

# Journal Pre-proof



Improved biodiversity detection using a large-volume environmental DNA sampler with in situ filtration and implications for marine eDNA sampling strategies

Annette F. Govindarajan, Luke McCartin, Allan Adams, Elizabeth Allan, Abhimanyu Belani, Rene Francolini, Justin Fujii, Daniel Gomez-Ibañez, Amy Kukulya, Fredrick Marin, Kaitlyn Tradd, Dana R. Yoerger, Jill M. McDermott, Santiago Herrera

PII: S0967-0637(22)00183-2

DOI: <https://doi.org/10.1016/j.dsr.2022.103871>

Reference: DSRI 103871

To appear in: *Deep-Sea Research Part I*

Received Date: 18 January 2022

Revised Date: 21 May 2022

Accepted Date: 29 August 2022

Please cite this article as: Govindarajan, A.F., McCartin, L., Adams, A., Allan, E., Belani, A., Francolini, R., Fujii, J., Gomez-Ibañez, D., Kukulya, A., Marin, F., Tradd, K., Yoerger, D.R., McDermott, J.M., Herrera, S., Improved biodiversity detection using a large-volume environmental DNA sampler with in situ filtration and implications for marine eDNA sampling strategies, *Deep-Sea Research Part I* (2022), doi: <https://doi.org/10.1016/j.dsr.2022.103871>.

This is a PDF file of an article that has undergone enhancements after acceptance, such as the addition of a cover page and metadata, and formatting for readability, but it is not yet the definitive version of record. This version will undergo additional copyediting, typesetting and review before it is published in its final form, but we are providing this version to give early visibility of the article. Please note that, during the production process, errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

© 2022 Published by Elsevier Ltd.

1 **Improved biodiversity detection using a large-volume environmental DNA sampler with in**  
2 **situ filtration and implications for marine eDNA sampling strategies**

3  
4 Annette F. Govindarajan<sup>a\*</sup>, Luke McCartin<sup>b</sup>, Allan Adams<sup>c,d,e</sup>, Elizabeth Allan<sup>e,f</sup>, Abhimanyu  
5 Belani<sup>e</sup>, Rene Francolini<sup>a,g,h</sup>, Justin Fujii<sup>e</sup>, Daniel Gomez-Ibanez<sup>e</sup>, Amy Kukulya<sup>e</sup>, Fredrick  
6 Marin<sup>e</sup>, Kaitlyn Tradd<sup>e</sup>, Dana R. Yoerger<sup>e</sup>, Jill M. McDermott<sup>i</sup>, Santiago Herrera<sup>b</sup>

7  
8 <sup>a</sup> Biology Department, Woods Hole Oceanographic Institution, Woods Hole, MA 02543, USA

9 <sup>b</sup> Department of Biological Sciences, Lehigh University, Bethlehem, PA 18015, USA

10 <sup>c</sup> Future Ocean Lab, Massachusetts Institute of Technology, Cambridge, MA 02139, USA

11 <sup>d</sup> Oceanic Labs Research Foundation, Cambridge, MA 02139, USA

12 <sup>e</sup> Department of Applied Ocean Physics and Engineering, Woods Hole Oceanographic  
13 Institution, Woods Hole, MA 02543, USA

14 <sup>f</sup> School of Marine and Environmental Affairs, University of Washington, Seattle, Washington,  
15 USA

16 <sup>g</sup> Bigelow Laboratory for Ocean Sciences, East Boothbay, Maine, 04544, USA

17 <sup>h</sup> School of Marine Sciences, Darling Marine Center, University of Maine, Walpole, Maine,  
18 04573, USA

19 <sup>i</sup> Department of Earth and Environmental Sciences, Lehigh University, Bethlehem, PA 18015,  
20 USA

21

22 \*corresponding author. Email address: [afrese@whoi.edu](mailto:afrese@whoi.edu) (A. F. Govindarajan)

23 **Keywords**

24 Environmental DNA, Metabarcoding, Biodiversity, Autonomous sampling, Mesopelagic, Gulf of  
25 Mexico  
26

Journal Pre-proof

27 **ABSTRACT**

28 Metabarcoding analysis of environmental DNA samples is a promising new tool for marine  
29 biodiversity and conservation. Typically, seawater samples are obtained using Niskin bottles and  
30 filtered to collect eDNA. However, standard sample volumes are small relative to the scale of the  
31 environment, conventional collection strategies are limited, and the filtration process is time  
32 consuming. To overcome these limitations, we developed a new large – volume eDNA sampler  
33 with in situ filtration, capable of taking up to 12 samples per deployment. We conducted three  
34 deployments of our sampler on the robotic vehicle *Mesobot* in the Flower Garden Banks  
35 National Marine Sanctuary in the northwestern Gulf of Mexico and collected samples from 20 to  
36 400 m depth. We compared the large volume (~40 – 60 liters) samples collected by *Mesobot*  
37 with small volume (~2 liters) samples collected using the conventional CTD rosette – mounted  
38 Niskin bottle approach. We sequenced the V9 region of 18S rRNA, which detects a broad range  
39 of invertebrate taxa, and found that while both methods detected biodiversity changes associated  
40 with depth, our large volume samples detected approximately 66% more taxa than the CTD  
41 small volume samples. We found that the fraction of the eDNA signal originating from  
42 metazoans relative to the total eDNA signal decreased with sampling depth, indicating that larger  
43 volume samples may be especially important for detecting metazoans in mesopelagic and deep  
44 ocean environments. We also noted substantial variability in biological replicates from both the  
45 large volume *Mesobot* and small volume CTD sample sets. Both of the sample sets also  
46 identified taxa that the other did not – although the number of unique taxa associated with the  
47 *Mesobot* samples was almost four times larger than those from the CTD samples. Large volume  
48 eDNA sampling with in situ filtration, particularly when coupled with robotic platforms, has



49 great potential for marine biodiversity surveys, and we discuss practical methodological and  
50 sampling considerations for future applications.

Journal Pre-proof

## 51 **Introduction**

52  
53 Marine ecosystems are facing a host of anthropogenic threats including global warming, ocean  
54 acidification, pollution, overfishing, and invasive species. It is critical to assess the impact of  
55 these threats on biodiversity (Brito-Morales et al., 2020; Sala et al., 2021; St John et al., 2016;  
56 Worm and Lotze, 2021). Metabarcoding analysis of environmental DNA (eDNA) is an important  
57 new tool that can efficiently and effectively help to fill this need (Gallego et al., 2020; Gilbey et  
58 al., 2021). DNA sequencing of the trace genetic remains of animals found in bulk environmental  
59 samples provides detailed information on the taxonomic makeup of marine communities, and  
60 leads to important insights on the diversity, distribution, and ecology of community inhabitants  
61 (e.g., Sawaya et al., 2018; Jeunen et al., 2019; Closek et al., 2019; Djurhuus et al., 2020; West et  
62 al., 2021; Visser et al., 2021). eDNA analyses are being increasingly applied to mid- and deep-  
63 water ocean ecosystems (Canals et al., 2021; Easson et al., 2020; Govindarajan et al., 2021;  
64 Laroche et al., 2020; Merten et al., 2021). These ecosystems are vast and the scales of  
65 biodiversity variation are less well known than freshwater and shallow coastal ecosystems, so  
66 key factors to consider are sample volume and the spatial scale of sampling. Advances in robotics  
67 and sampling technology could improve sampling strategies to these otherwise difficult to reach  
68 regions.

69

### 70 *1.1 Conventional eDNA sampling approaches*

71

72 For eDNA analyses in mid and deep-water oceanic environments, seawater is conventionally  
73 collected using Niskin bottles, which are triggered to collect water samples at a particular water

74 depth and location. Most commonly, the Niskin bottles are mounted on a conductivity  
75 temperature depth (CTD) rosette. A vertical profile of samples can be obtained with the CTD  
76 rosette at each location across a range of depths (Andruszkiewicz et al., 2017; Easson et al.,  
77 2020; Laroche et al., 2020; Govindarajan et al., 2021). Niskin bottles can also be mounted on  
78 other platforms, including remotely operated vehicles (ROVs) (Everett and Park, 2018). Upon  
79 recovery, the water samples are immediately filtered, and the filters are preserved for subsequent  
80 processing back in the laboratory. Niskin bottle sampling, however, has many limitations. The  
81 number, size, and deployment mode (e.g., on a CTD rosette) of the bottles is fixed, which  
82 confines experimental design. Sample volumes used for eDNA filtration typically range between  
83 1 to 5 liters and are limited by bottle size, competing scientific needs for sample water, and  
84 filtration capabilities (e.g., how quickly and how many samples can be filtered). Relative to the  
85 vastness of midwater habitats, these eDNA sampling volumes are minute (Govindarajan et al.,  
86 2021; Merten et al., 2021); and may be insufficient for obtaining representative eDNA snapshots,  
87 given that eDNA distributions appear to be patchy (Andruszkiewicz et al., 2017). Furthermore,  
88 limited sample volumes may fail to detect rare taxa, which can potentially have  
89 disproportionately important roles in ecosystem functioning (Bracken and Low, 2012; Dee et al.,  
90 2019) and may contribute to ecosystem health and resilience (Hughes et al., 2005; Isbell et al.,  
91 2011). However, the issue of optimizing sample volume is relatively poorly understood relative  
92 to other eDNA sampling and processing parameters, such as filter type and DNA extraction  
93 protocol (Dickie et al., 2018). Additional considerations for conventional eDNA sampling are the  
94 need to use a clean work area and sterile procedures during filtration to reduce the possibility of  
95 contamination during processing (Ruppert et al., 2019). Furthermore, the handling time involved  
96 for processing water samples collected with Niskin bottles can potentially take several hours,

97 during which time the eDNA samples may experience relatively warm temperatures and eDNA  
98 in the samples may potentially decay (Goldberg et al., 2016; Holman et al., 2021).

99

## 100 *1.2 New sampling approaches*

101

102 Integration of water collection with mobile platforms such as autonomous vehicles, combined  
103 with in situ filtration, allows for more efficient water sampling and a greater variety of  
104 experimental design possibilities than is achievable with Niskin bottle sampling. For example,  
105 Yamahara et al. (2019) coupled the Environmental Sample Processor (ESP) with a long-range  
106 autonomous underwater vehicle (LRAUV). The ESP sampler has the potential to collect and  
107 preserve up to 60 samples per deployment (Yamahara et al., 2019) and so can increase the scale  
108 of eDNA sampling efforts (Truelove et al., 2022). However, the ESP sampler requires  
109 approximately one hour to filter one liter of water, and so it may be best suited for applications  
110 that require small sample volumes. Autonomous approaches with in situ filtration have also been  
111 explored for zooplankton sampling. In Govindarajan et al. (2015) the Suspended Particulate  
112 Rosette (SUPR) sampler, originally designed for biogeochemical sampling, was fitted with mesh  
113 appropriate for invertebrate larval collection and integrated into a REMUS 600 AUV. “SUPR-  
114 REMUS” successfully collected barnacle larvae for DNA barcoding from a coastal embayment  
115 with complex bathymetry. For deep-sea environments where target species are relatively dilute,  
116 Billings et al. (2017) developed a very large volume plankton sampler for the AUV *Sentry*.

117

118 For midwater and deep sea eDNA collection, an in situ sampling approach similar to those for  
119 zooplankton described above could be taken, using relevant filter types and large seawater

120 sample volumes. Recently, a new autonomous vehicle, *Mesobot*, was designed for studying the  
121 ocean's midwater environments (Yoerger et al., 2021). *Mesobot* can operate fully autonomously  
122 or with a fiber optic tether and can survey. It can hold its depth in a Lagrangian manner or  
123 unobtrusively track slow-moving midwater animals, as well as collect image and sensor data  
124 such as conductivity, temperature, depth, dissolved oxygen, fluorometry and optical backscatter.  
125 *Mesobot* includes a number of features to minimize avoidance and attraction while operating,  
126 including white and red LED lighting and slow-turning, large diameter thrusters that reduce  
127 hydrodynamic disturbances (Yoerger et al., 2021). *Mesobot* also has payload space to  
128 accommodate additional instrumentation, such as an eDNA sampler. The combination of  
129 *Mesobot's* ability to drift with a parcel of water and track animals while obtaining imagery and  
130 sensor data make it a promising and insightful platform for water column eDNA sampling.

131

### 132 *1.3 Goals*

133

134 Our goals were to develop and present a new large-volume autonomous eDNA sampler with in  
135 situ filtration mounted on the midwater robot *Mesobot* and assess this approach for conducting  
136 midwater eDNA surveys relative to conventional CTD-mounted small-volume Niskin bottle  
137 sampling. Our study region was the Northwest Gulf of Mexico, and included two sites: Bright  
138 Bank in the Flower Garden Banks National Marine Sanctuary, and a deeper water location on the  
139 slope of the shelf south of Bright Bank. We sampled at depths ranging from 20 m to 400 m with  
140 both methods for their direct comparison. We tested the hypothesis that, because of the larger  
141 sample volumes, our eDNA sampler on *Mesobot* ("*Mesobot*" samples) would capture greater  
142 animal taxonomic diversity than the CTD rosette – mounted Niskin bottle sampling ("*CTD*"

143 samples) due to the detection of rare or patchily distributed taxa that were not captured in the  
144 small-volume CTD samples. We predicted that taxa identified from the CTD samples would be a  
145 subset of those detected in the *Mesobot* samples. As we expected that the most abundant taxa  
146 would be present in both sample sets, we also hypothesized that despite the differences in taxon  
147 detection, that overall patterns of community structure identified by the two approaches would be  
148 similar. To test these hypotheses, we sequenced the V9 barcode region of 18S rRNA to analyze  
149 the metazoan eDNA community and compared biodiversity metrics from both sample types. We  
150 also described the utility of our eDNA sampler for marine midwater biodiversity surveys,  
151 focusing on the topics of sampling volume and practical methodological issues.

152

## 153 **2 Material and Methods**

### 154 *2.1 Study site*

155 We conducted a cruise on the *R/V Manta* in September of 2019 out of Galveston, Texas, USA.  
156 The CTD samples presented here are a subset of a larger regional ecological survey investigating  
157 diversity patterns at mesophotic reef banks in the Northwest Gulf of Mexico. Our focal site was  
158 Bright Bank, located off of the coasts of Louisiana and Texas (Fig. 1). Bright Bank received  
159 federal protection in March 2021 as part of the recent expansion of the Flower Garden Banks  
160 National Marine Sanctuary (FGBNMS). Bright Bank is a shelf-edge carbonate bank that hosts a  
161 diverse mesophotic reef ecosystem spanning 117 to 34 m depth (<https://flowergarden.noaa.gov/>)  
162 and is an important habitat for commercially-important and threatened fish species (Dennis and  
163 Bright, 1988; Sammarco et al., 2016). We sampled eDNA using both the *Mesobot* sampler and  
164 CTD casts at two sites: 1) “Bright Bank” site, located within 3 nautical miles of the center of the  
165 bank; and 2) “Slope” site located in offshore water at the slope of the continental shelf,

166 approximately 21 nautical miles south of the bank and with a water depth of approximately 500  
167 m. No permits were required for our work.

## 168 *2.2 Large-volume eDNA sampler with in situ filtration*

169 We developed an adjustable volume eDNA sampler capable of filtering large seawater volumes  
170 (10s to 100s of liters) that can be mounted on autonomous platforms such as the hybrid robotic  
171 vehicle *Mesobot* (Fig. 2; Fig 3; Supplementary Fig. 1). The eDNA sampler consists of 12 pumps  
172 and 12 filters with one pump per filter. The sampler includes two identical pump arrays,  
173 originally designed and built as the core of the Midwater Oil Sampler (MOS), an AUV water  
174 sampler for oil spills. Each MOS pump array contains six submersible pumps (Shenzhen Century  
175 Zhongke Technology model DC40-1250) and a microprocessor that enables an external  
176 computer to command individual pumps and log pump status through an RS232 serial  
177 connection. The MOS pump array is potted in polyurethane and pressure tested to 6000 m depth.  
178 Water enters each filter-pump pair through a unique intake tube. After passing through the pump,  
179 the water exits the assembly through a common discharge tube where a flowmeter  
180 (Omega Engineering FPR-301) measures the flow. Flow measurements are processed and  
181 communicated to *Mesobot* at a frequency of 10 Hz by a secondary microprocessor mounted  
182 inside *Mesobot's* main housing. We built two spare pump arrays, so that upon retrieval  
183 of *Mesobot*, the used sampler can be quickly exchanged with a clean sampler.

184

185 The pumps are connected by bleach-sterilized plastic tubing to Mini Kleenpak capsule  
186 filters (Pall Corporation, Port Washington, New York, USA; cat. # KA02EAVP8G). Each  
187 filter is individually encapsulated and consists of an inner 0.2  $\mu\text{m}$  Polyethersulfone (PES) filter  
188 and an outer PES pre-filter with a variable pore size, resulting in an effective filtration area of

189 200 cm<sup>2</sup> for the entire filter capsule. Check valves prevent backflow from reaching any of the  
190 filters. Each pump filters seawater at a rate of approximately 2 L/min. Only one pump per MOS  
191 pump array can be run at a time, but both arrays can be run simultaneously allowing for duplicate  
192 samples to be taken at each of six sampling events.

193  
194 The eDNA sampler was mounted on the underside of *Mesobot* (Fig. 2). The timing and duration  
195 of sampling events were controlled by the main control computer inside the main housing of  
196 the *Mesobot* and communicated to the sampler via the secondary microprocessor. To ensure that  
197 samples were taken at the proper time, pump commands were interleaved in the mission control  
198 program sequence which includes motion commands such as depth changes.

199  
200 *2.3 Sampler deployments on Mesobot*

201  
202 Three fully autonomous, untethered *Mesobot* dives were conducted at the Bright Bank (dive  
203 MB009) and the Slope (dives MB011 and MB012) sites (Table 1). Prior to each dive, the  
204 sampler tubing was cleaned with 10% bleach and rinsed multiple times with ultrapure water. The  
205 sampler pumps were then primed by filling the filter capsules with ultrapure water. All filters had  
206 been sterilized by autoclaving before the cruise. An additional sealed filter capsule that was filled  
207 with ultrapure water was attached to *Mesobot*'s base to serve as a field control. It took  
208 approximately an hour and a half of time to complete the pre-dive sampler cleaning and priming  
209 steps by one person. At the start of each dive, *Mesobot* was lowered into the water from the  
210 vessel's A-frame and then released. *Mesobot* then executed the programmed sequence of depth  
211 changes and sampling operations. During these dives, *Mesobot* used its control system and



212 thrusters to hold depth precisely (+/- 1cm) while drifting with the ambient currents, much like a  
213 Lagrangian float (i.e, moving with the water parcel), as opposed to maintaining a Eulerian point  
214 of reference (ie., holding position as the water parcel moves by). During *Mesobot* deployments,  
215 an acoustic ultra-short baseline (LinkQuest TrackLink) tracking system was used to determine  
216 the position and depth of the AUV underwater. During each dive, *Mesobot* could drift several  
217 kilometers, accordingly we used the tracking information to follow the vehicle as it drifted and to  
218 ensure that the vessel was positioned appropriately to recover the vehicle when it returned to the  
219 surface at the end of the dive. To help locate the vehicle after it surfaced, the vehicle carried 3  
220 strobe lights, a VHF beacon, and an Iridium/GPS unit that transmitted the vehicle's surface  
221 position through a satellite link. The additional surface recovery aids were important on the last  
222 dive, MB012, when the USBL tracking system failed and the vehicle surfaced at night time  
223 about a kilometer from the expected position.

224  
225 For all deployments, twelve samples (consisting of 6 sets of duplicates, which served as  
226 biological replicates) were collected along vertical transects. At the Bright Bank site, samples  
227 were taken between 120 and 20 m; at the Slope site, samples were taken between 400 and 40 m  
228 over the course of two deployments (Table 1). Once *Mesobot* was recovered after each  
229 deployment, the filter capsules were removed from the sampler and drained, and the ends were  
230 sealed with parafilm. The sealed filter capsules were stored in coolers filled with dry ice within a  
231 few minutes of retrieval.

232

233 *2.4 Conventional CTD – mounted Niskin bottle sampling*

234

235 Seawater samples were collected using a Seabird SBE 19 CTD rosette equipped with twelve 2.5-  
236 liter Niskin bottles. Samples were collected in triplicate (i.e., three biological replicates) at four  
237 depths in each cast, with the target depths selected to complement the *Mesobot* sampling depths  
238 (Table 1). At the Bright Bank site, one CTD cast (“Cast 8”) was conducted and samples were  
239 collected between 40 and 100 m depth. At the slope site, two CTD casts were conducted and  
240 samples were collected at depths ranging from 40 to 100 m (“Cast 14”) and from 160 to 400 m  
241 (“Cast 15”) (Table 1).

242  
243 Once on board the ship, seawater from each Niskin bottle was either transferred to a sterile  
244 Whirl-Pak stand-up sample bag (Nasco Sampling, Madison, WI, USA) and filtered in the wet  
245 lab, or directly filtered from the Niskin bottle on deck. The entire volume of seawater from each  
246 bottle was filtered through a sterile 0.22  $\mu\text{m}$  PES Sterivex filter (MilliporeSigma, Burlington,  
247 MA USA). Sterivex filters have a surface area of 10  $\text{cm}^2$ . Water was filtered using a Masterflex  
248 L/S peristaltic pump (Masterflex, Vernon Hills, IL, USA) set to 60 RPM equipped with four  
249 Masterflex Easy-load II pump heads using Masterflex L/S 15 high-performance precision tubing.  
250 Prior to each cast, the tubing was sterilized by pumping a 10% bleach solution for 5 minutes with  
251 the pump set at 60 RPM. The tubing interior was then rinsed thoroughly by pumping ultrapure  
252 water for 5 minutes at the same flow rate. Following sample filtration, residual water was  
253 pumped out of the Sterivex filters, the filters were placed in sterile Whirl-pak bags, and the bags  
254 were placed on dry ice in a cooler for the remainder of the cruise. The volume of filtered water  
255 was measured with a graduated cylinder and recorded. The average volume of water filtered per  
256 Niskin bottle was  $2.22 \pm 0.25$  (SD) liters. For each CTD cast, a field control consisting of  
257 approximately 2 liters of ultrapure water was also processed in the same manner and using the

258 same equipment as the field samples. The total shipboard processing time for the Niskin bottles  
259 was approximately two hours per cast with two people. Upon return to port in Galveston, TX, the  
260 CTD and the *Mesobot* samples were shipped on dry ice to Woods Hole, MA. Upon arrival in  
261 Woods Hole, the filters were stored in a -80°C freezer until DNA extraction, which took place  
262 approximately three months later.

