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Supplemental Information for:

Geographically divergent evolutionary and ecological legacies shape mammal biodiversity in the global tropics and subtropics

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Supplemental Text and Results

Compilation of mammal community data

Our dataset of 515 mammal communities (Tables S1-4) was newly compiled for the purposes of this study and encompassed > 1.5 years (May 2017-December 2018) of data collection, screening, and standardization of species lists from multiple sources. We chose to compile community species lists by-hand from survey data rather than generate them from range maps because of the latter's spatial coarseness and well-documented proneness to both omission and commission errors (1-3). As such, relationships between species and their specific environmental associations, which 'scale up' to the level of community composition, are often muddled by range maps, though we acknowledge important efforts to combine these sources of data in new frameworks (4-5). Indeed, consulting (but not relying on) species range maps was a key component of our data screening and standardization process. Below, we provide details on the four key steps through which our survey-based community datasets were gathered and screened:

1) We compiled by-hand all possible sources of mammal community survey data from the Afrotropical, Indomalayan, Malagasy, and Neotropical biogeographic realms. This includes species lists from peer-reviewed papers in journals where mammal survey records are regularly published (e.g., *Check List, Journal of Mammalogy, Mammalia*, *Oryx*), natural history bulletins and government biodiversity surveys (e.g., *Bombay Natural History Society*, *Brunei Museum Journal*, *Bulletin of the American Society of Natural History*, and the survey 'Mammals of Chitwan National Park' carried out by ecologists in the Nepalese government), specialist handbooks and edited volumes, online biodiversity databases (e.g., 'Map of Life' hosted by multiple institutions including Yale University and the IUCN, as well as 'Biological Inventories of the World's Protected Areas' hosted by the University of California Davis), and survey-based community lists that have been published elsewhere—e.g., our Afrotropical data mainly derive from the multi-community datasets of Kamilar et al. (6) and Rowan et al. (7). Community datasets were then cropped to taxa generally weighing over 500 g on average, as survey records for small mammals are particularly sensitive to sampling effort (8).

2) With this initial compilation of communities, we preemptively removed community species lists that were likely erroneous, either because they contained very few taxa (e.g., richness < 5, which is suspect for tropical and subtropical regions), were focused on a single taxon or handful of taxa (e.g., primate-only surveys of forest regions), or consisted of unrealistic taxonomic lists. The latter includes both chimeric faunas consisting of species that almost certainly never occur in sympatry and those riddled with taxonomic errors to the extent that they were unusable (in practice, differentiating between the two can be difficult given variation in the scope and detail of data collection methods provided).

3) For the remaining communities, we obtained central latitude and longitude points and used these coordinates to obtain community species lists from shapefiles of species ranges from the IUCN Red List (9) using the packages *maptools* (10) and *raster* (11) in R (12). We then compared by-hand our community point data with

those generated from IUCN ranges to check for the congruence of taxa said to be present/absent, taking into account potential differences in species-level taxonomy (i.e., some of our checklists were published years ago and needed taxonomic updating). When these lists disagreed, often as a result of undersampling in our survey data or oversampling in the range maps, we investigated the likelihood of actual species presence/absence on a case-by-case basis using all possible sources, including georeferenced observations from the Global Biodiversity Information Facility (GBIF: www.gbif.org), expert distributional descriptions from handbooks and field guides, keyword searches on Google Scholar, and colleagues with expertise on particular mammal faunas of the world. Based on these sources, a decision was then made to add or remove the taxon from a given community list. For sake of clarity, we note that IUCN range maps were not used to construct community lists, but solely as a check of data quality that prompted us to seek out additional sources to ensure accuracy of the survey data.

4) All final community lists (the 515 used in this study) were updated by-hand to the most recent IUCN Red List species-level taxonomies. By taking the time to update all community species lists to the most up-to-date IUCN taxonomies, we have controlled for legacy effects in the community data and its influence on both intra- and inter-realm diversity patterns (e.g., two realms with identical α diversity might not appear as such simply because of differences in using old and less speciose versus new and more speciose taxonomies).

We provide the key references for the Afrotropical (6-7, 13-14), Indomalayan (15-53), Malagasy (54-57), and Neotropical (58-107) community datasets, as well as those we used for multiple realms (108-109). Additionally, we note two important points with regard to our community datasets: 1) each biogeographic realm analyzed in our study is made up of community lists derived from a mixture of data sources, meaning that any potential biases stemming from variation in source quality are limited; 2) the entire process of screening and standardizing community data was done by one of us (J.R.) so that there was no potential for biases to be introduced because of protocol variation among multiple recorders.

Testing for the effects of community spatial extent

The species-area relationship is a well-documented biogeographic pattern whereby community species richness increases as a function of the geographic sampling area (110, 111). Because our communities were compiled from species lists of parks and protected areas of varying size (Fig. S1), it is possible that species richness varies systematically in relation to community area, potentially confounding comparisons of phylogenetic and functional trait measures across the communities in our dataset. To test for confounding species-area relationships, we chose a subset of ~ 150 Afrotropical communities of varying richness, downloaded shapefiles of their geographic boundaries from the World Database on Protected Areas (WDPA), and calculated their terrestrial area in km^2. We find no relationship between area and species richness (R^2 = 0.003, p = 0.225), with the slope of the line being near-flat (Fig. S2). This is likely due to the fact that large-bodied mammals are highly mobile,

have weaker dispersal limits than smaller-bodied species (112), and are less likely to exhibit ecological zonation (113). Previous studies have found the lack of a species-area relationship in non-mammal vertebrate communities, such as birds (e.g., 114).

