

Table S1 The soil information

Type	pH	Soil particle			The total amount of heavy metals (mg·kg ⁻¹)				
		Sand	Silt	Clay	Cu	Zn	As	Cd	Pb
yellow brown soil	8.47	33.95%	62.80%	3.24%	62.10	897.69	54.89	1.97	252.21
The effective state of iron (mg·kg ⁻¹)		Cation exchange capacity (cmol·kg ⁻¹)		Soil moisture content (%)		Total organic carbon (g·kg ⁻¹)		Dissolved organic carbon (g·kg ⁻¹)	
	3.47	11.66		23.43		54.98		31.89	

Table S2 Taxonomic annotation results of species

Name	domain	phylum	class	order	family	genus	species
CK	50	35	125	309	667	2711	116
T1	67	47	146	285	1074	2922	154
T2	23	18	83	195	564	2044	106

Table S3 Table of taxonomic unit statistics for different treatment groups

Name	domain	phylum	class	order	family	genus	species
CK	1	20	54	111	168	250	67
T1	1	19	51	106	165	262	86
T2	1	22	59	122	190	295	77

Table S4 Average relative abundances of bacterial at phylum level in different treatments

Name	CK	T1	T2
<i>Actinobacteria</i>	56.94%	63.99%	72.62%
<i>Proteobacteria</i>	23.44%	20.81%	10.87%
<i>Firmicutes</i>	6.87%	6.78%	9.06%
<i>Chloroflexi</i>	4.89%	2.49%	3.59%
<i>Acidobacteria</i>	3.55%	2.28%	1.61%
<i>Gemmatimonadetes</i>	2.44%	1.70%	0.62%
<i>Rokubacteria</i>	0.96%	0.49%	0.77%
<i>Bacteroidetes</i>	0.27%	0.77%	0.24%
<i>Patescibacteria</i>	0.10%	0.13%	0.24%
<i>Nitrospirae</i>	0.10%	0.05%	0.05%

Table S5 Average relative abundances of bacterial at genus level in different treatments

Name	CK	T1	T2
<i>Nocardioides</i>	12.83%	17.32%	20.73%
<i>Bacillus</i>	5.49%	5.11%	5.82%
<i>Sphingomonas</i>	10.09%	4.19%	0.14%
<i>Marmoricola</i>	2.37%	2.39%	7.09%
<i>67-14</i>	4.00%	1.56%	1.26%
<i>Rhodococcus</i>	3.94%	0.96%	0.59%
<i>Ramlibacter</i>	1.82%	2.13%	0.61%
<i>Gaiella</i>	2.53%	0.98%	0.73%
<i>Microvirga</i>	1.42%	2.73%	0.05%
<i>Streptomyces</i>	2.15%	1.46%	0.45%

Table S6 Analysis of differences between groups by Adonis

Name	Df	SumsOfSqs	MeanSqs	F.Model	R ²	Pr(>F)
Treat1	2	1.654418	0.827209	11.810775	0.611616	0.001
Residuals	15	1.050577	0.070038	NaN	0.388384	NaN
Total	17	2.704995	NaN	NaN	1	NaN

