1   **Supplementary Information for**

2   **"Tagging of water masses with covariance of trace metals and prokaryotic taxa in the**

3   **Southern Ocean"**

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18   **This file includes:**

19   Supplemental Methods and Results.

20   Supplementary Figures 1 - 12.

21   Supplementary Table 1 - 4.

Supplementary Methods

The identification of water masses

Water masses were identified at each station from the vertical profile of physical properties (Fig. S1, Table S1) and geographical considerations, in particular the location of main Southern Ocean fronts as determined by Park et al (Park et al. 2019). The most abundant water masses of the Southern Ocean were identified from their neutral density, γ^n (Orsi et al. 1999; Bindoff and McDougall 2000; Talley et al. 2011), with highest values in water masses close to the bottom decreasing upwards; Antarctic Bottom Water (AABW, $\gamma^n > 28.27$ kg m^{-3}), Lower Circumpolar Deep Water (LCDW, $\gamma^n > 27.8$), Upper Circumpolar Deep Water (UCDW, $\gamma^n > 27.5$) and Antarctic Intermediate Water (AAIW, $\gamma^n > 27.2$). Within the LCDW density range, the presence of North Atlantic Deep Water (NADW) was determined from the salinity criterion S> 34.8 (Park et al. 1993, 2001). In the Aghulas Current sector, Arabian Sea Low Oxygen Water (ASLOW) was identified as a low-oxygen (< 165 µmol/kg) subsurface layer near $\gamma^n = 25.5$, whereas Red Sea Overflow Water (RSOW) was identified as interleaving saline layers within the AAIW salinity minimum, following Beal et al (Beal et al. 2006). The presence of mode waters (STMW) was assessed from the detection of a homogeneous low-potential vorticity layer in their corresponding density range.

Sample collection and analysis of environmental parameters

Concentration of trace metals. To sample seawater for trace metal determination, the trace metal clean rosette equipped with 24 GO-FLO bottles was deployed using a Kevlar wire. GO-FLO bottles and all sampling material were cleaned before the cruise following the GEOTRACES cookbook (Cutter et al. 2017). Immediately after recovery, the rosette was transferred into a clean container for sampling trace elements. Particle levels were controlled with a particle counter (Lighthouse HH3016) and when levels were adequate for ISO class 6 levels, sampling could begin. Bottles were pressurized with 0.2 µm-filtered nitrogen (Air Liquide®).

Samples dedicated to dissolved trace metal analyses were filtered on-line through a 0.45µm polyethersulfone filter (Supor®) and collected in duplicates in acid-cleaned 60mL LDPE bottles. All samples were acidified within 24h of collection with hydrochloric acid (HCl, ultrapure grade, Merck, final pH 1.8).

Concentrations of dissolved iron (dFe), manganese (dMn), copper (dCu), nickel (dNi) were analyzed using the preconcentration system seaFAST-pico™ coupled to a high-resolution magnetic sector field inductively-coupled plasma mass spectrometer (SF-ICP-MS, Element XR – Pôle Spectrométrie Ocean, Brest) following Tonnard et al. (Tonnard et al. 2020). Acidified MQ water with hydrochloric acid (HCl, ultrapure grade, Merck, 0.2‰, final pH 1.8) (n=9) was analyzed and used as the analytical blank (dFe=0.14±0.05 nmol L-1, dMn=0.08±0.04 nmol L-1, dCu=0.05±0.01 nmol L-1, dNi=0.06±0.01 nmol L-1). All trace metal data were above the detection limit (LOD), defined as three times the standard deviation (sd) of the blank. The reproducibility of our analyses has been verified with duplicat analyses (n=22). Reference seawater (NASS-7) and GEOTRACES consensus (GSC and GSP) seawaters were used to certify the accuracy of our analyses.

measured reference	dFe (nmol L^{-1})	dMn (nmol L^{-1})	dCu (nmol L^{-1})	dNi (nmol L^{-1})
NASS 7	**5.87±0.62**	**12.52±0.87**	**2.60±0.16**	**3.74±0.16**
(n=10)	*6.23±0.46*	*13.65±1.09*	*3.16±0.22*	*4.14±0.30*
GSC (n=15)	**1.76±0.35**	**1.87±0.31**	**1.08±0.19**	**3.81±0.66**
	1.53±0.12	*2.18±0.07*	*1.10±0.15*	*4.39±0.20*
GSP (n=2)	**0.18±0.02**	**0.65±0.04**	**0.55±0.08**	**2.77±0.06**
	0.16±0.04	*0.78±0.03*	*0.57±0.05*	*2.60±0.10*

Concentration of inorganic nutrients. To collect samples for the determination of the concentration of phosphate (PO_4^{3-}), nitrate (NO_3^-) and nitrite (NO_2^-), syringes (50 mL) were directly connected to the spigot of the Niskin bottles. The samples were drawn through a 0.45 μm Uptidisc (Whatman) adapted for the syringe. The samples (25 mL) were poisoned with mercuric chloride ($HgCl_2$, 20 mg L^{-1}, final concentration) and stored in the dark at room temperature for later analysis in the home lab as described in (Blain et al. 2015). Analyses were done on a segmented flow analyzer (Skalar) equipped with colorimetric detection using methods described in (Aminot and Kérouel 2007). The accuracy of the methods was assessed using reference material (Certipur, Merck). The precisions were in the range of 1–4 %, and the limit of detection was 0.02 μM for nitrate and nitrite, and 0.03 μM for phosphate.

Concentration of dissolved organic carbon (DOC). The concentration of DOC was determined in samples filtered through two combusted (450 °C, 4 h) GF/F filters. Subsamples of 10 mL (in duplicate) were transferred to pre-combusted glass ampoules and acidified with H_3PO_4 (final pH

78 = 2). The sealed glass ampoules were stored in the dark at room temperature until analysis. DOC

79 concentrations were measured on a Shimadzu TOC-L analyzer as described previously

80 (Hernandez-Magana et al. 2021). Consensus reference material (batch #04-21 DSR (700

81 m) consensus value [43-45] µM) provided in sealed glass ampoules (https://hansell-

82 lab.earth.miami.edu/consensus-reference-material/index.html) was injected every 12 to 17

83 samples to insure stable operating conditions. The measured DOC concentration of this reference

84 material was on average 44.7±2.0 µM.

85 *Apparent Oxygen Utilization (AOU)*. Dissolved oxygen concentrations (O_2 meas) were measured

86 using the calibrated oxygen sensor mounted on the CTD frame. The concentration of oxygen at

87 saturation (O_2 sat) was calculated using the solubility equation provided by Garcia et al (Garcia

88 and Gordon 1992), using temperature and salinity measured by the CTD sensor. AOU was

89 derived using the equation AOU = O_2 sat - O_2 meas.

90 *Enumeration of prokaryotic abundance.* To determine the abundance of prokaryotic cells, raw

91 seawater samples (1.45 mL) were fixed with glutaraldehyde (1% final concentration), incubated

92 at 4°C for 30 minutes, shock-frozen in liquid nitrogen and stored at -80°C until analyzed back in

93 the home laboratory. The prokaryotic cell abundance was determined by flow cytometry as

94 described previously (Hernandez-Magana et al. 2021). Counts were performed on a FACSCanto

95 II flow cytometer (Becton Dickinson) equipped with 3 air-cooled lasers: blue (argon 488 nm),

96 red (633 nm) and violet (407 nm). Cells were stained with SYBR Green I (Invitrogen –

97 Molecular Probes) at 0.025% (vol/vol) final concentration for 15 min at room temperature in the

98 dark. Stained prokaryotic cells were discriminated and enumerated according to their right-angle

99 light scatter (SSC) and green fluorescence at 530/30 nm. In a plot of green versus red

100 fluorescence, non-autofluorescent cells were distinguished from autofluorescent cells.

101 Fluorescent beads (1.002 µm; Polysciences Europe) were systematically added to each analyzed

102 sample as internal standard. The cell abundance was determined from the flow rate, which was

103 calculated with TruCount beads (BD biosciences).

104

DNA extraction

106 The Sterivex cartridges were opened according to Perrine's method (Cruaud et al. 2017), and the

107 0.22 µm membranes were cut into small pieces and transferred to 2 mL microtubes (Eppendorf).

108 The 0.8 µm membranes were also cut into pieces. To promote cell lysis, a solution containing

109 PW1 and lysozyme was added to the microtubes and incubated at 37°C for 45 min. To digest the

110   proteins in the cell lysate a proteinase K solution was added and incubated at 55°C for 1 h. DNA

111   was then extracted following the manufacturer's instructions of the DNeasy PowerWater Kit

112   (Qiagen). DNA concentrations were measured by a quantus fluorometer (Promega) with the

113   QuantiFluor® Double stranded DNA (dsDNA) system.

Supplementary Results

Microbial community composition

Regardless of free-living or particle-attached prokaryotes, prokaryotic communities from STSW differ from those in other zones of surface seawater (Fig. 2), where free-living prokaryotes from STSW were dominated by *Cyanobiaceae*, SAR11, SAR86, SAR116 and *Actinomarinaceae*, while other surface seawaters were dominated by SAR11, *Flavobacteriaceae*, *Rhodobacteraceae* and SAR86. The free-living prokaryotes from ASW also have abundant *Thioglobaceae* (Fig. S4), as well as particle-attached prokaryotes from STSW were primarily dominated by *Cyanobiaceae* and *Flavobacteriaceae* compared to other surface seawaters, with lower abundance of *Haileaceae*, *Rhodobacteraceae*, and *Rubritaleaceae* (Fig. S5). The free-living prokaryotic communities in seawater collected from below the surface contained abundant *Nitrosopumilaceae*, SAR406 and SAR324, whereas particle-attached prokaryotes in seawater collected from below the surface exhibited a greater number of ASVs compared to the free-living prokaryotic communities in surface seawater (Fig. S4 and S5).

Biogeographical barriers of water masses and sampling zones define specific prokaryotic taxa

in different samples

To further investigate whether each water mass or surface seawater contains specific prokaryotic taxa, the indicator species analysis was performed for each water mass or surface seawater. A total of 213 indicator species were identified in all samples of free-living prokaryotic communities, while 121 indicator species were identified in all samples of particle-attached prokaryotic communities. The list of indicator species, along with their indicator values and contributions to the prokaryotic community were shown in Table S2 and S3, where the contribution of indicator species to the free-living and particle-attached prokaryotic community is significantly lower in the STMW, AAIW, AICW, AAIW+RSOW, UCDW, LCDW and NADW/LCDW compared to other water masses and surface seawaters (Fig. S6), and indicator species in STSW contributed more than 60% to the free-living prokaryotic community, whereas indicator species in AABW contributed over 50% to the particle-attached prokaryotic community (Fig. S6). With the exception of ASW and STSW, there was rarely overlap between indicator species in free-living prokaryotic communities and those in particle-attached prokaryotic communities. The dominant indicator species of prokaryotic communities present in different water masses or surface seawaters belong to distinct taxa. For instance, for indicator species in

145   free-living prokaryotic communities, *Cyanobiaceae* and SAR11 dominate in STSW,

146   *Flavobacteriaceae* and SAR86 dominate in SASW, *Rhodobacteraceae* dominate in PFSW, and

147   *Flavobacteriaceae*, *Nitrincolaceae*, and *Rhodobacteraceae* dominate in ASW, *Thioglobaceae* are

148   the dominant indicator species in WW, while *Nitrosopumliaceae* dominate in AAIW and

149   AAIW+RSOW. In contrast, for indicator species in particle-attached prokaryotic communities,

150   *Cyanobiaceae* and *Rhodobacteraceae* dominate in STSW, *Cyanobiaceae* and *Flavobacteriaceae*

151   dominate in SASW, *Halieaceae* dominate in PFSW, *Flavobacteriaceae* dominate in ASW, and

152   *Pirellulaceae* dominate in WW (Fig. S6).

