

Supporting information:

Antibiotic resistance genes and their correlations with microbial community and metal resistance genes in full-scale biogas reactors as revealed by metagenomic analysis

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Table S1 Information of DNA yield and purity, metagenomic sequencing results and data accession ID

Sample name	DNA yield (ug DNA/mL sample)	260/280	Reads (100bp)	Tags (~170bp)	Accession number
MM1	4.2435	1.77	12,467,700×2	10,752,111	mgm4540030.3
MM2	5.2059	1.77	13,186,150×2	11,782,875	mgm4540034.3
MM3	10.75767	1.69	9,626,100×2	8,021,985	mgm4540043.3
MT1	6.3168	1.54	12,611,150×2	11,014,099	mgm4540036.3
MT2a	4.69755	1.51	12,821,750×2	9,064,863	mgm4540037.3
MT2b	5.454	1.52	13,163,550×2	9,977,217	mgm4540038.3
MT3a	3.889967	1.64	30,014,200×2	26,750,735	mgm4540039.3
MT3b	4.96515	1.68	18,662,400×2	16,452,526	mgm4540040.3
MT4	5.793667	1.46	16,272,400×2	14,852,689	mgm4540041.3
SM1	14.21548	1.82	15,306,650×2	12,779,969	mgm4540042.3
SM2	15.59173	1.83	10,569,300×2	9,369,214	mgm4540031.3
SM3	16.24618	1.8	11,968,650×2	10,656,756	mgm4540032.3
SM4	19.36293	1.82	10,761,650×2	9,199,240	mgm4540033.3
SM5	17.47845	1.79	12,027,200×2	9,804,037	mgm4540035.3

Table S2 Environmental variables used in CCA analysis

Sample name	HRT (days)	Operating temperature (°C)	VFA (mM)	Ammonia (g/L)	pH	Free ammonia (g/L)	Substrate
MM1	21	37	6.32	2.47	7.83	0.46	1
MM2	32	40	6.93	4.22	8.18	1.42	1
MM3	24	40	5.58	2.626875	7.75	0.42	1
MT1	22	52	1.95	2.53	7.82	0.46	1
MT2a	11	50	21.29	2.96	8.18	0.99	1
MT2b	22	52	10.74	3.3	8.36	1.44	1
MT3a	15	52	4.49	2.46	8.1	0.73	1
MT3b	18	52	1.05	2.31	8.1	0.69	1
MT4	11	53	15.67	2.38	8.03	0.63	1
SM1	24	37	1.19	0.47	7.01	0.02	0
SM2	30	37	0.65	0.92	7.11	0.04	0
SM3	25	39	0.64	0.53	7.1	0.02	0
SM4	19	37	0.6	1.1	7.33	0.07	0
SM5	22	36	1.7	1.24	7.53	0.13	0

Table S3 Inflation factor of each environmental variable

Parameter	Mean value	Standard deviation	Inflation factor
HRT	21.14	5.9	10.4
Temperature	43.85	7.01	5
VFA	5.63	6.09	5.2
ammonia	2.11	1.1	36.8
pH	7.75	0.44	42.8
free ammonia	0.54	0.47	22.2
substrate	0.64	0.48	12.9

