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Supplementary Materials for

The global distribution of plants used by humans

S. Pironon *et al*.

Corresponding author: S. Pironon, s.pironon@kew.org

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Other Supplementary Material for this manuscript includes the following:

MDAR Reproducibility Checklist

Materials and Methods

List of plant species used by humans

Analyses in this paper are based upon the "World Checklist of Useful Plant Species" (*21*). We use the term "utilised plant" to refer to vascular terrestrial plant species for which material and non-material benefits to humans have been documented and made publicly accessible. Uses may represent direct (e.g., food, medicine, material) or indirect benefits (e.g., contributions to environmental services such as water, soil or air quality protection). Utilised plants may be wild, introduced, cultivated or weeds. Their uses may have been reported at different time periods (from prehistory to contemporary times), scales (from local to global, by individuals or societies), and economic levels (from local personal use to commercial enterprise). Although commonly referred to as "useful" plants in the literature, we used the term "utilised" here to avoid relying on the subjective concept of "usefulness" and rather focus on the simple fact of a plant being known to be used. In fact, it is likely that all plants have an effective or potential use, but utilised plants are those for which the use by humans is documented in the scientific literature. This definition, derived from (*52*, *53*), was employed in the 2020 State of the World's Plants and Fungi report (*11*, *21*).

The checklist was compiled using 12 available datasets, of which five have a global coverage: *Crop Wild Relatives* ((*54*), https://www.cwrdiversity.org), Royal Botanic Gardens (RBG), Kew's *Economic Botany Collection* (http://apps.kew.org/ecbot/search), *Germplasm Resources Information Network* (GRIN) from the United States Department of Agriculture (USDA; https://www.ars-grin.gov), *Medicinal Plant Names Services* version 8.2 (http://www.kew.org/mpns (*55*, *56*)), and *Palms of the World Online* (http://www.palmweb.org); two cover primarily South-East Asia: *Plant Resources of South-East Asia* (PROSEA (*57*)) and *the indigenous knowledge of New Guinea's useful plants* (*58*, *59*); three span primarily Africa: *Plant Resources for Tropical Africa* (PROTA; https://www.prota4u.org/database), *Useful Plants of West Tropical Africa* (UPWTA; (*60*)) and *Survey of Economic Plants for Arid and Semi-Arid Lands* (http://apps.kew.org/sepasalweb/sepaweb); one has an American coverage: *Plants for Malaria, Plants for Fever: medicinal species in Latin America* (*61*); and one project (Project MGU – the Useful Plants Project (UPP; (*62*)) covers plants from both the Americas and Africa. A more comprehensive description of the data sources is provided in Table S1 and (*21*). We acknowledge that these 12 datasets do not constitute a complete list of all plant species used by humans across the world and knowledge gaps remain; nevertheless, this selection of such a range of large-scale databases covering different continents, disciplines, and taxonomic groups constitutes the most comprehensive source of utilised plant data. Because potential gaps, biases and uncertainties inevitably remain in plant use data, and those have not been assessed previously at global scale contrary to plant distribution data (e.g., (*22*)), we then adopted a cautious approach by mainly focusing our analyses on regional to continental differences and latitudinal gradients, and by avoiding over-interpretation. Our study thus emphasises the need for additional collection and collaboration efforts to document and understand the sampling distribution of plant use data at multiple spatial and temporal scales.

Describing plant uses requires a standardisation of use categories and terminologies. Our study used an adapted version of level 1 of the Economic Botany data standards (*20*) with the ten following plant use categories:

1. FOOD: Food for humans only, including beverages and food additives (*45*).
2. ANIMAL FOOD: Forage and fodder for vertebrate animals only.
3. INVERTEBRATE FOOD: Plants consumed by invertebrates used by humans, such as bees, silkworms, lac insects and edible grubs.
4. MEDICINES: Both human and veterinary.
5. POISONS: Plants which are poisonous to both vertebrates and invertebrates, both accidentally and intentionally, e.g., for hunting and fishing, molluscicides, herbicides, and insecticides.
6. MATERIALS: Woods, fibers, cork, cane, tannins, latex, resins, gums, waxes, oils, lipids, etc. and their derived products.
7. FUELS: charcoal, petroleum substitutes, fuel alcohols, etc. Given the importance of energy plants for people (*61*), those were distinguished from MATERIALS.
8. ENVIRONMENTAL USES: Examples include intercrops and nurse crops, ornamentals, barrier hedges, shade plants, windbreaks, soil improvers, plants for revegetation and erosion control, wastewater purifiers, indicators of the presence of metals, pollution, or underground water.
9. SOCIAL USES: Plants used for social purposes, which cannot be defined as food or medicine, for instance, masticatories, smoking materials, narcotics, hallucinogens and psychoactive drugs, and plants with ritual or religious significance.
10. GENE SOURCES: Wild relatives of major crops which may possess traits associated with biotic or abiotic resistance and may be valuable for breeding programs.

While original sources of data provide information about the identity of species uses, they do not consistently inform us about the parts of the plants that are used, the intensity of use, the identity and origin of the users, or the time at which the use has been observed; therefore, questions associated with this information have not been addressed in this study and will require further data collection at a smaller scale.

We standardised plant nomenclature and taxonomic following the World Checklist of Vascular Plants (WCVP) (*23*), which contains data for >1,400,000 scientific names found in the literature and >360,000 accepted names from >450 vascular plant families. To verify and correct species names, RBG Kew's semi-automated taxonomic names-reconciliation procedure was used (http://data1.kew.org/reconciliation/) to match names of each species of each source dataset against RBG Kew's taxonomic backbone on 26/11/2019. The backbone is built on the taxonomy from the WCVP employing names drawn from the International Plant Names Index (http://www.ipni.org). Once synonyms and non-accepted names were removed from the concatenated species lists, a total of 39,957 unique utilised plant species was retrieved (*21*).

Species distribution modelling

Our modelling framework follows standards and best practices recently highlighted in the literature (*64*, *65*), by pursuing the five following steps: 1. gathering and processing occurrence and environmental data, 2. selecting the modelling technique, 3. fitting models, 4. evaluating models, and 5. projecting species distribution.

1.a. Utilised plant occurrence data

We compiled occurrence records for each utilised plant species from the following seven databases: (i) Global Biodiversity Information Facility (GBIF, https://www.gbif.org; accessed on January-March 2020) using the function *get_gbifid* from the R package *taxize* for species name matching and then the function *occ_download* from the R package *rgbif* for downloading records; (ii) Botanical information and Ecology Network (BIEN version 4.1, https://bien.nceas.ucsb.edu/bien; accessed on January 2020) using the function *BIEN_occurrence_species* from the R package *BIEN*; (iii) RAINBIO, which provides direct access to wild and native species occurrence records from Sub-Saharan Africa, but from which we also obtained introduced and cultivated records directly from the authors (*66*); (iv) speciesLink, which provides occurrences for species found in Brazil (spLink, http://www.splink.org.br/); (v) BioTIME that provides local species assemblage data globally (*67*); (vi) Genesys from the global portal to information about Plant Genetic Resources for Food and Agriculture (PGRFA), discarding records from markets and stores (https://www.genesys-pgr.org); and (vii) the Crop Wild Relatives global occurrence database accessed via GBIF (http://www.cwrdiversity.org).

Because georeferencing errors, imprecisions and biases are common in occurrence databases and can significantly impact species distribution modelling (*68*), we first discarded possibly erroneous points found outside of each species' known geographic range according to the WCVP. Known ranges correspond to both species' native and introduced areas at the level-2 (regional or sub-continental scale) of the World Geographical Scheme for Recording Plant Distribution (WGSRPD) developed by the International Working Group on Taxonomic Databases for Plant Sciences (*69*). Here we used level-2 because level-1 (continental scale) was too coarse, and levels-3 and 4 (national/sub-national scales) were less reliable given a few countries have not been assessed by the WCVP and probabilities of assigning false presences and absences are significantly higher at local scale. We then used metadata information kept from primary data sources to only retain (i) records collected from 1945 onwards (*70*), and remove those with (ii) latitude or longitude coordinates out of their ranges ([−90, 90] and [−180, 180] respectively); (iii) coordinates uncertainty above 20 km; (iv) no decimal (i.e. rounded coordinates); (v) a count of individuals set to zero; (vi) both coordinates set to zero; (vii) coordinates equal to each other (i.e. latitude equals longitude); (viii) coordinates located within a buffer distance of ten kilometers around the centroids of countries, provinces, capitals, and botanical institutions, and (ix) within a buffer distance of 1km around the GBIF headquarters. We used the *cc_** functions from the R package *CoordinateCleaner* (*71*) to clean the data according to the nine points given above. To limit spatial autocorrelation and avoid redundant information (*72*), we finally kept only one record per ten arc-minutes (~20 km) grid cell for each species.

After cleaning, we did not retrieve any occurrence point for 4,270 utilised plant species. We thus performed analyses for 35,687 species (89% of the original list), of which 6,461 (18%) have reported uses for human food, 4,087 (11%) for animal food, 971 (3%) for invertebrate food, 23,842 (67%) for medicines, 2,816 (8%) for poisons, 12,418 (35%) for materials, 2,348 (7%) for fuels, 8,314 (23%) for environmental uses, 2,385 (7%) for social uses, and 4,713

(13%) for gene sources (considering that species can have more than one use). The final occurrence dataset contained >11 million records (Fig. S2).

1.b. Environmental data

We assembled an original set of 28 environmental variables. We used the 19 bioclimatic variables (temperature and precipitation averages over the 1979–2013 period) provided by the Climatologies at High resolution for the Earth's land Surface Areas (CHELSA v.1.2). CHELSA has recently shown to outperform other climate data products for predicting species distribution (*73*). We collected four terrain variables calculated from a Digital Elevation Model (DEM) provided by the Global Multi-resolution Terrain Elevation Database (GMTED) (*74*): terrain roughness (*R*) and Topographic Ruggedness Index (TRI), two measures of local terrain heterogeneity as the maximum difference and the square root of averaged differences in elevation found within 3-by-3 cell size windows around each grid cell, calculated using the *focal* function from the R package *raster*; Topographic Wetness Index (TWI), calculated with the GRASS GIS (version 7.6.0) (*75*) *r.topidx* module, that combines local land slope and the upslope area converging to a grid cell to describe hydrological processes contributing to soil wetness spatial patterns; and the land slope, calculated with the function *Slope* from the *Spatial Analyst toolbox* of ARC/INFO GIS ESRI (version 10.5). We used three soil related variables (averages across a range of 0-1m depth) obtained from the International Soil Reference and Information Centre (ISRIC; http://www.data.isric.org): soil organic carbon stock (SOC), soil pH, and soil water capacity (*76*). We also considered the Enhanced Vegetation Index (EVI) derived from MODIS time-series data spanning the 2000–2013 period, extracted from the LEFT tool (*77*), and the Human Footprint Index representing the anthropogenic impacts on the environment for the 1995–2004 period based on human population pressure, land use and infrastructure, and access, and produced by the Wildlife Conservation Society (WCS) and the Columbia University Center for International Earth Science Information Network (CIESIN) (*78*). The 28 variables were available for time slices that do not always match with each other's and occurrence data; however, we believe that considering a wide set of climatic, vegetation, edaphic, topographic, and human-related variables would better help unravel the distribution of utilised plants for the broad period going from mid-20th to early 21st century. For homogeneity and to match our occurrence records, all layers were resampled at a ten arc-min resolution and masked non-terrestrial lands based on the revised map of Terrestrial Ecoregions of the World (*79*), using the *Resample* and *ExtractbyMask* modules from the geoprocessing toolboxes *Data management* and *Spatial Analyst* of ArcGIS.

From this pool of 28 variables, we then made a sub-selection intending to: (i) capture most of the variation in environmental conditions across the world; (ii) limit multi-collinearity, and (iii) make the most sense ecologically (*80–82*). We performed a Principal Component Analysis (PCA) using the function *dudi.pca* from the R package *ade4* to assess how much of the variance is explained by the variables and correlations among them. Then, we carried out a stepwise selection and a pairwise correlation analysis to exclude (multi-)collinear variables. The former consists in iteratively computing the Variance Inflation Factor (VIF) (*83*) of each variable and excluding one variable at a time if its VIF value exceeds a threshold of ten, until all remaining variables have VIF values below ten. The latter consists in excluding variables with the highest VIF values out of pairs of highly correlated variables (i.e., Pearson's correlation coefficient $r > 0.7$). VIF analyses were conducted using functions *vifstep* and *vifcor* from the R package *usdm*. Based on the combination of these analyses and criteria, we finally selected nine predictors: precipitation seasonality, mean temperature of the coldest quarter, precipitation of the driest quarter, terrain roughness (*R*), Topographic Wetness Index (TWI), Enhanced Vegetation Index (EVI), Soil Organic Carbon stock (SOC), mean soil pH and the human footprint index. This diverse set of variables is well known to influence plant species distribution (*84–86*).

2. Algorithm selection

Occurrence records alone are unreliable to retrieve species richness patterns and macroecological transitions due to the numerous geographic and taxonomic biases that they contain (*22*, *87*). However, they have been shown to perform better when modelled along environmental gradients (*87*). To retrieve species composition and richness across space, we therefore decided to use a "stacked-species distribution" approach, which consists in stacking modelled species distribution maps (*88*). Species Distribution Models (SDMs) are probabilistic models relating species occurrence to environmental variables to project their distribution across space and/or time through an estimate of environmental similarity (*89*). Many species distribution modelling techniques are available, but we decided to use MaxEnt version 3.4.1. as it is a commonly used model that (i) relies on presence-only data and (ii) has shown to be one of the methods performing best in many different ecological contexts (*81*, *90*). Because SDMs are sensitive to sample size (*91*), simpler models are usually recommended when very few occurrence points are available for each species (*92*).

Geographic models (GMs) can provide a suitable alternative to SDMs since they do not rely on an environmental niche approach but rather consider the spatial structure of occurrence locations. They can recover endogenous spatial determinants such as dispersal limitation, which are particularly important factors shaping the distribution of small range species (*93*). Therefore, we decided to fit a GM for species having less than ten occurrence records. The minimum number of ten points to fit SDMs may prevent from overfitting, which often occurs when the number of explanatory variables (nine in our case) exceeds the number of predictors (low degree of freedom). Because GMs cannot be used for extremely low sample size (e.g., for very rare species), we simply rasterised occurrences for species having less than three points using the function *fasterize* from the R package *fasterize*.