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194

Subtropical Zone

ST2   ST3   ST5   ST8   ST11

Subantarctic Zone

ST14   ST15   ST16   ST38

Polar Frontal Zone

ST21   ST25   ST31   ST33   ST36

Antarctic Zone

ST29   ST30   ST42   ST44   ST46

ST58   ST63   ST68
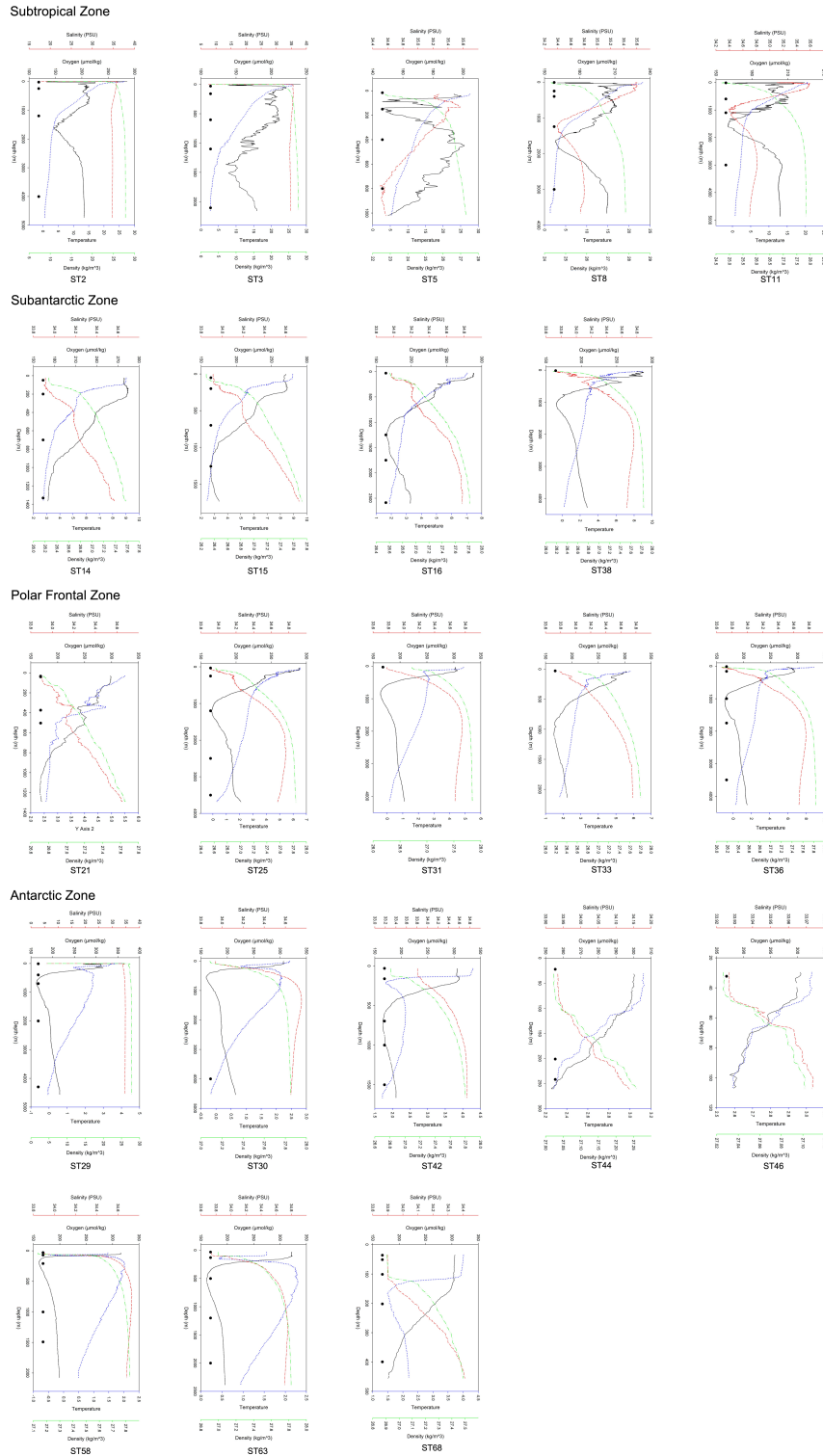
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196   Fig. S1. Vertical profiles of temperature (blue), salinity (red), oxygen (black) and density (green)
197   at the stations sampled in the present study. Dots represent the depths at which samples were
198   collected.

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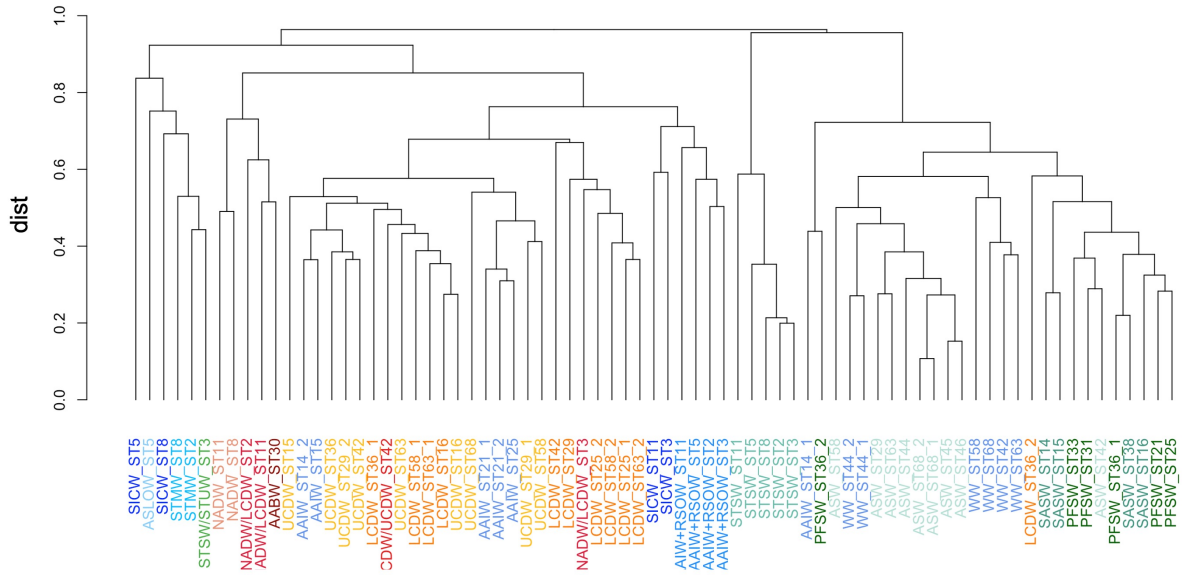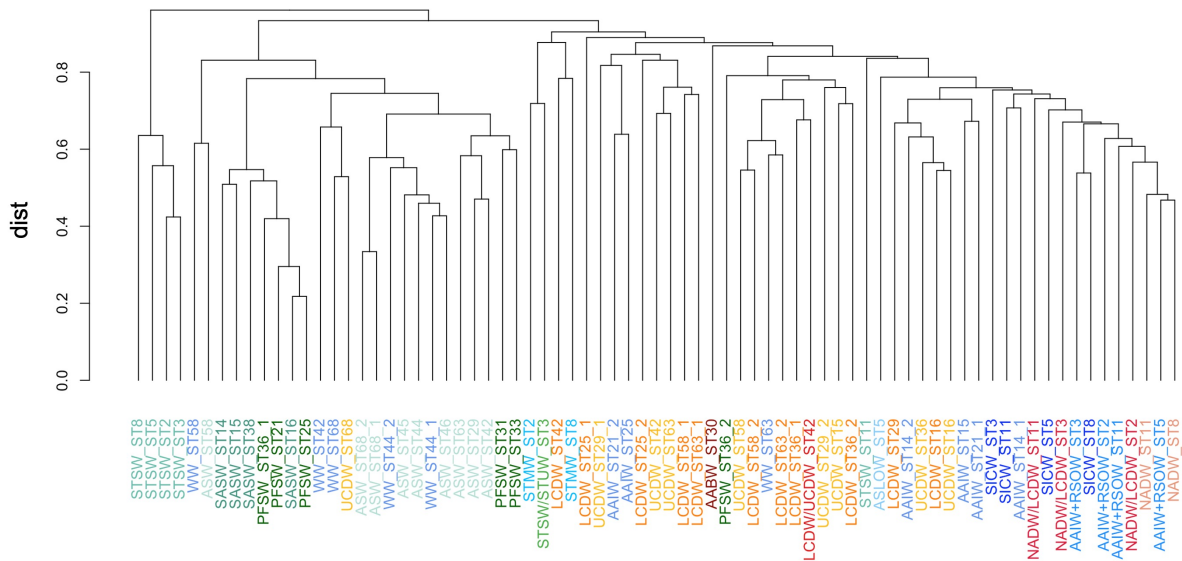
Fig. S2. Dendrograms showing hierarchical clustering of free-living and particle-attached prokaryotic community structure based on Bray-Curtis distances using the UPGMA method. Dendrograms are based on the relative abundance of prokaryotic taxa. Only those samples for which community composition of free living and particle attached prokaryotes are available are used here.

