Supplementary. The Effect of the Effluent from a Small-Scale Conventional Wastewater Treatment Plant Treating Municipal Wastewater on the Composition and Abundance of the Microbial Community, Antibiotic Resistome, and Pathogens in the Sediment and Water of a Receiving Stream

Table S1. Characteristics of qPCR primer pairs and programs. LOQ – limit of quantification per qPCR reaction.

Primers	Sequence 5'-3'	Target gene	Amplicon size (bp)	Primers concentration (µM)	qPCR program	LOQ	Reference	Amplification efficiency (standard)[2]	Amplification efficiency (samples)[2]
Arc519F	CAGYCGCCRCGGTAA	Archaeal 16S rRNA	393	0.6	50°C 2 min, 95°C 10 min; 35 cycles: 95°C 15 s; 56°C 30 s; 72°C 30s	1000	[1]	1.74 ± 0.04	1.93 ± 0.07
Arch910R	GAATWGGCGGGGGRGC								
Bact517F	GCCAGCAGCCGCGGTAA	Bacterial 16S rRNA	530	0.6	50°C 2 min, 95°C 10 min; 35 cycles: 95°C 30 s; 60°C 45 s; 72°C 45s	1000	[2]	1.88 ± 0.02	1.85 ± 0.05
Bact1028R	CGACARCCATGCASCACCT						[3]		
aadA-F	GCTGGCCGTRCATTTGTAC	*aadA*[1]	479	0.8	50°C 2 min, 95°C 10 min; 35 cycles: 95°C 15 s, 59°C 30 s, 72°C 30 s	25	[4]	1.72 ± 0.05	1.71 ± 0.07
aadA-R	AGCACTACATTYCGCTCATCG								
acrB-F	ATATCCTACGATTGCACCGC	*acrB*	160	0.8	50°C 2 min, 95°C 10 min; 40 cycles: 95°C 15 s, 58°C 30 s, 72°C 30 s	12	[5]	1.87 ± 0.10	1.84 ± 0.08
acrB-R	GGTACCCGTGGAGTCACTGT								
catQ-F	AGGTGCACTTACAGTATGACTGC	*catQ*	262	0.8	50°C 2 min, 95°C 10 min; 40 cycles: 95°C 15 s, 57°C 30 s, 72°C 30 s	12	[6]	1.90 ± 0.13	1.98 ± 0.07
catQ-R	AACGTGGGAAGTTCTCGTCATAC								
tetA F2	TCAATTTCCTGACGGGCTG	*tetA*	96	0.8	50°C 2 min, 95°C 10 min; 45 cycles: 95°C 15 s, 58°C 30 s, 72°C 30 s	25	[7]	1.93 ± 0.14	1.90 ± 0.12
tetA R2	GAAGCGAGCGGGTTGAGAG								
tetB-F1	AGTGCGCTTTGGATGCTG	*tetB*	101	0.8	50°C 2 min, 95°C 10 min; 45 cycles: 95°C 15 s, 58°C 30 s, 72°C 30 s	25	[7]	1.91 ± 0.08	1.94 ± 0.08
tetB-R1	TGAGGTGGTATCGGCAATGA								
tetQ-F	GCTCACATTGATGCAGGAAA	*tetQ*	153	0.8	50°C 2 min, 95°C 10 min; 35 cycles: 95°C 15 s, 58°C 30 s, 72°C 30 s	25	Modified from [5]	1.88 ± 0.08	2.00 ± 0.10
tetQ-R	CGTAGAAGCCCGRACAGTAA								
tetW-FC	GGGAAATTGTTCGGACAGAC	*tetW*	549	0.8	50°C 2 min, 95°C 10 min; 35 cycles: 95°C 15 s, 57°C 30 s, 72°C 30 s	25	[8]	1.83 ± 0.05	1.94 ± 0.10
tetW-RC	AACGGATACCATCCCTGACA								
sul1-F1	CTGAACGATATCCAAGGATTYCC	*sul1*	239	0.8	50°C 2 min, 95°C 10 min; 45 cycles: 95°C 15 s, 54°C 30 s, 72°C 30 s	25	[9]	1.81 ± 0.04	1.81 ± 0.06
sul1-R1	AAAAATCCCATCCCCGGRTC								
sul2-F	CTCAATGATATTCGCGGTTTYCC	*sul2*	245	0.6	50°C 2 min, 95°C 10 min; 45 cycles: 95°C 15 s, 58°C 30 s, 72°C 30 s	6	[10]	1.69 ± 0.06	1.84 ± 0.09
sul2-R	AAAAACCCCATGCCGGGRTC								
UP	ACCAAYGATATYGCGGTGAT	*blaCTX-M*	101	0.6	50°C 2min, 95°C 10min; 45 cycles: 95°C 15s, 56°C 30s, 72°C 30s	12	Modified from [11]	1.77 ± 0.07	1.62 ± 0.06
LP	ACATCGCGRCGGCKYTCT								
blaTEM1-F	CATTTYCGTGTCGCCCTTAT	*blaTEM1*	167	0.6	50°C 2 min, 95°C 10 min; 45 cycles: 95°C 15 s, 57°C 30 s, 72°C 30 s	50	[5]	1.88 ± 0.06	1.93 ± 0.07
blaTEM1-R	GGGCGAAAACTCTCAAGGAT								
blaOXA2F	TCTTCGCGATACTTTYCTCCA	*blaOXA2*	177	0.8	50°C 2 min, 95°C 10 min; 35 cycles: 95°C 15 s, 55°C 30 s, 72°C 30 s	12	[5]	1.91 ± 0.05	2.02 ± 0.10
blaOXA2R	ATCGCACAGGATCAAAAACC								
mexF-F1	CAGGACAAGCARTACCTGGTGGC	*mexF*	566	0.8	50°C 2 min, 95°C 10 min; 40 cycles: 95°C 15 s, 60°C 30 s, 72°C 30 s	12	This study	1.75 ± 0.04	1.80 ± 0.10
mexF-R2	AGGTARAYCTGCAGGGTGTCG								
QnrS-Ru	AAACACCTCGACTTAAGTCT	*qnrS*	169	0.4	50°C 2 min, 95°C 10 min; 45 cycles: 95°C 15 s, 52°C 30 s, 72°C 30 s	1000	[12]	1.90 ± 0.07	1.81 ± 0.07
QnrS-Fu	GTGAGTAATCGTATGTACTTTTGC								

[1] The primers amplify all *aadA* gene variants (*aadA1*-*aadA25*) except *aadA4*, *aadA5*, *aadA9*, and *aadA14*.

[2] Amplification efficiencies derived from LinRegPCR program are presented in the range of one to two, where one corresponds to no amplification (0% efficiency) and two corresponds to doubling of amplification product in each cycle (100% efficiency).

Table S2. The numbers of total reads and reads after quality trimming, coverage and diversity metrics, the proportions of classified reads (%) and the numbers of contigs in metagenomes of studied samples. E is the effluent of the wastewater treatment plant (WWTP), SW and RW are water samples, and SS and RS are sediment samples of the stream and river, respectively. SW$_{U}$ and SS$_{U}$ are the samples taken upstream of the WWTP discharge point and RW$_{U}$ and RS$_{U}$ are the samples taken from the river upstream of the stream inflow point. The number in the subscript of the sample code shows the distance (km) of the sampling point downstream from the WWTP discharge point.

Sample name	**No. of reads**	**No. of reads after quality trimming**	**Coverage**	**Diversity**	**Classified reads (%)**	**No. of contigs**
E	20911340	19655893	0.567	21.18	68.5	674253 (579158545 bp)
SW$_{U}$	18416530	17956649	0.503	21.49	68.0	593902 (454892072 bp)
SW$_{0.3}$	18563693	17523811	0.410	22.04	69.1	551181 (447254012 bp)
SS$_{U}$	22332423	21039728	0.162	23.63	70.8	325383 (207848632 bp)
SS$_{0.3}$	20180178	19025365	0.389	22.24	69.8	495233 (409619263 bp)
SS$_{2.7}$	22187376	20838296	0.168	23.57	72.3	257362 (152933903 bp)
SS$_{3.2}$	20827890	19390049	0.159	23.57	73.5	251018 (152254693 bp)
RS$_{U}$	23196456	21597354	0.156	23.72	73.2	302471 (180816447 bp)
RS$_{3.7}$	20940559	19430683	0.145	23.63	71.5	243151 (143192010 bp)

Table S3. The means and standard deviations (in parentheses) of physicochemical parameters in influent (IN) and effluent (E) of wastewater treatment plant (A), as well as values of individual measurements of physicochemical parameters of IN and E (B) over the 11-month period. ORP - oxidation-reduction potential; N_{tot} – content of total nitrogen; P_{tot} – content of total phosphorous; C_{tot} – content of total carbon; TOC – content of total organic carbon; DOC – content of dissolved organic carbon; TIC – content of total inorganic carbon, NM – not measured, NA – not applicable.

A – Means and standard deviations of physicochemical parameters													
Sample	**Temp (°C)**	**O_2 (mg/L)**	**pH**	**ORP (mV)**	**N_{tot} (mg/L)**	**NH_4-N (mg/L)**	**NO_3-N (mg/L)**	**P_{tot} (mg/L)**	**PO_4^{3-}-P (mg/L)**	**C_{tot} (mg/L)**	**TOC (mg/L)**	**DOC (mg/L)**	**TIC (mg/L)**
IN (n=2)	11.9 (2.3)	4.1 (1.1)	7.76 (0.12)	121 ±21	119 ±26	44.8 ±16.8	39.0 ± 51.7	14.5 ±3.5	13.2 ±3.0	333 ±50	249 ±51	130.00	83.50 ±2.12
E (n=3)	15.7 (2.3)	6.1 (0.8)	7.25 (0.28)	128 ±37	8.9 ±3.8	1.82 ±0.93	7.4 ±7.8	6.2 ±5.9	5.4 ±4.8	95 ±37	40 ±28	21.5 ±12.0	43.5 ±9.2
B – Values of measured physicochemical parameters of individual samples													
IN (05.12.2012)	10.2	4.9	7.84	136	137	32.9	75.5	17.0	15.3	368	285	NM	82
IN (20.11.2013)	13.5	3.3	7.67	107	100	56.7	2.4	12.0	11.0	298	213	130	85
E (05.12.2012)	13.4	6.8	7.18	164	10.0	1.16	16.5	3.0	2.7	69	32	NM	37
E (26.09.2013)	18.0	6.4	7.55	91	4.6	1.42	3.1	2.7	2.6	NA	17	13	NM
E (20.11.2013)	15.8	5.2	7.01	129	12.0	2.89	2.7	13.0	11.0	121	71	30	50

Table S4A. The means and standard deviations (in parentheses) of the target gene abundances and relative abundances in prokaryotic community of wastewater treatment plant influent (IN; n=3) and effluent (E; n=4) over a 11-month period. 16S$_{tot}$ – abundance of total prokaryotic community; B16S – abundance of bacterial 16S rRNA gene; A16S – abundance of archaeal 16S rRNA gene.

