

## Supplementary Information

Deep biogeographic barriers explain divergent global vertebrate communities

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**Supplementary Table 1: Functional traits used, and phylogenetic signal of these traits.** Blomberg's K is a metric of phylogenetic signal for continuous traits where 0 indicates no phylogenetic signal (complete randomness) and 1 indicates phylogenetic signal consistent with Brownian motion. Blomberg's K is shown for diet traits and bird foraging strata, where data are percentages used by a species, and for log body mass. Fritz & Purvis' D statistic is a similar metric of phylogenetic signal for binary traits. The D statistic, rescaled to allow comparison with K, is shown for mammal foraging strata, a categorical trait. Statistical significance was calculated by using randomization tests with 1,000 permutations for each trait. All traits have significant phylogenetic signal ( $K$  or  $D > 0$ ), but some traits are relatively evolutionarily labile ( $K$  or  $D < 1$ ), while other traits are phylogenetically conserved ( $K$  or  $D > 1$ ).

	Functional trait	Mammal	Bird
Diet	<i>Fish</i>	0.049 ( $p = 0.004$ )	0.657 ( $p < 0.001$ )
	<i>Fruit</i>	0.339 ( $p < 0.001$ )	0.511 ( $p < 0.001$ )
	<i>Other plant parts</i>	0.541 ( $p < 0.001$ )	0.969 ( $p < 0.001$ )
	<i>Invertebrates</i>	1.053 ( $p < 0.001$ )	0.949 ( $p < 0.001$ )
	<i>Nectar</i>	0.116 ( $p < 0.001$ )	1.744 ( $p < 0.001$ )
	<i>Carrion</i>	0.491 ( $p < 0.001$ )	0.798 ( $p < 0.001$ )
	<i>Seeds</i>	0.302 ( $p < 0.001$ )	0.632 ( $p < 0.001$ )
	<i>Vertebrates</i>	0.192 ( $p < 0.001$ )	0.809 ( $p < 0.001$ )
Foraging stratum	<i>Aerial</i>	1.345 ( $p < 0.001$ )	0.645 ( $p < 0.001$ )
	<i>Aquatic</i>	-	1.505 ( $p < 0.001$ )
	<i>Arboreal</i>	1.190 ( $p < 0.001$ )	-
	<i>Canopy</i>	-	0.496 ( $p < 0.001$ )
	<i>Ground</i>	1.202 ( $p < 0.001$ )	0.772 ( $p < 0.001$ )
	<i>Scansorial</i>	0.970 ( $p < 0.001$ )	-
	<i>Understory</i>	-	0.260 ( $p < 0.001$ )
	Log body mass	0.547 ( $p < 0.001$ )	7.929 ( $p < 0.001$ )

**Supplementary Table 2: Additional variables besides climate and biogeographic isolation.** For each variable, a model was run with that particular variable and the climate variables. We then compared the results to a model that only included climate. Variables that explained >1% of additional variance in comparison to the climate-only model, indicated by (\*), were included in final analyses. We ran models on species richness (SR) and functional richness (FR).

