

1 **Cobalamin and microbial plankton dynamics along a coastal to**
2 **offshore transect in the Eastern North Atlantic Ocean**

3 Vanessa Joglar*^{1,2}, X.A. Álvarez-Salgado³, Ana Gago-Martinez⁴, Jose M. Leao⁴, Clara Pérez-
4 Martínez⁵, Benjamin Pontiller⁵, Daniel Lundin⁵, Jarone Pinhassi⁵, Emilio Fernández^{1,2}, Eva
5 Teira^{1,2}

6

7 ¹ Centro de Investigación Mariña da Universidade de Vigo (CIM-UVIGO)

8 ² Departamento Ecoloxía e Bioloxía Animal, Universidade de Vigo, Campus Lagoas-Marcosende, Vigo,
9 36310, Spain

10 ³ CSIC, Instituto de Investigacións Mariñas, Eduardo Cabello 6, Vigo, 36208, Spain

11 ⁴ Food and Analytical Chemistry Department, Chemistry Faculty, Department of Analytical and Food
12 Chemistry, University of Vigo, Campus Universitario de Vigo, 36310 Vigo, Spain

13 ⁵ Centre for Ecology and Evolution in Microbial Model Systems – EEMiS, Linnaeus University,
14 Stuvaregatan 4, 39231 Kalmar, Sweden

15

16

17 *Correspondence to: Vanessa Joglar

18 Novo CACTI Lab.100
19 Campus As Lagoas-Marcosende
20 Universidad de Vigo
21 36310 Vigo
22 Spain

23 +34 986 818790

24 vanjoglar@gmail.com

25

26 **Summary**

27 Cobalamin (B12) is an essential cofactor that is exclusively synthesized by some prokaryotes
28 while many prokaryotes and eukaryotes require an external supply of B12. The spatial and
29 temporal availability of B12 is poorly understood in marine ecosystems. Field measurements of
30 B12 along with a large set of ancillary biotic and abiotic factors were obtained during three
31 oceanographic cruises in the NW Iberian Peninsula, covering different spatial and temporal
32 scales. B12 concentrations were remarkably low (< 1.5 pM) in all samples, being significantly
33 higher at the subsurface Eastern North Atlantic Central Water than at shallower depths,
34 suggesting that B12 supply in this water mass is greater than demand. Multiple regression
35 models excluded B12 concentration as predictive variable for phytoplankton biomass or
36 production, regardless of the presence of B12-requiring algae. Prokaryote production was the
37 best predictor for primary production, and eukaryote community composition was better
38 correlated with prokaryote community composition than with nutritional resources, suggesting
39 that biotic interactions play a significant role in regulating microbial communities. Interestingly,
40 co-occurrence network analyses based on 16S and 18S rRNA sequences allowed the
41 identification of significant associations between potential B12 producers and consumers (e.g
42 Thaumarchaeota and Dynophyceae, or *Amylibacter* and *Ostreococcus*, respectively), which can
43 now be investigated using model systems in the laboratory.

44

45 **Key words:** Vitamin B12, interactions, community composition, NW Iberian Peninsula.

46

47 **Introduction**

48 Cobalamin (B12) is an essential coenzyme involved in many important metabolic
49 pathways (e.g methionine or nucleotide synthesis) (Marsh, 1999; Madigan *et al.*, 2005;
50 Monteverde *et al.*, 2017). In addition, vitamin B12 (hereafter B12) may be an important
51 growth factor for phytoplankton (Droop, 1957; Provasoli, 1963; Carlucci *et al.*, 1969;
52 Haines and Guillard, 1974; Swift, 1980; Croft *et al.*, 2005, 2006; Sañudo-Wilhelmy *et*
53 *al.*, 2014). Vitamin B12 is a tetrapyrrolic cofactor containing a central cobalt atom, with
54 varying upper and lower axial ligands, resulting in several B12 analogs differing in
55 metabolic functions and bioavailability (Banerjee, 1997; Banerjee and Ragsdale, 2003;
56 Brown, 2005; Koutmos *et al.*, 2009). The active coenzymes methylcobalamin (MB12)
57 and adenosylcobalamin (AB12), as well as the non-catalytically active (transitive)
58 congeners cyanocobalamin (CB12) and hydroxycobalamin (HB12) result from
59 differences in the upper axial ligand (Banerjee, 1997; Brown, 2005). MB12 is the active
60 form of cobalamin that is used by organisms for the synthesis of methionine through the
61 cobalamin-dependent methionine synthase (MetH) (Matthews *et al.*, 2003) and AB12 is
62 the coenzyme for methylmalonyl-CoA mutase, which is an essential enzyme in the
63 metabolism of odd-chain fatty acids (Marsh, 1999). MB12 and AB12 are considered as
64 extremely photolabile and quickly degrade to HB12 when exposed to light (Juzeniene
65 and Nizauskaite, 2013; Juzeniene *et al.*, 2015; Vaid *et al.*, 2018). The lower axial ligand
66 of this molecule can also present diversity, with 5,6 dimethylbenzimidazole or adenine
67 building, respectively, cobalamin or pseudocobalamin (Stupperich and Krautler, 1988;
68 Watanabe *et al.*, 1999; Helliwell *et al.*, 2016; Heal *et al.*, 2017).

69

70 Compared to mineral nutrients and trace elements, much less is known about the spatial
71 and temporal availability of B12 in marine ecosystems, despite the recognition that

72 many microbial plankton species require an exogenous source of B12 (Carlucci and
73 Bowes, 1970; Croft *et al.*, 2005; Bertrand and Allen, 2012; Sañudo-Wilhelmy *et al.*,
74 2014; Paerl *et al.*, 2018). Dissolved B12 concentrations are typically very low
75 (picomolar range) and display pronounced spatial and temporal variation in marine
76 systems (Sañudo-Wilhelmy *et al.*, 2006, 2012; Panzeca *et al.*, 2009; Koch *et al.*, 2012;
77 Heal *et al.*, 2014; Cohen *et al.*, 2017; Suffridge *et al.*, 2018). A few studies observed
78 that intermediate-depth waters (~200–500 m) contain higher B12 levels than those
79 above and below that depth (Menzel and Spaeth, 1962; Carlucci and Cuhel, 1977;
80 Sañudo-Wilhelmy *et al.*, 2012). This spatial pattern is consistent with the “nutrient-like”
81 behavior of B12 proposed by Karl, (2002), being consumed in surface waters and
82 accumulated in subsurface waters.

83

84 It is important to note that, historically, liquid chromatography-mass spectrometry (LQ-
85 MS) only detected CB12 in marine system surveys (Okbamichael and Sañudo-
86 Wilhelmy, 2004; Sañudo-Wilhelmy *et al.*, 2006; Panzeca *et al.*, 2009). More recently,
87 Heal *et al.* (2014) developed a method to simultaneously detect four B12 congeners,
88 showing that HB12 was the more abundant form, representing ca. 78% of the total
89 dissolved B12 in coastal waters. A similar contribution of HB12 was measured in the
90 particulate pool by Heal *et al.* (2017) in oceanic waters. In contrast, the study by
91 Suffridge *et al.* (2018) found out that HB12 contributes to ca. 20% of total dissolved
92 B12 and 70% of total particulate B12.

93

94 Only selected prokaryotes are capable of *de novo* B12 synthesis, while many prokaryote
95 and eukaryote microbial species require an external supply of B12 (Carlucci and Bowes,
96 1970; Haines and Guillard, 1974; Helliwell *et al.*, 2011; Bertrand and Allen, 2012;

97 Sañudo-Wilhelmy *et al.*, 2014; Paerl *et al.*, 2015). Some algae have adapted to
98 overcome B12 limitation in the environment by using alternative enzymes (Bertrand *et*
99 *al.*, 2013; Helliwell *et al.*, 2014), whereas others require B12 and depend on an
100 exogenous source of this organic molecule (Bertrand *et al.*, 2012). It has been suggested
101 that phytoplankton may obtain B12 through interactions with prototrophic bacteria
102 (Haines and Guillard, 1974; Croft *et al.*, 2005; Amin *et al.*, 2012; Cooper and Smith,
103 2015). B12 is considered a key metabolite mediating the symbiotic relationships
104 between B12-auxotrophic algae and heterotrophic bacteria (Croft *et al.*, 2005; Amin *et*
105 *al.*, 2012; Cooper and Smith, 2015; Durham *et al.*, 2015). In this interaction, algae
106 obtain the vitamin directly from B12-synthesizing bacteria which, in return, receive
107 photosynthates (Croft *et al.*, 2005; Wagner-Döbler *et al.*, 2010; Grant *et al.*, 2014).

108

109 The NW Iberian coastal zone presents incised valleys called rías, which are
110 intermittently fertilized as a result of spring-summer upwelling events favored by
111 northerly winds along the shore (Wooster *et al.*, 1976; Blanton *et al.*, 1984; Gonzalez-
112 Nuevo *et al.*, 2014). Seasonality accounts for only 30% of the total annual variability in
113 the wind regime, with most of the variability being associated with events of shorter
114 temporal scales (Álvarez-Salgado *et al.*, 2003). These upwelling events inject cold and
115 nutrient-rich Eastern North Atlantic Central Water (ENACW) into the rías (Fraga, 1981;
116 Gómez-Gesteira *et al.*, 2001; Barton *et al.*, 2015). During the autumn and winter, when
117 high river flows are recorded, frequent downwelling episodes introduce nutrient-poor
118 surface waters of the adjacent shelf into the rías (Álvarez-Salgado *et al.*, 2000). A recent
119 study by Barber-Lluch *et al.* (2019) at a fixed shelf station off this area (stn 3 in Fig.
120 1A) showed a marked seasonal variability in the response of phytoplankton and bacteria
121 to inorganic nutrient and/or B12 additions in surface waters, with phytoplankton

122 responding at the beginning and at the end of the productive period. A detailed
123 experimental study by Joglar *et al.* (2020) at a shelf and an oceanic station off this area
124 (stn 3 and stn 6 in Fig.1A) also revealed that phytoplankton and prokaryotes frequently
125 respond to B12 and/or B1 additions. Overall, the magnitude of positive responses in the
126 sampling area after external B12 inputs was relatively small (Barber-Lluch *et al.*, 2019;
127 Joglar *et al.*, 2020), and the patterns of microbial responses appeared to be mostly
128 controlled by the prokaryote taxonomic composition (Joglar *et al.*, 2020).

129

130 The first few measurements of B12 availability in this area revealed consistently low
131 concentrations of this growth factor (< 2.7 pM of CB12+HB12) (Barber-Lluch *et al.*
132 2020; Joglar *et al.*, 2020). Nevertheless, the limited number of samples included in these
133 studies, together with the lack of concomitant measurements of microbial plankton
134 activity and diversity, precluded solid conclusions on the role of B12 in the dynamics of
135 the microbial plankton assemblage in this productive area.

136

137 Within this context, we conducted extensive fieldwork to explore B12 availability in the
138 coastal transition zone off the NW Iberian Peninsula covering, for the first time,
139 relevant spatial (cross-shelf and vertical) and temporal (daily and seasonal) scales. The
140 methodology could not be set up to accurately detect MB12 and AB12, and thus, total
141 B12 measured must be considered a conservative estimate of the total dissolved B12.
142 Furthermore, we combined B12 measurements with a detailed description of dissolved
143 inorganic nutrients and dissolved organic matter, phytoplankton and prokaryote biomass
144 and production, and microbial plankton community composition (based on partial 16S
145 and 18S rRNA gene sequences). Our general hypothesis was that dissolved B12

146 concentration influences the abundance, distribution, and activity of microbial plankton
147 and contributes to the delineation of ecological niches in this productive area.

148

149 **Results**

150 Three oceanographic cruises were conducted in different seasons (February, April and
151 August) in 2016. During the first day of each cruise, a cross-shelf transect was
152 performed to assess the spatial variability of B12 concentration. In addition, during the
153 next 7 days of each cruise, intensive sampling was carried out at a fixed coastal station
154 to study the short-term variability of B12 and its connection with biotic and abiotic
155 factors. It is important to note that the quantified B12 forms were CB12 and HB12, so
156 hereafter B12 refers to the sum of these two forms.

157

158 **Spatial variability**

159 *Thermohaline variables, nutrients, and chlorophyll a*

160 Different hydrographic conditions were found in the cross-shelf transect during each
161 cruise. In February, weak northerly winds and high precipitation prevailed prior to
162 cross-shelf sampling (Fig. 1B, 1C). The surface water temperature was constant
163 throughout the transect, slightly increasing from 13.5 °C in coastal waters to 13.9 °C in
164 oceanic waters (Fig. 2A). The temperature in deep waters was also lower in the coast
165 (11.6 °C) than in the adjacent ocean (12.5 °C). The homogeneous temperature in the
166 water column implied that the upper mixed layer (UML) was deep, exceeding 100 m at
167 several stations. The cold and nutrient-rich ENACW, which upper limit is defined by
168 the isopycnal level of 27 kg m^{-3} , was detected at the bottom in all stations during the
169 winter cruise.

170

171 Freshwater inputs of the rivers flowed out as a thin surface layer causing a slight
172 halocline at 10 m depth in the coastal stations. Chl-*a* was generally low along the
173 transect, ranging from 0.07 to 1.31 mg m⁻³ with the highest concentrations in the UML
174 without a clear inshore-offshore pattern (Fig. 2C). Nutrient concentrations were in the
175 range of 1.61-10.88 μM for DIN and 0.16-0.74 μM for HPO₄²⁻ (Fig. 2D and 2E).
176 Nutrient (i.e. DIN and HPO₄²⁻) concentrations increased with depth, being the highest at
177 the bottom of the shelf station (stn 3). In contrast, vitamin B12 concentrations ranged
178 from 0.19 to 0.97 pM and B12-hotspots were mostly distributed within the UML except
179 at stn 3 where highest concentrations were measured at the bottom (50 m depth) (Fig.
180 2F).

181

182 The April cruise was mostly characterized by a moderate downwelling turned into
183 upwelling at the end of the cruise (Fig. 1B). Temperature values varied slightly along
184 the transect being highest at the surface (ca. 13.3 °C) and gradually decreased in
185 subsurface waters to values lower than 13 °C (Fig. 2G). The salinity was homogeneous
186 along the water column and along the transect except in the coastal station (stn 3). In the
187 coastal station, a strong continental freshwater discharge resulted in a thin UML of low-
188 density water (Fig. 2H). In April, Chl-*a* concentrations increased with respect to
189 February within the UML and the subsurface layer (SSL), located between the UML
190 and the ENACW. Chl-*a* concentrations ranged from 0.08 in stn 6 to 2.61 mg m⁻³ in
191 surface waters in stn 3 (Fig. 2I). Nutrient concentrations were in the range of 1.12–9.72
192 μM for DIN and 0.12-0.49 μM for HPO₄²⁻ (Fig. 2J and K). B12 levels ranged from
193 0.12–0.91 pM being maximum below the UML throughout the transect, except at stn 4
194 (Fig. 2L). Stn 3 had the highest nutrient concentrations, associated with low salinity.

195

196 In August, the surface temperature ranged from 14.2 to 15.9 °C dropping to 13 °C at 20
197 m in stn 3. The 13 °C isotherm progressively deepened westwards. The ascending trend
198 of subsurface temperature, σ -t and nutrient concentrations isolines towards the coast,
199 indicate the upwelling of ENACW (Fig. 2M). The surface salinity values were higher
200 than 35.5 PSU along the transect, showing the negligible influence of the river
201 discharge (Fig. 2N). The thermohaline structure revealed the typical summer upwelling,
202 prevailing from day 1 to day 5 (Fig. 1C). Chl-*a* concentration was generally high in the
203 upper 30 m in shelf waters, where values higher than 5 mg m⁻³ were found. A
204 progressive decrease was observed from stn 3 (15.2 mg m⁻³) to stn 6 (1.28 mg m⁻³) (Fig.
205 2O). In August, nutrient levels were in the range of 0.12-11.0 µM for DIN and 0.02-
206 0.68 µM for HPO₄²⁻ (Fig. 2P and 2Q). Nutrients were depleted in the upper 25 m of the
207 water column, and a marked nutricline was visible along the transect. Below 25 m depth
208 nutrients increased towards the ENACW layer where the highest concentrations were
209 observed. B12 levels ranged from 0.15 to 0.92 pM and showed a distribution pattern
210 similar to that of inorganic nutrients (Fig. 2R).

