

Figure S1 a-f indicates the values of I_{geo} for Sb (a), As (b), Cd (c), Cr (d), Pb (e) and Cu (f) in TM, TS, MF, and PF, respectively. * above the bars indicate significant differences between different sites at the $p \leq 0.05$ level. TM, TS, MF, and PF indicates tailing residues, wasteland soils near to tailing reservoir, non-rhizosphere soils of maize, and non-rhizosphere soils of pepper, respectively.

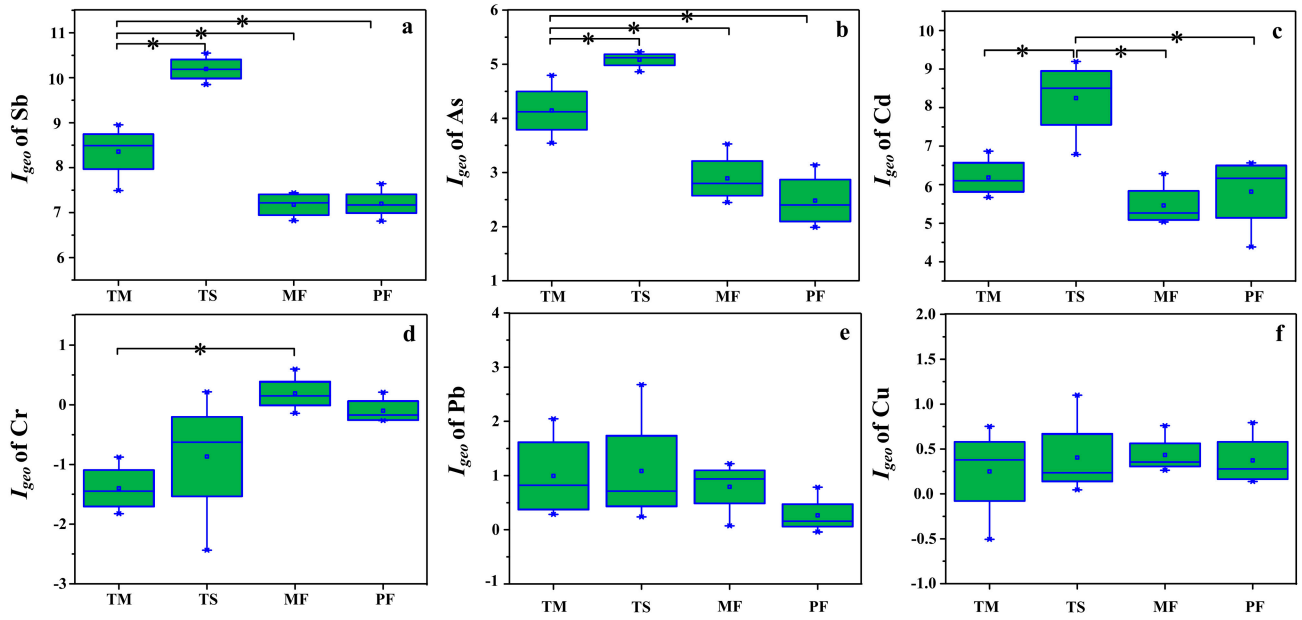


Figure S2 a-g Basic physicochemical properties of rhizosphere soils of 8 crops, including pH, EC, OM, total N concentration (Total N), total P concentration (Total P), available P concentration (AP), and available K concentration (AK). TM, TS, MF, and PF indicate tailing residues, wasteland soils near to tailing reservoir, non-rhizosphere soils of maize, and non-rhizosphere soils of pepper, respectively. Lowercase letters on the bars indicate significant differences among TS, PF, MF, and TM ($P \leq 0.05$).

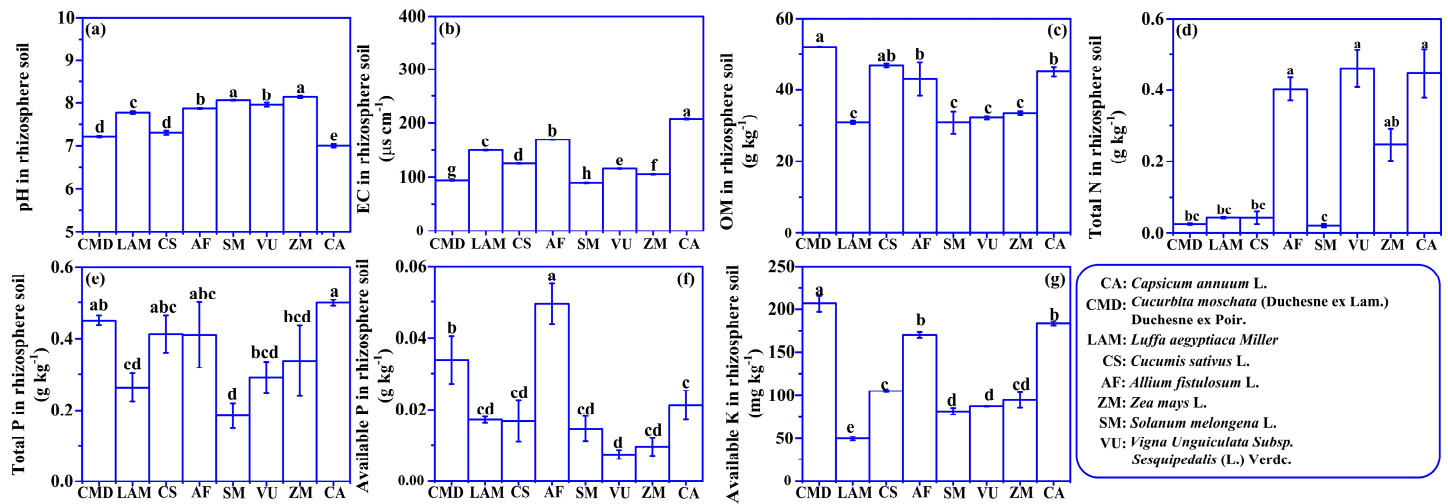


Figure S3 Alpha diversity indexes including dilution curve (a) and rank abundance curve (b). Beta diversity indexes including Non-Metric Multi-Dimensional Scaling analysis (NMDS, c) and Principal coordinates analysis (PCoA, d) of soil samples from different sites. TM, TS, MF, and PF indicates tailing residues, wasteland soils near to tailing reservoir, non-rhizosphere soils of maize, and non-rhizosphere soils of pepper, respectively.

