Supplementary Information for:

No evidence that warmer temperatures are associated with selection for smaller body sizes

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Methods and Results of the full phylogenetic random regression model

The models presented in the main text contains a random term for species to account for differences in selection among species. We present here a full phylogenetic random regression model that separates out the phylogenetic component of this species effect, to account for any lack of independence originating from shared evolutionary history among the species in the dataset. We constructed this elaboration for Models 1 and 2 of the main text, as these are the core models of our analysis. We followed the general recommendations developed by [1] and [2] to construct the models. Below we describe the construction of the phylogeny, and construction and results from the full phylogenetic random regression model.

Phylogeny construction

We constructed a phylogeny for the species in our selection database. Our target species consisted of nine birds, seven fish, seven insects, five mammals, three reptiles, and one amphibian (Table S1). We used GenBank to obtain mitogenomes for each of the 32 target species (or a congeneric or confamilial, if the target species was not available) plus two Cnidarian outgroup taxa (*Acropora aculeus* and *Nematostella* sp.). After extracting five mitochondrial loci (CO1, CO2, CO3, COB, and ND2), we aligned locus-specific alignments with MAFFT v7.215 [3]) in Geneious [4]. We used PartitionFinder2 [5] to determine optimal partitioning schemes and models of sequence evolution; GTR+G was used for all genes. We constrained the tree with a series of monophyletic statements and ran 10^7 MCMC generations with a linked clock and tree model in BEAST2 [6] via the CIPRES Science Gateway v. 3.3 [7]. We then used TreeAnnotator v.1.10 [6] with a 5% burn-in to get a single best tree with mean node heights and visualized the tree in FigTree v1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/). The tree was made ultrametric using the *compute.brlen* function in the R package *ape* [8]. The phylogeny is provided as a .nex file.

Meta-analytical model

Our phylogenetic random regression extension of Models 1 and 2 in the main text took the form

$$\beta_{ijk} = A + B\ t_{ijk} + \left(a_j + b_j.t_{ijk}\right) + \left(sp_k + sp\_b_k.t_{ijk}\right) + \left(sn_k + sn\_b_k.t_{ijk}\right) + \epsilon_{ijk} + e_{ijk},$$

where, as before: β_{ijk} is the i^{th} selection coefficient estimate for dataset j in species k; A and B are the fixed effect intercept and slope, respectively, of the regression of selection coefficients on annual temperature values, t_{ijk}; ϵ_{ijk} are measurement errors, $\epsilon_{ijk} \sim N\left(0, SE_{ijk}^2\right)$; and e_{ijk} are residuals distributed as $e_{ijk} \sim N(0, \sigma_e^2)$. In addition, this model contains the random intercepts sp_k and slopes sp_b_k for the phylogenetic component of the species effect, distributed as:

$$\begin{bmatrix} sp_k \\ sp\_b_k \end{bmatrix} \sim N\left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma_{sp}^2 & \sigma_{sp,sp\_b} \\ \sigma_{sp,sp\_b} & \sigma_{sp\_b}^2 \end{bmatrix}\right),$$

and intercepts and slopes sn_k and sn_b_k for the non-phylogenetic component of the species effect (with equivalent variances and covariance σ_{sn}^2, $\sigma_{sn\_b}^2$ and σ_{sn,sn_b}^2).

As above, the model was implemented in the R package MCMCglmm [9]. The prior and model were specified as follows:

```
 prior_PhyloRR=list(R=list(V=1,nu=0.002),
G=list(G1=list(V=diag(2),n=1,alpha.mu=rep(0,2),alpha.V=diag(2)*1000),
                                              G2=list(V=diag(1),n=0.002),
                                              G3=list(V=diag(1),n=0.002)))

model_PhyloRR<- MCMCglmm(estSelCoef~1+ envMeanCenter,
random=~us(1+envMeanCenter):dataset+Species+SpeciesPermEnv, mev=mev
,data=d_grads_time_ses_size_anim
,ginverse=list(Species=Ainv.UM),prior=pr_ Prior
,nitt=2600000,thin=2000,burnin=600000,verbose=FALSE)
```

All autocorrelation values were <0.05.

