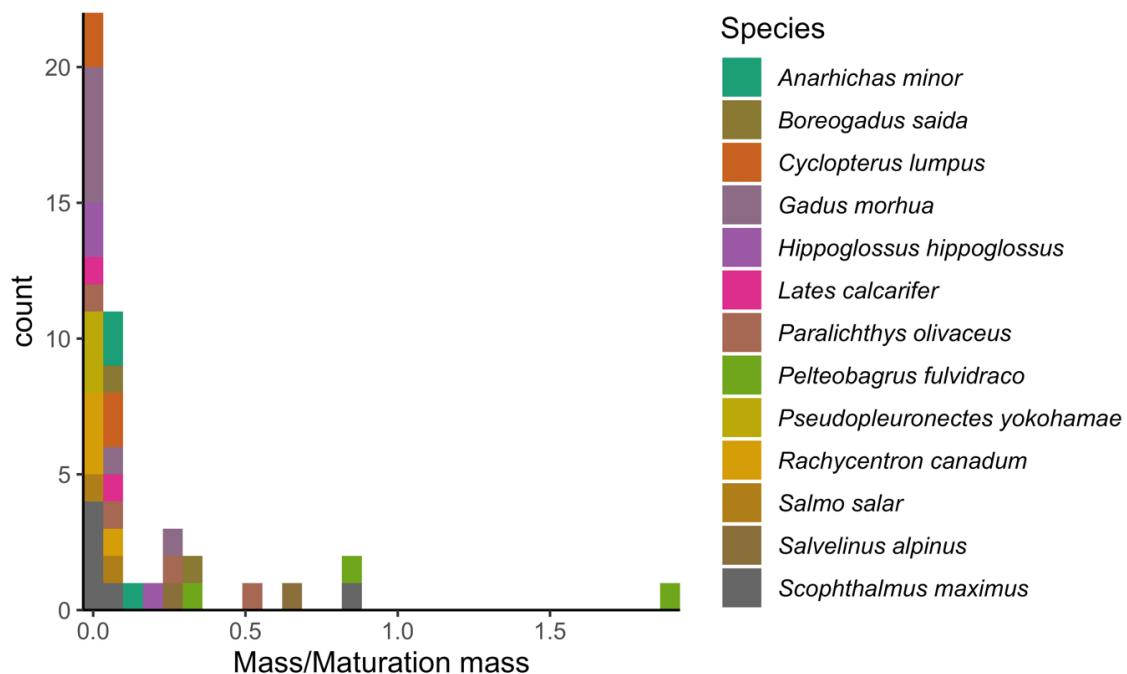


Fig. S2. The distribution of rescaled masses for individual observations (mass/mass at maturation), where color indicate species.

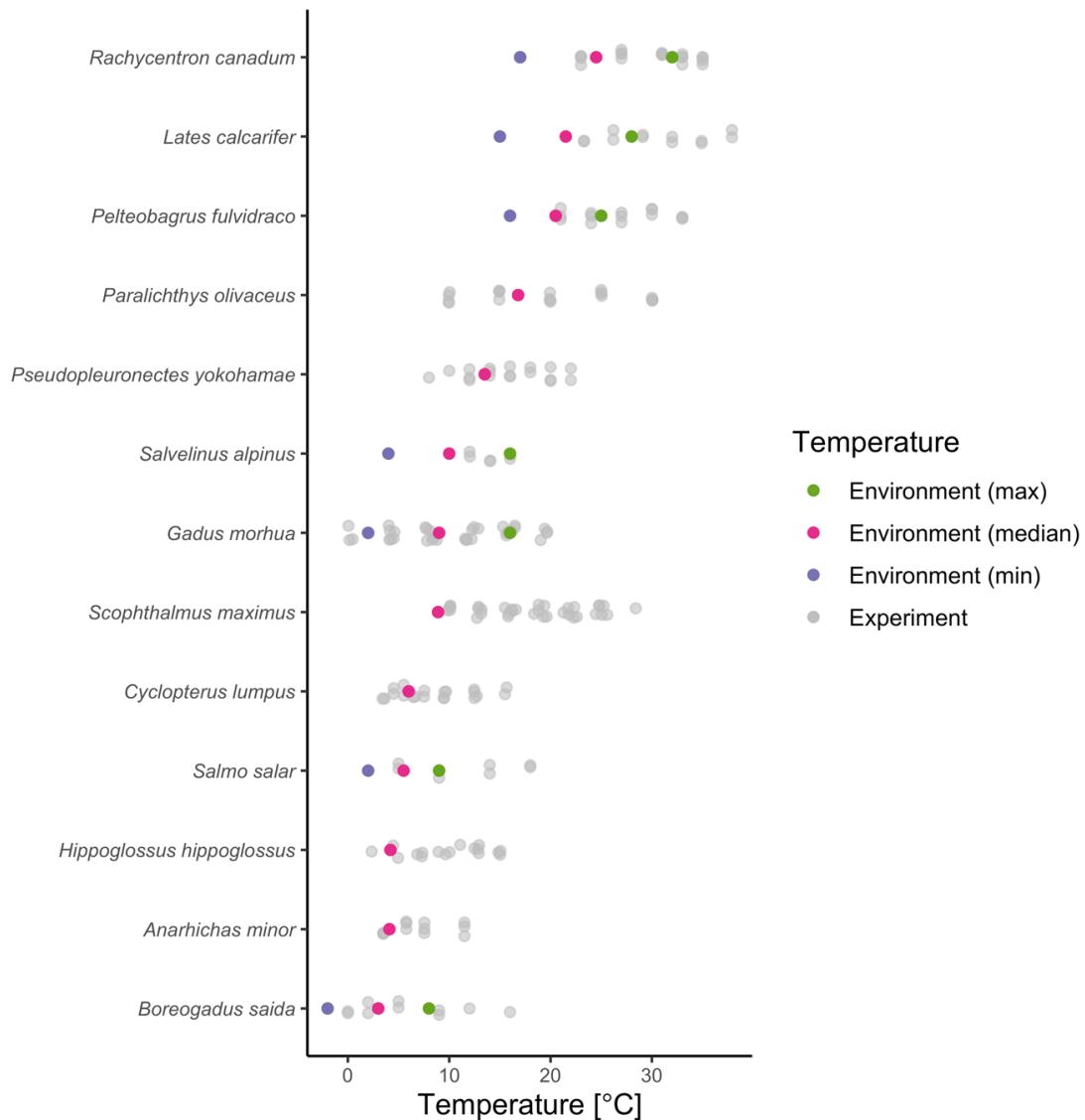


Fig. S3. Experimental temperatures (gray) in the growth rate data and environmental (min, median and max) temperatures (purple, pink and green, respectively). Missing temperatures means information was not available on FishBase. Experimental temperatures are jittered vertically for visibility.

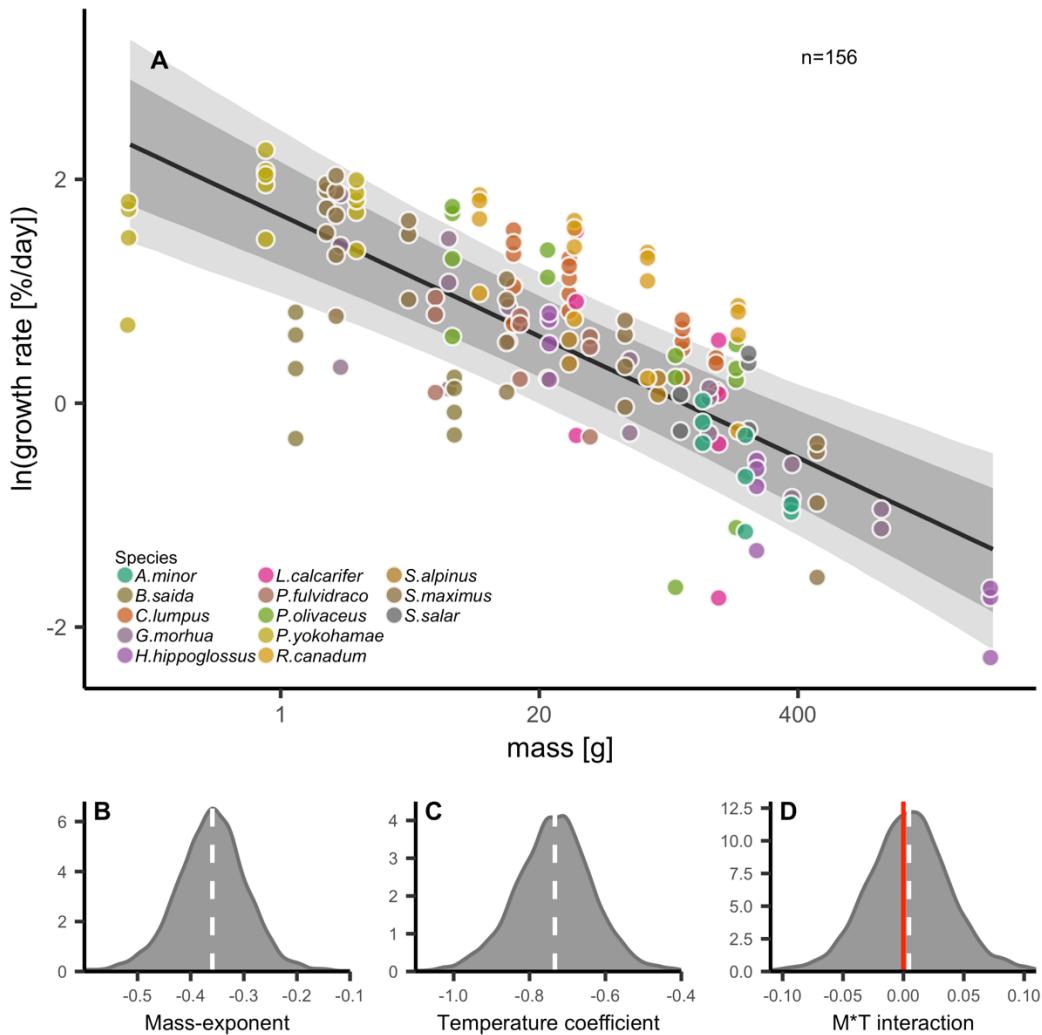


Fig. S4. Effects of temperature and body mass on body growth below optimum temperature. Panel A) shows the natural log of specific growth rate as a function of body mass on a logarithmic x-axis (for readability, note the model is fitted with $\ln(\text{mass})$ as a predictor), such that the slope corresponds to the mass-scaling exponent. Colors indicate species. The line in panel A is the global prediction from model M1 at the mean temperature in the growth data (14°C , but note the model is fitted using Arrhenius temperature). Shaded areas correspond to 80% and 95% credible intervals. Point colors indicate species. The bottom row shows the posterior distributions for (B) the global mass-scaling exponent, μ_{β_1} , (C) the global temperature coefficient, μ_{β_2} and (D) the global mass-temperature interaction, μ_{β_3} . Dashed white line shows the posterior median and red vertical line in (D) indicates zero.

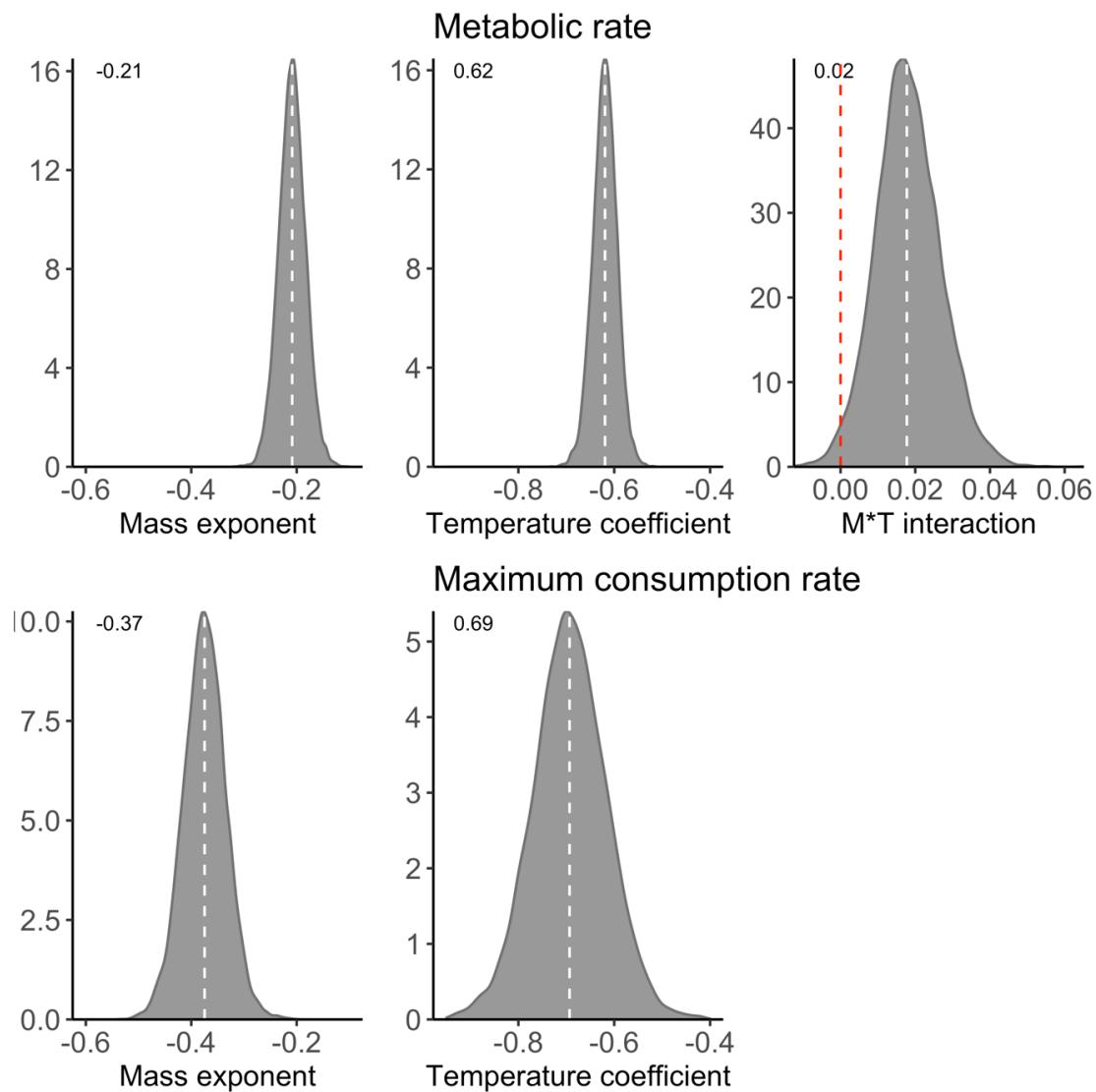


Fig. S5. Posterior distributions of the global intraspecific mass-specific mass exponents (μ_{β_1}) and temperature coefficients (μ_{β_2}) for metabolic rate (top) and maximum consumption rate (bottom). For metabolism, the global interaction coefficient (μ_{β_3}) is also shown (estimated and presented on an Arrhenius temperature scale), but for consumption this term was not included in the selected model. Numbers in the top left corner correspond to the posterior median. The axes are the same for each parameter for comparison between the two rates.

