Appendix S1

Journal name: Ecological Monographs

Title: Scale-dependent diversity–biomass relationships can be driven by tree mycorrhizal association and soil fertility.

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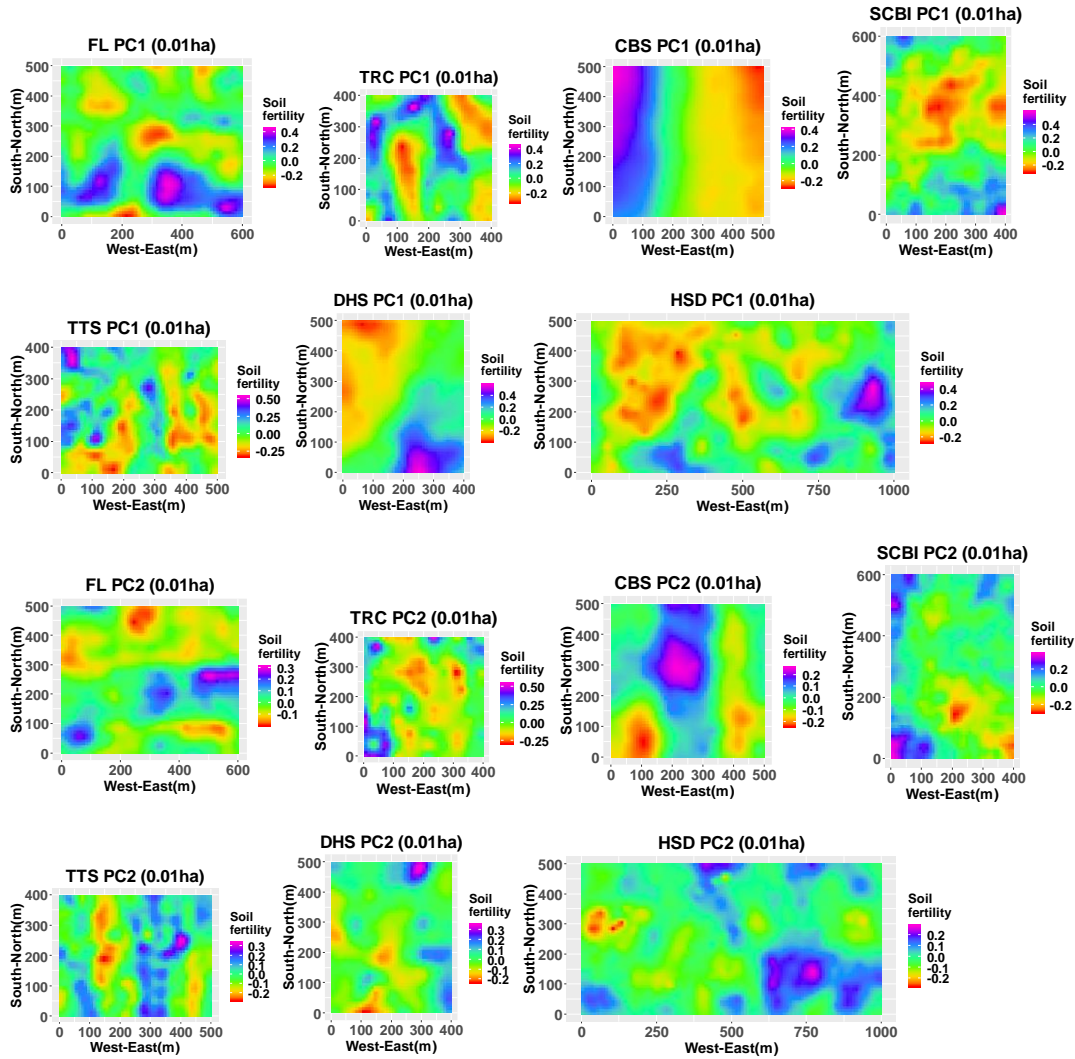
(a)
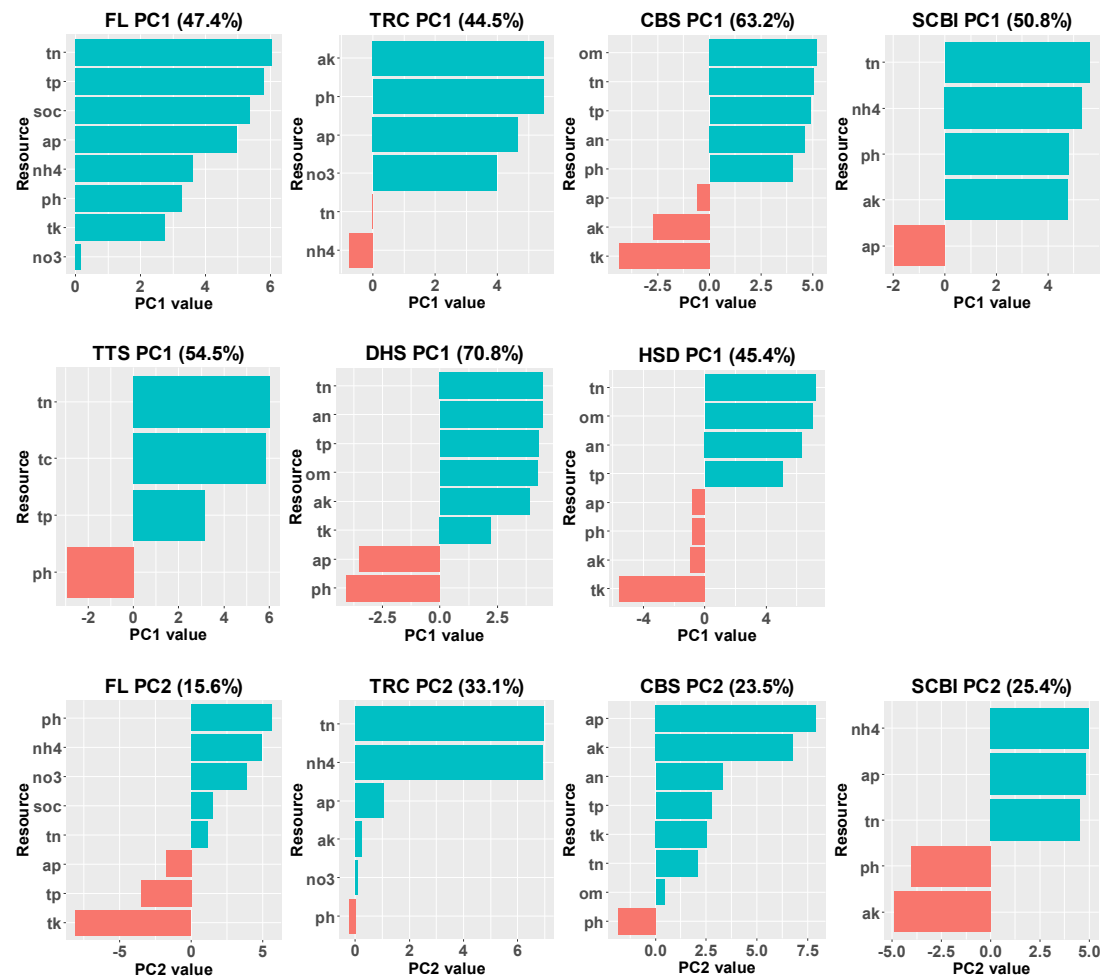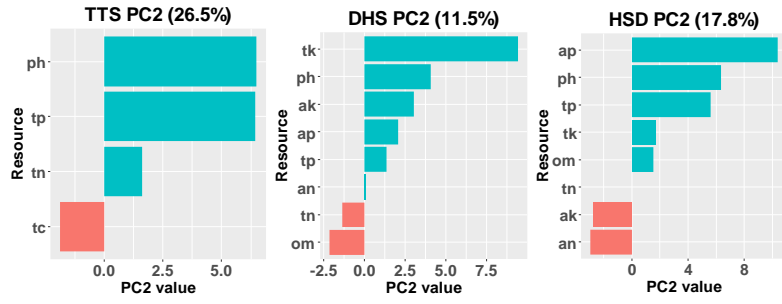
(b)