211

212 Despite the clear variation in hydrographic conditions in the cross-shelf section during
213 the different sampling periods, there were no significant differences in mean B12
214 concentrations among stations (ANOVA; df = 3, 57; P = 0.254), months (ANOVA; df =
215 2, 57; P = 0.398) or water layers (UML, SSL, and ENACW) (ANOVA; df = 2, 57; P =
216 0.154) (Supporting Information Fig. S1). In contrast, mean NO₃⁻ and HPO₄²⁻
217 concentrations were significantly higher in stn 3 than in stn 4 (Bonferroni, P = 0.006),
218 and 6 (Bonferroni, P < 0.042) and significantly higher in the ENACW than in UML

219 (Bonferroni, $P < 0.001$). However, no differences were observed between seasons
220 (Supporting Information Fig. S1).

221

222 **Temporal variability**

223 To investigate potential temporal patterns in the coastal stn 3 off the Ría de Vigo,
224 abiotic (dissolved vitamin B12, nutrients, and DOM) and biotic (phytoplankton and
225 prokaryote biomass and production as well as microbial taxonomic composition using
226 16S and 18S rRNA gene amplicon sequencing) variables were sampled daily or every
227 second day for one week at each cruise.

228

229 *Thermohaline variables, nutrients, and dissolved organic matter*

230 Precipitations before and at the beginning of the February cruise (Fig. 1C) caused a
231 persistent surface halocline, and a narrow UML, at the coastal station (Fig. 3B). The
232 vertical distribution of temperature (< 13 °C), salinity (> 35.5 PSU), and density σ -t ($>$
233 27 kg m^{-3}) in February indicated the presence of ENACW below 50 m depth throughout
234 the sampling period (Fig. 3A). The haline stratification was associated with the
235 development of a phytoplankton bloom in February. Increasing levels of Chl-*a* were
236 observed, reaching a maximum (10.5 mg m^{-3}) by the end of the cruise (Fig. 3C).
237 Nutrient concentrations were in the range of 2.4–12.0 μM for DIN, 1.1–7.8 for DON,
238 0.17–0.74 μM for HPO_4^{2-} and 45–69 μM for DOC (Fig. 3D-G). Relatively high
239 concentrations of DIN and HPO_4^{2-} were measured at UML, associated with low salinity,
240 yet, the highest values were observed in the ENACW. In contrast, maximum DON
241 concentration was observed at the subsurface layer. DOC concentration was high at the
242 surface but decreased below 15 m. The surface water was depleted in B12 with

243 concentrations < 0.3 pM along, while the ENACW had higher B12 concentrations,
244 peaking at 1.5 pM (Fig. 3H).

245

246 The April cruise coincided with prevailing downwelling conditions, as shown by the
247 negative upwelling index (UI) (Fig. 1C), when seawater temperatures ranged from 12.5
248 (in the deep water) to 14.6 °C (at the surface) (Fig. 3I). ENACW was not detected
249 during in April, with σ -t values < 27 kg m⁻³ reaching down to 80 m depth (Fig. 3I).
250 Surface salinity values ranged from 31 to 34.5 PSU due to the continental runoff
251 influence (Fig. 3J). Chl-*a* concentration ranged from 3 to 0.4 mg m⁻³ and decreased
252 towards the end of the sampling period (Fig. 3K). Progressive warming of the water
253 column was observed in this period, accompanied by a noticeable discharge of nutrient-
254 rich freshwater. Nutrient concentrations ranged between 0.4–14 μ M for DIN, 3.6–6.9
255 μ M for DON, 0.04–0.49 μ M for HPO₄²⁻, 57–102 μ M for DOC and 0.15–0.9 pM for
256 B12. The highest concentrations of DIN and DOC were always measured at the first 20
257 m (Fig. 3L and 3O), showing an inverse relationship with salinity. Surface DIN and
258 HPO₄²⁻ concentrations were close to 14 μ M and 0.5 μ M, respectively. In the SSL,
259 nutrient concentrations were very low, particularly after day 3. DON concentration was
260 homogeneous in the water column with values close to 6 μ M, (Fig. 3M). Interestingly,
261 B12 concentrations decreased throughout the sampling period, with values well below
262 0.2 pM in the whole water column at the end of the cruise (Fig. 3P).

263

264 Under the prevailing upwelling conditions found in August (Fig. 1B), surface salinity
265 values were higher than 35.2 PSU in the whole water column, indicating a negligible
266 influence of the river discharge (Fig. 3R). Surface seawater temperatures ranged from

267 13 to 15.1 °C. ENACW was detected below 30 m throughout the whole cruise (Fig.
268 3Q). During the summer upwelling, Chl-*a* was high in the upper 20 m, decreasing from
269 15.2 to 2.2 mg m⁻³ by the end of the cruise (Fig. 3S). Nutrient levels were in the range
270 of 0.3-11.4 μM for DIN, 2.0–5.2 for DON, 0.1-0.79 μM for HPO₄²⁻, 51–82 for DOC
271 and 0.12–0.92 pM for B12. In the upper 20 m of the water column DIN, HPO₄²⁻ and
272 B12 levels were depleted, except DIN and HPO₄²⁻ at day 7 (Fig. 3T, 3V and 3X). A
273 slight enrichment of organic nutrients (DON and DOC) was observed in surface waters,
274 decreasing at day 7. Below 20 m depth, inorganic nutrients (DIN and HPO₄²⁻) and B12
275 increased towards the bottom.

276

277 Vitamin B12 concentration did not vary among the three sampling periods (ANOVA; df
278 = 2, 59; *P* = 0.679) (Supporting Information Fig. S2). However, there were significant
279 differences between water layers at the coastal station (stn 3) (ANOVA; df = 2, 59; *P* <
280 0.001), with a significantly higher concentration [mean ± standard deviation (SD)] in
281 the ENACW (0.66 ± 0.107 pM) than in the UML (0.29 ± 0.049) (Bonferroni, *P* < 0.001)
282 and SSL (0.35 ± 0.03) (Bonferroni, *P* = 0.002) (Supporting Information Fig. S2). Both,
283 NO₃⁻ and HPO₄²⁻ followed a similar pattern to that of B12 at stn 3 (Supporting
284 Information Fig. S2). NO₃⁻ concentrations differed between layers (ANOVA, *P* <
285 0.001), while HPO₄²⁻ differed between seasons (ANOVA; df = 2, 59; *P* = 0.002) and
286 layers (ANOVA; df = 2, 59; *P* < 0.001). NO₃⁻ concentrations were higher in the
287 ENACW (9.84 ± 0.39 pM) than in the UML (4.46 ± 0.72 pM) (Bonferroni, *P* < 0.001)
288 and SSL (4.01 ± 0.45 pM) (Bonferroni, *P* < 0.001). HPO₄²⁻ concentrations showed
289 seasonal variability with lower values in April (0.26 ± 0.024 pM) than in February (0.39
290 ± 0.039) (Bonferroni, *P* = 0.069) and August (0.44 ± 0.043 pM) (Bonferroni, *P* =
291 0.003). A principal component analysis (PCA) was conducted to visualize vertical and

292 temporal patterns of the abiotic factors in stn 3 (Fig. 4A). The PCA highlighted the
293 differences between sampling months (Fig. 4A). The first principal component
294 explained 45.7% of total variation of abiotic factors, and the second principal
295 component explained 15.9% of total variation of abiotic factors. NO_2^- and NH_4^+
296 explained most of the variation in April, pointing out to a relatively high relevance of
297 regeneration processes. In contrast, B12 and inorganic nutrients such as SiO_4^{4-} , HPO_4^{2-}
298 and NO_3^- were positively correlated with ENACW sampled in February and August
299 indicating new production associated with the upwelling event. Salinity was strongly
300 related to subsurface samples in February and temperature was mostly related to UML
301 samples in April and August. Considering all the abiotic variables there were significant
302 differences between months (ANOSIM, $P = 0.001$) and between layers (ANOSIM, $P =$
303 0.001).

304

305 *Size-fractionated phytoplankton and prokaryote biomass and production*

306 Nano- and microphytoplankton (cell size $> 3 \mu\text{m}$) dominated over picophytoplankton
307 (cell size $< 3 \mu\text{m}$) except in April when picophytoplankton dominated throughout the
308 sampling period (Fig. 5A). In February, an increase in both picophytoplankton biomass
309 ($\text{Chl-}a < 3 \mu\text{m}$) and nano-microphytoplankton biomass ($\text{Chl-}a > 3 \mu\text{m}$) was noticeable
310 in the second half of the cruise (Fig. 5A and 5B). Primary production (PP) increased in
311 parallel to $\text{Chl-}a$ concentrations (Fig 5C and 5D). While picophytoplankton PP (PP < 3
312 μm) increased from $0.3 \text{ mg C m}^{-3} \text{ h}^{-1}$ at day 1 to $2.2 \text{ mg C m}^{-3} \text{ h}^{-1}$ at day 6 in surface
313 waters, nano-microphytoplankton PP (PP $> 3 \mu\text{m}$) increased from values close to 1 mg
314 $\text{C m}^{-3} \text{ h}^{-1}$ at the beginning of the cruise to $23 \text{ mg C m}^{-3} \text{ h}^{-1}$ at day 6 (Fig. 5C and 5D).
315 Total prokaryote biomass (PB) and heterotrophic prokaryote production (HPP)
316 decreased with depth (Fig. 5E and 5F). HPP ranged from $0.098 \text{ mg C m}^{-3} \text{ h}^{-1}$ in surface

317 waters to $0.015 \text{ mg C m}^{-3} \text{ h}^{-1}$ in the bottom, showing a slight increase in surface waters
318 towards the end of the cruise.

319

320 In April, Chl-*a* concentration was relatively low throughout the sampling period with
321 picophytoplankton as the main contributor to photosynthetic biomass (Fig. 5G). From
322 the third to the fifth day a slight increase in the picophytoplankton Chl-*a* up to 1.6 mg
323 m^{-3} was observed, while the maximum nano-microphytoplankton Chl-*a* was 1.4 mg m^{-3} ,
324 on day 1. A similar pattern was observed for PP, showing a peak of PP $< 3 \mu\text{m}$ (2.5 mg
325 $\text{C m}^{-3} \text{ h}^{-1}$) in surface waters on day 4 (Fig. 5I). On the other side, PP $> 3 \mu\text{m}$ remained
326 lower than $5 \text{ mg C m}^{-3} \text{ h}^{-1}$ even at the surface (Fig. 5J). PB in April was higher than
327 during the phytoplankton bloom in February (Fig. 5K). HPP values were low and
328 similar to those measured in February, ranging between $0.4\text{--}0.1 \text{ mg C m}^{-3} \text{ h}^{-1}$ (Fig. 5L).

329

330 During the August cruise, the influence of upwelling was reflected in Chl-*a* $> 3\mu\text{m}$,
331 which showed a high concentration (17.5 mg m^{-3}) at surface waters at the beginning of
332 the cruise (Fig. 5N). The PP $< 3 \mu\text{m}$ was close to $1 \text{ mg C m}^{-3} \text{ h}^{-1}$ at the surface while PP
333 $> 3 \mu\text{m}$ was substantially high, reaching values up to $40 \text{ mg C m}^{-3} \text{ h}^{-1}$ (Fig. 5O and 5P).
334 In the top 20 m, PB and HPP reached $\sim 60 \text{ mg C m}^{-3}$ and $2.5 \text{ mg C m}^{-3} \text{ h}^{-1}$, respectively
335 (Fig. 5Q and 5R). These values gradually decreased from day 5 when upwelling
336 intensity decreased (Fig. 1B).

337

338 Chl-*a* concentrations [mean \pm standard deviation (SD)] were significantly lower in
339 February ($1.66 \pm 0.41 \text{ mg m}^{-3}$) and April ($1.43 \pm 0.15 \text{ mg m}^{-3}$) than in August (4 ± 0.95
340 mg m^{-3}) (Bonferroni, $P = 0.033$), while PB was lower in February (1.19 mg C m^{-3}) than

341 in April ($5.8 \pm 0.5 \text{ mg C m}^{-3}$) (Bonferroni, $P = 0.000$) and August ($11.8 \pm 3.0 \text{ mg C m}^{-3}$)
342 (Bonferroni, $P = 0.000$) (Supporting Information Fig. S2). As expected, PP was
343 significantly higher during the summer upwelling ($15.5 \pm 3.4 \text{ mg C m}^{-3} \text{ h}^{-1}$) (Bonferroni,
344 $P = 0.000$), however HPP showed differences (ANOVA; $df = 2, 81$; $P < 0.001$ between
345 the three seasons, being lowest in February ($0.023 \pm 0.005 \text{ mg C m}^{-3} \text{ h}^{-1}$) and highest in
346 August ($0.48 \pm 0.12 \text{ mg C m}^{-3} \text{ h}^{-1}$) during the summer upwelling (Supporting
347 Information Fig. S2).

348

349 The PCA of biological variables of stn 3 showed that while $PP < 3 \mu\text{m}$ was linked to
350 UML and SSL in February and April, $PP > 3 \mu\text{m}$ and HPP were strongly associated with
351 the upwelling event in August. The two main components of PCA explained 89.8% of
352 the total variation of biological variables (Fig. 4B). There were significant differences in
353 the biotic variables between months (ANOSIM, $P = 0.001$) and layers (ANOSIM, $P =$
354 0.001) (Fig. 4B).

355

356 *Relationship between resources and microbial biomass and production*

357 We conducted a multiple linear regression analysis to explore the relationship between
358 microbial biomass and production and resource availability (Table 1). As we aimed at
359 explaining phytoplankton and prokaryote biomass and production from nutritional
360 resources, we used size-fractionated Chl-*a* and PP, bulk HPP, and PB as explained (i.e.
361 dependent) variables, and dissolved inorganic nutrients, dissolved organic matter, and
362 vitamin B12 concentrations as explanatory (i.e. independent) variables. We also
363 included PB and HPP as explanatory variables to model photosynthetic biomass and
364 production and additionally, total Chl-*a* and total PP to model PB and HPP, thereby

365 including the potential effect of the biotic interaction between autotrophs and
366 heterotrophs.

367

368 The resulting linear regression models explained more than 74% of variability of the
369 phytoplankton biomass (Chl-*a* < 3 μm, Chl-*a* > 3 μm and total Chl-*a*) and primary
370 production (PP < 3 μm, PP > 3 μm and total PP) and 65 and 81% of the PB and HPP,
371 respectively.

372

373 Multiple linear regression analysis indicated that although dissolved nutrients explained
374 a significant amount of the variability in Chl-*a* and PP, HPP was the most influential
375 variable for total and large phytoplankton biomass and production (Table 1). Similarly,
376 total PP had a strong influence on PB and HPP. Strikingly, B12 concentration only
377 significantly influenced PB.

378

379 *Microbial community structure*

380 The microbial community composition did not show pronounced differences between
381 samples, and samples tended to cluster by water mass and by sampling month (Fig. 6).

382 The class Flavobacteria clearly dominated in the UML and SSL, mostly in April and
383 August. Archaea (mostly belonging to the Thaumarcheota phylum) and the marine
384 alveolata groups (MALV) dominated the ENACW and the SSL in February (Fig. 6).

385 *Synechococcus*, Rhodobacterales, *Polaribacter*, *Ostreococcus*, *Micromonas*,
386 Bacillariophyta, and fungi were systematically more abundant in the UML and SSL,
387 showing very low abundances in the ENACW. In April, a well-defined microbial

388 community shift occurred between days 1-3 and days 5-7 in the UML and SSL.
389 *Ostreococcus* dominated the phytoplankton community during day 1 and 3, and
390 *Synechococcus*, *Thalassiosira* and other diatoms during day 5 and 7. The bacterial
391 groups *Amylibacter* and Oceanospirillales were more abundant during day 1 and 3 than
392 during day 5 and 7. The SAR11 clade was important during February in the UML and
393 SSL. Dinophyceae were relatively more abundant in summer.

