

Supplementary Materials

Table S1 Pearson correlation coefficients (all significant at p level of 0.05) between the species richness, phylogenetic diversity, functional diversity, conservation priority for taxonomic dimension, conservation priority for phylogenetic dimension, and conservation priority for functional trait dimension.

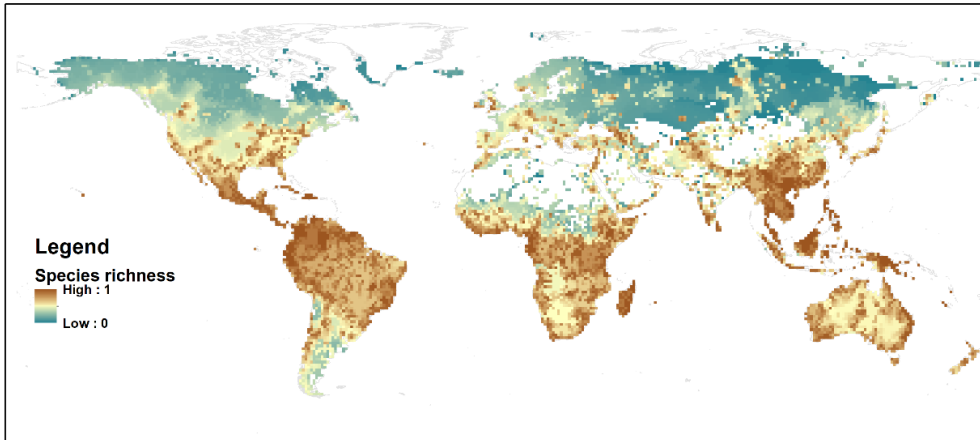
	taxonomic dimension	phylogenetic dimension	trait dimension
taxonomic dimension	1	0.766	0.763
phylogenetic dimension	0.766	1	0.982
trait dimension	0.763	0.982	1

Table S2 The 21 functional traits compiled and their completeness in the 54020 species included in the phylogeny. At the imputation, eight traits were selected to compute the functional trait diversity.

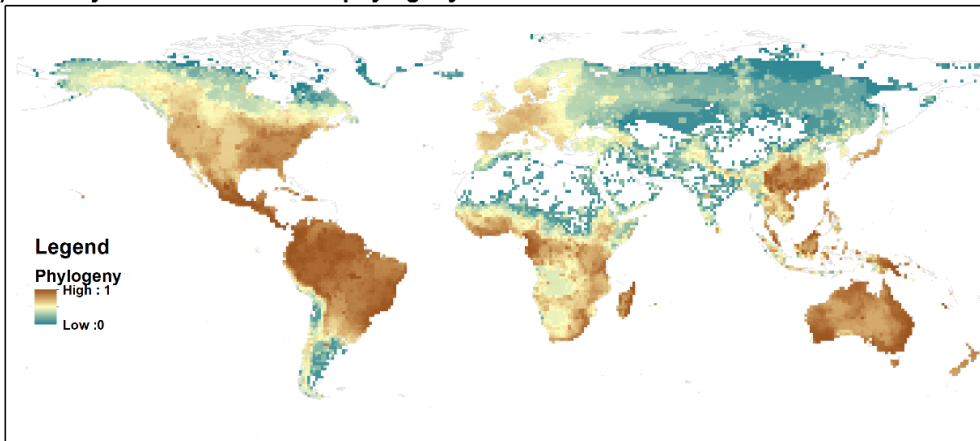
Trait name	Description	Missing species (totally 54,020 species)	Missing rate (%)	Selected
Leaf nitrogen content	Leaf nitrogen (N) content per leaf dry mass	50,441	93.37	√
Wood Density	Stem specific density (SSD)	47,608	88.13	√
Leaf K content	Leaf potassium (K) content per leaf dry mass	52,778	97.70	
Leaf P content	Leaf phosphorus (P) content per leaf dry mass	51,652	95.62	√
LDMC	Leaf dry matter content	53,227	98.53	√
Vegetative height	Plant maximum height	49,521	91.67	√
Leaf N:P	Leaf nitrogen/phosphorus (N/P) ratio	52,566	97.31	
Seed dry mass	Seed dry mass	49,348	91.35	√
SLA	specific leaf area (Leaf area per leaf dry mass, 1/LMA)	52,055	96.36	√
LA	Leaf area (in case of compound leaves: leaflet, petiole and rachis excluded)	53,221	98.52	√
SLAFM	Leaf area per leaf fresh mass (SLA based on leaf fresh mass)	53,739	99.48	
LA _{compoundleaf}	Leaf area (in case of compound leaves: leaf, petiole included)	53,355	98.77	
Leaf respiration rate	Leaf respiration rate per leaf area	53,802	99.60	
Wood N	Wood nitrogen (N) content per wood dry mass	53,989	99.94	
Leaf photosynthesis rate	Leaf photosynthesis rate per leaf area	53,252	98.58	
Seed germination rate	Seed germination rate (germination efficiency)	53,339	98.74	
LWR	Leaf dry mass per plant dry mass (leaf weight ratio)	53,828	99.64	

