

Removal of antibiotic resistance genes and co-selectors in a full-scale sewage treatment plant during drought and flood.

Supplementary Information

Text S1: In between samples, the sampling equipment was wiped with 70% ethanol for disinfection. Water quality parameters (pH, DO, conductivity) were measured using HQ40d Portable Water Quality Lab Package (Hach, USA) *in situ*. Before use, all glassware were washed thrice with soap and water, rinsed thrice with DI water, and submerged in a 10% nitric acid water bath overnight. Finally, they were rinsed thrice with DI water and then baked at 250 °C overnight.

Text S2: Solid phase extraction lines were prewashed with nanopure water and LC grade methanol. The metal frit ends of the solid phase extraction lines were submerged first in the 500 mL amber bottle containing methanol. Vacuum was applied to allow ~250 mL methanol to wash through the solid phase extraction lines and cartridges. Then, metal frits from methanol bottle were removed and inserted into the bottle containing nanopure water ~250 mL to flush through the lines. Conditioning was done with 6 mL of acetonitrile, followed by 6 mL nanopure water.

Text S3: LCMS Method

Acetonitrile (ACN) and methanol, both LCMS grade and ammonium acetate were purchased from Merck (Darmstadt, Germany). Formic acid (LC-MS grade) and disodium ethylenediamine tetraacetate (Na₂EDTA) ACS reagent were purchased from Sigma. The mobile phase used for Ciprofloxacin analysis was aqueous 0.1% formic acid in LCMS grade water (A) and methanol (B). The mobile phase used for triclosan was Aqueous 0.1%

Ammonium acetate in LCMS grade water (A) and Acetonitrile (B). Standards for antibiotics were purchased from Sigma. Stock solutions were prepared in wastewater as matrix.

Wastewater sample was used as a matrix blank and matrix spike was carried out evaluated to matrix interference.

Quality Assurance

Antibiotic standards were prepared using the starting mobile phase of the LC-MS/MS method with the solvent. An initial solution of 100 ppb ($\mu\text{g/L}$) was made and then it was serially diluted to obtain mixtures with concentrations of 75, 50, 25, 10, 5, 3, and 1 ppb. These standards were analysed by LC-MS/MS, with replicates for each concentration, to obtain the areas of both the quantifying and qualifying ions. The ion ratios were calculated by dividing the area of the quantifying ion by the area of the qualifying ion for each analyte. The average ion ratio and the deviations from the average value for the ion ratios were calculated at all concentrations for each compound. The ions selected for Ciprofloxacin and Triclosan were 332.10 < 314.10 and 287<35; 289<37 respectively.

Limits of Detection and Limits of Quantification values

Antimicrobials LOD LOQ

Ciprofloxacin 0.95 ng/L 2.90 ng/L

Triclosan 7.44 ng/L 22.57 ng/L

S/N value > 10

Table S1: List of primers used in the study.

Gene target	Forward Primer	Reverse Primer
16S rRNA gene (1369F - 1492R) ¹	CGGTGAATACGTTTCYCGG	GGWTACCTTGTTACGACTT
<i>gyrA</i> ²	GGTACACCGTCGCGTACTTT	CAACGAAATCGACCGTCTCT
<i>parC</i> ²	GCCTTGCGCTACATGAATTT	ACCATCAACCAGCGGATAAC
<i>acrA</i> ³	CTCTCAGGCAGCTTAGCCCTA A	TGCAGAGGTTTCAGTTTTGACT GTT
<i>acrB</i> ³	GGTCGATTCCGTTCTCCGTTA	CTACCTGGAAGTAAACGTCAT TGGT
<i>qepA</i> ⁴	GCAGGTCCAGCAGCGGGTAG	CTTCCTGCCCGAGTATCGTG
<i>ermB</i> ⁵	GATACCGTTTACGAAATTGG	GAATCGAGACTTGAGTGTGC
<i>vanA</i> (36F - 992R) ⁶	TTGCTCAGAGGAGCATGACG	TCGGGAAGTGCAATACCTGC
FAB RJH101 -102 ⁷	CATATGTAAATCTTGAAAAC AAAACGTATGTCAT	GGATCCTTATTTAATTGCGTG GAATCCGCTATC
<i>tetA</i> ⁸	GCGCGATCTGGTTCACTCG	AGTCGACAGYRGC GCCGGC
<i>bla</i> _{TEM} ⁸	ATGAGTATTCAACATTTCCG	CCAATGCTTAATCAGTGAGG
<i>tetQ</i> ⁹	AGAATCTGCTGTTTGCCAGTG	CGGAGTGTCAATGATATTGCA
<i>trb</i> ¹⁰	GGAAAGGCAACTGAATATCC	GCCGTCTTGATGTCACTTTC
<i>fabV</i> ¹¹	GATCACCCACGACATCTTCTG GAACGGTTCCATCGGC	GCCGATGGAACCGTTCCAGAA GATGTCGTGGGTGATC
<i>czcA</i> ¹²	GTTTGAACGTATCATTAGTTT	GTAGCCATCCGAAATATTCG

	C	
<i>chrA</i> ¹³	CTTATACGCTACGCCAACTG	GTAATGGCATTTCAGTCGCTTG
<i>chrB</i> ¹³	GTCGTTAGCTTGCCAACATC	CGGAAAGCAAGATGTTCGATCG
<i>sul1</i> ¹⁴	CGCACCGGAAACATCGCTGCA C	TGAAGTTCCGCCGCAAGGCTC G
<i>mecA</i> ¹⁵	CGCAACGTTCAATTTAATTTT GTTAA	CCACTTCATATCTTGTAACG
<i>tetW</i> ⁹	GAGAGCCTGCTATATGCCAGC	GGGCGTATCCACAATGTTAAC
<i>tetO</i> ⁹	ACGGARAGTTTATTGTATAACC	TGGCGTATCTATAATGTTGAC
<i>ermF</i> ⁵	CGACACAGCTTTGGTTGAAC	GGACCTACCTCATAGACAAG
<i>int1</i> ¹⁴	GGGTCAAGGATCTGGATTTTCG	ACATGCGTGTAATCATCGTC G
<i>mcr1</i> ^{16,17}	TCTTGTGGCGAGTGTGCCGT	CCAATGATACGCATGATAAAC GCTG
<i>mcr5</i> ¹⁷	GTGAAACAGGTGATCGTGACT TACCG	CGTGCTTTACACCGATCATGT GCT
<i>yccT</i> ¹⁸	GCATGCTGACCACCTTGA	CAGCGTGGTGGCAAAA
<i>mexF</i> ¹⁹	TGTACGCGAACGACTTCAAC	GAGGTGTCGCTGACCTTGAT
<i>bla_{OXA-1}</i> ²⁰	CAAGCCAAAGGCACGATAGT	ACGATTGCCTCCCTCTTGAA
<i>bla_{OXA-7}</i> ^{21,22}	GAAGCCGTCAATGGTGTTTT	ATGCCCTCACTTGCCATGAT
<i>qnrS</i> ²³	CAATCATACATATCGGCACC	TCAGGATAAACAACAATACCC
<i>sul2</i> ¹⁴	TCCGGTGGAGGCCGGTATCTG G	CGGGAATGCCATCTGCCTTGA G
Total <i>E. coli</i> ²⁴	TGGGAAGCGAAAATCCTG	CAGTACAGGTAGACTTCTG

Table S2: LOQ for each gene present in the samples.

Gene	LOQ (gene copy numbers/μL)	% Var
16S rRNA	10^2	24.1%
<i>yccT</i>	10^2	10.1%
<i>sul1</i>	10^1	15.5%
<i>sul2</i>	10^1	13.2%
<i>parC</i>	10^2	11.9%
<i>bla</i> _{OXA-1}	10^3	21.0%
<i>tetW</i>	10^1	8%
<i>ermF</i>	10^3	6%
<i>mcr5</i>	10^1	24.7%
<i>intI1</i>	10^2	14.7%

Table S3: Details of qPCR for all genes except *intI1* and *bla*_{OXA-1}

Step	Temperature	Time
Initial hold	50° C	120 secs
Initial denaturation	95° C	120 secs
Denaturation	95° C	15 secs
Annealing and Extension	60° C	60 secs
Repeat	Go to step 'Denaturation' step	Repeat 39 times
Denaturing gradient	60° C - 95° C gradient	15 mins

Table S4: Details of qPCR of *int11* and *bla*_{OXA-1}

Step	Temperature	Time
Initial hold	50° C	120 s
Initial denaturation	95° C	120 s
Denaturation	95° C	15 s
Annealing	60° C	60 s
Extension	72° C	60 s
Repeat	Go to step 'Denaturation' step	Repeat 39 times
Denaturing gradient	60° C - 95° C gradient	15 mins

Table S5: qPCR assay preparation

All the targeted gene markers	5µL SYBR Green, 1µL Forward Primer (5mM), 1µL Reverse Primer (5mM), 2µL DNA free water and 1µL DNA insert of the target gene.
<i>bla</i> _{OXA-1}	5µL SYBR Green, 0.8µL Forward Primer (5mM), 0.8µL Reverse Primer (5mM), 2.4µL DNA free water and 1µL DNA insert of the target gene.

Table S6: PCR conditions and PCR assay preparation

PCR type	Assay
PCR for presence/absence	5 μ L Hotstar master mix (Qiagen®, Hilden, Germany), 0.8 μ L Forward Primer (5mM), 0.8 μ L Reverse Primer (5mM), 2.4 μ L DNA free water and 1 μ L DNA insert of the target gene.
Gradient PCR	5 μ L Hotstar master mix (Qiagen®, Hilden, Germany), 0.8 μ L Forward Primer (5mM), 0.8 μ L Reverse Primer (5mM), 1.4 μ L DNA free water and 2 μ L DNA insert of the target gene.
M13 PCR	5 μ L Hotstar master mix (Qiagen®, Hilden, Germany), 1 μ L M13 Forward Primer (5mM), 1 μ L M13 Reverse Primer (5mM), 2.4 μ L DNA free water and 1 μ L DNA insert of the target gene.

Table S7: Median values of the levels of 16S rRNA gene copies (gene copy/L or gene copy/g), relative levels of the ARGs on log₁₀ scale (copy number/16S rRNA gene copies), and co-selectors (ppb) during the study period at different sampling locations within the targeted STP: IN – Grit chamber outlet, ATIN – Inlet of aeration tank i.e., sample collected post primary treatment, ATOUT – Outlet of aeration tank, MPIN – Inlet of maturation pond, and MPOUT – Outlet of maturation pond.