Likewise, because our communities vary significantly in spatial extent, there is a potential offset in the degree to which predictors derived from a central geospatial point (as done in this study) track predictors calculated from the community's entire spatial extent. To test for this, we sampled predictor grids across community extent for the subset of ~ 150 communities for which we collected WDPA shapefiles. We find that weighted predictor means, shown in Fig. S3 for modern temperature and precipitation, closely track the community's central predictor value irrespective of community size (area km^2), meaning that the latter reliably captures important among-community variation in climate and human impacts.

Dietary principal coordinates analysis

We used a subset of 13 food types included in MammalDIET (115) to characterize the dietary diversity of mammal communities (Table S1). For each species, MammalDIET rank scores were inverted so that ranks correspond to: 0=food type not consumed, 1=food type rarely consumed, 2=food type often consumed, 3=primary food type. Species dietary ranks were then collapsed using a Gower distance-based principal coordinates analysis (PCoA) using the package *vegan* (116) in R (12).

The first and second resulting PCoA axes (hereafter, Diet1 and Diet2) account for ~ 83% of the variation in species diets (Fig. S4). Diet1 (52.73%) separates species that feed on woody and herbaceous vegetation from those feeding on invertebrate and vertebrate (mammal, bird, fish, and reptiles and amphibians) prey. Thus, Diet1 essentially separates species along a trophic gradient from strict primary consumers (mainly ungulates in the orders Artiodactyla and Perissodactyla) from carnivores (mainly species in the order Carnivora). Generalized species that span trophic levels (i.e., omnivores), such as primates and suids, fall near the origin. Diet2 separates strict carnivores and strict leaf- or grass- feeding herbivores from more generalized species that include fruit, nectar, seeds, and other plant parts in their diets. These species are mainly mixed folivorous-frugivorous primates and rodents.

Phylogeny choice from the Faurby and Svenning treeblock

The Faurby and Svenning (117) treeblock contains 1000 mammalian phylogenies that vary in the details of their topology. In preliminary analyses and data exploration for this study, we ran analyses in which we randomly selected trees from the Faurby and Svenning treeblock and calculated NRI and NTI. Across all realms, we recovered near-identical results irrespective of the particular phylogeny used, which indicated to us that slight variations in tree topology had very little influence on the measurement of community phylogenetic structure (NRI/NTI). As such, and for sake of simplicity, we used the first topology (Tree1) of the Faurby and Svenning treeblock for all subsequent analyses. Because the NRI/NTI values from any one given topology are highly correlated with those from all others ($r = 0.95$-1.00), the choice of one particular tree over another has effectively no influence on the overall findings of our study.

Average model results

Following Burnham and Anderson (118) we averaged the top 95% of model weights to determine the influence of past and present climatic and anthropogenic factors on mammal community structure using the package *MuMIn* in R (119). Tables of these results are given in Tables S6-9: Afrotropics, Table S6; Indomalayan, Table S7; Malagasy, Table S8; Neotropics, Table S9. Variable importance (sum of AICc weights are shown in Fig. S5. For significant predictors, we show bivariate relationships in Figs. S6-9.

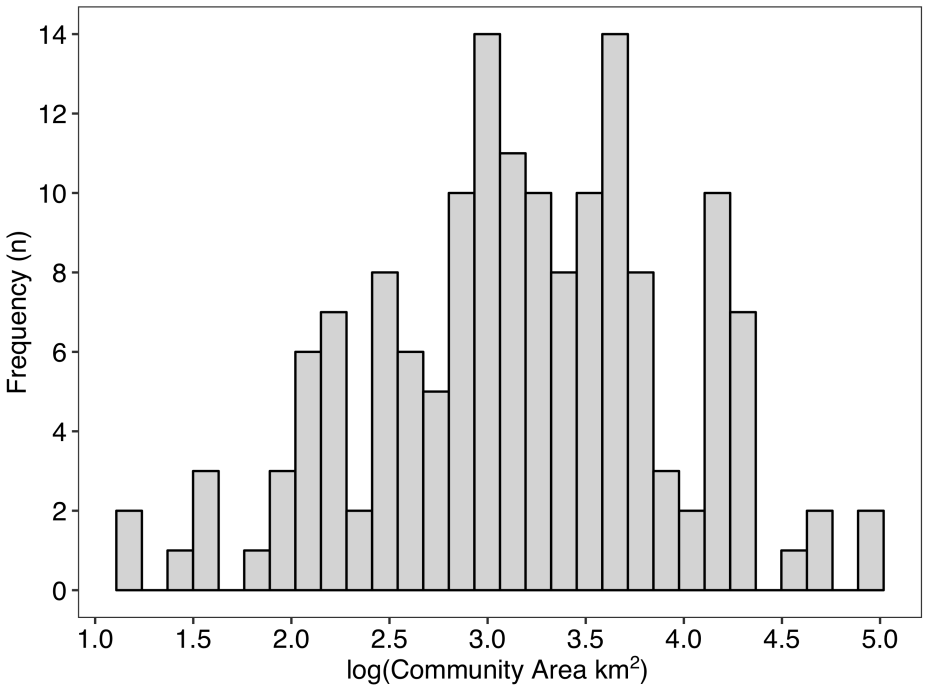

Fig. S1. Histogram (bins = 30) of community area (km^2) for a subset of ~ 150 communities from our dataset.