Gene	**Abundances of genes (copies/mL)**		**Relative abundances of genes (%)**	
	IN	**E**	**IN**	**E**
16S$_{tot}$	1.54x10^{8} (2.00x10^{8})	9.47x10^{7} (5.89x10^{7})	x	x
B16S	1.53x10^{8} (1.97x10^{8})	8.81x10^{7} (5.48x10^{7})	99.3 (0.4)	90.7 (7.6)
A16S	1.50x10^{6} (2.38x10^{6})	6.69x10^{6} (5.81x10^{6})	0.7 (0.4)	9.3 (7.6)
aadA	1.20x10^{6} (1.61x10^{6})	3.25x10^{5} (3.14x10^{5})	1.18 (0.89)	0.36 (0.23)
acrB	8.41x10^{3} (5.50x10^{3})	2.21x10^{4} (2.14x10^{4})	0.017 (0.016)	0.021 (0.017)
blaCTX-M	7.96x10^{3} (1.14x10^{4})	3.61x10^{4} (2.18x10^{4})	0.005 (0.002)	0.041 (0.004)
blaOXA2	4.39x10^{4} (7.42x10^{4})	1.67x10^{3} (1.52x10^{3})	0.015 (0.017)	0.002 (0.002)
blaTEM1	9.59x10^{3} (1.33x10^{4})	1.26x10^{4} (5.29x10^{3})	0.008 (0.005)	0.019 (0.012)
catQ	7.93x10^{3} (5.87x10^{3})	2.38x10^{3} (3.10x10^{3})	0.012 (0.008)	0.003 (0.003)
mexF	9.70x10^{4} (1.28x10^{5})	2.69x10^{4} (2.62x10^{4})	0.058 (0.008)	0.029 (0.012)
qnrS	2.38x10^{6} (2.07x10^{6})	4.27x10^{4} (1.84x10^{4})	3.38 (2.46)	0.088 (0.088)
sul1	1.55x10^{6} (1.94x10^{6})	1.41x10^{6} (1.35x10^{6})	0.99 (0.13)	1.33 (0.56)
sul2	1.15x10^{3} (1.94x10^{3})	1.24x10^{3} (4.67x10^{2})	0.0004 (0.0004)	0.0020 (0.0013)
tetA	2.47x10^{5} (2.08x10^{5})	1.21x10^{4} (8.33x10^{3})	0.242 (0.244)	0.013 (0.006)
tetB	4.09x10^{3} (2.02x10^{3})	1.80x10^{4} (1.16x10^{4})	0.025 (0.040)	0.017 (0.010)
tetQ	7.20x10^{5} (9.11x10^{5})	5.66x10^{4} (8.89x10^{4})	0.557 (0.154)	0.080 (0.107)
tetW	3.52x10^{5} (4.49x10^{5})	3.30x10^{3} (2.01x10^{3})	0.263 (0.063)	0.004 (0.002)

Table S4B. The target gene abundances (copies/mL) and relative abundances in prokaryotic community (%, given in parentheses) of individual samples of wastewater treatment plant influent (IN) and effluent (E) over a 11-month period. 16S$_{tot}$ – abundance of total prokaryotic community; B16S – abundance of bacterial 16S rRNA gene; A16S – abundance of archaeal 16S rRNA gene.

Gene	**IN** (05.12.2012)	**IN** (10.06.2013)	**IN** (20.11.2013)	**E** (05.12.2012)	**E** (10.06.2013)	**E** (26.09.2013)	**E** (20.11.2013)
16S$_{tot}$	3.82x10^{8}	7.46x10^{6}	7.40x10^{7}	8.38x10^{7}	1.20x10^{8}	1.57x10^{8}	1.85x10^{7}
B16S	3.78x10^{8} (98.89)	7.42x10^{6} (99.39)	7.38x10^{7} (99.72)	8.08x10^{7} (96.45)	1.15x10^{8} (96.01)	1.41x10^{8} (90.22)	1.48x10^{7} (80.16)
A16S	4.25x10^{6} (1.11)	4.56x10^{4} (0.61)	2.10x10^{5} (0.28)	2.97x10^{6} (3.55)	4.78x10^{6} (3.99)	1.53x10^{7} (9.78)	3.67x10^{6} (19.84)
aadA	3.06x10^{6} (0.81)	1.62x10^{5} (2.19)	3.92x10^{5} (0.53)	3.14x10^{5} (0.39)	7.66x10^{5} (0.66)	1.76x10^{5} (0.11)	4.24x10^{4} (0.29)
acrB	1.35x10^{4} (0.004)	2.61x10^{3} (0.035)	9.08x10^{3} (0.012)	1.50x10^{4} (0.019)	5.18x10^{4} (0.045)	2.04x10^{4} (0.013)	1.11x10^{3} (0.008)
blaCTX-M	2.11x10^{4} (0.006)	4.62x10^{2} (0.006)	2.33x10^{3} (0.003)	3.33x10^{4} (0.041)	4.75x10^{4} (0.041)	5.67x10^{4} (0.036)	6.87x10^{3} (0.046)
blaOXA2	1.30x10^{5} (0.034)	5.67x10^{2} (0.008)	1.63x10^{3} (0.002)	3.80x10^{3} (0.005)	1.19x10^{3} (0.001)	1.47x10^{3} (0.001)	2.18x10^{2} (0.002)
blaTEM1	2.49x10^{4} (0.007)	1.04x10^{3} (0.014)	2.84x10^{3} (0.004)	1.22x10^{4} (0.015)	1.73x10^{4} (0.015)	1.55x10^{4} (0.010)	5.34x10^{3} (0.036)
catQ	1.27x10^{4} (0.003)	1.38x10^{3} (0.019)	9.68x10^{3} (0.013)	6.97x10^{3} (0.009)	8.49x10^{2} (0.001)	1.47x10^{3} (0.001)	2.45x10^{2} (0.002)
mexF	2.43x10^{5} (0.064)	3.58x10^{3} (0.048)	4.45x10^{4} (0.060)	2.26x10^{4} (0.028)	1.57x10^{4} (0.014)	6.47x10^{4} (0.041)	4.77x10^{3} (0.032)
qnrS	4.57x10^{6} (1.21)	4.48x10^{5} (6.05)	2.13x10^{6} (2.88)	6.96x10^{4} (0.086)	3.01x10^{4} (0.026)	3.92x10^{4} (0.025)	3.18x10^{4} (0.215)
sul1	3.75x10^{6} (0.99)	6.37x10^{4} (0.86)	8.32x10^{5} (1.13)	5.89x10^{5} (0.73)	1.70x10^{6} (1.47)	3.19x10^{6} (2.04)	1.58x10^{5} (1.07)
sul2	3.38x10^{3} (0.0009)	1.70x10^{1} (0.0002)	4.00x10^{1} (0.0001)	1.50x10^{3} (0.0019)	1.58x10^{3} (0.0014)	1.31x10^{3} (0.0008)	5.58x10^{2} (0.0038)
tetA	3.46x10^{5} (0.092)	8.19x10^{3} (0.110)	3.87x10^{5} (0.525)	1.68x10^{4} (0.021)	1.02x10^{4} (0.009)	2.02x10^{4} (0.013)	1.27x10^{3} (0.009)
tetB	5.23x10^{3} (0.001)	5.28x10^{3} (0.071)	1.76x10^{3} (0.002)	2.30x10^{4} (0.028)	2.54x10^{4} (0.022)	2.30x10^{4} (0.015)	6.83x10^{2} (0.005)
tetQ	1.76x10^{6} (0.466)	5.45x10^{4} (0.735)	3.48x10^{5} (0.472)	1.90x10^{5} (0.235)	9.04x10^{3} (0.008)	1.76x10^{4} (0.011)	1.00x10^{4} (0.068)
tetW	8.64x10^{5} (0.229)	2.50x10^{4} (0.337)	1.66x10^{5} (0.225)	5.30x10^{3} (0.007)	2.67x10^{3} (0.002)	4.47x10^{3} (0.003)	7.72x10^{2} (0.005)

Table S5. The proportions of the most abundant bacterial genera (≥1 % at least in one sample) in the bacterial communities of studied samples. E is the effluent of the wastewater treatment plant (WWTP), SW and RW are water samples, and SS and RS are sediment samples of the stream and river, respectively. SW$_U$ and SS$_U$ are the samples taken upstream of the WWTP discharge point and RW$_U$ and RS$_U$ are the samples taken from the river upstream of the stream inflow point. The number in the subscript of the sample code shows the distance (km) of the sampling point downstream from the WWTP discharge point.

Genera	**Proportions of genera (%)**								
	Water samples			**Sediment samples**					
	E	**SW$_U$**	**SW$_{0.3}$**	**SS$_U$**	**SS$_{0.3}$**	**SS$_{2.7}$**	**SS$_{3.2}$**	**RS$_U$**	**RS$_{3.7}$**
Acidimicrobium	0.014	2.711	0.123	0.028	0.016	0.063	0.050	0.042	0.031
Acidovorax	0.807	2.437	0.601	0.309	0.335	0.364	0.506	0.279	0.316
Anaeromyxobacter	0.090	0.084	0.136	0.902	0.202	0.459	0.581	0.767	1.567
Aquabacterium	1.106	0.729	0.779	0.335	0.373	0.502	0.646	0.351	0.435
Bradyrhizobium	0.514	0.336	0.633	2.009	0.651	1.741	1.525	2.343	1.277
Ca. Accumulibacter	2.413	0.174	4.314	0.595	1.445	0.424	0.520	0.511	0.489
Ca. Nanopelagicus	0.001	7.134	0.284	0.002	0.001	0.001	0.001	0.002	0.001
Ca. Planktophila	0.003	7.834	0.344	0.005	0.004	0.006	0.005	0.008	0.005
Chitinophaga	0.659	0.224	0.698	0.348	1.008	0.360	0.380	0.318	0.392
Curvibacter	0.575	1.254	0.392	0.279	0.186	0.254	0.406	0.232	0.333
Dechloromonas	2.247	0.434	1.876	1.393	1.016	0.252	0.556	0.319	0.407
Flavobacterium	1.444	2.386	1.518	0.840	2.254	0.650	0.898	0.729	0.922
Geobacter	0.142	0.162	0.262	2.020	0.570	0.395	1.152	1.017	1.840
Geothrix	2.696	0.017	2.624	0.133	3.323	0.078	0.077	0.075	0.110
Gordonia	4.441	0.118	1.042	0.084	1.182	0.109	0.087	0.101	0.084
Haliscomenobacter	0.656	0.056	0.711	0.034	1.115	0.073	0.107	0.045	0.052
Hydrogenophaga	0.461	1.283	0.577	0.329	0.390	0.388	0.624	0.297	0.312
Ideonella	1.115	0.411	1.131	0.495	0.878	0.816	0.996	0.588	0.771
Limnohabitans	0.485	7.800	0.628	0.236	0.207	0.290	0.374	0.246	0.267
Mycobacterium	0.651	1.703	0.599	0.649	0.494	0.871	0.613	0.773	0.582
Nannocystis	1.247	0.035	0.446	0.059	0.079	0.078	0.081	0.064	0.062
Nitrospira	1.223	0.303	1.284	2.022	1.116	3.151	2.035	2.022	1.932
Novosphingobium	0.827	1.565	0.809	0.289	0.440	1.307	1.541	0.526	0.526
Pedobacter	0.709	0.462	0.763	0.395	1.156	0.348	0.392	0.330	0.433
Polynucleobacter	0.084	3.988	0.230	0.099	0.057	0.102	0.107	0.121	0.094
Pseudomonas	1.569	1.618	1.255	1.260	1.046	1.363	1.441	1.330	1.259
Rhodoferax	2.262	1.728	1.210	0.541	0.537	0.626	0.826	0.431	0.564
Rhodoluna	0.003	1.706	0.068	0.003	0.003	0.004	0.004	0.013	0.005
Rubrivivax	0.853	0.535	0.979	0.645	0.783	0.941	1.250	0.713	0.972
Sphingomonas	0.678	1.065	0.723	0.562	0.708	0.932	1.062	0.653	0.593
Streptomyces	1.566	1.186	1.681	2.414	1.663	2.604	2.032	2.765	2.411
Syntrophorhabdus	0.024	0.040	0.148	1.306	0.451	0.087	0.126	0.556	0.980
Tetrasphaera	1.239	0.066	1.689	0.061	1.209	0.103	0.084	0.073	0.077
Variovorax	0.794	0.741	0.750	0.772	0.562	1.108	1.225	0.944	0.872

Table S6. The proportions of the most abundant archaeal genera (≥1 % at least in one sample) in the archaeal communities of studied samples. E is the effluent of the wastewater treatment plant (WWTP), SW and RW are water samples, and SS and RS are sediment samples of the stream and river, respectively. SW_U and SS_U are the samples taken upstream of the WWTP discharge point and RW_U and RS_U are the samples taken from the river upstream of the stream inflow point. The number in the subscript of the sample code shows the distance (km) of the sampling point downstream from the WWTP discharge point.

