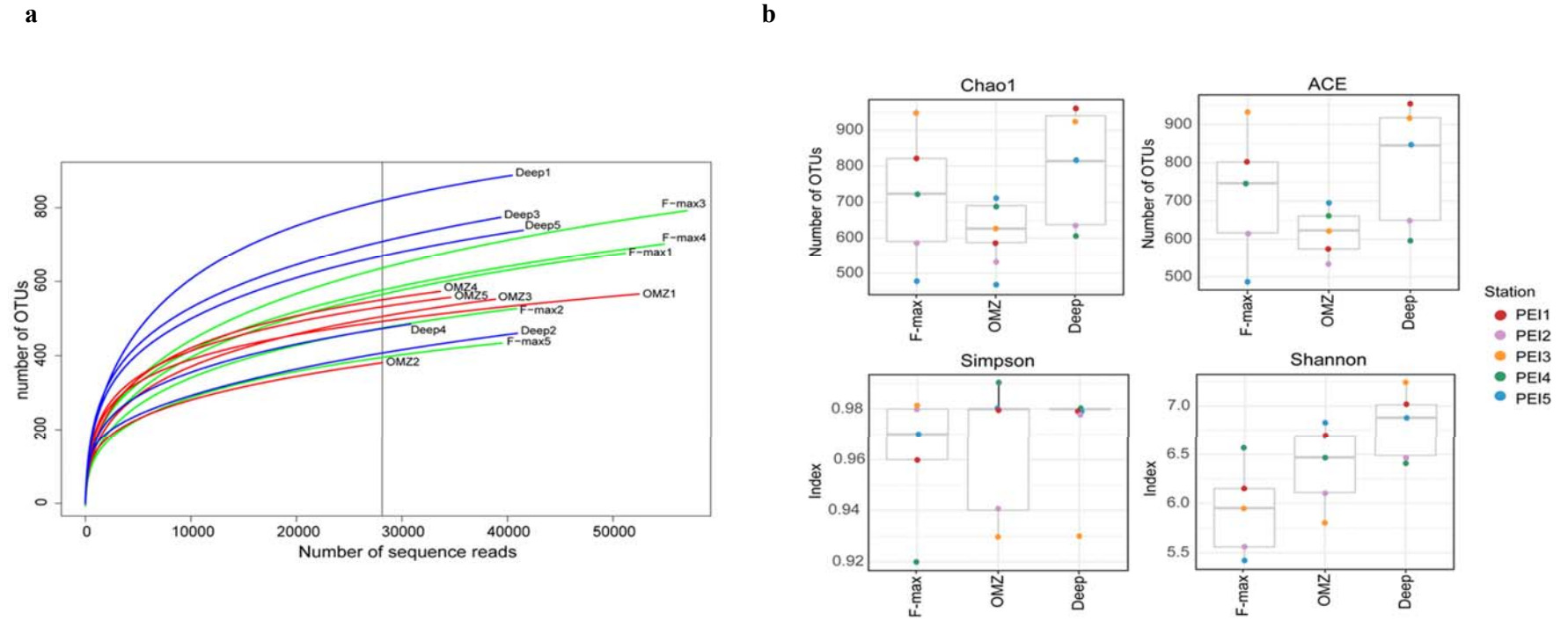
