

**Additional File 2:
SUPPLEMENTARY Material**

for

**Microbial Fingerprinting of Marine Water Masses in an Antarctic and
Hydrographically Complex Area**

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Supplementary Table 1. Water masses identified in the Gerlache–Bismarck Strait, along with their corresponding abbreviations.

Abbreviation	Oceanographic feature
STF	Surface water Thermal Front
SPF	Sub-Pycnocline Front
AASW	Antarctic Surface Waters
TBW	Transitional Zonal Waters with Bellingshausen Sea influence
GMW	Glacially Modified Waters
TWW	Transitional Zonal Waters with Weddell Sea Influence
CDW	Circumpolar Deep Waters

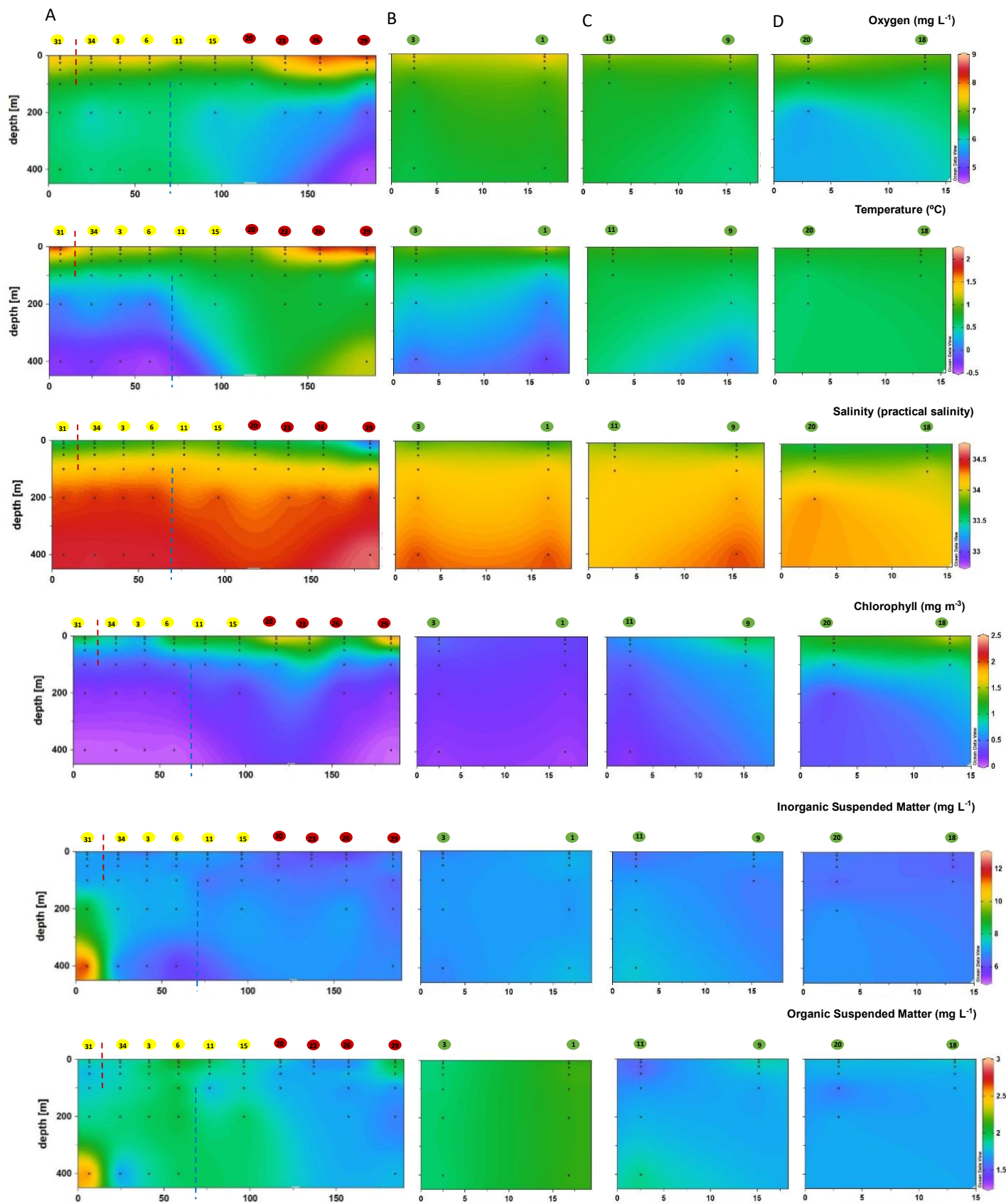
Supplementary Table 2. Water masses and their thermohaline indices (T, S). Values were obtained from: (1) Dierssen, HM, Smith, RC, Vernet, M. 2002. Glacial meltwater dynamics in coastal waters west of the Antarctic peninsula. *Proceedings of the National Academy of Sciences*, 99: 1790-1795; (2) García, MA, Castro, CG, Ríos, AF, Doval, MD, Rosón, G, Gomis, D, López, O. 2002. Water masses and distribution of physico-chemical properties in the Western Bransfield Strait and Gerlache Strait during Austral summer 1995/96. *Deep Sea Research Part II: Topical Studies in Oceanography*, 49: 585-602; (3) Parra, RRT, Laurido, ALC, Sánchez, JDI. 2020. Hydrographic conditions during two austral summer situations (2015 and 2017) in the Gerlache and Bismarck straits, northern Antarctic Peninsula. *Deep Sea Research Part I: Oceanographic Research Papers*, 161: 103278

Water masses	Temperature (°C)	Salinity (practical salinity)	References
Glacier Modified Waters (GMW)	3.10-3.20	32.50-32.70	1
Antarctic Surface Water (AASW)	1.00-2.50	33.36-34.11	2,3
Transitional Bellingshausen Water (TBW)	0.10-0.70	33.66-33.91	2
Transitional Weddell Water (TWW)	-0.70-0.30	34.50-34.60	2
Circumpolar Deep Water (CDW)	1.30-1.70	34.50-34.70	2,3

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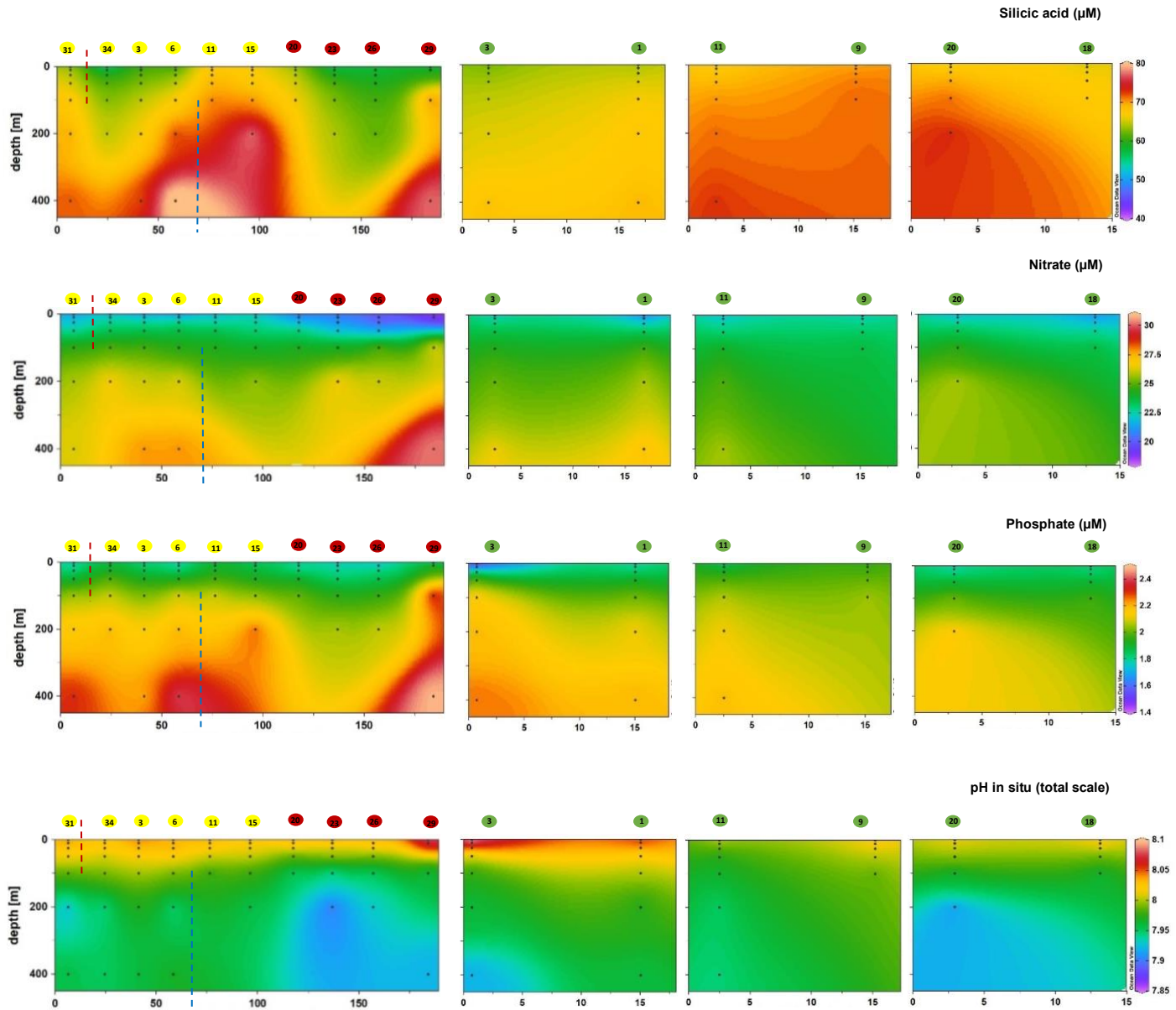
Supplementary Table 3. Details about the sampling stations.

Station	Depths [m]	Bottom Depth [m]	Dominant water mass	Sampling date [dd-mm-yyyy]	Latitude [degrees North]	Longitude [degrees East]
01	1, 10, 100	690	GMW	09-02-2020	-64,622283	-62,227017
03	1,10,100, 400	690	TBW	10-02-2020	-64,51105	-62,378617
06	1	617	AASW	10-02-2020	-64,5961	-62,678083
09	1	542	TBW	10-02-2020	-64,781083	-62,745417
11	1, 10, 100, 200	232	TBW	11-02-2020	-64,7046	-62,94385
15	1	258	TBW	11-02-2020	-64,845367	-63,203883
18	1	296	TBW	11-02-2020	-65,051633	-63,25855
20	1, 10, 100, 240	249	TBW	11-02-2020	-65,00665	-63,44775
23	1	347	AASW	12-02-2020	-64,911633	-63,697133
26	1, 10, 100, 400	474	GMW	12-02-2020	-64,829983	-64,075333
29	1, 10, 100, 400	1013	GMW	12-02-2020	-64,973433	-64,523633
31	1, 10, 100, 400	982	GMW	16-02-2020	-64,3223	-61,803267
34	1	795	TBW	16-02-2020	-64,425067	-62,092117



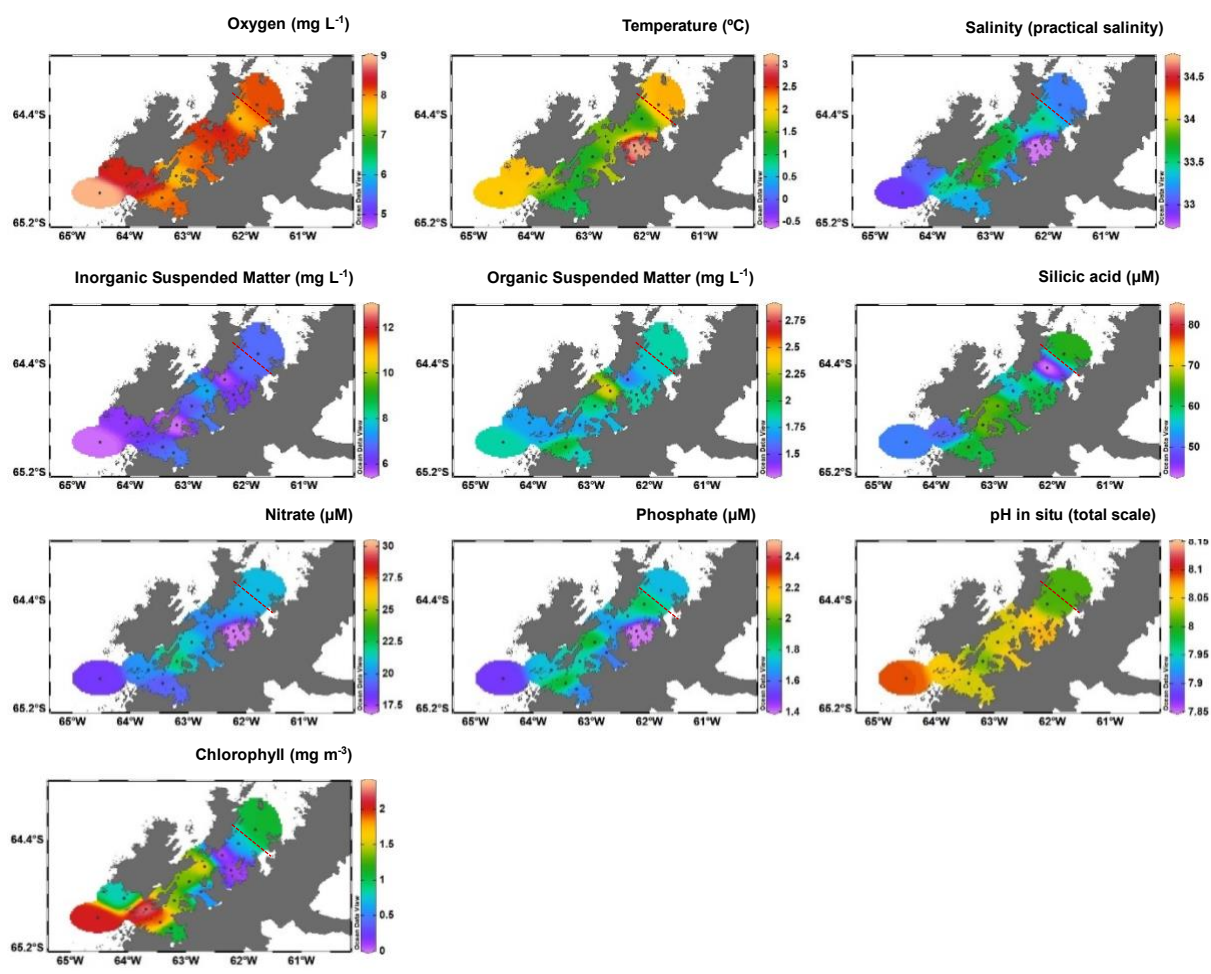
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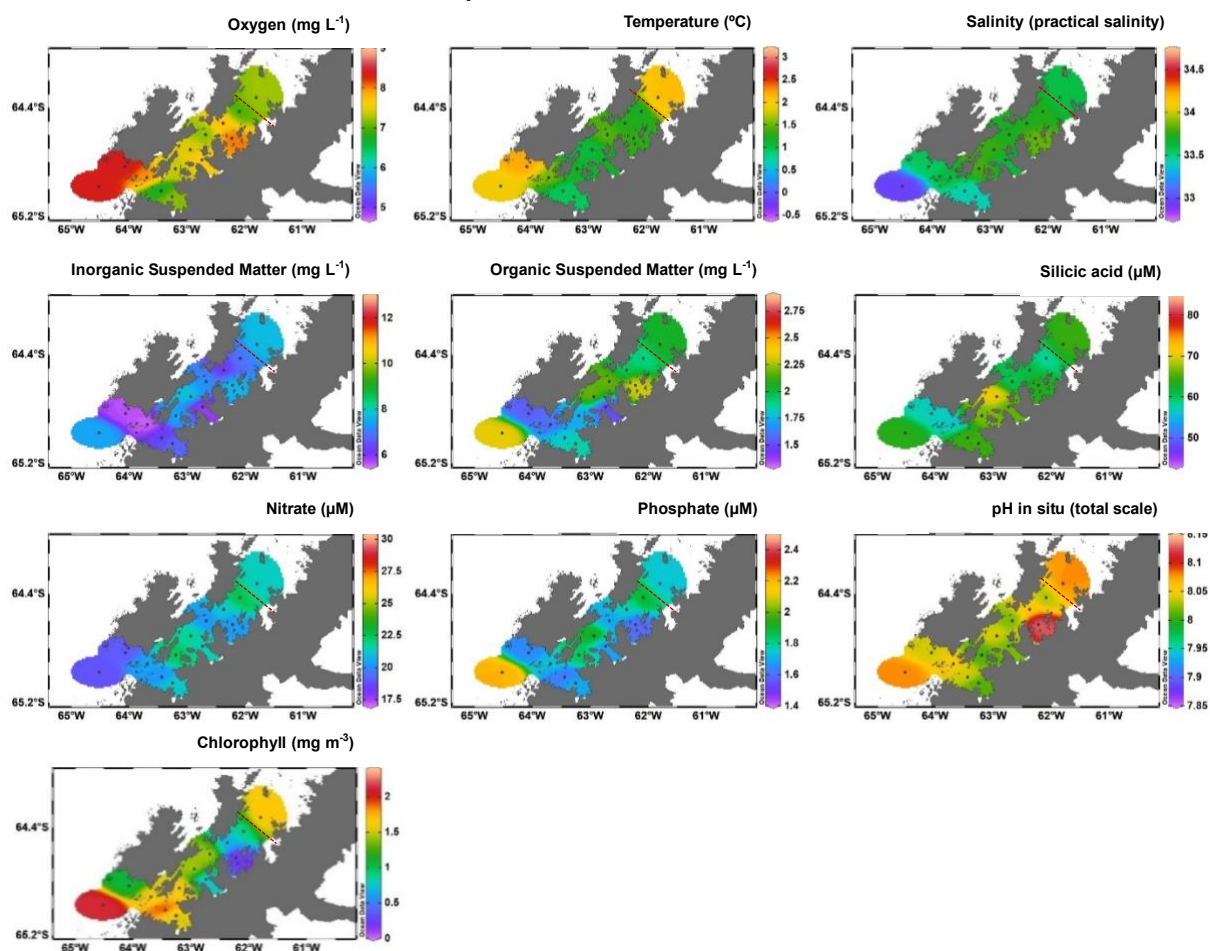
Supplementary Figure 1. Environmental variables considered in this study represented as vertical profiles. Each figure includes 13 vertical profiles (corresponding to 13 oceanographic stations), which are classified as Gerlache zone (yellow), fjords (green) and Bismarck zone (red). Each vertical profile includes 6 samples. Figures include the fronts: surface water thermal front (dashed red line) and the sub-pycnocline front (dashed blue line). The X axis represents the section distance (km). The sections represent (A) the transect including the central Gerlache and Bismarck stations, and the three different fjords (B: Wilhelmina Bay; C: Andvord Bay; D: Flandres Bay). Some stations (3, 11, 20) are duplicated to display differences between the inner and outer part of the fjords. The information regarding different stations is shown in Figure 2.

Environmental variables at 1 m depth



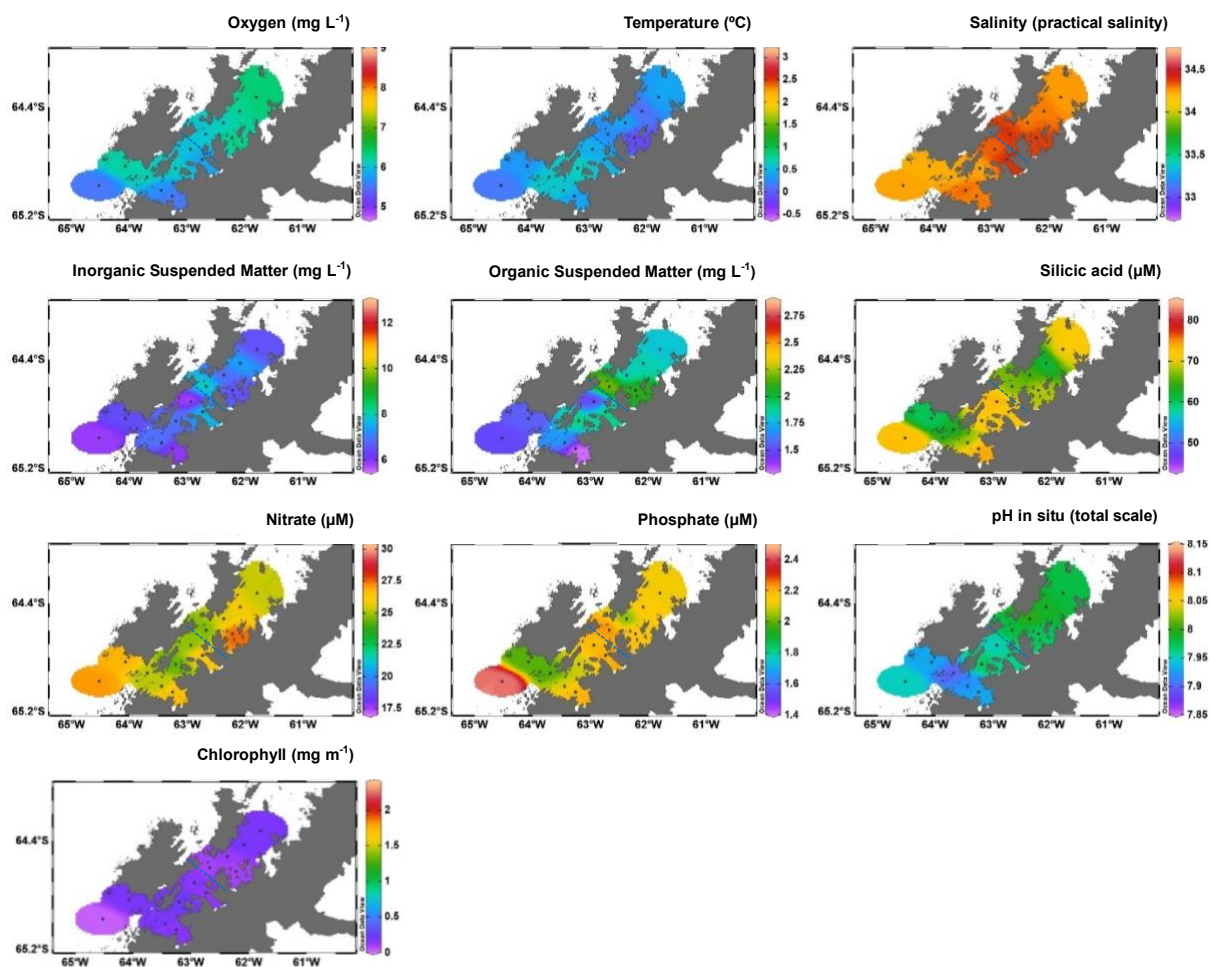
Supplementary Figure 2. Environmental variables at 1 m depth. Figures include the Surface water Thermal Front (dashed red line), situated from 1 to 100 m depth.

Environmental variables at 10 m depth



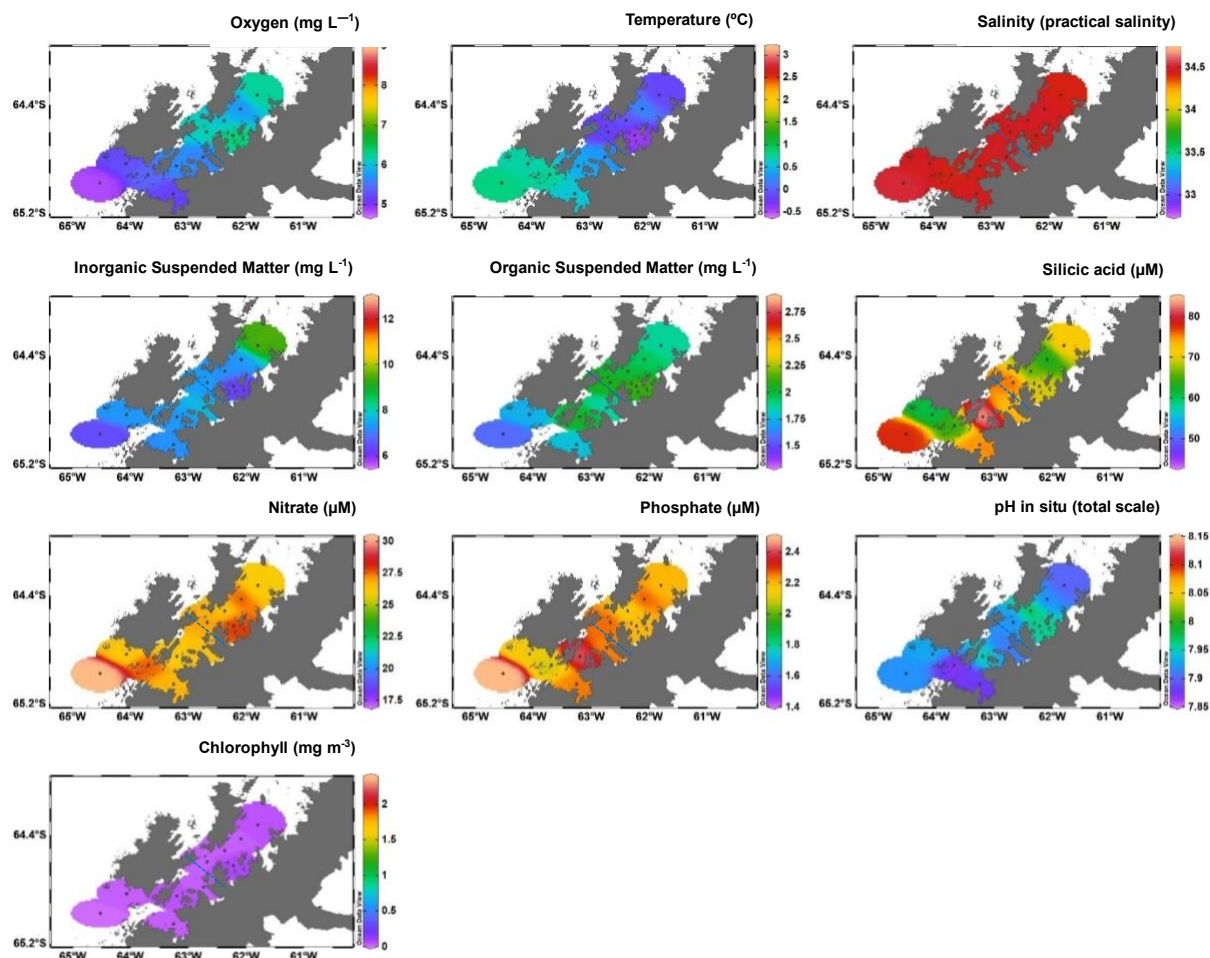
Supplementary Figure 3. Environmental variables at 10 m depth. Figures include the Surface water Thermal Front (dashed red line), situated from 1 to 100 m depth.