Stomata conductance	Stomata conductance per leaf area	53,542	99.12	
Fine root DM	Fine root dry mass to leaf dry mass ratio	53,948	99.87	
Leaf WUE	Leaf photosynthetic water use efficiency	53,970	99.91	
Wood DM	Wood dry mass per plant	54,012	99.99	

(a) Priority conservation areas: species richness



(b) Priority conservation areas: phylogeny



(c) Priority conservation areas: functional trait

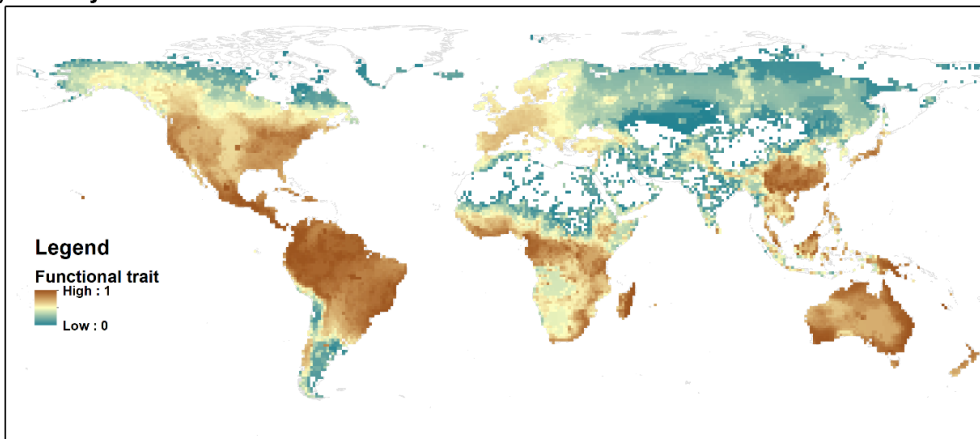


Fig. S1 The priority conservation areas showing the ranking from each of the three dimension analyses. (a) Species richness, (b) Phylogeny, and (c) Functional traits. The values of cell rank from 0 to 1 with the increase of the conservation importance.

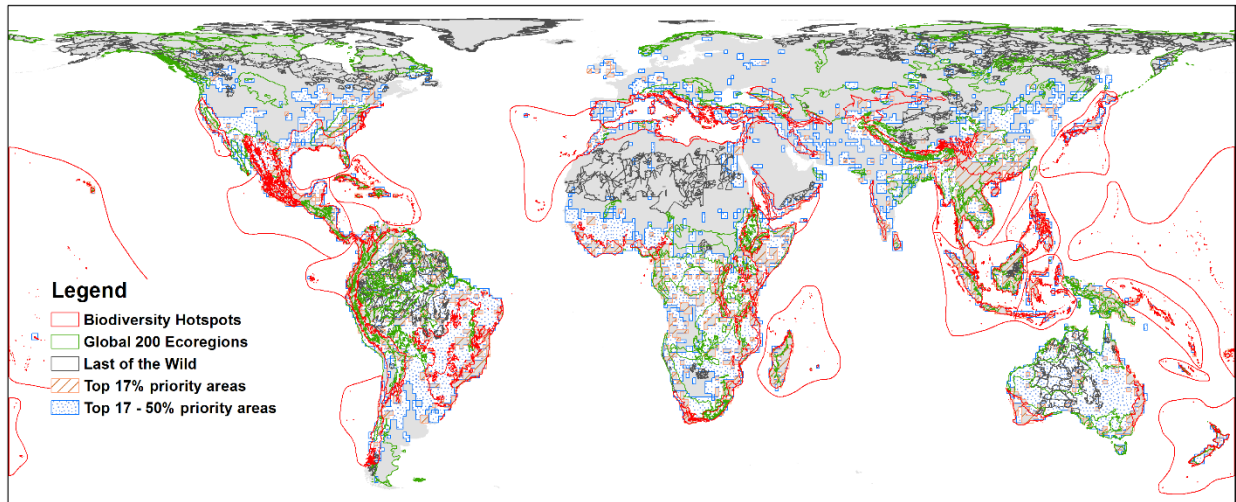


Fig. S2 Maps showing the top 17% (CBD 2020 target) and top 50% (CBD 2050 target) priority areas obtained in the study, Global 200 Ecoregions (G200), the Last of the Wild (LW), and the Biodiversity Hotspots (BH).

