

Supplementary Materials:

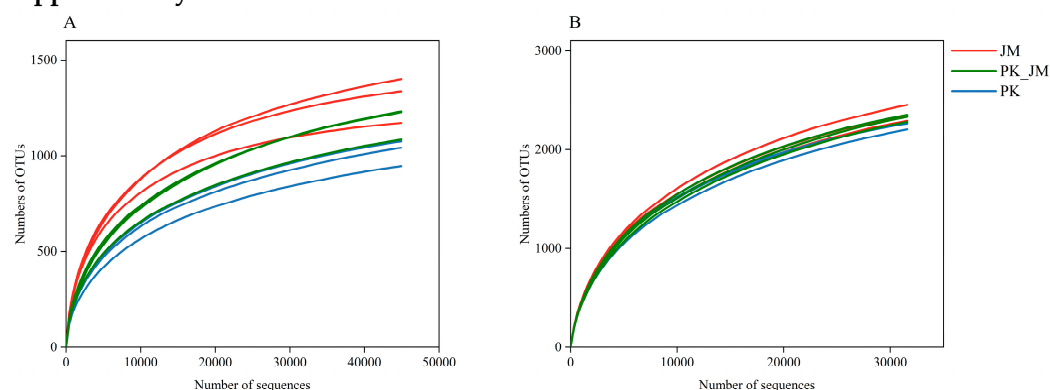


Figure S1. The Rarefaction curves of the number of operational taxonomic units (OTUs) for soil fungal (A) and bacterial (B) communities. Random subsamples of 44,925 and 31,586 gene per sample were used to generate the rarefaction curves. OTUs were delineated at 97% sequence similarity. JM for *Juglans mandshurica* plantations, PK_JM for *Pinus koraiensis* and *J. mandshurica* mixed plantations, PK for *P. koraiensis* plantations.

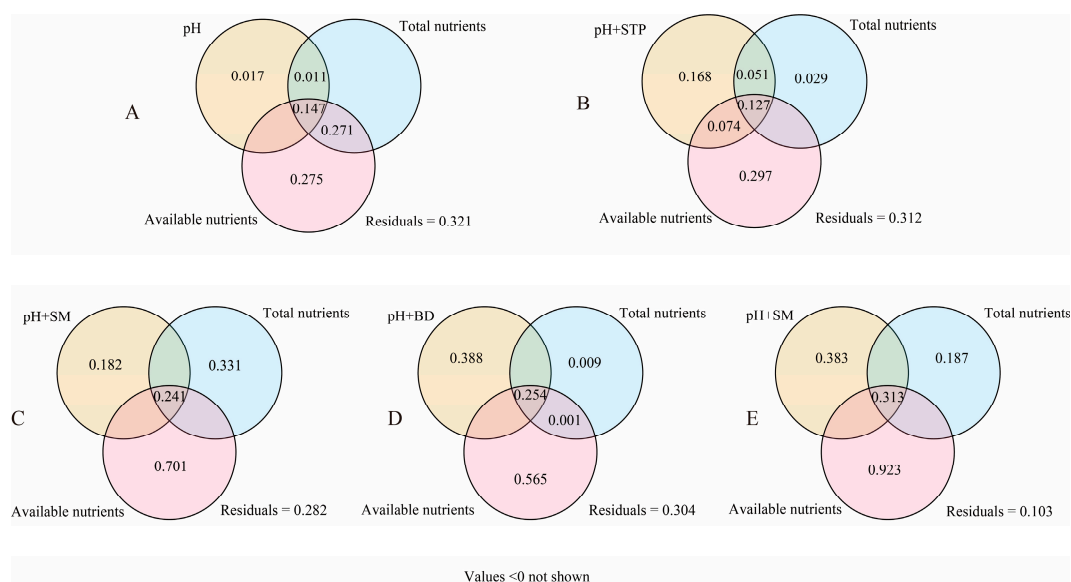


Figure S2. Venn diagram of variation partition analysis (VPA) showed the contributions of different types of soil variables to the variations in fungal Genus-level taxonomy (A) and function category based on FUNGuild database (B), bacterial Genus-level taxonomy (C) and function category based on FAPROTAX (D) and Bugbase databases (E). The soil variables in each subgraph were first screened by the results of tbrDA (Figure 6) and then classified by total nutrient content, available nutrient content, and soil pH with or without soil physical property.

