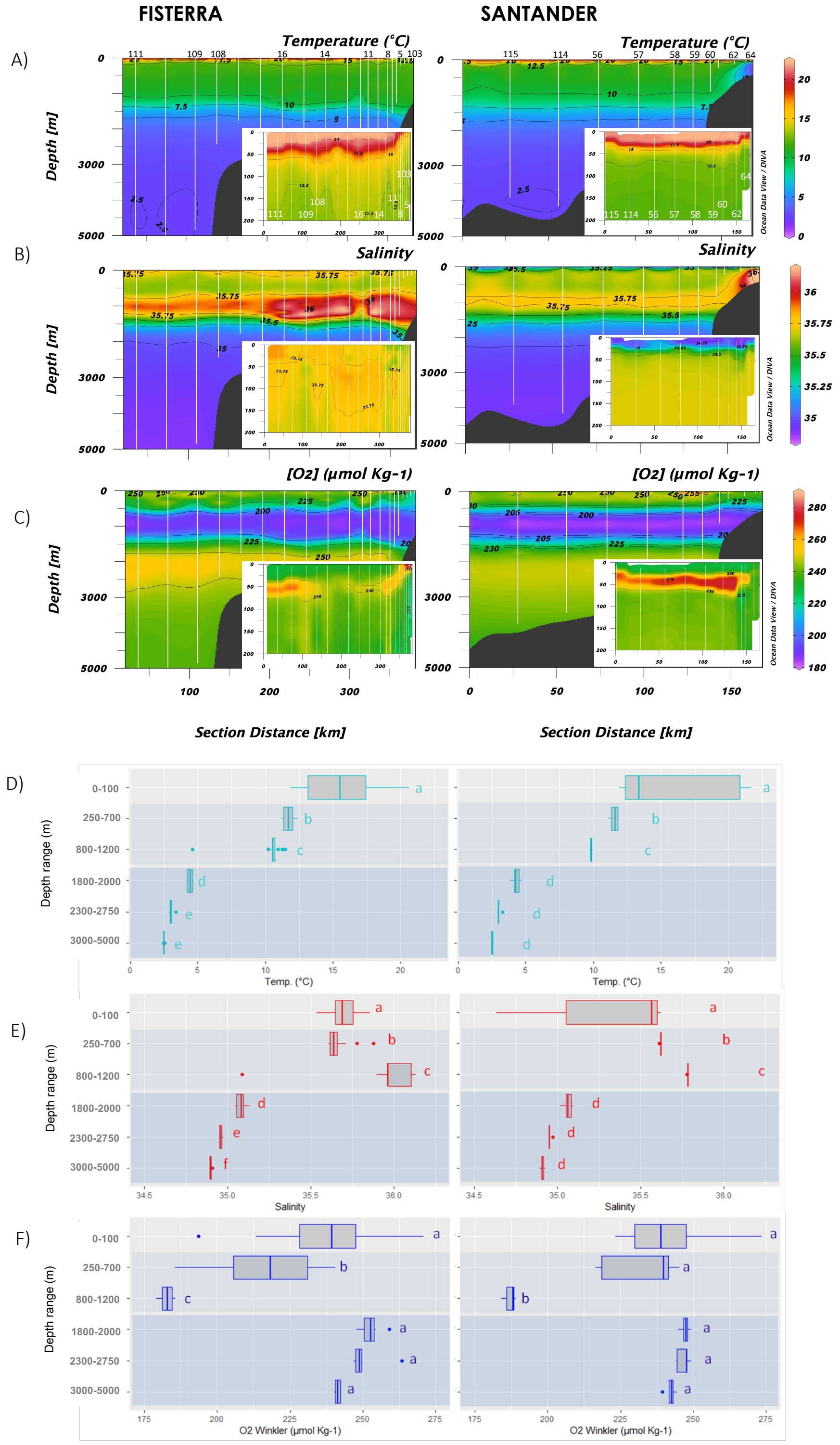
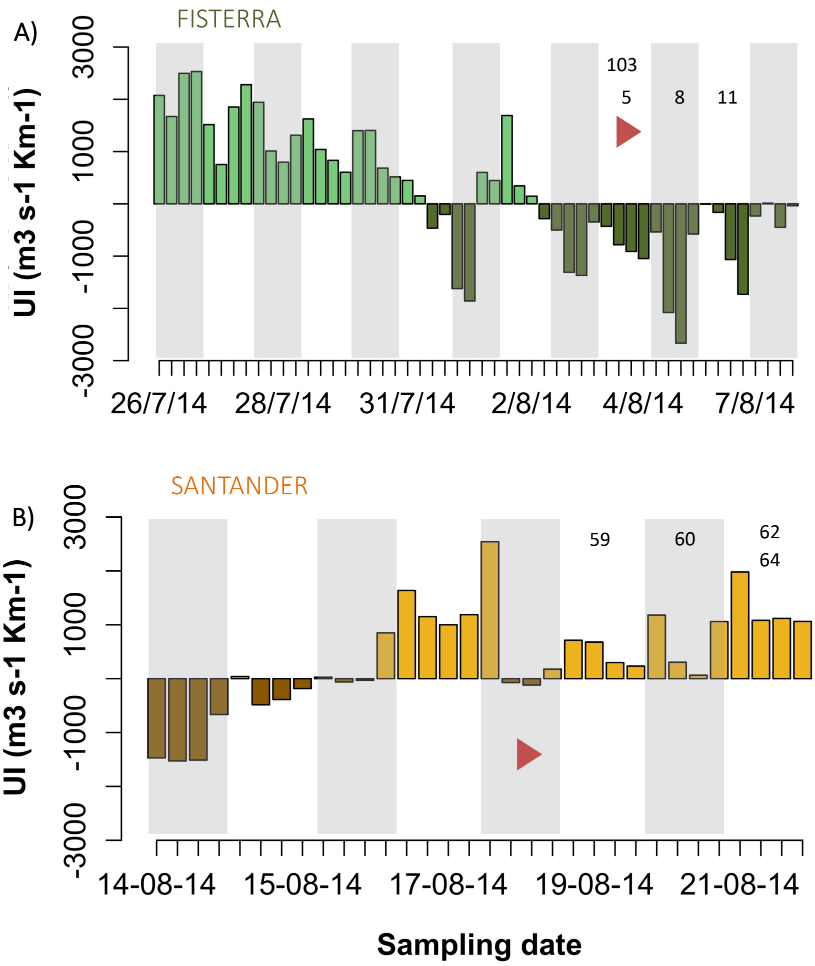
Supplementary Material

1 Supplementary Figures and Tables

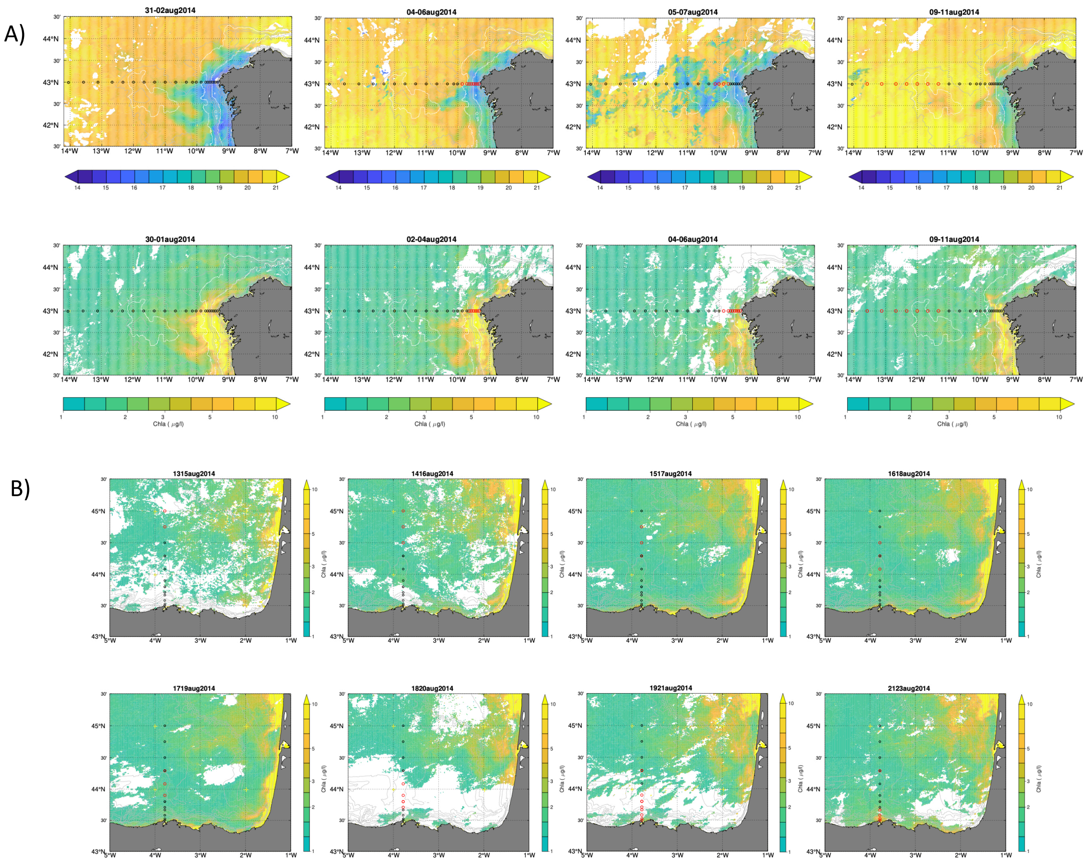
1.1 Supplementary Figures



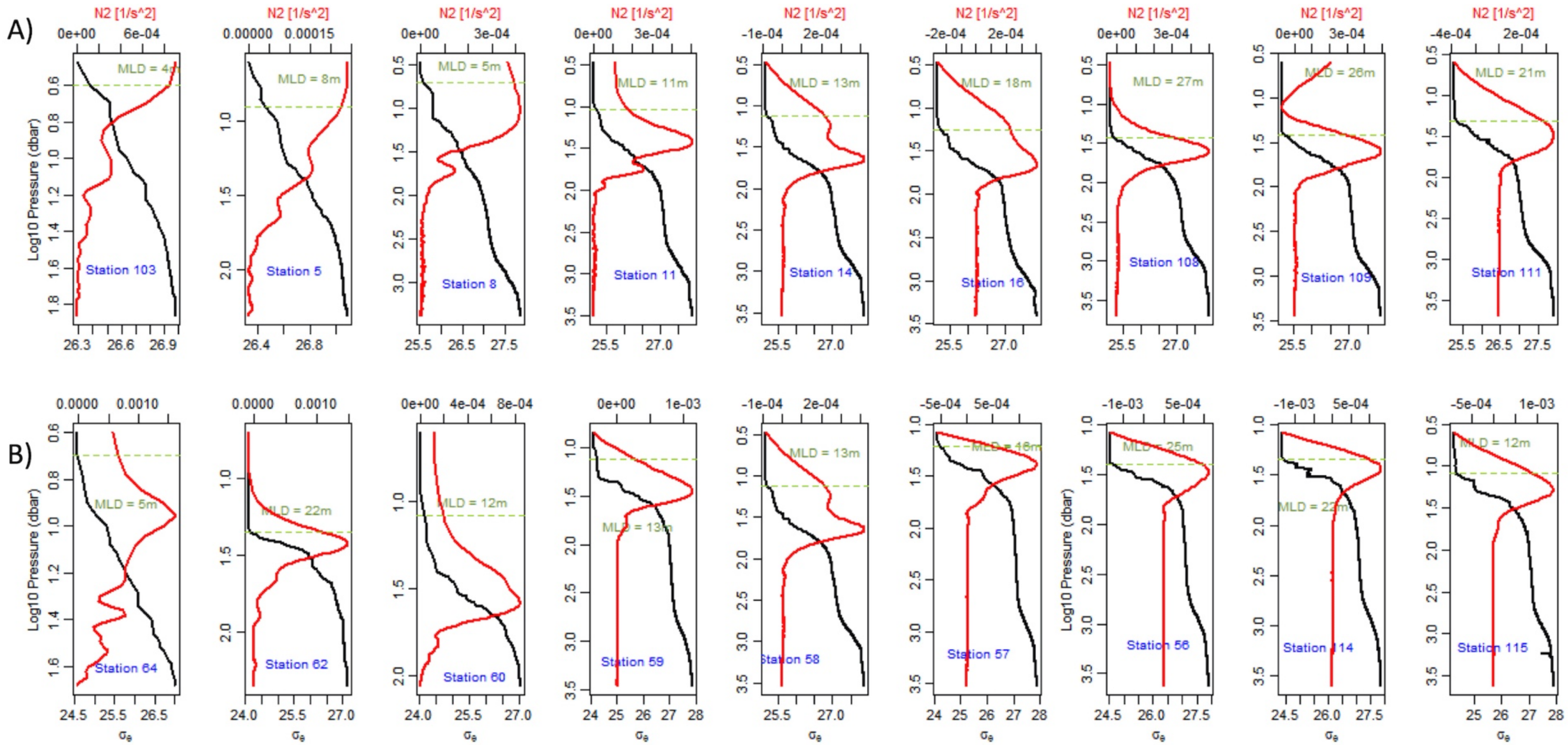
Supplementary Figure 1. Vertical sections of A) temperature (°C), B) salinity, and C) oxygen concentration (µmol kg^{-1}) in Fisterra (left) and Santander (right). Within each plot, a zoom for the first 200 m of the water column is shown. Numbers denote biological sampling stations (see Fig. 1). In the bottom panel, boxplots show the first and third quartiles of the distribution of values, as well as the medians, for D) temperature (°C), E) salinity, and F) oxygen concentration (µmol kg^{-1}), for the different sampling depth ranges along each transect. Dots represent outlier values. Different letters indicate significant differences (One-way ANOVA, and Tukey's test, $p < 0.001$) for each pair of depth ranges compared.