Gene	Inlet	ATIN	ATOUT	MPIN	MPOUT	FS
log 16SrRNA	9.51E+00	8.60E+00	9.82E+00	8.63E+00	8.56E+00	1.20E+01
<i>ycc T</i>	-7.16E-01	-2.02E-01	-9.93E-01	-1.19E+00	-1.03E+00	-2.86E+00
<i>int I1</i>	7.66E-02	1.76E-01	2.93E-01	6.58E-01	5.95E-01	-1.37E+00
<i>sul 1</i>	3.45E-01	4.65E-01	3.54E-01	4.86E-01	5.08E-01	-4.17E+00
<i>sul 2</i>	-2.33E+00	-2.32E+00	-2.64E+00	-2.39E+00	-2.38E+00	-7.21E+00
<i>par C</i>	-2.52E+00	-2.13E+00	-2.41E+00	-1.94E+00	-2.41E+00	-5.59E+00
<i>bla</i> _{OXA-1}	-3.75E+00	-1.63E+00	-4.42E+00	-6.74E+00	-1.65E+00	-2.22E+00
<i>tet W</i>	-7.25E-01	-3.92E-01	-1.07E+00	-8.71E-01	-7.36E-01	5.75E-01
<i>erm F</i>	2.03E-01	-2.06E-02	-9.38E-02	-3.04E-01	-1.68E-01	1.37E+00
<i>mcr 5</i>	-1.18E+00	-2.21E+00	-2.38E+00	-2.26E+00	-1.83E+00	-1.56E+00
Ciprofloxacin	102.27	87.49	87.21	74.37	44.37	27.17
Triclosan	172.88	135.80	109.46	113.06	104.38	0.00
Copper	0.80	0.72	0.29	0.53	0.14	0.00
Lead	0.31	0.29	0.21	0.11	0.00	0.00
Chromium	4.14	3.57	3.88	2.07	2.13	0.00

Table S8: Median values of the levels of 16S rRNA gene copies (gene copy/L or gene copy/g) and ARGs on log10 scale, and co-selectors (ppb) during the study period different sampling locations within the targeted STP: IN – Grit chamber outlet, ATIN – Inlet of aeration tank i.e., sample collected post primary treatment, ATOUT – Outlet of aeration tank, MPIN – Inlet of maturation pond, and MPOUT – Outlet of maturation pond in each season.

Gene	Season	Inlet	ATIN	ATOUT	MPIN	MPOUT
16SrRNA	Summer	3.41E+10	2.06E+08	2.22E+10	7.43E+09	2.10E+09
	Monsoon	1.52E+09	5.96E+08	6.35E+09	1.90E+08	3.52E+08
	Winter	1.67E+10	1.66E+08	3.89E+09	2.84E+08	1.87E+09
<i>yccT</i>	Summer	-1.08E+00	-1.45E+00	-7.91E-01	-2.63E+00	-3.13E+00
	Monsoon	-7.16E-01	-2.02E-01	-9.93E-01	-1.19E+00	-1.03E+00
	Winter	-9.05E-01	-4.75E-01	-6.95E-01	3.47E-01	-1.40E+00
<i>int11</i>	Summer	-2.39E+00	-2.22E+00	-2.22E+00	-1.87E+00	-2.37E+00
	Monsoon	1.19E+00	7.45E-01	6.01E-01	8.20E-01	1.04E+00
	Winter	-1.74E-01	-2.33E-01	8.29E-01	7.65E-01	2.61E-01
<i>sul1</i>	Summer	5.54E-01	4.15E-01	3.54E-01	2.92E-01	5.25E-01
	Monsoon	5.91E-01	7.53E-01	-4.58E-02	6.10E-01	2.17E-01
	Winter	3.23E-01	2.08E-01	8.80E-01	7.04E-01	6.64E-01
<i>sul2</i>	Summer	-2.56E+00	-2.32E+00	-2.75E+00	-2.46E+00	-2.41E+00
	Monsoon	-2.26E+00	-2.37E+00	-2.50E+00	-2.03E+00	-2.40E+00
	Winter	-1.95E+00	-1.67E+00	-1.79E+00	-4.38E-01	-1.44E+00
<i>parC</i>	Summer	-7.92E-01	-3.09E-01	1.96E-01	-2.60E-01	-3.15E-01
	Monsoon	-2.45E+00	-2.70E+00	-3.26E+00	-2.62E+00	-2.46E+00
	Winter	-3.95E+00	-1.92E+00	-2.50E+00	-1.52E+00	-2.98E+00
<i>bla_{OXA-1}</i>	Summer	-3.25E+00	-2.71E+00	-5.13E+00	-3.79E+00	-2.16E+00
	Monsoon	-8.21E+00	-3.02E+00	-4.00E+00	-5.09E+00	-1.64E+00
	Winter	-6.68E+00	-1.41E+00	-5.75E+00	-7.64E+00	-2.03E+00
<i>tetW</i>	Summer	-1.82E+00	-6.69E-01	-1.07E+00	-8.71E-01	-3.27E+00

	Monsoon	7.09E-02	2.95E-02	-9.23E-01	-6.78E-01	-5.21E-01
	Winter	-1.04E+00	-4.45E-01	-5.73E-01	-6.91E-01	-1.73E+00
<i>mcr5</i>	Summer	-3.01E+00	-3.70E+00	-3.20E+00	-3.76E+00	-2.66E+00
	Monsoon	-5.55E-01	-6.81E-01	-2.46E+00	-9.37E-01	-9.20E-01
	Winter	-2.34E+00	-2.37E+00	-2.24E+00	-2.48E+00	-2.41E+00
<i>ermF</i>	Summer	-5.39E-01	-5.76E-01	-4.61E-01	-7.16E-02	-2.74E+00
	Monsoon	6.99E-01	3.48E-01	1.19E-01	-1.27E-01	3.83E-01
	Winter	-3.72E-01	-6.19E-01	-2.85E-01	-4.60E-01	-1.51E+00
Ciprofloxacin	Summer	125.62	91.76	105.19	92.22	31.98
	Monsoon	103.04	90.32	89.43	78.48	46.04
	Winter	100.13	85.39	74.66	72.97	40.68
Triclosan	Summer	204.23	184.20	170.52	141.21	109.63
	Monsoon	188.77	154.25	128.39	134.81	110.64
	Winter	143.87	125.06	95.43	103.49	91.01
Copper	Summer	0.07	0.00	0.00	0.32	0.14
	Monsoon	0.83	0.73	0.40	0.32	0.00
	Winter	0.79	0.75	0.42	0.78	0.18
Lead	Summer	0.00	0.00	0.15	0.00	0.00
	Monsoon	0.37	0.25	0.22	0.09	0.00
	Winter	0.36	0.36	0.24	0.20	0.00
Chromium	Summer	0.00	1.27	0.41	0.00	0.00
	Monsoon	3.20	4.18	3.90	2.52	2.44
	Winter	4.37	3.86	4.11	3.80	3.77

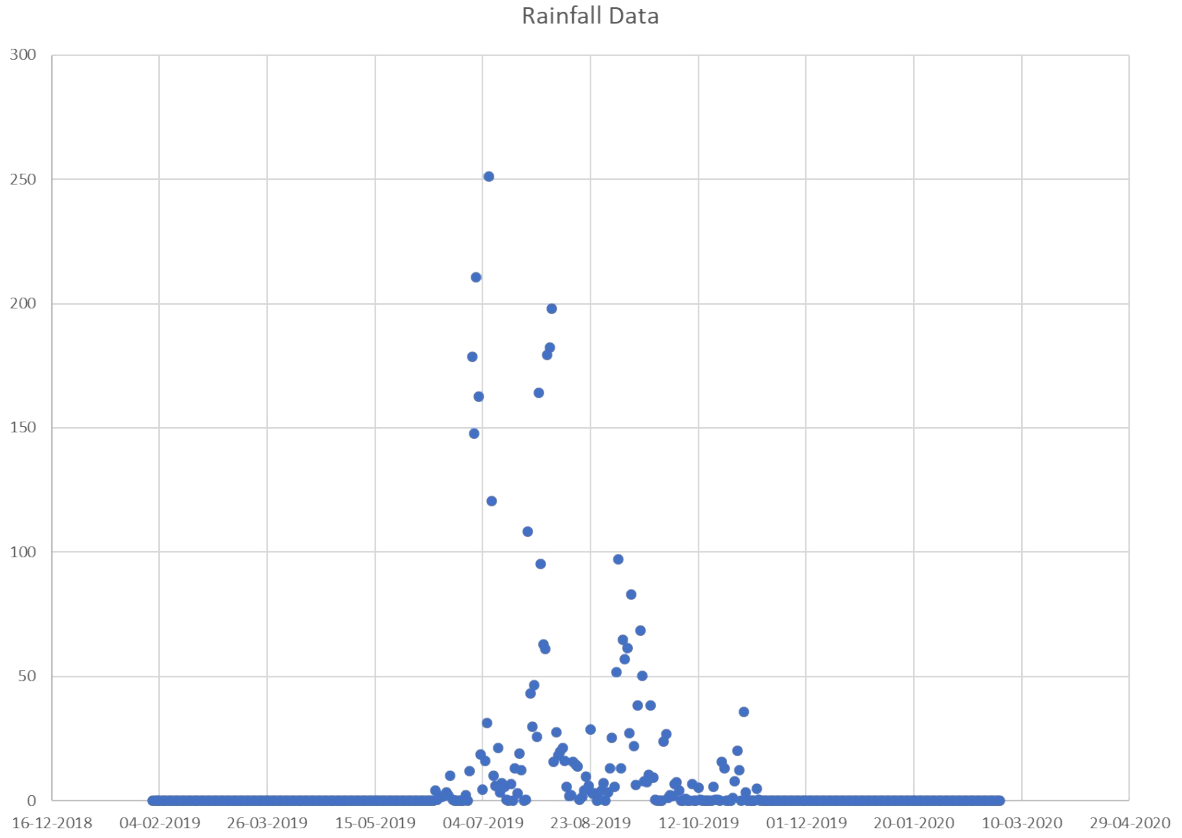


Figure S1: Average daily rainfall in mm during the sampling period in the city Chennai.

Data was obtained from IMD website^{25,26}.