394

395 The major microbial taxa were grouped into 3 different clusters depending on their
396 correlations with B12 and nutrient variables (Fig. 7). Cluster A (i.e. Archaea,
397 Oceanospirillales, SAR11, Dinophyceae, and MALV) correlated positively with
398 inorganic nutrients (e.g. HPO_4^{2-} , DIN, and NO_3^-), but negatively with NH_4^+ , NO_2^- and
399 organic nutrients (i.e. DOC and DON). This cluster showed significantly positive
400 Pearson correlation coefficients ($P < 0.01$) with B12 concentrations. An opposing
401 pattern was found for cluster C (i.e. *Ascidiaceihabitans*, *Amylibacter*, *Micromonas*,
402 *Ostreococcus*, *Synechococcus*, fungi, and *Planktomarina*) (Fig. 7). A significantly
403 negative correlation with B12 concentration was observed in *Planktomarina* ($R = -0.34$,
404 $P = 0.009$) and *Synechococcus* ($R = -0.34$, $P = 0.009$). This cluster showed a strong
405 negative correlation with inorganic nutrients, especially the *Planktomarina* bacteria, and
406 fungi, which had a particularly strong correlation with DON. A third cluster,
407 characterized by weak positive or negative correlations with nutrients, included
408 Ciliophora, Rhodobacterales, Flavobacteria, *Polaribacter*, *Skeletonema*, *Thalassiosira*,
409 and other Bacillariophyta. The strongest negative ($R = -0.43$, $P = 0.001$) correlation
410 with B12 was found for other Bacillariophyta (cluster B in Fig. 7). A Mantel test
411 revealed a weak but significant relationship between prokaryote community structure
412 (mostly composed of heterotrophs) and resources ($R = 0.17$, $P = 0.002$) and between

413 eukaryote community structure (mostly composed of autotrophs) and resources ($R =$
414 0.14 , $P = 0.01$). Interestingly, a significant relationship appeared between prokaryotes
415 and eukaryotes after correcting the effect of resources on both prokaryote and eukaryote
416 communities ($R = 0.41$, $P = 0.002$). Both microbial compartments were more related
417 among them than with resources.

418

419 *Co-occurrence networks*

420 In order to explore the potential interactions between major prokaryote and eukaryote
421 populations in the three different water layers, we examined the co-occurrence patterns
422 among the 50 most abundant amplicon sequence variants (ASVs) (25 eukaryotes and 25
423 prokaryotes) in each layer. From the 50 eligible nodes, 48 were included in UML and
424 SSL networks and 35 were included in the ENACW network (Fig. 8, Table 2). SSL and
425 ENACW networks were formed by only one component suggesting strong connectivity
426 between nodes (ASVs) below the UML. In contrast, 8 connected components composed
427 the UML network pointing out to a weak connectivity between ASVs at the surface.
428 Clustering coefficients (CL) were significantly higher than in random networks of the
429 same size (t-test, $P = 0.001$), whereas there were no significant differences between the
430 characteristic path lengths (CPL) and the random networks (CPLr). The considerably
431 higher CL of real versus random networks ($CL/CLr > 2$) is coherent with “small world”
432 network properties. The number of significant associations (edges), clustering
433 coefficients, the average number of neighbors and connectance, increased with depth
434 (UML < SSL < ENACW) (Table 2). Positive and negative co-occurrences in the built
435 networks are those where the two involved species coexist more and less frequently
436 than randomly expected, respectively (Veech, 2013). The proportion of negative co-
437 occurrences, potentially reflecting either niche partitioning or negative interactions, was

438 fairly similar in UML and SSL, 43 and 50% respectively, while in the ENACW most of
439 the interactions were positive, with only 33% of negative associations. In the UML, a
440 *Tenacibaculum* (Flavobacteriales) and a *Lonktanella* (Rhodobacterales) ASV showed
441 many negative co-occurrences with *Ostreococcus* and other Prasinophyceae ASVs
442 (Fig. 8A), while *Synechococcus* showed positive co-occurrences with *Thalassiosira*
443 *auguste-lienata*, *Chaetoceros tenuissimus*, and a fungal population (Fig. 8A). In the
444 SSL, several *Amylibacter* ASVs showed positive co-occurrences with Dinophyceae,
445 *Ostreococcus* and other Prasinophyceae ASVs (Fig. 8B). A large number of positive co-
446 occurrences in the ENACW suggests overlapping niches and/or intense ecological
447 interactions between Oceanospirillales or Thaumarchaeota and Dinophyceae, such as
448 *Gyrodinium*, or Thoracosphaeraceae (Fig. 8C). In contrast, most negative associations
449 involved Marine Alveolata ASVs (Fig. 8C).

450

451 **Discussion**

452 Cobalamin (vitamin B12) data were collected for the first time in the NW coast of the
453 Iberian Peninsula covering relevant spatial and temporal scales. This multidisciplinary
454 study revealed that CB12 and HB12 concentrations were lower than 1 pM in this
455 ecosystem, which is consistent with a tight coupling between B12 producers and
456 consumers.

457

458 *Spatial and temporal distribution of B12*

459 The individual active MB12 and AB12 forms of B12 were not measured in our
460 sampling area (Barber-Lluch *et al.* 2020), and thus the total B12 reported here is the
461 sum of HB12 and CB12. Overall, B12 levels in the NW Iberian margin were very low

462 (Fig. 2 and 3) and showed relatively small zonal variation (Fig. 2). CB12 concentration
463 varied between undetectable and 0.77 pM, within the range of values observed in the
464 Pacific Ocean (< 0.25 pM) (Cohen *et al.*, 2017), in the upwelling area of San Pedro
465 Basin (Panzeca *et al.*, 2009) or in a Mediterranean-Atlantic Ocean transect (0.01–2.5
466 pM) (Suffridge *et al.*, 2018), although two orders of magnitude lower than CB12
467 concentrations observed along the California-Baja California margin (Sañudo-Wilhelmy
468 *et al.*, 2012). Overall, HB12 represented 91.1% of the total B12 measured in this study.
469 The highest HB12 concentration registered in this study was 0.97 pM, also within the
470 range observed in the Mediterranean (0.01–3.31 pM) (Suffridge *et al.*, 2018). In
471 contrast, Heal *et al.* (2014) found consistently higher HB12 concentrations throughout a
472 vertical profile in inshore Pacific waters (1.56–5.8 pM). Considering that the two active
473 forms (i.e. MB12 and AB12) have been described as photolabile (Juzeniene and
474 Nizauskaite, 2013; Juzeniene *et al.*, 2015; Vaid *et al.*, 2018), it could be expected that
475 their contribution to the total dissolved pool in surface waters should be small. The only
476 two studies measuring the four B12 congeners (MB12, AB12, HB12 and CB12)
477 reported disparate average contribution of HB12 to the total dissolved B12 pool,
478 representing ca. 20% in oligotrophic oceanic waters (Suffridge *et al.*, 2018) and ca. 78%
479 in coastal waters (Heal *et al.*, 2014). Regardless of such differences, in both studies, the
480 contribution of the different B12 forms was relatively constant, which suggest that even
481 if we are underestimating the total B12 concentration, the variability patterns could be
482 taken as representative of those of total B12.

483

484 Compared with the relatively sharp spatial gradients observed in the North Pacific along
485 the California-Baja California margin (Sañudo-Wilhelmy *et al.*, 2012), we did not find
486 marked spatial patterns in the cross-shelf transects (Fig. 2). Although highly contrasted

487 areas were covered, Sañudo-Wilhelmy *et al.* (2012) found that areas of hundreds of
488 kilometers where B12 concentration was nearly undetectable, probably because they
489 only measured CB12. Our transect covered a less extensive area (Fig. 1) but both CB12
490 and HB12 were measured. Despite the lack of significant differences in B12
491 concentration along our transect (Supporting Information Fig. S1), higher values were
492 found in coastal stations during April and August (Fig. 2). Higher B12 concentrations
493 were observed within the UML in February, with the only exception of the innermost
494 coastal station (Fig. 2). Spatial patches above the nutricline (the location of which
495 frequently matches the UML limit) were also registered for B vitamins by Suffridge *et al.*
496 (2018), coinciding with intense biological activity. When considering the temporal
497 and vertical distribution of B12 at the innermost coastal station (stn 3) in February (Fig.
498 3 and 4), consistently higher B12 concentrations were found in the ENACW. On the
499 other hand, B12 depletion was observed in the UML during the entire sampling period,
500 regardless of the phytoplankton bloom development (Fig. 3 and 5). A similar pattern
501 was observed in August when the biological activity was high and the concentrations of
502 inorganic nutrients and B12 were the lowest in the surface and highest in the ENACW
503 (Fig. 2). The positive correlation between B12, SiO_4^{4-} , NO_3^- and HPO_4^{2-} concentrations
504 associated with the ENACW (Fig. 4) suggests that B12 follows a “nutrient-like” vertical
505 distribution (Karl, 2002; Grant *et al.*, 2014), showing higher concentrations in
506 intermediate water bodies (Sañudo-Wilhelmy *et al.*, 2012). We hypothesize that in this
507 coastal location, B12 could be produced by prototrophic prokaryotes and accumulated
508 in ENACW, transported to the photic zone through upwelling events or mixing
509 processes, and rapidly consumed in the UML. The high relative abundance of
510 Thaumarchaeota in ENACW (Fig. 6) supports this hypothesis, as this group seems to
511 play a major role in B12 production in aquatic ecosystems (Doxey *et al.*, 2015; Heal *et*

512 *al.*, 2017). The vitamin B12 depletion observed in surface waters is also coherent with
513 B12 degradation upon exposure to solar radiation (Juzeniene and Nizauskaite, 2013).

514

515 A remarkably different B12 distribution occurred in April at the coastal station (Fig.
516 3P), when the prevailing southerly winds likely promoted the onshore transport of B12
517 depleted oceanic water, resulting in very low B12 levels from day 5 to 7 (Fig. 1, 2 and
518 3). The hypothesis of oceanic waters moving towards the innermost coastal station
519 during days 5–7 is supported by the warmer water column temperatures observed at the
520 end of the April sampling period (Fig. 3) and by changes in the microbial community
521 composition (Fig. 6), particularly by the relative increase of *Synechococcus*, which tend
522 to be dominant in oceanic waters in this sampling area (Teira *et al.*, 2009, Joglar *et al.*
523 2020). Interestingly, *Synechococcus* is a cyanobacteria that produces and uses
524 pseudocobalamin (Helliwell *et al.*, 2016), which was not measured in this study.

525

526 *The role of vitamin B12 in the dynamics of microbial plankton*

527 According to recent experimental studies conducted by our research group in this area,
528 ambient B12 could occasionally limit primary production, particularly at the beginning
529 of the productive period in early spring (Barber-Lluch *et al.*, 2019; Joglar *et al.*, 2020).
530 In addition, a positive correlation was found between depth-averaged Chl-*a* and
531 dissolved B12 concentrations in this sampling area (Barber-Lluch *et al.*, 2020). In
532 contrast, using an extensively larger dataset than that of Barber-Lluch *et al.* (2020), the
533 multiple regression analyses conducted here did not include B12 concentration as a
534 predictive variable for chlorophyll-*a* or primary production (Table 1). A lack of
535 correlation between phytoplankton and B12 could derive from the presence of non-

536 auxotrophic groups. However, the phytoplankton community was composed of many
537 taxa that have been recognized to include B12-auxotrophs, such as Dinophyceae (Croft
538 *et al.*, 2005; Tang *et al.*, 2010), or *Ostreococcus*, *Micromonas*, *Skeletonema*, or
539 *Thalassiosira* (Swift, 1981; Croft *et al.*, 2005; Palenik *et al.*, 2007; Helliwell *et al.*,
540 2011; Ellis *et al.*, 2017; Cooper *et al.*, 2019), of which, only Dinophyceae abundance
541 showed a positive correlation with B12 (Fig. 6 and 7). Multiple regression models for
542 phytoplankton biomass and production included the concentration of NO_3^- , that was
543 inversely related to phytoplankton, as significant explanatory variable (Table 1). Such
544 negative relationships between primary producers and mineral nutrients have been
545 previously observed, reflecting nutrient exhaustion during phytoplankton growth (Fisher
546 *et al.*, 1992; Piehler *et al.*, 2004; Martínez-García *et al.*, 2010; Barber-Lluch *et al.*,
547 2019). Our findings thus contrast with similar studies in other coastal ecosystems
548 characterized by higher ambient B12 levels (0.3–158 pM of CB12), where a significant
549 and positive correlation was observed between CB12 and primary production rates
550 (Koch *et al.*, 2011).

551 Regardless of the contribution of inorganic nutrients to explaining phytoplankton
552 production and biomass, the variability explained by models including only nutrient
553 variables was relatively low (Adjusted $R^2 < 0.48$), except for the biomass of
554 picophytoplankton (Adjusted $R^2 = 0.79$) (Table 1). The fraction of variability explained
555 by the models considerably increased when both nutrients and prokaryote-related
556 variables (PB and HPP) were included (Adjusted $R^2 > 0.74$; Table 1), suggesting that
557 prokaryote activity largely influenced phytoplankton growth. In the case of prokaryotes,
558 only PB showed a positive relationship with the amount of dissolved vitamin B12
559 (Table 1), which is coherent with the fact that only prokaryotes have the capacity of *de*
560 *novo* synthesizing this compound (Roth *et al.*, 1996; Martens *et al.*, 2002; Warren *et al.*,

561 2002). Suffridge *et al.* (2018) found that both CB12 and HB12 contributed to explaining
562 the abundance of low nucleic acid bacteria in Atlantic waters. Interestingly, these
563 authors did not find any significant correlation with the active forms AB12 and MB12,
564 which were not detected in our study. Similarly, Gobler *et al.* (2007) also found a
565 significant relationship between bacterial densities and CB12 concentration in coastal
566 waters.

567

568 The lack of correlation between dissolved B12 concentration and phytoplankton
569 variables could be caused by a rapid turnover rate of this growth factor in surface waters
570 (Taylor and Sullivan, 2008), which is coherent with the constantly low concentration of
571 B12 in the sampling area and the small-magnitude response of phytoplankton to
572 experimental B12 additions (Barber-Lluch *et al.*, 2019; Joglar *et al.*, 2020), and suggest
573 a tight coupling between production and consumption of this growth factor. The
574 observed relationship between B12 and prokaryote biomass and the significant effect of
575 heterotrophic prokaryote production on phytoplankton biomass and production (Table
576 1), is consistent with the hypothesis of phytoplankton B12 acquisition through
577 interactions with bacteria, which may include intimate symbiotic relationships (Croft *et al.*
578 *et al.*, 2005; Amin *et al.*, 2012; Cooper and Smith, 2015; Seymour *et al.*, 2017). In such
579 intimate interactions, B12 molecules appear to accumulate in bacterial membranes, and
580 are rapidly assimilated by phytoplankton before being released into the environment
581 (Amin *et al.*, 2012). If phytoplankton obtain B12 mostly from closely associated
582 bacteria, then, changes in prokaryote community composition should have an impact on
583 primary producers. A relatively strong and significant relationship was indeed found
584 between eukaryote community composition, mostly dominated by phytoplankton taxa,
585 and the prokaryote community composition. These observations point to the inclusion

586 of microbial interactions as a key piece in future studies of vitamin B12 dynamics in the
587 marine environment.