Results

The results from the phylogenetic random regression were qualitatively the same as those presented in the main text. In particular, there was no evidence of an effect of temperature on either selection gradients (Table S3a) or selection differentials (Table S3b). There was also no support for any phylogenetic component to the species effect, nor for any variance in slopes or intercepts within either the phylogenetic or non-phylogenetic species effects for selection gradients (Table S3a) or differentials (Table S3b). The only exception from these phylogenetically informed results is that, although the estimates of the fixed effect intercepts are very similar (gradients 0.129, differentials 0.221 here; gradients 0.107, differentials 0.156 in the main text), the 95% CIs are considerably wider and hence span zero, reflecting the greater degree of uncertainty in the models incorporating phylogenetic effects.

Supplementary Tables

Table S1. Taxa included in the phylogenetic analysis, with GenBank accession numbers.

Group	Target Species	Sequence used	GenBank Accession	Sequence length
Amphibian	*Bufo valliceps*	*Bufo stejnegeri*	KR136211.1	17939
Bird	*Petrochelidon pyrrhonota*	*Cecropis daurica*	KJ499911.1	17949
Bird	*Parus caeruleus*	*Cyanistes cyanus*	KX388472.1	16788
Bird	*Ficedula albicollis*	*Ficedula albicollis*	KF293721.1	16787
Bird	*Malurus cyaeneus*	*Malurus melanocephalus*	KJ909199.1	15568
Bird	*Parus major*	*Parus major*	NC_026293.1	16776
Bird	*Setophaga caerulescens*	*Setophaga coronata*	FJ236285.1	15583
Bird	*Spheniscus magellanicus*	*Spheniscus magellanicus*	KU361806.1	16659
Bird	*Tachycineta bicolor*	*Tachycineta bicolor*	JQ071614.1	17945
Bird	*Zosterops lateralis chlorocephalus*	*Zosterops lateralis*	KC545407.1	17821
Cnidarian	*Acropora aculeus*	*Acropora aculeus*	NC_029251.1	18528
Cnidarian	*Nematostella*	*Nematostella sp*	DQ643835.1	16389
Fish	*Esox lucius*	*Esox lucius*	AP004103.1	16695
Fish	*Oncorhynchus kisutch*	*Oncorhynchus kisutch*	MF621751.1	16660
Fish	*Oncorhynchus mykiss*	*Oncorhynchus mykiss*	MF621750.1	16660
Fish	*Oncorhynchus nerka*	*Oncorhynchus nerka*	EF055889.1	16658
Fish	*Oncorhynchus tshawytscha*	*Oncorhynchus tshawytscha*	AF392054.1	16644
Fish	*Salmo salar*	*Salmo salar*	AF133701.1	16669
Fish	*Salmo trutta*	*Salmo trutta*	AM910409.1	16687
Insect	*Aquarius remigis*	*Aquarius paludum*	FJ456944.1	15380
Insect	*Calopteryx splendens*	*Atrocalopteryx melli*	MG011692.1	15562
Insect	*Tetraneura sorini*	*Eriosoma lanigerum*	KP722582.1	15640
Insect	*Ischnura elegans*	*Ischnura elegans*	KU958378.1	15962
Insect	*Oecanthus nigricornis*	*Oecanthus sinensis*	KY783908.1	16142
Insect	*Psilocorsis quercicella*	*Promalactis suzukiella*	KM875542.1	15507
Insect	*Scathophaga stercoraria*	*Scathophaga stercoraria*	KM200724.1	16223
Mammal	*Cervus elaphus*	*Cervus elaphus*	AB245427.2	16357
Mammal	*Crocidura russula*	*Crocidura russula*	NC_006893.1	17202
Mammal	*Chionomys nivalis*	*Microtus fortis*	JF261174.1	16310
Mammal	*Mirounga leonina*	*Mirounga leonina*	AM181023.1	16079
Mammal	*Ovis aries*	*Ovis aries*	NC_001941.1	16616
Reptile	*Anolis sagrei*	*Anolis carolinensis*	EU747728.2	17223
Reptile	*Lacerta agilis*	*Lacerta agilis*	NC_021766.1	17089
Reptile	*Nerodia sipedon*	*Nerodia sipedon*	JF964960.1	17706

Table S2. Full output from the meta-analytical models reported in the main text (Models 1 and 2), relating (2a) selection gradients and (2b) selection differentials to annual mean temperature. See Methods for full details of the model, which is set out in equation (2). Because effects of temperature may vary between study populations, we consider variation in slopes with temperature within each data-set, but there is no indication of any such variance in either gradients of differentials. Values shown are means of posterior distributions along with their 95% credible intervals.