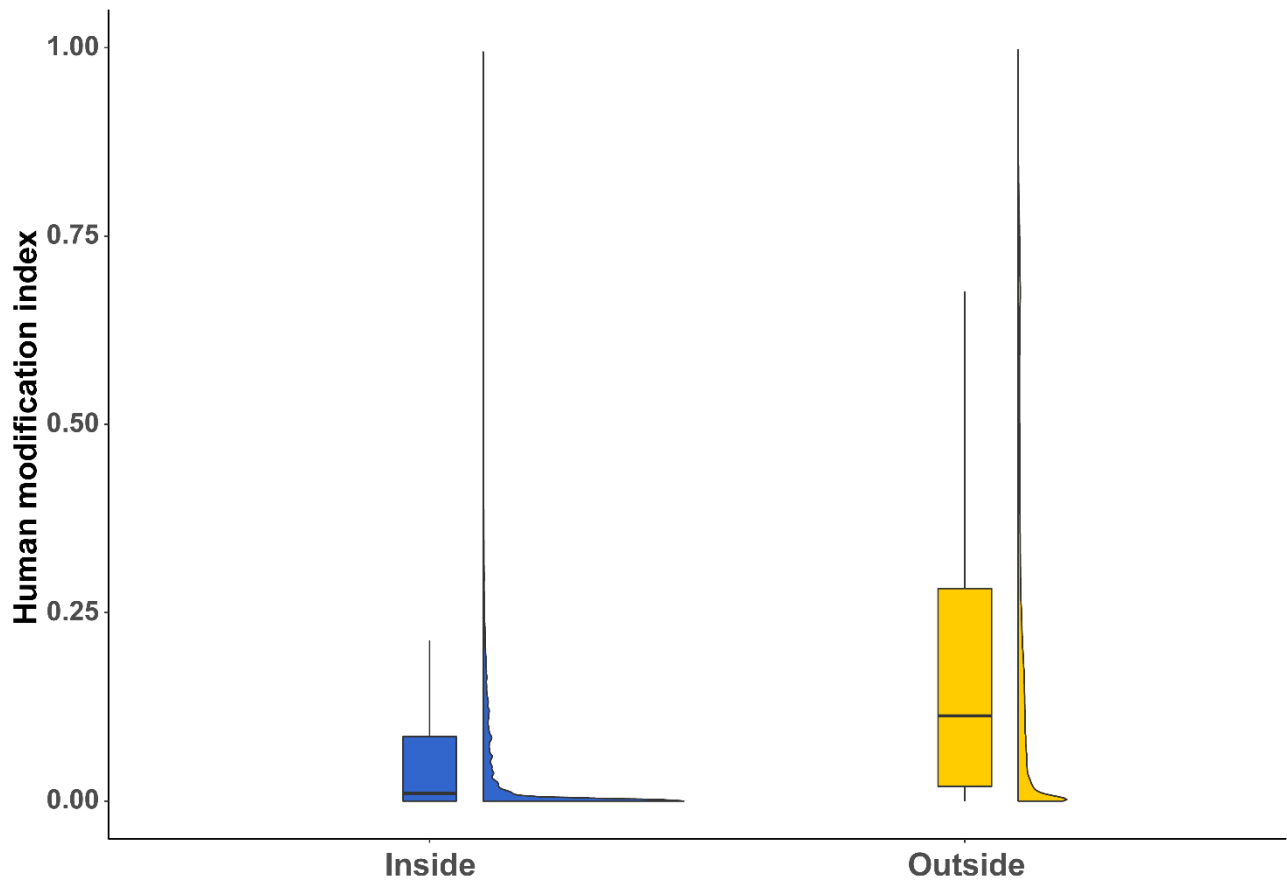


Fig. S3 Boxplot and density plot of the global human modification index inside and outside existing PAs. One-way ANOVA test: F-value = 4531569, $p < 0.0001$. Means are indicated by circles in the boxplots. Sample size of the inside and outside PAs is 8,577,868 and 125,609,765, respectively.

