

SUPPLEMENTARY TABLES

Table S1. Permutational multivariate analyses of variance (PERMANOVA) for ASV community structure in relation to depth using two distance matrices with 999 permutations.

a) PERMANOVA test in relation to depth.

Metrics	Df	Sums Sqs	Mean Sqs	F Model	R²	P (>F)
Bray-Curtis						
Depths	3	3.3108	1.1037	5.8799	0.4919	0.001 ***
Residuals	19	3.5661	0.1876		0.5089	
Total	22	6.8770			1	
Unweighted unifrac						
Depths	3	1.3992	0.4663	3.9344	0.4033	0.001 ***
Residuals	19	2.2523	0.1184		0.5969	
Total	22	3.6515			1	

b) PERMANOVA Pairwise test between depths.

Distance matrices			Bray-Curtis		Unweighted unifrac	
Group 1	Group 2	Sample size	pseudo-F	p-value	pseudo-F	p-value
BO	Bottom	11	7.903	0.003	4.8638	0.002
	DCM	12	3.602	0.013	3.3598	0.014
	Surface	12	3.1392	0.062	2.8524	0.062
Bottom	DCM	11	13.6169	0.004	6.3662	0.003
	Surface	11	8.16869	0.002	4.80779	0.002
DCM	Surface	12	2.40301	0.049	1.9133	0.081

Table S2. Analyses of similarity (ANOSIM) for ASV community structure in relation to depth using two distance matrices with 999 permutations.

a) ANOSIM test in relation to depth.

Metrics	R statistic	p-value
Bray-Curtis	0.6092	0.001 ***
Unweighted unifrac	0.5527	0.001 ***

b) ANOSIM Pairwise test between depths.

Distance matrices			Bray-Curtis		Unweighted unifrac	
Group 1	Group 2	Sample size	R	p-value	R	p-value
BO	Bottom	11	0.8935	0.006	0.8535	0.005
	DCM	12	0.3194	0.013	0.4611	0.017
	Surface	12	0.2906	0.063	0.3222	0.058
Bottom	DCM	11	1	0.002	0.9947	0.001
	Surface	11	0.873	0.002	0.8027	0.004
DCM	Surface	12	0.1906	0.102	0.1667	0.136

Table S3. Results of the statistical analysis (P-values) of the non-metric multidimensional scaling (NMDS) for the two ordination scores related to the environmental variables.

Variables	NMDS1	NMDS2	r ²	P (>r)	
Temperature	-0.97595	-0.21798	0.7561	0.000999	***
Oxygen	-0.90687	-0.42141	0.7473	0.000999	***
Salinity	-0.46847	-0.88348	0.4125	0.002997	**
Chlorophyll <i>a</i>	-0.89461	-0.44685	0.3074	0.028971	*

Table S4. Number of unique ASVs (only in one station) and shared ASVs by 2, 3, 4, 5, or 6 stations for each depth.

Depths / # of stations	Number of ASVs					
	1	2	3	4	5	6
Surface	1176	424	94	115	24	26
DCM	836	261	130	84	100	65
BO	1373	355	184	104	79	49
Bottom	744	184	87	55	62	-

Table S5a. Indicator ASVs at different depths (or combination of depths) in the eddy center (stations S30 and S31).

Groups	Indicator value	p-value	
Surface Center (# ASVs: 27)			
Planctomycetes; Planctomycetacia; Planctomycetales; Gimesiaceae; 7	0.954	0.01	**
Bacteroidetes; Bacteroidia; Flavobacteriales; Cryomorphaceae; 32	0.909	0.011	*
Gammaproteobacteria; EPR3968; O8a-Bc78; 1	0.973	0.012	*
Alphaproteobacteria; SAR11 clade; clade I; 25	0.852	0.013	*
Deltaproteobacteria; Bdellovibrionales; Bdellovibrionaceae; OM27 clade; 24	1	0.014	*
Bacteroidetes; Bacteroidia; Flavobacteriales; NS9 marine group; 55	1	0.014	*
Dependentiae; Babeliae; Babeliales; 1	1	0.014	*
Deltaproteobacteria; PB19; 33	1	0.014	*
Alphaproteobacteria; SAR11 clade; clade II; 67	0.998	0.014	*
Alphaproteobacteria; Rhodospirillales; Magnetospiraceae; 30	0.997	0.014	*
Deltaproteobacteria; PB19; 61	0.942	0.015	*
Deltaproteobacteria; NB1-j; 54	0.903	0.015	*
Marinimicrobia; SAR406 clade; 184	0.866	0.015	*
Gammaproteobacteria; HOC36; Ca. Thioglobus sp; REDSEA-S12_B1; 13	0.825	0.018	*
Chloroflexi; Dehalococcoidia; S085; Chloroflexus sp	0.808	0.02	*
Chloroflexi; Dehalococcoidia; SAR202 clade; 84	0.852	0.021	*
Chloroflexi; Dehalococcoidia; S085; Chloroflexus sp; 2	0.853	0.028	*
Bacteroidetes; Bacteroidia; Flavobacteriales; NS9 marine group; Flavobacteriia; 52	0.85	0.032	*
Gammaproteobacteria; Coxiellales; Coxiellaceae; Coxiella; 6	0.81	0.032	*
Gammaproteobacteria; Oceanospirillales; Pseudohongiellaceae; Pseudohongiella; 4	0.901	0.037	*
Marinimicrobia; SAR406 clade; 231	0.942	0.041	*
Alphaproteobacteria; Puniceispirillales; SAR116 clade; SCGC AAA015-N04	0.942	0.041	*
Planctomycetes; Pla3 lineage; 8	0.942	0.046	*
Gammaproteobacteria; 51	0.942	0.046	*
Gammaproteobacteria; EPR3968-O8a-Bc78; 11	0.942	0.046	*
Alphaproteobacteria; SAR11 clade; clade II; 72	0.798	0.046	*
DCM Center (# ASVs: 2)			
Gammaproteobacteria; Ectothiorhodospirales; Ectothiorhodospiraceae; 35	0.907	0.012	*
Gammaproteobacteria; OM182 clade; 13	0.919	0.021	*
BO Center (# ASVs: 6)			