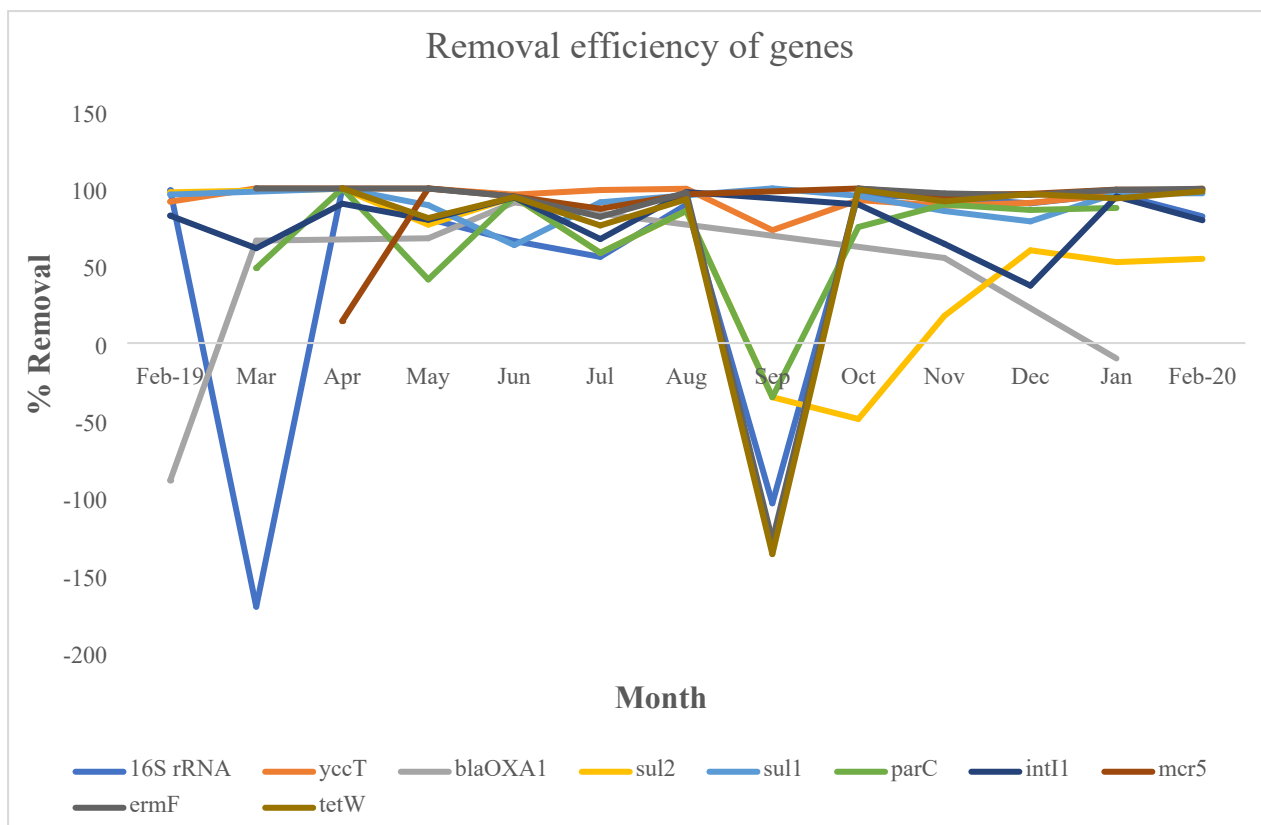


Figure S2: Removal efficiencies of the targeted genes in the STP from Feb 2019 (Feb19) all through the remaining months in 2019 till Feb 2020 (Feb 20).

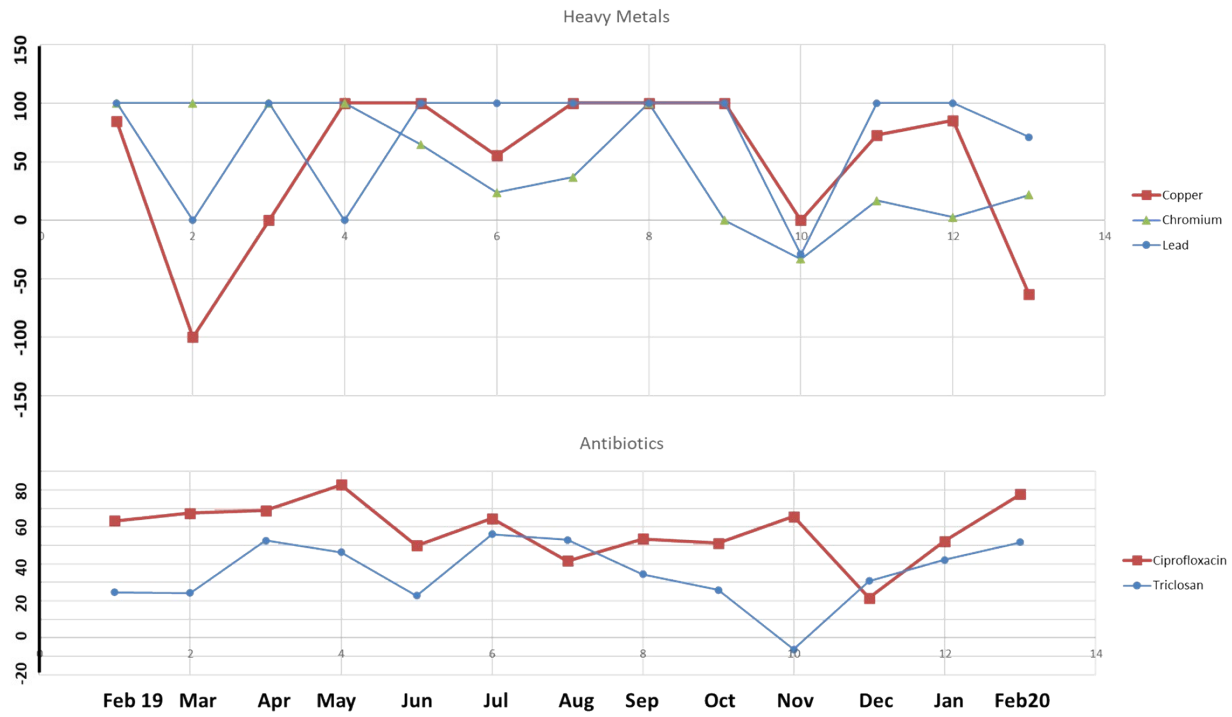


Figure S3: Removal efficiencies of the co-selectors from the STP from Feb 2019 (Feb19) all through the remaining months in 2019 till Feb 2020 (Feb 20).

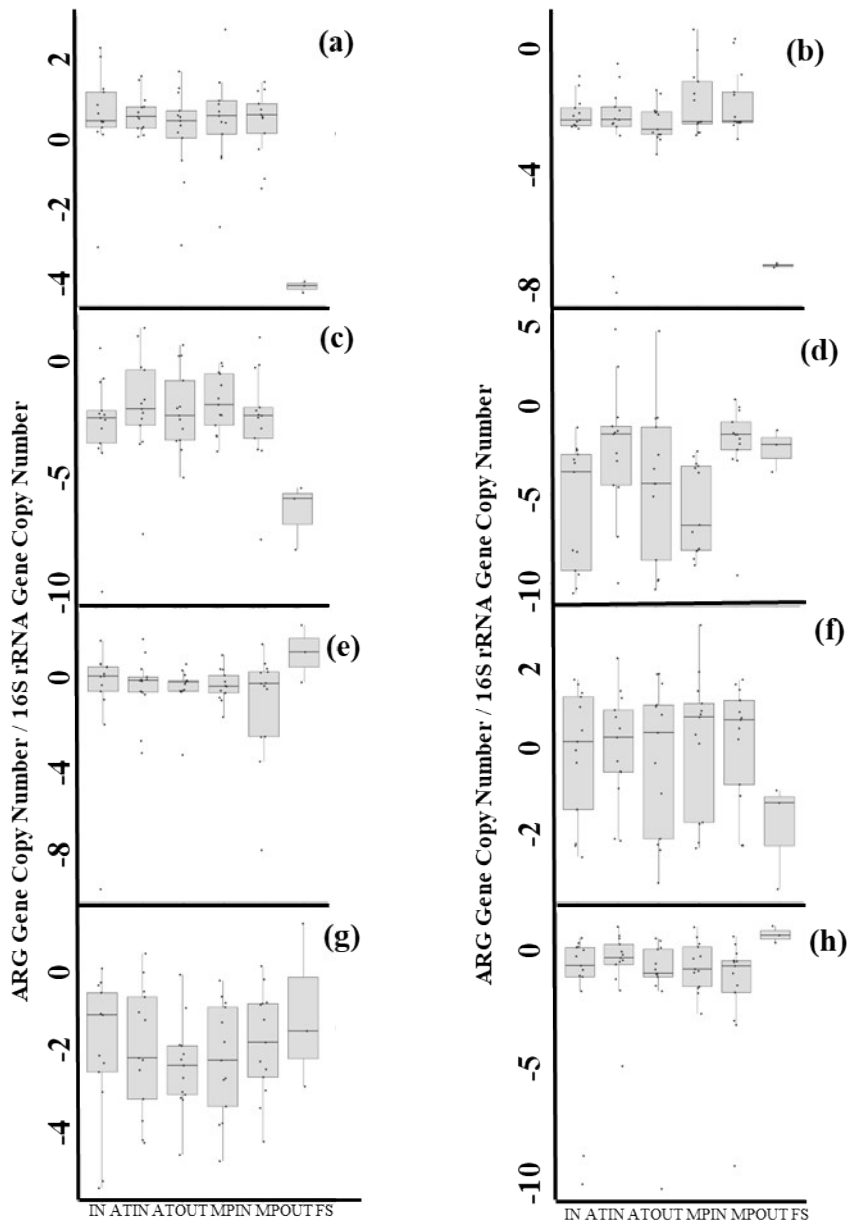


Figure S4: The overall relative abundance of the respective ARGs in the STP over the sampling period: a) *sul1*, b) *sul2*, c) *parC*, d) *bla*_{OXA-1}, e) *ermF*, f) *int11*, g) *mcr5*, and h) *tetW*. The x-axis represents different sampling locations within the targeted STP: IN – Grit chamber outlet (n=13), ATIN – Inlet of aeration tank i.e., sample collected post primary treatment (n=13), ATOUT – Outlet of aeration tank (n=13), MPIN – Inlet of maturation pond (n=13), MPOUT – Outlet of maturation pond and (n=13), FS - Final sludge collected after the drying of the anaerobically digested sludge (n=3).

