Electronic Supplementary Material (ESI) for Environmental Science: Water Research & Technology.

Supplemental Information

Bacterial communities in a Neotropical full-scale drinking water system including intermittent piped water supply, from sources to taps

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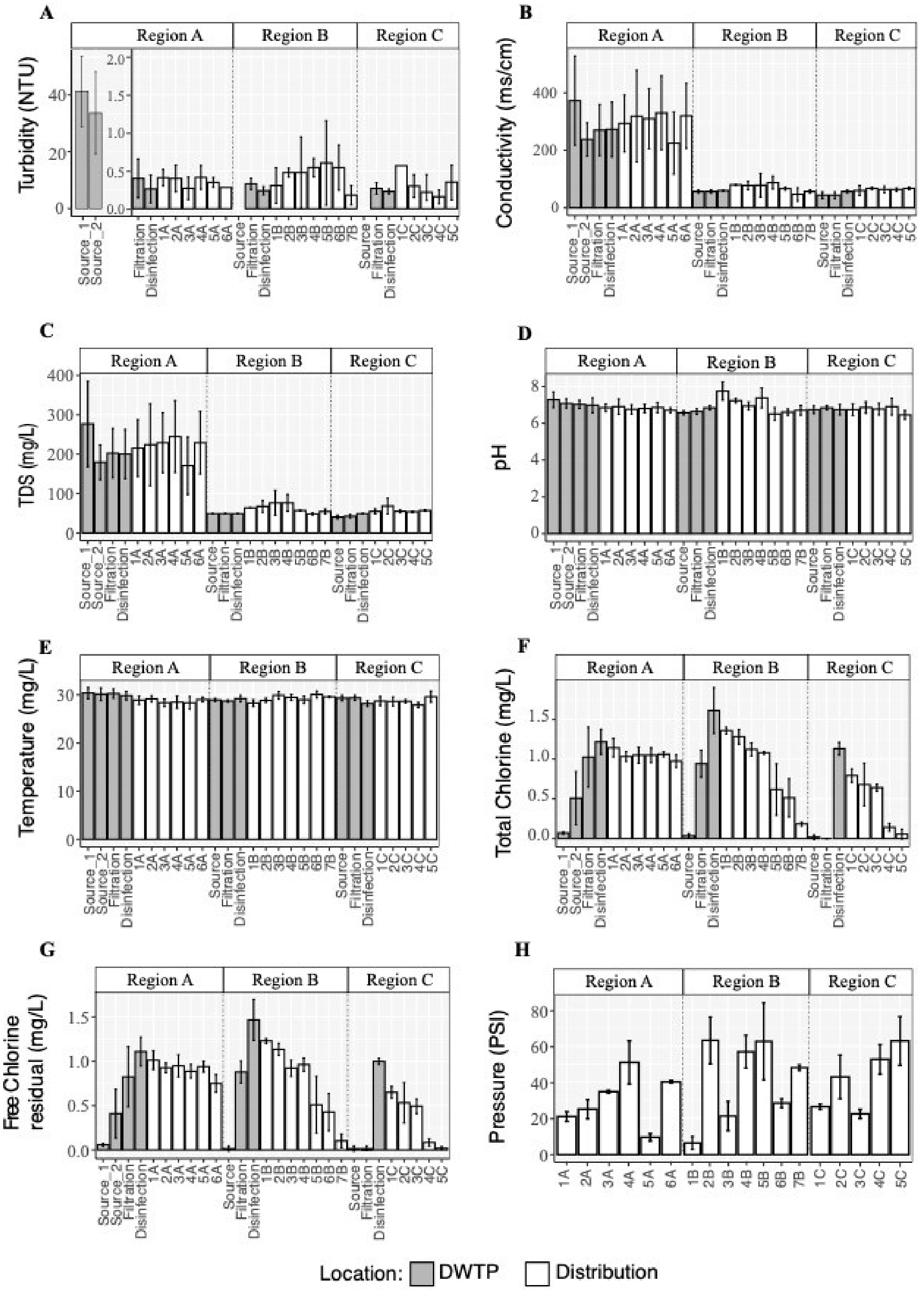
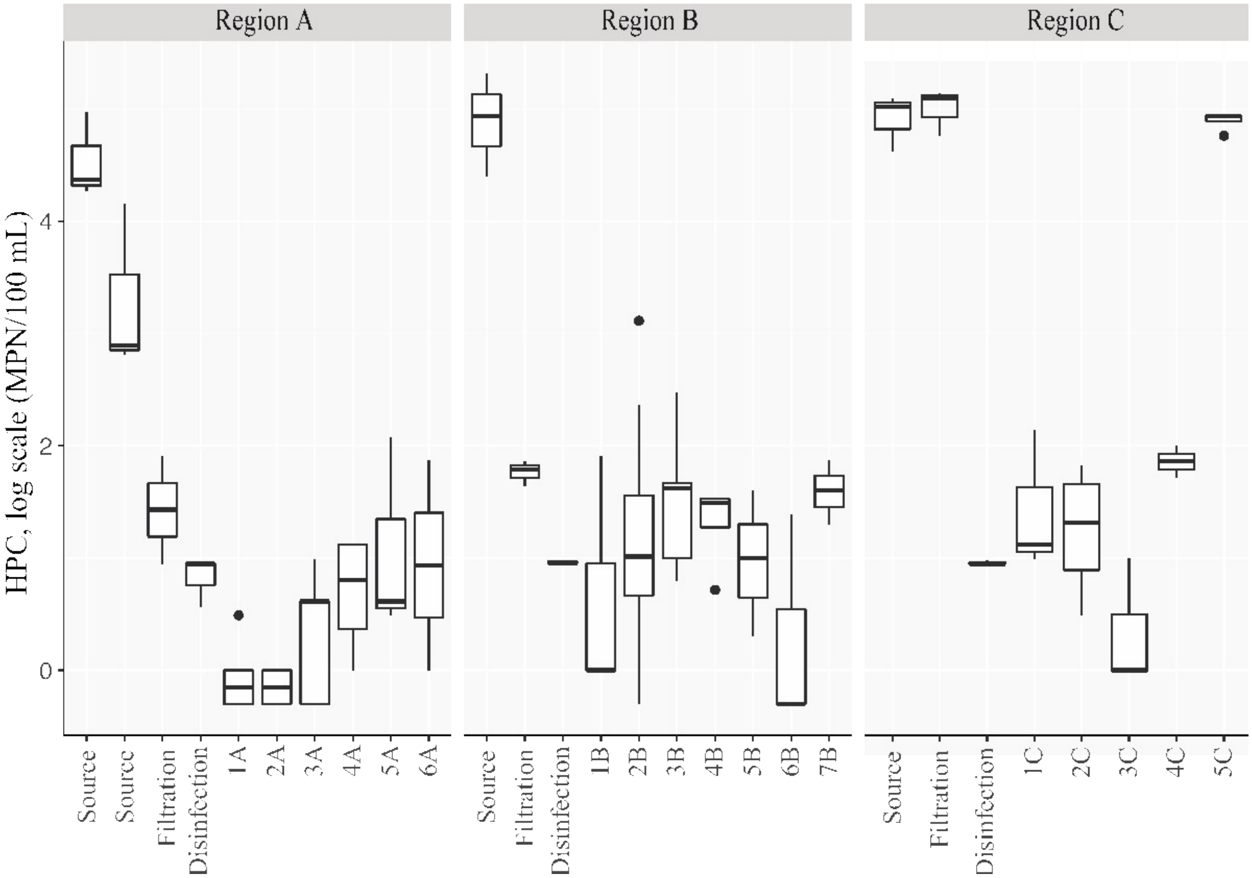
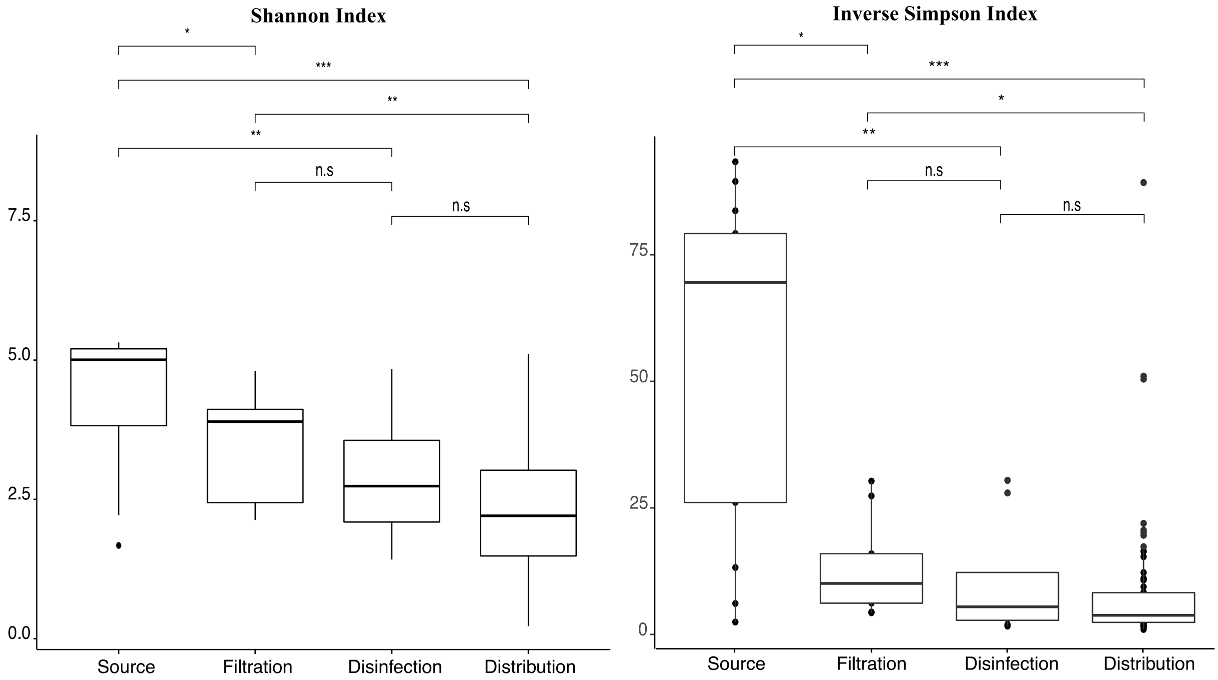
Supplemental Figure 1-8.
Supplemental Tables 1 & 4.
See Supplemental Tables 2 & 5 in excel document.