Genera	**Proportions of genera (%)**								
	Water samples			**Sediment samples**					
	E	**SW_U**	**$SW_{0.3}$**	**SS_U**	**$SS_{0.3}$**	**$SS_{2.7}$**	**$SS_{3.2}$**	**RS_U**	**$RS_{3.7}$**
Ca. Methanofastidiosum	1.195	0.943	1.131	0.651	1.685	0.696	0.863	0.787	0.744
Ca. Methanoperedens	2.499	1.202	1.018	1.327	1.095	2.376	2.404	5.201	1.765
Ca. Nitrosocosmicus	0.530	0.982	0.274	0.915	0.333	4.712	2.852	3.230	0.815
Ca. Nitrosopelagicus	0.167	2.326	0.072	0.026	0.043	0.075	0.106	0.100	0.036
Ca. Nitrosotenuis	0.502	0.896	0.190	0.281	0.197	1.267	3.006	1.126	0.355
Halobellus	0.803	1.030	0.321	0.304	0.212	0.940	0.914	0.569	0.272
Halococcus	1.070	0.959	0.366	0.350	0.216	1.124	1.109	0.620	0.341
Haloferax	1.830	1.375	0.606	0.587	0.464	1.803	1.695	1.141	0.535
Halorubrum	3.660	3.379	1.350	1.097	0.933	3.617	3.448	2.000	1.067
Halorussus	1.023	0.951	0.387	0.382	0.318	1.241	1.161	0.682	0.353
Methanobacterium	3.785	3.364	2.262	5.315	2.686	3.256	3.913	3.761	2.707
Methanobrevibacter	2.585	2.491	0.900	0.690	0.951	1.040	1.126	0.863	0.740
Methanocella	2.103	1.595	1.154	1.806	1.061	1.743	2.068	1.893	1.499
Methanococcus	0.655	1.187	0.319	0.269	0.264	0.375	0.360	0.331	0.288
Methanocorpusculum	1.864	0.362	0.760	0.318	0.670	0.246	0.202	0.212	0.294
Methanoculleus	2.767	2.106	2.368	3.421	2.668	2.617	2.855	3.080	3.339
Methanofollis	1.257	0.778	1.079	1.478	1.152	1.078	1.168	1.305	1.425
Methanolinea	0.621	0.464	0.998	1.993	1.384	0.728	0.613	1.207	1.822
Methanolobus	2.647	2.036	1.323	1.367	1.181	1.734	2.208	1.848	1.412
Methanomassiliicoccus	1.042	1.163	2.977	2.341	2.564	2.370	1.281	1.459	1.816
Methanomethylovorans	0.793	0.644	0.504	0.628	0.450	0.768	1.120	0.779	0.584
Methanoregula	2.595	3.977	17.909	20.061	21.570	3.543	3.883	9.595	20.182
Methanosarcina	10.035	6.995	7.542	6.257	7.121	7.828	8.563	7.340	4.919
Methanosphaerula	0.745	0.550	1.160	1.479	1.363	0.745	0.729	0.994	1.402
Methanospirillum	2.470	1.250	2.472	2.059	3.250	1.238	1.349	1.445	1.879
Methanothrix	9.614	14.249	32.502	25.738	31.902	9.046	9.826	17.168	30.144
Nitrosarchaeum	0.378	0.912	0.140	0.106	0.179	1.167	0.702	0.319	0.186
Nitrosopumilus	0.951	2.334	0.358	0.282	0.301	0.883	1.065	0.633	0.344
Nitrososphaera	0.683	0.534	0.228	0.613	0.337	4.176	2.291	2.672	0.762
Salinigranum	1.085	0.707	0.353	0.306	0.278	1.038	0.942	0.564	0.270
Thermococcus	2.031	1.847	0.979	0.941	0.786	1.622	1.712	1.459	1.010

Table S7. The abundances of bacterial and archaeal 16S rRNA genes (B16S and A16S, respectively) and antibiotic resistance genes (ARGs) in the studied water and sediment samples (A and B, respectively). E is the effluent of the wastewater treatment plant (WWTP), SW and RW are water samples, and SS and RS are sediment samples of the stream and river, respectively. SW$_{U}$ and SS$_{U}$ are the samples taken upstream of the WWTP discharge point and RW$_{U}$ and RS$_{U}$ are the samples taken from the river upstream of the stream inflow point. The number in the subscript of the sample code shows the distance (km) of the sampling point downstream from the WWTP discharge point. <LOQ denotes values below the limit of quantification.

Sample	**Abundances of target genes**															
	B16S	**A16S**	***aadA***	***acrB***	***bla CTX-M***	***bla OXA2***	***bla TEM1***	***catQ***	***mexF***	***qnrS***	***sul1***	***sul2***	***tetA***	***tetB***	***tetQ***	***tetW***
A (copies/mL)																
E	1.41x10^{8}	1.53x10^{7}	1.76x10^{5}	2.04x10^{4}	5.67x10^{4}	1.47x10^{3}	1.55x10^{4}	1.47x10^{3}	6.47x10^{4}	3.92x10^{4}	3.19x10^{6}	1.31x10^{3}	2.02x10^{4}	2.30x10^{4}	1.76x10^{4}	4.47x10^{3}
SW$_{U}$	3.58x10^{5}	2.25x10^{4}	<LOQ	1.27x10^{2}	2.91x10^{2}	<LOQ	5.53x10^{3}	<LOQ	5.75x10^{2}	<LOQ	<LOQ	<LOQ	1.28x10^{3}	1.36x10^{3}	<LOQ	5.00x10^{1}
SW$_{0.3}$	5.94x10^{6}	1.30x10^{6}	2.91x10^{3}	1.31x10^{3}	1.03x10^{4}	3.63x10^{1}	6.14x10^{3}	2.36x10^{2}	1.61x10^{4}	<LOQ	3.68x10^{4}	3.80x10^{2}	3.50x10^{3}	3.34x10^{3}	5.05x10^{2}	9.23x10^{2}
SW$_{2.7}$	4.80x10^{5}	6.46x10^{4}	<LOQ	1.77x10^{2}	8.16x10^{2}	<LOQ	6.19x10^{3}	<LOQ	1.13x10^{3}	<LOQ	3.25x10^{1}	2.12x10^{1}	2.24x10^{3}	2.20x10^{3}	<LOQ	4.02x10^{1}
SW$_{3.2}$	6.67x10^{5}	4.73x10^{4}	<LOQ	1.31x10^{2}	1.18x10^{3}	<LOQ	5.92x10^{3}	<LOQ	1.19x10^{3}	<LOQ	4.72x10^{1}	1.73x10^{1}	2.16x10^{3}	2.64x10^{3}	<LOQ	3.14x10^{1}
RW$_{U}$	3.12x10^{5}	2.32x10^{4}	<LOQ	1.01x10^{2}	2.45x10^{2}	<LOQ	4.31x10^{3}	<LOQ	2.63x10^{2}	<LOQ	<LOQ	<LOQ	1.44x10^{3}	1.52x10^{3}	<LOQ	4.00x10^{1}
RW$_{3.7}$	6.26x10^{5}	3.12x10^{4}	<LOQ	5.83x10^{1}	3.54x10^{2}	<LOQ	6.06x10^{3}	<LOQ	5.71x10^{2}	<LOQ	<LOQ	<LOQ	4.29x10^{3}	2.96x10^{3}	<LOQ	5.70x10^{1}
B (copies/g dw)																
SS$_{U}$	1.42x10^{10}	1.13x10^{9}	2.44x10^{5}	3.85x10^{7}	9.17x10^{7}	9.49x10^{4}	2.59x10^{6}	<LOQ	3.50x10^{7}	<LOQ	3.11x10^{5}	4.42x10^{5}	2.41x10^{7}	7.80x10^{5}	<LOQ	9.81x10^{5}
SS$_{0.3}$	2.60x10^{10}	8.02x10^{9}	1.73x10^{7}	7.71x10^{7}	1.02x10^{8}	8.41x10^{5}	3.07x10^{6}	3.92x10^{6}	7.78x10^{7}	<LOQ	9.25x10^{7}	1.84x10^{6}	1.84x10^{7}	1.93x10^{5}	6.70x10^{6}	2.86x10^{6}
SS$_{2.7}$	2.10x10^{9}	2.37x10^{8}	2.00x10^{5}	1.16x10^{7}	2.15x10^{7}	2.86x10^{4}	1.17x10^{6}	<LOQ	1.21x10^{7}	<LOQ	4.39x10^{5}	1.07x10^{5}	9.31x10^{6}	2.94x10^{5}	<LOQ	1.43x10^{5}
SS$_{3.2}$	1.22x10^{10}	1.01x10^{9}	1.22x10^{6}	4.61x10^{7}	7.25x10^{7}	1.90x10^{5}	1.65x10^{6}	<LOQ	8.94x10^{7}	<LOQ	2.82x10^{6}	4.85x10^{5}	1.59x10^{7}	4.51x10^{5}	<LOQ	9.36x10^{5}
RS$_{U}$	8.67x10^{9}	1.37x10^{9}	2.91x10^{5}	3.01x10^{7}	5.94x10^{7}	9.05x10^{4}	2.07x10^{6}	<LOQ	5.76x10^{7}	<LOQ	1.58x10^{5}	3.97x10^{5}	2.07x10^{7}	4.50x10^{5}	<LOQ	9.30x10^{5}
RS$_{3.7}$	3.80x10^{10}	8.89x10^{9}	2.03x10^{6}	1.08x10^{8}	2.15x10^{8}	3.66x10^{5}	4.09x10^{6}	<LOQ	1.69x10^{8}	<LOQ	1.31x10^{7}	1.52x10^{6}	4.34x10^{7}	1.03x10^{6}	<LOQ	3.20x10^{6}

Table S8. The relative abundances of archaea (arc%) and antibiotic resistance genes (ARGs) in prokaryotic communities of water and sediment samples (A and B, respectively). E is the effluent of the wastewater treatment plant (WWTP), SW and RW are water samples, and SS and RS are sediment samples of the stream and river, respectively. $\mathrm{SW_U}$ and $\mathrm{SS_U}$ are the samples taken upstream of the WWTP discharge point and $\mathrm{RW_U}$ and $\mathrm{RS_U}$ are the samples taken from the river upstream of the stream inflow point. The number in the subscript of the sample code shows the distance (km) of the sampling point downstream from the WWTP discharge point. <LOQ denotes values below the limit of quantification.

Sample	**Relative abundances of target genes (%)**													
	arc%	***aadA***	***acrB***	***bla CTX-M***	***bla OXA2***	***bla TEM1***	***catQ***	***mexF***	***qnrS***	***sul1***	***sul2***	***tetA***	***tetB***	***tetQ***	***tetW***
A															
E	9.78	0.1125	0.0130	0.0362	0.0009	0.0099	0.0009	0.0413	0.0250	2.0368	0.0008	0.0129	0.0147	0.0112	0.0029
$\mathrm{SW_U}$	5.92	<LOQ	0.0335	0.0765	<LOQ	1.4543	<LOQ	0.1513	<LOQ	<LOQ	<LOQ	0.3368	0.3580	<LOQ	0.0132
$\mathrm{SW_{0.3}}$	18.00	0.0401	0.0181	0.1424	0.0005	0.0848	0.0033	0.2217	<LOQ	0.5074	0.0052	0.0483	0.0461	0.0070	0.0127
$\mathrm{SW_{2.7}}$	11.87	<LOQ	0.0326	0.1498	<LOQ	1.1370	<LOQ	0.2077	<LOQ	0.0060	0.0039	0.4114	0.4046	<LOQ	0.0074
$\mathrm{SW_{3.2}}$	6.62	<LOQ	0.0183	0.1652	<LOQ	0.8285	<LOQ	0.1667	<LOQ	0.0066	0.0024	0.3026	0.3696	<LOQ	0.0044
$\mathrm{RW_U}$	6.93	<LOQ	0.0302	0.0731	<LOQ	1.2868	<LOQ	0.0786	<LOQ	<LOQ	<LOQ	0.4288	0.4555	<LOQ	0.0120
$\mathrm{RW_{3.7}}$	4.75	<LOQ	0.0089	0.0539	<LOQ	0.9212	<LOQ	0.0869	<LOQ	<LOQ	<LOQ	0.6527	0.4497	<LOQ	0.0087
B															
$\mathrm{SS_U}$	7.39	0.0016	0.2507	0.5976	0.0006	0.0169	<LOQ	0.2281	<LOQ	0.0020	0.0029	0.1571	0.0051	<LOQ	0.0064
$\mathrm{SS_{0.3}}$	23.54	0.0509	0.2264	0.3001	0.0025	0.0090	0.0115	0.2285	<LOQ	0.2718	0.0054	0.0541	0.0006	0.0197	0.0084
$\mathrm{SS_{2.7}}$	10.12	0.0085	0.4947	0.9176	0.0012	0.0498	<LOQ	0.5184	<LOQ	0.0188	0.0046	0.3977	0.0126	<LOQ	0.0061
$\mathrm{SS_{3.2}}$	7.66	0.0092	0.3487	0.5476	0.0014	0.0125	<LOQ	0.6757	<LOQ	0.0213	0.0037	0.1199	0.0034	<LOQ	0.0071
$\mathrm{RS_U}$	13.67	0.0029	0.2999	0.5910	0.0009	0.0206	<LOQ	0.5731	<LOQ	0.0016	0.0039	0.2056	0.0045	<LOQ	0.0093
$\mathrm{RS_{3.7}}$	18.96	0.0043	0.2303	0.4581	0.0008	0.0087	<LOQ	0.3607	<LOQ	0.0279	0.0032	0.0926	0.0022	<LOQ	0.0068

Table S9. Proportions of antibiotic resistance genes (ARGs, per 16S rRNA reads) in the metagenomes of studied samples. E is the effluent of the wastewater treatment plant (WWTP), SW and RW are water samples, and SS and RS are sediment samples of the stream and river, respectively. SW$_U$ and SS$_U$ are the samples taken upstream of the WWTP discharge point and RW$_U$ and RS$_U$ are the samples taken from the river upstream of the stream inflow point. The number in the subscript of the sample code shows the distance (km) of the sampling point downstream from the WWTP discharge point. ARGs subjected to the qPCR quantification are marked in bold. ABC – ATP-binding cassette type efflux complex; BAC – bacitracin; CHL – chloramphenicol; F – Fosfomycin; FOS – fosmidomycin; K – kasugamycin; MATE – multidrug and toxic compound extrusion type efflux complex; MFS – major facilitator superfamily efflux complex; MLS – macrolide-lincosamide-streptogramin; P – puromycin; Q – quinolone; R – rifamycin; RND – resistance-nodulation-division superfamily efflux complex; SMR – small multidrug resistance transporter complex; SUL – sulfonamide; TMP – trimethoprim.

