Supplementary Materials

The supporting information provides the detailed of number of ARGs subtypes in 17 water samples (Figure S1), bray-curtis-based principal coordinates analysis of relative and absolute abundance of antibiotic resistance genes (ARGs) in 17 water samples (Figure S2), relative and absolute abundance of mobile genetic elements (MGEs) in river water, source water and finished water (Figure S3), bray-curtis-based principal coordinates analysis of microbial communities in 17 water samples (Figure S4), bacteria proportion on phylum level of 17 water samples (Figure S5), river water quality parameters (Table S1), PCR primers for the investigated ARGs, MGEs and bacterial 16s rRNA gene (Table S2), quality control of the real-time qPCR methods for the all target genes (Table S3), absolute abundances (copies/mL water) and relative abundance (gene copies/16S rRNA gene) of the 17 ARGs and 2 MGEs in water samples (Tables S4 and S5), correlation of ARGs with MGEs (Table S6), coverage and diversity indices of bacterial communities by Miseq sequencing (Table S7), relative abundances of bacterial community compositions grouped by phylum in different water samples (Table S8), genera distribution patterns in 17 water samples (Table S9), Genera percentage of bacteria co-occurrence with ARGs (Table S10).

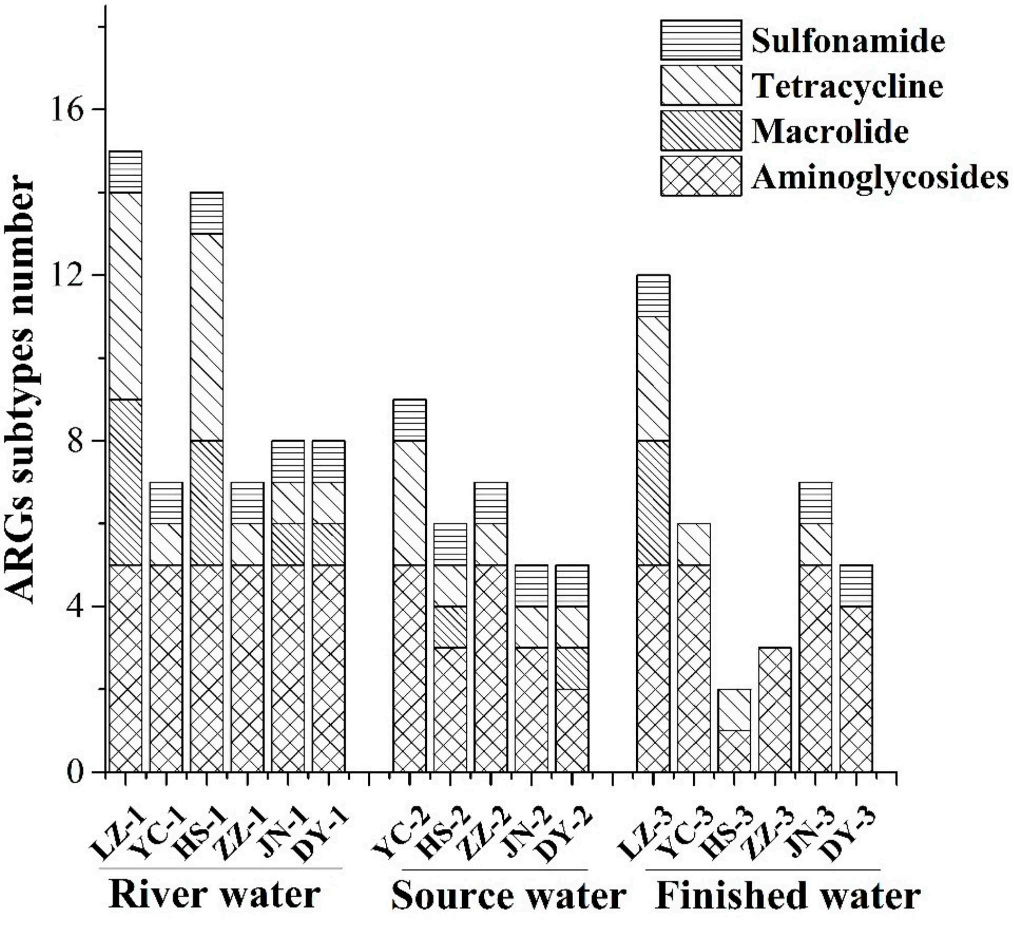

Figure S1. Number of ARGs subtypes in 17 water samples.