Table S4 List of the shared ARG subtypes and their abundance

	MM1	MM2	MM3	MT1	MT2a	MT2b	MT3a	MT3b	MT4	SM1	SM2	SM3	SM4	SM5
Lincosamide ucleotidyltransferase	2.30E-03	3.92E-03	4.86E-03	1.12E-03	7.49E-05	2.45E-04	3.60E-04	5.10E-04	3.00E-04	8.87E-04	1.19E-03	1.71E-03	9.09E-04	2.26E-04
Macrolide permease protein <i>macB</i>	1.24E-04	8.97E-04	4.22E-04	3.31E-04	2.34E-04	5.61E-04	2.88E-04	2.45E-04	2.06E-04	1.46E-04	7.62E-04	3.02E-04	4.46E-04	8.16E-04
Macrolide transporter ATP-binding(permease) protein	2.08E-04	2.00E-04	2.53E-04	4.96E-04	5.87E-04	2.35E-04	3.16E-04	3.60E-04	1.86E-04	4.39E-04	9.81E-05	5.03E-04	5.62E-04	5.59E-04
Macrolide-efflux protein	3.32E-04	3.03E-03	1.21E-03	1.25E-03	3.46E-04	8.06E-04	6.83E-04	6.72E-04	5.10E-04	3.51E-04	1.41E-03	1.61E-04	5.98E-04	2.97E-04
rRNA methyltransferase	3.90E-03	2.66E-03	1.03E-02	1.98E-03	3.28E-04	2.60E-04	2.42E-04	1.22E-03	1.41E-04	2.01E-03	3.61E-03	2.47E-03	8.00E-03	1.18E-03
Tetracycline resistance protein <i>tetW</i>	9.36E-03	2.14E-03	7.78E-03	1.36E-03	5.18E-04	1.29E-03	2.92E-04	3.39E-04	5.83E-04	2.68E-04	2.05E-03	1.18E-03	9.74E-04	2.83E-04
	1.10E-02	1.85E-03	1.17E-02	5.39E-04	7.20E-04	1.40E-03	2.45E-04	5.48E-04	5.65E-04	2.96E-04	1.59E-03	3.06E-04	1.04E-03	8.50E-04

Table S5 Profile of the microbial community composition in each sample

	MM1	MM2	MM3	MT1	MT2a	MT2b	MT3a	MT3b	MT4	SM1	SM2	SM3	SM4	SM5
<i>Acinetobacter johnsonii</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.00	0.00	0.00
<i>Acinetobacter unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.40	0.13	0.15	0.12
<i>Aerococcus viridans</i>	0.47	0.08	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Afipia unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.33	0.31	0.00	0.41
<i>Alicyclophilus unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.00	0.00	0.25	0.41	11.24	0.74	0.31
<i>Aminobacterium colombiense</i>	6.32	4.08	2.42	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Anaerobaculum hydrogeniformans</i>	0.00	0.00	0.00	3.56	0.00	0.00	0.09	3.87	0.00	0.00	0.00	0.00	0.00	0.00
<i>Anaerobaculum mobile</i>	0.00	0.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Anaerobaculum unclassified</i>	0.00	1.79	0.00	0.65	1.48	1.38	1.02	0.00	0.66	0.00	0.00	0.00	0.00	0.00
<i>Arcobacter unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00
<i>Azoarcus unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00
<i>Bacteroides coprosuis</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Bacteroides propionificiens</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00
<i>Bifidobacterium adolescentis</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.51	0.41	0.22	0.00
<i>Bifidobacterium longum</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.20	0.00	0.00
<i>Bifidobacterium minimum</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.32	0.00	0.00	0.00	0.00	0.00
<i>Bifidobacterium pseudolongum</i>	1.09	0.00	0.00	0.00	0.31	0.35	0.00	0.00	1.02	0.00	0.00	0.00	0.00	0.00
<i>Bifidobacterium thermophilum</i>	0.02	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Brachybacterium faecium</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.73	0.29	0.00	0.00	0.00	0.00	0.00	0.00
<i>Brachybacterium paraconglomeratum</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Brachybacterium unclassified</i>	0.00	0.00	0.20	0.00	0.00	0.00	0.61	0.40	0.10	0.00	0.00	0.00	0.00	0.00
<i>Brevibacterium unclassified</i>	0.00	0.62	0.00	0.00	0.00	0.00	0.41	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Butyrivibrio unclassified</i>	29.96	0.00	9.68	3.10	1.44	3.69	0.29	0.39	2.15	0.00	0.15	0.00	0.00	0.00
<i>Candidatus Accumulibacter phosphatis</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.00	0.00	0.04	0.02
<i>Candidatus Cloacimonas acidaminovorans</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	83.89	15.31	10.00	47.04	8.44
<i>Candidatus Nitrospira defluvii</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.57	0.90	0.00	1.30	0.00