Figure S2 The overall distribution patterns of tree diameter at breast height (i.e., dbh) and aboveground biomass (AGB) of AM and EM trees in seven forest plots (the abbreviations of the seven forest plots are consistent with Figure S1).
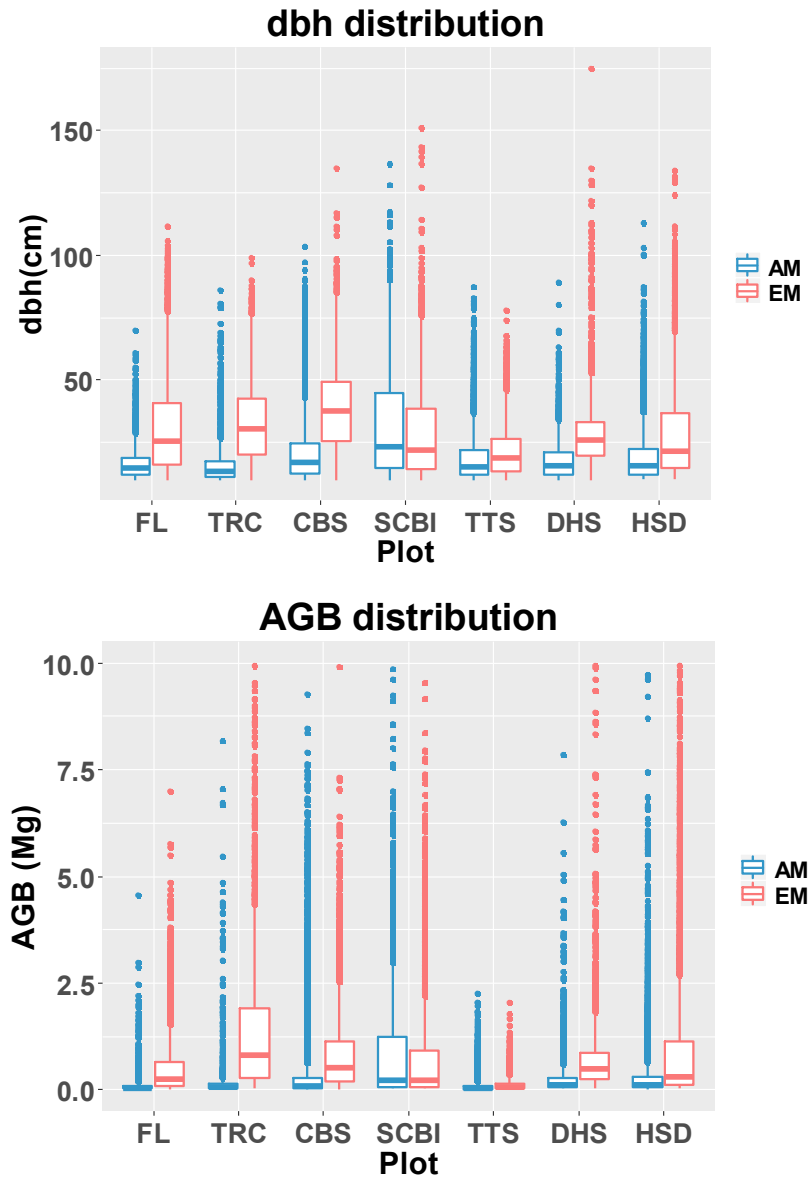
Figure S3 Graphical example showing how toroidal shift null model breaks the spatial relationship between AM and EM tree community with soil fertility. In this null model test, the entire communities of AM trees and EM trees were permutated in a random distance and direction, respectively, for 199 times. For instance, this simplified null model example selected the O_1 and O_2 as coordinate points to generate four subplots for AM and EM tree communities (i.e., A, B, C, and D for EM tree community, and a, b, c, and d for AM tree community), respectively. Then all the four subplots were shifted to new locations by some rules (here C to B, B to C, A to D, D to A; c to b, b to c, a to d, d to a) while holding the relative spatial positions of trees fixed within each subplot to get the new AM and EM tree communities. That is, all the points within the same subplot were shifted in the same distance and direction, while the points in different subplot were shifted in the different distance and direction. Because the coordinates of O_1 and O_2 are selected randomly and independently from each other, the final new AM and EM tree communities are distributed independently within the whole forest plot. Thus this mycorrhiza-dependent toroidal shift model removes the directional changes of AM and EM tree community performances along the soil fertility gradient while accounting for some important ecological processes (e.g., dispersal processes). Finally, these 199 new AM and EM tree communities were combined to generate 199 null communities. For the tree species not belonging to AM or EM types, we held their spatial information fixed in space in each null community.
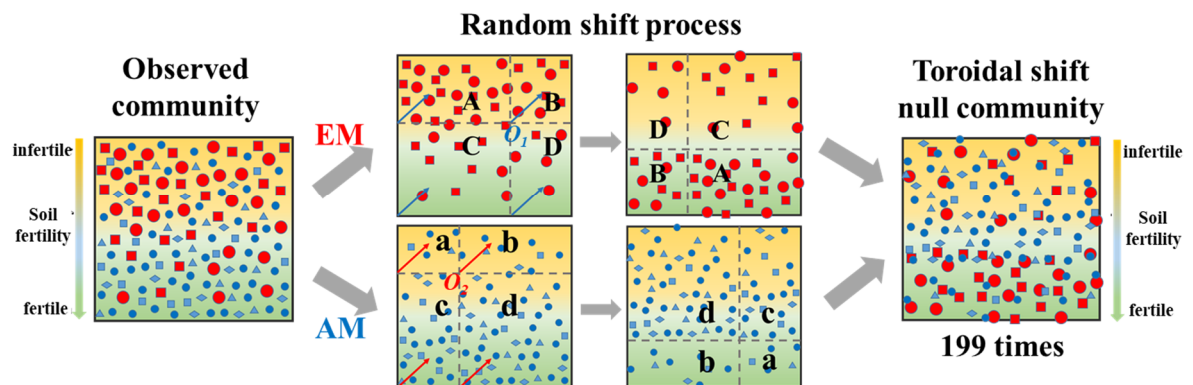
Figure S4 The results for the observed codispersion values, observed minus expected values (Obs. – Exp.) and significance test (Sig.) for the covariation between AM tree dominance (AMdomi) or EM tree dominance (EMdomi) and soil fertility. The abbreviations of the seven forest plots are consistent with Figure S1, and both the soil PC1 and PC2 values in Figure S1 were used in TTS and HSD as soil fertility, while the soil PC1 values were used in other five plots as soil fertility. The colour of each cell represents the value of the codispersion coefficient of the corresponding covariation: red, positive covariation; blue, negative covariation. For the significance test, brown represents significant covariation, whereas grey represents statistically insignificant covariation at the $P < 0.05$ level relative to the null expectation of the 199 null communities. (X: West-East direction; Y: South-North direction).

(a) FL (PC1)
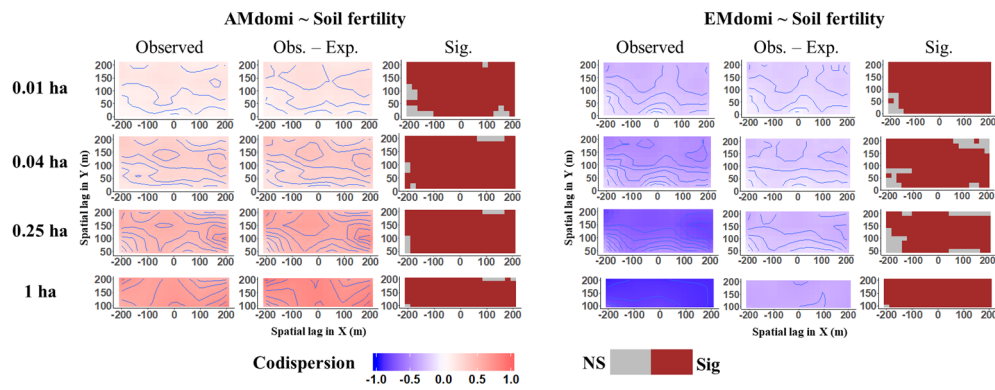
(b) TRC (PC1)
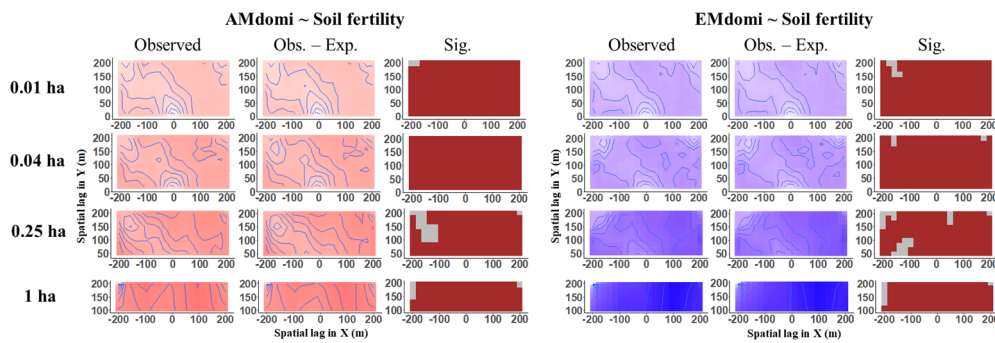
(c) CBS (PC1)

(d)   SCBI (PC1)
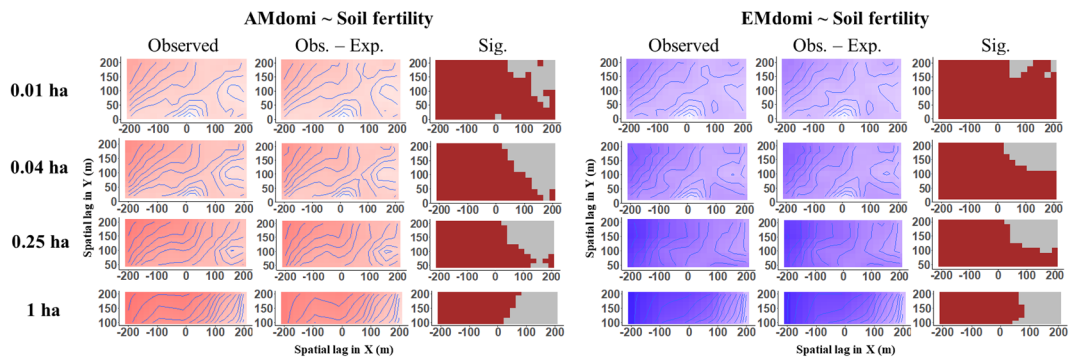
(e)   DHS (PC1)