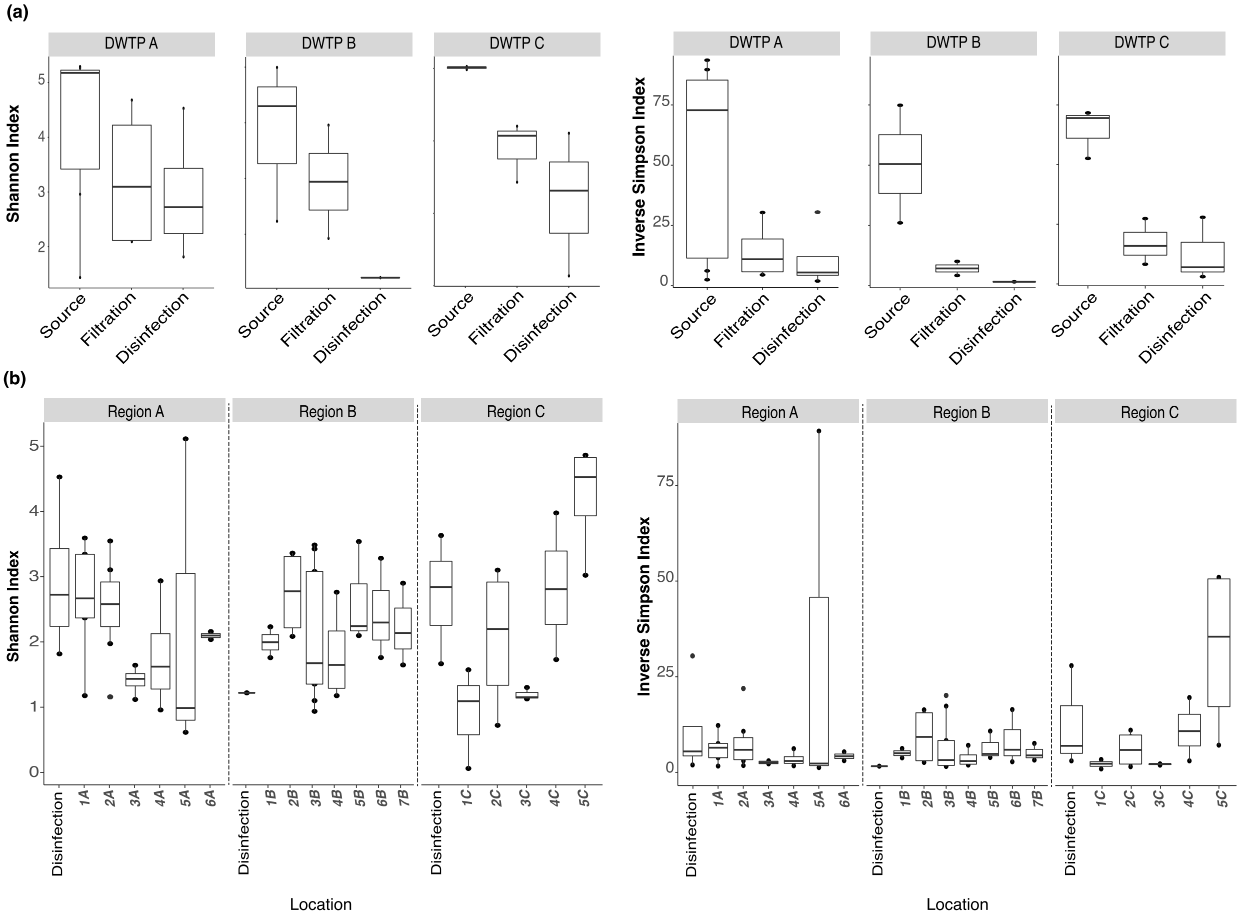
Supplemental Figure 1. Mean and standard deviation of water quality metrics measured in this study (on site). Each location was sampled three to four times. Measurements are divided in three regions that correspond to the three DWTPs that served Arraiján, Panama. Locations in the distribution system were labelled based on distance to the DWTP it is supplied from (i.e., the highest location number corresponds to the farthest location). Only Stable IWS samples were included for location 3B (IWS) in this part of the analysis. TDS = Total dissolved solids.