Alphaproteobacteria; Rickettsiales; S25-593; 18	0.956	0.013	*
Verrucomicrobia; Verrucomicrobiae; Opitutales; Puniceococcaceae; MB11C04 marine group; 21	0.966	0.016	*
Deltaproteobacteria; SAR324 clade marine group B; SAR324 cluster; 11	0.941	0.016	*
Nitrospinae; Nitrospina; Nitrospinales; Nitrospinaceae; Nitrospina; 19	0.858	0.024	*
Nitrospinae; Nitrospina; Nitrospinales; Nitrospinaceae; LS-NOB; 16	0.824	0.047	*
Chloroflexi; Dehalococcoidia; SAR202 clade; 7	0.841	0.049	*
Bottom Center (# ASVs: 77)			
Gammaproteobacteria; Oceanospirillales; Nitrincolaceae	0.937	0.005	**
Alphaproteobacteria; SAR11 clade; clade I; 27	0.946	0.015	*
Gammaproteobacteria; Methylococcales; Methylomonaceae; Milano-WF1B; 03; 1	0.939	0.015	*
Gammaproteobacteria; UBA10353 marine group; 24	0.925	0.015	*
Marinimicrobia; SAR406 clade; uncultured eubacterium OCS307; 5	0.921	0.015	*
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; NS2b marine group; 7	0.916	0.015	*
Alphaproteobacteria; Rhodospirillales; AEGEAN 169 marine group; 5	0.908	0.015	*
Gammaproteobacteria; Oceanospirillales; Pseudohongiellaceae; Pseudohongiella; 19	0.961	0.017	*
Marinimicrobia; SAR406 clade; hydrothermal vent metagenome; 9	0.925	0.017	*
Gammaproteobacteria; Ectothiorhodospirales; Ectothiorhodospiraceae; 3	0.954	0.022	*
Alphaproteobacteria; Rickettsiales; S25-593; 9	0.922	0.023	*
Chloroflexi; Dehalococcoidia; SAR202 clade; hydrothermal vent metagenome; 14	0.905	0.023	*
Deltaproteobacteria; Myxococcales; P3OB-42; 25	0.897	0.023	*
Alphaproteobacteria; SAR11 clade; clade II; 42	0.968	0.024	*
Marinimicrobia; SAR406 clade; 61	0.959	0.024	*
Gammaproteobacteria; HgCo23; 3	0.946	0.024	*
Marinimicrobia; SAR406 clade; Ca. Marinimicrobia; 1	0.919	0.025	*
Gammaproteobacteria; 20	0.882	0.028	*
Marinimicrobia; SAR406 clade; JGI-0000113 D11	0.88	0.03	*
Gammaproteobacteria; Methylococcales; Methylomonaceae; IheB2; 23	0.981	0.031	*
Verrucomicrobia; Verrucomicrobiae; Verrucomicrobiales; Rubritaleaceae; Roseibacillus; HF0500_18J03; 3	0.963	0.031	*
Actinobacteria; Acidimicrobia; Microtrichales; Microtrichaceae; 6	0.952	0.031	*
Alphaproteobacteria; SAR11 clade; clade I; 22	0.884	0.031	*
Gammaproteobacteria; Methylococcales; Methylomonaceae; Milano-WF1B; 03	0.943	0.032	*
Marinimicrobia; SAR406 clade; 220	0.858	0.032	*
Marinimicrobia; SAR406 clade; hydrothermal vent metagenome; 1	0.879	0.033	*
Alphaproteobacteria; Rickettsiales; S25-593; 8	0.904	0.034	*
Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas	0.999	0.035	*
Gammaproteobacteria; UBA10353 marine group; 1	0.938	0.036	*
Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Paracoccus	0.998	0.038	*
Bacteroidetes; Bacteroidia sphingobacteriales; Lentimicrobiaceae; deep sea	0.994	0.038	*
Alphaproteobacteria; Rhodospirillales; Magnetospiraceae; 48	0.968	0.038	*
Gammaproteobacteria; Methylococcales; Methylomonaceae; Milano-WF1B-03; 2	0.889	0.038	*
Alphaproteobacteria; Rhodospirillales; Magnetospiraceae	0.931	0.039	*
Gammaproteobacteria; UBA10353 marine group; 16	0.966	0.04	*
Nitrospinae; Nitrospina; Nitrospinales; Nitrospinaceae; Nitrospina; 23	0.961	0.04	*
Marinimicrobia; SAR406 clade; 17	0.915	0.041	*
Marinimicrobia; SAR406 clade; 94	0.85	0.046	*
Verrucomicrobia; Verrucomicrobiae; Opitutales; Puniceococcaceae; MB11C04 marine group; 1	1	0.048	*
Gammaproteobacteria; Oceanospirillales; Halomonadaceae; Halomonas	1	0.048	*
Margulisbacteria; 6	1	0.048	*
Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Brevundimonas	1	0.048	*
Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Aureimonas	1	0.048	*
Deltaproteobacteria; Bdellovibrionales; Bacteriovoracaceae; 5	1	0.048	*
Epsilonbacteraeota; Campylobacteria; Campylobacterales; Arcobacteraceae; Arcobacter; 1	1	0.048	*
Deltaproteobacteria; Bdellovibrionales; Bacteriovoracaceae; Peredibacter; 3	1	0.048	*

Deltaproteobacteria; Myxococcales; Blfdi19; 6	1	0.048	*
Gammaproteobacteria; Cellvibrionales spongiibacteraceae; BD- 7 clade; 3	1	0.048	*
Deltaproteobacteria; Myxococcales; P3OB-42; 18	1	0.048	*
Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Luteimonas	1	0.048	*
Verrucomicrobia; Verrucomicrobiae; Arctic97B-4 marine group; 31	1	0.048	*
Alphaproteobacteria; Parvibaculales; OCS116 clade; 10	1	0.048	*
Alphaproteobacteria; SAR11 clade; clade I; 21	1	0.048	*
Planctomycetes; Phycisphaerae; Phycisphaerales; Phycisphaeraceae; JL-ETNP-F27; 4	1	0.048	*
Nitrospirae; BMS9AB35; 2	1	0.048	*
Gammaproteobacteria; OM182 clade; 16	1	0.048	*
Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Paracoccus; 1	1	0.048	*
Bacteroidetes; Bacteroidia; Flavobacteriales; NS7 marine group; 16	1	0.048	*
Alphaproteobacteria; SAR11 clade; clade; I clade Ib; 12	1	0.048	*
Alphaproteobacteria; Puniceispirillales; SAR116 clade; 17	1	0.048	*
Marinimicrobia; SAR406 clade; Deferribacteres; 4	1	0.048	*
Nitrospirae; Nitrospira; Nitrospirales; Nitrospiraceae; Nitrospira; Nitrospirae; 3	1	0.048	*
Gammaproteobacteria; Alteromonadales; Idiomarinaceae; Idiomarina; Idiomarina baltica	1	0.048	*
Alphaproteobacteria; Acetobacterales; Acetobacteraceae; Roseomonas; Roseomonas sp	1	0.048	*
Alphaproteobacteria; Rhodospirillales; Magnetospiraceae; 35	1	0.048	*
Deltaproteobacteria; PB19; 60	1	0.048	*
Verrucomicrobia; Verrucomicrobiae; Opitutales; Puniceicoccaceae; MB11C04 marine group; 20	1	0.048	*
Verrucomicrobia; Verrucomicrobiae; Opitutales; Puniceicoccaceae; A714019; 4	1	0.048	*
Marinimicrobia; SAR406 clade; 294	1	0.048	*
Gammaproteobacteria; HgCo23	0.999	0.048	*
Nitrospinae; Nitrospina; Nitrospinales; Nitrospinaceae; Nitrospina	0.953	0.049	*
Chloroflexi; Dehalococcoidia; SAR202 clade; 83	0.918	0.049	*
Marinimicrobia; SAR406 clade; 116	0.907	0.049	*
Chloroflexi; Dehalococcoidia; SAR202 clade; 11	0.843	0.049	*
Alphaproteobacteria; SAR11 clade; clade I; 2	0.754	0.049	*
Surface Center + BO Center (# ASVs: 10)			
Chloroflexi; Dehalococcoidia; S085; Chloroflexus sp; 1	0.958	0.001	***
Chloroflexi; Dehalococcoidia; SAR202 clade; 51	0.945	0.001	***
Bacteroidetes; Bacteroidia; Flavobacteriales; NS9 marine group; Flavobacteriia; 11	0.9	0.002	**
Marinimicrobia; SAR406 clade; 103	0.877	0.003	**
Gammaproteobacteria; UBA10353 marine group; 19	0.927	0.004	**
Chloroflexi; JG30-KF-CM66; 5	0.91	0.004	**
Alphaproteobacteria; 5	0.889	0.004	**
Gammaproteobacteria; Thiomicrospirales; Thioglobaceae; SUP05 cluster; 15	0.854	0.005	**
Gammaproteobacteria; HOC36; Ca. Thioglobus sp REDSEA-S12_B1	0.809	0.006	**
Chloroflexi; Dehalococcoidia; SAR202 clade	0.827	0.009	**

