PREVALENCE OF ANTIBIOTIC RESISTANT GENES IN THE SAIGON RIVER IMPACTED BY ANTHROPOGENIC ACTIVITIES

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SUPPLEMENTARY MATERIALS

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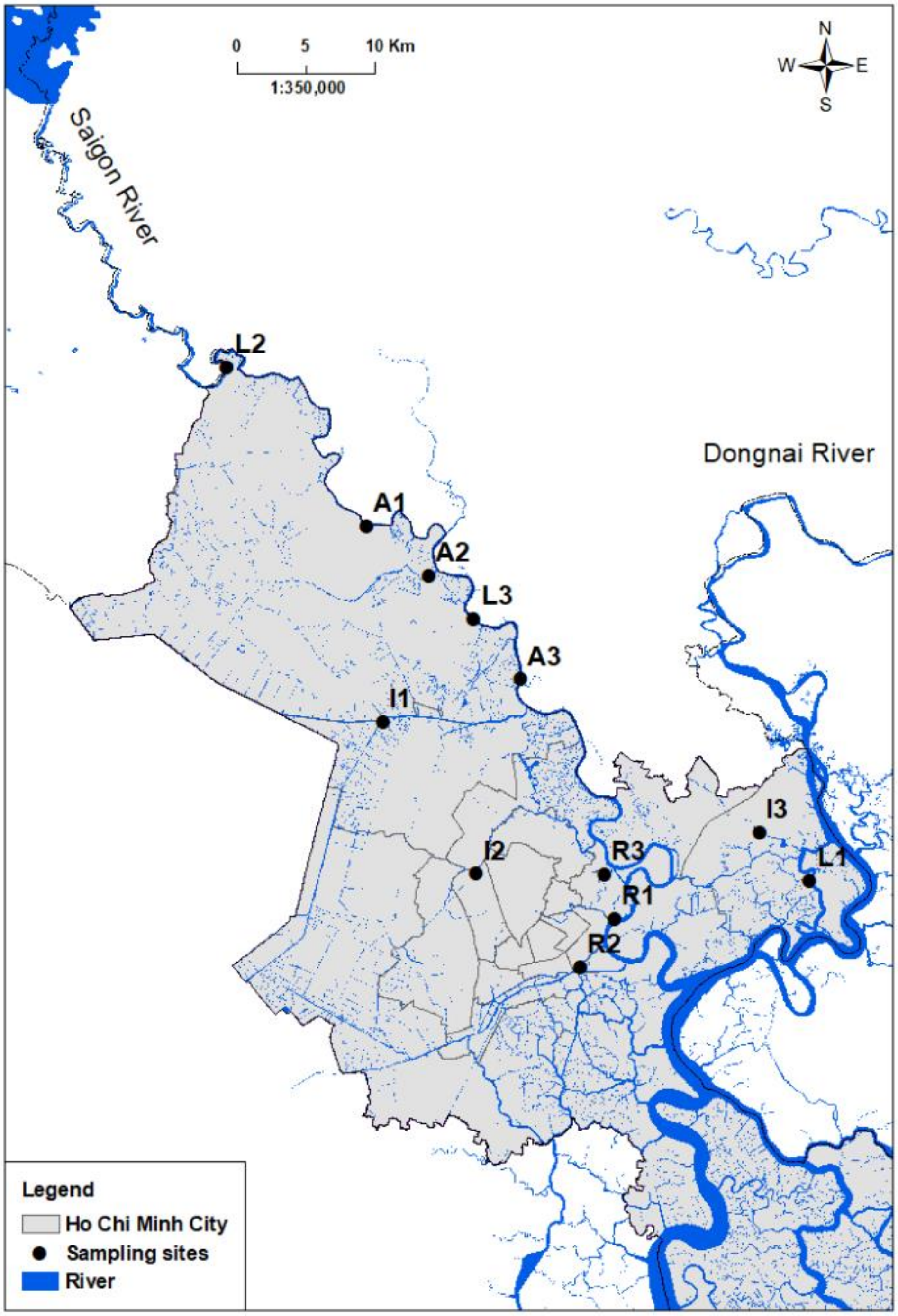

