Supplemental information

Microbiological water quality in a decentralized Arctic drinking water system

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General water quality

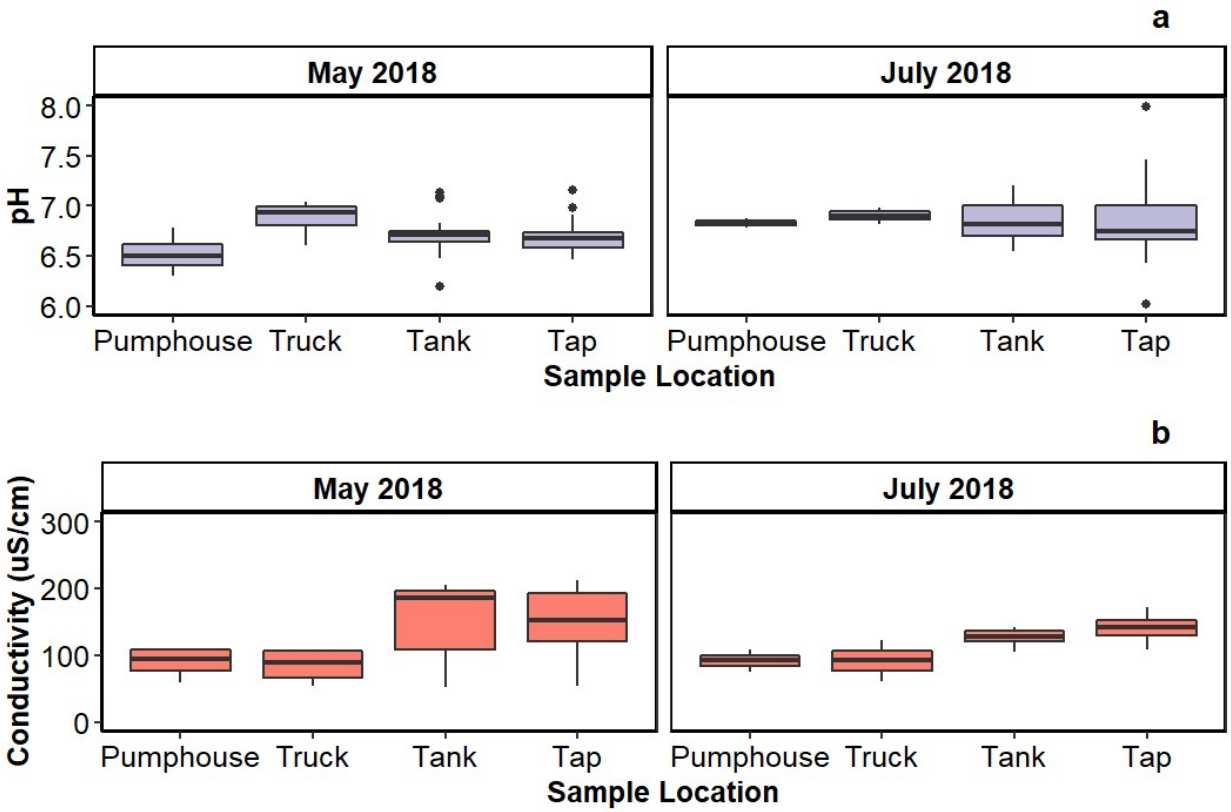

Figure S1 pH (a) and conductivity (b) measured in water gathered from the pumphouse, truck and storage tanks and taps in six buildings in Pond Inlet, NU, in July 2018

Table S1 Summary of chemical / physical water quality at different locations in the Pond Inlet drinking water system in May 2018 (median, min – max [n])