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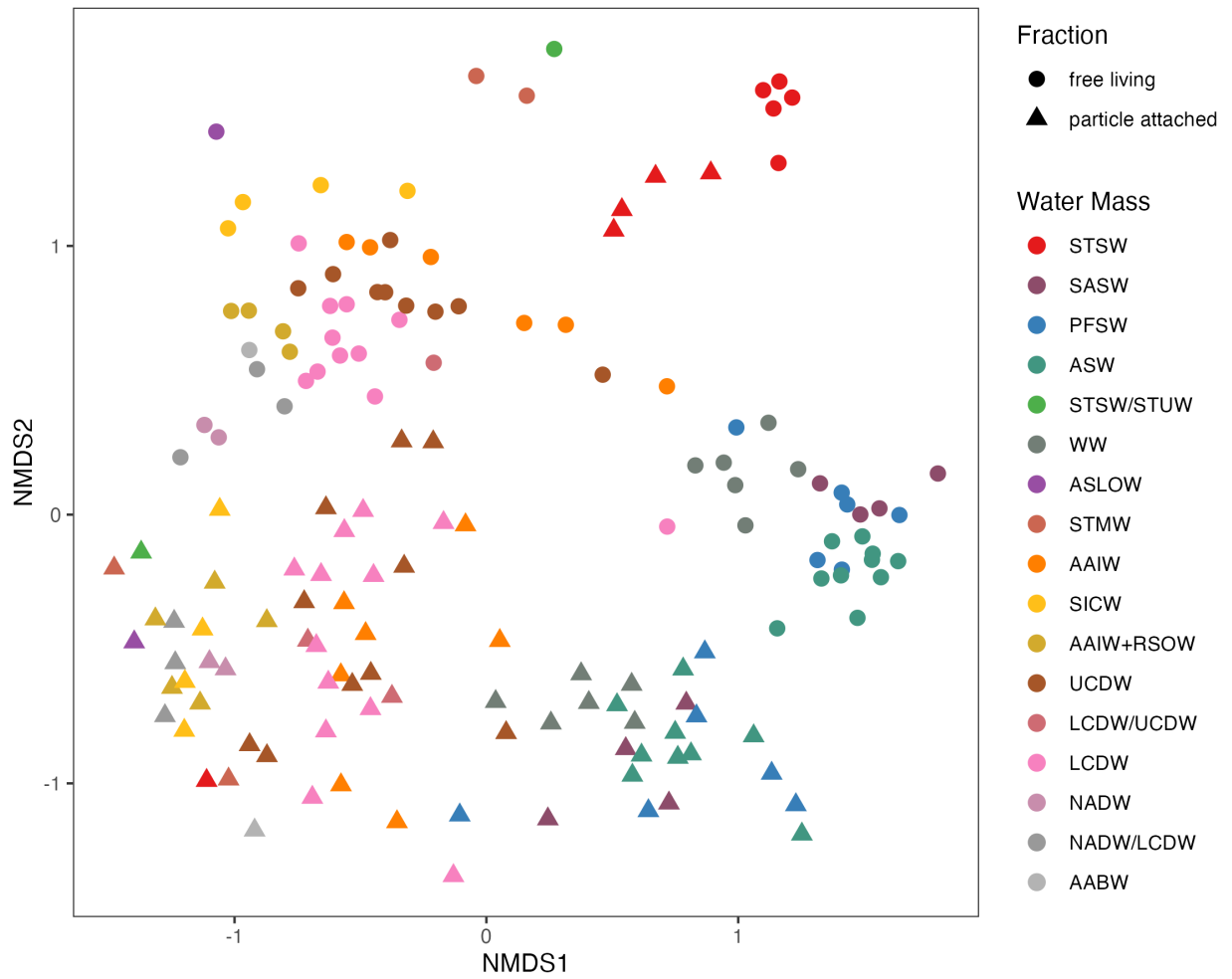
Fig. S3. Non-Metric Multidimensional Scale (NMDS) plots of free-living (circles) and particle-attached (triangles) prokaryotic communities based on Bray-Curtis dissimilarity. ANOSIM statistic: R: 0.7133, Significance: 1e-04.
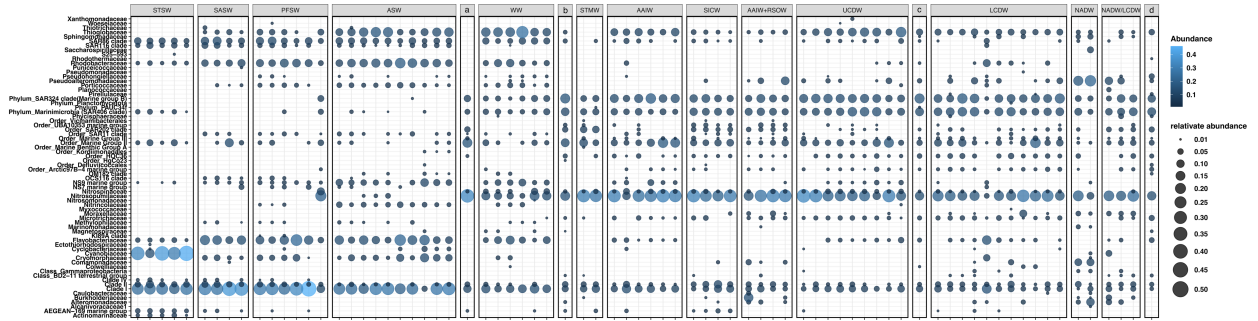
Fig. S4. Composition of the free-living prokaryotic communities in all samples of the present study. Taxonomic assignments are based on the Family level and only ASVs with a relative abundance of more than 1% in at least one sample are shown.

213
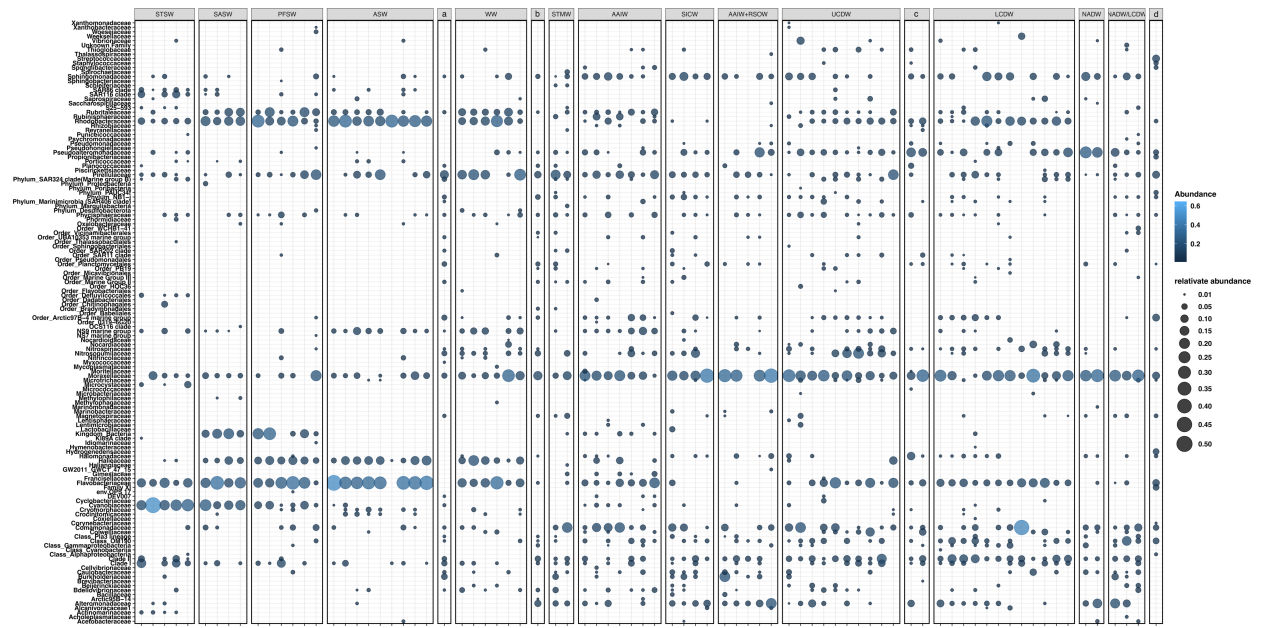
Fig. S5. Composition of the particle-attached prokaryotic communities in all samples of the present study. Taxonomic assignments are based on the Family level and only ASVs with a relative abundance of more than 1% in at least one sample are shown.

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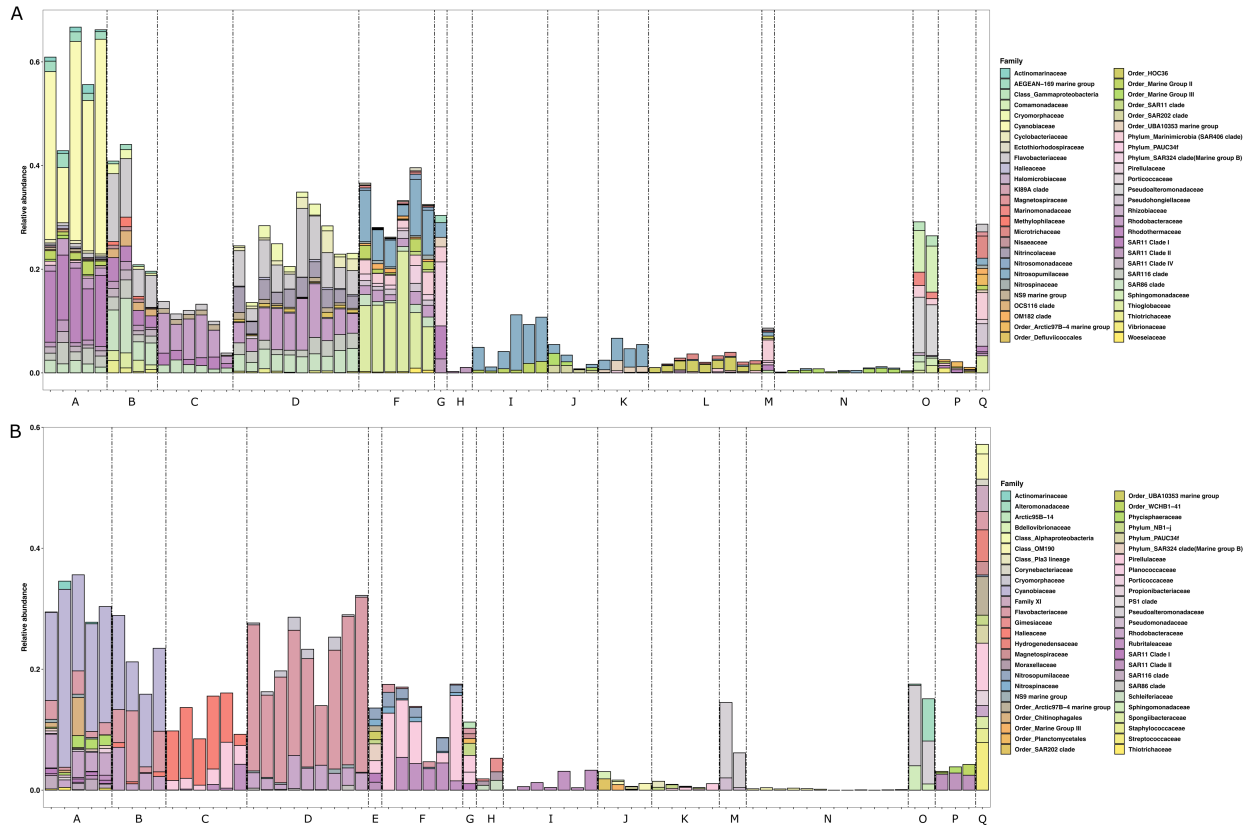
Fig. S6. Contribution of different indicator ASVs and their taxonomy in each sample (A, free-living prokaryotic community; B, particle-attached prokaryotic community). Surface waters and water masses were separated by vertical dashed lines. Taxonomic assignments are based on the Family level. A, STSW; B, SASW; C, PFSW; D, ASW; E, STSW/STUW; F, WW; G, ASLOW; H, STMW; I, AAIW; J, SICW; K, AAIW+RSOW; L, UCDW; M, LCDW/UCDW; N, LCDW; O, NADW; P, NADW/LCDW; Q, AABW.

