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Table S1. Interactive effects of afforestation and depth in top and deep soil layers. The chi-square and P-values were obtained for the interactions of afforestation and depth based on a generalized linear mixed effects model by using lme4 package. Target variables included soil physicochemical properties, alpha diversity, soil functions, dominant phyla, and families.

variable	Top soils (0-120 cm)		Deep soils (120-500 cm)	
	Chisq	*P.value*	*Chisq*	*P.value*
SOC	26.5836	**<0.0001**	6.7963	0.2362
TN	28.6466	**<0.0001**	3.4446	0.6318
C/N	6.6517	0.0839	2.1346	0.8302
OP	2.2584	0.5205	1.7675	0.8803
NH_4^+	7.784	0.0507	4.7339	0.4492
NO_3^-	14.3954	**0.0024**	14.1796	**0.0145**
pH	0.9899	0.8037	2.0167	0.8468
Moisture	24.168	**<0.0001**	28.6598	**<0.0001**
Observed	3.0712	0.3808	1.6873	0.8905
Shannon	3.0496	0.3840	0.7005	0.9829
C_{min}	8.2608	0.0409	10.7395	0.0568
N_{min}	2.4786	0.4792	13.407	**0.0198**
Vector length	6.5455	0.0879	31.4628	**<0.0001**
Vector angle	4.9277	0.1772	3.2801	0.6569
Multifunctionality	4.0492	0.2562	7.2639	0.2017
p_GAL15	9.5803	**0.0225**	5.6336	0.3435
p_Nitrospirota	3.8679	0.2761	4.5276	0.4762
p_Gemmatimonadota	4.271	0.2337	6.1278	0.2940
p_Verrucomicrobiota	6.0426	0.1096	3.3727	0.6427
p_Proteobacteria	0.3404	0.9523	4.7085	0.4525
p_Bacteroidota	1.9389	0.5852	3.7514	0.5857
p_Firmicutes	2.3522	0.5026	12.377	**0.0300**
p_Acidobacteriota	5.0429	0.1687	10.5415	0.0613
p_Actinobacteriota	16.1223	**0.0011**	6.4447	0.2653
p_Chloroflexi	2.4735	0.4801	1.118	0.9525
f_Gaiellaceae	4.2466	0.2360	2.1248	0.8316
f_GAL15	9.5803	**0.0225**	5.6336	0.3435
f_S085	6.4744	0.0907	4.7038	0.4531
f_JG30.KF.CM45	13.9775	**0.0029**	1.5532	0.9069
f_KD4.96	1.989	0.5747	2.0442	0.8430
f_Gitt.GS.136	2.5591	0.4647	9.9547	0.0765
f_P2.11E	9.605	0.0222	2.4822	0.7792
f_Pedosphaeraceae	7.8602	**0.0490**	3.6682	0.5981
f_Chthoniobacteraceae	5.6676	0.1290	3.2788	0.6571