Table S3a Selection gradients

Terms	**Intercepts**	**Slopes (on temperature)**
Random effects	*variance*	*covariance/variance*
data-set	σ_a^2=0.00078 (0.00015, 0.001572)	$\sigma_{a,b}$= -0.00051 (-0.00109, 0.00002) σ_b^2= 0.0010560 (0.00026, 0.00202)
species	σ_s^2= 0.01449 (0.00362, 0.02889)	
residual	σ_e^2= 0.01179 (0.01044, 0.01328)	
Fixed effects		
Intercept (A)	0.10784 (0.05084, 0.16778)	
Slope (B)	-0.00384 (-0.02012, 0.00879)	

Table S2b Selection differentials

Terms	**Intercepts**	**Slopes (on temperature)**
Random effects	*variance*	*covariance/variance*
data-set	σ_a^2=0.00033 (0.00000, 0.00081)	$\sigma_{a,b}$= -0.00001 (-0.00023,0.00020) σ_b^2= 0.00009 (0.00000,0.00033)
species	σ_s^2=0.03038 (0.00908, 0.05885)	
residual	σ_e^2=0.00249 (0.001925, 0.00316)	
Fixed effects		
Intercept (A)	0.15618 (0.07347, 0.25398)	
Slope (B)	0.00017 (-0.00868, 0.00829)	

Table S3. Results from the full meta-analytical phylogenetic random regression model relating (3a) selection gradients and (3b) selection differentials to annual mean temperature. For each of the three random effects of data-set, phylogenetic species effect (‘species:phylo’) and non-phylogenetic species effect (‘species:non-phylo’), the table shows the variance-covariance values for intercepts and slopes. Values shown are means of posterior distributions along with their 95% credible intervals.

Table S3a Selection gradients

Terms	**Intercepts**	**Slopes (on temperature)**
Random effects	*variance*	*covariance/variance*
data-set	σ_a^2= 0.000811 (0.00000, 0.001862)	$\sigma_{a,b}$= -0.000507 (-0.001351, 0.000256) σ_b^2= 0.001456 (0.000262, 0.002883)
species:phylo	σ_{sp}^2= 0.013811 (0.00000, 0.055788)	σ_{sp,sp_b}= -0.003459 (-0.024228, 0.010307) $\sigma_{sp\_b}^2$= 0.008642 (0.00000, 0.034667)
species:non-phylo	σ_{sn}^2= 0.015104 (0.001359, 0.031904)	σ_{sn,sn_b}= -0.006676 (-0.023249, 0.002748) $\sigma_{sn\_b}^2$= 0.007585 (0.00000, 0.028581)
residual	σ_e^2= 0.015418 (0.013401, 0.017394)	
Fixed effects		
Intercept (A)	0.129 (-0.057, 0.280)	
Slope (B)	0.079 (-0.229, 0.056)	

Table S3b Selection differentials

Terms	**Intercepts**	**Slopes (on temperature)**
Random effects	*variance*	*covariance/variance*
data-set	σ_a^2= 0. 000416 (0.00000, 0. 001003)	$\sigma_{a,b}$= 0. 000004 (-0. 000212, 0. 000219) σ_b^2= 0. 000071 (0. 000000, 0. 000266)
species:phylo	σ_{sp}^2= 0. 069346 (0.00000, 0. 21254)	σ_{sp,sp_b}= -0. 006309 (-0. 072251, 0. 028905) $\sigma_{sp\_b}^2$= 0. 024197 (0.00000, 0. 096782)
species:non-phylo	σ_{sn}^2= 0. 023494 (0.000002, 0. 067463)	σ_{sn,sn_b}= -0. 002173 (-0. 023711, 0. 016987) $\sigma_{sn\_b}^2$= 0.00014379 (0.00000, 0. 053242)
residual	σ_e^2= 0. 001832 (0. 001318, 0. 00233)	
Fixed effects		
Intercept (A)	0.221 (-0.087, 0.635)	
Slope (B)	0.025 (-0.239, 0.185)	