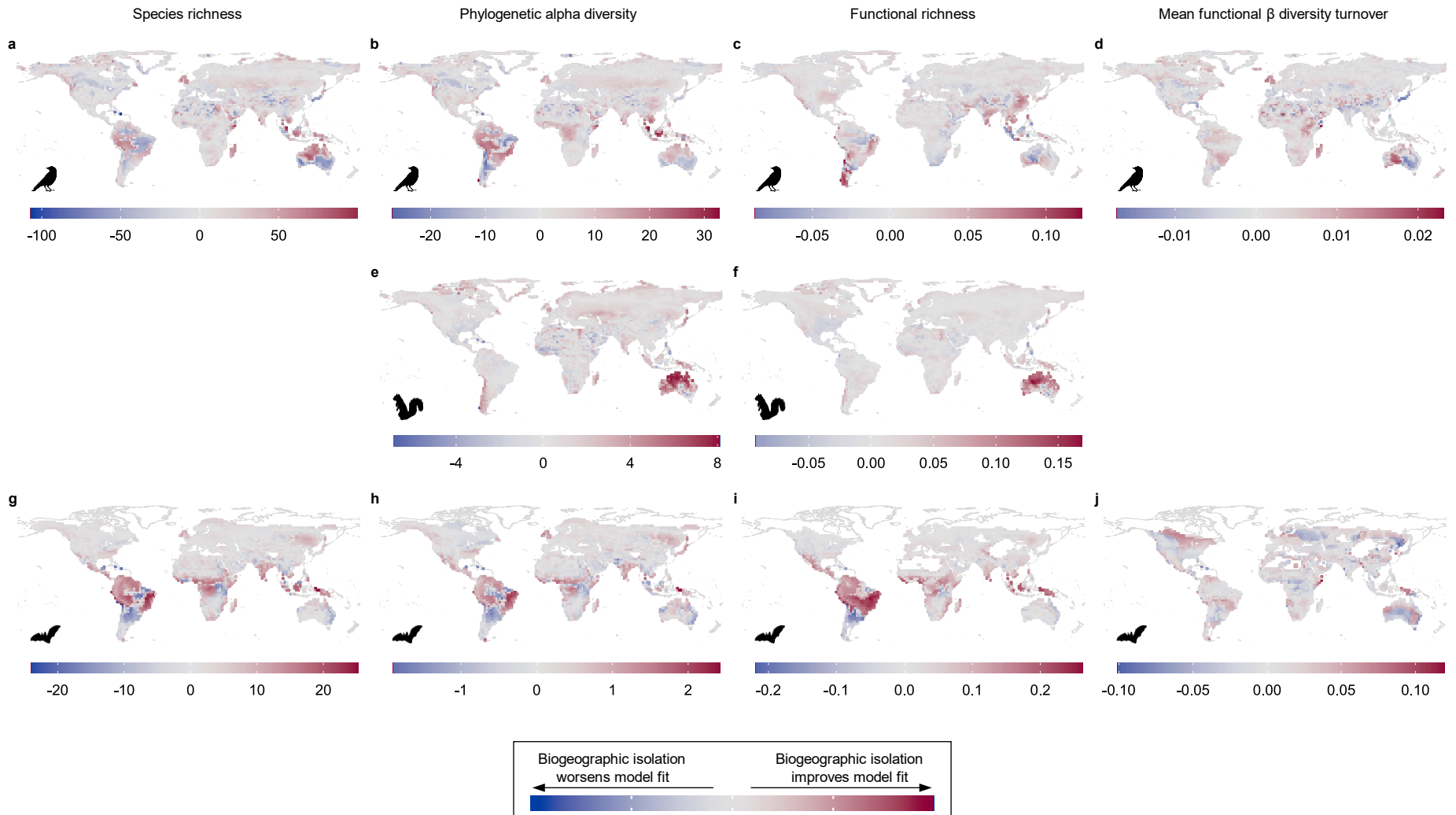
	Increase in R <sup>2</sup> compared to climate-only model					
	Bird		Mammal		Bat	
	SR	FR	SR	FR	SR	FR
*Landmass area	2.10%	0.67%	3.26%	1.85%	2.02%	0.92%
*Mean elevation	3.50%	2.62%	7.23%	2.85%	2.03%	0.62%
*Elevational range	4.20%	2.54%	4.57%	0.87%	2.17%	0.54%
Climatic distance, Present vs. Last Glacial Maximum	0.74%	0.46%	0.87%	0.04%	0.63%	0.24%
Climatic distance, Present vs. Mid-Holocene	<0.01%	0.25%	<0.01%	<0.01%	0.02%	0.03%
Past ice cover	0.83%	0.41%	0.99%	0.01%	0.75%	0.04%
Years since significant land conversion	0.05%	0.08%	<0.01%	0.04%	0.03%	<0.01%
Human Impact Index	<0.01%	0.39%	0.03%	0.04%	0.12%	1.69%