Figure S1. Map of all the sampling sites along the Saigon River in Ho Chi Minh City

Table S1. Detailed information of RT-PCR primers for quantification of the ARGs, integrons, and 16S rRNA gene

Target genes	**Amplicon length (bp)**	**Description**	**The sequences of forward and reverse primers**	**Annealing temp. (^{o}C)**	**References**
aac(6)-Ib-cr	179	Aminoglycoside resistance gene	F: GGAGAGCCGATTGGGTATG R: CATGTACACGGCTGGACCA	60	(Guillard *et al.*, 2010)
bla$_{CTX-M}$	232	B-lactam resistance gene	F: GGAATCTGACGCTGGGTAAA R: GGTTGAGGCTGGGTGAAGTA	56	(Ellem, Partridge and Iredell, 2011)
bla$_{SHV}$	105	B-lactam resistance gene	F: TCCCATGATGAGCACCTTTAAA R: TCCTGCTGGCGATAGTGGAT	55	(Roschanski *et al.*, 2014)
bla$_{TEM}$	100	B-lactam resistance gene	F: GCATCTTACGGATGGCATGA R: GTCCTCCGATCGTTGTCAGAA	61	(Roschanski *et al.*, 2014)
qnrA	159	Quinolone resistance gene	F: ATTTCTCACGCCAGGATTTG R: GCAGATCGGCATAGCTGAAG	56	(Marti and Balcázar, 2013)
qnrB	193	Quinolone resistance gene	F: TATGGCTCTGGCACTCGTT R: GCATCTTTCAGCATCGCAC	56	(Hamed *et al.*, 2018)
oqxB	131	Efflux pump	F: TCCTGATCTCCATTAACGCCCA R: ACCGGAACCCATCTCGATGC	56	(Hong *et al.*, 2009)
sul1	163	Sulfonamide resistance gene	F: CGCACCGGAAACATCGCTGCAC R: TGAAGTTCCGCCGCAAGGCTCG	60	(Pei *et al.*, 2006)
sul2	191	Sulfonamide resistance gene	F: TCCGGTGGAGGCCGGTATCTGG R: CGGGAATGCCATCTGCCTTGAG	60	(Pei *et al.*, 2006)
dfrA	273	Trimethoprim resistance gene	F: ACGGATCCTGGCTGTTGGTTGGACGC R: CGGAATTCACCTTCCGGCTCGATGTC	60	(Lee *et al.*, 2001)
intII1	196	IntIegrase class 1	F: GCCTTGATGTTACCCGAGAG R: GATCGGTCGAATGCGTGT	58	(Barraud *et al.*, 2010)
intII2	195	IntIegrase class 2	F: TGCTTTTCCCACCCTTACC R: GACGGCTACCCTCTGTTATCTC	58	(Barraud *et al.*, 2010)
intII3 -	138	IntIegrase class 3	F: GCCACCACTTGTTTGAGGA R: GGATGTCTGTGCCTGCTTG	58	(Barraud *et al.*, 2010)
16S rRNA	136	Total bacterial 16S rRNA gene	F: AAACTCAAAKGAATTGACGG R: CTCACRRCACGAGCTGAC	59	(Bacchetti De Gregoris *et al.*, 2011)

Table S2. Limit of detection values for all target ARGs in qPCR

Antibiotic resistance genes	Limit of detection (gene copies)
aac(6)-Ib-cr	52
blaCTX-M	40
blaTEM	93
blaSHV	88
qnrA	58
qnrB	48
sul1	49
sul2	57
dfrA	39
oqxB	71
intI1	47
intI2	47
intI3	67
16S rRNA	68

Table S3. The concentration (copies/mL) of the ARGs, Integrons, and 16S rRNA gene in the 12 sampling sites of the Saigon River influenced by different anthropogenic activities such as less-impacted areas (L), agricultural (A), industrial (I), and residential (R) activities during the wet and dry seasons. <LOD: Less than the limit of detection.