3. Model fitting

MaxEnt contrasts environmental conditions where species have been observed with conditions available or accessible in their surroundings (i.e., background region). Background selection is such a critical step of the modelling process (*64*) that we decided to individualise it for each species, as recommended in (*94*). We built an alpha-hull around occurrence points, which is a generalization of the convex-hull particularly useful for estimating species ranges whose habitat is irregularly shaped (*95*). Alpha-hulls were buffered using the "1/10th maximum" method to better account for spatially structured populations (*96*). We then selected the biomes (*79*) that intersect with the alpha-hull. To avoid extreme cases where a small alpha-hull intersects with biomes spreading over vast territories and provides an oversized background, we implemented two conditions: (i) the number of occurrence points lying inside each intersected biome must be higher or equal to ten, and (ii) the proportion of the biomes' area covered by the alpha-hull must be higher or equal to ten percent. If the conditions are not met for a particular biome, we then selected the ecoregion (*79*). Since the alpha-hull algorithm was set up to exclude up to 5% of the records (i.e., geographic outliers), we also searched for the ecoregion polygons occupied by these points and merged them back to the background. Thus, the background region extends to the boundaries of the biomes or ecoregions where species were found and where other populations could potentially occur.

Occurrence records are highly unevenly distributed in space and biased towards developed countries and sampling priorities of major botanical institutions (*22*, *97*). As this uneven geographic coverage may significantly impact species distribution modelling, we accounted for this bias by (i) generating a biased prior map giving a non-uniform weighting to background points (*90*, *98*, *99*), and (ii) integrating this map into the model building through the MaxEnt argument *biasfile*. This bias map representing the effort in sampling utilised plants was generated in two steps: (i) we used the *rasterize* function of the *raster* package in R to count the total number of utilised plant occurrence records found in each ten arc-min grid cell (based on the original dataset, before removing points occurring in the same cells), and (ii) we used the *kde2d* function from the R package *MASS* to interpolate these counts using a two-dimensional kernel density estimator with a two degrees bandwidth value (Fig. S1).

We ran MaxEnt models for 28,235 (79%) utilised plant species using the *biasfile*, a maximum number of 500 iterations and 50,000 samples from the background area. We specified an automatic selection of response shapes (hereafter called feature classes) and allowed MaxEnt to fit linear, quadratic, product (interaction) and hinge (threshold-like response) feature classes to the data. We used the complementary log-log output (cloglog), which is a more appropriate estimate of species probability of presence that avoids assumptions about species prevalence (*100*).

We fitted GMs for 5,464 (15%) utilised plant species using the Inverse Weighting Distance (IDW) method (*101*). IDW is a spatial interpolation model that computes the probability of occurrence as a weighted average of neighboring occurrences, with weights inversely proportional to the distance between locations. Distance-based GMs thus assume that species are more likely to occur close to known locations than further away (*93*). Since IDW requires absence data, we generated pseudo-absences to achieve a minimum prevalence of ten percent (i.e., 1:10 ratio between the number of cells occupied by species records and the number of non-occupied cells in the study ecoregion). IDW also requires a local neighborhood that we defined as the seven nearest locations using the function *geoIDW* from the R package *dismo*. Occurrence records were directly rasterised for the remaining 1,988 species (6%) that had less than three cleaned occurrence points.

4. Model evaluation

We used a species-specific tuning of the MaxEnt β regularization coefficient (hereafter called β multiplier) to assess the performance of our SDMs, as recommended in the literature (*98*, *102*). MaxEnt uses the β multiplier to prevent the model from overfitting, notably by penalizing the use of overly complex feature classes. We use the masked geographically structured approach (*102*) to explore a range of β multipliers based on (*103*, *104*): 1(default), 2, 6, 10.

This method is a variant of the *k-fold* cross-validation that provides a better ability to detect overfitting and more realistic estimates of model performance than other cross-validation approaches (*102*). We spatially segregated the occurrence records into $k=3$ geographical bins with approximately the same number of points in each bin using a customised algorithm using the *kmeans* function from the R package *stats*. Models were then trained iteratively using k-1 (= 2) bins and tested on the third. At each iteration, we calculated for each β multipliers: (i) the corrected Akaike Information criterion (AIC_c) (*103*, *105*) using the function *ic* from the R package *rmaxent*, (ii) the tenth percentile of the training omission rate (OR10) and (iii) the Area Under the Curve of the receiver operating characteristic on the testing dataset (AUC) as exported automatically from MaxEnt (*106*), and (iv) the maximum of the True Skill Statistics (TSS) (*107*) using the functions *prediction* and *performance* of the R package *ROCR*. We averaged these values over the iterations and ranked as *best model* the one with the regularization multiplier giving the lowest AIC_c. When the difference between the AIC_c values of the top models was not substantial (i.e., $\Delta AIC_c < 2$), we ranked them successively by the lowest $OR10_{test}$, highest TSS_{test} and highest AUC_{test} (where the subscript test indicates that the metric is calculated on the testing dataset). We therefore ranked the models according to their capacity to minimise overfitting before accounting for their discriminatory ability, as recommended in the literature (*102*, *108*).

GMs' predictions were assessed using the *leave-one-out* (LOO) method, a form of *k-fold* cross-validation suitable when sample size is small (*109*). LOO consists in iteratively training the model using *n-1* data points (where *n* is the total number of points) and testing on the withheld point. The AUC was computed and averaged across the iterations.

5. Projection of species distribution, richness, and endemism

Individual SDMs performed well according to AUC (mean AUC: 0.809 ± 0.121; Fig. S3), OR10 (mean OR10: 0.239 ± 0.137; Fig. S4), and TSS (mean TSS: 0.618 ± 0.160; Fig. S5) values, which indicate good discriminatory ability of the models and minimised overfitting. GMs indicate fair overall performance (mean AUC: 0.741 ± 0.177; Fig. S6). We therefore projected the probability of occurrence of each species from our SDMs and GMs onto the geographical area used for model training (background region) based on species biomes and/or ecoregions and known total range (i.e., native and introduced) or native range only according to the WCVP. Probabilities of one were assigned to the pixels occupied by the 1,988 (6%) utilised plant species represented by less than three records.

To retrieve species richness across space, we used a "Stacked-Species Distribution Models" (S-SDMs) approach, which consists in stacking individual species distribution maps obtained from SDMs (*88*). We summed species occurrence probabilities instead of using thresholded (binary) maps, as this has been shown to provide better estimates of species richness (*110*). We repeated this process considering species native and introduced ranges, and native ranges only to retrieve two global maps of species richness. Areas containing a large proportion of species with restricted ranges are potentially highly irreplaceable and do not match areas with high species richness, so they represent major targets for conservation (*5*, *6*, *111*). For this reason, we also estimated endemism as the sum of each species' occurrence probabilities weighted by the inverse of their range size calculated as the sum of the predicted probabilities within their study region (*112*, *113*). Finally, given that the location of the different uses of the 35,687 species remains largely unknown, we stress that our study does not intend to map the uses of plants but rather the distribution of species documented to be used somewhere in the world. Therefore, our results rather refer to a potential usage of the species occurring in different regions of the world rather than their actual use in those regions. Similarly, temporal variation in plant uses has not been quantified at such large taxonomic and spatial scales. Our results thus report a rather static view of the global distribution of plants used by humans.

Although we used extensive information and accounted for sampling biases in our modelling framework, SDM predictions can still suffer from data incompleteness and uncertainty (*22*). For this reason, we also mapped utilised plant species richness and weighted endemism using independent data from the WCVP at the level-3 of the WGSRPD (*69*). Level-3 provides plant species distribution data at a country scale for most of the world, except in a few large countries for which information is available at a sub-country scale. While species richness is simply the count of species found in each level-3 region, weighted endemism weighs each species by the total area of level-3 regions that it occupies. To account for differences in surface area between regions, we estimated a scaling exponent that describes the species-area relationship (SAR) between the counts of species (weighted or not) and the level-3 region areas (z-values range between 0.101 (social uses) and 0.141 (all uses)). Then, we used this exponent to rescale species counts for a standard area of 10,000 square kilometers as in (*114*). We executed this procedure for all utilised plant species together and for each individual use category.

Analyses

We investigated the variation of utilised plant species richness and weighted endemism across latitude, a well-known biogeographical gradient (*115*). To achieve this, we fitted Generalised Additive Models (GAM) between latitude and species richness/weighted endemism values across all pixels of our global maps following the approach from (*116*). Model fitting was performed using the function *bam* from the R package *mgcv* with our predicted estimates of species richness and weighted endemism per grid cell as response variable and a penalised cubic regression spline on the latitude of the grid cells as smooth term. Then, we predicted utilised plant species richness/endemism for each unique latitude value and divided each prediction by the total sum of the predictions to obtain a relative measure of utilised plant species richness/endemism along the latitudinal gradient. To better visualise differences among plant use categories, we considered species richness and endemism across all utilised plants grouped together as a baseline and then represented the deviation of the latitudinal patterns of each use category from this baseline. We used the function *hclust* from the *stats* package to assess (dis-)similarities and clustering among latitudinal profiles of each use by building dendrograms.

We assessed potential associations between distribution patterns in the diversity of all plant species, utilised plant species, and human cultures. To our knowledge, no continuous map is available for both overall plant richness and cultural diversity, thus we worked at a country scale. Estimates of human cultural diversity were compiled by (*117*) for 256 countries. Estimates of total vascular plant species richness/endemism and utilised plant species richness/endemism were compiled from the WCVP (*23*). Level-3 geographic data were aggregated at a country scale for each individual species using a global map of countries provided by the Database of Global Administrative Areas (GADM; http://www.gadm.org) version 3.6, before computing area-corrected richness and weighted endemism indices as described previously (Figs. S15-16). Due to geographic mismatches between certain botanical regions and countries, and the absence of cultural diversity data for certain territories, we only kept 163 countries for analyses. Cultural diversity is a composite index made of three estimates: total number of languages, religions, and ethnic groups per country (*117–119*). The cultural diversity index uses SAR to account for variable country sizes and ranges from 0 to 1, with values close to 0 indicating the least diverse countries and values close to 1 the most diverse ones. We assessed relationships between human cultural diversity, total plant, and utilised plant species richness/endemism using Generalised Least Squares (GLS) models with the *gls* function of the R package *nlme*. Unlike Ordinary Least Squares (OLS) models, GLSs allow to accommodate for potential spatial (auto-)correlation in the data. We used the latitude and longitude coordinates of the centroids of each country as spatial covariates, and tested three different correlation functions: exponential, gaussian and spherical. We fitted our GLS models using the restricted maximum likelihood method (REML) and selected the correlation structure with the lowest AIC. Analyses were repeated for all utilised plants together and for each individual use category separately.

We assessed spatial associations between utilised plant species richness, endemism, Indigenous lands, and protected areas at a finer resolution given the availability of raster maps for all variables. Indigenous lands represent areas managed and/or controlled by Indigenous Peoples (as defined by the International Labour Organization (*120*)). The global map was built based on 127 source documents and provides a percentage of each 50 km grid cell covered by Indigenous lands across the world (*34*). The completeness of this data cannot be guaranteed; it represents known Indigenous land areas based on publicly available geospatial data only. We used the World Database on Protected Areas (WDPA) (*121*) to extract the percentage of all protected areas contained in each 50 km cell of the Indigenous land grid. The WDPA is the most comprehensive global database of marine and terrestrial protected areas, comprising both spatial data with associated attribute data. It includes protected areas that meet definitions set by the International Union for Conservation of Nature (IUCN) and the Convention on Biological Diversity (CBD). Protected area coverage was calculated using ArcGIS and ESRI's Modelbuilder. Utilised plant species richness and endemism maps obtained from SDMs were aggregated to the same 50 km resolution using the *Resample* tool from the *Data Management* toolbox in ArcGIS. Spatial correlations between utilised plant species richness/endemism and both Indigenous lands and protected areas were assessed by computing Pearson's correlation coefficients across all values contained in 71 cells (~3,550km)-wide windows built around each pixel. This resulted in global maps indicating the strength and direction of regional correlations between the different variables. The size of the moving window was selected so that all pixels of the world map have a correlation value (i.e., all windows contain at least one Indigenous land and one protected area) and our analysis provides a broad estimate of the geographical variation of the correlations at large spatial scale. For this analysis we used the *focal* and *cor* functions from the *raster* and *stats* R packages, respectively. All analyses and data processing were based on the R statistical software version 3.6.1, ArcGIS version 10.5 and GRASS GIS version 7.6.0.

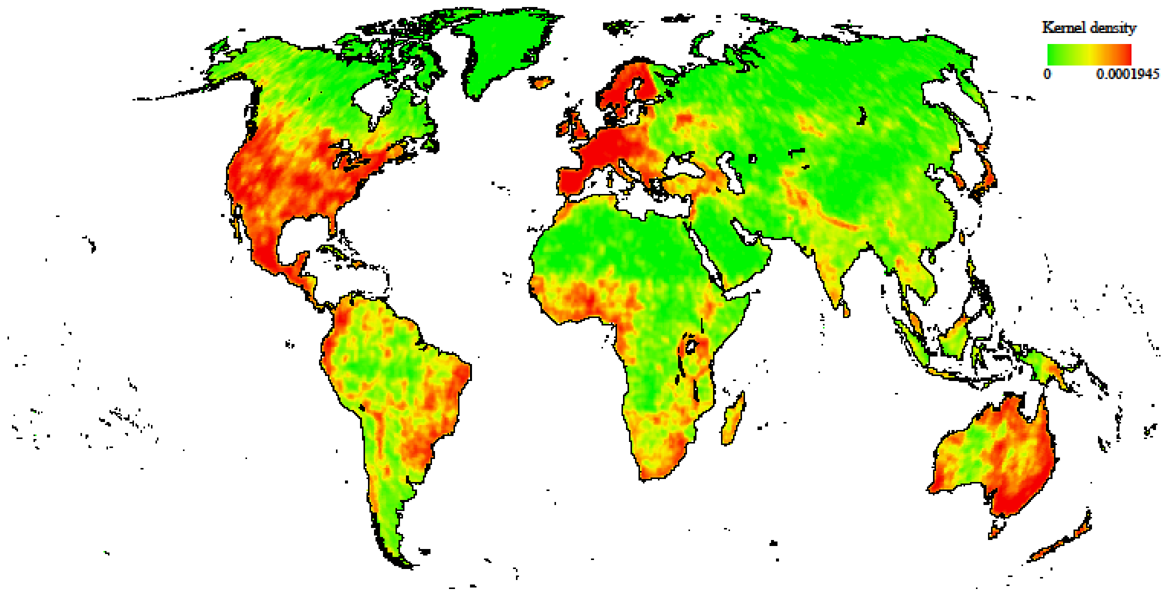


Figure S1. Sampling intensity in occurrence records for all utilised plant species. Red indicates high sampling density, whereas green indicates low sampling density based on counting the number of occurrence records available for all utilised plant species in each 400 km^2 grid cell and a kernel density probability approach providing a unitless relative index of density.