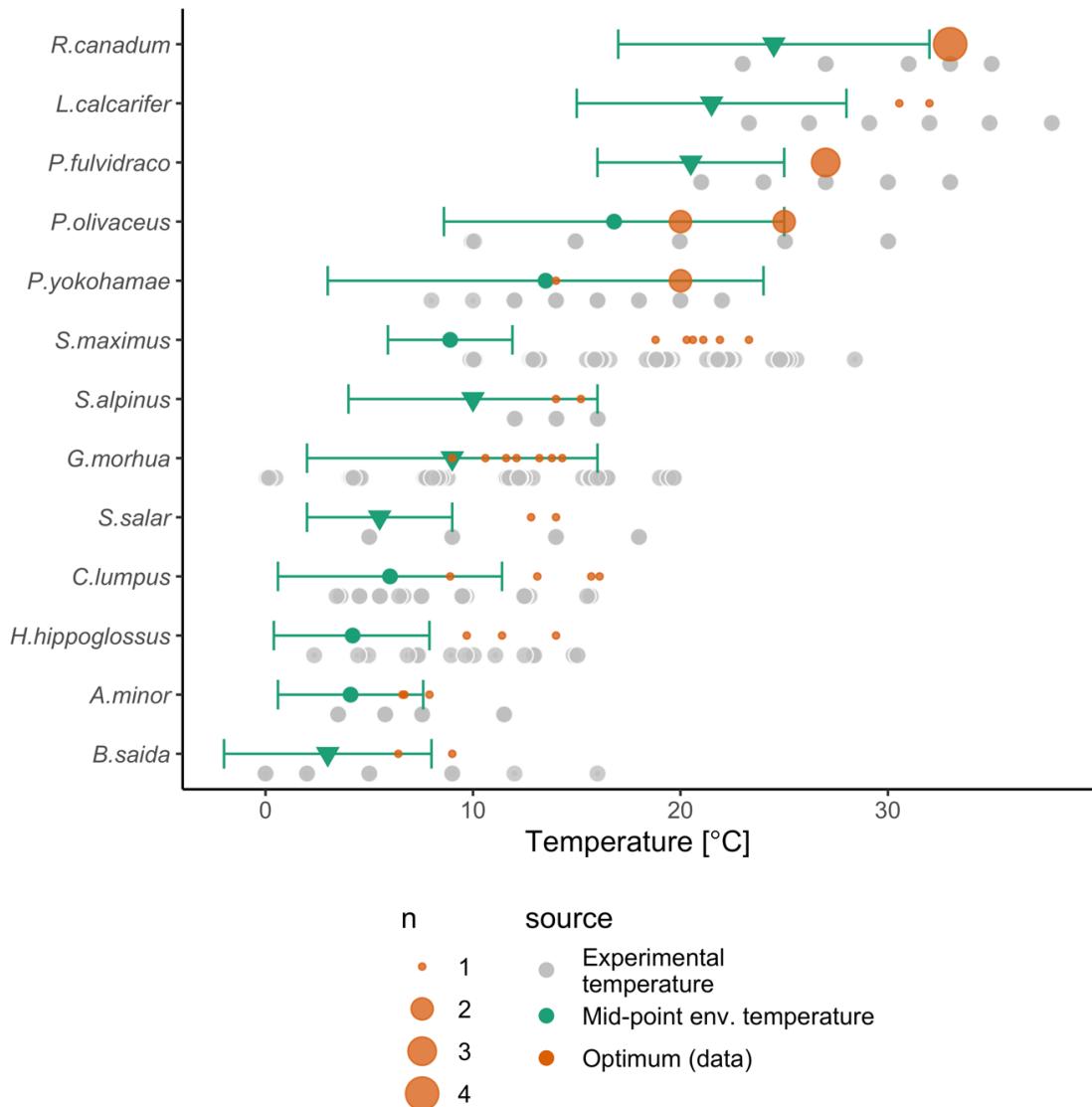


Fig. S6. Experimental temperatures (grey) overlap environmental temperatures (green), and optimum growth temperatures (orange) are typically at the upper end or above the environmental range. Horizontal green lines show the minimum and maximum environmental temperature based on either temperature in distribution range (triangles) or modelled distribution maps (circles), both taken from FishBase. The optimum growth temperatures are depicted for all size-classes per species, where the circle size is proportional to number of observations at that temperature.

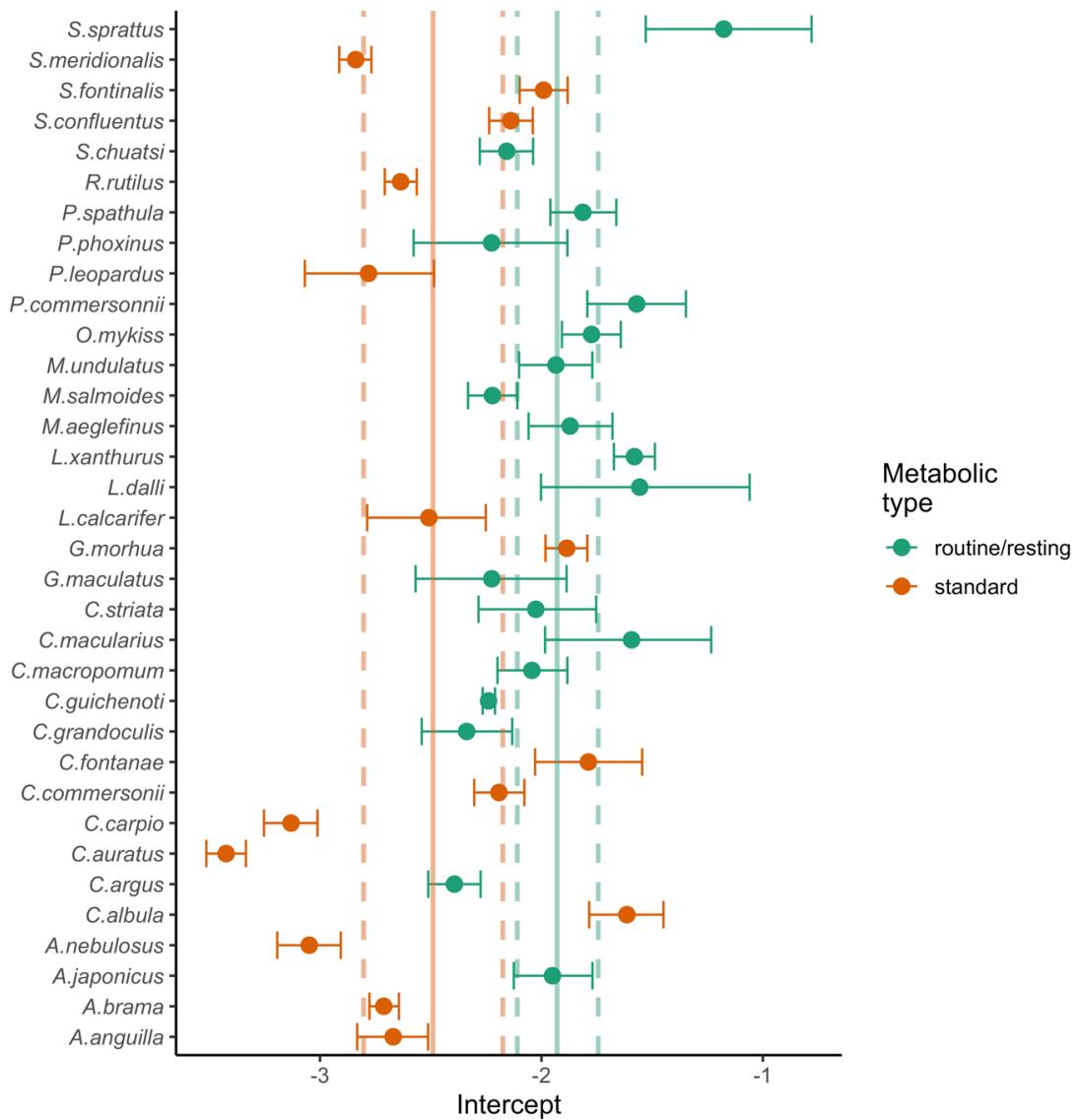


Fig. S7. Posterior median of species-level intercepts (points) and their 95% credible interval (horizontal error bars). Colors indicate the type of metabolism measurement for each species. Vertical solid lines are the posterior medians of the global intercepts (orange for standard metabolic rate, $\mu_{\beta_{0s}}$, and green for routine or resting metabolic rate, $\mu_{\beta_{0r}}$), and the dashed vertical lines show the 95% credible intervals for the global parameters.

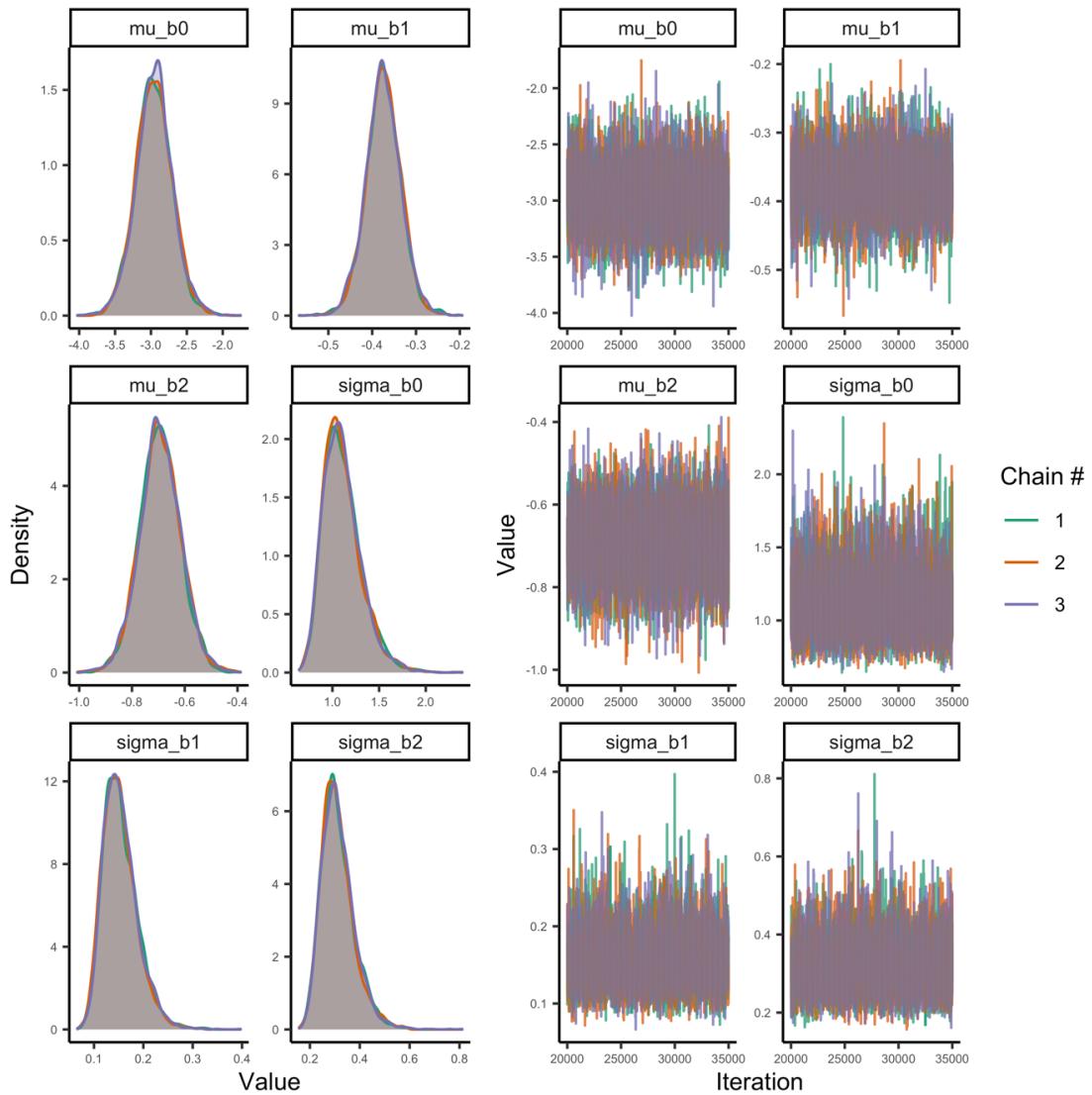


Fig. S8. Posterior densities and trace plots for evaluation of chain convergence (by chain, indicated by color), for the global-level parameters for the log-linear maximum consumption rate model at temperatures below peak temperatures.

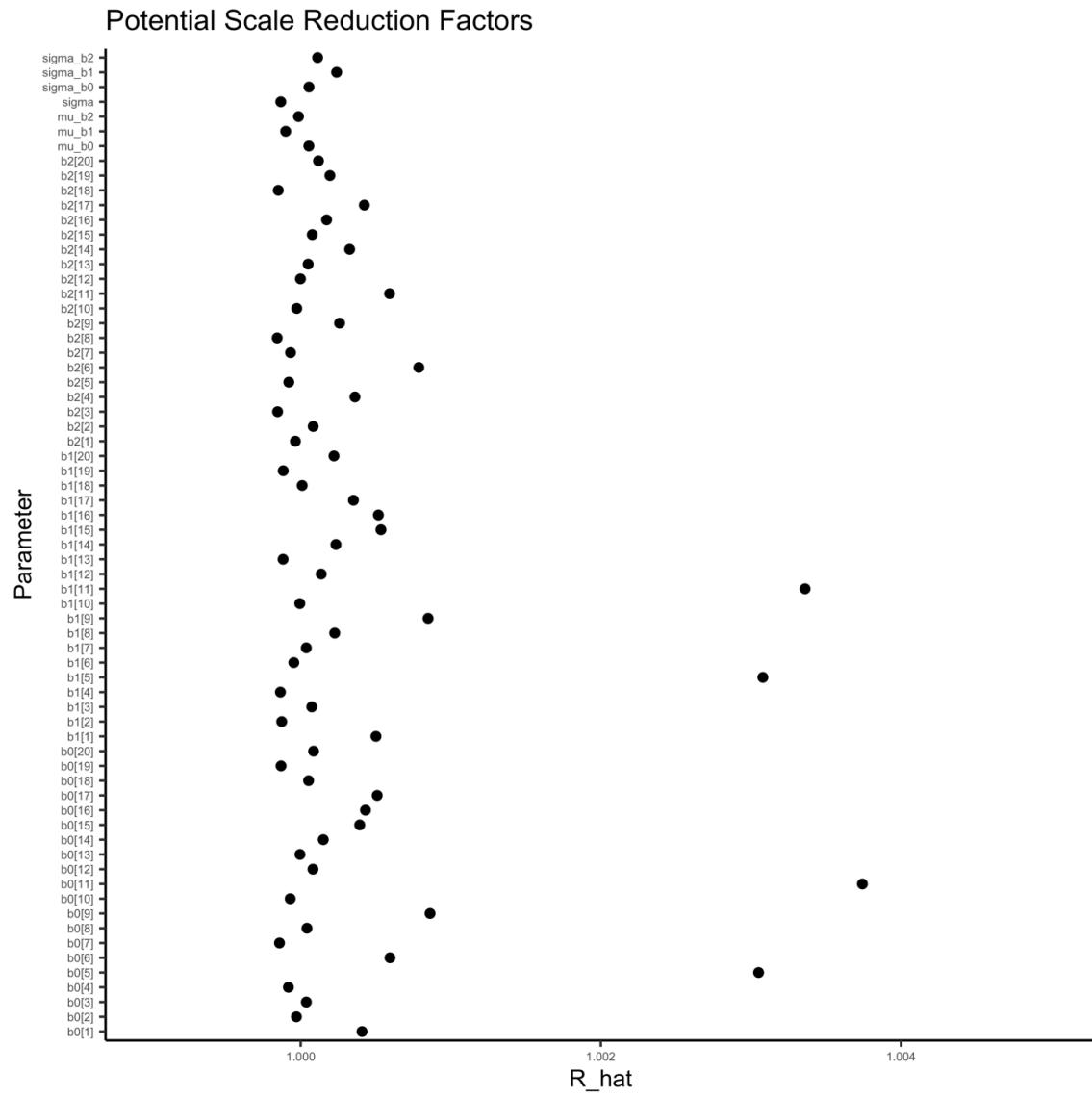


Fig. S9. Potential scale reduction factor (\hat{R}) for the log-linear maximum consumption rate model. This factor is based on the comparison of between and within-chain variation for the same parameter. A value close to one implies chains converged to the same distribution. The index of the parameter corresponds to species. The index of the parameter corresponds to species in alphabetical order.