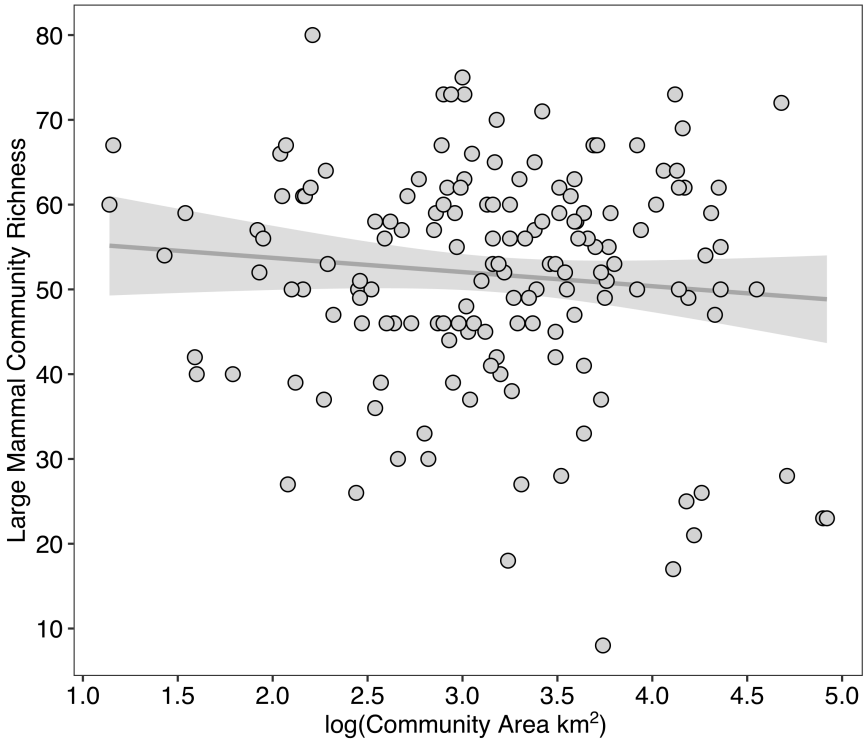

Fig. S2. Relationship between large mammal community richness and community area for ~ 150 communities from our dataset. Gray line indicates the linear fit, with shading showing the 95% CI of the relationship.

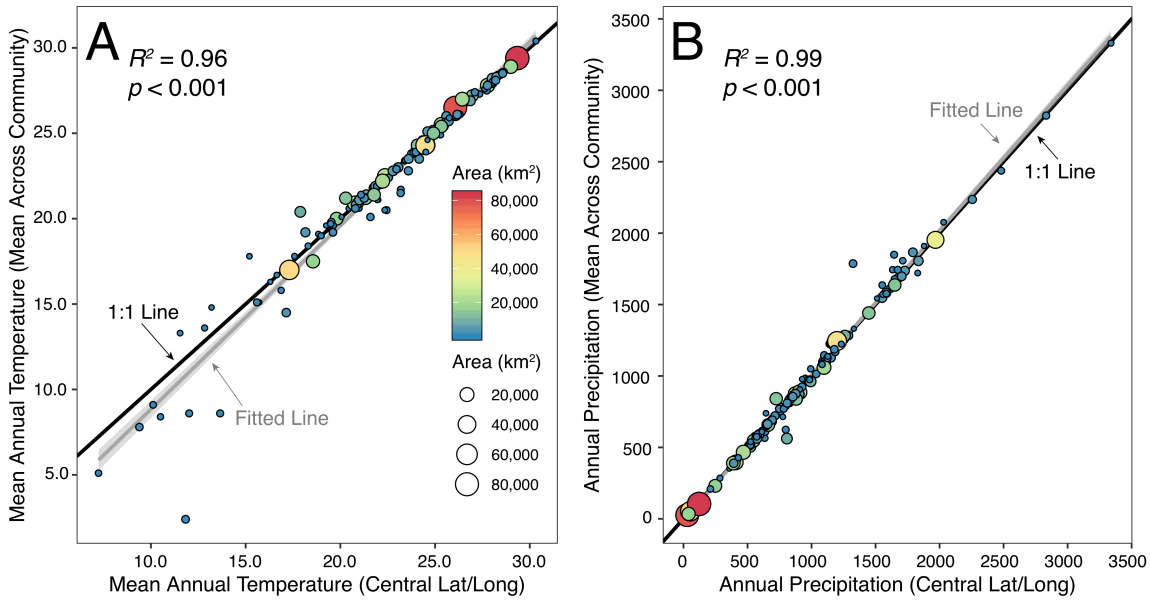

Fig. S3. Relationship between a community-wide weighted mean value (y-axis) and a central geospatial point (x-axis) and for modern mean annual temperature (A) and annual precipitation (B) across a subset of ~ 150 communities.