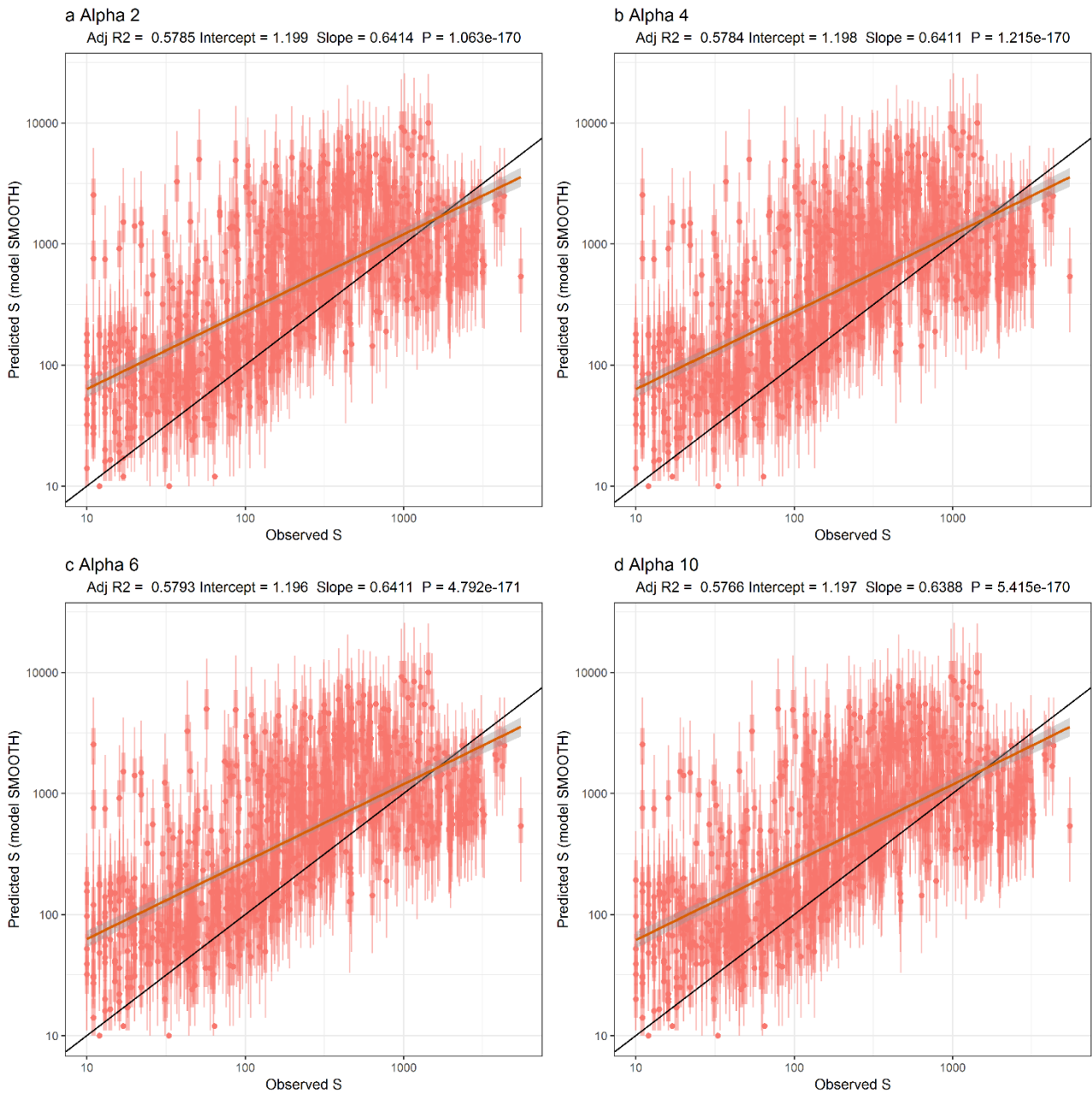
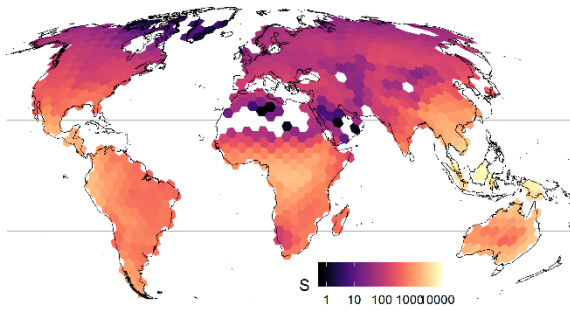
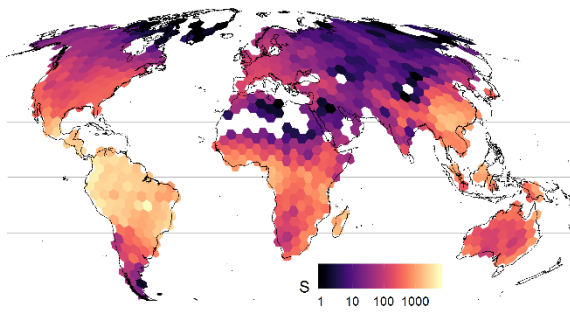


Fig. S4 External validation of the observed richness (S) from each alpha-value range map using the predictions of model SMOOTH at the grain of the 209,903 km² hexagons (Keil & Chase 2019). Each subplot shows how the observed S compares with predictions of model SMOOTH from Keil & Chase (2019). Provided are full Bayesian prediction intervals, reflecting both the uncertainty in model parameters, as well as the width of the negative binomial error distribution. Points are medians of posterior distributions of the predictions; thick transparent bars are 25% and 75% quantiles, thin lines are 2.5% and 97.5% quantiles of the posterior distributions. Solid diagonal line is 1:1 line, and solid red line is the regression line between the observed and predicted S , with the confidence intervals in shade. The model performance is provided above each subplot.

