Supplementary material

Higher Temperatures Do Not Always Achieve Better Antibiotic Resistance Genes Removal in Anaerobic Digestion of Swine Manure

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Text 1 Determination of antibiotics

The concentrations of twelve antibiotics including OTC, SM2 and CIP in fresh manure were very low (ppb level). Thus, only the antibiotics in T37A were determined and shown in this study. After centrifuging at 10,000 g, antibiotics in supernatant and pellet of manure slurry were extracted and measured separately. The supernatant was mixed with pure methanol (v:v=1:4), filtered through 0.45 μm membrane before determination. Antibiotics in pellet were extracted using the mixture of phosphate buffer (pH=3.0) and acetonitrile (1:1, v/v). The extract was also mixed with methanol and filtered before further analysis. All the samples were determined in duplicate. Control samples and spiked samples were also manipulated to obtain the recoveries of antibiotics. Antibiotics were finally detected and quantified by LC-MS/MS system (ABI 6500 Q-TRAP, Applied Biosystems, USA). The volumes of supernatant and wet weights of pellet were also recorded. The total antibiotic concentrations in manure slurry were therefore calculated.

Table S1 Experimental design and chemical properties of samples collected from different treatments.

#Sample ID	Temperature	Antibiotic spiking	Day	pH	NO_3^- (mg/L)	NH_4^+ (g/L)	TSS (g/L)	VSS (g/L)	VSS/TSS
D0	--	No	0	6.05±0.03	146.5±10.9	1.18±0.07	78.7±9.8	60.2±8.6	0.76±0.02
T25,D14	25	No	14	5.92±0.01	133.6±20.8	2.02±0.01	55.5±7.2	42.0±5.7	0.75±0.01
T25,D30	25	No	30	5.89±0.03	49.8±5.8	2.18±0.14	76.5±5.7	56.6±6.2	0.74±0.03
T37,D14	37	No	14	5.50±0.00	120.3±89.5	2.24±0.06	60.5±15.6	43.8±13.0	0.72±0.03
T37,D30	37	No	30	5.67±0.03	60.4±2.6	2.44±0.07	73.8±6.4	57.1±4.8	0.77±0.01
T37A,D14	37	Yes	14	5.49±0.01	126.4±57.8	2.19±0.10	45.7±7.1	33.8±5.5	0.74±0.01
T37A,D30	37	Yes	30	5.67±0.02	60.8±3.4	2.36±0.02	49.4±5.8	37.4±4.4	0.76±0.01
T55,D14	55	No	14	6.10±0.10	105.6±16.0	2.04±0.12	65.3±14.4	49.8±11.3	0.76±0.02
T55,D30	55	No	30	6.02±0.38	55.2±10.0	2.23±0.14	52.1±2.0	36.7±0.4	0.70±0.02

Table S2 ARG subtypes involved in network analysis according to fold change (FC) values of ARGs in samples of T37, T37A and T55 compared to that of T25 on day 30. The ARGs with three FC values >1 and minimum C_T value ≤ 21 are shown.

	Assay	FC values compared to T25D30			Maximum Relative abundance
		T37D30	T37D30A	T55D30	
Aminoglycosides	aac(6')-lb(akaaacA4)-01	1.56	1.26	2.44	9.67E-03
	aac(6')-lb(akaaacA4)-02	1.40	1.50	2.06	1.19E-02
	aac(6')-lb(akaaacA4)-03	1.28	1.27	1.52	1.33E-02
	aacC2	1.42	2.29	3.04	6.30E-03
	aadA-01	1.48	1.56	1.62	5.12E-02
	aadA-02	1.46	1.70	1.74	2.79E-02
	aadA1	1.18	1.34	1.01	2.98E-02
	aadA-1-01	1.51	1.28	1.28	1.96E-01
	aadA-1-02	2.42	2.23	2.48	4.03E-01
	aadA2-01	1.77	1.33	1.28	3.15E-02
	aadA2-02	1.57	1.88	1.62	3.58E-02
	aadA2-03	1.42	1.81	1.70	4.62E-02
	aadD	1.21	717.96	594.32	6.00E-03
	aadE	1.21	59399.46	62752.03	1.38E-01
	strB	1.08	1.17	2.75	3.31E-02
Beta_Lactamas	blaTEM	3.69	7.87	3.93	6.86E-03
	fox5	339.31	1.20	702.92	1.91E-03
(flor)/(chlor)/(am)phenicol	cmlA1-01	1.59	2.92	1.70	7.03E-03
	cmlA1-02	1.56	2.91	1.79	7.08E-03
	cmx(A)	1.34	1.11	1.68	9.56E-02
	floR	1.09	1.53	1.50	4.22E-02
MGEs	cIntI-1	1.21	1.20	2620.64	7.45E-03
	intI1	1.64	1.83	1.74	2.24E-02
	tnpA-05	1.58	3.05	2.95	1.63E-01
MLSB	ermB	1.38	1.35	4.32	1.91E-01
	ermT-01	1.83	2.11	4.83	3.69E-01
	ermT-02	1.32	1.54	3.24	1.93E-01
	lnuB-01	1.74	1.57	2.43	4.70E-02
	lnuB-02	1.81	1.51	2.40	5.65E-02
	mphA-01	1.21	1.20	1040.61	2.15E-03
	vatE-01	1.06	1.17	4.83	1.52E-01
	vatE-02	1.16	1.74	8.87	2.03E-01
Multidrug	qacEdelta1-01	1.42	1.21	1.39	5.13E-02
	qacEdelta1-02	1.38	1.27	1.54	7.15E-02
	qacH-01	1.21	1798.88	869.82	3.91E-03
	qacH-02	1.99	2.72	2.64	1.33E-03
Sulfonamides	dfrA1	2.13	1.67	4.86	6.10E-03
	dfrA12	1.97	3.16	1.75	2.99E-03
	sul2	1.23	1.38	1.81	4.27E-02
Tetracyclines	tet(32)	1.32	1.25	5.04	4.93E-01
	tetG-02	1.35	1.33	1.50	2.03E-02
	tetH	2.26	1.19	5.65	1.51E-03
	tetL-02	1.53	1.64	5.84	2.65E-02
	tetM-02	1.17	1.49	2.64	2.98E-02
	tetQ	10.77	13.10	1.74	1.99E-01
Other	sat4	1.58	1.21	1.62	5.18E-02

Table S3 Characteristics of microbial genera significantly correlated with over 10 ARGs in network analysis.

	Genera	Belong to	Maximum frequency	Number of correlated genes	Range of correlation efficiencies (ρ)	Number of strong correlation (ρ>0.8)	ARGs they strongly correlated with (ρ>0.8)
1	*Dorea*	*Firmicutes*	0.16%	20	0.496-0.856	6	ermB, ermT-01, ermT-02, tet(32), tetL-02, vatE-01
2	*Streptococcus*	*Firmicutes*	40.42%	16	0.499-0.919	7	ermB, ermT-01, ermT-02, tet(32), tetL-02, vatE-01, vatE-02
3	*Dokdonella*	*Proteobacteria*	0.01%	15	0.515-0.803	1	vatE-02
4	*Ruminococcus*	*Firmicutes*	0.29%	15	0.495-0.874	6	ermB, ermT-02, tet(32), tetL-02, vatE-01,vatE-02
5	*Proteiniclasticum*	*Firmicutes*	0.02%	14	0.487-0.717	0	
6	*Eubacterium*	*Firmicutes*	0.60%	14	0.495-0.822	1	vatE-01
7	*Lactobacillus*	*Firmicutes*	8.39%	14	0.506-0.873	6	ermB, ermT-02, tet(32), tetL-02, vatE-01,vatE-02
8	*Azomonas*	*Proteobacteria*	0.38%	14	0.498-0.752	0	
9	*Bacillus*	*Firmicutes*	0.27%	14	0.515-0.770	0	
10	*Rummeliibacillus*	*Firmicutes*	0.51%	13	0.512-0.811	1	vatE-01
11	*Hydrogenophaga*	*Proteobacteria*	0.07%	13	0.493-0.591	0	
12	*Wohlfahrtiimonas*	*Proteobacteria*	0.08%	13	0.500-0.611	0	
13	*Anaerococcus*	*Firmicutes*	0.08%	12	0.507-0.821	1	ermT-02
14	*Peptococcus*	*Firmicutes*	0.07%	11	0.489-0.836	4	ermB, ermT-02, tetL-02, vatE-01
15	*Facklamia*	*Firmicutes*	0.09%	11	0.521-0.800	0	
16	*Luteimonas*	*Proteobacteria*	0.06%	11	0.519-0.646	0	
17	*Oscillospira*	*Firmicutes*	0.36%	11	0.509-0.800	0	

