

## Supplemental Information

FIG S1. Comparison of salinity and temperature effects on Bacteroidales marker persistence with time. Individual panels represent different salinities or temperature, respectively.

FIG S2. The phylogenetic relationships of sample OTUs identified in this study, numbers in parentheses indicate number of sequences belonging to a particular OTU. The tree was inferred using the Neighbor joining method (2) using pairwise distances. Evolutionary distances we estimated using the Kimura-2 parameter method (1) and rate variation among sites was modeled using a gamma distribution and a shape parameter = 0.5. A total of 680 positions (including alignment gaps) were used in the final dataset and analyses was conducted using MEGA4 (3).

## References

1. **Kimura, M.** 1980. A simple method for estimating evolutionary rate of base substitutions through comparative studies of nucleotide sequences. *J. Mol. Evol.* **16**:111-120.
2. **Saitou, N., and M. Nei.** 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Mol. Biol. Evol.* **4**:406-425.
3. **Tamura, K., J. Dudley, M. Nei, and S. Kumar.** 2007. MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. *Mol. Biol. Evol.* **24**:1596-1599.

Figure S1.

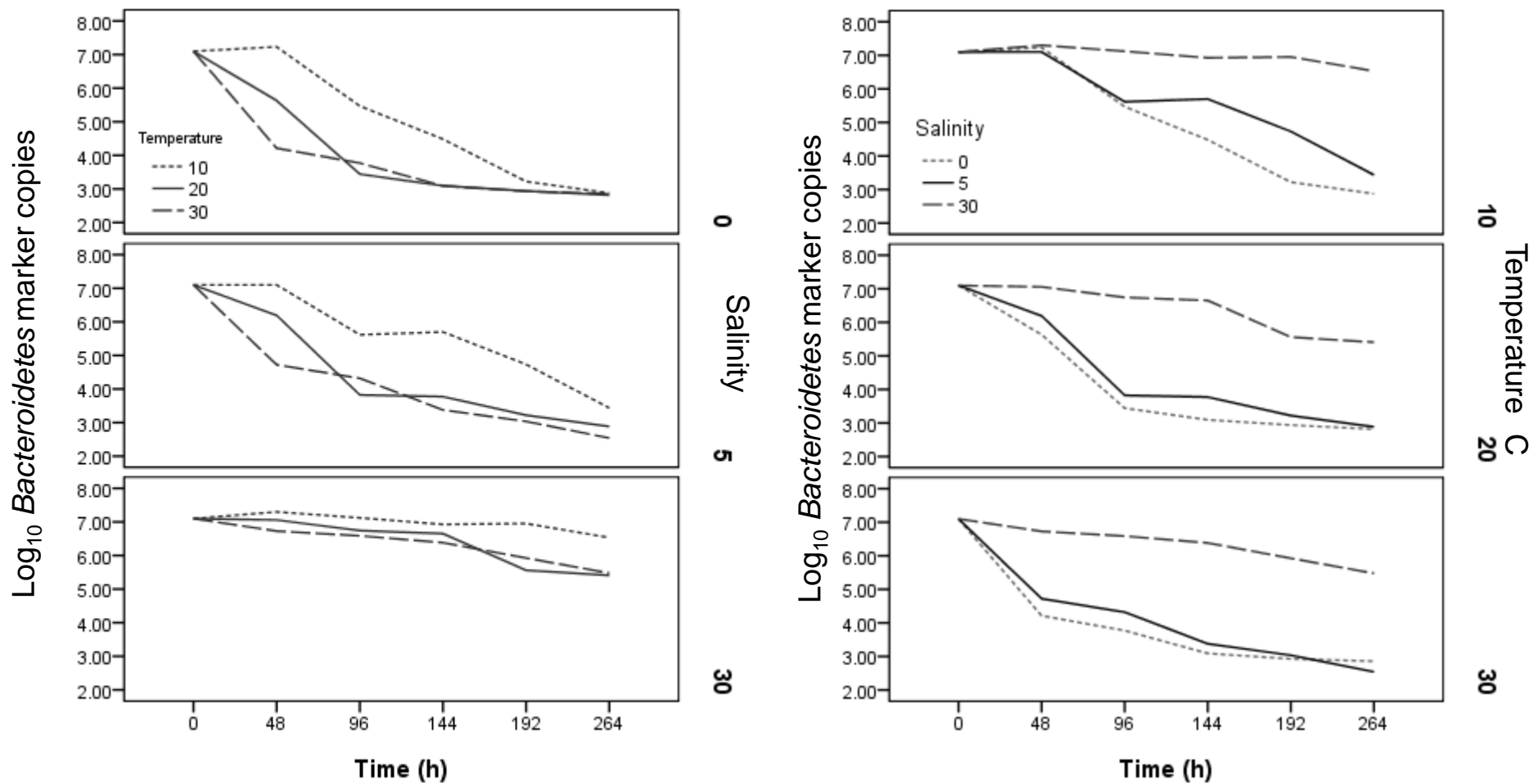


Figure S2.

