

Figure. S1 Sample strategy with nested design. Samples were taken from three sample sites from Beijing Songshan. At each sites, 21 nested samples were collected at distance of 1, 5, 20, 50 and 70m. At each sample point, five soil cores were collected and composited for microbial and soil analysis.

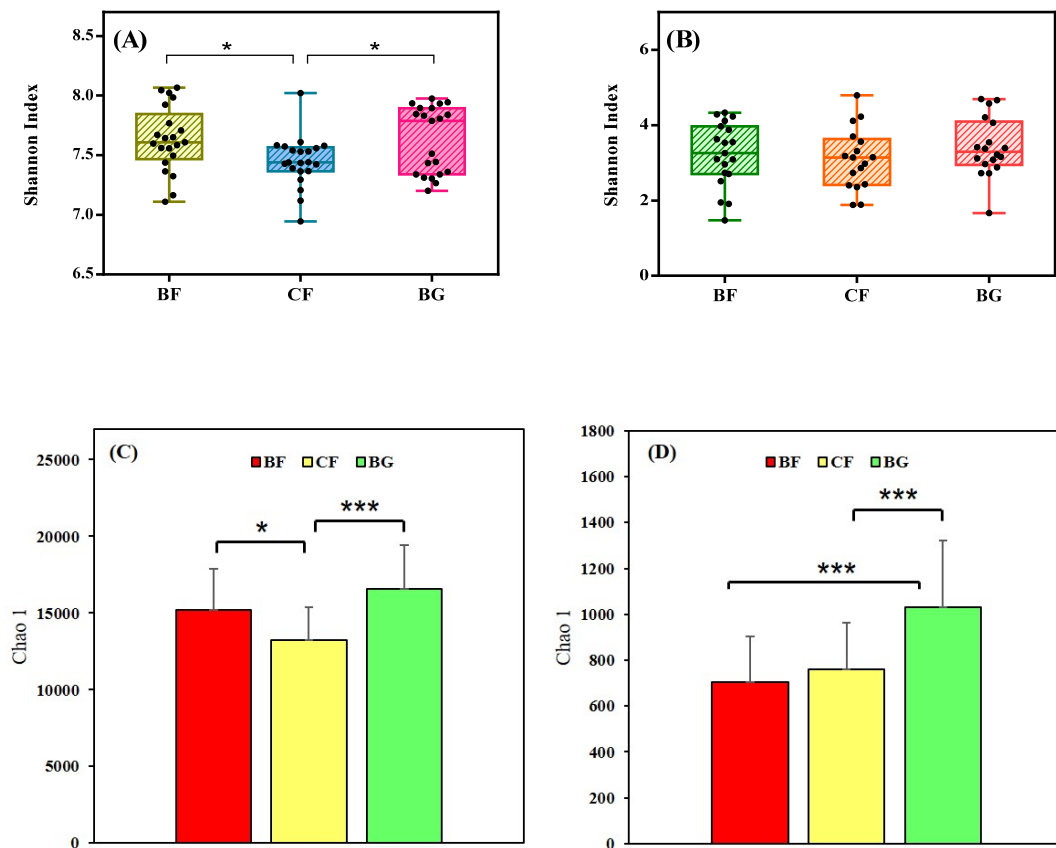


Figure. S2 Box-and-whiskers plots of α diversity for soil prokaryotic and fungal communities across three sample sites. (A) Box-and-whiskers plot of soil prokaryotic communities Shannon Index with significant difference ($*q < 0.05$); (B) Box-and-whiskers plot of soil fungal communities Shannon Index with no significance change. (C) Bar chart of Chao 1 of soil prokaryotic communities with significant difference ($*q < 0.05$); (D) Bar chart of Chao 1 soil fungal communities with no significance change. This indicates soil prokaryotic α diversity significantly decreased from broad-leaved forest to coniferous forest and increased from coniferous forest to alpine meadow.

