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Supplemental Information for:

Multiple spatial scales of bacterial and fungal structural and functional traits affect carbon mineralization

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Running title: Spatial scales of microbial C decomposition

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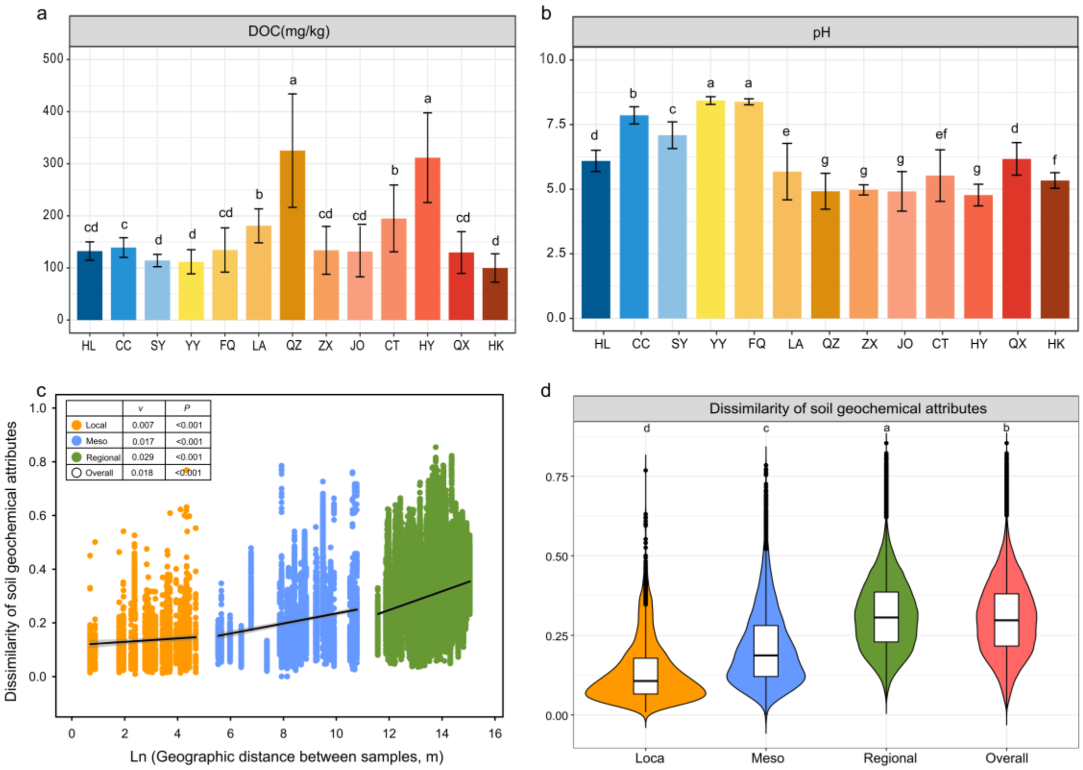

Figure S1 Patterns of abiotic factors (pH and dissolved organic carbon (DOC)) and spatial heterogeneity in 11 regions across China. Column plots show the average pH (a) and DOC (b) contents at each of the 11 regional sampling sites. The error bar represents the standard deviation value. Scatter plot (c) represents distance decay relationships (DDRs) between geographic distance and geochemical attributes based on Aitchison distance at different spatial scales. Guitar plot (d) represents the differences in soil geochemical properties at four spatial scales. Significant differences ($P < 0.05$) in gene abundance in each climatic zone-paired group are shown above the error bars via one-way ANOVA (multiple comparisons, Fisher’s LSD test).

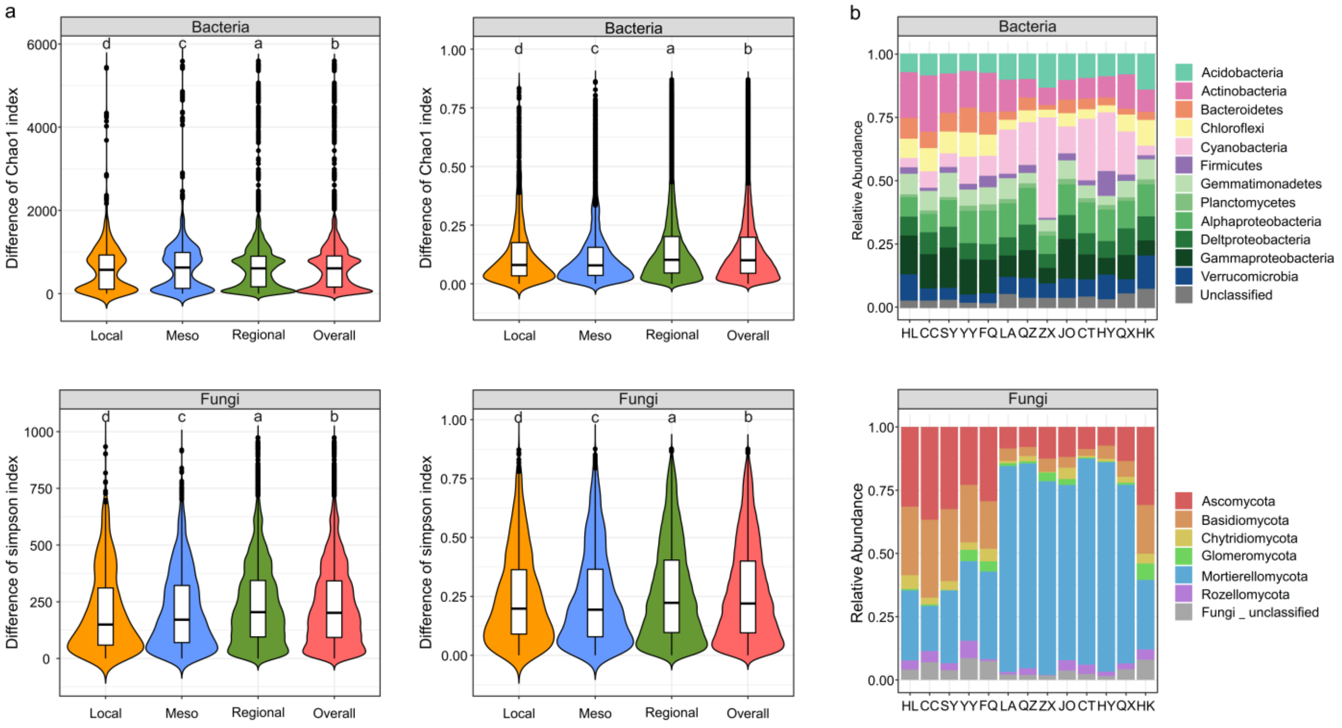

Figure S2 Biodiversity and composition of bacteria and fungi at different sampling sites. (a) Guitar plot representing the comparison of the α diversity of bacteria and fungi at four spatial scales via the Chao1 and Simpson indices. (b) Relative abundances of soil bacterial and fungal communities at the phylum or class level.