Seasons	Sites	*aac(6)-Ib-cr*	*blaCTX*	*blaTEM*	*blaSHV*	*qnrA*	*qnrB*	*sul1*	*sul2*	*dfrA*	*intI1*	*intI2*	*intI3*	*oqxB*	*16S rRNA*
Wet season	L1	1.9E+02	3.7E+00	1.0E+03	9.1E+02	8.8E+01	9.5E+01	2.5E+04	3.5E+03	8.8E+02	2.5E+04	2.7E+01	6.5E+02	5.0E+02	5.1E+05
	L2	<LOD	6.3E+00	3.3E+02	4.0E+02	7.4E+01	6.3E+00	1.5E+03	8.5E+01	2.7E+02	1.6E+03	2.9E+00	3.4E+00	5.3E+01	7.3E+04
	L3	1.9E+02	2.5E+00	5.3E+02	1.4E-01	7.9E+01	8.2E+01	1.5E+04	1.8E+03	5.7E+02	2.0E+04	2.7E+01	3.4E+02	2.5E+02	6.2E+05
	A1	2.4E+02	7.2E-03	2.4E+02	1.7E+02	1.2E+02	6.7E+01	1.2E+04	1.4E+03	1.2E+03	1.2E+04	1.6E+01	5.2E+02	1.8E+02	7.0E+05
	A2	4.6E+02	6.3E-01	4.6E+02	1.8E+04	2.7E+02	1.2E+02	3.7E+04	7.3E+03	2.1E+03	3.6E+04	7.8E+01	2.5E+03	2.2E+02	2.2E+06
	A3	1.5E+02	2.9E-02	2.2E+02	8.0E+02	1.2E+02	2.7E+02	1.9E+04	2.4E+03	4.0E+02	1.8E+04	3.5E+01	3.1E+02	2.3E+02	9.4E+05
	I1	2.4E+02	4.3E+00	6.9E+02	2.2E+02	2.8E+02	1.3E+02	2.0E+04	1.9E+03	3.7E+02	2.2E+04	4.2E+01	4.2E+02	3.3E+02	8.1E+05
	I2	5.8E+05	1.3E+03	6.8E+05	9.6E+03	7.9E+04	3.4E+03	6.4E+06	4.6E+05	2.9E+05	1.1E+07	1.0E+04	6.5E+04	2.2E+05	1.1E+08
	I3	1.6E+06	9.5E+02	6.7E+05	1.5E+04	1.6E+05	2.2E+03	8.9E+06	8.7E+05	4.9E+05	1.9E+07	3.5E+04	1.9E+05	2.9E+05	1.6E+08
	R1	6.0E+03	5.4E+01	5.0E+03	6.3E+01	5.7E+02	2.0E+03	1.3E+05	2.1E+04	3.8E+03	1.8E+05	1.0E+02	1.6E+03	3.0E+03	1.2E+07
	R2	1.2E+05	3.6E+02	1.5E+05	6.0E+02	1.2E+04	2.5E+03	1.7E+06	4.3E+05	5.2E+04	3.1E+06	2.7E+02	3.8E+04	5.8E+04	7.8E+07
	R3	5.5E+05	8.9E+02	3.3E+05	2.0E+02	3.3E+04	2.2E+04	4.8E+06	3.6E+05	1.9E+05	7.3E+06	5.5E+03	6.7E+04	1.1E+05	9.4E+07