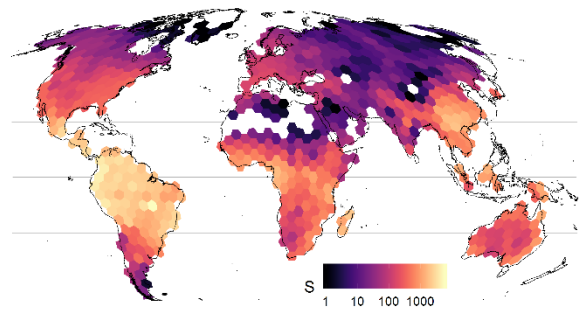
a Keil & Chase (2019)



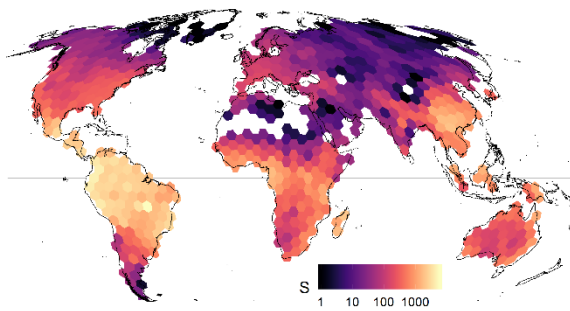
b Alpha 2



c Alpha 4



d Alpha 6



e Alpha 10

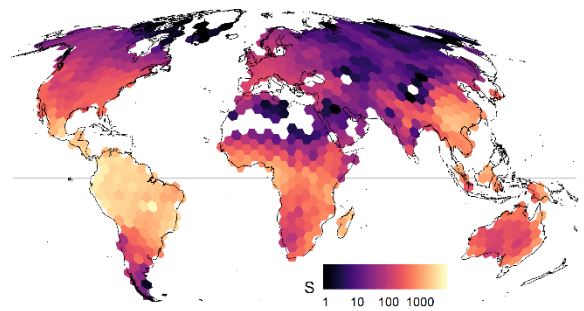
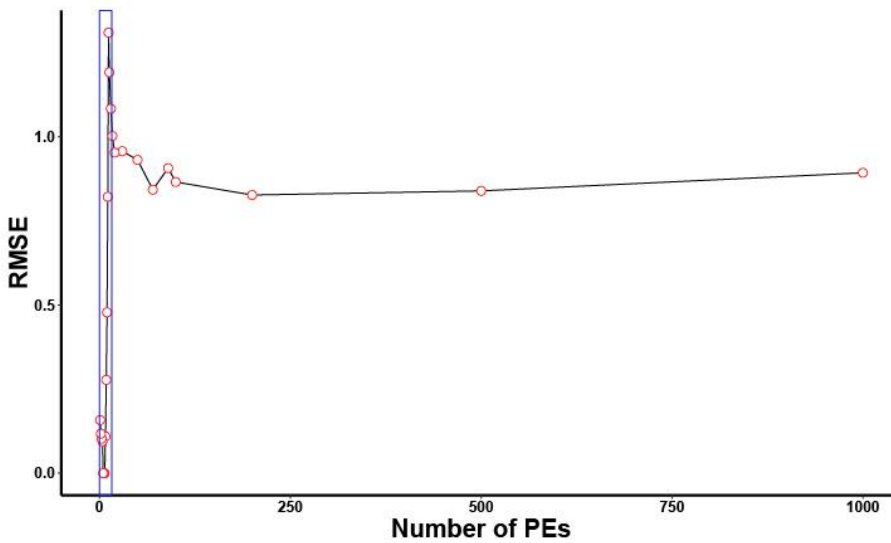


Fig. S5 Tree-species richness (S) at the grain of the 209,903 km² hexagons. (a) Predicted pattern from model SMOOTH in Keil & Chase (2019); (b-e), observed patterns of the alpha-level range maps at the same grain size. White hexagons represent data missing or $S = 0$.



Fig. S6 Time-calibrated phylogeny of the 46,752 tree species included in the study. Colors indicate main clades.

