The biogeography of relative abundance of soil fungi and bacteria in top surface soil

SUPPORTING ONLINE MATERIAL

Classification of vegetation biomes and vegetation types

Following the approach by Olson et al. 2006, vegetation biomes where the soil samples were collected were classified into tundra, boreal forests, montane grasslands, temperate conifer forests, temperate grasslands, temperate broadleaf forests, tropical forests, and Mediterranean & deserts. Mediterranean and deserts had low sample sizes and thus were combined into one vegetation biome. To determine the vegetation types in locations where the soil samples were collected, we used the Global 1-km Consensus Land Cover map[2]. The land cover map classifies vegetation or land cover types into Evergreen/Deciduous Needleleaf Trees, Evergreen Broadleaf Trees, Deciduous Broadleaf Trees, Mixed/Other Trees, Shrubs, Herbaceous Vegetation, Cultivated and Managed Vegetation, Regularly Flooded Vegetation, Urban/Built-up, Snow/Ice, Barren, and Open Water. We summed up the vegetation types of Evergreen/Deciduous Needleleaf Trees, Evergreen Broadleaf Trees, Deciduous Broadleaf Trees, Mixed/Other Trees and Shrubs to derive the total woody plant cover. To represent human activities (or land usage change), we used land cover of Cultivated and Managed Vegetation to derive the managed cover. Total vegetation cover is the sum of woody, herbaceous and managed vegetation cover. Then we classified our soil sample locations into vegetation types or ecosystems dominated by woody vegetation, managed vegetation, and herbaceous vegetation. To this end, we tested various thresholds of vegetation cover values and chose the one without overlaps among different vegetation types. That is, if the total vegetation cover was less than 20% or the cover of barren soil was greater than 50%, it was classified as barren soil. If the woody vegetation cover was larger than 20% and larger than the managed vegetation cover, it was classified into the vegetation type or ecosystem dominated by woody vegetation. If the managed vegetation cover was larger than 20% and

larger than the woody vegetation cover, it was classified into the vegetation type or ecosystem dominated by managed vegetation. The rest of sample sites were classified into herbaceous vegetation dominated ecosystem, if herbaceous vegetation cover was larger than 20%.

Environmental drivers

Based on previous studies[3–5], variables or covariates of climate, soil and human activities which likely affect F:B ratio or fungal proportion were selected for this study. They include climate conditions (aridity index, mean annual precipitation-MAP, mean annual temperature-MAT), soil properties (clay, silt and sand content, soil organic carbon-SOC, soil C:N ratio, pH, cation exchange capacity), vegetation index (net primary productivity-NPP, woody vegetation cover, herbaceous vegetation cover), and human activities (managed vegetation cover). All of these variables were derived from the global layers based on georeferenced coordinates of aggregated soil sample at 30 arc-seconds resolution. Machine-learning algorithm Random Forest was then used to determine variable importance for these 12 variable (Breiman 2001). We ran 1000 simulations of machine-learning algorithm random forest and reported mean values of mean decrease in accuracy (%IncMSE) and mean decrease gini (IncNodePurity) with 95% confidence interval. The greater the values of %IncMSE and IncNodePurity are, the more important the variables are.

Machine learning

Fungal proportion has the largest sample size (n = 3224 samples) and is the focus of our study. Because of better predictive strength, we used machine learning (random forest) to generate a spatially explicit map of fungal proportion at a global scale. The distinct soil samples (n = 3224) falling within the same 30 arc-seconds (~1-km^2) pixel were aggregated as an average, thus resulting in a total of 946 unique pixels across global as inputs into the geospatial modelling.

To generate a quantitative and mechanistic understanding of environmental controls on

fungal proportion across landscapes, we used a stack of ecologically relevant, global map layers including climatic, soil nutrient, soil chemical, soil physical, vegetative indices, radiation and topographic variables and anthropogenic covariates (Supplementary Table 1). All of these covariate map layers were standardized at 30 arc-seconds resolution (≈1km at the equator). When these global layers' resolution is higher than 30 arc-seconds, we downsampled these layers using a mean aggregation method. In contrast, if layers have a lower original resolution, we resampled these layers using simple upsampling (i.e., without interpolation) to align with the higher resolution grid. Each sample (plot)-specific independent variables were then derived from these ecologically relevant, global map layers based on each sample' georeferenced location.

The soil samples used for measuring soil microbes were collected from top soil surface (0-10/15 cm). To approximate the sampling soil depth, we thus used the soil variable at soil depth of 15 cm, thus resulting in a total of 90 ecologically relevant, global map layers. Geospatial modelling was used to investigate the dependence of fungal proportion on the 90 covariates. We followed recent advancements in machine learning for spatial prediction[6], and used random forest with a variety of parameters (i.e., variablesPerSplit 2, 3, 4, 5, 8, 10) to train the models and assessed each model using k-fold cross validation (with k = 10). This allowed us to quantify the coefficient of determination values for each fold of data in each model. Then we determined the mean and standard deviation values for the cross validated models. The model with the highest coefficient of determination values and lowest standard deviation were selected as the best model. The results showed that the final (best) model had a remarkably high strength of prediction (mean cross-validation R^2 = 0.43, standard deviation = 0.09). The "best model" with the highest coefficient of determination values and lowest standard deviation were then used to spatially explanate the fungal proportion at a global scale, with the derived 90 covariates on all the soil samples (n = 946). The results showed

again that the best performing model had remarkably high predictive strength at a global scale (overall $R^2 = 0.90$).

To account for the potential role of land usage change, we used the subset of data including only natural ecosystems (n = 1795) and aggregated the samples at 30 arc-seconds (~1-km^2) resolution as an average. We then used machine learning (random forest) to generate a spatially explicit map of fungal proportion at a global scale, using the derived 90 covariates on all the soil samples (n = 716) (Extended Fig. 1). The predictive strength of using data of natural ecosystems was lower than the case of using full dataset. But it still had good predictive strength with mean cross-validation $R^2 = 0.35$ and a final best model $R^2 = 0.91$ (Extended Fig. 9). In view of the minimal difference of the two scenarios, the main text reported results from the full dataset, whereas results from only the natural ecosystems was reported in the supplementary materials.