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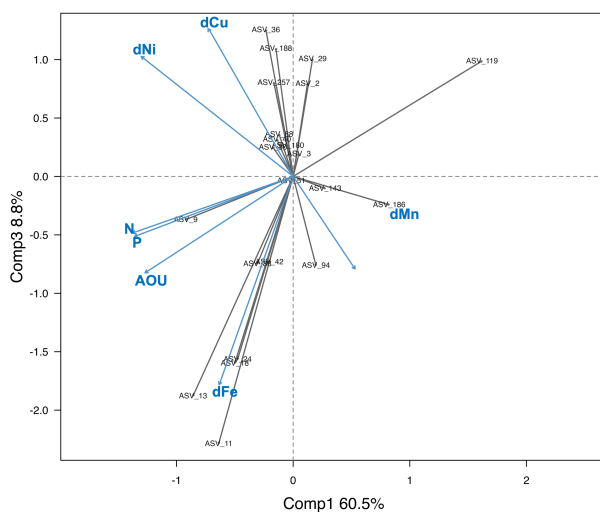
Fig. S7. Partial least squares regression analysis (PLSr) linking abundant ASVs (relative abundance ≥ 5% in at least one sample) with environmental variables. Blue short labels describe the environmental variables (AOU, apparent oxygen utilization; P, phosphate; N, nitrate; dMn, dissolved manganese; dFe, dissolved iron; dNi, dissolved nickel; dCu, dissolved copper) whereas grey short labels describe the ASVs.

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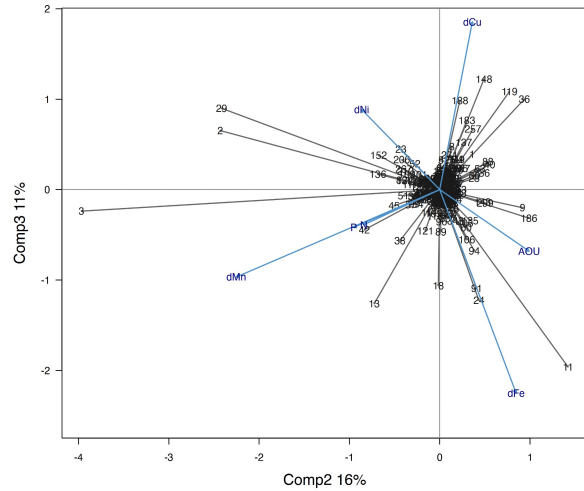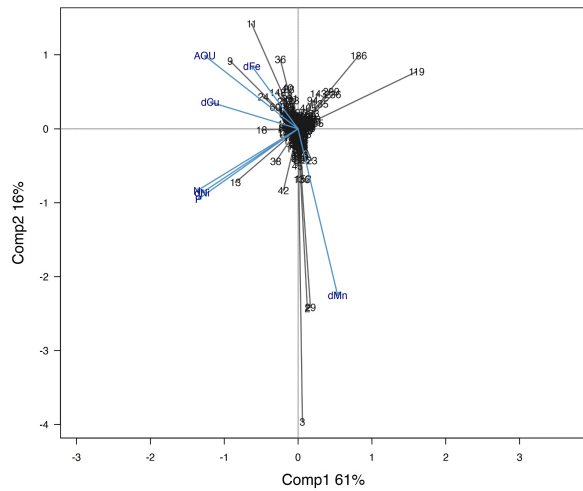
Fig. S8. Partial least squares regression analysis (PLSr) linking abundant ASVs (relative abundance ≥ 1% in at least one sample) with environmental variables. Blue short labels describe the environmental variables (AOU, apparent oxygen utilization; P, phosphate; N, nitrate; dMn, dissolved manganese; dFe, dissolved iron; dNi, dissolved nickel; dCu, dissolved copper) whereas grey short labels describe the ASVs.

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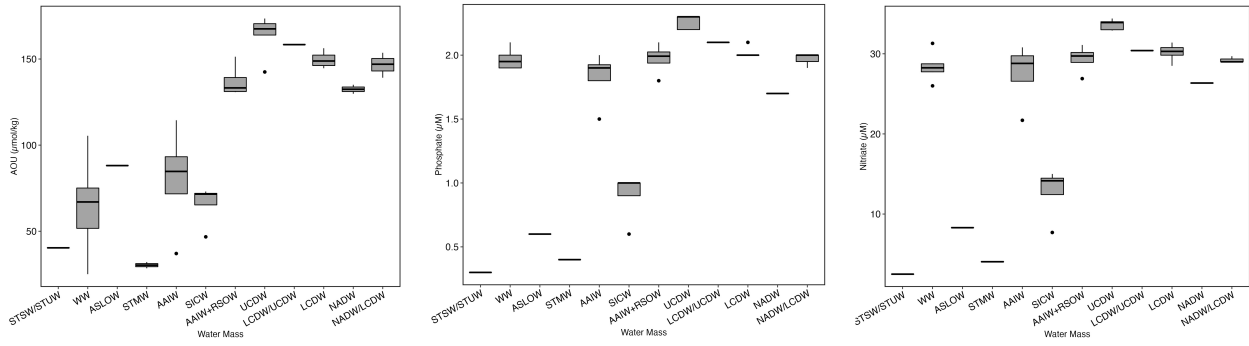
Fig. S9. The concentration of apparent oxygen utilization (AOU, μmol kg^{-1}), phosphate (μM) and nitrate (μM) in different surface waters and water masses (STSW/STUW, n=1; WW, n=6; ASLOW, n=1; STMW, n=2; AAIW, n=4; SICW, n=4; AAIW+RSOW, n=4; UCDW, n=5, LCDW/UCDW, n=1; LCDW, n=6; NADW, n=2; NADW/LCDW, n=3).

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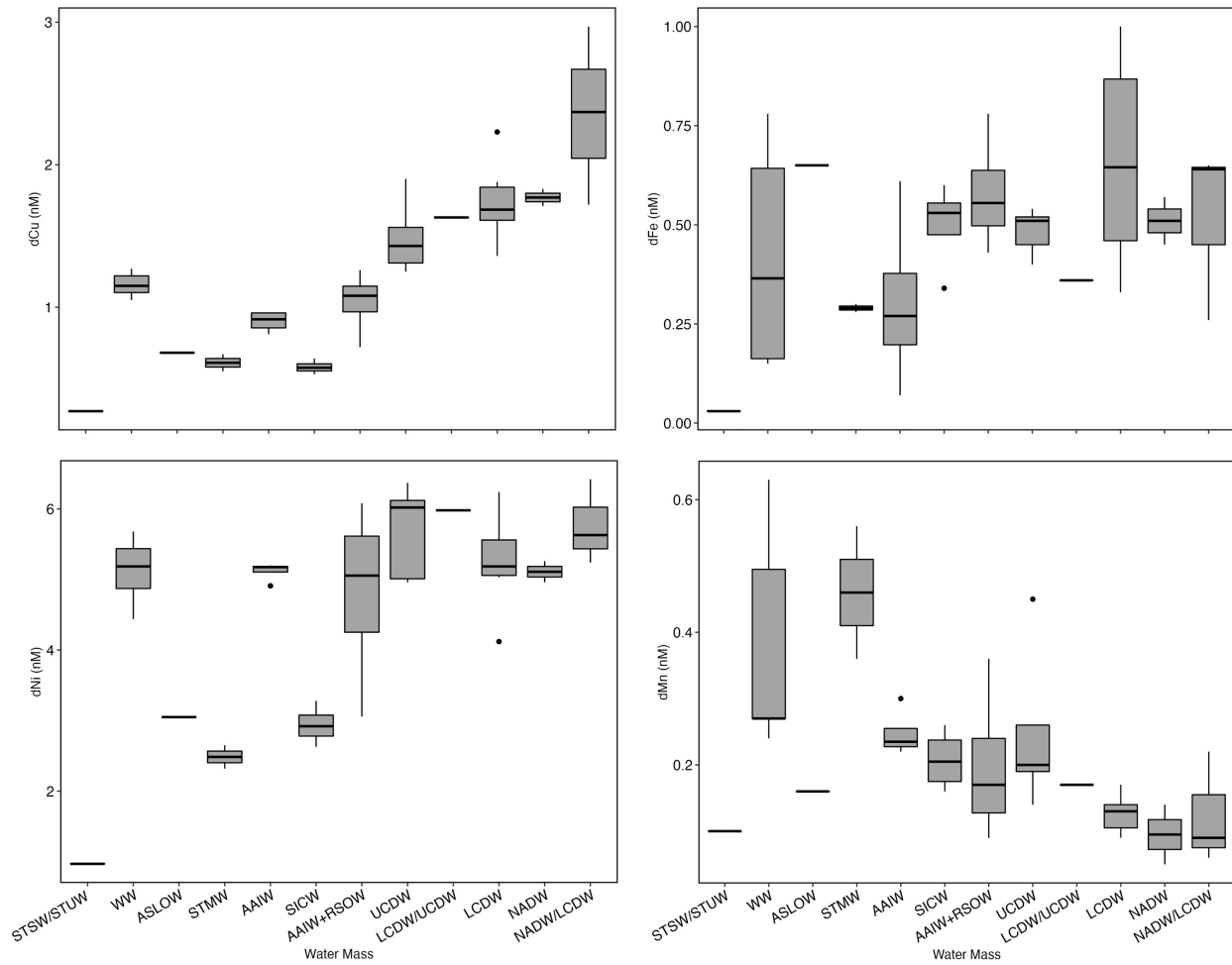
Fig. S10. The concentration of dissolved Cu (nM), dissolved Fe (nM), dissolved Ni (nM) and dissolved Mn (nM) in different surface waters and water masses (STSW/STUW, n=1; WW, n=6; ASLOW, n=1; STMW, n=2; AAIW, n=4; SICW, n=4; AAIW+RSOW, n=4; UCDW, n=5, LCDW/UCDW, n=1; LCDW, n=6; NADW, n=2; NADW/LCDW, n=3).

