

**Table S1.** Primer sets, sequences and conditions used in this study.

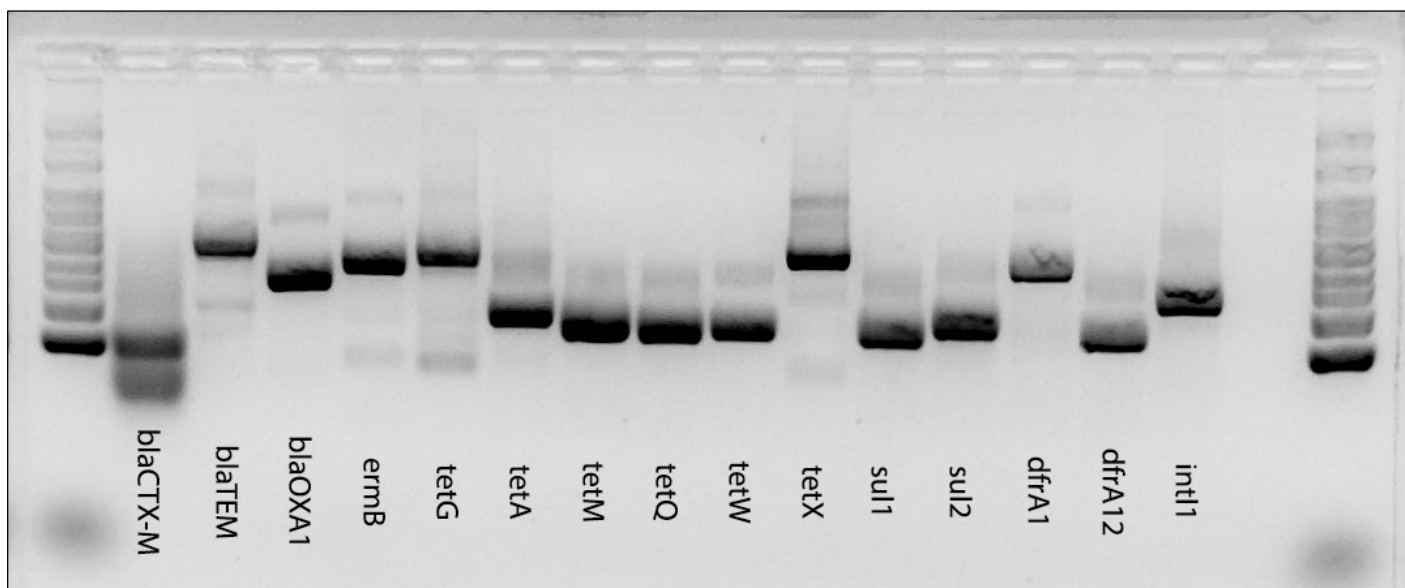
Antibiotic class / target	Primer set	Sequence (5'-3')	Amplicon size (bp)	PCR conditions
Beta-lactams	<i>bla</i> CTX-M-F	CTATGGCACCACCAACGATA	103	98°C x 12 min; 40 cycles of: 98°C x 30s, 55°C for 30 s and 72°C for 30s; Final extension 72°C x 5 min.
	<i>bla</i> CTX-M-R	ACGGCTTTCTGCCTTAGGTT		
	<i>bla</i> OXA-1-F	ACCAAAGACGTGGATGCAAT	325	
	<i>bla</i> OXA-1-R	TGCACCAGTTTTCCCATACA		
	<i>bla</i> TEM-F	CCCCGAAGAACGTTTTTC	516	
	<i>bla</i> TEM-R	ATCAGCAATAAACCAGC		
Macrolides	<i>erm</i> B-F	ACGACGAAACTGGCTAAAATAAGT	412	
	<i>erm</i> B-R	CTGTGGTATGGCGGGTAAGT		
Tetracyclines	<i>tet</i> A-F	GCTACATCCTGCTTGCC TTC	210	
	<i>tet</i> A-R	CATAGATCGCCGTGAAGAGG		
	<i>tet</i> G-F	GCTCGGTGGTATCTCTGCTC	468	
	<i>tet</i> G-R	AGCAACAGAATCGGGAACAC		
	<i>tet</i> M-F	ACAGAAAGCTTATTATATAAC	171	
	<i>tet</i> M-R	TGGCGTGTCTATGATGTTTAC		
	<i>tet</i> Q-F	AGAATCTGCTGTTTGCCAGTG	169	
	<i>tet</i> Q-R	CGGAGTGTCATGATATTGCA		
	<i>tet</i> W-F	GAGAGCCTGCTATATGCCAGC	168	
	<i>tet</i> W-R	GGGCGTATCCACAATGTTAAC		
	<i>tet</i> X-F	CAATAATTGGTGGTGGACCC	468	
	<i>tet</i> X-R	TTCTTACCTTGGACATCCCG		
Sulfonamides	<i>sul</i> 1-F	CACCGGAAACATCGCTGCA	158	
	<i>sul</i> 1-R	AAGTTCCGCCGCAAGGCT		
	<i>sul</i> 2-F	CTCCGATGGAGGCCGGTAT	190	
	<i>sul</i> 2-R	GGGAATGCCATCTGCCTTGA		
Trimetoprim-resistance	<i>dfr</i> A1-F	TGGTAGCTATATCGAAGAATGGAGT	425	
	<i>dfr</i> A1-R	TATGTTAGAGGCGAAGTCTTGGGTA		
Integrases	<i>int</i> 1-F	CCTCCCGCACGATGATC	280	
	<i>int</i> 1-R	TCCACGCATCGTCAGGC		
	<i>int</i> 2-F	TTATTGCTGGGATTAGGC	233	
	<i>int</i> 2-R	ACGGCTACCCTCTGTTATC		
Total bacteria (16S rRNA; qPCR) <sup>a</sup>	799F	AACMGGATTAGATACCCCKG	316	
	1115R	AGGGTTGCGCTCGTTG		
Total bacteria (16S rRNA; sequencing) <sup>b</sup>	341F	CCTACGGGNGGCWGCAG	464	95°C x 5 min; 35 cycles: 95°C x 30s, 55°C x 30 s and 72°C x 30s; Final extension: 72°C x 5 min.
	805R	GACTACHVGGGTATCTAATCC		

<sup>a</sup>Primer set selected to avoid chloroplast and mitochondria 16S rRNA amplification; <sup>b</sup>Primer set selected to amplify V3-V4 region of the 16S rRNA gene. Chloroplast and mitochondria reads were removed in analysis.