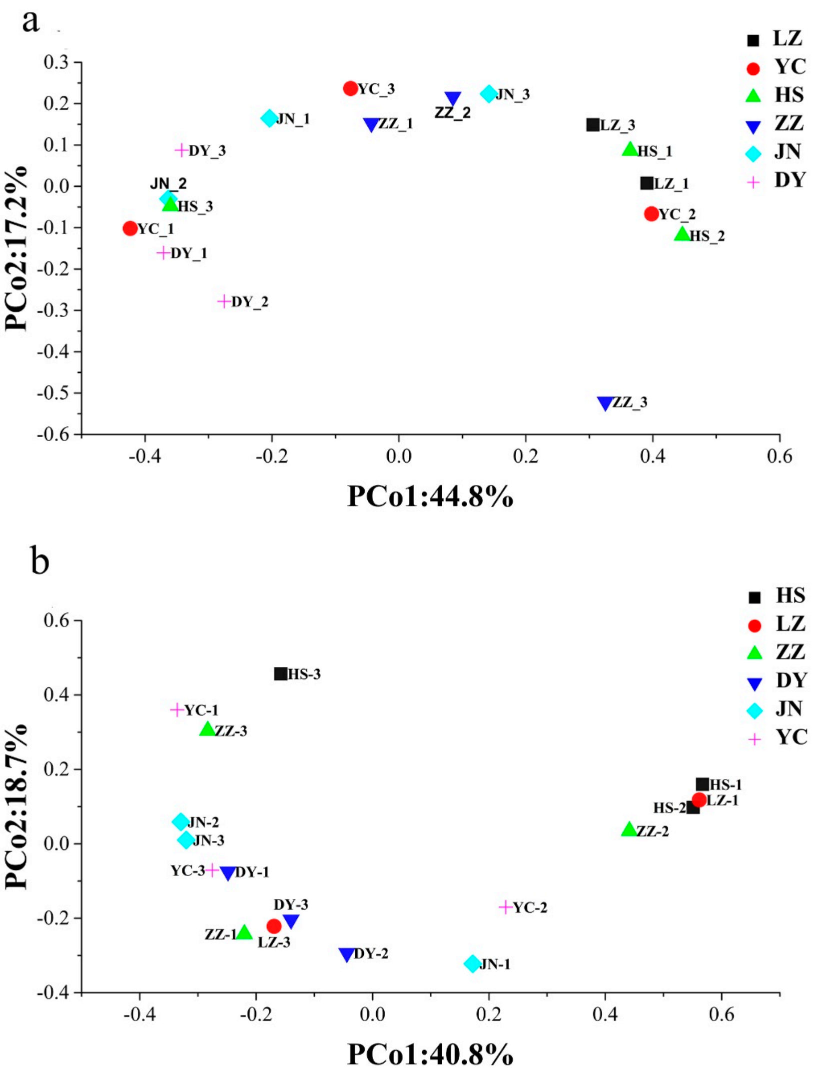

Figure S2. Bray-Curtis-based Principal coordinates analysis of (**a**) relative and (**b**) absolute abundance of ARGs in 17 water samples.

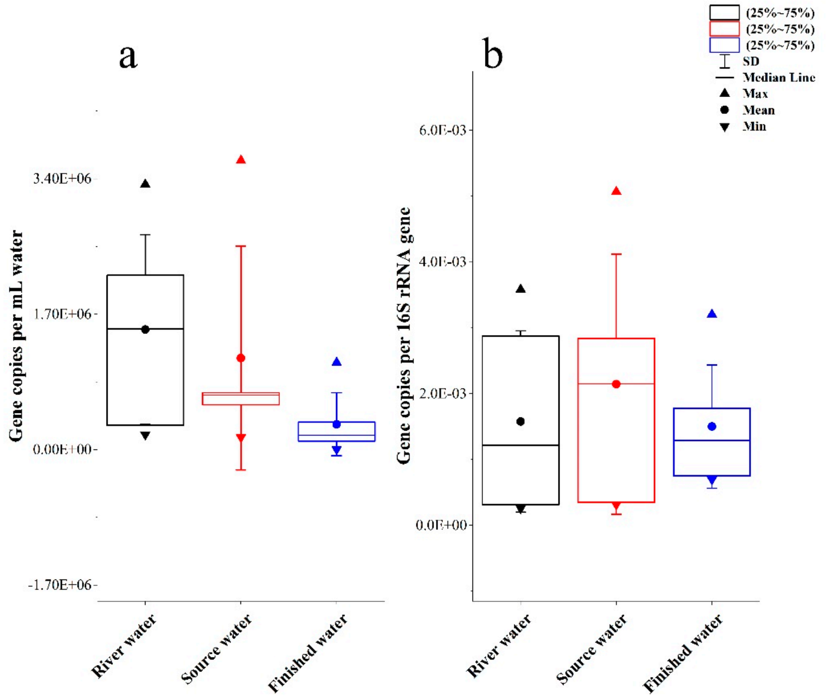

Figure S3. (**A**) Total absolute abundance of MGEs (copies/mL water) in river water, source water and finished water. (**B**) Total relative abundance of MGEs (copies/16S rRNA) in river water, source water and finished water.

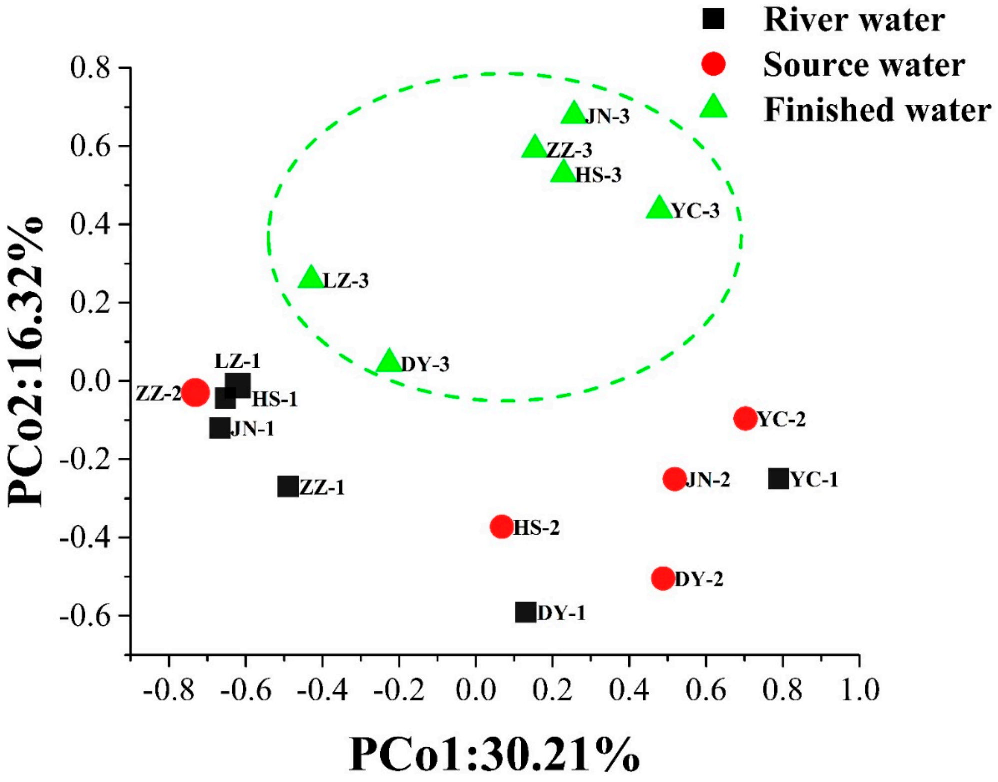

Figure S4. Bray-Curtis-based Principal coordinates analysis of microbial communities in 17 water samples.