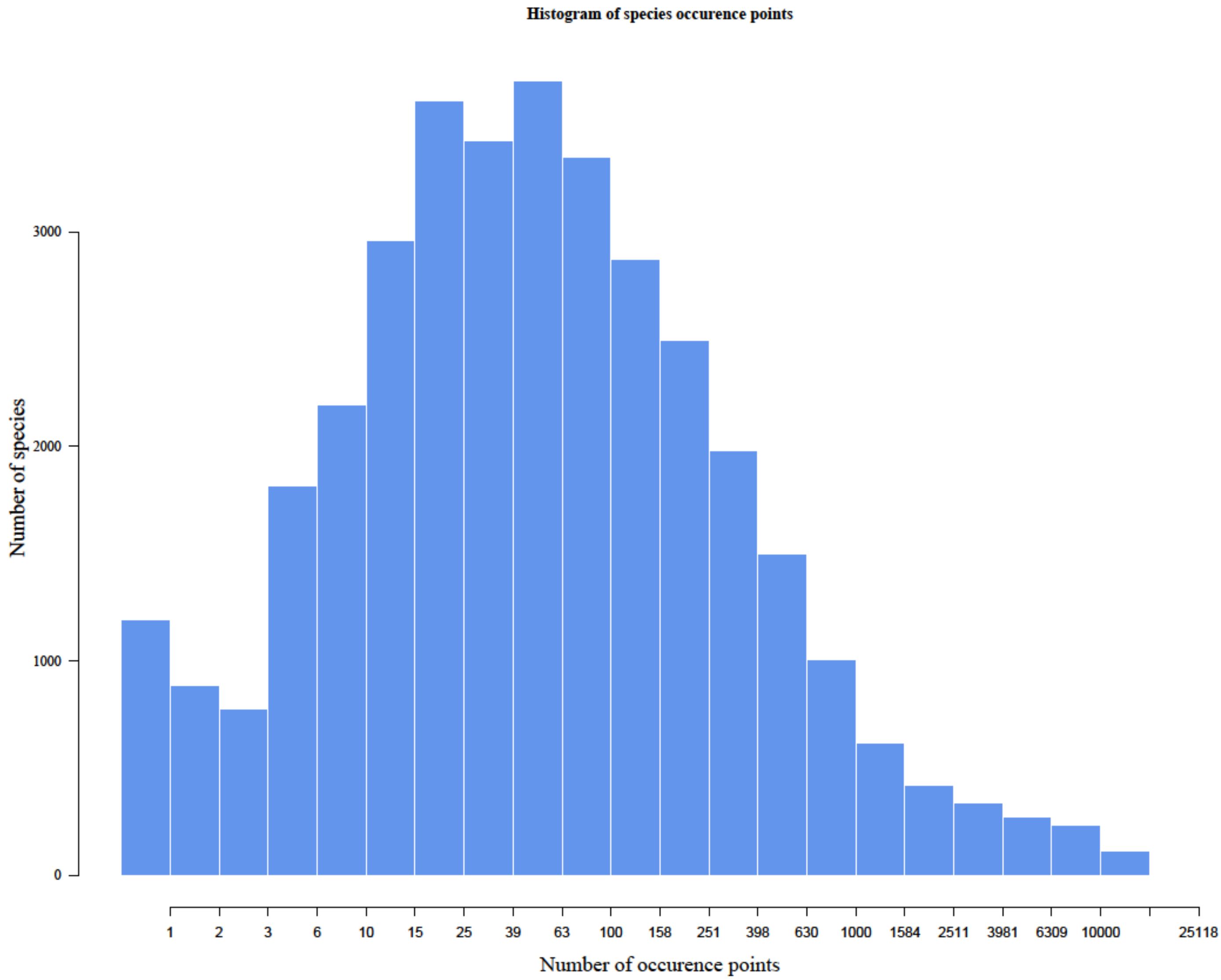


Figure S2. Number of occurrence records used for modelling the distribution of each utilised plant species.

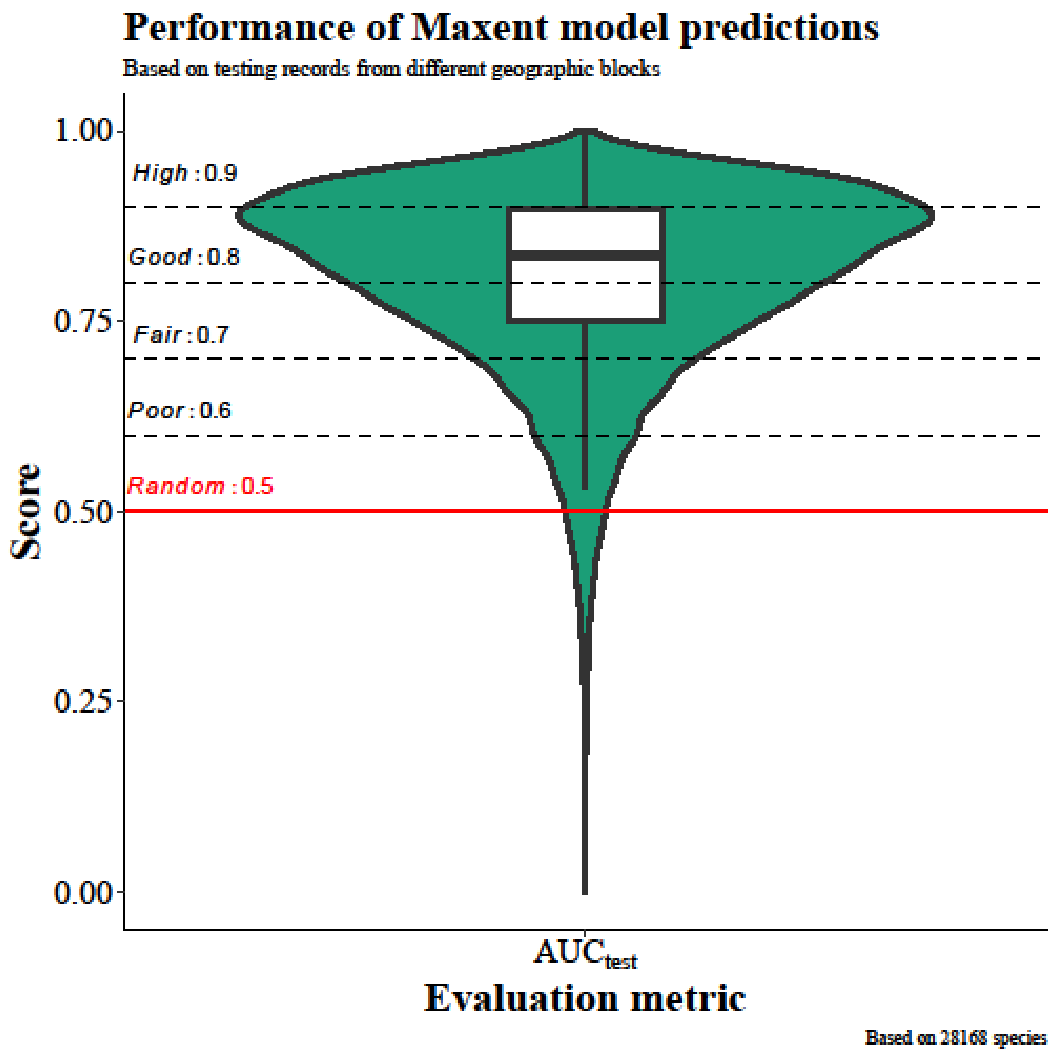


Figure S3. AUC evaluation scores of utilised plant species distribution models. Boxes represent upper and lower extremes, upper and lower quartiles, medians and outliers of AUC indices for all utilised plant species distribution models. Evaluation scores are given for MaxEnt models calibrated with more than ten occurrence records.

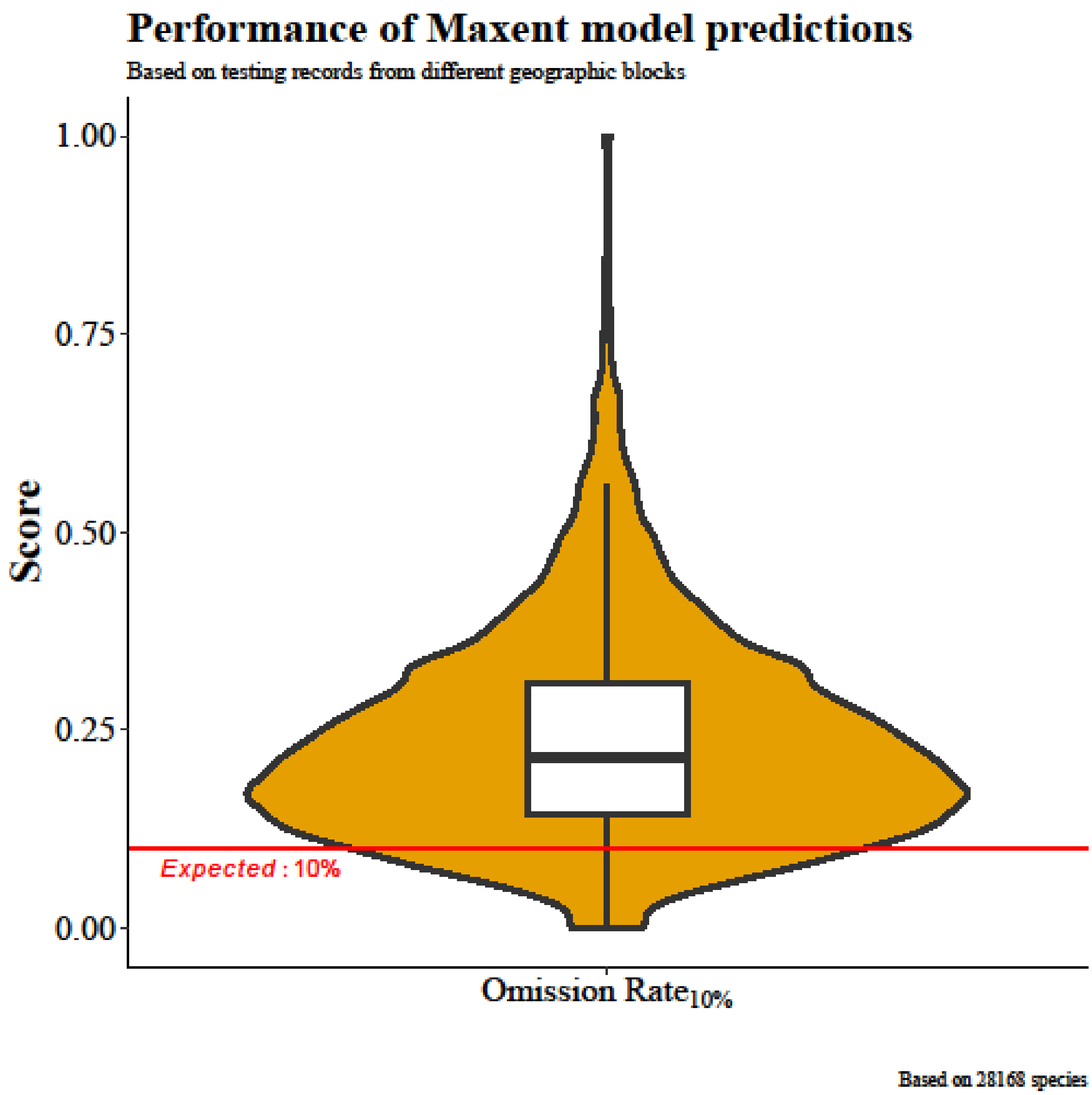


Figure S4. OR10 evaluation scores of utilised plant species distribution models. Boxes represent upper and lower extremes, upper and lower quartiles, medians and outliers of OR10 indices for all utilised plant species distribution models. Evaluation scores are given for MaxEnt models calibrated with more than ten occurrence records.