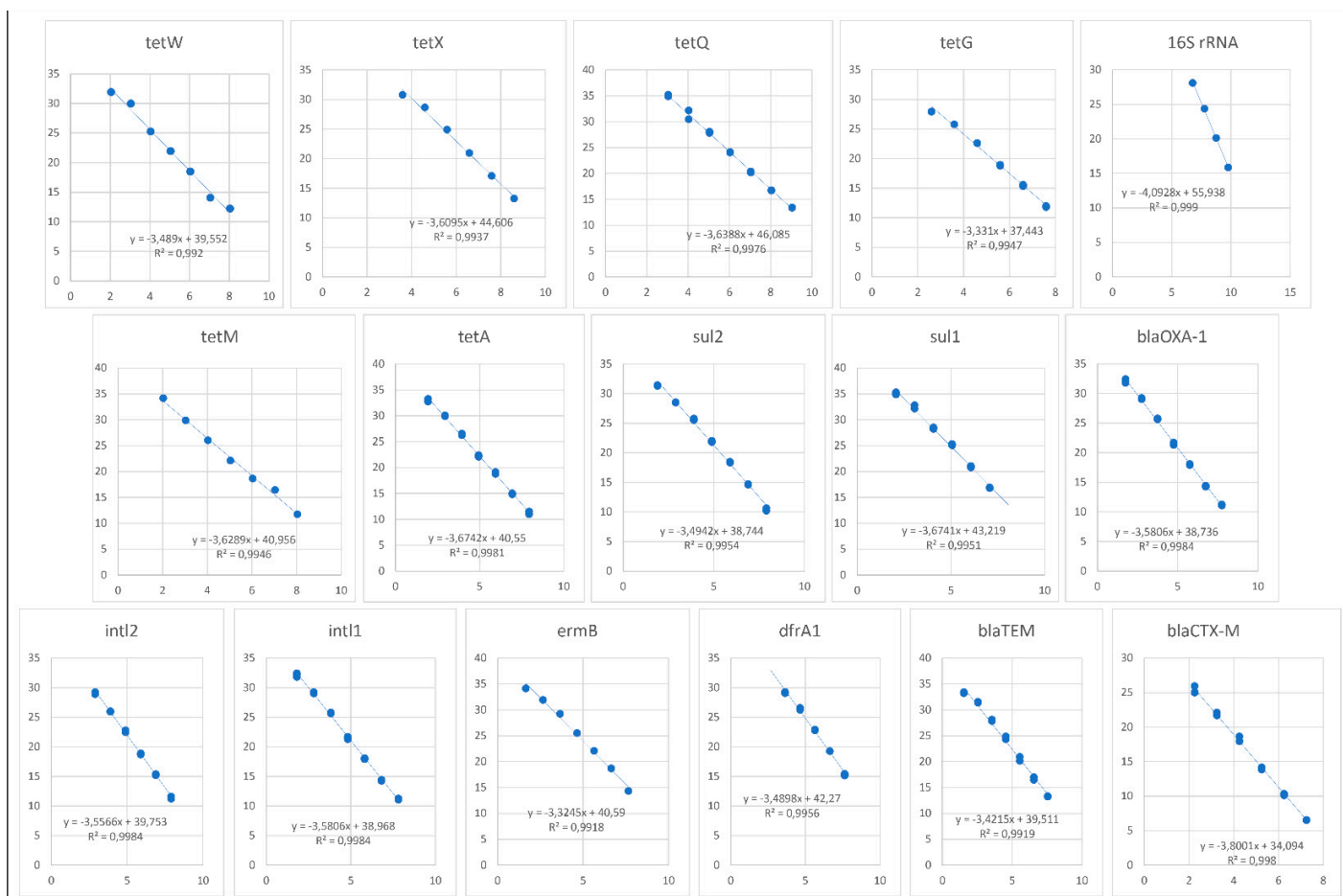
<sup>b</sup>Primers coupled to Illumina Inc. overhangs (341F = ACACTCTTTCCCTACACGACGCTCTTCCGATCT-primer sequence; 805R = GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT-primer sequence).

