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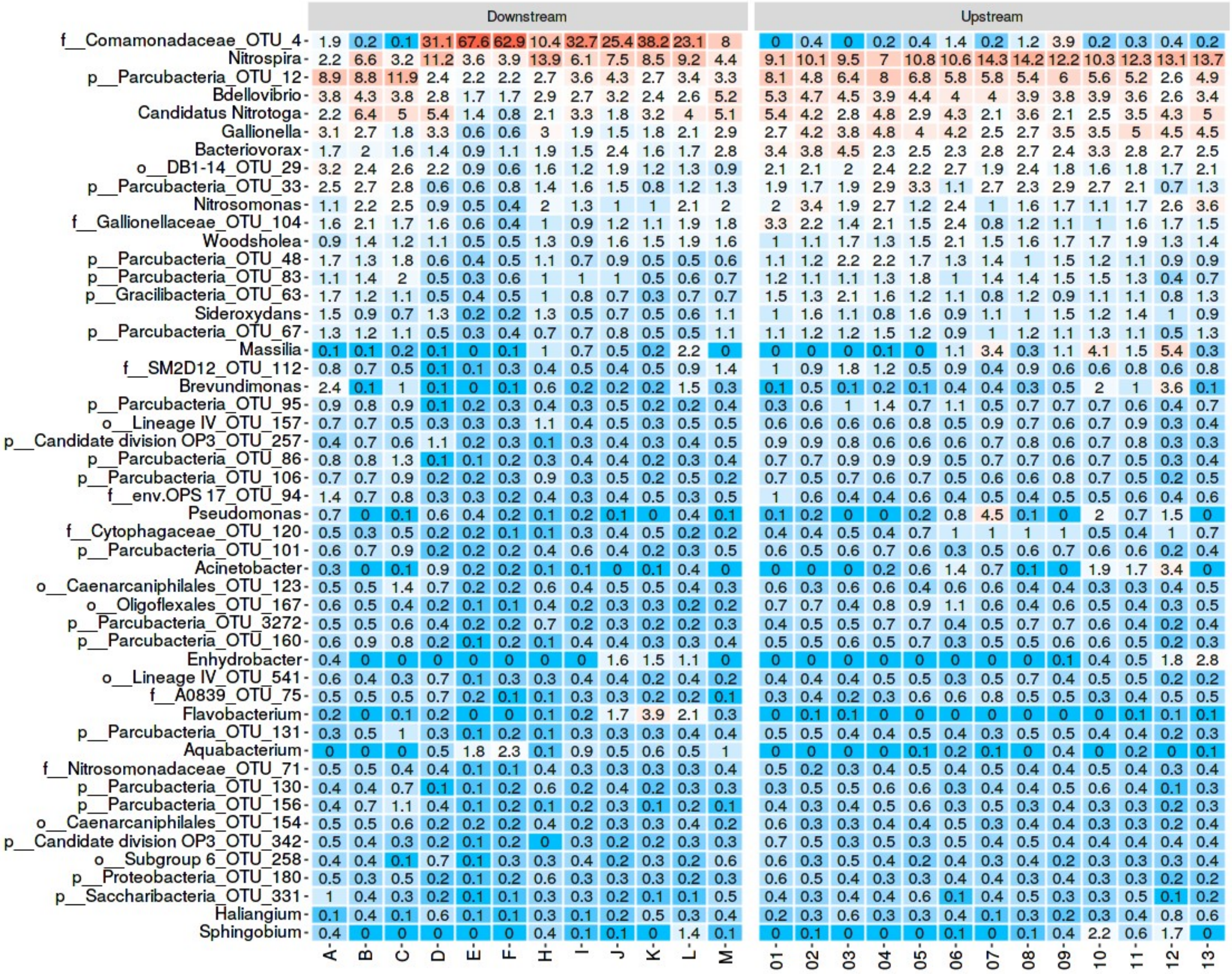
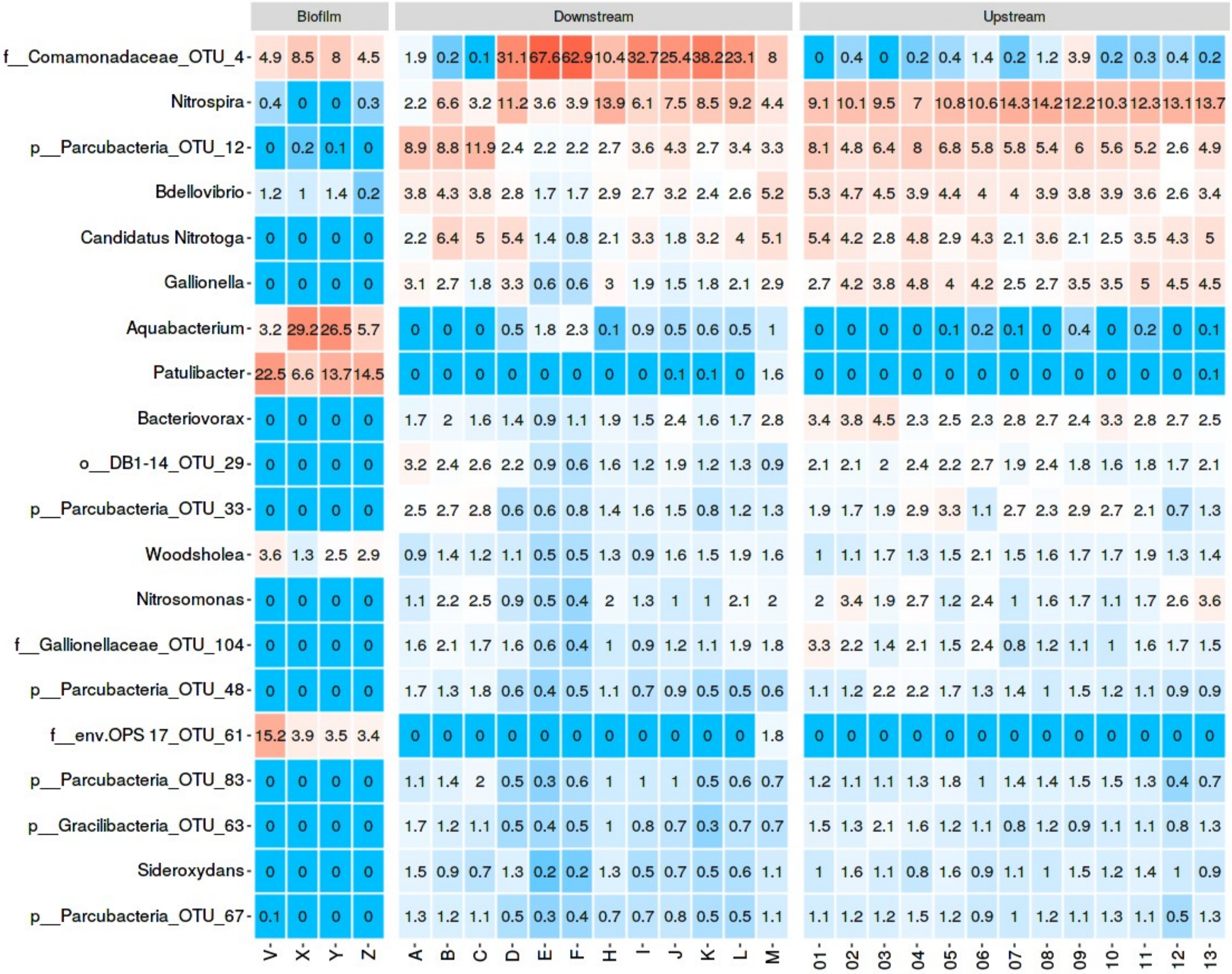
Supplementary information

Relative abundance of 25 water samples (downstream and upstream) and 4 biofilm samples.