Antibiotic resistance			**Proportion of genes (%)**								
Resistance type		**Resistance mechanism**	**Water**			**Stream sediment**					
	Resistance subtype (ARG)		**E**	**SW$_U$**	**SW$_{0.3}$**	**SS$_U$**	**SS$_{0.3}$**	**SS$_{2.7}$**	**SS$_{3.2}$**	**RS$_U$**	**RS$_{3.7}$**
Aminoglycoside	*aac(2´)-I*	Inactivation	0	0	0	0	0.035	0.043	0	0.021	0
	aac(3)-I	Inactivation	0.066	0.009	0.014	0.100	0.027	0.092	0.017	0.063	0.057
	aac(3)-IIIa	Inactivation	0.011	0	0	0	0	0	0.033	0	0
	aac(3)-IV	Inactivation	0	0	0	0.010	0	0.023	0.021	0.032	0.024
	aac(6')-31	Inactivation	0.034	0	0.022	0	0	0	0	0	0.015
	aac(6´)-I	Inactivation	0.015	0.012	0	0	0	0	0	0	0.017
	aac(6´)-II	Inactivation	0.121	0.082	0.103	0.020	0.028	0.196	0.113	0.125	0
	aad(6)	Inactivation	0.022	0	0	0	0	0	0	0	0
	aadA	**Inactivation**	**1.168**	**0**	**0.601**	**0**	**0.247**	**0.016**	**0.039**	**0**	**0.025**
	aadE	Inactivation	0.011	0	0.014	0	0.009	0	0.015	0	0
	ant(2´´)-I	Inactivation	0.018	0	0.029	0	0	0	0	0	0
	ant(9)-I	Inactivation	0	0	0	0	0.009	0	0	0	0
	aph(3´´´)-III	Inactivation	0	0	0.015	0	0	0	0	0	0
	aph(3´´)-I	Inactivation	0.142	0	0.193	0	0.042	0	0	0	0
	aph(3´)-I	Inactivation	0	0.045	0	0	0	0	0	0	0
	aph(6)-I	Inactivation	0.174	0	0.267	0	0.137	0	0	0	0
BA	*bacA*	Target alteration	6.203	6.912	5.386	4.033	3.226	5.665	7.484	4.962	4.002

Antibiotic resistance			**Proportion of genes (%)**								
Resistance type		**Resistance mechanism**	**Water**			**Stream sediment**					
	Resistance subtype (ARG)		**E**	**SW$_{U}$**	**SW$_{0.3}$**	**SS$_{U}$**	**SS$_{0.3}$**	**SS$_{2.7}$**	**SS$_{3.2}$**	**RS$_{U}$**	**RS$_{3.7}$**
	bcrA	Efflux: ABC	0	0.427	0.033	0.011	0.015	0.021	0.026	0.043	0.035
β-lactam	*AER-1*	Inactivation	0.040	0	0.100	0	0.028	0	0	0	0
	BEL-2	Inactivation	0.062	0	0.041	0	0	0	0	0	0
	BEL-3	Inactivation	0.098	0	0.041	0	0	0	0	0	0
	CfxA2	Inactivation	0.047	0	0.012	0	0	0	0	0	0
	FEZ-1	Inactivation	0	0	0	0	0.044	0	0.015	0	0
	IMP-5	Inactivation	0.440	0	0.114	0	0	0	0.017	0	0
	IMP-13	Inactivation	0.135	0	0	0	0	0	0	0	0
	IMP-15	Inactivation	0.050	0	0	0	0	0	0	0	0
	IMP-16	Inactivation	0	0	0.016	0	0	0	0	0	0
	IMP-24	Inactivation	0.010	0	0	0	0	0	0	0	0
	IMP-28	Inactivation	0.156	0	0	0	0	0	0	0	0
	IMP-29	Inactivation	0.985	0	0.150	0	0	0	0	0	0
	IMP-33	Inactivation	0	0	0	0	0	0	0.017	0	0
	IMP-37	Inactivation	0.443	0	0	0	0	0	0	0	0
	JOHN-1	Inactivation	0	0.010	0.008	0	0	0.036	0.011	0	0
	KHM-1	Inactivation	0	0.010	0	0	0	0.012	0	0	0
	LCR-1	Inactivation	0	0	0.046	0	0	0	0	0	0
	LEN-21	Inactivation	0	0	0.014	0	0	0	0	0	0
	LRA-1	Inactivation	0	0.008	0	0	0	0	0.014	0	0
	LRA-2	Inactivation	0	0	0.012	0	0.021	0.059	0.185	0	0.086
	LRA-3	Inactivation	0	0	0	0	0	0.027	0	0.012	0
	LRA-5	Inactivation	0	0	0	0	0	0.013	0	0	0
	LRA-8	Inactivation	0	0	0	0	0	0.008	0	0.013	0.013
	LRA-9	Inactivation	0	0	0	0	0	0	0.028	0	0
	LRA-12	Inactivation	0.010	0	0.067	0	0.069	0.030	0.042	0	0.026

Antibiotic resistance			**Proportion of genes (%)**								
Resistance type		**Resistance mechanism**	**Water**			**Stream sediment**					
	Resistance subtype (ARG)		**E**	**SW_{U}**	**$SW_{0.3}$**	**SS_{U}**	**$SS_{0.3}$**	**$SS_{2.7}$**	**$SS_{3.2}$**	**RS_{U}**	**$RS_{3.7}$**
	LRA-17	Inactivation	0	0	0	0	0	0.010	0.011	0	0
	LRA-19	Inactivation	0.020	0	0	0	0.044	0	0.027	0	0
	MOX-6	Inactivation	0	0	0.010	0	0	0	0	0	0
	OXA-2	Inactivation	0.152	0.048	0.108	0	0.079	0	0.039	0.015	0
	OXA-3	Inactivation	0.011	0	0	0	0	0	0	0.011	0
	OXA-5	Inactivation	0.202	0	0.058	0	0.063	0.017	0.016	0	0
	OXA-9	Inactivation	0.419	0	0.089	0	0.012	0	0	0	0
	OXA-10	Inactivation	0.222	0	0.090	0	0.026	0	0.017	0	0
	OXA-12	Inactivation	0	0.029	0	0	0	0	0	0	0
	OXA-13	Inactivation	0.023	0	0	0	0	0	0	0	0
	OXA-17	Inactivation	0	0	0.015	0	0	0	0	0	0
	OXA-20	Inactivation	0.175	0.009	0.104	0	0.013	0	0.016	0	0
	OXA-21	Inactivation	0.021	0	0.035	0	0.018	0	0	0	0
	OXA-34	Inactivation	0	0	0.015	0.013	0	0	0.015	0	0
	OXA-36	Inactivation	0	0	0	0.010	0	0	0	0	0
	OXA-37	Inactivation	0.069	0	0.074	0	0	0.017	0	0	0
	OXA-46	Inactivation	0.045	0	0.015	0	0.020	0	0	0	0
	OXA-47	Inactivation	0.011	0	0	0	0	0	0	0	0
	OXA-53	Inactivation	0.044	0	0	0	0	0	0	0	0
	OXA-54	Inactivation	0.011	0	0	0	0	0	0	0	0
	OXA-118	Inactivation	0.031	0.010	0	0	0.048	0	0	0	0
	OXA-119	Inactivation	0.033	0	0.059	0	0.025	0	0.016	0	0.015
	OXA-129	Inactivation	0.094	0	0.055	0	0.051	0	0.015	0	0
	OXA-141	Inactivation	0	0	0	0	0	0	0.015	0.015	0
	OXA-142	Inactivation	0.011	0	0	0	0.013	0	0	0	0
	OXA-147	Inactivation	0	0	0.015	0	0	0	0	0	0

Antibiotic resistance			**Proportion of genes (%)**								
Resistance type		**Resistance mechanism**	**Water**			**Stream sediment**					
	Resistance subtype (ARG)		**E**	**$\mathrm{SW_{U}}$**	**$\mathrm{SW_{0.3}}$**	**$\mathrm{SS_{U}}$**	**$\mathrm{SS_{0.3}}$**	**$\mathrm{SS_{2.7}}$**	**$\mathrm{SS_{3.2}}$**	**$\mathrm{RS_{U}}$**	**$\mathrm{RS_{3.7}}$**
	OXA-183	Inactivation	0.009	0	0	0	0	0	0	0	0
	OXA-205	Inactivation	0.081	0	0.088	0	0	0	0.013	0.012	0
	OXA-209	Inactivation	0.022	0.066	0	0	0.061	0	0	0.015	0.014
	OXA-226	Inactivation	0.022	0	0	0	0	0.016	0	0	0
	OXA-334	Inactivation	0.011	0	0	0	0	0	0	0	0
	PBP-1A	Target alteration	0	0	0	0	0.005	0	0	0	0
	PER-1	Inactivation	0	0.009	0	0	0	0	0	0	0
	PER-6	Inactivation	0	0.009	0	0	0	0	0	0	0
	SIM-1	Inactivation	0	0.010	0	0	0	0	0	0	0
	TEM-1	Inactivation	0.017	2.163	0.041	0.013	0.077	0	0	0	0.029
	TEM-6	Inactivation	0	0.401	0	0	0.012	0	0	0	0
	TEM-29	Inactivation	0	0.027	0	0	0	0	0	0	0
	TEM-43	Inactivation	0	0.036	0	0	0	0	0	0	0
	TEM-63	Inactivation	0	0.197	0	0	0	0	0	0	0
	TEM-75	Inactivation	0.012	0.330	0	0	0	0	0	0	0
	TEM-89	Inactivation	0	0.144	0	0	0	0	0	0	0
	TEM-91	Inactivation	0	0.531	0.010	0.017	0.012	0.009	0	0	0
	TEM-95	Inactivation	0	0.009	0	0	0	0	0	0	0
	TEM-106	Inactivation	0	0.049	0	0	0	0	0	0	0
	TEM-117	Inactivation	0	1.785	0.031	0.015	0.014	0.018	0	0	0
	TEM-118	Inactivation	0	0.798	0.015	0	0.026	0.017	0	0	0
	TEM-123	Inactivation	0	0.018	0	0	0	0	0	0	0
	TEM-154	Inactivation	0	0.055	0	0.013	0	0	0	0	0.014
	TEM-156	Inactivation	0	0.009	0	0	0	0	0	0	0
	TEM-157	Inactivation	0.011	1.113	0.028	0	0.036	0.031	0.044	0	0
	TEM-171	Inactivation	0	0.035	0.056	0	0	0	0	0	0