263

#### 264 *2.5 eDNA extraction*

265 For the *Mesobot* samples, Mini Kleenpak capsules were opened using a UV-sterilized 3-inch  
266 pipe cutter and the outer and inner PES filters were removed and dissected from the capsules  
267 using a sterile scalpel and forceps. For the majority of samples, each inner and outer filter was  
268 cut into six pieces, which were placed into sterile 5 ml centrifuge tubes, and the DNA was  
269 extracted from each of the 12 fractions of the filter using DNEasy Blood & Tissue DNA  
270 extraction kits (Qiagen, Germantown, MD, USA), with some modifications to the protocol. 900  
271 ul of Buffer ATL and 100 ul of proteinase K were added to each 5 ml centrifuge tube. The tubes  
272 were incubated at 56° for 3 hours and vortexed periodically during the incubation period.  
273 Following the incubation, 1000 µL of buffer AL and ethanol were added to each centrifuge tube.  
274 The entire volume of the lysate was spun through a single spin column in five steps. Washes  
275 were performed according to the manufacturer's protocol, and DNA extracted from each filter  
276 piece was eluted in 80 µL of AE buffer. The inner and outer filters for each 1/6<sup>th</sup> portion were  
277 extracted separately, resulting in a total of 12 extractions per sample. Inner and outer filter slices  
278 from three samples (1 replicate each from MB009-20 m, MB009-40 m, MB012-40 m; Table 1)  
279 were extracted in an analogous manner with the DNA Power Water kit (Qiagen, Germantown,  
280 MD, USA). The DNA concentration of each filter piece extraction was measured with a Qubit

281 fluorometer (Life Technologies, Carlsbad, CA, USA) using the 1X High-sensitivity double-  
282 stranded DNA assay. DNA extractions from inner filter pieces extracted using the Power Water  
283 kit yielded very low DNA concentrations. Therefore, these samples were not included in  
284 comparisons of total DNA yield. However, they were included in other analyses. Equal volumes  
285 of all inner 1/6<sup>th</sup> fractions were pooled yielding a pooled DNA extract for the inner filter for each  
286 sample. Outer 1/6<sup>th</sup> fractions were pooled in the same manner, resulting in a pooled DNA extract  
287 for the outer filter for each sample. These two pooled DNA extracts were processed separately  
288 for subsequent PCR, library preparation and sequencing.

289

290 For the CTD samples, genomic DNA from the Sterivex filters was extracted using DNEasy  
291 Blood & Tissue extraction kits following the manufacturer's protocol adapted to accommodate  
292 the Sterivex filter capsules (Govindarajan et al., 2021). DNA was eluted in 80  $\mu$ L of molecular-  
293 grade water. The DNA concentration of each Sterivex filter extraction was also measured with  
294 the Qubit 1X High-sensitivity double-stranded DNA assay.

295

## 296 *2.6 Library preparation and sequencing*

297 Library preparation and sequencing followed the approach in Govindarajan et al. (2021) with a  
298 few modifications. All PCR samples were diluted 1:10 in molecular-grade water to prevent  
299 possible inhibition (Andruszkiewicz et al., 2017). Duplicate 2.5  $\mu$ l aliquots from each sample  
300 were amplified in 25  $\mu$ L reactions with 12.5  $\mu$ L of KAPA HiFi HotStart ReadyMix (Kapa  
301 Biosciences, Wilmington, MA, USA), 0.5  $\mu$ L of 10  $\mu$ M forward and reverse primers (final  
302 concentrations of 0.200  $\mu$ M), and 9  $\mu$ L of molecular-grade water. The primers used were 1380F  
303 and 1510R, which amplify an 87 – 186 bp portion of the 18S rRNA V9 gene region (Amaral-

304 Zettler et al., 2009) with CS1 and CS2 linkers for subsequent ligation of Fluidigm adaptors. The  
305 primer sequences with linkers are:

306 ACACTGACGACATGGTTCTACACCCTGCCHTTTGTACACAC (1380F-w-CS1-F) and

307 TACGGTAGCAGAGACTTGGTCTCCTTCYGCAGGTTTCACCTAC (1510R-w-CS2-R).

308 Primers were ordered from Eurofins Genomics (Louisville, KY, USA) at 100  $\mu$ M concentration  
309 in TE buffer and diluted to 10  $\mu$ M to prepare the PCR reactions. Cycling conditions included an  
310 initial denaturation step at 95°C for 3 minutes; 25 cycles of 95°C for 30 seconds, 55°C for 30  
311 seconds, and 72°C for 30 seconds; and a final extension step of 72°C for 5 minutes. PCR  
312 products were visualized on a 1% agarose gel in TBE buffer stained with GelRed (Biotium,  
313 Fremont, California, USA) to determine the presence of amplicons of the expected size. The  
314 duplicate PCRs were pooled and sent to the Genome Research Core at the University of Illinois  
315 at Chicago (UIC).

316 At the UIC Genome Research Core, a second round of PCR amplification was conducted to  
317 ligate unique 10-base barcodes to each PCR product. The PCR was conducted using MyTaq HS  
318 2X master mix and the Access Array Barcode Library for Illumina (Fluidigm, South San  
319 Francisco, CA, USA). Cycling conditions included an initial denaturation step at 95°C for 5  
320 minutes; 8 cycles of 95°C for 30 seconds, 60°C for 30 seconds, and 72°C for 30 seconds; and a  
321 final 7-minute extension at 72°C. The barcoded PCR products were pooled and purified using  
322 1.0X Ampure beads (Beckman Coulter, Indianapolis, IN, USA). This method retains amplicons  
323 (with primers, linkers, and adapters) longer than 200 bp.

324

325 An initial paired-end, 150-basepair sequencing run on an Illumina MiniSeq platform was  
326 conducted to determine the expected number of reads per sample. Equal volumes of each library

327 were pooled, and the pooled libraries with a 15% phiX spike-in were sequenced. The volumes of  
328 each sample to be pooled for subsequent sequencing on an Illumina MiSeq were adjusted based  
329 on the relative number of reads produced by the initial MiniSeq run. Our goal was to obtain an  
330 equal sequencing depth among all field samples. Volumes pooled ranged from 1.0 to 30.0  $\mu\text{L}$ .  
331 The vast majority of the negative controls (filtration blanks, extraction blanks, and no-template  
332 controls) produced very few reads on the MiniSeq run. One  $\mu\text{L}$  of each negative control was  
333 pooled to increase the overall sequencing effort of the field samples; however, for the *Mesobot*  
334 filtration blanks, the volume was adjusted in the same manner as for the field samples. The  
335 volume-adjusted libraries were loaded on to a MiSeq platform and sequenced using v2 chemistry  
336 targeting paired-end 250 bp reads. De-multiplexing of reads was performed on the instrument. In  
337 addition to our sampler and Niskin bottle samples, additional Niskin bottle samples from the  
338 larger Bright Bank survey and their associated controls were also included in the sequencing  
339 runs. As these samples and controls were processed along with our focal samples, we included  
340 these additional controls in our sequence quality control (described below). In total, three MiSeq  
341 runs were conducted with the intent of obtaining a target depth of approximately 100,000 reads  
342 per sample. The same volume of all samples were included on each of the three runs.

343

#### 344 *2.7 Contamination controls*

345 Rigorous procedures to prevent and monitor contamination were taken at every step from sample  
346 collection through sequencing. During sampling filtration, all surfaces in the wet lab were  
347 cleaned with 10% bleach and rinsed multiple times with ultrapure water before every use. Nitrile  
348 gloves were worn and changed often. Field controls were taken for every *Mesobot* and CTD  
349 sampling event as described above. Back on shore, DNA extractions were conducted at WHOI in

350 the Govindarajan lab and PCR reactions were prepared at Lehigh University in the Herrera lab.  
351 Post-PCR products were handled for gel electrophoresis in a separate laboratory space at Lehigh  
352 University. All procedures in the WHOI, Lehigh, and UIC sequencing laboratories included the  
353 following measures to ensure sample integrity: 1) Nitrile lab gloves were always worn and  
354 changed frequently; 2) Pipettes were UV-sterilized before use and sterile filter tips were used; 3)  
355 All lab surfaces were cleaned with 10% bleach and rinsed with Milli Q water before each use; 4)  
356 PCR preparations were conducted in a PCR hood with a HEPA filter with positive airflow, and  
357 the work space was additionally decontaminated with UV light before each use; 5) Field controls  
358 were extracted, amplified and sequenced alongside the field samples; and 6) Six DNA extraction  
359 blanks were amplified and sequenced, and two PCR no-template controls (NTC) were included  
360 in each plate for the first round of PCR, pooled and sequenced.

361  
362 None of the negative controls (filtration blanks, extraction blanks and PCR NTCs) produced  
363 visible amplicons after the first PCR, and the vast majority produced far fewer sequencing reads  
364 than the field samples, as expected ( $105 \pm 137$  s.d. vs  $33,902 \pm 25,543$  s.d.). Two of the control  
365 sample libraries, a field negative control from a CTD cast not included in the data analysis and a  
366 PCR no-template control, produced more reads than expected (12,385 and 5,299, respectively).  
367 These and four other samples were re-sequenced to obtain correct data and to validate our initial  
368 sequencing results (Appendix 1).

369  
370 *2.8 Bioinformatics*  
371 Sequencing data was received as demultiplexed fastq.gz files for each sample and was processed  
372 using Quantitative Insights Into Microbial Ecology 2 (QIIME2) version 2020.11 (Bolyen et al.,

2019), following the general approach described in Govindarajan et al. (2021). Raw data was deposited in Dryad. Sequence quality plots were examined, forward primer sequences at the 5' end and reverse complements of reverse primers at the 3' end were trimmed using the Cutadapt QIIME2 plugin (Martin, 2011). Sequences were quality filtered, truncated to 120 base pairs in length, denoised, and merged using DADA2 (Callahan et al., 2016) within the QIIME2 platform. Sequences from each run were processed separately and merged after the DADA2 step. Singleton and doubleton (summed through the dataset) ASVs were removed from further analysis. These and subsequent merging and filtering steps were accomplished using the QIIME2 feature-table plugin. The resulting amplicon sequence variants (ASVs) were taxonomically classified using a naïve Bayesian classifier (Bokulich et al., 2018) that was trained on the Silva v.132 99% small subunit rRNA database (Quast et al., 2013) for the 18S V9 amplicon region. For each ASV in the dataset that was present in both the samples and in any of the controls, the maximum number of reads found in any control was subtracted from every sample (0.84% of the sample dataset). An additional 143 reads (0.00086% of the remaining sequences) that were classified as human and insect were removed. The resulting dataset was then filtered to include metazoan sequences only. Sampler inner and outer filters were analyzed both separately and together. Biodiversity was visualized using broad taxonomic categories (Silva levels 6 and 7; generally corresponding to order or family, respectively). The V9 marker is not used for species – level identification and species – level identification was outside the scope of this work. Rarefaction curves were generated in QIIME2 to assess and compare sequencing depths. After randomly sampling the data from each sample to the lowest sequencing depth of any field sample, Bray-Curtis dissimilarities were calculated in QIIME2 and were used to generate non-metric multidimensional scaling (nMDS) plots with sampling depth and sample type (*Mesobot* or



396 CTD) visualized using the package *vegan* 2.3\_5 (Oksanen et al., 2016) in R Version 4.0.4 (R  
397 Core Team, 2021). For the *Mesobot* filters, nMDS plots were also generated to compare the  
398 diversity collected on inner and outer filters. In this analysis, 4 samples with exceptionally low  
399 read counts on the inner filter were excluded, as described in the results section. Functional  
400 regressions of sampling depth against each nMDS axis were conducted to assess the significance  
401 of observed patterns (Ricker, 1973). Permutational multivariate analysis of variance  
402 (PERMANOVA) tests were conducted using the “adonis” function in *vegan* to assess the effects  
403 of sample type, sampling depth, and for *Mesobot* filters, inner and outer filter type. Taxon  
404 comparisons between sample categories (e.g., filter type, sampling approach, depth) were  
405 performed using an online Venn diagram tool from the University of Ghent  
406 (<http://bioinformatics.psb.ugent.be/webtools/Venn/>).

407

### 408 **3 Results**

#### 409 *3.1 Sampler performance, and sample collection summary*

410

411 The *Mesobot* sampler collected a total of 36 samples on three successful deployments (Table 1;  
412 Supplementary Table 1). Duplicate samples at 6 depths were obtained in each deployment, for a  
413 total of 12 samples per deployment. In the first deployment (MB009), the sampler pumps ran for  
414 20 minutes at 20 m depth intervals between 120 m and 20 m. In the second deployment  
415 (MB011), the sampler took 30-minute samples at 40 m depth intervals between 400 m and 200  
416 m. In the third deployment (MB012), the sampler took one pair of samples filtering for 30  
417 minutes at 320 m, and additional sample pairs filtering for 20 minutes at depths of 160 m, 100 m,  
418 80 m, 60 m, and 40 m. The length of time from the commencement of filtering of the first sample

419 to the return of *Mesobot* to the deck, when the samples were immediately preserved, was about 4  
420 hours for MB009 and MB011, and 3 hours and 15 minutes for MB012. For all deployments, the  
421 sampler flow rate was slightly over 2 liters per minute. The flow rate typically declined gradually  
422 over the sampling period, consistent with our expectation that material was accumulating on the  
423 filters (Supplementary Fig. 2).

424

### 425 *3.2 CTD data and Niskin bottle sample collection summary*

426 A total of 34 eDNA samples were collected with Niskin bottles over 3 CTD casts (Table 1;  
427 Supplementary Table 2). Twelve Niskin bottles were deployed on each CTD cast, but one  
428 sample was lost from Cast 8 (100 m) and another from Cast 15 (400 m) due to bottle  
429 malfunctions. The CTD profiles from these casts indicated a stratified water column with a  
430 thermocline beginning around 40 m at the Bright Bank site and 50 m at the Slope site, with the  
431 deep chlorophyll maximum (DCM, corresponding to peak fluorescence) slightly deeper than the  
432 thermocline (Supplementary Fig. 3).

433

### 434 *3.3 Total eDNA yield*

435 As expected given the larger sample volumes, the sampler collected more eDNA than the Niskin  
436 bottle sampling. However, the eDNA yield per liter of water filtered was comparable between  
437 methods for samples collected at the same depth (Fig. 4). eDNA concentration yields were  
438 higher in shallower water (i.e., less than 100 m), with the highest yields (up to ~628 ng per liter  
439 of water sampled) roughly coinciding with the approximate depth of the DCM (60 m)  
440 (Supplementary Fig. 3). eDNA yields were much lower at sampling depths greater than 100 m  
441 (Fig. 4). For the Bright site, where sampling depths ranged from 20 to 120 m, a regression of the

442 log of the amount of DNA collected per liter of water filtered and depth indicated no significant  
443 relationship (adjusted  $R^2 = -0.03866$ ,  $p = 0.619$ ), in contrast to the Slope site, where sampling  
444 depths ranged from 40 to 400 m (adjusted  $R^2 = 0.6856$ ,  $p = <0.0001$ ). For the *Mesobot* samples,  
445 the inner filters generally yielded slightly higher DNA concentrations than the outer filters  
446 (Wilcoxon signed rank test,  $p = 0.0003188$ ). There was greater variation at the Bright Bank site,  
447 where one inner filter yielded on average ~40 ng of DNA/L more than its corresponding outer  
448 filter (Fig. 5). For any given inner or outer filter from a *Mesobot* sample, the DNA  
449 concentrations of the extractions stemming from individual filter pieces were relatively similar in  
450 most cases, but a few samples (particularly those with the higher overall DNA yields) showed  
451 substantial variation (Fig. 5).

452

### 453 3.3 Metazoan sequence diversity

454 The number of metazoan reads varied greatly within and between *Mesobot* sampler and CTD  
455 datasets, and also between the Mini Kleenpak inner (*Mesobot*-inner, “MBI”) and outer (*Mesobot*-  
456 outer; “MBO”) filter dataset (Table 2; Supplementary Table 3). The MBO dataset consisted of 36  
457 samples with 1,096 metazoan ASVs and 2,700,417 metazoan reads. The mean number of reads  
458 per sample ranged from 23,530 to 207,391 with a mean of 75,012. The MBI dataset, with 36  
459 samples, in general had fewer metazoan ASVs (703), total sequences (582,246) and reads per  
460 sample (mean = 16,173.5 reads, min = 3 reads; max = 68,149 reads). For a given *Mesobot*  
461 sample, the majority of metazoan reads originated from the outer filter, both in terms of the  
462 percent of metazoan reads in the dataset (Fig. 6; paired t-test,  $p < 0.0001$ ) and in the absolute  
463 number of metazoan sequences (Supplementary Table 3). *Mesobot* samples from Bright Bank

464 (MB009) in general had proportionately more metazoan sequences on the outer filter than those  
465 from the Slope site (MB011 and MB012) (Fig. 6).

466

467 The CTD dataset included 34 samples with 517 metazoan ASVs and 1,477,377 metazoan  
468 sequences. The number of metazoan reads per sample ranged from 3,354 to 99,996, with a mean  
469 of 43,453, and in most samples, represented less than half of the total number of reads (Fig. 6),  
470 but in general the metazoan proportion was more similar to the *Mesobot* outer filters than the  
471 inner filters. Metazoan reads were proportionately more abundant in Bright Bank CTD samples  
472 (Cast 8) than in the Slope CTD samples (Casts 14 and 15) (Fig. 6)

473

474 Asymptotic rarefaction curves indicated that the sequencing depth was sufficient to capture the  
475 diversity in most of the CTD and *Mesobot* samples, and that *Mesobot* samples generally  
476 recovered more ASVs than the CTD samples (Fig. 7). The only exception to this pattern was one  
477 CTD sample from Cast 15, sampling at 240 m, which detected an unusually high number of  
478 ASVs (Fig. 7) although it had slightly less than the average number of sequence reads (40,691  
479 reads) (Supplementary Table 3).

480

### 481 3.5 Taxonomic composition of the inner and outer sampler filters

482

483 The *Mesobot* and CTD samples from both the Bright Bank and Slope sites were comprised of  
484 ASVs originating from a wide variety of animal groups (Supplementary Fig. 3; Supplementary  
485 Fig. 4). Samples were generally dominated by copepod reads (calanoid and cyclopoid) which  
486 often comprised the majority of metazoan reads, but ostracods (Halocyprida) and siphonophores

487 were also notably common. Siphonophores comprised the majority of metazoan reads in some  
488 samples, especially in CTD Cast 15 (e.g., at depths 160 m, 320 m, and 400 m at the Slope site).  
489 Ostracods were relatively abundant in some samples, especially in *Mesobot* deployment MB009  
490 (at the Bright Bank site) at sampling depths 80 m and greater, and in *Mesobot* deployment  
491 MB011 (the deep deployment at the Slope site). Very few reads were classified as fish. While the  
492 same broad taxonomic groups were generally present among samples, sample biological  
493 replicates varied substantially in the relative abundances of taxa (Supplementary Fig. 3;  
494 Supplementary Fig. 4). Occasionally, it appeared that one taxon would overwhelmingly  
495 dominate a particular sample but would be much less common in the corresponding duplicate  
496 sample (e.g., siphonophores in samples 320-1 and 400-1 in Cast 15, and in sample 160-1 in  
497 MB011; Supplementary Fig. 3).

498  
499 We compared the Silva level-7 taxa found in samples taken by both methods at a given site and  
500 depth. In all but one case, the *Mesobot* samples (duplicates for the site/depth pooled; representing  
501 ~80 – 120 liters of water sampled) detected, on average, 1.66 times more taxa than  
502 corresponding CTD samples (triplicates for the site/depth pooled, representing ~6 liters of water  
503 sampled) (Table 3; Appendix 2). There were between 22 – 33 shared taxa (detected in both  
504 sampling approaches) depending on the depth, representing on average 36% of all taxa detected  
505 at a given depth. There were typically more taxa unique to the *Mesobot* samples (25 – 40) than  
506 were unique to the CTD samples (2 – 12; Table 3), representing, on average, 43% (*Mesobot*) and  
507 11% (CTD) of all taxa at a given depth. The one exception was at the Slope site at 240 m depth,  
508 where there were 33 taxa detected by both sample types but the CTD samples detected 23 unique  
509 taxa and the *Mesobot* detected only 9 unique taxa. One of the CTD replicates from this depth was

510 the same sample noted to have an unusually high number of ASVs (Fig. 7). Also at the Slope  
511 site, one depth (320 m) was sampled during two Mesobot deployments (MB011 and MB012) as  
512 well as with the CTD. In this case, both *Mesobot* samplings detected more unique taxa than the  
513 CTD sampling, and also each *Mesobot* deployment detected several taxa that the other did not.

514  
515 The Bright Bank and Slope datasets were rarefied to their lowest sequencing depths (17,793 and  
516 3,354, respectively) before calculating Bray-Curtis dissimilarities. The nMDS and  
517 PERMANOVA analyses indicated structuring relative to sampling depth at the Bright Bank (Fig.  
518 8; sample type:  $R^2 = 0.06688$ ,  $p = 0.013$ ; depth:  $R^2 = 0.51695$ ,  $p = 0.001$ ) and Slope (Fig. 8;  
519 sample type:  $R^2 = 0.06181$ ,  $p = 0.001$ ; depth:  $R^2 = 0.41870$ ,  $p = 0.001$ ) sites. Sampling depth had  
520 a greater impact than sampling type at the Bright Bank site. These results were supported by  
521 functional regressions showed that sampling depth was strongly correlated with the first  
522 dimension (MDS1) (Bright Bank:  $R^2 = 0.7551$ ,  $p = 0$ ; Slope:  $R^2 = 0.6218$ ,  $p = 0$ ) but not the  
523 second (Bright Bank:  $R^2 = 0.005519$ ,  $p = 0.7439$ ; Slope  $R^2 = 0$ ,  $p = 0.9905$ ), and no obvious  
524 trend with sampling type (Supplementary Fig. 4).

525  
526 When the inner and outer filters for each *Mesobot* sampler sample were analyzed separately, the  
527 relative proportions of the most abundant taxa differed (Supplementary Fig. 5; Fig. 9). When  
528 calculating Bray-Curtis dissimilarities, the dataset was rarefied to 3,438 reads. Four samples  
529 from deployment MB009 (1 sample from 20 m, 2 samples from 40 m, and one sample from 100  
530 m) where the inner filters had read counts below this threshold were excluded. The  
531 PERMANOVA results indicated that sampling depth (Bright Bank:  $R^2 = 0.29513$ ,  $p = 0.001$ ;  
532 Slope:  $R^2 = 0.15503$ ,  $p = 0.01$ ) had a greater impact than filter type (Bright Bank:  $R^2 = 0.05691$ ,

533  $p = 0.123$ ; Slope:  $R^2 = 0.04972$ ,  $p = 0.02$ ). This was visualized in the nMDS plot (Fig. 9).  
534 Regressions showed that depth was correlated with the first dimension ( $R^2 = 0.8614$ ,  $p = 0$ ) but  
535 not the second ( $R^2 = 0.003707$ ,  $p = 0.7932$ ) (Supplementary Fig. 6). In general, gelatinous taxa  
536 including siphonophores, trachymedusae, and larvaceans (Oikopleuridae) were more abundant  
537 on the inner filters than the outer filters. Out of a total of 181 Silva level-7 (the most highly-  
538 resolved level in the Silva classification) taxa, 118 were found on both filter types, 18 on the  
539 inner filters only, and 45 on the outer filters only. Notably, there were no crustaceans or fish  
540 unique to the inner filters; while there were 7 crustaceans (5 copepods and two  
541 eumalacostracans) and two fish unique to the outer filters (Appendix 2). The taxa that were  
542 unique to the inner filters were primarily medusozoans, ctenophores, sponges, and polychaetes  
543 and other worm-like groups.