Supplementary Figures

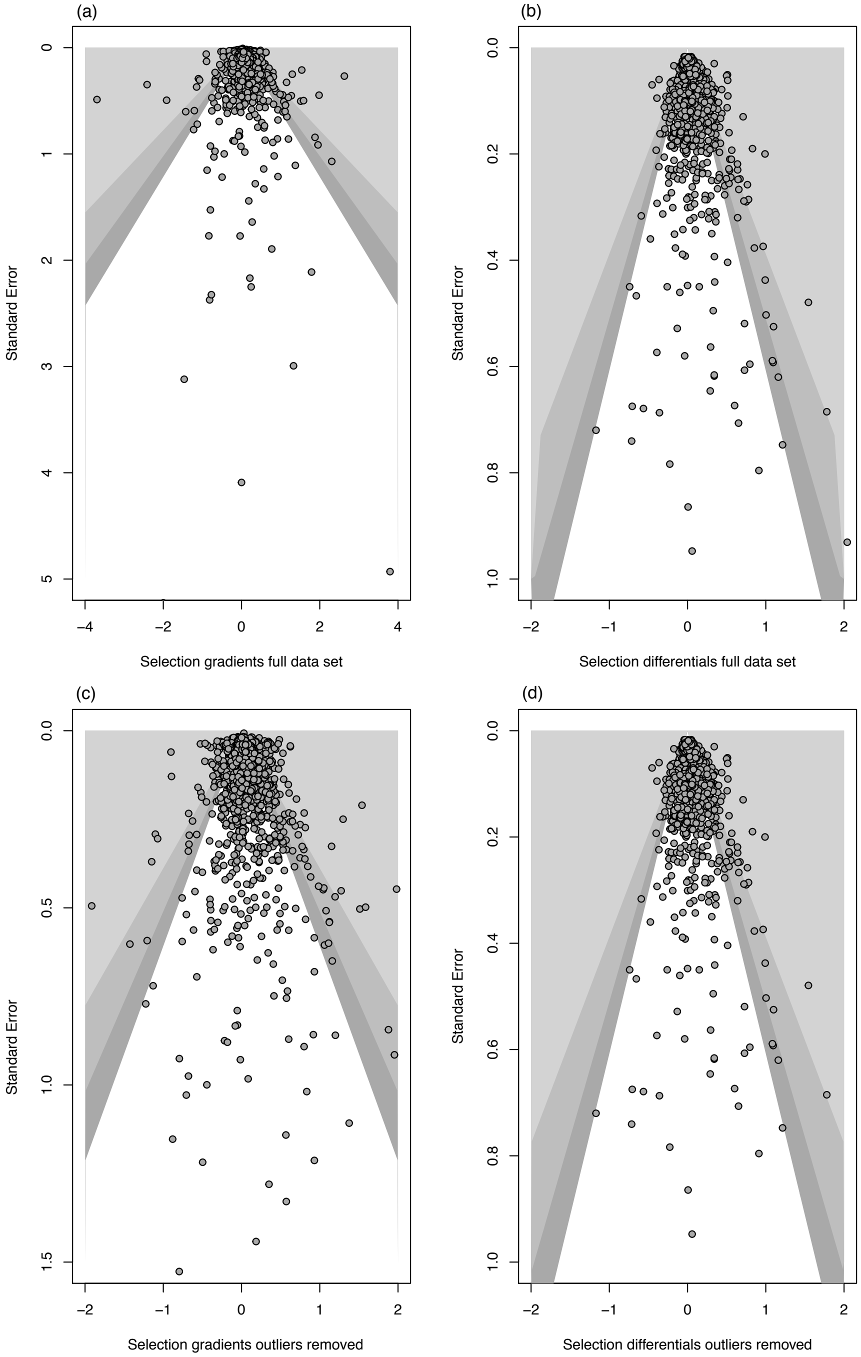

Figure S1. Funnel plots for selection gradients and differentials in the full data sets (a and b, gradients and differentials, respectively), and with large outliners removed to show more of the data (c and d, gradient and differentials, respectively. In all cases, there is no strong evidence for publication bias as the distributions of selection coefficients and their standard errors generate funnels that are all largely symmetrical. Each point is an individual selection coefficient and its corresponding standard error.

