

Table S1. Information of all functional genes.

Cycle	Gene category	Gene names	Gene number
C cycling 36	Starch	<i>Sga, amyX, apu, amyA, iso-plu</i>	5
	Hemicellulose	<i>abfA, manB, xylA</i>	3
	Cellulose	<i>Cdh, cex, naglu</i>	3
	Chitin	<i>chiA, exo-chi</i>	2
	Pectin	<i>pgu</i>	1
	Lignin	<i>mnp, glx, pox, lig</i>	4
	glucose	<i>gcd</i>	1
	C fixation	<i>rbcL, korA, acsE, accA, mct, mcrA, aclB, acsA, acsB, pccA, smtA, frdA, cdaR</i>	13
	Methane production	<i>pqq-mdh, mxaF</i>	2
	Methane oxidation	<i>pmoA, mmoX</i>	2
	Nitrification	<i>amoA1, amoB, amoA2, nxrA, hao</i>	5
		<i>narG, nirS2, nirK1, nirS1, nirS3, nirK2, nirK3, nosZ1, nosZ2</i>	9
	Denitrification		
N cycling 22	Assimilatory N reduction	<i>nasA</i>	1
	Dissimilatory N reduction	<i>napA</i>	1
	Anaerobic ammonium oxidation	<i>hzsB, hzsA, hzo</i>	3
	N fixation	<i>nifH</i>	1
	Ammonification	<i>ureC</i>	1
	Organic N mineralization	<i>gdhA</i>	1
	Organic P mineralization	<i>phoX, phoD, bpp, phnK, cphy</i>	5
P cycling 8	Inorganic P solubilization	<i>pqqC</i>	1
	Inorganic P biosynthesis	<i>ppk</i>	1
	Inorganic P hydrolysis	<i>ppx</i>	1
S cycling 5	S reduction	<i>dsrB, dsrA, apsA</i>	3
	S oxidation	<i>soxY, yedZ</i>	2
-	Phylogenetic marker	16S rRNA	1

Table S2. Richness and diversity of bacterial communities in different stand ages

Stand age	Soil layer (cm)	chao 1	observed species	shannnon	simpson
10a	0-20	6434.81±85.58Aa	5000.40±163.66Aa	9.15±0.24Aa	0.99±0.00Aa
	20-40	6462.10±28.76Aa	5222.90±76.15Aa	9.47±0.15Aa	0.99±0.00Aa
	40-60	6241.38±221.40Aa	4987.63±188.57Aa	9.11±0.22Aa	0.99±0.00Aa
15a	0-20	5868.27±189.59Ba	4704.23±196.70Aa	9.21±0.20Aa	0.99±0.00Aa
	20-40	5988.76±199.33ABa	4725.10±151.16BCa	9.17±0.25Aa	0.99±0.00Aa
	40-60	6186.12±250.99Aa	4934.60±137.60Aa	9.25±0.22Aa	0.99±0.01Aa
27a	0-20	6448.20±192.57Aa	4946.20±117.48Aa	9.24±0.19Aa	0.99±0.00Aa
	20-40	5589.25±48.34Bb	4431.80±43.50Cb	8.93±0.07Aa	0.99±0.00Aa
	40-60	6313.09±94.03Aa	4994.90±73.28Aa	9.29±0.09Aa	0.99±0.00Aa
55a	0-20	6608.64±104.16Aa	5180.07±108.80Aa	9.43±0.17Aa	0.99±0.00Aa
	20-40	6382.10±216.93Aa	5009.53±113.21ABa	9.29±0.10Aa	0.99±0.00Aa
	40-60	6261.08±123.30Aa	4951.17±81.89Aa	9.42±0.07Aa	0.99±0.00Aa
64a	0-20	6447.91±230.85Aa	5051.60±196.62Aa	9.31±0.18Aa	0.99±0.00Aa
	20-40	6449.90±163.71Aa	4999.93±129.59ABa	9.31±0.18Aa	0.99±0.00Aa
	40-60	6222.00±218.96Aa	4828.97±160.09Aa	9.00±0.26Aa	0.99±0.00Aa

Note: The data are shown as the means ± SD (n = 3). Different lowercase letters indicate significant differences among soil layers within the same stand age, while different uppercase letters indicate significant differences among stand ages within the same soil layer, both at p<0.05.

Table S3. Information of the normality of distribution of stand ages.