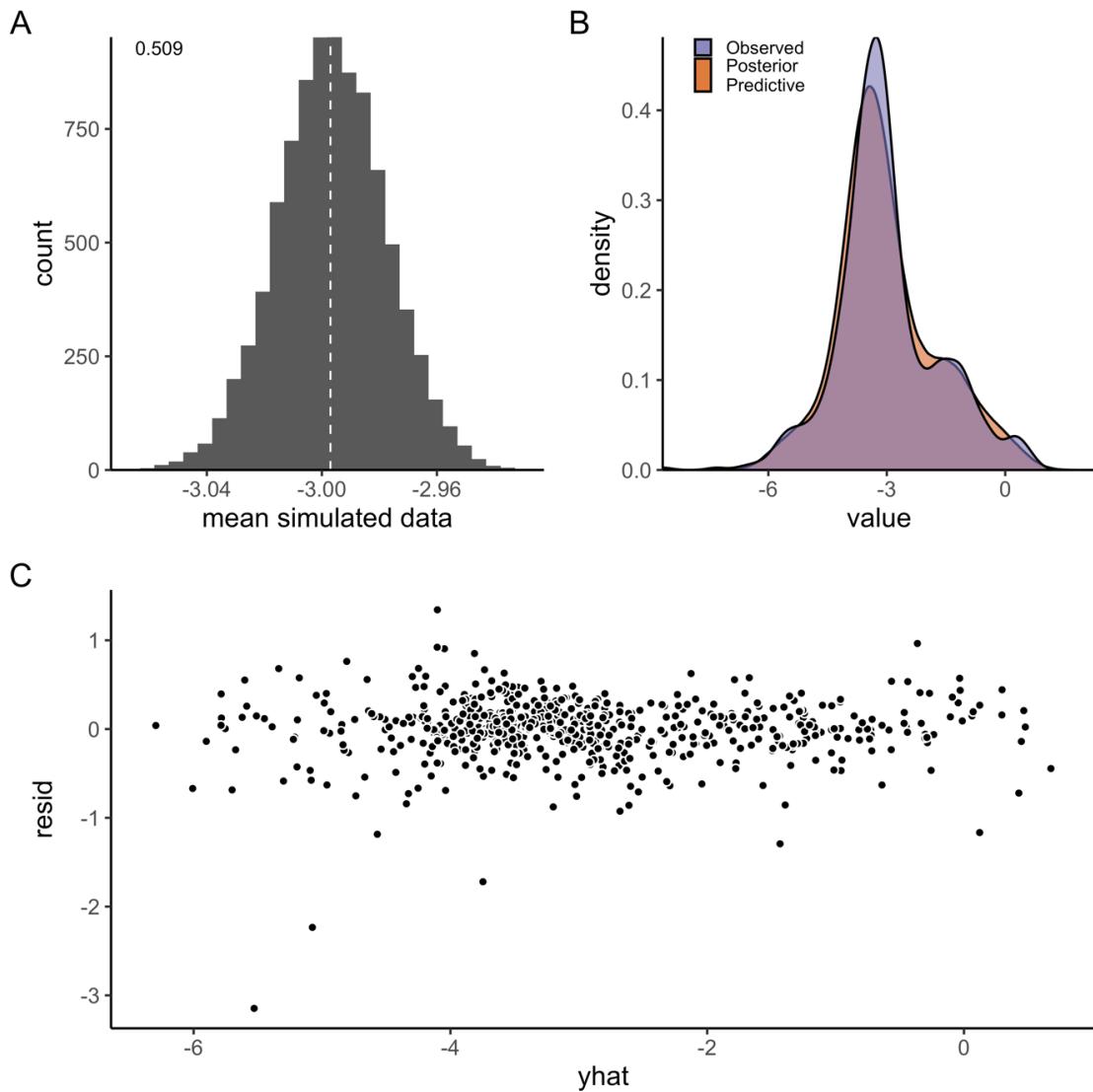


Fig. S10. A) Model fit (mean) for the log-linear model of maximum consumption rate at temperatures below temperature peak (by species). Fit is evaluated by simulating data from the likelihood (at each iteration of the MCMC chain), to compare how well it matches the original data. Each simulated data point is assigned a 0 or 1 if it is below or above the mean data point (the vertical line corresponds to the mean in data). The number in the plot corresponds to the mean of the vector of 0's and 1's. B) Posterior predictive distribution (orange) and distribution of data (purple). C) Difference between the observed value and the posterior median of the predicted value, plotted against fitted value.

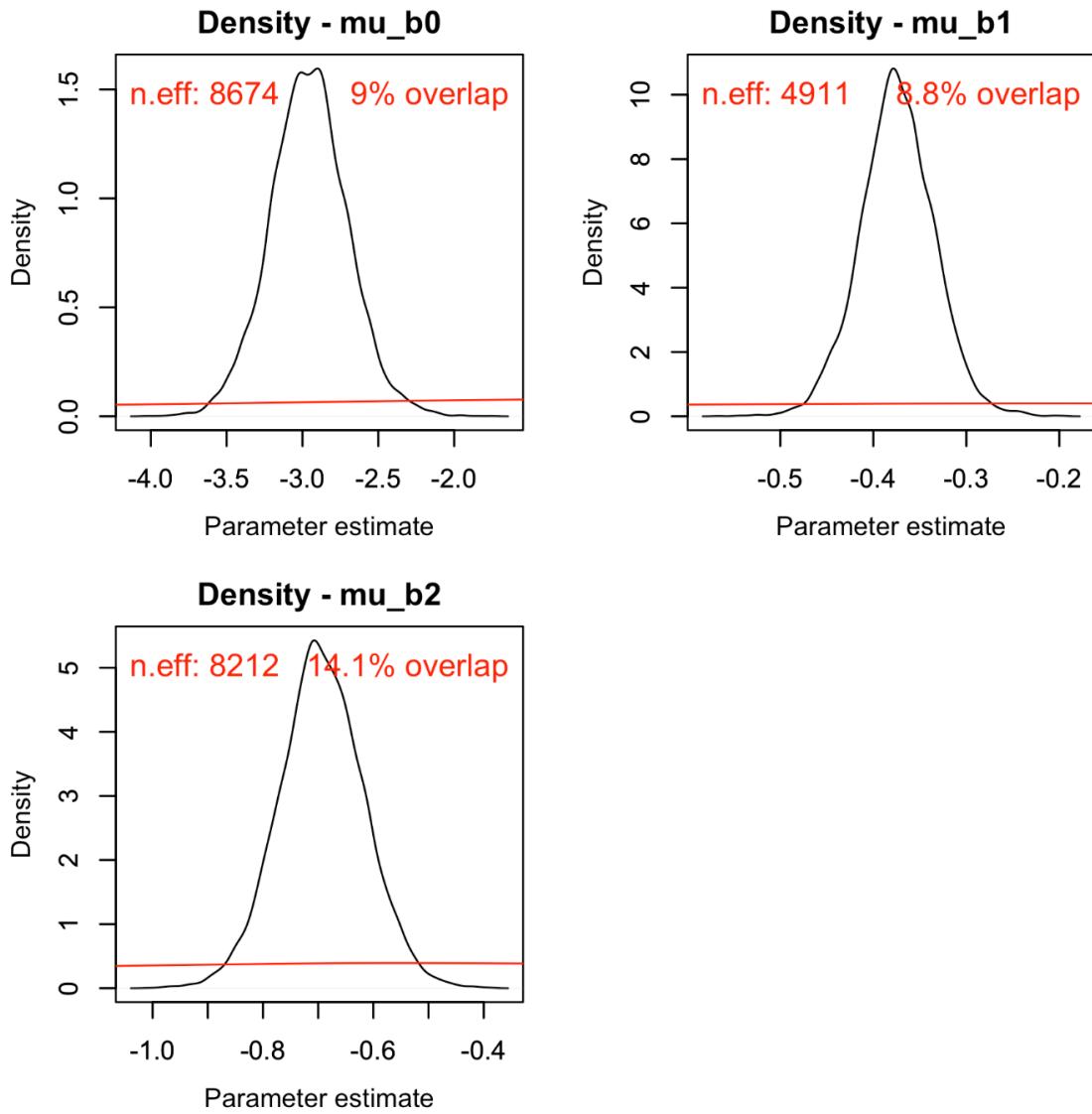


Fig. S11. Posterior (black) and prior distribution (red) for the global parameters in the log-linear model for maximum consumption rate, including their % overlap and effective sample size (n.eff).

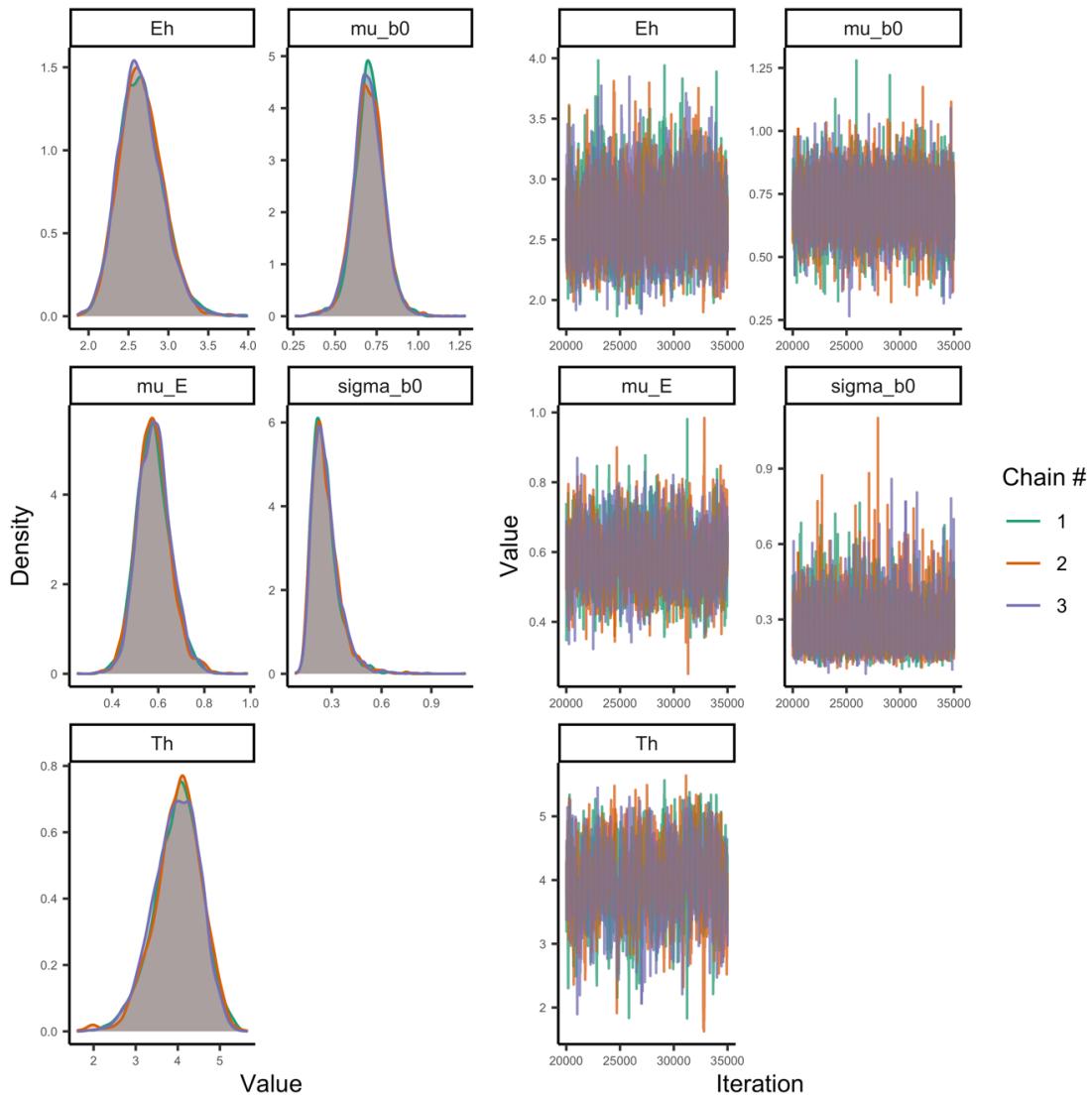


Fig. S12. Posterior densities and trace plots for evaluation of chain convergence (by chain, indicated by color), for the global-level parameters for the Sharpe-Schoolfield model fitted to maximum consumption rate data with temperatures including beyond peak temperatures.