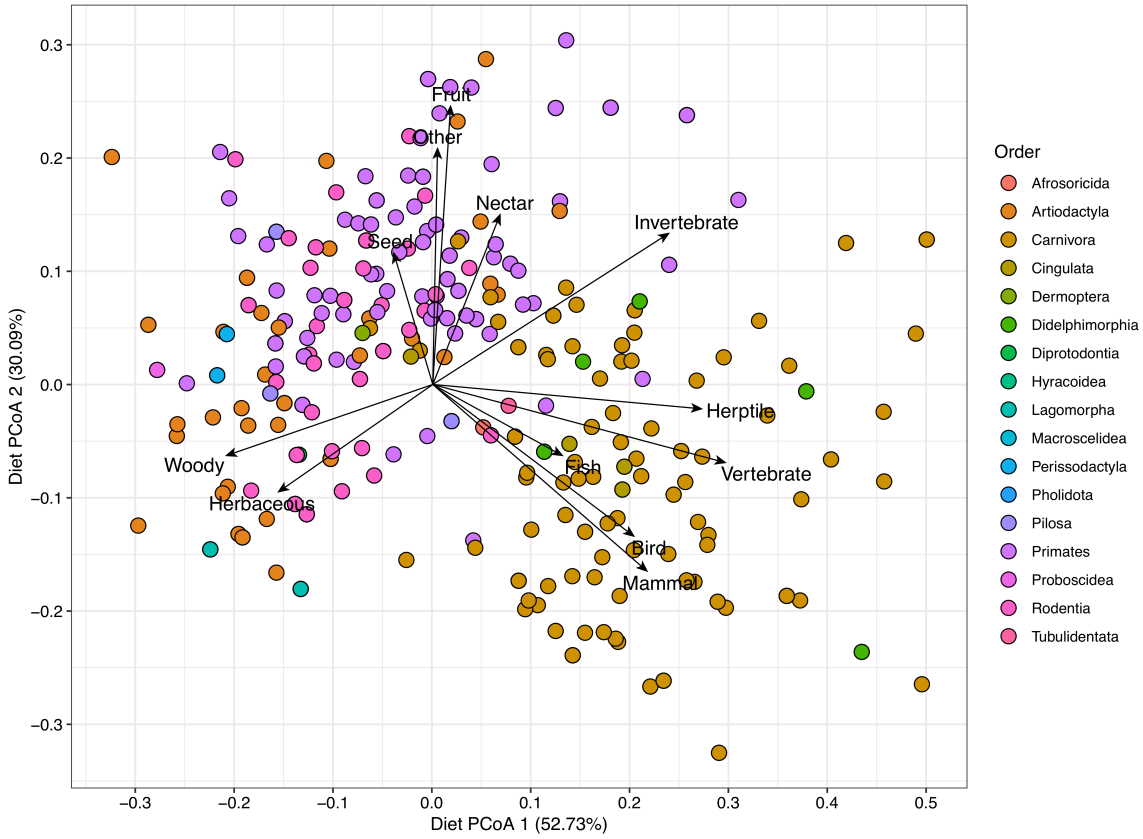

Fig. S4. Dietary principal coordinates analysis (PCoA) of 13 food types from MammalDIET across 852 mammal species in 17 orders. Collectively, PCoA Axis 1 (Diet1) and PCoA Axis 2 (Diet2) account for ~ 83% of variation in the dietary data.