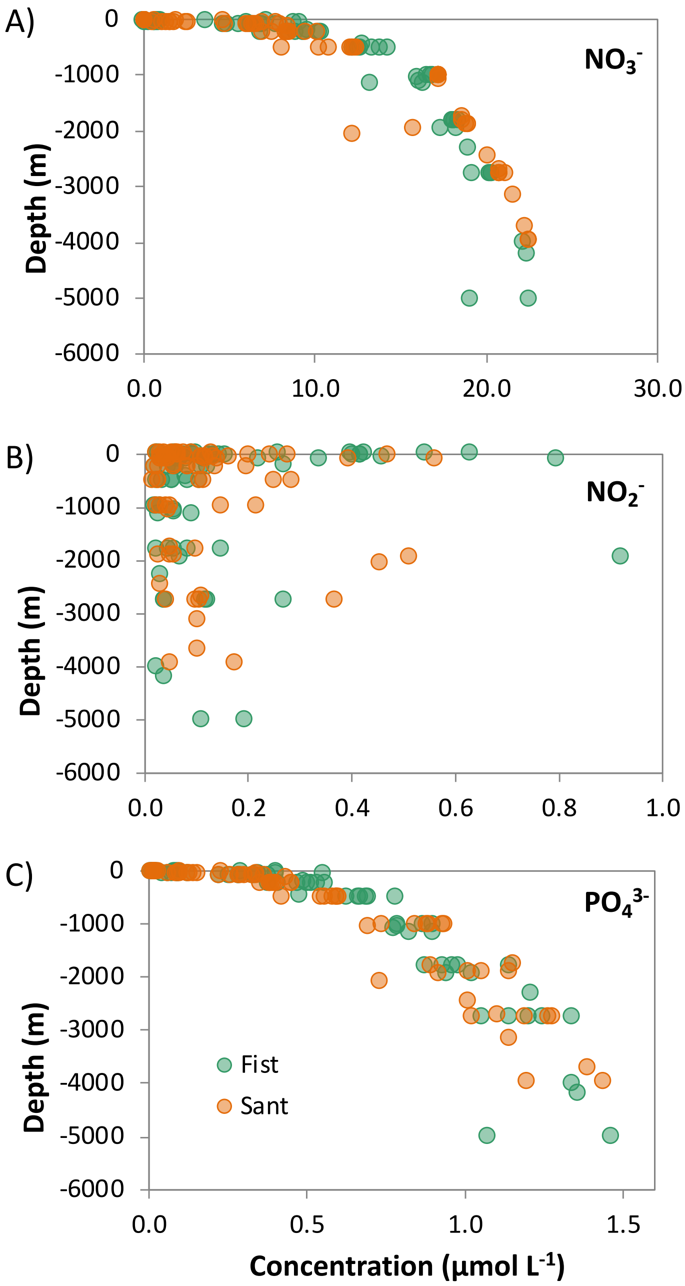
Supplementary Figure 2. Upwelling index (UI, m^3 s^{-1} km^{-1}, 6-hourly values) for A) Fisterra, and B) Santander, in the NW Iberian upwelling area during the period of survey (data source: http://www.indicedeafloramiento.ieo.es/). Alternate grey/white shadows indicate 24-h intervals. Red triangles denote the start of each sampling survey within the area of upwelling influence, and numbers indicate the biological sampling stations sampled each date.



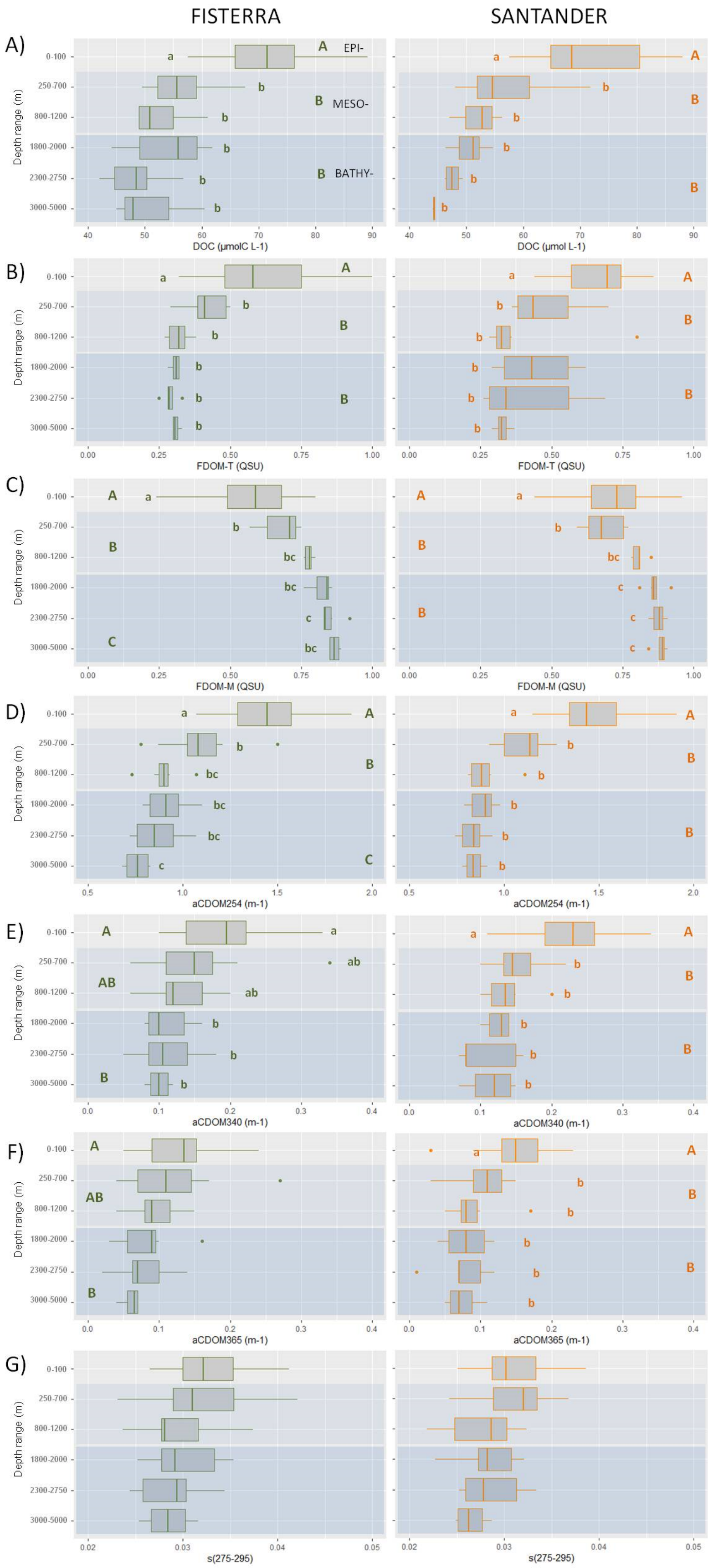
Supplementary Figure 3. Three-days composites of SST (sea surface temperature, º C) and chlorophyll concentration (µg L^{-1}) from satellite imagery, for A) Fisterra and B) Santander sections. Black circles represent MODUPLAN sampling stations. Larger red circles represent stations sampled during the corresponding period of time shown in the images.



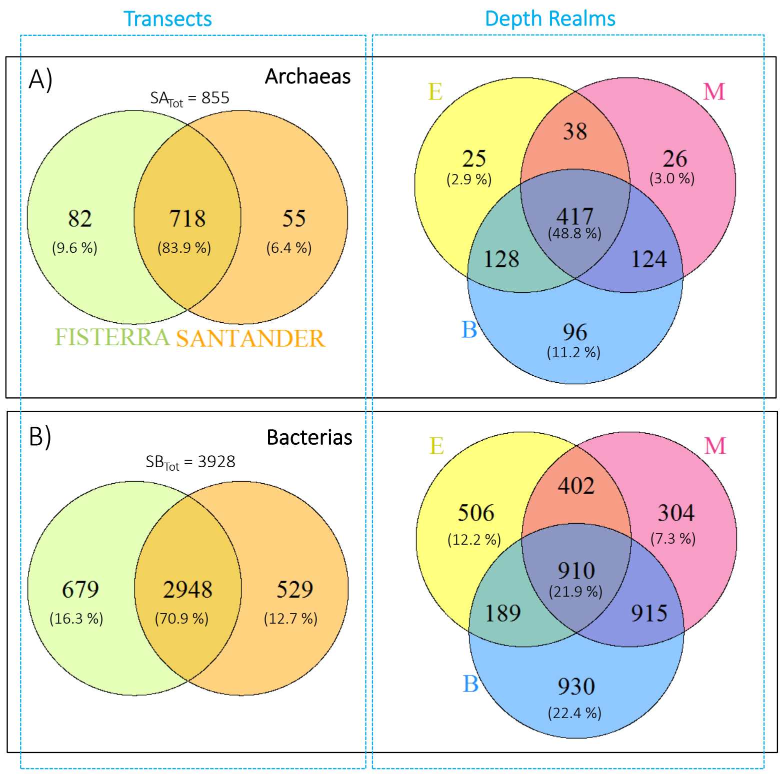
Supplementary Figure 4. Vertical profiles of the squared Brunt-Väisälä frequency (N^2, s^{-2}) (red line) for each sampling station in A) Fisterra and B) Santander sections from the Northwestern Iberian upwelling area to adjacent open-ocean. The green-dotted line shows the mixed layer depth (MLD), calculated as the depth where seawater density was 0.125 kg m^{-3} higher than the surface value. The black line represents the potential density anomaly (σ_θ), i.e., the surface-referenced potential density (ρ_θ) minus 1000 (Kg m^{-3}).