Shapiro-Wilk normality test		
Indicator	W	P values
BD	0.96728	0.23
SWC	0.98646	0.871
pH	0.97564	0.4549
TOC	0.98542	0.835
TP	0.9512	0.05641
TN	0.99055	0.9708
TC	0.98494	0.8177
NH ₄ ⁺ -N	0.98729	0.8972
AP	0.97964	0.6052
TK	0.9819	0.697
NO ₃ ⁻ -N	0.95732	0.09652
Ca ²⁺	0.95398	0.07195
Acid phosphatase	0.96054	0.1281
Catalase	0.99329	0.9956
Urease	0.98312	0.7467
Sucrase	0.98037	0.6349
Verrucomicrobiota	0.96922	0.2712
Acidobacteriota	0.97287	0.3663
Proteobacteria	0.97651	0.4857
Actinobacteriota	0.96077	0.1306
Chloroflexi	0.97627	0.477
RCP2-54	0.98369	0.7694
Planctomycetota	0.9884	0.9277
Myxococcota	0.96077	0.1307
WPS-2	0.98971	0.9566
Crenarchaeota	0.96779	0.2403
C degradation	0.96535	0.7843
C fixation	0.94062	0.3903
Methane metabolism	0.94726	0.4824
N Cycling	0.95438	0.5959
P Cycling	0.95032	0.5296
S Cycling	0.97167	0.8819

Table S4. Two-way ANOVA and *p* values of indicators.

Indicator	origin	F	<i>p</i> values
BD	age	0.776	0.549
	layer	0.098	0.907
	age×layer	0.97	0.477
SWC	age	7.858	<0.001
	layer	0.722	0.494
	age×layer	0.518	0.834
pH	age	89.604	<0.001
	layer	8.683	0.001
	age×layer	4.714	<0.001
TOC	age	174.257	0
	layer	75.244	0
	age×layer	0.596	0.773
TP	age	25.85	0
	layer	0.147	0.864
	age×layer	0.376	0.925
TN	age	6.806	0.001
	layer	57.677	0
	age×layer	1.73	0.132
TC	age	3.971	0.011
	layer	57.786	0
	age×layer	2.097	0.068
NH ₄ ⁺ -N	age	66.972	0
	layer	89.83	0
	age×layer	4.736	0.001
AP	age	3.03	0.033
	layer	71.766	0
	age×layer	1.721	0.134
TK	age	11.161	0
	layer	0.804	0.457
	age×layer	0.542	0.815
NO ₃ ⁻ -N	age	40.149	0
	layer	74.539	0
	age×layer	7.292	0
Ca ²⁺	age	6.099	0.001
	layer	0.15	0.861
	age×layer	1.239	0.312
Acid phosphatase	age	3.129	0.029
	layer	34.985	0
	age×layer	0.517	0.834
Catalase	age	55.76	0
	layer	0.144	0.867

	age×layer	0.382	0.922
	age	8.813	0
Urease	layer	15.564	0
	age×layer	2.602	0.027
	age	10.578	0
Sucrase	layer	13.793	0
	age×layer	0.406	0.908

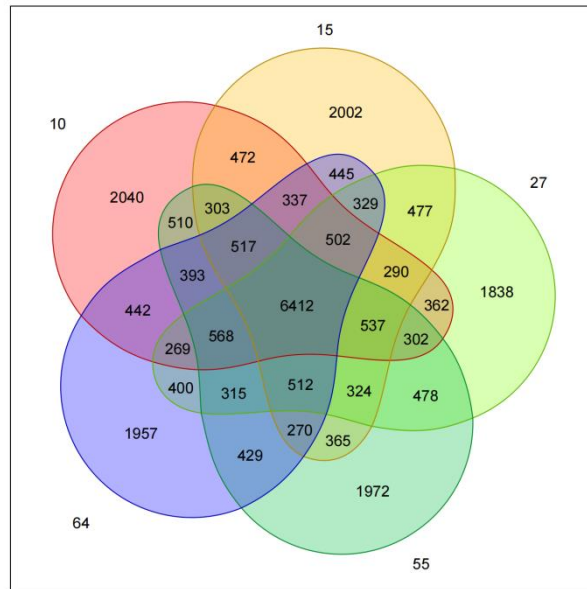


Figure S1. Venn diagram of bacterial OTUs distribution across different stand ages

