Supporting Materials

Table S1 Mean concentrations of antibiotics

Site	Sample Type	Tetracyclines (**µg/kg**)			Quinolones (**µg/kg**)		Sulfonamides (**µg/kg**)			
		CTC[a]	OTC	TCN	NOR	OLF	SMX	SDZ	SMN	SMR
CP	**Control Soil**	11.364	0.507	0.574	0.100	0.087	0.169	0.146	0.035	0
	Compost-amended Soil	102.421	191.843	89.377	0.205	0.025	7.926	0.021	0.179	0
	Compost	3443.832	818.471	502.775	5.422	8.047	16.578	2.179	0.208	0.181
	Manure	2793.496	241.961	178.243	6.799	10.039	21.514	1.340	0.807	0.192
DX	**Control Soil**	10.497	5.163	7.036	0.014	0.006	7.629	0.045	0.017	0.007
	Compost-amended Soil	95.434	0.771	1.833	1.494	0.020	7.772	0	0	0
	Compost	2244.113	8.766	117.416	4.122	16.156	6.933	0.934	0.156	0.157
	Manure	3763.561	3.325	162.006	4.537	0.280	14.781	0.597	0.148	0.259
HZ	**Control Soil**	1.944	0.048	0.108	1.059	0.004	0	0	0	0
	Compost-amended Soil	17.143	1.357	5.550	0.466	0.043	8.783	0.937	0.070	0
	Compost	5049.911	2948.120	227.718	88.056	2.729	16.096	73.006	0.332	0.423
	Manure	2902.975	15.546	166.690	1602.818	4.668	11.824	0.710	0.167	0.426
JG	**Control Soil**	5.128	12.127	0.576	0.042	0.015	7.288	0	0.565	0
	Compost-amended Soil	109.302	13.324	6.036	0.230	0.025	7.898	0.096	0.108	0.049
	Compost	9451.275	80.422	936.343	1.270	42.548	13.147	6.620	0.354	1.273
	Manure	1244.883	22.586	72.506	2.439	41.485	10.142	4.200	0.087	0.220
ZZ	**Control Soil**	4.483	12.689	0.578	0.705	0.021	0	0	0.419	0
	Compost-amended Soil	40.583	82.565	2.860	2.882	0.014	0	0	1.290	0
	Compost	7898.167	362.608	262.934	14.746	1.089	12.674	3.997	7.181	0.242
	Manure	10883.089	1168.248	431.762	6.235	2.358	15.302	2.198	2.351	0.204

Notes: a) Abbreviations: CTC: chlortetracycline; OTC: oxytetracycline; TCN: tetracycline; NOR: norfloxacin; OFL: ofloxacin; SMX: sulfamethoxazole; SDZ: sulfadiazine; SMN: sulfadimidine; SMR: sulfamerazine

Table S2 Pearson correlations between β-diversity (based on Bray-Curtis dissimilarity) of ARGs and bacterial OTUs in five sampling sites

Sample site	***r***	***P***
CP	0.718	**< 0.001**[a)]
DX	0.563	**< 0.001**
HZ	0.649	**< 0.001**
JG	0.536	**0.032**
ZZ	0.674	**< 0.001**

Notes: a) Significant *P*-values less than 0.050 are shown in bold

Table S3 Mantel tests between resistome and bacterial taxonomic distance matrices based on Bray-Curtis matrix

Samples	***r***	***P***
All samples	0.600	**0.001**[a)]
Manure	0.346	**0.001**
Compost	0.430	**0.001**
Compost-amended Soil	0.318	**0.001**
Control Soil	−0.018	0.481

Notes: a) Significant *P*-values less than 0.050 are shown in bold

Table S4 Significant, positive correlation pairs between bacterial genera and ARGs in the group of manure and compost samples. The significance of the Pearson correlation is determined by $P < 0.050$

Bacteria					ARG		Compost		Manure	
Phylum	Class	Order	Family	Genus	Name	Category	*r*	*P*	*r*	*P*
Proteobacteria	*Betaproteobacteria*	*Burkholderiales*	*Comamonadaceae*	*Giesbergeria*	*B_lactamase_A_5f0_2*	Antibiotic inactivation	0.466	0.044	0.705	0.001
Firmicutes	*Clostridia*	*Clostridiales*	*Clostridiaceae 2*	*Alkaliphilus*	*B_lactamase_A_5f0_firmicutes*	Antibiotic inactivation	0.693	0.001	0.742	0.000
Proteobacteria	*Gammaproteobacteria*	*Pseudomonadales*	*Moraxellaceae*	*Acinetobacter*	*B_lactamase_A_5f0_firmicutes*	Antibiotic inactivation	0.481	0.037	0.663	0.001
Proteobacteria	*Gammaproteobacteria*	*Xanthomonadales*	*Xanthomonadaceae*	*Stenotrophomonas*	*B_lactamase_A_5f0_firmicutes*	Antibiotic inactivation	0.698	0.001	0.691	0.001
Actinobacteria	*Actinobacteria*	*Coriobacteriales*	*Coriobacteriaceae*	*Olsenella*	*fosB*	Antibiotic inactivation	0.673	0.002	0.479	0.033
Firmicutes	*Clostridia*	*Clostridiales*	*Eubacteriaceae*	*Alkalibaculum*	*fosX*	Antibiotic inactivation	0.527	0.020	0.490	0.028
Firmicutes	*Erysipelotrichia*	*Erysipelotrichales*	*Erysipelotrichaceae*	*Catenibacterium*	*MFS_antibiotic_5f0_Firmicutes*	Antibiotic efflux	0.644	0.003	0.717	0.000