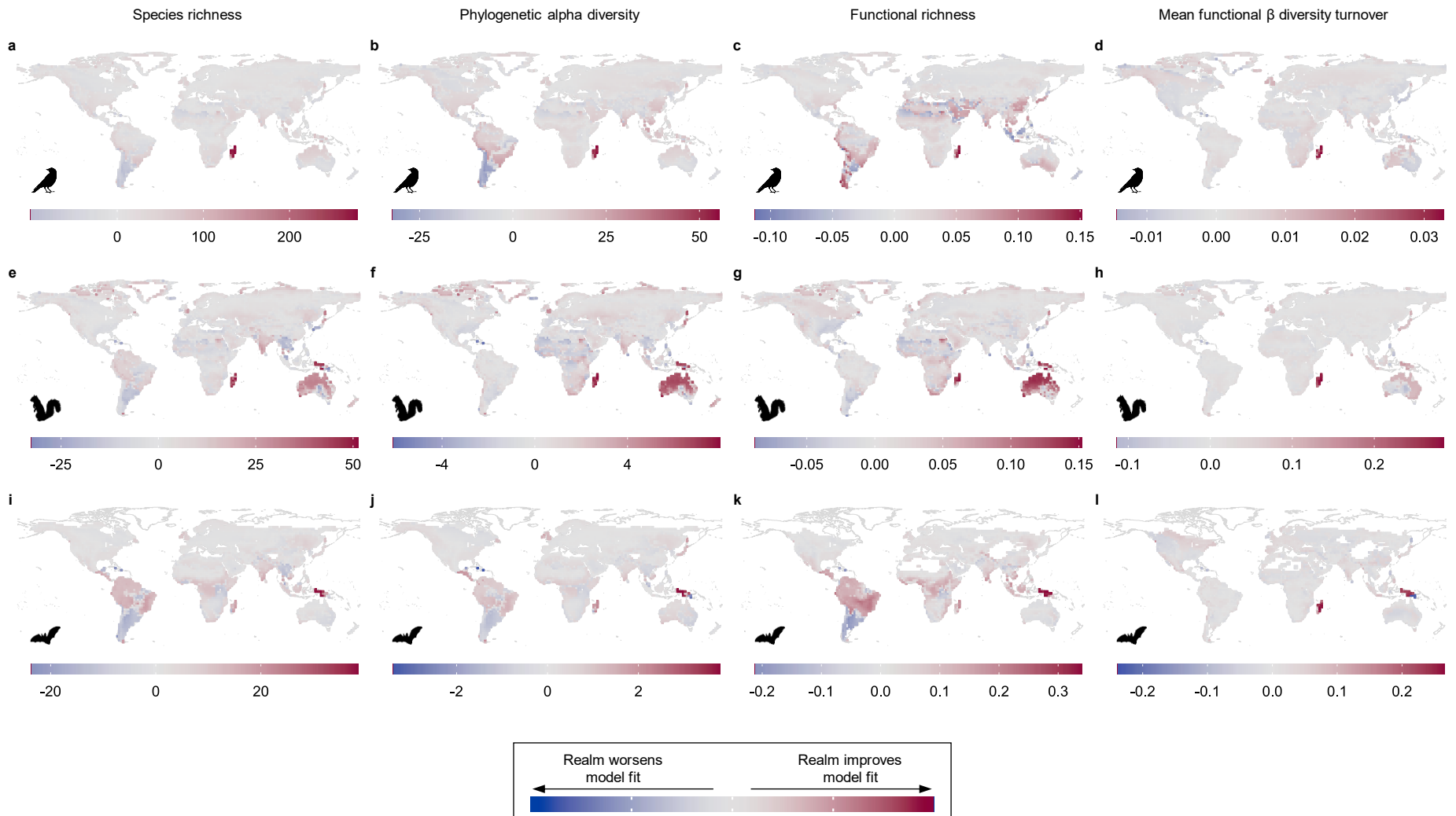
**Supplementary Table 4: Contemporary climate explains diversity as well as or better than past climate.**

Results shown for linear models of bird and mammal species richness (SR) or functional richness (FR). Each model included climate data from one of three time periods: the present, the Last Glacial Maximum, and the mid-Holocene. When non-contemporary climates had higher  $R^2$  values, they only increased the variance explained by < 1%. As such, we used only present-day climate in all analyses.