Parameter	Units	Source	Truck	Tanks	Taps[1]
Turbidity	NTU	2.94, 2.45 – 3.59 [4]	2.66, 2.54 – 2.83 [4]	2.78, 0.66 – 3.20 [22]	3.02, 1.04 – 5.12 [38]
Colour	CU	36, 35 – 37 [3]	31, 31 – 33 [3]	36, 32 – 39 [10]	40, 23 – 93 [36]
pH		6.51, 6.30 – 6.78 [4]	6.93, 6.60 – 7.04 [4]	6.70, 6.20 – 7.13 [22]	6.67, 6.47 – 7.16 [34]
Conductivity	uS/cm	94.7, 59.2 – 109.3 [4]	71.4, 53.7 – 108.7 [4]	186, 52.6 – 205.6 [22]	153, 53.0 – 211.8 [34]
Free Chlorine	mg/L	0.03, 0.02 – 0.03 [2]	0.12, 0.08 – 0.15 [4]	0.06, 0.03 – 0.09 [8]	0.08, 0.00 – 0.15 [29]
Total Chlorine	mg/L	0.02, 0 – 0.04 [4]	0.48, 0.40 – 0.53 [4]	0.16, 0.12 – 0.23 [8]	0.06, 0.00 – 0.22 [36]

[1]Tap water results represent "first flush" samples obtained randomly over the course of the day (random daytime samples)

Table S2 Summary of chemical / physical water quality at different locations in the Pond Inlet drinking water system in July 2018 (median, min – max [n])

Parameter	Units	Source	Truck	Tanks	Taps[1]
Turbidity	NTU	1.14, 1.08 – 1.21 [2]	1.54, 1.47 – 1.60 [2]	1.00, 0.80 – 1.55 [10]	1.26, 0.92 – 1.57 [8]
Colour	CU	23 [1]	20, 19 – 21 [2]	21, 10 – 23 [12]	20, 11 – 32 [12]
pH		6.83, 6.78 – 6.88 [2]	6.90, 6.82 – 6.98 [2]	6.82, 6.55 – 7.20 [10]	6.74, 6.02 – 7.99 [10]
Conductivity	uS/cm	91.9, 75.4 – 108.0 [2]	91.7, 61.2 - 122 [2]	128, 105 – 142 [10]	142, 108 – 172 [10]
Free Chlorine	mg/L	0.04 [1]	0.03 [1]	0.03, 0.02 – 0.21 [10]	0.03, 0.01 – 0.19 [10]
Total Chlorine	mg/L	0.05, 0.04 – 0.05 [2]	0.09, 0.03 – 0.14 [2]	0.05, 0.01 – 0.20 [10]	0.04, 0.01 – 0.20 [10]

[1]Tap water results represent "first flush" samples obtained randomly over the course of the day (random daytime samples)

Total coliforms

Duplicate samples collected from the pumphouse on May 18, 2018 had readings of 1 and 3.1 MPN/100mL. Positive readings were also obtained in duplicate pumphouse samples gathered on June 19, 2018 (1 and 12.4 MPN/100 mL), in a single sample gathered from the pumphouse on June 25 (12.4 MPN), and in a single sample from the pumphouse on November 7, 2018 (1 MPN/100mL). A first draw (RDT) sample gathered from the tap in Building 7 had a reading of 1 MPN/100 mL on October 24, 2018.

The majority of the Colilert™ results were below the detection limit (MPN < 1) resulting in a highly censored dataset (> 50% censored). The non-parametric Kruskal-Wallis test is recommended for comparing multiple groups censored datasets with a single detection limit (1) and was used in this study to determine if significant differences existed between the Colilert™ results from different sample locations or different sample months. The location where a sample was gathered was a significant factor ($p < 0.05$) but the month in which the sample was taken was not ($p > 0.05$). When the analysis was restricted to tap water samples, there were no significant differences based on location, indicating that the significant difference detected in the full dataset was related to the multiple pumphouse samples that had > 1 MPN.

Results of DNA analysis

16S (bacterial DNA) taxonomic profiles

Phylum level

Taxonomic profiles at the phylum level are presented in Figure S2 and summarized in Table S3. The pumphouse and truck samples were the only ones that contained more than 2.5% Verrucomicrobia. Cyanobacteria was present in the water sample from Building 3 (2.7%) and the biofilm from Building 5 as well as in the pumphouse and truck water samples at 1.8% and 1.1%,

respectively. Acidobacteria was present in the water sample from Building 6 at 8.6% and in the water samples from the pumphouse and truck at much lower abundances (0.07% ad 0.06%, respectively). Nitrospirae was present in the biofilm from the tank in Building 1 (13.7%) and the water sample from Building 6 (3.1%) but was not found in the water samples from the pumphouse or the truck.