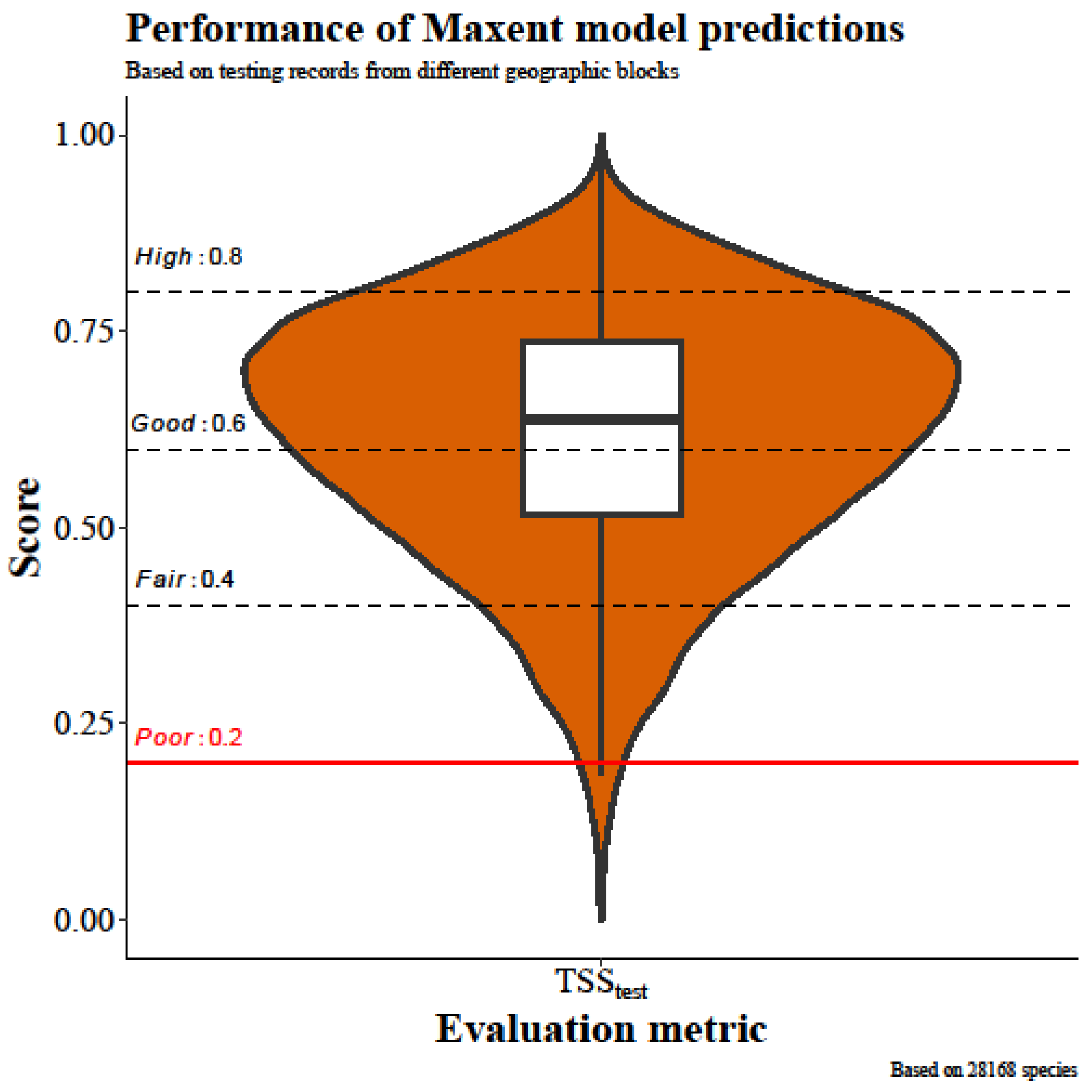


Figure S5. TSS evaluation scores of utilised plant species distribution models. Boxes represent upper and lower extremes, upper and lower quartiles, medians and outliers of TSS indices for all utilised plant species distribution models. Evaluation scores are given for MaxEnt models calibrated with more than ten occurrence records.

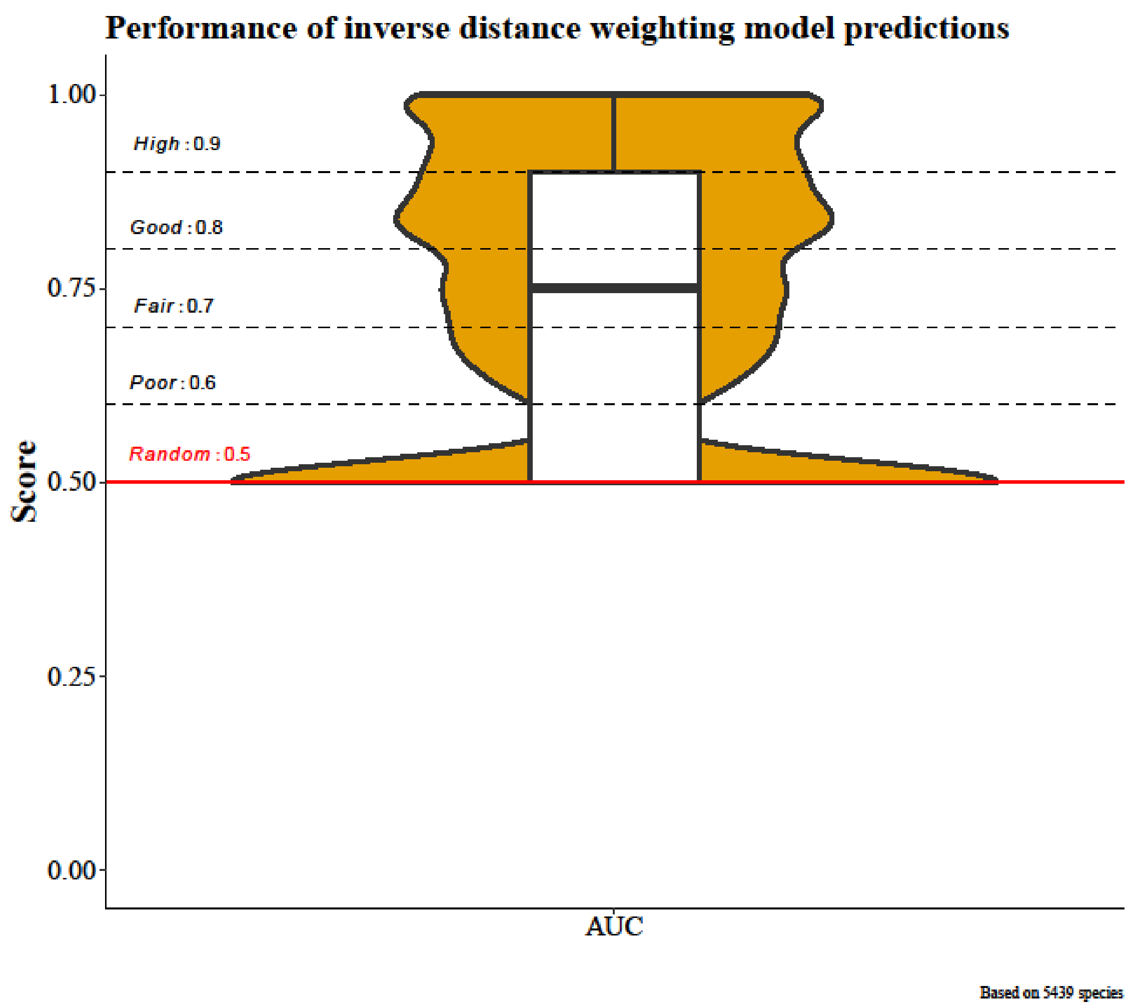


Figure S6. AUC evaluation scores of utilised plant species distribution models. Boxes represent upper and lower extremes, upper and lower quartiles, medians and outliers of AUC indices for all utilised plant species distribution models. Evaluation scores are given for geographic models (Inverse Distance Weighting) calibrated with less than ten occurrence records.

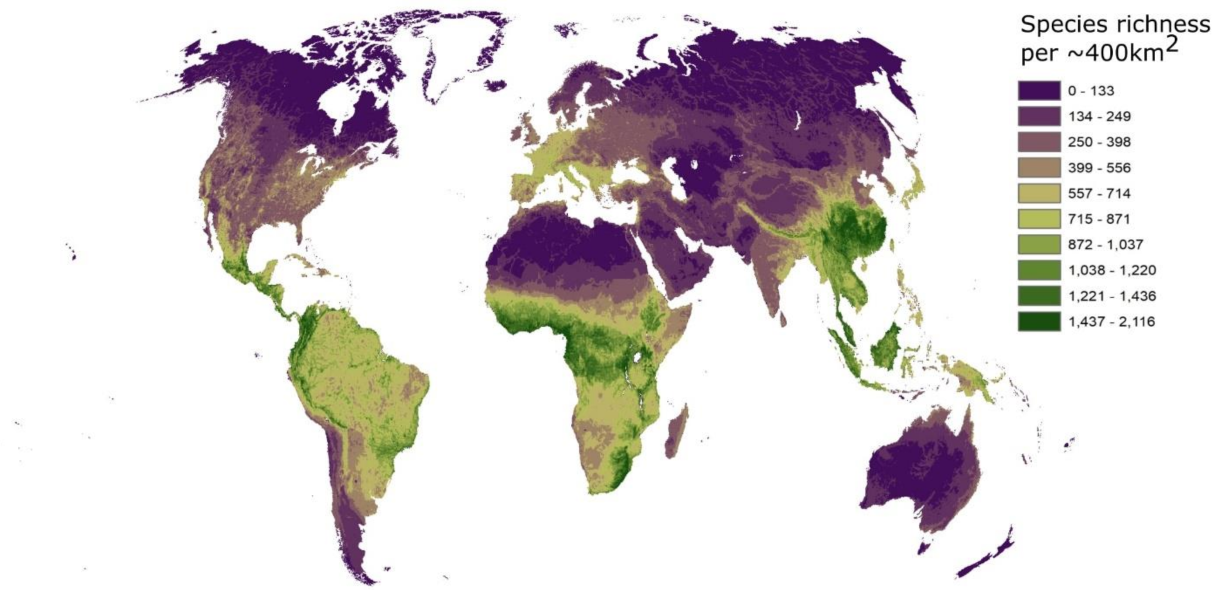


Figure S7. Global species richness of plants with known uses by humans. Utilised plant species richness corresponds to the sum of species occurrence probabilities predicted in each ten arc-minutes (~20 km) pixel found across their native ranges.

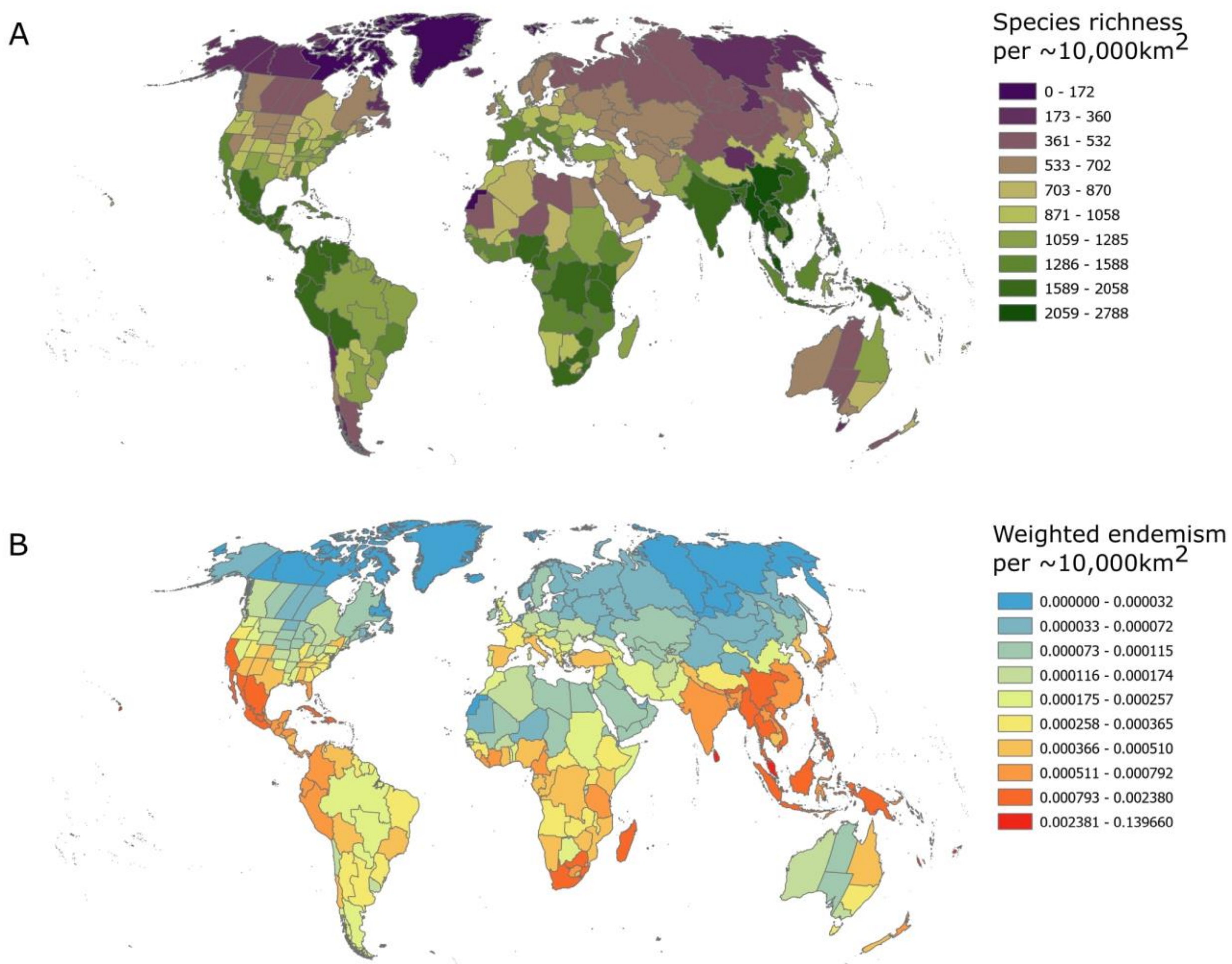


Figure S8. Global distribution of utilised plant species richness (A) and weighted endemism (B) at the level-3 (sub-national) of the World Geographical Scheme for Recording Plant Distribution (WGSRPD). Utilised plant species richness corresponds to the count of species found in each region. Utilised plant species endemism corresponds to the number of species present in each region weighted by the inverse of their range size calculated as the total area covered by the level-3 regions it occupies (i.e., weighted endemism). Geographic distribution for each species was retrieved from the World Checklist of Vascular Plants at the level-3 of the WGSRPD. To account for differences in surface area between regions, we estimated a scaling exponent that describes the species-area relationship (SAR) between the counts of species (weighted or not) and the level-3 region areas. We used this exponent to rescale species counts for a standard area of 10,000 square kilometers.