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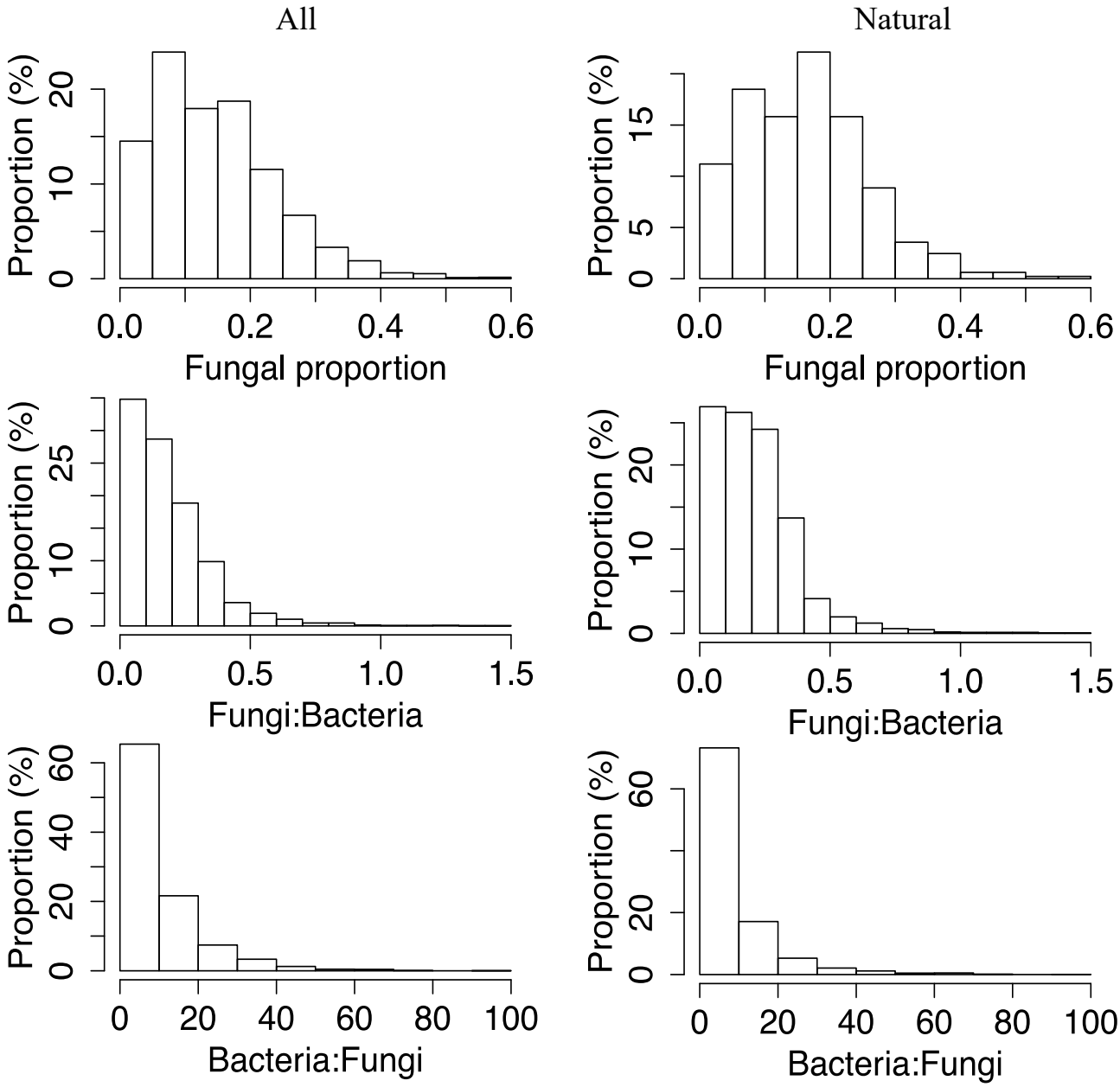

Fig. S1 Frequency distribution (%) of proportion of fungi, fungal and bacterial ratio and bacterial and fungal ratio. The data is derived from the original distinct soil samples (n = 3224 for all data and n = 1795 for natural ecosystems) before aggregation.

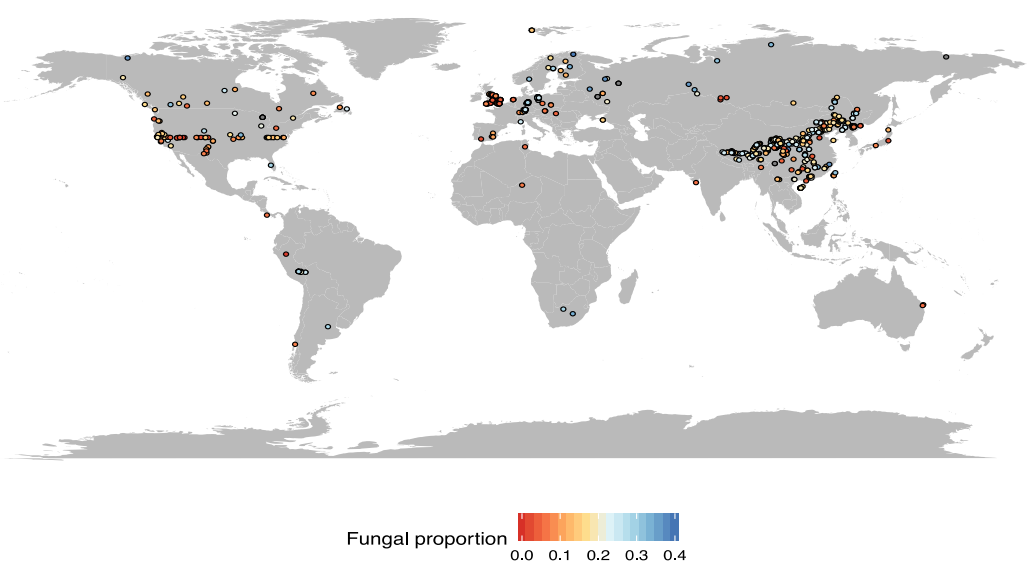

Fig. S2 Map of sample locations for fungal proportion using natural ecosystems. All data points (n = 1795) falling within the same 30 arc-seconds (~1-km^2) pixel were aggregated via an average (n = 716).