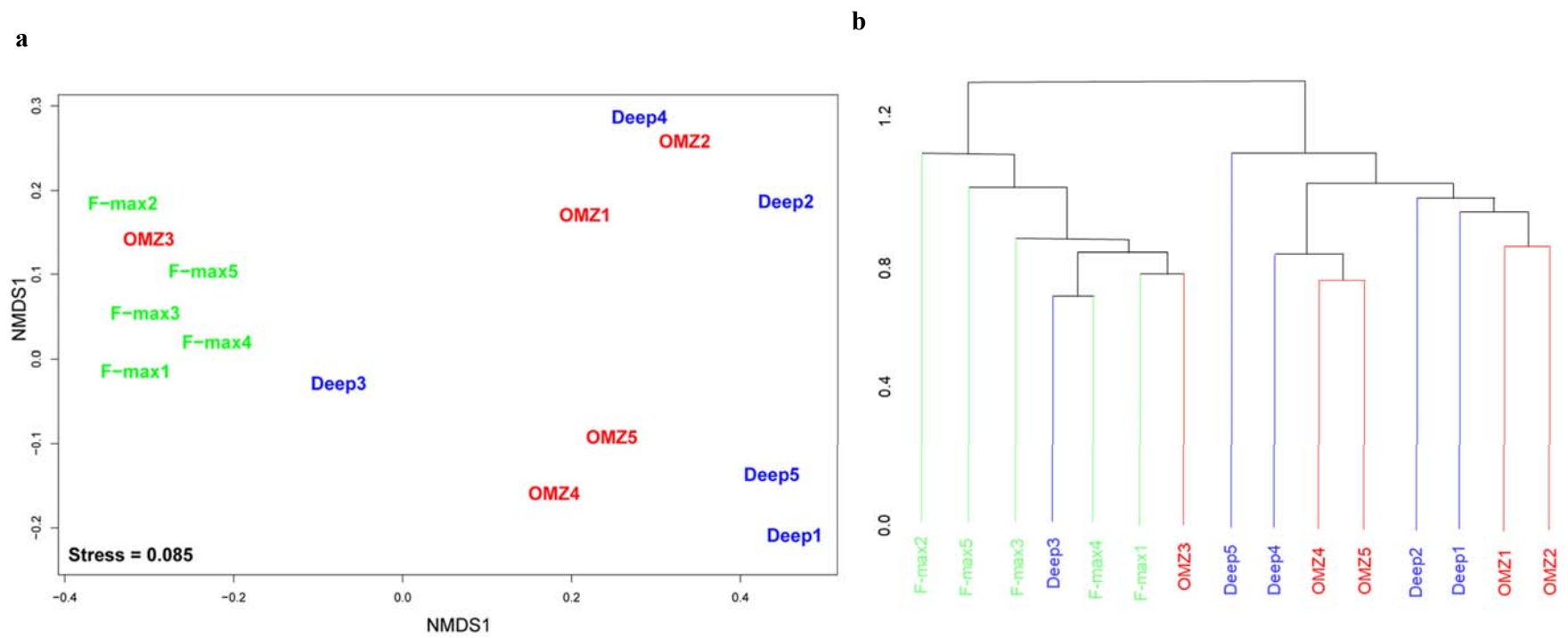