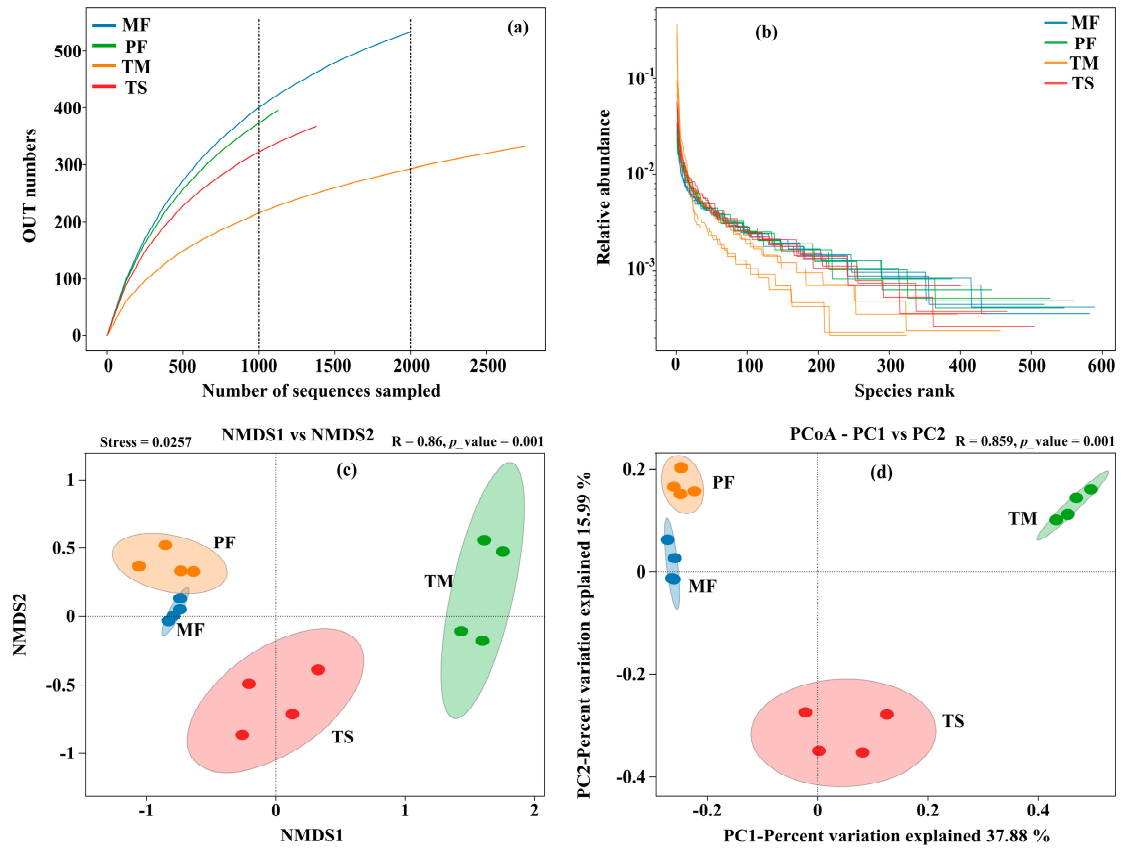


Figure S4 OUT numbers for MF, PF, TM, and TS (a). TM, TS, MF and PF indicates tailing residues, wasteland soils near to tailing reservoir, non-rhizosphere soils of maize, and non-rhizosphere soils of pepper, respectively. Alpha diversity index values of 16S rRNA bacterial libraries, including ACE (b) and Chao1 (c). (d) indicates the relative abundance of predominant bacterium at genus level.