544

#### 545 **4 Discussion**

546

547 We built a large – volume eDNA sampler and successfully deployed it during three dives using  
548 *Mesobot* as our sampling platform. Our sampler filtered approximately 20 – 30 times more  
549 volume per sample (~40-60 liters) than our conventionally – obtained CTD samples (~2 liters).  
550 Our hypothesis, that there would be more taxa identified from the large – volume *Mesobot*  
551 samples, was supported. We found 66% more taxa in *Mesobot* samples than CTD samples. We  
552 also found that the majority of taxa found in the CTD samples were also found in corresponding  
553 *Mesobot* samples (78% on average). However, there was substantial variation between replicates  
554 in both the *Mesobot* and CTD sample sets. Despite recovering fewer overall taxa, the CTD  
555 samples captured unique taxa corresponding to 11% of all taxa sampled at a given depth

556 (compared to 43% taxa sampled only by *Mesobot*). *Mesobot* and CTD sample sets both showed  
557 that community composition patterns are strongly associated with depth, thus supporting our  
558 hypothesis that, despite the differences in taxon detection, the overall community patterns  
559 revealed by both methods would be similar.

560

#### 561 *4.1 Sampling volume*

562 While highly variable in both sampling types, our *Mesobot* eDNA capture rate (in terms of the  
563 total DNA concentration of our extractions as measured by the Qubit fluorometer) was in the  
564 same range as for the CTD sampling, after accounting for sample volume and depth. Our study  
565 shows a decrease in eDNA concentration with depth that is consistent with previous studies  
566 (Govindarajan et al., 2021; McClenaghan et al., 2020). This finding indicates that greater sample  
567 volumes may be needed for mid and deep water eDNA biodiversity analyses. This is especially  
568 true when the focal organisms are animals (as opposed to microbes) – given the small fraction (of  
569 metazoan sequence reads we observed in our samples (e.g., <50% in most and <10 % in  
570 some), when the eDNA signal is inhomogeneous, and when the detection of rare taxa is an  
571 objective of the study. Because our eDNA sampler can efficiently pump a much larger volume  
572 than that which can be captured by a single Niskin bottle, it represents an improved tool for  
573 collecting eDNA at deeper ocean depths (i.e., below ~100 m).

574

575 Studies in other environments have similarly demonstrated that increasing sample volumes can  
576 improve biodiversity detection (Bessey et al., 2020; Hestetun et al., 2021; Schabacker et al.,  
577 2020; Sepulveda et al., 2019), and future work should evaluate the optimal sampling volume and  
578 strategy as a function of the environment and the biology of target taxa (Mächler et al., 2016).



579 For example, it is often of interest to obtain vertical profiles in mesopelagic studies, as the  
580 vertical dimension is a key axis for environmental variables such as light availability, and for  
581 ecological processes such as diel vertical migration. Future studies could explore whether it is  
582 advantageous to adjust sampling volume with depth (e.g., Laroche et al., 2020), for vertical  
583 sampling transects that run from shallow water (e.g., < 100 m, or above the thermocline or  
584 DCM) to deep water (e.g., > 100, or below the thermocline or DCM).

585

#### 586 *4.2 Integrated versus point sampling*

587 Our conclusion that larger sample volumes are associated with greater biodiversity detection  
588 result from a comparison of two different sampling approaches, and it is possible that factors  
589 inherent to those approaches also contributed to our results. Our eDNA sampler filtered over 20  
590 to 30 minute time intervals while *Mesobot* was drifting at constant depth. While *Mesobot*  
591 samples are integrated over time, the Niskin bottles collected the entire sample volume  
592 instantaneously at a single point in the water column. Importantly, *Mesobot* was moving  
593 passively with the ambient water, and so was likely sampling from the same water parcel  
594 throughout the filtration period. A possible exception could have occurred, however, if an internal  
595 wave passed through during the sampling period – such as was noted, for example, during a  
596 *Mesobot* animal tracking deployment in Monterey Bay (Yoerger et al., 2021). The presence of  
597 internal waves could be assessed in future *Mesobot* sampling deployments with the addition of  
598 co-registered CTD sensor data.

599

600 Sampling approaches and theory are understudied aspects of eDNA protocols (Dickie et al.,  
601 2018), and should be further explored. To better tease apart the co-varying factors of volume,

602 space, and time, sampling experiments could be conducted in a mesocosm where the diversity is  
603 known, and the proportion of diversity recovered using different sampling volumes and intervals  
604 collected by moving and stationary samplers could be determined. Alternatively, sampling  
605 experiments could be conducted in the field by co-collecting independent samples with different  
606 filtration durations (i.e., collecting a single sample over 30 minutes, while collecting series of 6  
607 consecutive samples, each filtered for 5 minutes).

608

#### 609 *4.3 Autonomous sampling with a robotic platform*

610 The combination of autonomous sampling with robotic platforms and molecular sensing is  
611 extremely powerful and has great potential to reveal biological patterns and processes in poorly  
612 understood midwater ecosystems (McQuillan and Robidart, 2017). Our sampler was mounted on  
613 *Mesobot*, a midwater robot that can operate up to 1000 m depth and track particles and animals  
614 while utilizing a wide variety of sensors (Yoerger et al., 2021). *Mesobot* can also behave in a  
615 Lagrangian manner, drifting with a water parcel, allowing continuous sampling and sensing of  
616 that parcel. Our cruise was the second-ever midwater deployment of *Mesobot*. Since our cruise,  
617 the capabilities and operation readiness of the vehicle have expanded, opening up the possibility  
618 of integrating eDNA results with other sensed data, making it possible to test a wide variety of  
619 midwater hypotheses (Lindsay, 2021). *Mesobot* now carries machine-vision monochrome stereo  
620 cameras (Allied Vision G-319B) that enable real-time tracking of midwater targets (Yoerger et  
621 al., 2021), a color camera (Sony UMC-SC3A) that provides high-quality color video (HD or 4K)  
622 and high-resolution stills (12 MP), and a high-sensitivity radiometer (Oceanic Labs) which can  
623 measure downwelling irradiance. Future *Mesobot* – sampler deployments could take advantage  
624 of these sensors - for example, eDNA results could be compared to simultaneously-collected

625 imaging and could potentially provide taxonomic resolution to ecological and behavioral  
626 observations. Another exciting strategy would be to use *Mesobot*'s ability to maintain its position  
627 to take samples at a constant depth over the course of a zooplankton diurnal migraton cycle,  
628 while simultaneously recording irradiance (which likely triggers most migrations (Brierley,  
629 2014)). Our eDNA sampler could also be integrated on to other platforms, including  
630 observational networks for long term monitoring of ocean health (Thorrold et al., 2021).  
631  
632 Yamahara et al. (2019) and Truelove et al. (2022) also coupled an autonomous eDNA sampler  
633 with in situ filtration (the Environmental Sample Processor) to a robotic vehicle (a long range  
634 AUV, or LRAUV), but their approach differed from ours in terms of both their vehicle and their  
635 sampler. By moving in tight circles within the drifting water mass (Zhang et al., 2020), the  
636 LRAUV can hold its position in a parcel of water during sample collection in a quasi-Lagrangian  
637 fashion (Truelove et al. 2022). Their sampler can collect up to 60 samples in a deployment,  
638 which are then preserved in situ – an important feature for long term sampler deployments.  
639 However, their sampler requires about an hour to filter a single liter of water, while ours filters  
640 that volume in about 30 seconds. While their ability of the ESP sampler to collect and preserve  
641 large numbers of samples has great potential for increasing the scale of eDNA sampling, their  
642 longer filtration time increases the possibility of collecting samples that integrate temporal  
643 phenomena occurring within a water parcel, such as diel vertical migration, as well as greatly  
644 limiting collection volumes. As sampling and platform technologies evolve, it is likely that  
645 multiple approaches will be needed to address a diverse range of ecological questions and  
646 observational needs in different ocean environments.  
647

648 *4.4 Filters for large – volume sampling*

649 Our Mini Kleenpak sampler filters had an outer filter with variable-sized pores and an inner filter  
650 with 0.2  $\mu\text{m}$  pores and an effective filtration area of 200  $\text{cm}^2$ . For comparison, the Sterivex filters  
651 were made of the same material (PES) and the same pore size, but had an order of magnitude  
652 smaller filtration area (10  $\text{cm}^2$ ). Our sampler outer filters essentially served as a prefilter to the  
653 inner filters, and we processed and analyzed both, which added to the effort and cost involved.  
654 The processing included dividing each inner and outer filter into 6 pieces and extracting each,  
655 and then pooling and sequencing the inner and outer pieces separately. Thus, each *Mesobot*  
656 sample required 12 extractions and 2 pooled PCR reactions per sample for sequencing (versus 1  
657 extraction and 1 pooled PCR reaction for each CTD sample). There is clearly a tradeoff between  
658 sample volumes and project cost and effort. As this was the first time that we were aware of that  
659 Mini Kleenpak filters were used for eDNA sampling, we elected to process the entirety of the  
660 filter area; however, this is an aspect of our protocol which could be refined in the future, as we  
661 discuss in section 4.4.

662

663 The outer Mini Kleenpak filters contained a much larger proportion of metazoan sequence reads  
664 than the inner filters, indicating a greater retention of animal eDNA on those filters. As the filter  
665 pore spaces became reduced or blocked over the course of filtering, it is possible that the  
666 effective pore size of the outer filter was reduced. Thus, we might expect that very small  
667 particulates or extracellular DNA could be found on both filters, but that larger particulates or  
668 even whole animals would be found primarily on the outer filters. We also acknowledge the  
669 possibility that the pore sizes of both filters could have been enlarged due to our relatively high  
670 flow rate, causing larger particulates to be pushed through to the inner filter, or smaller

671 particulates to escape the filters entirely. The taxa found on both filter types included a broad  
672 range of animal groups (e.g., medusozoans, polychaete worms and other worm-like animals,  
673 crustaceans, and fish). However, there were many additional taxa found only on the outer filters,  
674 including crustacean taxa, which may suggest their eDNA signal is associated with larger  
675 particles and/or that the outer filters retained zooplankton as well as eDNA.

676  
677 Previous studies that used larger sample volumes have taken different approaches with filter  
678 selection. Small (submicron) pore size filters which are typically used in eDNA sampling may  
679 have slow filtration rates and the filters could become easily clogged (Turner et al., 2014). Some  
680 researchers obtain higher sample volumes by utilizing multiple submicron-opening filters  
681 (Goldberg et al., 2016; Mächler et al., 2016); but this requires longer processing time and higher  
682 costs associated with additional DNA extractions, PCR, and sequencing. Other studies have  
683 utilized larger-pore size filters (Schabacker et al., 2020), but the disadvantage is that taxa that  
684 have eDNA predominantly associated with smaller particles could be missed (Sepulveda et al.,  
685 2019). Additionally, when large volumes are filtered, it is likely that some intact animals are  
686 collected in addition to eDNA. The ideal filter pore size depends on the form of the eDNA of the  
687 target taxa; however, eDNA particle sizes are known for only very few taxa (Jo et al., 2019;  
688 Moushomi et al., 2019; Turner et al., 2014) Sometimes, a pre-filter to screen out large particles  
689 and even whole organisms is used, but using pre-filters may result in the detection of fewer taxa  
690 (Djurhuus et al., 2018), unless the pre-filter is also processed.

691

692 *4.5 Logistical considerations*

693 From the field perspective, our sampler required about an hour and a half of effort per  
694 deployment to prime the pumps, and upon retrieval, the sampler samples could be immediately  
695 stored. In contrast, the CTD sampling and processing required more time after retrieval (about  
696 four hours of effort per deployment) to filter the same number of samples (12) with around 20 –  
697 30 times less volume per sample. In situations where the number of samples is greater or the  
698 sample volumes are larger, the post-retrieval processing time would be even longer, potentially  
699 allowing the eDNA signal to decay. Thus, reduction of post-retrieval shipboard processing time  
700 is an important advantage of using a sampler with in situ filtration.

701  
702 Laboratory time and costs are also important to consider. If multiple filters are used to obtain the  
703 large volume, the cost of DNA extraction is multiplied. Here, we utilized a single large-area  
704 filter, and our DNA extraction protocol necessitated dividing up the filter into pieces for  
705 individual extractions. Ideally, only a portion of the filter could be processed and the remainder  
706 could be archived (Sepulveda et al., 2019). However, it would need to be shown first that the  
707 DNA is distributed evenly throughout the filter, and our data suggest that this is not necessarily  
708 the case. An alternative to this issue would be to develop a DNA extraction protocol that  
709 processes the whole filter without having to partition it. Moreover, depending on the goal of the  
710 study, it might be acceptable to extract only the outer filters which capture the majority of  
711 metazoan diversity. Alternatively, the sampler design could be adapted to accommodate other  
712 filter types that have only larger openings. Future research with the Mini Kleenpak and other  
713 large surface area filters should explore refinements to the DNA extraction protocol to reduce the  
714 cost and labor involved, while preserving the ability to detect a wide range of taxa.

715

716 Another relevant sample processing feature that impacts the quantity of taxa detected and should  
717 be further explored is the number of PCR replicates in the library preparation step (Ruppert et al.,  
718 2019). Increasing the number of PCR replicates increases the number of taxa identified (Ficetola  
719 et al., 2015), but also adds to the time and cost of the project. Here, we used duplicate PCRs, but  
720 future work should evaluate the benefits of increased replication as this is likely especially  
721 important for large volume samples.

722

#### 723 *4.6 General biodiversity observations*

724 Our eDNA analyses from both the *Mesobot* sampler and the CTD sampling revealed a broad  
725 range of invertebrate taxa, consistent with what other studies have found with the 18S V9 marker  
726 (Blanco-Bercial, 2020; Bucklin et al., 2019; Govindarajan et al., 2021). The paucity of fish reads  
727 is also consistent with these other studies, and prior observations that the V9 marker  
728 preferentially amplifies taxa other than fish (Sawaya et al., 2019). Sequence reads from  
729 crustacean taxa including calanoid and cyclopid copepods and ostracods were especially  
730 abundant in most samples. Siphonophore reads were also common in samples collected at 80  
731 meters and deeper. While the 18S V9 marker detects a wide variety of taxa, it lacks the  
732 resolution to identify most taxa to species (Blanco-Bercial, 2020; Bucklin et al., 2016; Wu et al.,  
733 2015) and we did not attempt species-level identification in this study. However, future analyses  
734 of these samples with other markers could reveal valuable ecological insights on target species.  
735 In particular, markers targeting fish such as 12S (e.g., Miya et al., 2015) and anthozoans will be  
736 especially relevant for our study site. Additionally, independent methods of characterizing  
737 biodiversity such as analyses of net tows and video are important to relate eDNA signatures to  
738 community composition (Closek et al., 2019; Govindarajan et al., 2021; Stoeckle et al., 2021).

739 *Mesobot* also has imaging capability (Yoerger et al., 2021) and future studies combining  
740 *Mesobot* imaging with our eDNA sampler will reveal further insights into mesophotic and deep  
741 water biodiversity.

742

#### 743 *4.7 Biodiversity changes with depth*

744 Despite differences in taxon detection, both of our large and small volume sampling approaches  
745 revealed significant changes in community structure with depth. This is an important finding as it  
746 shows that despite the small volumes of water that are sampled, community biodiversity trends  
747 can still be detected using conventional CTD/Niskin bottle sampling – which is the most  
748 common approach to marine eDNA sampling. Furthermore, despite a myriad of processes that  
749 could potentially blur eDNA signatures in oceanic environments – such as particle sinking, ocean  
750 currents, vertical mixing, and biologically-mediated transport such as diel vertical migration, our  
751 results and other recent studies indicate that eDNA signatures may remain localized. Our finding  
752 that eDNA detected diversity changes on the order of 10s of meters in depth are consistent with  
753 modeling results that show midwater eDNA signatures remain within 20 meters of their origin in  
754 the vertical direction (Allan et al., 2021), and add to a growing body of field evidence from  
755 pelagic systems demonstrating that eDNA can detect biodiversity changes with depth (Canals et  
756 al., 2021; Easson et al., 2020; Govindarajan et al., 2021).

757

#### 758 *4.8 Variation between replicates*

759 Environmental DNA analyses often show substantial variability between replicates (Beentjes et  
760 al., 2019) as we observed here. The optimal number of replicates to include in any eDNA study  
761 depends on the study system and goals; however, replication strategies in eDNA studies are



762 inconsistent, and generally not optimized (Dickie et al., 2018). The variation observed here and  
763 elsewhere (e.g., Andruszkiewicz et al., 2017; Govindarajan et al., 2021) with CTD sampling  
764 suggests that read abundances in individual samples may not be representative of community  
765 proportions and that absences of taxa may be false negatives. This variation indicates that eDNA  
766 distributions are patchy within a given location or depth, even if eDNA communities are  
767 distinguishable between depths.

768  
769 At our Slope site, the eDNA community at 320 m depth was sampled during both the MB011  
770 and MB012 deployments, as well as with one CTD cast. We found that despite the more  
771 intensive sampling effort, each sampling event still recovered unique taxa, and in particular the  
772 MB012 sampling event recovered several more taxa (63) than the MB011 sampling event (39)  
773 despite similar sample volumes. These differences may be related to eDNA patchiness in the  
774 horizontal direction. In mesopelagic depths such as this sampling location, diel vertical migration  
775 can create variation in horizontal zooplankton distributions (Chen et al., 2021), which could  
776 result in patchy eDNA distributions. More research on the spatial distribution of eDNA in the  
777 horizontal dimension of midwater environments would be insightful for optimizing eDNA  
778 sampling strategies.

779  
780 Larger-volume sampling might be expected to lead to more consistent results in biological  
781 replicates (which are sampled at the same and location). However, we found that the relative  
782 proportions of taxa differed substantially between replicates even in our large-volume *Mesobot*  
783 samples. Given the volume of water that we sampled (~40 - 60 of liters), it is highly likely that  
784 small zooplankton were collected along with the eDNA. This possibility is also consistent with

785 our observation of several crustacean taxa unique to the outer filters. If zooplankton are retained  
786 on the filters, they would likely be contributing disproportionately to the eDNA reads in that  
787 particular sample. Thus, paradoxically, while larger volumes may smooth out variation in eDNA  
788 particle distributions, the collection of small zooplankton in addition to particles may introduce a  
789 new source of variation. The introduction of a pre-filter to screen out the zooplankton, is not a  
790 straightforward solution, as discussed in sections 4.4.

791

## 792 **5 Conclusions**

793

794 We introduced a new eDNA sampler that is capable of filtering large volumes of seawater in  
795 situ. We mounted the sampler on the midwater robot *Mesobot* and conducted three successful  
796 deployments at two sites in the Flower Garden Banks region of the Gulf of Mexico where we  
797 collected samples between 20 and 400 m water depth. We additionally sampled and analyzed  
798 eDNA from three CTD casts from the same sites and depths. While both approaches detected  
799 biodiversity patterns with depth on the scale of 10s of meters, we found that our large volume  
800 samples detected more animal taxa than our conventionally – collected small volume CTD  
801 samples. Large-volume sampling could be especially important to consider for mid and deep-  
802 water marine environments, and in any environment where eDNA is dilute or patchily –  
803 distributed, and when the detection of rare taxa is a goal.

804

## 805 **Funding**

806 This research is part of the Woods Hole Oceanographic Institution's Ocean Twilight Zone  
807 Project, funded as part of The Audacious Project housed at TED, and a result of research funded

808 by the National Oceanic and Atmospheric Administration's Oceanic and Atmospheric Research,  
809 Office of Ocean Exploration and Research, under award NA18OAR0110289 to Lehigh  
810 University (SH and JM co-PIs). The work of AA was supported in part by the Future Oceans Lab  
811 Acceleration Fund. The work on the sampler pumps was supported by funding from UNH  
812 Subaward No. 19-015 on NOAA Federal Award No. NA17NOS0080203 to AK.

813

#### 814 **Acknowledgements**

815 We thank the Scibotics Lab (WHOI) for contributing their midwater oil samplers to the eDNA  
816 sampler development, Katie Foley (Lehigh) for assistance with CTD sample processing in the  
817 field, and James MacMillan (FGBNMS) for assistance with CTD deployments, Erin Frates  
818 (WHOI) for assistance with laboratory sample processing, Peter Wiebe (WHOI) for discussions  
819 on data analysis, and Sarah Stover (WHOI) for proof-reading the manuscript. We thank Jessica  
820 Labonté and the Ocean & Coastal Studies laboratories of Texas A&M University at Galveston  
821 for access to ultrapure water. We also thank the Flower Garden Banks National Marine  
822 Sanctuary and the captain and crew of *R/V Manta*.

823 **Table 1.** Summary of samples collected, including the *Mesobot*-mounted sampler samples and  
 824 the CTD- mounted Niskin bottle samples. Additional sampling details for the *Mesobot* samples  
 825 are in Supplementary Table 1 and details for the CTD samples are in Supplementary Table 2.

826

Cast or Dive	Date	Time (UTC)	Site	Station	Latitude	Longitude	Depth range (m)	Bottom depth (m)	# samples
8	9/25/19	16:29	Bright Bank	Bright Bank	27.84239	-93.268503	100 - 40	154	11
14	9/26/19	17:36	Slope	Slope	27.54012	-93.35027	100 - 40	507	12
15	9/26/19	21:01	Slope	Slope	27.54607	-93.38611	400 - 160	482	11
MB009	9/25/19	15:25	Bright Bank	Bright Bank	27.8485	-93.2576	20 - 120	155	12
MB011	9/26/19	17:11	Slope	Slope	27.53905	-93.34029	200 - 400	488	12
MB012	9/26/19	23:29	Slope	Slope	27.53905	-93.34029	40 - 320	510	12

827

828

829 **Table 2.** Metazoan sequence summary.

830

	<i>Mesobot-Inner</i>	<i>Mesobot-Outer</i>	<b>CTD</b>
<b># samples</b>	36	36	34
<b># sequences (total)</b>	582,246	2,700,417	1,477,377
<b># ASVs</b>	703	1096	517
<b>Minimum # sequences/sample</b>	3	25,350	3,354
<b>Maximum # sequences/sample</b>	68,149	207,391	99,996
<b>Mean # sequences/sample</b>	16,173.5	75,012	43,452

831

832

833 **Table 3.** Number of Level-7 taxa at in CTD and *Mesobot* samples from common sites/depths  
 834 from A) comparisons between 2 sample sets; and B) comparisons between 3 samples sets. \*CTD  
 835 filter volumes not measured; approximations assume 2.2 liters per bottle.

