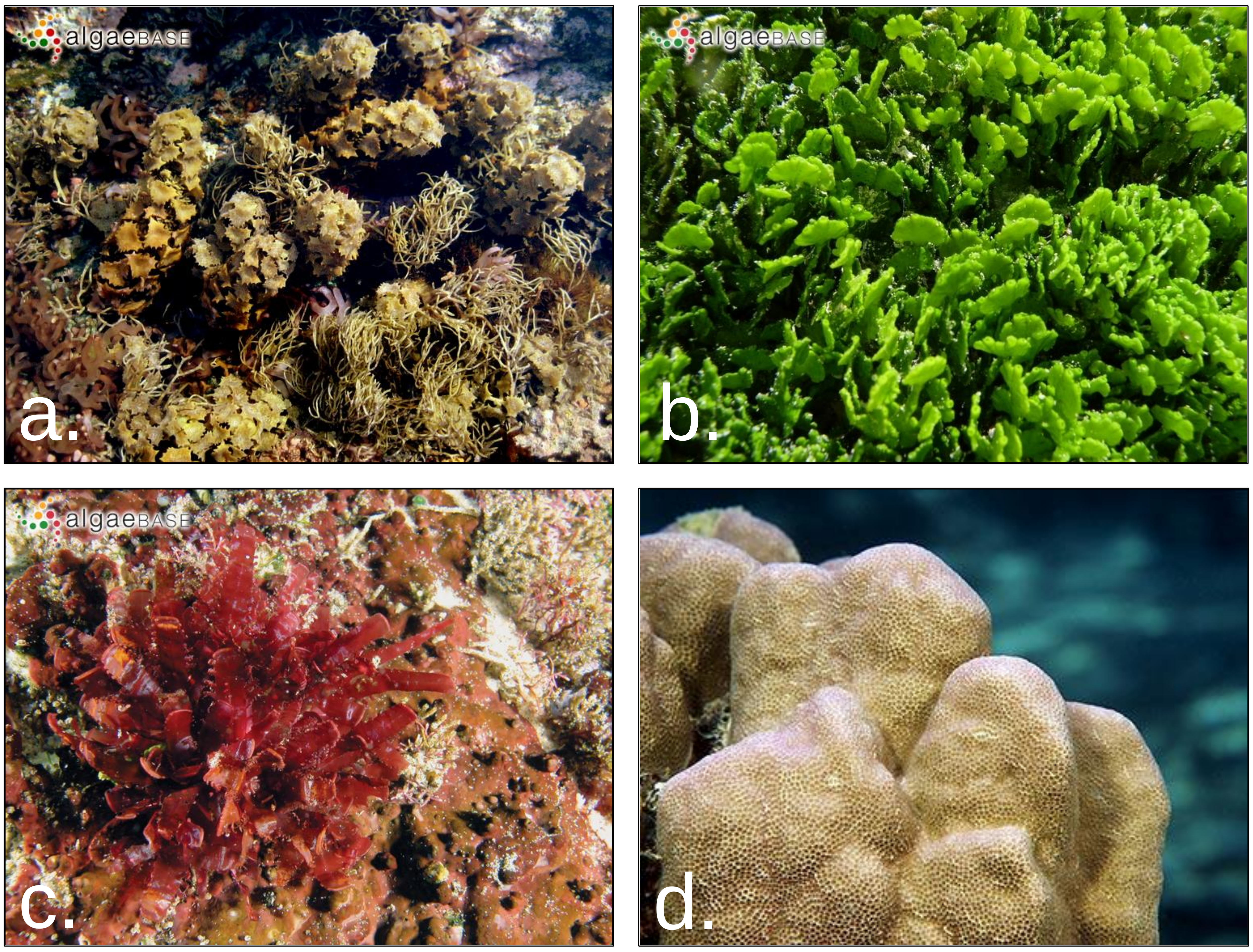
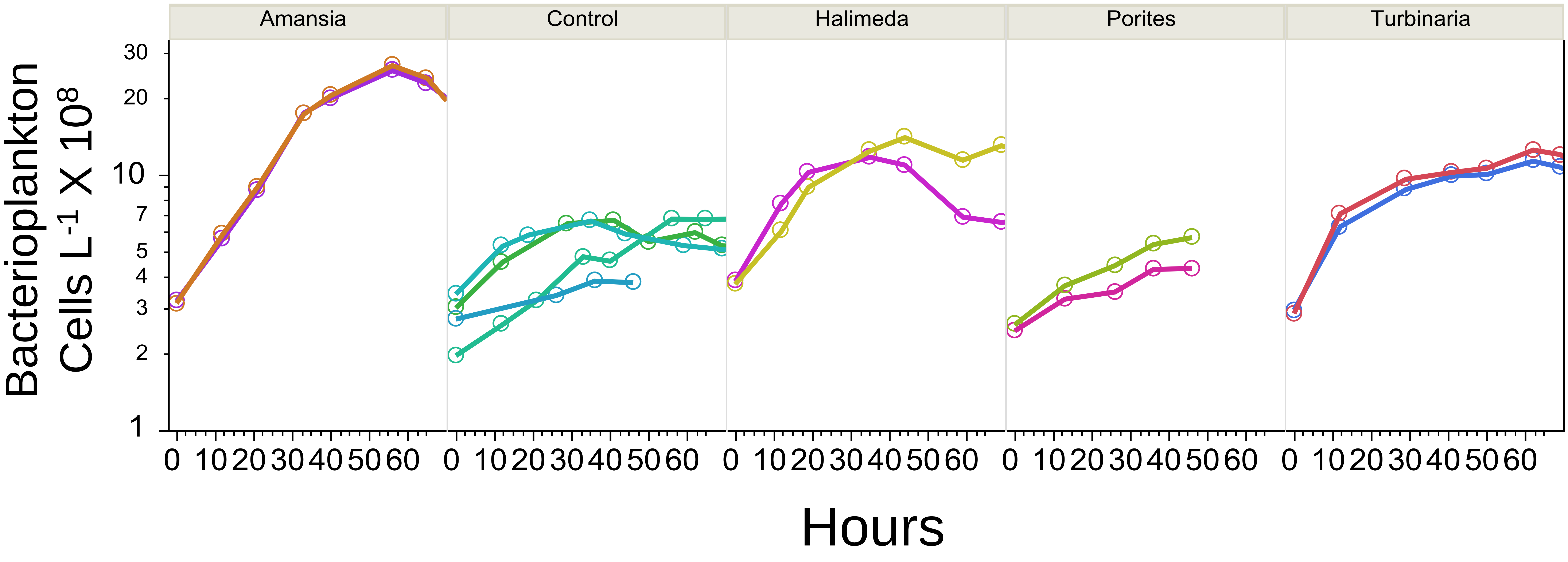


Supplementary Figure S1. Example photographs of the four benthic primary producers found in lagoonal reefs on the north shore of Moorea, French Polynesia used to produce exudates in this study. Species are as follows: a)*Turbinaria ornata* – Ochrophyta; b) *Halimeda opuntia* – Chlorophyta; c) *Amansia rhodantha* – Rhodophyta; *Porites lobata* - Cnidaria. Photos a-c sourced from AlgaeBase: Guiry, M.D. & Guiry, G.M. 2011. http://www.algaebase.org, National University of Ireland, Galway; photo d sourced from MCR-LTER at http://mcr.lternet.edu/education with respective copyrights: a) Eric Coppejans(eric.coppejans@ugent.be); b) John Huisman (j.huisman@murdoch.edu.au); c) Heroen Verbruggen (heroen.verbruggen@gmail.com); d) Matthew Meier (matt@matthewmeierphoto.com).