Dry season	L1	5.7E+02	4.3E+01	8.8E+02	6.7E+03	3.9E+02	3.7E+01	3.4E+02	5.7E+03	1.3E+03	1.6E+03	2.3E+02	4.4E+02	8.0E+02	3.3E+04
	L2	8.1E+01	8.0E+00	8.3E+02	1.8E+03	6.2E+02	1.4E+02	1.1E+03	4.4E+03	2.7E+03	1.5E+03	2.4E+02	2.2E+02	9.8E+02	2.6E+06
	L3	2.8E+03	4.7E+00	1.6E+03	4.9E+02	1.7E+02	1.0E+01	2.7E+04	3.1E+05	2.0E+04	3.2E+04	2.2E+01	3.8E+02	1.7E+03	1.6E+04
	A1	1.5E+03	5.8E+01	5.1E+04	6.3E+03	9.9E+02	1.3E+02	1.8E+04	6.8E+04	1.3E+04	1.5E+04	2.6E+02	3.4E+02	7.5E+02	3.7E+05
	A2	1.4E+04	2.6E+02	1.6E+03	1.7E+04	2.5E+03	1.1E+02	1.0E+05	3.7E+05	9.1E+04	7.3E+04	2.3E+02	1.5E+03	1.6E+03	1.3E+06
	A3	1.1E+04	6.4E+02	9.6E+03	6.2E+03	2.4E+03	3.5E+03	1.8E+05	7.0E+05	6.2E+04	2.2E+05	2.7E+02	4.8E+03	4.5E+03	2.4E+06
	I1	2.1E+04	7.1E+02	2.7E+03	9.1E+03	8.8E+03	8.6E+02	4.1E+05	1.3E+06	1.1E+05	2.6E+05	3.0E+02	2.0E+03	5.5E+03	5.3E+06
	I2	1.5E+07	2.0E+04	1.2E+07	1.4E+05	2.6E+05	5.3E+03	4.4E+07	3.8E+07	5.6E+06	2.7E+07	1.8E+04	1.6E+05	4.6E+05	1.6E+08
	I3	5.7E+06	8.7E+03	2.9E+06	8.1E+04	1.2E+05	2.7E+03	1.5E+07	1.0E+07	2.1E+06	1.3E+07	7.9E+03	5.1E+04	2.1E+05	6.2E+07
	R1	7.7E+03	1.4E+02	8.2E+03	1.5E+03	1.9E+02	7.1E+03	4.6E+04	2.2E+05	7.9E+03	6.1E+04	5.1E+01	9.8E+02	1.6E+03	1.1E+06
	R2	9.5E+05	2.9E+03	1.0E+06	6.3E+04	1.2E+04	4.2E+03	3.9E+06	9.7E+06	5.5E+05	3.3E+06	2.0E+03	4.7E+04	8.0E+04	1.8E+07
	R3	2.7E+06	7.8E+03	1.9E+06	2.9E+05	4.4E+04	2.8E+04	2.1E+07	2.2E+07	1.1E+06	1.1E+07	6.5E+03	1.3E+05	2.3E+05	5.8E+07
Average	L	6.2E+02	1.1E+01	8.6E+02	1.7E+03	2.4E+02	6.2E+01	1.2E+04	5.5E+04	4.4E+03	1.4E+04	9.2E+01	3.4E+02	7.1E+02	6.3E+05
	A	4.6E+03	1.6E+02	1.1E+04	8.0E+03	1.1E+03	7.0E+02	6.2E+04	1.9E+05	2.8E+04	6.1E+04	1.5E+02	1.7E+03	1.3E+03	1.3E+06