836 **A.**

Site	Depth (m)	# taxa shared	# taxa unique to CTD samples	# taxa unique to <i>Mesobot</i> samples	Sample volume (l)	
					CTD:	MB:
Bright Bank	40	29	2	40	CTD:	6.84
					MB:	120.95
	60	27	6	30	CTD:	6.82
					MB:	129.96
	80	25	12	34	CTD:	6.41
					MB:	122.15
	100	22	5	33	CTD:	4.4
					MB:	122.17
Slope	40	28	3	30	CTD:	7.2
					MB:	85.91
	60	22	0	28	CTD:	7.16
					MB:	79.96
	80	22	11	29	CTD:	5.9
					MB:	88.29
	100	24	9	25	CTD:	7.02
					MB:	86.1
	240	33	23	9	CTD:	6.91
					MB:	125.71
	400	24	10	45	CTD:	~4.4*
					MB:	119.38

837

838 **B.**

Slope	Depth (m)	# taxa shared-all	# taxa shared CTD-MB011	# taxa shared CTD-MB012	# taxa shared MB011-MB012	# taxa unique to CTD	# taxa unique to MB011	# taxa unique to MB012
Sample volumes (l): CTD: ~6.6*; MB011: 120.45; MB012: 120.62								

839

840 **References**

- 841 Allan, E.A., DiBenedetto, M.H., Lavery, A.C., Govindarajan, A.F., Zhang, W.G., 2021.  
842 Modeling characterization of the vertical and temporal variability of environmental DNA  
843 in the mesopelagic ocean. *Sci Rep* 11, 21273. [https://doi.org/10.1038/s41598-021-00288-](https://doi.org/10.1038/s41598-021-00288-5)  
844 5
- 845 Amaral-Zettler, L.A., McCliment, E.A., Ducklow, H.W., Huse, S.M., 2009. A Method for  
846 Studying Protistan Diversity Using Massively Parallel Sequencing of V9 Hypervariable  
847 Regions of Small-Subunit Ribosomal RNA Genes. *PLOS ONE* 4, e6372.  
848 <https://doi.org/10.1371/journal.pone.0006372>
- 849 Andruszkiewicz, E.A., Starks, H.A., Chavez, F.P., Sassoubre, L.M., Block, B.A., Boehm, A.B.,  
850 2017. Biomonitoring of marine vertebrates in Monterey Bay using eDNA metabarcoding.  
851 *PLOS ONE* 12, e0176343. <https://doi.org/10.1371/journal.pone.0176343>
- 852 Beentjes, K.K., Speksnijder, A.G.C.L., Schilthuizen, M., Hoogeveen, M., Hoorn, B.B. van der,  
853 2019. The effects of spatial and temporal replicate sampling on eDNA metabarcoding.  
854 *PeerJ* 7, e7335. <https://doi.org/10.7717/peerj.7335>
- 855 Bessey, C., n.d. Maximizing fish detection with eDNA metabarcoding - Bessey - 2020 -  
856 Environmental DNA - Wiley Online Library [WWW Document]. URL  
857 <https://onlinelibrary.wiley.com/doi/full/10.1002/edn3.74> (accessed 12.28.21).
- 858 Billings, A., Kaiser, C., Young, C.M., Hiebert, L.S., Cole, E., Wagner, J.K.S., Van Dover, C.L.,  
859 2017. SyPRID sampler: A large-volume, high-resolution, autonomous, deep-ocean  
860 precision plankton sampling system. *Deep Sea Research Part II: Topical Studies in*  
861 *Oceanography, Advances in deep-sea biology: biodiversity, ecosystem functioning and*  
862 *conservation* 137, 297–306. <https://doi.org/10.1016/j.dsr2.2016.05.007>

- 863 Blanco-Bercial, L., 2020. Metabarcoding Analyses and Seasonality of the Zooplankton  
864 Community at BATS. *Front. Mar. Sci.* 7. <https://doi.org/10.3389/fmars.2020.00173>
- 865 Bokulich, N.A., Kaehler, B.D., Rideout, J.R., Dillon, M., Bolyen, E., Knight, R., Huttley, G.A.,  
866 Gregory Caporaso, J., 2018. Optimizing taxonomic classification of marker-gene  
867 amplicon sequences with QIIME 2's q2-feature-classifier plugin. *Microbiome* 6, 90.  
868 <https://doi.org/10.1186/s40168-018-0470-z>
- 869 Bolyen, E., Rideout, J.R., Dillon, M.R., Bokulich, N.A., Abnet, C.C., Al-Ghalith, G.A.,  
870 Alexander, H., Alm, E.J., Arumugam, M., Asnicar, F., Bai, Y., Bisanz, J.E., Bittinger, K.,  
871 Brejnrod, A., Brislawn, C.J., Brown, C.T., Callahan, B.J., Caraballo-Rodríguez, A.M.,  
872 Chase, J., Cope, E.K., Da Silva, R., Diener, C., Dorrestein, P.C., Douglas, G.M., Durall,  
873 D.M., Duvallet, C., Edwardson, C.F., Ernst, M., Estaki, M., Fouquier, J., Gauglitz, J.M.,  
874 Gibbons, S.M., Gibson, D.L., Gonzalez, A., Gorlick, K., Guo, J., Hillmann, B., Holmes,  
875 S., Holste, H., Huttenhower, C., Huttley, G.A., Janssen, S., Jarmusch, A.K., Jiang, L.,  
876 Kaehler, B.D., Kang, K.B., Keefe, C.R., Keim, P., Kelley, S.T., Knights, D., Koester, I.,  
877 Kosciulek, T., Kreps, J., Langille, M.G.I., Lee, J., Ley, R., Liu, Y.-X., Loftfield, E.,  
878 Lozupone, C., Maher, M., Marotz, C., Martin, B.D., McDonald, D., McIver, L.J., Melnik,  
879 A.V., Metcalf, J.L., Morgan, S.C., Morton, J.T., Naimey, A.T., Navas-Molina, J.A.,  
880 Nothias, L.F., Orchanian, S.B., Pearson, T., Peoples, S.L., Petras, D., Preuss, M.L.,  
881 Pruesse, E., Rasmussen, L.B., Rivers, A., Robeson, M.S., Rosenthal, P., Segata, N.,  
882 Shaffer, M., Shiffer, A., Sinha, R., Song, S.J., Spear, J.R., Swafford, A.D., Thompson,  
883 L.R., Torres, P.J., Trinh, P., Tripathi, A., Turnbaugh, P.J., Ul-Hasan, S., van der Hooft,  
884 J.J.J., Vargas, F., Vázquez-Baeza, Y., Vogtmann, E., von Hippel, M., Walters, W., Wan,  
885 Y., Wang, M., Warren, J., Weber, K.C., Williamson, C.H.D., Willis, A.D., Xu, Z.Z.,



- 886 Zaneveld, J.R., Zhang, Y., Zhu, Q., Knight, R., Caporaso, J.G., 2019. Reproducible,  
887 interactive, scalable and extensible microbiome data science using QIIME 2. *Nat*  
888 *Biotechnol* 37, 852–857. <https://doi.org/10.1038/s41587-019-0209-9>
- 889 Bracken, M.E.S., Low, N.H.N., 2012. Realistic losses of rare species disproportionately impact  
890 higher trophic levels. *Ecology Letters* 15, 461–467. [https://doi.org/10.1111/j.1461-](https://doi.org/10.1111/j.1461-0248.2012.01758.x)  
891 [0248.2012.01758.x](https://doi.org/10.1111/j.1461-0248.2012.01758.x)
- 892 Brierley, A.S., 2014. Diel vertical migration. *Current Biology* 24, R1074–R1076.  
893 <https://doi.org/10.1016/j.cub.2014.08.054>
- 894 Brito-Morales, I., Schoeman, D.S., Molinos, J.G., Burrows, M.T., Klein, C.J., Arafeh-Dalmau,  
895 N., Kaschner, K., Garilao, C., Kesner-Reyes, K., Richardson, A.J., 2020. Climate  
896 velocity reveals increasing exposure of deep-ocean biodiversity to future warming. *Nat.*  
897 *Clim. Chang.* 10, 576–581. <https://doi.org/10.1038/s41558-020-0773-5>
- 898 Bucklin, A., Lindeque, P.K., Rodriguez-Ezpeleta, N., Albaina, A., Lehtiniemi, M., 2016.  
899 Metabarcoding of marine zooplankton: prospects, progress and pitfalls. *J Plankton Res*  
900 38, 393–400. <https://doi.org/10.1093/plankt/fbw023>
- 901 Bucklin, A., Yeh, H.D., Questel, J.M., Richardson, D.E., Reese, B., Copley, N.J., Wiebe, P.H.,  
902 2019. Time-series metabarcoding analysis of zooplankton diversity of the NW Atlantic  
903 continental shelf. *ICES J Mar Sci* 76, 1162–1176. <https://doi.org/10.1093/icesjms/fsz021>
- 904 Callahan, B.J., McMurdie, P.J., Rosen, M.J., Han, A.W., Johnson, A.J.A., Holmes, S.P., 2016.  
905 DADA2: High-resolution sample inference from Illumina amplicon data. *Nature Methods*  
906 13, 581–583. <https://doi.org/10.1038/nmeth.3869>
- 907 Canals, O., Mendibil, I., Santos, M., Irigoien, X., Rodríguez-Ezpeleta, N., 2021. Vertical  
908 stratification of environmental DNA in the open ocean captures ecological patterns and

- 909 behavior of deep-sea fishes. *Limnology and Oceanography Letters* 6, 339–347.  
910 <https://doi.org/10.1002/lol2.10213>
- 911 Chen, B., Masunaga, E., Smith, S.L., Yamazaki, H., 2021. Diel vertical migration promotes  
912 zooplankton horizontal patchiness. *J Oceanogr* 77, 123–135.  
913 <https://doi.org/10.1007/s10872-020-00564-4>
- 914 Closek, C.J., Santora, J.A., Starks, H.A., Schroeder, I.D., Andruszkiewicz, E.A., Sakuma, K.M.,  
915 Bograd, S.J., Hazen, E.L., Field, J.C., Boehm, A.B., 2019. Marine Vertebrate  
916 Biodiversity and Distribution Within the Central California Current Using Environmental  
917 DNA (eDNA) Metabarcoding and Ecosystem Surveys. *Frontiers in Marine Science* 6,  
918 732. <https://doi.org/10.3389/fmars.2019.00732>
- 919 Dee, L.E., Cowles, J., Isbell, F., Pau, S., Gaines, S.D., Reich, P.B., 2019. When Do Ecosystem  
920 Services Depend on Rare Species? *Trends in Ecology & Evolution* 34, 746–758.  
921 <https://doi.org/10.1016/j.tree.2019.03.010>
- 922 Dennis, G.D., Bright, T.J., 1988. Reef Fish Assemblages on Hard Banks in the Northwestern  
923 Gulf of Mexico. *Bulletin of Marine Science* 43, 280–307.
- 924 Dickie, I.A., Boyer, S., Buckley, H.L., Duncan, R.P., Gardner, P.P., Hogg, I.D., Holdaway, R.J.,  
925 Lear, G., Makiola, A., Morales, S.E., Powell, J.R., Weaver, L., 2018. Towards robust and  
926 repeatable sampling methods in eDNA-based studies. *Molecular Ecology Resources* 18,  
927 940–952. <https://doi.org/10.1111/1755-0998.12907>
- 928 Djurhuus, A., Pitz, K., Sawaya, N.A., Rojas-Márquez, J., Michaud, B., Montes, E., Muller-  
929 Karger, F., Breitbart, M., 2018. Evaluation of marine zooplankton community structure  
930 through environmental DNA metabarcoding. *Limnology and Oceanography: Methods* 16,  
931 209–221. <https://doi.org/10.1002/lom3.10237>

- 932 Easson, C.G., Boswell, K.M., Tucker, N., Warren, J.D., Lopez, J.V., 2020. Combined eDNA and  
933 Acoustic Analysis Reflects Diel Vertical Migration of Mixed Consortia in the Gulf of  
934 Mexico. *Frontiers in Marine Science* 7, 552. <https://doi.org/10.3389/fmars.2020.00552>
- 935 Everett, M.V., Park, L.K., 2018. Exploring deep-water coral communities using environmental  
936 DNA. *Deep Sea Research Part II: Topical Studies in Oceanography, Results of*  
937 *Telepresence-Enabled Oceanographic Exploration* 150, 229–241.  
938 <https://doi.org/10.1016/j.dsr2.2017.09.008>
- 939 Ficetola, G.F., Pansu, J., Bonin, A., Coissac, E., Giguët-Covex, C., De Barba, M., Gielly, L.,  
940 Lopes, C.M., Boyer, F., Pompanon, F., Rayé, G., Taberlet, P., 2015. Replication levels,  
941 false presences and the estimation of the presence/absence from eDNA metabarcoding  
942 data. *Molecular Ecology Resources* 15, 543–556. [https://doi.org/10.1111/1755-](https://doi.org/10.1111/1755-0998.12338)  
943 [0998.12338](https://doi.org/10.1111/1755-0998.12338)
- 944 Gallego, R., Jacobs-Palmer, E., Cribari, K., Kelly, R.P., 2020. Environmental DNA  
945 metabarcoding reveals winners and losers of global change in coastal waters. *Proceedings*  
946 *of the Royal Society B: Biological Sciences* 287, 20202424.  
947 <https://doi.org/10.1098/rspb.2020.2424>
- 948 Gilbey, J., Carvalho, G., Castilho, R., Coscia, I., Coulson, M.W., Dahle, G., Derycke, S.,  
949 Francisco, S.M., Helyar, S.J., Johansen, T., Junge, C., Layton, K.K.S., Martinsohn, J.,  
950 Matejusova, I., Robalo, J.I., Rodríguez-Ezpeleta, N., Silva, G., Strammer, I., Vasemägi,  
951 A., Volckaert, F.A.M., 2021. Life in a drop: Sampling environmental DNA for marine  
952 fishery management and ecosystem monitoring. *Marine Policy* 124, 104331.  
953 <https://doi.org/10.1016/j.marpol.2020.104331>

- 954 Goldberg, C.S., Turner, C.R., Deiner, K., Klymus, K.E., Thomsen, P.F., Murphy, M.A., Spear,  
955 S.F., McKee, A., Oyler-McCance, S.J., Cornman, R.S., Laramie, M.B., Mahon, A.R.,  
956 Lance, R.F., Pilliod, D.S., Strickler, K.M., Waits, L.P., Fremier, A.K., Takahara, T.,  
957 Herder, J.E., Taberlet, P., 2016. Critical considerations for the application of  
958 environmental DNA methods to detect aquatic species. *Methods in Ecology and*  
959 *Evolution* 7, 1299–1307. <https://doi.org/10.1111/2041-210X.12595>
- 960 Govindarajan, A.F., Francolini, R.D., Jech, J.M., Lavery, A.C., Llopiz, J.K., Wiebe, P.H., Zhang,  
961 W. (Gordon), 2021. Exploring the Use of Environmental DNA (eDNA) to Detect Animal  
962 Taxa in the Mesopelagic Zone. *Front. Ecol. Evol.* 9, 574877.  
963 <https://doi.org/10.3389/fevo.2021.574877>
- 964 Govindarajan, A.F., Pineda, J., Purcell, M., Breier, J.A., 2015. Species- and stage-specific  
965 barnacle larval distributions obtained from AUV sampling and genetic analysis in  
966 Buzzards Bay, Massachusetts, USA. *Journal of Experimental Marine Biology and*  
967 *Ecology* 472, 158–165. <https://doi.org/10.1016/j.jembe.2015.07.012>
- 968 Hestetun, J.T., Lanzén, A., Dahlgren, T.G., 2021. Grab what you can—an evaluation of spatial  
969 replication to decrease heterogeneity in sediment eDNA metabarcoding. *PeerJ* 9, e11619.  
970 <https://doi.org/10.7717/peerj.11619>
- 971 Holman, L.E., Chng, Y., Rius, M., n.d. How does eDNA decay affect metabarcoding  
972 experiments? *Environmental DNA* n/a. <https://doi.org/10.1002/edn3.201>
- 973 Hughes, T.P., Bellwood, D.R., Folke, C., Steneck, R.S., Wilson, J., 2005. New paradigms for  
974 supporting the resilience of marine ecosystems. *Trends in Ecology & Evolution* 20, 380–  
975 386. <https://doi.org/10.1016/j.tree.2005.03.022>

- 976 Isbell, F., Calcagno, V., Hector, A., Connolly, J., Harpole, W.S., Reich, P.B., Scherer-Lorenzen,  
977 M., Schmid, B., Tilman, D., van Ruijven, J., Weigelt, A., Wilsey, B.J., Zavaleta, E.S.,  
978 Loreau, M., 2011. High plant diversity is needed to maintain ecosystem services. *Nature*  
979 477, 199–202. <https://doi.org/10.1038/nature10282>
- 980 Jo, T., Arimoto, M., Murakami, H., Masuda, R., Minamoto, T., 2019. Particle Size Distribution  
981 of Environmental DNA from the Nuclei of Marine Fish. *Environ. Sci. Technol.* 53, 9947–  
982 9956. <https://doi.org/10.1021/acs.est.9b02833>
- 983 Laroche, O., Kersten, O., Smith, C.R., Goetze, E., 2020. Environmental DNA surveys detect  
984 distinct metazoan communities across abyssal plains and seamounts in the western  
985 Clarion Clipperton Zone. *Molecular Ecology* 29, 4588–4604.  
986 <https://doi.org/10.1111/mec.15484>
- 987 Lindsay, D.J., 2021. Stealthy tracking of deep ocean organisms with Mesobot. *Science Robotics*  
988 6, eabj3949. <https://doi.org/10.1126/scirobotics.abj3949>
- 989 Mächler, E., Deiner, K., Spahn, F., Altermatt, F., 2016. Fishing in the Water: Effect of Sampled  
990 Water Volume on Environmental DNA-Based Detection of Macroinvertebrates. *Environ.*  
991 *Sci. Technol.* 50, 305–312. <https://doi.org/10.1021/acs.est.5b04188>
- 992 McClenaghan, B., Fahner, N., Cote, D., Chawarski, J., McCarthy, A., Rajabi, H., Singer, G.,  
993 Hajibabaei, M., 2020. Harnessing the power of eDNA metabarcoding for the detection of  
994 deep-sea fishes. *PLOS ONE* 15, e0236540. <https://doi.org/10.1371/journal.pone.0236540>
- 995 McQuillan, J.S., Robidart, J.C., 2017. Molecular-biological sensing in aquatic environments:  
996 recent developments and emerging capabilities. *Current Opinion in Biotechnology,*  
997 *Energy biotechnology • Environmental biotechnology* 45, 43–50.  
998 <https://doi.org/10.1016/j.copbio.2016.11.022>

- 999 Merten, V., Bayer, T., Reusch, T.B.H., Puebla, O., Fuss, J., Stefanschitz, J., Lischka, A., Hauss,  
1000 H., Neitzel, P., Piatkowski, U., Czudaj, S., Christiansen, B., Denda, A., Hoving, H.-J.T.,  
1001 2021. An Integrative Assessment Combining Deep-Sea Net Sampling, in situ  
1002 Observations and Environmental DNA Analysis Identifies Cabo Verde as a Cephalopod  
1003 Biodiversity Hotspot in the Atlantic Ocean. *Frontiers in Marine Science* 9, Art.Nr.  
1004 760108. <https://doi.org/10.3389/fmars.2021.760108>
- 1005 Miya, M., Sato, Y., Fukunaga, T., Sado, T., Poulsen, J.Y., Sato, K., Minamoto, T., Yamamoto,  
1006 S., Yamanaka, H., Araki, H., Kondoh, M., Iwasaki, W., n.d. MiFish, a set of universal  
1007 PCR primers for metabarcoding environmental DNA from fishes: detection of more than  
1008 230 subtropical marine species. *Royal Society Open Science* 2, 150088.  
1009 <https://doi.org/10.1098/rsos.150088>
- 1010 Moushomi, R., Wilgar, G., Carvalho, G., Creer, S., Seymour, M., 2019. Environmental DNA  
1011 size sorting and degradation experiment indicates the state of *Daphnia magna*  
1012 mitochondrial and nuclear eDNA is subcellular. *Sci Rep* 9, 12500.  
1013 <https://doi.org/10.1038/s41598-019-48984-7>
- 1014 Oksanen J, Blanchet FG, Friendly M, Kindt R, Legendre P, McGlinn D, Minchin PR, O'hara  
1015 RB, Simpson GL, Solymos P, Stevens MH, 2016. *vegan*: Community Ecology Package.  
1016 R package version 2.4-3. Vienna: R Foundation for Statistical Computing.
- 1017 Quast, C., Pruesse, E., Yilmaz, P., Gerken, J., Schweer, T., Yarza, P., Peplies, J., Glöckner, F.O.,  
1018 2013. The SILVA ribosomal RNA gene database project: improved data processing and  
1019 web-based tools. *Nucleic Acids Res* 41, D590–D596. <https://doi.org/10.1093/nar/gks1219>
- 1020 Ricker, W.E., 1973. Linear Regressions in Fishery Research. *Journal of the Fisheries Board of*  
1021 *Canada*. <https://doi.org/10.1139/f73-072>

- 1022 Ruppert, K.M., Kline, R.J., Rahman, M.S., 2019. Past, present, and future perspectives of  
1023 environmental DNA (eDNA) metabarcoding: A systematic review in methods,  
1024 monitoring, and applications of global eDNA. *Global Ecology and Conservation* 17,  
1025 e00547. <https://doi.org/10.1016/j.gecco.2019.e00547>
- 1026 Sala, E., Mayorga, J., Bradley, D., Cabral, R.B., Atwood, T.B., Auber, A., Cheung, W., Costello,  
1027 C., Ferretti, F., Friedlander, A.M., Gaines, S.D., Garilao, C., Goodell, W., Halpern, B.S.,  
1028 Hinson, A., Kaschner, K., Kesner-Reyes, K., Leprieur, F., McGowan, J., Morgan, L.E.,  
1029 Mouillot, D., Palacios-Abrantes, J., Possingham, H.P., Rechberger, K.D., Worm, B.,  
1030 Lubchenco, J., 2021. Protecting the global ocean for biodiversity, food and climate.  
1031 *Nature* 592, 397–402. <https://doi.org/10.1038/s41586-021-03371-z>
- 1032 Sammarco, P., Nuttall, M., Beltz, D., Hickerson, E., Schmahl, G.P., 2016. Patterns of  
1033 Mesophotic Benthic Community Structure on Banks Off vs Inside the Continental Shelf  
1034 Edge, Gulf of Mexico. *Gulf of Mexico Science* 33.  
1035 <https://doi.org/10.18785/goms.3301.07>
- 1036 Sawaya, N.A., Djurhuus, A., Closek, C.J., Hepner, M., Olesin, E., Visser, L., Kelble, C.,  
1037 Hubbard, K., Breitbart, M., 2019. Assessing eukaryotic biodiversity in the Florida Keys  
1038 National Marine Sanctuary through environmental DNA metabarcoding. *Ecology and*  
1039 *Evolution* 9, 1029–1040. <https://doi.org/10.1002/ece3.4742>
- 1040 Schabacker, J.C., Amish, S.J., Ellis, B.K., Gardner, B., Miller, D.L., Rutledge, E.A., Sepulveda,  
1041 A.J., Luikart, G., 2020. Increased eDNA detection sensitivity using a novel high-volume  
1042 water sampling method. *Environmental DNA* 2, 244–251.  
1043 <https://doi.org/10.1002/edn3.63>

