Biodiversity Monitoring Stations for Benthic Macrofauna and Meiofauna in the Disko Fan and Hatton Basin Conservation Areas

Kevin Jacobs, Marième Bouchard Marmen, Beatriz Rincón, Barry MacDonald, Camille Lirette, Olivia Gibb, Margaret Treble, Ellen Kenchington

Fisheries and Oceans Canada
Maritimes Region
Bedford Institute of Oceanography
PO Box 1006
Dartmouth, Nova Scotia
B2Y 4A2

2022

Canadian Technical Report of
Fisheries and Aquatic Sciences 3487

Fisheries and Oceans Canada | Pêches et Océans Canada

Canada

Canadian Technical Report of Fisheries and Aquatic Sciences

Technical reports contain scientific and technical information that contributes to existing knowledge but which is not normally appropriate for primary literature. Technical reports are directed primarily toward a worldwide audience and have an international distribution. No restriction is placed on subject matter and the series reflects the broad interests and policies of Fisheries and Oceans Canada, namely, fisheries and aquatic sciences.

Technical reports may be cited as full publications. The correct citation appears above the abstract of each report. Each report is abstracted in the data base *Aquatic Sciences and Fisheries Abstracts*.

Technical reports are produced regionally but are numbered nationally. Requests for individual reports will be filled by the issuing establishment listed on the front cover and title page.

Numbers 1-456 in this series were issued as Technical Reports of the Fisheries Research Board of Canada. Numbers 457-714 were issued as Department of the Environment, Fisheries and Marine Service, Research and Development Directorate Technical Reports. Numbers 715-924 were issued as Department of Fisheries and Environment, Fisheries and Marine Service Technical Reports. The current series name was changed with report number 925.

Rapport technique canadien des sciences halieutiques et aquatiques

Les rapports techniques contiennent des renseignements scientifiques et techniques qui constituent une contribution aux connaissances actuelles, mais qui ne sont pas normalement appropriés pour la publication dans un journal scientifique. Les rapports techniques sont destinés essentiellement à un public international et ils sont distribués à cet échelon. II n'y a aucune restriction quant au sujet; de fait, la série reflète la vaste gamme des intérêts et des politiques de Pêches et Océans Canada, c'est-à-dire les sciences halieutiques et aquatiques.

Les rapports techniques peuvent être cités comme des publications à part entière. Le titre exact figure au-dessus du résumé de chaque rapport. Les rapports techniques sont résumés dans la base de données *Résumés des sciences aquatiques et halieutiques*.

Les rapports techniques sont produits à l'échelon régional, mais numérotés à l'échelon national. Les demandes de rapports seront satisfaites par l'établissement auteur dont le nom figure sur la couverture et la page du titre.

Les numéros 1 à 456 de cette série ont été publiés à titre de Rapports techniques de l'Office des recherches sur les pêcheries du Canada. Les numéros 457 à 714 sont parus à titre de Rapports techniques de la Direction générale de la recherche et du développement, Service des pêches et de la mer, ministère de l'Environnement. Les numéros 715 à 924 ont été publiés à titre de Rapports techniques du Service des pêches et de la mer, ministère des Pêches et de l'Environnement. Le nom actuel de la série a été établi lors de la parution du numéro 925.

Canadian Technical Report
of Fisheries and Aquatic Sciences 3487

2022

Biodiversity Monitoring Stations for Benthic Macrofauna and Meiofauna in the Disko Fan and Hatton Basin Conservation Areas

by

Kevin Jacobs[1,2], Mariève Bouchard Marmen[1], Beatriz Rincón, Barry MacDonald[1], Camille Lirette[1], Olivia Gibb[3], Margaret Treble[2], Ellen Kenchington[1]

[1] Ocean and Ecosystem Sciences Division
Fisheries and Oceans Canada
Bedford Institute of Oceanography
PO Box 1006
Dartmouth, Nova Scotia
B2Y 4A2

[2] Arctic and Aquatic Research Division
Fisheries and Oceans Canada
Freshwater Institute
501 University Crescent
Winnipeg, Manitoba
R3T 2N6

[3] Environmental Sciences Division
Fisheries and Oceans Canada
Northwest Atlantic Fisheries Centre
PO Box 5667
St. John's, Newfoundland and Labrador
A1C 5X1

© Her Majesty the Queen in Right of Canada, 2022.

Cat. No. Fs97-6/3487E-PDF ISBN 978-0-660-43884-9 ISSN 1488-5379

Correct citation for this publication:

Jacobs, K., Bouchard Marmen, M., Rincón, B., MacDonald, B., Lirette, C., Gibb, O., Treble, M., and Kenchington, E. 2022. Biodiversity Monitoring Stations for Benthic Macrofauna and Meiofauna in the Disko Fan and Hatton Basin Conservation Areas. Can. Tech. Rep. Fish. Aquat. Sci. 3487: vi + 86 p.

TABLE OF CONTENTS

ABSTRACT

Jacobs, K., Bouchard Marmen, M., Rincón, B., MacDonald, B., Lirette, C., Gibb, O., Treble, M., and Kenchington, E. 2022. Biodiversity Monitoring Stations for Benthic Macrofauna and Meiofauna in the Disko Fan and Hatton Basin Conservation Areas. Can. Tech. Rep. Fish. Aquat. Sci. 3487: vi + 86 p.

In 2012 and 2013, Fisheries and Oceans Canada surveyed the benthos in two areas closed to bottom contact fishing, the Narwhal Overwintering and Coldwater Coral Zone (now the Disko Fan Conservation Area, DFCA), and the Hatton Basin Voluntary Coral Protection Zone (now the Hatton Basin Conservation Area, HBCA). Samples were collected following protocols recommended by the Arctic Council's Circumpolar Biodiversity Monitoring Plan for the purposes of providing baseline data for future monitoring of benthic invertebrates in this sensitive region, and for facilitating pan-Arctic comparisons of benthic communities. Five biodiversity monitoring stations were established, four in the DFCA and one in the HBCA, each of which was fully sampled according to those protocols with Van Veen grabs or box corers, drop cameras and temperature recorders attached to the gear. This report summarises the grab/core-sampled benthic fauna collected during the 2012 survey of the Conservation Areas and complements another report documenting the epibenthos from the camera transects in the DFCA. Here we report on macrofauna in the 1-cm size fraction, and on foraminiferan meiofauna.

RÉSUMÉ

Jacobs, K., Bouchard Marmen, M., Rincón, B., MacDonald, B., Lirette, C., Gibb, O., Treble, M., and Kenchington, E. 2022. Biodiversity Monitoring Stations for Benthic Macrofauna and Meiofauna in the Disko Fan and Hatton Basin Conservation Areas. Can. Tech. Rep. Fish. Aquat. Sci. 3487: vi + 86 p.

En 2012 et 2013, Pêches et Océans Canada a effectué des relevés du benthos dans deux zones fermées à la pêche entrant en contact avec le fond : la zone d'hivernage du narval et de coraux d'eaux froides (l'actuelle aire de conservation de Disko Fan, ou ACDF) et la zone de protection volontaire des coraux dans le bassin Hatton (l'actuelle aire de conservation du bassin Hatton, ou ACBH). Des échantillons ont été prélevés selon les protocoles recommandés dans le Plan de surveillance de la biodiversité circumpolaire du Conseil de l'Arctique dans le but de fournir des données de référence pour la surveillance future des invertébrés benthiques dans cette région sensible, ainsi que de faciliter les comparaisons des communautés benthiques à l'échelle de l'Arctique. Cinq stations de surveillance de la biodiversité ont été établies, quatre dans l'aire de conservation de Disko Fan et une dans l'aire de conservation du bassin Hatton, et chacune d'entre elles a été entièrement échantillonnée conformément à ces protocoles avec des bennes Van Veen ou des carottiers à boîte, des caméras sous-marines et des enregistreurs de température fixés à l'engin. Ce rapport résume la faune benthique prélevée à l'aide de bennes ou de carottiers lors du relevé de 2012 dans les aires de conservation et complète un autre rapport documentant l'épibenthos d'après les transects couverts par des caméras dans l'aire de conservation de Disko Fan. Nous présentons ici un rapport sur la macrofaune dans la classe de taille de 1 cm, et sur la méiofaune foraminifère.

INTRODUCTION

The deep-ocean environment is understudied globally (Brito-Morales et al., 2020). This is particularly true in Arctic deep-water benthic systems. The Arctic is also undergoing rapid environmental change. Polar regions on Earth are experiencing the most rapid effects of global warming, including change in air temperature (Osborne et al., 2018), sea-ice thickness (Osborne et al., 2018) and extent (Serreze et al., 2007), system productivity, salinity (Shu et al., 2018) and species distributions. Due to increased concentration of carbon dioxide in the atmosphere the world's oceans are also acidifying, increasing stress on calcifying organisms. Ocean acidification poses a threat to Canadian Arctic cold-water corals, especially to the scleractinian corals (Maier et al., 2012), and to gorgonian corals which secrete magnesium calcite (Orr et al., 2005). Increased periods of open water also bring the potential for increased economic activity and resource exploitation impacting the marine environment. Examples include but are not limited to, increased ship traffic to support tourism and transportation of goods, bottom-contact fishing, hydrocarbon extraction, invasive-species introductions, noise, and contaminants.

The rapid pace of change and paucity of baseline data from the Arctic provide impetus for increased knowledge of species distributions and abundances. Despite this necessity, scientific work in the Arctic offshore environment is complicated by the need for large vessels, and the associated financial and logistical constraints of working in this area. As such, historically, scientific work in the Arctic has been incomplete and fragmented in both space and time (Niemi et al., 2019).

Currently, scientific work in the Arctic is often coordinated by national governments, and facilitated through international partnerships. For example, Canada is a party to the Arctic Council with seven other nations. The Arctic Council's Conservation of Arctic Flora and Fauna (CAFF) working group established the Arctic Marine Biodiversity Monitoring Plan to facilitate the collection of baseline data in this sensitive region (Gill et al., 2011). "The monitoring plan is a pan-Arctic, long-term, integrated biodiversity monitoring plan produced by CAFF's Circumpolar Biodiversity Monitoring Program (CBMP)" (Circumpolar Biodiversity Monitoring Program Marine Steering Group, 2015). The goals of the program include coordinating the specific parameters measured, methodologies, indicators and sampling designs used by nations conducting Arctic science, to ensure comparability and support evidence-based decision making. Here, we report on data collected from the eastern Canadian Arctic in support of the CAFF for the purposes of providing baseline data for future monitoring of this sensitive region and of facilitating pan-Arctic comparisons of benthic communities.

OVERVIEW OF THE ARCTIC MARINE BIODIVERSITY MONITORING PLAN SAMPLING APPROACH RELEVANT TO THIS STUDY

Data in this report were collected and subsequently processed and analyzed following standards outlined in the Arctic Marine Biodiversity Monitoring Plan (Gill et al., 2011) for benthic

communities, produced by the CAFF's CBMP. In this plan the benthos (excluding fish and plankton which are addressed separately in their report) are divided into three Focal Ecosystem Components (FECs): 1) macrofauna and megafauna, 2) macroalgae (coastal), and 3) meiofauna and microbes (Table 1). Macrofauna are defined as infauna > 1 cm and are always sampled by quantitative grab (Gill et al., 2011). Megafauna includes both sessile and motile epifauna > 1 cm (or larger than 4 mm, depending on the size of the semi-quantitative trawl net mesh used) (Gill et al., 2011) and so includes the same size fraction as the macrofauna. Table 2 shows the essential, recommended, and suggested gear, sampling scheme, and recommended sample analysis for macrofauna from the CBMP, while Table 3 provides the same information for megafauna. Only stations that sampled all FECs are considered CBMP monitoring stations, however other processed samples can serve monitoring purposes (e.g., monitoring of conservation areas) and so are included herein.

Table 1. Summary of the priority parameters and biodiversity indicators for three Focal Ecosystem Component (FEC) categories of the benthos. [Adapted from the CBMP (Gill et al., 2011).]

Category	FEC	Key Parameters	Indicators
Benthic fauna & microbes	Macrofauna & megafauna	- Abundance - Biomass (wet weight) - Species composition - Barcoding, other genomics	- Abundance; community composition - Biomass; community composition - Size-frequency distribution (for selected, mainly pan-Arctic species) - Diversity indices (e.g. Shannon, Simpson) - Distribution
Benthic fauna & microbes	Meiofauna & microbes	- Abundance - Biomass (wet weight) - Species composition - Barcoding, other genomics	- Abundance; community composition/structure - Biomass; community composition - Diversity indices (e.g. Shannon, Simpson) - Distribution
Benthic flora	Macroalgae	- Abundance - Biomass (wet weight) - Species composition - Barcoding, other genomics	- Abundance; community composition - Biomass; community composition - Diversity indices (e.g. Shannon, Simpson) - Distribution

Table 2. Essential, recommended, and suggested gear, sampling scheme, and sample analysis for macrofauna. [Adapted from the CBMP (Gill et al., 2011).]

	Essential	Recommended	Suggested
Gear	Small quantitative grabs (e.g., 0.1 m^2 Van Veen grab) for shelf and larger quantitative box cores for deeper sampling	Preserve subsamples in 95% non-denatured molecular-grade ethanol for barcoding and genomics	
Sampling scheme	3-5 replicate sediment grabs per station	Sediment chlorophyll	Information on other drivers (shipping, development, harvest)
	Station depth	Water column properties (salinity, temperature) from CTD casts	
	Grain size from visual categories or physical sampling	Water column chlorophyll (direct measurements or from satellite data)	
Sample analysis	Species-level detail desirable. Abundance counts and biomass (wet-weight, from preserved samples)	Genomics/barcoding to confirm identifications, and examine pan-Arctic distribution patterns	Size-frequency distribution of select target species of regional and/or pan-Arctic relevance
	Standardize sample abundance and biomass to 1 m^2		
	Vouchering of specimens, archiving of samples		

Table 3. Essential, recommended, and suggested gear, sampling scheme, and sample analysis for megafauna. [Adapted from the CBMP (Gill et al., 2011).]

	Essential	Recommended	Suggested
Gear	Semi-quantitative trawl types and associated gear metadata	Under-water imaging (video or still photography) transects to complement trawl samples Preserve subsamples in 95% non-denatured molecular-grade ethanol for barcoding and genomics	
Sampling scheme	One trawl per station Substrate type and grain size from visual inspection of trawl catch, from imagery, or from accompanying grab samples Station depth	Water properties (salinity, temperature) from CTD casts Water-column chlorophyll (either from direct measurements or from satellite data) Separate grab sample for quantitative grain-size determination	Information on other drivers (shipping, development, harvest) acquired from appropriate sources
Sample analysis	Species-level detail desirable. Abundance counts and biomass (wet-weight from fresh or preserved samples) Vouchering of specimens, archiving of samples	Genomics/barcoding to confirm identifications and examine pan-Arctic distribution patterns	Size-frequency distribution of select target species of regional and/or pan-Arctic relevance, invasive species, and species vulnerable to physical stress from trawling

The Arctic Ocean is affected by strong shelf-basin gradients with respect to biogeochemical processes (Monier et al., 2014; Coupel et al., 2015; Ardyna et al., 2014; Niemi et al., 2019). Primary production is typically higher near the coasts generally decreasing off shore (Gill et al., 2011). However, zones of upwelling and ocean currents can contribute to hotspots of productivity in offshore areas (Mundy et al., 2009; Tremblay et al., 2011, 2014, 2015). In particular, filter-feeding organisms, such as cold-water corals, benefit from strong currents which supply food and nutrients (Lim et al., 2020). The Arctic Marine Biodiversity Monitoring Plan identifies the need for sampling transects along gradients such as transition areas based on depth, fishing activity, ice cover, water masses and/or productivity, and specifically areas such as the ice edge and polynyas.

Establishment of CBMP Monitoring Sites in the Eastern Canadian Arctic

In support of its commitment to the Arctic Council, in 2012 and 2013 Fisheries and Oceans Canada (DFO) conducted benthic photo transects complemented by ship-based sediment and water column sampling in the eastern Canadian Arctic (Baffin Bay and the Davis Strait), following the methodology outlined in the CBMP (Baker et al., 2018). The first mission took place on board the CCGS *Henry Larsen* (mission code: LAR2012003) from 13 September to 15 October, 2012 with collaboration from the University of Quebec at Rimouski and Laval University. This mission undertook research as far north as Lancaster Sound. The second mission took place on board the CCGS *Hudson* from 23 August to 12 September, 2013 (mission code: HUD2013029) and was led by Natural Resources Canada (NRCan). It reached Pond Inlet, Baffin Island (Figure 1).

The surveys included two sites selected for long-term monitoring: the Disko Fan Conservation Area (DFCA) (Hiltz et al., 2018), and the Hatton Basin Conservation Area (HBCA), both subsequently designated as marine refuges by DFO and located in the Davis Strait (Figures 1, 2) and considered Ecologically and Biologically Significant Areas (DFO, 2011; Kenchington et al., 2011). Significant concentrations of cold-water corals and sponges have been found in these sites (DFO, 2010; Kenchington et al., 2010, 2018a) and conservation measures prohibit all bottom-contact fishing activities (Government of Canada, 2018), making them good candidates for monitoring the impacts of climate change.

Bottom-contact fishing was first restricted in the DFCA in 1998 to minimize impacts on food availability and winter habitat of narwhal (Hiltz et al., 2018). After the discovery of gorgonian corals in the area, the conservation objectives were expanded and the area was named the Narwhal Overwintering and Coldwater Coral Zone. A prohibition on all bottom-contact gear fishing for Greenland halibut was instituted in 2008. In 2017 the site was renamed the Disko Fan Conservation Area, with associated area-based fishing closures, contributing to Canada's Marine Conservation Targets. The DFCA is recognized as an important over-wintering habitat for narwhal (*Monodon monoceros*). This is supported by stable isotope, stomach content and diving behaviour analyses, which indicated the diet of narwhal is largely dependent on benthic organisms and habitats (Peklova et al., 2012; Laidre and Heide-Jørgensen, 2005; Laidre et al., 2003; Watt et al., 2013,

2015, 2017). Understanding the benthic habitats that support these higher trophic levels is a critical element in the protection and conservation of species such as narwhals.

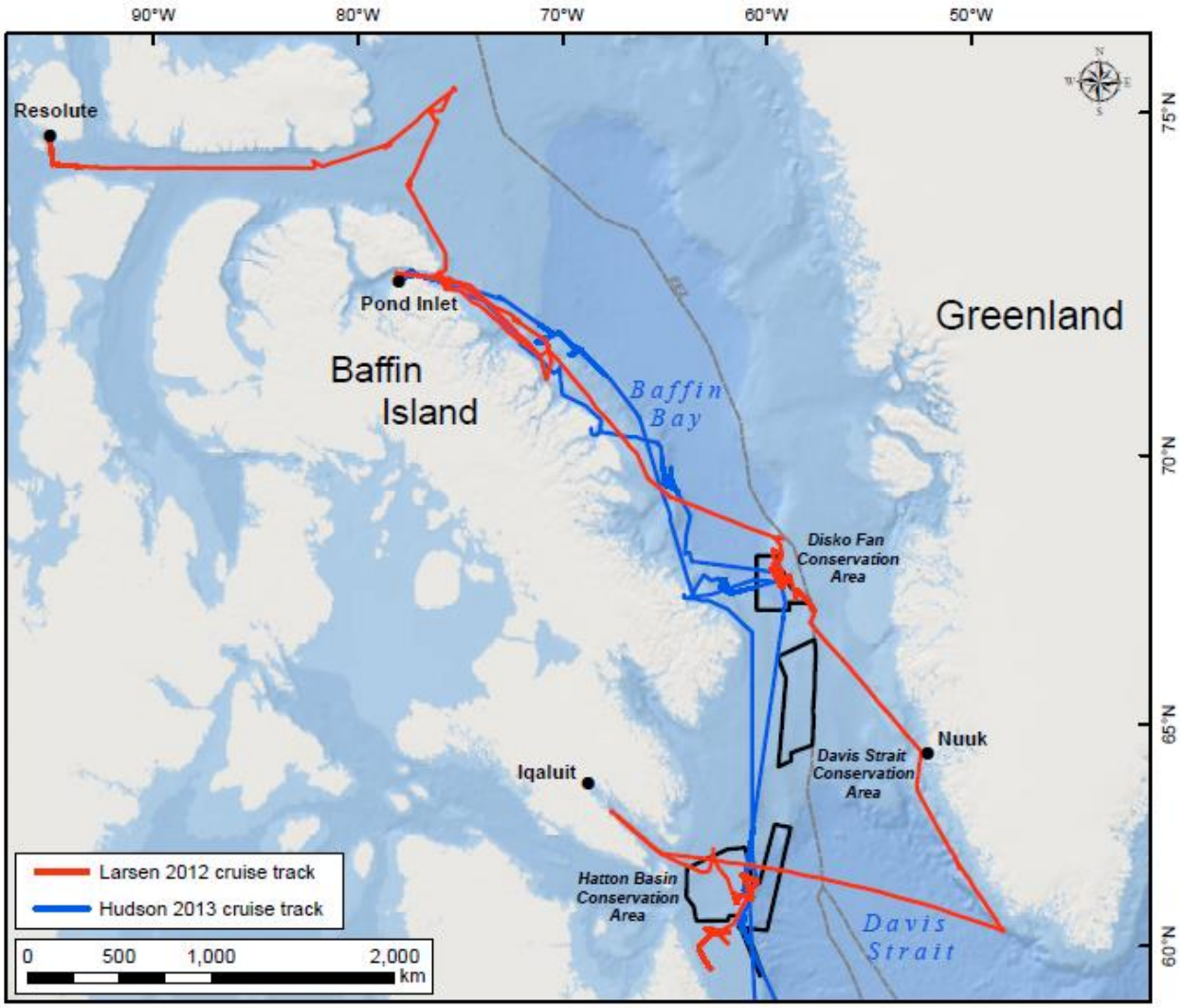


Figure 1. Cruise tracks of the CCGS *Henry Larsen* 2012 (red) and CCGS *Hudson* 2013 (blue) cruises carried out in the eastern Arctic. Closed areas (black outline) show the Disko Fan Conservation Area (DFCA), the Davis Strait Conservation Area, and Hatton Basin Conservation Area (HBCA).

Standardized biomass of sensitive benthic megafaunal species (large and small gorgonian corals, sea pens, large-sized sponges) estimated from DFO research vessel trawl surveys conducted throughout the region (in Canadian waters) were previously reported in Kenchington et al. (2016 and 2018a). Species distribution models produced from those data interpolate the probability of occurrence to unsampled areas (Beazley et al., 2016, 2019a; Murillo et al., 2018, 2019). Megafauna > 1 cm observed on the photo transects (Table 3) were previously described by Baker et al. (2018), and all photos and associated data are publicly available in an open access data repository

(Kenchington et al., 2018b) and on the CAFF Arctic Biodiversity Data Service data portal. Water depth and temperature were continuously recorded on the photo transects *in situ* using a SBE 39 temperature-pressure recorder attached to the 4K Camera system during deployment. Substrate type was determined for each transect by visual assessment of the photos, and categorized following a modified version of the Wentworth classification based on the relative proportions of mud, sand, and gravel (Baker et al., 2018).

Meiofauna and macrofauna, identified from sediment samples obtained from Van Veen grabs and box corers collected in 2012, are reported herein to complete the documentation of the FECs at the monitoring stations in the DFCA (Appendix A). Data on macrofauna from the HBCA are also summarized, although the meiofauna from that location have not been processed. Due to the general paucity of benthic data from this region we have also compiled and reported on unprocessed benthic samples collected from these cruises held at the Bedford Institute of Oceanography (BIO), Dartmouth, Nova Scotia (available upon request), largely from the HBCA, to facilitate future monitoring.

METHODS

SITE SELECTION

Two sites were considered suitable for the establishment of long-term monitoring stations in the eastern Canadian Arctic. Their selection was informed by knowledge of sponge and coral habitats through previous trawl surveys (Kenchington et al., 2010), and the desire to sample within and around the Narwhal Overwintering and Coldwater Coral Zone, and the Hatton Basin Voluntary Coral Protection Zone established by some of the shrimp fishing companies at the time. These zones were specifically highlighted as high priorities for benthic sampling by DFO managers.

In the DFCA, sampling stations included north-south and east-west gradients across the continental shelf, that included key transitions in fishing activity, ice cover, water masses, productivity, and depth strata: ~400 m and ~600 m (Figures 2, 3). Station BB1_C_400 m and BB1_D are just outside the DFCA boundaries and so serve as areas subject to differences in fishing pressure as suggested by Gill et al. (2011) (Table 2). In the HBCA stations DS1_T and DS1-Q lie just outside the boundary of the closed area and so also serve as comparative areas for monitoring fishing impacts. Tables 4 and 5 provide a summary of all of the stations sampled for sediment in 2012 and 2013, respectively, even though not all of them have been processed to date. While more samples were taken than have been processed, only those that have been processed for megafauna, macrofauna and foraminiferan meiofauna, with sufficient replication, are considered CBMP monitoring stations. In future, more CBMP monitoring stations may be added if the unprocessed samples and/or new samples are assessed for these FEC components.

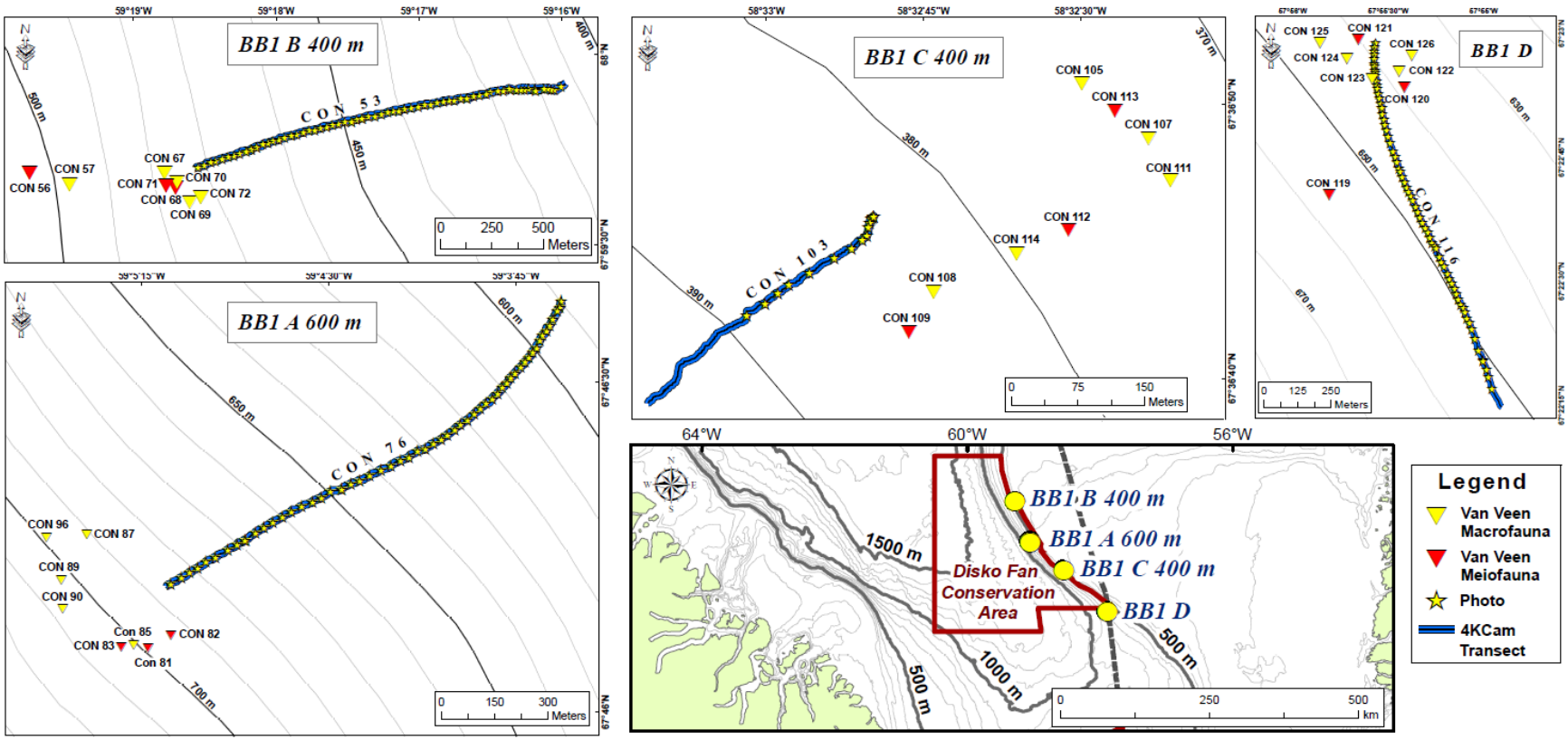


Figure 2. Four locations in or adjacent to the DFCA where sediment samples were collected along with the locations of associated photo transects. These four locations constitute the CBMP monitoring stations as all Focal Ecosystem Components (FEC) are processed. Consecutive Operation Numbers (Con) associated with all samples are indicated on each map and sediment samples are detailed in Table 4.

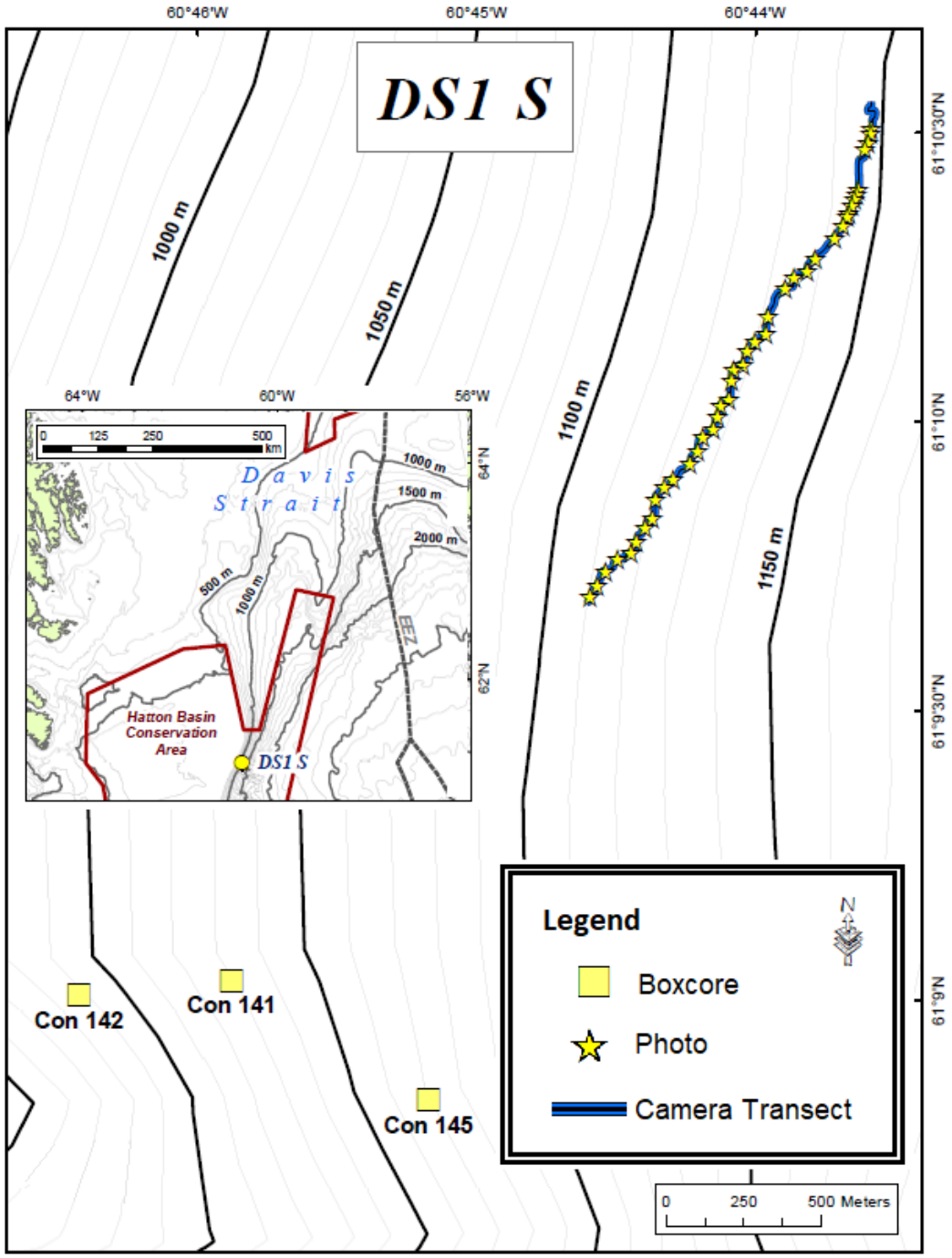


Figure 3. Box core sampling locations in the HBCA in relation to the location of the unprocessed photo transect. Samples from Consecutive Operation Numbers (Con) 141, 142 and 145 were processed for macrofauna in the 1-cm size fraction and further details are provided in Table 4. This location is considered a monitoring station for macrofauna, and data on other FEC have been collected and await processing. The inset shows its location within the HBCA.

Table 4. Details for benthic sediment samples details from the 2012 CCGS *Henry Larsen* mission. CON = Consecutive Operation Number. CBMP monitoring stations are shaded (all FEC processed). *Indicates biomass data for each unique taxon collected in the 1-cm size fraction, in addition to abundance. Subscript 'm' indicates that the sediments were sampled for meiofauna. All others were sampled for macrofauna.