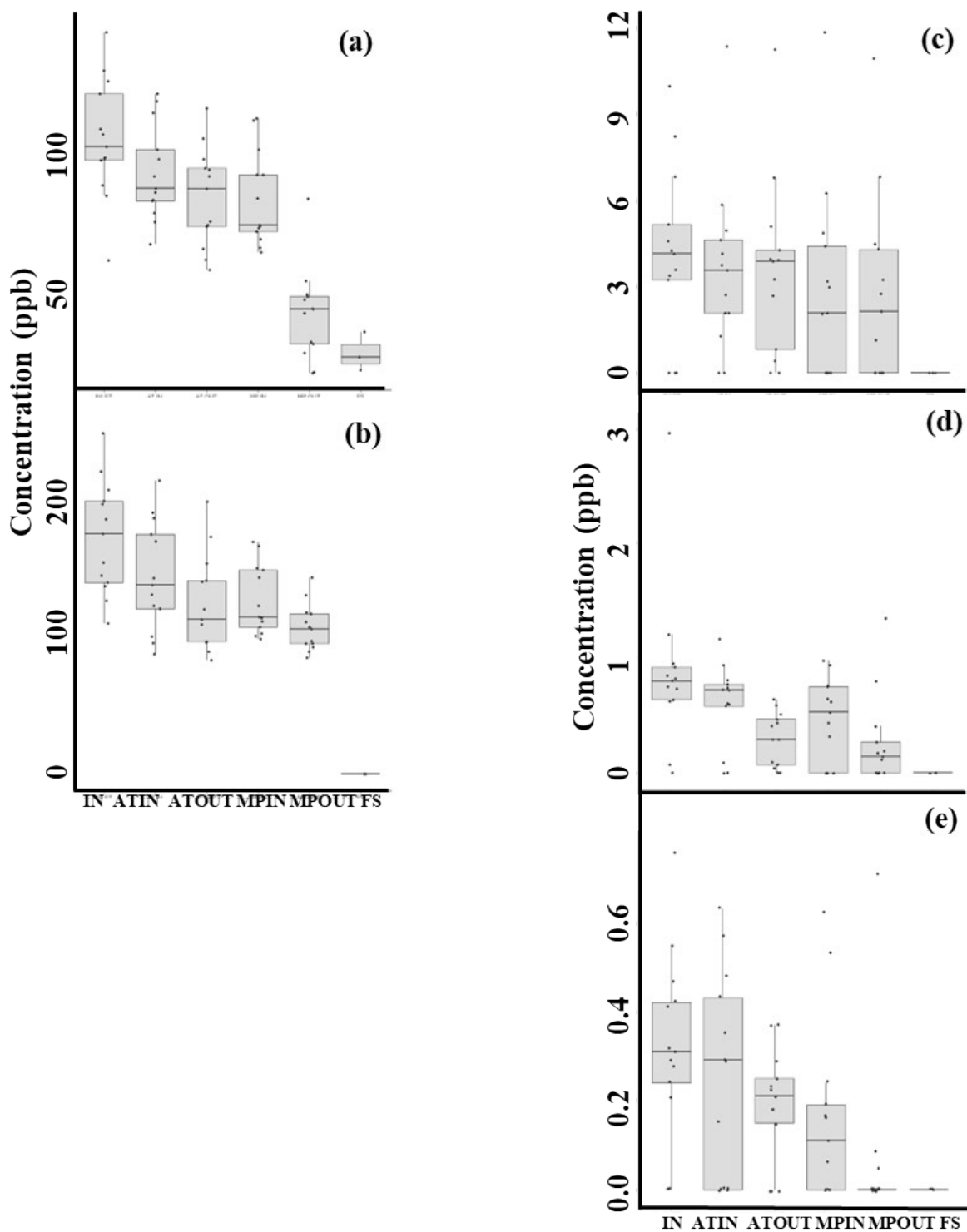


Figure S5: The y-axis represents the levels of co-selective agents over the sampling period: **a.** Ciprofloxacin, **b.** Triclosan, **c.** Chromium, **d.** Copper, and **e.** Lead in ppb. The x-axis represents different sampling locations within the targeted STP: IN – Grit chamber outlet (n=13), ATIN – Inlet of aeration tank i.e., sample collected post primary treatment (n=13),

ATOUT – Outlet of aeration tank (n=13), MPIN – Inlet of maturation pond (n=13), and MPOUT – Outlet of maturation pond and (n=13), FS - Final sludge collected after the drying of the anaerobically digested sludge (n=3).

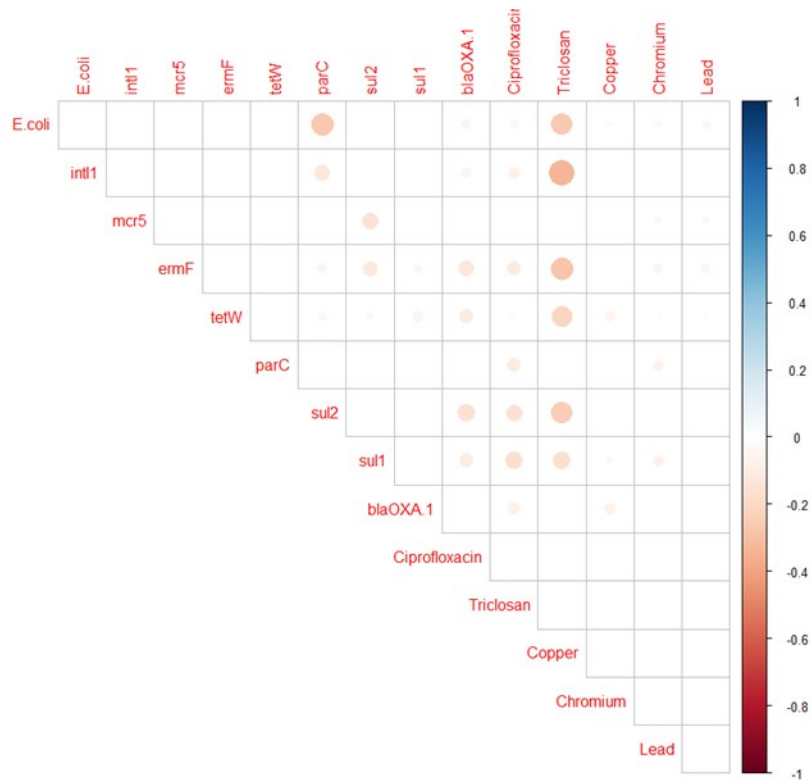


Figure S6: The correlogram indicating Spearman correlation coefficient (when p-value <0.05) between the relative levels of the ARGs and the co-selective agents (having the absolute values)

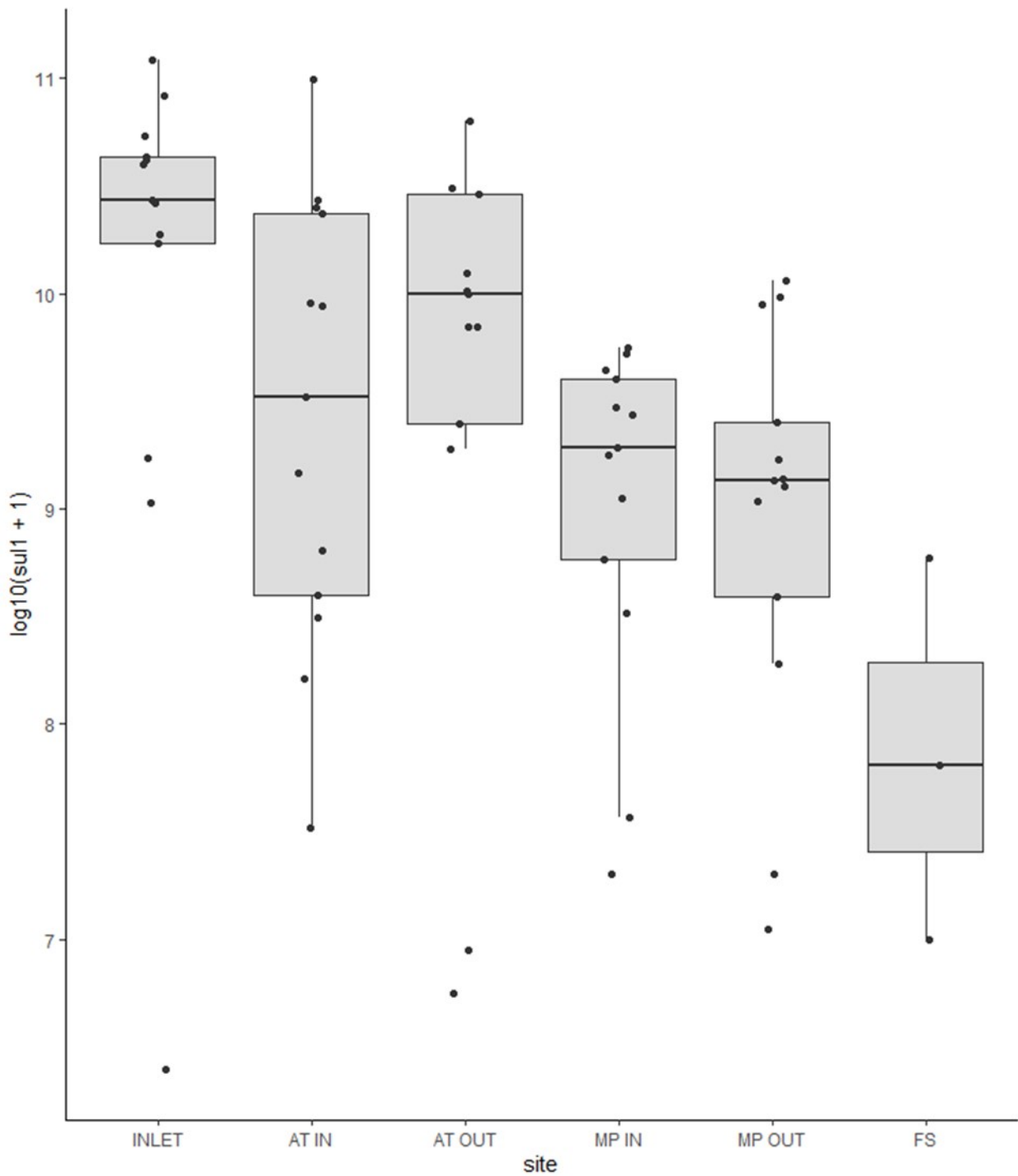


Figure S7: The y-axis represents the absolute abundance of *sul1* at different sites in the STP over the sampling period. The x-axis represents different sampling locations within the targeted STP: IN – Grit chamber outlet (n=13), ATIN – Inlet of aeration tank i.e., sample collected post primary treatment (n=13), ATOUT – Outlet of aeration tank (n=13), MPIN –

Inlet of maturation pond (n=13), and MPOUT – Outlet of maturation pond and (n=13), FS - Final sludge collected after the drying of the anaerobically digested sludge (n=3).