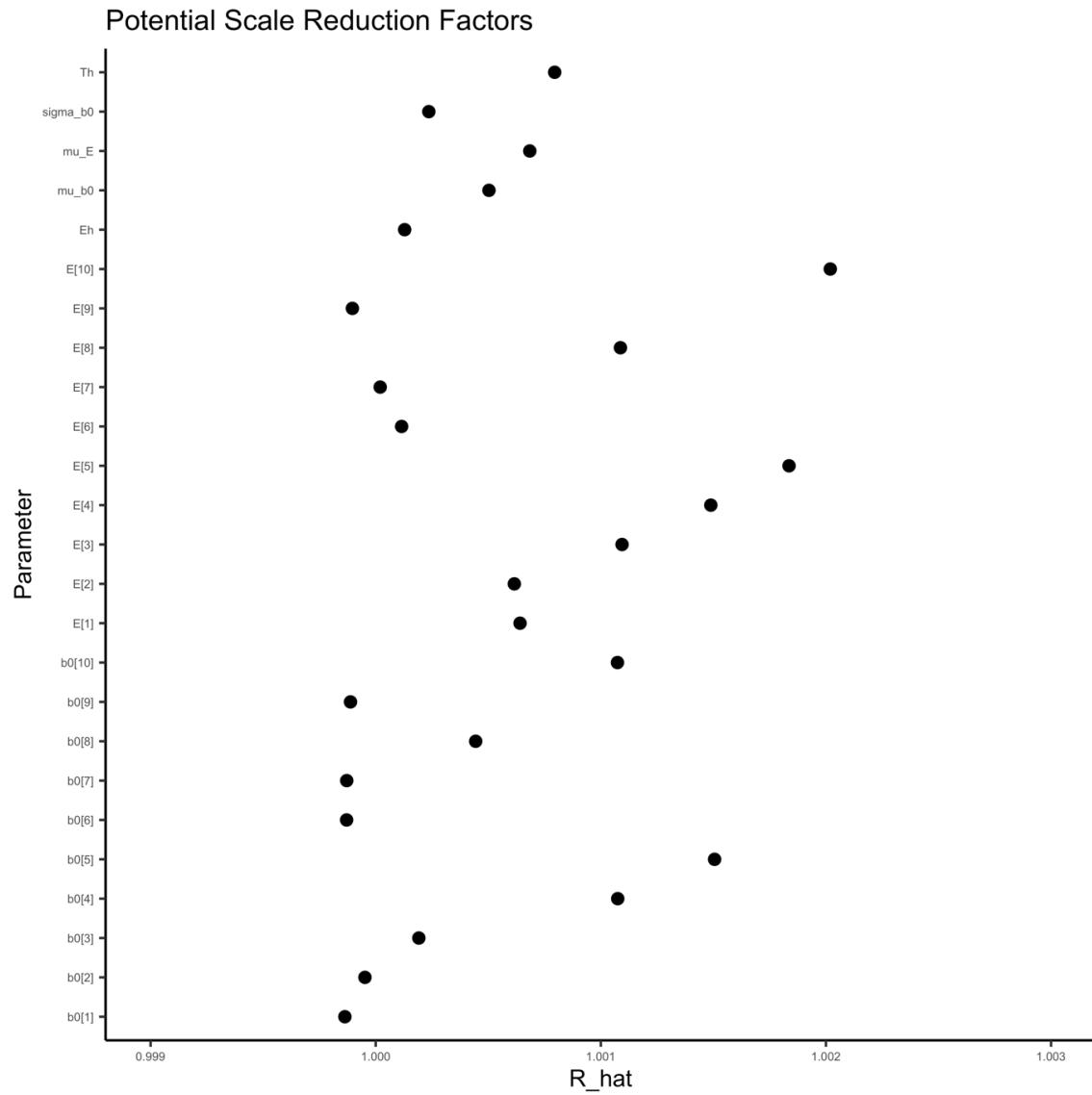


Fig. S13. Potential scale reduction factor (\hat{R}) for the Sharpe-Schoolfield model fitted to maximum consumption rate data (including data beyond peak). This factor is based on the comparison of between and within-chain variation for the same parameter. A value close to one implies chains converged to the same distribution. The index of the parameter corresponds to species in alphabetical order.

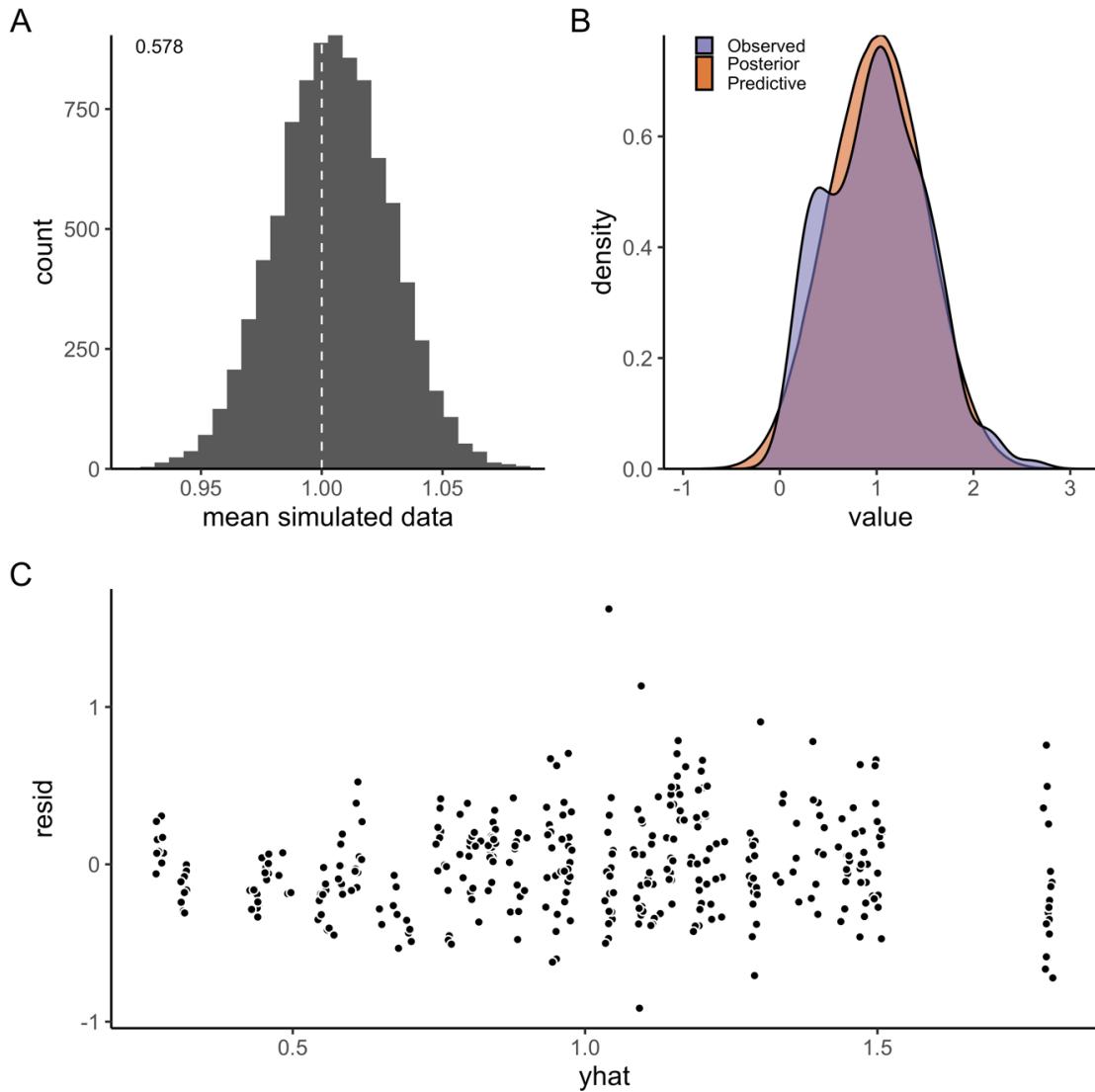


Fig. S14. A) Model fit (mean) for the Sharpe-Schoolfield model fitted to maximum consumption rate data including temperatures beyond peak (by species). Fit is evaluated by simulating data from the likelihood (at each iteration of the MCMC chain), to compare how well it matches the original data. Each simulated data point is assigned a 0 or 1 if it is below or above the mean data point (the vertical line corresponds to the mean in data). The number in the plot corresponds to the mean of the vector of 0's and 1's. B) Posterior predictive distribution (orange) and distribution of data (purple). C) Difference between the observed value and the posterior median of the predicted value, plotted against fitted value.

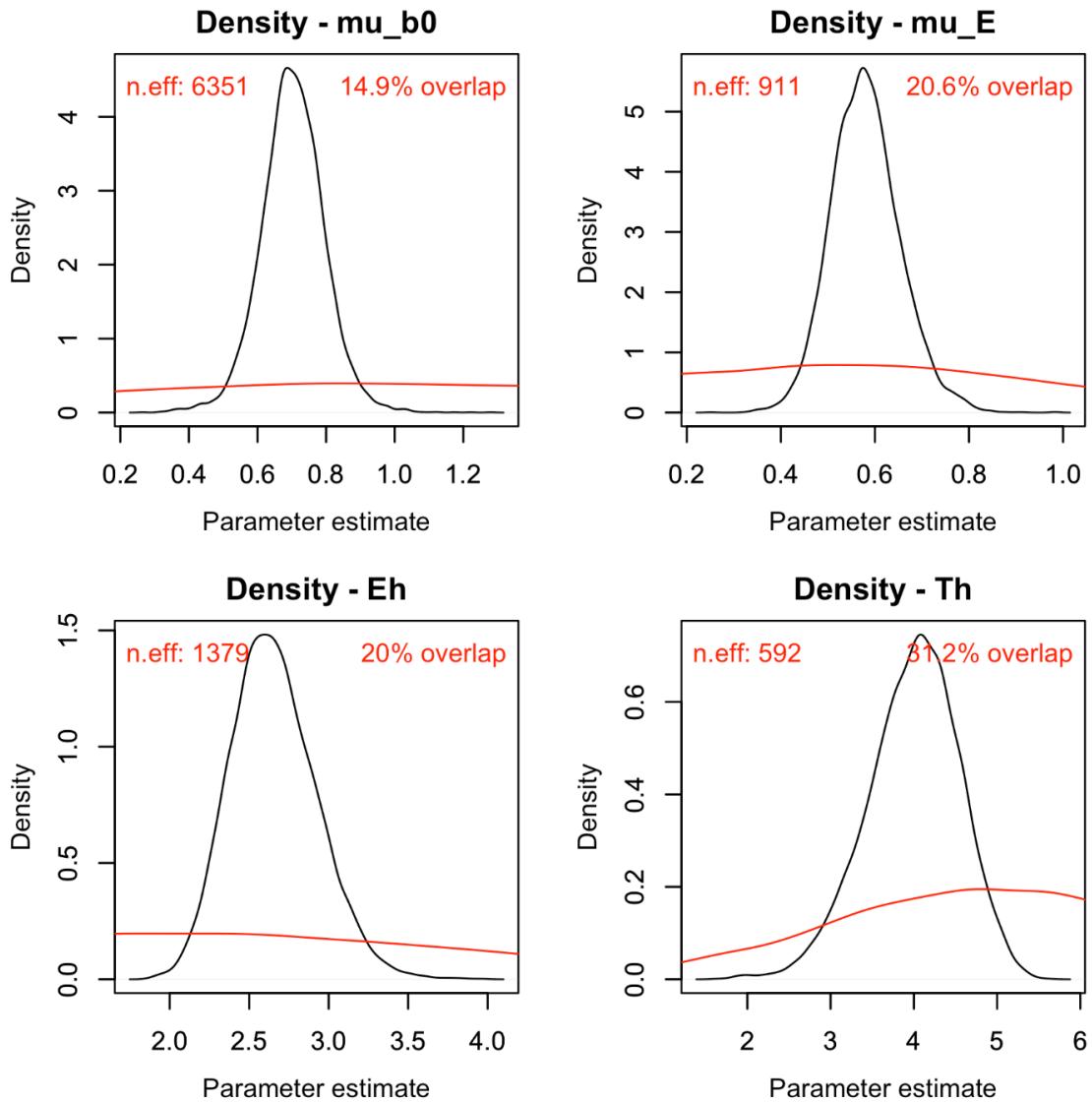


Fig. S15. Posterior (black) and prior distribution (red) for the global parameters in the Sharpe-Schoolfield model for maximum consumption rate including data beyond peak, including their % overlap (rounded) and effective sample size (n.eff).

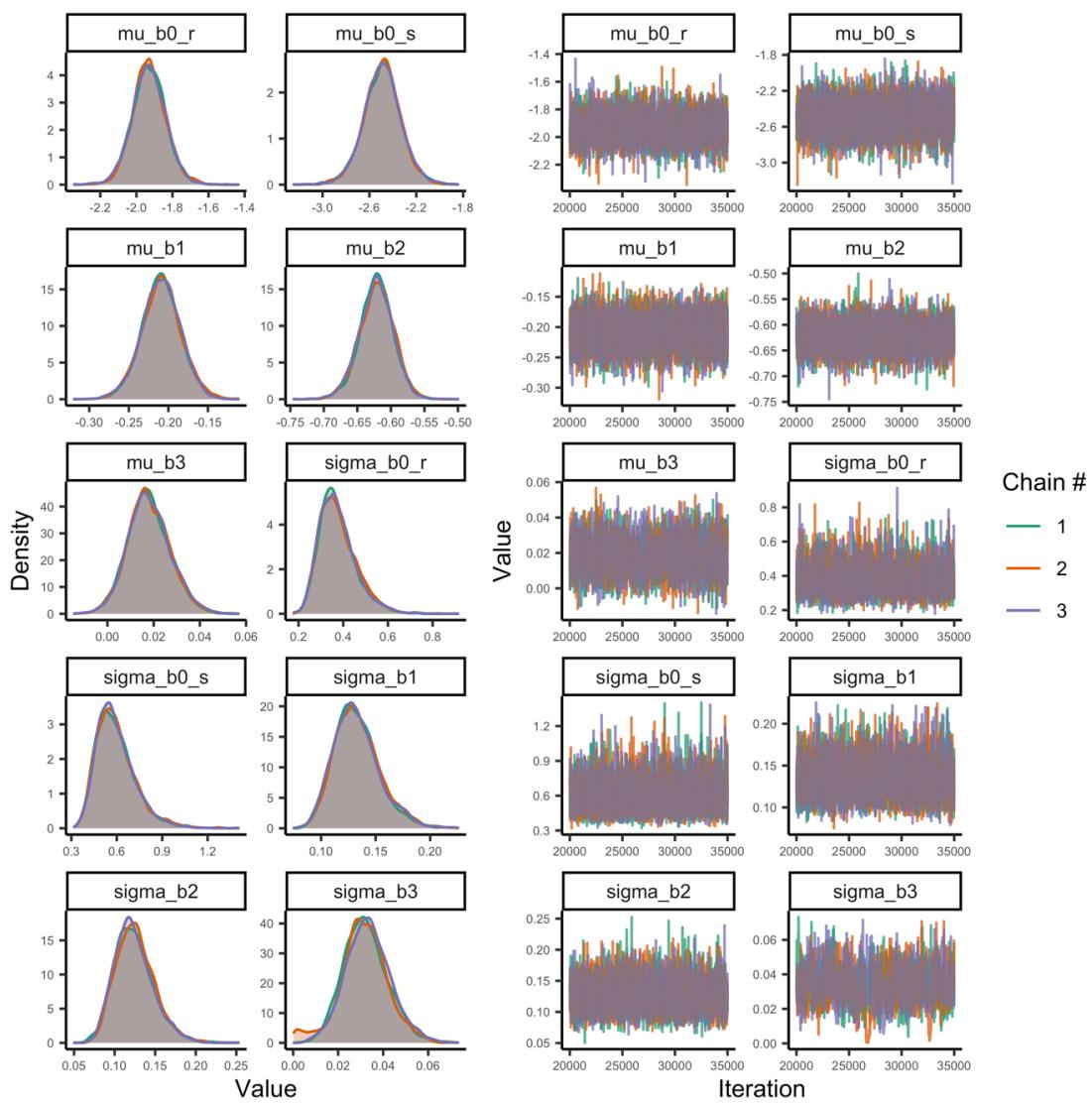


Fig. S16. Posterior densities and trace plots for evaluation of chain convergence (by chain, indicated by color), for the global-level parameters for the metabolic rate model at temperatures below peak temperatures.