Antibiotic resistance			**Proportion of genes (%)**								
Resistance type		**Resistance mechanism**	**Water**			**Stream sediment**					
	Resistance subtype (ARG)		**E**	**SW_U**	**$SW_{0.3}$**	**SS_U**	**$SS_{0.3}$**	**$SS_{2.7}$**	**$SS_{3.2}$**	**RS_U**	**$RS_{3.7}$**
	TEM-177	Inactivation	0	0.318	0.028	0	0.012	0	0	0	0
	TEM-178	Inactivation	0	0.322	0	0	0	0	0	0	0
	TEM-183	Inactivation	0	0.009	0	0	0	0	0	0	0
	TEM-184	Inactivation	0	0.018	0	0	0	0	0	0	0
	TEM-185	Inactivation	0	0.009	0	0	0	0	0	0	0
	TEM-187	Inactivation	0	0.824	0	0	0.033	0	0.015	0	0.014
	TEM-193	Inactivation	0	0.009	0	0	0	0	0	0	0
	TEM-195	Inactivation	0	0.118	0	0	0	0	0	0	0
	TEM-197	Inactivation	0	0.009	0	0	0	0	0	0	0
	TEM-205	Inactivation	0.011	0.323	0.014	0	0	0	0	0	0
	TEM-209	Inactivation	0	0.132	0.014	0	0	0	0	0	0
	THIN-B	Inactivation	0	0	0	0.006	0	0	0.021	0.025	0.012
	VEB-1	Inactivation	0	0	0	0	0.051	0	0	0	0
	ampC	Inactivation	0.006	0	0	0	0	0	0	0	0
	penA	Target alteration	0	0	0	0	0	0	0.005	0	0
	Class A β-lactamase	Inactivation	0.251	0	0.249	0	0.098	0.029	0.014	0	0
	Class B β-lactamase	Inactivation	0.012	0.080	0.016	0	0	0	0	0	0
	Class C β-lactamase	Inactivation	0.015	0.030	0.053	0	0.022	0	0.009	0	0
	metallo-β-lactamase	Inactivation	0.058	0	0.012	0	0.012	0.015	0	0	0
CHL	*catA*	Inactivation	0	0	0.010	0	0	0	0	0	0
	catB	Inactivation	0.015	0	0	0	0	0	0.011	0	0
	Chloramphenicol acetyltransferase cat	Inactivation	0.015	0	0	0	0.056	0	0.014	0.027	0.018
	Chloramphenicol exporter	Efflux: MFS	0.031	0	0.020	0	0	0.011	0	0	0
	floR	Efflux: MFS	0.038	0	0.056	0	0	0	0	0	0
F	*fosX*	Inactivation	0.018	0	0.022	0.019	0	0	0	0.016	0.033
FO	*rosA*	Efflux: MFS	0.243	0.143	0.403	0.354	0.321	0.566	0.324	0.360	0.259

Antibiotic resistance			**Proportion of genes (%)**								
Resistance type		**Resistance mechanism**	**Water**			**Stream sediment**					
	Resistance subtype (ARG)		**E**	**SW$_U$**	**SW$_{0.3}$**	**SS$_U$**	**SS$_{0.3}$**	**SS$_{2.7}$**	**SS$_{3.2}$**	**RS$_U$**	**RS$_{3.7}$**
	rosB	Efflux: MFS	0.586	0.248	0.497	0.505	0.365	0.692	0.890	0.601	0.311
K	*ksgA*	Inactivation	0.019	0.038	0.014	0	0.008	0.046	0	0	0
Macrolide-lincosamide-streptogramin (MLS)	*ereA*	Inactivation	0.294	0	0.072	0	0.008	0	0	0	0
	erm(35)	Target alteration	0.033	0	0.036	0	0.041	0	0	0	0
	erm(38)	Target alteration	0	0	0	0	0	0.011	0	0	0
	erm(39)	Target alteration	0	0	0.016	0	0	0.018	0	0	0
	ermB	Target alteration	0.048	0	0.016	0	0.091	0	0	0	0
	ermF	Target alteration	0.315	0	0.220	0	0.086	0	0	0	0
	ermX	Target alteration	0	0	0	0	0.013	0	0	0	0
	lsa	Target protection	0	0	0.007	0.008	0.041	0	0.008	0	0
	macA	Efflux: ABC	0.122	0.068	0.116	0.015	0.039	0.036	0.111	0.052	0.045
	macB	Efflux: ABC	0.999	0.455	1.036	1.512	0.977	1.767	1.690	1.829	1.543
	mefA	Efflux: MFS	0.038	0	0.020	0	0.017	0	0	0	0.009
	mphA	Inactivation	0.058	0	0.126	0	0.195	0	0	0	0
	msrC	Target protection	0.004	0	0.004	0	0	0	0	0	0
	tlcC	Target protection	0.003	0	0.009	0	0	0	0	0	0
	vatA	Inactivation	0.008	0	0.034	0	0	0	0	0	0
	vatB	Inactivation	0	0	0.037	0	0.032	0.042	0.014	0	0
ABC	*ABC transporter*	Efflux: ABC	0.311	0.206	0.347	0.412	0.257	0.712	0.576	0.618	0.371
	bcr	Efflux: ABC	0	0	0.010	0	0.017	0	0	0	0
RND	*tolC*	Regulation	0	0.040	0.041	0	0.008	0	0	0	0
	acrA	Efflux: RND	0	0.004	0.026	0.043	0.014	0.006	0.009	0.015	0.069
	acrB	**Efflux: RND**	**0.348**	**0.278**	**0.553**	**0.847**	**0.398**	**0.391**	**0.665**	**0.629**	**0.591**
	acrF	Efflux: RND	0.009	0.010	0.015	0.029	0.019	0.013	0.032	0.012	0.019
	adeB	Efflux: RND	0.018	0.057	0.046	0.013	0.023	0.004	0.012	0.016	0.023
	adeC	Efflux: RND	0	0	0.004	0	0	0	0	0	0

Antibiotic resistance			**Proportion of genes (%)**								
Resistance type		**Resistance mechanism**	**Water**			**Stream sediment**					
	Resistance subtype (ARG)		**E**	**SW_U**	**$SW_{0.3}$**	**SS_U**	**$SS_{0.3}$**	**$SS_{2.7}$**	**$SS_{3.2}$**	**RS_U**	**$RS_{3.7}$**
	adeJ	Efflux: RND	0.006	0.016	0.028	0.025	0.013	0.008	0.018	0.021	0.029
	adeK	Efflux: RND	0.007	0	0	0	0	0	0	0	0
	amrB	Efflux: RND	0.081	0.058	0.078	0.054	0.043	0.087	0.065	0.031	0.040
	bpeF	Efflux: RND	0.008	0.029	0.030	0.006	0.021	0.067	0.061	0.030	0.032
	ceoB	Efflux: RND	0.009	0.070	0.036	0.038	0.032	0.115	0.070	0.051	0.036
	cmeB	Efflux: RND	0.085	0.017	0.031	0.027	0.013	0.035	0.037	0.016	0.033
	mdtA	Efflux: RND	0.007	0.028	0	0	0.004	0	0.005	0	0
	mdtB	Efflux: RND	0.431	0.500	0.618	0.689	0.523	1.308	0.936	1.034	0.677
	mdtC	Efflux: RND	0.278	0.239	0.315	0.321	0.270	0.641	0.490	0.469	0.319
	mdtD	Efflux: RND	0.013	0.016	0	0	0	0	0	0	0
	mdtE	Efflux: RND	0	0.014	0	0	0	0	0	0	0
	mdtF	Efflux: RND	0.057	0.032	0.047	0.024	0.005	0.028	0.047	0.023	0.028
	mexA	Efflux: RND	0	0.051	0.019	0.037	0.006	0.012	0.041	0.020	0.043
	mexB	Efflux: RND	0.116	0.094	0.173	0.165	0.094	0.075	0.134	0.102	0.100
	mexC	Efflux: RND	0.392	0.063	0.220	0.035	0.044	0.076	0.037	0.034	0.084
	mexD	Efflux: RND	1.094	0.096	0.415	0.077	0.073	0.052	0.063	0.051	0.057
	mexE	Efflux: RND	0.052	0.037	0.048	0.088	0.107	0.022	0.098	0.042	0.084
	mexF	**Efflux: RND**	**0.411**	**0.396**	**0.515**	**0.667**	**0.410**	**1.128**	**1.132**	**0.810**	**0.630**
	mexI	Efflux: RND	0.055	0.025	0.088	0.192	0.096	0.200	0.186	0.161	0.160
	mexT	Efflux: RND	1.062	0.092	0.258	0.012	0.024	0.089	0.083	0.012	0
	mexW	Efflux: RND	0.204	0.239	0.243	0.204	0.160	0.324	0.278	0.171	0.138
	mexY	Efflux: RND	0.036	0.032	0.018	0.021	0.008	0.010	0.020	0.024	0.035
	mtrE	Efflux: RND	0.007	0	0	0.007	0	0.028	0.008	0	0.013
	opcM	Efflux: RND	0.004	0	0	0	0	0	0	0	0
	oprA	Efflux: RND	0.006	0.033	0.014	0	0.011	0	0.012	0	0.005
	oprC	Efflux: RND	0.013	0.028	0.021	0.019	0.022	0.028	0.028	0.024	0.011

Antibiotic resistance			**Proportion of genes (%)**								
Resistance type		**Resistance mechanism**	**Water**			**Stream sediment**					
	Resistance subtype (ARG)		**E**	**SW$_{U}$**	**SW$_{0.3}$**	**SS$_{U}$**	**SS$_{0.3}$**	**SS$_{2.7}$**	**SS$_{3.2}$**	**RS$_{U}$**	**RS$_{3.7}$**
	oprJ	Efflux: RND	0.123	0.004	0.112	0	0.026	0	0	0	0
	oprM	Efflux: RND	0.101	0.040	0.193	0.032	0.070	0.053	0.060	0.070	0.042
	oprN	Efflux: RND	0.013	0.035	0.008	0	0.007	0	0	0	0
	sdeY	Efflux: RND	0	0	0	0	0	0	0	0.004	0
	smeB	Efflux: RND	0.005	0.022	0.015	0.075	0.023	0.020	0.074	0.025	0.058
	smeD	Efflux: RND	0.099	0.028	0.307	0.167	0.145	0.102	0.226	0.124	0.208
	smeE	Efflux: RND	0.049	0.007	0.117	0.052	0.070	0.040	0.094	0.027	0.045
	smeF	Efflux: RND	0.005	0	0.016	0	0.019	0	0	0.007	0
	Multidrug transporter	Efflux: RND	1.068	0.850	1.908	1.855	1.624	1.059	2.388	1.518	1.650
MATE	*mdtK*	Efflux: MATE	0.010	0.006	0	0	0	0	0.006	0	0
MFS	*emrA*	Efflux: MFS	0.020	0.038	0.036	0.018	0.043	0.009	0.025	0.072	0.029
	emrB	Efflux: MFS	0.012	0.065	0.052	0.015	0.028	0.067	0.045	0.008	0.023
	emrD	Efflux: MFS	0	0.020	0	0	0	0	0	0	0
	emrK	Efflux: MFS	0	0.020	0	0	0	0	0	0.010	0
	emrB-qacA family MFS transporter	Efflux: MFS	0.009	0.061	0.098	0.105	0.057	0.165	0.388	0.074	0.272
	MFS transporter	Efflux: MFS	0.007	0.011	0	0	0	0	0	0	0
	mdfA	Efflux: MFS	0.023	0.023	0	0	0	0	0	0	0
	mdtG	Efflux: MFS	0	0.026	0	0	0	0	0	0	0
	mdtH	Efflux: MFS	0.007	0.006	0	0	0	0	0	0	0
	mdtL	Efflux: MFS	0.015	0.033	0	0	0	0	0	0	0
	mdtM	Efflux: MFS	0	0.025	0	0	0	0	0	0	0
	mdtN	Efflux: MFS	0	0.015	0.023	0	0.005	0	0	0	0
	mdtO	Efflux: MFS	0	0.011	0	0	0	0	0	0	0
	mdtP	Efflux: MFS	0	0.019	0	0	0	0	0	0	0
SM	*abeS*	Efflux: SMR	0.018	0	0	0	0	0	0	0	0

