

Benthic protists: the under-charted majority

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Abstract

Marine protist diversity inventories have largely focused on planktonic environments, while benthic protists have received relatively little attention. We therefore hypothesize that current diversity surveys have only skimmed the surface of protist diversity in marine sediments, which may harbour greater diversity than planktonic environments. We tested this by analyzing sequences of the hypervariable V4 18S rRNA from benthic and planktonic protist communities sampled in European coastal regions. Despite a similar number of OTUs in both realms, richness estimations indicated that we recovered at least 70% of the diversity in planktonic protist communities, but only 33% in benthic communities. There was also little overlap of OTUs between planktonic and benthic communities, as well as between separate benthic communities. We argue that these patterns reflect the heterogeneity and diversity of benthic habitats. A comparison of all OTUs against the Protist Ribosomal Reference database showed that a higher proportion of benthic than planktonic protist diversity is missing from public databases; similar results were obtained by comparing all OTUs against environmental references from NCBI's Short Read Archive. We suggest that the benthic realm may therefore be the world's 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, Holzmänn 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

extracellular DNA may severely bias the environmental sequencing studies (Dell'Anno and Danovaro 2005). Furthermore, specific techniques and expensive equipment are required to access these physically remote environments (Orcutt *et al.* 2011). Published benthic studies of protists are thus not only restricted in geographic scope, but also in their comparisons to the overlying planktonic protists. Despite our limited knowledge of benthic protists, there is strong agreement among microbial ecologists that marine coastal sediments play a pivotal role for the diversity and dynamics of overlying plankton communities by acting as seedbanks (Marcus and Boreo 1998). The benthic species reservoir consists of both truly active benthic species and resting stages of dormant planktonic species. Most of the latter occur in low abundances, but blooms can be initiated in response to environmental changes (Marcus and Boreo 1998). Furthermore, studies on microfossil protists have suggested that several planktonic lineages have evolved from benthic ancestors, which have colonized the pelagic realm on different occasions (Leckie 2009).

In this study, we used previously published data from Massana *et al.* (2015) that surveyed protist diversity in European coastal waters and sediments from Norway to Bulgaria using the V4 region of the 18S rRNA. Massana *et al.* (2015) provided a general taxonomic overview of planktonic and benthic protists, with particular attention on examining differences in size-fractionated planktonic protist communities and comparing results obtained from DNA and RNA templates. Building upon this initial study, here we focus on a more detailed comparison of benthic and planktonic protist diversity, with a special emphasis on the richness and phylogenetic novelty contained in marine benthic protist assemblages, two topics that were not covered by Massana *et al.* (2015). Our results not only support previous notions of more diverse benthic than planktonic protist communities, but also present clear

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indications of a higher degree of novelty in genetic signatures within benthic communities.

Methods

Sampling, pyrosequencing and data processing

In the framework of the BioMarKs project (Dunthorn *et al.* 2014a; Logares *et al.* 2014; Massana *et al.* 2015), water samples from the surface and deep chlorophyll maximum (DCM) layer, and sediment samples were collected from six different European coastal sites including the Skagerrak, the English Channel, the Atlantic Ocean, the Mediterranean Sea and the Black Sea (Table 1). For details on sampling protocols, nucleic acid extraction, 454-pyrosequencing of the hypervariable V4 18S rDNA region and data processing see Massana *et al.* (2015). Briefly, RNA from benthic samples was extracted from 2.5 g of surficial sediment using the Power Soil RNA kit (MoBio, Carlsbad, United States). RNA from planktonic samples was extracted with the NucleoSpin RNA kit (Macherey-Nagel, Düren, Germany) from filters of DCM and surface water samples collected with Niskin bottles. Both extraction kits are specifically optimized to gain high RNA yields from the respective samples and are routinely used in environmental high-throughput sequencing (HTS) studies. Because of the difficulties in RNA extractions from sediment samples (Hurt *et al.* 2001), using an optimized kit for the recovery of nucleic acids from benthic samples was especially important. By targeting environmental (e)RNA rather than environmental (e)DNA we minimized potential biases induced by accumulation and preservation of extracellular eDNA in sediments (Dell’Anno and Danovaro 2005; Stoeck *et al.* 2007). The effect of extracellular eDNA is less critical when only water 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
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11 151 (Stoeck *et al.* 2010). This primer pair, though, does not cover Foraminifera and
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13 152 several excavate lineages that are important contributors to benthic protist
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15 153 communities but whose taxonomy is not very well delineated by the V4 region
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17 154 (Pawlowski *et al.* 2011; Lax and Simpson 2013). In contrast to other barcode genes,
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19 155 the V4 region does allow for better comparisons with published full-length 18S rRNA
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21 156 Sanger sequencing studies and has a better database coverage for taxonomic
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23 157 assignment (Stoeck *et al.* 2010; Dunthorn *et al.* 2012). Pyrosequencing of the
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25 158 amplified PCR product was conducted on a 454 GS FLX Titanium system (454 Life
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27 159 Sciences, USA). Resulting 454 reads were subject of a strict quality filtering,
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29 160 including two steps of chimera checking in UCHIME (Edgar *et al.* 2011) and
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31 161 ChimeraSlayer (Haas *et al.* 2011). All quality sequences were then clustered into
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33 162 OTUs using USEARCH (Edgar 2010) on a 97% sequence similarity value. In a
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35 163 second step of quality filtering, one representative of each OTU was subject to a
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37 164 BLASTn analysis against NCBI's nucleotide database release 183.0. All OTUs
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39 165 assigned to Bacteria, Archaea, Metazoa, Embryophyta and OTUs with less than 80%
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41 166 similarity to database entries were removed from the dataset. The final dataset
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43 167 included 430 894 V4 18S RNA sequences, which clustered into 12 438 distinct
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45 168 OTUs. The complete BioMarks sequencing dataset is available at the European
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47 169 Nucleotide Archive under the study accession number PRJEB9133.
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56 171 *Taxonomic assignment of OTUs*
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172 To search for the best hit of each OTU to a described organism, we conducted
173 a local BLASTn analysis (using default settings) against the protist reference
174 database PR² (Guillou *et al.* 2012). Additionally, we compared our environmental
175 data against reference data of previous environmental HTS diversity surveys of
176 protists using a similar BLASTn analysis. To build this environmental reference
177 database, we manually screened NCBI's Short Read Archive (SRA) for studies that
178 at least partially included protist data of the eukaryotic 18S gene (according to the
179 experiment's descriptions in the SRA). After downloading the respective data, we
180 removed all references shorter than 100 bp. The final customized SRA reference
181 database consisted of 11 708 385 references from 167 datasets (Supplemental
182 Table S1).

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184 *Statistical analyses and diversity measures*

185 All statistical and diversity analyses were performed in R Studio (version
186 2.15.1, <http://r-project.org>). Following recommendations of previous studies
187 (Dunthorn *et al.* 2014b) we relied on incidence-based rather than abundance-based
188 data to avoid biases induced by uneven gene copy numbers among different protist
189 taxa. Species richness was estimated with the incidence-based coverage estimator
190 (ICE) as implemented in the 'fossil' package (Vavrek 2011). ICE appropriately
191 estimates asymptotic species richness from datasets containing many rare species
192 (Colwell *et al.* 2012), which we expect in benthic protist communities. Additional
193 species richness estimations in CatchAll (Bunge *et al.* 2012) are provided as
194 supplemental material (Supplemental Fig. S2). Non-metric multidimensional scaling
195 (NMDS) using (binary-) Jaccard distances as a measure of β -diversity was performed
196 with the 'vegan' package (Oksanen *et al.* 2015). Non-parametrical, two-sided
197 Kolmogorov-Smirnov tests (KS-tests) using 1000 bootstrap replicates were used to

198 assess the significance of sequence divergence distribution from planktonic and
199 benthic datasets in the package 'Matching' (Sekhon 2011).

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201 **Results**

202 *Comparison of planktonic and benthic protist diversity*

203 The number of quality filtered sequences among the three habitats differed:
204 206 602 from the surface, 184 192 from the DCM, and 40 100 from the sediment
205 (Table 1). Despite these differences, the sequences clustered into similar numbers of
206 OTUs: 5747 in the surface, 5685 in the DCM, and 5616 in the sediment. However,
207 ICE-based richness estimates predicted a difference in the number of total OTUs
208 between the plankton and the sediment: 7763 from the surface, 8140 from the DCM,
209 and 16 652 from the sediment (Fig. 1A). The proportion of OTUs thus not detected
210 through our sequencing effort was 26% in surface, 30.2% in the DCM, and 66.3% in
211 the sediment. Richness estimations based on abundance data revealed similar
212 trends but predicted even more undetected OTUs (Supplemental Fig. S2). The
213 observed trends on OTU richness were further congruent with rarefaction results of
214 sequencing data, which were closer to saturation for water column than for sediment
215 samples (Supplemental Fig. S3). Differences in community composition between
216 plankton and benthos were first shown by the number of shared and exclusive OTUs
217 (Fig. 1B). Of 7729 non-singleton OTUs observed in total, only 708 (9.2%) were
218 shared among all three habitats. This low number is, in part, explained by the low
219 number of co-occurring OTUs in plankton and benthos: the plankton had 4368 non-
220 singleton OTUs not found in the benthos, of which 701 were exclusively found in the
221 surface and 762 were exclusively found in the DCM; the benthos had 2364 non-
222 singleton OTUs not found in the plankton.

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223 NMDS analysis further demonstrated the partitioning of the observed diversity
224 patterns in plankton and benthos (Fig. 2). Since differentiation in size fractions was
225 only possible for planktonic samples and beyond the scope of this work, we pooled
226 planktonic data of different size fractions from the same sampling events. In this
227 analysis, surface and DCM samples clustered closely together, indicating a higher
228 similarity in community composition among plankton samples than among benthos
229 samples. Sediment samples were separated from the water communities in the
230 analysis. In contrast to the narrow cluster of surface and DCM samples, the sediment
231 samples were more widely distributed, indicating high dissimilarity in community
232 composition between individual samples. This also applied to sediment samples from
233 the same sampling site taken in consecutive years, as shown by the large distances
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,

the OTUs detected in the benthos accounted for more than 70% of the OTUs. These groups comprised the Apicomplexa (Alveolata), Apusomonadidae (Incertae Sedis), Centrohelida (Hacrobia), Discosea and Tubulinea (both Amoebozoa), as well as the previously mentioned Cercozoa and Fungi. Further groups mainly detected in the benthos included Ciliophora (Alveolata), Bacilliarophyceae and Labyrinthulomycetes (both Stramenopiles). Dinoflagellates, however, as the taxonomic group with highest OTU richness in total, were predominantly detected in planktonic samples. Acantharea (Rhizaria), MAST (Stramenopiles) and MALV (Alveolata) are three other taxonomic groups with heterotrophic members that were distinctively more often detected in planktonic than in benthic samples. Similar observations were made among the predominantly phototrophic groups Chlorophyta (Archaeplastida), Chrysophyceae and Dictyochophyceae (both Stramenopiles), and Haptophyta (Hacrobia). Supplemental figures S4 and S5 provide a closer look on the occurrence and distribution of phototrophic taxa and show that Cryptophyta and Rhodophyta were also mostly found in planktonic samples, while more diatoms were found in the benthos (677 OTUs) than in the plankton (445 OTUs).

Database coverage and genetic divergence of plankton and benthos OTUs

To assess how well the observed diversity of OTUs matched previously collected data, we calculated their degree of genetic similarity to reference sequences of the taxonomically curated PR² database and to environmental reference sequences of earlier protist diversity inventories deposited in NCBI's SRA (Fig. 5). In both BLAST analyses, the novelty profile was much higher for benthic OTUs, while surface and DCM OTUs exhibited an almost identical profile. Moreover, the genetic similarity of BioMarKs OTUs to PR² references (Fig. 5A) was significantly lower ($p < 0.001$) than to environmental references of the SRA database (Fig. 5B).

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275 Considering that 71.8% of the planktonic OTUs in our study can be assigned on a
276 97%-sequence similarity value to references in PR², this database misses 28.2% of
277 the potentially detectable plankton species (conservative estimate, see discussion).
278 Among benthic protist communities 74.4% of the OTUs did not retrieve a
279 taxonomically assigned hit in PR² at the same threshold of 97% similarity. Regarding
280 the SRA BLAST results, 78.6% of the planktonic OTUs in our study (n=8988 OTUs)
281 were at least 97% similar to previously deposited environmental references,
282 compared to only 42.7% of the OTUs from benthic samples (n=2400 OTUs). These
283 numbers illustrate that the vast majority of planktonic OTUs had already been
284 detected in previous environmental diversity surveys. This, however, was not the
285 case for benthic OTUs. Thus, BioMarks benthos analyses contributed a high
286 proportion of novel OTUs to the environmental reference database.