Potential Scale Reduction Factors

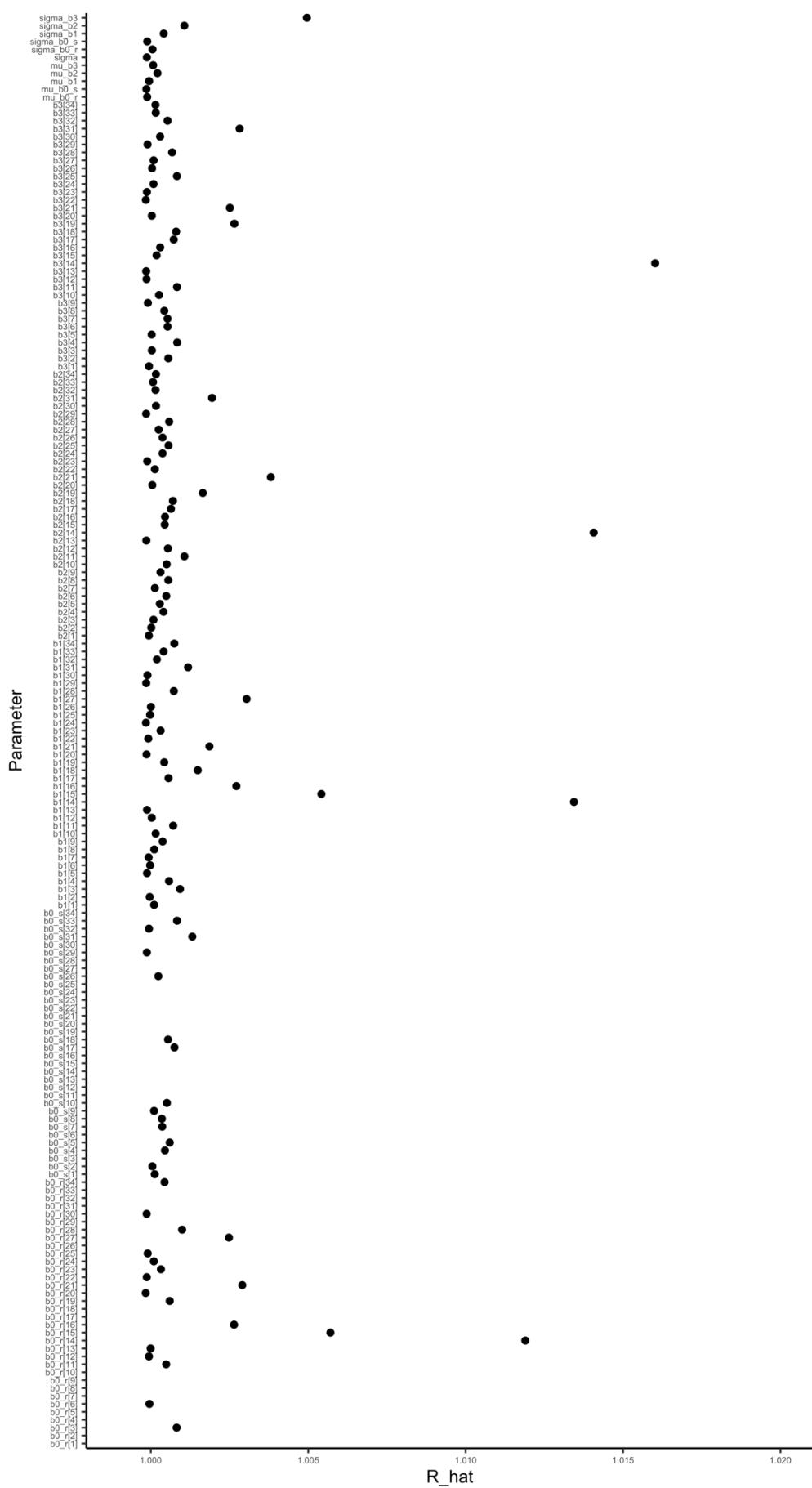


Fig. S17. Potential scale reduction factor (\hat{R}) for the metabolic rate model. This factor is based on the comparison of between and within-chain variation for the same parameter. A value close to one implies chains converged to the same distribution. The index of the parameter corresponds to species in alphabetical order.

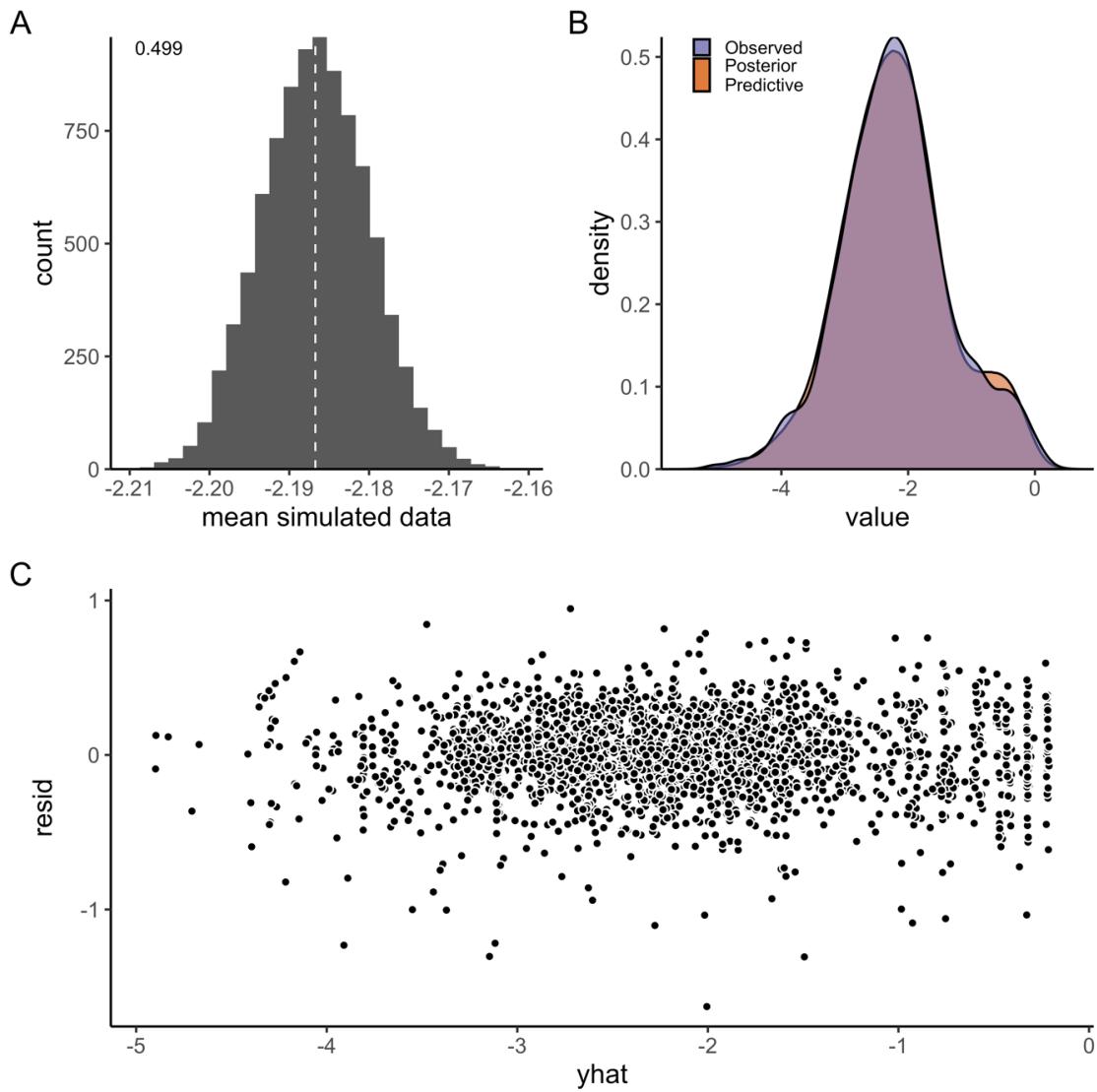


Fig. S18. A) Model fit (mean) for the log-linear model of metabolic rate. Fit is evaluated by simulating data from the likelihood (at each iteration of the MCMC chain), to compare how well it matches the original data. Each simulated data point is assigned a 0 or 1 if it is below or above the mean data point (the vertical line corresponds to the mean in data). The number in the plot corresponds to the mean of the vector of 0's and 1's. B) Posterior predictive distribution (orange) and distribution of data (purple). C) Difference between the observed value and the posterior median of the predicted value, plotted against fitted value.

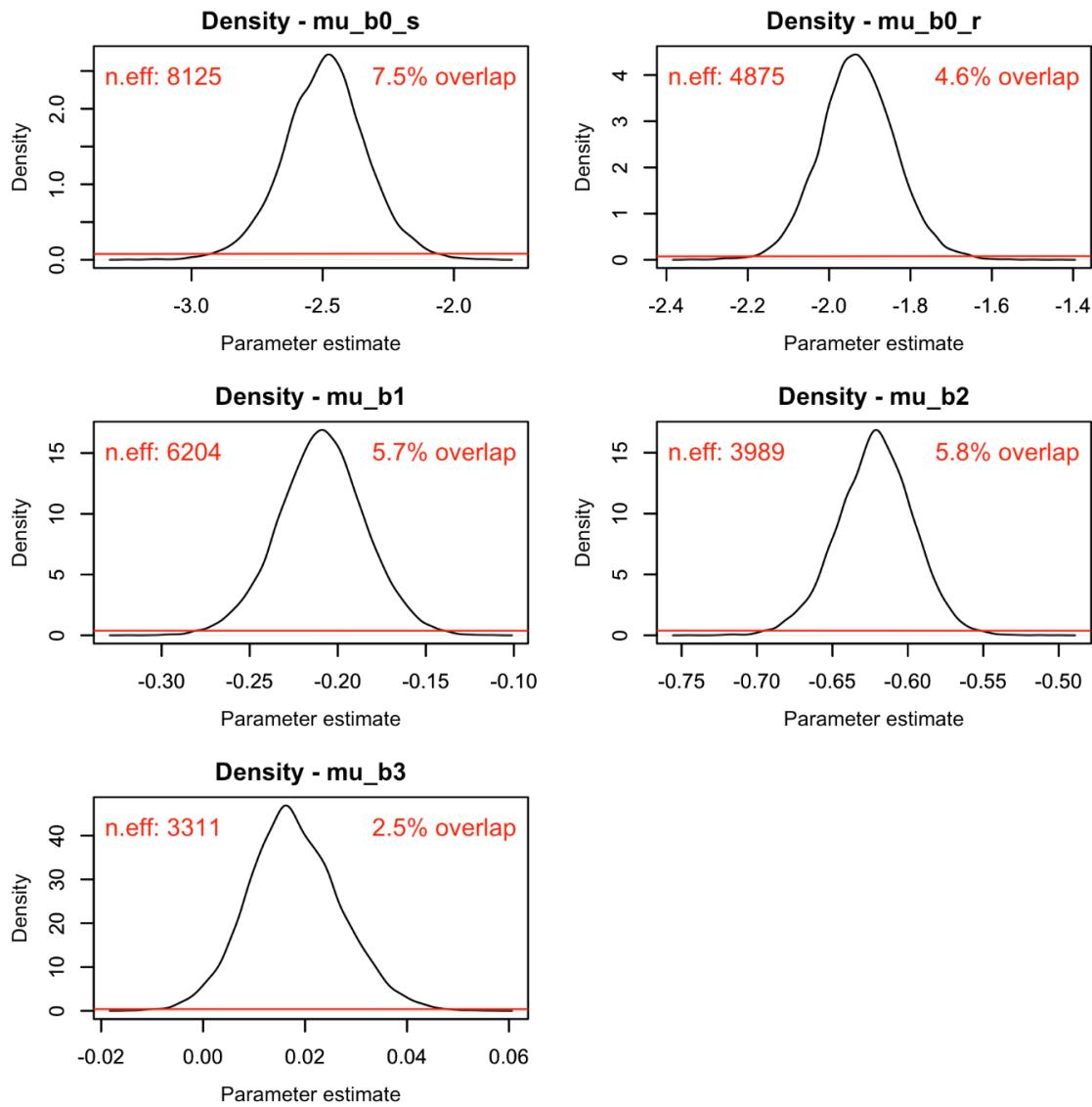


Fig. S19. Posterior (black) and prior distribution (red) for the global parameters in the model for metabolic rate, including their % overlap and effective sample size (n.eff).