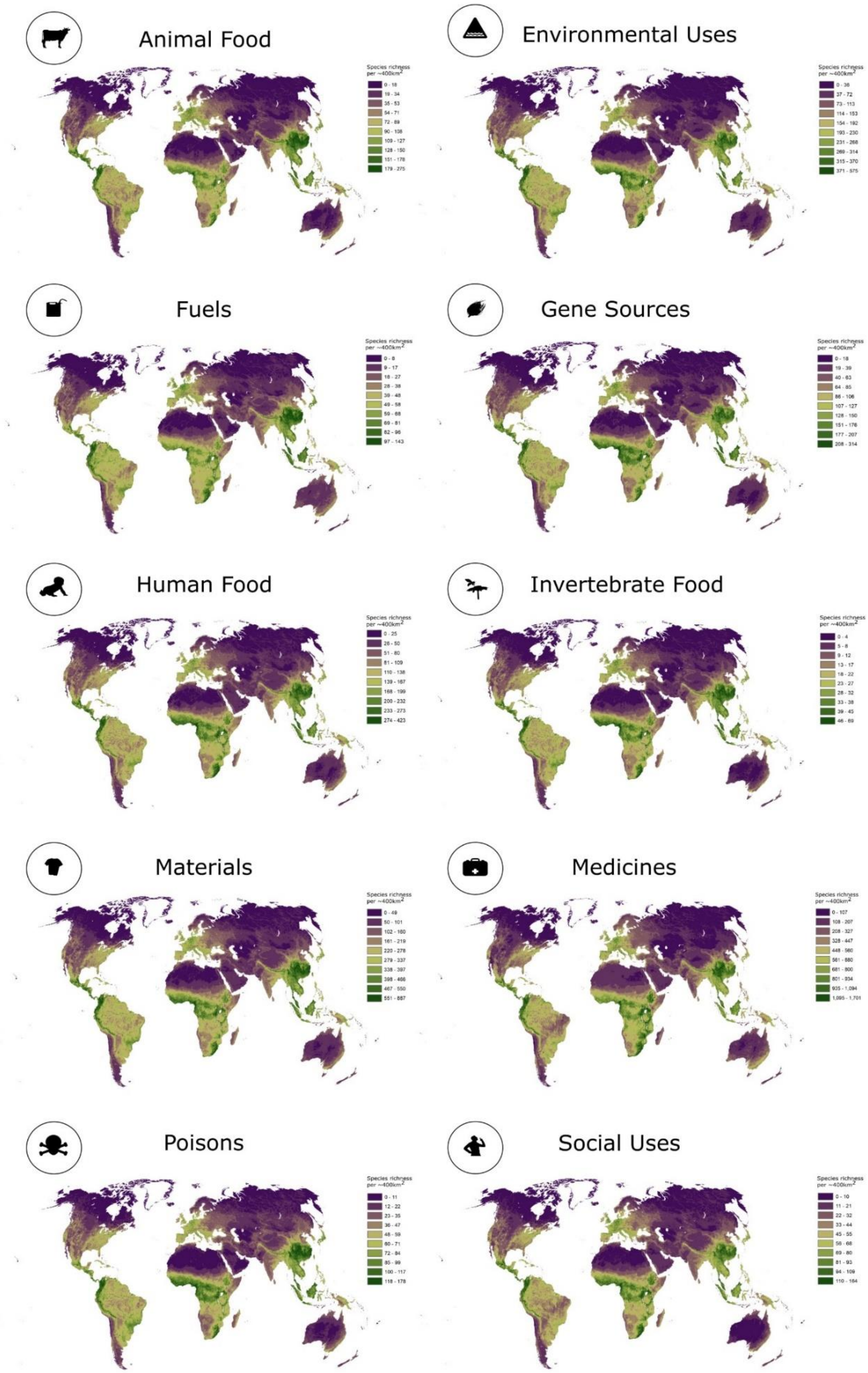
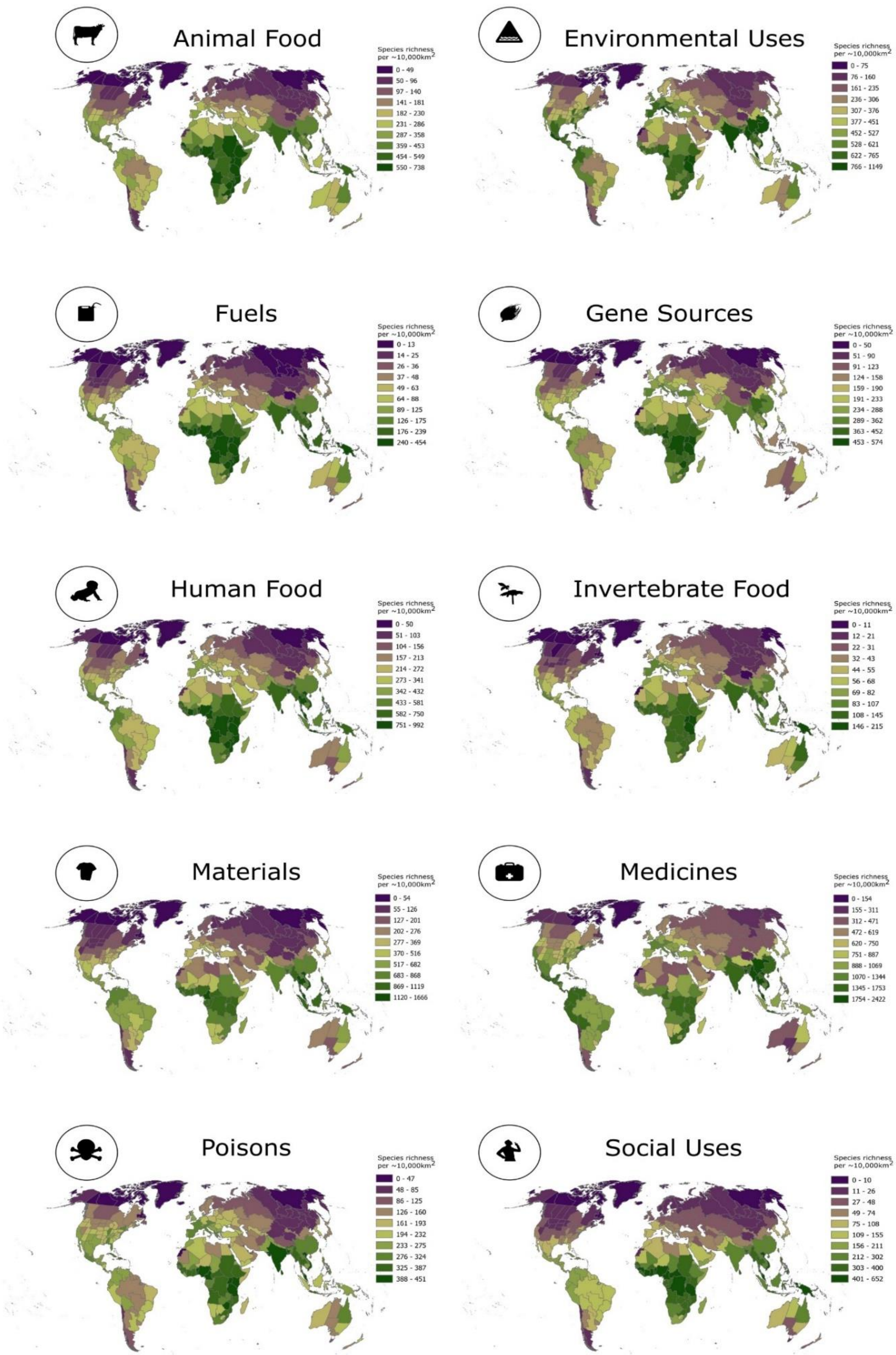

Animal Food
Environmental Uses
Fuels
Gene Sources
Human Food
Invertebrate Food
Materials
Medicines
Poisons
Social Uses

Figure S9. Global distribution of utilised plant species richness across ten categories of uses. Utilised plant species richness corresponds to the sum of each species occurrence probabilities predicted in each pixel by our “stacked-species distribution modelling” approach.



Animal Food
Species richness per ~10,000km2
0 - 49
50 - 96
97 - 140
141 - 181
182 - 230
231 - 286
287 - 358
359 - 453
454 - 549
550 - 738
Environmental Uses
Species richness per ~10,000km2
0 - 75
76 - 160
161 - 235
236 - 306
307 - 376
377 - 451
452 - 527
528 - 621
622 - 765
766 - 1149
Fuels
Species richness per ~10,000km2
0 - 13
14 - 25
26 - 36
37 - 48
49 - 63
64 - 88
89 - 125
126 - 175
176 - 239
240 - 454
Gene Sources
Species richness per ~10,000km2
0 - 50
51 - 90
91 - 123
124 - 158
159 - 190
191 - 233
234 - 288
289 - 362
363 - 452
453 - 574
Human Food
Species richness per ~10,000km2
0 - 50
51 - 103
104 - 156
157 - 213
214 - 272
273 - 341
342 - 432
433 - 581
582 - 750
751 - 992
Invertebrate Food
Species richness per ~10,000km2
0 - 11
12 - 21
22 - 31
32 - 43
44 - 55
56 - 68
69 - 82
83 - 107
108 - 145
146 - 215
Materials
Species richness per ~10,000km2
0 - 54
55 - 126
127 - 201
202 - 276
277 - 369
370 - 516
517 - 682
683 - 868
869 - 1119
1120 - 1666
Medicines
Species richness per ~10,000km2
0 - 154
155 - 311
312 - 471
472 - 619
620 - 750
751 - 887
888 - 1069
1070 - 1344
1345 - 1753
1754 - 2422
Poisons
Species richness per ~10,000km2
0 - 47
48 - 85
86 - 125
126 - 160
161 - 193
194 - 232
233 - 275
276 - 324
325 - 387
388 - 451
Social Uses
Species richness per ~10,000km2
0 - 10
11 - 26
27 - 48
49 - 74
75 - 108
109 - 155
156 - 211
212 - 302
303 - 400
401 - 652

Figure S10. Global distribution of utilised plant species richness at the level-3 (sub-national) of the World Geographical Scheme for Recording Plant Distribution (WGSRPD) across ten categories of uses. Utilised plant species richness corresponds to the count of species found in each region. Geographic distribution for each species was retrieved from the World Checklist of Vascular Plants at the level-3 of the WGSRPD. To account for differences in surface area between regions, we estimated a scaling exponent that describes the species-area relationship (SAR) between the counts of species and the level-3 region areas. We used this exponent to rescale species counts for a standard area of 10,000 square kilometers.

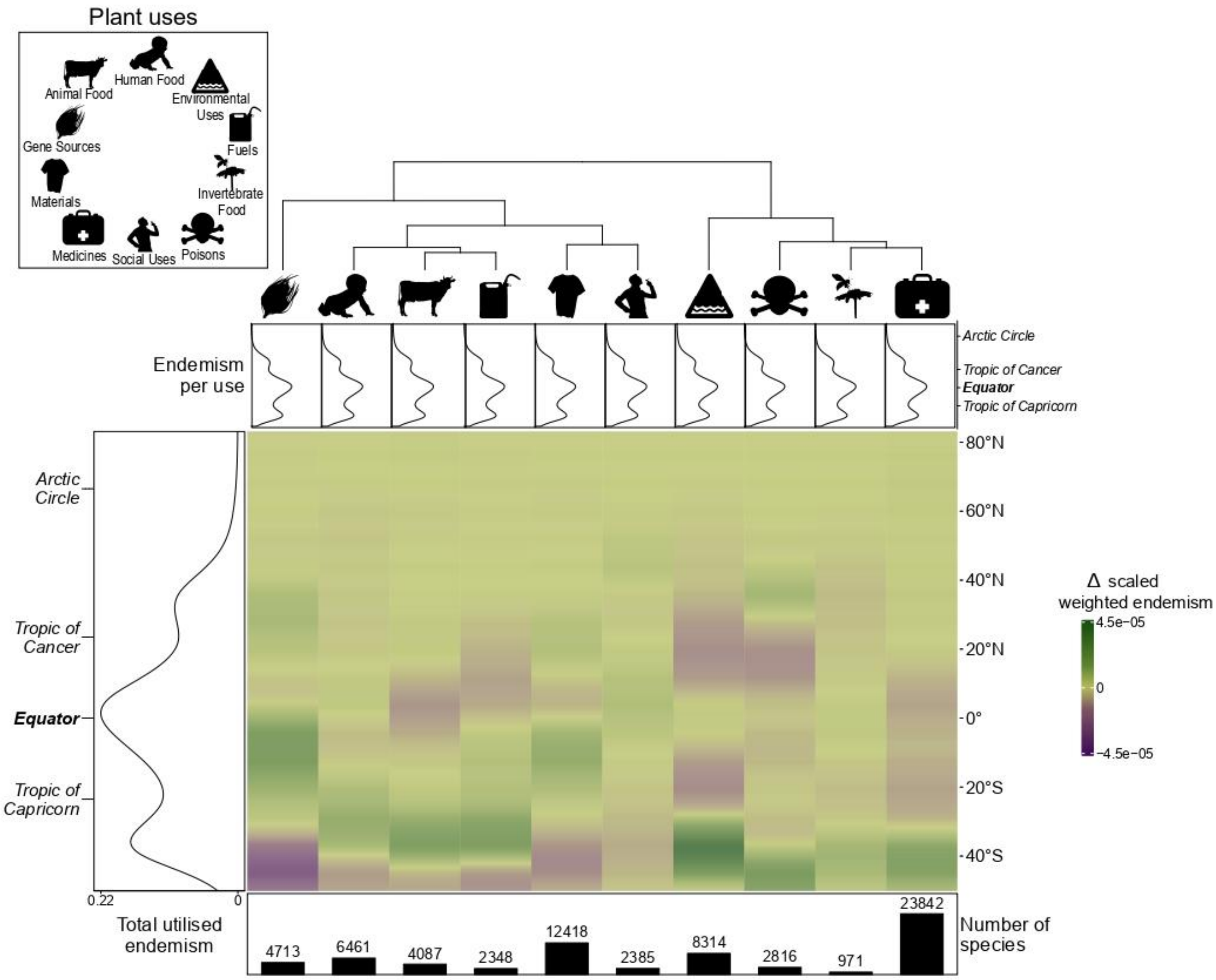


Figure S11. Latitudinal distribution of utilised plant species endemism across ten categories of uses. The black curve on the left represents the latitudinal distribution of all utilised plant species endemism. The dendrogram on the top orders the ten use categories according to the (dis-)similarity of their species endemism latitudinal profiles. Black curves underneath the dendrogram correspond to the species endemism latitudinal profile for each use category. The heatmap describes the latitudinal variation in the deviation of utilised plant species endemism for the ten plant use categories from total utilised plant species endemism. Colors indicate higher (green) or lower (purple) proportions in utilised plant species endemism of a given use relative to the total utilised plant species endemism pattern. The bar chart underneath the heatmap shows the number of species considered in each use category.