<i>Candidatus Saccharimonas aalborgensis</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.71	0.00	0.00	0.00
<i>Clostridium sticklandii</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00
<i>Collinsella aerofaciens</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.14	0.17	0.00
<i>Collinsella unclassified</i>	0.19	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
<i>Comamonas unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.15	0.00	0.00	0.00
<i>Corynebacterium ammoniagenes</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Corynebacterium casei</i>	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	0.00
<i>Corynebacterium crenatum</i>	0.00	0.00	1.05	0.00	0.00	0.83	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Corynebacterium glutamicum</i>	0.08	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
<i>Corynebacterium maris</i>	0.50	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
<i>Corynebacterium nuruki</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Corynebacterium urealyticum</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.23	0.01	0.00	0.00	0.00	0.00	0.00	0.00
<i>Dietzia unclassified</i>	0.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.45	0.00
<i>Dorea unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00
<i>Enterococcus faecium</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Escherichia unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.11	0.12	0.00	0.00
<i>Eubacterium hallii</i>	0.15	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
<i>Eubacterium rectale</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.27	0.00	0.00	0.00
<i>Faecalibacterium prausnitzii</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00
<i>Fervidobacterium unclassified</i>	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
<i>Hyphomicrobium unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.10
<i>Lactobacillus amylovorus</i>	13.27	0.94	4.54	5.25	0.00	0.28	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Lactobacillus coryniformis</i>	0.03	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
<i>Lactobacillus crispatus</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.42	0.00	0.00	0.00	0.00	0.00
<i>Lactobacillus curvatus</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.25	0.00	0.00	0.00	0.00	0.00
<i>Lactobacillus delbrueckii</i>	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	0.00
<i>Lactobacillus johnsonii</i>	0.15	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
<i>Lactobacillus malefermentans</i>	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	0.00
<i>Lactobacillus otakiensis</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.11	0.04	0.00	0.00	0.00	0.00	0.00	0.00

<i>Lactobacillus parabrevis</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Lactobacillus phage Lc Nu</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Lactobacillus reuteri</i>	2.58	1.08	0.82	0.59	0.07	0.31	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00
<i>Lactobacillus sakei</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.30	0.00	0.00	0.00	0.00	0.00
<i>Lactobacillus salivarius</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.00	0.00	0.00	0.00	0.00
<i>Lactobacillus vaginalis</i>	0.00	0.25	0.00	0.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Lactococcus garvieae</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00
<i>Lactococcus lactis</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.24	0.00	0.00	0.00	0.00	0.00
<i>Leucobacter unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.21	0.37	0.04	0.00
<i>Limnohabitans unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.13	0.00
<i>Megasphaera unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.20	0.00	0.00	0.00	0.00	0.00
<i>Mesotoga prima</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.44	0.00	1.22	0.26	0.35
<i>Mesotoga unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.64	0.00	0.97
<i>Methanobacterium unclassified</i>	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	1.78
<i>Methanobrevibacter ruminantium</i>	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	0.00
<i>Methanobrevibacter smithii</i>	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.16	0.27	0.00	0.27	0.06
<i>Methanobrevibacter unclassified</i>	20.99	0.00	8.19	1.98	0.81	1.96	0.37	0.39	0.75	0.01	0.00	0.11	0.17	0.23
<i>Methanoculleus bourgensis</i>	0.00	12.72	0.48	0.62	9.70	10.41	13.84	14.47	19.22	0.00	0.00	0.00	0.61	0.00
<i>Methanoculleus marisnigri</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.17	0.00
<i>Methanoculleus unclassified</i>	0.52	54.23	1.53	2.93	34.97	28.06	41.65	45.92	54.44	0.10	0.00	0.07	2.42	0.00
<i>Methanosaeta concilii</i>	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	2.54	64.62	44.80	33.03	52.72
<i>Methanosaeta harundinacea</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.45	2.07	0.03	23.85
<i>Methanosaeta unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.54	0.00	0.00	0.00	0.00
<i>Methanosarcina barkeri</i>	0.00	0.00	0.00	2.58	0.00	0.00	0.00	0.00	0.34	0.00	0.00	0.00	0.00	0.00
<i>Methanosarcina mazei</i>	0.00	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Methanosarcina unclassified</i>	0.10	0.15	0.31	18.41	0.00	0.00	0.00	0.05	2.36	0.00	0.00	0.00	0.00	0.00
<i>Methanospaera stadtmanae</i>	1.29	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Methanospirillum hungatei</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.64	1.27	1.36	1.53	0.48
<i>Microtholunatus phosphovoratus</i>	0.00	0.00	15.69	0.00	0.00	0.00	22.70	18.13	0.00	0.00	0.00	0.00	0.00	0.00

