

Supplemental Files

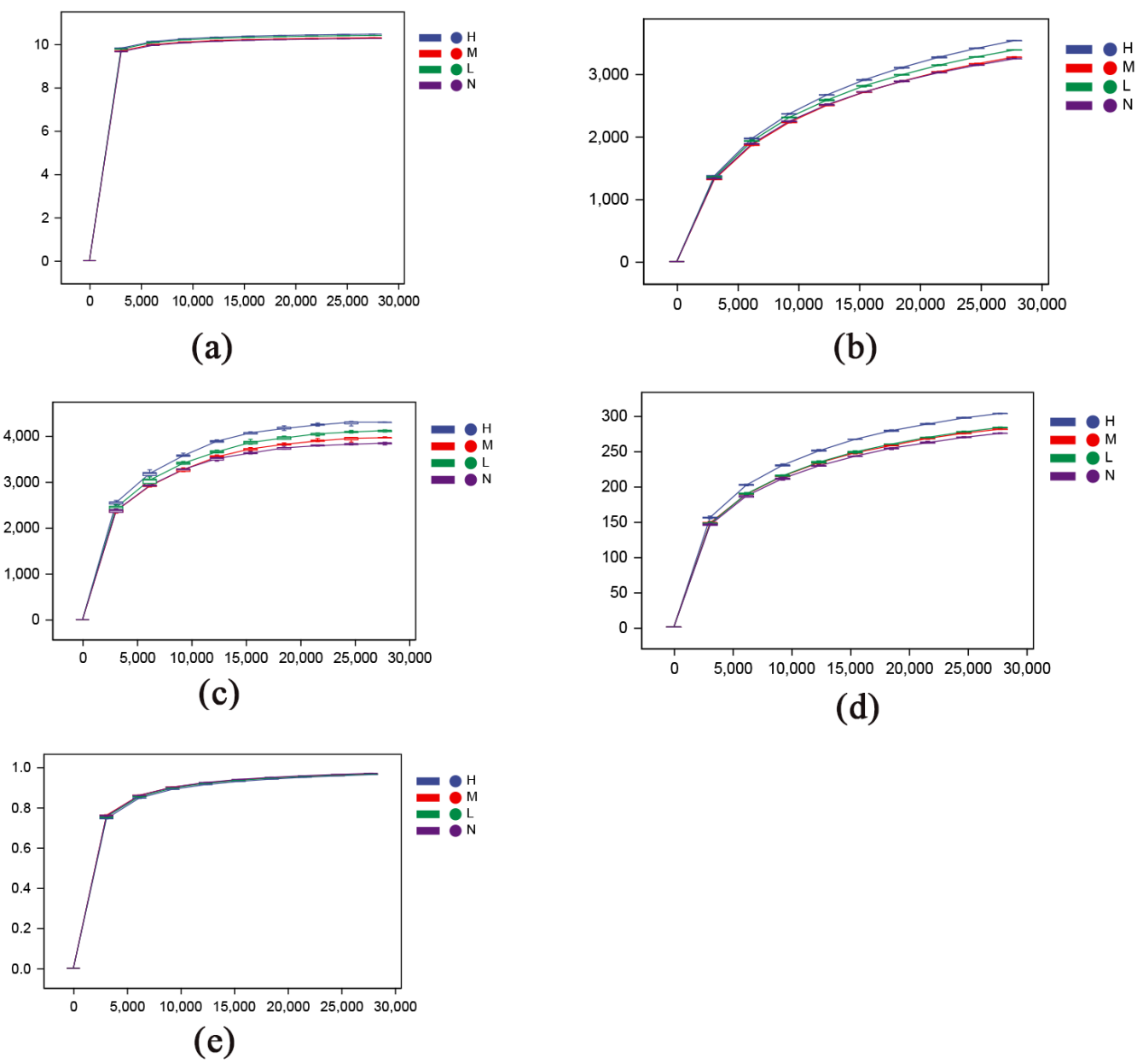


Figure S1. (a-e) Rarefaction curves at Shannon index, observed species, Chao1 index, Good's coverage, and Faith pd values level with different degrees of regeneration, respectively.