588

589 *Interactions between eukaryotes and prokaryotes as possible sources of B12.*

590 Recent experimental work demonstrated that dissolved B12 concentrations do not
591 provide enough information about the balance between B12 release by prokaryotes and
592 its consumption by prokaryotes and eukaryotes (Villegas-Mendoza *et al.*, 2019).
593 Therefore, despite its very low ambient concentration, we cannot disregard B12 as a
594 factor playing a significant role in microbial plankton dynamics in this coastal system.
595 We built co-occurrence networks for the different water layers to identify potential
596 biotic interactions between prokaryotes and eukaryotes that might involve B12 trading
597 (Fig. 8). The significant relationship found between prokaryote and eukaryote (mostly
598 phytoplankton) communities strongly suggests that biotic interactions might be playing
599 a critical role in the functioning of microbial communities in this coastal ecosystem.
600 Such dependence can involve phytoplankton-derived organic compounds required by
601 heterotrophic bacteria in exchange for nutrients or bacterial products required by
602 phytoplankton (Amin *et al.*, 2015; Durham *et al.*, 2015; Cirri and Pohnert,
603 2019)(Durham *et al.*, 2015).

604

605 The first study aimed at evaluating the interactions between algae and bacteria was
606 carried out in 1974, revealing that cultures with B12-producing bacteria enhanced
607 growth of B12-consuming algae (Haines and Guillard, 1974). There are many other
608 recent pieces of experimental evidence of biotic interactions between bacteria and
609 phytoplankton involving B12. For example, a vitamin B12-poor environment induces a

610 symbiotic relationship between *Lobomonas*, a B12-auxotroph green alga, and the
611 heterotrophic bacteria *Mesorhizobium* acting as the ultimate source of the vitamin
612 (Kazamia *et al.*, 2012). *Dinoroseobacter shibae*, a marine bacteria belonging to
613 Rhodobacterales, isolated from dinoflagellates (Biebl *et al.*, 2005) supplies B1 and B12
614 to its hosts in exchange for fixed carbon (Wagner-Döbler *et al.*, 2010), and *Ruegeria*
615 *pomeroyi* also provides B12 to the diatom *Thalassiosira pseudonana* in exchange for
616 organosulfurized compounds (Durham *et al.*, 2015).

617

618 The strong positive co-occurrences found in the ENACW involving Thaumarchaeota or
619 Oceanospirillales and dinoflagellates (Fig. 8C), suggests that these groups share
620 ecological niche, showing very similar correlations with resource variables, such as
621 inorganic nutrients or B12 (Fig. 7). It is important to note that co-occurrence does not
622 necessarily imply the existence of positive interaction, still, it has been demonstrated
623 that species that mutually benefit from each other tend to evolve towards ecological
624 niche convergence (Elias *et al.*, 2008). While many Dinophyceae have an absolute
625 requirement for exogenous B12 (Tang *et al.*, 2010; Koch *et al.*, 2014), both
626 Thaumarchaeota and Oceanospirillales have been reported to play an important role in
627 B12 biosynthesis within aquatic environments (Bertrand *et al.*, 2015; Doxey *et al.*,
628 2015), suggesting that these significant positive co-occurrences may involve B12
629 supply. Previous studies also suggested that the strong correlation between archaea and
630 phytoplankton found in marine systems could imply the archaeal supply of B12 to algae
631 (Rodionov *et al.*, 2003; Fietz *et al.*, 2011; Heal *et al.*, 2017). Furthermore, the
632 demonstration of the ability of bacteria to directly affect gene expression in some
633 Dinophyceae (Moustafa *et al.*, 2010; Gong *et al.*, 2017), suggests a close relationship
634 between these microbial planktonic groups.

635 In the subsurface layer, *Amylibacter* ASVs, belonging to the Rhodobacteraceae family,
636 and *Ostreococcus* ASVs also appeared to coexist (Fig. 8B), sharing an ecological niche
637 (Fig. 7). It has been previously reported that *Ostreococcus* B12 requirements can be
638 provided by associated Rhodobacteraceae (Cooper *et al.*, 2019) Thus, the significant co-
639 occurrence observed might reflect a mutualistic interaction between *Amylibacter* and
640 *Ostreococcus* mediated by vitamin B12.

641

642 Competition among microbes for essential limiting nutrients is also common in marine
643 ecosystems. In the oceans, phytoplankton growth is often limited by the availability of
644 macronutrients such as nitrogen and phosphorus (Elser *et al.*, 1995; Joint *et al.*, 2002;
645 Lovdal *et al.*, 2008) or micronutrients such as iron or vitamins (Bertrand *et al.*, 2011;
646 Amin *et al.*, 2012; Koch *et al.*, 2012; Barber-Lluch *et al.*, 2019). Recent work point to
647 bacteria as a major sink of B12, potentially competing for this resource with
648 phytoplankton (Koch *et al.*, 2012; Heal *et al.*, 2017).

649

650 In the UML, significantly negative occurrences between *Tenacibaculum*, belonging to
651 Flavobacteriaceae, and the diatoms *Minidiscus* or *Thalassiosira* sp. were observed (Fig.
652 8A), suggesting competition-exclusion relationships. All currently sequenced
653 Flavobacteriaceae are predicted to be B12-auxotrophs (Sañudo-Wilhelmy *et al.*, 2014),
654 an trait also found in many diatoms (Croft *et al.*, 2006; Tang *et al.*, 2010; Bertrand and
655 Allen, 2012). As an example, *Thalassiosira* species have been reported of being B12-
656 dependent (Croft *et al.*, 2005; Sañudo-Wilhelmy *et al.*, 2014). Diatoms may increase
657 their cobalamin acquisition machinery in response to B12 scarcity (Bertrand and Allen,
658 2012), which may improve their competitiveness against auxotrophic bacteria for the

659 acquisition of B12. Interestingly, there were also some positive co-occurrences between
660 *Synechococcus* ASVs and *Thalassiosira* or *Chaetoceros tenuissimus* ASVs.
661 *Synechococcus* has been described as a major producer of pseudocobalamin, a chemical
662 variant of B12 that can be remodeled by certain algae (Helliwell *et al.*, 2016; Heal *et al.*,
663 2017; Helliwell, 2017).

664

665 In summary, our results suggest that ambient B12 concentration *per se* does not
666 contribute to ecological niche definition and does not appear to play a strong role in
667 regulating microbial plankton dynamics in this upwelling system. Instead, heterotrophic
668 prokaryote production appeared to be strongly related to phytoplankton biomass and
669 primary production. The relatively high abundance of taxa previously described as B12-
670 auxotrophs in this sampling area suggests that there might be a close balance between
671 B12 production and consumption, which may result in low dissolved B12
672 concentrations. Interestingly, the co-occurrence analyses allowed the identification of
673 interactions potentially involving B12 that can be subsequently tested with model
674 systems in the laboratory. The fact that prokaryote and eukaryote taxonomic
675 composition showed higher correlation between them than with nutritional resources,
676 suggests that the biotic interactions between phytoplankton and prokaryotes may
677 represent a predominant driving force of oceanic microbial community dynamics.

678

679 **Experimental procedures**

680 **Survey area**

681 The Ría de Vigo (NW Spain) is a coastal embayment and its main tributary into the
682 innermost part of the Ría is the Oitabén-Verdugo River. This Ría is affected by

683 intermittent upwelling of cold and inorganic nutrient-rich subsurface water from April
684 to September and downwelling of warm and nutrient poor shelf surface water from
685 October to March. Despite this seasonality, short-term variability in the wind regime is
686 recurrent and significant in the area, with upwelling and downwelling events occurring
687 within each season (Figueiras *et al.*, 2002; Piedracoba *et al.*, 2005; Barton *et al.*, 2016).
688 The Ría de Vigo and its adjacent shelf is a highly productive and very dynamic coastal
689 system, where microbial community composition varies over short temporal and spatial
690 scales (Cermeño *et al.*, 2006).

691

692 **Field observations**

693 Field measurements were obtained during the ‘ENVISION’ cruises held in 2016 aboard
694 the R/V Ramón Margalef. Cruises were carried out in February, coinciding with the
695 spring bloom, in April under upwelling relaxation, and in August during the upwelling
696 event.

697

698 In order to describe the spatial variability, a total of 9 stations were occupied (Fig. 1A)
699 along a zonal transect of the Ría de Vigo from the inner continental shelf (42 °N, 8.88
700 °W) to open ocean waters on the shelf-break (42.142 °N, 9.708 °W) during the first day
701 of each cruise (day 1). At each station, vertical profiles of temperature and salinity were
702 recorded using a regular CTD-rosette sampler down to a maximum depth of 200 m.
703 Seawater samples for chemical and biological analyses were collected at 4 stations (stn
704 3, stn 4, stn 5 and stn 6), hereafter referred to as biological stations. Stn 3 and stn 4 are
705 considered as on-shelf stations since their depth is less than 200 m, being stn 3 closer to
706 the mouth of the Ría de Vigo. In contrast, the deeper stn 5 and 6 are considered as shelf-
707 break stations, with stn 6 being the most oceanic sampling point. Seawater samples for

708 vitamin B12, inorganic nutrients, and total chlorophyll *a* concentration were drawn from
709 5 depths at each station. In order to explore temporal variability, the on-shelf stn 3 (Fig.
710 1A) was visited daily from day 1 to day 7 during each cruise. This station was
711 intensively sampled for vitamin B12, inorganic nutrients and dissolved organic matter,
712 size-fractionated chlorophyll *a*, size-fractionated primary production, prokaryote
713 biomass and prokaryote heterotrophic production. The sampling depths were chosen
714 based on the vertical profiles of chlorophyll *a* fluorescence and temperature considering
715 the downward CTD casts.

716

717 Upwelling index (UI) was estimated from surface winds in a 2° x 2° cell centered at 42
718 °N, 10 °W. Daily UI values were computed by the Instituto Español de Oceanografía
719 (www.indicedeafloramiento.ieo.es) from sea level pressure fields over the ocean
720 supplied by the US Navy Operational Global Atmospheric Prediction System
721 (NOGAPS) model maintained by FNMOC (Fleet Numerical Meteorology and
722 Oceanography Center) (Gonzalez-Nuevo *et al.*, 2014). Precipitation data was
723 downloaded from the meteorological station Illas Cies (ID 10125) run by the Regional
724 Weather Forecast Agency-Meteogalicia (www.meteogalicia.gal).

725

726 **Size-fractionated chlorophyll *a* concentration**

727 Chlorophyll *a* (Chl-*a*) concentration was measured as a phytoplankton biomass proxy.
728 A volume of 300 mL of water samples were sequentially filtered through 3 and 0.2 µm
729 pore-size polycarbonate filters and frozen at -20 °C until analysis. Chl-*a* from samples
730 was extracted with 90% (v/v) acetone (HPLC grade) at 4 °C overnight in dark
731 conditions. Chl-*a* fluorescence was determined with a TD-700 Turner Designs
732 fluorometer calibrated with pure Chl-*a* standard solution.

733

734 **Size-fractionated primary production**

735 Size-fractionated photosynthetic carbon incorporation rates were estimated using ^{14}C -
736 sodium bicarbonate according to Marañón *et al.* (2001). In brief, 100 μL $\text{NaH}^{14}\text{CO}_3$
737 stock solution (126 $\mu\text{Ci mL}^{-1}$ specific activity) were added to seawater samples
738 transferred to acid-cleaned polycarbonate bottles. For each sample, three light and one
739 dark bottles were incubated for ~6 hours (typically from 11:00 to 17:00 h, local time)
740 under *in situ* irradiance and temperature conditions. At the end of the incubation,
741 samples were gently sequentially filtered through 3 μm and 0.2 μm pore-size Whatman
742 PC filters. Non-assimilated radioactive ^{14}C was removed by exposing the filters to 10%
743 (v/v) HCl for 12 hours and constant shaking. After decontamination of inorganic ^{14}C ,
744 filters were transferred to scintillation vials to which 4 mL of scintillation cocktail
745 (Ultima Gold XR, Perkin Elmer) was added before measuring the radioactivity signal as
746 disintegrations per minute (DPM) in a Perkin Elmer TriCarb 3100 TR counter.

747

748 **Prokaryote biomass and production**

749 Unfiltered seawater samples (2 mL) for prokaryote biomass (PB) quantification were
750 preserved with 1% (v/v) paraformaldehyde + 0.05% (v/v) glutaraldehyde incubated for
751 20 min at room temperature and stored at -80 °C after being flash-frozen with liquid
752 nitrogen.

753

754 The abundance of heterotrophic prokaryotes was determined using a FACSCalibur flow
755 cytometer equipped with a laser emitting at 488nm. Samples were stained with SYBR
756 Green DNA fluorochrome prior to analysis, and prokaryote abundance was detected by

757 their signature of side scatter (SSC) and green fluorescence as described by Gasol and
758 Del Giorgio (2000). The empirical calibration between light side scatter (SSC) and cell
759 diameter described by Calvo-Díaz and Moran (2006) was used to estimate the
760 biovolume (BV) of cells. BV was converted into biomass by using the allometric factor
761 of Norland (1993) ($\text{fg C cell}^{-1} = 120 \times \text{BV}^{0.72}$) for the coastal samples and using the
762 open ocean conversion factor for the oceanic samples ($\text{fg C cell}^{-1} = 350 \times \text{BV}$).

763

764 Heterotrophic prokaryote production (HPP) was measured following the ^3H -leucine
765 incorporation method (Smith and Azam, 1992). Three replicates and two killed control
766 of unfiltered seawater were sampled (1 mL). Samples were spiked with 40 μL leucine
767 ($47 \mu\text{Ci mL}^{-1}$ specific activity stock solution) and incubated for 90 min in the same
768 conditions as PP samples. Processed samples were analyzed in a Perkin Elmer TriCarb
769 3100 TR counter, and the HPP was calculated from the leucine uptake rates using a
770 theoretical leucine to a carbon conversion factor of $3.1 \text{ kg C mol Leu}^{-1}$ (Smith and
771 Azam, 1992).

772

773 **Inorganic and organic nutrients**

774 Aliquots for inorganic nutrient determinations (ammonium, nitrite, nitrate, phosphate
775 and silicate) were collected in first place and directly from the Niskin bottle in order to
776 avoid contamination. 5% (v/v) HCl precleaned 50 mL polyethylene bottles were filled
777 with the sample employing free-contamination plastic gloves and immediately frozen at
778 $-20 \text{ }^\circ\text{C}$ until analysis by standard colorimetric methods with an Alliance Futura
779 segmented flow analyzer (Grasshoff *et al.*, 1999). The measurement error was $0.1 \mu\text{mol}$
780 L^{-1} for nitrate, $0.02 \mu\text{mol L}^{-1}$ for nitrite and phosphate and $0.05 \mu\text{mol L}^{-1}$ for

781 ammonium and silicate. Dissolved inorganic nitrogen (DIN) concentration was
782 calculated as the sum of the ammonium, nitrite and nitrate concentration.

783 Dissolved organic carbon (DOC) and total dissolved nitrogen (TDN) samples were
784 collected in 250 mL acid-washed all-glass flasks and were gently filtered through acid
785 rinsed 0.2 μm Pall Supor filters. Filtration was done in an acid-cleaned all-glass
786 filtration device under low pressure of high purity N_2 . About 15 mL of the filtrate was
787 collected in pre-combusted (450 $^\circ\text{C}$ for 24 h) Wheaton amber glass vials of 20 mL,
788 stopped with acid-cleaned PTFE lined caps and immediately frozen at -20 $^\circ\text{C}$ until
789 simultaneous DOC and TDN analysis in the base laboratory. After defrosting, samples
790 were acidified with 150 μL of 25% (v/v) H_3PO_4 and analyzed in a Shimadzu TOC-V
791 analyzer coupled in series with a TNM-1 chemiluminescence detector. The
792 measurement error was 0.7 $\mu\text{mol L}^{-1}$ for DOC and 0.3 $\mu\text{mol L}^{-1}$ for TDN. Reference
793 materials provided by D. A. Hansell (University of Miami) were analyzed to check the
794 accuracy of the instruments. Dissolved organic nitrogen was obtained subtracting
795 ammonium, nitrite and nitrate to TDN.