Julien Day	Station	Site Location	CON	Operation	Latitude (decimal degrees)	Longitude (decimal degrees)	Depth (m)
270	BB1_B_400 m	DFCA	56	Van Veen$_m$	67.9939	-59.3280	506
270	BB1_B_400 m	DFCA	*57	Van Veen	67.9934	-59.3233	504
271	BB1_B_1000 m	DFCA	63	Van Veen$_m$	67.9727	-59.5264	940
271	BB1_B_400 m	DFCA	*67	Van Veen	67.9941	-59.3123	476
271	BB1_B_400 m	DFCA	68	Van Veen$_m$	67.9935	-59.3109	476
271	BB1_B_400 m	DFCA	*69	Van Veen	67.9929	-59.3092	476
271	BB1_B_400 m	DFCA	*70	Van Veen	67.9937	-59.3108	475
271	BB1_B_400 m	DFCA	71	Van Veen$_m$	67.9935	-59.3120	479
271	BB1_B_400 m	DFCA	*72	Van Veen	67.9931	-59.3080	473
272	BB1_A_600 m	DFCA	81	Van Veen$_m$	67.7679	-59.0862	700
272	BB1_A_600 m	DFCA	82	Van Veen$_m$	67.7683	-59.0847	699
272	BB1_A_600 m	DFCA	83	Van Veen$_m$	67.7679	-59.0880	705
273	BB1_A_600 m	DFCA	*85	Van Veen	67.7680	-59.0872	701
273	BB1_A_600 m	DFCA	*87	Van Veen	67.7707	-59.0905	696
273	BB1_A_600 m	DFCA	*89	Van Veen	67.7696	-59.0921	706
273	BB1_A_600 m	DFCA	*90	Van Veen	67.7688	-59.0920	710
273	BB1_A_600 m	DFCA	*96	Van Veen	67.7706	-59.0932	707
274	BB1_C_1000 m	DFCA	100	Box Corer$_m$	67.5265	-58.6119	1016
274	BB1_C_1000 m	DFCA	*101	Box Corer	67.5270	-58.6061	1010
274	BB1_C_400 m	DFCA	*105	Van Veen	67.6141	-58.5415	375
274	BB1_C_400 m	DFCA	*107	Van Veen	67.6135	-58.5397	376
274	BB1_C_400 m	DFCA	*108	Van Veen	67.6119	-58.5453	385
274	BB1_C_400 m	DFCA	109	Van Veen$_m$	67.6115	-58.5460	387
275	BB1_C_400 m	DFCA	*111	Van Veen	67.6131	-58.5391	372
275	BB1_C_400 m	DFCA	112	Van Veen$_m$	67.6126	-58.5418	377
275	BB1_C_400 m	DFCA	113	Van Veen$_m$	67.6138	-58.5406	376
275	BB1_C_400 m	DFCA	*114	Van Veen	67.6123	-58.5431	379
275	BB1_D	DFCA	119	Van Veen$_m$	67.3778	-57.9299	662
275	BB1_D	DFCA	120	Van Veen$_m$	67.3815	-57.9235	643
275	BB1_D	DFCA	121	Van Veen$_m$	67.3830	-57.9276	644
275	BB1_D	DFCA	*122	Van Veen	67.3820	-57.9240	644
275	BB1_D	DFCA	*123	Van Veen	67.3817	-57.9263	647
275	BB1_D	DFCA	*124	Van Veen	67.3824	-57.9285	648
275	BB1_D	DFCA	*125	Van Veen	67.3829	-57.9309	650
275	BB1_D	DFCA	*126	Van Veen	67.3825	-57.9229	642

Julien Day	Station	Site Location	CON	Operation	Latitude (decimal degrees)	Longitude (decimal degrees)	Depth (m)
283	DS1_S	HBCA	*141	Box Corer	61.1513	-60.7666	1051
283	DS1_S	HBCA	*142	Box Corer	61.1510	-60.7758	1012
283	DS1_S	HBCA	*145	Box Corer	61.1476	-60.7551	1093

Table 5. Details for benthic sediment samples collected during the 2013 CCGS *Hudson* mission. Station DS1_S was also sampled in 2012. The CBMP focal ecosystem components have been sampled with sufficient replication at stations DS1_I, DS1_G, DS1_S and DS1_Q (shaded) and they could, therefore, be confirmed as CBMP monitoring stations once the samples are processed. CON = Consecutive Operation Number. Subscript 'm' indicates that the sediments were sampled for meiofauna. *Station just outside HBCA boundary.

Julien Day	Station	Site Location	CON	Operation	Latitude (decimal degrees)	Longitude (decimal degrees)	Depth (m)
235	DS1_S	HBCA	8	Van Veen	61.2726	-60.8730	*552*
235	DS1_S	HBCA	9	Van Veen	61.2728	-60.8726	552
235	DS1_S	HBCA	13	Van Veen$_m$	61.2728	-60.8734	554
236	DS1_T*	HBCA	18	Van Veen	61.5391	-60.4891	1065
236	DS1_T*	HBCA	19	Van Veen	61.5391	-60.4887	1059
236	DS1_T*	HBCA	21	Van Veen	61.5392	-60.4888	1059
236	DS1_G	HBCA	25	Van Veen	61.6691	-61.1221	554
236	DS1_G	HBCA	26	Van Veen	61.6715	-61.1185	554
236	DS1_G	HBCA	28	Van Veen	61.6707	-61.1287	551
236	DS1_G	HBCA	29	Van Veen	61.6708	-61.1293	551
236	DS1_G	HBCA	31	Van Veen	61.6706	-61.1303	554
236	DS1_G	HBCA	32	Van Veen$_m$	61.6710	-61.1294	553
236	DS1_G	HBCA	33	Van Veen	61.6705	-61.1309	554
236	DS1_G	HBCA	34	Van Veen	61.6705	-61.1305	554
236	DS1_G	HBCA	35	Van Veen$_m$	61.6724	-61.1286	555
236	DS1_G	HBCA	36	Van Veen$_m$	61.6722	-61.1301	556
237	DS1_I	HBCA	39	Van Veen	61.3437	-61.1179	555
237	DS1_I	HBCA	41	Van Veen	61.3412	-61.1235	557
237	DS1_I	HBCA	42	Van Veen	61.3426	-61.1223	554
237	DS1_I	HBCA	43	Van Veen$_m$	61.3440	-61.1218	556
237	DS1_I	HBCA	46	Van Veen$_m$	61.3441	-61.1230	557
237	DS1_I	HBCA	50	Van Veen	61.3460	-61.1251	563
237	DS1_I	HBCA	51	Van Veen	61.3450	-61.1237	557
237	DS1_I	HBCA	53	Van Veen$_m$	61.3436	-61.1200	559
246	GSCA0068	Pond Inlet	76	Box Corer	72.8164	-77.4275	1068
247	GSCA0072	Scott Trough	80	Box Corer	71.3968	-70.1474	443
250	GSCA0078	Home Trough	86	Box Corer	68.3088	-63.7963	1147

Julien Day	Station	Site Location	CON	Operation	Latitude (decimal degrees)	Longitude (decimal degrees)	Depth (m)
251	GSCA0083	HBCA	91	Box Corer	67.7819	-59.5387	1338
253	DS1_T	HBCA	93	Van Veen$_m$	61.5384	-60.4814	1057
255	DS1_Q*	HBCA	105	Box Corer	60.6197	-61.3486	451
255	DS1_Q*	HBCA	106	Box Corer$_m$	60.6200	-61.3477	451
255	DS1_Q*	HBCA	107	Box Corer$_m$	60.6201	-61.3495	451
255	DS1_Q*	HBCA	108	Box Corer$_m$	60.6192	-61.3490	451
255	DS1_Q*	HBCA	109	Box Corer	60.6172	-61.3477	452
255	DS1_Q*	HBCA	110	Box Corer	60.6164	-61.3446	443
255	DS1_Q*	HBCA	111	Box Corer	60.6302	-61.3603	456
255	DS1_Q*	HBCA	112	Box Corer$_m$	60.6293	-61.3589	456
255	DS1_Q*	HBCA	113	Box Corer$_m$	60.6297	-61.3589	460
255	DS1_Q*	HBCA	115	Box Corer$_m$	60.6294	-61.3587	458
255	DS1_Q*	HBCA	116	Box Corer	60.6299	-61.3602	458
255	DS1_Q*	HBCA	117	Box Corer	60.6188	-61.3461	450

AT-SEA COLLECTION AND PROCESSING PROCEDURES

The at-sea collection and data processing procedures are described for each FEC below. Any deviations from the CAFF sampling protocols are highlighted. In general, initial examination of the macrofauna took place at sea and was followed up with more detailed review upon return to the Bedford Institute of Oceanography (BIO) in Dartmouth, Nova Scotia.

Macrofauna

Sediments containing macrofaunal organisms were sampled using either a mega-box corer or a Van Veen grab. The mega-box corer (Figure 4A) holds a 0.25 m^2 stainless steel sample box (50 × 50 cm) that has a maximum sediment penetration of 60 cm. The smaller Van Veen grab (Figure 4B) is capable of sampling 0.145 m^2 (15 × 15 in = 38.1 × 38.1 cm) from the sediment surface, and was typically used on coarser substrate which was not effectively sampled by the box corer.

Following the CAFF sampling scheme for macrofauna (Table 2), three to five replicate sediment samples per station were targeted (Tables 4, 5). Ship position (latitude and longitude) and total water column depth (m) were recorded from either the Regulus II or Aldebaran II ship navigation systems once a sample was taken.

Once the gear was retrieved and secured on deck, a photo was taken with a label to identify the station and Consecutive Operation Number (CON) to document the surface of the sediment. Any large and delicate megafauna or macrofauna were removed from the surface of the sample, and the sample was then shovelled into pre-measured buckets to calculate sediment volume. Any

megafaunal organisms present on the sediment surface or attached to rocks were also processed and included in the collections.

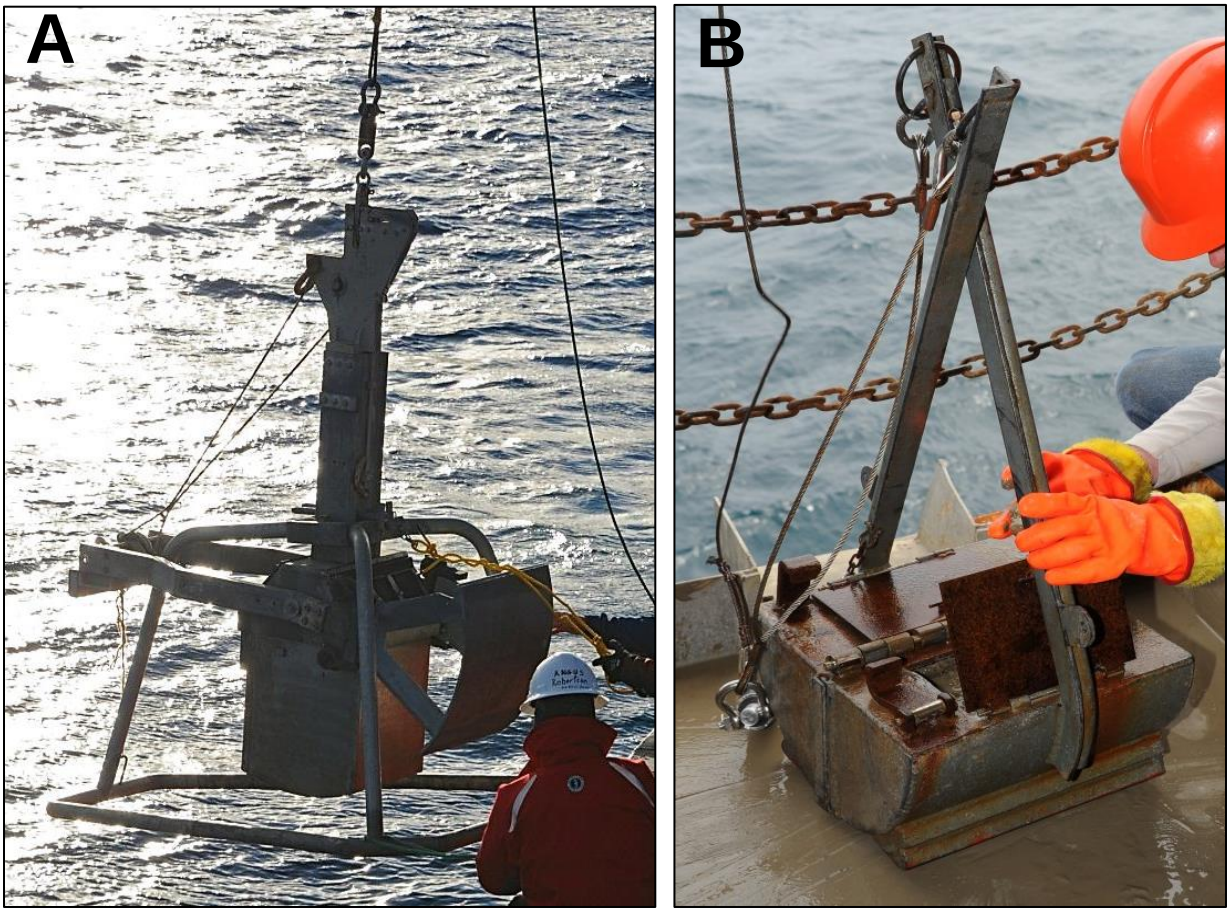


Figure 4. A) Mega-box corer and B) Van Veen grab systems used to collect sediment samples during the 2012 and 2013 DFO Arctic cruises.

Samples were washed onto a sieve table using a sea-water hose. Grain size was not visually assessed directly from these samples, as stated in the CBMP protocol, nor were surface subsamples collected from the grabs for future grain-size analysis. However, surficial sediment was qualitatively classified using the relative proportions of mud, sand, and gravel for each station based on the benthic imagery collected (Baker et al., 2018).

Washed sediment samples were then sorted using mesh sieves into three different size fractions (1 cm, 1 mm, and 0.5 mm) (Gill et al., 2011). The 1-mm and 0.5-mm size fractions were separately placed in a bucket and preserved in 10% formalin (4% formaldehyde buffered with sodium borate) for later taxonomic processing. The 1-cm size fraction was processed immediately when possible.

Some larger specimens (e.g., large sponges) were bagged and frozen. Encrusting fauna on rocks were also taxonomically assessed. Most specimens were preserved in 10% formalin, but some calcareous specimens (e.g., sponges and bryozoans) were preserved in 70% ethanol to prevent degradation of spicules and other features used for taxonomic identification.

All specimens from the 1-cm size fraction were identified to species when possible, or to the lowest practicable taxonomic classification. Those specimens which could not be fully identified were given morphotype designations at taxonomic levels where identifications were confirmed (e.g., Actiniaria sp. 1). Final taxonomic identifications were made by para-taxonomists at BIO (Dartmouth, Nova Scotia) upon return, with the aid of relevant taxonomic keys. The taxonomic authority used was the World Register of Marine Species (WoRMS). Identification of the specimens from the 1-mm and 0.5-mm size fractions has not been completed.

All specimens were counted for each taxon to obtain taxon abundance (Table 1). For colonial organisms each colony was counted. A unique collection number was assigned to each group of specimens identified as the same taxon, for a given sediment sample. Biomass was determined as the wet-weight (before or after preservation) of each taxon (Table 1) and recorded in milligrams for most samples (see Table 4). Encrusting taxa could not be weighed.

Abundance and biomass of each taxon was standardized to 1 m^2. Abundance, biomass, and other metadata collected during taxonomic processing were recorded in a Microsoft Access database. To aid in cataloging, all unique taxa in the 1-cm size fraction were photographed with a scale bar using a high-quality macro-photography system (Nikon D300), or a Nikon SMZ1500 stereomicroscope and attached Nikon DS-Ri1 camera for smaller specimens.

Sample processing and identification were completed for all of the specimens from the selected monitoring stations in the 1-cm size fraction in all samples collected in 2012. The remaining samples, primarily from the HBSC, are stored at the Bedford Institute of Oceanography, pending funding and/or capacity for further analysis.

Size Frequency Distributions

Protocols were established prior to going to sea for the measurement of snow crabs, ophiuroids and bivalves for the "size-frequency distribution indicator for selected pan-Arctic species" (Tables 2, 3) following Gill et al. (2011). All measurements were to be recorded using electronic calipers in millimeters to two decimal places. For the ophiuroids, the largest diameter across the central disc was to be recorded. Three measurements were to be recorded for bivalves: 1) length, measured as the greatest distance from the anterior to the posterior end of the shell, 2) width, the distance between the furthest expansion of the left and right valves when the shell is closed, and 3) height, the maximum distance between the dorsal and ventral edges of the shell.

DNA Sequencing and Barcoding

Specimens in the 1-cm size fraction were processed for DNA sequencing as soon after collection as possible. Typically, one specimen per unique taxon per location (e.g., DFCA) was preserved for sequencing purposes. Samples requiring sequencing were immediately given a temporary identification and photographed. Tissue was subsampled when possible and preserved in 95% non-denatured ethanol, which was changed after 24 hours. Specimens sampled for genetics were assigned a unique number (GEN#) which was entered into the collection database.

Genomic DNA was extracted from samples preserved in 95% ethanol using a DNeasy®Tissue Kit (Qiagen) following the manufacture's protocol, then PCR –amplified with one of the following primer pairs: ITS2.2 5'-CCT GGT TAG TTT CTT TTC CTC CGC-3' and RA2 5'-GTC CCT GCC CTT TGT ACA CA-3' to obtain internal transcribe spacer regions ITS1 and ITS2 (Wörheide, 1998), HCO2198 5'-TAA ACT TCA GGG TGA CCA AAA AAT CA-3' and LCO1490 5'-GGT CAA CAA ATC ATA AAG ATA TTG G-3' (Folmer et al., 1994) or dgHCO 5'-TAA ACT TCA GGG TGA CCA AAR AAY CA-3' and dgLCO 5'-GGT CAA CAA ATC ATA AAG AYA TYG G-3' (Meyer, 2003) to obtain a fragment of the mitochondrial cytochrome oxidase subunit I gene. PCR products were purified using standard protocols and sent for Sanger DNA sequencing at Genewiz Inc., NJ. Good quality sequences were searched using the BLAST (https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE_TYPE=BlastSearch) search engine for closest matches in the NCBI database.

Meiofauna

Sediment subsamples were taken from three box corers or Van Veen grabs per station (Tables 4, 5) that were dedicated solely to meiofauna sampling (i.e. not used for macrofauna). From each of those sediment samples, seven subsamples of the sediment surface were collected by injecting a 60 ml modified syringe (needle end cut off to expose the full bore of the syringe) into the top of the sample (preferably in an undisturbed section and evenly distributed). A 5 cc portion of the surface sediment layer was extracted and the top centimeter of sediment placed into a plastic container. From those seven sediment subsamples, three were fixed in 10% formalin for general taxonomy, three were fixed in 70% ethanol for taxonomy of calcareous organisms such as foraminiferans, and one was frozen at -20ºC for DNA analysis (not performed).

Identification of the foraminiferans was achieved for stations BB1_A_600 m, BB1_B_400 m, BB1_C_400 m, and BB1_D. None of the 2013 samples (Table 5) were processed (14 × 3 replicates) along with CON 63 and 100 from 2012; only 1 of 3 replicates was processed for sediment samples taken from CONs 56, 68, 81, 82, 83, 109, 112, 113, 120, 121 (Table 4). Nematodes and other non-foraminiferan meiofauna were not identified.

Tubular species commonly found in the > 250-µm size fraction including *Rhabdammina* spp. and *Hyperammina* spp. were often found fragmented. Most fragments were recognizable, however,

when in doubt the fragment was tabulated as *Rhabdammina*/*Hyperammina* spp. Each fragment was counted as one individual, which likely exaggerated their total numbers. Also, certain agglutinated species of foraminifera are segmented and therefore the grouping "agglutinated fragment/unknown" was added to the taxon list.

Some calcareous species were classified as "reworked" and counted separately. These reworked specimens were identified as thick and robust, dark, and often eroded and/or broken, which appeared quite different from their thin and fragile counterparts. Unfortunately there are no guidelines for classifying specimens as reworked and therefore tabulation was done in a discretionary manner.

Many samples contained diatoms and sponge spicules but those were not tabulated. Sponge spicules were also used in the constructing the tests made by the agglutinated foraminiferan *Saccorhiza ramosa*.

DATA ANALYSES

Indices of species diversity, richness and evenness were calculated from the standardized abundance data for the 1-cm size fraction and meiofauna according to the CBMP protocol (Table 1) using the software Primer 7.0 (Clarke and Gorley, 2015). Each of the indices calculated describes a different facet of the community: Margalef Species Richness (d) incorporates the number of individuals in the index corrected for sampling effort. Pielou's Evenness, J′, is a measure of equitability calculated on the basis of the ratio of Shannon Diversity divided by the maximum possible value of Shannon Diversity if all species were equally numerous. The Shannon Diversity index, H′, was calculated based on the natural logarithm, and is sensitive to the level of sampling effort, therefore, caution is advised when comparing DS1_S station (three samples) and BB1 stations (five samples per station; except BB1_C_1000 m). Simpson's Index is the probability that any two individuals from a sample chosen at random would be from the same species. ANOVA tests, assessed at $\alpha = 0.05$, were performed on each diversity index testing for differences among all stations and among DFCA stations (except BB1_C_1000 m). For significant ANOVA tests, Student *t* tests were performed on each pair of stations to identify stations contributing to the difference. Retrospective power analyses ($\alpha = 0.05$) were conducted when the null hypotheses failed to be rejected, to assess whether the lack of statistical significance could be the result of low sample size. Values for the least significant number (LSN) of samples were also estimated. LSN is the number of samples needed to reduce the variance of the estimates enough to achieve a significant result for a given α, effect size and root mean square error. These tests will inform future sampling efforts. ANOVAs and *t*-tests were performed with JMP 15. 1.0 software (SAS Institute Inc., Cary, North Carolina, USA).

Shade plots (Clarke et al., 2014) were constructed from the standardized data to aid in selecting the type of data transformation. Untransformed, square-root and log(x+1)-transformed data were reviewed for both abundance and biomass data. Colouring in the shade plots gradate in linear proportion to abundance/biomass, with white space denoting absence of a taxon. Transformed

standardized abundance/biomass data were used to construct a Bray-Curtis similarity matrix between samples. This matrix was used to perform cluster and non-multidimensional scaling (nMDS) analyses. Unweighted pair-group method with arithmetic mean (UPGMA) clustering was performed using a Type 1 similarity profile test (SIMPROF) with 999 permutations within variables testing the null hypothesis of no multivariate structure. The SIMPROF test provides stopping rules for the clustering algorithm (Clarke et al., 2008), and significance was determined at $\alpha = 0.05$. Analysis of similarity (ANOSIM) was used to test the null hypothesis of no difference in macrofaunal communities among stations followed by pairwise tests between every pair of stations. For meiofauna, similarity matrices were constructed using all individual sediment samples (N = 16) and using averaged abundance data for the two sediment samples that had three replicates (N = 12). The latter were used to construct the UPGMA dendrograms, nMDS ordination and ANOSIM tests. A similar analytical approach was followed to look at the relationship between taxa. Transformed standardized abundance data from the 1-cm size fraction for macrofauna were used to construct a Bray-Curtis similarity matrix between taxa that were present in five or more of the 24 samples (> 20%) in order to examine taxon associations. For meiofaunal species the variable selection was based on presence in five or more of the 12 samples (> 41%). The matrices were each clustered using the UPGMA algorithm and SIMPROF test. Cophenetic correlations were calculated for all cluster analyses to evaluate whether the dendrograms were a good representation of the similarity matrices. All analyses were performed in Primer 7.0.

Environmental Gradients

In addition to the data directly collected at the time of sampling, a wide range of abiotic factors used in species distribution modeling in this region (Beazley et al., 2016) and published in an open access data repository (Beazley et al., 2019a; Beazley et al., 2019b) were used to characterize the stations and act as covariates in some analyses. Interpolated environmental variables based on modelled data (Beazley et al., 2018) were linked to the data from the sediment samples based on geolocation. Modelled environmental variables were utilized to compare sample locations with respect to likely drivers of community assemblage and diversity and included mean depth (m), mean bottom salinity, mean spring ice cover (% ice cover, Julian Days 91 – 181, 1° grid cell), mean bottom temperature (°C), mean spring chlorophyl *a* concentration (mg m^{-3}), mean bottom current (m s^{-1}) and mean annual primary production (mg C m^{-2} day^{-1}).

Environmental variables from each of the five DFCA stations were normalized by subtracting the mean and dividing by the standard deviation for each variable. Only the DFCA stations were analyzed as they underwent a similar level of taxonomic scrutiny. Euclidean distances between pairs of stations were calculated from the normalized data and a UPGMA cluster analysis with SIMPROF test was performed. A principal components analysis was used to ordinate the stations and the loadings of the environmental variables on each of the first two PCA axes were used to assess the degree to which the stations differed environmentally across all variables. All of these analyses were performed in Primer 7.0. Linear regressions between depth and the diversity indices

for each sample shown in Appendix C were calculated with 95% confidence intervals with JMP software. Equations for significant regressions were presented.

RESULTS

The sampling details for all of the sediments that were successfully processed are provided in Table 6. In total 36 independent sediment samples were fully processed, 24 for macrofauna in the 1-cm size fraction, and 12 for meiofauna. Replicate samples were taken from two of the samples processed for meiofauna.

MACROFAUNA 1-CM SIZE FRACTION

Diversity Indices

In total, 101 taxa were identified from 24 sediment samples collected from six stations (BB1_A_600 m, BB1_B_400 m, BB1_C_1000 m, BB1_C_400 m, BB1_D, and DS1_S) in the DFCA and HBCA (Appendix B). Those taxa were drawn from 12 phyla (Annelida, Arthropoda, Brachiopoda, Bryozoa, Chordata, Cnidaria, Echinodermata, Mollusca, Nemertea, Platyhelminthes, Porifera, and Sipuncula) and 51 families, with the Annelida being the most diverse, followed by the Porifera, Echinodermata and Bryozoa (Figure 5). The diversity indices for each sample are provided in Appendix C with averaged data for the number of taxa (S), total abundance (N) and biomass (B) per m^2, Margalef's Species Richness (d), Pielou's Evenness (J′), Shannon Diversity (H′) and Simpson's Index summarized by station in Table 7. BB1_C_1000 m did not have replicate samples and so does not meet the standards for CBMP monitoring stations; it is only included for comparison with the other values given that it comes from the deepest sample (1010 m) (Table 7).

Both the Porifera and Bryozoa likely contain more diversity in the 1-cm size fraction than identified here, as only 16% of the former and none of the later were identified to species. Cnidarians were also poorly identified with only 9% identified to species. Annelida had the highest identification success with 52% identified to species and 81% to genus (Appendix B). Additionally, data from station DS1_S in the HBCA underestimate diversity as the samples were not given the same level of scrutiny in the lab. This is particularly true for the Bryozoa but applies to other taxa as well. As a result the taxa are mutually exclusive among the BB1 samples and among the DS1_S samples but not between the two sites (DFCA and HBCA). Despite this, the DS1_S station was the most diverse (Table 7). ANOVA found significant differences in S and N among stations within DFCA (Appendix C), with BB1_C_400 m having a greater mean number of species (S) and larger mean abundance/m^2 (N) than the other DFCA stations. Power for non-significant tests was low, ranging from 0.14 to 0.47 with very large sample sizes estimated to detect significant effects (29 to 99 samples) (Appendix C). When stations from the HBCA were included in the ANOVA, significant differences were found in B, S, N, d and J′ (Table 7, Appendix C). HBCA station DS1_S had significantly higher values for S, B, N and d and significantly lower

values for J′ compared to the other stations, except with BB1_C_400 m which did not differ from DS1_S in S and N, also being higher than the other DFCA stations.

Community Similarity Based on Abundance

After examining shade plots showing the effect of square-root and log(x+1) transformations (Appendix D) the standardized abundance data were log(x+1)-transformed, resulting in an increase in the importance of less abundant taxa.

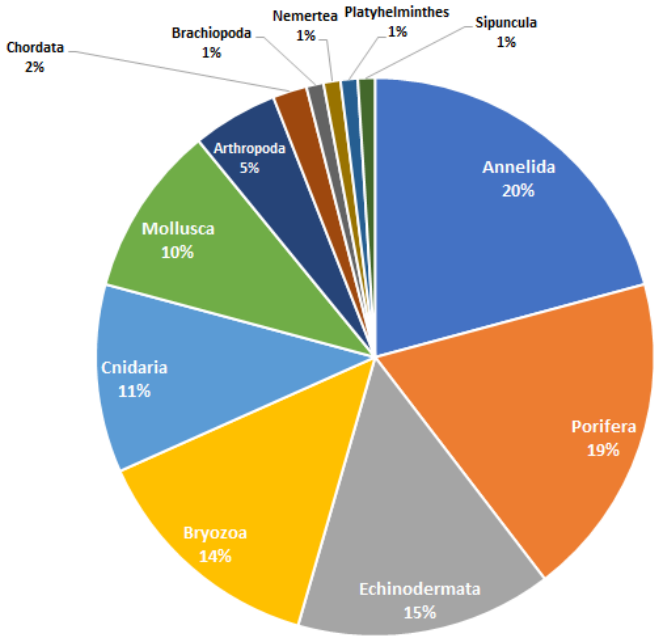


Figure 5. Proportion of macrofaunal taxa > 1 cm by phylum identified from sediment samples taken from biodiversity monitoring stations in the Disko Fan and Hatton Basin Conservation Areas. The total number of taxa (S) over all stations was 101.

The dendrogram of samples clustered according to their Bray-Curtis similarity (Appendix E) had a cophenetic correlation of 0.83 and showed that the macrofaunal communities in the HBCA samples (station DS1_S) are significantly different from those in the DFCA (Figure 6). There is a tendency for samples from the same station to group together within the DFCA stations, but those from BB1_C_400 m are significantly different from the others (Figure 6). Station BB1_B_400 m is the most diverse spreading across three cluster groups (Figure 6). This same pattern is visualized in the nMDS plot with the similarity of the samples from each station shown (Figure 7). The highest similarity between samples was 68.1%, for samples from CON 124 and CON 122 (BB1_D). Of the 276 pairwise similarities, 121 (44%) had no similarity between samples (Bray-Curtis Similarity = 0.0). ANOSIM found that the macrofaunal communities were significantly different among stations (Global R: 0.651; P = 0.001), with nine pairs of stations having significantly different species compositions (Table 8). However, adjusting the P-value to account for multiple testing (P = 0.003) would discount those differences.

Table 6. Details of sediment sampling locations and fully processed focal ecosystem component identifications reported herein.

Julien Day	Station	Site Location	CON	Sampling Gear	Latitude (decimal degrees)	Longitude (decimal degrees)	Depth (m)	Meiofauna Abundance	Macrofauna Abundance (1-cm Size Fraction)	Macrofauna Biomass (1-cm Size Fraction)
270	BB1_B_400 m	DFCA	56	Van Veen	67.9939	-59.3280	506	x		
270	BB1_B_400 m	DFCA	57	Van Veen	67.9934	-59.3233	504		x	x
271	BB1_B_400 m	DFCA	67	Van Veen	67.9941	-59.3123	476		x	x
271	BB1_B_400 m	DFCA	68	Van Veen	67.9935	-59.3109	476	x		
271	BB1_B_400 m	DFCA	69	Van Veen	67.9929	-59.3092	476		x	x
271	BB1_B_400 m	DFCA	70	Van Veen	67.9937	-59.3108	475		x	x
271	BB1_B_400 m	DFCA	71	Van Veen	67.9935	-59.3120	479	x		
271	BB1_B_400 m	DFCA	72	Van Veen	67.9931	-59.3080	473		x	x
272	BB1_A_600 m	DFCA	81	Van Veen	67.7679	-59.0862	700	x		
272	BB1_A_600 m	DFCA	82	Van Veen	67.7683	-59.0847	699	x		
272	BB1_A_600 m	DFCA	83	Van Veen	67.7679	-59.0880	705	x		
273	BB1_A_600 m	DFCA	85	Van Veen	67.7680	-59.0872	701		x	x
273	BB1_A_600 m	DFCA	87	Van Veen	67.7707	-59.0905	696		x	x
273	BB1_A_600 m	DFCA	89	Van Veen	67.7696	-59.0921	706		x	x
273	BB1_A_600 m	DFCA	90	Van Veen	67.7688	-59.0920	710		x	x
273	BB1_A_600 m	DFCA	96	Van Veen	67.7706	-59.0932	707		x	x
274	BB1_C_1000 m	DFCA	101	Box Corer	67.5270	-58.6061	1010		x	x
274	BB1_C_400 m	DFCA	105	Van Veen	67.6141	-58.5415	375		x	x
274	BB1_C_400 m	DFCA	107	Van Veen	67.6135	-58.5397	376		x	x
274	BB1_C_400 m	DFCA	108	Van Veen	67.6119	-58.5453	385		x	x
274	BB1_C_400 m	DFCA	109	Van Veen	67.6115	-58.5460	387	x		
275	BB1_C_400 m	DFCA	111	Van Veen	67.6131	-58.5391	372		x	x
275	BB1_C_400 m	DFCA	112	Van Veen	67.6126	-58.5418	377	x		
275	BB1_C_400 m	DFCA	113	Van Veen	67.6138	-58.5406	376	x		

Julien Day	Station	Site Location	CON	Sampling Gear	Latitude (decimal degrees)	Longitude (decimal degrees)	Depth (m)	Meiofauna Abundance	Macrofauna Abundance (1-cm Size Fraction)	Macrofauna Biomass (1-cm Size Fraction)
275	BB1_C_400 m	DFCA	114	Van Veen	67.6123	-58.5431	379		x	x
275	BB1_D	DFCA	119	Van Veen	67.3778	-57.9299	662	x		
275	BB1_D	DFCA	120	Van Veen	67.3815	-57.9235	643	x		
275	BB1_D	DFCA	121	Van Veen	67.3830	-57.9276	644	x		
275	BB1_D	DFCA	122	Van Veen	67.382	-57.9240	644		x	x
275	BB1_D	DFCA	123	Van Veen	67.3817	-57.9263	647		x	x
275	BB1_D	DFCA	124	Van Veen	67.3824	-57.9285	648		x	x
275	BB1_D	DFCA	125	Van Veen	67.3829	-57.9309	650		x	x
275	BB1_D	DFCA	126	Van Veen	67.3825	-57.9229	642		x	x
283	DS1_S	HBCA	141	Box Corer	61.1513	-60.7666	1051		x	x
283	DS1_S	HBCA	142	Box Corer	61.1510	-60.7758	1012		x	x
283	DS1_S	HBCA	145	Box Corer	61.1476	-60.7551	1093		x	x

Table 7. Mean ± standard deviation of depth, number of taxa (S), abundance (N), biomass (B), Margalef's Species Richness (d), Pielou's Evenness (J′), Shannon Diversity (H′) and Simpson's Index for macrofauna in the > 1-cm size fraction for each biodiversity monitoring station. Stations of similar depth are shown together. *Does not meet the criteria for the CBMP due to insufficient replication (Table 4).