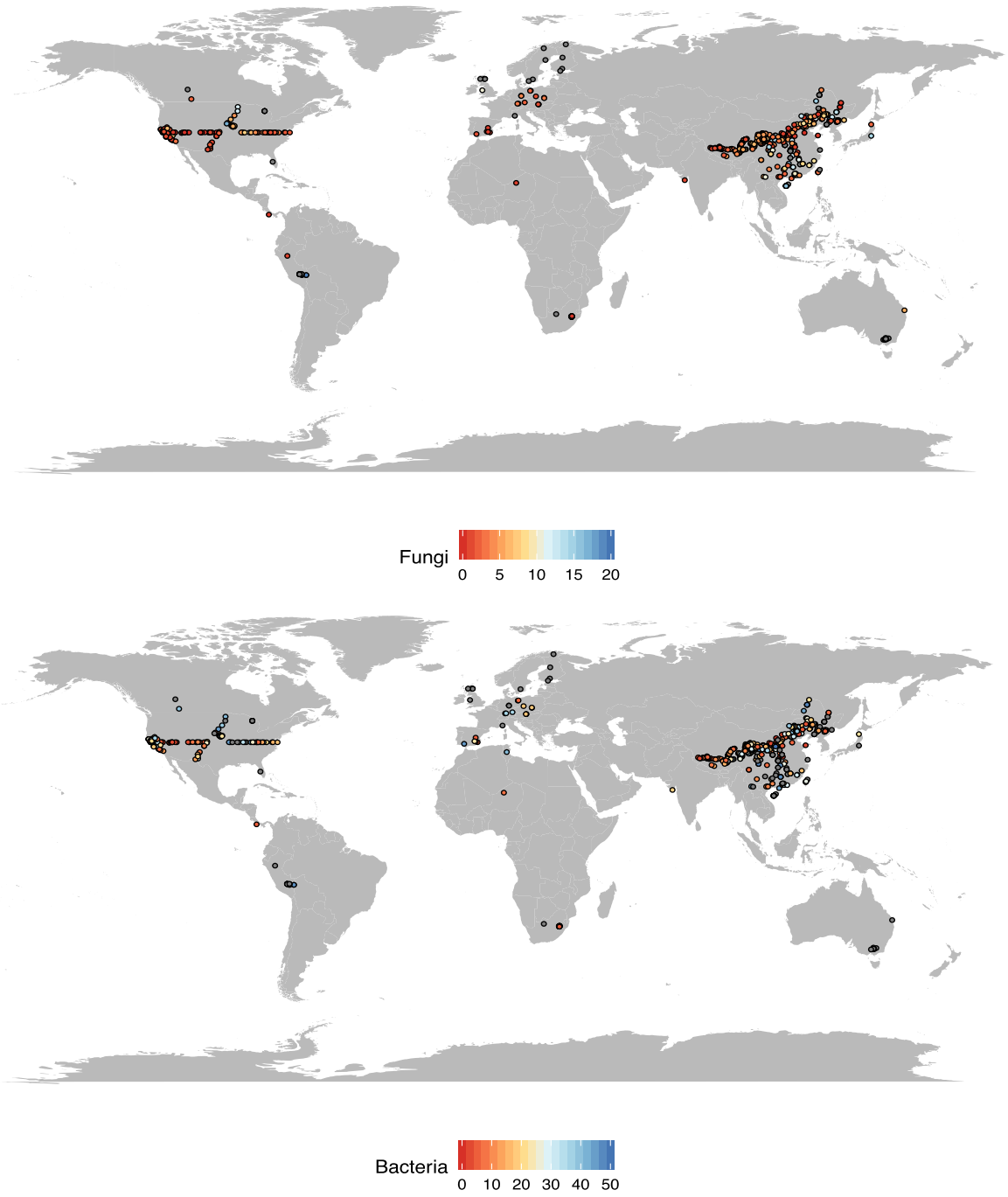

Fig. S3 Map of sample locations for abundance of fungi and bacteria. All data points (n = 2753 for fungi and n = 2759 for bacteria) falling within the same 30 arc-seconds (~1-km^2) pixel were aggregated via an average (n = 646 and n = 647 for both fungi and bacteria, respectively).