Table S4 Primer list used in this study

Gene Name	Forward Primer	Reverse Primer	Classification	Mechanism
16S rRNA	GGGTTGCGCTCGTTGC	ATGGYTGTCGTCAGCTCGTG		
aac	CCCTGCGTTGTGGCTATGT	TTGGCCACGCCAATCC	Aminoglycoside	deactivate
aac(6')I1	GACCGGATTAAGGCCGATG	CTTGCCTTGATATTCAGTTTTTATAACCA	Aminoglycoside	deactivate
aac(6')-Ib(aka aacA4)-01	GTTTGAGAGGCAAGGTACCGTAA	GAATGCCTGGCGTGTTTGA	Aminoglycoside	deactivate
aac(6')-Ib(aka aacA4)-02	CGTCGCCGAGCAACTTG	CGGTACCTTGCCTCTCAAACC	Aminoglycoside	deactivate
aac(6')-Ib(aka aacA4)-03	AGAAGCACGCCCGACACTT	GCTCTCCATTCAGCATTGCA	Aminoglycoside	deactivate
aac(6')-II	CGACCCGACTCCGAACAA	GCACGAATCCTGCCTTCTCA	Aminoglycoside	deactivate
aac(6')-Iy	GCTTTGCGGATGCCTCAAT	GGAGAACAAAAATACCTTCAAGGAAA	Aminoglycoside	deactivate
aacA/aphD	AGAGCCTTGGGAAGATGAAGTTT	TTGATCCATACCATAGACTATCTCATCA	Aminoglycoside	deactivate
aacC	CGTCACTTATTCGATGCCCTTAC	GTCGGGCGCGGCATA	Aminoglycoside	deactivate
aacC1	GGTCGTGAGTTCGGAGACGTA	GCAAGTTCCCGAGGTAATCG	Aminoglycoside	deactivate
aacC2	ACGGCATTCTCGATTGCTTT	CCGAGCTTCACGTAAGCATTT	Aminoglycoside	deactivate
aacC4	CGGCGTGGGACACGAT	AGGGAACCTTTGCCATCAACT	Aminoglycoside	deactivate
aadA-01	GTTGTGCACGACGACATCATT	GGCTCGAAGATACCTGCAAGAA	Aminoglycoside	deactivate
aadA-02	CGAGATTCTCCGCGCTGTA	GCTGCCATTCTCCAAATTGC	Aminoglycoside	deactivate
aadA1	AGCTAAGCGCGAACTGCAAT	TGGCTCGAAGATACCTGCAA	Aminoglycoside	deactivate
aadA-1-01	AAAAGCCCGAAGAGGAACTTG	CATCTTTCACAAAGATGTTGCTGTCT	Aminoglycoside	deactivate
aadA-1-02	CGGAATTGAAAAAACTGATCGAA	ATACCGGCTGTCCGTCATTT	Aminoglycoside	deactivate
aadA2-01	ACGGCTCCGCAGTGGAT	GGCCACAGTAACCAACAAATCA	Aminoglycoside	deactivate
aadA2-02	CTTGTCGTGCATGACGACATC	TCGAAGATACCCGCAAGAATG	Aminoglycoside	deactivate
aadA2-03	CAATGACATTCTTGCGGGTATC	GACCTACCAAGGCAACGCTATG	Aminoglycoside	deactivate
aadA5-01	ATCACGATCTTGCGATTTTGCT	CTGCGGATGGGCCTAGAAG	Aminoglycoside	deactivate

aadA5-02	GTTCTTGCTCTTGCTCGCATT	GATGCTCGGCAGGCAAAC	Aminoglycoside	deactivate
aadA9-01	CGCGGCAAGCCTATCTTG	CAAATCAGCGACCGCAGACT	Aminoglycoside	deactivate
aadA9-02	GGATGCACGCTTGGATGAA	CCTCTAGCGGCCGGAGTATT	Aminoglycoside	deactivate
aadD	CCGACAACATTTCTACCATCCTT	ACCGAAGCGCTCGTCGTATA	Aminoglycoside	deactivate
aadE	TACCTTATTGCCCTTGGAAGAGTTA	GGAACTATGTCCCTTTTAATTCTACAATCT	Aminoglycoside	deactivate
aph	TTTCAGCAAGTGGATCATGTTAAAAT	CCAAGCTGTTTCCACTGTTTTTC	Aminoglycoside	deactivate
aph(2')-Id-01	TGAGCAGTATCATAAGTTGAGTGAAAAG	GACAGAACAATCAATCTCTATGGAATG	Aminoglycoside	deactivate
aph(2')-Id-02	TAAGGATATACCGACAGTTTTGGAAA	TTTAATCCCTCTTCATACCAATCCATA	Aminoglycoside	deactivate
aph6ia	CCCATCCCATGTGTAAGGAAA	GCCACCGCTTCTGCTGTAC	Aminoglycoside	deactivate
aphA1(aka kanR)	TGAACAAGTCTGGAAAGAAATGCA	CCTATTAATTTCCCCTCGTCAAAAA	Aminoglycoside	deactivate
spcN-01	AAAAGTTCGATGAAACACGCCTAT	TCCAGTGGTAGTCCCCGAATC	Aminoglycoside	deactivate
spcN-02	CAGAATCTTCCTGAAAAGTTTGATGAA	CGCAGACACGCCGAATC	Aminoglycoside	deactivate
str	AATGAGTTTTGGAGTGTCTCAACGTA	AATCAAAACCCCTATTAAAGCCAAT	Aminoglycoside	deactivate
strA	CCGGTGGCATTTGAGAAAAA	GTGGCTCAACCTGCGAAAAG	Aminoglycoside	deactivate
strB	GCTCGGTCGTGAGAACAATCT	CAATTTCGGTCGCCTGGTAGT	Aminoglycoside	deactivate
ampC/blaDHA	TGGCCGCAGCAGAAAGA	CCGTTTTATGCACCCAGGAA	Beta_Lactamase	deactivate
ampC-01	TGGCGTATCGGGTCAATGT	CTCCACGGGCCAGTTGAG	Beta_Lactamase	deactivate
ampC-02	GCAGCACGCCCCGTAA	TGTACCCATGATGCGCGTACT	Beta_Lactamase	deactivate
ampC-04	TCCGGTGACGCGACAGA	CAGCACGCCGGTGAAAGT	Beta_Lactamase	deactivate
ampC-05	CTGTTCGAGCTGGGTTCTATAAGTAAA	CAGTATCTGGTCACCGGATCGT	Beta_Lactamase	deactivate
ampC-06	CCGCTCAAGCTGGACCATAC	CCATATCCTGCACGTTGGTTT	Beta_Lactamase	deactivate
ampC-07	CCGCCCAGAGCAAGGACTA	GCTCGACTTCACGCCGTAAG	Beta_Lactamase	deactivate
ampC-09	CAGCCGCTGATGAAAAAATATG	CAGCGAGCCCACTTCGA	Beta_Lactamase	deactivate
bla1	GCAAGTTGAAGCGAAAGAAAAGA	TACCAGTATCAATCGCATATACACCTAA	Beta_Lactamase	deactivate
bla-ACC-1	CACACAGCTGATGGCTTATCTAAAA	AATAAACGCGATGGGTTCCA	Beta_Lactamase	deactivate

blaCMY	CCGCGGCGAAATTAAGC	GCCACTGTTTGCCTGTCAGTT	Beta_Lactamase	deactivate
blaCMY2-01	AAAGCCTCAT GGGTGCATAAA	ATAGCTTTTGTTTGCCAGCATCA	Beta_Lactamase	deactivate
blaCMY2-02	GCGAGCAGCCTGAAGCA	CGGATGGGCTTGTCCTCTT	Beta_Lactamase	deactivate
blaCTX-M-01	GGAGGCGTGACGGCTTTT	TTCAGTGCGATCCAGACGAA	Beta_Lactamase	deactivate
blaCTX-M-02	GCCGCGGTGCTGAAGA	ATCGGATTATAGTTAACCAGGTCAGATTT	Beta_Lactamase	deactivate
blaCTX-M-03	CGATACCACCACGCCGTTA	GCATTGCCCAACGTCAGATT	Beta_Lactamase	deactivate
blaCTX-M-04	CTTGGCGTTGCGCTGAT	CGTTCATCGGCACGGTAGA	Beta_Lactamase	deactivate
blaCTX-M-05	GCGATAACGTGGCGATGAAT	GTCGAGACGGAACGTTTCGT	Beta_Lactamase	deactivate
blaCTX-M-06	CACAGTTGGTGACGTGGCTTAA	CTCCGCTGCCGGTTTTATC	Beta_Lactamase	deactivate
blaGES	GCAATGTGCTCAACGTTCAAG	GTGCCTGAGTCAATTCTTTCAAAG	Beta_Lactamase	deactivate
blaIMP-01	AACACGGTTTGGTGGTTCTTGTA	GCGCTCCACAAACCAATTG	Beta_Lactamase	deactivate
blaIMP-02	AAGGCAGCATTTCCTCTCATTTT	GGATAGATCGAGAATTAAGCCACTCT	Beta_Lactamase	deactivate
bla-L1	CACCGGGTTACCAGCTGAAG	GCGAAGCTGCGCTTGTAGTC	Beta_Lactamase	deactivate
blaMOX/blaCMY	CTATGTCAATGTGCCGAAGCA	GGCTTGTCCTCTTTCGAATAGC	Beta_Lactamase	deactivate
blaOCH	GGCGACTTGCGCCGTAT	TTTTCTGCTCGGCCATGAG	Beta_Lactamase	deactivate
blaOKP	GCCGCCATCACCATGAG	GGTGACGTTGTCACCGATCTG	Beta_Lactamase	deactivate
blaOXA1/blaOXA30	CGGATGGTTTGAAGGGTTTATTAT	TCTTGGCTTTTATGCTTGATGTTAA	Beta_Lactamase	deactivate
blaOXA10-01	CGCAATTATCGGCCTAGAAACT	TTGGCTTTCCGTCCCATTT	Beta_Lactamase	deactivate
blaOXA10-02	CGCAATTATCGGCCTAGAAACT	TTGGCTTTCCGTCCCATTT	Beta_Lactamase	deactivate
blaOXY	CGTTCAGGCGGCAGGTT	GCCGCGATATAAGATTTGAGAATT	Beta_Lactamase	deactivate
blaPAO	CGCCGTACAACCGGTGAT	GAAGTAATGCGGTTCTCCTTTCA	Beta_Lactamase	deactivate
blaPER	TGCTGGTTGCTGTTTTTGTGA	CCTGCGCAATGATAGCTTCAT	Beta_Lactamase	deactivate
blaPSE	TTGTGACCTATTCCCCTGTAATAGAA	TGCGAAGCACGCATCATC	Beta_Lactamase	deactivate
blaROB	GCAAAGGCATGACGATTGC	CGCGCTGTTGTCGCTAAA	Beta_Lactamase	deactivate
blaSFO	CCGCCGCCATCCAGTA	GGGCCGCCAAGATGCT	Beta_Lactamase	deactivate