**Table S2.** qPCR standard curve sequences synthesized in this study.

Gene	Amplicon Size (bp)	GeneBank Accession No.	Sequence (5' – 3')
<i>blaCTX-M</i>	103	KT867021.1	CTATGGCACCACCAACGATATCGCGGTGATCTGGCCAAAAGATCGTGCGCCGCTGATTCTGGTCACTTACTTCACCCAGCCTCAACCTAAGGCAGAAAGCCGT
<i>blaTEM</i>	516	KT867019.1	CCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGTGCGGTATTATCCCGTGTTGACGCCGGGCAAGAGCAACTCGGTGCGCCGATACACTATTCTCAGAATGACTTGGTTGAGTACTCAC CAGTCACAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGTGCCATAAACCATGAGTGATAACACTGCTGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTT TGCACAACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCACGATGCCTGCAGCAATGGCAACAACGTTGCGCAAACTATTAAGTGGCG AACTACTTACTCTAGCTTCCCAGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCCTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGAT
<i>blaOXA-1</i>	325	KR338947.1	ACCAAAGACGTGGATGCAATTTTCTGTTGTTTGGGTTTCGCAAGAAATAACCCAAAAAATTGGATTAAATAAAATCAAGAATTATCTCAAAGATTTTGATTATGGAAATCAAGACTTCTCTGGAGATAAAAGAAAGA AACACCGATTAAACAGAAGCATGGCTCGAAAGTAGCTTAAAAATTCCACAGAAGAACAAATTCAATTCTGCGTAAAAATTATTAATCACAATCTCCCAGTTAAAACTCAGCCATAGAAAAACCATAGAGAAC ATGTATCTACAAGATCTGGATAATAGTACAAAACCTGTATGGGAAAACTGGTGCA
<i>ermB</i>	412	EU595407.1	ACGACGAAACTGGCTAAAAATAAGTAAACAGGTAACGTCTATTGAATTAGACAGTCATCTATTCAACTTATCGTCAGAAAAATTAAAACTGAATACTCGTGTCACTTTAATTCACCAAGATATTCTACAGTTTCAATT CCCTAACAAACAGAGGTATAAAATTGTTGGGAATATTCCCTACCATTAAAGCACACAAATTATTAAAAAAGTGGTTTTTGAAAGCCATGCGTCTGACATCTATCTGATTGTTGAAGAAGGATTCTACAAGCGTACC TTGGATATTCACCGAACACTAGGGTTGCTCTTGACACACTCAAGTCTCGATTGACCAATTGCTTAAGCTGCCAGCGGAATGCTTTCATCCTAAACCAAAAAGTAAACAGTGTCTTAATAAACTTACCCGCCATACCAC AG
<i>tetA</i>	210	KF240812.1	GCTACATCCTGCTTGCTTCGCGACACGGGGATGGATGGCGTTCCCGATCATGGTCTGCTTGCTTCGGGTGGCATCGGAATGCCGGCGCTGCAAGCAATGTTGTCCAGGCAGGTGGATGAGGAACGTCAGGGGCA GCTGCAAGGCTCACTGGCGGCGCTCACCAGCCTGACCTCGATCGTCGGACCCCTCCTCTTCACGGCGATCTATG
<i>tetG</i>	468	KJ603219.1	GCTCGGTGGTATCTCTGCTCATGCCCCGTTTATCGCCGCCGCCCTTCTCAACGGGTTCGCGTTCTGCTTGCTGTCATTTTCTCAAGGAGACTCATCACAGCCATGGCGGGACCGGAAAGCCGGTTTCGATCAAAC CATTGCTTCTGTTACGGCTGGATGATGATTTGCGCGGGCTAGGTGCGCTTTTCGCAGTTTTCTTCATTATTCAACTGATCGGCCAAGTGCCTGCAGCCCTATGGGTCATATATGGCGAGGACCGTTTTTCAGTGGAAC ACCGCGACCGTTGGTTTGTGCTCGCTCGCGGCGTTTTGGGGCAACACATGCGATCTTCCAAGCGTTTGTACCAGCCCGCTTTCAGCCGCGCTTGAGAGAGCGGCGCACGCTGCTGTTTGGCATGGCTGCGGATGCGACTG GCTTCGTTCTTCTGGCTTTTGCCACGCAGGGATGGATGGTGTTCGGATTCTGTTGCT
<i>tetM</i>	171	KR270482.1	ACAGAAAGCTTATTATATAACAGTGGAGCGATTACAGAATTAGGAAGCGTGGACAAAGGTACAACGAGGACGGATAATACGCTTTTAGAACGTCAGAGAGGAATTACAATTCAGACAGGAATAACCTCTTTTCAG TGGGAAAATACGAAGGTGAACATCATAGACACGCCA
<i>tetQ</i>	169	KX034803.1	AGAATCTGCTGTTTGCCAGTGGAGCAACGGAAAAAGTGCGGCCGTGTGGATAATGGTGACACCATAACGGACTCTATGGATATAGAGAAACGTAGAGGAATTACTGTCCGGGCTTCTACGACATCTATTATCTGGA ATGGAGTGAAATGCAATATCATTGACACTCCG