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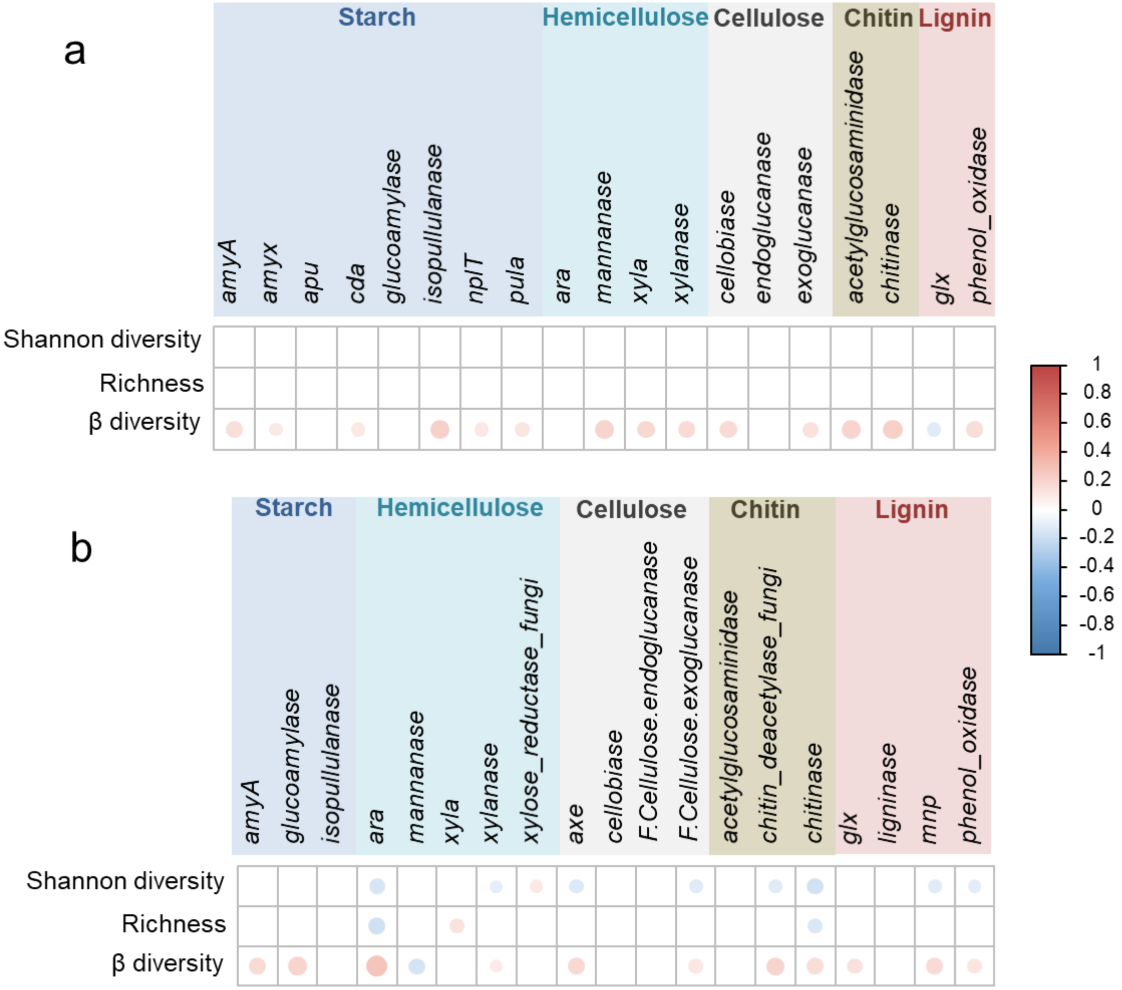


Figure S3 Pearson's correlations between bacterial (a) and fungal (b) diversity and carbon functional genes. The color points indicate a significant correlation coefficient ($P < 0.05$; bluer indicates a stronger negative correlation, and redder indicates a stronger positive correlation).

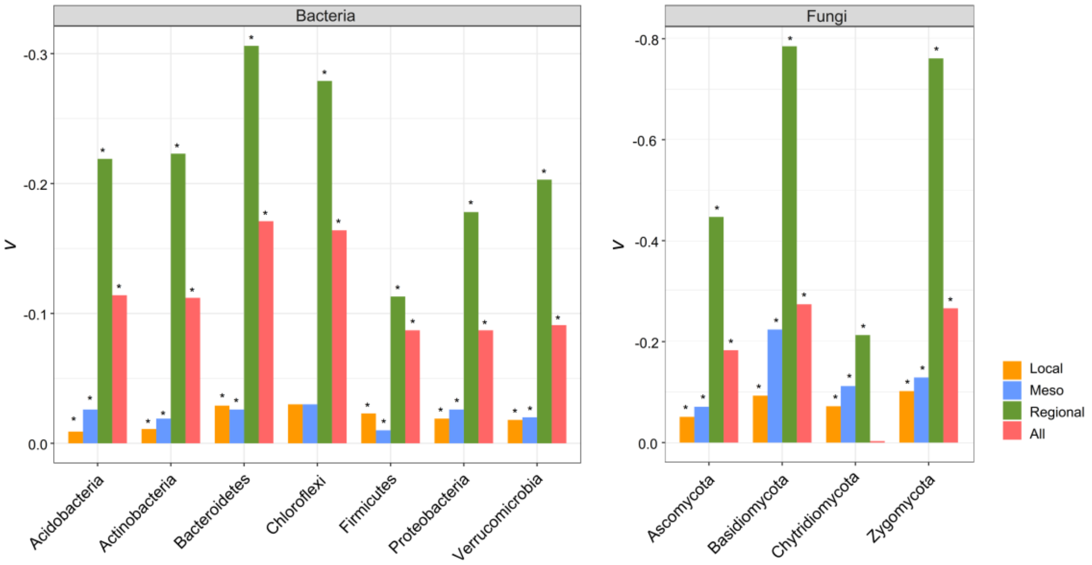


Figure S4 Spatial turnover rates of the highly abundant soil bacteria and fungi at the phylum level. The column plot shows the changes in turnover rates (*v*) for bacteria (left) and fungi (right) based on distance decay relationships. The significant differences ($P < 0.01$) in *v* values in each phylum group are tagged by the asterisk via one-way ANOVA (multiple comparisons, Fisher's LSD test).