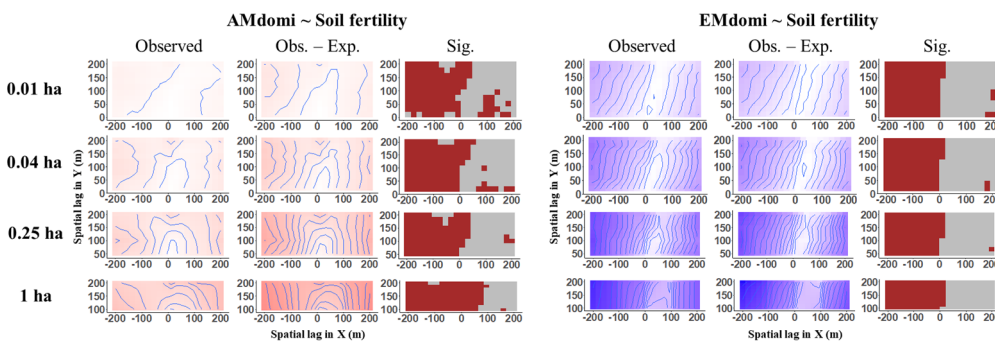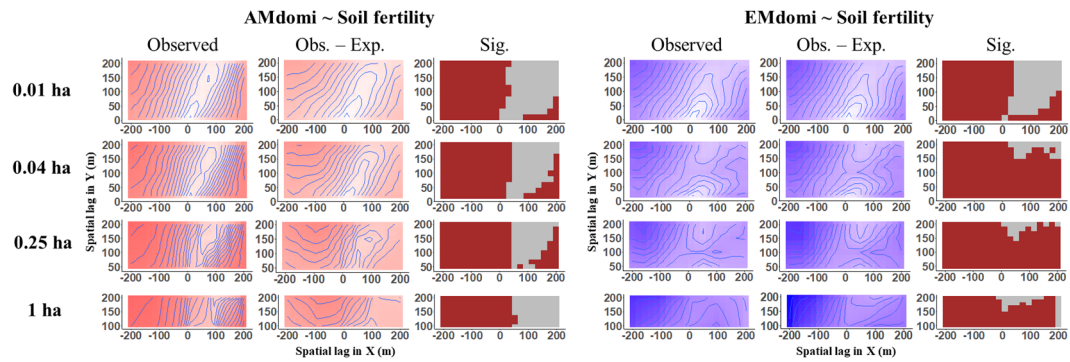**(f)   TTS (PC1)**
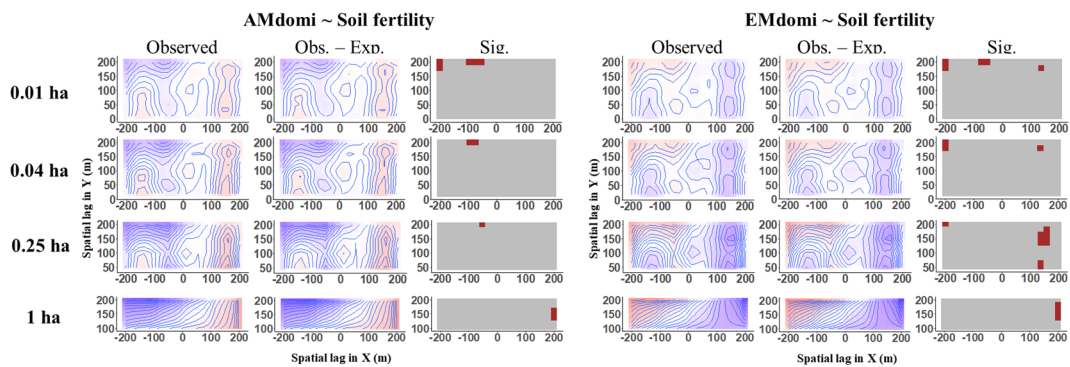
(g)   TTS (PC2)
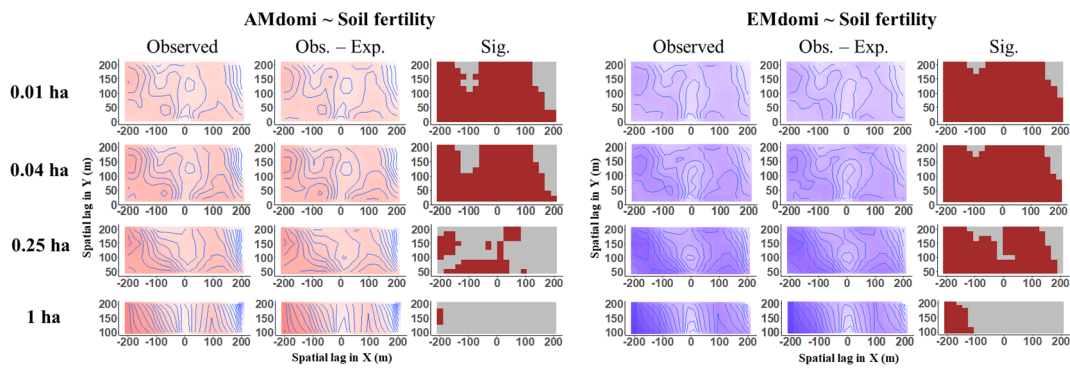
(h)   HSD (PC1)
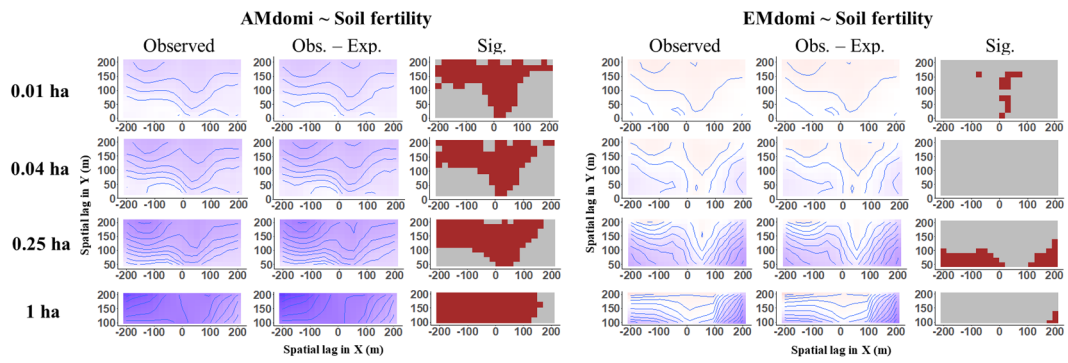
(i)   HSD (PC2)
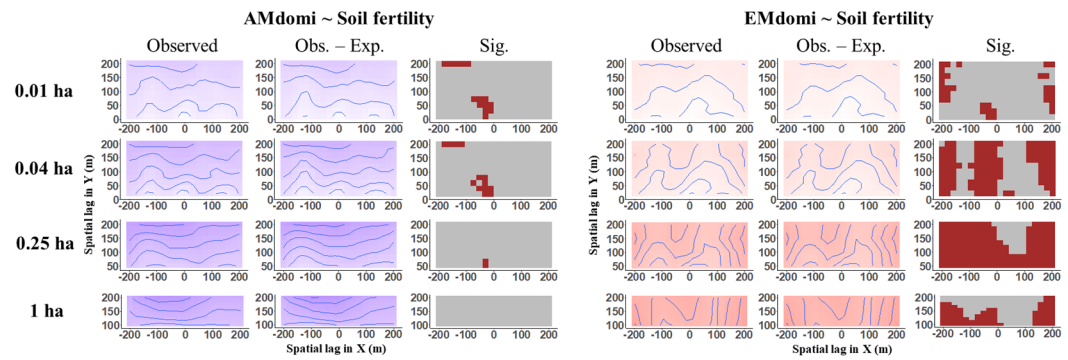
Figure S5 The final structural equation models (SEM) with the lowest Akaike Information Criterion (AIC) score in seven plots at different scales (panel a for AM tree dominance case (AM domi), and panel b for EM tree dominance case (EM domi); the abbreviations of the seven forest plots are consistent with Figure S1). Soil PC1: the soil PC1 values in Figure S1; Soil PC2: the soil PC2 values in Figure S1. The coefficients are standardised coefficients for each causal path. Solid blue arrows indicate positive effects, while solid red arrows indicate negative effects. The arrow thickness is proportional to the absolute value of standardised coefficients. The dashed lines indicate non-significant effects at $P < 0.05$. Significances are $*P < 0.05$, $**P < 0.01$, and $***P < 0.001$. The statistical criteria to evaluate the performance of SEMs were also reported (chi-square test (Chisq $P > 0.05$); Bentler's comparative fit index (CFI > 0.9); The root mean square error of approximation (RMSEA < 0.05); The standardized root mean square residual (SRMR < 0.05)).