	Downstream												Upstream												
	A	B	C	D	E	F	H	I	J	K	L	M	01	02	03	04	05	06	07	08	09	10	11	12	13
f__Comamonadaceae_OTU_4	1.9	0.2	0.1	31.1	67.6	62.9	10.4	32.7	25.4	38.2	23.1	8	0	0.4	0	0.2	0.4	1.4	0.2	1.2	3.9	0.2	0.3	0.4	0.2
Nitrospira	2.2	6.6	3.2	11.2	3.6	3.9	13.9	6.1	7.5	8.5	9.2	4.4	9.1	10.1	9.5	7	10.8	10.6	14.3	14.2	12.2	10.3	12.3	13.1	13.7
p__Parcubacteria_OTU_12	8.9	8.8	11.9	2.4	2.2	2.2	2.7	3.6	4.3	2.7	3.4	3.3	8.1	4.8	6.4	8	6.8	5.8	5.8	5.4	6	5.6	5.2	2.6	4.9
Bdellovibrio	3.8	4.3	3.8	2.8	1.7	1.7	2.9	2.7	3.2	2.4	2.6	5.2	5.3	4.7	4.5	3.9	4.4	4	4	3.9	3.8	3.9	3.6	2.6	3.4
Candidatus Nitrotoga	2.2	6.4	5	5.4	1.4	0.8	2.1	3.3	1.8	3.2	4	5.1	5.4	4.2	2.8	4.8	2.9	4.3	2.1	3.6	2.1	2.5	3.5	4.3	5
Gallionella	3.1	2.7	1.8	3.3	0.6	0.6	3	1.9	1.5	1.8	2.1	2.9	2.7	4.2	3.8	4.8	4	4.2	2.5	2.7	3.5	3.5	5	4.5	4.5
Bacteriovorax	1.7	2	1.6	1.4	0.9	1.1	1.9	1.5	2.4	1.6	1.7	2.8	3.4	3.8	4.5	2.3	2.5	2.3	2.8	2.7	2.4	3.3	2.8	2.7	2.5
o__DB1-14_OTU_29	3.2	2.4	2.6	2.2	0.9	0.6	1.6	1.2	1.9	1.2	1.3	0.9	2.1	2.1	2	2.4	2.2	2.7	1.9	2.4	1.8	1.6	1.8	1.7	2.1
p__Parcubacteria_OTU_33	2.5	2.7	2.8	0.6	0.6	0.8	1.4	1.6	1.5	0.8	1.2	1.3	1.9	1.7	1.9	2.9	3.3	1.1	2.7	2.3	2.9	2.7	2.1	0.7	1.3
Nitrosomonas	1.1	2.2	2.5	0.9	0.5	0.4	2	1.3	1	1	2.1	2	2	3.4	1.9	2.7	1.2	2.4	1	1.6	1.7	1.1	1.7	2.6	3.6
f__Gallionellaceae_OTU_104	1.6	2.1	1.7	1.6	0.6	0.4	1	0.9	1.2	1.1	1.9	1.8	3.3	2.2	1.4	2.1	1.5	2.4	0.8	1.2	1.1	1	1.6	1.7	1.5
Woodsholea	0.9	1.4	1.2	1.1	0.5	0.5	1.3	0.9	1.6	1.5	1.9	1.6	1	1.1	1.7	1.3	1.5	2.1	1.5	1.6	1.7	1.7	1.9	1.3	1.4
p__Parcubacteria_OTU_48	1.7	1.3	1.8	0.6	0.4	0.5	1.1	0.7	0.9	0.5	0.5	0.6	1.1	1.2	2.2	2.2	1.7	1.3	1.4	1	1.5	1.2	1.1	0.9	0.9
p__Parcubacteria_OTU_83	1.1	1.4	2	0.5	0.3	0.6	1	1	1	0.5	0.6	0.7	1.2	1.1	1.1	1.3	1.8	1	1.4	1.4	1.5	1.5	1.3	0.4	0.7
p__Gracilibacteria_OTU_63	1.7	1.2	1.1	0.5	0.4	0.5	1	0.8	0.7	0.3	0.7	0.7	1.5	1.3	2.1	1.6	1.2	1.1	0.8	1.2	0.9	1.1	1.1	0.8	1.3