Family level

Figure S3 and Table S4 summarize the family level taxonomic profiles of the water and biofilm samples analyzed in this study. All of the water samples and most of the biofilm samples contained ASVs from the family *Sphingomonadceae*, though the abundance varied from 7.1% in the biofilm sample from Building 5 to 65% in the tap water sample from Building 1. Bacteria from this family are ubiquitous in the environment, including in tap water and health-care settings, and have been associated with opportunistic infections (Vaz-Moreira *et al.*, 2011). All of the water samples also contained ASVs associated with the family *Burkholderiaceae* and the majority contained ASVs from the family *Pirellulaceae*.

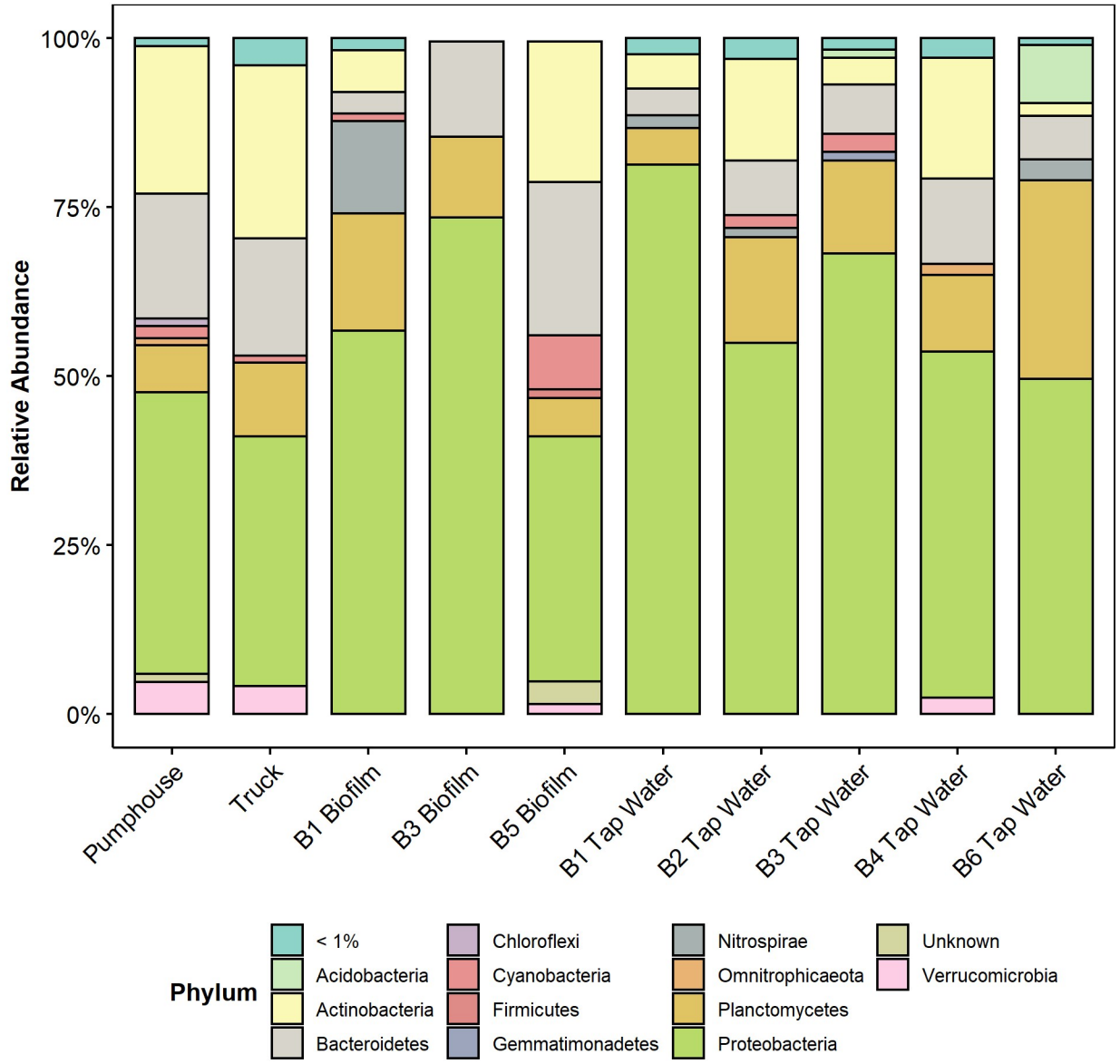

Figure S2 Distribution of bacterial phyla (abundance > 1%) measured in water and biofilm samples gathered from the Pond Inlet drinking water system in May 2018.