blaSHV-01	TCCCATGATGAGCACCTTTAAA	TTCGTCACCGGCATCCA	Beta_Lactamase	deactivate
blaSHV-02	CTTTCCCATGATGAGCACCTTT	TCCTGCTGGCGATAGTGGAT	Beta_Lactamase	deactivate
blaTEM	AGCATCTTACGGATGGCATGA	TCCTCCGATCGTTGTCAGAAGT	Beta_Lactamase	deactivate
blaTLA	ACACTTTGCCATTGCTGTTTATGT	TGCAAATTTCGGCAATAATCTTT	Beta_Lactamase	deactivate
blaVEB	CCCGATGCAAAGCGTTATG	GAAAGATTCCCTTTATCTATCTCAGACAA	Beta_Lactamase	deactivate
blaVIM	GCACTTCTCGCGGAGATTG	CGACGGTGATGCGTACGTT	Beta_Lactamase	deactivate
blaZ	GGAGATAAAGTAACAAATCCAGTTAGATATGA	TGCTTAATTTTCCATTTGCGATAAG	Beta_Lactamase	deactivate
cepA	AGTTGCGCAGAACAGTCCTCTT	TCGTATCTTGCCCGTCGATAAT	Beta_Lactamase	deactivate
cfiA	GCAGCGTTGCTGGACACA	GTTCGGGATAAACGTGGTGACT	Beta_Lactamase	deactivate
cfxA	TCATTCCTCGTTCAAGTTTTCAGA	TGCAGCACCAAGAGGAGATGT	Beta_Lactamase	deactivate
cphA-01	GCGAGCTGCACAAGCTGAT	CGGCCCAGTCGCTCTTC	Beta_Lactamase	deactivate
cphA-02	GTGCTGATGGCGAGTTTCTG	GGTGTGGTAGTTGGTGTTGATCAC	Beta_Lactamase	deactivate
fox5	GGTTTGCCGCTGCAGTTC	GCGGCCAGGTGACCAA	Beta_Lactamase	deactivate
mecA	GGTTACGGACAAGGTGAAATACTGAT	TGTCTTTTAATAAGTGAGGTGCGTTAATA	Beta_Lactamase	protection
ndm-1	ATTAGCCGCTGCATTGAT	CATGTCGAGATAGGAAGTG	Beta_Lactamase	eactivate
pbp	CCGGTGCCATTGGTTTAGA	AAAATAGCCGCCCCAAGATT	Beta_Lactamase	protection
pbp2x	TTTCATAAGTATCTGGACATGGAAGAA	CCAAAGGAAACTTGCTTGAGATTAG	Beta_Lactamase	protection
Pbp5	GGCGAACTTCTAATTAATCCTATCCA	CGCCGATGACATTCTTCTTATCTT	Beta_Lactamase	protection
penA	AGACGGTAACGTATAACTTTTTGAAAGA	GCGTGTAGCCGGCAATG	Beta_Lactamase	protection
catA1	GGGTGAGTTTCACCAGTTTTGATT	CACCTTGTCGCCTTGCGTATA	FCA	deactivate
catB3	GCACTCGATGCCTTCCAAAA	AGAGCCGATCCAAACGTCAT	FCA	deactivate
catB8	CACTCGACGCCTTCCAAAG	CCGAGCCTATCCAGACATCATT	FCA	deactivate
cfr	GCAAAATTCAGAGCAAGTTACGAA	AAAATGACTCCCAACCTGCTTTAT	FCA	deactivate
cmlA1-01	TAGGAAGCATCGGAACGTTGAT	CAGACCGAGCACGACTGTTG	FCA	efflux
cmlA1-02	AGGAAGCATCGGAACGTTGA	ACAGACCGAGCACGACTGTTG	FCA	efflux

cmx(A)	GCGATCGCCATCCTCTGT	TCGACACGGAGCCTTGGT	FCA	efflux
floR	ATTGTCTTCACGGTGTCCGTTA	CCGCGATGTCGTCGAACT	FCA	efflux
qnrA	AGGATTTCTCACGCCAGGATT	CCGCTTTCAATGAAACTGCAA	FCA	unknown
cIntI-1	GGCATCCAAGCAGCAAG	AAGCAGACTTGACCTGA	MGEs/Integrase	integrase
intI-1	CGAACGAGTGGCGGAGGGTG	TACCCGAGAGCTTGGCACCCA	MGEs/Integrase	integrase
IS613	AGGTTCGGACTCAATGCAACA	TTCAGCACATACCGCCTTGAT	MGEs/Transposase	transposase
tnpA-01	CATCATCGGACGGACAGAATT	GTCGGAGATGTGGGTGTAGAAAGT	MGEs/Transposase	transposase
tnpA-02	GGGCGGGTCGATTGAAA	GTGGGCGGGATCTGCTT	MGEs/Transposase	transposase
tnpA-03	AATTGATGCGGACGGCTTAA	TCACCAAACTGTTTATGGAGTCGTT	MGEs/Transposase	transposase
tnpA-04	CCGATCACGGAAAGCTCAAG	GGCTCGCATGACTTCGAATC	MGEs/Transposase	transposase
tnpA-05	GCCGCACTGTCGATTTTTATC	GCGGGATCTGCCACTTCTT	MGEs/Transposase	transposase
tnpA-07	GAAACCGATGCTACAATATCCAATTT	CAGCACCGTTTGCAGTGTAAG	MGEs/Transposase	transposase
Tp614	GGAAATCAACGGCATCCAGTT	CATCCATGCGCTTTTGTCTCT	MGEs/Transposase	transposase
carB	GGAGTGAGGCTGACCGTAGAAG	ATCGGCGAAACGCACAAA	MLSB	efflux
ereA	CCTGTGGTACGGAGAATTCATGT	ACCGCATTCGCTTTGCTT	MLSB	deactivate
ereB	GCTTTATTTCAGGAGGCGGAAT	TTTTAAATGCCACAGCACAGAATC	MLSB	deactivate
erm(34)	GCGCGTTGACGACGATTT	TGGTCATACTCGACGGCTAGAAC	MLSB	protection
erm(35)	TTGAAAACGATGTTGCATTAAGTCA	TCTATAATCACAACTAACCACTTGAACGT	MLSB	protection
erm(36)	GGCGGACCGACTTGCAT	TCTGCGTTGACGACGGTTAC	MLSB	protection
ermA	TTGAGAAGGGATTTGCGAAAAG	ATATCCATCTCCACCATTAATAGTAAACC	MLSB	protection
ermA/ermTR	ACATTTTACCAAGGAACTTGTGGAA	GTGGCATGACATAAACCTTCATCA	MLSB	protection
ermB	TAAAGGGCATTTAACGACGAAACT	TTTATACCTCTGTTTGTTAGGGAATTGAA	MLSB	protection
ermC	TTTGAAATCGGCTCAGGAAAA	ATGGTCTATTTCAATGGCAGTTACG	MLSB	protection
ermF	CAGCTTTGGTTGAACATTTACGAA	AAATTCCTAAAATCACAACCGACAA	MLSB	protection
ermJ/ermD	GGACTCGGCAATGGTCAGAA	CCCCGAAACGCAATATAATGTT	MLSB	protection