Antibiotic resistance			**Proportion of genes (%)**								
Resistance type		**Resistance mechanism**	**Water**			**Stream sediment**					
	Resistance subtype (ARG)		**E**	**SW_{U}**	**$SW_{0.3}$**	**SS_{U}**	**$SS_{0.3}$**	**$SS_{2.7}$**	**$SS_{3.2}$**	**RS_{U}**	**$RS_{3.7}$**
	emrE	Efflux: SMR	0	0.079	0.068	0.027	0	0	0.064	0.076	0.021
	qacEΔ1	Efflux: SMR	0.912	0	0.498	0	0.325	0	0	0	0
Polymyxin	*arnA*	Target alteration	0.106	0.104	0.094	0.147	0.115	0.104	0.069	0.164	0.116
	Icr-Mo	Target alteration	0	0.008	0	0	0	0.006	0.005	0	0
	mcr-1.5	Target alteration	0.003	0	0	0	0	0	0	0	0
	mcr-3	Target alteration	0	0.010	0	0	0	0	0	0	0
	mcr-4	Target alteration	0	0.008	0	0	0.010	0	0	0	0
	mcr-5	Target alteration	0.011	0.006	0	0	0	0	0.008	0	0.004
P	*Puromycin resistance protein*	Efflux: MFS	0	0	0.009	0	0	0	0	0	0
Q	*abaQ*	Efflux: MFS	0	0	0	0	0	0.017	0	0	0
	norB	Efflux: MFS	0	0	0	0	0	0	0.014	0	0
	qepA	Efflux: MFS	0.003	0.049	0.047	0.075	0.020	0.138	0.105	0.074	0.042
	qnrB	Target protection	0.014	0	0	0	0	0	0	0	0
R	*arr*	Inactivation	0.648	0.025	0.513	0.079	0.496	0.523	0.333	0.293	0.140
	Rifampin monooxygenase	Inactivation	0	0.009	0.008	0	0.005	0.055	0.021	0.025	0.008
SUL	***sul1***	**Target replacement**	**5.383**	**0**	**1.803**	**0**	**0.817**	**0.018**	**0.035**	**0**	**0.047**
	sul2	**Target replacement**	**0.230**	**0**	**0.436**	**0**	**0.398**	**0**	**0**	**0**	**0**
	sul4	Target replacement	0.079	0	0.046	0.135	0.048	0.075	0.084	0.071	0.260
Tetracycline	*otrA*	Target protection	0.005	0.002	0	0.009	0.010	0.052	0.030	0.042	0.012
	tet32	Target protection	0	0.008	0.012	0	0.004	0	0	0	0
	tet35	Efflux: ABC	0	0	0.011	0	0.012	0	0	0	0
	tet39	Efflux: MFS	0.020	0	0	0	0	0	0.005	0	0
	tet41	Efflux: MFS	0.008	0	0.010	0	0	0	0	0	0
	tet43	Efflux: MFS	0.034	0	0.012	0	0.024	0.026	0.021	0	0
	tet44	Target protection	0.009	0	0.006	0	0	0	0	0	0
	tetA	**Efflux: MFS**	**0.037**	**0.015**	**0.038**	**0**	**0.010**	**0.022**	**0.021**	**0**	**0.008**
	tetC	Efflux: MFS	0	0.012	0.052	0	0.017	0.006	0	0	0

Antibiotic resistance			Proportion of genes (%)								
Resistance type		**Resistance mechanism**	**Water**			**Stream sediment**					
	Resistance subtype (ARG)		**E**	**SW_U**	**$SW_{0.3}$**	**SS_U**	**$SS_{0.3}$**	**$SS_{2.7}$**	**$SS_{3.2}$**	**RS_U**	**$RS_{3.7}$**
	tetE	Efflux: MFS	0.015	0	0	0	0	0	0	0	0
	tetG	Efflux: MFS	0.041	0	0.107	0	0.050	0	0	0	0
	tetM	Target protection	0	0	0.031	0	0.020	0	0.023	0	0
	tetO	Target protection	0	0	0	0	0	0	0.003	0	0
	tetP	Efflux: MFS	0.040	0.015	0.034	0.003	0.047	0.004	0.039	0.010	0.029
	tetQ	**Target protection**	**0.042**	**0**	**0.018**	**0**	**0**	**0**	**0**	**0**	**0**
	tetR	Regulation	0.016	0	0	0	0	0	0	0	0
	tetT	Target protection	0.017	0.002	0.024	0	0.010	0	0	0	0.004
	tetV	Efflux: MFS	0.015	0.012	0	0	0	0.091	0.016	0.029	0
	tetW	**Target protection**	**0.037**	**0**	**0.006**	**0**	**0.021**	**0**	**0**	**0**	**0**
	tetX	Inactivation	0.039	0	0	0	0.009	0	0	0	0
	tetX1	Inactivation	0.009	0	0	0	0	0	0	0	0
	tetX2	Inactivation	0.128	0	0.034	0	0.023	0	0	0	0
	tetX3	Inactivation	0	0	0	0	0.017	0	0	0	0
	tetX4	Inactivation	0.008	0	0.010	0	0.009	0	0	0	0
	Tetracycline resistance protein	Efflux: MFS	0.005	0.004	0.019	0	0	0.011	0	0	0.005
TMP	*dfrA1*	Target replacement	0	0	0	0	0	0	0.012	0	0.019
	dfrB1	Target replacement	0.032	0	0	0	0.034	0	0	0	0
	dfrB2	Target replacement	0.021	0.095	0.044	0	0.085	0.193	0.159	0.228	0.200
	dfrB3	Target replacement	0.038	0	0.101	0.049	0	0.262	0	0.237	0.026
	dfrB6	Target replacement	0.112	0	0	0.070	0.066	0.055	0.291	0.048	0.088
Vancomycin	*vanA*	Target alteration	0	0	0.007	0	0	0	0	0	0.022
	vanC	Target alteration	0	0	0.006	0	0.008	0	0.039	0.006	0.007
	vanD	Target alteration	0.006	0.026	0	0	0	0	0	0	0.011
	vanG	Target alteration	0	0	0.012	0	0.006	0	0	0	0.006
	vanH	Target alteration	0	0.016	0	0	0	0.013	0.030	0.023	0

Antibiotic resistance			**Proportion of genes (%)**								
Resistance type		**Resistance mechanism**	**Water**			**Stream sediment**					
	Resistance subtype (ARG)		**E**	**SW_U**	**$SW_{0.3}$**	**SS_U**	**$SS_{0.3}$**	**$SS_{2.7}$**	**$SS_{3.2}$**	**RS_U**	**$RS_{3.7}$**
	vanR	Regulation	0.085	0.127	0.079	0.254	0.090	0.961	0.646	0.262	0.130
	vanS	Regulation	0.021	0	0	0.065	0.028	0.179	0.042	0.046	0.034
	vanX	Target alteration	0	0	0	0	0	0	0.019	0	0
	vanY	Target alteration	0	0	0	0	0	0	0.007	0	0
Other/regulation	*gadX*	Regulation	0	0.019	0	0	0	0	0	0	0
	H-NS	Regulation	0	0.024	0	0	0	0	0.045	0	0
	LuxR	Regulation	0	0.021	0	0	0	0	0	0	0
	cAMP-regulatory protein	Regulation	0.194	0.312	0.109	0.115	0.085	0.164	0.099	0.043	0.047
	cob(I)	Regulation	0.030	0.039	0	0.031	0	0	0.015	0	0
	rpsD	Regulation	0	0	0	0.014	0	0	0	0	0
	tsnR	Regulation	0	0	0	0	0	0.016	0	0	0
	cpxR	Regulation	1.178	0.562	0.975	0.853	0.726	1.217	1.170	0.983	0.838
	arlR	Regulation	0.068	0	0.011	0	0.008	0.046	0.053	0	0.018
ARG proportion (%)			**31.886**	**24.332**	**23.904**	**14.968**	**15.600**	**20.836**	**23.416**	**17.262**	**14.715**
ARG subtypes detected			**160**	**130**	**147**	**66**	**129**	**91**	**109**	**73**	**82**

Table S10. Statistically significant Pearson correlations (R) between physicochemical parameters in water as well as sediment and (A) target gene abundances, and (B) target gene relative abundances in prokaryotic community. Statistically significant partial correlations between physicochemical parameters and ARGs (in case of ARGs abundances *16Stot* is used as covariable and in case of ARGs relative abundances B16S relative abundance in prokaryotic community is used as covariable) are given in bold italic. Temp – temperature; N_{tot} – total nitrogen; P_{tot} – total phosphorous; TOC – total organic carbon; *$16S_{tot}$* – total prokaryotic community abundance; *B16S* – bacteria specific 16S rRNA gene; *A16S* – archaea specific 16S rRNA gene.

Target gene	**Physicochemical parameters**												
	Water										**Sediment**		
	Temp	**O_2 conc**	**pH**	**N_{tot}**	**NH_4-N**	**NO_3-N**	**P_{tot}**	**PO_4^{3-}-P**	**SO_4^{2-}**	**pH**	**TOC %**	**N_{tot}**	**P_{tot}**
A													
$16S_{tot}$					0.87*		0.95**	0.88*		-0.84*			
B16S					0.86*		0.95**	0.87*		-0.83*			
A16S					0.95**		0.99***	0.93**		-0.83*	0.87*		
aadA										-0.86*	0.87*	0.89*	0.91*/ ***0.88****
acrB					0.92**		0.96**	0.90*		-0.81*			
blaCTX-M					0.96**		0.99***/ ***0.90****	0.98***/ ***0.97*****					
blaOXA2										-0.93**	0.89*	0.85*	0.81*
mexF					0.94**		0.99***	0.95**					
sul1					0.87*		0.94**	0.85*			0.82*	0.84*	0.85*
sul2					0.98***/ ***0.92****		0.99***/ ***0.95****	0.98***/ ***0.90****		-0.90*		0.82*	
tetW							0.88*			-0.85*			
B													
B16S					-0.96**		-0.93**	-0.91*			-0.84*	-0.86*	-0.83*
A16S					0.96**		0.93**	0.91*			0.84*	0.86*	0.83*
aadA												0.87*	0.95**/ ***0.93****
acrB										0.83*	-0.87*		
blaCTX-M				0.95**/ ***0.96****		0.92**/ ***0.98*****			0.91*	0.94**/ ***0.90****		-0.81*	
blaOXA2													0.83*
blaTEM1					-0.83*		-0.90*	-0.86*		0.82*			
mexF					0.86*			0.86*					

sul1					0.84*		0.93**	0.82*			0.85*	0.92**	0.98***/ ***0.96*****
sul2					0.97**		0.91*	0.95**					
tetA							-0.85*			0.90*			
tetB			0.85*		-0.85*		-0.95**	-0.86*		0.87*			
tetW	0.92**/ ***0.93****	-0.89*/ **-*****0.89****											

* p<0.05; ** p<0.01; *** p<0.001

Table S11. Proportions of pathogens in the bacterial communities of studied samples. E is the effluent of the wastewater treatment plant (WWTP), SW and RW are water samples, and SS and RS are sediment samples of the stream and river, respectively. SW$_U$ and SS$_U$ are the samples taken upstream of the WWTP discharge point and RW$_U$ and RS$_U$ are the samples taken from the river upstream of the stream inflow point. The number in the subscript of the sample code shows the distance (km) of the sampling point downstream from the WWTP discharge point.