(a)
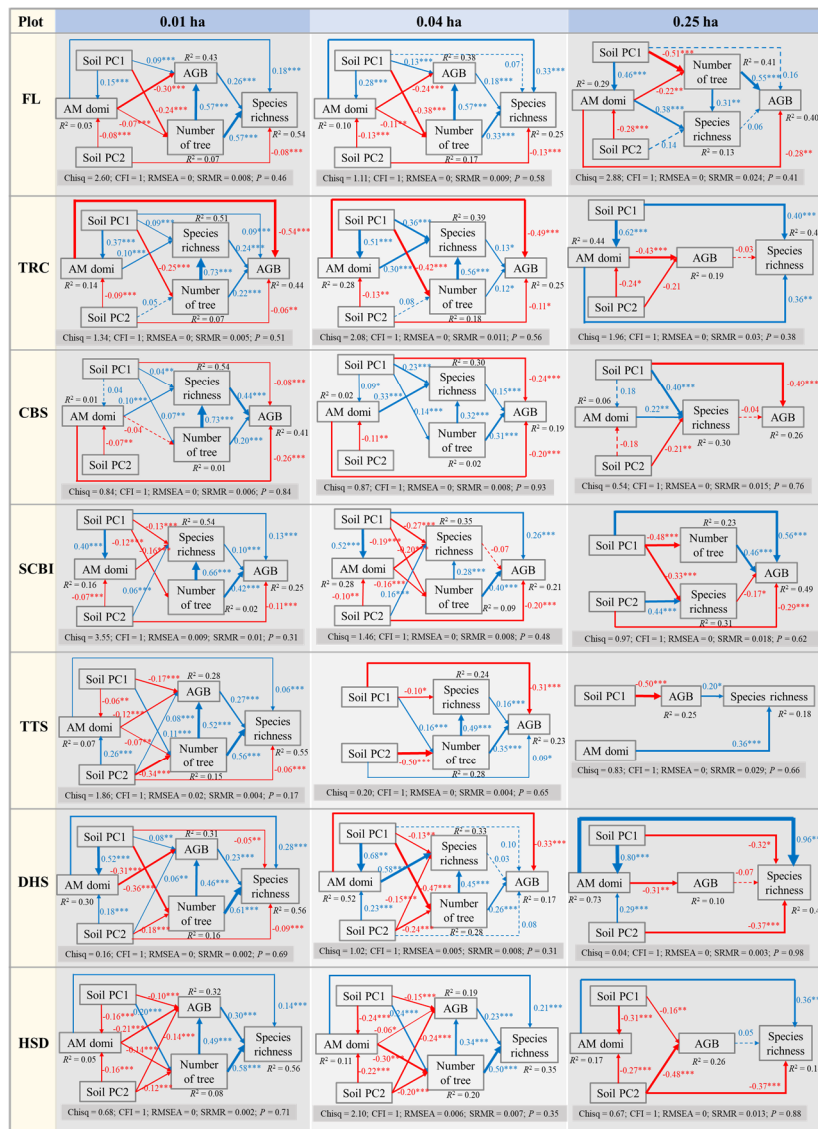
(b)
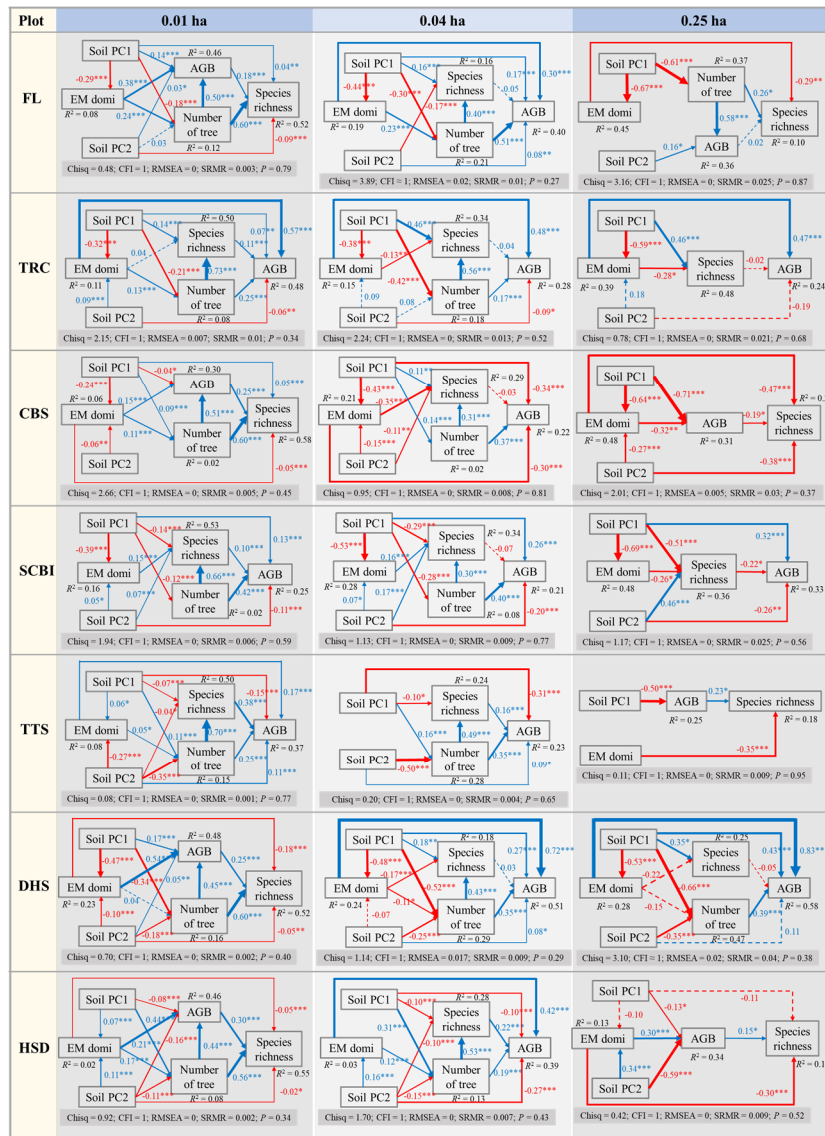
Figure S6 The linear and nonlinear relationships between AM tree dominance and species richness (a) or biomass (b) across 0.01–1 ha scales in seven studied forests (the abbreviations of the seven forest plots are consistent with Figure S1). The lines indicate the regression curves and the shaded areas represent the 95% credible intervals of the regression, with red lines representing the linear relationship while blue lines representing the nonlinear relationships (here y = a*x^2 + b*x + c). The R^2 and *P*-value of each linear and nonlinear model are shown with different font sizes, with large fonts indicating the linear (large red font) or nonlinear (large blue font) model has a lower AIC score.

(a)
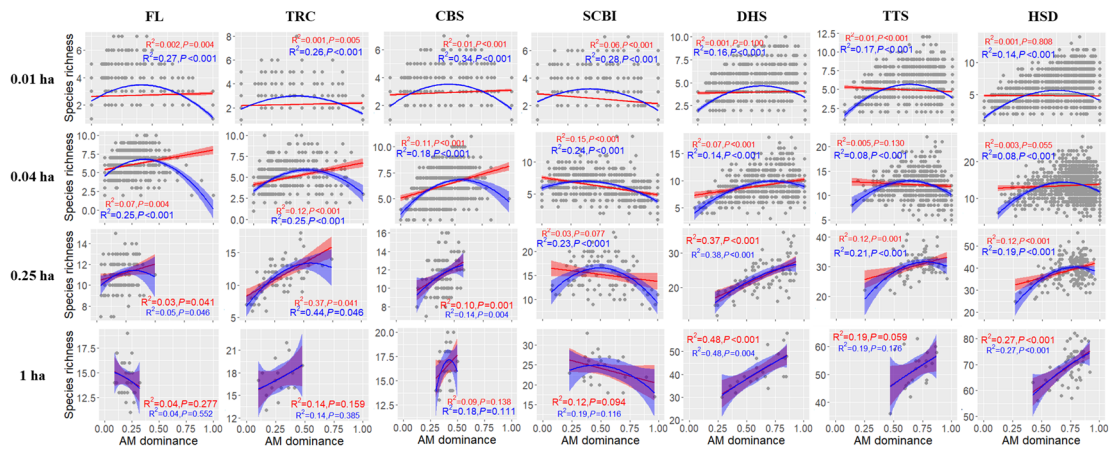
(b)
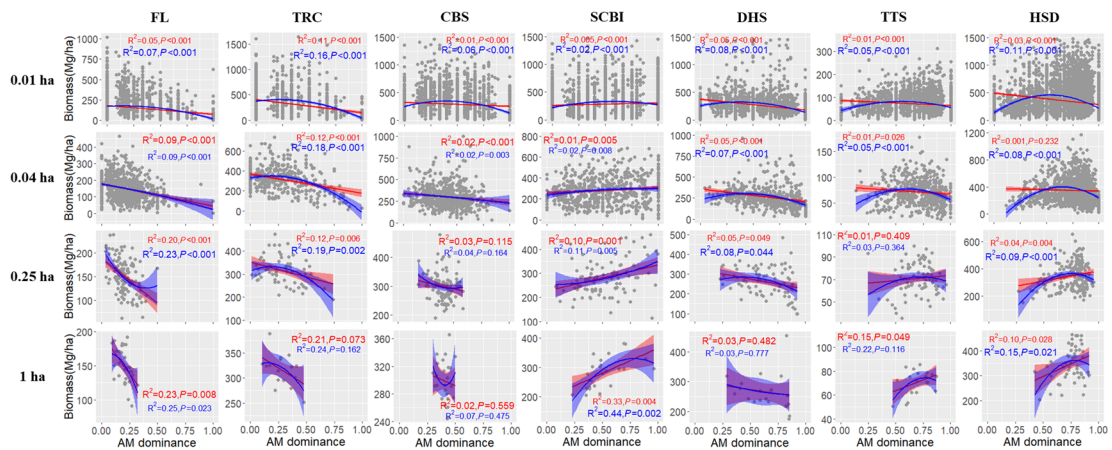
Figure S7 The codispersion results for the covariation between species richness and aboveground biomass after reassigning the mycorrhizal types for tree species with uncertain information or contradictory reports (see the Method section in the main text for details). The abbreviations of the seven forest plots are consistent with Figure S1. (a) the observed results for each forest, and the color of each cell represents whether observed covariation is positive (i.e., positive DBR; red) or negative (i.e., negative DBR; blue). (b) the expected results of null forests (199 times) where soil-related changes in the tree mycorrhizal dominance are excluded, and the color of each cell represents the same meaning as panel a. (c) the significance test for mycorrhizal dominance effect using observed – null results, where the color of each cell represents whether the observed covariation is significantly more positive (i.e., positive effect; brown) or more negative (i.e., negative effect; blue) at the *P* < 0.05 level relative to the null expectation of the 199 null communities.

