Title: Landscape effects on global soil pathogenic fungal diversity across spatial scales

Supplementary Information

Supplementary Tables 1–9

Supplementary Figs. 1–31

Supplementary Table 1. Predictors, coefficients (estimate slope), standard errors (se), t-values and *p*-values of the multivariate Generalized Additive Models for Location, Scale, and Shape (GAMLSS) on (a) leaf/fruit/seed-associated (LFSA) and (b) root-associated (RA) fungal alpha diversity within the 500 m radius around the sampling plot. Statistical tests are two-sided Wald tests from multivariate GAMLSS without adjustment for multiple comparisons. Significance relationships are marked in bold.

(a) LFSA fungi

		Overall				**Forest**				**Grassland**			
Predictor	**Diversity**	**Coefficient**	**se**	**t-value**	***p*-value**	**Coefficient**	**se**	**t-value**	***p*-value**	**Coefficient**	**se**	**t-value**	***p*-value**
Landscape complexity	Richness	**0.037**	**0.011**	**3.355**	**0.001**	0.008	0.014	0.584	0.560	**0.062**	**0.029**	**2.165**	**0.032**
	Shannon	0.021	0.011	1.795	0.073	0.015	0.018	0.840	0.402	0.018	0.024	0.769	0.444
	Abundance	**0.042**	**0.012**	**3.435**	**0.001**	**-0.037**	**0.014**	**-2.551**	**0.011**	**0.081**	**0.030**	**2.662**	**0.009**
Grass cover	Richness	0.004	0.064	0.057	0.955	<0.001	0.111	-0.002	0.999	-0.060	0.113	-0.534	0.595
	Shannon	-0.056	0.067	-0.836	0.403	-0.030	0.138	-0.216	0.829	-0.022	0.094	-0.237	0.813
	Abundance	0.063	0.072	0.875	0.382	0.041	0.113	0.359	0.720	0.041	0.107	0.384	0.702
Crop cover	Richness	**0.226**	**0.060**	**3.754**	**<0.001**	0.063	0.106	0.595	0.553	**-0.436**	**0.107**	**-4.087**	**<0.001**
	Shannon	**0.155**	**0.063**	**2.444**	**0.015**	-0.098	0.132	-0.742	0.459	**-0.333**	**0.089**	**-3.736**	**<0.001**
	Abundance	**0.268**	**0.068**	**3.925**	**<0.001**	**0.222**	**0.108**	**2.062**	**0.040**	-0.148	0.102	-1.454	0.148
Tree cover	Richness	-0.102	0.071	-1.442	0.150	-0.116	0.118	-0.985	0.326	**-0.636**	**0.135**	**-4.726**	**<0.001**
	Shannon	-0.124	0.075	-1.660	0.098	-0.218	0.147	-1.485	0.139	**-0.469**	**0.112**	**-4.174**	**<0.001**
	Abundance	-0.026	0.080	-0.321	0.749	-0.087	0.120	-0.726	0.469	-0.167	0.090	-1.854	0.066
Longitude	Richness	-0.007	0.031	-0.218	0.828	-0.016	0.030	-0.524	0.601	0.120	0.135	0.885	0.378
	Shannon	0.005	0.032	0.151	0.880	-0.012	0.037	-0.331	0.741	**0.288**	**0.113**	**2.547**	**0.012**
	Abundance	-0.017	0.035	-0.493	0.622	-0.057	0.030	-1.883	0.061	0.146	0.152	0.959	0.339

(Continued from previous page)		**Overall**				**Forest**				**Grassland**			
Predictor	**Diversity**	**Coefficient**	**se**	**t-value**	***p*-value**	**Coefficient**	**se**	**t-value**	***p*-value**	**Coefficient**	**se**	**t-value**	***p*-value**
Latitude	Richness	**-0.099**	**0.036**	**-2.717**	**0.007**	**-0.089**	**0.039**	**-2.314**	**0.022**	-0.023	0.083	-0.279	0.781
	Shannon	**-0.129**	**0.038**	**-3.392**	**0.001**	**-0.117**	**0.048**	**-2.441**	**0.016**	0.071	0.069	1.036	0.302
	Abundance	-0.020	0.041	-0.497	0.619	**-0.134**	**0.039**	**-3.421**	**0.001**	0.175	0.095	1.843	0.068
Elevation	Richness	-0.070	0.044	-1.613	0.107	-0.067	0.062	-1.071	0.285	**-0.418**	**0.113**	**-3.715**	**<0.001**
	Shannon	-0.012	0.046	-0.258	0.797	-0.083	0.078	-1.065	0.288	**-0.294**	**0.094**	**-3.134**	**0.002**
	Abundance	0.031	0.049	0.621	0.535	-0.029	0.063	-0.466	0.642	-0.191	0.118	-1.613	0.109
MAT	Richness	**0.095**	**0.042**	**2.258**	**0.024**	**0.102**	**0.048**	**2.107**	**0.036**	0.127	0.220	0.577	0.565
	Shannon	0.064	0.044	1.444	0.149	0.052	0.060	0.863	0.389	0.246	0.183	1.343	0.182
	Abundance	**0.223**	**0.047**	**4.693**	**<0.001**	0.080	0.049	1.624	0.106	-0.010	0.237	-0.044	0.965
MAP	Richness	-0.003	0.034	-0.081	0.935	**-0.129**	**0.042**	**-3.086**	**0.002**	**-0.240**	**0.108**	**-2.226**	**0.028**
	Shannon	-0.063	0.036	-1.768	0.078	-0.097	0.052	-1.855	0.065	**-0.219**	**0.090**	**-2.431**	**0.016**
	Abundance	0.049	0.038	1.272	0.204	-0.141	**0.042**	**-3.331**	**0.001**	-0.198	0.121	-1.643	0.103
Clay	Richness	**0.175**	**0.033**	**5.264**	**<0.001**	0.250	**0.034**	**7.306**	**<0.001**	-0.111	0.082	-1.343	0.182
	Shannon	**0.117**	**0.035**	**3.357**	**0.001**	0.122	**0.043**	**2.864**	**0.005**	**-0.166**	**0.069**	**-2.415**	**0.017**
	Abundance	**0.109**	**0.038**	**2.893**	**0.004**	0.245	**0.035**	**7.050**	**<0.001**	0.151	0.091	1.653	0.101
Silt	Richness	-0.029	0.033	-0.873	0.383	-0.035	0.033	-1.044	0.298	**0.236**	**0.088**	**2.677**	**0.008**
	Shannon	-0.011	0.034	-0.308	0.758	-0.001	0.042	-0.030	0.976	**0.266**	**0.073**	**3.621**	**<0.001**
	Abundance	**-0.099**	**0.037**	**-2.664**	**0.008**	**-0.071**	**0.034**	**-2.094**	**0.038**	-0.188	0.096	-1.965	0.052
pH	Richness	**0.290**	**0.040**	**7.217**	**<0.001**	**0.203**	**0.045**	**4.503**	**<0.001**	**0.345**	**0.080**	**4.318**	**<0.001**
	Shannon	**0.300**	**0.042**	**7.095**	**<0.001**	**0.275**	**0.056**	**4.895**	**<0.001**	**0.236**	**0.067**	**3.541**	**0.001**
	Abundance	**0.175**	**0.045**	**3.852**	**<0.001**	0.087	0.046	1.898	0.059	**0.227**	**0.091**	**2.502**	**0.014**

(Continued from previous page)		**Overall**				**Forest**				**Grassland**			
Predictor	**Diversity**	**Coefficient**	**se**	**t-value**	***p*-value**	**Coefficient**	**se**	**t-value**	***p*-value**	**Coefficient**	**se**	**t-value**	***p*-value**
Nitrogen	Richness	0.045	0.029	1.532	0.126	0.020	0.034	0.581	0.562	0.076	0.055	1.382	0.169
	Shannon	0.046	0.031	1.504	0.133	0.003	0.043	0.067	0.947	0.055	0.046	1.202	0.232
	Abundance	0.033	0.033	1.007	0.314	0.026	0.035	0.750	0.454	-0.066	0.061	-1.082	0.281
C/N ratio	Richness	**-0.128**	**0.032**	**-4.075**	**<0.001**	-0.039	0.034	-1.129	0.260	-0.107	0.071	-1.512	0.133
	Shannon	**-0.219**	**0.033**	**-6.619**	**<0.001**	**-0.185**	**0.043**	**-4.334**	**<0.001**	-0.044	0.059	-0.738	0.462
	Abundance	**-0.126**	**0.036**	**-3.523**	**<0.001**	-0.050	0.035	-1.446	0.150	-0.037	0.079	-0.470	0.639

(b) RA fungi

		Overall				**Forest**				**Grassland**			
Predictor	**Diversity**	**Coefficient**	**se**	**t-value**	***p*-value**	**Coefficient**	**se**	**t-value**	***p*-value**	**Coefficient**	**se**	**t-value**	***p*-value**
Landscape complexity	Richness	<0.001	0.015	0.023	0.981	-0.044	0.025	-1.741	0.083	0.044	0.034	1.285	0.201
	Shannon	0.007	0.016	0.469	0.639	-0.023	0.025	-0.923	0.357	0.001	0.038	0.033	0.974
	Abundance	0.024	0.016	1.497	0.135	0.034	0.026	1.314	0.190	-0.037	0.044	-0.848	0.398
Grass cover	Richness	0.025	0.090	0.276	0.783	-0.233	0.199	-1.171	0.243	-0.085	0.135	-0.629	0.530
	Shannon	0.024	0.092	0.264	0.792	-0.172	0.197	-0.876	0.382	-0.115	0.149	-0.771	0.442
	Abundance	0.086	0.095	0.906	0.365	0.073	0.203	0.362	0.718	-0.066	0.172	-0.385	0.701
Crop cover	Richness	0.106	0.085	1.245	0.214	-0.082	0.190	-0.435	0.664	-0.137	0.128	-1.069	0.287
	Shannon	0.053	0.087	0.607	0.544	-0.075	0.188	-0.399	0.691	-0.153	0.141	-1.082	0.281
	Abundance	**0.276**	**0.089**	**3.090**	**0.002**	**0.568**	**0.193**	**2.940**	**0.004**	**-0.420**	**0.163**	**-2.576**	**0.011**
Tree cover	Richness	0.184	0.100	1.837	0.067	-0.352	0.211	-1.669	0.097	-0.122	0.162	-0.753	0.453
	Shannon	0.176	0.103	1.717	0.087	-0.263	0.208	-1.264	0.208	0.052	0.178	0.292	0.771
	Abundance	**0.268**	**0.105**	**2.546**	**0.011**	0.303	0.215	1.410	0.160	-0.187	0.206	-0.907	0.366

(Continued from previous page)		Overall				Forest				Grassland			
Predictor	**Diversity**	**Coefficient**	**se**	**t-value**	***p*-value**	**Coefficient**	**se**	**t-value**	***p*-value**	**Coefficient**	**se**	**t-value**	***p*-value**
Longitude	Richness	-0.058	0.043	-1.337	0.182	-0.064	0.053	-1.210	0.228	-0.215	0.162	-1.324	0.188
	Shannon	-0.029	0.044	-0.649	0.517	-0.033	0.052	-0.621	0.535	-0.245	0.179	-1.371	0.173
	Abundance	0.007	0.045	0.157	0.876	0.033	0.054	0.614	0.540	-0.027	0.207	-0.131	0.896
Latitude	Richness	0.023	0.051	0.448	0.655	-0.031	0.069	-0.447	0.655	**0.370**	**0.099**	**3.724**	**<0.001**
	Shannon	0.007	0.052	0.137	0.891	-0.009	0.068	-0.136	0.892	**0.294**	**0.109**	**2.692**	**0.008**
	Abundance	0.002	0.054	0.046	0.964	0.027	0.070	0.379	0.705	**0.267**	**0.127**	**2.109**	**0.037**
Elevation	Richness	0.021	0.062	0.345	0.730	-0.131	0.111	-1.178	0.240	0.077	0.135	0.571	0.569
	Shannon	0.030	0.063	0.483	0.630	-0.106	0.110	-0.961	0.338	0.020	0.149	0.132	0.895
	Abundance	0.086	0.065	1.323	0.187	0.141	0.113	1.245	0.215	-0.128	0.172	-0.741	0.460
MAT	Richness	-0.077	0.059	-1.296	0.196	**-0.356**	**0.086**	**-4.129**	**<0.001**	0.425	0.263	1.613	0.109
	Shannon	-0.088	0.061	-1.453	0.147	**-0.310**	**0.085**	**-3.633**	**<0.001**	0.257	0.290	0.884	0.378
	Abundance	-0.072	0.062	-1.159	0.247	-0.118	0.088	-1.348	0.179	0.393	0.336	1.170	0.244
MAP	Richness	-0.017	0.048	-0.346	0.729	**0.148**	**0.075**	**1.983**	**0.049**	0.086	0.129	0.664	0.508
	Shannon	-0.044	0.049	-0.893	0.372	0.107	0.074	1.449	0.149	0.113	0.143	0.795	0.428
	Abundance	0.098	0.050	1.943	0.053	**0.257**	**0.076**	**3.381**	**0.001**	-0.125	0.165	-0.758	0.450
Clay	Richness	**0.108**	**0.047**	**2.312**	**0.021**	0.088	0.061	1.444	0.150	0.123	0.099	1.249	0.214
	Shannon	**0.106**	**0.048**	**2.199**	**0.028**	0.058	0.060	0.955	0.341	0.183	0.109	1.681	0.095
	Abundance	0.033	0.049	0.664	0.507	0.039	0.062	0.627	0.531	-0.005	0.126	-0.043	0.966
Silt	Richness	-0.088	0.046	-1.903	0.058	-0.050	0.060	-0.838	0.403	-0.132	0.106	-1.249	0.214
	Shannon	-0.092	0.047	-1.951	0.052	-0.039	0.059	-0.664	0.507	-0.179	0.116	-1.542	0.126
	Abundance	-0.087	0.049	-1.797	0.073	**-0.133**	**0.061**	**-2.192**	**0.030**	0.127	0.135	0.946	0.346

(Continued from previous page)		**Overall**				**Forest**				**Grassland**			
Predictor	**Diversity**	**Coefficient**	**se**	**t-value**	***p*-value**	**Coefficient**	**se**	**t-value**	***p*-value**	**Coefficient**	**se**	**t-value**	***p*-value**
pH	Richness	0.014	0.057	0.243	0.808	0.142	0.081	1.761	0.080	-0.157	0.096	-1.636	0.104
	Shannon	0.018	0.058	0.313	0.755	**0.201**	**0.080**	**2.515**	**0.013**	-0.200	0.106	-1.893	0.061
	Abundance	0.099	0.060	1.654	0.099	**0.279**	**0.082**	**3.402**	**0.001**	0.110	0.122	0.900	0.370
Nitrogen	Richness	**-0.093**	**0.041**	**-2.255**	**0.025**	**-0.181**	**0.061**	**-2.944**	**0.004**	**-0.144**	**0.066**	**-2.185**	**0.031**
	Shannon	**-0.103**	**0.042**	**-2.418**	**0.016**	**-0.168**	**0.061**	**-2.759**	**0.006**	**-0.168**	**0.073**	**-2.317**	**0.022**
	Abundance	**-0.093**	**0.044**	**-2.139**	**0.033**	-0.092	0.063	-1.470	0.143	-0.140	0.084	-1.673	0.097
C/N ratio	Richness	0.026	0.044	0.580	0.562	**0.223**	**0.061**	**3.634**	**<0.001**	0.021	0.085	0.249	0.803
	Shannon	0.047	0.046	1.038	0.300	**0.229**	**0.061**	**3.772**	**<0.001**	0.035	0.093	0.373	0.710
	Abundance	0.011	0.047	0.242	0.809	0.114	0.062	1.821	0.070	-0.067	0.108	-0.618	0.538

Supplementary Table 2. Responses of different pathogenic fungal genus to landscape complexity at the 500 m radius around the sampling plot. Shown are the coefficients (estimate slope), standard errors (se), t-value and *p*-value of the multivariate Generalized Additive Models for Location, Scale, and Shape (GAMLSS). Statistical tests are two-sided Wald tests from multivariate GAMLSS without multiple-comparison adjustment. Significance relationships are marked in bold.

Pathogenic group	**Genus**	**Diversity**	**Coeff-icient**	**se**	**t-value**	***p*-value**
LFSA fungi	*Discosia*	Richness	**0.034**	**0.010**	**3.285**	**0.001**
		Shannon	0.014	0.011	1.310	0.191
		Abundance	**0.042**	**0.012**	**3.442**	**<0.001**
	Neodevriesia	Richness	**0.049**	**0.016**	**3.032**	**0.003**
		Shannon	0.032	0.016	1.965	0.051
		Abundance	**0.054**	**0.016**	**3.384**	**<0.001**
	Parafabraea	Richness	-0.025	0.016	-1.537	0.125
		Shannon	-0.031	0.017	-1.813	0.071
		Abundance	-0.010	0.017	-0.575	0.566
	Pseudofabraea	Richness	0.018	0.014	1.269	0.205
		Shannon	0.020	0.014	1.440	0.150
		Abundance	0.009	0.015	0.584	0.560
	Pseudophaeomoniella	Richness	0.009	0.016	0.544	0.586
		Shannon	<0.001	<0.001	0.227	0.810
		Abundance	-0.001	0.015	-0.078	0.938
RA fungi	*Entoloma*	Richness	0.008	0.016	0.534	0.594
		Shannon	**0.037**	**0.016**	**2.284**	**0.023**
		Abundance	0.023	0.016	1.427	0.154
	Exophiala	Richness	-0.012	0.013	-0.909	0.364
		Shannon	0.019	0.016	1.179	0.239
		Abundance	0.022	0.014	1.542	0.124
	Hygrocybe	Richness	-0.009	0.016	-0.527	0.599
		Shannon	-0.005	0.017	-0.296	0.767
		Abundance	-0.004	0.017	-0.221	0.826
	Oidiodendron	Richness	0.004	0.014	0.285	0.776
		Shannon	0.010	0.015	0.643	0.521
		Abundance	0.005	0.015	0.306	0.759

Supplementary Table 3. The correlation of the leaf/fruit/seed-associated (LFSA) and root-associated (RA) fungal alpha diversity and eight landscape metrics at the 500 m radius around the sampling plot. The diversity indices include richness, Shannon diversity and the relative abundance of the fungi. The eight landscape metrics include landscape division index (Division), edge density (ED), patch density (PD), largest patch index (LPI), landscape shape index (LSI), patch richness (PR), modified Simpson diversity index (MSIDI), and Shannon diversity index (SHDI). Statistical significance is determined using two-sided Spearman's rank correlation tests without multiple-comparison adjustment. Shown are the correlation *r*-value and significance *p*- value, and significant relationships are marked in bold.