Environmental variables at 100 m depth



Supplementary Figure 4. Environmental variables at 100 m depth. Figures include the Sub-Pycnocline Front (the dashed blue line), situated below 100 m depth.

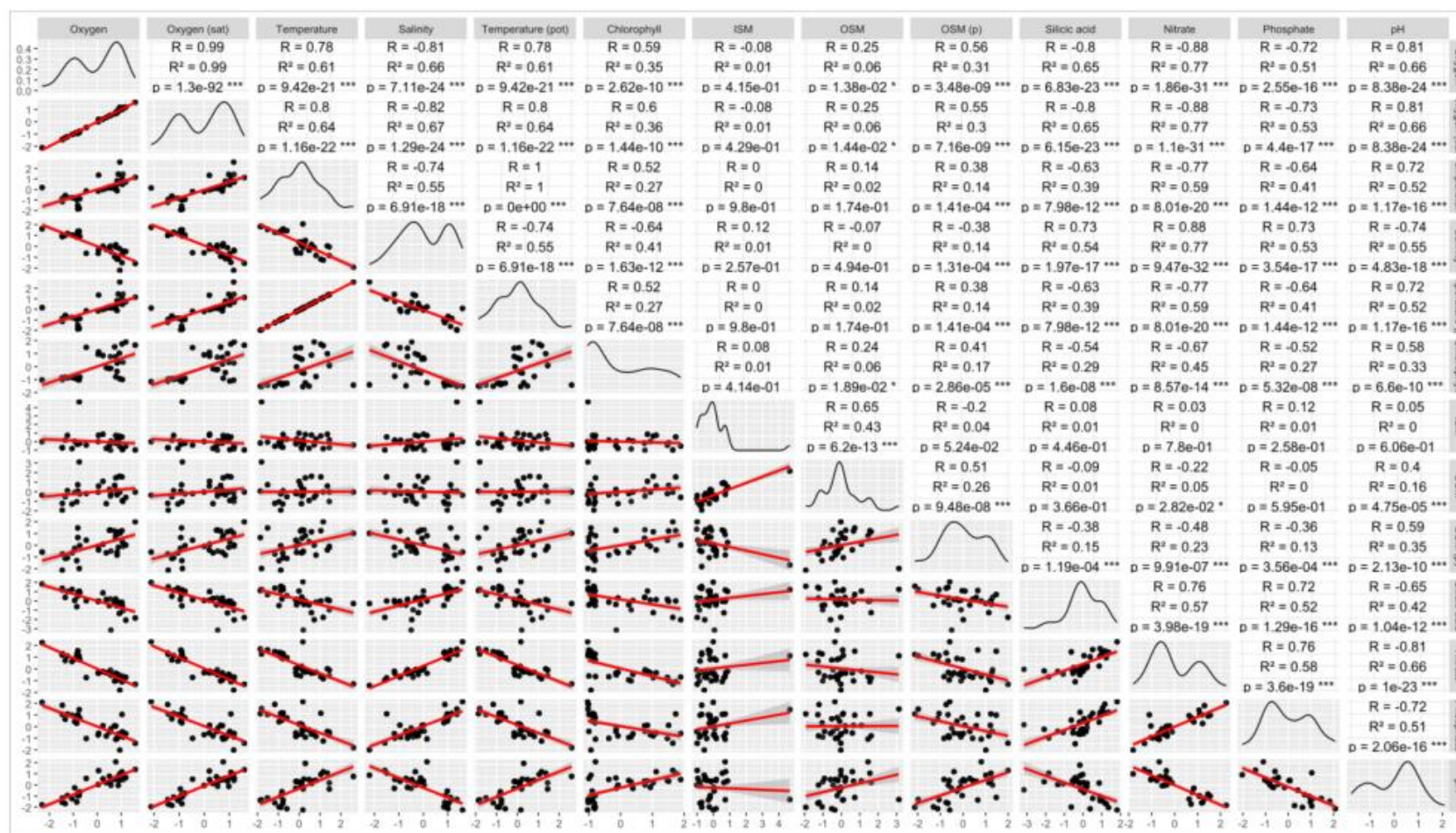
Environmental variables at 200 - 400 m depth



Supplementary Figure 5. Environmental variables at intermediate and deep depths. Figures include the sub-pycnocline front (the dashed blue line) situated below 100 m depth.

Supplementary Material

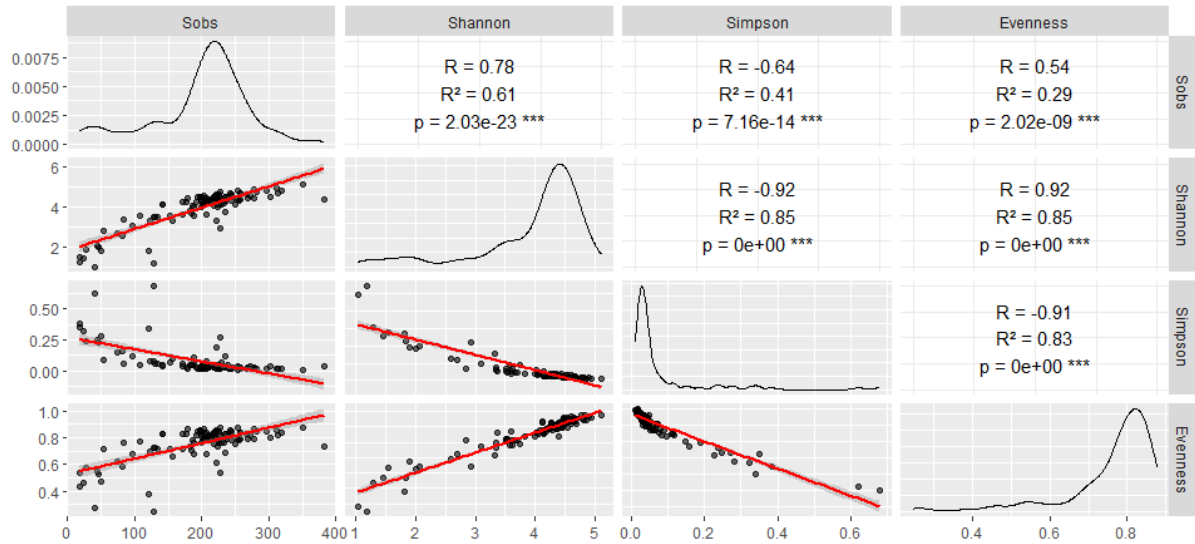
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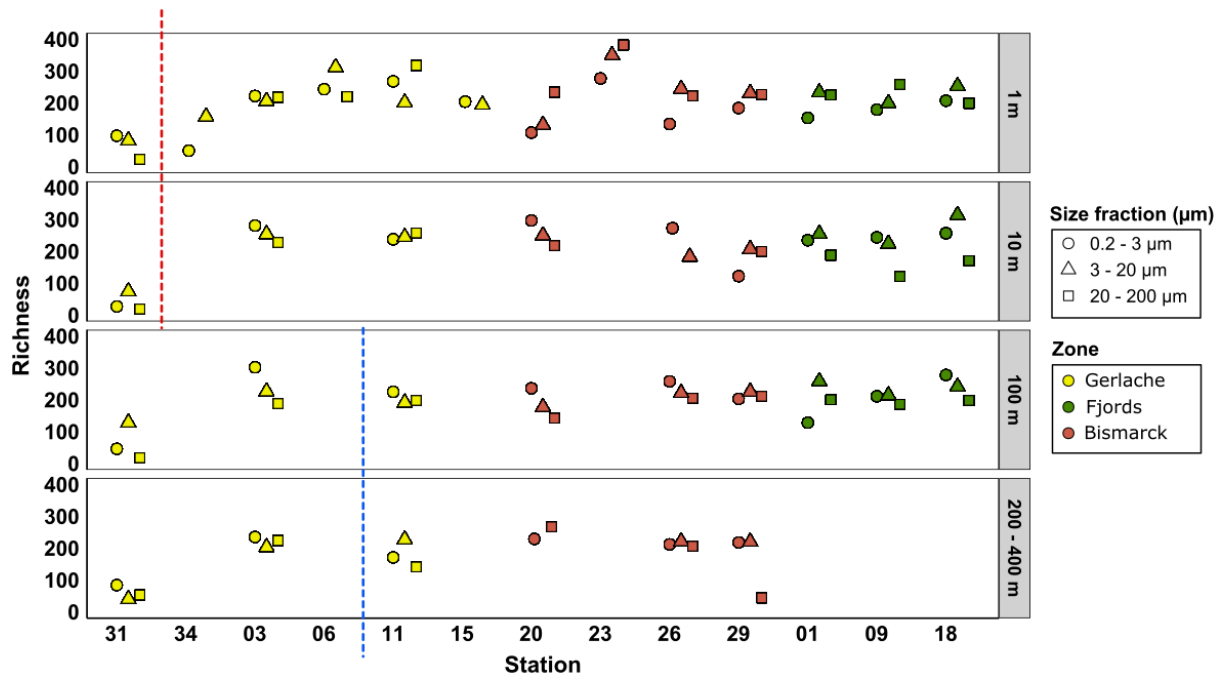
Supplementary Figure 6. Correlations (Spearman method) among the different environmental variables included in this study. Some of the environmental variables (partial pressure of CO₂, potential temperature and oxygen saturation percentage) correlated with other variables (with *in situ* pH, temperature and oxygen concentration, respectively) and were discarded for subsequent analysis (*bioenv* function).

Supplementary Material

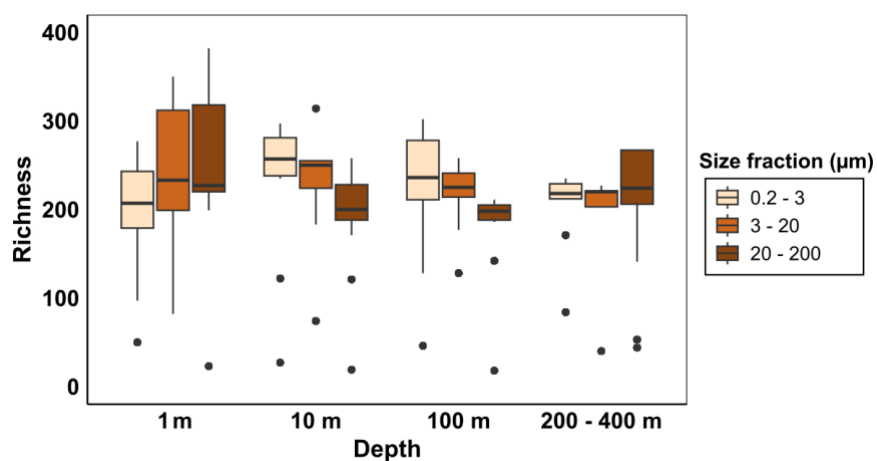
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Supplementary Figure 7. Results of the correlations (Spearman method) conducted between the different alpha diversity indices. The upper right section displays the correlation value R (coefficient of correlation), R^2 (coefficient of determination), the p-values, and the significance of the p-values (thresholds considered in this study were 0.001***, 0.01**, and 0.05*).



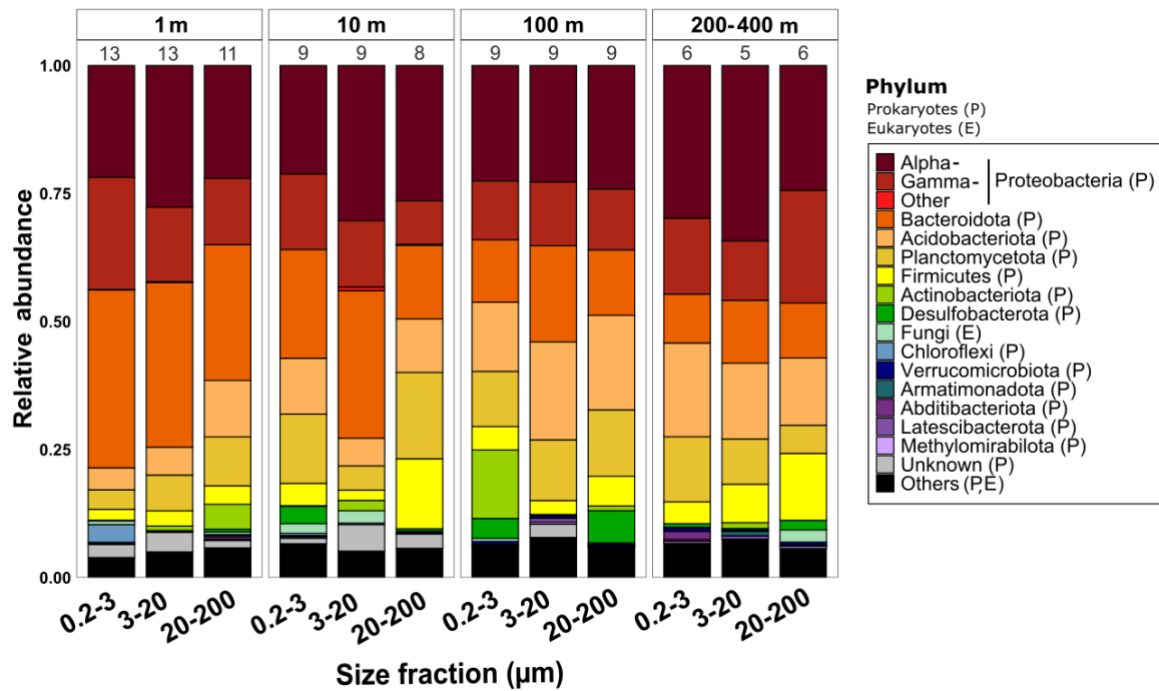
Supplementary Figure 8. Dotplot showing richness values (number of ASVs) along the Gerlache-Bismarck Strait, for each station, size fraction and depth. Stations are classified as Gerlache Strait zone (yellow), fjords (green) and Bismarck Strait zone (red). Figure includes the fronts: surface water thermal front (dashed red line) and the sub-pycnocline front (dashed blue line). A Kruskal-Wallis test revealed differences among size fractions (p -value $< 0.001^{***}$), stations (p -value $< 0.001^{***}$) and depths (p -value $< 0.001^{***}$). Samples from stations 34, 15, 20, and 26 were excluded due to insufficient sequencing depth.



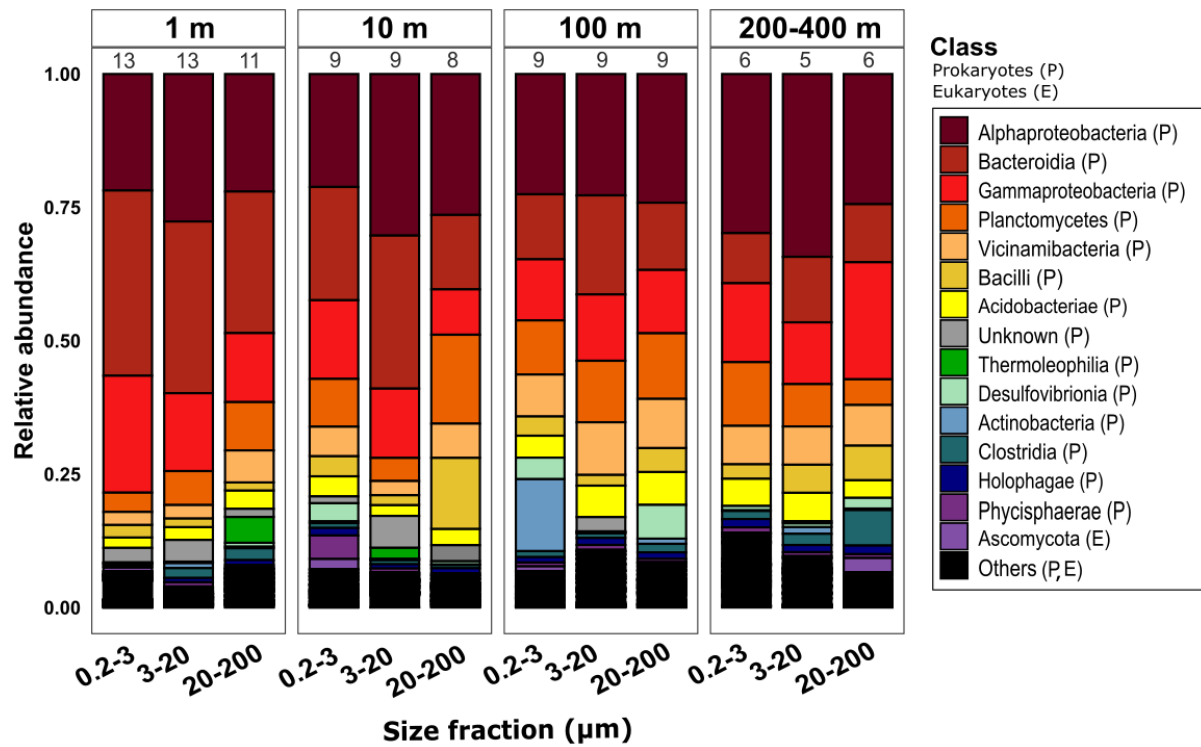
Supplementary Figure 9. Boxplot showing richness values (number of ASVs) for each size fraction and depth. The Kruskal-Wallis test revealed that richness was significantly different among size fractions and depths (p-value < 0.001).

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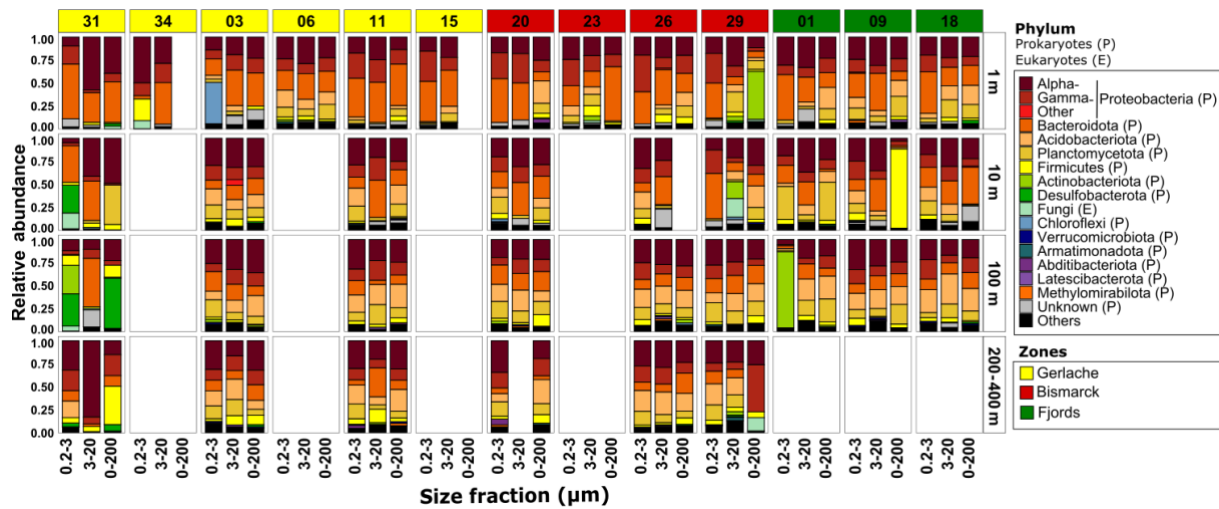
Supplementary Figure 10. Bar plot depicting the microbial community composition (represented at the Phylum level) of the Gerache-Bismarck Strait, at each depth and size-fraction. This plot includes samples from the channel, offshore and fjords. Only the 15 most abundant taxonomic groups (Prokaryotes and Eukaryotes) at the Phylum level are represented. The remaining groups were grouped together as 'Others,' along with those with an abundance of less than 1% per sample. The X-axis represents the size fractions and the Y-axis shows the relative abundance (%) grouped by depth. The number above the bars represent the N number (number of samples included in each bar).



Supplementary Figure 11. Bar plot depicting the microbial community composition (represented at the Class level) of the Gerache-Bismarck Strait, at each depth, and size fraction. This plot includes samples from the Gerlache Strait zone (yellow), Bismarck Strait zone (red) and fjords (green). Only the 15 most abundant taxonomic groups (Prokaryotes and Eukaryotes) at the Class level are represented. The remaining groups were grouped together as 'Others,' along with those with an abundance of less than 1% per sample. The X-axis represents the size fractions and the Y-axis shows the relative abundance (%) grouped by depth.

Supplementary Material

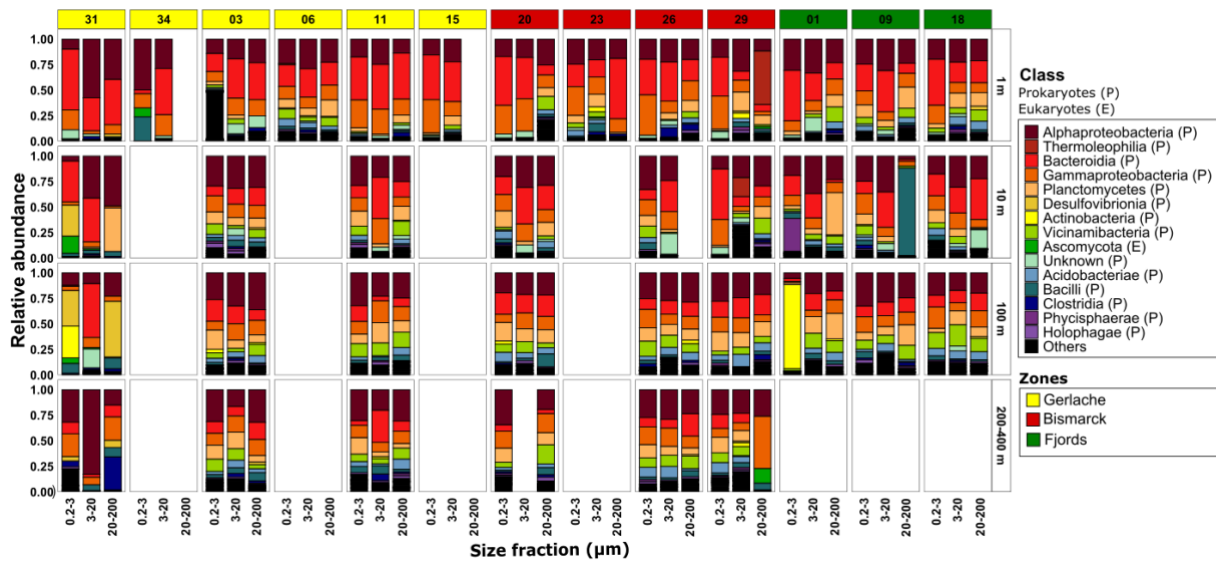
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Supplementary Figure 12. Bar plot showing the microbial community composition (represented at the Phylum level) of the Gerache-Bismarck Strait, at each station, depth, and size-fraction. This plot includes samples from the Gerlache Strait zone (yellow), Bismarck Strait zone (red) and fjords (green). Only the 15 most abundant taxonomic groups (Prokaryotes and Eukaryotes) at the Phylum level are represented. The remaining groups were grouped together as 'Others,' along with those with an abundance of less than 1% per sample. The X-axis represents the size fractions and the Y-axis shows the relative abundance (%) grouped by depth. Samples from stations 34, 15, 20, and 26 were excluded due to low sequencing depth.

