GOLDER
MEMBER OF WSP

FINAL REPORT

Chapter 5.0 Substrate, Macroflora and Benthic Epifauna

2021 Marine Environmental Effects Monitoring Program (MEEMP) and Non-Indigenous Species / Aquatic Invasive Species (NIS/AIS) Monitoring Program

Submitted to:

Baffinland Iron Mines Corporation

2275 Upper Middle Road East, Suite 300
Oakville, ON L6H 0C3

Submitted by:

Golder Associates Ltd.

Suite 200 - 2920 Virtual Way Vancouver, BC, V5M 0C4 Canada

+1 604 296 4200

1663724-349e-R-Rev0-44000

21 October 2022

Table of Contents

TABLES

FIGURES

APPENDICES

ACRONYMS AND ABBREVIATIONS

Acronym or Abbreviation	Definition
AIS/NIS	Aquatic Invasive Species/ Non-Indigenous Species
BACI	Before-After-Control-Impact
CD	Chart Datum
EEM	Environmental Effects Monitoring
ERP	Early Revenue Phase
FEIS	Final Environmental Impact Statement
M	meter
Mm	millimeter
MANOVA	Multivariate Analysis of Variance
MEEMP	Marine Environmental Effects Monitoring Program
MFEAP	Marine Foreshore Environment Assessment Procedure
NIS/AIS	Non-Indigenous Species/Aquatic Invasive Species
No.	Number
org./quadrat	Organism per quadrat
PC	Project Certificate
QA/QC	Quality Assurance and Quality Control
ROV	Remotely Operated Vehicle
SDI	Simpson’s Diversity Index
Unid.	unidentified
ZOI	Zone of Influence
%	Percent

5.0 SUBSTRATE, MACROFLORA AND BENTHIC EPIFAUNA

5.1 Introduction

This chapter presents the results of the substrate, macroflora and benthic epifaunal monitoring program, a component of the larger Marine Environmental Effects Monitoring Program (MEEMP) conducted at Milne Port and in Milne Inlet during the 2021 open-water season. This component was developed in consideration of the potential Project-related impacts to the marine environment as identified in the 2012 Final Environmental Impact Statement (FEIS, Baffinland 2012) and subsequent addendums, as well as monitoring requirements outlined in the Project Certificate (PC) Conditions described in in Chapter 1.0, Table 1-2. PC Conditions related to the monitoring of substrate, macroflora, and epifauna included PC Conditions No. 76, 83 (a), 87, 99 (a), and 99 (c).

5.1.1 Objectives

The overall MEEMP objectives are outlined in Section 1.3 of Chapter 1.0 (Program Overview). Objectives specific to the substrate, macroflora, and benthic epifaunal component are as follows:

- Monitor potential changes in substrate conditions or in the macrofloral and benthic epifaunal community at Milne Port and in a nearby Reference Area for the purpose of identifying Project-related effects.
- Verify predictions made in the FEIS regarding effects on Arctic char *(Salvelinus alpinus)* habitat.
- Recommend necessary and appropriate changes to survey methodology for future years, if warranted.

5.2 Study Design

5.2.1 Background

The 2014 to 2017 MEEMP study design monitored for changes to the benthic community with epifauna[1] and epiflora[2] as indicators, using towed underwater video transect surveys. The use of epifauna and epiflora as effect indicators deviated from the standard Environmental Effects Monitoring (EEM) methodology (Environment Canada 2010; 2012) and presented a number of challenges, including 1) high temporal and spatial variability due to the mobile and transient nature of many epifaunal species, 2) typical low resolution of video survey data compared to laboratory analysis for species identification, enumeration and substrate classification, and 3) difficulty in distinguishing between live epiflora (e.g., kelp) and detrital vegetation debris using video survey methods, which can result in inaccurate results.

In 2018, a new survey design was implemented, based on a Before-After-Control-Impact (BACI) approach. Towed underwater video transects were replaced with five belt transects (1 m x 5 m plots) permanently installed on the seabed in each exposure (impact) and reference (control) areas. Monitoring was conducted using a remotely operated vehicle (ROV) underwater video system. In addition to informing this component of the MEEMP, taxonomic data were also used to inform the NIS/AIS program (Chapter 8.0). In 2019, underwater video monitoring of epifauna and macroflora communities within permanent belt transects continued for a second year.

[1] benthic invertebrates living on the substrate

[2] marine vegetation attached to the substrate (e.g. kelp)

The belt transects deployed in 2018 were composed of two 1-m-long, 5-cm-diameter aluminum pipes filled with concrete connected by two 5-m-long steel chains attached to both ends of the pipes (Figure 5-1). In 2019, it was determined that the flexible design was not suitable for the environment, as five of the ten deployed transects were dragged from their original position due to presumed interactions with the sea-ice during spring break-out or had become embedded in the sediment and thus obscured from detection.

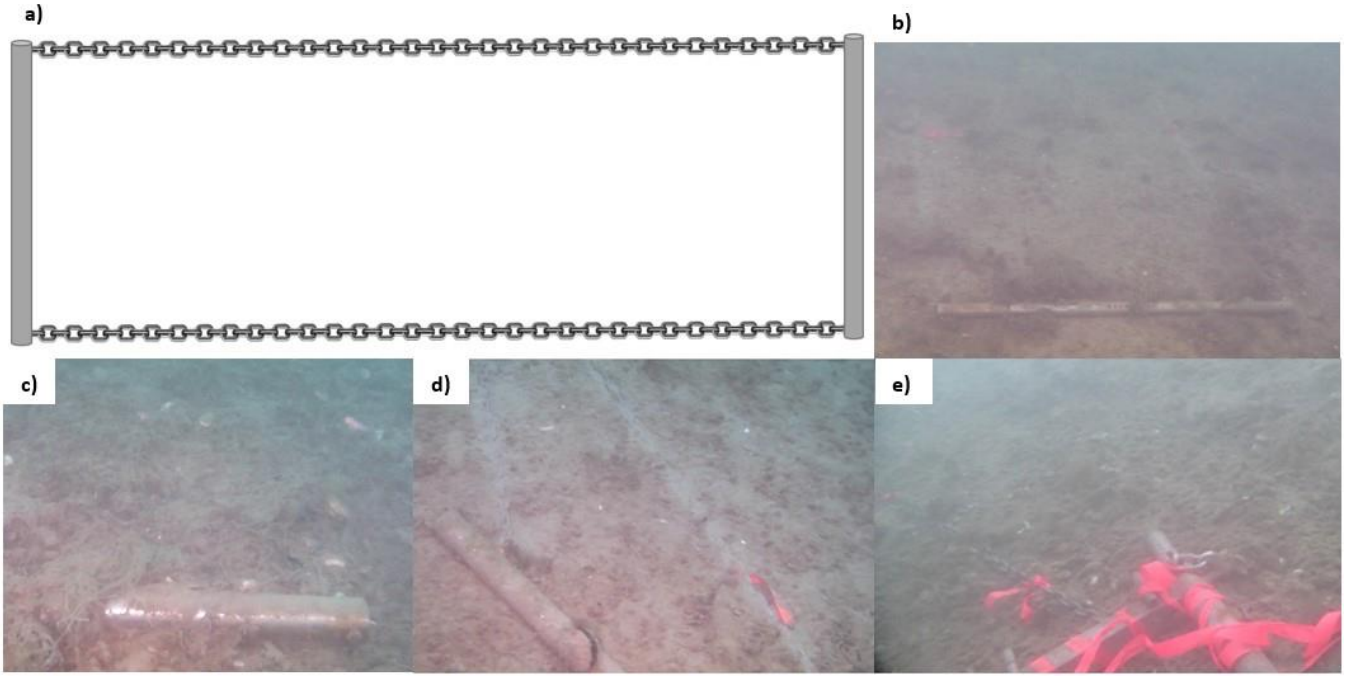


Figure 5-1: Belt Transects Used for Epifauna and Macroflora Surveys in 2018-2019. a) Diagram of Belt Transect Layout; b) Photo of Deployed Belt Transect; c, d and e) Belt Transects Embedded in Sediment and/or Shifted from Original Deployment Position

5.2.2 Modifications to the Program (2020 and 2021)

The program was modified in 2020 to replace the belt transects described above, which had been determined to be ineffective due to a large number of the deployed transects being dragged out of position or embedded within the underlying sediment within one year of deployment, presumably due to interactions with sea-ice. Modifications to the program in 2020 included the use of divers to undertake biophysical surveys of permanent, heavy-duty steel quadrats to improve the resolution of taxonomic identification. A total of ten 1 m x 1 m square quadrats were fabricated onsite in 2020 and installed on the sea bottom in Milne Port, five in the exposure area (Q1 through Q5) and five in a reference area (Q6 through Q10) (Figure 5-2). An additional ten square steel quadrats were fabricated and deployed in 2021 (Q11 through Q20; 5 in each exposure and reference area), doubling the total number of quadrats relative to 2020.

Surveys conducted in 2020 indicated that Q9 was dominated by hard substrate (boulder) and supported different ecological communities relative to the soft substrate quadrats. Therefore, in 2021, Q9 was relocated to a different area to maintain comparability between quadrats.

In previous years, taxonomic resolution was relatively coarse because of poor visibility due to suspended particles in the water column and the use of a ROV-based underwater video survey for monitoring. Survey of the quadrats was performed by a combination of divers and ROV in 2020[3] and exclusively by divers in 2021. Rationale for dropping use of the ROV is that divers are more accurately able to distinguish unique taxa (i.e., differentiate between detrital algae or non-living organisms), move vegetation aside to observe the underlying substrate and marine organisms, and collect specimens from the quadrats for identification purposes.

5.2.3 Indicators

Effect indicators selected to evaluate potential Project-induced changes in substrate, macroflora and epifauna include taxa richness (number of unique taxa present), relative abundance, Simpson's Diversity Index (SDI), density (motile taxa) and percent cover (macroflora and sessile invertebrates). These indicators are described in detail in Section 5.3.2. The indicators are calculated from data collected in both reference and exposure areas and analyzed statistically to evaluate Project-related effects within the study area.

The 2020 field season was the first year in which data were collected using steel quadrats, precluding the ability to make quantitative temporal comparisons to previous years. Upon reviewing the data collected in 2020, it was noted that the data had been collected with a coarser taxonomic resolution than in 2021 (due to differing field methodologies), which would affect how the data compared between the two survey years. Therefore, quantitative comparisons to 2020 data could not be made and a qualitative comparison has been provided where reasonable to do so. The 2021 quadrat survey results will serve as a benchmark for quantitative comparisons to future survey years so long as field methodologies remain consistent.

5.3 Materials and Methods

5.3.1 Field Methodology

Twenty 1 m x 1 m square steel quadrats were fabricated on site and were inset with 0.075 m metal bars to create nine smaller squares (sub-quadrats, approximately 0.22 m x 0.22 m) to allow for accurate and repeatable area measurements and scaling (for ROV observations). The quadrats were slowly lowered to the sea floor from a vessel: ten in the exposure area and ten in a reference area (Table 5-1, Figure 5-2). The reference area was established in 2013 and selected for its proximity to Milne Port while residing outside of the main zone of influence (ZOI) of Project activities (SEM 2014). Ten of the quadrats (Q1 through Q10) were deployed and surveyed in 2020, and an additional ten quadrats were deployed in 2021 (Q11 through Q20). The quadrats were deployed from the field vessel at the locations of the old belt transects, in water depths of approximately -5 to -16 m Chart Datum (CD). Each quadrat was marked with fluorescent spray paint to aid in relocating them in subsequent surveys.

[3] Divers surveyed quadrats in the reference area (Q6, Q8, Q9, Q10), but were unable to survey the quadrats in the exposure area due to time constraints in the field program (these were subsequently completed using ROV-video surveys).

Table 5-1: Quadrat Locations

Area	Quadrat	UTM Coordinates (17W)		Depth (m below CD) [1]	Deployment Date	Survey Date (2021)
		Easting (m)	Northing (m)			
Milne Port	Q1	502828	7976382	-9.1	12 August 2020	14 August
	Q2	503039	7976480	-9.8	12 August 2020	Not surveyed[2]
	Q3	504208	7976659	-10.9	12 August 2020	15 August
	Q4	504363	7976611	-12.2	12 August 2020	6 August
	Q5	504802	7976731	-12.4	12 August 2020	6 August
	Q11	502820	7976371	-7.6	10 August 2021	14 August
	Q12	503041	7976474	-6.0	7 August 2021	11 August
	Q13	504210	7976643	-8.0	10 August 2021	15 August
	Q14	504350	7976589	-7.7	6 August 2021	16 August
	Q15	504800	7976721	-7.4	6 August 2021	6 August
Reference Area	Q6	506563	7979107	-15.9	13 August 2020	8 August
	Q7	506774	7979170	-10.2	13 August 2020	16 August
	Q8	506957	7979457	-10.7	13 August 2020	16 August
	Q9	506963	7979448	-9.3	11 August 2021[3]	Not surveyed[4]
	Q10	506584	7979115	-6.5	13 August 2020	8 August
	Q16	506567	7979090	-5.7	8 August 2021	8 August
	Q17	506774	7979163	-8.9	11 August 2021	16 August
	Q18	506956	7979452	-10.2	11 August 2021	16 August
	Q19	506961	7979458	-8.0	11 August 2021	Not surveyed[4]
	Q20	506588	7979125	-11.2	8 August 2021	8 August

Note: [1] Diver depth gauge was converted to meters chart datum (CD), estimated using tide table for Milne Inlet, Nunavut (http://www.tides.gc.ca/eng [accessed October 2021]). The negative (-) numbers indicate 'below' CD. [2] Q2 was not located by divers. [3] Q9 was relocated from hard substrate to soft substrate. [4] Q9 and Q19 were not surveyed due to time constraints.

Figure 5-2: Locations of Survey Quadrats for Monitoring Substrate, Macroflora and Epifauna (2021)

Field surveys of the quadrats were conducted in August 2021 by Golder's occupational (SCUBA-based) dive team composed of marine biologists and scientific divers. The dive team is certified in accordance with Canadian Standard Association Z275:4-97 and WorkSafe BC Regulations Part 24. Dive surveys were conducted from Baffinland's 30-foot Research Vessel.

Field surveys included the following components:

- Deployment of additional ten steel quadrats: five in exposure area and five in the Reference Area.
- Retrieval and relocation of Q9 from hard substrate to soft substrate.
- Subtidal dive quadrat surveys to quantitatively evaluate macroalgae, sessile and motile invertebrates and fish occurrence (commonly termed epifauna) within both the exposure area and reference area.
- Opportunistic observations[4] of macroalgae, fish and motile/sessile invertebrates during quadrat surveying.

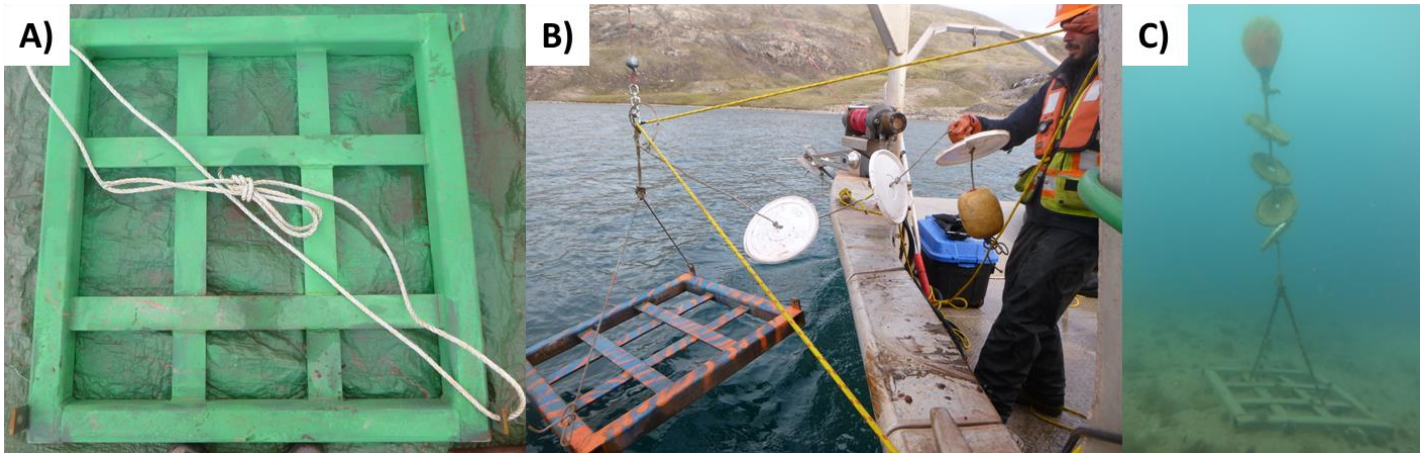


Figure 5-3: A) Example of 1 x 1 m Steel Quadrat Deployed in 2021; B) Active Deployment of Survey Quadrat; C) Underwater Photo of Quadrat (Q5) With Attached Settlement Plates for NIS/AIS Monitoring.

5.3.1.1 Quadrat Survey

Biophysical data within each quadrat was recorded by one diver while another diver collected representative photographs of the survey quadrat[5]. Observations within the sub-quadrats were recorded in a systematic way, with the top end of the quadrat (sub-quadrat 1,2,3) on the upslope and the bottom of the quadrat (sub-quadrat 7,8,9) on the down slope so the observations by sub-quadrat could be repeatable each year. A quadrat specific marker (a string with knots) was added to each of the quadrats deployed in 2021 at the corner representing sub-quadrat 1.

[4] Opportunistic observations refer to observations that were recorded during diver-collected photo or video to document presence/absence in a qualitative manner rather than quantitatively assessed during the quadrat survey.

[5] Underwater imagery collected using a SONY RX100 V camera in Fantasea underwater housing and Big Blue video light for all underwater surveys. The camera has high definition video capability and still photography features.

Quantitative data were collected in general accordance with DFO's Marine Foreshore Environmental Assessment Procedure (DFO 2002). Quadrat data were recorded on project-specific datasheets, and included the following information[6]:

- Substrate type was visually estimated according to the size ranges: bedrock; boulder (>256 mm diameter); cobble (64 to 256 mm); gravel (2 to 64 mm); sand (0.0625 to 2 mm); silt/mud/clay (<0.0625 mm) and relative composition (i.e., as a percent areal coverage).
- Macroalgae was identified to the lowest practical level (LPL) and total areal coverage was estimated.
- Sessile invertebrates, such as clams and mussels, were identified to LPL and total areal coverage was estimated (as above).
- Motile invertebrates (e.g., urchins, limpets) and fish were identified to LPL and enumerated. Abundance was estimated if relatively large numbers of motile species were present.
- Photographs showing representative biological features and aiding in species identification were taken.

During the 2021 field program, divers were unable to relocate quadrat Q2 after undertaking a thorough search along the depth contour -3 to -12 m CD (Q2 was deployed in approximately -10 m CD), extending approximately 25 m to the west and east of the original Q2 location. This quadrat was assumed to have been dragged from its original position by sea-ice during the spring break-out period. Quadrats Q9 and Q19 were not surveyed in 2021 due to time constraints resulting from several storm days which precluded dive operations.

5.3.1.2 Opportunistic Specimen Collection

Opportunistic samples of epifauna and macroflora were collected to enhance taxonomic resolution, particularly in cases where organisms may be suspected to be non-indigenous to the area. Specimens were collected using the following protocol:

- Divers collected specimens into sealed ziploc bags and brought to the surface in a mesh bag.
- Discretion was used to sample only one representative individual or portion of a macroalgae to avoid over-harvesting from the quadrats which could have future implications on the community assemblage (experimental design interaction).
- Samples were placed into 120-mL clear glass jars and preserved. Macroflora samples collected for DNA barcoding were preserved with 90% ethanol and samples collected for taxonomic analysis were preserved in a 10% buffered formalin solution. The jars were then sealed and inverted several times to promote homogenization and saturation with the preservative. Jars were labeled internally and externally with water-resistant labels.
- Samples were sent to Biologica Environmental Services Ltd. (Biologica) for taxonomic identifications and genetic analysis (DNA-barcoding) (macroflora only). Macroflora samples sent for DNA-barcoding were first analyzed for morphological identification by an algae taxonomist (Dr. Sandra Lindstrom, UBC) to verify DNA sequencing success. Whole specimen or tissue samples of taxa sent for DNA verification were sent to the Canadian Centre for DNA Barcoding (CCDB) at the University of Guelph for barcoding.

[6] Recorded data were in general accordance with Fisheries and Oceans Canada (DFO) Marine Foreshore Environment Assessment Procedure (MFEAP) (provided in Appendix A)

5.3.2 Data Analysis

Diver-collected quadrat data were entered into an electronic database by one biologist and verified by second biologist for transcription errors. Field-based identifications were updated where lab identifications of opportunistically sampled specimens resulted in improved taxonomic resolution.

Statistical analysis was based on four indicators: taxa richness (to the lowest practicable level), relative abundance, Simpson's Diversity Index, organism density (motile taxa) and percent cover (macroflora and sessile invertebrates).

Due to inconsistent sampling methodologies between 2021 and previous survey years, a quantitative statistical analysis was not possible between the 2021 quadrat survey data and that from previous years (i.e., interannual comparisons). A qualitative comparison between years has been provided. Results from 2021 surveys will act as a baseline to monitor for changes in future survey years, with 2021 comprising the first year of quantitative annual comparisons.

Richness

Richness is defined as the total number of unique taxa per quadrat. This metric provides an indication of the diversity (number of different species) in the local ecological community. A higher richness value typically indicates a healthier and more balanced community. Mean taxa richness and standard error of the mean was calculated based on number of taxa by area (Exposure, Reference).

Simpson's Diversity Index

Simpson's Diversity Index (SDI) measures the proportional distribution of organisms in the community, which considers the density and taxonomic richness of the community. Certain conditions may favour one taxa over another, resulting in the community being dominated by a few taxa, which is reflected in decreased diversity (Simpson 1949). The SDI values range between zero and one, where lower values indicate a less diverse community dominated by few taxonomic groups and higher values indicate a community consisting of more taxa among which density is more evenly distributed. The SDI was calculated using the formula provided by Krebs (Krebs 1999):

$$SDI = 1 - \sum_{i=1}^{S} (p_i)^2$$

Where:

- SDI = Simpson's Diversity Index
- S = the total number of taxa
- p_i = the proportion of the i^{th} taxon (of each unique taxa out of the total abundance of the sample)

For categorization of diversity, SDI values <0.250 were considered to have very low diversity, 0.250 to 0.499 had low diversity, 0.500 to 0.750 were moderately diverse and >0.750 were considered to have high diversity (Table 5-2).

Table 5-2: Diversity Categories for Simpson's Diversity Index (SDI) Values

SDI Value	Diversity Category
<0.250	Very Low
0.250 through 0.499	Low
0.500 through 0.750	Moderate
>0.750	High

Mean SDI and standard error of the mean were calculated for each exposure and reference areas.

Organism Density

For motile invertebrates and fish, mean density (organisms/quadrat) and standard error of the mean were calculated for each exposure and reference areas.

Percent Cover

For macroalgae and sessile invertebrates, mean percent areal cover (total cover) and standard error of the mean was calculated by area (Exposure, Reference). Relative abundance was calculated as percent cover standardized out of 100% for substrate, macroflora, sessile and motile epifauna.

5.3.2.1 Statistical Analysis

5.3.2.1.1 ANOVA and ANCOVA

Differences in substrate, detritus and debris, macroalgae, and benthic epifauna between the exposure area and reference area were analyzed using an analysis of variance (ANOVA) and/or an analysis of covariance (ANCOVA). The ANOVA compares the means of a variable between two or more groups; specifically for these analyses, a one-way ANOVA was used as opposed to a two-way ANOVA as only one independent variable was tested (i.e., exposure versus reference site). The ANCOVA is an extension of the ANOVA and is used to compare the means of a variable between two or more groups while correcting for variability due to another variable (i.e., covariate). Both analyses seek an F value, which is the ratio of the two mean square values being tested, and a p-value, which is calculated based on the F value. A large F value indicates that the variation among the group means is higher than can be accounted for by chance (Zar 2010). Percent cover, density, taxa richness, and diversity (i.e., SDI) of macroflora, sessile, and motile benthic epifauna were used as dependent variables. P-values <0.05 are considered to indicate significance between groups. Analysis was conducted using R statistical software version 4.1.2 (R Core Team 2013).

5.3.2.1.2 Taxa Accumulation

A taxa accumulation curve was calculated for quadrats surveyed in 2021 to provide an estimate of the effort required to fully characterize the quadrat benthic community assemblage, in accordance with Baffinland's commitment made in response to DFO Technical Comment 17 on the 2020 MEEMP and NIS/AIS Monitoring Program Report (Golder 2021). A taxa accumulation curve illustrates how the number of unique taxa (or species) increases as the number of samples are accumulated; in other words, the harder one looks (i.e., the higher the sampling effort), the more unique taxa are found. The curve reaches an asymptote when all taxa within the given community assemblage have been sampled and the community assemblage is assumed to have been fully

described. The observed species (or taxa) curve (S_{obs}) is plotted and the sample (i.e., quadrat) order is randomized and permutated 999 times, resulting in an averaged curve describing a smooth relationship of the average number of species (or taxa) for each number of replicates and the standard error of the mean (i.e. permutations). This is equivalent to station-based rarefaction curves. Analysis was conducted using PRIMER-E statistical software version 7 (Clarke and Gorley 2014, Clarke and Gorley 2015).

5.3.2.1.3 Power Analysis

A power analysis was conducted using the 2021 data to estimate the sample size needed to detect Project-related change based on levels of observed variability among quadrats, in accordance with Baffinland's commitment made in response to DFO Technical Comment 16 and 17 on the 2020 MEEMP and NIS/AIS Monitoring Program Report (Golder 2021).

5.3.3 Quality Management

Quality assurance and quality control (QA/QC) procedures were applied to the field collection, data analysis, and reporting tasks within the chapter component to verify that the data presented were valid and of acceptable quality to address objectives stated in Section 5.1.1.

5.3.3.1 Field QA/QC

QA/QC measures for quantitative and qualitative data collected during quadrat surveys, included:

- Field survey data sheets were checked and cross-validated before in the field.
- Taxa identifications, including common and species name, were verified using references[7].
- Dive survey video, photographs and datasheets were saved to a laptop computer and external hard drive at the end of each field day. Once in the office, the survey data were uploaded to Golder's SharePoint site.

5.3.3.2 Laboratory and Data Analysis QA/QC

The following QA/QC measures were implemented:

- Taxa common name/species name and recorded observations were verified using references[7].
- Transcribed diver-collected data was reviewed for transcription errors by a second biologist.
- Calculations were verified by a second biologist for errors as part of the data review process.

[7] References used during the surveys, included: Mecklenburg et al. (2007), Küpper et al. (2016), Coad and Reist (2018), Golder (2021), WoRMS (2021), Guiry and Guiry (2021)

5.4 Results

This section presents results form the 2021 quadrat sampling program at Milne Port. Representative photographs are provided in Appendix 5B. Quadrat/transect data in tabulated form are presented in Appendix 5C. ANOVA / ANCOVA results are presented in Appendix 5D. Results of the power analysis are provided in Appendix 5E. A taxa list with common and scientific names is provided in Appendix 5F. Taxonomy and algae DNA barcoding results are presented in Appendix 8B-2 (Chapter 8.0).

During field surveys, it was noted that Q12 had been deployed too shallow (-6 m CD) from desired target depth (-7 to -9 m CD) in an area consisting of a high percentage of sand (approximately 90%), trace macroalgae (6%) and no sessile or motile epifauna (Appendix 5B – Photo 1). Macroalgae and epifuana was observed within deeper depths at this location; therefore, the placement of this quadrat within the shallows is considered an outlier. The results from Q12 were not included in the data analysis for 2021 and the location of Q12 should be reassessed for future surveys.

5.4.1 Substrate

Substrate was composed predominantly of silt and sand for all quadrats in both the exposure area and reference area (Figure 5-4, Figure 5-5A), as observed in previous years. Quadrats Q1, Q11, Q14 within the exposure area contained majority sand (ranging 55 to 59%), while silt was more dominant in the other quadrats within both the exposure area (ranging between 50 to 72%) and reference area (ranging between 55 and 79%). The ANOVA/ANCOVA analyses found significant differences in the percent cover of substrate types between the exposure area and reference area for sand and silt, with p-values of 0.003 and 0.032, respectively (Table 5-3). Specifically, the ANCOVA results indicate that silt was slightly higher in the reference area compared to the exposure area; this could be explained by the larger proportion of sand in Q1, Q11, and Q14 within the exposure area.

Other substrate types present in small proportions within each area included cobble (0 to 4%), gravel (0 to 12%), and shell (0-6%). Bedrock was observed in small proportions in Q20 (6% bedrock). When surveying Q20, it was noted that the quadrat had traveled across the sediment surface interface over a steep slope during deployment, causing the sediment to be disturbed and exposing some underlaying bedrock (Appendix 5B – Photo 43). Generally, the proportion of substrate types are similar between the exposure area and reference area, although the substrate recorded in the reference area quadrats do contain slightly higher silt.

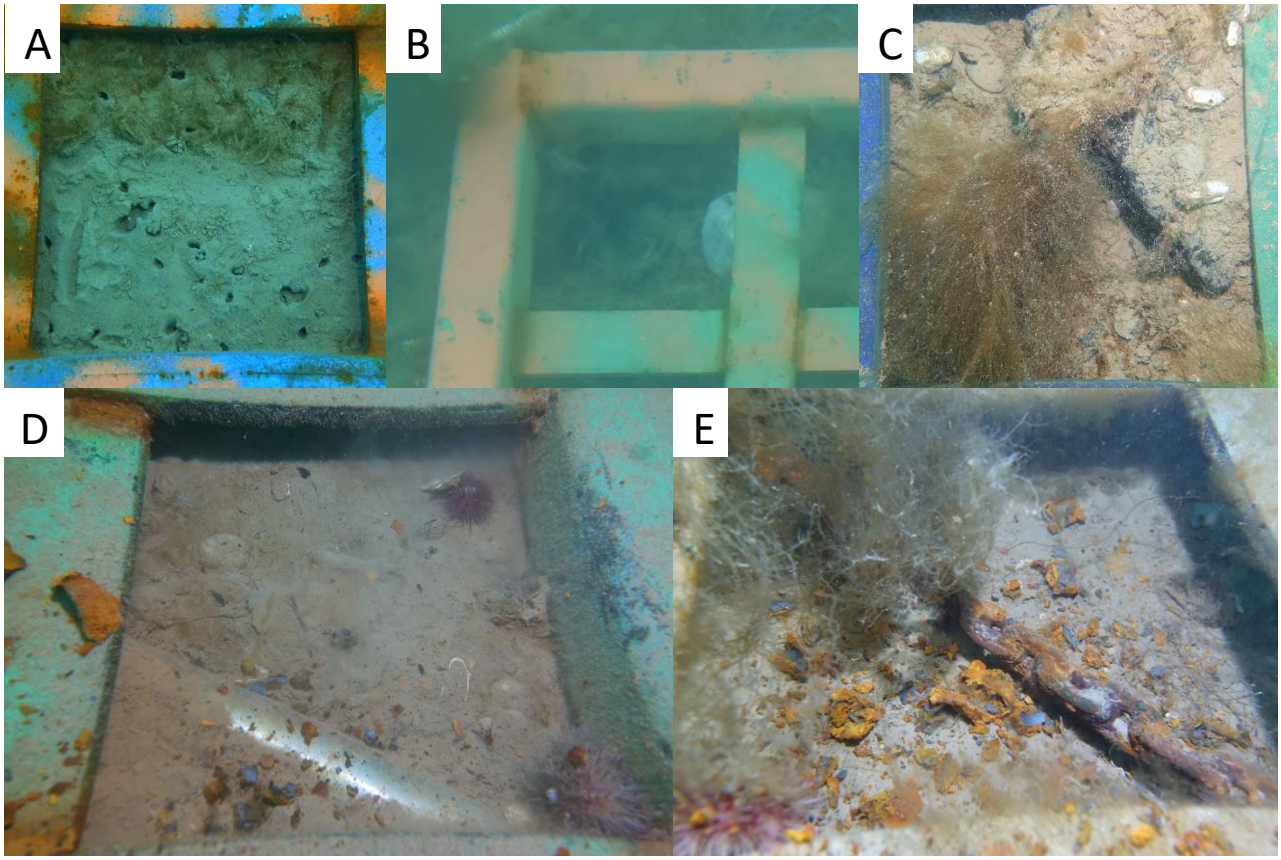


Figure 5-4: Substrate Types Observed in Survey Quadrats at Milne Port: A) Silt/Sand, B) Cobble, C) Bedrock and D) Anthropogenic Debris (i.e., Metal Frame from Old Belt Transect and Chain).