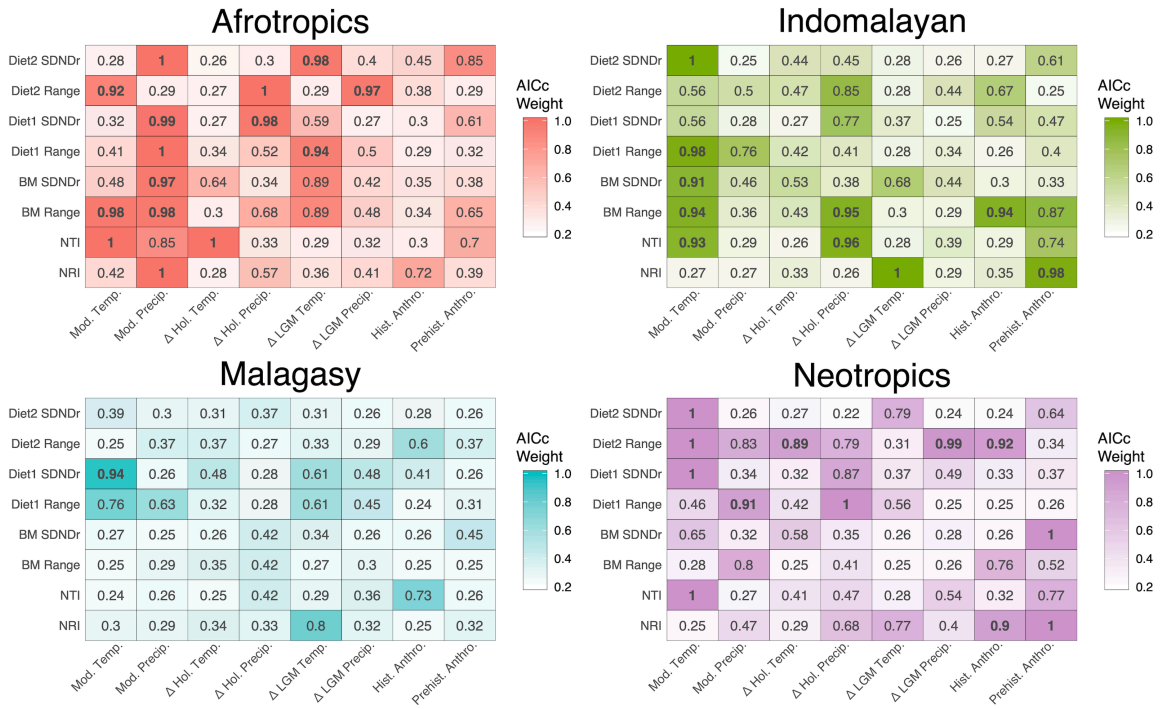

Fig. S5. Heatmaps of AICc weights (variable importance) for past and present climate and human impacts on mammal community structure. Values in bold indicate predictors that were significant in the average model (top 95% of model weights).

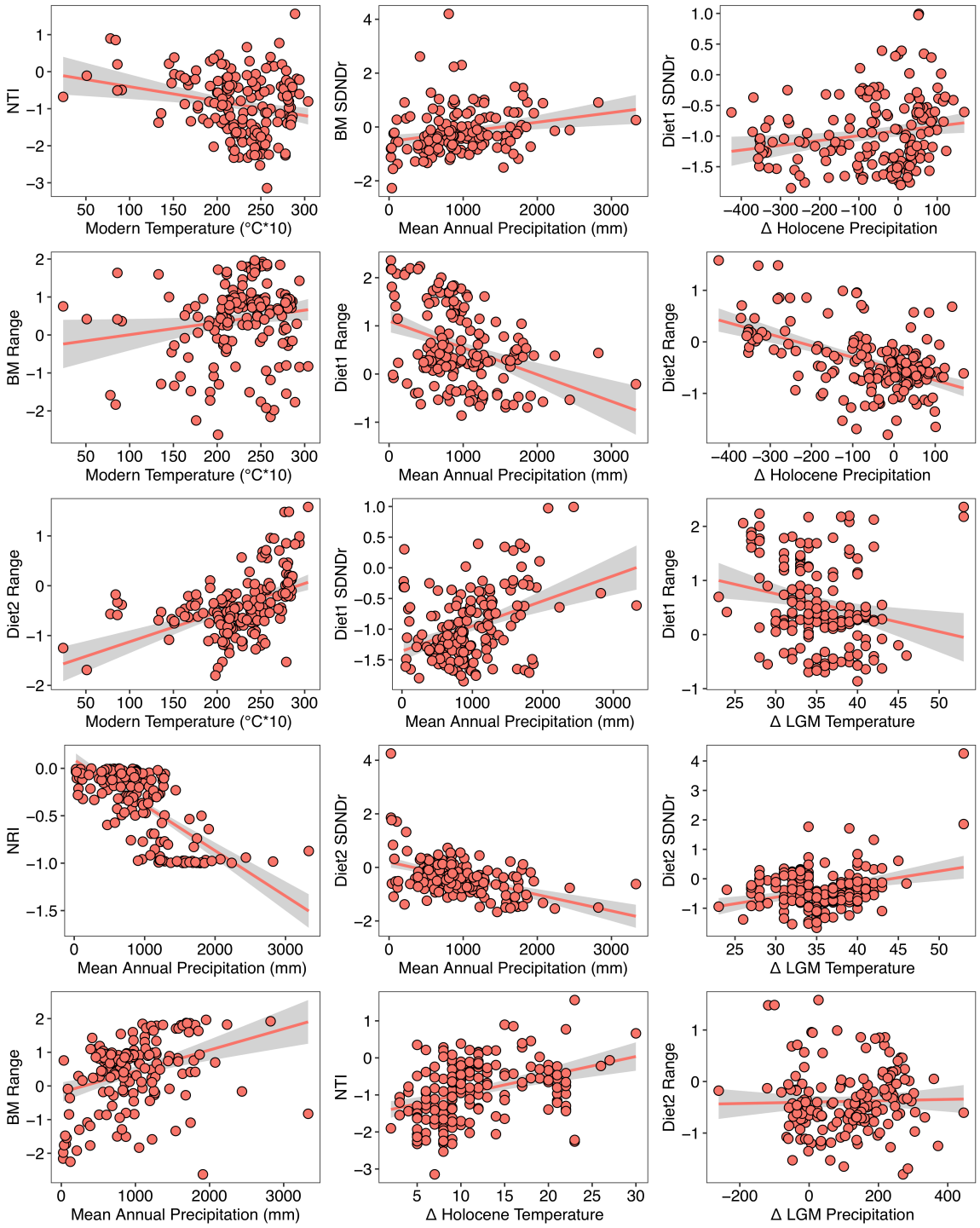

Fig. S6. Scatterplots of significant variables in the average model predicting Afrotropical mammal community structure.