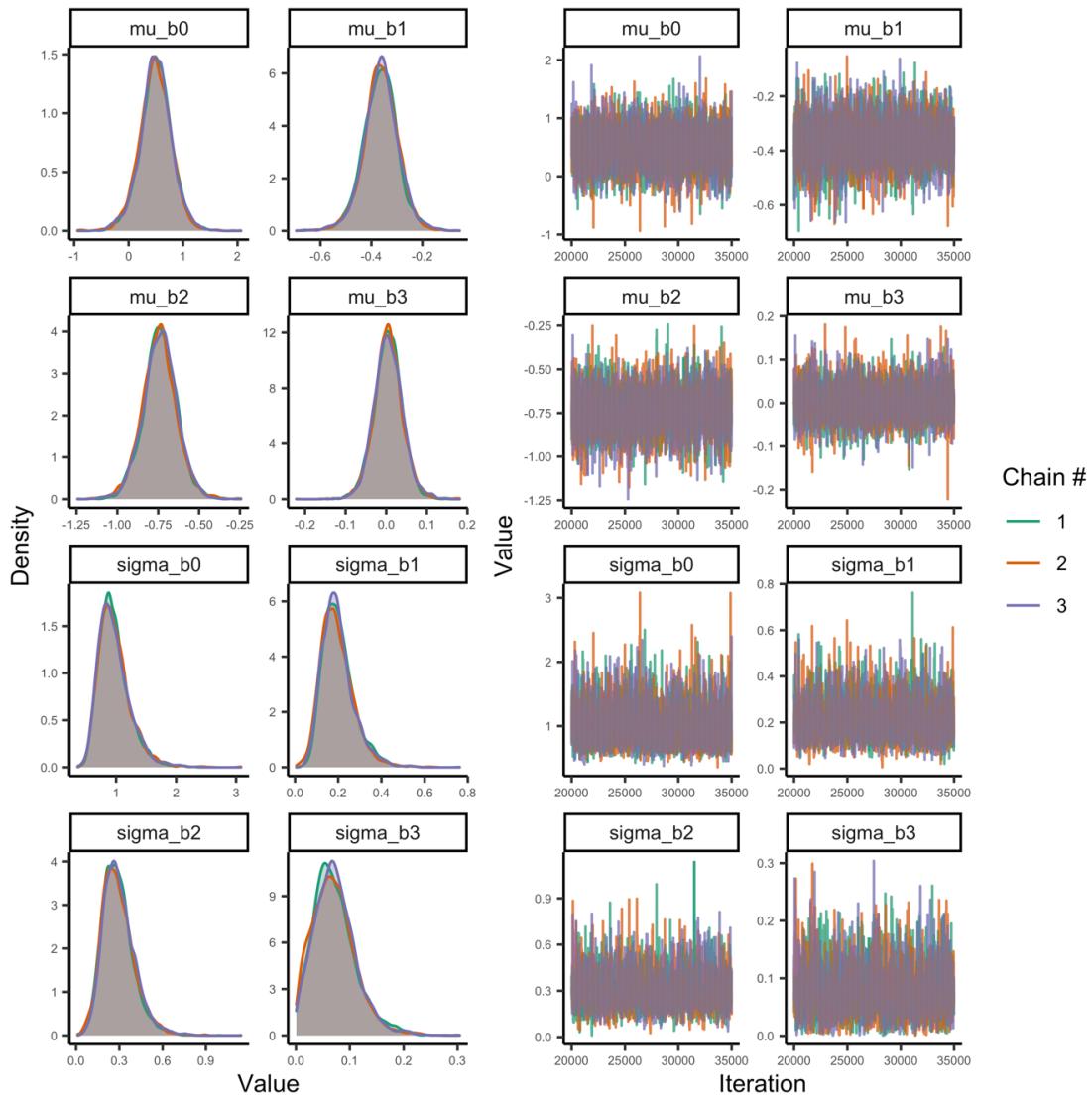


Fig. S20. Posterior densities and trace plots for evaluation of chain convergence (by chain, indicated by color), for the global-level parameters for the growth rate model at temperatures below optimum temperatures.

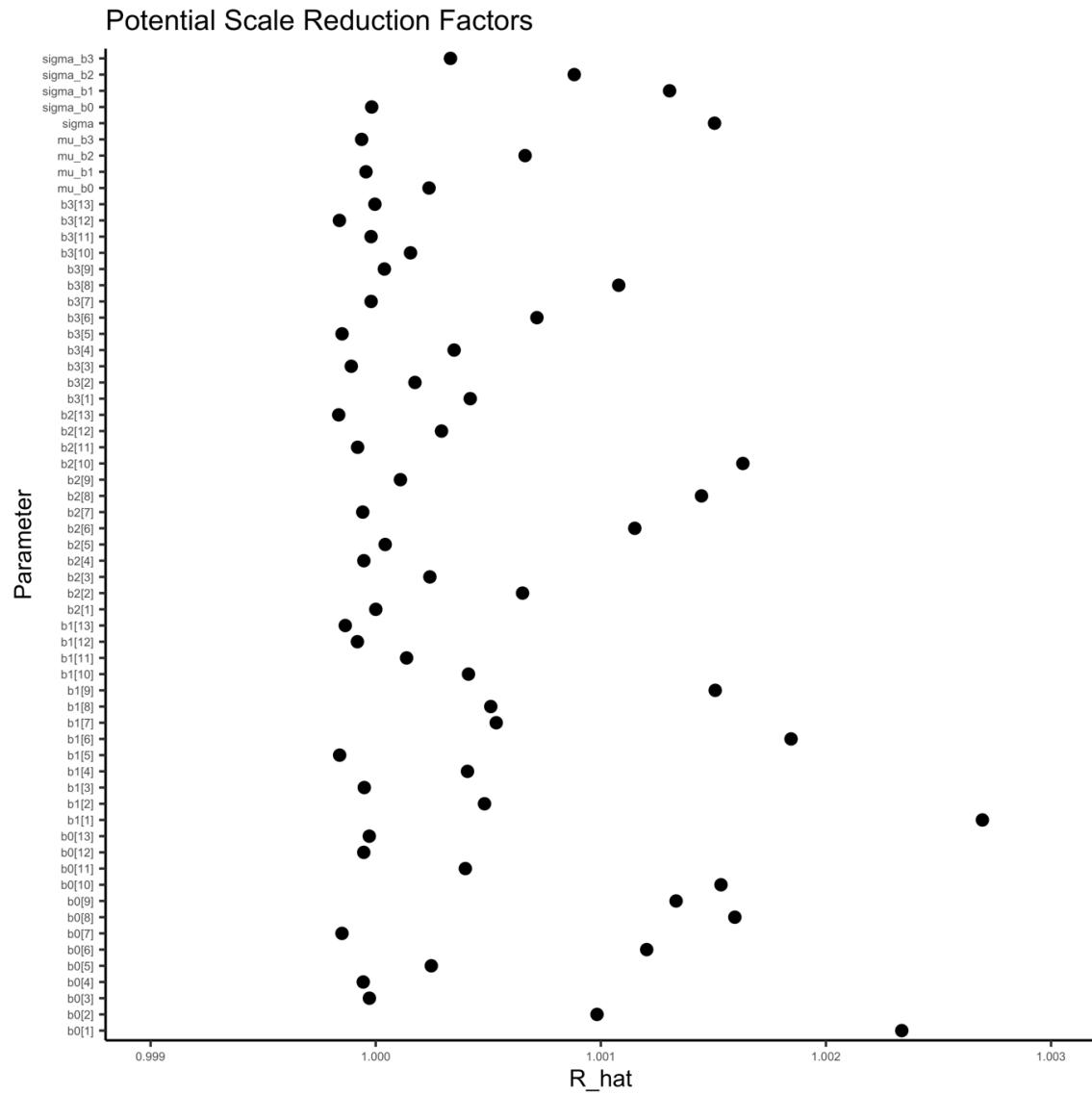


Fig. S21. Potential scale reduction factor (\hat{R}) for the growth rate model. This factor is based on the comparison of between and within-chain variation for the same parameter. A value close to one implies chains converged to the same distribution. The index of the parameter corresponds to species in alphabetical order.

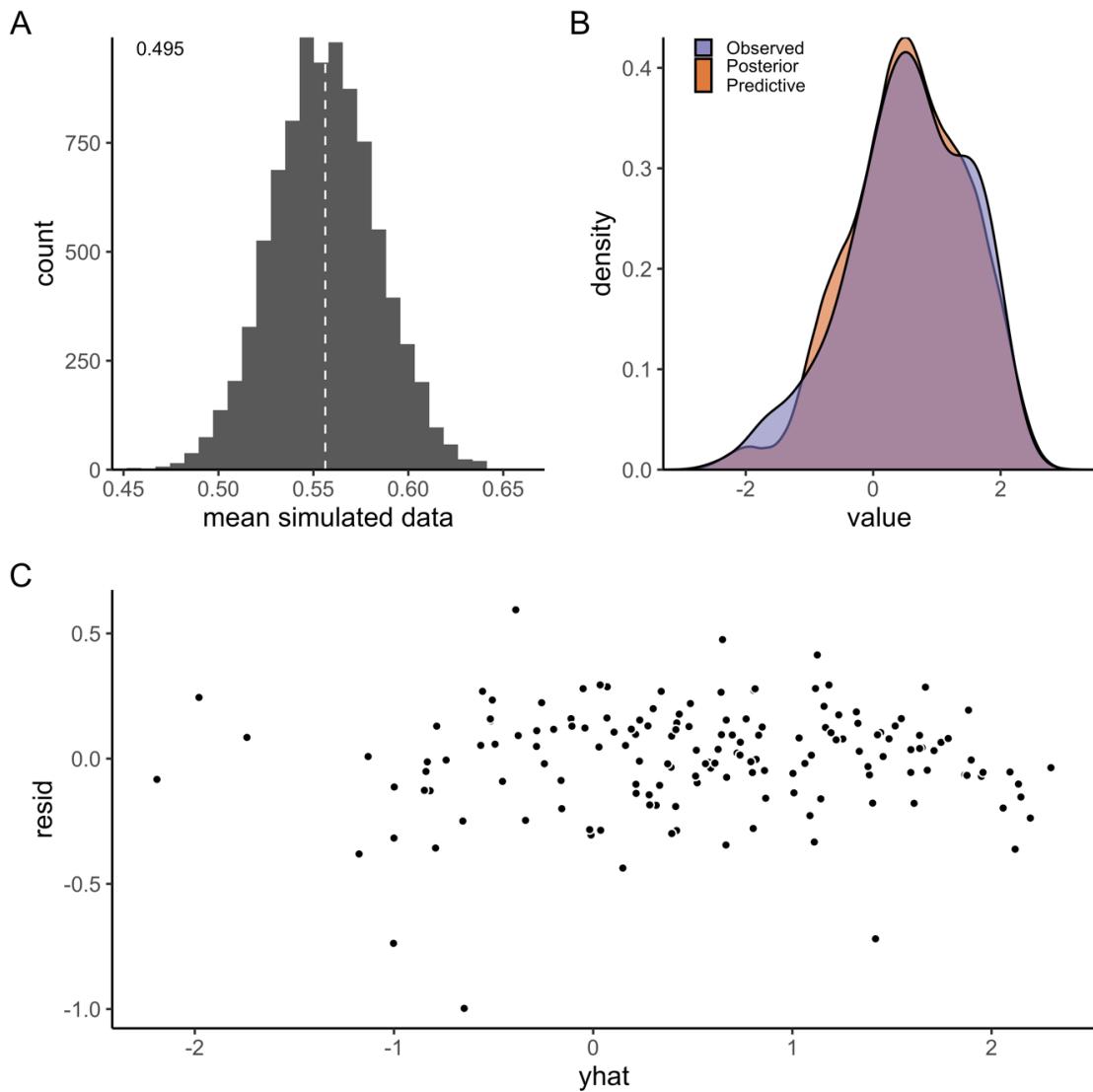


Fig. S22. A) Model fit (mean) for the model of growth at temperatures below temperature optimum (by species). Fit is evaluated by simulating data from the likelihood (at each iteration of the MCMC chain), to compare how well it matches the original data. Each simulated data point is assigned a 0 or 1 if it is below or above the mean data point (the vertical line corresponds to the mean in data). The number in the plot corresponds to the mean of the vector of 0's and 1's. B) Posterior predictive distribution (orange) and distribution of data (purple). C) Difference between the observed value and the posterior median of the predicted value, plotted against fitted value.

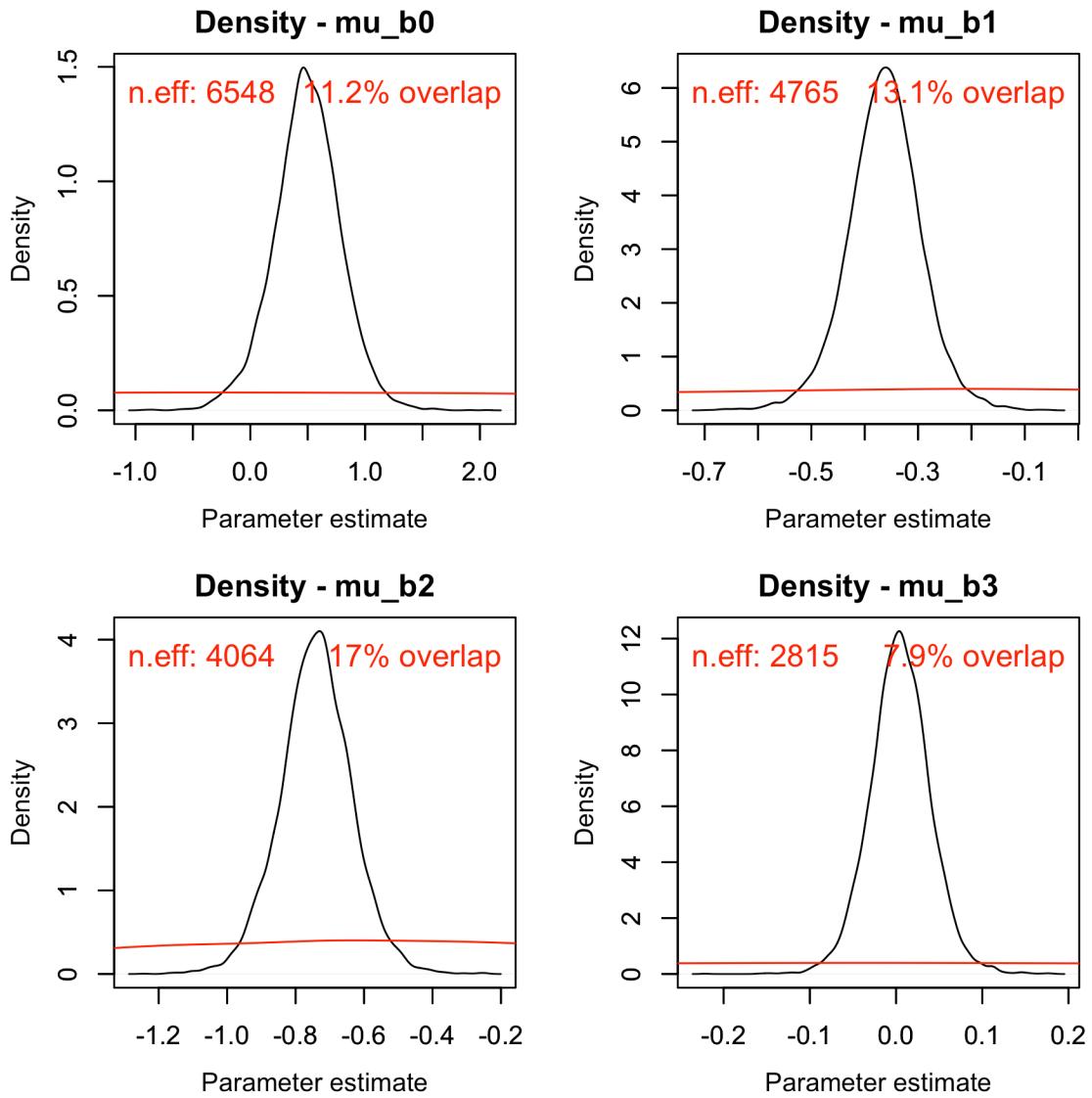


Fig. S23. Posterior (black) and prior distribution (red) for the global parameters in the model for growth rate, including their % overlap and effective sample size (n.eff).