Sideroxydans	1.5	0.9	0.7	1.3	0.2	0.2	1.3	0.5	0.7	0.5	0.6	1.1	1	1.6	1.1	0.8	1.6	0.9	1.1	1	1.5	1.2	1.4	1	0.9
p__Parcubacteria_OTU_67	1.3	1.2	1.1	0.5	0.3	0.4	0.7	0.7	0.8	0.5	0.5	1.1	1.1	1.2	1.2	1.5	1.2	0.9	1	1.2	1.1	1.3	1.1	0.5	1.3
Massilia	0.1	0.1	0.2	0.1	0	0.1	1	0.7	0.5	0.2	2.2	0	0	0	0	0.1	0	1.1	3.4	0.3	1.1	4.1	1.5	5.4	0.3
f__SM2D12_OTU_112	0.8	0.7	0.5	0.1	0.1	0.3	0.4	0.5	0.4	0.5	0.9	1.4	1	0.9	1.8	1.2	0.5	0.9	0.4	0.9	0.6	0.6	0.8	0.6	0.8
Brevundimonas	2.4	0.1	1	0.1	0	0.1	0.6	0.2	0.2	0.2	1.5	0.3	0.1	0.5	0.1	0.2	0.1	0.4	0.4	0.3	0.5	2	1	3.6	0.1
p__Parcubacteria_OTU_95	0.9	0.8	0.9	0.1	0.2	0.3	0.4	0.3	0.5	0.2	0.2	0.4	0.3	0.6	1	1.4	0.7	1.1	0.5	0.7	0.7	0.7	0.6	0.4	0.7
o__Lineage IV_OTU_157	0.7	0.7	0.5	0.3	0.3	0.3	1.1	0.4	0.5	0.3	0.5	0.5	0.6	0.6	0.6	0.6	0.8	0.5	0.9	0.7	0.6	0.7	0.9	0.3	0.4
p__Candidate division OP3_OTU_257	0.4	0.7	0.6	1.1	0.2	0.3	0.1	0.3	0.4	0.3	0.4	0.5	0.9	0.9	0.8	0.6	0.6	0.6	0.7	0.8	0.6	0.7	0.8	0.3	0.3
p__Parcubacteria_OTU_86	0.8	0.8	1.3	0.1	0.1	0.2	0.3	0.4	0.4	0.2	0.3	0.4	0.7	0.7	0.9	0.9	0.9	0.5	0.7	0.7	0.6	0.7	0.5	0.3	0.4
p__Parcubacteria_OTU_106	0.7	0.7	0.9	0.2	0.2	0.3	0.9	0.3	0.5	0.2	0.5	0.2	0.7	0.5	0.7	0.6	0.7	0.5	0.6	0.6	0.8	0.7	0.5	0.2	0.5
f__env.OPS 17_OTU_94	1.4	0.7	0.8	0.3	0.3	0.2	0.4	0.3	0.4	0.5	0.3	0.5	1	0.6	0.4	0.4	0.6	0.4	0.5	0.4	0.5	0.5	0.6	0.4	0.6
Pseudomonas	0.7	0	0.1	0.6	0.4	0.2	0.1	0.2	0.1	0	0.4	0.1	0.1	0.2	0	0	0.2	0.8	4.5	0.1	0	2	0.7	1.5	0
f__Cytophagaceae_OTU_120	0.5	0.3	0.5	0.2	0.2	0.1	0.1	0.3	0.4	0.5	0.2	0.2	0.4	0.4	0.5	0.4	0.7	1	1	1	1	0.5	0.4	1	0.7
p__Parcubacteria_OTU_101	0.6	0.7	0.9	0.2	0.2	0.2	0.4	0.6	0.4	0.2	0.3	0.5	0.6	0.5	0.6	0.7	0.6	0.3	0.5	0.6	0.7	0.6	0.6	0.2	0.4
Acinetobacter	0.3	0	0.1	0.9	0.2	0.2	0.1	0.1	0	0.1	0.4	0	0	0	0	0.2	0.6	1.4	0.7	0.1	0	1.9	1.7	3.4	0
o__Caenarcaniphilales_OTU_123	0.5	0.5	1.4	0.7	0.2	0.2	0.6	0.4	0.5	0.5	0.4	0.3	0.6	0.3	0.6	0.6	0.4	0.6	0.6	0.4	0.4	0.3	0.3	0.4	0.5