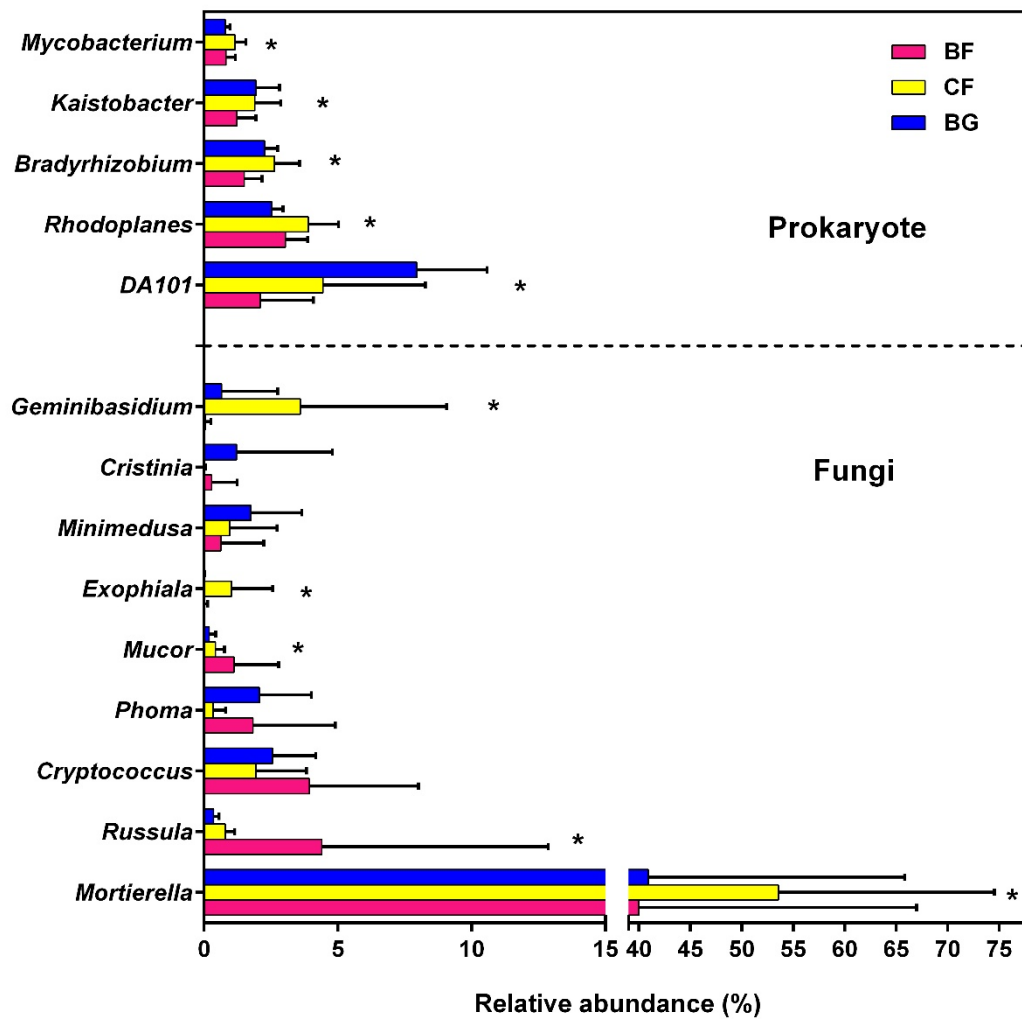


Figure. S3 Relative abundance of dominant genus (>1%) detected in soil microbial communities across three sample sites. Significant results are indicated by $*P < 0.05$.

