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Dominik Forster, Micah Dunthorn, Frédéric Mahé, John R. Dolan, Stéphane Audic, David Bass, Lucie Bittner, Christophe Boutte, Richard Christen, Jean-Michel Claverie, et al.

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## Benthic protists: the under-charted majority

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1  
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3 52 **Abstract**  
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5 53 Marine protist diversity inventories have largely focused on planktonic  
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7 54 environments, while benthic protists have received relatively little attention. We  
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9 55 therefore hypothesize that current diversity surveys have only skimmed the surface  
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11 56 of protist diversity in marine sediments, which may harbour greater diversity than  
12  
13 57 planktonic environments. We tested this by analyzing sequences of the hypervariable  
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15 58 V4 18S rRNA from benthic and planktonic protist communities sampled in European  
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17 59 coastal regions. Despite a similar number of OTUs in both realms, richness  
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19 60 estimations indicated that we recovered at least 70% of the diversity in planktonic  
20  
21 61 protist communities, but only 33% in benthic communities. There was also little  
22  
23 62 overlap of OTUs between planktonic and benthic communities, as well as between  
24  
25 63 separate benthic communities. We argue that these patterns reflect the heterogeneity  
26  
27 64 and diversity of benthic habitats. A comparison of all OTUs against the Protist  
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29 65 Ribosomal Reference database showed that a higher proportion of benthic than  
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31 66 planktonic protist diversity is missing from public databases; similar results were  
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33 67 obtained by comparing all OTUs against environmental references from NCBI's Short  
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35 68 Read Archive. We suggest that the benthic realm may therefore be the world's  
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37 69 largest reservoir of marine protist diversity, with most taxa at present undescribed.  
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## 70 Introduction

71 Molecular studies of marine plankton have uncovered an enormous diversity  
72 of protists, many of which could not be assigned to any accession in taxonomic  
73 reference databases (e.g., de Vargas *et al.* 2015). Planktonic studies have thus  
74 found a very large pool of unknown marine protist species. However, initial molecular  
75 studies unveiled highly diverse protist communities from marine benthic habitats  
76 which exhibit key ecosystem functions and whose diversity may even exceed that of  
77 planktonic protists. Most of these benthic studies were conducted in hydrothermal  
78 vent systems (Edgcomb *et al.* 2002; López-García *et al.* 2003; López-García,  
79 Vereshchaka and Moreira 2007) and anoxic sediments (Dawson and Pace 2002;  
80 Stoeck and Epstein 2003; Takishita *et al.* 2005), both of which environments  
81 emerged as hotspots of protist biodiversity. More recently, similarly high diversity was  
82 reported from deep-sea and coastal sediments, with many genetic signatures only  
83 distantly related to taxonomically described protists (Scheckenbach *et al.* 2010;  
84 Pawlowski *et al.* 2011; Bik *et al.* 2012; Gong *et al.* 2015). At least for the three major  
85 protist lineages of ciliates, diatoms and foraminifera, the existing species inventories  
86 of morphologically delineated species support a higher and distinctively different  
87 diversity of benthic compared to planktonic species (Patterson, Larsen and Corliss  
88 1989; Mann and Evans 2007; Pawlowski, Holzmann and Tyszka 2013).

89 Marine benthic studies, though, remain scarce and limited compared to the  
90 considerably larger amount of planktonic studies. Based on the sparse and locally  
91 restricted amount of data, no consensus has been reached on the extent of microbial  
92 eukaryotic diversity in marine sediments (Epstein and López-García 2007; Fierer  
93 2008; Bik *et al.* 2012). Methodological difficulties are a partial explanation for this  
94 undersampling. The clean extraction of nucleic acids from environmental marine  
95 sediment samples is challenging (Hurt *et al.* 2001) and extensive amounts of

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3 96 extracellular DNA may severely bias the environmental sequencing studies  
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5 97 (Dell'Anno and Danovaro 2005). Furthermore, specific techniques and expensive  
6  
7 98 equipment are required to access these physically remote environments (Orcutt *et al.*  
8  
9 99 2011). Published benthic studies of protists are thus not only restricted in geographic  
10  
11 100 scope, but also in their comparisons to the overlying planktonic protists. Despite our  
12  
13 101 limited knowledge of benthic protists, there is strong agreement among microbial  
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15 102 ecologists that marine coastal sediments play a pivotal role for the diversity and  
16  
17 103 dynamics of overlying plankton communities by acting as seedbanks (Marcus and  
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19 104 Boreo 1998). The benthic species reservoir consists of both truly active benthic  
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21 105 species and resting stages of dormant planktonic species. Most of the latter occur in  
22  
23 106 low abundances, but blooms can be initiated in response to environmental changes  
24  
25 107 (Marcus and Boreo 1998). Furthermore, studies on microfossil protists have  
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27 108 suggested that several planktonic lineages have evolved from benthic ancestors,  
28  
29 109 which have colonized the pelagic realm on different occasions (Leckie 2009).

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34 110 In this study, we used previously published data from Massana *et al.* (2015)  
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36 111 that surveyed protist diversity in European coastal waters and sediments from  
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38 112 Norway to Bulgaria using the V4 region of the 18S rRNA. Massana *et al.* (2015)  
39  
40 113 provided a general taxonomic overview of planktonic and benthic protists, with  
41  
42 114 particular attention on examining differences in size-fractionated planktonic protist  
43  
44 115 communities and comparing results obtained from DNA and RNA templates. Building  
45  
46 116 upon this initial study, here we focus on a more detailed comparison of benthic and  
47  
48 117 planktonic protist diversity, with a special emphasis on the richness and phylogenetic  
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50 118 novelty contained in marine benthic protist assemblages, two topics that were not  
51  
52 119 covered by Massana *et al.* (2015). Our results not only support previous notions of  
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54 120 more diverse benthic than planktonic protist communities, but also present clear  
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3 121 indications of a higher degree of novelty in genetic signatures within benthic  
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5 122 communities.

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## 10 11 12 125 **Methods**

### 13 14 126 *Sampling, pyrosequencing and data processing*

15  
16 127 In the framework of the BioMarKs project (Dunthorn *et al.* 2014a; Logares *et*  
17  
18 128 *al.* 2014; Massana *et al.* 2015), water samples from the surface and deep chlorophyll  
19  
20 129 maximum (DCM) layer, and sediment samples were collected from six different  
21  
22 130 European coastal sites including the Skagerrak, the English Channel, the Atlantic  
23  
24 131 Ocean, the Mediterranean Sea and the Black Sea (Table 1). For details on sampling  
25  
26 132 protocols, nucleic acid extraction, 454-pyrosequencing of the hypervariable V4 18S  
27  
28 133 rDNA region and data processing see Massana *et al.* (2015). Briefly, RNA from  
29  
30 134 benthic samples was extracted from 2.5 g of surficial sediment using the Power Soil  
31  
32 135 RNA kit (MoBio, Carlsbad, United States). RNA from planktonic samples was  
33  
34 136 extracted with the NucleoSpin RNA kit (Macherey-Nagel, Düren, Germany) from  
35  
36 137 filters of DCM and surface water samples collected with Niskin bottles. Both  
37  
38 138 extraction kits are specifically optimized to gain high RNA yields from the respective  
39  
40 139 samples and are routinely used in environmental high-throughput sequencing (HTS)  
41  
42 140 studies. Because of the difficulties in RNA extractions from sediment samples (Hurt  
43  
44 141 *et al.* 2001), using an optimized kit for the recovery of nucleic acids from benthic  
45  
46 142 samples was especially important. By targeting environmental (e)RNA rather than  
47  
48 143 environmental (e)DNA we minimized potential biases induced by accumulation and  
49  
50 144 preservation of extracellular eDNA in sediments (Dell'Anno and Danovaro 2005;  
51  
52 145 Stoeck *et al.* 2007). The effect of extracellular eDNA is less critical when only water  
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54 146 samples are analyzed (Logares *et al.* 2014), but relevant for a comparison of water  
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3 147 with sediment samples. Extracted RNA was then transcribed to cDNA for further  
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5 148 processing.

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7 149 Targeted amplification of the hypervariable V4 18S rDNA region was  
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9 150 performed with the eukaryotic primer pair TAREuk454FWD1 and TAREukREV3  
10  
11 151 (Stoeck *et al.* 2010). This primer pair, though, does not cover Foraminifera and  
12  
13 152 several excavate lineages that are important contributors to benthic protist  
14  
15 153 communities but whose taxonomy is not very well delineated by the V4 region  
16  
17 154 (Pawlowski *et al.* 2011; Lax and Simpson 2013). **In contrast to other barcode genes,**  
18  
19 155 **the V4 region does allow for better comparisons with published full-length 18S rRNA**  
20  
21 156 **Sanger sequencing studies and has a better database coverage for taxonomic**  
22  
23 157 **assignment** (Stoeck *et al.* 2010; Dunthorn *et al.* 2012). Pyrosequencing of the  
24  
25 158 amplified PCR product was conducted on a 454 GS FLX Titanium system (454 Life  
26  
27 159 Sciences, USA). Resulting 454 reads were subject of a strict quality filtering,  
28  
29 160 including two steps of chimera checking in UCHIME (Edgar *et al.* 2011) and  
30  
31 161 ChimeraSlayer (Haas *et al.* 2011). All quality sequences were then clustered into  
32  
33 162 OTUs using USEARCH (Edgar 2010) on a 97% sequence similarity value. In a  
34  
35 163 second step of quality filtering, one representative of each OTU was subject to a  
36  
37 164 BLASTn analysis against NCBI's nucleotide database release 183.0. All OTUs  
38  
39 165 assigned to Bacteria, Archaea, Metazoa, Embryophyta and OTUs with less than 80%  
40  
41 166 similarity to database entries were removed from the dataset. The final dataset  
42  
43 167 included 430 894 V4 18S RNA sequences, which clustered into 12 438 distinct  
44  
45 168 OTUs. The complete BioMarKs sequencing dataset is available at the European  
46  
47 169 Nucleotide Archive under the study accession number PRJEB9133.  
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56 171 *Taxonomic assignment of OTUs*  
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3 172 To search for the best hit of each OTU to a described organism, we conducted  
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5 173 a local BLASTn analysis (using default settings) against the protist reference  
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7 174 database PR<sup>2</sup> (Guillou *et al.* 2012). Additionally, we compared our environmental  
8  
9 175 data against reference data of previous environmental HTS diversity surveys of  
10  
11 176 protists using a similar BLASTn analysis. To build this environmental reference  
12  
13 177 database, we manually screened NCBI's Short Read Archive (SRA) for studies that  
14  
15 178 at least partially included protist data of the eukaryotic 18S gene (according to the  
16  
17 179 experiment's descriptions in the SRA). After downloading the respective data, we  
18  
19 180 removed all references shorter than 100 bp. The final customized SRA reference  
20  
21 181 database consisted of 11 708 385 references from 167 datasets (Supplemental  
22  
23 182 Table S1).  
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#### 31 184 *Statistical analyses and diversity measures*

32 185 All statistical and diversity analyses were performed in R Studio (version  
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34 186 2.15.1, <http://r-project.org>). Following recommendations of previous studies  
35  
36 187 (Dunthorn *et al.* 2014b) we relied on incidence-based rather than abundance-based  
37  
38 188 data to avoid biases induced by uneven gene copy numbers among different protist  
39  
40 189 taxa. Species richness was estimated with the incidence-based coverage estimator  
41  
42 190 (ICE) as implemented in the 'fossil' package (Vavrek 2011). ICE appropriately  
43  
44 191 estimates asymptotic species richness from datasets containing many rare species  
45  
46 192 (Colwell *et al.* 2012), which we expect in benthic protist communities. Additional  
47  
48 193 species richness estimations in CatchAll (Bunge *et al.* 2012) are provided as  
49  
50 194 supplemental material (Supplemental Fig. S2). Non-metric multidimensional scaling  
51  
52 195 (NMDS) using (binary-) Jaccard distances as a measure of  $\beta$ -diversity was performed  
53  
54 196 with the 'vegan' package (Oksanen *et al.* 2015). Non-parametrical, two-sided  
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56 197 Kolmogorov-Smirnov tests (KS-tests) using 1000 bootstrap replicates were used to  
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3 198 assess the significance of sequence divergence distribution from planktonic and  
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5 199 benthic datasets in the package 'Matching' (Sekhon 2011).  
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## 10 201 **Results**

### 11 202 *Comparison of planktonic and benthic protist diversity*

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14 203 The number of quality filtered sequences among the three habitats differed:  
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16 204 206 602 from the surface, 184 192 from the DCM, and 40 100 from the sediment  
17  
18 205 (Table 1). Despite these differences, the sequences clustered into similar numbers of  
19  
20 206 OTUs: 5747 in the surface, 5685 in the DCM, and 5616 in the sediment. However,  
21  
22 207 ICE-based richness estimates predicted a difference in the number of total OTUs  
23  
24 208 between the plankton and the sediment: 7763 from the surface, 8140 from the DCM,  
25  
26 209 and 16 652 from the sediment (Fig. 1A). The proportion of OTUs thus not detected  
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28 210 through our sequencing effort was 26% in surface, 30.2% in the DCM, and 66.3% in  
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30 211 the sediment. Richness estimations based on abundance data revealed similar  
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32 212 trends but predicted even more undetected OTUs (Supplemental Fig. S2). The  
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34 213 observed trends on OTU richness were further congruent with rarefaction results of  
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36 214 sequencing data, which were closer to saturation for water column than for sediment  
37  
38 215 samples (Supplemental Fig. S3). Differences in community composition between  
39  
40 216 plankton and benthos were first shown by the number of shared and exclusive OTUs  
41  
42 217 (Fig. 1B). Of 7729 non-singleton OTUs observed in total, only 708 (9.2%) were  
43  
44 218 shared among all three habitats. This low number is, in part, explained by the low  
45  
46 219 number of co-occurring OTUs in plankton and benthos: the plankton had 4368 non-  
47  
48 220 singleton OTUs not found in the benthos, of which 701 were exclusively found in the  
49  
50 221 surface and 762 were exclusively found in the DCM; the benthos had 2364 non-  
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52 222 singleton OTUs not found in the plankton.  
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3 223 NMDS analysis further demonstrated the partitioning of the observed diversity  
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5 224 patterns in plankton and benthos (Fig. 2). Since differentiation in size fractions was  
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7 225 only possible for planktonic samples and beyond the scope of this work, we pooled  
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9 226 planktonic data of different size fractions from the same sampling events. In this  
10  
11 227 analysis, surface and DCM samples clustered closely together, indicating a higher  
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13 228 similarity in community composition among plankton samples than among benthos  
14  
15 229 samples. Sediment samples were separated from the water communities in the  
16  
17 230 analysis. In contrast to the narrow cluster of surface and DCM samples, the sediment  
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19 231 samples were more widely distributed, indicating high dissimilarity in community  
20  
21 232 composition between individual samples. This also applied to sediment samples from  
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23 233 the same sampling site taken in consecutive years, as shown by the large distances  
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25 234 between both samples from Naples and both samples from Oslo.  
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### 236 *Taxonomic affiliation of plankton and benthos OTUs*

237 Most OTUs in each habitat were assigned to the groups of Alveolata,  
238 Stramenopiles and Rhizaria (Fig. 3). While the Alveolata dominated the planktonic  
239 communities (3281 OTUs in surface, 3638 OTUs in DCM samples), rhizarian OTUs  
240 of the phylum Cercozoa dominated the benthic communities (1566 of 1622 benthic  
241 rhizarian OTUs). Approximately the same proportion of OTUs was assigned to  
242 Stramenopiles in all three habitats. The number of OTUs from the Amoebozoa,  
243 Apusozoa, Opisthokonta (predominantly fungi), and Picozoa were notably higher in  
244 the benthos than in the plankton. In contrast, Archaeplastida and Hacrobia were  
245 more diverse in planktonic (238 and 309 OTUs in surface samples; 175 and 264  
246 OTUs in DCM samples) than in benthic communities (50 and 179 OTUs).

247 On a lower taxonomic level, we observed a higher OTU richness in benthic  
248 samples for 10 of the 19 most abundant groups (Fig. 4). In seven of these groups,

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3 249 the OTUs detected in the benthos accounted for more than 70% of the OTUs. These  
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5 250 groups comprised the Apicomplexa (Alveolata), Apusomonadidae (Incertae Sedis),  
6  
7 251 Centrohelida (Hacrobia), Discosea and Tubulinea (both Amoebozoa), as well as the  
8  
9 252 previously mentioned Cercozoa and Fungi. Further groups mainly detected in the  
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11 253 benthos included Ciliophora (Alveolata), Bacilliarophyceae and Labyrinthulomycetes  
12  
13 254 (both Stramenopiles). Dinoflagellates, however, as the taxonomic group with highest  
14  
15 255 OTU richness in total, were predominantly detected in planktonic samples.  
16  
17 256 Acantharea (Rhizaria), MAST (Stramenopiles) and MALV (Alveolata) are three other  
18  
19 257 taxonomic groups with heterotrophic members that were distinctively more often  
20  
21 258 detected in planktonic than in benthic samples. Similar observations were made  
22  
23 259 among the predominantly phototrophic groups Chlorophyta (Archaeplastida),  
24  
25 260 Chrysophyceae and Dictyochophyceae (both Stramenopiles), and Haptophyta  
26  
27 261 (Hacrobia). Supplemental figures S4 and S5 provide a closer look on the occurrence  
28  
29 262 and distribution of phototrophic taxa and show that Cryptophyta and Rhodophyta  
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31 263 were also mostly found in planktonic samples, while more diatoms were found in the  
32  
33 264 benthos (677 OTUs) than in the plankton (445 OTUs).  
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#### 41 266 *Database coverage and genetic divergence of plankton and benthos OTUs*

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43 267 To assess how well the observed diversity of OTUs matched previously  
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45 268 collected data, we calculated their degree of genetic similarity to reference  
46  
47 269 sequences of the taxonomically curated PR<sup>2</sup> database and to environmental  
48  
49 270 reference sequences of earlier protist diversity inventories deposited in NCBI's SRA  
50  
51 271 (Fig. 5). In both BLAST analyses, the novelty profile was much higher for benthic  
52  
53 272 OTUs, while surface and DCM OTUs exhibited an almost identical profile. Moreover,  
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55 273 the genetic similarity of BioMarKs OTUs to PR<sup>2</sup> references (Fig. 5A) was significantly  
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57 274 lower ( $p < 0.001$ ) than to environmental references of the SRA database (Fig. 5B).  
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3 275 Considering that 71.8% of the planktonic OTUs in our study can be assigned on a  
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5 276 97%-sequence similarity value to references in PR<sup>2</sup>, this database misses 28.2% of  
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7 277 the potentially detectable plankton species (conservative estimate, see discussion).  
8  
9 278 Among benthic protist communities 74.4% of the OTUs did not retrieve a  
10  
11 279 taxonomically assigned hit in PR<sup>2</sup> at the same threshold of 97% similarity. Regarding  
12  
13 280 the SRA BLAST results, 78.6% of the planktonic OTUs in our study (n=8988 OTUs)  
14  
15 281 were at least 97% similar to previously deposited environmental references,  
16  
17 282 compared to only 42.7% of the OTUs from benthic samples (n=2400 OTUs). These  
18  
19 283 numbers illustrate that the vast majority of planktonic OTUs had already been  
20  
21 284 detected in previous environmental diversity surveys. This, however, was not the  
22  
23 285 case for benthic OTUs. Thus, BioMarks benthos analyses contributed a high  
24  
25 286 proportion of novel OTUs to the environmental reference database.  
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29  
30 287 On closer examination of the PR<sup>2</sup> BLAST results, the mean sequence  
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32 288 divergence of OTUs detected in surface and DCM samples from references of the  
33  
34 289 taxonomic reference database was 2.6% (Fig. 6). By contrast, the mean sequence  
35  
36 290 divergence of OTUs from sediment samples to PR<sup>2</sup> accessions was 6.6%, indicating  
37  
38 291 that the benthic compartment contains protist species more distantly related to  
39  
40 292 previously deposited taxa than the planktonic compartment. Specifically among the  
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42 293 Alveolata, Hacrobia, Opisthokonta, Rhizaria and Stramenopiles, the difference in  
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44 294 divergence between plankton and benthos was statistically significant ( $p < 0.001$ ). For  
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46 295 example, while the mean sequence divergence of OTUs assigned to Rhizaria from  
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48 296 PR<sup>2</sup> references was 3.5% in both the surface and DCM, the averaged divergence  
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50 297 was 8.2% in the sediment.  
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## 58 300 Discussion