Supplementary Figure S2. Replicate bacterioplankton growth curves over time in each treatment.

Supplementary Figures S3. Complete phylogeny of all OTUs analyzed in this study and nearest neighbors. Bars at right of each OTU give relative abundance of each taxa in each treatment. Note that this is downloadable as a separate file for full resolution.

Turbinaria		Halimeda	
Alphaproteobacteria_Rhodobacteraceae_uncultured_OTU1	20.2%	Alphaproteobacteria_Rhodobacteraceae_uncultured_OTU1	27.8%
Gammaproteobacteria_Vibrionaceae_Photobacterium_OTU59	10.0%	Alphaproteobacteria_Rhodobacteraceae_Thalassobius_OTU14	20.6%
Alphaproteobacteria_Rhodobacteraceae_Thalassobius_OTU14	5.8%	Flavobacteria_Flavobacteriaceae_Formosa_OTU8	4.5%
Gammaproteobacteria_Vibrionaceae_Vibrio_OTU33	5.8%	Gammaproteobacteria_Alteromonadaceae_Porticoccus_OTU106	3.5%
Gammaproteobacteria_Vibrionaceae_Photobacterium_OTU102	5.3%	Flavobacteria_Flavobacteriaceae_NS5_marine_group_OTU7	3.5%
Flavobacteria_Flavobacteriaceae_NS5_marine_group_OTU7	4.1%	Cyanobacteria_Synechococcus__OTU22	3.3%
Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU39	4.1%	Flavobacteria_Cryomorphaceae_Owenweeksia_OTU23	1.8%
Alphaproteobacteria_Rhodobacteraceae_Ruegeria_OTU100	3.6%	Gammaproteobacteria_Alteromonadaceae_OM60(NOR5)_clade_OTU5	1.8%
Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU95	2.5%	Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU4	1.6%
Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU56	2.2%	Gammaproteobacteria_Litoricolaceae_Litoricola_OTU2	1.5%
Gammaproteobacteria_Litoricolaceae_Litoricola_OTU2	2.0%	Gammaproteobacteria_Oceanospirillaceae_Oceanobacter_OTU21	1.4%
Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU18	1.8%	Flavobacteria_NS9_marine_group__OTU55	1.4%
Gammaproteobacteria_Alteromonadaceae_OM60(NOR5)_clade_OTU5	1.7%	Betaproteobacteria_Methylophilaceae_OM43_clade_OTU10	1.3%
Gammaproteobacteria_Oceanospirillaceae_Marinomonas_OTU210	1.3%	Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU95	1.3%
Alphaproteobacteria_Rhodobacteraceae_Albimonas_OTU174	1.2%	Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU56	1.2%
Amansia		**Porites**	
Alphaproteobacteria_Rhodobacteraceae_uncultured_OTU1	33.5%	Alphaproteobacteria_Rhodobacteraceae_uncultured_OTU1	26.2%
Alphaproteobacteria_Rhodobacteraceae_Thalassobius_OTU14	26.2%	Alphaproteobacteria_Rhodobacteraceae_Thalassobius_OTU14	9.0%
Flavobacteria_Flavobacteriaceae_NS5_marine_group_OTU7	8.2%	Betaproteobacteria_Methylophilaceae_OM43_clade_OTU10	4.3%
Gammaproteobacteria_Vibrionaceae_Vibrio_OTU33	5.8%	Alphaproteobacteria_Hyphomonadaceae_uncultured_OTU50	3.5%
Flavobacteria_Flavobacteriaceae_NS5_marine_group_OTU29	3.2%	Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU56	2.8%
Gammaproteobacteria_Oleiphilaceae_Oleiphilus_OTU3	2.2%	Gammaproteobacteria_Alteromonadaceae_OM60(NOR5)_clade_OTU5	2.6%
Alphaproteobacteria_Rhodobacteraceae_Tropicibacter_OTU32	1.5%	Alphaproteobacteria_Rhodobacteraceae_Tropicibacter_OTU32	1.8%
Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU56	1.4%	Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU95	1.7%
Gammaproteobacteria_Alteromonadaceae_OM60(NOR5)_clade_OTU5	1.2%	Gammaproteobacteria_Oleiphilaceae_Oleiphilus_OTU3	1.6%
Gammaproteobacteria_Oceanospirillaceae_Marinomonas_OTU210	1.0%	Alphaproteobacteria_Sneathiellaceae_Sneathiella_OTU108	1.6%
Cyanobacteria_Synechococcus__OTU22	1.0%	Alphaproteobacteria_Sneathiellaceae_Sneathiella_OTU115	1.5%
Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU95	1.0%	Gammaproteobacteria_Litoricolaceae_Litoricola_OTU2	1.4%
Flavobacteria_Flavobacteriaceae_Mesoflavibacter_OTU259	0.9%	Gammaproteobacteria_Alteromonadaceae__OTU332	1.3%
Gammaproteobacteria_Litoricolaceae_Litoricola_OTU2	0.7%	Cyanobacteria_Synechococcus__OTU22	1.1%
Flavobacteria_Cryomorphaceae_Owenweeksia_OTU162	0.6%	Gammaproteobacteria_KI89A_clade__OTU68	1.0%