## Supplementary Files

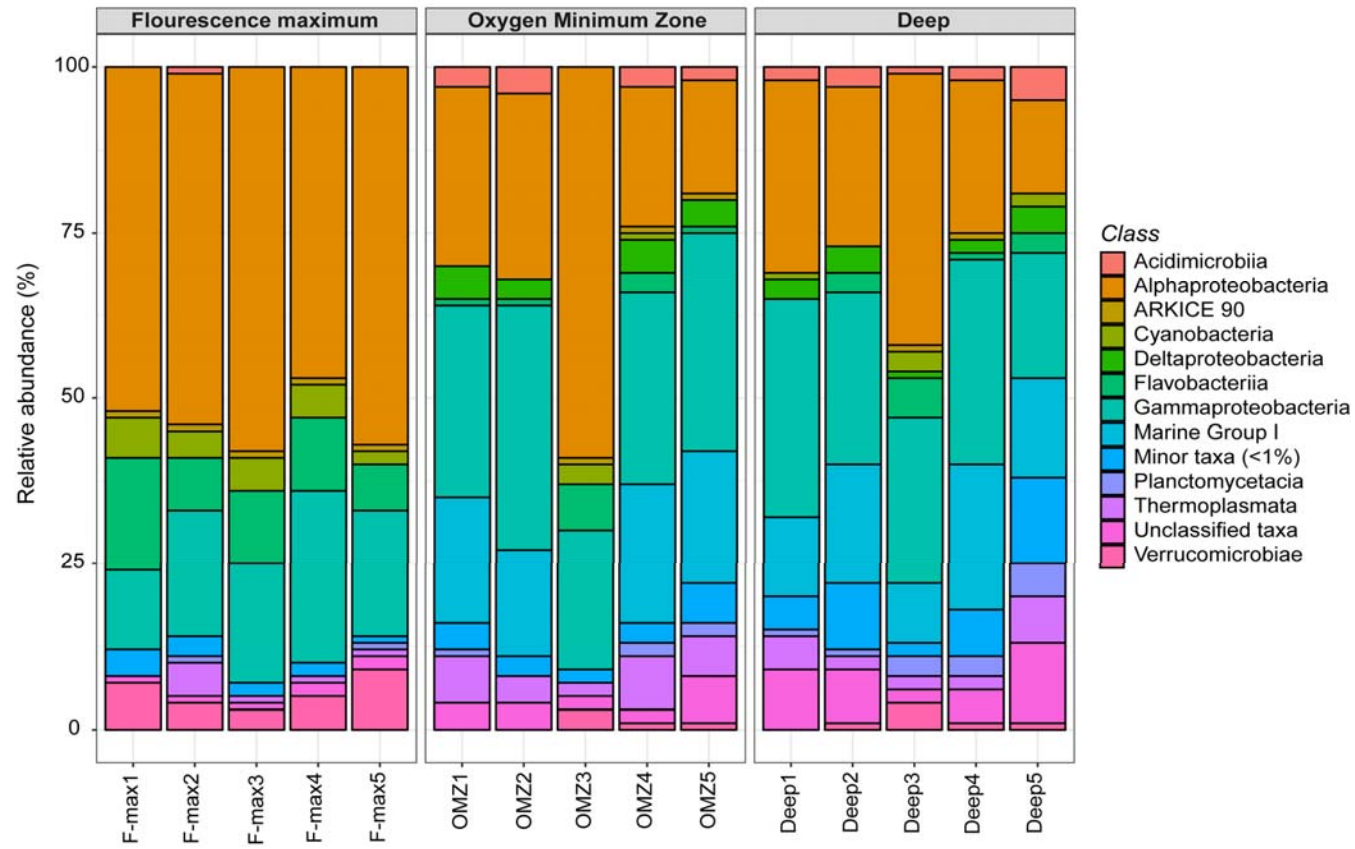
## 6S rRNA gene sequences obtained from three seafloor samples by three different



**Fig. S1** Rarefaction and alpha diversity analyses. (a) Rarefaction curves illustrating the number of OTUs (clustered at 3% dissimilarity cut-off) from 16S rRNA sequence reads. (b) Boxplots of alpha diversity estimator calculations of all PEI stations



**Fig. S2** Beta-diversity of PEI samples. (a) Non-metric multidimensional scaling (NMDS) ordination bacterial and archaeal communities (2D stress = 0.085) based on operational taxonomic units (OTUs) across all samples. (b) Hierarchical clustering tree on the OTU level based on the Bray-Curtis distance



**Fig. S3** The relative abundance of dominant (>1%) bacterial and archaeal taxa at class level across F-max, OMZ and Deep samples

**Table S1** Geographical and physicochemical variables of oceanic samples obtained in the vicinity of the PEIs during the 2015 Marion relief cruise on-board the SA Agulhas II RV

*PEI, Prince Edwards Islands; SASW, Sub-Antarctic Surface Water; AAIW, Antarctic Intermediate Water; NADW, North Atlantic Deep Water; AASW, Antarctic Surface Water; AABW, Antarctic*