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3 301 *High  $\alpha$ - and  $\beta$ -diversity shapes coastal benthic protist communities*

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5 302 The  $\alpha$ - and  $\beta$ -diversity patterns (Figs. 1 and 2) of protists along the European  
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7 303 coastline support previous notions of highly diverse protist communities from different  
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9 304 benthic habitats in the world's oceans (Dawson and Pace 2002; Edgcomb *et al.*  
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11 305 2002; López-García *et al.* 2003; Stoeck and Epstein 2003; Takishita *et al.* 2005;  
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13 306 López-García, Vereshchaka and Moreira 2007; Scheckenbach *et al.* 2010;  
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16 307 Pawlowski *et al.* 2011; Bik *et al.* 2012; Gong *et al.* 2015). A direct comparison of OTU  
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18 308 numbers to many of these initial studies is difficult, since most relied on clone library  
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20 309 approaches (Dawson and Pace 2002; Edgcomb *et al.* 2002; López-García *et al.*  
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22 310 2003; Stoeck and Epstein 2003; Takishita *et al.* 2005; López-García, Vereshchaka  
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24 311 and Moreira 2007; Scheckenbach *et al.* 2010) that produced fewer genetic signatures  
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26 312 than the current pyrosequencing approach. Consequently, Scheckenbach *et al.*  
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28 313 (2010) estimated a mean OTU richness of 489 in benthic biodiversity hotspots, such  
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30 314 as hydrothermal vents, and 1240 in abyssal sediments. These numbers would be  
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32 315 well below the mean estimated species richness of 2776 OTUs in BioMarKs  
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34 316 sediment samples. Other studies relying on 454 pyrosequencing detected similarly  
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36 317 high benthic diversity (Pawlowski *et al.* 2011; Bik *et al.* 2012; Gong *et al.* 2015). One  
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38 318 of these surveys observed between 393 and 1049 protist OTUs and estimated  
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40 319 between 421 and 1051 OTUs in coastal sediment sites of the Yellow Sea (Gong *et*  
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42 320 *al.* 2015). OTU richness in European coastal sediment samples was higher, with  
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44 321 observed protist OTU numbers ranging from 493 to 2499 and estimated OTU  
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46 322 numbers ranging from 721 to 3573. The BioMarKs numbers are closer to those  
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48 323 observed in Arctic and Southern Ocean deep-sea samples (between 942 and 1756  
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50 324 observed OTUs) (Pawlowski *et al.* 2011).

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56 325 In contrast to most previous studies, our data allowed us to analyze benthic  
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58 326 communities in the context of planktonic communities from overlying water masses of

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3 327 the euphotic zone. Such data are scarcely available for protists and usually limited to  
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5 328 specific lineages. One example is a Sanger sequencing study that focused on ciliates  
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7 329 (Doherty *et al.* 2010), which reported little overlap between genetic signatures of  
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9 330 benthic and planktonic communities in the Gulf of Maine and Long Island Sound.  
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11 331 This finding corroborates our observations on whole protist communities in European  
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13 332 coastal habitats (Fig. 1B). More data exists, however, for benthic-planktonic  
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15 333 community comparisons of marine bacteria. Zinger *et al.* (2011) showed that  
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17 334 bacterial OTU richness and  $\beta$ -diversity was much higher in coastal sediments than in  
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19 335 coastal surface waters. Similar results were obtained in an arctic fjord HTS survey  
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21 336 (Teske *et al.* 2011). These patterns nicely reflect those obtained in our study on  
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23 337 protists.  
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27 338 Building upon the Massana *et al.* (2015) study, we targeted the question of the  
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29 339 magnitude of benthic compared to planktonic diversity by contrasting the degree of  
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31 340 observed richness with the degree of estimated richness (Fig. 1A). In the same  
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33 341 context, we highlighted how much of this observed diversity likely represented novel  
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35 342 diversity (Figs. 5 and 6), a previously unexamined topic. Furthermore, we contrasted  
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37 343 the  $\beta$ -diversity among benthic and planktonic communities (Fig. 2), illustrating small  
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39 344 overlap between benthic and planktonic diversity, but also among benthic  
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41 345 communities in particular. Given that biodiversity is considered to be higher in coastal  
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43 346 than in open ocean habitats (Gray 1997; Zinger *et al.* 2011), the BioMarkS data  
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45 347 suggest that marine coastal sediments may be the world's largest reservoir of protist  
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47 348 diversity, much of which is still undetected and most of which is still undescribed in  
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49 349 public databases.  
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54 350 One major factor that might promote high diversity in benthic protist  
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56 351 communities is a large number of distinct benthic habitats due to horizontal and  
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58 352 vertical gradients in both physical and chemical characteristics. Even at microscale,  
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3 353 habitat heterogeneity in marine sediments reflects gradients in grain-sizes, oxygen  
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5 354 concentration or organic matter content (Pedersen, Smets and Dechesne 2015). The  
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7 355 diversity of physico-chemical microhabitats likely promotes the existence of highly  
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9 356 specialized organisms and is probably an important driver for species-richness  
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11 357 patterns (Hortal *et al.* 2009). We thus argue that our findings of high protist richness  
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13 358 and heterogeneity at comparably small geographical scales represents a general  
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15 359 trend in benthic diversity, which is well supported by previous findings, *e.g.* in the  
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17 360 Yellow Sea, where high  $\alpha$ - and  $\beta$ -diversity patterns in coastal marine sediments were  
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19 361 unveiled (Gong *et al.* 2015). To further investigate the effect of niche partitioning,  
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21 362 species-area relationships and distance-decay relationships on small spatial and  
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23 363 temporal scales could be analyzed for planktonic and benthic protists at the same  
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25 364 locales (Franzén, Schweiger and Betzholtz 2012; Zinger, Boetius and Ramette  
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27 365 2014). In addition to habitat heterogeneity, geological structures at the seafloor may  
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29 366 act as biogeographical barriers. Even locally, this results in a spatial separation of  
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31 367 protist communities (Scheckenbach *et al.* 2010). Both factors, niche partitioning and  
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33 368 allopatric speciation processes may work *in concerto* to generate and maintain a high  
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35 369 diversity of protists in sediments. In direct comparison, environmental heterogeneity  
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37 370 is surely much more pronounced in the benthos (Orcutt *et al.* 2011) than in the  
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39 371 plankton, although the pelagic realm may create patchy distributions of protists as  
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41 372 well (Menden-Deuer and Fredrickson 2010; Dolan and Stoeck 2011).

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43 373 Additional reasons for diverging protist communities between individual  
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45 374 benthic sites (Fig. 2) may also be of technical nature: we found that all sediment  
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47 375 samples were severely undersampled as a result of their high diversity  
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49 376 (Supplemental Fig. S3). Because of this undersampling, community divergence  
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51 377 among different sediment samples may be artificially inflated. It is, however,  
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53 378 reasonable to assume that with increasing sampling effort the proportion of OTUs  
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3 379 that are shared between two samples and the proportion of OTUs that are unique to  
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5 380 each of these samples would remain similar. We therefore argue that the observed  
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7 381 high Jaccard-distance between the sediment protist communities is more due to true  
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9 382 (biological) heterogeneity in species memberships rather than to (technical)  
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11 383 undersampling.  
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### 16 385 *Different protist taxon groups thrive in plankton and benthos*

18 386 Benthic protist diversity uncovered by environmental HTS is comprised of i)  
19 387 resident species of truly benthic origin; ii) transient species, which spend at least part  
20 388 of their life cycle living actively in or on sediments; iii) non-resident species of  
21 389 planktonic origin present as inactive resting stages, or as recently settled cells. OTUs  
22 390 of resident species clearly dominated the benthic protist communities in our analyses  
23 391 (Fig. 1B). Though transient species are commonly found among different taxonomic  
24 392 groups (Garstecki *et al.* 2000), we found only little overlap between benthic and  
25 393 planktonic OTUs (Figs. 1B and 2). A notable fraction of this overlap was related to  
26 394 diatoms, Chrysophyceae and Chlorophyta (Supplemental Fig. S4). Since all of these  
27 395 groups include species of planktonic origin which are able to form benthic resting  
28 396 stages (McQuoid and Hobson 1996; Duff, Zeeb and Smol 2013), we cannot rule out  
29 397 that at least some of the phototrophic OTUs in sediments could correspond to  
30 398 phytoplankton cysts or cells that had sunk to the sea floor shortly before sampling.  
31 399 Genetic signatures of the planktonic diatom family Leptocylindraceae in sediment  
32 400 samples represent such a peculiar case (Nanjappa *et al.* 2014). However, particularly  
33 401 among phototrophic protists, diatoms were more often detected in the benthos than  
34 402 in the plankton. Indeed this group is known to harbour a larger diversity of benthic  
35 403 than planktonic species, especially in shallow coastal waters (Mann and Evans  
36 404 2007). Regarding the small amount of shared OTUs between benthos and plankton

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3 405 in general, we argue that genetic signatures of dead or sinking organisms or  
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5 406 dissolved RNA were considerably limited.  
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7 407 A striking difference in the community composition between planktonic and  
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9 408 benthic protists at a higher taxonomic level is the dominance of numerous previously  
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11 409 undescribed Rhizaria in coastal sediments. More than 95% of these rhizarian OTUs  
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13 410 were assigned to the phylum Cercozoa (Supplemental Fig. S6), which have emerged  
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15 411 as an abundant and diverse lineage in several other benthic protist diversity studies  
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17 412 (summarized by Epstein and López-García, 2008). This phylum comprises a large  
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19 413 number of gliding zooflagellates, filose and often large reticulose amoebae, which are  
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21 414 well adapted to a psammophilic lifestyle (Bass *et al.* 2009; Howe *et al.* 2011), but  
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23 415 also occur as parasites of invertebrates, algae and stramenopiles with benthos-  
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25 416 associated stages of their lifecycles (Hartikainen *et al.* 2014). Recent studies on  
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27 417 cercozoans could link many previously uncultured environmental sequences to novel  
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29 418 benthic cercozoans (Chantangsi and Leander 2010; Howe *et al.* 2011; Berney *et al.*  
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31 419 2013). In addition, genetically divergent benthic cercozoans, both free-living and  
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33 420 parasitic, are common and diverse but rarely detected in eukaryote-wide  
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35 421 environmental surveys, *e.g.* the amoeboid-flagellate *Reticulamoeba* (Bass *et al.* 2012)  
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37 422 or the parasitic *Ascetospora* (Hartikainen *et al.* 2014). These examples further  
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39 423 emphasize the importance of this phylum in the marine benthos.  
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45 424 Among the most abundant taxonomic groups we observed a trend of  
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47 425 distinctively higher OTU richness in benthic than in planktonic communities (Fig. 4).  
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49 426 Beside Cercozoa, this trend was especially prominent for Discosea and Tubulinea,  
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51 427 two groups of rhizopod Amoebozoa, which are common inhabitants of coastal  
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53 428 benthic ecosystems (Garstecki and Arndt 2000). Likewise, the detection of a high  
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55 429 proportion of saprotrophic fungi that contribute to detritus processing in marine  
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57 430 sediments is not surprising (Richards *et al.* 2012). Higher OTU richness in benthic  
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3 431 samples, though less pronounced, was also observed for ciliates. This result is  
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5 432 supported by previous morphological and molecular studies that reported higher  
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7 433 benthic than planktonic ciliate diversity (Patterson, Larsen and Corliss 1989; Doherty  
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9 434 *et al.* 2010). As discussed above, the situation was similar for diatoms.

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11 435 We detected an inverse trend in diversity among the Acantharea,  
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13 436 Dinoflagellata and MALV, all of which are commonly observed in planktonic  
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15 437 communities (Guillou *et al.* 2008; Jeong *et al.* 2010; Massana 2011; Decelle *et al.*  
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17 438 2013). Acantharea and dinoflagellates are mostly planktonic organisms and both  
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19 439 groups comprise mixotrophs or members with phototrophic symbionts (Gilg *et al.*  
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21 440 2010; Hansen 2010). MALV, on the other hand, can be found as parasites of ciliates,  
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23 441 dinoflagellates, radiolarians and fish eggs (Massana 2011) and are known to form  
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25 442 planktonic lifecycles (Guillou *et al.* 2008). Unicellular Archaeplastida (Chlorophyta)  
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27 443 and Hacrobia (Haptophyta) were also largely missing from benthos samples but  
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29 444 occurred in plankton samples. These groups mainly consist of autotrophic organisms  
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31 445 performing carbon fixation (Vaulot *et al.* 2008; Not *et al.* 2012) and are major  
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33 446 contributors to the pico- and nanoplankton diversity and biomass across the world's  
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35 447 oceans (Bittner *et al.* 2013; Egge *et al.* 2015).

#### 448 449 *High degree of genetic novelty among benthic protist assemblages*

450 The genetic divergence of benthic OTUs from reference sequences described  
451 the marine coastal benthic realm as a habitat having a vast majority of protist  
452 diversity still uncharted. This applied to both BLAST analyses, against the curated  
453 PR<sup>2</sup> reference database and the environmental genetic signatures of the SRA  
454 database. Thereby, the mean sequence similarity to taxonomic references (93.4%,  
455 Fig. 5A) and to environmental references (95.4%, Fig. 5B) was higher than reported  
456 from abyssal sediment communities of protists (87% similarity to taxonomic

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3 457 references, 89% to environmental references) (Scheckenbach *et al.* 2010). Recent  
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5 458 advances in sequencing technologies enable the detection and assemblage of a  
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7 459 broader diversity of genetic signatures in environmental microbial surveys than ever,  
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9 460 but there still remains a clear discrepancy between what can be detected and what  
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11 461 can be taxonomically assigned. This discrepancy is especially pronounced among  
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13 462 benthic organisms, which display a much higher novelty in genetic diversity surveys  
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15 463 than planktonic organisms (Figs. 5 and 6). A promising approach towards exploring  
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17 464 this novel diversity is the combination of multiple SRA datasets in network analyses  
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19 465 to screen for groups of sequences that do not have closely described relatives  
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21 466 (Forster *et al.* 2015). Such highly divergent groups detected in independent  
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23 467 environmental samples have a high potential to represent genuine undescribed  
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25 468 organisms. The design of novel probes and primer-sets specifically for these groups  
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27 469 will in turn enable the targeted recovery and identification of the respective organisms  
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29 470 from life samples by molecular methods (Gimmler and Stoeck 2015). As our picture  
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31 471 of protist diversity heavily depends on the coverage of available public databases  
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33 472 (Pawlowski *et al.* 2012), increasing the efforts to isolate, cultivate and describe  
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35 473 benthic protist species will also help to link genetic signatures obtained in  
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37 474 environmental sequencing studies to a real biological entity with a phylogenetic  
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39 475 context. Although the isolation of individual specimen remains a challenging task,  
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41 476 methods exist to successfully address organisms in benthos samples. For example,  
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43 477 even small flagellates can be isolated by quantitative centrifugation (Starink *et al.*  
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45 478 1994). More recently, a serial dilution method enabled the recovery of diatom spores  
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47 479 from coastal sediment samples (Montresor *et al.* 2013). First studies on highly  
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49 480 divergent BioMarKs sediment OTUs already led to the discovery of novel cercozoan  
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51 481 vampirellids (Berney *et al.* 2013) and opisthokont Fonticulida (del Campo *et al.*  
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53 482 2015), two groups that were mostly known from soil or freshwater samples.  
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3 483 Regarding the divergence of benthic OTUs from publicly available reference  
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5 484 sequences, we suppose that we are just scratching the surface of protist diversity in  
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7 485 coastal sediments. Thus, we understand the BioMarKs data as a starting point that  
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9 486 may guide the discovery of more novel benthic protist diversity by further taxon-  
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11 487 specific screening.  
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## 18 490 **Conclusions**

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21 491 Over the last 60 years, our perception of marine benthic environments has  
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23 492 changed from being biologically inert deserts towards being highly heterogeneous  
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25 493 habitats teeming with a multitude of microbial organisms. Even though new  
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27 494 technologies allow for addressing this vast diversity, the results of the BioMarKs  
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29 495 project strongly imply that the most part of benthic protist diversity remains a black  
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31 496 box. While sampling the deep-seafloor surely imposes many challenges and  
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33 497 restrictions that have lagged the exploration of benthic diversity, our data show that it  
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35 498 is not mandatory to focus on such remote environments when looking for highly  
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37 499 diverse protist communities. From a quantitative (*i.e.* OTU richness) and qualitative  
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39 500 (*i.e.* degree of genetic divergence) point of view, coastal sediments inhabit  
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41 501 intriguingly rich protist assemblages on local and regional scales. Increasing the  
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43 502 efforts to explore these assemblages will be beneficial to learn more about the  
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45 503 dispersal patterns of benthic protists, their roles in ecosystem functioning and to  
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47 504 complement current species inventories by identifying many still unknown organisms.  
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36 522 The authors declare that they have no conflict of interest.  
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523 **References**

- 524 Bass D, Chao EE-Y, Nikolaev S *et al.* Phylogeny of novel naked filose and reticulose Cercozoa:  
525 Granofilosea cl. n. and Proteomyxidea revised. *Protist* 2009;**160**:75–109.
- 526 Bass D, Yabuki A, Santini S *et al.* Reticulamoeba is a long-branched granofilosean (Cercozoa) that is  
527 missing from sequence databases. *PLoS ONE* 2012;**7**:e49090.
- 528 Berney C, Romac S, Mahé F *et al.* Vampires in the oceans: predatory cercozoan amoebae in marine  
529 habitats. *ISME J* 2013;**7**:2387–99.
- 530 Bik HM, Sung W, De Ley P *et al.* Metagenetic community analysis of microbial eukaryotes illuminates  
531 biogeographic patterns in deep-sea and shallow water sediments. *Mol Ecol* 2012;**21**:1048–  
532 59.
- 533 Bittner L, Gobet A, Audic S *et al.* Diversity patterns of uncultured Haptophytes unravelled by  
534 pyrosequencing in Naples Bay. *Mol Ecol* 2013;**22**:87–101.
- 535 Bunge J, Woodard L, Böhning D *et al.* Estimating population diversity with CatchAll. *Bioinformatics*  
536 2012;**28**:1045–7.
- 537 del Campo J, Mallo D, Massana R *et al.* Diversity and distribution of unicellular opisthokonts along the  
538 European coast analysed using high-throughput sequencing. *Environ Microbiol*  
539 2015;**17**:3195–207.
- 540 Chantangsi C, Leander BS. An SSU rDNA barcoding approach to the diversity of marine interstitial  
541 cercozoans, including descriptions of four novel genera and nine novel species. *Int J Syst Evol*  
542 *Microbiol* 2010;**60**:1962–77.
- 543 Colwell RK, Chao A, Gotelli NJ *et al.* Models and estimators linking individual-based and sample-based  
544 rarefaction, extrapolation and comparison of assemblages. *J Plant Ecol* 2012;**5**:3–21.
- 545 Dawson SC, Pace NR. Novel kingdom-level eukaryotic diversity in anoxic environments. *Proc Natl*  
546 *Acad Sci* 2002;**99**:8324–9.
- 547 Decelle J, Martin P, Paborstava K *et al.* Diversity, ecology and biogeochemistry of cyst-forming  
548 Acantharia (Radiolaria) in the oceans. *PLoS ONE* 2013;**8**:e53598.
- 549 Dell'Anno A, Danovaro R. Extracellular DNA plays a key role in deep-sea ecosystem functioning.  
550 *Science* 2005;**309**:2179–2179.
- 551 Doherty M, Tamura M, Vriezen JAC *et al.* Diversity of Oligotrichia and Choreotrichia ciliates in coastal  
552 marine sediments and in overlying plankton. *Appl Environ Microbiol* 2010;**76**:3924–35.
- 553 Dolan JR, Stoeck T. Repeated sampling reveals differential variability in measures of species richness  
554 and community composition in planktonic protists. *Environ Microbiol Rep* 2011;**3**:661–6.
- 555 Duff K, Zeeb BA, Smol JP. *Atlas of Chrysophycean Cysts*. Dordrecht: Springer Science & Business  
556 Media, 2013.
- 557 Dunthorn M, Klier J, Bunge J *et al.* Comparing the hyper-variable V4 and V9 regions of the small  
558 subunit rDNA for assessment of ciliate environmental diversity. *J Eukaryot Microbiol*  
559 2012;**59**:185–7.