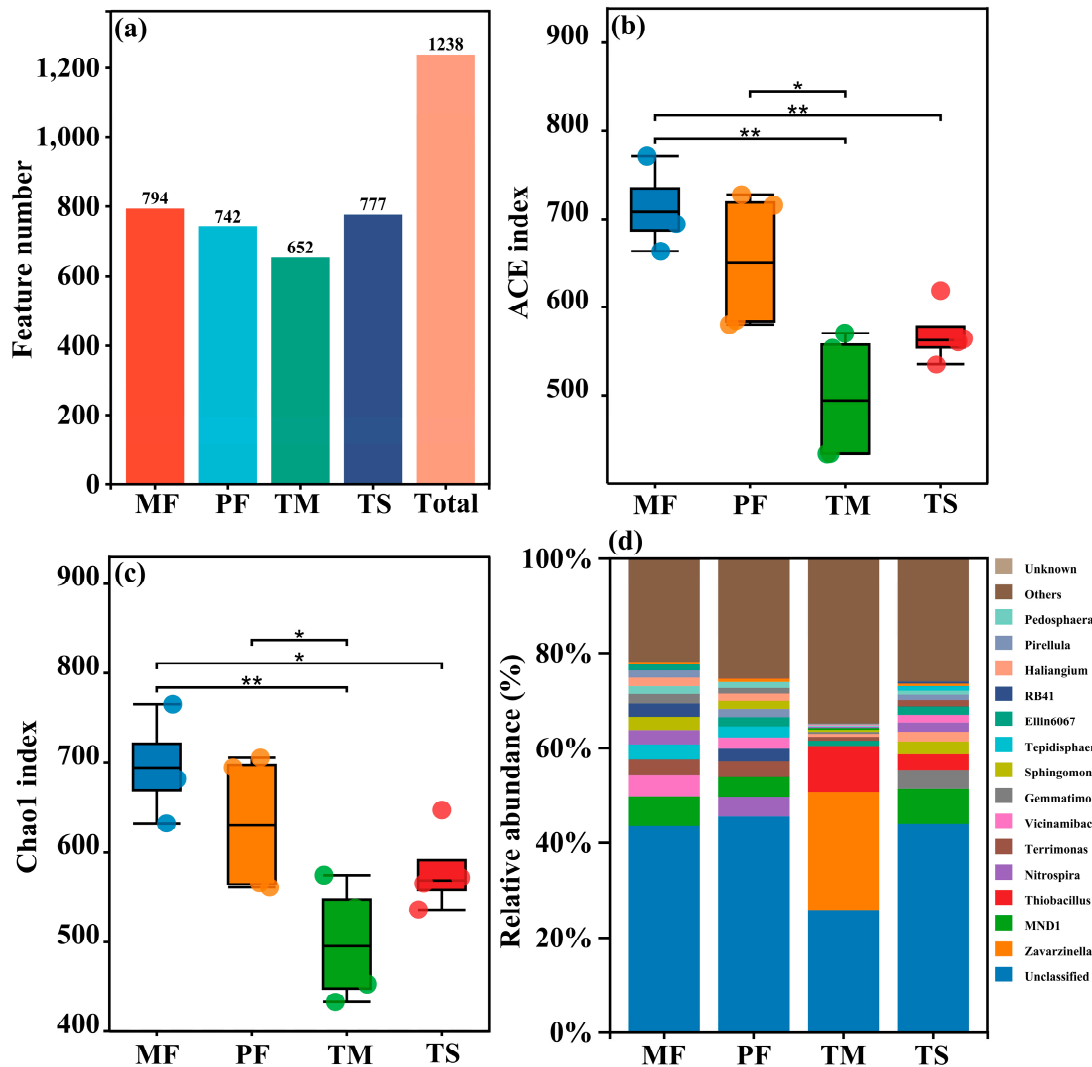


Figure S5 Relative abundances of the major phyla with significant differences among MF, PF, TM, and TS. ** and * above the bars indicate significant differences between different sites at the $p \leq 0.01$ and $p \leq 0.05$ level, respectively. TM, TS, MF, and PF indicates tailing residues, wasteland soils near to tailing reservoir, non-rhizosphere soils of maize, and non-rhizosphere soils of pepper, respectively.

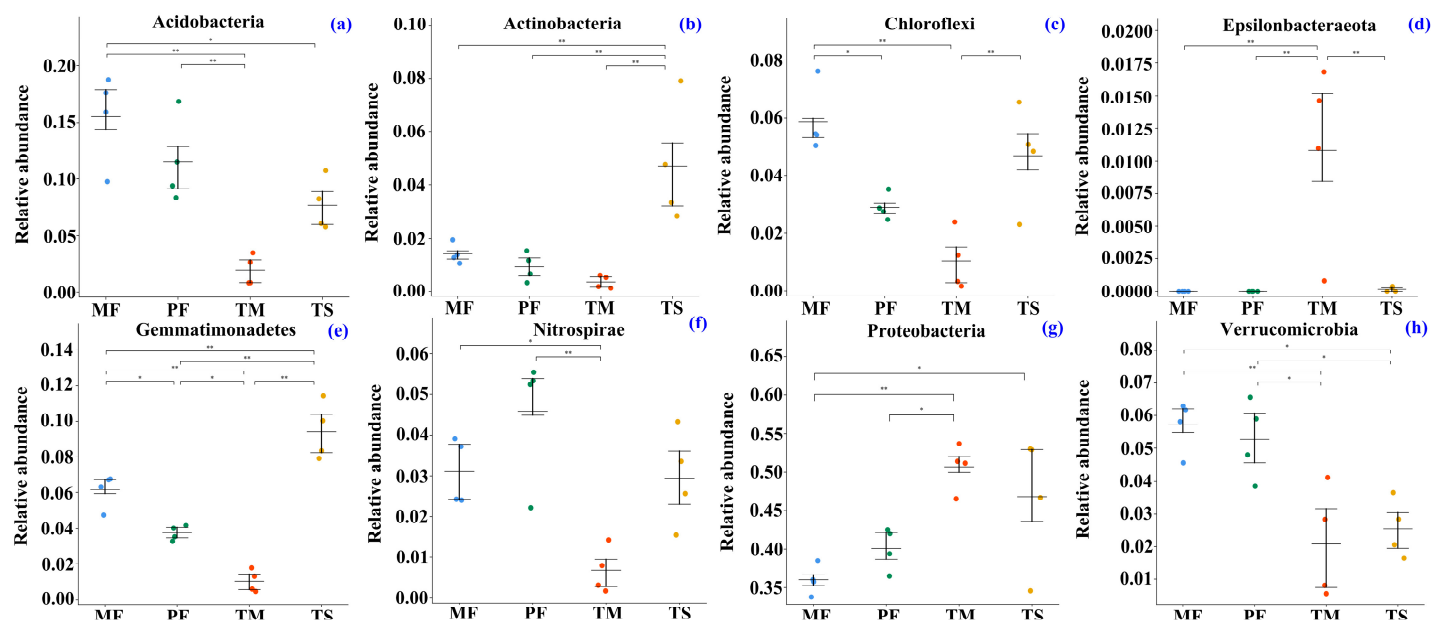


Table S1 Limits for metalloid concentrations in agricultural soils and eatable parts of crops.