Site	Station	Depth (m)	S	N (no./m^2)	B (mg/m^2)	d	J′	H′	Simpson's Index
DFCA	BB1_B_400 m	480 ± 13	6.0 ± 4.3	42.8 ± 29.0	13883 ± 11024	1.24 ± 0.97	0.99 ± 0.02	1.48 ± 0.97	0.67 ± 0.38
DFCA	BB1_C_400 m	377.4 ± 4.9	14.4 ± 7.4	412.4 ± 425.7	90637 ± 139458	2.37 ± 1.12	0.88 ± 0.14	2.14 ± 0.67	0.84 ± 0.10
DFCA	BB1_A_600 m	704 ± 5.5	5.2 ± 2.3	40 ± 14.1	22331 ± 31060	1.12 ± 0.52	0.97 ± 0.03	1.53 ± 0.48	0.77 ± 0.12
DFCA	BB1_D	646.2 ± 3.2	6.4 ± 1.7	59.3 ± 24.1	23411 ± 30834	1.33 ± 0.30	0.96 ± 0.05	1.76 ± 0.26	0.83 ± 0.06
HBCA	DS1_S	1052 ± 40.5	19 ± 2.6	478.7 ± 342.7	282698 ± 298407	3.00 ± 0.34	0.64 ± 0.26	1.88 ± 0.73	0.69 ± 0.27
DFCA	BB1_C_1000 m*	1010	6	69	5212	1.18	0.90	1.61	0.77

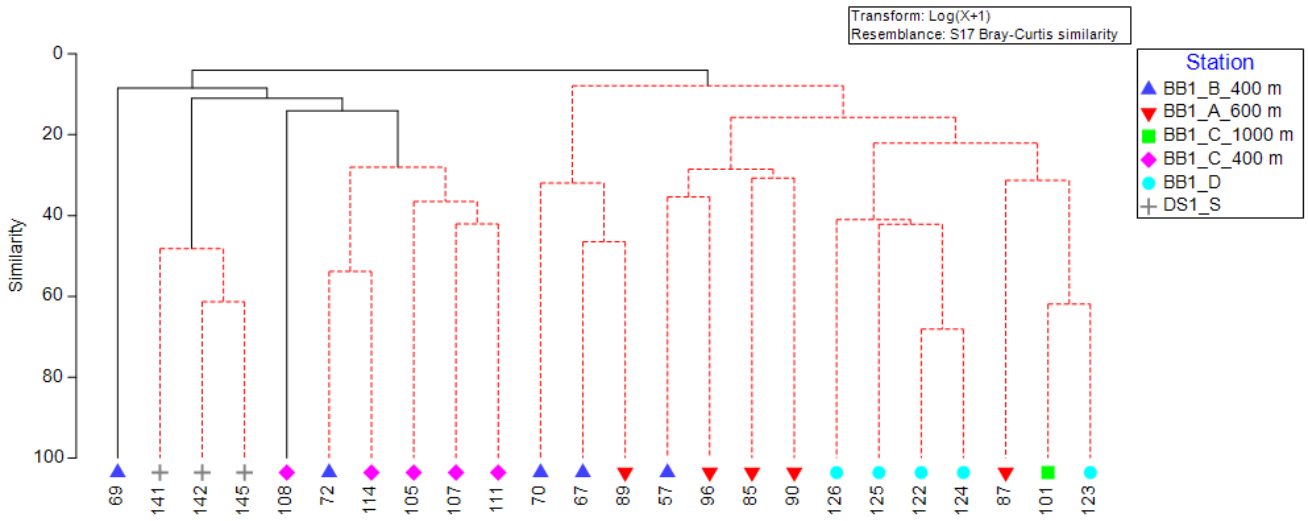


Figure 6. Unweighted group-average (UPGMA) cluster analysis of macrofaunal communities (1-cm size fraction) based on Bray-Curtis similarity of log(x+1)-transformed standardized abundance. Significant clusters ($\alpha = 0.05$) assessed through 999 permutations are shown in red. Samples are labelled by CON (Consecutive Operation Number) and colour-coded by station (see Table 4).

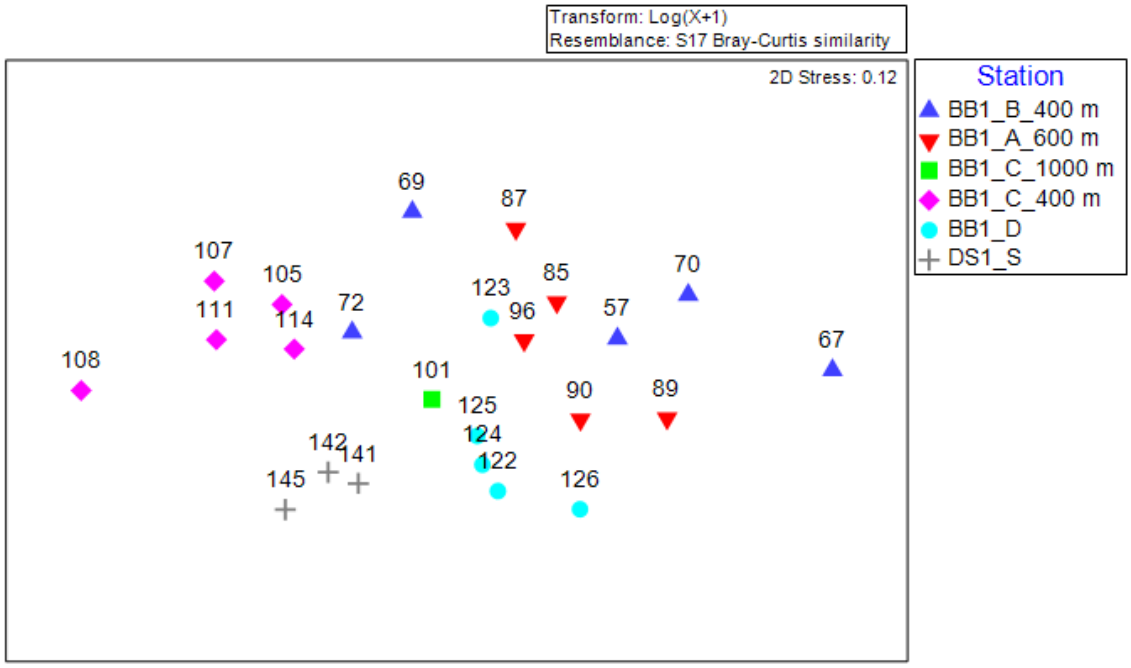


Figure 7. Non-metric multidimensional scaling analysis (nMDS) of macrofaunal communities (1-cm size fraction) based on Bray-Curtis similarity of log(x+1)-transformed standardized abundance. Samples are labelled by CON (Consecutive Operation Number) (Table 4) and colour-coded by station.

Table 8. Analysis of Similarities (ANOSIM) pairwise significance tests based on Bray-Curtis similarity calculated from log(x+1)-transformed macrofaunal abundance (1-cm size fraction). *Indicates pairs of stations with significantly different species compositions ($\alpha = 0.05$).

Groups	R Statistic	P
BB1_B_400 m, BB1_A_600 m	0.236	6.3
BB1_B_400 m, BB1_C_1000 m	0.440	16.7
BB1_B_400 m, BB1_C_400 m*	0.550	0.8
BB1_B_400 m, BB1_D*	0.678	0.8
BB1_B_400 m, DS1_S*	0.518	3.6
BB1_A_600 m, BB1_C_1000 m	0.640	16.7
BB1_A_600 m, BB1_C_400 m*	0.896	0.8
BB1_A_600 m, BB1_D*	0.502	3.2
BB1_A_600 m, DS1_S*	0.744	1.8
BB1_C_1000 m, BB1_C_400 m	0.840	16.7
BB1_C_1000 m, BB1_D	-0.080	66.7
BB1_C_1000 m, DS1_S	1.000	25.0
BB1_C_400 m, BB1_D*	0.952	0.8
BB1_C_400 m, DS1_S*	0.908	1.8
BB1_D, DS1_S*	0.990	1.8

Numerically, Bryozoa dominated the samples (measured as individual colonies) with 56% of the standardized 4277.4 counts drawn from that phylum. Following the Bryozoa, were Annelida (polychaetes), Porifera, Mollusca and Cnidaria (Figure 8). The mean abundance/m^2 of macrofauna > 1 cm varied by an order of magnitude among stations (Table 7). Stations BB1_C_400 m and DS1_S had the highest total standardized abundances with large numbers of bryozoan colonies accounting for much of their difference from the other stations (Figure 9). The most abundant individual taxa were Bryozoa spp., Bryozoa Cyclostomatida sp. 1, Bryozoa Flustrina sp. 1, Anthozoa spp. and Bryozoa Cyclostomatida sp. 3, together accounting for 48.8% of total standardized abundance (Appendix F). The most abundant of the Annelida was the bamboo worm, *Nicomache* (*Loxochona*) *quadrispinata*, while 46 other taxa were only recorded once (Appendix F). The full data matrix of the standardized abundance (number/m^2) of the 101 taxa × 24 samples is provided in Appendix G.

The variability among replicates within stations visualized in the nMDS plot (Figure 7) is illustrated in Figure 10 where large differences in the replicates at station BB1_C_400 m and in station DS1_S, created largely by differences in the numbers of Bryozoa colonies, are shown.

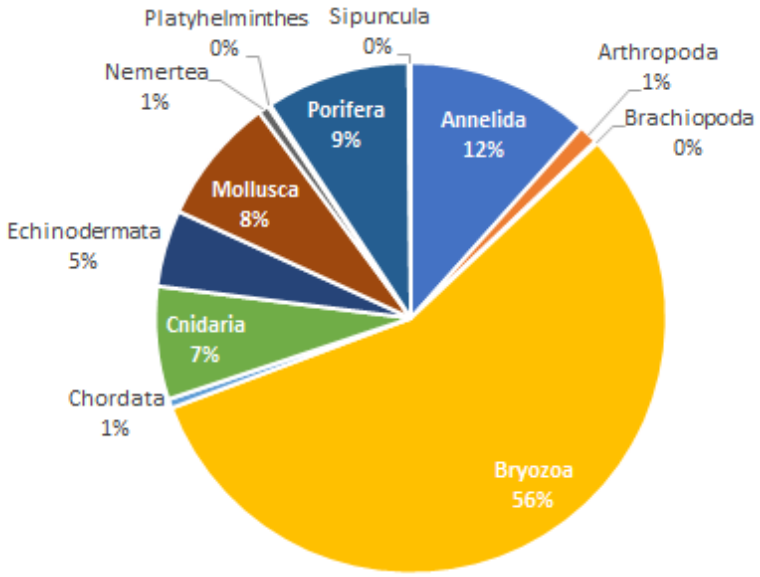


Figure 8. Proportion of total abundance by phylum identified from macrofaunal taxa > 1 cm recorded from the 24 sediment samples taken from the biodiversity monitoring stations in the Disko Fan and Hatton Basin Conservation Areas, eastern Canadian Arctic. The total number of individuals recorded after standardization was 4277.4.

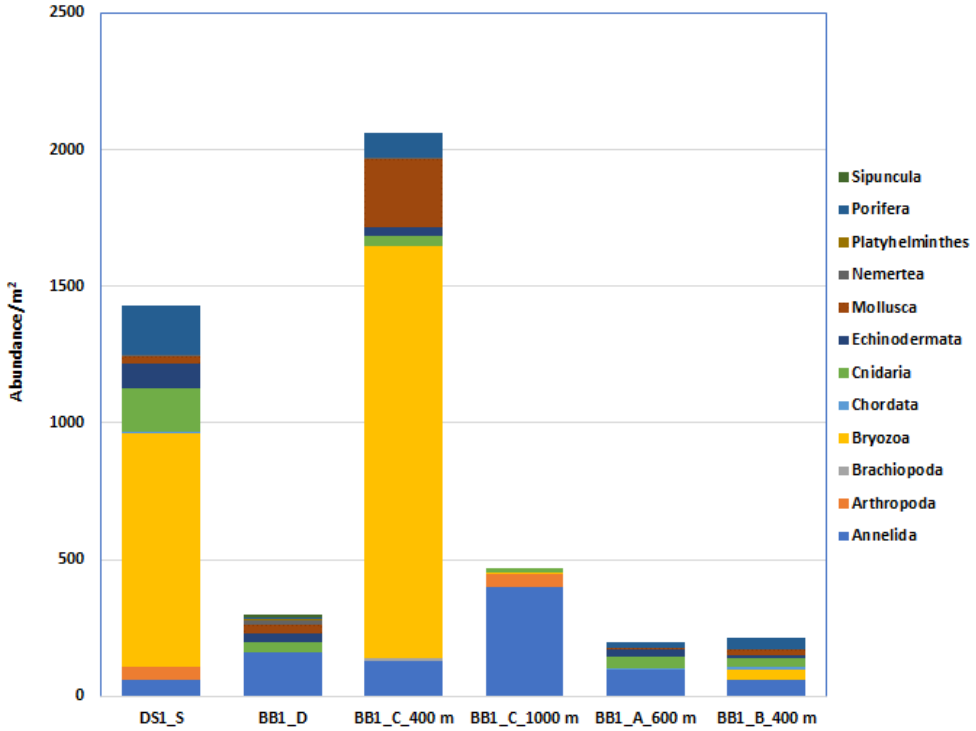


Figure 9. Total abundance/m^2 by phylum identified from macrofaunal taxa > 1 cm recorded from each of the biodiversity monitoring stations in the Disko Fan and Hatton Basin Conservation Areas, eastern Canadian Arctic. The total number of individuals recorded after standardization was 4277.4. Phyla colours in the bars follow the vertical order in the legend.

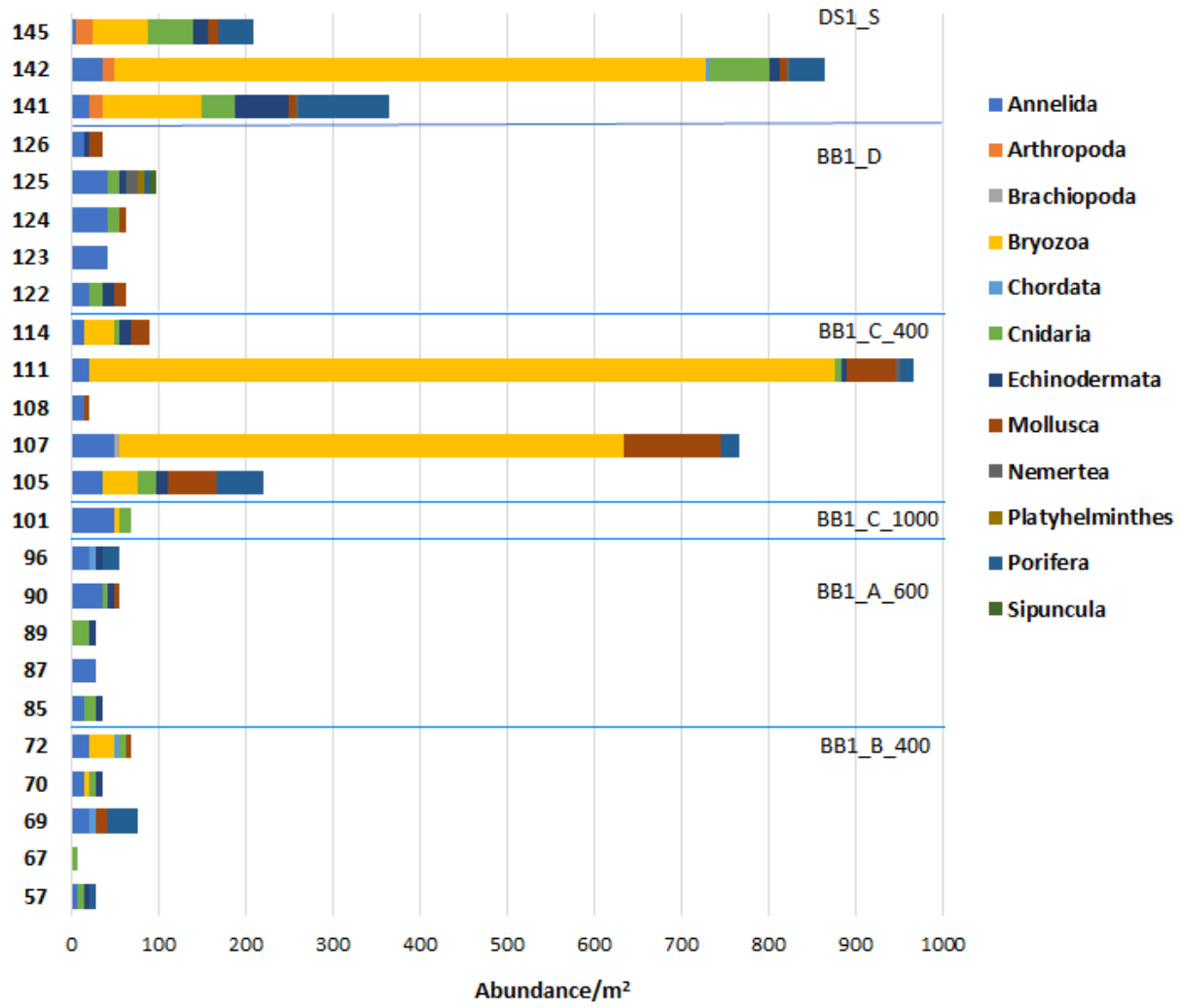


Figure 10. Total abundance/m^2 by phylum identified from macrofaunal taxa > 1 cm recorded from each of the 24 samples drawn from the biodiversity monitoring stations in the Disko Fan and Hatton Basin Conservation Areas, eastern Canadian Arctic. Blue lines separate the replicates within each station, with station name to the upper right of each group.

Twelve taxa occurred in at least 5 of the 24 samples (> 20%) and so were examined for associations between them (Figure 11). Cophenetic correlation was 0.84 indicating that the dendrogram is a very good representation of the similarity matrix. The SIMPROF test applied to the UPGMA cluster identified two significant groupings with the greatest similarity between taxa shown between two bryozoans.

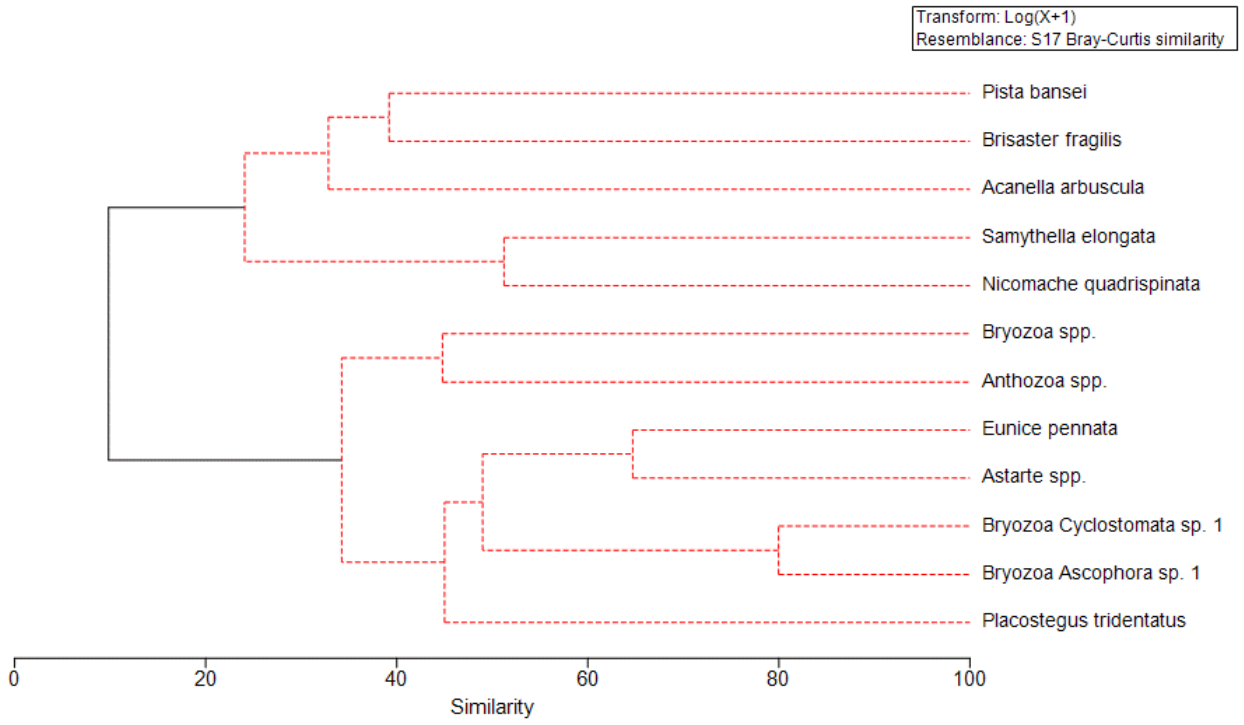


Figure 11. Unweighted group-average cluster analysis (UPGMA) of macrofaunal taxa (1-cm size fraction) based on Bray-Curtis similarity of log(x+1)-transformed standardized abundance. Significant clusters ($\alpha = 0.05$) assessed through 999 permutations are shown in red. Only taxa that occurred in 5 or more samples were included in the analyses.

Environmental Relationships

The mean values for the variables used in the PCA are shown in Table 9. Stations BBI_C_400 m and BB1_D have higher mean bottom temperatures than the other stations. Although not included in the multivariate analyses, the HBCA station DS1_S although deeper is much warmer and more productive than the DFCA stations. The first principal component axis (PCA) accounted for 61.6% of the variation and the second for 25.7%, together accounting for 87.2% of the variation in the data, indicating that the two dimensions of the PCA shown in the plane of Figure 12, are a very good description of the structure in the higher dimensional space created by all seven variables. The coefficients of the eigenvectors (Figure 12) show that all of the stations differ from one another in one or more variables. This suggests that each station will have value for biodiversity monitoring as different aspects of the environment are expected to change differentially.

UPGMA cluster of the stations is shown in Figure 13. The cophenetic correlation was 0.78, indicating that the dendrogram is a good representation of the similarity matrix. Two cluster groups were formed, one with station BB1_D and BB1_C_400 m and the other with the remaining stations. Each station was also significantly different from others in its cluster. Thus the stations represent different environments within the DFCA.

Significant linear regressions were found between depth and the number of species per station (S), abundance (N), and Margalef's species richness (d), all showing decreases with increased depth (Figure 14).

Table 9. Environmental variables (Beazley et al., 2018) for each of the five stations in the DFCA used in the PCA, and for DS1_S in HBCA.

Station	Mean Depth (m)	Mean Bottom Salinity	Mean Spring Ice Cover (Proportion)	Mean Bottom Temperature (°C)	Mean Spring Chlorophyll *a* Concentration (mg m^{-3})	Mean Bottom Current (m s^{-1})	Mean Annual Primary Production (mg C m^{-2} day^{-1})
BB1_A_600 m	704.75	34.48	0.84	0.57	0.40	0.01	598.93
BB1_B_400 m	480.8	34.48	0.86	0.66	0.40	0.02	608.97
BB1_C_1000 m	1012.5	34.49	0.79	0.55	0.52	0.01	620.87
BB1_C_400 m	377.4	34.47	0.79	0.78	0.55	0.02	623.85
BB1_D	646.2	34.46	0.69	0.79	0.68	0.02	610.65
DS1_S	1052.0	34.90	0.25	3.79	1.04	0.01	666.05

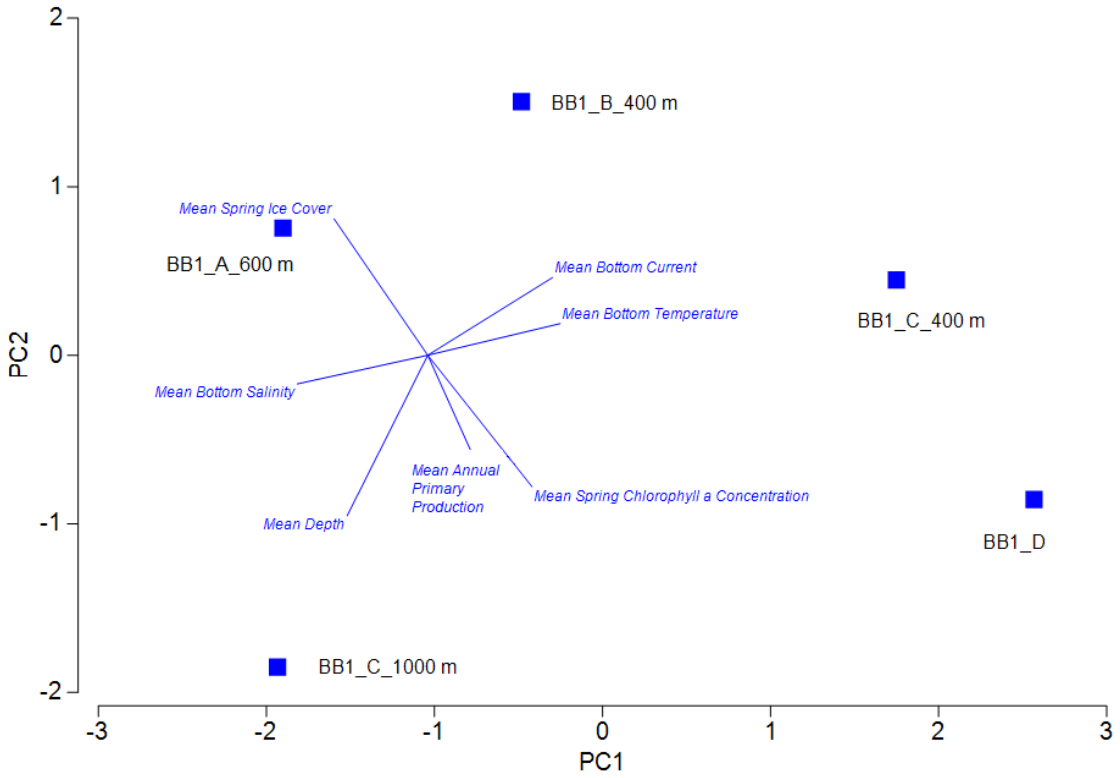


Figure 12. Position of the five stations in the DFCA along the first two axes of a principal components analysis. The coefficients of each of the seven environmental variables used in the analysis (Table 9) are overlain. Their vector length reflects the importance of each variable to PC1 and PC2.

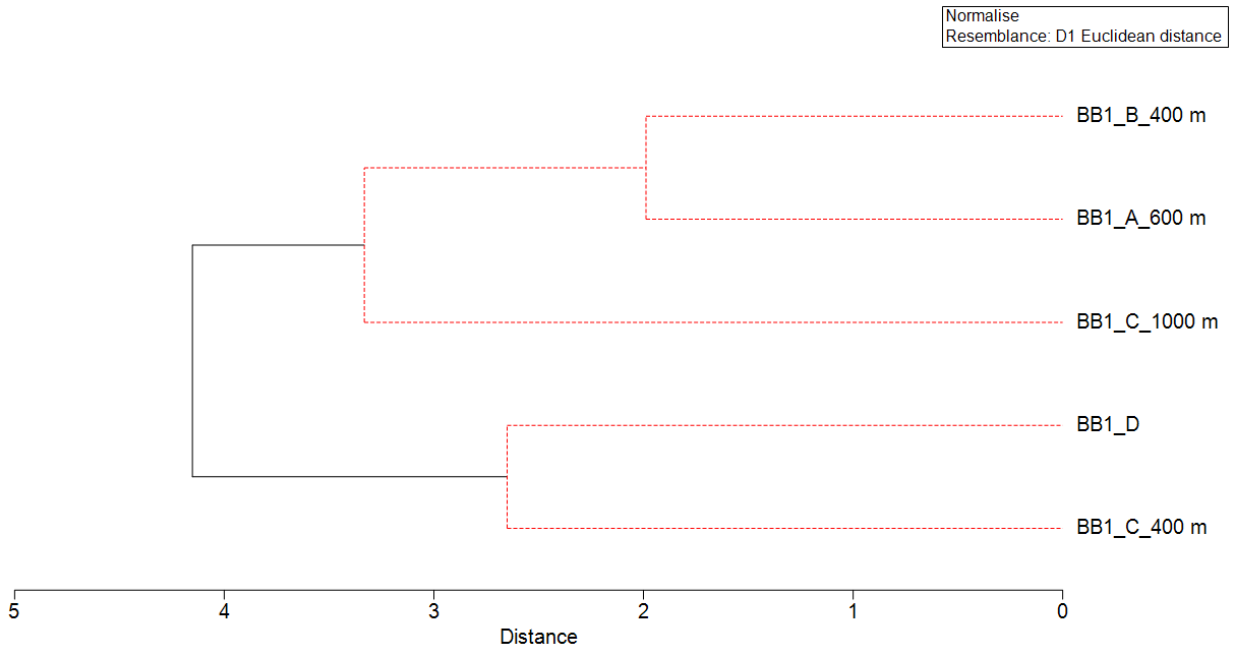


Figure 13. Unweighted group-average (UPGMA) cluster analysis of stations based on Euclidean distances of normalized environmental variables for the DFCA stations (Table 9). Significant clusters ($\alpha = 0.05$) assessed through 999 permutations are shown in red.

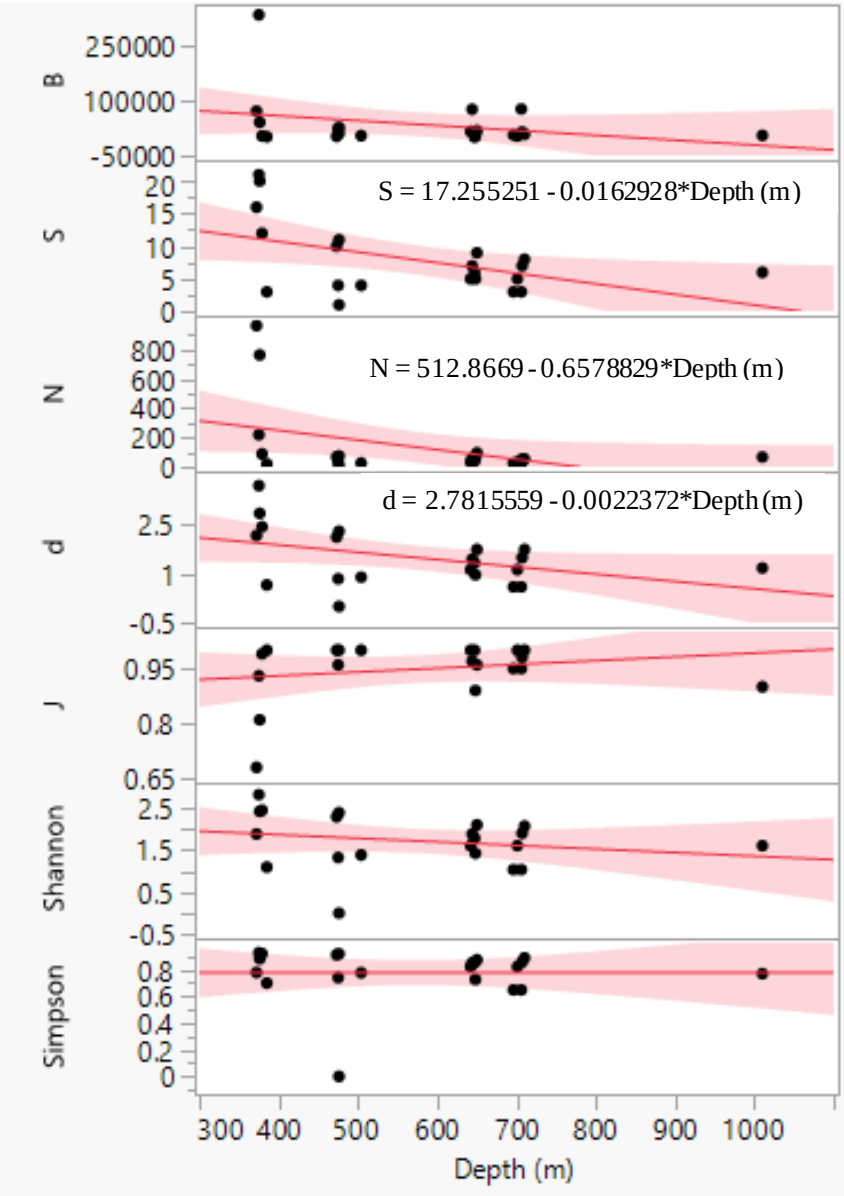


Figure 14. Linear regressions of the diversity indices for each of the samples in the DFCA (Appendix C) with depth, showing the 95% confidence intervals around the fit. Regression equations are shown for significant relationships ($P \leq 0.05$).

Community Similarity Based on Biomass

Of the 101 taxa identified, biomass was recorded for 90. Eight bryozoan colonial taxa were not weighed (Bryozoa Flustrina sp. 1, 2, 4, 10, 15, and Bryozoa Cyclostomatida sp. 1, 3, 4) along with the single specimen collections of *Eulalia* sp. 1, Platyhelminthes spp. and Polychaeta sp. 2. In some cases the lack of data from the bryozoans was because the taxon was associated with cobble/gravel and difficult to separate. Consequently, 90 taxa had biomass data recorded and these were drawn from 11 phyla (Platyhelminthes no longer represented). Of those, biomass was dominated by sponges and cnidarians (Figure 15). Sponges of the family Theneidae, accounted for

46.4% of the total biomass. The glass sponge, *Asconema foliatum*, ranked second, accounting for 19.5%, while the burrowing heart urchin *Brisaster fragilis* ranked third with 9% of the total biomass (Appendix H). These three species accounted for 75% of the cumulative biomass, with 13 species accounting for 95%. Bryozoan Flustrina sp. 17 and *Astarte* spp. were the highest ranking macrofaunal species accounting for 1.4 and 1.0% of total biomass respectively (Appendix H). Biomass varied greatly among samples both within and between stations (Figure 16) and was highly influenced by presence of Porifera (Figure 16). There was also a high degree of variability among replicates within stations (Figure 17), also influenced by poriferan biomass. The full data matrix of the standardized wet weight biomass (g/m^2) of the 90 taxa × 24 samples is provided in Appendix I, including total weights for each of the 11 phyla for which biomass was recorded.