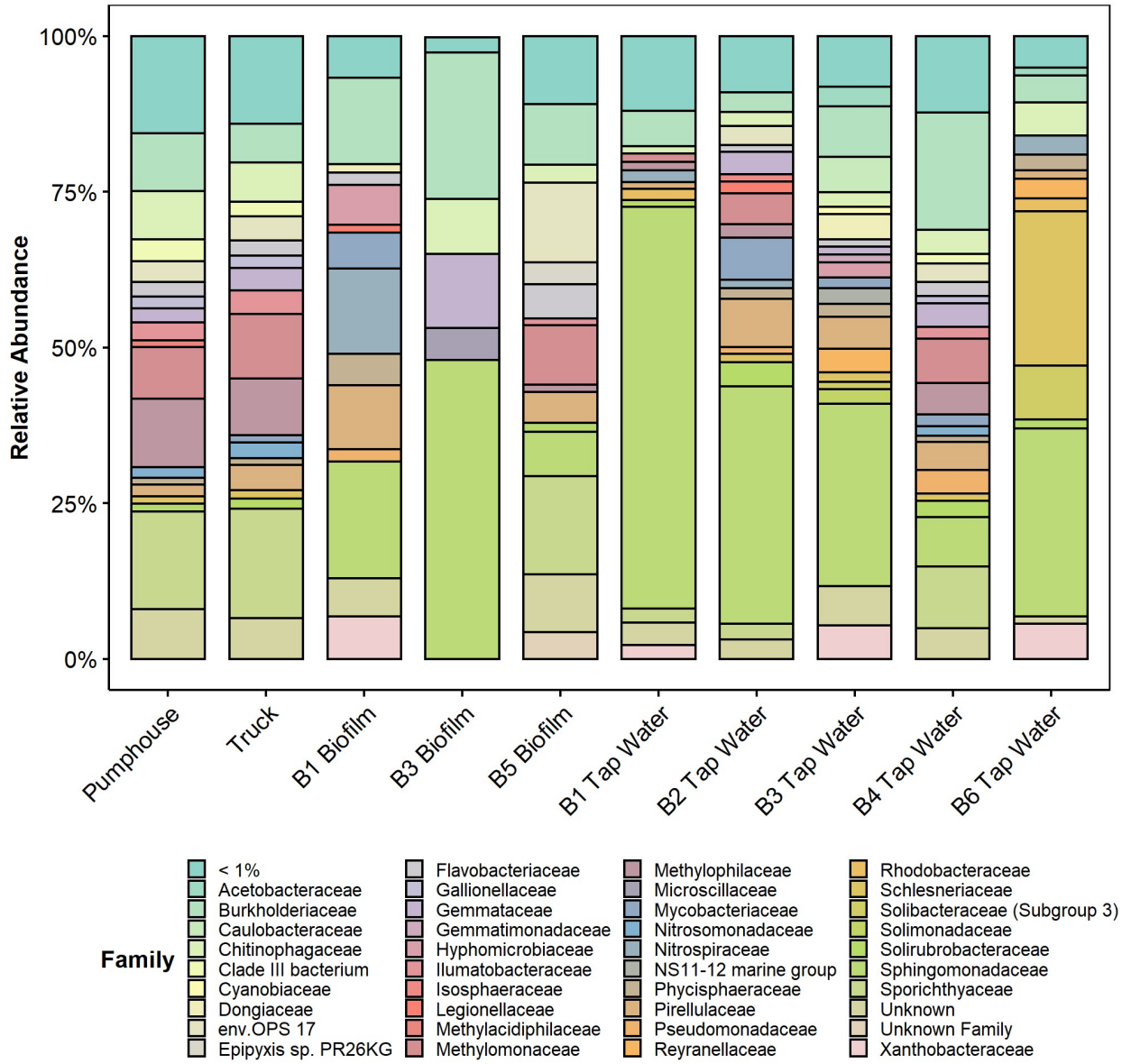

Figure S3 Distribution of bacterial families (abundance > 1%) measured in water and biofilm samples gathered from the Pond Inlet drinking water system in May 2018