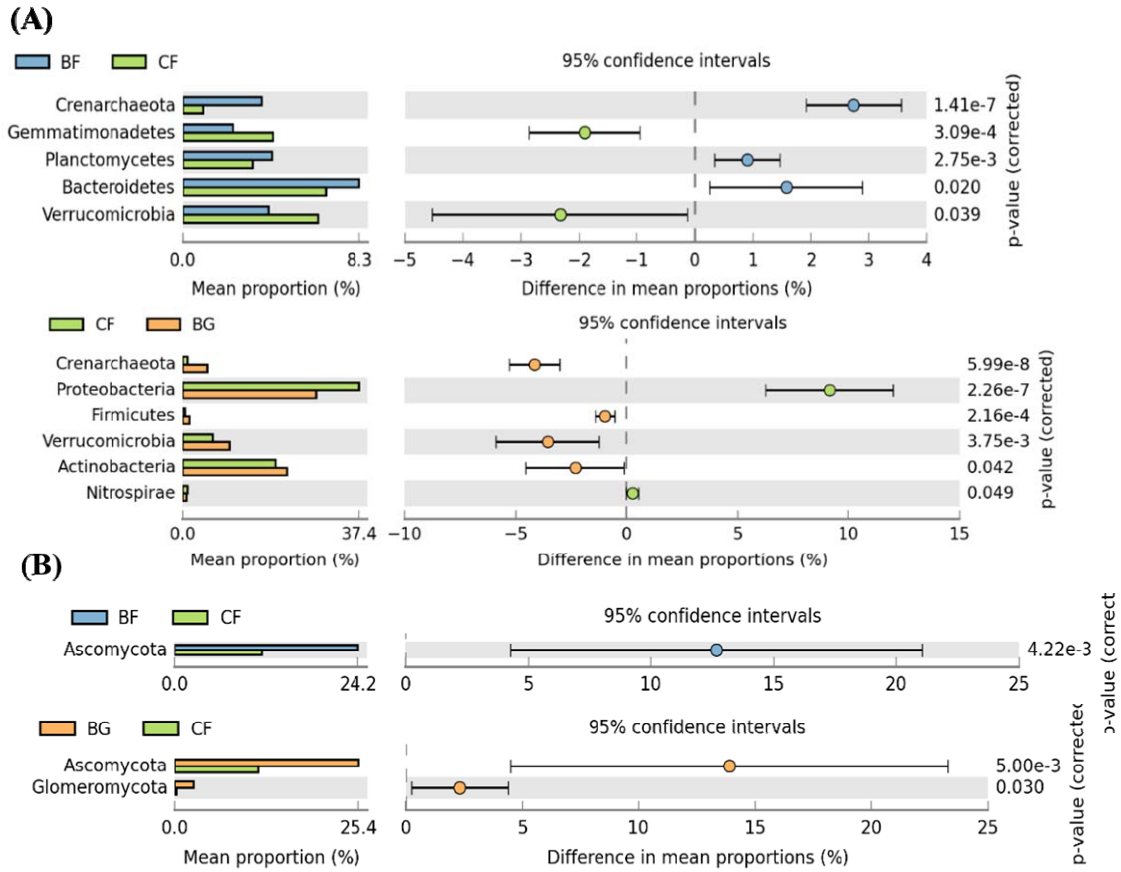


Figure. S4 Relative abundance difference of dominant phylum across two degenerative abundance. (A) Relative abundance difference of soil prokaryotic communities during forest degeneration process; (B) Relative abundance difference of soil fungal communities during forest degeneration process.