Firmicutes	*Erysipelotrichia*	*Erysipelotrichales*	*Erysipelotrichaceae*	*Holdemania*	*MFS_antibiotic_5f0_Firmicutes*	Antibiotic efflux	0.601	0.007	0.559	0.010
Firmicutes	*Clostridia*	*Clostridiales*	*Lachnospiraceae*	*Catonella*	*Tet*	Antibiotic efflux	0.479	0.038	0.488	0.029
Firmicutes	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	*Clostridium IV*	*Tet*	Antibiotic efflux	0.600	0.007	0.637	0.003
Firmicutes	*Clostridia*	*Clostridiales*	*Ruminococcaceae*	*Subdoligranulum*	*Tet*	Antibiotic efflux	0.671	0.002	0.509	0.022
Proteobacteria	*Gammaproteobacteria*	*Enterobacteriales*	*Enterobacteriaceae*	*Pseudocitrobacter*	*Tet*	Antibiotic efflux	0.558	0.013	0.568	0.009
Proteobacteria	*Gammaproteobacteria*	*Pseudomonadales*	*Moraxellaceae*	*Acinetobacter*	*Tet*	Antibiotic efflux	0.823	0.000	0.914	0.000
Firmicutes	*Clostridia*	*Clostridiales*	*ClostridialesIncertae Sedis XI*	*Tissierella*	*Van_2*	Target protection/redundancy	0.581	0.009	0.470	0.037
Firmicutes	*Clostridia*	*Clostridiales*	*Eubacteriaceae*	*Alkalibaculum*	*vgb*	Antibiotic inactivation	0.571	0.011	0.622	0.003

Table S5 Significant, positive correlation pairs between bacterial genera and ARGs in the group of compost-amended soil and control soil samples. The significance of the Pearson correlation is determined by $P < 0.050$

Bacteria					**ARG**		**Control soil**		**Compost-amended soil**	
Phylum	Class	Order	Family	Genus	Name	Category	*r*	*P*	*r*	*P*
Actinobacteria	*Actinobacteria*	*Actinomycetales*	*Microbacteriaceae*	*Diaminobutyricimonas*	*ABC_antibiotic_transporter*	Antibiotic efflux	0.450	0.047	0.505	0.023
Actinobacteria	*Actinobacteria*	*Actinomycetales*	*Micromonosporaceae*	*Dactylosporangium*	*b_lactamase*	Antibiotic inactivation	0.623	0.003	0.509	0.022
Actinobacteria	*Actinobacteria*	*Actinomycetales*	*Micromonosporaceae*	*Luedemannella*	*b_lactamase*	Antibiotic inactivation	0.493	0.027	0.607	0.005
Proteobacteria	*Alphaproteobacteria*	*Rhizobiales*	*Bradyrhizobiaceae*	*Bradyrhizobium*	*b_lactamase*	Antibiotic inactivation	0.513	0.021	0.638	0.002
Proteobacteria	*Betaproteobacteria*	*Ferritrophicales*	*Ferritrophicaceae*	*Ferritrophicum*	*b_lactamase*	Antibiotic inactivation	0.454	0.044	0.533	0.015
Actinobacteria	*Actinobacteria*	*Actinomycetales*	*Pseudonocardiaceae*	*Alloactinosynnema*	*B_lactamase_5f0_D*	Antibiotic inactivation	0.499	0.025	0.625	0.003
Proteobacteria	*Alphaproteobacteria*	*Rhizobiales*	*Aurantimonadaceae*	*Fulvimarina*	*B_lactamase_5f0_D*	Antibiotic inactivation	0.513	0.021	0.556	0.011