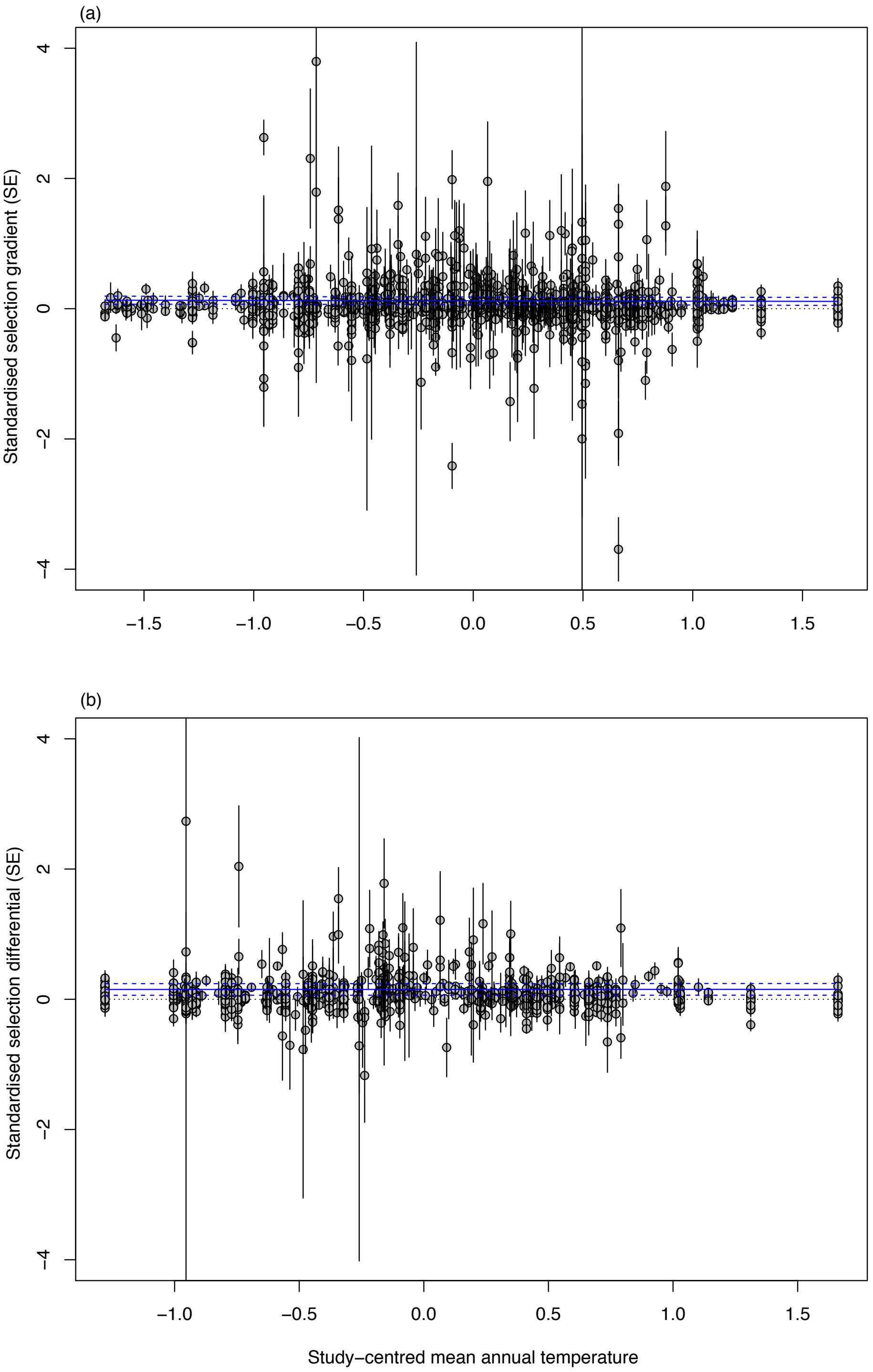

Figure S2. The full data set from figure 1 in the main text, showing large outliers.