	I	3.8E+06	5.2E+03	2.7E+06	4.2E+04	1.1E+05	2.4E+03	1.2E+07	8.5E+06	1.4E+06	1.2E+07	1.2E+04	7.9E+04	2.0E+05	8.4E+07
	R	7.3E+05	2.0E+03	5.7E+05	6.0E+04	1.7E+04	1.1E+04	5.2E+06	5.5E+06	3.1E+05	4.2E+06	2.4E+03	4.7E+04	8.1E+04	4.3E+07

Table S4. The relative abundance of the ARGs, and Integrons in the 12 sampling sites of the Saigon River influenced by different anthropogenic activities such as less-impacted areas (L), agricutural (A), industrial (I), and residential (R) activities during the wet and dry seasons. NA: not available

Seasons	**Sites**	***aac(6)-Ib-cr***	***blaCTX***	***blaTEM***	***blaSHV***	***qnrA***	***qnrB***	***sul1***	***sul2***	***dfrA***	***intI1***	***intI2***	***intI3***	***oqxB***
Wet season	L1	3.6E-04	7.2E-06	2.0E-03	1.8E-03	1.7E-04	1.8E-04	4.9E-02	6.8E-03	1.7E-03	4.9E-02	5.2E-05	1.3E-03	9.7E-04
	L2	*NA*	8.6E-05	4.6E-03	5.4E-03	1.0E-03	8.6E-05	2.0E-02	1.2E-03	3.7E-03	2.2E-02	3.9E-05	4.7E-05	7.3E-04
	L3	3.1E-04	4.1E-06	8.5E-04	2.3E-07	1.3E-04	1.3E-04	2.5E-02	2.9E-03	9.2E-04	3.2E-02	4.3E-05	5.5E-04	4.0E-04
	I1	3.0E-04	5.3E-06	8.5E-04	2.8E-04	3.4E-04	1.6E-04	2.5E-02	2.3E-03	4.6E-04	2.8E-02	5.2E-05	5.3E-04	4.1E-04
	I2	5.2E-03	1.2E-05	6.1E-03	8.6E-05	7.1E-04	3.0E-05	5.8E-02	4.2E-03	2.6E-03	9.7E-02	9.4E-05	5.8E-04	2.0E-03
	I3	9.6E-03	5.8E-06	4.1E-03	9.1E-05	9.9E-04	1.3E-05	5.4E-02	5.3E-03	3.0E-03	1.2E-01	2.1E-04	1.2E-03	1.8E-03
	A1	3.4E-04	1.0E-08	3.5E-04	2.5E-04	1.7E-04	9.7E-05	1.7E-02	2.0E-03	1.8E-03	1.7E-02	2.3E-05	7.5E-04	2.6E-04
	A2	2.1E-04	2.9E-07	2.1E-04	8.2E-03	1.3E-04	5.8E-05	1.7E-02	3.4E-03	9.8E-04	1.7E-02	3.6E-05	1.2E-03	1.0E-04
	A3	1.6E-04	3.0E-08	2.3E-04	8.5E-04	1.3E-04	2.9E-04	2.0E-02	2.6E-03	4.2E-04	1.9E-02	3.7E-05	3.3E-04	2.5E-04