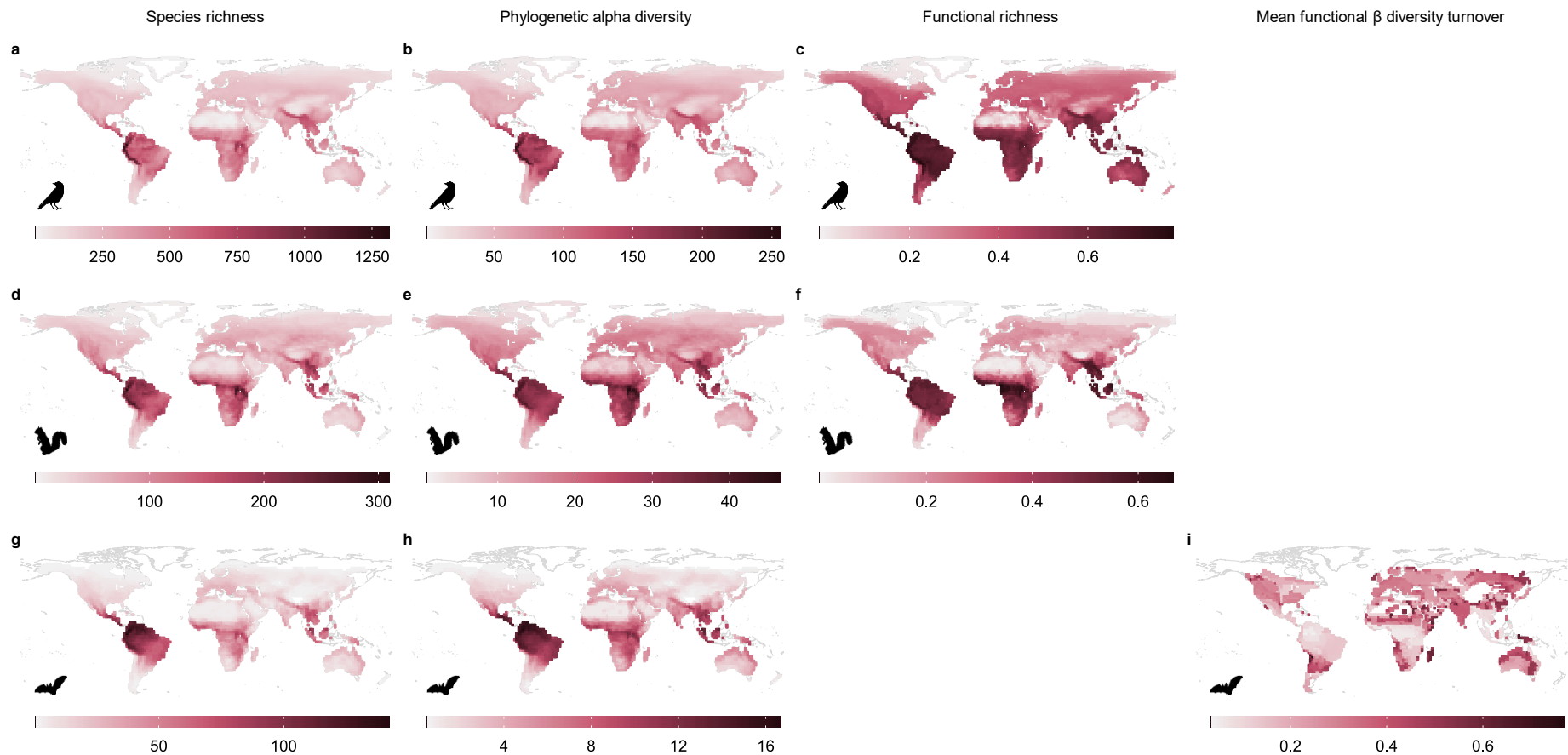
Taxon	Metric	Climate period	$R^2$ for model containing these variables	
			Climate, elevation, area	Climate, elevation, area, biogeographic isolation
Bird	SR	Present	80.2%	82.6%
		Last Glacial Maximum	79.2%	81.3%
		Mid-Holocene	80.3%	82.5%
Bird	FR	Present	85.8%	88.5%
		Last Glacial Maximum	79.6%	85.5%
		Mid-Holocene	84.8%	88.1%
Mammal	SR	Present	80.0%	84.5%
		Last Glacial Maximum	79.9%	85.3%
		Mid-Holocene	80.3%	84.2%
Mammal	FR	Present	82.8%	87.1%
		Last Glacial Maximum	81.5%	86.7%
		Mid-Holocene	82.5%	86.3%



**Supplementary Fig. 1: Differences in residuals in models with vs. without biogeographic isolation.** Differences in residuals were calculated as the absolute value of residuals in the environment-only model minus the absolute value of residuals in the global model using the residuals values of each grid cell. Scales differ for each plot based on the units of the response variable. Positive values indicate that including biogeographic isolation improved model fit for the grid cells, while negative values indicate that including biogeographic isolation worsened model fit. For birds (a-d), biogeographic isolation did not consistently improve model fit for any regions. For mammals (e-f), biogeographic isolation improved model fit for regions such as Australia. Maps for mammal species richness and mean functional beta diversity turnover are shown in Fig. 3 of the main text. For bats (g-j), biogeographic isolation improved model fit across tropical forest regions, at least for alpha diversity metrics (g-i). Maps are shown with an equirectangular projection.