(a) Root mean squared error (RMSE) of each imputation with different phylogenetic eigenvectors (PEs)



(b) Root mean squared error (RMSE) of each imputation with PEs less than 15 (subset of above figure in blue box)

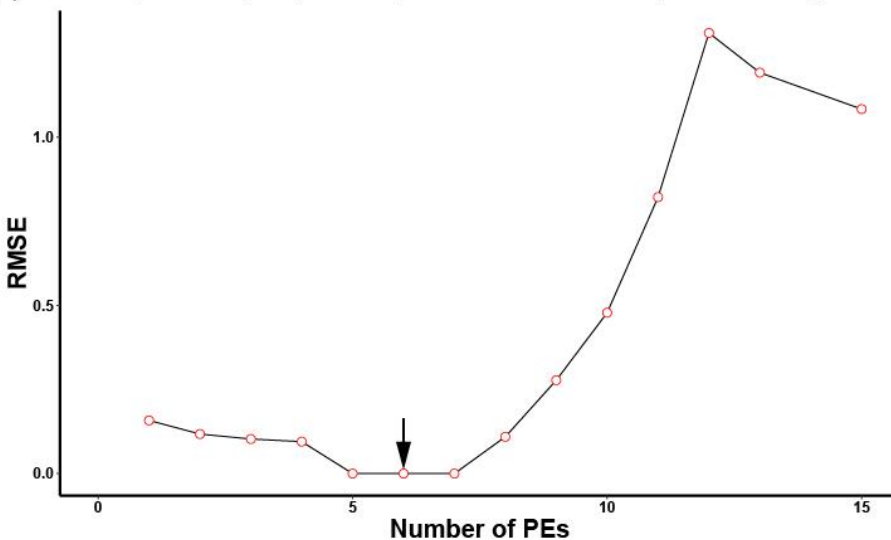


Fig. S7 Root mean squared errors (RMSEs) from each Bayesian Hierarchical Probabilistic Matrix Factorization (BHPMF) imputation using different numbers of phylogenetic eigenvectors (PEs). RMSE is a quadratic scoring rule that also measures the average magnitude of the error; it is the square root of the average of squared differences between prediction and actual observation. It can range from zero to ∞ and is indifferent to the direction of errors. It is negatively oriented scores, which means lower values are better. The RMSE is the biggest for the imputation with 12 PEs, then it decreases with increasing PEs, and keeps stable at about 0.85 until the imputation with 1000 PEs (the maximum number of PEs investigated) (a). (b) The imputation with six PEs has the smallest RMSE value (0.087), followed by imputations with five or seven PEs (0.089). Thus, the final imputation selected six PEs (the black arrow in (b), which is an enlarged figure to show the part in the blue box in (a)).