- 1  
2  
3 560 Dunthorn M, Otto J, Berger SA *et al.* Placing environmental next-generation sequencing amplicons  
4 561 from microbial eukaryotes into a phylogenetic context. *Mol Biol Evol* 2014a;**31**:993–1009.  
5  
6 562 Dunthorn M, Stoeck T, Clamp J *et al.* Ciliates and the rare biosphere: a review. *J Eukaryot Microbiol*  
7 563 2014b;**61**:404–9.  
8  
9 564 Edgar RC. Search and clustering orders of magnitude faster than BLAST. *Bioinformatics*  
10 565 2010;**26**:2460–1.  
11  
12 566 Edgar RC, Haas BJ, Clemente JC *et al.* UCHIME improves sensitivity and speed of chimera detection.  
13 567 *Bioinformatics* 2011;**27**:2194–200.  
14  
15 568 Edgcomb VP, Kysela DT, Teske A *et al.* Benthic eukaryotic diversity in the Guaymas Basin  
16 569 hydrothermal vent environment. *Proc Natl Acad Sci* 2002;**99**:7658–62.  
17  
18 570 Egge ES, Johannessen TV, Andersen T *et al.* Seasonal diversity and dynamics of haptophytes in the  
19 571 Skagerrak, Norway, explored by high-throughput sequencing. *Mol Ecol* 2015;**24**:3026–42.  
20  
21 572 Epstein S, López-García P. “Missing” protists: a molecular prospective. *Biodivers Conserv*  
22 573 2007;**17**:261–76.  
23  
24 574 Fierer N. Microbial biogeography: patterns in microbial diversity across space and time. In: Zengler K  
25 575 (ed.). *Accessing Uncultivated Microorganisms: From the Environment to Organisms and*  
26 576 *Genomes and Back*. Washington, DC: ASM Press, 2008, 95–115.  
27  
28 577 Forster D, Bittner L, Karkar S *et al.* Testing ecological theories with sequence similarity networks:  
29 578 marine ciliates exhibit similar geographic dispersal patterns as multicellular organisms. *BMC*  
30 579 *Biol* 2015;**13**:16.  
31  
32 580 Franzén M, Schweiger O, Betzholtz P-E. Species-area relationships are controlled by species traits.  
33 581 *PLoS ONE* 2012;**7**:e37359.  
34  
35 582 Garstecki T, Arndt H. Seasonal abundances and community structure of benthic rhizopods in shallow  
36 583 lagoons of the southern Baltic Sea. *Eur J Protistol* 2000;**36**:103–15.  
37  
38 584 Garstecki T, Verhoeven R, Wickham SA *et al.* Benthic–pelagic coupling: a comparison of the  
39 585 community structure of benthic and planktonic heterotrophic protists in shallow inlets of the  
40 586 southern Baltic. *Freshw Biol* 2000;**45**:147–67.  
41  
42 587 Gilg IC, Amaral-Zettler LA, Countway PD *et al.* Phylogenetic affiliations of mesopelagic Acantharia and  
43 588 acantharian-like environmental 18S rRNA genes off the Southern California coast. *Protist*  
44 589 2010;**161**:197–211.  
45  
46 590 Gimmler A, Stoeck T. Mining environmental high-throughput sequence data sets to identify divergent  
47 591 amplicon clusters for phylogenetic reconstruction and morphotype visualization. *Environ*  
48 592 *Microbiol Rep* 2015;**7**:679–86.  
49  
50 593 Gong J, Shi F, Ma B *et al.* Depth shapes  $\alpha$ - and  $\beta$ -diversities of microbial eukaryotes in surficial  
51 594 sediments of coastal ecosystems. *Environ Microbiol* 2015;**17**:3722–37.  
52  
53 595 Gray JS. Marine biodiversity: patterns, threats and conservation needs. *Biodivers Conserv*  
54 596 1997;**6**:153–75.  
55  
56  
57  
58  
59  
60



- 1  
2  
3 597 Guillou L, Bachar D, Audic S *et al.* The protist ribosomal reference database (PR2): a catalog of  
4 598 unicellular eukaryote small sub-unit rRNA sequences with curated taxonomy. *Nucleic Acids*  
5 599 *Res* 2012;D597–604.  
6  
7 600 Guillou L, Viprey M, Chambouvet A *et al.* Widespread occurrence and genetic diversity of marine  
8 601 parasitoids belonging to Syndiniales (Alveolata). *Environ Microbiol* 2008;**10**:3349–65.  
9  
10 602 Haas BJ, Gevers D, Earl AM *et al.* Chimeric 16S rRNA sequence formation and detection in Sanger and  
11 603 454-pyrosequenced PCR amplicons. *Genome Res* 2011;**21**:494–504.  
12  
13 604 Hansen PJ. The role of photosynthesis and food uptake for the growth of marine mixotrophic  
14 605 dinoflagellates. *J Eukaryot Microbiol* 2010;**58**:203–14.  
15  
16 606 Hartikainen H, Ashford OS, Berney C *et al.* Lineage-specific molecular probing reveals novel diversity  
17 607 and ecological partitioning of haplosporidians. *ISME J* 2014;**8**:177–86.  
18  
19 608 Hortal J, Triantis KA, Meiri S *et al.* Island species richness increases with habitat diversity. *Am Nat*  
20 609 2009;**174**:E205–17.  
21  
22 610 Howe AT, Bass D, Scoble JM *et al.* Novel cultured protists identify deep-branching environmental  
23 611 DNA clades of Cercozoa: new genera Tremula, Micrometopion, Minimassisteria, Nudifila,  
24 612 Peregrinia. *Protist* 2011;**162**:332–72.  
25  
26 613 Hurt RA, Qiu X, Wu L *et al.* Simultaneous recovery of RNA and DNA from soils and sediments. *Appl*  
27 614 *Environ Microbiol* 2001;**67**:4495–503.  
28  
29 615 Jeong HJ, Yoo YD, Kim JS *et al.* Growth, feeding and ecological roles of the mixotrophic and  
30 616 heterotrophic dinoflagellates in marine planktonic food webs. *Ocean Sci J* 2010;**45**:65–91.  
31  
32 617 Lax G, Simpson AGB. Combining molecular data with classical morphology for uncultured  
33 618 phagotrophic euglenids (Excavata): a single-cell approach. *J Eukaryot Microbiol* 2013;**60**:615–  
34 619 25.  
35  
36 620 Leckie RM. Seeking a better life in the plankton. *Proc Natl Acad Sci* 2009;**106**:14183–4.  
37  
38 621 Logares R, Audic S, Bass D *et al.* Patterns of rare and abundant marine microbial eukaryotes. *Curr Biol*  
39 622 2014;**24**:813–21.  
40  
41 623 López-García P, Philippe H, Gail F *et al.* Autochthonous eukaryotic diversity in hydrothermal sediment  
42 624 and experimental microcolonizers at the Mid-Atlantic Ridge. *Proc Natl Acad Sci U S A*  
43 625 2003;**100**:697–702.  
44  
45 626 López-García P, Vereshchaka A, Moreira D. Eukaryotic diversity associated with carbonates and fluid–  
46 627 seawater interface in Lost City hydrothermal field. *Environ Microbiol* 2007;**9**:546–54.  
47  
48 628 Mann DG, Evans KM. Molecular genetics and the neglected art of diatomics. In: Brodie J, Lewis J  
49 629 (eds.). *Unravelling the Algae: The Past, Present, and Future of Algal Systematics*. Boca Raton,  
50 630 FL, USA: CRC Press, Taylor and Francis Group, 2007, 231–66.  
51  
52 631 Marcus NH, Boreo F. Minireview: the importance of benthic-pelagic coupling and the forgotten role  
53 632 of life cycles in coastal aquatic systems. *Limnol Oceanogr* 1998;**43**:763–8.  
54  
55 633 Massana R. Eukaryotic picoplankton in surface oceans. *Annu Rev Microbiol* 2011;**65**:91–110.  
56  
57  
58  
59  
60

- 1  
2  
3 634 Massana R, Gobet A, Audic S *et al.* Marine protist diversity in European coastal waters and sediments  
4 635 as revealed by high-throughput sequencing. *Environ Microbiol* 2015;**17**:4035–49.
- 5  
6 636 McQuoid MR, Hobson LA. Diatom resting stages. *J Phycol* 1996;**32**:889–902.
- 7  
8 637 Menden-Deuer S, Fredrickson K. Structure-dependent, protistan grazing and its implication for the  
9 638 formation, maintenance and decline of plankton patches. *Mar Ecol Prog Ser* 2010;**420**:57–71.
- 10  
11 639 Montresor M, Di Prisco C, Sarno D *et al.* Diversity and germination patterns of diatom resting stages  
12 640 at a coastal Mediterranean site. *Mar Ecol Prog Ser* 2013;**484**:79–95.
- 13  
14 641 Nanjappa D, Audic S, Romac S *et al.* Assessment of species diversity and distribution of an ancient  
15 642 diatom lineage using a DNA metabarcoding approach. *PLoS ONE* 2014;**9**:e103810.
- 16  
17 643 Not F, Siano R, Kooistra WHCF *et al.* Diversity and ecology of eukaryotic marine phytoplankton. In:  
18 644 Piganeau G (ed.). *Advances in Botanical Research: Genomic Insight into the Biology of Algae*.  
19 645 Amsterdam, Netherlands: Elsevier, 2012, 1–53.
- 20  
21 646 Oksanen J, Blanchet FG, Kindt R *et al.* *Vegan: Community Ecology Package. R Package Version 2.2-1.*,  
22 647 2015.
- 23  
24 648 Orcutt BN, Sylvan JB, Knab NJ *et al.* Microbial ecology of the dark ocean above, at, and below the  
25 649 seafloor. *Microbiol Mol Biol Rev* 2011;**75**:361–422.
- 26  
27  
28 650 Patterson DJ, Larsen J, Corliss JO. The ecology of heterotrophic flagellates and ciliates living in marine  
29 651 sediments. *Prog Protistol* 1989;**3**:185–277.
- 30  
31 652 Pawlowski J, Audic S, Adl S *et al.* CBOL protist working group: barcoding eukaryotic richness beyond  
32 653 the animal, plant, and fungal kingdoms. *PLoS Biol* 2012;**10**:e1001419.
- 33  
34 654 Pawlowski J, Christen R, Lecroq B *et al.* Eukaryotic richness in the abyss: insights from pyrotag  
35 655 sequencing. *PLoS ONE* 2011;**6**:e18169.
- 36  
37 656 Pawlowski J, Holzmann M, Tyszka J. New supraordinal classification of Foraminifera: molecules meet  
38 657 morphology. *Mar Micropaleontol* 2013;**100**:1–10.
- 39  
40 658 Pedersen LL, Smets BF, Dechesne A. Measuring biogeochemical heterogeneity at the micro scale in  
41 659 soils and sediments. *Soil Biol Biochem* 2015;**90**:122–38.
- 42  
43 660 Richards TA, Jones MDM, Leonard G *et al.* Marine fungi: their ecology and molecular diversity. *Annu*  
44 661 *Rev Mar Sci* 2012;**4**:495–522.
- 45  
46 662 Scheckenbach F, Hausmann K, Wylezich C *et al.* Large-scale patterns in biodiversity of microbial  
47 663 eukaryotes from the abyssal sea floor. *Proc Natl Acad Sci* 2010;**107**:115–20.
- 48  
49 664 Sekhon JS. Multivariate and propensity score matching software with automated balance  
50 665 optimization: the matching package for R. *J Stat Softw* 2011;**42**.
- 51  
52  
53 666 Starink M, Bär-Gilissen M-J, Bak RPM *et al.* Quantitative centrifugation to extract benthic protozoa  
54 667 from freshwater sediments. *Appl Environ Microbiol* 1994;**60**:167–73.
- 55  
56 668 Stoeck T, Bass D, Nebel M *et al.* Multiple marker parallel tag environmental DNA sequencing reveals  
57 669 a highly complex eukaryotic community in marine anoxic water. *Mol Ecol* 2010;**19**:21–31.
- 58  
59  
60

- 1  
2  
3 670 Stoeck T, Epstein S. Novel eukaryotic lineages inferred from small-subunit rRNA analyses of oxygen-  
4 671 depleted marine environments. *Appl Environ Microbiol* 2003;**69**:2657–63.  
5  
6 672 Stoeck T, Zuendorf A, Breiner H-W *et al.* A molecular approach to identify active microbes in  
7 673 environmental eukaryote clone libraries. *Microb Ecol* 2007;**53**:328–39.  
8  
9 674 Takishita K, Miyake H, Kawato M *et al.* Genetic diversity of microbial eukaryotes in anoxic sediment  
10 675 around fumaroles on a submarine caldera floor based on the small-subunit rDNA phylogeny.  
11 676 *Extremophiles* 2005;**9**:185–96.  
12  
13 677 Teske A, Durbin A, Ziervogel K *et al.* Microbial community composition and function in permanently  
14 678 cold seawater and sediments from an arctic fjord of Svalbard. *Appl Environ Microbiol*  
15 679 2011;**77**:2008–18.  
16  
17 680 de Vargas C, Audic S, Henry N *et al.* Eukaryotic plankton diversity in the sunlit ocean. *Science*  
18 681 2015;**348**:1261605.  
19  
20 682 Vaulot D, Eikrem W, Viprey M *et al.* The diversity of small eukaryotic phytoplankton ( $\leq 3 \mu\text{m}$ ) in  
21 683 marine ecosystems. *FEMS Microbiol Rev* 2008;**32**:795–820.  
22  
23 684 Vavrek MJ. fossil: palaeoecological and palaeogeographical analysis tools. *Palaeontol Electron*  
24 685 2011;14:1T.  
25  
26 686 Zinger L, Amaral-Zettler LA, Fuhrman JA *et al.* Global patterns of bacterial beta-diversity in seafloor  
27 687 and seawater ecosystems. *PLoS ONE* 2011;**6**:e24570.  
28  
29 688 Zinger L, Boetius A, Ramette A. Bacterial taxa–area and distance–decay relationships in marine  
30 689 environments. *Mol Ecol* 2014;**23**:954–64.  
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691 **Table 1 Overview of BioMarKs samplings along the European coastline.**

Sampling Event	Latitude/Longitude	Oceanic region	Quality sequences per sampled habitat		
			Surface water	DCM	Sediment
Blanes	41°40'N/2°48'E	Mediterranean Sea	16 568	n.d.	3576
Gijon	43°40'N/5°35'W	Atlantic Ocean	20 966	n.d.	n.d.
Naples 2009	40°48'N/14°15'E	Mediterranean Sea	62 250	52 114	15 739
Naples 2010	40°48'N/14°15'E	Mediterranean Sea	22 132	31 268	3159
Oslo 2009	59°16'N/10°43'E	Skagerrak	33 133	36 988	12 835
Oslo 2010	59°16'N/10°43'E	Skagerrak	19 316	24 819	3071
Roscoff	48°46'E/3°57'W	English Channel	9298	n.d.	1720
Varna	43°10'N/28°50'E	Black Sea	22 939	39 003	n.d.