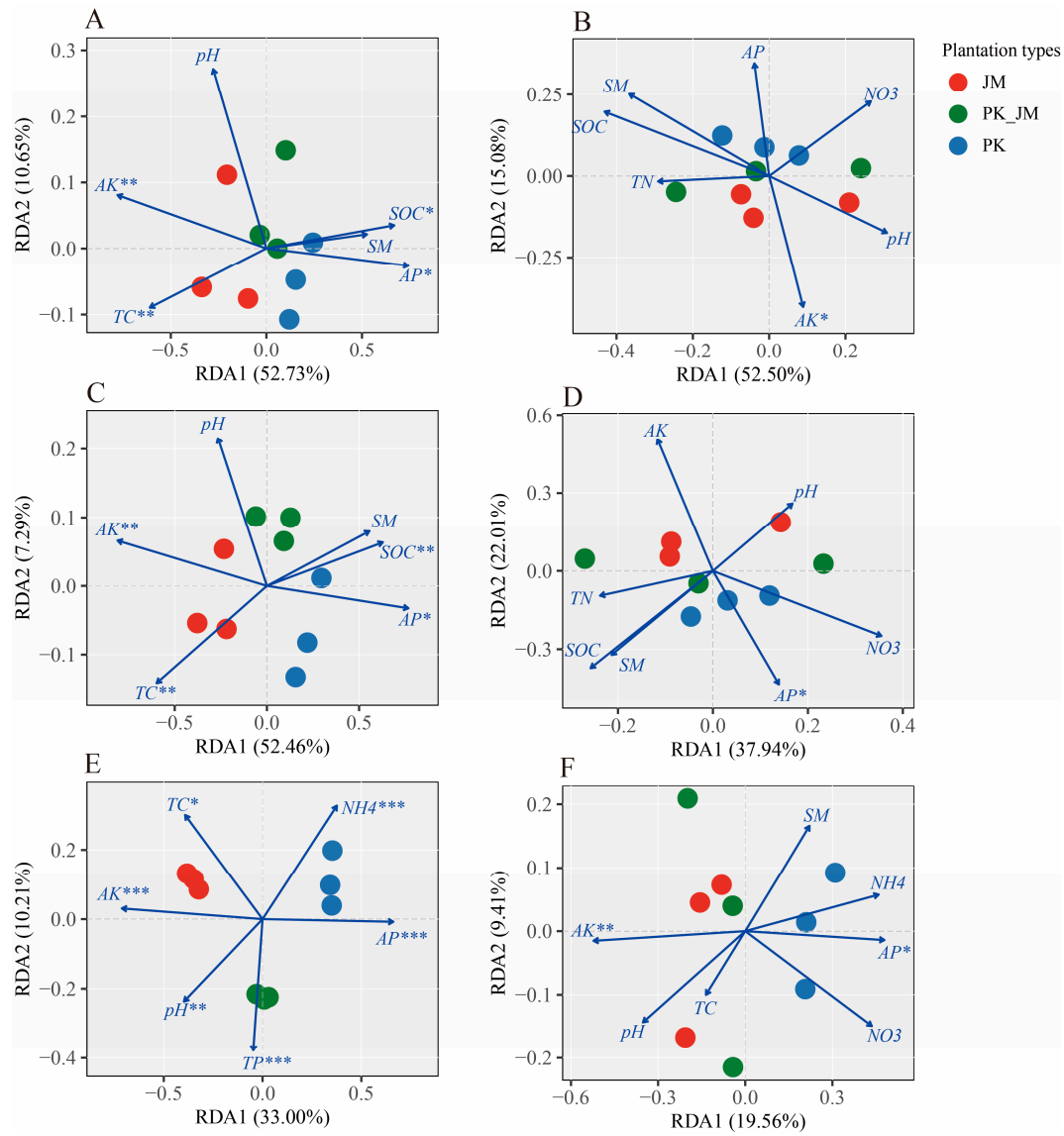


Figure S3. The results of Redundancy analysis (RDA) showed the correlation between the soil physicochemical parameters and microbial community composition in different taxonomy levels: fungal phylum (A), class (C), and OTU (E) levels, and bacterial phylum (B), class (D), and OTU (F) levels. JM for *Juglans mandshurica* plantations, PK_JM for *Pinus koraiensis* and *J. mandshurica* mixed plantations, PK for *P. koraiensis* plantations.