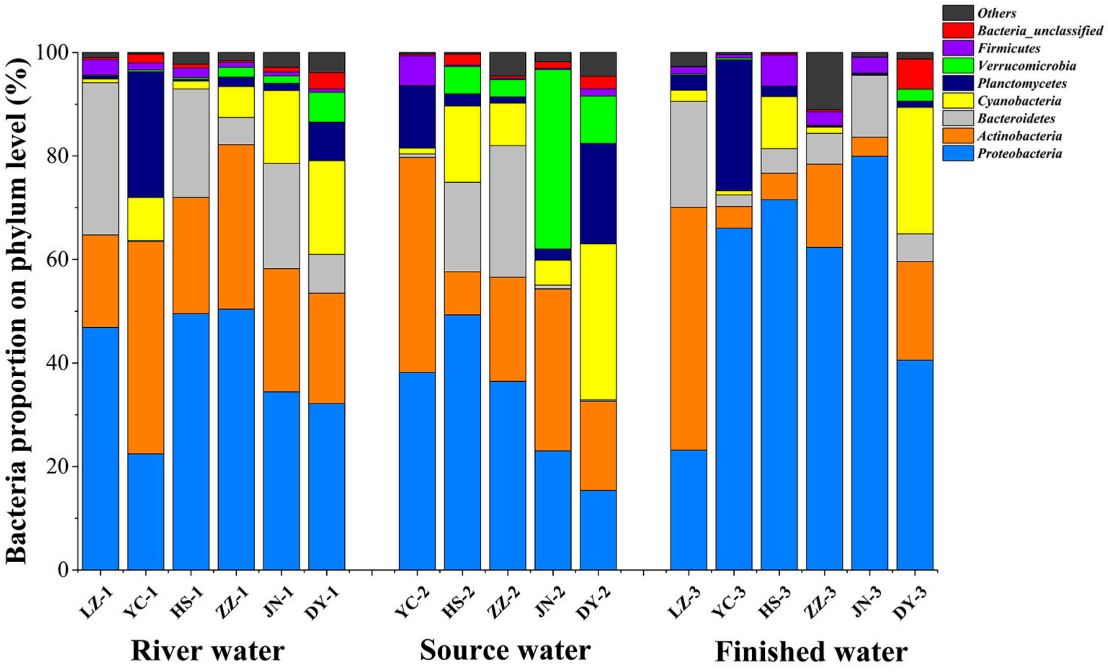

Figure S5. Bacteria proportion on phylum level of 17 water samples.

Table S1. River water quality parameters.

Water Quality Parameters	Lanzhou	Yinchuan	Hohhot	Zhengzhou	Jinan	Dongying
Water Temperature/°C	5	1.5	2.5	8	7	9.4
pH	8.1	7.66	7.7	8.19	8.32	8.68
TOC/(mg/L)	1.92	2.15	3.21	2.78	2.86	2.96
TN/(mg/L)	2.51	2.29	4.68	5.51	4.4	3.61
TP/(mg/L)	0.049	0.021	0.093	0.078	0.039	0.036

Table S2. PCR primers for the investigated ARGs, MGEs and bacterial 16s rRNA gene.

Antibiotics	Mechanism of resistance	Gene	Forward Primers (5'-3')	Reverse Primers (5'-3')	Annealing temp. (°C)	Amplicon length (bp)	Reference
Aminoglycosides	Nucleotidyl-transferases	*aadB*	TGGTGGTACTTCATCGGCATA	GTTACTTGACTGCGAACCTGCT	58	175	[1]
		aadE	GATCTTACCTTATTGCCCTTGGA	GCGCTTGGCTTTCTTACATG	58	143	[1]
	Phosphor-transferases	*aphA1*	AAACGTCTTGCTCGAGGC	CAAACCGTTATTCATTCGTGA	55	500	[2]
		strA	CCTGGTGATAACGGCAATTC	CCAATCGCAGATAGAAGGC	55	546	[3]
		strB	ATCGTCAAGGGATTGAAACC	GGATCGTAGAACATATTGGC	56	509	[3]
Macrolid	Inactivat	*ereA*	AACACCCTGAA	CTTCACATCCG	56	466	[4]

e	ing enzyme (esterase)		CCCAAGGGACG	GATTCGCTCGA			
	rRNA methylase	*ermF*	CGGGTCAGCACTTTACTATTG	GGACCTACCTCATAGACAAG	50	465	[5]
		ermG	GTGAGGTAACTCGTAATAAGCTG	CCTCTGCCATTAACAGCAATG	63	255	[6]
		ermX	GAGATCGGRCCAGGAAGC	GTGTGCACCATCGCCTGA	61	488	[7]
	Efflux	*mefA*	AGTATCATTAATCACTAGTGC	TTCTTCTGGTACTAAAAGTGG	54	348	[4]
Tetracycline	Efflux	*tetA*	GCTACATCCTGCTTGCCTTC	CATAGATCGCCGTGAAGAGG	61	210	[8]
		tetG	GCTCGGTGGTATCTCTGCTC	AGCAACAGAATCGGGAACAC	60	468	[8]
	Ribosomal Protection	*tetO*	AGAATCTGCTGTTTGCCAGTG	CGGAGTGTCAATGATATTGCA	63	169	[8]
		tetQ	AACTTAGGCATTCTGGCTCAC	TCCCACTGTTCCATATCGTCA	60	515	[9]
		tetW	GAGAGCCTGCTATATGCCAGC	GGGCGTATCCACAATGTTAAC	64	168	[10]
	Enzymatic	*tetX*	CAATAATTGGTGGTGGACCC	TTCTTACCTTGGACATCCCG	55	468	[8]
Sulfonamide	Dihydropteroate synthase folP	*sulII*	TCCGGTGGAGGCCGGTATCTGG	CGGGAATGCCATCTGCCTTGAG	60	191	[11]
Mobile element	Integron	*intI1*	CCTCCCGCACGATGATC	TCCACGCATCGTCAGGC	55	280	[12]
	Transposons	*Tn916*	TCCTACAGCGACAGCCAGTGA	TGCGTTGCTTTGGTCTGCTGGT	50	142	[13]
Bacterial 16S rRNA gene			CCTACGGGAGGCAGCAG	TTACCGCGGCTGCTGGCAC	55	193	[10]

Table S3. Quality control of the real-time qPCR methods for the all target genes.