287 On closer examination of the PR² BLAST results, the mean sequence
288 divergence of OTUs detected in surface and DCM samples from references of the
289 taxonomic reference database was 2.6% (Fig. 6). By contrast, the mean sequence
290 divergence of OTUs from sediment samples to PR² accessions was 6.6%, indicating
291 that the benthic compartment contains protist species more distantly related to
292 previously deposited taxa than the planktonic compartment. Specifically among the
293 Alveolata, Hacrobia, Opisthokonta, Rhizaria and Stramenopiles, the difference in
294 divergence between plankton and benthos was statistically significant ($p<0.001$). For
295 example, while the mean sequence divergence of OTUs assigned to Rhizaria from
296 PR² references was 3.5% in both the surface and DCM, the averaged divergence
297 was 8.2% in the sediment.

300 **Discussion**

301 *High α - and β -diversity shapes coastal benthic protist communities*

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

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

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the euphotic zone. Such data are scarcely available for protists and usually limited to specific lineages. One example is a Sanger sequencing study that focused on ciliates (Doherty *et al.* 2010), which reported little overlap between genetic signatures of benthic and planktonic communities in the Gulf of Maine and Long Island Sound. This finding corroborates our observations on whole protist communities in European coastal habitats (Fig. 1B). More data exists, however, for benthic-planktonic community comparisons of marine bacteria. Zinger *et al.* (2011) showed that bacterial OTU richness and β -diversity was much higher in coastal sediments than in coastal surface waters. Similar results were obtained in an arctic fjord HTS survey (Teske *et al.* 2011). These patterns nicely reflect those obtained in our study on protists.

Building upon the Massana *et al.* (2015) study, we targeted the question of the magnitude of benthic compared to planktonic diversity by contrasting the degree of observed richness with the degree of estimated richness (Fig. 1A). In the same context, we highlighted how much of this observed diversity likely represented novel diversity (Figs. 5 and 6), a previously unexamined topic. Furthermore, we contrasted the β -diversity among benthic and planktonic communities (Fig. 2), illustrating small overlap between benthic and planktonic diversity, but also among benthic communities in particular. Given that biodiversity is considered to be higher in coastal than in open ocean habitats (Gray 1997; Zinger *et al.* 2011), the BioMarkS data suggest that marine coastal sediments may be the world's largest reservoir of protist diversity, much of which is still undetected and most of which is still undescribed in public databases.

One major factor that might promote high diversity in benthic protist communities is a large number of distinct benthic habitats due to horizontal and vertical gradients in both physical and chemical characteristics. Even at microscale,

habitat heterogeneity in marine sediments reflects gradients in grain-sizes, oxygen concentration or organic matter content (Pedersen, Smets and Dechesne 2015). The diversity of physico-chemical microhabitats likely promotes the existence of highly specialized organisms and is probably an important driver for species-richness patterns (Hortal *et al.* 2009). We thus argue that our findings of high protist richness and heterogeneity at comparably small geographical scales represents a general trend in benthic diversity, which is well supported by previous findings, *e.g.* in the Yellow Sea, where high α - and β -diversity patterns in coastal marine sediments were unveiled (Gong *et al.* 2015). To further investigate the effect of niche partitioning, species-area relationships and distance-decay relationships on small spatial and temporal scales could be analyzed for planktonic and benthic protists at the same locales (Franzén, Schweiger and Betzholtz 2012; Zinger, Boetius and Ramette 2014). In addition to habitat heterogeneity, geological structures at the seafloor may act as biogeographical barriers. Even locally, this results in a spatial separation of protist communities (Scheckenbach *et al.* 2010). Both factors, niche partitioning and allopatric speciation processes may work *in concerto* to generate and maintain a high diversity of protists in sediments. In direct comparison, environmental heterogeneity is surely much more pronounced in the benthos (Orcutt *et al.* 2011) than in the plankton, although the pelagic realm may create patchy distributions of protists as well (Menden-Deuer and Fredrickson 2010; Dolan and Stoeck 2011).

Additional reasons for diverging protist communities between individual benthic sites (Fig. 2) may also be of technical nature: we found that all sediment samples were severely undersampled as a result of their high diversity (Supplemental Fig. S3). Because of this undersampling, community divergence among different sediment samples may be artificially inflated. It is, however, reasonable to assume that with increasing sampling effort the proportion of OTUs

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379 that are shared between two samples and the proportion of OTUs that are unique to
380 each of these samples would remain similar. We therefore argue that the observed
381 high Jaccard-distance between the sediment protist communities is more due to true
382 (biological) heterogeneity in species memberships rather than to (technical)
383 undersampling.

384
385 *Different protist taxon groups thrive in plankton and benthos*

386 Benthic protist diversity uncovered by environmental HTS is comprised of i)
387 resident species of truly benthic origin; ii) transient species, which spend at least part
388 of their life cycle living actively in or on sediments; iii) non-resident species of
389 planktonic origin present as inactive resting stages, or as recently settled cells. OTUs
390 of resident species clearly dominated the benthic protist communities in our analyses
391 (Fig. 1B). Though transient species are commonly found among different taxonomic
392 groups (Garstecki *et al.* 2000), we found only little overlap between benthic and
393 planktonic OTUs (Figs. 1B and 2). A notable fraction of this overlap was related to
394 diatoms, Chrysophyceae and Chlorophyta (Supplemental Fig. S4). Since all of these
395 groups include species of planktonic origin which are able to form benthic resting
396 stages (McQuoid and Hobson 1996; Duff, Zeeb and Smol 2013), we cannot rule out
397 that at least some of the phototrophic OTUs in sediments could correspond to
398 phytoplankton cysts or cells that had sunk to the sea floor shortly before sampling.
399 Genetic signatures of the planktonic diatom family Leptocylindraceae in sediment
400 samples represent such a peculiar case (Nanjappa *et al.* 2014). However, particularly
401 among phototrophic protists, diatoms were more often detected in the benthos than
402 in the plankton. Indeed this group is known to harbour a larger diversity of benthic
403 than planktonic species, especially in shallow coastal waters (Mann and Evans
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 *Ascetosporea* (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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431 samples, though less pronounced, was also observed for ciliates. This result is
432 supported by previous morphological and molecular studies that reported higher
433 benthic than planktonic ciliate diversity (Patterson, Larsen and Corliss 1989; Doherty
434 *et al.* 2010). As discussed above, the situation was similar for diatoms.

435 We detected an inverse trend in diversity among the Acantharea,
436 Dinoflagellata and MALV, all of which are commonly observed in planktonic
437 communities (Guillou *et al.* 2008; Jeong *et al.* 2010; Massana 2011; Decelle *et al.*
438 2013). Acantharea and dinoflagellates are mostly planktonic organisms and both
439 groups comprise mixotrophs or members with phototrophic symbionts (Gilg *et al.*
440 2010; Hansen 2010). MALV, on the other hand, can be found as parasites of ciliates,
441 dinoflagellates, radiolarians and fish eggs (Massana 2011) and are known to form
442 planktonic lifecycles (Guillou *et al.* 2008). Unicellular Archaeplastida (Chlorophyta)
443 and Hacrobia (Haptophyta) were also largely missing from benthos samples but
444 occurred in plankton samples. These groups mainly consist of autotrophic organisms
445 performing carbon fixation (Vaulot *et al.* 2008; Not *et al.* 2012) and are major
446 contributors to the pico- and nanoplankton diversity and biomass across the world's
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 PR² 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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483 Regarding the divergence of benthic OTUs from publicly available reference
484 sequences, we suppose that we are just scratching the surface of protist diversity in
485 coastal sediments. Thus, we understand the BioMarKs data as a starting point that
486 may guide the discovery of more novel benthic protist diversity by further taxon-
487 specific screening.

488
489
490 **Conclusions**

491 Over the last 60 years, our perception of marine benthic environments has
492 changed from being biologically inert deserts towards being highly heterogeneous
493 habitats teeming with a multitude of microbial organisms. Even though new
494 technologies allow for addressing this vast diversity, the results of the BioMarKs
495 project strongly imply that the most part of benthic protist diversity remains a black
496 box. While sampling the deep-seafloor surely imposes many challenges and
497 restrictions that have lagged the exploration of benthic diversity, our data show that it
498 is not mandatory to focus on such remote environments when looking for highly
499 diverse protist communities. From a quantitative (*i.e.* OTU richness) and qualitative
500 (*i.e.* degree of genetic divergence) point of view, coastal sediments inhabit
501 intriguingly rich protist assemblages on local and regional scales. Increasing the
502 efforts to explore these assemblages will be beneficial to learn more about the
503 dispersal patterns of benthic protists, their roles in ecosystem functioning and to
504 complement current species inventories by identifying many still unknown organisms.

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506
507 **Funding**

1
2
3 508 This work was supported by the European Commission and is part of the EU-FP7
4
5 509 ERA-net program BiodivERsA, under the project BioMarKs [2008-6530]. DF was
6
7 510 supported by a graduate scholarship of Stipendienstiftung Rheinland-Pfalz. MD and
8
9 511 FM were supported by the Deutsche Forschungsgemeinschaft [grant #DU1319/1-1].
10
11 512 TS was supported by the Deutsche Forschungsgemeinschaft [grant #STO414/11-1].
12
13 513 DV was supported by the European Union [grants MicroB3/FP7-287589,
14
15 514 MaCuMBA/FP7-KBBE-2012-6-311975].
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517 **Acknowledgements**

25 518 We would like to thank the Regional Computing Center at the University of
26
27 519 Kaiserslautern for providing computational resources.
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521 **Conflict of interest**

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36 522 The authors declare that they have no conflict of interest.
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References

Bass D, Chao EE-Y, Nikolaev S *et al.* Phylogeny of novel naked filose and reticulose Cercozoa: Granofilosea cl. n. and Proteomyxidea revised. *Protist* 2009;**160**:75–109.

Bass D, Yabuki A, Santini S *et al.* Reticulamoeba is a long-branched granofilosean (Cercozoa) that is missing from sequence databases. *PLoS ONE* 2012;**7**:e49090.

Berney C, Romac S, Mahé F *et al.* Vampires in the oceans: predatory cercozoan amoebae in marine habitats. *ISME J* 2013;**7**:2387–99.

Bik HM, Sung W, De Ley P *et al.* Metagenetic community analysis of microbial eukaryotes illuminates biogeographic patterns in deep-sea and shallow water sediments. *Mol Ecol* 2012;**21**:1048–59.

Bittner L, Gobet A, Audic S *et al.* Diversity patterns of uncultured Haptophytes unravelled by pyrosequencing in Naples Bay. *Mol Ecol* 2013;**22**:87–101.

Bunge J, Woodard L, Böhning D *et al.* Estimating population diversity with CatchAll. *Bioinformatics* 2012;**28**:1045–7.

del Campo J, Mallo D, Massana R *et al.* Diversity and distribution of unicellular opisthokonts along the European coast analysed using high-throughput sequencing. *Environ Microbiol* 2015;**17**:3195–207.

Chantangsi C, Leander BS. An SSU rDNA barcoding approach to the diversity of marine interstitial cercozoans, including descriptions of four novel genera and nine novel species. *Int J Syst Evol Microbiol* 2010;**60**:1962–77.

Colwell RK, Chao A, Gotelli NJ *et al.* Models and estimators linking individual-based and sample-based rarefaction, extrapolation and comparison of assemblages. *J Plant Ecol* 2012;**5**:3–21.

Dawson SC, Pace NR. Novel kingdom-level eukaryotic diversity in anoxic environments. *Proc Natl Acad Sci* 2002;**99**:8324–9.

Decelle J, Martin P, Paborstava K *et al.* Diversity, ecology and biogeochemistry of cyst-forming Acantharia (Radiolaria) in the oceans. *PLoS ONE* 2013;**8**:e53598.

Dell’Anno A, Danovaro R. Extracellular DNA plays a key role in deep-sea ecosystem functioning. *Science* 2005;**309**:2179–2179.

Doherty M, Tamura M, Vriezen JAC *et al.* Diversity of Oligotrichia and Choreotrichia ciliates in coastal marine sediments and in overlying plankton. *Appl Environ Microbiol* 2010;**76**:3924–35.

Dolan JR, Stoeck T. Repeated sampling reveals differential variability in measures of species richness and community composition in planktonic protists. *Environ Microbiol Rep* 2011;**3**:661–6.

Duff K, Zeeb BA, Smol JP. *Atlas of Chrysophycean Cysts*. Dordrecht: Springer Science & Business Media, 2013.

Dunthorn M, Klier J, Bunge J *et al.* Comparing the hyper-variable V4 and V9 regions of the small subunit rDNA for assessment of ciliate environmental diversity. *J Eukaryot Microbiol* 2012;**59**:185–7.

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

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

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

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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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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.