		Overall		**Forest**		**Grassland**	
	metrics	***r*-value**	***p*-value**	***r*-value**	***p*-value**	***r*-value**	***p*-value**
Richness LFSA fungi	Division	**0.156**	**<0.001**	**0.134**	**0.030**	**0.265**	**<0.001**
	ED	**0.197**	**<0.001**	**0.194**	**0.002**	**0.307**	**<0.001**
	PD	**0.226**	**<0.001**	**0.181**	**0.003**	**0.352**	**<0.001**
	LPI	**-0.137**	**<0.001**	**-0.130**	**0.034**	**-0.245**	**0.001**
	LSI	**0.197**	**<0.001**	**0.191**	**0.002**	**0.312**	**<0.001**
	PR	**0.227**	**<0.001**	0.119	0.053	**0.324**	**<0.001**
	MSIDI	**0.176**	**<0.001**	**0.154**	**0.012**	**0.242**	**0.001**
	SHDI	**0.201**	**<0.001**	**0.156**	**0.011**	**0.274**	**<0.001**
Richness RA fungi	Division	**0.093**	**0.036**	0.057	0.353	0.112	0.131
	ED	0.081	0.068	0.056	0.362	0.084	0.258
	PD	**0.106**	**0.016**	0.073	0.236	0.107	0.150
	LPI	**-0.091**	**0.041**	-0.060	0.330	-0.107	0.150
	LSI	0.080	0.071	0.062	0.314	0.080	0.283
	PR	**0.144**	**0.001**	0.099	0.110	0.105	0.156
	MSIDI	**0.100**	**0.024**	0.053	0.395	0.107	0.148
	SHDI	**0.114**	**0.010**	0.071	0.250	0.104	0.162
Shannon LFSA fungi	Division	**0.159**	**<0.001**	**0.151**	**0.014**	**0.257**	**<0.001**
	ED	**0.187**	**<0.001**	**0.195**	**0.001**	**0.303**	**<0.001**
	PD	**0.224**	**<0.001**	**0.194**	**0.002**	**0.354**	**<0.001**
	LPI	**-0.141**	**0.001**	**-0.143**	**0.020**	**-0.241**	**0.001**
	LSI	**0.188**	**<0.001**	**0.193**	**0.002**	**0.305**	**<0.001**
	PR	**0.235**	**<0.001**	**0.124**	**0.044**	**0.345**	**<0.001**
	MSIDI	**0.176**	**<0.001**	**0.160**	**0.009**	**0.238**	**0.001**
	SHDI	**0.205**	**<0.001**	**0.168**	**0.006**	**0.269**	**<0.001**
Shannon RA fungi	Division	**0.091**	**0.039**	0.064	0.302	0.083	0.263
	ED	0.074	0.095	0.051	0.413	0.051	0.493
	PD	**0.096**	**0.030**	0.082	0.183	0.062	0.403
	LPI	**-0.091**	**0.040**	-0.064	0.300	-0.080	0.283
	LSI	0.072	0.103	0.055	0.377	0.047	0.527
	PR	**0.126**	**0.004**	0.105	0.090	0.066	0.373
	MSIDI	**0.092**	**0.038**	0.054	0.383	0.080	0.284
	SHDI	**0.100**	**0.023**	0.073	0.238	0.069	0.353
Abundance LFSA fungi	Division	**0.135**	**0.002**	0.069	0.265	**0.264**	**<0.001**
	ED	**0.182**	**<0.001**	**0.138**	**0.025**	**0.297**	**<0.001**
	PD	**0.195**	**<0.001**	0.117	0.057	**0.314**	**<0.001**
	LPI	**-0.121**	**0.006**	-0.067	0.281	**-0.247**	**0.001**
	LSI	**0.182**	**<0.001**	**0.133**	**0.031**	**0.304**	**<0.001**
	PR	**0.168**	**<0.001**	0.035	0.566	**0.276**	**<0.001**
	MSIDI	**0.147**	**0.001**	0.081	0.188	**0.242**	**0.001**
	SHDI	**0.160**	**<0.001**	0.074	0.229	**0.261**	**<0.001**
Abundance RA fungi	Division	**0.094**	**0.033**	0.050	0.419	**0.150**	**0.043**
	ED	**0.091**	**0.040**	0.061	0.323	0.126	0.090
	PD	**0.119**	**0.007**	0.078	0.209	0.142	0.056
	LPI	**-0.090**	**0.042**	-0.051	0.408	**-0.147**	**0.047**
	LSI	**0.094**	**0.034**	0.070	0.256	0.128	0.084
	PR	**0.163**	**<0.001**	0.101	0.102	**0.154**	**0.038**
	MSIDI	**0.106**	**0.017**	0.044	0.478	**0.153**	**0.039**
	SHDI	**0.124**	**0.005**	0.066	0.288	**0.149**	**0.044**

Supplementary Table 4. Generalized dissimilarity modeling (GDM) results for LFSA (a) and RA (b) fungal Sørensen beta dissimilarity for all plots. The table shows the sum of coefficients (SC; cumulative sum of the three I-spline coefficients per predictor) and the relative contribution (RC, %) of each predictor. Predictors include landscape complexity, grass cover, crop cover, tree cover, mean annual temperature (MAT), mean annual precipitation (MAP), spatial distance, elevation, clay content, silt content, soil pH, nitrogen content, and C/N ratio. Landscape complexity, grass cover, crop cover, and tree cover are calculated within buffer radii ranging from 250 m to 10,000 m as competing models.

	250 m		**500 m**		**1000 m**		**2000 m**		**5000 m**		**10000 m**	
	SC	RC	SC	RC	SC	RC	SC	RC	SC	RC	SC	RC
(a) LFSA fungi												
Landscape complexity	0.003	0.02	0.095	0.81	0.097	0.84	0.046	0.39	0.000	0.00	0.000	0.00
Grass cover	0.760	6.39	0.762	6.46	0.716	6.13	0.813	6.77	0.555	4.56	0.638	5.15
Crop cover	0.411	3.50	0.371	3.19	0.314	2.72	0.238	2.01	0.275	2.29	0.232	1.90
Tree cover	0.617	5.21	0.618	5.25	0.523	4.49	0.558	4.65	0.651	5.34	0.669	5.38
MAT	3.538	29.8	3.462	29.4	3.450	29.58	3.646	30.5	3.958	32.64	4.045	32.69
MAP	0.229	1.95	0.192	1.65	0.161	1.39	0.167	1.40	0.134	1.11	0.142	1.16
Spatial distance	1.027	8.75	0.995	8.55	1.008	8.74	1.019	8.6	0.997	8.29	0.967	7.89
Elevation	0.000	0.00	0.000	0.00	0.000	0.00	0.016	0.14	0.062	0.51	0.050	0.41
Clay	0.493	4.20	0.483	4.15	0.488	4.23	0.506	4.27	0.506	4.21	0.490	4.00
Silt	0.067	0.56	0.065	0.56	0.118	1.01	0.161	1.34	0.145	1.18	0.190	1.53
pH	2.879	24.5	2.840	24.4	2.933	25.42	2.968	25.0	3.002	24.97	3.048	24.86
Nitrogen	0.593	5.04	0.574	4.92	0.544	4.7	0.519	4.36	0.558	4.62	0.610	4.95
C/N ratio	1.175	10.0	1.237	10.6	1.240	10.75	1.257	10.6	1.234	10.27	1.238	10.09
(b) RA fungi												
Landscape complexity	0.059	0.18	0.000	0.00	0.021	0.06	0.000	0	0.255	0.75	0.175	0.49
Grass cover	0.700	2.17	0.805	2.52	1.588	4.85	1.988	5.84	1.872	5.60	1.974	5.67
Crop cover	0.067	0.21	0.304	0.96	0.067	0.21	0.063	0.19	0.000	0.00	0.000	0.00
Tree cover	1.850	5.72	1.681	5.22	1.695	5.15	1.920	5.6	3.686	10.96	3.425	9.78
MAT	7.582	23.7	7.161	22.5	6.997	21.51	7.136	21.1	7.243	21.82	7.751	22.43
MAP	3.556	11.0	3.689	11.5	3.794	11.58	4.036	11.9	2.691	8.05	2.784	7.99
Spatial distance	0.790	2.46	0.447	1.40	0.168	0.51	0.000	0.00	0.000	0.00	0.000	0.00
Elevation	3.846	11.9	3.657	11.4	3.520	10.75	3.422	10.1	3.366	10.07	3.235	9.30
Clay	0.901	2.79	1.164	3.63	1.452	4.42	1.754	5.14	1.652	4.93	1.878	5.38
Silt	0.494	1.52	0.651	2.02	0.623	1.89	0.802	2.34	0.630	1.87	0.995	2.84
pH	11.202	35.2	11.215	35.5	11.57	35.74	11.66	34.7	10.951	33.15	11.435	33.23
Nitrogen	0.253	0.79	0.283	0.89	0.281	0.86	0.240	0.71	0.118	0.36	0.235	0.68
C/N ratio	0.733	2.30	0.758	2.40	0.800	2.47	0.837	2.49	0.803	2.43	0.760	2.21

Supplementary Table 5. Generalized dissimilarity modeling (GDM) results for LFSA (a) and RA (b) fungal Sørensen beta dissimilarity for forest ecosystems. The table shows the sum of coefficients (SC; cumulative sum of the three I-spline coefficients per predictor) and the relative contribution (RC, %) of each predictor. Predictors include landscape complexity, grass cover, crop cover, tree cover, mean annual temperature (MAT), mean annual precipitation (MAP), spatial distance, elevation, clay content, silt content, soil pH, nitrogen content, and C/N ratio. Landscape complexity, grass cover, crop cover, and tree cover are calculated within buffer radii ranging from 250 m to 10,000 m as competing models.

	250 m		**500 m**		**1000 m**		**2000 m**		**5000 m**		**10000 m**	
	SC	RC	SC	RC	SC	RC	SC	RC	SC	RC	SC	RC
(a) LFSA fungi												
Landscape complexity	0.156	1.67	0.414	4.39	0.423	4.47	0.470	4.96	0.048	0.53	0.078	0.85
Grass cover	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00
Crop cover	0.118	1.26	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00
Tree cover	0.331	3.56	0.221	2.34	0.080	0.85	0.000	0.00	0.047	0.50	0.233	2.47
MAT	3.398	36.05	3.556	37.2	3.632	37.91	3.603	37.56	3.515	38.46	3.625	38.83
MAP	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00
Spatial distance	1.510	16.22	1.430	15.15	1.473	15.57	1.493	15.76	1.608	17.82	1.493	16.2
Elevation	0.186	2.00	0.217	2.3	0.236	2.49	0.276	2.90	0.201	2.22	0.206	2.23
Clay	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00
Silt	0.446	4.79	0.456	4.83	0.474	5.01	0.477	5.03	0.469	5.20	0.485	5.26
pH	1.889	20.29	1.792	18.98	1.838	19.42	1.867	19.7	1.900	21.06	1.896	20.56
Nitrogen	0.572	6.15	0.594	6.29	0.567	6	0.543	5.73	0.557	6.17	0.545	5.91
C/N ratio	0.750	7.99	0.810	8.52	0.789	8.27	0.796	8.34	0.730	8.04	0.713	7.68
(b) RA fungi												
Landscape complexity	0.272	1.68	0.000	0.00	0.000	0.00	0.000	0.00	0.510	2.97	1.404	8.01
Grass cover	0.120	0.75	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00
Crop cover	0.068	0.43	0.716	4.22	0.367	2.22	0.279	1.7	0.234	1.37	0.161	0.92
Tree cover	0.704	4.29	0.773	4.49	0.643	3.86	0.706	4.27	1.364	8.03	1.196	6.93
MAT	5.769	35.82	5.901	34.97	5.881	35.76	5.932	36.19	6.041	35.61	5.955	34.37
MAP	0.989	6.17	1.022	6.08	1.050	6.41	0.997	6.11	0.698	4.13	0.549	3.19
Spatial distance	0.157	0.97	0.196	1.16	0.206	1.25	0.197	1.19	0.221	1.3	0.328	1.89
Elevation	1.059	6.55	1.074	6.34	0.985	5.97	0.945	5.74	0.862	5.07	0.877	5.05
Clay	0.276	1.7	0.361	2.12	0.326	1.96	0.280	1.69	0.236	1.38	0.180	1.03
Silt	1.206	7.42	1.186	6.96	1.227	7.39	1.228	7.42	1.099	6.43	1.050	6.02
pH	2.734	17.05	2.851	16.96	2.884	17.61	2.867	17.57	2.821	16.71	2.667	15.48
Nitrogen	2.202	13.58	2.277	13.4	2.334	14.09	2.352	14.25	2.251	13.19	2.159	12.39
C/N ratio	0.577	3.60	0.555	3.30	0.572	3.49	0.631	3.87	0.643	3.81	0.815	4.73

Supplementary Table 6. Generalized dissimilarity modeling (GDM) results for LFSA (a) and RA (b) fungal Sørensen beta dissimilarity for grassland ecosystem. The table shows the sum of coefficients (SC; cumulative sum of the three I-spline coefficients per predictor) and the relative contribution (RC, %) of each predictor. Predictors include landscape complexity, grass cover, crop cover, tree cover, mean annual temperature (MAT), mean annual precipitation (MAP), spatial distance, elevation, clay content, silt content, soil pH, nitrogen content, and C/N ratio. Landscape complexity, grass cover, crop cover, and tree cover are calculated within buffer radii ranging from 250 m to 10,000 m as competing models.

	250 m		**500 m**		**1000 m**		**2000 m**		**5000 m**		**10000 m**	
	SC	RC	SC	RC	SC	RC	SC	RC	SC	RC	SC	RC
(a) LFSA fungi												
Landscape complexity	0.000	0.00	0.081	0.83	0.169	1.76	0.220	2.30	0.134	1.45	0.080	0.87
Grass cover	0.122	1.32	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00
Crop cover	0.318	3.48	0.241	2.54	0.224	2.36	0.261	2.78	0.463	5.10	0.516	5.62
Tree cover	0.176	1.92	0.080	0.84	0.036	0.38	0.005	0.05	0.000	0.00	0.000	0.00
MAT	1.491	16.2	1.628	17.06	1.621	16.97	1.576	16.66	1.460	15.99	1.604	17.36
MAP	0.082	0.90	0.125	1.31	0.109	1.14	0.119	1.26	0.168	1.84	0.164	1.78
Spatial distance	1.075	11.76	1.185	12.5	1.188	12.51	1.175	12.5	1.054	11.6	1.034	11.27
Elevation	0.332	3.63	0.453	4.78	0.463	4.87	0.416	4.43	0.265	2.91	0.195	2.13
Clay	0.195	2.13	0.170	1.80	0.177	1.87	0.169	1.8	0.114	1.26	0.113	1.23
Silt	0.398	4.24	0.439	4.50	0.441	4.52	0.434	4.49	0.424	4.54	0.397	4.21
pH	2.480	27.1	2.512	26.44	2.485	26.13	2.475	26.26	2.455	26.97	2.509	27.31
Nitrogen	0.530	5.79	0.548	5.76	0.547	5.75	0.534	5.67	0.529	5.82	0.546	5.94
C/N ratio	1.978	21.53	2.062	21.63	2.073	21.72	2.064	21.82	2.059	22.54	2.054	22.27
(b) RA fungi												
Landscape complexity	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00
Grass cover	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00
Crop cover	0.000	0.00	0.000	0.0	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00
Tree cover	0.057	0.13	0.090	0.20	0.113	0.25	0.134	0.30	0.151	0.36	0.181	0.42
MAT	3.969	8.90	3.976	9.00	3.995	9.13	4.030	9.20	4.053	9.87	4.013	9.51
MAP	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00
Spatial distance	32.382	71.88	31.930	71.54	31.513	71.26	31.441	71.1	28.742	69.31	29.872	70.11
Elevation	4.163	9.23	4.151	9.29	4.135	9.34	4.137	9.34	4.142	9.97	4.107	9.63
Clay	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00	0.000	0.00
Silt	0.657	1.43	0.663	1.46	0.663	1.47	0.662	1.47	0.648	1.53	0.651	1.50
pH	2.949	6.61	2.945	6.66	2.940	6.71	2.945	6.72	2.863	6.97	2.908	6.89
Nitrogen	0.171	0.38	0.175	0.39	0.179	0.4	0.173	0.39	0.162	0.39	0.169	0.4
C/N ratio	0.656	1.45	0.651	1.45	0.635	1.43	0.649	1.46	0.664	1.6	0.662	1.55

Supplementary Table 7. Metrics used at landscape level to quantify landscape complexity.

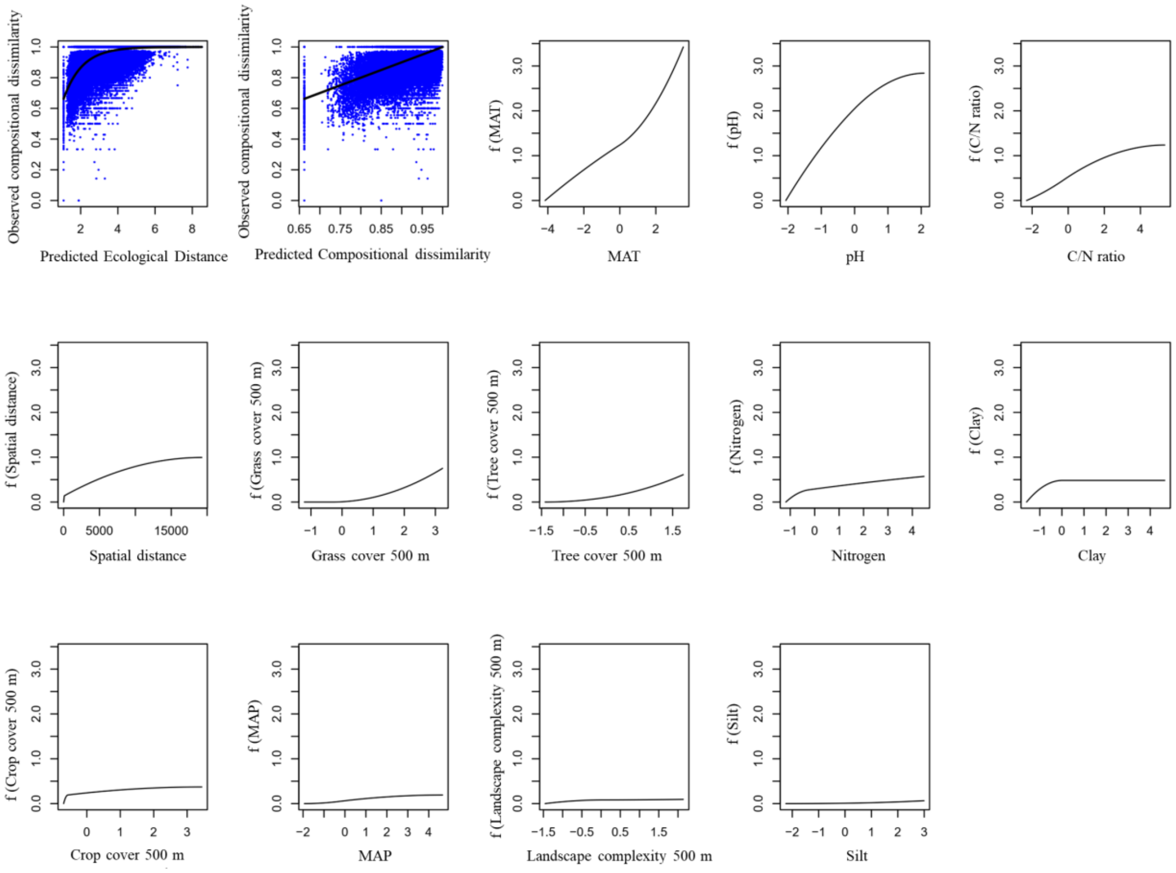
Metrics (units)	Name	Description	Type
Division	Landscape division index	The metric quantifies the probability that two randomly selected points in a landscape are not in the same patch. Higher value means the landscape is divided into many small patches, reducing connectivity.	Aggregation metric
ED	Edge density (meters per hectare)	The total lengths of all edge segments in relation to the total landscape area. The metric describes the configuration heterogeneity of the landscape and increases as the landscape edge gets more complex.	Area and edge metric
PD	Patch density (number per 100 hectares)	Ratio of number of patches and the total landscape area. The metric describes the configuration heterogeneity of the landscape and increases as the patch configuration gets more complex.	Aggregation metric
LPI	Largest patch index (%)	Ratio of the landscape area covered by the largest patch in the landscape. The metric measures dominance and spatial continuity of the largest habitat patch and increases as the largest patch is larger.	Area and edge metric
LSI	Landscape shape index	Ratio of the actual landscape edge length and the hypothetical minimum landscape edge length. The higher the LSI value, the more complex the landscape shape.	Aggregation metric
PR	Patch richness	The metric measures the number of unique patch types (land cover classes) present in a landscape and is the simplest measure of compositional heterogeneity. Higher value means more diverse land cover types present.	Diversity metric
MSIDI	Modified Simpson diversity index	The metric measures landscape diversity and the value increases as the number of patches increases and landscape proportions are more equally distributed.	Diversity metric
SHDI	Shannon diversity index	The metric describes diversity of landscape, which considers both the number and abundance of each class. The value increases as the number of classes increases while the proportions are equally distributed.	Diversity metric

Supplementary Table 8. The correlation of the landscape complexity and the corresponding eight landscape metrics across six spatial scales. The landscape complexity variables (i.e. landscape complexity 250, 500, 1,000, 2,000, 5,000 and 10,000) correspond to the minus of the first PCA axis of the eight landscape metrics at their respective spatial scales. The eight landscape metrics include landscape division index (Division), edge density (ED), patch density (PD), largest patch index (LPI), landscape shape index (LSI), patch richness (PR), modified Simpson diversity index (MSIDI), and Shannon diversity index (SHDI). Statistical significance is determined using two-sided Spearman's correlation tests without adjustment for multiple comparisons. Shown are *r*-values and significance levels (*p*-values) of correlations.