f_Nitrospiraceae	3.8679	0.2761	4.5276	0.4762
f_Gemmatimonadaceae	4.2699	0.2338	6.0934	0.2972

f_Vicinamibacteraceae	0.6001	0.8964	5.5451	0.3530
f_Paenibacillaceae	2.4098	0.4918	31.8597	**<0.0001**
f_Bryobacteraceae	4.9313	0.1769	1.8656	0.8674
f_Solibacteraceae	18.2596	**0.0004**	8.5728	0.1274
f_Polyangiaceae	2.8483	0.4156	2.9266	0.7113
f_BIrii41	4.6985	0.1953	2.0648	0.8401
f_Haliangiaceae	1.1558	0.7636	6.7615	0.2390
f_Methyloligellaceae	7.4773	0.0581	1.6091	0.9001
f_Beijerinckiaceae	0.5461	0.9086	6.5017	0.2604
f_Xanthobacteraceae	4.7836	0.1883	7.0563	0.2165
f_Hyphomicrobiaceae	5.0557	0.1678	3.3891	0.6402
f_Rhizobiales_Incertae_Sedis	3.4186	0.3315	2.5139	0.7744
f_Rhizobiaceae	1.9124	0.5908	8.8052	0.1171
f_Hyphomonadaceae	0.5841	0.9001	4.6285	0.4629
f_Sphingomonadaceae	0.491	0.9209	2.038	0.8439
f_Caulobacteraceae	4.2417	0.2365	5.1226	0.4011
f_Rhodobacteraceae	8.5997	**0.0351**	5.9658	0.3096
f_Dongiaceae	6.0632	0.1086	1.8575	0.8685
f_Reyranellaceae	6.8721	0.0761	3.1533	0.6764
f_Solimonadaceae	5.6451	0.1302	3.3436	0.6472
f_Hymenobacteraceae	2.7456	0.4325	7.4252	0.1909
f_Microscillaceae	2.3306	0.5067	3.8728	0.5679
f_Chitinophagaceae	4.7719	0.1893	2.0611	0.8406
f_Blastocatellaceae	3.9887	0.2627	5.5244	0.3553
f_Pyrinomonadaceae	11.5749	**0.0090**	4.0932	0.5361
f_0319.7L14	8.8271	**0.0317**	20.0395	**0.0012**
f_MB.A2.108	4.282	0.2326	12.2323	**0.0317**
f_Rubrobacteriaceae	4.6391	0.2002	4.919	0.4258
f_Ilumatobacteraceae	3.8126	0.2824	1.5556	0.9066
f_IMCC26256	7.8027	0.0503	2.4826	0.7791
f_Streptomycetaceae	9.8772	**0.0196**	4.0909	0.5364
f_Nocardioidaceae	15.3536	**0.0015**	2.3437	0.7998
f_Pseudonocardiaceae	4.671	0.1975	10.7637	0.0563
f_Dietziaceae	3.0118	0.3898	2.6229	0.7579
f_Mycobacteriaceae	2.2963	0.5132	15.5643	**0.0082**
f_Micrococcaceae	7.7261	0.0520	5.5912	0.3480
f_Micromonosporaceae	2.2197	0.5281	5.1293	0.4003
f_Geodermatophilaceae	1.252	0.7406	3.0377	0.6942