o__Oligoflexales_OTU_167	0.6	0.5	0.4	0.2	0.1	0.1	0.4	0.2	0.3	0.3	0.2	0.2	0.7	0.7	0.4	0.8	0.9	1.1	0.6	0.4	0.6	0.5	0.4	0.3	0.5
p__Parcubacteria_OTU_3272	0.5	0.5	0.6	0.4	0.2	0.2	0.7	0.2	0.3	0.2	0.2	0.3	0.4	0.5	0.5	0.7	0.7	0.4	0.5	0.7	0.7	0.6	0.4	0.2	0.4
p__Parcubacteria_OTU_160	0.6	0.9	0.8	0.2	0.1	0.2	0.1	0.4	0.4	0.3	0.3	0.4	0.5	0.5	0.6	0.5	0.7	0.3	0.5	0.5	0.6	0.6	0.5	0.2	0.3
Enhydrobacter	0.4	0	0	0	0	0	0	0	1.6	1.5	1.1	0	0	0	0	0	0	0	0	0	0.1	0.4	0.5	1.8	2.8
o__Lineage IV_OTU_541	0.6	0.4	0.3	0.7	0.1	0.3	0.3	0.4	0.4	0.2	0.4	0.2	0.4	0.4	0.4	0.5	0.5	0.3	0.5	0.7	0.4	0.5	0.5	0.2	0.2
f__A0839_OTU_75	0.5	0.5	0.5	0.7	0.2	0.1	0.1	0.3	0.3	0.2	0.2	0.1	0.3	0.4	0.2	0.3	0.6	0.6	0.8	0.5	0.5	0.3	0.4	0.5	0.5
Flavobacterium	0.2	0	0.1	0.2	0	0	0.1	0.2	1.7	3.9	2.1	0.3	0	0.1	0.1	0	0	0	0	0	0	0	0.1	0.1	0.1
p__Parcubacteria_OTU_131	0.3	0.5	1	0.3	0.1	0.2	0.1	0.3	0.3	0.3	0.4	0.4	0.5	0.5	0.4	0.4	0.5	0.4	0.3	0.5	0.5	0.4	0.4	0.2	0.3
Aquabacterium	0	0	0	0.5	1.8	2.3	0.1	0.9	0.5	0.6	0.5	1	0	0	0	0	0.1	0.2	0.1	0	0.4	0	0.2	0	0.1
f__Nitrosomonadaceae_OTU_71	0.5	0.5	0.4	0.4	0.1	0.1	0.4	0.3	0.3	0.3	0.3	0.4	0.5	0.2	0.3	0.4	0.5	0.4	0.5	0.4	0.4	0.5	0.4	0.3	0.4
p__Parcubacteria_OTU_130	0.4	0.4	0.7	0.1	0.1	0.2	0.6	0.2	0.4	0.2	0.3	0.3	0.3	0.5	0.5	0.6	0.6	0.3	0.4	0.4	0.5	0.6	0.4	0.1	0.3
p__Parcubacteria_OTU_156	0.4	0.7	1.1	0.4	0.1	0.2	0.1	0.2	0.3	0.1	0.2	0.1	0.4	0.3	0.4	0.5	0.6	0.3	0.5	0.3	0.4	0.3	0.3	0.2	0.3
o__Caenarcaniphilales_OTU_154	0.5	0.5	0.6	0.2	0.2	0.2	0.4	0.2	0.3	0.3	0.4	0.2	0.6	0.3	0.3	0.4	0.4	0.5	0.3	0.4	0.4	0.3	0.3	0.2	0.4
p__Candidate division OP3_OTU_342	0.5	0.4	0.3	0.2	0.1	0.2	0	0.3	0.2	0.2	0.3	0.3	0.7	0.5	0.3	0.5	0.3	0.5	0.4	0.5	0.4	0.4	0.4	0.4	0.4
o__Subgroup 6_OTU_258	0.4	0.4	0.1	0.7	0.1	0.3	0.3	0.4	0.2	0.3	0.2	0.6	0.6	0.3	0.5	0.4	0.2	0.4	0.3	0.4	0.2	0.3	0.3	0.3	0.4
