Supplementary Material:

Depleted dissolved organic carbon and distinct Bacterial communities in the water column of a rapid-flushing coral reef ecosystem

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Table S1. Pyrosequencing collection metadata and sequence read information. Samples were collected January 12-14, 2008 at depths ranging from 1-5 m. Reads denotes the number of 16S rRNA gene V6 sequences derived from two pooled replicate libraries collected at each sampling station. OTUs denotes the number of unique operational taxonomic units after sequences were dereplicated according to the RefHVR8 SILVA-derived rRNA reference database (http://vamps.mbl.edu). Collection metadata include latitude/longitude (decimal degrees), depth (z), temperature, salinity, and concentrations of chlorophyll *a*, nitrate+nitrite (N+N), soluble reactive phosphorus (SRP), silicate, particulate organic carbon (POC), particulate organic nitrogen (PON), dissolved organic carbon (DOC), and bacterioplankton cell density (Bacteria).

Station	Date	Reads	OTUs	Lat	Lon	z m	Temp °C	Salinity PSU	Chl. a µg L^{-1}	N+N µM	SRP µM	SiO_3 µM	POC µM	PON µM	DOC µM	Bacteria 10^8 L^{-1}
Offshore 130 km	13	39024	1542	-16.377	-150.145	2	28.24	35.97	0.030	N/C	N/C	N/C	N/C	N/C	N/C	N/C
Offshore 5 km	14	38192	1355	-17.427	-149.814	5	28.01	35.89	0.055	0.337	0.121	1.538	2.43	0.39	69.8	5.21
Forereef	14	47074	2724	-17.475	-149.837	5	28.15	35.91	0.206	0.634	0.115	0.900	3.65	0.39	71.4	5.13
Bay	12	43356	1871	-17.493	-149.822	5	28.64	35.91	0.434	0.191	0.133	1.777	7.35	0.95	61.7	6.97
Backreef (Lagoon)	12	37712	3477	-17.478	-149.842	1	28.45	35.90	0.093	0.407	0.143	1.448	4.68	0.44	64.4	3.82
Backreef (Fringe)	12	31954	2940	-17.485	-149.834	5	28.23	35.91	0.077	0.339	0.137	1.317	3.11	0.32	64.9	3.61

Fig S1. Concentrations of bacterioplankton and DOC in synoptic surveys conducted Aug-Sept 2008. Depth profiles of DOC and bacteria (a) collected 08/23/08 (Forereef and Offshore) and 08/25/08 (Backreef and Bay; see Fig. 1 for profile locations) show consistent concentrations over depth and spatial patterns which corroborate the 10m depth-averaged time series data in Fig. 3. Two synoptic surface surveys of DOC (b and c) and bacterioplankton (d and e) conducted 1 week apart (09/02 and 09/08/08) show temporal stability of spatial trends in the Backreef and Bay habitats corroborating results of the higher resolution 2009 surface synoptic survey (Fig. 2).