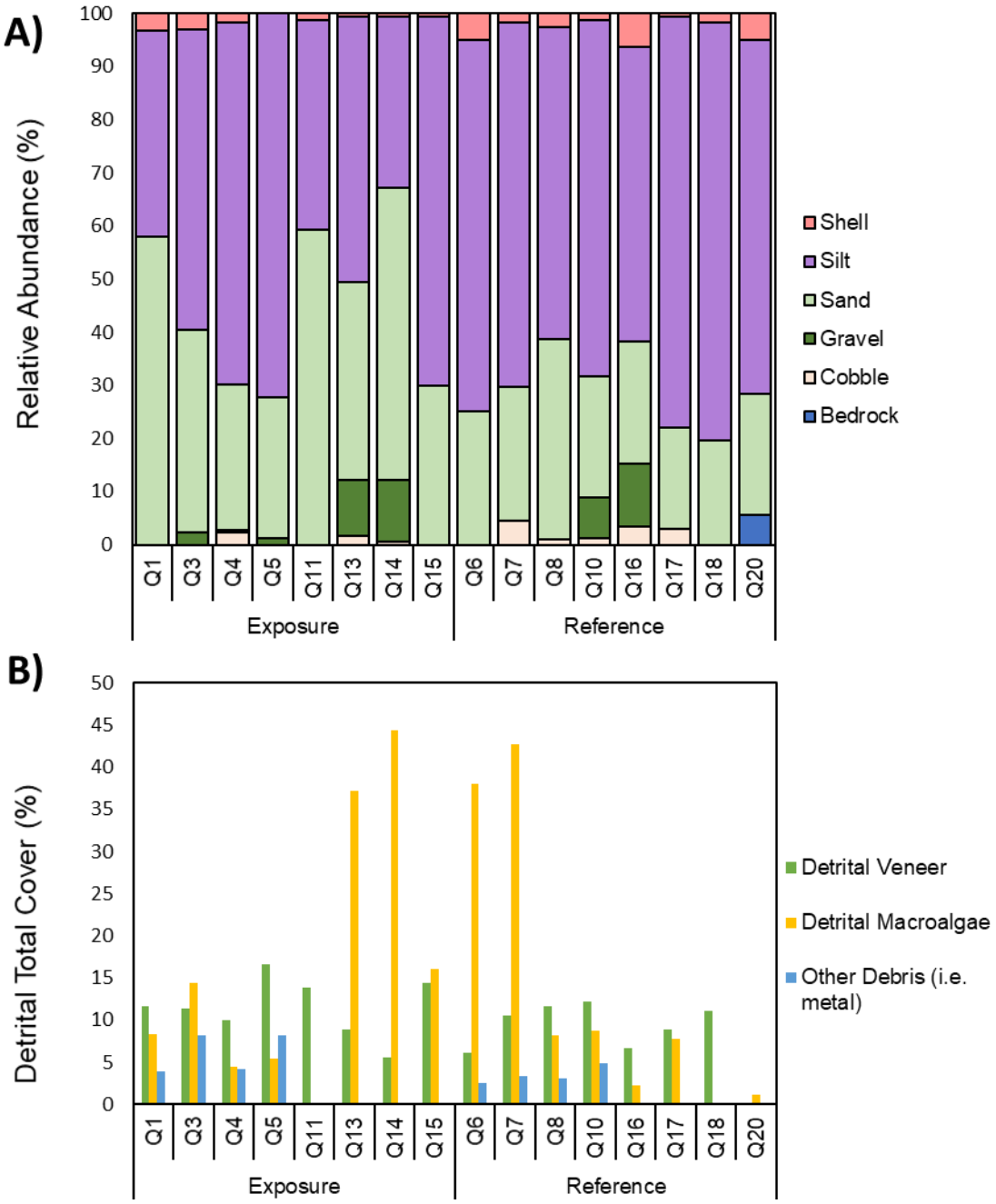


Figure 5-5: Relative Abundance of Substrate Types (A) and Total Percent Cover of Detrital Veneer, Macroalgae and other Anthropogenic Debris (B) during Quadrat Surveys in Milne Port (2021).

Detritus and debris were present in all quadrats in 2021 (Figure 5-5B). Total percent cover of detritus and debris was calculated separately from substrate composition, as it was present over the existing substrate, resulting in overall percent compositions greater than 100%. Detritus and debris were categorized into three groups: detrital veneer, detrital macroalgae, and other debris (i.e. metal). The detrital veneer was organic and appeared to consist of phytoplankton/diatoms and silt; this layer was present within equal ranges between the exposure area (6 to 17%) and reference area (0 to 12%). Detrital (or drift) macroalgae was present in all quadrats in various percent cover, except for Q11 in the exposure area and Q18 in the reference area, which had none. Highest percent cover was recorded in Q13, Q14, Q6, and Q7 (ranging 37 to 44%). Other debris consisted of rusting metal pieces from the suspended anchor chain maintaining the settlement plates buoyant (used for NIS/AIS monitoring [Chapter 8]) above the quadrat, for those quadrats deployed in 2020 (Q1 through Q10). It also includes aluminum metal piping from the old belt transects observed in Q5, as was noted in 2020. No significant differences were found between the reference area and the exposure area for detrital/debris cover (Table 5-3).

Power to detect the observed effect size was only sufficient for percent fines (that is, the combined silt and clay values), but not for detrital algae or detrital veneer (Appendix 5E). An analysis based on eight samples (quadrats) would have sufficient power to detect an effect size of ±40% for percent fines. An increase in effort to 25 quadrats per area would result in sufficient power to detect a ±40% effect size for detrital veneer, but not detrital algae.

Table 5-3: ANOVA and ANCOVA Results of Parameter Effects of Percent Cover on Substrate and Detrital Types – Quadrat Surveys at Milne Port (2021)

Response	Covariate	Percent (%) Cover	
		F-value	Pr(>F)
Bedrock[1]	-	-	-
Cobble	-	2.386	0.143
Gravel	Depth (m)	0.006[2]	0.937
Sand	-	**13.010**	**0.003**
Silt	Depth (m)	**5.700**	**0.032**
Shell	-	3.997	0.064
Detrital/Debris Cover			
Organic Veneer	-	3.398	0.086
Detrital Algae	-	0.046	0.833
Debris (e.g., metal)	Depth (m)	0.456	0.510

Note: Substrate composition refers to the number of substrate types per quadrat location. Residuals and intercept are not presented in this table. See Appendix 5D for full results. Bold text indicates significant p-value <0.05.

[1] Bedrock was not analyzed due to not enough data present between sites.

[2] A Kruskall-Wallis Test, the non-parametric version of an ANOVA, was run instead of an ANOVA on cobble as the data did not meet the assumptions of an ANOVA. Instead of an f-value, a chi-squared value is given.

5.4.2 Macroflora

Macroflora identified in quadrats belonged to three larger taxonomic classifications: Ochrophyta (brown algae), Rhodophyta (red algae) and Chlorophyceae (green algae). Samples opportunistically collected and sent to laboratories for identification improved taxonomic resolution of the 2021 quadrat data compared to earlier years. DNA barcoding results matched the identifications based on morphological features (see Table 8-10 in Chapter 8 for a comparison of results and Appendix 8D-4 for laboratory results). Brown algae were resolved to seven distinct taxa, four of which were defined to species level: rockweed (*Fucus distichus*), sugar kelp (*Saccharina latissima*), sieve kelp (*Agarum clathratum*) and *Halosiphon tomentosus* (Appendix 5B – Photo 16, 19, 20, 39). Two filamentous brown algae were identified to genus level – *Pylaiella* spp. and acid weed (*Desmarestia* spp.) – while a third filamentous brown algae was identified as cf. *Coelocladia arctica*[8] by the taxonomic laboratory (Appendix 5B – Photo 32, 39, 45). Red algae were identified to four distinct taxa, of which three were resolved to species level via taxonomic analysis of samples: *Savoiea arctica*, *Coccotylus truncatus*, and Dilsea [*Dilsea socialis*]) (Appendix 5B – Photo 18, 24, 40). An encrusting coralline red algae was identified to the Order Corallinales, though morphological similarities between taxa within the Order prevented further resolution. Green algae were categorized as two types of filamentous algae, distinguished from one another based on general morphology. Taxonomic analysis confirmed one to be *Chaetomorpha melagonium* (Appendix 5B – Photo 25); however, the other was not collected and remains unidentified.

Macroalgae percent cover varied among quadrats (from 2 to 38%) but were in the same range in both exposure and reference areas (18 ± 5% and 18 ± 4%, respectively) (Table 5-4; Figure 5-6). A total of six out of 16 quadrats surveyed had macroalgae cover above 29%, including three in the exposure area (Q13, Q14, and Q15) and three in the reference area (Q7, Q16, and Q17; Figure 5-6A). The most abundant macroalgae type was brown filamentous algae (various taxa), present in all quadrats except Q1 (Figure 5-6B). *Pylaiella* spp. is a brown filamentous alga, abundant within several quadrats, but unique from other brown algae taxa in the dataset due to it being a fast-growing ephemeral macroalgae. Ephemeral algae are transient, exist for a short period of time, and vary widely in abundance during a given period; in contrast, other brown algae found in the surveys are slower-growing annual or perennial species whose growing characteristics do not fluctuate as much. Sugar kelp (*Saccharina latissima*) and sieve kelp (*Agarum clathratum*) were present in generally low proportions in several quadrats within both exposure and reference areas, although Q5 in the exposure area contained 48% sieve kelp.

Taxa richness was similar between the exposure area and reference areas, ranging between two to seven taxa, and three to six taxa, respectively (Figure 5-6C). SDI ranged between Very Low (<0.250) to Moderate (0.500 to 0.750) in the exposure area and Low (0.250 to 0.499) to High (>0.750) in the reference area (Figure 5-6D), with similar mean values for each area (0.513 ± 0.084 and 0.545 ± 0.040, respectively). Diversity was highest at Q15 and lowest at Q14, both occurring in the exposure area. SDI was high in Q15 due to six unique taxa present in roughly equal proportions, while Q14 had moderate taxa richness (4), but a low SDI as a result of the presence of a single dominant taxon – acid weed (*Desmarestia* spp.) at 93% relative abundance.

No statistically significant differences were detected between the exposure area and reference area for any of the indicators measured (i.e., total percent cover, taxa richness, or SDI (Table 5-5). Overall, these results indicate that the exposure and reference areas were comparable for these indicators. Power to detect the observed effect size was not sufficient for any of the macroflora variables (Appendix 5E). An increase in effort to 25 quadrats per area would result in sufficient power to detect a ±40% effect size for all three variables.

[8] cf. “compare with”, in taxonomy refers to a taxonomic designation that indicates an inexact match to the indicated taxon. The specimen may represent a similar related species, an undescribed morph, or the specimen may be lacking characteristics that allow for a positive identification.

It should be noted that quadrats with high macroalgae cover in 2020 were observed to have high detrital algae cover in 2021, suggesting that there was little distinction made between attached/living and detrital macroflora in 2020. Regardless, a quantitative interannual comparison of macroalgae percent cover was not performed due to a change in survey methods (i.e., from video to divers with opportunistic sample collection) in 2021 that considerably improved taxonomic resolution (thereby influencing taxa richness and diversity calculations) between the two years.

Table 5-4: Quadrat Survey Results for Macroflora - Milne Port (2021)

Survey Area	Quadrat	Macroalgae			
		Total Cover (%)	Taxa Richness	SDI	Dominant Taxa
Exposure	Q1	9	2	0.208	*Pylaiella* spp., *Coccotylus truncatus*
	Q3	3	3	0.528	cf. *Coelocladia arctica*, *Pylaiella* spp.
	Q4	8	2	0.484	Acid weed, red filamentous algae
	Q5	3	3	0.636	Sieve kelp, acid weed
	Q11	13	7	0.685	*Pylaiella* spp., *Coccotylus truncatus*, *Halosiphon tomentosus*
	Q13	38	5	0.606	cf. *Coelocladia arctica*, acid weed
	Q14	36	4	0.125	Acid weed, sugar kelp
	Q15	31	6	0.832	cf. *Coelocladia arctica*, *Coccotylus truncatus*, brown filamentous algae
	Mean ± SE	**18 ± 5**	**4 ± 0.7**	**0.513 ± 0.084**	
Reference	Q6	2	3	0.508	Brown filamentous algae, green filamentous algae
	Q7	29	5	0.618	Acid weed, cf. *Coelocladia arctica*, *Coccotylus truncatus*
	Q8	11	5	0.512	*Halosiphon tomentosus*, green filamentous algae, acid weed
	Q10	13	3	0.310	*Pylaiella* spp., brown filamentous algae
	Q16	29	6	0.508	*Pylaiella* spp., Dilsea
	Q17	38	6	0.604	Acid weed, *Pylaiella* spp., *Coccotylus truncatus*
	Q18	13	5	0.663	Acid weed, *Pylaiella* spp., *Halosiphon tomentosus*
	Q20	10	4	0.638	Acid weed, sugar kelp
	Mean ± SE	**18 ± 4**	**5 ± 0.4**	**0.545 ± 0.040**	

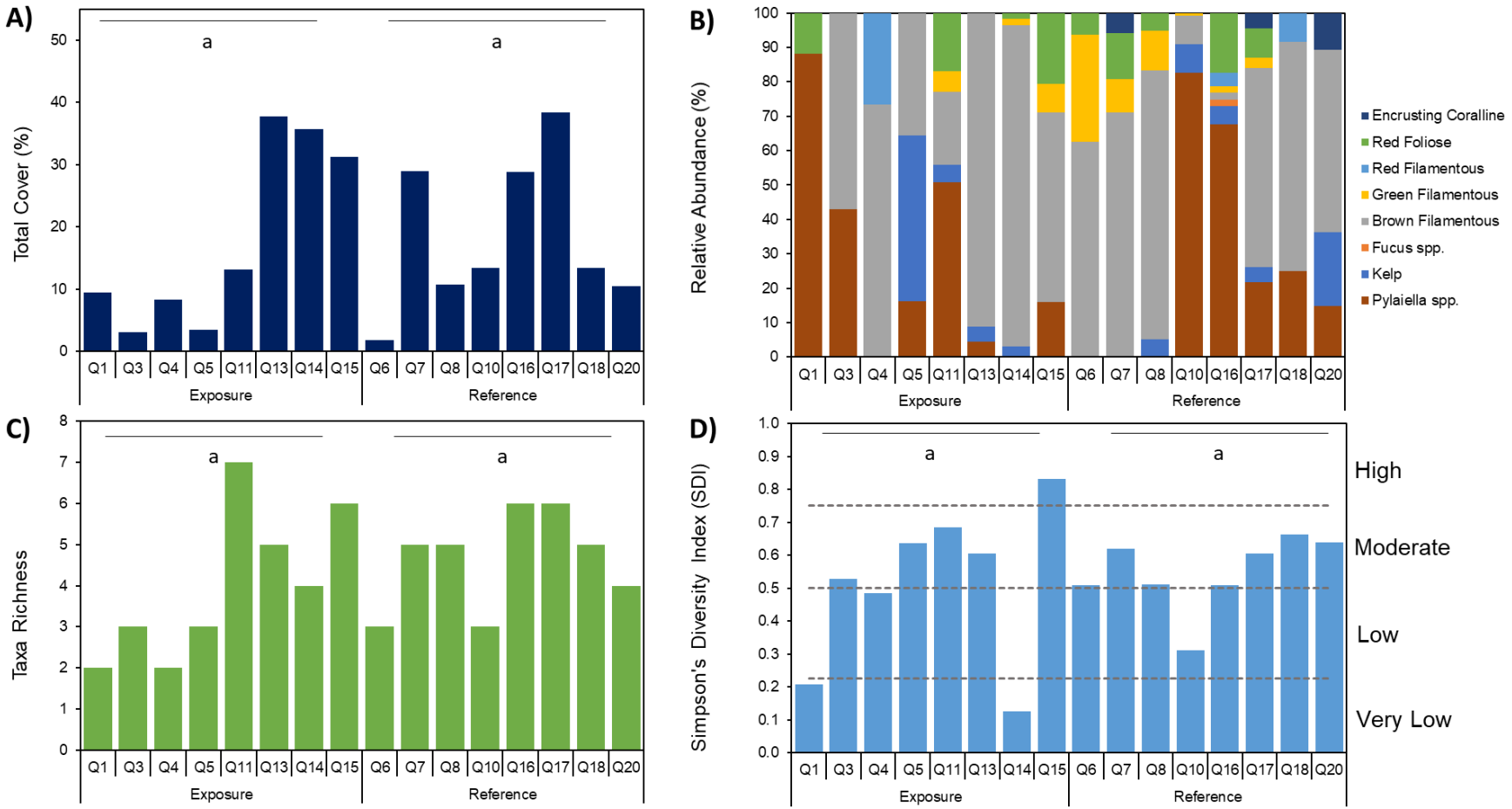


Figure 5-6: Total Percent Cover (A), Relative Abundance (B), Taxa Richness and (C) Simpson's Diversity Index (D) of Macroflora Recorded in Survey Quadrats in Milne Port in 2021. Letters Indicate Statistical Significance ($p<0.05$) Between Groups.

Table 5-5: ANOVA and ANCOVA Results of Parameter Effects of Total Percent Cover, Taxa Richness, Simpson's Diversity Index on Macroflora – Quadrat Surveys in Milne Port (2021)

Response	Covariate	F-value	Pr(>F)
Total Percent Cover	-	1.218	0.287
Taxa Richness	Depth (m)	1.258	0.281
Simpson's Diversity Index (SDI)	Percent (%) Cover of Fines (Silt/Clay)	0.964	0.343

Note: Residuals and intercept are not presented in this table. Response variables without a covariate were analyzed using an ANOVA while response variables with covariates were analyzed using an ANCOVA. See Appendix 5D for full results. Bold text indicates significant p-value <0.05.

5.4.3 Benthic Epifauna

Benthic epifauna identified in the quadrats belonged to seven phyla: Annelida (worms), Platyhelminthes, Cnidaria, Arthropoda, Chordata, Echinodermata, and Mollusca. Taxonomic identification of collected specimens improved resolution of the 2021 quadrat data compared to earlier years.

Phylum Annelida was represented by three distinct taxa, one of which was identified to species level (cone worm [*Cistenides granulata*], Appendix 5B – Photo 3). Two species of sabellid worms (Family Sabellidae) were distinguished but unable to be identified (Appendix 5B – Photo 23) while a single flat worm (Phylum Platyhelminthes) was observed and also remains unidentified. The phylum Echinodermata was represented by brittle stars (Family Ophiuridae) and green urchin (*Strongylocentrotus droebachiensis*), and the phylum Cnidaria was represented by an individual burrowing anemone, Ceriantharia indet. (Appendix 5B – Photo 26, 31). The majority of species identified in the quadrats belonged to the phylum Mollusca, with four species identified: wrinkled rock borer clam (*Hiatella arctica*), icelandic scallop (*Chlamys islandica*), northern astarte clam (*Astarte borealis*), and Greenland glass-scallop (*Similipecten greenlandicus)* (Appendix 5B – Photo 8, 28, 29, 43). Several specimens were able to be resolved as far as genus, including: blunt gaper (*Mya* spp.), Margarite snail (*Margarites* spp.), and clams of the genus Astarte and Macoma (Appendix 5B – Photo 7, 40). Phylum Arthropoda was represented by two species of shrimp (Pandalus shrimp [*Pandalus* spp.], and sculptured shrimp [*Sclerocrangon boreas*]) (Appendix 5B – Photo 13. 27), as well as unidentified barnacles and amphipods. Phylum Chordata was represented by tunicates (Subphylum Tunicata) of which one was identified to genus level (*Polycarpa* spp.), fish from the sculpin family (Cottidae) and a type of pout (cf. *Gymnelus* spp.) (Appendix 5B – Photo 4, 15, 44)

5.4.3.1 Sessile Epifauna

Total percent cover of sessile epifauna varied among quadrats in both exposure and reference areas but, on average, was lower in the reference area (26 ± 3% and 18 ± 4%, respectively) (Table 5-6, Figure 5-7). Wrinkled rock borer clam was the dominant sessile epifauna taxa in the majority of quadrats, aside from Q10, Q14, Q16, and Q17 where cone and sabellid worms were the most dominant taxa. The 2021 results are consistent with 2020 results, where wrinkled rock borer clam was the most dominant taxa for most quadrats, while cone worms, unidentified tube worms, and feather worms (these could be Sabellid worms) were the dominant taxa in Q10.

Taxa richness was similar between the exposure area (5 ± 0.5 taxa) and reference area (6 ± 0.6 taxa) (Figure 5-7C). Taxa richness values were higher in several quadrats in 2021 compared to 2020, which is attributed to changes in survey methodology that improved taxonomic resolution. SDI ranged between Very Low (<0.250) to Moderate (0.500 to 0.750) in both areas (Figure 5-6D), with no difference in mean values (0.427 ± 0.055 SDI for

exposure area; 0.479 ± 0.079 SDI for reference area). Diversity was very low for Q1, Q8, and Q18 due to a high proportion of wrinkled-rock borer clam dominating the total percent cover. Because taxa richness is part of the SDI calculation, comparing this indicator between the two years is not warranted as it is already accounted for.

No statistically significant differences were detected between the exposure area and reference area for total percent cover, taxa richness, or diversity (SDI) of sessile epifauna (Table 5-7). Overall, this suggests that the exposure and reference areas were comparable with respect to these indicators; however, the power analysis indicated that there was inadequate power to detect the observed effect size for any of the assessed variables (Appendix 5E). An increase in survey effort to 25 quadrats per area would be needed to have sufficient power to detect a ±40% effect size for SDI and taxa richness, but not for sessile epifauna density.

Table 5-6: Quadrat Survey Results for Sessile Epifauna - Milne Port (2021)

Survey Area	Quadrat	Sessile Epifauna			
		Total Cover (%)	Taxa Richness	SDI	Dominant Taxa
Exposure	Q1	32	5	0.215	Wrinkled rock-borer, cone worm
	Q3	32	5	0.420	Wrinkled rock-borer, blunt gaper
	Q4	16	7	0.341	Wrinkled rock-borer, cone worm
	Q5	19	5	0.586	Wrinkled rock-borer, unidentified (unid.) clam
	Q11	35	6	0.363	Wrinkled rock-borer, cone worm
	Q13	24	4	0.658	Wrinkled rock-borer, cone worm, sabellid worm
	Q14	13	3	0.547	Sabellid worm, cone worm, wrinkled rock-borer
	Q15	34	3	0.285	Wrinkled rock-borer, cone worm
	Mean ± SE	**26 ± 3**	**5 ± 0.5**	**0.427 ± 0.055**	
Reference	Q6	10	6	0.468	Wrinkled rock-borer, blunt gaper
	Q7	7	7	0.713	Wrinkled rock-borer, sabellid worm, burrowing anemone
	Q8	37	8	0.201	Wrinkled rock-borer, blunt gaper
	Q10	9	4	0.655	Cone worm, wrinkled rock-borer
	Q16	14	6	0.620	Cone worm, wrinkled rock-borer, blunt gaper
	Q17	6	5	0.645	Sabellid worm, wrinkled rock-borer
	Q18	31	5	0.109	Wrinkled rock-borer, blunt gaper
	Q20	30	9	0.422	Wrinkled rock-borer, cone worm
	Mean ± SE	**18 ± 4**	**6 ± 0.6**	**0.479 ± 0.079**	

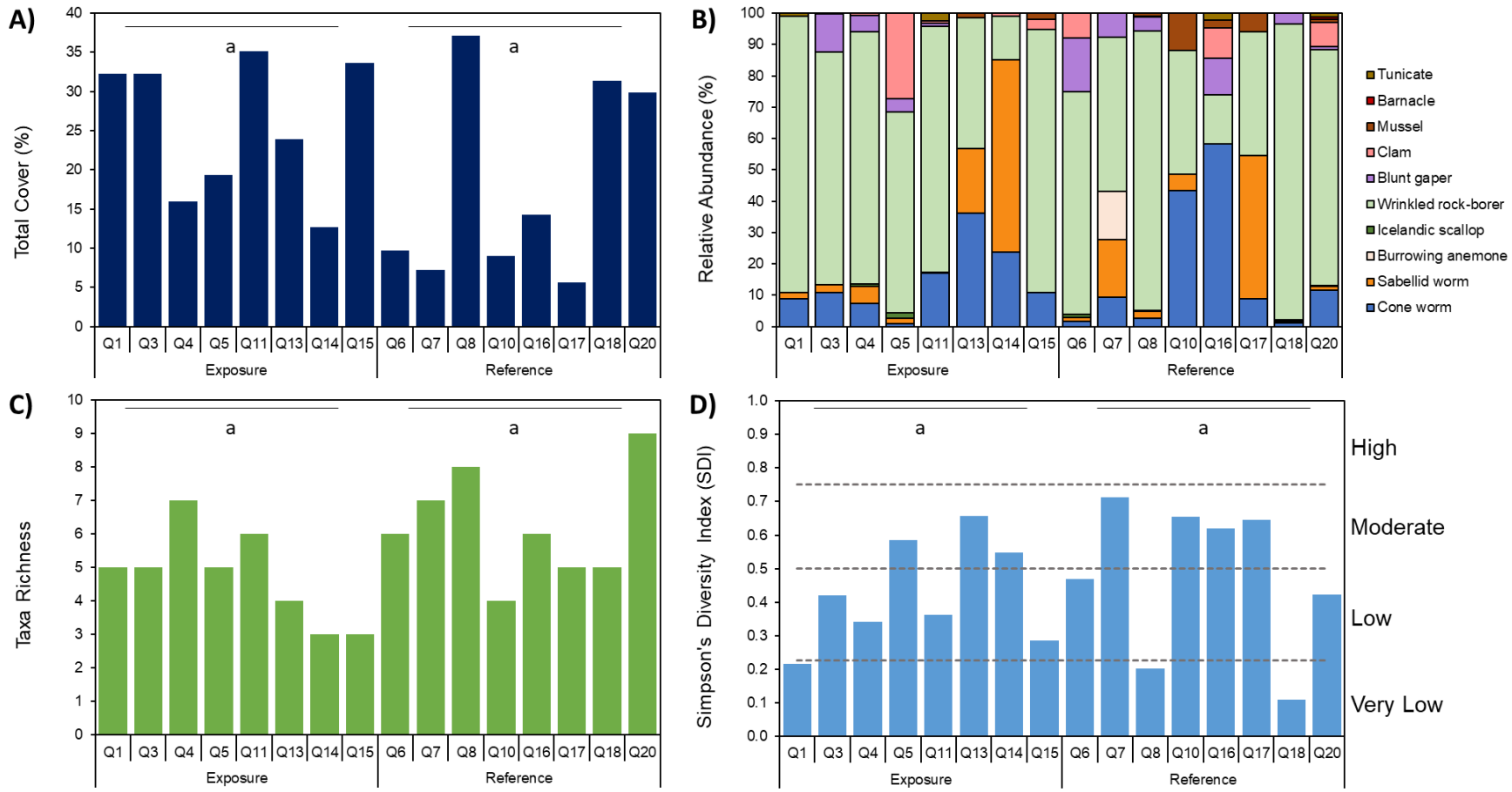


Figure 5-7: Total Percent Cover (A), Relative Abundance (B), Taxa Richness and (C) Simpson's Diversity Index (D)) of Sessile Epifauna Recorded in Survey Quadrats in Milne Port (2021). Letters Indicate Statistical Significance (p<0.05) Between Groups.

Table 5-7: ANOVA and ANCOVA Results of Parameter Effects of Total Percent Cover, Taxa Richness, and Simpson's Diversity Index on Sessile Epifauna – Quadrat Surveys in Milne Port (2021)

Response	Covariate	F-value	Pr(>F)
Percent Cover	Percent (%) Cover of Fines (Silt/Clay)	1.194	0.293
Taxa Richness	-	0.664	0.428
Diversity (SDI)	-	0.951	0.345

Note: Residuals and intercept are not presented in this table. Response variables without a covariate were analyzed using an ANOVA while response variables with covariates were analyzed using an ANCOVA. See Appendix 5D for full results. Bold text indicates significant p-value <0.05.

5.4.3.2 Motile Epifauna

Motile epifauna density was generally low but within the same range for the exposure and reference areas, where all quadrats contained densities below 20 organisms/quadrat except for Q6, which had a density of 74 organisms/quadrat (Table 5-8, Figure 5-8). Q13 and Q15 contained no motile epifauna. Green urchins were the dominant motile epifaunal species recorded in the exposure area; however, Icelandic glass-scallop was the sole motile organism recorded in Q11. In contrast, several quadrats in the reference area were largely dominated by brittle stars (Q6, Q8, Q10, Q18, and Q20), while others contained a variety of taxa (Q7, Q16, and Q17) (Figure 5-8B).

Taxa richness was similar between the two survey areas (ranging 0 – 4 in exposure area; 1 - 5 in the reference area) (Figure 5-8C). Several quadrats within both the exposure area and reference area had a diversity of zero: these were quadrats without any motile epifauna (Q13 and Q15) or quadrats that contained only one or two organisms of a single taxa (Q8, Q10, Q11, and Q14) (Figure 5-8D). SDI reached as high as moderate (0.500 to 0.750) in quadrats within the exposure area and up to High (>0.750) in the reference area. A similar variation in taxa richness and diversity between exposure and reference area was observed in 2020 and 2021, indicating that there is no difference between the years.

No statistically significant differences were detected between the exposure and references for any indicators measured (i.e., density, taxa richness, or diversity (SDI); Table 5-7). Overall, these results indicate that the exposure and reference areas were comparable for these indicators, however, the power analysis indicated that there was inadequate power to detect the observed effect size for any of the assessed variables (Appendix 5E). An increase in survey effort to 25 quadrats per area would be needed to have sufficient power to detect a ±40% effect size for density and taxa richness, but not for SDI.

Table 5-8: Quadrat Survey Results for Motile Epifauna - Milne Port (2021)

Survey Area	Quadrat	Motile Epifauna			
		Density (org/quadrat)	Taxa Richness	SDI	Dominant Taxa
Exposure	Q1	9	4	0.519	Green urchin
	Q3	16	4	0.602	Green urchin, brittle star
	Q4	13	4	0.391	Green urchin
	Q5	20	4	0.415	Green urchin
	Q11	1	1	0.000	Icelandic scallop
	Q13	0	0	0.000	No motile epifauna
	Q14	1	1	0.000	Green urchin
	Q15	0	0	0.000	No motile epifauna
	Mean ± SE	**8 ± 3**	**2 ± 0.7**	**0.241 ± 0.094**	
Reference	Q6	74	5	0.371	Brittle star
	Q7	5	4	0.720	Brittle star
	Q8	2	1	0.000	Brittle star
	Q10	1	1	0.000	Brittle star
	Q16	4	3	0.813	Snail, brittle star, margarite snail
	Q17	3	3	0.667	Brittle star, snail, limpet
	Q18	2	2	0.500	Brittle star, juvenile fish
	Q20	13	3	0.272	Brittle star
	Mean ± SE	**13 ± 9**	**3 ± 0.5**	**0.418 ± 0.111**	

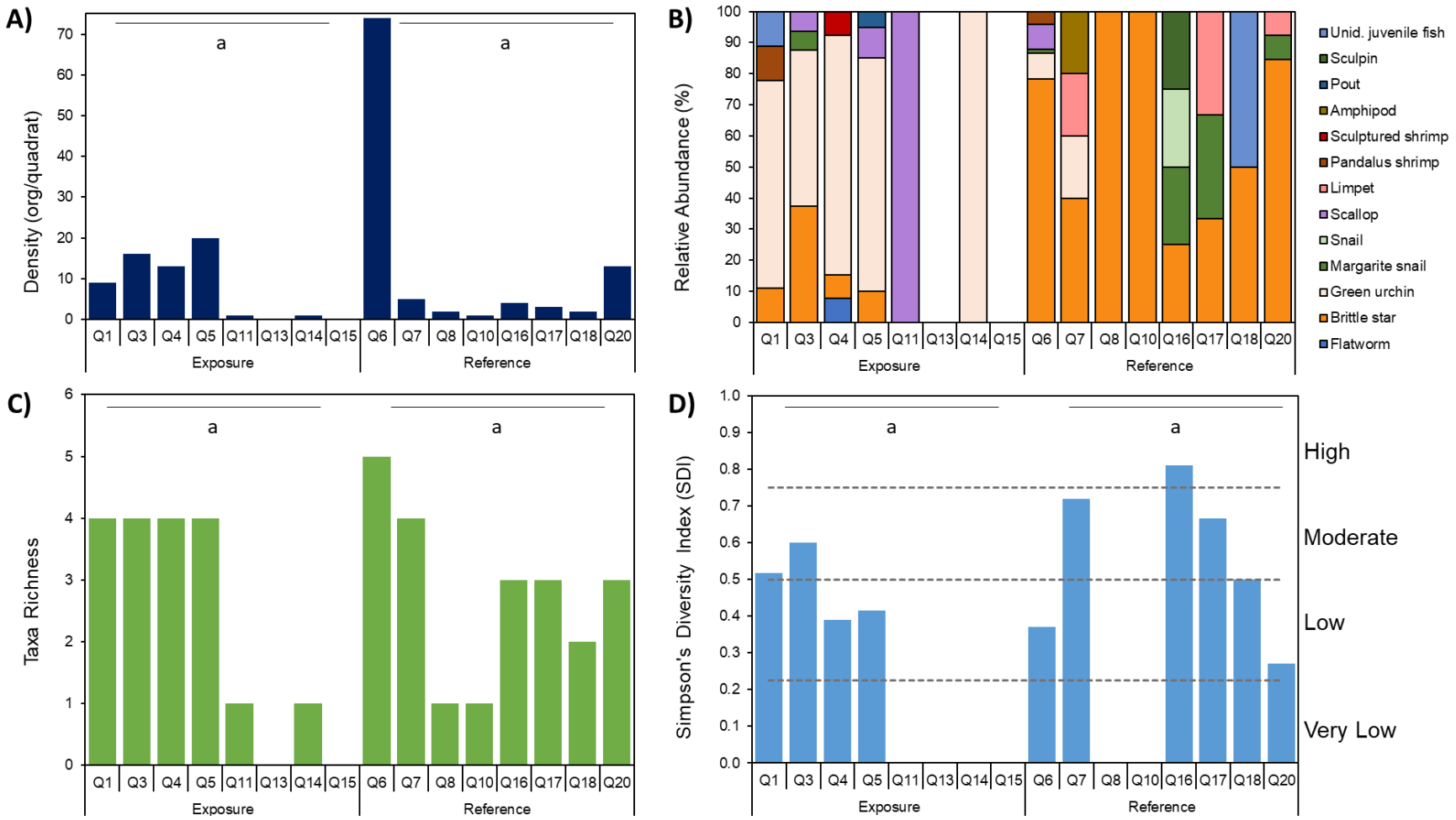


Figure 5-8: Density (A), Relative Abundance (B), Taxa Richness and (C) Simpson's Diversity Index (D) of Motile Epifauna Recorded in Survey Quadrats in Milne Port in 2021. Letters Indicate Statistical Significance (p<0.05) Between Groups.