Metal(loid)s		Sb	As	Cd	Cr	Pb	Cu					
Background values		2.98	15.7	0.126	71.4	29.7	27.3					
Risk controlling concentration of metal(loid) in agricultural lands (pH > 7.5, GB15618-2018)		---	25	0.6	250	170	100					
Risk intervention concentration of metal(loid) in agricultural lands (pH > 7.5, GB15618-2018)		---	100	4	1300	1000	---					
Plant species		National food safety standards–limit of pollutants in foods (GB 2762–2022)										
CA	---	0.5	0.05	0.50	0.10	---						
CMD	---	0.5	0.05	0.50	0.10	---						
LAM	---	0.5	0.05	0.50	0.10	---						
CS	Sb	---	As	0.5	Cd	0.05	Cr	0.50	Pb	0.10	Cu	---
AF	(mg kg ⁻¹)	---	(mg kg ⁻¹)	0.5	(mg kg ⁻¹)	0.2	(mg kg ⁻¹)	0.50	(mg kg ⁻¹)	0.30	(mg kg ⁻¹)	---
ZM	---	0.5	0.10	1.0	0.20	---						
SM	---	0.5	0.05	0.50	0.10	---						
VU	---	0.5	0.1	0.50	0.20	---						

Table S2 Assessment standards for soil pollution degree based on the geo-accumulation index (I_{geo}) and the potential ecological risk indexes (E_{ir} and RI).

Grade of I_{geo}		Value of I_{geo}	Degree of contamination
0		≤ 0	Unpolluted
1		0-1	Slightly polluted
2		1-2	Moderately polluted
3		2-3	Moderately severely polluted
4		3-4	Severely polluted
5		4-5	Severely extremely polluted
6		> 5	Extremely polluted
E_{ir}^j value	Individual pollution level	RI value	Comprehensive pollution level
< 40	Low	$RI < 150$	Low
$40 \leq E_{ir}^j < 80$	Moderate	$RI: 150 - 300$	Moderate
$80 \leq E_{ir}^j < 160$	Considerable	$RI: 300 - 600$	High
$160 \leq E_{ir}^j < 320$	High	$RI: \geq 600$	Serious
$E_{ir}^j \geq 320$	Very high		

Table S3 Concentrations of metal(loid)s in different tissues of plants and in rhizosphere soils of 8 crops.

	Plant species	Cr (mg kg ⁻¹)	Cu (mg kg ⁻¹)	As (mg kg ⁻¹)	Cd (mg kg ⁻¹)	Sb (mg kg ⁻¹)	Pb (mg kg ⁻¹)
Roots	CA	4.94	10.26	1.36	1.10	4.34	0.65
	CMD	3.83	9.53	4.25	0.85	7.18	1.91
	LAM	2.81	14.26	1.57	0.79	1.35	0.60
	CS	2.78	10.79	2.64	1.09	1.72	1.21
	AF	2.13	17.14	4.45	1.05	1.68	0.64
	ZM	3.92	6.90	1.33	0.42	5.10	0.80
	SM	7.68	9.60	3.34	2.11	5.08	1.06
	VU	2.53	6.75	0.52	0.35	1.25	0.41
	PM	2.48	12.10	46.10	0.57	548.6	3.64
	ECL	1.06	7.96	11.03	1.25	127.8	1.88
	BP	1.35	3.25	5.31	0.18	51.20	0.57
	AC	2.43	8.22	4.79	0.83	25.15	0.79
	IC	2.10	5.91	12.34	0.36	45.89	1.50
	CT	2.24	8.30	25.05	0.50	571.7	1.86
Stems	CA	3.14	9.84	0.64	1.30	2.26	0.29
	CMD	0.67	5.32	0.76	0.32	2.36	0.25
	LAM	3.52	8.86	2.37	0.94	2.57	0.74
	CS	0.38	8.52	7.41	0.74	9.79	1.05
	ZM	0.48	2.05	0.62	0.42	1.46	0.16
	SM	0.86	5.89	0.44	0.99	0.87	0.09
	VU	0.71	6.09	0.53	0.37	1.54	0.15
	PM	0.16	9.03	3.33	1.85	9.49	0.53
	ECL	0.49	3.88	3.34	1.37	12.40	0.46
	BP	0.83	3.29	4.76	0.41	34.78	2.28
	AC	0.13	5.94	3.05	0.56	86.87	0.60
	IC	1.66	1.60	1.03	0.43	2.32	0.12
	CT	0.48	7.65	2.33	0.45	43.39	0.24
Leaves	CA	0.51	13.95	7.06	1.69	18.17	2.38
	CMD	1.36	17.06	2.99	0.19	11.02	1.21
	LAM	0.62	17.95	4.87	0.85	10.96	3.65
	CS	0.32	17.52	3.30	0.29	9.04	0.75
	AF	0.21	4.28	0.42	0.33	1.23	0.12
	ZM	1.78	7.56	3.23	0.17	5.64	1.14
	SM	1.14	12.50	8.64	1.82	15.47	1.76
	VU	0.34	11.81	3.26	0.16	8.06	0.81
	PM	0.56	12.77	26.54	0.65	275.7	4.96
	ECL	0.34	12.78	19.14	1.36	77.31	2.70
	BP	0.55	3.61	25.50	0.27	55.34	3.76
	AC	0.30	19.68	30.44	1.44	63.01	3.17

	IC	0.74	2.18	11.79	0.20	14.43	1.66
	CT	0.55	12.72	8.16	0.42	126.6	1.94
Fruits	CA	0.31	10.23	0.56	0.56	2.38	0.13
	CMD	0.22	7.90	0.33	0.29	0.96	0.03
	LAM	0.19	13.92	0.68	0.48	0.94	0.05
	CS	0.11	10.80	0.93	0.39	0.57	0.09
	ZM	0.08	3.35	0.07	0.25	0.22	0.04
	SM	0.25	11.46	0.52	1.99	1.44	0.07
	VU	0.16	8.19	0.28	0.28	0.51	0.02
Metal(loid)							
concentrations in rhizosphere soils of crops	Cr	Cu	As	Cd	Sb	Pb	
	(mg kg ⁻¹)	(mg kg ⁻¹)	(mg kg ⁻¹)	(mg kg ⁻¹)	(mg kg ⁻¹)	(mg kg ⁻¹)	
CA	445.3	11.87	18046	4.10	464.7	17.67	
CMD	551.2	8.86	22769	3.89	490.1	17.95	
LAM	163.7	11.06	18703	3.99	130.2	18.71	
CS	315.5	10.46	22599	4.21	177.4	20.33	
AF	327.5	9.22	19273	4.05	144.7	19.10	
ZM	419.2	9.69	23111	4.04	423.2	19.35	
SM	591.6	8.49	23090	3.95	541.9	18.14	
VU	498.2	9.60	22726	3.90	166.7	19.49	