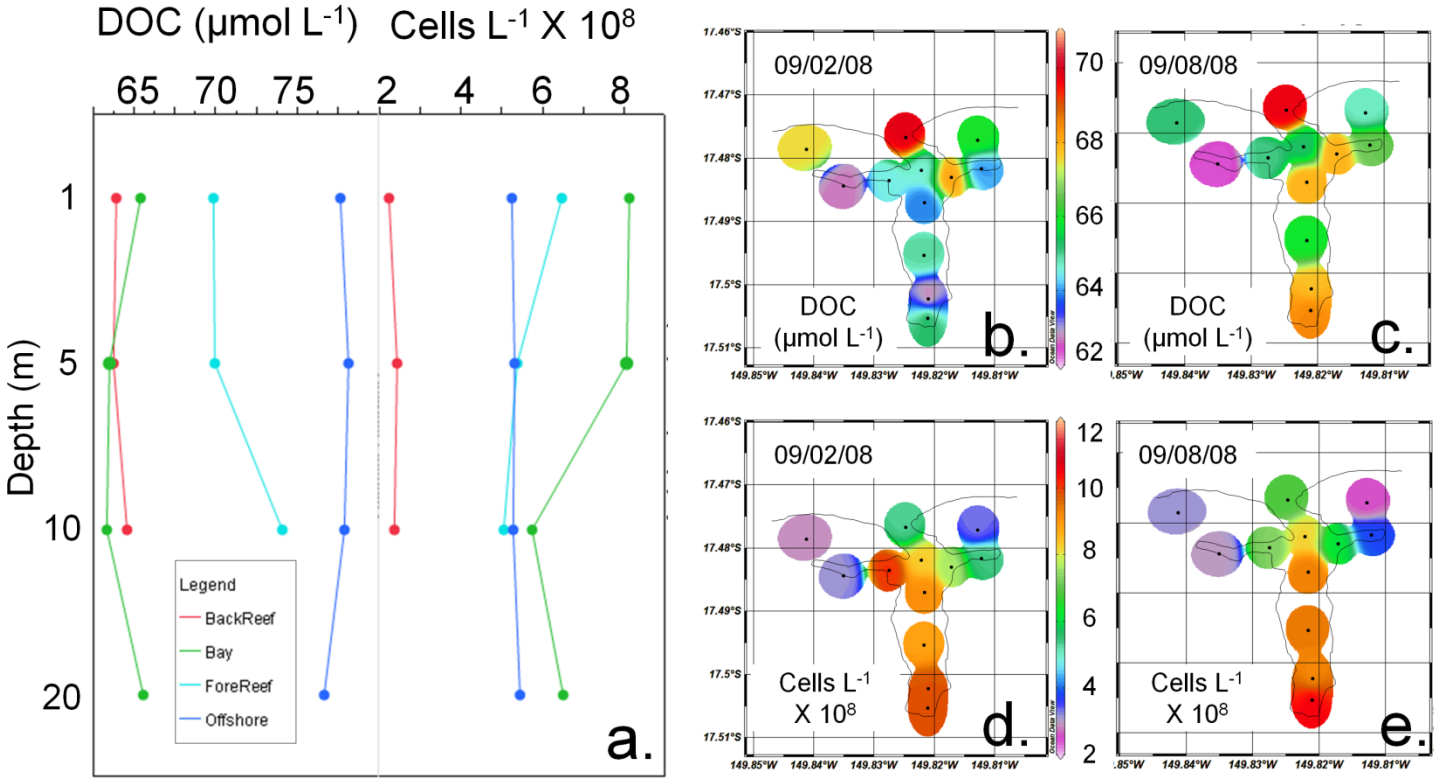


Fig S2. Comparison of ancillary nutrient and particulate organic matter concentrations among sampling habitats averaged over the upper 10m of the water column through time. As noted in the text, significant differences between habitats (assessed via Tukey post hoc test pairwise $p < 0.05$) were found only for nitrate in Winter (Backreef > Offshore) and for particulate measures (Bay higher than other habitats for POC, PON, and Chl. A in both seasons). Abbreviations are as follows: SRP – soluble reactive phosphate, Chl. a – chlorophyll a, POC – particulate organic carbon, PON – particulate organic nitrogen. Particulate variables were log-transformed to approximate the normal distribution in statistical tests.