Table 5-9: ANOVA and ANCOVA Results of Parameter Effects of Total Percent Cover, Taxa Richness, and Simpson's Diversity Index on Motile Epifauna – Quadrat Surveys in Milne Port (2021)

Response	Covariate	F-value	Pr(>F)
Density	Depth (m)	0.001	0.974
Taxa Richness	Depth (m)	0.094	0.763
Diversity (SDI)	Percent (%) Cover of Fines (Silt/Clay)	0.376	0.220

Note: Residuals and intercept are not presented in this table. Response variables without a covariate were analyzed using an ANOVA while response variables with covariates were analyzed using an ANCOVA. See Appendix 5D for full results. Bold text indicates significant p-value <0.05.

5.4.4 Relative Richness and Diversity

Taxa richness varied between and among quadrats (Figure 5-9A), with no apparent relationship observed between macroflora, sessile epifauna, or motile epifauna. Statistical analysis yielded no significant differences between the exposure area or reference area for any of the comparisons. Overall, Q7 and Q8 in the reference area stand out as harbouring the overall greatest taxa richness with the highest values for each macroflora, sessile and motile epifauna relative to other quadrats.

Diversity of macroflora, sessile epifauna and motile epifauna ranged from very low to high (Figure 5-9B); however, statistically significant differences in diversity were not found for any of the comparisons. Overall, Q7 and Q17 displayed the greatest diversity, where macrofauna, sessile and motile epifauna values were all characterized as moderate. No quadrat had Very Low or Low diversity values across all benthic community components (i.e., macroflora, sessile or motile epifauna).

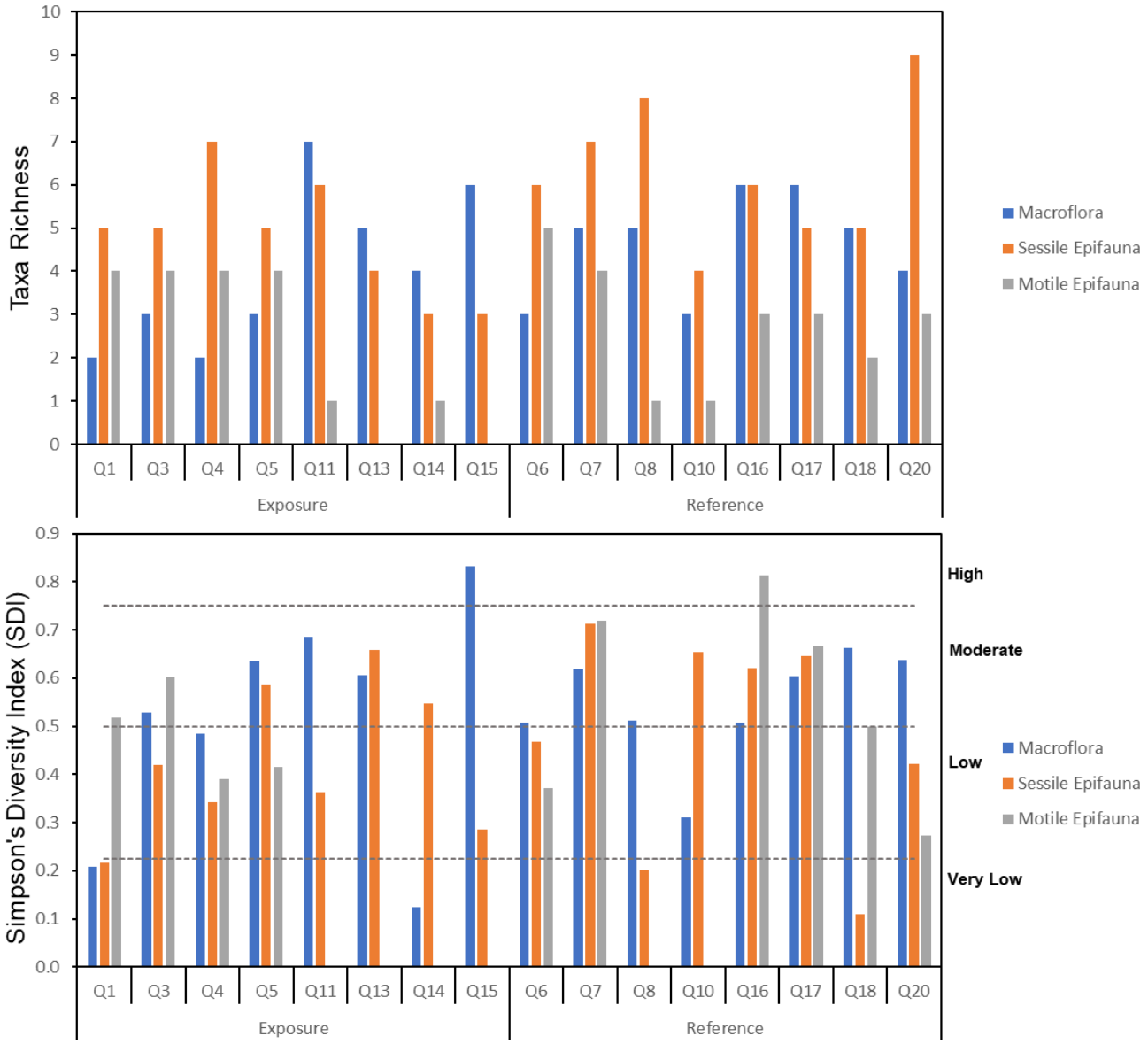


Figure 5-9: Taxa Richness (A) and Simpson's Diversity Index (SDI) (B) for Macroflora, Sessile Epifauna and Motile Epifauna – Quadrat Surveys in Milne Port (2021).

5.4.5 Sampling Effort

A taxa accumulation curve was calculated for quadrats surveyed in 2021 to provide an estimate of the effort required to fully characterize the quadrat benthic community assemblage (macroalgae, sessile and motile epifauna) (Figure 5-10). The accumulated species (or taxa) observed curve (S_{obs}) shows the mean number of species (or taxa) for each number of permutation and Standard Error (SE) of the mean.

The taxa accumulation curve for the 2021 sampling effort approached, but did not reach, an asymptote for the 17 quadrats sampled. This indicates that sampling in 2021 did not full attain levels to fully describe the overall benthic community assemblage.

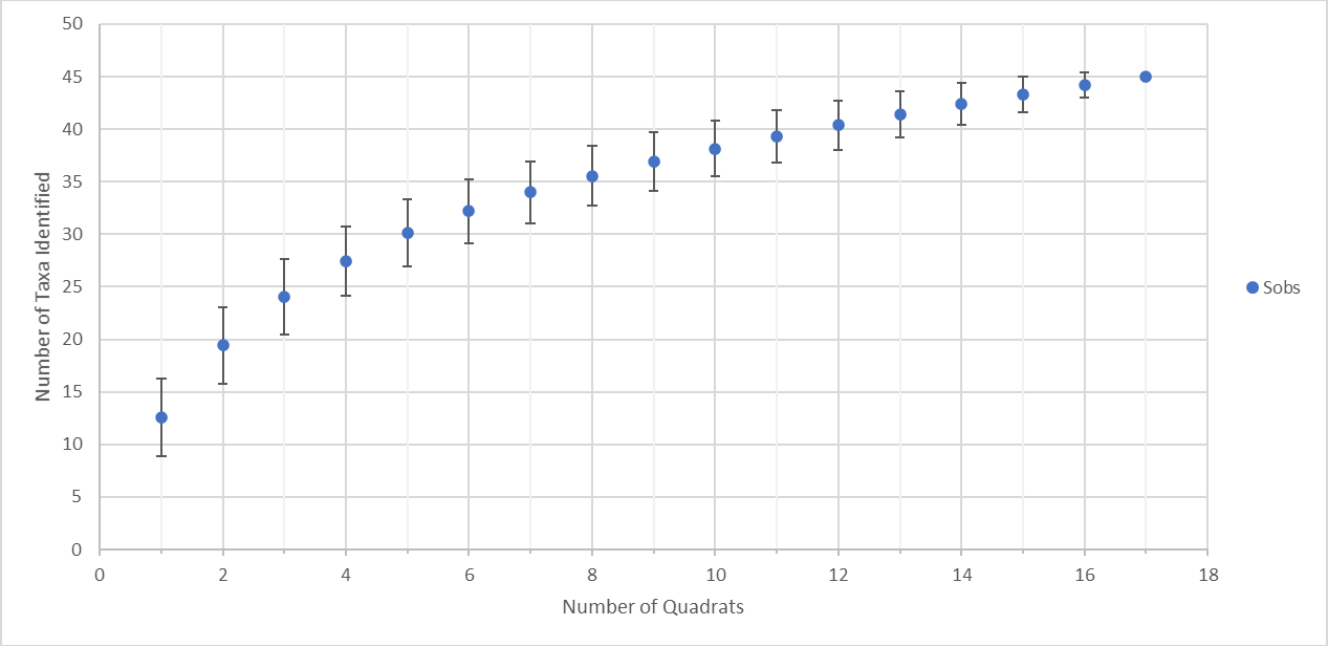


Figure 5-10: Taxa Accumulation Curve for Quadrat Benthic Community Assemblage in Milne Port (2021).

5.4.6 Opportunistic Fish Observations

A species of eelpout (*Lycodes* spp.) was observed residing within the hollow frame of Q1 in Milne Port (Appendix B - Photo 6). Identification to species level was not possible because only part of the head was visible.

When searching for Q2 in Milne port, several sand lance (*Ammodytes* spp.) where observed emerging from the sandy sediment (-4 to -6 m CD depth) as divers approached, however their elusive behaviour precluded video/photo documentation.

5.5 Discussion

Taxonomic resolution was improved in 2021 due to the exclusive use of divers for data collection, which enabled opportunistic collection of samples for taxonomic and/or genetic analysis. In contrast, the methodology employed in 2020 used a combination of ROV underwater video surveys and dive surveys, hence taxonomic resolution was relatively coarse. Accordingly, quantitative comparisons between the two years were not possible and the 2021 quadrat survey results will serve as a baseline for future years. Golder recommends that methodologies remain consistent moving forward to allow for multi-year comparisons.

Substrate type was similar among quadrats and between the exposure and reference areas. A detrital layer, comprised of organic detritus and other debris, was present in all quadrats; the extent and composition of the detrital layer was variable with no significant differences between reference and exposure areas. Substrate within the quadrats was dominated by soft silt and sand, consistent with what has been previously documented. While there were some statistically significant differences in sand and silt percent cover between the exposure and reference areas (silt was slightly higher in the reference area), these likely reflect natural variability driven by the dynamic estuarine nature of Milne Port, which produces fine-scale spatial variation in substrate characteristics due to internal mixing and sediment redistribution processes as well as the influence of features such as Phillips Creek. Similar macroflora and benthic epifaunal taxa were observed in 2021 as in previous years (2018-2020). Indicators (i.e., percent cover, density, species richness, and diversity) were shown to be variable within and among quadrats and between the reference and exposure areas; however, no statistically significant differences were noted between the exposure and reference areas for any of the indicators evaluated. Overall, results of this survey suggest that substrate, macrofloral and epibenthic community assemblages are comparable between the exposure and reference areas with no obvious evidence of Project-related influence or impairment.

The survey design in 2021 aimed to sample a total of 20 quadrats; however, four of these quadrats could not be surveyed in 2021 for various reasons. Quadrat Q2 could not be relocated after an extensive dive search, and time constraints prevented surveying Q9 and Q19 due to several inclement weather days that prevented safe diving operations. Q12 was excluded from the data analysis as an outlier, having been deployed in shallow water (-6 m CD) susceptible to ice scour, which limits macroflora and epifauna density. Effect size was explored on 2021 data using a power analysis to estimate the sample size needed to detect Project-related change based on levels of observed variability among quadrats, and whether the sample size (16 quadrats) was adequate to fully describe the benthic community assemblage. The results of the power analysis indicate that the power to detect the observed effect size was not sufficient for any of the assessed variables (indicators). This was not unexpected given epifaunal communities are commonly associated with high temporal and spatial variability; this is the reason standard EEM practice generally recommends monitoring benthic infauna rather than epifauna (Environment Canada 2012). In addition, the taxa accumulation curve completed for the 2021 epifauna data suggested that the benthic community assemblage has not been fully characterized by the current sampling effort (i.e., 16 quadrats), although the curve appears to be reaching its asymptote.

The results of the power analysis indicate that the sample size of the current study design is not sufficient for detecting small-scale differences between exposure and reference area, though large-scale differences would likely be noted. An increase in effort to 25 quadrats per area would result in sufficient power to detect a ±40% effect size for most, but not all, indicators; however, the diving effort involved with surveying a total of 50 quadrats within the limited open-water season in the region would not be realistic to complete within the timeframe available for summer field program. Use of alternative and/or supplemental methodologies, such as ROV and underwater video, have already been explored in previous years and replaced with divers due to challenges in

collecting data at acceptable taxonomic resolution. Three options were discussed with the MEWG about how best to move forward: (i) remove this component entirely from the MEEMP and focus on other components that have the ability to detect change with statistical power (e.g., benthic infauna, sediment quality); (ii) maintain the current sampling methodology (as this has produced the highest resolution in the data thus far) and current sampling effort (i.e., detection of large-scale trends only), accepting the associated statistical limitations; or, (iii) add a minimum of two additional quadrats in each survey area to increase the number of indices for which ±40% change can be detected from two to six. It was ultimately decided to increase the number of quadrats in each area by three, to 13, for a total sample size of 26 quadrats across both areas. The additional quadrats will be deployed in summer 2022.

5.6 Conclusions and Recommendations

Surveys in 2021 exclusively utilized divers to collect quadrat data, which improved taxonomic resolution for characterizing the benthic community assemblage. It is recommended that a diver-based methodology permanently replace the combined use of ROVs and underwater video. Not only will this enable data collection to occur in a standardized manner, but also enables collection of specimens for taxonomic verification and hence improves the resolution of this component. Future dive surveys should analyze the quadrats as a whole (not by sub-quadrat) to reduce diving time. Further, a new quadrat should be deployed to replace the missing quadrat (Q2) and the location of Q12 should be moved to a deeper site so that it can be included in analyses moving forward. Future field surveys should incorporate enough field days to buffer for inclement weather.

Overall, macrofloral and benthic epifaunal community assemblages are comparable between exposure and reference areas. Observations reveal no evidence of spatial or temporal trends that might be associated with Project-induced effects from construction or operation activities and Milne Port. However, these results should be interpreted with some caution, as a power analysis and a taxa accumulation curve on 2021 data indicate that the current sample size of 16 quadrats is not adequate to detect small-scale significant differences in indicators in substrate, macroflora, or benthic epifauna, or to fully characterize the benthic community assemblage. Rather, the number of quadrats would need to more than double (at least 25 quadrats in each area) to detect a 40% change (i.e., effect size).

Given that sampling effort to date has not been adequate to detect community change with acceptable statistical power, three additional survey quadrats will be deployed in each of the study and reference areas (total of six additional quadrats) in 2022. This is a commitment made by Baffinland through ongoing discussions with the MEWG.

5.7 Closure

We trust this information is sufficient for your needs at this time. Should you have any questions or concerns, please do not hesitate to contact Phil Rouget, on behalf of the undersigned, at 604-230-7630.

Golder Associates Ltd.

Niallan O'Brien, BSc
Marine Ecologist

Kristin Westman, MSc, RPBio
Marine Biologist

Phil Rouget, MSc, RPBio
Senior Marine Biologist

Shawn Redden, RPBio
Associate, Senior Fisheries Biologist

NOB/KW/PR/SR/lih

https://golderassociates.sharepoint.com/sites/11206g/deliverables (do not use)/issued to client_for wp/300-399/1663724-349e-r-rev0/1663724-349e-rev0-44000 2021 meemp 5.0 substrate macroflora epifauna_21oct_22.docx

5.8 References

Baffinland (Baffinland Iron Mines Corporation). 2012. Mary River Project – Final Environmental Impact Statement. February 2012.

Clarke KR and Gorley RN, Somerfield PJ, and RM Warwick. 2014. Change in Marine communities: An approach to Statistical Analysis and Interpretation. 3rd edition. PRIMER-E: Plymouth

Clarke KR and Gorley RN. 2015, PRIMER-E: Plymouth

Coad BW and Reist JD, editors. 2018. Marine Fishes of Arctic Canada. Toronto: University of Toronto Press. 632 p.

Environment Canada. 2012. Metal Mining Technical Guidance for Environmental Effects Monitoring. EN14-61/2012E-PDF

Fox J, and Weisberg S. 2018. Bootstrapping Regression Models in R. An Appendix to An R Companion to Applied Regression, 3rd edition, https://socialsciences.mcmaster.ca/jfox/Books/Companion/appendices/Appendix-Bootstrapping.pdf.

Golder. 2021. 2020 Milne Inlet Marine Environmental Effects Monitoring Program (MEEMP) and Aquatic Invasive Species (AIS) Monitoring Program: Mary River Project. Submitted to Baffinland Iron Mines Corporation, Oakville, ON. Golder Associates Ltd. Golder Report Number 1663724-281-R-Rev1-34000; 18 August 2021. 1581 p.

Guiry MD, Guiry GM. 2021. AlgaeBase. World-wide electronic publication, National University of Ireland, Galway; [accessed November 2021]. https://www.algaebase.org

Krebs CJ. 1999. Ecological Methodology, 2nd edn Addison wesly Longman, Menlo Park.

Küpper FC, Peters AF, Shewring DM, Sayer MDJ, Mystikou A, Brown H, Azzopardi E, Dargent O, Strittmatter M, Brennan D, Asensi AO, van West P, Wilce RT. 2016. Arctic Marine Phytobenthos of Northern Baffin Island. Journal of Phycology 52(4):532-49.

Mecklenburg CW, Stein DL, Sheiko BA, Chernova NW, Mecklenburg TA, Holladay BA. 2007. Russian-American Long-Term Census of the Arctic: Benthic Fishes Trawled in the Chukchi Sea and Bering Strait, August 2004. Northwestern Naturalist 88:168-187.

R Core Team. 2021. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/.

Simpson E. 1949. Measurement of Diversity. Nature. 163(4148):688.

WoRMS (WoRMS Editorial Board). 2021. World Register of Marine Species. Flanders Belgium: Flanders Marine Institute; [accessed November 2021]. http://www.marinespecies.org/index.php

Zar JH. 2010. Biostatistical Analysis, Fifth edition. Pearson. 960 p.

APPENDIX 5A

Marine Foreshore Environmental Assessment Procedure

MARINE FORESHORE ENVIRONMENTAL ASSESSMENT PROCEDURE

Marine development projects have the potential to effect fish[1] and fish habitat[2]. Fisheries and Oceans Canada (DFO) is responsible for the protection and management of fish habitats under the authority of the *Fisheries Act* and may request plans, specifications and environmental assessments specific to marine projects where more detailed information is required. Assessments may be necessary for all types of projects, including, but not limited to aquaculture, log handling, industrial port development, marinas, private moorage facilities, marine repair facilities, pipeline or outfall installations, vessel launches or barge ramps, dredging projects and shoreline protection projects (breakwaters and seawalls). Presented below are standardized, transect-based assessment procedures intended to provide DFO with the basic information required to determine the potential effects of a development project on fish habitat.

Assessment Area

For comparative purposes, the assessment area should include both the foreshore site proposed for development as well as the adjacent foreshore. This will provide a context for the project and may provide data about cumulative effects if similar developments already occur on-site. A large scale site plan, preferably an enlargement of the hydrographic chart, with a small scale insert of the general geographic location will serve as a base map of the study area.

Tidal Height and Water Depth Measurements

The lowest normal tide (0.0 m), or chart datum, will be used as the reference point for the measurement of tidal height and water depth. Tidal height is recorded as positive relative to chart datum, while water depth below chart datum will be recorded as a negative value. For example, if the assessment is made when the tide is at 2 m, and observations are taken at a water depth of 6 m, then the depth will be recorded as -4 m. Tidal height will be corrected using the closest secondary port to the reference port found in the Canadian Tide and Current Tables, with further correction made for daylight savings time as required.

Transect Layout

Transects should be established perpendicular to the shoreline at regular intervals both within and adjacent to the proposed or active development area so as to sample representative fish habitat conditions. A preliminary low water reconnaissance or dive survey may be advisable to establish

---

[1] shellfish, crustaceans, marine animals and any parts of shellfish, crustaceans or marine animals, and the eggs, sperm, spawn, larvae, spat and juvenile stages of fish, shellfish, crustaceans and marine animals;

[2] shellfish, crustaceans, marine animals and any parts of shellfish, crustaceans or marine animals, and the eggs, sperm, spawn, larvae, spat and juvenile stages of fish, shellfish, crustaceans and marine animals;

appropriate boundaries for the assessment. Transects should begin at the highest high water mark (HHWM: distance referenced as Station 0.0 m) and, at a minimum, extend to a depth of -20 m (–30 m if the development has the potential to effect deeper benthic habitats). Though small-scale intertidal projects may only require intertidal transects, care must be taken to ensure that a representative sample is collected across the proposed development area. Procedural manuals are available from DFO if sampling of intertidal clam or benthic invertebrates is required. To ensure complete assessment of marine plants and animals in the photic zone, deeper transects may be necessary, especially to determine the effects of sunken debris or woodwaste accumulations resulting from existing developments. Transects should be spaced approximately 25 m apart, although this interval may vary depending on the width of the site. The number of transects required will depend on the nature of the foreshore development proposed, anticipated effects of the development, and local site conditions (tides and currents, geography, fetch, geology, etc.). Transects should be individually numbered and indicated on the site plan, and their commencement point referenced to benchmarks, where possible.

Recording Observations

Habitat inventories should be conducted during the more productive spring and summer months. At that time, algae and saltmarsh species are more readily identifiable, enabling a better assessment of the productive capacity of the site.

Observations should be recorded every 5 m along the transect or at significant changes in habitat type. Observations should include substrate type and composition, presence and relative abundance of marine animals and plants, and any other notable features (e.g., debris accumulations) using the following format:

Substrate

Substrate types are to be subdivided into the following size class categories:

- Bedrock
- Boulder (>256 mm diameter)
- Cobble (64-256 mm diameter)
- Gravel (2-64 mm diameter)
- Sand (0.0625-2 mm diameter)
- Silt/Mud/Clay (<0.0625 mm diameter)

Substrate types are recorded cumulatively as percentages out of a total of 100% (e.g., Boulder 5%; Cobble 15%; Gravel 60%, Sand 20%)

Marine Plants

Marine plants include rooted vascular vegetation (e.g., eelgrass, saltmarsh vegetation, etc.) and marine algae (e.g., rockweed, kelp, etc.). Marine plant observations are recorded as percent areal coverage estimated per 5 m × 1 m transect segment. Observations can be recorded as percentages (5%, 10%, 15%, etc.) or by utilizing the following areal coverage classes:

+	<5%
1	5-25%
2	>25-50%
3	>50-75%
4	>75-100%

Sessile Animals

Many marine animals permanently attached to substrates function as important fish habitat (e.g., barnacles, bay mussels, etc.). Sessile animals are recorded as percent areal coverage along the transect line using either estimated percentages or by areal coverage classes, as presented above.

Motile Animals

Motile animals include fish and marine invertebrates such as crabs and snails. These can be individually counted along the transect or, where too numerous, their estimated numbers can be recorded. Population estimates will most likely be applied to species such as herring or mysid shrimp that naturally occur in large numbers.

Other Features

Accumulations of wood bark and debris, sunken logs or other waste materials arising from onsite or nearby development activities should also be recorded. For wood bark and related small size debris, observations are recorded as percent areal coverage estimates per 5 m × 1 m transect segment and estimated deposition depth (e.g., 15% / 10 cm). For larger materials (sunken logs, wood chunks, etc.), observations can be recorded by individual piece count or by estimate of percent areal coverage.

Observations should be correlated to the transect distance from the HHWM and (corrected) tidal height or water depth (e.g., Sta. 0+80 m / +4.5 m), with information compiled in tabular form, by transect. Common names of observed animals and plants are acceptable for the data table; a species list with scientific names should, however, be appended to the report.

General marine plant categories (e.g., rockweed, eelgrass, bull kelp, saltmarsh, etc.) and any other notable features should be sketched to scale directly on a copy of the site plan, drawings or photographs of the site. A site profile should be prepared for each transect showing the slope of the foreshore and the location of indicator marine plants or invertebrates. A sketch of the proposed marine development should be superimposed over the site plan so that any potential effect of the project on fish habitat is clear. Compensatory habitat proposed for offsetting altered habitat should also be sketched on site maps and profiles to enable review of the positioning of replacement habitat relative to the project.

Photographic Documentation

It is essential to produce a photographic record along the intertidal and subtidal transects. A videographic record of subtidal transects is also recommended. Photos and videos provide a real-time record of characteristic fish habitat at the proposed site and can be invaluable to future post-development site monitoring. Photographic records also facilitate comparison of the productivity of natural habitats with any compensatory habitat constructed to offset habitat losses. As visibility may be a problem, careful attention should be given to appropriate tidal levels, and midday lighting conditions are recommended. Aerial photos, taken at low tide, are often useful to put the site into context with the surrounding area and to verify information provided from other sources.

Assessment reports should include photographs of representative fish habitat types. Depending upon the scope of the proposed foreshore development, an unedited, labelled copy of the assessment video may also be required for the report submission. The video footage should be referenced with pertinent information (e.g., time, date, depth, heading, etc.), and a written or recorded interpretation should accompany the video.

Summary of information to be submitted

1. Basemap showing tenure area boundaries, surrounding area, transect locations and sampling stations
2. Shoreline video/photographs of intertidal zone
3. Underwater video/photographs of transects
4. Tabular data for each transect describing substrate type and composition, marine plants, sessile and motile marine animals, and other notable features
5. Habitat map showing location of different substrate types, plants, animals and operational infrastructure
6. Profile diagrams of each transect showing slope, sediment types and the major marine plants or animals observed
7. Photographs of site and aerial photographs if available.

APPENDIX 5B

Photographs

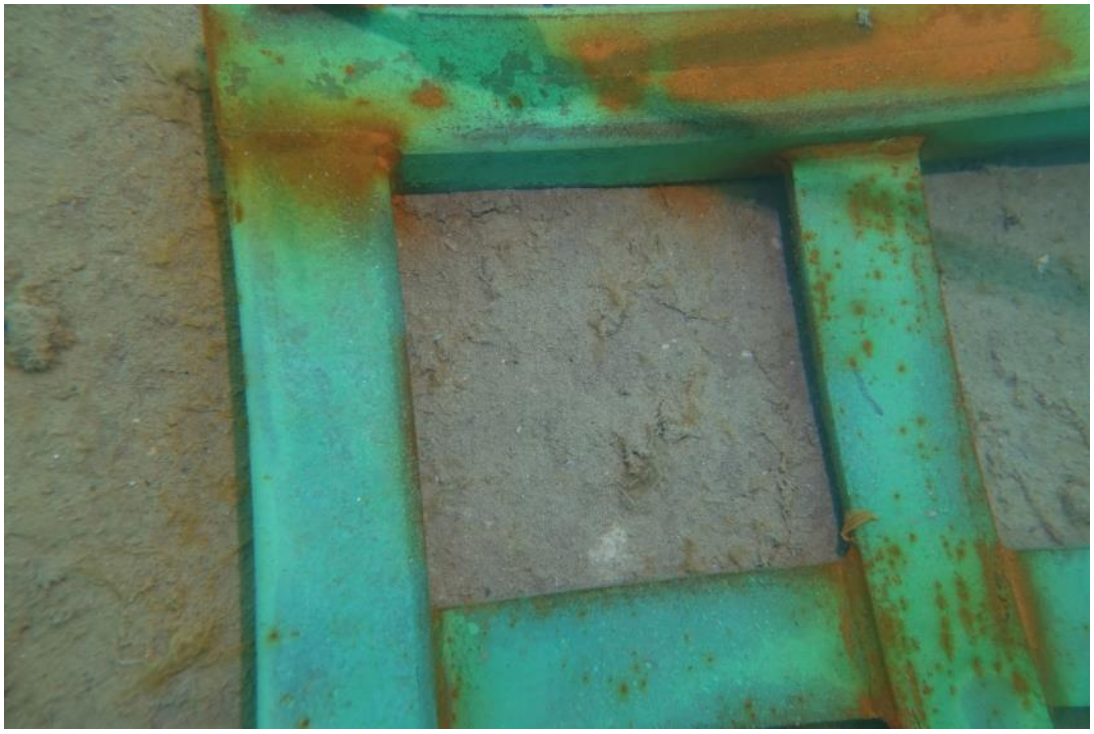


Photo 1: Photo of Q12 deployed in Milne Port in 2021.

Photo 2: Diver surveying Q11 in Milne Port (2021).

Photo 3: Wrinkled Rock-borer Clam (*Hiatella artica*) and Cone Worm (*Cistenides granulata,* Yellow Arrow) in Q1 in Milne Port (2021).

Photo 4: Orange Tunicate (*Polycarpa* spp.) Identified in Q1 in in Milne Port (2021).

Photo 5: Shrimp (*Pandalus* spp.) and Brown Filamentous Algae Recorded in Q1 in Milne Port (2021).

Photo 6: Eelpout (*Lycodes* spp.) Inside Steel Frame of Q1 in Milne Port (2021).

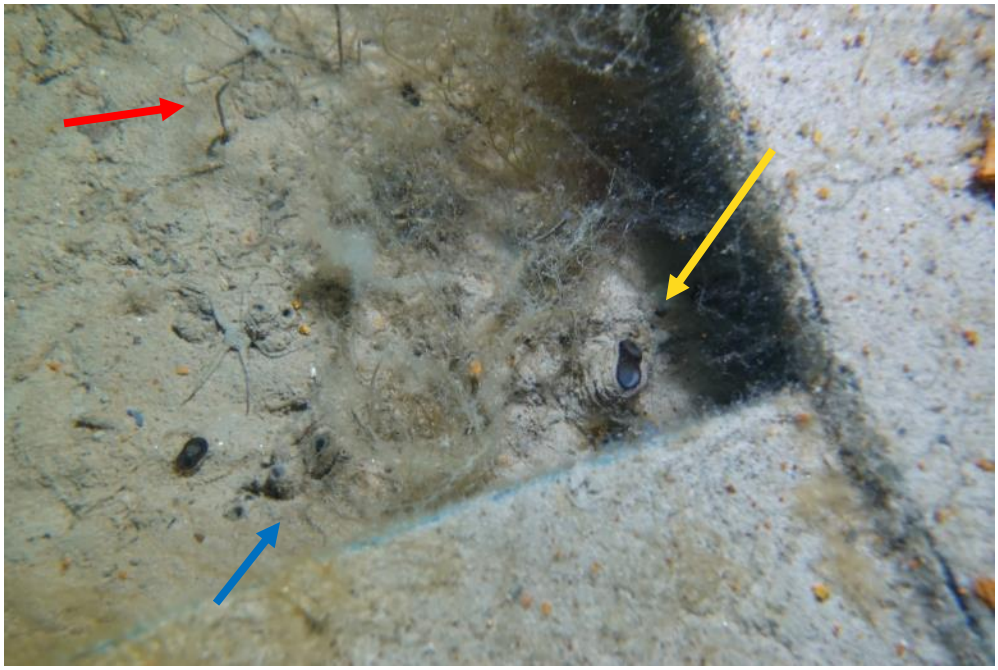


Photo 7: Blunt Gaper (*Mya* spp., Yellow Arrow), Wrinkled Rock-borer Clam (Blue Arrow), Brittle Star and Polychaete Tube Casing (Red Arrow) in Q3 in Milne Port (2021).

Photo 8: Icelandic Scallop (*Chlamys islandica*) in Q3 in Milne Port (2021).

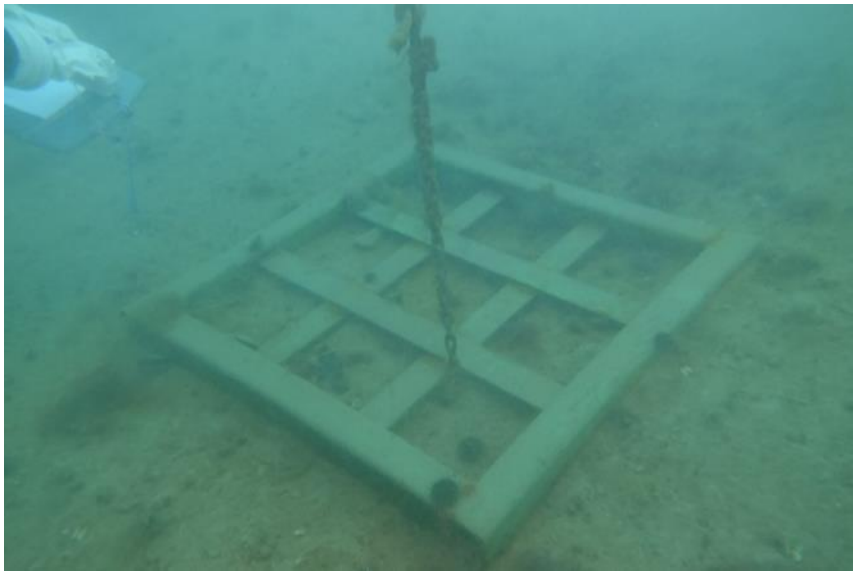


Photo 9: Photo of Q4 in Milne Port (2021).