796

797 **Vitamin B12**

798 Seawater samples (2 L) for dissolved vitamin analysis were taken at five depths in the
799 station closet to the coast (stn 3) on day 1, day 3, day 5 and day 7 of the cruise and in all
800 biological stations during the day 1 of the cruise. Samples were filtered through 0.2 μm
801 Sterivex filter units under dim light conditions, and frozen at -20 $^\circ\text{C}$ until further
802 analysis. The methodology for concentration and detection of B12 was adapted from
803 Sañudo-Wilhelmy *et al.* (2012), Heal *et al.* (2014) and Suffridge *et al.* (2017) and is
804 fully described in Barber-Lluch *et al.* (2020). The pH of 1 L of water was adjusted to

805 6.5 and pre-concentrated using a solid-phase extraction (SPE) column (Econo-Pac®
806 Chromatography Columns BioRad) with 20 mL bed volume filled with 5 g of HF-
807 Bondesil C18 resin (Agilent Technologies) at a flow rate of 1 mL min⁻¹, avoiding light
808 exposure. The B12 vitamin retained on stationary phase were eluted using 12 mL of
809 methanol (MeOH) LCMS grade. The eluate was evaporated under nitrogen stream
810 using N₂ gas Turbovap until obtain the final volume of 300 -500 µL of sample, and then
811 was frozen at -20 °C until analysis.

812

813 The analysis of dissolved vitamin B12 concentrations in water samples were carried out
814 by LC-MS/MS, following the conditions described by Barber-Lluch *et al.* (2020). We
815 analyzed two B12-forms; cyanocobalamin (CB12) and hydroxocobalamin (HB12), as
816 we could not successfully set up the method for adenosylcobalamin (AB12) and
817 methylcobalamin methylcobalamin (MB12) measurement. Both MB12 and AB12
818 standards were highly unstable during the analyses, rapidly converting to HB12, which
819 precluded us to obtain an accurate calibration curve for these two congeners (see
820 Barber-Lluch *et al.* 2020). It is important to note that photodegradation was minimized
821 covering samples and lab materials with black opaque plastics. Briefly, quantification of
822 dissolved B12 (HB12 and CB12) was carried out using an Agilent 1290 Infinity LC
823 system (Agilent Technologies, Waghauseel Wiesental, Germany), coupled to an Agilent
824 G6460A triple quadrupole mass spectrometer equipped with an Agilent Jet Stream ESI
825 source. The LC system used a C18 reversed-phase column Agilent Zorbax SB-C18
826 Rapid Resolution HT (2.1 × 50 mm, 1.8 µm) with a 10 µL sample loop. Mass Hunter
827 Workstation software B.04.01 from Agilent Technologies was used for data acquisition
828 and quantitative analysis. The mobile phase was (A) metanol and (B) wáter both LCMS
829 grade and both buffered to pH 5.0 with 0.5% (v/v) of acetic acid (LCMS grade). The

830 chromatographic conditions consist in a isocratic condition of 7% of mobile phase B
831 during 2 min, a gradient from 7 to 100% of mobile phase B were set up for the next 9
832 min, an isocratic condition with 100% B for 2.5 min and returning to initial conditions
833 until completing 15 min of run. Limits of detection (LODs) and limits of quantification
834 (LOQs) were determined using sequential dilutions of the lowest point of the calibration
835 curves. LODs were defined as the lowest detectable concentration of the analyte with a
836 signal-to-noise (S/N) ratio for the qualitative transition of at least 3. In the same way,
837 LOQs were defined as the lowest quantifiable concentration with a S/N ratio of 10 for
838 the quantitative transition. The LODs obtained were 0.04 for hydroxocobalamin (HB12)
839 and 0.01 pmol L⁻¹ for cyanocobalamin (CB12), while the LOQs values were 0.05 and
840 0.025 pmol L⁻¹ for HB12 and CB12, respectively. The relative standard deviation of
841 triplicate injections was lower than 5% for both B12 congeners.

842

843 Standard of CB12 and HB12 were added in triplicate to a blank of seawater for recovery
844 studies following the conditions described by Barber-Lluch *et al.* (2020) and the
845 average B12 recovery percentage after pre-concentration and extraction of B-vitamin
846 spiked samples was 93%.

847

848 **Microbial community composition**

849 DNA samples were taken in the coastal station (stn 3) during the three ENVISION
850 cruises. In particular, sampling for microbial plankton community composition was
851 carried out on day 1, day 3, day 5 and day 7 at 5 different depths from surface to 80 m
852 depth. 2 L water samples were sequentially filtered through 3 µm pore size
853 polycarbonate filters and 0.2 µm pore size Sterivex Filter Units and immediately frozen

854 in liquid nitrogen and preserved at -80 °C. DNA contained in particles retained in the 3
855 µm and 0.2 µm filters was extracted by using the PowerSoil DNA isolation kit (MoBio
856 Laboratories Inc., CA, USA) and the PowerWater DNA isolation kit (MoBio
857 Laboratories Inc., CA, USA), respectively, according to the manufacturer's instructions.
858 Prokaryote community composition was assessed by sequencing the V4 and V5 regions
859 of the 16S rRNA gene (16S rDNA) from 0.2 µm Serivex by using the universal primers
860 "515F and 926R" (Parada *et al.*, 2016). Eukaryote community composition from both 3
861 µm and 0.2 µm filters was assessed by sequencing the V4 region from the 18S rRNA
862 gene (18S rDNA) using the primers "TAReuk454FWD1" and "TAReukREV3"
863 (Logares *et al.*, 2014). Amplified regions were sequenced with the Illumina MiSeq
864 platform (paired-end reads; 2 × 300 bp) at the Research and Testing Laboratory
865 (Lubbock, TX, USA) and subsequently analyzed following the DADA2 pipeline
866 (Callahan *et al.*, 2016). The SILVA reference database (Quast *et al.*, 2012) was used for
867 taxonomic assignment of 16S ASVs (amplicon sequence variant). The PR2 (Guillou *et*
868 *al.*, 2013) and the marine protist database from the BioMarks project (Massana *et al.*,
869 2015) were used for the taxonomic assignment of 18S ASVs. The data for this study
870 have been deposited in the European Nucleotide Archive (ENA) at EMBL-EBI
871 (<https://www.ebi.ac.uk/ena>) under accession numbers PRJEB36188 (16S sequences)
872 and PRJEB36099 (18S sequences).

873 The ASV tables of prokaryotes and eukaryotes were subsampled to the number of reads
874 present in the sample with the lowest number of reads, which was 2080 and 1286, for
875 16S rDNA and 18S rDNA, respectively. Rarefaction curves suggest that these minimum
876 sample sizes were adequate to describe prokaryote and eukaryote communities in our
877 samples (Supporting Information Fig. S3). A total of 1550 unique ASVs of prokaryotes
878 were identified. As many ASVs of eukaryotes were present in both size fractions, we

879 combined datasets derived from the 0.2 and the 3 μm filters for eukaryote community
880 analyses. Reads from each filter size were normalized by the filter DNA yield as
881 explained in Dupont *et al.* (2015) and Hernández-Ruiz *et al.* (2018) obtaining 2293
882 unique 18S ASVs. The sequence abundances of the subsampled ASV tables were
883 transformed using the centered log-ratio (clr) (Fernandes *et al.*, 2014; Gloor *et al.*,
884 2017). Zero values were replaced by the minimum value that was larger than 0 divided
885 by 2.

886

887 **Statistical analyses**

888 Water samples were classified for statistical analyses in three water bodies according to
889 their potential density. The upper mixed layer (UML) was determined as the depth
890 where potential density was 0.1 kg m^{-3} higher than in the surface layer (Fernández-
891 Castro *et al.*, 2014). Eastern North Atlantic Central Water (ENACW) was defined as the
892 depth where potential density ($\sigma\text{-t}$) was higher than 27 kg m^{-3} (potential temperature
893 about $12 \text{ }^\circ\text{C}$) (Pollard and Pu, 1985; Ríos *et al.*, 1992; Liu and Tanhua, 2019). Samples
894 between the UML and the ENACW layer were classified as sub-surface (SSL).

895 Normal distribution was tested by a Kolmogorov-Smirnov test and variables were log-
896 transformed when it was necessary to obtain normality. Analysis of variance (ANOVA)
897 with Bonferroni's pairwise *post-hoc* tests were used to explore the effect of sampling
898 month, water layer and sampling station on B12, NO_3^- and HPO_4^{2-} concentrations in the
899 transect (stn 3 to 6), and on B12, NO_3^- , HPO_4^{2-} concentrations, phytoplankton and
900 prokaryote biomass and production along the short-term time series at stn 3. To evaluate
901 the spatial variability, the effect of water layer and sampling month and station were

902 evaluated with samples collected on day 1 of each cruise while temporal variability was
903 evaluated with samples taken at stn 3 from day 1 to day 7.

904

905 The environmental (temperature, salinity, inorganic nutrients, dissolved organic carbon,
906 dissolved organic nitrogen, and B12) and biological (size-fractionated phytoplankton
907 biomass and production, and prokaryote biomass and production) data were transformed
908 with the square root function to homogenize values, normalized and a Principal
909 Component Analysis (PCA) were conducted to explore the data. Hierarchical cluster
910 analysis was applied to classify individual samples based on the clr abundances of main
911 microbial taxa using Euclidean distance. The depicted microbial taxa were carefully
912 defined based on their abundance and relevance. The criteria to subdivide a taxonomic
913 level was that the relative abundance of the resulting subgroups (lower taxonomic
914 levels) was higher than 5 % in at least one sample. No subdivisions were made for
915 kingdoms or phyla with low relative abundance (e.g Planctomycetes, Verrucomicrobia,
916 Fungi, Rhizaria). Two-way crossed analysis of similarities (ANOSIM, 999
917 permutations) were applied to the Euclidean distance matrices of (a) environmental
918 variables, and (b) biological variables to evaluate differences among sampling months
919 and layers. A partial mantel test was used to explore the relationship between the
920 distance matrices built from (a) resource variables, (b) clr abundance of major eukaryote
921 taxa, and (c) clr abundance of major prokaryote taxa. For this analysis, only resource
922 variables (i.e, inorganic nutrients, dissolved organic carbon and nitrogen, and vitamin
923 B12) were considered as the main factors directly impacting microbial growth.

924

925 Multiple linear regression analysis was conducted to explore the relationship between
926 resource variables and both prokaryote and phytoplankton production and biomass. The

927 influence of dissolved nutrients (including NO_3^- , NO_2^- , NH_4^+ , SiO_4^{4-} , HPO_4^{2-} , dissolved
928 organic carbon, dissolved organic nitrogen, and B12 concentrations) on the microbial
929 community structure was explored by calculating the Pearson coefficient between
930 normalized nutrients and the clr abundance of the main taxonomic groups.

931

932 Species co-occurrence analysis was completed using R studio with the package “co-
933 occur” (Griffith *et al.*, 2016), using the default settings of the package. Co-occurrence
934 patterns among pairs of microbial ASVs based on presence/absence data were assessed
935 with the probabilistic approach of Veech (Veech, 2013) to determine positive, negative
936 and random (i.e. not significant) co-occurrence among species. A co-association
937 network was inferred and visualized for each water body with Cytoscape v3.7.1
938 (Shannon *et al.*, 2003). To visualize the networks we filtered the infrequent ASVs
939 selecting the top 50 most abundant ASVs at each layer (25 prokaryote ASVs and 25
940 eukaryote ASVs). Networks were compared against 100 randomized versions generated
941 preserving the degree of nodes and edges applying Erdős–Rényi model by using the
942 Network Randomizer App. Topological parameters were calculated with the Network
943 Analyzer tool implemented in the Cytoscape software and these parameters were
944 compared between random and co-occurrence networks to evaluate the arbitrariness of
945 the community structure along the water column.

946

947 *Author contribution.* Eva Teira designed the experiments and Vanessa Joglar carried
948 them out with contributions of Clara Pérez-Martínez, Benjamin Pontiller, Emilio
949 Fernández and Eva Teira. X. A. Álvarez-Salgado was responsible for measuring
950 inorganic and organic nutrients and Ana Gago and Jose M. Leao for dissolved B12

951 concentrations. Daniel Lundin, Benjamin Pontiller and Jarone Pinhassi processed the
952 sequencing data. Vanessa Joglar and Eva Teira interpreted the results and prepared the
953 manuscript. All authors contributed to the further development of the manuscript and
954 approved the final version.

955

956 *Competing interests.* The authors declare that they have no conflict of interest.

957

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969

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- 1304

1305 **Tables and Figures**

1306 **Table 1:** Multiple linear regression models for the variables listed in the first column,
1307 showing the Beta coefficients for the different explanatory variables in rows. The last
1308 column (resource variables) shows the R2 adjusted of the models excluding biotic
1309 variables (i.e. PB, HPP, PP, and Chl-*a*). B12: vitamin B12 (CB12+HB12), NO₃⁻: nitrate,
1310 NO₂⁻: nitrite, NH₄⁺: ammonium, HPO₄²⁻: phosphate, SiO₄⁴⁻: silicate, DOC: dissolved
1311 organic carbon, DON: dissolved organic nitrogen, Chl-*a* < 3 μm: picophytoplankton
1312 biomass, Chl-*a* > 3 μm: nano-microplankton biomass, Chl-*a*: total phytoplankton
1313 biomass, PP < 3 μm: picophytoplankton production, PP > 3 μm: nano-
1314 microphytoplankton production, PP: total primary production, PB: prokaryote biomass,
1315 HPP: heterotrophic prokaryote production. X: variable not entered to create the model,
1316 ni: variable not included by the model.

1317

1318 **Table 2:** Topology of the co-occurrence networks in the upper mixed layer (UML),
1319 subsurface layer (SSL) and Eastern North Atlantic Central Water (ENACW). CL,
1320 clustering coefficient; CPL, characteristic path length; CL:CLr and CPL:CPLr ratios
1321 between de CL or CPL of the real network and the mean CL or CPL of 100 random
1322 networks of the same size (indicated with r).

1323

1324 **Figure 1:** (A) The NW Iberian margin (arrow) and locations of the stations that were
1325 sampled highlighting the biological stations (stars). Temporal variability was studied in
1326 stn 3 (red). (B) Daily coastal upwelling index (UI) and (C) daily precipitations during
1327 each sampling period. Vertical red line shows when cross-shelf transect was sampled.

1328

1329 **Figure 2:** Vertical distribution in the cross-shelf section from stn 3 to stn 6 of
1330 temperature (°C) showing water layer limits with dotted lines in (A) February, (G) April
1331 and (M) August. The upper mixed layer (UML) and the subsurface layer (SSL) is
1332 separated by the mixed layer deep (MLD) and the Eastern North Atlantic Central Water
1333 (ENACW) is located below the thick dashed line ($\sigma-t$, 27 kg m^{-3}). The thick dashed line
1334 (potential density 27 kg m^{-3}) separates the SSL from ENACW since the upper limit of
1335 ENACW is defined as the depth where the potential density ($\sigma-t$) is greater than 27 kg
1336 m^{-3} (potential temperature about $12 \text{ }^\circ\text{C}$). Salinity (PSU) in (B) February, (H) April and
1337 (N) August; chlorophyll *a* (Chl-*a*) (mg m^{-3}) in February (C), April (I) and August (O);
1338 dissolved inorganic nitrogen (DIN) (μM) in February (D), April (J) and August (P);
1339 phosphate (HPO_4^{2-}) (μM) in February (E), April (K) and August (Q); and vitamin B12
1340 (pM) in February (F), April (L) and August (R) are also shown.

1341

1342 **Figure 3:** Time course of vertical distribution of physicochemical variables at stn 3 over
1343 the 7-day sampling period. Water layer limits are shown with dotted lines in the
1344 temperature (°C) plots in (A) February, (L) April and (Q) August. Upper mixed layer
1345 (UML) and subsurface layer (SSL) are separated by mixed layer deep (MLD) and the
1346 Eastern North Atlantic Central Water (ENACW) shown below the thick dashed line ($\sigma-$
1347 t , 27 kg m^{-3}). Temporal sections of salinity (PSU) in (B) February, (J) April and (R)
1348 August; chlorophyll *a* (Chl-*a*) (mg m^{-3}) in (C) February, (K) April and (S) August;
1349 dissolved inorganic nitrogen (DIN) (μM) in (D) February, (L) April and (T) August;
1350 dissolved organic nitrogen (DON) (μM) in (E) February, (M) April and (U) August;
1351 phosphate (HPO_4^{2-}) (μM) in (F) February, (N) April and (V) August; dissolved organic
1352 carbon (DOC) (μM) in (G) February, (O) April and (W) August; and B12 (pM) in (H)
1353 February, (P) April and (X) August are also shown.