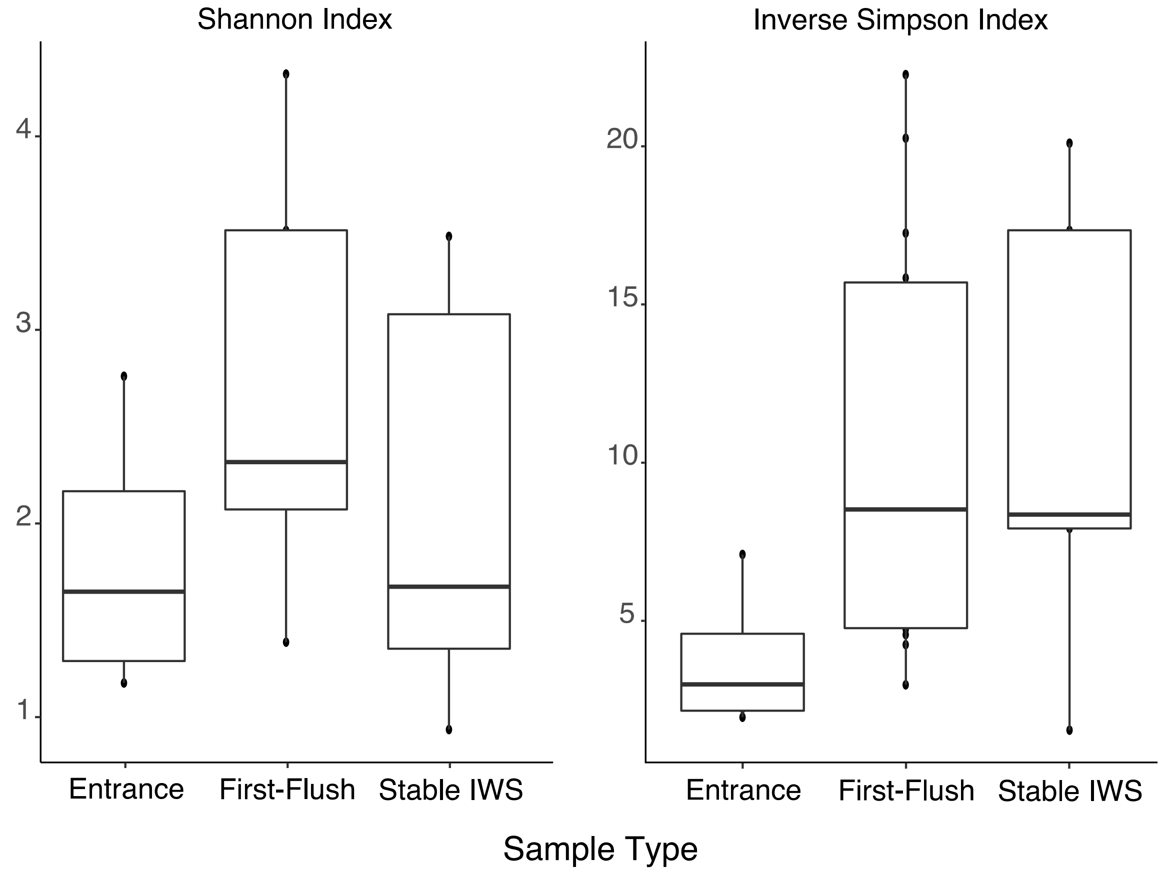
Supplemental Figure 2. Heterotrophic plate count (HPC) concentrations found across sample types and sampling locations. Measurements are divided in three regions that correspond to the three DWTPs that served Arraiján, Panama. Locations in the distribution system were labelled based on distance to the DWTP it is supplied from (i.e., the highest location number corresponds to the farthest location). Only Stable IWS samples were included for location 3B (IWS) in this part of the analysis. MPN = Most probable number.