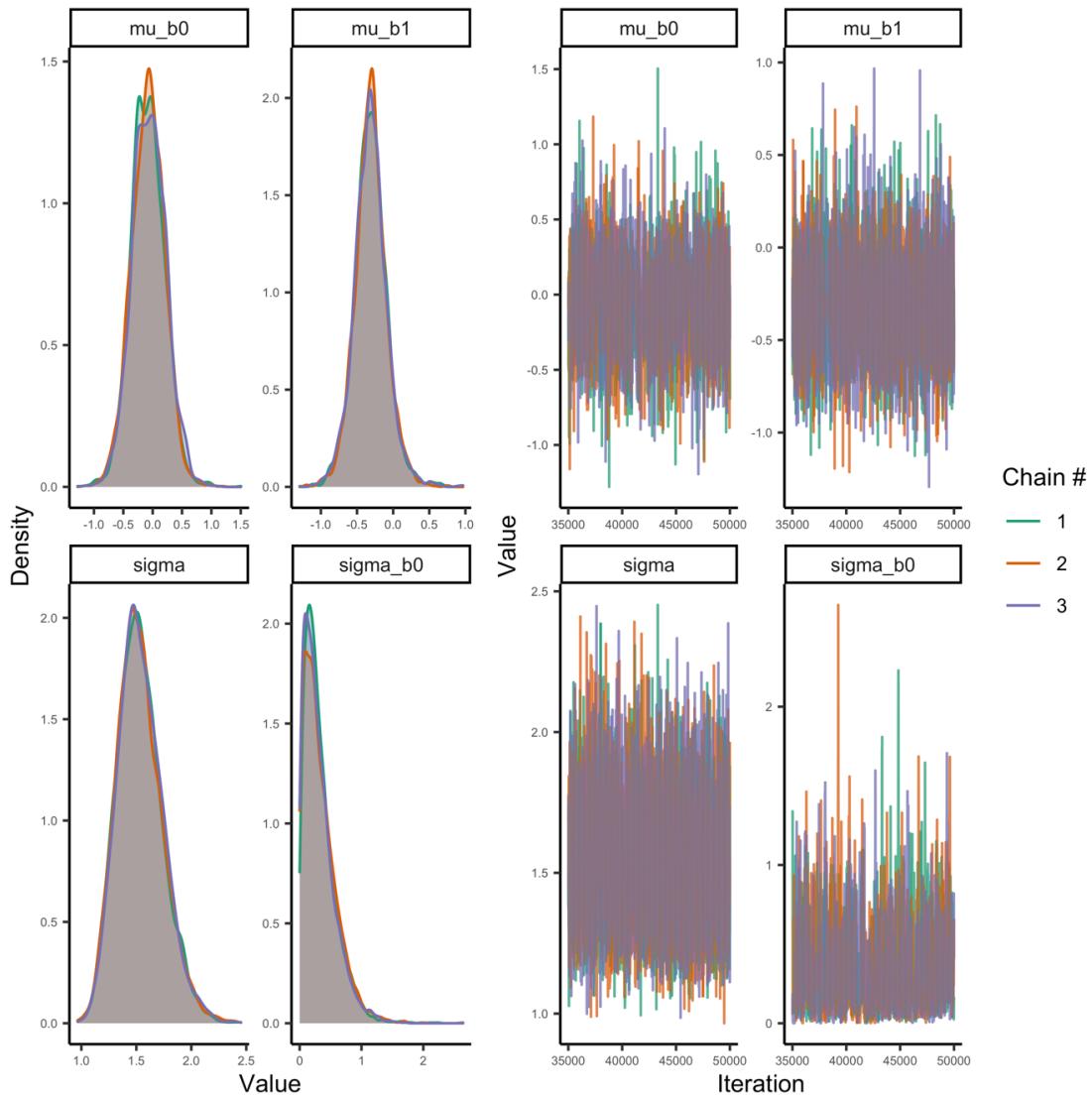


Fig. S24. Posterior densities and trace plots for evaluation of chain convergence (by chain, indicated by color), for the global-level parameters for the T_{opt} model.

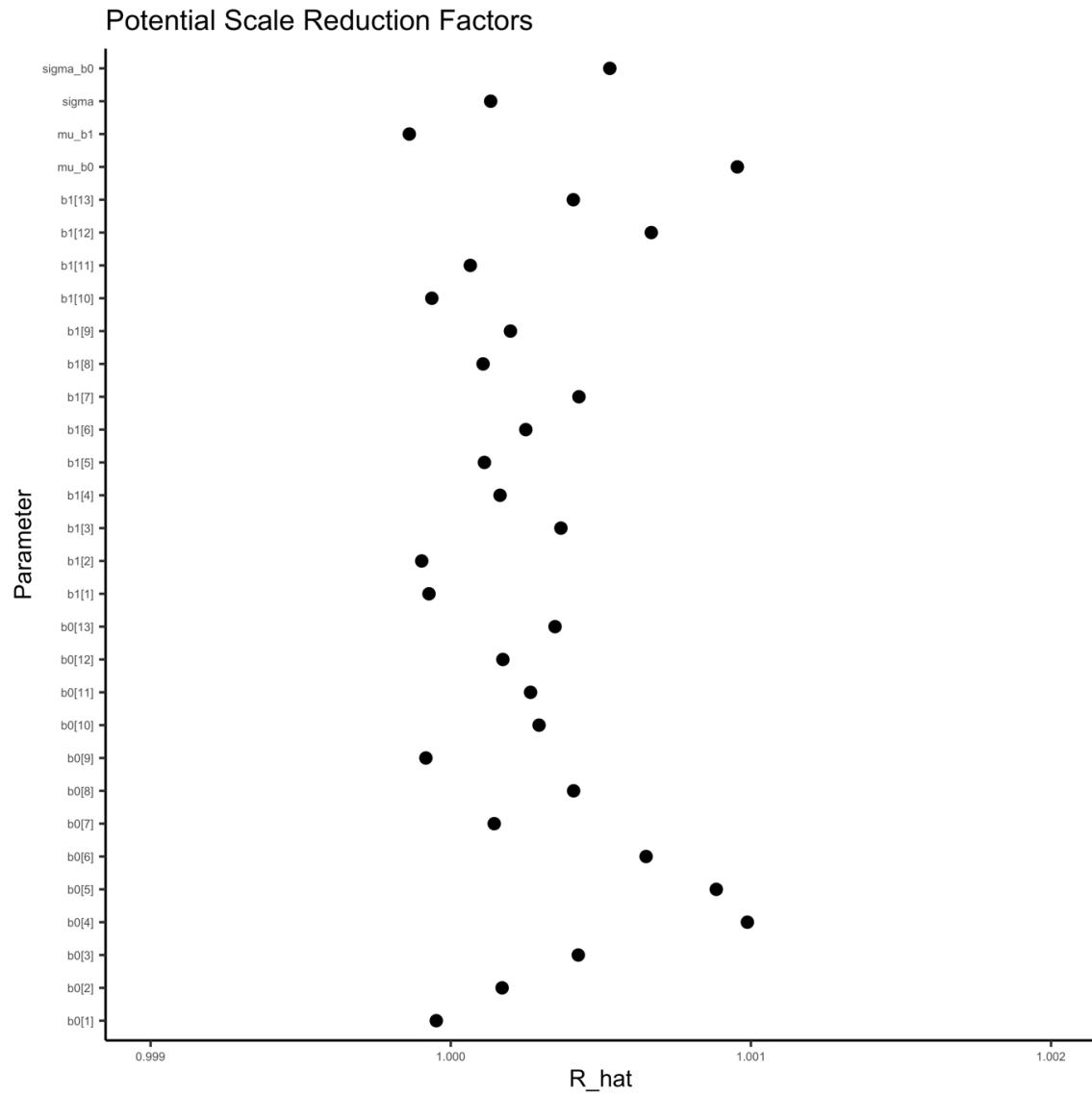


Fig. S25. Potential scale reduction factor (\hat{R}) for the T_{opt} model. This factor is based on the comparison of between and within-chain variation for the same parameter. A value close to one implies chains converged to the same distribution. The index of the parameter corresponds to species in alphabetical order.

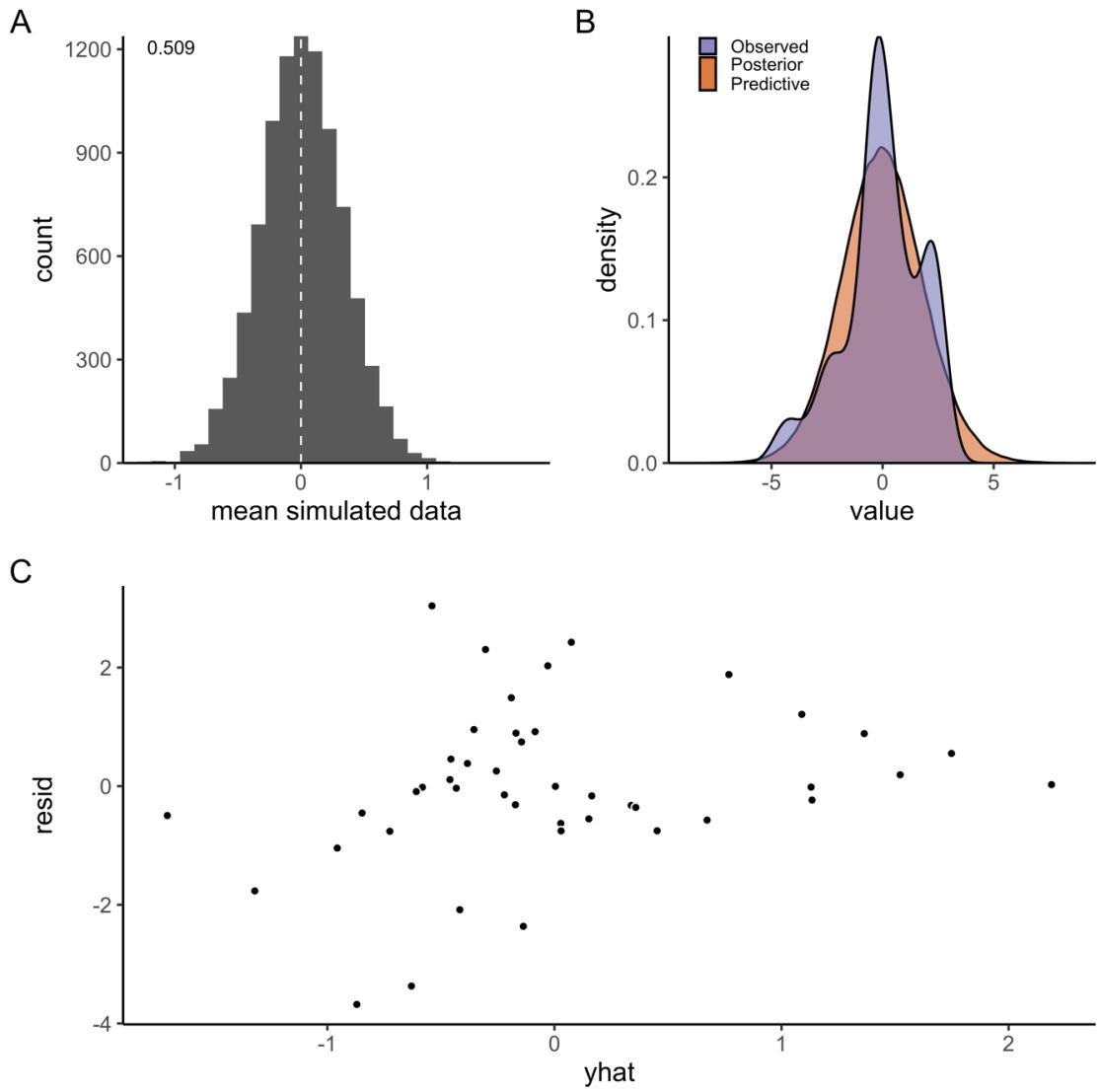


Fig. S26. A) Model fit (mean) for the model of optimum growth temperature as a function of body mass. Fit is evaluated by simulating data from the likelihood (at each iteration of the MCMC chain), to compare how well it matches the original data. Each simulated data point is assigned a 0 or 1 if it is below or above the mean data point (the vertical line corresponds to the mean in data). The number in the plot corresponds to the mean of the vector of 0's and 1's. B) Posterior predictive distribution (orange) and distribution of data (purple). C) Difference between the observed value and the posterior median of the predicted value, plotted against fitted value.

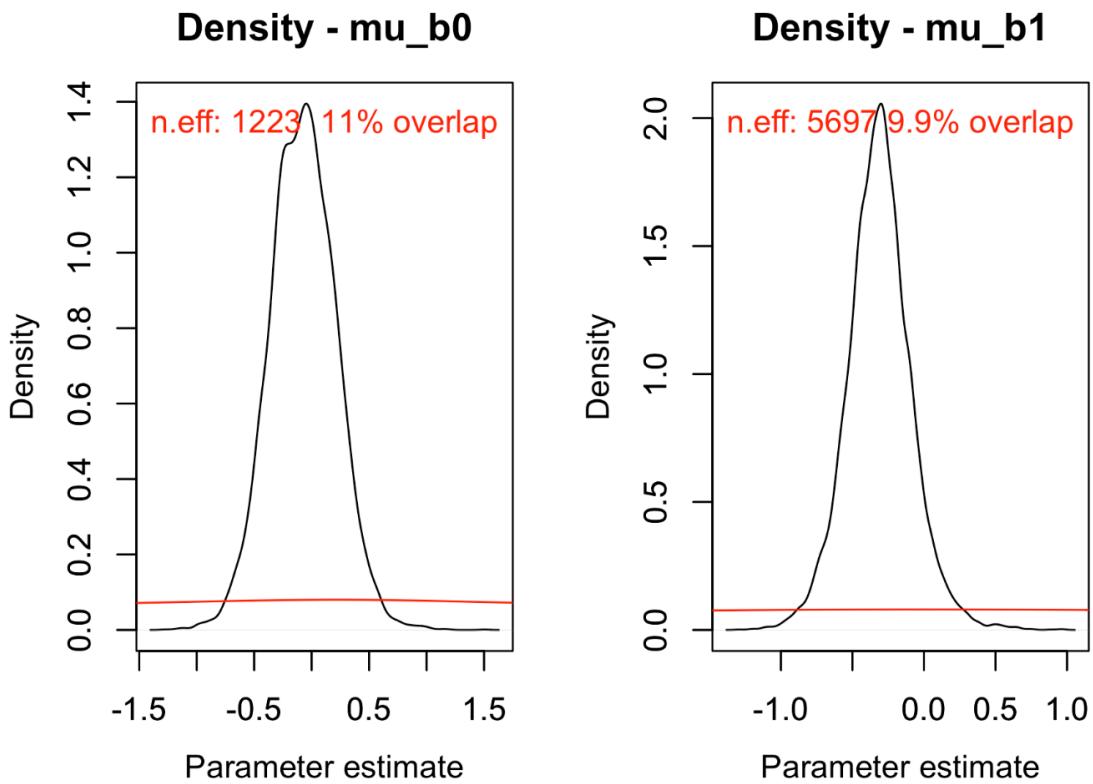


Fig. S27. Posterior (black) and prior distribution (red) for the global parameters in the model for T_{opt} , including their % overlap and effective sample size (n.eff).