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

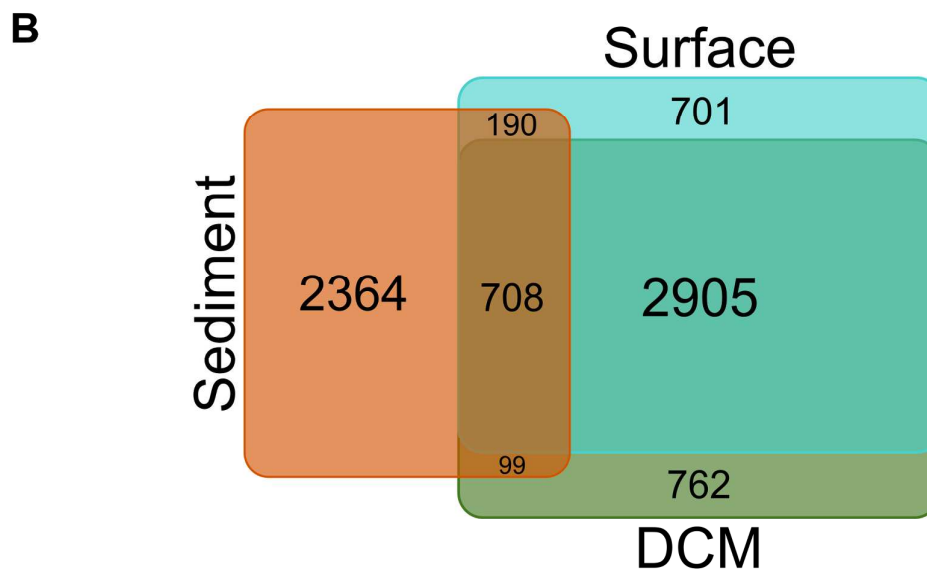
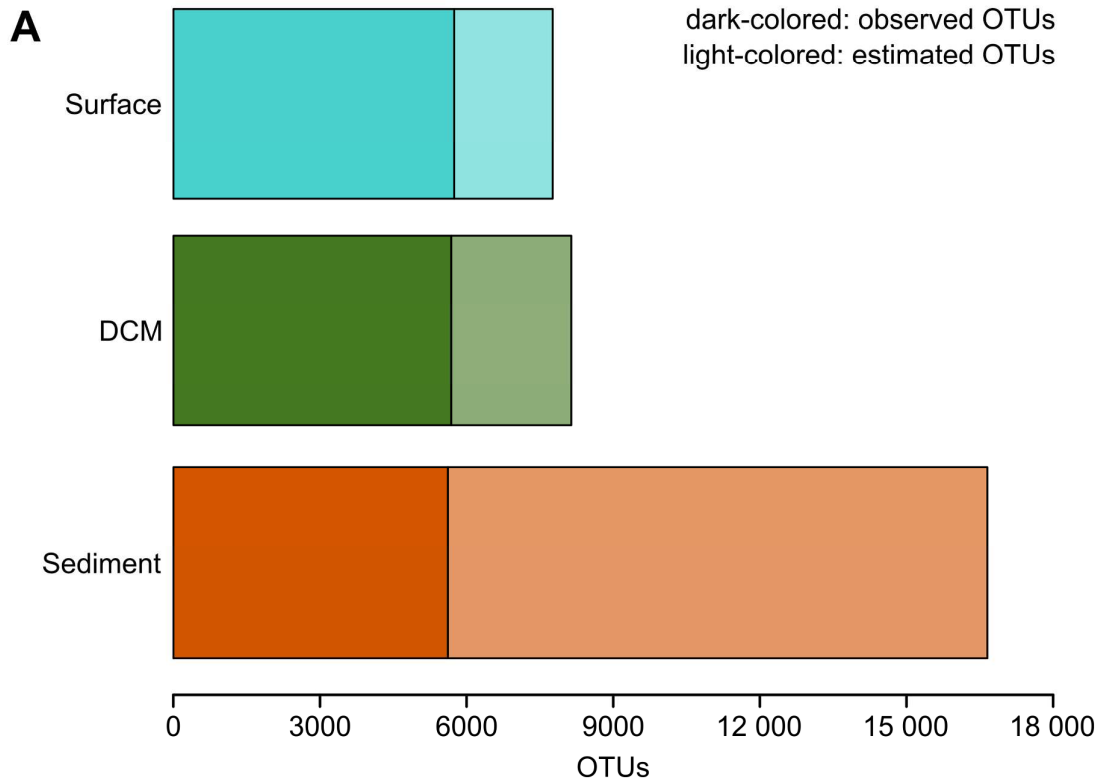
Total number of surface water quality sequences: 206 602.

Total number of DCM quality sequences: 184 192.

Total number of sediment quality sequences: 40 100.

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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 proportionally approximated to the number of OTUs from the respective habitat.



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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.

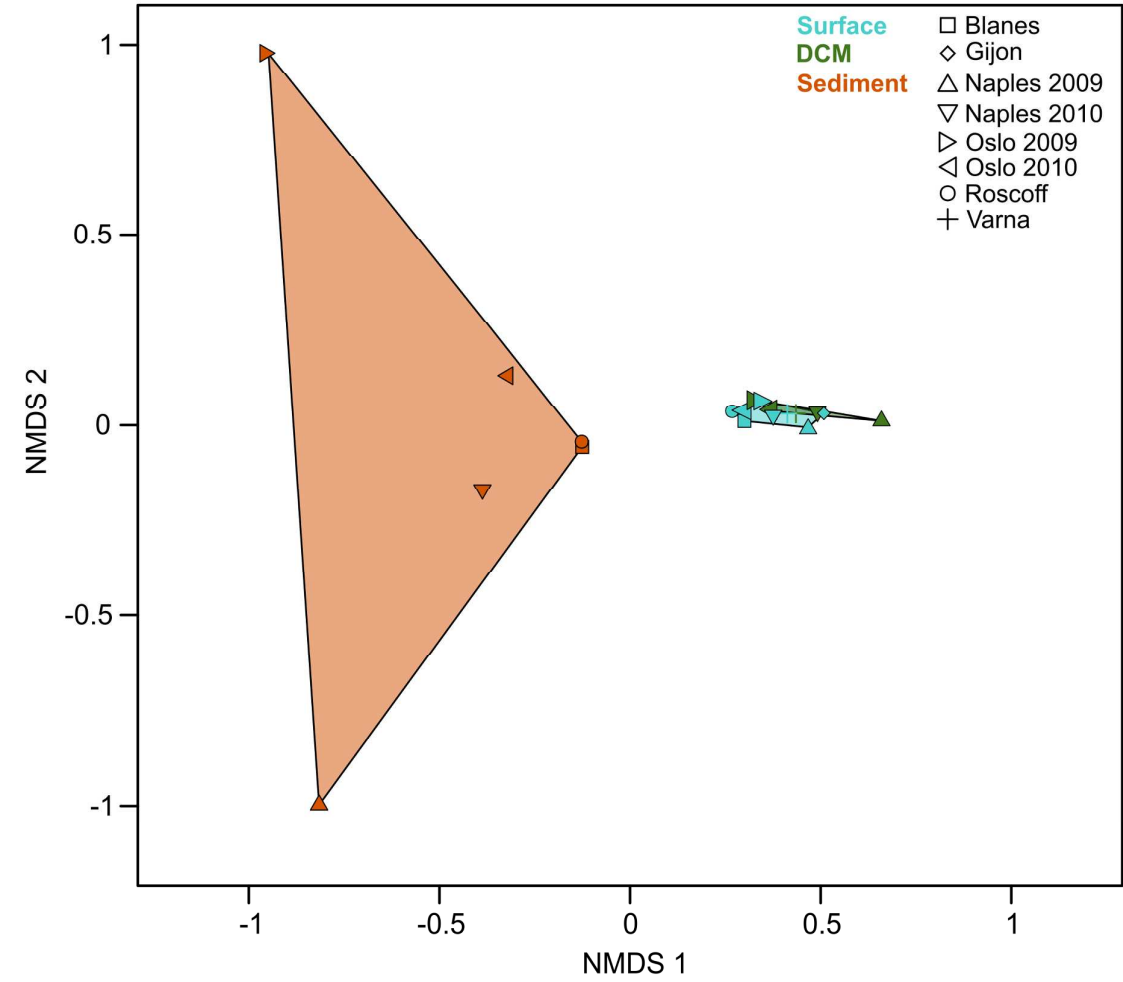
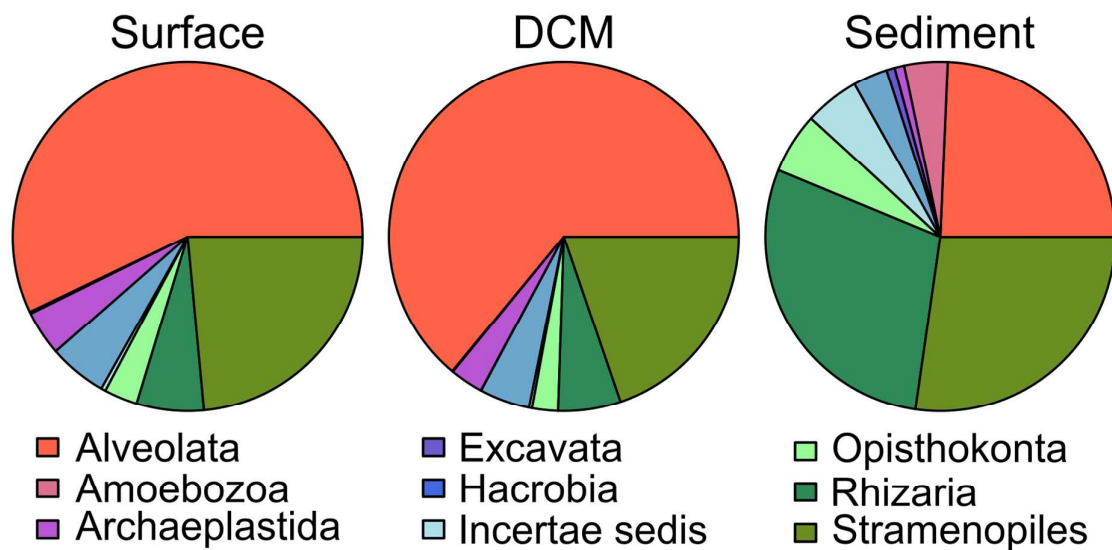


Fig. 3 Taxonomic community compositions as revealed by the PR² database.

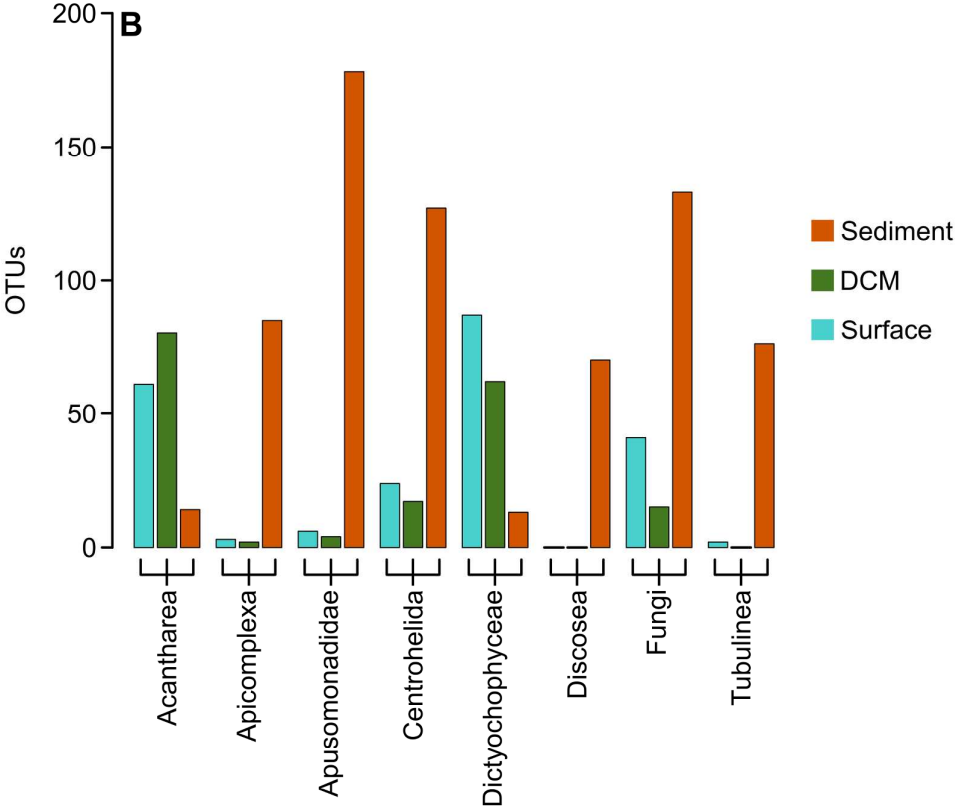
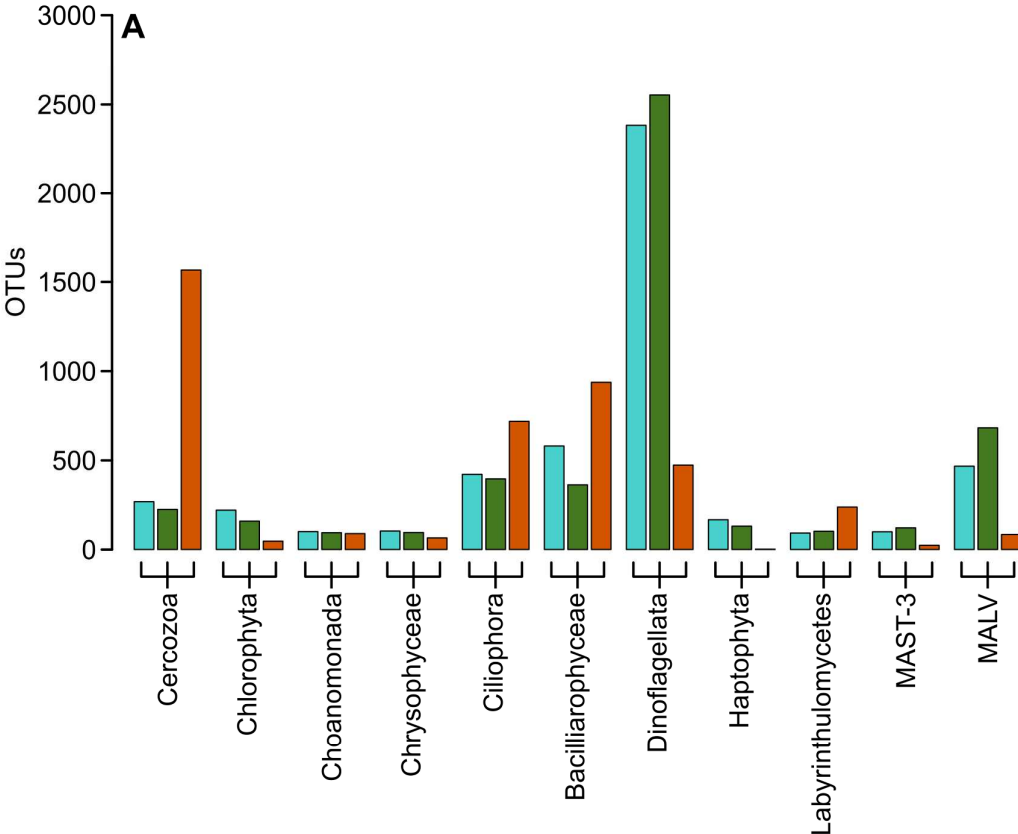
The pie charts reflect the distribution of OTUs within major protist groups, by pooling the data of all samples from each habitat. The surface dataset included 5747 distinct OTUs, the DCM dataset 5685 distinct OTUs and the sediment dataset 5616 distinct OTUs.