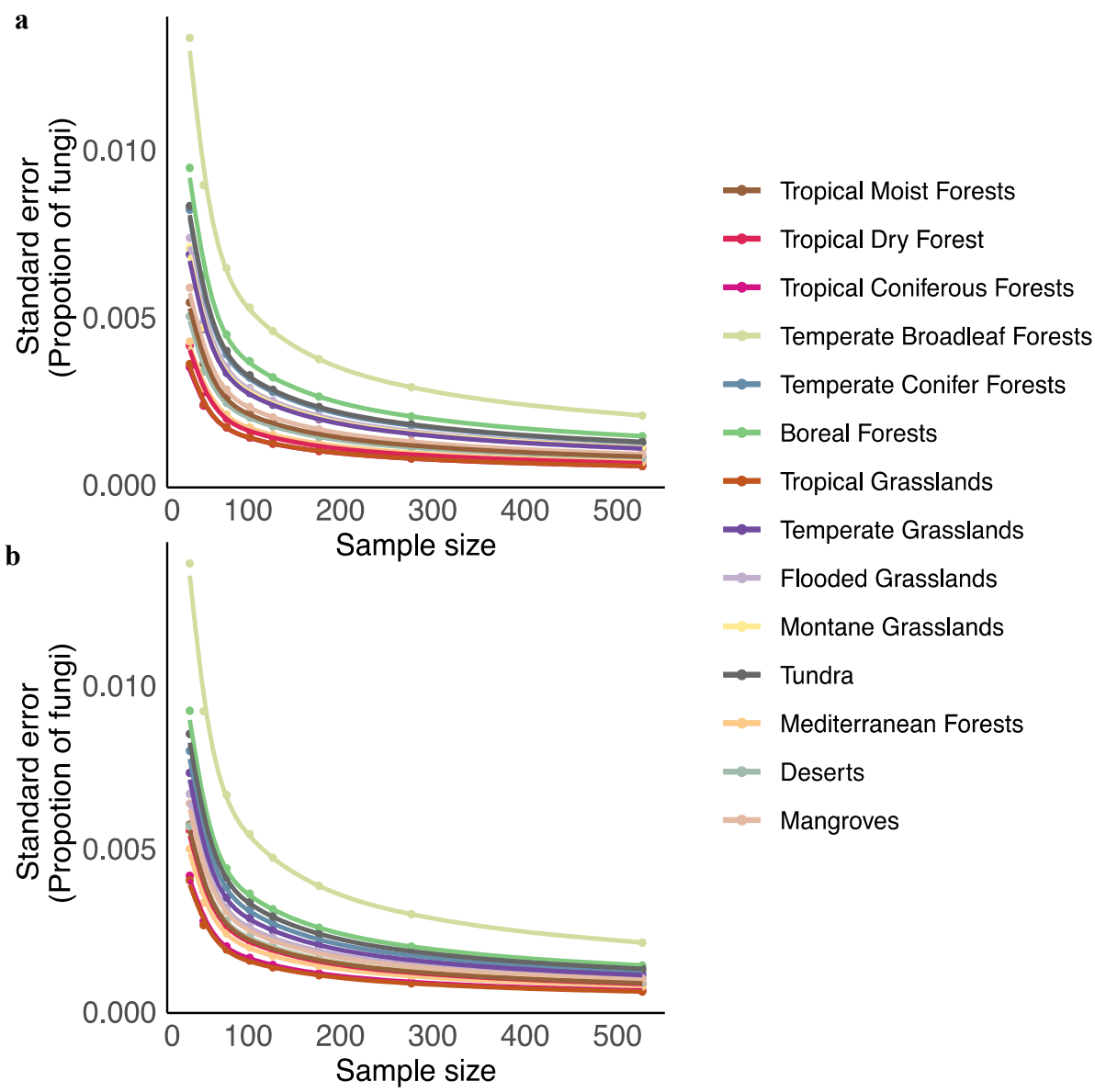

Fig. S4 The standard error of the predicted mean values of fungal proportion decrease with increasing sample size, quantified by the 1000 bootstrapping. a, the scenario of using full dataset. b, the scenario of using dataset with natural ecosystems.

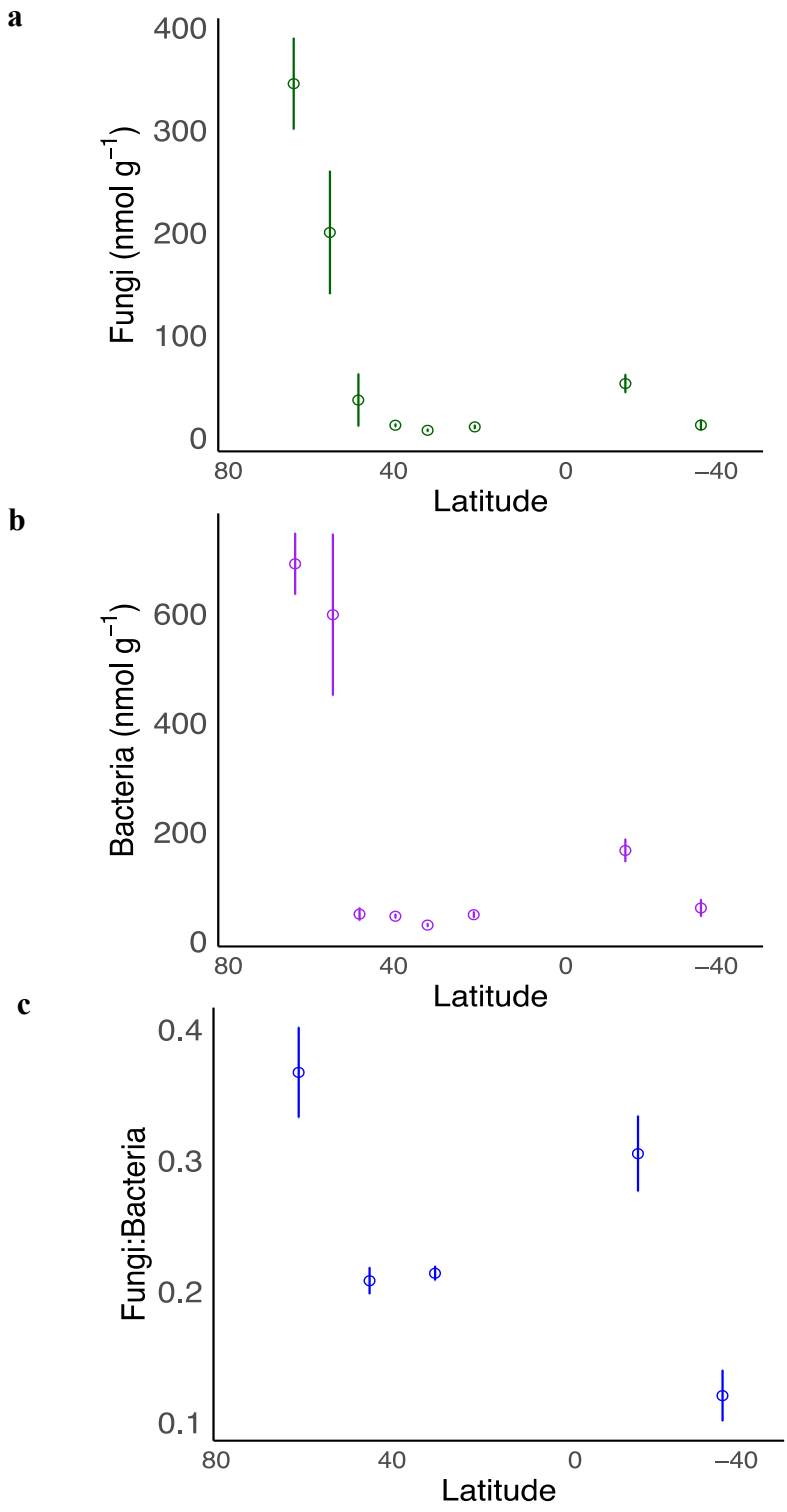

Fig. S5 Abundance of fungi (a), bacteria (b), and fungi and bacteria ratio (c) derived from PLFA as affected by latitude.