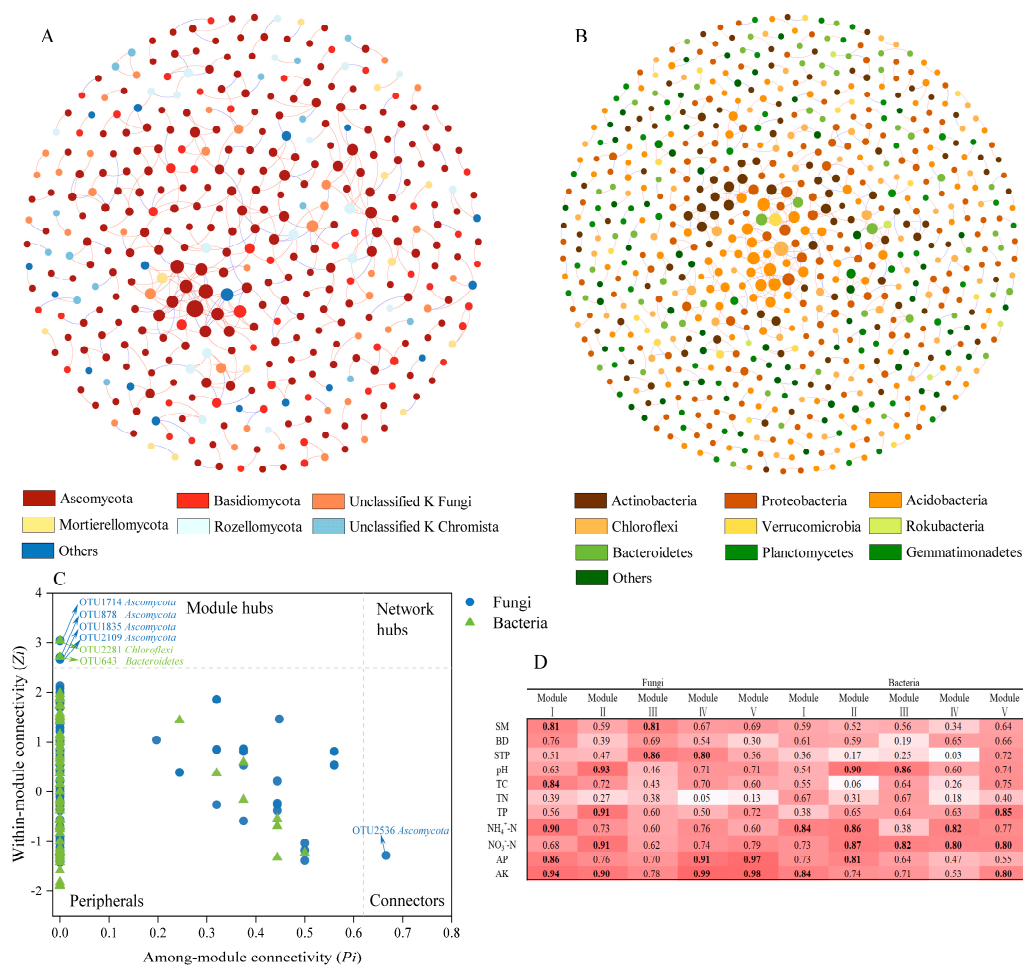


Figure S4. The patterns of soil fungal (A) and bacterial (B) co-occurrence networks. Each node represented one type of OTUs and was colored by phylum taxonomic categories. Positive links between nodes were shown in red, and negative links were in blue. The size of each node was proportional to the number of degrees. Topological role of each node (OTU) in the soil fungal and bacterial co-occurrence networks was indicated by the Zi-Pi plot (C). The network hubs are determined by $Z_i > 2.5$ and $P_i > 0.62$, and the peripherals are characterized by $Z_i < 2.5$ and $P_i < 0.62$. The nodes with $Z_i > 2.5$ are identified as module hubs, and those with $P_i > 0.62$ are connectors. We also showed the Spearman's correlations between soil variables and the sub-networks in fungal and bacterial communities (D). Significant correlation coefficients ($P < 0.05$) were shown in bold. BD, Bulk density; SM, Soil moisture; STP, Soil total porosity; TC, Total carbon; TN, Total nitrogen; TP, Total phosphorus; $\text{NH}_4^+\text{-N}$, Ammonium nitrogen; $\text{NO}_3^-\text{-N}$, Nitrate nitrogen; AP, Available phosphorus; AK, Available potassium.