<i>Nakamurella multipartita</i>	0.00	0.00	0.00	0.00	2.69	3.20	0.65	0.50	0.00	0.00	0.00	0.00	0.00	0.00
<i>Nocardioides unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.11	0.52	0.45
<i>Oligella unclassified</i>	0.12	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
<i>Olsenella unclassified</i>	0.94	0.00	0.00	0.00	0.15	0.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04
<i>Paracoccus unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.22	0.27	0.00	0.00
<i>Peptostreptococcaceae noname unclassified</i>	18.72	3.45	9.07	5.71	7.00	3.86	0.52	0.00	4.38	0.00	0.00	0.00	0.00	0.00
<i>Phascolarctobacterium succinatutens</i>	0.00	0.00	0.62	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Polaromonas unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.71	0.29	0.00
<i>Porcine bocavirus 3</i>	0.00	0.00	1.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Porcine type C oncovirus</i>	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10
<i>Porphyromonas asaccharolytica</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Prevotella paludivivens</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.00	0.00	0.12	0.00
<i>Pseudomonas caeni</i>	0.00	0.00	1.57	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Pseudomonas unclassified</i>	0.00	0.00	2.19	1.70	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.48
<i>Pseudoxanthomonas unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00
<i>Rhodopseudomonas palustris</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.14	0.65	0.00	0.07
<i>Rhodopseudomonas unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.73
<i>Ruminococcus bromii</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.41	0.00	0.04	0.00
<i>Ruminococcus flavefaciens</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00
<i>Ruminococcus torques</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.00	0.00	0.00
<i>Sphaerochaeta unclassified</i>	0.00	0.00	1.10	0.40	2.11	1.82	0.64	0.53	0.23	0.30	0.08	0.00	0.33	0.00
<i>Sphingopyxis unclassified</i>	0.00	0.00	0.00	0.00	0.98	0.47	0.03	0.03	0.00	0.00	0.74	1.93	0.00	0.22
<i>Staphylococcus lentus</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.67	0.12	0.00	0.00	0.00	0.00	0.00	0.00
<i>Subdoligranulum unclassified</i>	0.65	0.00	1.41	0.37	0.00	0.00	0.00	0.00	0.06	0.00	0.48	0.45	0.21	0.16
<i>Syntrophomonas wolfei</i>	0.00	0.00	5.58	0.00	0.00	0.00	0.00	0.00	0.00	0.52	0.24	0.00	0.47	0.06
<i>Tepidanaerobacter acetatoxydans</i>	0.00	2.73	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Tetrasphaera elongata</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.40	0.41	3.08	0.00
<i>Thauera aminoaromatica</i>	0.00	0.00	0.02	0.00	0.00	0.00	0.01	0.00	0.00	0.21	0.00	0.07	0.00	0.00
<i>Thauera phenylacetica</i>	0.00	0.00	0.36	0.00	0.00	0.00	0.01	0.00	0.00	0.10	0.03	0.63	0.00	0.00

<i>Thauera terpenica</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.44	1.76	0.01	0.24
<i>Thauera unclassified</i>	0.00	0.00	14.90	0.00	0.00	0.00	2.13	1.45	0.00	2.04	0.57	6.56	0.00	0.76
<i>Thermoanaerobacter mathranii</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00
<i>Thermoanaerobacter thermohydrosulfuricus</i>	1.33	17.56	4.85	52.00	32.42	28.38	3.82	5.16	11.42	0.00	0.00	0.00	0.00	0.82
<i>Thermobifida fusca</i>	0.00	0.00	0.85	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Thiomonas unclassified</i>	0.00	0.00	2.03	0.00	0.00	0.00	0.16	0.00	0.00	0.17	4.37	3.88	2.41	0.77
<i>Thiothrix unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00
<i>Variovorax unclassified</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.11	0.03	0.00

Table S6 Potential ARGs host revealed by co-occurrence between ARGs subtype and microbial taxa