Photo 10: Green Urchin (*Strongylocentrotus droebachiensis*) Observed in Q4 in Milne Port (2021).

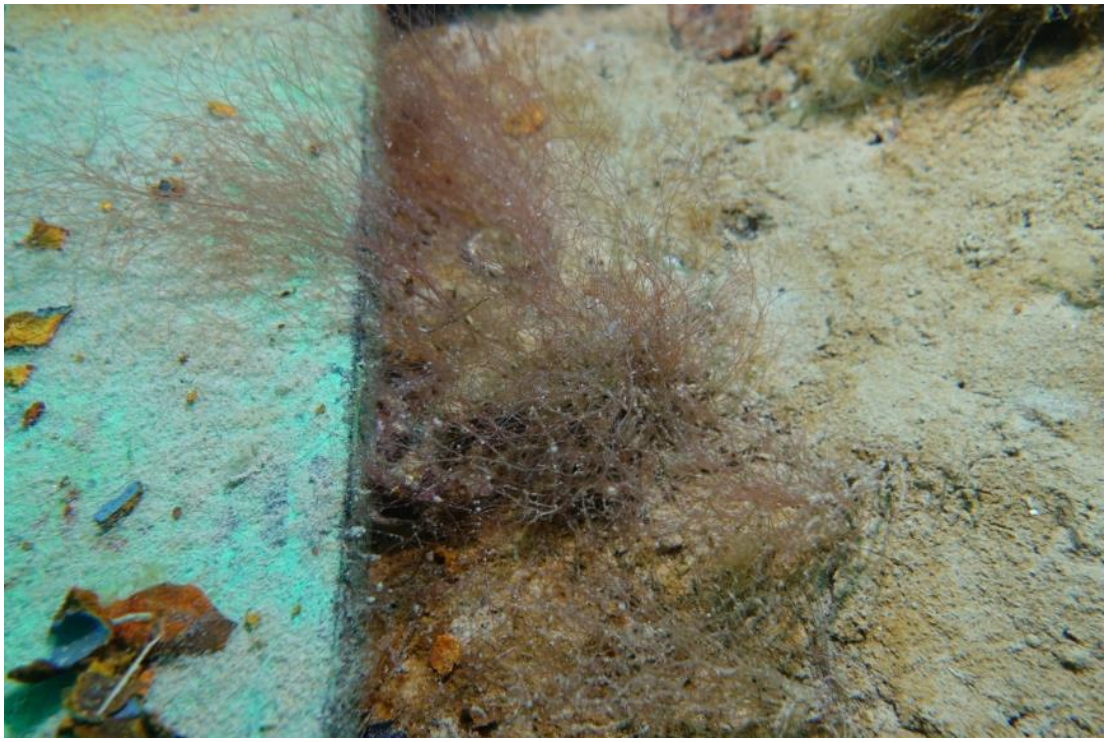


Photo 11: Red Filamentous Macroalgae in Q4 in Milne Port (2021).

Photo 12: Whelk (*Buccinum hydrophanum*) Recorded on Quadrat Frame (Q4) in Milne Port (2021).

Photo 13: Wrinkled Rock-borer Clam Siphons (Blue Arrow) and Shrimp (*Sclerocrangon boreas*) Recorded in Q4 in Milne Port (2021).

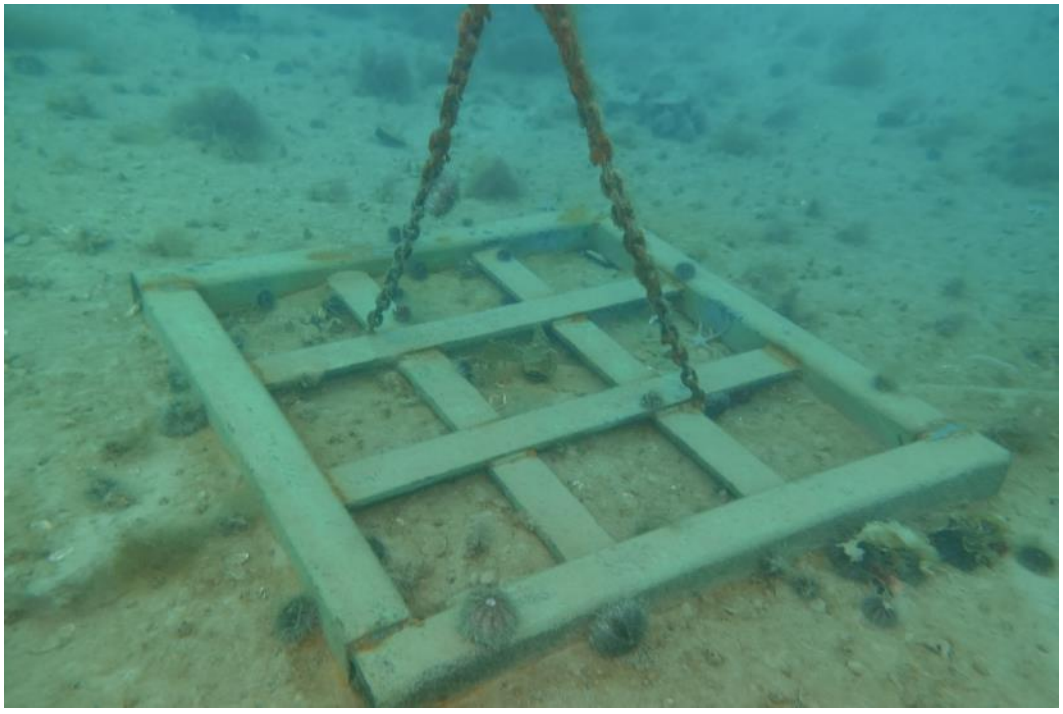


Photo 14: Photo of Q5 in Milne Port (2021).

Photo 15: Pout (*Gymnelus* spp.) observed in Q5 in Milne Port (2021).

Photo 16: Sieve Kelp (*Agarum clathratum*) and Green urchin in Q5 in Milne Port (2021).

Photo 17: Photo of Q5 in Milne Port (2021) Showing Old Belt Transect Frame, Green Urchin, Brittle Star and Wrinkled Rock-borer Clam.

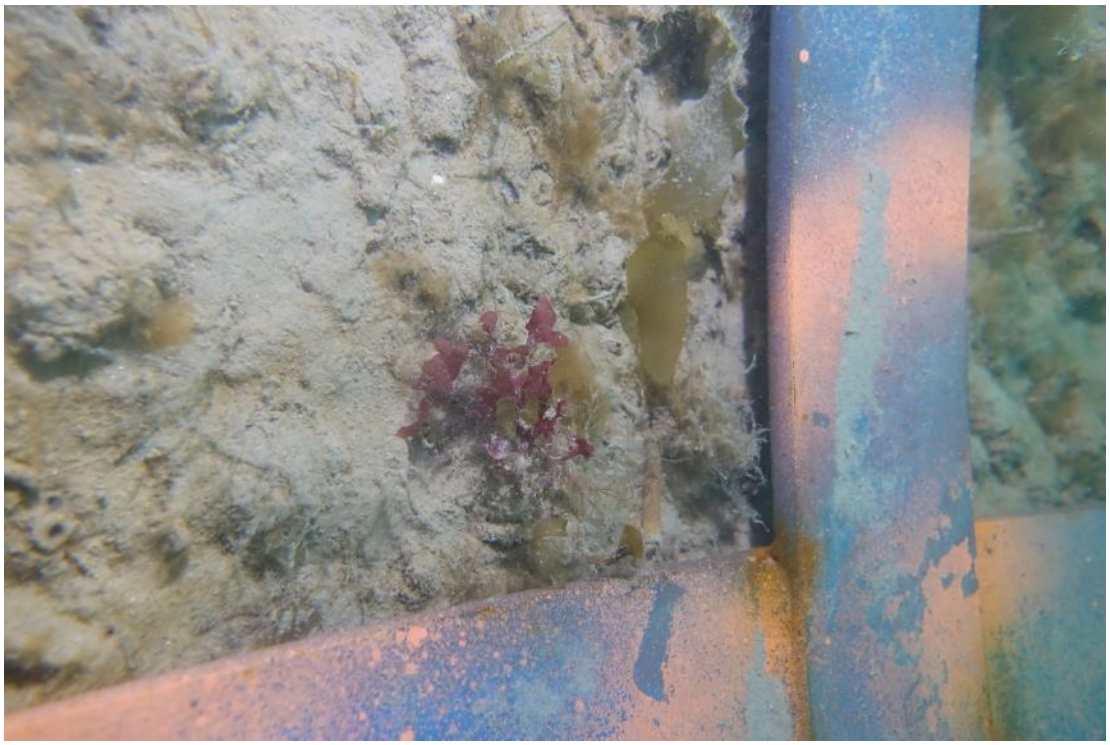


Photo 18: Sugar Kelp (*Saccharina latissima*) and Red Foliose Algae (*Coccotylus truncatus*) in Q11 in Milne Port (2021).

Photo 19: Brown Filamentous Algae (*Halosiphon tomentosus)* in Q11 in Milne Port (2021).

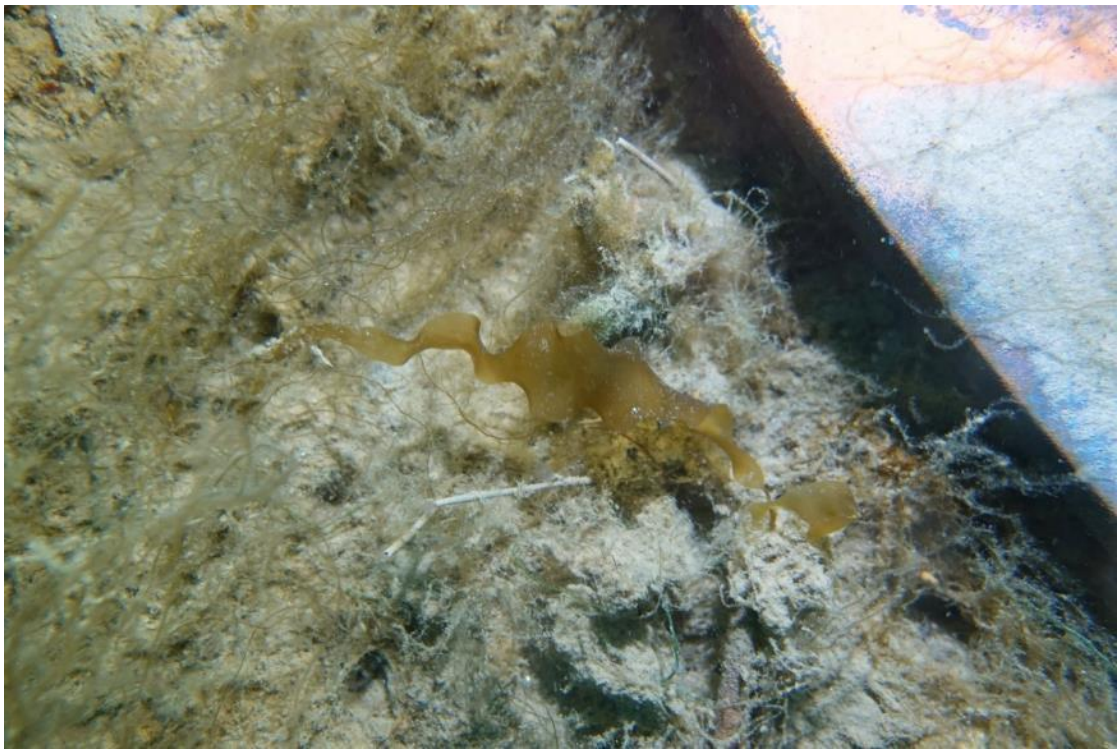


Photo 20: Sugar Kelp and Brown Filamentous Algae in Q13 in Milne Port (2021).

Photo 21: Sabellid Worm, Brown Filamentous Algae (*H. tomentosus*) and Sugar Kelp in Q13 in Milne Port (2021).

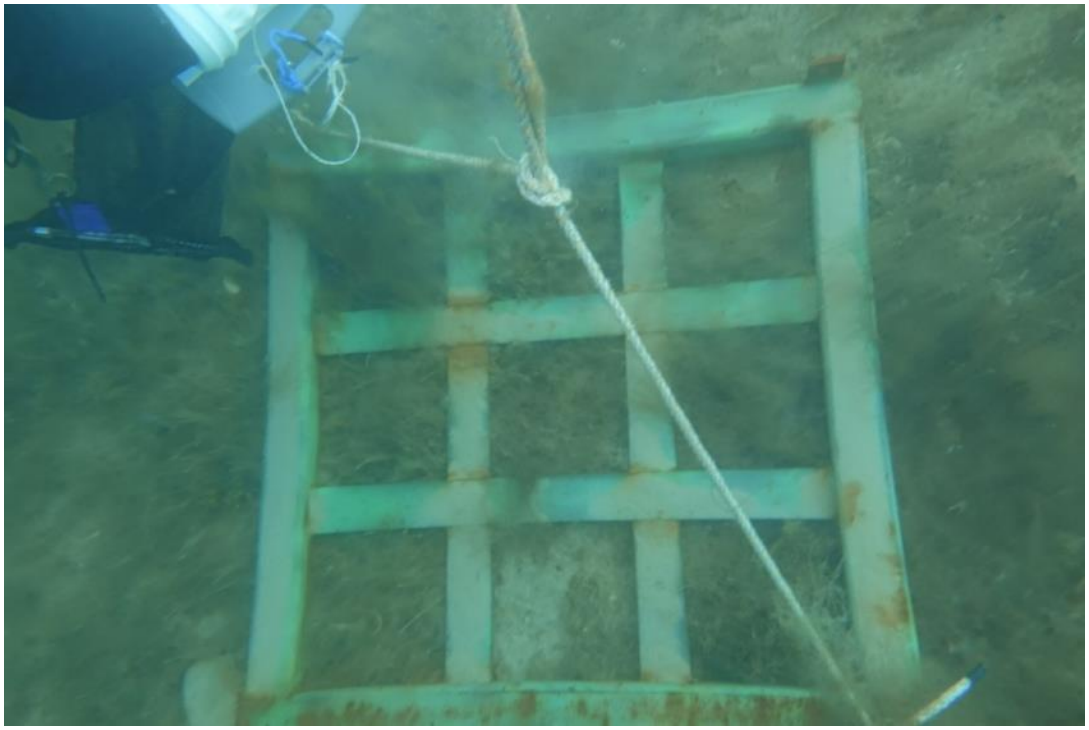


Photo 22: Photo of Q14 in Milne Port (2021).

Photo 23: Sabellid Worm, Polychaete Worm Casing and Brown Filamentous Algae in Q14 in Milne Port (2021).

Photo 24: Photo of Q15 With Red Foliose Algae (*Coccotylus truncatus*), Green Filamentous Algae, Brown Filamentous Algae (cf. *Coelocladia arctica*) in Milne Port (2021).

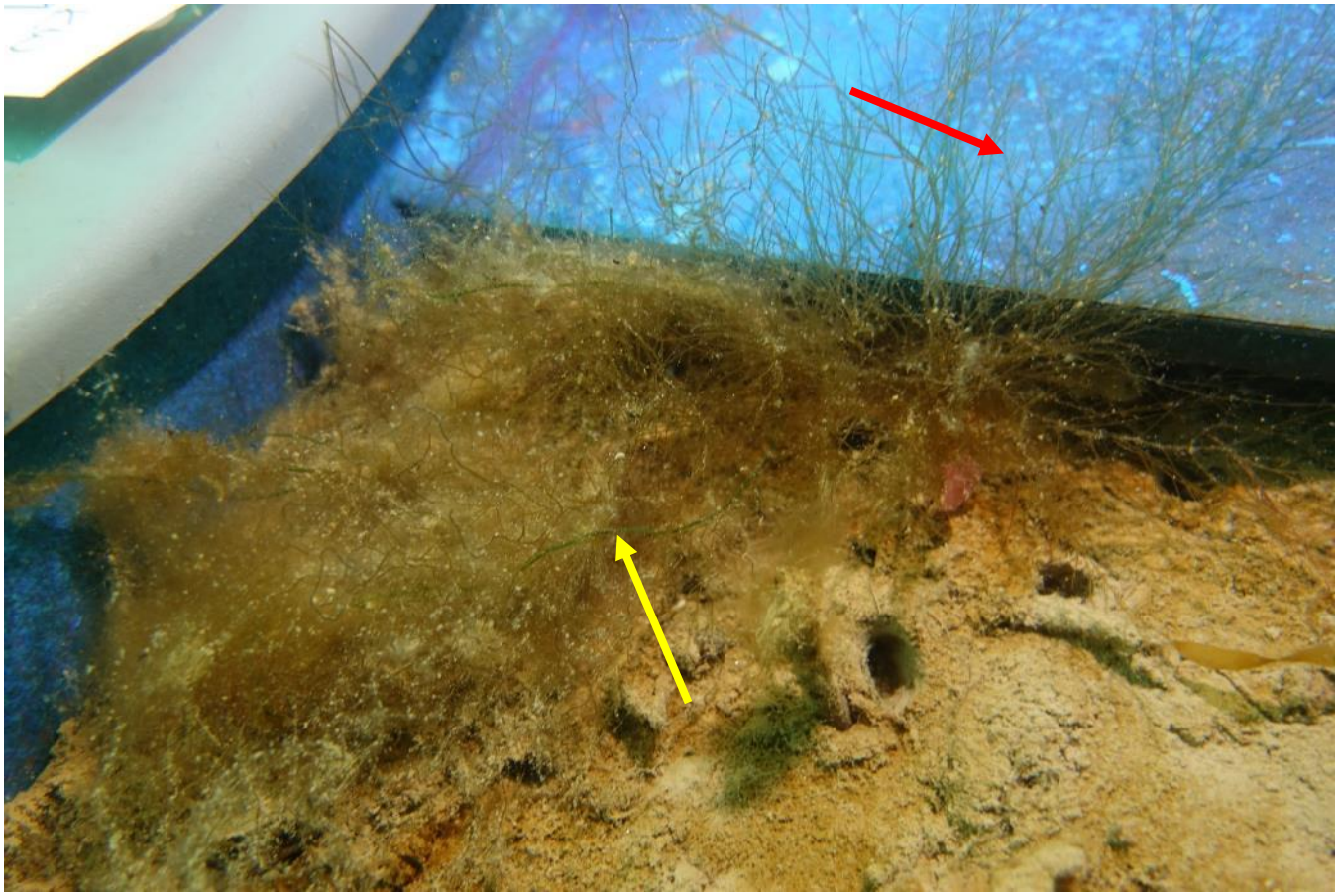


Photo 25: Green Filamentous Algae (*Chaetomorpha melagonium*, Yellow Arrow) and Acid Weed (*Desmarestia* sp., Red Arrow) in Q15 in Milne Port (2021).

Photo 26: Brittle Stars, Green Urchin, Greenland Scallop (*Similipecten greenlandicus*) and Detrital Algae in Q6 in Reference Area (2021).

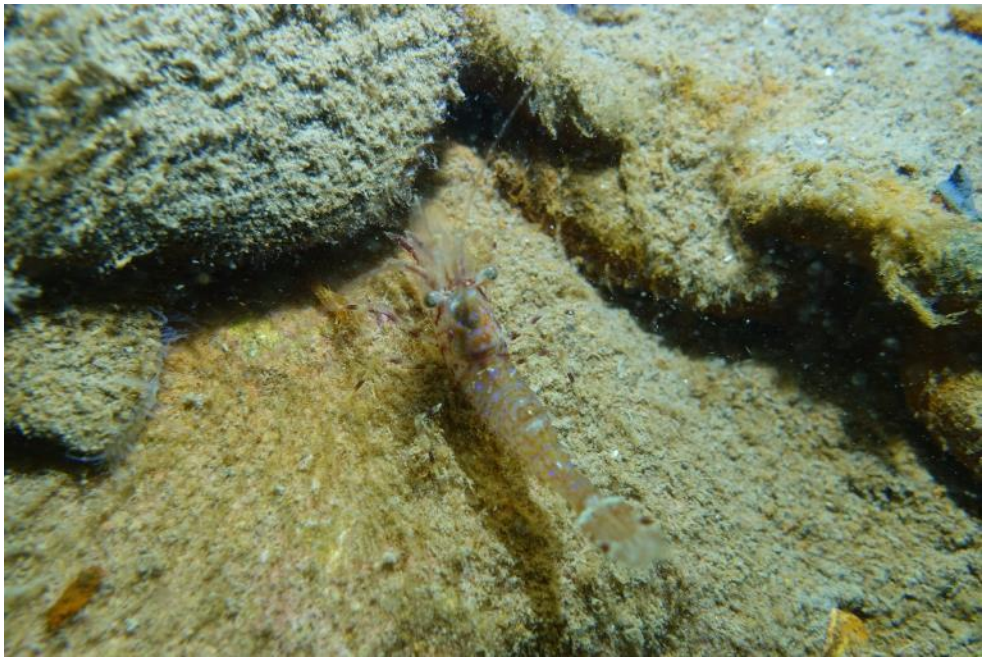


Photo 27: Shrimp (*Pandalus* spp.) and Icelandic Scallop in Q6 in Reference Area (2021).

Photo 28: Greenland Scallop, Brittle Stars, Siphon of Wrinkled Rock-borer Clam) and Brown Diatoms on Sediment in Q6 in Reference Area (2021).

Photo 29: Wrinkled Rock-borer Clam, Brittle stars and Brown Diatoms on Sediment in Q6 in Reference Area (2021).

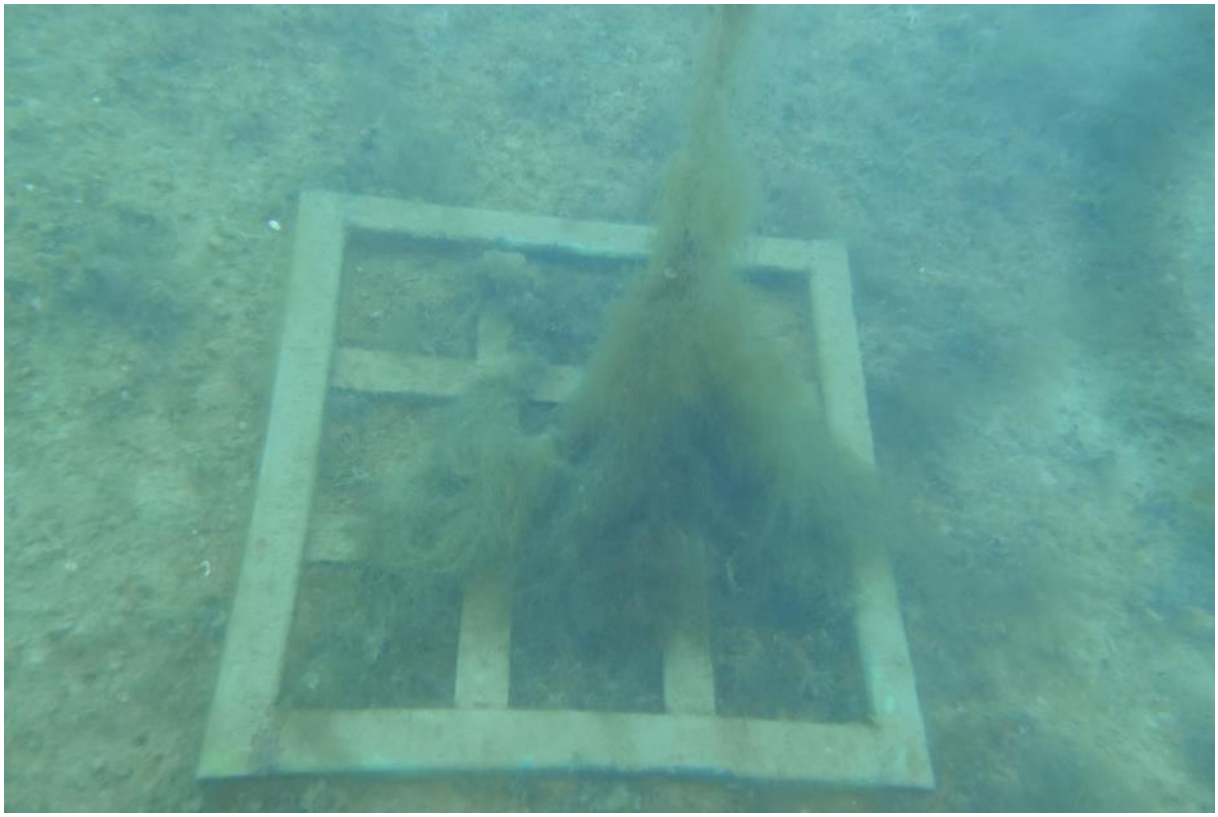


Photo 30: Photo of Q7 in Reference Area (2021) Showing Macroalgae Attached to Suspended Chain.

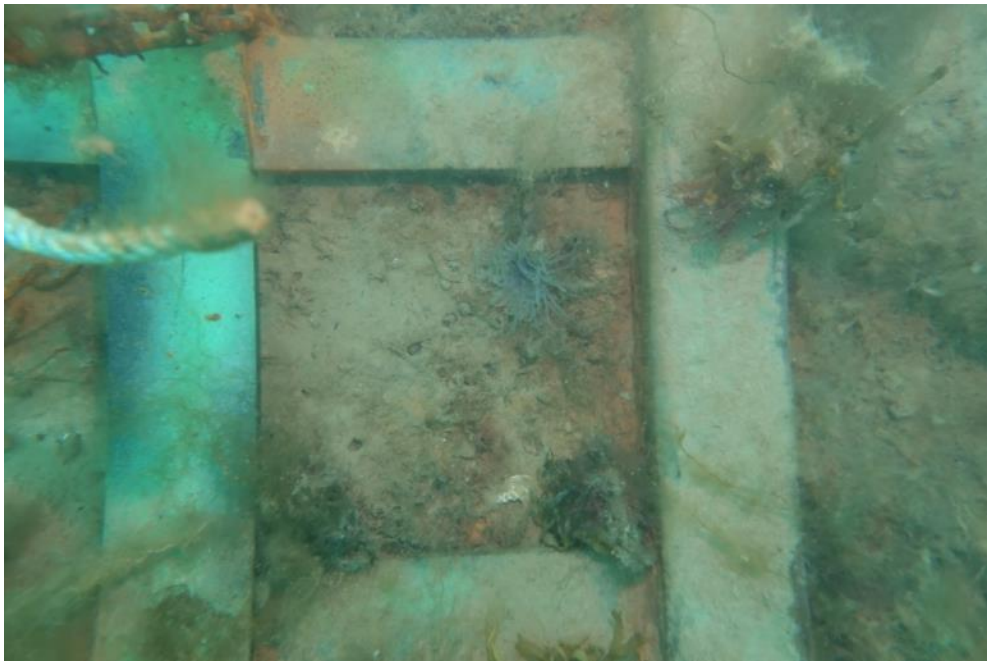


Photo 31: Burrowing Anemone (Ceriantharia indet.), Green Urchin Covered in Detrital Algae, Wrinkled Rock-borer Clam, Brown Filamentous Algae (cf. *Coelocladia arctica*) in Q7 in Reference Area (2021).

Photo 32: Acid Weed in Q7 in Reference Area (2021).

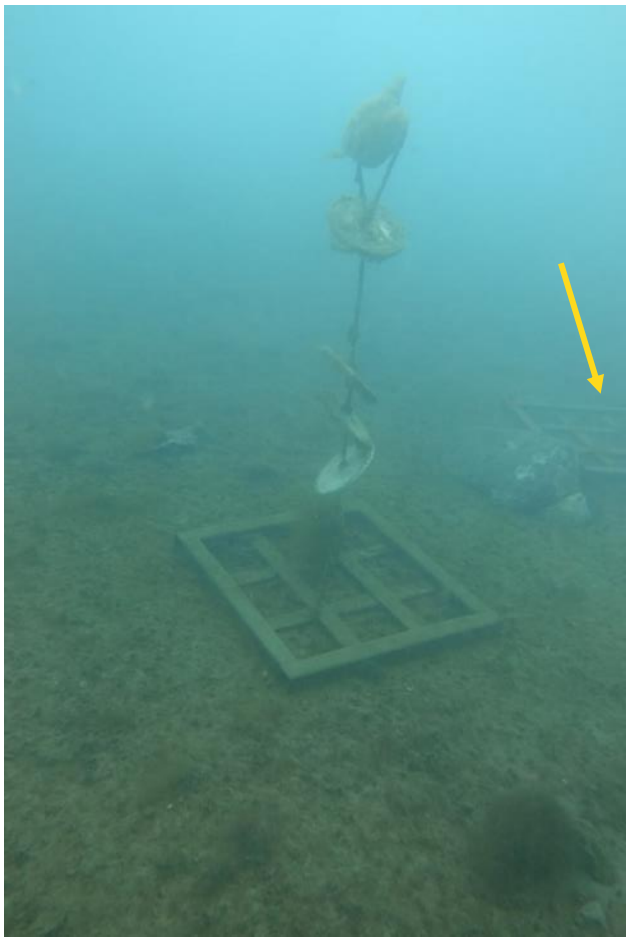


Photo 33: Photo of Q8 and Q18 (Yellow Arrow) in Reference Area (2021).

Photo 34: Wrinkled Rock-borer Clam Siphons, Greenland scallop and Brown Diatoms on Sediment in Q8 in Reference Area (2021).

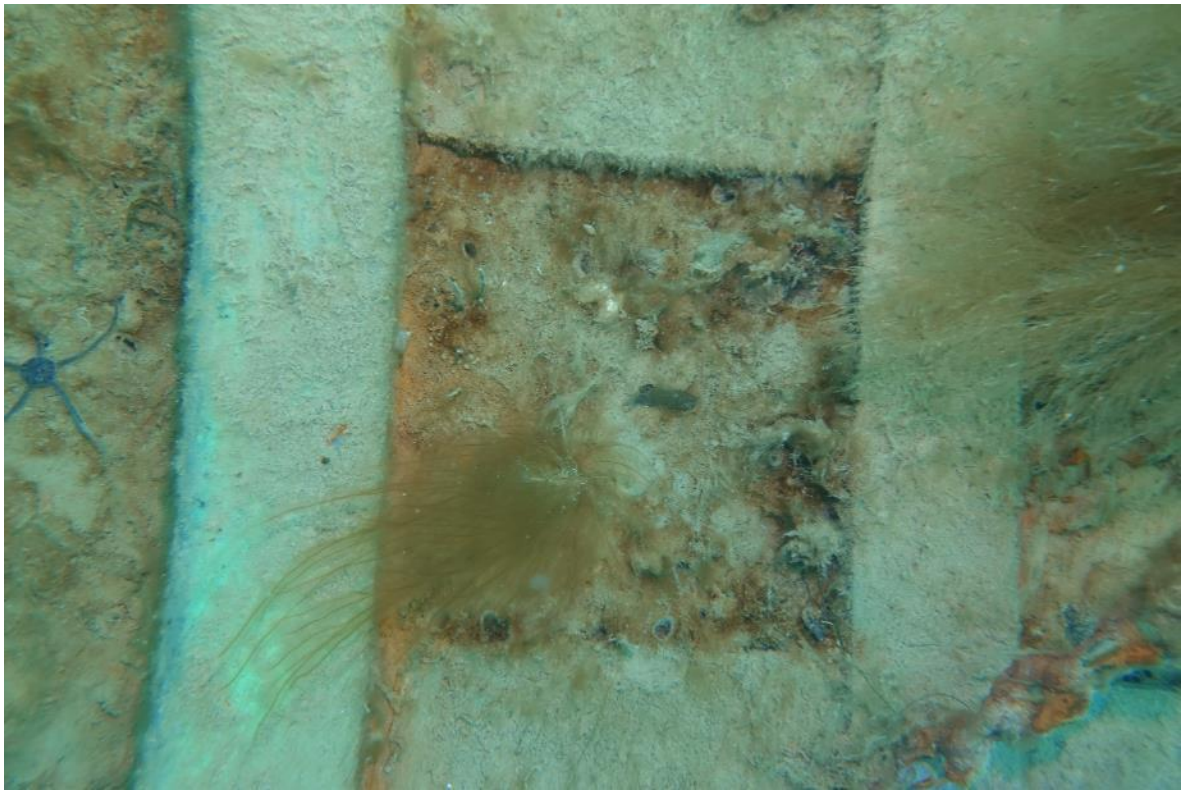


Photo 35: Photo of Q8 with *H. tomentosus* and Siphon Holes of Wrinkled Rock-borer Clam and Blunt Gaper in Reference Area (2021).