73 **Table S3** Percent distribution of bacterial phyla measured in water and biofilm samples gathered from the Pond Inlet drinking water system
74 in May 2018

Phylum	**PH**	**TR**	**B1_B**	**B2_B**	**B3_B**	**B5_B**	**B1_W**	**B2_W**	**B3_W**	**B4_W**	**B6_W**
Acidobacteria	--	--	--	--	--	--	--	--	--	--	8.6%
Actinobacteria	21.8%	25.6%	6.2%	6.5%	--	20.8%	5.1%	15.1%	3.9%	17.9%	--
Bacteroidetes	18.5%	17.3%	3.2%	--	14.1%	22.7%	4.0%	8.1%	7.3%	12.6%	6.4%
Cyanobacteria	--	--	--	--	--	8.0%	--	--	2.7%	--	--
Nitrospirae		--	13.7%	--	--	--	--	--	--	--	3.1%
Planctomycetes	6.9%	10.9%	17.3%	--	11.9%	5.6%	5.4%	15.7%	13.7%	11.4%	29.4%
Proteobacteria	41.6%	36.9%	56.7%	93.5%	73.5%	36.2%	81.3%	54.9%	68.2%	51.2%	49.5%
Verrucomicrobia	4.7%	4.1%	--	--	--	--	--	--	--	--	--
Total > 2.5%	***93.5%***	***84.8%***	***97.1%***	***100%***	***99.5%***	***93.3%***	***95.8%***	***93.8%***	***95.8%***	***93.1%***	***97.0%***
< 2.5%	***6.5%***	***15.2%***	***2.9%***	***0%***	***0.5%***	***6.7%***	***4.2%***	***6.2%***	***4.2%***	***6.9%***	***3.0%***
Total	***100%***	***100%***	***100%***	***100%***	***100%***	***100%***	***100%***	***100%***	***100%***	***100%***	***100%***
Number of Phyla > 2.5%	***5***	***5***	***5***	***2***	***3***	***5***	***4***	***4***	***5***	***4***	***5***

Table S4 Percent distribution of bacterial families measured in water and biofilm samples gathered from the Pond Inlet drinking water system in May 2018

Family	PH	TR	B1_B	B2_B	B3_B	B5_B	B1_W	B2_W	B3_W	B4_W	B6_W
Bacterium	3.4%	--	--	--	--	--	--	--	--	--	--
Acetobacteraceae	--	--	--	--	--	--	--	--	3.1%	--	--
Burkholderiaceae	9.3%	6.1%	13.8%	--	23.5%	9.8%	5.7%	3.1%	8.1%	18.9%	4.4%
Caulobacteraceae	--	--	--	--	--	--	--	--	5.7%	--	--
Chitinophagaceae	7.7%	6.3%	--	--	8.9%	2.9%	--	--	--	3.8%	5.3%
Clade III	3.5%	--	--	--	--	--	--	--	--	--	--
Dongiaceae	--	--	--	--	--	--	--	--	4.0%	--	--
Env.OPS 17	3.4%	4.0%	--	--	--	12.7%	--	3.0%	--	3.0%	--
Epipxis sp. PR26KG	--	--	--	--	--	3.6%	--	--	--	--	--
Flavobacteriaceae	--	--	--	--	--	5.5%	--	--	--	--	--
Gemmataceae	--	3.5%	--	--	2.3%	--	--	3.7%	--	--	--
Hyphomicrobiaceae	--	--	6.4%	--	--	--	--	--	--	--	--
Illumatobacteraceae	2.9%	3.8%	--	--	--	--	--	--	--	--	--
Methylomonaceae	8.3%	10.3%	--	--	--	9.6%	--	4.9%	--	7.2%	--
Methylophilaceae	10.9%	9.1%	--	--	--	--	--	--	--	--	--
Microscillaceae	--	--	--	--	5.1%	--	--	--	--	--	--
Moraxellaceae	--	--	--	93.5%	--	--	--	--	--	--	--
Mycobacteriaceae	--	--	5.8%	--	--	--	--	6.8%	--	--	--
Nitrosomondaceae	--	2.5%	--	--	--	--	--	--	--	--	--
Nitrospiraceae	--	--	13.7%	--	--	--	--	--	--	--	--
NS11-12 marine group	--	--	--	--	--	--	--	--	2.7%	--	--
Phycisphaeraceae	--	--	4.9%	--	--	--	--	--	--	--	--
Pirellulaceae	--	4.0%	10.3%	--	--	5.0%	--	7.7%	5.2%	4.5%	--
Propionibacteriaceae	--	--	--	6.5%	--	--	--	--	--	--	--
Pseudomonadaceae	--	--	--	--	--	--	--	--	--	3.8%	--
Reyranellaceae	--	--	--	--	--	--	--	--	3.8%	--	3.1%
Schlesneriaceae	--	--	--	--	--	--	--	--	--	--	24.8%
Solibacteracea	--	--	--	--	--	--	--	--	--	--	8.6%
Solirubacteraceae	--	--	--	--	--	--	--	3.8%	--	2.6%	--
Sphingomonadaceae	--	--	18.7%	--	48%	7.1%	64.5%	38%	29.3%	7.8%	30.1%
Sporichthyaceae	15.7%	17.6%	--	--	--	15.8%	--	2.5%	--	9.9%	--