Station number (PEI-X)	Sample name	Sample type	Water mass	Sampling date (dd/mm/yy)	Long (E°)	Lat (S°)	Salinity (PSU)	Oxygen (ml/l)	Temp (°C)	Fluor (mg/m <sup>3</sup> )	Depth (m)	Sounding (m)
PEI1	F-max1	F-max	SASW	04/23/2015	37.296	45.748	33.81	6.66	7.29	2.54	37.68	2579
	OMZ1	Oxy-min	AAIW				34.56	3.79	2.69	0.77	1214.23	
	Deep1	Deep	NADW				34.78	4.50	2.07	0.77	2531.52	
PEI2	F-max2	F-max	SASW	04/24/2015	37.309	46.752	33.84	6.47	7.75	1.80	46.60	3302
	OMZ2	Oxy-min	AAIW				34.60	3.79	2.66	0.78	1315.78	
	Deep2	Deep	NADW				34.73	4.45	4.1	0.78	3242.46	
PEI3	F-max3	F-max	SASW*	04/26/2015	37.900	46.750	33.81	6.59	7.04	1.98	50.57	210
	OMZ3	Oxy-min	SASW*				34.05	5.98	5.95	0.78	197.26	
	Deep3	Deep	SASW*				34.05	6.01	5.95	0.78	199.24	
PEI4	F-max4	F-max	SASW	04/25/2015	38.500	46.750	33.80	6.66	6.68	1.98	44.62	1022
	OMZ4	Oxy-min	AAIW*				34.46	3.94	2.85	0.78	1002.17	
	Deep4	Deep	AAIW*				34.56	4.00	2.4	0.78	1013.23	
PEI5	F-max5	F-max	AASW	04/25/2015	37.301	47.501	33.76	6.92	4.77	1.67	68.42	4137
	OMZ5	Oxy-min	AAIW				34.55	3.73	2.57	0.78	979.40	
	Deep5	Deep	AABW				34.66	4.78	0.21	0.78	4057.09	

*Bottom Water; Long, Longitude; Lat, Latitude; Temp, Temperature; Fluor, Fluorescence; \* shallow stations without water mass variation.*

**Table S2** Nutrient and extracellular enzyme concentrations of seawater samples obtained along the PEI transect.

Station number (PEI-X)	Sample name	Silicate ( $\mu\text{m/L}$ )	Nitrate ( $\mu\text{m/L}$ )	Phosphate ( $\mu\text{m/L}$ )	AP (mmol.h.ml)	NAG (mmol/h/ml)	LAP (mmol/h/ml)	BG (mmol/h/ml)	BX (mmol/h/ml)
PEI1	F-max1	2.00	13.24	1.27	0.0150	0.00150	0.02100	0.02234	0.00310
	OMZ1	62.44	35.19	2.76	0.00450	0.00028	0.00510	0.00100	0.00120
	Deep1	70.45	32.41	2.98	0.00180	0.00012	0.00230	0.00030	0.00048
PEI2	F-max2	1.62	15.96	1.13	0.01230	0.00130	0.01900	0.01876	0.00220
	OMZ2	76.77	34.43	2.30	0.00380	0.00032	0.00310	0.00090	0.00098
	Deep2	121.68	27.82	3.30	0.00020	0.00003	0.00056	0.00002	0.00066
PEI3	F-max3	2.20	17.11	1.46	0.02876	0.00355	0.03500	0.03344	0.00430
	OMZ3	10.65	26.27	1.56	0.01134	0.00230	0.02900	0.00153	0.00290
	Deep3	13.67	25.30	1.63	0.01240	0.00340	0.04330	0.00298	0.00322
PEI4	F-max4	2.50	18.19	1.34	0.02100	0.00312	0.02900	0.02990	0.00390
	OMZ4	58.70	38.41	2.29	0.00376	0.00190	0.00450	0.00123	0.00067
	Deep4	64.98	38.55	2.28	0.00361	0.00140	0.00520	0.00113	0.00047
PEI5	F-max5	3.50	19.10	1.34	0.01110	0.00089	0.01100	0.01209	0.00190
	OMZ 5	50.93	37.86	2.00	0.00250	0.00004	0.00920	0.00119	0.00056
	Deep5	135.07	14.19	3.90	0.00010	0.00002	0.00012	0.00001	0.00003

AP, Alkaline phosphate; NAG, N-acetyl- $\beta$ -glucosidase; LAP, Leucine aminopeptidase; BG,  $\beta$ -Glucosidase; BX,  $\beta$ -Xylosidase.

**Table S3** Extracellular enzymes and their reported function in the marine ecosystem. Information was retrieved from Sinsabaugh *et al.* (2012), Arnosti (2014), Kellogg and Deming (2014) and Baltar *et al.* (2017).