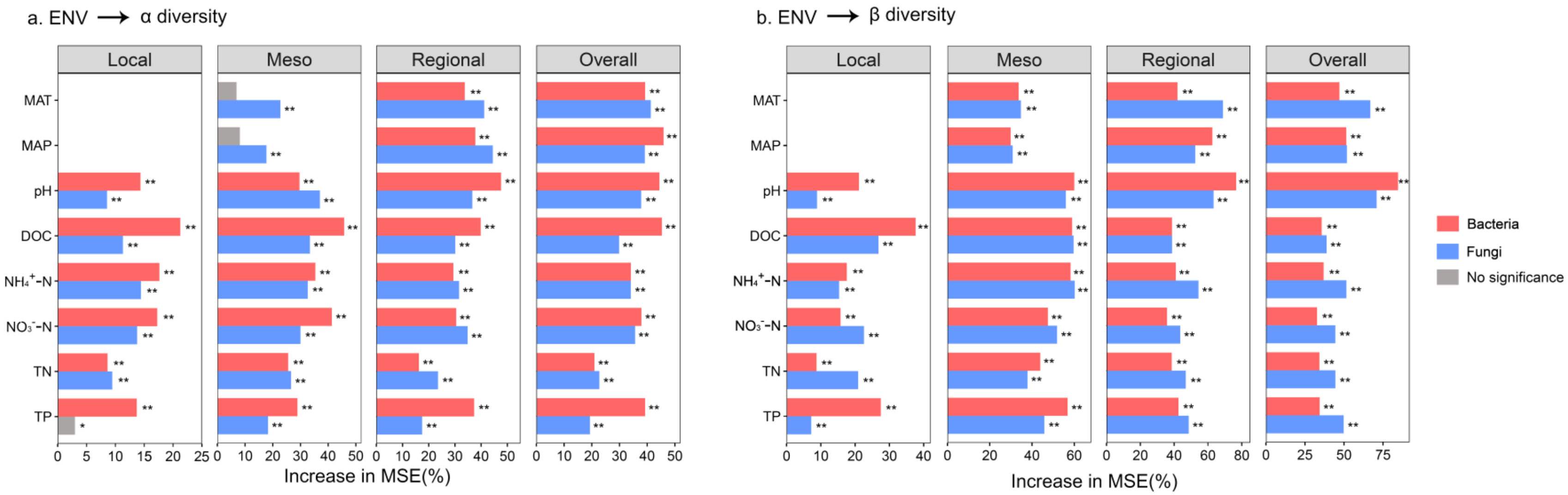


Figure S5 Effects of the main environmental driving factors on the α and β diversity of soil microbial communities in paddy fields. Contribution of environmental factors to (a) α diversity and (b) β diversity at four spatial scales. The average predictive values of bacterial and fungal diversity caused by environmental factors (% of increasing mean squared error (MSE)) were calculated using random forest (RF) analysis. ENV: environmental variables; MAT: mean annual temperature; MAP: mean annual precipitation. The significance levels of the predictors are as follows: * $P < 0.05$; ** $P < 0.01$.

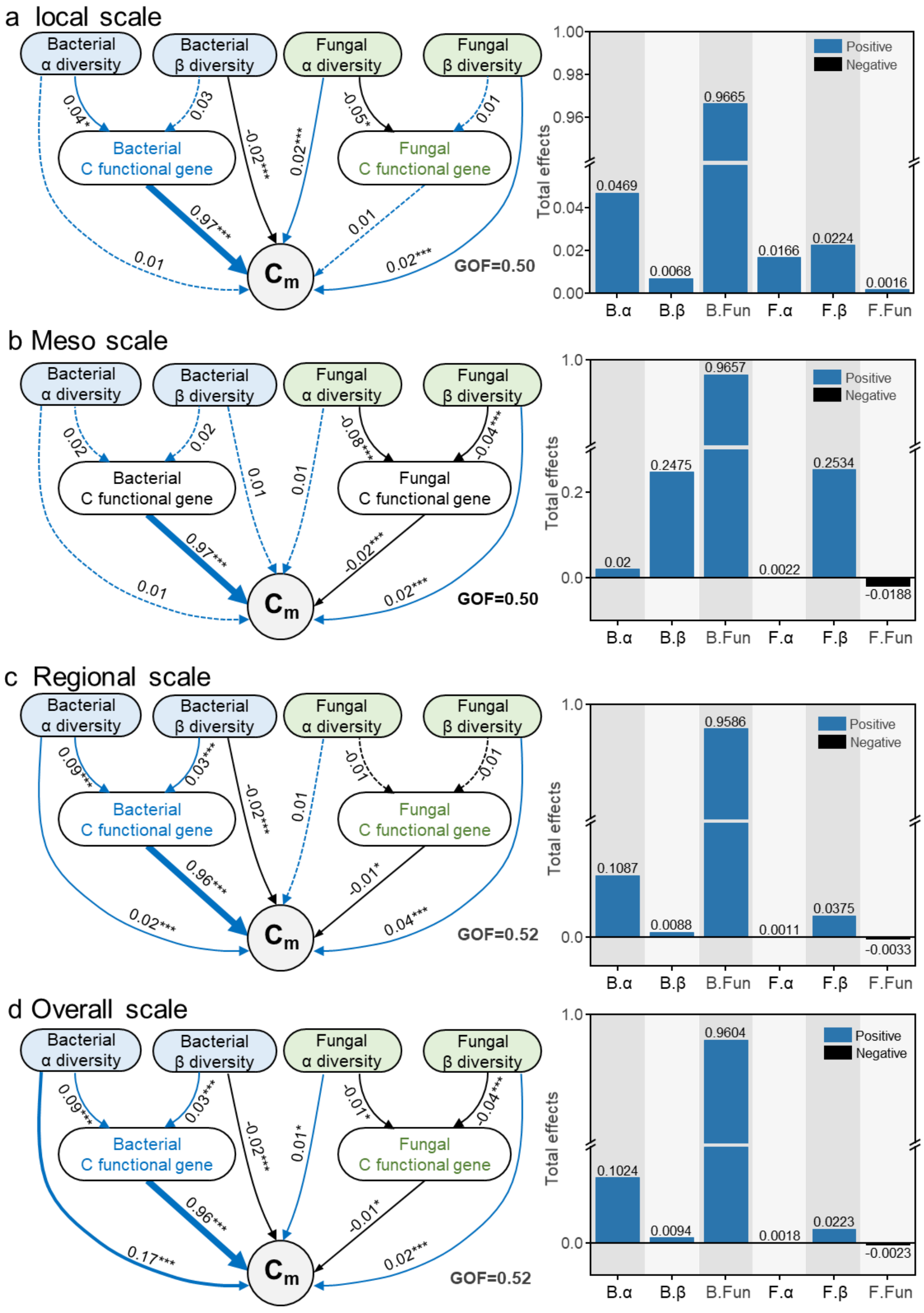
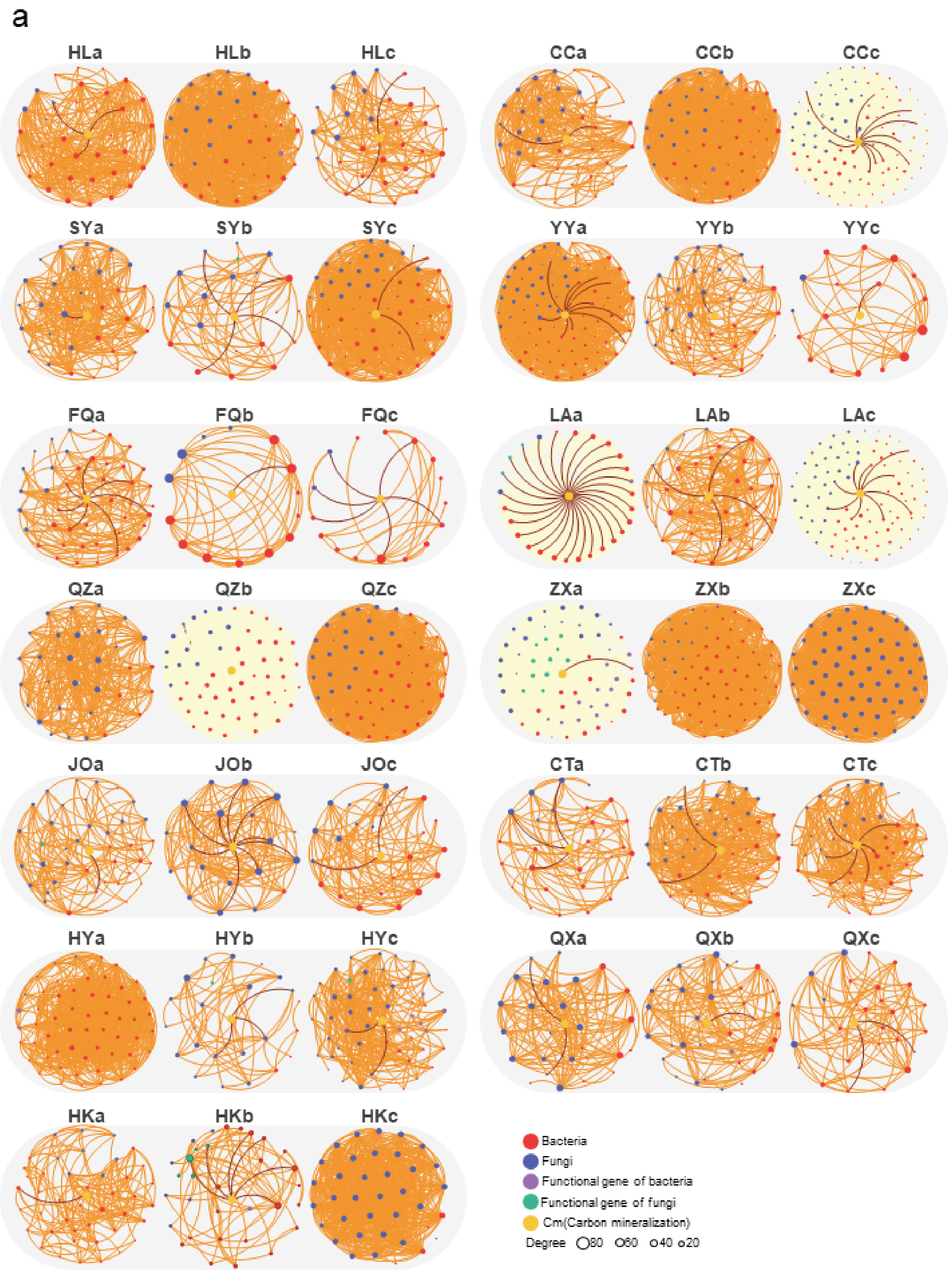