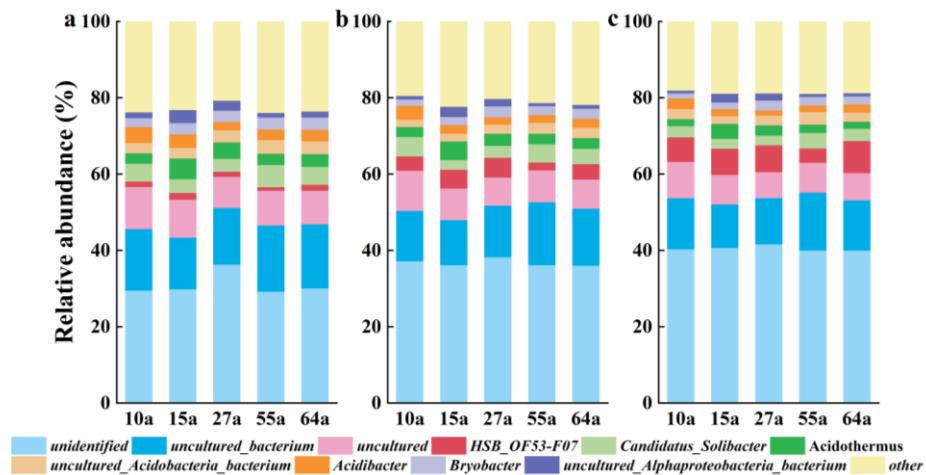
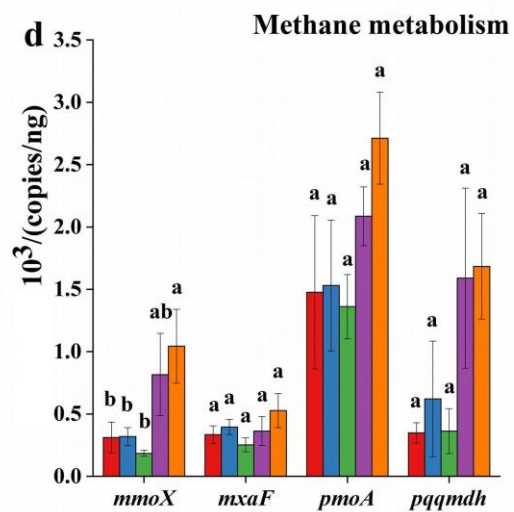
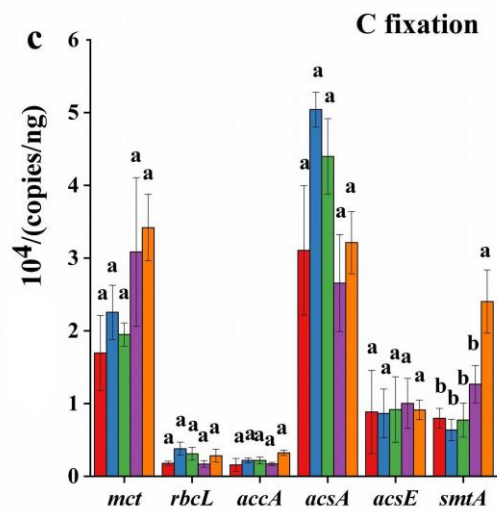
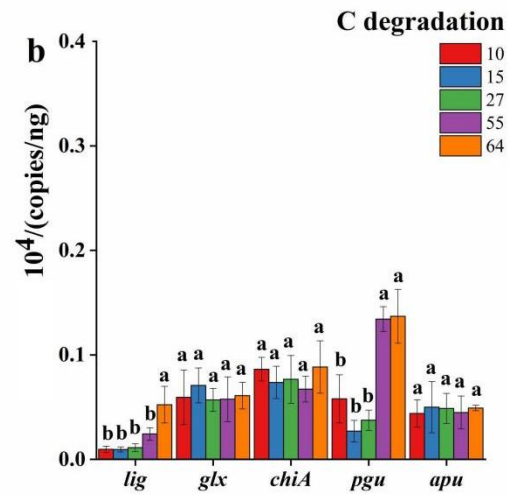
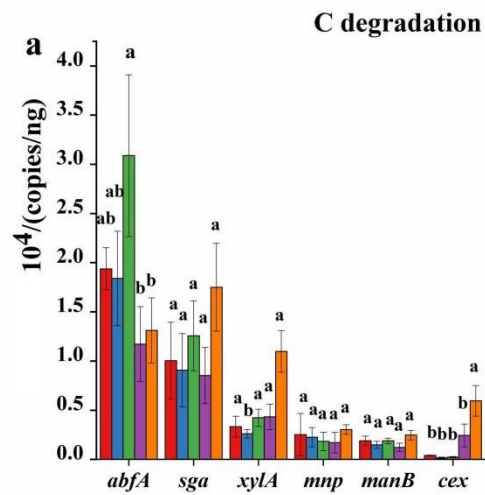


Figure S2. Relative abundance of bacterial community composition at the level of genus. Panels a, b, and c represent soil layers of 0-20 cm, 20-40 cm, and 40-60 cm in sequence.