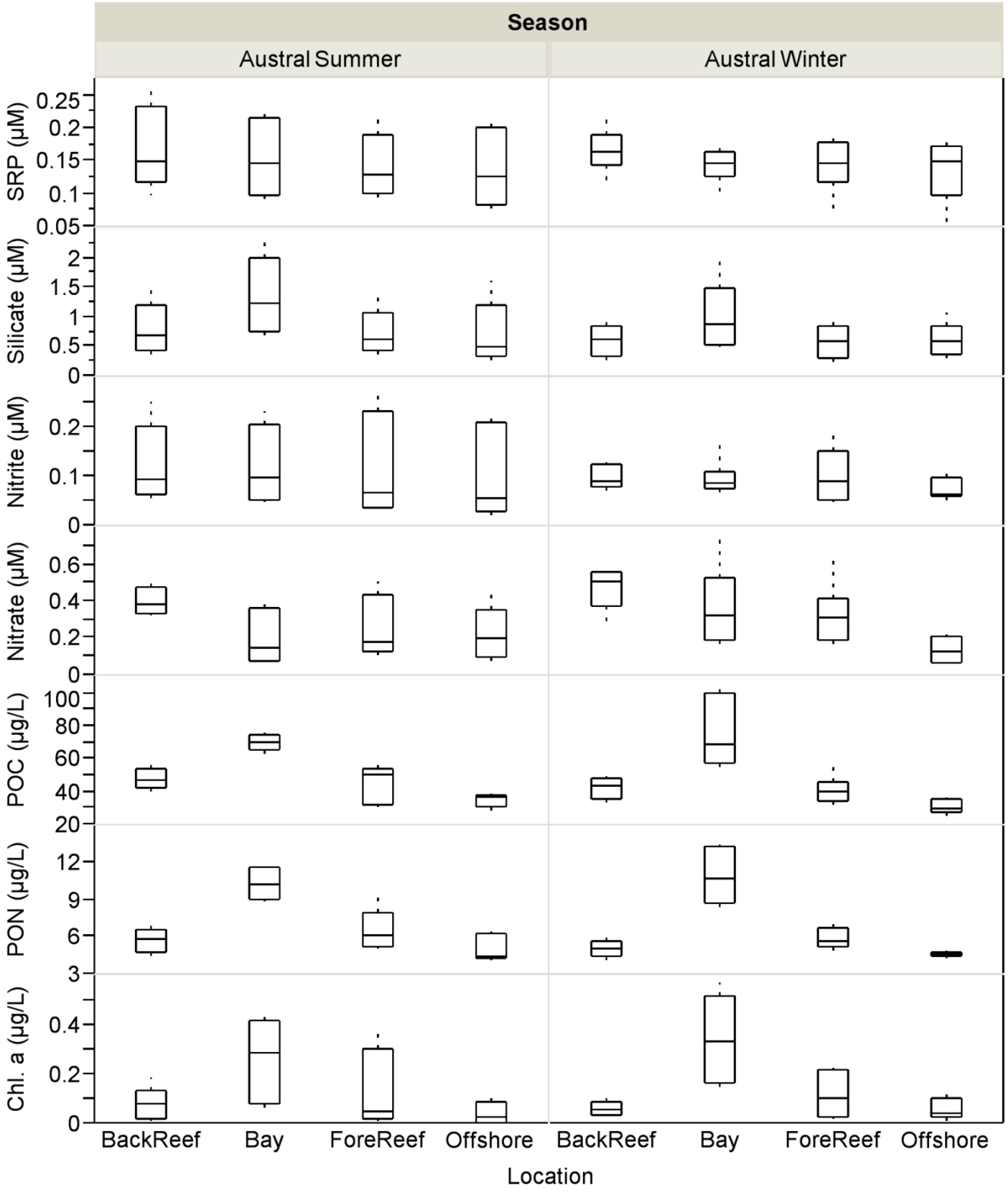
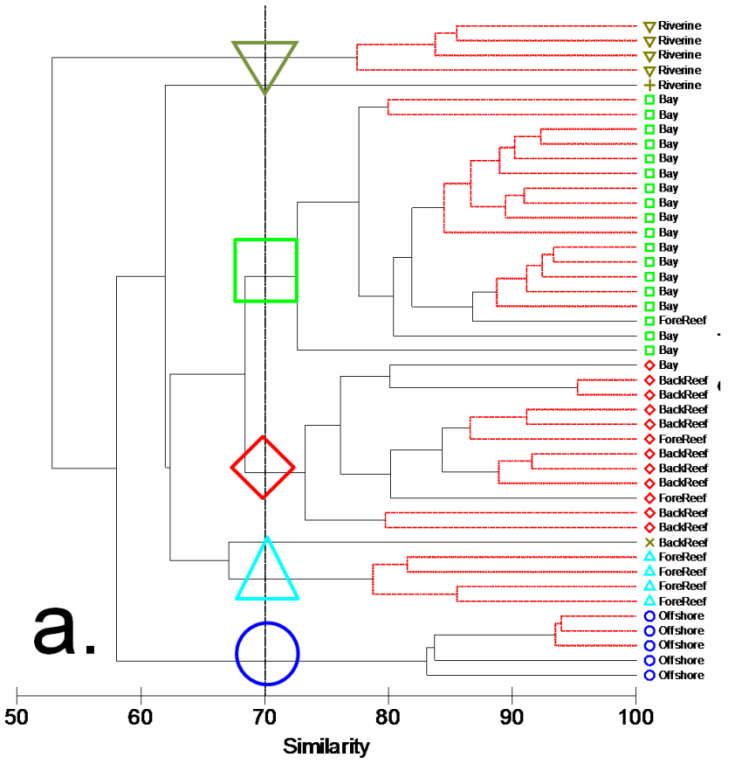