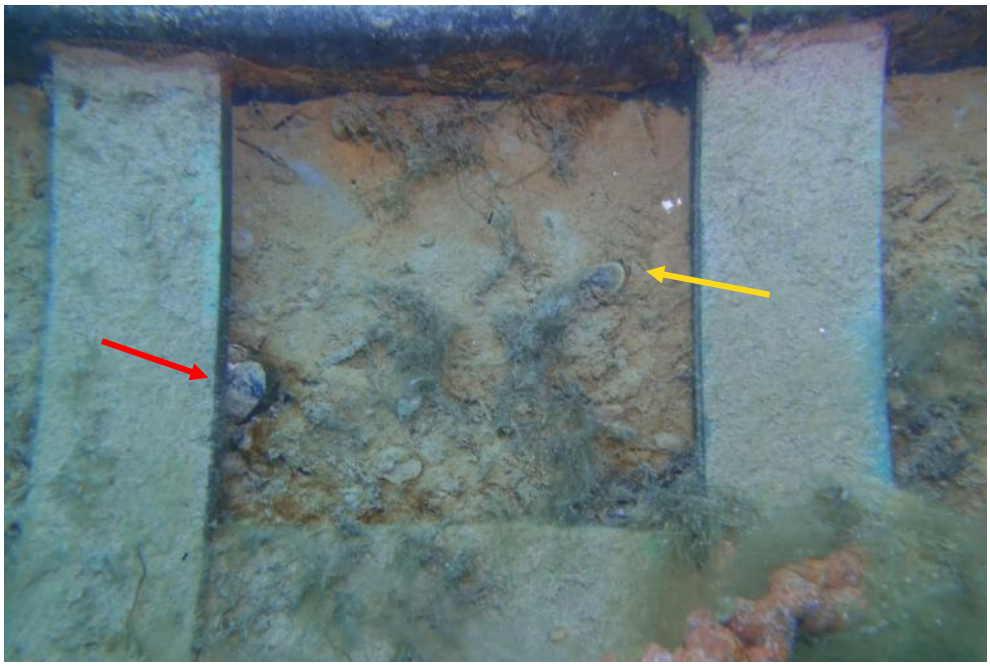


Photo 36: Photo of Q10 with Unidentified Mussel (Red Arrow), Olive Green Mussel (Yellow Arrow) and Brown Filamentous Algae in Reference Area (2021).

Photo 37: Sugar Kelp in Q10 in Reference Area (2021).

Photo 38: Sculpin (Cottidae indet.) in Q16 in Reference Area (2021).

Photo 39: Sugar Kelp and *Pylaiella* spp. in Q16 in Reference Area (2021).

Photo 40: Snail (Margarite spp.) and Dilsea (*Dilsea socialis*) in Q16 in Reference Area (2021).

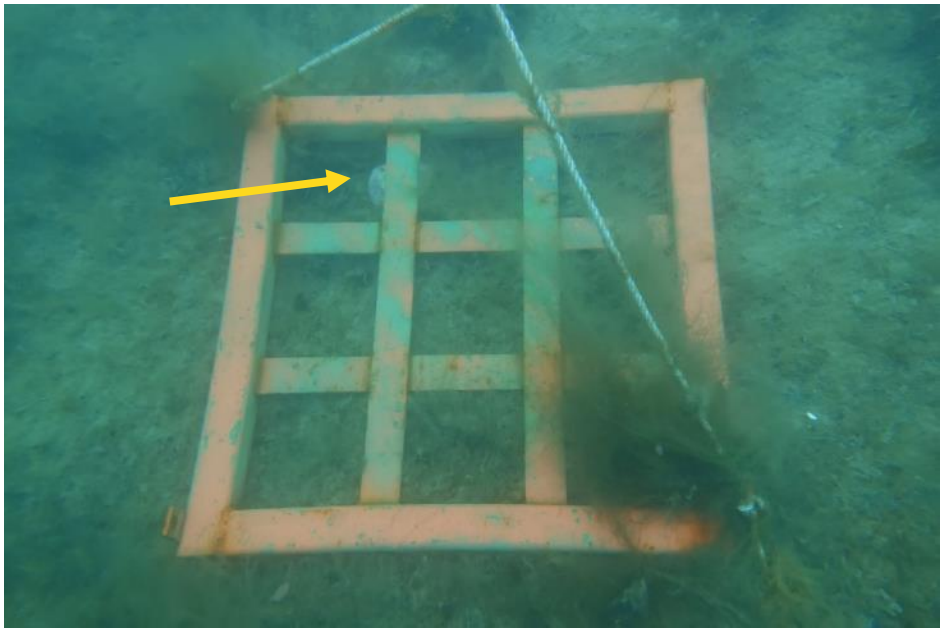


Photo 41: Q17 in Reference Area (2021). Cobble with Encrusting Coralline Algae (Yellow Arrow) and Detrital Algae.

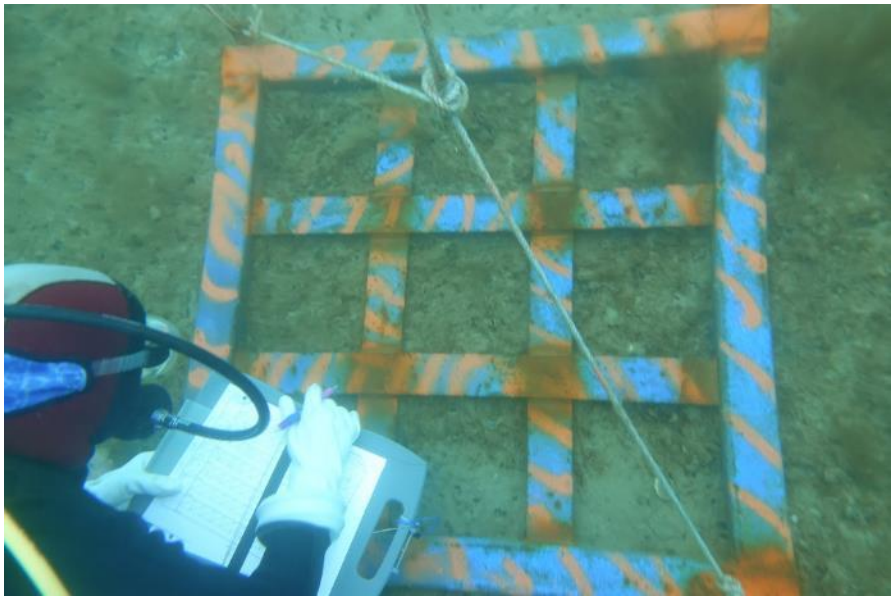


Photo 42: Diver Surveying Q18 in Reference Area (2021).

Photo 43: Brittle star, Sugar Kelp and Exposed Wrinkled Rock-borer Clam in Q20 in Reference Area (2021).

Photo 44: Orange Tunicate (Polycarpa spp.) and Brittle Star in Q20 in Reference Area (2021).

Photo 45: Photo of Q20 with Bedrock and Silt/Sand Substrate, Acid Weed and Wrinkled Rock-borer Clam in Reference Area (2021).

APPENDIX 5C

Quadrat Survey Data

Location/Quadrat Number	UTM (17W) Easting (m)	UTM (17W) Northing (m)	Survey Date	Quadrat Sub-number	Depth (m) Chart Datum	Substrate (% cover)									Macroalgae (% Cover)																
																Kelp		Brown						Green			Red				
						Bedrock	Cobble	Gravel	Sand	Silt	Shell -whole/crushed	Detrital veneer	Other debris (i.e., metal)	Brown diatom mat	Detrital Algae	Sugar kelp *Saccharina latissima*	Sieve kelp *Agarum clathratum*	Rockweed *Fucus distichus*	*Pylaiella* spp.	*Halosiphon tomentosus*	Acid weed *Desmarestia* spp.	Brown filamentous 1 cf. *Coelocladia arctica*	Brown filamentous algae	*Chaetomorpha melagonium*	Short green filamentous 1 Indet. 1	Green filamentous Indet.	*Savoiea arctica*	*Coccotylus truncatus*	*Dilsea socialis*	Red filamentous Rhodophyta indet.	Encrusting coralline Corallinales indet.
Q1	502828	7976382	14-Aug-21	1	-8.9	-	-	-	60	40	<5	30	-	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				2	-9.0	-	-	-	60	40	<5	15	-	-	2-	-	-	-	-	-	-	-	-	-	-	-	-	<5	-	-	-
				3	-9.1	-	-	-	60	40	-	15	-	-	15	-	-	-	5	-	-	-	-	-	-	-	-	<5	-	-	-
				4	-9.0	-	-	-	60	40	<5	10	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				5	-9.2	-	-	-	60	40	<5	10	15	-	-	-	-	-	10	-	-	-	-	-	-	-	-	-	-	-	-
				6	-9.3	-	-	-	60	40	-	5	<1	-	-	-	-	-	15	-	-	-	-	-	-	-	-	-	-	-	-
				7	-9.2	-	-	-	60	40	<5	10	-	-	-	-	-	-	10	-	-	-	-	-	-	-	-	-	-	-	-
				8	-9.3	-	-	-	60	40	-	5	7	-	-	-	-	-	20	-	-	-	-	-	-	-	-	-	-	-	-
				9	-9.3	-	-	-	60	40	<5	5	7	-	-	-	-	-	15	-	-	-	-	-	-	-	-	-	-	-	-
Q3	504208	7976659	15-Aug-21	1	-10.4	-	-	5	40	50	5	7	<5	-	-	-	-	-	<5	-	1	-	-	-	-	-	-	-	-	-	-
				2	-11.0	-	-	5	35	50	10	10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				3	-11.1	-	-	-	40	60	-	20	-	-	15	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				4	-11.0	-	-	-	40	60	-	10	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				5	-11.0	-	-	-	40	60	-	0	45	20	3-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				6	-11.0	-	-	5	35	55	5	20	<2	-	-	-	-	-	-	-	-	10	-	-	-	-	-	-	-	-	-
				7	-11.0	-	-	5	38	57	<1	5	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				8	-10.8	-	-	-	37	58	<5	10	7	-	5	-	-	-	7	-	-	5	-	-	-	-	-	-	-	-	-
				9	-10.9	-	-	-	40	60	<1	20	5	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Q4	504363	7976611	06-Aug-21	1	-12.1	-	-	-	30	70	-	10	-	2	2	-	-	-	-	-	20	-	-	-	-	-	-	-	-	-	-
				2	-12.2	-	-	-	25	70	5	10	<1	10	-	-	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-
				3	-12.2	-	-	-	30	70	<2	10	<1	10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				4	-12.2	-	-	5	23	70	2	10	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				5	-12.3	-	-	-	28	70	2	10	5	5	-	-	-	-	-	-	5	-	-	-	-	-	-	-	-	<5	-
				6	-12.2	-	-	-	30	70	-	10	5	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	15	-
				7	-12.2	-	-	-	25	70	5	10	10	10	-	-	-	-	-	-	10	-	-	-	-	-	-	-	-	-	-
				8	-12.3	-	20	-	25	55	-	10	5	5	-	-	-	-	-	-	10	-	5	-	-	-	-	-	-	-	-
				9	-12.3	-	-	-	30	70	-	10	10	10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Q5	504802	7976731	06-Aug-21	1	-12.4	-	-	5	30	65	-	20	-	5	-	-	-	-	-	-	-	-	<1	-	-	-	-	-	-	-	-
				2	-12.4	-	-	-	30	70	-	20	<1	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				3	-12.4	-	-	<5	30	65	-	20	20	<5	-	-	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-
				4	-12.4	-	-	-	25	75	-	20	5	5	-	-	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-
				5	-12.4	-	-	-	25	75	-	10	27	<5	35	-	15	-	<5	-	-	-	-	-	-	-	-	-	-	-	-
				6	-12.4	-	-	-	25	75	-	20	-	<5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				7	-12.4	-	-	-	25	75	-	10	<1	10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				8	-12.4	-	-	-	25	75	-	10	20	<5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				9	-12.4	-	-	-	25	75	-	20	-	10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Q6	506563	7979107	08-Aug-21	1	-15.4	-	-	-	25	70	5	-	-	-	8-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				2	-15.7	-	-	-	25	70	5	<5	-	10	-	-	-	-	-	-	-	-	<5	-	-	<5	-	<1	-	-	-
				3	-15.9	-	-	-	30	70	-	10	-	20	2-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				4	-16.0	-	-	-	25	70	5	10	-	<5	-	-	-	-	-	-	-	-	5	-	-	-	-	-	-	-	-
				5	-16.0	-	-	-	25	70	5	10	20	5	5-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				6	-16.0	-	-	-	30	70	-	10	-	10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				7	-16.0	-	-	-	25	70	5	10	<2	20	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				8	-16.2	-	-	-	20	70	10	-	-	-	7-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				9	-16.2	-	-	-	20	70	10	-	-	-	1--	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Q7	506774	7979170	16-Aug-21	1	-10.1	-	-	-	30	70	<1	20	-	-	4-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				2	-10.1	-	10	-	25	65	-	20	-	10	2-	-	-	-	-	-	5	10	-	-	-	-	-	<5	-	-	-
				3	-10.2	-	-	-	30	70	-	15	2	7	15	-	-	-	-	-	5	-	-	<5	-	-	-	-	-	-	-
				4	-10.1	-	-	-	25	70	5	20	-	5	1-	-	-	-	-	-	10	-	-	<5	-	-	-	<5	-	-	-
				5	-10.1	-	-	-	20	80	<5	-	25	-	1--	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				6	-10.2	-	-	-	20	80	-	10	-	-	3-	-	-	-	-	-	-	10	-	<5	-	-	-	<5	-	-	-
				7	-10.2	-	-	-	30	70	<5	5	3	20	4-	-	-	-	-	-	25	-	-	10	-	-	-	-	-	-	-
				8	-10.2	-	-	-	30	70	-	-	-	-	1--	-	-	-	-	-	75	20	-	-	-	-	-	5	-	-	20
				9	-10.2	-	30	-	20	50	-	5	-	-	-	-	-	-	-	-	40	-	-	-	-	-	-	15	-	-	-
Q8	506957	7979457	16-Aug-21	1	-10.5	-	-	-	35	60	5	10	-	30	45	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-	-
				2	-10.7	-	5	-	35	60	-	10	-	35	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				3	-10.7	-	5	-	35	60	-	10	2	35	-	-	-	-	-	-	-	-	-	-	-	<5	-	-	-	-	-
				4	-10.7	-	-	-	40	60	<5	10	-	35	-	5	-	-	-	15	-	-	-	-	-	-	-	-	-	-	-
				5	-10.7	-	-	-	40	60	<5	10	20	35	-	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-	-
				6	-10.7	-	-	-	40	60	-	10	-	30	-	-	-	-	-	10	-	-	-	-	-	-	-	-	-	-	-
				7	-10.7	-	-	-	40	60	<8	15	5	20	-	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-	-
				8	-10.7	-	-	-	40	60	-	15	<1	35	-	-	-	-	-	15	-	-	-	-	-	<5	-	-	-	-	-
				9	-10.7	-	-	-	40	60	-	15	-	5	-	-	-	-	-	10	-	-	-	-	-	<1	-	5	-	-	-
Q10	506584	7979115	08-Aug-21	1	-6.1	-	-	20	20	60	-	10	<1	2	-	-	-	-	10	-	-	-	-	-	-	-	-	-	-	-	-
				2	-6.4	-	-	5	25	70	-	20	<1	10	-	-	-	-	-	-	-	-	10	-	-	-	-	-	-	-	-
				3	-6.5	-	-	-	25	70	5	10	-	-	-	-	-	-	10	-	-	-	-	-	-	-	-	-	-	-	-
				4	-6.4	-	-	-	30	70	-	10	-	<1	2-	-	-	-	10	-	-	-	-	-	-	-	-	-	-	-	-
				5	-6.6	-	-	10	20	70	-	10	35	-	-	-	-	-	10	-	-	-	-	-	-	-	-	-	-	-	-
				6	-6.6	-	-	15	20	65	-	15	7	2	-	-	-	-	25	-	-	-	-	-	-	-	-	-	-	-	-
				7	-6.5	-	10	10	20	60	<1	15	-	-	1-	5	-	-	10	-	-	-	-	-	-	<1	-	-	-	-	-
				8	-6.6	-	-	10	20	70	-	10	-	-	5	-	-	-	20	-	-	-	-	-	-	-	-	-	-	-	-
				9	-6.9	-	-	-	25	70	5	10	-	2	-	<5	-	-	5	-	-	-	-	-	-	-	-	-	-	-	-
Q11	502820	7976371	14-Aug-21	1	-7.5	-	-	-	60	40	-	20	-	-	-	5	-	-	10	-	-	-	-	<1	-	-	-	5	-	-	-
				2	-7.6	-	-	-	60	40	<1	20	-	<1	-	-	-	-	5	-	-	-	-	-	-	-	-	5	-	-	-
				3	-7.5	-	-	-	60	40	-	15	-	-	-	-	-	-	15	-	-	-	-	-	-	-	-	5	-	-	-
				4	-7.6	-	-	-	60	40	<5	20	-	-	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-	-	-
				5	-7.6	-	-	-	60	40	<1	10	-	-	-	<1	-	-	20	-	-	-	-	-	-	-	-	5	-	-	-
				6	-7.6	-	-	-	60	40	<1	10	-	-	-	-	-	-	-	15	-	-	-	-	-	-	-	-	-	-	-
				7	-7.6	-	-	-	60	40	<1	10	-	-	-	-	-	-	-	-	5	-	-	1	<5	-	-	-	-	-	-
				8	-7.7	-	-	-	60	40	<1	10	-	-	-	-	-	-	<5	-	5	-	-	-	-	-	-	-	-	-	-
				9	-7.7	-	-	-	60	40	<1	10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Q12	503041	7976474	11-Aug-21	1	-6.0	-	-	-	90	10	-	15	-	-	-	-	-	-	<5	-	-	-	-	-	-	-	-	-	-	-	-
				2	-6.0	-	-	5	85	10	-	15	-	-	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-	-	-
				3	-6.0	-	-	7	83	10	-	15	-	-	-	-	-	-	<5	-	-	-	-	-	-	-	-	-	-	-	-
				4	-6.0	-	-	<1	82	10	8	15	-	-	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-	-	-
				5	-6.0	-	-	-	90	10	-	15	-	-	-	-	-	-	<1	-	-	-	-	-	-	-	-	-	-	-	-
				6	-6.0	-	-	<5	85	10	5	10	-	-	-	-	-	-	<5	-	-	-	-	-	-	-	-	-	-	-	-
				7	-6.0	-	10	-	85	5	-	10	-	-	-	-	-	-	10	-	5	-	-	-	-	-	-	-	-	-	-
				8	-6.0	-	-	-	90	10	-	10	-	-	-	-	-	-	<5	-	5	-	-	-	-	-	-	-	-	-	-
				9	-6.0	-	-	-	90	10	-	10	-	-	5	-	-	-	<5	-	-	-	-	-	-	-	-	-	-	-	-
Q13	504210	7976643	15-Aug-21	1	-7.9	-	-	10	40	50	-	10	-	5	1-	<5	-	-	-	-	10	-	-	-	-	-	-	-	-	-	-
				2	-7.9	-	5	10	38	47	<5	5	-	-	45	-	-	-	-	-	10	5	-	-	-	-	-	-	-	-	-
				3	-7.9	-	-	10	40	50	-	5	-	-	8-	-	-	-	-	-	-	60	-	-	-	-	-	-	-	-	-
				4	-8.0	-	-	5	35	60	-	10	-	1	65	<5	-	-	10	-	35	-	-	-	-	-	-	-	-	-	-
				5	-8.1	-	-	10	40	50	-	15	-	2	1-	5	-	-	-	5	-	10	-	-	-	-	-	-	-	-	-
				6	-8.1	-	-	10	40	50	-	5	-	-	15	-	-	-	-	5	15	25	-	-	-	-	-	-	-	-	-
				7	-8.1	-	-	10	40	50	-	15	-	-	4-	-	-	-	-	-	30	5	-	-	-	-	-	-	-	-	-
				8	-8.1	-	10	10	35	45	-	10	-	-	3-	-	-	-	5	-	15	30	-	-	-	-	-	-	-	-	-
				9	-8.1	-	-	20	30	50	-	5	-	-	4-	-	-	-	-	-	30	20	-	-	-	-	-	-	-	-	-

Location/Quadrat Number	Quadrat Sub-number	Invertebrates (Sessile: % cover; Motile: number of Individuals)																											Fish		
		Annelida				Platyhelminthes	Echinodermata		Cnidaria	Mollusca													Crustacea				Tunicata				
		Cone worm *Cistenides granulata*	Small sabellid worm spp. 1 Sabellidae indet.	Large sabellid worm spp. 2 Sabellidae indet.	tubes[1] Polychaeta indet.	Flat worm Platyhelminthes	Brittle star Opiuridae indet.	Green urchin *Strongylocentrotus droebachiensis*	Burrowing anemone Ceriantharia indet.	Margarite snail *Margarites* spp.	Snail Vetigastropoda indet.	Scallop *Similipecten greenlandicus*	Icelandic scallop *Chlamys islandica*	Wrinkled rock-borer *Hiatella arctica*	Blunt gaper *Mya* spp.	Northern astarte *Astarte borealis*	Astarte Clam *Astarte* spp.	Macoma clam *Macoma* spp.	Clam Bivalvia indet.	Limpet Lottiidae indet.	Mussel Mytilida indet.	Green mussel spp. 1 Mytilida indet.	Pandalus shrimp *Pandalus* spp.	Sculptured shrimp *Sclerocrangon boreas*	Barnacle Balanomorpha indet.	Amphipod Amphipoda Indet.	Orange tunicate spp. 1 *Polycarpa* spp.	Tunicate Tunicata indet.	Pout cf. *Gymnelus* spp.	Sculpin Cottidae indet.	Unid. Juvenile fish
Q1	1	6	-	1	-	-	-	2	-	-	-	-	-	60	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	2	-	-	-	-	-	-	1	-	-	-	-	-	40	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	3	-	-	-	-	-	-	-	-	-	-	-	-	40	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	4	5	-	-	-	-	-	1	-	-	-	-	-	20	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	5	6	2	-	-	-	-	-	-	-	-	-	-	40	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	6	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	3	-	-	-	-
	7	5	1	-	-	-	1	-	-	-	-	-	-	16	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	8	2	-	1	-	-	-	-	-	-	-	-	-	40	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	9	3	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Q3	1	-	-	-	-	-	-	1	-	-	-	-	-	40	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	2	2	-	-	-	-	-	1	-	-	-	-	-	20	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	3	5	-	-	-	-	1	2	-	-	-	-	-	16	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	4	-	-	-	-	-	2	1	-	-	-	-	-	30	8	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-
	5	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	6	-	-	-	-	-	-	-	-	-	-	1	-	40	10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	7	26	-	-	-	-	-	-	-	1	-	-	-	10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	8	-	5	-	-	-	3	1	-	-	-	-	-	30	13	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	9	-	2	-	-	-	-	1	-	-	-	-	-	30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Q4	1	2	1	-	-	-	-	3	-	-	-	-	-	30	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	2	3	-	-	-	-	-	1	-	-	-	-	-	20	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	3	2	-	-	-	-	-	1	-	-	-	-	-	20	-	-	-	<1	-	-	-	-	-	-	-	-	-	-	-	-	-
	4	-	-	-	2	-	-	1	-	-	-	-	-	6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	5	2	-	1	-	-	1	-	-	-	-	-	-	6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	6	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-
	7	2	4	2	-	-	-	1	-	-	-	-	1	12	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	8	-	-	-	-	-	-	1	-	-	-	-	-	8	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	9	-	-	-	-	1	-	2	-	-	-	-	-	14	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Q5	1	-	-	3	-	-	-	2	-	-	-	1	1	20	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-
	2	-	-	-	1	-	-	-	-	-	-	-	-	26	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	3	-	-	-	-	-	1	3	-	-	-	-	-	12	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	4	-	-	-	-	-	-	1	-	-	-	-	-	20	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	5	-	-	-	-	-	-	3	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	6	2	-	-	-	-	-	3	-	-	-	-	-	20	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	7	-	-	-	1	-	1	-	-	-	-	-	-	-	-	-	-	-	25	-	-	-	-	-	-	-	-	-	-	-	-
	8	-	-	-	-	-	-	2	-	-	-	-	-	10	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	9	-	-	-	-	-	-	1	-	-	-	1	1	4	-	-	-	-	23	-	-	-	-	-	-	-	-	-	-	-	-
Q6	1	-	-	-	3	-	6	2	-	1	-	1	-	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	2	-	-	-	2	-	6	1	-	-	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	3	-	-	-	-	-	22	1	-	-	-	2	-	-	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-	-	-
	4	-	-	-	-	-	5	-	-	-	-	-	-	12	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	5	-	-	-	-	-	4	-	-	-	-	-	1	8	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-
	6	2	-	-	-	-	5	-	-	-	-	-	-	18	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-
	7	-	-	-	-	-	7	-	-	-	-	1	-	12	3	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-
	8	-	-	-	-	-	1	1	-	-	-	1	-	12	3	-	1	-	<1	-	-	-	-	-	-	-	-	-	-	-	-
	9	-	-	1	-	-	2	1	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Q7	1	2	-	5	-	-	-	-	-	-	-	-	-	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	2	3	1	-	-	-	-	-	-	-	-	-	-	-	3	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-
	3	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	4	-	-	-	-	-	-	-	-	-	-	-	-	4	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-
	5	-	-	-	-	-	-	-	-	-	-	-	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	6	-	-	3	-	-	-	1	10	-	-	-	-	14	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	7	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	8	-	-	2	-	-	1	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	9	-	-	-	-	-	1	-	-	-	-	-	-	8	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-
Q8	1	6	2	-	-	-	-	-	-	-	-	-	-	20	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	2	-	-	-	-	-	-	-	-	-	-	-	-	30	5	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	3	-	1	1	-	-	-	-	-	-	-	-	-	50	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	4	-	-	-	-	-	-	-	-	-	-	-	-	32	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	5	-	-	-	-	-	-	-	-	-	-	-	-	42	-	-	-	-	-	-	3	-	-	-	-	-	-	-	-	-	-
	6	-	-	1	-	-	-	-	-	-	-	-	-	32	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	7	-	2	-	-	-	-	-	-	-	-	-	-	26	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	8	3	-	-	-	-	1	-	-	-	-	-	-	42	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	9	-	-	-	-	-	1	-	-	-	-	-	1	24	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Q10	1	3	-	-	-	-	-	-	-	-	-	-	-	18	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	2	2	1	-	-	-	-	-	-	-	-	-	-	6	-	-	-	-	-	-	3	2	-	-	-	-	-	-	-	-	-
	3	5	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	4	6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	5	6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	6	5	-	-	-	-	-	-	-	-	-	-	-	6	-	-	-	-	-	-	3	-	-	-	-	-	-	-	-	-	-
	7	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	8	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	9	-	2	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	3	-	-	-	-	-	-	-	-	-	-
Q11	1	2	-	-	-	-	-	-	-	-	-	-	-	28	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	2	5	1	-	-	-	-	-	-	-	-	-	-	20	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	3	6	-	-	-	-	-	-	-	-	-	-	-	40	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-
	4	11	-	-	-	-	-	-	-	-	-	-	-	40	-	-	-	-	3	-	-	-	-	-	-	-	5	-	-	-	-
	5	8	-	-	-	-	-	-	-	-	-	-	-	30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	6	5	-	-	-	-	-	-	-	-	-	-	-	20	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	7	-	-	-	-	-	-	-	-	-	-	1	-	20	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	8	12	-	-	-	-	-	-	-	-	-	-	-	30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	9	8	-	-	-	-	-	-	-	-	-	-	-	20	-	-	-	-	-	-	-	-	-	-	-	-	3	-	-	-	-
Q12	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	7	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	8	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	9	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Q13	1	9	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	2	6	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	3	11	-	-	-	-	-	-	-	-	-	-	-	18	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-
	4	5	3	-	-	-	-	-	-	-	-	-	-	12	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	5	8	30	-	-	-	-	-	-	-	-	-	-	20	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	6	15	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	7	15	-	-	-	-	-	-	-	-	-	-	-	40	-	-	-	-	-	-	3	-	-	-	-	-	-	-	-	-	-
	8	5	8	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	9	6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Q14	504350	7976589	16-Aug-21	1	-7.6	-	5	10	35	50	-	10	-	3	45	-	-	-	-	-	30	-	-	-	-	-	-	-	-	-	-	3	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<1	-	-	-	-	-	-	-	-	-	-	-	-
				2	-7.6	-	-	15	45	40	-	<5	-	-	15	-	-	-	-	-	40	-	-	-	-	<1	-	-	-	-	-	9	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				3	-7.7	-	-	5	60	35	-	5	-	-	4-	-	-	-	-	-	40	-	-	-	-	-	-	-	-	-	-	-	10	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				4	-7.6	-	-	10	60	30	-	5	-	-	8-	-	-	-	-	-	40	-	-	-	-	5	-	-	-	-	-	6	13	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				5	-7.6	-	-	10	60	30	-	5	-	-	8-	5	-	-	-	-	30	-	-	-	-	-	-	5	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				6	-7.8	-	-	10	60	30	-	5	-	1	1-	-	-	-	-	-	25	-	-	-	-	-	-	-	-	-	-	3	5	-	-	-	-	-	-	-	-	-	-	10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				7	-7.7	-	-	15	60	25	-	5	-	-	1--	5	-	-	-	-	40	-	-	-	-	-	-	-	-	-	-	3	11	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				8	-7.8	-	-	15	55	25	5	5	-	-	2-	-	-	-	-	-	30	-	-	-	-	-	-	-	-	-	-	3	10	-	-	-	-	-	-	-	-	-	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				9	-7.8	-	-	15	60	25	-	5	-	-	1-	-	-	-	-	-	25	-	-	-	-	-	-	-	-	-	-	-	10	-	-	-	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Q15	504800	7976721	06-Aug-21	1	-7.4	-	-	-	30	70	-	20	-	15	-	-	-	-	10	-	10	15	-	1	-	-	-	<5	-	-	-	6	-	-	-	-	-	-	-	-	-	-	-	20	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				2	-7.4	-	-	-	30	70	-	10	-	2	-	-	-	-	-	-	-	10	-	1	10	-	-	15	-	-	-	8	-	-	-	-	-	-	-	-	-	-	-	24	-	-	-	-	10	-	-	-	-	-	-	-	-	-	-	-	-
				3	-7.4	-	-	-	30	70	-	10	-	-	8-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				4	-7.4	-	-	-	30	70	-	10	-	5	25	-	-	-	10	-	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				5	-7.4	-	-	-	30	70	<5	20	-	7	-	-	-	-	5	-	-	15	-	1	-	-	-	10	-	-	-	8	-	-	-	-	-	-	-	-	-	-	-	40	-	-	-	-	-	-	3	-	-	-	-	-	-	-	-	-	-
				6	-7.4	-	-	-	30	70	-	15	-	5	-	-	-	-	5	-	10	10	-	-	-	-	-	-	-	-	-	8	-	-	1	-	-	-	-	-	-	-	-	40	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				7	-7.6	-	-	-	30	70	-	10	-	7	-	-	-	-	5	-	-	-	20	<5	-	-	-	15	-	-	-	5	-	-	-	-	-	-	-	-	-	-	-	30	-	-	-	-	-	-	3	-	-	-	-	-	-	-	-	-	-
				8	-7.6	-	-	-	30	70	-	15	-	2	-	-	-	-	5	-	-	20	30	-	-	-	-	8	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	20	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				9	-7.5	-	-	-	30	70	-	20	-	2	-	-	-	-	5	-	-	10	-	<5	-	-	-	<5	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	20	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Q16	506567	7979090	08-Aug-21	1	-5.6	-	-	20	20	50	10	5	-	-	2-	-	-	-	15	-	-	-	-	-	-	-	-	-	10	-	-	21	-	-	-	-	-	-	-	-	-	-	-	14	-	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				2	-5.6	-	-	10	25	55	10	10	-	-	-	-	-	-	20	-	-	-	-	-	-	-	-	-	15	-	-	12	-	-	-	-	-	-	-	-	-	-	-	-	3	-	-	-	-	-	3	-	-	-	-	-	3	-	-	1	-
				3	-5.7	-	-	12	23	55	10	10	-	-	-	-	-	-	15	-	-	-	-	-	-	-	-	-	10	-	-	11	-	-	-	-	-	-	-	-	-	-	-	-	13	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				4	-5.7	-	25	12	12	44	7	10	-	-	-	-	-	<5	-	-	-	-	<5	<5	-	-	-	-	10	10	-	5	-	-	-	-	-	-	-	1	-	-	-	6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				5	-5.7	-	-	5	35	60	<5	5	-	-	-	10	-	-	5	-	-	-	-	-	-	-	-	-	-	-	-	8	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				6	-5.7	-	5	10	25	60	<5	5	-	-	-	-	-	-	20	-	-	-	-	-	-	-	-	-	-	-	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				7	-5.7	-	-	20	20	55	5	5	-	-	-	2	-	-	10	-	-	-	-	-	-	-	-	-	-	-	-	11	-	-	-	-	-	-	-	-	1	-	-	-	-	-	1	-	8	-	-	-	-	-	-	-	-	-	-	-	-
				8	-5.8	-	-	20	20	55	5	5	-	-	-	2	-	-	10	-	-	-	-	-	-	-	-	-	-	-	-	6	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				9	-5.9	-	-	-	30	70	-	5	-	-	-	-	-	-	80	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Q17	506774	7979163	16-Aug-21	1	-8.9	-	15	-	15	70	-	-	-	7	7-	-	-	-	-	-	-	-	-	-	-	<5	-	-	-	-	15	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-
				2	-9.0	-	12	-	18	70	-	10	-	<5	-	-	-	-	-	-	45	-	-	-	-	-	-	-	-	-	-	2	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				3	-8.9	-	-	-	20	80	<5	10	-	10	-	-	-	-	10	-	-	-	-	-	-	5	-	<5	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				4	-8.9	-	-	-	20	80	-	10	-	15	-	-	-	-	10	-	5	-	-	-	-	-	-	-	-	-	-	-	6	-	-	-	-	-	-	-	-	-	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				5	-8.9	-	-	-	20	80	-	10	-	-	-	-	-	-	10	-	10	-	-	-	-	-	-	-	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				6	-8.9	-	-	-	20	80	-	10	-	10	-	5	-	-	15	-	20	-	-	-	-	-	-	15	-	-	-	2	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				7	-9.0	-	-	-	20	80	-	10	-	10	-	-	-	-	15	-	40	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				8	-9.0	-	-	-	20	80	-	10	-	-	-	-	-	-	15	-	40	-	-	-	-	-	-	-	-	-	-	2	-	1	-	-	1	-	-	-	-	-	-	6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				9	-9.0	-	-	-	20	80	-	10	-	-	-	10	-	-	-	-	40	-	-	-	-	-	-	10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6	-	-	-	-	-	-	3	-	-	-	-	-	-	-	-	-	-
Q18	506956	7979452	16-Aug-21	1	-9.8	-	-	-	20	80	-	-	-	40	-	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-	-	3	1	-	-	-	-	-	-	-	-	-	-	38	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				2	-10.1	-	-	-	20	80	-	20	-	40	-	-	-	-	-	-	20	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	36	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				3	-10.1	-	-	-	20	80	-	20	-	30	-	-	-	-	-	-	40	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	22	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				4	-10.2	-	-	-	20	80	-	10	-	30	-	-	-	-	<5	-	-	-	-	-	-	-	<5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	24	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
				5	-10.4	-	-	-	20	80	-	15	-	15	-	-	-	-	5	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	22	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				6	-10.4	-	-	-	20	80	-	10	-	30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				7	-10.3	-	-	-	20	80	<5	10	-	20	-	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	18	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				8	-10.3	-	-	-	20	80	<5	10	-	-	-	-	-	-	20	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	46	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				9	-10.3	-	-	-	20	80	<5	5	-	20	-	-	-	-	-	-	-	-	-	-	-	-	<5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Q20	506588	7979125	08-Aug-21	1	-10.9	-	-	-	25	70	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	-	-	2	-	-	-	-	-	-	16	3	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				2	-11.0	-	-	-	25	70	5	-	-	-	-	<5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	-	-	5	-	-	-	-	-	-	46	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				3	-11.1	-	-	-	25	70	5	-	-	-	-	<5	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-	8	-	3	-	-	-	-	-	-	-	-	-	60	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				4	-11.2	-	-	-	25	70	5	-	-	-	5	<5	-	-	10	-	5	-	-	-	-	-	-	-	-	-	-	3	-	-	-	-	-	-	-	1	-	-	-	6	-	-	<1	-	-	-	-	-	-	-	-	-	3	-	-	-	-
				5	-11.3	50	-	-	5	40	5	-	-	-	-	-	-	-	-	-	25	-	-	-	-	-	-	-	-	-	10	6	-	-	-	-	-	-	-	-	-	-	1	14	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-
				6	-11.4	-	-	-	25	70	5	-	-	-	-	-	-	-	-	-	15	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	26	-	5	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-
				7	-11.3	-	-	-	25	70	5	-	-	-	-	-	-	-	<2	-	-	-	-	-	-	-	-	-	-	-	-	5	-	-	-	-	3	-	-	-	-	-	-	4	-	-	5	-	-	-	3	-	-	-	-	-	-	-	-	-	-
				8	-11.2	-	-	-	25	70	5	-	-	-	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6	-	-	-	-	-	-	-	-	-	-	-	10	-	-	<1	-	<1	-	-	-	-	-	-	-	-	-	-	-	-
				9	-11.2	-	-	-	25	70	5	-	-	-	5	-	-	-	<2	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	-	-	1	-	-	-	-	-	-	20	-	-	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-