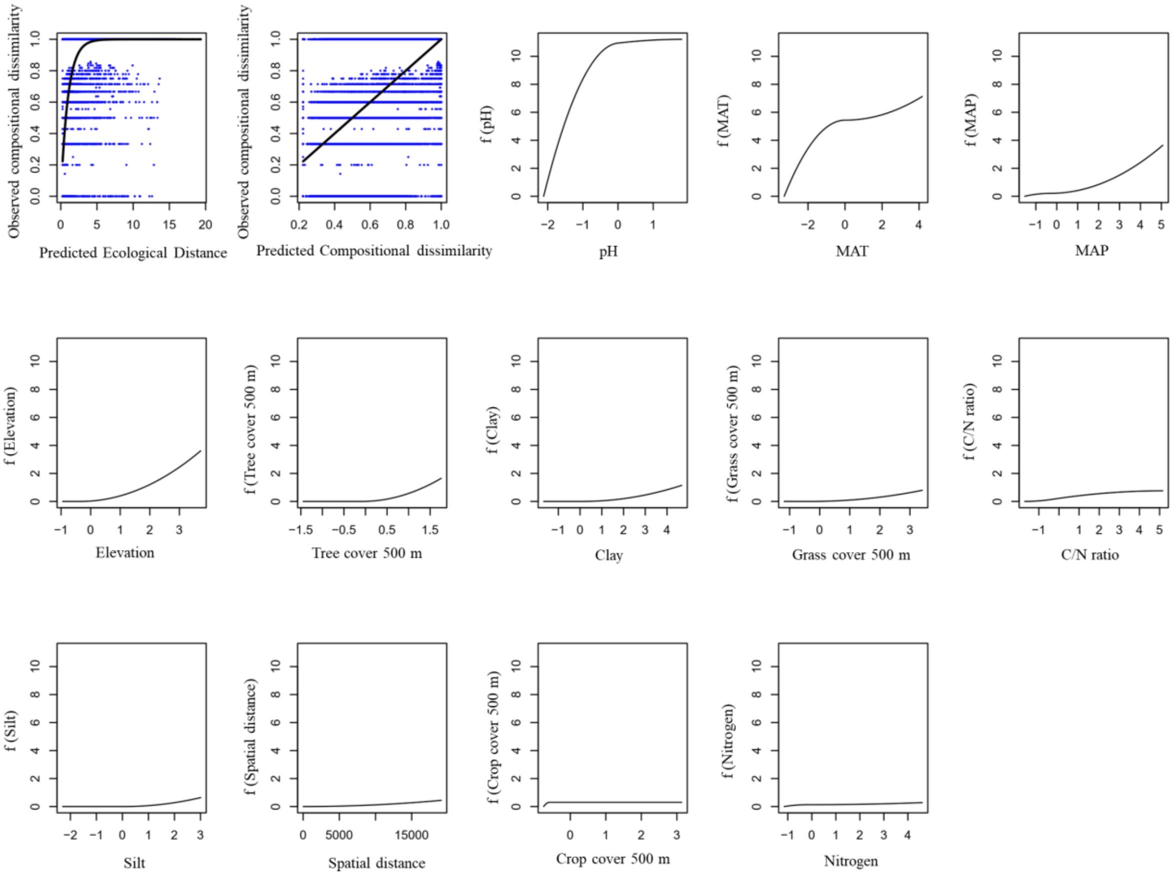
	Landscape complexity 250		**Landscape complexity 500**		**Landscape complexity1000**		**Landscape complexity2000**		**Landscape complexity 5000**		**Landscape complexity 10000**	
	r	***p***	***r***	***p***	***r***	***p***	***r***	***p***	***r***	***p***	***r***	***p***
Division	0.980	<0.001	0.979	<0.001	0.976	<0.001	0.973	<0.001	0.963	<0.001	0.960	<0.001
ED	0.975	<0.001	0.981	<0.001	0.975	<0.001	0.962	<0.001	0.952	<0.001	0.942	<0.001
PD	0.966	<0.001	0.947	<0.001	0.930	<0.001	0.896	<0.001	0.867	<0.001	0.857	<0.001
LPI	-0.966	<0.001	-0.960	<0.001	-0.955	<0.001	-0.953	<0.001	-0.932	<0.001	-0.939	<0.001
LSI	0.975	<0.001	0.981	<0.001	0.975	<0.001	0.962	<0.001	0.952	<0.001	0.942	<0.001
PR	0.936	<0.001	0.875	<0.001	0.767	<0.001	0.617	<0.001	0.288	<0.001	-0.056	0.207
MSIDI	0.982	<0.001	0.985	<0.001	0.893	<0.001	0.924	<0.001	0.940	<0.001	0.928	<0.001
SHDI	0.980	<0.001	0.980	<0.001	0.981	<0.001	0.970	<0.001	0.946	<0.001	0.903	<0.001

Supplementary Table 9. Spatial autocorrelation of predicted soil pathogenic fungal alpha diversity based on multivariate Generalized Additive Models for Location, Scale, and Shape (GAMLSS). Moran's I values and corresponding *p*-values are reported for the richness, Shannon diversity, and relative abundance of LFSA and RA fungi, derived from six competing models evaluated at six different landscape spatial scales (250 m to 10,000 m radii). Statistical tests were two-sided.

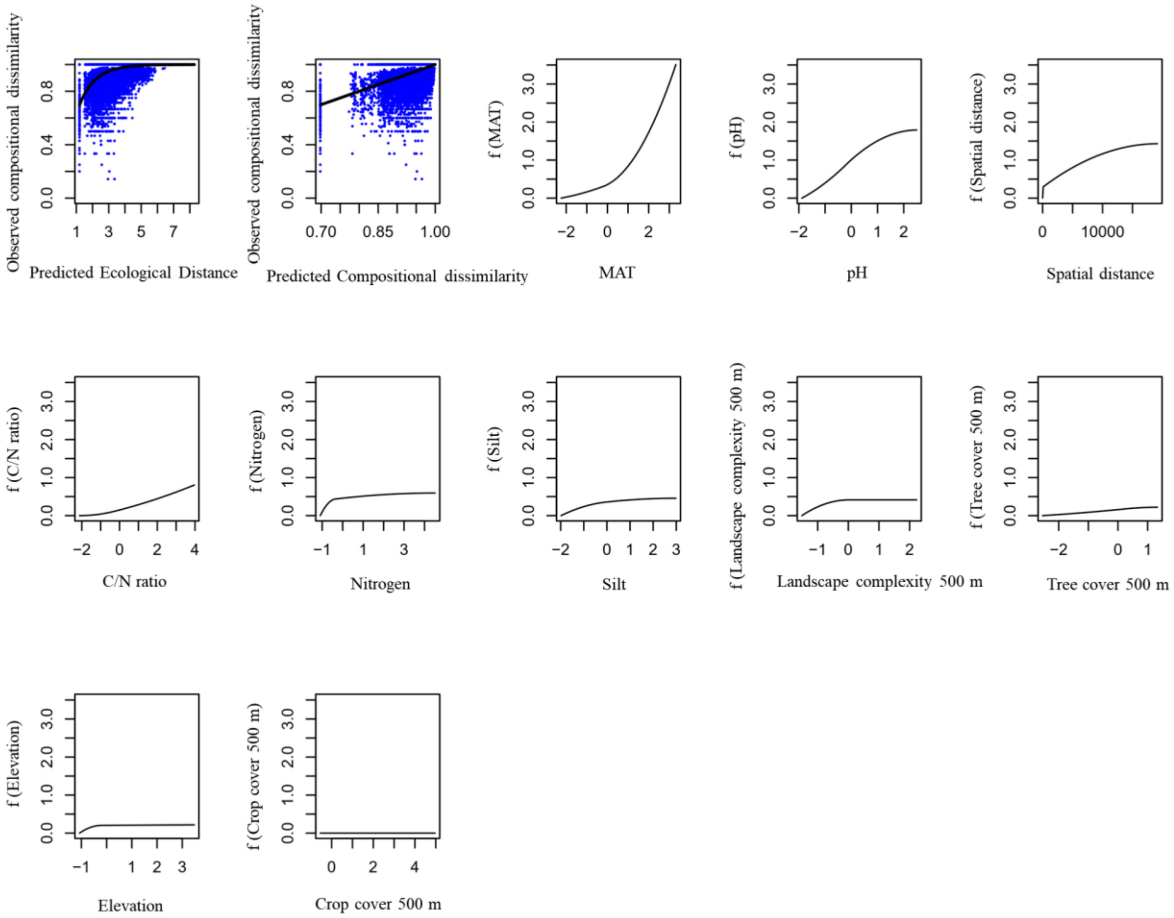
Diversity indices	Scale	Moran's I	*p*-value
Richness of LFSA fungi	250	0.011	0.093
Richness of LFSA fungi	500	0.011	0.093
Richness of LFSA fungi	1000	0.021	0.011
Richness of LFSA fungi	2000	0.008	0.152
Richness of LFSA fungi	5000	0.004	0.261
Richness of LFSA fungi	10000	0.004	0.280
Shannon of LFSA fungi	250	0.003	0.291
Shannon of LFSA fungi	500	0.000	0.401
Shannon of LFSA fungi	1000	0.006	0.206
Shannon of LFSA fungi	2000	-0.003	0.544
Shannon of LFSA fungi	5000	0.000	0.415
Shannon of LFSA fungi	10000	0.000	0.424
Abundance of LFSA fungi	250	0.011	0.093
Abundance of LFSA fungi	500	0.013	0.063
Abundance of LFSA fungi	1000	0.020	0.012
Abundance of LFSA fungi	2000	0.016	0.033
Abundance of LFSA fungi	5000	0.013	0.061
Abundance of LFSA fungi	10000	0.014	0.048
Richness of RA fungi	250	0.009	0.128
Richness of RA fungi	500	0.006	0.193
Richness of RA fungi	1000	0.003	0.302
Richness of RA fungi	2000	0.007	0.173
Richness of RA fungi	5000	0.010	0.118
Richness of RA fungi	10000	0.013	0.066
Shannon of RA fungi	250	-0.004	0.588
Shannon of RA fungi	500	-0.005	0.627
Shannon of RA fungi	1000	-0.011	0.818
Shannon of RA fungi	2000	-0.010	0.795
Shannon of RA fungi	5000	-0.006	0.675
Shannon of RA fungi	10000	-0.006	0.669
Abundance of RA fungi	250	-0.008	0.739
Abundance of RA fungi	500	-0.011	0.817
Abundance of RA fungi	1000	-0.012	0.851
Abundance of RA fungi	2000	-0.014	0.895
Abundance of RA fungi	5000	-0.015	0.917
Abundance of RA fungi	10000	-0.015	0.922



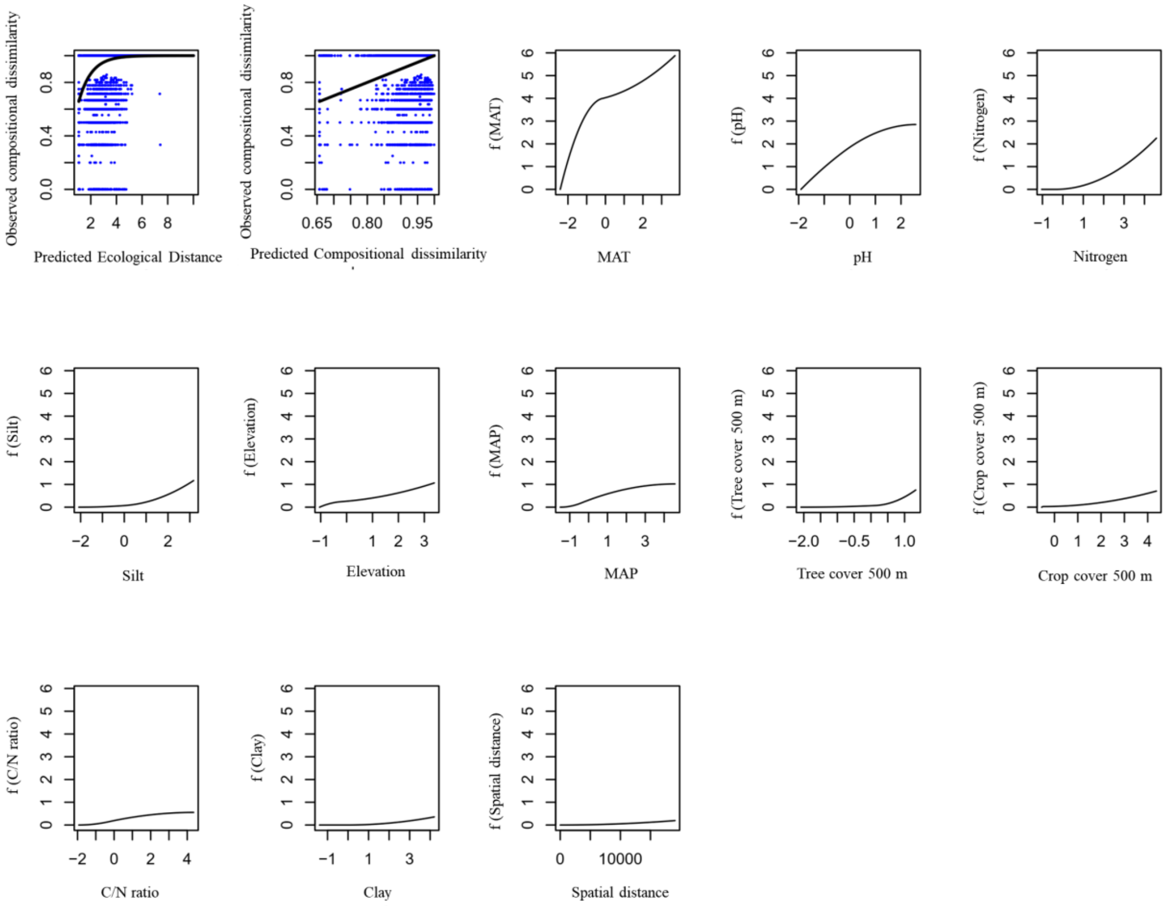
Supplementary Fig. 1. Generalized Dissimilarity Modelling (GDM) of LFSA fungal community beta diversity in relation to local and landscape variables within the 500 m radius for all plots. The plots show the fitted I-spline partial functions for each environmental predictor included in the GDM, illustrating their relative contributions to compositional dissimilarity (Sørensen beta dissimilarity) of soil pathogenic fungi across sites (predictors contributing no deviance explained were not presented). N = 511 biologically independent samples. The percent deviance explained of the model is 37.20.



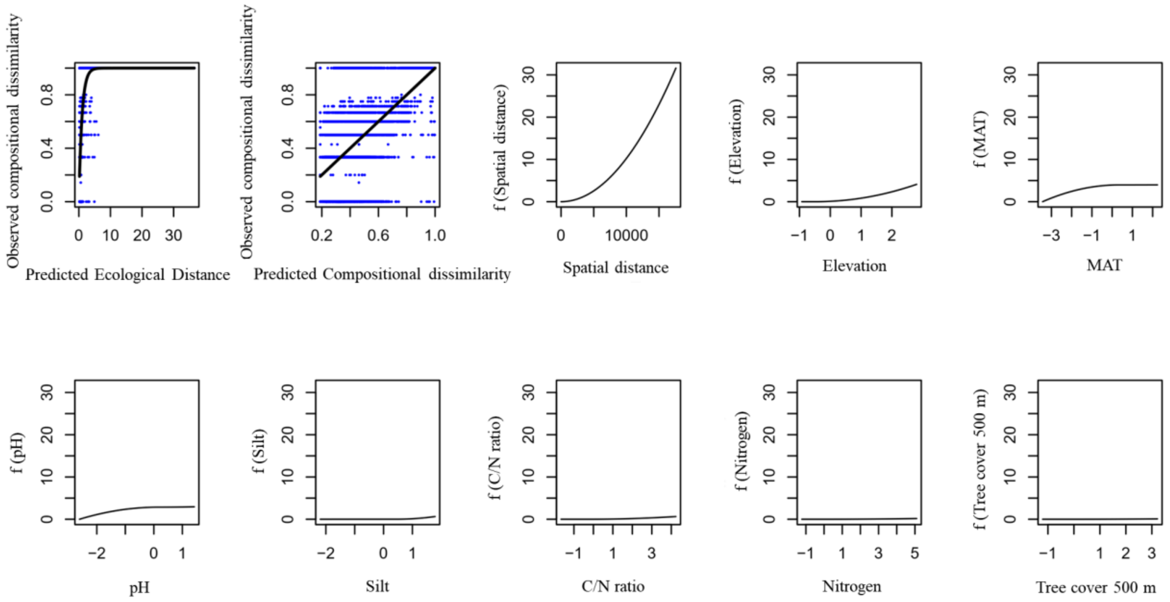
Supplementary Fig. 2. Generalized Dissimilarity Modelling (GDM) of RA fungal community beta diversity in relation to local and landscape variables within the 500 m radius for all plots. The plots show the fitted I-spline partial functions for each environmental predictor included in the GDM, illustrating their relative contributions to compositional dissimilarity (Sørensen beta dissimilarity) of soil pathogenic fungi across sites (predictors contributing no deviance explained were not presented). N = 511 biologically independent samples. The percent deviance explained of the model is 52.78.



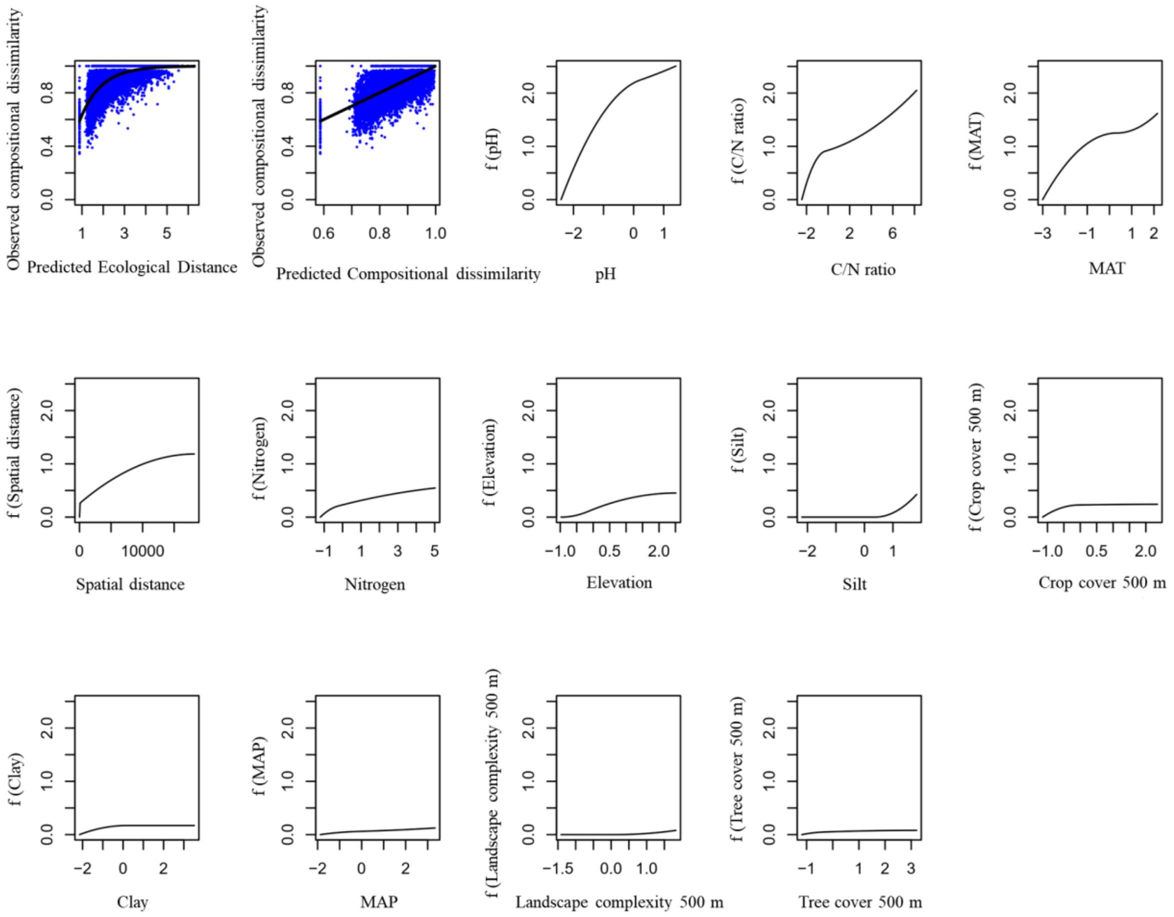
Supplementary Fig. 3. Generalized Dissimilarity Modelling (GDM) of LFSA fungal community beta diversity in relation to local and landscape variables within the 500 m radius in forest ecosystems. The plots show the fitted I-spline partial functions for each environmental predictor included in the GDM, illustrating their relative contributions to compositional dissimilarity (Sørensen beta dissimilarity) of soil pathogenic fungi across sites (predictors contributing no deviance explained were not presented). N = 264 forest plots. The percent deviance explained of the model is 25.21.