Supplementary Material

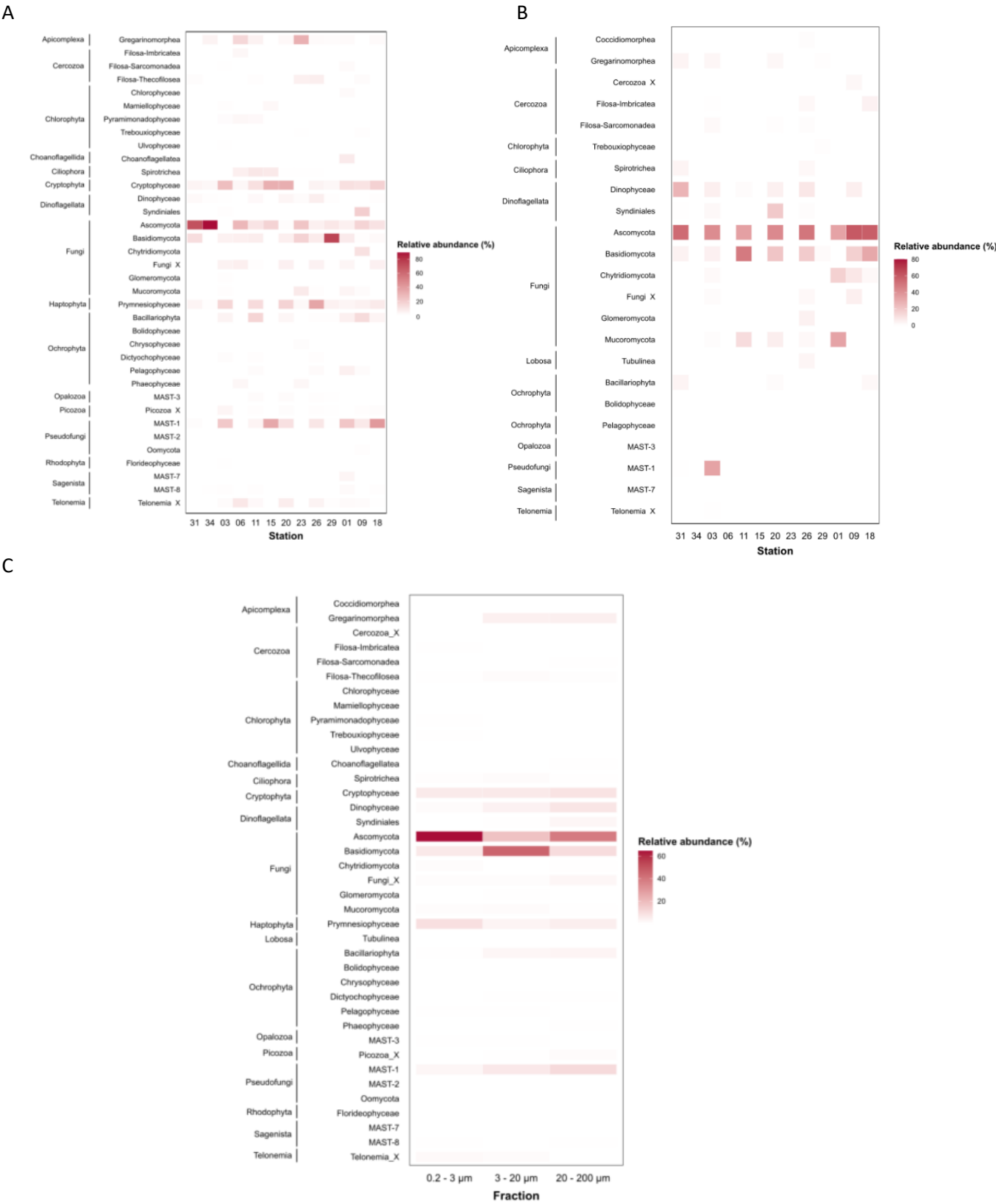
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Supplementary Figure 13. Bar plot showing the microbial community composition (represented at the Class taxonomic level) of the Gerache-Bismarck Strait, at each station, depth, and size fraction. This plot includes samples from the Gerlache Strait zone (yellow), Bismarck Strait zone (red) and fjords (green). Only the 15 most abundant taxonomic groups (Prokaryotes and Eukaryotes) at the Class level are represented. The remaining groups were grouped together as 'Others,' along with those with an abundance of less than 1% per sample. The X-axis represents the size fractions and the Y-axis shows the relative abundance (%) grouped by depth. Samples from stations 34, 15, 20, and 26 were excluded due to low sequencing depth.

Supplementary Material

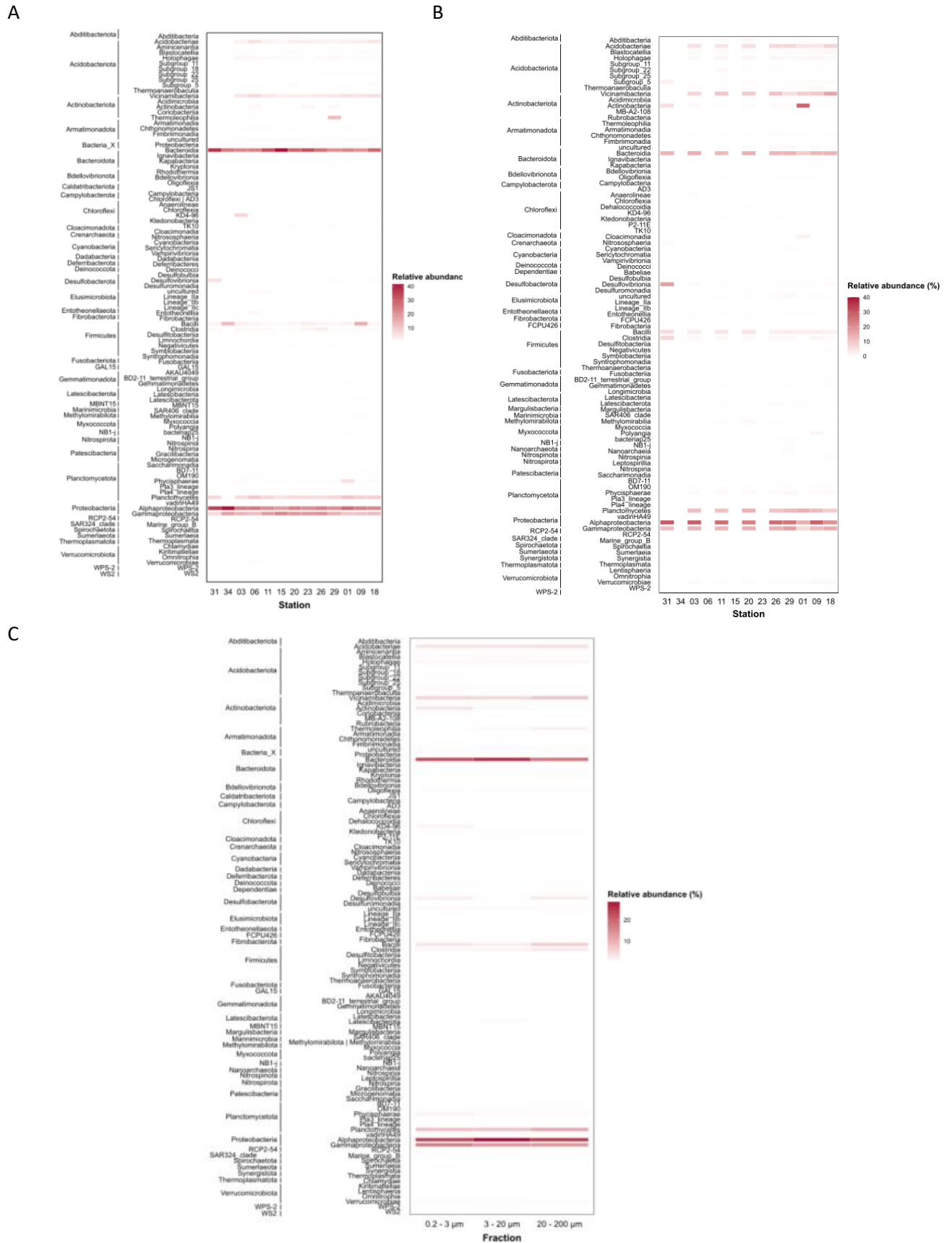
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Supplementary Figure 14. Heatmaps revealing the relative abundance of Eukaryotes (at Phylum and Class level) at (A) surface waters (from 1 to 100 m), (B) at deep waters (from 200 to 400 m) and (C) at each size fraction.

Supplementary Material

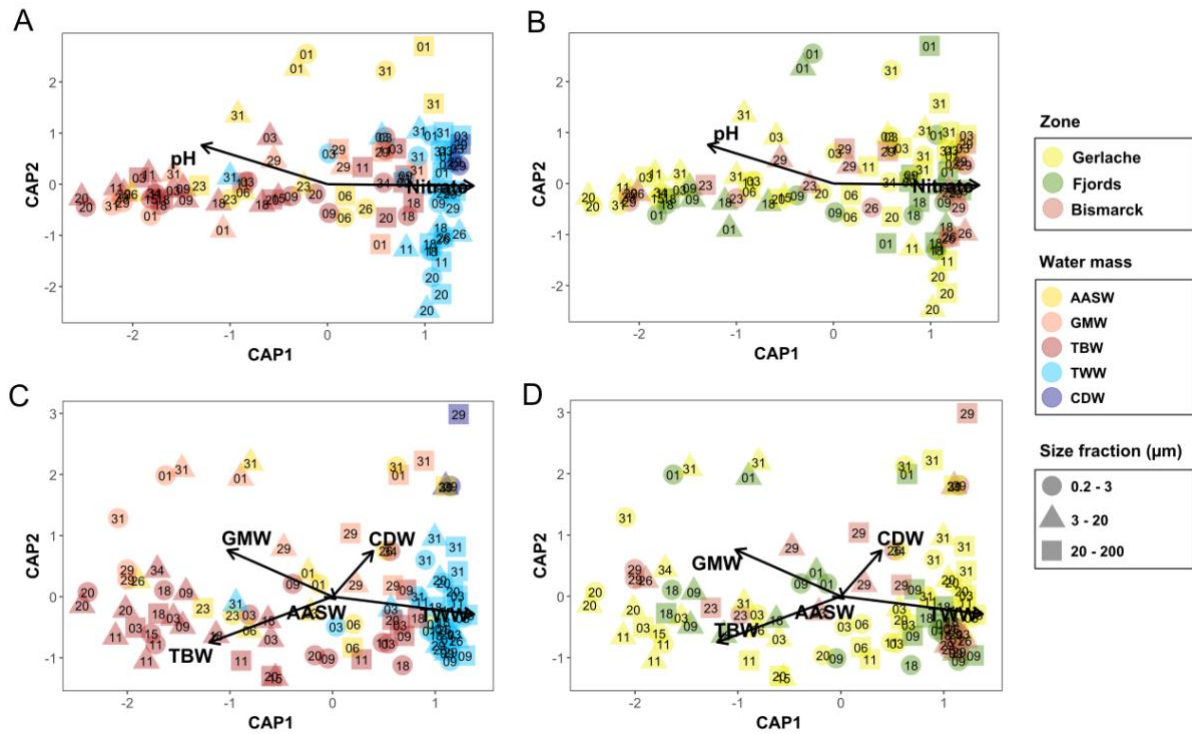
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Supplementary Figure 15. Heatmap revealing the relative abundance of Prokaryotes (at Class and Order level) at (A) surface waters (from 1 to 100 m), (B) at deep waters (from 200 to 400 m) and (C) at each size fraction.

Supplementary Material

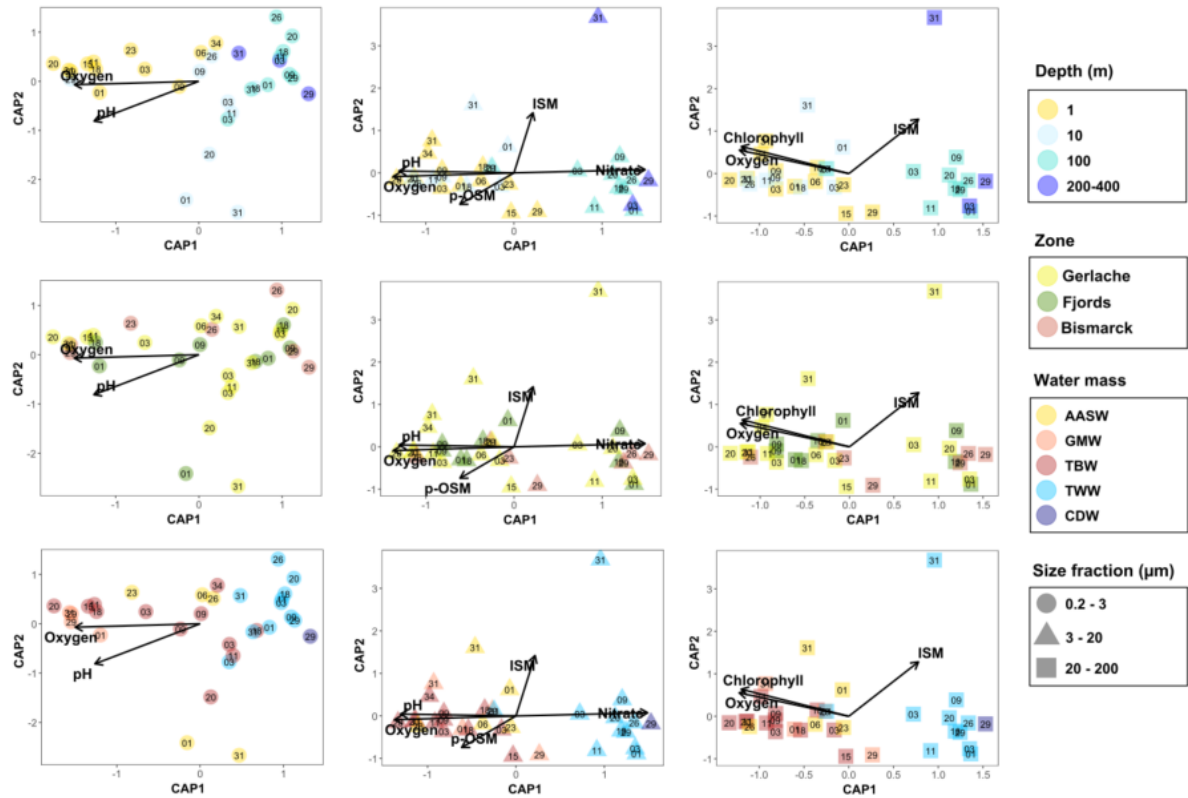
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Supplementary Figure 16. Distance-based redundancy analysis (dbRDA) showing the influence of (A, B) biogeochemical variables and (C, D) water masses on microbial community composition. Ordinations are colored by water mass (A, C) and zone (B, D). Details regarding the dbRDA ordination and the selection of variables using the *bioenv* function procedure are included in the Materials and Methods section.

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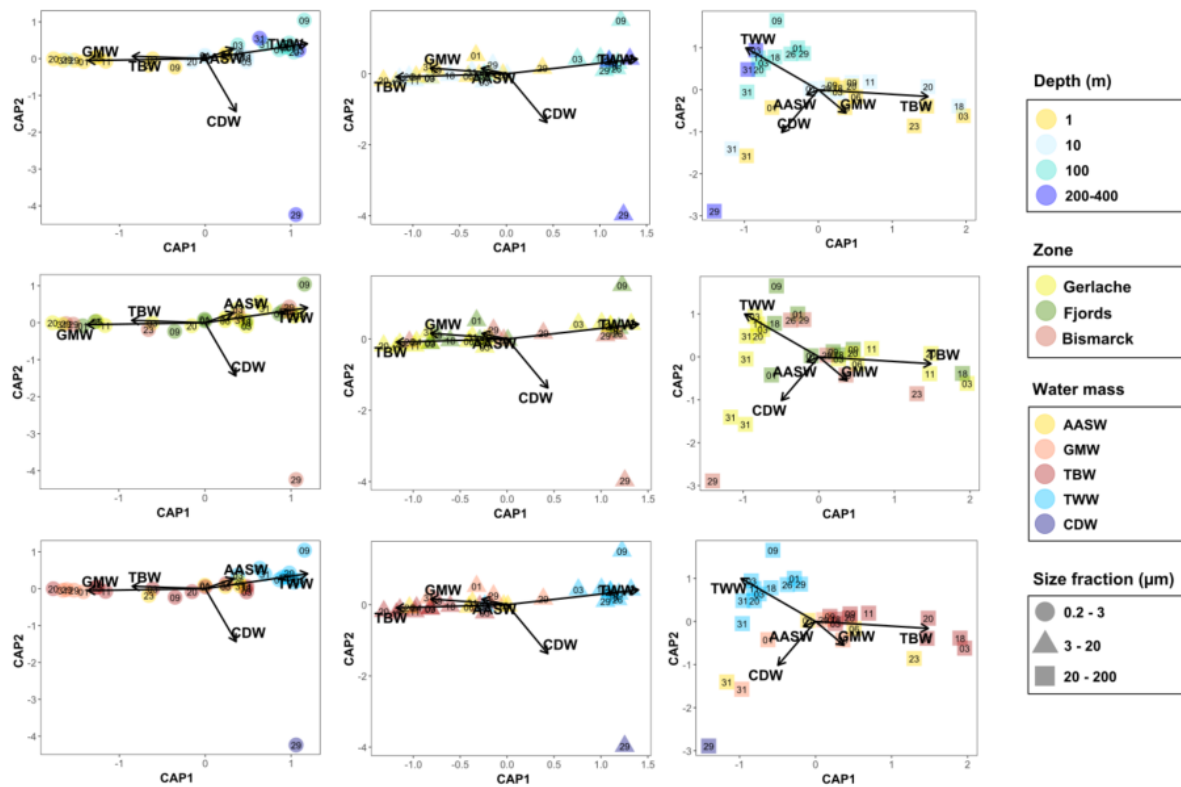
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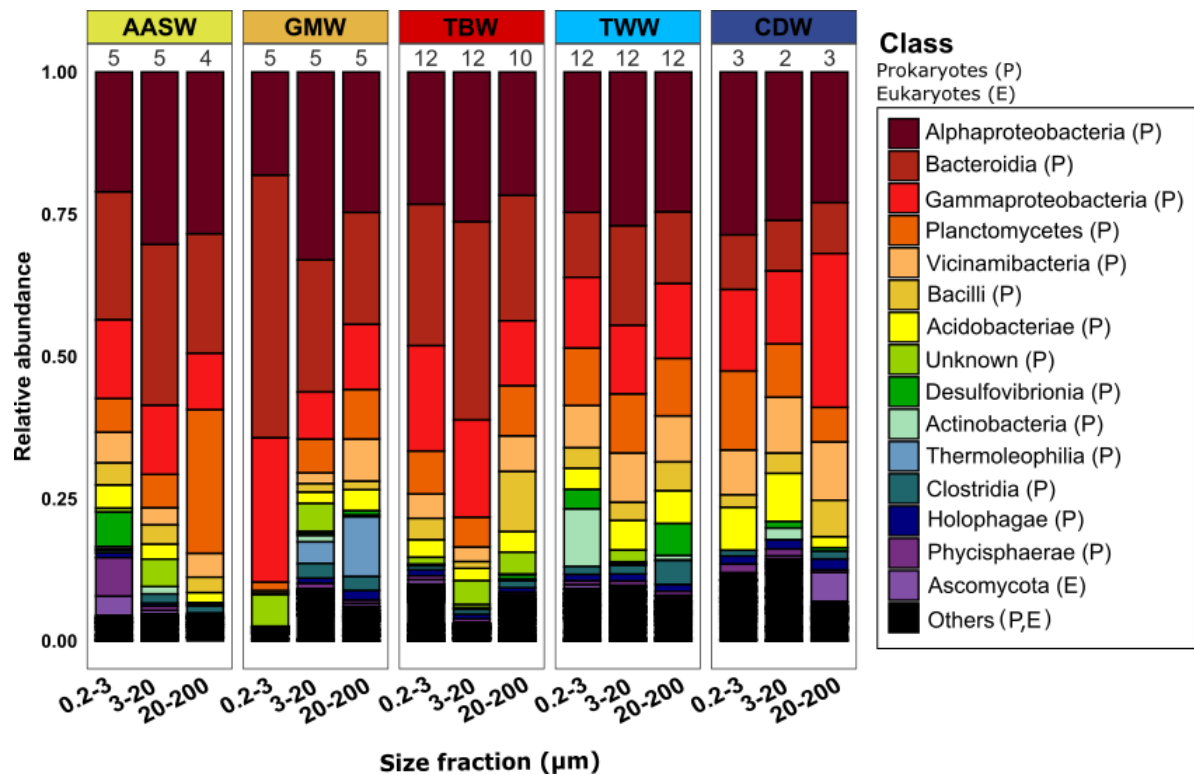
Supplementary Figure 17. Distance-based redundancy analysis (dbRDA) showing the influence of biogeochemical variables on microbial community composition, for each size-fraction. Samples are colored by depth, zone and water mass.

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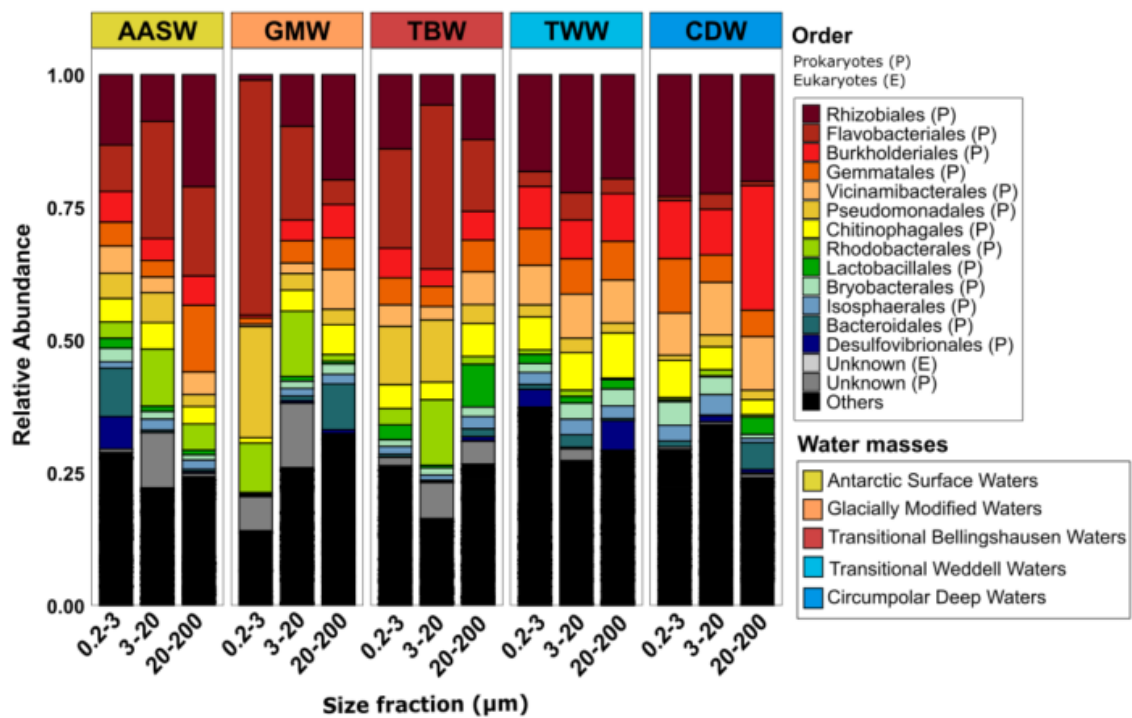
Supplementary Figure 18. Distance-based redundancy analysis (dbRDA) showing the influence of water masses on microbial community composition, for each size-fraction. Samples are colored by depth, zone and water mass.



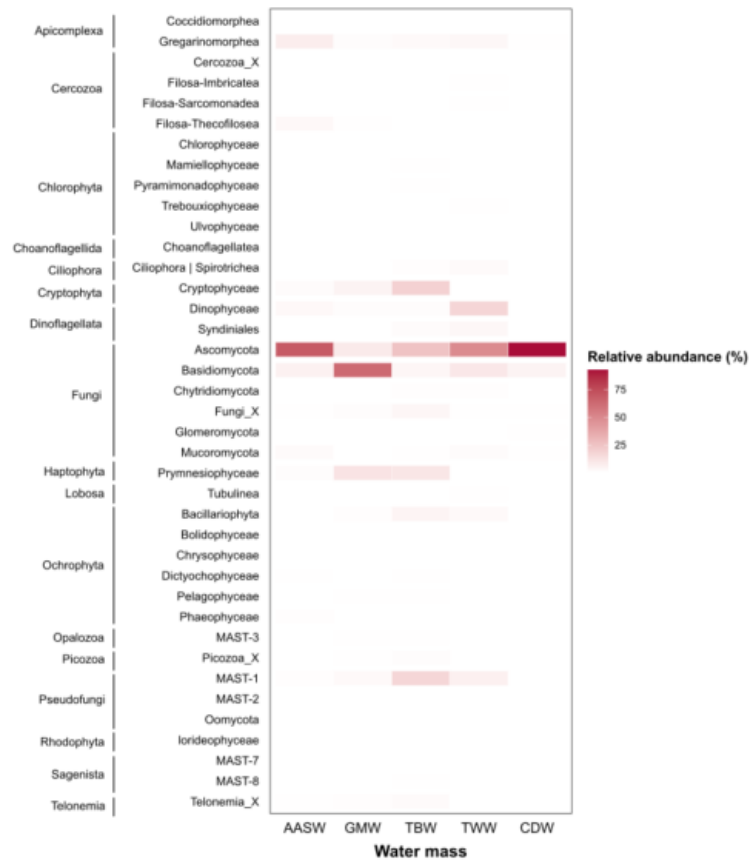
Supplementary Figure 19. Bar plot showing the microbial community composition (represented at the Class level) in each water mass, and size fraction. Only the 15 most abundant taxonomic groups (Prokaryotes and Eukaryotes) at the Class level are represented. The remaining groups were grouped together as 'Others,' along with those with an abundance of less than 1% per sample.