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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).

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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.

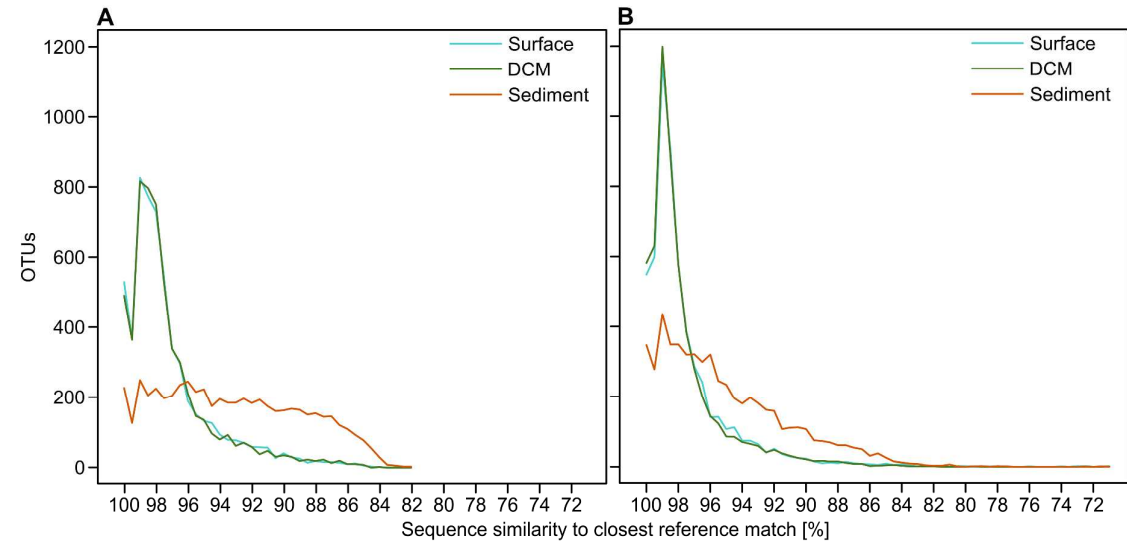


Fig. 6 Sequence divergence of OTUs to their closest taxonomic hit. Each boxplot comprises the sequence divergence values of all OTUs within a given taxonomical group from the same habitat to their closest reference in the PR² database. The taxonomic assignment is shown at the supergroup level. Missing 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.

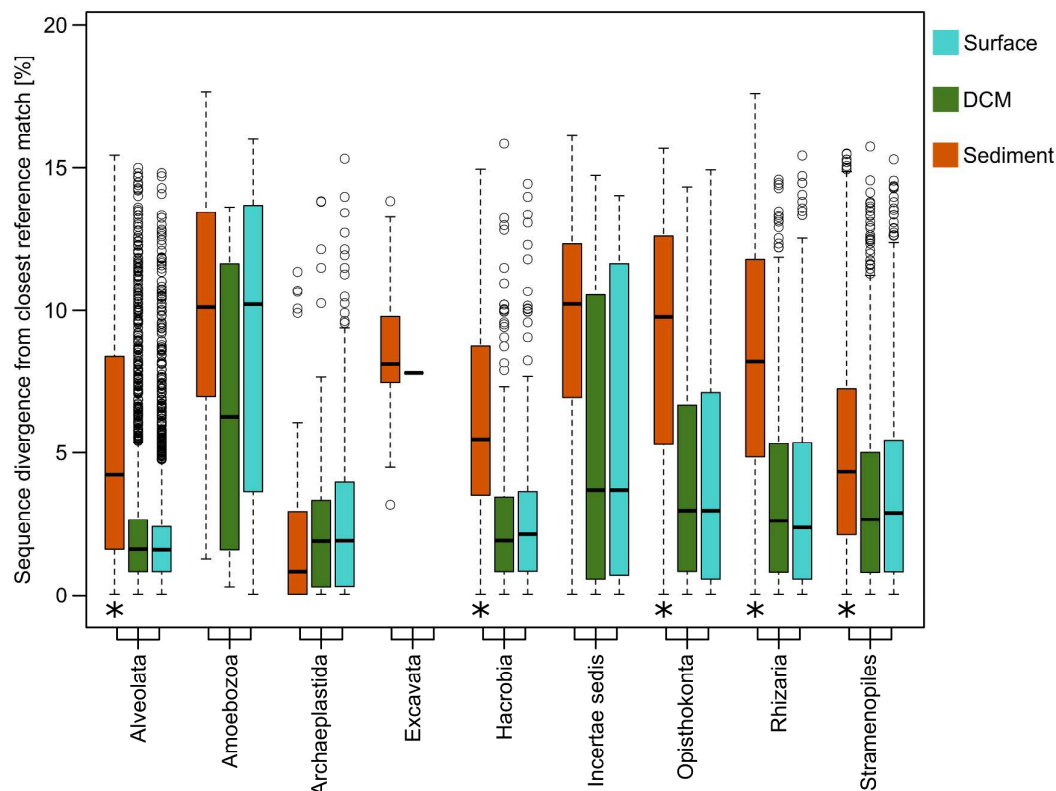


Table 1 Overview of BioMarKs samplings along the European coastline.

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Total number of surface water quality sequences: 206 602.

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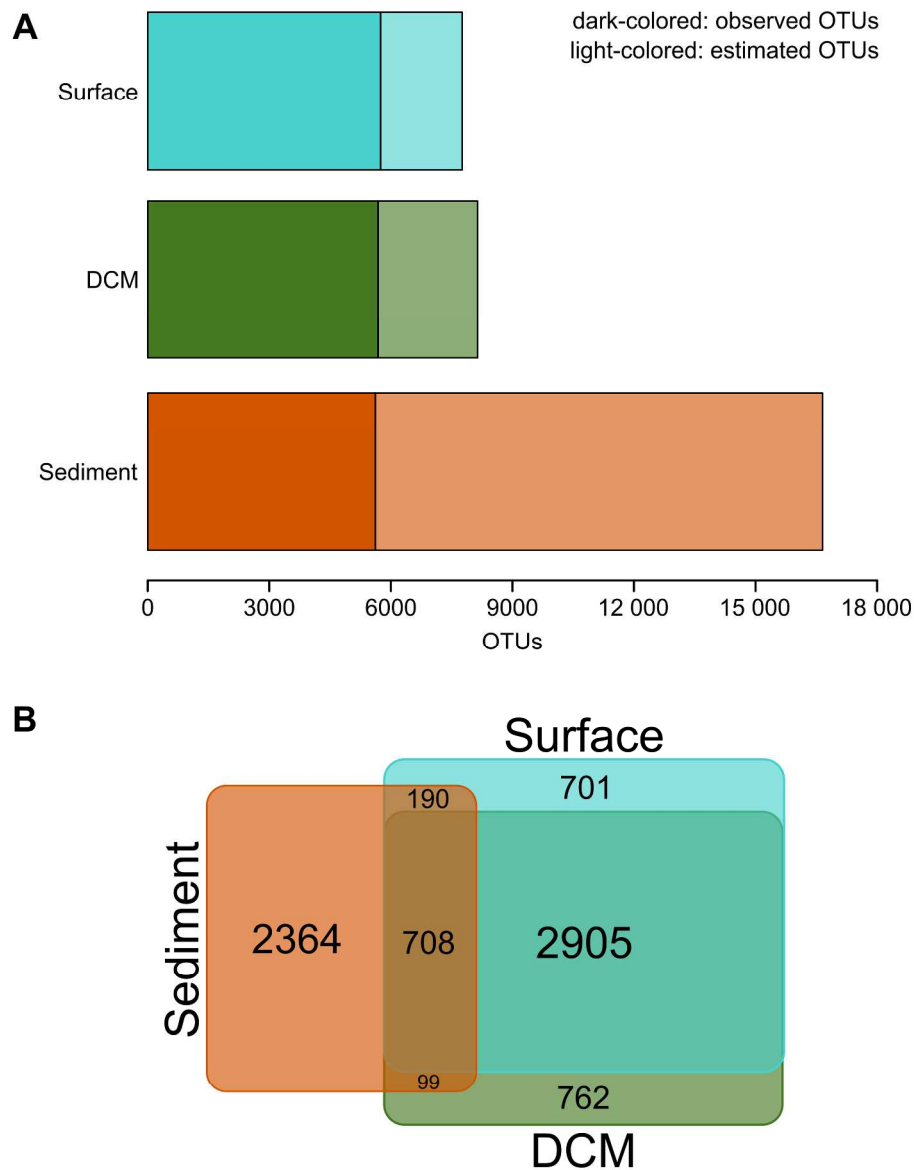


Fig. 1 OTU richness and shared OTUs of planktonic and benthic protist communities. (A) For each habitat the bars show the number of observed (left, dark colored part) and estimated OTUs (right, lighter colored part). Estimations are based on the incidence-based coverage estimator (ICE). (B) The Venn-Diagram 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.