Control		**Ambient**	
Alphaproteobacteria_Rhodobacteraceae_uncultured_OTU1	28.5%	Cyanobacteria_Synechococcus__OTU22	23.2%
Betaproteobacteria_Methylophilaceae_OM43_clade_OTU10	6.1%	Alphaproteobacteria_SAR11_clade_Pelagibacter_OTU9	10.2%
Gammaproteobacteria_Oleiphilaceae_Oleiphilus_OTU3	4.2%	Alphaproteobacteria_Rhodobacteraceae_uncultured_OTU1	8.0%
Cyanobacteria_Synechococcus__OTU22	4.0%	Alphaproteobacteria_SAR11_clade_Surface_1_OTU43	7.1%
Gammaproteobacteria_Alteromonadaceae_OM60(NOR5)_clade_OTU5	3.7%	Alphaproteobacteria_SAR11_clade_Surface_1_OTU81	2.3%
Flavobacteria_Flavobacteriaceae_NS5_marine_group_OTU7	3.5%	Flavobacteria_Flavobacteriaceae_NS5_marine_group_OTU7	2.1%
Alphaproteobacteria_SAR11_clade_Pelagibacter_OTU9	3.5%	Gammaproteobacteria_Alteromonadaceae_OM60(NOR5)_clade_OTU5	1.9%
Alphaproteobacteria_SAR11_clade_Surface_1_OTU43	3.1%	Alphaproteobacteria_SAR116_clade__OTU15	1.8%
Alphaproteobacteria_Rhodobacteraceae_Thalassobius_OTU14	3.1%	Alphaproteobacteria_SAR116_clade__OTU36	1.7%
Flavobacteria_Flavobacteriaceae_Formosa_OTU8	2.7%	Gammaproteobacteria_Litoricolaceae_Litoricola_OTU2	1.5%
Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU95	2.2%	Flavobacteria_Cryomorphaceae_Owenweeksia_OTU23	1.4%
Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU4	1.8%	Alphaproteobacteria_Rhodobacteraceae_Thalassobius_OTU14	1.4%
Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU56	1.4%	Gammaproteobacteria_SAR86_clade__OTU47	1.3%
Alphaproteobacteria_SAR116_clade__OTU15	1.4%	Cyanobacteria_Chloroplast__OTU225	1.3%
Gammaproteobacteria_Litoricolaceae_Litoricola_OTU2	1.3%	Gammaproteobacteria_SAR86_clade__OTU91	1.2%

Supplementary Table S4. Fifteen most common OTUs in each treatment, with mean relative abundances. A set of six OTUs which were common to most treatments are color-coded for ease of visualization of shifts in dominance from Ambient Waters to experimental treatments.

Supplementary Table S5. OTU mean relative abundances among treatments with ANOVA and Dunnet's tests for significant differences among treatments. ANOVA p-values in ***bold italic*** are significant after multiple comparison corrections. Mean relative abundances significantly different from Control treatments (Dunnet's p < 0.05) are underlined; those in bold are higher while those in italics are lower than Control cultures. *Note that for OTUs statistical tests did not include Ambient comparisons.

	ANOVA $F_{4,15}$		Mean Relative Abundance					
OTU	p-value	q-value	Turbinaria	Halimeda	Amansia	Porites	Control	Ambient*
Gammaproteobacteria_Vibrionaceae_Photobacterium_OTU102	***0.0000***	***0.0002***	**5.29%**	0.00%	0.00%	0.00%	0.09%	0.00%
Gammaproteobacteria_Vibrionaceae_Photobacterium_OTU59	***0.0000***	***0.0002***	**9.99%**	0.00%	0.00%	0.09%	0.17%	0.00%
Alphaproteobacteria_Hyphomonadaceae_uncultured_OTU50	***0.0000***	***0.0002***	0.07%	0.30%	0.06%	**3.49%**	0.32%	0.04%
Alphaproteobacteria_SAR11_clade_Pelagibacter_OTU9	***0.0000***	***0.0002***	*0.62%*	*0.83%*	*0.53%*	*0.80%*	3.54%	10.23%
Alphaproteobacteria_SAR11_clade_Surface_1_OTU43	***0.0000***	***0.0002***	*0.27%*	*0.52%*	*0.06%*	*0.68%*	3.07%	7.12%
Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU18	***0.0001***	***0.0002***	**1.75%**	0.04%	0.06%	0.42%	0.09%	0.00%
Alphaproteobacteria_Rhodobacteraceae_Thalassobius_OTU14	***0.0001***	***0.0002***	5.83%	**20.55%**	**26.20%**	9.02%	3.05%	1.36%
Alphaproteobacteria_Rhodobacteraceae_Ruegeria_OTU100	***0.0004***	***0.0005***	**3.62%**	0.04%	0.13%	0.30%	0.07%	0.00%
Alphaproteobacteria_Sneathiellaceae_Sneathiella_OTU115	***0.0023***	***0.0032***	0.00%	0.00%	0.00%	**1.52%**	0.00%	0.00%
Gammaproteobacteria_Pseudoalteromonadaceae_Algicola_OTU6	***0.0025***	***0.0032***	**0.61%**	0.00%	0.06%	0.10%	0.16%	0.08%
Cyanobacteria_Synechococcus__OTU22	***0.0026***	***0.0032***	*0.79%*	3.33%	*0.96%*	*1.10%*	4.02%	23.20%