<b>Extracellular enzyme</b>	<b>Functional activity</b>	<b>Nutrient result and function in marine ecosystem</b>	<b>Substrate proxy</b>
<b><math>\beta</math>-Glucosidase (BG)</b>	Hydrolyses non-reducing D-glucose residues in polysaccharides	Release of glucose. aids in carbon acquisition	4-Methylumbelliferyl $\beta$ -D-glucopyranoside
<b><math>\beta</math>-Xylosidase (BX)</b>	Hydrolyses xylans by cleaving non-reducing D-xylose	Releases xylose; Aids in carbon acquisition and POM degradation	4-Methylumbelliferyl $\beta$ -D-xylopyranoside
<b>N-acetylglucosaminidase (NAG)</b>	Hydrolyses chitin related oligopolymers by acting on D-glucosaminide residues	Releases glucosamine residues; Aids in nitrogen acquisition	4-Methylumbelliferyl N-acetyl- $\beta$ -D-glucosaminide
<b>Alkaline phosphatase (AP)</b>	Hydrolyses phosphate from compounds such as nucleotides. proteins and monoesters	Releases inorganic phosphorus; Aids in phosphorus acquisition	4-Methylumbelliferyl phosphate
<b>Leucine aminopeptidase (LAP)</b>	Degrades polypeptides by removing N-terminal amino acids	Releases amino acids; Aids in nitrogen acquisition	L-Leucine-7-amido-4-methylcoumarin hydrochloride

**Table S4** OTU observations, alpha diversity indices and good's coverage at 3% genetic dissimilarity derived from 16S rRNA gene analysis of PEI seawater samples.

Sample name	High quality reads	Observed OTUs	ACE	Chao1	Shannon	Good's coverage (%)	$\beta$ -diversity	Gamma
F-max1	51147	565	801.67	821	6.15	99.32	1.75	1183
F-max2	40831	482	616.77	590	5.56	99.54	2.21	
F-max3	56977	647	935.08	960	5.95	99.19	1.49	
F-max4	54816	570	746.47	723	6.57	99.44	1.69	
F-max5	39448	386	489.10	465	5.42	99.65	2.71	
OMZ1	52420	481	574.56	587	6.69	99.65	2.04	1153
OMZ2	28117	381	533.87	532	6.11	99.60	3.03	
OMZ3	38825	499	623.10	626	5.81	99.54	2.08	
OMZ4	33598	543	660.60	690	6.47	99.54	2.01	
OMZ5	34591	540	694.75	711	6.83	99.52	2.07	
Deep1	40405	807	954.19	955	7.01	99.34	1.72	1530
Deep2	40901	401	650.05	637	6.49	99.51	3.36	
Deep3	39337	706	917.79	940	7.23	99.33	1.98	
Deep4	30793	465	595.39	609	6.46	99.58	3.14	
Deep5	41459	670	845.48	814	6.88	99.42	2.07	
<b>Total</b>	<b>623665*</b>	<b>1891*</b>						

\*A total of 1891 different OTUs were obtained after all samples were normalised to 28117 reads; PD = Phylogenetic diversity



**Table S5** Statistical significance of the nMDS plot using *adonis* analysis.

	<i>adonis</i> R <sup>2</sup>	<i>adonis</i> p
<b>All</b>	0.34	<b>0.005</b>
<b>F-max vs OMZ</b>	0.37	<b>0.017</b>
<b>OMZ vs Deep</b>	0.10	0.593
<b>F-max vs Deep</b>	0.36	<b>0.014</b>

Bold values are significant values ( $p < 0.05$ );  $p$ -values were adjusted using the Benjamini and Hochberg method for multiple testing using the stats R package.