Family	**PH**	**TR**	**B1_B**	**B2_B**	**B3_B**	**B5_B**	**B1_W**	**B2_W**	**B3_W**	**B4_W**	**B6_W**
Unknown Family	--	--	--	--	--	7.4%	--	--	--	--	--
Xamthobacteraceae	--	--	6.9%	--	--	--	--	--	5.3%	--	5.6%
Total > 2.5%	***65.1%***	***67.2%***	***80.5%***	***100%***	***87.8%***	***79.4%***	***70.2%***	***73.5%***	***67.2%***	***61.7%***	***81.9%***
< 2.5%	***34.9%***	***32.8%***	***19.5%***	***0%***	***12.2%***	***20.6%***	***29.8%***	***26.5%***	***32.8%***	***38.3%***	***18.1%***
Total	***100%***	***100%***	***100%***	***100%***	***100%***	***100%***	***100%***	***100%***	***100%***	***100%***	***100%***
# of Families > 2.5%	***9?***	***10***	***8***	***2***	***5***	***11?***	***2***	***9***	***9***	***9***	***7***

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Table S5 Percent distribution of bacterial genera measured in water and biofilm samples gathered from the Pond Inlet drinking water system in May 2018

Genus	PH	TR	B1_B	B2_B	B3_B	B5_B	B1_W	B2_W	B3_W	B4_W	B6_W
Acinetobacter	--	--	--	93.5%	--	--	--	--	--	--	--
Altererythrobacter	--	--	--	--	41.7%	--	--	--	--	--	--
Aquabacterium	--	--	--	--	--	--	4.4%	--	--	--	4.4%
Bradyrhizobium	--	--	--	--	--	--	--	--	--	--	2.6%
Candidatus Methylopumilus	5.2%	4.5%	--	--	--	--	--	--	--	2.6%	--
Candidatus Ovatusbacter	--	--	--	--	--	4.3%	--	--	--	--	--
CL500-29 marine group	2.9%	3.8%	--	--	--	--	--	--	--	--	--
Conexibacter	--	--	--	--	--	--	--	3.8%	--	2.6%	--
Cutibacterium	--	--	--	6.5%	--	--	--	--	--	--	--
Dongia	--	--	--	--	--	--	--	--	4.0%	--	--
Epipyxis sp. PR26KG	--	--	--	--	--	3.6%	--	--	--	--	--
Flavisolibacter	--	--	--	--	--	--	--	--	--	--	4.9%
Flavobacterium	--	--	--	--	--	5.5%	--	--	--	--	--
hgcl clade	14.5%	16.3%	--	--	--	15.3%	--	--	--	9.0%	--
Hyphomicrobium	--	--	5.6%	--	--	--	--	--	--	--	--
Lacibacter	--	--	--	--	8.0%	--	--	--	--	--	--
Methylobacter	7.2%	9.3%	--	--	--	9.6%	--	4.3%	--	6.9%	--
Methylotenera	4.8%	3.9%	--	--	--	--	--	--	--	--	--
Mycobacterium	--	--	5.8%	--	--	--	--	6.8%	--	--	--
Nitrospira	--	--	13.7%	--	--	--	--	--	--	--	3.1%
Novosphingobium	--	--	--	--	--	--	38.8%	--	4.7%	--	3.8%
Paludibaculum	--	--	--	--	--	--	--	--	--	--	8.6%
Phenylobacterium	--	--	--	--	--	--	--	--	5.2%	--	--
Pirellula	--	--	3.2%	--	--	--	--	--	--	--	--
Planctopirus	--	--	--	--	--	--	--	--	--	--	24.8%
Polaromonas	--	--	--	--	2.6%	--	--	--	--	--	--
Polymorphobacter	--	--	--	--	--	--	--	--	--	--	11.3%
Pseudomonas	--	--	--	--	--	--	--	--	--	3.8%	--
Reyranella	--	--	--	--	--	--	--	--	3.8%	--	3.1%
Rhizobacter	--	--	--	--	--	--	--	--	4.0%	--	--
Rhodoferax	3.6%	--	4.0%	--	--	--	--	--	--	--	--