- 1044 Sepulveda, A.J., Schabacker, J., Smith, S., Al-Chokhachy, R., Luikart, G., Amish, S.J., 2019.  
1045 Improved detection of rare, endangered and invasive trout in using a new large-volume  
1046 sampling method for eDNA capture. *Environmental DNA* 1, 227–237.  
1047 <https://doi.org/10.1002/edn3.23>
- 1048 St John, M.A., Borja, A., Chust, G., Heath, M., Grigorov, I., Mariani, P., Martin, A.P., Santos,  
1049 R.S., 2016. A dark hole in our understanding of marine ecosystems and their services:  
1050 Perspectives from the mesopelagic community. *Front. Mar. Sci.* 3.  
1051 <https://doi.org/10.3389/fmars.2016.00031>
- 1052 Stoeckle, M.Y., Adolf, J., Charlop-Powers, Z., Dunton, K.J., Hinks, G., VanMorter, S.M., 2021.  
1053 Trawl and eDNA assessment of marine fish diversity, seasonality, and relative abundance  
1054 in coastal New Jersey, USA. *ICES Journal of Marine Science* 78, 293–304.  
1055 <https://doi.org/10.1093/icesjms/fsaa225>
- 1056 Thorrold, S.R., Adams, A., Bucklin, A., Buesseler, K., Fischer, G., Govindarajan, A., Hoagland,  
1057 P., Jin, D., Lavery, A., Llopez, J., Madin, L., Omand, M., Renaud, P.G., Sosik, H.M.,  
1058 Wiebe, P., Yoerger, D.R., Zhang, W. (Gordon), 2021. Twilight Zone Observation  
1059 Network: A distributed observation network for sustained, real-time interrogation of the  
1060 ocean's twilight zone. *Marine Technology Society Journal* 55, 92–93.  
1061 <https://doi.org/10.4031/MTSJ.55.3.46>
- 1062 Truelove, N.K., Patin, N.V., Min, M., Pitz, K.J., Preston, C.M., Yamahara, K.M., Zhang, Y.,  
1063 Raanan, B.Y., Kieft, B., Hobson, B., Thompson, L.R., Goodwin, K.D., Chavez, F.P., n.d.  
1064 Expanding the temporal and spatial scales of environmental DNA research with  
1065 autonomous sampling. *Environmental DNA* n/a. <https://doi.org/10.1002/edn3.299>



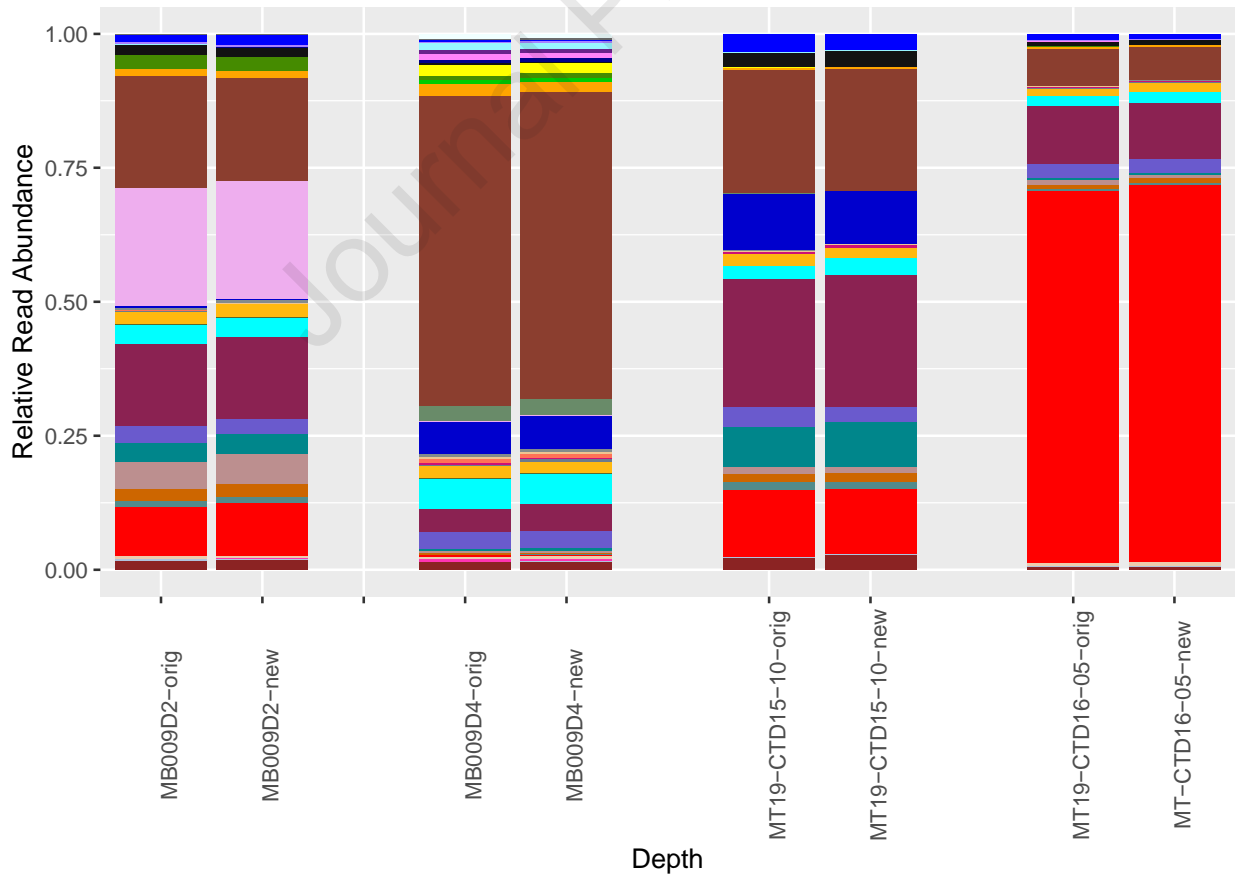
- 1066 Turner, C.R., Barnes, M.A., Xu, C.C.Y., Jones, S.E., Jerde, C.L., Lodge, D.M., 2014. Particle  
1067 size distribution and optimal capture of aqueous microbial eDNA. *Methods in Ecology*  
1068 *and Evolution* 5, 676–684. <https://doi.org/10.1111/2041-210X.12206>
- 1069 Worm, B., Lotze, H.K., 2021. Chapter 21 - Marine biodiversity and climate change, in: Letcher,  
1070 T.M. (Ed.), *Climate Change (Third Edition)*. Elsevier, pp. 445–464.  
1071 <https://doi.org/10.1016/B978-0-12-821575-3.00021-9>
- 1072 Wu, S., Xiong, J., Yu, Y., 2015. Taxonomic Resolutions Based on 18S rRNA Genes: A Case  
1073 Study of Subclass Copepoda. *PLoS One* 10.  
1074 <https://doi.org/10.1371/journal.pone.0131498>
- 1075 Yamahara, K.M., Preston, C.M., Birch, J., Walz, K., Marin, R., Jensen, S., Pargett, D., Roman,  
1076 B., Ussler, W., Zhang, Y., Ryan, J., Hobson, B., Kieft, B., Raanan, B., Goodwin, K.D.,  
1077 Chavez, F.P., Scholin, C., 2019. In situ Autonomous Acquisition and Preservation of  
1078 Marine Environmental DNA Using an Autonomous Underwater Vehicle. *Frontiers in*  
1079 *Marine Science* 6, 373. <https://doi.org/10.3389/fmars.2019.00373>
- 1080 Yoerger, Dana R., Govindarajan, A.F., Howland, J.C., Llopiz, J.K., Wiebe, P.H., Curran, M.,  
1081 Fujii, J., Gomez-Ibanez, D., Katija, K., Robison, B.H., Hobson, B.W., Risi, M., Rock,  
1082 S.M., 2021. A hybrid underwater robot for multidisciplinary investigation of the ocean  
1083 twilight zone. *Science Robotics*. <https://doi.org/10.1126/scirobotics.abe1901>
- 1084 Yoerger, Dana R, Robison, B.H., Rock, S.M., Govindarajan, A.F., Katija, K., 2021. Mesobot: a  
1085 New Autonomous Robot for Midwater Research and Exploration. *Science Robotics* 22.
- 1086 Zhang, Y., Kieft, B., Hobson, B.W., Ryan, J.P., Barone, B., Preston, C.M., Roman, B., Raanan,  
1087 B.-Y., Marin III, R., O'Reilly, T.C., Rueda, C.A., Pargett, D., Yamahara, K.M., Poulos,  
1088 S., Romano, A., Foreman, G., Ramm, H., Wilson, S.T., DeLong, E.F., Karl, D.M., Birch,

1089 J.M., Bellingham, J.G., Scholin, C.A., 2020. Autonomous Tracking and Sampling of the  
1090 Deep Chlorophyll Maximum Layer in an Open-Ocean Eddy by a Long-Range  
1091 Autonomous Underwater Vehicle. IEEE Journal of Oceanic Engineering 45, 1308–1321.  
1092 <https://doi.org/10.1109/JOE.2019.2920217>  
1093

Journal Pre-proof

## Appendix 1.

Two control samples were mis-processed during the MiSeq runs and produced a large number of sequencing reads: after the DADA2 and quality control steps, there were 119,646 reads in the CTD control (for Cast 16; which was part of the larger Bright Bank Survey but not analyzed here) and 116,805 reads in one of the PCR no template controls. These same controls had no detectable DNA after the library preparation PCRs and produced extremely few reads during the preliminary Miniseq run. We re-sequenced new aliquots from these two controls, plus four additional environmental samples (2 *Mesobot* and 2 CTD samples), across 3 new MiSeq runs with the same target sequencing depth as in the original MiSeq runs. As expected, the suspect controls produced very few reads in the second sequencing run series: after the dada2 and quality control steps, there were 0 reads in the CTD control and 112 reads in the PCR no template control. The taxonomic composition of the data from the re-sequenced environmental samples was nearly identical to the composition of the data from samples in the original run series (Supplementary Figure 1). There was no evidence that these or any other environmental samples or controls were compromised in the original MiSeq runs. We suspect the issue arose from an isolated cross-contamination event related to shipping the samples to the sequencing facility or at the sequencing facility during library preparation or sequencing. We therefore proceeded with our data from the original sequencing run series, with the substitution of the two mis-processed control data with the control data from the re-sequenced run.



**Appendix 2.**

Each sheet lists the results of the Silva level-7 taxa comparisons, including between the Mesobot inner and outer. The number of taxa in each shared or unique category is given, as well as a list of those taxa.

Journal Pre-proof

Names	total	elements
inner outer	118	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Sipuncula;D_9_Phascolosomatiformes;D_10_Apionsoma misakianum
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Myodocopa;D_10_Halocyprida;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Thaliacea;D_9_Salpida;D_10_Iasis cylindrica
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Lobata;D_8_Undescribed Lobata sp. 4
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Bilateria;D_6_uncultured;D_7_uncultured eukaryote
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;D_11_Gaetanus variabilis
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;D_11_Candacia discadata
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;D_11_Neocalanus flemingeri
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Terebellida;D_10_Anobothrus gracilis
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Opheliidae;D_10_Ophelina acuminata
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_Liriope tetraphylla
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;D_11_Euchaeta concinna
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Anthoathecata;D_9_Solanderia secunda
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;__;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Pleurobrachia bachei
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;D_11_Heterostylites major
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Hormiphora plumosa
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;__;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Anthoathecata;D_9_Hydractinia sp. MMM-2016
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Spionida;D_10_Caulleriella parva
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Capitellida;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Eumalacostraca;D_10_Peracarida;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;D_11_Metridia asymmetrica
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Anthoathecata;D_9_Fabienna sphaerica
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Heterobranchia;D_9_Desmopterus papilio
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Myodocopa;D_10_Halocyprida;D_11_Conchoecia sp. SN008
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_uncultured marine eukaryote
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_Oithona sp. 1 New Caledonia-RJH-2001
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;D_11_Centropages furcatus
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Narcomedusae;D_9_uncultured eukaryote
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Platyctenida;D_8_Coeloplana bannwarthii
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Pteriomorphia;D_9_Arcoida;D_10_Glycymeris sp.
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Thaliacea;D_9_Salpida;D_10_Cyclosalpa polae
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;D_11_uncultured eukaryote
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;D_11_Sapphirina darwinii
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_uncultured eukaryote
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;D_11_Scolecithricella longispinosa
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;D_9_Sagitta sp. DP-2006
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Scyphozoa;D_7_Semaeostomeae;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Eumalacostraca;D_10_Eucarida;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hexacorallia;D_8_Zoantharia;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;D_11_uncultured eukaryote
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Pleurobrachia brunnea
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Caenogastropoda;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Echinodermata;D_7_Ophiuroidea;D_8_Gorgonocephalus eucnemis
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Leptotheccata;D_9_Blackfordia virginica
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;D_10_metagenome
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Echinodermata;D_7_Holothuroidea;D_8_Holothuria forskali
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_uncultured metazoan
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_Pantachogon haeckeli
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Enteropneusta;D_8_Ptychoderidae;D_9_Enteropneusta sp. extrawide-lipped
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Anopla;D_8_Palaeonemertea;D_9_Palaeonemertea sp. MCZ IZ 45654
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Anopla;D_8_Heteronemertea;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Heteroconchia;D_9_Veneroida;D_10_Protothaca jedoensis
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Echinodermata;D_7_Asteroidea;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Leptotheccata;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Heterobranchia;D_9_Limacina retroversa
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Siphonostomatoida;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Bilateria;D_6_Annelida;D_7_uncultured metazoan
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Maxillopoda;D_9_Copepoda;D_10_uncultured eukaryote
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Heteroconchia;D_9_Veneroida;D_10_Candidatus Thiodiazotropha endoloripes
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Anopla;D_8_Heteronemertea;D_9_Cerebratulus lacteus (milky ribbon-worm)
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Terebellida;D_10_Lanice conchilega
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Monogononta;D_8_Ploimida;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;__;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;D_10_Alciopina sp. THS-2006
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Anopla;D_8_Monostilifera;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Echinodermata;D_7_Echinoidea;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Siphonophorae;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Heterobranchia;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Spionida;D_10_Prionospio cirrifera
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hexacorallia;D_8_Scleractinia;D_9_Orbicella franksi
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;D_11_Pleuromamma borealis
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Anthoathecata;D_9_Podocoryna exigua
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Brachiopoda;D_7_Phoroniformea;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Sabellida;D_10_Owenia fusiformis



D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Gastropoda;D\_8\_Caenogastropoda;D\_9\_Planaxis sulcatus  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Scolecida;D\_9\_Spionida;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_6\_Tentaculata;D\_7\_Cydippida;D\_8\_Undescribed mertensiid sp. 3  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Thaliacea;D\_9\_Salpida;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_9\_Decapodiformes;D\_10\_Teuthida;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Hydroidolina;D\_8\_Leptothecata;D\_9\_Aequorea aequorea  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_9\_Copelata;D\_10\_Oikopleuridae;D\_11\_uncultured eukaryote  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);\_\_;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_9\_Copelata;D\_10\_Oikopleuridae;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_6\_Gastrotricha;D\_7\_Chaetonotida;D\_8\_uncultured eukaryote  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Hexacorallia;D\_8\_Ceriantharia;D\_9\_Pachycerianthus fimbriatus  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_6\_Scyphozoa;D\_7\_Coronatae;D\_8\_Atolla vanhoeffeni  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_9\_Copepoda;D\_10\_Calanoida;D\_11\_Junceella aquamata  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Palpata;D\_9\_Phyllodocida;D\_10\_Conchoecia sp. OC-2001  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_6\_Tentaculata;D\_7\_Cydippida;D\_8\_Lampea pancerina  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_9\_Copepoda;D\_10\_Calanoida;D\_11\_Haloptilus longicornis  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Hexacorallia;D\_8\_Actiniaria;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Hydroidolina;D\_8\_Siphonophorae;D\_9\_Nanomia bijuga  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Hydroidolina;D\_8\_Anthoathecata;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_9\_Copelata;D\_10\_Oikopleuridae;D\_11\_uncultured metazoan  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_9\_Copepoda;D\_10\_Poecilostomatoida;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Hydroidolina;D\_8\_Siphonophorae;D\_9\_uncultured eukaryote  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Gymnolaemata;D\_8\_Cheilostomatida;D\_9\_Smittidea spinigera  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_9\_Copepoda;D\_10\_Harpacticoida;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_9\_Copepoda;D\_10\_Calanoida;D\_11\_marine metagenome  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Hydroidolina;D\_8\_Anthoathecata;D\_9\_Pandea sp. AGC-2005  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_11\_Neopterygii;D\_12\_Teleostei;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Trachylinae;D\_8\_Narcomedusae;D\_9\_Solmissus marshalli  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Rhabdocoela;D\_9\_Neodalyellida;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Hydroidolina;\_\_;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_9\_Myodocopa;D\_10\_Halocyprida;D\_11\_marine metagenome  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Pteriomorphia;D\_9\_Mytiloida;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Sagittoidea;D\_8\_Aphragmophora;D\_9\_Aidanosagitta neglecta  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Sagittoidea;D\_8\_Aphragmophora;D\_9\_Decipisagitta decipiens  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Enteropneusta;D\_8\_Ptychoderidae;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Octocorallia;D\_8\_Alyconacea;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_9\_Copepoda;D\_10\_Cyclopoida;D\_11\_Oithona sp. 2 New Caledonia-RJH-2004  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_9\_Copepoda;D\_10\_Cyclopoida;D\_11\_uncultured eukaryote  
 45 outer D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Pteriomorphia;D\_9\_Pterioda;D\_10\_Atrina pectinata  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_9\_Copepoda;D\_10\_Harpacticoida;D\_11\_Canuella perplexa  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Hydroidolina;D\_8\_Anthoathecata;D\_9\_Cytaeis sp. MAN-2015  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Scolecida;D\_9\_Terebellida;D\_10\_Sternaspis scutata  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Scolecida;D\_9\_Capitellida;D\_10\_Dasybranchus caducus  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Trachylinae;D\_8\_Narcomedusae;D\_9\_Cunina frugifera  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_6\_Echinodermata;D\_7\_Ophiuroidea;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Palpata;D\_9\_Phyllodocida;D\_10\_Salvatoria kerguelensis  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Palpata;D\_9\_Phyllodocida;D\_10\_Lepidonotus sublevis  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Scolecida;D\_9\_Capitellida;D\_10\_Heteromastus filiformis  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Protobranchia;D\_9\_Nuculanoida;D\_10\_Nuculana pernula  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Hydroidolina;D\_8\_Anthoathecata;D\_9\_Porpita sp. AGC-2001  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_9\_Copepoda;D\_10\_Cyclopoida;D\_11\_Anthessius sp. New Caledonia-RJH-2004  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_9\_Copepoda;D\_10\_Calanoida;D\_11\_Pareucalanus attenuatus  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Hirudinida;\_\_;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_11\_Neopterygii;D\_12\_Teleostei;D\_13\_Gadus morhua (Atlantic cod)  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_9\_Copepoda;D\_10\_Poecilostomatoida;D\_11\_Clausidium vancouverense  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_5\_Demospongiae;D\_6\_Tetractinellida;D\_7\_Candidatus Entotheonella sp. TSY1  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_9\_Eumalacostraca;\_\_;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Scolecida;D\_9\_Terebellida;D\_10\_Pectinaria koreni  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_6\_Echinodermata;D\_7\_Holothuroidea;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Palpata;D\_9\_Sabellida;D\_10\_Lamellibrachia sp. L1 DH-2004  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Myzostomida;D\_8\_Myzostomidae;D\_9\_Myzostoma polycyclus  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Digenea;\_\_;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Octocorallia;D\_8\_Pennatulacea;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Thaliacea;D\_9\_Salpida;D\_10\_Salpa thompsoni  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Palpata;D\_9\_Eunicida;D\_10\_Paramphinome jeffreysii  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_9\_Eumalacostraca;D\_10\_Eucarida;D\_11\_Albunea catherinae  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Monogononta;D\_8\_Ploimida;D\_9\_Brachionus calyciflorus  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Pteriomorphia;D\_9\_Ostreoida;D\_10\_Saccostrea glomerata  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_6\_Echinodermata;D\_7\_Ophiuroidea;D\_8\_Amphipholis squamata  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Scolecida;D\_9\_Terebellida;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Hydroidolina;D\_8\_Anthoathecata;D\_9\_Corymorpha glacialis  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Polyplacophora;D\_8\_Neoloricata;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Palpata;D\_9\_Phyllodocida;D\_10\_Kefersteinia cirrata  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Gastropoda;D\_8\_Heterobranchia;D\_9\_Cylichna cylindracea  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Scolecida;\_\_;\_\_  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_9\_Copepoda;D\_10\_Calanoida;D\_11\_Subeucalanus pileatus  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_11\_Neopterygii;D\_12\_Teleostei;D\_13\_Salmo salar (Atlantic salmon)  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Hexacorallia;D\_8\_Zoantheria;D\_9\_Palythoa variabilis  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_6\_Nuda;D\_7\_Beroida;D\_8\_Beroe cucumis  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_8\_Palpata;D\_9\_Phyllodocida;D\_10\_Nephtys hombergii  
 D\_0\_Eukaryota;D\_1\_Opisthokonta;D\_2\_Holozoa;D\_3\_Metazoa (Animalia);D\_7\_Gastropoda;D\_8\_Caenogastropoda;D\_9\_Pomacea canaliculata