Table S2. Mantel tests of soil physicochemical properties against bacterial community composition (ASV table), phylogenetic turnover (β-nearest taxon index, βNTI) and Bray-Curtis-based Raup-Crick (RC$_{bray}$) of bacterial communities in top and deep soil layers.

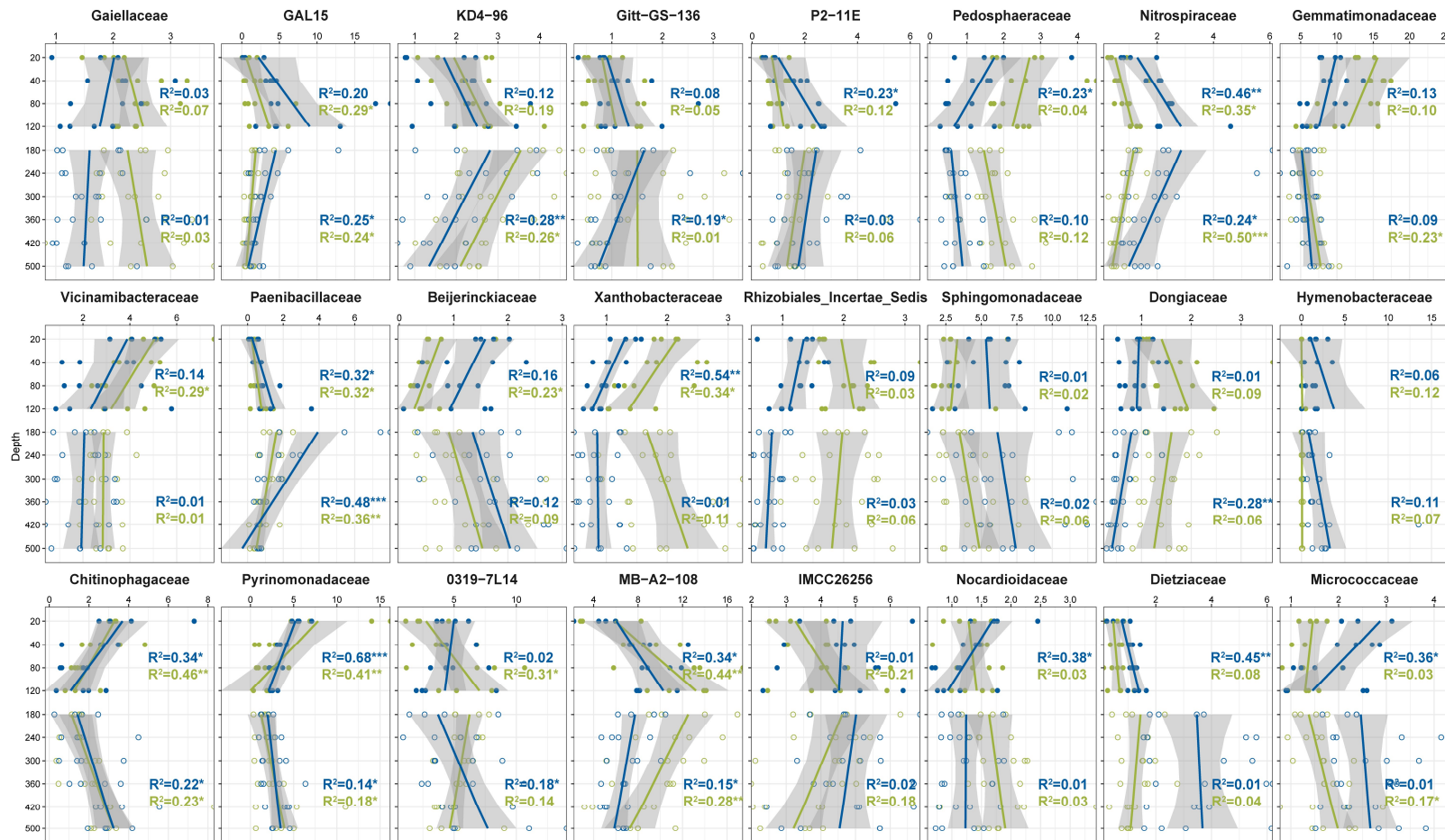|	ASV		βNTI		RC$_{bray}$	
	Top	Deep	Top	Deep	Top	Deep
SOC	**0.451*****	0.010	0.092	-0.011	**0.402*****	0.041
TN	**0.429*****	-0.017	0.057	0.020	**0.378****	0.023
OP	0.140	0.048	-0.083	0.071	**0.141***	0.088
C/N	**0.190***	-0.053	**0.263****	-0.010	**0.161***	0.003
NH$_4^+$	**0.253****	**0.191****	0.147	**0.158****	**0.132***	**0.206*****
NO$_3^-$	**0.433*****	**0.367****	0.141	**0.284*****	**0.420*****	**0.329*****
pH	**0.173****	-0.070	0.082	-0.058	0.090	0.008
Moisture	0.036	**0.639*****	0.113	**0.353*****	**0.188***	**0.632*****
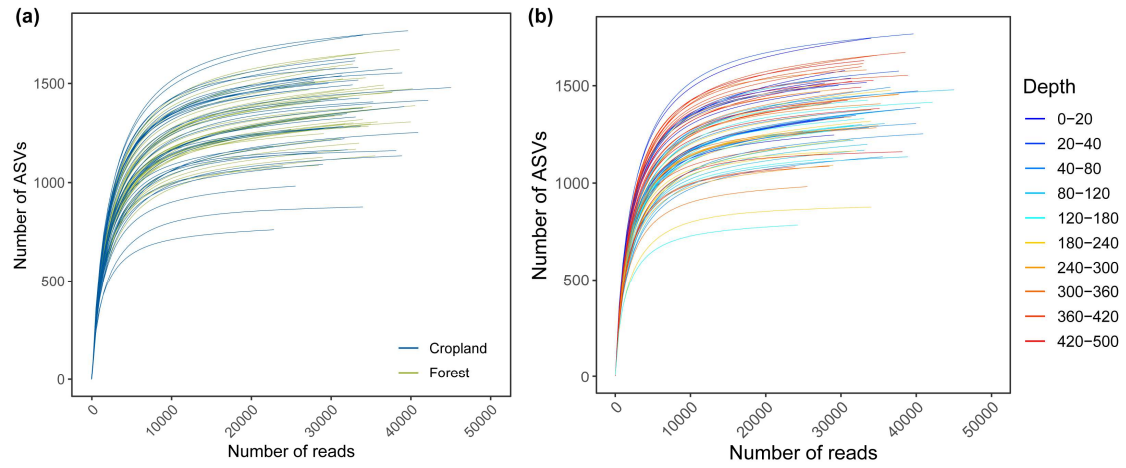
Figure S1. Rarefaction curves showing the saturation of ASV saturation. Rarefaction curves are labeled with (a) afforestation and (b) depth.

Figure S2. Variation in soil properties, functions, alpha diversity, community composition and dominant phyla with depth. The lines denote the least-squares linear regressions across soil depth, with 95% confidence intervals. The response patterns of most measured parameters to afforestation (cropland [blue] vs. forest [light green]) were markedly different between top (0-120 cm) and deep (120-500 cm) layers. R^2 is explained variance. Asterisks denote *, P < 0.05, ** P < 0.01, and *** P < 0.001.

Figure S3 Variation in dominant families (relative abundance greater than 1%) with depth. The lines denote the least-squares linear regressions across soil depth, with their 95% confidence intervals. The response patterns of most measured parameters to afforestation (cropland [blue] vs. forest [light green]) were markedly different between top (0-120 cm) and deep (120-500 cm) layer. R^2 is explained variance. Asterisks denote * P < 0.05, ** P < 0.01, and *** P < 0.001.