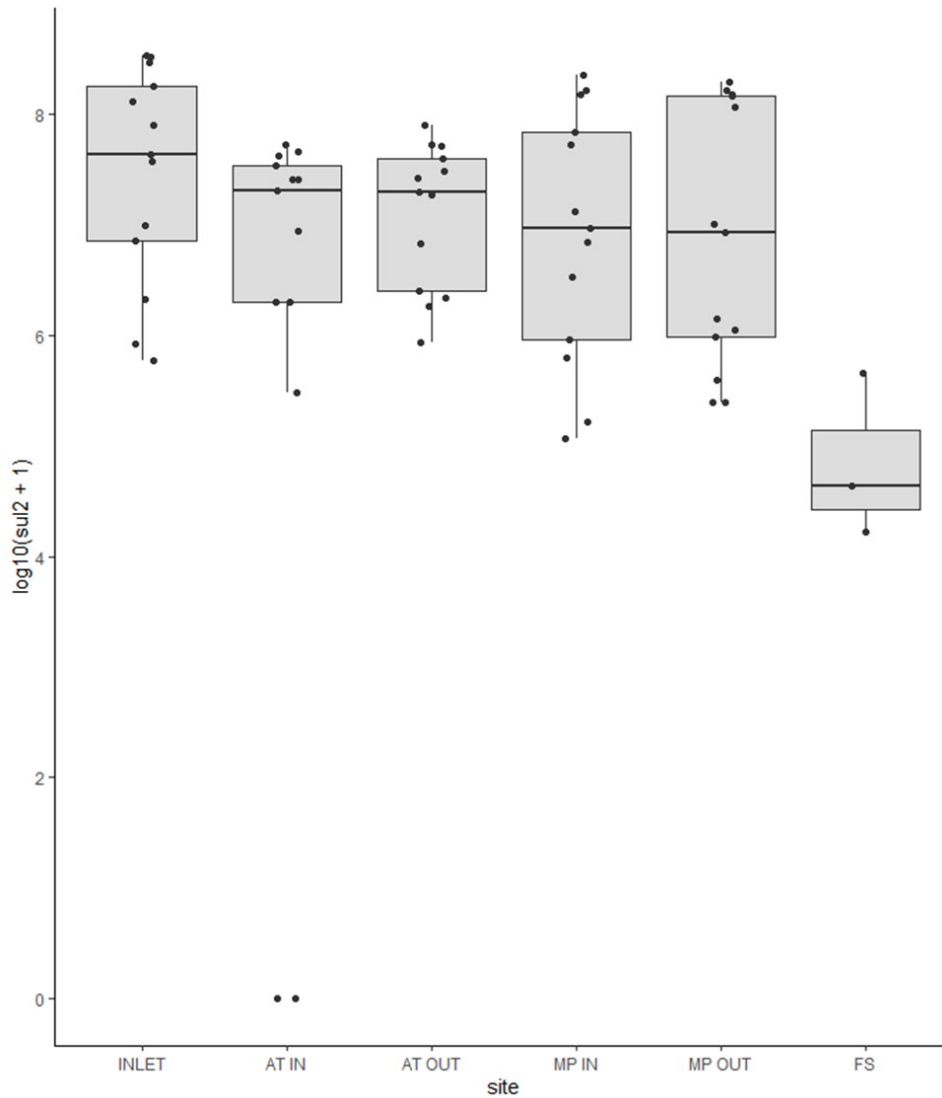


Figure S8: The y-axis represents the absolute abundance of *sul2* at different sites in the STP over the sampling period. The x-axis represents different sampling locations within the targeted STP: IN – Grit chamber outlet (n=13), ATIN – Inlet of aeration tank i.e., sample collected post primary treatment (n=13), ATOUT – Outlet of aeration tank (n=13), MPIN – Inlet of maturation pond (n=13), and MPOUT – Outlet of maturation pond and (n=13), FS - Final sludge collected after the drying of the anaerobically digested sludge (n=3).

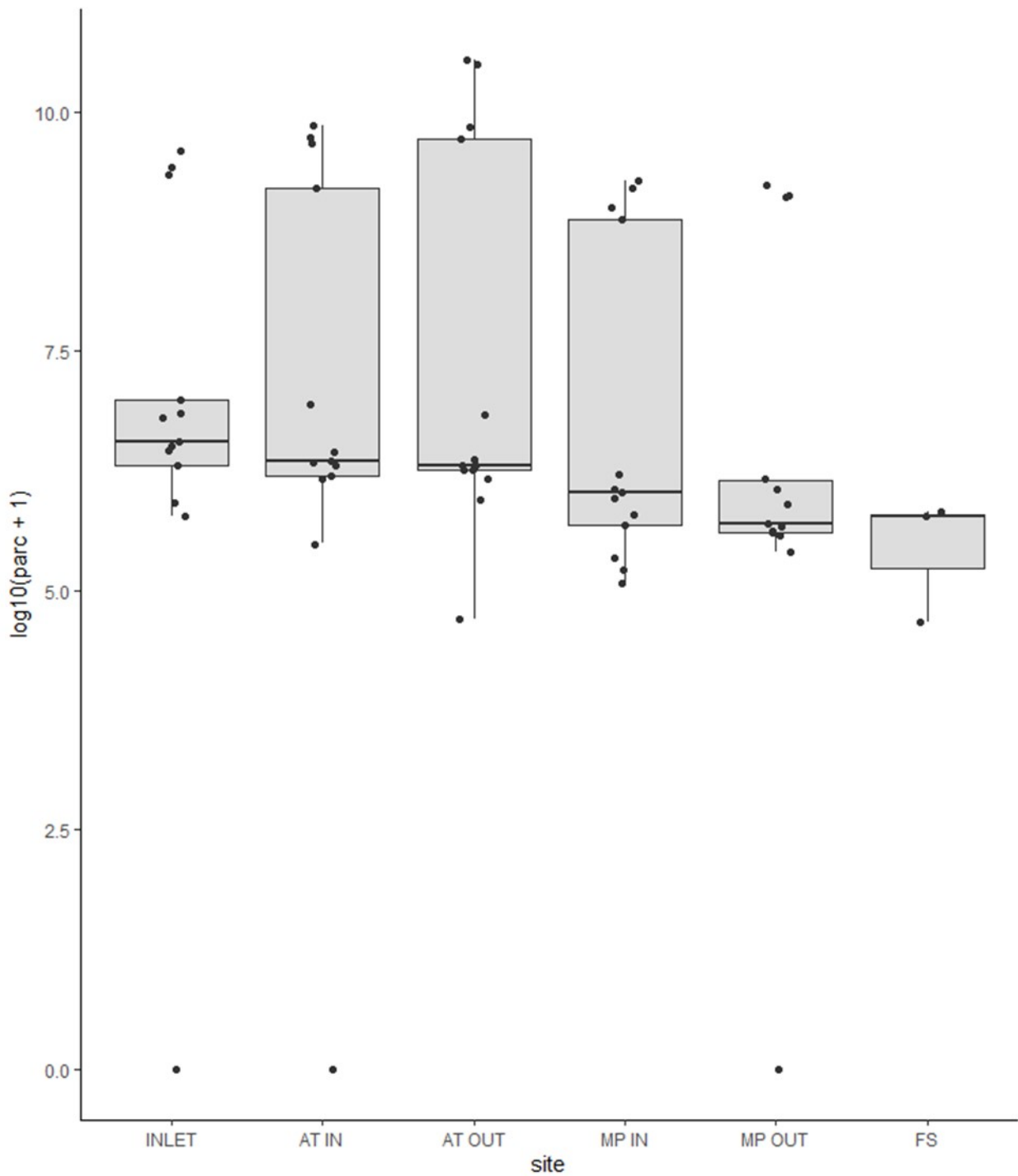


Figure S9: The y-axis represents the absolute abundance of *parC* at different sites in the STP over the sampling period. The x-axis represents different sampling locations within the targeted STP: IN – Grit chamber outlet (n=13), ATIN – Inlet of aeration tank i.e., sample collected post primary treatment (n=13), ATOUT – Outlet of aeration tank (n=13), MPIN –

Inlet of maturation pond (n=13), and MPOUT – Outlet of maturation pond and (n=13), FS - Final sludge collected after the drying of the anaerobically digested sludge (n=3).

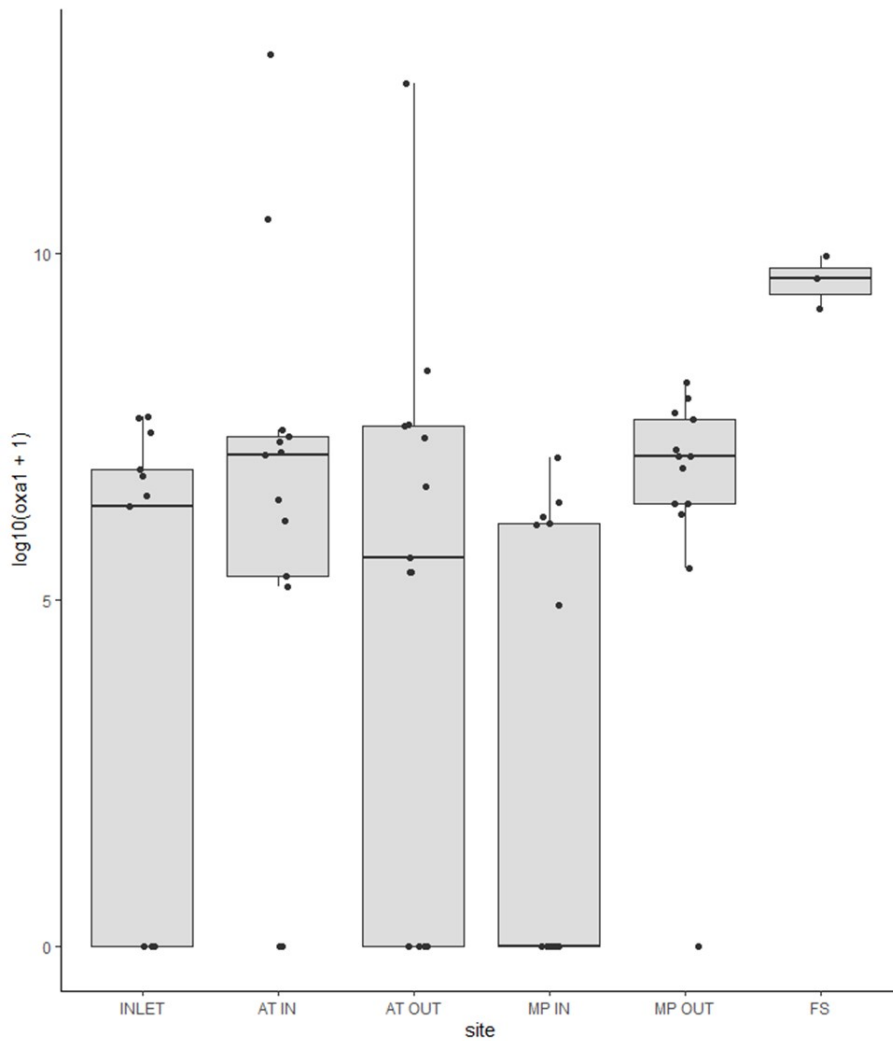


Figure S10: The y-axis represents the absolute abundance of *bla*_{OXA-1} at different sites in the STP over the sampling period. The x-axis represents different sampling locations within the targeted STP: IN – Grit chamber outlet (n=13), ATIN – Inlet of aeration tank i.e., sample collected post primary treatment (n=13), ATOUT – Outlet of aeration tank (n=13), MPIN – Inlet of maturation pond (n=13), and MPOUT – Outlet of maturation pond and (n=13), FS - Final sludge collected after the drying of the anaerobically digested sludge (n=3).