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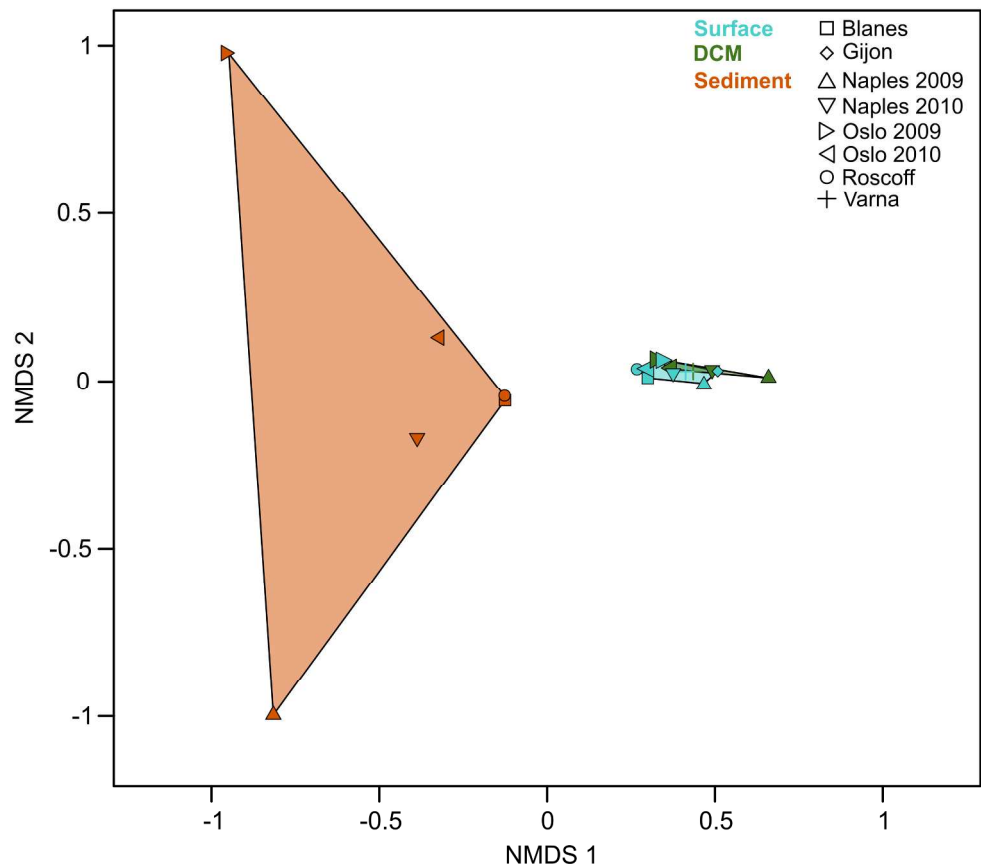


Fig. 2 Beta diversity analysis of single sampling events. The NMDS is based on binary-Jaccard distances between protist communities of single samples (NMDS stress level = 0.2). Colors of the data points were chosen with respect to their habitat affiliation. Data points of the same affiliation were linked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

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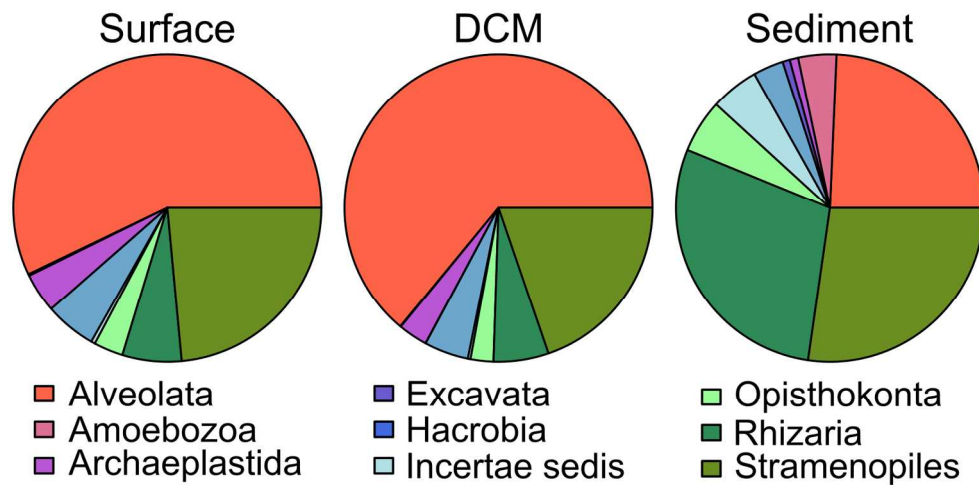


Fig. 3 Taxonomic community compositions as revealed by the PR2 database. The pie charts reflect the distribution of OTUs within major protist groups, by pooling the data of all samples from each habitat. The surface dataset included 5747 distinct OTUs, the DCM dataset 5685 distinct OTUs and the sediment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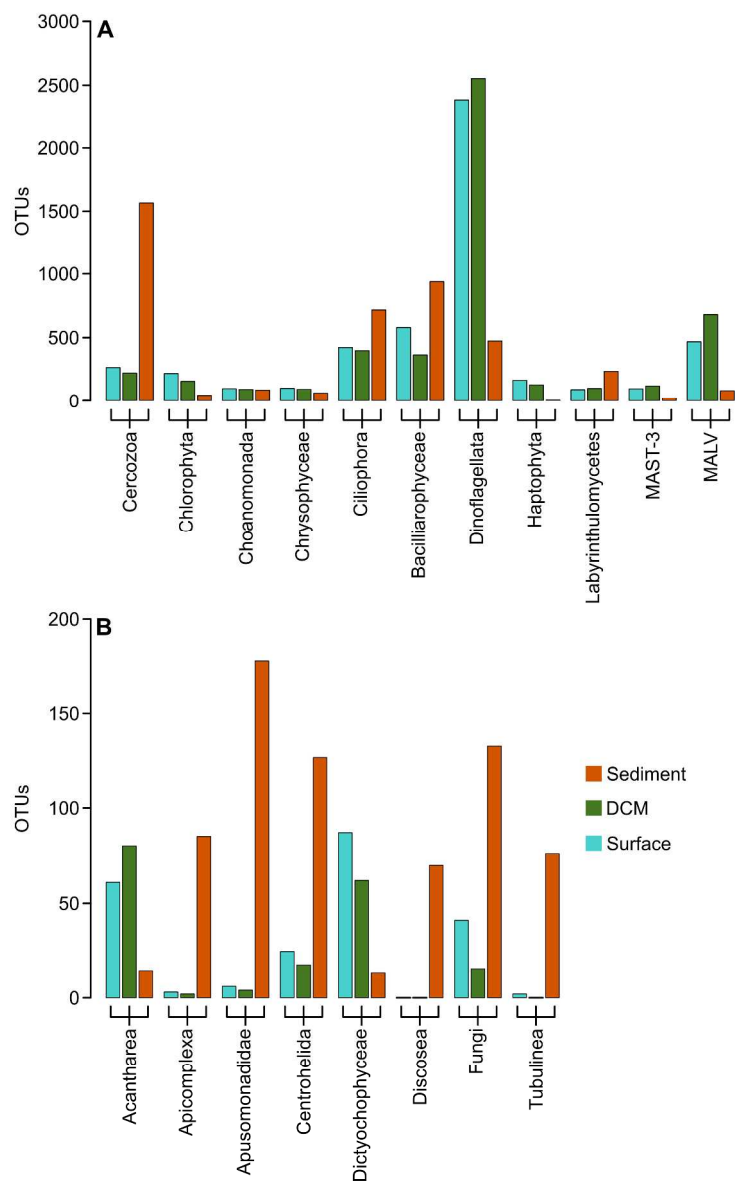


Fig. 4 Number of OTUs within taxonomic groups in planktonic and benthic samples. Only groups contributing to at least 1% of the OTU number in either surface, DCM or sediment communities were considered. Note the different scale among the two panels, to display taxonomic groups with more than 200 OTUs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

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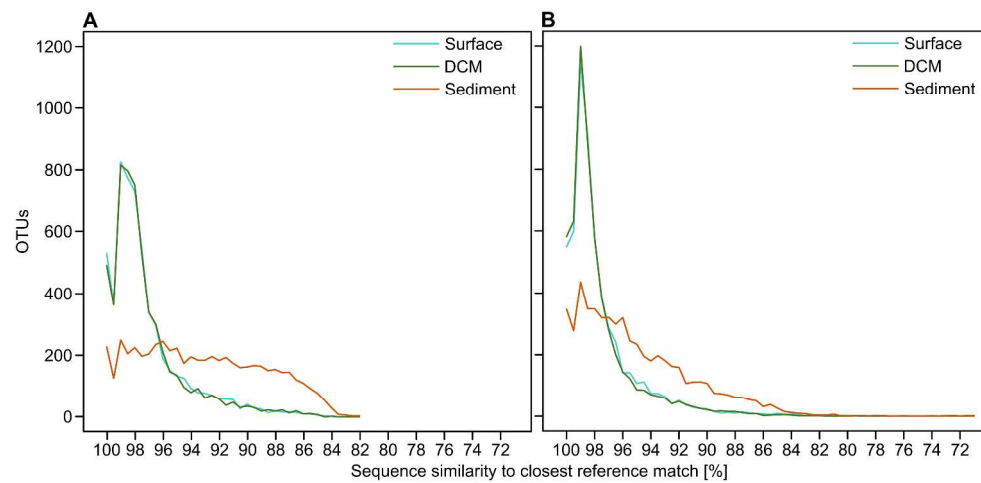


Fig. 5 Rank abundance curves displaying the sequence similarity distribution of OTUs against reference databases. Results are shown for two different BLAST queries, against the PR2 database (A) and against a custom-built subset of NCBI's Short Read Archive (B). The curves display the number of OTUs with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

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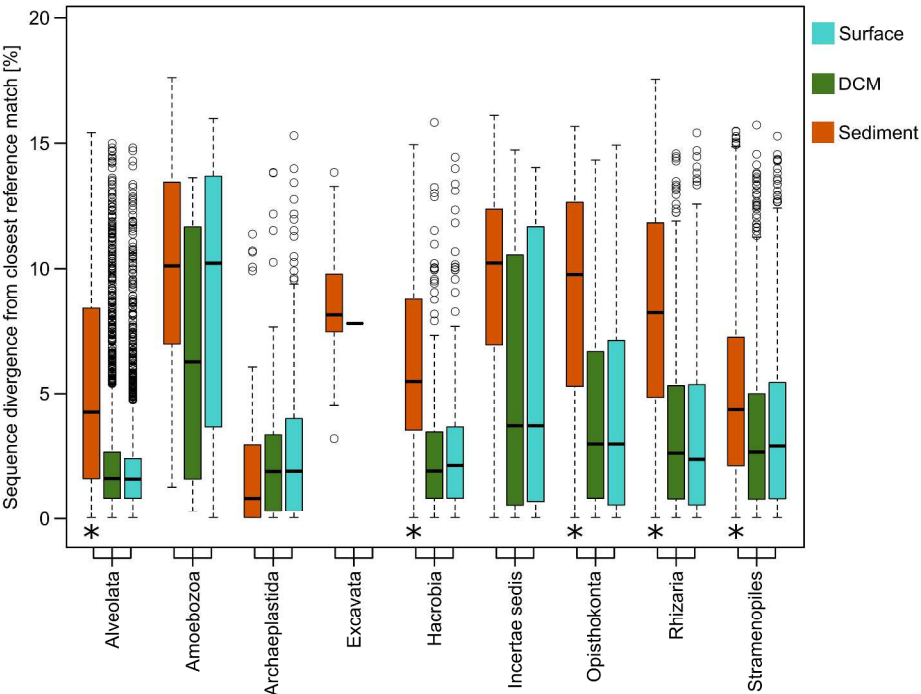


Fig. 6 Sequence divergence of OTUs to their closest taxonomic hit. Each boxplot comprises the sequence divergence values of all OTUs within a given taxonomical group from the same habitat to their closest reference in the PR2 database. The taxonomic assignment is shown at the supergroup level. Missing 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.

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Benthic protists: the under-charted majority

Dominik Forster, Micah Dunthorn, Frédéric Mahé, John R. Dolan, Stéphane Audic,
David Bass, Lucie Bittner, Christophe Boutte, Richard Christen, Jean-Michel
Claverie, Johan Decelle, Bente Edvardsen, Elianne Egge, Wenche Eikrem,
Angélique Gobet, Wiebe H.C.F. Kooistra, Ramiro Logares, Ramon Massana, Marina
Montresor, Fabrice Not, Hiroyuki Ogata, Jan Pawlowski, Massimo C. Pernice, Sarah
Romac, Kamran Shalchian-Tabrizi, Nathalie Simon, Thomas Richards, Sébastien
Santini, Diana Sarno, Raffaele Siano, Daniel Vaultot, Patrick Wincker, Adriana
Zingone, Colomban de Vargas, Thorsten Stoeck

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Supplemental Table S1 Additional information of the SRA database. The table includes all 167 distinct datasets used to build our custom subset of the SRA. We screened the complete archive for protist datasets of the eukaryotic 18S gene. After downloading the respective data, we removed all sequences shorter than 100 bp. The final customized SRA reference database consisted of 11 708 385 sequences. Information in the table was downloaded directly from NCBI's SRA platform along with the respective sequences.

Supplemental Fig. 2 Observed and estimated OTU richness calculated by abundance-based analyses. Additionally to incidence-based ICE analyses (Fig.1) we estimated OTU richness with the abundance-based CatchAll tool. In direct comparison ICE and CatchAll results show the same trends, though the estimated richness of the abundance-based analyses always exceeded the one of the incidence-based analyses. For each habitat the plot shows the amount of observed and estimated OTUs. The left, dark colored part of each bar shows the actually observed number of OTUs, the right, light colored part of each bar shows how many more OTUs were estimated to be in each dataset by extrapolation of the data.

Supplemental Fig. S3 Normalized rarefaction curves of sampled habitats. Sequence data of all single sampling events were pooled with regard to the respective habitat. Each habitat rarefaction curve was normalized to 40 100 sequences, which equals the smallest total amount of sequences found in any of the three habitats. Depicted is the amount of SSU V4 rDNA sequences in relation to the amount of resulting OTUs into which the sequences were clustered.

Supplemental Fig. S4 Community composition among phototrophic protist taxon groups. Represented are all phototrophic groups detected in BioMarkS. The upper bar shows the phototrophic OTUs exclusively found in the plankton, the middle bar the phototrophic OTUs present in both plankton and benthos and the lower bar the phototrophic OTUs exclusively found in the benthos. Dinoflagellates were not considered in the analyses.

Supplemental Fig. S5 Occurrence of each phototrophic protist taxon group in the sampled habitats. For each phototrophic taxon group, the bars indicate the fraction of OTUs which was found exclusively in the plankton, in both plankton and benthos and exclusively in the benthos. Dinoflagellates were not considered in these analyses.