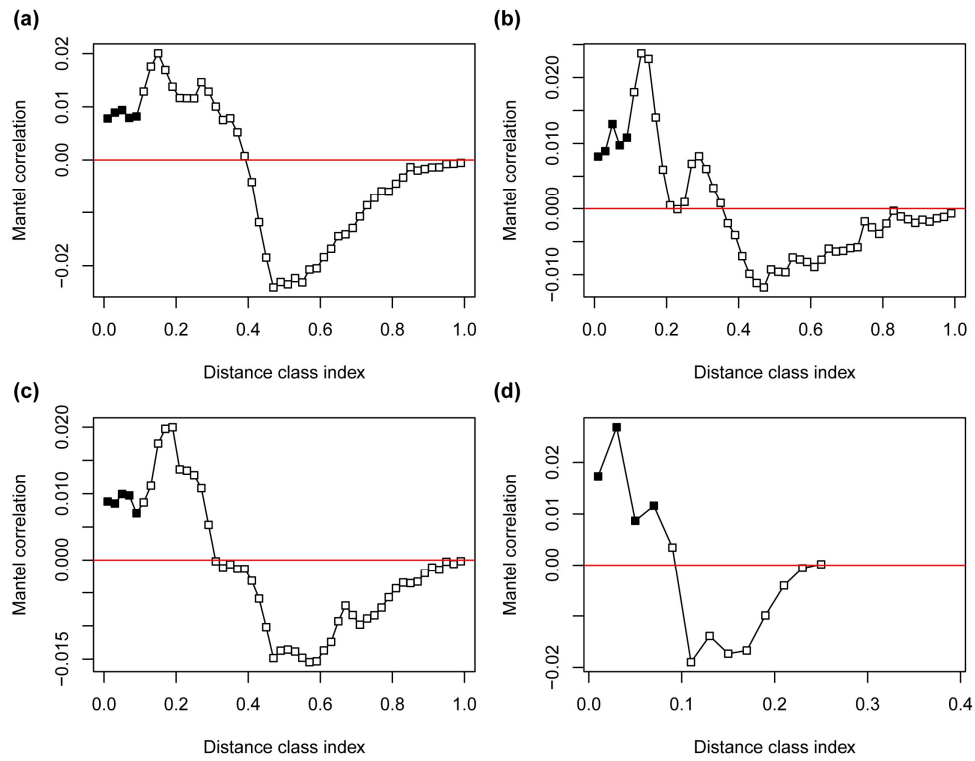
Figure S4. Phylogenetic Mantel correlogram for: top layer in cropland **(a)**, deep layer in cropland **(b)**, top layer in forest **(c)**, and deep layer in forest **(d)**. The plots show significant phylogenetic signal across relatively short phylogenetic distances. Solid circles denote significant correlations ($P < 0.05$).
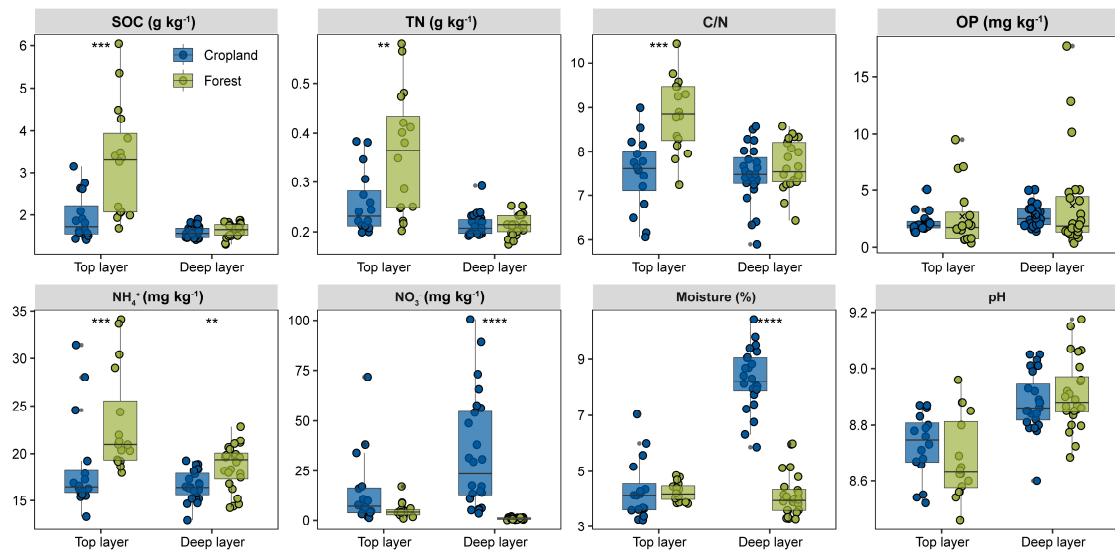
Figure S5. Soil physicochemical properties affected by afforestation and soil depth (top vs. deep layers). Significant differences were based on the Wilcoxon test. Asterisks denote * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$. Legend: SOC, soil organic carbon; TN, soil total nitrogen; C/N, ratio of carbon to nitrogen; OP, available phosphorus; NH_4^+, ammonium; NO_3^-, nitrate; pH, soil pH; and Moisture, soil moisture.