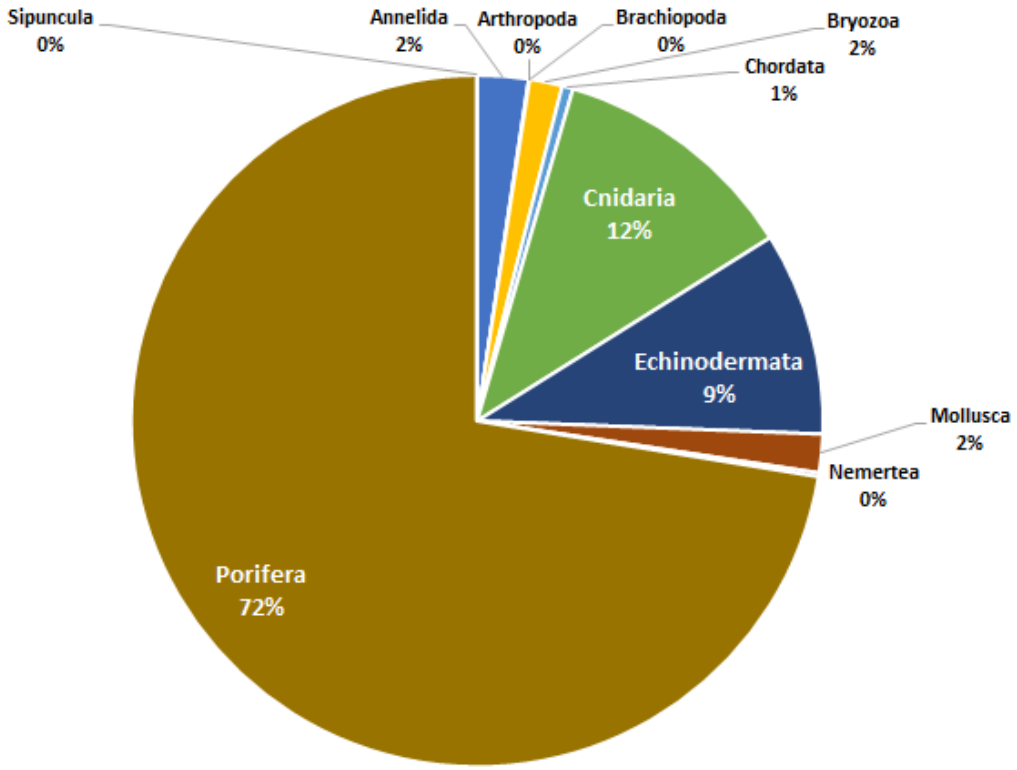


Figure 15. Proportion of total biomass by phylum identified from macrofaunal taxa > 1 cm recorded from the 24 sediment samples taken from the biodiversity monitoring stations in the Disko Fan and Hatton Basin Conservation Areas, eastern Canadian Arctic. The total biomass of individuals recorded after standardization was 1604.626 g.

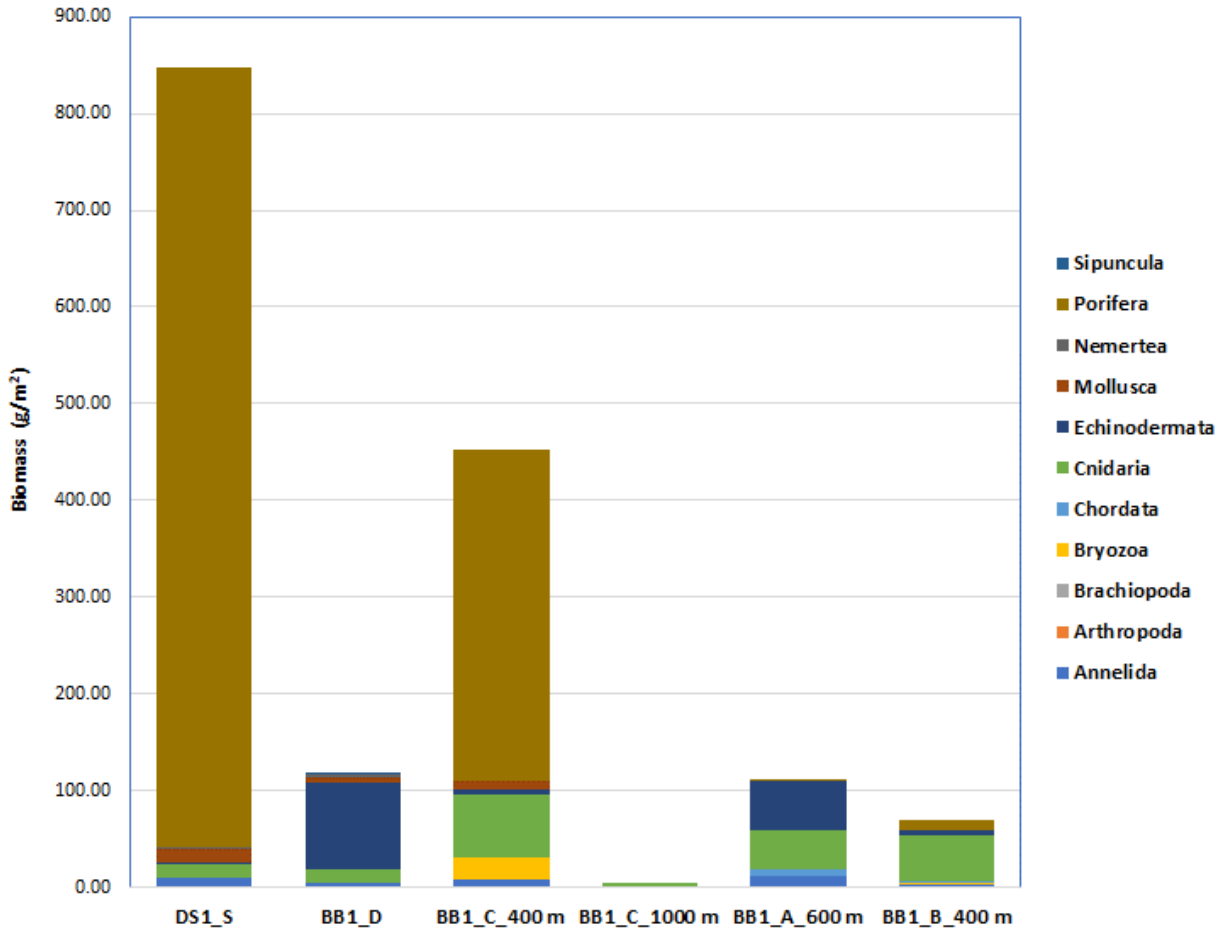


Figure 16. Total biomass in g/m^2 by phylum identified from macrofaunal taxa > 1 cm recorded from each of the CBMP biodiversity monitoring stations in the Disko Fan and Hatton Basin Conservation Areas, eastern Canadian Arctic. The total biomass of individuals recorded after standardization was 1604.626 g. Phyla colours in the bars follow the vertical order in the legend. Station DS1_S was positioned inside a significant concentration of sponges identified from trawl surveys (Kenchington et al., 2010).

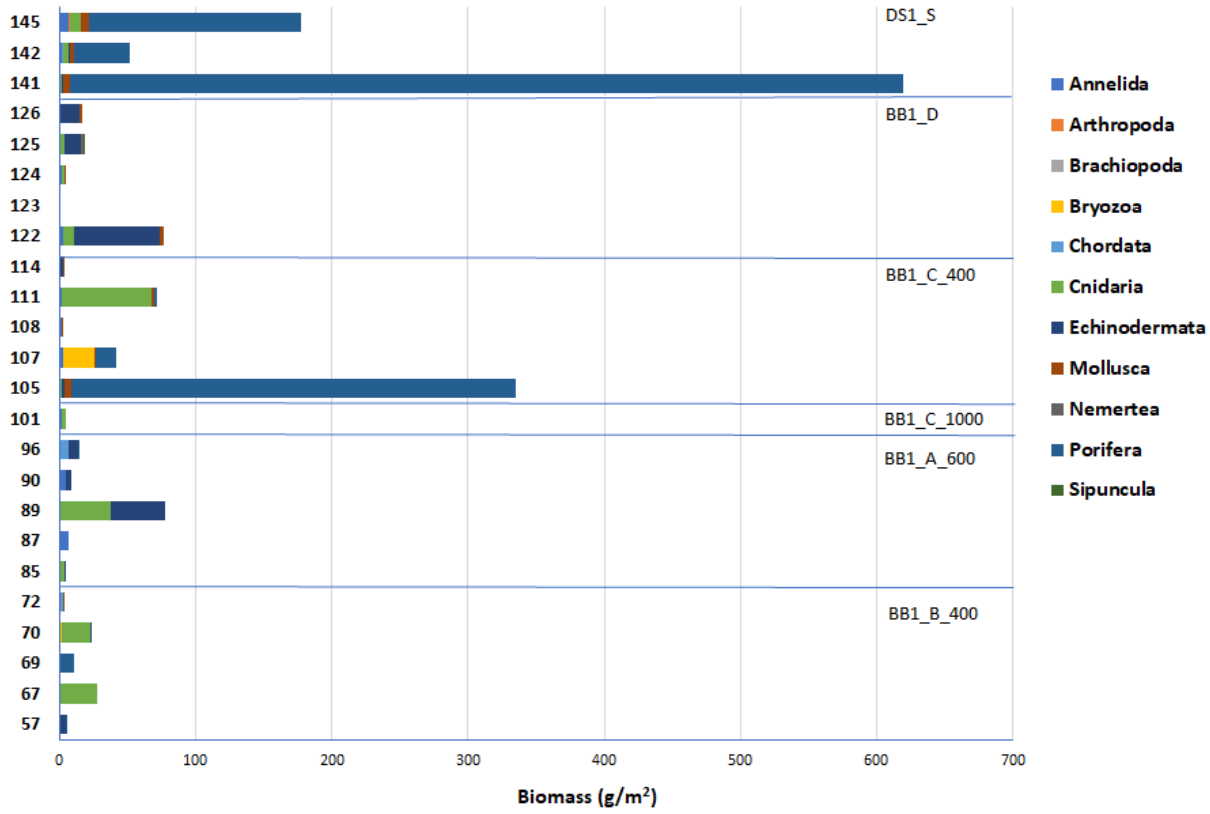


Figure 17. Total wet weight biomass in g/m^2 by phylum identified from macrofaunal taxa > 1 cm recorded from each of the 24 samples drawn from the CBMP biodiversity monitoring stations in the Disko Fan and Hatton Basin Conservation Areas, eastern Canadian Arctic. Blue lines separate the replicates within each station, with station name to the upper right of each group.

After examination of shade plots showing the effect of log(x+1) transformation (Appendix J), the standardized biomass data were log(x+1)-transformed, resulting in an increase in importance of lighter-weight taxa and reducing Porifera's impact.

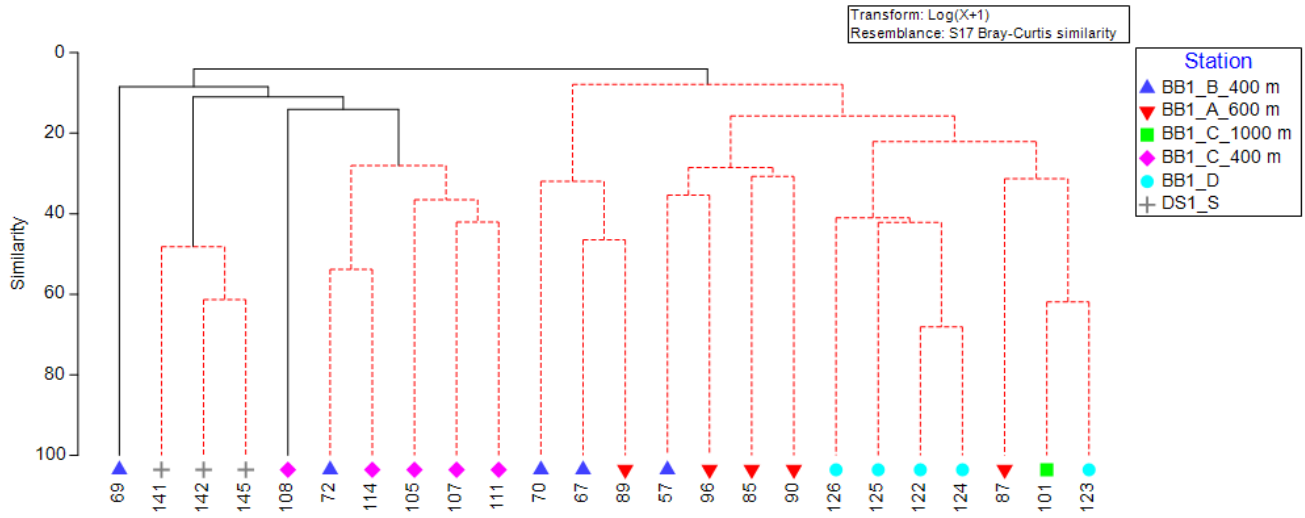


Figure 18. Unweighted group average cluster analysis of macrofaunal communities (1-cm size fraction) based on Bray-Curtis similarity of log(x+1)-transformed standardized biomass. Significant clusters ($\alpha = 0.05$) assessed through 999 permutations are shown in red. Samples are labelled by CON (Consecutive Operation Number) and station (see Table 4).

Table 10. Analysis of Similarities (ANOSIM) pairwise significance tests based on Bray-Curtis similarity calculated from log(x+1)-transformed standardized macrofaunal biomass (1-cm size fraction). * indicates pairs of stations with significantly different species compositions ($\alpha = 0.05$).

Groups	R Statistic	P
BB1_B_400 m, BB1_A_600 m	0.196	11.1
BB1_B_400 m, BB1_C_1000 m	0.48	16.7
BB1_B_400 m, BB1_C_400 m*	0.574	0.8
BB1_B_400 m, BB1_D*	0.574	0.8
BB1_B_400 m, DS1_S*	0.487	3.6
BB1_A_600 m, BB1_C_1000 m	0.68	16.7
BB1_A_600 m, BB1_C_400 m*	0.896	0.8
BB1_A_600 m, BB1_D*	0.472	2.4
BB1_A_600 m, DS1_S*	0.733	1.8
BB1_C_1000 m, BB1_C_400 m	1	16.7
BB1_C_1000 m, BB1_D	0.36	33.3
BB1_C_1000 m, DS1_S	1	25.0
BB1_C_400 m, BB1_D*	0.944	0.8
BB1_C_400 m, DS1_S*	0.959	1.8
BB1_D, DS1_S*	0.969	1.8

The dendrogram of samples clustered according to their Bray-Curtis similarity (Appendix K) had a good cophenetic correlation of 0.80 and showed that the macrofaunal communities in the HBCA samples (station DS1_S) are clustered with those from BB1_C_400 m and are significantly different from the others (Figure 18). Station BB1_B_400 m is the most diverse spreading across

four cluster groups (Figure 18), as was seen with the abundance data. This same pattern was visualized in the nMDS plot with the similarity of the samples from each station shown (Figure 19). There the samples from BBI_B_400 m are less mixed with the other groups but the stress level is relatively high (0.12). ANOSIM found that the macrofaunal communities were significantly different among stations (Global R: 0.65; P = 0.001), with nine pairs of stations having significantly different species compositions (Table 10). These are the same nine pairs that differed in their community composition based on abundance. Adjusting the P-value to account for multiple testing (P = 0.003) would discount those differences.

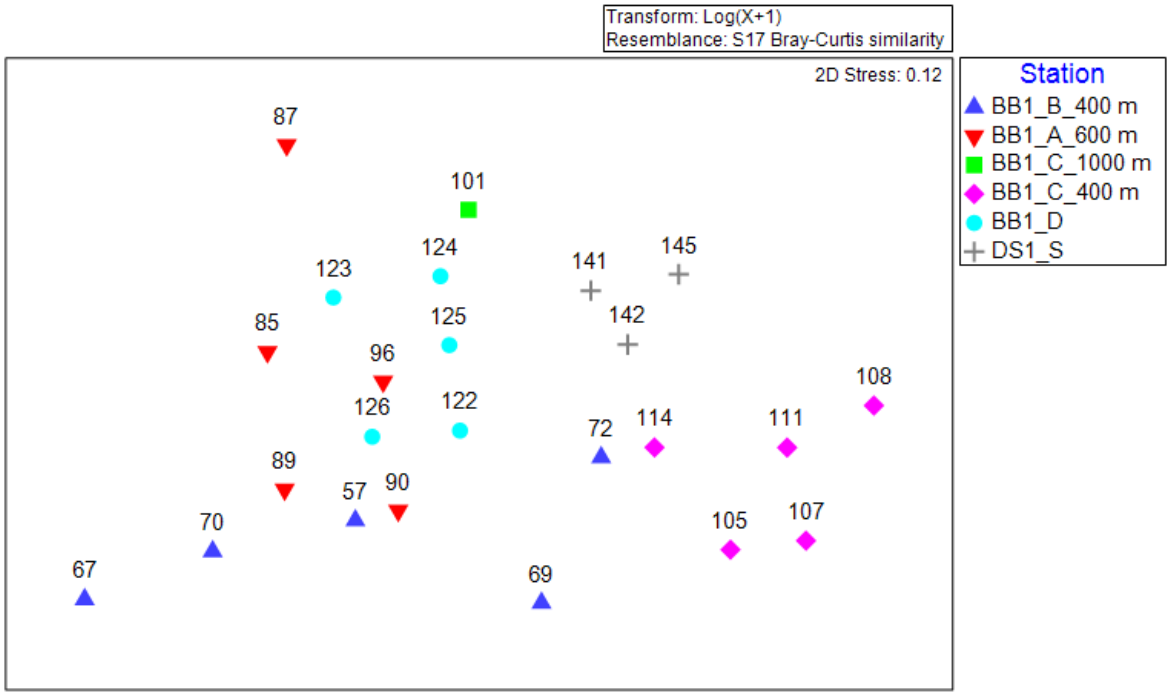


Figure 19. Non-metric multidimensional scaling analysis (nMDS) of macrofaunal communities (1-cm size fraction) based on Bray-Curtis similarity of log(x+1)-transformed standardized biomass. Samples are labelled by CON (Consecutive Operation Number) (Table 4) and colour-coded by station.

Size Frequency Distributions of Selected Species

Not enough samples of snow crabs, ophiuroids or bivalves were collected to provide sufficient data on the size frequencies for these species. Snow crabs (*Chionoecetes opilio*) were too large for the sampling gear employed. Ophiurids were only recorded in small numbers (Appendix G) spread over at least nine taxa (Appendices B and F), with five single counts, and a maximum count of nine individuals for *Amphiura* spp., a mixed species taxon. Similarly for the bivalve molluscs, only four taxa were identified (Appendices B and F) with two of those single counts (Appendix G), and a maximum count of seven for *Astarte* spp., a mixed species taxon.

DNA Sequencing and Barcoding of Macrofauna

Genetic samples were collected from 61 distinct specimens, or group of specimens, sampled from 14 sediment samples taken in eastern Davis Strait. However, only 32 samples produced good or adequate sequence data. Of those, 20 returned sequence matches in BLAST, with sequence similarity ranging from 78 to 98 which are not close enough for identification purposes; 4 retumed matches of 99 or 100 which can be used to identify the taxa. The remaining 12 samples did not return a match. This could be due to sequencing issues or to lack of representation in the BLAST database. Two samples of sponge which were identified as *Thenea valdiviae* returned 100% matches. An unknown nemertean was identified as *Nipponnemertes pulchra* (99% sequence similarity) and an unknown annelid was identified as *Glycera capitata*. Collectively, the effort put into collecting and processing these data did not return the anticipated benefits due to poor sequence quality and/or poor matching success, possibly due to initial handling and storage conditions at sea and to a lack of reference material in the databases for some groups.

MEIOFAUNA

All sediment samples contained both calcareous and agglutinated species. In total, 41 agglutinated taxa were identified, including 36 to species, four to genus, and one general taxon. Calcareous foraminifera were identified to 46 taxa, including 34 species, 11 others identified to genus, and one general taxon. Additionally, three species of planktonic foraminifera were present, giving a total of 90 taxa (Appendix L). Data are presented as total counts per 5 cc (Appendix M). Total abundance of each of these three groups (agglutinated, calcareous and planktonic) varied greatly among stations (Figure 20). Calcareous foraminifera were particularly dominant at station BB1_C_400 m, accounting for 72% of total abundance, but only ranged from 4–24% of abundance at the other stations. Agglutinated species were the most numerous group at stations BB1_B_400 m, BB1_A_600 m and BB1_D. They accounted for 8–91% of total abundance across stations. Planktonic species constituted 2–26% of total abundance at each station with the larger proportion found at station BB1_B_400 m and the largest absolute numbers at station BB1_C_400 m.

The planktonic species *Neogloboquadrina pachyderma sinistral* dominated abundance, accounting for 15.6% of the cumulative total abundance (Appendix N), although that abundance was largely accumulated in sample CON 109, with two others also having high abundance but at an order of magnitude less (CON 56, CON 68). *Textularia torquata,* an agglutinated species, was the second most dominant with 10.1%, while a calcareous species, *Cibicides lobatus*, was third with 7.6% of total abundance. Only eight taxa accounted for 50% of the foraminiferan abundance (Appendix N).

The calcareous specimens were very fragile due to partial dissolution. This can occur due to preservation in water or alcohol that has not been buffered to a pH of approximately 8, but can also be due to natural processes at the collection site. Baffin Bay and Davis Strait carbonate dissolution occurs in Holocene sediments at depths > 900 m due to low carbonate saturation states (Azetsu-Scott et al., 2010) and oxidation of organic matter related to high productivity (Aksu,

1983; de Vernal et al., 1992; Osterman and Nelson, 1989; Schröeder-Adams and Van Rooyen, 2011). Given the fragile nature of the specimens, some identifying features were missing, and therefore the groupings "*Cassidulina*/*Islandiella* spp." and "calcareous fragment/unknown" were added to the species list.

Meiofauna from the CON 109 sediment sample (BB1_C_400 m) had the largest total abundance (Figure 21), being an order of magnitude greater than that observed in any of the other samples (Appendix O). The highest species diversity was found in the CON 113 sediment sample from the same station. There, 56 taxa were identified in the single 5 cc sediment sub-sample (Appendix O). These higher values explain the higher mean total abundance and number of taxa observed at this station compared with other stations (Table 11). There was less variability among the replicates from a single sediment sample (Figure 21), although more variability in within-sample replicates was seen in the CON 71 sediment sample than from the CON 119 sediment sample (Figure 21). Stations differed significantly in ANOVA tests of the number of species (S), and in Shannon Diversity (H′) and Simpson's Index (Appendix O), with BB1_D having significantly fewer taxa (S) than BB1_C_400 m and BB1_B_400 m, and lower Shannon Diversity (H′) and Simpson's Index than BB1_C_400 m. Power was low for the non-significant tests, ranging from 0.16 to 0.47 and LSN estimated sample sizes of 15 to 41 are needed to detect effects of stations for those variables (Appendix O).

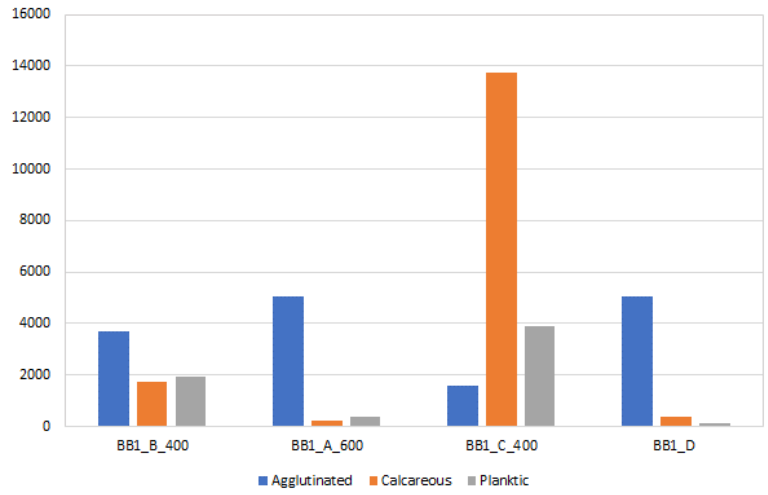


Figure 20. Total abundance of agglutinated, calcified and planktic foraminifera found at each of the four biodiversity stations in the DFCA (stations BB1_A_600 m, BB1_B_400 m, BB1_C_400 m, and BB1_D). Average abundance for replicate samples CONs 71 and 119 were used.

Examination of shade plots (Appendix P) showed that a log(x+1) transformation improved the representation of all taxa and so Bray-Curtis similarity matrices (Appendix Q) were calculated from log(x+1)-transformed meiofaunal abundance/ 5 cc. Multivariate analyses were based on the similarity matrix (not shown) replacing averaged values for the three replicates in each of the CON 71 and CON 119 sediment samples (Appendix M).

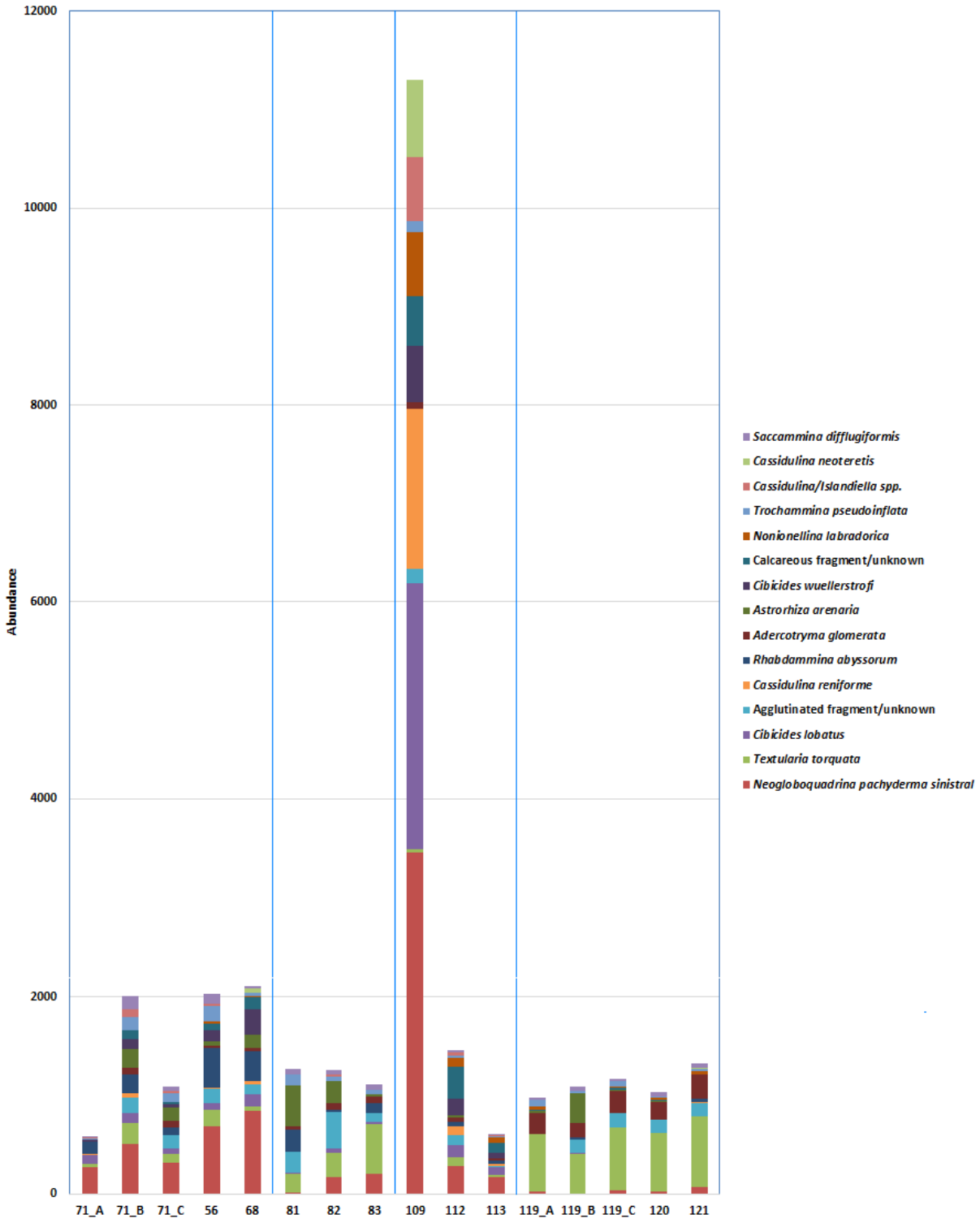


Figure 21. Meiofaunal abundance/5 cc by taxon from each of the sediment samples (Consecutive Operation Number shown) drawn from four CBMP biodiversity monitoring stations in the Disko Fan Conservation Area (Table 4). Blue lines separate the replicates within each station, and A, B, C denote replicates within one sediment sample. Only taxa with total abundance across all samples > 700 were included (Appendix N).

Table 11. Mean ± standard deviation of depth, number of taxa (S), abundance (N), Margalef's Species Richness (d) and Pielou's Evenness (J′), Shannon Diversity (H′) and Simpson's Index for meiofauna from each biodiversity monitoring station sampled in the DFCA.

Station	Depth (m)	S	N (/5cc)	d	J′	H′	Simpson's Index
BB1_B_400 m	487 ± 17	45 ± 3	2464 ± 528	5.71 ± 0.33	0.76 ± 0.04	2.90 ± 0.18	0.89 ± 0.03
BB1_C_400 m	380 ± 6	48 ± 8	6412 ± 8224	6.01 ± 1.96	0.80 ± 0.04	3.11 ± 0.24	0.93 ± 0.02
BB1_A_600 m	701 ± 3	37 ± 3	1900 ± 148	4.73 ± 0.31	0.81 ± 0.02	2.90 ± 0.12	0.91 ± 0.02
BB1_D	650 ± 11	32 ± 3	1849 ± 110	4.18 ± 0.41	0.74 ± 0.03	2.57 ± 0.17	0.85 ± 0.03

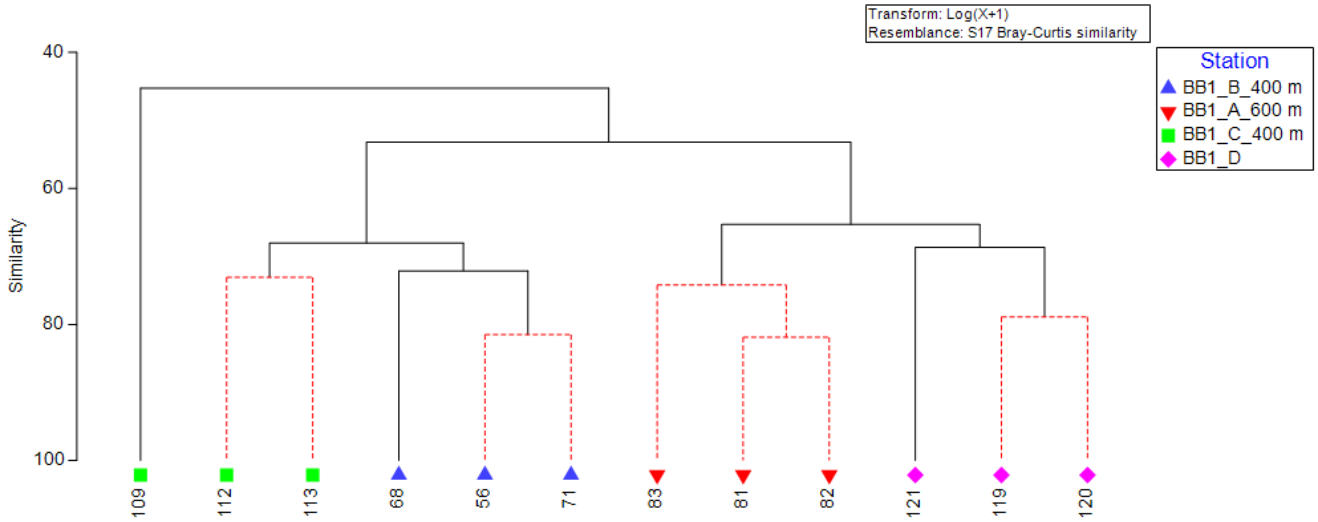


Figure 22. Unweighted group-average (UPGMA) cluster analysis of meiofaunal communities based on Bray-Curtis similarity of log(x+1)-transformed abundance (/5 cc). Significant clusters (α = 0.05) assessed through 999 permutations are shown in red. Samples are labelled by CON (Consecutive Operation Number) and colour-coded by station (see Table 4).

The dendrogram of samples clustered according to their Bray-Curtis similarity (Figure 22) had a high cophenetic correlation of 0.83 and showed that the meiofaunal communities in the DFCA samples formed clusters of samples from the same stations, most of which were significant in the SIMPROF test. Although the data were transformed, the CON 109 sample from the sediments collected at BB1_C_400 m remains distinct. This same pattern was seen in the nMDS plot with the similarity of the samples from each station shown (Figure 23). The stress level is very low for this ordination (2-D Stress: 0.08) indicating that the two dimensions capture much of the variation expressed at higher dimensions. ANOSIM found that the meiofaunal communities were significantly different among stations (Global R: 0.784; P = 0.001), although no pairwise comparisons of stations were statistically significant even without adjusting the P-value to account for multiple testing.

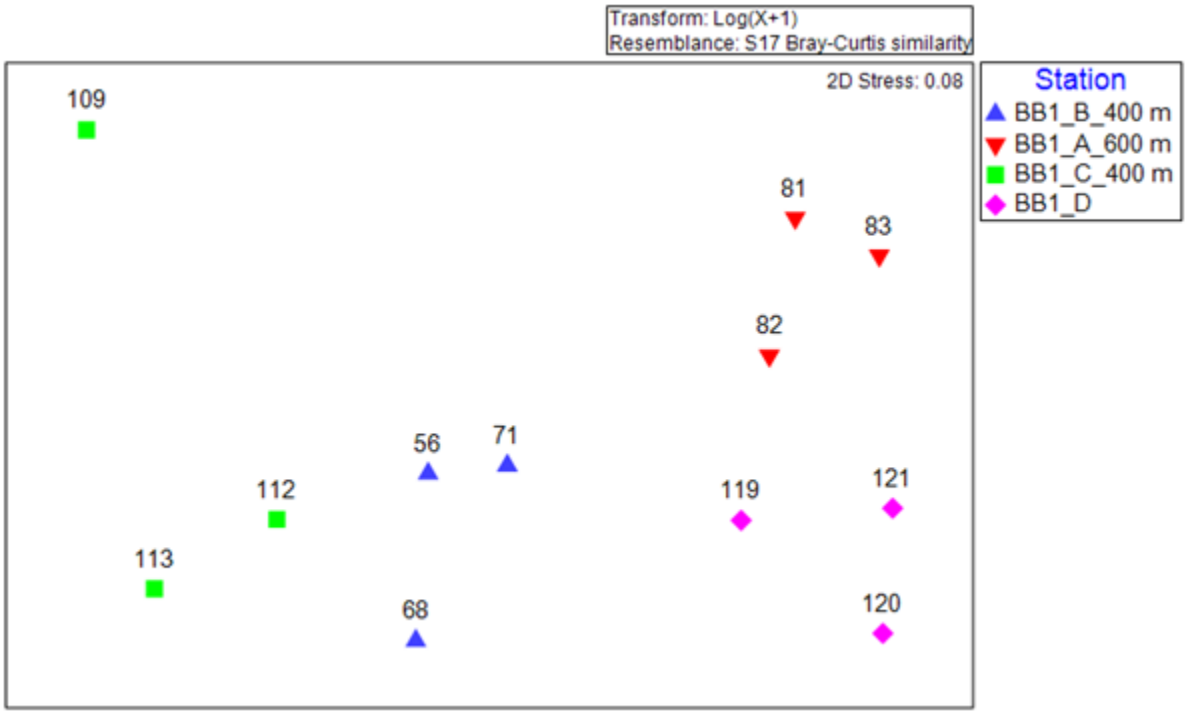


Figure 23. Non-metric multidimensional scaling analysis (nMDS) of meiofaunal communities based on Bray-Curtis similarity of log(x+1)-transformed abundance (/5 cc). Samples are labelled by CON (Consecutive Operation Number) (Table 4) and colour-coded by station.