Notes: P = Present [1]Tubes: likley sabellid worm, though animal inside tube was not observed during survey. Grey highlighting indicates sessile invertebrates

APPENDIX 5D

ANOVA and ANCOVA Analysis

APP 5D_ANOVA/ANCOVA 2021

NOB

14 February 2022

```
## -- Attaching packages --------------------------------------- tidyverse
1.3.1 --

## v ggplot2 3.3.5     v purrr   0.3.4
## v tibble  3.1.6     v dplyr   1.0.7
## v tidyr   1.2.0     v stringr 1.4.0
## v readr   2.1.2     v forcats 0.5.1

## -- Conflicts ------------------------------------------
tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()

##
## Attaching package: 'rstatix'

## The following object is masked from 'package:stats':
##
##     filter

## Loading required package: carData

##
## Attaching package: 'car'

## The following object is masked from 'package:dplyr':
##
##     recode

## The following object is masked from 'package:purrr':
##
##     some
```

```
# Correlation Tests for Substrate

## Bedrock - Depth
cor.test(anco.quad$depth, anco.quad$bedrock, method = "pearson")

##
##  Pearson's product-moment correlation
##
## data:  anco.quad$depth and anco.quad$bedrock
## t = -0.66622, df = 15, p-value = 0.5154
## alternative hypothesis: true correlation is not equal to 0
```

```
## 95 percent confidence interval:
##  -0.6011856  0.3387175
## sample estimates:
##        cor
## -0.1695267
```

```
## Bedrock ~ Fines
cor.test(anco.quad$fines, anco.quad$bedrock, method = "pearson")
```

```
##
##  Pearson's product-moment correlation
##
## data:  anco.quad$fines and anco.quad$bedrock
## t = 0.46907, df = 15, p-value = 0.6458
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.3825153  0.5680520
## sample estimates:
##       cor
## 0.1202352
```

```
## Boulder ~ Depth
cor.test(anco.quad$depth, anco.quad$boulder, method = "pearson")
```

```
##
##  Pearson's product-moment correlation
##
## data:  anco.quad$depth and anco.quad$boulder
## t = NA, df = 15, p-value = NA
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  NA NA
## sample estimates:
## cor
##  NA
```

```
# Boulder ~ Fines
cor.test(anco.quad$fines, anco.quad$boulder, method = "pearson")
```

```
##
##  Pearson's product-moment correlation
##
## data:  anco.quad$fines and anco.quad$boulder
## t = NA, df = 15, p-value = NA
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  NA NA
## sample estimates:
## cor
##  NA
```

```r
## Cobble ~ Depth
cor.test(anco.quad$depth, anco.quad$cobble, method = "pearson")

##
##  Pearson's product-moment correlation
##
## data:  anco.quad$depth and anco.quad$cobble
## t = 0.91804, df = 15, p-value = 0.3731
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.2811681  0.6403075
## sample estimates:
##       cor
## 0.2306467

## Cobble ~ Fines
cor.test(anco.quad$fines, anco.quad$cobble, method = "pearson")

##
##  Pearson's product-moment correlation
##
## data:  anco.quad$fines and anco.quad$cobble
## t = 0.5413, df = 15, p-value = 0.5963
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.3666191  0.5804448
## sample estimates:
##       cor
## 0.1384165

## Gravel ~ Depth
cor.test(anco.quad$depth, anco.quad$gravel, method = "pearson")

##
##  Pearson's product-moment correlation
##
## data:  anco.quad$depth and anco.quad$gravel
## t = 2.4288, df = 15, p-value = 0.02819
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.06801017 0.80608910
## sample estimates:
##       cor
## 0.5312878

## Gravel ~ Fines
cor.test(anco.quad$fines, anco.quad$gravel, method = "pearson")

##
##  Pearson's product-moment correlation
##
```

```
## data:  anco.quad$fines and anco.quad$gravel
## t = -1.2526, df = 15, p-value = 0.2295
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.6867865  0.2029402
## sample estimates:
##        cor
## -0.3077203
```

```
## Sand ~ Depth
cor.test(anco.quad$depth, anco.quad$sand, method = "pearson")
```

```
##
##  Pearson's product-moment correlation
##
## data:  anco.quad$depth and anco.quad$sand
## t = 1.6648, df = 15, p-value = 0.1167
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.1058280  0.7358735
## sample estimates:
##       cor
## 0.3949038
```

```
## Sand ~ Fines
cor.test(anco.quad$fines, anco.quad$sand, method = "pearson")
```

```
##
##  Pearson's product-moment correlation
##
## data:  anco.quad$fines and anco.quad$sand
## t = -11.947, df = 15, p-value = 4.593e-09
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.9826296 -0.8670476
## sample estimates:
##        cor
## -0.9512617
```

```
## Shell ~ Depth
cor.test(anco.quad$depth, anco.quad$shell, method = "pearson")
```

```
##
##  Pearson's product-moment correlation
##
## data:  anco.quad$depth and anco.quad$shell
## t = -0.87214, df = 15, p-value = 0.3969
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.6334445  0.2917671
## sample estimates:
```

```
##        cor
## -0.2196856
```

```
## Shell ~ Fines
cor.test(anco.quad$fines, anco.quad$shell, method = "pearson")
```

```
##
##  Pearson's product-moment correlation
##
## data:  anco.quad$fines and anco.quad$shell
## t = 0.17732, df = 15, p-value = 0.8616
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.4446836  0.5150589
## sample estimates:
##       cor
## 0.0457367
```

```
## Detrial veneer ~ Depth
cor.test(anco.quad$depth, anco.quad$detrital.veneer, method = "pearson")
```

```
##
##  Pearson's product-moment correlation
##
## data:  anco.quad$depth and anco.quad$detrital.veneer
## t = 0.65806, df = 15, p-value = 0.5205
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.3405540  0.5998583
## sample estimates:
##       cor
## 0.1675097
```

```
## Detrial veneer ~ Fines
cor.test(anco.quad$fines, anco.quad$detrital.veneer, method = "pearson")
```

```
##
##  Pearson's product-moment correlation
##
## data:  anco.quad$fines and anco.quad$detrital.veneer
## t = -0.19659, df = 15, p-value = 0.8468
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.5187005  0.4406881
## sample estimates:
##         cor
## -0.05069443
```

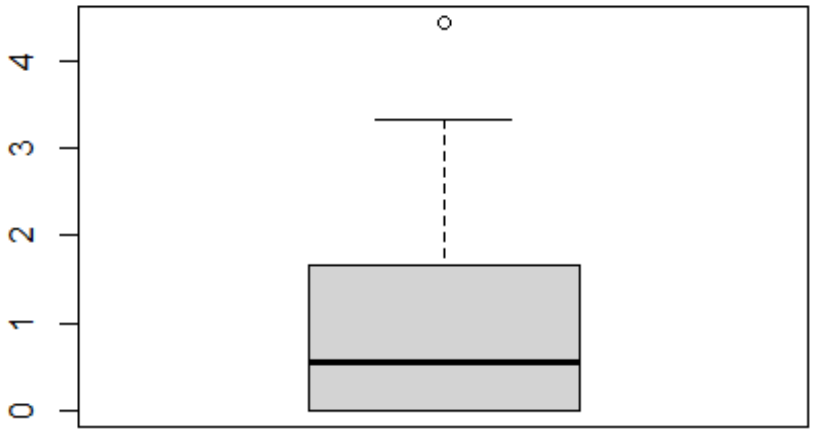
```
## Debris other - Depth
cor.test(anco.quad$depth, anco.quad$debris.other, method = "pearson")
```

```
##
##  Pearson's product-moment correlation
##
## data:  anco.quad$depth and anco.quad$debris.other
## t = -1.8869, df = 15, p-value = 0.07869
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.75886822  0.05405098
## sample estimates:
##       cor
## -0.437972
```

```
## Debris other - Fines
cor.test(anco.quad$fines, anco.quad$debris.other, method = "pearson")
```

```
##
##  Pearson's product-moment correlation
##
## data:  anco.quad$fines and anco.quad$debris.other
## t = 0.91468, df = 15, p-value = 0.3748
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.2819455  0.6398091
## sample estimates:
##       cor
## 0.2298472
```

```
# Assumption Testing for ANOVA/ANCOVA

## Cobble, covariate = na
### Outliers
boxplot(anco.quad$cobble)
```



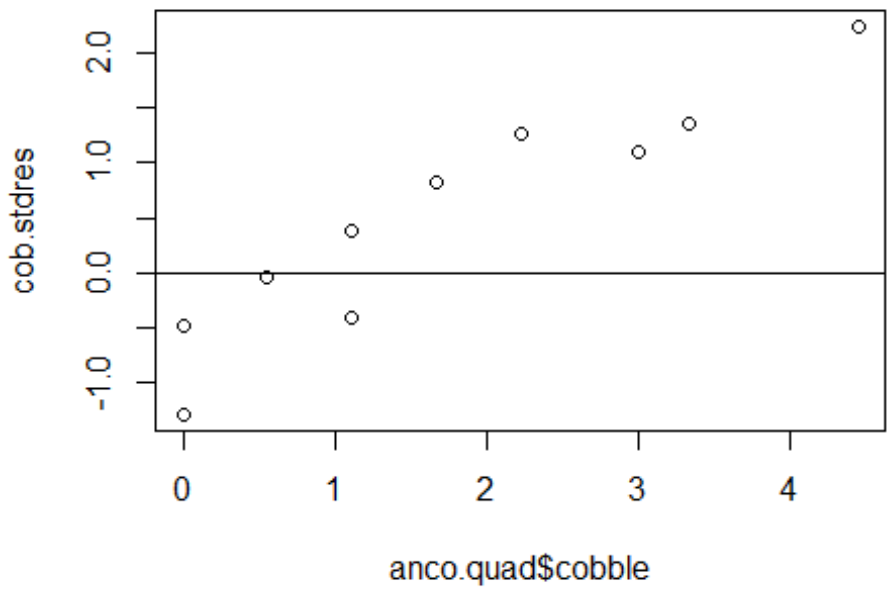

```
boxplot.stats(anco.quad$cobble)$out # 4.444, 3.333
```

```
## [1] 4.444444
```

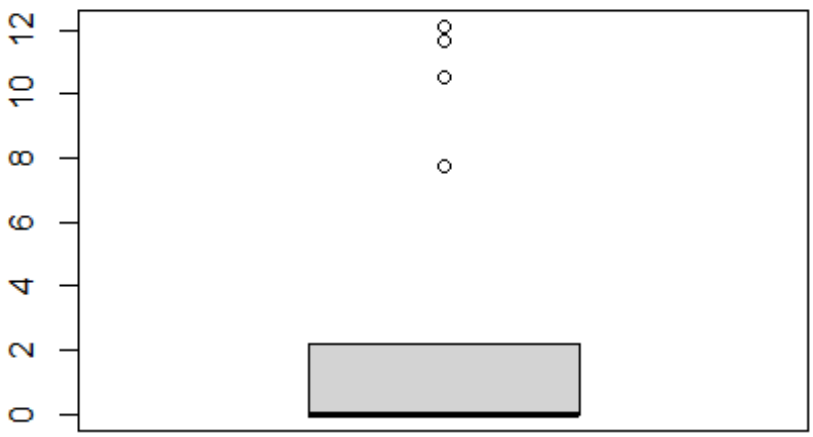
```
model.cob.0 <- lm(cobble ~ site, data = anco.quad)
cob.stdres <- rstandard(model.cob.0)
cob.stdres
```

```
##           1           2           3           4           5           6
## -0.48766062 -0.48766062  1.26791762 -0.48766062 -0.48766062  0.39012850
##           7           8           9          10          11          12
##  0.82902306 -0.04876606 -0.48766062 -1.29391510  2.24499799 -0.40918683
##          13          14          15          16          17
## -0.40918683  1.36026972  1.09485124 -1.29391510 -1.29391510
```

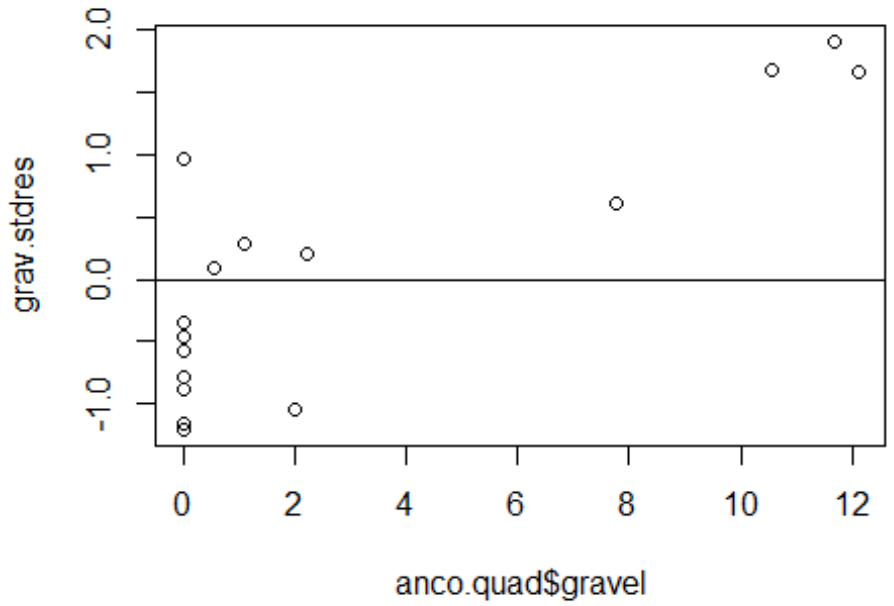
```
plot(anco.quad$cobble, cob.stdres)
abline(0,0)
```




```
### Normality of Residuals
model.cob <- lm(cobble ~  site, data = anco.quad)
shapiro.test(model.cob$residuals)

##
##  Shapiro-Wilk normality test
##
## data:  model.cob$residuals
## W = 0.90107, p-value = 0.0708

### Homogeneity of Variance
leveneTest(model.cob$residuals ~ site, data = anco.quad)

## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1  2.3135  0.149
##       15

## Gravel, covariate = Depth
### Outliers
boxplot(anco.quad$gravel)
```




```
boxplot.stats(anco.quad$gravel)$out

## [1] 10.555556 11.666667  7.777778 12.111111

model.grv.0 <- lm(gravel ~ depth + site, data = anco.quad)
grav.stdres <- rstandard(model.grv.0)
plot(anco.quad$gravel, grav.stdres)
abline(0,0)
```

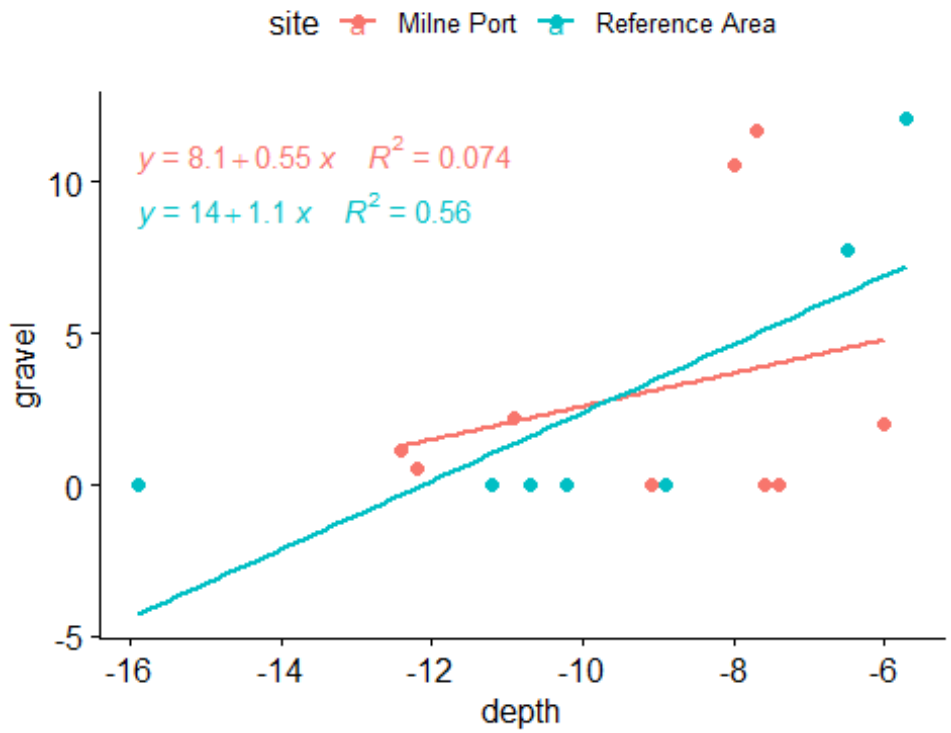



```
### Normality of Residuals
model.grv <- lm(gravel ~ depth + site, data = anco.quad)
shapiro.test(model.grv$residuals)

##
##  Shapiro-Wilk normality test
##
## data:  model.grv$residuals
## W = 0.91194, p-value = 0.1079

### Homogeneity of Regression Slopes
anco.quad %>% anova_test(gravel ~ site*depth)

## Coefficient covariances computed by hccm()

## ANOVA Table (type II tests)
##
##       Effect DFn DFd     F     p p<.05     ges
## 1       site   1  13 0.006 0.938       0.00048
## 2      depth   1  13 5.218 0.040     * 0.28600
## 3 site:depth   1  13 0.496 0.494       0.03700

### Homogeneity of Variance
levene_test(model.grv$residuals ~ site, data = anco.quad)

## # A tibble: 1 x 4
##     df1   df2 statistic     p
```

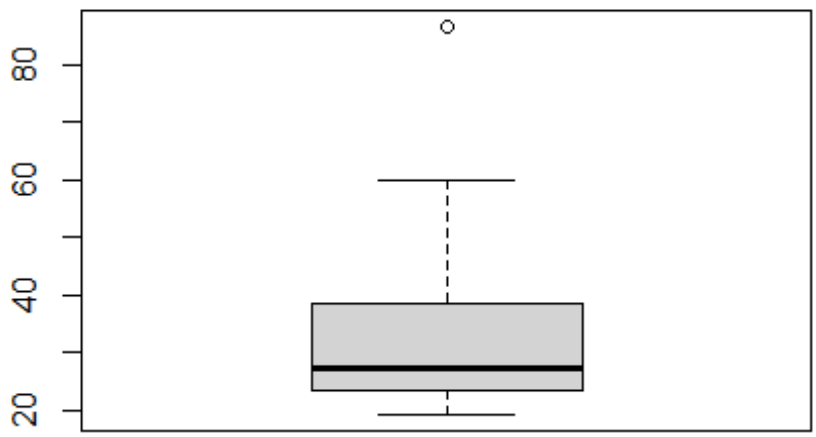
```
##   <int> <int>     <dbl> <dbl>
## 1     1    15     0.795 0.387
```

```
### Linearity
ggscatter(
  anco.quad, x = "depth", y = "gravel",
  color = "site", add = "reg.line"
)+
  stat_regline_equation(
    aes(label = paste(..eq.label.., ..rr.label.., sep = "~~~~"), color =
site)
  )
```

```
## `geom_smooth()` using formula 'y ~ x'
```




```
## Sand, covariate = na
### Outliers
boxplot(anco.quad$sand)
```



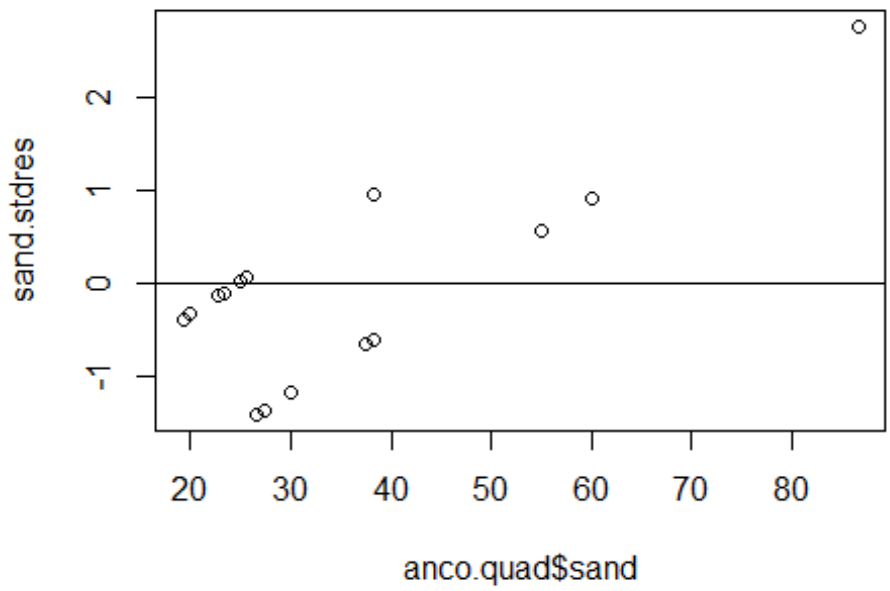

```
boxplot.stats(anco.quad$sand)$out
```

```
## [1] 86.66667
```

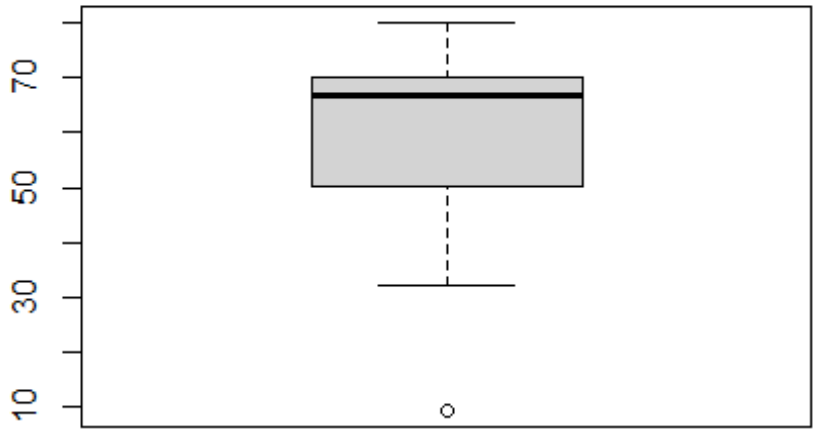
```
model.sand <- lm(sand ~ site, data = anco.quad)
sand.stdres <- rstandard(model.sand)
sand.stdres
```

```
##           1           2           3           4           5           6
##  0.91687018 -0.59261121 -1.35896331 -1.40540889  0.91687018  2.77469344
##           7           8           9          10          11          12
## -0.64679773  0.56852832 -1.17318098  0.02633217  0.06534279  0.96258709
##          13          14          15          16          17
## -0.12971032 -0.09069970 -0.37937829 -0.32476342 -0.12971032
```

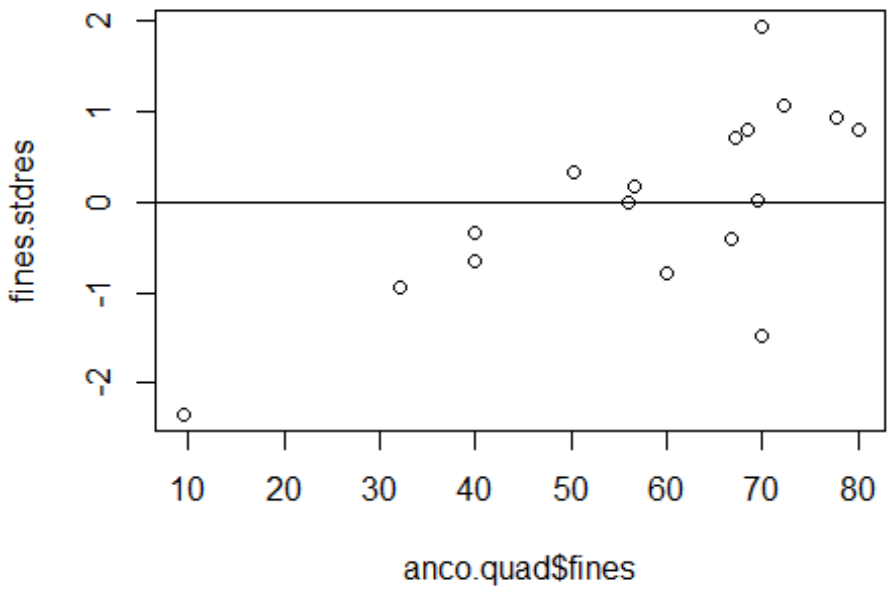
```
plot(anco.quad$sand, sand.stdres)
abline(0,0)
```




```
###Log transformation
anco.quad$sand.LOG <- log10(anco.quad$sand)
### Normality of Residuals
model.snd <- lm(sand.LOG ~ site, data = anco.quad)
shapiro.test(model.snd$residuals)

##
##  Shapiro-Wilk normality test
##
## data:  model.snd$residuals
## W = 0.96451, p-value = 0.7171

### Homogeneity of Variance
levene_test(model.snd$residuals ~ site, data = anco.quad)

## # A tibble: 1 x 4
##     df1   df2 statistic      p
##   <int> <int>     <dbl>  <dbl>
## 1     1    15      4.04 0.0628

### Fines, covariate = Depth
### Outliers
boxplot(anco.quad$fines)
```




```
boxplot.stats(anco.quad$fines)$out

## [1] 9.444444

model.fines <- lm(fines ~ depth + site, data = anco.quad)
fines.stdres <- rstandard(model.fines)
plot(anco.quad$fines, fines.stdres)
abline(0,0)
```

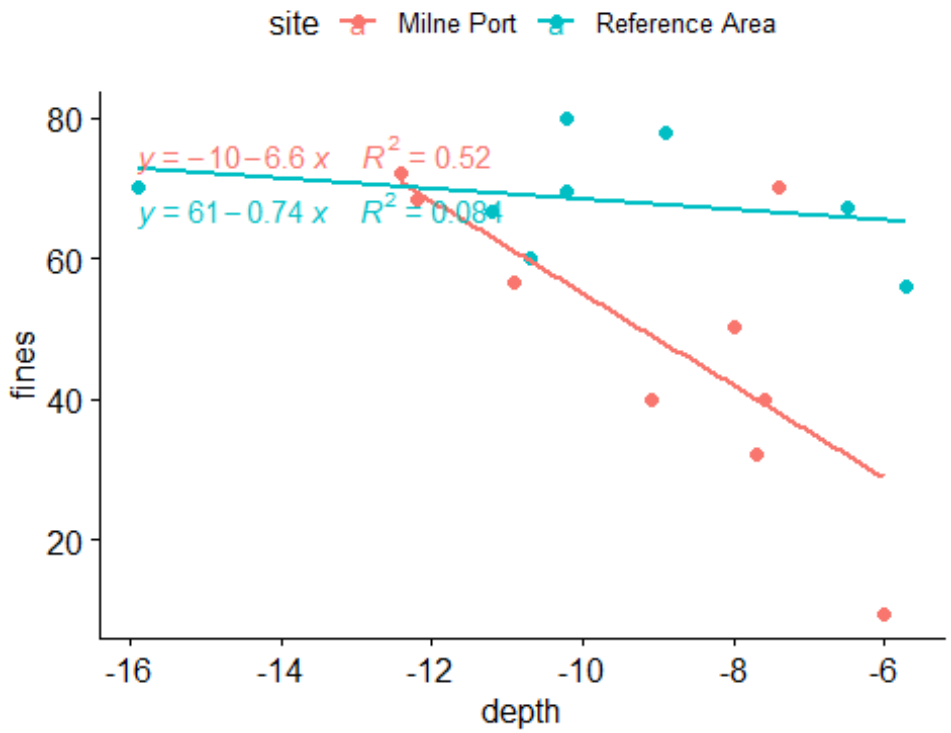



```
### Normality of Residuals
model.fine <- lm(fines ~ depth + site, data = anco.quad)
shapiro.test(model.fine$residuals)

##
##  Shapiro-Wilk normality test
##
## data:  model.fine$residuals
## W = 0.98147, p-value = 0.9693

### Homogeneity of Regression Slopes
anco.quad %>% anova_test(fines ~ site*depth)

## Coefficient covariances computed by hccm()

## ANOVA Table (type II tests)
##
##       Effect DFn DFd     F     p p<.05   ges
## 1       site   1  13 7.551 0.017     * 0.367
## 2      depth   1  13 6.029 0.029     * 0.317
## 3 site:depth   1  13 5.548 0.035     * 0.299

### Homogeneity of Variance
levene_test(model.fine$residuals ~ site, data = anco.quad)

## # A tibble: 1 x 4
##     df1   df2 statistic     p
```

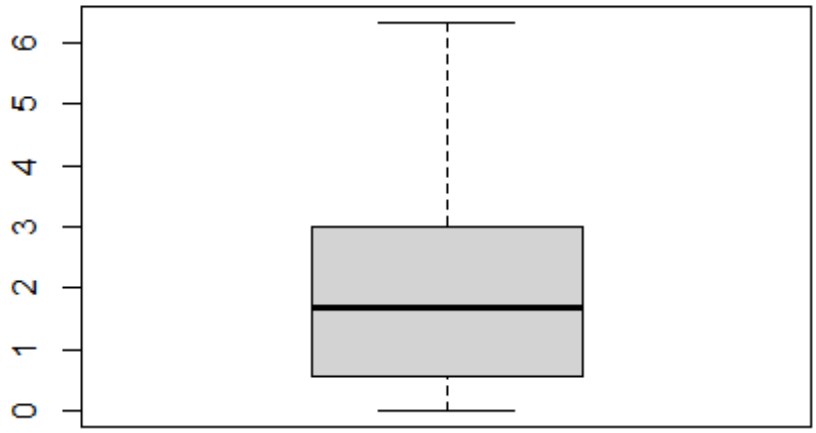
```
##   <int> <int>     <dbl> <dbl>
## 1     1    15      1.06 0.319
```

```
### Linearity
ggscatter(
  anco.quad, x = "depth", y = "fines",
  color = "site", add = "reg.line"
)+
  stat_regline_equation(
    aes(label = paste(..eq.label.., ..rr.label.., sep = "~~~~"), color =
site)
  )
```