Figure S6 Structural equation models at four spatial scales. a, The local scale (1-100 m); b, The meso scale (0.5-50 km); c, The regional scale (100-3500 km), and d, the overall scale (1 m-3500 km). Cm represents carbon mineralization. The significance levels of the predictors are as follows: * *P* < 0.05; ** *P* < 0.01, *** *P* < 0.001.


a
HLa
HLb
HLc
CCa
CCb
CCc
SYa
SYb
SYc
YYa
YYb
YYc
FQa
FQb
FQc
LAa
LAb
LAc
QZa
QZb
QZc
ZXa
ZXb
ZXc
JOa
JOb
JOc
CTa
CTb
CTc
HYa
HYb
HYc
QXa
QXb
QXc
HKa
HKb
HKc
Bacteria
Fungi
Functional gene of bacteria
Functional gene of fungi
Cm(Carbon mineralization)
Degree 80 60 40 20

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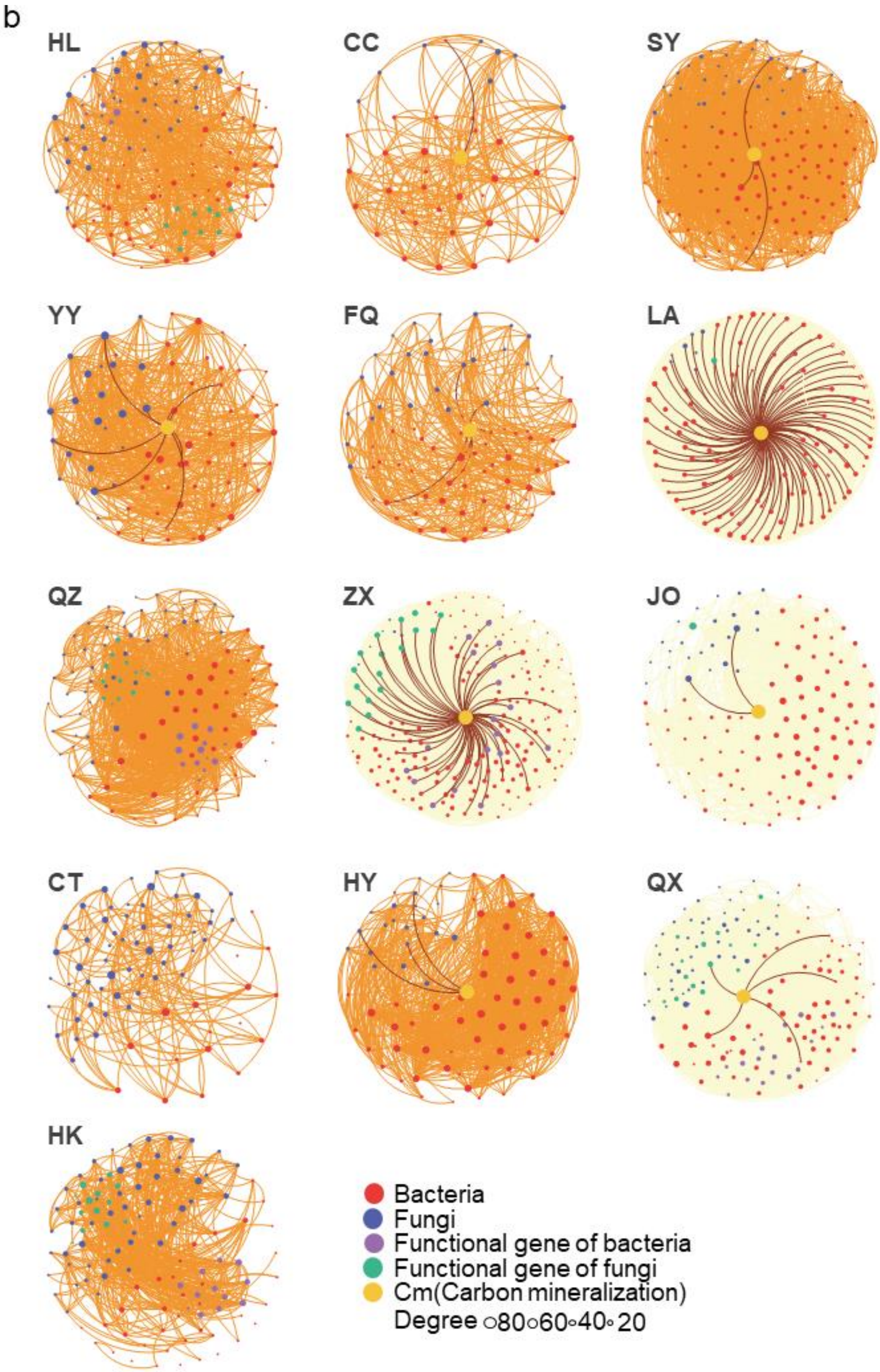