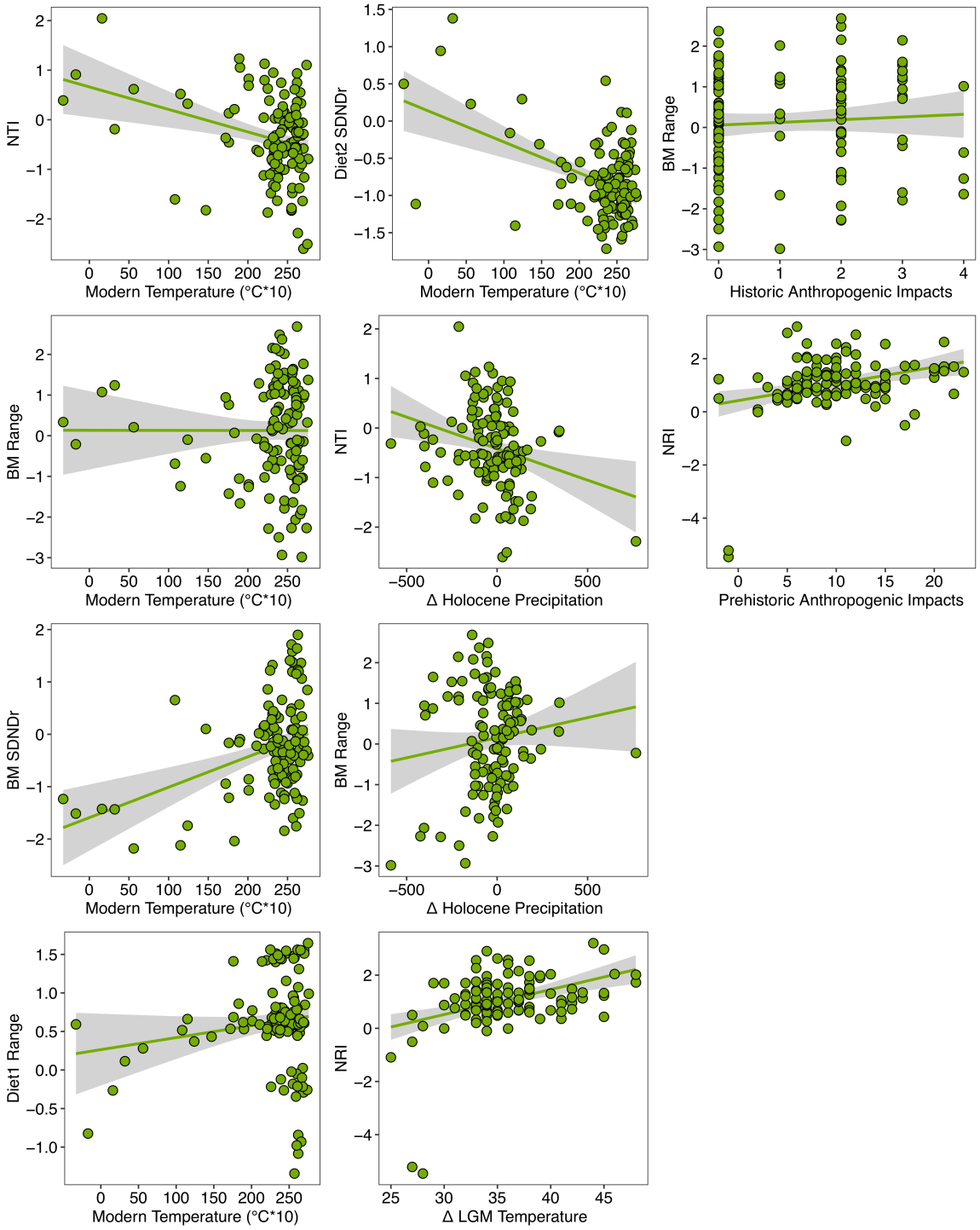

Fig. S7. Scatterplots of significant variables in the average model predicting Indomalayan mammal community structure.

