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Supplemental Information for

**Ultrafiltration and Microarray Detect Microbial Source Tracking Marker and  
Pathogen Genes in Riverine and Marine Systems**

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14 Table S1. qPCR reactions used in this study

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Organism (gene target)	Primer (F and R) and Probe (P) Sequence (5'-3')	Standard Curve	Reaction efficiency (R <sup>2</sup> )	Reference
Enterococcus spp. (23S rRNA)	F: GAGAAATTCCAAACGAACTTG R: CAGTGCTCTACCTCCATCATT P: TGGTTCTCTCCGAAATAGCTTTAGGGCTA	y= -0.3597x+11.966	130% (0.994)	(1)
Bacteroidales (16S rRNA)	F: GGGGTTCTGAGAGGAAGGT R: CCGTCATCCTTCACGCTACT P: CAATATTCCTCACTGCTGCCTCCCGTA	y=-0.3297x+13.839	114% (0.997)	(2)
E. coli (uidA)	F: GTCCAAAGCGGCGATTTG R: CAGGCCAGAAGTTCTTTTTTCCA P: ACGGCAGAGAAGGTA	y=-0.3373x+13.371	118 % (0.997)	(3)
Salmonella spp. (invA)	F: CGTTTCCTGCGGTA CTGTTAATT R: AGACGGCTGGTACTGATCGATAA P: CCACGCTCTTTCGTCT	y=-0.3238x+13.87	112% (0.994)	(3)
Brevibacterium sp. LA35 (16S rRNA)	F: ACCGGATACGACCATCTGC R: TCCCCAGTGTCAGTCACAGC P: CAGCAGGGAAGAAGCCTTCGGGTGACGGTA	y=-0.2649x+10.38	84% (0.999)	(4)
Staphylococcus aureus (sec)	F: CGTATTAGCAGAGACCAACCA R: GTGAATTTACTCGCTTTGTGCAA P: ACCCTACGCCAGATGA	y=-0.2904x+12.366	109% (0.996)	(3)
Norovirus (RNA polymerase)	F: GCYATGTTCCGYTGGATGC R: GTCCTTAGACGCCATCATCATT	y=-0.3743x+11.279	138% (0.992)	(5)
Polyomavirus (T antigen)	F: AGT CTT TAG GGT CTT CTA CCT TT R: GGT GCC AAC CTA TGG AAC AG	y=-0.3761x+12.673	121% (0.987)	(6)
Human Bacteroidales (16s rRNA)	F: ATCATGAGTTCACATGTCCG R: TACCCCGCCTACTATCTAATG	y=-0.3038x+11.095	101% (0.998)	(7)
Adenovirus (hexon gene)	F: GGACGCCTCGGAGTACCTGAG R: ACIGTGGGGTTTCTGAACTTGTT P: CTGGTGCAGTTCGCCCCGTGCCA	y= -0.3545x +6.6727	89% (0.986)	(8)

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