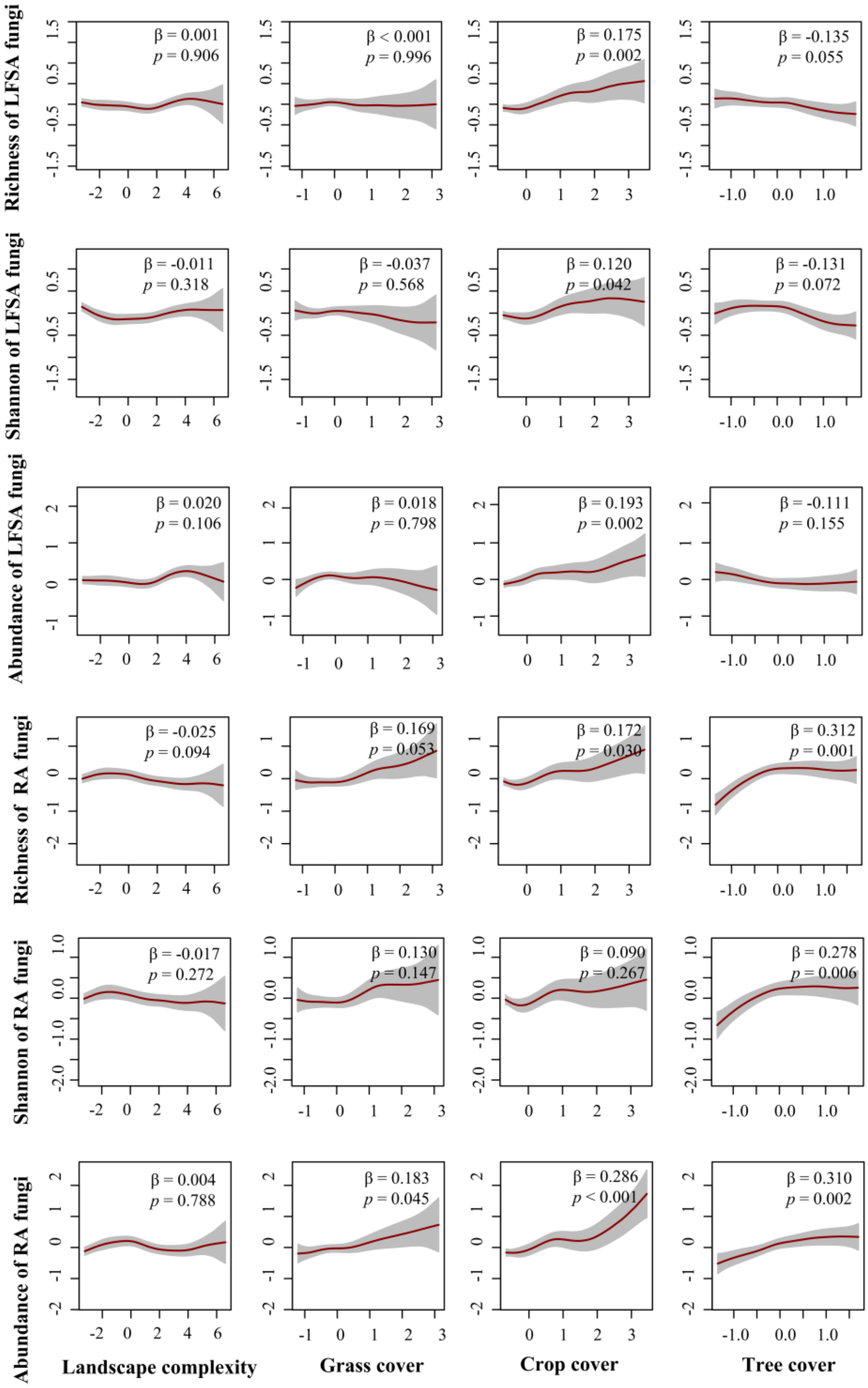
Supplementary Fig. 4. Generalized Dissimilarity Modelling (GDM) of RA fungal community beta diversity in relation to local and landscape variables within the 500 m radius in forest ecosystems. The plots show the fitted I-spline partial functions for each environmental predictor included in the GDM, illustrating their relative contributions to compositional dissimilarity (Sørensen beta dissimilarity) of soil pathogenic fungi across sites (predictors contributing no deviance explained were not presented). N = 264 forest plots. The percent deviance explained of the model is 14.63.



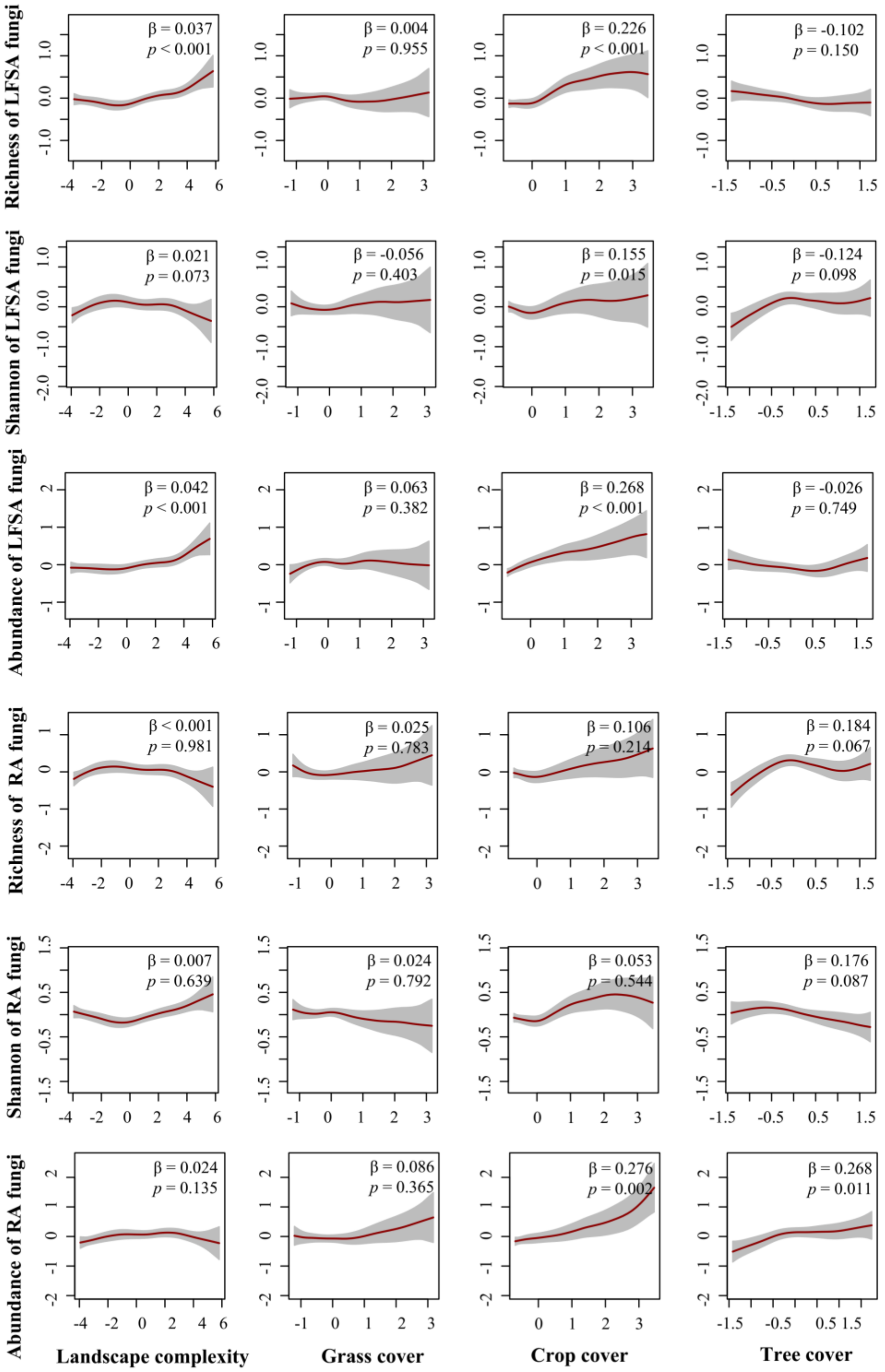
Supplementary Fig. 5. Generalized Dissimilarity Modelling (GDM) of RA fungal community beta diversity in relation to local and landscape variables within the 500 m radius in grassland ecosystem. The plots show the fitted I-spline partial functions for each environmental predictor included in the GDM, illustrating their relative contributions to compositional dissimilarity (Sørensen beta dissimilarity) of soil pathogenic fungi across sites (predictors contributing no deviance explained were not presented). N = 183 grassland plots. The percent deviance explained of the model is 60.90.



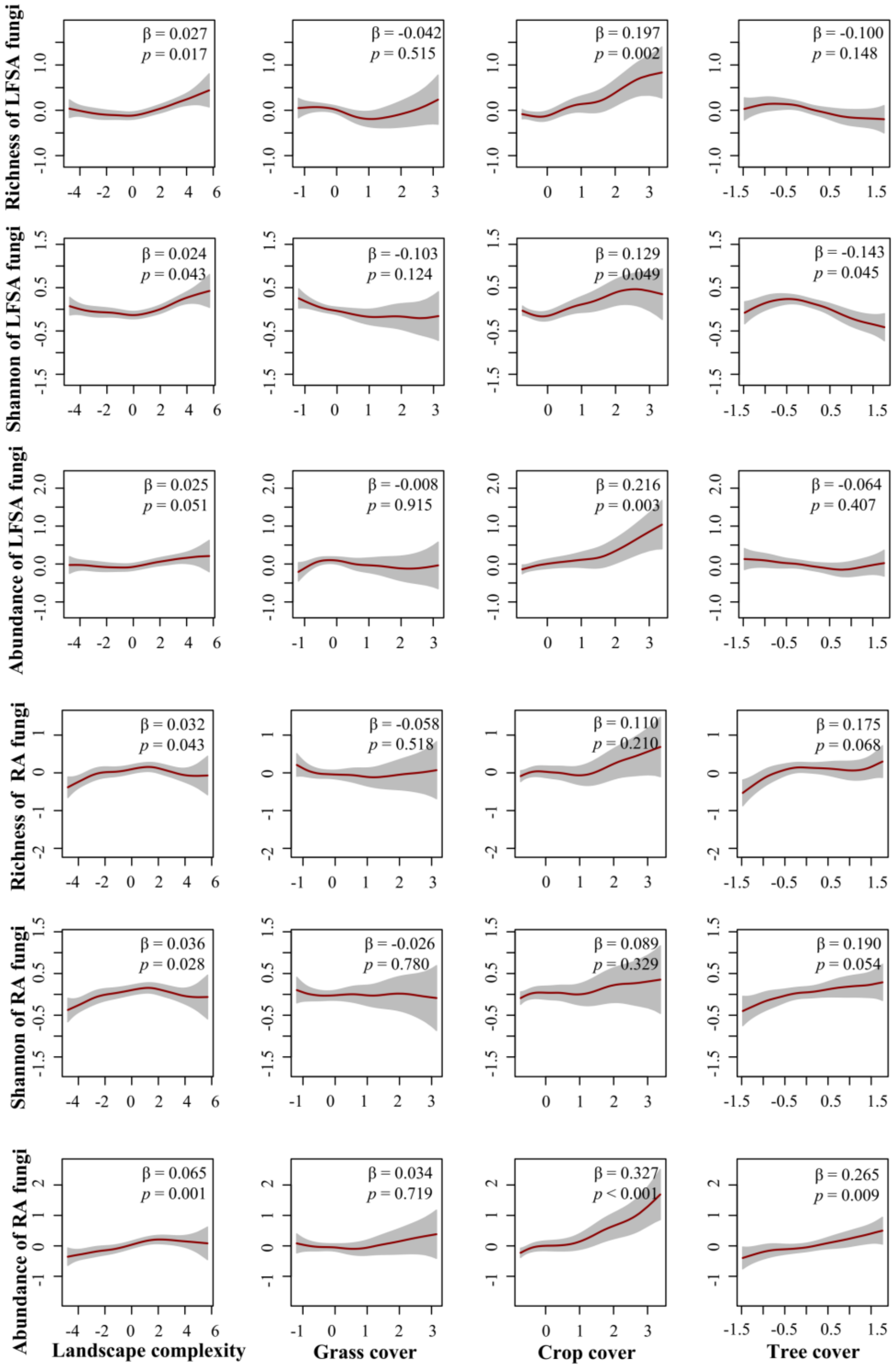
Supplementary Fig. 6. Generalized Dissimilarity Modelling (GDM) of LFSA fungal community beta diversity in relation to local and landscape variables within the 500 m radius in grassland ecosystems. The plots show the fitted I-spline partial functions for each environmental predictor included in the GDM, illustrating their relative contributions to compositional dissimilarity (Sørensen beta dissimilarity) of soil pathogenic fungi across sites (predictors contributing no deviance explained were not presented). N = 183 grassland plots. The percent deviance explained of the model is 53.47.



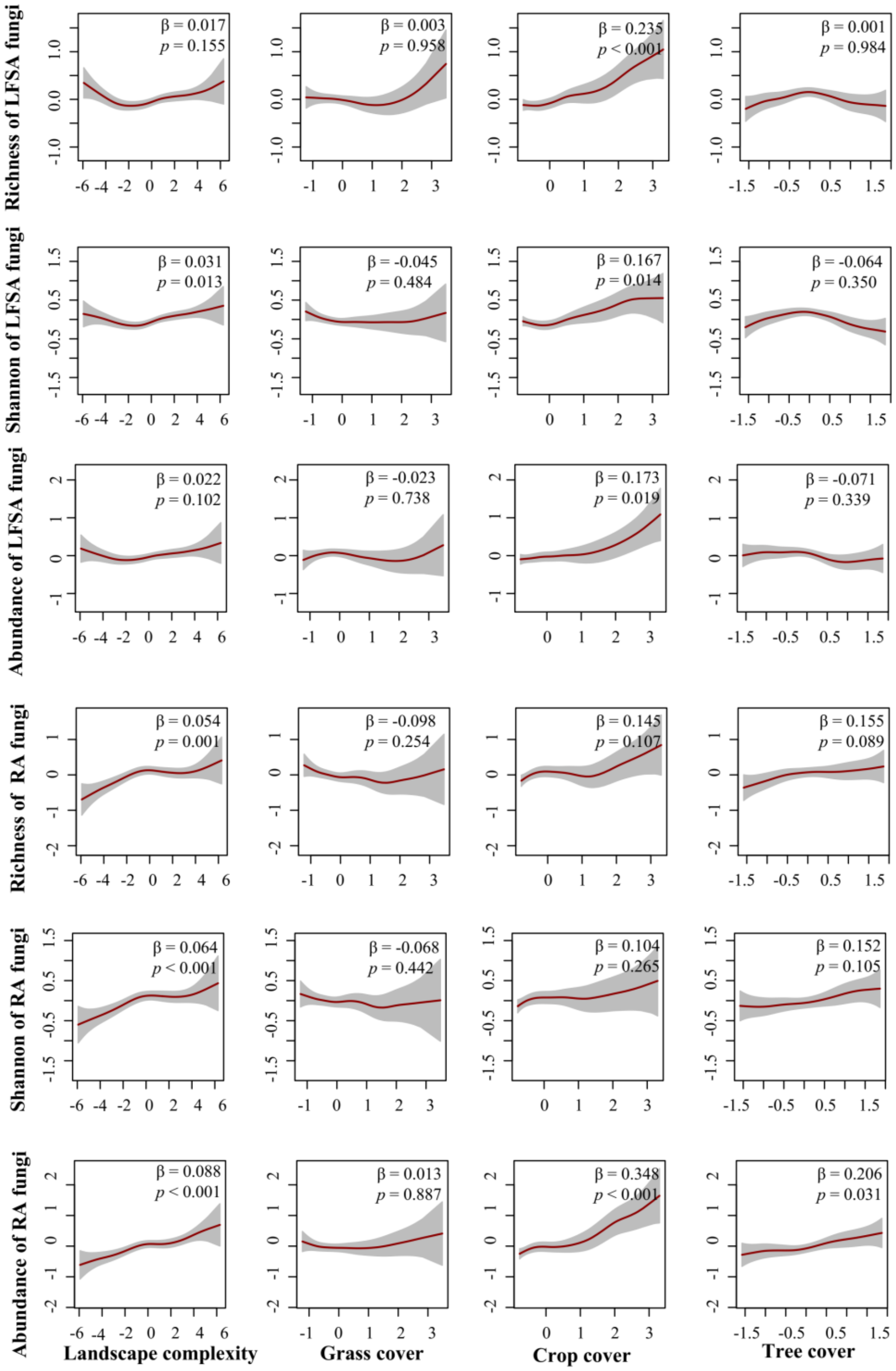
Supplementary Fig. 7. The partial regression of leaf/fruit/seed-associated (LFSA) and root-associated (RA) fungal alpha diversity to landscape complexity, grass cover, crop cover, and tree cover within the 250 m radius for all the 511 plots. Shown are the parameter estimate (standardized regression coefficient) and *p*-value from multivariable Generalized Additive Models for Location, Scale, and Shape (GAMLSS). Light coloured shade is the region within the 95% CIs.



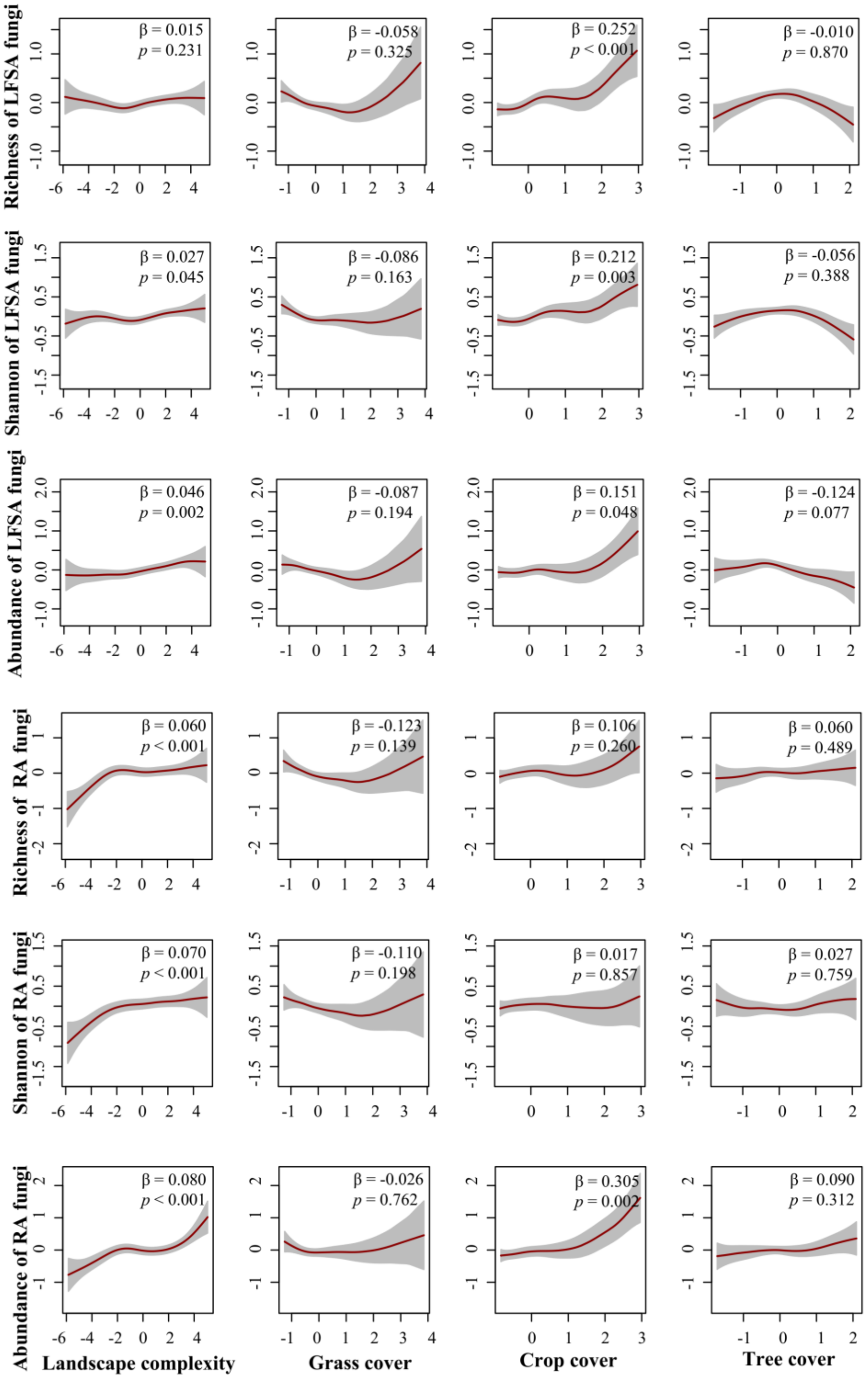
Supplementary Fig. 8. **The partial regression of leaf/fruit/seed-associated (LFSA) and root-associated (RA) fungal alpha diversity to landscape complexity, grass cover, crop cover, and tree cover within the 500 m radius for all the 511 plots.** Shown are the parameter estimate (standardized regression coefficient) and *p*-value from multivariable Generalized Additive Models for Location, Scale, and Shape (GAMLSS). Light coloured shade is the region within the 95% CIs.