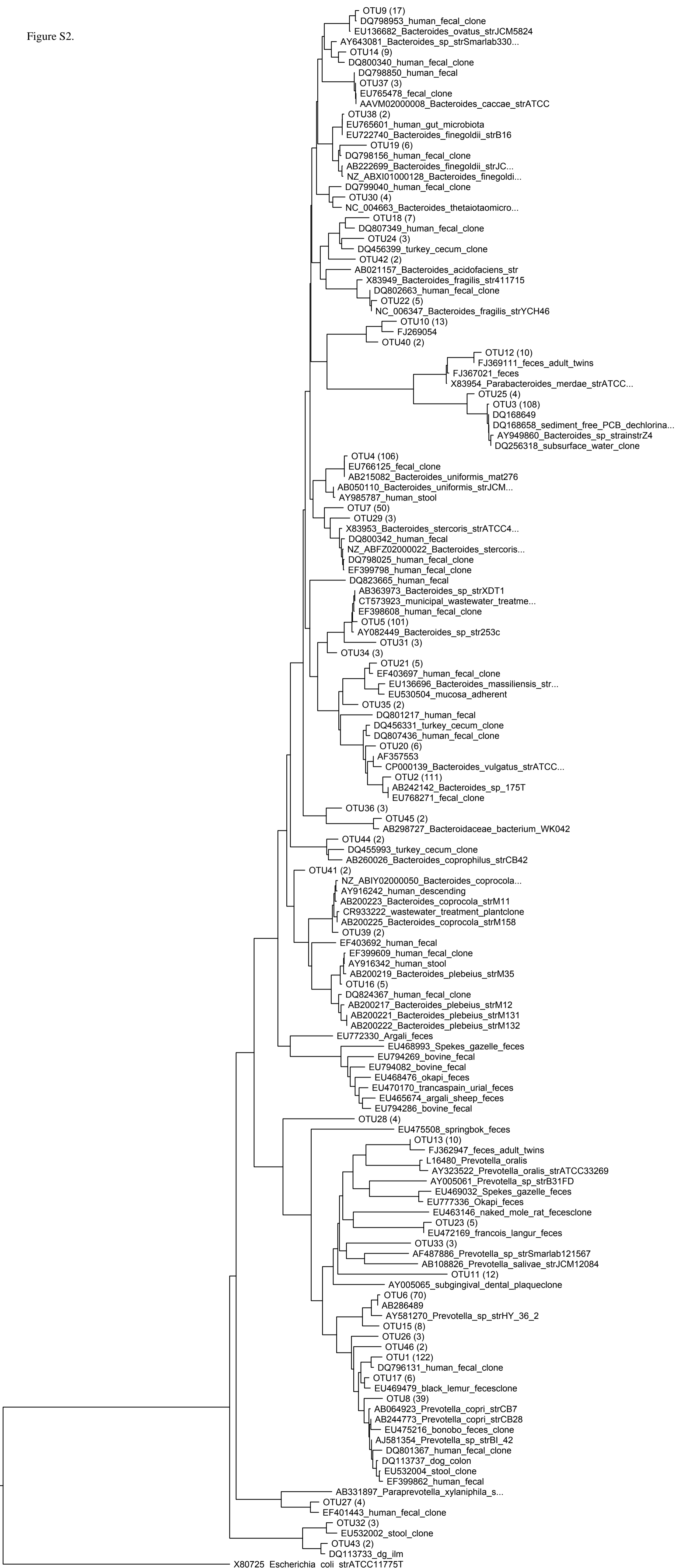


Table S1. Results of Multi-Response Permutation Procedures (MRPP) using Bray-Curtis distance and 95% OTU cutoff value

	Within group distance			Between group pairwise comparisons		
	mean distance	Test statistic $T$	$p$ (all groups)	Salinity (‰)	Test statistic $T$	$p$
Salinity						
0 ‰	0.707			0 ‰ - 5 ‰	0.736	0.754
5 ‰	0.573	-1.686	0.06	0 ‰ - 30 ‰	326	0.597
30 ‰	0.467			5 ‰ - 30 ‰	-4.691	0.0006
Temperature						
20°C	0.605					
30°C	0.534	-0.426	0.283			