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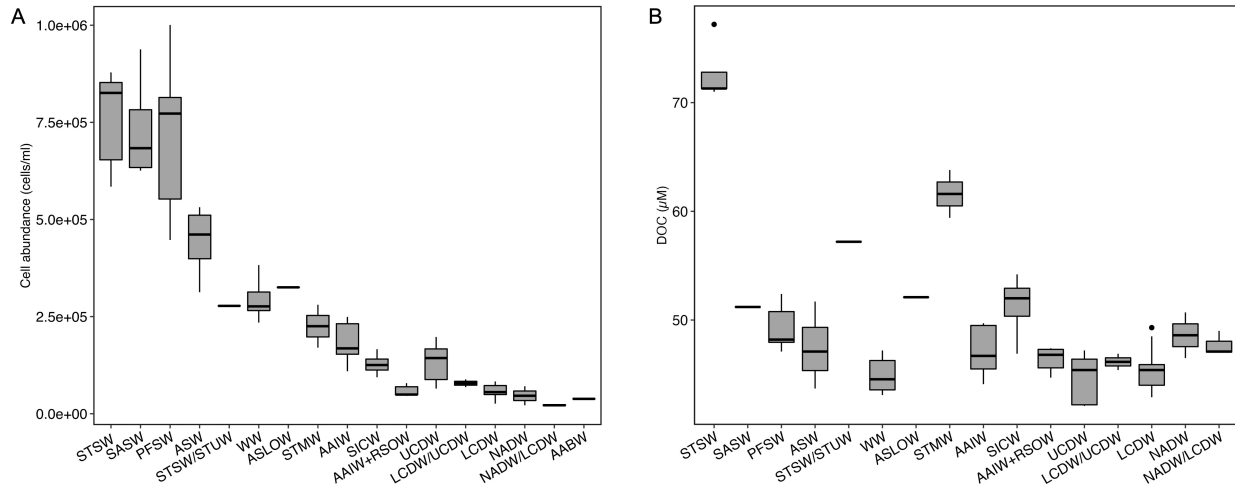
Fig. S11. A. Cell abundance of prokaryotes in different surface waters and water masses (STSW, n=5; SASW, n=4; PFSW, n=6; ASW, n=10; STSW/STUW, n=1; WW, n=6; ASLOW, n=1; STMW, n=2; AAIW, n=7; SICW, n=4; AAIW+RSOW, n=5; UCDW, n=10, LCDW/UCDW, n=2; LCDW, n=11; NADW, n=2; NADW/LCDW, n=3; AABW, n=1). B. DOC concentrations in different surface waters and water masses (STSW, n=5; SASW, n=1; PFSW, n=6; ASW, n=9; STSW/STUW, n=1; WW, n=6; ASLOW, n=1; STMW, n=2; AAIW, n=5; SICW, n=4; AAIW+RSOW, n=5; UCDW, n=9, LCDW/UCDW, n=2; LCDW, n=12; NADW, n=2; NADW/LCDW, n=3).
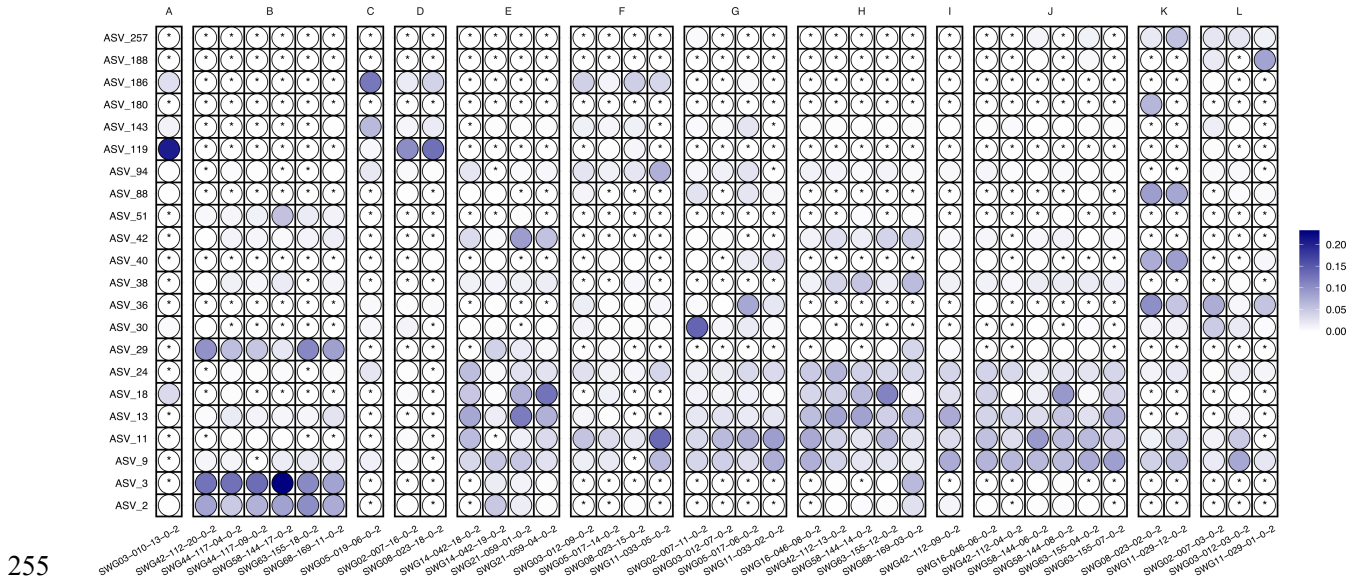
Fig.S12. Relative abundance of 22 abundant ASVs (relative abundance of ASVs >=5% in at least one sample) in different free-living prokaryotic community samples. Asterisks indicates that the relative abundance of ASV is 0. A. STSW/STUW; B. WW; C. ASLOW; D. STMW; E. AAIW; F. SICW; G. AAIW+RSOW; H. UCDW; I. LCDW/UCDW; J. LCDW; K. NADW; L. NADW/LCDW.

Table S1. List of physical properties of water masses.

Station No	CTD No	Cast No	Depth (m)	Water Mass	Salinity (PSU)	Pot Temperature (°C)	Pot density [0dbar] (kg/m³)	Neutral density (kg/m³)	Oxygen (umol/kg)	Identification criteria	Ref
ST2	7	16	249.9	STMW	35.545	16.482	26.0551632466777	26.087468834384	207.579	homogeneous low PV layer	Fine, 1993 (10.1016/0967-0637(93)90043-3)
ST2	7	11	1200.6	AAIW+RSOW	34.427	4.746	27.2498667794093	27.4423923895027	179.594	interleaving saline layers within the AAIW	Talley et al 2011; Beal et al, 2006 (doi:10.1175/JPO2964.1)
ST2	7	3	4003.2	NADW/LCDW	34.73	0.784	27.842481221277	28.1976476883103	203.112	LCDW density range, S<34.8	Park et al 2001 (doi:10.1029/2000JC900087)
ST3	10	13	160	STSW/STUW	35.605	18.229	25.6786367159675	25.7221425183528	191.442	subsurface salinity maximum	O'Connor et al 2005 (doi :10.1016/j.dsr.2005.01.011)
ST3	12	9	603.3	SICW	34.993	11.44	26.6893060666093	26.7596181683323	194.683	main T-S relationship of subtropical gyre	Talley et al 2011
ST3	12	7	1100.7	AAIW+RSOW	34.451	5.439	27.1882269138691	27.359486285587	174.923	interleaving saline layers within the AAIW	Talley et al 2011; Beal et al, 2006 (doi:10.1175/JPO2964.1)
ST3	12	3	2103.5	NADW/LCDW	34.753	2.522	27.7305490567642	27.9468405335601	173.793	LCDW density range, S<34.8	Park et al 2001 (doi:10.1029/2000JC900087)
ST5	19	6	150.6	ASLOW	35.419	17.612	25.688323515395	25.7007623188467	146.678	O_2 < 165 μmol/kg near $\gamma^n \approx$ 25.5	Beal et al, 2006 (doi:10.1175/JPO2964.1)
ST5	17	14	400	SICW	35.072	12.032	26.6389327300101	26.6855696591062	191.429	main T-S relationship of subtropical gyre	Talley et al 2011
ST5	17	6	800.1	AAIW+RSOW	34.588	6.906	27.1071916637377	27.214363338085	159.915	interleaving saline layers within the AAIW	Talley et al 2011; Beal et al, 2006 (doi:10.1175/JPO2964.1)
ST8	23	18	251	STMW	35.559	16.624	26.0325847634213	26.0683316807629	210.543	homogeneous low PV layer	Fine, 1993 (10.1016/0967-0637(93)90043-3)
ST8	23	15	401.1	SICW	35.345	14.387	26.3714162616204	26.4174190878478	203.342	main T-S relationship of subtropical gyre	Talley et al 2011
ST8	23	9	1245.2	AAIW+RSOW	34.395	4.769	27.2218894171219	27.3738466568966	187.213	interleaving saline layers within the AAIW	Talley et al 2011; Beal et al, 2006 (doi:10.1175/JPO2964.1)
ST8	23	2	2997.8	NADW	34.801	1.996	27.812585157096	28.0568551786749	201.833	S>34.8 within the LCDW density range	Park et al 2001 (doi:10.1029/2000JC900087)
ST11	33	5	599.3	SICW	34.891	10.726	26.7399469190682	26.8158099047443	197.539	main T-S relationship of subtropical gyre	Talley et al 2011
ST11	33	2	1098.8	AAIW+RSOW	34.489	5.029	27.2667672400903	27.4007604959657	157.273	interleaving saline layers within the AAIW	Talley et al 2011; Beal et al, 2006 (doi:10.1175/JPO2964.1)
ST11	29	12	2999.9	NADW	34.812	1.986	27.8221960805638	28.0648238964805	196.643	S>34.8 within the LCDW density range	Park et al 2001 (doi:10.1029/2000JC900087)
ST11	29	1	5386.7	NADW/LCDW	34.693	0.246	27.8449728249379	28.2619961185337	200.192	LCDW density range, S<34.8	Park et al 2001 (doi:10.1029/2000JC900087)
ST14	42	19	199.6	AAIW	33.992	5.433	26.8255686247987	26.9108843778332	269.723	27.2 > γ^n	Park et al 1993 (doi:10.1029/93JC00938)
ST14	42	18	699.6	AAIW	34.243	3.396	27.2439055136099	27.4211990552994	207.194	27.5 > γ^n > 27.2	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST14	42	5	1332.9	UCDW	34.542	2.703	27.546108911356	27.7618596132586	164.899	27.8 > γ^n > 27.5	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST15	44	19	200.5	AAIW	33.995	5.554	26.8134338733303	26.9124165926688	270.032	27.5 > γ^n > 27.2	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST15	44	17	700.2	AAIW	34.252	3.38	27.2526077611283	27.4224774513361	205.038	27.5 > γ^n > 27.2	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011