ARGs Subtypes		Standard Curve	R^2	Amplification Efficiencies (%)	Detection Limits (copies/μL added DNA)
	16S rRNA	y=−3.27logx+36.63	0.995	102	1.70E+03
aminoglycosides	*aadB*	y=−3.32logx+39.08	0.998	100	4.80E+01
	aadE	y=−3.39logx+38.63	0.997	97.2	2.20E+02
	aphA1	y=−3.48logx+36.72	0.998	93.8	2.60E+01
	strA	y=−3.35logx+38.78	0.999	98.8	4.80E+01
	strB	y=−3.47logx+39.04	0.999	94.2	8.40E+01
marcolide	*ereA*	y=−3.27logx+34.73	0.997	102.21	1.76E+02
	ermF	y=−3.57logx+37.75	0.998	90.6	1.46E+02
	ermG	y=−3.48logx+40.93	0.999	93.8	2.70E+01
	ermX	y=−3.39logx+36.57	0.998	97.24	2.33E+02
	mefA	y=−3.53logx+39.95	0.998	92	7.80E+01
tetracycline	*tetA*	y=−3.67logx+38.37	0.994	87.27	3.40E+01
	tetG	y=−3.31logx+32.96	0.999	100.5	3.03E+02
	tetO	y=−3.67logx+36.84	0.993	87.27	3.21E+02
	tetQ	y=−3.73logx+43.34	0.994	85.39	2.86E+03
	tetW	y=−3.41logx+37.13	0.997	96.45	9.90E+01
	tetX	y=−3.45logx+36.78	0.998	94.92	1.63E+02
sulfonamide	*sulII*	y=−3.34logx+38.54	0.996	99.3	2.40E+01
MGEs	*intI1*	y=−3.48logx+37.75	0.999	93.8	1.40E+01
	Tn916	y=−3.05logx+33.89	0.992	112.75	1.07E+02

Table S4. Absolute abundances of the 17 ARGs and 2 MGEs (copies/mL water) in water samples.

Sample	16S rRNA gene	*aadB*	*aadE*	*aphA1*	*strA*	*strB*	*ereA*	*ermF*	*ermG*	*ermX*	*mefA*	*tetA*	*tetG*	*tetO*	*tetQ*	*tetW*	*tetX*	*sulII*	*intI1*	*Tn916*
LZ_1	2.19E+06	2.12E+02	5.03E+02	8.05E+02	7.55E+03	9.90E+03	8.96E+01	1.44E+03	0	6.35E+01	4.29E+03	5.56E+01	1.38E+02	5.51E+02	0	3.04E+02	1.38E+02	1.17E+03	1.02E+04	4.38E+02
	(1.67E+5)	(2.36E+1)	(2.78E+1)	(3.43E+1)	(4.02E+2)	(2.20E+2)	(6.10E+0)	(1.41E+2)	-	(2.92E+0)	(2.90E+2)	(7.60E+0)	(1.03E+1)	(3.08E+1)	-	(3.48E+1)	(2.49E+1)	(1.38E+1)	(1.74E+2)	(5.02E+1)
LZ_3	1.97E+05	1.21E+02	6.74E+01	1.04E+01	3.22E+02	4.60E+02	1.12E+01	2.04E+02	0	0	7.18E+01	0	0	2.42E+01	0	8.85E+00	1.90E+01	4.67E+01	1.18E+03	3.06E+01
	(1.45E+4)	(1.44E+1)	(5.37E+0)	(2.67E-1)	(1.84E+1)	(2.52E+1)	(7.98E-1)	(7.82E+0)	-	-	(8.39E+0)	-	-	(4.31E+0)	-	(1.66E+0)	(9.91E-1)	(2.82E+0)	(1.54E+1)	(5.08E+0)
YC_1	3.06E+05	4.74E+00	5.18E+00	9.23E+00	2.08E+01	1.42E+02	0	0	0	0	0	2.54E+00	0	0	0	0	0	3.27E+01	1.90E+02	1.45E+01
	(1.19E+4)	(5.59E-1)	(1.51E-1)	(1.06E-1)	(1.27E+0)	(6.40E+0)	-	-	-	-	-	(3.51E-1)	-	-	-	-	-	(1.63E+0)	(1.59E+1)	(3.84E+0)
YC_2	1.56E+05	5.84E+02	1.24E+02	4.46E+00	3.03E+03	2.39E+03	0	0	0	0	0	2.64E+01	0	1.91E+01	0	0	2.20E+01	9.29E+01	1.72E+03	1.84E+01
	(7.30E+3)	(1.09E+2)	(6.89E+0)	(2.01E+0)	(4.96E+2)	(2.66E+1)	-	-	-	-	-	(4.83E-1)	-	(1.54E+0)	-	-	(3.62E+0)	(4.80E+0)	(1.44E+1)	(8.75E-1)
YC_3	3.46E+05	6.00E+00	8.08E+00	2.01E+00	3.71E+02	4.55E+02	0	0	0	0	0	3.21E+00	0	0	0	0	0	0	6.82E+02	2.91E+01
	(9.04E+3)	(3.98E-1)	(7.69E-1)	(2.00E-1)	(3.66E+1)	(3.56E+1)	-	-	-	-	-	(2.54E-1)	-	-	-	-	-	-	(2.59E+1)	(2.76E+1)
HS_1	3.33E+06	1.47E+02	1.22E+02	4.67E+01	1.28E+04	1.07E+04	3.59E+02	1.49E+03	0	0	1.18E+03	7.50E+01	5.82E+02	2.06E+02	0	8.11E+01	2.41E+02	1.96E+03	2.34E+04	2.84E+02
	(2.10E+5)	(1.88E+1)	(7.20E+0)	(2.62E+0)	(3.59E+2)	(1.74E+2)	(2.18E+1)	(1.96E+2)	-	-	(6.01E+1)	(6.59E+0)	(8.82E+1)	(1.52E+1)	-	(4.43E+0)	(1.62E+1)	(1.92E+2)	(5.71E+1)	(2.75E+1)
HS_2	7.17E+05	0	1.05E+01	0	7.78E+03	6.89E+03	0	2.51E+01	0	0	0	1.03E+02	0	0	0	0	0	8.81E+01	9.24E+03	7.23E+01
	(4.20E+4)	-	(5.57E-1)	-	(1.99E+2)	(1.50E+2)	-	(2.87E+0)	-	-	-	(1.60E+1)	-	-	-	-	-	(3.50E+0)	(3.47E+2)	(3.54E+1)
HS_3	1.09E+05	0	7.31E+00	0	0	0	0	0	0	0	0	5.04E+00	0	0	0	0	0	0	1.11E+02	9.18E+00
	(1.69E+3)	-	(3.18E+0)	-	-	-	-	-	-	-	-	(1.05E+0)	-	-	-	-	-	-	(7.24E+0)	(1.07E+0)
ZZ_1	1.90E+05	8.17E+00	1.01E+01	6.64E+00	1.09E+02	2.93E+02	0	0	0	0	0	7.09E+01	0	0	0	0	0	7.93E+02	8.37E+02	2.24E+01
	(8.97E+3)	(1.06E+0)	(4.73E+0)	(4.90E-1)	(9.39E+0)	(1.30E+1)	-	-	-	-	-	(2.31E+1)	-	-	-	-	-	(1.32E+1)	(6.97E+1)	(3.57E+0)
ZZ_2	3.63E+06	9.47E+01	1.00E+02	1.27E+01	9.20E+02	6.43E+02	0	0	0	0	0	3.05E+01	0	0	0	0	0	4.45E+02	1.62E+04	2.75E+01
	(2.07E+5)	(1.15E+1)	(7.64E+0)	(4.17E-1)	(1.93E+1)	(4.90E+1)	-	-	-	-	-	(2.33E+0)	-	-	-	-	-	(1.36E+1)	(5.96E+2)	(3.20E+0)
ZZ_3	4.75E+03	0	7.90E+00	0	1.66E+02	1.70E+02	0	0	0	0	0	0	0	0	0	0	0	0	1.69E+01	0
	(2.02E+2)	-	(2.43E+0)	-	(1.09E+1)	(1.03E+0)	-	-	-	-	-	-	-	-	-	-	-	-	(1.05E+0)	-
JN_1	1.74E+06	4.72E+01	2.02E+01	5.95E+01	2.12E+02	1.83E+03	0	5.70E+01	0	0	0	1.66E+01	0	0	0	0	0	2.07E+03	3.06E+03	5.37E+01
	(2.85E+5)	(6.01E+0)	(1.46E+0)	(5.04E+0)	(1.63E+1)	(1.58E+2)	-	(3.64E+0)	-	-	-	(2.98E+0)	-	-	-	-	-	(1.31E+1)	(2.26E+1)	(2.56E+1)