<i>tetW</i>	168	EF489472.1	GAGAGCCTGCTATATGCCAGCGGAGCCATTTACAGAACGGGGAGCGTCGAAAAAGGGACAACGAGGACGGACACCATGTTTTTGAGAGCGGCAGCGTGGGATTACCATTCAAGCGGCAGTCACTTCTTCCAGTGG CACAGATGTAAAGTTAACATTGTGGATACGCC
<i>tetX</i>	468	KF905572.1	CAATAATTGGTGGTGGACCCGTTGGACTGACTATGGCAAAATTATTACAGCAAAACGGCATAGACGTTTCAGTTTACGAAAGAGACAACGACCGAGAGGGCAAGAATTTTTGGTGGAACCCCTTGACCTACACAAAG GTTCAAGGTCAGGAAGCAATGAAAAAAGCGGGATTGTTACAAACTTATTATGACTTAGCCTTACCAATGGGTGTAAATATTGCTGATGAAAAAGGCAATATTTTATCCACAAAAAATGTAAAGCCCGAAAAATCGAT TTGACAATCCTGAAATAAACAGAAATGACTTAAGGGCTATCTTGTTGAATAGTTTAGAAAACGACACGGTTATTGGGATAGAAAACCTTGTTATGCTTGAACCTGGTAAGAAGAAGTGGACACTAACTTTTGAGAA TAAACCGAGTGAAACAGCAGATTGGTTATTCTTGCCAATGGCGGGATGTCCAAGGTAAGAA
<i>sul1</i>	158	KJ801663.1	CACCGGAAACATCGCTGCACGTGCTGTGCAACCTTCAAAAGCTGAAGTCGGCGTTGGGGCTTCCGCTATTGGTCTCGGTGTCGCGGAAATCCTTCTTGGGCGCCACCGTTGGCCTTCCTGTAAAGGATCTGGGTCCA GCGAGCCTTGCGGCGGAACTT
<i>sul2</i>	190	KC898873.1	CTCCGATGGAGGCCGGTATCTGGCGCCAGACGCAGCCATTGCGCAGGCGCGTAAGCTGATGGCCGAGGGGGCAGATGTGATCGACCTCGGTCCGGCATCCAGCAATCCCGACGCCGCGCCTGTTTCGTCCGACAC AGAAATCGCGCGTATCGCGCCGGTGCTGGACGCGCTCAAGGCAGATGGCATTCCC
<i>dfrA1</i>	425	KC862256.1	TGGTAGCTATATCGAAGAATGGAGTTATCGGGAATGGCCCTGATATTCCATGGAGTGCCAAAGGTGAACAGCTCCTGTTTAAAGCTATTACCTATAACCAATGGCTGTTGGTTGGACGCAAGACTTTTGAATCAAT GGGAGCATTACCCAACCGAAAAGTATGCGGTGCTAACACGTTCAAGTTTTACATCTGACAATGAGAACGTAGTGATCTTTCCATCAATTAAGATGCTTTAACCAACCTAAAGAAAAATAACGGATCATGTCAATTGTT TCAGGTGGTGGGAGATATACAAAAGCCTGATCGATCAAGTAGATACACTACATATATCTACAATAGACATCGAGCCGGAAGGTGATGTTACTTTTCTGAAATCCCCAGCAATTTTAGGCCAGTTTTTACCCAAG ACTTCGCCTCTAACATA
<i>int11</i>	280	JN837682.1	CCTCCCGCACGATGATCGTGCCGTGATCGAAATCCAGATCCTTGACCCGCAGTTGCAAAACCTCACTGATCCGCATGCCGTTCCATACAGAAGCTGGGCGAACAAACGATGCTCGCCTTCCAGAAAACCGAGGAT GCGAACCATTTCATCCGGGGTCAGCACCAACCGGCAAGCGCCGCGACGGCCGAGGTCTTCCGATCTCCTGAAGCCAGGGCAGATCCGTGCACAGCACCTTGCCGTAGAAGAACAGCAAGGCCGCCAATGCCTGACG ATGCGTGGA
<i>int12</i>	233	FJ785524.1	TTATTGCTGGGATTAGGCGCGTGGGCAGTAGGCTGTTTCTGCTTTTCCACCCCTTACCGTCATGCACAGTGATGCAGCCATTATCAAAATCAAAATCTTTAACC CGCAAAACGCAAGCATTCATTAATGCGCAAACT GCACCATACAGCAGCGTAAAAATAACTTGTTGCGAGTATCCATAACCTGCAAAATGCGTTGCACTTCATTGTCAGAGATAACAGAGGGTAGCCGT
<i>16S rRNA</i>	799	CP119116.1	CGAAGACTGACGCTCAGGTGCGAAAAGCGTGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGA CCGCTTGGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATTGACGGGGGGCCGCACAAGCGGTGGAGCATGTGGTTTAATTTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATCCACGGAAAGTTTTCAG AGATGAGAAATGTGCCTTCGGGAACCGTGAGACAGGTGCTGCATGGCTGTCGTGAGTGTGTAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGGTCCGGCCGGGAAC AAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTACAATGGCGCATACAAAGAGAAGCGACCTCGCGAGAGCAAGCGGACCT CATAAAGTGCCTGCTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGTAGTAATCGTGGATCAGAATGCCACGGTGAATACGTTCCCGGGCCTTGACACACCGCCCGTCACACCATGGGAG TGGGTTGCAAAAGAAGTAGGTAGCTTAACCTTCGGGAGGGCGCTTACCACCTTGTGATTTCATGACTGGGGTGAAGTCGTAACAAGGTAACCGTAGGGGAACCTGCGGTTGGATCACCTCCTTA