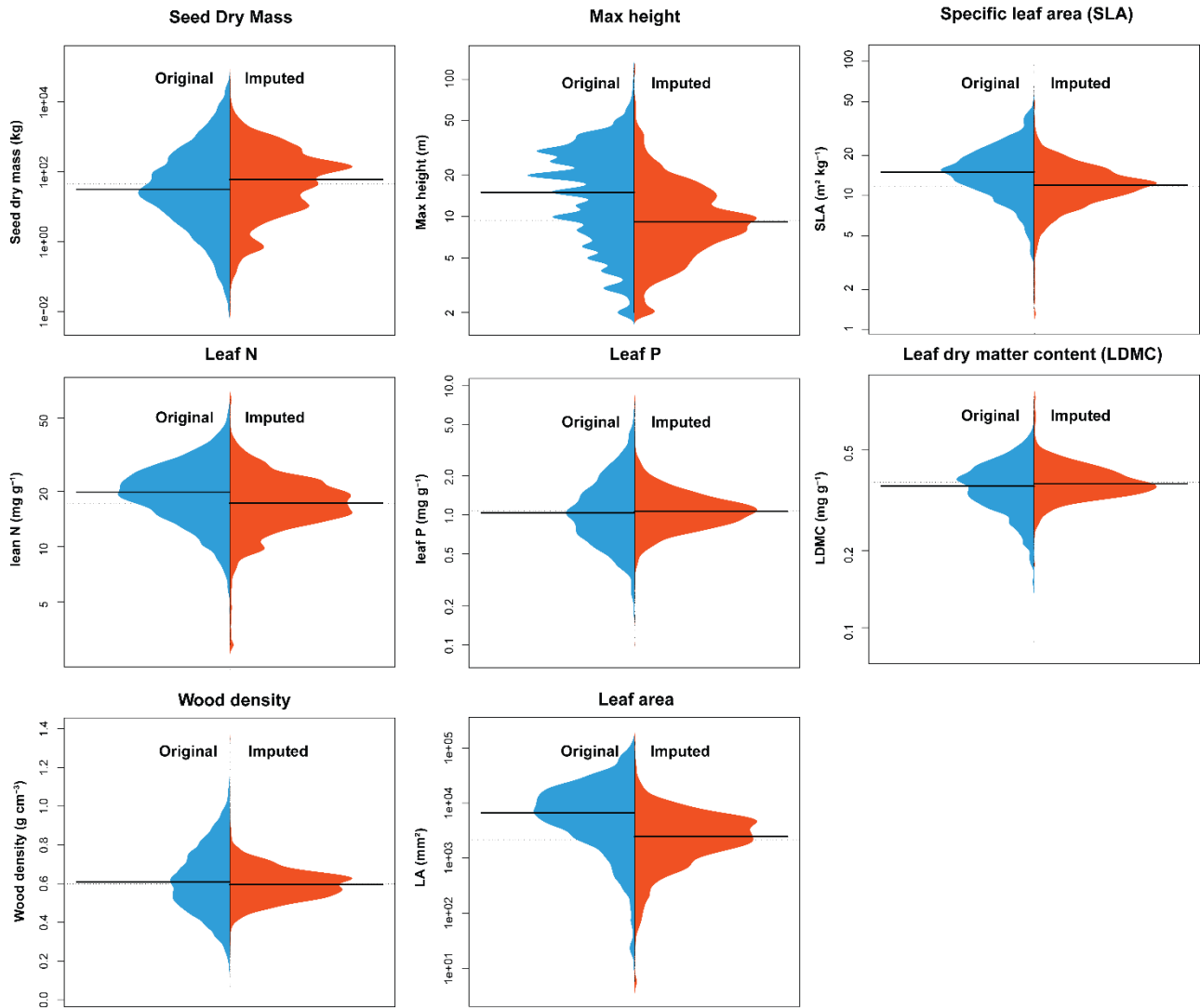


Fig. S8 Asymmetric beanplots to compare the density distributions of original and imputed data for the eight functional traits used to calculate functional diversity. The black line indicates the median of each dataset.