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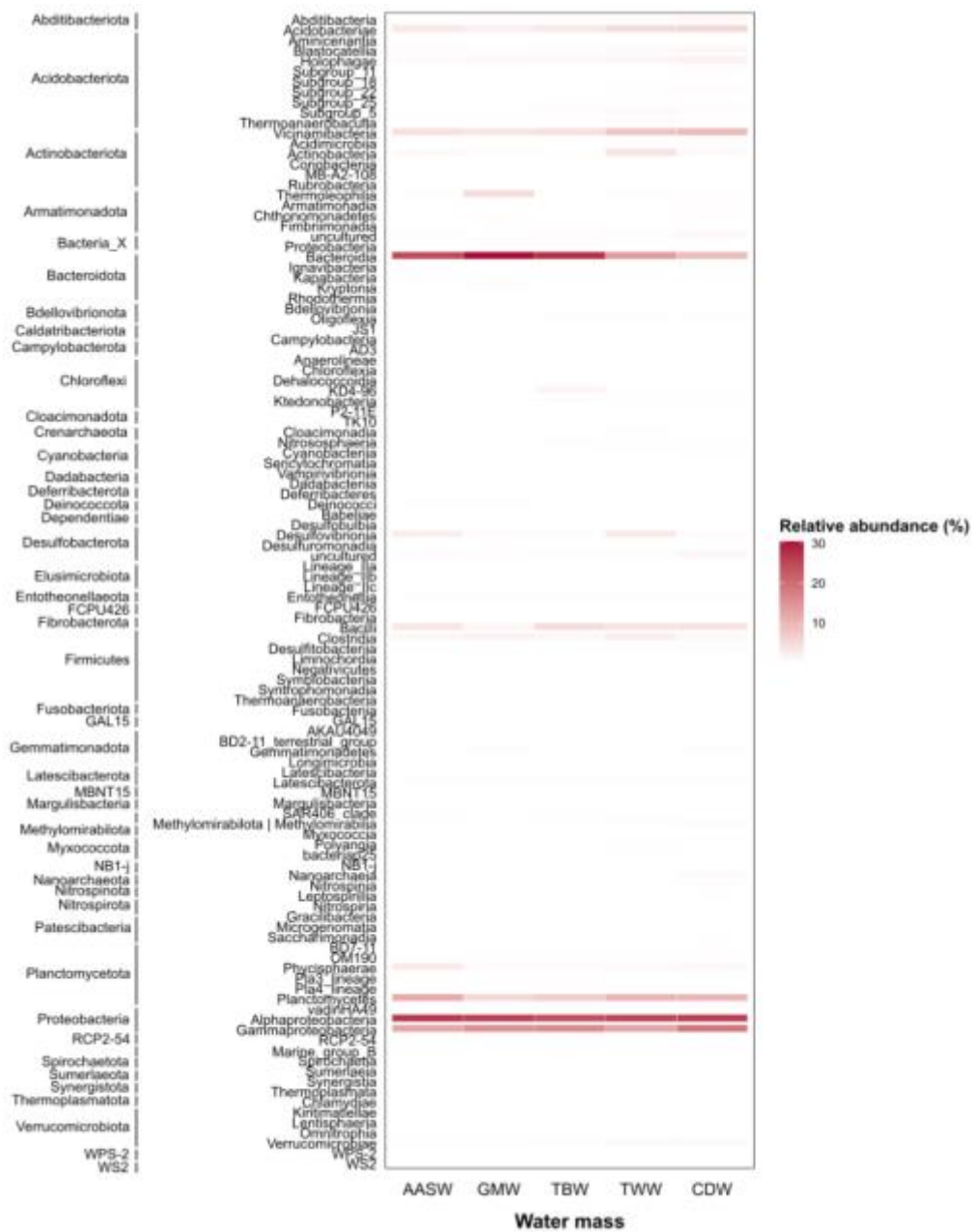
Supplementary Figure 20. Bar plot showing the microbial community composition (represented at the Order level) in each water mass, and size fraction. Only the 15 most abundant taxonomic groups (Prokaryotes and Eukaryotes) at the Order level are represented. The remaining groups were grouped together as 'Others,' along with those with an abundance of less than 1% per sample.



Supplementary Figure 21. Heatmap revealing the relative abundance of Eukaryotes (at Phylum and Class level) for each water mass.

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Supplementary Figure 22. Heatmap revealing the relative abundance of Prokaryotes (at Class and Order level) for each water mass.

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Supplementary Table 4. List of indicator microorganisms for each water mass.

Water mass	ASV	Rel. Abundance (%)	Phylum, Class, Order, Family, Genus, Species
AASW	PROK_00996	0.3032741	Bacteroidota, Bacteroidia, Flavobacteriales, Flavobacteriaceae, NS4 marine group, Unknown
AASW	PROK_00089	1.138694	Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, <i>Ascidiaeihabitans</i> , Unknown
AASW	EUK_0021	0.280528	Cercozoa, Filosa-Thecofilosea, Cryomonadida, Cryothecomonas-lineage, <i>Cryothecomonas</i> , <i>Cryothecomonas aestivalis</i>
AASW	PROK_09764	0.08661222	Planctomycetota, Planctomycetes, Isosphaerales, Isosphaeraceae, Uncultured, Unknown
AASW	PROK_02031	0.2228458	Proteobacteria, Alphaproteobacteria, Rhizobiales, Xanthobacteraceae, <i>Bradyrhizobium</i> , Unknown
AASW	PROK_08135	0.06187353	Firmicutes, Clostridia, Oscillospirales, Oscillospiraceae, <i>Colidextribacter</i> , Unknown
AASW	PROK_09207	0.06191184	Proteobacteria, Alphaproteobacteria, Tistrellales, Geminicoccaceae, Candidatus Alysiosphaera, Unknown
AASW	PROK_08149	0.07430341	Acidobacteriota, Acidobacteriae, Bryobacterales, Bryobacteraceae, <i>Bryobacter</i> , Unknown
AASW	PROK_06091	0.0989854	Firmicutes, Clostridia, Lachnospirales, Lachnospiraceae, Oribacterium, Uncultured organism
AASW	EUK_0048	1.138614	Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes, Aspergillus, Unknown
AASW	PROK_03214	0.09907121	Bacteroidota, Bacteroidia, Chitinophagales, Uncultured, Uncultured, bacterium episymbiont
AASW	PROK_01171	0.1815781	Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, <i>Octadecabacter</i> , Uncultured bacterium
AASW	PROK_03613	0.1155402	Proteobacteria, Alphaproteobacteria, Rhizobiales, Xanthobacteraceae, <i>Rhodoplanes</i> , metagenome
AASW	PROK_02019	0.03712412	Fusobacteriota, Fusobacteriia, Fusobacteriales, Fusobacteriaceae, <i>Fusobacterium</i> , Unknown
AASW	PROK_04801	0.1855976	Acidobacteriota, Acidobacteriae, Acidobacteriales, Uncultured, Uncultured, Unknown
AASW	PROK_00518	0.4083653	Bacteroidota, Bacteroidia, Flavobacteriales, Flavobacteriaceae, <i>Polaribacter</i> , Unknown
AASW	PROK_03718	0.5325077	Bacteroidota, Bacteroidia, Chitinophagales, Chitinophagaceae, <i>Flaviaesturariibacter</i> , Uncultured bacterium
AASW	PROK_07543	0.1238237	Proteobacteria, Gammaproteobacteria, Burkholderiales, Burkholderiaceae, <i>Lautropia</i> , Uncultured bacterium
AASW	PROK_02729	0.3838534	Armatimonadota, Uncultured, Uncultured, Uncultured, Uncultured, Unknown
AASW	PROK_04507	0.08662294	Bacteroidota, Bacteroidia, Chitinophagales, Saprospiraceae, Uncultured, Uncultured marine
AASW	PROK_06672	0.08661222	Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiales Incertae Sedis, <i>Nordella</i> , Uncultured bacterium

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AASW	PROK_07515	0.08667657	Rhodobacterales, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhodobacteraceae, <i>Yoonia-Loktanelia</i> , Uncultured bacterium
AASW	PROK_04170	0.3219814	Planctomycetota, Planctomycetes, Gemmatales, Gemmataceae, Gemmata, Uncultured bacterium
AASW	PROK_03363	0.0495356	Verrucomicrobiota, Verrucomicrobiae, Verrucomicrobiales, Rubritaleaceae, <i>Rubritalea</i> , Uncultured bacterium
AASW	PROK_05647	0.06186587	Proteobacteria, Alphaproteobacteria, Elsterales, Uncultured, Uncultured, Uncultured bacterium
AASW	PROK_02139	0.06187353	Bacteroidota, Bacteroidia, Flavobacteriales, NS9 marine group, NS9 marine group, Uncultured Flavobacterium
AASW	PROK_01053	0.978207	Bacteroidota, Bacteroidia, Chitinophagales, Chitinophagaceae, Uncultured, Unknown
CDW	PROK_05932	0.04950904	Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, <i>Sphingomonas</i> , Unknown
CDW	PROK_03369	0.1649893	Proteobacteria, Gammaproteobacteria, Burkholderiales, Oxalobacteraceae, <i>Massilia</i> , Unknown
CDW	PROK_06577	0.1113724	Thermoplasmatota, Thermoplasmata, Marine Group II, Marine Group II, Marine Group II, unidentified archaeon
CDW	PROK_01387	0.08664439	Proteobacteria, Gammaproteobacteria, Enterobacterales, Erwiniaceae, Unknown, Unknown
CDW	PROK_04212	0.123793	Proteobacteria, Gammaproteobacteria, Burkholderiales, Oxalobacteraceae, <i>Massilia</i> , Unknown
CDW	PROK_09655	0.03712871	Planctomycetota, Planctomycetes, Isosphaerales, Isosphaeraceae, Uncultured, Uncultured bacterium
CDW	PROK_00551	3.069687	Planctomycetota, Planctomycetes, Gemmatales, Gemmataceae, Uncultured, Uncultured bacterium
CDW	PROK_00195	0.3217623	Firmicutes, Negativicutes, Veillonellales-Selenomonadales, Veillonellaceae, <i>Veillonella</i> , Unknown
CDW	PROK_03028	0.3835684	Planctomycetota, Planctomycetes, Isosphaerales, Isosphaeraceae, Unknown, Unknown
CDW	PROK_01874	0.3835684	Acidobacteriota, Blastocatellia, 11-24, 11-24, 11-24, Uncultured Acidobacteriales
CDW	PROK_01047	1.138473	Bacteroidota, Bacteroidia, Chitinophagales, Chitinophagaceae, Uncultured, Unknown
CDW	PROK_03266	0.2723446	Proteobacteria, Alphaproteobacteria, Rhizobiales, Beijerinckiaceae, Unknown, Unknown
CDW	PROK_01375	0.3547855	Proteobacteria, Gammaproteobacteria, Burkholderiales, Oxalobacteraceae, <i>Massilia</i> , Unknown
CDW	PROK_00647	1.83123	Bacteroidota, Bacteroidia, Chitinophagales, Chitinophagaceae, <i>Flavisolibacter</i> , Unknown
CDW	PROK_00554	1.535033	Acidobacteriota, Vicinamibacteria, Vicinamibacteriales, Uncultured, Uncultured, Uncultured Acidobacteria
CDW	EUK_0032	0.2478622	Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes, Unknown, Unknown
CDW	PROK_02085	0.6557783	Proteobacteria, Gammaproteobacteria, Gammaproteobacteria Incertae Sedis, Unknown Family, <i>Acidibacter</i> , Uncultured Steroidobact
CDW	PROK_02447	0.3341998	Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Unknown

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CDW	PROK_00598	0.9530883	Acidobacteriota, Vicinamibacteria, Vicinamibacterales, Vicinamibacteraceae, Vicinamibacteraceae, Unknown
CDW	PROK_00489	0.8086476	Acidobacteriota, Holophagae, Subgroup 7, Subgroup 7, Subgroup 7, Unknown
CDW	PROK_03425	0.1484965	Proteobacteria, Alphaproteobacteria, Rhizobiales, Xanthobacteraceae, Unknown, Unknown
CDW	PROK_08312	0.06188885	Planctomycetota, Phycisphaerae, Tepidisphaerales, WD2101 soil group, WD2101 soil group, Uncultured soil
CDW	PROK_01550	0.2804586	Acidobacteriota, Holophagae, Subgroup 7, Subgroup 7, Subgroup 7, Unknown
CDW	PROK_03935	0.1856665	Proteobacteria, Alphaproteobacteria, Rhizobiales, Beijerinckiaceae, Unknown, Unknown
CDW	PROK_06113	0.1237777	Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, <i>Sphingomonas</i> , Unknown
CDW	PROK_01786	0.494927	Planctomycetota, Planctomycetes, Isosphaerales, Isosphaeraceae, <i>Aquisphaera</i> , Unknown
CDW	EUK_0052	0.7065824	Fungi, Ascomycota, Saccharomycotina, Saccharomycetales, <i>Debaryomyces</i> , Unknown
CDW	PROK_02670	0.1979953	Proteobacteria, Alphaproteobacteria, Rhizobiales, Beijerinckiaceae, <i>Microvirga</i> , Unknown
CDW	PROK_01323	1.683168	Acidobacteriota, Vicinamibacteria, Vicinamibacterales, Vicinamibacteraceae, Vicinamibacteraceae, Unknown
CDW	PROK_00060	43.9315	Proteobacteria, Gammaproteobacteria, Burkholderiales, Oxalobacteraceae, <i>Massilia</i> , Unknown
CDW	PROK_02255	0.3960396	Proteobacteria, Gammaproteobacteria, Burkholderiales, Alcaligenaceae, <i>Alcaligenes</i> , Unknown
CDW	PROK_03375	0.3960396	Thermoplasmata, Thermoplasmata, Marine Group II, Marine Group II, Marine Group II, unidentified archaeon
CDW	EUK_0126	0.3219416	Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes, Unknown, Unknown
CDW	PROK_00786	3.217822	Armatimonadota, Uncultured, Uncultured, Uncultured, Uncultured, Uncultured Firmicutes
CDW	PROK_06615	0.2474635	Proteobacteria, Alphaproteobacteria, Rhizobiales, Beijerinckiaceae, Methylobacterium-Methylorubrum, Unknown
CDW	PROK_06835	0.1981179	Planctomycetota, Planctomycetes, Isosphaerales, Isosphaeraceae, Uncultured, Uncultured bacterium
CDW	PROK_03697	0.3219416	Proteobacteria, Gammaproteobacteria, Gammaproteobacteria Incertae Sedis, Unknown Family, Candidatus Berkiella, Unknown
CDW	PROK_03786	0.1485149	Proteobacteria, Alphaproteobacteria, Rhizobiales, Xanthobacteraceae, Uncultured, Unknown
CDW	PROK_07457	0.1484781	Proteobacteria, Alphaproteobacteria, Rhizobiales, Beijerinckiaceae, <i>Psychroglaciecola</i> , Unknown
CDW	PROK_06560	0.3711952	Proteobacteria, Alphaproteobacteria, Elsteriales, Uncultured, Uncultured, Unknown
CDW	PROK_03167	0.8415842	Proteobacteria, Gammaproteobacteria, Burkholderiales, SC-I-84, SC-I-84, Uncultured beta
CDW	PROK_02467	0.6438831	Acidobacteriota, Thermoanaerobaculia, Thermoanaerobaculales, Thermoanaerobaculaceae, Subgroup 10, Acidobacteria bacterium

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CDW	PROK_00790	2.377415	Acidobacteriota, Vicinamibacteria, Vicinamibacteriales, Uncultured, Uncultured, Unknown
CDW	PROK_02328	0.9156149	Acidobacteriota, Acidobacteriae, Acidobacteriales, Uncultured, Uncultured, Uncultured Acidobacteriaceae
CDW	PROK_02396	0.1732244	Firmicutes, Bacilli, Lactobacillales, Lactobacillaceae, Levilactobacillus, Unknown
CDW	PROK_03041	0.3467063	Acidobacteriota, Acidobacteriae, Solibacteriales, Solibacteraceae, Candidatus Solibacter, Unknown
CDW	PROK_05910	0.2969562	Proteobacteria, Gammaproteobacteria, Burkholderiales, Nitrosomonadaceae, <i>Nitrosospira</i> , Unknown
CDW	PROK_01527	1.287129	Methylomirabilota, Methylomirabilia, Rokubacteriales, Rokubacteriales, Rokubacteriales, Uncultured bacterium
CDW	PROK_04067	0.2228826	Proteobacteria, Alphaproteobacteria, Rhizobiales, Beijerinckiaceae, <i>Microvirga</i> , Unknown
CDW	PROK_05421	0.2722098	Crenarchaeota, Nitrososphaeria, Nitrosopumilales, Nitrosopumilaceae, Nitrosopumilaceae, Unknown
CDW	PROK_06482	0.2722098	Chloroflexi, Anaerolineae, Anaerolineales, Anaerolineaceae, UTCFX1, Unknown
CDW	PROK_03014	0.4210005	Planctomycetota, Planctomycetes, Gemmatales, Gemmataceae, Uncultured, Uncultured bacterium
CDW	PROK_07778	0.1732244	Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, <i>Sphingomonas</i> , Unknown
CDW	PROK_04965	0.2475248	Planctomycetota, Planctomycetes, Planctomycetales, Rubinisphaeraceae, SH-PL14, Unknown
CDW	PROK_00856	1.088839	Acidobacteriota, Acidobacteriae, Bryobacteriales, Bryobacteraceae, Bryobacter, Unknown
CDW	PROK_07784	0.2227723	Methylomirabilota, Methylomirabilia, Rokubacteriales, Rokubacteriales, Rokubacteriales, Uncultured bacterium
CDW	PROK_01520	1.658005	Planctomycetota, Planctomycetes, Gemmatales, Gemmataceae, Gemmata, Uncultured bacterium
CDW	PROK_03211	0.569166	Proteobacteria, Gammaproteobacteria, Burkholderiales, SC-I-84, SC-I-84, Unknown
CDW	PROK_01980	0.6930693	Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, <i>Pseudomonas</i> , Unknown
CDW	PROK_01076	0.07423905	Firmicutes, Bacilli, Lactobacillales, Lactobacillaceae, Leuconostoc, Unknown
CDW	PROK_03212	0.3474808	Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, <i>Sphingomonas</i> , Unknown
CDW	PROK_00344	0.7446016	Proteobacteria, Gammaproteobacteria, Enterobacteriales, Alteromonadaceae, <i>Alishewanella</i> , Unknown
CDW	PROK_07211	0.1237624	Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, <i>Sphingomonas</i> , Unknown
GMW	EUK_0010	0.2878188	Haptophyta, Prymnesiophyceae, Prymnesiales, Chrysochromulinaceae, <i>Chrysochromulina</i> , <i>Chrysochromulina simplex</i>
GMW	PROK_00122	0.5299768	Bacteroidota, Bacteroidia, Flavobacteriales, Crocinitomicaceae, Crocinitomix, Uncultured Crocinitomix
GMW	PROK_01668	0.07423905	Firmicutes, Clostridia, Oscillospirales, Ruminococcaceae, Faecalibacterium, Unknown

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GMW	PROK_04471	0.5196733	Proteobacteria, Gammaproteobacteria, Beggiatoales, Beggiatoaceae, Uncultured, Uncultured bacterium
GMW	PROK_10101	0.06187353	Proteobacteria, Alphaproteobacteria, Rhizobiales, Xanthobacteraceae, Uncultured, Uncultured forest
GMW	PROK_11095	0.06187353	Bacteroidota, Bacteroidia, Cytophagales, Microscillaceae, Uncultured, Uncultured soil
GMW	PROK_07200	0.1113586	Proteobacteria, Alphaproteobacteria, Acetobacterales, Acetobacteraceae, Uncultured, Unknown
GMW	PROK_11193	0.0989854	Verrucomicrobiota, Verrucomicrobiae, Chthoniobacteriales, Chthoniobacteraceae, Candidatus Udaeobacter, Unknown
GMW	PROK_00694	0.3340757	Firmicutes, Clostridia, Peptostreptococcales-Tissierellales, Peptostreptococcaceae, <i>Peptostreptococcus</i> , Uncultured bacterium
GMW	PROK_08860	0.07425743	Actinobacteriota, Actinobacteria, Corynebacteriales, Mycobacteriaceae, <i>Mycobacterium</i> , Unknown
GMW	PROK_02165	0.7671368	Acidobacteriota, Vicinamibacteria, Vicinamibacteriales, Uncultured, Uncultured, Unknown
GMW	PROK_03897	0.210396	Acidobacteriota, Blastocatellia, 11-24, 11-24, 11-24, Uncultured Acidobacteria
TBW	PROK_00456	0.286005	Bacteroidota, Bacteroidia, Flavobacteriales, Cryomorphaceae, Uncultured, Uncultured bacterium
TBW	PROK_00103	0.4795891	Bacteroidota, Bacteroidia, Flavobacteriales, NS9 marine group, NS9 marine group, Uncultured Flavobacteriia
TBW	PROK_00110	1.078588	Bacteroidota, Bacteroidia, Flavobacteriales, Cryomorphaceae, NS10 marine group, Uncultured Flavobacteriia
TBW	PROK_00085	1.463046	Bacteroidota, Bacteroidia, Flavobacteriales, NS7 marine group, NS7 marine group, Uncultured bacterium
TBW	PROK_02457	0.06049274	Proteobacteria, Alphaproteobacteria, Parvibaculales, OCS116 clade, OCS116 clade, Unknown
TBW	PROK_00062	0.903456	Bacteroidota, Bacteroidia, Flavobacteriales, Flavobacteriaceae, NS2b marine group, Unknown
TBW	PROK_00649	0.1287224	Proteobacteria, Gammaproteobacteria, Burkholderiales, Methylophilaceae, OM43 clade, Unknown
TBW	PROK_00316	0.6236183	Bacteroidota, Bacteroidia, Flavobacteriales, Cryomorphaceae, NS10 marine group, Uncultured Bacteroidetes/Chlorobi
TBW	PROK_03146	0.08248783	Unknown, Unknown, Unknown, Unknown, Unknown, Unknown
TBW	PROK_00036	0.938887	Proteobacteria, Gammaproteobacteria, Pseudomonadales, Thioglobaceae, SUP05 cluster, Uncultured marine
TBW	PROK_06319	0.05939124	Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Uncultured, Unknown
TBW	PROK_00232	0.2009114	Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudohongiellaceae, <i>Pseudohongiella</i> , Unknown
TBW	EUK_0014	0.3972969	Cryptophyta, Cryptophyceae, Cryptomonadales, Cryptomonadales X, <i>Geminigera</i> , <i>Geminigera cryophila</i>
TBW	PROK_01050	0.115483	Marinimicrobia (SAR406 clade), Marinimicrobia (SAR406 clade), Marinimicrobia (SAR406 clade), Marinimicrobia (SAR406 clade), Uncultured marine
TWW	PROK_01014	0.4269142	Proteobacteria, Gammaproteobacteria, Burkholderiales, Nitrosomonadaceae, Ellin6067, Unknown

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TWW	PROK_02182	0.1773488	Proteobacteria, Gammaproteobacteria, Burkholderiales, Oxalobacteraceae, <i>Massilia</i> , <i>Duganella</i> sp.
TWW	PROK_01064	0.1273345	Proteobacteria, Gammaproteobacteria, Xanthomonadales, Rhodanobacteraceae, <i>Rhodanobacter</i> , <i>Rhodanobacter</i> sp.

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Supplementary Table 5. List of the core microbes of each water mass.

Water Mass	ASVs	Rel. Abundance (%)	Phylum, Class, Order, Family, Genus, Species
CDW	PROK_00001	17.01	Proteobacteria, Alphaproteobacteria, Rhizobiales, Beijerinckiaceae, <i>Methylobacterium-Methylorubrum</i> , Unknown
CDW	PROK_00011	0.92	Firmicutes, Bacilli, Staphylococcales, Staphylococcaceae, <i>Staphylococcus</i> , Unknown
CDW	PROK_00046	0.26	Proteobacteria, Gammaproteobacteria, Enterobacterales, Enterobacteriaceae, <i>Escherichia-Shigella</i> , Unknown
CDW	PROK_00094	1.24	Proteobacteria, Gammaproteobacteria, Burkholderiales, Oxalobacteraceae, <i>Massilia</i> , Unknown
CDW	PROK_00156	0.58	Proteobacteria, Gammaproteobacteria, Burkholderiales, Oxalobacteraceae, <i>Massilia</i> , Unknown
CDW	PROK_00173	0.41	Proteobacteria, Gammaproteobacteria, Burkholderiales, Oxalobacteraceae, <i>Massilia</i> , Unknown
TWW	PROK_00001	15.28	Proteobacteria, Alphaproteobacteria, Rhizobiales, Beijerinckiaceae, <i>Methylobacterium-Methylorubrum</i> , Unknown
TWW	PROK_00046	0.46	Proteobacteria, Gammaproteobacteria, Enterobacterales, Enterobacteriaceae, <i>Escherichia-Shigella</i> , Unknown
TWW	PROK_00094	1.03	Proteobacteria, Gammaproteobacteria, Burkholderiales, Oxalobacteraceae, <i>Massilia</i> , Unknown
TWW	PROK_00156	0.69	Proteobacteria, Gammaproteobacteria, Burkholderiales, Oxalobacteraceae, <i>Massilia</i> , Unknown
GMW	PROK_00001	8.31	Proteobacteria, Alphaproteobacteria, Rhizobiales, Beijerinckiaceae, <i>Methylobacterium-Methylorubrum</i> , Unknown
GMW	PROK_00003	5.15	Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, <i>Sulfitobacter</i> , Unknown
GMW	PROK_00020	0.97	Bacteroidota, Bacteroidia, Flavobacteriales, Flavobacteriaceae, <i>Ulvibacter</i> , Uncultured marine
GMW	PROK_00024	3.93	Bacteroidota, Bacteroidia, Flavobacteriales, Cryomorphaceae, Uncultured, marine metagenome
GMW	PROK_00032	2.93	Bacteroidota, Bacteroidia, Flavobacteriales, Flavobacteriaceae, <i>Polaribacter</i> , Unknown
GMW	PROK_00043	4.68	Bacteroidota, Bacteroidia, Flavobacteriales, Cryomorphaceae, <i>Vicingus</i> , Uncultured bacterium
AASW	PROK_00001	11.39	Proteobacteria, Alphaproteobacteria, Rhizobiales, Beijerinckiaceae, <i>Methylobacterium-Methylorubrum</i> , Unknown
AASW	PROK_00003	2.85	Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, <i>Sulfitobacter</i> , Unknown
AASW	PROK_00015	1.46	Proteobacteria, Gammaproteobacteria, Pseudomonadales, Nitrospiraceae, Uncultured, Uncultured marine
TBW	PROK_00001	8.06	Proteobacteria, Alphaproteobacteria, Rhizobiales, Beijerinckiaceae, <i>Methylobacterium-Methylorubrum</i> , Unknown
TBW	PROK_00003	2.91	Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, <i>Sulfitobacter</i> , Unknown
TBW	PROK_00015	3.86	Proteobacteria, Gammaproteobacteria, Pseudomonadales, Nitrospiraceae, Uncultured, Uncultured marine
TBW	PROK_00020	1.87	Bacteroidota, Bacteroidia, Flavobacteriales, Flavobacteriaceae, <i>Ulvibacter</i> , Uncultured marine

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TBW	PROK_00024	2.99	Bacteroidota, Bacteroidia, Flavobacteriales, Cryomorphaceae, Uncultured, marine metagenome
TBW	PROK_00027	1.93	Proteobacteria, Pseudomonadales, Gammaproteobacteria, Nitrincolaceae, Uncultured, Uncultured marine
TBW	PROK_00032	1.39	Bacteroidota, Bacteroidia, Flavobacteriales, Flavobacteriaceae, <i>Polaribacter</i> , Unknown
TBW	PROK_00036	0.80	Proteobacteria, Gammaproteobacteria, Pseudomonadales, Thioglobaceae, SUP05 cluster, Uncultured marine
TBW	PROK_00045	1.00	Bacteroidota, Bacteroidia, Flavobacteriales, Flavobacteriaceae, NS5 marine group, Unknown
TBW	PROK_00059	0.75	Proteobacteria, Alphaproteobacteria, SAR11 clade, Clade I, Clade Ia, Unknown
TBW	PROK_00094	0.57	Proteobacteria, Gammaproteobacteria, Burkholderiales, Oxalobacteraceae, <i>Massilia</i> , Unknown

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Supplementary Table 6. DNA sequences of the indicator microbes.