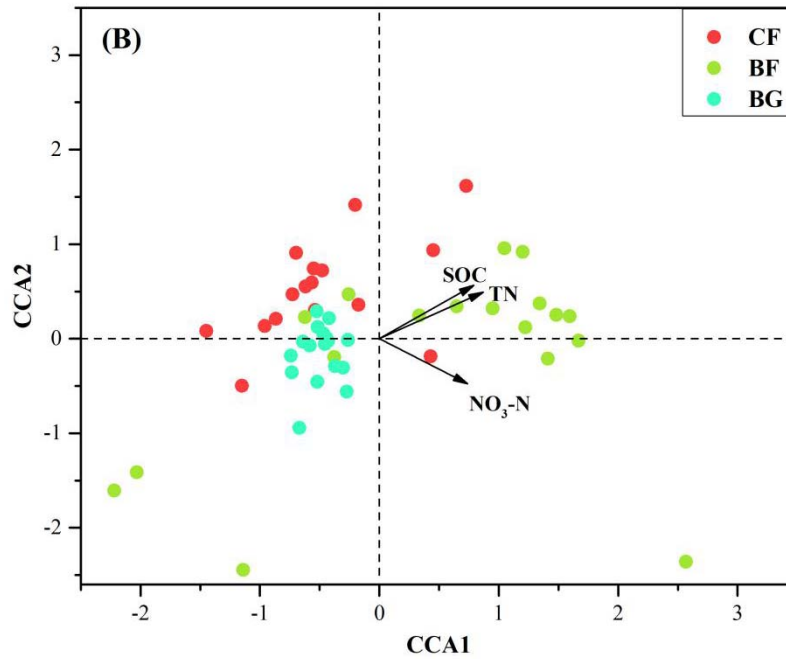
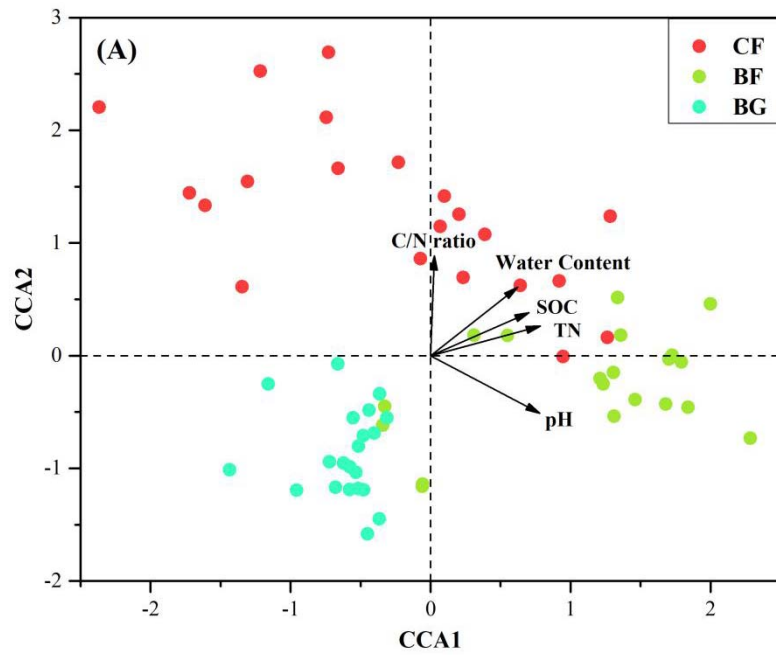


Figure. S5 Canonical Correspondence Analysis plot of prokaryotic and fungal community across three sample sites. (A) CCA plot of soil prokaryotic communities; (B) CCA plot of soil fungal communities. Different land use type were separated clearly by different colors and indicated community structure changed during forest degenerative succession processes. And arrows represent environmental factors related to microbial community structure change during forest degradation processes.