Table S5b. Indicator ASVs at different depths (or combination of depths) in the eddy edges (stations S24, S25, S26, and S32).

Groups	Indicator value	p-value	
Surface Edge (# ASVs: 23)			
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; NS2b marine group; 1	0.986	0.002	**
Verrucomicrobia; Verrucomicrobiae; Opitutales; Puniceicoccaceae; Pelagicoccus	0.972	0.002	**
Alphaproteobacteria; SAR11 clade; clade I; clade Ib; 2	0.958	0.002	**
Bacteroidetes; Bacteroidia; Flavobacteriales; Crocinitomicaceae; Fluviicola; 11	0.929	0.002	**
Gammaproteobacteria; SAR86 clade; 45	0.892	0.003	**
Cyanobacteria; Oxyphotobacteria; Synechococcales; Cyanobiaceae; Synechococcus CC9902; 3	0.895	0.004	**
Cyanobacteria; Oxyphotobacteria; Synechococcales; Cyanobiaceae; Synechococcus	0.863	0.004	**

CC9902; 19			
Gammaproteobacteria; SAR86 clade; 20	0.849	0.005	**
Cyanobacteria; Oxyphotobacteria; Synechococcales; Cyanobiaceae; Synechococcus			
CC9902; 12	0.848	0.006	**
Planctomycetes; Planctomycetacia; Pirellulales; Pirellulaceae; Pirellula	0.902	0.008	**
Deltaproteobacteria; Bdellovibrionales; Bdellovibrionaceae; OM27 clade; 135	0.899	0.011	*
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; NS4 marine group; 22	0.852	0.012	*
Cyanobacteria; Oxyphotobacteria; Synechococcales; Cyanobiaceae; Synechococcus			
CC9902; 15	0.831	0.013	*
Gammaproteobacteria; SAR86 clade; HF0070_25G02; 6	0.868	0.014	*
Bacteroidetes; Bacteroidia; Flavobacteriales; NS9 marine group; 91	0.847	0.016	*
Gammaproteobacteria; Cellvibrionales; Halieaceae; OM60(NOR5) clade 13	0.789	0.02	*
Planctomycetes; Planctomycetacia; Pirellulales; Pirellulaceae; Rubripirellula; 6	0.846	0.029	*
Gammaproteobacteria; SAR86 clade; 5	0.799	0.03	*
Gammaproteobacteria; Coxiellales; Coxiellaceae; Coxiella; Legionellales	0.848	0.031	*
Alphaproteobacteria; Parvibaculales; Parvibaculaceae; 2	0.864	0.043	*
Actinobacteria; Acidimicrobiia; Microtrichales; Ilumatobacteraceae; 2	0.837	0.046	*
Alphaproteobacteria; Puniceispirillales; SAR116 clade; SAR116 cluster; REDSEA			
S10_B10N8; 1	0.812	0.048	*
Gammaproteobacteria; Cellvibrionales; Halieaceae; OM60(NOR5) clade 2	0.798	0.049	*
DCM Edge (# ASVs: 14)			
Bacteroidetes; Bacteroidia; Flavobacteriales; NS9 marine group; 123	0.93	0.002	**
Bacteroidetes; Bacteroidia; Flavobacteriales; Cryomorphaceae; 18	0.927	0.002	**
Cyanobacteria; Oxyphotobacteria; Synechococcales; Cyanobiaceae; Synechococcus			
CC9902; 4	0.929	0.004	**
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; NS2b marine group; 15	0.89	0.005	**
Actinobacteria; Acidimicrobiia; Actinomarinales; Actinomarinaceae; Ca. Actinomarina; 15	0.872	0.008	**
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; NS5 marine group; 9	0.836	0.015	*
Alphaproteobacteria; SAR11 clade; clade I; 20	0.84	0.019	*
Bacteroidetes; Bacteroidia; Flavobacteriales; NS9 marine group; 120	0.874	0.023	*
Actinobacteria; Acidimicrobiia; Actinomarinales; Actinomarinaceae; Ca. Actinomarina; 14	0.819	0.026	*
Planctomycetes; Phycisphaerae; Phycisphaerales; Phycisphaeraceae; CL500-3; 2	0.848	0.029	*
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; NS5 marine group; 42	0.802	0.03	*
Gammaproteobacteria; Cellvibrionales; Halieaceae; OM60(NOR5) clade 8	0.853	0.031	*
Gammaproteobacteria; SAR86 clade; 11	0.772	0.035	*
Deltaproteobacteria; Desulfarculales; Desulfarculaceae; 6	0.786	0.044	*
BO Edge (# ASVs: 3)			
Bacteroidetes; Bacteroidia; Flavobacteriales; NS7 marine group; 3	0.862	0.007	**
Alphaproteobacteria; Rhodospirillales; AEGEAN 169 marine group; 48	0.845	0.018	*
Gammaproteobacteria; HOC36; Ca.; Thioglobus sp; REDSEA S12_B1; 12	0.851	0.041	*
Bottom Edge (# ASVs: 19)			
Gammaproteobacteria; UBA10353 marine group; 26	0.963	0.001	***
Gammaproteobacteria; UBA10353 marine group; 2	0.992	0.002	**
Actinobacteria; Acidimicrobiia; Microtrichales; Microtrichaceae; Sva0996 marine group; 41	0.987	0.002	**
Alphaproteobacteria; SAR11 clade; clade II; 26	0.967	0.002	**
Alphaproteobacteria; SAR11 clade; clade I; clade Ib; 14	0.966	0.002	**
Alphaproteobacteria; SAR11 clade; clade I; 33	0.966	0.002	**
Bacteroidetes; Bacteroidia; Flavobacteriales; NS9 marine group; 5	0.95	0.002	**
Gammaproteobacteria; SAR86 clade; 32	0.923	0.002	**
Planctomycetes; Phycisphaerae; Phycisphaerales; Phycisphaeraceae; JL-ETNP-F27; 7	0.929	0.003	**
Alphaproteobacteria; SAR11 clade; clade II; 39	0.949	0.006	**
Nitrospinae; Nitrospina; Nitrospinales; Nitrospinaceae; Nitrospina; 24	0.925	0.006	**
Gammaproteobacteria; SAR86 clade; KTc1121; 2	0.824	0.019	*
Verrucomicrobia; Verrucomicrobiae; Arctic97B-4 marine group; 49	0.819	0.019	*
Alphaproteobacteria; Rickettsiales	0.837	0.02	*
Nitrospinae; Nitrospina; Nitrospinales; Nitrospinaceae; Nitrospina; 17	0.849	0.03	*