692 DCM, deep-chlorophyll maximum; n.d., no data available.

693 Total number of surface water quality sequences: 206 602.

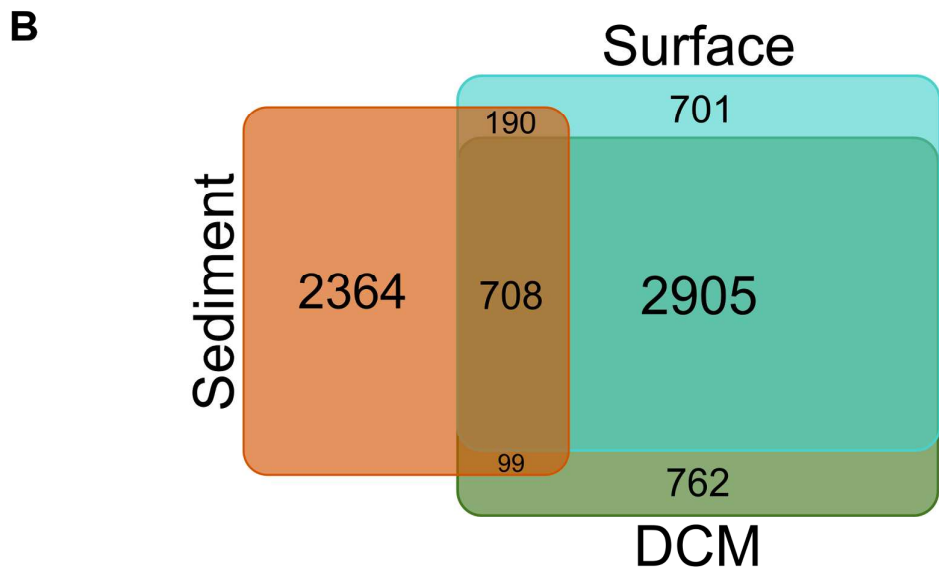
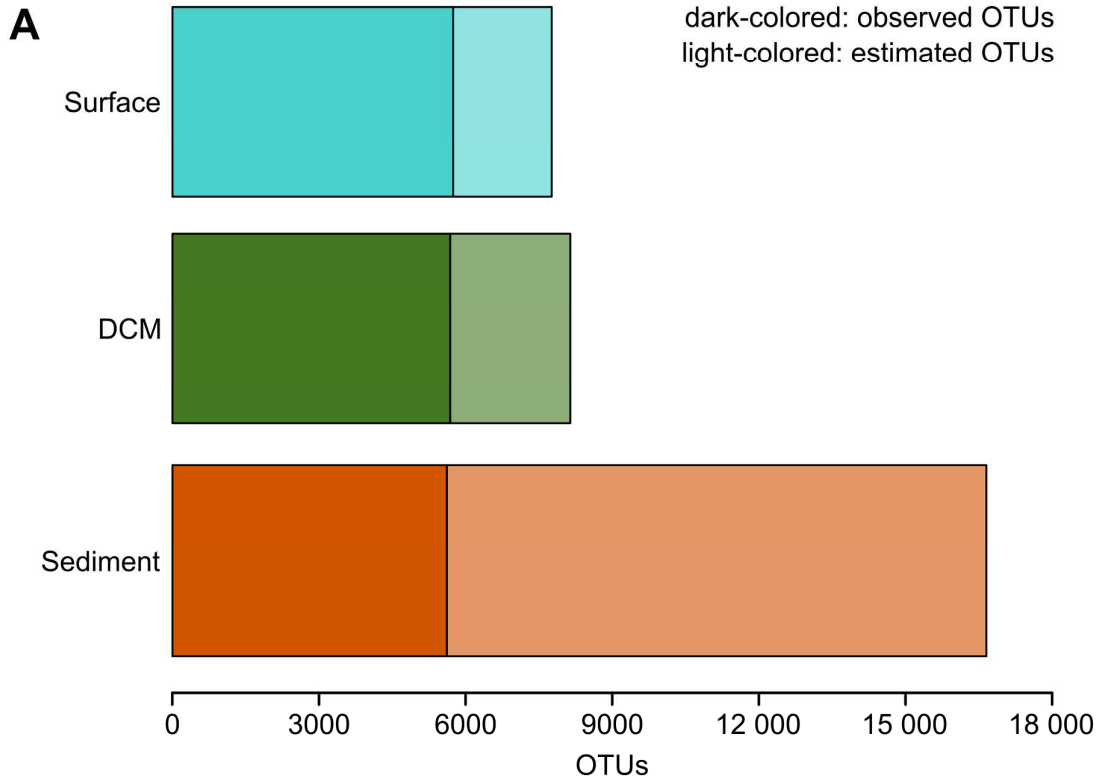
694 Total number of DCM quality sequences: 184 192.

695 Total number of sediment quality sequences: 40 100.

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3 697 **Fig. 1 OTU richness and shared OTUs of planktonic and benthic protist**  
4 **communities.** (A) For each habitat the bars show the number of observed (left, dark  
5 698 **communities.** (A) For each habitat the bars show the number of observed (left, dark  
6 colored part) and estimated OTUs (right, lighter colored part). Estimations are based  
7 699 colored part) and estimated OTUs (right, lighter colored part). Estimations are based  
8 on the incidence-based coverage estimator (ICE). (B) The Venn-Diagram highlights  
9 700 on the incidence-based coverage estimator (ICE). (B) The Venn-Diagram highlights  
10 701 how many non-singleton OTUs were shared between all habitats, shared between  
11 702 how many non-singleton OTUs were shared between all habitats, shared between  
12 703 any two of the sampled habitats or exclusively detected in a single habitat. Numbers  
13 704 indicate the amount of OTUs which fall into the respective category. The area of each  
14 705 category was proportionally approximated to the number of OTUs from the respective  
15 habitat.  
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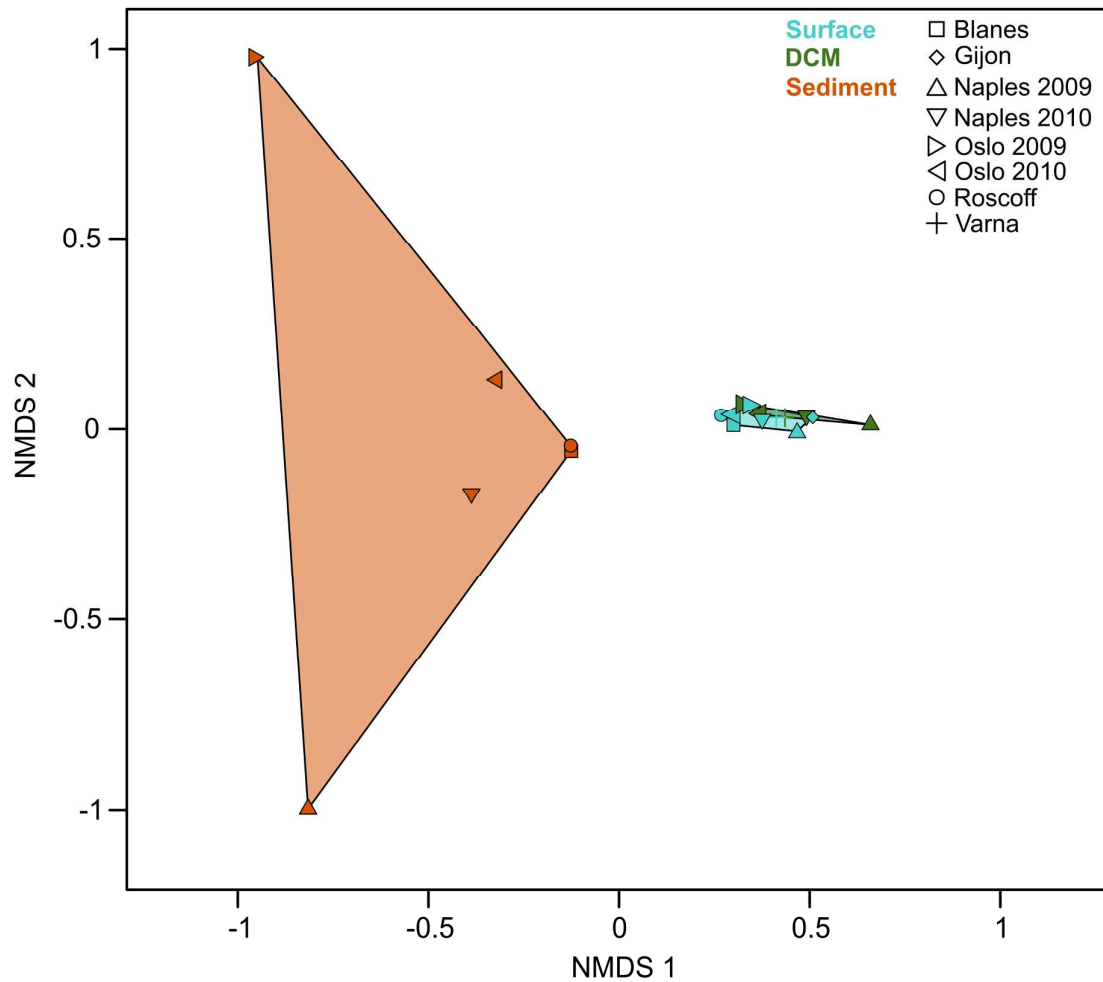


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3 709 **Fig. 2 Beta diversity analysis of single sampling events.** The NMDS is based on  
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5 710 binary-Jaccard distances between protist communities of single samples (NMDS  
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7 711 stress level = 0.2). Colors of the data points were chosen with respect to their habitat  
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10 712 affiliation. Data points of the same affiliation were linked and the area between the  
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12 713 linked points was colored with respect to their habitat affiliation.  
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3 717 **Fig. 3 Taxonomic community compositions as revealed by the PR<sup>2</sup> database.**

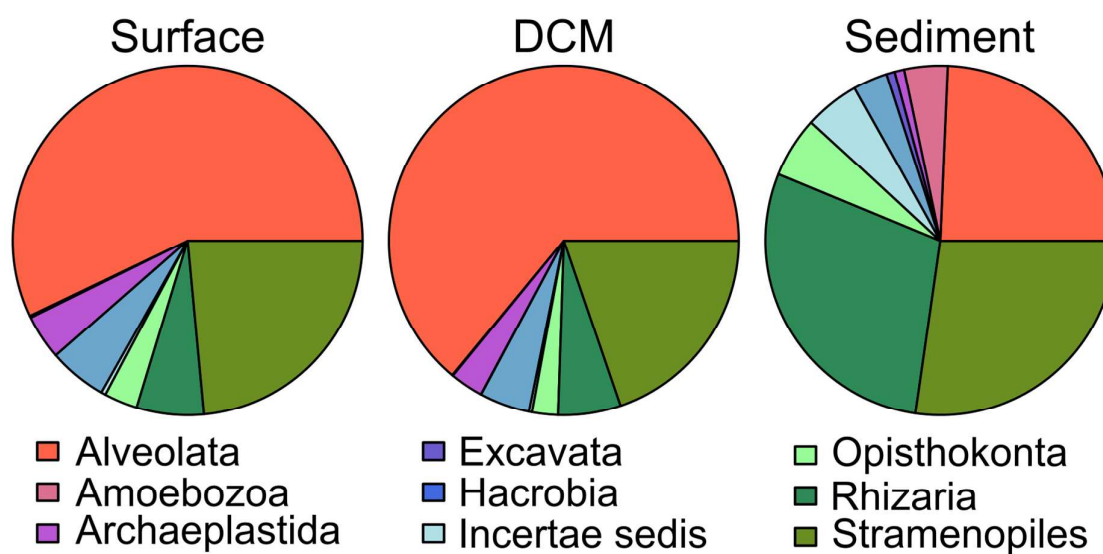
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5 718 The pie charts reflect the distribution of OTUs within major protist groups, by pooling

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7 719 the data of all samples from each habitat. The surface dataset included 5747 distinct

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9 720 OTUs, the DCM dataset 5685 distinct OTUs and the sediment dataset 5616 distinct

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11 721 OTUs.

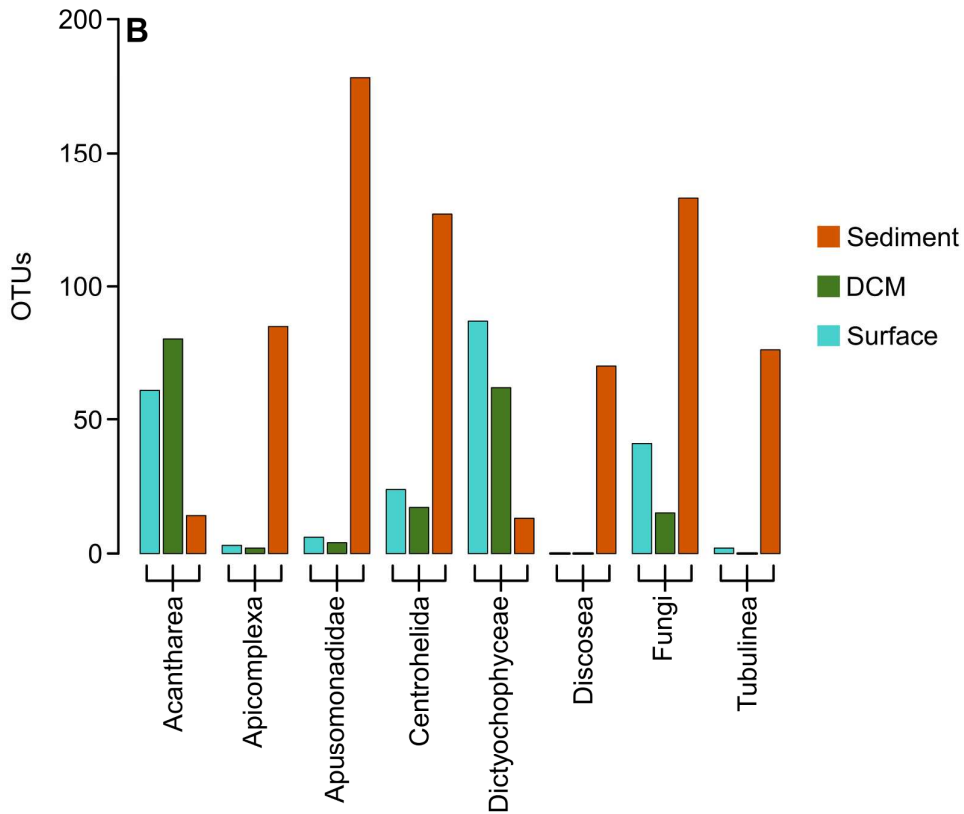
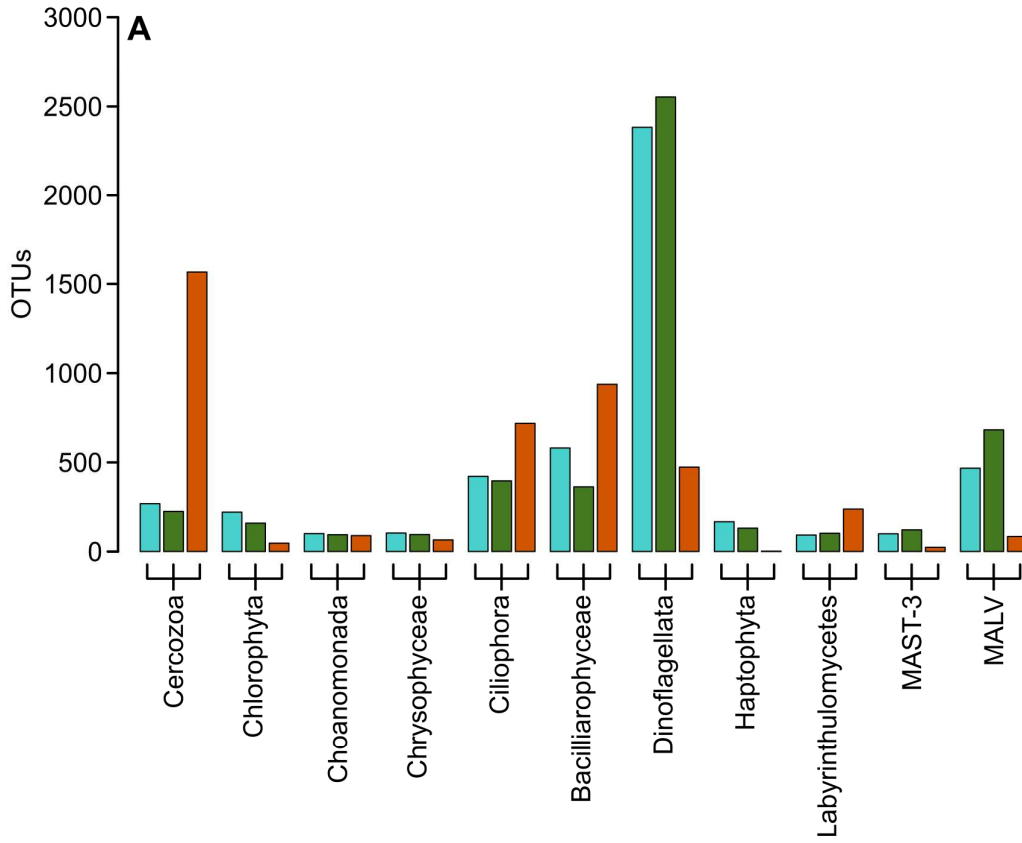
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3 725 **Fig. 4 Number of OTUs within taxonomic groups in planktonic and benthic**  
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5 726 **samples.** Only groups contributing to at least 1% of the OTU number in either  
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7 727 surface, DCM or sediment communities were considered. Note the different scale  
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9 728 among the two panels, to display taxonomic groups with more than 200 OTUs in total  
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11 729 (A) or with less than 200 OTUs in total (B).  
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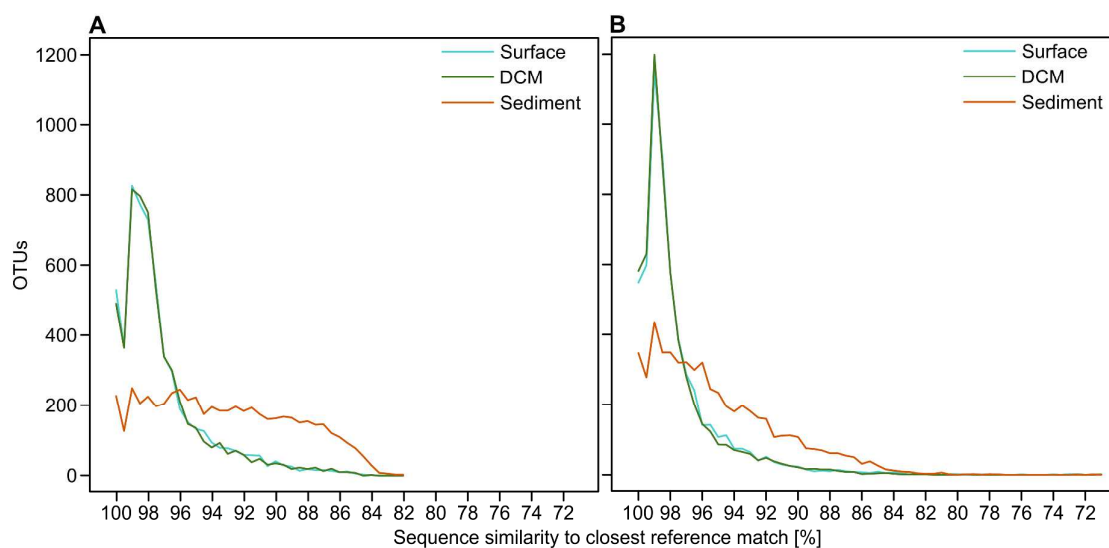