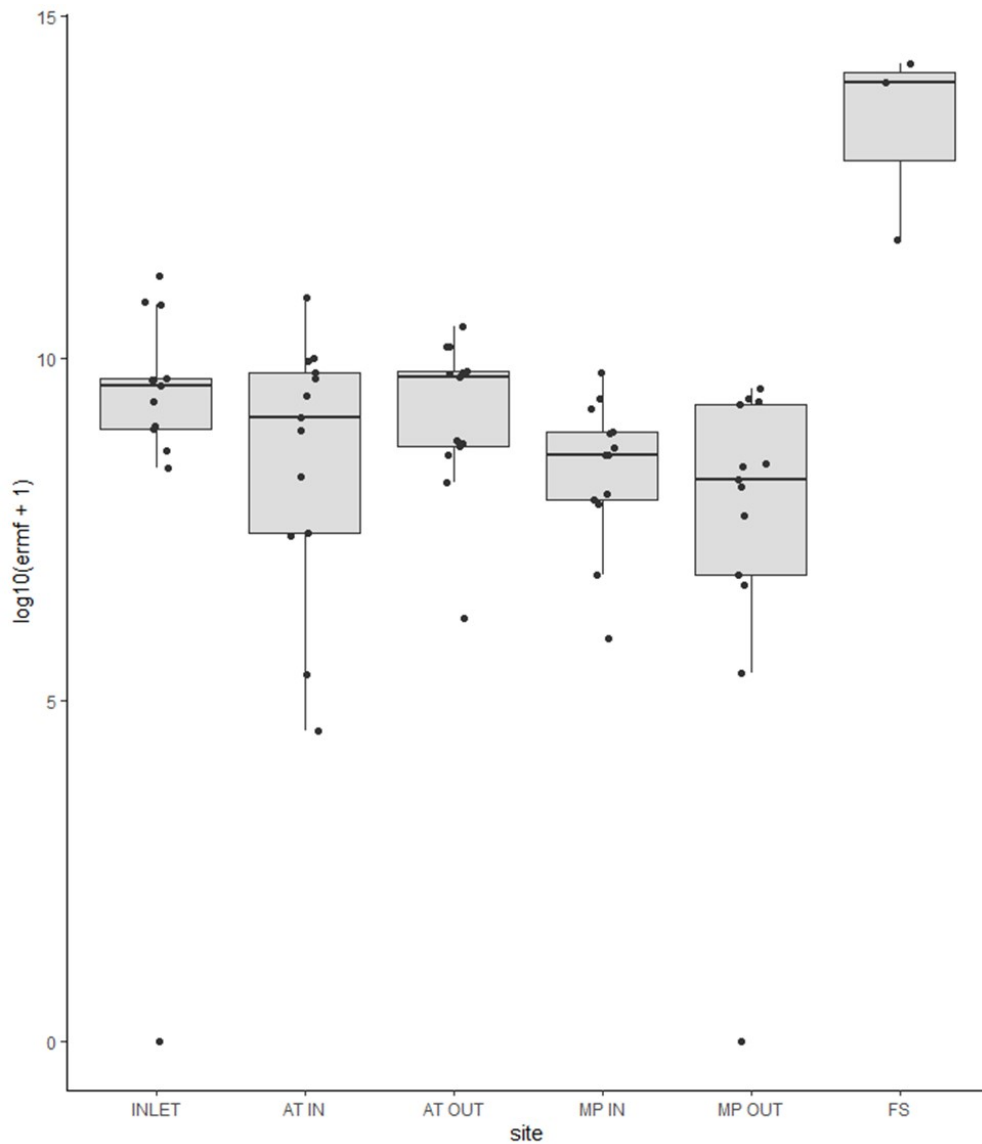


Figure S11: The y-axis represents the absolute abundance of *ermF* at different sites in the STP over the sampling period. The x-axis represents different sampling locations within the targeted STP: IN – Grit chamber outlet (n=13), ATIN – Inlet of aeration tank i.e., sample collected post primary treatment (n=13), ATOUT – Outlet of aeration tank (n=13), MPIN – Inlet of maturation pond (n=13), and MPOUT – Outlet of maturation pond and (n=13), FS - Final sludge collected after the drying of the anaerobically digested sludge (n=3).

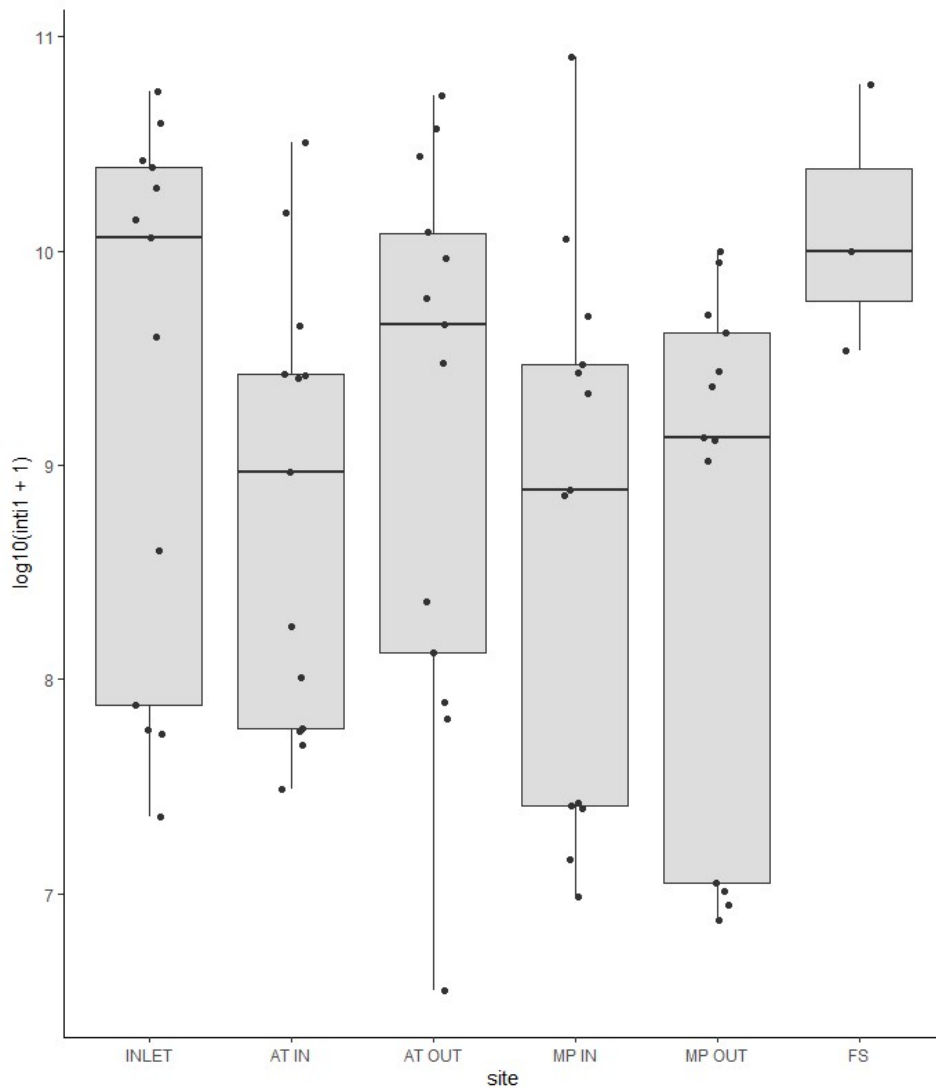


Figure S12: The y-axis represents the absolute abundance of *intI1* at different sites in the STP over the sampling period. The x-axis represents different sampling locations within the targeted STP: IN – Grit chamber outlet (n=13), ATIN – Inlet of aeration tank i.e., sample collected post primary treatment (n=13), ATOUT – Outlet of aeration tank (n=13), MPIN – Inlet of maturation pond (n=13), and MPOUT – Outlet of maturation pond and (n=13), FS - Final sludge collected after the drying of the anaerobically digested sludge (n=3).