	R1	4.9E-04	4.4E-06	4.1E-04	5.2E-06	4.7E-05	1.7E-04	1.1E-02	1.7E-03	3.1E-04	1.5E-02	8.6E-06	1.3E-04	2.4E-04
	R2	1.6E-03	4.6E-06	1.9E-03	7.7E-06	1.6E-04	3.2E-05	2.1E-02	5.5E-03	6.6E-04	3.9E-02	3.4E-06	4.9E-04	7.3E-04
	R3	5.9E-03	9.5E-06	3.5E-03	2.2E-06	3.5E-04	2.3E-04	5.1E-02	3.8E-03	2.1E-03	7.8E-02	5.9E-05	7.2E-04	1.2E-03
Dry season	L1	1.7E-02	1.3E-03	2.7E-02	2.0E-01	1.2E-02	1.1E-03	1.0E-02	1.7E-01	4.0E-02	4.8E-02	7.1E-03	1.3E-02	2.4E-02
	L2	3.2E-05	3.2E-06	3.2E-04	6.9E-04	2.4E-04	5.6E-05	4.4E-04	1.7E-03	1.1E-03	5.7E-04	9.5E-05	8.7E-05	3.8E-04
	L3	1.7E-01	2.9E-04	9.7E-02	3.0E-02	1.0E-02	6.1E-04	1.7E+00	1.9E+01	1.2E+00	1.9E+00	1.4E-03	2.3E-02	1.0E-01
	I1	4.0E-03	1.3E-04	5.0E-04	1.7E-03	1.7E-03	1.6E-04	7.7E-02	2.4E-01	2.1E-02	4.9E-02	5.6E-05	3.8E-04	1.0E-03
	I2	9.4E-02	1.2E-04	7.3E-02	8.7E-04	1.6E-03	3.3E-05	2.7E-01	2.4E-01	3.5E-02	1.7E-01	1.1E-04	1.0E-03	2.8E-03
	I3	9.1E-02	1.4E-04	4.7E-02	1.3E-03	2.0E-03	4.4E-05	2.4E-01	1.7E-01	3.3E-02	2.1E-01	1.3E-04	8.2E-04	3.4E-03
	A1	4.1E-03	1.6E-04	1.4E-01	1.7E-02	2.7E-03	3.7E-04	5.0E-02	1.9E-01	3.5E-02	4.1E-02	7.1E-04	9.3E-04	2.1E-03
	A2	1.0E-02	1.9E-04	1.2E-03	1.2E-02	1.8E-03	7.9E-05	7.8E-02	2.8E-01	6.8E-02	5.5E-02	1.7E-04	1.1E-03	1.2E-03
	A3	4.7E-03	2.6E-04	3.9E-03	2.6E-03	9.7E-04	1.4E-03	7.5E-02	2.9E-01	2.5E-02	8.9E-02	1.1E-04	2.0E-03	1.8E-03
	R1	6.7E-03	1.2E-04	7.1E-03	1.3E-03	1.6E-04	6.2E-03	4.0E-02	1.9E-01	6.9E-03	5.3E-02	4.5E-05	8.5E-04	1.4E-03
	R2	5.2E-02	1.6E-04	5.7E-02	3.5E-03	6.9E-04	2.3E-04	2.2E-01	5.3E-01	3.0E-02	1.8E-01	1.1E-04	2.6E-03	4.4E-03
	R3	4.7E-02	1.4E-04	3.3E-02	5.1E-03	7.7E-04	4.8E-04	3.6E-01	3.8E-01	1.8E-02	1.9E-01	1.1E-04	2.2E-03	4.1E-03