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3 733 **Fig. 5 Rank abundance curves displaying the sequence similarity distribution**  
4 **of OTUs against reference databases.** Results are shown for two different BLAST  
5 734 **queries, against the PR<sup>2</sup> database (A) and against a custom-built subset of NCBI's**  
6  
7 735 **queries, against the PR<sup>2</sup> database (A) and against a custom-built subset of NCBI's**  
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9 736 **Short Read Archive (B). The curves display the number of OTUs with a given**  
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11 737 **similarity with the closest match from the respective reference database. Sequence**  
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13 738 **similarities are binned in 0.5 % intervals.**  
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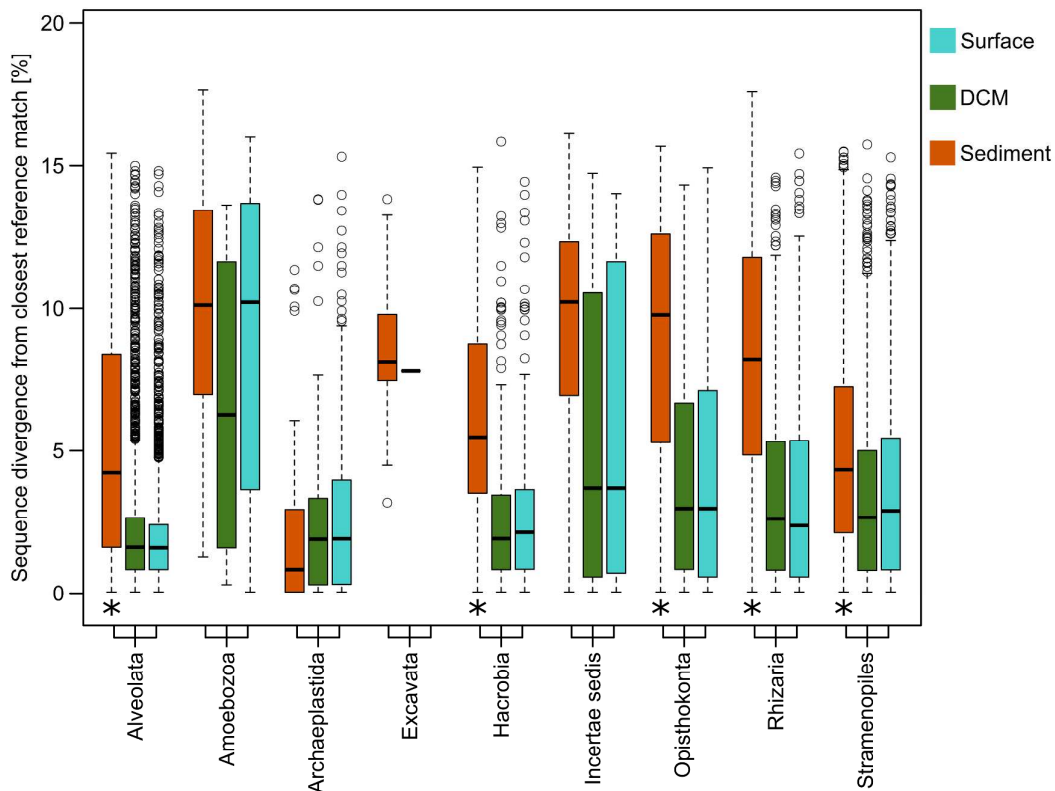
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742 **Fig. 6 Sequence divergence of OTUs to their closest taxonomic hit.** Each  
 743 boxplot comprises the sequence divergence values of all OTUs within a given  
 744 taxonomical group from the same habitat to their closest reference in the PR<sup>2</sup>  
 745 database. The taxonomic assignment is shown at the supergroup level. Missing  
 746 boxplots indicate that the taxonomical group was not detected in the respective  
 747 habitat. For each taxonomic group, differences between the distribution of sequence  
 748 dissimilarity values of sediment OTUs to planktonic OTUs was tested for significance  
 749 ( $p < 0.001$ , indicated by stars). The distribution of sequence dissimilarity values was  
 750 never significantly different between DCM and surface OTUs. Black bars represent  
 751 the median of each boxplot, the part of the box above the median represents the  
 752 upper quartile; accordingly, the part of the box below the median represents the  
 753 lower quartile. Circles show the outliers of each group of data.



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Total number of surface water quality sequences: 206 602.

Total number of DCM quality sequences: 184 192.

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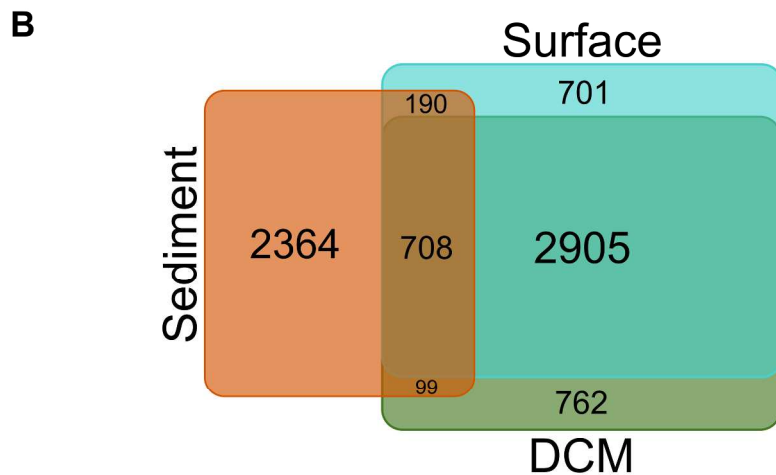
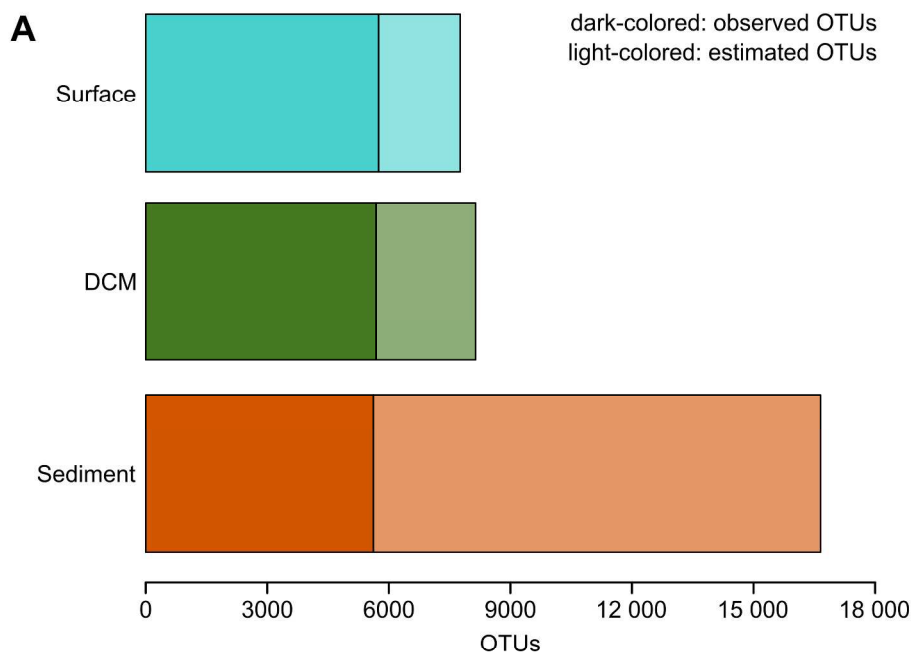


Fig. 1 OTU richness and shared OTUs of planktonic and benthic protist communities. (A) For each habitat the bars show the number of observed (left, dark colored part) and estimated OTUs (right, lighter colored part). Estimations are based on the incidence-based coverage estimator (ICE). (B) The Venn-Diagram highlights how many non-singleton OTUs were shared between all habitats, shared between any two of the sampled habitats or exclusively detected in a single habitat. Numbers indicate the amount of OTUs which fall into the respective category. The area of each category was proportional approximated to the number of OTUs from the respective habitat.  
228x290mm (300 x 300 DPI)

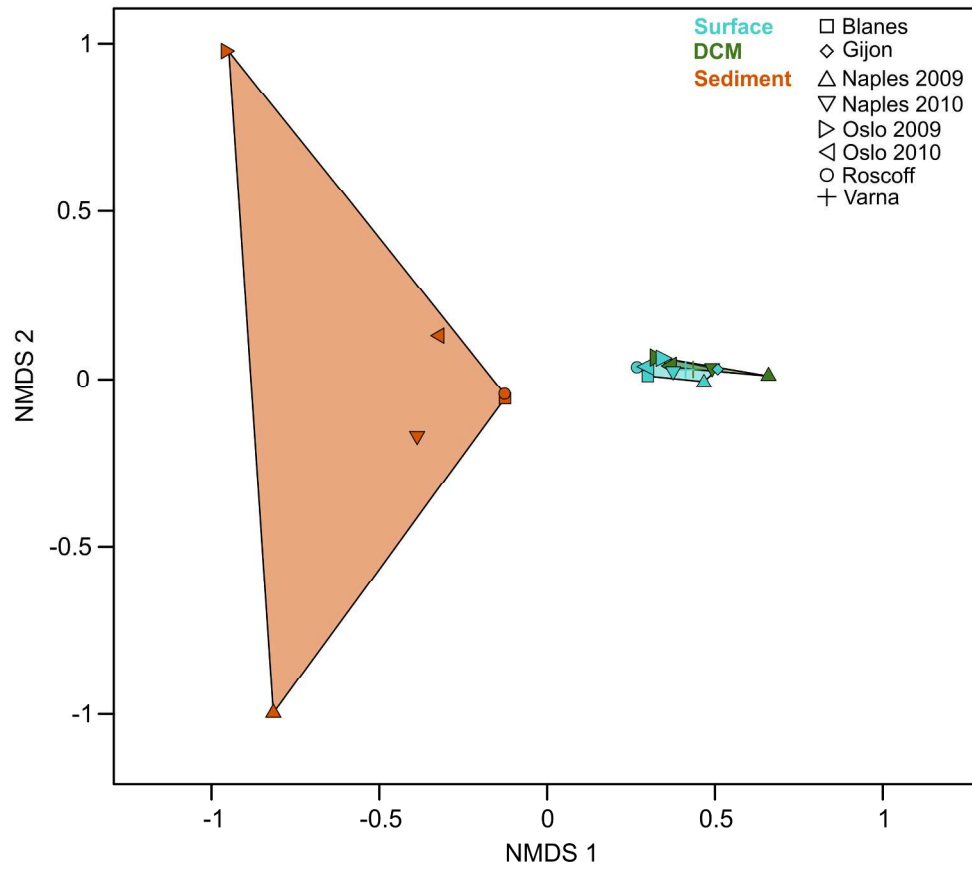


Fig. 2 Beta diversity analysis of single sampling events. The NMDS is based on binary-Jaccard distances between protist communities of single samples (NMDS stress level = 0.2). Colors of the data points were chosen with respect to their habitat affiliation. Data points of the same affiliation were linked and the area between the linked points was colored with respect to their habitat affiliation.  
 228x200mm (300 x 300 DPI)

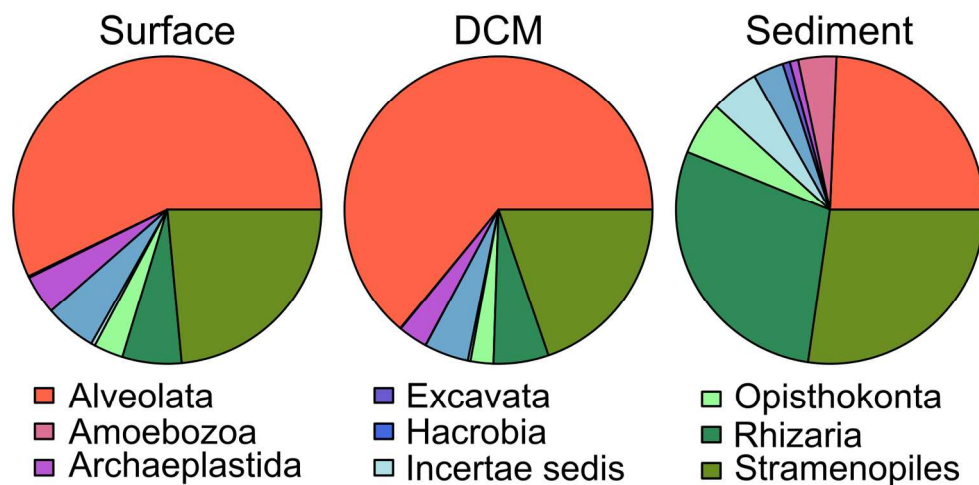


Fig. 3 Taxonomic community compositions as revealed by the PR2 database. The pie charts reflect the distribution of OTUs within major protist groups, by pooling the data of all samples from each habitat. The surface dataset included 5747 distinct OTUs, the DCM dataset 5685 distinct OTUs and the sediment dataset 5616 distinct OTUs.  
160x79mm (300 x 300 DPI)



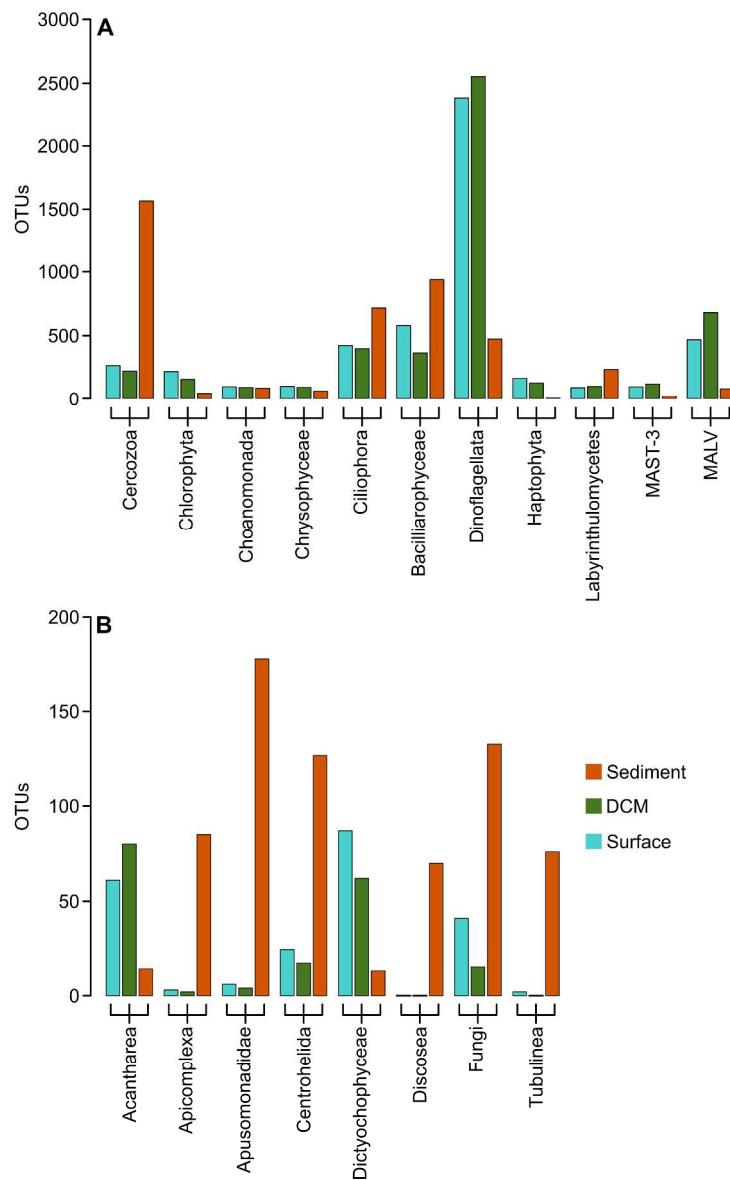


Fig. 4 Number of OTUs within taxonomic groups in planktonic and benthic samples. Only groups contributing to at least 1% of the OTU number in either surface, DCM or sediment communities were considered. Note the different scale among the two panels, to display taxonomic groups with more than 200 OTUs in total (A) or with less than 200 OTUs in total (B).

228x360mm (300 x 300 DPI)

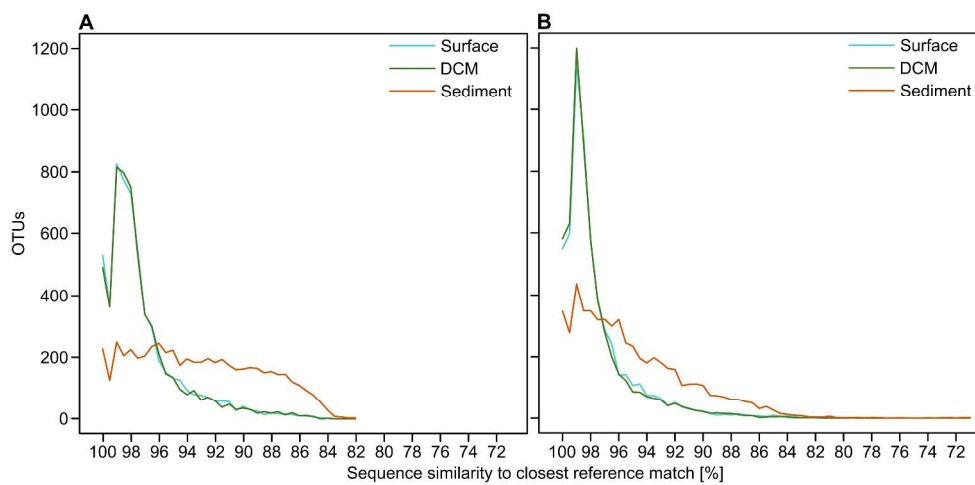


Fig. 5 Rank abundance curves displaying the sequence similarity distribution of OTUs against reference databases. Results are shown for two different BLAST queries, against the PR2 database (A) and against a custom-built subset of NCBI's Short Read Archive (B). The curves display the number of OTUs with a given similarity with the closest match from the respective reference database. Sequence similarities are binned in 0.5 % intervals.

336x169mm (300 x 300 DPI)

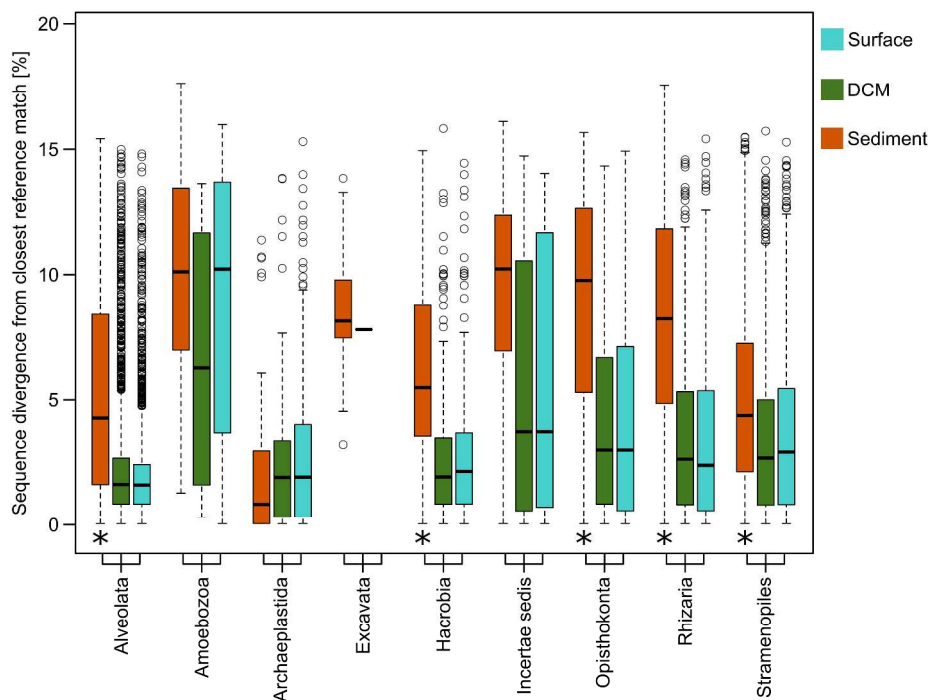


Fig. 6 Sequence divergence of OTUs to their closest taxonomic hit. Each boxplot comprises the sequence divergence values of all OTUs within a given taxonomical group from the same habitat to their closest reference in the PR2 database. The taxonomic assignment is shown at the supergroup level. Missing boxplots indicate that the taxonomical group was not detected in the respective habitat. For each taxonomic group, differences between the distribution of sequence dissimilarity values of sediment OTUs to planktonic OTUs was tested for significance ( $p < 0.001$ , indicated by stars). The distribution of sequence dissimilarity values was never significantly different between DCM and surface OTUs. Black bars represent the median of each boxplot, the part of the box above the median represents the upper quartile; accordingly, the part of the box below the median represents the lower quartile. Circles show the outliers of each group of data.