Supplemental Fig. S6 Community composition across different taxonomic levels. The pie charts reflect the proportion of taxonomic groups of the total microbial eukaryote community in each habitat. The inner ring is equivalent to Fig. 4 and represents the taxonomical assignment into major protist groups (corresponding to the left part of the taxonomic legend). The outer ring represents the taxonomical assignment at the phylum level (corresponding to the right part of the taxonomic legend). Only phyla which contributed with at least 5% to the total community were considered with a specific color in the outer ring. Exact proportions are given in square brackets behind the taxonomical group names.

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10	ERX250343
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12	SRX006203
13	SRX006204
14	SRX037894
15	SRX037895
16	SRX037896
17	SRX050582
18	SRX050583
19	SRX057201
20	SRX057202
21	SRX099033
22	SRX154532
23	SRX155674
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13 Gene expression during the initiation phase of growth in the dinoflagellate *Alexandrium catenella* (Dinophyceae)
14 community profiling of Mirs Bay seawater by 18S rRNA V4 amplicon 454 sequencing
15 community profiling of Tolo Harbor seawater by 18S rRNA V4 amplicon 454 sequencing
16 Pooled bacterial amplicons from 10 Arctic marine surface water samples from 2003-2009 plus 2010
17 Pooled archaeal amplicons from 10 Arctic marine surface water samples from 2003-2009 plus 2010
18 Pooled eukarya amplicons from 10 Arctic marine surface water samples from 2003-2009 plus 2010
19 Marine microbial eukaryote community analysis in Korea
20 Marine microbial eukaryote community analysis in Korea
21 GS_FLX sequencing for environmental diversity study using the SSU rRNA as taxonomic marker
22 GS_FLX_Titanium sequencing for environmental diversity study using the SSU rRNA as taxonomic marker
23 RN_RepliG_Sequencing
24 Pooled sample of 12 Arctic (Amundsen Gulf and Franklin Bay) sea ice samples from 2008
25 microbial diversity of ornamental fish aquarium water sample D1
26 microbial diversity of ornamental fish aquarium water sample E1
27 microbial diversity of ornamental fish aquarium water sample D2
28 microbial diversity of ornamental fish aquarium water sample A1
29 microbial diversity of ornamental fish aquarium water sample A2
30 microbial diversity of ornamental fish aquarium water sample E2
31 microbial diversity of ornamental fish aquarium water sample E1.V4
32 microbial diversity of ornamental fish aquarium water sample D1.V4
33 microbial diversity of ornamental fish aquarium water sample A1.V4
34 microbial diversity of ornamental fish aquarium water sample A2.V4
35 microbial diversity of ornamental fish aquarium water sample D2.V4
36 microbial diversity of ornamental fish aquarium water sample E2.V4
37 microbial diversity of ornamental fish aquarium water sample B2.V4
38 Pooled samples of protist communities at 8 depth from Lake A in May 2008
39 Pooled samples of protist communities at 4 depths from Lake A in August 2008
40 Pooled samples of protist communities at 5 depths from Lake A in July 2009
41 Environmental Samples from ANT-XXVI/3-NS
42 Partial ribosomal gene sequences Ciliates in DHABs in the Mediterranean Sea
43 V4 18S rRNA amplicons from cDNA prepared from different microbialite sediment samples from Highborne Cay, B
44 V4 amplicons (18S rRNA) of eukaryotes obtained from cDNA prepared from various microbialite samples from Sha
45 ANT XXVI/3 - WE
46 a test of 16-18s universal primers using sponge samples
47 Comparative Microbial Analysis to Understand Taxonomic Fingerprints of Healthy Coral Holobiont Communities at
48 Protistan communities of the upper Arctic Ocean
49 Comparative Microbial Analysis to Understand Taxonomic Fingerprints of Healthy Coral Holobiont Communities at

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Comparative Microbial Analysis to Understand Taxonomic Fingerprints of Healthy Coral Holobiont Communities at
Exp1.Ward Hunt Lake Dilution Experiment Eukaryotes RNA

Characterisation of uncultured marine eukaryotes in the Canada Basin

Chukchi Sea < 3 um Stn BS1
Chukchi Sea < 3 um Stn AN1
Chukchi Sea < 3 um Stn KS6
Chukchi Sea < 3 um Stn EC5
Chukchi Sea < 3 um Stn HLY
Chukchi Sea < 3 um Stn CC18
Chukchi Sea < 3 um Stn CN3
Chukchi Sea < 3 um Stn CN14
Chukchi Sea < 3 um Stn BCH7
Chukchi Sea < 3 um Stn IE
Chukchi Sea < 3 um Stn HSN5
Chukchi Sea > 3 um Stn BS1
Chukchi Sea > 3 um Stn AN1
Chukchi Sea > 3 um Stn KS6
Chukchi Sea > 3 um Stn CHA1
Chukchi Sea > 3 um Stn EC5
Chukchi Sea > 3 um Stn HLY
Chukchi Sea > 3 um Stn CC18
Chukchi Sea > 3 um Stn CN3
Chukchi Sea > 3 um Stn CN14
Chukchi Sea > 3 um Stn BCH7
Chukchi Sea > 3 um Stn IE
Chukchi Sea > 3 um Stn HSN5

454

Sequences from three sediments

Design and validation of four primers for next-generation sequencing to target the 18S rRNA gene of gastrointestinal
Design and validation of four primers for next-generation sequencing to target the 18S rRNA gene of gastrointestinal
Design and validation of four primers for next-generation sequencing to target the 18S rRNA gene of gastrointestinal
454 pyrosequencing of plankton community collected from Hamilton harbour
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
28 Eukaryota Arctic Ocean Survey
29 Eukaryota Arctic Ocean Survey
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31 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
26 Protists in Havre-aux-Maisons Lagoon
27 Protists in Havre-aux-Maisons Lagoon
28 Protists in Havre-aux-Maisons Lagoon
29 Protists in Havre-aux-Maisons Lagoon
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	uncultured marine eukaryote	454 GS FLX Titanium
20	uncultured marine eukaryote	454 GS FLX Titanium
21	metagenomes	454 GS FLX
22	metagenomes	454 GS FLX Titanium
23	Rotylenchulus reniformis	454 GS FLX Titanium
24	marine metagenome	454 GS FLX Titanium
25	metagenomes	454 GS FLX
26	metagenomes	454 GS FLX
27	metagenomes	454 GS FLX
28	metagenomes	454 GS FLX
29	metagenomes	454 GS FLX
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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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Montipora digitata	454 GS FLX Titanium
Porites cylindrica	454 GS FLX Titanium
Isopora palifera	454 GS FLX Titanium
Isopora palifera	454 GS FLX Titanium
Isopora palifera	454 GS FLX Titanium
Montipora digitata	454 GS FLX Titanium
Montipora digitata	454 GS FLX Titanium
Montipora digitata	454 GS FLX Titanium
Seriatopora hystrix	454 GS FLX Titanium
Seriatopora hystrix	454 GS FLX Titanium
Seriatopora hystrix	454 GS FLX Titanium
Porites cylindrica	454 GS FLX Titanium
Porites cylindrica	454 GS FLX Titanium
Porites cylindrica	454 GS FLX Titanium
aquatic metagenome	454 GS FLX Titanium
marine metagenome	454 GS FLX Titanium
marine metagenome	454 GS FLX Titanium
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marine metagenome	454 GS FLX Titanium
marine metagenome	454 GS FLX Titanium
gut metagenome	454 GS FLX
marine sediment metagenome	454 GS FLX+
gut metagenome	454 GS FLX Titanium
gut metagenome	454 GS FLX Titanium
gut metagenome	454 GS FLX Titanium
freshwater metagenome	454 GS FLX Titanium
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
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57	uncultured eukaryote	454 GS FLX Titanium
58	uncultured eukaryote	454 GS FLX Titanium
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454 GS FLX Titanium
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454 GS FLX+
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
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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
17	Universite Laval	SRP005272
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19	Universite Laval	SRP005272
20	Inha univ.	SRP006126
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22	University of Kaiserslautern	SRP003169
23	University of Kaiserslautern	SRP003169
24	University of Kaiserslautern	SRP003169
25	Alabama A&M University	SRP008476
26	Universite Laval	SRP013740
27	MBL	SRP013874
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47	Université Laval	SRP014823
48	Alfred Wegener Institute for Polar and Marine Rese	SRP016049
49	University of Kaiserslautern	SRP017187
50	Woods Hole Oceanographic Institution	SRP017332
51	Woods Hole Oceanographic Institution	SRP017334
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53	Alfred Wegener Institute for Polar and Marine Rese	SRP016049
54	hkust-kaust	SRP021898
55	University of Sydney	SRP022083
56	Laval University	SRP022176
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58	University of Sydney	SRP022083
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19	Universit* Laval	SRP027540
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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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55	RCEES, Chinese Academy of Sciences	SRP038053
56	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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34	Institute of Shandong River Wetlands	SRP045389
35	Alfred Wegener Instiute	SRP048617
36	Woods Hole Oceanographic Institution	SRP049010
37	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	Composition and genetic diversity of picoeukaryotes in subtropical coastal waters as revealed by 454 sequencing-l
17	Microbial Community Diversity Response to a Changing Arctic Ocean
18	Microbial Community Diversity Response to a Changing Arctic Ocean
19	Microbial Community Diversity Response to a Changing Arctic Ocean
20	Microbial Community Diversity Response to a Changing Arctic Ocean
21	Marine microbial eukaryote community analysis in Korea
22	Marine microbial eukaryote community analysis in Korea
23	Error rate of 454 GS FLX sequenced V4 and V9 PCR amplicons of various protists
24	Error rate of 454 GS FLX sequenced V4 and V9 PCR amplicons of various protists
25	Error rate of 454 GS FLX sequenced V4 and V9 PCR amplicons of various protists
26	Rotylenchulus reniformisGenome sequencing
27	Arctic sea ice Targeted Locus (Loci)
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
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39	Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water
40	Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water
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42	Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water
43	Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water
44	Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water
45	Lake A protist communities
46	Lake A protist communities
47	Lake A protist communities
48	Marine eukaryotic protists Metagenome
49	Partial ribosomal RNA gene of DHAB Ciliates
50	Partial ribosomal RNA gene of DHAB Ciliates
51	Highborne Bay eukaryotic small subunit ribosomal RNA diversity
52	Shark Bay eukaryotic small subunit ribosomal RNA diversity
53	Marine eukaryotic protists Metagenome
54	Sponge metagenome
55	Sponge metagenome
56	Reef-building coral species harbour Chromera velia and apicomplexan “type-N” (cf. Gemmocystis cylindrus) on the
57	Protistan communities of the upper Arctic Ocean (18S SSU-rRNA Targeted Locus)
58	Reef-building coral species harbour Chromera velia and apicomplexan “type-N” (cf. Gemmocystis cylindrus) on the
59	Reef-building coral species harbour Chromera velia and apicomplexan “type-N” (cf. Gemmocystis cylindrus) on the
60	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
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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
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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)
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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)
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6	Uncultured eukaryotes Targeted Locus (Loci)
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32	Uncultured eukaryotes Targeted Locus (Loci)
33	Eukaryota Arctic Ocean Survey Targeted Locus (Loci)
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2 Eukaryota Arctic Ocean Survey Targeted Locus (Loci)
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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
1						
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
15	SRS152378		105.05	2	93195	46778615
16	SRS152378		190.11	2	174077	86125205
17	SRS182654		3.27	1	3025	1487037
18	SRS182654		4.98	1	4575	2292151
19	SRS086207		22.19	1	53155	10757013
20	SRS086207		14.35	1	15221	5812974
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
27	SRS346708		14.43	1	13015	7108579
28	SRS346709		17.94	1	16171	8854309
29	SRS346705		3.35	1	8248	1578966
30	SRS346704		2.99	1	7443	1424093
31	SRS346707		3.3	1	8032	1538044
32	SRS346708		3.96	1	9691	1858955
33	SRS346706		3.07	1	7788	1489084
34	SRS346709		3.29	1	8133	1555000
35	SRS348706		3.9	1	9538	1827278
36	SRS355910		86.28	1	72724	36293480
37	SRS355910		42.46	1	35716	17867669
38	SRS355910		76.54	2	66130	34180949
39	SRS367508		378.84	1	300582	180399874
40	SRS375573		540.47	1	513347	236974344
41	SRS377421		277.64	1	260367	120224628
42	SRS377419		293.83	1	273186	128190762
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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2	SRS419339	0.81	1	7392	1559199
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
18	SRS474328	8.68	1	7316	3910652
19	SRS474346	18.1	1	15303	8161494
20	SRS474349	15.9	1	13493	7128393
21	SRS474350	13.83	1	11664	6215030
22	SRS474351	16.15	1	13734	7262782
23	SRS474352	18.29	1	15517	8240291
24	SRS474353	11.44	1	9655	5121533
25	SRS474354	17.62	1	14747	7924648
26	SRS474356	16.06	1	13611	7207989
27	SRS474357	17.41	1	14939	7808117
28	SRS474358	9.22	1	7748	4147573
29	SRS474359	13.97	1	12148	6399423
30	SRS474360	18.17	1	15778	8326048
31	SRS474361	13.18	1	11435	5969057
32	SRS474362	8.88	1	7728	4058666
33	SRS474363	13.63	1	11864	6249808
34	SRS474364	12.67	1	11010	5797710
35	SRS474365	12.04	1	10497	5506280
36	SRS474366	14.59	1	12686	6679449
37	SRS474367	14.41	1	12487	6529205
38	SRS474368	14.11	1	12243	6426116
39	SRS474369	14.04	1	12182	6373006
40	SRS474371	9.96	1	8600	4515861
41	SRS498636	297.51	1	337737	130753424
42	SRS507106	219.12	1	860390	354289445
43	SRS514888	5.06	1	22051	10260945
44	SRS514890	2.82	1	11405	5460929
45	SRS514891	1.69	1	9223	3633683
46	SRS559023	209.76	4	1714374	329548979
47	SRS563175	169.38	2	789405	273242265
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2	SRS569198	521.92	1	498945	236436763
3	SRS579457	11.73	1	10432	5170818
4	SRS579488	10.13	1	8796	4472640
5	SRS579489	10.83	1	9743	4774971
6	SRS579508	10.88	1	9487	4807091
7	SRS579509	10.08	1	8872	4460573
8	SRS579510	8.73	1	7592	3840296
9	SRS579511	11.39	1	10188	5037956
10	SRS579512	8.88	1	7740	3918258
11	SRS579513	11.34	1	9971	5060281
12	SRS579514	9.92	1	8615	4382786
13	SRS579515	12.26	1	10827	5479712
14	SRS579516	10.81	1	9410	4779994
15	SRS579517	11.2	1	9851	4988947
16	SRS579518	10.54	1	9167	4636301
17	SRS579519	10.48	1	9209	4650741
18	SRS579520	10.89	1	9398	4783119
19	SRS579521	11.97	1	10539	5349735
20	SRS579522	11.62	1	10111	5108976
21	SRS579523	10.54	1	9432	4725730
22	SRS579524	9.49	1	8300	4179958
23	SRS579525	11.33	1	10010	5047486
24	SRS579526	11.09	1	9847	4830421
25	SRS579527	10.63	1	9333	4732068
26	SRS579528	8.71	1	7578	3833004
27	SRS584239	9.26	1	9027	4434127
28	SRS584240	8.98	1	8782	4296411
29	SRS584241	12.45	1	12226	5973192
30	SRS584242	12.22	1	12079	5870832
31	SRS584243	9.91	1	9660	4741315
32	SRS584244	11.71	1	11525	5643505
33	SRS584245	12.91	1	12567	6203763
34	SRS584246	12.43	1	12097	5938216
35	SRS584248	18.89	1	18592	9110667
36	SRS584249	13.26	1	13090	6382758
37	SRS584251	12.93	1	12647	6195428
38	SRS584252	12.38	1	12162	5972069
39	SRS584257	10.22	1	9454	4727038
40	SRS584258	9.5	1	8796	4397118
41	SRS584324	11.74	1	10844	5394881
42	SRS584326	11.33	1	10463	5210335
43	SRS584327	11.8	1	10936	5474639
44	SRS584345	13.6	1	12616	6222179
45	SRS584346	12.56	1	11734	5854858
46	SRS584357	11.93	1	11028	5503305
47	SRS584358	13.44	1	12395	6210778
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SRS584359	14.03	1	12942	6456278
SRS584360	8.6	1	7907	3955921
SRS584361	14.47	1	13365	6677072
SRS584362	12.43	1	11770	5895814
SRS584363	12.81	1	12106	6060868
SRS584364	13.81	1	13145	6534390
SRS584365	13.88	1	13345	6585414
SRS584366	7.25	1	6960	3450835
SRS584367	15.2	1	14340	7186457
SRS584368	15.66	1	14810	7397424
SRS584369	14.13	1	13423	6633286
SRS584370	14.5	1	13560	6756945
SRS584372	13.97	1	13192	6577063
SRS584373	14.7	1	13435	6832284
SRS584374	13.14	1	12472	6190537
SRS569198	2726.45	1	1135587	1033738707
SRS629197	12.05	1	10283	5062010
SRS629198	12.16	1	10368	5109882
SRS629199	8.25	1	6992	3454326
SRS629200	13.76	1	11779	5796806
SRS629201	12.28	1	10494	5171193
SRS629202	12.39	1	10538	5211005
SRS629203	13.89	1	11819	5847093
SRS629204	13.02	1	11077	5470294
SRS629205	15.87	1	13484	6676694
SRS629206	11.71	1	9963	4932541
SRS677471	193.28	1	155510	90495203
SRS715739	0.72	4	34093	1251455
SRS722944	270.9	1	229068	122310596
SRS752744	1809.99	1	1566895	865799314