Table S4 Numbers of species at different levels in MF, PF, TM, and TS. The TM, TS, MF and PF indicates tailing residues, wasteland soils near to tailing reservoir, non-rhizosphere soils of maize, and non-rhizosphere soils of pepper, respectively.

Sample	Kindom	Phylum	Class	Order	Family	Genus	Species
MF1	1	11	22	48	66	104	94
MF 2	1	13	24	48	63	94	79
MF 3	1	14	22	51	70	103	92
MF 4	1	15	27	52	70	108	101
PF1	1	14	24	48	59	80	76
PF 2	1	17	29	52	65	104	93
PF 3	1	14	24	49	66	95	84
PF 4	1	15	25	56	73	106	100
TM1	1	19	31	60	87	134	108
TM2	1	17	30	53	75	121	102
TM3	1	16	24	49	72	115	97
TM4	1	15	26	54	76	119	95
TS1	1	15	27	51	68	98	85
TS2	1	14	22	48	62	97	84
TS3	1	16	27	54	76	117	94
TS4	1	17	28	54	69	102	84
Total	1	19	39	82	120	206	180

Table S5 Results of ANOVA analysis for the relative abundances of microbial communities (at genus levels). TM, TS, MF, and PF indicates tailing residues, wasteland soils near to tailing reservoir, non-rhizosphere soils of maize, and non-rhizosphere soils of pepper, respectively.

Phylum	Genus	Relative abundances (on average)				Results of ANOVA analysis (<i>p</i> values)					
		MF	TM	PF	TS	MF/T	MF/P	MF/T	TM/P	TM/T	PF/T
						M	F	S	F	S	S
Proteobacteria	<i>Reyranella</i>	0.002759	0.000227	0.003245	0.001478	*	ns	ns	**	ns	ns
	<i>Defluviimonas</i>	0	0.003082	0	0.000271	**	ns	ns	**	*	ns
	<i>Dongia</i>	0.006741	0.00018	0.011384	0.000974	**	ns	*	***	ns	***
	<i>Phenyllobacterium</i>	0.002543	0.000058	0.002501	0.001493	**	ns	ns	**	ns	ns
	<i>Rhodobacter</i>	0.000193	0.008247	0.000519	0.00067	***	ns	ns	***	***	ns
	<i>Sphingomonas</i>	0.028707	0.004198	0.0174	0.027357	***	ns	ns	ns	**	ns
	<i>Tabrizicola</i>	0	0.004156	0	0	***	ns	ns	***	***	ns
	<i>Hyphococcus</i>	0	0.001604	0	0	***	ns	ns	***	***	ns
	<i>Bradyrhizobium</i>	0.002211	0.000171	0.00334	0.001656	*	ns	ns	***	ns	ns
	<i>Annwoodia</i>	0	0.009109	0	0.000329	**	ns	ns	**	**	ns
	<i>Gallionella</i>	0	0.004328	0	0.00079	**	ns	ns	**	*	ns
	<i>Ideonella</i>	0.003035	0.024301	0.001845	0.006965	*	ns	ns	**	*	ns
	<i>Pseudolabrys</i>	0.00103	0.00020	0.00488	0.00050	ns	***	ns	***	ns	***
		9	4	9	5						
	<i>Sulfurisoma</i>	0	0.003988	0	0	**	ns	ns	**	**	ns
	<i>Sulfuritalea</i>	0	0.011619	0	0	**	ns	ns	**	**	ns
	<i>MND1</i>	0.06244	0.003729	0.04097	0.069367	**	ns	ns	ns	**	ns
	<i>Thiobacillus</i>	0.000111	0.091031	0.000317	0.025113	**	ns	ns	**	*	ns
	<i>Sulfurovum</i>	0	0.00956	0	0.000155	**	ns	ns	**	**	ns
	<i>Thermomonas</i>	0	0.004902	0.000129	0.000198	***	ns	ns	***	***	ns
	<i>Poivalibacter</i>	0.004817	0.000261	0.004008	0.001348	***	ns	**	**	ns	*
	<i>Geobacter</i>	0	0.008474	0	0	*	ns	ns	*	*	ns
Bacteroidota	<i>Flavihumibacter</i>	0.000937	0.011385	0.001118	0.001979	***	ns	ns	***	***	ns
	<i>Flavisolibacter</i>	0.010006	0.000201	0.010488	0.004607	**	ns	ns	**	ns	ns
	<i>Crocinitomix</i>	0	0.000282	0	0	*	ns	ns	*	*	ns
	<i>Runella</i>	0.000089	0.002214	0	0.000187	**	ns	ns	**	**	ns
	<i>Niastella</i>	0.00244	0	0.00342	0.00041	ns	ns	ns	*	ns	*
		8		9	2						
	<i>Sediminibacterium</i>	0	0.001529	0	0	***	ns	ns	***	***	ns
	<i>Adhaeribacter</i>	0.002773	0	0.000721	0	**	*	**	ns	ns	ns
Acidobacteriota	<i>Terrimonas</i>	0.034655	0.009049	0.034919	0.014476	**	ns	**	**	ns	**
	<i>Vicinamibacter</i>	0.04385	0.001438	0.022866	0.018437	***	**	**	**	*	ns
	<i>RB41</i>	0.028547	0.000494	0.028772	0.005451	*	ns	*	*	ns	*
	<i>Geothrix</i>	0	0.005343	0	0	*	ns	ns	*	*	ns
	<i>Bryobacter</i>	0.003345	0	0.000777	0.001082	**	*	*	ns	ns	ns
Verrucomicrobiota	<i>Candidatus_Solibacter</i>	0.001163	0	0.001765	0	**	ns	**	***	ns	***
	<i>Candidatus_Udaeobacter</i>	0.004969	0	0.007595	0.000093	*	ns	*	**	ns	**
	<i>Chthoniobacter</i>	0.005749	0.000212	0.003909	0.000496	*	ns	*	ns	ns	ns
Planctomycetota	<i>Pedosphaera</i>	0.017765	0.002378	0.011968	0.010361	***	*	*	**	**	ns
	<i>Gemmata</i>	0.003859	0.000262	0.005188	0.002676	*	ns	ns	**	ns	ns
	<i>Pirellula</i>	0.015004	0.000847	0.01742	0.009909	*	ns	ns	**	ns	ns
	<i>Singulisphaera</i>	0.000642	0.000058	0.000103	0.000578	**	**	ns	ns	*	*
	<i>Zavarzinella</i>	0.005013	0.230923	0.006524	0.006396	**	ns	ns	**	**	ns
Bacillota	<i>Tepidisphaera</i>	0.032047	0.000178	0.022151	0.011041	***	ns	**	**	ns	ns
	<i>Fusibacter</i>	0	0.000763	0	0	*	ns	ns	*	*	ns
Gemmatimonadetes (also called	<i>Gemmatimonas</i>	0.020435	0.004323	0.013973	0.037815	*	ns	**	ns	***	***