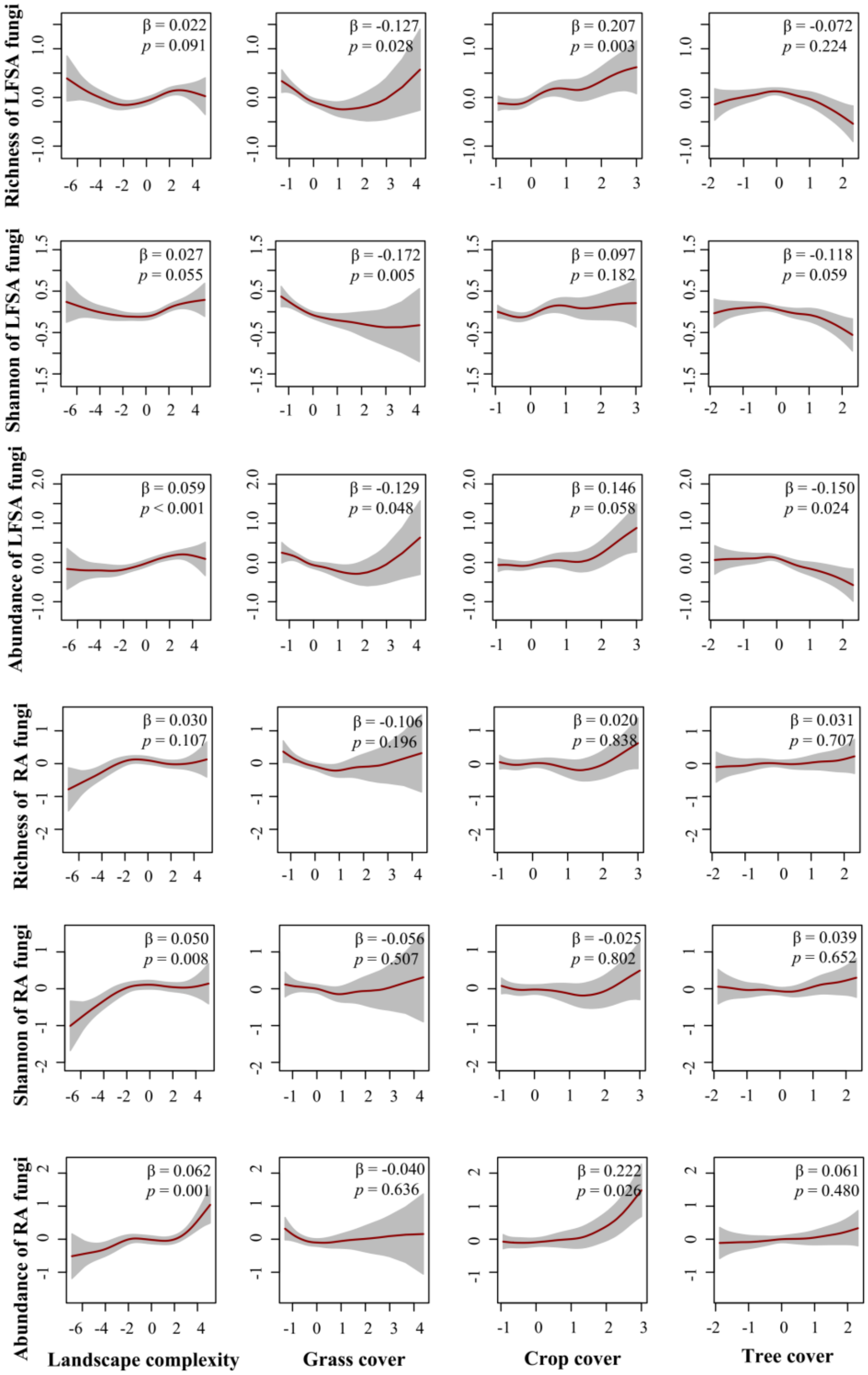
Supplementary Fig. 9. **The partial regression of leaf/fruit/seed-associated (LFSA) and root-associated (RA) fungal alpha diversity to landscape complexity, grass cover, crop cover, and tree cover within the 1,000 m radius for all the 511 plots.** Shown are the parameter estimate (standardized regression coefficient) and *p*-value from multivariable Generalized Additive Models for Location, Scale, and Shape (GAMLSS). Light coloured shade is the region within the 95% CIs.



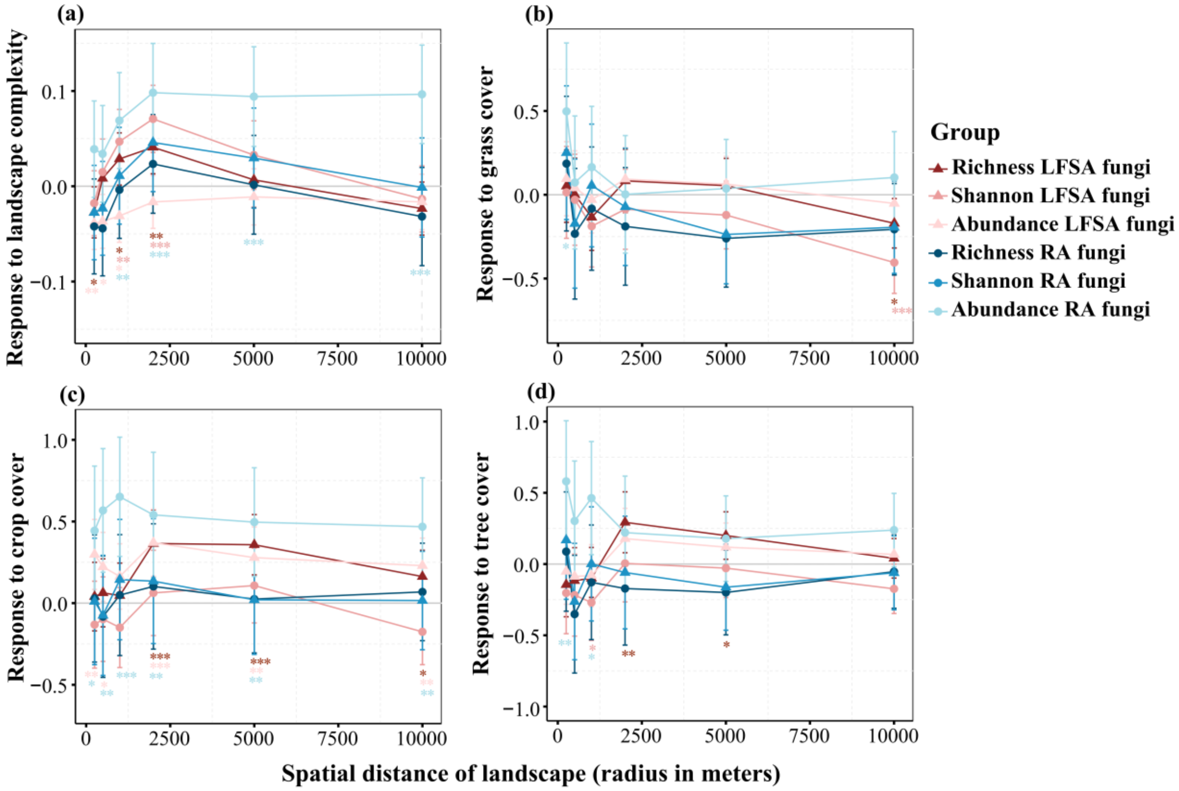
Supplementary Fig. 10. **The partial regression of leaf/fruit/seed-associated (LFSA) and root-associated (RA) fungal alpha diversity to landscape complexity, grass cover, crop cover, and tree cover within the 2,000 m radius for all the 511 plots**. Shown are the parameter estimate (standardized regression coefficient) and *p*-value from multivariable Generalized Additive Models for Location, Scale, and Shape (GAMLSS). Light coloured shade is the region within the 95% CIs.



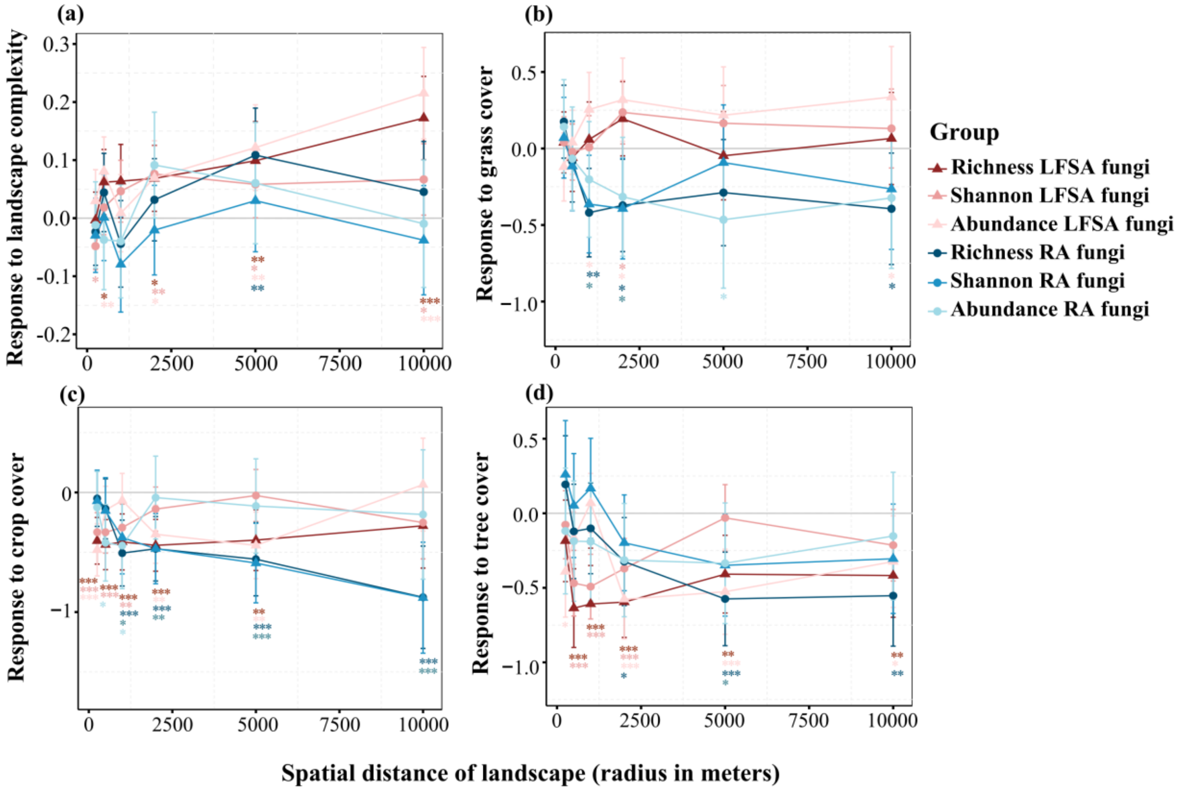
Supplementary Fig. 11. The partial regression of leaf/fruit/seed-associated (LFSA) and root-associated (RA) fungal alpha diversity to landscape complexity, grass cover, crop cover, and tree cover within the 5,000 m radius to all the 511 plots. Shown are the parameter estimate (standardized regression coefficient) and *p*-value from multivariable Generalized Additive Models for Location, Scale, and Shape (GAMLSS). Light coloured shade is the region within the 95% CIs.



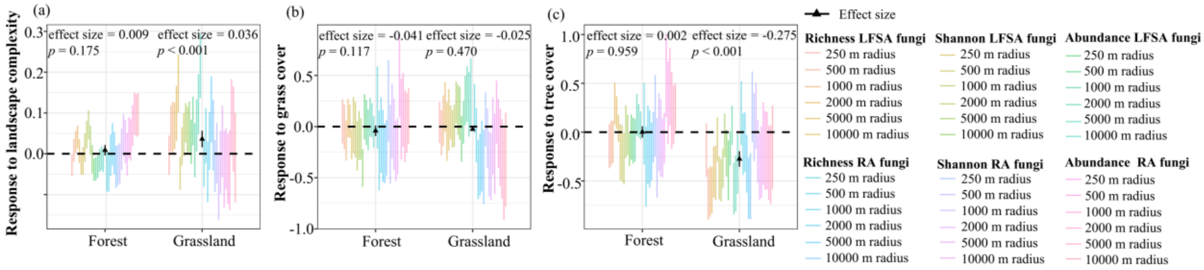
Supplementary Fig. 12. The partial regression of leaf/fruit/seed-associated (LFSA) and root-associated (RA) fungal alpha diversity to landscape complexity, grass cover, crop cover, and tree cover within the 10,000 m radius for all the 511 plots. Shown are the parameter estimate (standardized regression coefficient) and *p*-value from multivariable Generalized Additive Models for Location, Scale, and Shape (GAMLSS). Light coloured shade is the region within the 95% CIs.



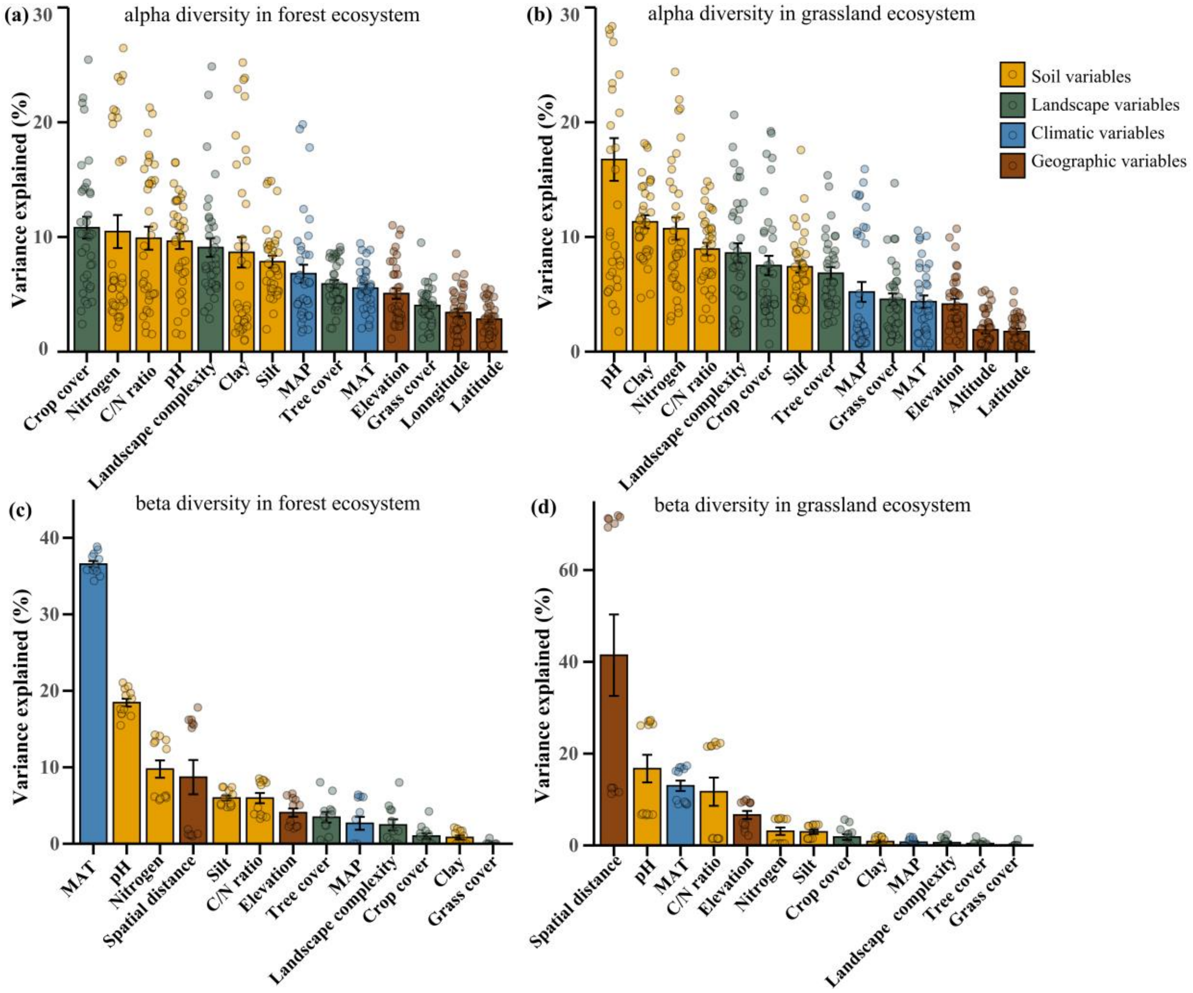
Supplementary Fig. 13. Landscape effects on leaf/fruit/seed-associated and root-associated fungal alpha diversity across spatial scales in forest ecosystems. Leaf/fruit/seed-associated (LFSA) and root-associated (RA) fungal diversity as affected by (a) landscape complexity, (b) grass cover, (c) crop cover, and (d) tree cover across six spatial scales (250 m, 500 m, 1,000 m, 2,000 m, 5,000 m, and 10,000 m radii) (n = 264 forest plots). Data are presented as model-estimated standardized regression coefficients ±95% confidence intervals (CIs) derived from multivariate Generalized Additive Models for Location, Scale, and Shape (GAMLSS). Red lines from dark to light indicate the richness, Shannon diversity and relative abundance of LFSA fungi, while the blue lines correspond to those of RA fungi. Statistical significance is determined using two-sided Wald tests from multivariate GAMLSS without adjustment for multiple comparisons. Significance levels are indicated as *** $p \leq 0.001$; ** $p \leq 0.01$; * $p \leq 0.05$.