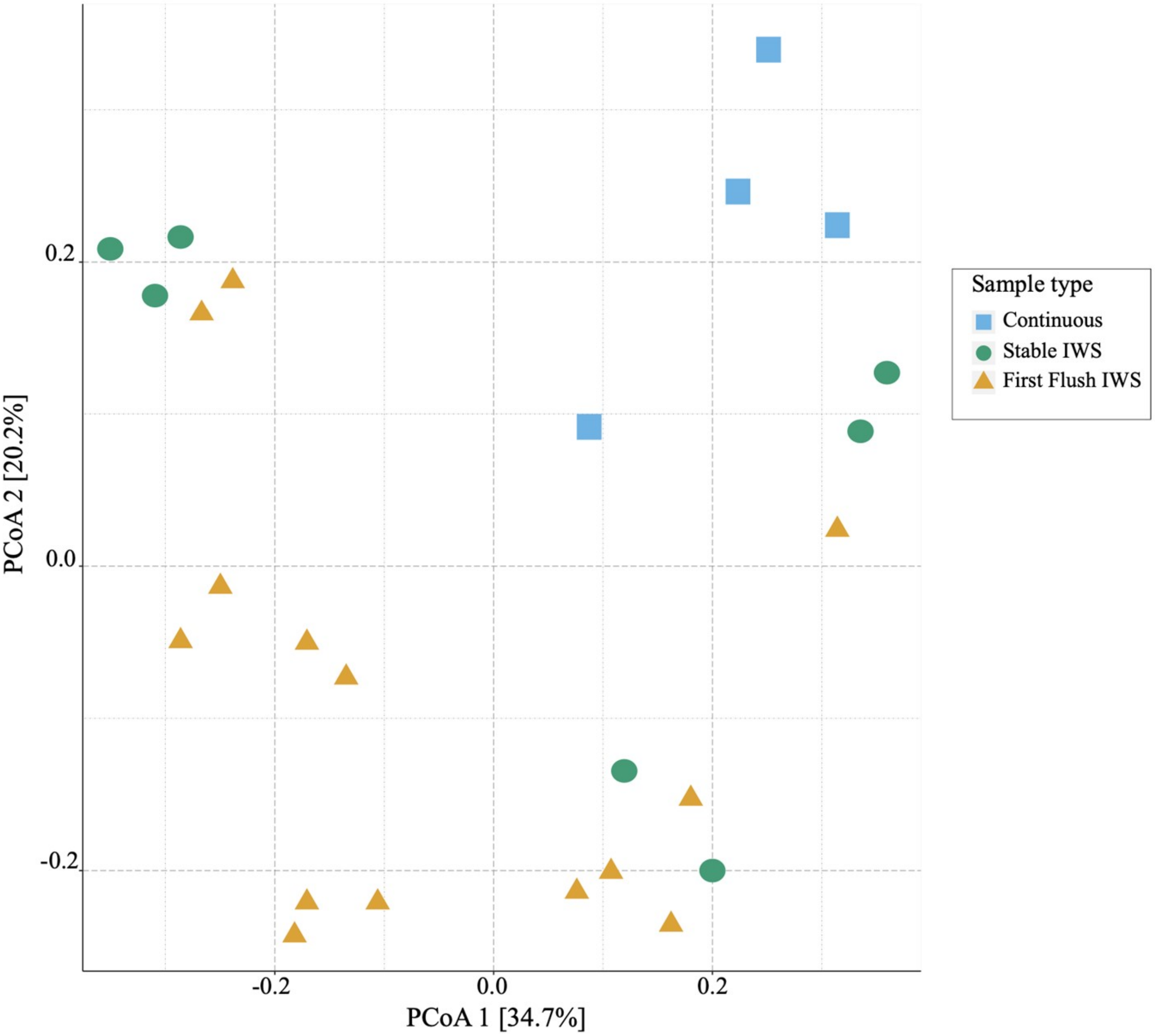
Supplemental Figure 3. Alpha diversity metrics (Shannon and Inverse Simpson Indices) for the different sample types in this study. Asterix represent statistical significance (Kruskal-Wallis tests with bonferroni corrections) * = ($p < 0.05$), ** = ($p < 0.01$), *** = ($p < 0.001$).