Table S1. The basic situation of the three forest types.

Stand	Species	Existing density (No.·ha ⁻¹)	Average tree height (m)	Mean breast diameter (cm)	Mean individual volume (m ³)	Stand volume (m ³ ·ha ⁻¹)
JM	<i>J. mandshurica</i>	800	13.1	14.8	0.116	88.25
PK_JM	<i>J. mandshurica</i>	578	13.2	19.1	0.187	90.95
	<i>P. koraiensis</i>	522	8.5	10.9	0.051	25.17
PK	<i>P. koraiensis</i>	750	11.4	13.6	0.092	64.05

JM for *Juglans mandshurica* plantations, PK_JM for *Pinus koraiensis* and *J. mandshurica* mixed plantations, PK for *P. koraiensis* plantations. The stand volum of PK_JM is the accumulation of Manchurian walnut and Korean pine in the mixed plantation.

Table S2. The effects of plantation types on the relative abundance of soil fungal phyla and classes.

Taxonomy	The relative abundance (%)	GLMM
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		JM	PK_JM	PK	F	P
Phyla	Ascomycota	64.03±3.71 b	77.00±1.95 a	76.33±1.28 a	8.338	0.019*
	Basidiomycota	5.77±0.50 b	6.59±0.23 b	9.69±0.28 a	34.301	0.001**
	Unclassified K Fungi	8.64±1.59 a	5.05±0.50 a	4.67±1.42 a	3.001	0.125
	Mortierellomycota	6.39±1.18 a	3.55±1.37 a	4.72±0.40 a	1.780	0.247
	Rozellomycota	7.65±1.70 b	4.27±1.20 ab	1.41±0.39 a	6.554	0.031*
	Unclassified K Chromista	6.60±1.55 a	2.66±0.38 b	2.14±0.63 b	6.079	0.036*
Classes	Leotiomycetes	23.24±2.58 b	37.42±4.49 a	45.24±1.18 a	13.214	0.006**
	Sordariomycetes	24.27±1.61 a	16.42±1.90 b	10.98±0.33 c	21.226	0.002**
	Unclassified k Fungi	8.65±1.57 a	5.06±0.50 a	4.67±1.44 a	3.020	0.124
	Unclassified p Ascomycota	2.41±0.42 b	7.82±1.43 a	6.95±0.89 a	8.419	0.018*
	Dothideomycetes	5.41±0.22 ab	6.99±1.11 a	3.87±0.54 b	4.681	0.060
	Mortierellomycetes	6.45±1.22 a	3.56±1.35 a	4.71±0.40 a	1.837	0.239
	Eurotiomycetes	3.52±0.23 a	3.78±0.25 a	5.41±0.75 a	4.599	0.062
	Rozellomycotina cls Incertae sedis	7.32±1.65 a	3.79±1.13 ab	1.34±0.39 b	6.543	0.031*
	Unclassified k Chromista	6.58±1.56 a	2.67±0.39 b	2.14±0.64 b	5.885	0.038*
	Pezizomycetes	4.69±0.07 a	3.98±0.19 a	2.32±0.41 b	21.397	0.002**
	Agaricomycetes	3.83±0.41 a	2.41±0.06 a	3.50±0.83 a	1.922	0.226
	Tremellomycetes	1.42±0.24 b	3.15±0.26 ab	4.68±1.11 a	5.864	0.039*

Mean ± Standard Error. Different lowercase letters in the same row indicate significant differences ($P < 0.05$) amongst the three plantation types based on the results of the generalized linear mixed model (GLMM) with Tukey's multiple comparisons. *, $P < 0.05$; **, $P < 0.01$; *** $P < 0.001$. JM for *Juglans mandshurica* plantations, PK_JM for *Pinus koraiensis* and *J. mandshurica* mixed plantations, PK for *P. koraiensis* plantations.

Table S3. The effects of plantation types on the relative abundance of soil bacterial phyla and classes.