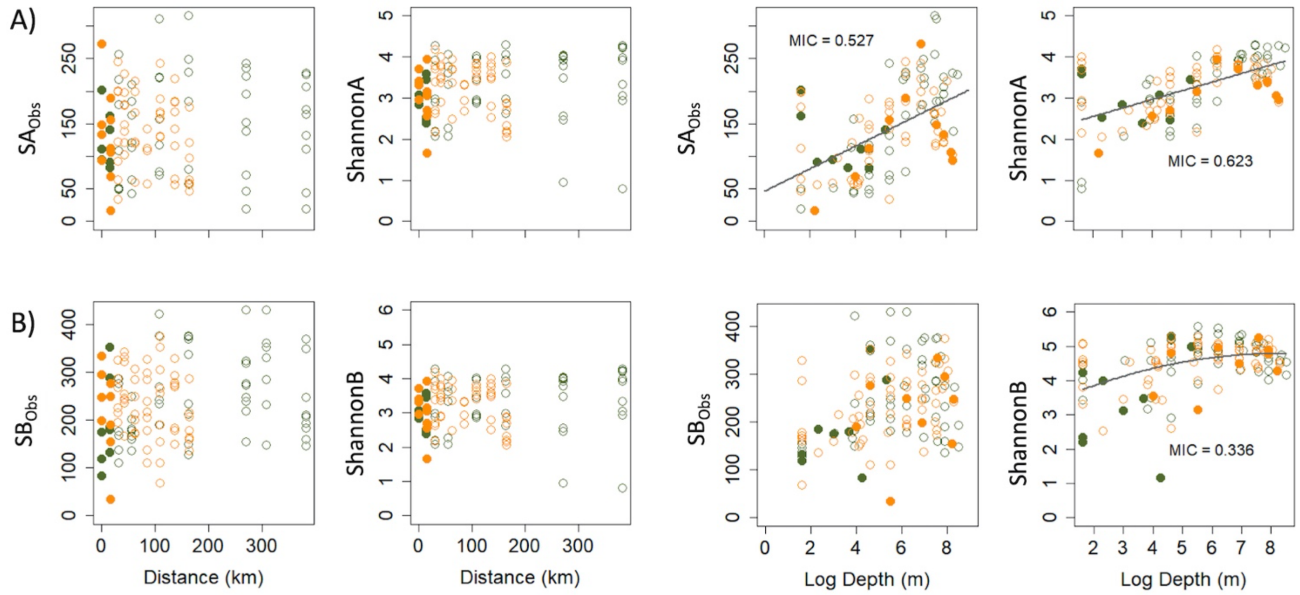
Supplementary Figure 5. Vertical profiles of the concentration of inorganic nutrients: A) nitrate (NO_3^-); B) nitrite, (NO_2^-); and C) phosphate (PO_4^{3-}); all expressed as µM (µmol L^{-1}), in Fisterra (green) and Santander (orange) sections from the Northwestern Iberian upwelling area to adjacent open-ocean.


FISTERRA
SANTANDER
A)
B)
C)
D)
E)
F)
G)
EPI-
MESO-
BATHY-
Depth range (m)
DOC (µmolC L-1)
DOC (µmol L-1)
FDOM-T (QSU)
FDOM-M (QSU)
aCDOM254 (m-1)
aCDOM340 (m-1)
aCDOM365 (m-1)
s(275-295)

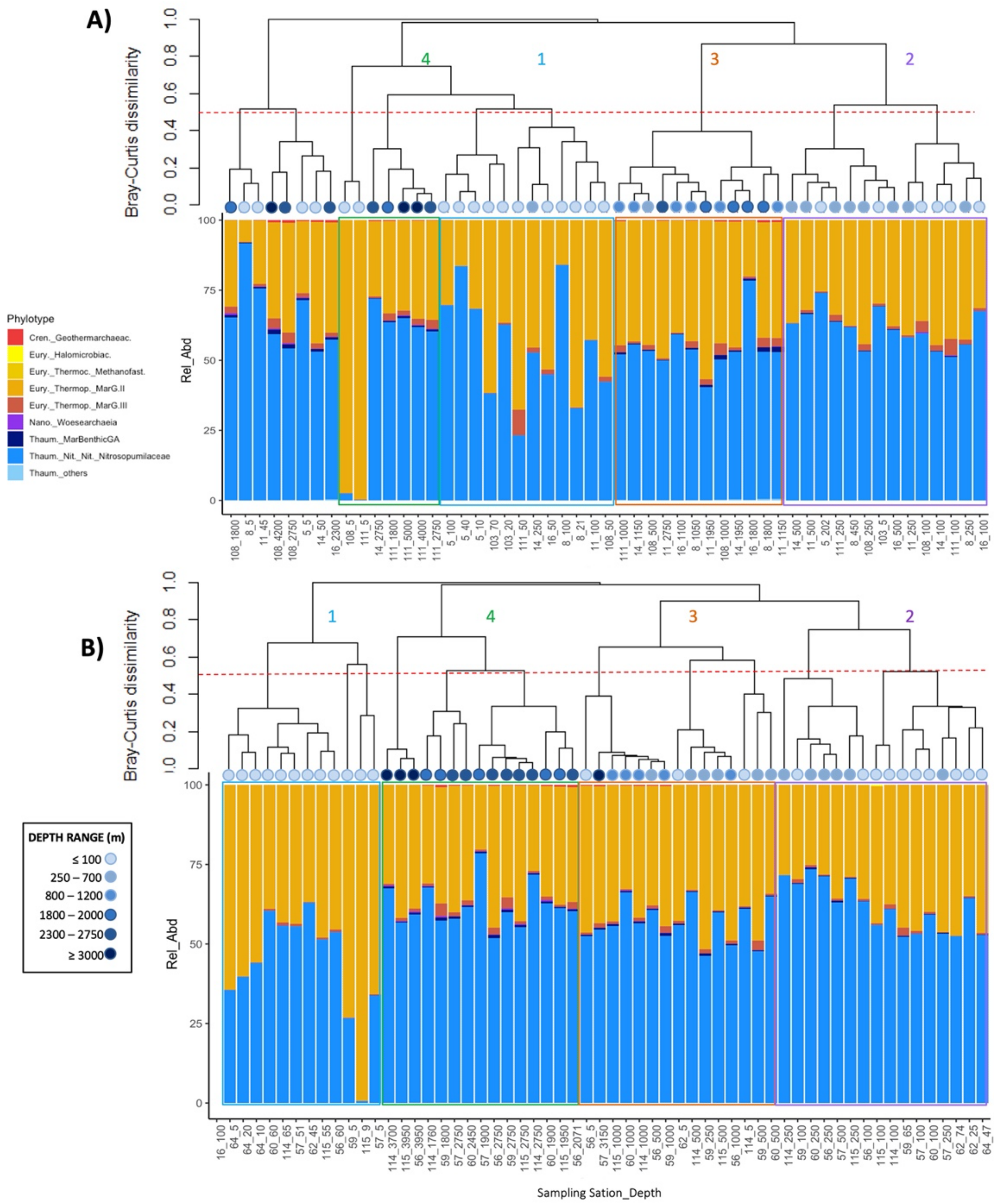
Supplementary Figure 6. Average A) DOC concentration (µmolC L^{-1}), B) FDOM-T (QSU), C) FDOM-M (QSU), D) aCDOM254 (m^{-1}), E) aCDOM340 (m^{-1}), F) aCDOM365 (m^{-1}), and G) s(275-295), in the three depth realms (epi-, meso- and bathy-pelagic) and the different sampling depth ranges (0-100, 250-700, 800-1200, 1800-2000, 2300-2750, and 3000-5000), for Fisterra (left) and Santander (right) sections from the Northwestern Iberian upwelling area to adjacent open-ocean. The boxplots were constructed with the first and third quartiles of the distribution of values, and the medians. Dots represent outlier values. Different capital letters indicate significant (One-way ANOVA and Tukey's test, p-value < 0.001) differences among depth realms, while different lowercase letters indicate significant (One-way ANOVA and Tukey's test, p-value < 0.001) differences among depth ranges.



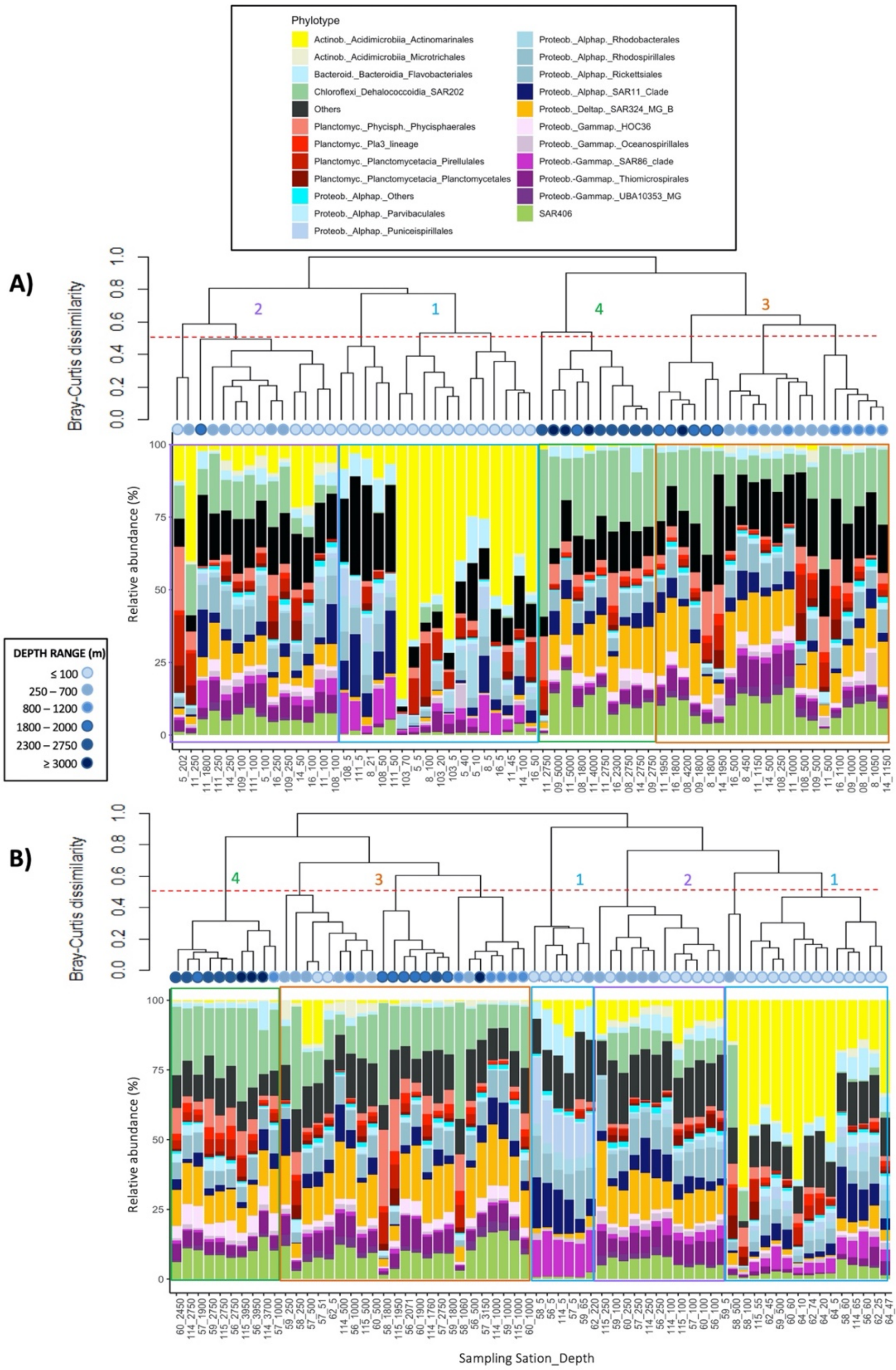
Supplementary Figure 7. Venn diagrams, showing the number (and the percentage of the observed ASV richness) of unique and shared ASVs of A) Archaea and B) Bacteria, between transects (left panel, Fisterra and Santander) and among depth realms (right panel, E =epi-, M = meso- and B = bathypelagic).