**Figure S1.** qPCR standards specificity amplification. First and last wells loaded with 1000 bp ladder.



**Figure S2.** Linearized standard curves for ARGs assayed in this study. X axis represents log value, whereas Y axis corresponds to obtained Ct values. Equations in graph were used for copy number calculations.

**Table S3.** Variance explanation of the sampled microbial communities.

<b>PERMANOVA<sup>±</sup></b>	<b>Df</b>	<b>Sq. sum</b>	<b>R<sup>2</sup></b>	<b>F</b>	<b>p-value&gt;F</b>
Sampling site	3	8387	0.11226	4.5515	2E-04***
Sample type	2	47893	0.64108	38.9869	1E-04***
Residual	30	18426	0.24756		
Total	35	74706	1.00000		

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1

<sup>±</sup>Values obtained via 9999 permutations performed to the distance matrix.

**Table S4.** Total log ARGs copy abundances observed in this study.

	Slurry				Rhizosphere				Bulk soil			
	RMS	FRS	ESS	SGS	RMR	FRR	ESR	SGR	RMB	FRB	ESB	SGB
16S rRNA	4E+09 ± 1E+09 Ba	3E+09 ± 1E+09 Ba	9E+09 ± 3E+09 Aa	3E+09 ± 2E+09 Ba	6E+08 ± 5E+08 Cb	5E+08 ± 9E+07 Cb	5E+08 ± 2E+08 Cb	3E+08 ± 7E+07 Cb	3E+07 ± 2E+07 Cb	1E+08 ± 5E+08 Cb	1E+08 ± 2E+07 Cb	8E+07 ± 6E+07 Cb
<i>intl1</i>	5E+02 ± 1E+02 Ba	2E+03 ± 2E+03 Aa	5E+02 ± 2E+02 Ba	5E+02 ± 1E+02 Ba	6E+01 ± 2E+01 Ca	2E+01 ± 2E+00 Cb	6E+01 ± 6E+00 Cb	5E+01 ± 3E+01 Cb	2E+01 ± 7E+00 Ca	2E+01 ± 9E+00 Cb	4E+01 ± 8E+00 Cb	1E+01 ± 2E+00 Cb
<i>intl2</i>	3E+03 ± 1E+03 Ba	3E+03 ± 2E+03 Ba	7E+04 ± 2E+04 Aa	4E+03 ± 3E+03 Ba	9E+01 ± 4E+01 Cb	4E+01 ± 2E+01 Cb	1E+02 ± 2E+01 Cb	1E+02 ± 8E+01 Cb	1E+02 ± 4E+01 Cb	4E+01 ± 6E+00 Cb	4E+01 ± 1E+01 Cb	3E+01 ± 5E+00 Cb
<i>Tetracyclines</i>												
<i>tetA</i>	9E+03 ± 2E+03 Ba	7E+03 ± 2E+03 Ba	2E+04 ± 8E+03 Aa	1E+04 ± 3E+03 Ba	7E+02 ± 2E+02 Cb	1E+02 ± 1E+01 Cb	7E+02 ± 1E+02 Cb	4E+02 ± 2E+02 Cb	1E+02 ± 2E+01 Cb	1E+02 ± 9E+00 Cb	3E+02 ± 5E+01 Cb	9E+01 ± 2E+01 Cb
<i>tetG</i>	2E+03 ± 1E+03 Aa	8E+02 ± 3E+02 CBCa	2E+03 ± 1E+03 Aa	1E+03 ± 2E+02 BC*	5E+02 ± 1E+02 CDb	2E+01 ± 4E+00 Db	1E+02 ± 2E+01 CDb	7E+01 ± 4E+01 CD	2E+01 ± 8E+00 Db	3E+01 ± 1E+01 Db	2E+02 ± 8E+01 CDb	n.d
<i>tetM</i>	1E+05 ± 4E+04 Ba	4E+04 ± 1E+04 Ca	9E+04 ± 1E+04 Ba	1E+06 ± 2E+02 Aa	3E+02 ± 1E+02 Db	1E+02 ± 5E+01 Db	2E+02 ± 7E+01 Db	2E+02 ± 8E+01 Db	5E+02 ± 4E+02 Db	8E+01 ± 8E+00 Db	3E+01 ± 1E+01 Db	4E+01 ± 3E+01 Db
<i>tetQ</i>	5E+05 ± 3E+05 BCa	2E+05 ± 6E+04 Ca	7E+05 ± 1E+05 Ba	5E+06 ± 4E+06 Aa	8E+02 ± 8E+02 Db	2E+02 ± 9E+01 Db	6E+02 ± 3E+02 Db	6E+02 ± 4E+02 Db	1E+03 ± 3E+02 Db	9E+02 ± 7E+02 Db	5E+01 ± 2E+01 Db	1E+02 ± 1E+02 Db
<i>tetW</i>	2E+03 ± 1E+03 BCa	3E+02 ± 1E+02 BCa	1E+03 ± 4E+02 Aa	2E+03 ± 9E+02 Ba	8E+01 ± 4E+01 Cb	7E+01 ± 2E+01 Cb	1E+02 ± 5E+01 Cb	1E+02 ± 6E+01 Cb	2E+02 ± 8E+01 Cb	4E+01 ± 9E+00 Cb	6E+01 ± 2E+01 Cb	4E+01 ± 1E+01 Cb
<i>tetX</i>	7E+03 ± 2E+03 Fb	9E+03 ± 5E+03 Fa	2E+04 ± 6E+03 EFc	2E+04 ± 1E+04 EFb	6E+04 ± 5E+04 CDb	6E+03 ± 1E+03 Fab	1E+05 ± 3E+04 Ba	5E+04 ± 3E+04 DEa	3E+05 ± 1E+05 Aa	5E+03 ± 1E+05 Fb	8E+04 ± 3E+04 Cb	6E+03 ± 2E+03 Fb
<i>Sulfonamides</i>												
<i>sul1</i>	3E+04 ± 5E+03 Ba	3E+04 ± 8E+03 BCa	6E+04 ± 2E+04 Aa	2E+04 ± 1E+04 CDa	5E+03 ± 4E+03 DEb	3E+02 ± 8E+01 Eb	4E+03 ± 1E+03 DEb	1E+03 ± 9E+02 Eb	1E+02 ± 6E+01 Ec	1E+02 ± 4E+01 Eb	4E+03 ± 1E+03 DEb	1E+02 ± 9E+01 DEc
<i>sul2</i>	1E+04 ± 1E+03 Ba	5E+03 ± 4E+03 BCa	3E+04 ± 1E+04 Aa	6E+03 ± 4E+03 BC*	6E+02 ± 2E+02 Cb	4E+01 ± 5E+00 Cb	4E+02 ± 7E+01 Cb	3E+02 ± 2E+02 C	7E+01 ± 3E+01 Cc	4E+01 ± 6E+00 Cb	5E+02 ± 2E+02 Cb	n.d
<i>Beta-lactams</i>												
<i>blaTEM</i>	7E+02 ± 5E+01 Aa	9E+01 ± 4E+01 Ca	5E+02 ± 1E+02 ABa	6E+02 ± 4E+02 Aa	3E+01 ± 1E+01 Cb	2E+01 ± 8E+00 Cb	4E+01 ± 2E+01 Cb	4E+01 ± 2E+01 Cb	6E+01 ± 3E+01 Cb	1E+01 ± 1E+00 Cb	2E+01 ± 7E+00 Cb	2E+01 ± 3E+00 Cb
<i>blaOXA-1</i>	5E+02 ± 1E+02 A*	2E+03 ± 1E+03 A*	5E+02 ± 1E+02 A*	5E+02 ± 1E+02 A*	3E+01 ± 1E+01 B	7E+02 ± 9E+01 A	4E+01 ± 7E+00 B	2E+01 ± 9E+00 B	n.d	n.d	n.d	n.d
<i>blaCTX-M</i>	5E+01 ± 5E+01 Aab	6E+01 ± 4E+01 Aa	6E+01 ± 3E+01 A	5E+01 ± 6E+01 Aa	6E+01 ± 2E+01 Aa	5E+01 ± 4E+01 Ab	n.d	9E+00 ± 5E+01 BCb	2E+01 ± 6E+00 Bb	1E+01 ± 1E+01 BCb	n.d.	9E+00 ± 1E+01 Bb
<i>Macrolides and Trimetoprim</i>												
<i>ermB</i>	1E+05 ± 2E+04 BCa	3E+05 ± 3E+04 B*	8E+05 ± 2E+05 Aa	1E+05 ± 1E+05 BC*	2E+02 ± 6E+01 Cb	5E+01 ± 2E+01 Cb	7E+02 ± 1E+02 Cc	6E+02 ± 3E+02 C	2E+02 ± 6E+01 Cb	n.d	1E+02 ± 8E+01 Cb	n.d
<i>dfpA1</i>	1E+04 ± 6E+03 B*	8E+03 ± 9E+02 B**	1E+05 ± 7E+04 Aa	1E+04 ± 1E+03 B*	9E+02 ± 6E+02 B	n.d	3E+03 ± 7E+02 Bb	6E+02 ± 3E+02 B	n.d	n.d	7E+03 ± 4E+03 Bb	n.d

Values after ± symbol represent mean standard deviation (SD).