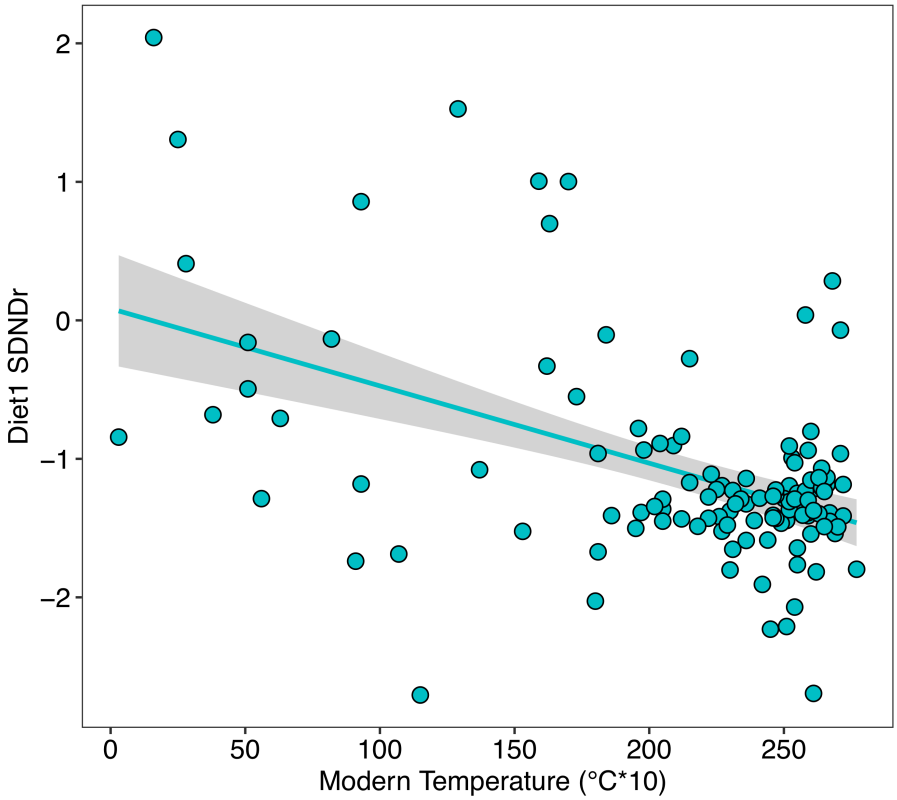

Fig. S8. Scatterplot of the significant variable (modern temperature) in the average model predicting Malagasy mammal community structure.

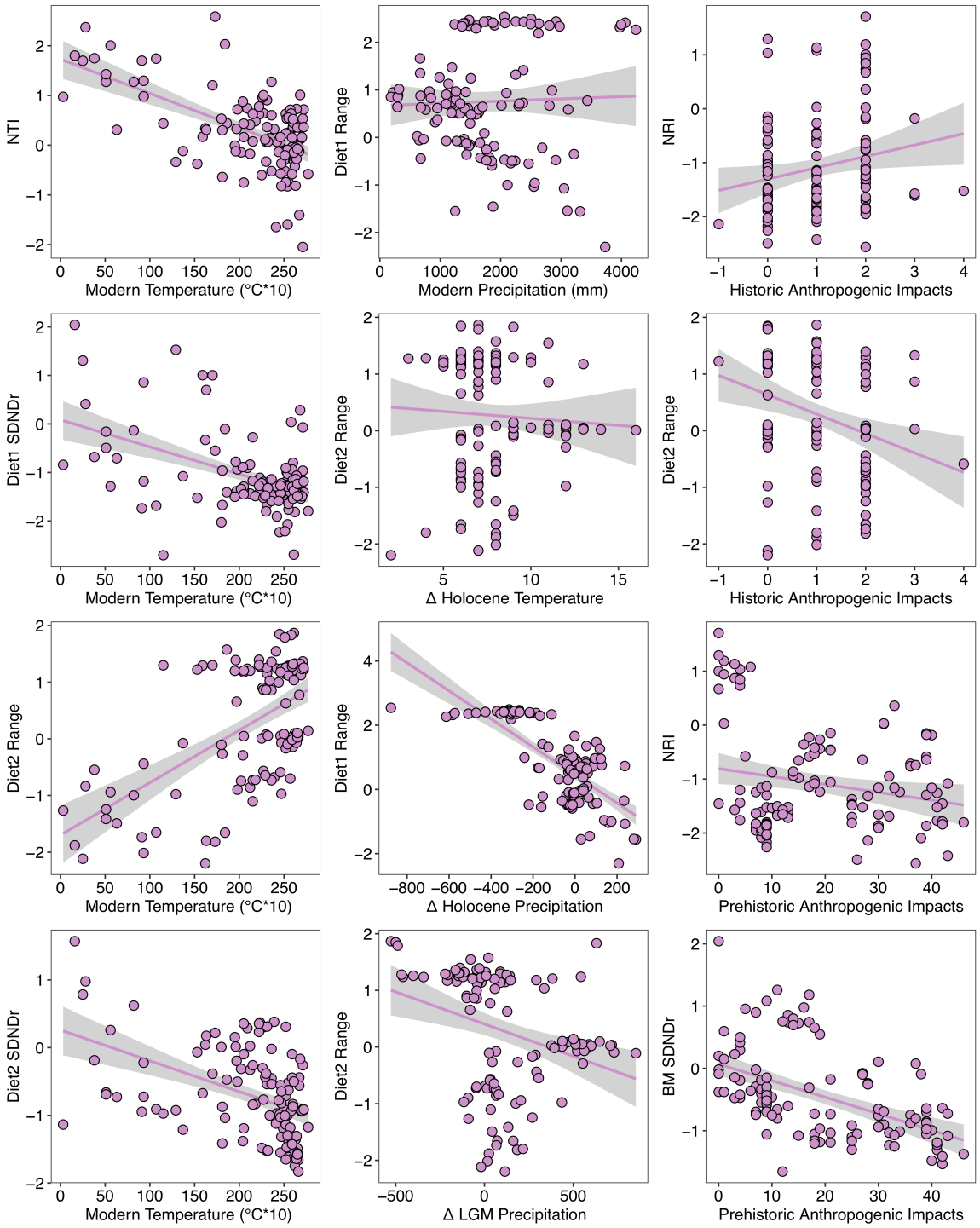

Fig. S9. Scatterplots of significant variables in the average model predicting Neotropical mammal community structure.