Table S5. The correlation coefficient values of Pearson and Spearman analysis between water quality parameters and the absolute abundance (copies/ml) of all ARGs, integrons, and the 16S rRNA gene in the surface water. The correlation was considered significant only if the p-value was less than 0.05, and highlighted with bold format.

		pH	**Temperature**	**Conductivity**	**Salinity**	**Turbidity**	**DO**	**P-PO43-**	**N-NH4+**	**N-NO2-**	**N-NO3-**	**BOD5**
aac(6)-Ib-cr	**Pearson**	**0.448**	**0.449**	0.025	0.061	0.205	**-0.433**	0.153	0.013	-0.157	-0.074	**0.582**
	Spearman	**0.645**	**0.524**	**0.777**	**0.787**	-0.071	**-0.409**	**0.526**	**0.461**	**-0.429**	-0.328	**0.783**
blaCTX	**Pearson**	**0.491**	**0.489**	0.113	0.159	0.210	**-0.441**	0.208	0.057	-0.168	-0.092	**0.581**
	Spearman	**0.648**	**0.502**	**0.754**	**0.766**	-0.161	-0.295	**0.456**	**0.451**	**-0.512**	**-0.473**	**0.752**
blaTEM	**Pearson**	**0.438**	**0.406**	0.049	0.084	0.114	-0.394	0.241	0.000	-0.144	-0.071	**0.499**
	Spearman	**0.640**	**0.447**	**0.732**	**0.745**	-0.186	-0.339	**0.512**	**0.434**	**-0.456**	-0.353	**0.754**
blaSHV	**Pearson**	**0.410**	0.357	0.273	0.343	0.038	-0.401	0.235	0.104	-0.147	-0.099	**0.295**
	Spearman	**0.465**	0.330	**0.457**	**0.479**	-0.100	-0.291	0.389	0.235	-0.310	-0.363	**0.301**
qnrA	**Pearson**	**0.476**	**0.428**	-0.050	-0.024	0.206	**-0.569**	**0.304**	0.287	-0.218	-0.106	**0.752**
	Spearman	**0.556**	**0.405**	**0.640**	**0.646**	-0.099	**-0.496**	**0.578**	**0.466**	**-0.527**	**-0.502**	**0.833**
qnrB	**Pearson**	**0.301**	**0.237**	0.294	0.338	-0.204	-0.330	0.358	**0.427**	-0.122	-0.118	**0.144**
	Spearman	**0.618**	**0.444**	**0.709**	**0.704**	-0.254	-0.355	0.526	**0.477**	-0.220	-0.212	**0.666**
sul1	**Pearson**	**0.497**	**0.443**	0.072	0.120	0.117	**-0.525**	0.366	0.157	-0.194	-0.099	**0.583**
	Spearman	**0.615**	**0.445**	**0.625**	**0.633**	0.098	**-0.520**	**0.567**	**0.505**	-0.401	-0.168	**0.774**
sul2	**Pearson**	**0.483**	**0.455**	0.217	0.271	0.065	-0.382	0.218	0.009	-0.149	-0.089	**0.414**
	Spearman	**0.572**	**0.502**	**0.736**	**0.750**	-0.095	-0.279	0.397	0.365	-0.356	-0.399	**0.663**
dfrA	**Pearson**	**0.456**	**0.456**	0.049	0.085	0.201	**-0.419**	0.160	0.017	-0.158	-0.080	**0.577**
	Spearman	**0.531**	**0.444**	0.697	0.709	-0.164	-0.367	0.415	0.354	-0.382	**-0.472**	**0.723**
intI1	**Pearson**	**0.517**	**0.442**	0.014	0.048	0.136	**-0.630**	0.419	0.416	-0.240	-0.125	**0.747**
	Spearman	**0.625**	**0.456**	**0.624**	**0.634**	0.129	**-0.511**	0.543	0.527	-0.407	-0.133	**0.786**
intI2	**Pearson**	**0.354**	0.266	-0.051	-0.036	0.041	**-0.534**	0.280	0.407	-0.204	-0.101	**0.604**
	Spearman	**0.568**	0.384	0.648	0.654	-0.123	**-0.473**	**0.528**	**0.505**	**-0.482**	**-0.501**	**0.797**
intI3	**Pearson**	**0.487**	0.388	0.094	0.131	-0.026	**-0.595**	0.402	**0.460**	-0.233	-0.130	**0.582**
	Spearman	**0.619**	0.369	**0.633**	**0.639**	0.061	**-0.512**	**0.587**	**0.521**	-0.396	-0.196	**0.721**
oqxB	**Pearson**	**0.541**	**0.440**	0.057	0.095	0.104	**-0.632**	**0.476**	**0.457**	-0.243	-0.132	**0.736**
	Spearman	**0.626**	**0.478**	**0.730**	**0.740**	-0.155	-0.361	**0.492**	**0.468**	**-0.513**	-0.398	**0.805**
16s rRNA	**Pearson**	**0.488**	0.359	-0.054	-0.035	0.031	**-0.625**	**0.471**	**0.627**	-0.219	-0.141	**0.699**
	Spearman	**0.598**	0.368	**0.485**	**0.486**	0.029	**-0.580**	**0.522**	**0.534**	-0.331	-0.237	**0.848**

Table S6. The p value of Pearson and Spearman analysis between water quality parameters and ARGs, integrons, and the 16S rRNA gene in the surface water.