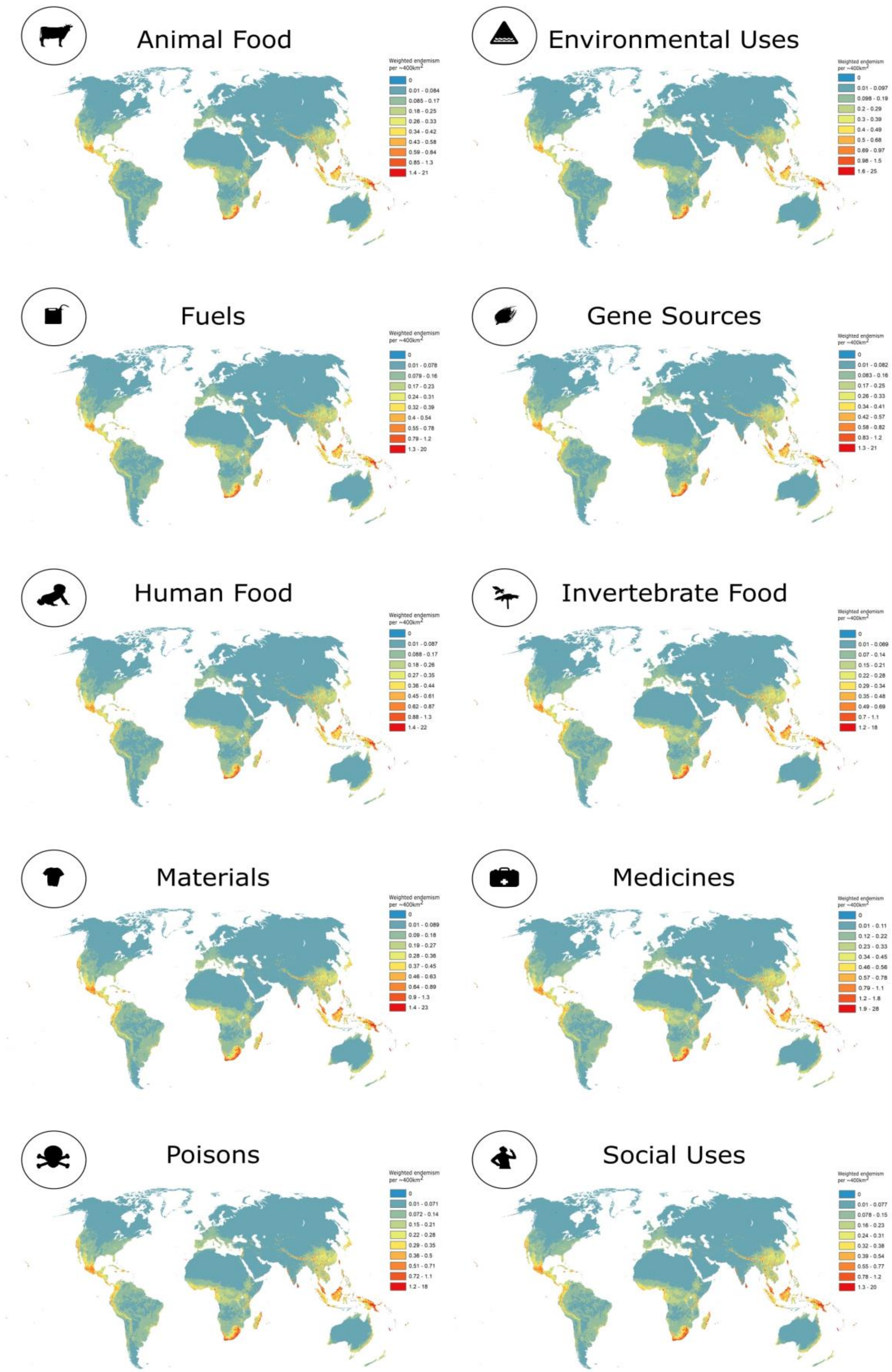

Animal Food
Weighted endemism per ~400km²
0
0.01 - 0.084
0.085 - 0.17
0.18 - 0.25
0.26 - 0.33
0.34 - 0.42
0.43 - 0.58
0.59 - 0.84
0.85 - 1.3
1.4 - 21
Environmental Uses
Weighted endemism per ~400km²
0
0.01 - 0.097
0.098 - 0.19
0.2 - 0.29
0.3 - 0.39
0.4 - 0.49
0.5 - 0.68
0.69 - 0.97
0.98 - 1.5
1.6 - 25
Fuels
Weighted endemism per ~400km²
0
0.01 - 0.078
0.079 - 0.16
0.17 - 0.23
0.24 - 0.31
0.32 - 0.39
0.4 - 0.54
0.55 - 0.78
0.79 - 1.2
1.3 - 20
Gene Sources
Weighted endemism per ~400km²
0
0.01 - 0.082
0.083 - 0.16
0.17 - 0.25
0.26 - 0.33
0.34 - 0.41
0.42 - 0.57
0.58 - 0.82
0.83 - 1.2
1.3 - 21
Human Food
Weighted endemism per ~400km²
0
0.01 - 0.087
0.088 - 0.17
0.18 - 0.26
0.27 - 0.35
0.36 - 0.44
0.45 - 0.61
0.62 - 0.87
0.88 - 1.3
1.4 - 22
Invertebrate Food
Weighted endemism per ~400km²
0
0.01 - 0.069
0.07 - 0.14
0.15 - 0.21
0.22 - 0.28
0.29 - 0.34
0.35 - 0.48
0.49 - 0.69
0.7 - 1.1
1.2 - 18
Materials
Weighted endemism per ~400km²
0
0.01 - 0.089
0.09 - 0.18
0.19 - 0.27
0.28 - 0.36
0.37 - 0.45
0.46 - 0.63
0.64 - 0.89
0.9 - 1.3
1.4 - 23
Medicines
Weighted endemism per ~400km²
0
0.01 - 0.11
0.12 - 0.22
0.23 - 0.33
0.34 - 0.45
0.46 - 0.56
0.57 - 0.78
0.79 - 1.1
1.2 - 1.8
1.9 - 28
Poisons
Weighted endemism per ~400km²
0
0.01 - 0.071
0.072 - 0.14
0.15 - 0.21
0.22 - 0.28
0.29 - 0.35
0.36 - 0.5
0.51 - 0.71
0.72 - 1.1
1.2 - 18
Social Uses
Weighted endemism per ~400km²
0
0.01 - 0.077
0.078 - 0.15
0.16 - 0.23
0.24 - 0.31
0.32 - 0.38
0.39 - 0.54
0.55 - 0.77
0.78 - 1.2
1.3 - 20

Figure S12. Global distribution of utilised plant species endemism across ten categories of uses. Utilised plant species endemism corresponds to the sum of each species occurrence probabilities predicted in each pixel weighted by the inverse of their range size calculated as the sum of the predicted probabilities within their study region (i.e., weighted endemism).

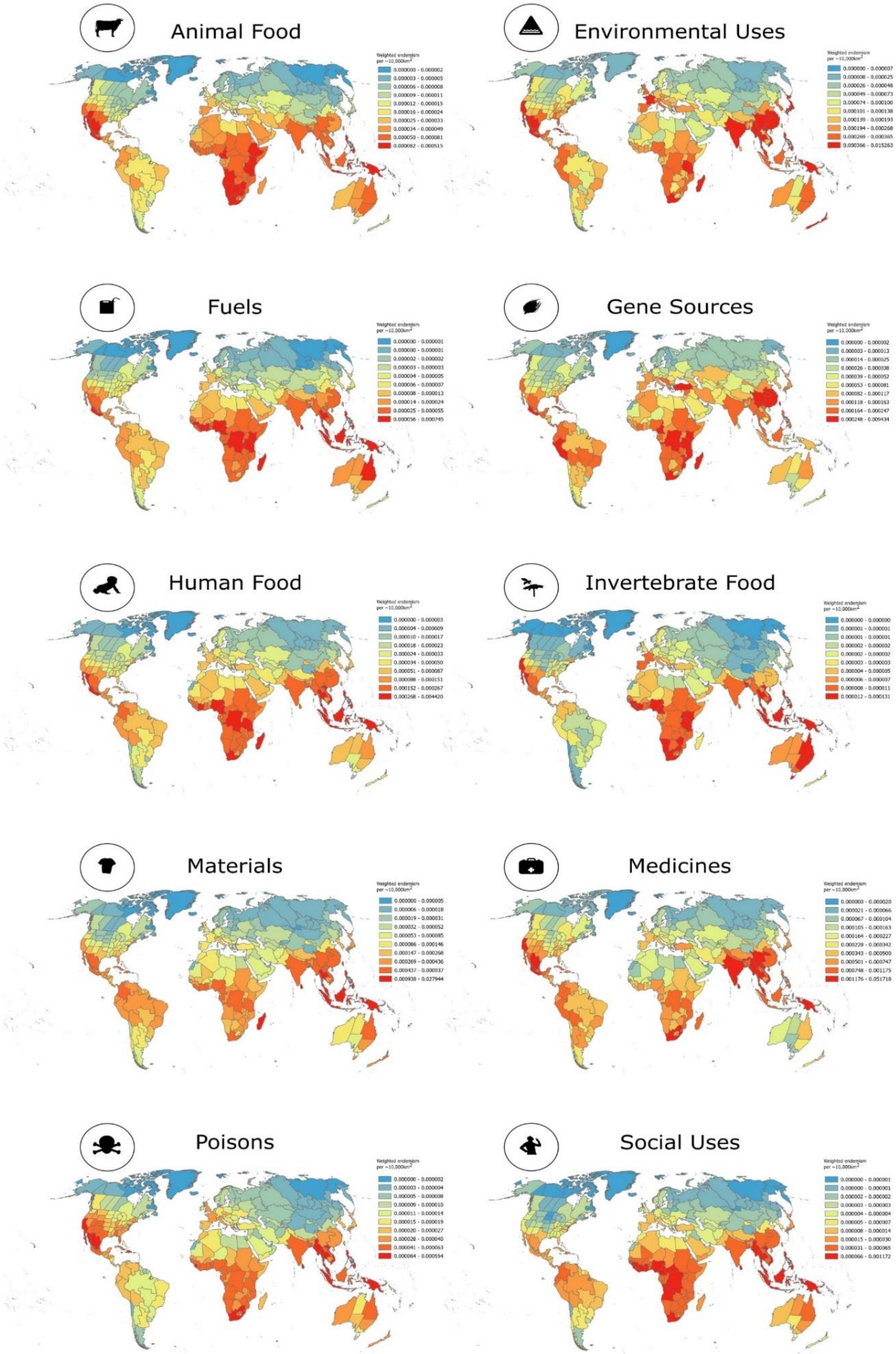

Animal Food
Environmental Uses
Fuels
Gene Sources
Human Food
Invertebrate Food
Materials
Medicines
Poisons
Social Uses

Figure S13. Global distribution of utilised plant species endemism at the level-3 (sub-national) of the World Geographical Scheme for Recording Plant Distribution (WGSRPD) across ten categories of uses. Utilised plant species endemism corresponds to the number of species present in each region weighted by the inverse of their range size calculated as the total area covered by the level-3 regions it occupies (i.e., weighted endemism). Geographic distribution for each species was retrieved from the World Checklist of Vascular Plants at the level-3 of the WGSRPD. To account for differences in surface area between regions, we estimated a scaling exponent that describes the species-area relationship (SAR) between the counts of species and the level-3 region areas. We used this exponent to rescale species counts for a standard area of 10,000 square kilometers.

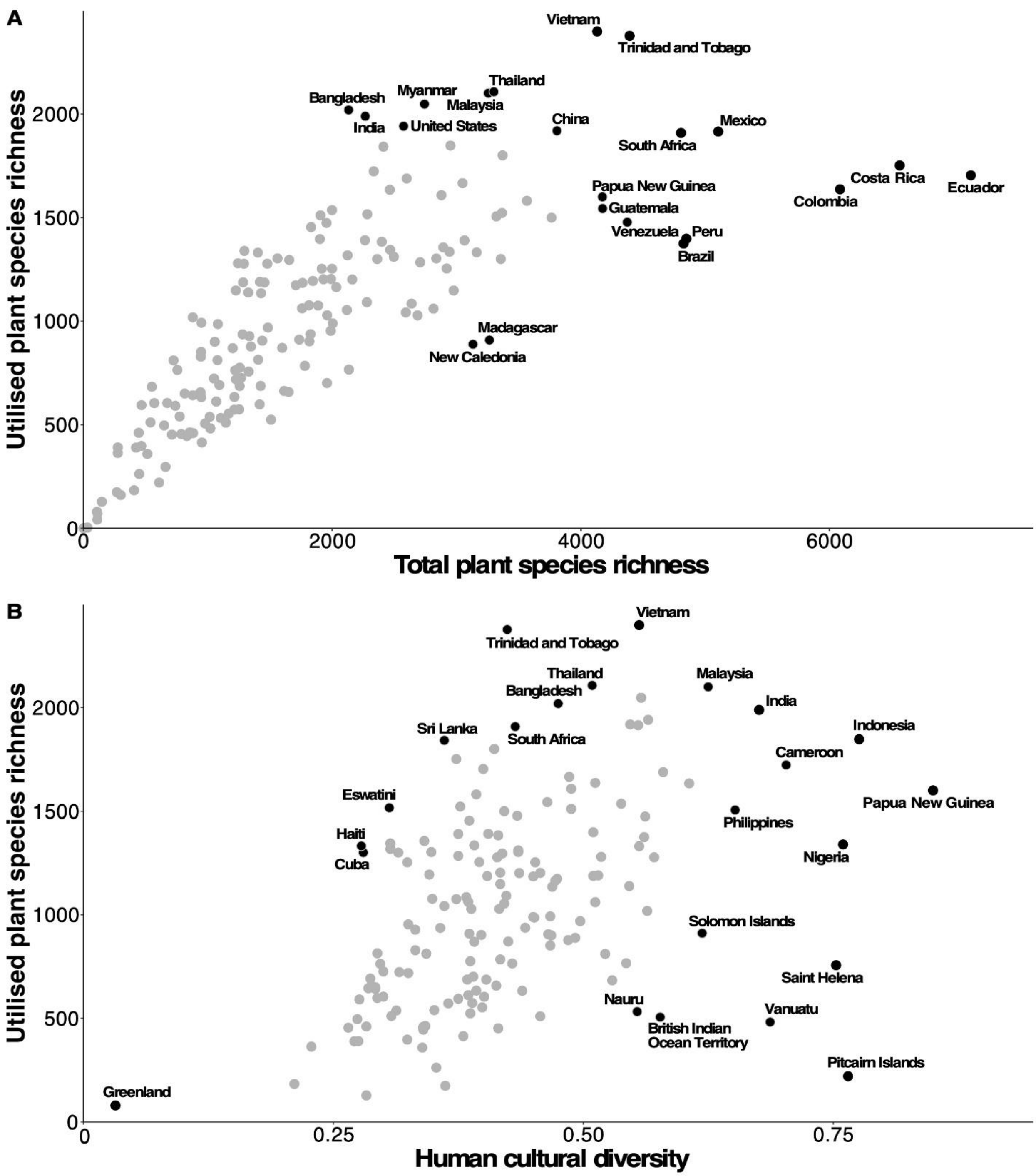


Figure S14. Relationships between utilised plant species richness and total plant species richness (A), and human cultural diversity (B) across 163 countries/territories. Geographic distribution for each species was derived from the World Checklist of Vascular Plants at the level-3 of the WGSRPD. To account for differences in surface area between regions, we estimated a scaling exponent that describes the species-area relationship (SAR) between the counts of species and the region areas. We used this exponent to rescale species counts for a standard area of 10,000 square kilometers.