ermK-01	GTTTGATATTGGCATTGTCAGAGAAA	ACCATTGCCGAGTCCACTTT	MLSB	protection
ermK-02	GAGCCGCAAGCCCCTTT	GTGTTTCATTTGACGCGGAGTAA	MLSB	protection
ermT-01	GTTCACTAGCACTATTTTTAATGACAGAAGT	GAAGGGTGTCTTTTTAATACAATTAACGA	MLSB	protection
ermT-02	GTAAAATCCCTAGAGAATACTTTCATCCA	TGAGTGATATTTTTGAAGGGTGTCTT	MLSB	protection
ermX	GCTCAGTGGTCCCCATGGT	ATCCCCCCGTCAACGTTT	MLSB	protection
ermY	TTGTCTTTGAAAGTGAAGCAACAGT	TAACGCTAGAGAACGATTTGTATTGAG	MLSB	protection
lmrA-01	TCGACGTGACCGTAGTGAACA	CGTGACTACCCAGGTGAGTTGA	MLSB	efflux
lnuA-01	TGACGCTCAACACACTCAAAAA	TTCATGCTTAAGTTCCATACGTGAA	MLSB	deactivate
lnuB-01	TGAACATAATCCCCTCGTTTAAAGAT	TAATTGCCCTGTTTCATCGTAAATAA	MLSB	deactivate
lnuB-02	AAAGGAGAAGGTGACCAATACTCTGA	GGAGCTACGTCAAACAACCAGTT	MLSB	deactivate
lnuC	TGGTCAATATAACAGATGTAAACCAGATTT	CACCCCAGCCACCATCAA	MLSB	deactivate
matA/mel	TAGTAGGCAAGCTCGGTGTTGA	CCTGTGCTATTTTAAGCCTTGTTTCT	MLSB	efflux
mdtA	CCTAACGGGCGTGACTTCA	TTCACCTGTTTCAAGGGTCAAA	MLSB	efflux
mefA	CCGTAGCATTGGAACAGCTTTT	AAACGGAGTATAAGAGTGCTGCAA	MLSB	efflux
mphA-01	CTGACGCGCTCCGTGTT	GGTGGTGCATGGCGATCT	MLSB	deactivate
mphA-02	TGATGACCCTGCCATCGA	TTCGCGAGCCCCTCTTC	MLSB	deactivate
mphB	CGCAGCGCTTGATCTTGTAG	TTACTGCATCCATACGCTGCTT	MLSB	deactivate
mphC	CGTTTGAAGTACCGAATTGGAAA	GCTGCGGGTTTGCCTGTA	MLSB	deactivate
msrA-01	CTGCTAACACAAGTACGATTCCAAAT	TCAAGTAAAGTTGTCTTACCTACACCATT	MLSB	efflux
msrC-01	TCAGACCGGATCGGTTGTC	CCTATTTTTTGGAGTCTTCTCTCTAATGTT	MLSB	efflux
oleC	CCCGGAGTCGATGTTCGA	GCCGAAGACGTACACGAACAG	MLSB	efflux
pikR1	TCGACATGCGTGACGAGATT	CCGCGAATTAGGCCAGAA	MLSB	protection
pikR2	TCGTGGGCCAGGTGAAGA	TTCCCCTTGCCGGTGAA	MLSB	protection
vatB-01	GGAAAAAGCAACTCCATCTCTTGA	TCCTGGCATAACAGTAACATTCTGA	MLSB	deactivate
vatB-02	TTGGGAAAAAGCAACTCCATCT	CAATCCACACATCATTTCCAACA	MLSB	deactivate

vatC-01	CGGAAATTGGGAACGATGTT	GCAATAATAGCCCCGTTTCCTA	MLSB	deactivate
vatC-02	CGATGTTTGGATTGGACGAGAT	GCTGCAATAATAGCCCCGTTT	MLSB	deactivate
vatE-01	GGTGCCATTATCGGAGCAAAT	TTGGATTGCCACCGACAAT	MLSB	deactivate
vatE-02	GACCGTCCTACCAGGCGTAA	TTGGATTGCCACCGACAATT	MLSB	deactivate
vgaA-01	CGAGTATTGTGGAAAGCAGCTAGTT	CCCGTACCGTTAGAGCCGATA	MLSB	efflux
vgaA-02	GACGGGTATTGTGGAAAGCAA	TTTCCTGTACCATTAGATCCGATAATT	MLSB	efflux
vgb-01	AGGGAGGGTATCCATGCAGAT	ACCAAATGCGCCCGTTT	MLSB	deactivate
vgbB-01	CAGCCGGATTCTGGTCCTT	TACGATCTCCATTCAATTGGGTAAA	MLSB	efflux
vgbB-02	ATACGAGCTGCCTAATAAAGGATCTT	TGTGAACCACAGGGCATTATCA	MLSB	deactivate
acrA-01	CAACGATCGGACGGGTTTC	TGGCGATGCCACCGTACT	Multidrug	efflux
acrA-02	GGTCTATCACCCTACGCGCTATC	GCGCGCACGAACATACC	Multidrug	efflux
acrA-03	CAGACCCGCATCGCATATT	CGACAATTTCGCGCTCATG	Multidrug	efflux
acrA-04	TACTTTGCGCGCCATCTTC	CGTGCGCGAACGAACAT	Multidrug	efflux
acrA-05	CGTGCGCGAACGAACA	ACTTTGCGCGCCATCTTC	Multidrug	efflux
acrB-01	AGTCGGTGTTCGCCGTTAAC	CAAGGAAACGAACGCAATACC	Multidrug	efflux
acrF	GCGGCCAGGCACAAAA	TACGCTCTTCCCACGGTTTC	Multidrug	efflux
acrR-01	GCGCTGGAGACACGACAAC	GCCTTGCTGCGAGAACAAA	Multidrug	efflux
acrR-02	GATGATACCCCCTGCTGTGAGA	ACCAAACAAGAAGCGCAAGAA	Multidrug	efflux
adeA	CAGTTCGAGCGCCTATTTCTG	CGCCCTGACCGACCAAT	Multidrug	efflux
ceoA	ATCAACACGGACCAGGACAAG	GGAAAGTCCGCTCACGATGA	Multidrug	efflux
cmeA	GCAGCAAAGAAGAAGCACCAA	AGCAGGGTAAGTAAAACTAAGTGGTAAATCT	Multidrug	efflux
cmr	CGGCATCGTCAGTGGAATT	CGGTTCCGAAAAAGATGGAA	Multidrug	efflux
emrD	CTCAGCAGTATGGTGGTAAGCATT	ACCAGGCGCCGAAGAAC	Multidrug	efflux
marR-01	GCGGCGTACTGGTGAAGCTA	TGCCCTGGTCGTTGATGA	Multidrug	efflux
mdetl1	ATACAGCAGTGGATATTGGTTTAATTGT	TGCATAAGGTGAATGTTCCATGA	Multidrug	efflux

mdtE/yhiU	CGTCGGCGCACTCGTT	TCCAGACGTTGTACGGTAACCA	Multidrug	efflux
mepA	ATCGGTCGCTCTTCGTTCAC	ATAAATAGGATCGAGCTGCTGGAT	Multidrug	efflux
mexA	AGGACAACGCTATGCAACGAA	CCGGAAAGGGCCGAAAT	Multidrug	efflux
mexD	TTGCCACTGGCTTTCATGAG	CACTGCGGAGAACTGTCTGTAGA	Multidrug	efflux
mexE	GGTCAGCACCGACAAGGTCTAC	AGCTCGACGTACTTGAGGAACAC	Multidrug	efflux
mexF	CCGCGAGAAGGCCAAGA	TTGAGTTCGGCGGTGATGA	Multidrug	efflux
mtrC-01	GGACGGGAAGATGGTCCAA	CGTAGCGTTCCGGTTCGAT	Multidrug	efflux
mtrC-02	CGGAGTCCATCGACCATTTG	ATCGTCGGCAAGGAGAATCA	Multidrug	efflux
mtrD-02	GGTCGGCACGCTCTTGTC	TGAAGAATTTGCGCACCACTAC	Multidrug	efflux
mtrD-03	CCGCCAAGCCGATATAGACA	GGCCGGGTTGCCAAA	Multidrug	efflux
oprD	ATGAAGTGGAGCGCCATTG	GGCCACGGCGAACTGA	Multidrug	efflux
oprJ	ACGAGAGTGGCGTCGACAA	AAGGCGATCTCGTTGAGGAA	Multidrug	efflux
pmrA	TTTGCAGGTTTTGTTCCTAATGC	GCAGAGCCTGATTTCTCCTTTG	Multidrug	efflux
putitive multidrug	AATTTTGCCGATTATTGCTGAAA	GATTGTCATCATTCGTTTATCACCAA	Multidrug	efflux
qac	CAATAATAACCGAAATAATAGGGACAAGTT	AATAAGTGTTCCTAGTGTTGGCCATAG	Multidrug	efflux
qacA	TGGCAATAGGAGCTATGGTGTTT	AAGGTAACACTATTTTCGGTCCAAATC	Multidrug	efflux
qacA/qacB	TTTAGGCAGCCTCGCTTCA	CCGAATCCAAATAAAACCCAATAA	Multidrug	efflux
qacEdelta1-01	TCGCAACATCCGCATTAAAA	ATGGATTTCAGAACCAGAGAAAGAAA	Multidrug	efflux
qacEdelta1-02	CCCCTTCCGCCGTTGT	CGACCAGACTGCATAAGCAACA	Multidrug	efflux
qacH-01	GTGGCAGCTATCGCTTGGAT	CCAACGAACGCCCACAA	Multidrug	efflux
qacH-02	CATCGTGCTTGTGGCAGCTA	TGAACGCCCAGAAGTCTAGTTTT	Multidrug	efflux
rarD-02	TGACGCATCGCGTGATCT	AAATTTTCTGTGGCGTCTGAATC	Multidrug	efflux
sdeB	CACTACCGCTTCCGCACTTAA	TGAAAAAACGGGAAAAGTCCAT	Multidrug	efflux
tolC-01	GGCCGAGAACCTGATGCA	AGACTTACGCAATTCCGGGTTA	Multidrug	efflux
tolC-02	CAGGCAGAGAACCTGATGCA	CGCAATTCCGGGTTGCT	Multidrug	efflux