(a) Observed spatial DBRs
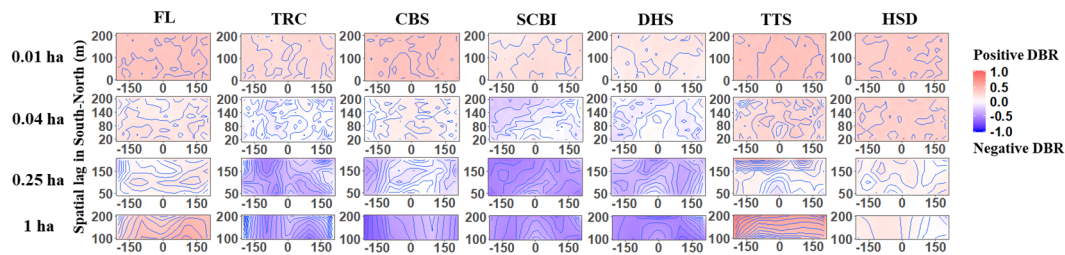
(b) Spatial DBRs without mycorrhizal dominance effect (null results)
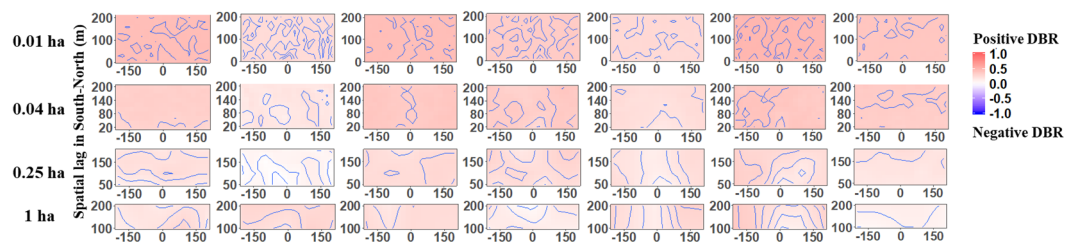
(c) Mycorrhizal dominance effect (observed – null)
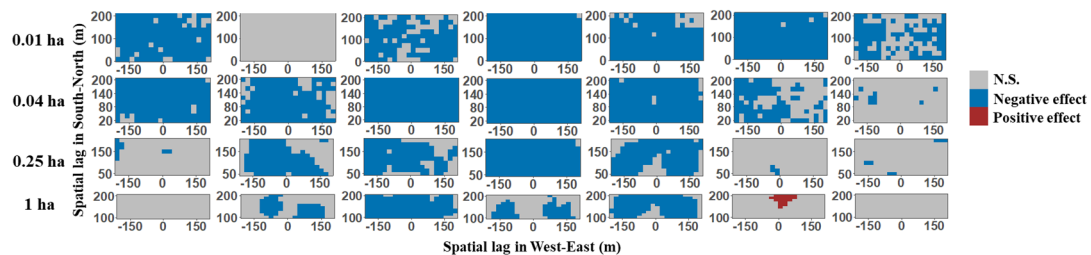
Figure S8 Association between tree species richness and AGB with the soil fertility information at larger scales for seven forest plots (the abbreviations of the seven forest plots are consistent with Figure S1). The colors of points represent the soil fertility property of quadrats deriving from Figure S1 (orange: infertile (IF); blue: fertile (F); the soil PC2 values in Figure S1 were used in TTS and HSD as soil fertility, while the soil PC1 values were used in other five plots as soil fertility). The outlines of AM, EM, and the whole tree community DBRs are drawn with blue, red, and black ellipses for the forest plots with observed soil fertility patterns. Because the points in one group (e.g., AM) overlap points in other groups (e.g., EM) in some plots (e.g., SCBI), we translate all points along diversity or AGB axis for these overlapped groups with no effect on the point patterns within each group to better present their patterns.
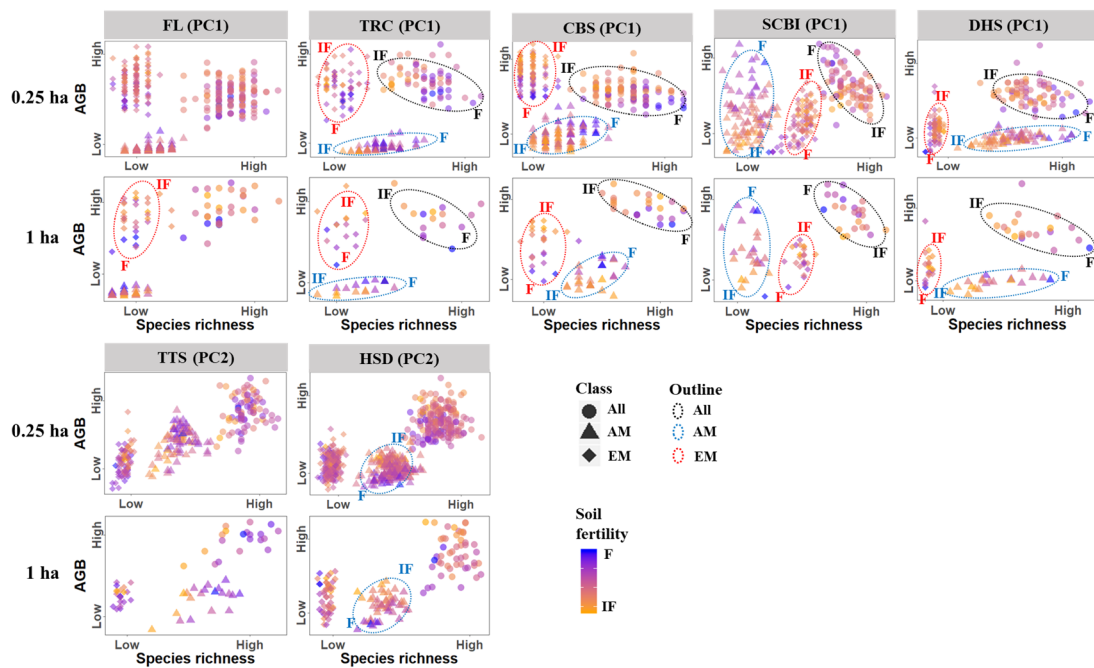
Figure S9 The data characteristics of quadrat aboveground biomass (AGB), number of trees, and species richness across spatial scales (0.0025–1 ha) in seven studied forests (the abbreviations of the seven forest plots are consistent with Figure S1). Panel a is about the mean value (dots) and standard deviation (SD; vertical bars), while panel b is about the coefficient of variation (CV = SD/mean × 100%) of quadrat AGB, number of trees (TN), and species richness (SR). Black: all trees; red: EM trees; blue: AM trees. The results between 0.04 ha and 0.25 ha scales are covered with grey ribbon.

(a)
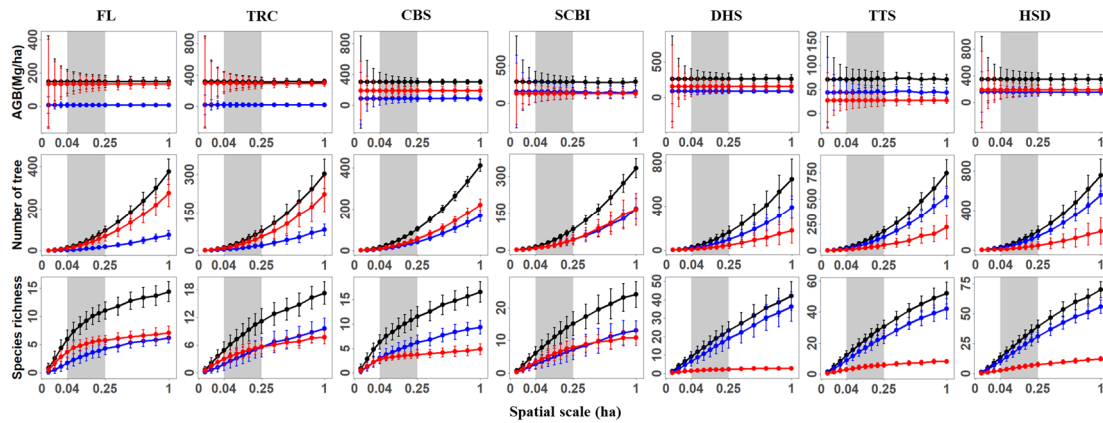
(b)
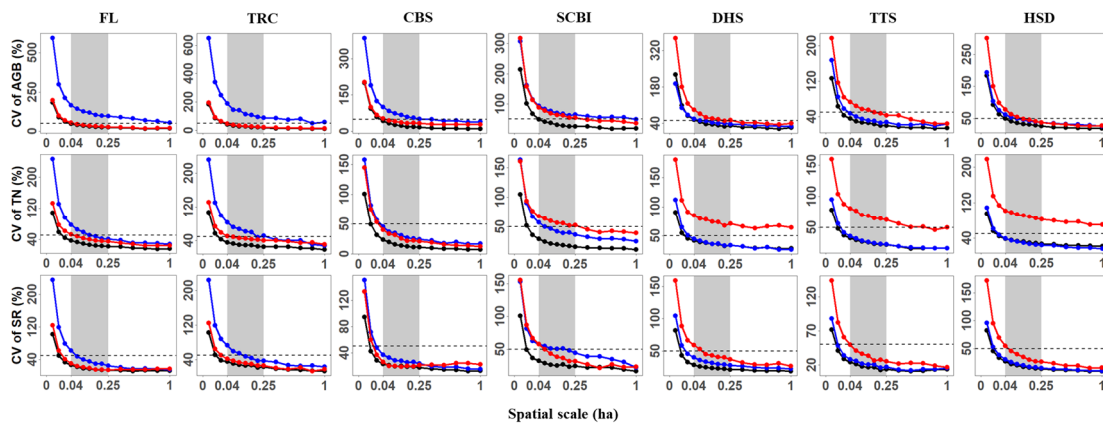
Section S1 Soil sampling and soil physiochemical analyses

Overall, as the important components of the ForestGEO global observational network, all our studied forests have implemented a standard protocol to measure the physical and chemical properties of soils (see Anderson-Teixeira *et al.*, 2015 and Davies *et al.*, 2021 for details). Here, to show that our soil dataset can be used to conduct the statistical analyses across 0.01–1 ha (i.e. 10 m × 10 m to 100 m × 100 m) scales, we selected the Changbaishan plot as one example to introduce the protocol in detail.

Soil sampling: In 2007, soils in this site were sampled using a regular grid of points every 30 m. To capture the variation in soil nutrients at finer scales (e.g. 10 m), two additional sample points at 2, 5, or 15 m were selected in a random compass direction from the grid point (Figure S10). In total, 967 points were sampled in this 25 ha plot in the same day. At each sample point, we collected three randomly allocated soil samples with an auger (50 mm inner diameter, 10 cm in depth) and pooled them to get one composite sample. Each sample contained 500 g topsoil (0–10 cm depth) and all soil samples were air-dried in the same place. Note that to ensure that the soil characteristics in this site did not change in these years, we have resampled the soils in the same sample points in 2019 and found no significant difference between these two datasets (unpublished data).

Soil physiochemical analyses: Eight soil properties (pH, organic matter, total nitrogen (N), available N, total phosphorus (P), available P, total potassium (K) and available K) were analyzed according to the standard method (Lu, 1999; Wang *et al.*, 2012). Specifically, soil pH in water (1:1) was measured by Beckman glass electrode. Soil organic matter was determined colorimetrically by the dichromate oxidation method. Total N was determined colorimetrically on the KCl extracts using the Kjeldahl method. Available N was alkali dispelled by 1 mol/L NaOH. Total P was determined by molybdenum antimony blue colorimetry after extraction using $HClO_4$ – H_2SO_4. Available P content was extracted using a 0.05 mol/L HCL – 0.025 mol/L H_2SO_4 solution. Total K was determined by digesting in hydrofluoric acid and then measured by atomic absorption spectrometer. Available K was extracted with

ammonium acetate and then measured by atomic absorption spectrometer.
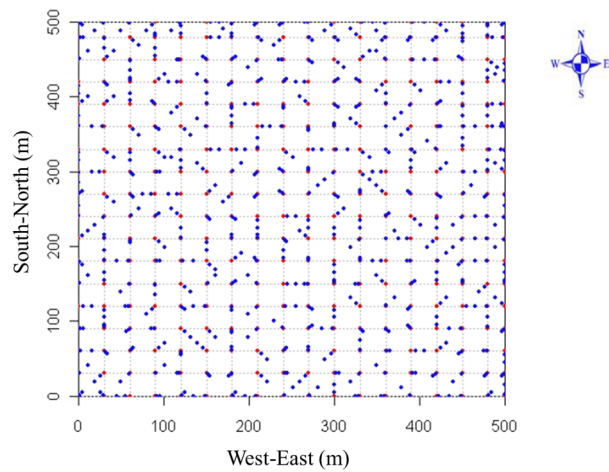
Figure S10 The map of soil sampling points in Changbaishan plot. The dashed lines represent the boundaries of 30 m × 30 m grids, and the red points denote the grid points and the blue points denote the supplementary sampling points.