336x250mm (300 x 300 DPI)

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3 **1 Benthic protists: the under-charted majority**  
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4 Dominik Forster, Micah Dunthorn, Frédéric Mahé, John R. Dolan, Stéphane Audic,

5 David Bass, Lucie Bittner, Christophe Boutte, Richard Christen, Jean-Michel

6 Claverie, Johan Decelle, Bente Edvardsen, Elianne Egge, Wenche Eikrem,

7 Angélique Gobet, Wiebe H.C.F. Kooistra, Ramiro Logares, Ramon Massana, Marina

8 Montresor, Fabrice Not, Hiroyuki Ogata, Jan Pawlowski, Massimo C. Pernice, Sarah

9 Romac, Kamran Shalchian-Tabrizi, Nathalie Simon, Thomas Richards, Sébastien

10 Santini, Diana Sarno, Raffaele Siano, Daniel Vaultot, Patrick Wincker, Adriana

11 Zingone, Colomban de Vargas, Thorsten Stoeck

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3 12 **Supplemental Table S1 Additional information of the SRA database.** The table  
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5 13 includes all 167 distinct datasets used to build our custom subset of the SRA. We  
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7 14 screened the complete archive for protist datasets of the eukaryotic 18S gene. After  
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9 15 downloading the respective data, we removed all sequences shorter than 100 bp.  
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11 16 The final customized SRA reference database consisted of 11 708 385 sequences.  
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14 17 Information in the table was downloaded directly from NCBI's SRA platform along  
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16 18 with the respective sequences.  
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20 20 **Supplemental Fig. 2 Observed and estimated OTU richness calculated by**  
21 **abundance-based analyses.** Additionally to incidence-based ICE analyses (Fig.1)  
22 we estimated OTU richness with the abundance-based CatchAll tool. In direct  
23 comparison ICE and CatchAll results show the same trends, though the estimated  
24 richness of the abundance-based analyses always exceeded the one of the  
25 incidence-based analyses. For each habitat the plot shows the amount of observed  
26 and estimated OTUs. The left, dark colored part of each bar shows the actually  
27 observed number of OTUs, the right, light colored part of each bar shows how many  
28 more OTUs were estimated to be in each dataset by extrapolation of the data.  
29

30 **Supplemental Fig. S3 Normalized rarefaction curves of sampled habitats.**

31 Sequence data of all single sampling events were pooled with regard to the  
32 respective habitat. Each habitat rarefaction curve was normalized to 40 100  
33 sequences, which equals the smallest total amount of sequences found in any of the  
34 three habitats. Depicted is the amount of SSU V4 rDNA sequences in relation to the  
35 amount of resulting OTUs into which the sequences were clustered.  
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3 37 **Supplemental Fig. S4 Community composition among phototrophic protist**  
4 **taxon groups.** Represented are all phototrophic groups detected in BioMarkKs. The  
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7 38  
8 39 upper bar shows the phototrophic OTUs exclusively found in the plankton, the middle  
9  
10 40 bar the phototrophic OTUs present in both plankton and benthos and the lower bar  
11  
12 41 the phototrophic OTUs exclusively found in the benthos. Dinoflagellates were not  
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14 42 considered in the analyses.  
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19 44 **Supplemental Fig. S5 Occurrence of each phototrophic protist taxon group in**  
20 **the sampled habitats.** For each phototrophic taxon group, the bars indicate the  
21  
22 45  
23 46 fraction of OTUs which was found exclusively in the plankton, in both plankton and  
24  
25 47 benthos and exclusively in the benthos. Dinoflagellates were not considered in these  
26  
27 48 analyses.  
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32 50 **Supplemental Fig. S6 Community composition across different taxonomic**  
33 **levels.** The pie charts reflect the proportion of taxonomic groups of the total microbial  
34  
35 51  
36 52 eukaryote community in each habitat. The inner ring is equivalent to Fig. 4 and  
37  
38 53 represents the taxonomical assignment into major protist groups (corresponding to  
39  
40 54 the left part of the taxonomic legend). The outer ring represents the taxonomical  
41  
42 55 assignment at the phylum level (corresponding to the right part of the taxonomic  
43  
44 56 legend). Only phyla which contributed with at least 5% to the total community were  
45  
46 57 considered with a specific color in the outer ring. Exact proportions are given in  
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48 58 square brackets behind the taxonomical group names.  
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2	Experiment Accession
3	ERX145205
4	ERX145206
5	ERX145207
6	ERX145208
7	ERX250340
8	ERX250341
9	ERX250342
10	ERX250343
11	SRX003229
12	SRX006203
13	SRX006204
14	SRX037894
15	SRX037895
16	SRX037896
17	SRX050582
18	SRX050583
19	SRX057201
20	SRX057202
21	SRX099033
22	SRX154532
23	SRX155674
24	SRX155675
25	SRX155676
26	SRX155677
27	SRX155678
28	SRX155679
29	SRX157990
30	SRX157991
31	SRX157992
32	SRX157993
33	SRX157994
34	SRX157995
35	SRX157996
36	SRX176181
37	SRX176184
38	SRX176202
39	SRX193126
40	SRX204625
41	SRX206793
42	SRX206833
43	SRX270898
44	SRX272400
45	SRX275327
46	SRX275961
47	SRX276149
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2 SRX276150  
3 SRX276151  
4 SRX276152  
5 SRX276153  
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7 SRX276156  
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9 SRX276163  
10 SRX276164  
11 SRX276166  
12 SRX276167  
13 SRX276171  
14 SRX276172  
15 SRX276173  
16 SRX325682  
17 SRX340975  
18 SRX341060  
19 SRX341082  
20 SRX341087  
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30 SRX341098  
31 SRX341099  
32 SRX341100  
33 SRX341101  
34 SRX341102  
35 SRX341103  
36 SRX341104  
37 SRX341105  
38 SRX341107  
39 SRX341108  
40 SRX341110  
41 SRX373203  
42 SRX382997  
43 SRX391657  
44 SRX391659  
45 SRX391660  
46 SRX472244  
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2 SRX484165  
3 SRX497463  
4 SRX497495  
5 SRX497496  
6 SRX497527  
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9 SRX497530  
10 SRX497531  
11 SRX497532  
12 SRX497533  
13 SRX497534  
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24 SRX497545  
25 SRX497546  
26 SRX497547  
27 SRX504293  
28 SRX504294  
29 SRX504295  
30 SRX504296  
31 SRX504297  
32 SRX504477  
33 SRX504478  
34 SRX504479  
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38 SRX504485  
39 SRX504515  
40 SRX504517  
41 SRX504584  
42 SRX504585  
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44 SRX504604  
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2 SRX504618  
3 SRX504619  
4 SRX504620  
5 SRX504621  
6 SRX504622  
7 SRX504623  
8 SRX504624  
9 SRX504625  
10 SRX504626  
11 SRX504627  
12 SRX504628  
13 SRX504630  
14 SRX504631  
15 SRX504632  
16 SRX504635  
17 SRX528337  
18 SRX575253  
19 SRX575254  
20 SRX575255  
21 SRX575256  
22 SRX575257  
23 SRX575258  
24 SRX575259  
25 SRX575261  
26 SRX575263  
27 SRX575264  
28 SRX673677  
29 SRX719588  
30 SRX734515  
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2 Experiment Title  
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14 Gene expression during the initiation phase of growth in the dinoflagellate *Alexandrium catenella* (Dinophyceae)  
15 community profiling of Mirs Bay seawater by 18S rRNA V4 amplicon 454 sequencing  
16 community profiling of Tolo Harbor seawater by 18S rRNA V4 amplicon 454 sequencing  
17 Pooled bacterial amplicons from 10 Arctic marine surface water samples from 2003-2009 plus 2010  
18 Pooled archaeal amplicons from 10 Arctic marine surface water samples from 2003-2009 plus 2010  
19 Pooled eukarya amplicons from 10 Arctic marine surface water samples from 2003-2009 plus 2010  
20 Marine microbial eukaryote community analysis in Korea  
21 Marine microbial eukaryote community analysis in Korea  
22 GS\_FLX sequencing for environmental diversity study using the SSU rRNA as taxonomic marker  
23 GS\_FLX\_Titanium sequencing for environmental diversity study using the SSU rRNA as taxonomic marker  
24 RN\_RepliG Sequencing  
25 Pooled sample of 12 Arctic (Amundsen Gulf and Franklin Bay) sea ice samples from 2008  
26  
27 microbial diversity of ornamental fish aquarium water sample D1  
28 microbial diversity of ornamental fish aquarium water sample E1  
29 microbial diversity of ornamental fish aquarium water sample D2  
30 microbial diversity of ornamental fish aquarium water sample A1  
31 microbial diversity of ornamental fish aquarium water sample A2  
32 microbial diversity of ornamental fish aquarium water sample E2  
33 microbial diversity of ornamental fish aquarium water sample E1.V4  
34 microbial diversity of ornamental fish aquarium water sample D1.V4  
35 microbial diversity of ornamental fish aquarium water sample A1.V4  
36 microbial diversity of ornamental fish aquarium water sample A2.V4  
37 microbial diversity of ornamental fish aquarium water sample D2.V4  
38 microbial diversity of ornamental fish aquarium water sample E2.V4  
39 microbial diversity of ornamental fish aquarium water sample B2.V4  
40 Pooled samples of protist communities at 8 depth from Lake A in May 2008  
41 Pooled samples of protist communities at 4 depths from Lake A in August 2008  
42 Pooled samples of protist communities at 5 depths from Lake A in July 2009  
43 Environmental Samples from ANT-XXVI/3-NS  
44 Partial ribosomal gene sequences Ciliates in DHABs in the Mediterranean Sea  
45 V4 18S rRNA amplicons from cDNA prepared from different microbialite sediment samples from Highborne Cay, B  
46 V4 amplicons (18S rRNA) of eukaryotes obtained from cDNA prepared from various microbialite samples from Sha  
47 ANT XXVI/3 - WE  
48 a test of 16-18s universal primers using sponge samples  
49 Comparative Microbial Analysis to Understand Taxonomic Fingerprints of Healthy Coral Holobiont Communities at  
50 Protistan communities of the upper Arctic Ocean  
51 Comparative Microbial Analysis to Understand Taxonomic Fingerprints of Healthy Coral Holobiont Communities at  
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3 Comparative Microbial Analysis to Understand Taxonomic Fingerprints of Healthy Coral Holobiont Communities at  
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7 Comparative Microbial Analysis to Understand Taxonomic Fingerprints of Healthy Coral Holobiont Communities at  
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10 Comparative Microbial Analysis to Understand Taxonomic Fingerprints of Healthy Coral Holobiont Communities at  
11 Comparative Microbial Analysis to Understand Taxonomic Fingerprints of Healthy Coral Holobiont Communities at  
12 Comparative Microbial Analysis to Understand Taxonomic Fingerprints of Healthy Coral Holobiont Communities at  
13 Comparative Microbial Analysis to Understand Taxonomic Fingerprints of Healthy Coral Holobiont Communities at  
14 Comparative Microbial Analysis to Understand Taxonomic Fingerprints of Healthy Coral Holobiont Communities at  
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17 Comparative Microbial Analysis to Understand Taxonomic Fingerprints of Healthy Coral Holobiont Communities at  
18 Comparative Microbial Analysis to Understand Taxonomic Fingerprints of Healthy Coral Holobiont Communities at  
19 Exp1. Ward Hunt Lake Dilution Experiment Eukaryotes RNA  
20

21 Characterisation of uncultured marine eukaryotes in the Canada Basin

22 Chukchi Sea < 3 um Stn BS1

23 Chukchi Sea < 3 um Stn AN1

24 Chukchi Sea < 3 um Stn KS6

25 Chukchi Sea < 3 um Stn EC5

26 Chukchi Sea < 3 um Stn HLY

27 Chukchi Sea < 3 um Stn CC18

28 Chukchi Sea < 3 um Stn CN3

29 Chukchi Sea < 3 um Stn CN14

30 Chukchi Sea < 3 um Stn BCH7

31 Chukchi Sea < 3 um Stn IE

32 Chukchi Sea < 3 um Stn HSN5

33 Chukchi Sea > 3 um Stn BS1

34 Chukchi Sea > 3 um Stn AN1

35 Chukchi Sea > 3 um Stn KS6

36 Chukchi Sea > 3 um Stn CHA1

37 Chukchi Sea > 3 um Stn EC5

38 Chukchi Sea > 3 um Stn HLY

39 Chukchi Sea > 3 um Stn CC18

40 Chukchi Sea > 3 um Stn CN3

41 Chukchi Sea > 3 um Stn CN14

42 Chukchi Sea > 3 um Stn BCH7

43 Chukchi Sea > 3 um Stn IE

44 Chukchi Sea > 3 um Stn HSN5

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46 Sequences from three sediments