**Table S6** The core microbiome across and between all sample depths.

	Class level	Lowest taxa assignment	Taxa group	Count	Relative abundance (%)
<b>All (n=71)</b>	Acidimicrobiia	Sva0996 marine group	f	2	2.82
	Alphaproteobacteria	PS1 clade	f	1	1.41
		AEGEAN-169 marine group	g	2	2.82
		SAR11 clade	o	16	22.54
	Cyanobacteria	<i>Prochlorococcus</i>	g	2	2.82
		<i>Synechococcus</i>	g	1	1.41
	Deltaproteobacteria	SAR324 clade (Marine group B)	p	2	2.82
	Flavobacteriia	NS5 marine group	g	3	4.23
	Gammaproteobacteria	<i>Pseudoalteromonas</i>	g	2	2.82
		<i>Alteromonas</i>	g	1	1.41
		SAR86 clade	f	15	21.13
		<i>Pseudohongiella</i>	g	2	2.82
	Marine Group I	<i>Candidatus Nitrosopumilus</i>	g	10	14.08
	Planctomycetacia	<i>Planctomycetaceae</i>	f	1	1.41
Thermoplasmata	Marine Group II	f	5	7.04	
Marinimicrobia (SAR406 clade)*	Unassigned	*	5	7.04	
Verrucomicrobiae	<i>Roseibacillus</i>	g	1	1.41	
<b>F-max (n=34)</b>	Alphaproteobacteria	<i>PS1 clade</i>	f	1	2.94
		<i>Rhodobacteraceae</i>	g	1	2.94
		AEGEAN-169 marine group	o	2	5.88
		SAR11 clade	o	10	29.41
	Bacteroidetes	NS5 marine group	g	5	14.71
	Cyanobacteria	<i>Prochlorococcus</i>	g	2	5.88
		<i>Synechococcus</i>	g	1	2.94
	Euryarchaeota	Marine Group II	f	1	2.94
	Gammaproteobacteria	SAR86 clade	f	9	26.47
	Marinimicrobia (SAR406 clade)	Unassigned	*	1	2.94
Verrucomicrobiae	<i>Roseibacillus</i>	g	1	2.94	

*f* = family; *o* = order; *g* = genus; \* = unassigned

<b>OMZ (n=41)</b>	Acidimicrobiia	Sva0996 marine group	f	1	2.44
	Alphaproteobacteria	SAR11 clade	o	11	26.83
		PS1 clade	f	1	2.44
		AEGEAN-169 marine group	g	1	2.44
	Deltaproteobacteria	SAR324 clade(Marine group B)	o	1	2.44
	Flavobacteriia	NS5 marine group	g	2	4.88
	Gammaproteobacteria	JL-ETNP-Y6	f	1	2.44
		Pseudoalteromonas	g	2	4.88
		ZD0417 marine group	g	1	2.44
		SAR86 clade	f	3	7.32
		<i>Pseudomonas</i>	g	1	2.44
		<i>Pseudohongiella</i>	g	1	2.44
	Marine Group I	Marine Group I	c	7	17.07
	Marinimicrobia (SAR406 clade)	Unassigned	*	3	7.32
Thermoplasmata	Marine Group II	f	4	9.76	
Verrucomicrobia	<i>Roseibacillus</i>	g	1	2.44	
<b>Deep (n=41)</b>	Acidimicrobiia	Sva0996 marine group	f	1	2.44
	Alphaproteobacteria	PS1 clade	f	1	2.44
		SAR11 clade	o	6	14.63
		AEGEAN-169 marine group	g	1	2.44
	Deltaproteobacteria	SAR324 clade(Marine group B)	o	1	2.44
	Flavobacteriia	NS5 marine group	g	2	4.88
	Gammaproteobacteria	JL-ETNP-Y6	f	7	17.07
		Pseudoalteromonas	g	2	4.88
		SAR86 clade	f	3	7.32
		<i>Pseudohongiella</i>	g	1	2.44
		<i>Pseudomonas</i>	g	1	2.44
	Marine Group I	Candidatus Nitrosopumilus	g	9	17.07
	Marinimicrobia (SAR406 clade)	Unassigned	*	3	7.32
	Thermoplasmata	Marine Group II	f	2	9.76
Verrucomicrobiae	<i>Roseibacillus</i>	g	1	2.44	

*f* = family; *o* = order; *g* = genus; \* = unassigned taxa group