Gemmatimonadota)											
Flavobacteria	<i>Flavobacterium</i>	0.004032	0.012003	0.007955	0.00071	ns	ns	ns	ns	*	ns
Chloroflexi	<i>UTCFX1</i>	0.01171	0.001335	0.008955	0.006988	**	ns	ns	*	ns	ns
Nitrospirota	<i>Nitrospira</i>	0.028569	0.002752	0.040509	0.017533	**	ns	ns	***	ns	**
Myxococcota	<i>Haliangium</i>	0.01726	0.005999	0.015792	0.018665	*	ns	ns	*	**	ns
Actinomycetota	<i>Yonghaparkia</i>	0	0.000611	0	0	**	ns	ns	**	**	ns
-----	<i>Unclassified</i>	0.434967	0.270026	0.454394	0.448126	*	ns	ns	**	**	ns
Unknown	<i>ADurb.Bin063-1</i>	0.004296	0.000923	0.005651	0.001868	ns	ns	ns	*	ns	ns

⁽¹⁾ Values are means \pm SD (n = 4). *, ** and *** indicate significant differences at 0.05, 0.01 and 0.001 level,

respectively. ns indicates non-significant differences.

Table S6 Relative abundances of microbial communities (at phylum and genus levels) classified into different phenotypes based on BUGbase prediction analysis. TM, TS, MF, and PF indicates tailing residues, wasteland soils near to tailing reservoir, non-rhizosphere soils of maize, and non-rhizosphere soils of pepper, respectively.

Phenotypes			MF	PF	TM	TS
Aerobic	Phyla	Acidobacteria	0.059038	0.060656	0	0.025365
		Actinobacteria	0	0	0	0.046584
		Bacteroidetes	0.069057	0.075527	0.050921	0.066727
		Planctomycetes	0.052669	0.050047	0	0.045417
		Proteobacteria	0.107302	0.130725	0.195023	0.200437
		Verrucomicrobia	0.043118	0.04243	0	0
	Genera	<i>f_Chitinophagaceae</i>	0.043399	0.040044	0.013826	0.030258
		<i>f_Comamonadaceae</i>	0	0	0.006467	0.004404
		<i>f_Cytophagaceae</i>	0.005645	0.007625	0.008815	0.007837
		<i>f_Ellin515</i>	0	0.006183	0	0
		<i>f_Ellin517</i>	0	0	0	0.005956
		<i>f_Ellin6075</i>	0.007431	0	0	0.010165
		<i>f_Gaiellaceae</i>	0	0	0	0.016527
		<i>f_Haliangiaceae</i>	0.006205	0.007929	0.005773	0.011429
		<i>f_Methylophilaceae</i>	0	0	0	0.007679
		<i>f_Nitrosomonadaceae</i>	0	0	0.006019	0
		<i>f_Pirellulaceae</i>	0.012706	0.020344	0	0.024847
		<i>f_Saprospiraceae</i>	0.004816	0.007208	0	0.015094
		<i>f_Sinobacteraceae</i>	0.00634	0	0	0.03772
		<i>f_Sphingomonadaceae</i>	0.005902	0	0	0
		<i>f_Xanthomonadaceae</i>	0.007788	0.016864	0.007626	0.018181
		<i>f_auto67_4W</i>	0	0.005471	0	0
		<i>Candidatus_Koribacter</i>	0	0	0	0.005142
		<i>DA101</i>	0.005831	0.009349	0	0
		<i>Flaviumibacter</i>	0	0	0.011951	0
		<i>Flavisolibacter</i>	0.007332	0.008139	0	0
		<i>Flavobacterium</i>	0	0	0.004423	0
		<i>Gallionella</i>	0	0	0.007684	0
		<i>Gemmata</i>	0.006275	0	0	0
		<i>Hydrogenophaga</i>	0	0	0.02949	0
		<i>Kaistobacter</i>	0.016322	0.013204	0	0.024178
		<i>Limnohabitans</i>	0.00869	0.009478	0	0.009188
		<i>Luteolibacter</i>	0	0	0.006255	0
		<i>Lysobacter</i>	0	0.00526	0	0
		<i>Pirellula</i>	0.023672	0.011554	0	0
		<i>Planctomyces</i>	0.004933	0.009829	0	0.011062
		<i>Polaromonas</i>	0	0	0	0.004891
		<i>Rhodoferrax</i>	0	0	0.038869	0
		<i>Sulfuritalea</i>	0	0	0.012274	0
		<i>Thermomonas</i>	0.005558	0.009762	0.007662	0
Anaerobic	Phyla	Acidobacteria	0.094999	0.051555	0.018529	0.048347
		Planctomycetes	0.155424	0.129525	0	0.06801
		Proteobacteria	0	0	0.031714	0
	Genera	<i>f_Desulfobulbaceae</i>	0	0	0.003752	0
		<i>f_Helicobacteraceae</i>	0	0	0.009405	0
		<i>f_Holophagaceae</i>	0	0	0.003983	0
		<i>f_Opitutaceae</i>	0.002433	0	0.006963	0.00403
		<i>f_Pelobacteraceae</i>	0	0	0.001861	0
		<i>f_RB40</i>	0.005066	0.002778	0	0.001913
		<i>f_SB-1</i>	0	0	0.004186	0
		<i>f_Thiotrichaceae</i>	0	0	0.002465	0.001816
		<i>f_mb2424</i>	0.014838	0.003107	0	0.00647
		<i>Geobacter</i>	0	0	0.006502	0
		<i>Geothrix</i>	0	0	0.004736	0
		<i>Leptospira</i>	0	0	0.002761	0.005326
		<i>Opitutus</i>	0.004305	0.00237	0	0.00393
Contains_Mobile_Elements	Phyla	Bacteroidetes	0.067609	0.072968	0	0.066407
		Cyanobacteria	0	0	0.337385	0
		Gemmatimonadetes	0	0	0	0.090378
		Planctomycetes	0.208093	0.179572	0	0.113427
		Proteobacteria	0.278866	0.302607	0.496047	0.417947
		Verrucomicrobia	0.049857	0	0	0
	Genera	<i>f_Chitinophagaceae</i>	0.043399	0.040044	0.013826	0.030258
		<i>f_Comamonadaceae</i>	0	0.015395	0.013136	0