Cyanobacteria_Chloroplast__OTU85	***0.0032***	***0.0036***	*0.00%*	*0.04%*	*0.00%*	*0.00%*	0.36%	0.77%
Flavobacteria_NS9_marine_group__OTU38	***0.0073***	***0.0075***	*0.10%*	0.62%	*0.17%*	*0.28%*	1.00%	0.10%
Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU39	***0.0108***	***0.0102***	**4.08%**	0.00%	0.00%	0.69%	0.92%	0.03%
Gammaproteobacteria_Oceanospirillaceae_Pseudospirillum_OTU52	***0.0114***	***0.0102***	0.00%	**0.31%**	0.06%	0.12%	0.06%	0.23%
Flavobacteria_Flavobacteriaceae_Gilvibacter_OTU239	***0.0146***	***0.0123***	0.00%	0.00%	0.00%	0.31%	0.09%	0.00%
Gammaproteobacteria_Pseudoalteromonadaceae_Algicola_OTU27	***0.0175***	***0.0138***	**0.54%**	0.00%	0.00%	0.09%	0.03%	0.00%
Gammaproteobacteria_Alteromonadaceae_Porticoccus_OTU642	***0.0228***	***0.0161***	0.00%	0.00%	0.00%	**0.22%**	0.00%	0.00%
Gammaproteobacteria_Pseudoalteromonadaceae_Pseudoalteromonas_OTU17	***0.0230***	***0.0161***	**1.12%**	0.04%	0.00%	0.00%	0.03%	0.31%
Alphaproteobacteria_Rhodobacteraceae_Thalassobius_OTU173	***0.0240***	***0.0161***	0.00%	0.04%	0.00%	**0.16%**	0.00%	0.00%
Flavobacteria_Cryomorphaceae_Owenweeksia_OTU162	***0.0278***	***0.0169***	0.00%	**0.73%**	0.57%	0.09%	0.00%	0.00%
Alphaproteobacteria_SAR116_clade__OTU15	***0.0281***	***0.0169***	*0.05%*	*0.08%*	*0.00%*	*0.06%*	1.44%	1.85%
Alphaproteobacteria_Erythrobacteraceae_Erythrobacter_OTU197	***0.0289***	***0.0169***	0.02%	0.00%	0.00%	0.51%	0.13%	0.05%
Flavobacteria_Flavobacteriaceae_Formosa_OTU8	***0.0331***	***0.0173***	0.28%	4.48%	0.00%	0.06%	2.74%	0.78%
Flavobacteria_Cryomorphaceae_Fluviicola_OTU854	***0.0334***	***0.0173***	0.00%	0.19%	**0.31%**	0.00%	0.00%	0.00%
Gammaproteobacteria_Alteromonadaceae_Teredinibacter_OTU136	***0.0351***	***0.0173***	0.00%	0.00%	0.00%	**0.58%**	0.00%	0.00%
Alphaproteobacteria_Rhodobacteraceae_Albimonas_OTU174	***0.0353***	***0.0173***	**1.22%**	0.00%	0.18%	0.06%	0.11%	0.00%
Flavobacteria_Flavobacteriaceae_Tenacibaculum_OTU336	0.0362	0.0173	0.02%	0.04%	0.00%	0.43%	0.11%	0.00%
Planctomycetes_OM190__OTU744	0.0384	0.0173	0.00%	0.00%	0.00%	0.18%	0.00%	0.00%
Alphaproteobacteria_Rhodobacteraceae_uncultured_OTU177	0.0392	0.0173	0.00%	0.04%	0.06%	0.65%	0.16%	0.00%
Gammaproteobacteria_Pseudoalteromonadaceae_Pseudoalteromonas_OTU314	0.0429	0.0173	0.73%	0.00%	0.00%	0.03%	0.00%	0.04%
Gammaproteobacteria_Alteromonadaceae_Marinobacter_OTU157	0.0433	0.0173	0.00%	0.07%	0.06%	0.73%	0.27%	0.00%
Alphaproteobacteria_SAR116_clade__OTU86	0.0436	0.0173	0.02%	0.00%	0.00%	0.03%	0.33%	0.26%
Deltaproteobacteria_Bacteriovoraceae_Bacteriovorax_OTU48	0.0438	0.0173	0.02%	0.24%	0.18%	0.61%	0.07%	0.03%
Gammaproteobacteria_Pseudoalteromonadaceae_Algicola_OTU30	0.0452	0.0173	0.18%	0.00%	0.00%	0.00%	0.03%	0.00%
Flavobacteria_NS9_marine_group__OTU55	0.0475	0.0177	0.10%	1.35%	0.36%	0.96%	0.14%	0.02%
Alphaproteobacteria_Rhodobacteraceae_Dinoroseobacter_OTU399	0.0509	0.0182	0.00%	0.00%	0.00%	0.16%	0.04%	0.00%
Flavobacteria_Flavobacteriaceae_Winogradskyella_OTU149	0.0514	0.0182	0.25%	0.17%	0.00%	0.85%	0.14%	0.00%
Flavobacteria_Flavobacteriaceae_Sufflavibacter_OTU688	0.0555	0.0187	0.14%	0.00%	0.00%	0.20%	0.00%	0.00%
Gammaproteobacteria_Alcanivoracaceae_Alcanivorax_OTU527	0.0571	0.0187	0.00%	0.00%	0.00%	0.21%	0.00%	0.00%
Flavobacteria_Flavobacteriaceae_NS5_marine_group_OTU29	0.0572	0.0187	0.41%	0.55%	3.17%	0.06%	0.58%	0.33%
Flavobacteria_Flavobacteriaceae_Psychroserpens_OTU628	0.0605	0.0193	0.05%	0.04%	0.00%	0.43%	0.03%	0.00%
Betaproteobacteria_Methylophilaceae_uncultured_OTU153	0.0715	0.0223	0.00%	0.00%	0.00%	0.63%	0.00%	0.00%
Flavobacteria_Flavobacteriaceae_Sandarakinotalea_OTU167	0.0756	0.0228	0.09%	0.40%	0.06%	0.00%	0.00%	0.00%
Alphaproteobacteria_Hyphomonadaceae_Maricaulis_OTU322	0.0767	0.0228	0.00%	0.00%	0.00%	0.16%	0.10%	0.00%
Flavobacteria_Flavobacteriaceae_NS4_marine_group_OTU591	0.0781	0.0228	0.02%	0.00%	0.00%	0.07%	0.00%	0.23%