Proteobacteria	*Alphaproteobacteria*	*Rhizobiales*	*Methylocystaceae*	*Methylosinus*	*B_lactamase_5f0_D*	Antibiotic inactivation	0.474	0.035	0.622	0.003
Proteobacteria	*Gammaproteobacteria*	*Oceanospirillales*	*Hahellaceae*	*Kistimonas*	*fosA*	Antibiotic inactivation	0.512	0.021	0.582	0.007
Armatimonadetes	*Armatimonadetes Gp5*	*Armatimonadetes Gp5*	*Armatimonadetes Gp5*	*Armatimonadetes Gp5*	*MFS_antibiotic*	Antibiotic efflux	0.510	0.021	0.634	0.003
Acidobacteria	*Acidobacteria Gp11*	*Gp11*	*Gp11*	*Gp11*	*Van*	Target protection/redundancy	0.459	0.042	0.502	0.024
Bacteroidetes	*Sphingobacteriia*	*Sphingobacteriales*	*Saprospiraceae*	*Phaeodactylibacter*	*Van*	Target protection/redundancy	0.513	0.021	0.519	0.019
Chloroflexi	*Caldilineae*	*Caldilineales*	*Caldilineaceae*	*Caldilinea*	*Van*	Target protection/redundancy	0.606	0.005	0.579	0.007
Firmicutes	*Negativicutes*	*Selenomonadales*	*Acidaminococcaceae*	*Succiniclasticum*	*Van*	Target protection/redundancy	0.500	0.025	0.503	0.024
Proteobacteria	*Betaproteobacteria*	*Burkholderiales*	*Burkholderialesincertaesedis*	*Aquabacterium*	*Van*	Target protection/redundancy	0.512	0.021	0.706	0.001

Proteobacteria	*Betaproteobacteria*	*Ferritrophicales*	*Ferritrophicaceae*	*Ferritrophicum*	*Van*	Target protection/redundancy	0.482	0.031	0.514	0.020
Proteobacteria	*Betaproteobacteria*	*Rhodocyclales*	*Rhodocyclaceae*	*Ferribacterium*	*Van*	Target protection/redundancy	0.533	0.016	0.527	0.017