Genus	**PH**	**TR**	**B1_B**	**B2_B**	**B3_B**	**B5_B**	**B1_W**	**B2_W**	**B3_W**	**B4_W**	**B6_W**
Rhodopseudomonas	--	--	5.7%	--	--	--	--	--	--	--	--
Rhodovarius	--	--	--	--	--	--	--	--	3.0%	--	--
Sediminibacterium	5.3%	3.7%	--	--	--	--	--	--	--	2.6%	--
SM1A02	--	--	5.0%	--	--	--	--	--	--	--	--
Sphingomonas	--	--	16.6%	--	--	6.6%	25.4%	35.6%	23.0%	6.7%	12.6%
Undibacterium	--	--	--	--	--	4.7%	--	2.8%	--	12.0%	--
Total > 2.5%	***43.5%***	***41.5%***	***59.6%***	***100%***	***52.3%***	***49.6%***	***68.6%***	***53.3%***	***47.7%***	***46.2%***	***79.2%***
< 2.5%	***56.5%***	***58.5%***	***40.4%***	***0%***	***47.7%***	***50.4%***	***31.4%***	***46.7%***	***52.3%***	***53.8%***	***20.8%***
Total	***100%***	***100%***	***100%***	***100%***	***100%***	***100%***	***100%***	***100%***	***100%***	***100%***	***100%***
Number of Genera > 2.5%	*7*	***6***	***8***	***2***	***3***	*7*	***3***	***5***	*7*	***8***	***10***

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Table S6 Relative abundances of eukaryotic organisms present in the Pond Inlet water and biofilm samples. Cumulatively, these organisms represent the majority (greater than or equal to 70%) of ASVs in each sample

	Pumphouse	Truck	B4 Water	B2 Biofilm	B5 Biofilm
Genus					
Symbiodinium	n.d.	n.d.	n.d	83.1%	28.6%
Cladophora	n.d	n.d.	n.d	1.8%	1.0%
Biecheleria	22.9%	14.0%	11.4%	n.d.	16.1%
Tetrahymena	n.d.	n.d.	<1%	n.d.	5.0%
Coniochaeta	n.d	n.d.	2.9%	n.d.	n.d.
Rhizoclosmatium	n.d.	n.d.	2.9%	n.d.	n.d.
Order					
Syndiniales G1	n.d.	n.d.	n.d.	2.9%	<1%
Cyclopoida	64.9%	67.1%	20.4%	n.d.	16.7%
Ploimida	n.d.	<1%	n.d.	n.d.	2.6%
Cercomonas	n.d.	n.d.	32.7%	n.d.	n.d.
Class					
Demospongiae	n.d.	n.d.	<1%	4.5%	6.2%