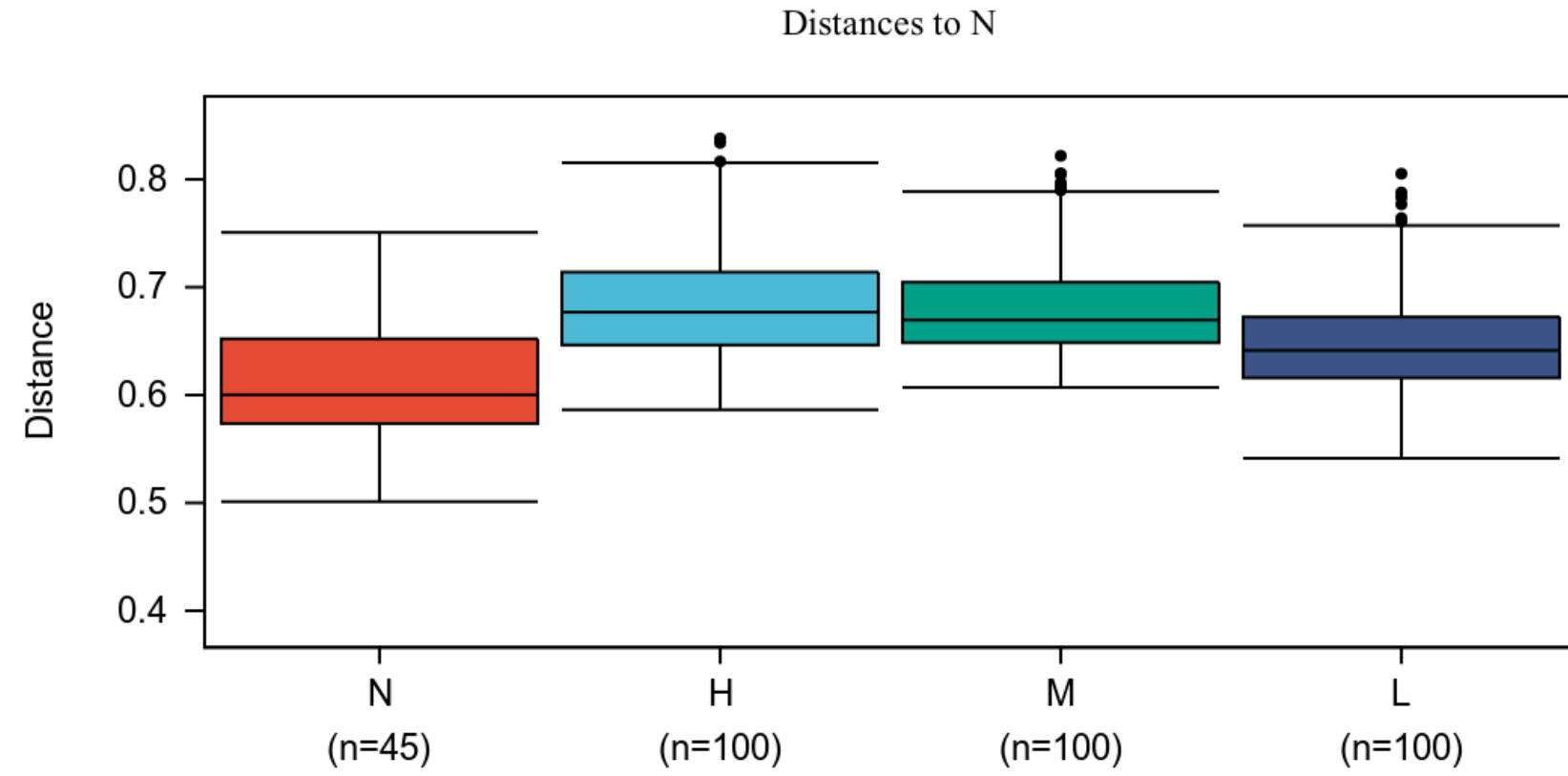


Figure S2. Dissimilarity distance showing the differences in bacterial structure between Inter-group with different degrees of regeneration.

Table S1. Analysis of similarities (ANOSIM) and permutational multivariate analysis of variance (PERMANOVA) based on Bray Curtis distance with different regeneration degree

Group1	Group2	F	P	R ²
all	-	2.487012	0.001	0.404
H	M	1.474092	0.002	0.158
H	L	1.652074	0.004	0.211
H	N	3.325409	0.001	0.606
M	L	1.496214	0.003	0.172
M	N	4.218141	0.001	0.749
L	N	2.659608	0.001	0.521

Table S2. Soil bacterial community co-occurrence network characteristics with different regeneration degree

Group	Number of nodes	Number of edges	Positive edges	Negative edges	avg K	Den.	ACC	AWD	Modularity	GD	N/P cohesion	No. of modules
N	99	664	586(88.25%)	78(11.75%)	13.414	0.137	0.605	10.469	0.562	2.911	13.31%	5
L	100	579	506(87.39%)	73(12.61%)	11.58	0.117	0.588	8.988	0.575	2.962	14.43%	7
M	99	530	478(90.19%)	52(9.18%)	10.707	0.109	0.585	8.238	0.629	2.969	10.88%	7
H	100	502	484(96.41%)	18(3.59%)	10.04	0.101	0.624	8.156	0.681	3.567	3.70%	8