Table S7 Lefse results

Name	Abundance	Group	LDA score	P value
<i>Bacteria.Actinobacteria.Actinobacteria.Streptomyces</i>	4.33852	CK	3.93019	0.00051
<i>Bacteria.Actinobacteria.Thermoleophilia.Gaiellales.Gaiellaceae.Gaiella</i>	4.40374	CK	3.95709	0.00091
<i>Bacteria.Actinobacteria.Acidimicrobiia</i>	4.54048	CK	3.94438	0.00294
<i>Bacteria.Actinobacteria.Thermoleophilia</i>	5.06777	CK	4.61275	0.00051
<i>Bacteria.Chloroflexi.KD4_96.KD4_96.KD4_96.KD4_96</i>	4.31198	CK	3.81568	0.00255
<i>Bacteria.Acidobacteria</i>	4.54963	CK	3.98171	0.00063
<i>Bacteria.Proteobacteria</i>	5.37000	CK	4.79988	0.00234
<i>Bacteria.Proteobacteria.Alphaproteobacteria</i>	5.22731	CK	4.76585	0.00168
<i>Bacteria.Actinobacteria.Thermoleophilia.Gaiellales.Gaiellaceae</i>	4.40374	CK	3.95709	0.00091
<i>Bacteria.Proteobacteria.Alphaproteobacteria.Sphingomonadales.Sphingomonadaceae</i>	5.03409	CK	4.71877	0.00051
<i>Bacteria.Gemmatimonadetes.Gemmatimonadetes.Gemmatimonadales.Gemmatimonadaceae</i>	4.35795	CK	3.92982	0.00051
<i>Bacteria.Gemmatimonadetes.Gemmatimonadetes.Gemmatimonadales</i>	4.35795	CK	3.92982	0.00051
<i>Bacteria.Chloroflexi.KD4_96.KD4_96.KD4_96</i>	4.31198	CK	3.81568	0.00255
<i>Bacteria.Chloroflexi</i>	4.68963	CK	4.06918	0.00051
<i>Bacteria.Proteobacteria.Alphaproteobacteria.Sphingomonadales.Sphingomonadaceae.Sphingomonas</i>	5.00407	CK	4.69396	0.00051
<i>Bacteria.Actinobacteria.Actinobacteria.Streptomyces.Streptomyces</i>	4.33227	CK	3.92317	0.00051
<i>Bacteria.Actinobacteria.Actinobacteria.Corynebacteriales</i>	4.72017	CK	4.31070	0.00340
<i>Bacteria.Actinobacteria.Actinobacteria.Streptomyces.Streptomyces</i>	4.33852	CK	3.93019	0.00051
<i>Bacteria.Proteobacteria.Alphaproteobacteria.Sphingomonadales</i>	5.03409	CK	4.71877	0.00051
<i>Bacteria.Actinobacteria.Thermoleophilia.Solirubrobacterales.67_14</i>	4.60167	CK	4.13580	0.00108
<i>Bacteria.Actinobacteria.Actinobacteria.Corynebacteriales.Nocardiaceae</i>	4.60449	CK	4.21611	0.00340

<i>Bacteria.Actinobacteria.Thermoleophilia.Gaiellales</i>	4.69671	CK	4.27053	0.00051
<i>Bacteria.Gemmatimonadetes.Gemmatimonadetes</i>	4.35795	CK	3.92982	0.00051
<i>Bacteria.Actinobacteria.Actinobacteria.Corynebacteriales.Nocardiaceae.Rhodococcus</i>	4.59526	CK	4.21514	0.00340
<i>Bacteria.Actinobacteria.Thermoleophilia.Solirubrobacterales.67_14.67_14</i>	4.60167	CK	4.13580	0.00108
<i>Bacteria.Chloroflexi.KD4_96.KD4_96</i>	4.31198	CK	3.81568	0.00255
<i>Bacteria.Actinobacteria.Thermoleophilia.Solirubrobacterales</i>	4.79047	CK	4.32340	0.00051
<i>Bacteria.Chloroflexi.KD4_96</i>	4.31198	CK	3.81568	0.00255
<i>Bacteria.Proteobacteria.Alphaproteobacteria.Rhizobiales.Xanthobacteraceae</i>	4.22676	T1	3.81568	0.00051
<i>Bacteria.Proteobacteria.Alphaproteobacteria.Rhizobiales</i>	4.88550	T1	4.44849	0.00051
<i>Bacteria.Proteobacteria.Alphaproteobacteria.Rhizobiales.Beijerinckiaceae</i>	4.56167	T1	4.26282	0.00051
<i>Bacteria.Proteobacteria.Gammaproteobacteria.Betaproteobacteriales.Burkholderiaceae.Ramlibacter</i>	4.32757	T1	3.88138	0.00812
<i>Bacteria.Proteobacteria.Alphaproteobacteria.Rhizobiales.Beijerinckiaceae.Microvirga</i>	4.43539	T1	4.14754	0.00063
<i>Bacteria.Actinobacteria.Actinobacteria.Micrococcales.Intrasporangiaceae</i>	4.61530	T1	4.04263	0.00212
<i>Bacteria.Actinobacteria.Actinobacteria.Micrococcales.Micrococcaceae.Paenarthrobacter</i>	4.36060	T2	4.04315	0.00051
<i>Bacteria.Actinobacteria.Actinobacteria.Micrococcales.Micrococcaceae.Arthrobacter</i>	4.27182	T2	3.96538	0.00051
<i>Bacteria.Actinobacteria.Actinobacteria.Propionibacteriales.Nocardioideaceae.Marmoricola</i>	4.85053	T2	4.36906	0.00340
<i>Bacteria.Actinobacteria</i>	5.86107	T2	4.89146	0.00186
<i>Bacteria.Actinobacteria.Actinobacteria.Micrococcales.Micrococcaceae</i>	5.42922	T2	4.99824	0.00127
<i>Bacteria.Actinobacteria.Actinobacteria</i>	5.82315	T2	5.11724	0.00051
<i>Bacteria.Actinobacteria.Actinobacteria.Propionibacteriales.Nocardioideaceae</i>	5.50193	T2	4.79919	0.00294
<i>Bacteria.Actinobacteria.Actinobacteria.Propionibacteriales.Nocardioideaceae.Nocardioides</i>	5.31660	T2	4.58349	0.00141