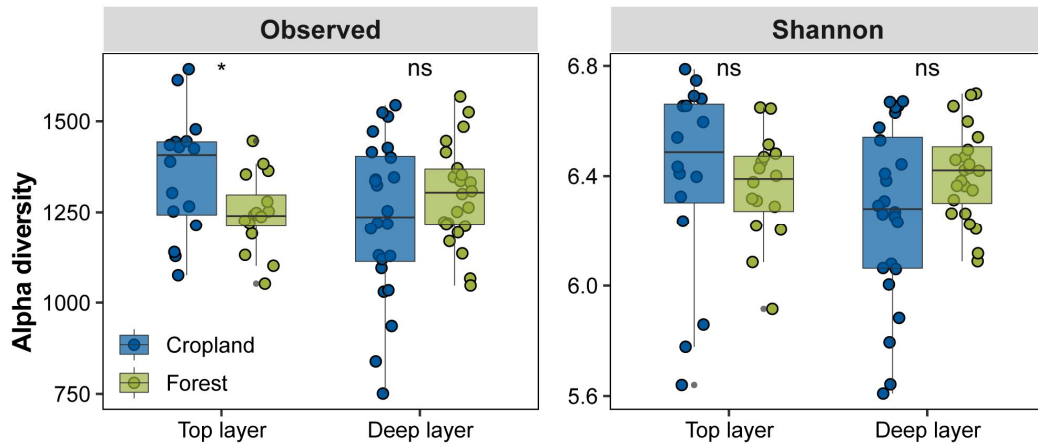
Figure S6. Soil bacterial alpha diversity affected by afforestation and soil depth (top vs. deep layer). Significant differences were based on the Wilcoxon test. Asterisks denote * P < 0.05, ** P < 0.01 and *** P < 0.001.
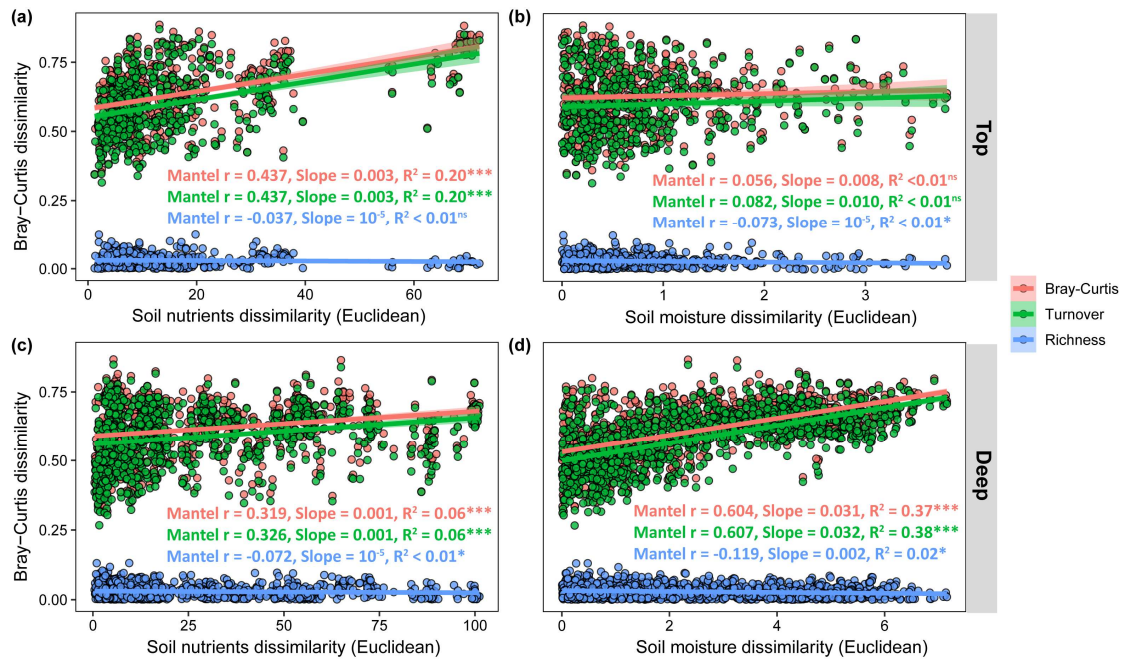
Figure S7. Relationship of beta-diversity of microbial communities (Bray-Curtis dissimilarity) to soil nutrients (**a** and **c**) and moisture (**b** and **d**) dissimilarities (Euclidean distance) in top and deep layers after afforestation, respectively. Soil nutrients include SOC, TN OP, NH_4^+ and NO_3^-. The beta-diversity (Bray-Curtis dissimilarity) was partitioned into two components, the abundance gradient (richness) and the balanced variation (turnover), using the bray.part function of the betapart package. Asterisks denote * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$.