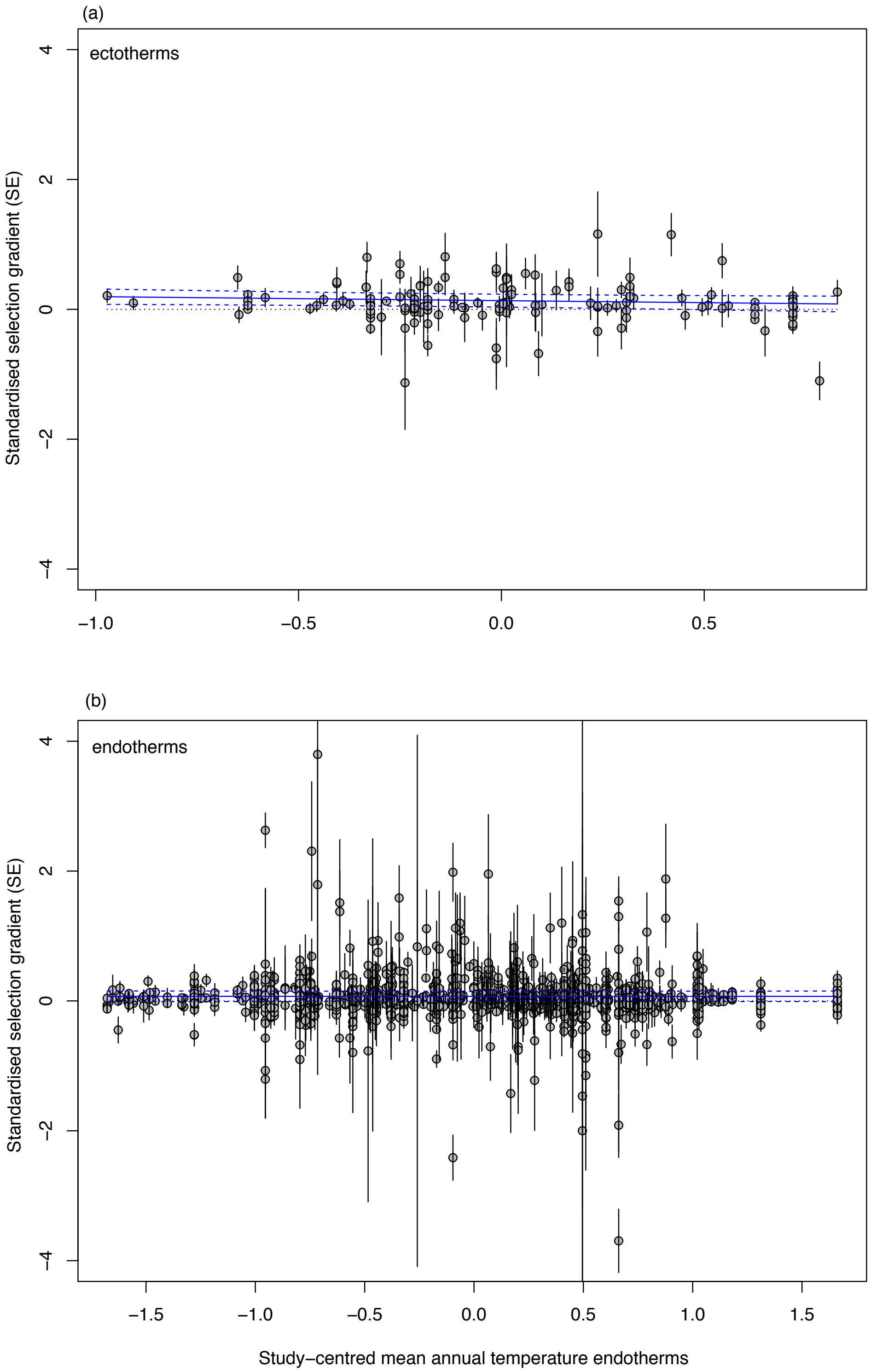

Figure S3. The full data set from figure 2 in the main text, showing large outliers.