c

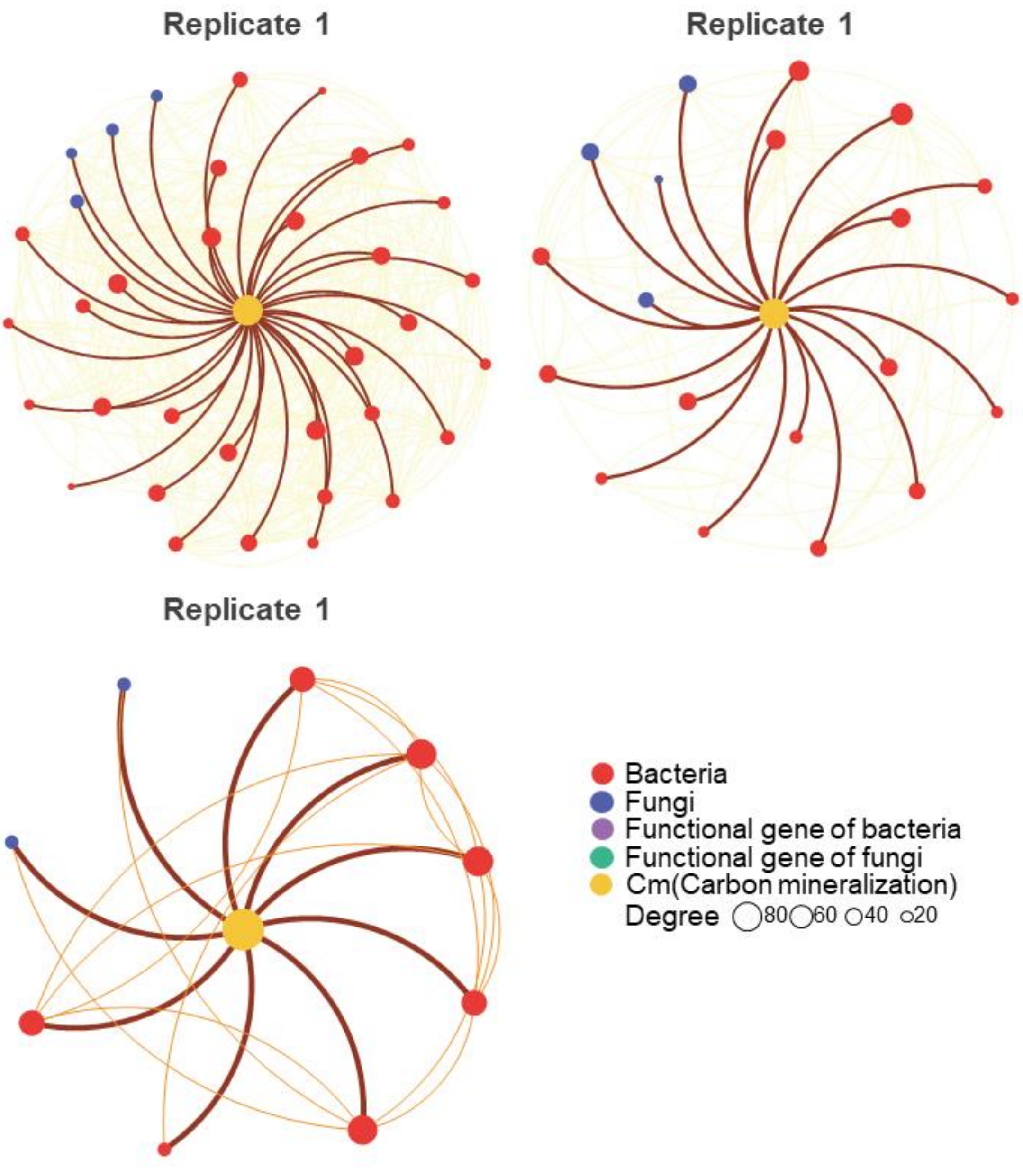
Replicate 1
Replicate 1
Replicate 1
● Bacteria
● Fungi
● Functional gene of bacteria
● Functional gene of fungi
● Cm(Carbon mineralization)
Degree ○80 ○60 ○40 ○20

Figure S7 Co-occurrence network analyses linked to heterotopic respiration (RH, equal to carbon mineralization) at local (a), meso (b) and regional (c) scales. The network pathway shows the fundamental linkages between functional bacterial and fungal communities and related genes that induce carbon mineralization. Each node at each site represents an operational taxonomic unit (OTU, at the genus level) of bacteria or fungi contributing to carbon mineralization, each node represents the critically functional genes regulating carbon mineralization processes, and each edge represents a positive or negative interaction.