Fifty-three taxa occurred in at least 5 of the 12 samples and so were examined for associations between them (Figure 24). Cophenetic correlation among taxa was 0.74, indicating that the cluster dendrogram is a good representation of the similarity matrix. The SIMPROF test applied to the UPGMA cluster identified eleven significant groupings with the greatest similarity between taxa shown between *Textularia torquata* and the agglutinated fragment class at 91.6% similarity, raising the possibility that the agglutinated fragment class may have been composed of this species. *Adercotryma glomerata* joined this cluster at 19% similarity forming a distinct clade. The next most similar species pair was *Textularia earlandi* and *Trochammina nana* with 90.6% similarity. Amongst the calcareous foraminifera, the closest similarity was found between *Fissurina marginata* and *Stetsonia arctica* with 88% similarity. The calcareous fragment class showed 86% similarity to *Pullenia osloensis*.

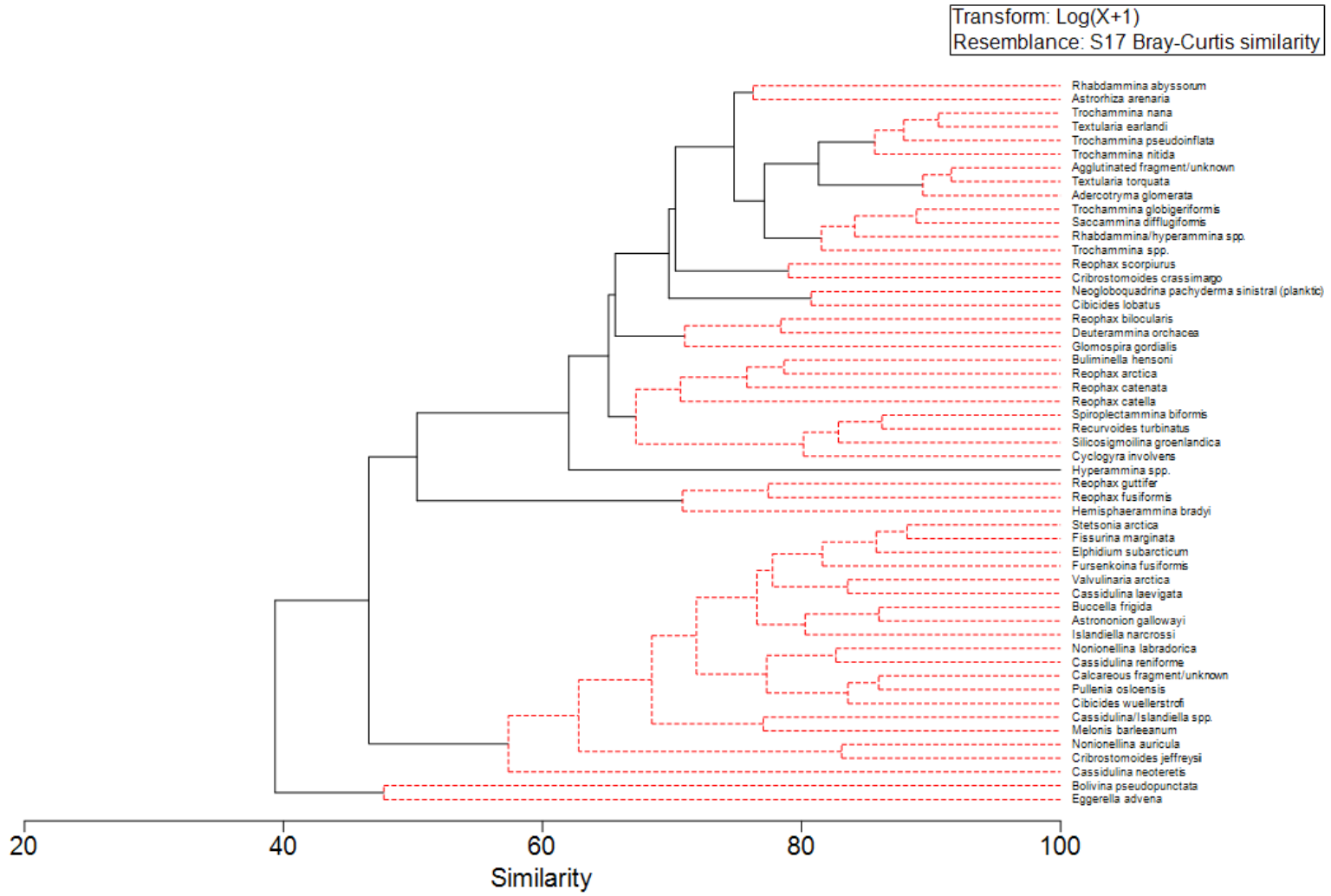


Figure 24. Unweighted group-average cluster analysis (UPGMA) of meiofaunal taxa based on Bray-Curtis similarity of log(x+1)-transformed abundance (per 5 cc). Significant clusters ($\alpha = 0.05$) assessed through 999 permutations are shown in red. Only taxa that occurred in 5 or more samples were included in the analyses.

DESCRIPTIVE OVERVIEW OF FAUNA AT CBMP MONITORING STATIONS

BB1_A_600 m
Depth ~ 700 m
Operation – 8 successful replicate Van Veen grabs processed
Substrate – Sandy mud with gravel
Large macrofauna (> 1 cm) – Dominated by the small suspension feeding gorgonian coral *Acanella arbuscula* and surface deposit feeding terebellid and ampharetid polychaetes. The burrowing heart urchin *Brisaster fragilis* was also common and sea pens were present.
Meiofauna – Agglutinated species were common with the most abundant species *Textularia torquata*.

Station BB1_A_600 m was the deepest of the four biodiversity monitoring sites at BB1 and the only one with gorgonian corals. Station A had a population of *Acanella arbuscula*, which anchors in soft sediment. All of the *Acanella* specimens collected were small, indicating recent, successful recruitment. Soft bottom fauna was most similar to BB1_B_400 m, with surface deposit feeding terebellid polychaetes common and the presence of sea pens. Most sea pens were also small, indicating recent, successful recruitment. Hard bottom fauna were sparse. Burrowing urchins, *Brisaster fragilis*, were common at station BB1_A_600 m (occurring in three of five samples). This station was most similar to station BB1_D with respect to the meiofaunal community and both were dominated by agglutinated species.

BB1_B_400 m
Depth ~ 500 m
Operation – 8 successful replicate Van Veen grabs processed
Substrate – Sandy mud with gravel
Large macrofauna (> 1 cm) – Dominated by filter feeding sponges, with hard substrate encrusting tubiculous serpulid polychaetes and bryozoans common. Soft-bottom taxa including surface deposit feeding terebellid polychaetes and suspension feeding sea pens were also common.
Meiofauna – The planktic foraminiferan *Neogloboquadrina pachyderma sinistral* was the most abundant species at this station. The vagile textulariid, *Rhabdammina abyssorum*, was also abundant.

The larger macrofauna was dominated by filter and suspension feeders, with surface deposit feeders common. Substrate type and soft-bottom fauna were most similar to the immediately adjacent station BB1_A_600 m, even though separated by 200 m in depth. Sea pens were only observed at stations BB1_A_600 m and BB1_B_400 m, and surface deposit feeding terebellids were common in both areas. These two faunal components were absent or nearly so at station BB1_C_400 m. Sea pens collected were small, indicating recent, successful recruitment. Hard-bottom fauna were most similar to BB1_C_400 m, with sponges, serpulid polychaetes, and

bryozoans common at both stations. Meiofaunal communities were most similar to BB1_C_400 m at similar depths.

BB1_C_400 m
Depth ~ 400m
Operation – 8 successful replicate Van Veen grabs processed
Substrate – Gravel with sandy mud
Large macrofauna (> 1 cm) – Dominated by limpets, with other hard substrate taxa common: chitons and filter- or suspension-feeding encrusting bryozoans, sponges and tubiculous serpulid polychaetes. Subsurface deposit feeding maldanid polychaetes and omnivorous eunicid polychaetes were common, and brittle stars in general were found in three of the five sediment samples, with no one particular species or feeding mode/lifestyle common. This station had the highest species diversity and biomass of the BB1 stations.
Meiofauna – Calcareous species greatly dominated abundance with two species of *Cibicides* the most common. The planktic foraminiferan *Neogloboquadrina pachyderma sinistral* was the most abundant species at this station.

The shallowest of the four sites, also with the greatest proportion of gravel; the volume of material retained on the 1-mm sieve was several times greater than at other stations. Station BB1_C_400 m was the only station where upright cyclostome bryozoan lace-corals, limpets and chitons were common. The compliment of hard bottom filter- and suspension-feeding taxa at BB1_C_400 m was most similar to BB1_B_400 m, the station most similar in depth. The compliment of soft-bottom taxa differed from both BB1_A_600 m and BB1_B_400 m, with surface deposit feeding terebellid and ampharetid polychaetes nearly absent. Omnivorous eunicid polychaetes and subsurface deposit feeding maldanid polychaetes were common. Maldanids were also common at the immediately adjacent station BB1_D, indicating a change in at least some aspects of the soft bottom benthic macrofaunal community between stations BB1_A_600 m/BB1_B_400 m and BB1_C_400 m /BB1_D, mainly surface deposit feeders at one end of BB1 and subsurface deposit feeders at the other. BB1_C_400 m was also the only BB1 station where the burrowing urchin *Brisaster fragilis* was absent. Most distinctive meiofaunal community with high numbers of calcareous foraminifera. Most similar to BB1_B_400 m.

BB1_D
Depth ~ 600m
Operation – 8 successful replicate Van Veen grabs processed
Sediment – Gravel with sandy mud
Large macrofauna (> 1 cm) – Dominated by subsurface deposit feeding maldanid polychaetes, with tusk shells, surface deposit-feeding ampharetid polychaetes, suspension-feeding anemones, and filter-feeding sponges common.
Meiofauna – Agglutinated species were common with the most abundant species *Textularia torquata*.

Only BB1_A_600 m was deeper than station BB1_D, and this was the only other station where scaphopods were observed, but these two stations were also separated by the greatest distance, at opposite ends of BB1. The amount of gravel present appeared intermediate between stations BB1_B_400 m and BB1_C_400, but this abundance of hard substrate appeared covered by a thin layer of sandy mud. With the exception of some sponge, encrusting taxa were uncommon at station BB1_D. The commonly occurring anemone was a colonial form with a bulbous base, possibly for anchoring in soft sediments. The dominance of subsurface deposit feeding maldanid polychaetes, with surface deposit feeding terebellids nearly absent, indicated a soft bottom macrofauna most similar to station BB1_C_400, different in some aspects from BB1_B_400 m and BB1_A_600 m. However, the numbers of colonial anemones and tusk shells suggest some soft bottom community characteristics unique to station BB1_D at BB1. Meiofaunal community very similar to BB1_A_600 m. Both are dominated by agglutinated species.

DISCUSSION

Our study has increased the knowledge of benthic marine diversity within the eastern Canadian Arctic. Four stations within or straddling the DFCA (Figure 2) met the requirements for benthic monitoring stations under the CAFF-CBMP using samples processed to date. Another station in the HBCA (DS1_S) was partially processed for macrofauna in the 1-cm size fraction but samples for meiofauna have been collected and stored and a photo transect has been conducted (Figure 3). Thus, samples from DS1_S should have high priority for processing in future.

Analysis of macrofaunal communities from the 1-cm size fraction indicate significant differences in community composition in biomass and abundance between all five fully sampled stations in all pairwise combinations except for BB1_B_400 m and BB1_A_600 m (Tables 8, 10). This does not necessarily limit the utility of those stations as CBMP monitoring stations, as their different environments, as shown by our analyses, indicates that their constituent species may respond differently to different stressors. Replicate samples within stations clustered together, except for BB1_B_400 m, indicating that the number of replicates sampled (5) was sufficient. There is no clear reason why this one station had higher variability among replicates, but future sampling efforts could consider increasing the number of replicates at this station to try to reduce this variability. Significant differences among stations within/adjacent to the DFCA were only seen in the number (S) and abundance of species (N). Spatial differences among stations are not a prerequisite for monitoring temporal changes but it does indicate the magnitude of future effects that could be distinguished based on the variance in the data. While only limited comparisons could be made, the data indicate the samples within/adjacent to the Disko Fan and Hatton Basin Conservation Areas represent different macrofaunal assemblages and habitats and are found in very different environments. Further processing of the samples from the 2013 expedition that focused on the Hatton Basin and those remaining samples from the 2012 mission will be invaluable in assessing the baseline conditions of the Conservation Areas and of the HBCA in particular.

The most comparable study to ours is that by Hansen et al. (2019), who conducted quantitative sampling of infaunal communities with 0.1 m^2 Van Veen grabs and a 0.0143 m^2 Haps-corer on the northeast Greenland shelf. They found that annelids and arthropods were dominant, followed by echinoderms and molluscs. This contrasts with our stations, where the numerically dominant phyla in the samples were Bryozoa, followed by the annelids, together accounting for 68% of macrofaunal abundance. Most likely this difference was due to differences in substrate, with the samples from the northeast Greenland shelf drawn from fine muds, while the samples from our study were taken from gravel with sandy mud. The bryozoans would be associated with the gravel.

Biomasses from northeast Greenland samples ranged between < 0.1 and 63 g wet weight m^{-2}. However, that range excluded two stations located on the continental slopes that had high biomasses of epifauna associated with dense stands of bamboo corals. Abundances ranged between 40 and 1,240 individuals m^{-2}. Hansen et al. (2019) were able to compare their results with a number of previous studies conducted with the same sampling design off west Greenland (shelf plains, banks, fjords and shelf slopes). Compared to the west Greenland studies, Hansen et al. (2019) considered their samples to generally have low densities, with arthropods and annelids averaging about 400 individuals m^{-2}, and the corresponding biomass averaging 10 g m^{-2}. This biomass of the infauna was said to be about 30 times lower and the abundance about 7 times lower than on the west Greenland shelves. Our estimates of average abundance over all taxa ranged in the DFCA between 40 and 412 individuals m^{-2}, with the corresponding biomass ranging between averages of 13.9 and 90.6 g m^{-2}. This would render the DFCA samples 'low' in abundance and biomass compared with the northeast Greenland shelf, and more so when compared with west Greenland (inferred from Hansen et al., 2019). In the single station in the HBCA, which averaged 479 individuals m^{-2} with biomass on average 283 g m^{-2}, biomass was more comparable to that of west Greenland, but in our case it was heavily comprised of sponges, which were not considered in the above comparison (Hansen et al., 2019).

Hansen et al. (2019) identified more than the 101 macrofaunal taxa reported here, with 298 taxa found in their sediment samples. The most species-rich phyla were annelids (88 taxa), followed by arthropods (71 taxa), bryozoans (35 taxa), molluscs (30 taxa), echinoderms (23 taxa), cnidarians (20 taxa), sponges (15 taxa) and 8 other phyla contributing with 16 additional taxa. Annelids was also the most species-rich phylum in our study, but with only 21 taxa identified, and arthropods were much less speciose (5 taxa), as were most other phyla. Only poriferans were more species-rich in our study compared to Hansen et al. (2019), with 19 taxa identified and those believed to be severely underestimated. The Shannon diversity index showed an average value between 1.48 and 2.14 at our stations which was much lower than the 3.54 reported for the northeast Greenland samples.

The meiofauna from ten fjords in Baffin Island were previously studied from sediments collected with Van Veen grabs, for the purpose of examining environmental relationships with species composition (Schafer and Cole, 1988). In those settings, 75% of the taxa were agglutinated and the total number of individuals averaged 111 per cubic centimeter of sediment. In this study of offshore locations, abundance of foraminifera was an order of magnitude higher, with averages

per 5 cubic centimeters ranging from 1859 to 6412. The dominant species in the fjords (*Textularia earlandi*, *Spiroplectammina biformis*, *Trochammina nana*, *Reophax arctica*) were present in our samples but at most accounting for 1.5% of total abundance. Interestingly, two of these species, *T. earlandi* and *T. nana* were strongly associated in our samples, with 91.6% similarity. They formed a significant clade with two other species of *Trochammina* (*T. pseudoinflata* and *T. nitida*).

The average number of foraminiferan taxa per 5 cubic centimeters ranged from 32 to 48 at the different stations and the standard deviation was very small for all, suggesting that species number and related diversity indicators will be good indicators for monitoring change. The percentage of agglutinated taxa may be positively correlated with water depth and percent silt in the sediments (Schafer and Cole, 1988). We did not have accurate measures of silt content but stations BB1_A_600 m and BB1_D which had the highest percentage of agglutinated taxa were from the deeper locations with water depths averaging 701 meters and 650 meters, respectively. It may be useful to monitor the percentage of agglutinated species given its environmental sensitivities (Schafer and Cole, 1988).

The large megabenthic epifauna is recommended by the CBMP to be sampled by trawl or with *in situ* imagery (Gill et al., 2011). Kenchington et al. (2016) used kernel density estimation to model biomass estimates and predicted distributions based on presence/absence data from multi-species trawl surveys in this region. Using species distribution models it is possible to interpolate predictions to un-surveyed areas with similar environmental characteristics as the occurrence data. Prediction maps of distribution were made for large gorgonian corals, sea pens, small gorgonian corals, and sponge grounds. Large gorgonian corals identified from the trawl catches included *Acanthogorgia armata, Paramuricea* spp., *Primnoa resedaeformis*, *Paragorgia arborea*, *Radicipes* spp. and *Keratoisis* sp. as well as unidentified species (Kenchington et al., 2012). Stations BB1_A_600 m, BB1_C 400 m, BB1_C_1000 m, and BB1_D corresponded with areas predicted to have large gorgonian corals. Some of these may correspond to the Anthozoa spp. taxon collected here, and *Radicipes* spp. which were observed by Baker et al. (2018) in the DFCA.

Murillo et al. (2018), in examining samples collected by trawl surveys, found that the glass sponge *Asconema foliatum* and demosponge *Mycale (Mycale) lingua* were the second and third most common species in the region, with the genus-level taxon *Thenea* spp. the most common. Theneidae spp. were identified from the box corer samples at station DS1_S in Hatton Basin and our genetic confirmation of *Thenea valdiviae* further supports the presence of *Thenea* spp. observed by Murillo et al. (2018). *A. foliatum* was one of only three sponges identified to the species level in our study. It was found only at station BB1_C_400 m in the DFCA. Similar to the larger corals, it is considered megafauna that is best sampled using other sampling gear.

Habitat heterogeneity plays an important role in the diversity and assemblage of benthic organisms, providing physical habitat for soft corals and gorgonians to anchor on (Baker et al., 2012; Long et al., 2020). Sediment characteristics such as grain size were not assessed as part of the benthic monitoring during this survey. However, in Baffin Bay, the basin sediment has been reported to generally be comprised of fine silts and clays, while coarser fine sediments have been

observed in the lower slopes (Baker and Friedman, 1973). General sediment composition can be gained from data collected as part of the photo transects. It is recommended that further surveys consider obtaining sediment samples for grain size and chemical analysis such as percentage organic carbon, and archived for other potential analyses (e.g., microplastic).

Data collected at these CBMP biodiversity monitoring stations will serve as the baseline for monitoring changes in the conservation areas. The DFCA was established to protect cold-water corals and the overwintering habitat of narwhal. It is known to include concentrations of large gorgonian corals including high densities of bamboo corals, which in turn provide habitat for commercially harvested species such as Greenland halibut and northern shrimp (DFO, 2007; DFO, 2019; Hiltz et al., 2018). Similarly, the HBCA is a highly productive area established to protect gorgonian corals, sponges and other coral species (DFO, 2019). Our results also show the areas contained numerous taxa of Annelida, Arthropoda, Bryozoa, Echinodermata, and Mollusca, all of which provide ecological functions and support the lifecycles of commercial fish species, and marine mammals such as narwhal.

Protected areas can be an effective tool in biodiversity conservation, food provisioning, and carbon storage (Sala et al., 2021). Despite the adoption of protected areas to reduce fishing pressures, there remain many external and internal threats to Arctic marine ecosystems. With global climate change the region is expected to become ice free for longer, the water fresher, and more acidic which will drive changes in habitat suitability for benthic species. Foraminifera are expected to be particularly sensitive to changes in ocean carbonate chemistry, particularly for calcareous species which are susceptible to dissolution of their skeletons under low pH conditions. However, foraminiferal species' responses have been shown to vary considerably, under experimental conditions, in response to multiple stressors such as deoxygenation, warming and acidification (Bernhard et al. 2021). As for many ecosystem components, while some species may decrease in abundance, others are likely to be unaffected or even increase under future conditions.

DATA ACCESS

Data collected from this project will be made available on the Government of Canada Open Data Portal https://open.canada.ca/en/open-data. Data will also be submitted to the CAFF Arctic Biodiversity Data Service (ABDS) data portal https://abds.is/index.php/contribute-data.

ACKNOWLEDGEMENTS

In 2012, a joint project between the Department of Fisheries and Oceans Canada's (DFO) Maritimes and Central and Arctic (C&A) Regions was initiated with the primary objective to conduct *in situ* benthic surveys in Davis Strait and Baffin Bay for the purpose of identifying vulnerable marine ecosystems (VMEs) and ecologically and biologically significant areas

(EBSAs), and to provide baseline data on the distribution and abundance of benthic invertebrates for assessing the impacts of climate change. The project was funded by DFO's International Governance Strategy (IGS) Research Fund to Ellen Kenchington and Margaret Treble (DFO-C&A), through the project: "Identification and Characterization of Benthic VMEs and EBSAs in Baffin Bay and Davis Strait, Sub Arctic/Eastern Arctic" which ran from April 2011 to March 2014.

Many people contributed to this work, both at sea and in the lab. In particular we thank the Captains and crews of the Canadian Coast Guard Ships (CCGS) *Henry Larsen* and *Hudson*, as well as colleagues with the University of Quebec at Rimouski (UQAR), Laval University (ArcticNet), and Natural Resources Canada (NRCan). In particular we thank Andrew Cogswell (DFO) chief scientist for the Larsen mission in 2012 and Calvin Campbell (NRCan) chief scientist for the Hudson mission in 2013. Robert Benjamin led the implementation of IT logistics in support of data acquisition and links with the ship's navigation systems. We further thank Vladimir Kostylev for use of the corers and grabs, and logistical support from Angus Robertson and Bob Murphy (NRCan), and from Kirk Phelan and Kelly Bentham (DFO). Many scientific staff from all four organizations (UQAR, ArcticNet, DFO, NRCan) contributed to the sample collections and we are very grateful to all. Most notably Kevin MacIsaac, Merlin Best, Lindsay Beazley, Lynne Anstey and Shawn Roach (DFO) were an integral part of this project. Although all of the at-sea identifications were re-examined in the lab upon return by co-authors of this report, we are very grateful to the preliminary identifications done by the scientists while at sea and for their contributions to the successful processing of sediment samples. Lynne Anstey put considerable time and effort into processing genetic samples. We thank Dr. F. Javier Murillo for his assistance in identifying macrofauna in the lab and along with Brighid Odenthal (DFO) for providing a review of this report prior to publication.

REFERENCES

Aksu, A.E. 1983. Holocene and Pleistocene dissolution cycles in deep-sea cores of Baffin Bay and Davis Strait: Palaeoceanographic implications. Mar. Geol. 53: 331–348.

Ardyna, M., Babin, M., Gosselin, M., Devred, E., Rainville, L., and Tremblay, J.-É. 2014. Recent Arctic Ocean sea ice loss triggers novel fall phytoplankton blooms. Geophys. Res. Lett. 41: 6207–6212.

Azetsu-Scott, K., Clarke, A., Falkner, K., Hamilton, J., Jones, E.P., Lee, C., Petrie, B., Prinsenberg, S., Starr, M., and Yeats, P. 2010. Calcium carbonate saturation states in the waters of the Canadian Arctic Archipelago and the Labrador Sea. J. Geophys. Res. Oceans 115(C11).

Baker, S.R., and Friedman, G.M. 1973. Sedimentation in an Arctic marine environment: Baffin Bay between Greenland and the Canadian Arctic Archipelago. Geol. Surv. Canada Paper 71-23, pp. 471–491.

Baker, E., Beazley, L., McMillan, A., Rowsell, J., and Kenchington, E. 2018. Epibenthic Megafauna of the Disko Fan Conservation Area in the Davis Strait (Eastern Arctic) Identified from In Situ Benthic Image Transects. Can. Tech. Rep. Fish. Aquat. Sci. 3272: vi + 388 p.

Baker, K. D., Wareham, V. E., Snelgrove, P. V., Haedrich, R. L., Fifield,D. A., Edinger, E. N., et al. 2012. Distributional patterns of deep-sea coral assemblages in three submarine canyons off Newfoundland, Canada. Mar. Ecol. Prog. Ser. 445: 235–249.

Brito-Morales, I., Schoeman, D. S., Molinos, J. G., Burrows, M. T., Klein, C. J., Arafeh-Dalmau, N., et al. 2020. Climate velocity reveals increasing exposure of deep-ocean biodiversity to future warming. Nature Climate Change 10(6), 576.

Beazley, L., Murillo, F.J., Kenchington, E., Guijarro, J., Lirette, C., Siferd, T., et al. 2016. Species Distribution Modelling of Corals and Sponges in the Eastern Arctic for Use in the Identification of Significant Benthic Areas. Can. Tech. Rep. Fish. Aquat. Sci. 3175: vii + 210p.

Beazley, L., Guijarro, J. Lirette, C., Wang, Z., and Kenchington, E. 2018. Characteristics of Environmental Data Layers for Use in Species Distribution Modelling in the Eastern Canadian Arctic and Sub-Arctic Regions. Can. Tech. Rep. Fish. Aquat. Sci. 3248: vii + 488p.

Beazley, L., Murillo, F.J., Kenchington, E., Guijarro-Sabaniel, J., Lirette, C., Siferd, T., et al. 2019a. Species Distribution Modelling of Corals and Sponges in the Eastern Arctic for Use in the Identification of Significant Benthic Areas. Mendeley Data V1, doi: 10.17632/mcb726kcbx.1

Beazley, L., Guijarro-Sabaniel, J., Lirette, C., Wang, Z., and Kenchington, E. 2019b. Characteristics of Environmental Data Layers for Use in Species Distribution Modelling in the Eastern Canadian Arctic and Sub-Arctic Regions. Mendeley Data, V2, doi: 10.17632/zmwyjs222s.2

Bernhard, J.M., Wit, J.C., Starczak, V.R., Beaudoin, D.J., Phalen, W.G., and McCorkle, D.C. 2021. Impacts of multiple stressors on a benthic foraminiferal community: A long-term experiment assessing response to ocean acidification, hypoxia and warming. Front. Mar. Sci., https://doi.org/10.3389/fmars.2021.643339

Circumpolar Biodiversity Monitoring Program Marine Steering Group. 2015. Arctic Marine Biodiversity Monitoring Plan Annual Plan 2014: Annual Report on the Implementation of the Circumpolar Biodiversity Monitoring Program's Arctic Marine Biodiversity Monitoring Plan (CBMP-Marine Plan). CAFF Monitoring Report No.15. CAFF International Secretariat, Akureyri, Iceland. ISBN: 978-9935-431-42-4

Clarke, K.R. and Gorley, R.N. 2015. PRIMER v7: User Manual/Tutorial. PRIMER-EPlymouth.

Clarke, K.R., Somerfield, P.J., and Gorley, R.N. 2008. Testing of null hypotheses in exploratory community analyses: Similarity profiles and biota-environment linkage J. Exp. Mar. Biol. Ecol. 366: 56-69.

Clarke, K.R., Tweedley, J.R., and Valesini, F.J. 2014. Simple shade plots aid better long-term choices of data pre-treatment in multivariate assemblage studies J. Mar. Biol. Assoc. UK 94: 1-16.

Coupel, P., Matsuoka, A., Diana, R.P., Gosselin, M., Marie, D., Tremblay, J.-É., and Babin, M. 2015. Pigment signatures of phytoplankton communities in the Beaufort Sea. Biogeosci. 12: 991–1006.

de Vernal, A., Bilodeau, G., Hillaire-Marcel, C., and Kassou, N. 1992. Quantitative assessment of carbonate dissolution in marine sediments from foraminifer linings vs shell ratios: Davis Strait northwest North Atlantic. Geology 20(6): 527-530.

DFO. 2007. Development of a Closed Area in NAFO 0A to protect Narwhal Over-Wintering Grounds, including Deep-sea Corals. DFO Can. Sci. Advis. Sec. Sci. Resp. 2007/002.

DFO. 2010. Occurrence, Sensitivity to Fishing, and Ecological Function of Corals, Sponges, and Hydrothermal vents in Canadian waters. DFO Can. Sci. Advis. Sec. Sci. Advis. Rep. 2010/041.

DFO. 2011. Identification of Ecologically and Biologically Significant Areas (EBSA) in the Canadian Arctic. DFO Can. Sci. Advis. Sec. Sci. Advis. Rep. 2011/055.

DFO. 2019. List of Marine Refuges. https://www.dfo-mpo.gc.ca/oceans/oecm-amcepz/refuges/ Accessed 2021-04-14.

Folmer, O., Black, M., Hoeh, W., Lutz, R., and Vrijenhoek, R. 1994. DNA primers for amplification of mitochondrial cytochrome *c* oxidase subunit I from diverse metazoan invertebrates. Mol. Mar. Biol. Biotechnol. 3: 294-297.

Gill M.J., Crane, K., Hindrum, R., Arneberg, P., Bysveen, I., Denisenko, N.V., et al. 2011. Arctic Marine Biodiversity Monitoring Plan (CBMP-MARINE PLAN). CAFF Monitoring Series Report No.3, April 2011,CAFF International Secretariat, Akureyri, Iceland. ISBN 1. 978-9979-9778-7-2

Government of Canada. 2018. New marine refuges off the coasts of Nunavut and Newfoundland and Labrador. News Release. https://www.canada.ca/en/fisheries-oceans/news/2017/12/new_marine_refugesoffthecoastsofnunavutandnewfoundlandandlabrador.html Accessed 2020-12-11.

Hansen, J.L.S., Sejr, M.K., Holm-Hansen, T.H., and Andersen, O.G.N. 2019. Benthic macrofauna communities on the Northeast Greenland shelf 2017. Results and data from the NEG Dana cruise 2017. Aarhus University, DCE – Danish Centre for Environment and Energy, 35 pp. Scientific Report No. 361. http://dce2.au.dk/pub/SR361.pdf

Hiltz, E., Fuller, S. D., and Mitchell, J. 2018. Disko Fan Conservation Area: a Canadian case study. Parks 24 Special Issue June 2018. doi: 10.2305/IUCN.CH.2018.PARKS-24-SIEH.en

Kenchington, E., Lirette, C., Cogswell, A., Archambault, D., Archambault, P., Benoit, H., et al. 2010. Delineating Coral and Sponge Concentrations in the Biogeographic Regions of the East Coast of Canada Using Spatial Analyses. DFO Can. Sci. Advis. Sec.t Res. Doc. 2010/041. iv + 207 pp.

Kenchington, E., Link, H., Roy, V., Archambault, P., Siferd, T., Treble, M., and Wareham, V. 2011. Identification of mega- and macrobenthic Ecologically and Biologically Significant Areas (EBSAs) in the Hudson Bay Complex, the Western and Eastern Canadian Arctic. DFO Can. Sci. Advis. Sec. Res. Doc. 2011/071. vi + 52 p.

Kenchington, E., Siferd, T., and Lirette, C. 2012. Arctic Marine Biodiversity: Indicators for Monitoring Coral and Sponge Megafauna in the Eastern Arctic. DFO Can. Sci. Advis. Sec. Res. Doc. 2012/003: v + 37p.

Kenchington, E., L. Beazley, C. Lirette, F.J. Murillo, J. Guijarro, V. Wareham, K. Gilkinson, M. Koen Alonso, H. Benoît, H. Bourdages, B. Sainte-Marie, M. Treble, and T. Siferd. 2016. Delineation of Coral and Sponge Significant Benthic Areas in Eastern Canada Using Kernel Density Analyses and Species Distribution Models. DFO Can. Sci. Advis. Sec. Res. Doc. 2016/093. vi + 178 p.

Kenchington, E., Lirette, C., Murillo, F., Beazley, L., Guijarro-Sabaniel, J., Wareham, V., et al. 2018a. Kernel Density Analyses of Coral and Sponge Catches from Research Vessel Survey Data for Use in Identification of Significant Benthic Areas. Mendeley Data, V2, doi: 10.17632/dtk86rjm86.2

Kenchington, E., Baker, E., and Beazley, L. 2018b. In Situ Benthic Image Transects from the Disko Fan Conservation Area in the Davis Strait (Eastern Arctic). Mendeley Data, V3, doi: 10.17632/cr3xvztwrj.3

Laidre, K.L., and Heide-Jørgensen, M.P. 2005. Winter feeding intensity of narwhals (*Monodon monoceros*). Mar. Mamm. Sci. 21: 45–57.

Laidre, K.L., Heide-Jørgensen, M.P., Dietz, R., Hobbs, R.C., and Jørgensen, O.A. 2003. Deep-diving by narwhals *Monodon monoceros*: differences in foraging behavior between wintering areas? Mar. Ecol. Prog. Ser. 261: 269–281.

Lim, A., Wheeler, A.J., Price, D.M., O'Reilly, L., Harris, K., and Conti, L. 2020. Influence of benthic currents on cold-water coral habitats: a combined benthic monitoring and 3D photogrammetric investigation. Sci. Rep. 10: 19433.