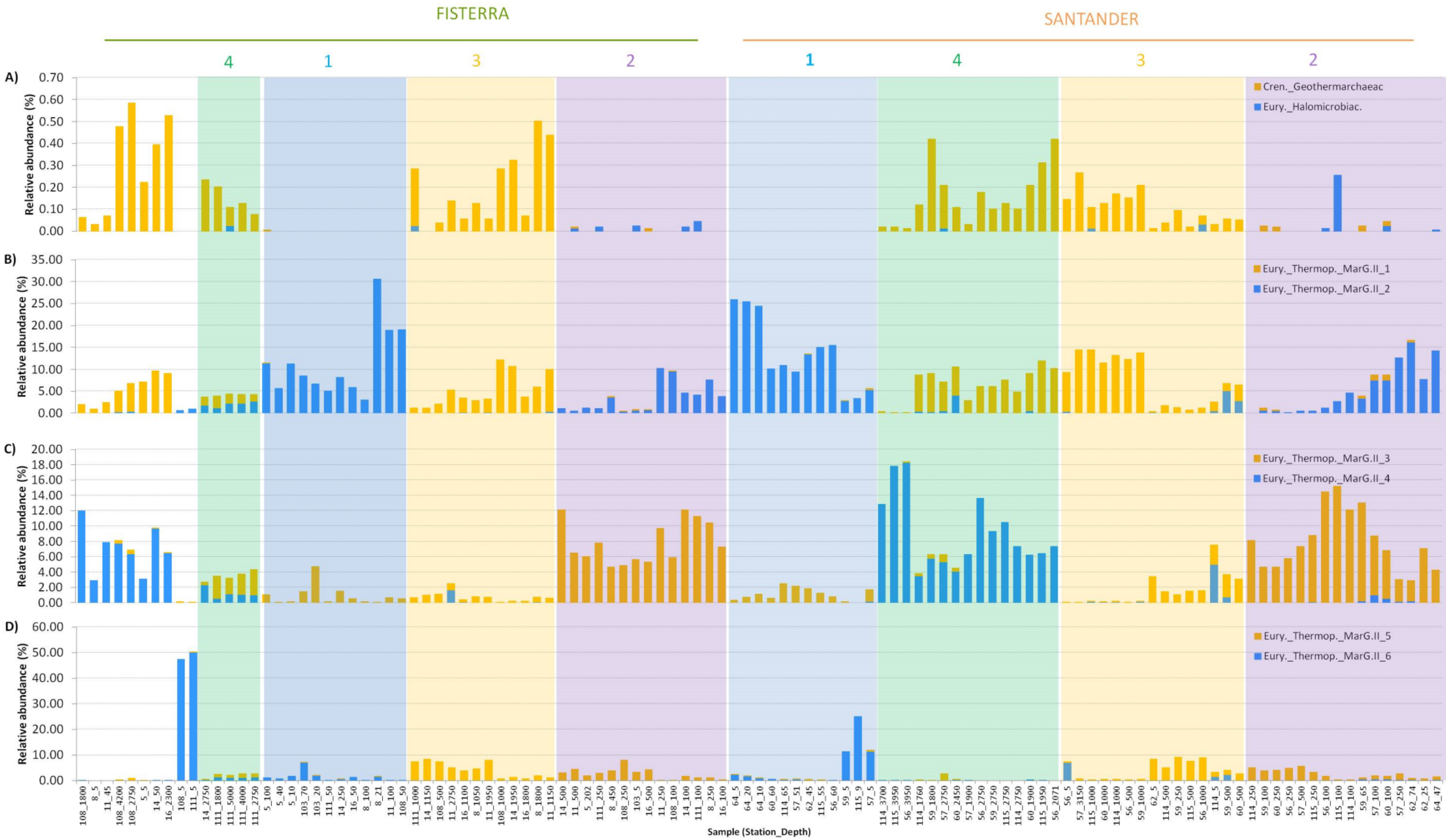
Supplementary Figure 8. Spatial variability of alpha-diversity for A) Archaea and B) Bacteria. S_{Obs}, observed ASV richness per sample, and Shannon diversity index, plotted against distance from the coast (horizontal variability) and sampling depth (vertical variability). For informative purpose, colors show Fisterra in orange and Santander in green, and close circles represent the two sampling stations closer to the coast, while open circles are open-ocean samples. All samples were grouped into a unique dataset for statistical analysis and model fitting. MIC is the Maximal information Coefficient, only shown when correlation was found to be significant ($p < 0.01$) by the MINE analysis. For these cases, grey line represents the (linear or quadratic) model significantly fitted to data. The values for the parameters describing these models are available at Table S4.



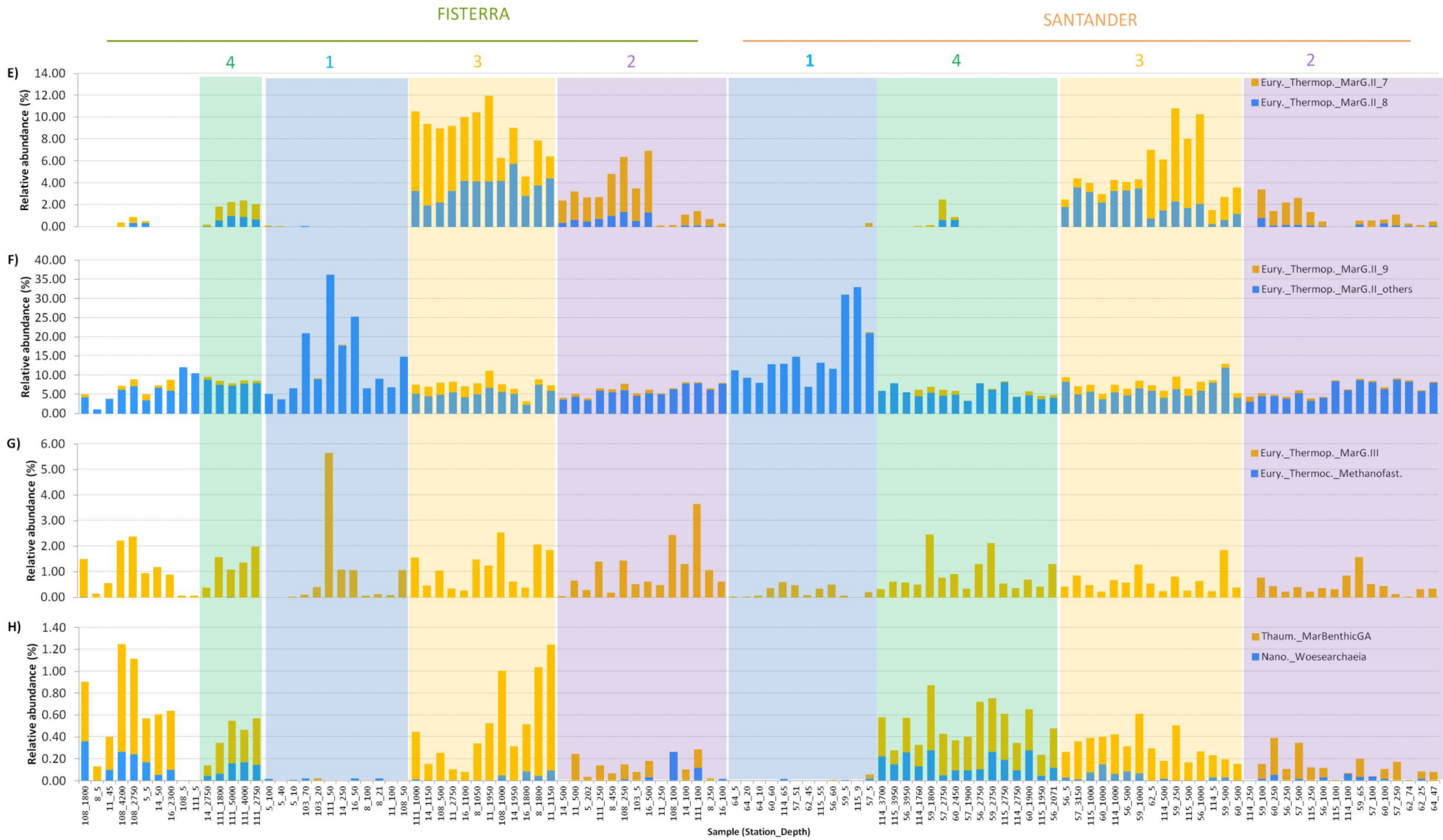
Supplementary Figure 9. Cluster dendrogram based on Bray-Curtis dissimilarity (after Hellinger transformation) among samples, associated to the plot of community composition in terms of the relative abundance (%) of Archaea phylotypes per sample, pooled at family level, for A) Fisterra, and B) Santander sections. Boxes help to visualize the 4 different clusters: cluster 1 = *upper subsurface* (≤100 m, blue); cluster 2 = *lower subsurface* (100 - 500 m, purple); cluster 3 = *intermediate* (500 - 2000 m, orange); cluster 4 = *deep* communities (≥2000 m, green). See Table 2 for further details on the taxonomy of archaeal phylotypes.



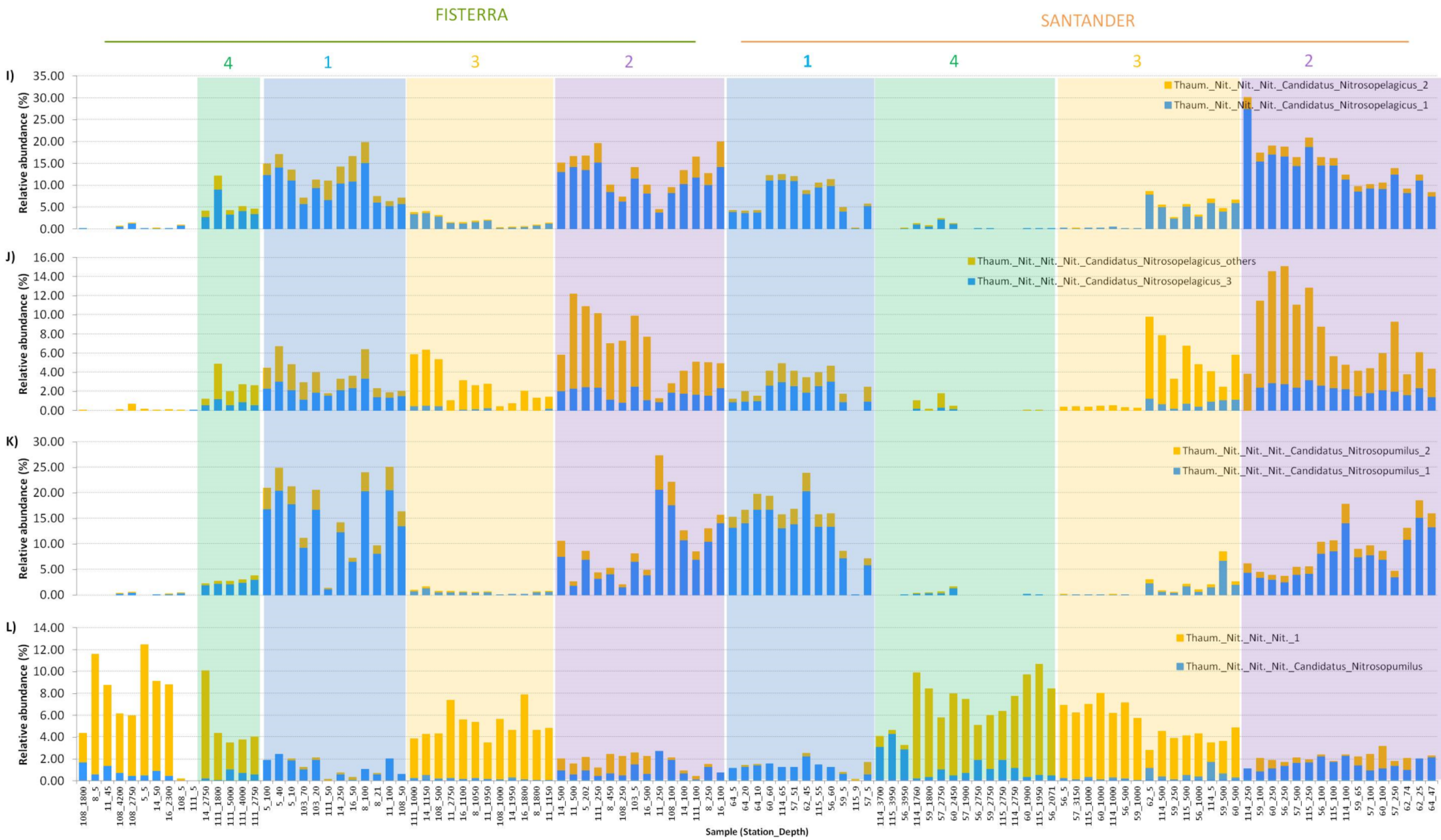
Supplementary Figure 10. Cluster dendrogram based on Bray-Curtis dissimilarity (after Hellinger transformation) among samples, associated to the plot of community composition in terms of the relative abundance (%) of Bacteria phylotypes per sample, pooled at order level, for A) Fisterra, and B) Santander sections. Boxes help to visualize the 4 different clusters: cluster 1 = *upper subsurface* (≤100 m, blue); cluster 2 = *lower subsurface* (100 - 500 m, purple); cluster 3 = *intermediate* (500 - 2000 m, orange); cluster 4 = *deep* communities (≥2000 m, green). See Table 2 for further details on the taxonomy of archaeal phylotypes.