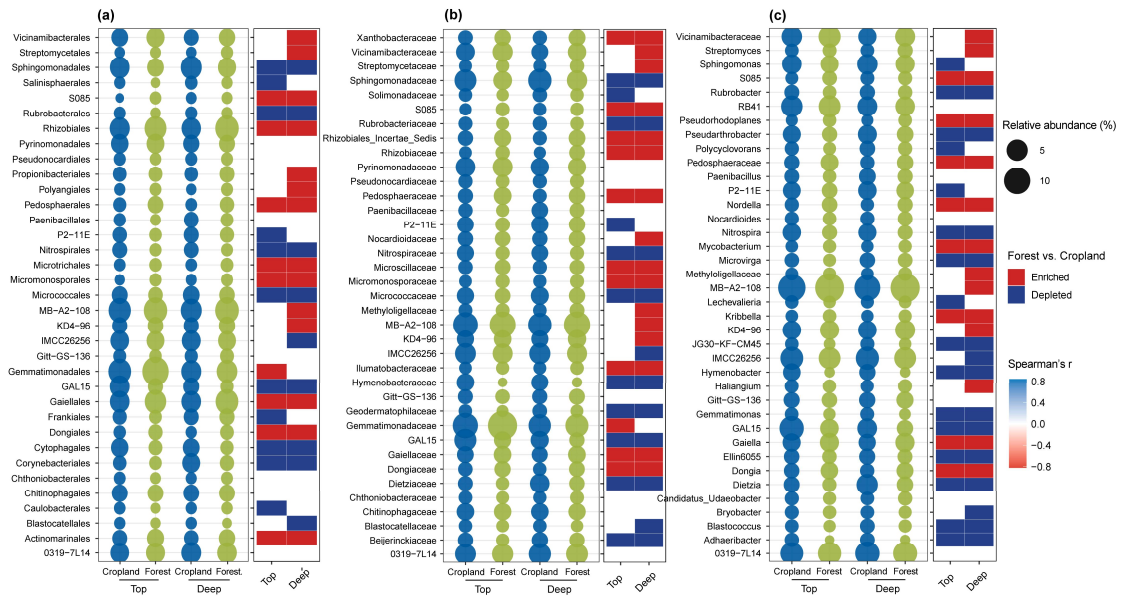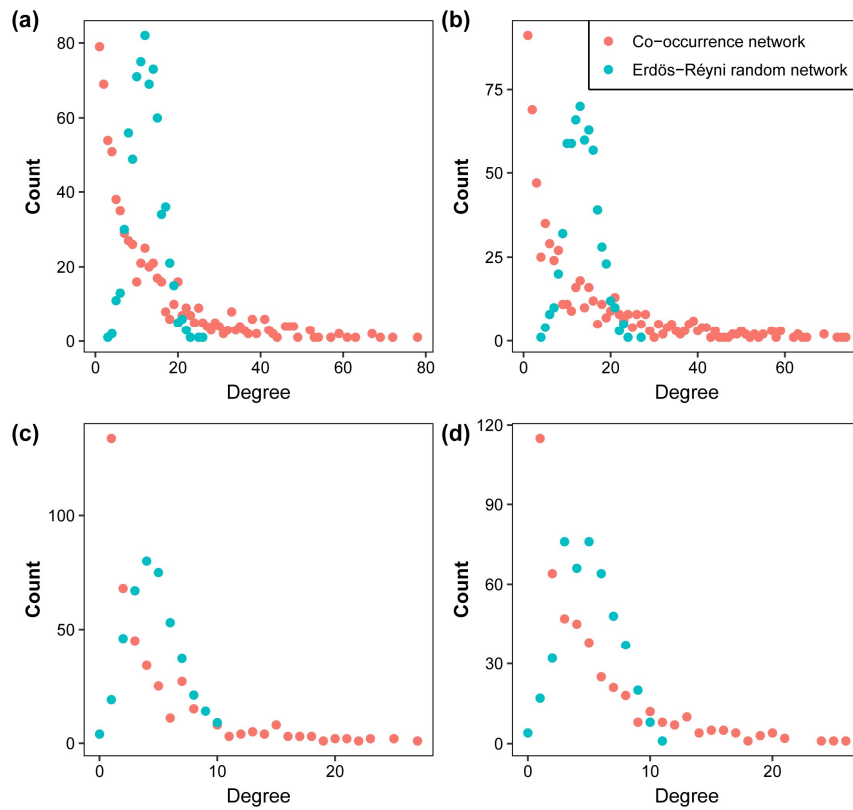
Figure S8. Dominant bacterial orders **(a)**, families **(b)** and genera **(c)** affected by afforestation and soil depth (top vs. deep layer). Bubble plot showing the relative abundance of the bacterial orders (>0.5%), families (>0.5%) and genera (>0.3%). Heatmaps showing the significant changes in relative abundance of dominant taxa induced by afforestation (cropland was used as control) in top and deep soils based on the Wilcoxon test at P < 0.05 level. Only taxa with significant changes are filled with color. Red or blue colors indicated that the taxa were enriched or depleted in forest, respectively.