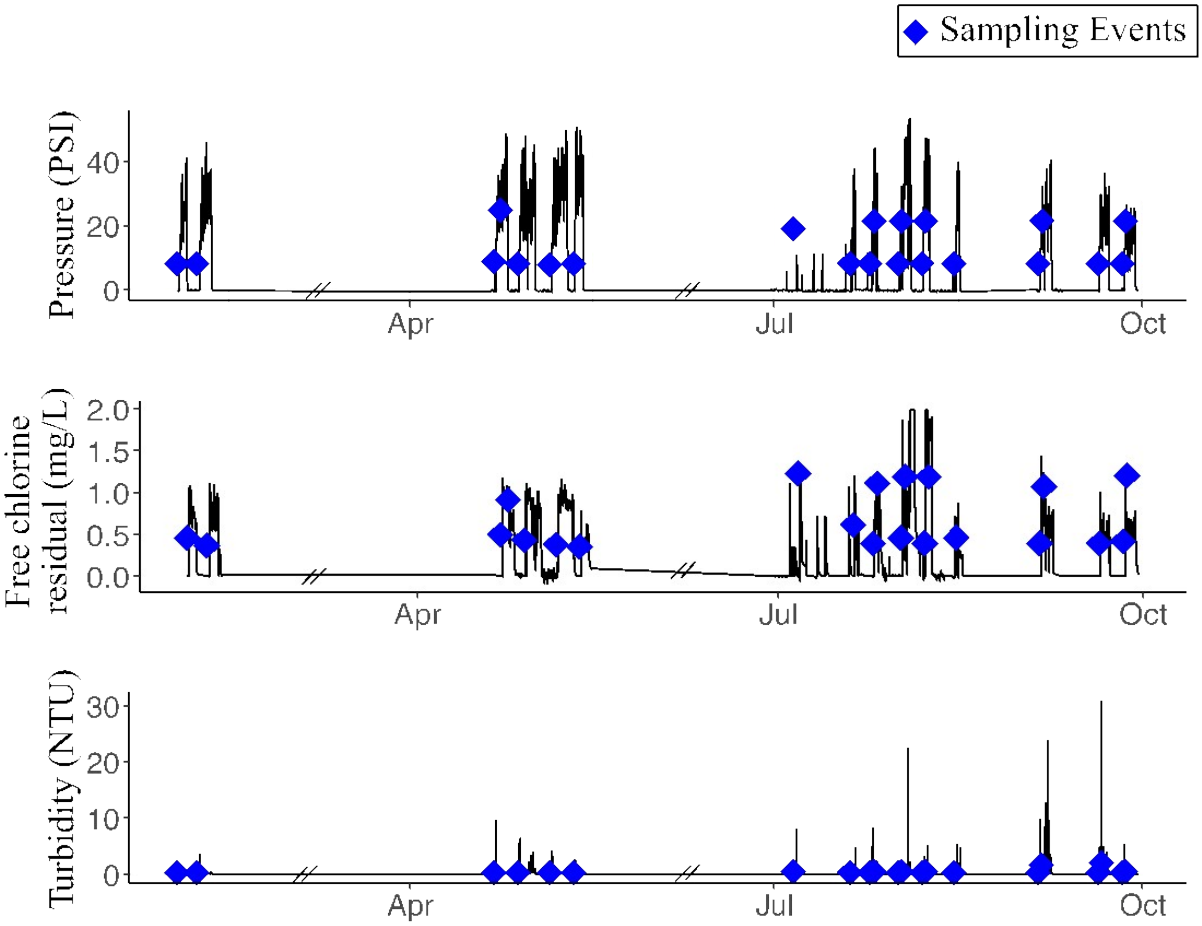
Supplemental Figure 4. Alpha diversity (Shannon and Inverse Simpson Indices) in the drinking water system of Arraijan, Panama by region and sampling location: (a) Shannon and Inverse Simpson diversity across treatment processes at each drinking water treatment plant; (b) Shannon and Inverse Simpson diversity across the various sampling locations in the distribution system.