D\_0\_\_Eukaryota;D\_1\_\_Opisthokonta;D\_2\_\_Holozoa;D\_3\_\_Metazoa (Animalia);D\_7\_\_Anopla;D\_8\_\_Heteronemertea;D\_9\_\_Gorgonorhynchus albocinctus  
 D\_0\_\_Eukaryota;D\_1\_\_Opisthokonta;D\_2\_\_Holozoa;D\_3\_\_Metazoa (Animalia);D\_9\_\_Phyllopora;D\_10\_\_Diplostraca;D\_11\_\_Pleuroxus aduncus  
 18 D\_0\_\_Eukaryota;D\_1\_\_Opisthokonta;D\_2\_\_Holozoa;D\_3\_\_Metazoa (Animalia);D\_7\_\_Hydroidolina;D\_8\_\_Leptothecata;D\_9\_\_Clytia sp. AGC-2001  
 D\_0\_\_Eukaryota;D\_1\_\_Opisthokonta;D\_2\_\_Holozoa;D\_3\_\_Metazoa (Animalia);D\_7\_\_Chromadorea;D\_8\_\_Monhysterida;\_\_  
 D\_0\_\_Eukaryota;D\_1\_\_Opisthokonta;D\_2\_\_Holozoa;D\_3\_\_Metazoa (Animalia);D\_5\_\_Demospongiae;D\_6\_\_Suberitida;D\_7\_\_Terpios aploos  
 D\_0\_\_Eukaryota;D\_1\_\_Opisthokonta;D\_2\_\_Holozoa;D\_3\_\_Metazoa (Animalia);D\_8\_\_Heteroconchia;D\_9\_\_Veneroida;\_\_  
 D\_0\_\_Eukaryota;D\_1\_\_Opisthokonta;D\_2\_\_Holozoa;D\_3\_\_Metazoa (Animalia);D\_7\_\_Sagittoidea;D\_8\_\_Aphragmophora;D\_9\_\_Sagitta elegans  
 D\_0\_\_Eukaryota;D\_1\_\_Opisthokonta;D\_2\_\_Holozoa;D\_3\_\_Metazoa (Animalia);D\_8\_\_Palpata;D\_9\_\_Eunicida;D\_10\_\_Ninnoe nigripes  
 D\_0\_\_Eukaryota;D\_1\_\_Opisthokonta;D\_2\_\_Holozoa;D\_3\_\_Metazoa (Animalia);D\_6\_\_Tentaculata;D\_7\_\_Cydippida;D\_8\_\_Haeckelia rubra  
 D\_0\_\_Eukaryota;D\_1\_\_Opisthokonta;D\_2\_\_Holozoa;D\_3\_\_Metazoa (Animalia);D\_7\_\_Hexacorallia;D\_8\_\_Antipatharia;D\_9\_\_Antipathes fiordensis  
 D\_0\_\_Eukaryota;D\_1\_\_Opisthokonta;D\_2\_\_Holozoa;D\_3\_\_Metazoa (Animalia);D\_8\_\_Scolecida;D\_9\_\_Terebellida;D\_10\_\_Lysilla sp. THS-2012  
 D\_0\_\_Eukaryota;D\_1\_\_Opisthokonta;D\_2\_\_Holozoa;D\_3\_\_Metazoa (Animalia);D\_7\_\_Hydroidolina;D\_8\_\_Anthoathecata;D\_9\_\_Hybocodon chilensis  
 D\_0\_\_Eukaryota;D\_1\_\_Opisthokonta;D\_2\_\_Holozoa;D\_3\_\_Metazoa (Animalia);D\_7\_\_Hydroidolina;D\_8\_\_Leptothecata;D\_9\_\_Rhacostoma atlanticum  
 D\_0\_\_Eukaryota;D\_1\_\_Opisthokonta;D\_2\_\_Holozoa;D\_3\_\_Metazoa (Animalia);D\_5\_\_Demospongiae;D\_6\_\_Poecilosclerida;\_\_  
 D\_0\_\_Eukaryota;D\_1\_\_Opisthokonta;D\_2\_\_Holozoa;D\_3\_\_Metazoa (Animalia);D\_6\_\_Scyphozoa;D\_7\_\_Rhizostomeae;\_\_  
 D\_0\_\_Eukaryota;D\_1\_\_Opisthokonta;D\_2\_\_Holozoa;D\_3\_\_Metazoa (Animalia);D\_7\_\_Chromadorea;D\_8\_\_Rhabditida;D\_9\_\_Rhabditophanes sp. KR3021  
 D\_0\_\_Eukaryota;D\_1\_\_Opisthokonta;D\_2\_\_Holozoa;D\_3\_\_Metazoa (Animalia);D\_8\_\_Scolecida;D\_9\_\_Capitellida;D\_10\_\_Notomastus latericeus  
 D\_0\_\_Eukaryota;D\_1\_\_Opisthokonta;D\_2\_\_Holozoa;D\_3\_\_Metazoa (Animalia);D\_7\_\_Hydroidolina;D\_8\_\_Anthoathecata;D\_9\_\_Ectopleura marina  
 D\_0\_\_Eukaryota;D\_1\_\_Opisthokonta;D\_2\_\_Holozoa;D\_3\_\_Metazoa (Animalia);D\_8\_\_Palpata;D\_9\_\_Phyllodocida;D\_10\_\_Goniada brunnea  
 D\_0\_\_Eukaryota;D\_1\_\_Opisthokonta;D\_2\_\_Holozoa;D\_3\_\_Metazoa (Animalia);D\_7\_\_Monogononta;D\_8\_\_Ploimida;D\_9\_\_metagenome

Journal Pre-proof



Names	total	elements
CTD8-40 MB009-40	29	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Pleuromamma borealis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Neocalanus flemingeri D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Opheliidae;D_10_Ophelina acuminata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;__;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;__;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);__;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Scyphozoa;D_7_Coronatae;D_8_Atolla vanhoeffeni D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Junceella aquamata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Centropages furcatus D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;D_10_Conchoecia sp. OC-2001 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hexacorallia;D_8_Actiniaria;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;D_11_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;D_11_Sapphirina darwinii D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Siphonophorae;D_9_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Caenogastropoda;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_Pantachogon haeckeli D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_marine metagenome D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Bilateria;D_6_Annelida;D_7_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Maxillopoda;D_9_Copepoda;D_10_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Myodocopa;D_10_Halocyprida;D_11_marine metagenome D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Heterobranchia;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_Oithona sp. 2 New Caledonia-RJH-2004 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_uncultured eukaryote
CTD8-40	2	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Sipuncula;D_9_Phascosomatiformes;D_10_Apiosoma misakianum D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Echinodermata;D_7_Ophiuroidea;_
MB009-40	40	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Myodocopa;D_10_Halocyprida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Digenea;__;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Lobata;D_8_Undescribed Lobata sp. 4 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Bilateria;D_6_uncultured;D_7_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Spionida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Eunicida;D_10_Paramphinome jeffreysii D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Harpacticoida;D_11_Canuella perplexa D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Candacia discadata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_Liriope tetraphylla D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Anthoathecata;D_9_Solanderia secunda D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Pleurobrachia bachei D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hexacorallia;D_8_Ceriantharia;D_9_Pachycerianthus fimbriatus D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_uncultured marine eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Narcomedusae;D_9_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Haloptilus longicornis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Platyctenida;D_8_Coeloplana bannwarthii D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;D_10_Salvatoria kerguelensis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Capitellida;D_10_Heteromastus filiformis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Anthoathecata;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Thaliacea;D_9_Salpida;D_10_Cyclosalpa polae D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Heterobranchia;D_9_Cylichna cylindracea D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;D_9_Sagitta sp. DP-2006 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Pleurobrachia brunnea D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Subeucalanus pileatus D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Echinodermata;D_7_Holothuroidea;D_8_Holothuria forskali D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Enteropneusta;D_8_Ptychoderidae;D_9_Enteropneusta sp. extrawide-lipped D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Harpacticoida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Anopla;D_8_Heteronemertea;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Echinodermata;D_7_Asteroidea;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Leptothecata;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Siphonostomatoida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_11_Neopterygii;D_12_Teleostei;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Echinodermata;D_7_Holothuroidea;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;__;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;__;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Enopla;D_8_Monostilifera;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;D_9_Aidanosagitta neglecta D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;D_9_Decipisagitta decipiens



Names	total	elements		
CTD8-60 MBOI	27	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Myodocopa;D_10_Halocyprida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Siphonophorae;D_9_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;D_9_Sagitta sp. DP-2006 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Bilateria;D_6_uncultured;D_7_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;D_11_Gaetanus variabilis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;D_11_Neocalanus flemingeri D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_Pantachogon haeckeli D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;__;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;D_11_marine metagenome D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;__;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Leptothecata;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);__;__;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;D_11_Metridia asymmetrica D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Heterobranchia;D_9_Desmopterus papilio D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Bilateria;D_6_Annelida;D_7_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_uncultured marine eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Maxillopoda;D_9_Copepoda;D_10_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;D_11_Junceella aquamata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;D_11_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_uncultured eukaryote		
	CTD8-60	6	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;D_11_Pleuromamma borealis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Undescribed mertensiid sp. 3 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Pleurobrachia bachei D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Platyctenida;D_8_Coeloplana banwarthii D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Anthoathecata;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Phyllopoda;D_10_Diplostraca;D_11_Pleuroxus aduncus	
		MB009-60	30	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Pteriomorphia;D_9_Pterioidea;D_10_Atrina pectinata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Pleurobrachia brunnea D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Spionida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Caenogastropoda;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;D_11_Candacia discaudata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Opheliidae;D_10_Ophelina acuminata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;D_11_Pareucalanus attenuatus D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoidea;D_11_Euchaeta concinna D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Anthoathecata;D_9_Solanderia secunda D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Enteropneusta;D_8_Ptychoderidae;D_9_Enteropneusta sp. extrawide-lipped D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Harpacticoida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Leptothecata;D_9_Aequorea aequorea D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Echinodermata;D_7_Asteroidea;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Eumalacostraca;D_10_Peracarida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Scaphozoa;D_7_Coronatae;D_8_Atolla vanhoeffeni D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Siphonostomatoida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Anthoathecata;D_9_Hybocodon chilensis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Terebellida;D_10_Lanice conchilega D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Pteriomorphia;D_9_Ostreoida;D_10_Saccostrea glomerata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Narcomedusae;D_9_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Pteriomorphia;D_9_Mytiloida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Thaliacea;D_9_Salpida;D_10_Cyclosalpa polae D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;D_9_Aidanosagitta neglecta D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;D_11_Sapphirina darwinii D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Enteropneusta;D_8_Ptychoderidae;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Heterobranchia;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Caenogastropoda;D_9_Pomacea canaliculata

Names	total	elements		
CTD8-80 MBOI	25	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Myodocopa;D_10_Halocyprida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Neocalanus flemingeri D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;__;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Hormiphora plumosa D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;__;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);__;__;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_uncultured marine eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_Oithona sp. 1 New Caledonia-RJH-2001 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Demospongiae;D_6_Poecilosclerida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;D_10_Conchoecia sp. OC-2001 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;D_11_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Siphonophorae;D_9_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;D_10_metagenome D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_Pantachogon haeckeli D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Bilateria;D_6_Annelida;D_7_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Myodocopa;D_10_Halocyprida;D_11_marine metagenome D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;D_9_Decipisagitta decipiens D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_uncultured eukaryote		
	CTD8-80	12	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Undescribed mertensiid sp. 3 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Eumalacostraca;D_10_Peracarida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Demospongiae;D_6_Dictyoceratida;D_7_Hippospongia communis (horse sponge) D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Eumalacostraca;D_10_Eucarida;D_11_Munida iris D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Anthoathecata;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Scolecida;D_9_Terebellida;D_10_Terebellides californica D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Calcinea;D_7_Clathrinida;D_8_Leucetta sp. Manuel H2 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Eumalacostraca;D_10_Eucarida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_11_Neopterygii;D_12_Teleostei;D_13_Salmo salar (Atlantic salmon) D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Demospongiae;__;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Demospongiae;D_6_Verongiida;D_7_Smenospongia aurea D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gymnolaemata;D_8_Cheilostomatida;D_9_Schizomavella linearis	
		MB009-80	34	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Pleuromamma borealis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Spionida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Gaetanus variabilis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Candacia discaudata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Euchaeta concinna D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Heterostylites major D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Anthoathecata;D_9_Hydractinia sp. MMM-2016 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Metridia asymmetrica D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Heterobranchia;D_9_Desmopterus papilio D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Centropages furcatus D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hexacorallia;D_8_Actiniaria;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Heterobranchia;D_9_Cylichna cylindracea D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;D_9_Sagitta sp. DP-2006 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Pleurobrachia brunnea D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Caenogastropoda;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gymnolaemata;D_8_Cheilostomatida;D_9_Smittoidea spinigera D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Pareucalanus attenuatus D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Harpacticoida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Hirudinida;__;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Heteroconchia;D_9_Veneroidea;D_10_Protothaca jedoensis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Echinodermata;D_7_Asteroidea;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Demospongiae;D_6_Tetractinellida;D_7_Candidatus Entotheonella sp. TSY1 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Siphonostomatoida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Maxillopoda;D_9_Copepoda;D_10_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Narcomedusae;D_9_Solmissus marshalli D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;__;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Echinodermata;D_7_Echinoidea;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Enopla;D_8_Monostilifera;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Heterobranchia;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Spionida;D_10_Prionospio cirrifera



Names	total	elements
CTD8-100 MBI	22	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Myodocopa;D_10_Halocyprida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Siphonophorae;D_9_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Gaetanus variabilis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Undescribed mertensiid sp. 3 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Candacia discaudata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_Pantachogon haeckeli D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;__;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;__;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Anthoathecata;D_9_Hydractinia sp. MMM-2016 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);__;__;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Anthoathecata;D_9_Pandea sp. AGC-2005 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Bilateria;D_6_Annelida;D_7_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_uncultured marine eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Siphonostomatoida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_11_Neopterygii;D_12_Teleostei;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hexacorallia;D_8_Actiniaria;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;D_11_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_uncultured eukaryote
CTD8-100	5	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Hormiphora plumosa D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Anthoathecata;D_9_Turritopsis nutricula D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Demospongiae;D_6_Tetractinellida;D_7_Rhabdastrella globostellata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Anopla;D_8_Heteronemertea;D_9_Gorgonorhynchus albocinctus
MB009-100	33	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;D_9_Sagitta sp. DP-2006 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Pleuromamma borealis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Pleurobrachia brunnea D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Sabellida;D_10_Owenia fusiformis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Spionida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Caenogastropoda;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;D_10_metagenome D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Neocalanus flemingeri D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Euchaeta concinna D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_marine metagenome D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Heterostylytes major D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Leptotheccata;D_9_Aequorea aequorea D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Leptotheccata;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Echinodermata;D_7_Asteroidea;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Metridia asymmetrica D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Gastrotricha;D_7_Chaetonotida;D_8_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Heterobranchia;D_9_Limacina retroversa D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Maxillopoda;D_9_Copepoda;D_10_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_Oithona sp. 1 New Caledonia-RJH-2001 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Junceella aquamata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Anopla;D_8_Heteronemertea;D_9_Cerebratulus lacteus (milky ribbon-worm) D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Narcomedusae;D_9_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Myodocopa;D_10_Halocyprida;D_11_marine metagenome D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;D_10_Nephtys hombergii D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;D_9_Aidanosagitta neglecta D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;D_11_Sapphirina darwinii D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Scolecithricella longispinosa D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Heterobranchia;__

Names	total	elements
CTD14-40 MBI	28	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Thaliacea;D_9_Salpida;D_10_lasis cylindrica D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Siphonophorae;D_9_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Leptothecata;D_9_Blackfordia virginica D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_Liriope tetrphylla D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_Pantachogon haeckeli D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Pleurobrachia bachei D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_marine metagenome D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;__;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);__;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Bilateria;D_6_Annelida;D_7_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Siphonostomatoida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Maxillopoda;D_9_Copepoda;D_10_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Junceella aquamata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;D_10_Conchoecia sp. OC-2001 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;__;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Narcomedusae;D_9_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Platyctenida;D_8_Coeloplana bannwarthii D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Siphonophorae;D_9_Nanomia bijuga D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;D_11_Sapphirina darwinii D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Heterobranchia;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_Oithona sp. 2 New Caledonia-RJH-2004 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_uncultured eukaryote
CTD14-40	3	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Pleurobrachia brunnea D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Undescribed mertensiid sp. 3 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;__;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;__;_
MB012-40	30	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;D_9_Sagitta sp. DP-2006 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Eumalacostraca;D_10_Eucarida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Pleuromamma borealis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Brachiopoda;D_7_Phoroniformea;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Caenogastropoda;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Echinodermata;D_7_Holothuroidea;D_8_Holothuria forskali D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Candacia discadata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Neocalanus flemingeri D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Euchaeta concinna D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Harpacticoida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Anopla;D_8_Heteronemertea;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Echinodermata;D_7_Asteroidea;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Eumalacostraca;D_10_Peracarida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Metridia asymmetrica D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hexacorallia;D_8_Ceriantharia;D_9_Pachycerianthus fimbriatus D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_uncultured marine eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_11_Neopterygii;D_12_Teleostei;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Centropages furcatus D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Echinodermata;D_7_Holothuroidea;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;__;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Myodocopa;D_10_Halocyprida;D_11_marine metagenome D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Haloptilus longicornis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;D_10_Nephtys hombergii D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hexacorallia;D_8_Actiniaria;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;D_10_Alciopina sp. THS-2006 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;D_11_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;D_9_Decipisagitta decipiens D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;D_9_Aidanosagitta neglecta



Names	total	elements	
CTD14-60 MBI	22	D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Thaliacea;D_9__Salpida;D_10__Iasis cylindrica	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Hydroidolina;D_8__Siphonophorae;D_9__uncultured eukaryote	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Calanoida;D_11__uncultured eukaryote	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_5__Bilateria;D_6__uncultured;D_7__uncultured eukaryote	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_6__Echinodermata;D_7__Ophiuroidea;D_8__Gorgonocephalus eucnemis	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Hydroidolina;D_8__Leptothecata;D_9__Blackfordia virginica	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Trachylinae;D_8__Trachymedusae;D_9__Pantachogon haeckeli	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_6__Tentaculata;__;_	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Oikopleuridae;D_11__uncultured eukaryote	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);__;_	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_5__Bilateria;D_6__Annelida;D_7__uncultured metazoan	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Cyclopoida;D_11__uncultured marine eukaryote	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Siphonostomatoida;_	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Maxillopoda;D_9__Copepoda;D_10__uncultured eukaryote	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Hydroidolina;__;_	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_6__Tentaculata;D_7__Platyctenida;D_8__Coeloplana bannwarthii	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Oikopleuridae;D_11__uncultured metazoan	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Poecilostomatoida;D_11__Sapphirina darwinii	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Poecilostomatoida;D_11__uncultured eukaryote	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Gastropoda;D_8__Heterobranchia;_	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Cyclopoida;_	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Cyclopoida;D_11__uncultured eukaryote	
	MB012-60	28	D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Myodocopa;D_10__Halocyprida;_
			D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Sagittoidea;D_8__Aphragmophora;D_9__Sagitta sp. DP-2006
			D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_6__Scyphozoa;D_7__Semaestomeae;_
			D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Calanoida;D_11__Pleuromamma borealis
			D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_6__Tentaculata;D_7__Lobata;D_8__Undescribed Lobata sp. 4
			D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Gastropoda;D_8__Caenogastropoda;_
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Calanoida;D_11__Gaetanus variabilis	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Calanoida;D_11__Candacia discaudata	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Calanoida;D_11__Neocalanus flemingeri	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Scolecida;D_9__Opheliidae;D_10__Ophelina acuminata	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Trachylinae;D_8__Trachymedusae;D_9__Liriope tetraphylla	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Harpacticoida;_	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_6__Tentaculata;D_7__Cydippida;D_8__Hormiphora plumosa	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;__;_	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_6__Echinodermata;D_7__Asteroidea;_	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Calanoida;D_11__Metridia asymmetrica	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Gastropoda;D_8__Heterobranchia;D_9__Desmopterus papilio	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Gastropoda;D_8__Heterobranchia;D_9__Limacina retroversa	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Anopla;D_8__Heteronemertea;D_9__Cerebratulus lacteus (milky ribbon-worm)	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Palpata;__;_	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Trachylinae;D_8__Narcomedusae;D_9__uncultured eukaryote	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Calanoida;D_11__Haloptilus longicornis	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Palpata;D_9__Phyllodocida;_	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Hydroidolina;D_8__Anthoathecata;_	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Sagittoidea;D_8__Aphragmophora;D_9__Decipisagitta decipiens	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Calanoida;D_11__Scolecithricella longispinosa	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Gastropoda;D_8__Caenogastropoda;D_9__Pomacea canaliculata	
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Scolecida;D_9__Spionida;D_10__Prionospio cirrifera	

Names	total	elements
CTD14-80 MBI	22	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Thaliacea;D_9_Salpida;D_10_lasis cylindrica
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Siphonophorae;D_9_uncultured eukaryote
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_uncultured eukaryote
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Caenogastropoda;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Gaetanus variabilis
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Neocalanus flemingeri
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_uncultured metazoan
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_Pantachogon haeckeli
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;__;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;__;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;D_11_uncultured eukaryote
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);__;__;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Metridia asymmetrica
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Bilateria;D_6_Annelida;D_7_uncultured metazoan
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_uncultured marine eukaryote
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_Oithona sp. 1 New Caledonia-RJH-2001
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;D_11_uncultured metazoan
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;D_11_Sapphirina darwinii
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_uncultured eukaryote
CTD14-80	11	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Undescribed mertensiid sp. 3
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;__;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_marine metagenome
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Hormiphora plumosa
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Leptothecata;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Anthoathecata;D_9_Pandea sp. AGC-2005
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Leptothecata;D_9_Clytia gracilis
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;__;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_10_Myodocopa;D_11_marine metagenome
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Siphonophorae;D_9_Nanomia bijuga
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;D_9_Decipisagitta decipiens
MB012-80	29	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Myodocopa;D_10_Halocyprida;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Pleuromamma borealis
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Bilateria;D_6_uncultured;D_7_uncultured eukaryote
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;D_10_metagenome
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Candacia discaudata
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_Liriope tetraphylla
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Pareucalanus attenuatus
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Thaliacea;D_9_Salpida;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Harpacticoida;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Heterostylites major
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Monogononta;D_8_Ploimida;D_9_Brachionus calyciflorus
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Chromadorea;D_8_Monhysterida;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Eumalacostraca;D_10_Peracarida;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Heterobranchia;D_9_Limacina retroversa
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Siphonostomatoida;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Maxillopoda;D_9_Copepoda;D_10_uncultured eukaryote
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_11_Neopterygii;D_12_Teleostei;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Monogononta;D_8_Ploimida;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Haloptilus longicornis
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Platyctenida;D_8_Coeloplana bannwarthii
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;D_10_Lepidonotus sublevis
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;D_10_Alcipina sp. THS-2006
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Enopla;D_8_Monostilifera;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;D_11_uncultured eukaryote
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Heterobranchia;__
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Spionida;D_10_Prionospio cirrifera
		D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hexacorallia;D_8_Scleractinia;D_9_Orbicella franksi



Names	total	elements
CTD14-100 MI	24	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Thaliacea;D_9_Salpida;D_10_lasis cylindrica D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Siphonophorae;D_9_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Bilateria;D_6_uncultured;D_7_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_Pantachogon haeckeli D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;__;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Heteroconchia;D_9_Veneroida;D_10_Protothaca jedsensis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);__;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Metridia asymmetrica D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Bilateria;D_6_Annelida;D_7_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_uncultured marine eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Siphonostomatoida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_Oithona sp. 1 New Caledonia-RJH-2001 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;__;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Siphonophorae;D_9_Nanomia bijuga D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;D_11_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_uncultured eukaryote
CTD14-100	9	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;D_9_Sagitta sp. DP-2006 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Leptothecata;D_9_Blackfordia virginica D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Undescribed mertensiid sp. 3 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Pleurobrachia bachei D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_11_Neopterygii;D_12_Teleostei;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Leptothecata;D_9_Rhacostoma atlanticum D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Platyctenida;D_8_Coeloplana bannwarthii D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Haloptilus longicornis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;D_9_Decipisagitta decipiens
MB012-100	25	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Myodocopa;D_10_Halocyprida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Scyphozoa;D_7_Semaeostomeae;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Eumalacostraca;D_10_Eucarida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Pleuromamma borealis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Lobata;D_8_Undescribed Lobata sp. 4 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Spionida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Caenogastropoda;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Gaetanus variabilis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;D_10_metagenome D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Candacia discaudata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Neocalanus flemingeri D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Thaliacea;D_9_Salpida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Harpacticoida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Heterostylites major D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;__;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Gastrotricha;D_7_Chaetonotida;D_8_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Maxillopoda;D_9_Copepoda;D_10_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;D_10_Conchoecia sp. OC-2001 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Echinodermata;D_7_Echinoidea;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;D_11_Sapphirina darwinii D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Scolecithricella longispinosa D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Spionida;D_10_Prionospio cirrifera D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hexacorallia;D_8_Scleractinia;D_9_Orbicella franksi