tolC-03	GCCAGGCAGAGAACCTGATG	CGCAATTCCGGGTTGCT	Multidrug	efflux
ttgA	ACGCCAATGCCAAACGATT	GTCACGGCGCAGCTTGA	Multidrug	efflux
ttgB	TCGCCCTGGATGTACACCTT	ACCATTGCCGACATCAACAAC	Multidrug	efflux
yceE/mdtG-01	TGGCACAAAATATCTGGCAGTT	TTGTGTGGCGATAAGAGCATTAG	Multidrug	efflux
yceE/mdtG-02	TTATCTGTTTTCTGCTCACCTTCTTTT	GCGTGGTGACAAACAGGCTTA	Multidrug	efflux
yceL/mdtH-01	TCGGGATGGTGGGCAAT	CGATAACCGAGCCGATGTAGA	Multidrug	efflux
yceL/mdtH-02	CGCGTGAAACCTTAAGTGCTT	AGACGGCTAAACCCCATATAGCT	Multidrug	efflux
yceL/mdtH-03	CTGCCGTTAAATGGATGTATGC	ACTCCAGCGGGCGATAGG	Multidrug	efflux
yidY/mdtL-01	GCAGTTGCATATCGCCTTCTC	CTTCCCGGCAAACAGCAT	Multidrug	efflux
yidY/mdtL-02	TGCTGATCGGGATTCTGATTG	CAGGCGCGACGAACATAAT	Multidrug	efflux
fabK	TTTCAGCTCAGCACTTTGGTCAT	AAGGCATCTTTTTCAGCCAGTTC	Others	deactivate
imiR	CCGGACTAGAGCTTCATGTAAGC	CCCACGCGGTACTCTTGTAAA	Others	unknown
nisB	GGGAGAGTTGCCGATGTTGTA	AGCCACTCGTTAAAGGGCAAT	Others	unknown
speA	GCAAGAGGTATTTGCTCAACAAGA	CAGGGTCACCCTCATAAAGAAAA	Others	unknown
bacA-01	CGGCTTCGTGACCTCGTT	ACAATGCGATACCAGGCAAAT	Others/bacitracin	deactivate
bacA-02	TTCCACGACACGATTAAGTCATTG	CGGCTCTTTCGGCTTCAG	Others/bacitracin	deactivate
fosB	TCACTGTAACTAATGAAGCATTAGACCAT	CCATCTGGATCTGTAAAGTAAAGAGATC	Others/fosfomycin	deactivate
fosX	GATTAAGCCATATCACTTTAATTGTGAAAG	TCTCCTTCCATAATGCAAATCCA	Others/fosfomycin	deactivate
nimE	TGCGCCAAGATAGGGCATA	GTCGTGAATTCGGCAGGTTTA	Others/nitroimidazole	unknown
pncA	GCAATCGAGGCGGTGTTC	TTGCCGCAGCCAATTCA	Others/Pyrazinamide	unknown
sat4	GAATGGGCAAAGCATAAAAACTTG	CCGATTTTGAAACCACAATTATGATA	Others/streptothricin	deactivate
dfrA1	GGAATGGCCCTGATATTCCA	AGTCTTGCGTCCAACCAACAG	Sulfonamides	deactivate
dfrA12	CCTCTACCGAACCGTCACACA	GCGACAGCGTTGAAACAACTAC	Sulfonamides	deactivate
folA	CGAGCAGTTCCTGCCAAAG	CCCAGTCATCCGGTTCATAATC	Sulfonamides	deactivate
sul1	CAGCGCTATGCGCTCAAG	ATCCCGCTGCGCTGAGT	Sulfonamides	protection

sul2	TCATCTGCCAAACTCGTCGTTA	GTCAAAGAACGCCGCAATGT	Sulfonamides	protection
sulA/folP-01	CAGGCTCGTAAATTGATAGCAGAAG	CTTTCCTTGCGAATCGCTTT	Sulfonamides	protection
sulA/folP-03	CACGGCTTCGGCTCATGT	TGCCATCCTGTGACTAGCTACGT	Sulfonamides	protection
tet(32)	CCATTACTTCGGACAACGGTAGA	CAATCTCTGTGAGGGCATTTAACA	Tetracyclines	protection
tet(34)	CTTAGCGCAAACAGCAATCAGT	CGGTGATACAGCGCGTAAACT	Tetracyclines	unknown
tet(35)	ACCCCATGACGTACCTGTAGAGA	CAACCCACACTGGCTACCAGTT	Tetracyclines	unknown
tet(36)-01	AGAATACTCAGCAGAGGTCAGTTCCT	TGGTAGGTCGATAACCCGAAAAT	Tetracyclines	protection
tet(36)-02	TGCAGGAAAGACCTCCATTACAG	CTTTGTCCACACTTCCACGTACTATG	Tetracyclines	protection
tet(37)	GAGAACGTTGAAAAGGTGGTGAA	AACCAAGCCTGGATCAGTCTCA	Tetracyclines	unknown
tetA-01	GCTGTTTGTTCTGCCGGAAA	GGTTAAGTTCCTTGAACGCAAACT	Tetracyclines	efflux
tetA-02	CTCACCAGCCTGACCTCGAT	CACGTTGTTATAGAAGCCGCATAG	Tetracyclines	efflux
tetB-01	AGTGCGCTTTGGATGCTGTA	AGCCCCAGTAGCTCCTGTGA	Tetracyclines	efflux
tetB-02	GCCCAGTGCTGTTGTTGTCAT	TGAAAGCAAACGGCCTAAATACA	Tetracyclines	efflux
tetC-01	CATATCGCAATACATGCGAAAAA	AAAGCCGCGGTAAATAGCAA	Tetracyclines	efflux
tetC-02	ACTGGTAAGGTAAACGCCATTGTC	ATGCATAAACCAGCCATTGAGTAAG	Tetracyclines	efflux
tetD-01	TGCCGCGTTTGATTACACA	CACCAGTGATCCCGGAGATAA	Tetracyclines	efflux
tetD-02	TGTCATCGCGCTGGTGATT	CATCCGCTTCCGGGAGAT	Tetracyclines	efflux
tetE	TTGGCGCTGTATGCAATGAT	CGACGACCTATGCGATCTGA	Tetracyclines	efflux
tetG-01	TCAACCATTGCCGATTCGA	TGGCCCGGCAATCATG	Tetracyclines	efflux
tetG-02	CATCAGCGCCGGTCTTATG	CCCCATGTAGCCGAACCA	Tetracyclines	efflux
tetH	TTTGGGTCATCTTACCAGCATTAA	TTGCGCATTATCATCGACAGA	Tetracyclines	efflux
tetJ	GGGTGCCGCATTAGATTACCT	TCGTCCAATGTAGAGCATCCATA	Tetracyclines	efflux
tetK	CAGCAGTCATTGGAAAATTATCTGATTATA	CCTTGTACTAACCTACCAAAAATCAAAATA	Tetracyclines	efflux
tetL-01	AGCCCGATTTATTCAAGGAATTG	CAAATGCTTTCCCCCTGTTCT	Tetracyclines	efflux
tetL-02	ATGGTTGTAGTTGCGCGCTATAT	ATCGCTGGACCGACTCCTT	Tetracyclines	efflux

tetM-01	CATCATAGACACGCCAGGACATAT	CGCCATCTTTTGCAGAAATCA	Tetracyclines	protection
tetM-02	TAATATTGGAGTTTTAGCTCATGTTGATG	CCTCTCTGACGTTCTAAAAGCGTATTAT	Tetracyclines	protection
tetO-01	ATGTGGATACTACAACGCATGAGATT	TGCCTCCACATGATATTTTTCCT	Tetracyclines	protection
tetPA	AGTTGCAGATGTGTATAGTCGTAAACTATCTATT	TGCTACAAGTACGAAAACAAAACTAGAA	Tetracyclines	efflux
tetPB-01	ACACCTGGACACGCTGATTTT	ACCGTCTAGAACGCGGAATG	Tetracyclines	protection
tetPB-02	TGATACACCTGGACACGCTGAT	CGTCCAAAACGCGGAATG	Tetracyclines	protection
tetPB-03	TGGGCGACAGTAGGCTTAGAA	TGACCCTACTGAAACATTAGAAATATACCT	Tetracyclines	protection
tetPB-04	AGTGGTGCAAATACTGAAAAAGTTGT	TTTGTTCCTTCGTTTTGGACAGA	Tetracyclines	protection
tetPB-05	CTGAAGTGGAGCGATCATTCC	CCCTCAACGGCAGAAATAACTAA	Tetracyclines	protection
tetQ	CGCCTCAGAAGTAAGTTCATACACTAAG	TCGTTCATGCGGATATTATCAGAAT	Tetracyclines	protection
tetR-02	CGCGATAGACGCCTTCGA	TCCTGACAACGAGCCTCCTT	Tetracyclines	efflux
tetR-03	CGCGATGGAGCAAAAGTACAT	AGTGAAAAACCTTGTTGGCATAAAA	Tetracyclines	efflux
tetS	TTAAGGACAAACTTTCTGACGACATC	TGTCTCCCATTGTTCTGGTTCA	Tetracyclines	protection
tetT	CCATATAGAGGTTCCACCAAATCC	TGACCCTATTGGTAGTGGTTCTATTG	Tetracyclines	protection
tetU-01	GTGGCAAAGCAACGGATTG	TGCGGGCTTGCAAAACTATC	Tetracyclines	unknown
tetV	GCGGGAACGACGATGTATATC	CCGCTATCTCACGACCATGAT	Tetracyclines	efflux
tetX	AAATTTGTTACCGACACGGAAGTT	CATAGCTGAAAAAATCCAGGACAGTT	Tetracyclines	unknown
vanA	AAAAGGCTCTGAAAACGCAGTTAT	CGGCCGTTATCTTGTAAAAACAT	Vancomycin	protection
vanB-01	TTGTCGGCGAAGTGGATCA	AGCCTTTTTCCGGCTCGTT	Vancomycin	protection
vanB-02	CCGGTCGAGGAACGAAATC	TCCTCCTGCAAAAAAAGATCAAC	Vancomycin	protection
vanC-01	ACAGGGATTGGCTATGAACCAT	TGACTGGCGATGATTTGACTATG	Vancomycin	protection
vanC-03	AAATCAATACTATGCCGGGCTTT	CCGACCGCTGCCATCA	Vancomycin	protection
vanC1	AGGCGATAGCGGGTATTGAA	CAATCGTCAATTGCTCATTTCC	Vancomycin	protection
vanC2/vanC3	TTTGACTGTCGGTGCTTGTGA	TCAATCGTTTCAGGCAATGG	Vancomycin	protection
vanG	ATTTGAATTGGCAGGTATACAGGTTA	TGATTTGTCTTTGTCCATACATAATGC	Vancomycin	protection