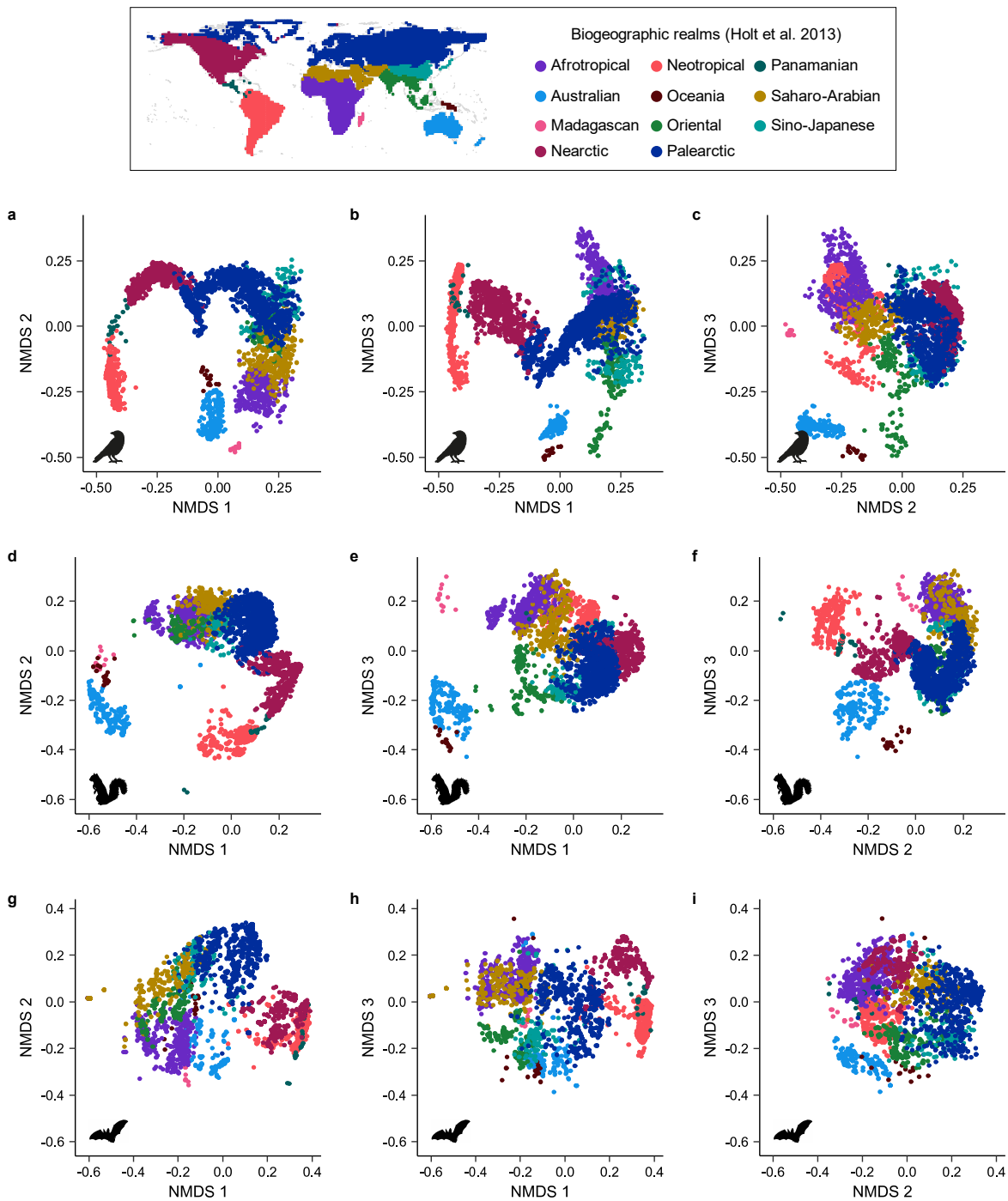


**Supplementary Fig. 2: Differences in residuals in models with vs. without realm as a categorical variable.** See legend for Supplementary Fig. 1. All plots are analogous to Supplementary Fig. 1, except for plots e & h, which are analogous to Fig. 3 of the main text. In all cases, models were ran using ‘realm’ as a discrete, categorical variable, rather than using continuous biogeographic isolation quantified using phylobetadiversity. Realms from Holt et al.<sup>1</sup>.