ST15	44	11	1259.1	UCDW	34.557	2.676	27.5604647817793	27.7649585646118	164.059	$27.8 > \gamma^n > 27.5$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST16	46	8	1249.5	UCDW	34.563	2.603	27.5716173452624	27.7971108868545	159.717	$27.8 > \gamma^n > 27.5$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST16	46	6	1750.3	LCDW	34.733	2.308	27.7326897386749	27.9507425406034	172.962	$28.27 > \gamma^n > 27.8$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST16	46	2	2588	LCDW	34.782	1.715	27.8192188272114	28.0846887626661	192.375	$28.27 > \gamma^n > 27.8$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST21	59	4	374.2	AAIW	34.178	3.922	27.140232916003	27.2782962947142	231.481	$27.5 > \gamma^n > 27.2$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST21	59	1	503.3	AAIW	34.13	3.107	27.1808354939772	27.3766797602976	240.945	$27.5 > \gamma^n > 27.2$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST25	67	10	251.1	AAIW	33.913	4.668	26.8506416901885	27.2037526447239	237.438	$27.5 > \gamma^n > 27.2$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST25	67	1	1200.3	LCDW/UCDW	34.23	2.566	27.3085555537166	27.8140564912859	160.328	$\gamma^n \sim 27.8$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST25	69	7	2499.3	LCDW	34.767	1.635	27.8132206843454	28.0845038360383	188.684	$28.27 > \gamma^n > 27.8$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST25	69	2	3500.2	LCDW	34.694	0.382	27.8379856633751	28.2162527795133	196.184	$28.27 > \gamma^n > 27.8$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST36	100	2	998.5	UCDW	34.559	2.553	27.5727341171535	27.761628833942	159.897	$27.8 > \gamma^n > 27.5$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST36	97	9	1749.1	LCDW	34.749	2.151	27.7584418444042	27.9911537859391	177.888	$28.27 > \gamma^n > 27.8$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST36	97	4	3497.5	LCDW	34.691	0.334	27.8383456964279	28.235136177162	195.511	$28.27 > \gamma^n > 27.8$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST29	78	14	398.9	UCDW	34.324	2.363	27.4008025985891	27.6130331932602	185.542	$27.8 > \gamma^n > 27.5$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST29	78	11	700.6	UCDW	34.567	2.367	27.5949107919882	27.8318430711255	158.609	$27.8 > \gamma^n > 27.5$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST29	78	7	2000.5	LCDW	34.742	1.358	27.8133954174459	28.115481716819	186.163	$28.27 > \gamma^n > 27.8$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST29	78	2	4297.1	AABW	34.661	-0.328	27.8492381904691	28.3327286956579	209.581	$\gamma^n > 28.27$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST30	79	3	4000.2	AABW	34.663	-0.273	27.8481672150585	28.323089033201	208.122	$\gamma^n > 28.27$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST42	112	20	161.3	WW	33.879	2.084	27.0670372077204	27.2500402293351	308.149	Subsurface Tmin layer near 200m	Park et al 1998 (doi :10.1016/S0924-7963(98)00026-8)
ST42	112	13	696.7	UCDW	34.557	2.32	27.5908256987207	27.8477071026222	165.646	$27.8 > \gamma^n > 27.5$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST42	112	9	1001	LCDW/UCDW	34.696	2.225	27.7099444856833	27.9449011216986	171.639	$\gamma^n \sim 27.8$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST42	112	4	1502.2	LCDW	34.75	1.749	27.7909615856988	28.0480804288143	189.21	$28.27 > \gamma^n > 27.8$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST44	117	9	201.5	WW	34.057	2.378	27.1859402080474	27.260863118825	267.885	Subsurface Tmin layer near 200m	Park et al 1998 (doi :10.1016/S0924-7963(98)00026-8)
ST44	117	4	242.2	WW	34.123	2.281	27.2466865470171	27.3068240396447	254.715	Subsurface Tmin layer near 200m	Park et al 1998 (doi :10.1016/S0924-7963(98)00026-8)
ST58	144	17	70.3	WW	34.259	-0.237	27.5198956601041	27.7328603823068	247.349	Subsurface Tmin layer near 200m	Park et al 1998 (doi :10.1016/S0924-7963(98)00026-8)

ST58	144	14	209.3	UCDW	34.625	2.008	27.6706021130617	27.9166877854586	161.467	$27.8 > \gamma^n > 27.5$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST58	144	8	1001	LCDW	34.726	1.307	27.8041582921064	28.0987965257788	191.639	$28.27 > \gamma^n > 27.8$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST58	144	6	1491.1	LCDW	34.704	0.784	27.8215516882344	28.1646032627964	195.648	$28.27 > \gamma^n > 27.8$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST63	155	18	129.9	WW	33.996	0.456	27.271112783958	27.4493708185415	299.032	Subsurface Tmin layer near 200m	Park et al 1998 (doi :10.1016/S0924-7963(98)00026-8)
ST63	155	12	499.8	UCDW	34.593	2.262	27.6244389226906	27.8540413050866	156.448	$27.8 > \gamma^n > 27.5$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST63	155	7	1199.6	LCDW	34.749	1.837	27.7833929407282	28.0418382214248	180.433	$28.27 > \gamma^n > 27.8$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST63	155	4	1999.1	LCDW	34.73	1.091	27.8223071623083	28.1387029050168	188.545	$28.27 > \gamma^n > 27.8$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011
ST68	169	11	201.9	WW	34.072	1.563	27.2608193824401	27.4419568751932	265.613	Subsurface Tmin layer near 200m	Park et al 1998 (doi :10.1016/S0924-7963(98)00026-8)
ST68	169	3	399.4	UCDW	34.381	2.143	27.4643801336806	27.6766091833312	188.991	$27.8 > \gamma^n > 27.5$	Orsi et al 1999, Bindoff and McDougall, 2000, Talley et al 2011

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263   Table S2. List of indicator species with their indicator value, p-value and frequency in each

264   surface water and water mass in the free-living prokaryotic community.

Water Mass	Family	Indicator Value	p-value	Frequency
	ASV_78_Cryomorphaceae	0.48	0.029	23
	ASV_132_Cyclobacteriaceae	0.70	0.002	33
	ASV_214_Flavobacteriaceae	0.52	0.001	21
	ASV_32_Flavobacteriaceae	0.41	0.003	32
	ASV_456_Flavobacteriaceae	0.62	0.049	12
	ASV_49_Flavobacteriaceae	0.39	0.044	37
	ASV_70_Flavobacteriaceae	0.68	0.001	17
	ASV_80_Flavobacteriaceae	0.52	0.001	23
	ASV_5_Halieaceae	0.40	0.027	27
	ASV_104_Nitrincolaceae	0.61	0.001	24
	ASV_72_Nitrincolaceae	0.48	0.002	28
ASW	ASV_168_NS9 marine group	0.69	0.001	13
	ASV_262_Order_Defluviicoccales	0.45	0.009	23
	ASV_539_Porticoccaceae	0.50	0.031	16
	ASV_147_Rhodobacteraceae	0.52	0.004	23
	ASV_34_Rhodobacteraceae	0.59	0.001	26
	ASV_57_Rhodobacteraceae	0.54	0.001	31
	ASV_87_Rhodobacteraceae	0.70	0.01	20
	ASV_505_SAR116 clade	0.73	0.002	13
	ASV_71_SAR116 clade	0.43	0.001	31
	ASV_100_SAR86 clade	0.65	0.001	23
	ASV_103_SAR86 clade	0.70	0.001	27
	ASV_707_SAR86 clade	0.65	0.028	9
	ASV_545_Thiotrichaceae	0.48	0.047	13
	ASV_304_Actinomarinaceae	0.89	0.001	6
	ASV_1030_AEGEAN-169 marine group	0.80	0.015	4
	ASV_261_AEGEAN-169 marine group	0.89	0.001	8
	ASV_3144_AEGEAN-169 marine group	0.80	0.047	4
	ASV_187_SAR11 Clade I	1.00	0.001	5
STSW	ASV_209_SAR11 Clade I	0.75	0.001	8
	ASV_256_SAR11 Clade I	0.83	0.001	6
	ASV_484_SAR11 Clade I	0.80	0.027	4
	ASV_567_SAR11 Clade I	0.80	0.009	4
	ASV_58_SAR11 Clade I	0.68	0.002	13

	ASV_702_SAR11 Clade I	1.00	0.001	5
	ASV_769_SAR11 Clade I	0.80	0.003	4
	ASV_780_SAR11 Clade I	0.80	0.017	4
	ASV_807_SAR11 Clade I	0.80	0.009	4
	ASV_910_SAR11 Clade I	0.80	0.036	4
	ASV_462_SAR11 Clade II	0.83	0.021	6
	ASV_520_SAR11 Clade II	1.00	0.001	5
	ASV_561_SAR11 Clade IV	0.74	0.029	6
	ASV_840_SAR11 Clade IV	0.86	0.032	8
	ASV_287_Cyanobiaceae	0.80	0.012	4
	ASV_451_Cyanobiaceae	0.80	0.012	4
	ASV_470_Cyanobiaceae	0.80	0.012	4
	ASV_56_Cyanobiaceae	0.94	0.001	7
	ASV_625_Cyanobiaceae	0.80	0.01	4
	ASV_642_Cyanobiaceae	0.80	0.018	4
	ASV_65_Cyanobiaceae	0.96	0.001	6
	ASV_8_Cyanobiaceae	0.86	0.001	14
	ASV_833_Cyanobiaceae	0.80	0.008	4
	ASV_912_Cyanobiaceae	0.80	0.01	4
	ASV_495_Cyclobacteriaceae	0.80	0.01	4
	ASV_474_Flavobacteriaceae	0.80	0.044	4
	ASV_783_Flavobacteriaceae	1.00	0.001	5
	ASV_660_Halieaceae	1.00	0.001	5
STSW	ASV_926_KI89A clade	1.00	0.001	5
	ASV_611_NS9 marine group	0.80	0.03	4
	ASV_1525_OCS116 clade	0.72	0.042	6
	ASV_1087_Order_Marine Group II	0.73	0.043	5
	ASV_548_Order_Marine Group II	0.80	0.045	4
	ASV_729_Order_Marine Group II	0.95	0.001	6
	ASV_759_Order_Marine Group II	0.80	0.043	4
	ASV_1017_Order_Marine Group III	0.72	0.05	7
	ASV_613_SAR406 clade	0.77	0.025	5
	ASV_392_Rhodobacteraceae	0.80	0.045	4
	ASV_395_Rhodobacteraceae	0.99	0.001	6
	ASV_467_Rhodobacteraceae	0.77	0.044	8
	ASV_541_Rhodobacteraceae	0.68	0.048	5
	ASV_1048_SAR116 clade	0.82	0.001	6
	ASV_191_SAR116 clade	0.95	0.001	7
	ASV_290_SAR116 clade	0.95	0.001	7
	ASV_388_SAR116 clade	0.92	0.001	6