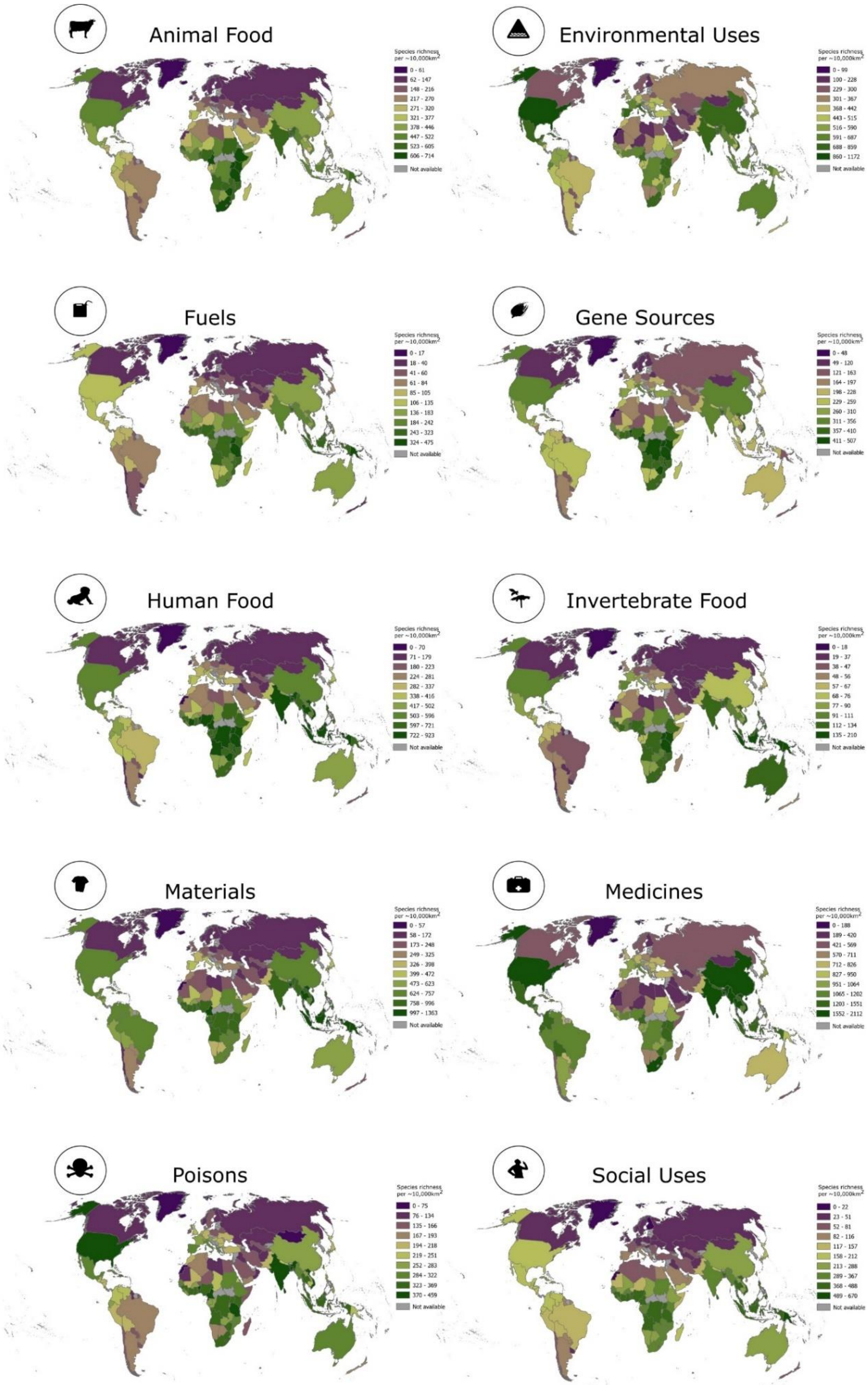

Animal Food
Species richness per ~10,000km²
0 - 61
62 - 147
148 - 216
217 - 270
271 - 320
321 - 377
378 - 446
447 - 522
523 - 605
606 - 714
Not available
Environmental Uses
Species richness per ~10,000km²
0 - 99
100 - 228
229 - 300
301 - 367
368 - 442
443 - 515
516 - 590
591 - 687
688 - 859
860 - 1172
Not available
Fuels
Species richness per ~10,000km²
0 - 17
18 - 40
41 - 60
61 - 84
85 - 105
106 - 135
136 - 183
184 - 242
243 - 323
324 - 475
Not available
Gene Sources
Species richness per ~10,000km²
0 - 48
49 - 120
121 - 163
164 - 197
198 - 228
229 - 259
260 - 310
311 - 356
357 - 410
411 - 507
Not available
Human Food
Species richness per ~10,000km²
0 - 70
71 - 179
180 - 223
224 - 281
282 - 337
338 - 416
417 - 502
503 - 596
597 - 721
722 - 923
Not available
Invertebrate Food
Species richness per ~10,000km²
0 - 18
19 - 37
38 - 47
48 - 56
57 - 67
68 - 76
77 - 90
91 - 111
112 - 134
135 - 210
Not available
Materials
Species richness per ~10,000km²
0 - 57
58 - 172
173 - 248
249 - 325
326 - 398
399 - 472
473 - 623
624 - 757
758 - 996
997 - 1363
Not available
Medicines
Species richness per ~10,000km²
0 - 188
189 - 420
421 - 569
570 - 711
712 - 826
827 - 950
951 - 1064
1065 - 1202
1203 - 1551
1552 - 2112
Not available
Poisons
Species richness per ~10,000km²
0 - 75
76 - 134
135 - 166
167 - 193
194 - 218
219 - 251
252 - 283
284 - 322
323 - 369
370 - 459
Not available
Social Uses
Species richness per ~10,000km²
0 - 22
23 - 51
52 - 81
82 - 116
117 - 157
158 - 212
213 - 288
289 - 367
368 - 488
489 - 670
Not available

Figure S15. Global distribution of utilised plant species richness at a country/territory scale across ten categories of uses. Utilised plant species richness corresponds to the count of species found in each region. Geographic distribution for each species was derived from the World Checklist of Vascular Plants at the level-3 of the WGSRPD. To account for differences in surface area between regions, we estimated a scaling exponent that describes the species-area relationship (SAR) between the counts of species and the region areas. We used this exponent to rescale species counts for a standard area of 10,000 square kilometers.

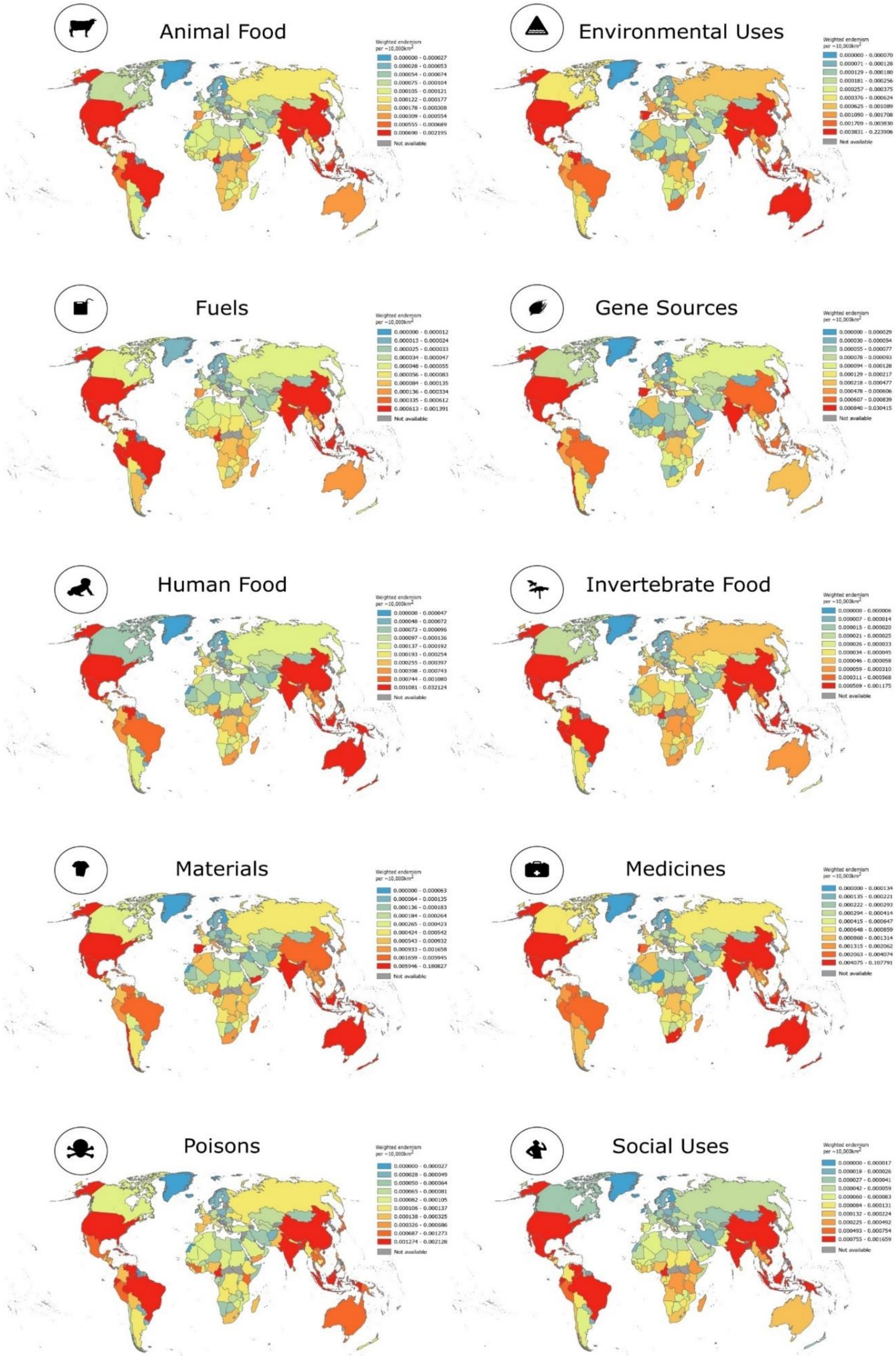

Animal Food
Weighted endemism
per ~10,000km^2
0.000000 - 0.000027
0.000028 - 0.000053
0.000054 - 0.000074
0.000075 - 0.000104
0.000105 - 0.000121
0.000122 - 0.000177
0.000178 - 0.000308
0.000309 - 0.000554
0.000555 - 0.000689
0.000690 - 0.002195
Not available
Environmental Uses
Weighted endemism
per ~10,000km^2
0.000000 - 0.000070
0.000071 - 0.000128
0.000129 - 0.000180
0.000181 - 0.000256
0.000257 - 0.000375
0.000376 - 0.000624
0.000625 - 0.001089
0.001090 - 0.001708
0.001709 - 0.003830
0.003831 - 0.223906
Not available
Fuels
Weighted endemism
per ~10,000km^2
0.000000 - 0.000012
0.000013 - 0.000024
0.000025 - 0.000033
0.000034 - 0.000047
0.000048 - 0.000055
0.000056 - 0.000083
0.000084 - 0.000135
0.000136 - 0.000334
0.000335 - 0.000612
0.000613 - 0.001391
Not available
Gene Sources
Weighted endemism
per ~10,000km^2
0.000000 - 0.000029
0.000030 - 0.000054
0.000055 - 0.000077
0.000078 - 0.000093
0.000094 - 0.000128
0.000129 - 0.000217
0.000218 - 0.000477
0.000478 - 0.000606
0.000607 - 0.000839
0.000840 - 0.030415
Not available
Human Food
Weighted endemism
per ~10,000km^2
0.000000 - 0.000047
0.000048 - 0.000072
0.000073 - 0.000096
0.000097 - 0.000136
0.000137 - 0.000192
0.000193 - 0.000254
0.000255 - 0.000397
0.000398 - 0.000743
0.000744 - 0.001080
0.001081 - 0.032124
Not available
Invertebrate Food
Weighted endemism
per ~10,000km^2
0.000000 - 0.000006
0.000007 - 0.000014
0.000015 - 0.000020
0.000021 - 0.000025
0.000026 - 0.000033
0.000034 - 0.000045
0.000046 - 0.000058
0.000059 - 0.000310
0.000311 - 0.000568
0.000569 - 0.001175
Not available
Materials
Weighted endemism
per ~10,000km^2
0.000000 - 0.000063
0.000064 - 0.000135
0.000136 - 0.000183
0.000184 - 0.000264
0.000265 - 0.000423
0.000424 - 0.000542
0.000543 - 0.000932
0.000933 - 0.001658
0.001659 - 0.005945
0.005946 - 0.180827
Not available
Medicines
Weighted endemism
per ~10,000km^2
0.000000 - 0.000134
0.000135 - 0.000221
0.000222 - 0.000293
0.000294 - 0.000414
0.000415 - 0.000647
0.000648 - 0.000859
0.000860 - 0.001314
0.001315 - 0.002062
0.002063 - 0.004074
0.004075 - 0.107791
Not available
Poisons
Weighted endemism
per ~10,000km^2
0.000000 - 0.000027
0.000028 - 0.000049
0.000050 - 0.000064
0.000065 - 0.000081
0.000082 - 0.000105
0.000106 - 0.000137
0.000138 - 0.000325
0.000326 - 0.000686
0.000687 - 0.001273
0.001274 - 0.002128
Not available
Social Uses
Weighted endemism
per ~10,000km^2
0.000000 - 0.000017
0.000018 - 0.000026
0.000027 - 0.000041
0.000042 - 0.000059
0.000060 - 0.000083
0.000084 - 0.000131
0.000132 - 0.000224
0.000225 - 0.000492
0.000493 - 0.000754
0.000755 - 0.001659
Not available

Figure S16. Global distribution of utilised plant species endemism at a country/territory scale across ten categories of uses. Utilised plant species endemism corresponds to the number of species present in each region weighted by the inverse of their range size calculated as the total area covered by the regions it occupies (i.e., weighted endemism). Geographic distribution for each species was retrieved from the World Checklist of Vascular Plants at the level-3 of the WGSRPD. To account for differences in surface area between regions, we estimated a scaling exponent that describes the species-area relationship (SAR) between the counts of species and the region areas. We used this exponent to rescale species counts for a standard area of 10,000 square kilometers.