Taxonomy		Plantation types			GLMM	
		JM	PK_JM	PK	F	P
Phyla	Actinobacteria	32.75±1.52 a	29.23±2.06 a	25.20±1.97 a	4.105	0.075
	Proteobacteria	29.40±2.12 a	31.52±4.07 a	33.90±0.87 a	0.695	0.535
	Acidobacteria	12.52±1.57 a	13.04±2.82 a	13.62±1.35 a	0.074	0.929
	Chloroflexi	7.95±0.76 a	7.74±1.73 a	7.42±0.42 a	0.056	0.946
	Verrucomicrobia	5.61±1.39 a	7.51±1.84 a	7.04±1.05 a	0.455	0.655
	Rokubacteria	4.11±0.23 a	3.13±0.25 a	3.77±0.38 a	2.818	0.137
	Bacteroidetes	2.82±0.34 a	2.72±0.25 a	2.89±0.17 a	0.098	0.908
	Planctomycetes	1.02±0.14 a	1.20±0.14 a	1.20±0.20 a	0.438	0.664
	Gemmatimonadetes	1.02±0.15 b	0.96±0.14 b	1.66±0.11 a	8.116	0.020*
Classes	Actinobacteria	32.76±1.52 a	29.23±2.06 a	25.20±1.97 a	4.105	0.075
	Alphaproteobacteria	17.07±0.69 a	21.05±3.37 a	23.41±0.96 a	2.422	0.169
	Subgroup 6	6.48±0.88 a	6.82±2.22 a	5.73±0.65 a	0.152	0.862
	Gammaproteobacteria	7.49±0.97 a	6.41±0.65 a	5.60±0.12 a	1.964	0.221
	Verrucomicrobiae	5.61±1.39 a	7.51±1.84 a	7.04±1.05 a	0.455	0.655
	Deltaproteobacteria	4.84±0.47 a	4.05±0.40 a	4.88±0.25 a	1.450	0.306
	KD4-96	3.72±0.63 a	3.70±1.14 a	2.90±0.29 a	0.370	0.706
	NC 10	4.11±0.23 a	3.13±0.25 a	3.77±0.38 a	2.818	0.137
	Bacteroidia	2.74±0.32 a	2.66±0.25 a	2.83±0.17 a	0.117	0.892
	Blastocatellia Subgroup 4	2.02±0.31 a	2.18±0.54 a	1.96±0.21 a	0.091	0.914
	Acidobacteriia	1.44±0.119 b	1.68±0.39 b	3.46±0.28 a	13.700	0.006**
	Anaerolineae	1.15±0.06 a	1.18±0.28 a	0.94±0.10 a	0.538	0.610
	Subgroup 17	0.83±0.11 a	0.75±0.26 a	0.66±0.12 a	0.224	0.806

Mean ± Standard Error. Different lowercase letters in the same row indicate significant differences ($P < 0.05$) amongst the three plantation types based on the results of the generalized linear mixed model (GLMM) with Tukey's multiple

comparisons. *, $P < 0.05$; **, $P < 0.01$; *** $P < 0.001$. JM for *Juglans mandshurica* plantations, PK_JM for *Pinus koraiensis* and *J. mandshurica* mixed plantations, PK for *P. koraiensis* plantations.

Table S4. The changes of soil fungal functional guilds composition in different plantation types.

FUNGuilds		JM (%)	PK_JM (%)	PK (%)
Pathotroph	Animal Pathogen	23.41±1.56 ab	27.68±3.03 a	17.64±0.92 b
	Plant Pathogen	6.57±0.92 a	5.57±0.96 a	4.40±0.83 a
	Fungal Parasite	1.05±0.11 b	2.73±0.21 ab	4.35±1.08 a
		31.03±2.22 ab	35.98±1.87 a	26.39±1.56 b
Saprotroph	Undefined Saprotroph	21.49±1.12 a	19.69±0.91 a	22.66±0.20 a
	Plant Saprotroph	1.49±0.30 b	0.89±0.18 b	2.64±0.40 a
	Dung Saprotroph	0.82±0.11 a	0.65±0.09 a	0.84±0.21 a
	Leaf Saprotroph	0.34±0.05 a	0.21±0.04 b	0.15±0.02 b
	Wood Saprotroph	0.29±0.07 a	0.12±0.02 b	0.10±0.01 b
	Soil Saprotroph	0.11±0.01 a	0.02±0.00 b	0.01±0.00 b
	Litter Saprotroph	0.10±0.04 a	0.03±0.01 ab	0.01±0.00 b
		24.65±1.30 ab	21.61±0.85 b	26.40±0.08 a
Symbiotroph	Ectomycorrhizal	1.09±0.10 a	0.93±0.14 a	2.43±0.83 a
	Endophyte	8.06±1.14 a	5.30±1.23 a	6.50±0.69 a
	Ericoid Mycorrhizal	0.10±0.03 c	0.53±0.06 b	1.24±0.01 a
		9.26±1.11 a	6.76±1.12 a	10.16±1.51 a
Others		0.12±0.03 b	0.09±0.04 b	0.45±0.14 a
Undefined		34.58±3.46 a	35.05±1.69 a	37.47±0.71 a