p__Proteobacteria_OTU_180	0.5	0.3	0.5	0.2	0.1	0.2	0.6	0.3	0.3	0.3	0.2	0.3	0.6	0.5	0.4	0.3	0.3	0.4	0.4	0.3	0.4	0.3	0.3	0.2	0.2
p__Saccharibacteria_OTU_331	1	0.4	0.3	0.2	0.1	0.1	0.3	0.3	0.2	0.1	0.1	0.5	0.4	0.3	0.4	0.4	0.6	0.1	0.4	0.5	0.3	0.3	0.5	0.1	0.2
Haliangium	0.1	0.4	0.1	0.6	0.1	0.1	0.3	0.1	0.2	0.5	0.3	0.4	0.2	0.3	0.6	0.3	0.3	0.4	0.1	0.3	0.2	0.3	0.4	0.8	0.6
Sphingobium	0.4	0	0	0	0	0	0.4	0.1	0.1	0	1.4	0.1	0	0.1	0	0	0	0.1	0	0.1	0.4	2.2	0.6	1.7	0

Figure SI.1: The 50 most abundant bacteria (phylum, genus) found with amplicon sequencing in **downstream (A-M)** and **upstream (01-13) water samples**. The water samples were taken from September 19, 2017 to October 13, 2017. The colour bar indicates percentage relative abundance in the samples.



	Biofilm				Downstream												Upstream												
	V	X	Y	Z	A	B	C	D	E	F	H	I	J	K	L	M	01	02	03	04	05	06	07	08	09	10	11	12	13
f__Comamonadaceae_OTU_4	4.9	8.5	8	4.5	1.9	0.2	0.1	31.1	67.6	62.9	10.4	32.7	25.4	38.2	23.1	8	0	0.4	0	0.2	0.4	1.4	0.2	1.2	3.9	0.2	0.3	0.4	0.2
Nitrospira	0.4	0	0	0.3	2.2	6.6	3.2	11.2	3.6	3.9	13.9	6.1	7.5	8.5	9.2	4.4	9.1	10.1	9.5	7	10.8	10.6	14.3	14.2	12.2	10.3	12.3	13.1	13.7
p__Parcubacteria_OTU_12	0	0.2	0.1	0	8.9	8.8	11.9	2.4	2.2	2.2	2.7	3.6	4.3	2.7	3.4	3.3	8.1	4.8	6.4	8	6.8	5.8	5.8	5.4	6	5.6	5.2	2.6	4.9
Bdellovibrio	1.2	1	1.4	0.2	3.8	4.3	3.8	2.8	1.7	1.7	2.9	2.7	3.2	2.4	2.6	5.2	5.3	4.7	4.5	3.9	4.4	4	4	3.9	3.8	3.9	3.6	2.6	3.4
Candidatus Nitrotoga	0	0	0	0	2.2	6.4	5	5.4	1.4	0.8	2.1	3.3	1.8	3.2	4	5.1	5.4	4.2	2.8	4.8	2.9	4.3	2.1	3.6	2.1	2.5	3.5	4.3	5
Gallionella	0	0	0	0	3.1	2.7	1.8	3.3	0.6	0.6	3	1.9	1.5	1.8	2.1	2.9	2.7	4.2	3.8	4.8	4	4.2	2.5	2.7	3.5	3.5	5	4.5	4.5
Aquabacterium	3.2	29.2	26.5	5.7	0	0	0	0.5	1.8	2.3	0.1	0.9	0.5	0.6	0.5	1	0	0	0	0	0.1	0.2	0.1	0	0.4	0	0.2	0	0.1
Patulibacter	22.5	6.6	13.7	14.5	0	0	0	0	0	0	0	0	0.1	0.1	0	1.6	0	0	0	0	0	0	0	0	0	0	0	0	0.1