Supplementary Figure 11 A-D)



Supplementary Figure 11 E-H)



Supplementary Figures 11 I-L)

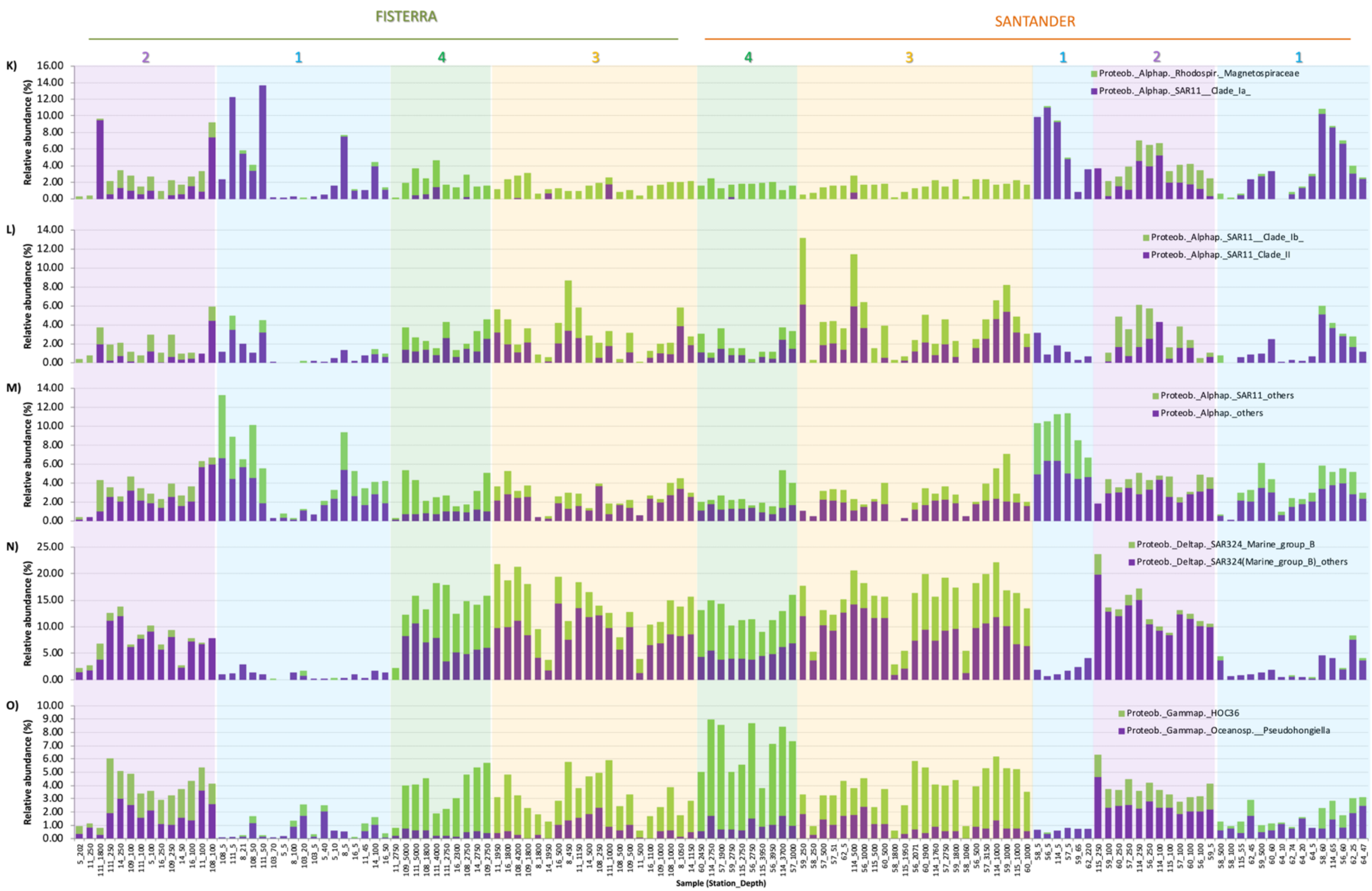
Supplementary Figure 11 M-P)

Supplementary Figure 11, A) to P). Relative abundance of the 32 archaeal abundant phylotypes per sample, in Fisterra (left) and Santander (right) transects. Colored boxes and numbers show the corresponding cluster displayed in Figure 3 (blue is cluster 1, *upper subsurface*; purple is cluster 2, *lower subsurface*; orange is cluster 3, *intermediate*; and green is cluster 4, *deep*). See further details about archaeal phylotypes nomenclature in Table 2.

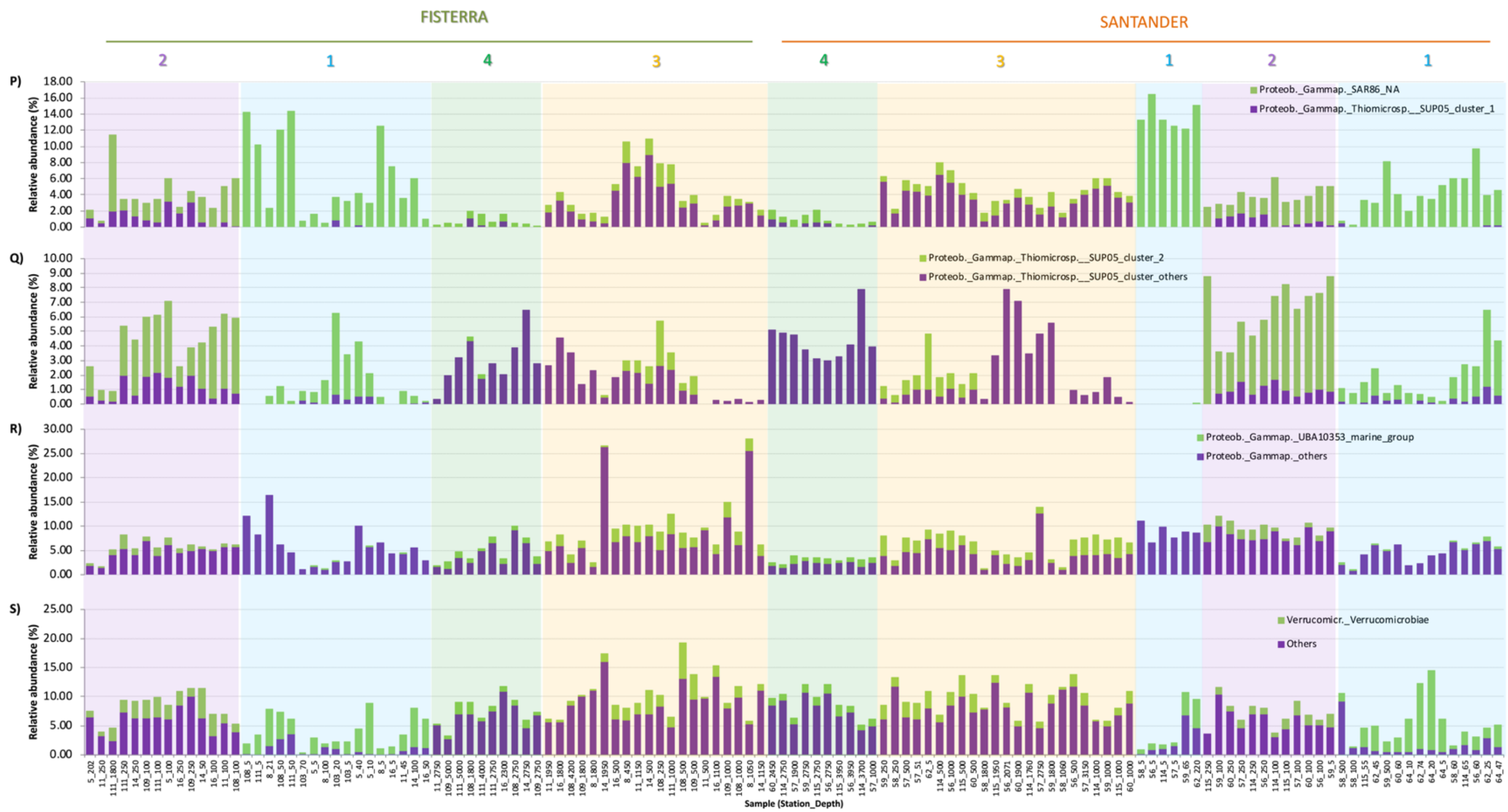
In general, the abundant phylotypes conforming archaeal communities displayed 3 different vertical patterns of relative abundance through the water column: 1) some phylotypes were very abundant at the upper and lower subsurface communities (clusters 1, 2 or both) to then almost disappear at intermediate and deep samples (e.g., *MarGII_2* (Euryarchaeota) (Supplementary Figure S11,B) and *C.Nitrosopumilus*_1 (Thaumarchaeota) (Supplementary Figure S11,K), while some others showed 2) the opposite trend (i.e., high abundance in clusters 3, 4 or both but very low abundance or absence in subsurface clusters 1 and 2; e.g. *MarGII_4* (Euryarchaeota) (Supplementary Figure S11,C) and *Thaum_Nit._Nit._Nit._others,* a group of 296 ASVs (Thaumarchaeota) (Supplementary Figure S11,P). Finally, 3) some phylotypes, such as *MarGII_others* (Euryarchaeota, composed by 237 ASVs) (Supplementary Figure S9,F) and *C.Nitrosopumilus_2* (Thaumarchaeota) (Supplementary Fiure S9,K), were found at pretty constant relative abundance throughout the water column. For instance, the 3 vertical patterns of relative abundance were found for 7 abundant ASVs within the Family *Nitrosopumilaceae* (Thaum._Nit_Nit_Nit_ 1 to 7): *Thaum._Nit_Nit_Nit_1* (Supplementary Figure S9,L) was abundant in clusters 3 and 4, i.e., intermediate and deep communities (~ 8% in both transects), decreasing to less than 1% of the samples in subsurface waters (clusters 1 and 2); *Thaum._Nit_Nit_Nit_2* and *Thaum._Nit_Nit_Nit_3* (Supplementary Information Fig. S9M) were almost absent at upper subsurface (cluster 1) but showed a slightly increased at lower subsurface (cluster 2), where they are present in low abundance (~ 1%). At intermediate waters (cluster 3), they both reached about 3% of the community, but while *Thaum._Nit_Nit_Nit_2* kept this relative abundance in deep communities, *Thaum._Nit_Nit_Nit_3* decreased again to very low relative abundance (~1%); *Thaum._Nit_Nit_Nit_4, Thaum._Nit_Nit_Nit_5* (Supplementary Information Fig. S9N) and *Thaum._Nit_Nit_Nit_6* (Supplementary Figure S11O) were almost completely absent at subsurface waters (cluster 1 and 2), they appeared in very low abundance at intermediate waters (cluster 3) and finally reached important relative abundance (~ 5% each) at deeper communities (cluster 4); Finally, *Thaum._Nit_Nit_Nit_7* (Supplementary Figure S11O) was almost absent from upper subsurface assemblages (cluster 1), then increased its relative abundance trough lower subsurface (cluster 2) and intermediate waters (cluster 3), to then decreased again at deeper communities (cluster 4).