Mean ± Standard Error. Different lowercase letters in the same row indicate significant differences ($P < 0.05$) amongst the three plantation types based on the results of the generalized linear mixed model (GLMM) with Tukey's multiple comparisons. JM for *Juglans mandshurica* plantations, PK_JM for *Pinus koraiensis* and *J. mandshurica* mixed plantations, PK for *P. koraiensis* plantations.

Table S5. Mantel test results for the correlation between soil microbial community with functional groups and soil variables.

Soil Variables	Fungalgenus taxonomy		Fungalfunction froups		Bacterialgenus taxonomy		Bacterialecological froups		Bacterialphenotypes froups	
	R ²	P	R ²	P	R ²	P	R ²	P	R ²	P
pH	0.924	0.002**	0.881	0.002**	0.289	0.355	0.755	0.019*	0.399	0.221
TC	0.709	0.025*	-	-	0.301	0.349	-	-	-	-
TP	0.823	0.004**	0.725	0.011*	-	-	0.405	0.206	0.200	0.506
NH ₄ ⁺ -N	0.765	0.015*	0.715	0.017*	0.241	0.443	0.825	0.004**	0.414	0.219
NO ₃ ⁻ -N	-	-	0.297	0.343	0.349	0.271	0.750	0.014*	0.309	0.327
AP	0.918	0.003**	0.303	0.363	0.658	0.036*	0.577	0.085	0.574	0.093
AK	0.974	<0.001***	0.262	0.428	0.885	0.004**	0.590	0.065	0.799	0.007**
STP	-	-	0.431	0.209	-	-	-	-	-	-
SM	-	-	-	-	0.563	0.071	-	-	0.402	0.220
BD	-	-	-	-	-	-	0.361	0.271	-	-

TC, total carbon; TP, total phosphorus; NH₄⁺-N, ammonium; NO₃⁻-N, nitrate-nitrogen; AP, available phosphorus; AK, available potassium. STP, soil total porosity; SM, soil moisture; BD, bulk density. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.

Table S6. Mantel test results for the correlation between soil microbial community and soil variables in different taxonomy levels.

Soil Variables	Fungal phylum taxonomy		Fungal class taxonomy		Fungal OTU taxonomy		Bacterial phylum taxonomy		Bacterial class taxonomy		Bacterial OTU taxonomy	
	R ²	P	R ²	P	R ²	P	R ²	P	R ²	P	R ²	P
pH	0.589	0.067	0.203	0.483	0.884	0.006**	0.310	0.338	0.286	0.374	0.386	0.238
TC	0.767	0.010*	0.811	0.007**	0.752	0.013*	-	-	-	-	0.261	0.401

TN	-	-	-	-	-	-	0.101	0.743	0.065	0.841	-	-
TP	-	-	-	-	0.925	<0.001***	-	-	-	-	-	-
SOC	0.749	0.017*	0.759	0.008**			0.390	0.217	0.488	0.113	-	-
NH ₄ ⁺ -N	-	-	-	-	0.886	0.005**	-	-	-	-	0.351	0.279
NO ₃ ⁻ -N	-	-	-	-	-	-	0.341	0.296	0.349	0.271	0.378	0.226
AP	0.701	0.036*	0.774	0.016*	0.908	<0.001***	0.576	0.070	0.659	0.047*	0.740	0.017*
AK	0.881	0.004**	0.883	0.002**	0.975	<0.001***	0.791	0.012*	0.885	0.004**	0.889	0.003**
STP	-	-	-	-	-	-	-	-	-	-	-	-
SM	0.451	0.160	0.479	0.131	-	-	0.558	0.077	0.566	0.098	0.412	0.213
BD	-	-	-	-	-	-	-	-	-	-	-	-

TC, total carbon; TN, total nitrogen; TP, total phosphorus; SOC, soil organic carbon; NH₄⁺-N, ammonium nitrogen; NO₃⁻-N, nitrate nitrogen; AP, available phosphorus; AK, available potassium. STP, soil total porosity; SM, soil moisture; BD, bulk density. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.