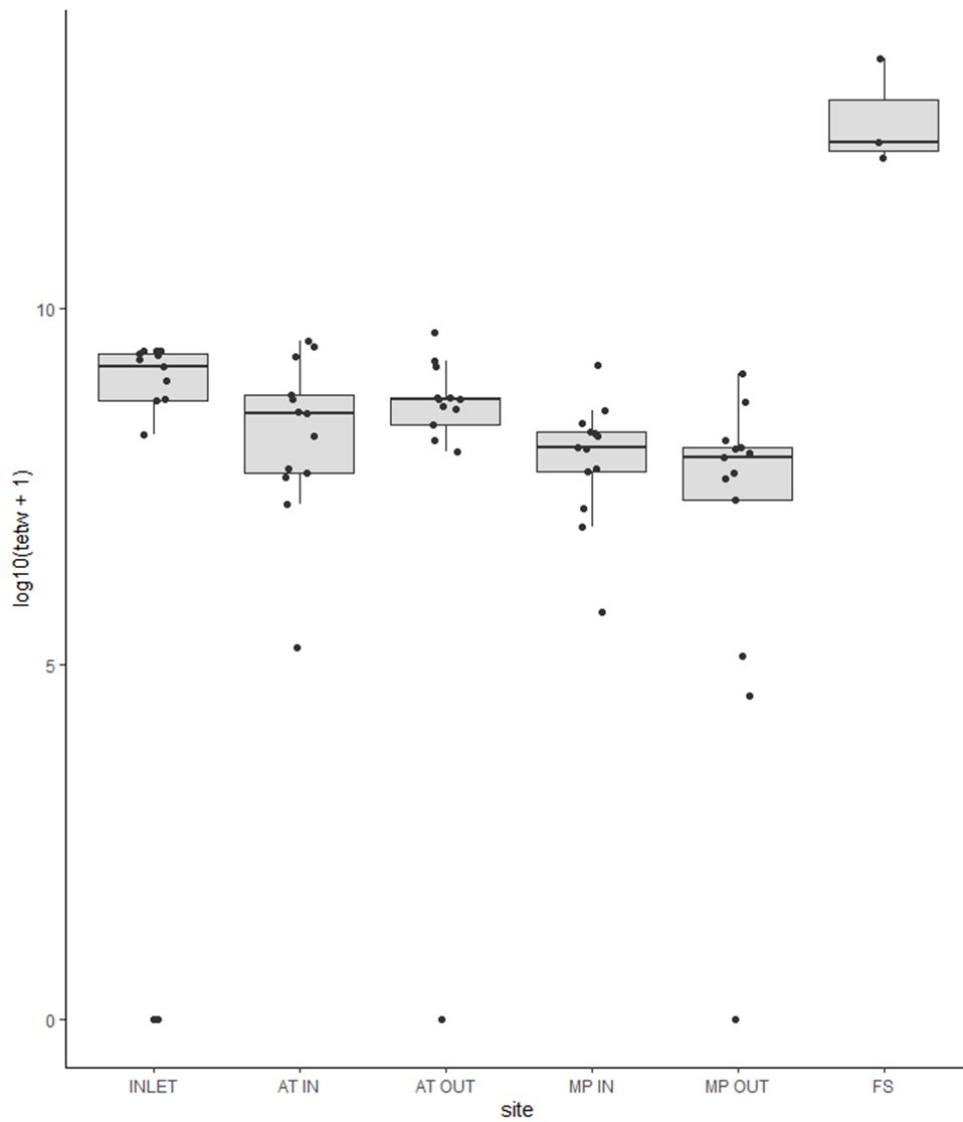


Figure S13: The y-axis represents the absolute abundance of *tetW* at different sites in the STP over the sampling period. The x-axis represents different sampling locations within the targeted STP: IN – Grit chamber outlet (n=13), ATIN – Inlet of aeration tank i.e., sample collected post primary treatment (n=13), ATOUT – Outlet of aeration tank (n=13), MPIN – Inlet of maturation pond (n=13), and MPOUT – Outlet of maturation pond and (n=13), FS - Final sludge collected after the drying of the anaerobically digested sludge (n=3).

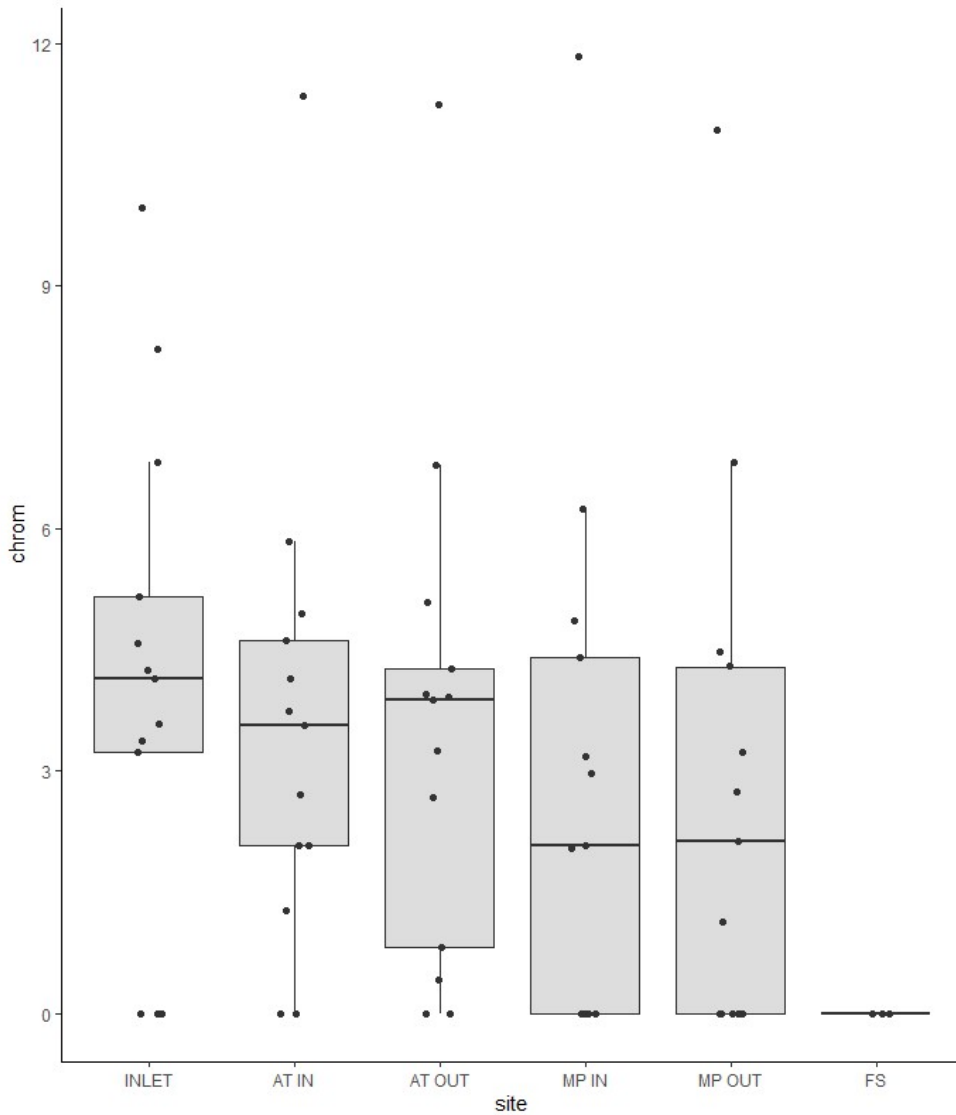


Figure S14: The y-axis represents the concentration of chromium at different sites in the STP over the sampling period. The x-axis represents different sampling locations within the targeted STP: IN – Grit chamber outlet (n=13), ATIN – Inlet of aeration tank i.e., sample collected post primary treatment (n=13), ATOUT – Outlet of aeration tank (n=13), MPIN – Inlet of maturation pond (n=13), and MPOUT – Outlet of maturation pond and (n=13), FS - Final sludge collected after the drying of the anaerobically digested sludge (n=3).

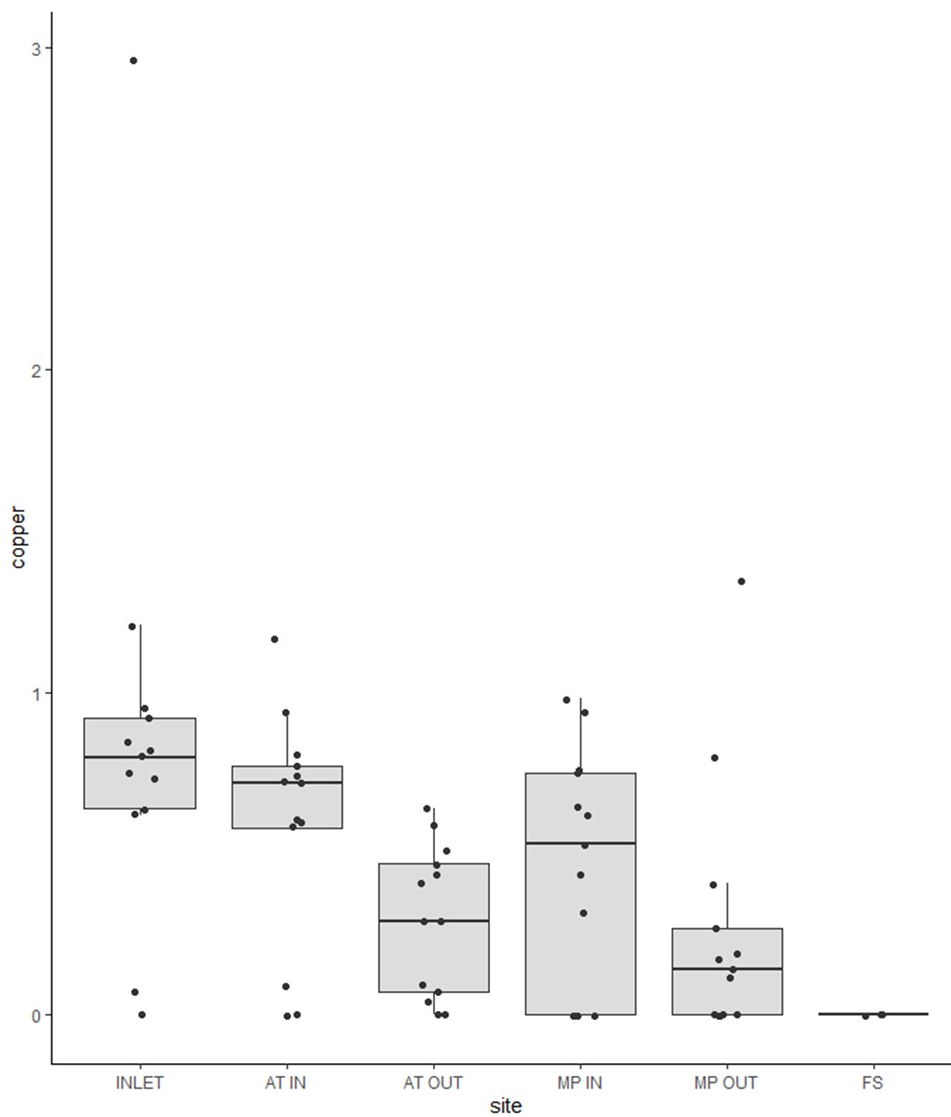


Figure S15: The y-axis represents the concentration of copper at different sites in the STP over the sampling period. The x-axis represents different sampling locations within the targeted STP: IN – Grit chamber outlet (n=13), ATIN – Inlet of aeration tank i.e., sample collected post primary treatment (n=13), ATOUT – Outlet of aeration tank (n=13), MPIN – Inlet of maturation pond (n=13), and MPOUT – Outlet of maturation pond and (n=13), FS - Final sludge collected after the drying of the anaerobically digested sludge (n=3).