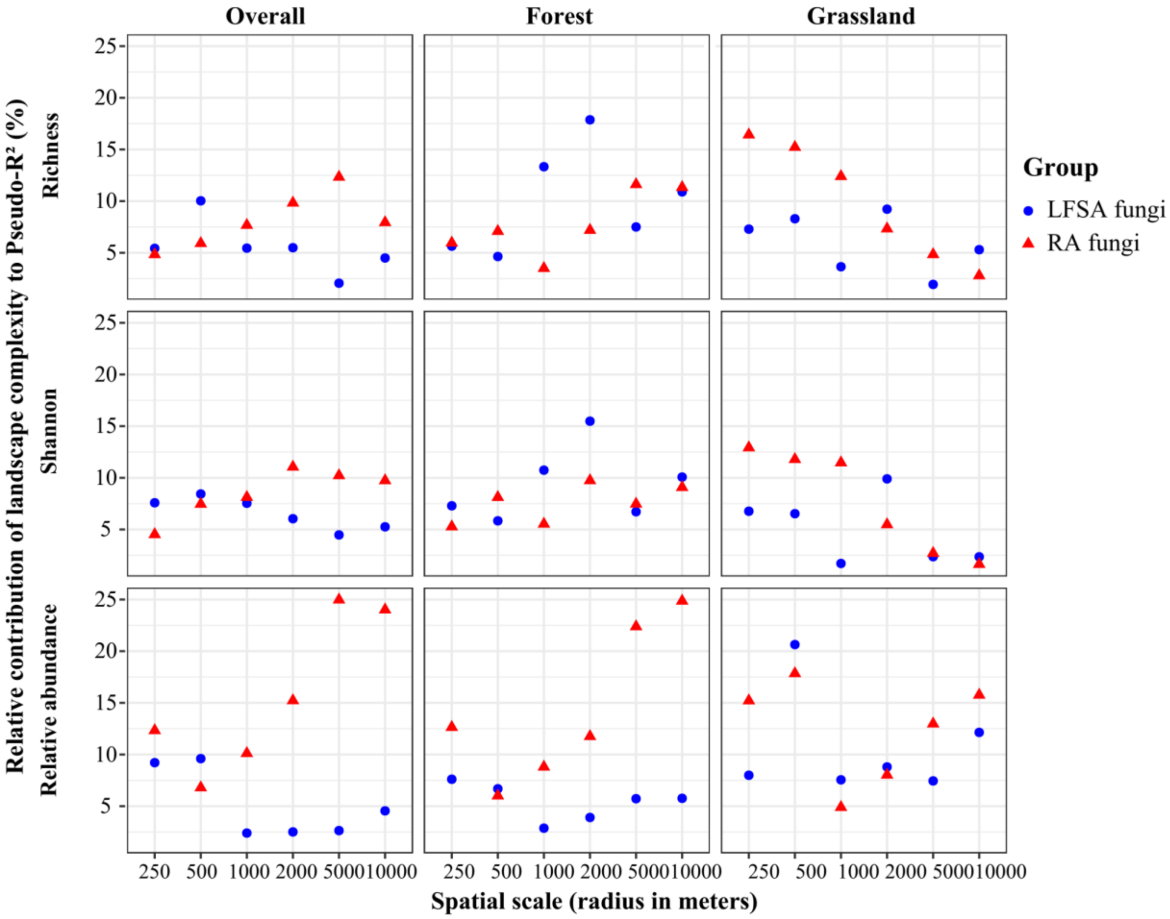
Supplementary Fig. 14. Landscape effects on leaf/fruit/seed-associated and root-associated fungal alpha diversity across spatial scales in grassland ecosystems. Leaf/fruit/seed-associated (LFSA) and root-associated (RA) fungal diversity as affected by (a) landscape complexity, (b) grass cover, (c) crop cover, and (d) tree cover across six spatial scales (250 m, 500 m, 1,000 m, 2,000 m, 5,000 m, and 10,000 m radii) (n = 183 grassland plots). Data are presented as model-estimated standardized regression coefficients ±95% confidence intervals (CIs) derived from multivariate Generalized Additive Models for Location, Scale, and Shape (GAMLSS). Red lines from dark to light indicate the richness, Shannon diversity and relative abundance of LFSA fungi, while the blue lines correspond to those of RA fungi. Statistical significance is determined using two-sided Wald tests from multivariate GAMLSS without adjustment for multiple comparisons. The significance levels are indicated as *** $p \leq 0.001$; ** $p \leq 0.01$; * $p \leq 0.05$.



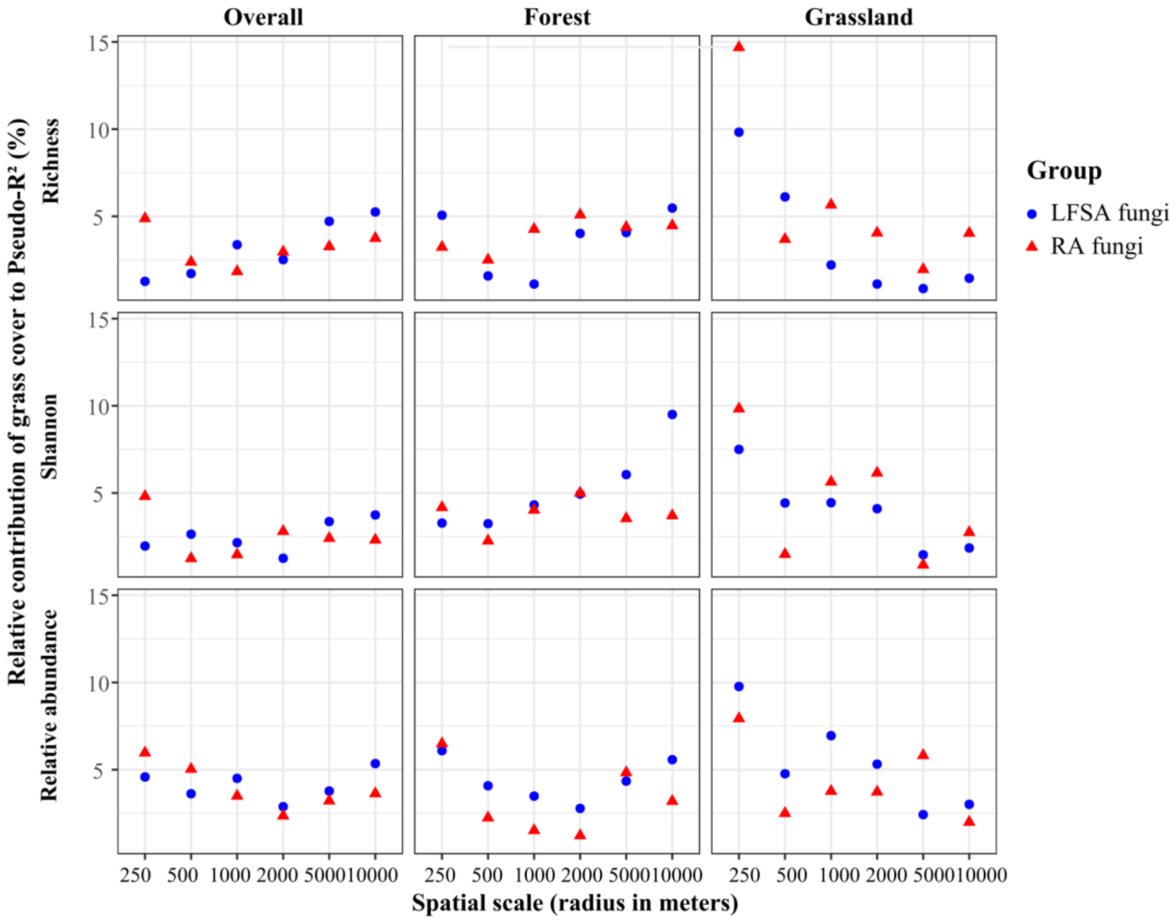
Supplementary Fig. 15. **Overall landscape effects on soil pathogenic fungal alpha diversity across ecosystems.** Overall effects of (a) landscape complexity, (b) grass cover, and (c) tree cover on soil pathogenic fungal alpha diversity between forest and grassland ecosystems. Colored lines denote the 95% confidence intervals of model-estimated standardized regression coefficients across two fungal groups (LFSA and RA fungi), three diversity indices (richness, Shannon diversity, and relative abundance), and six spatial scales (250 m to 10,000 m radii) from multivariate Generalized Additive Models for Location, Scale, and Shape (GAMLSS). Black triangles represent the overall effect sizes. Effect sizes are estimated using random-effects meta-analyses (n = 36 biologically independent samples), and statistical significance is evaluated using two-sided z-tests without adjustment for multiple comparisons. Effect size values and associated *p*-values are reported for each category.



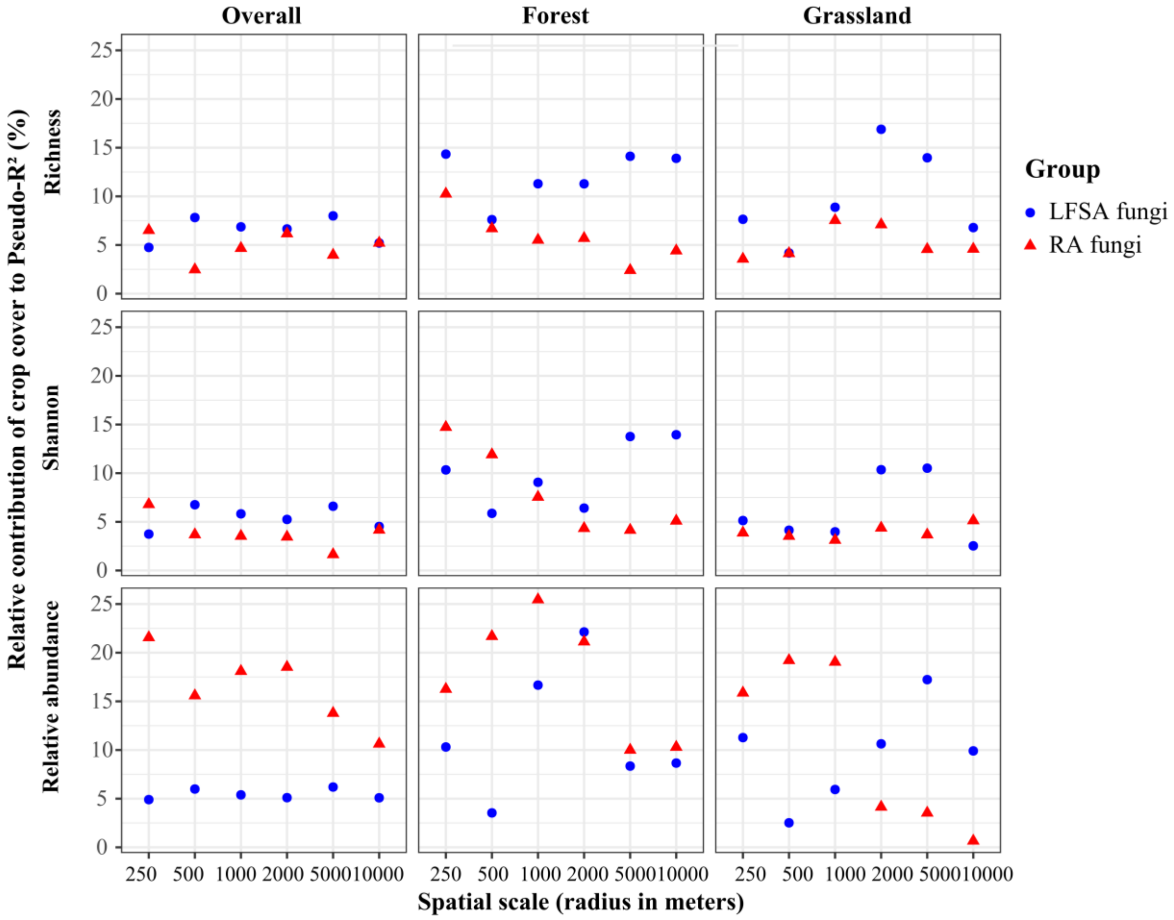
Supplementary Fig. 16. Relative contributions of environmental predictors to soil pathogenic fungal alpha and beta diversity across ecosystems. Average relative contribution (proportion of variance explained, %) of each predictor variable to soil pathogenic fungal (a)–(b) alpha (n = 36 biologically independent samples) and (c)–(d) beta (n = 12 biologically independent samples) diversity, covering two fungal groups (LFSA and RA fungi), four diversity indices (richness, Shannon diversity, and relative abundance for alpha diversity and Sørensen dissimilarity for beta diversity), and six spatial scales (250 m to 10,000 m radii) between forest and grassland ecosystems, respectively. Data are shown as mean ± s.e. Predictor variables are categorized into four groups: soil, landscape, climatic, and geographic factors.



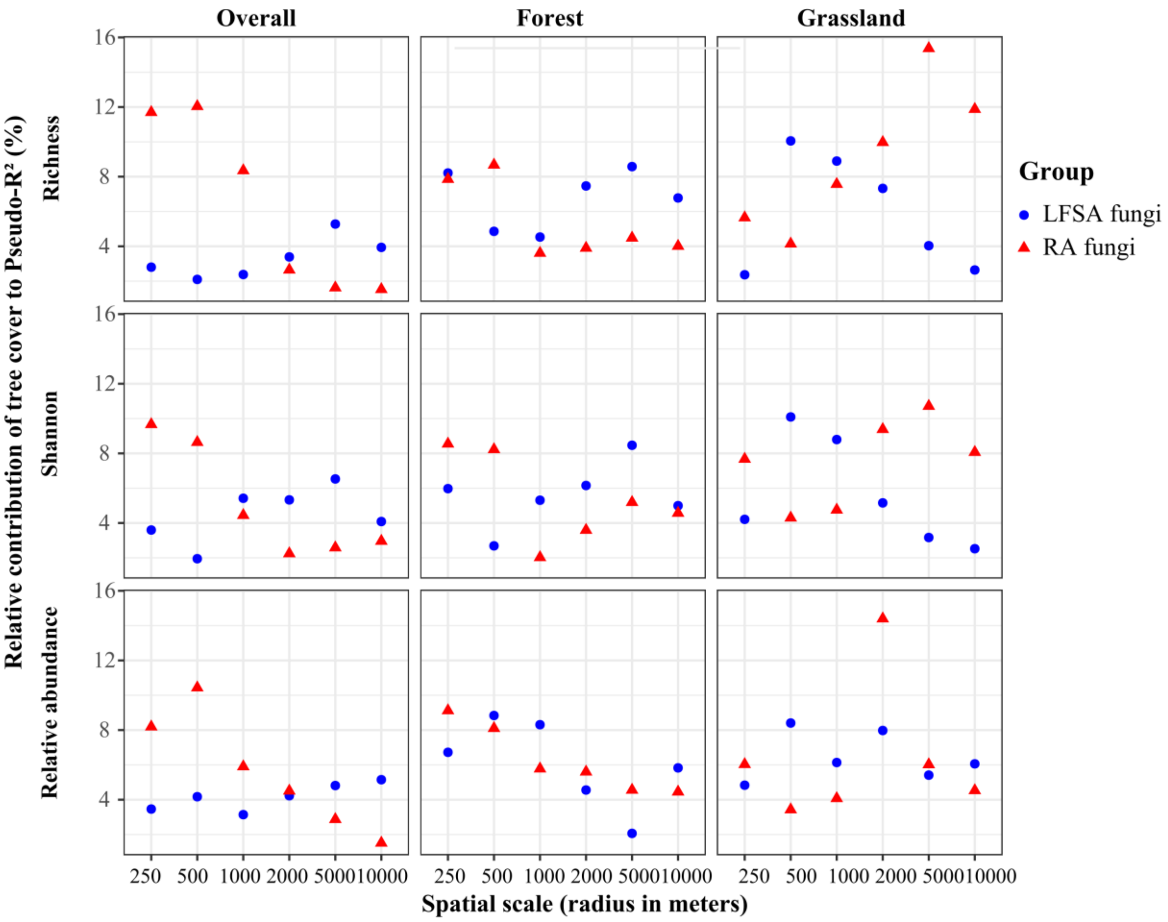
Supplementary Fig. 17. Relative contribution of landscape complexity to leaf/fruit/seed-associated and root-associated fungal alpha diversity across spatial scales (250 m to 10,000 m radii). Relative contribution (proportion of variance explained, %) of landscape complexity to the Pseudo-R ^{2}of multivariate Generalized Additive Models for Location, Scale, and Shape (GAMLSS) on leaf/fruit/seed-associated (LFSA) and root-associated (RA) fungal alpha diversity (richness, Shannon diversity and relative abundance) for overall plots (n = 511 plots), forest (n = 264 plots) and grassland (n = 183 plots) ecosystems.



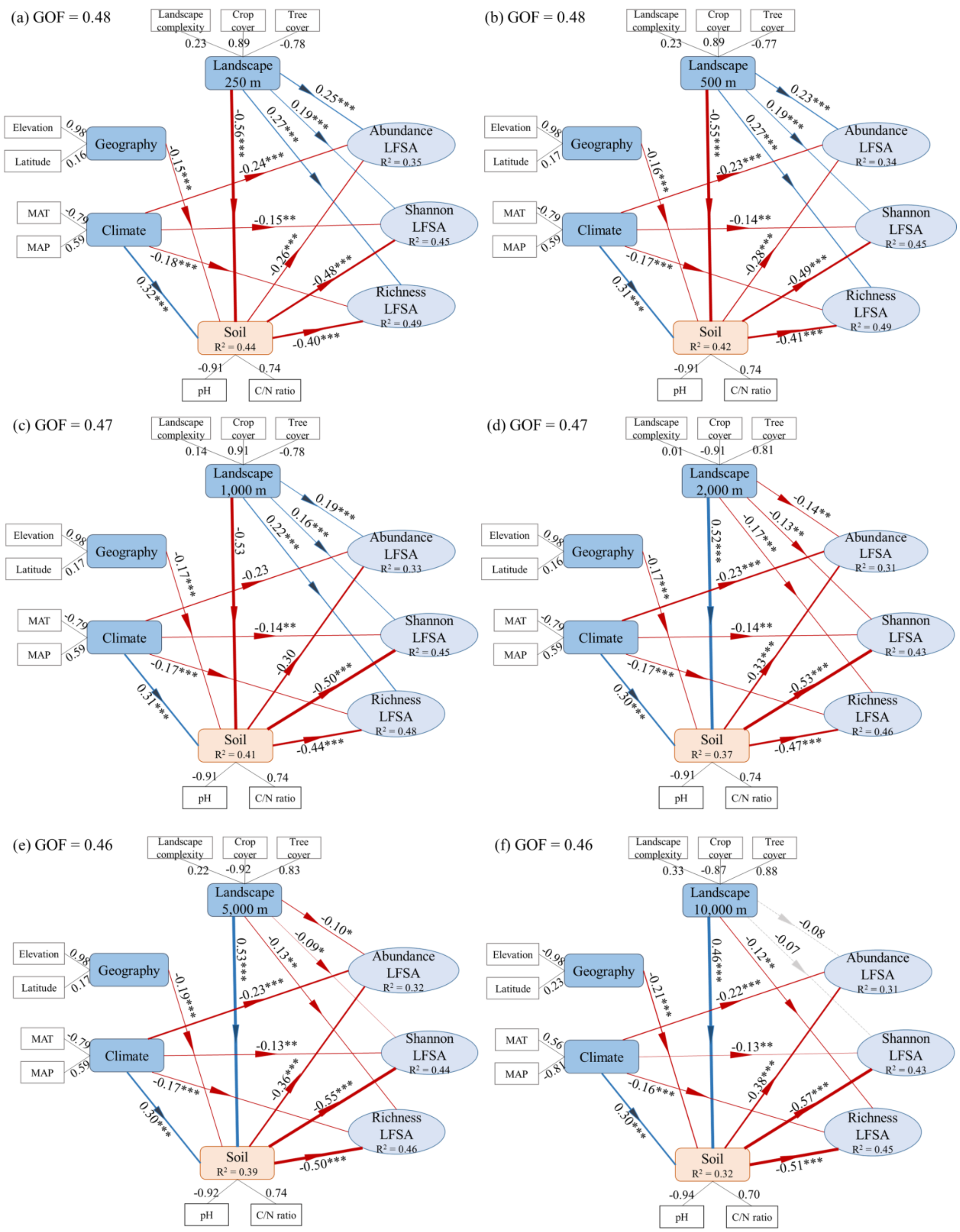
Supplementary Fig. 18. Relative contribution of grass cover to leaf/fruit/seed-associated and root-associated fungal alpha diversity across spatial scales (250 m to 10,000 m radii). Relative contribution (proportion of variance explained, %) of landscape complexity to the Pseudo-R ²of multivariate Generalized Additive Models for Location, Scale, and Shape (GAMLSS) on leaf/fruit/seed-associated (LFSA) and root-associated (RA) fungal alpha diversity (richness, Shannon diversity and relative abundance) for overall plots (n = 511 plots), forest (n = 264 plots) and grassland (n = 183 plots) ecosystems.