Supplementary Figure 12 A-E)

Supplementary Figure 12 F-J)



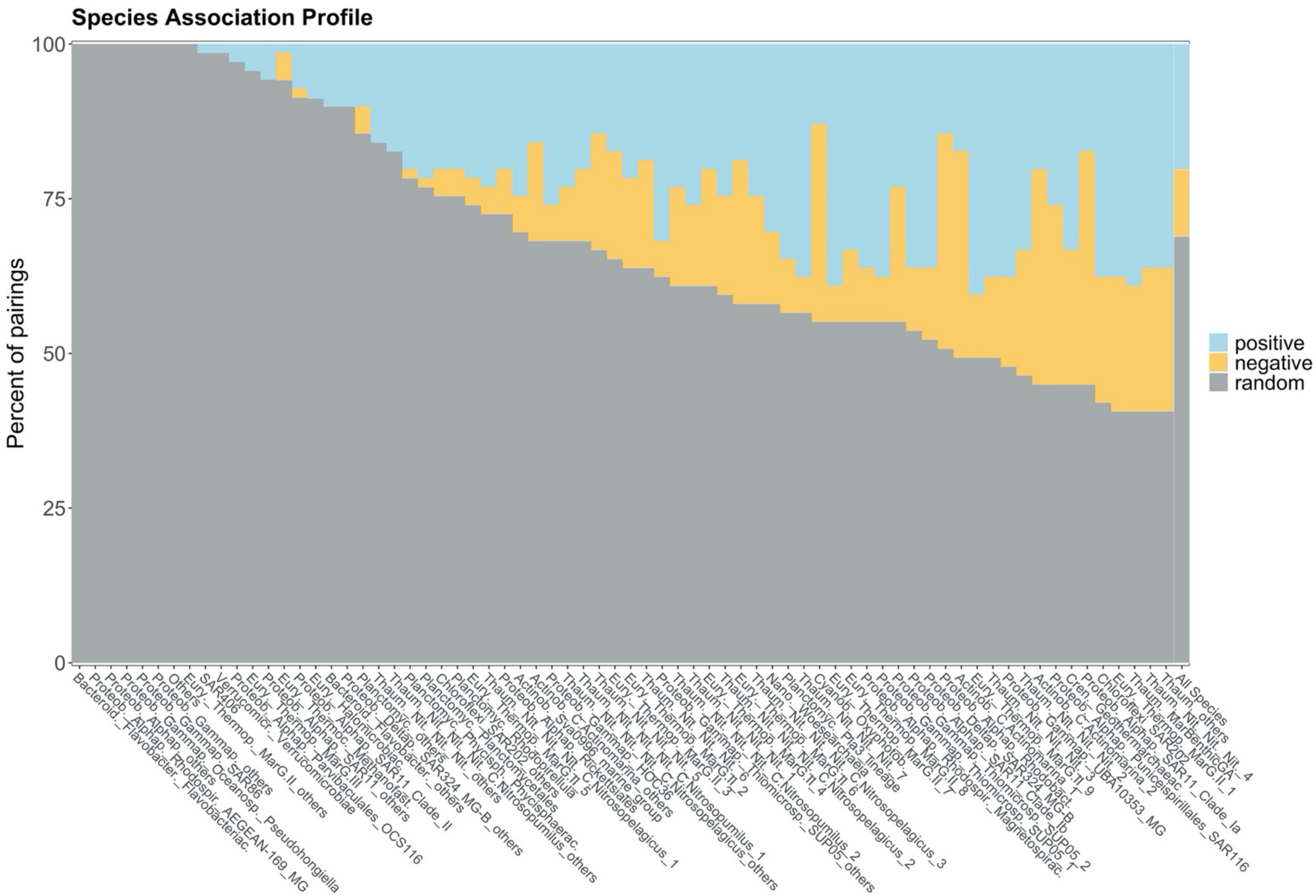
Supplementary Figure 12 K-O)



Supplementary Figure 12 P-S)

Supplementary Figure 12 A) to S). Relative abundance of the 38 bacterial abundant phylotypes per sample, in Fisterra (left) and Santander (right) transects. Colored boxes and numbers show the corresponding cluster displayed in Figure 4 (blue is cluster 1, *upper subsurface*; purple is cluster 2, *lower subsurface*; orange is cluster 3, *intermediate*; and green is cluster 4, *deep*). See further details about archaeal phylotypes nomenclature in Table 3.

The same 3 vertical patterns of relative abundance (as for Archaea, Supplementary Figure S11), were found for Bacteria: some groups were present through the whole water column, keeping fairly low and constant relative abundance (such as *Sva0996_marine_group* (Actinobacteria) (Supplementary Figure S112B) and *Phycisphaeraceae* (Planctomycetes) (Supplementary Figure S12,F), sometimes increasing their presence at subsurface (e.g., *AEGEAN-169_marine group* (Alphaproteobacteria) in clusters 1 and 2, Supplementary Figure S12,J) or at deep waters (for instance *HOC36* (Gammaproteobacteria) at clusters 3 and 4, Supplementary Figure S12O); some phylotypes were (almost) specific of subsurface waters, with high relative abundance in cluster 1 and 2 (e.g., *C.Actinomarina_1* (Actinobacteria) (Supplementary Figure S12,A), Cyanobacteria (Supplementary Figure S12,E), and *SAR86* (Gammaproteobacteria) (Supplementary Figure S12,P); and finally some others were very abundant at intermediated and deep waters (clusters 3 and 4) but very low at subsurface communities (clusters 1 and 2) (e.g., *SAR202_others* (Chloroflexi) (Supplementary Figure S12,D), *SAR406* (Marinimicrobia) (Supplementary Figure S12,E) or *SAR324_marine group B* (Deltaproteobacteria) (Supplementary Figure S12,N).



Supplementary Figure 13. Percentage of associations among abundant phylotypes in the co-occurrence semi-matrix (Figure 5 in the main text). A few abundant phylotypes, in the left extreme, showed completely random (grey) relationships with the others, while most phylotypes showed positive (blue) and/or negative (orange) co-occurrence patterns with up to ~ 60% of the other phylotypes. See Table 2 and Table 3 in the main text for further details on Archaea and Bacteria nomenclature, respectively

1.2 Supplementary Tables

Supplementary Table 1. Probe sequences and formamine concentrations used for CARD-FISH analysis.

Probe	**Organism**	**Sequence (5'→3')**	**FA* (%)**	**Reference**
NON338	Negative control	ACTCCTACGGGAGGCAGC	55	(Wallner *et al.,* 1993)
Cren537	Thaumarchaeota	TGACCACTTGAGGTGCTG	20	(Teira *et al.,* 2004)
Eury806	Euryarchaeota	CACAGCGTTTACACCTAG	20	(Teira *et al.,* 2004)
EUB338I	Bacteria	GCTGCCTCCCGTAGGAGT	55	(Amann *et al.*, 1990)
EUB338 II	Bacteria	GCAGCCACCCGTAGGTGT	55	(Daims *et al.*, 1999)
EUB338 III	Bacteria	GCTGCCACCCGTAGGTGT	55	(Daims *et al.*, 1999)

*Formamide (FA) concentration in percent of hybridization buffer

Supplementary Table 2. Concentration (µmol L-1) of inorganic nutrients (phosphate, PO43-; nitrite, NO2-; nitrate, NO3-; inorganic nitrogen, NO2-+NO3-) in the different stations and sampling depths, in A) Fisterra and B) Santander sections.

A)

Section	**Station**	**Depth (m)**	**PO_4^{3-}**	**NO_2^-**	**NO_3^-**	**$NO_2^- + NO_3^-$**
FISTERRA	103	5	0.294	0.259	3.611	3.870
		20	0.403	0.417	7.183	7.600
		45	0.552	0.415	8.799	9.214
		70	0.403	0.458	9.135	9.593
	5	5	0.078	0.542	0.689	1.231
		10	0.087	0.629	0.833	1.462
		40	0.349	0.402	6.063	6.465
		100	0.377	0.336	6.970	7.306
		202	0.487	0.269	9.583	9.852
	8	5	0.018	0.425	0.029	0.454
		21	0.090	0.131	0.999	1.130
		100	0.220	0.795	4.828	5.623
		250	0.380	0.108	6.845	6.953
		450	0.476	0.081	12.781	12.862
		1050	0.788	0.055	15.933	15.988
		1800	0.929	0.058	18.367	18.425
	11	5	0.017	0.056	0.001	0.057
		45	0.121	0.095	0.833	0.928
		100	0.282	0.219	5.536	5.755
		250	0.516	0.060	9.331	9.391
		500	0.784	0.051	13.849	13.900
		1150	0.897	0.090	16.369	16.459
		1950	0.941	0.067	18.252	18.319
		2750	1.246	0.270	20.261	20.531
	14	5	0.014	0.399	0.009	0.408
		70	0.090	0.128	0.708	0.836

	100	0.336	0.113	6.334	6.447
	250	0.474	0.046	8.464	8.510
	500	0.689	0.033	12.624	12.657
	1150	0.822	0.028	13.242	13.270
	1950	1.020	0.922	17.357	18.279
	2750	1.337	0.119	20.344	20.463
16	5	0.005	0.026	0.001	0.027
	50	0.074	0.125	0.630	0.755
	100	0.255	0.081	4.593	4.674
	250	0.499	0.020	9.382	9.402
	500	0.671	0.021	14.238	14.259
	1100	0.776	0.057	16.093	16.150
	1800	0.871	0.047	18.070	18.117
	2300	1.211	0.029	18.979	19.008
108	5	0.012	0.022	0.000	0.022
	50	0.064	0.155	0.320	0.475
	100	0.326	0.066	6.189	6.255
	250	0.535	0.121	10.337	10.458
	500	0.694	0.104	13.344	13.448
	1000	0.789	0.022	16.841	16.863
	1800	0.978	0.148	18.165	18.313
	2750	1.201	0.039	20.301	20.340
	4200	1.360	0.038	22.409	22.447
109	5	0.025	0.098	0.003	0.101
	50	0.091	0.077	0.641	0.718
	100	0.366	0.067	7.675	7.742
	250	0.558	0.059	10.303	10.362
	500	0.666	0.083	12.222	12.305
	1000	0.897	0.032	16.511	16.543
	1800	1.139	0.085	18.113	18.198
	2750	1.140	0.122	19.229	19.351

	5000	1.461	0.108	22.520	22.628
111	5	0.012	0.089	0.010	0.099
	50	0.040	0.145	0.114	0.259
	100	0.285	0.060	6.862	6.922
	250	0.407	0.055	8.831	8.886
	500	0.629	0.054	12.522	12.576
	1000	0.865	0.017	16.761	16.778
	1800	0.964	0.024	18.082	18.106
	2750	1.054	0.036	20.163	20.199
	4000	1.338	0.023	22.210	22.233
	5000	1.072	0.192	19.098	19.290