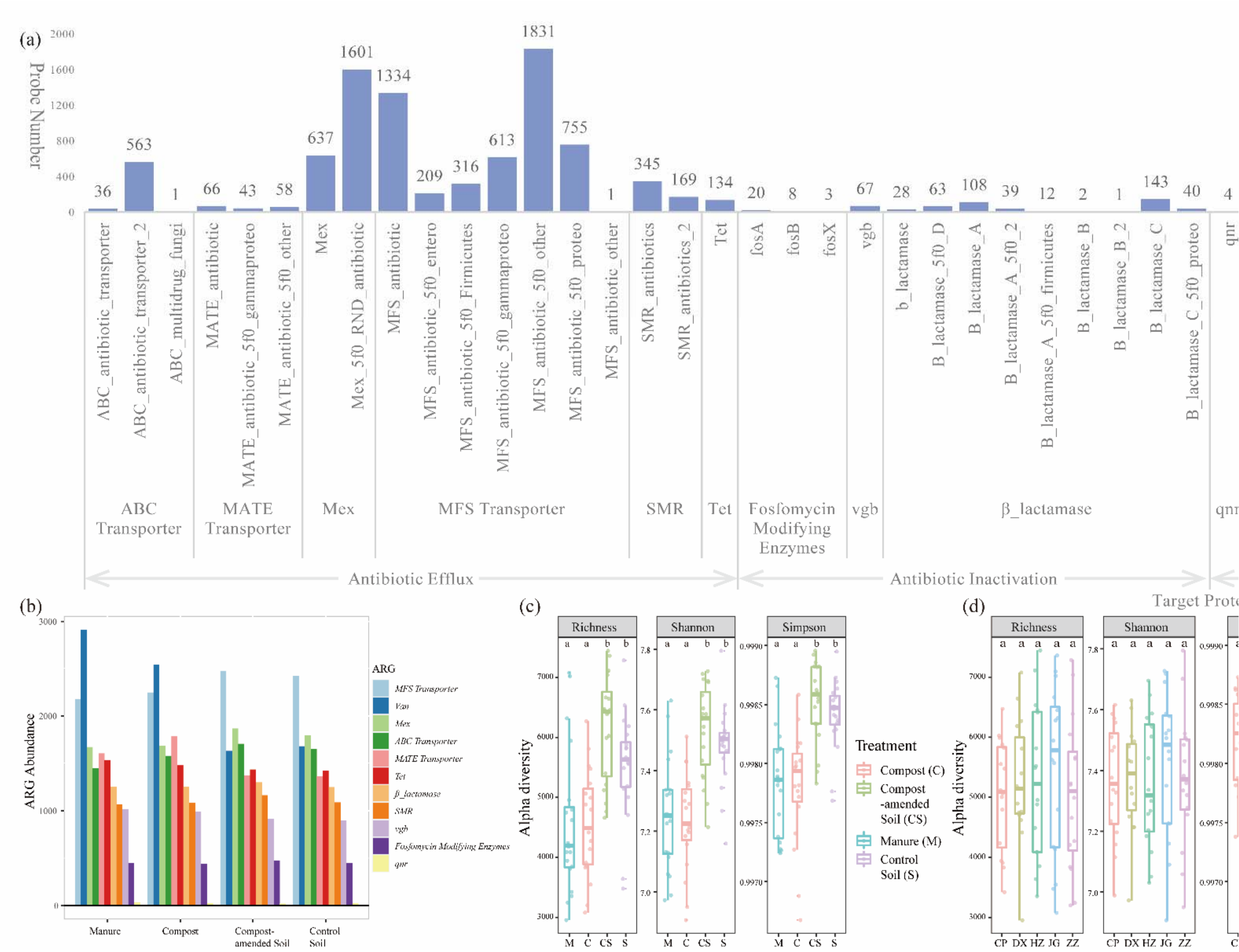

Fig. S1 Detected resistome in samples. (a) The probe number of detected resistome assigned to different types; (b) ARG abundances in manure, compost, compost-amended soil, and control soil; (c) α-diversity of resistome in manure, compost, compost-amended soil, and control soil, “a” and “b” represent difference by Tukey HSD test; (d) α-diversity of resistome in CP, DX, HZ, JG, and ZZ sites, “a” represent difference by Tukey HSD test

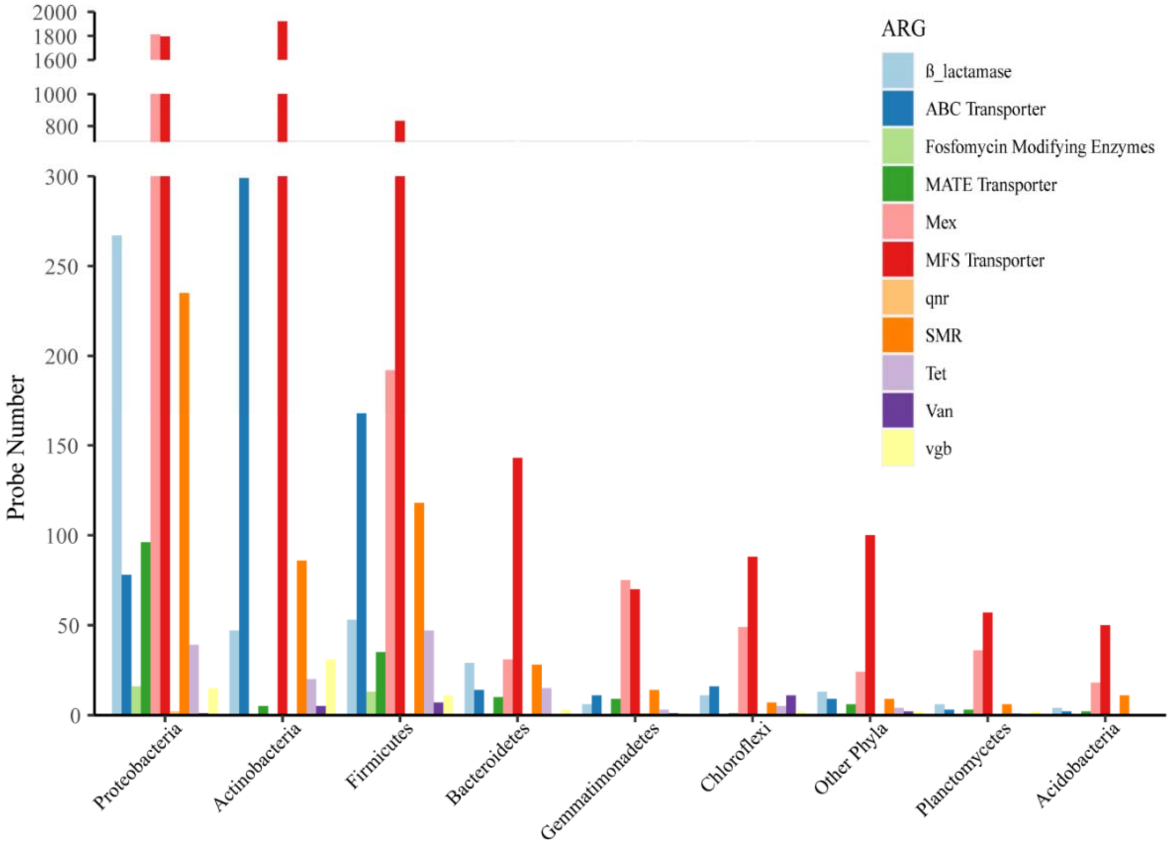

Fig. S2 The probe number of ARGs categorized by their predicted taxonomic origin. The probe number of ARGs is indicated on the *y*-axis. The ARG types are color-coded