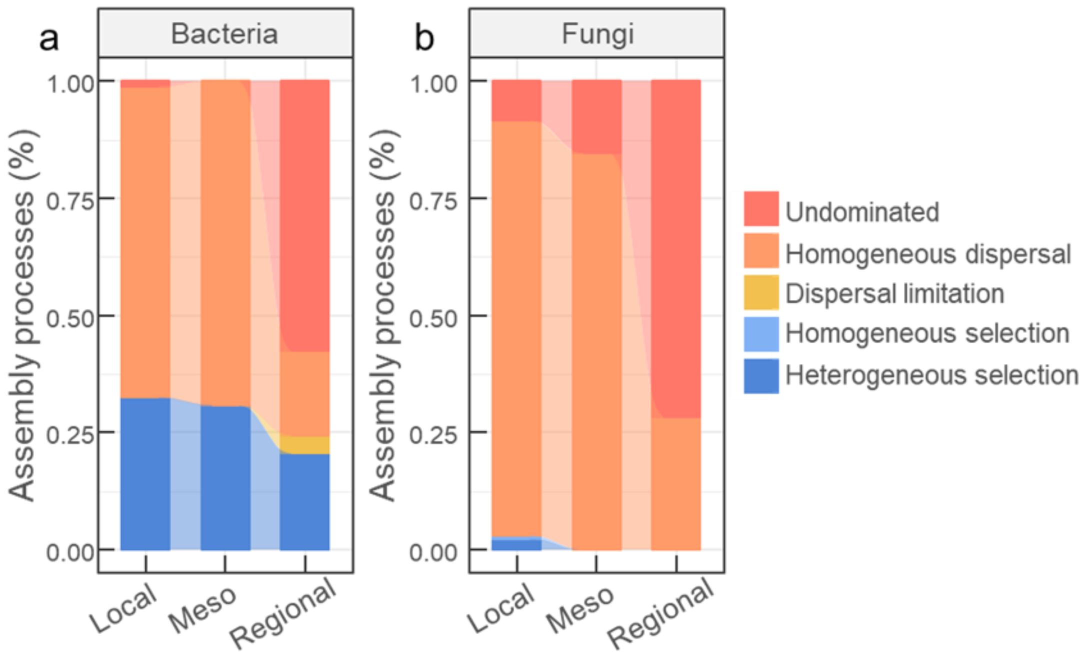

Figure S8 Community assembly processes at different scales in bacteria and fungi. A null model approach was used to calculate the weighted β nearest taxon index (βNTI) and Bray–Curtis-based Raup-Crick (RCbray) values to distinguish the ecological processes that regulate community construction. Deterministic processes include heterogeneous selection (βNTI > 2) and homogeneous selection (βNTI < -2); stochastic processes include homogeneous dispersal (|βNTI| < 2, RCbray < -0.95) and the dispersal limit (|βNTI| < 2, RCbray > 0.95); undominated processes (|βNTI| < 2 and |RCbray| < 0.95) indicate that the composition turnover is not dominated by any single process mentioned above.

Table S1 Environmental factors in each paddy field soil sample.

Plot	Coordinates	pH	DOC (mg/kg)	NO_3^{-}N (mg/kg)	NH_4^+-N (mg/kg)	TN (g/kg)	TP (g/kg)	MAT (°C)	MAP (mm)
HLa	47.579°N, 126.884°E	5.87±0.16	137.19±8.79	0.78±0.80	8.60±1.59	3.03±0.34	1.02±0.08	1.5	556
HLb	47.566°N, 126.892°E	5.84±0.16	144.60±10.26	2.07±2.24	4.84±0.79	3.20±0.28	0.88±0.03	1.5	556
HLc	47.554°N, 126.929°E	6.57±0.32	107.52±5.97	1.60±0.72	5.04±0.66	2.76±0.22	0.83±0.04	1.5	556
CCa	44.207°N, 125.572°E	7.58±0.20	135.33±15.44	5.21±1.40	4.95±0.80	2.49±0.32	0.86±0.05	5.6	520
CCb	44.205°N, 125.576°E	7.96±0.41	127.92±26.84	6.70±1.70	4.69±0.81	2.31±0.23	0.65±0.03	5.6	520
CCc	44.207°N, 125.569°E	8.01±0.12	137.19±11.53	9.58±2.05	4.78±0.59	2.64±0.55	0.81±0.03	5.6	520
SYa	41.516°N, 123.353°E	7.61±0.27	106.92±9.34	1.95±2.73	5.45±0.57	1.34±0.19	0.51±0.04	8.4	399
SYb	41.525°N, 123.322°E	7.17±0.07	99.55±7.64	1.18±1.49	5.35±1.60	1.30±0.12	0.62±0.17	8.4	399
SYc	41.502°N, 123.324°E	6.48±0.23	117.98±9.23	0.70±1.16	5.23±0.80	1.55±0.14	0.46±0.03	8.4	399
YYa	35.003°N, 114.129°E	8.40±0.09	107.52±34.22	23.75±7.00	1.71±0.30	0.98±0.37	0.66±0.06	14.4	550
YYb	35.001°N, 114.052°E	8.45±0.17	92.69±15.43	27.88±13.29	2.68±0.49	1.12±0.24	0.81±0.05	14.4	550
YYc	35.003°N, 114.089°E	8.43±0.17	140.89±17.26	28.19±13.22	2.63±0.54	1.17±0.24	0.79±0.07	14.4	550
FQa	34.958°N, 114.574°E	8.30±0.15	81.57±54.75	25.62±5.20	1.51±0.48	1.33±0.37	0.68±0.06	13.9	615
FQb	34.804°N, 114.457°E	8.44±0.04	127.92±13.37	31.60±7.51	1.65±0.26	1.53±0.30	0.84±0.13	13.9	615
FQc	34.933°N, 114.573°E	8.39±0.08	81.57±31.83	24.39±9.45	1.45±0.55	0.88±0.37	0.61±0.07	13.9	615
LAa	30.230°N, 119.796°E	7.10±0.64	164.10±13.28	20.57±8.14	4.42±0.98	0.36±0.28	0.56±0.05	16.1	783
LAb	30.097°N, 119.766°E	4.93±0.18	199.78±25.83	8.66±8.57	12.44±3.33	1.01±0.17	0.42±0.03	16.1	783
LAc	30.084°N, 119.732°E	5.01±0.19	199.78±18.12	36.18±8.41	6.34±0.63	1.22±0.15	0.49±0.10	16.1	783
QZa	28.834°N, 118.869°E	4.52±0.09	230.10±71.29	3.53±1.46	29.59±11.15	2.46±0.43	0.41±0.09	17.9	1971
QZb	28.083°N, 118.432°E	4.70±0.08	430.63±48.81	3.96±6.31	9.77±1.70	2.58±0.14	0.60±0.07	17.9	1971
QZc	28.855°N, 119.014°E	5.53±0.94	333.70±72.08	3.62±3.65	17.17±5.51	2.05±0.17	0.47±0.05	17.9	1971
ZXa	27.661°N, 117.012°E	5.10±0.20	137.04±18.86	10.84±5.35	5.06±1.48	1.15±0.42	0.44±0.05	17	1934
ZXb	27.755°N, 116.995°E	4.99±0.17	111.80±37.43	23.13±13.69	9.39±13.54	1.60±0.46	0.34±0.03	17	1934
ZXc	27.742°N, 116.976°E	4.82±0.10	124.42±50.39	30.64±7.65	5.45±1.24	1.56±0.35	0.34±0.02	17	1934
JOa	27.067°N, 118.367°E	5.82±0.22	108.19±6.65	27.97±12.48	3.16±0.65	0.86±0.08	1.03±0.20	18.8	1971
JOb	27.050°N, 118.303°E	4.07±0.32	106.39±19.37	3.70±6.22	7.69±4.30	1.03±0.26	0.49±0.09	18.8	1971
JOc	27.083°N, 118.432°E	4.86±0.19	202.07±26.62	0.62±1.30	5.98±1.70	1.74±0.42	0.67±0.09	18.8	1971
CTa	25.861°N, 116.176°E	4.87±0.19	196.16±36.86	31.53±14.79	7.00±2.07	1.77±0.15	0.63±0.10	18.4	1700
CTb	25.882°N, 116.142°E	6.57±1.12	105.16±32.47	24.92±16.80	5.27±1.92	1.66±0.21	0.45±0.13	18.4	1700
CTc	25.866°N, 116.183°E	5.12±0.15	293.33±37.42	3.49±7.89	11.68±2.07	1.84±0.14	0.62±0.03	18.4	1700
HYa	26.856°N, 113.019°E	4.92±0.61	310.53±54.01	16.13±4.16	5.38±0.88	1.60±0.26	0.40±0.01	18.1	1500
HYb	26.898°N, 113.054°E	4.76±0.27	370.78±127.23	16.65±17.81	7.24±2.39	1.68±0.53	0.36±0.06	18.1	1500
HYc	26.813°N, 113.016°E	4.63±0.23	240.25±61.15	28.48±16.89	8.55±7.12	1.93±0.29	0.40±0.06	18.1	1500
QXa	23.634°N, 112.842°E	6.61±0.63	114.94±16.21	7.85±4.15	3.16±0.93	1.58±0.33	0.51±0.03	21.6	2216
QXb	23.618°N, 112.813°E	5.61±0.28	88.49±12.58	4.61±3.63	3.76±0.36	1.49±0.47	0.52±0.05	21.6	2216
QXc	23.685°N, 112.930°E	6.29±0.45	134.58±42.28	0.95±1.10	4.64±0.70	1.94±0.23	0.46±0.05	21.6	2216
HKa	19.897°N, 110.425°E	5.42±0.21	125.36±15.50	0.39±0.29	4.64±0.82	1.24±0.19	0.25±0.02	23.8	1686
HKb	19.841°N, 110.417°E	4.99±0.16	106.92±35.45	24.91±15.21	23.66±14.88	1.45±0.19	0.45±0.09	23.8	1686
HKc	19.758°N, 110.512°E	5.58±0.14	90.33±26.91	1.77±3.02	16.78±15.91	2.01±0.64	0.56±0.09	23.8	1686