Water mass	ASV	DNA sequence
AASW	PROK_00996	TACGGAGGATCCAAGCGTTATCCGGAATCATTGGGTTTAAAGGGTCCGCAGGCGGTCTTTAAGTCAGAGGTGAAAGCCTACAGCTCAACTGTAGAAGGCCTTTGAAACTGAAAGACTTGAGTTATTGTGAAGTGGTTA GAATGTGTGGTGTAGCGGTGAAATGCATAGATATCACACAGAATACCAATTGCGAAGGCAGATCACTAACATATACTGACGCTCATGGACGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCC GTAACGATGGATACTAGCTGTTCTGCTAACATTGGTTAGATGAGTGGCTAAGCGAAAGTGATAAGTATCCACCTGGGGAGTACGGTCGCAAGACTG
AASW	PROK_00089	TACGGAGGGGGTTAGCGTTGTTCCGAATTACTGGGCGTAAAGCGCACGTAGGCGGATTAGAAAAGTTAGAGGTGAAATCCCAGGGGCTCAACCCTGGAAGTGCCTTTAAAACTCCTAGTCTTGAGTTGAGAGAGGTGAGT GGAATTCGAAGTGTAGAGGTGAAATTCGTAGATATTTGGAGGAACACCAAGTGGCGAAGGCGGCTCACTGGCTCGATACTGACGCTGAGGTGCGAAAGTGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACAC CGTAAACGATGAATGCCAGTCGTCGGGTAGTATACTATTCCGGTGACACACCTAACGGATTAAGCATTCCGCTGGGGAGTACGGTCGCAAGATTA
AASW	EUK_0021	TTCCAGCTCCAAGAGCGTATATTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATTTCTGGTACAACGCGCCTGGCCCGCTTTTAGTGAGTGCCGGTGCGCTTGCATCCTTCTAGAAAACGTTTCTACCTGGGCAAC CGGGCCGGAAGTCTGCGATCTAGATCTTTTACTTTGAAAAAATTAGAGTGTAAAGCAGGCTTTTGTGTGAATACATTAAGGATGTCTTTAATCAAGAACGAAAGTTGGGGGATCGAAGACGATCAGATACCCTCGTA GTCTCAACCATAAACTATGCCAACTAGGGATGGGTGAACGTGTTTTTGTGACTCATCTGCACCTTATGAGAAATCAAAGTCTTTGGGTTCCGGGGGAGTATGGTCGCAAGGCTG
AASW	PROK_09764	GACGAACCGTGCGAACGTTATTCGGAATCACTGGGCTTAAAGCGCGTGTAGGCGGCCCGCACGTCCGGCGTGAATCCCCCGGCTCAACCGGGGAGGGGCGCGGATACGACCGGGCTGGAGGGGGTAGGGGG AGCCGGAACCTACCGTGGAGCGGTGAAATGCGTTGAGATCGTGAGGAACGCCGTGGCGAAGCGGGCTCTGACCCCGCCTGACGCTGAGACGCGAAAGCCAGGGGAGCGAACGGGATTAGATACCCCGGTAGTC CTGGCCGTAACCATGGGCACTGGGTAGGGGGCTCGCGATGGGCTCCCTGCCGACGCAAGCGTGAAGTGCCCGCCTGGGGAGTATGGTCGCAAGGCTG
AASW	PROK_02031	TACGAAGGGGGCTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGTGCCTAGGCGGGTCTTTAAGTCAGGGGTGAAATCTGGAGCTCAACTCCAGAAGTGCCTTTGATACTGAGGATCTTGAGTCCGGGAGAGGTGAG TGGAATCGCAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCAAGTGGCGAAGGCGGCTCACTGGCCCGTACTGACGCTGAGGCGCAAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCAC GCCGTAACGATGAATGCCAGCGTTAGTGGGTTTACTCACTAGTGGCGCAGCTAACGCTTTAAGCATTCCGCTGGGGAGTACGGTCGCAAGATTA
AASW	PROK_08135	TACGTAGGTGCAAGCGTTATCCGGAATTAAGGGTGTAAAGGGCGTGTAGGCGGGACTGCAAGTCAGGCGTGAACCAAGGGGCTCAACCCTTGGCTGCGTTTGAACTGTAGTTCTTGAGTACTGGAGAGGCAGA TGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAAGTGGCGAAGGCGATCTGCTGGACAGCAACTGACGCTAAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCAC GCTGTAACGATGGATACTAGGTGTGGGGGTCTGACCCCTCCGTGCCGACGTAACGCAATAAGTATCCACCTGGGGAGTACGATCGCAAGGTTG
AASW	PROK_09207	GACGGAGGGTGTAGCGTTGTTCCGAATCACTGGGCGTAAAGGGGCGTGAAGCGGCCGCCGCTCGGACGTGAAGAGCCCGGGCTCAACCCGGAACGCGTCCGATACGGGGCGGCTCGAGGCCGGGAGAGGGG GGTGAATACCCAGTGTAGAGGTGAAATTCGTAGATATTTGGTGGAAACACCGGTGGCGAAGCGGCCCTGGCCCGTCTGACGCTGAGGCGCAAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCC ACGCCCTAACGATGTGGGCTGGGCGTGGGGGGCTCGCCCCCGGTGCCGAGCTAACGCGGTAAGCCACCGCCTGGGGAGTACGGCCGCAAGGTTA
AASW	PROK_08149	TACGTAGGCAGCGAGCGTTGTTCCGAGTTACTGGGCGTAAAGCGTGCGTAGGCGGTGGCCTAAGTCTGTTGTGAAATCTCCCGCTTAACCGGGAGGGTGCGGCGGAACTGGGTTGCTGGAGTGCGGGAGAGGTAA GCGGAATTCGGGTGTAGCGGTGAAATGCGTAGATATCGGGAGGAACACCTGCGGTGTAGACGGCTTACTGGACCGTAAGTACGCTGAGGCACGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCAC GCCCTAACGATGCATACTTGGTGTGGGCGAGTTCAGTCTGCTCGTGCCGAAGCTAACGCGATAAGTATGCCGCTGGGGAGTACGGTCGCAAGGCTG
AASW	PROK_06091	TACGTAGGGGGCAAGCGTTATCCGGAATTAAGGGTGTAAAGGGGAGCGTAGACGGAGTGGCAAGTCTGAAGTGAACACCTGGGCTTAACCTGGGGACTGCTTTGAACTGTAACTAGAGTGTGGAGAGGTAAG TGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATGACTCAGAAACACCGATTGCGAAGGCGAGCTTACTGGAACAATACTGACGTTGAGGCTCGAAAGCGTGGGGATCAAACAGGATTAGATACCCTGGTAGTCCACG CTGTAACGATGAATACTAGGTGTGGGGTGCAAAGCATCTCGGTGCCGTGCTAACGCAATAAGTATCCACCTGGGGAGTACGTTGCAAGAATG
AASW	EUK_0048	TTCCAGCTCCAATAGCGTATATTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGTCTGGCTGGCCGGTCCGCTCACCGGAGTACTGGTCCGGCTGGACCTTCTCTTCTGGGGAACTCATGGCCTTCACTG GCTGTGGGGGGAACCAAGGACTTTTACTGTGAAAAAATTAGAGTGTCAAAGCAGGCTTTGCTCGAATACATTAGCATAGGATGTTTTTCAATTAATCAGGGAACGAAAGTTAGGGGATCGAAGACGATCAGATACCGTCG TAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGCGGTGTTTCTATGATGACCCGCTCGGCACCTTACGAGAAATCAAAGTTTTTGGGTTCTGGGGGAGTATGGTCGCAAGGCTG
AASW	PROK_03214	TACGGAGGGTGCAGCGTTATCCGGAATTAAGGGTGTAAAGGGTGCAGGCGGTAAATTAAGTCAGTGGTGAAAGCCTACAGCTCAACTGTAGAAGTGCATTGAACTGAAATACTTGAGTGTGGTAGAGGTAGGC GGAATGAGTCATGTAGCGGTGAAATGCATAGATATGACTCAGAAACACCGATTGCGAAGGCGAGCTTACTAAACCATTAAGTACGCTCAGGCACGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCC CTAACGATGTTCACTCGATATTTGCGATAAAGTGTCAAGCGAAAGCGTTAAGTGAACACCTGGGGAGTACGATCGCAAGGTTG
AASW	PROK_01171	TACGGAGGGGGTTAGCGTTGTTCCGAATTACTGGGCGTAAAGCGCACGTAGGCGGACTATTAAGTAGAGGGTGAATCCCAGGGGCTCAACCCTGGAAGTGCCTTCTATACTGGTAGTCTTGAGTTGAGAGAGGTGAGT GGAATTCGAGTGTAGAGGTGAAATTCGTAGATATTCGAGAGGAACACCAAGTGGCGAAGGCGGCTCACTGGCTCGATACTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGC CGTAAACGATGAATGCCAGACGTTGGGGGGCTTCCCTTCAGTGTACACTTAACGGATTAAGCATTCCGCTGGGGAGTACGGTCGCAAGATTA
AASW	PROK_03613	TACGAAGGGGGCTAGCGTTGCTCGGAATCACTGGGCGTAAAGCGCACGTAGGCGGATTTAAGTCAGGGGTGAAATCTGGAGCTCAACTCCAGAAGTGCCTTTGATACTGGGAATCTCGAGTCCGGAAGAGGTGAG TGGAATCGCAGTGTAGAGGTGAAATTCGTAGATATTCGAAAGAACACCAAGTGGCGAAGGCGGCTCACTGGTCCGGTACTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACG CCGTAACGATGGATGCTAGCGTTGGCCGGTTTACCAGTGTAGGCGCAGCTAACGCTTTAAGCATCCCGCTGGGGAGTACGGTCGCAAGATTA

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AASW	PROK_02019	TACGTATGTCGCAAGCGTTATCCGGATTATTGGGCGTAAAGCGCGTCTAGGCGGTTTGATAAGTCTGATGTGAAATGCGGGGCTCAACTCCGTATTGCGTTGGAACTGTCAAAGTACTGAGAGAGGTGGGCG GAACTACAAGTGTAGAGGTGAAATTCGTAGATATTTGTAGGAATGCCGATGGAGAAGTCAAGTCACTGGACAGATACTGACGCTAAAGCGCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC GTAACGATGATTACTAGGTGTTGGGGTTCGAACCTCAGCGCCCAAGCTAACGCGATAAGTAATCCGCTGGGGAGTACGTACGCAAGTATG
AASW	PROK_04801	TACAGAGGGTCCGAGCGTTATCCGGAATCATTGGGTTTAAAGGGTCCGAGGCGGTCAATTAAGTCAAGAGGTGAAATCCCATAGCTCAACTATGGAAGTCCCTTTGATACTGTTGACTTGAGTCATATGGAAGTAGATA GTGGAATTTCCGGTGTAGCGGTGAAATGCGTAGATATCGGAAGGAACACCTGTGGCGAAAGCGGCTCTCTGGACCACAACTGACGCTGAGGCGCGAAAGCTAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTA GCCCTAAACGATGATTGCTTGCTGTGATCGGTACCCAACTCCGATTGTGGCGAAGCTAACGCGATAAGCAATCCGCTGGGGAGTACGGTCGCAAGGCTG
AASW	PROK_00518	TACGGAGGGTCCGAGCGTTATCCGGAATCATTGGGTTTAAAGGGTCCGAGGCGGTCAATTAAGTCAAGAGGTGAAATCCCATAGCTCAACTATGGAAGTCCCTTTGATACTGTTGACTTGAGTCATATGGAAGTAGATA GAATGTGTAGTGTAGCGGTGAAATGCATAGATATTACACAGAATACCGATTGCGAAGGCAGTCTACTACGTATGTACTGACGCTGAGGGACGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCC GTAACGATGGATACTAGTTGTTGGGCATTAGCTCAGTGACTAAGCGAAAGTGATAAGTATCCCACTGGGGAGTACGGTCGCAAGACTG
AASW	PROK_03718	TACGGAGGGTCCGAGCGTTATCCGGAATCATTGGGTTTAAAGGGTCCGAGGCGGTCAATTAAGTCAAGAGGTGAAATCCCATAGCTCAACTATGGAAGTCCCTTTGATACTGTTGACTTGAGTCATATGGAAGTAGATA GGAATATGTCATGTAGCGGTGAAATGCTTAGATATGACATAGAACACCGATTGCGAAGGCAGCTCGTACACGAACATTGACTCTGAGGCACGAAAGCGTGGGGATCAAACAGGATTAGATACCCTGGTAGTCCACGCC CTAAACGATGGATACTCGACATACGCGATACACGGTGTGTCTGAGCGAAAGCATTAAATATCCCACTGGGAAGTACGACCGCAAGGTTG
AASW	PROK_07543	TACGTAGGGTCCGAGCGTTATCCGGAATCATTGGGTTTAAAGGGTCCGAGGCGGTCAATTAAGTCAAGAGGTGAAATCCCATAGCTCAACTATGGAAGTCCCTTTGATACTGTTGACTTGAGTCATATGGAAGTAGATA TGGAAATCCGCGTGTAGCAGTGAATGCGTAGATATGCGGAGGAACACCGATGGCGAAGGCAGCCTCTGGGATAACACTGACGCTCATGACGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACG CCCTAAACGATGTCTACTAGTTGTGCGGAATTAATTTCTTGTTAAGCAGCTAACGCGGGAAGTAGACCGCTGGGGAGTACGGTCGCAAGATTA
AASW	PROK_02729	TACGTAGGGGGCAAGCGTTTCCGGATTACTGGGCGTAAAGCGCGTGTAGGCGGGACGAAAGTCCGTTGTGAAAGCCCCCGCTCAACGGGGGAAGGTCGCTGAAAGTCCGTTTCTGAGGGCGCGAGAGGGAA GTGGAATTGCTGGTGTAGCGGTGAAATGCGTAGAGATCAGCAGGAACACCGTGGCGAAGGCGGCTCTCTGGGCGCGCCTGACGCTGAGACGCGAAAGCGTGGGGAGCGAACGGGATTAGATACCCCGGTAGTCCA CGCGTAAACGATGGTCACTAGGTGTATGGGTATCGACCCCCATGGGCCGAGCTAACGCAATAAGTGACCCGCTGGGGAGTACGGCCGCAAGGTTG
AASW	PROK_04507	TACGGAGGGTCCGAGCGTTATCCGGAATCATTGGGTTTAAAGGGTCCGAGGCGGTCAATTAAGTCAAGAGGTGAAATCCCATAGCTCAACTATGGAAGTCCCTTTGATACTGTTGACTTGAGTCATATGGAAGTAGATA GGAATGAGTCATGTAGCGGTGAAATGCATAGATATGACTTAGAACACCAATTGCGTAGGCAGCTAGCTAGGCATATATTGACGCTGAGGCACGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGC CCTAAACGATGTTACTCGATGTTTGGGCTTCGGCTTGAGCATCAAAGGGAACCAATTAAGTAAACCACTGGGGAGTACGTTCCGAAGAATG
AASW	PROK_06672	TACGAAGGGGGTAGCGTTTTCGGAATCATTGGGCGTAAAGCGCACGTAGGCGGGTGTGTAAGTCAAGGGTGAATCCCGAGCTCAACTCCGGAATGCCTTTGATACTGGCAACCTAGAGGCCGGAAGAGGTTAG TGGAAATCCAGTGTAGAGGTGAAATTCGTAGATATTGGGAAGAACCAGTGGCGAAGGCGGCTAACTGGTCCGGTACTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACG CCGTAACATATGGATGCTAGCGCTCAGCGGGCTTGCCGTTGGTGGCGAGCTAACGCATTAAGCATCCCGCTGGGGAGTACGGTCGCAAGATTA
AASW	PROK_07515	TACGGAGGGGGTAGCGTTTTCGGAATCATTGGGCGTAAAGCGCACGTAGGCGGGTGTGTAAGTCAAGGGTGAATCCCGAGCTCAACTCCGGAATGCCTTTGATACTGGCAACCTAGAGGCCGGAAGAGGTTAG GGAATCCGAGTGTAGAGGTGAAATTCGTAGATATTGCGAGGAACACCAAGTGGCGAAGGCGGCTTACTGGCTCGATACTGACGCTGAGGTGCGAAAGTGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACAC CGTAAACGATGAATGCCAGACGTGAGGGGGCTTGCCCTTTGGTGTACACCTAACGGATTAAGCATTCCGCTGGGGAGTACGGTCGCAAGATTA
AASW	PROK_04170	GACGAACCGTGCGAACGTTTTCGGAATCATTGGGCGTAAAGGGCGCGTAGGCGGACCGCAAGTCCGTTGGTGAATCCTCCAGCTCAACTGGAGAACTGCCGCGGATACTGGAGGTCTCGAGGGAGGTAGGGGCAA GCGGAAGTGTGGGTGGAGCGGTGAAATGCGTTGATATCCACAGGAACCTCCGTTGGCGAAGGCGGCTTGTGGACCTTTTCTGACGCTGAGGCGCGAAAGCCAGGGGAGCAAACGGGATTAGATACCCCGGTAGTCCCT GGCCCTAAACGATGGTACTAGATAGTAGACATAGCATGGGTTTACTGTGCAAGCAAAGTCTAAGTACCCCGCTGGGGAGTATGGTCGCAAGGCTG
AASW	PROK_03363	TACGAAGGTCCGAGCGTTATCCGGAATCATTGGGTTTAAAGGGTCCGAGGCGGTCAATTAAGTCAAGAGGTGAAATCCCATAGCTCAACTATGGAAGTCCCTTTGATACTGGCAACCTAGAGGTGAGGTTAGGAGAGGTAAGT GGAATTTTGGTGTAGCAGTGAATGCGTAGATATCAAGAGGAAGACCAATGGCGAAAGCAGGTTACTGGACATTACTGACGCTGAGGCTCGAAGGCTAGGGTAGCGAAAGGGATTAGATACCCTGTAGTCTAGC AGTAAACGATGTGCGCTTGGTGTGGGAGGGTTCGACCCCTTCGTGCCGAGCTAACGCGTTAAGCGCACCGCTGGGGAGTACGGTCGCAAGACTA
AASW	PROK_05647	TACGAAGGGGGCGAGCGTTTTCGGAATCATTGGGCGTAAAGGGCGCGTAGGCGGCGGATCAAGTCAAGTGTGAAAGCCCCGGGCTCAACTCCGGAAGTGCCTCGAGACTGTTTGTGAGTTCCGGAGAGGAGC GTGGAATCCAGTGTAGAGGTGAAATTCGTAGATATTGGGAAGAACCAGTGGCGAAGGCGGCTTGTGGACCGAGACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCCA CGCGTAAACGATGTGTCTAGACGTTGGGGAGCCTAGCTCTCGGTGTCGACCAACGCTGTAAGCACACCGCTGGGGAGTACGGCCGCAAGGTTA
AASW	PROK_02139	TACGGAGGATGCAAGCGTTATCCGGAATCATTGGGTTTAAAGGGTCCGAGGCGGTCAATTAAGTCAAGAGGTGAAATCCCATAGCTCAACTATGGAAGTCCCTTTGATACTGGCAACCTAGAGGTGAGGTTAGGAGAGGTAAGT GAATGCGTCATGTAGCGGTGAAATGCACAGATATGACGCGAAGACCAATTCGGAAGGCAGCTCACTAATGTATTATTGACGCTGAGGGACGAAAGCATGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCATGCC GTAACGATGATTACTCGGTATTAGTCTGACTAGTGCTAAGCGAAAGTGATAAGTATCCCACTGGGGAGTACGCTCGCAAGAGTG
AASW	PROK_01053	TACGGAGGGTCCGAGCGTTATCCGGAATCATTGGGTTTAAAGGGTCCGAGGCGGTCAATTAAGTCAAGAGGTGAAATCCCATAGCTCAACTATGGAAGTCCCTTTGATACTGGCAACCTAGAGGTGAGGTTAGGAGAGGTAAG GGAATATGTCATGTAGCGGTGAAATGCTTAGATATGACATAGAACACCAATTCGGAAGGCAGCTGGCTACACGAATATTGACACTGATGACGAAAGCGTGGGGATCAAACAGGATTAGATACCCTGGTAGTCCACGCC CTAAACGATGGATACTCGACATACGCGATATACTGTGTGTCTGAGCGAAAGCATTAAATATCCCACTGGGAAGTACGATCGCAAGATTG
CDW	PROK_05932	TACGGAGGGGGTAGCGTTTTCGGAATCATTGGGCGTAAAGCGCACGTAGGCGGGTGTGTAAGTCAAGAGGTGAAATCCCATAGCTCAACTATGGAAGTCCCTTTGATACTGGCAACCTAGAGGTGAGGTTAGGAGAGGTAAG TGGAAATCCGAGTGTAGAGGTGAAATTCGTAGATATTGGAAGAACCAGTGGCGAAGGCGACTTACTGGACACATATTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACG CCGTAACGATGATGACTAGCTGTGCGGGCGCTTAGCGTTCCGGTGGCGAGCTAACGCGTTAAGTATCCGCTGGGGAGTACGGCCGCAAGGTTA

Microbial Fingerprinting of Marine Water Masses in an Antarctic and Hydrographically Complex Area

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Microbial Fingerprinting of Marine Water Masses in an Antarctic and Hydrographically Complex Area