Gammaproteobacteria; Oceanospirillales; Pseudohongiellaceae; Pseudohongiella; 18	0.863	0.031	*
Nitrospirae; BMS9AB35; 3	0.849	0.033	*
Alphaproteobacteria; SAR11 clade; clade I; 17	0.804	0.033	*
Planctomycetes; Planctomycetacia; Pirellulales; Pirellulaceae; Rhodopirellula; hydrothermal vent metagenome	0.844	0.046	*
Surface Edge + DCM Edge (# ASVs: 2)			
Verrucomicrobia; Verrucomicrobiae; Verrucomicrobiales; DEV007	0.821	0.023	*
Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; 18	0.754	0.024	*
DCM Edge + BO Edge (# ASVs: 6)			
Actinobacteria; Acidimicrobiia; Microtrichales; Microtrichaceae; Sva0996 marine group; 15	0.834	0.012	*
Cyanobacteria; Oxyphotobacteria; Synechococcales; Cyanobiaceae; Synechococcus CC9902; 9	0.833	0.019	*
Planctomycetes; Planctomycetacia; Pirellulales; Pirellulaceae; Blastopirellula; 22	0.831	0.019	*
Actinobacteria; Acidimicrobiia; Actinomarinales; Actinomarinaceae; Ca. Actinomarina; 1	0.817	0.02	*
Bacteroidetes; Bacteroidia; Flavobacteriales; NS9 marine group; 1	0.787	0.037	*
Gammaproteobacteria; HOC36; 6	0.77	0.045	*

Table S5c. Indicator ASVs from a combination of depths between the eddy center and the eddy edges.

Groups	Indicator value	p-value	
Surface Center + BO Edge (# ASVs: 22)			
Acidobacteria; Subgroup 21; 1	0.888	0.004	**
Deinococcus; Thermus; Deinococci; Deinococcales; Trueperaceae; Truepera	0.864	0.004	**
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; NS4 marine group; 19	0.842	0.004	**
Gemmatimonadetes; BD2-11 terrestrial group; 8	0.862	0.005	**
Gammaproteobacteria; SAR86 clade; KTc1121	0.812	0.005	**
Planctomycetes; Planctomycetacia; Planctomycetales; 10	0.844	0.006	**
Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Roseobacter clade; NAC11-7 lineage; 3	0.854	0.007	**
Actinobacteria; Acidimicrobiia; Microtrichales; Microtrichaceae; Sva0996 marine group; 6	0.855	0.008	**
Planctomycetes; Planctomycetacia; Pirellulales; Pirellulaceae; Pir4 lineage	0.872	0.009	**
Gammaproteobacteria; KI89A clade; 14	0.84	0.009	**
Gammaproteobacteria; UBA10353 marine group; 25	0.804	0.009	**
Marinimicrobia; SAR406 clade; 203	0.737	0.009	**
Firmicutes; 3	0.861	0.011	*
Gammaproteobacteria; Steroidobacterales; Woeseiaceae; Woeseia; 5	0.843	0.012	*
Gemmatimonadetes; BD2-11 terrestrial group; AD66-C11; 2	0.838	0.013	*
Acidobacteria; Subgroup; 21	0.83	0.015	*
Gammaproteobacteria; SAR86 clade;KTc1121; 4	0.753	0.019	*
Deltaproteobacteria; Bdellovibrionales; Bdellovibrionaceae; OM27 clade; 25	0.823	0.021	*
Planctomycetes; Planctomycetacia; Pirellulales; Pirellulaceae; 29	0.811	0.021	*
Deltaproteobacteria; NB1-j; uncultured myxobacterium HF0200_01L06; 1	0.821	0.022	*
Gammaproteobacteria; Steroidobacterales; Woeseiaceae; Woeseia; 2	0.816	0.023	*
Actinobacteria; Acidimicrobiia; Microtrichales; Microtrichaceae; Sva0996 marine group; 20	0.776	0.032	*
DCM Center + Surface Edge (# ASVs: 34)			
Alphaproteobacteria; Rhodospirillales; AEGEAN 169 marine group; 67	0.939	0.001	***
Dadabacteria; Dadabacteriia; Dadabacteriales; marine metagenome	0.918	0.001	***
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; NS2b marine group; 13	0.891	0.001	***
Gammaproteobacteria; SAR86 clade; 70	0.888	0.001	***
Gammaproteobacteria; SAR86 clade; 52	0.84	0.001	***
Alphaproteobacteria; SAR11 clade; clade II; 64	0.789	0.001	***
Alphaproteobacteria; Rickettsiales; S25-593; 14	0.906	0.002	**
Gammaproteobacteria; SAR86 clade; 71	0.875	0.002	**
Alphaproteobacteria; SAR11 clade; clade II; 7	0.826	0.003	**
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; NS5 marine group;	0.859	0.006	**