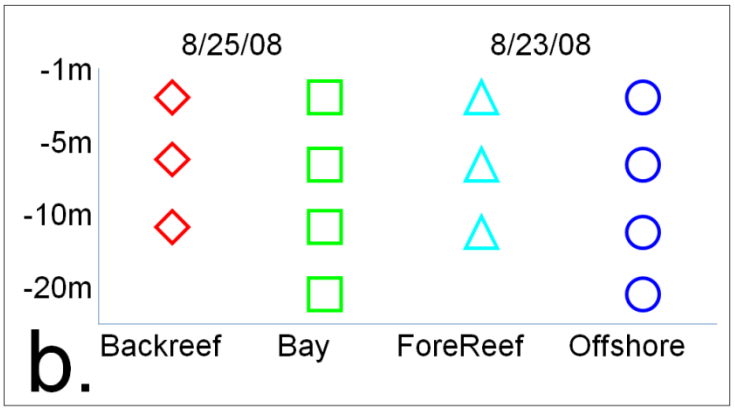
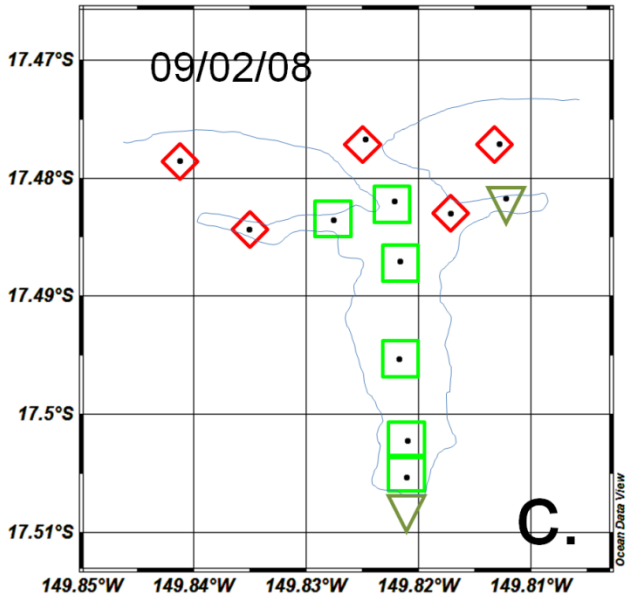