Section S2 One example for the interpretation of codispersion analysis

Codispersion analysis is a nonparametric approach to quantify the spatial covariation of two or more spatially explicit datasets (Cuevas *et al*., 2013). So far, this method have been widely applied to dealing with many ecological issues, including the species co-occurrence patterns (Buckley *et al*., 2016a; Wang *et al*., 2016), the spatial patterns in species-environment relationships (Cuevas *et al*., 2013; Buckley *et al*., 2016b), the landscape classification from remotely sensed image data (Vallejos *et al*., 2015), and the role of foundation species in driving species diversity (Ellison *et al*., 2019).

Take the case of the codispersion analysis of aboveground biomass (AGB) of EM trees and soil fertility at 20 m scale in Changbaishan plot, these two data contain regular 20 m × 20 m rasters with the spatial information of AGB and soil fertility in this plot (Figure S11a, b). To get the codispersion patterns of these two variables, this method firstly needs to smooth the spatial variation surface for each individual dataset (i.e. AGB and soil fertility) and their intersection (AGB ~ soil fertility) using an Epanechnikov kernel function across all studied spatial lags (i.e. distance between rasters). Then, the semivariograms for AGB and soil fertility and the semi-cross-variogram of their intersection are computed for the kernel-smoothed surfaces (Figure S11c; Cuevas *et al*., 2013). Finally, the codispersion coefficient is computed for each spatial lag as the semi-cross-variogram divided by the square root of the product of the semivariograms for each of these two variables (Figure S11d; Buckley *et al*., 2016b). Note that the value of the codispersion coefficient ranges from -1 to 1, where the positive (negative) values represent the positive (negative) covariation between AGB and soil fertility, and the strength of the covariation increases with the increasing absolute value of the codispersion coefficient. More details about the R codes and the statistical information of this method can be found in Cuevas *et al*., 2013 and Buckley *et al*., 2016b.

From the spatial patterns of AGB and soil fertility in Changbaishan plot at 20 m scale (Figure S11a, b), we can find an obvious east-west gradient for both the soil fertility and AGB of EM trees. Specifically, there were greater AGB (i.e. higher AGB

value) in eastern quadrats compared with the western quadrats, while the soils in eastern quadrats were more infertile (i.e. lower fertility value) than those in western quadrats. That is, the spatial patterns of the changes in AGB and soil fertility were opposite with each other (i.e. negative covariation) in this forest. Thus, the codispersion coefficients of these two variables were negative in most spatial lags (Figure S11d).
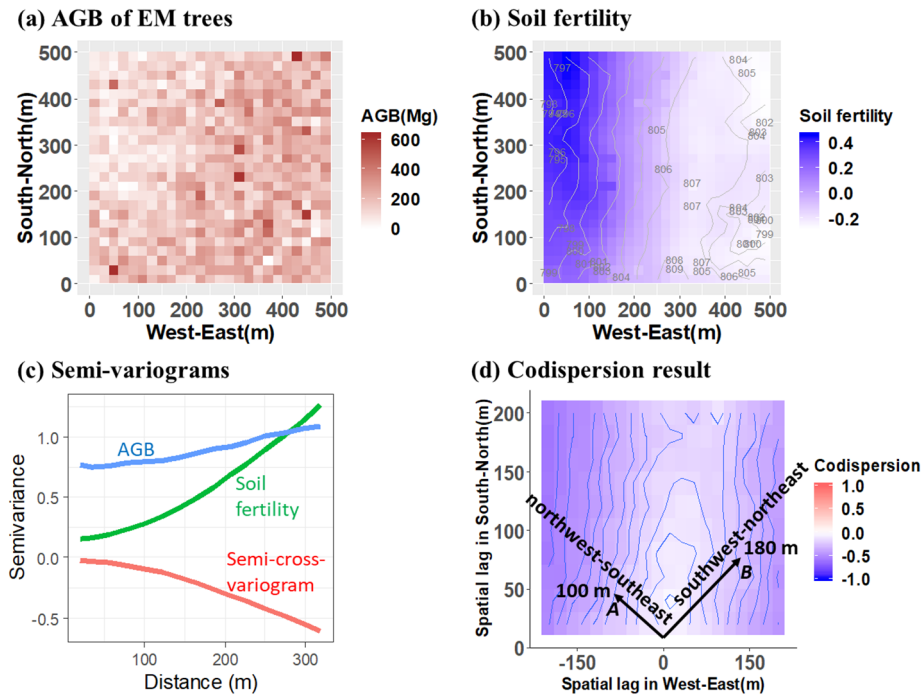
Figure S11 Case example of the codispersion analysis. Panels a and b show the spatial patterns of AGB of EM trees and soil fertility, respectively. Panel c represents the semi-variograms for AGB of EM trees (blue line) and soil fertility (green line) and their semi-cross-variogram (red line). Panel d shows the final codispersion result indicating the spatial covariation between AGB and soil fertility.

One great advantage of the codispersion method is the detailed distance and direction (or anisotropy) information of studied covariation. For the direction, the two axes of the codispersion results represent north-south and west-east direction, respectively, thus each spatial lag in the codispersion maps represents one certain direction. For the distance, the spatial lag values in each axis represent the studied distance over which the covariation between the two variables is computed. For

instance, the codispersion value in *A* point (Figure S11d) represents the covariation result over 100 m (distance) in northwest-southeast (direction), while the codispersion value in *B* point represents the covariation result over 180 m (distance) in southwest-northeast (direction). Thus we can see from Figure S11d that, there was an obvious west-east (but not north-south) trend in the covariation between AGB and soil fertility, because the codispersion values mainly changed in this direction (i.e. the directional changes in color in Figure S11d). This is a signal of anisotropy. Moreover, we can also read that, the covariation changed with studied distance, because the greater codispersion values (i.e. the dark color in Figure S11d) mainly occurred in lags far away from the original point.

Table S1 Soil variables [mean (standard deviation)] used to quantify the soil fertility gradient in seven forest plots. "na" represents that there is no information about this soil variable in this forest plot.

Soil variables		FL	TRC	CBS	SCBI	TTS	DHS	HSD
nitrogen (N)	total N (g kg⁻¹)	11.76	3.20 (0.90)	6.40 (1.42)	4.19	3.20 (0.70)	1.18 (0.50)	1.53 (0.25)
	available N (mg kg⁻¹)	na	na	502.66	na	na	201.76	154.00
	NH_4^+ (mg kg⁻¹)	7.55 (1.35)	2.82 (0.95)	na	4.15	na	na	na
	NO_3^- (mg kg⁻¹)	0.016	0.283	na	na	na	na	na
phosphorus (P)	total P (g kg⁻¹)	0.92 (0.21)	na	1.26 (0.31)	na	0.26 (0.10)	0.28 (0.05)	0.101
	available P (mg kg⁻¹)	4.81 (2.42)	10.47	8.46 (0.81)	19.99	na	1.81 (1.05)	1.61 (0.46)
potassium (K)	total K (g kg⁻¹)	3.53 (0.34)	na	16.49	na	na	18.24	25.56
	available K (mg kg⁻¹)	na	104.06	259.60	174.61	na	55.03	79.15
soil organic matter (g kg⁻¹)		na	na	164.75	na	na	60.96	38.67
soil total carbon (g kg⁻¹)		na	na	na	na	44.68	na	na
soil organic carbon (g kg⁻¹)		154.54	na	na	na	na	na	na
pH		4.69 (0.39)	5.53 (0.60)	5.45 (0.10)	5.06	4.15 (0.14)	3.75 (0.08)	4.48 (0.08)

Abbreviations: FL: Fenglin; TRC: Tyson Research Center; CBS: Changbaishan; SCBI: Smithsonian Conservation Biology Institute; TTS: Tiantongshan; DHS: Dinghushan; HSD: Heishiding.

Table S2 The direct, indirect, and total effects of number of tree (TN), AM tree dominance (AMdomi), soil PC1 (Soil1), and soil PC2 (Soil2) on species richness and aboveground biomass in our structural equation models (Figure S5; the abbreviations of the seven forest plots are consistent with Table S1). Significance levels: ns, nonsignificant at $P \geq 0.05$; *, $P < 0.05$;**, $P < 0.01$; ***, $P < 0.001$.