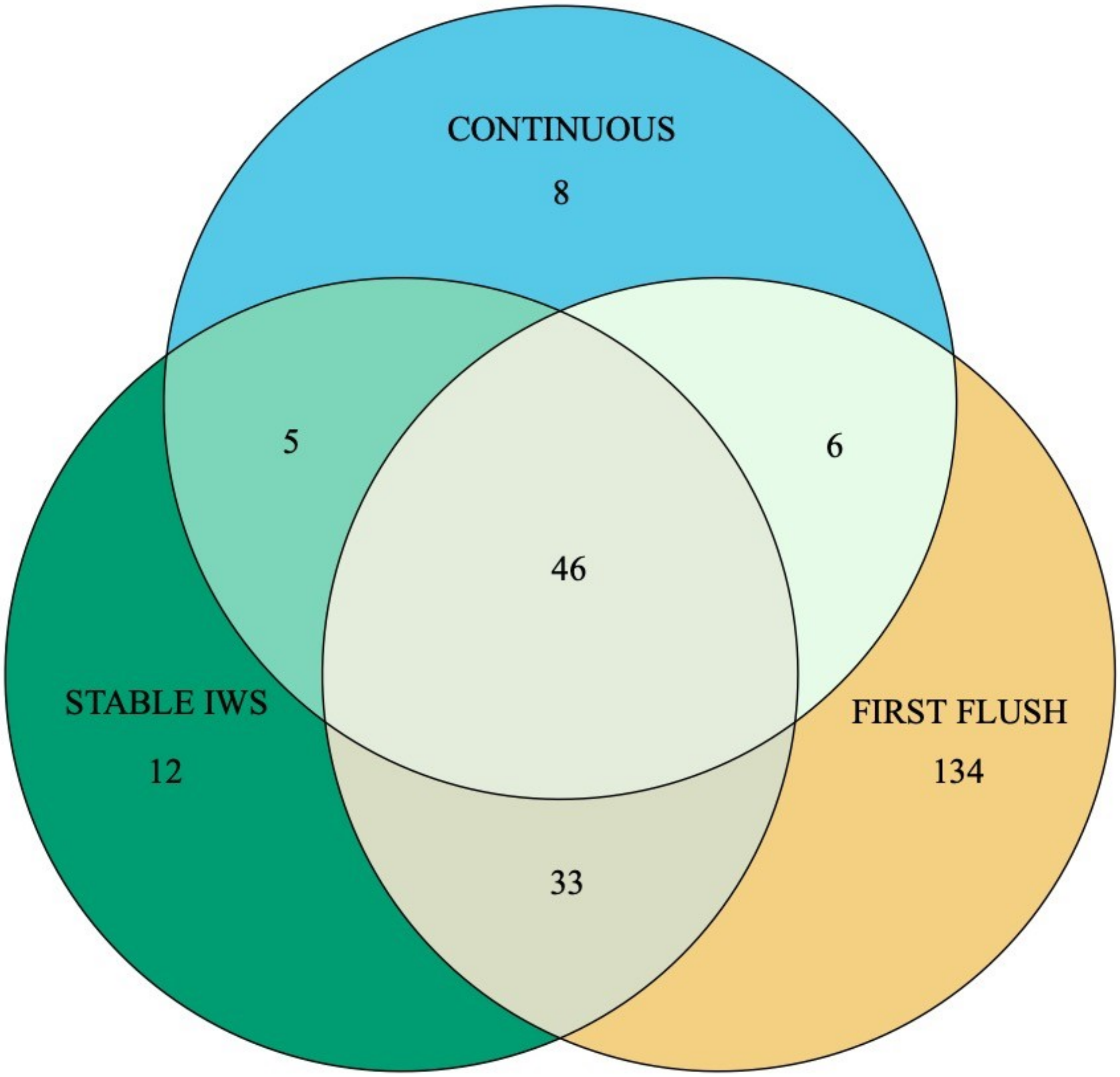
Supplemental Figure 5. Microbial community diversity in stable and intermittent water supply. Shannon and Inverse Simpson diversity indices for each sample type in the IWS zone.



Supplemental Figure 6. Principal Coordinate Analysis (PCoA) using weighted UniFrac distance of all samples taken at the section of the drinking water distribution with IWS. Continuous samples are the samples taken at the entrance of the IWS neighbourhood.



Supplemental Figure 7. Continuous monitoring data of water quality measurements during IWS for the duration of the study. Blue diamonds indicate grab samples collected for both water quality control and 16S rRNA gene sequencing. High turbidity at the beginning of supply while chlorine measurements are zero may be due to air that was trapped in the pipes being expelled through the sensor.



Supplemental Figure 8. Venn Diagram of shared and unique number of ASVs between IWS sample types.