B)

Section	**Station**	**Depth (m)**	**PO_4^{3-}**	**NO_2^-**	**NO_3^-**	**NO_2^- + NO_3^-**
SANTANDER	63	5	0.023	0.029	0.087	0.116
		10	0.031	0.075	0.614	0.689
		20	0.100	0.200	1.843	2.043
		30	0.231	0.276	4.683	4.959
		50	0.341	0.040	7.706	7.746
		75	0.364	0.030	7.984	8.014
		123	0.431	0.029	8.420	8.449
	62	5	0.018	0.092	-0.001	0.091
		25	0.010	0.469	0.022	0.491
		45	0.125	0.243	2.525	2.768
		74	0.325	0.080	6.889	6.969
		220	0.387	0.056	10.087	10.143
	60	5	0.017	0.059	0.018	0.077
		60	0.087	0.111	1.279	1.390

	100	0.261	0.038	6.564	6.602
	250	0.383	0.020	8.317	8.337
	500	0.543	0.107	12.293	12.400
	1000	0.738	0.022	17.213	17.235
	1900	1.055	0.050	18.957	19.007
	2450	1.013	0.032	20.126	20.158
59	65	0.062	0.046	0.465	0.511
	5	0.019	0.059	0.012	0.071
	100	0.290	0.140	6.418	6.558
	250	0.393	0.103	8.430	8.533
	500	0.595	0.026	12.398	12.424
	1000	0.929	0.148	17.178	17.326
	1900	1.139	0.055	18.994	19.049
	2700	1.103	0.108	20.738	20.846
58	5	0.019	0.054	0.025	0.079
	60	0.101	0.161	1.561	1.722
	100	0.282	0.559	6.031	6.590
	250	0.396	0.055	8.478	8.533
	500	0.595	0.027	12.252	12.279
	1060	0.695	0.047	17.249	17.296
	1800	0.891	0.100	18.609	18.709
57	5	0.018	0.022	0.013	0.035
	51	0.092	0.065	1.074	1.139
	250	0.353	0.084	6.944	7.028
	250	0.451	0.084	9.422	9.506
	500	0.582	0.249	12.134	12.383
	1000	0.878	0.215	17.194	17.409
	1900	1.008	0.026	18.842	18.868
	2750	1.023	0.369	21.078	21.447
	3150	1.140	0.101	21.624	21.725
56	5	0.005	0.064	0.013	0.077

	60	0.144	0.118	1.595	1.713
	100	0.224	0.394	4.753	5.147
	250	0.387	0.195	7.511	7.706
	500	0.421	0.284	8.090	8.374
	1000	0.936	0.041	17.185	17.226
	2071	0.730	0.453	12.246	12.699
	2750	1.275	0.041	20.752	20.793
	3950	1.195	0.175	22.467	22.642
114	5	0.021	0.129	0.015	0.144
	65	0.154	0.132	2.412	2.544
	100	0.341	0.118	6.176	6.294
	250	0.451	0.028	8.469	8.497
	500	0.557	0.016	10.285	10.301
	1000	0.841	0.031	17.179	17.210
	1760	1.152	0.049	18.556	18.605
	2750	1.190	0.100	20.786	20.886
	3700	1.391	0.101	22.256	22.357
115	9	0.021	0.037	0.020	0.057
	55	0.130	0.110	1.772	1.882
	100	0.303	0.045	6.330	6.375
	250	0.402	0.136	8.418	8.554
	500	0.604	0.115	10.830	10.945
	1000	0.887	0.050	17.250	17.300
	1950	0.920	0.510	15.793	16.303
	2750	1.262	0.106	20.791	20.897
	3950	1.440	0.049	22.463	22.512

Supplementary Table 3. Contribution of Bacteria and Archaea (as % of total prokaryotic cells; % DAPI) throughout the water column, for A) Fisterra (stations 8, 11, 16 and 111) and B) Santander (stations 115, 57, 60), determined by CARD-FISH.

A)

Station	Depth (m)	Bacteria %DAPI	Thaum. %DAPI	Eury. %DAPI	Tot. Archaea %DAPI	Recovery (%)
8	1800	67.20	7.57	1.05	8.61	75.8
	1050	53.53	8.06	1.20	9.26	62.8
	450	51.06	11.03	0.00	11.03	62.1
	250	57.31	12.38	2.74	15.12	72.4
	100	62.98	3.35	0.97	4.31	67.3
	21	54.12	17.95	2.01	19.96	74.1
	5	68.57	6.18	3.74	9.92	78.5
11	2750	51.11	10.87	4.43	15.31	66.4
	1950	56.94	10.48	5.00	15.48	72.4
	1150	49.68	13.32	5.17	18.49	68.2
	500	48.93	11.89	6.74	18.62	67.6
	100	49.37	15.92	6.00	21.92	71.3
	45	60.00	11.66	5.86	17.51	77.5
	5	66.96	10.06	8.44	18.50	85.5

16	2300	74.34	10.46	5.17	15.63	90.0
	1950	67.97	15.15	6.74	21.89	89.9
	1150	64.00	18.09	10.24	28.33	92.3
	500	64.55	10.81	6.00	16.81	81.4
	250	55.77	8.21	5.86	14.07	69.8
	100	53.76	9.57	8.44	18.01	71.8
	50	52.51	5.97	5.13	11.10	63.6
111	5000	65.02	23.23	-	-	
	4000	62.65	22.09	3.79	25.88	88.5
	2750	73.69	18.85	7.34	26.19	99.9
	1800	59.48	-	-	-	
	1000	68.96	21.17	7.03	28.20	97.2
	250	61.78	13.47	7.48	20.95	82.7
	100	65.51	13.67	6.85	20.51	86.0
	50	56.68	18.73	6.29	25.02	81.7
	5	66.68	29.45	9.91	39.36	106.0

B)

Station	Depth (m)	Bacteria %DAPI	Thaum. %DAPI	Eury. %DAPI	Tot. Archaea %DAPI	Recovery (%)
60	2450	67.64	21.02	3.20	24.22	91.86
	1900	-	11.40	4.27	15.67	
	1000	-	23.45	5.45	28.90	
	500	56.02	11.11	3.00	14.11	70.14
	250	58.02	8.03	7.10	15.13	73.15
	100	57.37	7.00	5.71	12.71	70.09
	60	72.55	8.11	5.92	14.03	86.58
	5	70.44	-	6.75	6.75	
57	3150	61.28	20.43	3.00	23.43	84.71
	2750	66.87	13.74	3.43	17.17	84.04
	1900	59.97	10.62	5.00	15.62	75.59
	1000	56.96	22.23	5.37	27.60	84.57
	500	66.34	12.56	7.61	20.17	86.50
	250	65.69	17.90	7.00	24.90	90.60
	100	86.63	8.57	10.76	19.33	105.95
	51	64.15	7.15	8.92	16.07	80.22

	9	72.42	12.09	7.87	19.96	92.38
115	3950	69.86	21.55	6.44	27.99	97.84
	2750	62.71	14.49	4.56	19.05	81.76
	1950	72.59	11.68	3.89	15.57	88.16
	1000	66.78	23.43	5.80	29.23	96.01
	500	67.84	10.51	9.50	20.00	87.85
	250	65.82	17.34	7.51	24.85	90.67
	100	57.48	-	14.28	-	
	55	73.10	-	8.59	-	
	9	77.12	-	13.74	-	

Supplementary Table 4. Good's coverage estimator, showing the proportion of the population represented by the ASVs included in the sample. *Nº sing.* denotes the number of singletons (abundance =1) in the sample. *Nº seqs.* is the number of sequences.

	RAW ARCHAEA			RAW BACTERIA			RAREFIED ARCHAEA			RAREFIED BACTERIA		
Sample (Station_Depth)	**Nº sing.**	**Nº seqs.**	**Good's**	**Nº sing.**	**Nº seqs.**	**Good's**	**Nº sing.**	**Nº seqs.**	**Good's**	**Nº sing.**	**Nº seqs.**	**Good's**
103_70	0	64223	100.00	1	47278	100.00	9	9718	99.91	25	2002	98.75
103_20	0	30197	100.00	5	19067	99.97	3	9718	99.97	42	2002	97.90
103_5	0	38746	100.00	4	19330	99.98	9	9718	99.91	34	2002	98.30
5_202	0	20174	100.00	10	18499	99.95	4	9718	99.96	67	2002	96.65
5_100	0	25125	100.00	13	13023	99.90	2	9718	99.98	82	2002	95.90
5_40	0	36495	100.00	2	20456	99.99	4	9718	99.96	38	2002	98.10
5_10	0	44140	100.00	3	24677	99.99	5	9718	99.95	39	2002	98.05
5_5	1	33903	100.00	4	38084	99.99	6	9718	99.94	51	2002	97.45
8_1800	2	39929	99.99	6	14595	99.96	8	9718	99.92	62	2002	96.90
8_1050	2	27728	99.99	1	12067	99.99	6	9718	99.94	20	2002	99.00
8_450	2	58565	100.00	2	18796	99.99	10	9718	99.90	54	2002	97.30
8_250	1	27558	100.00	NS	NS	NS	0	9718	100.00	NS	NS	NS
8_100	0	20466	100.00	0	11510	100.00	1	9718	99.99	14	2002	99.30
8_21	0	33902	100.00	2	8243	99.98	0	9718	100.00	22	2002	98.90
8_5	0	12805	100.00	4	12859	99.97	1	9718	99.99	22	2002	98.90
11_2750	0	20725	100.00	3	6513	99.95	1	9718	99.99	18	2002	99.10
11_1950	2	27176	99.99	4	6557	99.94	4	9718	99.96	18	2002	99.10

11_1150	1	31127	100.00	5	16673	99.97	5	9718	99.95	45	2002	97.75
11_500	3	27331	99.99	1	7610	99.99	7	9718	99.93	16	2002	99.20
11_250	0	25215	100.00	3	14289	99.98	3	9718	99.97	29	2002	98.55
11_100	0	31182	100.00	5	9811	99.95	3	9718	99.97	23	2002	98.85
11_45	0	53349	100.00	3	31282	99.99	7	9718	99.93	37	2002	98.15
14_2750	3	122329	100.00	2	10294	99.98	17	9718	99.83	31	2002	98.45
14_1950	2	129545	100.00	11	41086	99.97	27	9718	99.72	104	2002	94.81
14_1150	5	34499	99.99	8	14216	99.94	8	9718	99.92	72	2002	96.40
14_500	0	22800	100.00	6	13837	99.96	1	9718	99.99	40	2002	98.00
14_250	1	39957	100.00	4	8824	99.95	0	9718	100.00	31	2002	98.45
14_100	0	34120	100.00	8	27288	99.97	4	9718	99.96	60	2002	97.00
14_50	4	52334	99.99	11	47567	99.98	12	9718	99.88	156	2002	92.21
16_2300	4	80670	100.00	6	19789	99.97	18	9718	99.81	82	2002	95.90
16_1800	2	82365	100.00	12	39546	99.97	22	9718	99.77	126	2002	93.71
16_1100	0	46114	100.00	8	22139	99.96	11	9718	99.89	100	2002	95.01
16_500	2	46731	100.00	6	9837	99.94	17	9718	99.83	43	2002	97.85
16_250	NS	NS	NS	8	21009	99.96	NS	NS	NS	100	2002	95.01
16_100	0	25131	100.00	3	9128	99.97	4	9718	99.96	32	2002	98.40
16_50	0	27349	100.00	1	9311	99.99	1	9718	99.99	21	2002	98.95
16_5	NS	NS	NS	0	15356	100.00	NS	NS	NS	25	2002	98.75
108_4200	1	17619	99.99	10	16834	99.94	3	9718	99.97	69	2002	96.55
108_2750	4	29185	99.99	8	15514	99.95	7	9718	99.93	49	2002	97.55
108_1800	0	48167	100.00	9	24009	99.96	9	9718	99.91	81	2002	95.95