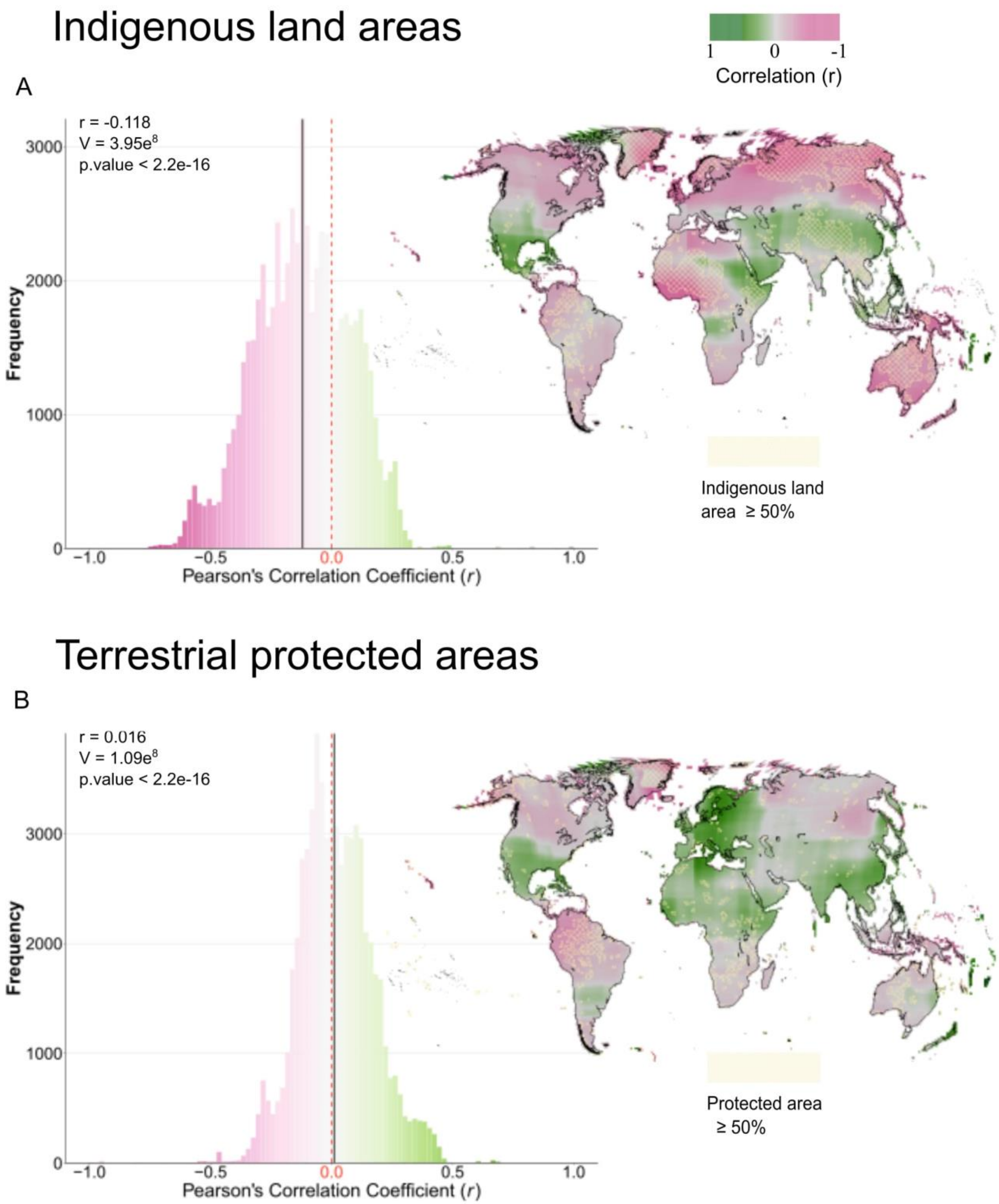


Figure S17. Spatial correlations between utilised plant species endemism and proportions of both Indigenous lands and terrestrial protected areas. Pearson's correlation coefficients were computed across all values contained in 71 cells (~3,550km)-wide windows built around each pixel. Pixel color indicates regions where utilised plant species endemism is positively (green) or negatively (pink) correlated with the proportion of Indigenous lands and terrestrial protected areas. Regions crossed in beige indicate pixels containing more than 50% of Indigenous lands and protected areas. All Indigenous lands and protected areas are thus not represented on the maps, although they are all accounted for in the analyses. Frequencies of Pearson's correlation coefficients found across the world are given in histograms. The median correlation across the world is indicated by the black vertical line, while zero correlation is indicated by the red dashed line. One-sample Wilcoxon signed rank tests were performed to assess whether median correlations are significantly different from zero.

Dataset	Source	Acronym	Number of species	Geographic extent	Description
Crop wild relative inventory	https://www.cwrdiversity.org Dempewolf *et al.* 2014	CWR	2,459	Global	A global priority Crop Wild Relatives inventory, based on both gene pool and taxon group concepts
Economic Botany Collection	http://apps.kew.org/ecbot/search	EcBot	8,162	Global	RBG Kew's Economic Botany Collection containing over 120,000 specimens/objects
Germplasm Resources Information Network, United States Department of Agriculture	https://www.ars-grin.gov	GRIN	10,988	Global	Online database of taxonomic information on cultivated plants from the USDA-ARS germplasm resources information network (GRIN)
Medicinal Plant Names Services version 8.2	http://www.kew.org/mpns	MPNS	26,690	Global	Global resource for medicinal plant names with access to information about plants and plant products
Palms of the world online	http://www.palmweb.org	PalmWeb	152	Global	An online palm encyclopaedia gleaned from taxonomic publications
Plant resources of South-East Asia	Jansen *et al.* 1991	PROSEA	4,182	South-East Asia	Book inventorying useful plants of a core area (Brunei, Indonesia, Malaysia, New Guinea, the Philippines and Singapore) occurring and used also in neighbouring areas (Burma, Cambodia, Laos, Thailand and Vietnam). Based on literature review.
Indigenous knowledge of New Guinea's useful plants	Cámara-Leret *et al.* 2019	NewGuinea	3,071	New Guinea	Quantitative review of 488 references reporting indigenous knowledge and plant uses in New Guinea
Plant Resources of Tropical Africa	https://www.prota4u.org/database	PROTA	4,534	Sub-Saharan Africa	Online resource of useful plant information from Sub-Saharan Africa
Useful Plants of West Tropical Africa	Burkill 1994	UPWTA	3,349	Western Africa	Database of useful plants from West tropical Africa
Survey of Economic Plants for Arid and Semi-Arid Lands	http://apps.kew.org/sepasalweb/sepaweb	SEPASAL	3,479	Arid and semi-arid African lands	Database of 16,407 uses records for species from the African Arid and Semi-Arid areas
Plants for Malaria, plants for fever	Milliken 1997	MALARIA	748	Latin America	Literature review of plant species used to treat malaria and fever
Project MGU-Useful Plants Project	Ulian *et al.* 2017	UPP	905	Sub-Saharan Africa and Mesoamerica	Database compiling plant uses by local communities and partners of the UPP project from Botswana, South Africa, Mali, Kenya and Mexico

Table S1. Data sources of the World Checklist of Useful Plant Species.

Variable	Response	Standardised regression coefficient + 95% Confidence Interval			Student's t-test		
		Estimate	Lower CI	Upper CI	t-value	*p*-value[1]	Correlation[2]
Total plant species richness							
	All uses	0.865	0.782	0.947	20.703	1.86e-48***	exponential
	Animal Food	0.676	0.573	0.779	12.966	3.24e-27***	exponential
	Environmental Uses	0.874	0.765	0.982	15.890	1.66e-35***	exponential
	Fuels	0.494	0.392	0.597	9.518	1.89e-17***	exponential
	Gene Sources	0.747	0.631	0.863	12.705	2.38e-26***	exponential
	Human Food	0.692	0.589	0.796	13.184	1.04e-27***	exponential
	Invertebrate Food	0.684	0.567	0.801	11.554	3.95e-23***	exponential
	Materials	0.662	0.570	0.754	14.256	9.81e-31***	exponential
	Medicines	0.822	0.737	0.906	19.232	1.29e-44***	sperical
	Poisons	0.788	0.668	0.908	12.995	3.60e-27***	exponential
	Social Uses	0.522	0.431	0.613	11.305	1.99e-22***	exponential
Human cultural diversity							
	All uses	0.358	0.235	0.481	5.743	4.52e-08***	gaussian
	Animal Food	0.306	0.194	0.419	5.394	2.42e-07***	sperical
	Environmental Uses	0.349	0.217	0.481	5.217	5.53e-07***	sperical
	Fuels	0.377	0.275	0.479	7.322	1.10e-11***	sperical
	Gene Sources	0.314	0.183	0.445	4.737	4.74e-06***	exponential
	Human Food	0.355	0.239	0.471	6.043	1.01e-08***	exponential
	Invertebrate Food	0.392	0.268	0.517	6.219	4.14e-09***	exponential
	Materials	0.352	0.244	0.460	6.451	1.24e-09***	gaussian
	Medicines	0.328	0.204	0.451	5.242	4.93e-07***	gaussian
	Poisons	0.342	0.208	0.476	5.030	1.29e-06***	exponential
	Social Uses	0.323	0.223	0.424	6.359	2.01e-09***	exponential

[1] Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

[2] Name of the correlation structure function selected for accommodating spatial autocorrelation

Table S2. Generalised Least Squares (GLS) summary statistics for the relationships between utilised plant species richness and total plant species richness, and human cultural diversity across 163 countries/territories. GLS models account for potential spatial (auto-)correlation in the data. Latitudinal and longitudinal coordinates of the centroids of each country were used as spatial covariates, and three different correlation functions were tested: exponential, gaussian and spherical. GLS models were fitted using the restricted maximum likelihood method (REML) and the correlation structure with the lowest AIC was selected. Analyses were repeated for all utilised plant species together and for each individual use category separately. Human cultural diversity is a composite index made of three estimates: total number of languages, religions, and ethnic groups per country. Total vascular plant species richness and utilised plant species richness were compiled from the World Checklist of Vascular Plants.

Variable	Response	Standardised regression coefficient + 95% Confidence Interval			Student's t-test		
		Estimate	Lower CI	Upper CI	t-value	*p*-value[(1)]	Correlation[(2)]
Total plant species endemism							
	All uses	0.297	0.213	0.381	7.001	5.54e-11***	gaussian
	Animal Food	0.016	-0.118	0.149	0.231	8.18e-01	gaussian
	Environmental Uses	0.065	0.007	0.123	2.209	2.85e-02*	gaussian
	Fuels	-0.046	-0.174	0.082	-0.713	4.77e-01	gaussian
	Gene Sources	0.435	0.371	0.498	13.456	1.79e-28***	gaussian
	Human Food	0.146	0.030	0.263	2.477	1.42e-02*	sperical
	Invertebrate Food	-0.066	-0.196	0.064	-1.003	3.17e-01	gaussian
	Materials	0.184	0.111	0.256	5.009	1.38e-06***	gaussian
	Medicines	0.353	0.218	0.488	5.153	7.00e-07***	sperical
	Poisons	0.087	-0.048	0.222	1.279	2.03e-01	gaussian
	Social Uses	-0.009	-0.134	0.116	-0.146	8.84e-01	gaussian
Human cultural diversity							
	All uses	0.060	-0.037	0.157	1.218	2.25e-01	gaussian
	Animal Food	0.312	0.181	0.443	4.696	5.65e-06***	gaussian
	Environmental Uses	0.008	-0.050	0.066	0.269	7.88e-01	gaussian
	Fuels	0.340	0.217	0.462	5.453	1.83e-07***	gaussian
	Gene Sources	0.002	-0.104	0.108	0.038	9.70e-01	gaussian
	Human Food	-0.028	-0.171	0.116	-0.381	7.04e-01	sperical
	Invertebrate Food	0.336	0.209	0.463	5.223	5.37e-07***	gaussian
	Materials	0.013	-0.065	0.090	0.328	7.43e-01	gaussian
	Medicines	0.055	-0.108	0.218	0.670	5.04e-01	exponential
	Poisons	0.245	0.109	0.380	3.568	4.74e-04***	gaussian
	Social Uses	0.327	0.205	0.448	5.317	3.47e-07***	gaussian

(1) Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(2) Name of the correlation structure function selected for accommodating spatial autocorrelation

Table S3. Generalised Least Squares (GLS) summary statistics for the relationships between utilised plant species endemism and total plant species endemism, and human cultural diversity across 163 countries/territories. GLS models account for potential spatial (auto-)correlation in the data. Latitudinal and longitudinal coordinates of the centroids of each country were used as spatial covariates, and three different correlation functions were tested: exponential, gaussian and spherical. GLS models were fitted using the restricted maximum likelihood method (REML) and the correlation structure with the lowest AIC was selected. Analyses were repeated for all utilised plant species together and for each individual use category separately. Human cultural diversity is a composite index made of three estimates: total number of languages, religions, and ethnic groups per country. Total vascular plant species endemism and utilised plant species endemism were compiled from the World Checklist of Vascular Plants.

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