n.d. = not detected

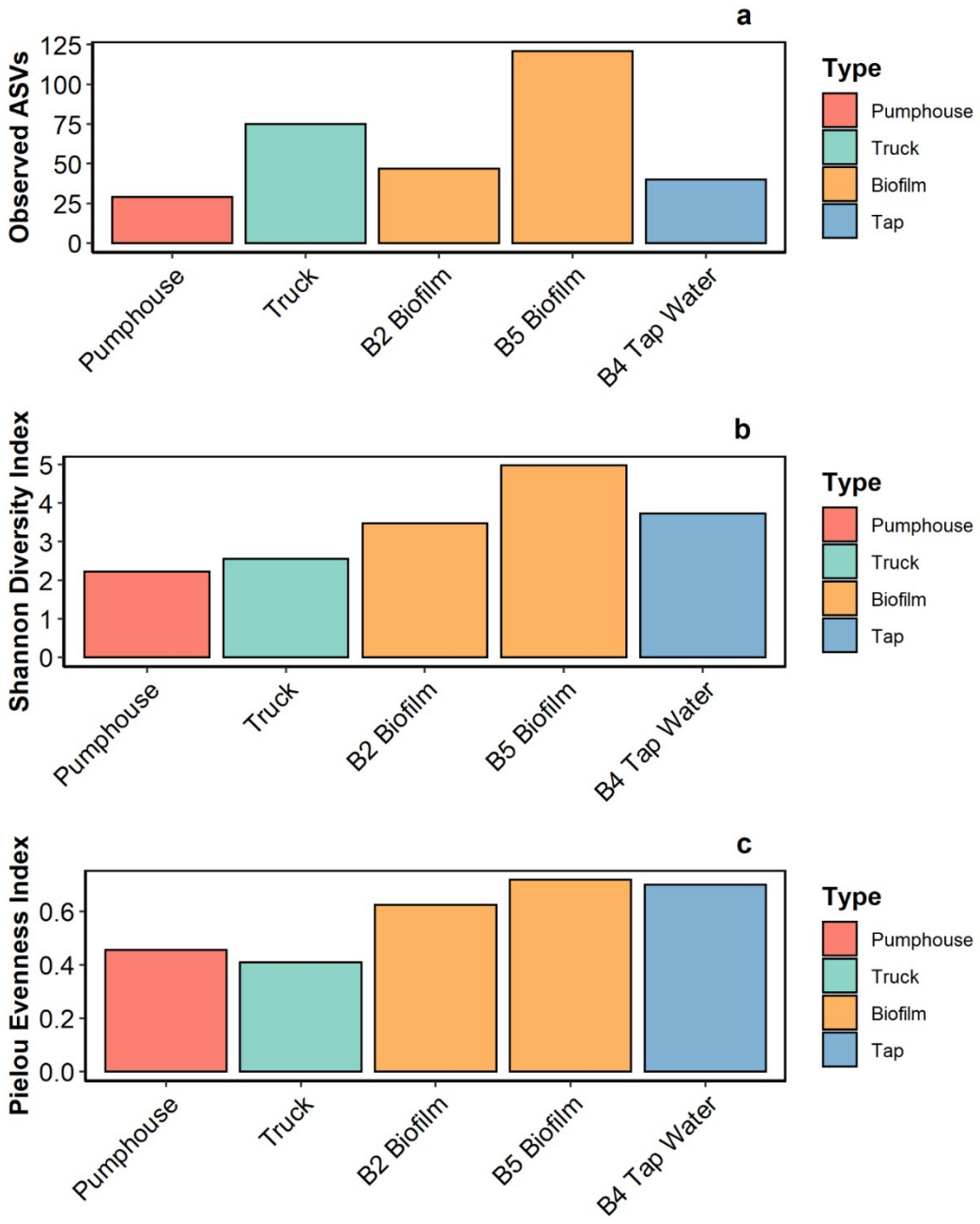

Figure S4 Richness (a), Shannon Diversity Index (b), and Pielou Evenness Index (c) of eukaryotic organisms detected in five samples gathered from various points in the Pond Inlet drinking water system in May 2018.

References

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2. Vaz-Moreira I, Nunes OC, Manaia CM. Diversity and Antibiotic Resistance Patterns of Sphingomonadaceae Isolates from Drinking Water. Applied and Environmental Microbiology. 2011 Aug 15;77(16):5697–706.