Bacteriovorax	0	0	0	0	1.7	2	1.6	1.4	0.9	1.1	1.9	1.5	2.4	1.6	1.7	2.8	3.4	3.8	4.5	2.3	2.5	2.3	2.8	2.7	2.4	3.3	2.8	2.7	2.5
o__DB1-14_OTU_29	0	0	0	0	3.2	2.4	2.6	2.2	0.9	0.6	1.6	1.2	1.9	1.2	1.3	0.9	2.1	2.1	2	2.4	2.2	2.7	1.9	2.4	1.8	1.6	1.8	1.7	2.1
p__Parcubacteria_OTU_33	0	0	0	0	2.5	2.7	2.8	0.6	0.6	0.8	1.4	1.6	1.5	0.8	1.2	1.3	1.9	1.7	1.9	2.9	3.3	1.1	2.7	2.3	2.9	2.7	2.1	0.7	1.3
Woodsholea	3.6	1.3	2.5	2.9	0.9	1.4	1.2	1.1	0.5	0.5	1.3	0.9	1.6	1.5	1.9	1.6	1	1.1	1.7	1.3	1.5	2.1	1.5	1.6	1.7	1.7	1.9	1.3	1.4
Nitrosomonas	0	0	0	0	1.1	2.2	2.5	0.9	0.5	0.4	2	1.3	1	1	2.1	2	2	3.4	1.9	2.7	1.2	2.4	1	1.6	1.7	1.1	1.7	2.6	3.6
f__Gallionellaceae_OTU_104	0	0	0	0	1.6	2.1	1.7	1.6	0.6	0.4	1	0.9	1.2	1.1	1.9	1.8	3.3	2.2	1.4	2.1	1.5	2.4	0.8	1.2	1.1	1	1.6	1.7	1.5
p__Parcubacteria_OTU_48	0	0	0	0	1.7	1.3	1.8	0.6	0.4	0.5	1.1	0.7	0.9	0.5	0.5	0.6	1.1	1.2	2.2	2.2	1.7	1.3	1.4	1	1.5	1.2	1.1	0.9	0.9
f__env.OPS 17_OTU_61	15.2	3.9	3.5	3.4	0	0	0	0	0	0	0	0	0	0	0	1.8	0	0	0	0	0	0	0	0	0	0	0	0	0
p__Parcubacteria_OTU_83	0	0	0	0	1.1	1.4	2	0.5	0.3	0.6	1	1	1	0.5	0.6	0.7	1.2	1.1	1.1	1.3	1.8	1	1.4	1.4	1.5	1.5	1.3	0.4	0.7
p__Gracilibacteria_OTU_63	0	0	0	0	1.7	1.2	1.1	0.5	0.4	0.5	1	0.8	0.7	0.3	0.7	0.7	1.5	1.3	2.1	1.6	1.2	1.1	0.8	1.2	0.9	1.1	1.1	0.8	1.3
Sideroxydans	0	0	0	0	1.5	0.9	0.7	1.3	0.2	0.2	1.3	0.5	0.7	0.5	0.6	1.1	1	1.6	1.1	0.8	1.6	0.9	1.1	1	1.5	1.2	1.4	1	0.9
p__Parcubacteria_OTU_67	0.1	0	0	0	1.3	1.2	1.1	0.5	0.3	0.4	0.7	0.7	0.8	0.5	0.5	1.1	1.1	1.2	1.2	1.5	1.2	0.9	1	1.2	1.1	1.3	1.1	0.5	1.3

Figure SI.2: The 20 most abundant bacteria (phylum, genus) found with amplicon sequencing in **biofilm samples (V-Z)** listed alongside with **downstream (A-M)** and **upstream (01-13) water samples**. V and Z were taken from the *bottom part* of the pipe and X and Y from the *upper part* of the pipe. The colour bar indicates percentage relative abundance in the samples.