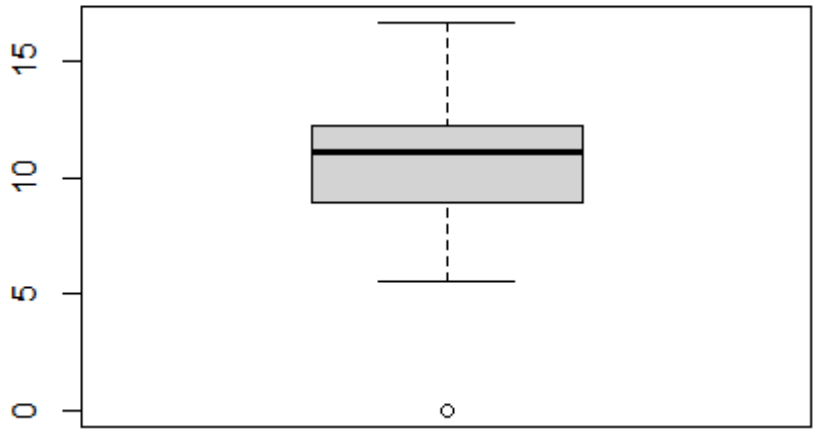
```
## `geom_smooth()` using formula 'y ~ x'
```




```
### Shell, covariate = na
### Outliers
boxplot(anco.quad$shell)
```




```
boxplot.stats(anco.quad$shell)$out

## numeric(0)

### Normality of Residuals
model.shell <- lm(shell ~  site, data = anco.quad)
shapiro.test(model.shell$residuals)

##
##  Shapiro-Wilk normality test
##
## data:  model.shell$residuals
## W = 0.93159, p-value = 0.2314

### Homogeneity of Variance
leveneTest(model.shell$residuals ~ site, data = anco.quad)

## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1  2.4423  0.139
##       15

### Detrital Veneer, covariate = na \
### Outliers
boxplot(anco.quad$detrital.veneer)
```



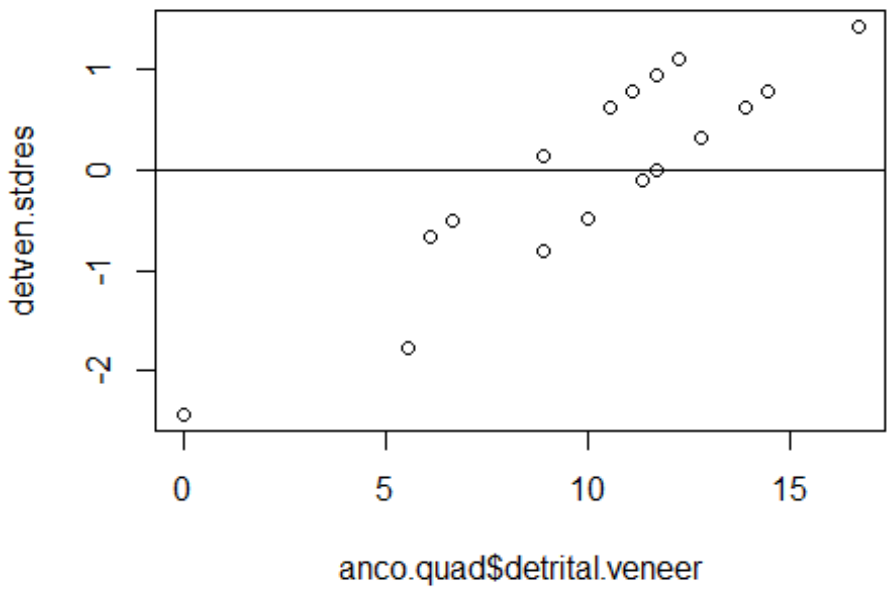

```
boxplot.stats(anco.quad$detrital.veneer)$out
```

```
## [1] 0
```

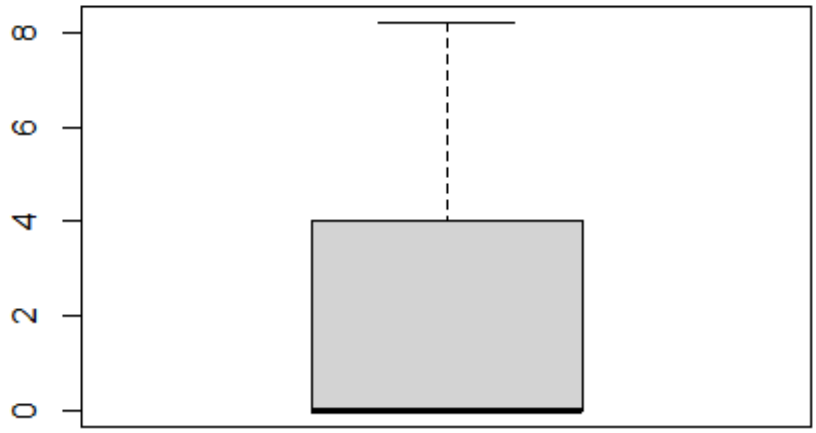
```
model.detven <- lm(detrital.veneer ~ site, data = anco.quad)
detven.stdres <- rstandard(model.detven)
detven.stdres
```

```
##            1            2            3            4            5
6
## -0.007116307 -0.103186471 -0.487467115  1.433936114  0.633351435
0.313117564
##            7            8            9           10           11
12
## -0.807700987 -1.768402601  0.793468369 -0.665703646  0.625357971
0.948123375
##           13           14           15           16           17
##  1.109506075 -0.504320944  0.141209864  0.786740671 -2.440913367
```

```
plot(anco.quad$detrital.veneer, detven.stdres)
abline(0,0)
```

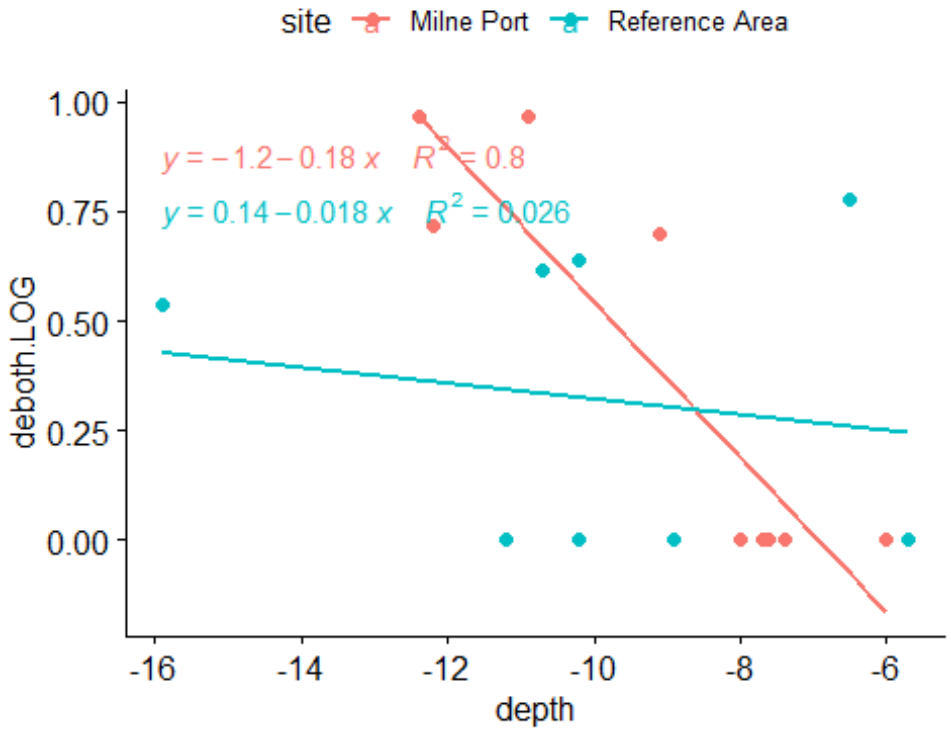



```
### Normality of Residuals
model.det.ven <- lm(detrital.veneer ~  site, data = anco.quad)
shapiro.test(model.det.ven$residuals)

##
##  Shapiro-Wilk normality test
##
## data:  model.det.ven$residuals
## W = 0.93467, p-value = 0.2603

### Homogeneity of Variance
leveneTest(model.det.ven$residuals ~ site, data = anco.quad)

## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1  0.2027  0.659
##       15

### Debris Other, covariate = Depth
### Outliers
boxplot(anco.quad$debris.other)
```

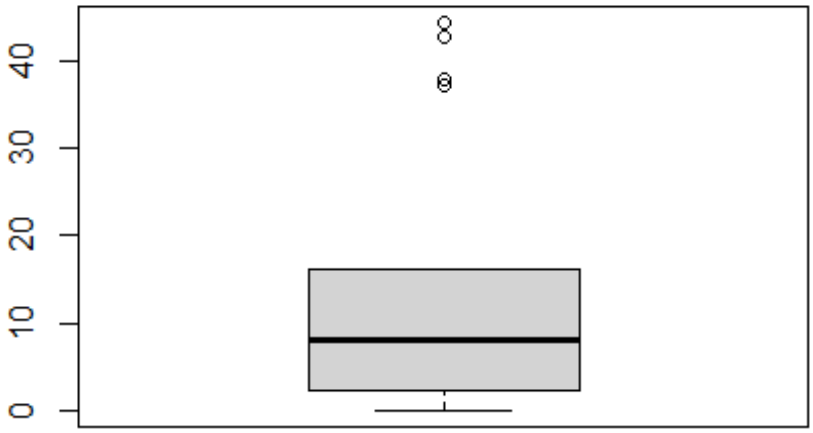



```
boxplot.stats(anco.quad$debris.other)$out

## numeric(0)

### Log transformation
anco.quad$deboth.LOG <- log10(anco.quad$debris.other + 1)
### Normality of Residuals
model <- lm(deboth.LOG ~ depth + site, data = anco.quad)
shapiro.test(model$residuals)

##
##  Shapiro-Wilk normality test
##
## data:  model$residuals
## W = 0.8997, p-value = 0.06715

### Homogeneity of Regression Slopes
anco.quad %>% anova_test(deboth.LOG ~ site*depth)

## Coefficient covariances computed by hccm()

## ANOVA Table (type II tests)
##
##       Effect DFn DFd     F     p p<.05   ges
## 1       site   1  13 0.666 0.429       0.049
## 2      depth   1  13 7.584 0.016     * 0.368
## 3 site:depth   1  13 7.438 0.017     * 0.364
```

```
### Homogeneity of Variance
levene_test(model$residuals ~ site, data = anco.quad)

## # A tibble: 1 x 4
##     df1   df2 statistic     p
##   <int> <int>     <dbl> <dbl>
## 1     1    15     0.345 0.566

### Linearity
ggscatter(
  anco.quad, x = "depth", y = "deboth.LOG",
  color = "site", add = "reg.line"
)+
  stat_regline_equation(
    aes(label = paste(..eq.label.., ..rr.label.., sep = "~~~~"), color =
site)
  )

## `geom_smooth()` using formula 'y ~ x'
```




```
### Detrital algae, covariate = na \
### Outliers
boxplot(anco.quad$detrital.algae)
```



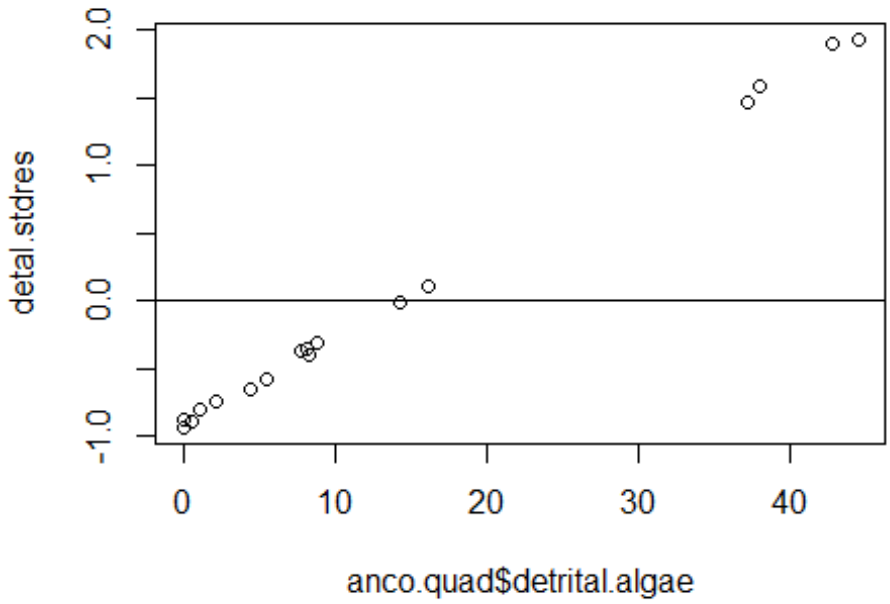

```
boxplot.stats(anco.quad$detrital.algae)$out
```

```
## [1] 37.22222 44.44444 38.00000 42.77778
```

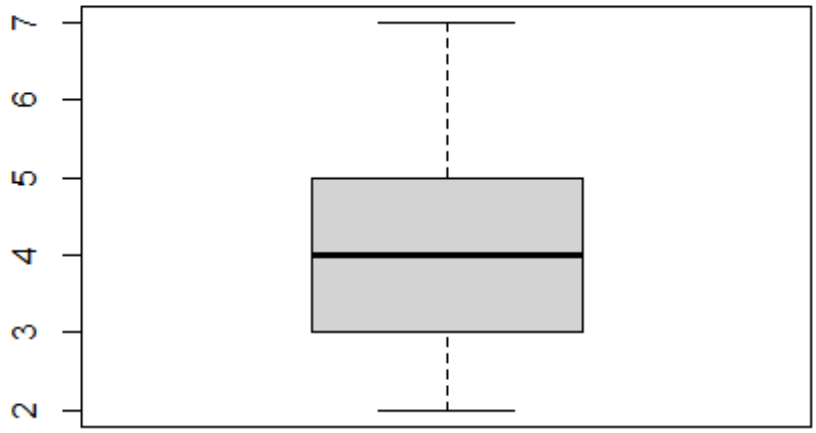
```
model.detal <- lm(detrital.algae ~ site, data = anco.quad)
detal.stdres <- rstandard(model.detal)
detal.stdres
```

```
##           1           2           3           4           5           6
## -0.40105445 -0.01355452 -0.65221181 -0.58762849 -0.93924879 -0.90336917
##           7           8           9          10          11          12
##  1.46468593  1.93112102  0.10126027  1.58847122  1.89947526 -0.35711220
##          13          14          15          16          17
## -0.31371628 -0.74044276 -0.37881015 -0.88509580 -0.81276928
```

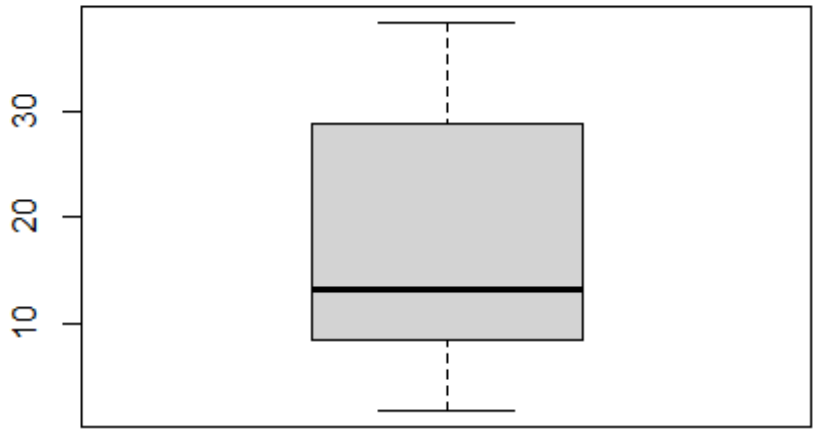
```
plot(anco.quad$detrital.algae, detal.stdres)
abline(0,0)
```




```
### Log transformation
anco.quad$detal.LOG <- log10(anco.quad$detrital.algae + 1)
### Normality of Residuals
model.det.al <- lm(detal.LOG ~  site, data = anco.quad)
shapiro.test(model.det.al$residuals)

##
##  Shapiro-Wilk normality test
##
## data:  model.det.al$residuals
## W = 0.93994, p-value = 0.3175

### Homogeneity of Variance
leveneTest(model.det.al$residuals ~ site, data = anco.quad)

## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1  0.0035 0.9537
##       15

## Macroflora Taxa Richness, covariate = na
### Outliers
boxplot(anco.quad$macro.taxa.richness)
```

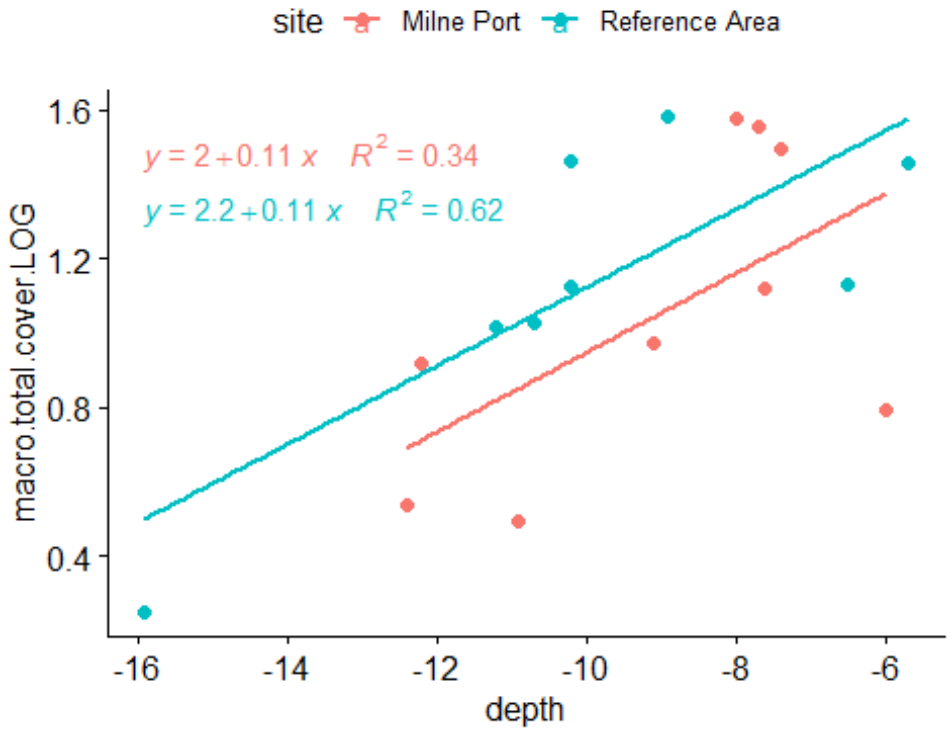



```
boxplot.stats(anco.quad$macro.taxa.richness)$out

## integer(0)

### Normalty of Residuals
model.mtr <- lm(macro.taxa.richness ~  site, data = anco.quad)
shapiro.test(model.mtr$residuals)

##
##  Shapiro-Wilk normality test
##
## data:  model.mtr$residuals
## W = 0.921, p-value = 0.1535

###  Homogeneity of Variance
leveneTest(model.mtr$residuals ~ site, data = anco.quad)

## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1  1.0787 0.3154
##       15

## Macroflora Total Cover, covariate = Depth
###  OUTLIERS
boxplot(anco.quad$macro.total.cover, y = "macro.total.cover")
```

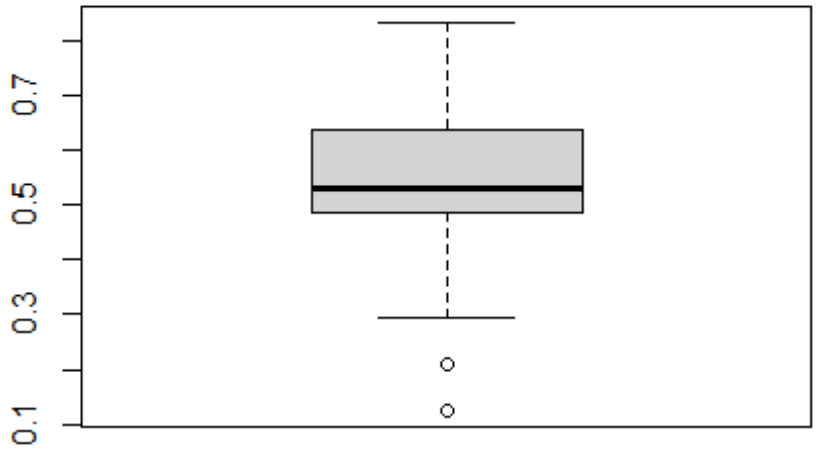



```
boxplot.stats(anco.quad$macro.total.cover)$out

## numeric(0)

### Log transformation
anco.quad$macro.total.cover.LOG <- log10(anco.quad$macro.total.cover)
###  Normality of Residuals
model <- lm(macro.total.cover.LOG ~ depth + site, data = anco.quad)
shapiro.test(model$residuals)

##
##  Shapiro-Wilk normality test
##
## data:  model$residuals
## W = 0.95049, p-value = 0.4644

###  Homogeneity of Regression Slopes
anco.quad %>% anova_test(macro.total.cover.LOG ~ site*depth)

## Coefficient covariances computed by hccm()

## ANOVA Table (type II tests)
##
##       Effect DFn DFd        F     p p<.05      ges
## 1       site   1  13  1.16900 0.299       8.20e-02
## 2      depth   1  13 11.67200 0.005     * 4.73e-01
## 3 site:depth   1  13  0.00044 0.984       3.38e-05
```

```
###  Homogeneity of Variance
levene_test(model$residuals ~ site, data = anco.quad)

## # A tibble: 1 x 4
##     df1   df2 statistic     p
##   <int> <int>     <dbl> <dbl>
## 1     1    15     0.903 0.357

###  Linearity
ggscatter(
  anco.quad, x = "depth", y = "macro.total.cover.LOG",
  color = "site", add = "reg.line"
)+
  stat_regline_equation(
    aes(label = paste(..eq.label.., ..rr.label.., sep = "~~~~"), color =
site)
)

## `geom_smooth()` using formula 'y ~ x'
```




```
## Macroflora SDI, covariate = fines
### Outliers
boxplot(anco.quad$macro.sdi)
```



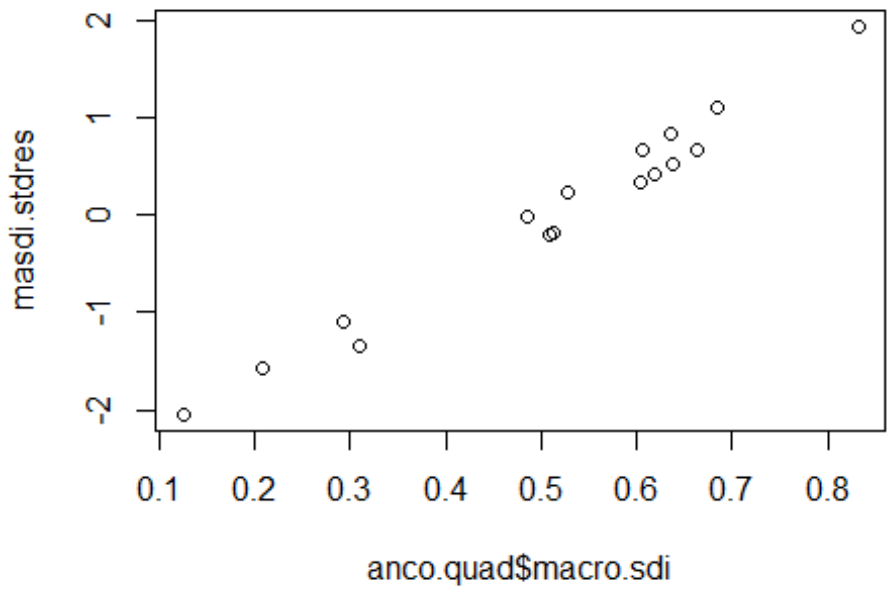

```
boxplot.stats(anco.quad$macro.sdi)$out
```

```
## [1] 0.2076125 0.1249988
```

```
model.masdi <- lm(macro.sdi ~ site, data = anco.quad)
masdi.stdres <- rstandard(model.masdi)
masdi.stdres
```

```
##           1           2           3           4           5           6
## -1.58029479  0.22270899 -0.02270065  0.82887856  1.10413233 -1.09779522
##           7           8           9          10          11          12
##  0.65862240 -2.04512029  1.93156868 -0.21239795  0.41441887 -0.18778435
##          13          14          15          16          17
## -1.33368806 -0.21278432  0.33588527  0.66876919  0.52758135
```

```
plot(anco.quad$macro.sdi, masdi.stdres)  # no outliers with res > 3.5
```

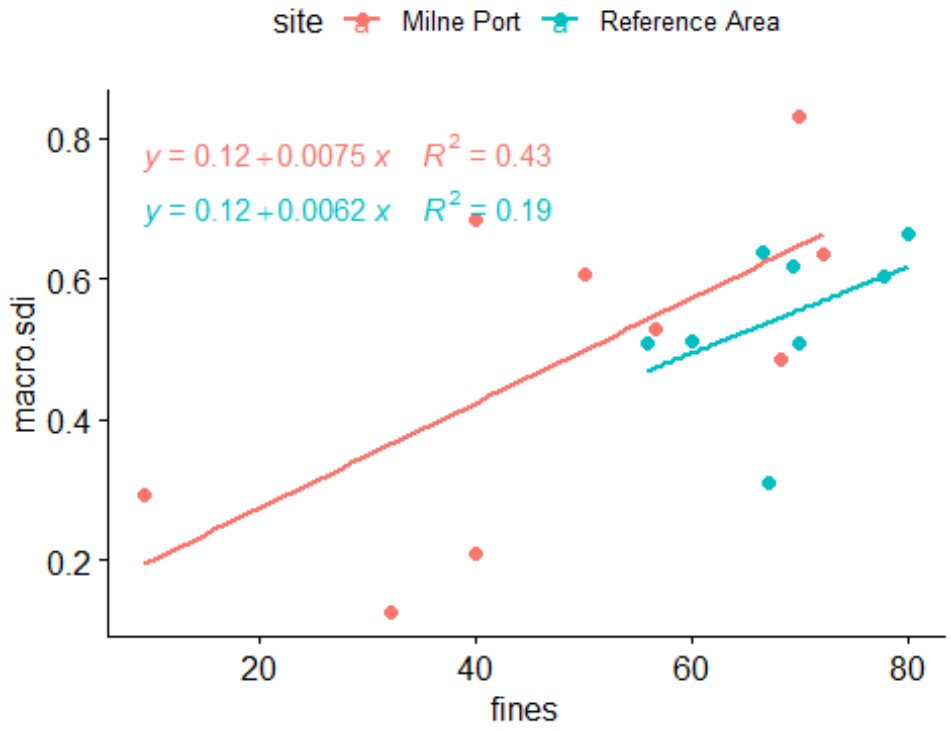



```
### Normality of Residuals
model <- lm(macro.sdi ~ fines + site, data = anco.quad)
shapiro.test(model$residuals) # p-value = 0.1696

##
##  Shapiro-Wilk normality test
##
## data:  model$residuals
## W = 0.9503, p-value = 0.4613

### Homogeneity of Regression Slopes
anco.quad %>% anova_test(macro.sdi ~ site*fines)

## Coefficient covariances computed by hccm()

## ANOVA Table (type II tests)
##
##       Effect DFn DFd     F     p p<.05   ges
## 1       site   1  13 0.897 0.361       0.065
## 2      fines   1  13 8.316 0.013     * 0.390
## 3 site:fines   1  13 0.028 0.870       0.002

### Homogeneity of Variance
levene_test(model$residuals ~ site, data = anco.quad)

## # A tibble: 1 x 4
##     df1   df2 statistic      p
```

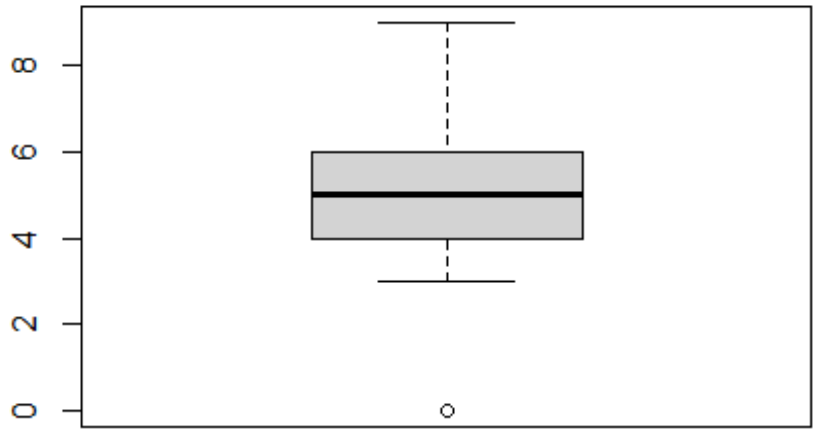
```
##   <int> <int>     <dbl>  <dbl>
## 1     1    15      3.17 0.0954
```

```
### Linearity
ggscatter(
  anco.quad, x = "fines", y = "macro.sdi",
  color = "site", add = "reg.line"
)+
  stat_regline_equation(
    aes(label = paste(..eq.label.., ..rr.label.., sep = "~~~~"), color =
site)
  )
```

```
## `geom_smooth()` using formula 'y ~ x'
```




```
## Sessile Taxa Richness, covariate = fines
### Outliers
boxplot(anco.quad$sessile.taxa.richness)
```



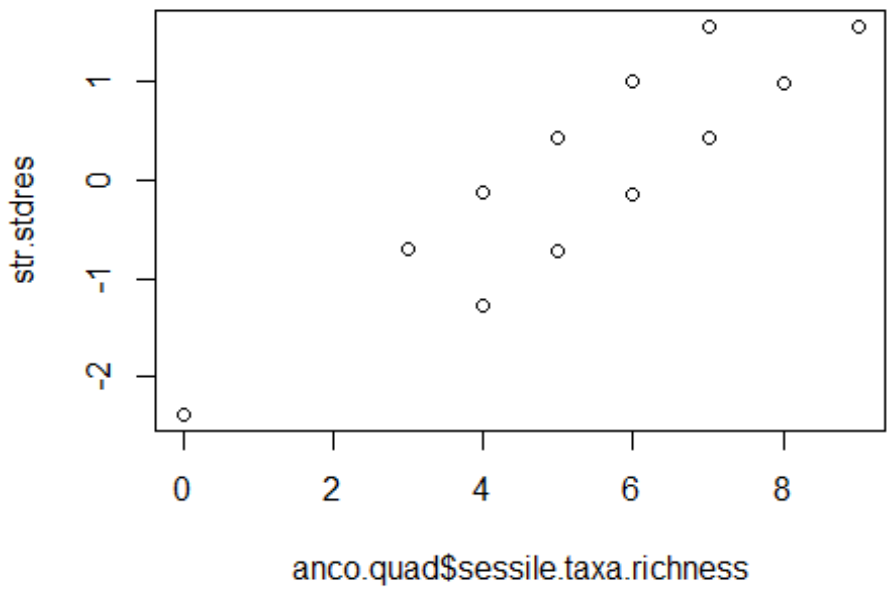

```
boxplot.stats(anco.quad$sessile.taxa.richness)$out
```

```
## [1] 0
```

```
model.str <- lm(sessile.taxa.richness ~ site, data = anco.quad)
str.stdres <- rstandard(model.str)
str.stdres
```

```
##          1          2          3          4          5          6
7
##  0.4386438  0.4386438  1.5665850  0.4386438  1.0026144 -2.3812092 -
0.1253268
##          8          9         10         11         12         13
14
## -0.6892974 -0.6892974 -0.1421072  0.4263217  0.9947506 -1.2789651 -
0.1421072
##         15         16         17
## -0.7105362 -0.7105362  1.5631795
```

```
plot(anco.quad$sessile.taxa.richness, str.stdres)  # no outliers with res >
3.5
```

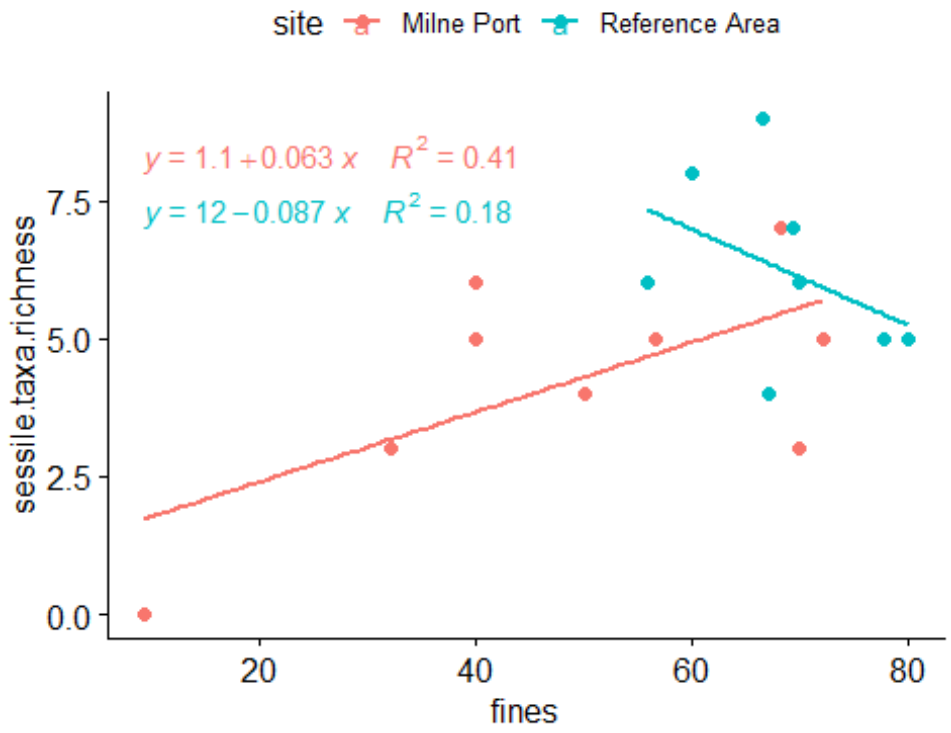



```
### Normality of Residuals
model <- lm(sessile.taxa.richness ~ fines + site, data = anco.quad)
shapiro.test(model$residuals) # p-value = 0.1696

##
##  Shapiro-Wilk normality test
##
## data:  model$residuals
## W = 0.94172, p-value = 0.3391

### Homogeneity of Regression Slopes
anco.quad %>% anova_test(sessile.taxa.richness ~ site*fines)

## Coefficient covariances computed by hccm()

## ANOVA Table (type II tests)
##
##       Effect DFn DFd     F     p p<.05   ges
## 1       site   1  13 1.388 0.260       0.096
## 2      fines   1  13 2.915 0.112       0.183
## 3 site:fines   1  13 3.275 0.094       0.201

### Homogeneity of variance
levene_test(model$residuals ~ site, data = anco.quad)

## # A tibble: 1 x 4
##     df1   df2 statistic     p
```