Note: avg K, average degree; Den., density; ACC, average clustering coefficient; AWD, average weighted degree; GD, average path distance; N/P cohesion, proportion of negatively correlated connections

Table S3. Topological properties of potential functional co-occurrence networks of soil bacterial communities with different regeneration degree

Group	Number of nodes	Number of edges	avg. degree	den.	avg.CC	Avg. weighted degree	Mod. degree	Avg. path distance
N	99	2415	48.788	0.498	0.843	41.148	0.258	1.632
L	99	4129	83.414	0.851	0.982	75.968	0.015	1.058
M	100	3344	66.88	0.676	0.85	55.49	0.129	1.369
H	99	3372	68.121	0.695	0.864	57.623	0.093	1.431

Note: avg. degree, average degree; den., density; avg.CC, average clustering coefficient; Avg. weighted degree, average weighted degree; Mod. Degree, modularity; Avg. path distance, average path distance

Table S4. Percent variance explained of the degree of regeneration by each environmental factor.

Name	Explains %	Contribution %	pseudo-F	P
Metabolism	47.2	48.5	34	0.002
avg K	22.1	22.7	26.7	0.002
H. Pielou	8.9	9.1	14.7	0.002
ST	4	4.1	7.9	0.006
INV	1	1.1	5.4	0.022
LAI	1.6	1.7	5	0.036
Density	1.6	1.6	4.3	0.042
Tit Max.	1.1	1.2	3.8	0.05
RLI	0.5	0.5	3.3	0.054
H. Simpson	1.4	1.4	3.1	0.06
H. Shannon	1.2	1.3	2.7	0.098
AK	1.2	1.2	2.5	0.11
Altitude	1	1	2.3	0.13
PHO	0.4	0.4	2.3	0.13
URE	0.4	0.4	2.2	0.136
SW	0.8	0.8	2	0.166
AN	0.2	0.2	1.2	0.318
Tit T	0.2	0.2	1	0.32
H	0.1	0.1	0.7	0.434
AP	<0.1	<0.1	0.5	0.536
Chao1	<0.1	<0.1	0.4	0.55
Slope	<0.1	<0.1	0.4	0.596
CO	<0.1	<0.1	0.2	0.73
Shannon	<0.1	<0.1	0.1	0.772

Table S5. Correlation analysis of several environmental factors with regeneration.