MAP: mean annual precipitation, MAT: mean annual temperature, SOM: soil organic matter.

Table S2 Pearson correlation analyses between carbon mineralization and the soil physical or chemical properties.

	DOC	NO_3^--N	NH_4^+-N	TN	TP	pH
r	0.098*	0.021	0.083	-0.048	0.044	0.177***
P	0.042	0.667	0.084	0.316	0.359	<0.001

*** $P < 0.001$; ** $P < 0.01$; * $P < 0.05$

Table S3 Comparison of the α diversities of the soil bacterial and fungal communities at each sampling site.

Sites	Bacteria		Fungi	
	Richness index	Shannon index	Richness index	Shannon index
HL	4233.42 ± 277.41	7.24 ± 0.18	791.15 ± 138.49	4.26 ± 0.73
CC	4112.39 ± 328.60	7.27 ± 0.16	761.55 ± 123.07	4.77 ± 0.67
SY	4511.21 ± 299.81	7.41 ± 0.15	631.55 ± 177.06	4.08 ± 0.71
YY	4148.03 ± 408.95	7.29 ± 0.24	789.67 ± 187.59	4.57 ± 0.69
FQ	4172.00 ± 325.84	7.28 ± 0.22	642.18 ± 140.74	4.13 ± 0.79
LA	4303.55 ± 371.50	7.24 ± 0.22	582.70 ± 123.09	3.73 ± 0.71
QZ	4015.21 ± 469.69	7.14 ± 0.27	677.09 ± 136.98	4.06 ± 0.47
ZX	3269.00 ± 595.84	6.68 ± 0.42	639.88 ± 204.29	4.18 ± 0.71
JO	3829.88 ± 507.98	6.95 ± 0.37	651.24 ± 133.40	4.04 ± 0.71
CT	4333.03 ± 320.29	7.21 ± 0.22	677.27 ± 143.40	4.05 ± 0.58
HY	4256.64 ± 345.00	7.15 ± 0.21	677.94 ± 129.93	4.01 ± 0.59
QX	4059.85 ± 558.91	7.14 ± 0.34	709.39 ± 115.62	4.38 ± 0.5
HK	3458.48 ± 375.32	6.96 ± 0.21	630.03 ± 134.22	4.28 ± 0.55

Table S4 Parameters of the distance decay relationships for the bacterial and fungal communities at the phylum or class levels at four spatial scales.

	Bacteria				Fungi			
	Local	Meso	Regional	Overall	Local	Meso	Regional	Overall
Slope(*v*)	-0.020	-0.025	-0.217	-0.105	-0.060	-0.095	-0.671	-0.208
P value	<0.001	< 0.001	< 0.001	< 0.001	<0.001	<0.001	< 0.001	< 0.001
r square	0.007	0.011	0.127	0.219	0.022	0.079	0.320	0.243

Bacteria

	Local	Meso	Regional	Overall
Acidobacteria	-0.009***	-0.026***	-0.219***	-0.114***
Actinobacteria	-0.011***	-0.019***	-0.223***	-0.112***
Bacteroidetes	-0.029***	-0.026***	-0.306***	-0.171***
Chloroflexi	-0.030***	-0.030***	-0.279***	-0.164***
Firmicutes	-0.023***	-0.010***	-0.113***	-0.087***
Verrucomicrobia	-0.018***	-0.020***	-0.203***	-0.091***
Proteobacteria	-0.019***	-0.026***	-0.178***	-0.087***
α-proteobacteria	-0.019***	-0.014***	-0.175***	-0.082***
β- proteobacteria	-0.008***	-0.023***	-0.121***	-0.084***
γ- proteobacteria	-0.030***	0.006***	-0.239***	-0.125***
δ- proteobacteria	-0.019***	-0.048***	-0.204***	-0.086***

Fungi

	Local	Meso	Regional	Overall
Ascomycota	-0.051***	-0.071***	-0.447***	-0.183***
Basidiomycota	-0.093***	-0.224***	-0.785***	-0.274***
Chytridiomycota	-0.072***	-0.112***	-0.213***	0.003***
Zygomycota	-0.102***	-0.129***	-0.761***	-0.266***

* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$

Table S5 Top 10 microbial taxa of the co-occurrence network based on weight scale among four spatial scales.