Flavobacterium sp; 1			
Gammaproteobacteria; SAR86 clade; 25	0.821	0.006	**
Gammaproteobacteria; SAR86 clade; 41	0.859	0.007	**
Alphaproteobacteria; Puniceispirillales; SAR116 clade; 16	0.829	0.007	**
Gammaproteobacteria; SAR86 clade; 7	0.824	0.007	**
Verrucomicrobia; Verrucomicrobiae; Pedosphaerales; Pedosphaeraceae; SCGC AAA164-E04	0.863	0.011	*
Cyanobacteria; Oxyphotobacteria; Synechococcales; Cyanobiaceae; Synechococcus CC9902; 17	0.821	0.014	*
Alphaproteobacteria; SAR11 clade; clade II	0.806	0.014	*
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; NS5 marine group; 36	0.809	0.017	*
Alphaproteobacteria; Rhodospirillales; AEGEAN 169 marine group; 46	0.843	0.018	*
Gammaproteobacteria; SAR86 clade; HF0070_25G02	0.82	0.02	*
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; NS2b marine group; 12	0.809	0.024	*
Bacteroidetes; Bacteroidia; Flavobacteriales; NS9 marine group; 101	0.805	0.025	*
Alphaproteobacteria; Rhodospirillales; AEGEAN 169 marine group; 1	0.804	0.027	*
Alphaproteobacteria; Rhodospirillales; AEGEAN 169 marine group; 4	0.806	0.029	*
Actinobacteria; Acidimicrobia; Actinomarinales; Actinomarinae; Ca. Actinomarina; 22	0.788	0.029	*
Alphaproteobacteria; SAR11 clade; clade IV; 4	0.803	0.031	*
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; NS2b marine group; 9	0.81	0.032	*
Gammaproteobacteria; SAR86 clade; HF0070_25G02; 1	0.805	0.039	*
Gammaproteobacteria; SAR86 clade; 69	0.801	0.041	*
Actinobacteria; Acidimicrobia; Actinomarinales; Actinomarinae; Ca. Actinomarina; 20	0.774	0.041	*
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; NS2b marine group; 21	0.789	0.044	*
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; NS2b marine group; 6	0.755	0.046	*
Gammaproteobacteria; SAR86 clade; HF0070_25G02; 3	0.779	0.048	*
Alphaproteobacteria; SAR11 clade; clade II; 47	0.754	0.048	*
BO Center + DCM Edge (# ASVs: 1)			
Planctomycetes; Planctomycetacia; Pirellulales; Pirellulaceae; 5	0.741	0.045	*
BO Center + Bottom Edge (# ASVs: 2)			
Gammaproteobacteria; Thiomicrospirales; Thioglobaceae; SUP05 cluster; 1	0.856	0.006	**
Marinimicrobia; SAR406 clade; JGI 0000113-D11; 3	0.808	0.02	*
Bottom Center + Bottom Edge (# ASVs: 42)			
Gammaproteobacteria; Thiomicrospirales; Thioglobaceae; SUP05 cluster; 14	0.997	0.001	***
Actinobacteria; Acidimicrobia; Microtrichales; Microtrichaceae; Sva0996 marine group; 6	0.989	0.001	***
Gammaproteobacteria; Arenicellales; Arenicellaceae	0.977	0.001	***
Marinimicrobia; SAR406 clade; OCS307; 6	0.97	0.001	***
Gammaproteobacteria; Thiomicrospirales; Thioglobaceae; SUP05 cluster	0.97	0.001	***
Bacteroidetes; Bacteroidia; Flavobacteriales; NS9 marine group; hydrothermal vent metagenome; 11	0.968	0.001	***
Actinobacteria; Acidimicrobia; Microtrichales; Microtrichaceae; Sva0996 marine group; 1	0.956	0.001	***
Gammaproteobacteria; Thiomicrospirales; Thioglobaceae; 3	0.95	0.001	***
Alphaproteobacteria; SAR11 clade; clade II; 60	0.949	0.001	***
Deltaproteobacteria; SAR324 clade marine group B; 20	0.94	0.001	***
Alphaproteobacteria; SAR11 clade; clade II; 41	0.937	0.001	***
Gammaproteobacteria; Thiomicrospirales; Thioglobaceae; 1	0.937	0.001	***
Gammaproteobacteria; SAR86 clade; 9	0.934	0.001	***
Deltaproteobacteria; SAR324 clade marine group B; 29	0.917	0.001	***
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; NS4 marine group; 14	0.946	0.002	**
Alphaproteobacteria; SAR11 clade; 4	0.94	0.002	**
Deltaproteobacteria; SAR324 clade marine group B; SAR324 cluster; 6	0.926	0.002	**
Deltaproteobacteria; SAR324 clade marine group B; 34	0.921	0.002	**
Deltaproteobacteria; SAR324 clade marine group B; SAR324 cluster; 1	0.869	0.002	**
Gammaproteobacteria; AT-s2; 59	0.932	0.003	**
Deltaproteobacteria; SAR324 clade marine group B; SAR324 cluster; 16	0.919	0.003	**
Marinimicrobia; SAR406 clade; 127	0.918	0.003	**
Gammaproteobacteria; HOC36; Ca. Thioglobus sp; REDSEA S12_B1; 17	0.907	0.003	**

Marinimicrobia; SAR406 clade; OCS307; 3	0.898	0.003	**
Verrucomicrobia; Verrucomicrobiae; Arctic97B-4 marine group; 32	0.925	0.004	**
Gammaproteobacteria; UBA10353 marine group; 4	0.898	0.008	**
Bacteroidetes; Bacteroidia; Flavobacteriales; NS9 marine group; 46	0.869	0.008	**
Dadabacteria; Dadabacteriia; Dadabacteriales; marine metagenome; 3	0.89	0.009	**
Marinimicrobia; SAR406 clade; hydrothermal vent metagenome; 4	0.894	0.012	*
Gammaproteobacteria; UBA10353 marine group; 32	0.898	0.014	*
Marinimicrobia; SAR406 clade; hydrothermal vent metagenome; 4	0.885	0.014	*
Deltaproteobacteria; SAR324 clade marine group B; SAR324 cluster; 17	0.865	0.014	*
Gammaproteobacteria; SAR86 clade; KTc1121; 6	0.87	0.015	*
Gammaproteobacteria; Methylococcales; Methylomonaceae; IheB2-23; 2	0.884	0.016	*
Alphaproteobacteria; SAR11 clade; clade I; 4	0.854	0.016	*
Marinimicrobia; SAR406 clade; Deferribacteres; 2	0.88	0.017	*
Chloroflexi; Dehalococcoidia; SAR202 clade; 52	0.843	0.019	*
Verrucomicrobia; Verrucomicrobiae; Arctic97B-4 marine group; 45	0.908	0.021	*
Marinimicrobia; SAR406 clade; hydrothermal vent metagenome; 7	0.814	0.025	*
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; Lutibacter; 1	0.899	0.031	*
Marinimicrobia; SAR406 clade; 34	0.829	0.036	*
Nitrospinae; Nitrospina; Nitrospinales; Nitrospinaceae; Nitrospina; 2	0.951	0.039	*
Surface Center + BO Center + BO Edge (# ASVs: 24)			
Gammaproteobacteria; SAR86 clade; KTc1121; 7	0.872	0.001	***
Alphaproteobacteria; Rhodovibrionales; Kiloniellaceae; 2	0.864	0.002	**
Gammaproteobacteria	0.918	0.003	**
Gemmatimonadetes; BD2-11; terrestrial group; AD66- C11; 1	0.895	0.003	**
Gammaproteobacteria; HOC36; 1	0.846	0.004	**
Gammaproteobacteria; Steroidobacterales; Woeseiaceae; Woeseia; 15	0.884	0.005	**
Acidobacteria; Subgroup 6; 6	0.856	0.005	**
Marinimicrobia; SAR406 clade; 14	0.853	0.005	**
Gammaproteobacteria; SAR86 clade; KTc1121; 3	0.825	0.006	**
Gemmatimonadetes; BD2-11 terrestrial group; 12	0.861	0.007	**
Gammaproteobacteria; HOC36; 12	0.822	0.007	**
Gammaproteobacteria; UBA10353 marine group; 11	0.858	0.01	**
Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Ascidiaceihabitans; 1	0.85	0.01	**
Gammaproteobacteria; Thiomicrospirales; Thioglobaceae; SUP05 cluster; 12	0.831	0.012	*
Margulisbacteria; 49	0.812	0.015	*
Marinimicrobia; SAR406 clade; 10	0.788	0.02	*
Acidobacteria; Subgroup 6; AD248-D7-1A	0.784	0.025	*
Chloroflexi; Dehalococcoidia; SAR202 clade; Chloroflexi HF4000_28F02; 3	0.813	0.026	*
Gammaproteobacteria; KI89A clade; 17	0.778	0.032	*
Gammaproteobacteria; UBA10353 marine group; 31	0.742	0.039	*
Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; 17	0.778	0.044	*
Gammaproteobacteria; Cellvibrionales; Porticoccaceae; SAR92 clade	0.801	0.048	*
Actinobacteria; Acidimicrobia; Microtrichales; Microtrichaceae; Sva0996 marine group; 4	0.768	0.048	*
Gammaproteobacteria; Thiomicrospirales; Thioglobaceae; SUP05 cluster; 13	0.8	0.049	*
Surface Center + BO Center + Bottom Edge (# ASVs: 1)			
Alphaproteobacteria; SAR11 clade; clade II; 5	0.807	0.019	*
Surface Center + DCM Edge + BO Edge (# ASVs: 14)			
Marinimicrobia; SAR406 clade; 289	0.977	0.001	***
Gammaproteobacteria; UBA10353 marine group; 33	0.917	0.001	***
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; NS2b marine group; 8	0.848	0.001	***
Gammaproteobacteria; UBA10353 marine group; 10	0.844	0.001	***
Gammaproteobacteria; UBA10353 marine group; 8	0.842	0.001	***
Planctomycetes; Planctomycetacia; Pirellulales; Pirellulaceae; Blastopirellula; 2	0.808	0.001	***
Gammaproteobacteria; SAR86 clade; 24	0.882	0.002	**
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; NS2b marine group; 3	0.828	0.002	**
Gammaproteobacteria; UBA10353 marine group; 7	0.81	0.003	**