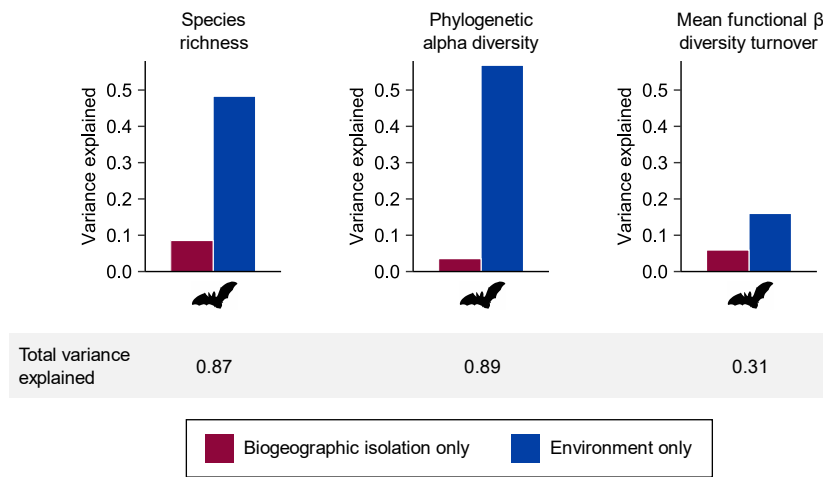


**Supplementary Fig. 3: Global biodiversity patterns for (a-c) birds, (d-f) mammals, and (g-i) bats.** Bird and mammal mean functional beta diversity turnover are shown in Fig. 4 of the main text. Bat functional richness is shown in Fig. 6 of the main text. Maps are shown with an equirectangular projection.