STSW	ASV_483_SAR86 clade	0.80	0.03	4
	ASV_499_SAR86 clade	0.93	0.001	8
	ASV_569_SAR86 clade	0.77	0.023	5
	ASV_584_SAR86 clade	1.00	0.001	5
SASW	ASV_574_AEGEAN-169 marine group	0.76	0.01	10
	ASV_166_Cryomorphaceae	0.50	0.012	28
	ASV_112_Flavobacteriaceae	0.46	0.003	32
	ASV_124_Flavobacteriaceae	0.41	0.014	23
	ASV_129_Flavobacteriaceae	0.55	0.003	25
	ASV_21_Flavobacteriaceae	0.52	0.019	28
	ASV_394_Flavobacteriaceae	0.86	0.001	7
	ASV_204_Methylophilaceae	0.45	0.049	28
	ASV_269_Nisaeaceae	0.39	0.014	26
	ASV_122_OCS116 clade	0.42	0.023	33
	ASV_156_SAR11 Clade I	0.59	0.01	27
	ASV_350_SAR11 Clade II	0.60	0.001	24
	ASV_195_SAR11 Clade IV	0.59	0.001	23
	ASV_169_SAR116 clade	0.69	0.002	20
	ASV_216_SAR86 clade	0.65	0.03	16
	ASV_243_SAR86 clade	0.60	0.03	8
	ASV_509_SAR86 clade	0.80	0.001	8
	ASV_92_SAR86 clade	0.55	0.014	28
	ASV_182_Thioglobaceae	0.49	0.015	17
	ASV_213_Thiotrichaceae	0.53	0.046	23
PFSW	ASV_123_SAR11 Clade I	0.38	0.031	29
	ASV_140_NS9 marine group	0.43	0.002	27
	ASV_177_Flavobacteriaceae	0.55	0.001	18
	ASV_26_Rhodobacteraceae	0.41	0.027	25
	ASV_260_Rhodobacteraceae	0.45	0.01	22
	ASV_33_Rhodobacteraceae	0.36	0.006	30
	ASV_387_SAR11 Clade I	0.56	0.014	12
	ASV_6_Rhodobacteraceae	0.32	0.045	32
	ASV_819_Flavobacteriaceae	0.54	0.031	12
	ASV_82_SAR86 clade	0.32	0.015	29
WW	ASV_29_Candidatus Nitrosopumilus	0.54	0.041	34
	ASV_749_Family_Ectothiorhodospiraceae	0.67	0.004	19
	ASV_201_Family_OM182 clade	0.45	0.002	29
	ASV_109_Family_SAR86 clade	0.36	0.01	29

	ASV_178_Lentibacter	0.43	0.001	29
	ASV_510_LS-NOB	0.66	0.004	12
	ASV_883_Magnetospira	0.72	0.013	11
	ASV_684_Nitrosomonas	0.65	0.027	13
	ASV_267_Order_Marine Group II	0.76	0.001	15
	ASV_320_Order_SAR11 clade	0.33	0.049	27
WW	ASV_117_Pseudohongiella	0.40	0.001	30
	ASV_139_Roseobacter clade NAC11-7 lineage	0.39	0.003	32
	ASV_210_SAR324 clade(Marine group B)	0.64	0.023	22
	ASV_136_SAR406 clade	0.63	0.002	24
	ASV_375_SAR406 clade	0.57	0.001	21
	ASV_3_SUP05 cluster	0.48	0.001	36
	ASV_817_Sva0996 marine group	0.68	0.002	15
	ASV_537_Woeseia	0.77	0.001	16
	ASV_5394_AEGEAN-169 marine group	1.00	0.044	1
	ASV_1443_Nitrosopumilaceae	0.79	0.043	3
	ASV_724_Order UBA10353 marine group	0.89	0.05	2
	ASV_143_SAR11 Clade I	0.52	0.041	40
ASLOW	ASV_3042_SAR11 Clade II	0.98	0.049	3
	ASV_186_SAR324 clade(Marine group B)	0.57	0.048	10
	ASV_2261_SAR406 clade	0.79	0.045	6
	ASV_442_SAR406 clade	0.48	0.031	15
	ASV_4703_SAR406 clade	0.89	0.04	2
STMW	ASV_2579_SAR11 Clade II	0.81	0.046	3
	ASV_1371_Nitrosopumilaceae	0.83	0.001	6
	ASV_42_Nitrosopumilaceae	0.48	0.01	38
AAIW	ASV_424_Nitrosopumilaceae	0.68	0.032	10
	ASV_688_Order_Marine Group II	0.67	0.013	11
	ASV_809_Order_Marine Group II	0.79	0.027	7
	ASV_1981_Nitrosopumilaceae	0.90	0.006	7
AAIW+RSOW	ASV_91_Nitrosopumilaceae	0.33	0.025	34
	ASV_422_Order_UBA10353 marine group	0.62	0.045	16
	ASV_1825_SAR324 clade(Marine group B)	0.71	0.039	7
	ASV_805_Nitrosopumilaceae	0.71	0.032	11
SICW	ASV_716_Order_Marine Group III	0.81	0.043	6
	ASV_741_Order_SAR202 clade	1.00	0.001	4
UCDW	ASV_286_Microtrichaceae	0.46	0.035	24
	ASV_981_Nitrosopumilaceae	0.54	0.014	14

UCDW	ASV_105_Order_HOC36	0.32	0.024	37
	ASV_1948_Rhodobacteraceae	0.72	0.035	9
	ASV_763_SAR406 clade	0.52	0.039	17
LCDW	ASV_650_Nitrosopumilaceae	0.56	0.042	11
	ASV_384_Order_Marine Group III	0.91	0.001	10
NADW	ASV_59_Class_Gammaproteobacteria	0.44	0.014	46
	ASV_88_Comamonadaceae	0.77	0.021	19
	ASV_318_Marinomonadaceae	0.78	0.028	11
	ASV_40_Pseudoalteromonadaceae	0.72	0.007	26
	ASV_46_Pseudoalteromonadaceae	0.39	0.043	38
	ASV_410_Rhizobiaceae	0.80	0.031	12
	ASV_328_SAR406 clade	0.59	0.035	13
	ASV_341_SAR86 clade	0.46	0.033	21
	ASV_133_Sphingomonadaceae	0.73	0.013	19
	ASV_1452_Thioglobaceae	0.98	0.002	3
NADW/LCDW	ASV_246_Order_Arctic97B-4 marine group	0.80	0.001	12
	ASV_869_Order_Marine Group II	0.47	0.04	14
	ASV_2150_SAR11 Clade I	0.97	0.001	6
	ASV_2284_SAR406 clade	0.94	0.001	7
	ASV_329_Vibrionaceae	0.82	0.046	6
LCDW/UCDW	ASV_44_Flavobacteriaceae	0.76	0.007	11
	ASV_1601_Halomicrobiaceae	0.65	0.003	12
	ASV_982_Microtrichaceae	0.73	0.004	10
	ASV_1172_Nitrosopumilaceae	0.82	0.001	8
	ASV_792_Nitrosopumilaceae	0.54	0.025	11
	ASV_837_Order_HOC36	0.81	0.003	8
	ASV_543_Order_SAR202 clade	0.32	0.034	26
	ASV_891_Phylum_PAUC34f	0.61	0.001	17
	ASV_1539_SAR11 Clade I	0.83	0.004	9
	ASV_617_SAR11 Clade I	0.52	0.012	12
	ASV_629_SAR11 Clade I	0.60	0.001	12
	ASV_1817_SAR324 clade(Marine group B)	0.72	0.038	6
	ASV_814_SAR324 clade(Marine group B)	0.60	0.025	9
	ASV_116_SAR406 clade	0.31	0.031	35
	ASV_1332_SAR406 clade	0.78	0.001	10
	ASV_1564_SAR406 clade	0.73	0.008	7
	ASV_327_SAR406 clade	0.51	0.044	21
	ASV_402_SAR406 clade	0.42	0.01	19
	ASV_645_SAR406 clade	0.54	0.003	13

LCDW/UCDW	ASV_244_Sphingomonadaceae	0.78	0.025	5
	ASV_1651_Flavobacteriaceae	0.95	0.006	4
	ASV_39_Flavobacteriaceae	0.89	0.001	11
	ASV_978_Magnetospiraceae	0.88	0.011	6
	ASV_1447_Marinimicrobia (SAR406 clade)	0.95	0.004	3
	ASV_271_Marinimicrobia (SAR406 clade)	0.61	0.043	13
	ASV_409_Marinimicrobia (SAR406 clade)	0.47	0.046	19
	ASV_839_Marinimicrobia (SAR406 clade)	0.77	0.003	14
	ASV_84_Microtrichaceae	0.49	0.006	30
	ASV_832_Nitrosopumilaceae	0.73	0.039	6
	ASV_151_Nitrospinaceae	0.43	0.001	24
	ASV_2148_OM182 clade	0.99	0.008	2
AABW	ASV_1373_Order_Arctic97B-4 marine group	0.71	0.022	10
	ASV_319_Order_Arctic97B-4 marine group	0.97	0.009	2
	ASV_948_Order_Arctic97B-4 marine group	0.74	0.019	6
	ASV_412_Order_Marine Group II	0.47	0.023	21
	ASV_1057_Order_UBA10353 marine group	0.75	0.023	7
	ASV_247_Pirellulaceae	0.54	0.001	22
	ASV_179_Pseudohongiellaceae	0.74	0.007	17
	ASV_2778_Pseudohongiellaceae	0.86	0.02	4
	ASV_1753_Rhodothermaceae	0.89	0.042	5
	ASV_962_SAR11 Clade I	0.61	0.002	13
	ASV_393_SAR11 Clade II	0.70	0.005	8
	ASV_291_Thioglobaceae	0.77	0.037	9

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266   Table S3. List of indicator species with their indicator value, p-value and frequency in each

267   surface water and water mass in the particle-attached prokaryotic community.