CDW	PROK_02085	TACAGAGGGTGAAGCGTTAATCGGAATTACTGGGCGTAAAGCGTGCGCAGACGGTTGCGTAAGTCAGATGTGAAAGCCCCGGGCTCAACCTGGGAATTGCATTTGAGACTGCGTAGCTAGGGTGCAGAAAGGGGAA GCGGAATTTCCGGTGTAGCGGTGAAATGCGTAGATATCGGAAGGAACACCAAGTGGCGAAAGCGGCTTCTGGTCCAGCACCGACGTTAGGACGAGAAAGCGTGGGGAGCAAAACAGGATTAGATACCTGGTAGTCCAC GCCATAAACGATGAGAACTAGACGTTGAAGGGGTAAAGCCCTCCAGTGTCTAGCTAACGCGCTAAGTTCTCCGCTGGGGAGTACGGCCGCAAGGTTG
CDW	PROK_02447	TACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGCGCGCGCAGGTGGTTTCTTAAGTCTGATGTGAAAGCCACGGCTCAACCGTGGAGGGTCATTGGAACCTGGGAACTTGAGTG CAGAAGAGGAAAG TGGAAATCCAGGTGTAGCGGTGAAATGCGTAGAGATTTGGAGGAACACCAAGTGGCGAAGGCGCACTTTCTGGTCTGTAAGTACACTGAGGCGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCTGGTAGTCCACG CCGTAACGATGAGTGCTAAGTGTAGAGGGTTTCCGCCCTTATGCTGCTGACGCTAACGCATTAAGCACTCCGCTGGGGAGTACGGTCGCAAGACTG
CDW	PROK_00598	TACAGAGGGGGCAAGCGTTGTTCGGAATTACTGGGCGTAAAGGGCGCGTAGGGCGGCTTCTAAGTCAAGCTGAAATCCCCGGGCTCAACCCGGGAAGTGCCTCCGATACTGGGAGGCTTGAATCCGGGAGAGGGAT GCGGAATTCAGGTGTAGCGGTGAAATGCGTAGATATCTGGAGGAACACCGGTGGCGAAGGCGGCATCTGGACCGGCATTGACGCTGAGGCGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCCGGTAGTCCCT GGCCCTAAACGATGAATGCTTGGTGTGGCGGGTATCGATCCCTGCCGTGCCGAAGCTAACGCATTAAGCATTCCGCTGGGGAGTACGGTCGCAAGGCTG
CDW	PROK_00489	TACAGAGGGGGCAAGCGTTATTTCGGAATTATTGGGCGTAAAGGGCGCGTAGGGCGGCTTGGCAAGTGGAAGGTGAAATCCCTCGGCTTAACCGAGGAAGTGCCTCCAACTGCTTTGCTTGAGGCCGGGAGAGGCGAG TGGAAATCCAGGTGTAGCGGTGAAATGCGTAGATATTGGGAGGAACACCAAGTGGCGAAGGCGGCTCGCTGGACCGGTTCTGACGCTGAGGCGCGAAAGCGTGGGGAGCAACAGGATTAGATACCCCGGTAGTCCAC GCTGTAACGATGAGTGCTTGGTGTAGCGGGTATCGACCCCTGCTGTGCCGAAGTCAACACATTAAGCACTCCGCTGGGGAGTACGGTCGCAAGGCTG
CDW	PROK_03425	TACGAAGGGGGCTAGCGTTGCTCGGAATTACTGGGCGTAAAGGGCGCGTAGGGCGGCTTCTAAGTCAAGGGGTGAAATCCCTGGAGCTCAACTCCGAACTGCCTTTGATACTGGCGAGCTTGAGTCGGGAGAGGTGAG TGGAACTGCGAGTGTAGAGGTGAAATTCGTAGATATTGCAAGAACACCAAGTGGCGAAGGCGGCTCACTGGCCCGTACTGACGCTGAGGTGCGAAAGCGTGGGGAGCAACAGGATTAGATACCTGGTAGTCCAC GCCGTAACGATGGATGCTAGCGTTGGCGGGTTACTCGTCACTGCGCAGCTAACGCATTAAGCATCCCGCTGGGGAGTACGGTCGCAAGATTA
CDW	PROK_08312	GACAGAGTCTCGAGCGTTAGGCGGAATCACTGGGCTTAAAGCGTGTGTAGGCGGACTTCTAAGTACCTTGTAATCCACGGCTTAACCGTGGAACTGCTTGGTATACTGTTGTCTTGGGTGCTAGGGGCTACTG GAACAAACGGTGGAGCGGTGAAATGCGTAGATATCGTTTGAACGCCAATGGTGAAACAAGTAGCTGGGGATGACCCGACGCTGAGACACGAAAGCCAGGGGAGCGAACGGGATTAGATACCCCGGTAGTCTTGGC TGTAACGATGTCGACTAGATCGTGGTGGCTCTGACGCCGTACGGTGAAGCAAAAGTGCTAAGTCAAGCGCTGGGAAGTACGGTCGCAAGGCTA
CDW	PROK_01550	TACAGAGGGGGCAAGCGTTATTTCGGAATTATTGGGCGTAAAGGGCGCGTAGGGCGGCTTCTAAGTCAAGGGGTGAAATCCCTGGGCTTAACCGAGGAAGTGCCTGCCAGACTGGATTGCTTGAGTCGGGAGAGGTGA GTGGAATTCAGGTGTAGCGGTGAAATGCGTAGATATTGGGAGGAACACCAAGTGGCGAAGGCGGCTCACTGGACCGGAAGTACGCTGAGGCGCGAAAGCGTGGGGAGCAACAGGATTAGATACCTGGTAGTCCAC CGCCGTAACGATGAGTGCTTGGTGTAGCGGGTATCGACCCCTGCTGTGCCGAAGTCAACACATTAAGCACTCCGCTGGGGAGTACGGTCGCAAGACTG
CDW	PROK_03935	TACGAAGGGGGCTAGCGTTGCTCGGAATTACTGGGCGTAAAGGGCGCGTAGGGCGGCTTCTAAGTCAAGGGGTGAAAGCCAGGGCTCAACCTGGAAATGCCTTCGATACTGTTTGCTAGAGACCGGAAGAGGTAA GTGGAAGTGCAGTGTAGAGGTGAAATTCGTAGATATTGCAAGAACACCAAGTGGCGAAGGCGGCTTACTGGTCCGGTCTGACGCTGAGGCGCGAAAGCGTGGGGAGCAACAGGATTAGATACCTGGTAGTCCAC GCTGTAACGATGGATGCTAGCGTTGGCCAGCTTGTGGTCACTGCGCAGCTAACGCTTTAAGCATCCCGCTGGGGAGTACGGTCGCAAGATTA
CDW	PROK_06113	TACGAGGGGGCTAGCGTTGCTCGGAATTACTGGGCGTAAAGGGCGCGTAGGGCGGCTTCTAAGTCAAGGGGTGAAATCCCTGGGCTTAACCGAGGAAGTGCCTTGAAGTGCATCGCTTGAACA TCGGAGAGGTAAAGT GGAATTCAGGTGTAGAGGTGAAATTCGTAGATATTGGAAGAACACCAAGTGGCGAAGGCGGCTTACTGGACGATTGTTGACGCTGAGGTGCGAAAGCGTGGGGAGCAACAGGATTAGATACCTGGTAGTCCACGC CGTAAACGATGATGACTAGCTGTGGGGCGCTTAGCGTTTGGTGGCGCAGCTAACCGTTAAGTCATCCGCTGGGGAGTACGGCCGCAAGGTTA
CDW	PROK_01786	GACGAACCGTGCGAACGTTATTTCGGAATTACTGGGCTTAAAGCGCGTGTAGGCGGGCGGGACGTCGCTCGCTGAAATCCCCGGGCTCAACCGGGGAACGGGCGCCGAAACGCCCGCTCTCAGGGACGTAGGGGGA CCTGGAAGTCCCGTGGAGCGGTGAAATGCGTTGAGATCGGAAGGAACGCCGTGGCGAAAGCGAGGTCTGGACGCTTCTGACGCTGAGACGCGAAAGCTAGGGGAGCGAACGGGATTAGATACCCCGGTAGTCC TAGCCGTAACGATGGGCACTGGGTAGGGGCTCGCCGATGGGCTCCCTGCCGAGCGAAAGCGTGAAGTGCCCGCTGGGGAGTATGGTCGCAAGGCTG
CDW	EUK_0052	TTCCAGCTCCAATAGCGTATATAAAGTTGTTGCAAGTTAAAAAGCTGTAGTTGAACCTTGGGCTTGGTTGGCCGGTCCGCTTTTGGCGAGTACTGGACCCAACCGAGCCTTCTCTGCTGAACCTTTCGCCCTTGTG GTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATAGAGTGTTCAAAGCAGGCGCTTGTCTGCAATATATTAGCATGAAGGACGTTTTTCAATTAAGAAGCAAAAGTTAGGGGATCGAAGATGATCAGATACCGTCGT AGTCTTAACCATAACTATGCCGACTAGGGATCGGGTGTGTTCTTTTGTGACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTG
CDW	PROK_02670	TACGAAGGGGGCTAGCGTTGTTTCGGAATTACTGGGCGTAAAGGGCGCGTAGGGCGGCTTATAAGTCCGGGGTGAAGGCTGTGGCTCAACACAGAAATGCCTTCGATACTGTATGGCTTGAGACCGGAAGAGGTAG TGGAACTGCGAGTGTAGAGGTGAAATTCGTAGATATTGCAAGAACACCAAGTGGCGAAGGCGGCTAAGTGGTCCGGTCTGACGCTGAGGCGCGAAAGCGTGGGGAGCAACAGGATTAGATACCTGGTAGTCCACG CCGTAACGATGAATGCCAGCGTTGGCGAGCTTGTCTGCTAGTGGCGCAGCTAACGCTTTAAGCATTCCGCTGGGGAGTACGGTCGCAAGATTA
CDW	PROK_01323	TACAGAGGGGGCAAGCGTTGTTTCGGAATTACTGGGCGTAAAGGGCGCGTAGGGCGGCTTCTAAGTCAAGCTGAAATCCCTGGGCTCAACCCAGGAAGTGCCTCCGATACTGGAAGGCTTGAATCCGGGAGAGGGATG CGGAATTCAGGTGTAGCGGTGAAATGCGTAGATATCTGGAGGAACACCGGTGGCGAAGGCGGCATCTGGACCGGATTGACGCTGAGGCGCGAAAGCCAGGGGAGCAACAGGATTAGATACCCCGGTAGTCCCTG GCCCTAAACGATGAATGCTTGGTGTGGCGGGTATCGATCCCTGCCGTGCCGAAGCTAACGCATTAAGCATTCCGCTGGGGAGTACGGTCGCAAGGCTG
CDW	PROK_00060	TACGTAGGGTGAAGCGTTAATCGGAATTACTGGGCGTAAAGCGTGCGCAGGCGGTTTTGTAAGTCTGTCTGTAAGGCCCGGGCTTAACCTGGGAATTGCGATGGAGACTGCAAGGCTTGAATCTGGCAGAGGGGGG TAGAATTCACGTGTAGCAGTGAAATGCGTAGAGATGTGGAGGAACACCGATGGCGAAGGCGAGCCCTGGGTCAAGATTGACGCTATGACGAGAAAGCGTGGGGAGCAACAGGATTAGATACCTGGTAGTCCACG CCCTAAACGATGTCTACTAGTTGTCCGGTCTTAATTGACTTGGTAACGAGCTAACGCGTGAAGTAGACCGCTGGGGAGTACGGTCGCAAGATTA
CDW	PROK_02255	TACGTAGGGTGAAGCGTTAATCGGAATTACTGGGCGTAAAGGGCGCGTAGGGCGGCTTCTGGAAGAAAGATGTGAAATCCGAGGGCTCAACCTGGGAAGTGCATTTTAACTGCCGAGCTAGAGTATGTAGAGGGGGG TAGAATTCACGTGTAGCAGTGAAATGCGTAGATATGTGGAGGAATACCGATGGCGAAGGCGAGCCCTGGGATAACTGACGCTCAGACACGAAAGCGTGGGGAGCAACAGGATTAGATACCTGGTAGTCCACG CCCTAAACGATGTCAACTAGCTGTTGGGGCCGTTAGGCCCTAGTAGCGCAGCTAACGCGTGAAGTTGACCGCTGGGGAGTACGGTCGCAAGATTA

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Microbial Fingerprinting of Marine Water Masses in an Antarctic and Hydrographically Complex Area

CDW	PROK_03375	TACCGGCGCCTCAAGTGGTAGTCGCTTTTATTGGGCTAAACGCTCCGTAGCCGGTCTGATACATTCTGGGTAATCAACCAGCTTAAGTGGTTGAATTCTGCGAGGACGGTCAGACTGGGACCGGGAGAGGTGTGGGGTACGCTCAGGGTAGGGGTAATCTCTGTATCCTGAGCGGACCCTGTTGCGAAGGCGCCACACTAGAACGGATCCGACGGTCAGGGACGAAGCCTAGGGGCACGAACCGGATTAGATACCCGGGTAGTCTAGGTGTAACGCTGTGGACTTGATGTTGGGGGTGCTCCGAGCACTCTAGTGTCAAGCGAAGGTGATAAGTCCACTGCCTGGGAAGTACGGTCGCAAGGCTG
CDW	EUK_0126	TTCCAGCTCCAATAGCGTATATTAAAGTTGTTGCAATTAAAAAGCTCGTAGTTGAACCTTGGGTCTGGCTGGCCGGTCCGCCTACCCGCGAGTACTGGTCCGGCTGGACCTTCTCTGGGGAACTCATGGCCTTCACTGGCTGTGGGGGGAACAGGACTTTTACTGTGAAAAAATTAGAGTGTCAAAGCAGGCCTTGTCTGAATACATTAGCATGCCAAGGACGCTTCCGTTGATCAGGGGCTAAGGTTAGGGGATCGAAGACGATTAGATACCGTCGTAGTCTTAACAGCAAACTATGCCGACTAGGGATTGGACTTGGCTTTATGGCTTGTCCAGCACCTTAGCGAAAGCAAAGTTTGGGTTCTGGGGGAGTACGGGACGCAAGGCTG
CDW	PROK_00786	TACGTAGGGGGCGAGCGTTGTCGGAATTACTGGGCGTAAAGCGCTGTAGGCGGGAAGTTACGTCGAGCTGAAAGCGGGGGCTCAACCCCGAGCGCGTTCGAAACGGACTTCTTCTGAGGGTCGAAGAGGAGCGTGAATTCCCGGTGTAGCGGTGAAATGCGTAGAGATCGGGAGGAACACCCATGGCGAAGGCGAGCTCTGGTCGGCATCTGACGCTGAGAGGCGAAAGCGTGGGGAGCGAACGGGATTAGATACCCCGGTAGTCCACGCGGTAACGATGGTCACTAGGTGTACGCGGTATCGACCCGCTGGTGCCGACGTAACGCAAGTAAGTACCCGCTGGGGAGTACGGCCGCAAGGTTG
CDW	PROK_06615	TACGAAGGGGGCTAGCGTTGCTCGGAATTACTGGGCGTAAAGGGCGCGTAGGCGGGTCTGCAAGTCGGGGGTGAAAGCCTGTGGCTCAACCACAGAATGGCCTTCGATACTGGCGGGCTTGAGACCGGAAGAGGACAGCGGAAGTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCACTGGCGAAGGCGGCTGTCTGGTCCGGTTCTGACGCTGAGGCGCGAAAGCGTGGGGAGCAACAGGATTAGATACCTTGGTAGTCCACGCTGTAACGATGAATGCTAGCCGTTGGGGTGCATGCACCGCAGTGGCGCGCTAACGCATTAAGCATTCCGCTGGGGAGTACGGTCGCAAGATTA
CDW	PROK_06835	GACGAACCGTGCGAACGTTATTTCGGAATTACTGGGCTTAAAGCGCGTGTAGGCGGGCCGGCACGTCGACTGCTGAAAGCCCCGGCTCAACCGGGGAACGGGCATCGATACGACCGGCTGGAGGGGGTAGGGGAGCCGGAAGTCCAGGTGTAGAGGTGAAATGCGTTGAGATCGTGAGGAACGCCGTGGCGAAGCGGGCTCTGGACCCCACTGACGCTGAGACGCGAAAGCCAGGGGAGCGAACGGGATTAGATACCCCGGTAGTCCGTGCGCTAAACCATGAGCACTGGGTAGGGGGCTCGCCGATGGGCTCCCTGCCGACGCGAAAGCGTGAAGTGCTCCGCTGGGGAGTATGGTCGCAAGGCTG
CDW	PROK_03697	TACAGAGGGTGCAGCGTTAATCGGAATTACTGGGCGTAAAGGGCGCGTAGGTTGGTTAATTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAATGGCATATGAAACTGGTTGGCTAGAGTTCCGGAGAGGGGAGTGGAATTTCCGGTGTAGCGGTGAAATGCGTAGATATCGGAAGGAACACCACTGGCGAAGGCGACTTCTGGCCGATACTGACACTGAGGCGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCTTGGTAGTCCACGCTGTAACGATGAGAACTAGATGTTAGGTGGCTTAGACCATTTAGTATCGCAGCAACGCGTTAAGTTCTCCGCTGGGGAGTACGGTCGCAAGATTA
CDW	PROK_03786	TACGAAGGGGGCTAGCGTTGCTCGGAATTACTGGGCGTAAAGGGCGCGTAGGCGGATTGCTAAGTCAGGGGTGAAATCCTGGAGCTCAACTCCAGAACTGCCTTGATACTGGCGGTCTCGAGTCGGGAGAGGTGAGTGGAACTGCGAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCACTGGCGAAGGCGGCTCACTGGCCCGTACTGACGCTGAGGTGCGAAAGCGTGGGGAGCAACAGGATTAGATACCTTGGTAGTCCACGCCGTAACGATGGATGCTAGCCGTTGGTGGGTTTACCCTTCACTGGCGCAGCTAACGCATTAAGCATCCGCTGGGGAGTACGGTCGCAAGATTA
CDW	PROK_07457	TACGAAGGGGGCTAGCGTTGCTCGGAATTACTGGGCGTAAAGGGCGCGTAGGCGGATTCTAAGTCGGGGGTGAAAGCCTGAGGCTCAACCTCAGAATTGCCTTCGATACTGGAAATCTTGAGACCGGAAGAGGTGAGTGGAACTGCGAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCACTGGCGAAGGCGGCTCACTGGTCCGGTTCTGACGCTGAGGCGCGAAAGCGTGGGGAGCAACAGGATTAGATACCTTGGTAGTCCACGCCGTAACGATGGATGCTAGCCGTTGGCGGGTTTACCCTCAGTGGCGCAGCTAACGCATTAAGCATCCGCTGGGGAGTACGGTCGCAAGATTA
CDW	PROK_06560	TACGAAGGGGGCGAGCGTTGTTTCGGAATTACTGGGCGTAAAGGGCGCGTAGGCGGCTGTTTGTTCAGGCGTGAAAGCCCCGGCTTAACCTGGGAAGTGCCTTGAGACGGACGGGTAGAGTTCCGGAGAGGAGAGCGGAATTCAGTGTAGAGGTGAAATTCGTAGATATTGGGAAGAACACCGGTGGCGAAGGCGGCTCTCTGGACCGAGACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAACAGGATTAGATACCTTGGTAGTCCACGCTGTAACGATGTGTCTAGACGTTGGGGAGCCTAGCTCTTCGGTGTGCGAGCTAACCGGTAAGCACACCGCTGGGGAGTACGGCCGCAAGGTTA
CDW	PROK_03167	TACGTAGGGTGCAGCGTTAATCGGAATTACTGGGCGTAAAGCGTGCGCAGGCGGTTCTGTGATGTCTGGTGTGAAAGCCCCGGGCTTAACCTGGGAATTGCATTGGAAGTACGGGGCTGGAGTGTGGCAGAGGGGGGTGGAATTCACGCTGTAGCAGTGAAATGCGTAGAGATGTGGAGGAACACCGATGGCGAAGGCGAGCCCCCTGGGTAACACTGACGCTCATGCACGAAGCGTGGGGAGCAACAGGATTAGATACCTTGGTAGTCCACGCCCTAAACGATGGCAACTGGGTGTTGGGGAAGCGATTCTCAGTACCGTAGCTAACCGTGAAGTTGCCGCTGGGGAGTACGGCCGCAAGGTTA
CDW	PROK_02467	TACGAGGGGGCGAGCGTTATTTCGGAATTATTGGGCGTAAAGGGCGCGTAGGCGGCTATTCAAGTCAAAGGTGAAATCCCTCGGCTCAACTGAGGAAGTGCCTTGAAACTGGATGGCTTGGAGCGGGAGGGGGTAGCGGAATTCAGTGTAGCGGTGAAATGCGTAGATATTGGGAGGAACACCACTGGCGAAGGCGGCTACCTGGACCGGTTCTGACGCTGATGCGCGAAAGCGTGGGTAGCAACAGGATTAGATACCTTGGTAGTCCACGCTGTAACGATGGGTGCTCGGTGTGCGGGTATCGACCCCTGCGGTGCCTTAGCCAACGCGTTAAGCACCCGCTGGGGAGTACGGTCGCAAGGCTG
CDW	PROK_00790	TACGGGGGGGGCAAGCGTTGTTTCGGAATTACTGGGCGTAAAGGGCTCGTAGGCGGCCAACTAAGTCAGACGTGAAATCCCCAGGCTCAACCTGGGAAGTGCCTGATACTGGATGGCTTGAATCCGGGAGAGGGGATGCAGAATTCAGGTGTAGCGGTGAAATGCGTAGATATTCGGAGGAATACCGGTGGCGAAGGCGGCATCTGGACCGGCATTGACGCTGAGGAGCGAAAGCTAGGGGAGCAACGGGATTAGATACCCCGGTAGTCCCTAGCCCTAAACGATGAATGCTTGGTGTAAACGGGTATCGATCCCTGTTGTGCCGAAGCTAACGCATTAAGCATTCCGCTGGGGAGTACGGTCGCAAGGCTG
CDW	PROK_02328	TACGAGGGGGCGAGCGTTGTTTCGGAATTATTGGGCGTAAAGGGCGCGTAGGCGGCTGCGGTAAGTCACCTGTGAAAGCTTGGGCTCAACTCAGAGGCTGAGGCGGTAAGTGCCTTGAAGTGTGAGTGTGGGAGAGGTGCGTGAATTCCCGGTGTAGCGGTGAAATGCGTAGATATCGGGAGGAACACCTGTGGCGAAGGCGGCACTGGACCACAACTGACGCTGAGGCGCGAAAGCTAGGGGAGCAACAGGATTAGATACCTTGGTAGTCTTAGCCCTAAACTATGGATGCTTGGTGTGATCGGTACCAATCCGATCGTCCGTAGCTAACGCGTTAAGCATCCGCTGGGGAGTACGGTCGCAAGGCTG
CDW	PROK_02396	TACGTAGGTGCAAGCGTTGTCGCGATTATTGGGCGTAAAGCGAGCGCAGCGGTTTCTAAGTCTGATGTGAAAGCCTTGGCTTAACCGGAGAAAGTGCATCGGAAACTGGGAGACTTGAGTGCAGAAGAGGACAGTGGAACTCCATGTGTAGCGGTGGAATGCGTAGATATATGGAAGAACACCACTGGCGAAGGCGGCTGTCTAGTCTGTAAGTACGCTGAGGCTCGAAAGCATGGGTAGCAAAACAGGATTAGATACCTTGGTAGTCCATGCCGTAACGATGAGTGTAGGTGTTGGAGGGTTTCCGCCCTCAGTGCCGACGCTAACGCATTAAGCATCCGCTGGGGAGTACGACCGCAAGGTTG
CDW	PROK_03041	TACGTAGGCGAGCGTTGTTTCGGAATTACTGGGCGTAAAGGGTGTGTAGGCGGTTGTTAAGTTTGGTGTGAAATCTCCGGCTCAACTGGGAGGCTGCGCCGAATCTGAATGACTTCGAGTGCGGGAGAGGAGAGTGGAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGTGGTGTAGACGGCTCTCTGGACCGTAAGTACGCTGAGACACGAAGCGTGGGTAGCAACAGGATTAGATACCTTGGTAGTCCACGCCCTAAACGATGCATATTTGGTGTGGGCGAGTTATTCTGTCCGTGCCGAGCTAACCGTTAAATATGCCGCTGGGGAGTACAGTCGCAAGGCTG

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Microbial Fingerprinting of Marine Water Masses in an Antarctic and Hydrographically Complex Area