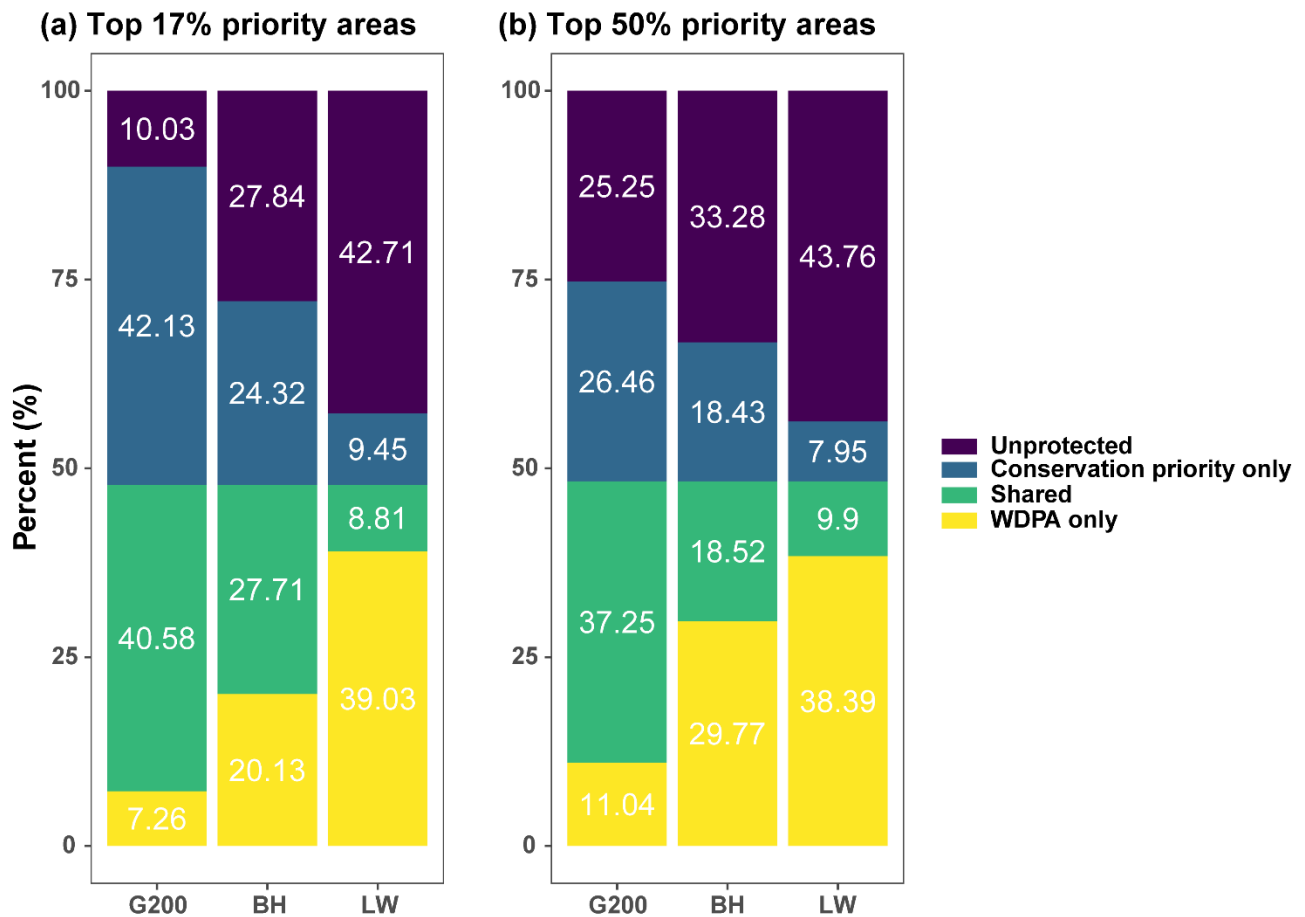


Fig. S9 Percentages of the top 17% (CBD 2020 target) and top 50% (CBD 2050 target) priority areas for tree diversity covered by the existing protected areas (WDPA) or by each global biodiversity conservation priority framework (G200, BH, and LW). Data were from the combined priority areas, i.e., combining the top priority areas of the three diversity dimensions. Unprotected: areas not overlapping with either WDPA or the conservation priority framework; Conservation priority only: areas overlapping with conservation priority framework only; Shared: areas overlapping with both WDPA and conservation priority framework; WDPA only: areas overlapping with WDPA only. G200: Global 200 Ecoregions; BH: Biodiversity Hotspots; LW: Last of the Wild.

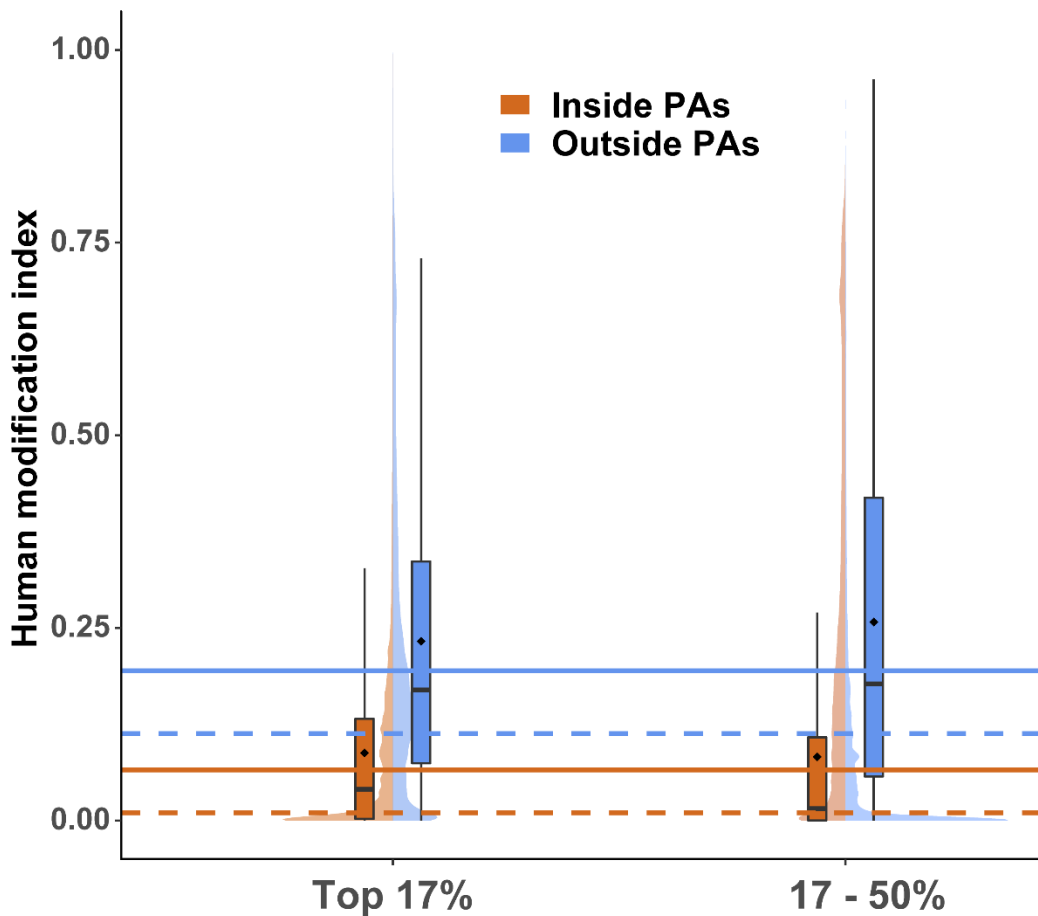


Fig. S10 Split violin density plot of the human modification index across tree diversity conservation categories (top 17%, and top 17 - 50% of the priority scores from the Zonation prioritization). Data were from the combined priority areas, i.e., combining the top priority areas of the three diversity dimensions. Each category is divided into two groups: areas inside (dark orange) and outside (light blue) protected areas (PAs, following the World Database on Protected Areas (WDPA) database). For each category, there are two subplots: a boxplot and density plot. Medians and means each are indicated by solid lines and points in the boxplots. The horizontal solid lines and dashed lines indicate the global mean and median human modification values for the areas inside and outside PAs, respectively. All values were obtained from 1- km² resolution input layers (see Methods for more information).