		<i>f_Cytophagaceae</i>	0	0	0.008815	0
		<i>f_Gaiellaceae</i>	0	0	0	0.016527
		<i>f_Haliangiaceae</i>	0	0	0	0.011429
		<i>f_Helicobacteraceae</i>	0	0	0.009405	0
		<i>f_Pirellulaceae</i>	0.012706	0.020344	0	0.024847
		<i>f_Rhodospirillaceae</i>	0	0.008127	0	0
		<i>f_Saprospiraceae</i>	0	0	0	0.015094
		<i>f_Sinobacteraceae</i>	0.015878	0.00996	0	0.043395
		<i>f_Syntrophobacteraceae</i>	0.020697	0.014675	0	0
		<i>f_Xanthomonadaceae</i>	0	0.016864	0	0.018181
		DA101	0	0.009349	0	0
		Flaviumibacter	0	0	0.011951	0
		Flavisolibacter	0	0.008139	0	0
		Hydrogenophaga	0	0	0.02949	0
		Kaistobacter	0.016322	0.013204	0	0.024178
		Leptothrix	0.012255	0	0.045823	0.023755
		Limnhabitans	0.00869	0.009478	0	0.009188
		Methylibium	0.017709	0.027357	0.016105	0.013662
		Pirellula	0.023672	0.011554	0	0
		Planctomyces	0	0.009829	0	0.011062
		Rhodobacter	0	0	0.009401	0
		Rhodoferrax	0	0	0.038869	0
		Rubrivivax	0	0	0.025478	0
		Sulfuritalea	0	0	0.012274	0
		Thermomonas	0	0.009762	0	0
		Thiobacillus	0	0	0.080586	0.023508
Facultatively_Anaerobic	Phyla	Proteobacteria	0.057932	0.084933	0.257655	0.101216
	Genera	<i>f_Comamonadaceae</i>	0	0.014295	0	0
		<i>f_Rhodospirillaceae</i>	0	0.008127	0	0
		Leptothrix	0.012255	0	0.045823	0.023755
		Methylibium	0.017709	0.027357	0.016105	0.013662
		Rhodobacter	0	0	0.009401	0
		Rubrivivax	0	0	0.025478	0
		Thiobacillus	0	0	0.080586	0.023508
Forms_Biofilms	Phyla	Acidobacteria	0.154037	0.112211	0	0.073712
		Nitrospirae	0.146483	0.20991	0	0.087702
		Planctomycetes	0.208093	0.179572	0	0.113427
		Proteobacteria	0.22553	0.253981	0.479719	0.395495
		Verrucomicrobia	0.049857	0	0	0
	Genera	<i>f_0319-6A21</i>	0.080294	0.111443	0	0.025122
		<i>f_Comamonadaceae</i>	0	0.015395	0.013136	0
		<i>f_Gaiellaceae</i>	0	0	0	0.016527
		<i>f_Pirellulaceae</i>	0.012706	0.020344	0	0.024847
		<i>f_Sinobacteraceae</i>	0.015878	0	0	0.043395
		<i>f_Xanthomonadaceae</i>	0	0.016864	0	0.018181
		<i>f_mb2424</i>	0.014838	0	0	0
		Hydrogenophaga	0	0	0.02949	0
		Kaistobacter	0.016322	0.013204	0	0.024178
		Leptothrix	0.012255	0	0.045823	0.023755
		Methylibium	0.017709	0.027357	0.016105	0.013662
		Nitrospira	0.064048	0.094547	0	0.042784
		Pirellula	0.023672	0.011554	0	0
		Rhodoferrax	0	0	0.038869	0
		Rubrivivax	0	0	0.025478	0
		Sulfuritalea	0	0	0.012274	0
		Thiobacillus	0	0	0.080586	0.023508
Gram_Negative	Phyla	Acidobacteria	0.154037	0.112211	0	0.073712
		Bacteroidetes	0.069057	0.075527	0.055107	0.066727
		Cyanobacteria	0	0	0.337385	0
		Gemmatimonadetes	0	0	0	0.090378
		Nitrospirae	0.146483	0.20991	0	0.087702
		Planctomycetes	0.209478	0.179936	0	0.117155
		Proteobacteria	0.278866	0.302607	0.50441	0.417947
	Genera	<i>f_0319-6A21</i>	0.080294	0.111443	0	0.025122
		<i>f_Chitinophagaceae</i>	0.043399	0.040044	0.013826	0.030258
		<i>f_Comamonadaceae</i>	0	0.015395	0.013136	0
		<i>f_Haliangiaceae</i>	0	0	0	0.011429
		<i>f_Pirellulaceae</i>	0.012706	0.020344	0	0.024847
		<i>f_Saprospiraceae</i>	0	0	0	0.015094
		<i>f_Sinobacteraceae</i>	0.015878	0	0	0.043395
		<i>f_Syntrophobacteraceae</i>	0.020697	0.014675	0	0
		<i>f_Xanthomonadaceae</i>	0	0.016864	0	0.018181
		<i>f_mb2424</i>	0.014838	0	0	0
		Flaviumibacter	0	0	0.011951	0
		Hydrogenophaga	0	0	0.02949	0
		Kaistobacter	0.016322	0.013204	0	0.024178