vanHB	GAGGTTTCCGAGGCGACAA	CTCTCGGCGGCAGTCGTAT	Vancomycin	protection
vanHD	GTGGCCGATTATACCGTCATG	CGCAGGTCATTCAGGCAAT	Vancomycin	protection
vanRA-01	CCCTTACTCCCACCGAGTTTT	TTCGTCGCCCCATATCTCAT	Vancomycin	protection
vanRA-02	CCACTCCGGCCTTGTCATT	GCTAACCACATTCCCCTTGTTTT	Vancomycin	protection
vanRB	GCCCTGTCGGATGACGAA	TTACATAGTCGTCTGCCTCTGCAT	Vancomycin	protection
vanRC	TGCGGGAAAAACTGAACGA	CCCCCCATACGGTTTTGATTA	Vancomycin	protection
vanRC4	AGTGCTTTGGCTTATCTCGAAAA	TCCGGCAGCATCACATCTAA	Vancomycin	protection
vanRD	TTATAATGGCAAGGATGCACTAAAGT	CGTCTACATCCGGAAGCATGA	Vancomycin	protection
vanSA	CGCGTCATGCTTTCAAAATTC	TCCGCAGAAAGCTCAATTTGTT	Vancomycin	protection
vanSB	GCGCGGCAAATGACAAC	TTTGCCATTTTATTCGCACTGT	Vancomycin	protection
vanSC-02	GCCATCAGCGAGTCTGATGA	CAGCTGGGATCGTTTTTCCTT	Vancomycin	protection
vanSE	TGGCCGAAGAAGCAGGAA	CAATAATACTCGTCAAAGGAGTTCTCA	Vancomycin	protection
vanTC-01	CACACGCATTTTTTCCCATCTAG	CAGCCAACAGATCATCAAAACAA	Vancomycin	protection
vanTC-02	ACAGTTGCCGCTGGTGAAG	CGTGGCTGGTCGATCAAAA	Vancomycin	protection
vanTE	GTGGTGCCAAGGAAGTTGCT	CGTAGCCACCGCAAAAAAAT	Vancomycin	protection
vanTG	CGTGTAGCCGTTCCGTTCTT	CGGCATTACAGGTATATCTGGAAA	Vancomycin	protection
vanWB	CGGACAAAGATACCCCCTATAAAG	AAATAGTAAATTGCTCATCTGGCACAT	Vancomycin	protection
vanWG	ACATTTTCATTTTGGCAGCTTGTAC	CCGCCATAAGAGCCTACAATCT	Vancomycin	protection
vanXA	CGCTAAATATGCCACTTGGGATA	TCAAAAGCGATTCAGCCAACT	Vancomycin	protection
vanXB	AGGCACAAAATCGAAGATGCTT	GGGTATGGCTCATCAATCAACTT	Vancomycin	protection
vanXD	TAAACCGTGTTATGGGAACGAA	GCGATAGCCGTCCCATAAGA	Vancomycin	protection
vanYB	GGCTAAAGCGGAAGCAGAAA	GATATCCACAGCAAGACCAAGCT	Vancomycin	protection
vanYD-01	AAGGCGATACCCTGACTGTCA	ATTGCCGGACGGAAGCA	Vancomycin	protection
vanYD-02	CAAACGGAAGAGAGGTCACTTACA	CGGACGGTAATAGGGACTGTTC	Vancomycin	protection

Fig. S1. The number of ARGs and MGEs that can be detected using 295 primer sets.

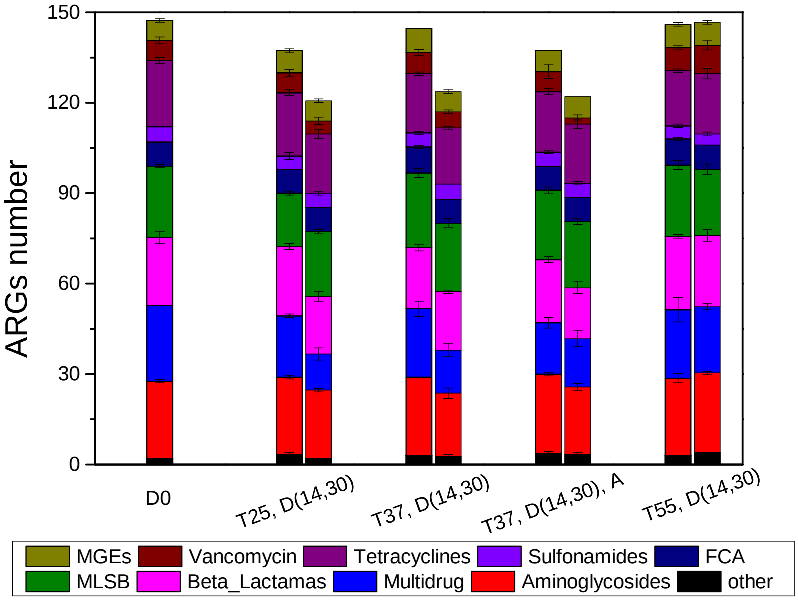
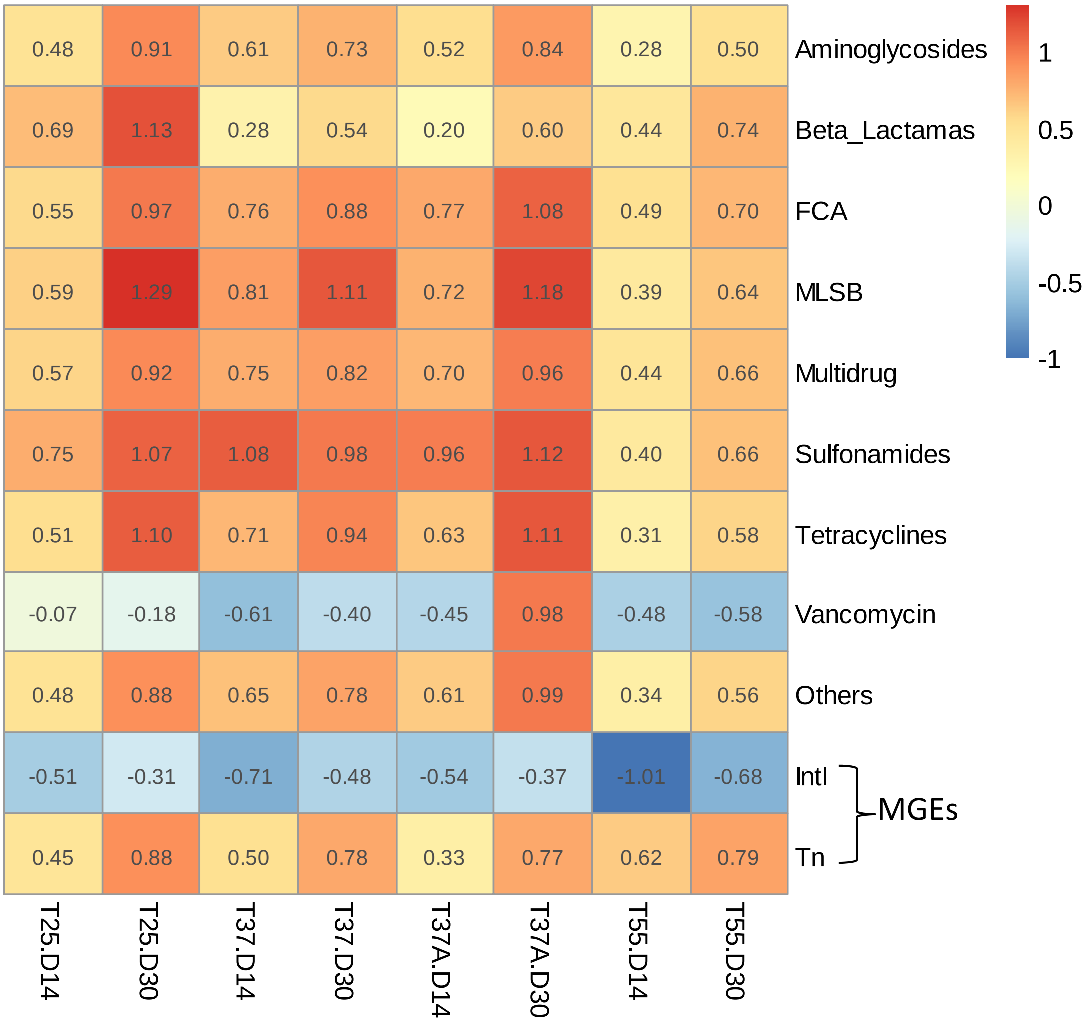


Fig. S2. Average log removal of ARG types and MGEs on days 14 and 30 compared to day 0. *IntI*: integrase genes; *Tn*: transposase genes. The number in the cell indicates the log removal.