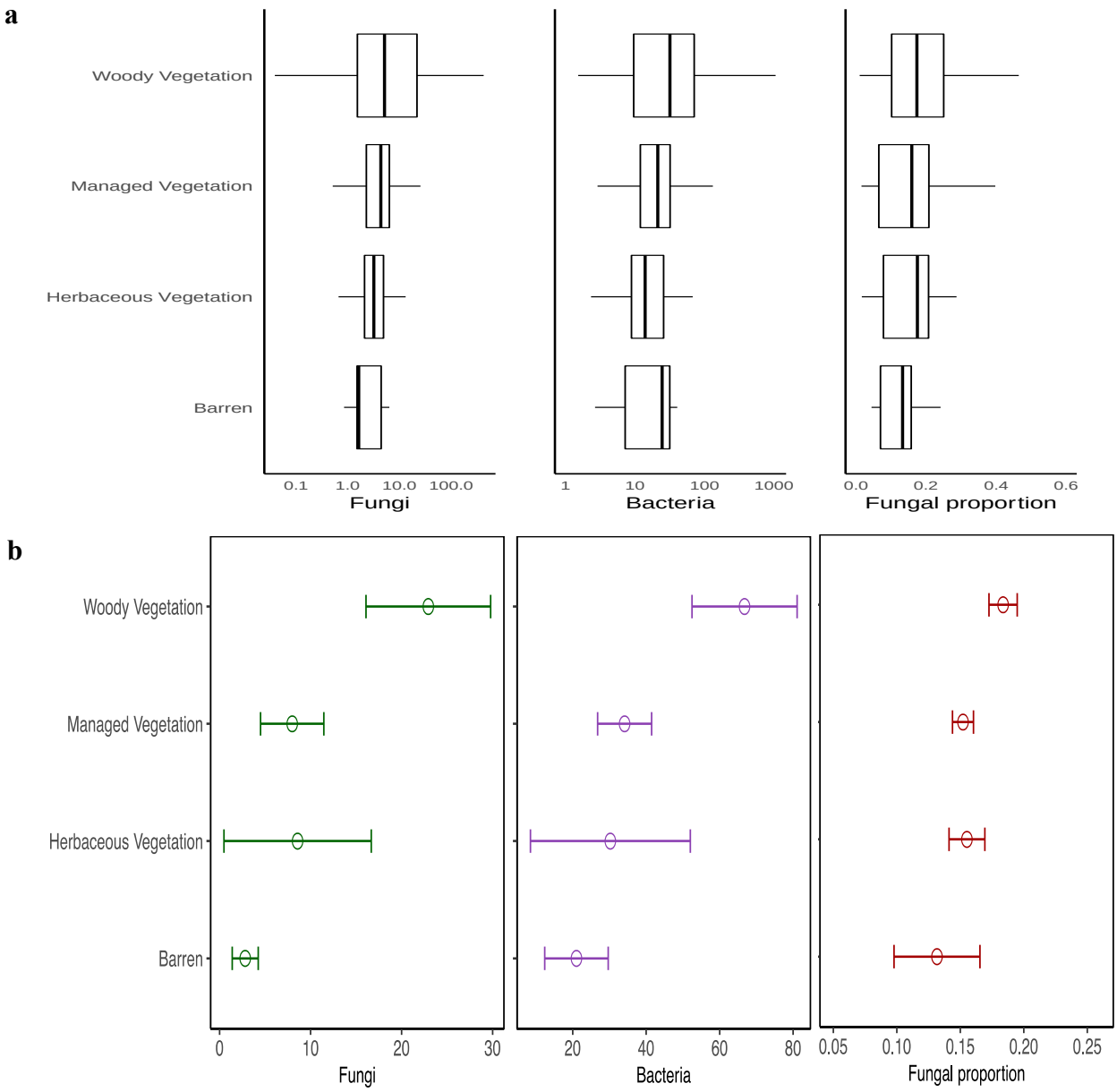

Fig. S6 The median and interquartile range (a) and mean ± 95 CIs (b) of abundance of fungi and bacteria and fungal proportion across vegetation types. Mediterranean and desert have low sample sizes (<25) and thus were combined.

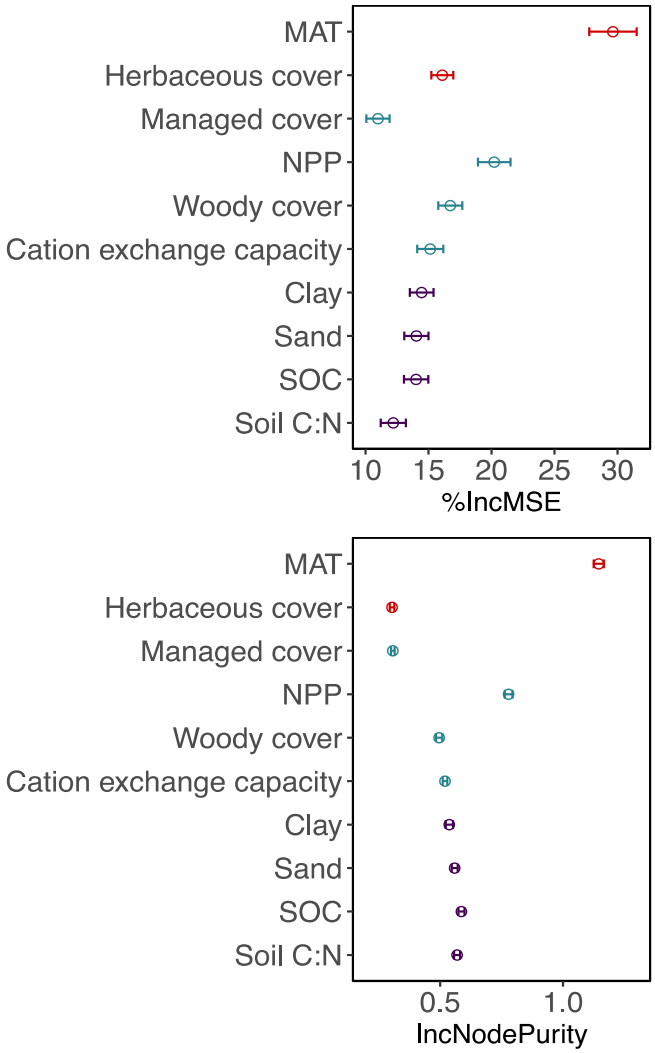

Fig. S7 Mean decrease in accuracy (%IncMSE, mean and SD) and mean decrease gini (IncNodePurity, mean and SD) estimated from 1000 simulations of random forests. This is used to evaluate the importance of top environmental drivers on proportion of fungi derived from natural ecosystems.

