Supplementary Material Table 4. SIMPER analysis of taxonomic groups (family level) driving Bray Curtis dissimilarity between Marine and West/River samples. Average abundance is square root transformed. Top 35% dissimilarity shown. Average dissimilarity = 44.17.

Species	Group WEST/RIVER Av.Abund	Group MARINE Av.Abund	Av.Diss	Diss/SD	Contrib%	Cum.%
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Microbacteriaceae	0.39	0.22	1.95	1.87	4.41	4.41
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Halomonadaceae	0.06	0.25	1.69	2.41	3.82	8.23
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Acidimicrobiales;f__OCS155	0.09	0.21	1.14	1.99	2.59	10.82
k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__Flavobacteriaceae	0.23	0.36	1.13	2.17	2.55	13.37
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__;f__	0.1	0.21	0.95	1.76	2.14	15.51
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rickettsiales;f__Pelagibacteraceae	0.07	0.17	0.87	2.24	1.97	17.48
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__	0.11	0.02	0.87	0.84	1.97	19.45
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae	0.62	0.54	0.87	1.41	1.96	21.41
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Chromatiales;f__	0.13	0.05	0.75	0.81	1.69	23.1
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Rhodocyclales;f__Rhodocyclaceae	0.12	0.07	0.71	1.27	1.6	24.71
k__Bacteria;p__Cyanobacteria;c__Synechococcophycideae;o__Synechococcales;f__Synechococcaceae	0.07	0.13	0.7	1.59	1.58	26.28
k__Bacteria;p__Bacteroidetes;c__[Saprospirae];o__[Saprospirales];f__Saprospiraceae	0.11	0.12	0.57	1.44	1.3	27.58
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__OM60	0.09	0.15	0.57	1.8	1.29	28.87
k__Bacteria;p__Cyanobacteria;c__Chloroplast;o__Stramenopiles;f__	0.12	0.08	0.53	0.99	1.2	30.07
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Erythrobacteraceae	0.1	0.04	0.52	2.1	1.18	31.25
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae	0.07	0.05	0.51	1.24	1.15	32.4
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Oceanospirillaceae	0.1	0.08	0.49	1.27	1.12	33.52
k__Bacteria;p__Bacteroidetes;c__Sphingobacteriia;o__Sphingobacteriales;f__	0.11	0.06	0.46	1.6	1.04	34.56
k__Bacteria;p__Bacteroidetes;c__[Rhodothermi];o__[Rhodothermales];f__[Balneolaceae]	0.01	0.07	0.45	1.45	1.02	35.58