Alphaproteobacteria; SAR11 clade; clade IV; 1	0.84	0.004	**
Marinimicrobia; SAR406 clade; 30	0.793	0.009	**
Actinobacteria; Acidimicrobiia; Actinomarinales; Actinomarinaceae; Ca. Actinomarina; 4	0.768	0.026	*
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; Tenacibaculum; 4	0.768	0.043	*
Firmicutes; 4	0.845	0.044	*
Surface Center + BO Edge + Bottom Edge (# ASVs: 1)			
Planctomycetes; Planctomycetacia; Pirellulales; Pirellulaceae; Blastopirellula; 4	0.741	0.038	*
DCM Center + Surface Edge + DCM Edge (# ASVs: 18)			
Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobacteraceae; REDSEA S03_B4; 1	0.903	0.001	***
Alphaproteobacteria; Parvibaculales; OCS116 clade; 9	0.835	0.001	***
Actinobacteria; Acidimicrobiia; Microtrichales; Microtrichaceae; Sva0996 marine group; 40	0.878	0.002	**
Alphaproteobacteria; SAR11 clade; clade I; 5	0.838	0.002	**
Alphaproteobacteria; SAR11 clade; clade I; 13	0.814	0.002	**
Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobacteraceae; REDSEA S03_B4	0.79	0.004	**
Gammaproteobacteria; Ectothiorhodospirales; Ectothiorhodospiraceae; 42	0.869	0.005	**
Actinobacteria; Acidimicrobiia; Actinomarinales; Actinomarinaceae; Ca. Actinomarina; 23	0.833	0.005	**
Alphaproteobacteria; SAR11 clade; clade II; 31	0.833	0.006	**
Alphaproteobacteria; Rhodospirillales; AEGEAN 169 marine group; 16	0.815	0.006	**
Alphaproteobacteria; SAR11 clade; clade IV	0.826	0.007	**
Alphaproteobacteria; SAR11 clade; clade I; clade Ib; 27	0.823	0.008	**
Alphaproteobacteria; SAR11 clade; clade I; clade Ia; 1	0.751	0.016	*
Cyanobacteria; Oxyphotobacteria; Synechococcales; Cyanobiaceae; Cyanobium PCC-6307; 1	0.765	0.019	*
Cyanobacteria; Oxyphotobacteria; Synechococcales; Cyanobiaceae; Cyanobium PCC-6307; 2	0.76	0.026	*
Cyanobacteria; Oxyphotobacteria; Synechococcales; Cyanobiaceae; Cyanobium PCC-6307	0.747	0.033	*
Alphaproteobacteria; SAR11 clade; clade IV; 6	0.79	0.036	*
Gammaproteobacteria; HOC36; 7	0.746	0.037	*
DCM Center + DCM Edge + BO Edge (# ASVs: 4)			
Gammaproteobacteria; SAR86 clade; 72	0.821	0.01	**
Actinobacteria; Acidimicrobiia; Actinomarinales; Actinomarinaceae; Ca. Actinomarina; 8	0.771	0.022	*
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; NS5 marine group; 4	0.784	0.028	*
Actinobacteria; Acidimicrobiia; Actinomarinales; Actinomarinaceae; Ca. Actinomarina; 11	0.759	0.031	*
BO Center + Bottom Center + Bottom Edge (# ASVs: 9)			
Deltaproteobacteria; SAR324 clade marine group B; SAR324 cluster; 4	0.867	0.001	***
Deltaproteobacteria; SAR324 clade marine group B; SAR324 cluster	0.859	0.001	***
Gammaproteobacteria; UBA10353 marine group; 17	0.91	0.002	**
Gammaproteobacteria; HOC36; Ca. Thioglobus sp; REDSEA S12_B1; 10	0.883	0.003	**
Gammaproteobacteria; Thiomicrospirales; Thioglobaceae; SUP05 cluster; 4	0.877	0.004	**
Gammaproteobacteria; UBA10353 marine group; 27	0.844	0.007	**
Gammaproteobacteria; Thiomicrospirales; Thioglobaceae; SUP05 cluster; 9	0.846	0.012	*
Gammaproteobacteria; Thiomicrospirales; Thioglobaceae; SUP05 cluster; 16	0.827	0.017	*
Deltaproteobacteria; SAR324 clade marine group B; 8	0.859	0.044	*
Surface Center + DCM Center + DCM Edge + BO Edge (# ASVs: 2)			
Alphaproteobacteria; SAR11 clade; clade I; clade Ia; 13	0.77	0.014	*
Actinobacteria; Acidimicrobiia; Actinomarinales; Actinomarinaceae; Ca. Actinomarina; 12	0.728	0.041	*
Surface Center + BO Center + DCM Edge + BO Edge (# ASVs: 6)			
Actinobacteria; Acidimicrobiia; Microtrichales; Microtrichaceae; Sva0996 marine group; 10	0.828	0.001	***
Actinobacteria; Acidimicrobiia; Microtrichales; Microtrichaceae; Sva0996 marine group; 21	0.815	0.001	***
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; NS4 marine group; 1	0.798	0.01	**
Alphaproteobacteria; SAR11 clade; clade I; clade Ib; 22	0.761	0.021	*
Marinimicrobia; SAR406 clade; 6	0.756	0.027	*
Alphaproteobacteria; SAR11 clade; clade IV; 2	0.753	0.027	*
Surface Center + BO Center + BO Edge + Bottom Edge (# ASVs: 6)			
Gammaproteobacteria; HOC36; Ca. Thioglobus sp; REDSEA S12_B1; 20	0.871	0.001	***