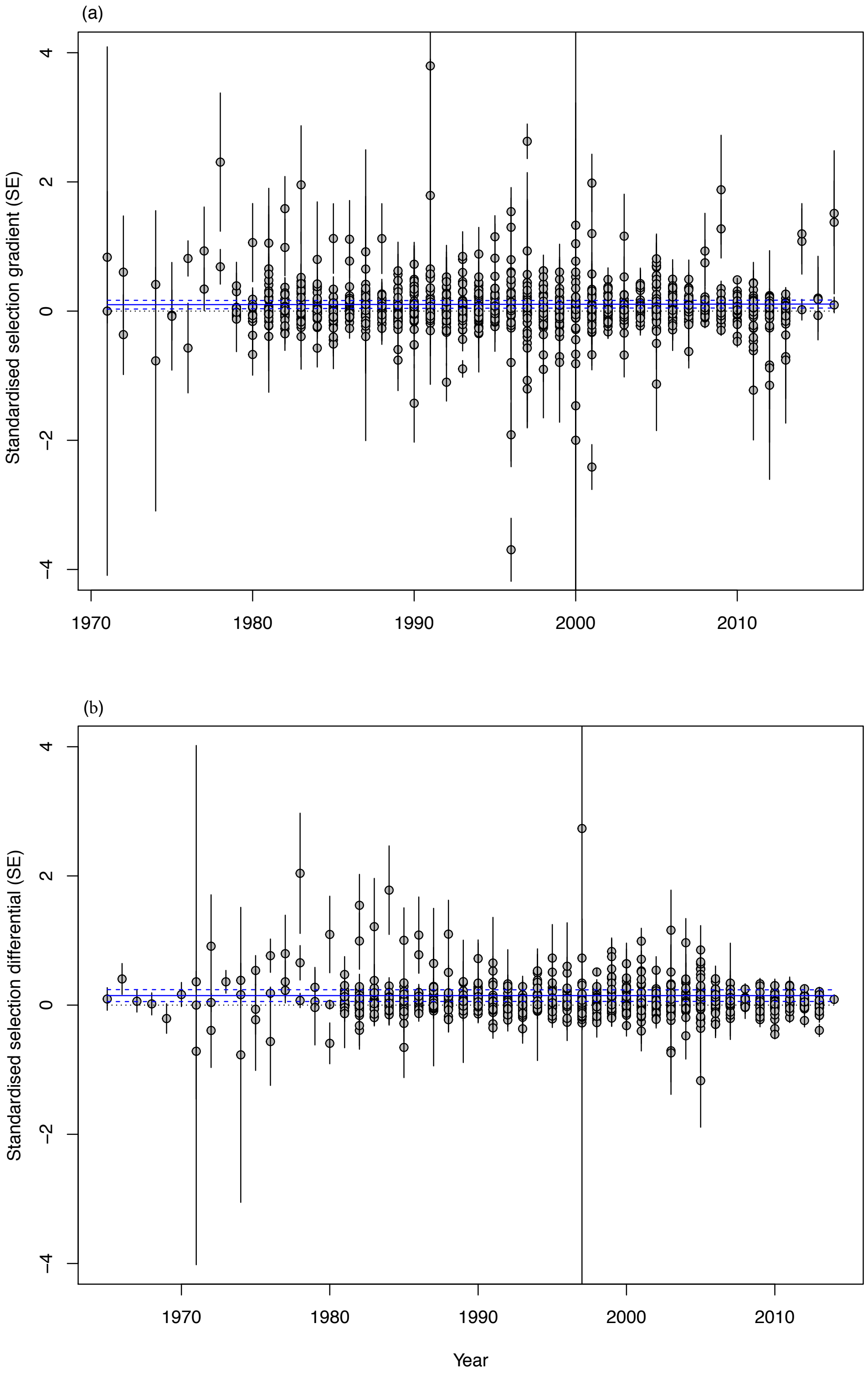

Figure S4. The full data set from figure 3 in the main text, showing large outliers.

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