Variable	Scale (ha)	Plot	Effect on aboveground biomass			Effect on species richness		
			direct	indirect	total	direct	indirect	total
AMdomi	0.01	FL	-0.30***	-0.04***	-0.34***	0.176***	-0.119***	0.057*
		TRC	-0.54***	0.025***	-0.52***	0.102***	-	0.102***
		CBS	-0.26***	0.038***	-0.23***	0.104***	-0.027 ns	0.077***
		SCBI	-	-0.02***	-0.02***	-0.16***	-	-0.16***
		TTS	-0.12***	-0.037**	-0.16***	0.06***	-0.05***	0.012 ns
		DHS	-0.31***	-	-0.31***	0.279***	-0.07***	0.208***
		HSD	-0.21***	-0.07***	-0.28***	0.135***	-0.14***	-0.007 ns
	0.04	FL	-0.24***	-0.061**	-0.30***	0.328***	-0.079***	0.249***
		TRC	-0.485***	0.039*	-0.45***	0.298***	-	0.298***
		CBS	-0.20***	0.05**	-0.15***	0.331***	-	0.331***
		SCBI	-	-0.05*	-0.05*	-0.20***	-0.044**	-0.24***
		TTS	-	-	-	-	-	-
		DHS	-0.33***	0.017 ns	-0.32***	0.578***	-	0.578***
		HSD	-0.064*	-0.1***	-0.17***	0.214***	-0.17***	0.047 ns
	0.25	FL	-0.275**	-0.097 ns	-0.37***	0.375***	-0.069*	0.306**
		TRC	-0.43***	-	-0.43***	0.364**	0.012 ns	0.376**
		CBS	-	-0.008 ns	-0.008 ns	0.224**	-	0.224**
		SCBI	-	-	-	-	-	-
		TTS	-	-	-	0.364***	-	0.364***
		DHS	-0.311**	-	-0.311**	0.958***	0.023 ns	0.981***
		HSD	-	-	-	0.358***	-	0.358***
TN	0.01	FL	0.572***	-	0.572***	0.565***	0.15***	0.715***
		TRC	0.223***	0.177***	0.40***	0.73***	-	0.73***
		CBS	0.198***	0.318***	0.516***	0.73***	-	0.73***
		SCBI	0.419***	0.068***	0.487***	0.662***	-	0.662***
		TTS	0.518***	-	0.518***	0.558***	0.141***	0.699***
		DHS	0.462***	-	0.462***	0.609***	0.106***	0.715***
		HSD	0.485***	-	0.485	0.567***	0.146***	0.713***
	0.04	FL	0.569***	-	0.569***	0.33***	0.103***	0.433***
		TRC	0.115*	0.074*	0.188***	0.558***	-	0.558***
		CBS	0.308***	0.048**	0.356***	0.317***	-	0.317***
		SCBI	0.399***	-0.019 ns	0.38***	0.277***	-	0.277***
		TTS	0.348***	0.078**	0.426***	0.492***	-	0.492***
		DHS	0.257***	0.013 ns	0.271***	0.449***	-	0.449***
		HSD	0.341***	-	0.341***	0.5***	0.078***	0.578***
	0.25	FL	0.549***	0.02 ns	0.569***	0.314**	-	0.314**
		TRC	-	-	-	-	-	-
		CBS	-	-	-	-	-	-
		SCBI	0.459***	-	0.459***	-	-	-
		TTS	-	-	-	-	-	-
		DHS	-	-	-	-	-	-
		HSD	-	-	-	-	-	-

Table S2 (continued).

Variable	Scale (ha)	Plot	Effect on aboveground biomass			Effect on species richness		
			direct	indirect	total	direct	indirect	total
		FL	0.091***	-0.18***	-0.09***	-	-0.08***	-0.08***
		TRC	0.085***	-0.23***	-0.15***	0.094***	-0.146***	-0.051*
		CBS	-0.08***	0.02*	-0.06***	0.037**	0.054***	0.092***
	0.01	SCBI	0.134***	-0.06***	0.069**	-0.13***	-0.14***	-0.28***
		TTS	-0.17***	0.064***	-0.11***	-	0.012 ns	0.012 ns
		DHS	0.078**	-0.33***	-0.25***	-0.051**	-0.056**	-0.11***
		HSD	-0.1***	0.13***	0.03*	-	0.059***	0.059***
		FL	0.129***	-0.28***	-0.15***	0.065 ns	-0.008 ns	0.057 ns
		TRC	-	-0.25***	-0.25***	0.356***	-0.082*	0.274***
		CBS	-0.24***	0.058**	-0.18***	0.227***	0.075***	0.302***
Soil1	**0.04**	SCBI	0.258***	-0.059**	0.199***	-0.27***	-0.16***	-0.43***
		TTS	-0.31***	0.041*	-0.27***	-0.096*	0.08***	-0.016 ns
		DHS	0.101 ns	-0.35***	-0.25***	-0.126*	0.183***	0.057 ns
		HSD	-0.15***	0.097***	-0.049 ns	-	0.037*	0.037*
		FL	0.157 ns	-0.41***	-0.25**	-	0.014 ns	0.014 ns
		TRC	-	-0.27***	-0.27***	0.395***	0.224**	0.619***
		CBS	-0.49***	-0.014 ns	-0.50***	0.399***	0.04 ns	0.439***
	0.25	SCBI	0.56***	-0.164*	0.396***	-0.33***	-	-0.33***
		TTS	-0.5***	-	-0.5***	-	-0.1 ns	-0.1 ns
		DHS	-	-0.249**	-0.249**	-0.323*	0.769***	0.446***
		HSD	-0.156**	-	-0.156**	-	-0.12***	-0.12***
		FL	-	0.023***	0.023***	-0.08***	-0.014***	-0.095***
		TRC	-0.064**	0.061***	-0.003 ns	-	0.023 ns	0.023 ns
		CBS	-	0.018**	0.018**	-	-0.007**	-0.007**
	0.01	SCBI	-0.11***	0.007**	-0.1***	0.064***	0.011**	0.075***
		TTS	0.083***	-0.21***	-0.13***	-0.06***	-0.15***	-0.22***
		DHS	0.06**	-0.14***	-0.08***	-0.09***	-0.047**	-0.13***
		HSD	-0.14***	-0.024**	-0.17***	-	-0.13***	-0.13***
		FL	-	0.032**	0.032**	-0.13***	-0.042***	-0.176***
		TRC	-0.107*	0.073**	-0.034 ns	-	0.003 ns	0.003 ns
		CBS	-	0.023*	0.023*	-	-0.037**	-0.037**
Soil2	**0.04**	SCBI	-0.20***	-0.011 ns	-0.21***	0.161***	0.02**	0.182***
		TTS	0.092*	-0.18***	-0.083 ns	-	-0.25***	-0.25***
		DHS	0.082 ns	-0.14***	-0.061 ns	-0.15***	0.022 ns	-0.132**
		HSD	-0.24***	-0.06***	-0.29***	-	-0.2***	-0.2***
		FL	-	0.086*	0.086*	0.143 ns	-0.105**	0.038 ns
		TRC	-0.209 ns	0.102*	-0.107 ns	-	-0.08 ns	-0.08 ns
		CBS	-	0.007 ns	0.007 ns	-0.214**	-0.041 ns	-0.255**
	0.25	SCBI	-0.29***	-0.077 ns	-0.37***	0.439***	-	0.439***
		TTS	-	-	-	-	-	-
		DHS	-	-0.09**	-0.09**	-0.37***	0.278***	-0.089 ns
		HSD	-0.48***	-	-0.48***	-	-0.121**	-0.121**

Table S3 The direct, indirect, and total effects of number of tree (TN), EM tree dominance (EMdomi), soil PC1 (Soil1), and soil PC2 (Soil2) on species richness and aboveground biomass in our structural equation models (Figure S5; the abbreviations of the seven forest plots are consistent with Table S1). Significance levels: ns, nonsignificant at $P \geq 0.05$; *, $P < 0.05$;**, $P < 0.01$; ***, $P < 0.001$.

Variable	Scale (ha)	Plot	Effect on aboveground biomass			Effect on species richness		
			direct	indirect	total	direct	indirect	total
EMdomi	**0.01**	FL	0.375***	0.123***	0.498***	-	0.216***	0.216***
		TRC	0.574***	0.036***	0.609***	0.037 ns	0.092***	0.129***
		CBS	0.15***	0.054***	0.204***	-0.05***	0.101***	0.049*
		SCBI	-	0.015***	0.015***	0.145***	-	0.145***
		TTS	0.167***	0.013*	0.18***	-	0.036*	0.036*
		DHS	0.543***	0.017 ns	0.56***	-0.18***	0.16***	-0.023 ns
		HSD	0.437***	0.073***	0.51***	-0.05***	0.221***	0.169***
	0.04	FL	0.298***	0.118***	0.415***	-	0.092***	0.092***
		TRC	0.483***	-0.005 ns	0.478***	-0.129**	-	-0.129**
		CBS	-0.3***	0.011 ns	-0.28***	-0.35***	-	-0.35***
		SCBI	-	-0.011 ns	-0.011 ns	0.16***	-	0.16***
		TTS	-	-	-	-	-	-
		DHS	0.723***	-0.043**	0.68***	-0.17***	-0.046*	-0.22***
		HSD	0.423***	0.023***	0.445***	-	0.062***	0.062***
	0.25	FL	-	-	-	-0.292**	-	-0.292**
		TRC	0.473***	0.006 ns	0.479***	-0.28*	-	-0.28*
		CBS	-0.316**	-	-0.316**	-0.47***	0.058 ns	-0.41***
		SCBI	-	0.058 ns	0.058 ns	-0.26*	-	-0.26*
		TTS	-	-	-	-0.35***	-	-0.35***
		DHS	0.828***	-0.048 ns	0.78***	-0.218 ns	-	-0.218 ns
		HSD	0.299***	-	0.299***	-0.30***	0.044*	-0.26***
TN	**0.01**	FL	0.504***	-	0.504***	0.602***	0.093***	0.695***
		TRC	0.248***	0.08***	0.328***	0.725***	-	0.725***
		CBS	0.509***	-	0.509***	0.599***	0.129***	0.727***
		SCBI	0.418***	0.068***	0.487***	0.664***	-	0.664***
		TTS	0.253***	0.265***	0.518***	0.699***	-	0.699***
		DHS	0.445***	-	0.445***	0.599***	0.112***	0.711***
		HSD	0.439***	-	0.439***	0.556***	0.13***	0.685***
	0.04	FL	0.51***	0.02 ns	0.53***	0.401***	-	0.401***
		TRC	0.167***	0.022 ns	0.189***	0.556***	-	0.556***
		CBS	0.365***	-0.009 ns	0.355***	0.305***	-	0.305***
		SCBI	0.398***	-0.02 ns	0.378***	0.297***	-	0.297***
		TTS	0.348***	0.078**	0.426***	0.492***	-	0.492***
		DHS	0.351***	0.013 ns	0.364***	0.425***	-	0.425***
		HSD	0.191***	0.116***	0.306***	0.528***	-	0.528***
	0.25	FL	0.582***	-	0.582***	0.264*	0.014 ns	0.278**
		TRC	-	-	-	-	-	-
		CBS	-	-	-	-	-	-
		SCBI	-	-	-	-	-	-
		TTS	-	-	-	-	-	-
		DHS	0.386***	-	0.386***	-	-	-
		HSD	-	-	-	-	-	-

Table S3 (continued).