CDW	PROK_05910	TACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGTGCGCAGGCGGTTTTGTAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAAGTCGCTTTGAAACTACAAGGCTAGAGTGTGGCAGAGGGGGG TGGAAATCCACGTGTAGCAGTGAAATGCGTAGAGATGTGGAGGAACACCGATGGCGAAGGCAGCCCCCTGGGTAACTGACGCTCAGGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCAC GCCCTAAACGATGTCAACTAGTTGTCGGGTCTTAACGGACTTGGTAACGCAGCTAACGCGTGAAGTTGACCGCTGGGGAGTACGGTCGCAAGATTA
CDW	PROK_01527	GACAGAGGGGGCAAGCGTTGCTCGGAATCACTGGGCGTAAAGGGCGCGTAGGCGGGATGGCAAGTCGCTCGTAAATCCTTCGCCCCAACCGAAGAACGTCGGCCGATACTGCCGTTCTTGAGGGATGCAGAGGAGA CTGGAATTCGCGGTGTAGCGGTGAAATGTGTAGAGATCGGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCATTTCTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACGGGATTAGATACCCCGGTAGTCCA CGCTGTAACGATGACGACTAGGTGTGGGGGGGTTAGTCCCTTCGTCGCCGAGCTAACGCATTAAGTCGTCGCCCTGGGGAGTACGGCCGCAAGGTTG
CDW	PROK_04067	TACGAAGGGGGCTAGCGTTGTTTCGGAATCACTGGGCGTAAAGGGCGCGTAGGCGGCTTGATAAGTCGGGGGTGAAAGCCTGTGGCTCAACCAAGCAATTCCTTGCCTTCGATACTGTCTGGCTTGAGACCGGAAGAGGTAAG TGGAACTGCGAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCACTGGCGAAGGCGGCTTACTGGTCCGTTCTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACG CCGTAAACGATGAATGCCAGCGTTGGGCGAGCTTGCTGCTCAGTGGCGCAGCTAACGCTTTAAGCATTCCGCTGGGGAGTACGGTCGCAAGATTA
CDW	PROK_05421	AACCAGACCTCAAGTGGTCAGGATGATTATTGGGCTAAAGCATCCGTAGCCGGCTCTGTAAGTTTTCGGTTAAATCTATGCGCTCAACGTATGGGCTGCCGAAATACTGCAGAGATAGGGAGTGGGAGAGGTAGAC GGTACTCGGTAGGAAGGGGTAATTCCTTTGATCTATCGATGACCACCTGTGGCGAAGGCGGTCTACCAGAACACGTTTCGACGGTGAAGGATGAAAGCTGGGGAGCAAACCGGATTAGATACCCCGGTAGTCCCAGC TGTAACGATGCAGACTCGATGATGCATTGGCATATAGCCAGTGCAGTGTCCGAGGGAAGCCGTTAAGTCTGCCCTGGGAAGTACGTACGCAAGTATG
CDW	PROK_06482	AACGTAGGAGGCAAGCGTTATCCGGATTCACTGGGCGTAAAGCGCGTGCAGGTGGCGCGTAAAGTTGGGCGTGAATCTCCCGCTCAACTGGGAGAGGTCTGCCAATACTACCGTCTTGAGAGCAGAAAGGGAAG ATGGAATTCGCGGTGTAGTGGTGAATGCGTAGATATCGGGAGGAACACCACTGGCGAAGGCGATCTTCTGGTCTGTTCTGACACTCAGACGCGACAGCTAGGGTAGTAACGGGATTAGAGACCCCGGTAACTCTAG CCGTAAACGATGTGAACCTGGCGTTGGTGGTTAACTCCATCAGTGCCGTAGCAAACGCGATAAGTTACCCTGGGACTACGGCCGCAAGGTTA
CDW	PROK_03014	GACGAACCGTGCTAACGTTGTTTCGGAATCACTGGGCTTAAAGGGCGCGTAGGCGGGCCGGAAGTCAAGGGGTGAAAGCCCGCGGCTCAACCGCGGAAGCGCTTTGATACTGCCGGCTCGAGGGGGGTAGGGGCGT GCGGAACCTCCGGTGGAGCGGTGAAATGCGTAGATATCGGAAGGAACACCGGTGGCGAAGGCGCGCTGGACCCCTCTGACGCTGAGGCGCGAAAGCCAGGGGAGCAAACGGGATTAGATACCCCGGTAGTCCCT GGCCCTAAACGATGGGTACTAGGTAGTGGGCTTACATGGGCTCACTGCCGAAGCAAAAGTGTAAAGTACCCCGCTGGGGAGTATGGTCGCAAGGCTG
CDW	PROK_07778	TACGGAAGGGGGCTAGCGTTGTTTCGGAATCACTGGGCTTAAAGGGCGCGTAGGCGGCTTTGTAAGTTAGAGGTGAAAGCCAGGGCTCAACCTCGGAATTGCTTTAAGACTGCATCGCTTGAACATCGGAGAGGTAAGT GGAATTCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAAGAACACCACTGGCGAAGGCGACTTACTGGACGATTGTTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGC CGTAAACGATGATGACTAGCTGTCCGGCTCTTGAGTTTCGGTGGCGCAGCTAACGCCTTAAGTCATCCGCTGGGGAGTACGGCCGCAAGGTTA
CDW	PROK_04965	TACGGAAGGGGGCTAGCGTTGTTTCGGAATCACTGGGCTTAAAGGGCGCGTAGGCGGCTTTGTAAGTTAGAGGTGAAAGCCAGGGCTCAACCTCGGAATTGCTTTAAGACTGCATCGCTTGAACATCGGAGAGGTAAGT GGAATTCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAAGAACACCACTGGCGAAGGCGACTTACTGGACGATTGTTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGC CGTAAACGATGATGACTAGCTGTCCGGCTCTTGAGTTTCGGTGGCGCAGCTAACGCCTTAAGTCATCCGCTGGGGAGTACGGCCGCAAGGTTA
CDW	PROK_00856	TACGTAGGCAGCAAGCGTTGTTTCGGAATCACTGGGCTTAAAGGGCGCGTAGGCGGCTTTGTAAGTTAGAGGTGAAAGCCAGGGCTCAACCTCGGAATTGCTTTAAGACTGCATCGCTTGAACATCGGAGAGGTAAGT GCGGAATTCGCGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGTGGTGTAGACGCTTACTGGACCATGACTGACGCTGAGGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCAC GCCCTAAACGATGCACACTTGGTGTGAGCGATTCAATTCGTTCTGTCGCCGAGCTAACGCGTTAAGTGTGCCGCTGGGGAGTACGGTCGCAAGGCTG
CDW	PROK_07784	GACAGAGGGGGCAAGCGTTGCTCGGAATCACTGGGCGTAAAGGGCGCGTAGGCGGGATGGCAAGTCGCTCGTAAATCCCTCGGCTCAACTGAGGAACGTCGATCGATACTGCCGTTCTTGAGGATTGCAGAGGAGA CTGGAATTCGCGGTGTAGCGGTGAAATGTGTAGAGATCGGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCAATTCCTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCCGGTAGTCCA CGCTGTAACGATGACGACTAGGTGTGGGGGGGTTAGTCCCTTCGTCGCCGAGCTAACGCATTAAGTCGTCGCCCTGGGGAGTACGGCCGCAAGGTTG
CDW	PROK_01520	GACGAACCGTGCGAACGTTGTTTCGGAATCACTGGGCTTAAAGGGCGCGTAGGCGGCCCCGCCGCTCCGGGTGAAATCTCCCGCTCAACCGGAGAACCGGCCCTCGGATACGGGCGGGTGGAGGGGGTAGGGGCG GGCGGAACGTGGGTGGAGCGGTGAAATGCGTTGAGATCCACAGGAACCTCCGTGGCGAAGGCGGCCGCTGGACCCCTCTGACGCTGAGGCGCGAAAGCCAGGGGAGCGAACGGGATTAGATACCCCGGTAGTC CTGGCCCTAAACGTTGAGGACTAGGTAGTACCCGGGTATGGGTTACTGCCGAGCGAAAGTGTAAAGTCTCCGCTGGGGAGTATGGTCGCAAGGCTG
CDW	PROK_03211	TACGTAGGGTGCGAGCGTTAATCGGAATCACTGGGCGTAAAGCGTGCGCAGGCGGTTTCGCTGTCTGTCTGTGTAAGGCCCGGGCTTAACCTGGGAATGCGATGGAACTGGCGAGCTGGAGTGGCGCAGAGGGGG GTGGAATTCGCGGTGTAGCAGTGAAATGCGTAGAGATGCGGAGGAACACCGATGGCGAAGGCGAGCCCCCTGGGTGACACTGACGCTCAGGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA CGCCCTAAACGATGTCAACTGGGTGTTGGGAAGCGATTCCCTAGTACCGTAGCTAACGCGTGAAGTTGACCGCTGGGGAGTACGGCCGCAAGGTTA
CDW	PROK_01980	TACAGAGGGTGCAAGCGTTAATCGGAATCACTGGGCTTAAAGGGCGCGTAGGCGGCTTTGTAAGTTAGAGGTGAAATCCCGGGCTCAACCTGGGAATGCATTCAAAGTGTGAGCTAGAGTATGGTAGAGGGTGG TGGAAATTCGCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCACTGGCGAAGGCGACCACTGGACTGATACTGACACTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACG CCGTAAACGATGTCAACTAGCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGACCGCTGGGGAGTACGGCCGCAAGGTTA
CDW	PROK_01076	TACGTATGTCCGAGCGTTATCCGATTATTGGGCGTAAAGCGAGCGCAGACGTTTATTAAGTCTGATGTGAAAGCCCCGGAGCTCAACTCCGGAATGGCATTGGAATCTGTTAATTGAGTGACGTAGAGGTAAGT GGAACCTCATGTGTAGCGGTGGAATGCGTAGATATAGGAAGAACACCACTGGCGAAGGCGGCTTACTGGACTGCAACTGACGTTGAGGCTCGAAAGTGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACAC CGTAAACGATGAACACTAGGTGTAGGAGGTTCCGCTCTTAGTGCCGAAGCTAACGCATTAAGTTGACCGCTGGGGAGTACGACCGCAAGGTTG
CDW	PROK_03212	TACGGAAGGGGGCTAGCGTTGTTTCGGAATCACTGGGCTTAAAGGGCGCGTAGGCGGCTTTGTAAGTTAGAGGTGAAATCCCGGGCTCAACCTGGGAATGCATTCAAAGTGTGAGCTGCATAGAATTGTGGAGAGGTGAG TGGAAATTCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAAGAACACCACTGGCGAAGGCGACTCACTGGACACATATTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACG CCGTAAACGATGATGACTAGCTGTCCGGGCTCATGGAGTTTCGGTGGCGCAGCTAACGCGTTAAGTCATCCGCTGGGGAGTACGGCCGCAAGGTTA

Supplementary Material

Microbial Fingerprinting of Marine Water Masses in an Antarctic and Hydrographically Complex Area

CDW	PROK_00344	TACGGAGGGTGAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGCTTTTAAAGTCGGATGTGAAAGCCCCGGGCTCAACCTGGGAATTGCATCTGATACTGGGAAGCTAGAGTATGTGAGAGGGGGTAGAATTCCAAGTGTAGCGGTGAAATGCGTAGAGATTTGGAGGAATACCAAGTGGCGAAGGCGGCCCTGGCACAATACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCTACTAGATGTTGAGGTCCTTGTACTTTGAGTATCGCAGCTAACGCATTAAGTAGACCGCCTGGGGAGTACGGTCGCAAGATTA
CDW	PROK_07211	TACGGAGGGGGCTAGCGTTGTTCCGAATTACTGGGCGTAAAGCGCACGTAGGCGGCTTTGTAAGTTAGAGGTGAAAGCCCCGGGCTCAACTCCGGAATGCCTTAAAGACTGCATCGCTAGAATTGTGGAGAGGTGAGTGGAAATCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAAGAACCAGTGGCGAAGGCGACTACTGGACACATATTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGATGACTAGCTGTCGGGGCTCTTGGAGTTTCGGTGGCGCAGCTAACCGCTTAAGTATCCGCTGGGGAGTACGGCCGCAAGGTTA
GMW	EUK_0010	TTCCAGCTCCAATAGCGTATATTAAAGTTGTTGCACTTAGAACGCTCGTAGTCGGATTTCCGGGCGAGTCCGACCGGTCTGCCGATGGGTATGCACTGGCCGAGTGTCTTTTGGCCGAGACCGTGCCTACTCTTAAGTACGCGGGGGCGGAGACGGCACTTTTACTTTGAAAAATCAGAGTGTTCAGCAGGCGAGCTCGCTCTTGCATGGATTAGAGGGATGTTTTACTGATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATACCGTCTGAGTCTTAACCATAAACCATGCCGACTAGGGATTGGAGGATGTTCACTGATTGACTCCTTCAGCACCTTACGGGAAACTAAAGTCTTTGGGTTCCGGGGGGAGTATGGTCGCAAGGCTG
GMW	PROK_00122	TACGGAGGGTCCAAGCGTTATCCGGAATCATTGGGTTTAAAGGGTGCAGGCGGTTTATTAAAGTCAGTGGTGAAATCTCGGGGCTCAACCTCGAAACTGCCATTGATACTGATAAACTTGAGTTCAGTTGGAGTAGGCGGAATGTGTAGTGTAGCGGTGAAATGCTTAGATATTACACAGAACCCGATAGCGAAGGCGAGCTTACTAACTGATACTGACGCTGAGGACGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACTATGATTACTCGATATTGGCGATATACTGTCACTGTCTAAGCGAAAGTGATAAGTAATCCACCTGGGGAGTACGGTCGCAAGATTG
GMW	PROK_01668	AACGTAGGTCAACAAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGCAGGCGGGAAGCAAGTTGGAAGTGAAATCCATGGGCTCAACCCATGAAGTCTTCAAAGTCTTTTCTTGTAGTAGTGCAGAGGTAGGCGGAATTCGGGTGTAGCGGTGGAATGCGTAGATATCGGGAGGAACACCAAGTGGCGAAGGCGGCTACTGGGCACCACTGACGCTGAGGCTCGAAAGTGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACACTGTAAACGATGATTACTAGGTGTTGGAGGATTGACCCCTTCAGTGCCGCAAGTAAACACAATAAGTAATCCACCTGGGGAGTACGACCGCAAGGTTG
GMW	PROK_04471	TACAGAGGGTGAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGTAGGTGTTTTGTAAGTTGGATGTGAAATCCCCGGGCTTAACTCGGGAAGTGCATTCAATACTGCCTACTAGAGTCTGGTAGAGGGAAGCGGAATTCACATGTAGCGGTGAAATGCGTAGATATGTGGAGGAACATCAATGGCGAAGGCGAGCTTCTGGACTGATACTGACACTGAGGTGCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCCTAAACGATGAGAACTAGATGTTGGGGAGTTTATCTTCTAGTGTGCGCAGCTAACGCGTTAAGTTCTCCGCTGGGGAGTACGGCCGCAAGGTTG
GMW	PROK_10101	TACGAAGGGGGCTAGCGTTGCTCGGAATTACTGGGCGTAAAGCGCACGTAGGCGGCTTTTAAAGTCAGGGGTGAAATCCTGGAGCTCAACTCCAGAAGTGCCTTGTAGTGAAGCTTGAGTCCGGGAGAGGTGAGTGGAACTGCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAAGAACCAGTGGCGAAGGCGGCTACTGGCCCGTACTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCTGTAACGATGGATGCTAGCGGTTGTCGGGTTTACTCGTCAGTGCGCAGCTAACGCATTAAGCATCCGCTGGGGAGTACGGTCGCAAGATTA
GMW	PROK_11095	TACGTAGGTGCAAGCGTTGTCGGGATTTATTGGGTTTAAAGGGTGCCTAGGTGGTCTTATTAAAGTCAGTGTGAAATATCCCGGCTTAACTCCGGAAGGTTGGCATTGATACTGATGGACTTGAGTGAGTTGAGGTAGGCGGAATTCAGCGGTGTAGCGGTGAAATGCTTAGATATCGTCAAGAACCACATAGCGAAGGCGAGCTTACTAAGCTCTAAGTACACTGACACTGATGCACGAAAGTGTGGGGATCAAACAGGATTAGATACCCTGGTAGTCCACACTGTAACCGTTGATTACTCGATGTTGGCGATACACAGTCAGCGTCTTAGCGCAAGCGATAAGTAAATCCACCTGGGGAGTACGGCCGCAACGGTG
GMW	PROK_07200	TACGAAGGGGGCTAGCGTTGCTCGGAATTACTGGGCGTAAAGGGCGCGTAGGCGGCTTTGTAAGTCAGAGGTGAAATCCTGGGCTTAACTCCGGAAGTGCCTTGTAGTGAAGTGTGAGTGAAGAGAGGGTGTGGAATTCAGTGTAGAGGTGAAATTCGTAGATATTCGGAAGAACCAGTGGCGAAGGCGGCGACCTGGTCTTTGACTGACGCTGAGGCGGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACCGCTGTAACGATGTGCGCTGGATGTTGGGCGACCTAGTCTGCTCAGTGTGCGCAGCTAACGCGCTAAGCGCACCGCTGGGGAGTACGGCCGCAAGGTTG
GMW	PROK_11193	TACAGAGGTCTCAAGCGTTGTTCCGGAATCATTGGGCGTAAAGGGTGCCTAGGTGGCGCTGTAAGTCGGGTGTGAAATTTCCGAGCTTAACTCCGAAACTGCATTGATACTGCGGTGCTTGAGGACTGGAGAGGAGACTGGAATTCATGGTGTAGCAGTGAAATGCGTAGAGATCATGAGGAAGACCAGTGGCGAAGGCGGGTCTCTGGACAGTTCCTGACGCTGAGGCACGAAAGTTCAGGGGAGCAAACAGGATTAGATACCCCGGTAGTCTGACAGTAAACGGTGCACGTTTGGTGTGGGAGGATTGACCCCTTCTGCGCCGAGCTAACGCGTTAAACGTGCCCTGGGGAGTACGGTCGCAAGATTA
GMW	PROK_00694	TACGTAGGGGGCTAGCGTTATCCGGAATTACTGGGCGTAAAGGGTGCCTAGGTGGTCTTTTAAAGTCAGGTGGTTAAAGGCTACGGCTCAACCGTAGTTAGCTTCCGAAACTGGAAGACTTGAGTGCAGGAGAGGAAAGTGGAAATTCAGTGTAGCGGTGAAATGCGTAGATATTGGGAGGAACACCAAGTAGCGAAGGCGGCTTTCTGGACTGCAACTGACACTGAGGCACGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCTGTAACGATGAGTACTAGGTGTCGGGGGTTACCCCTCGGTGCCGAGCTAACGCATTAAGTACTCCGCTGGGGAGTACGCACGCAAGGTG
GMW	PROK_08860	TACGTAGGGTGCAGCGTTGTCGGGAATTACTGGGCGTAAAGAGCTCGTAGGTGTTTTGTCGCGTTGTTCTGTAAGTGCACAGCTTAACTGTGGGCGTGCAGGCGATACGGGCAGACTGGAGTACTGCAGGGGAGATTGGAAATTCCTGGTGTAGCGGTGGAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCGGGTCTCTGGGCAGTAACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACCGTGGTACTAGGTGTGGGTTTCTTCTTGGGATCCGTGCCGTAGCTAACGCATTAAGTACCCCGCTGGGGAGTACGGCCGCAAGGCTA
GMW	PROK_02165	TACAGAGGTGGCAAGCGTTATCCGGAATTACTGGGCGTAAAGGGCGCGTAGGCGGCTTAAAGTCAGAGCTGAAATCCTGGGCTTAACTGGGAAGTGCCTGATACTGGACGGCTTGAGTAGGGAGAGGGATGTAGAATTCAGGTGTAGCGGTGAAATGCGTAGATATCTGGAGGAATACCGGTGGCGAAGGCGGCATCTGGACCATTACTGACGCTGATGCGGAAAGCTAGGGGAGCAAACAGGATTAGATACCCCGGTAGTCTAGCCCTAAACGATGAATGCTTGGTGTGGCGGGTATCGATCCCTGCCGTGCCGAAGCTAACGCATTAAGCATTCCGCTGGGGAGTACGGTCGCAAGGCTG
GMW	PROK_03897	TACGTAGGTGCAAGCGTTGTTCCGGAATTATTGGGCGTAAAGGGCGCGTAGGCGGCGGTTAAGTCAGCTGTGAAAGCCCCGGGCTCAACCCCGAGGGTTCGGCTGATACTGGTGGCTAGAGTACGGAAGAGGTAGCTGGAATTCGGGTGTAGCGGTGAAATGCGTAGATATCGGGAGGAACACCTGAGGCGAAGGCGGGTACTGGGCCGATACTGACGCTGATGCGCGAAAGCCAGGGGAGCGAACGGGATTAGATACCCCGGTAGTCTCTGGCCCTAAACGATGGACACTTGGTGTGTCGGGTCTTACAGTCCCGGCTGCCGAGCTAACGCGTTAAGTGTCCCGCTGGGGAGTACGGTCGCAAGGCTG
TBW	PROK_00456	TACGGAGGGTCCAAGCGTTATCCGGAATTACTGGGCGTAAAGGGCGCGTAGGCGGCTTAAAGTCAGAGCTGAAATCCTGGGCTTAACTGGGAAGTGCCTTGTAGTGAAGACTGCTATTGAAACTGTCAAGCTTGAATCTAGTTGAAGTGGGCGGAATACATCATGTAGCGGTGAAATGCATAGATATGATGTGGAACGCCGATTGCGAAGGCGAGCTACTAAGTTAGTATTGACGCTGAGGCACGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGGTCACTCGCTGTTGGCGACATAATGTCAGTGGCTGAGCGAAAGCATTAAAGTACCCACCTGGGGAGTACGTTGCAAGAATG

Microbial Fingerprinting of Marine Water Masses in an Antarctic and Hydrographically Complex Area

TBW	PROK_00103	TACGGAGGGTGCAAGCGTTATCCGGATTATTAGGTTTAAAGGGTCCGACGGCGGAATTTAAGTCAGTGGTGAAGCCTACAGCTCAACTGTAGAAGTCGCATTGAAACTGATATTTCTTGAGTAGATGAAGTGGCGG GAATATGTCATGTAGCGGTGAAATGCATAGATATGACATGGAACACCAATTGCGAAGGCAGCTCACTAACTATTACTGACGCTCATGAACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCC TAAACTATGATCACTAGATGTTGGCGATATAATTGTCAGTGTTTTAGAGAAATCGTTAAGTGATCCACCTGGGGAGTACGTTTCGAAGAATG
TBW	PROK_00110	TACGGAGGATGCGAGCGTTATCCGGATTATTGGGTTTAAAGGGTCCGACGGCGGACCAATCAGTCAGTGGTGAAATCCAATCGCTTAACGATTGAACTGCCATTGATACTGTTGGTCTTGAGTCTAGTTGACGTAGCGG GAATGTGACATGTAGCGGTGAAATGCATAGATATGTCACAGAACACCAATTGCGAAGGCAGCTTACGAAACTACGACTGACGCTCATGGACGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTGGTAGTCCACGCC GTAAACGATGATCACTCGATGTCACGATATACTGTTGGTGCTTAGCGAAAGTTTAAGTGATCCACCTGGGGAGTACGTTTCGAAGAATG
TBW	PROK_00085	TACGGAGGGTGCAAGCGTTATCCGGATTATTAGGTTTAAAGGGTCCGACGGCGGAATTTAAGTCAGTGGTGAAGCCCATAGCTCAACTATGGAATGCCATTGAACTGAATTTCTGAATATGATTGAAGCAGCGC GAATATGTCATGTAGCGGTGAAATGCTTAGATATGACATAGAACACCGATAGCGAAGGCAGCTTGCTAAGTCATTATTGACGCTGAGGGACGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCC GTAAACGATGATTACTAGCTATTGGCGATATACTGTCAGTGGCAAAGCGAAAGTGTTAAGTAATCCACCTGGGGAGTACGATCGAAGGTTG
TBW	PROK_02457	TACGGAGGGGGCTAACGTTGTTCCGAATTACTGGGCGTAAAGCGCGCGTAGGCGGATTAGACAGTTGAGGGTGAAATCCCGGAGCTTAACCTCCGGAACGTCCTTCAATACTACTAATCTTGAGTTGCGAAGAGGTGAGT GGAATTCCTAGTGTAGAGGTGAAATTCGTAGATATTAGGAAGAACATCAGTGGCGAAGGCAGCTCACTGGTCCGATACTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGC CGTAAACGATGGAAGCTAGTTGTCGGGCGGCATGCCGTTCCGTGACACAGTGAACGATTAAGCTTCCCGCTGGGGAGTACGATCGCAAGATTA
TBW	PROK_00062	TACGGAGGATCCAAGCGTTATCCGAATTATTGGGTTTAAAGGGTCCGACGGTGAAGCAATTAAGTCAGAGGTGAAATCTCGACGCTCAACTGTAGAATTGCCTTTGAAACTGGTGTCTTGAGTCAATTGAAGTGGTTA GAATGTGTAGTGAGCGGTGAAATGCATAGATATTACACAGAATACCAATTGCGAAGGCAGATCACTAATAATGTACTGACACTGATGGACGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTGGTAGTCCACGCC TAAACGATGTTACTAGCTGTTCCGACTTCGGTCTGAGTGGCTAAGCGAAAGTGATAAGTAACCCACCTGGGGAGTACGTTTCGAAGAATG
TBW	PROK_00649	TACATAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGTTTCGACGGCTGTTTTACAAGTCAGATGTGAATCCCGAGCTCAACTGGGAACGCGTTTGAACTGTAAGACTAGAGTGTGTGACAGGGGGGT AGAATTCACAGTGTAGCAGTGAAATGCGTAGATATGTGGAGGAATACCAATGGCGAAGGCAGCCCCCTGGGATAACACTGACGCTCATGAACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGC CCTAAACGATGTCTACTAGTTGTTGGTGGAGTAAATCCATGAGTAACGCAGCTAACGCGTGAAGTAGACCGCTGGGGAGTACGGTCGCAAGATTA
TBW	PROK_00316	TACGGAGGATCCAAGCGTTATCCGGATTATTGGGTTTAAAGGGTCCGACGGCGATCAATAAGTCAGTGGTGAAGCCCATAGCTCAACTATGGAACGCCATTGAACTGTTGATCTTGAGTCTAGTTGACGTAGCGC GAATGTGACATGTAGCGGTGAAATGCATAGATATGTCACAGAACCAAAATTGCGAAGGCAGCTTACGAAACTAGACTGACGCTCATGGACGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGT AAACGATGATCACTCGATGTCGCGCATATACTGTCGGTGTCCAAGCGAAAGTATTAAGTGATCCACCTGGGGAGTACGTTTCGAAGAATG
TBW	PROK_03146	TACGGGGAGAGTGAGCGTTATTCAGAATGACTGGGCGTAAAGGGTACGTAGGCTGTTTTTAGGTTGAAGGTGTAAGTTTCAAGCTTTACTTGAAGAATATTTTCAAAACCAAAAATCTAGAGCTTGAGTGAGGAGAGT AGAATTTTTAGTGGAGAGGTGAAATTCGTAGAGATTTAAAGGAATGTCAAGGCGAAAGCAACTCTCTGAATCAAAGCTGACGCTGAGGTACGAAAGCGTAGTTAGCAAGTGGGATTAGAGACCCCATAGTCTACGCAG TCAACGATGCCGGTTCATCCTTGCGTTAAAAATGCAGGGGTTTAGCTAACGCGTCAAACCGGCCGCTGAGGACTATGGCCGCAAGGTTA
TBW	PROK_00036	TACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGTGCGTAGGCGGTTTAAAGTCAGATGTGAAGCCCCGGGCTTAACCTGGGAACGTCATTTGAACTGGTCAACTAGAGTATGGTAGAGGAAAG TGGAAATTCGTGTTAGCGGTGAAATGCGTAGATATCAGAAGGAACCTTATGGCGAAGGCAACTTCTGGACCAACTACTGACGCTGAGGTACGAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGC CGTAAACGATGATAACTAGCCGTTGGGGGGATTACCCCTTAGTGCGCAAGCTAACGCGTTAAGTTATCCGCTGGGGAGTACGGCCGCAAGGTTA
TBW	PROK_06319	TACGGAGGGGGTTAGCGTTGTTCCGAATTACTGGGCGTAAAGCGCACGTAGGCGGATTAGTAAGTGAGGGGTGAAATCCCGAGGCTCAACCTCGGAACGTCCTTTCATACTGCTAGTCTAGAGTTGAGAGAGGTGAG TGGAAATTCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAACACCAGTGGCGAAGGCAGGCTCACTGGCTCGATACTGACGCTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACG CCGTAACGATGAGAGCTAGTCGTCGGGGGCGATGCCCTTCGGTGACGCAGTTAACGCATTAAGCTCTCCGCTGGGGAGTACGGTCGCAAGATTA
TBW	PROK_00232	TACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGCGGTTTCGGTAAGTTGGATGTGAAGGCCAGGGCTCAACCTTGGAACTGCATTCAAACCTGCCAGGCTAGAGTACGGTAGAGGGGG GTAGAATTCACGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAATACCAAGTGGCGAAGCGGCCCTGGATCGATCACTGACGTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA CGCTGTAAACGATGTCAACTAGCCGTTGGAGGGGTAATCCCTTAGTGCGCAGCTAACGCAATAAGTTGACCGCTGGGGAGTACGGTCGCAAGATTA
TBW	EUK_0014	TTCCAGCTCTAATAGCGTATATTTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTCGGATGTCGGGCTCGGGCAGGCTGTCGGCTTCGGTCGAGCGCAGGCTCGGGTCTTTCTGCCTGAGGATCCATTGCACTTTATTGTGG AGGTGGGGACGCAGGCCGTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCTACGCTTGAATACATTAGCATGGAACAAAGGATGTTTTATTGATCAAGAACGAAAGTTAGGGGATCGAAGACGATCAGATACCCT CGTAGTCTTAACCATAACTATGCCGACTAGGGATCAGTGGATGTCAATTTGCGACTCCATTGGCACCTTGTGAGAAATCAAAGTTTTTGGGTTCCGGGGGGAGTATGGTCGCAAGGCTG
TBW	PROK_01050	TACGAGGGGTGCAAGCGTTGTCGGAATCATTGGGCGTAAAGGGTCCGTAGGCGTTTCAATAAGTCATTTGTGAAGACACCCGGCTCAACCGGTGGCCCGCATTCGAAACTGTTGAAATAGAGTATAGGAGAGGGAAAG TGGAAATTCGTGTTAGCGGTGACATGCGTAGATATCAGGAGGAACCAAAATGGCGAAGGCAGCTTTCTGCCCTATTACTGACGTGAGGGACGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACG CCGTAAACGATGTAGTATTGGTGTGGGGGAAATCGACCCCTCGGTACCGGAGTAAACGATTAAGTACTCCGCTGGGAACATCGTCCGCAAGGATG
TWW	PROK_01014	TACGTAGGGTGCGAGCGTTAATCGGAATTACTGGGCGTAAAGCGTGCGCAGGCGGTTTTGTAAGCCAGATGTGAATCCCGGGGCTTAACCTGGGAATGGCATTGGGACTGCAAGGCTGGAGTGCGGCAGAGGAGAC TGGAAATTCGTGTTAGCAGTGAAATGCGTAGATATCAGGAGGAACACCGATGGCGAAGGCAGGTCTCTGGGCTGACACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACG CCCTAAACGATGTCGACTGTTGTTGGGGGTTTGACACTCTCAGTAACGAAGCTAACGCGTGAAAGTCGACCGCTGGGGAGTACGGCCGCAAGGTTA
TWW	PROK_02182	TACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGTGCGCAGGCGGTTTTGTAAGTCTGTCTGTAATCCCGGGGCTTAACCTGGGAATGGCGATGGAGACTGCGAGGCTAGAGTTTGGCAGAGGGGG GTAGAATTCACGTGTAGCAGTGAAATGCGTAGAGATGTGGAGGAACACCGATGGCGAAGGCAGGCCCTGGGTCAAACCTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCAC GCCCTAAACGATGTCTACTAGTTGTTGGGCTTTAATTGACTTAGTAACGCAAGTAAACGCTGAAAGTGAAGTACCGCTGGGGAGTACGTTTCGAAGAATTA

Supplementary Material

Microbial Fingerprinting of Marine Water Masses in an Antarctic and Hydrographically Complex Area

TWW	PROK_01064	TACGAAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGGGTGCGTAGGCGGTTAGTTAAGTCTGTTGTGAAATCCCCGGGCTCAACCTGGGAATGGCAATGGATACTGGCTAGCTAGAGTGTGTCAGAGGATGG TGGAATTTCCGGTGTAGCGGTGAAATGCGTAGAGATCGGAAGGAACATCAGTGGCGAAGGCGGCCATCTGGGACAACACTGACGCTGAAGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCAC GCCCTAAACGATGCGAACTGGATGTTGGTCTCAACTCGGAGATCAGTGTGCAAGCTAACGCGTTAAGTTCGCCGCCTGGGGAGTACGGTCGCAAGACTG
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Supplementary Material

Microbial Fingerprinting of Marine Water Masses in an Antarctic and Hydrographically Complex Area

Supplementary Table 7. DNA sequences of the core microbes.