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2 FTP Path to Experiment
3 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/ERX/ERX145/ERX145205
4 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/ERX/ERX145/ERX145206
5 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/ERX/ERX145/ERX145207
6 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/ERX/ERX145/ERX145208
7 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/ERX/ERX250/ERX250340
8 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/ERX/ERX250/ERX250341
9 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/ERX/ERX250/ERX250342
10 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/ERX/ERX250/ERX250343
11 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX003/SRX003229
12 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX006/SRX006203
13 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX006/SRX006204
14 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX037/SRX037894
15 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX037/SRX037895
16 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX037/SRX037896
17 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX050/SRX050582
18 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX050/SRX050583
19 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX057/SRX057201
20 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX057/SRX057202
21 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX099/SRX099033
22 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX154/SRX154532
23 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX155/SRX155674
24 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX155/SRX155675
25 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX155/SRX155676
26 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX155/SRX155677
27 ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-instant/reads/ByExp/sra/SRX/SRX155/SRX155678
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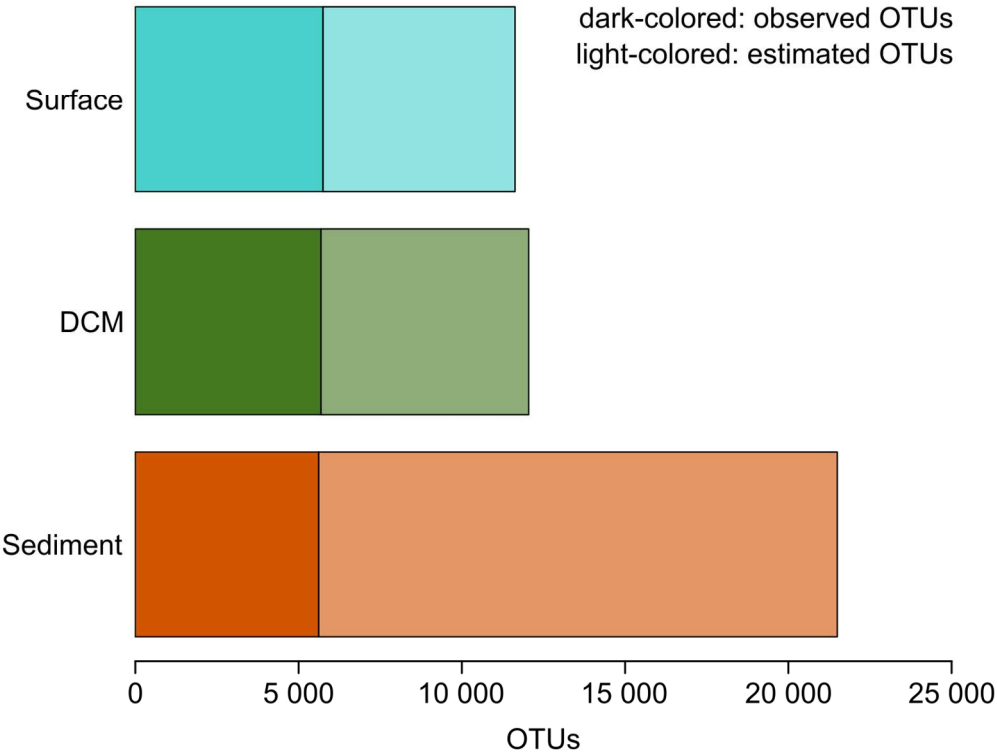
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Library Name	Library Strategy	Library Source	Library Selection
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Tintinnid_ITS_lib	AMPLICON	GENOMIC	PCR
Tintinnid_SSU_lib	AMPLICON	GENOMIC	PCR
Tintinnid_ITS_lib	AMPLICON	GENOMIC	PCR
LOHAFEX library of sample day_-1	AMPLICON	METAGENOMIC	PCR
LOHAFEX library of sample day_9	AMPLICON	METAGENOMIC	PCR
LOHAFEX library of sample day_18	AMPLICON	METAGENOMIC	PCR
LOHAFEX library of sample day_36	AMPLICON	METAGENOMIC	PCR
SUBINI	EST	TRANSCRIPTOMIC	RANDOM
MB	AMPLICON	GENOMIC	PCR
TH	AMPLICON	GENOMIC	PCR
AMCEpooledBACT	AMPLICON	OTHER	PCR
AMCEpooledARCH	AMPLICON	OTHER	PCR
AMCEpooledEUK	AMPLICON	OTHER	PCR
Ciliate-specific	AMPLICON	METAGENOMIC	PCR
Eukaryote-universal	AMPLICON	METAGENOMIC	PCR
GS_FLX	AMPLICON	METAGENOMIC	PCR
GS_FLX_Titanium	AMPLICON	METAGENOMIC	PCR
Lib_RepliGRN	WGS	GENOMIC	unspecified
ASID	AMPLICON	METAGENOMIC	PCR
VS-454-MBL:assay:D1.3_Bacteria	AMPLICON	METAGENOMIC	PCR
VS-454-MBL:assay:E1.5_Bacteria	AMPLICON	METAGENOMIC	PCR
VS-454-MBL:assay:D2.4_Bacteria	AMPLICON	METAGENOMIC	PCR
VS-454-MBL:assay:A1.1_Bacteria	AMPLICON	METAGENOMIC	PCR
VS-454-MBL:assay:A2.2_Bacteria	AMPLICON	METAGENOMIC	PCR
VS-454-MBL:assay:E2.6_Bacteria	AMPLICON	METAGENOMIC	PCR
VS-454-MBL:assay:E1.V4.11_Bacteria	AMPLICON	METAGENOMIC	PCR