Genus	ARGs subtype	ARGs type	Reference ^a
<i>Thiomonas</i>	<i>sul1</i>	Sulfonamide	Not available
	<i>sul2</i>	Sulfonamide	Not available
	hydrophobe_amphiphile efflux-1 (HAE1) family protein	Multidrug	Not available
	<i>mexB</i>	MLS	Not available
	undecaprenol kinase	Bacitracin	Not available
	undecaprenyl-diphosphatase	Bacitracin	Not available
	aminoglycoside resistance protein	Aminoglycoside	Not available
<i>Lactobacillus</i>	<i>ermT</i>	MLS	http://ardb.cbcb.umd.edu/cgi/search.cgi?db=T&and0=O&term=ermT&field=af& Whitehead and Cotta, 2001
	<i>tetPA</i>	Tetracycline	Not available
	<i>tetPB</i>	Tetracycline	Not available
	erythromycin resistance methylase	MLS	[1, 2]
	streptomycin adenylyltransferase	Aminoglycoside	Not available
<i>Peptostreptococcaceae</i>	<i>tetPB</i>	Tetracycline	Not available
	streptomycin adenylyltransferase	Aminoglycoside	Not available
<i>Butyrivibrio</i>	<i>tetPB</i>	Tetracycline	Not available

^a: The reference listed in this column verified the same host information for the related ARGs as that revealed by co-occurrence results.

Table S7 The co-occurring patterns between ARGs subtypes and MRGs

ARG type	ARG subtype	MRG
Acriflavine	<i>acrB</i>	MGR-Ag
		MRG-As
		MRG-Cu
		MRG-Fe
		MRG-Hg
		MRG-Mn
		MRG-Pb
		MRG-Te
		MRG-Zn
Aminoglycoside	aminoglycoside resistance protein	MRG-Au
		MRG-Cu
Bacitracin	undecaprenol kinase	MGR-Ag
		MRG-As
		MRG-Au
		MRG-Cu
		MRG-Fe
		MRG-Hg
		MRG-Mn
		MRG-Pb
		MRG-Sb
	undecaprenyl-diphosphatase	MRG-Te
		MRG-Zn
		MGR-Ag
		MRG-Cu
		MRG-Fe
		MRG-Hg
		MRG-Pb
		MRG-Sb
		MRG-Te
		MRG-Zn
MLS	<i>mexB</i>	MRG-As
		MRG-Hg
		MRG-Te
	<i>strB</i>	MRG-Au

Table S7 The co-occurring patterns between ARGs subtypes and MRGs (continued)

ARG type	ARG subtype	MRGs
Multidrug	hydrophobe_ amphiphile efflux-1 (HAE1) family protein	MRG-Mn
		MRG-Pb
		MRG-Te
		MRG-Zn
		MGR-Ag
		MRG-Cu
	multidrug efflux protein	MRG-Mn
Sulfonamide	<i>sul1</i>	MGR-Ag
		MRG-Cu
		MRG-Fe
		MRG-Hg
		MRG-Mg
		MRG-Mn
		MRG-Te
		MRG-Zn
	<i>sul2</i>	MRG-As
		MRG-Au
		MRG-Hg
		MRG-Te
Others	RND protein	MGR-Ag
		MRG-As
		MRG-Cu
		MRG-Fe
		MRG-Hg
		MRG-Ni
		MRG-Pb
		MRG-Sb
		MRG-Te
		MRG-Zn

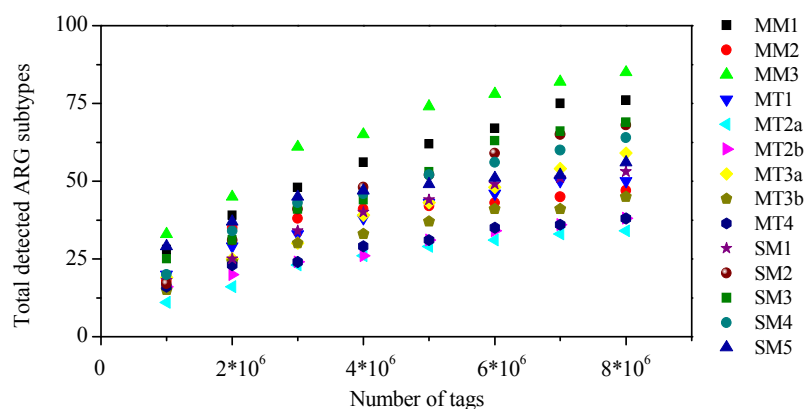


Fig S1 Rarefaction curve showing the sequencing depth was sufficient to characterize the ARGs profiles at subtype level