<i>Bacteria.Firmicutes.Bacilli.Bacillales.Planococcaceae</i>	4.15433	T2	3.82217	0.00310
<i>Bacteria.Actinobacteria.Actinobacteria.Propionibacteriales</i>	5.50317	T2	4.80074	0.00294
<i>Bacteria.Actinobacteria.Actinobacteria.Micrococcales.Micrococcaceae.Arthrobacter.Arthrobacter_crystallopoietes</i>	4.19569	T2	3.89835	0.00044
<i>Bacteria.Actinobacteria.Actinobacteria.Micrococcales</i>	5.49261	T2	5.00721	0.00212

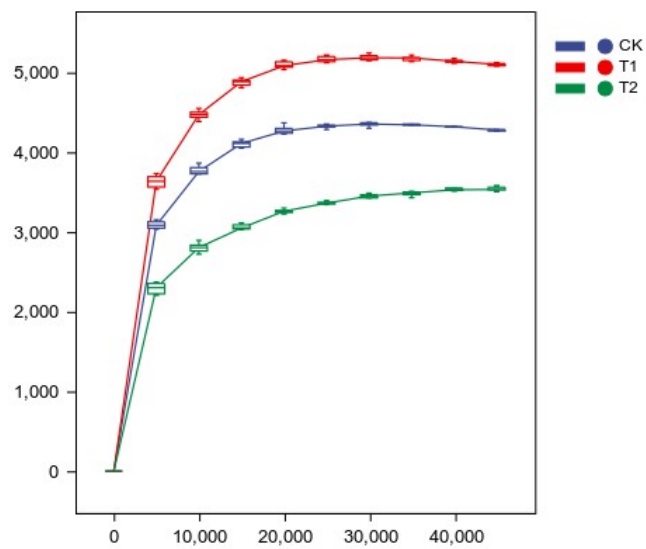


Fig. S1 The species accumulation and diversity curves of different treatments

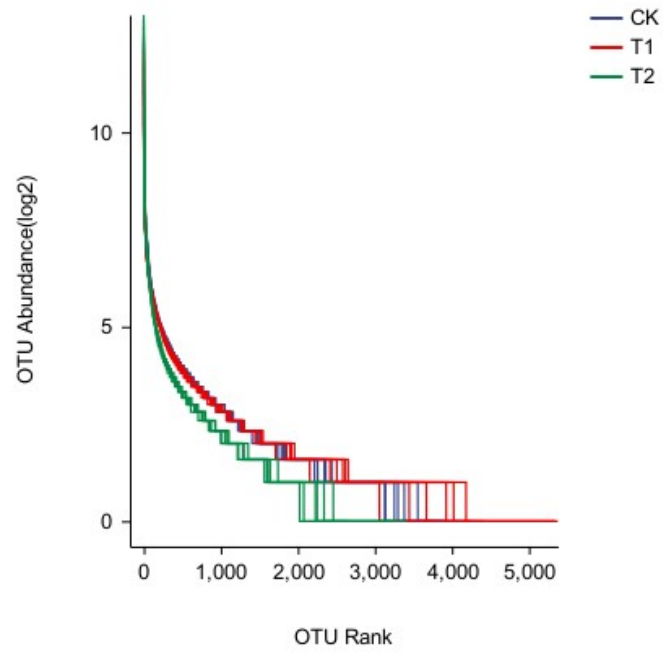


Fig. S2 Rank abundance curves