47 Design and validation of four primers for next-generation sequencing to target the 18S rRNA gene of gastrointesti

48 Design and validation of four primers for next-generation sequencing to target the 18S rRNA gene of gastrointesti

49 Design and validation of four primers for next-generation sequencing to target the 18S rRNA gene of gastrointesti

50 454 pyrosequencing of plankton community collected from Hamilton harbour

51 454 pyrosequencing of plankton community collected from Nanaimo harbour

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2 Investigating marine microbial plankton in meso-eutrophic ecosystem (Eastern English Channel)  
3 JB121SF\_DNA  
4 JB121SF\_RNA GoMA July 2010  
5 JB121SCM\_DNA GoMA July 2010  
6 JB121SCM\_RNA GoMA July 2010  
7 JB700SF\_DNA GoMA July 2010  
8 JB700SF\_RNA GoMA July 2010  
9 JB700SCM\_DNA GoMA July 2010  
10 JB700SCM\_RNA GoMA July 2010  
11 JB601SF\_DNA GoMA July 2010  
12 JB601SF\_RNA GoMA July 2010  
13 JB601SCM\_DNA GoMA July 2010  
14 JB601SCM\_RNA GoMA July 2010  
15 NEC211SF\_DNA  
16 NEC211SF\_RNA GoMA July 2010  
17 NEC211SCM\_DNA GoMA July 2010  
18 NEC211SCM\_RNA GoMA July 2010  
19 NEF43SF\_DNA GoMA July 2010  
20 NEF43SF\_RNA GoMA July 2010  
21 NEF43SCM\_DNA GoMA July 2010  
22 NEF43SCM\_RNA GoMA July 2010  
23 NEF512SF\_DNA GoMA July 2010  
24 NEF512SF\_RNA GoMA July 2010  
25 NEF512SCM\_DNA GoMA July 2010  
26 NEF512SCM\_RNA GoMA July 2010  
27 Eukaryota Arctic Ocean Survey  
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- 19 Eukaryota Arctic Ocean Survey
- 20 Eukaryota Arctic Ocean Survey
- 21 Marine microbial community structure assessed from combined metagenomic analysis and ribosomal tag pyroseq
- 22 Protists in Havre-aux-Maisons Lagoon
- 23 Protists in Havre-aux-Maisons Lagoon
- 24 Protists in Havre-aux-Maisons Lagoon
- 25 Protists in Havre-aux-Maisons Lagoon
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- 30 Protists in Havre-aux-Maisons Lagoon
- 31 Protists in Havre-aux-Maisons Lagoon
- 32 Protists in Havre-aux-Maisons Lagoon
- 33 Protists in Havre-aux-Maisons Lagoon
- 34 Eukaryotic Plankton Assemblages Inhabiting Saline Lakes in the Qaidam Basin
- 35 Marine picoplankton
- 36 Deep Hypersaline Anoxic Basin sediment microbial eukaryotes
- 37 Three years diversity in the Eastern English Channel
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2	Organism Name	Instrument
3	marine metagenome	454 GS FLX
4	marine metagenome	454 GS FLX
5	marine metagenome	454 GS FLX
6	marine metagenome	454 GS FLX
7	marine metagenome	454 GS FLX
8	aquatic metagenome	454 GS FLX Titanium
9	aquatic metagenome	454 GS FLX Titanium
10	aquatic metagenome	454 GS FLX Titanium
11	aquatic metagenome	454 GS FLX Titanium
12	Alexandrium catenella	454 GS FLX
13	marine metagenome	454 GS FLX
14	marine metagenome	454 GS FLX
15	marine metagenome	454 GS FLX Titanium
16	marine metagenome	454 GS FLX Titanium
17	marine metagenome	454 GS FLX Titanium
18	marine metagenome	454 GS FLX Titanium
19	marine metagenome	454 GS FLX Titanium
20	uncultured marine eukaryote	454 GS FLX Titanium
21	uncultured marine eukaryote	454 GS FLX Titanium
22	metagenomes	454 GS FLX
23	metagenomes	454 GS FLX Titanium
24	Rotylenchulus reniformis	454 GS FLX Titanium
25	marine metagenome	454 GS FLX Titanium
26	metagenomes	454 GS FLX
27	metagenomes	454 GS FLX
28	metagenomes	454 GS FLX
29	metagenomes	454 GS FLX
30	metagenomes	454 GS FLX
31	metagenomes	454 GS FLX
32	metagenomes	454 GS FLX
33	metagenomes	454 GS FLX
34	metagenomes	454 GS FLX
35	metagenomes	454 GS FLX
36	metagenomes	454 GS FLX
37	metagenomes	454 GS FLX
38	metagenomes	454 GS FLX
39	metagenomes	454 GS FLX
40	metagenomes	454 GS FLX
41	metagenomes	454 GS FLX
42	metagenomes	454 GS FLX
43	metagenomes	454 GS FLX
44	freshwater metagenome	454 GS FLX Titanium
45	freshwater metagenome	454 GS FLX Titanium
46	freshwater metagenome	454 GS FLX Titanium
47	uncultured marine eukaryote	454 GS FLX Titanium
48	marine metagenome	454 GS FLX Titanium
49	eukaryote XCL-2011	454 GS FLX Titanium
50	eukaryote XCL-2011	454 GS FLX Titanium
51	marine metagenome	454 GS FLX
52	Suberites ficus	454 GS FLX Titanium
53	Isopora palifera	454 GS FLX Titanium
54	marine metagenome	454 GS FLX Titanium
55	Seriatopora hystrix	454 GS FLX Titanium
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2	Montipora digitata	454 GS FLX Titanium
3	Porites cylindrica	454 GS FLX Titanium
4	Isopora palifera	454 GS FLX Titanium
5	Isopora palifera	454 GS FLX Titanium
6	Isopora palifera	454 GS FLX Titanium
7	Isopora palifera	454 GS FLX Titanium
8	Montipora digitata	454 GS FLX Titanium
9	Montipora digitata	454 GS FLX Titanium
10	Montipora digitata	454 GS FLX Titanium
11	Montipora digitata	454 GS FLX Titanium
12	Seriatopora hystrix	454 GS FLX Titanium
13	Seriatopora hystrix	454 GS FLX Titanium
14	Seriatopora hystrix	454 GS FLX Titanium
15	Seriatopora hystrix	454 GS FLX Titanium
16	Porites cylindrica	454 GS FLX Titanium
17	Porites cylindrica	454 GS FLX Titanium
18	Porites cylindrica	454 GS FLX Titanium
19	aquatic metagenome	454 GS FLX Titanium
20	marine metagenome	454 GS FLX Titanium
21	marine metagenome	454 GS FLX Titanium
22	marine metagenome	454 GS FLX Titanium
23	marine metagenome	454 GS FLX Titanium
24	marine metagenome	454 GS FLX Titanium
25	marine metagenome	454 GS FLX Titanium
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27	marine metagenome	454 GS FLX Titanium
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32	marine metagenome	454 GS FLX Titanium
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40	marine metagenome	454 GS FLX Titanium
41	marine metagenome	454 GS FLX Titanium
42	marine metagenome	454 GS FLX Titanium
43	marine metagenome	454 GS FLX Titanium
44	marine metagenome	454 GS FLX Titanium
45	marine metagenome	454 GS FLX Titanium
46	marine metagenome	454 GS FLX Titanium
47	marine metagenome	454 GS FLX Titanium
48	marine metagenome	454 GS FLX Titanium
49	marine metagenome	454 GS FLX Titanium
50	marine metagenome	454 GS FLX Titanium
51	gut metagenome	454 GS FLX
52	marine sediment metagenome	454 GS FLX+
53	gut metagenome	454 GS FLX Titanium
54	gut metagenome	454 GS FLX Titanium
55	gut metagenome	454 GS FLX Titanium
56	gut metagenome	454 GS FLX Titanium
57	freshwater metagenome	454 GS FLX Titanium
58	marine metagenome	454 GS FLX Titanium
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2	marine metagenome	454 GS FLX Titanium
3	uncultured eukaryote	454 GS FLX Titanium
4	uncultured eukaryote	454 GS FLX Titanium
5	uncultured eukaryote	454 GS FLX Titanium
6	uncultured eukaryote	454 GS FLX Titanium
7	uncultured eukaryote	454 GS FLX Titanium
8	uncultured eukaryote	454 GS FLX Titanium
9	uncultured eukaryote	454 GS FLX Titanium
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15	uncultured eukaryote	454 GS FLX Titanium
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22	uncultured eukaryote	454 GS FLX Titanium
23	uncultured eukaryote	454 GS FLX Titanium
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25	uncultured eukaryote	454 GS FLX Titanium
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32	uncultured eukaryote	454 GS FLX Titanium
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41	uncultured eukaryote	454 GS FLX Titanium
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51	uncultured eukaryote	454 GS FLX Titanium
52	uncultured eukaryote	454 GS FLX Titanium
53	uncultured eukaryote	454 GS FLX Titanium
54	uncultured eukaryote	454 GS FLX Titanium
55	uncultured eukaryote	454 GS FLX Titanium
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57	uncultured eukaryote	454 GS FLX Titanium
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2	uncultured eukaryote	454 GS FLX Titanium
3	uncultured eukaryote	454 GS FLX Titanium
4	uncultured eukaryote	454 GS FLX Titanium
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7	uncultured eukaryote	454 GS FLX Titanium
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15	uncultured eukaryote	454 GS FLX Titanium
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20	uncultured eukaryote	454 GS FLX Titanium
21	marine metagenome	454 GS FLX+
22	marine metagenome	454 GS FLX Titanium
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34	aquatic metagenome	454 GS FLX
35	marine metagenome	454 GS FLX
36	marine sediment metagenome	454 GS FLX Titanium
37	marine metagenome	454 GS FLX Titanium
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2	Submitter	Study Accession
3	ESE	ERP001773
4	ESE	ERP001773
5	ESE	ERP001773
6	ESE	ERP001773
7	ESE	ERP001773
8	MPIMM	ERP002513
9	MPIMM	ERP002513
10	MPIMM	ERP002513
11	MPIMM	ERP002513
12	MPIMM	ERP002513
13	CNRS/UNIVERSITE MONTPELLIER 2	SRP000647
14	The Chinese University of Hong Kong	SRP000936
15	The Chinese University of Hong Kong	SRP000936
16	The Chinese University of Hong Kong	SRP000936
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21	Inha univ.	SRP006126
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23	University of Kaiserslautern	SRP003169
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25	University of Kaiserslautern	SRP003169
26	Alabama A&M University	SRP008476
27	Universite Laval	SRP013740
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44	Université Laval	SRP014823
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47	Université Laval	SRP014823
48	Alfred Wegener Institute for Polar and Marine Rese	SRP016049
49	University of Kaiserslautern	SRP017187
50	University of Kaiserslautern	SRP017187
51	Woods Hole Oceanographic Institution	SRP017332
52	Woods Hole Oceanographic Institution	SRP017334
53	Woods Hole Oceanographic Institution	SRP017334
54	Alfred Wegener Institute for Polar and Marine Rese	SRP016049
55	hkust-kaust	SRP021898
56	University of Sydney	SRP022083
57	Laval University	SRP022176
58	University of Sydney	SRP022083
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19	Universit* Laval	SRP027540
20	Universite Laval	SRP029291
21	Université Laval	SRP029300
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50	AWI	SRP032538
51	University of Bergen	SRP033298
52	University of Vermont	SRP034591
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54	University of Vermont	SRP034591
55	University of Vermont	SRP034591
56	RCEES, Chinese Academy of Sciences	SRP038053
57	RCEES, Chinese Academy of Sciences	SRP039005
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2	Universite du Littoral Cote d'Opale	SRP039908
3	Université Laval	SRP040423
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21	Universite du Littoral Cote d'Opale	SRP039908
22	Universié Laval	SRP043016
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32	Universié Laval	SRP043016
33	Universié Laval	SRP043016
34	Institute of Shandong River Wetlands	SRP045389
35	Alfred Wegener Instiute	SRP048617
37	Woods Hole Oceanographic Institution	SRP049010
38	Universite du Littoral Cote d'Opale	SRP039908
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2 Study Title  
3 Accuracy of protist diversity assessments: morphology compared to cloning and direct pyrosequencing of 18S rRN  
4 Accuracy of protist diversity assessments: morphology compared to cloning and direct pyrosequencing of 18S rRN  
5 Accuracy of protist diversity assessments: morphology compared to cloning and direct pyrosequencing of 18S rRN  
6 Accuracy of protist diversity assessments: morphology compared to cloning and direct pyrosequencing of 18S rRN  
7 Accuracy of protist diversity assessments: morphology compared to cloning and direct pyrosequencing of 18S rRN  
8 Microbial community response during the iron fertilization experiment LOHAFEX  
9 Microbial community response during the iron fertilization experiment LOHAFEX  
10 Microbial community response during the iron fertilization experiment LOHAFEX  
11 Microbial community response during the iron fertilization experiment LOHAFEX  
12 Microbial community response during the iron fertilization experiment LOHAFEX  
13 Alexandrium catenella  
14 Composition and genetic diversity of picoeukaryotes in subtropical coastal waters as revealed by 454 sequencing-l  
15 Composition and genetic diversity of picoeukaryotes in subtropical coastal waters as revealed by 454 sequencing-l  
16 Microbial Community Diversity Response to a Changing Arctic Ocean  
17 Microbial Community Diversity Response to a Changing Arctic Ocean  
18 Microbial Community Diversity Response to a Changing Arctic Ocean  
19 Marine microbial eukaryote community analysis in Korea  
20 Marine microbial eukaryote community analysis in Korea  
21 Error rate of 454 GS FLX sequenced V4 and V9 PCR amplicons of various protists  
22 Error rate of 454 GS FLX sequenced V4 and V9 PCR amplicons of various protists  
23 Rotylenchulus reniformis Genome sequencing  
24 Arctic sea ice Targeted Locus (Loci)  
25 Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water  
26 Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water  
27 Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water  
28 Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water  
29 Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water  
30 Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water  
31 Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water  
32 Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water  
33 Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water  
34 Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water  
35 Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water  
36 Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water  
37 Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water  
38 Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water  
39 Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water  
40 Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water  
41 Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water  
42 Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water  
43 Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water  
44 Lake A protist communities  
45 Lake A protist communities  
46 Lake A protist communities  
47 Marine eukaryotic protists Metagenome  
48 Partial ribosomal RNA gene of DHAB Ciliates  
49 Highborne Bay eukaryotic small subunit ribosomal RNA diversity  
50 Shark Bay eukaryotic small subunit ribosomal RNA diversity  
51 Marine eukaryotic protists Metagenome  
52 Sponge metagenome  
53 Reef-building coral species harbour Chromera velia and apicomplexan "type-N" (cf. Gemmocystis cylindrus) on the  
54 Protistan communities of the upper Arctic Ocean (18S SSU-rRNA Targeted Locus)  
55 Reef-building coral species harbour Chromera velia and apicomplexan "type-N" (cf. Gemmocystis cylindrus) on the  
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2 Reef-building coral species harbour Chromera velia and apicomplexan “type-N” (cf. Gemmocystis cylindrus) on the  
3 Reef-building coral species harbour Chromera velia and apicomplexan “type-N” (cf. Gemmocystis cylindrus) on the  
4 Reef-building coral species harbour Chromera velia and apicomplexan “type-N” (cf. Gemmocystis cylindrus) on the  
5 Reef-building coral species harbour Chromera velia and apicomplexan “type-N” (cf. Gemmocystis cylindrus) on the  
6 Reef-building coral species harbour Chromera velia and apicomplexan “type-N” (cf. Gemmocystis cylindrus) on the  
7 Reef-building coral species harbour Chromera velia and apicomplexan “type-N” (cf. Gemmocystis cylindrus) on the  
8 Reef-building coral species harbour Chromera velia and apicomplexan “type-N” (cf. Gemmocystis cylindrus) on the  
9 Reef-building coral species harbour Chromera velia and apicomplexan “type-N” (cf. Gemmocystis cylindrus) on the  
10 Reef-building coral species harbour Chromera velia and apicomplexan “type-N” (cf. Gemmocystis cylindrus) on the  
11 Reef-building coral species harbour Chromera velia and apicomplexan “type-N” (cf. Gemmocystis cylindrus) on the  
12 Reef-building coral species harbour Chromera velia and apicomplexan “type-N” (cf. Gemmocystis cylindrus) on the  
13 Reef-building coral species harbour Chromera velia and apicomplexan “type-N” (cf. Gemmocystis cylindrus) on the  
14 Reef-building coral species harbour Chromera velia and apicomplexan “type-N” (cf. Gemmocystis cylindrus) on the  
15 Reef-building coral species harbour Chromera velia and apicomplexan “type-N” (cf. Gemmocystis cylindrus) on the  
16 Reef-building coral species harbour Chromera velia and apicomplexan “type-N” (cf. Gemmocystis cylindrus) on the  
17 Reef-building coral species harbour Chromera velia and apicomplexan “type-N” (cf. Gemmocystis cylindrus) on the  
18 Reef-building coral species harbour Chromera velia and apicomplexan “type-N” (cf. Gemmocystis cylindrus) on the  
19 Ward Hunt Lake Dilution Experiment Eukarya  
20 Uncultured marine eukaryotes Targeted Locus (Loci)  
21 Surface ocean Targeted Locus (Loci)  
22 Surface ocean Targeted Locus (Loci)  
23 Surface ocean Targeted Locus (Loci)  
24 Surface ocean Targeted Locus (Loci)  
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48 Surface ocean Targeted Locus (Loci)  
49 Surface ocean Targeted Locus (Loci)  
50 Gut content of salps Targeted Locus (Loci)  
51 Environmental eukaryotes Metagenome  
52 Design and validation of three primer sets to target the 18S rRNA gene of rumen protozoa.  
53 Design and validation of three primer sets to target the 18S rRNA gene of rumen protozoa.  
54 Design and validation of three primer sets to target the 18S rRNA gene of rumen protozoa.  
55 454 pyrosequencing of plankton sample collected from Hamilton Harbour  
56 Plankton sample collected from Nanaimo Harbour Targeted Locus (Loci)  
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2 Marine metagenome Targeted Locus (Loci)  
3 Uncultured eukaryotes Targeted Locus (Loci)  
4 Uncultured eukaryotes Targeted Locus (Loci)  
5 Uncultured eukaryotes Targeted Locus (Loci)  
6 Uncultured eukaryotes Targeted Locus (Loci)  
7 Uncultured eukaryotes Targeted Locus (Loci)  
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32 Uncultured eukaryotes Targeted Locus (Loci)  
33 Eukaryota Arctic Ocean Survey Targeted Locus (Loci)  
34 Eukaryota Arctic Ocean Survey Targeted Locus (Loci)  
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2 Eukaryota Arctic Ocean Survey Targeted Locus (Loci)  
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18 Eukaryota Arctic Ocean Survey Targeted Locus (Loci)  
19 Eukaryota Arctic Ocean Survey Targeted Locus (Loci)  
20 Eukaryota Arctic Ocean Survey Targeted Locus (Loci)  
21 Marine metagenome Targeted Locus (Loci)  
22 Protists in Havre-aux-Maisons Lagoon, Magdalen Islands, Quebec, Canada  
23 Protists in Havre-aux-Maisons Lagoon, Magdalen Islands, Quebec, Canada  
24 Protists in Havre-aux-Maisons Lagoon, Magdalen Islands, Quebec, Canada  
25 Protists in Havre-aux-Maisons Lagoon, Magdalen Islands, Quebec, Canada  
26 Protists in Havre-aux-Maisons Lagoon, Magdalen Islands, Quebec, Canada  
27 Protists in Havre-aux-Maisons Lagoon, Magdalen Islands, Quebec, Canada  
28 Protists in Havre-aux-Maisons Lagoon, Magdalen Islands, Quebec, Canada  
29 Protists in Havre-aux-Maisons Lagoon, Magdalen Islands, Quebec, Canada  
30 Protists in Havre-aux-Maisons Lagoon, Magdalen Islands, Quebec, Canada  
31 Protists in Havre-aux-Maisons Lagoon, Magdalen Islands, Quebec, Canada  
32 Protists in Havre-aux-Maisons Lagoon, Magdalen Islands, Quebec, Canada  
33 Protists in Havre-aux-Maisons Lagoon, Magdalen Islands, Quebec, Canada  
34 aquatic metagenome Genome sequencing  
35 Marine picoplankton Targeted Locus (Loci)  
36 Environmental pyrotags for eukaryotes Targeted Locus (Loci)  
37 Marine metagenome Targeted Locus (Loci)  
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	Sample Accession	Sample Title	Total Size, Mb	Total RUNs	Total Spots	Total Bases
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2						
3	ERS169722	marine metagenome	23.79	1	21827	9839469
4	ERS169723	marine metagenome	21.43	1	23993	8082496
5	ERS169724	marine metagenome	18.76	1	17244	7794090
6	ERS169725	marine metagenome	17.47	1	19798	6666525
7	ERS249848		85.86	1	72440	38229935
8	ERS249849		102.95	1	81845	47054441
9	ERS249850		118.91	1	98290	53957382
10	ERS249851		100.9	1	88895	43788914
11	SRS002344		35.51	1	71986	18253824
12	SRS004112		61.34	1	100911	27881207
13	SRS004113		53.61	1	87392	24193478
14	SRS152378		75.57	2	74742	32439603
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19	SRS086207		22.19	1	53155	10757013
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21	SRS265308		1523.59	1	1206043	732000297
22	SRS345723		115.48	1	97702	48782681
23	SRS346704		12.67	1	11368	6229595
24	SRS346705		15.56	1	14233	7736979
25	SRS346706		9.52	1	8332	4512789
26	SRS346707		11	1	9993	5429341
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28	SRS346709		17.94	1	16171	8854309
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31	SRS346707		3.3	1	8032	1538044
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35	SRS348706		3.9	1	9538	1827278
36	SRS355910		86.28	1	72724	36293480
37	SRS355910		42.46	1	35716	17867669
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40	SRS375573		540.47	1	513347	236974344
41	SRS377421		277.64	1	260367	120224628
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43	SRS415390		351.24	1	278116	166721838
44	SRS417793		4.62	1	11325	6671280
45	SRS418650		0.91	1	7981	1692614
46	SRS419165		322.41	1	273168	144033297
47	SRS419338		0.41	1	3871	806497
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3	SRS419340	1.04	1	11758	2445426
4	SRS418650	0.68	1	3132	976006
5	SRS418650	1.64	1	7869	2535594
6	SRS418650	5.82	1	21910	8789284
7	SRS419339	0.82	1	3714	1214580
8	SRS419339	1.77	1	8746	2761817
9	SRS419339	1.93	1	7460	2842999
10	SRS419338	4.94	1	18201	7310788
11	SRS419338	1.04	1	3904	1497539
12	SRS419338	0.82	1	3682	1202397
13	SRS419340	0.99	1	4352	1465489
14	SRS419340	0.91	1	4454	1311120
15	SRS419340	0.89	1	3886	1329835
16	SRS463199	196.76	2	173394	87300958
17	SRS474263	162.05	1	144296	73326694
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47	SRS584358	13.44	1	12395	6210778
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21	SRS629200	13.76	1	11779	5796806
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23	SRS629202	12.39	1	10538	5211005
24	SRS629203	13.89	1	11819	5847093
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29	SRS715739	0.72	4	34093	1251455
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31	SRS752744	1809.99	1	1566895	865799314
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## FTP Path to Experiment