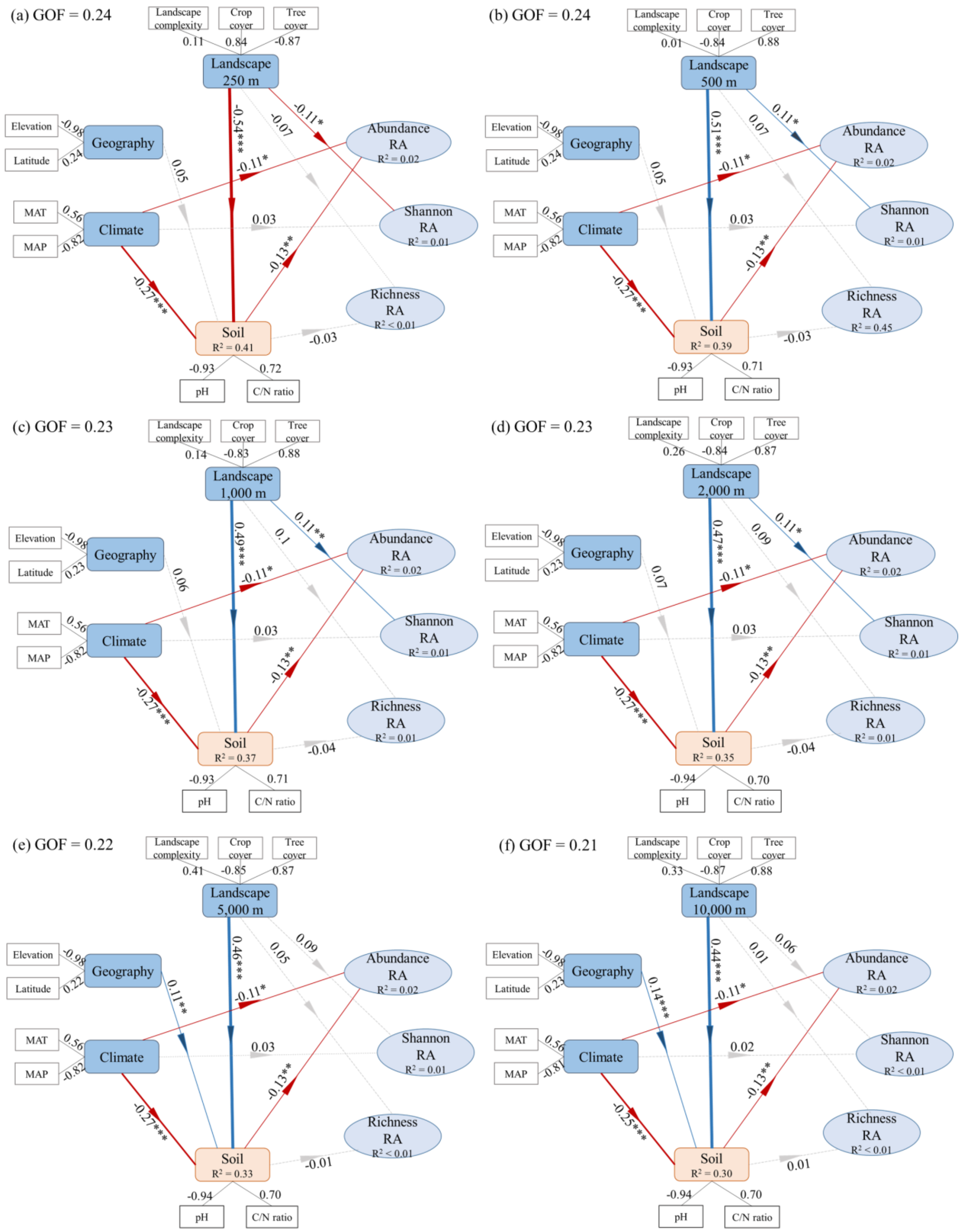
Supplementary Fig. 19. Relative contribution of crop cover to leaf/fruit/seed-associated and root-associated fungal alpha diversity across spatial scales (250 m to 10,000 m radii). Relative contribution (proportion of variance explained, %) of landscape complexity to the Pseudo-R ^{2}of multivariate Generalized Additive Models for Location, Scale, and Shape (GAMLSS) on leaf/fruit/seed-associated (LFSA) and root-associated (RA) fungal alpha diversity (richness, Shannon diversity and relative abundance) for overall plots (n = 511 plots), forest (n = 264 plots) and grassland (n = 183 plots) ecosystems.



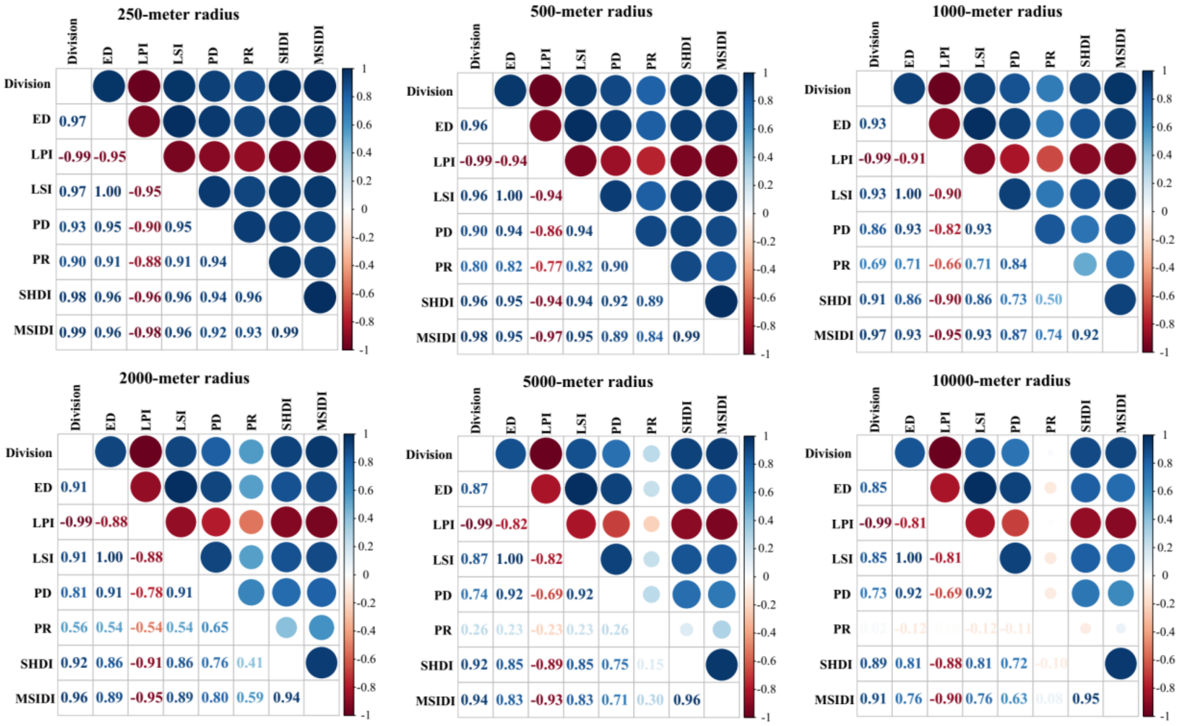
Supplementary Fig. 20. Relative contribution of tree cover to leaf/fruit/seed-associated and root-associated fungal alpha diversity across spatial scales (250 m to 10,000 m radii). Relative contribution (proportion of variance explained, %) of landscape complexity to the Pseudo-R ^{2}of multivariate Generalized Additive Models for Location, Scale, and Shape (GAMLSS) on leaf/fruit/seed-associated (LFSA) and root-associated (RA) fungal alpha diversity (richness, Shannon diversity and relative abundance) for overall plots (n = 511 plots), forest (n = 264 plots) and grassland (n = 183 plots) ecosystems.



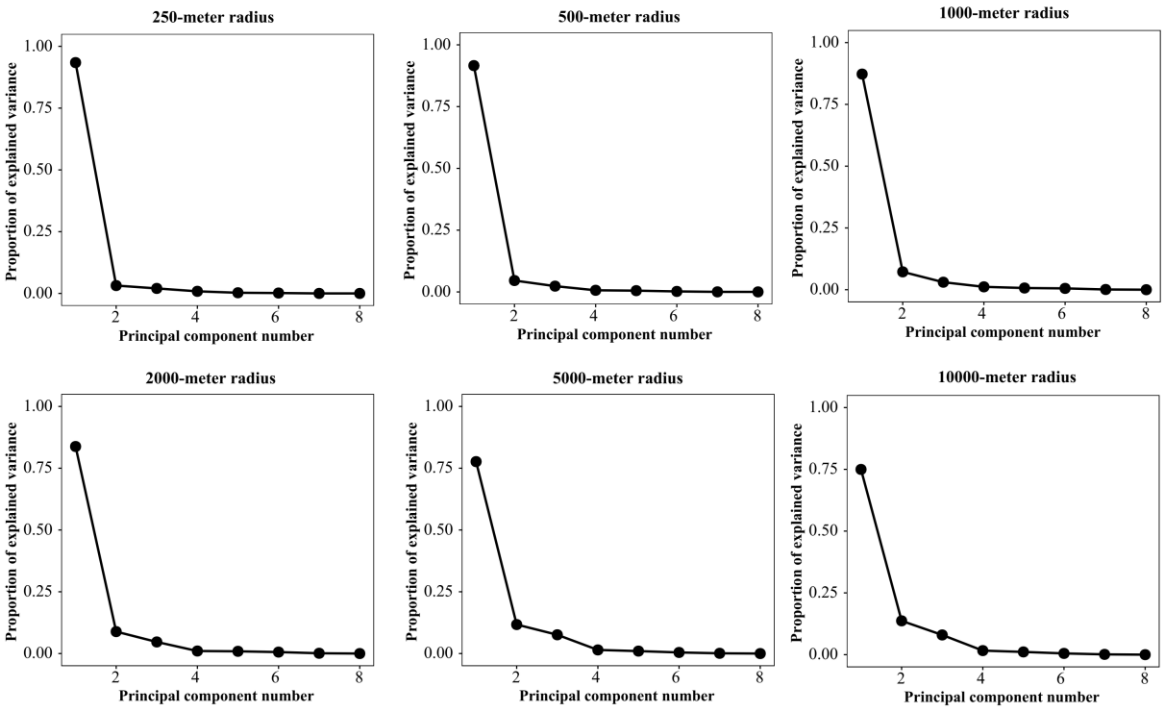
Supplementary Fig. 21. Optimal direct and indirect drivers of soil leaf/fruit/seed-associated fungal alpha diversity. Partial Least Squares Path Modeling (PLSPM) assesses the direct and indirect effects of landscape (across six spatial scales), geographic, climatic, and soil factors on leaf/fruit/seed-associated (LFSA) fungal alpha diversity, including richness, Shannon diversity, and relative abundance, across all plots (n = 511 plots). Panels (a)–(f) show the effects of landscape factors at different spatial scales (i.e., 250 m, 500 m, 1,000 m, 2,000 m, 5,000 m, and 10,000 m radii). Solid and dashed arrows represent significant or non-significant pathways, respectively, with standardized path coefficients shown alongside each path. Significance levels are denoted as $*p < 0.05$, $**p < 0.01$, $***p < 0.001$. Arrow widths reflect the relative strength of the path coefficients. The R^2 values indicate the proportion of variance explained for each response variable. The landscape latent variable includes landscape complexity, crop cover, and tree cover; the geographic variable includes elevation and latitude; the climatic variable includes MAT and MAP; and the soil variable includes soil pH and C/N ratio. The values linking indicators to latent variables represent loadings, with higher loadings indicating stronger associations with the corresponding latent construct. GoF indicates the goodness-of-fit of the model.



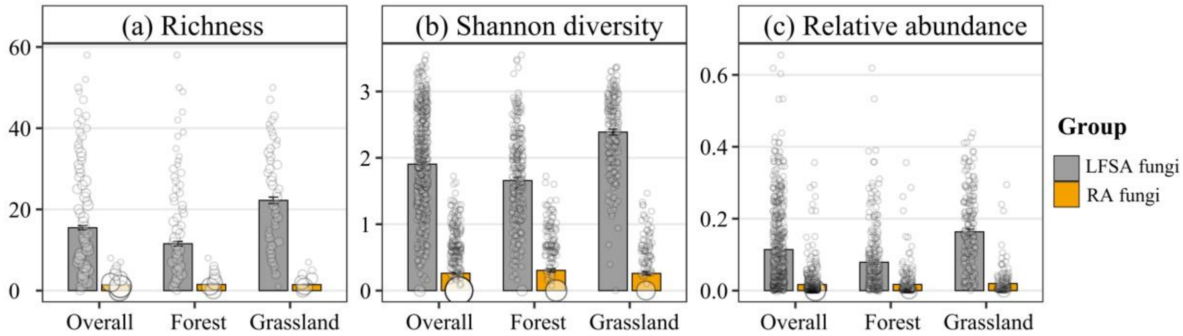
Supplementary Fig. 22. Optimal direct and indirect drivers of soil root-associated fungal alpha diversity. Partial Least Squares Path Modeling (PLSPM) assesses the direct and indirect effects of landscape (across six spatial scales), geographic, climatic, and soil factors on root-associated (RA) fungal alpha diversity, including richness, Shannon diversity, and relative abundance, across all plots (n = 511 plots). Panels (a)–(f) show the effects of landscape factors at different spatial scales (i.e., 250 m, 500 m, 1,000 m, 2,000 m, 5,000 m, and 10,000 m radii). Solid and dashed arrows represent significant or non-significant pathways, respectively, with standardized path coefficients shown alongside each path. Significance levels are denoted as $*p < 0.05$, $**p < 0.01$, $***p < 0.001$. Arrow widths reflect the relative strength of the path coefficients. The R^2 values indicate the proportion of variance explained for each response variable. The landscape latent variable includes landscape complexity, crop cover, and tree cover; the geographic variable includes elevation and latitude; the climatic variable includes MAT and MAP; and the soil variable includes soil pH and C/N ratio. The values linking indicators to latent variables represent loadings, with higher loadings indicating stronger associations with the corresponding latent construct. GoF indicates the goodness-of-fit of the model.



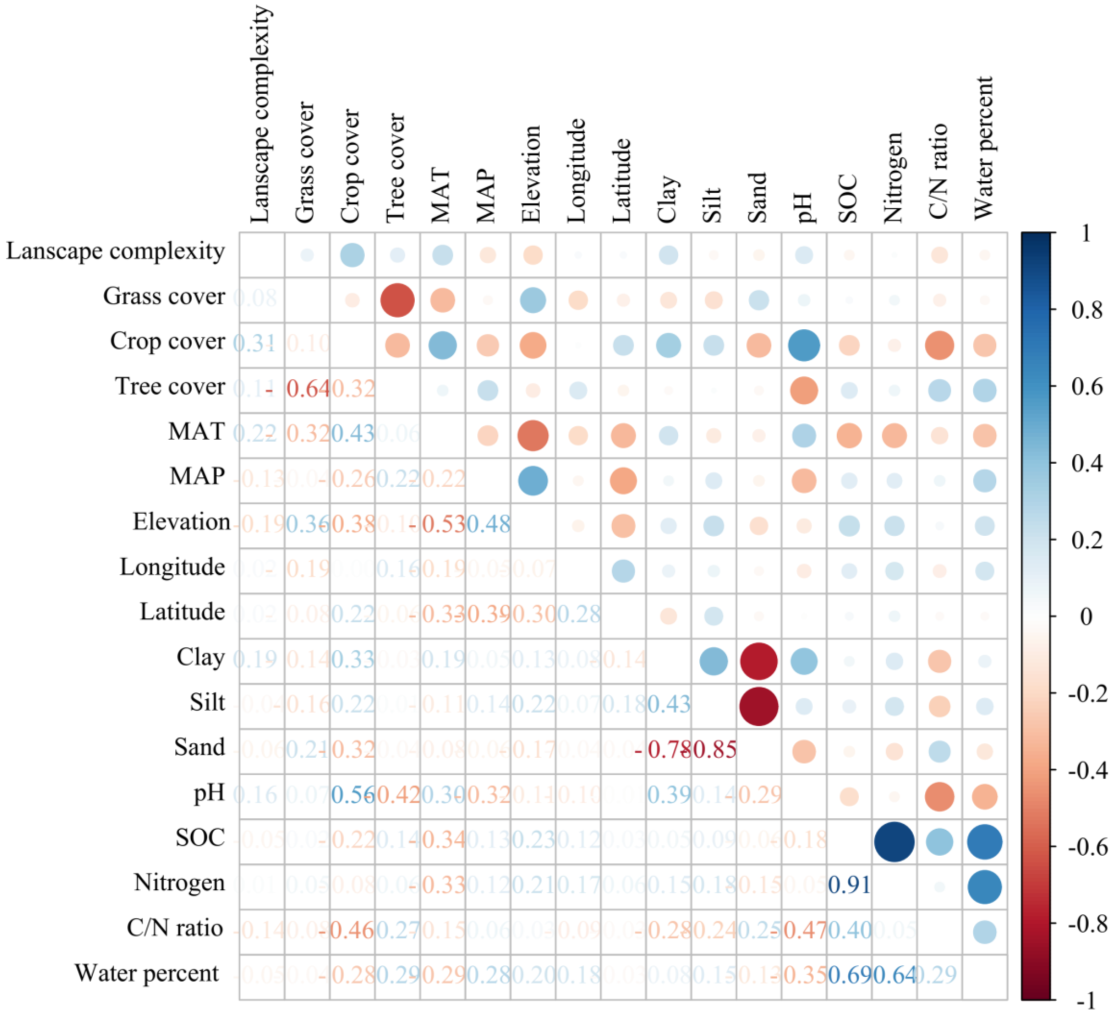
Supplementary Figure 23. The two-sided Spearman's correlation of eight landscape metrics across six spatial scales (250 m, 500 m, 1,000 m, 2,000 m, 5,000 m, and 10,000 m radii). N = 511 biologically independent samples without adjustment for multiple comparisons. The metrics include, landscape division index (Division), edge density (ED), largest patch index (LPI), landscape shape index (LSI), patch density (PD), Patch richness (PR), Shannon diversity index (SHDI), modified Simpson's diversity index (MSIDI).



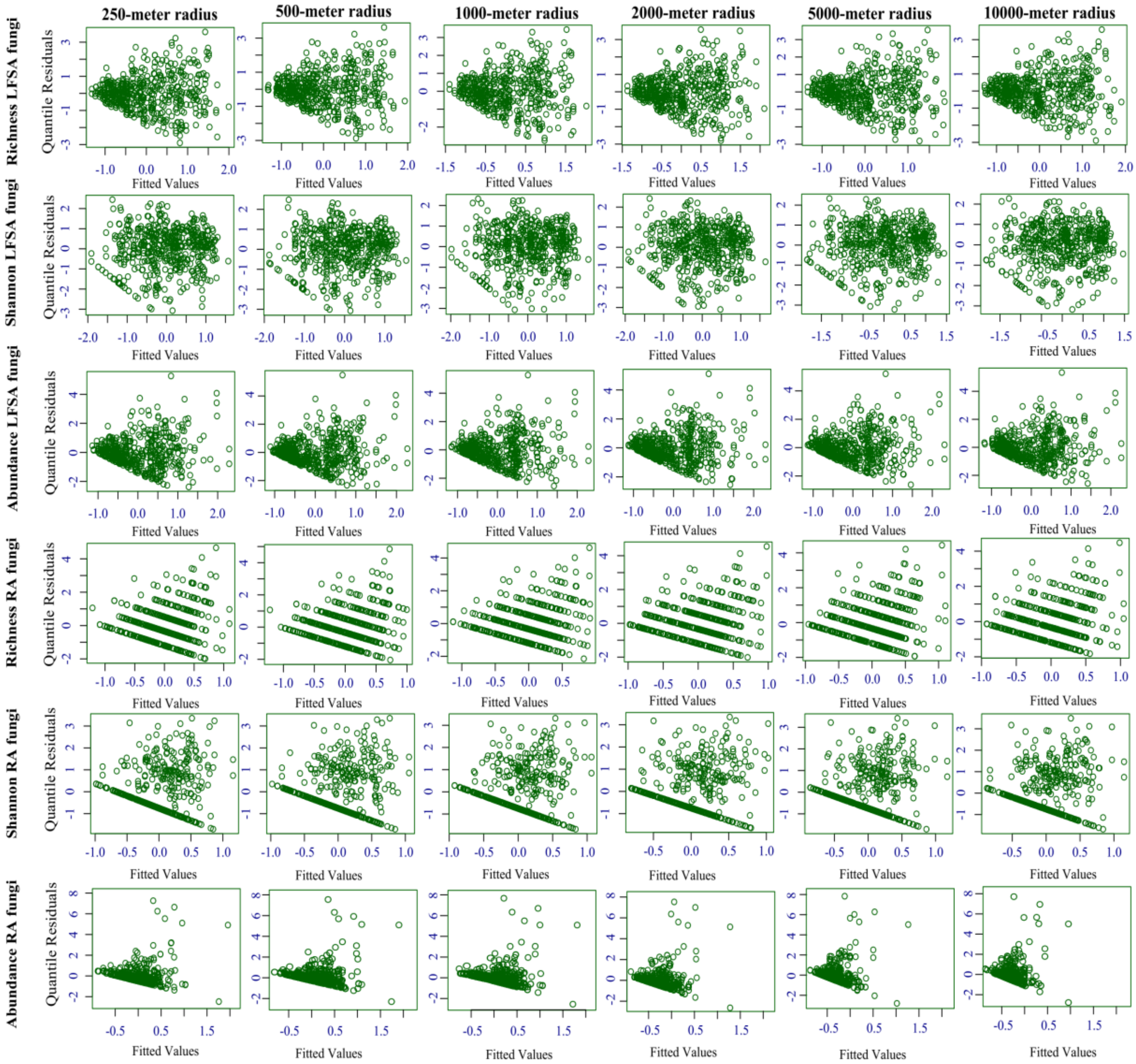
Supplementary Figure 24. Proportion of variance explained by each principal component derived from principal component analysis (PCA) of eight landscape metrics across six spatial scales (250 m, 500 m, 1,000 m, 2,000 m, 5,000 m, and 10,000 m radii). N = 511 biologically independent samples without adjustment for multiple comparisons. The analyzed metrics include landscape division index (Division), edge density (ED), largest patch index (LPI), landscape shape index (LSI), patch density (PD), patch richness (PR), Shannon diversity index (SHDI), and modified Simpson's diversity index (MSIDI).