JN_2	6.85E+05	0	2.87E+00	0	4.14E+02	2.11E+02	0	0	0	0	0	2.39E+00	0	0	0	0	0	1.93E+01	4.34E+02	5.44E+01
	(1.63E+4)	-	(1.27E-1)	-	(4.79E+1)	(4.46E+0)	-	-	-	-	-	(4.04E-1)	-	-	-	-	-	(4.21E+0)	(2.39E+1)	(2.28E+1)
JN_3	1.65E+05	1.24E+01	5.85E+00	1.54E+01	3.25E+02	3.68E+02	0	0	0	0	0	3.91E+00	0	0	0	0	0	8.16E+00	4.83E+02	2.29E+01
	(8.75E+3)	(4.27E-2)	(1.18E+0)	(1.13E+0)	(9.63E+0)	(1.66E+1)	-	-	-	-	-	(2.34E-1)	-	-	-	-	-	(3.13E-1)	(4.17E+1)	(5.92E+0)
DY_1	1.29E+06	6.45E+01	3.06E+01	2.91E+00	1.38E+02	1.18E+02	0	7.91E+01	0	0	0	9.42E+00	0	0	0	0	0	7.31E+02	2.33E+02	4.87E+01
	(2.64E+4)	(1.31E+1)	(2.87E-1)	(6.80E-1)	(1.59E+1)	(4.00E+0)	-	(3.13E+1)	-	-	-	(9.88E-1)	-	-	-	-	-	(4.07E+1)	(6.73E+0)	(2.60E+1)
DY_2	5.64E+05	1.34E+02	7.12E+01	0	0	0	0	1.17E+02	0	0	0	9.39E+00	0	0	0	0	0	2.55E+03	4.39E+02	2.96E+01
	(9.53E+3)	(1.40E+1)	(1.02E+1)	-	-	-	-	(1.02E+1)	-	-	-	(8.15E-1)	-	-	-	-	-	(1.07E+2)	(3.79E+1)	(8.93E+0)
DY_3	1.09E+06	0.00E+00	1.52E+01	11	112	65	0	0.00E+00	0	0	0	0.00E+00	0	0	0	0	0	8.45E+01	1.62E+03	1.35E+01
	(7.20E+4)	-	(2.20E+0)	(5.86E-1)	(4.33E+0)	(5.45E+0)	-	-	-	-	-	-	-	-	-	-	-	(1.37E+0)	(7.63E+1)	(2.72E+0)

*numbers in brackets are standard error of above.

Table S5. Relative abundances of the 18 ARGs and 2 MGEs (gene copies/16S rRNA gene copies) in water samples.