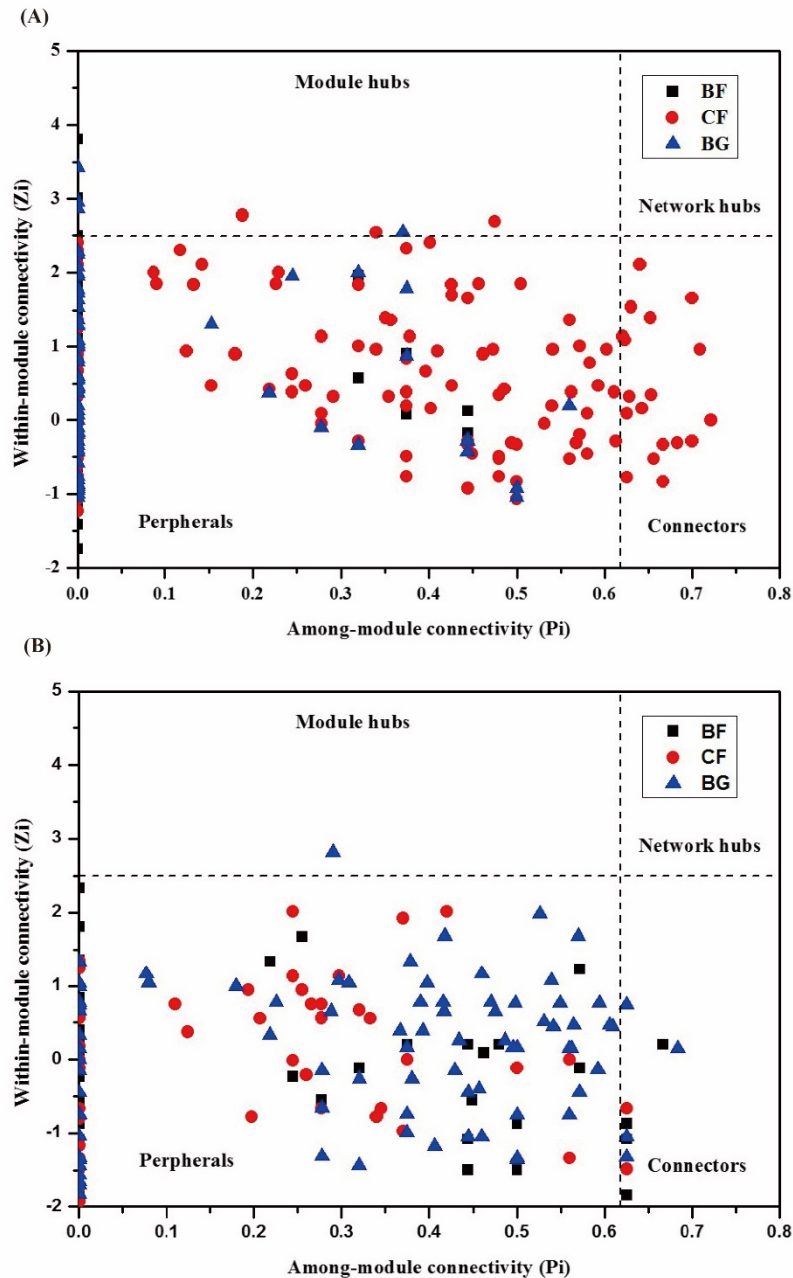


Figure. S6 Z-P plot showing the distribution of OTUs based on their topological roles. Each color represents a kind of land use type, BF, CF, BG. The topological role of each OTU was determined according to the scatter plot of within module connectivity (Z_i) and among-module connectivity (P_i). (A) Z-P plot of prokaryotic community MENs; (B) Z-P plot of fungal community MENs.

Table S1. Soil characteristics (\pm se) of the soil samples across three sample sites.

Site	n	TN [%]	Available P [mg/kg]	NO ₃ -N [mg/kg]	NH ₄ -N [mg/kg]	SOC [%]	Water Content [%]	pH	C/N ratio
BF	21	0.49 \pm 0.23 ^a	2.87 \pm 1.64 ^a	50.23 \pm 24.32 ^a	5.67 \pm 2.89 ^a	6.97 \pm 2.85 ^a	22.12 \pm 9.20 ^a	6.94 \pm 0.37 ^a	11.43 \pm 0.72 ^b
CF	21	0.44 \pm 0.25 ^a	2.85 \pm 2.35 ^a	64.35 \pm 24.66 ^a	4.75 \pm 1.99 ^a	5.88 \pm 3.59 ^a	25.01 \pm 6.72 ^a	6.09 \pm 0.56 ^c	13.05 \pm 1.11 ^a
BG	21	0.34 \pm 0.07 ^b	2.08 \pm 2.51 ^a	38.08 \pm 22.48 ^a	5.33 \pm 3.05 ^a	3.73 \pm 0.82 ^b	14.62 \pm 4.43 ^b	6.42 \pm 0.19 ^b	11.01 \pm 0.26 ^b

Table S2. Analysis of covariance (ANOVA) to test the impact of soil characteristics. Significant results are indicated by * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$. In this table Sum of Squares, degrees of freedom (*df*), mean squares (*MS*), and *F*-values are presented.