Long, S., Sparrow-Scinocca, B., Blicher, M. E., Arboe, N. H., Fuhrmann, M., Kemp, K. M., et al. 2020. Identification of a soft coral garden candidate vulnerable marine ecosystem (VME) using video imagery, Davis Strait, West Greenland. Front. Mar. Sci. 7.

Maier, C., Watremez, P., Taviani, M., Weinbauer, M. G., and Gattuso, J. P. 2012. Calcification rates and the effect of ocean acidification on Mediterranean cold-water corals. Proc. Roy. Soc. Biol. Sci. 279(1734): 1716–1723.

Meyer, C.P. 2003. Molecular systematics of coweries (Gastropoda: Cypraeidae) and diversification patterns in the tropics. Biol. J. Linnean Soc., 79: 401-459.

Monier, A., Comte, J., Babin, M., Forest, A., Matsuoka, A., and Lovejoy, C. 2014. Oceanographic structure drives the assembly processes of microbial eukaryotic communities. ISME J. 9: 990–1002.

Mundy, C.J., Gosselin, M., Ehn, J., Gratton, Y., Rossnagel, A., Barber, D.G., et al. 2009. Contribution of under-ice primary production to an ice-edge upwelling phytoplankton bloom in the Canadian Beaufort Sea. Geophys. Res. Lett. 36: L17601.

Murillo, F. J., Kenchington, E., Tompkins, G., Beazley, L., Baker, E., Knudby, A., and Walkusz, W. 2018. Sponge assemblages and predicted archetypes in the eastern Canadian Arctic. Mar. Ecol. Progr. Ser. 597: 115–135.

Murillo, F.J., Kenchington, E., Tompkins MacDonald, G., Beazley, L., Baker, E., Knudby, A., and Walkusz, W. 2019. Sponge Assemblages and Predicted Archetypes in the Eastem Canadian Arctic. Mendeley Data, V1, doi: 10.17632/vb4xvxk86v.1

Niemi, A., Ferguson, S., Hedges, K., Melling, H., Michel, C., Ayles, B., et al. 2019. State of Canada's Arctic Seas. Can. Tech. Rep. Fish. Aquat. Sci. 3344: xv + 189 p.

Osborne, E., Richter-Menge, J., and Jeffries, M. (eds.). 2018. Arctic report card 2018. Available from: https://www.arctic.noaa.gov/Report-Card [accessed 11 February 2019].

Orr, J. C., Fabry, V. J., Aumont, O., Bopp, L., Doney, S. C., Feely, R. A., et al. 2005. Anthropogenic ocean acidification over the twenty-first century and its impact on calcifying organisms. Nature 437(7059): 681–686.

Osterman, L.E., and Nelson, A.R. 1989. Latest Quaternary and Holocene paleoceanography of the eastern Baffin Island continental shelf Canada: benthic foraminiferal evidence. Can J. Earth Sci. 26: 2236-2248.

Peklova, I., Hussey, N.E., Hedges, K.J., Treble, M.A., and Fisk, A.T. 2012. Depth and temperature preferences of the deepwater flatfish Greenland halibut *Reinhardtius hippoglossoides* in an Arctic marine ecosystem. Mar. Ecol. Prog. Ser. 467: 193–205.

Sala, E., Mayorga, J., Bradley, D., Cabral, R. B., Atwood, T. B., Auber, A., et al. 2021. Protecting the global ocean for biodiversity, food and climate. Nature 592: 397–402.

Schafer, C.T., and Cole, F.E. 1988. Environmental associations of Baffin Island fjord agglutinated foraminifera. Abh. Geol. B.-A. 41: 307-323.

Schröeder-Adams, C. and Van Rooyen, D. 2011. Response of recent benthic foraminiferal assemblages to contrasting environments in Baffin Bay and the northern Labrador Sea, Northwest Atlantic. Arctic 64: 317–341.

Serreze, M. C., Barrett, A. P., Slater, A. G., Woodgate, R. A., Aagaard, K., Lammers, R., et al. 2007. The large-scale freshwater cycle of the Arctic. J. Geophys. Res. 111, C11010.

Shu Q. Qiao, F. Song, Z., Zhao, J., and Li, X. 2018. Projected freshening of the Arctic Ocean in the 21st century. J. Geophys. Res. Oceans 123: 9232–9244.

Tremblay, J.-É., Bélanger, S., Barber, D.G., Asplin, M., Martin, J., Darnis, G., et al. 2011. Climate forcing multiplies biological productivity in the coastal Arctic Ocean. Geophys. Res. Lett. 38: L18604.

Tremblay, J.-É., Raimbault, P., Garcia, N., Lansard, B., Babin, M., and Gagnon, J. 2014. Impact of river discharge, upwelling and vertical mixing on the nutrient loading and productivity of the Canadian Beaufort Shelf. Biogeosci. 11: 4853–4868.

Tremblay, J.-É., Anderson, L.G., Matrai, P., Coupel, P., Bélanger, S., Michel, C., and Reigstad, M. 2015. Global and regional drivers of nutrient supply, primary production and CO2 drawdown in the changing Arctic Ocean. Prog. Oceanogr. 139: 171–196.

Watt, C.A., Heide-Jørgensen, M.P., and Ferguson, S.H. 2013. How adaptable are narwhal? A comparison of foraging patterns among the world's three narwhal populations. Ecosphere 4: 71.

Watt, C.A., Orr, J.R., Heide-Jørgensen, M.P., Nielsen, N.H., and Ferguson, S.H. 2015. Differences in dive behaviour among the world's three narwhal *Monodon monoceros* populations correspond with dietary differences. Mar. Ecol. Prog. Ser. 525: 273–285.

Watt, C.A., Orr, J. R., and Ferguson, S. H. 2017. Spatial distribution of narwhal (*Monodon monoceros*) diving for Canadian populations helps identify important seasonal foraging areas. Can. J. Zool. 95: 41–50.

Wörheide, G. 1998. The reef cave dwelling ultraconservative coralline demosponge *Astrosclera willeyana* Lister 1900 from the Indo-Pacific: Micromorphology, ultrastructure, biocalcification, isotope record, taxonomy, biogeography, phylogeny. Facies 38: 1-88.

APPENDIX A: SAMPLING OVERVIEW

Table 1. Summary of all operations (camera, core/grab) at CBMP biodiversity monitoring stations in the Disko Fan and Hatton Basin Conservation Areas for which data have been analysed. Stations sampled and processed for all focal ecosystem components are in bold font and boxed.

Site	Station Group	Station Code	Benthic imagery	Sediment samples for macrofauna/ megafauna > 1 cm	Sediment samples for meiofauna
Disko Fan Conservation Area	BB1_A	**BB1_A_600 m**	**4K Camera**	**5 Van Veen grabs**	**3 Van Veen grabs**
	BB1_B	**BB1_B_400 m**	**4K Camera**	**5 Van Veen grabs**	**3 Van Veen grabs**
		BB1_B_600 m	4K Camera	-	-
		BB1_B_1000 m	4K Camera	-	
	BB1_C	**BB1_C_400 m**	**4K Camera**	**5 Van Veen grabs**	**3 Van Veen grabs**
		BB1_C_1000 m	4K Camera	1 box core	-
	BB1_D	**BB1_D**	**4K Camera**	**5 Van Veen grabs**	**3 Van Veen grabs**
Hatton Basin Conservation Area	DS1_S	DS1		3 box cores	-

APPENDIX B: MACROFAUNAL TAXON LIST (1-CM SIZE FRACTION)

Table 1. List of 101 taxa identified from the 1-cm size fraction of the sediment samples from stations BB1_A_600 m, BB1_B_400 m, BB1_C_1000 m, BB1_C_400 m, BB1_D, and DS1_S in the Disko Fan and Hatton Basin Conservation Areas.

Identified Taxon	Phylum	Class	Order	Family	Genus	Species
Eunice pennata	Annelida	Polychaeta	Eunicida	Eunicidae	*Eunice*	*pennata*
Scoletoma fragilis	Annelida	Polychaeta	Eunicida	Lumbrineridae	*Scoletoma*	*fragilis*
Glycera capitata	Annelida	Polychaeta	Phyllodocida	Glyceridae	*Glycera*	*capitata*
Aglaophamus malmgreni	Annelida	Polychaeta	Phyllodocida	Nephtyidae	*Aglaophamus*	*malmgreni*
Eulalia sp. 1	Annelida	Polychaeta	Phyllodocida	Phyllodocidae	*Eulalia*	
Polynoidae spp.	Annelida	Polychaeta	Phyllodocida	Polynoidae		
Syllidae spp.	Annelida	Polychaeta	Phyllodocida	Syllidae		
Potamilla sp. 1	Annelida	Polychaeta	Sabellida	Sabellidae	*Potamilla*	
Placostegus tridentatus	Annelida	Polychaeta	Sabellida	Serpulidae	*Placostegus*	*tridentatus*
Serpulidae sp. 2	Annelida	Polychaeta	Sabellida	Serpulidae		
Samythella elongata	Annelida	Polychaeta	Terebellida	Ampharetidae	*Samythella*	*elongata*
Pista bansei	Annelida	Polychaeta	Terebellida	Terebellidae	*Pista*	
Polycirrus sp. 1	Annelida	Polychaeta	Terebellida	Terebellidae	*Polycirrus*	
Terebellides gracilis	Annelida	Polychaeta	Terebellida	Trichobranchidae	*Terebellides*	*gracilis*
Terebellides stroemii	Annelida	Polychaeta	Terebellida	Trichobranchidae	*Terebellides*	*stroemii*
Clymenura spp.	Annelida	Polychaeta		Maldanidae	*Clymenura*	
Maldanella davisi	Annelida	Polychaeta		Maldanidae	*Maldanella*	*davisi*
Nicomache (Loxochona) quadrispinata	Annelida	Polychaeta		Maldanidae	*Nicomache*	*quadrispinata*
Petaloproctus tenuis	Annelida	Polychaeta		Maldanidae	*Petaloproctus*	*tenuis*
Praxillura spp.	Annelida	Polychaeta		Maldanidae	*Praxillura*	
Polychaeta sp. 2	Annelida	Polychaeta				
Caprellidae spp.	Arthropoda	Malacostraca	Amphipoda	Caprellidae		
Diastylis spp.	Arthropoda	Malacostraca	Cumacea	Diastylidae	*Diastylis*	
Janiroidea sp. 1	Arthropoda	Malacostraca	Isopoda			
Scalpellidae sp. 1	Arthropoda	Thecostraca	Scalpellomorpha	Scalpellidae		
Verruca spp.	Arthropoda	Thecostraca	Verrucomorpha	Verrucidae	*Verruca*	
Brachipoda spp.	Brachiopoda					
Bryozoa Flustrina sp. 1	Bryozoa	Gymnolaemata	Cheilostomatida			
Bryozoa Flustrina sp. 2	Bryozoa	Gymnolaemata	Cheilostomatida			
Bryozoa Flustrina sp. 4	Bryozoa	Gymnolaemata	Cheilostomatida			
Bryozoa Flustrina sp. 7	Bryozoa	Gymnolaemata	Cheilostomatida			
Bryozoa Flustrina sp. 10	Bryozoa	Gymnolaemata	Cheilostomatida			
Bryozoa Flustrina sp. 11	Bryozoa	Gymnolaemata	Cheilostomatida			

Identified Taxon	Phylum	Class	Order	Family	Genus	Species
Bryozoa Flustrina sp. 15	Bryozoa	Gymnolaemata	Cheilostomatida			
Bryozoa Flustrina sp. 17	Bryozoa	Gymnolaemata	Cheilostomatida			
Bryozoa Cyclostomatida sp. 1	Bryozoa	Stenolaemata	Cyclostomatida			
Bryozoa Cyclostomatida sp. 2	Bryozoa	Stenolaemata	Cyclostomatida			
Bryozoa Cyclostomatida sp. 3	Bryozoa	Stenolaemata	Cyclostomatida			
Bryozoa Cyclostomatida sp. 4	Bryozoa	Stenolaemata	Cyclostomatida			
Bryozoa Cyclostomatida sp. 5	Bryozoa	Stenolaemata	Cyclostomatida			
Bryozoa spp.	Bryozoa					
Ascidiacea sp. 1 (colonial)	Chordata	Ascidiacea				
Ascidiacea sp. 2 (solitary)	Chordata	Ascidiacea				
Clavularia sp. 1	Cnidaria	Anthozoa	Alcyonacea	Clavulariidae	*Clavularia*	
Acanella arbuscula	Cnidaria	Anthozoa	Alcyonacea	Isididae	*Acanella*	*arbuscula*
Duva florida	Cnidaria	Anthozoa	Alcyonacea	Nephtheidae	*Duva*	*florida*
Nephtheidae spp.	Cnidaria	Anthozoa	Alcyonacea	Nephtheidae		
Pennatula sp. 1	Cnidaria	Anthozoa	Pennatulacea		*Pennatula*	
Pennatulacea sp. 1	Cnidaria	Anthozoa	Pennatulacea			
Cerianthidae spp.	Cnidaria	Anthozoa	Spirularia	Cerianthidae		
Anthozoa spp.	Cnidaria	Anthozoa				
Anthoathecata sp. 1	Cnidaria	Hydrozoa	Anthoathecata			
Cladocarpus sp. 1	Cnidaria	Hydrozoa	Leptothecata	Aglaopheniidae	*Cladocarpus*	
Hydrozoa spp.	Cnidaria	Hydrozoa				
Asteroidea sp. 1	Echinodermata	Asteroidea				
Hathrometra sp. 1	Echinodermata	Crinoidea	Comatulida	Antedonidae	*Hathrometra*	
Rhizocrinidae sp. 1	Echinodermata	Crinoidea	Comatulida	Rhizocrinidae		
Brisaster fragilis	Echinodermata	Echinoidea	Spatangoida	Schizasteridae	*Brisaster*	*fragilis*
Psolus sp. 1	Echinodermata	Holothuroidea	Dendrochirotida	Psolidae	*Psolus*	
Holothuroidea spp.	Echinodermata	Holothuroidea				
Amphiura fragilis	Echinodermata	Ophiuroidea	Amphilepidida	Amphiuridae	*Amphiura*	*fragilis*
Amphiura spp.	Echinodermata	Ophiuroidea	Amphilepidida	Amphiuridae	*Amphiura*	
Ophiopholis aculeata	Echinodermata	Ophiuroidea	Amphilepidida	Ophiopholidae	*Ophiopholis*	*aculeata*
Ophiacantha bidentata	Echinodermata	Ophiuroidea	Ophiacanthida	Ophiacanthidae	*Ophiacantha*	*bidentata*
Ophiolycus purpureus	Echinodermata	Ophiuroidea	Ophioscolecida	Ophioscolecidae	*Ophiolycus*	*purpureus*
Ophiura sarsii	Echinodermata	Ophiuroidea	Ophiurida	Ophiuridae	*Ophiura*	*sarsii*
Ophiuroidea sp. 1	Echinodermata	Ophiuroidea				
Ophiuroidea sp. 2	Echinodermata	Ophiuroidea				
Ophiuroidea sp. 3	Echinodermata	Ophiuroidea				
Bathyarca spp.	Mollusca	Bivalvia	Arcida	Arcidae	*Bathyarca*	
Astarte spp.	Mollusca	Bivalvia	Carditida	Astartidae	*Astarte*	

Identified Taxon	Phylum	Class	Order	Family	Genus	Species
Cyclopecten hoskynsi	Mollusca	Bivalvia	Pectinida	Propeamussiidae	*Cyclopecten*	*hoskynsi*
Poromya granulata	Mollusca	Bivalvia		Poromyidae	*Poromya*	*granulata*
Polinices sp. 1	Mollusca	Gastropoda	Littorinimorpha	Naticidae	*Polinices*	
Marginellidae sp. 1	Mollusca	Gastropoda	Neogastropoda	Marginellidae		
Patellogastropoda sp. 1	Mollusca	Gastropoda				
Patellogastropoda sp. 2	Mollusca	Gastropoda				
Polyplacophora spp.	Mollusca	Polyplacophora				
Scaphopoda spp.	Mollusca	Scaphopoda				
Nemertea spp.	Nemertea					
Platyhelminthes spp.	Platyhelminthes					
Leucosolenida sp. 1	Porifera	Calcarea	Leucosolenida			
Calcarea sp. 1	Porifera	Calcarea				
Janulum spinispiculum	Porifera	Demospongiae	Axinellida	Raspailiidae	*Janulum*	*spinispiculum*
cf. Iriciniidae spp.	Porifera	Demospongiae	Dictyoceratida	Iriciniidae		
Haplosclerida spp.	Porifera	Demospongiae	Haplosclerida			
Iophon spp.	Porifera	Demospongiae	Poecilosclerida	Acarnidae	*Iophon*	
Asbestopluma sp. 1	Porifera	Demospongiae	Poecilosclerida	Cladorhizidae	*Asbestopluma*	
Esperiopsidae sp. 1	Porifera	Demospongiae	Poecilosclerida	Esperiopsidae		
Hymedesmia sp. 2	Porifera	Demospongiae	Poecilosclerida	Hymedesmiidae	*Hymedesmia*	
Sceptrella sp. 1	Porifera	Demospongiae	Poecilosclerida	Latrunculiidae	*Sceptrella*	
Microcionidae sp. 1	Porifera	Demospongiae	Poecilosclerida	Microcionidae		
Mycale (Rhaphidotheca) marshallhalli	Porifera	Demospongiae	Poecilosclerida	Mycalidae	*Mycale*	*marshallhalli*
Polymastiidae sp. 1	Porifera	Demospongiae	Polymastiida	Polymastiidae		
cf. *Halichondria* spp.	Porifera	Demospongiae	Suberitida	Halichondriidae	*Halichondria*	
Tethya sp. 1	Porifera	Demospongiae	Tethyida	Tethyidae	*Tethya*	
Theneidae spp.	Porifera	Demospongiae	Tetractinellida	Theneidae		
Demospongiae sp. 1	Porifera	Demospongiae				
Asconema foliatum	Porifera	Hexactinellida	Lyssacinosida	Rossellidae	*Asconema*	*foliatum*
Porifera spp.	Porifera					
Sipuncula spp.	Sipuncula					

APPENDIX C: MACROFAUNAL DIVERSITY INDICES BY STATION

Table 1. Macrofaunal indicators for the 1-cm size fraction for the eastern Canadian Arctic biodiversity monitoring sites (Disko Fan and Hatton Basin Conservation Areas). Abundance (N), Biomass (B), S = number of species, d = Margalef Species Richness, J′ = Pielou's Evenness. All data were standardized to values/m^2. CON=Consecutive Operation Number. *Indicates significant differences among all stations (ANOVA); ǂIndicates significant difference among DFCA stations (ANOVA). Retrospective power and least significant number (LSN) calculations for non-significant ANOVAǂ.

Site	Station	CON	Latitude	Longitude	Depth (m)	Total B* (mg/m^2)	S*ǂ	N*ǂ ($no./m^2$)	d*	J′*	Shannon H′(log_e)	Simpson Index
DFCA	BB1_B_400 m	57	67.9934	-59.3233	504	4750.34	4	27.59	0.90	1.00	1.39	0.778
DFCA	BB1_B_400 m	67	67.9941	-59.3123	476	27586.21	1	6.90	0.00	-	0.00	0.000
DFCA	BB1_B_400 m	69	67.9929	-59.3092	476	10708.28	11	75.86	2.31	1.00	2.40	0.921
DFCA	BB1_B_400 m	70	67.9937	-59.3108	475	23284.14	4	34.48	0.85	0.96	1.33	0.742
DFCA	BB1_B_400 m	72	67.9931	-59.308	473	3090.34	10	68.97	2.13	1.00	2.30	0.913
DFCA	BB1_A_600 m	85	67.768	-59.0872	701	3982.76	5	34.48	1.13	1.00	1.61	0.824
DFCA	BB1_A_600 m	87	67.7707	-59.0905	696	6762.76	3	27.59	0.60	0.95	1.04	0.649
DFCA	BB1_A_600 m	89	67.7696	-59.0921	706	77435.86	3	27.59	0.60	0.95	1.04	0.649
DFCA	BB1_A_600 m	90	67.7688	-59.092	710	8647.59	8	55.17	1.75	1.00	2.08	0.891
DFCA	BB1_A_600 m	96	67.7706	-59.0932	707	14827.59	7	55.17	1.50	0.98	1.91	0.859
DFCA	BB1_C_1000 m	101	67.527	-58.6061	1010	5212.41	6	68.97	1.18	0.90	1.61	0.771
DFCA	BB1_C_400 m	105	67.6141	-58.5415	375	334675.86	21	220.69	3.71	0.93	2.83	0.928
DFCA	BB1_C_400 m	107	67.6135	-58.5397	376	41273.10	20	765.52	2.86	0.81	2.43	0.884
DFCA	BB1_C_400 m	108	67.6119	-58.5453	385	1736.55	3	20.69	0.66	1.00	1.10	0.701
DFCA	BB1_C_400 m	111	67.6131	-58.5391	372	71706.90	16	965.52	2.18	0.68	1.89	0.780
DFCA	BB1_C_400 m	114	67.6123	-58.5431	379	3796.55	12	89.66	2.45	0.99	2.46	0.922
DFCA	BB1_D	122	67.382	-57.924	644	76842.07	7	62.07	1.45	0.97	1.89	0.853
DFCA	BB1_D	123	67.3817	-57.9263	647	774.48	6	41.38	1.34	1.00	1.79	0.854
DFCA	BB1_D	124	67.3824	-57.9285	648	4264.83	5	62.07	0.97	0.89	1.43	0.728
DFCA	BB1_D	125	67.3829	-57.9309	650	18398.62	9	96.55	1.75	0.96	2.11	0.876
DFCA	BB1_D	126	67.3825	-57.9229	642	16773.79	5	34.48	1.13	1.00	1.61	0.824
HBCA	DS1_S	141	61.1513	-60.7666	1051	619534.40	21	364.00	3.39	0.78	2.38	0.855
HBCA	DS1_S	142	61.151	-60.7758	1012	51406.40	20	864.00	2.81	0.35	1.04	0.375
HBCA	DS1_S	145	61.1476	-60.7551	1093	177154.00	16	208.00	2.81	0.80	2.22	0.842
Power	ANOVA DFCA stations					0.23			0.47	0.37	0.20	0.14
LSN	ANOVA DFCA stations					57			29	34	66	99

APPENDIX D: EFFECT OF DATA TRANSFORMATION ON MACROFAUNAL ABUNDANCE

Untransformed Standardized Abundance

Square-Root Transformed Standardized Abundance

Log(x+1)-Transformed Standardized Abundance

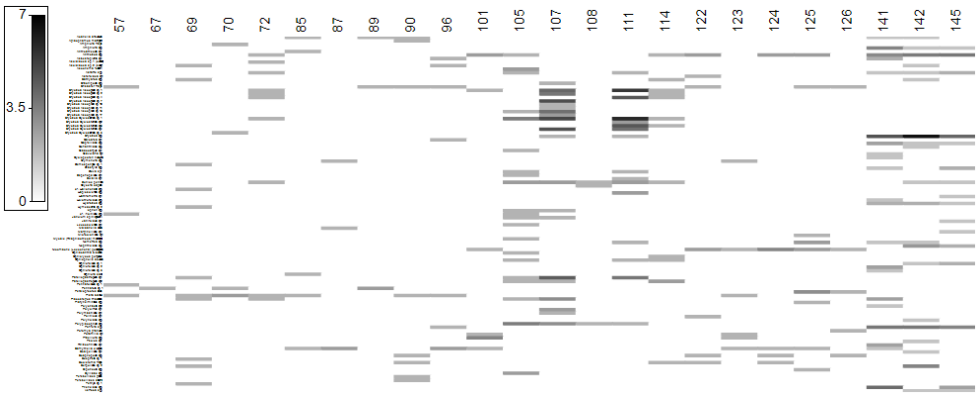


Figure 1. Shade plots showing the effect of transformation on the standardized abundance of macrofaunal taxa by sample (labelled by Consecutive Operation Number). Scale bars of the abundance for each plot are shown in the upper left.

APPENDIX E: SIMILARITY IN ABUNDANCE AMONG MACROFAUNAL COMMUNITIES

57	**57**																							
67	0.0	**67**																						
69	13.3	0.0	**69**																					
70	24.1	37.7	13.1	**70**																				
72	14.3	0.0	19.0	14.0	**72**																			
85	22.2	0.0	12.5	21.5	13.3	**85**																		
87	0.0	0.0	0.0	0.0	0.0	24.1	**87**																	
89	27.4	46.5	0.0	26.3	0.0	24.1	0.0	**89**																
90	33.3	0.0	10.5	16.3	11.1	30.8	0.0	35.4	**90**															
96	35.4	0.0	21.9	17.2	11.6	32.5	24.6	18.9	26.1	**96**														
101	0.0	0.0	0.0	0.0	23.6	16.8	19.6	0.0	0.0	14.1	**101**													
105	7.3	0.0	11.6	0.0	30.0	0.0	0.0	0.0	0.0	0.0	6.6	**105**												
107	0.0	0.0	9.8	0.0	25.1	0.0	0.0	0.0	0.0	0.0	5.4	39.6	**107**											
108	0.0	0.0	0.0	0.0	15.4	0.0	0.0	0.0	0.0	0.0	0.0	15.2	12.2	**108**										
111	0.0	0.0	5.6	0.0	29.0	0.0	0.0	0.0	0.0	0.0	6.4	33.5	42.1	14.5	**111**									
114	0.0	0.0	8.6	0.0	53.8	0.0	0.0	0.0	9.9	0.0	20.8	28.0	23.7	13.1	32.6	**114**								
122	17.2	0.0	0.0	0.0	11.4	0.0	0.0	18.3	38.4	13.4	31.7	6.5	0.0	0.0	0.0	20.1	**122**							
123	20.0	0.0	11.8	19.4	12.5	36.4	43.0	0.0	14.3	30.1	61.9	0.0	0.0	0.0	0.0	0.0	14.7	**123**						
124	0.0	0.0	0.0	0.0	12.6	18.3	21.7	0.0	28.7	15.1	51.4	6.8	0.0	0.0	0.0	21.9	68.1	33.5	**124**					
125	13.9	0.0	0.0	0.0	9.8	13.0	14.6	14.6	10.9	22.6	38.1	5.9	0.0	0.0	5.7	8.8	40.1	24.4	44.2	**125**				
126	22.2	0.0	0.0	0.0	0.0	0.0	0.0	24.1	30.8	16.3	16.8	0.0	0.0	0.0	0.0	0.0	47.6	18.2	36.6	39.0	**126**			
141	0.0	0.0	5.7	0.0	16.3	10.7	5.7	5.7	4.9	17.7	13.4	11.7	8.3	0.0	10.5	5.5	8.2	5.2	13.9	16.6	0.0	**141**		
142	0.0	0.0	15.7	0.0	16.2	5.8	0.0	6.2	5.3	12.3	9.1	11.4	6.9	6.3	14.4	15.1	8.9	0.0	9.4	13.0	0.0	46.3	**142**	
145	0.0	0.0	0.0	0.0	20.5	0.0	0.0	0.0	0.0	8.2	10.8	13.7	7.6	7.7	13.3	12.1	10.5	0.0	11.3	9.5	0.0	50.1	61.3	**145**
Site	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	HBCA	HBCA	HBCA
Station	BB1_B_400 m	BB1_B_400 m	BB1_B_400 m	BB1_B_400 m	BB1_B_400 m	BB1_A_600 m	BB1_A_600 m	BB1_A_600 m	BB1_A_600 m	BB1_A_600 m	BB1_C_1000 m	BB1_C_400 m	BB1_C_400 m	BB1_C_400 m	BB1_C_400 m	BB1_C_400 m	BB1_D	BB1_D	BB1_D	BB1_D	BB1_D	DS1_S	DS1_S	DS1_S

Figure 1. Bray-Curtis similarity among macrofaunal communities (> 1-cm size fraction) based on log (x+1)-transformed standardized abundance. Samples are labelled by Consecutive Operation Number (in bold, black for rows, white for columns), site and station.

APPENDIX F: RANKED MACROFAUNAL TAXON ABUNDANCE

Table 1. Standardized abundance in ranked order for each of the 101 macrofaunal taxa (> 1-cm size fraction) recorded from 24 sediment samples collected from six stations (Appendix G). Percent and cumulative percent abundance for each taxon provided.

Taxon	A	% A	Cumulative % A
Bryozoa spp.	869.8	20.3	20.3
Bryozoa Cyclostomatida sp. 1	551.7	12.9	33.2
Bryozoa Flustrina sp. 1	324.1	7.6	40.8
Anthozoa spp.	175.9	4.1	44.9
Bryozoa Cyclostomatida sp. 3	165.5	3.9	48.8
Patellogastropoda sp. 1	137.9	3.2	52.0
Bryozoa Flustrina sp. 15	124.1	2.9	54.9
Porifera spp.	114.9	2.7	57.6
Bryozoa Flustrina sp. 11	110.3	2.6	60.2
Bryozoa Cyclostomatida sp. 2	103.4	2.4	62.6
Nicomache (Loxochona) quadrispinata	75.9	1.8	64.3
Esperiopsidae sp. 1	70.1	1.6	66.0
Polyplacophora spp.	69.0	1.6	67.6
Theneidae spp.	68.0	1.6	69.2
Samythella elongata	66.1	1.5	70.7
Pista bansei	62.1	1.5	72.2
Bryozoa Flustrina sp. 4	55.2	1.3	73.5
Bryozoa Flustrina sp. 10	55.2	1.3	74.8
Placostegus tridentatus	53.4	1.2	76.0
Brisaster fragilis	48.3	1.1	77.1
Astarte spp.	36.7	0.9	78.0
Amphiura spp.	36.0	0.8	78.8
Serpulidae sp. 2	34.9	0.8	79.6
Praxillura spp.	34.5	0.8	80.5
Acanella arbuscula	28.7	0.7	81.1
Nemertea spp.	28.7	0.7	81.8
Scoletoma fragilis	27.6	0.6	82.4
Petaloproctus tenuis	27.6	0.6	83.1
Pennatulacea sp. 1	27.6	0.6	83.7
Patellogastropoda sp. 2	27.6	0.6	84.4
Scaphopoda spp.	27.6	0.6	85.0
Nephtheidae spp.	24.0	0.6	85.6
Ophiopholis aculeata	20.7	0.5	86.1
Caprellidae spp.	20.0	0.5	86.5
Holothuroidea spp.	20.0	0.5	87.0
Ascidiacea sp. 2 (solitary)	17.8	0.4	87.4

Taxon	A	% A	Cumulative % A
Bathyarca spp.	17.8	0.4	87.8
Asbestopluma sp. 1	14.9	0.3	88.2
Glycera capitata	13.8	0.3	88.5
Syllidae spp.	13.8	0.3	88.8
Potamilla sp. 1	13.8	0.3	89.1
Polychaeta sp. 2	13.8	0.3	89.5
Janiroidea sp. 1	13.8	0.3	89.8
Bryozoa Flustrina sp. 7	13.8	0.3	90.1
Bryozoa Cyclostomatida sp. 5	13.8	0.3	90.4
Clavularia sp. 1	13.8	0.3	90.8
Iophon spp.	13.8	0.3	91.1
Hymedesmia sp. 2	13.8	0.3	91.4
Demospongiae sp. 1	13.8	0.3	91.7
Asconema foliatum	13.8	0.3	92.1
Rhizocrinidae sp. 1	12.0	0.3	92.3
Ophiura sarsii	12.0	0.3	92.6
Ophiuroidea sp. 1	12.0	0.3	92.9
Cyclopecten hoskynsi	12.0	0.3	93.2
Verruca spp.	8.0	0.2	93.4
Eunice pennata	6.9	0.2	93.5
Aglaophamus malmgreni	6.9	0.2	93.7
Eulalia sp. 1	6.9	0.2	93.8
Polycirrus sp. 1	6.9	0.2	94.0
Terebellides gracilis	6.9	0.2	94.2
Terebellides stroemii	6.9	0.2	94.3
Clymenura spp.	6.9	0.2	94.5
Maldanella davisi	6.9	0.2	94.7
Diastylis spp.	6.9	0.2	94.8
Brachipoda spp.	6.9	0.2	95.0
Bryozoa Flustrina sp. 17	6.9	0.2	95.1
Bryozoa Flustrina sp. 2	6.9	0.2	95.3
Bryozoa Cyclostomatida sp. 4	6.9	0.2	95.5
Ascidiacea sp. 1 (colonial)	6.9	0.2	95.6
Duva florida	6.9	0.2	95.8
Pennatula sp. 1	6.9	0.2	95.9
Anthoathecata sp. 1	6.9	0.2	96.1
Hydrozoa spp.	6.9	0.2	96.3
Asteroidea sp. 1	6.9	0.2	96.4
Amphiura fragilis	6.9	0.2	96.6
Ophiacantha bidentata	6.9	0.2	96.7
Ophiolycus purpureus	6.9	0.2	96.9

Taxon	A	% A	Cumulative % A
Ophiuroidea sp. 3	6.9	0.2	97.1
Poromya granulata	6.9	0.2	97.2
Platyhelminthes spp.	6.9	0.2	97.4
Leucosolenida sp. 1	6.9	0.2	97.6
Calcarea sp. 1	6.9	0.2	97.7
Sceptrella sp. 1	6.9	0.2	97.9
Microcionidae sp. 1	6.9	0.2	98.0
Mycale (Rhaphidotheca) marshallhalli	6.9	0.2	98.2
Polymastiidae sp. 1	6.9	0.2	98.4
cf. *Halichondria* spp.	6.9	0.2	98.5
Tethya sp. 1	6.9	0.2	98.7
Sipuncula spp.	6.9	0.2	98.8
Polynoidae spp.	4.0	0.1	98.9
Scalpellidae sp. 1	4.0	0.1	99.0
Cerianthidae spp.	4.0	0.1	99.1
Cladocarpus sp. 1	4.0	0.1	99.2
Hathrometra sp. 1	4.0	0.1	99.3
Psolus sp. 1	4.0	0.1	99.4
Ophiuroidea sp. 2	4.0	0.1	99.5
Polinices sp. 1	4.0	0.1	99.6
Marginellidae sp. 1	4.0	0.1	99.7
Janulum spinispiculum	4.0	0.1	99.8
cf. Iricinidae spp.	4.0	0.1	99.9
Haplosclerida spp.	4.0	0.1	100.0
Total Abundance	4277.4		

APPENDIX G: MACROFAUNAL TAXON ABUNDANCE BY SAMPLE

Table 1. Abundance/m² for each of 101 macrofaunal taxa (> 1-cm size fraction), by phylum, for each sample (labelled by Consecutive Operation Number) in each station. Note: Taxa are mutually exclusive within the BB1 stations, and within the DS1_S station but not between the two groups, as the DS1_S samples were not fully identified to species in some groups (e.g., Bryozoa, Porifera). Phylum total abundances (used to generate Figure 10) are rounded to whole numbers.