Fig S3. Spatial differentiation of bacterioplankton community composition in synoptic surveys Aug-Sept 2008. DNA samples collected at various locations and depths are symbol/color coded according to 5 community types defined as 70% Bray-Curtis similarity UPGMA clusters of 16S bacterial rRNA TRFLP fingerprints (a). Note that community types were homogenous over depth (b) and through time (b,c,d) but differed consistently by habitat (b,c,d; see Fig 1. for profile locations). Red lines within the dendrogram denote samples not significantly different at 95% confidence level by SIMPROF.







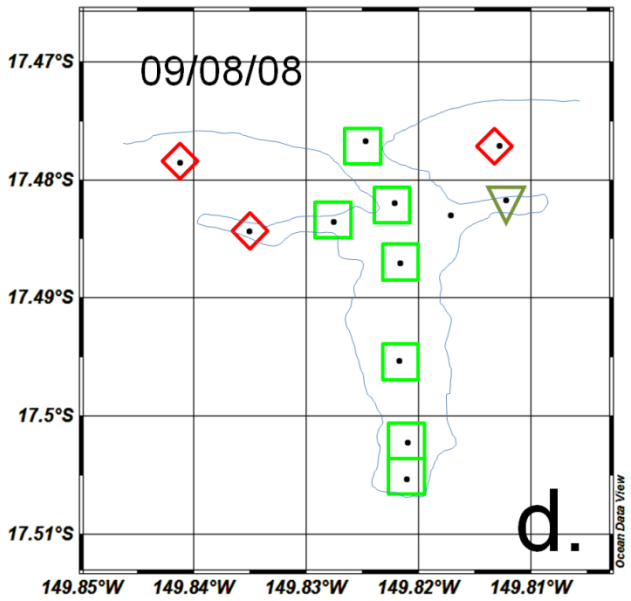


Fig S4. Effect of taxonomic level and binary vs. relativized data analysis on habitat differentiation among bacterioplankton communities. Cluster dendrograms generated from comparing 16S V6 tag pyrosequencing data among samples (Fig. 5) at two taxonomic levels (reference OTU [a,b] and Order [c,d]) and using relative abundance [a,c] or presence/absence [b,d] data to generate the similarity matrices. Note that tree structure is similar across taxonomic levels and that nearshore localities show differences in community structure using presence/absence data, suggesting that species identities, rather than simply abundances, differ between habitats. Red lines within the dendrogram denote samples not significantly different at the 95% confidence level by SIMPROF.