		Sum of Squares	df	Mean Square	F	P value
TN	Between Groups	0.254	2	0.127	3.090	0.05*
	Within Groups	2.465	60	0.041		
	Total	2.719	62			
Available P	Between Groups	6.641	2	3.321	0.674	0.52
	Within Groups	221.729	45	4.927		
	Total	228.370	47			
NO ₃ -N	Between Groups	5688.299	2	2844.149	5.022	0.01**
	Within Groups	25482.923	45	566.287		
	Total	31171.222	47			
NH ₄ -N	Between Groups	7.915	2	3.958	0.319	0.73
	Within Groups	745.393	60	12.423		
	Total	753.308	62			
SOC	Between Groups	58.819	2	29.410	4.025	0.02*
	Within Groups	438.450	60	7.307		
	Total	497.269	62			
Water Content	Between Groups	1207.337	2	603.669	12.114	<0.001***
	Within Groups	2990.052	60	49.834		
	Total	4197.390	62			
pH	Between Groups	7.167	2	3.584	21.048	<0.001***
	Within Groups	9.876	58	0.170		
	Total	17.043	60			
C/N ratio	Between Groups	49.021	2	24.510	40.522	<0.001***
	Within Groups	36.292	60	0.605		
	Total	85.313	62			

Table S3. Dissimilarity tests of soil microbial community structure between three sample sites with three different statistical approaches. Significant results are indicated by * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

Dissimilarity tests Method	Prokaryote				Fungi			
	Global test	Pairwise composition			Global test	Pairwise composition		
		BF	CF			BF	CF	
MRPP	0.72(0.001)	CF	0.71(0.001)		0.70(0.001)	CF	0.73(0.001)	
δ (P-value)		BG	0.70(0.001)	0.68(0.001)		BG	0.73(0.001)	0.65(0.001)
ANOSIM	0.41(0.001)	CF	0.35(0.001)		0.31(0.001)	CF	0.28(0.001)	
R (P-value)		BG	0.54(0.001)	0.57(0.001)		BG	0.40(0.001)	0.24(0.001)
PERMANOV	3.04(0.001)	CF	2.95(0.001)		5.76(0.001)	CF	5.50(0.001)	
A		BG	3.78(0.001)	4.03(0.001)		BG	7.01(0.001)	4.47(0.001)
F (P-value)								

Table S4. Topological properties of the empirical molecular networks (MENs) and associated random MENs of soil microbial communities across three sample sites

Topological properties	Prokaryote			Fungi		
	BF	CF	BG	BF	CF	BG
Similarity threshold (S_t)	0.85	0.86	0.84	0.55	0.55	0.55
Total nodes	276	338	326	51	56	97
Total links	254	911	373	136	237	602
R ² of power law	0.992	0.985	0.997	0.255	0.374	0.432
Average Connectivity (avgK)	1.84	5.39	2.288	5.333	8.464	12.412
Average geodesic distance (GD)	0.248	1.89	0.957	3.248	2.528	2.756
Average clustering coefficient (avgCC)	0.107	0.197	0.130	0.365	0.576	0.492
Modularity (No of modules)	0.918 (65)	0.498 (52)	0.841 (76)	0.474 (4)	0.293 (5)	0.339 (4)
Average geodesic distance (GD)	2.887± 0.519	3.076± 0.118	3.018± 0.295	2.554± 0.051	2.211± 0.037	2.234± 0.023
Average clustering coefficient (avgCC)	0.005± 0.003	0.048± 0.007	0.009± 0.004	0.132± 0.023	0.338± 0.028	0.278± 0.016
Modularity (No of modules)	0.849± 0.009	0.381± 0.006	0.727± 0.010	0.320± 0.015	0.199± 0.010	0.179± 0.007