Station	BB1_B_400 m					BB1_A_600 m					BB1_C_1000 m	BB1_C_400 m						BB1_D					DS1_S		
Taxon/Phylum	57	67	69	70	72	85	87	89	90	96	101	105	107	108	111	114	122	123	124	125	126	141	142	145
Annelida	7	0	21	14	21	14	28	0	34	21	48	34	48	14	21	14	21	41	41	41	14	20	36	4
Eunice pennata	0	0	0	0	6.9	0	0	0	0	0	0	13.8	13.8	6.9	13.8	6.9	0	0	0	0	0	0	4	4
Scoletoma fragilis	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	6.9	6.9	0	6.9	0	0	0	0	0
Glycera capitata	0	0	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0
Aglaophamus malmgreni	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eulalia sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0
Polynoidae spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0
Syllidae spp.	0	0	0	0	0	0	0	0	0	0	0	13.8	0	0	0	0	0	0	0	0	0	0	0	0
Potamilla sp.1	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	6.9	0	0	0	0	0	0
Placostegus tridentatus	0	0	6.9	0	6.9	0	0	0	0	0	0	6.9	20.7	0	0	0	0	0	0	0	0	12	0	0
Serpulidae sp. 2	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	28	0
Samythella elongata	0	0	0	0	0	6.9	13.8	0	0	13.8	6.9	0	0	0	0	0	0	6.9	6.9	6.9	0	4	0	0
Pista bansei	6.9	0	6.9	13.8	6.9	6.9	0	0	6.9	6.9	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0
Polycirrus sp.1	0	0	0	0	0	0	0	0	0	0	0	0	13.8	0	0	0	0	0	0	0	0	0	0	0
Terebellides gracilis	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Terebellides stroemii	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Clymenura spp.	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0
Maldanella davisi	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nicomache (Loxochona) quadrispinata	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	13.8	6.9	27.6	13.8	6.9	0	0	0
Petaloproctus tenuis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	20.7	6.9	0	0	0
Praxillura spp.	0	0	0	0	0	0	0	0	0	0	27.6	0	0	0	0	0	0	6.9	0	0	0	0	0	0
Polychaeta sp.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
Arthropoda	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	16	12	20

Station	BB1_B_400 m					BB1_A_600 m					BB1_C_1000 m	BB1_C_400 m					BB1_D					DS1_S		
Taxon/Phylum	57	67	69	70	72	85	87	89	90	96	101	105	107	108	111	114	122	123	124	125	126	141	142	145
Caprellidae spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12	4	4
Diastylis spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	8
Janiroidea sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4
Scalpellidae sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0
Verruca spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	4
Brachiopoda	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	0	0	0	0	0	0	0	0
Brachipoda spp.	0	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0
Bryozoa	0	0	0	7	28	0	0	0	0	0	7	41	579	0	855	34	0	0	0	0	0	112	680	64
Bryozoa Flustrina sp. 1	0	0	0	0	6.9	0	0	0	0	0	6.9	0	62.1	0	241.4	6.9	0	0	0	0	0	0	0	0
Bryozoa Flustrina sp. 10	0	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0
Bryozoa Flustrina sp. 11	0	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0
Bryozoa Flustrina sp. 15	0	0	0	0	0	0	0	0	0	0	0	6.9	48.3	0	0	0	0	0	0	0	0	0	0	0
Bryozoa Flustrina sp. 17	0	0	0	0	0	0	0	0	0	0	0	0	13.8	0	0	0	0	0	0	0	0	0	0	0
Bryozoa Flustrina sp. 2	0	0	0	0	6.9	0	0	0	0	0	0	0	41.4	0	0	6.9	0	0	0	0	0	0	0	0
Bryozoa Flustrina sp. 4	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	96.6	6.9	0	0	0	0	0	0	0	0
Bryozoa Flustrina sp. 7	0	0	0	0	0	0	0	0	0	0	0	0	124.1	0	0	0	0	0	0	0	0	0	0	0
Bryozoa Cyclost. sp. 1	0	0	0	0	6.9	0	0	0	0	0	0	34.5	151.7	0	351.7	6.9	0	0	0	0	0	0	0	0
Bryozoa Cyclost. sp. 5	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bryozoa Cyclost. sp.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13.8	0	0	0	0	0	0	0	0	0
Bryozoa Cyclost. sp.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.6	6.9	0	0	0	0	0	0	0	0
Bryozoa Cyclost. sp.4	0	0	0	0	0	0	0	0	0	0	0	0	117.2	0	48.3	0	0	0	0	0	0	0	0	0
Bryozoa spp.	0	0	0	0	0	0	0	0	0	0	0	0	6.9	0	6.9	0	0	0	0	0	0	112	680	64
Chordata	0	0	7	0	7	0	0	0	0	7	0	0	0	0	0	0	0	0	0	0	0	0	4	0
Ascidiacea sp.1 (colonial)	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascidiacea sp.2 (solitary)	0	0	6.9	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0	4	0
Cnidaria	7	7	0	7	7	14	0	21	7	0	14	21	0	0	7	7	14	0	14	14	0	40	68	52
Clavularia sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
Acanella arbuscula	0	0	0	0	0	6.9	0	6.9	6.9	0	0	0	0	0	0	0	0	0	0	0	0	4	4	0
Duva florida	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	6.9	0	0	0	0	0	0	0	0	0
Nephtheidae spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	16	8
Pennatula sp. 1	0	6.9	0	6.9	0	0	0	13.8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pennatulacea sp. 1	6.9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cerianthidae spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0

Station	BB1_B_400 m					BB1_A_600 m					BB1_C_1000 m	BB1_C_400 m					BB1_D					DS1_S		
Taxon/Phylum	57	67	69	70	72	85	87	89	90	96	101	105	107	108	111	114	122	123	124	125	126	141	142	145
Anthozoa spp.	0	0	0	0	6.9	0	0	0	0	0	13.8	6.9	0	0	0	6.9	13.8	0	13.8	13.8	0	24	36	40
Anthoathecata sp.1	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cladocarpus sp.1	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0
Hydrozoa spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	8	4
Echinodermata	7	0	0	7	0	7	0	7	7	7	0	14	0	0	7	14	14	0	0	7	7	60	12	16
Asteroidea sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0
Hathrometra sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4
Rhizocrinidae sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12	0	0
Brisaster fragilis	6.9	0	0	0	0	0	0	6.9	6.9	6.9	0	0	0	0	0	0	6.9	0	0	6.9	6.9	0	0	0
Psolus sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0
Holothuroidea spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
Amphiura fragilis	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Amphiura spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	28	4	4
Ophiopholis aculeata	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	6.9	6.9	0	0	0	0	0	0	0	0
Ophiacantha bidentata	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0
Ophiolycus purpureus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0
Ophiura sarsii	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ophiuroidea sp. 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	8
Ophiuroidea sp. 2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12	0	0
Ophiuroidea sp. 3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
Mollusca	0	0	14	0	7	0	0	0	7	0	0	55	110	7	55	21	14	0	7	0	14	8	8	12
Bathyarca spp.	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	4	0
Astarte spp.	0	0	0	0	6.9	0	0	0	0	0	0	6.9	0	0	6.9	0	0	0	0	0	0	4	4	8
Cyclopecten hoskynsi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
Poromya granulata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0
Polinices sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0
Marginellidae sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4
Patellogastropoda sp.1	0	0	6.9	0	0	0	0	0	0	0	0	6.9	82.8	0	41.4	0	0	0	0	0	0	0	0	0
Patellogastropoda sp.2	0	0	0	0	0	0	0	0	0	0	0	6.9	6.9	0	0	13.8	0	0	0	0	0	0	0	0
Polyplacophora spp.	0	0	0	0	0	0	0	0	0	0	0	34.5	20.7	6.9	6.9	0	0	0	0	0	0	0	0	0
Scaphopoda spp.	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	6.9	0	6.9	0	6.9	0	0	0
Nemertea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	0	14	0	4	4	0
Nemertea spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	13.8	0	4	4	0

Station	BB1_B_400 m					BB1_A_600 m					BB1_C_1000 m	BB1_C_400 m					BB1_D					DS1_S		
Taxon/Phylum	57	67	69	70	72	85	87	89	90	96	101	105	107	108	111	114	122	123	124	125	126	141	142	145
Platyhelminthes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	0
Platyhelminthes spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0
Porifera	7	0	34	0	0	0	0	0	0	21	0	55	21	0	14	0	0	0	0	7	0	104	40	40
Leucosolenida sp.1	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0
Calcarea sp.1	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Janulum spinispiculum	0	0	0	0	0	0	0	0	0	0	0	6.9	6.9	0	0	0	0	0	0	0	0	0	0	0
cf. Iriciniidae spp.	6.9	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0
Haplosclerida spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13.8	0	0	0	0	0	0	0	0	0
Iophon spp.	0	0	0	0	0	0	0	0	0	0	0	6.9	6.9	0	0	0	0	0	0	0	0	0	0	0
Asbestopluma sp.1	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	8	0	0
Esperiopsidae sp.1	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0
Hymedesmia sp. 2	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sceptrella sp. 1	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Microcionidae sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0
Mycale (*Rhaphidotheca*) *marshallhalli*	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0
Polymastiidae sp.1	0	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0
cf. *Halichondria* spp.	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tethya sp. 1	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Theneidae spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56	0	12
Demospongiae sp. 1	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Asconema foliatum	0	0	0	0	0	0	0	0	0	0	0	13.8	0	0	0	0	0	0	0	0	0	0	0	0
Porifera spp.	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0	0	0	0	0	0	0	0	40	40	28
Sipuncula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0
Sipuncula spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6.9	0	0	0	0

APPENDIX H: MACROFAUNAL TAXON BIOMASS (1-CM SIZE FRACTION)

Table 1. Standardized wet weight biomass (B)in ranked order for each of 90 macrofaunal taxa (> 1-cm size fraction) recorded from 24 sediment samples (Appendix G). Percent and cumulative percent biomass for each taxon are provided.

Taxon	B (mg)	% B	Cumulative % B
Theneidae spp.	745060.00	46.4	46.4
Asconema foliatum	313641.38	19.5	66.0
Brisaster fragilis	144047.59	9.0	75.0
Pennatula sp. 1	76551.72	4.8	79.7
Duva florida	65621.38	4.1	83.8
Porifera spp.	61774.25	3.8	87.7
Anthozoa spp.	25922.52	1.6	89.3
Bryozoa Flustrina sp. 17	22697.93	1.4	90.7
Astarte spp.	16324.87	1.0	91.7
Eunice pennata	13926.61	0.9	92.6
Janulum spinispiculum	13793.10	0.9	93.4
Acanella arbuscula	13543.45	0.8	94.3
Iophon spp.	10696.55	0.7	95.0
Ascidiacea sp. 2 (solitary)	6158.92	0.4	95.3
Maldanella davisi	5506.90	0.3	95.7
Scoletoma fragilis	4900.00	0.3	96.0
Sceptrella sp. 1	3448.28	0.2	96.2
Polinices sp. 1	2994.48	0.2	96.4
Nemertea spp.	2937.32	0.2	96.6
Patellogastropoda sp. 1	2766.21	0.2	96.7
Haplosclerida spp.	2300.00	0.1	96.9
Placostegus tridentatus	2226.39	0.1	97.0
Nephtheidae spp.	2171.60	0.1	97.2
Ophiacantha bidentata	2074.48	0.1	97.3
Ascidiacea sp.1 (colonial)	2068.97	0.1	97.4
cf. *Halichondria* spp.	2068.97	0.1	97.5
Hymedesmia sp. 2	2068.97	0.1	97.7
Cerianthidae spp.	2059.20	0.1	97.8
Praxillura spp.	1895.17	0.1	97.9
Poromya granulata	1849.66	0.1	98.0
Asbestopluma sp. 1	1780.00	0.1	98.1
Bryozoa Cyclostomatida sp. 5	1732.41	0.1	98.3
Ophiolycus purpureus	1716.55	0.1	98.4
Polyplacophora spp.	1517.93	0.1	98.5
Demospongiae sp. 1	1504.14	0.1	98.5
Pista bansei	1447.59	0.1	98.6

Taxon	B (mg)	% B	Cumulative % B
Nicomache (*Loxochona*) *quadrispinata*	1440.69	0.1	98.7
Ophiopholis aculeata	1306.90	0.1	98.8
Samythella elongata	1305.59	0.1	98.9
Clymenura spp.	1057.24	0.1	99.0
Patellogastropoda sp. 2	1037.24	0.1	99.0
Glycera capitata	966.90	0.1	99.1
Terebellides gracilis	926.21	0.1	99.1
Terebellides stroemii	926.21	0.1	99.2
cf. Iricinidae spp.	834.48	0.1	99.3
Scaphopoda spp.	809.66	0.1	99.3
Bathyarca spp.	721.61	0.0	99.3
Polymastiidae sp. 1	689.66	0.0	99.4
Polynoidae spp.	634.00	0.0	99.4
Mycale (*Rhaphidotheca*) *marshallhalli*	624.14	0.0	99.5
Marginellidae sp. 1	550.00	0.0	99.5
Tethya sp. 1	518.62	0.0	99.5
Rhizocrinidae sp. 1	511.60	0.0	99.6
Ophiuroidea sp. 1	492.80	0.0	99.6
Amphiura spp.	485.60	0.0	99.6
Aglaophamus malmgreni	429.66	0.0	99.7
Leucosolenida sp. 1	413.79	0.0	99.7
Amphiura fragilis	391.72	0.0	99.7
Ophiura sarsii	387.59	0.0	99.7
Microcionidae sp. 1	344.83	0.0	99.7
Holothuroidea spp.	343.60	0.0	99.8
Diastylis spp.	308.80	0.0	99.8
Serpulidae sp. 2	302.55	0.0	99.8
Pennatulacea sp. 1	276.55	0.0	99.8
Asteroidea sp. 1	267.59	0.0	99.8
Esperiopsidae sp. 1	240.00	0.0	99.9
Sipuncula spp.	233.10	0.0	99.9
Hydrozoa spp.	218.80	0.0	99.9
Hathrometra sp. 1	190.80	0.0	99.9
Verruca spp.	175.60	0.0	99.9
Cyclopecten hoskynsi	159.20	0.0	99.9
Ophiuroidea sp. 3	145.60	0.0	99.9
Clavularia sp. 1	140.40	0.0	99.9
Brachipoda spp.	137.24	0.0	99.9
Polycirrus sp. 1	130.34	0.0	100.0
Syllidae spp.	116.55	0.0	100.0
Bryozoa spp.	111.60	0.0	100.0

Taxon	B (mg)	% B	Cumulative % B
Psolus sp. 1	92.40	0.0	100.0
Ophiuroidea sp. 2	92.00	0.0	100.0
Calcarea sp. 1	68.97	0.0	100.0
Caprellidae spp.	64.00	0.0	100.0
Potamilla sp. 1	44.83	0.0	100.0
Anthoathecata sp. 1	44.14	0.0	100.0
Janiroidea sp. 1	42.00	0.0	100.0
Scalpellidae sp. 1	35.60	0.0	100.0
Petaloproctus tenuis	26.90	0.0	100.0
Bryozoa Flustrina sp. 7	6.90	0.0	100.0
Cladocarpus sp. 1	6.21	0.0	100.0
Bryozoa Flustrina sp. 11	0.69	0.0	100.0
Bryozoa Cyclostomatida sp. 2	0.69	0.0	100.0
Total Biomass	1604625.83		

APPENDIX I: MACROFAUNAL TAXON BIOMASS BY SAMPLE

Table 1. Wet weight biomass (g/m²) for 90 macrofaunal taxa (> 1-cm size fraction), by phylum, for each sample (labelled by Consecutive Operation Number) in each station. Note: Taxa are mutually exclusive within the BB1 stations, and within the DS1_S station but not between the two groups as the DS1_S samples were not fully identified to species in some groups (e.g., Bryozoa, Porifera). Phylum total biomasses (used to generate Figure 15) are provided.

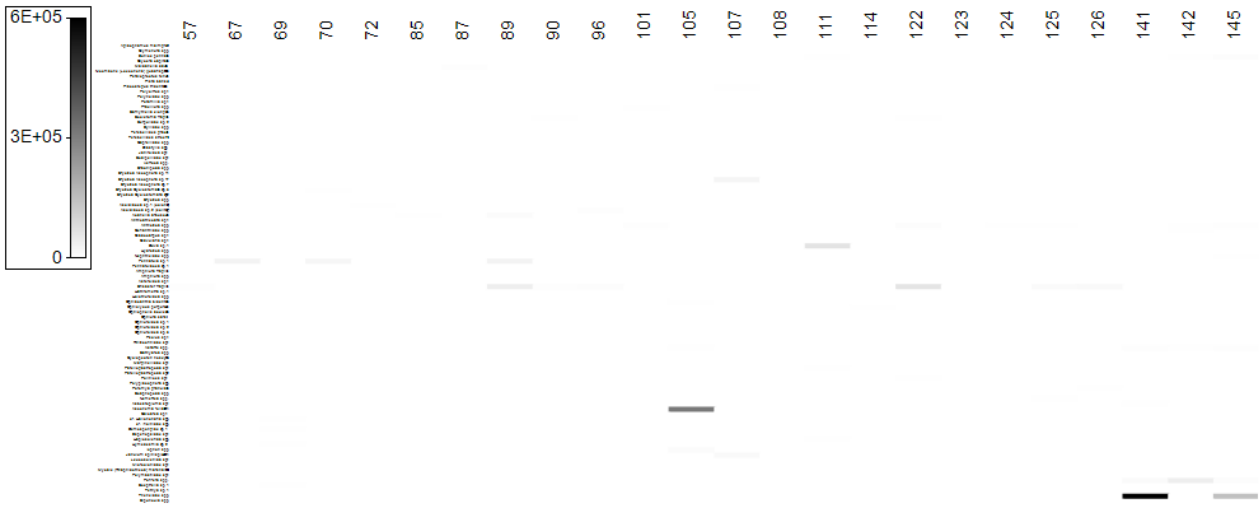
Station	BB1_B_400 m					BB1_A_600 m					BB1_C_1000 m	BB1_C_400 m					BB1_D					DS1_S		
Taxon/Phylum	57	67	69	70	72	85	87	89	90	96	101	105	107	108	111	114	122	123	124	125	126	141	142	145
Annelida	0.15	0	0.52	0.47	0.87	0.25	6.76	0	4.67	0.53	1.63	0.93	2.39	1.64	1.93	1.07	2.39	0.77	1.30	0.41	0.22	0.14	2.01	7.13
Aglaophamus malmgreni	0	0	0	0	0	0	0	0	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Clymenura spp.	0	0	0	0	0	0	1.06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eunice pennata	0	0	0	0	0.39	0	0	0	0	0	0	0.66	1.09	0.67	1.93	0.86	0	0	0	0	0	0	1.19	7.13
Glycera capitata	0	0	0	0	0	0	0	0	0	0	0	0	0	0.97	0	0	0	0	0	0	0	0	0	0
Maldanella davisi	0	0	0	0	0	0	5.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nicomache (Loxochona) quadrispinata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27	0.17	0.46	0.33	0.21	0	0	0
Petaloproctus tenuis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01	0.01	0	0	0
Pista bansei	0.15	0	0.06	0.47	0.04	0.14	0	0	0.06	0.35	0	0	0	0	0	0	0	0.17	0	0	0	0	0	0
Placostegus tridentatus	0	0	0.34	0	0.44	0	0	0	0	0	0	0.15	1.18	0	0	0	0	0	0	0	0	0.12	0	0
Polycirrus sp. 1	0	0	0	0	0	0	0	0	0	0	0	0	0.13	0	0	0	0	0	0	0	0	0	0	0
Polynoidae spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.63	0
Potamilla sp. 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0	0	0	0	0
Praxillura spp.	0	0	0	0	0	0	0	0	0	0	1.61	0	0	0	0	0	0	0.28	0	0	0	0	0	0
Samythella elongata	0	0	0	0	0	0.11	0.20	0	0	0.18	0.02	0	0	0	0	0	0	0.10	0.61	0.06	0	0.02	0	0
Scoletoma fragilis	0	0	0	0	0	0	0	0	2.33	0	0	0	0	0	0	0.21	2.12	0	0.23	0	0	0	0	0
Serpulidae sp. 2	0	0	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.19	0
Syllidae spp.	0	0	0	0	0	0	0	0	0	0	0	0.12	0	0	0	0	0	0	0	0	0	0	0	0
Terebellides gracilis	0	0	0	0	0	0	0	0	0.93	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Terebellides stroemii	0	0	0	0	0	0	0	0	0.93	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Arthropoda	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04	0.17	0.42
Caprellidae spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0.03
Diastylis spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.31
Janiroidea sp. 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04
Scalpellidae sp. 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04	0
Verruca spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.14	0.04
Brachiopoda	0	0	0	0	0	0	0	0	0	0	0	0	0.14	0	0	0	0	0	0	0	0	0	0	0
Brachipoda spp.	0	0	0	0	0	0	0	0	0	0	0	0	0.14	0	0	0	0	0	0	0	0	0	0	0
Bryozoa	0	0	0	1.73	0.01	0	0	0	0	0	0	0	22.70	0	0	0	0	0	0	0	0	0.05	0.01	0.05

Station	BB1_B_400 m					BB1_A_600 m					BB1_C_1000 m	BB1_C_400 m					BB1_D					DS1_S		
Taxon/Phylum	57	67	69	70	72	85	87	89	90	96	101	105	107	108	111	114	122	123	124	125	126	141	142	145
Bryozoa Flustrina sp. 11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bryozoa Flustrina sp. 17	0	0	0	0	0	0	0	0	0	0	0	0	22.70	0	0	0	0	0	0	0	0	0	0	0
Bryozoa Flustrina sp. 7	0	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bryozoa Cyclostomatida sp. 5	0	0	0	1.73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bryozoa Cyclostomatida sp. 2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bryozoa spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.05	0.01	0.05
Chordata	0	0	0.14	0	2.07	0	0	0	0	5.85	0	0	0	0	0	0	0	0	0	0	0	0	0.17	0
Ascidiacea sp. 1 (colonial)	0	0	0	0	2.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascidiacea sp. 2 (solitary)	0	0	0.14	0	0	0	0	0	0	5.85	0	0	0	0	0	0	0	0	0	0	0	0	0.17	0
Cnidaria	0.28	27.59	0	20.69	0.10	3.34	0	38.02	0.14	0	3.58	0.34	0	0	65.29	0.08	7.86	0	2.81	2.81	0	1.38	4.55	7.71
Acanella arbuscula	0	0	0	0	0	3.30	0	9.75	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0.21	0.15	0
Anthoathecata sp. 1	0	0	0	0	0	0.04	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anthozoa spp.	0	0	0	0	0.10	0	0	0	0	0	3.58	0	0	0	0	0.08	7.86	0	2.81	2.81	0	0.91	2.11	5.67
Cerianthidae spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.06	0
Cladocarpus sp. 1	0	0	0	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0
Clavularia sp. 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.14	0	0
Duva florida	0	0	0	0	0	0	0	0	0	0	0	0.33	0	0	65.29	0	0	0	0	0	0	0	0	0
Hydrozoa spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.12	0.09	0.01
Nephtheidae spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.14	2.03
Pennatula sp. 1	0	27.59	0	20.69	0	0	0	28.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pennatulacea sp. 1	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Echinodermata	4.26	0	0	0.39	0	0.39	0	39.41	3.83	7.19	0	2.94	0	0	0.36	1.79	63.27	0	0	11.98	14.37	1.35	0.51	0.50
Amphiura fragilis	0	0	0	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Amphiura spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.25	0.15	0.08
Asteroidea sp. 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27	0	0	0	0	0	0	0
Brisaster fragilis	4.26	0	0	0	0	0	0	39.41	3.83	7.19	0	0	0	0	0	0	63.00	0	0	11.98	14.37	0	0	0
Hathrometra sp. 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.19
Holothuroidea spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.34	0	0
Ophiacantha bidentata	0	0	0	0	0	0	0	0	0	0	0	2.07	0	0	0	0	0	0	0	0	0	0	0	0
Ophiolycus purpureus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.72	0	0	0	0	0	0	0	0
Ophiopholis aculeata	0	0	0	0	0	0	0	0	0	0	0	0.87	0	0	0.36	0.08	0	0	0	0	0	0	0	0
Ophiura sarsii	0	0	0	0	0	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ophiuroidea sp. 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.27	0.22
Ophiuroidea sp. 2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.09	0	0
Ophiuroidea sp. 3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.15	0	0
Psolus sp. 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.09	0
Rhizocrinidae sp. 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.51	0	0
Mollusca	0	0	0.44	0	0.05	0	0	0	0	0	0	4.01	1.63	0.10	1.75	0.86	3.32	0	0.15	0	2.18	4.77	3.25	6.23
Astarte spp.	0	0	0	0	0.05	0	0	0	0	0	0	2.98	0	0	0.10	0	0	0	0	0	0	4.61	2.92	5.68
Bathyarca spp.	0	0	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0.13	0	0	0	0	0	0	0.33	0
Cyclopecten hoskynsi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.16	0	0

Station	BB1_B_400 m					BB1_A_600 m					BB1_C_1000 m	BB1_C_400 m					BB1_D					DS1_S		
Taxon/Phylum	57	67	69	70	72	85	87	89	90	96	101	105	107	108	111	114	122	123	124	125	126	141	142	145
Marginellidae sp. 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.55
Patellogastropoda sp. 1	0	0	0.18	0	0	0	0	0	0	0	0	0.06	1.03	0	1.50	0	0	0	0	0	0	0	0	0
Patellogastropoda sp. 2	0	0	0	0	0	0	0	0	0	0	0	0.20	0.10	0	0	0.73	0	0	0	0	0	0	0	0
Polinices sp. 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.99	0	0	0	0	0	0	0
Polyplacophora spp.	0	0	0	0	0	0	0	0	0	0	0	0.78	0.49	0.10	0.15	0	0	0	0	0	0	0	0	0
Poromya granulata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.85	0	0	0
Scaphopoda spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.33	0	0.15	0	0.33	0	0	0
Nemertea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.07	0	0	0	0	2.62	0	0.19	0.05	0
Nemertea spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.07	0	0	0	0	2.62	0	0.19	0.05	0
Porifera	0.07	0	9.61	0	0	0	0	0	0	1.25	0	326.45	14.41	0	2.30	0	0	0	0	0.34	0	611.63	40.69	155.11
Asbestopluma sp. 1	0	0	0	0	0	0	0	0	0	0.18	0	0	0	0	0	0	0	0	0	0	0	1.60	0	0
Asconema foliatum	0	0	0	0	0	0	0	0	0	0	0	313.64	0	0	0	0	0	0	0	0	0	0	0	0
Calcarea sp. 1	0	0	0	0	0	0	0	0	0	0.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cf. *Halichondria* spp.	0	0	2.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
cf. Iricinidae spp.	0.07	0	0	0	0	0	0	0	0	0	0	0.77	0	0	0	0	0	0	0	0	0	0	0	0
Demospongiae sp. 1	0	0	1.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Esperiopsidae sp. 1	0	0	0	0	0	0	0	0	0	0	0	0.24	0	0	0	0	0	0	0	0	0	0	0	0
Haplosclerida spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.30	0	0	0	0	0	0	0	0	0
Hymedesmia sp. 2	0	0	2.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Iophon spp.	0	0	0	0	0	0	0	0	0	0	0	10.35	0.34	0	0	0	0	0	0	0	0	0	0	0
Janulum spinispiculum	0	0	0	0	0	0	0	0	0	0	0	0.41	13.38	0	0	0	0	0	0	0	0	0	0	0
Leucosolenida sp. 1	0	0	0	0	0	0	0	0	0	0	0	0.41	0	0	0	0	0	0	0	0	0	0	0	0
Microcionidae sp. 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.34	0	0	0	0
Mycale (Rhaphidotheca) marshallhalli	0	0	0	0	0	0	0	0	0	0	0	0.62	0	0	0	0	0	0	0	0	0	0	0	0
Polymastiidae sp. 1	0	0	0	0	0	0	0	0	0	0	0	0	0.69	0	0	0	0	0	0	0	0	0	0	0
Porifera spp.	0	0	0	0	0	0	0	0	0	1.00	0	0	0	0	0	0	0	0	0	0	0	12.27	40.69	7.81
Sceptrella sp. 1	0	0	3.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tethya sp. 1	0	0	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Theneidae spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	597.76	0	147.30
Sipuncula	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.23	0	0	0	0
Sipuncula spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.23	0	0	0	0

APPENDIX J: EFFECT OF DATA TRANSFORMATION ON MACROFAUNAL BIOMASS

Untransformed Standardized Biomass



Log(x+1)-Transformed Standardized Biomass

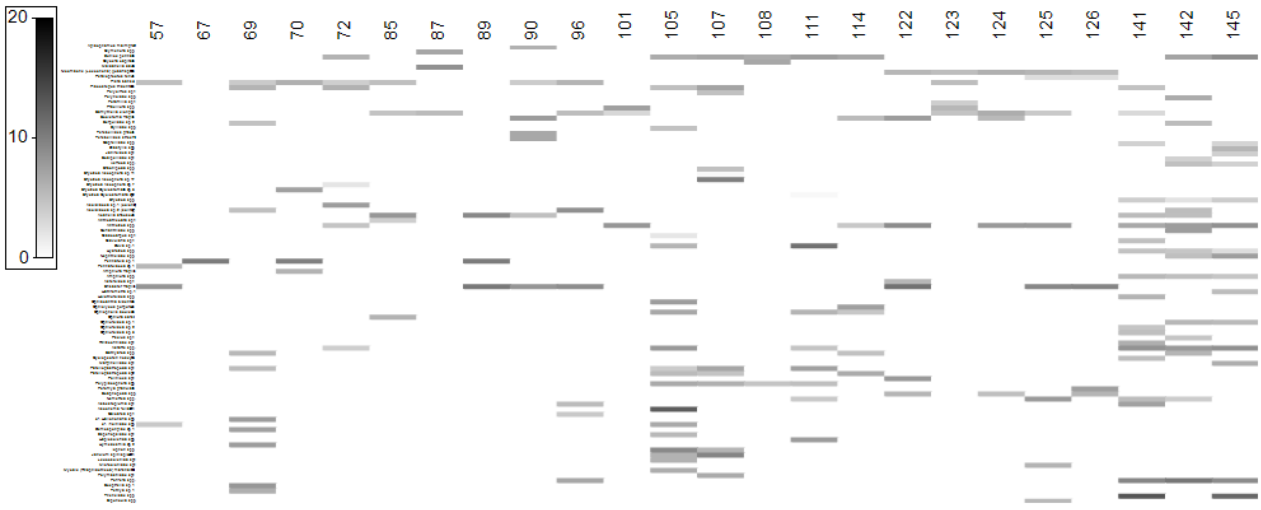


Figure 1. Shade plots showing the effect of transformation on the standardized biomass of macrofaunal taxa (> 1-cm size fraction) by sample (labelled by Consecutive Operation Number). Scale bars of the biomass for each plot are shown in the upper left.

APPENDIX K: SIMILARITY IN BIOMASS AMONG MACROFAUNAL COMMUNITIES

57	**57**																							
67	0.0	**67**																						
69	9.1	0.0	**69**																					
70	18.9	50.0	8.5	**70**																				
72	13.4	0.0	19.0	12.0	**72**																			
85	19.6	0.0	8.7	17.4	12.4	**85**																		
87	0.0	0.0	0.0	0.0	0.0	19.4	**87**																	
89	31.4	50.8	0.0	33.4	0.0	28.1	0.0	**89**																
90	36.2	0.0	7.2	10.9	9.7	24.9	0.0	35.3	**90**															
96	39.2	0.0	16.2	15.7	9.7	26.7	15.8	23.7	27.5	**96**														
101	0.0	0.0	0.0	0.0	17.4	13.4	15.7	0.0	0.0	9.8	**101**													
105	6.1	0.0	10.0	0.0	19.9	0.0	0.0	0.0	0.0	0.0	0.0	**105**												
107	0.0	0.0	15.6	0.0	22.3	0.0	0.0	0.0	0.0	0.0	0.0	40.5	**107**											
108	0.0	0.0	0.0	0.0	23.0	0.0	0.0	0.0	0.0	0.0	0.0	16.7	24.1	**108**										
111	0.0	0.0	8.5	0.0	22.3	0.0	0.0	0.0	0.0	0.0	0.0	37.8	29.6	30.8	**111**									
114	0.0	0.0	9.1	0.0	28.0	0.0	0.0	0.0	12.7	0.0	14.8	20.9	20.0	22.6	23.7	**114**								
122	22.0	0.0	0.0	0.0	10.6	0.0	0.0	25.6	32.7	18.2	22.9	0.0	0.0	0.0	0.0	21.0	**122**							
123	21.0	0.0	9.0	19.1	13.1	37.1	20.6	0.0	11.8	28.3	40.7	0.0	0.0	0.0	0.0	0.0	13.3	**123**						
124	0.0	0.0	0.0	0.0	14.1	16.1	20.4	0.0	14.4	13.7	44.5	0.0	0.0	0.0	0.0	27.4	57.4	35.4	**124**					
125	23.1	0.0	0.0	0.0	11.0	10.9	11.9	23.7	17.6	27.8	32.6	0.0	0.0	0.0	8.2	9.7	45.0	25.3	44.8	**125**				
126	30.9	0.0	0.0	0.0	0.0	0.0	0.0	31.4	21.8	23.4	0.0	0.0	0.0	0.0	0.0	0.0	49.6	18.6	33.5	43.4	**126**			
141	0.0	0.0	5.3	0.0	17.9	11.8	4.4	7.4	6.3	19.0	14.8	11.2	5.1	0.0	10.6	5.7	8.2	4.3	13.5	18.5	0.0	**141**		
142	0.0	0.0	17.4	0.0	20.3	7.4	0.0	7.3	6.5	15.7	12.1	13.0	7.7	10.3	19.3	21.6	9.5	0.0	11.0	14.8	0.0	40.7	**142**	
145	0.0	0.0	0.0	0.0	21.6	0.0	0.0	0.0	0.0	9.6	13.9	13.5	8.1	11.1	15.9	16.0	11.4	0.0	12.2	10.7	0.0	47.5	53.2	**145**
Site	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	DFCA	HBCA	HBCA	HBCA
Station	BB1_B_400 m	BB1_B_400 m	BB1_B_400 m	BB1_B_400 m	BB1_B_400 m	BB1_A_600 m	BB1_A_600 m	BB1_A_600 m	BB1_A_600 m	BB1_A_600 m	BB1_C_1000 m	BB1_C_400 m	BB1_C_400 m	BB1_C_400 m	BB1_C_400 m	BB1_C_400 m	BB1_D	BB1_D	BB1_D	BB1_D	BB1_D	DS1_S	DS1_S	DS1_S

Figure 1. Bray-Curtis similarity among macrofaunal communities (> 1-cm size fraction) based on log (x+1)-transformed standardized biomass. Samples are labelled by Consecutive Operation Number (in bold, black for rows, white for columns), site and station.