Figure S9. Redundancy analysis (RDA) showing the major drivers influencing dominant soil bacterial taxa in top and deep layers after afforestation at order **(a)**, family **(b)**, and genus **(c)** levels. The individual effect of each soil property was calculated by the rdacca.hp package.

Figure S10. Distribution of degrees for the co-occurrence network (Red) and Erdos-Renyi random network (Blue) for soil bacteria communities in top layer in cropland **(a)**, top layer in forest **(b)**, deep layer in cropland **(c)**, and deep layer in forest **(d)**.
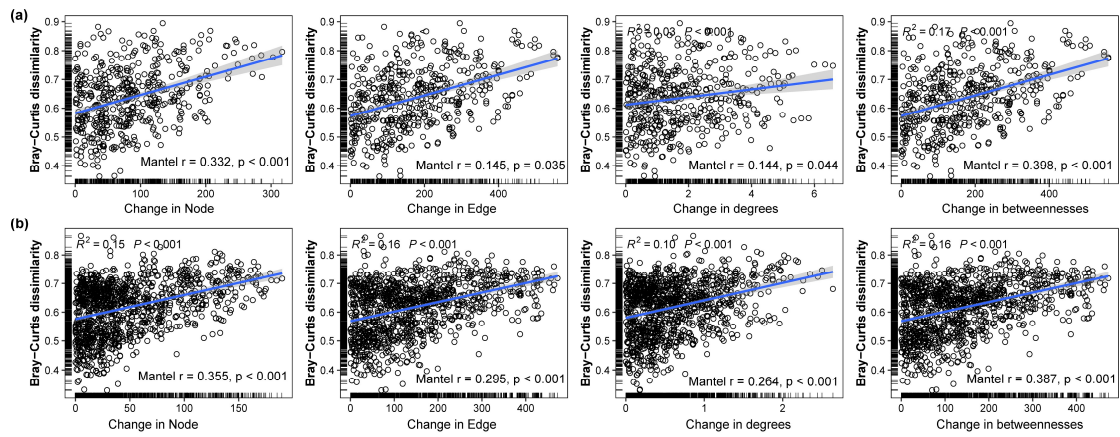
Figure S11. Relationships between potential biotic interactions (co-occurrence network properties) and beta diversity of bacterial community composition (Bray-Curtis dissimilarity) in top **(a)** and deep layers **(b)**, respectively. Network properties include node, edge, degree and betweenness. Dissimilarity distance matrix of network properties were calculated based on Euclidean distances. Linear relationships were evaluated by the Mantel test.