Marinimicrobia; SAR406 clade; 248	0.861	0.002	**
Actinobacteria; Acidimicrobiia; Microtrichales; Microtrichaceae; Sva0996 marine group; 44	0.822	0.002	**
Alphaproteobacteria; SAR11 clade; clade I; 1	0.808	0.005	**
Actinobacteria; Acidimicrobiia; Microtrichales; Microtrichaceae; Sva0996 marine group; 11	0.801	0.009	**
Gammaproteobacteria; UBA10353 marine group; 22	0.746	0.042	*
Surface Center + BO Center + Bottom Center + Bottom Edge (# ASVs: 1)			
Alphaproteobacteria; SAR11 clade; clade I; 3	0.786	0.008	**
BO Center + Bottom Center + BO Edge + Bottom Edge (# ASVs: 1)			
Gammaproteobacteria; HOC36; Ca. Thioglobus sp; REDSEA S12_B1; 1	0.735	0.047	*
Surface Center + DCM Center + BO Center + DCM Edge + BO Edge (# ASVs: 7)			
Alphaproteobacteria; Rhodospirillales; AEGEAN 169 marine group; 42	0.824	0.002	**
Verrucomicrobia; Verrucomicrobiae; Verrucomicrobiales; DEV007; hydrothermal vent metagenome; 8	0.821	0.003	**
Alphaproteobacteria; Rhodospirillales; AEGEAN 169 marine group; 14	0.83	0.004	**
Alphaproteobacteria; SAR11 clade; clade I; clade Ia; 4	0.742	0.02	*
Gammaproteobacteria; HOC36; 8	0.744	0.033	*
Alphaproteobacteria; Rhodospirillales; AEGEAN 169 marine group; 68	0.739	0.045	*
Gammaproteobacteria; HOC36; 17	0.732	0.047	*
Surface Center + DCM Center + Surface Edge + DCM Edge + BO Edge (# ASVs: 1)			
Alphaproteobacteria; SAR11 clade; clade I; clade Ia; 7	0.865	0.001	***
Surface Center + BO Center + DCM Edge + BO Edge + Bottom Edge (# ASVs: 1)			
Alphaproteobacteria; SAR11 clade; clade I; 16	0.838	0.002	**
Surface Center + DCM Center + BO Center + Surface Edge + DCM Edge + BO Edge (# ASVs: 3)			
Alphaproteobacteria; SAR11 clade; clade I; clade Ia; 14	0.798	0.002	**
Alphaproteobacteria; SAR11 clade; clade I; clade Ia	0.784	0.002	**
Alphaproteobacteria; SAR11 clade; clade I; clade Ia; 5	0.735	0.021	*

SUPPLEMENTARY FIGURES

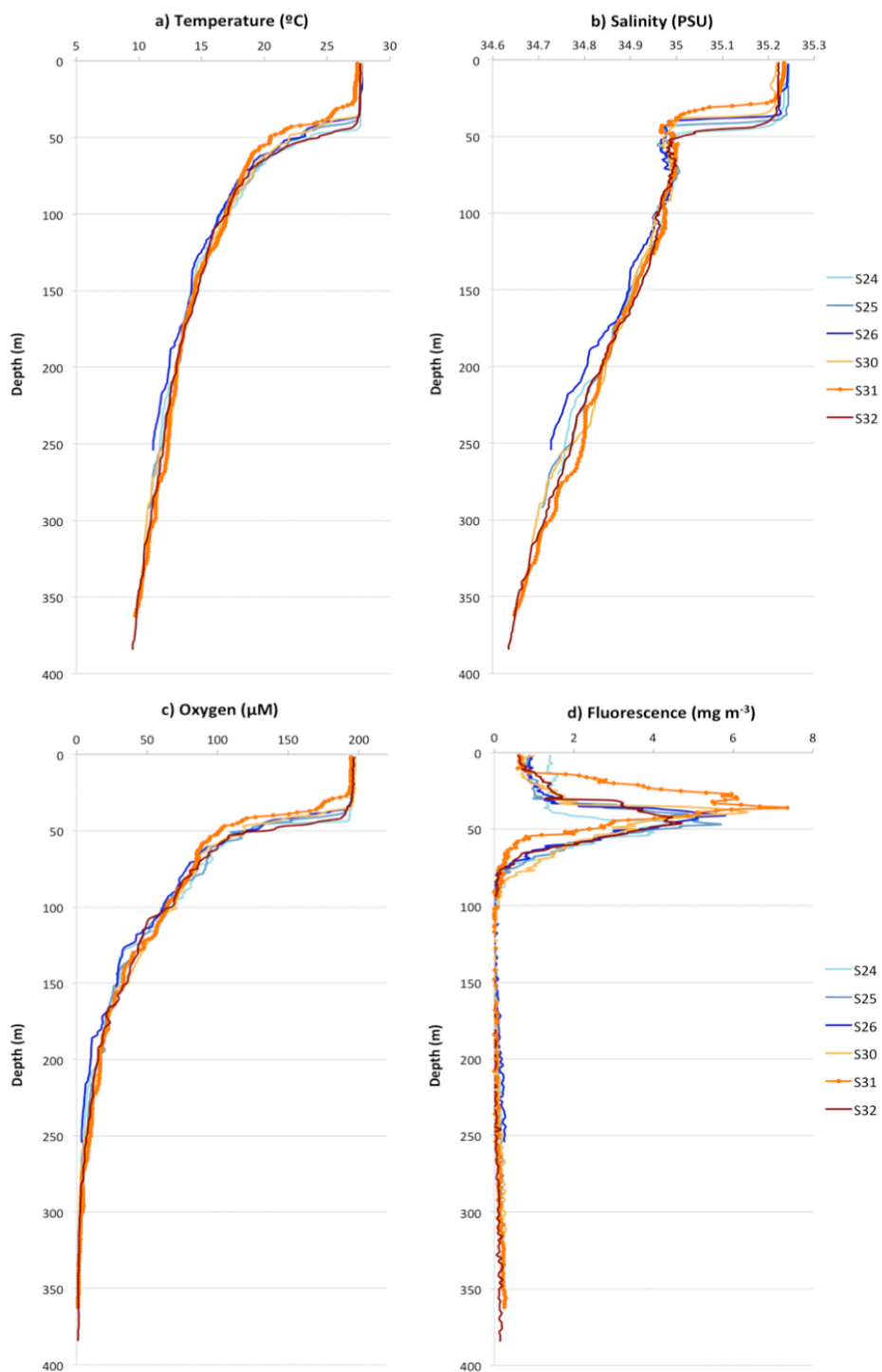


Fig. S1. Vertical profiles of environmental variables in the six sampling stations: a) temperature, b) salinity, c) dissolved oxygen, and d) chlorophyll *a* (fluorescence). The dotted profile denotes the station S31 (located just within the eddy core).