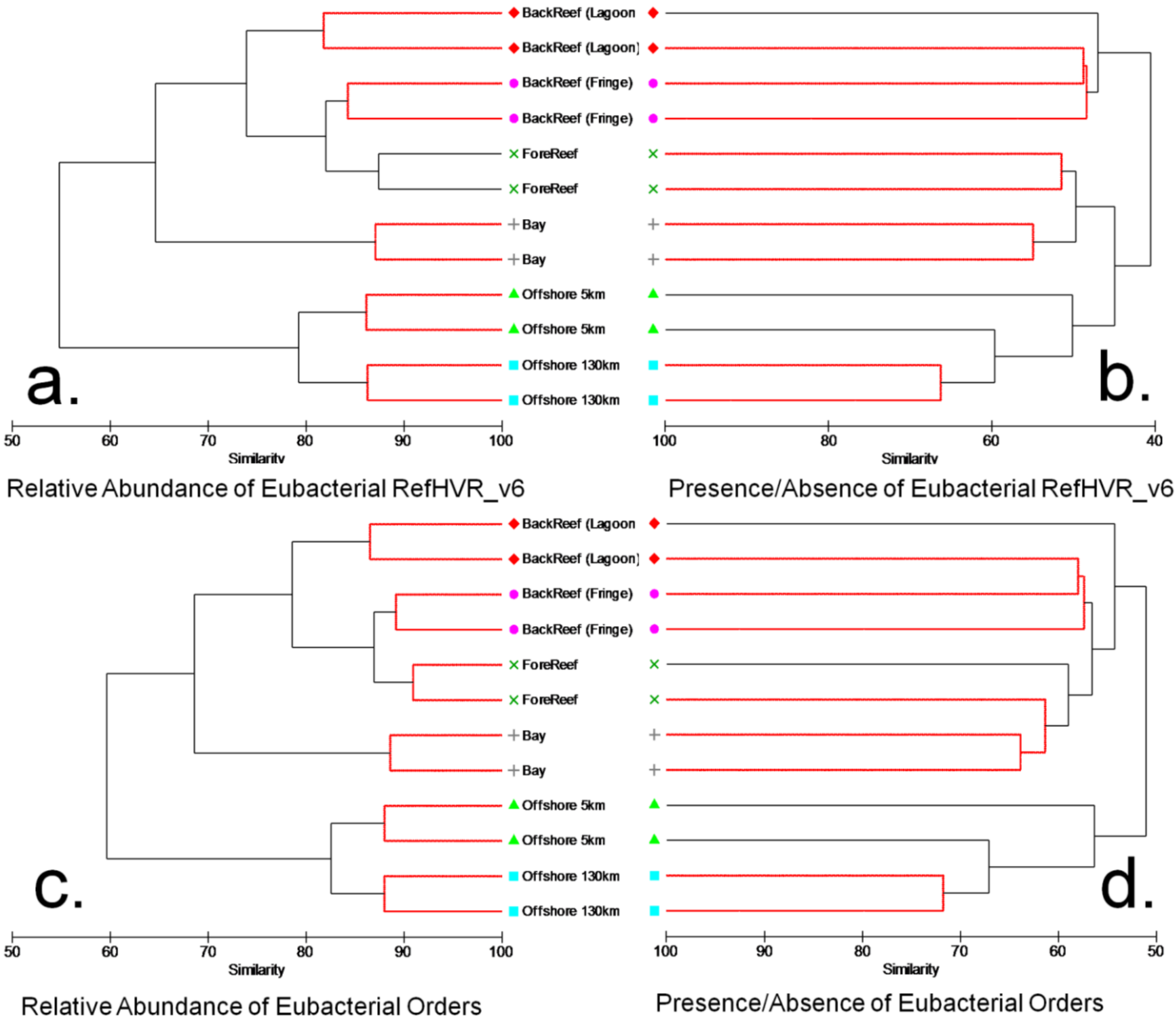
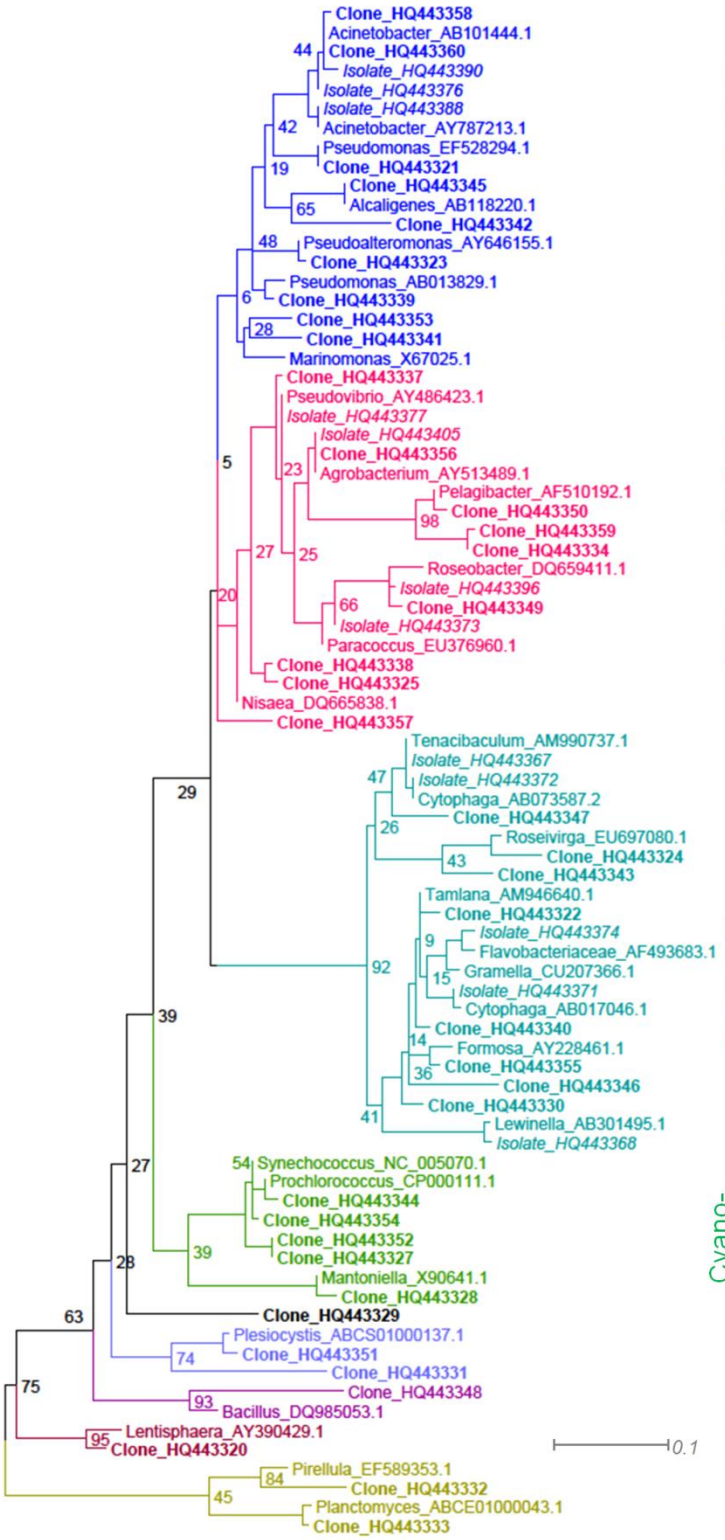