Uppercase characters after each value represent statistical differentiation among all samples for the row as revealed by Tukey HSD test ( $P \leq 0.05$ ).

Lowercase character after each value represent statistical differentiation among the slurry, rhizosphere and bulk soil of each sampling site as revealed by Tukey HSD test ( $P \leq 0.05$ ).

\*Statistical differentiation revealed by t-test as only two sampled matrixes from the sampling site presented the target ARG ( $P \leq 0.05$ ). Remark added to the higher compared value.

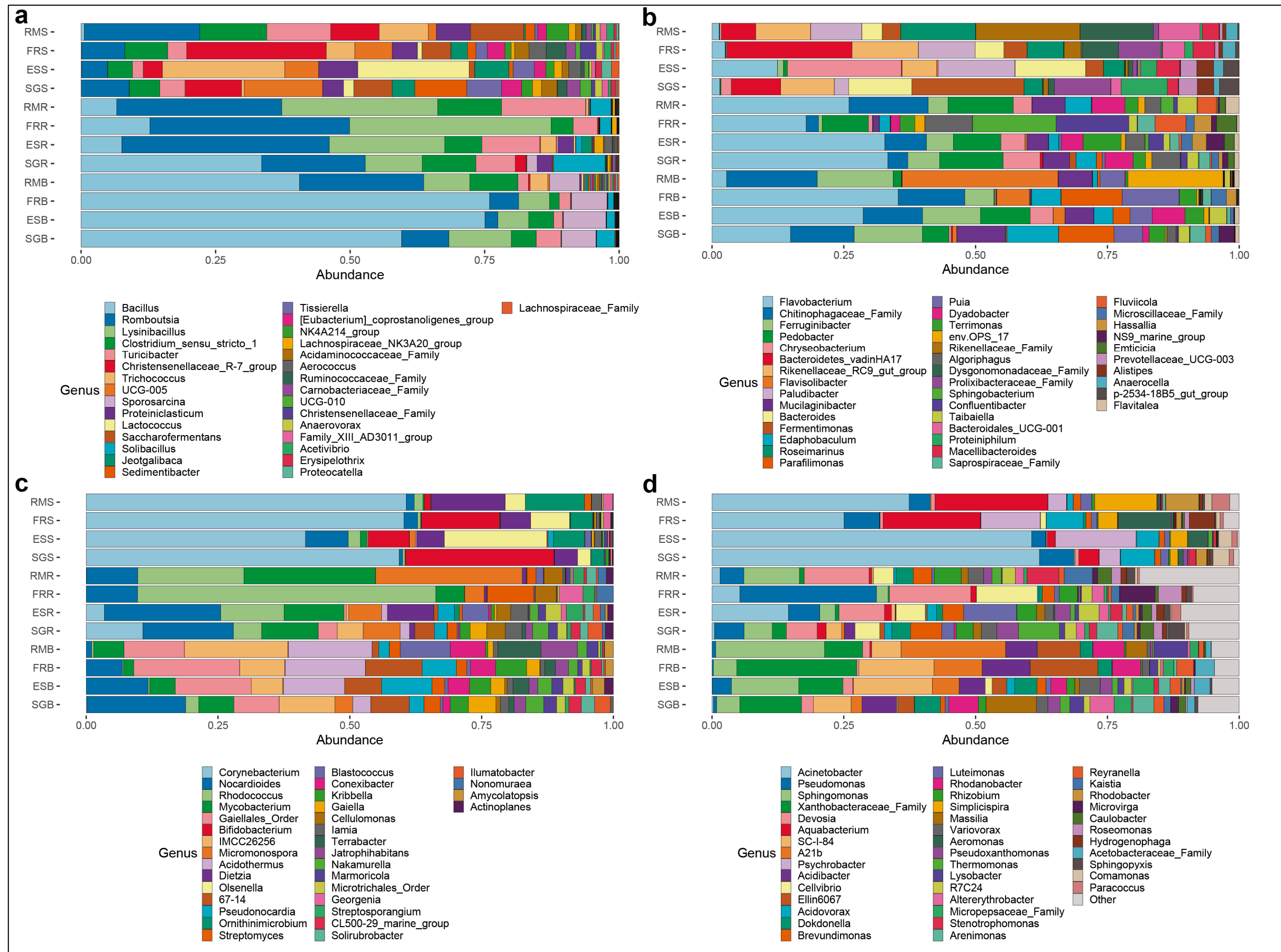
\*\*ARG only detected in this niche from the sampling site.

n.d.: not detected by qPCR.