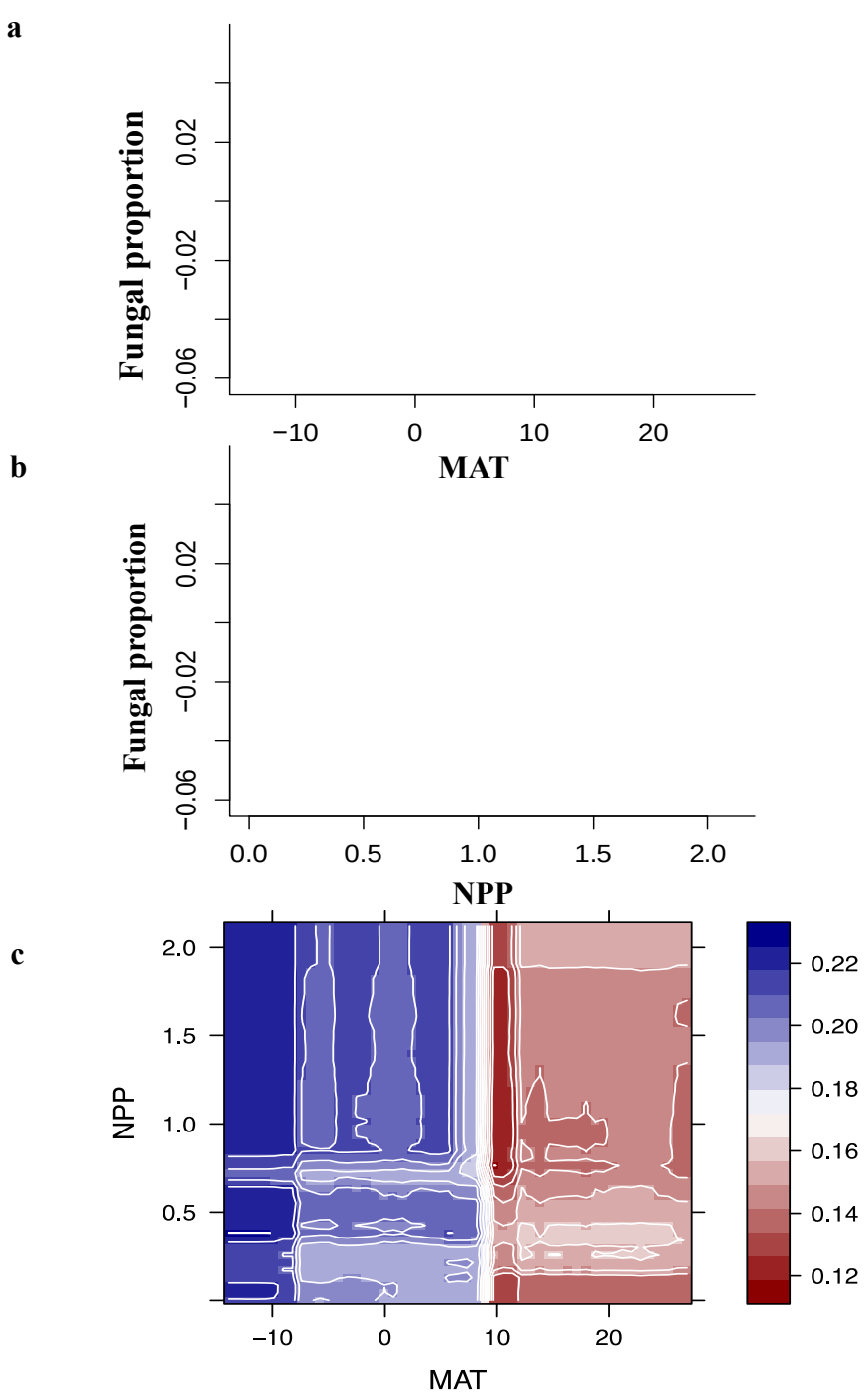

Fig. S8 Fungal proportion is primarily associated with net primary productivity and climate using data set of natural ecosystems. a–**b**, Partial feature contributions of primary environmental variables (**a**, MAT; **b**, NPP) to proportion of fungi. **c**, Partial feature contributions of primary environmental variable interactions (MAT vs NPP) to proportion of fungi.