Figure S5. Maximum likelihood tree showing phylogenetic context of 16S rRNA clones generated randomly from a sample of BackReef water collected 3/2007. Sequences were aligned to the greengenes 16S rRNA core alignment via NAST (DeSantis, et al. 2006a, 2006b) and post-curated by GBLOCKS via the Phylogeny.fr pipeline (Dereeper et al 2008). The tree was built from sequences spanning 520 positions using the HKY85 evolution model within the PhyML software package (Guindon and Gascuel 2003) with branch support values displayed as percentages derived from 100 bootstraps and scale bar showing substitutions per base. Nearest neighbor isolate sequences aligned from the greengenes database were used to scaffold the tree and **Clone** and *Isolate* accessions HQ443320-HQ443409 denote the source of the sequence. To the right of each clone and selected isolates are restriction lengths using the HaeIII enzyme and primers 8f and 519r. Both *in silico* (predicted from sequence) and measured lengths (derived from TRFLP of cloned amplicons) are listed, and replicate clones are noted where removed for clarity. Clones used for TRFLP peak identification in Fig. 5 are noted. Note that while the closest isolated relative of clone HQ443344 used in Fig 5b is annotated as *Prochlorococcus*, the top five NCBI RefSeq Blast hits for this clone (genomic sequences assembled without isolation) are in the genus *Synechococcus*.



Accession/Genus	*In Silico* TRF	Measured TRF	Notes
HQ443358	254	253	
Acinetobacter	200		
HQ443360	253	252	3 addtl clones
HQ443390			
HQ443376			
HQ443388			
Acinetobacter	200		
Pseudomonas	39		
HQ443321	39	32	
HQ443345	225	224	
Alcaligenes	226		
HQ443342	39	32	
Pseudoalteromonas	39		
HQ443323	39	32	2 addtl clones
Pseudomonas	39		
HQ443339	272	272	
HQ443353	39	32	
HQ443341	39	32	
Marinomonas	322		
HQ443337	192	191	Fig. 5e
Pseudovibrio			
HQ443377			
HQ443405			
HQ443356	191	188	
Agrobacterium	191		
Pelagibacter			
HQ443350	117	113	Fig. 5d
HQ443359	293	292	Fig. 5a
HQ443334	293		
Roseobacter	39		
HQ443396			
HQ443349	39	32	2 addtl clones
HQ443373			
Paracoccus			
HQ443338	227	227	
HQ443325	224	224	2 addtl clones
Nisaea	150		
HQ443357	202	201	
Tenacibaculum			
HQ443367			
HQ443372			
073587.2			
HQ443347	39	32	
Roseivirga	39		
HQ443324	39	32	
HQ443343	521	524	
Tamlana	39		
HQ443322			
HQ443374			
Flavobacteriaceae			
Gramella			
HQ443371			
Cytophaga			
HQ443340	286	285	Fig. 5c
Formosa	39		
HQ443355	410	409	Fig. 5f
HQ443346	39	32	
HQ443330	39	32	
Lewinella			
HQ443368			
Synechococcus			
Prochlorococcus			
HQ443344	290	289	Fig. 5b; 24 addtl clones
HQ443354	138	136	
HQ443352	305		
HQ443327	305	305	
Mantoniella			
HQ443328			
HQ443329	231	231	
Plesiocystis	39		
HQ443351	39	32	
HQ443331	213	212	
HQ443348	322	321	
Bacillus	309		
Lentisphaera	404		
HQ443320	401	401	
Pirellula	247		
HQ443332	240	240	
Planctomyces	296		
HQ443333	283	283	