Flavobacteria_Flavobacteriaceae_Tenacibaculum_OTU481	0.0819	0.0234	0.89%	0.00%	0.00%	0.03%	0.06%	0.00%
Flavobacteria_Flavobacteriaceae_Tenacibaculum_OTU483	0.0879	0.0237	0.25%	0.00%	0.06%	0.03%	0.00%	0.08%
Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU4	0.0894	0.0237	0.46%	1.56%	0.00%	0.90%	1.75%	0.08%
Flavobacteria_Flavobacteriaceae_Krokinobacter_OTU298	0.0898	0.0237	0.32%	0.04%	0.06%	0.26%	0.00%	0.00%
Flavobacteria_Flavobacteriaceae_Winogradskyella_OTU125	0.0907	0.0237	0.52%	0.04%	0.00%	0.69%	0.03%	0.04%
Gammaproteobacteria_Alteromonadaceae__OTU293	0.0934	0.0237	0.52%	0.00%	0.00%	0.45%	0.11%	0.00%
Flavobacteria_Flavobacteriaceae_Croceibacter_OTU849	0.0936	0.0237	0.00%	0.00%	0.00%	0.13%	0.00%	0.00%
Gammaproteobacteria_SAR86_clade__OTU47	0.1039	0.0253	0.00%	0.69%	0.00%	0.00%	0.92%	1.29%
Gammaproteobacteria_Alteromonadaceae_Congregibacter_OTU158	0.1049	0.0253	0.00%	0.00%	0.00%	0.39%	0.11%	0.04%
Gammaproteobacteria_OM182_clade__OTU377	0.1056	0.0253	0.00%	0.00%	0.00%	0.27%	0.09%	0.00%
Actinobacteria_Acidimicrobiales_OCS155_marine_group_OTU180	0.1201	0.0271	0.00%	0.00%	0.24%	0.03%	0.00%	0.18%
Gammaproteobacteria_Alteromonadaceae__OTU332	0.1210	0.0271	0.70%	0.00%	0.00%	1.35%	0.20%	0.00%
Alphaproteobacteria_Rhodobacteraceae_Rhodobacter_OTU596	0.1211	0.0271	0.00%	0.00%	0.00%	0.13%	0.00%	0.00%
Flavobacteria_NS9_marine_group__OTU34	0.1212	0.0271	0.05%	0.00%	0.00%	0.00%	0.25%	0.04%
Alphaproteobacteria_Rhodobacteraceae_uncultured_OTU426	0.1231	0.0271	0.02%	0.12%	0.00%	0.09%	0.00%	0.00%
Flavobacteria_Cryomorphaceae_Owenweeksia_OTU146	0.1269	0.0275	0.14%	1.00%	0.45%	0.16%	0.00%	0.00%
Flavobacteria_Cryomorphaceae_NS10_marine_group_OTU1514	0.1295	0.0276	0.00%	0.20%	0.00%	0.00%	0.00%	0.00%
Gammaproteobacteria_Oceanospirillaceae_Marinomonas_OTU210	0.1356	0.0285	1.35%	0.00%	1.04%	0.00%	0.03%	0.00%
Betaproteobacteria_Methylophilaceae_OM43_clade_OTU10	0.1421	0.0290	0.39%	1.34%	0.00%	4.26%	6.11%	0.38%
Gammaproteobacteria_Oceanospirillaceae_Neptuniibacter_OTU44	0.1426	0.0290	0.00%	0.22%	0.06%	0.03%	0.00%	0.04%
Flavobacteria_NS9_marine_group__OTU547	0.1462	0.0293	0.00%	0.17%	0.00%	0.10%	0.00%	0.00%
Flavobacteria_Flavobacteriaceae_Polaribacter_OTU203	0.1549	0.0306	0.37%	0.00%	0.00%	0.32%	0.14%	0.00%
Alphaproteobacteria_SAR11_clade_Surface_1_OTU81	0.1621	0.0312	0.12%	0.16%	0.24%	0.67%	0.63%	2.32%
Alphaproteobacteria_Rhodobacteraceae_Roseobacter_clade_DC5-80-3_lineage_OTU126	0.1628	0.0312	0.02%	0.07%	0.12%	0.13%	0.00%	0.00%
Alphaproteobacteria_Rhodobacteraceae_Shimia_OTU529	0.1647	0.0312	0.05%	0.00%	0.00%	0.09%	0.00%	0.00%
Flavobacteria_Flavobacteriaceae_Polaribacter_OTU553	0.1676	0.0313	0.00%	0.00%	0.00%	0.12%	0.03%	0.00%
Flavobacteria_Flavobacteriaceae_NS5_marine_group_OTU7	0.1721	0.0317	4.10%	3.47%	8.22%	0.10%	3.55%	2.15%
Deltaproteobacteria_SAR324_clade(Marine_group_B)__OTU169	0.1759	0.0319	0.00%	0.00%	0.00%	0.00%	0.07%	0.42%
Deferribacteres_SAR406_clade(Marine_group_A)__OTU88	0.1931	0.0346	0.05%	0.23%	0.00%	0.03%	0.60%	0.77%
Gammaproteobacteria_Alteromonadaceae_OM60(NOR5)_clade_OTU76	0.2008	0.0355	0.85%	0.54%	0.06%	0.19%	0.18%	0.39%
Deltaproteobacteria_Bacteriovoraceae_Peredibacter_OTU101	0.2067	0.0360	0.00%	0.04%	0.00%	0.80%	0.04%	0.02%
Betaproteobacteria_Methylophilaceae_OM43_clade_OTU97	0.2299	0.0391	0.05%	0.04%	0.00%	0.06%	0.19%	0.47%
Gammaproteobacteria_KI89A_clade__OTU68	0.2299	0.0391	0.00%	0.15%	0.00%	1.01%	0.11%	0.04%
Gammaproteobacteria_Alteromonadaceae_Aestuariibacter_OTU61	0.2381	0.0400	0.18%	0.00%	0.00%	0.14%	0.00%	0.02%
Alphaproteobacteria_SAR116_clade__OTU12	0.2457	0.0407	0.10%	0.12%	0.00%	0.12%	0.37%	0.21%
Alphaproteobacteria_SAR116_clade__OTU26	0.2484	0.0407	0.57%	0.20%	0.00%	0.19%	1.01%	0.59%
Gammaproteobacteria_Alteromonadaceae_OM60(NOR5)_clade_OTU5	0.2557	0.0408	1.71%	1.77%	1.17%	2.65%	3.72%	1.95%
Alphaproteobacteria_Rhodobacteraceae_Roseobacter_clade_DC5-80-3_lineage_OTU107	0.2566	0.0408	0.00%	0.00%	0.00%	0.00%	0.42%	0.13%