Pathogen	**Proportion of pathogens (%)**								
	E	**SW$_U$**	**SW$_{0.3}$**	**SS$_U$**	**SS$_{0.3}$**	**SS$_{2.7}$**	**SS$_{3.2}$**	**RS$_U$**	**RS$_{3.7}$**
Achromobacter xylosoxidans	0.01663	0.01584	0.01324	0.00788	0.00843	0.01001	0.01046	0.00891	0.00829
Acinetobacter baumannii	0.02481	0.02799	0.02086	0.00769	0.01301	0.00843	0.01256	0.00761	0.00858
Acinetobacter haemolyticus	0.00100	0.00059	0.00036	0.00038	0.00028	0.00019	0.00037	0.00032	0.00034
Acinetobacter junii	0.00380	0.00261	0.00123	0.00074	0.00067	0.00062	0.00064	0.00053	0.00051
Acinetobacter lwoffii	0.00072	0.00069	0.00036	0.00020	0.00024	0.00021	0.00023	0.00024	0.00029
Acinetobacter nosocomialis	0.00105	0.00168	0.00087	0.00034	0.00032	0.00033	0.00039	0.00018	0.00030
Bacillus anthracis	0.00061	0.00089	0.00074	0.00077	0.00086	0.00057	0.00061	0.00071	0.00114
Bordetella pertussis	0.01306	0.00946	0.01225	0.01190	0.01030	0.01242	0.01347	0.01194	0.01238
Brucella abortus	0.00036	0.00027	0.00024	0.00016	0.00039	0.00033	0.00038	0.00024	0.00025
Brucella canis	0.00013	0.00002	0.00018	0.00003	0.00018	0.00008	0.00010	0.00007	0.00002
Brucella melitensis	0.00021	0.00041	0.00018	0.00021	0.00020	0.00046	0.00046	0.00030	0.00029
Brucella ovis	0.00007	0.00002	0.00006	0.00006	0.00008	0.00008	0.00005	0.00006	0.00010
Brucella suis	0.00056	0.00041	0.00047	0.00040	0.00044	0.00043	0.00052	0.00033	0.00025
Burkholderia cenocepacia	0.01184	0.01003	0.01028	0.00783	0.00773	0.00897	0.00972	0.00795	0.00772
Burkholderia cepacia	0.01096	0.00883	0.00948	0.00697	0.00652	0.00829	0.00839	0.00730	0.00664
Burkholderia pseudomallei	0.03463	0.03884	0.03168	0.01960	0.01979	0.02180	0.02084	0.02078	0.02009
Campylobacter coli	0.00099	0.00183	0.00089	0.00082	0.00104	0.00046	0.00057	0.00046	0.00067
Campylobacter jejuni	0.00190	0.00262	0.00198	0.00193	0.00218	0.00134	0.00127	0.00177	0.00184
Chlamydia pneumoniae	0.00075	0.00095	0.00085	0.00066	0.00087	0.00055	0.00053	0.00071	0.00073
Chlamydia trachomatis	0.00670	0.00451	0.00484	0.00223	0.00425	0.00149	0.00181	0.00159	0.00212
Citrobacter amalonaticus	0.00075	0.00047	0.00049	0.00046	0.00043	0.00047	0.00056	0.00042	0.00051
Citrobacter freundii	0.03459	0.00944	0.05084	0.00771	0.07140	0.02725	0.02520	0.01002	0.01242
Citrobacter koseri	0.00046	0.00045	0.00037	0.00047	0.00040	0.00057	0.00040	0.00034	0.00044
Citrobacter youngae	0.00021	0.00019	0.00012	0.00016	0.00008	0.00013	0.00017	0.00019	0.00008
Clostridioides difficile	0.00413	0.00545	0.00529	0.00324	0.00525	0.00259	0.00240	0.00285	0.00361
Clostridium botulinum	0.00460	0.00413	0.00431	0.00420	0.00591	0.00280	0.00293	0.00362	0.00448
Clostridium perfringens	0.00204	0.00249	0.00228	0.00225	0.00313	0.00113	0.00114	0.00136	0.00221
Clostridium tetani	0.00038	0.00058	0.00088	0.00080	0.00089	0.00039	0.00040	0.00056	0.00075

Pathogen	Proportion of pathogens (%)								
	E	SW_U	$SW_{0.3}$	SS_U	$SS_{0.3}$	$SS_{2.7}$	$SS_{3.2}$	RS_U	$RS_{3.7}$
Enterobacter asburiae	0.00069	0.00066	0.00079	0.00043	0.00041	0.00056	0.00068	0.00058	0.00069
Enterobacter cloacae	0.00336	0.00409	0.00373	0.00231	0.00233	0.00222	0.00275	0.00229	0.00210
Enterobacter hormaechei	0.00393	0.00285	0.00266	0.00151	0.00150	0.00113	0.00130	0.00131	0.00110
Enterobacter kobei	0.00054	0.00037	0.00065	0.00024	0.00049	0.00033	0.00036	0.00015	0.00036
Enterococcus faecalis	0.00701	0.01864	0.00830	0.00618	0.01334	0.00735	0.00603	0.00724	0.01177
Enterococcus faecium	0.02379	0.06015	0.02404	0.01353	0.02889	0.01514	0.05648	0.03206	0.02221
Escherichia coli	0.03942	0.04339	0.02904	0.02168	0.02220	0.02148	0.02349	0.01870	0.02132
Francisella tularensis	0.00026	0.00045	0.00041	0.00040	0.00039	0.00008	0.00024	0.00020	0.00025
Haemophilus influenzae	0.00213	0.00424	0.00182	0.00132	0.00149	0.00107	0.00130	0.00091	0.00121
Haemophilus parainfluenzae	0.00272	0.00128	0.00111	0.00086	0.00080	0.00076	0.00086	0.00084	0.00092
Helicobacter pylori	0.00263	0.00366	0.00297	0.00226	0.00279	0.00181	0.00191	0.00205	0.00240
Klebsiella aerogenes	0.00168	0.00174	0.00167	0.00135	0.00144	0.00139	0.00134	0.00148	0.00140
Klebsiella oxytoca	0.00311	0.00206	0.00292	0.00221	0.00232	0.00201	0.00206	0.00189	0.00230
Klebsiella pneumoniae	0.02724	0.02839	0.02757	0.02024	0.01917	0.01940	0.02116	0.02380	0.01783
Legionella pneumophila	0.00610	0.00527	0.00628	0.00473	0.00544	0.00445	0.00487	0.00444	0.00507
Listeria monocytogenes	0.00213	0.00304	0.00283	0.00213	0.00252	0.00134	0.00177	0.00164	0.00191
Micrococcus luteus	0.00227	0.00292	0.00273	0.00219	0.00204	0.00215	0.00224	0.00207	0.00223
Moraxella catarrhalis	0.00218	0.00182	0.00119	0.00056	0.00065	0.00067	0.00070	0.00060	0.00052
Morganella morganii	0.00162	0.00162	0.00145	0.00104	0.00119	0.00105	0.00099	0.00105	0.00114
Mycobacterium tuberculosis	0.02436	0.02238	0.02197	0.01989	0.01837	0.02190	0.02029	0.02057	0.02022
Mycobacteroides abscessus	0.05611	0.03808	0.03870	0.01834	0.02480	0.02153	0.01895	0.01982	0.01832
Mycoplasma genitalium	0.00004	0.00006	0.00001	0.00006	0.00003	0.00002	0.00002	0.00004	0.00008
Mycoplasma pneumoniae	0.00008	0.00018	0.00004	0.00010	0.00010	0.00006	0.00005	0.00005	0.00008
Neisseria gonorrhoeae	0.00163	0.00101	0.00128	0.00093	0.00087	0.00117	0.00116	0.00118	0.00115
Neisseria meningitidis	0.00416	0.00375	0.00363	0.00309	0.00260	0.00258	0.00279	0.00286	0.00290
Proteus mirabilis	0.00275	0.00222	0.00119	0.00048	0.00071	0.00038	0.00066	0.00051	0.00052
Proteus penneri	0.00007	0.00010	0.00006	0.00007	0.00005	0.00003	0.00005	0.00005	0.00004
Proteus vulgaris	0.00013	0.00031	0.00028	0.00018	0.00032	0.00013	0.00015	0.00017	0.00018
Providencia rettgeri	0.00089	0.00112	0.00073	0.00072	0.00058	0.00071	0.00074	0.00053	0.00063
Providencia stuartii	0.00148	0.00070	0.00104	0.00061	0.00091	0.00053	0.00060	0.00060	0.00059
Pseudomonas aeruginosa	0.07725	0.03252	0.05980	0.03308	0.03852	0.03736	0.03948	0.03262	0.03488
Pseudomonas fluorescens	0.03167	0.02812	0.02593	0.02268	0.02268	0.02733	0.02907	0.02146	0.02180
Pseudomonas putida	0.01265	0.01138	0.01184	0.01026	0.01026	0.01168	0.01304	0.00994	0.00972

Pathogen	**Proportion of pathogens (%)**								
	E	**$\mathrm{SW_{U}}$**	**$\mathrm{SW_{0.3}}$**	**$\mathrm{SS_{U}}$**	**$\mathrm{SS_{0.3}}$**	**$\mathrm{SS_{2.7}}$**	**$\mathrm{SS_{3.2}}$**	**$\mathrm{RS_{U}}$**	**$\mathrm{RS_{3.7}}$**
Pseudomonas sp.	0.01832	0.01151	0.01020	0.00431	0.00625	0.00688	0.00943	0.00416	0.00488
Pseudomonas stutzeri	0.02123	0.01634	0.01860	0.01497	0.01401	0.01657	0.01835	0.01647	0.01535
Ralstonia mannitolilytica	0.00400	0.00380	0.00313	0.00148	0.00171	0.00187	0.00171	0.00170	0.00169
Ralstonia pickettii	0.00726	0.00480	0.00585	0.00518	0.00394	0.00636	0.00643	0.00593	0.00494
Raoultella planticola	0.00074	0.00083	0.00091	0.00072	0.00072	0.00058	0.00121	0.00129	0.00094
Rickettsia prowazekii	0.00020	0.00053	0.00017	0.00030	0.00032	0.00031	0.00038	0.00026	0.00033
Salmonella enterica	0.02172	0.01320	0.01731	0.01797	0.01221	0.01134	0.01024	0.00999	0.01044
Serratia liquefaciens	0.00064	0.00139	0.00066	0.00043	0.00038	0.00043	0.00048	0.00036	0.00051
Serratia marcescens	0.00687	0.00434	0.00476	0.00320	0.00337	0.00369	0.00370	0.00309	0.00345
Serratia odorifera	0.00066	0.00051	0.00057	0.00039	0.00042	0.00072	0.00069	0.00046	0.00051
Shigella dysenteriae	0.00019	0.00018	0.00010	0.00013	0.00015	0.00011	0.00012	0.00007	0.00015
Shigella flexneri	0.00351	0.00071	0.00084	0.00031	0.00056	0.00022	0.00034	0.00028	0.00037
Shigella sonnei	0.00055	0.00302	0.00057	0.00036	0.00053	0.00041	0.00042	0.00029	0.00034
Staphylococcus aureus	0.00358	0.00498	0.00445	0.00417	0.00388	0.00308	0.00286	0.00325	0.00379
Staphylococcus epidermidis	0.00078	0.00117	0.00067	0.00056	0.00064	0.00061	0.00067	0.00054	0.00060
Staphylococcus intermedius	0.00004	0.00005	0.00009	0.00005	0.00010	0.00002	0.00005	0.00003	0.00005
Staphylococcus lugdunensis	0.00008	0.00001	0.00004	0.00001	0.00001	NA	NA	0.00005	0.00001
Staphylococcus pseudintermedius	0.00279	0.00250	0.00140	0.00040	0.00066	0.00048	0.00034	0.00026	0.00029
Stenotrophomonas maltophilia	0.02502	0.01658	0.02350	0.01309	0.01800	0.01638	0.01806	0.01304	0.01343
Streptococcus agalactiae	0.00134	0.00239	0.00133	0.00112	0.00149	0.00069	0.00101	0.00091	0.00130
Streptococcus anginosus	0.00035	0.00110	0.00042	0.00024	0.00039	0.00022	0.00016	0.00010	0.00015
Streptococcus constellatus	0.00010	0.00007	0.00003	0.00009	0.00007	0.00008	0.00004	0.00002	0.00003
Streptococcus pneumoniae	0.02112	0.01588	0.01210	0.00361	0.00590	0.00385	0.00380	0.00330	0.00357
Streptococcus pyogenes	0.00058	0.00141	0.00101	0.00077	0.00099	0.00096	0.00061	0.00082	0.00117
Vibrio cholerae	0.00745	0.00575	0.00549	0.00419	0.00512	0.00425	0.00455	0.00431	0.00429
Vibrio parahaemolyticus	0.00966	0.00837	0.00805	0.00599	0.00677	0.00555	0.00623	0.00572	0.00633
Vibrio vulnificus	0.00260	0.00208	0.00202	0.00169	0.00182	0.00159	0.00177	0.00143	0.00173
Yersinia enterocolitica	0.00212	0.00229	0.00198	0.00093	0.00117	0.00128	0.00146	0.00089	0.00105
Yersinia pestis	0.00058	0.00033	0.00054	0.00034	0.00039	0.00027	0.00054	0.00027	0.00037
Total proportion of detected pathogens	**0.688**	**0.606**	**0.591**	**0.373**	**0.487**	**0.411**	**0.470**	**0.384**	**0.387**