	T25.D14	T25.D30	T37.D14	T37.D30	T37A.D14	T37A.D30	T55.D14	T55.D30
Aminoglycosides	0.48	0.91	0.61	0.73	0.52	0.84	0.28	0.50
Beta_Lactamas	0.69	1.13	0.28	0.54	0.20	0.60	0.44	0.74
FCA	0.55	0.97	0.76	0.88	0.77	1.08	0.49	0.70
MLSB	0.59	1.29	0.81	1.11	0.72	1.18	0.39	0.64
Multidrug	0.57	0.92	0.75	0.82	0.70	0.96	0.44	0.66
Sulfonamides	0.75	1.07	1.08	0.98	0.96	1.12	0.40	0.66
Tetracyclines	0.51	1.10	0.71	0.94	0.63	1.11	0.31	0.58
Vancomycin	-0.07	-0.18	-0.61	-0.40	-0.45	0.98	-0.48	-0.58
Others	0.48	0.88	0.65	0.78	0.61	0.99	0.34	0.56
IntI	-0.51	-0.31	-0.71	-0.48	-0.54	-0.37	-1.01	-0.68
Tn	0.45	0.88	0.50	0.78	0.33	0.77	0.62	0.79

Fig.S3. The alpha-diversity indices of microbial communities in the samples collected from different days.

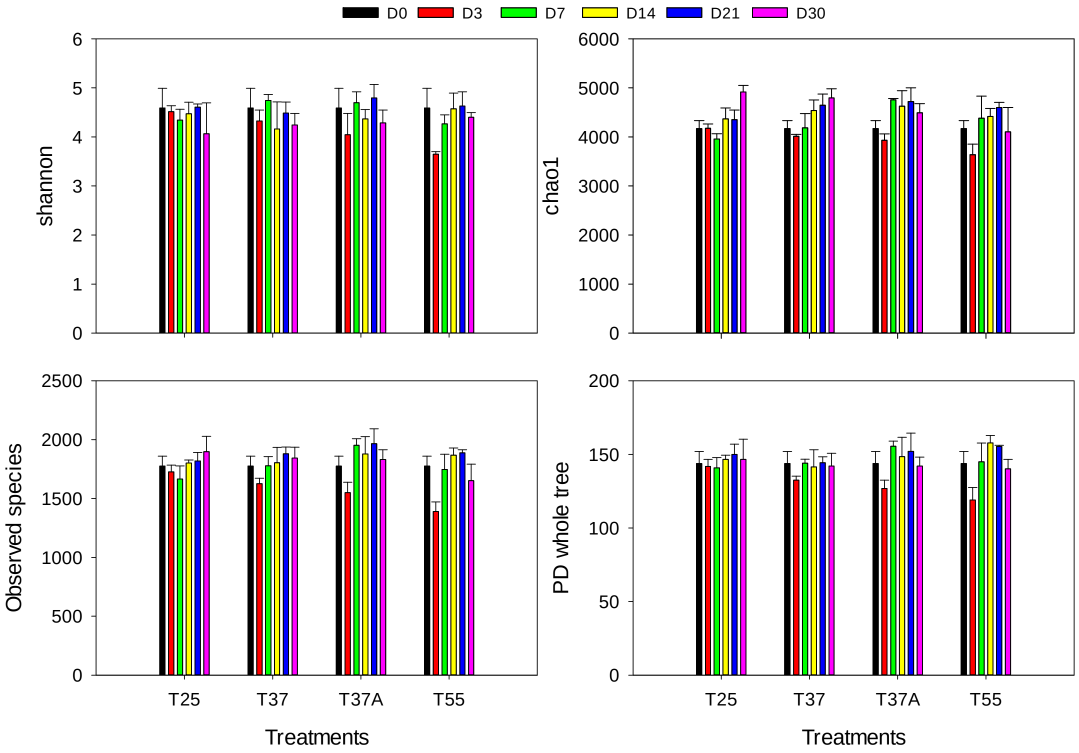


Fig. S4. Principal component analysis (PCA) based on the euclidean distance showing the overall distribution pattern of microbial communities in all treatments.

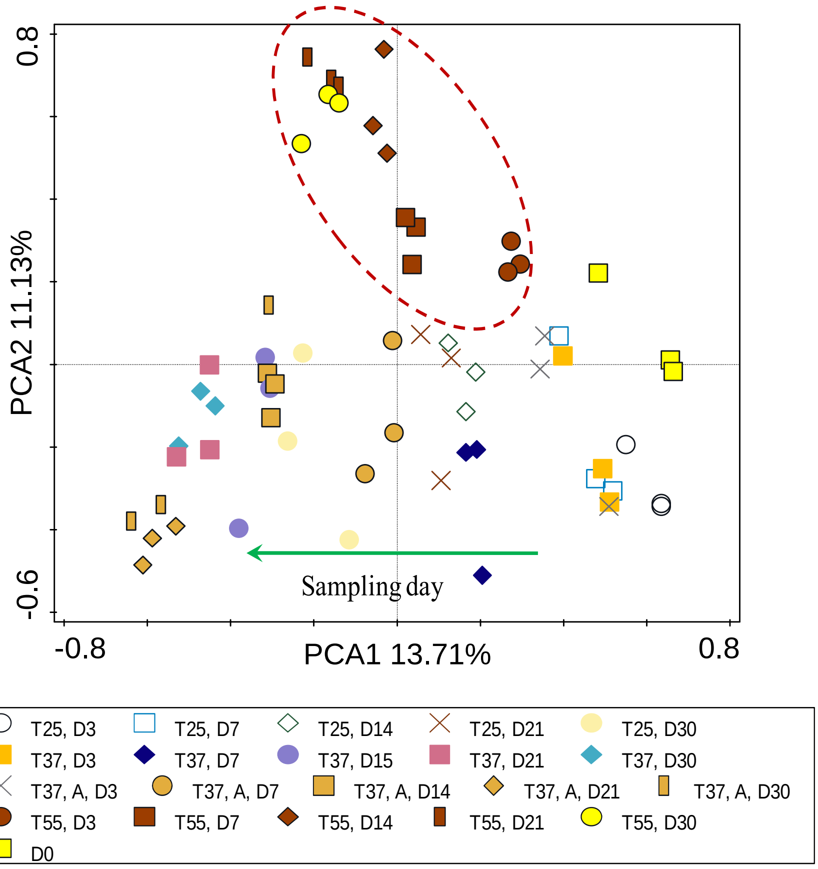


Fig. S5. Variation of bacterial and archaeal phyla in manure slurry during anaerobic digestion.

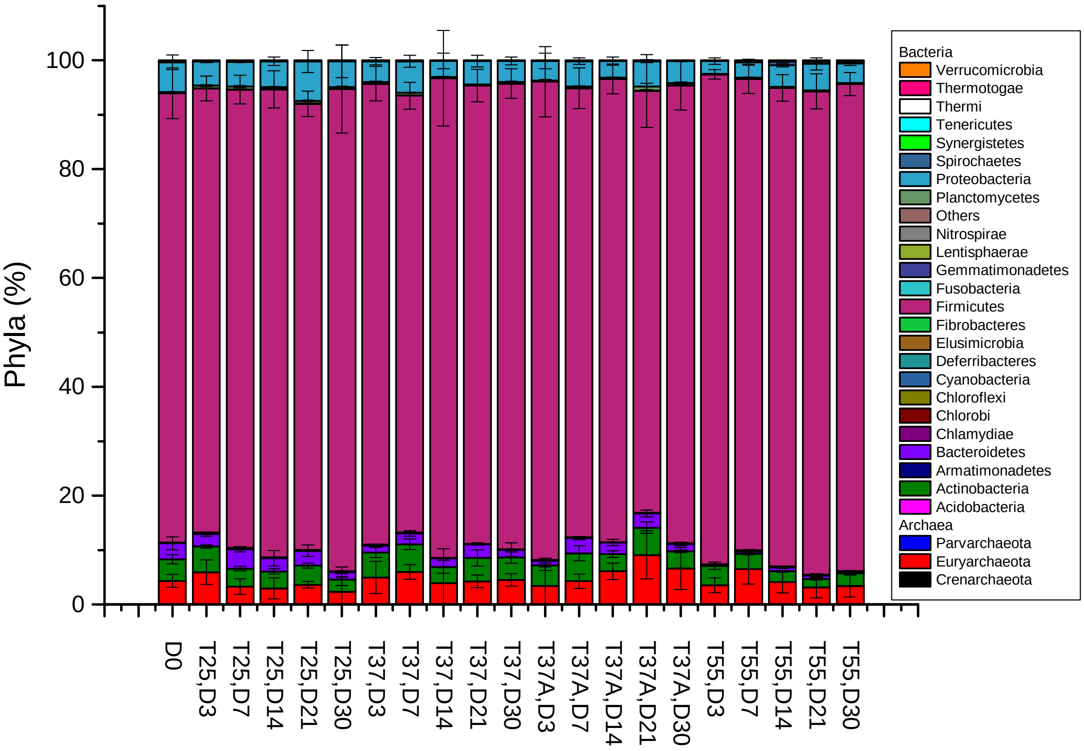
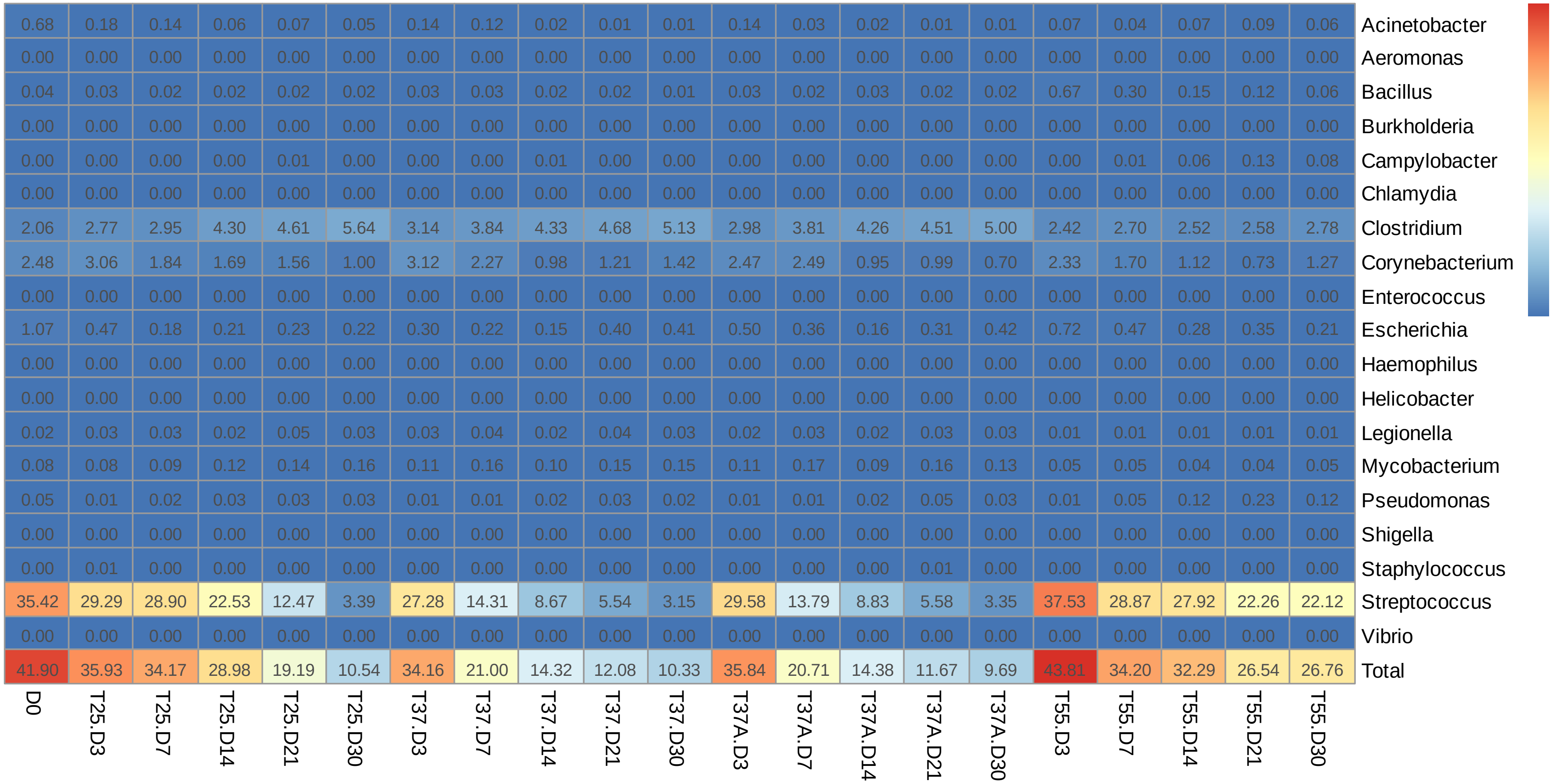