108_1000	3	43727	99.99	9	16606	99.95	11	9718	99.89	64	2002	96.80
108_500	2	32696	99.99	9	30369	99.97	14	9718	99.86	115	2002	94.26
108_250	4	52719	99.99	13	12172	99.89	13	9718	99.87	47	2002	97.65
108_100	0	25163	100.00	6	12274	99.95	1	9718	99.99	29	2002	98.55
108_50	0	24181	100.00	5	15250	99.97	3	9718	99.97	42	2002	97.90
108_5	0	14739	100.00	2	12121	99.98	0	9718	100.00	23	2002	98.85
109_5000	NS	NS	NS	2	7891	99.97	NS	NS	NS	21	2002	98.95
109_2750	NS	NS	NS	3	12991	99.98	NS	NS	NS	40	2002	98.00
109_1800	NS	NS	NS	6	13587	99.96	NS	NS	NS	67	2002	96.65
109_1000	NS	NS	NS	6	17605	99.97	NS	NS	NS	80	2002	96.00
109_500	NS	NS	NS	9	18418	99.95	NS	NS	NS	93	2002	95.35
109_250	NS	NS	NS	17	21672	99.92	NS	NS	NS	114	2002	94.31
109_100	NS	NS	NS	9	23481	99.96	NS	NS	NS	81	2002	95.95
111_5000	2	41206	100.00	3	11885	99.97	11	9718	99.89	34	2002	98.30
111_4000	3	37798	99.99	0	13254	100.00	15	9718	99.85	39	2002	98.05
111_2750	1	39002	100.00	3	7126	99.96	13	9718	99.87	17	2002	99.15
111_1800	1	22191	100.00	2	8195	99.98	3	9718	99.97	22	2002	98.90
111_1000	1	23150	100.00	8	27505	99.97	6	9718	99.94	102	2002	94.91
111_250	3	27009	99.99	10	7479	99.87	9	9718	99.91	24	2002	98.80
111_100	0	29705	100.00	8	18151	99.96	5	9718	99.95	95	2002	95.25
111_50	0	18748	100.00	2	11441	99.98	1	9718	99.99	25	2002	98.75
111_5	0	47676	100.00	1	10923	99.99	3	9718	99.97	21	2002	98.95

115_3950	1	41069	100.00	2	20393	99.99	4	9718	99.96	57	2002	97.15
115_2750	1	53677	100.00	5	19057	99.97	5	9718	99.95	82	2002	95.90
115_1950	1	50223	100.00	4	25499	99.98	11	9718	99.89	81	2002	95.95
115_1000	1	72347	100.00	1	9674	99.99	26	9718	99.73	25	2002	98.75
115_500	1	26214	100.00	10	10197	99.90	6	9718	99.94	41	2002	97.95
115_250	1	32514	100.00	1	2413	99.96	5	9718	99.95	1	2002	99.95
115_100	2	63073	100.00	5	15956	99.97	10	9718	99.90	58	2002	97.10
115_55	0	52248	100.00	8	20065	99.96	1	9718	99.99	51	2002	97.45
115_9	0	22994	100.00	NS	NS	NS	0	9718	100.00	NS	NS	NS
114_3700	0	59071	100.00	0	10088	100.00	7	9718	99.93	21	2002	98.95
114_2750	1	52911	100.00	7	19368	99.96	2	9718	99.98	74	2002	96.30
114_1760	1	54611	100.00	9	19408	99.95	12	9718	99.88	88	2002	95.60
114_1000	0	34474	100.00	6	14537	99.96	4	9718	99.96	41	2002	97.95
114_500	2	41681	100.00	2	8214	99.98	13	9718	99.87	20	2002	99.00
114_250	0	9718	100.00	7	10614	99.93	0	9718	100.00	47	2002	97.65
114_100	1	44721	100.00	6	7392	99.92	6	9718	99.94	27	2002	98.65
114_65	0	28767	100.00	6	11613	99.95	0	9718	100.00	33	2002	98.35
114_5	2	32496	99.99	2	17257	99.99	10	9718	99.90	13	2002	99.35
56_3950	1	45825	100.00	2	15310	99.99	7	9718	99.93	47	2002	97.65
56_2750	0	28000	100.00	7	25079	99.97	4	9718	99.96	103	2002	94.86
56_2071	0	36354	100.00	9	21758	99.96	3	9718	99.97	79	2002	96.05
56_1000	3	27548	99.99	10	11160	99.91	6	9718	99.94	44	2002	97.80
56_500	0	47358	100.00	13	20528	99.94	8	9718	99.92	94	2002	95.30

56_250	1	46533	100.00	6	8802	99.93	7	9718	99.93	42	2002	97.90
56_100	0	45627	100.00	6	10540	99.94	11	9718	99.89	31	2002	98.45
56_60	0	33227	100.00	8	14137	99.94	4	9718	99.96	34	2002	98.30
56_5	2	37772	99.99	2	12794	99.98	12	9718	99.88	18	2002	99.10
57_3150	1	44641	100.00	5	19458	99.97	9	9718	99.91	80	2002	96.00
57_2750	2	22354	99.99	3	10800	99.97	5	9718	99.95	26	2002	98.70
57_1900	2	45293	100.00	4	9223	99.96	4	9718	99.96	30	2002	98.50
57_1000	NS	NS	NS	3	13812	99.98	NS	NS	NS	67	2002	96.65
57_500	0	15253	100.00	14	13909	99.90	5	9718	99.95	77	2002	96.15
57_250	1	30171	100.00	11	8410	99.87	0	9718	100.00	26	2002	98.70
57_100	0	14293	100.00	11	13346	99.92	1	9718	99.99	55	2002	97.25
57_51	0	20880	100.00	12	17156	99.93	0	9718	100.00	81	2002	95.95
57_5	2	31126	99.99	3	26420	99.99	8	9718	99.92	21	2002	98.95
58_1800	NS	NS	NS	4	12179	99.97	NS	NS	NS	37	2002	98.15
58_1060	NS	NS	NS	1	3771	99.97	NS	NS	NS	6	2002	99.70
58_500	NS	NS	NS	7	10394	99.93	NS	NS	NS	32	2002	98.40
58_250	NS	NS	NS	12	19848	99.94	NS	NS	NS	68	2002	96.60
58_100	NS	NS	NS	1	9697	99.99	NS	NS	NS	15	2002	99.25
58_60	NS	NS	NS	5	34123	99.99	NS	NS	NS	60	2002	97.00
58_5	NS	NS	NS	0	2002	100.00	NS	NS	NS	0	2002	100.00
59_2750	0	40270	100.00	4	35463	99.99	3	9718	99.97	131	2002	93.46
59_1800	3	35635	99.99	5	16424	99.97	4	9718	99.96	47	2002	97.65

59_1000	4	49399	99.99	7	21319	99.97	11	9718	99.89	65	2002	96.75
59_500	0	15194	100.00	5	18725	99.97	2	9718	99.98	32	2002	98.40
59_250	3	26202	99.99	5	3726	99.87	8	9718	99.92	8	2002	99.60
59_100	1	33923	100.00	11	17728	99.94	12	9718	99.88	90	2002	95.50
59_65	2	31566	99.99	4	16582	99.98	9	9718	99.91	15	2002	99.25
59_5	0	39611	100.00	18	21216	99.92	3	9718	99.97	101	2002	94.96
60_2450	1	25502	100.00	5	14369	99.97	2	9718	99.98	54	2002	97.30
60_1900	1	24992	100.00	5	8376	99.94	3	9718	99.97	20	2002	99.00
60_1000	1	48382	100.00	11	12562	99.91	15	9718	99.85	76	2002	96.20
60_500	0	22880	100.00	11	12606	99.91	4	9718	99.96	53	2002	97.35
60_250	2	39256	99.99	13	11061	99.88	8	9718	99.92	62	2002	96.90
60_100	1	20271	100.00	16	11960	99.87	4	9718	99.96	44	2002	97.80
60_60	0	20168	100.00	5	11791	99.96	1	9718	99.99	24	2002	98.80
62_220	NS	NS	NS	2	20546	99.99	NS	NS	NS	29	2002	98.55
62_74	2	29718	99.99	3	21809	99.99	5	9718	99.95	39	2002	98.05
62_45	0	28719	100.00	9	14116	99.94	3	9718	99.97	40	2002	98.00
62_25	0	20526	100.00	9	9890	99.91	2	9718	99.98	35	2002	98.25
62_5	1	24477	100.00	10	11319	99.91	5	9718	99.95	50	2002	97.50
64_47	1	24954	100.00	4	10930	99.96	2	9718	99.98	31	2002	98.45
64_20	1	19276	99.99	1	18447	99.99	1	9718	99.99	29	2002	98.55
64_10	1	17891	99.99	6	21886	99.97	3	9718	99.97	38	2002	98.10
64_5	0	16792	100.00	6	16511	99.96	1	9718	99.99	30	2002	98.50

NS = no sample available.

Both for Archaea and Bacteria, even after rarefaction to an equal-level sampling effort (9718 reads per sample for Archaea and 2002 reads per sample for Bacteria), samples showed a very high Good's coverage estimator, meaning that they are representative of the natural communities sampled (1).

Supplementary Table 5. Linear or quadratic models fitted to observed ASV richness (S_{Obs}) and Shannon diversity index per sample (dependent variable, *y*) for Archaea and Bacteria, as a function of distance to the coast (horizontal variability; *x*) or sampling depth (vertical variability; *x*). Linear model: y = Param1 * x + Intercept; Quadratic model: y = Param1 * x2 + Param2 * x + intercept.

		Distance			**Depth**		
	Diversity metric	**param.1** (± s.e.)	**param.2 (± s.e.)**	**intercept (± s.e.)**	**param. 1 (± s.e.)**	**param.2 (± s.e.)**	**intercept (± s.e.)**
ARCHAEA	**S_{Obs}**	-	-	-	17.277 (± 2.699)	-	46.487 (± 15.759)
	p-value	-	-	-	3.90E-03	-	4.06E-09
	Shannon	-	-	-	0.208 (± 0.026)	-	2.133 (± 0.152)
	p-value	-	-	-	1.80E-12	-	< 2E-16
BACTERIA	**S_{Obs}**	-	-	-	-	-	-
	p-value	-	-	-	-	-	-
	Shannon	-	-	-	0.392 (± 0.150)	-0.024 (±0.015)	3.169 (± 0.353)
	p-value	-	-	-	9.96E-03	0.106	3.63E-15

Supplementary Table 6. Spearman's rank correlation coefficient between diversity metrics (observed ASV richness (S_{Obs}) and Shannon diversity index) for Archaea and Bacteria, and abiotic variables (after removing highly collinear variables): *Sal*, salinity; *NO_2^-*, nitrite concentration; *FDOM-T*, fluorescence of protein-like compounds; *FDOM-M*, fluorescence of humic-like DOM; *aCDOM254*, absorbtion coefficient at 254 nm; *s(275-295)*, spectral slope between 275 and 295 nm.

	ARCHAEA		**BACTERIA**	
	SA_{Obs}	**ShannonA**	**SB_{Obs}**	**ShannonB**
Sal	0.007	-0.076	0.031	0.107
NO_2^- (µM)	-0.208	-0.266	-0.158	-0.226
FDOM-T (QSU)	-0.450	-0.459	-0.302	-0.290
FDOM-M (QSU)	0.295	0.359	0.146	0.013
aCDOM254 (m^{-1})	-0.490	-0.541	-0.228	-0.181
s(275-295)	-0.064	-0.112	-0.162	-0.079