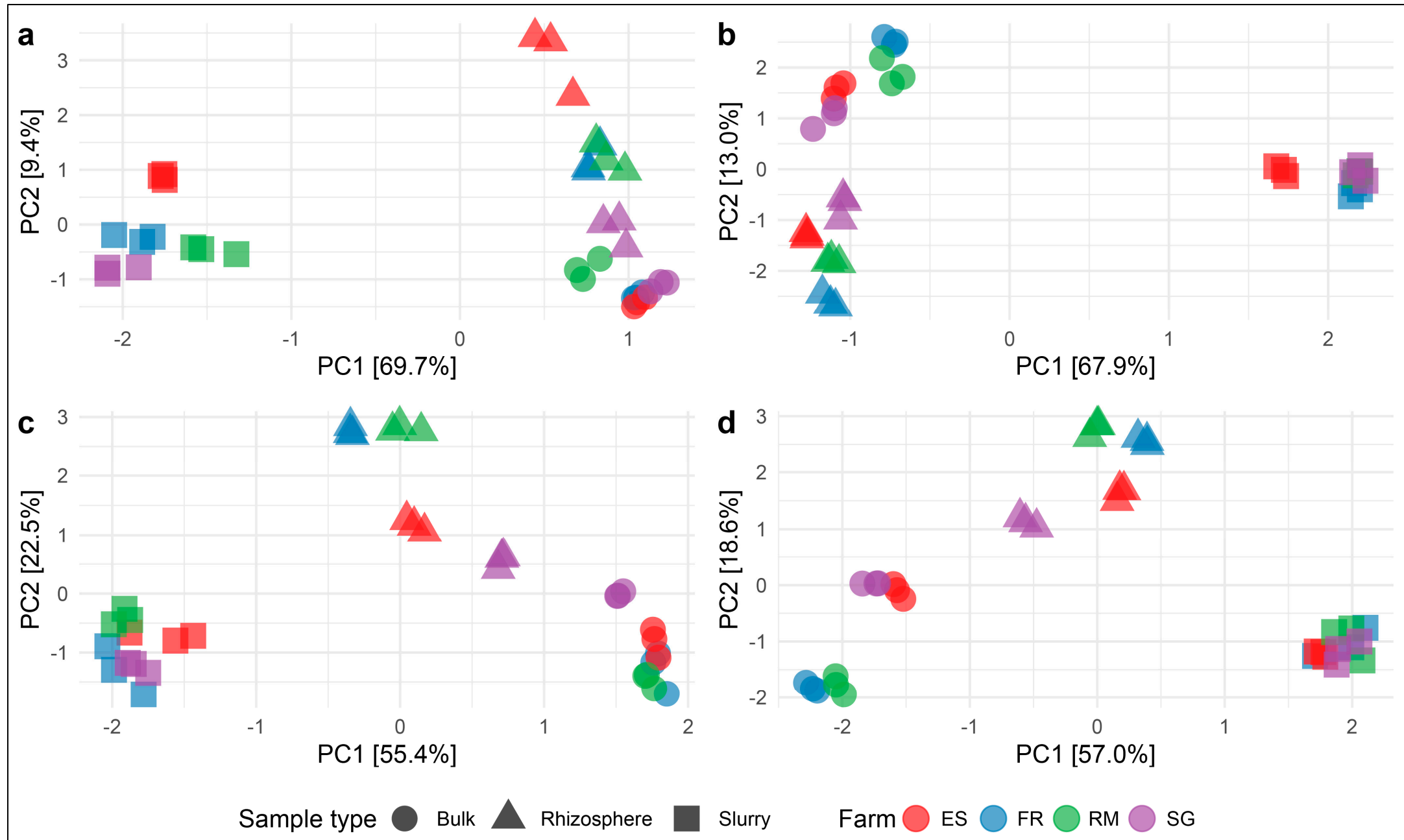
**Table S5.** Relative abundance between ARGs and total bacteria (log ARG:16S rRNA copies per g<sup>-1</sup> soil) observed in this study.