										Tit											H.		H,	H.		avg		
	Number	ATH	Altitude	Slope	Density	H	CO	RLI	LAI	Tit T	Max.	SW	ST	AN	AP	AK	PHO	INV	URE	Shannon	Pielou	Simpson	Shannon	Chao1	N/P	K	Modularity	Metabolism
Number	1																											
ATH	0.057	1																										
Altitude	0.094	-0.302	1																									
Slope	-0.246	-.472**	0.298	1																								
Density	0.065	0.099	0.201	-0.131	1																							
H	0.030	0.089	-0.019	0.306	0.009	1																						
CO	0.023	-0.077	-0.215	-0.172	-.614**	-0.096	1																					
RLI	-0.124	-0.044	-0.183	-0.044	-.657**	-0.031	.949**	1																				
LAI	0.069	0.050	0.153	0.090	.629**	0.034	-.958**	-.958**	1																			
Tit T	-0.122	-0.221	.336*	-0.001	.469**	-0.101	-0.068	-0.080	-0.024	1																		
Tit Max.	-0.040	-0.250	0.248	0.052	.406**	-0.229	-0.090	-0.145	0.041	.752**	1																	
SW	-0.188	-0.138	.352*	0.271	-.365*	0.166	0.138	0.259	-0.199	-0.135	-.411**	1																
ST	0.136	-.465**	0.013	0.126	-0.140	-0.069	.509**	.438**	-.505**	-0.017	0.014	0.167	1															
AN	-.406**	-0.293	.366*	.408**	-0.228	0.033	-0.071	0.006	0.003	0.023	-0.036	.473**	-0.051	1														
AP	-0.142	0.044	-0.228	0.124	0.061	0.158	0.024	0.044	0.007	0.177	0.085	-0.182	-0.137	-0.076	1													
AK	-0.178	0.036	0.080	0.140	0.030	0.104	-0.068	-0.059	-0.001	-0.005	-0.194	0.145	-0.047	.351*	-0.171	1												
PHO	-.327*	-0.104	-0.005	0.000	0.099	-0.041	-0.079	-0.061	0.109	-0.032	-0.125	-0.042	-0.053	0.237	0.264	0.269	1											
INV	-0.067	0.047	-.371*	-0.120	-0.220	0.106	-0.064	-0.080	0.099	-.322*	-0.290	-0.026	0.038	-0.183	0.250	-0.099	0.125	1										
URE	-0.112	-0.014	-0.070	-0.110	0.119	-.357*	-0.234	-0.239	0.211	0.282	0.106	-0.153	-.391*	-0.011	0.096	0.269	0.258	-0.007	1									
H. Shannon	-0.129	0.174	.356*	-0.042	0.247	-0.109	0.086	0.112	-0.087	0.084	-0.046	0.202	0.177	0.040	-0.086	0.016	0.071	-0.312	-0.308	1								
H. Pielou	-.350*	.421**	0.140	0.028	0.033	0.212	0.004	0.119	-0.126	0.134	0.007	0.201	-0.163	0.195	0.126	0.120	0.110	-0.308	-0.238	.510**	1							
H. Simpson	-0.044	-0.005	.387*	0.044	0.219	-0.154	0.064	0.132	-0.048	0.160	-0.019	0.227	0.185	0.033	0.085	-0.159	0.101	-0.258	-0.285	.886**	.389*	1						
Shannon	0.191	-0.067	0.084	-0.115	-0.024	-0.029	0.139	0.133	-0.057	-0.056	-0.072	0.129	0.166	-0.177	0.104	-.583**	-0.115	-0.139	-0.216	0.221	0.036	.380*	1					
Chao1	0.280	0.122	0.168	-0.301	0.038	0.082	0.158	0.136	-0.110	0.027	-0.034	0.084	0.065	-0.220	0.101	-.368*	-0.196	-0.193	-.364*	.390*	0.230	.460**	.772**	1				
N/P	-.947**	-0.142	-0.181	0.202	-0.117	0.060	0.059	0.191	-0.138	0.116	-0.013	0.147	-0.057	.381*	0.274	0.139	.433**	0.129	0.057	0.086	.385*	0.060	-0.148	-0.227	1			
avg K	-.715**	-.551**	0.284	.569**	0.018	0.155	-0.029	0.077	-0.068	.345*	0.154	.371*	0.136	.568**	0.125	0.257	0.210	-0.168	0.016	0.063	0.188	0.087	-0.170	-0.250	.726**	1		
Modularity	.891**	.339*	-0.010	-.349*	0.034	-0.114	-0.008	-0.131	0.089	-0.229	-0.024	-0.257	-0.018	-.477**	-0.262	-0.207	-.428**	-0.023	-0.069	-0.109	-.326*	-0.118	0.148	0.231	-.949**	-.890**	1	
Metabolism	.964**	0.127	0.181	-0.238	0.161	-0.047	-0.082	-0.221	0.176	-0.107	-0.036	-0.143	0.050	-.391*	-0.223	-0.126	-.340*	-0.108	-0.021	-0.047	-.380*	0.000	0.175	0.255	-.987**	-.723**	.922**	1

The main variables measured in each sample plot were as follows: (1) topographic factors (altitude, slope); (2) stand structure factors (Density, diameter at breast height, height(H)); (3) light factors (canopy opening (CO), relative light intensity (RLI), and leaf area index (LAI) in the sample plot); (4) soil characteristics: soil moisture (SW), soil temperature (ST), available nitrogen (AN), available phosphorus (AP), available potassium (AK), phosphatase (PHO), invertase (INV), urease (URE); (5) litter characteristics: litter thickness (Tit T), and their maximum water holding capacity (Tit Max.); (6) herbaceous diversity: Shannon index (H. Shannon), Simpson index (H. Simpson), evenness index (H. Pielou); (7) Soil bacteria composition and network structure: Shannon index(Shannon), Chao1, N/P cohesion(N/P), average degree(avg K), Modularity, metabolic functions(Metabolism)

Table S6. Percent variance explained of the extent of regeneration by each soil bacterial community.