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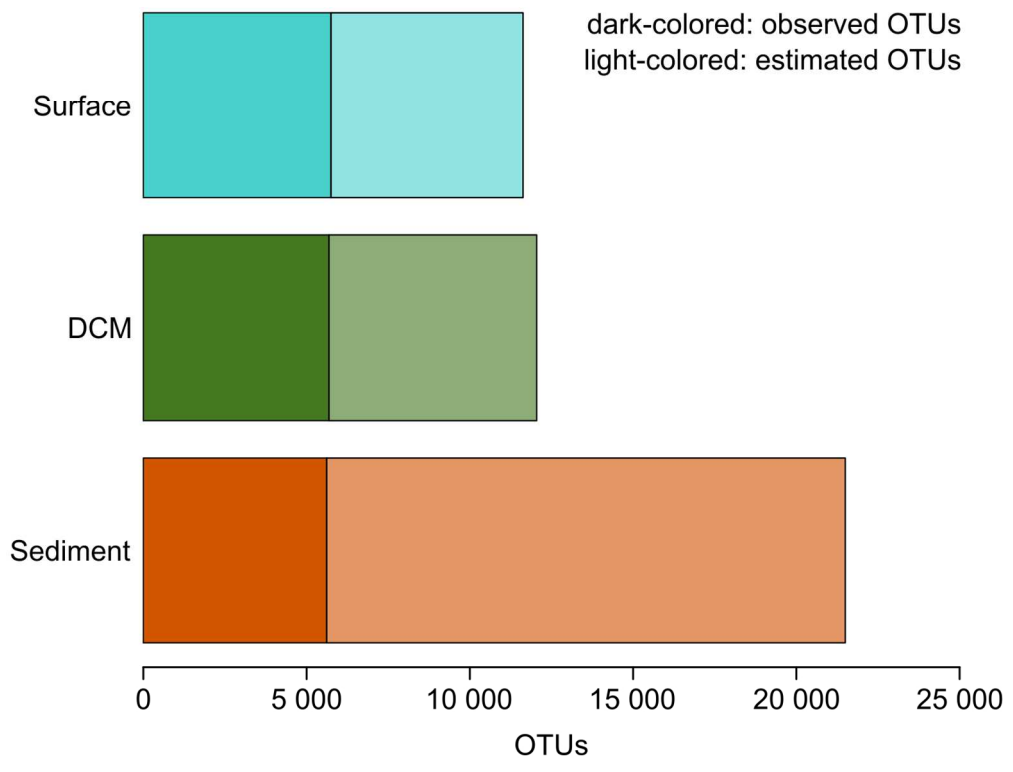
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5	Tintinnid_SSU_lib	AMPLICON	GENOMIC	PCR
6	Tintinnid_ITS_lib	AMPLICON	GENOMIC	PCR
7				
8	LOHAFEX library of sample day_-1	AMPLICON	METAGENOMIC	PCR
9	LOHAFEX library of sample day_9	AMPLICON	METAGENOMIC	PCR
10	LOHAFEX library of sample day_18	AMPLICON	METAGENOMIC	PCR
11	LOHAFEX library of sample day_36	AMPLICON	METAGENOMIC	PCR
12				
13	SUBINI	EST	TRANSCRIPTOMIC	RANDOM
14				
15	MB	AMPLICON	GENOMIC	PCR
16	TH	AMPLICON	GENOMIC	PCR
17	AMCEpooledBACT	AMPLICON	OTHER	PCR
18	AMCEpooledARCH	AMPLICON	OTHER	PCR
19	AMCEpooledEUK	AMPLICON	OTHER	PCR
20	Ciliate-specific	AMPLICON	METAGENOMIC	PCR
21	Eukaryote-universal	AMPLICON	METAGENOMIC	PCR
22				
23	GS_FLX	AMPLICON	METAGENOMIC	PCR
24	GS_FLX_Titanium	AMPLICON	METAGENOMIC	PCR
25				
26	Lib_RepliGRN	WGS	GENOMIC	unspecified
27	ASID	AMPLICON	METAGENOMIC	PCR
28	VS-454-MBL:assay:D1.3_Bacteria	AMPLICON	METAGENOMIC	PCR
29	VS-454-MBL:assay:E1.5_Bacteria	AMPLICON	METAGENOMIC	PCR
30	VS-454-MBL:assay:D2.4_Bacteria	AMPLICON	METAGENOMIC	PCR
31	VS-454-MBL:assay:A1.1_Bacteria	AMPLICON	METAGENOMIC	PCR
32	VS-454-MBL:assay:A2.2_Bacteria	AMPLICON	METAGENOMIC	PCR
33	VS-454-MBL:assay:E2.6_Bacteria	AMPLICON	METAGENOMIC	PCR
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35	VS-454-MBL:assay:D1.V4.9_Bacteria	AMPLICON	METAGENOMIC	PCR
36	VS-454-MBL:assay:A1.V4.7_Bacteria	AMPLICON	METAGENOMIC	PCR
37	VS-454-MBL:assay:A2.V4.8_Bacteria	AMPLICON	METAGENOMIC	PCR
38	VS-454-MBL:assay:D2.V4.10_Bacteria	AMPLICON	METAGENOMIC	PCR
39	VS-454-MBL:assay:E2.V4.12_Bacteria	AMPLICON	METAGENOMIC	PCR
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56	PRJNA193567	AMPLICON	METAGENOMIC	PCR
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58	JS_NGS176-2_short	AMPLICON	METAGENOMIC	PCR
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3	JS_NGS66-2_short	AMPLICON	METAGENOMIC	PCR
4	JS_NGS42a_EUK1	AMPLICON	METAGENOMIC	PCR
5	JS_NGS42a-EUK-A7	AMPLICON	METAGENOMIC	PCR
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7	JS_NGS60a_EUK1	AMPLICON	METAGENOMIC	PCR
8	JS_NGS60a-EUKA7	AMPLICON	METAGENOMIC	PCR
9	JS_NGS60a_bact	AMPLICON	METAGENOMIC	PCR
10	JS_NGS176-2_bact	AMPLICON	METAGENOMIC	PCR
11	JS_NGS176-2_EUK1	AMPLICON	METAGENOMIC	PCR
12	JS_NGS176-2-EUK-A7	AMPLICON	METAGENOMIC	PCR
13	JS_NGS66-2-EUK-A7	AMPLICON	METAGENOMIC	PCR
14	JS_NGS66-2_EUK1	AMPLICON	METAGENOMIC	PCR
15	JS_NGS66-2_bact	AMPLICON	METAGENOMIC	PCR
16	WHL_DilEXEuk	AMPLICON	METAGENOMIC	PCR
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51		AMPLICON	GENOMIC	PCR
52	ThreeSeds	AMPLICON	METAGENOMIC	PCR
53		AMPLICON	GENOMIC	PCR
54		AMPLICON	GENOMIC	PCR
55		AMPLICON	GENOMIC	PCR
56		AMPLICON	GENOMIC	PCR
57	Hamilton-18S_Replicate	AMPLICON	METAGENOMIC	PCR
58	Nanaimo plankton	AMPLICON	GENOMIC	PCR
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3		AMPLICON	METAGENOMIC	PCR
4		AMPLICON	METAGENOMIC	cDNA
5	JB121SF_RNA	AMPLICON	METAGENOMIC	PCR
6	JB121SCM_DNA	AMPLICON	METAGENOMIC	cDNA
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12	JB601SF_DNA	AMPLICON	METAGENOMIC	cDNA
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14	JB601SCM_DNA	AMPLICON	METAGENOMIC	cDNA
15	JB601SCM_RNA	AMPLICON	METAGENOMIC	PCR
16	NEC211SF_DNA	AMPLICON	METAGENOMIC	cDNA
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20	NEF43SF_DNA	AMPLICON	METAGENOMIC	cDNA
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27	NEF512SCM_RNA	AMPLICON	METAGENOMIC	PCR
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29	HB_2010_710_34m_euk	AMPLICON	GENOMIC	PCR
30	HB_2010_699_6m_euk	AMPLICON	GENOMIC	PCR
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33	HB_2010_709_30m_euk	AMPLICON	GENOMIC	PCR
34	HB_2010_745_10m_euk	AMPLICON	GENOMIC	PCR
35	HB_2010_745_47m_euk	AMPLICON	GENOMIC	PCR
36	HB_2010_706_10m_euk	AMPLICON	GENOMIC	PCR
37	HB_2010_706_30m_euk	AMPLICON	GENOMIC	PCR
38	HB_2010_706_40m_euk	AMPLICON	GENOMIC	PCR
39	LS_2006_301_25m_euk	AMPLICON	GENOMIC	PCR
40	LS_2008_303_16m_euk	AMPLICON	GENOMIC	PCR
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42	CB_2011_314_18m_euk	AMPLICON	GENOMIC	PCR
43	CB_2011_314_2m_euk	AMPLICON	GENOMIC	PCR
44	BB_2005_131_40m_euk	AMPLICON	GENOMIC	PCR
45	BB_2005_131_5m_euk	AMPLICON	GENOMIC	PCR
46	BB_2005_100_22m_euk	AMPLICON	GENOMIC	PCR
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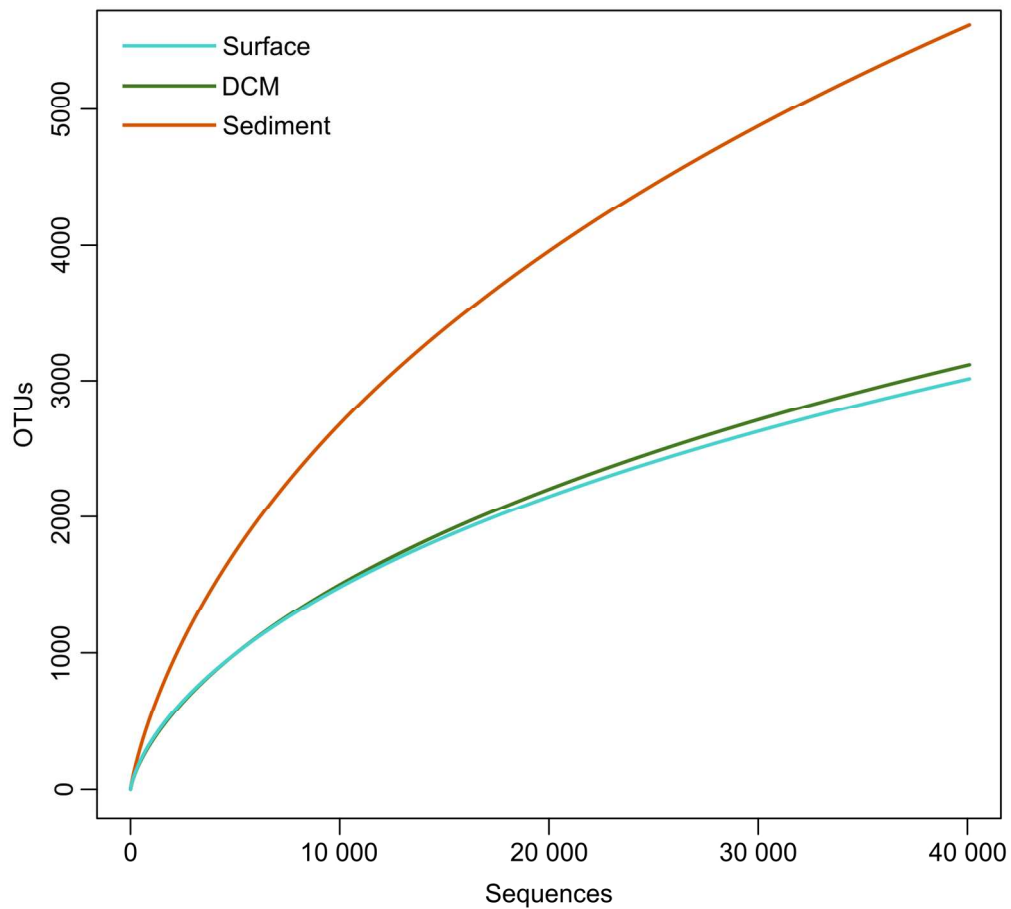
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8	BB_2006_123_45m_euk	AMPLICON	GENOMIC	PCR
9	BB_2006_123_10m_euk	AMPLICON	GENOMIC	PCR
10	Lv_2007_VB0603_5m_euk	AMPLICON	GENOMIC	PCR
11	Lv_2007_VB1007_7m_euk	AMPLICON	GENOMIC	PCR
12	Lv_2007_VB1607_8m_euk	AMPLICON	GENOMIC	PCR
13	Lv_2007_VB2107_7m_euk	AMPLICON	GENOMIC	PCR
14	Lv_2007_VB3807_6m_euk	AMPLICON	GENOMIC	PCR
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16	Lv_2007_VB7207_5m_euk	AMPLICON	GENOMIC	PCR
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136x102mm (300 x 300 DPI)

Review

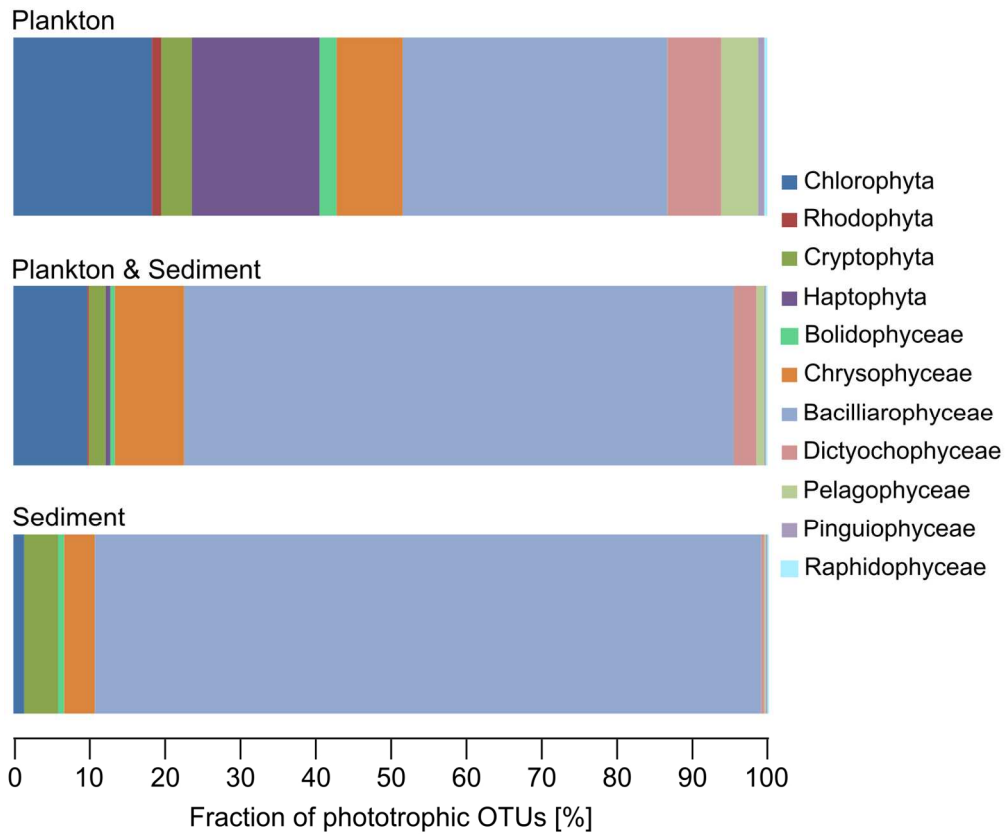


152x138mm (300 x 300 DPI)

ew

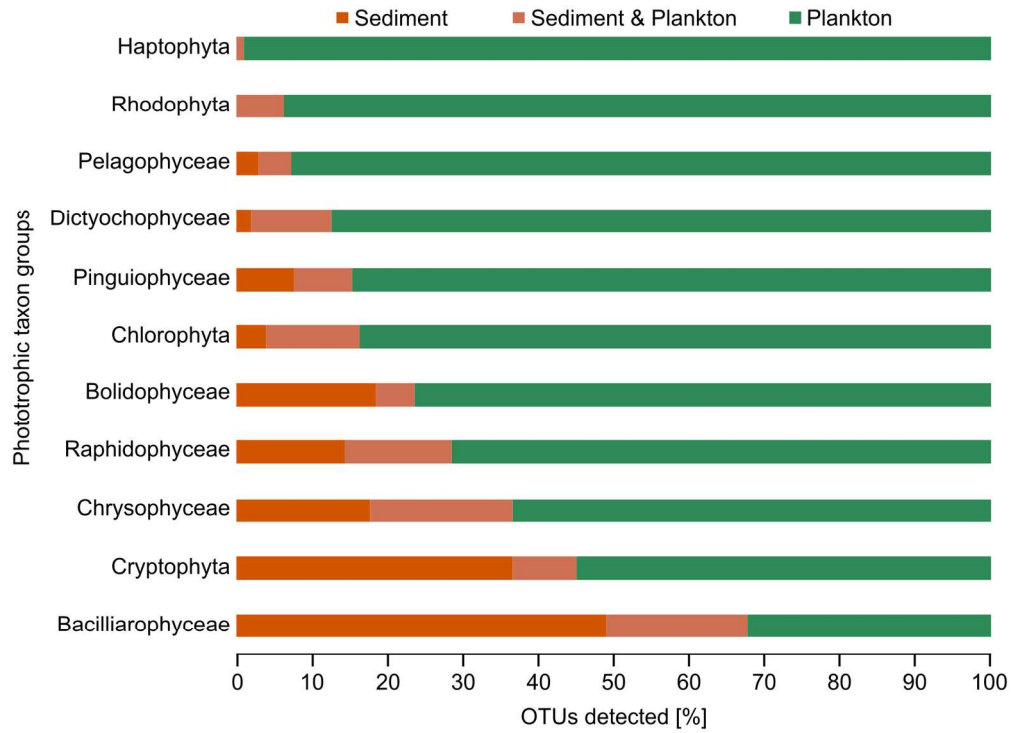


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145x122mm (300 x 300 DPI)

view

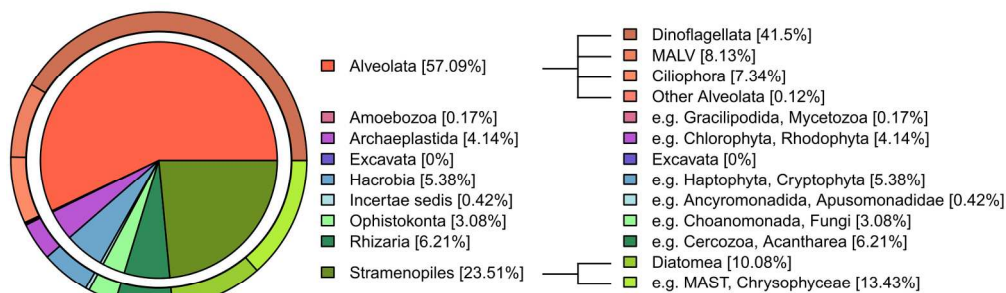


160x116mm (300 x 300 DPI)

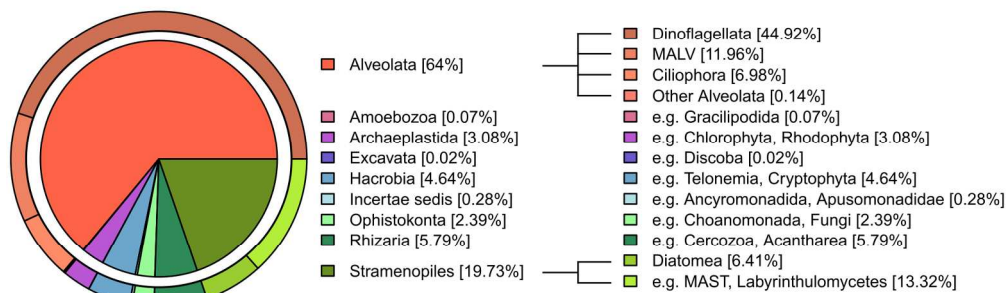
Review

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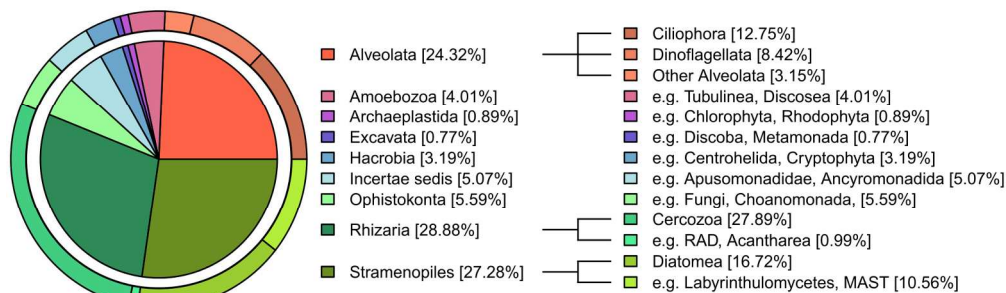
Surface



DCM



Sediment



171x178mm (300 x 300 DPI)