Variable	Scale (ha)	Plot	Effect on aboveground biomass			Effect on species richness		
			direct	indirect	total	direct	indirect	total
Soil1	0.01	FL	0.138***	-0.20***	-0.06**	0.038**	-0.08***	-0.04*
		TRC	0.065**	-0.22***	-0.15***	0.142***	-0.16***	-0.022 ns
		CBS	-0.039*	0.011 ns	-0.027 ns	0.048***	0.058***	0.106***
		SCBI	0.134***	-0.07***	0.069**	-0.14***	-0.14***	-0.28***
		TTS	-0.15***	0.012 ns	-0.14***	-0.07***	0.079***	0.011 ns
		DHS	0.165***	-0.41***	-0.24***	-	-0.078***	-0.078***
		HSD	-0.084***	0.12***	0.036**	-	0.088***	0.088***
	0.04	FL	0.168***	-0.28**	-0.11**	0.156***	-0.12***	0.034 ns
		TRC	-	-0.23***	-0.23***	0.46***	-0.19***	0.274***
		CBS	-0.34***	0.173***	-0.16***	0.11**	0.193***	0.303***
		SCBI	0.258***	-0.09***	0.167***	-0.29***	-0.17***	-0.46***
		TTS	-0.31***	0.041*	-0.27***	-0.096*	0.08***	-0.016 ns
		DHS	0.266***	-0.53***	-0.26***	0.176**	-0.14***	0.036 ns
		HSD	-0.1***	0.039**	-0.06*	-0.1***	0.165***	0.07*
	0.25	FL	-	-0.36***	-0.36***	-	0.034 ns	0.034 ns
		TRC	-	-0.29***	-0.29***	0.463***	0.165*	0.628***
		CBS	-0.71***	0.201**	-0.51***	-	0.429***	0.429***
		SCBI	0.323***	0.112*	0.436***	-0.51***	0.18*	-0.33***
		TTS	-0.5***	-	-0.5***	-	-0.114*	-0.114*
		DHS	0.429***	-0.71***	-0.284**	0.35**	0.116 ns	0.466***
		HSD	-0.125*	-0.03 ns	-0.156**	-0.105 ns	0.012 ns	-0.093 ns
Soil2	0.01	FL	0.033*	0.016 ns	0.049**	-0.09***	0.026*	-0.068***
		TRC	-0.06**	0.049***	-0.008 ns	-	0.003 ns	0.003 ns
		CBS	-	-0.009**	-0.009**	-	0.003*	0.003*
		SCBI	-0.11***	0.007**	-0.1***	0.068***	0.007*	0.075***
		TTS	0.11***	-0.15***	-0.036 ns	-0.035*	-0.24***	-0.28***
		DHS	0.054**	-0.13***	-0.08***	-0.054**	-0.08***	-0.13***
		HSD	-0.16***	-0.004 ns	-0.16***	-0.02*	-0.12***	-0.14***
	0.04	FL	0.078**	-0.008 ns	0.07*	-0.17***	-	-0.17***
		TRC	-0.089*	0.054*	-0.036 ns	-	0.031 ns	0.031 ns
		CBS	-	0.047**	0.047**	-0.113**	0.053***	-0.06 ns
		SCBI	-0.2***	-0.011 ns	-0.21***	0.171***	0.011 ns	0.182***
		TTS	0.092*	-0.18***	-0.083 ns	-	-0.248***	-0.248***
		DHS	0.078*	-0.14***	-0.06 ns	-	-0.1***	-0.1***
		HSD	-0.27***	0.016 ns	-0.26***	-0.10***	-0.08***	-0.19***
	0.25	FL	0.164*	-	0.164*	-	0.004 ns	0.004 ns
		TRC	-0.192 ns	0.085 ns	-0.107 ns	-	-0.05 ns	-0.05 ns
		CBS	-	0.086*	0.086*	-0.38***	0.127**	-0.253**
		SCBI	-0.259**	-0.101*	-0.36***	0.456***	-	0.456***
		TTS	-	-	-	-	-	-
		DHS	0.114 ns	-0.134**	-0.02 ns	-	-	-
		HSD	-0.59***	0.102***	-0.48***	-	-0.188***	-0.188***

Table S4 Numerical output from the linear fits of the generalized least squares methods of log-transformed species richness on log-transformed aboveground biomass at different scales for all forest plots (the abbreviations of the seven forest plots are consistent with Table S1). Note: CI-low and CI-high show the lower and upper confidence limits of slope coefficients. Significance levels of slope coefficients are shown: ns, nonsignificant at $P \geq 0.05$; *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$. The model with the lowest AIC score is selected as the optimal model.

Plots	Scales (ha)	models	slope	CI-low	CI-high	*P*-value	AIC	optimal model
	0.01	non-spatial	1.24	1.17	1.31	< 0.001***	8061.22	spatial
	0.01	spatial	1.26	1.18	1.33	< 0.001***	8043.17	
	0.04	non-spatial	0.46	0.33	0.60	< 0.001***	1274.49	spatial
FL	0.04	spatial	0.55	0.41	0.68	< 0.001***	1222.40	
	0.25	non-spatial	0.18	-0.14	0.51	0.271 ns	28.97	spatial
	0.25	spatial	0.10	-0.19	0.38	0.510 ns	10.68	
	1	non-spatial	0.58	0.03	1.13	0.040*	-9.43	non-spatial
	1	spatial	0.62	0.07	1.16	0.028*	-6.82	
	0.01	non-spatial	0.92	0.80	1.04	< 0.001***	4829.65	spatial
	0.01	spatial	0.94	0.82	1.06	< 0.001***	4829.45	
	0.04	non-spatial	0.003	-0.13	0.13	0.965 ns	611.26	spatial
TRC	0.04	spatial	0.02	-0.11	0.15	0.771 ns	610.23	
	0.25	non-spatial	-0.21	-0.39	-0.03	0.023*	-22.73	non-spatial
	0.25	spatial	-0.21	-0.39	-0.03	0.023*	-18.73	
	1	non-spatial	-0.20	-0.61	0.20	0.301 ns	-16.18	non-spatial
	1	spatial	-0.20	-0.61	0.20	0.301 ns	-12.18	
	0.01	non-spatial	1.38	1.29	1.46	< 0.001***	6626.50	non-spatial
	0.01	spatial	1.38	1.30	1.47	< 0.001***	6629.85	
	0.04	non-spatial	0.20	0.06	0.35	0.004**	725.05	non-spatial
CBS	0.04	spatial	0.21	0.06	0.35	0.004**	729.05	
	0.25	non-spatial	-0.22	-0.39	-0.05	0.013*	-78.78	non-spatial
	0.25	spatial	-0.19	-0.36	-0.01	0.039*	-75.70	
	1	non-spatial	-0.38	-0.68	-0.07	0.017*	-35.65	spatial
	1	spatial	-0.32	-0.61	-0.03	0.032*	-38.52	
	0.01	non-spatial	0.92	0.81	1.02	< 0.001***	7523.55	spatial
	0.01	spatial	0.95	0.85	1.05	< 0.001***	7520.43	
	0.04	non-spatial	-0.09	-0.21	0.03	0.148 ns	1038.75	non-spatial
SCBI	0.04	spatial	-0.05	-0.18	0.07	0.410 ns	1040.66	
	0.25	non-spatial	-0.47	-0.67	-0.28	< 0.001***	8.31	spatial
	0.25	spatial	-0.31	-0.52	-0.09	0.006**	-1.08	
	1	non-spatial	-0.56	-0.99	-0.13	0.012*	-8.21	non-spatial
	1	spatial	-0.37	-0.78	0.04	0.075 ns	-5.54	
	0.01	non-spatial	0.91	0.83	0.99	< 0.001***	4985.25	spatial
	0.01	spatial	0.93	0.85	1.01	< 0.001***	4958.57	
	0.04	non-spatial	0.02	-0.14	0.18	0.778 ns	788.62	spatial
DHS	0.04	spatial	0.11	-0.05	0.28	0.188 ns	731.13	
	0.25	non-spatial	-0.38	-0.71	-0.05	0.023*	51.46	spatial
	0.25	spatial	-0.13	-0.48	0.22	0.457 ns	44.44	
	1	non-spatial	-0.49	-1.00	0.03	0.062 ns	0.39	non-spatial
	1	spatial	-0.49	-1.00	0.03	0.062 ns	4.39	

Table S4 (continued).

Plots	Scales (ha)	models	slope	CI-low	CI-high	*P*-value	AIC	optimal model
TTS	0.01	non-spatial	0.91	0.85	0.97	< 0.001***	3948.43	spatial
	0.01	spatial	0.93	0.86	0.99	< 0.001***	3916.51	
	0.04	non-spatial	0.47	0.34	0.60	< 0.001***	424.81	spatial
	0.04	spatial	0.51	0.39	0.64	< 0.001***	350.84	
	0.25	non-spatial	0.38	0.05	0.71	0.026*	-14.00	spatial
	0.25	spatial	-0.02	-0.34	0.30	0.912 ns	-29.87	
	1	non-spatial	0.69	0.26	1.11	0.003**	-15.57	spatial
	1	spatial	0.28	-0.14	0.70	0.173 ns	-17.06	
HSD	0.01	non-spatial	1.17	1.12	1.22	< 0.001***	13062.31	spatial
	0.01	spatial	1.18	1.13	1.23	< 0.001***	12995.69	
	0.04	non-spatial	0.77	0.67	0.88	< 0.001***	1994.26	spatial
	0.04	spatial	0.81	0.70	0.91	< 0.001***	1916.11	
	0.25	non-spatial	0.26	-0.02	0.54	0.066 ns	64.17	spatial
	0.25	spatial	0.10	-0.16	0.36	0.465 ns	14.00	
	1	non-spatial	0.33	-0.29	0.94	0.291 ns	-5.10	spatial
	1	spatial	0.37	-0.22	0.96	0.213 ns	-18.51	

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