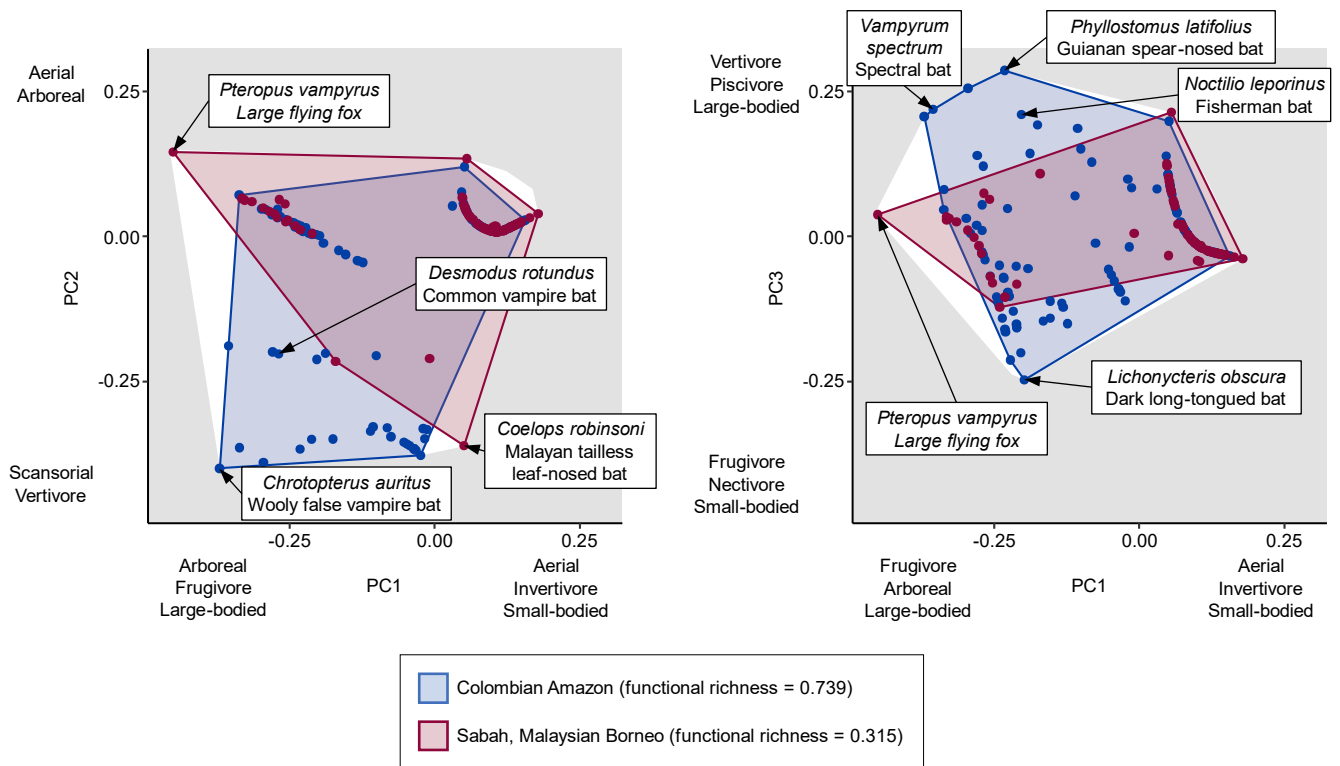




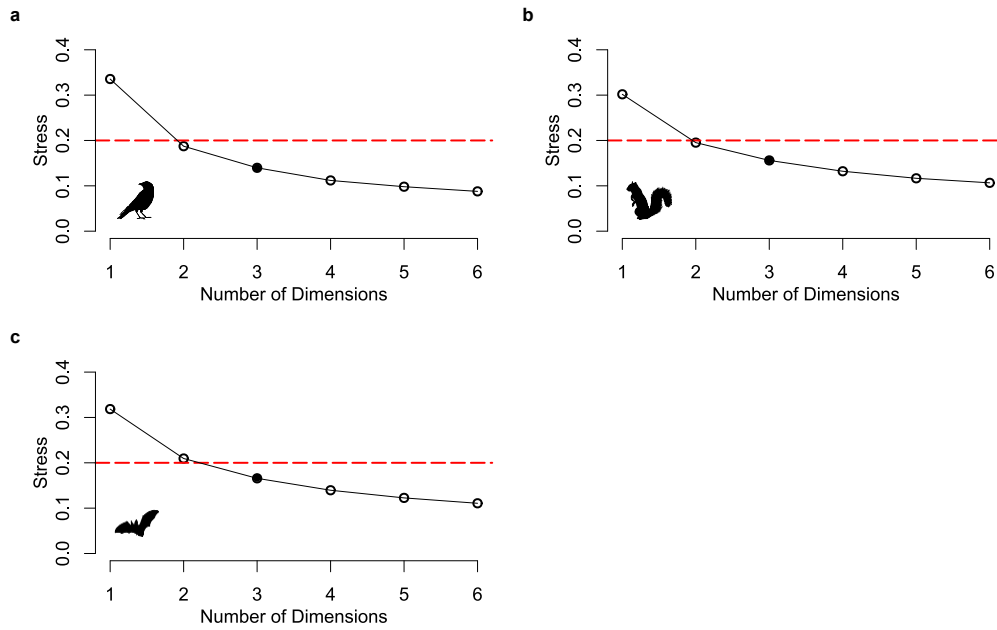
**Supplementary Fig. 4: Biogeographic isolation as quantified by phylobetadiversity, with NMDS plots in three dimensions.** Phylobetadiversity is shown for (a-c) birds, (d-f) mammals, and (g-i) bats with points colored by biogeographic realm, as categorized by Holt et al.<sup>1</sup>. Plots g and h highlight the biogeographic rift between the Neotropics (Neotropical, Panamanian) and Paleotropics (Afrotropics, Oriental) for bats. The NMDS axes shown here differ from the axes shown in Fig. 1 of the main text, where NMDS were fitted using only two axes (for visualization purposes only). These three NMDS axes were used in analyses as ‘biogeographic isolation’ (stress values 0.156 for mammals, 0.140 for birds, 0.166 for bats).