APPENDIX L: MEIOFAUNAL TAXON LIST

Table 1. List of 90 meiofaunal taxa identified from the 5cc sediment samples from stations BB1_A_600 m, BB1_B_400 m, BB1_C_400 m, and BB1_D. All taxa belong to the phylum Foraminifera. Note nomenclature changes for some taxa.

Identified Taxon	Class	Order	Family	Genus	Species
Agglutinated Species					
Adercotryma glomerata	Globothalamea	Lituolida	Adercotrymidae	*Adercotryma*	*glomerata*
Astrorhiza arenaria	Monothalamea	Astrorhizida	Astrorhizidae	*Astrorhiza*	*arenaria*
Bathysiphon rufus	Monothalamea	Astrorhizida	Rhabdamminidae	*Bathysiphon*	*rufus*
Cribrostomoides crassimargo	Globothalamea	Lituolida	Ammosphaeroidinidae	*Cribrostomoides*	*crassimargo*
Cribrostomoides jeffreysii	Globothalamea	Lituolida	Ammosphaeroidinidae	*Cribrostomoides*	*jeffreysii*
Cribrostomoides subglobosum	Globothalamea	Lituolida	Ammosphaeroidinidae	*Cribrostomoides*	*subglobosum*
Deuterammina orchacea	Globothalamea	Lituolida	Trochamminidae	*Lepidodeuterammina*	*ochracea*
Eggerella advena	Globothalamea	Textulariida	Eggerellidae	*Eggerella*	*advena*
Glomospira gordialis	Tubothalamea	Spirillinida	Ammodiscidae	*Glomospira*	*gordialis*
Hemisphaerammina bradyi	Monothalamea	Astrorhizida	Stegnamminidae	*Hemisphaerammina*	*bradyi*
Hemisphaerammina spp.	Monothalamea	Astrorhizida	Stegnamminidae	*Hemisphaerammina*	
Hyperammina spp.	Monothalamea	Astrorhizida	Hyperamminidae	*Hyperammina*	
Psammosphaera fusca	Monothalamea	Astrorhizida	Psammosphaeridae	*Psammosphaera*	*fusca*
Recurvoides turbinatus	Globothalamea	Lituolida	Ammosphaeroidinidae	*Recurvoides*	*turbinatus*
Reophax arctica	Nodosariata		Reophacidae	*Cuneata*	*arctica*
Reophax bacillaris	Nodosariata		Hormosinidae	*Hormosina*	*bacillaris*
Reophax bilocularis	Nodosariata		Reophacidae	*Reophax*	*bilocularis*
Reophax catella	Nodosariata		Reophacidae	*Leptohalysis*	*catella*
Reophax catenata	Nodosariata		Reophacidae	*Reophax*	*catenata*
Reophax dentaliniformis	Nodosariata		Reophacidae	*Nodulina*	*dentaliniformis*
Reophax fusiformis	Nodosariata		Reophacidae	*Reophax*	*fusiformis*
Reophax guttifer	Nodosariata		Reophacidae	*Hormosinelloides*	*guttifer*
Reophax nodulosa	Nodosariata		Reophacidae	*Pseudonodosinella*	*nodulosa*

Identified Taxon	**Class**	**Order**	**Family**	**Genus**	**Species**
Reophax scorpiurus	Nodosariata		Reophacidae	*Reophax*	*scorpiurus*
Rhabdammina abyssorum	Monothalamea	Astrorhizida	Rhabdamminidae	*Rhabdammina*	*abyssorum*
Rhabdammina linearis	Monothalamea	Astrorhizida	Rhabdamminidae	*Rhabdammina*	*linearis*
Saccammina difflugiformis	Monothalamea	Astrorhizida	Saccamminidae	*Saccammina*	*difflugiformis*
Saccammina sphaerica	Monothalamea	Astrorhizida	Saccamminidae	*Saccammina*	*sphaerica*
Saccorhiza ramosa	Monothalamea	Astrorhizida	Hyperamminidae	*Saccorhiza*	*ramosa*
Silicosigmoilina groenlandica	Tubothalamea	Miliolida	Miliamminidae	*Silicosigmoilina*	*groenlandica*
Spiroplectammina biformis	Globothalamea	Lituolida	Spiroplectamminidae	*Spiroplectammina*	*biformis*
Textularia earlandi	Globothalamea	Textulariida	Textulariidae	*Textularia*	*earlandi*
Textularia torquata	Globothalamea	Textulariida	Textulariidae	*Textularia*	*torquata*
Trochammina globigeriformis	Globothalamea	Lituolida	Trochamminidae	*Trochammina*	*globigeriformis*
Trochammina nana	Globothalamea	Lituolida	Trochamminidae	*Trochammina*	*nana*
Trochammina nitida	Globothalamea	Lituolida	Trochamminidae	*Trochammina*	*nitida*
Trochammina pseudoinflata	Globothalamea	Lituolida	Trochamminidae	*Trochammina*	*pseudoinflata*
Trochammina squamata	Globothalamea	Lituolida	Trochamminidae	*Trochammina*	*squamata*
Trochammina spp.	Globothalamea	Lituolida	Trochamminidae	*Trochammina*	
Rhabdammina/Hyperammina spp.	Monothalamea	Astrorhizida	Rhabdamminidae/ Hyperamminidae	*Rhabdammina/ Hyperammina*	
Agglutinated fragment/unknown					
Calcareous Species					
Astacolus spp.	Nodosariata	Vaginulinida	Vaginulinidae	*Astacolus*	
Astrononion gallowayi	Globothalamea	Rotaliida	Astrononionidae	*Astrononion*	*gallowayi*
Bolivina pseudopunctata	Globothalamea	Rotaliida	Bolivinitidae	*Bolivina*	*pseudopunctata*
Buccella frigida	Globothalamea	Rotaliida	Trichohyalidae	*Buccella*	*frigida*
Buliminella hensoni	Globothalamea	Rotaliida	Buliminellidae	*Buliminella*	*hensoni*
Cassidulina laevigata	Globothalamea	Rotaliida	Cassidulinidae	*Cassidulina*	*laevigata*
Cassidulina neoteretis	Globothalamea	Rotaliida	Cassidulinidae	*Cassidulina*	*neoteretis*
Cassidulina reniforme	Globothalamea	Rotaliida	Cassidulinidae	*Cassidulina*	*reniforme*
Cibicides lobatus	Globothalamea	Rotaliida	Cibicididae	*Lobatula*	*lobatula*

Identified Taxon	Class	Order	Family	Genus	Species
Cibicides wuellerstrofi	Globothalamea	Rotaliida	Cibicididae	*Cibicidoides*	*wuellerstorfi*
Cyclogyra involvens	Tubothalamea	Miliolida	Cornuspiridae	*Cyclogyra*	*involvens*
Dentalina spp.	Nodosariata	Nodosariida	Nodosariidae	*Dentalina*	
Elphidium bartletti	Globothalamea	Rotaliida	Elphidiidae	*Elphidium*	*bartletti*
Elphidium excavatum *f. clavata*	Globothalamea	Rotaliida	Elphidiidae	*Elphidium*	*excavatum*
Elphidium subarcticum	Globothalamea	Rotaliida	Elphidiidae	*Elphidium*	*subarcticum*
Elphidium spp.	Globothalamea	Rotaliida	Elphidiidae	*Elphidium*	
Epistominella exigua	Globothalamea	Rotaliida	Pseudoparrellidae	*Epistominella*	*exigua*
Epistominella takayanagii	Globothalamea	Rotaliida	Pseudoparrellidae	*Epistominella*	*takayanagii*
Fissurina marginata	Nodosariata	Polymorphinida	Ellipsolagenidae	*Fissurina*	*marginata*
Fissurina spp.	Lecanoromycetes	Ostropales	Graphidaceae	*Fissurina*	
Fursenkoina fusiformis	Globothalamea	Rotaliida	Bolivinitidae	*Fursenkoina*	*fusiformis*
Globobulimina spp.	Globothalamea	Rotaliida	Globobuliminidae	*Globobulimina*	
Haynesina germanica	Globothalamea	Rotaliida	Haynesinidae	*Haynesina*	*germanica*
Islandiella helenae	Globothalamea	Rotaliida	Cassidulinidae	*Islandiella*	*helenae*
Islandiella norcrossi	Globothalamea	Rotaliida	Cassidulinidae	*Islandiella*	*norcrossi*
Lagena mollis	Nodosariata	Nodosariida	Lagenidae	*Lagena*	*mollis*
Lagena spp.	Nodosariata	Nodosariida	Lagenidae	*Lagena*	
Lenticulina spp.	Nodosariata	Vaginulinida	Vaginulinidae	*Lenticulina*	
Melonis barleeanum	Globothalamea	Rotaliida	Melonidae	*Melonis*	*barleeanum*
Nonionella auricula	Globothalamea	Rotaliida	Nonionidae	*Nonionella*	*auricula*
Nonionellina labradorica	Globothalamea	Rotaliida	Nonionidae	*Nonionellina*	*labradorica*
Oolina globosa	Nodosariata	Polymorphinida	Ellipsolagenidae	*Oolina*	*globosa*
Oolina hexagona	Nodosariata	Polymorphinida	Ellipsolagenidae	*Oolina*	*hexagona*
Oolina spp.	Nodosariata	Polymorphinida	Ellipsolagenidae	*Oolina*	
Oridosalis umbonatus	Globothalamea	Rotaliida	Alabaminidae	*Oridorsalis*	*umbonatus*
Planispirinoides bucculentus	Tubothalamea	Miliolida	Miliolidae	*Planispirinoides*	*bucculentus*
Pullenia bulloides	Globothalamea	Rotaliida	Pulleniidae	*Pullenia*	*bulloides*
Pullenia osloensis	Globothalamea	Rotaliida	Pulleniidae	*Pullenia*	*osloensis*

Identified Taxon	**Class**	**Order**	**Family**	**Genus**	**Species**
Quinqueloculina seminulum	Tubothalamea	Miliolida	Hauerinidae	*Quinqueloculina*	*seminulum*
Quinqueloculina spp.	Tubothalamea	Miliolida	Hauerinidae	*Quinqueloculina*	
Spiroloculina spp.	Tubothalamea	Miliolida	Spiroloculinidae	*Spiroloculina*	
Stetsonia arctica	Globothalamea	Rotaliida	Pseudoparrellidae	*Stetsonia*	*arctica*
Trifarina fluens	Globothalamea	Rotaliida	Uvigerinidae	*Trifarina*	*fluens*
Valvulineria arctica	Globothalamea	Rotaliida	Cancrisidae	*Valvulineria*	*arctica*
Cassidulina/Islandiella spp.	Globothalamea	Rotaliida	Cassidulinidae	*Cassidulina/Islandiella*	
Calcareous fragment/unknown					
Planktic Species					
Neogloboquadrina pachyderma subsp. *sinistral*	Globothalamea	Rotaliida	Globorotaliidae	*Neogloboquadrina*	*pachyderma*
Neogloboquadrina pachyderma subsp. *dextral*	Globothalamea	Rotaliida	Globorotaliidae	*Neogloboquadrina*	*pachyderma*
Globigerina bulloides	Globothalamea	Rotaliida	Globigerinidae	*Globigerina*	*bulloides*

APPENDIX M: MEIOFAUNAL ABUNDANCE BY SAMPLE

Table 1. Abundance of meiofauna per 5 cc sample by taxon for each of the replicate samples (labelled by Consecutive Operation Number, CON) from four of the biodiversity monitoring stations in the DFCA. Codes A, B, C denote replicate samples from the same sediment sample (CON 71 or 119). All other sample codes represent single 5cc samples. See Table 4 for sample location details. Samples from the same station are colour-coded for ease of reference.

Station	BB1_B_400 m					BB1_A_600 m			BB1_C_400 m			BB1_D				
Taxon	71_A	71_B	71_C	56	68	81	82	83	109	112	113	119_A	119_B	119_C	120	121
Adercotryma glomerata	0	66	60	24	36	42	66	66	72	48	25	216	150	222	186	252
Astrorhiza arenaria	0	186	132	42	132	414	222	18	0	18	2	18	306	18	12	0
Bathysiphon rufus	0	6	0	12	0	0	0	12	0	0	0	0	0	0	6	0
Cribrostomoides crassimargo	0	24	6	12	24	30	36	42	36	18	7	0	0	0	0	6
Cribrostomoides jeffreysii	10	36	36	24	36	0	0	0	0	42	8	24	12	6	12	0
Cribrostomoides subglobosum	0	0	0	0	0	0	6	6	0	0	1	0	0	0	0	0
Deuterammina orchacea	0	24	0	60	18	36	18	0	0	12	0	60	6	42	30	0
Eggerella advena	0	6	0	24	0	0	0	6	0	0	0	6	0	12	12	0
Glomospira gordialis	0	12	18	12	6	6	6	0	36	6	1	12	0	18	30	0
Hemisphaerammina bradyi	0	36	12	24	0	36	6	0	0	0	0	0	0	6	0	0
Hemisphaerammina spp.	0	0	0	0	0	0	0	0	0	0	0	0	12	6	0	0
Hyperammina spp.	0	0	6	0	6	42	6	12	0	6	3	0	18	0	6	6
Psammosphaera fusca	4	0	0	0	0	24	18	0	0	0	0	0	0	0	6	0
Recurvoides turbinatus	0	24	6	0	6	30	54	24	72	0	3	12	48	36	18	30
Reophax arctica	0	24	0	0	0	12	12	12	0	6	0	72	48	36	36	30
Reophax bacillaris	0	0	0	0	0	30	0	0	0	0	0	0	0	0	0	0
Reophax bilocularis	1	6	6	72	6	18	30	24	0	0	0	18	12	12	12	0
Reophax catella	3	18	24	6	36	0	12	0	0	30	2	0	24	90	138	30
Reophax catenata	0	66	24	24	0	18	12	6	36	54	0	30	0	42	84	6
Reophax dentaliniformis	6	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Reophax fusiformis	0	24	6	6	0	66	36	6	0	0	0	6	12	0	0	6
Reophax guttifer	0	12	6	0	0	30	18	6	0	0	0	6	0	0	0	0
Reophax nodulosa	0	0	0	0	0	0	0	0	0	12	0	0	0	6	30	0
Reophax scorpiurus	15	36	30	18	12	18	18	108	0	24	10	0	12	0	0	0
Rhabdammina abyssorum	127	186	84	402	306	216	30	102	0	42	30	0	18	0	0	24
Rhabdammina linearis	0	0	0	0	0	0	6	0	0	0	0	0	0	0	0	0
Saccammina difflugiformis	10	132	54	102	24	60	48	60	0	18	12	24	48	24	42	48

Station	BB1_B_400 m					BB1_A_600 m			BB1_C_400 m			BB1_D				
Taxon	71_A	71_B	71_C	56	68	81	82	83	109	112	113	119_A	119_B	119_C	120	121
Saccammina sphaerica	1	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Saccorhiza ramosa	0	0	0	0	0	54	12	78	36	0	0	0	0	0	0	0
Silicosigmoilina groenlandica	2	0	0	0	0	6	18	18	36	0	1	36	18	12	30	36
Spiroplectammina biformis	5	24	12	0	0	42	24	36	36	0	4	114	72	78	126	96
Textularia earlandi	5	18	30	24	12	54	36	42	36	6	2	12	30	42	84	132
Textularia torquata	38	204	90	162	42	192	240	504	36	90	22	588	408	642	600	714
Trochammina globigeriformis	12	126	48	60	12	36	54	30	0	0	2	72	18	12	24	24
Trochammina nana	4	30	24	18	30	54	24	42	72	12	5	6	24	18	36	12
Trochammina nitida	28	42	42	48	6	18	42	90	36	12	3	30	48	6	66	0
Trochammina pseudoinflata	16	138	84	156	42	108	42	36	108	18	3	66	18	48	18	24
Trochammina squamata	0	0	0	0	0	12	0	0	0	0	0	0	0	0	0	0
Trochammina spp.	2	60	42	30	6	48	36	0	0	0	0	6	24	42	30	60
Rhabdammina/hyperammina spp.	0	126	90	126	72	24	24	0	0	66	11	6	66	0	24	30
Agglutinated fragment/unknown	0	162	138	144	102	222	372	96	144	96	18	0	126	138	132	132
Astacolus spp.	0	6	0	0	0	0	0	0	0	6	0	0	0	0	0	0
Astrononion gallowayi	0	12	6	0	6	0	6	0	288	36	25	0	0	0	0	0
Bolivina pseudopunctata	0	0	6	6	0	0	0	0	0	12	3	6	0	60	0	0
Buccella frigida	1	18	0	6	6	0	0	0	360	30	67	0	0	0	0	0
Buliminella hensoni	23	84	18	6	0	0	18	6	0	6	0	54	6	18	30	6
Cassidulina laevigata	19	24	0	12	54	0	0	0	288	0	19	0	0	0	0	0
Cassidulina neoteretis	0	6	0	0	36	0	0	0	792	6	1	0	0	0	0	6
Cassidulina reniforme	14	48	0	18	24	0	0	0	1620	90	24	0	6	0	0	18
Cibicides lobatus	83	102	54	66	126	6	42	24	2700	132	74	0	12	6	0	0
Cibicides wuellerstrofi	15	108	36	114	258	0	0	0	576	174	56	0	0	0	0	0
Cyclogyra involvens	3	0	6	12	18	12	12	12	108	0	2	24	18	24	18	24
Dentalina spp.	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0
Elphidium bartletti	0	0	0	0	0	0	0	0	36	0	0	0	0	0	0	0
Elphidium exclavatum. *f. clavata*	9	0	0	0	0	0	0	6	324	0	1	0	0	0	0	0
Elphidium subarcticum	3	30	0	12	0	0	0	0	144	78	18	0	6	0	0	0
Elphidium spp.	1	0	0	0	0	0	0	12	540	0	6	0	0	0	0	0
Epistominella exigua	1	0	6	0	0	0	0	0	0	6	1	0	0	0	0	6
Epistominella takayanagii	0	0	0	0	6	0	0	0	0	0	0	0	0	0	0	0
Fissurina marginata	0	18	24	12	6	0	0	0	396	12	8	0	0	12	0	0
Fissurina spp.	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Station	BB1_B_400 m					BB1_A_600 m			BB1_C_400 m			BB1_D				
Taxon	71_A	71_B	71_C	56	68	81	82	83	109	112	113	119_A	119_B	119_C	120	121
Fursenkoina fusiformis	0	24	0	30	12	0	0	0	72	36	8	84	0	6	0	0
Globobulimina spp.	0	0	0	0	0	0	0	0	0	6	4	0	0	0	0	0
Haynesina germanica	0	0	0	0	0	0	0	0	0	0	7	0	0	0	0	0
Islandiella helenae	8	0	6	0	12	0	0	0	0	12	3	0	0	0	0	0
Islandiella narcrossi	0	18	0	12	0	6	0	0	504	42	34	0	0	0	0	0
Lagena mollis	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lagena spp.	0	0	0	6	0	0	0	0	0	12	5	0	0	0	0	0
Lenticulina spp.	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Melonis barleeanum	0	30	18	12	0	18	24	18	288	84	49	24	0	0	0	18
Nonionellina auricula	0	42	6	30	12	0	0	0	0	84	22	0	0	0	6	0
Nonionellina labradorica	1	0	6	18	6	0	0	0	648	90	59	36	0	18	18	30
Oolina globosa	0	0	0	0	0	0	0	0	36	0	0	0	0	0	0	0
Oolina hexagona	0	0	6	0	0	0	0	0	0	0	0	0	0	0	0	0
Oolina spp.	0	0	0	0	0	6	0	0	0	0	0	0	0	0	0	0
Ordosalis umbonatus	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Planispirinoides bucculentus	1	0	0	6	6	0	0	0	0	0	0	0	0	0	0	0
Pullenia bulloides	0	0	0	0	0	0	0	0	144	0	5	0	0	0	0	0
Pullenia osloensis	0	48	12	72	18	0	0	0	180	90	21	6	0	12	6	0
Quinqueloculina seminulum	0	0	0	0	6	0	0	0	0	0	0	0	0	0	0	0
Quinqueloculina spp.	0	0	0	0	0	0	0	0	0	0	1	0	12	0	0	0
Spiroloculina spp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0
Stetsonia arctica	13	0	0	12	0	0	0	0	216	18	8	12	6	0	0	0
Trifarina fluens	0	0	0	0	0	0	0	0	36	6	1	0	0	0	0	0
Valvulinaria arctica	0	18	0	12	24	0	0	0	180	18	7	0	0	0	0	0
Cassidulina/Islandiella spp.	4	78	18	24	0	0	18	0	648	36	17	0	0	0	0	6
Calcareous fragment/unknown	3	84	24	66	126	0	0	6	504	324	99	12	0	18	6	0
Neogloboquadrina pachyderma sinistral (planktic)	268	510	312	690	846	12	174	198	3456	276	169	18	0	30	18	72
Neogloboquadrina pachyderma dextral (planktic)	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Globigerina bulloides (planktic)	0	0	0	0	54	0	0	0	0	0	0	0	0	0	0	0

APPENDIX N: RANKED TAXON ABUNDANCE OF MEIOFAUNA

Table 1. Meiofaunal abundance in ranked order for each of 90 foraminiferan taxa recorded from 16, 5-cc sediment samples collected from four CBMP biodiversity monitoring stations in the DFCA (Appendix M). Percent and cumulative percent abundance for each taxon are provided.

Taxon	Abundance	% A	Cumulative %A
Neogloboquadrina pachyderma sinistral (planktic)	7049	15.6	15.6
Textularia torquata	4572	10.1	25.8
Cibicides lobatus	3427	7.6	33.4
Agglutinated fragment/unknown	2022	4.5	37.9
Cassidulina reniforme	1862	4.1	42.0
Rhabdammina abyssorum	1567	3.5	45.5
Adercotryma glomerata	1531	3.4	48.9
Astrorhiza arenaria	1520	3.4	52.2
Cibicides wuellerstrofi	1337	3.0	55.2
Calcareous fragment/unknown	1272	2.8	58.0
Nonionellina labradorica	930	2.1	60.1
Trochammina pseudoinflata	925	2.1	62.2
Cassidulina/Islandiella spp.	849	1.9	64.0
Cassidulina neoteretis	847	1.9	65.9
Saccammina difflugiformis	706	1.6	67.5
Spiroplectammina biformis	669	1.5	69.0
Rhabdammina/Hyperammina spp.	665	1.5	70.4
Islandiella narcrossi	616	1.4	71.8
Melonis barleeanum	583	1.3	73.1
Textularia earlandi	565	1.3	74.4
Elphidium spp.	559	1.2	75.6
Trochammina globigeriformis	530	1.2	76.8
Trochammina nitida	517	1.1	77.9
Buccella frigida	488	1.1	79.0
Fissurina marginata	488	1.1	80.1
Pullenia osloensis	465	1.0	81.1
Cassidulina laevigata	416	0.9	82.0
Reophax catella	413	0.9	83.0
Trochammina nana	411	0.9	83.9
Reophax catenata	402	0.9	84.8
Trochammina spp.	386	0.9	85.6
Astrononion gallowayi	379	0.8	86.5
Recurvoides turbinatus	363	0.8	87.3

Taxon	Abundance	% A	Cumulative %A
Elphidium exclavatum *f. clavata*	340	0.8	88.0
Deuterammina orchacea	306	0.7	88.7
Reophax scorpiurus	301	0.7	89.4
Cyclogyra involvens	293	0.7	90.0
Elphidium subarcticum	291	0.6	90.7
Reophax arctica	288	0.6	91.3
Stetsonia arctica	285	0.6	91.9
Buliminella hensoni	275	0.6	92.5
Fursenkoina fusiformis	272	0.6	93.1
Valvulinaria arctica	259	0.6	93.7
Cribrostomoides jeffreysii	246	0.5	94.3
Cribrostomoides crassimargo	241	0.5	94.8
Reophax bilocularis	217	0.5	95.3
Silicosigmoilina groenlandica	213	0.5	95.8
Nonionellina auricula	202	0.4	96.2
Saccorhiza ramosa	180	0.4	96.6
Reophax fusiformis	168	0.4	97.0
Glomospira gordialis	163	0.4	97.3
Pullenia bulloides	149	0.3	97.7
Hemisphaerammina bradyi	120	0.3	97.9
Hyperammina spp.	111	0.2	98.2
Bolivina pseudopunctata	93	0.2	98.4
Reophax guttifer	78	0.2	98.6
Eggerella advena	66	0.1	98.7
Globigerina bulloides (planktic)	54	0.1	98.8
Psammosphaera fusca	52	0.1	98.9
Reophax nodulosa	48	0.1	99.0
Trifarina fluens	43	0.1	99.1
Islandiella helenae	41	0.1	99.2
Bathysiphon rufus	36	0.1	99.3
Elphidium bartletti	36	0.1	99.4
Oolina globosa	36	0.1	99.5
Reophax bacillaris	30	0.1	99.5
Lagena spp.	23	0.1	99.6
Epistominella exigua	20	0.0	99.6
Hemisphaerammina spp.	18	0.0	99.7
Cribrostomoides subglobosum	13	0.0	99.7
Planispirinoides bucculentus	13	0.0	99.7
Quinqueloculina spp.	13	0.0	99.8

Taxon	Abundance	% A	Cumulative %A
Reophax dentaliniformis	12	0.0	99.8
Trochammina squamata	12	0.0	99.8
Astacolus spp.	12	0.0	99.8
Globobulimina spp.	10	0.0	99.9
Saccammina sphaerica	7	0.0	99.9
Haynesina germanica	7	0.0	99.9
Rhabdammina linearis	6	0.0	99.9
Epistominella takayanagii	6	0.0	99.9
Oolina hexagona	6	0.0	99.9
Oolina spp.	6	0.0	99.9
Quinqueloculina seminulum	6	0.0	100.0
Spiroloculina spp.	6	0.0	100.0
Fissurina spp.	5	0.0	100.0
Dentalina spp.	3	0.0	100.0
Neogloboquadrina pachyderma dextral (planktic)	2	0.0	100.0
Lagena mollis	1	0.0	100.0
Lenticulina spp.	1	0.0	100.0
Ordosalis umbonatus	1	0.0	100.0

APPENDIX O: MEIOFAUNAL DIVERSITY INDICES BY STATION

Table 1. Meiofaunal indicators for the biodiversity monitoring sites established in the DFCA of the eastern Canadian Arctic. S = number of species, Abundance (N), d = Margalef's Species Richness, J′ = Pielou's Evenness. All data /5 cc sediment. Replicates A, B, C are from the same sediment sample. CON=Consecutive Operation Number. *Indicates significant difference among stations (ANOVA, α = 0.05). Retrospective power and least significant number (LSN) calculations for non-significant ANOVA.

Site	Station	CON	Replicate	Latitude	Longitude	Depth (m)	S*	N	d	J'	Shannon* H'(loge)	Simpson* Index
DFCA	BB1_B_400 m	71	A	67.9935	-59.312	479	40	768	5.870	0.666	2.455	0.832
DFCA	BB1_B_400 m	71	B	67.9935	-59.312	479	51	3174	6.201	0.857	3.368	0.947
DFCA	BB1_B_400 m	71	C	67.9935	-59.312	479	43	1674	5.658	0.840	3.159	0.933
					Average CON	71	45	1872	5.910	0.787	2.994	0.904
DFCA	BB1_B_400 m	56		67.9939	-59.328	506	48	2886	5.899	0.776	3.004	0.906
DFCA	BB1_B_400 m	68		67.9935	-59.3109	476	43	2634	5.332	0.714	2.686	0.862
DFCA	BB1_A_600 m	81		67.7679	-59.0862	700	37	2058	4.719	0.824	2.976	0.918
DFCA	BB1_A_600 m	82		67.7683	-59.0847	699	39	1878	5.041	0.810	2.969	0.914
DFCA	BB1_A_600 m	83		67.7679	-59.088	705	34	1764	4.415	0.783	2.761	0.885
DFCA	BB1_C_400 m	109		67.6115	-58.546	387	40	15876	4.032	0.766	2.826	0.900
DFCA	BB1_C_400 m	112		67.6126	-58.5418	377	48	2358	6.052	0.847	3.277	0.944
DFCA	BB1_C_400 m	113		67.6138	-58.5406	376	56	1003	7.959	0.798	3.213	0.936
DFCA	BB1_D	119	A	67.3778	-57.9299	662	33	1716	4.297	0.741	2.591	0.850
DFCA	BB1_D	119	B	67.3778	-57.9299	662	32	1644	4.186	0.768	2.661	0.881
DFCA	BB1_D	119	C	67.3778	-57.9299	662	35	1818	4.530	0.732	2.603	0.845
					Average CON	119	33	1726	4.338	0.747	2.618	0.859
DFCA	BB1_D	120		67.3815	-57.9235	643	35	1938	4.492	0.765	2.719	0.873
DFCA	BB1_D	121		67.383	-57.9276	644	29	1884	3.713	0.708	2.384	0.821
Power								0.16	0.35	0.47		
LSN								41	19	15		

APPENDIX P: EFFECT OF TRANSFORMATION ON MEIOFAUNAL ABUNDANCE

Untransformed Abundance

Log(x+1)-transformed Abundance

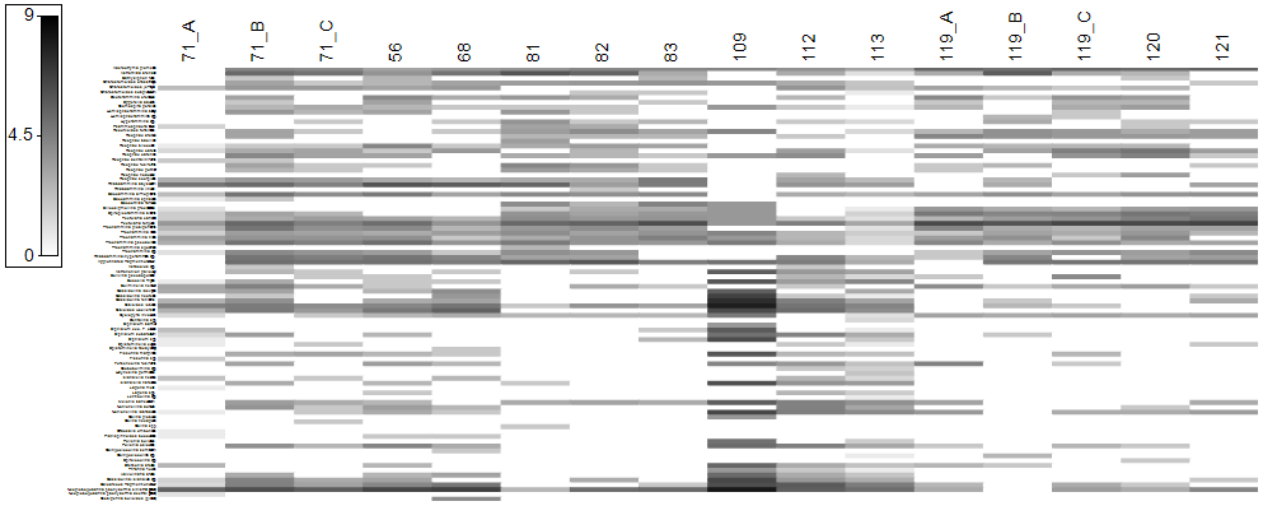


Figure 1. Shade plots showing the effect of transformation on the abundance of meiofaunal taxa by 5-cc sample (labelled by Consecutive Operation Number). Scale bars of the abundance for each plot are shown in the upper left.

APPENDIX Q: SIMILARITY IN ABUNDANCE AMONG MEIOFAUNAL COMMUNITIES

BB1_B_400	**71A**	**71A**														
	71B	47.5	**71B**													
	71C	52.0	75.0	**71C**												
	56	50.9	81.3	74.8	**56**											
	68	50.7	70.1	69.9	72.1	**68**										
BB1_A_600	**81**	36.0	62.7	65.1	58.3	51.6	**81**									
	82	44.8	68.4	75.0	62.0	56.6	81.9	**82**								
	83	46.9	58.3	64.4	56.0	49.5	71.7	76.7	**83**							
BB1_C_400	**109**	33.3	54.4	43.9	51.3	48.7	36.5	40.6	42.2	**109**						
	112	44.9	72.7	66.2	72.9	68.2	43.4	51.4	44.3	57.8	**112**					
	113	53.1	60.5	58.8	64.7	63.1	37.0	44.4	43.1	54.8	73.1	**113**				
BB1_D	**119A**	40.1	57.6	61.1	59.9	46.9	58.6	62.0	61.0	38.9	47.6	40.7	**119A**			
	119B	46.9	57.3	62.2	55.5	54.7	66.5	71.6	65.0	31.1	46.0	40.7	61.4	**119B**		
	119C	37.9	58.9	65.1	60.4	54.4	58.9	63.5	59.2	40.0	50.5	40.5	75.6	66.1	**119C**	
	120	38.5	58.0	63.2	57.3	52.9	61.3	66.1	62.3	35.3	48.2	37.0	74.2	69.0	81.2	**120**
	121	41.5	54.0	63.1	51.5	49.7	61.2	68.7	64.2	38.3	49.0	44.9	61.6	69.1	63.7	68.3

Figure 1. Bray-Curtis similarity among meiofaunal communities based on log (x+1)-transformed abundance. Samples are labelled by Consecutive Operation Number (in bold, black by row and white by column) and station. All stations are in the DFCA. Comparisons of within-sample replicates are lightly shaded.