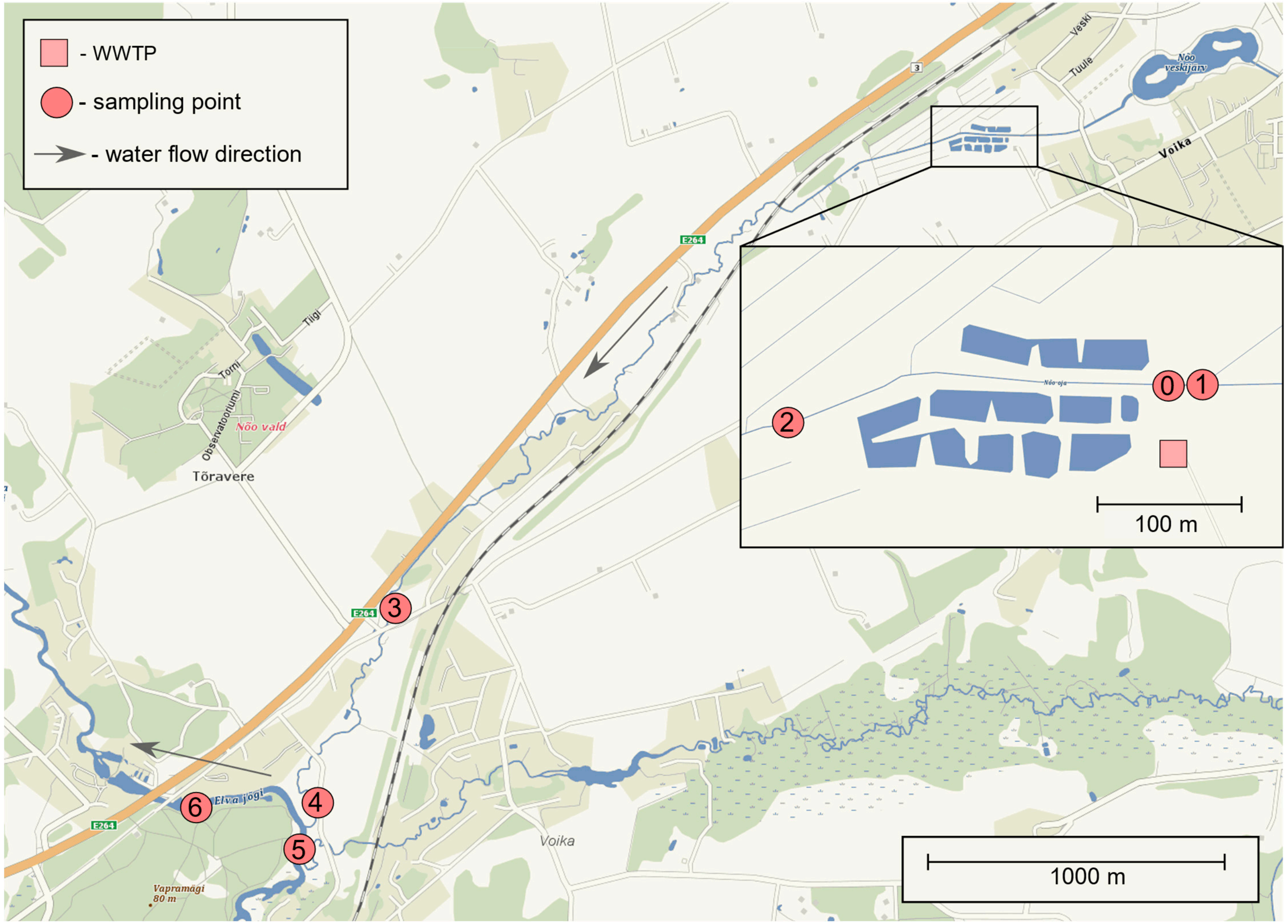

Figure S1. A map showing the locations of wastewater treatment plant (WWTP) of Nõo and sampling points on the Nõo steam and Elva river. 0 is the WWTP discharge point, 1 is the stream sampling point locating upstream of the WWTP discharge point; 2, 3 and 4 are the stream sampling points downstream at the distance of 0.3, 2.7 and 3.2 km of the WWTP discharge point; and 5 and 6 are the river sampling points locating upstream of the Nõo stream inflow point and downstream of the stream inflow at the 3.7 km distance from the WWTP discharge point, respectively.

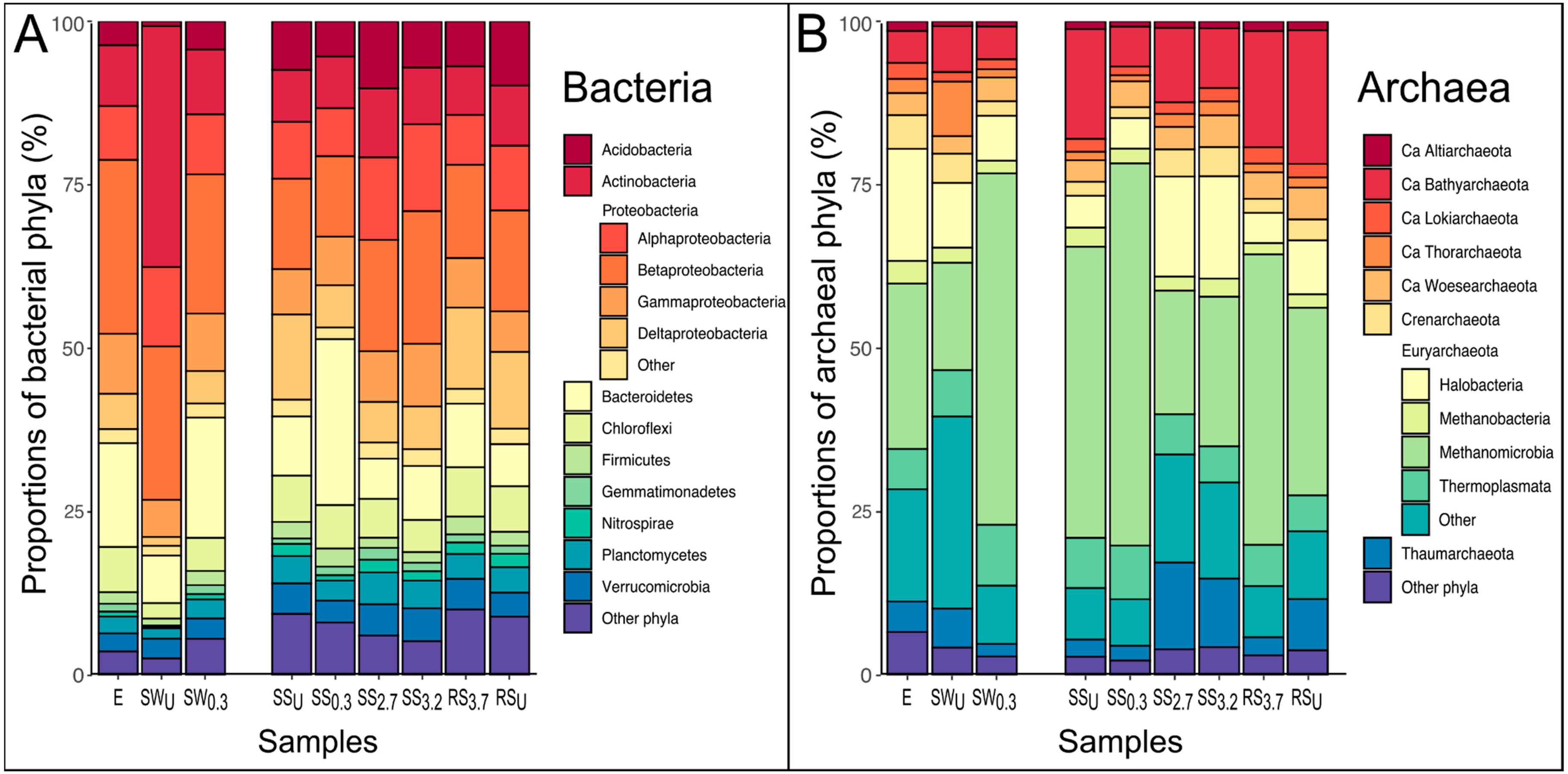

Figure S2. The bacterial (A) and archaeal (B) community taxonomy of wastewater treatment plant (WWTP) effluent (E), stream water upstream (SW_U) and downstream ($SW_{0.3}$) of WWTP discharge, as well as stream sediment upstream (SS_U) and downstream ($SS_{0.3}$-$SS_{3.2}$) of WWTP discharge and river sediment upstream (RS_U) and downstream ($RS_{3.7}$) of stream inflow at phylum level. *Proteobacteria* and *Euryarchaeota* are presented at class level. The subscript number in the sample code indicates distance (in km) from the WWTP discharge.

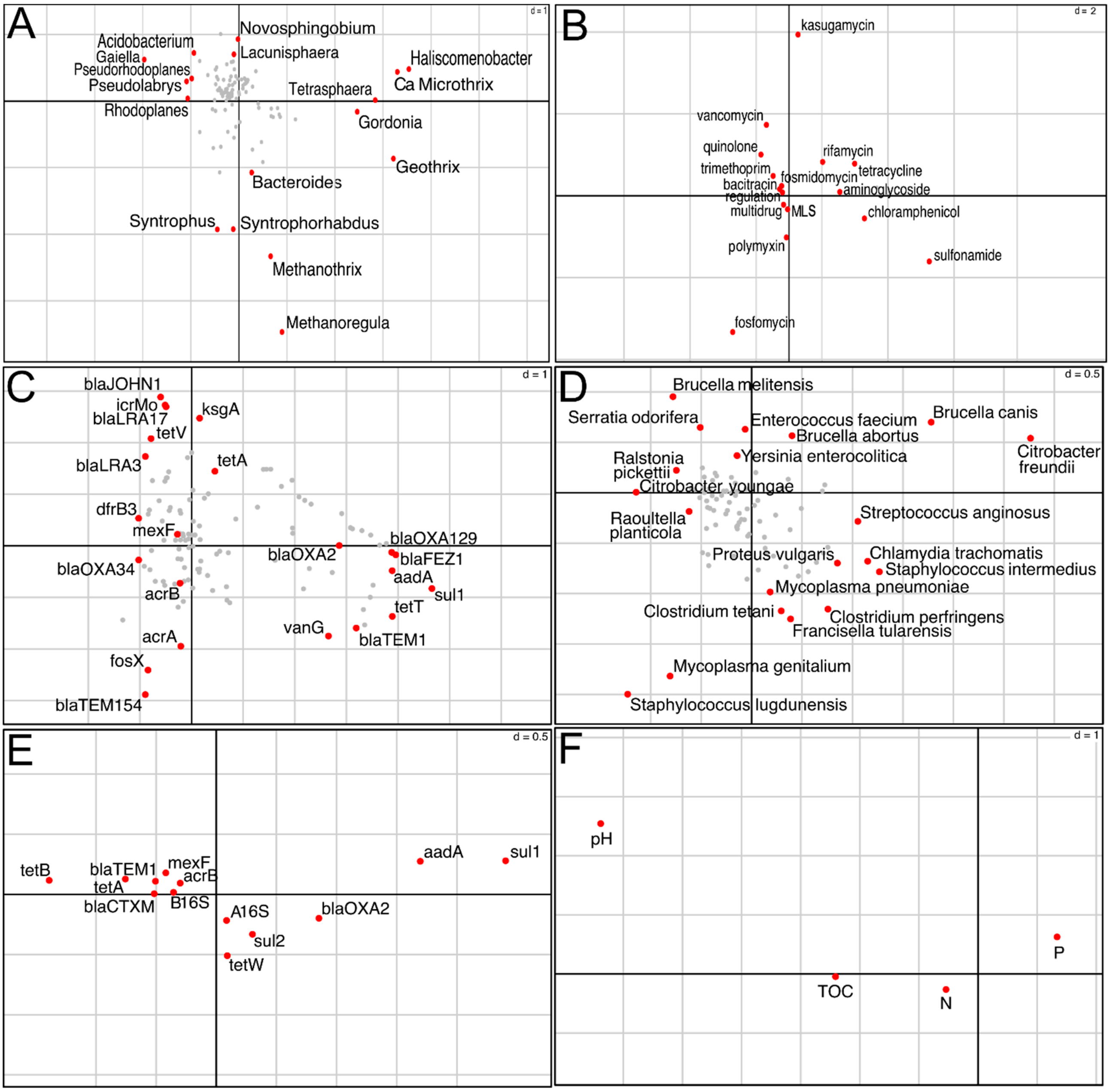

Figure S3. Multiple co-inertia analysis results based on six sediment-specific data sets. Shown are variable spaces for each data set (microbial genera proportions in prokaryotic community (A), antibiotic resistance type (B) and ARG subtype (C) proportions, pathogen proportions (D), target gene abundances (E) and sediment physicochemical parameters (F). TOC – total organic carbon, N – total nitrogen, P – total phosphorous content in sediment.

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