Phylum	Explains %	Contribution %	pseudo- F	P
Nitrospirae	9.2	16.4	3.8	0.022
Latescibacteria	8.4	15.1	4	0.014
Acidobacteria	6	10.8	2.6	0.098
Actinobacteria	4.9	8.8	2.4	0.078
Patescibacteria	4.6	8.2	2.4	0.09
Entotheonellaeota	4.2	7.4	2.1	0.122
Dependentiae	3.9	7	2.1	0.116
Firmicutes	3.7	6.7	2	0.134
Gemmatimonadetes	2.3	4.1	1.3	0.332
Rokubacteria	2	3.7	1.1	0.332
Bacteroidetes	1.8	3.3	1	0.372
Planctomycetes	1.7	3.1	0.9	0.38
Verrucomicrobia	1.6	2.9	0.9	0.46
Chloroflexi	0.9	1.6	0.5	0.572
Proteobacteria	0.5	0.8	0.2	0.778

Table S7. Correlation analysis of soil bacterial communities at phyla levels with regeneration

	Number	ATH	Proteo.	Actino.	Acido.	Chlo.	Rok.	Gem.	Verru.	Bac.	Firm.	Nitro.	Pates.	Lates.	Planct.	Dep.	Ento.
Number	1																
ATH	0.057	1															
Proteo.	0.077	0.119	1														
Actino.	0.030	-0.068	-0.136	1													
Actino.	0.045	-0.254	-0.286	-.756**	1												
Chlo.	-0.119	0.198	-.675**	-.328*	.332*	1											
Rok.	-.313*	-0.079	-.323*	-.657**	.653**	.471**	1										
Gem.	-0.109	0.238	-.570**	-.359*	.334*	.737**	.395*	1									
Verru.	0.165	-0.029	-0.156	-0.172	0.249	-0.116	0.089	0.121	1								
Bac.	0.230	0.012	0.066	0.049	0.100	-0.243	-0.189	-0.167	-0.086	1							
Firm.	-0.157	0.014	0.021	.518**	-.674**	-0.218	-.379*	-0.287	-0.164	-0.211	1						
Nitro.	-.423**	-0.068	-0.129	-.458**	.416**	.365*	.718**	0.098	-0.215	-0.235	-0.252	1					
Pates.	-.395*	0.067	-0.195	-0.042	0.017	0.194	-0.163	0.277	0.056	.352*	0.029	-.454**	1				
Lates.	-0.186	0.236	-.392*	-.518**	.450**	.736**	.642**	.677**	-0.241	-0.100	-.410**	.501**	0.090	1			
Planct.	0.012	0.019	-0.239	-0.284	.381*	0.079	0.227	.325*	.600**	-0.202	-0.249	0.049	-0.036	0.171	1		
Dep.	-0.002	0.229	-0.214	-0.292	0.055	.444**	0.266	.456**	-0.086	0.071	0.098	0.076	.412**	.347*	0.033	1	
Ento.	0.230	0.141	-0.307	-0.134	0.227	.327*	0.267	.403**	0.000	0.048	-.338*	0.084	-0.099	.417**	.335*	.357*	1

Abbreviations of soil bacterial communities at phyla level are as follows: Proteo., Proteobacteria; Actino., Actinobacteria; Acido., Acidobacteria; Chlo., Chloroflexi; Rok., Rokubacteria; Gem., Gemmatimonadetes; Verru., Verrucomicrobia; Bac., Bacteroidetes; Firm., Firmicutes; Nitro., Nitrospirae; Pates., Patescibacteria; Lates., Latescibacteria; Planct., Planctomycetes; Dep., Dependientiae; Ento., Enttheonellaeota

Table S8. SEM model fit indices for all factors

Statistics		Absolute fit index			Baseline Comparisons				
Fitting Index	χ^2 test(χ^2)	Chi-square/ p -value degree of Freedom(χ^2 /df)	Goodness of Fit Index (GFI)	Root Mean Square Error of Approximation (RMSEA)	Normed Fit Index (NFI)	Comparative Fit Index (CFI)	Incremental Fit Index (IFI)	Relative Fit Index (RFI)	Non-normed Fit Index (TLI)
	95.882	1.88	0.918	0.027	0.924	0.958	0.957	0.972	0.979
Fitting standards	The smaller the better	<5	≥ 0.80	<0.08	≥ 0.80	≥ 0.80	≥ 0.80	≥ 0.80	≥ 0.80
Ideal value	The smaller the better	<3	>0.90	<0.05	>0.90	>0.90	>0.90	>0.90	>0.90

Table S9. Indirect, direct, and total effects between the observed variables in the SEM (standardized results)

Observed variables		Direct effects	Indirect effects	Total effects
Bacteria	Regeneration	0.84	-	0.84
Altitude	Regeneration	0.01	0.378	0.388
Soil	Regeneration	-0.17	-0.697	-0.867
Herb	Regeneration	-0.03	-0.235	-0.265
Tit T	Regeneration	0.003	-0.126	-0.123
Regeneration	avg K	-0.70	-	-0.70
Soil	Bacteria	-0.83	-	-0.83