		pH	**Temperature**	**Conductivity**	**Salinity**	**Turbidity**	**DO**	**P-PO43-**	**N-NH4+**	**N-NO2-**	**N-NO3-**	**BOD5**
aac(6)-Ib-cr	Pearson	0.0282	0.0279	0.9081	0.7773	0.3371	0.0347	0.4959	0.9527	0.4844	0.7300	0.0028
	Spearman	0.0007	0.0086	0.0000	0.0000	0.7406	0.0472	0.0120	0.0267	0.0466	0.1179	0.0000
blaCTX	Pearson	0.0148	0.0152	0.6007	0.4583	0.3246	0.0309	0.3541	0.7969	0.4538	0.6676	0.0029
	Spearman	0.0006	0.0124	0.0000	0.0000	0.4527	0.1616	0.0331	0.0310	0.0148	0.0196	0.0000
blaTEM	Pearson	0.0324	0.0491	0.8193	0.6959	0.5956	0.0568	0.2800	0.9999	0.5214	0.7415	0.0131
	Spearman	0.0008	0.0285	0.0000	0.0000	0.3840	0.1056	0.0148	0.0386	0.0331	0.0906	0.0000
blaSHV	Pearson	0.0468	0.0871	0.1972	0.1012	0.8599	0.0520	0.2927	0.6366	0.5139	0.6468	0.1616
	Spearman	0.0220	0.1150	0.0249	0.0179	0.6420	0.1682	0.0735	0.2801	0.1603	0.0816	0.1533
qnrA	Pearson	0.0186	0.0370	0.8151	0.9118	0.3347	0.0037	0.1694	0.1847	0.3302	0.6219	0.0000
	Spearman	0.0048	0.0495	0.0008	0.0007	0.6449	0.0137	0.0049	0.0249	0.0118	0.0125	0.0000
qnrB	Pearson	0.1530	0.2645	0.1628	0.1061	0.3394	0.1154	0.1019	0.0423	0.5874	0.5829	0.5016
	Spearman	0.0013	0.0299	0.0001	0.0001	0.2312	0.0886	0.0120	0.0213	0.3260	0.3196	0.0004
sul1	Pearson	0.0135	0.0302	0.7396	0.5765	0.5868	0.0085	0.0936	0.4733	0.3876	0.6452	0.0028
	Spearman	0.0014	0.0292	0.0011	0.0009	0.6478	0.0091	0.0059	0.0140	0.0640	0.4331	0.0000
sul2	Pearson	0.0169	0.0254	0.3084	0.2003	0.7621	0.0654	0.3295	0.9664	0.5092	0.6802	0.0441
	Spearman	0.0035	0.0125	0.0000	0.0000	0.6595	0.1876	0.0674	0.0872	0.1036	0.0533	0.0004
dfrA	Pearson	0.0250	0.0253	0.8210	0.6927	0.3458	0.0415	0.4760	0.9388	0.4821	0.7118	0.0032
	Spearman	0.0075	0.0296	0.0002	0.0001	0.4429	0.0775	0.0548	0.0977	0.0791	0.0198	0.0001
intI1	Pearson	0.0097	0.0306	0.9485	0.8236	0.5249	0.0010	0.0522	0.0481	0.2822	0.5603	0.0000
	Spearman	0.0011	0.0252	0.0011	0.0009	0.5490	0.0107	0.0091	0.0098	0.0600	0.5354	0.0000
intI2	Pearson	0.0897	0.2086	0.8115	0.8666	0.8482	0.0072	0.2062	0.0538	0.3625	0.6393	0.0018
	Spearman	0.0038	0.0640	0.0006	0.0005	0.5654	0.0195	0.0116	0.0140	0.0232	0.0127	0.0000
intI3	Pearson	0.0158	0.0611	0.6627	0.5433	0.9042	0.0022	0.0634	0.0272	0.2957	0.5435	0.0029
	Spearman	0.0013	0.0763	0.0009	0.0008	0.7775	0.0106	0.0041	0.0108	0.0682	0.3596	0.0001
oqxB	Pearson	0.0064	0.0316	0.7911	0.6580	0.6288	0.0009	0.0250	0.0282	0.2752	0.5377	0.0000
	Spearman	0.0011	0.0180	0.0001	0.0000	0.4702	0.0829	0.0201	0.0242	0.0146	0.0539	0.0000
16s rRNA	Pearson	0.0156	0.0851	0.8028	0.8715	0.8860	0.0011	0.0271	0.0014	0.3275	0.5101	0.0001
	Spearman	0.0021	0.0771	0.0162	0.0160	0.8941	0.0030	0.0127	0.0087	0.1318	0.2640	0.0000