

	Pump House	Supply Plant
<i>Manganese (µg/L)*</i>	32.62 ± 12.32	26.3 ± 16.74
<i>Temperature (°C)</i>	14.9 ± 4.1	15.8 ± 3.4
pH	5.25 ± 0.43	5.10 ± 0.53
<i>Turbidity (NTU)</i>	0.790 ± 0.51	0.733 ± 0.50
<i>DOC (mg/L)*</i>	3.260 ± 0.33	2.99 ± 0.361
<i>TOC (mg/L)*</i>	3.530 ± 0.49	3.08 ± 0.741
<i>Colour (NTU)</i>	14 ± 10	15 ± 14

Supplemental Table 1. Average influent water quality conditions for the Pump House and Supply Plant reactors. (* P < 0.05)

	Pump House	Supply Plant
<i>Manganese (µg/cm²)</i>	11.0 ± 4.8	36.2 ± 16.0
<i>tATP (pg/cm²)</i>	15600 ± 9700	17600 ± 8800
MOB (CFU/cm ²)	99 ± 33	178 ± 56

Supplemental Table 2. Surface density of Mn, tATP and MOB on coupons in the Pump House and Supply Plant reactors.

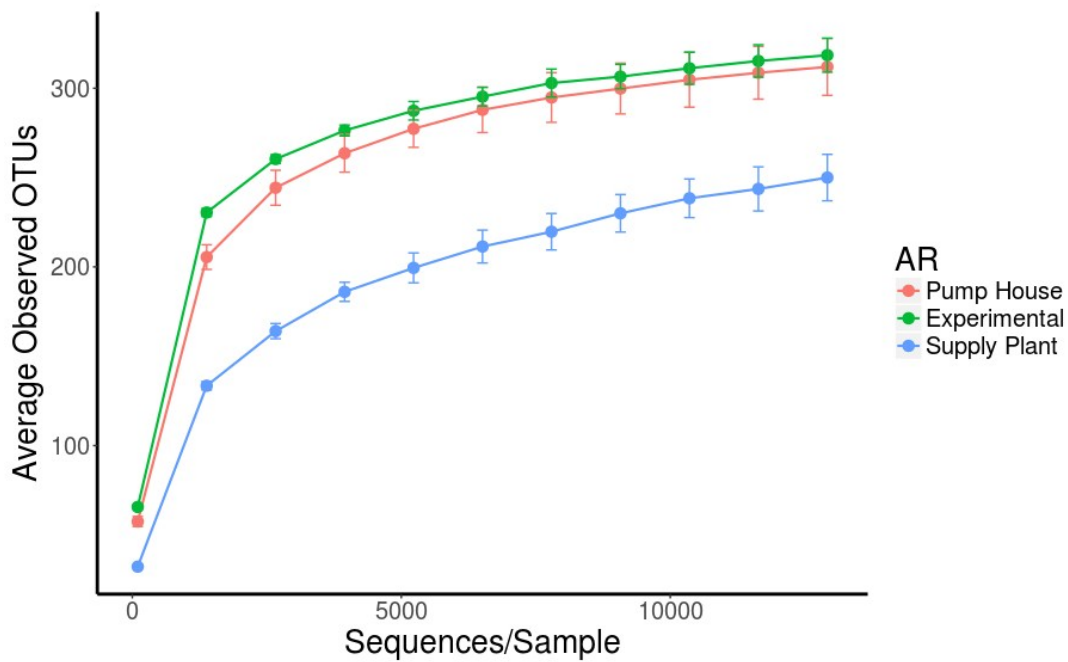
% Atomic Composition

	C	N	O	Al	Si	Cl	Mn	Fe
Pump House	62.91	4.37	29.54	0.33	0.58	0.05	1.03	1.18
Supply Plant	53.31	6.10	36.03	0.64	0.19	0.00	2.53	1.19

Table 3. Average atomic composition (%) of the Pump House and Supply Plant coupon surface elements obtained through EDS analysis.

	Pump House	Supply Plant
<i>Class</i>	15	11
<i>Order</i>	9	5
<i>Family</i>	8	3
<i>Genus</i>	5	1

Supplemental Table 4. Relative abundance (%) of known MOB in Pump House and Supply Plant biofilms at the class, order, family and genus level.



Supplemental Figure 1. Alpha rarefaction curves of biofilm communities within the Pump House, Experimental, and Supply Plant reactors.

Leptothrix discophora SS-1	MofA	304	IHLHGG	384	WYHDHT	1173	HPVHGHLL	1278	HCHILGHEENDF
Bacillus SG-1	MnxG	527	MHIHFV	572	FFHDHL	281	HVFHYHVVH	334	HVHLYPHFGIGM
Pedomicrobium sp. ACM 3067	MoxA	129	IHWHGQ	170	MYHPHA	265	HPIHMHGY	318	HCHKSHHTMNAM
Bacillus pumilus WH4	CotA	101	VHLHGG	149	WYHDHA	419	HPIHLHLV	491	HCHILEHEDYDM
Excherichia coli str. K-12 (MG1655)	CueO	100	LHWHGL	139	WFHPHQ	443	HPFHIIHGT	499	HCHLLEHEDTGM
Candidatus Koribacter versatilis	ABF43180	134	LHFHGL	178	WYHPHI	485	HAFHIIHQL	546	HCHLLDHEDKGM
Candidatus Koribacter versatilis	ABF41129	130	LHFHGL	174	WYHPHV	481	HAFHIIHQL	541	HCHLLEHEDRGM
Candidatus Koribacter versatilis	ABF42365	415	IHWHGI	461	IYHTHA	234	HPMHLHGA	291	HCHFHAHISHDE
Candidatus Koribacter versatilis	ABF40498	132	IHFHGT	175	WYHPHP	453	HTFHIIHQQV	512	HCHILAHEDSGM

Figure 7. Sequence alignment of MCO binding motifs A-D of CotA, CueO, MofA, MnxG, MoxA and four MCO homologues in *Candidatus Koribacter*. Homologues are identified by their GenBank Accession Numbers. The cofactor copper-binding histidine residues are highlighted.