Water Mass	ASVs	DNA Sequence
CDW	PROK_00001	TACGAAGGGGGCTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGCGCGTAGGCGCGTTTTAAGTCGGGGGTGAAAGCCTGTGGCTCAACCACAGAATGGCCTTCGATACTGGGACGCTTGAGTATGGTAGAGTTG GTGGAAGTGCAGGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACCACGGTGGCGAAGGCGGCCAACTGGACCATTACTGACGCTGAGGCGCGAAAGCGTGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA CGCCGTAACGATGAATGCCAGCTGTTGGGGTGCTTGACCCGAGTAGCGCAGCTAACGCTTTGAGCAITCCGCCTGGGGAGTACGGTCGCAAGATTA
CDW	PROK_00011	TACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCTAGGCGGTTTTTAAGTCTGATGTGAAAGCCCACGGCTCAACCTGGGAACTGCATCTGATACTGGCAAGCTTGAGTCTCGTAGAGGGGG TGGAAATCCATGTGTAGCGGTGAAATGCGCAGAGATATGGAGGAACACCGATGGCGAAGGCGCAGTTTCTGGTCTGTAAGTACGCTGATGTGCGAAAGCGTGGGGATCAAACAGGATTAGATACCCTGGTAGTCCACG CCGTAACGATGAGTGCTAAGTGTAGGGGGTTCCGCCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCCGAAGGTTG
CDW	PROK_00046	TACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGACGGCGGTTTGTAAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATCTGATACTGGCAAGCTTGAGTCTCGTAGAGGGGG TAGAATTCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCAC GCCGTAACGATGTGCACTTGAGGTTGTGCCCTTGAGGCGTGCTTCCGAGCTAACGCGTTAAGTCGACCGCTGGGGAGTACGGCCGCAAGGTTA
CDW	PROK_00094	TACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGTGCGCAGGCGTTTTGTAAAGTCTGTCTGTGAAAGCCCCGGGCTCAACCTGGGAATTGCGATGGAGACTGCAAGGCTTGAATCTGGCAGAGGGGG TAGAATTCACGTGTAGCAGTGAAATGCGTAGAGATGTGGAGGAACACCGATGGCGAAGGCGAGCCCCCTGGGTCAAGATTGACGCTATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACG CCCTAACGATGTCTACTAGTTGTCGGGTTTAATTAACCTGGTAACGCAGCTAACGCGTGAAGTAGACCGCTGGGGAGTACGGTCGCAAGATTA
CDW	PROK_00156	TACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGTGCGCAGGCGTTTTGTAAAGTCTGTCTGTGAAATCCCCGGGCTCAACCTGGGAATTGCGATGGAGACTGCAAGGCTGGAGTCTGGCAGAGGGGG TAGAATTCACGTGTAGCAGTGAAATGCGTAGAGATGTGGAGGAACACCGATGGCGAAGGCGAGCCCCCTGGGTCAAGACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACG CCCTAACGATGTCTACTAGTTGTCGGGTTTAATTAACCTGGTAACGCAGCTAACGCGTGAAGTAGACCGCTGGGGAGTACGGTCGCAAGATTA
CDW	PROK_00173	TACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGTGCGCAGGCGTTTTGTAAAGTCTGTCTGTGAAATCCCCGGGCTCAACCTGGGAATTGCGATGGAGACTGCAAGGCTGGAGTCTGGCAGAGGGGG TAGAATTCACGTGTAGCAGTGAAATGCGTAGAGATGTGGAGGAACACCGATGGCGAAGGCGAGCCCCCTGGGTCAAGACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACG CCCTAACGATGTCTACTAGTTGTCGGGTTTAATTAACCTGGTAACGCAGCTAACGCGTGAAGTAGACCGCTGGGGAGTACGGTCGCAAGATTA
TWW	PROK_00001	TACGAAGGGGGCTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGCGCGTAGGCGCGTTTTAAGTCGGGGGTGAAAGCCTGTGGCTCAACCACAGAATGGCCTTCGATACTGGGACGCTTGAGTATGGTAGAGTTG GTGGAAGTGCAGGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACCACGGTGGCGAAGGCGGCCAACTGGACCATTACTGACGCTGAGGCGCGAAAGCGTGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA CGCCGTAACGATGAATGCCAGCTGTTGGGGTGCTTGACCCGAGTAGCGCAGCTAACGCTTTGAGCAITCCGCCTGGGGAGTACGGTCGCAAGATTA
TWW	PROK_00046	TACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGACGGCGGTTTGTAAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATCTGATACTGGCAAGCTTGAGTCTCGTAGAGGGGG TAGAATTCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCAC GCCGTAACGATGTGCACTTGAGGTTGTGCCCTTGAGGCGTGCTTCCGAGCTAACGCGTTAAGTCGACCGCTGGGGAGTACGGCCGCAAGGTTA
TWW	PROK_00094	TACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGTGCGCAGGCGTTTTGTAAAGTCTGTCTGTGAAATCCCCGGGCTCAACCTGGGAATTGCGATGGAGACTGCAAGGCTTGAATCTGGCAGAGGGGG TAGAATTCACGTGTAGCAGTGAAATGCGTAGAGATGTGGAGGAACACCGATGGCGAAGGCGAGCCCCCTGGGTCAAGATTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACG CCCTAACGATGTCTACTAGTTGTCGGGTTTAATTAACCTGGTAACGCAGCTAACGCGTGAAGTAGACCGCTGGGGAGTACGGTCGCAAGATTA
TWW	PROK_00156	TACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGTGCGCAGGCGTTTTGTAAAGTCTGACGTGAAATCCCCGGGCTCAACCTGGGAATTGCGATGGAGACTGCAAGGCTGGAGTCTGGCAGAGGGGG TAGAATTCACGTGTAGCAGTGAAATGCGTAGAGATGTGGAGGAACACCGATGGCGAAGGCGAGCCCCCTGGGTCAAGACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACG CCCTAACGATGTCTACTAGTTGTCGGGTTTAATTAACCTGGTAACGCAGCTAACGCGTGAAGTAGACCGCTGGGGAGTACGGTCGCAAGATTA
GMW	PROK_00001	TACGAAGGGGGCTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGCGCGTAGGCGCGTTTTAAGTCGGGGGTGAAAGCCTGTGGCTCAACCACAGAATGGCCTTCGATACTGGGACGCTTGAGTATGGTAGAGTTG GTGGAAGTGCAGGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACCACGGTGGCGAAGGCGGCCAACTGGACCATTACTGACGCTGAGGCGCGAAAGCGTGGGAGCAAACAGGATTAGATACCCTGGTAGTCCA CGCCGTAACGATGAATGCCAGCTGTTGGGGTGCTTGACCCGAGTAGCGCAGCTAACGCTTTGAGCAITCCGCCTGGGGAGTACGGTCGCAAGATTA
GMW	PROK_00003	TACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGTGCGCAGGCGTTTTGTAAAGTCTGTCTGTGAAATCCCCGGGCTCAACCTGGGAATTGCGATGGAGACTGCAAGGCTGGAGTCTGGCAGAGGGGG TAGAATTCACGTGTAGCAGTGAAATGCGTAGAGATGTGGAGGAACACCGATGGCGAAGGCGAGCCCCCTGGGTCAAGACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACG CCCTAACGATGTCTACTAGTTGTCGGGTTTAATTAACCTGGTAACGCAGCTAACGCGTGAAGTAGACCGCTGGGGAGTACGGTCGCAAGATTA
GMW	PROK_00020	TACGGAGGGTGCAAGCGTTATCCGGAATCATTGGGTTTAAAGGTCCTGAGGCGGCTATTAAAGTCAGAGGTGAAAGTTTGACAGCTCAACTGTAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTGCAAGTTG GAATAAGTAGTGTAGCGGTGAAATGCATAGATATTAAGTAATACCAATTGCGAAGGCGAGTCACTAATAATATATTGACGCTGAGGGACGAAAGCGTGGGGAGCGAAGAGGATTAGATACCCTGGTAGTCCACGCCG TAAACGATGGATACTAGCTGTTCCGATTATCTGAGTGGCTAAGCGAAAGTGATAAGTATCCACCTGGGGAGTACGTTGCAAGAATG

Supplementary Material

Microbial Fingerprinting of Marine Water Masses in an Antarctic and Hydrographically Complex Area

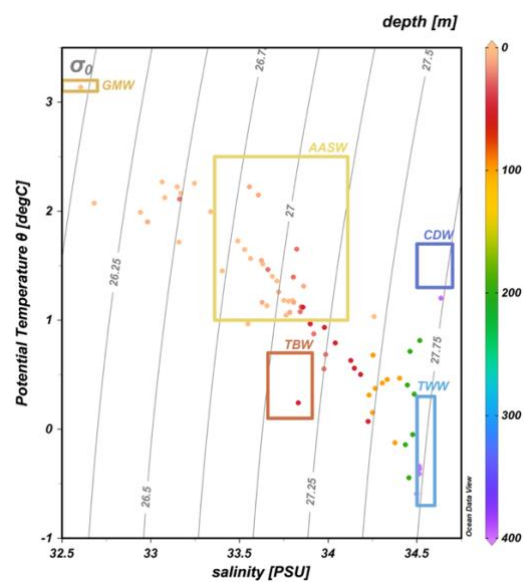
GMW	PROK_00024	TACGGAGGGTCCAAGCGTTATCCGATTATTGGGTTTAAAGGGTCCGTAGGCGGGTCATTAAAGTCAGTGGTGAAATCCTACAGCTCAACTGTAGAAGTCCATTGAACTGGTGACCTTGAATAAATTGAAGTAGGCGG GAATGTGTATGTAGCGGTGAAATGCTTAGATATGCCACAGAACACCGATTGCGAAGGCAGCTTACTAAGTTATTATTGACGCTGAGGGACGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCG TAAACGATGTATACTCGTTGCTAGCGATACACAGTTAGTGACCAAGCGAAAGTATTAAGTATACCACCTGGGGAGTACGATCGCAAGATTG
GMW	PROK_00032	TACGGAGGGTCCGAGCGTTATCCGGAATCATTGGGTTTAAAGGGTCCGAGGCGGTCTATTAAAGTCAGAGGTGAAATCCCATAGCTCAACTATGGAAGTGCCTTTGATACTGGTTGACTTGAGTCATATGGAAGTGGATA GAATGTGTAGTGTAGCGGTGAAATGCATAGATATTACACAGAATACCGATTGCGAAGGCAGTCCACTACGTATGTACTGACGCTGAGGGACGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCC GTAACGATGGATACTAGTTGTTGGGATTATCTCAGTGACTAAGCGAAAGTGATAAGTATCCACCTGGGGAGTACGGTCGCAAGACTG
GMW	PROK_00043	TACGGAGGGTCCAAGCGTTATCCGGAATCATTGGGTTTAAAGGGTCCGTAGGCGGGGAGAATAAGTCAGTGGTGAAAGCCCTACAGCTCAACTGTAGAAGTGCCTTTGATACTGGTTGACTTGAGTCATATGGAAGTGGGCG GAATATATCATGTAGCGGTGAAATGCATAGATATGATATAGAACACCGATTGCGAAGGCAGTCACTAACTAATATTGACGCTGAGGGACGAAAGGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACACCG TAAACGATGATTACTCGATGCTAGCGATATACTGTTAGTGTCTAAGCGAAAGCGATAAGTATCCACCTGGGGAGTACGGTCGCAAGATTG
AASW	PROK_00001	TACGAAGGGGGGTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGCGCGTAGGCGGCGTTTTAAGTCGGGGGTGAAAGCCCTGTGGCTCAACCACAGAATGGCCTTCGATACTGGGACGCTTGAGTATGGTAGAGGTTG GTGGAAGTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCGGTGGCGAAGGCGGCCAACTGGACCATTACTGACGCTGAGGCGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCA CGCCGTAACGATGAATGCCAGCTGTTGGGGTCTTGACCCGAGTAGCGCAGCTAACGCTTTGAGCATTCCGCTGGGGAGTACGGTCGCAAGATTG
AASW	PROK_00003	TACGTAGGGTGCAAGCGTTAATCGGAATTAAGCGGCTGAAAGCGTGGCGAGGCGGTTTTGTAAGTCTGCTGTAAGTCCCGGGCTCAACTGGGAATTGCGATGGAGACTGCAAGGCTGGAGTCTGGCAGAGGGGG TAGAATTCACGTGTAGCAGTGAAATGCGTAGAGATGTGGAGGAACACCGATGGCGAAGGCAGCCCCCTGGGTCAAGACTGACGCTCATGCACGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACG CCCTAACGATGTCTACTAGTTGTGCGGTCTTAATTGACTTGGTAACGACGCTAACGCGTGAAGTAGACCGCTGGGGAGTACGGTCGCAAGATTG
AASW	PROK_00015	TACGGAGGGTCAAGCGTTAATCGGAATTAAGCGGCTGAAAGCGCGCTAGGTTGTTTAAAGTCGGAATGTGAAAGCCCTGGGCTCAACTAGGAATTGCATCCCAAAGTGGCAGACTAGAGTACAAGAGAGGGGTG TGGAAATTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACATCAGTGGCGAAGGCGACGCCCTGGCTTGATACTGACACTGAGGTGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACG CCGTAACGATGTCTACTAGCGTTGGGGGACTTGATCCCTAGTGGCGAAGCTAACGCGATAAGTAGACCGCTGGGGAGTACGGTCGCAAGATTG
TBW	PROK_00001	TACGAAGGGGGGTAGCGTTGCTCGGAATCACTGGGCGTAAAGGGCGCGTAGGCGGCGTTTTAAGTCGGGGGTGAAAGCCCTGTGGCTCAACCACAGAATGGCCTTCGATACTGGGACGCTTGAGTATGGTAGAGGTTG GTGGAAGTCCGAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGAACACCGGTGGCGAAGGCGGCCAACTGGACCATTACTGACGCTGAGGCGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCA CGCCGTAACGATGAATGCCAGCTGTTGGGGTCTTGACCCGAGTAGCGCAGCTAACGCTTTGAGCATTCCGCTGGGGAGTACGGTCGCAAGATTG
TBW	PROK_00003	TACGTAGGGTGCAAGCGTTAATCGGAATTAAGCGGCTGAAAGCGCGCTAGGTTGTTTAAAGTCGCTGTAAGTCCCGGGCTCAACTGGGAATTGCGATGGAGACTGCAAGGCTGGAGTCTGGCAGAGGGGG TAGAATTCACGTGTAGCAGTGAAATGCGTAGAGATGTGGAGGAACACCGATGGCGAAGGCAGCCCCCTGGGTCAAGACTGACGCTCATGCACGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACG CCCTAACGATGTCTACTAGTTGTGCGGTCTTAATTGACTTGGTAACGACGCTAACGCGTGAAGTAGACCGCTGGGGAGTACGGTCGCAAGATTG
TBW	PROK_00015	TACGGAGGGTCAAGCGTTAATCGGAATTAAGCGGCTGAAAGCGCGCTAGGTTGTTTAAAGTCGGAATGTGAAAGCCCTGGGCTCAACTAGGAATTGCATCCCAAAGTGGCAGACTAGAGTACAAGAGAGGGGTG TGGAAATTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACATCAGTGGCGAAGGCGACGCCCTGGCTTGATACTGACACTGAGGTGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACG CCGTAACGATGTCTACTAGCGTTGGGGGACTTGATCCCTAGTGGCGAAGCTAACGCGATAAGTAGACCGCTGGGGAGTACGGTCGCAAGATTG
TBW	PROK_00020	TACGGAGGGTCCAAGCGTTATCCGGAATCATTGGGTTTAAAGGGTCCGTAGGCGGGCTATTAAAGTCAGAGGTGAAAGTTTGACGCTCAACTGTAAAATTGCCTTTGAACTGGTAGTCTTGAATTATTATGAAGTGGTTA GAATAAGTAGTGTAGCGGTGAAATGCATAGATATTACTTAGAATACCAATTGCGAAGGCAGATCACTAATAATATATTGACGCTGAGGGACGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCG TAAACGATGGATACTAGCTGTTCCGATTATCTGAGTGGCTAAGCGAAAGTGATAAGTATCCACCTGGGGAGTACGTTGCAAGAAATG
TBW	PROK_00024	TACGGAGGGTCCAAGCGTTATCCGGAATCATTGGGTTTAAAGGGTCCGTAGGCGGGTCATTAAAGTCAGTGGTGAAATCCTACAGCTCAACTGTAGAAGTGCCTTTGAACTGGTGACCTTGAATAAATTGAAGTAGGCG GAATGTGTATGTAGCGGTGAAATGCTTAGATATGCCACAGAACACCGATTGCGAAGGCAGCTTACTAAGTTATTATTGACGCTGAGGGACGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCG TAAACGATGTATACTCGTTGCTAGCGATACACAGTTAGTGACCAAGCGAAAGTATTAAGTATACCACCTGGGGAGTACGATCGCAAGATTG
TBW	PROK_00027	TACGGAGGGTCAAGCGTTAATCGGAATTAAGCGGCTGAAAGCGCGCTAGGTTGTTTAAAGTCGGAATGTGAAAGCCCTGGGCTCAACTAGGAATTGCATCCCAAAGTGGCAAACTAGAGTACAAGAGAGGGGTG TGGAAATTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACATCAGTGGCGAAGGCGACGCCCTGGCTTGATACTGACACTGAGGTGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACG CCGTAACGATGTCTACTAGCGTTGGGGGACTTGATCCCTAGTGGCGAAGCTAACGCGATAAGTAGACCGCTGGGGAGTACGGTCGCAAGATTG
TBW	PROK_00032	TACGGAGGGTCCGAGCGTTATCCGGAATCATTGGGTTTAAAGGGTCCGTAGGCGGGTCATTAAAGTCAGAGGTGAAATCCCATAGCTCAACTGTAGAAGTGCCTTTGATACTGGTTGACTTGAGTCATATGGAAGTGGATA GAATGTGTAGTGTAGCGGTGAAATGCATAGATATTACACAGAATACCGATTGCGAAGGCAGTCCACTACGTATGTACTGACGCTGAGGGACGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCC GTAACGATGGATACTAGTTGTTGGGATTATCTCAGTGACTAAGCGAAAGTGATAAGTATCCACCTGGGGAGTACGGTCGCAAGACTG
TBW	PROK_00036	TACGGAGGGTCAAGCGTTAATCGGAATTAAGCGGCTGAAAGCGCGCTAGGTTGTTTAAAGTCAGATGTGAAAGCCCGGGCTTAACCTGGGAAGTGCATTGAAACTGGTCAACTAGAGTATGGTAGAGGAAAG TGGAAATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGAAGGAACATCAATGGCGAAGGCAACTTTCTGGACCAATACTGACGCTGAGGTACGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTGGTAGTCCACGC CGTAAACGATGATAACTAGCCGTTGGGGGATTACCCCTTAGTGGCGAAGCTAACGCGTTAAGTATCCGCTGGGGAGTACGGTCGCAAGGTTA
TBW	PROK_00045	TACGGAGGATCCAAGCGTTATCCGGAATCATTGGGTTTAAAGGGTCCGTAGGCGGCTCTTTAAGTCAGAGGTGAAATCCCATAGCTCAACTGTAGAAGTGCCTTTGATACTGAAAGACTTGAGTTATTGTGAAGTAGTTA GAATGTGTGGTGTAGCGGTGAAATGCATAGAGATCACACAGAATACCGATTGCGAAGGCAGATTACTAACATATACTGACGCTGAGGGACGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTGGTAGTCCACGCC GTAACGATGGATACTAGCTGTTGACCAACATTGGTTGGTTGAGTGGCTAAGCGAAAGTGATAAGTATCCACCTGGGGAGTACGGTCGCAAGACTG

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TBW	PROK_00059	TACGAAGGGACCTAGCGTAGTTCGGAATTACTGGGCTTAAAGAGTTCGTAGGTGGTTGAAAAAGTTGGTGGTGAAATCCCAGAGCTTAACTCTGGAAGTCCATCAAACTTTTCAGCTAGAGTATGATAGAGGAAAGC AGAATTTCTAGGTAGAGGTGAAATTCGTAGATATTAGAAAGAATACCAATTGCGAAGGCAGCTTTCTGGATCATTACTGACACTGAGGAACGAAAGCATGGGTAGCGAAGAGGATTAGATACCCTCGTAGTCCATGCC GTAAACGATGTGTGTAGACGTTGAAATTTATTTTCAGTGTCGCAGGGAAACCGATAAACACACCGCCTGGGGAGTACGACCGCAAGGTTA
TBW	PROK_00094	TACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGTGCGCAGGCGTTTTGTAAGTCTGTCTGTAAAGCCCCGGGCTCAACCTGGGAATTGCGATGGAGACTGCAAGGCTTGAATCTGGCAGAGGGGGG TAGAATTCACGTGTAGCAGTGAAATGCGTAGAGATGTGGAGGAACACCGATGGCGAAGGCAGCCCCCTGGGTCAAGATTGACGCTCATGCACGAAAGCGTGGGGAGCAACAGGATTAGATACCCTGGTAGTCCACG CCCTAAACGATGTCTACTAGTTGTCGGGTTTTAATTAACCTTGGTAAACGCAGCTAACGCGTGAAGTAGACCGCCTGGGGAGTACGGTCGCAAGATTA

Supplementary Table 8. Different metrics of co-occurrence networks calculated for each of the water masses considered in this study.

	Nodes	Edges	Average distance	Modularity index	Average degree	Average clustering	Average density
General	384	776	2.1798	0.5855	4.0417	0.4535	0.0105
AASW	137	722	2.1404	0.3465	10.5401	0.5767	0.0775
GMW	112	849	2.0343	0.2233	15.1607	0.6081	0.1366
TBW	264	748	2.1587	0.4298	5.6667	0.4704	0.0215
TWW	176	138	1.3067	0.9579	1.5682	0.4912	0.0089
CDW	42	83	2.5034	0.5784	3.9524	0.4071	0.0964



Supplementary Figure 23. Temperature-Salinity (T-S) diagram with water mass cores included. Details about water masses are included in Supplementary Table 2. Triangles applied: GMW-AASW-TBW; AASW-TBW-TWW; TBW-TWW-CDW.

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Supplementary Table 9. Formulas used for calculating alpha diversity. For the Shannon index: p_i is the relative abundance of species i . For the Simpson index: n_i is the number of reads belonging to species i and N is the total number of reads. For the Pielou index: p_i is the proportion of the total sample represented by species i and S is the number of species in a sample.

Shannon index (H')	Simpson index (D')	Pielou index (J')
$H' = -\sum(p_i \ln(p_i))$	$D' = \sum n_i(n_i-1)/N(N-1)$	$J' = -\sum p_i \ln(p_i)/\ln(S)$