ARG/16S	RMS	FRS	ESS	SGS	RMR	FRR	ESR	SGR	RMB	FRB	ESB	SGB
<i>tetA</i>	2.2E-06 ± 9.1E-07 BC	2.2E-06 ± 9.3E-07 BC	2.3E-06 ± 1.5E-06 BC	4.6E-06 ± 3.4E-06 AB	1.8E-06 ± 1.4E-06 BCD	3.0E-07 ± 5.4E-08 D	1.3E-06 ± 4.0E-07 CD	1.3E-06 ± 5.3E-07 CD	6.7E-06 ± 5.0E-06 A	7.0E-07 ± 1.4E-07 CD	2.8E-06 ± 1.4E-06 ABC	2.6E-06 ± 1.7E-06 ABC
<i>tetG</i>	6.3E-07 ± 4.5E-07 ABC	2.7E-07 ± 8.8E-08 BCD	2.9E-07 ± 1.8E-07 BCD	4.3E-07 ± 4.3E-07 BCD	2.1E-06 ± 4.0E-06 ABC	4.3E-08 ± 1.2E-08 CD	2.1E-07 ± 6.9E-08 BCD	2.1E-07 ± 1.0E-07 BCD	1.2E-06 ± 1.0E-06 AB	2.2E-07 ± 2.6E-07 BCD	2.0E-06 ± 1.1E-06 A	n.d.
<i>tetM</i>	2.6E-05 ± 8.5E-06 B	1.1E-05 ± 8.6E-06 BCD	1.2E-05 ± 4.7E-06 BC	4.8E-04 ± 4.0E-04 A	1.3E-06 ± 2.3E-06 CD	2.5E-07 ± 8.9E-08 D	3.3E-07 ± 1.3E-07 D	4.8E-07 ± 2.0E-07 CD	3.4E-05 ± 4.2E-05 B	6.2E-07 ± 5.2E-07 CD	1.9E-07 ± 1.8E-07 D	9.8E-07 ± 1.7E-06 CD
<i>tetQ</i>	1.1E-04 ± 4.3E-05 B	5.8E-05 ± 1.8E-05 D	8.7E-05 ± 3.7E-05 BC	1.9E-03 ± 1.2E-03 A	3.1E-06 ± 4.2E-06 E	3.6E-07 ± 2.3E-07 E	1.0E-06 ± 3.4E-07 E	1.8E-06 ± 1.1E-06 E	4.8E-05 ± 4.4E-05 CD	6.7E-06 ± 5.9E-06 E	4.8E-07 ± 1.8E-07 E	2.4E-06 ± 1.6E-06 E
<i>tetW</i>	4.6E-07 ± 6.7E-07 BC	8.5E-08 ± 3.1E-08 C	1.8E-07 ± 8.5E-08 BC	1.5E-06 ± 2.8E-06 BC	2.8E-07 ± 2.6E-07 BC	1.5E-07 ± 6.0E-08 BC	2.6E-07 ± 1.4E-07 BC	3.7E-07 ± 1.6E-07 BC	9.2E-06 ± 8.8E-06 A	2.7E-07 ± 6.4E-08 BC	5.9E-07 ± 1.9E-07 BC	1.2E-06 ± 1.1E-06 B
<i>tetX</i>	2.0E-06 ± 8.9E-07 C	3.0E-06 ± 1.2E-06 C	2.3E-06 ± 7.3E-07 C	6.1E-06 ± 3.7E-06 C	2.2E-04 ± 2.8E-04 BC	1.4E-05 ± 3.7E-06 C	2.3E-04 ± 3.2E-05 BC	1.5E-04 ± 8.8E-05 BC	1.5E-02 ± 1.4E-02 A	3.6E-05 ± 4.6E-06 BC	9.2E-04 ± 4.4E-04 B	1.3E-04 ± 6.8E-05 BC
<i>sul1</i>	8.5E-06 ± 3.2E-06 BC	8.4E-06 ± 1.5E-06 BC	7.9E-06 ± 4.8E-06 BC	5.2E-06 ± 2.6E-06 BCD	1.9E-05 ± 2.4E-05 B	6.2E-07 ± 2.0E-07 E	8.5E-06 ± 2.6E-06 BC	4.9E-06 ± 2.8E-06 CDE	5.8E-06 ± 4.4E-06 BCD	8.0E-07 ± 3.0E-07 DE	3.7E-05 ± 1.4E-05 A	4.0E-06 ± 3.2E-06 CDE
<i>sul2</i>	3.2E-06 ± 1.5E-06 BCD	1.6E-06 ± 4.8E-07 CDEF	4.1E-06 ± 2.5E-06 AB	2.1E-06 ± 9.1E-07 BCDE	1.1E-06 ± 8.0E-07 FG	8.1E-08 ± 1.7E-08 GH	8.4E-07 ± 2.0E-07 EFG	1.0E-06 ± 6.5E-07 DEFG	4.1E-06 ± 4.1E-06 ABC	2.6E-07 ± 6.9E-08 GH	5.4E-06 ± 1.6E-06 A	n.d.
<i>blaTEM</i>	1.5E-07 ± 2.2E-07 B	2.8E-08 ± 1.0E-08 B	5.8E-08 ± 2.8E-08 B	4.9E-07 ± 9.2E-07 B	1.0E-07 ± 8.5E-08 B	4.8E-08 ± 2.0E-08 B	8.3E-08 ± 4.5E-08 B	1.2E-07 ± 5.3E-08 B	3.0E-06 ± 2.8E-06 A	9.7E-08 ± 1.5E-08 B	1.9E-07 ± 6.1E-08 B	4.7E-07 ± 4.6E-07 B
<i>blaOXA-1</i>	1.3E-07 ± 6.0E-08 B	3.9E-07 ± 3.3E-07 A	5.7E-08 ± 1.8E-08 BC	1.8E-07 ± 1.1E-07 B	8.1E-08 ± 8.2E-08 BC	1.8E-07 ± 2.1E-07 CD	7.7E-08 ± 1.9E-08 B	8.0E-08 ± 2.6E-08 B	n.d.	n.d.	n.d.	n.d.
<i>blaCTX-M</i>	1.1E-08 ± 1.0E-08 ABCD	1.8E-08 ± 1.3E-08 ABC	6.9E-09 ± 4.3E-09 AB	1.6E-08 ± 1.2E-08 ABCDE	2.0E-07 ± 1.6E-07 A	4.5E-08 ± 9.7E-08 BCDE	9.3E-09 ± 4.8E-09 E	2.8E-08 ± 1.9E-08 DE	7.9E-07 ± 7.7E-07 ABCDE	8.3E-08 ± 7.8E-08 CDE	7.6E-08 ± 4.5E-08 DE	4.6E-07 ± 8.7E-07 CDE
<i>dfpA1</i>	3.7E-06 ± 1.4E-06 C	1.7E-06 ± 2.2E-06 CD	1.8E-05 ± 1.3E-05 B	2.4E-06 ± 2.2E-06 CD	1.3E-06 ± 1.8E-06 CD	n.d.	5.5E-06 ± 2.2E-06 C	1.8E-06 ± 8.0E-07 CD	n.d.	n.d.	7.6E-05 ± 4.5E-05 A	n.d.
<i>ermB</i>	2.8E-05 ± 1.2E-05 C	6.9E-05 ± 5.0E-05 B	1.1E-04 ± 4.8E-05 A	2.7E-05 ± 2.9E-05 C	5.8E-07 ± 5.1E-07 D	6.1E-08 ± 6.4E-08 D	1.2E-06 ± 5.7E-07 D	2.1E-06 ± 9.9E-07 D	5.0E-06 ± 8.4E-06 D	n.d.	1.3E-06 ± 1.0E-06 D	n.d.
<i>intl1</i>	1.5E-07 ± 7.0E-08 DE	4.5E-07 ± 3.8E-07 B	6.6E-08 ± 2.1E-08 DE	1.8E-07 ± 1.5E-07 DE	1.5E-07 ± 1.1E-07 DE	5.3E-08 ± 1.1E-08 E	1.1E-07 ± 2.3E-08 DE	1.6E-07 ± 7.4E-08 CDE	9.1E-07 ± 4.0E-07 A	1.4E-07 ± 6.1E-08 DE	4.1E-07 ± 1.1E-07 BC	2.9E-07 ± 2.2E-07 BCD
<i>intl2</i>	6.5E-07 ± 5.8E-07 A	7.9E-07 ± 9.4E-07 B	8.2E-06 ± 4.9E-06 A	9.6E-07 ± 8.2E-07 B	2.2E-07 ± 1.7E-07 B	8.2E-08 ± 1.6E-08 B	2.4E-07 ± 5.6E-08 B	4.6E-07 ± 2.3E-07 B	6.1E-06 ± 6.1E-06 B	2.9E-07 ± 7.5E-08 B	4.0E-07 ± 2.3E-07 B	7.1E-07 ± 6.0E-07 B

Values after ± symbol represent mean standard deviation (SD). Presented data is in log format.  
Uppercase characters after each value represent statistical differentiation among all samples for the row as revealed by Tukey HSD test ( $P \leq 0.05$ ).  
n.d.: not detected by qPCR.



**Figure S3.** Taxonomic assignment at top genus level for (a) Firmicutes, (b) Bacteroidota, (c) Actinobacteria, and (d) Proteobacteria. ‘Other’ represents taxa under 0.05% relative abundance towards total ASV assignments. Sample names ending with S, R and B correspond to slurry, rhizosphere, or bulk soil, respectively.



**Figure S4.** Principal component analysis (PCA) for (a) Firmicutes, (b), Bacteroidota, (c) Actinobacteria, and (d) Proteobacteria.