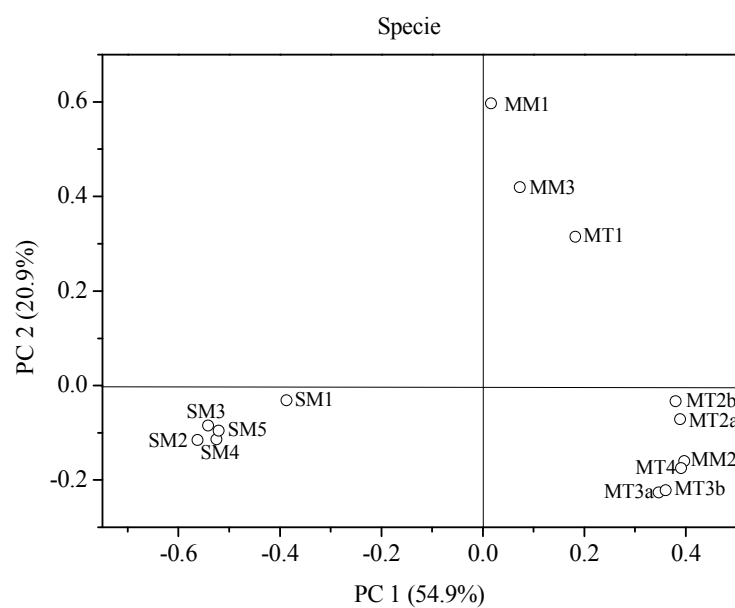


Fig S2 PCA analysis of all the samples based on microbial community compositions

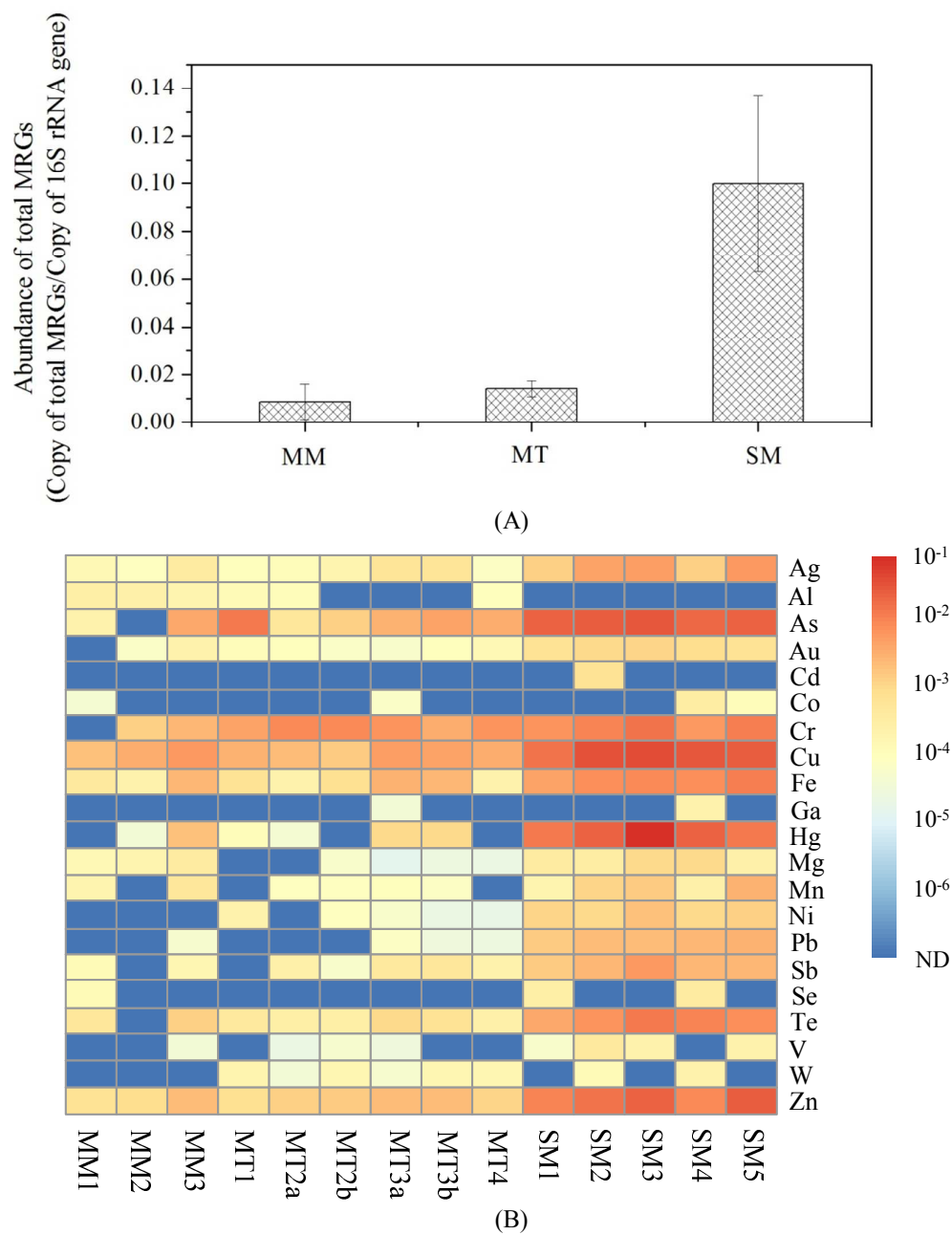


Fig S3 The abundance (A) and profile (B) of MRGs composition in each sample

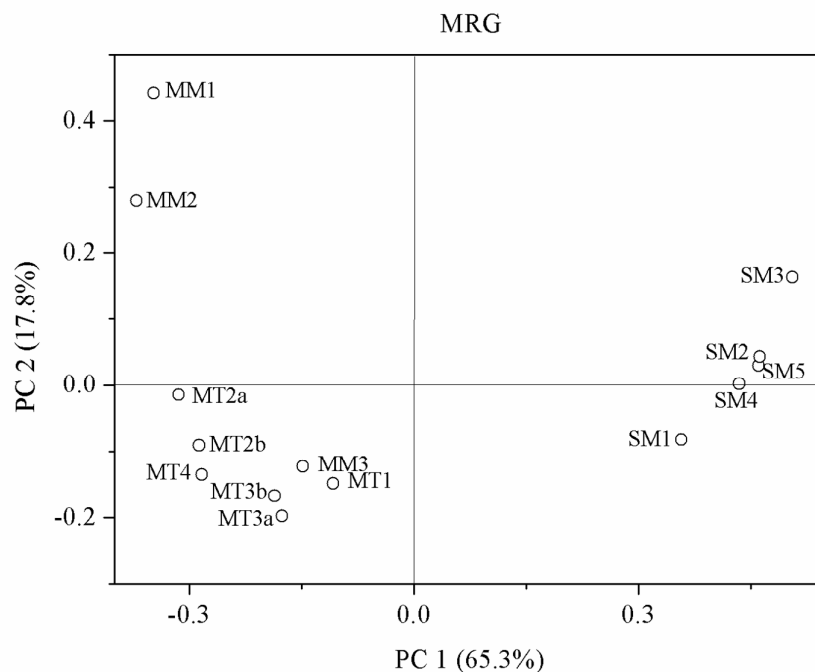


Fig S4 PCA analysis of all the samples based on MRGs compositions

References:

1. Gfeller, K. Y.; Roth, M.; Meile, L.; Teuber, M., Sequence and genetic organization of the 19.3-kb erythromycin- and dalbapristin-resistance plasmid pLME300 from *Lactobacillus fermentum* ROT1. *Plasmid* **2003**, *50*, (3), 190-201.
2. Begovic, J.; Huys, G.; Mayo, B.; D'Haene, K.; Florez, A. B.; Lozo, J.; Kojic, M.; Strahinic, I.; Topisirovic, L., Human vaginal *Lactobacillus rhamnosus* harbor mutation in 23S rRNA associated with erythromycin resistance. *Research in Microbiology* **2009**, *160*, (6), 421-426.