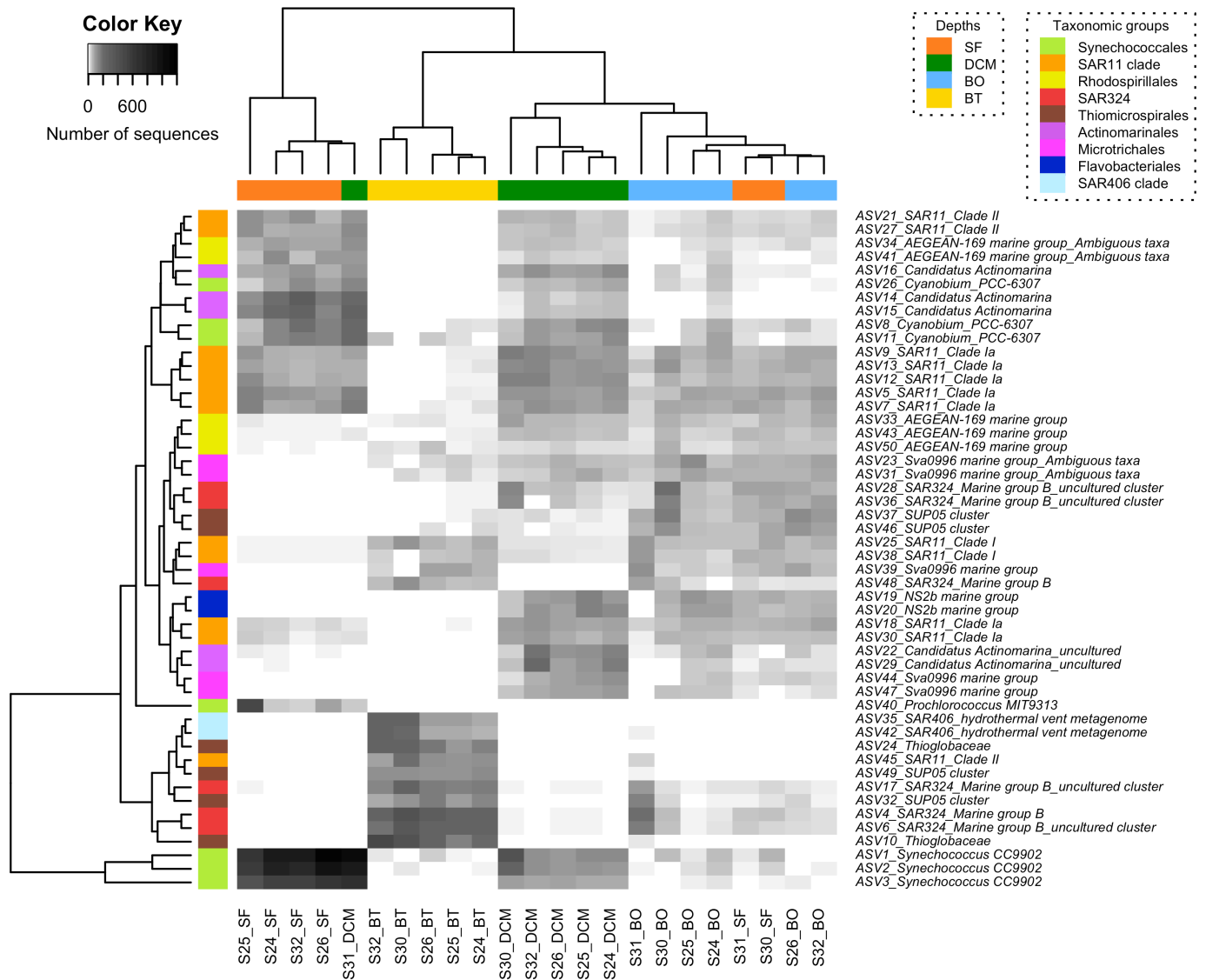


Fig. S2. Heatmap showing the abundance distribution of the 50 most abundant ASVs (contributing >0.3% of the total sequences). The color key scale represents the number of sequences detected for each sample (white color denotes zero sequences). Rows indicate ASVs and columns indicate the samples from the two transects. The dendrograms show the hierarchical clustering among samples and ASVs, respectively. The samples were labelled with the station name, followed by the sampling depth (SF, surface; DCM, deep chlorophyll maximum; BO, base of the oxycline; BT, bottom).

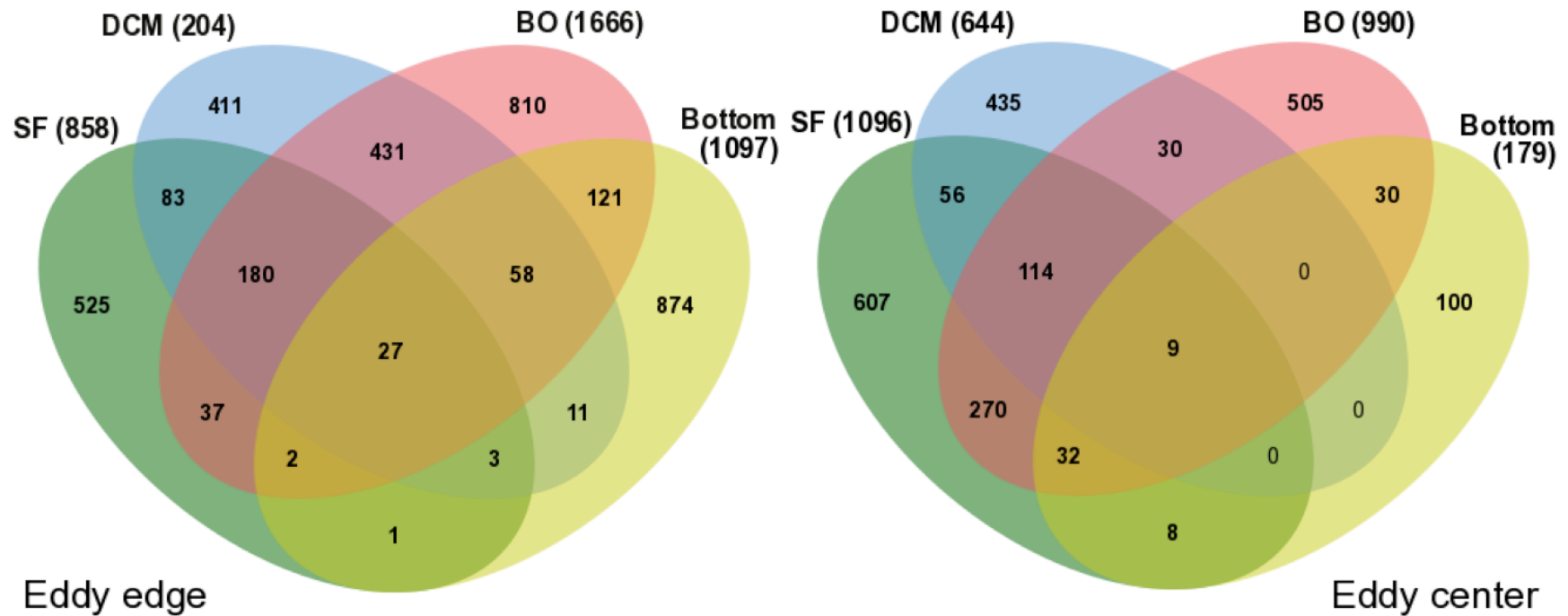


Fig. S3. Venn diagrams showing the numbers of shared and unique ASVs among the sampling depths (SF, surface; DCM, deep chlorophyll maximum; BO, base of the oxycline; and bottom) for the stations located at the eddy edges (S24, S25, S26, and 232) and those located at the eddy center (S30 and S31). The total number of ASVs at each depth for a given location is indicated in parentheses.