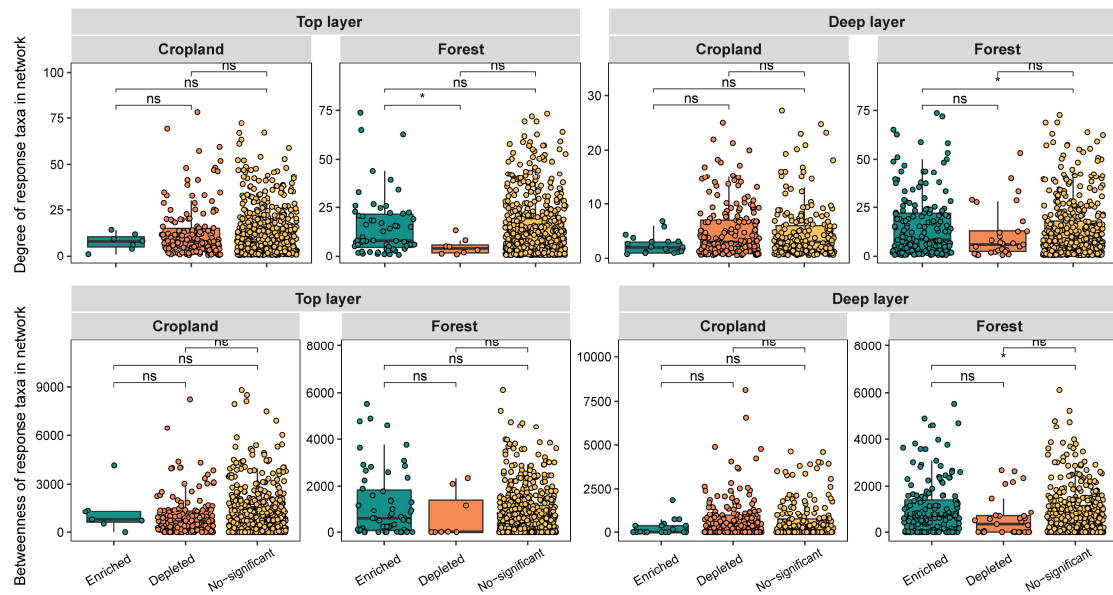
Figure S12. Node connectedness (degree) and centrality (betweenness) of bacterial networks. Nodes in each network were divided into three categories based on *DESeq2* differential abundance analysis, i.e., enriched, depleted and non-significant after afforestation. Although the number of ASVs responsive to afforestation was smaller than non-responsive ASVs in all networks, the enriched ASVs after afforestation in network had higher connectedness and centrality. Asterisk denote significant differences based on Wilcoxon texts. Asterisks denote * P < 0.05, ** P < 0.01 and *** P < 0.001.
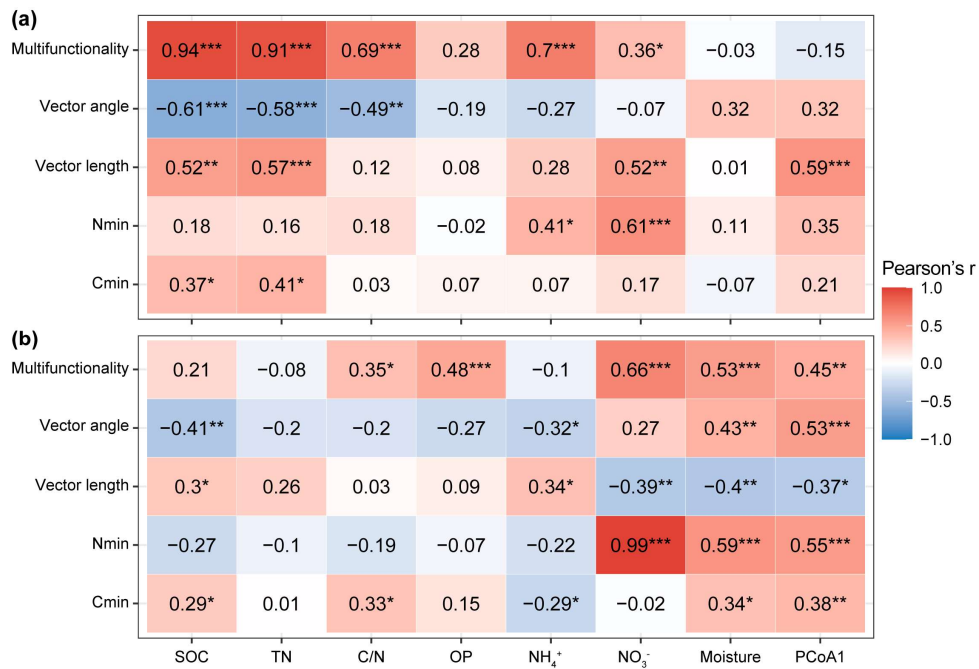
Figure S13. Pearson's correlations of the soil functions (soil organic carbon and nitrogen mineralization, vector length, vector angle and multifunctionality) to soil physicochemical properties and bacterial community composition in top **(a)** and deep layers **(b)**, respectively. Bacterial community diversity was quantified by using the first axis of PCoA (PCoA1) based on Bray-Curtis distance. Vector length represents relative C vs. nutrient limitation, and the vector angle denotes the relative P vs. N limitation. C_{min} and N_{min} denote the organic carbon and nitrogen mineralization, respectively. Legend: SOC, soil organic carbon; TN, soil total nitrogen; C/N, ratio of carbon to nitrogen; OP, available phosphorus; NH_4^+, ammonium; NO_3^-, nitrate; pH, soil pH; and Moisture, soil moisture. Asterisks denote * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$.