Table S5 Information on the module hubs and connectors of soil microbial MENs

	Sites	Node	Topological roles	Module	Classification		
Prokaryote	BF	OTU_564	Module hubs	A1	Pirellulaceae	(Planctomycetes)	
		OTU_78	Module hubs	A5	Sinobacteraceae	(Proteobacteria)	
		OTU_200	Module hubs	A3	Sinobacteraceae	(Proteobacteria)	
	CF	OTU_83	Module hubs	B1	<i>DA101</i>	(Verrucomicrobia)	
		OTU_271	Module hubs	B3	iii1-15	(Acidobacteria)	
		OTU_90	Module hubs	B1	Koribacteraceae	(Acidobacteria)	
		OTU_19042	Connectors	B4	iii1-15	(Acidobacteria)	
		OTU_100	Connectors	B3	Ellin329	(Proteobacteria)	
		OTU_162	Connectors	B4	iii1-15	(Acidobacteria)	
		OTU_49	Connectors	B1	Solibacterales	(Acidobacteria)	
		OTU_89484	Connectors	B2	Rhodospirillaceae	(Proteobacteria)	
		OTU_878	Connectors	B5	iii1-15	(Acidobacteria)	
		OTU_67843	Connectors	B4	<i>Burkholderiaceae</i>	(Proteobacteria)	
		OTU_27893	Connectors	B1	<i>Candidatus Solibacter</i>	(Acidobacteria)	
		OTU_1348	Connectors	B5	mb2424	(Acidobacteria)	
		OTU_103745	Connectors	B2	iii1-15	(Acidobacteria)	
		OTU_56352	Connectors	B2	iii1-15	(Acidobacteria)	
		OTU_569	Connectors	B3	IS-44	(Proteobacteria)	
		OTU_182	Connectors	B3	Rhodospirillaceae	(Proteobacteria)	
		OTU_14416	Connectors	B2	Gaiellaceae	(Actinobacteria)	
		OTU_471	Connectors	B3	CCU21	(Acidobacteria)	
		OTU_319	Connectors	B3	Solibacterales	(Acidobacteria)	
		OTU_5843	Connectors	B3	Acidimicrobiales	(Actinobacteria)	
		OTU_102471	Connectors	B2	<i>Rubrivivax</i>	(Proteobacteria)	
		OTU_529	Connectors	B1	Gaiellales	(Actinobacteria)	
		BG	OTU_39210	Module hubs	C1	iii1-15	(Acidobacteria)
			OTU_17210	Module hubs	C5	<i>Rhodoplanes</i>	(Proteobacteria)
			OTU_181	Module hubs	C2	0319-6A21	(Nitrospirae)
			OTU_93	Module hubs	C3	<i>Phenylobacterium</i>	(Proteobacteria)
		Fungi	BF	OTU_6404	Connectors	a3	<i>Pleosporales_unidentified</i>
	OTU_24			Connectors	a2	<i>Exophiala</i>	(Ascomycota)
	OTU_369			Connectors	a1	<i>Ascomycota_unidentified</i>	(Ascomycota)
OTU_3158	Connectors			a3	<i>Tetracladium</i>	(Ascomycota)	
CF	OTU_24		Connectors	b1	<i>Exophiala</i>	(Ascomycota)	
	OTU_162		Connectors	b3	<i>Trichosporon</i>	(Basidiomycota)	
BG	OTU_8222		Connectors	c2	<i>Pleosporales_unidentified</i>	(Ascomycota)	
	OTU_101		Connectors	c2	<i>Alternaria</i>	(Ascomycota)	
	OTU_274		Connectors	c3	<i>Clavaria</i>	(Basidiomycota)	
	OTU_4161		Connectors	c4	<i>Mortierella</i>	(Zygomycota)	
		OTU_39	Module hubs	c2	<i>Davidiella</i>	(Ascomycota)	

Table S6 Correlation between dominant genera and soil nutrients SOC and TN. Significant results are indicated by * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

Dominant Genus	SOC		TN	
	<i>r</i>	<i>P</i>	<i>r</i>	<i>P</i>
<i>DA101</i>	-0.306	0.016*	-0.34	0.006**
<i>Rhodoplanes</i>	0.378	0.002**	0.399	0.001***
<i>Kaistobacter</i>	0.328	0.015*	0.355	0.008**
<i>Bradyrhizobium</i>	-0.057	0.656	-0.016	0.900
<i>Mycobacterium</i>	0.226	0.0741	0.158	0.216
<i>Mortierella</i>	0.126	0.919	0.129	0.917
<i>Russula</i>	0.211	0.086	0.260	0.05*
<i>Mucor</i>	0.648	<0.001***	0.639	<0.001***
<i>Geminibasidium</i>	-0.219	0.110	0.263	0.055
<i>Exophiala</i>	-0.270	0.042*	-0.175	0.192