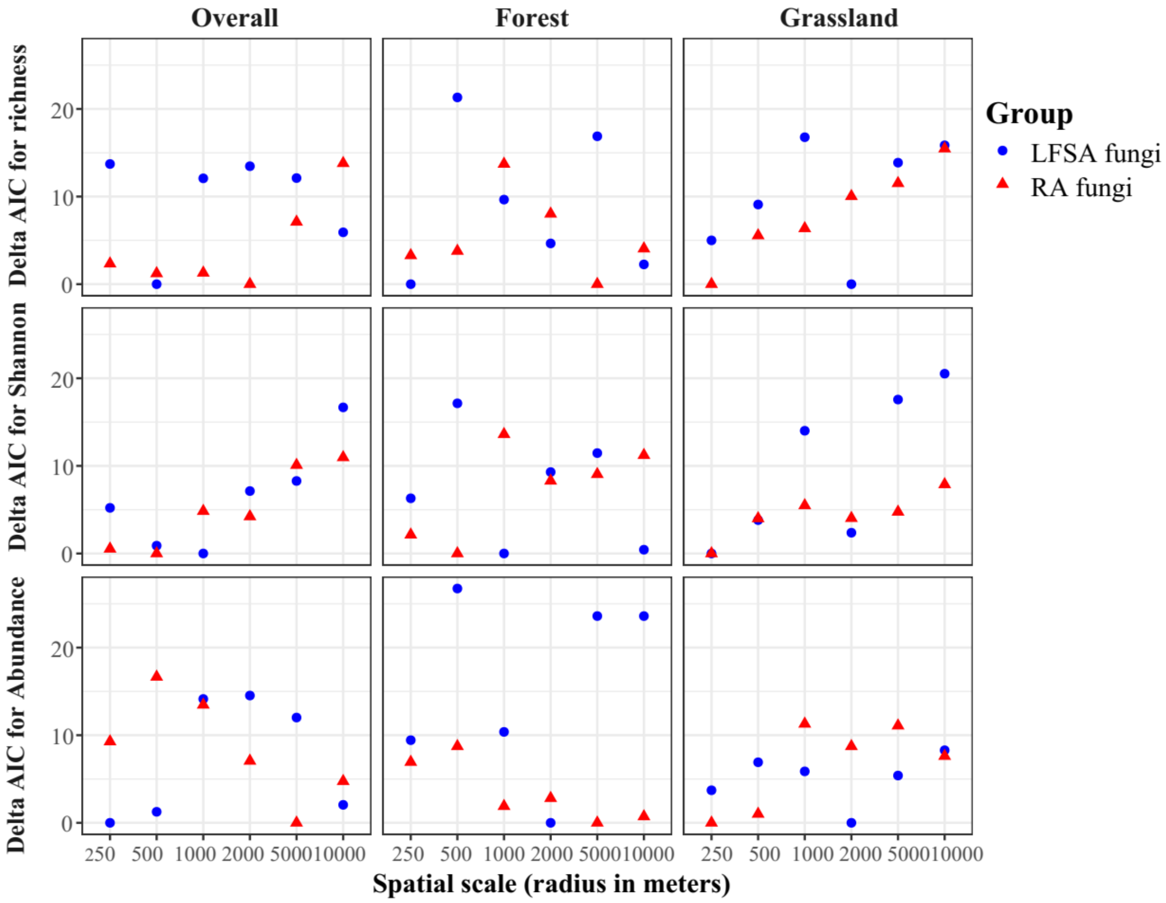
Supplementary Fig. 25. Alpha diversity of soil pathogenic fungi. Panels (a)–(c) display the richness, Shannon diversity, and relative abundance (mean ± s.e.) of leaf/fruit/seed-associated (LFSA) and root-associated (RA) fungal communities across all plots (n = 511 plots), forest (n = 264 plots) and grassland (n = 183 plots) ecosystems. The circles represent the original diversity values of each plot, with larger circles indicate more frequent values.



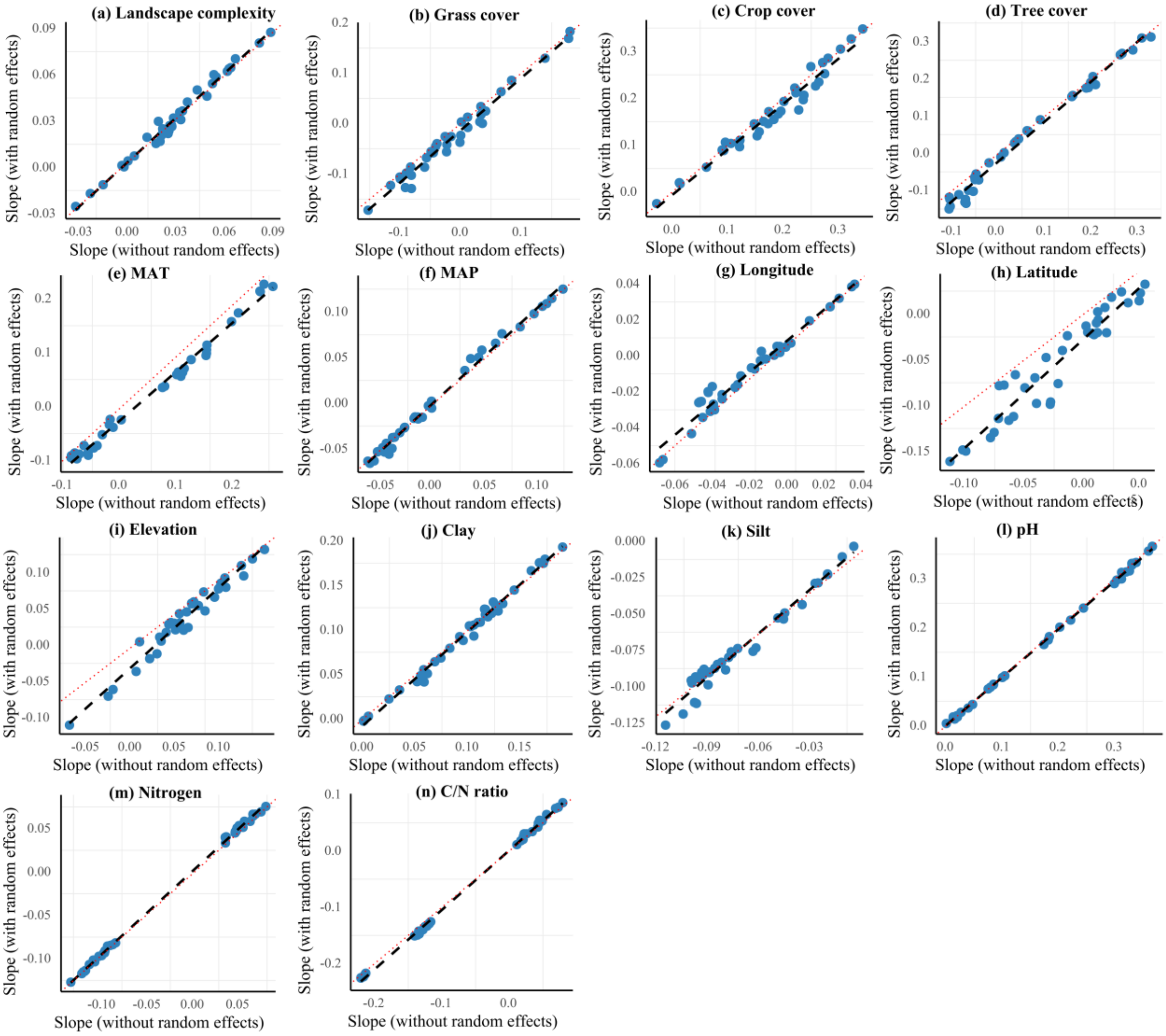
Supplementary Fig. 26. The two-sided Spearman's correlation of landscape, geographic, climatic and soil factors. N = 511 biologically independent samples without adjustment for multiple comparisons. Landscape factors include the landscape complexity index, grass cover, crop cover and tree cover (at the spatial distance of 500 m). Geographic factors include elevation, longitude and latitude. Climatic factors include mean annual temperature (MAT) and mean annual precipitation (MAP). Soil factors include soil clay content, silt content, sand content, pH, soil organic carbon (SOC), total nitrogen content, SOC/total nitrogen (C/N) ratio and water percent. Since soil sand content, SOC and water percent had high correlations with other variables, they are not included in further analysis. Blue shading represents positive correlations, and red shading represents negative correlations.



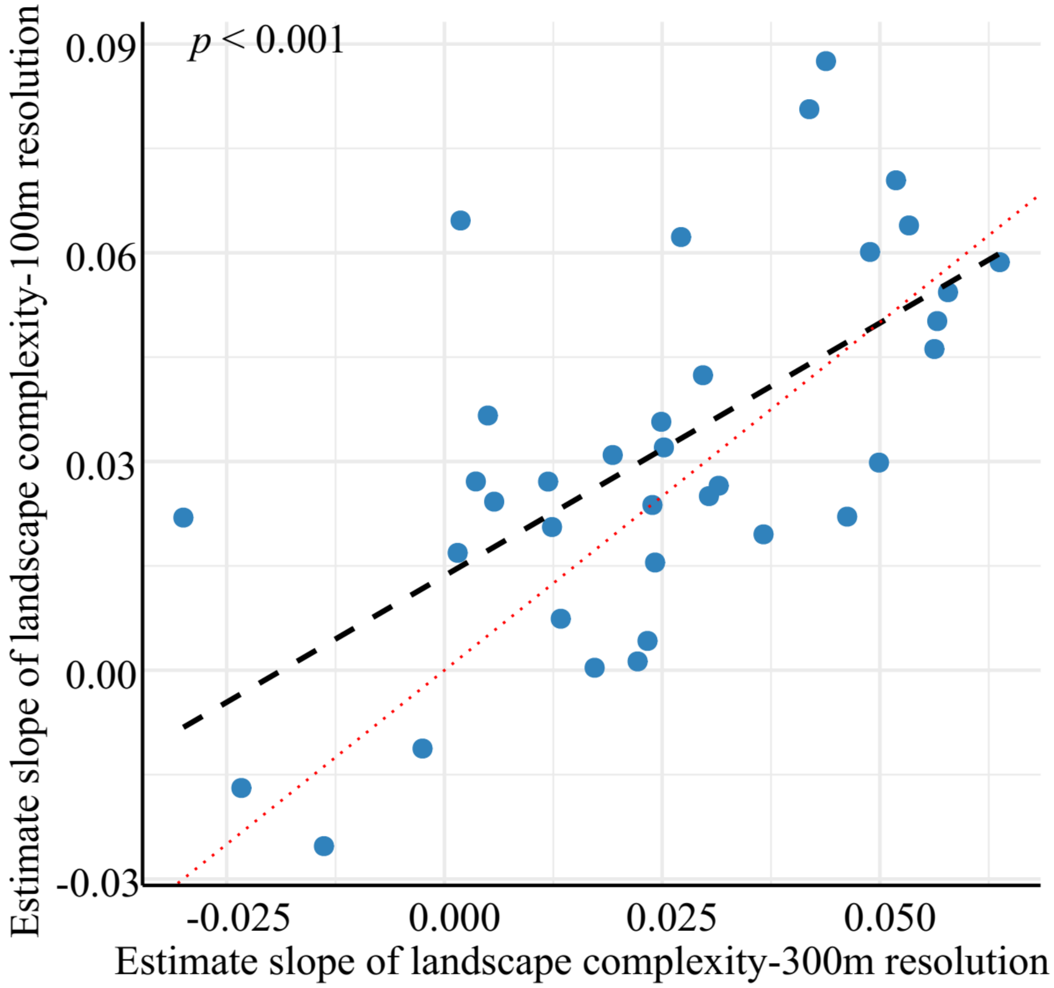
Supplementary Fig. 27. Quantile residual diagnostics for multivariate generalized additive models of soil pathogenic fungal diversity. Plots of quantile residuals against fitted values to assess the homogeneity of residual variances from the multivariate Generalized Additive Models for Location, Scale, and Shape (GAMLSS). Models are fitted for soil fungal richness, Shannon diversity, and relative abundance of leaf/fruit/seed-associated (LFSA) and root-associated (RA) fungi, evaluated across six competing models at spatial scales ranging from 250 m to 10,000 m radii for all 511 plots.



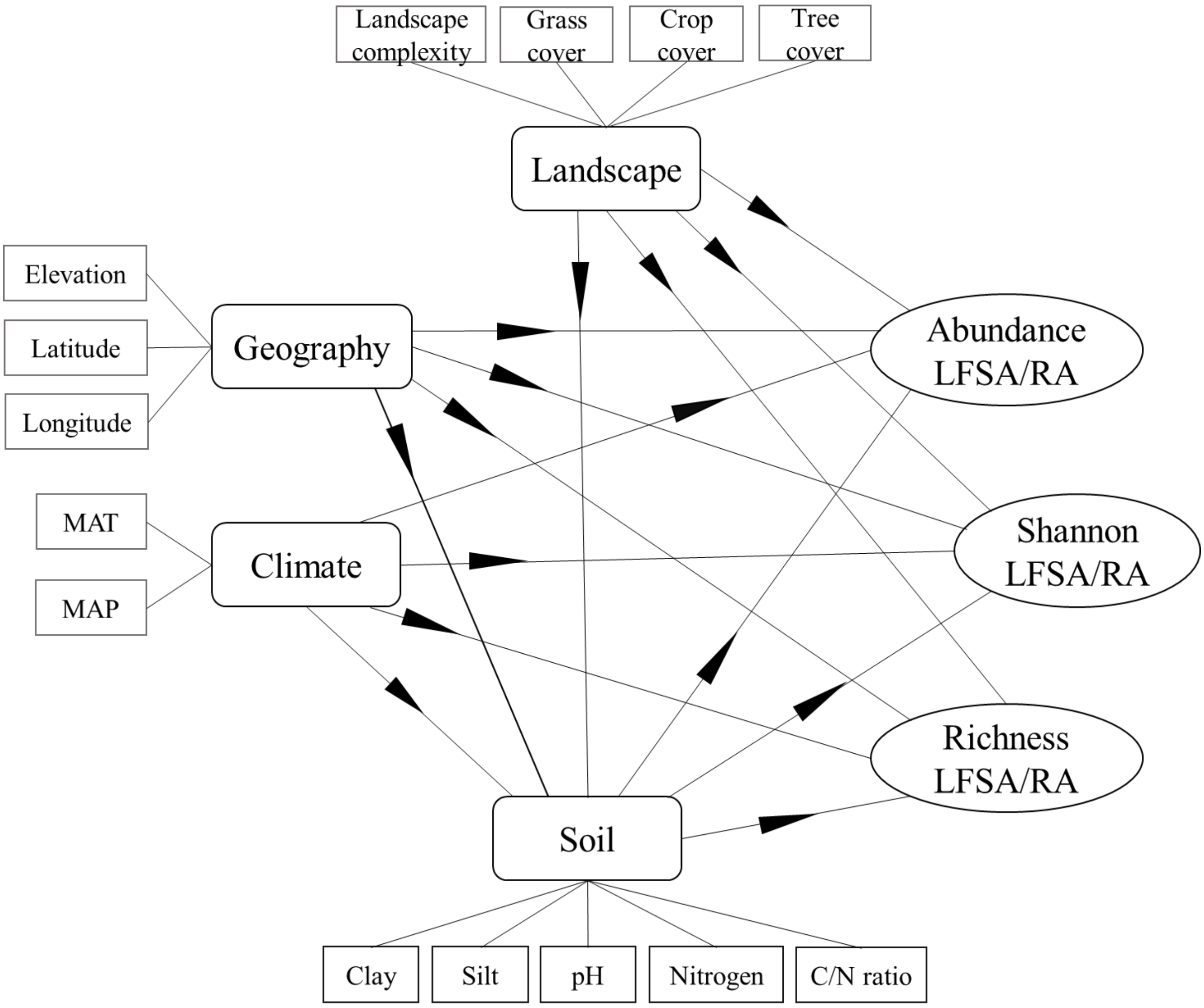
Supplementary Fig. 28. Model performance of multivariate generalized additive models for soil pathogenic fungal alpha diversity across spatial scales (250 m to 10,000 m radii). The delta-AIC of all multivariate Generalized Additive Models for Location, Scale, and Shape (GAMLSS) on leaf/fruit/seed-associated (LFSA) and root-associated (RA) fungal alpha diversity for overall plots (n = 511 plots), forest (n = 264 plots) and grassland (n = 183 plots) ecosystems. The lower AIC, the better the model.



Supplementary Fig. 29. Consistency of estimate slopes from multivariate Generalized Additive Models for Location, Scale, and Shape (GAMLSS) with and without site as a random effect for each environmental variable. (a)–(n) show the results for individual environmental variables, including landscape variables of landscape complexity, grass cover, crop cover and tree cover (within the 500 m radius around the sampling coordinate), climatic variables of mean annual temperature (MAT) and mean annual precipitation (MAP), geographic variables of longitude, latitude, and elevation, and soil variables of soil clay content (clay), silt content (silt), pH, total nitrogen content (nitrogen) and soil organic carbon/total nitrogen (C/N) ratio. Points indicate paired slope estimates (n = 36 biologically independent samples), with the dashed red line showing the 1:1 relationship.



Supplementary Fig. 30. Comparison of estimate slopes for the relationships between landscape complexity calculated from 100 m- and 300 m-resolution land cover maps and soil pathogenic fungal alpha diversity. Estimate slopes are obtained from multivariate Generalized Additive Models for Location, Scale, and Shape (GAMLSS) across two fungal groups (LFSA and RA fungi), three alpha diversity indices (richness, Shannon diversity, and relative abundance) and six landscape spatial scales (250–10,000 m radii). Points indicate paired slope estimates (n = 36 biologically independent samples), with the dashed red line showing the 1:1 relationship.



Supplementary Fig. 31. Hypothesized direct and indirect effects of landscape, geography, climate and soil variables on soil pathogenic fungal alpha diversity based on Partial Least Squares Path Modeling (PLSPM). The landscape latent variable includes landscape complexity, grass cover, crop cover, and tree cover; the geographic variable includes elevation, latitude, and longitude; the climatic variable includes MAT and MAP; and the soil variable includes soil clay, silt, pH, nitrogen, and C/N ratio. Response variables are the richness, Shannon diversity, and relative abundance of leaf/fruit/seed-associated (LFSA) and root-associated (RA) fungi. The final model was assessed with Goodness-of-Fit (GoF) value.