1354

1355 **Figure 4:** (A) Principal component analysis (PCA) of the abiotic factors measured at stn
1356 3: temperature (T), salinity (Sal), nitrate (NO_3^-), phosphate (HPO_4^{2-}), silicate (SiO_4^{4-}),
1357 dissolved vitamin B12 (B12), nitrite (NO_2^-), ammonium (NH_4^+), dissolved organic
1358 nitrogen (DON) and dissolved organic carbon (DOC). (B) PCA of biological variables
1359 measured at stn 3: picophytoplankton biomass ($\text{Chl-}a < 3 \mu\text{m}$), nano-
1360 microphytoplankton biomass ($\text{Chl-}a > 3 \mu\text{m}$), picophytoplankton production ($\text{PP} < 3$
1361 μm), nano-microphytoplankton production ($\text{PP} > 3 \mu\text{m}$), prokaryote biomass (PB) and
1362 heterotrophic prokaryote production (HPP). Different symbols stand for different water
1363 layers: upper mixed layer (UML), subsurface layer (SSL), and the Eastern North
1364 Atlantic Central Water (ENACW). Different colors represent different sampling
1365 months: February (green), April (blue) and August (pink).

1366

1367 **Figure 5:** Time course of the vertical distribution of the biological variables at stn 3
1368 over the 7-day sampling period. (A) picophytoplankton biomass ($\text{Chl-}a < 3 \mu\text{m}$), (B)
1369 nano-microphytoplankton biomass ($\text{Chl-}a > 3 \mu\text{m}$), (C) primary production of
1370 picophytoplankton ($\text{PP} < 3 \mu\text{m}$), (D) primary production of nano-microphytoplankton
1371 ($\text{PP} > 3 \mu\text{m}$), (E) prokaryote biomass (PB) and (F) heterotrophic prokaryote production
1372 (HPP).

1373

1374 **Figure 6:** Time course of the relative abundance of the main taxonomic groups of
1375 prokaryotes and eukaryotes at stn 3 over the 7-day sampling period. Different symbols
1376 stand for different water layers: the upper mixed layer (UML), subsurface layer (SSL)
1377 and the Eastern North Atlantic Central Water (ENACW). Different colors represent
1378 different sampling months: February (green), April (blue) and August (pink) showing

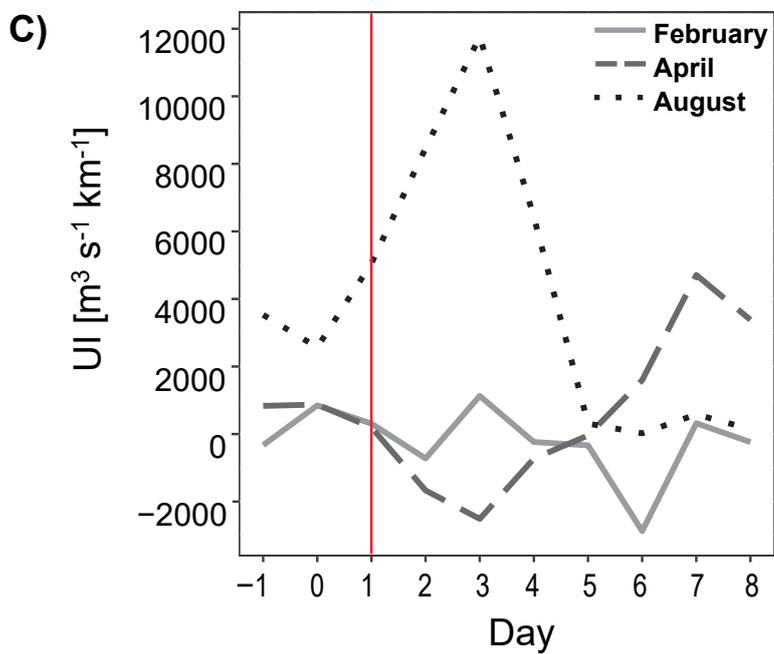
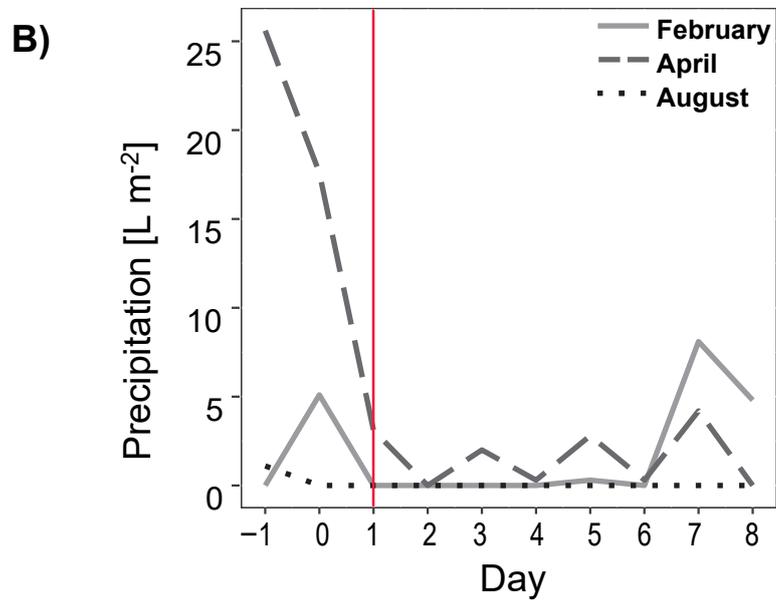
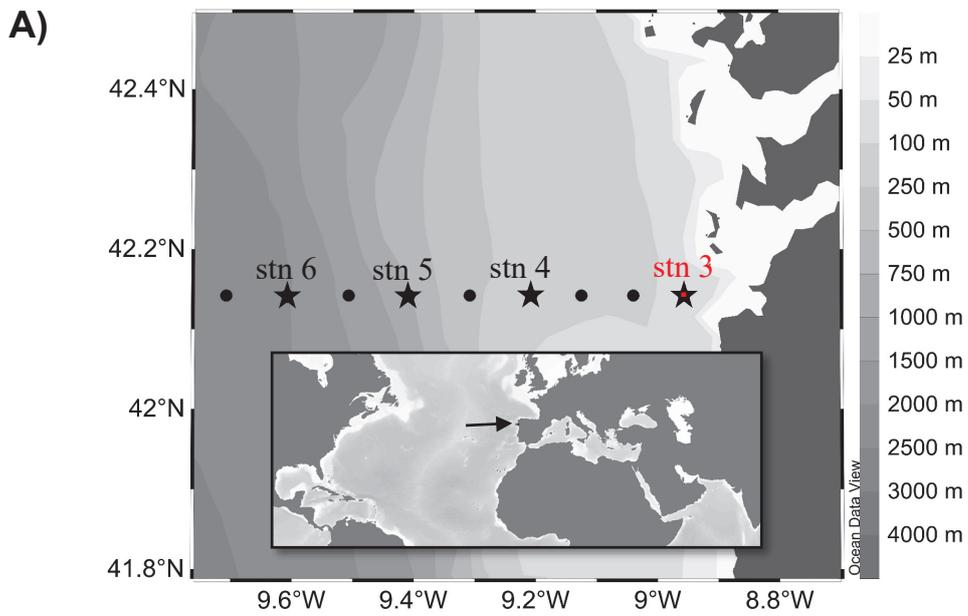
1379 the sampling day. The dendrogram represents the hierarchical clustering of individual
1380 samples based on the clr abundances of major microbial taxa using Euclidean distance.

1381

1382 **Figure 7:** Pearson correlation between the clr-abundance of the main taxonomic groups
1383 and resource variables: nitrate (NO_3^-), dissolved inorganic nitrogen (DIN), phosphate
1384 (HPO_4^{2-}), silicate (SiO_4^{4-}), total dissolved nitrogen (TDN), dissolved vitamin B12
1385 (B12), nitrite (NO_2^-), ammonium (NH_4^+), dissolved organic nitrogen (DON) and
1386 dissolved organic carbon (DOC). The dendrogram represents the hierarchical clustering
1387 of taxonomic groups based on their correlations with abiotic factors (Euclidean
1388 distances). Asterisks indicate statistically significant Pearson correlations.

1389

1390 **Figure 8:** Co-occurrence networks of the 50 most abundant and frequent prokaryote
1391 (diamonds: Archaea, circles: Bacteria) and eukaryote ASVs (hexagons). (A) Upper
1392 mixed layer (UML), (B) subsurface layer and (SSL) (C) Eastern North Atlantic Central
1393 Water (ENACW). Red and blue edges represent positive and negative associations,
1394 respectively. The width of the edges is proportional to the significance level of positive
1395 (coexistence) or negative (mutual exclusion) co-occurrence patterns.