Sample	*aadB*	*aadE*	*aphA1*	*strA*	*strB*	*ereA*	*ermF*	*ermG*	*ermX*	*mefA*	*tetA*	*tetG*	*tetO*	*tetQ*	*tetW*	*tetX*	*sulII*	*intI1*	*Tn916*
LZ_1	5.46E-05	1.30E-04	2.07E-04	1.94E-03	2.55E-03	5.13E-05	8.28E-04	0	3.64E-05	9.03E-04	3.19E-05	7.92E-05	3.09E-04	0	1.70E-04	7.88E-05	2.45E-04	2.63E-03	2.46E-04
	(7.51E-6)	(1.49E-5)	(1.01E-5)	(2.18E-4)	(2.39E-4)	(6.26E-6)	(1.29E-4)	-	(4.31E-6)	(1.29E-4)	(6.12E-6)	(1.16E-5)	(3.84E-5)	-	(2.63E-5)	(1.56E-5)	(1.57E-5)	(2.19E-4)	(3.98E-5)
LZ_3	3.10E-04	1.72E-04	2.64E-05	8.23E-04	1.17E-03	7.34E-05	1.33E-03	0	0	2.33E-04	0	0	1.56E-04	0	5.71E-05	1.24E-04	1.53E-04	3.00E-03	2.00E-04
	(5.92E-5)	(2.12E-5)	(1.63E-6)	(8.43E-5)	(3.82E-5)	(1.09E-5)	(1.41E-4)	-	-	(2.16E-5)	-	-	(1.88E-5)	-	(6.93E-6)	(1.11E-5)	(2.09E-5)	(2.50E-4)	(4.38E-5)
YC_1	7.81E-06	7.44E-06	1.33E-05	2.99E-05	2.03E-04	0	0	0	0	0	8.28E-06	0	0	0	0	0	4.81E-05	2.73E-04	4.31E-05
	(5.57E-7)	(1.58E-7)	(3.95E-7)	(2.95E-6)	(4.29E-6)	-	-	-	-	-	(8.54E-7)	-	-	-	-	-	(3.43E-6)	(1.36E-5)	(1.31E-5)
YC_2	6.75E-04	1.50E-04	5.21E-06	3.63E-03	2.88E-03	0	0	0	0	0	6.92E-05	0	8.26E-05	0	7.00E-06	9.49E-05	2.00E-04	2.07E-03	7.95E-05
	(1.39E-4)	(1.53E-5)	(2.19E-6)	(4.26E-4)	(1.03E-4)	-	-	-	-	-	(4.38E-6)	-	(9.27E-6)	-	(1.21E-5)	(1.39E-5)	(1.68E-5)	(1.14E-4)	(6.07E-6)
YC_3	7.99E-06	1.17E-05	2.91E-06	5.38E-04	6.57E-04	0	0	0	0	0	9.25E-06	0	0	0	0	0	0	9.85E-04	6.11E-05
	(7.36E-7)	(8.21E-7)	(3.66E-7)	(6.45E-5)	(4.02E-5)	-	-	-	-	-	(5.03E-7)	-	-	-	-	-	-	(3.88E-5)	(5.67E-5)
HS_1	2.20E-05	1.84E-05	7.04E-06	1.93E-03	1.61E-03	1.08E-04	4.49E-04	0	0	1.32E-04	2.26E-05	1.74E-04	4.65E-05	0	1.83E-05	7.26E-05	2.19E-04	3.52E-03	6.40E-05
	(1.43E-6)	(1.18E-6)	(8.33E-7)	(1.47E-4)	(9.02E-5)	(5.40E-6)	(8.15E-5)	-	-	(1.20E-5)	(3.14E-6)	(1.57E-5)	(6.17E-6)	-	(2.02E-6)	(8.50E-6)	(1.17E-5)	(2.12E-4)	(9.27E-6)
HS_2	0	5.74E-06	0	4.23E-03	3.74E-03	0	1.61E-05	0	0	0	6.76E-05	0	0	0	0	0	2.89E-05	5.02E-03	4.66E-05
	-	(5.58E-7)	-	(3.31E-4)	(1.47E-4)	-	(2.55E-6)	-	-	-	(1.21E-5)	-	-	-	-	-	(7.37E-7)	(3.49E-4)	(2.03E-5)
HS_3	0	3.35E-05	0	0	0	0	0	0	0	0	4.65E-05	0	0	0	0	0	0	5.12E-04	1.85E-04
	-	(1.42E-5)	-	-	-	-	-	-	-	-	(1.03E-5)	-	-	-	-	-	-	(3.02E-5)	(2.16E-5)
ZZ_1	1.45E-05	1.78E-05	1.18E-05	1.93E-04	5.19E-04	0	0	0	0	0	3.70E-04	0	0	0	0	0	7.60E-04	1.48E-03	4.27E-05
	(2.47E-6)	(7.87E-6)	(3.57E-7)	(2.47E-5)	(6.34E-6)	-	-	-	-	-	(1.06E-4)	-	-	-	-	-	(3.50E-5)	(1.47E-4)	(5.32E-6)
ZZ_2	1.65E-05	1.74E-05	2.21E-06	1.61E-04	1.12E-04	0	0	0	0	0	1.06E-05	0	0	0	0	0	8.17E-05	2.83E-03	1.01E-05
	(1.28E-6)	(1.18E-6)	(1.39E-7)	(1.11E-5)	(7.86E-6)	-	-	-	-	-	(3.75E-7)	-	-	-	-	-	(7.14E-6)	(5.81E-5)	(1.72E-6)
ZZ_3	0	8.25E-04	0	1.76E-02	1.79E-02	0	0	0	0	0	0	0	0	0	0	0	0	1.78E-03	0
	-	(2.19E-4)	-	(1.87E-3)	(7.20E-4)	-	-	-	-	-	-	-	-	-	-	-	-	(1.11E-4)	-
JN_1	1.38E-05	5.87E-06	1.74E-05	6.16E-05	5.39E-04	0	1.71E-05	0	0	0	5.09E-06	0	0	0	0	0	2.30E-04	8.96E-04	1.60E-05
	(2.80E-6)	(7.19E-7)	(3.68E-6)	(8.65E-6)	(1.33E-4)	-	(2.74E-6)	-	-	-	(1.88E-6)	-	-	-	-	-	(4.95E-5)	(1.66E-4)	(7.04E-6)
JN_2	0	2.10E-06	0	3.02E-04	1.54E-04	0	0	0	0	0	3.49E-06	0	0	0	0	0	1.03E-05	3.17E-04	3.17E-05
	-	(9.13E-8)	-	(3.41E-5)	(6.84E-6)	-	-	-	-	-	(6.11E-7)	-	-	-	-	-	(2.02E-6)	(2.11E-5)	(1.25E-5)
JN_3	3.77E-05	1.79E-05	4.67E-05	9.89E-04	1.12E-03	0	0	0	0	0	2.38E-05	0	0	0	0	0	1.23E-05	1.47E-03	6.86E-05

	(1.86E-6)	(4.47E-6)	(1.22E-6)	(2.47E-5)	(4.31E-5)	-	-	-	-	-	(6.57E-7)	-	-	-	-	-	(8.71E-7)	(1.19E-4)	(1.43E-5)
DY_1	5.59E-05	2.65E-05	2.52E-06	1.20E-04	1.02E-04	0	9.05E-05	0	0	0	7.35E-06	0	0	0	0	0	2.36E-04	2.01E-04	5.63E-05
	(1.17E-5)	(4.18E-7)	(5.18E-7)	(1.27E-5)	(1.49E-6)	-	(3.66E-5)	-	-	-	(6.29E-7)	-	-	-	-	-	(1.26E-5)	(6.23E-6)	(3.10E-5)
DY_2	8.69E-05	4.62E-05	0	0	0	0	1.24E-04	0	0	0	1.67E-05	0	0	0	0	0	1.36E-03	2.84E-04	3.16E-05
	(7.73E-6)	(7.36E-6)	-	-	-	-	(9.11E-6)	-	-	-	(1.43E-6)	-	-	-	-	-	(7.33E-5)	(2.08E-5)	(1.01E-5)
DY_3	0	6.94E-06	5.10E-06	5.12E-05	2.96E-05	0	0	0	0	0	0	0	0	0	0	0	3.31E-05	7.41E-04	1.05E-05
	-	(5.76E-7)	(3.22E-7)	(4.75E-6)	(5.47E-7)	-	-	-	-	-	-	-	-	-	-	-	(2.61E-6)	(1.53E-5)	(1.66E-6)

*numbers in brackets are standard error of above.

Table S6. Correlation of ARGs with MGEs.