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VS-454-MBL:assay:B2.V4.13_Bacteria	AMPLICON	METAGENOMIC	PCR
	AMPLICON	METAGENOMIC	PCR
	AMPLICON	METAGENOMIC	PCR
	AMPLICON	METAGENOMIC	PCR
	AMPLICON	GENOMIC	PCR
	RNA-Seq	GENOMIC	PCR
	AMPLICON	METATRANSCRIPTOMIC	RANDOM
	AMPLICON	TRANSCRIPTOMIC	RANDOM
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	AMPLICON	METAGENOMIC	PCR
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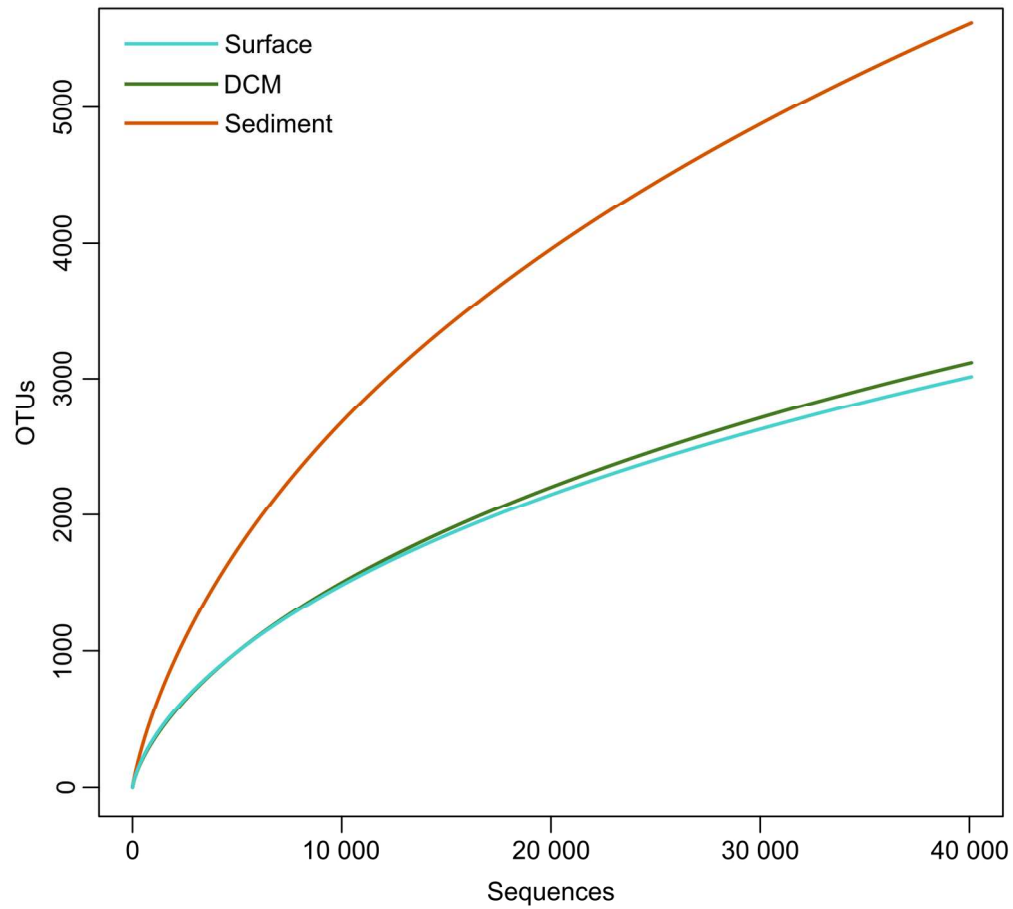
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8	JB700SF_DNA	AMPLICON	METAGENOMIC	PCR
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15	JB601SCM_DNA	AMPLICON	METAGENOMIC	PCR
16	JB601SCM_RNA	AMPLICON	METAGENOMIC	cDNA
17				
18	NEC211SF_DNA	AMPLICON	METAGENOMIC	PCR
19	NEC211SF_RNA	AMPLICON	METAGENOMIC	cDNA
20	NEC211SCM_DNA	AMPLICON	METAGENOMIC	PCR
21	NEC211SCM_RNA	AMPLICON	METAGENOMIC	cDNA
22				
23	NEF43SF_DNA	AMPLICON	METAGENOMIC	PCR
24	NEF43SF_RNA	AMPLICON	METAGENOMIC	cDNA
25	NEF43SCM_DNA	AMPLICON	METAGENOMIC	PCR
26	NEF43SCM_RNA	AMPLICON	METAGENOMIC	cDNA
27				
28	NEF512SF_DNA	AMPLICON	METAGENOMIC	PCR
29	NEF512SF_RNA	AMPLICON	METAGENOMIC	cDNA
30	NEF512SCM_DNA	AMPLICON	METAGENOMIC	PCR
31	NEF512SCM_RNA	AMPLICON	METAGENOMIC	cDNA
32				
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34	HB_2010_710_34m_euk	AMPLICON	GENOMIC	PCR
35	HB_2010_699_6m_euk	AMPLICON	GENOMIC	PCR
36	HB_2010_699_15m_euk	AMPLICON	GENOMIC	PCR
37	HB_2010_709_9m_euk	AMPLICON	GENOMIC	PCR
38	HB_2010_709_30m_euk	AMPLICON	GENOMIC	PCR
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40	HB_2010_745_10m_euk	AMPLICON	GENOMIC	PCR
41	HB_2010_745_47m_euk	AMPLICON	GENOMIC	PCR
42	HB_2010_706_10m_euk	AMPLICON	GENOMIC	PCR
43	HB_2010_706_30m_euk	AMPLICON	GENOMIC	PCR
44	HB_2010_706_40m_euk	AMPLICON	GENOMIC	PCR
45	LS_2006_301_25m_euk	AMPLICON	GENOMIC	PCR
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47	LS_2008_303_2m_euk	AMPLICON	GENOMIC	PCR
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50	CB_2011_314_2m_euk	AMPLICON	GENOMIC	PCR
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53	BB_2005_131_5m_euk	AMPLICON	GENOMIC	PCR
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55	BB_2005_100_5m_euk	AMPLICON	GENOMIC	PCR
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57	BB_2008_108_20m_euk	AMPLICON	GENOMIC	PCR
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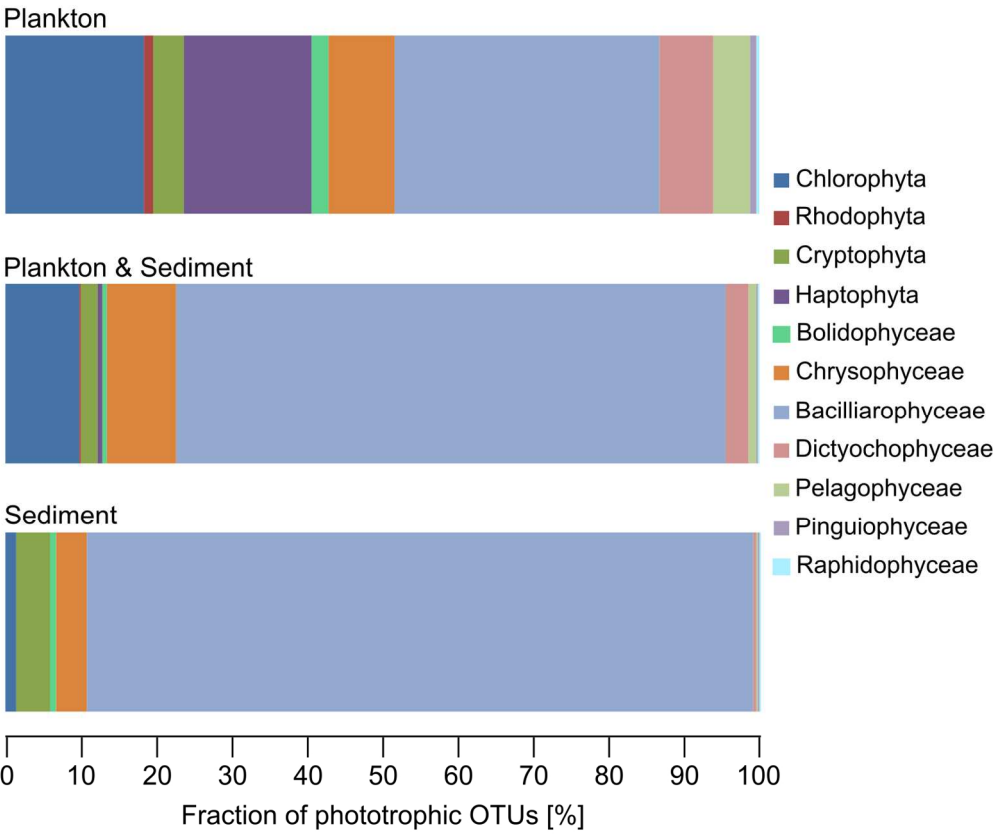
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6	BB_2006_BA0405_28m_euk	AMPLICON	GENOMIC	PCR
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11	Lv_2007_VB1007_7m_euk	AMPLICON	GENOMIC	PCR
12	Lv_2007_VB1607_8m_euk	AMPLICON	GENOMIC	PCR
13	Lv_2007_VB2107_7m_euk	AMPLICON	GENOMIC	PCR
14	Lv_2007_VB3807_6m_euk	AMPLICON	GENOMIC	PCR
15	Lv_2007_VB3807_100m_euk	AMPLICON	GENOMIC	PCR
16	Lv_2007_VB7207_5m_euk	AMPLICON	GENOMIC	PCR
17	EEC_2013_De novo	WGS	METAGENOMIC	RANDOM
18		AMPLICON	GENOMIC	PCR
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32		AMPLICON	GENOMIC	PCR
33		AMPLICON	GENOMIC	PCR
34		CLONE	GENOMIC	unspecified
35		AMPLICON	GENOMIC	PCR
36	031814MPtarEuk	AMPLICON	METATRANSCRIPTOMIC	RT-PCR
37		AMPLICON	METAGENOMIC	PCR
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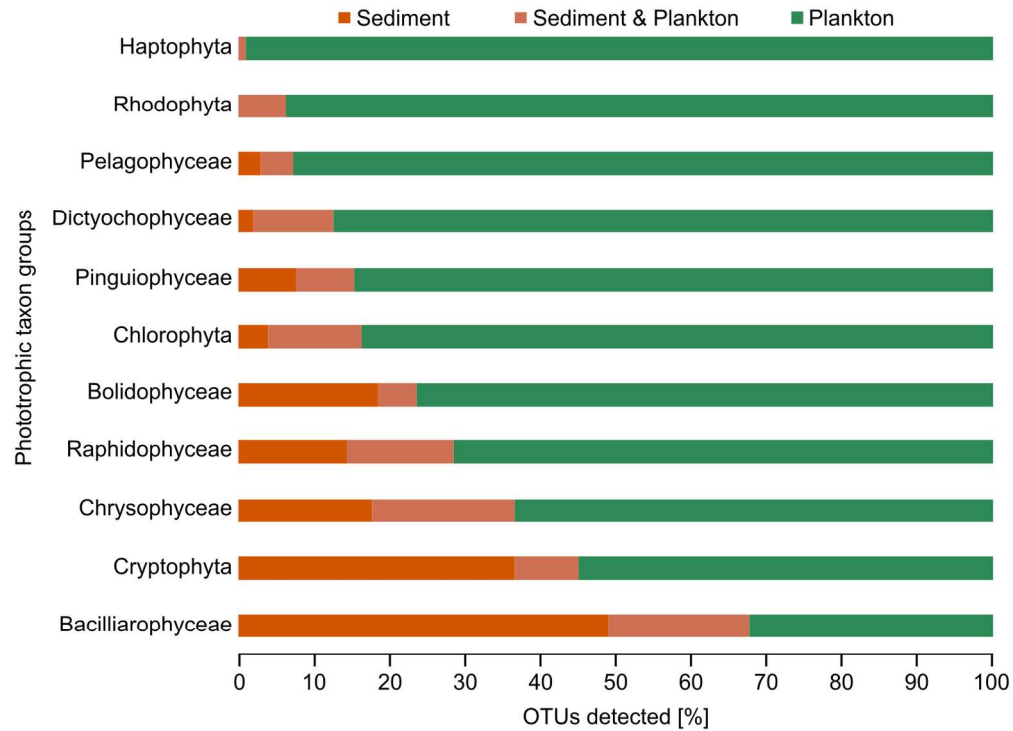
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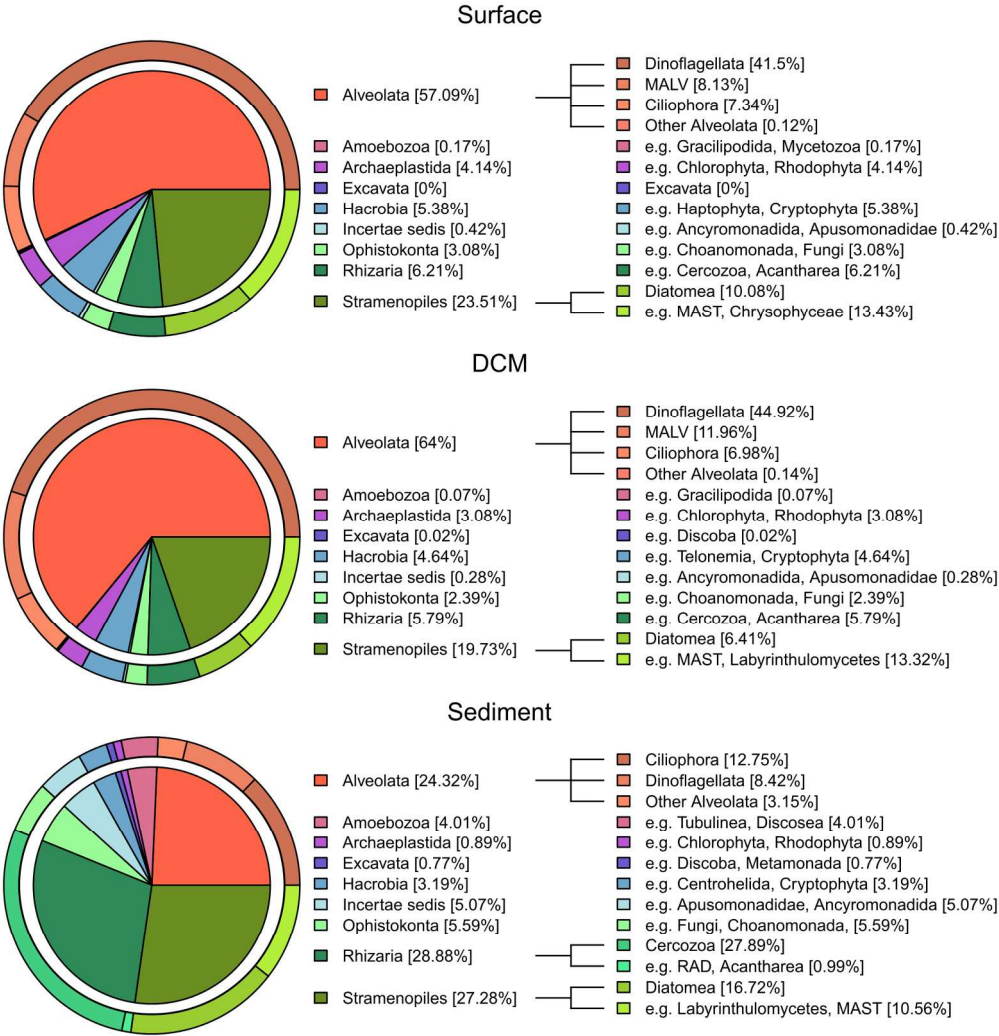
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