Cyanobacteria_Chloroplast__OTU225	0.2592	0.0408	0.02%	0.00%	0.00%	0.00%	0.24%	1.25%
Actinobacteria_Acidimicrobiales_Acidimicrobiaceae_OTU188	0.2620	0.0408	0.00%	0.15%	0.00%	0.00%	0.25%	0.44%
Alphaproteobacteria_Sneathiellaceae_Sneathiella_OTU108	0.2644	0.0408	0.00%	0.00%	0.00%	1.55%	0.00%	0.00%
Alphaproteobacteria_Kordiimonadaceae_Kordiimonas_OTU541	0.2779	0.0424	0.18%	0.00%	0.00%	0.13%	0.00%	0.00%
Alphaproteobacteria_Rhodobacteraceae_Thalassobius_OTU41	0.3050	0.0460	0.16%	0.93%	0.49%	0.56%	0.51%	0.00%
Gammaproteobacteria_Litoricolaceae_Litoricola_OTU2	0.3093	0.0461	1.96%	1.52%	0.66%	1.44%	1.29%	1.45%
Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU51	0.3269	0.0470	1.10%	0.48%	0.24%	0.87%	0.49%	0.08%
Alphaproteobacteria_SAR116_clade__OTU179	0.3285	0.0470	0.00%	0.00%	0.00%	0.03%	0.22%	0.68%
Alphaproteobacteria_Sneathiellaceae_Sneathiella_OTU195	0.3289	0.0470	0.00%	0.00%	0.00%	0.43%	0.11%	0.00%
Flavobacteria_Cryomorphaceae_Owenweeksia_OTU726	0.3322	0.0470	0.02%	0.08%	0.12%	0.03%	0.00%	0.00%
Gammaproteobacteria_Oleiphilaceae_Oleiphilus_OTU13	0.3326	0.0470	0.00%	0.04%	0.00%	0.06%	0.16%	0.00%
Flavobacteria_Cryomorphaceae_Owenweeksia_OTU23	0.3490	0.0482	0.02%	1.85%	0.00%	0.06%	0.33%	1.41%
Gammaproteobacteria_Alteromonadaceae_OM60(NOR5)_clade_OTU63	0.3505	0.0482	0.36%	0.38%	0.00%	0.41%	0.56%	0.11%
Flavobacteria_Flavobacteriaceae_Croceitalea_OTU435	0.3660	0.0482	0.00%	0.17%	0.00%	0.15%	0.03%	0.04%
Gammaproteobacteria_Alteromonadaceae_Porticoccus_OTU106	0.3687	0.0482	0.00%	3.51%	0.00%	0.03%	0.00%	0.00%
Flavobacteria_Flavobacteriaceae_Winogradskyella_OTU757	0.3752	0.0482	0.31%	0.12%	0.00%	0.28%	0.00%	0.00%
Alphaproteobacteria_Rhodobacteraceae_uncultured_OTU1	0.3861	0.0482	20.17%	27.82%	33.52%	26.18%	28.45%	8.04%
Alphaproteobacteria_SAR116_clade__OTU397	0.3970	0.0482	0.00%	0.00%	0.00%	0.06%	0.00%	0.13%
Alphaproteobacteria_SAR11_clade_Surface_4_OTU92	0.3970	0.0482	0.00%	0.00%	0.00%	0.03%	0.00%	0.41%
Deltaproteobacteria_Bacteriovoraceae_Peredibacter_OTU401	0.3970	0.0482	0.00%	0.00%	0.00%	0.20%	0.00%	0.00%
Alphaproteobacteria_SM2D12__OTU105	0.3970	0.0482	0.00%	0.25%	0.00%	0.00%	0.00%	0.00%
Chloroflexi_SAR202_clade__OTU567	0.3970	0.0482	0.00%	0.04%	0.00%	0.00%	0.00%	0.13%
Alphaproteobacteria_Hyphomonadaceae_Hellea_OTU359	0.3970	0.0482	0.00%	0.00%	0.06%	0.00%	0.00%	0.04%
Gammaproteobacteria_Alteromonadaceae_BD1-7_clade_OTU1060	0.3970	0.0482	0.00%	0.46%	0.00%	0.00%	0.00%	0.00%
Gammaproteobacteria_Alteromonadaceae_Teredinibacter_OTU24	0.3970	0.0482	0.00%	0.00%	0.00%	0.40%	0.00%	0.00%
Alphaproteobacteria_Rhodobacteraceae_Donghicola_OTU360	0.3970	0.0482	0.00%	0.00%	0.00%	0.42%	0.00%	0.00%
Alphaproteobacteria_Rhodobacteraceae_Ruegeria_OTU351	0.4014	0.0482	0.00%	0.12%	0.00%	0.06%	0.04%	0.00%
Gammaproteobacteria_Alteromonadaceae_Aestuariibacter_OTU315	0.4049	0.0482	0.02%	0.00%	0.06%	0.50%	0.44%	0.00%
Gammaproteobacteria_Vibrionaceae_Vibrio_OTU33	0.4078	0.0482	5.81%	0.12%	5.81%	0.25%	0.28%	0.22%
Alphaproteobacteria_Rhodobacteraceae_uncultured_OTU291	0.4096	0.0482	0.00%	0.00%	0.00%	0.06%	0.04%	0.00%
Gammaproteobacteria_Alteromonadaceae_Melitea_OTU405	0.4129	0.0482	0.00%	0.00%	0.00%	0.25%	0.20%	0.00%
Alphaproteobacteria_Rhodobacteraceae_Roseovarius_OTU255	0.4255	0.0493	0.00%	0.00%	0.18%	0.09%	0.00%	0.00%
Alphaproteobacteria_SAR116_clade__OTU96	0.4349	0.0499	0.18%	0.08%	0.00%	0.00%	0.06%	0.02%
Flavobacteria_Cryomorphaceae_Owenweeksia_OTU349	0.4397	0.0500	0.00%	0.17%	0.00%	0.03%	0.00%	0.00%
Flavobacteria_Flavobacteriaceae_Mesoflavibacter_OTU259	0.4564	0.0514	0.00%	0.16%	0.91%	0.10%	0.00%	0.00%
Gammaproteobacteria_Oceanospirillaceae_Oceanospirillum_OTU35	0.4591	0.0514	0.00%	0.00%	0.00%	0.23%	0.04%	0.00%
Alphaproteobacteria_Rhodobacteraceae_Roseobacter_clade_NAC11-7_lineage_OTU165	0.4651	0.0515	0.18%	0.24%	0.19%	0.58%	0.23%	0.04%