Water Mass	Family	Indicator Value	p-value	Frequency
	ASV_78_Cryomorphaceae	0.80	0.001	11
	ASV_10_Flavobacteriaceae	0.35	0.018	45
	ASV_17_Flavobacteriaceae	0.73	0.003	25
	ASV_32_Flavobacteriaceae	0.61	0.001	24
	ASV_49_Flavobacteriaceae	0.50	0.003	21
ASW	ASV_50_Flavobacteriaceae	0.47	0.03	26
	ASV_70_Flavobacteriaceae	0.91	0.001	12
	ASV_283_NS9 marine group	0.58	0.044	14
	ASV_34_Rhodobacteraceae	0.59	0.004	19
	ASV_87_Rhodobacteraceae	0.59	0.045	17
	ASV_100_SAR86 clade	0.61	0.044	10
	ASV_1310_Actinomarinaceae	0.60	0.047	3
	ASV_56_Cyanobiaceae	0.79	0.004	5
	ASV_586_Cyanobiaceae	0.59	0.032	5
	ASV_65_Cyanobiaceae	0.91	0.001	11
	ASV_8_Cyanobiaceae	0.78	0.016	8
	ASV_966_Cyanobiaceae	0.78	0.044	5
	ASV_378_Flavobacteriaceae	0.80	0.042	4
	ASV_516_Flavobacteriaceae	0.80	0.014	4
	ASV_564_Flavobacteriaceae	0.80	0.041	4
STSW	ASV_783_Flavobacteriaceae	1.00	0.001	5
	ASV_611_NS9 marine group	0.80	0.049	4
	ASV_361_Order_Chitinophagales	0.59	0.05	6
	ASV_317_Phycisphaeraceae	1.00	0.001	5
	ASV_686_Porticoccaceae	0.80	0.026	4
	ASV_1427_PS1 clade	0.80	0.027	4
	ASV_392_Rhodobacteraceae	0.80	0.047	4
	ASV_395_Rhodobacteraceae	0.80	0.036	4
	ASV_467_Rhodobacteraceae	0.80	0.02	4
	ASV_469_Rhodobacteraceae	0.80	0.015	4
	ASV_475_Rhodobacteraceae	0.80	0.028	4
	ASV_541_Rhodobacteraceae	0.80	0.026	4
	ASV_758_Rhodobacteraceae	0.80	0.035	4
	ASV_1151_Rubritaleaceae	0.80	0.04	4
	ASV_256_SAR11 Clade I	0.80	0.008	4

STSW	ASV_520_SAR11 Clade II	0.80	0.034	4
	ASV_290_SAR116 clade	0.80	0.028	4
	ASV_388_SAR116 clade	0.80	0.026	4
	ASV_703_SAR324 clade(Marine group B)	0.77	0.014	5
	ASV_1359_Thiotrichaceae	0.80	0.04	4
SASW	ASV_25_Cyanobiaceae	0.57	0.001	33
	ASV_309_Cyanobiaceae	1.00	0.001	4
	ASV_478_Flavobacteriaceae	0.97	0.001	5
	ASV_86_Flavobacteriaceae	0.83	0.007	9
	ASV_673_Halieaceae	0.72	0.017	7
	ASV_75_Rhodobacteraceae	0.60	0.028	20
STSW/STUW	ASV_119_Nitrosopumilaceae	0.80	0.042	2
	ASV_4520_Nitrospinaceae	1.00	0.034	1
	ASV_958_Order_Arctic97B-4 marine group	0.83	0.031	4
	ASV_3143_Order_UBA10353 marine group	1.00	0.026	1
	ASV_486_Phylum_NB1-j	0.60	0.001	17
	ASV_1965_Pirellulaceae	0.95	0.033	2
	ASV_1998_Pirellulaceae	0.93	0.031	2
	ASV_181_SAR11 Clade I	0.88	0.016	7
	ASV_217_SAR11 Clade II	0.68	0.05	9
	ASV_186_SAR324 clade(Marine group B)	0.72	0.048	4
	ASV_354_SAR324 clade(Marine group B)	0.82	0.034	6
PFSW	ASV_5_Halieaceae	0.30	0.024	36
	ASV_97_Pirellulaceae	0.63	0.029	28
	ASV_364_Rubritaleaceae	0.67	0.05	10
WW	ASV_310_Flavobacteriaceae	0.67	0.019	13
	ASV_29_Nitrosopumilaceae	0.88	0.001	11
	ASV_152_Nitrospinaceae	0.75	0.018	8
	ASV_20_Pirellulaceae	0.50	0.042	22
	ASV_67_Rubritaleaceae	0.54	0.013	17
ASLOW	ASV_1815_Arctic95B-14	0.93	0.037	5
	ASV_3428_Flavobacteriaceae	0.97	0.033	2
	ASV_1513_Magnetospiraceae	0.92	0.025	3
	ASV_937_Order_Planctomycetales	0.78	0.027	6
	ASV_2235_Phylum_NB1-j	0.98	0.047	2
	ASV_2768_Phylum_NB1-j	0.85	0.036	3
	ASV_1185_Pirellulaceae	0.84	0.034	2
	ASV_2973_Pirellulaceae	0.95	0.034	3

ASLOW	ASV_427_Planococcaceae	0.72	0.039	10
	ASV_3381_SAR11 Clade I	1.00	0.047	1
STMW	ASV_622_Gimesiaceae	1.00	0.004	2
	ASV_527_Moraxellaceae	0.77	0.033	5
	ASV_572_Schleiferiaceae	0.76	0.05	3
AAIW	ASV_212_Rubritaleaceae	0.65	0.006	24
AAIW+RSOW	ASV_1201_Class_Pla3 lineage	0.80	0.045	4
	ASV_960_Phylum_NB1-j	0.76	0.035	5
	ASV_911_Pirellulaceae	0.80	0.035	4
SICW	ASV_1474_Bdellovibrionaceae	0.72	0.047	5
	ASV_535_Class_OM190	0.71	0.046	4
	ASV_1396_Order_Marine Group III	0.50	0.049	2
	ASV_1862_Order_SAR202 clade	0.50	0.047	2
LCDW	ASV_797_Class_OM190	0.68	0.005	11
NADW	ASV_180_Alteromonadaceae	0.96	0.035	4
	ASV_40_Pseudoalteromonadaceae	0.62	0.016	33
	ASV_133_Sphingomonadaceae	0.49	0.04	28
NADW/LCDW	ASV_1400_Phycisphaeraceae	0.65	0.049	3
	ASV_2659_Order_WCHB1-41	0.66	0.039	3
	ASV_53_SAR11 Clade II	0.39	0.001	30
LCDW/UCDW	ASV_141_Pseudoalteromonadaceae	0.49	0.021	22
	ASV_19_Pseudoalteromonadaceae	0.43	0.025	46
	ASV_857_Pseudomonadaceae	0.93	0.006	6
AABW	ASV_1008_Spongiibacteraceae	0.88	0.018	6
	ASV_1757_Class_Alphaproteobacteria	0.99	0.032	2
	ASV_1221_Class_OM190	0.97	0.043	2
	ASV_2022_Class_OM190	1.00	0.03	1
	ASV_1171_Corynebacteriaceae	0.80	0.016	9
	ASV_848_Family XI	1.00	0.04	1
	ASV_556_Flavobacteriaceae	0.94	0.001	11
	ASV_1051_Hydrogenedensaceae	1.00	0.04	1
	ASV_1610_Hydrogenedensaceae	1.00	0.041	1
	ASV_589_Magnetospiraceae	0.73	0.034	12
	ASV_978_Magnetospiraceae	0.87	0.032	4
	ASV_222_Nitrosopumilaceae	0.58	0.036	8
	ASV_319_Order_Arctic97B-4 marine group	0.94	0.003	4
	ASV_777_Order_Arctic97B-4 marine group	0.84	0.004	9
	ASV_2349_Phylum_NB1-j	1.00	0.042	1

	ASV_1554_Phylum_PAUC34f	1.00	0.042	1
	ASV_2525_Phylum_PAUC34f	1.00	0.037	1
	ASV_1160_Pirellulaceae	1.00	0.036	1
	ASV_247_Pirellulaceae	0.91	0.005	13
AABW	ASV_864_Propionibacteriaceae	0.96	0.001	11
	ASV_174_Rhodobacteraceae	0.42	0.047	21
	ASV_54_Staphylococcaceae	0.75	0.032	15
	ASV_1468_Streptococcaceae	1.00	0.036	1
	ASV_2018_Streptococcaceae	1.00	0.04	1
	ASV_873_Streptococcaceae	1.00	0.034	1

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Table S4. Taxonomic of 22 abundant ASVs (ASVs with a relative abundance of ≥ 5% in at least one sample).

ASV	Kingdom	Phylum	Class	Order	Family	Genus	Species
ASV_11	Archaea	Crenarchaeota	Nitrososphaeria	Nitrosopumilales	Nitrosopumilaceae	Family_Nitrosopumilaceae	Family_Nitrosopumilaceae
ASV_119	Archaea	Crenarchaeota	Nitrososphaeria	Nitrosopumilales	Nitrosopumilaceae	Candidatus Nitrosopelagicus	Genus_Candidatus Nitrosopelagicus
ASV_13	Bacteria	SAR324 clade(Marine group B)	Phylum_SAR324 clade	Phylum_SAR324 clade	Phylum_SAR324 clade	Phylum_SAR324 clade	Phylum_SAR324 clade
ASV_143	Bacteria	Proteobacteria	Alphaproteobacteria	SAR11 clade	Clade I	Clade Ib	Genus_Clade Ib
ASV_18	Archaea	Thermoplasmatota	Thermoplasmata	Marine Group II	Order_Marine Group II	Order_Marine Group II	Order_Marine Group II
ASV_180	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacterales	Alteromonadaceae	Aestuariibacter	aggregatus
ASV_186	Bacteria	SAR324 clade(Marine group B)	Phylum_SAR324 clade	Phylum_SAR324 clade	Phylum_SAR324 clade	Phylum_SAR324 clade	Phylum_SAR324 clade
ASV_188	Bacteria	SAR324 clade(Marine group B)	Phylum_SAR324 clade	Phylum_SAR324 clade	Phylum_SAR324 clade	Phylum_SAR324 clade	Phylum_SAR324 clade
ASV_2	Bacteria	Proteobacteria	Alphaproteobacteria	SAR11 clade	Clade I	Clade Ia	Genus_Clade Ia
ASV_24	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Thioglobaceae	SUP05 cluster	Genus_SUP05 cluster
ASV_257	Archaea	Crenarchaeota	Nitrososphaeria	Nitrosopumilales	Nitrosopumilaceae	Family_Nitrosopumilaceae	Family_Nitrosopumilaceae
ASV_29	Archaea	Crenarchaeota	Nitrososphaeria	Nitrosopumilales	Nitrosopumilaceae	Candidatus Nitrosopumilus	Genus_Candidatus Nitrosopumilus
ASV_3	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Thioglobaceae	SUP05 cluster	Genus_SUP05 cluster
ASV_30	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	Cupriavidus	metallidurans
ASV_36	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacterales	Pseudoalteromonadaceae	Pseudoalteromonas	Genus_Pseudoalteromonas
ASV_38	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Thioglobaceae	SUP05 cluster	Genus_SUP05 cluster
ASV_40	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacterales	Pseudoalteromonadaceae	Pseudoalteromonas	Genus_Pseudoalteromonas
ASV_42	Archaea	Crenarchaeota	Nitrososphaeria	Nitrosopumilales	Nitrosopumilaceae	Candidatus Nitrosopumilus	Genus_Candidatus Nitrosopumilus
ASV_51	Bacteria	Bacteroidota	Bacteroidia	Flavobacteriales	NS9 marine group	Family_NS9 marine group	Family_NS9 marine group
ASV_88	Bacteria	Proteobacteria	Gammaproteobacteria	Burkholderiales	Comamonadaceae	Aquabacterium	parvum
ASV_9	Bacteria	SAR324 clade(Marine group B)	Phylum_SAR324 clade	Phylum_SAR324 clade	Phylum_SAR324 clade	Phylum_SAR324 clade	Phylum_SAR324 clade
ASV_94	Archaea	Crenarchaeota	Nitrososphaeria	Nitrosopumilales	Nitrosopumilaceae	Family_Nitrosopumilaceae	Family_Nitrosopumilaceae

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