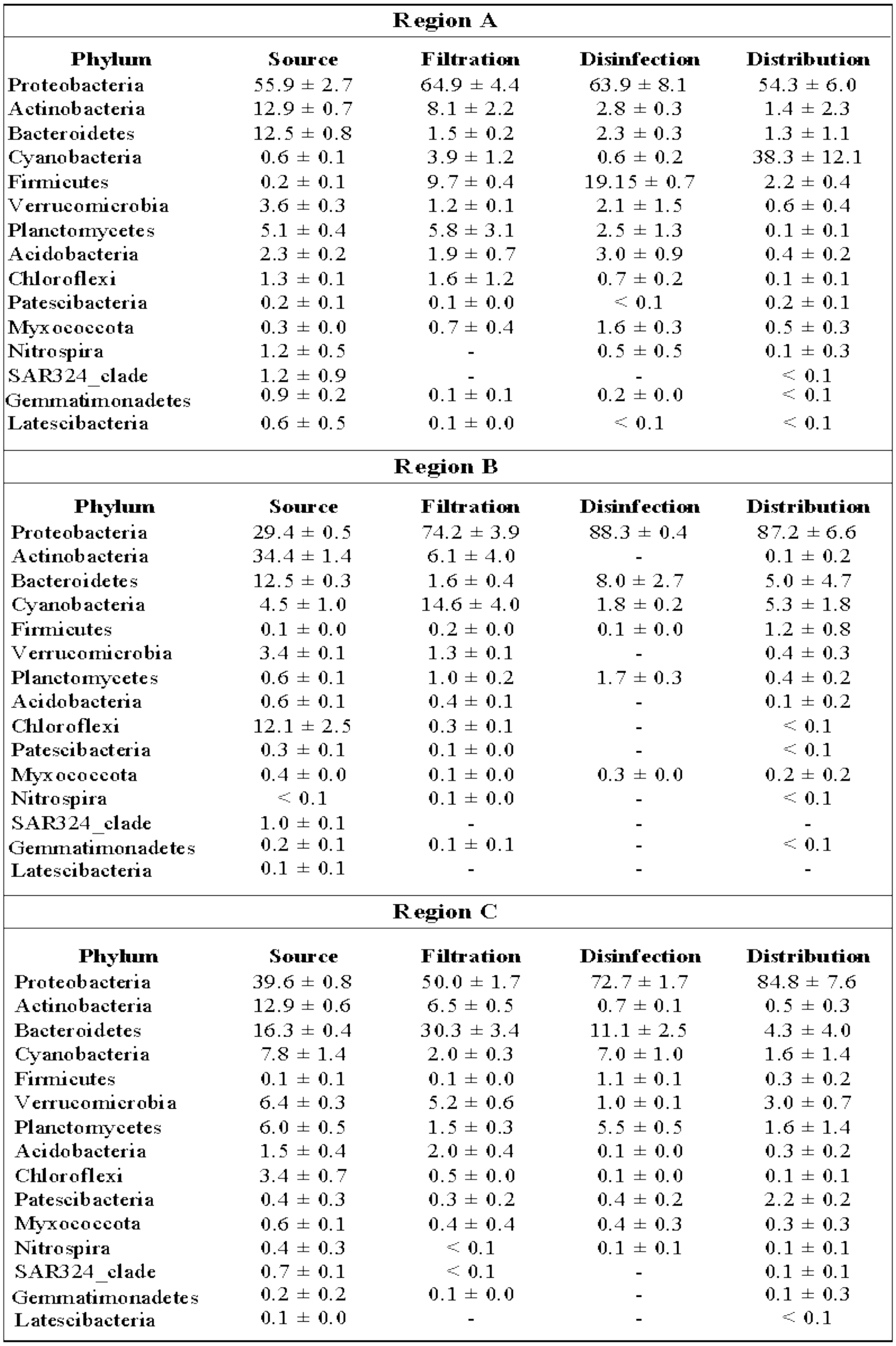
Supplemental Table 1. General parameters for the three DWTPs in this study. ACP = Panama Canal Authority. IDAAN = Panama's Institute of National Aqueducts and Sewers. ACP and IDAAN are governmental agencies. Aguas Panama is a private entity that sells water to IDAAN for its distribution. Gatun lake is a large artificial lake (425 km^2) that forms a major part of the Panama Canal. * Drinking water conventional treatment included: 1) potassium aluminium sulfate, sodium silicofluoride and calcium hydroxide as coagulants and additives; 2) rapid sand filtration with gravel, sand and anthracite media; and 3) chlorination using chlorine gas.

	DWTP A	**DWTP B**	**DWTP C**
Year of construction	1915	2002	2014
Regions served	Arraiján & La Chorrera	Arraiján	Panama City & Arraiján
Elevation (m)	60	123	122
Administered by	ACP	Aguas Panama	IDAAN
Population served	199,777	278,157	128,091
Source water	Chagres River & Gatún Lake (2 intakes)	Gatún Lake (1 intake)	Gatún Lake (1 intake)
Capacity (MGDs)	31.6	20.1	13.4
Treatment*	Conventional	Conventional	Conventional
Filtration cleaning cycle	52-60 hours/turbidity check	52-60 hours/turbidity check	60-72 hours/turbidity check
Number of filter	20	10	11

Supplemental Table 3: Monitoring data for IWS based on grab samples. Shown are mean and standard deviations. Letters indicate significant differences between sample types ($p < 0.05$) based on Kruskal-Wallis and pairwise Wilcox (with Benjamini-Hochberg correction) tests.

Sampling Location	**Upstream Entrance**	**Downstream First Flush**	**Downstream Stable**
Supply Type	Continuous	IWS	IWS
Free Chlorine (mg/L)	1.0 ± 0.1^{a}	0.3 ± 0.1^{b}	0.9 ± 0.1^{a}
Total Chlorine (mg/L)	1.1 ± 0.0^{a}	0.5 ± 0.1^{b}	1.1 ± 0.1^{a}
Turbidity (NTU)	0.5 ± 0.1^{a}	1.7 ± 0.5^{a}	0.5 ± 0.5^{a}
pH	7.4 ± 0.5^{a}	7.4 ± 0.4^{a}	6.9 ± 0.2^{a}
Temperature □	29.5 ± 0.6^{a}	31.1 ± 1.4^{b}	29.9 ± 0.8^{a}
Conductivity (µS/cm)	0.1 ± 0.0^{a}	0.08 ± 0.03^{b}	0.1 ± 0.0^{b}
TDS (mg/L)	76.5 ± 21.3^{a}	69.3 ± 21.1^{b}	76.5 ± 31.7^{a}
Pressure (PSI)	59.0 ± 10.4^{a}	7.5 ± 2.5^{b}	21.5 ± 8.2^{c}
HPC (MPN/100mL)	22.0 ± 14^{a}	$4.3\text{x}10^{4} \pm 2.8\text{x}10^{4\,b}$	70.0 ± 109.0^{c}

Supplemental Table 4. Mean relative abundance and standard deviation of phyla found in Arraiján’s DWDS by sample type and region.