		<i>Leptothrix</i>	0.012255	0	0.045823	0.023755		
		<i>Methylibium</i>	0.017709	0.027357	0.016105	0.013662		
		<i>Nitrospira</i>	0.064048	0.094547	0	0.042784		
		<i>Pirellula</i>	0.023672	0.011554	0	0		
		<i>Rhodoferax</i>	0	0	0.038869	0		
		<i>Rubrivivax</i>	0	0	0.025478	0		
		<i>Sulfuritalea</i>	0	0	0.012274	0		
		<i>Thiobacillus</i>	0	0	0.080586	0.023508		
Gram_Positive	Phyla	Actinobacteria	0.01267	0.007562	0	0.047523		
		Armatimonadetes	0	0	0	0.009281		
		Chloroflexi	0	0	0	0.006973		
	Genera	<i>f_Gaiellaceae</i>	0.003571	0.002568	0	0.016527		
		<i>Agromyces</i>	0.001697	0	0	0		
		<i>Iamia</i>	0	0	0	0.002203		
<i>PSB-M-3</i>		0	0	0.002811	0			
Potentially_Pathogenic	Phyla	Proteobacteria	0.18266	0.215064	0.445623	0.34203		
	Genera	<i>f_Comamonadaceae</i>	0	0.015395	0.013136	0		
		<i>f_Sinobacteraceae</i>	0.015878	0.00996	0	0.043395		
		<i>f_Xanthomonadaceae</i>	0	0.016864	0	0.018181		
		<i>Hydrogenophaga</i>	0	0	0.02949	0		
		<i>Leptothrix</i>	0.012255	0	0.045823	0.023755		
		<i>Limnohabitans</i>	0.00869	0.009478	0	0.009188		
		<i>Methylibium</i>	0.017709	0.027357	0.016105	0.013662		
		<i>Rhodoferax</i>	0	0	0.038869	0		
		<i>Rubrivivax</i>	0	0	0.025478	0		
		<i>Sulfuritalea</i>	0	0	0.012274	0		
		<i>Thermomonas</i>	0	0.009762	0	0		
		<i>Thiobacillus</i>	0	0	0.080586	0.023508		
		Stress_Tolerant	Phyla	Bacteroidetes	0.068674	0.075406	0.049645	0.066485
				Cyanobacteria	0	0	0.335617	0
Gemmatimonadetes	0.049453			0	0	0.090378		
Planctomycetes	0.209478			0.179936	0	0.117155		
Proteobacteria	0.210961			0.262067	0.47538	0.376934		
Verrucomicrobia	0.049857			0	0	0		
Genera	<i>f_Chitinophagaceae</i>		0.043399	0.040044	0.013826	0.030258		
	<i>f_Comamonadaceae</i>		0	0.015395	0.013136	0		
	<i>f_Cytophagaceae</i>		0	0	0.008815	0		
	<i>f_Gaiellaceae</i>		0	0	0	0.016527		
	<i>f_Haliangiaceae</i>		0	0	0	0.011429		
	<i>f_Pirellulaceae</i>		0.012706	0.020344	0	0.024847		
	<i>f_Rhodospirillaceae</i>		0	0.008127	0	0		
	<i>f_Saprospiraceae</i>		0	0	0	0.015094		
	<i>f_Sinobacteraceae</i>		0.015878	0.00996	0	0.043395		
	<i>f_Xanthomonadaceae</i>		0	0.016864	0	0.018181		
	<i>DA101</i>		0	0.009349	0	0		
	<i>Flaviumibacter</i>		0	0	0.011951	0		
	<i>Flavisolibacter</i>		0	0.008139	0	0		
	<i>Hydrogenophaga</i>		0	0	0.02949	0		
	<i>Leptothrix</i>		0.012255	0	0.045823	0.023755		
	<i>Limnohabitans</i>		0.00869	0.009478	0	0.009188		
	<i>Methylibium</i>		0.017709	0.027357	0.016105	0.013662		
	<i>Pirellula</i>		0.023672	0.011554	0	0		
	<i>Planctomyces</i>		0	0.009829	0	0.011062		
	<i>Rhodobacter</i>		0	0	0.009401	0		
	<i>Rhodoferax</i>		0	0	0.038869	0		
	<i>Rubrivivax</i>		0	0	0.025478	0		
	<i>Sulfuritalea</i>		0	0	0.012274	0		
	<i>Thermomonas</i>		0	0.009762	0	0		
	<i>Thiobacillus</i>		0	0	0.080586	0.023508		