Names	total	elements		
CTD15-240 MI	33	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Myodocopa;D_10_Halocyprida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Thaliacea;D_9_Salpida;D_10_Iasis cylindrica D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Siphonophorae;D_9_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;D_9_Sagitta sp. DP-2006 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Gaetanus variabilis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;D_10_metagenome D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Undescribed mertensiid sp. 3 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Neocalanus flemingeri D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_Pantachogon haeckeli D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;__; D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;__; D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);__; D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Eumalacostraca;D_10_Peracarida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Metridia asymmetrica D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Siphonostomatoida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Bilateria;D_6_Annelida;D_7_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_11_Neopterygii;D_12_Teleostei;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Narcomedusae;D_9_Cunina frugifera D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Narcomedusae;D_9_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Siphonophorae;D_9_Nanomia bijuga D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;D_11_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Thaliacea;D_9_Salpida;D_10_Cyclosalpa polae D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Heterobranchia;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_uncultured eukaryote		
	CTD15-240	23	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Bilateria;D_6_uncultured;D_7_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Pleurobrachia brunnea D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Eunicida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Spionida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Opheliidae;D_10_Ophelina acuminata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Pareucalanus attenuatus D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Leptothecata;D_9_Aequorea aequorea D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Echinodermata;D_7_Asteroidea;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Leptothecata;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copelata;D_10_Oikopleuridae;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Bdelloidea;D_8_Adinetida;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Anthoathecata;D_9_Fabienna sphaerica D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Heterobranchia;D_9_Desmopterus papilio D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Scyphozoa;D_7_Coronatae;D_8_Atolla vanhoeffeni D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_uncultured marine eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Maxillopoda;D_9_Copepoda;D_10_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Junceella aquamata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Pteriomorphia;D_9_Ostreoida;D_10_Saccostrea glomerata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;__; D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Platyctenida;D_8_Coeloplana bannwarthii D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hexacorallia;D_8_Actiniaria;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;D_11_Sapphirina darwinii D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_Oithona sp. 2 New Caledonia-RJH-2004	
		MB011-240	9	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Caenogastropoda;__ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Candacia discadata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_Liriope tetraphylla D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Heterostylites major D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Demospongiae;D_6_Suberitida;D_7_Terpis aploos D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Gastrotricha;D_7_Chaetonotida;D_8_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_Oithona sp. 1 New Caledonia-RJH-2001 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Myodocopa;D_10_Halocyprida;D_11_marine metagenome D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Scolecithricella longispinosa

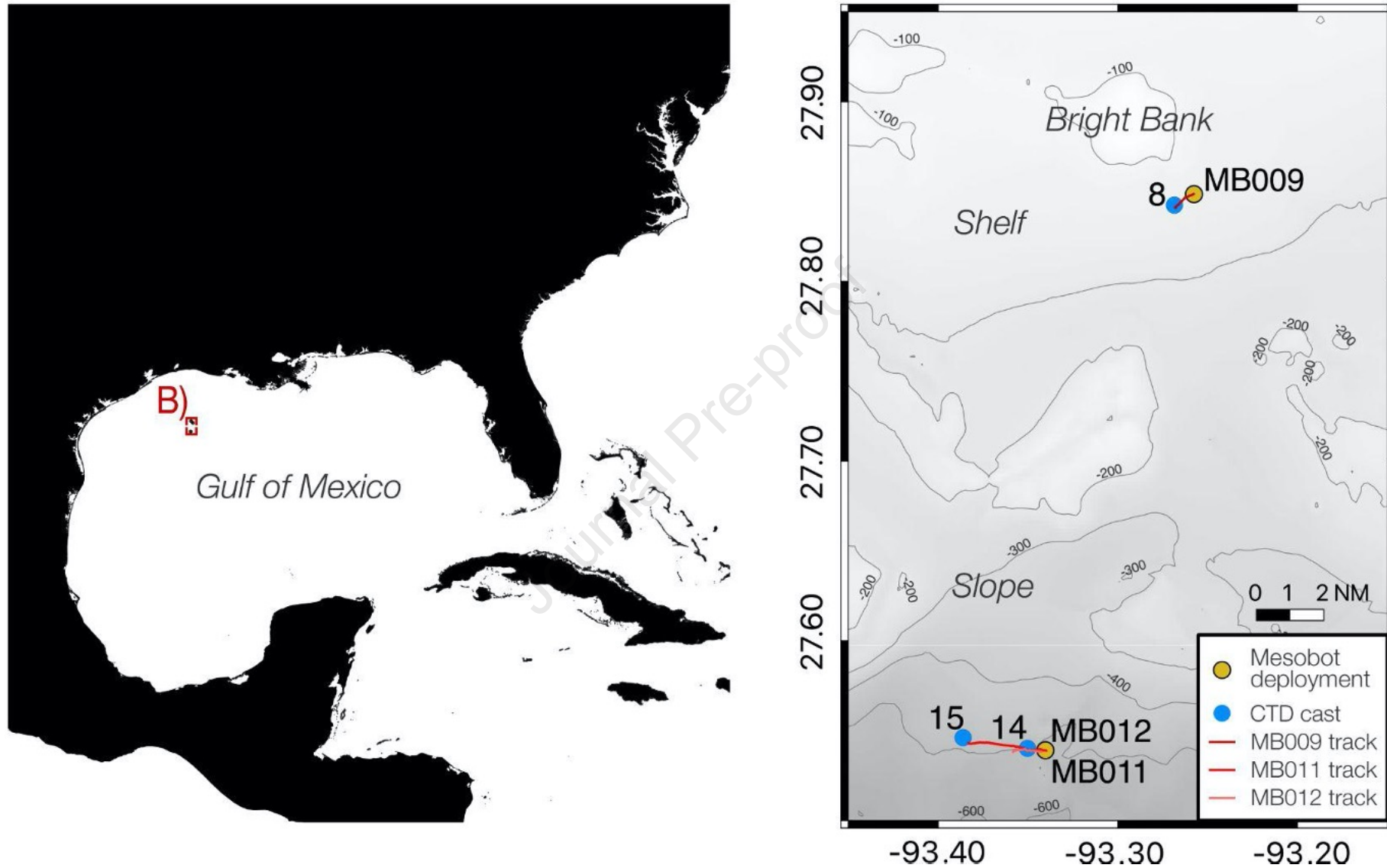


Names	total	elements
CTD15-320 MI	13	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;__;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Heterostylites major D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;__;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Oikopleuridae;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);__;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Oikopleuridae;D_11_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Siphonophorae;D_9_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Eumalacostraca;D_10_Eucarida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_Pantachogon haeckeli D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Bilateria;D_6_Annelida;D_7_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_uncultured eukaryote
CTD15-320 MI	2	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Anthoathecata;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;D_11_uncultured eukaryote
CTD15-320 MI	4	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Lobata;D_8_Undescribed Lobata sp. 4 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_uncultured marine eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_11_Neopterygii;D_12_Teleostei;D_13_Salmo salar (Atlantic salmon) D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Anthoathecata;D_9_Pandea sp. AGC-2005
MB011-320 M	17	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Myodocopa;D_10_Halocyprida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Thaliacea;D_9_Salpida;D_10_lasis cylindrica D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Pleuromamma borealis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Metridia asymmetrica D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hexacorallia;D_8_Ceriantharia;D_9_Pachycerianthus fimbriatus D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_Oithona sp. 1 New Caledonia-RJH-2001 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Haloptilus longicornis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Poecilostomatoida;D_11_Sapphirina darwinii D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Scolecithricella longispinosa D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Siphonostomatoida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_11_Neopterygii;D_12_Teleostei;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Myodocopa;D_10_Halocyprida;D_11_marine metagenome D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Gastropoda;D_8_Heterobranchia;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Spionida;D_10_Prionospio cirrifera D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;_ CTD15-320
CTD15-320	8	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Undescribed mertensiid sp. 3 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_Liriope tetraphylla D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Pleurobrachia bachei D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Hormiphora plumosa D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Siphonophorae;D_9_Nanomia bijuga D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Demospongiae;D_6_Haplosclerida;D_7_Haliclona sp. NBL-2014 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Trachylinae;D_8_Trachymedusae;D_9_uncultured metazoan D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Monogononta;D_8_Ploimida;D_9_metagenome
MB011-320	7	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Tentaculata;D_7_Cydippida;D_8_Haekelia rubra D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Spionida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_Candacia discaudata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Anthoathecata;D_9_Hydractinia sp. MMM-2016 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hexacorallia;D_8_Zoantheria;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;__;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Echinodermata;D_7_Echinoidea;_ MB012-320
MB012-320	29	D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Sipuncula;D_9_Phascosomatiformes;D_10_Apionsoma misakianum D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Octocorallia;D_8_Pennatulacea;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hexacorallia;D_8_Antipatharia;D_9_Antipathes fiordensis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Opheliidae;D_10_Ophelina acuminata D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Decapodiformes;D_10_Teuthida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Leptothecata;D_9_Aequorea aequorea D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Scolecida;D_9_Spionida;D_10_Cauleriella parva D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Anthoathecata;D_9_Fabienna sphaerica D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Gastrotricha;D_7_Chaetonotida;D_8_uncultured eukaryote D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_5_Demospongiae;D_6_Poecilosclerida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hexacorallia;D_8_Actiniaria;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Scyphozoa;D_7_Semaestomeae;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Leptothecata;D_9_Blackfordia virginica D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;D_9_Phyllodocida;D_10_metagenome D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Cyclopoida;D_11_Anthessius sp. New Caledonia-RJH-2004 D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Copepoda;D_10_Calanoida;D_11_marine metagenome D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Anopla;D_8_Heteronemertea;D_9_Cerebratulus lacteus (milky ribbon-worm) D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Monogononta;D_8_Ploimida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_6_Nuda;D_7_Beroida;D_8_Beroe cucumis D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Palpata;__;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_8_Pteriomorphia;D_9_Mytiloida;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;D_9_Sagitta elegans D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Sagittoidea;D_8_Aphragmophora;D_9_Aidanosagitta neglecta D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Enopla;D_8_Monostilifera;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Hydroidolina;D_8_Siphonophorae;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Octocorallia;D_8_Alcyonacea;_ D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_7_Myzostomida;D_8_Myzostomidae;D_9_Myzostoma polycyclus D_0_Eukaryota;D_1_Opisthokonta;D_2_Holozoa;D_3_Metazoa (Animalia);D_9_Phyllopoda;D_10_Diplostraca;D_11_Pleuroxus aduncus

Names	total	elements
CTD15-400 MI	24	D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Sipuncula;D_9__Phascolosomatiformes;D_10__Apionsoma misakianum
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_6__Tentaculata;D_7__Lobata;D_8__Undescribed Lobata sp. 4
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Scolecida;D_9__Terebellida;D_10__Anobothrus gracilis
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Scolecida;D_9__Opheliidae;D_10__Ophelina acuminata
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_6__Tentaculata;__;
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;__;
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copelata;D_10__Oikopleuridae;D_11__uncultured eukaryote
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);__;
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Calanoida;D_11__Metridia asymmetrica
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_6__Gastrotricha;D_7__Chaetonotida;D_8__uncultured eukaryote
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Hydroidolina;D_8__Siphonophorae;D_9__uncultured eukaryote
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Calanoida;__
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Calanoida;D_11__uncultured eukaryote
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Trachylinae;D_8__Trachymedusae;D_9__Pantachogon haeckeli
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Enteropneusta;D_8__Ptychoderidae;D_9__Enteropneusta sp. extrawide-lipped
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Hydroidolina;D_8__Anthoathecata;D_9__Pandea sp. AGC-2005
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_11__Neopterygii;D_12__Teleostei;__
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Hydroidolina;__;
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Myodocopa;D_10__Halocyprida;D_11__marine metagenome
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Palpata;D_9__Phyllodocida;__
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Enopla;D_8__Monostilifera;__
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Hydroidolina;D_8__Siphonophorae;__
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Anopla;D_8__Heteronemertea;D_9__Gorgonrhyinchus albocinctus
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Cyclopoida;D_11__uncultured eukaryote
CTD15-400	10	D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Hydroidolina;D_8__Leptotheicata;D_9__Clytia sp. AGC-2001
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_6__Tentaculata;D_7__Cydippida;D_8__Undescribed mertensiid sp. 3
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Gastropoda;__;
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_6__Scyphozoa;D_7__Coronatae;D_8__Atolla vanhoeffeni
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Hydroidolina;D_8__Leptotheicata;D_9__Rhacostoma atlanticum
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Thaliacea;D_9__Salpida;D_10__Cyclosalpa polae
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Poecilostomatoida;D_11__uncultured eukaryote
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Scolecida;D_9__Capitellida;D_10__Metasychis disparidentata
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_5__Bilateria;D_6__Mollusca;D_7__Bathypecten vulcani
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Cyclopoida;__
MB011-400	45	D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Thaliacea;D_9__Salpida;D_10__lasis cylindrica
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_5__Bilateria;D_6__uncultured;D_7__uncultured eukaryote
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Scolecida;D_9__Terebellida;D_10__Lysilla sp. THS-2012
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Thaliacea;D_9__Salpida;__
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Calanoida;D_11__Heterostylites major
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Hydroidolina;D_8__Anthoathecata;D_9__Cytaeis sp. MAN-2015
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Scolecida;D_9__Spionida;D_10__Caulleriella parva
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Scolecida;D_9__Terebellida;D_10__Sternaspis scutata
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copelata;D_10__Oikopleuridae;__
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Scolecida;D_9__Capitellida;__
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Eumalacostraca;D_10__Peracarida;__
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Hydroidolina;D_8__Anthoathecata;D_9__Fabienna sphaerica
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Cyclopoida;D_11__Oithona sp. 1 New Caledonia-RJH-2001
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Calanoida;D_11__Haloptilus longicornis
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Scolecida;D_9__Terebellida;__
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Hexacorallia;D_8__Actiniaria;__
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Hydroidolina;D_8__Anthoathecata;D_9__Corymorpha glacialis
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copelata;D_10__Oikopleuridae;D_11__uncultured metazoan
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Protobranchia;D_9__Nuculanoida;D_10__Nuculana pernula
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Trachylinae;D_8__Trachymedusae;D_9__uncultured eukaryote
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Calanoida;D_11__Scolecithricella longispinosa
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Chromadorea;D_8__Rhabditida;D_9__Rhabditophanes sp. KR3021
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Scolecida;D_9__Capitellida;D_10__Notomastus latericeus
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Eumalacostraca;D_10__Eucarida;__
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Heteroconchia;D_9__Veneroida;__
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Gastropoda;D_8__Caenogastropoda;__
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Gymnolaemata;D_8__Cheilostomatida;D_9__Smittoidea spinigera
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Palpata;D_9__Phyllodocida;D_10__metagenome
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Cyclopoida;D_11__Anthessius sp. New Caledonia-RJH-2004
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_11__Neopterygii;D_12__Teleostei;D_13__Gadus morhua (Atlantic cod)
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Anopla;D_8__Heteronemertea;__
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Hydroidolina;D_8__Leptotheicata;__
		D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Gastropoda;D_8__Heterobranchia;D_9__Limacina retroversa
	D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_9__Copepoda;D_10__Siphonostomatoida;__	
	D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_5__Bilateria;D_6__Annelida;D_7__uncultured metazoan	
	D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Palpata;D_9__Phyllodocida;D_10__Goniada brunnea	
	D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Heteroconchia;D_9__Veneroida;D_10__Candidatus Thiodiazotropha endoloripes	
	D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_6__Echinodermata;D_7__Holothuroidea;__	
	D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Palpata;D_9__Sabellida;D_10__Lamellibrachia sp. L1 DH-2004	
	D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Palpata;__;	
	D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_8__Palpata;D_9__Eunicida;D_10__Ninoe nigripes	
	D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Sagittoidea;D_8__Aphragmophora;D_9__Decipisagitta decipiens	
	D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Enteropneusta;D_8__Ptychoderidae;__	
	D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Gastropoda;D_8__Caenogastropoda;D_9__Pomacea canaliculata	
	D_0__Eukaryota;D_1__Opisthokonta;D_2__Holozoa;D_3__Metazoa (Animalia);D_7__Gastropoda;D_8__Heterobranchia;__	

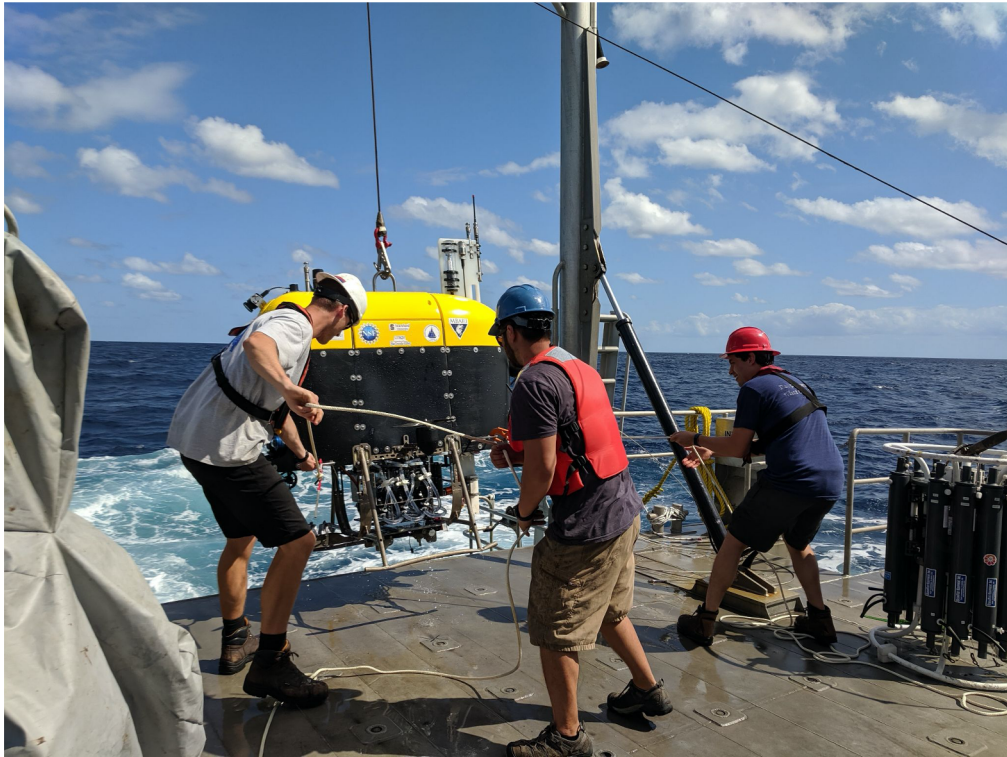


A)



**Fig. 1.** Map of study area. A) location in the Gulf of Mexico; B) close up of study area including Bright Bank and the deeper site. Blue dots indicate CTD locations and yellow dots indicate *Mesobot* deployment locations (MB009, MB011, and MB012). Red lines indicate the *Mesobot* tracks.

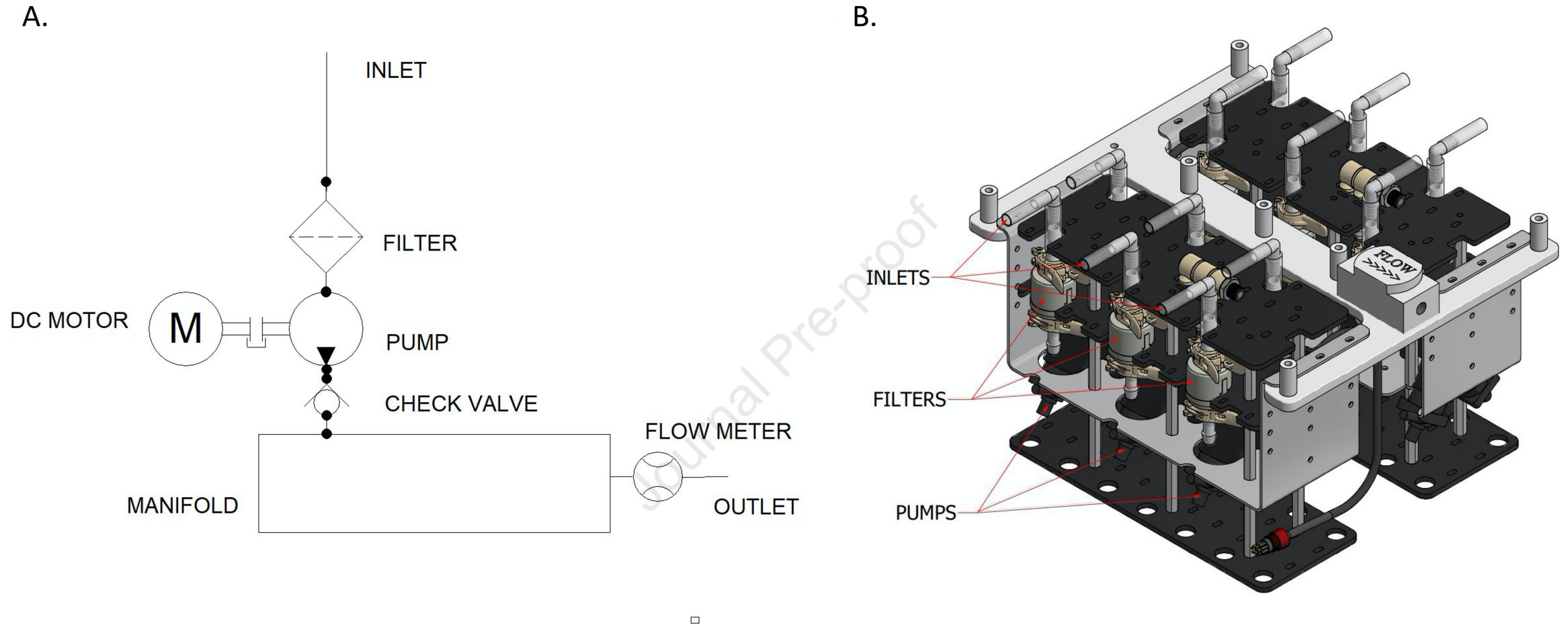
A.



B.