Resistance genes[a]	***intI1***	***Tn916***
aadB	0.156	0.253
aadE	0.099	-0.056
aphA1	0.189	0.665**
strA	0.255	-0.187
strB	0.232	-0.164
ereA	0.500*	0.488*
ermF	0.393	0.728**
ermG	–	–
ermX	0.185	0.635**
mefA	0.297	0.741**
tetA	0.086	-0.024
tetG	0.407	0.249
tetO	0.353	0.801**
tetQ	–	–
tetW	0.303	0.770**
tetX	0.461	0.639**
sulII	-0.192	-0.088
intI1	1	0.203
Tn916	0.203	1

* Numbers denote statistically significant correlations, *, $p < 0.05$, **, $p<0.01$ (Pearson coefficient, bivariate analysis).

[a] Units of resistance genes or intI1 used in correlation analysis are gene copies per 16s rDNA genes copies.

Table S7. Coverage and diversity indices of bacterial communities by Miseq sequencing.

Samples	OTUs	ACE	Chao	Shannon index	Simpson index	NO. of Reads	Coverage (%)
LZ_1	364	464	454	4.11	0.0441	9367	98.9
LZ_3	294	462	422	3.53	0.0715	9593	99.0
YC_1	278	381	381	3.38	0.0743	18055	99.5
YC_2	333	404	414	3.41	0.0906	17243	99.5
YC_3	230	301	294	1.96	0.3721	11426	99.4
HS_1	596	712	705	4.56	0.0265	15757	99.1
HS_2	298	392	378	3.45	0.0657	18549	99.5
HS_3	352	431	426	3.53	0.0679	18725	99.5
ZZ_1	548	692	692	4.28	0.0358	14510	98.9
ZZ_2	605	704	708	4.71	0.0231	15348	99.1
ZZ_3	457	520	516	4.04	0.0386	14751	99.4
JN_1	475	659	641	4.69	0.0176	10159	98.5
JN_2	261	348	340	3.39	0.0836	10923	99.3
JN_3	324	458	458	1.99	0.4349	17350	99.3
DY_1	606	716	729	4.49	0.0287	17057	99.2
DY_2	417	508	520	3.97	0.0483	13893	99.2
DY_3	268	410	382	3.84	0.0597	11729	99.3

Table S8. Relative abundances of bacterial community compositions grouped by phylum in different water samples. The abundance is presented in terms of the percentage of the targeted phylum in the total sequences of a sample (%).

Taxon	LZ_1	LZ_3	YC_1	YC_2	YC_3	HS_1	HS_2	HS_3	ZZ_1	ZZ_2	ZZ_3	JN_1	JN_2	JN_3	DY_1	DY_2	DY_3
Proteobacteria	46.88	23.17	22.45	38.18	66.06	49.53	49.31	71.55	50.42	36.46	62.33	34.43	23.02	79.94	32.19	15.40	40.55
Actinobacteria	17.87	46.89	41.00	41.54	4.18	22.45	8.30	5.13	31.76	20.11	16.07	23.81	31.29	3.69	21.29	17.19	19.05
Bacteroidetes	29.42	20.50	0.25	0.68	2.23	20.97	17.31	4.73	5.24	25.41	5.96	20.29	0.72	11.95	7.48	0.28	5.35
Cyanobacteria	0.70	2.15	8.28	1.11	0.81	1.52	14.74	10.07	5.99	8.23	1.19	14.12	4.82	0.14	18.12	30.13	24.44
Planctomycetes	0.59	2.92	24.29	12.03	25.32	0.36	2.37	1.99	1.84	1.21	0.23	1.41	2.17	0.24	7.47	19.41	1.20
Verrucomicrobia	0.18	0.24	0.38	0.08	0.35	0.36	5.28	0.05	1.90	3.34	0.13	1.42	34.66	0.03	5.77	9.17	2.30
Firmicutes	2.98	1.36	1.35	5.76	0.67	1.82	0.26	6.01	0.97	0.29	2.64	0.76	0.25	3.10	0.62	1.41	0.02
Bacteria_unclassified	0.41	0.11	1.71	0.31	0.04	0.72	2.09	0.26	0.30	0.40	0.38	0.92	1.28	0.01	3.17	2.40	5.83
Chloroflexi	0.20	1.06	0.18	0.16	0.00	1.26	0.04	0.03	0.38	2.44	0.38	0.36	1.06	0.03	1.87	1.41	0.10
Deinococcus-Thermus	0.00	0.00	0.00	0.00	0.07	0.01	0.01	0.10	0.02	0.01	10.25	0.02	0.04	0.06	0.01	0.24	0.00
Gemmatimonadetes	0.20	0.02	0.00	0.00	0.01	0.22	0.01	0.01	0.33	0.98	0.19	0.96	0.00	0.28	0.02	0.00	0.00
Acidobacteria	0.04	0.29	0.00	0.01	0.14	0.27	0.04	0.03	0.32	0.35	0.03	0.17	0.00	0.01	0.48	0.11	0.10
Candidate_division_OD1	0.11	0.90	0.02	0.01	0.00	0.17	0.03	0.00	0.00	0.08	0.01	0.13	0.00	0.00	0.34	0.42	0.09
TM6	0.06	0.04	0.06	0.08	0.03	0.05	0.02	0.04	0.13	0.07	0.02	0.12	0.51	0.11	0.19	0.45	0.01
Chlorobi	0.14	0.02	0.00	0.00	0.04	0.10	0.00	0.01	0.10	0.10	0.02	0.50	0.00	0.32	0.04	0.01	0.10
Chlamydiae	0.04	0.03	0.01	0.02	0.00	0.03	0.00	0.00	0.02	0.07	0.01	0.03	0.03	0.01	0.28	0.71	0.06
Armatimonadetes	0.01	0.02	0.03	0.01	0.07	0.01	0.05	0.01	0.14	0.32	0.06	0.49	0.01	0.07	0.00	0.01	0.01
WCHB1-60	0.03	0.00	0.02	0.03	0.00	0.01	0.00	0.00	0.06	0.02	0.00	0.02	0.10	0.00	0.42	0.55	0.01
Spirochaetae	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.01	0.02	0.01	0.02	0.00	0.00	0.02	0.04	0.76
Candidate_division_TM	0.07	0.07	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.08	0.42	0.00

7																	
Nitrospirae	0.01	0.01	0.00	0.00	0.00	0.08	0.00	0.00	0.03	0.05	0.09	0.02	0.00	0.00	0.05	0.07	0.00
Candidate_division_OP3	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	0.00	0.08	0.06	0.00
Fusobacteria	0.00	0.16	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
SM2F11	0.00	0.00	0.00	0.00	0.00	0.00	0.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BD1-5	0.04	0.03	0.00	0.01	0.00	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00
Candidate_division_OP11	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	0.00	0.02	0.05	0.01
Candidate_division_BRC1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.04	0.00	0.01	0.00	0.00	0.00	0.00	0.00
SHA-109	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	0.05	0.00

Table S9. Genera distribution patterns in 17 water samples.