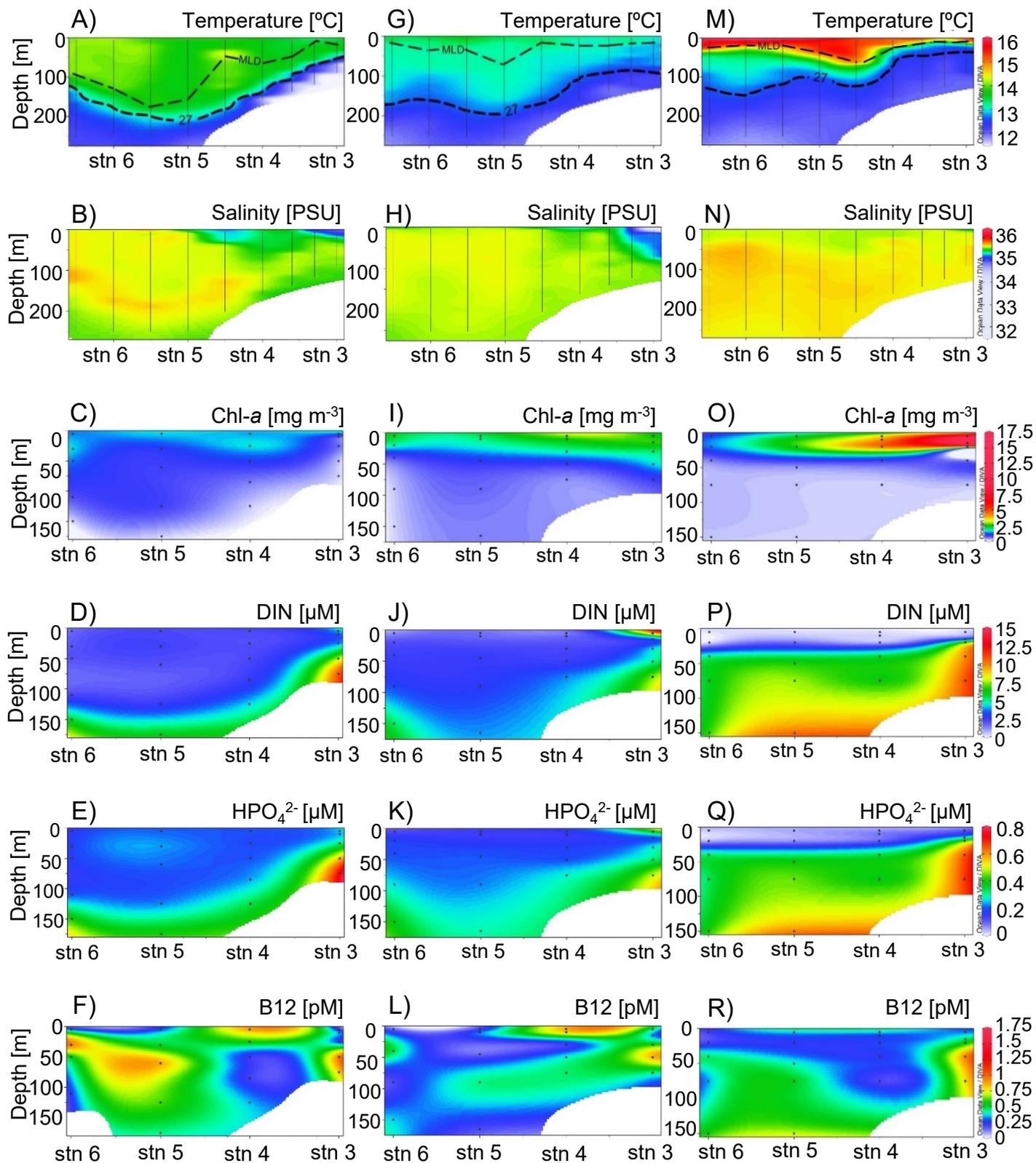


Spatial section

February

April

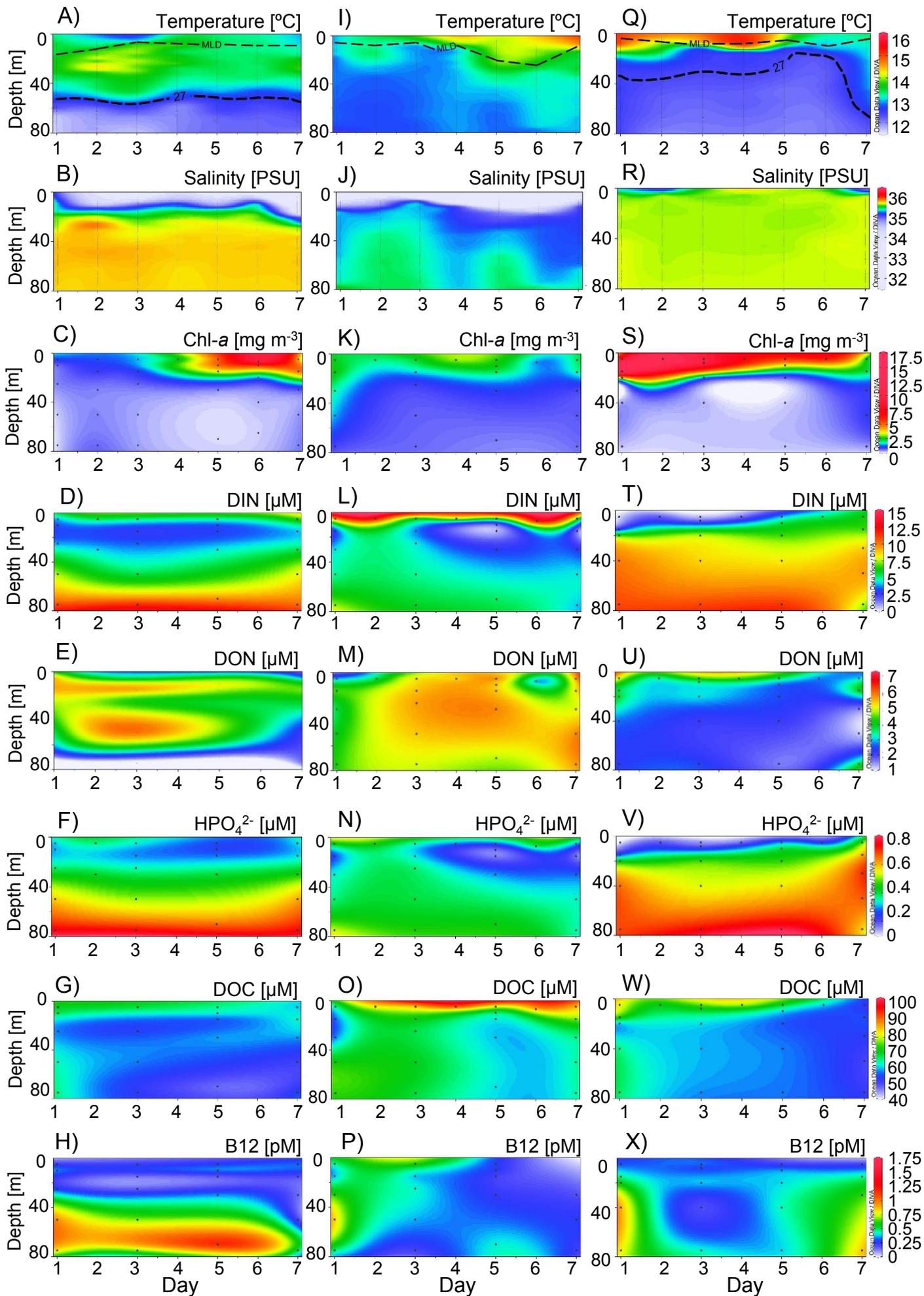
August

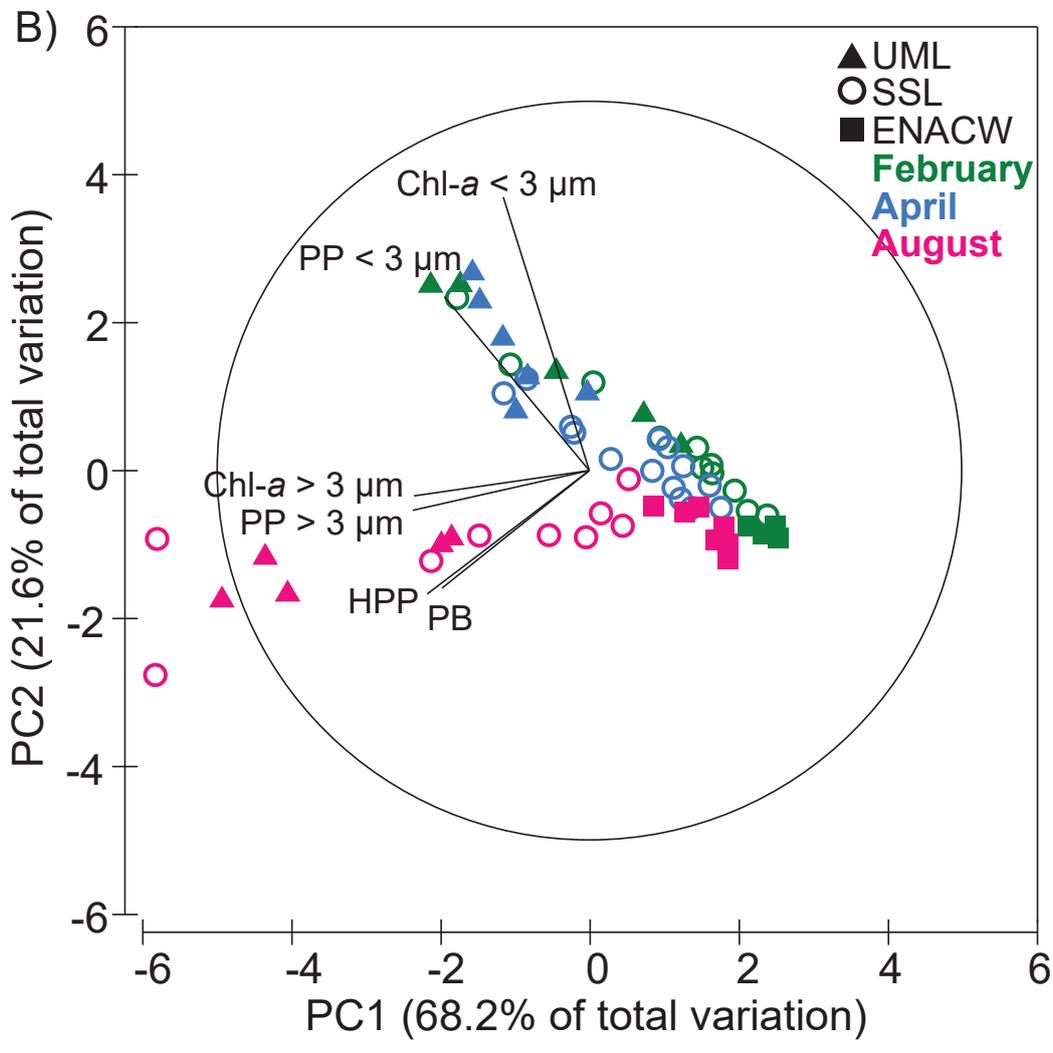
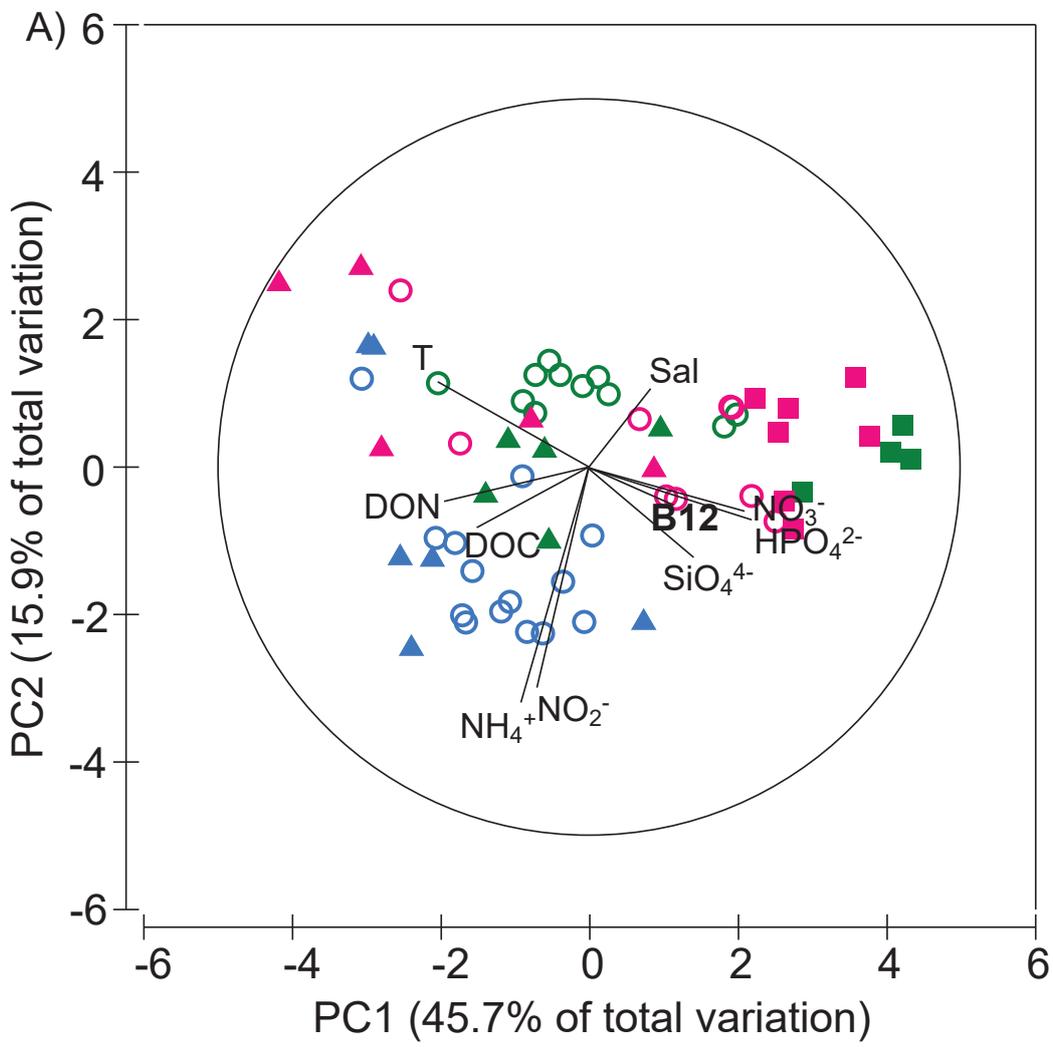