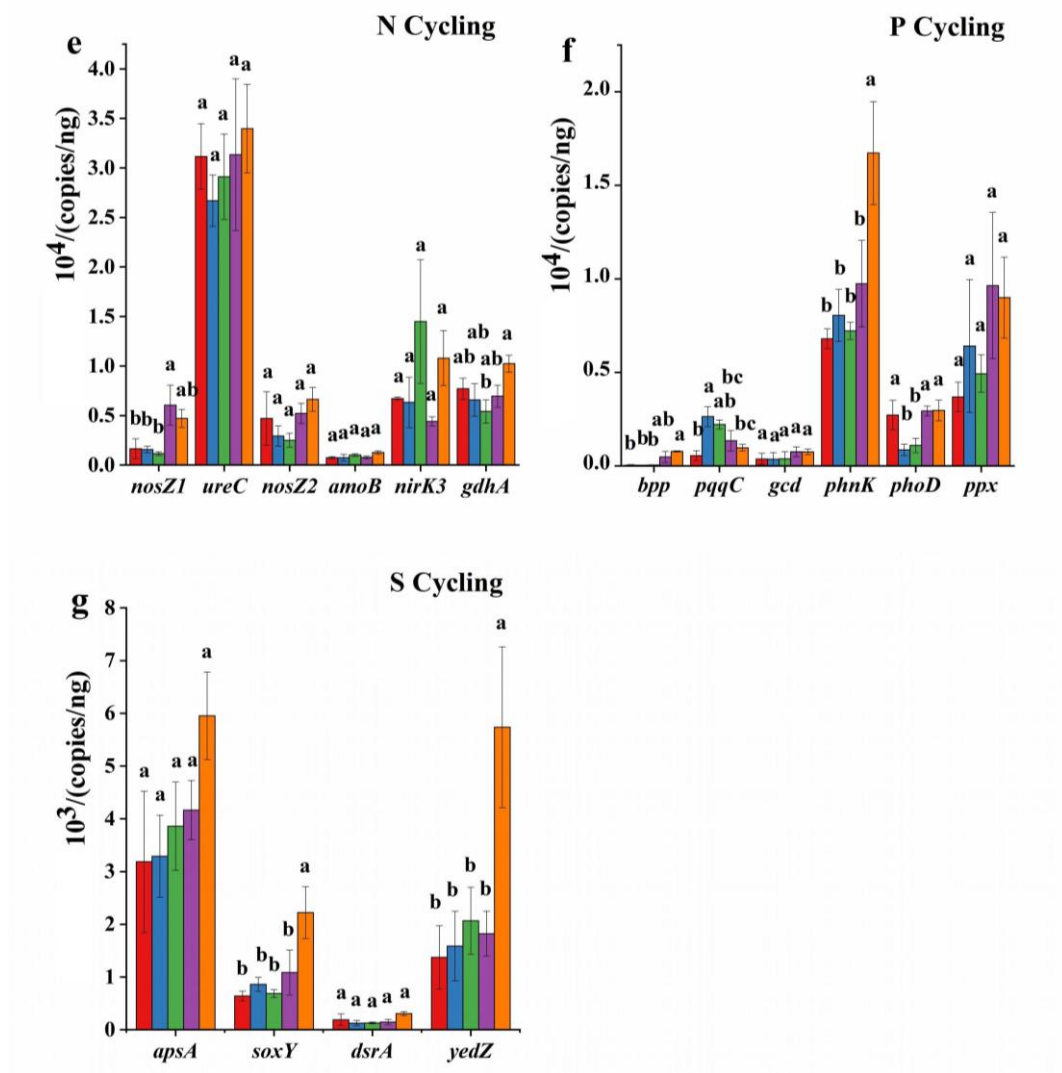


Figure S3. Absolute abundance of soil bacterial functional genes, measured as more than 10^3 copies/ng across various stand ages. Different lowercase letters indicate significant differences among stand ages at $p < 0.05$.