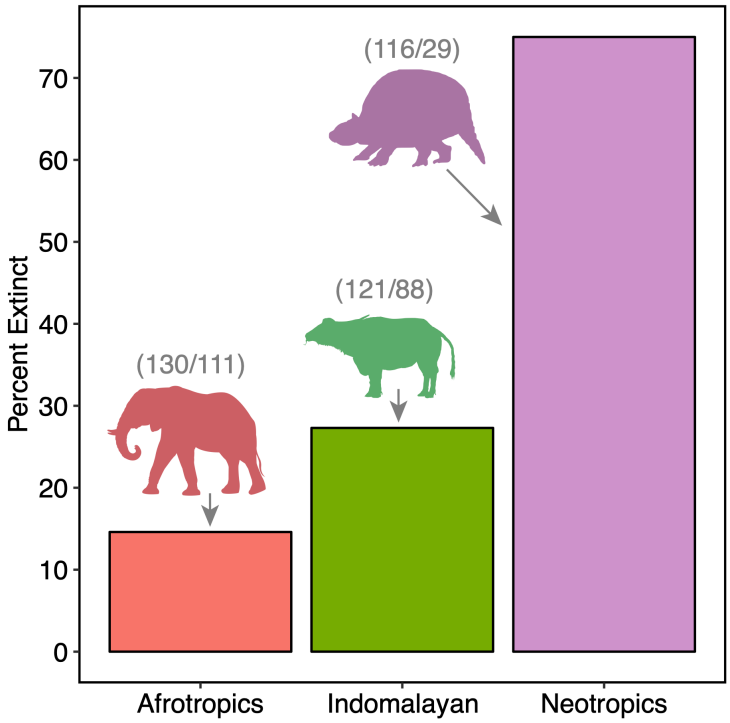

Fig. S10. Differences in late Quaternary extinctions of terrestrial large-bodied (here, species ≥ 10 kg) herbivores across three continental realms. Values in parentheses above silhouettes indicate: late Quaternary species richness/present-day species richness.

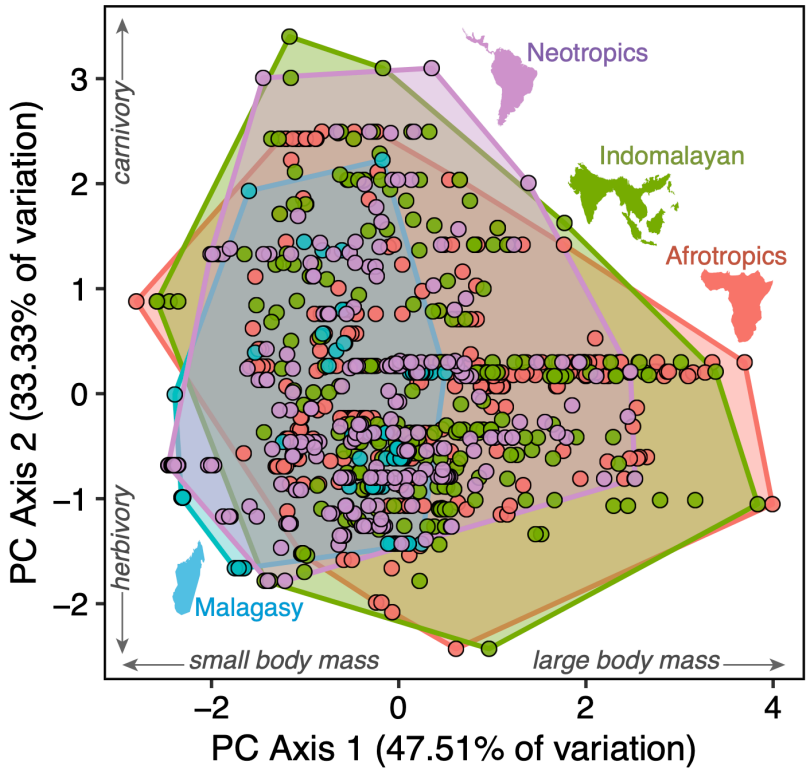

Fig. S11. Principal components analysis representing the functional trait space of large mammal assemblages across the world's tropical and subtropical realms, wherein each point represents a species colored by its respective realm. Convex hulls show the size and geometry of functional trait space across each realm. Collectively, the first and second axes account for ~ 80% of among-realm functional trait variation.

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