Local scale:

IDs	**PCC**	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**Generalist**
B.OTU_117	0.814982	Acidobacteria	Acidobacteria_Gp7	Unclassified	Unclassified	Gp7	
B.OTU_374	0.803222	Acidobacteria	Acidobacteria_Gp16	Unclassified	Unclassified	Gp16	
B.OTU_149	0.798395	Acidobacteria	Acidobacteria_Gp7	Unclassified	Unclassified	Gp7	
B.OTU_435	0.798036	Crenarchaeota	Thermoprotei	Unclassified	Unclassified	Haliangium	
B.OTU_183	0.792578	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Arenimonas	
B.OTU_27	0.789504	Proteobacteria	Betaproteobacteria	Unclassified	Unclassified	Gallionellaceae	
B.OTU_58	0.784711	Unclassified	Unclassified	Unclassified	Unclassified	Conexibacter	
B.OTU_106	0.777052	Firmicutes	Bacilli	Bacillales	Bacillaceae 1	Bacillus	*
B.OTU_29465	0.776457	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingosinicella	
B.OTU_155	-0.77503	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	Leptolinea	
F.OTU_309	0.80638	Basidiomycota	Unclassified	Unclassified	Unclassified	Basidiomycota	
F.OTU_80	0.80624	Basidiomycota	Agaricomycetes	Agaricales	Unclassified	Agaricomycetidae	
F.OTU_147	0.805087	Ascomycota	Sordariomycetes	Sordariomycetes_Incertae sedis_Incertae sedis	Sordariomycetes_Incertae sedis_Incertae sedis_Incertae sedis	Myrmecridium	
F.OTU_183	0.792336	Ascomycota	Unclassified	Unclassified	Unclassified	Rhizophydiales	
F.OTU_65	0.780108	Basidiomycota	Unclassified	Unclassified	Unclassified	Taphrinales	
F.OTU_41	0.777533	Ascomycota	Leotiomycetes	Helotiales	Unclassified	Leotiomycetes	

Meso scale：

IDs	**PCC**	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**Generalist**
B.OTU_38594	0.86854	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Pseudolabrys	*
B.OTU_79	0.85869	Proteobacteria	Alphaproteobacteria	Alphaproteobacteria_incertae_sedis	Unclassified	Rhizomicrobium	*
B.OTU_440	0.85668	Acidobacteria	Acidobacteria_Gp16	Unclassified	Unclassified	Blastochloris	*
B.OTU_1211	0.85551	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Hyphomicrobiaceae	*
B.OTU_213	0.85544	Proteobacteria	Deltaproteobacteria	Unclassified	Unclassified	Desulfomonile	
B.OTU_7	0.84793	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Hyphomicrobiaceae	*
B.OTU_404	0.84625	Acidobacteria	Acidobacteria_Gp3	Unclassified	Unclassified	Gp3	
B.OTU_16916	0.83794	Acidobacteria	Acidobacteria_Gp1	Unclassified	Unclassified	Gp1	
B.OTU_109	0.83787	Acidobacteria	Acidobacteria_Gp1	Unclassified	Unclassified	Gp1	
B.OTU_12760	0.83588	Proteobacteria	Deltaproteobacteria	Unclassified	Unclassified	Geobacteraceae	*
F.OTU_33	0.80022	Unclassified	Unclassified	Unclassified	Unclassified	Chlamydomonadaceae	

Regional scale:

IDs	PCC	Phylum	Class	Order	Family	Genus	Generalist
B.OTU_256	0.50532	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	Steroidobacter*	*
B.OTU_29599	0.43651	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Comamonas*	*
B.OTU_10378	0.41951	Acidobacteria	Acidobacteria_Gp4	Unclassified	Unclassified	Gp4*	*
B.OTU_8262	0.41296	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas*	*
B.OTU_186	0.38843	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae	Streptomyces*	*

B.OTU_42	0.37918	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas*	*
B.OTU_675	0.36482	Actinobacteria	Actinobacteria	Unclassified	Unclassified	Gaiella*	*
B.OTU_204	0.35866	Unclassified	Unclassified	Unclassified	Unclassified	Nitrospira*	*
B.OTU_33074	0.35662	Proteobacteria	Unclassified	Unclassified	Unclassified	Desulfuromonadale*	*
B.OTU_76	0.35578	Proteobacteria	Unclassified	Unclassified	Unclassified	Phenylobacterium*	*
F.OTU_277	0.39507	Basidiomycota	Agaricomycetes	Agaricales	Bolbitiaceae	Panaeolina*	*
F.OTU_194	0.34907	Unclassified	Unclassified	Unclassified	Unclassified	Neochloridaceae*	*
F.OTU_282	0.34283	Unclassified	Unclassified	Unclassified	Unclassified	Scenedesmaceae*	*
F.OTU_18708	0.33698	Ascomycota	Sordariomycetes	Sordariales	Unclassified	Lasiosphaeriaceae*	*
F.OTU_250	0.3277	Unclassified	Unclassified	Unclassified	Unclassified	Oenantheae*	*
F.OTU_181	0.32652	Basidiomycota	Agaricomycetes	Agaricales	Typhulaceae	Sclerotium*	*
F.OTU_291	0.32148	Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	Cordyceps*	*
F.OTU_184	-0.3024	Ascomycota	Dothideomycetes	Pleosporales	Unclassified	Pleosporomycetidae*	*
F.OTU_5	-0.3097	Ascomycota	Dothideomycetes	Pleosporales	Unclassified	Pleosporales*	*
F.OTU_236	-0.3169	Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Dimorphospora*	*

Overall scale:

IDs	PCC	Phylum	Class	Order	Family	Genus
B.OTU_57	0.287305	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
B.OTU_256	0.26814	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	Steroidobacter
B.OTU_29465	0.267937	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingosinicella
B.OTU_675	0.264271	Actinobacteria	Actinobacteria	Unclassified	Unclassified	Streptomyces
B.OTU_10378	0.256388	Acidobacteria	Acidobacteria_Gp4	Unclassified	Unclassified	Terrimonas
B.OTU_38594	0.254731	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Pseudolabrys

B.OTU_30	0.237072	Nitrospira	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira
B.OTU_8262	0.235644	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas
B.OTU_74	0.233084	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	Desulfobacterium
B.OTU_29599	0.230999	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Desulfobacca
F.OTU_277	0.260429	Basidiomycota	Agaricomycetes	Agaricales	Bolbitiaceae	Panaeolina
F.OTU_67	0.241479	Basidiomycota	Unclassified	Unclassified	Unclassified	Scenedesmaceae
F.OTU_194	0.207878	Unclassified	Unclassified	Unclassified	Unclassified	Neochloridaceae
F.OTU_28617	-0.20106	Ascomycota	Dothideomycetes	Pleosporales	Unclassified	Pleosporales
F.OTU_236	-0.211165	Ascomycota	Leotiomycetes	Helotiales	Helotiaceae	Dimorphospora
F.OTU_184	-0.223271	Ascomycota	Dothideomycetes	Pleosporales	Unclassified	Pleosporomycetidae
F.OTU_5	-0.244125	Ascomycota	Dothideomycetes	Pleosporales	Unclassified	Pleosporales

[a] represents a generalist taxon that was detected three or more times among the four-scale samples.