Distribution Pattern	Genera	Pattern Description
A	*hgcI_clade* *Cyanobacteria_norank* *Albidiferax* *Rhodobacteraceae_unclassified* *Arenimonas* *Comamonadaceae_unclassified* *Hydrogenophaga* *Gaiellales_uncultured* *GKS98_freshwater_group* *Planctomycetaceae_unclassified* *MNG7_norank* *PeM15_norank* *Legionella* *Acidimicrobiales_unclassified* *Solirubrobacterales_unclassified*	Prevalent in all water type, while dominant in river water and source water.
B	*Pseudomonas* *Massilia* *Acinetobacter* *Sphingomonas* *Methylobacterium* *Brevundimonas* *Deinococcus*	Enriched in finished water, but not prevalent in river water and source water.
C	*Mycobacterium* *CL500–29_marine_group* *LD29_norank* *Synechococcus* *Planctomycetaceae_unclassified* *Actinobacteria_unclassified* *Rhodobacter* *Bacteria_unclassified*	Mainly prevalent in river water and source water, but not in finished water.

Table S10. Genera percentage of bacteria co-occurrence with ARGs.

Genus	LZ_1	LZ_3	YC_1	YC_2	YC_3	HS_1	HS_2	HS_3	ZZ_1	ZZ_2	ZZ_3	JN_1	JN_2	JN_3	DY_1	DY_2	DY_3
Brevundimonas	3.42E-03	7.30E-04	9.42E-04	1.28E-02	2.01E-03	1.14E-03	4.15E-03	1.39E-02	2.34E-03	1.43E-03	1.02E-01	2.85E-03	9.52E-03	4.09E-03	1.17E-03	7.20E-05	8.53E-05
Methylobacterium	1.07E-04	1.42E-02	1.55E-03	1.45E-03	2.45E-03	9.52E-04	1.29E-03	2.53E-02	2.76E-04	3.00E-03	2.49E-01	2.95E-04	5.31E-03	9.28E-03	8.09E-03	3.60E-04	8.53E-05

Reference

1. Tian, Z.; Zhang, Y.; Yu, B.; Yang, M. Changes of resistome, mobilome and potential hosts of antibiotic resistance genes during the transformation of anaerobic digestion from mesophilic to thermophilic. *Water Res.* **2016**, *98*, 261–269.
2. Shahada, F.; Chuma, T.; Tobata, T.; Okamoto, K.; Sueyoshi, M.; Takase, K. Molecular epidemiology of antimicrobial resistance among salmonella enterica serovar infantis from poultry in kagoshima, japan. *Int. J. Antimicrob. Agents* **2006**, *28*, 302–307.
3. Lanz, R.; Kuhnert, P.; Boerlin, P. Antimicrobial resistance and resistance gene determinants in clinical *Escherichia coli* from different animal species in switzerland. *Vet. Microbiol.* **2003**, *91*, 73–84.
4. Sutcliffe, J.; Grebe, T.; Tait-Kamradt, A.; Wondrack, L. Detection of erythromycin-resistant determinants by pcr. *Antimicrob. Agents Chemother.* **1996**, *40*, 2562–2566.
5. Chung, W.O.; Werckenthin, C.; Schwarz, S.; Roberts, M.C. Host range of the ermf rrna methylase gene in bacteria of human and animal origin. *J. Antimicrob. Chemother.* **1999**, *43*, 5–14.
6. Koike, S.; Aminov, R.I.; Yannarell, A.C.; Gans, H.D.; Krapac, I.G.; Chee-Sanford, J.C.; Mackie, R.I. Molecular ecology of macrolide–lincosamide–streptogramin b methylases in waste lagoons and subsurface waters associated with swine production. *Microb. Ecol.* **2010**, *59*, 487–498.
7. Chen, J.; Yu, Z.; Michel, F.C.; Wittum, T.; Morrison, M. Development and application of real-time pcr assays for quantification of erm genes conferring resistance to macrolides-lincosamides-streptogramin b in livestock manure and manure management systems. *Appl. Environ. Microbiol.* **2007**, *73*, 4407–4416.
8. Ng, L.-K.; Martin, I.; Alfa, M.; Mulvey, M. Multiplex pcr for the detection of tetracycline resistant genes. *Mol. Cell. Probes* **2001**, *15*, 209–215.
9. Aminov, R.; Garrigues-Jeanjean, N.; Mackie, R. Molecular ecology of tetracycline resistance: Development and validation of primers for detection of tetracycline resistance genes encoding ribosomal protection proteins. *Appl. Environ. Microbiol.* **2001**, *67*, 22–32.
10. Koike, S.; Krapac, I.; Oliver, H.; Yannarell, A.; Chee-Sanford, J.; Aminov, R.; Mackie, R. Monitoring and source tracking of tetracycline resistance genes in lagoons and groundwater adjacent to swine production facilities over a 3-year period. *Appl. Environ. Microbiol.* **2007**, *73*, 4813–4823.
11. Pei, R.; Kim, S.-C.; Carlson, K.H.; Pruden, A. Effect of river landscape on the sediment concentrations of antibiotics and corresponding antibiotic resistance genes (arg). *Water Res.* **2006**, *40*, 2427–2435.
12. Goldstein, C.; Lee, M.D.; Sanchez, S.; Hudson, C.; Phillips, B.; Register, B.; Grady, M.; Liebert, C.; Summers, A.O.; White, D.G. Incidence of class 1 and 2 integrases in clinical and commensal bacteria from livestock, companion animals, and exotics. *Antimicrob. Agents Chemother.* **2001**, *45*, 723–726.
13. Liu, M.; Ding, R.; Zhang, Y.; Gao, Y.; Tian, Z.; Zhang, T.; Yang, M. Abundance and distribution of macrolide-lincosamide-streptogramin resistance genes in an anaerobic-aerobic system treating spiramycin production wastewater. *Water Res.* **2014**, *63*, 33–41.