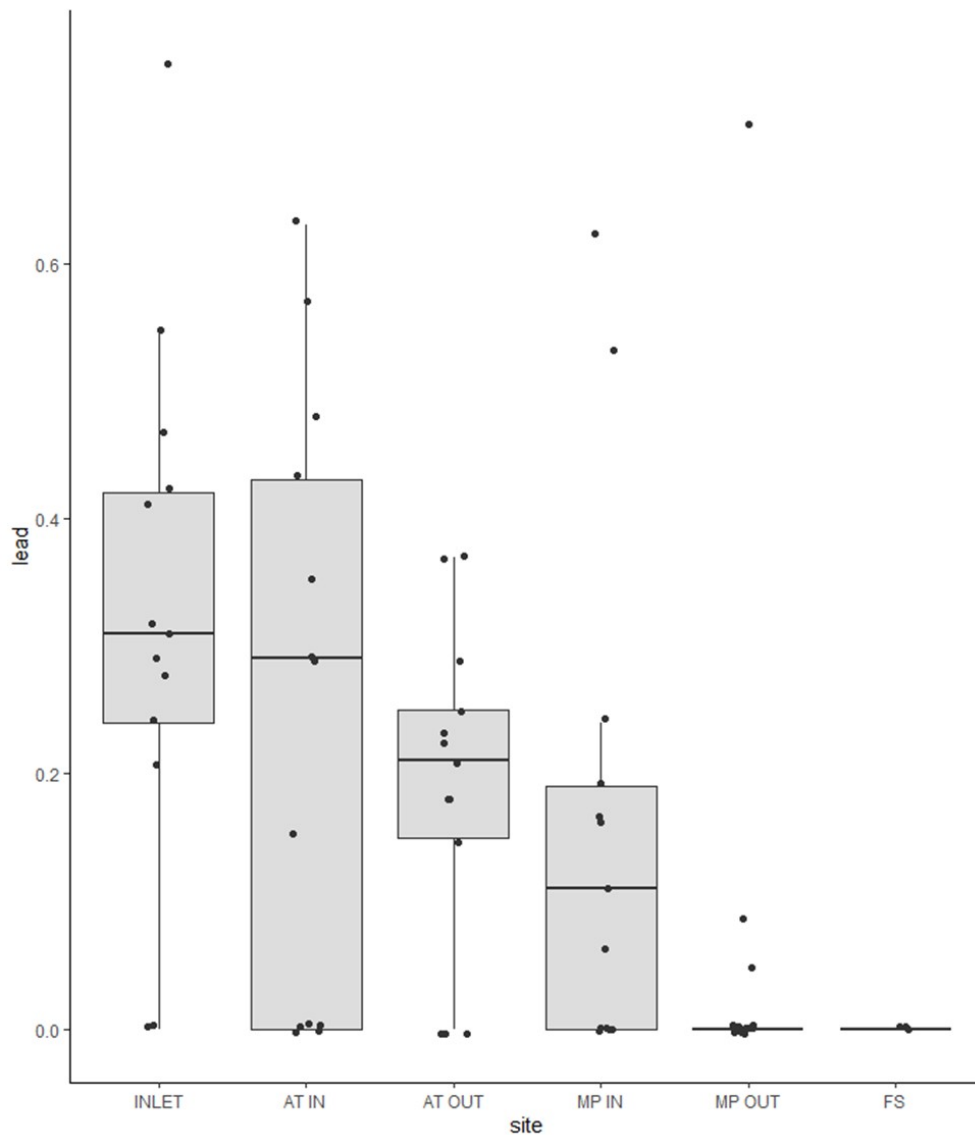


Figure S16: The y-axis represents the concentration of lead at different sites in the STP over the sampling period. The x-axis represents different sampling locations within the targeted STP: IN – Grit chamber outlet (n=13), ATIN – Inlet of aeration tank i.e., sample collected post primary treatment (n=13), ATOUT – Outlet of aeration tank (n=13), MPIN – Inlet of maturation pond (n=13), and MPOUT – Outlet of maturation pond and (n=13), FS - Final sludge collected after the drying of the anaerobically digested sludge (n=3).

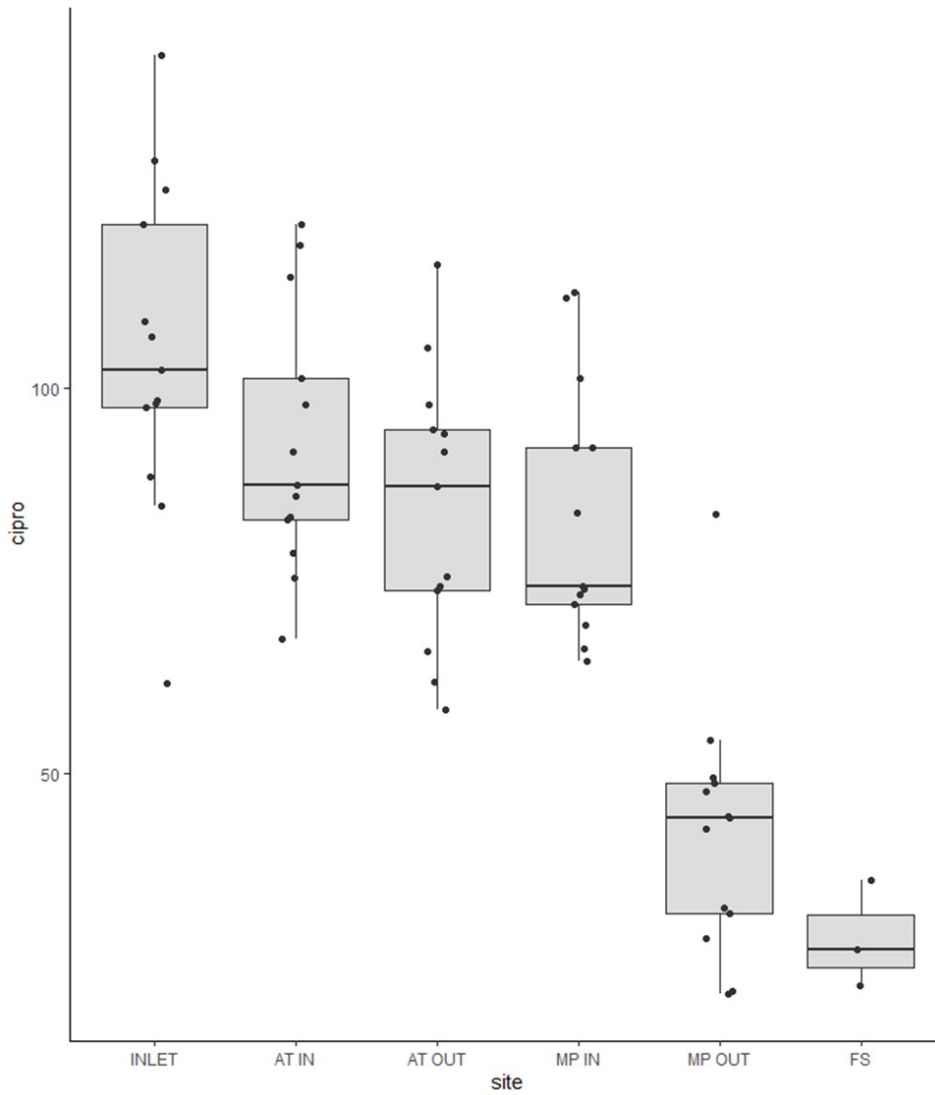


Figure S17: The y-axis represents the concentration of ciprofloxacin at different sites in the STP over the sampling period. The x-axis represents different sampling locations within the targeted STP: IN – Grit chamber outlet (n=13), ATIN – Inlet of aeration tank i.e., sample collected post primary treatment (n=13), ATOUT – Outlet of aeration tank (n=13), MPIN – Inlet of maturation pond (n=13), and MPOUT – Outlet of maturation pond and (n=13), FS - Final sludge collected after the drying of the anaerobically digested sludge (n=3).

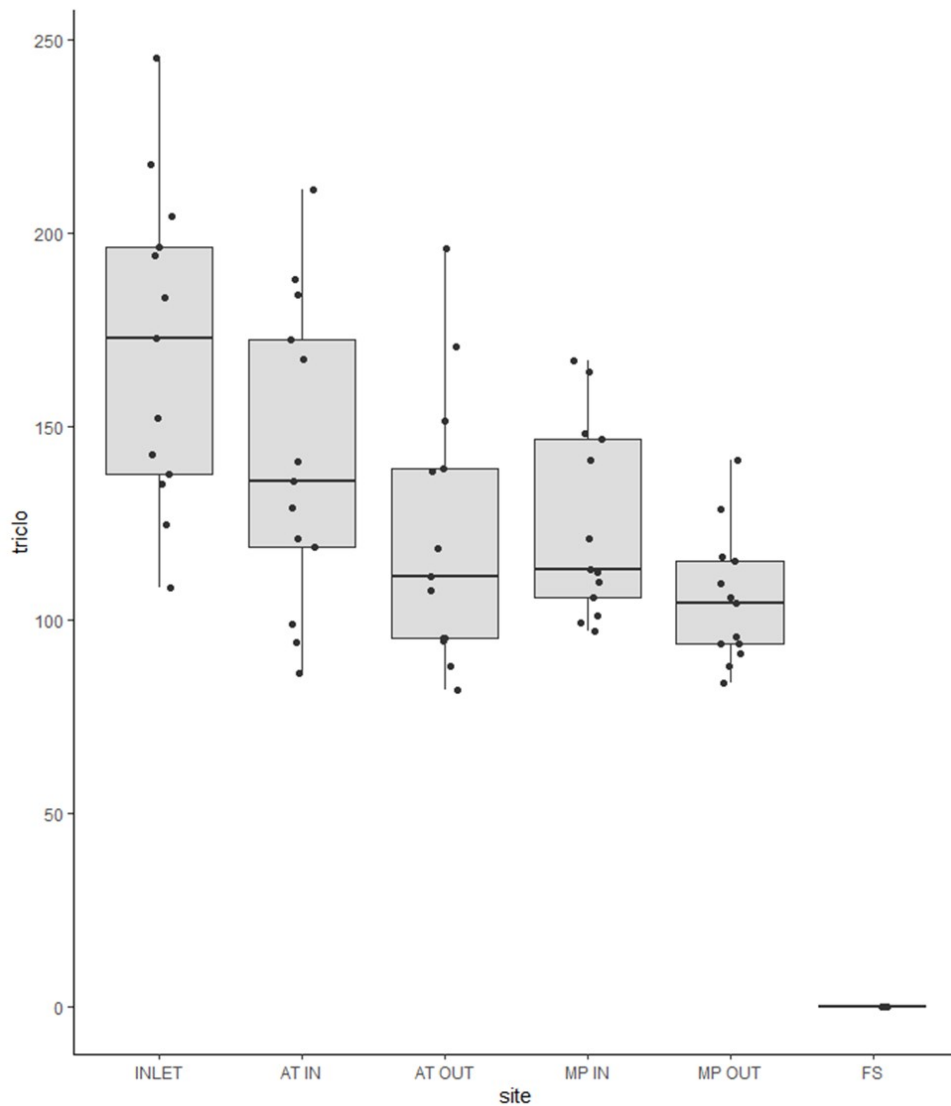


Figure S18: The y-axis represents the concentration of triclosan at different sites in the STP over the sampling period. The x-axis represents different sampling locations within the targeted STP: IN – Grit chamber outlet (n=13), ATIN – Inlet of aeration tank i.e., sample collected post primary treatment (n=13), ATOUT – Outlet of aeration tank (n=13), MPIN – Inlet of maturation pond (n=13), and MPOUT – Outlet of maturation pond and (n=13), FS - Final sludge collected after the drying of the anaerobically digested sludge (n=3).

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