February

April

August

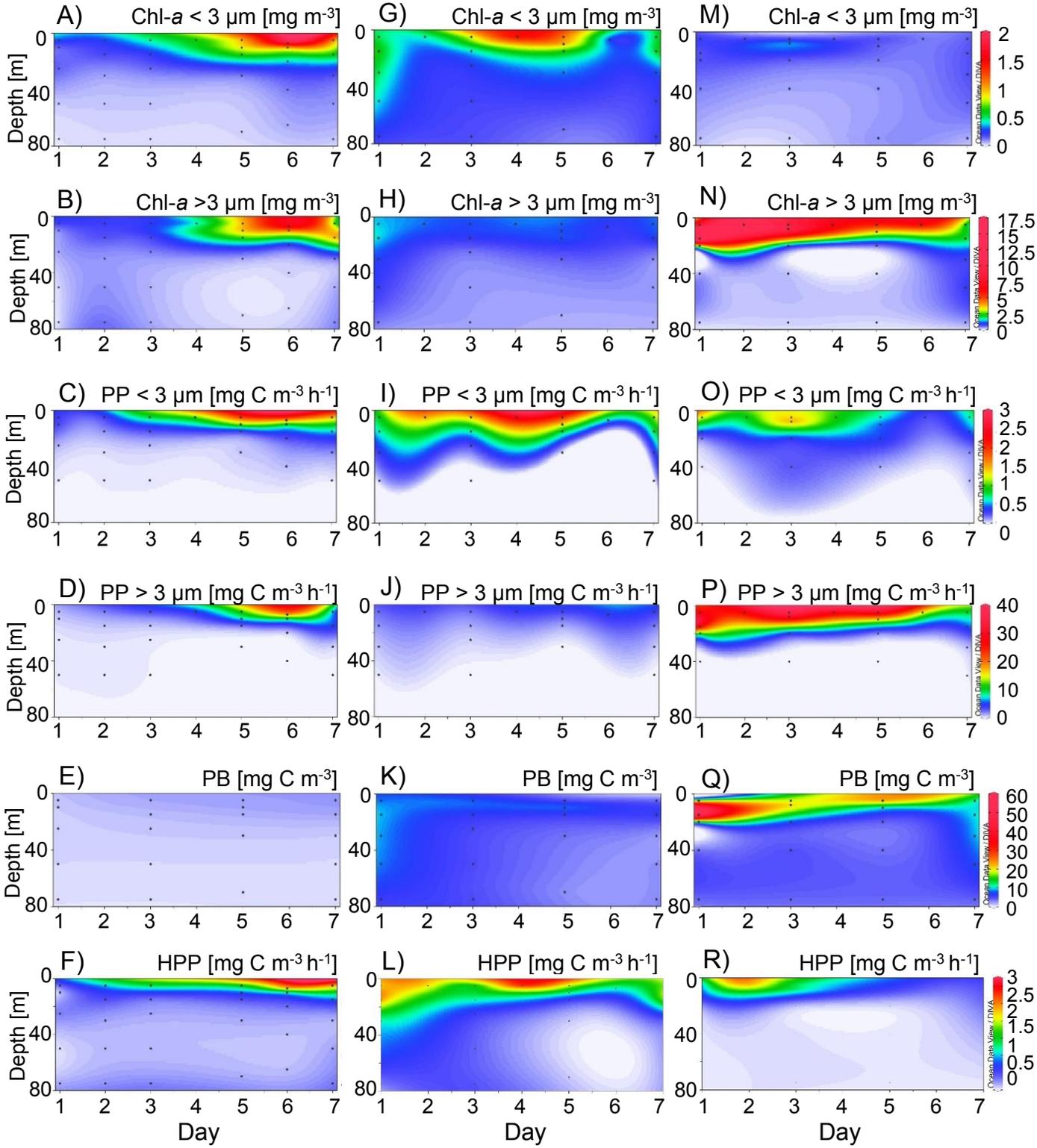




February

April

August



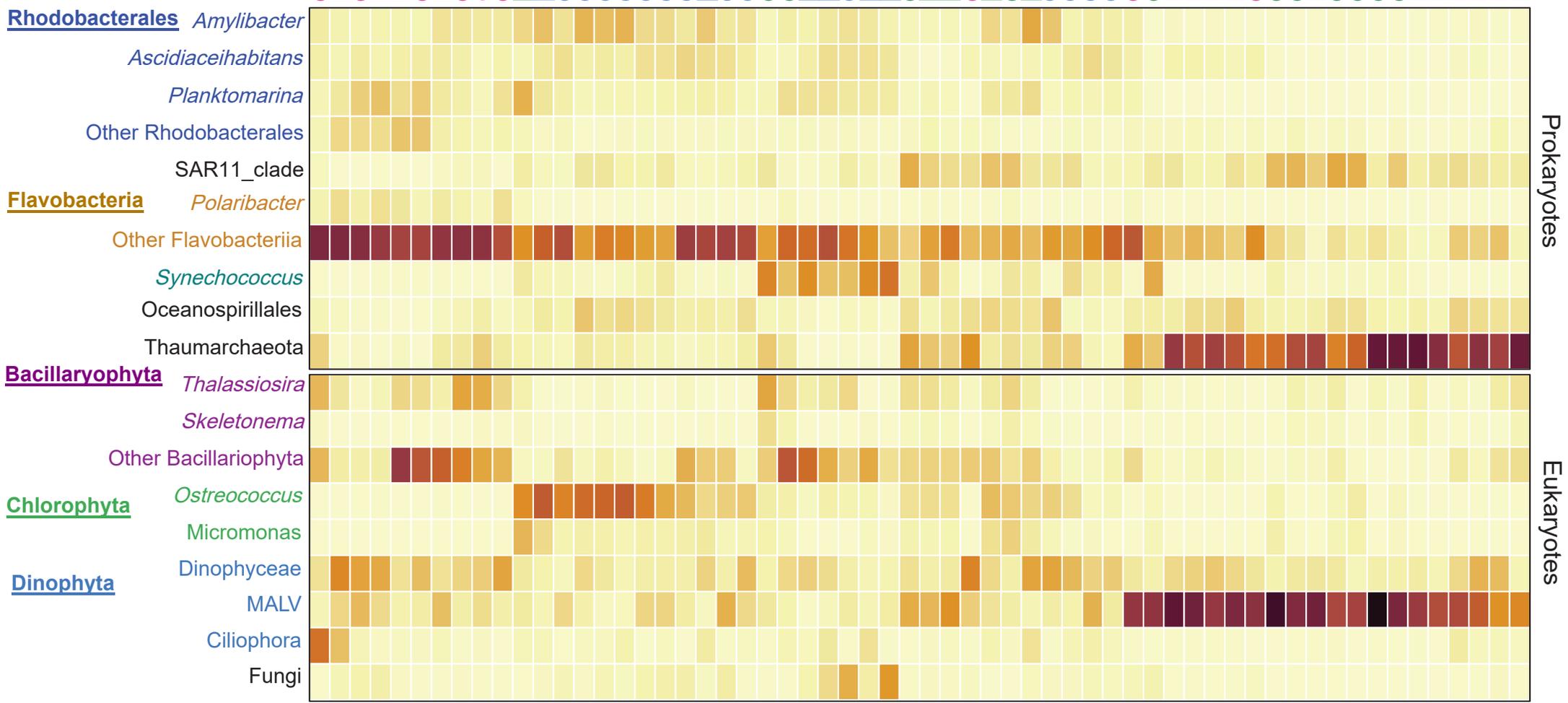
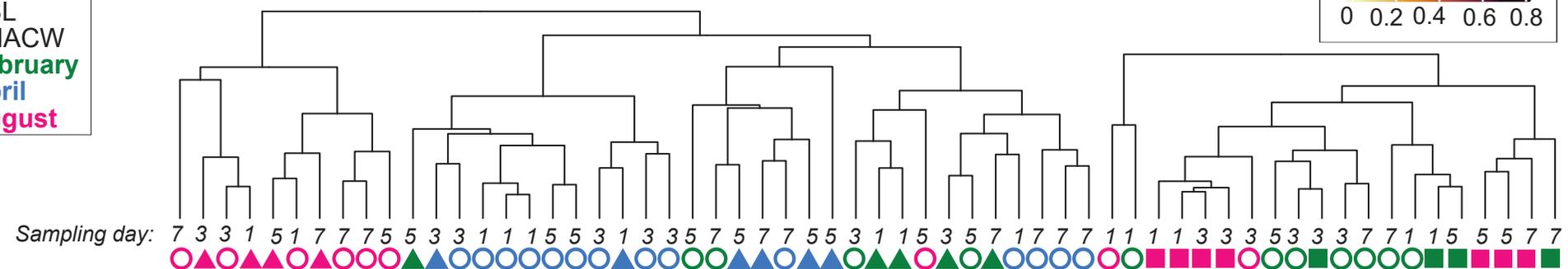
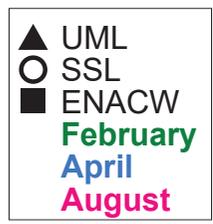
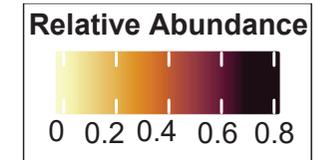
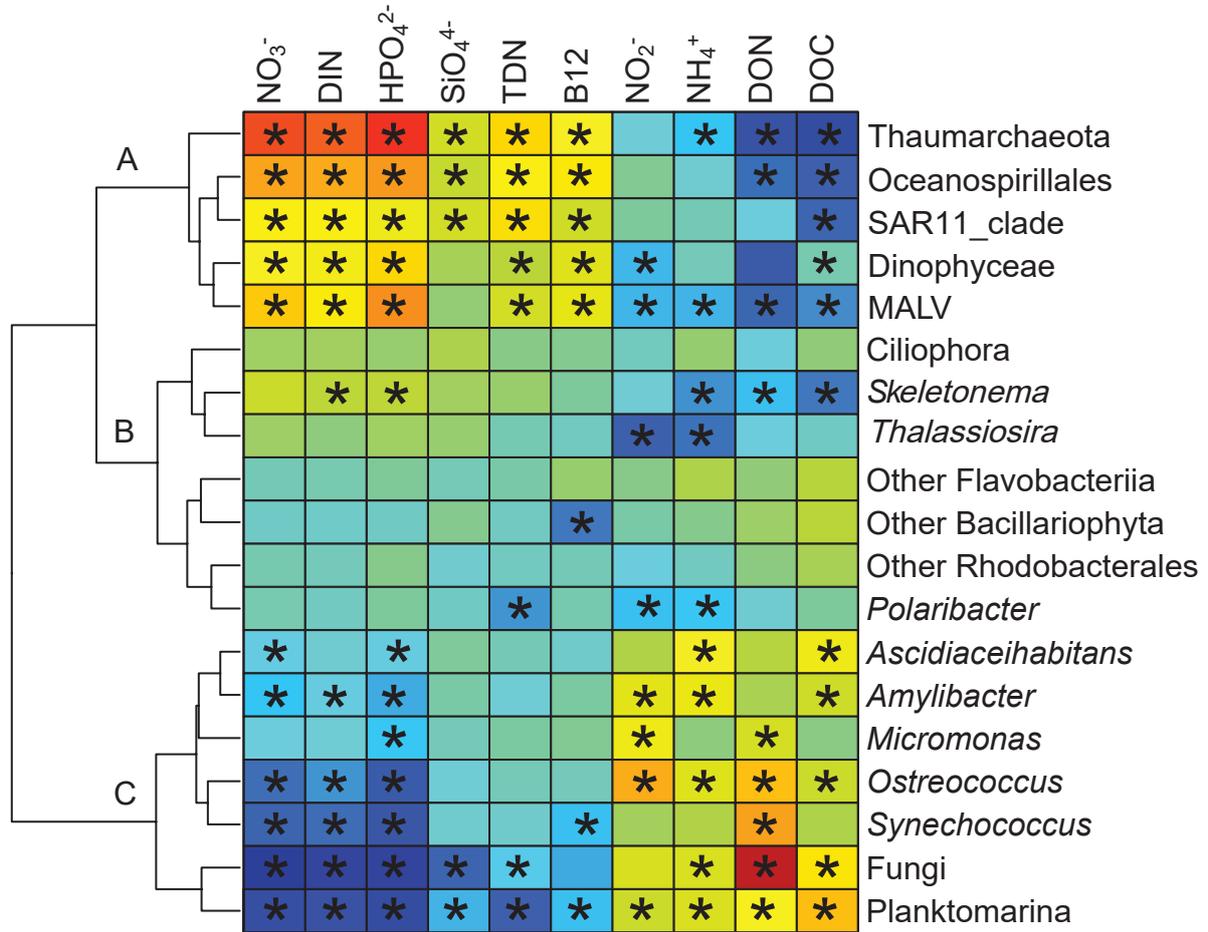


Figure 7



Pearson correlation coefficient

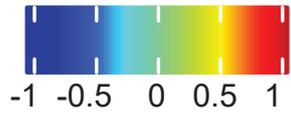
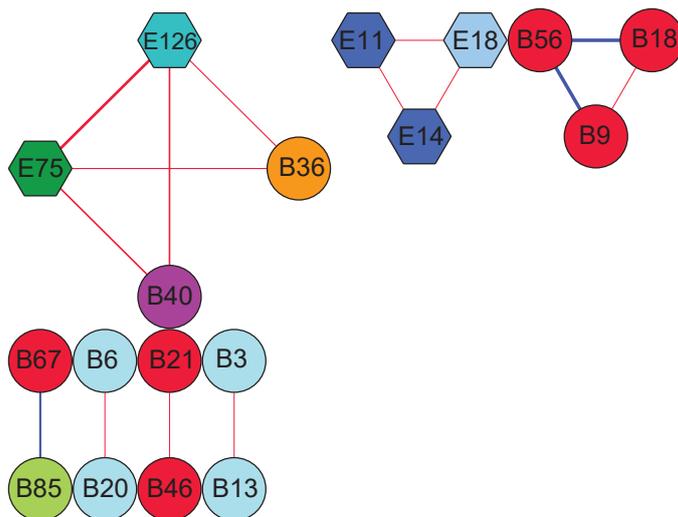
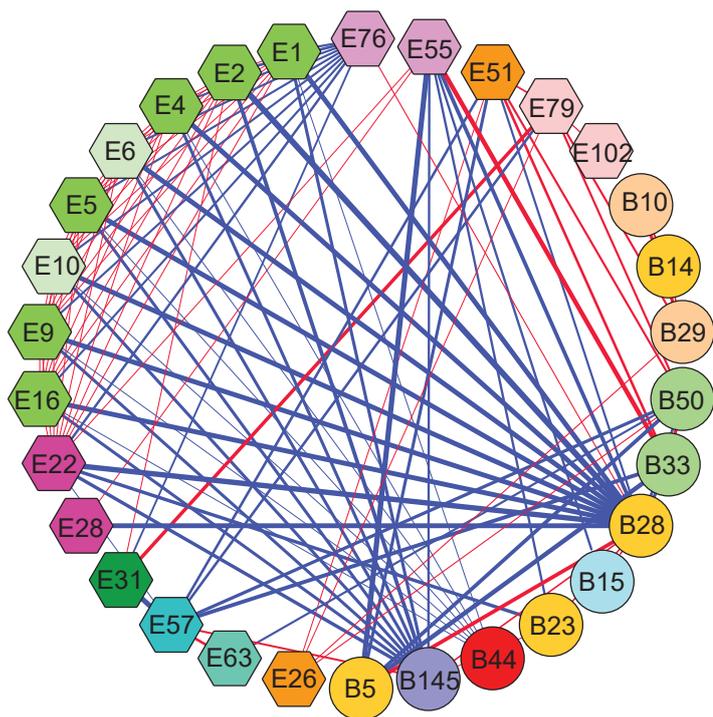
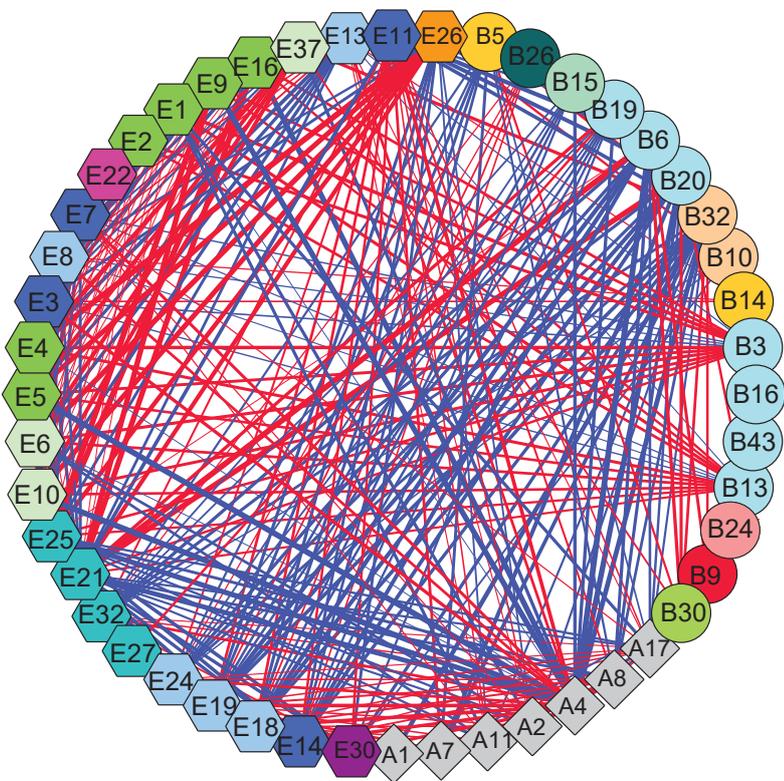


Figure 9

A) UML



B) SSL



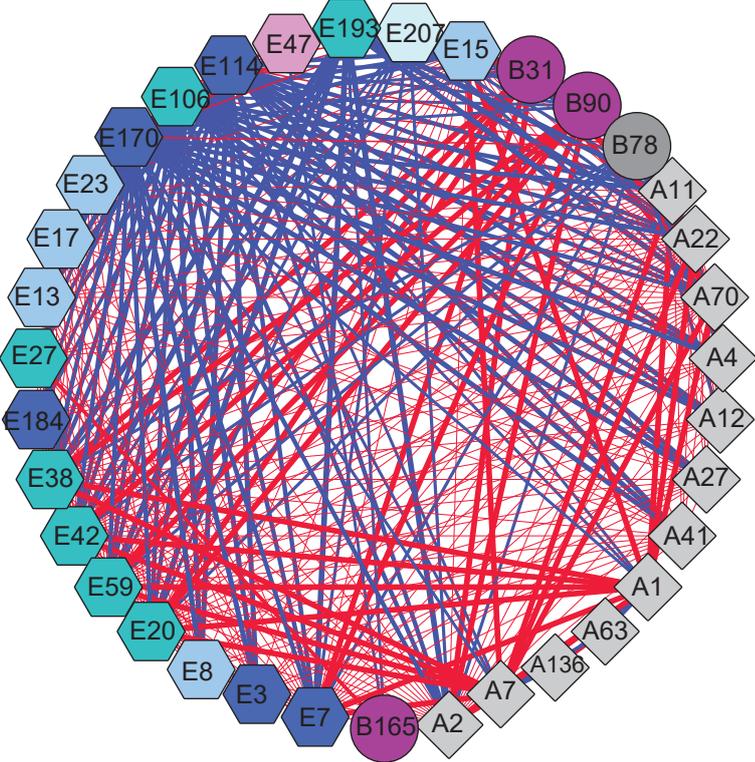
Prokaryotes

- ◇ Thaumarchaeota
- *Loktanella*
- Deltaproteobacteria
- *Ascidiaceihabitants*
- Flavobacteriaceae
- *Tenacibaculum*
- *Amylibacter*
- *Ulvibacter*
- *Synechococcus*
- Oceanospirillales
- Acidimicrobiales
- *Planktomarina*
- Candidatus Pelagibacter

Eukaryotes

- ◇ MALV-I
- ◇ MALV-II
- ◇ Dinophyceae
- ◇ Prasinophyceae
- ◇ *Ostreococcus lucimarinus*
- ◇ Other Chlorophyta
- ◇ *Chaetoceros tenuissimus*
- ◇ *Thalassiosira*
- ◇ *Minidiscus trioculatus*
- ◇ *Skeletonema marinoi*
- ◇ Fungi

C) ENACW



ID	Taxa	ID	Taxa
A1	Thaumarchaeota	E1	<i>Ostreococcus lucimarinus</i>
A11	Thaumarchaeota	E10	Prasinophyceae
A12	Thaumarchaeota	E102	<i>Chaetoceros tenuissimus</i>
A136	Thaumarchaeota	E106	<i>Apicomplexa</i>
A17	Thaumarchaeota	E11	MALV-II
A2	Thaumarchaeota	E114	MALV-II
A22	Thaumarchaeota	E126	Dinophyceae
A27	Thaumarchaeota	E13	MALV-I
A4	Thaumarchaeota	E14	MALV-II
A41	Thaumarchaeota	E15	MALV-I
A63	Thaumarchaeota	E16	<i>Ostreococcus lucimarinus</i>
A7	Thaumarchaeota	E17	MALV-I
A70	Thaumarchaeota	E170	MALV-II
A8	Thaumarchaeota	E18	MALV-I
B10	<i>Ascidiaecihabitans</i>	E184	MALV-II
B13	<i>Amylibacter</i>	E19	MALV-I
B14	<i>Tenacibaculum</i>	E193	<i>Apicomplexa</i>
B145	<i>Loktanella</i>	E2	<i>Ostreococcus lucimarinus</i>
B15	<i>Amylibacter</i>	E20	Dinophyceae
B16	<i>Amylibacter</i>	E207	Filosa-Chlorarachnea
B165	<i>Oceanospirillales</i>	E21	Dinophyceae
B18	<i>Planktomarina</i>	E22	<i>Minidiscus trioculatus</i>
B19	<i>Amylibacter</i>	E23	MALV-I
B20	<i>Amylibacter</i>	E24	MALV-I
B21	<i>Planktomarina</i>	E25	<i>Balechina pachydermata</i>
B23	<i>Tenacibaculum</i>	E26	Exobasidiomycetes
B24	Acidimicrobiales	E27	<i>Gyrodinium fusiforme</i>
B26	<i>Pelagibacter</i>	E28	<i>Minidiscus trioculatus</i>
B28	<i>Tenacibaculum</i>	E3	MALV-II
B29	<i>Ascidiaecihabitans</i>	E30	<i>Skeletonema marinoi</i>
B3	<i>Amylibacter</i>	E31	Pyramimonadales
B30	<i>Ulvibacter</i>	E32	Dinophyceae
B31	<i>Oceanospirillales</i>	E37	Prasinophyceae
B32	<i>Ascidiaecihabitans</i>	E38	<i>Gyrodinium spirale</i>
B33	<i>Synechococcus</i>	E4	<i>Ostreococcus lucimarinus</i>
B36	Flavobacteriaceae	E42	Thoracosphaeraceae
B40	<i>Oceanospirillales</i>	E47	<i>Thalassiosira</i>
B43	<i>Amylibacter</i>	E5	<i>Ostreococcus lucimarinus</i>
B44	<i>Planktomarina</i>	E51	Tremellomycetes
B46	<i>Planktomarina</i>	E55	<i>Thalassiosira anguste-lineata</i>
B5	<i>Tenacibaculum</i>	E57	<i>Prorocentrum</i>
B50	<i>Synechococcus</i>	E59	Thoracosphaeraceae
B56	<i>Planktomarina</i>	E6	Prasinophyceae
B6	<i>Amylibacter</i>	E63	Prorocentrum
B67	<i>Planktomarina</i>	E7	MALV-II
B78	Deltaproteobacteria	E75	<i>Botryococcus braunii</i>
B85	<i>Ulvibacter</i>	E76	<i>Thalassiosira pseudonana</i>
B9	<i>Planktomarina</i>	E79	<i>Chaetoceros tenuissimus</i>
B90	<i>Oceanospirillales</i>	E8	MALV-I
		E9	<i>Ostreococcus lucimarinus</i>