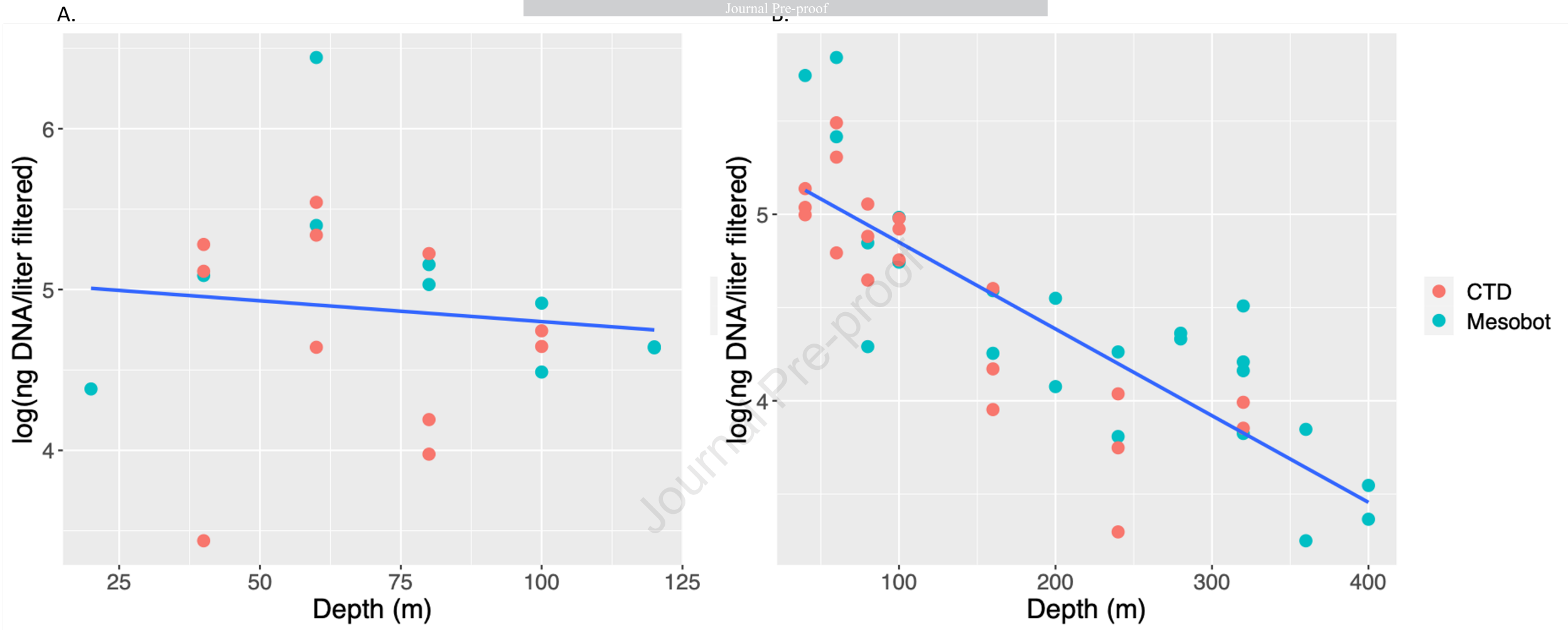


**Fig. 2.** A) *Mesobot* with the eDNA sampler being retrieved after a deployment on the R/V Manta; B) close-up of the eDNA sampler.

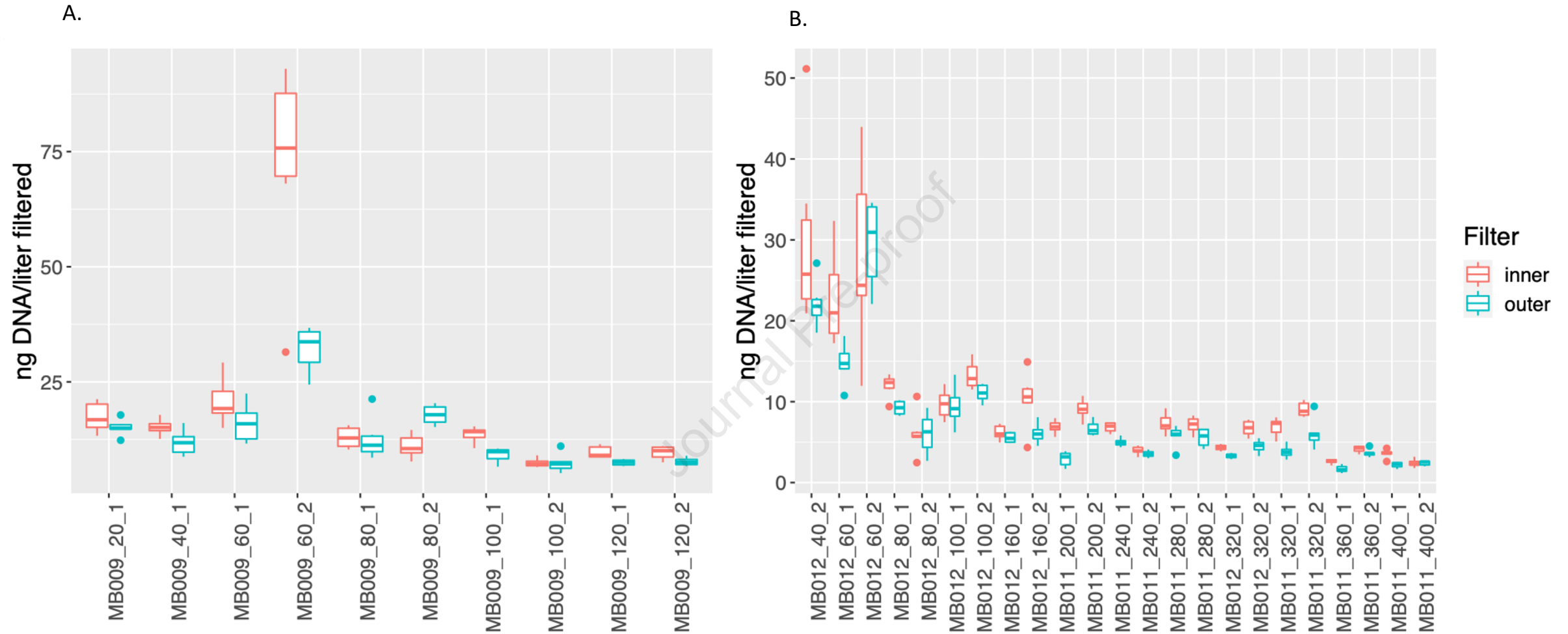


**Fig. 3.** Sampler design. A) Schematic of one pump/filter channel. Each sampler has 6 such channels that flow into a common manifold with an outlet through a single flowmeter. All 6 pumps are controlled by a single microcontroller; B) CAD drawing of the complete sampler. *Mesobot* carried two such samplers for a total of 12 pump/filter units on each dive.

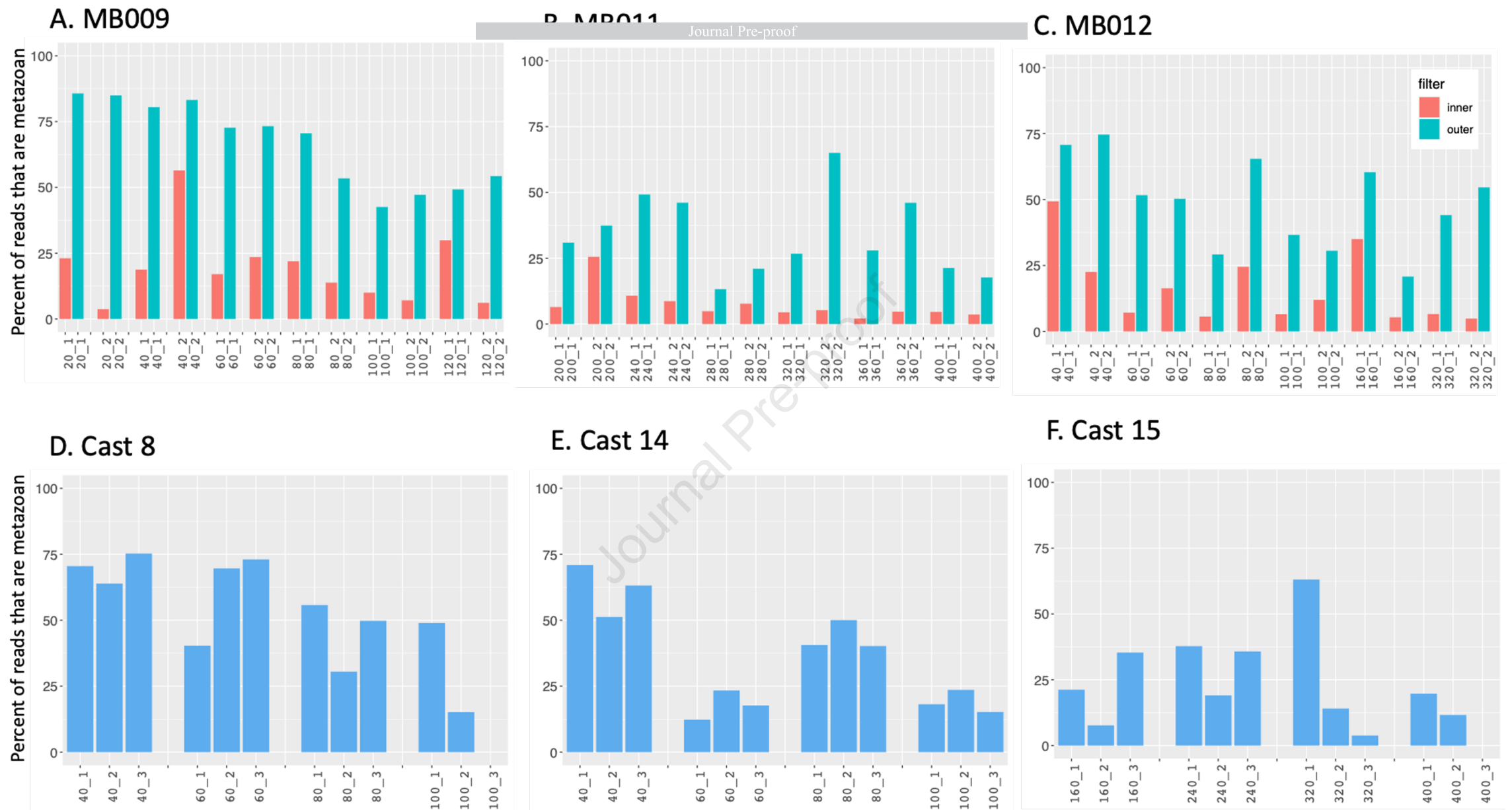




**Fig. 4.** log DNA yield versus depth for the *Mesobot* and CTD samples at the A) Bright and B) Slope sites. DNA yields refer to the total amount (ng) of DNA extracted divided by the filtration volume; for *Mesobot* samples - yields from individually-extracted filter pieces are summed. There was no significant relationship with depth for the Bright site (adjusted  $R^2 = -0.03866$ ;  $p = 0.619$ ); but there was for the Slope site (adjusted  $R^2 = 0.6856$ ,  $p = 0$ )

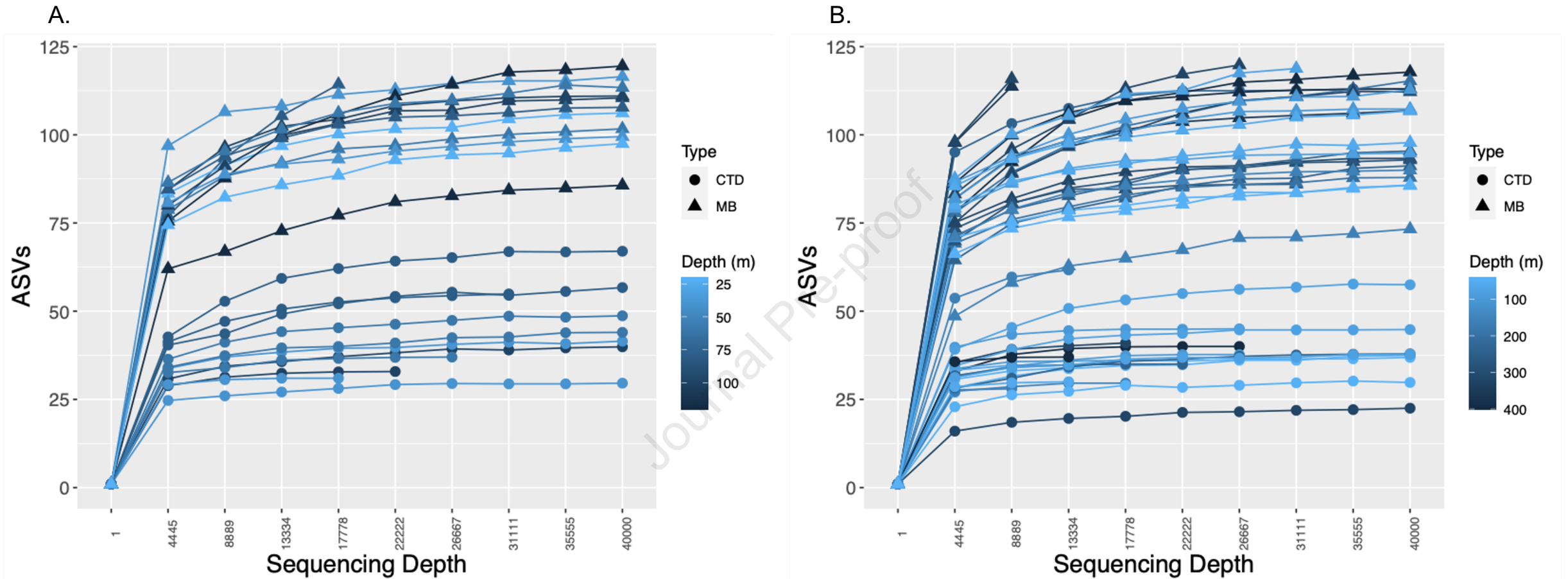


**Fig. 5.** Boxplots of DNA yields (ng DNA per liter of water filtered) of inner and outer filter slices from each *Mesobot* sample. A) Bright Bank site; B) Slope site. Sample names on the x-axis are formatted as “deployment\_depth\_replicate”.

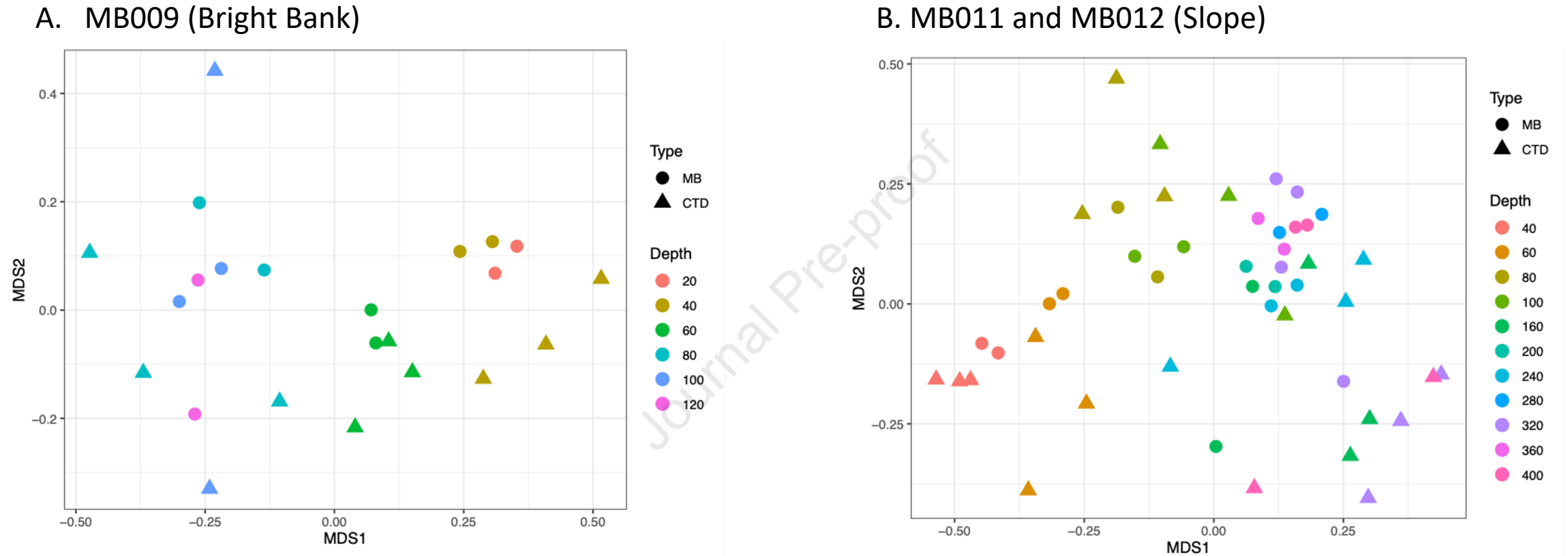


**Fig. 6.** Percent metazoan and non-metazoan reads from the inner and outer *Mesobot* sample filters (A-C); and the CTD samples (D-F). Sample names on the x-axis are formatted as depth\_replicate. Note we do not have samples for one of the replicates of Cast 8 - 100 m and for Cast 15 - 400 m, due to bottle mishaps. MB009 and Cast 8 originate from the Bright Bank site and MB011, MB012, Cast 14, and Cast 15 originate from the Slope site.



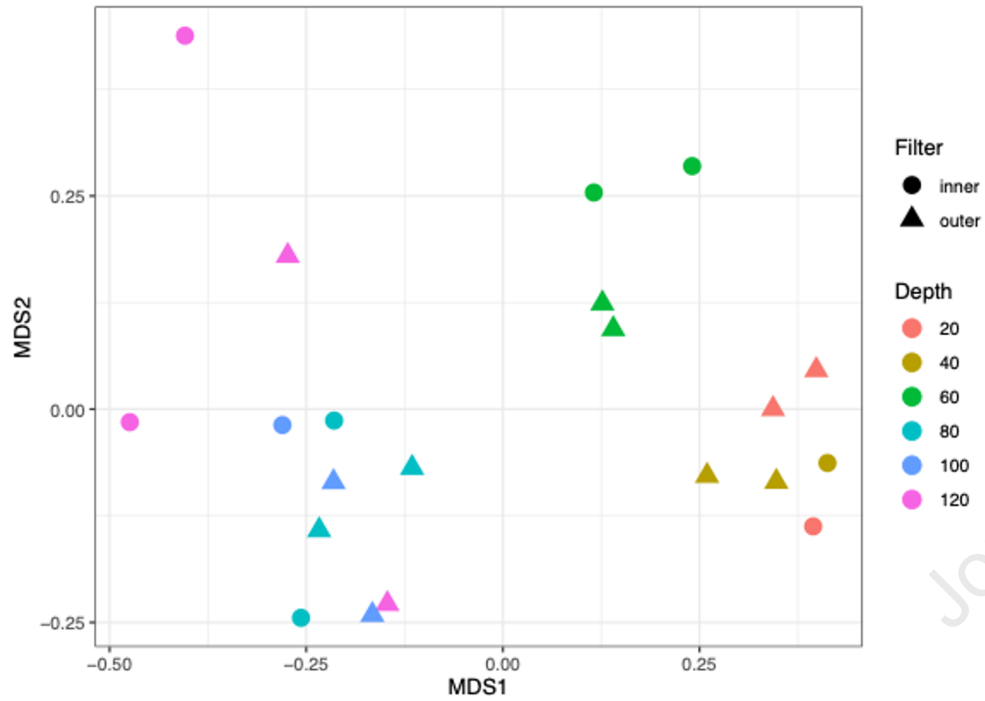


**Fig. 7.** Number of metazoan ASV's in the A) Bright Bank site (MB009 and Cast 8); and B) Slope site (MB011, MB012, Cast 14, and Cast 15). *Mesobot* sampler (MB) samples represent the merged inner and outer filter datasets. Sampling depth is indicated by shade. As some samples had extremely high read counts (>100,000), curves are truncated at 40,000 in order to visualize all samples, including those with much lower read counts. Total read counts for all samples are in Supplementary Table 3.

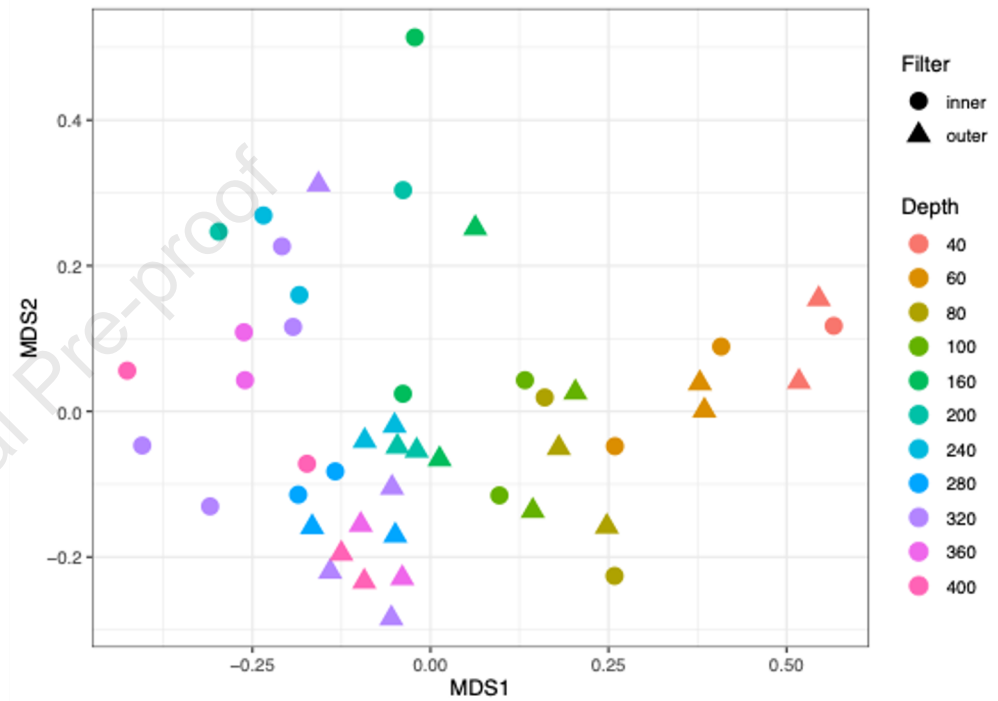


**Fig. 8.** nMDS plots based on Bray-Curtis dissimilarities from the A) MB009 deployment (Bright Bank site), stress = 0.1511615; and B) MB011 and MB012 deployments (Slope site), stress = 0.1815937.

A. MB009 (Bright Bank)



B. MB011 and MB012 (Slope)



**Fig. 9.** nMDS plots based on Bray-Curtis dissimilarities comparing inner and outer filters and depth from the A) MB009 deployment (Bright Bank site), stress = 0.1436734; and B) the MB011 and MB012 deployments (Slope site), stress = 0.1856701.

## Highlights

- A large-volume eDNA sampler was developed and deployed on the midwater robot *Mesobot*
- Compared to conventional small-volume samples, the sampler detected more metazoan taxa
- Both sampling approaches detected community changes with depth on the scale of 10's of meters
- The metazoan eDNA signal declined with depth
- Large volume sampling may be especially important in the mesopelagic and deep sea

**Declaration of interests**

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests:

Dana Yoerger reports a relationship with Gulf of Mexico Research Initiative that includes: board membership and consulting or advisory. Amy Kukulya, Daniel Gomez-Ibanez, and Abhimanyu Belani has patent Mapper and Sampler for Autonomous Analyte Detection and Recovery pending to Amy Kukulya, Daniel Gomez-Ibanez, and Abhimanyu Belani.