Table S1. Explanation of data columns (G=growth data, T_{opt}=optimum growth temperature data, C=maximum consumption data, M=metabolism data).

Column	Explanation	Datasets
<i>growth_rate %/day</i>	Main response variable.	G, T _{opt}
<i>opt_temp_c</i>	Main response variable.	T _{opt}
<i>initial_mass_g</i>	Body mass [g] at the onset of the growth trial.	G, T _{opt}
<i>final_mass_g</i>	Body mass [g] at the end of the growth trial.	G, T _{opt}
<i>geom_mean_mass_g</i>	Geometric mean mass in t ₁ and t ₂ of the growth trial.	G, T _{opt}
<i>size_group</i>	Representative body mass of size group in the growth trial, in case initial, final or geometric body mass could not be retrieved.	G, T _{opt}
<i>consumption</i>	Main response variable.	C
<i>metabolic_rate</i>	Main response variable.	M
<i>type</i>	Type of respiration measurement (resting, routine, standard).	M
<i>unit</i>	Unit of response variable.	C, M
<i>original_unit</i>	Original unit of response variable. If different from “ <i>unit</i> ”, see “ <i>notes</i> ” column for information on conversion.	C, M
<i>mass_g</i>	Body mass in experiment [g]. Some studies report body masses before and some after the feeding trials. See “ <i>notes</i> ”.	C, M
<i>temp_c</i>	Experimental temperature [°C].	G, C, M
<i>above_peak_temp</i>	Is the experiment conducted at temperature above peak temperature for the given size group? Y/N.	G, C, M
<i>common_name</i>	Common name of species.	G, T _{opt} , C, M
<i>species</i>	Scientific name of species.	G, T _{opt} , C, M
<i>genus</i>	Genus of species.	G, T _{opt} , C, M
<i>family</i>	Family of species.	G, T _{opt} , C, M
<i>order</i>	Order of species.	G, T _{opt} , C, M
<i>habitat</i>	Species natural habitat, taken from FishBase (4).	G, T _{opt} , C, M
<i>lifestyle</i>	Lifestyle of species, taken from FishBase (4).	G, T _{opt} , C, M
<i>biogeography</i>	Biogeography of species, taken from FishBase (4).	G, T _{opt} , C, M
<i>trophic_level</i>	Trophic level of species, taken from FishBase (4).	G, T _{opt} , C, M
<i>w_maturity_g</i>	Body mass [g] at maturation taken from FishBase (4). If not available, weight was estimated from length using species-specific allometric weight-length, else taken from alternative sources (see “ <i>notes</i> ”). Used to estimate relative body size across species in the data and to normalize optimum growth temperatures across species.	G, T _{opt}

w_max_published_g	Max. published weight [g] taken from FishBase (4). If not available, weight was estimated from length using species-specific allometric weight-length, else taken from alternative sources (see " notes "). Used to estimate relative body size across species in the data.	G, T _{opt} , C, M
env_temp_min	Min. environmental temperature [°C], taken from FishBase (4). If not available on FishBase, data were taken from alternative sources (see " notes "). Used to compare experimental temperatures to common temperatures for species.	G, T _{opt} , C, M
env_temp_max	Max. environmental temperature [°C], taken from FishBase (4). If not available on FishBase, data were taken from alternative sources (see " notes "). Used to compare experimental temperatures to common temperatures for species.	G, T _{opt} , C, M
env_temp_mid	Median of environmental temperature [°C], taken from FishBase (4). If not available on FishBase, data were taken from alternative sources (see " notes "). Used to compare experimental temperatures to common temperatures for species.	G, T _{opt} , C, M
pref_temp_mid	Median of preferred temperature [°C], taken from FishBase (4). If not available on FishBase, data were taken from alternative sources (see " notes "). Used to compare experimental temperatures to common temperatures for species.	G, T _{opt} , C, M
notes	This column contains additional information, including if data were sent by authors, if any column above has data that is not from the main source (i.e. FishBase), how certain metrics were calculated, alternative common names, comments on the experimental protocol, information on conversion to standard " unit ", source of the data (literature search or cited in paper from literature search)	G, T _{opt} , C, M
reference	Source (See Table S2).	G, T _{opt} , C, M

Table S2. Species, common name, the data set(s) in which they appear and the sources (G=growth data, T_{opt}=optimum growth temperature data, C=maximum consumption data, M=metabolism data). If more than one data and source, the sources are in order (1 study per species and rate).

Species	Common name	Datasets	Source
<i>Pseudopleuronectes yokohamae</i>	Marbled flounder	G, T _{opt} , C	(5)
<i>Cyclopterus lumpus</i>	Lumpfish	G, T _{opt}	(6)
<i>Paralichthys olivaceus</i>	Japanese flounder (alt. bastard halibut, Japanese halibut or Olive flounder)	G, T _{opt} , C	(7)
<i>Salvelinus alpinus</i>	Arctic char	G, T _{opt}	(8)
<i>Salmo salar</i>	Atlantic salmon	G, T _{opt}	(9)
<i>Lates calcarifer</i>	Barramundi	G, T _{opt} , C, M	(10) (10) (10) (11)
<i>Gadus morhua</i>	Atlantic cod	G, T _{opt} , M	(12)(13)
<i>Hippoglossus hippoglossus</i>	Atlantic halibut	G, T _{opt}	(14)
<i>Scophthalmus maximus</i>	Turbot	G, T _{opt}	(15)
<i>Boreogadus saida</i>	Arctic cod	G, T _{opt}	(16)
<i>Rachycentron canadum</i>	Cobia	G, T _{opt} , C	(17)
<i>Pelteobagrus fulvidraco</i>	Yellow catfish	G, T _{opt} , C	(18)
<i>Anarhichas minor</i>	Spotted wolffish	G, T _{opt}	(19)
<i>Oncorhynchus mykiss</i>	Rainbow trout	C, M	(20)
<i>Perca fluviatilis</i>	Eurasian perch	C	(21)
<i>Phoxinus phoxinus</i>	Eurasian minnow	C, M	(22)
<i>Coregonus hoyi</i>	Bloater	C	(23)
<i>Pomoxis annularis</i>	White crappie	C	(24)
<i>Gambusia affinis</i>	Western mosquitofish	C	(25)
<i>Morone saxatilis</i>	Striped bass	C	(26)
<i>Salvelinus fontinalis</i>	Brook trout	C, M	(27) (28)
<i>Leuciscus leuciscus</i>	Dace	C	(29)
<i>Lepomis microlophus</i>	Redear sunfish	C	(30)
<i>Channa argus</i>	Chinese snakehead (alt. Northern snakehead or Snakehead)	C, M	(31) (32)
<i>Siniperca chuatsi</i>	Mandarin fish	C, M	(31) (32)
<i>Gasterosteus aculeatus</i>	Three-spined stickleback	C	(33)
<i>Salmo trutta</i>	Brown trout	C	(34)
<i>Epinephelus coioides</i>	Orange-spotted grouper	C	(35)
<i>Coregonus albula</i>	Vendace	M	(36)
<i>Coregonus fontanae</i>	Stechlin cisco	M	(36)
<i>Abramis brama</i>	Common bream	M	(36)
<i>Rutilus rutilus</i>	Common roach	M	(36)
<i>Salvelinus confluentus</i>	Bull trout	M	(37)
<i>Catostomus commersonii</i>	White sucker	M	(28)
<i>Cyprinus carpio</i>	Common carp	M	(28)
<i>Ameiurus nebulosus</i>	Brown bullhead	M	(28)
<i>Silurus meridionalis</i>	Southern catfish	M	(38)
<i>Carassius auratus</i>	Goldfish	M	(39)
<i>Pomadasys commersonii</i>	Spotted grunter	M	(40)

<i>Melanogrammus aeglefinus</i>	Haddock	M	(41)
<i>Centropristes striata</i>	Black sea bass	M	(42)
<i>Anguilla anguilla</i>	European eel	M	(43)
<i>Micropterus salmoides</i>	Largemouth bass	M	(44)
<i>Cyprinodon macularius</i>	Desert pupfish	M	(45)
<i>Micropogonias undulatus</i>	Atlantic croaker	M	(46)
<i>Leiostomus xanthurus</i>	Spot	M	(46)
<i>Coreius guichenoti</i>	Largemouth bronze gudgeon	M	(47)
<i>Sprattus sprattus</i>	European sprat	M	(48)
<i>Plectropomus leopardus</i>	Leopard coral grouper	M	(49)
<i>Galaxias maculatus</i>	Common galaxias	M	(50)
<i>Polyodon spathula</i>	American paddlefish (alt. Mississippi paddlefish)	M	(51)
<i>Argyrosomus japonicus</i>	Mulloway	M	(52)
<i>Lythrypnus dalli</i>	Bluebanded goby	M	(53)
<i>Collossoma macropomum</i>	Tambaqui (alt. Cachama)	M	(54)
<i>Carassius auratus grandoculis</i>	Round crucian carp (alt. Nigorobuna)	M	(55)

Table S3. Description of model parameters (type and their interpretation in brackets) and their prior distributions (see ‘Model description’ and equations 1-3 in the main text). N refers to a normal distribution (mean and standard deviation, s.d.) and U to a uniform distribution (interval). For simplicity, only the parameters of the full model are shown here (i.e., with most coefficients varying by species), but note that when a model is fitted with a common rather than species-varying coefficient, for example β_1 instead of $\beta_{1j} \sim N(\mu_{\beta_1}, \sigma_{\beta_1})$, we use the same prior for β_1 as for μ_{β_1} .

Model	Parameter	Description	Prior distribution
Log-linear regressions for growth, consumption and metabolism	$\mu_{\beta_{0s}}$	Hyperparameter (average intercept for standard metabolic rate across species) <i>Only for metabolism model.</i>	$N(-2, 5)$
	$\mu_{\beta_{0r}}$	Hyperparameter (average intercept for routine and resting metabolic rate across species). <i>Only for metabolism model.</i>	$N(-1, 5)$
	μ_{β_0}	Hyperparameter (average intercept across species). <i>Only for consumption and growth models.</i>	$N(0, 5)$
	μ_{β_1}	Hyperparameter (average mass coefficient across species)	$N(-0.25, 1)$
	μ_{β_2}	Hyperparameter (average temperature coefficient across species)	$N(-0.6, 1)$
	μ_{β_3}	Hyperparameter (average interaction coefficient across species)	$N(0, 1)$
	$\sigma_{\beta_{0s}}$	Hyperparameter (s.d. of species-intercepts for standard metabolic rate)	$U(0, 10)$
	$\sigma_{\beta_{0r}}$	Hyperparameter (s.d. of species-intercepts for routine and resting metabolic rate)	$U(0, 10)$
	σ_{β_1}	Hyperparameter (s.d. of species mass coefficients)	$U(0, 10)$
	σ_{β_2}	Hyperparameter (s.d. of species temperature coefficients)	$U(0, 10)$
	σ_{β_3}	Hyperparameter (s.d. of species interaction coefficients)	$U(0, 10)$
	σ	Parameter (s.d.)	$U(0, 10)$
Sharpe-Schoolfield (unimodal consumption data)	$\mu_{C_{0j}}$	Hyperparameter (average consumption at reference temperature [-10 on centered scale] across species)	$N(1, 1)$
	μ_{E_j}	Hyperparameter (average activation energy across species)	$N(0.5, 0.5)$
	E_h	Parameter (common rate of decline with temperature)	$N(2, 2)$
	T_h	Parameter (common temperature at which half the rate is reduced due to high temperatures)	$N(5, 2)$
	σ_{E_j}	Hyperparameter (s.d. of species-varying activation energies)	$U(0, 3)$
	$\sigma_{C_{0j}}$	Hyperparameter (s.d. of species-varying average consumption)	$U(0, 3)$
	σ	Parameter (s.d.)	$U(0, 3)$
Linear	μ_{β_0}	Hyperparameter (average intercept across species)	$N(0, 5)$

T_{opt} models	μ_{β_1}	Hyperparameter (average mass coefficient across species)	$N(0, 5)$
	σ_{β_0}	Hyperparameter (s.d. of species-intercepts)	$U(0, 10)$
	σ_{β_1}	Hyperparameter (s.d. of species mass coefficients)	$U(0, 10)$
	σ	Parameter (s.d.)	$U(0, 10)$

Table S4. Model comparison for the log-linear regressions of how consumption, metabolism and growth depend on mass and temperature below optimum temperatures (see ‘*Model description*’ and equations 1-3 in the main text). The column m*t indicates whether the model for the rate includes an interactive effect of mass and temperature. The models differ in which coefficients vary among species and which are common, where β_0 is the intercept, β_1 mass coefficient (mass-exponent on linear scale), β_2 temperature coefficient (corresponding to the negative activation energy) and β_3 interaction between mass and temperature. The WAIC columns shows ΔWAIC and absolute WAIC in brackets, rounded to the nearest decimal, where ΔWAIC is the difference between each models’ WAIC and the lowest WAIC across models. Bold indicates models with $\Delta\text{WAIC} < 2$.

Model	m*t	Species-varying parameter(s)	WAIC metabolism	WAIC consumption	WAIC growth
M1	Yes	$\beta_0, \beta_1, \beta_2, \beta_3$	0 (273.2)	4.3 (564.5)	0 (47.2)
M2		$\beta_0, \beta_1, \beta_2$	1.27 (274.5)	3.1 (563.4)	7.2 (54.4)
M3a		β_0, β_1	306.1 (579.3)	148.1 (708.4)	23.4 (70.6)
M3b		β_0, β_2	387.5 (660.7)	70.1 (630.4)	32.6 (79.8)
M4		β_0	649.6 (922.8)	189.9 (750.2)	43.5 (90.7)
M5		$\beta_0, \beta_1, \beta_2$	5.0 (278.2)	0 (560.2)	5.5 (52.7)
M6a	No	β_0, β_1	347.8 (621.0)	166.1 (726.3)	22.1 (69.3)
M6b		β_0, β_2	388.9 (662.1)	74.1 (634.4)	34.3 (81.5)
M7		β_0	682.2 (955.4)	213.9 (774.2)	44.9 (92.1)

Table S5. Comparison of the two models fitted to optimum growth temperature data. The WAIC columns shows Δ WAIC and absolute WAIC in brackets, rounded to the nearest decimal, where Δ WAIC is the difference between each models' WAIC and the lowest WAIC across models. Bold indicates models with Δ WAIC < 2.

Model	Species-varying parameter(s)	WAIC
M1	β_0, β_1	0 (177.3)
M2	β_0	1 (178.3)

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