Region A

Phylum	Source	Filtration	Disinfection	Distribution
Proteobacteria	55.9 ± 2.7	64.9 ± 4.4	63.9 ± 8.1	54.3 ± 6.0
Actinobacteria	12.9 ± 0.7	8.1 ± 2.2	2.8 ± 0.3	1.4 ± 2.3
Bacteroidetes	12.5 ± 0.8	1.5 ± 0.2	2.3 ± 0.3	1.3 ± 1.1
Cyanobacteria	0.6 ± 0.1	3.9 ± 1.2	0.6 ± 0.2	38.3 ± 12.1
Firmicutes	0.2 ± 0.1	9.7 ± 0.4	19.15 ± 0.7	2.2 ± 0.4
Verrucomicrobia	3.6 ± 0.3	1.2 ± 0.1	2.1 ± 1.5	0.6 ± 0.4
Planctomycetes	5.1 ± 0.4	5.8 ± 3.1	2.5 ± 1.3	0.1 ± 0.1
Acidobacteria	2.3 ± 0.2	1.9 ± 0.7	3.0 ± 0.9	0.4 ± 0.2
Chloroflexi	1.3 ± 0.1	1.6 ± 1.2	0.7 ± 0.2	0.1 ± 0.1
Patescibacteria	0.2 ± 0.1	0.1 ± 0.0	< 0.1	0.2 ± 0.1
Myxococcota	0.3 ± 0.0	0.7 ± 0.4	1.6 ± 0.3	0.5 ± 0.3
Nitrospira	1.2 ± 0.5	-	0.5 ± 0.5	0.1 ± 0.3
SAR324_clade	1.2 ± 0.9	-	-	< 0.1
Gemmatimonadetes	0.9 ± 0.2	0.1 ± 0.1	0.2 ± 0.0	< 0.1
Latescibacteria	0.6 ± 0.5	0.1 ± 0.0	< 0.1	< 0.1

Region B

Phylum	Source	Filtration	Disinfection	Distribution
Proteobacteria	29.4 ± 0.5	74.2 ± 3.9	88.3 ± 0.4	87.2 ± 6.6
Actinobacteria	34.4 ± 1.4	6.1 ± 4.0	-	0.1 ± 0.2
Bacteroidetes	12.5 ± 0.3	1.6 ± 0.4	8.0 ± 2.7	5.0 ± 4.7
Cyanobacteria	4.5 ± 1.0	14.6 ± 4.0	1.8 ± 0.2	5.3 ± 1.8
Firmicutes	0.1 ± 0.0	0.2 ± 0.0	0.1 ± 0.0	1.2 ± 0.8
Verrucomicrobia	3.4 ± 0.1	1.3 ± 0.1	-	0.4 ± 0.3
Planctomycetes	0.6 ± 0.1	1.0 ± 0.2	1.7 ± 0.3	0.4 ± 0.2
Acidobacteria	0.6 ± 0.1	0.4 ± 0.1	-	0.1 ± 0.2
Chloroflexi	12.1 ± 2.5	0.3 ± 0.1	-	< 0.1
Patescibacteria	0.3 ± 0.1	0.1 ± 0.0	-	< 0.1
Myxococcota	0.4 ± 0.0	0.1 ± 0.0	0.3 ± 0.0	0.2 ± 0.2
Nitrospira	< 0.1	0.1 ± 0.0	-	< 0.1
SAR324_clade	1.0 ± 0.1	-	-	-
Gemmatimonadetes	0.2 ± 0.1	0.1 ± 0.1	-	< 0.1
Latescibacteria	0.1 ± 0.1	-	-	-

Region C

Phylum	Source	Filtration	Disinfection	Distribution
Proteobacteria	39.6 ± 0.8	50.0 ± 1.7	72.7 ± 1.7	84.8 ± 7.6
Actinobacteria	12.9 ± 0.6	6.5 ± 0.5	0.7 ± 0.1	0.5 ± 0.3
Bacteroidetes	16.3 ± 0.4	30.3 ± 3.4	11.1 ± 2.5	4.3 ± 4.0
Cyanobacteria	7.8 ± 1.4	2.0 ± 0.3	7.0 ± 1.0	1.6 ± 1.4
Firmicutes	0.1 ± 0.1	0.1 ± 0.0	1.1 ± 0.1	0.3 ± 0.2
Verrucomicrobia	6.4 ± 0.3	5.2 ± 0.6	1.0 ± 0.1	3.0 ± 0.7
Planctomycetes	6.0 ± 0.5	1.5 ± 0.3	5.5 ± 0.5	1.6 ± 1.4
Acidobacteria	1.5 ± 0.4	2.0 ± 0.4	0.1 ± 0.0	0.3 ± 0.2
Chloroflexi	3.4 ± 0.7	0.5 ± 0.0	0.1 ± 0.0	0.1 ± 0.1
Patescibacteria	0.4 ± 0.3	0.3 ± 0.2	0.4 ± 0.2	2.2 ± 0.2
Myxococcota	0.6 ± 0.1	0.4 ± 0.4	0.4 ± 0.3	0.3 ± 0.3
Nitrospira	0.4 ± 0.3	< 0.1	0.1 ± 0.1	0.1 ± 0.1
SAR324_clade	0.7 ± 0.1	< 0.1	-	0.1 ± 0.1
Gemmatimonadetes	0.2 ± 0.2	0.1 ± 0.0	-	0.1 ± 0.3
Latescibacteria	0.1 ± 0.0	-	-	< 0.1