Alphaproteobacteria_Rhodospirillaceae_AEGEAN-169_marine_group_OTU134	0.4675	0.0515	0.00%	0.08%	0.00%	0.03%	0.00%	0.23%
Alphaproteobacteria_Kordiimonadaceae_Kordiimonas_OTU520	0.4718	0.0515	0.00%	0.13%	0.00%	0.15%	0.06%	0.00%
Alphaproteobacteria_SAR116_clade__OTU36	0.4768	0.0516	0.49%	0.24%	0.06%	0.44%	0.75%	1.74%
Alphaproteobacteria_SAR11_clade_Surface_1_OTU168	0.4806	0.0516	0.18%	0.00%	0.00%	0.03%	0.07%	0.57%
Gammaproteobacteria_Vibrionaceae_Photobacterium_OTU1518	0.4837	0.0516	0.12%	0.00%	0.00%	0.00%	0.03%	0.00%
Alphaproteobacteria_SAR11_clade_Deep_1_OTU497	0.4914	0.0520	0.00%	0.04%	0.18%	0.03%	0.00%	0.16%
Alphaproteobacteria_S25-593__OTU387	0.5023	0.0523	0.02%	0.00%	0.00%	0.09%	0.06%	0.32%
Gammaproteobacteria_Oceanospirillaceae_Oceanobacter_OTU21	0.5026	0.0523	0.00%	1.39%	0.06%	0.73%	1.03%	0.09%
Flavobacteria_Cryomorphaceae_NS10_marine_group_OTU1838	0.5167	0.0534	0.00%	0.12%	0.13%	0.00%	0.00%	0.00%
Flavobacteria_Cryomorphaceae_Owenweeksia_OTU603	0.5273	0.0534	0.00%	0.04%	0.13%	0.03%	0.00%	0.00%
Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU56	0.5319	0.0534	2.16%	1.18%	1.38%	2.81%	1.44%	0.49%
Flavobacteria_NS9_marine_group__OTU121	0.5321	0.0534	0.00%	0.00%	0.12%	0.00%	0.04%	0.08%
Alphaproteobacteria_Rhodobacteraceae_Loktanella_OTU147	0.5333	0.0534	0.05%	0.13%	0.00%	0.03%	0.00%	0.00%
Alphaproteobacteria_Rhodobacteraceae_uncultured_OTU619	0.5426	0.0540	0.00%	0.00%	0.00%	0.09%	0.09%	0.00%
Flavobacteria_Flavobacteriaceae_NS2b_marine_group_OTU75	0.5493	0.0542	0.29%	0.07%	0.00%	0.07%	0.28%	0.77%
Alphaproteobacteria_Phyllobacteriaceae_Hoeflea_OTU323	0.5532	0.0542	0.10%	0.00%	0.36%	0.24%	0.06%	0.00%
Alphaproteobacteria_SAR11_clade_Surface_1_OTU161	0.5584	0.0543	0.00%	0.07%	0.00%	0.00%	0.03%	0.13%
Gammaproteobacteria_Oleiphilaceae_Oleiphilus_OTU3	0.5803	0.0547	0.40%	0.17%	2.16%	1.60%	4.21%	0.13%
Gammaproteobacteria_SAR86_clade__OTU417	0.5810	0.0547	0.00%	0.08%	0.00%	0.00%	0.04%	0.07%
Gammaproteobacteria_Colwelliaceae_Thalassomonas_OTU65	0.6017	0.0547	0.10%	0.00%	0.00%	0.03%	0.03%	0.00%
Alphaproteobacteria_Rhodospirillaceae_AEGEAN-169_marine_group_OTU45	0.6033	0.0547	0.41%	0.00%	0.00%	0.00%	0.59%	0.33%
Gammaproteobacteria_Oceanospirillaceae_Neptuniibacter_OTU78	0.6047	0.0547	0.00%	0.04%	0.12%	0.10%	0.00%	0.00%
Flavobacteria_NS9_marine_group__OTU380	0.6074	0.0547	0.02%	0.04%	0.00%	0.06%	0.00%	0.13%
Alphaproteobacteria_SAR11_clade_Deep_2_OTU226	0.6082	0.0547	0.02%	0.00%	0.06%	0.03%	0.00%	0.06%
Flavobacteria_NS9_marine_group__OTU164	0.6155	0.0547	0.00%	0.00%	0.00%	0.00%	0.04%	0.19%
Alphaproteobacteria_SAR116_clade__OTU295	0.6155	0.0547	0.00%	0.00%	0.00%	0.00%	0.08%	0.29%
Flavobacteria_Cryomorphaceae_Owenweeksia_OTU191	0.6155	0.0547	0.00%	0.00%	0.00%	0.00%	0.04%	0.13%
Gammaproteobacteria_SAR86_clade__OTU166	0.6155	0.0547	0.00%	0.00%	0.00%	0.00%	0.07%	0.55%
Alphaproteobacteria_Rhodobacteraceae_uncultured_OTU371	0.6155	0.0547	0.00%	0.00%	0.00%	0.00%	0.07%	0.00%
Cyanobacteria_Chloroplast__OTU256	0.6155	0.0547	0.00%	0.00%	0.00%	0.00%	0.16%	0.15%
Flavobacteria_Flavobacteriaceae_NS4_marine_group_OTU137	0.6288	0.0556	0.14%	0.26%	0.00%	0.03%	0.60%	1.17%
Alphaproteobacteria_Rhodobacteraceae_Labrenzia_OTU540	0.6443	0.0562	0.05%	0.00%	0.00%	0.23%	0.11%	0.00%
Alphaproteobacteria_Kordiimonadaceae_Kordiimonas_OTU616	0.6496	0.0562	0.00%	0.00%	0.00%	0.21%	0.29%	0.00%
Gammaproteobacteria_Oceanospirillaceae_Marinomonas_OTU270	0.6570	0.0562	0.00%	0.00%	0.26%	0.00%	0.22%	0.27%
Flavobacteria_Flavobacteriaceae_Kordia_OTU455	0.6747	0.0562	0.02%	0.00%	0.06%	0.07%	0.03%	0.00%
Flavobacteria_Flavobacteriaceae_NS5_marine_group_OTU111	0.6758	0.0562	0.07%	0.04%	0.00%	0.00%	0.03%	0.23%
Planctomycetes_Planctomycetaceae_Planctomyces_OTU294	0.6812	0.0562	0.00%	0.00%	0.00%	0.03%	0.04%	0.05%
Gammaproteobacteria_SAR86_clade__OTU91	0.6836	0.0562	0.00%	0.04%	0.00%	0.00%	0.06%	1.20%
Alphaproteobacteria_SAR11_clade_Surface_4_OTU80	0.6846	0.0562	0.00%	0.04%	0.00%	0.00%	0.06%	0.21%