Fig. S6. The detection frequencies (%) of potential pathogenic bacteria during anaerobic digestion in this study based on the information on website http://www.mgc.ac.cn/cgi-bin/VFs/jsif/main.cgi.



D0	T25.D3	T25.D7	T25.D14	T25.D21	T25.D30	T37.D3	T37.D7	T37.D14	T37.D21	T37.D30	T37A.D3	T37A.D7	T37A.D14	T37A.D21	T37A.D30	T55.D3	T55.D7	T55.D14	T55.D21	T55.D30	
0.68	0.18	0.14	0.06	0.07	0.05	0.14	0.12	0.02	0.01	0.01	0.14	0.03	0.02	0.01	0.01	0.07	0.04	0.07	0.09	0.06	Acinetobacter
0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	Aeromonas
0.04	0.03	0.02	0.02	0.02	0.02	0.03	0.03	0.02	0.02	0.01	0.03	0.02	0.03	0.02	0.02	0.67	0.30	0.15	0.12	0.06	Bacillus
0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	Burkholderia
0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.06	0.13	0.08	Campylobacter
0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	Chlamydia
2.06	2.77	2.95	4.30	4.61	5.64	3.14	3.84	4.33	4.68	5.13	2.98	3.81	4.26	4.51	5.00	2.42	2.70	2.52	2.58	2.78	Clostridium
2.48	3.06	1.84	1.69	1.56	1.00	3.12	2.27	0.98	1.21	1.42	2.47	2.49	0.95	0.99	0.70	2.33	1.70	1.12	0.73	1.27	Corynebacterium
0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	Enterococcus
1.07	0.47	0.18	0.21	0.23	0.22	0.30	0.22	0.15	0.40	0.41	0.50	0.36	0.16	0.31	0.42	0.72	0.47	0.28	0.35	0.21	Escherichia
0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	Haemophilus
0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	Helicobacter
0.02	0.03	0.03	0.02	0.05	0.03	0.03	0.04	0.02	0.04	0.03	0.02	0.03	0.02	0.03	0.03	0.01	0.01	0.01	0.01	0.01	Legionella
0.08	0.08	0.09	0.12	0.14	0.16	0.11	0.16	0.10	0.15	0.15	0.11	0.17	0.09	0.16	0.13	0.05	0.05	0.04	0.04	0.05	Mycobacterium
0.05	0.01	0.02	0.03	0.03	0.03	0.01	0.01	0.02	0.03	0.02	0.01	0.01	0.02	0.05	0.03	0.01	0.05	0.12	0.23	0.12	Pseudomonas
0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	Shigella
0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	Staphylococcus
35.42	29.29	28.90	22.53	12.47	3.39	27.28	14.31	8.67	5.54	3.15	29.58	13.79	8.83	5.58	3.35	37.53	28.87	27.92	22.26	22.12	Streptococcus
0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	Vibrio
41.90	35.93	34.17	28.98	19.19	10.54	34.16	21.00	14.32	12.08	10.33	35.84	20.71	14.38	11.67	9.69	43.81	34.20	32.29	26.54	26.76	Total

Fig. S7. Dynamics of OTC, SM2 and CIP in manure slurry of antibiotic-spiking treatment (T37A) during anaerobic digestion. (A) Antibiotic concentrations in supernatant. (B) Antibiotic concentrations in pellet. (C) Total concentrations calculated from those in supernatant and pellet.

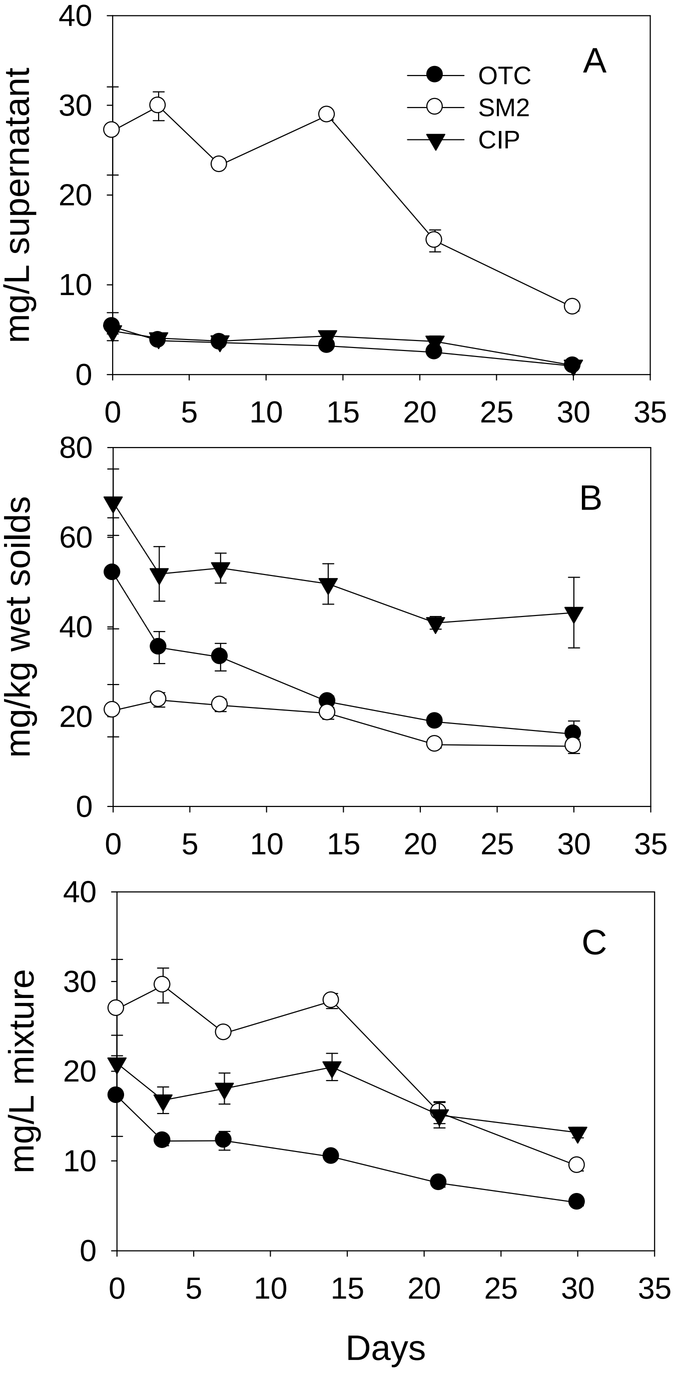


Fig. S8. Schematic description of anaerobic digestion experimental setup.