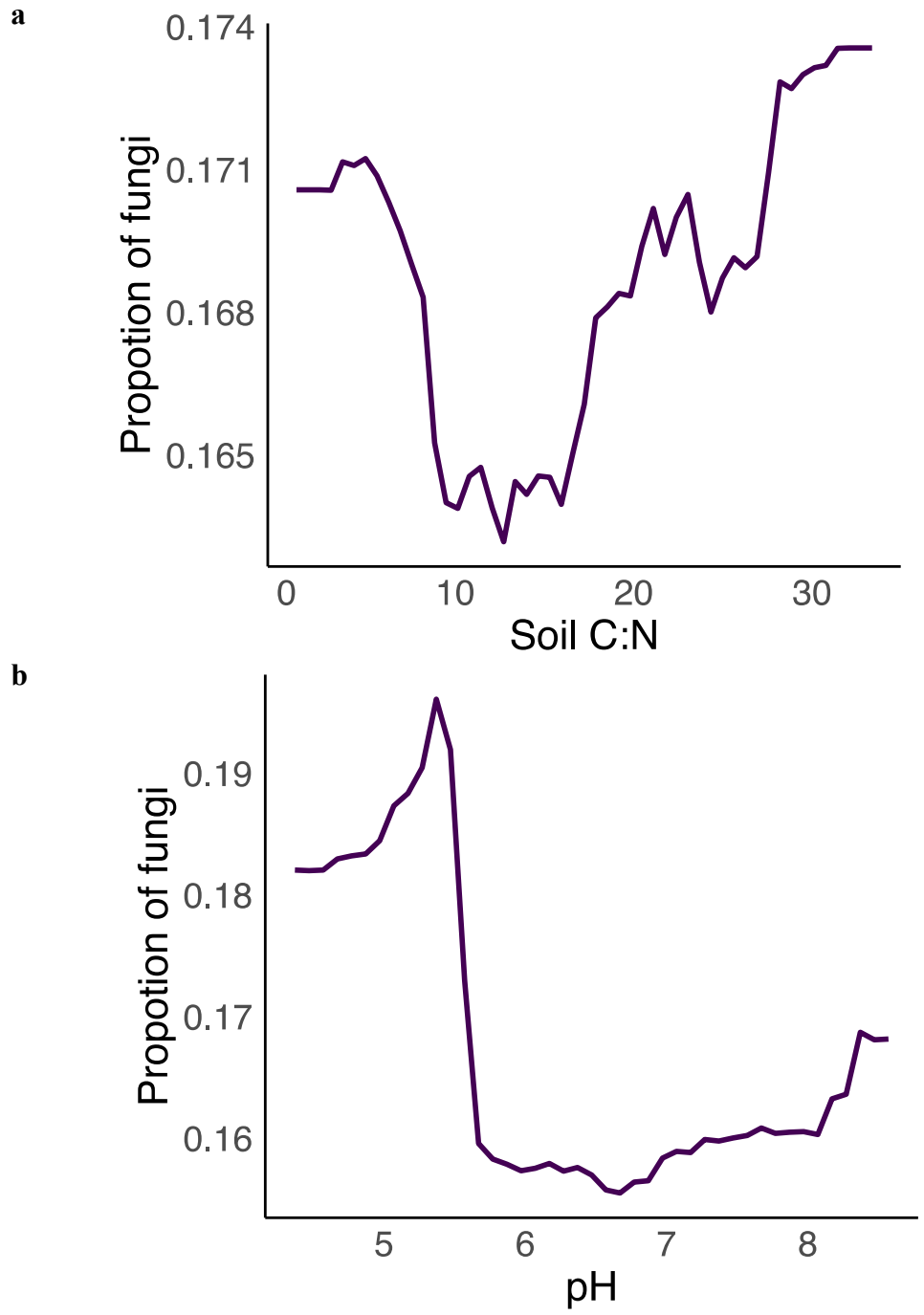

Fig. S9 Partial feature contributions of soil C:N (a) and pH (b) to fungal proportion.

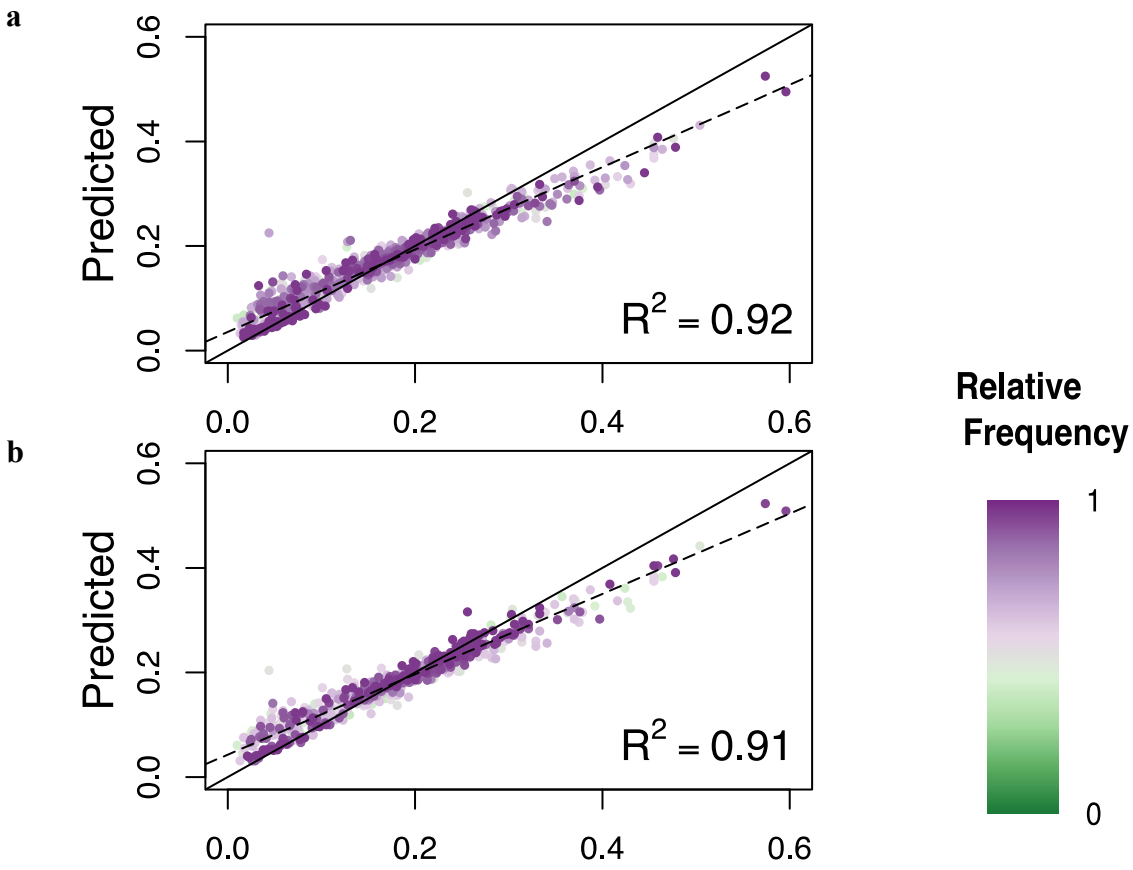

Fig. S10 Model and data validation in the final model. a, the scenario of using full dataset for fungal proportion; b, the scenario of using dataset from natural ecosystems for fungal proportion; C. Heat plots showing the relationships between predicted versus observed values of fungal proportion for the best final models. Dashed diagonal lines indicate fitted relationships, while solid diagonal lines indicate a 1:1 relationship between predicted and observed points.