Flavobacteria_Flavobacteriaceae_Kordia_OTU620	0.6854	0.0562	0.07%	0.04%	0.06%	0.09%	0.00%	0.00%
Alphaproteobacteria_Rhodobacteraceae_Tropicibacter_OTU32	0.6867	0.0562	1.21%	0.88%	1.50%	1.78%	0.92%	0.14%
Deltaproteobacteria_Bacteriovoraceae_Peredibacter_OTU19	0.6876	0.0562	0.00%	0.20%	0.00%	0.27%	0.15%	0.02%
Gammaproteobacteria_OM182_clade__OTU109	0.6902	0.0562	0.00%	0.23%	0.06%	0.06%	0.25%	0.18%
Alphaproteobacteria_SAR11_clade_Surface_1_OTU329	0.6911	0.0562	0.00%	0.00%	0.06%	0.10%	0.04%	0.22%
Alphaproteobacteria_SAR11_clade_Surface_3_OTU198	0.6949	0.0562	0.00%	0.04%	0.00%	0.09%	0.04%	0.09%
Alphaproteobacteria_Rhodospirillaceae_AEGEAN-169_marine_group_OTU99	0.7164	0.0576	0.16%	0.04%	0.00%	0.06%	0.19%	0.59%
Flavobacteria_NS9_marine_group__OTU46	0.7260	0.0580	0.55%	0.46%	0.48%	0.22%	0.30%	0.53%
Actinobacteria_Acidimicrobiales_OCS155_marine_group_OTU207	0.7423	0.0590	0.10%	0.08%	0.00%	0.00%	0.21%	0.14%
Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU95	0.7521	0.0592	2.52%	1.27%	0.95%	1.68%	2.16%	0.45%
Flavobacteria_Flavobacteriaceae_Croceitalea_OTU20	0.7539	0.0592	0.18%	0.19%	0.06%	0.27%	0.06%	0.00%
Actinobacteria_Acidimicrobiales_Sva0996_marine_group_OTU127	0.7898	0.0616	0.11%	0.07%	0.00%	0.03%	0.08%	0.17%
Alphaproteobacteria_Rhodobacteraceae_Rhodobacter_OTU16	0.7937	0.0616	0.29%	0.10%	0.06%	0.24%	0.11%	0.08%
Flavobacteria_NS9_marine_group__OTU84	0.8103	0.0625	0.14%	0.29%	0.18%	0.03%	0.22%	0.08%

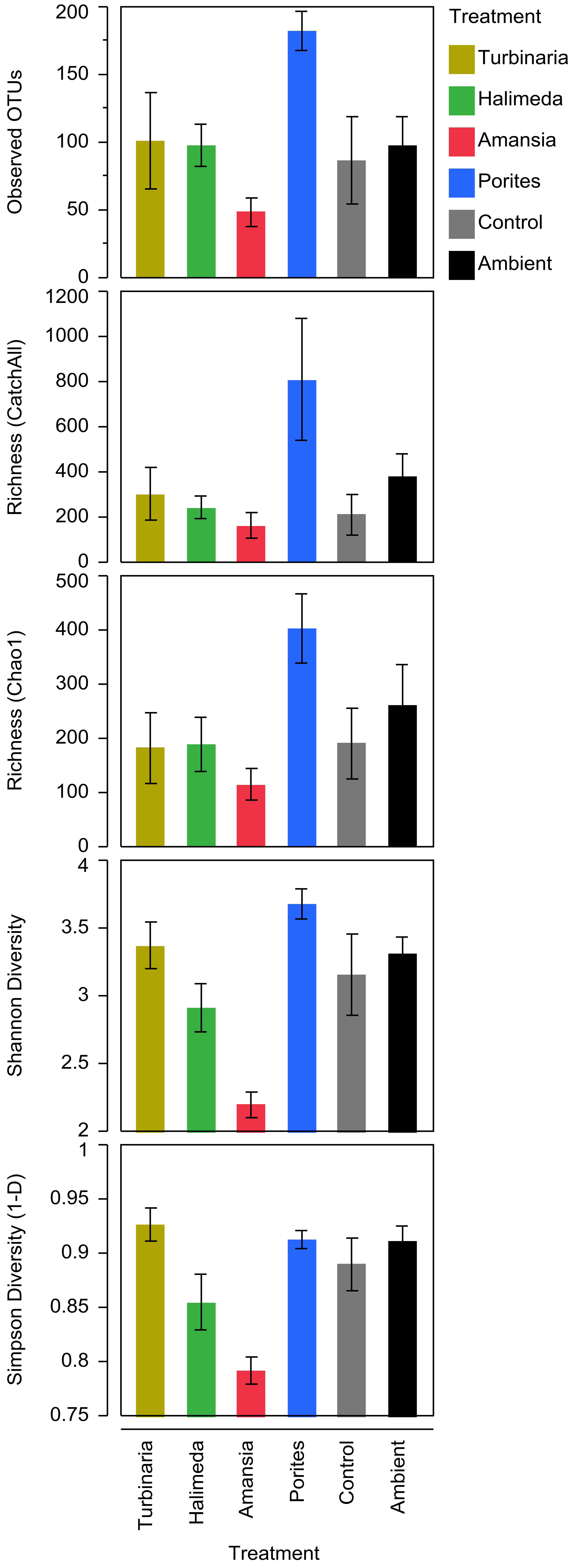
Supplementary Figure S6. Maximum-likelihood phylogeny of selected OTUs differing significantly among treatments and their nearest cultured isolate neighbors.

Flavobacteria_Flavobacteriaceae_Tenacibaculum_OTU336
Flavobacteria_Flavobacteriaceae_Winogradskyella_OTU149
Flavobacteria_NS9_marine_group__OTU55
Alphaproteobacteria_Rhodobacteraceae_uncultured_OTU1
Alphaproteobacteria_Rhodobacteraceae_uncultured_OTU177
Deltaproteobacteria_Bacteriovoraceae_Bacteriovorax_OTU48
Gammaproteobacteria_Alteromonadaceae_Alteromonas_OTU4
Gammaproteobacteria_Alteromonadaceae_Marinobacter_OTU157

Supplementary Table S7. Eight taxa which were enriched in all dilution culture incubations (exudate-amendments and controls) relative to ambient waters.

Treatment Code	Replicate Bottle	Start Date 2010	Multiplex Barcode	Sequence Reads	Observed OTUs	CatchAll Richness	Chao1 Richness	Shannon Diversity	Simpson Diversity*
Turbinaria	1	9/8	ACACGTCA	1393	171	518	305	3.64	0.94
Turbinaria	2	9/8	ACACGTGT	213	59	127	84	3.41	0.95
Turbinaria	3	9/8	ACACTCTC	377	73	262	159	3.05	0.90
Amansia	1	9/9	ACACTGTG	574	50	134	123	2.12	0.78
Amansia	2	9/9	ACAGACAG	187	30	82	61	2.09	0.78
Amansia	3	9/9	ACAGAGAC	515	66	271	162	2.38	0.82
Halimeda	1	9/10	ACAGCTCA	796	121	304	187	3.27	0.91
Halimeda	2	9/10	ACAGCTGT	502	68	143	104	2.75	0.83
Halimeda	3	9/10	ACAGGAGT	865	104	280	276	2.72	0.83
Porites	1	9/13	ACAGGTGA	1157	202	1351	530	3.90	0.93
Porites	2	9/13	ACAGTCAC	995	154	518	320	3.57	0.90
Porites	3	9/13	ACAGTGAG	1030	190	560	361	3.58	0.91
Control	1	9/8	ACACTCAG	154	32	47	45	2.84	0.91
Control	2	9/9	ACAGACTC	334	51	100	196	2.61	0.83
Control	3	9/10	ACAGGACA	598	88	259	163	3.18	0.87
Control	4	9/13	ACAGTCTG	873	176	445	358	3.98	0.95
Ambient	1	9/8	ACACTGAC	79	33	66	57	3.05	0.94
Ambient	2	9/9	ACAGAGTG	261	70	217	211	3.15	0.91
Ambient	3	9/10	ACAGGTCT	1061	150	616	378	3.41	0.90
Ambient	4	9/10	ACACGACT	208	56	186	100	3.33	0.94
Ambient	5	9/12	ACACGAGA	405	112	523	283	3.13	0.85
Ambient	6	9/13	ACAGTGTC	464	165	659	540	3.83	0.92

Supplementary Table S8. Sequence reads, observed OTUs, diversity indices, and richness estimates for each sample. Multiplex barcodes are listed to associate each sequence set with the SRA Accession. *Simpson Diversity here is calculated as 1-D.



Supplementary Figure S9: Mean OTU diversity indices among treatments. Whiskers represent one standard error of the mean. Data are listed in Table S8.