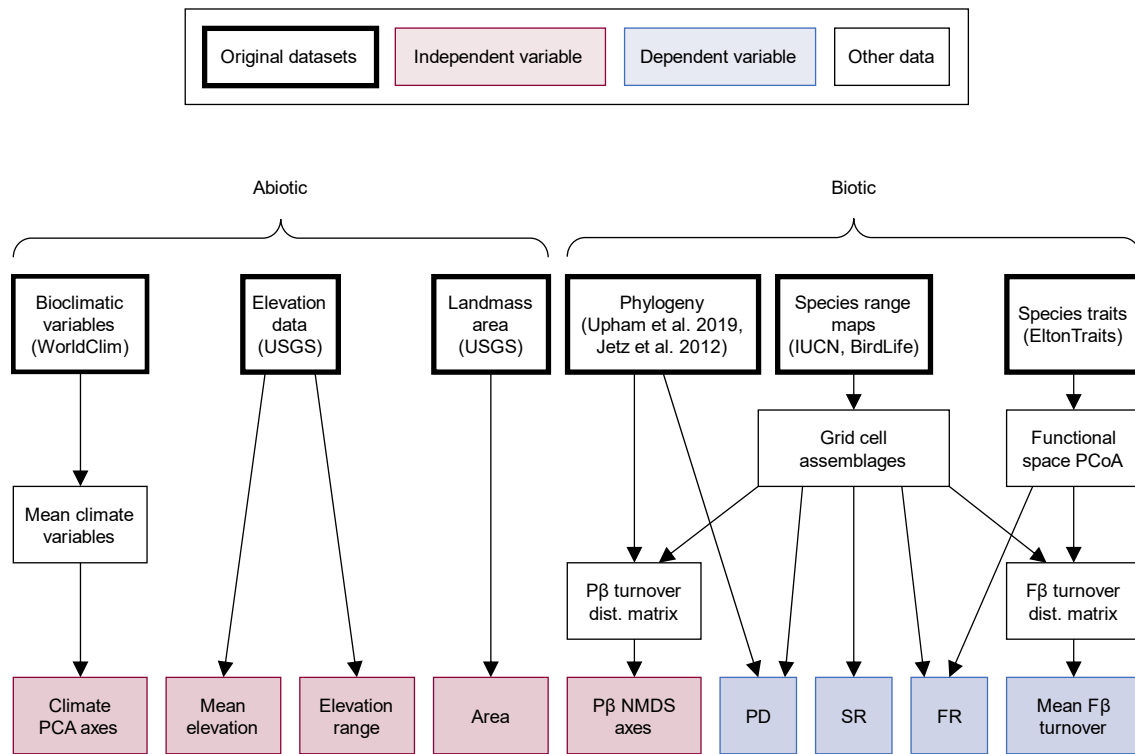
**Supplementary Fig. 5: Bat variance partitioning results.** In contrast to functional richness (Fig. 6 of the main text), environment explains much more variance than biogeographic isolation for species richness, phylogenetic alpha diversity, and mean functional beta diversity turnover. For each metric, total variance explained includes the variance explained by biogeographic isolation only (red), environment only (including climate, elevation, topography, and landmass area variables; blue), and shared between biogeographic isolation and environment (not shown). Variance explained was calculated by comparing adjusted  $R^2$  values among a biogeographic isolation model, an environment model, and a global model that included both biogeographic isolation and environment variables.



**Supplementary Fig. 6: High functional richness in a Neotropical bat assemblage compared to a Palearctic bat assemblage.** The three PCoA axes shown were calculated using trait data from all bat species. Functional richness is the proportion of total functional space occupied by an assemblage, where the white polygons represent the total functional space of all bat species. In this example, the Colombian assemblage contains many vertivorous and piscivorous species which the Malaysian assemblage lacks.



**Supplementary Fig. 7: Phylobetadiversity NMDS scree plots for (a) birds, (b) mammals, and (c) bats.** According to commonly used guidelines, stress values  $< 0.2$  (the red dashed line) indicate that the NMDS is an acceptable representation of distances, while stress values  $< 0.1$  indicate a very good representation. Based on these scree plots and desire for parsimony in our models, we used three NMDS dimensions (filled circles) in all analyses to represent biogeographic isolation.



**Supplementary Fig. 8: Schematic of methods, deriving variables used in analyses from original data products.** Publicly available data products were used to calculate variables for each 2° grid cell. Biotic variables were recalculated separately for each taxon (birds, mammals, bats; see Methods). For each dependent variable (phylogenetic alpha diversity (PD), species richness (SR), functional richness (FR), mean functional beta ( $F\beta$ ) diversity turnover), we used linear regression including all independent variables shown. In linear regressions, ‘environment’ variables included four climate PCA axes with quadratic terms, mean elevation with a quadratic term, elevation range, and log landmass area. ‘Biogeographic isolation’ variables included three phylobetadiversity ( $P\beta$ ) NMDS axes with quadratic terms and pairwise interactions among axes (see Methods). We then used variance partitioning to calculate the variance explained by biogeographic isolation only, environment only, and shared between biogeographic isolation and environment.

## Supplementary References

1. Holt, B. G. *et al.* An update of Wallace's zoogeographic regions of the world. *Science* **339**, 74–78 (2013).