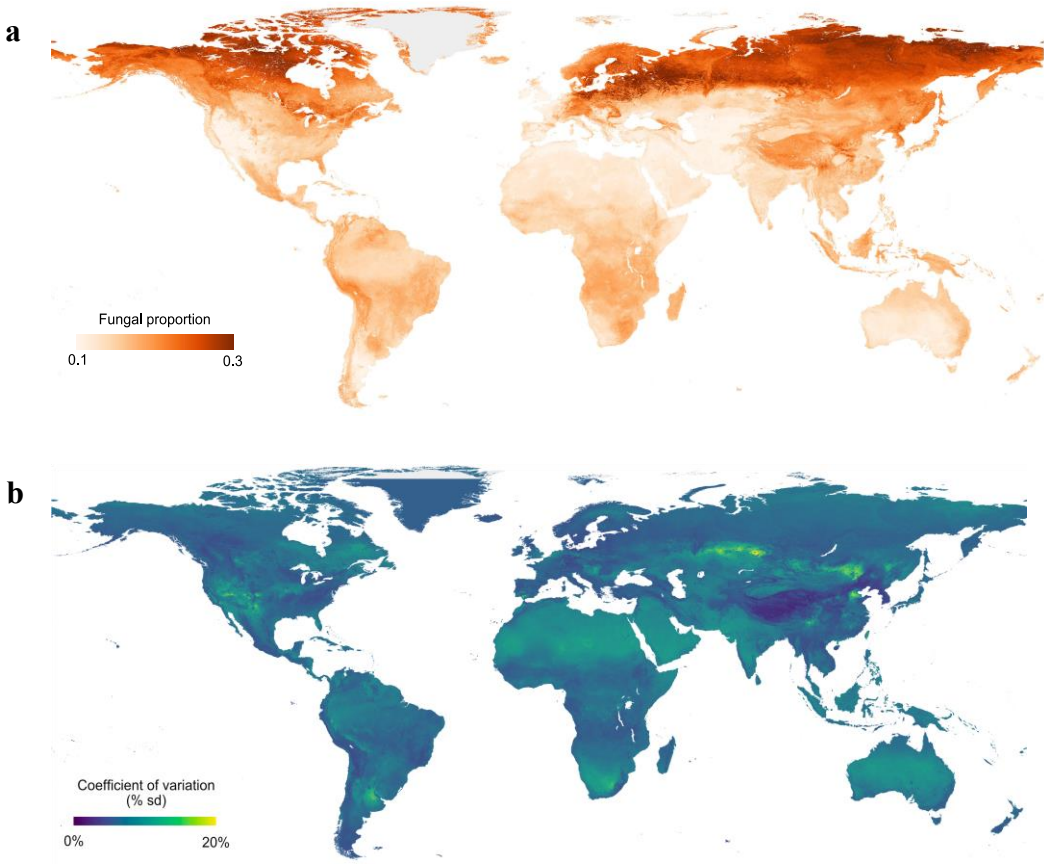

Fig. S11 Global map of fungal proportion (a) and bootstrapped (100 iterations) coefficient of variation (b) at the 30 arcsec (approximately 1 km) pixel scale using the data with natural ecosystems. Bootstrapped coefficient of variation is standard deviation divided by the mean predicted value as a measure of prediction accuracy. Sampling was stratified by biome.

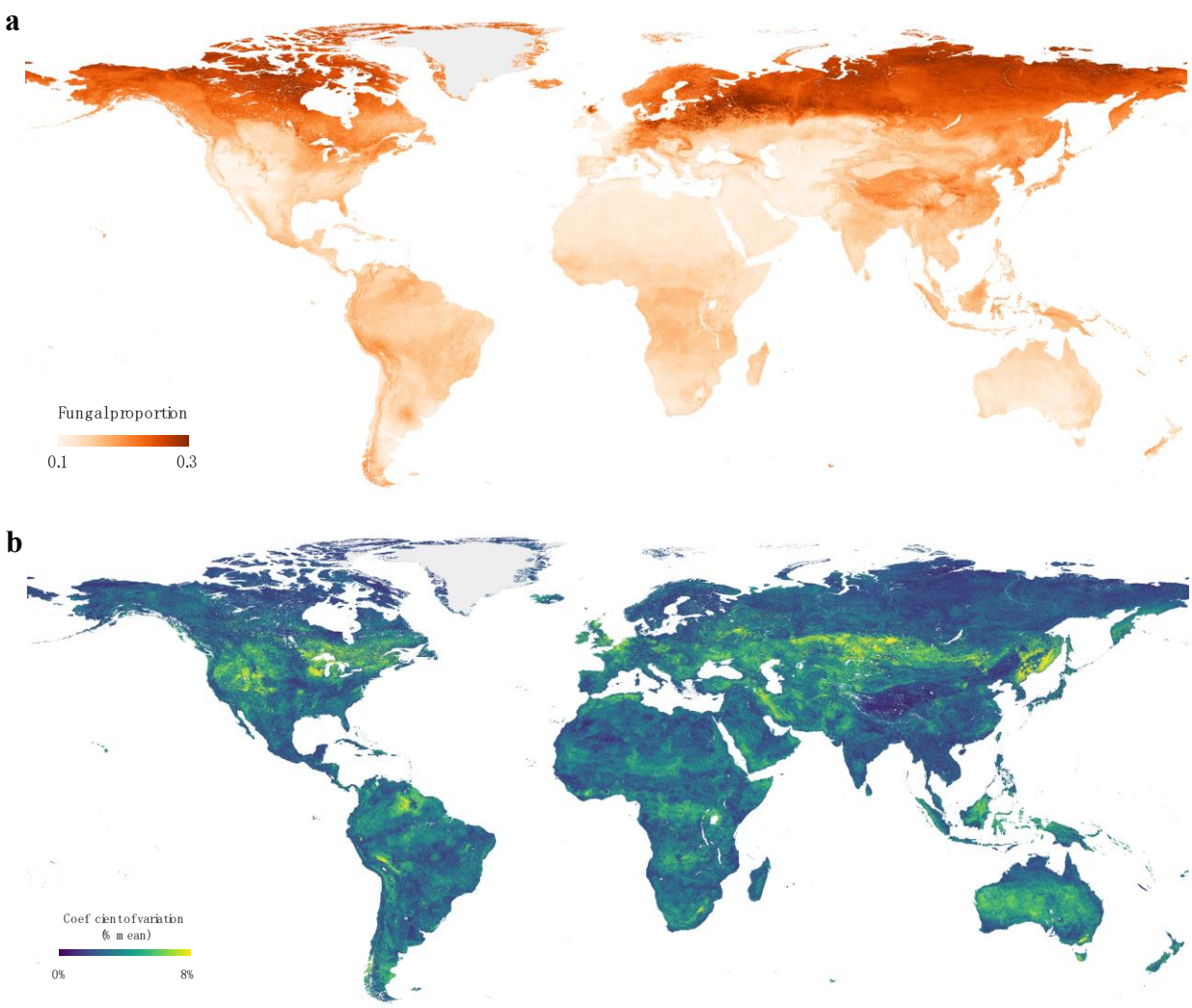

Fig. S12 Global map of fungal proportion (a) and bootstrapped (100 iterations) coefficient of variation (b) at the 30 arcsec (approximately 1 km) pixel scale using full data. Bootstrapped coefficient of variation is standard deviation divided by the mean predicted value as a measure of prediction accuracy. Samples were selected by randomly sampling 90% full datasets with replacement to account for the unbalanced sample distribution.

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