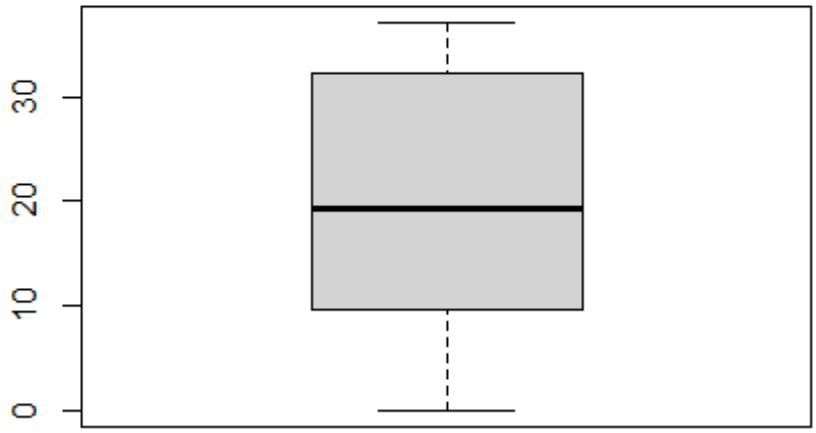
```
##   <int> <int>     <dbl> <dbl>
## 1     1    15     0.318 0.581
```

```
### Linearity
ggscatter(
  anco.quad, x = "fines", y = "sessile.taxa.richness",
  color = "site", add = "reg.line"
)+
  stat_regline_equation(
    aes(label = paste(..eq.label.., ..rr.label.., sep = "~~~~"), color =
site)
  )
```

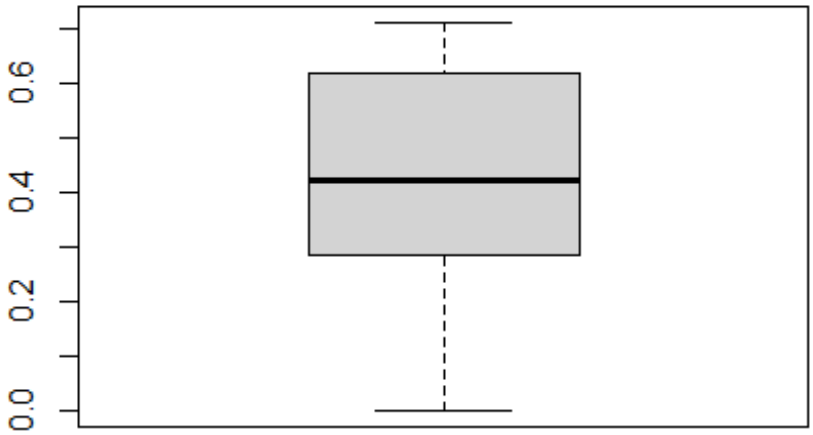
```
## `geom_smooth()` using formula 'y ~ x'
```



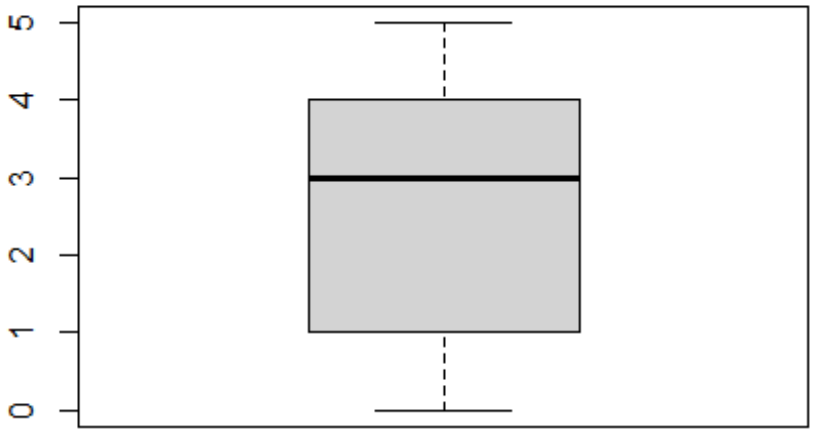

```
## Sessile Total Cover, covariate = na ###
### Outliers
boxplot(anco.quad$sessile.total.cover)
```




```
boxplot.stats(anco.quad$sessile.total.cover)$out

## numeric(0)

### Normality of Residuals
model.stc <- lm(sessile.total.cover ~  site, data = anco.quad)
shapiro.test(model.stc$residuals) # p-value = 0.1535

##
##  Shapiro-Wilk normality test
##
## data:  model.stc$residuals
## W = 0.93385, p-value = 0.2522

### Homogeneity of Variance
leveneTest(model.stc$residuals ~ site, data = anco.quad)

## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1  0.0367 0.8506
##       15

## Sessile SDI, covariate = na
### Outliers
boxplot(anco.quad$sessile.sdi)
```




```
boxplot.stats(anco.quad$sessile.sdi)$out

## numeric(0)

### Normality of Residuals
model.ssdi <- lm(sessile.sdi ~  site, data = anco.quad)
shapiro.test(model.ssdi$residuals) # p-value = 0.1535

##
##  Shapiro-Wilk normality test
##
## data:  model.ssdi$residuals
## W = 0.92537, p-value = 0.182

### Homogeneity of Variance
leveneTest(model.ssdi$residuals ~ site, data = anco.quad)

## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1  0.2135 0.6507
##       15

## Motile Taxa Richness, covariate = depth
### OUTLIERS
boxplot(anco.quad$motile.taxa.richness)
```




```
boxplot.stats(anco.quad$motile.taxa.richness)$out
```

```
## integer(0)
```

```
### Normality of Residuals
model <- lm(motile.taxa.richness ~ depth + site, data = anco.quad)
shapiro.test(model$residuals) # p-value = 0.1696
```

```
##
##  Shapiro-Wilk normality test
##
## data:  model$residuals
## W = 0.96763, p-value = 0.7757
```

```
### Homogeneity of Regression Slopes
anco.quad %>% anova_test(motile.taxa.richness ~ site*depth)
```

```
## Coefficient covariances computed by hccm()
```

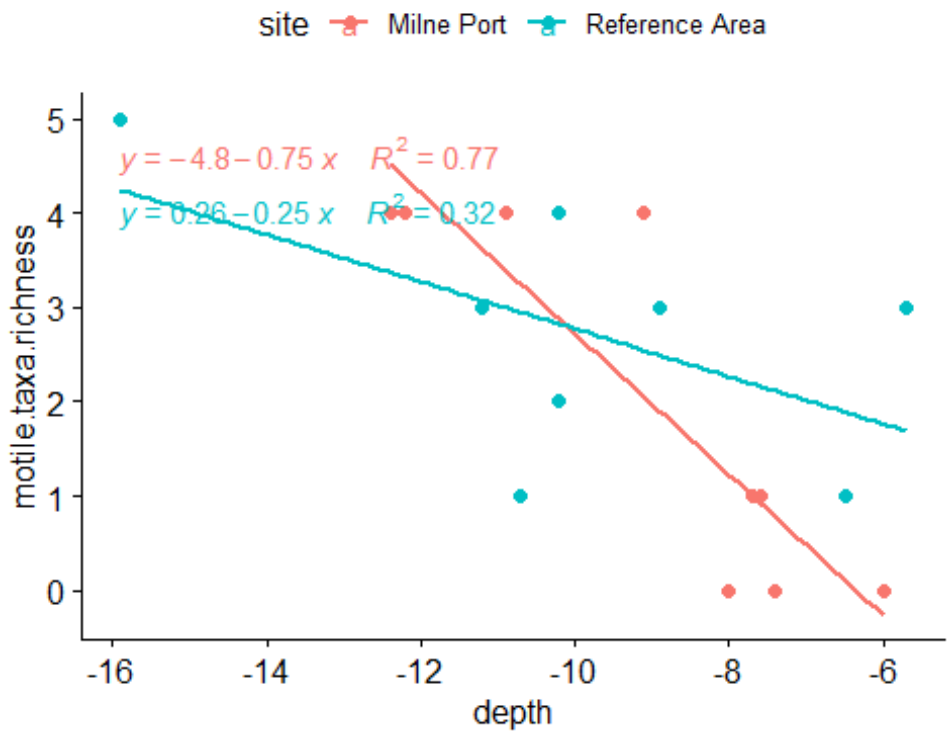
```
## ANOVA Table (type II tests)
##
##       Effect DFn DFd      F     p p<.05   ges
## 1       site   1  13  0.447 0.516       0.033
## 2      depth   1  13 17.260 0.001     * 0.570
## 3 site:depth   1  13  5.211 0.040     * 0.286
```

```
### Homogeneity of Variance
levene_test(model$residuals ~ site, data = anco.quad)
```

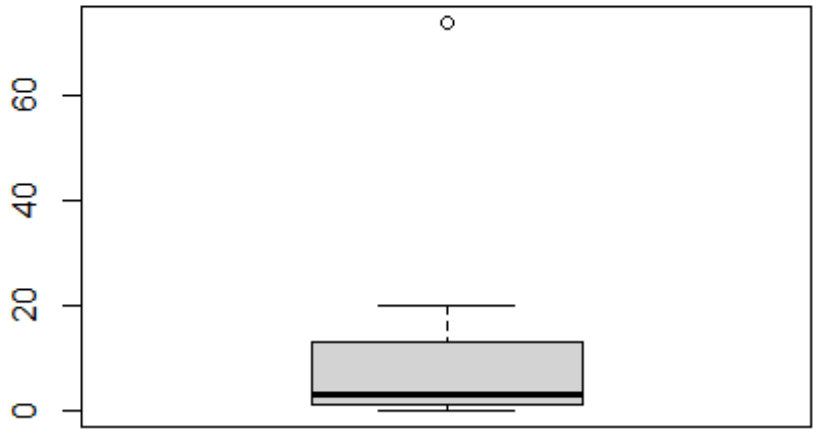
```
## # A tibble: 1 x 4
##     df1   df2 statistic     p
##   <int> <int>     <dbl> <dbl>
## 1     1    15 0.0000260 0.996
```

```
### Linearity
ggscatter(
  anco.quad, x = "depth", y = "motile.taxa.richness",
  color = "site", add = "reg.line"
)+
  stat_regline_equation(
    aes(label = paste(..eq.label.., ..rr.label.., sep = "~~~~"), color =
site)
  )
```

```
## `geom_smooth()` using formula 'y ~ x'
```




```
## Motile Density, covariate = Depth
### OUTLIERS
boxplot(anco.quad$motile.density)
```



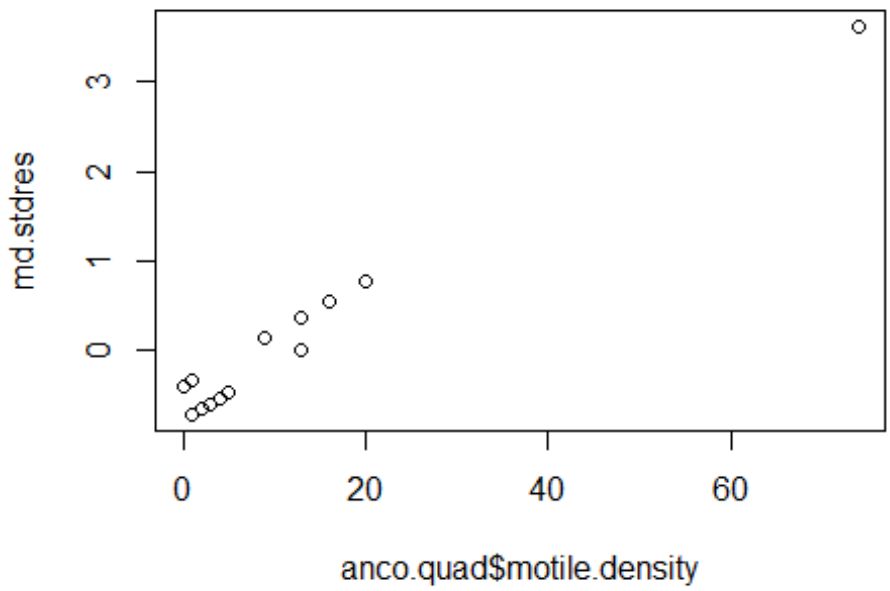

```
boxplot.stats(anco.quad$motile.density)$out
```

```
## [1] 74
```

```
model.md <- lm(motile.density ~ site, data = anco.quad)
md.stdres <- rstandard(model.md)
md.stdres
```

```
##          1          2          3          4          5          6
7
##  0.1374930  0.5499719  0.3731952  0.7856742 -0.3339115 -0.3928371 -
0.3928371
##          8          9         10         11         12         13
14
## -0.3339115 -0.3928371  3.6228746 -0.4751311 -0.6533053 -0.7126966 -
0.5345225
##         15         16         17
## -0.5939139 -0.6533053  0.0000000
```

```
plot(anco.quad$motile.density, md.stdres)  # 1 > 3.5
```

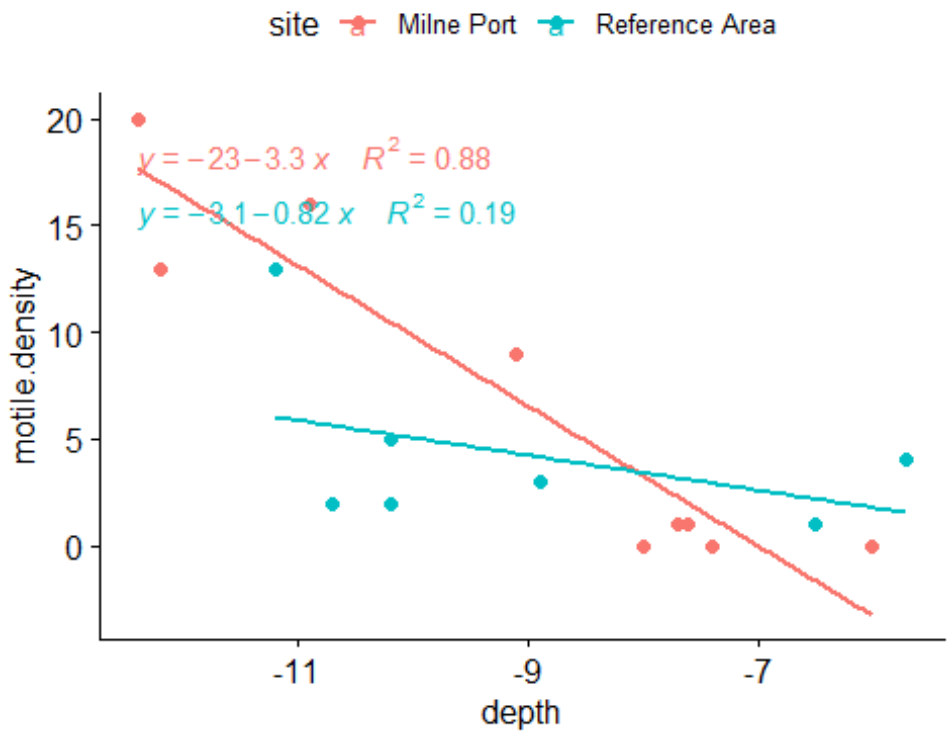



```
outliers <- boxplot(anco.quad$motile.density, plot=FALSE)$out
anco.quad.md <- anco.quad[-which(anco.quad$motile.density %in% outliers),]
### Normality of Residuals
model <- lm(motile.density ~ depth + site, data = anco.quad.md)
shapiro.test(model$residuals) # p-value = 0.1696

##
##  Shapiro-Wilk normality test
##
## data:  model$residuals
## W = 0.95749, p-value = 0.6165

### Homogeneity of Regression Slopes
anco.quad.md %>% anova_test(motile.density ~ site*depth)

## Coefficient covariances computed by hccm()

## ANOVA Table (type II tests)
##
##       Effect DFn DFd      F         p p<.05   ges
## 1       site   1  12  1.958 0.187000       0.140
## 2      depth   1  12 30.509 0.000131     * 0.718
## 3 site:depth   1  12  8.406 0.013000     * 0.412

### Homogeneity of Variance
levene_test(model$residuals ~ site, data = anco.quad.md)
```

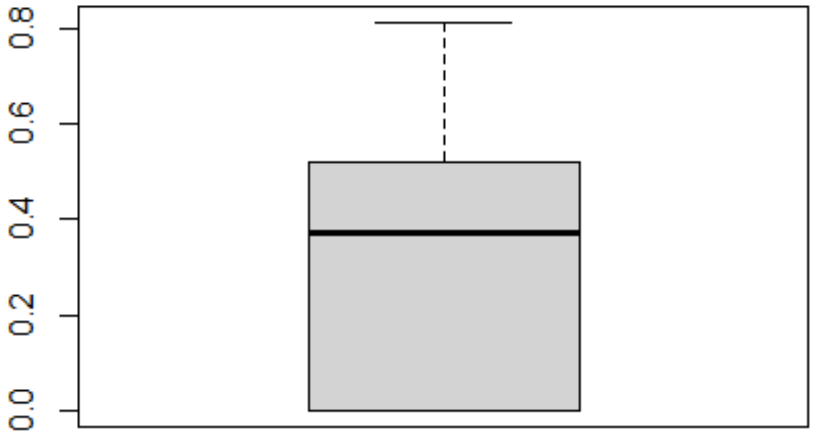
```
## # A tibble: 1 x 4
##     df1   df2 statistic     p
##   <int> <int>     <dbl> <dbl>
## 1     1    14     0.639 0.438
```

```
### Linearity
ggscatter(
  anco.quad.md, x = "depth", y = "motile.density",
  color = "site", add = "reg.line"
)+
  stat_regline_equation(
    aes(label = paste(..eq.label.., ..rr.label.., sep = "~~~~"), color =
site)
  )
```

```
## `geom_smooth()` using formula 'y ~ x'
```




```
## Motile SDI, covariate = Fines
### Outliers
boxplot(anco.quad$motile.sdi)
```




```
boxplot.stats(anco.quad$motile.sdi)$out
```

```
## numeric(0)
```

```
### Normality of Residuals
model <- lm(motile.sdi ~ fines + site, data = anco.quad)
shapiro.test(model$residuals) # p-value = 0.1696
```

```
##
##  Shapiro-Wilk normality test
##
## data:  model$residuals
## W = 0.96321, p-value = 0.6924
```

```
### Homogeneity of Regression Slopes
anco.quad %>% anova_test(motile.sdi ~ site*fines)
```

```
## Coefficient covariances computed by hccm()
```

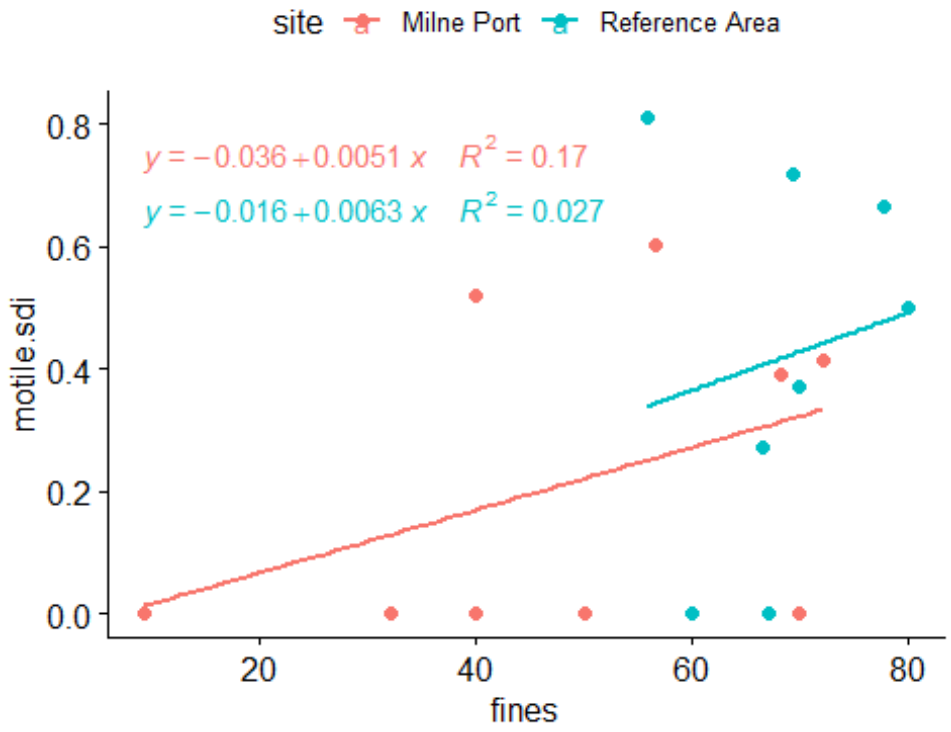
```
## ANOVA Table (type II tests)
##
##       Effect DFn DFd     F     p p<.05      ges
## 1       site   1  13 0.349 0.565       0.026000
## 2      fines   1  13 1.245 0.285       0.087000
## 3 site:fines   1  13 0.007 0.935       0.000534
```

```
### Homogeneity of Variance
levene_test(model$residuals ~ site, data = anco.quad)
```

```
## # A tibble: 1 x 4
##     df1   df2 statistic     p
##   <int> <int>     <dbl> <dbl>
## 1     1    15     0.612 0.446
```

```
### Linearity
ggscatter(
  anco.quad, x = "fines", y = "motile.sdi",
  color = "site", add = "reg.line"
)+
  stat_regline_equation(
    aes(label = paste(..eq.label.., ..rr.label.., sep = "~~~~"), color =
site)
  )
```

```
## `geom_smooth()` using formula 'y ~ x'
```




```
# ANOVA/ANCOVA Testing and Post-Hoc Testing

## Cobble
res.aov.cob <- anco.quad %>% anova_test(cobble ~ site)

## Coefficient covariances computed by hccm()

res.aov.cob

## ANOVA Table (type II tests)
##
```

```
##   Effect DFn DFd     F     p p<.05   ges
## 1   site   1  15 2.386 0.143       0.137

pwc <- anco.quad %>% tukey_hsd(cobble ~ site)
pwc

## # A tibble: 1 x 9
##   term  group1  group2 null.value estimate conf.low conf.high p.adj
p.adj.signif
## * <chr> <chr>   <chr>       <dbl>    <dbl>    <dbl>     <dbl> <dbl> <chr>
## 1 site  Milne ~ Refer~          0     1.01   -0.383      2.40 0.143 ns

## Gravel + Depth
res.aov.grav <- anco.quad %>% anova_test(gravel ~ depth + site)

## Coefficient covariances computed by hccm()

get_anova_table(res.aov.grav)

## ANOVA Table (type II tests)
##
##   Effect DFn DFd     F     p p<.05      ges
## 1  depth   1  14 5.413 0.036     * 0.279000
## 2   site   1  14 0.006 0.937       0.000462

grav <- anco.quad %>%
  emmeans_test(
    gravel ~ site, covariate = depth,
    p.adjust.method = "bonferroni"
  )
grav

## # A tibble: 1 x 9
##   term       .y.    group1     group2      df statistic     p p.adj
p.adj.signif
## * <chr>      <chr>  <chr>      <chr>    <dbl>     <dbl> <dbl> <dbl> <chr>
## 1 depth*site gravel Milne Port Referen~    14   -0.0804 0.937 0.937 ns

get_emmeans(grav)

## # A tibble: 2 x 8
##   depth site           emmean    se    df conf.low conf.high method
##   <dbl> <fct>           <dbl> <dbl> <dbl>    <dbl>     <dbl> <chr>
## 1 -9.45 Milne Port       2.75  1.38    14   -0.212      5.71 Emmeans test
## 2 -9.45 Reference Area   2.91  1.46    14   -0.231      6.05 Emmeans test

## Sand
res.aov.sand <- anco.quad %>% anova_test(sand.LOG ~ site)

## Coefficient covariances computed by hccm()

res.aov.sand
```

```
## ANOVA Table (type II tests)
##
##   Effect DFn DFd     F     p p<.05   ges
## 1   site   1  15 13.01 0.003     * 0.464

pwc <- anco.quad %>% tukey_hsd(sand.LOG ~ site)
pwc

## # A tibble: 1 x 9
##   term  group1     group2         null.value estimate conf.low conf.high
p.adj
## * <chr> <chr>      <chr>               <dbl>    <dbl>    <dbl>     <dbl>
<dbl>
## 1 site  Milne Port Reference Area          0   -0.255   -0.405    -0.104
0.00259
## # ... with 1 more variable: p.adj.signif <chr>

## Fines + Depth
res.aov.fines <- anco.quad %>% anova_test(fines ~ depth + site)

## Coefficient covariances computed by hccm()

get_anova_table(res.aov.fines)

## ANOVA Table (type II tests)
##
##   Effect DFn DFd     F     p p<.05   ges
## 1  depth   1  14 4.551 0.051       0.245
## 2   site   1  14 5.700 0.032     * 0.289

fines <- anco.quad %>%
  emmeans_test(
    fines ~ site, covariate = depth,
    p.adjust.method = "bonferroni"
  )
fines

## # A tibble: 1 x 9
##   term       .y.   group1     group2     df statistic      p  p.adj
p.adj.signif
## * <chr>      <chr> <chr>      <chr>   <dbl>     <dbl>  <dbl>  <dbl> <chr>
## 1 depth*site fines Milne Port Refere~    14     -2.39 0.0316 0.0316 *

get_emmeans(fines)

## # A tibble: 2 x 8
##   depth site           emmean    se    df conf.low conf.high method
##   <dbl> <fct>           <dbl> <dbl> <dbl>    <dbl>     <dbl> <chr>
## 1 -9.45 Milne Port       50.0  4.85    14     39.6      60.4 Emmeans test
## 2 -9.45 Reference Area   67.0  5.15    14     56.0      78.1 Emmeans test
```

```r
## Shell
res.aov.shell <- anco.quad %>% anova_test(shell ~ site)

## Coefficient covariances computed by hccm()

res.aov.shell

## ANOVA Table (type II tests)
##
##   Effect DFn DFd     F     p p<.05  ges
## 1   site   1  15 3.997 0.064       0.21

pwc <- anco.quad %>% tukey_hsd(shell ~ site)
pwc

## # A tibble: 1 x 9
##   term  group1  group2 null.value estimate conf.low conf.high p.adj
p.adj.signif
## * <chr> <chr>   <chr>       <dbl>    <dbl>    <dbl>     <dbl> <dbl> <chr>
## 1 site  Milne ~ Refer~          0     1.63   -0.108      3.37 0.064 ns

## Detrital Veneer
res.aov.detven <- anco.quad %>% anova_test(detrital.veneer ~ site)

## Coefficient covariances computed by hccm()

res.aov.detven

## ANOVA Table (type II tests)
##
##   Effect DFn DFd     F     p p<.05   ges
## 1   site   1  15 3.382 0.086       0.184

pwc.dv <- anco.quad %>% tukey_hsd(detrital.veneer ~ site)
pwc.dv

## # A tibble: 1 x 9
##   term  group1 group2 null.value estimate conf.low conf.high  p.adj
p.adj.signif
## * <chr> <chr>  <chr>       <dbl>    <dbl>    <dbl>     <dbl>  <dbl> <chr>
## 1 site  Milne~ Refer~          0    -3.29    -7.10     0.523 0.0858 ns

## Debris Other + Depth
anco.quad$deboth.LOG <- log10(anco.quad$debris.other + 1)
res.aov.dbo <- anco.quad %>% anova_test(deboth.LOG ~ depth + site)

## Coefficient covariances computed by hccm()

get_anova_table(res.aov.dbo)

## ANOVA Table (type II tests)
##
##   Effect DFn DFd     F     p p<.05   ges
```

```
## 1  depth   1  14 5.195 0.039     * 0.271
## 2   site   1  14 0.456 0.510       0.032
```

```
dbo <- anco.quad %>%
  emmeans_test(
    deboth.LOG ~ site, covariate = depth,
    p.adjust.method = "bonferroni"
  )
dbo
```

```
## # A tibble: 1 x 9
##   term       .y.        group1   group2    df statistic     p p.adj
p.adj.signif
## * <chr>      <chr>      <chr>    <chr>  <dbl>     <dbl> <dbl> <dbl> <chr>
## 1 depth*site deboth.LOG Milne P~ Refer~    14     0.675 0.510 0.510 ns
```

```
get_emmeans(dbo)
```

```
## # A tibble: 2 x 8
##   depth site           emmean    se    df conf.low conf.high method
##   <dbl> <fct>           <dbl> <dbl> <dbl>    <dbl>     <dbl> <chr>
## 1 -9.45 Milne Port      0.404 0.121    14   0.146      0.663 Emmeans test
## 2 -9.45 Reference Area  0.284 0.128    14   0.0101     0.559 Emmeans test
```

```
## Detrital Algae
anco.quad$detal.LOG <- log10(anco.quad$detrital.algae + 1)
res.aov.detal <- anco.quad %>% anova_test(detal.LOG ~ site)
```

```
## Coefficient covariances computed by hccm()
```

```
res.aov.detal
```

```
## ANOVA Table (type II tests)
##
##   Effect DFn DFd     F     p p<.05   ges
## 1   site   1  15 0.046 0.833       0.003
```

```
pwc.da <- anco.quad %>% tukey_hsd(detal.LOG ~ site)
pwc.da
```

```
## # A tibble: 1 x 9
##   term  group1  group2 null.value estimate conf.low conf.high p.adj
p.adj.signif
## * <chr> <chr>   <chr>       <dbl>    <dbl>    <dbl>     <dbl> <dbl> <chr>
## 1 site  Milne ~ Refer~          0  -0.0598   -0.652     0.532 0.833 ns
```

```
## Macroalgae Taxa Richness
res.aov.mtr <- anco.quad %>% anova_test(macro.taxa.richness ~ site)
```

```
## Coefficient covariances computed by hccm()
```

```
res.aov.mtr
```

```
## ANOVA Table (type II tests)
##
##   Effect DFn DFd     F     p p<.05   ges
## 1   site   1  15 1.218 0.287       0.075

pwc.mtr <- anco.quad %>% tukey_hsd(macro.taxa.richness ~ site)
pwc.mtr

## # A tibble: 1 x 9
##   term  group1  group2 null.value estimate conf.low conf.high p.adj
p.adj.signif
## * <chr> <chr>   <chr>       <dbl>    <dbl>    <dbl>     <dbl> <dbl> <chr>
## 1 site  Milne ~ Refer~          0    0.847   -0.789      2.48 0.287 ns

## Macroalgae Total Cover + Depth
res.aov.mtc <- anco.quad %>% anova_test(macro.total.cover.LOG ~ depth + site)

## Coefficient covariances computed by hccm()

get_anova_table(res.aov.mtc)

## ANOVA Table (type II tests)
##
##   Effect DFn DFd      F     p p<.05   ges
## 1  depth   1  14 12.569 0.003     * 0.473
## 2   site   1  14  1.258 0.281       0.082

mtc <- anco.quad %>%
  emmeans_test(
    macro.total.cover.LOG ~ site, covariate = depth,
    p.adjust.method = "bonferroni"
  )
mtc

## # A tibble: 1 x 9
##   term       .y.          group1 group2    df statistic     p p.adj
p.adj.signif
## * <chr>      <chr>        <chr>  <chr>  <dbl>     <dbl> <dbl> <dbl> <chr>
## 1 depth*site macro.total~ Milne~ Refer~    14     -1.12 0.281 0.281 ns

get_emmeans(mtc)

## # A tibble: 2 x 8
##   depth site           emmean    se    df conf.low conf.high method
##   <dbl> <fct>           <dbl> <dbl> <dbl>    <dbl>     <dbl> <chr>
## 1 -9.45 Milne Port       1.01 0.105    14    0.782      1.23 Emmeans test
## 2 -9.45 Reference Area   1.18 0.112    14    0.941      1.42 Emmeans test

## Macroalgae Taxa Richness
res.aov.mtr <- anco.quad %>% anova_test(macro.taxa.richness ~ site)

## Coefficient covariances computed by hccm()
```

```
res.aov.mtr
```

```
## ANOVA Table (type II tests)
##
##   Effect DFn DFd     F     p p<.05   ges
## 1   site   1  15 1.218 0.287       0.075
```

```
pwc.mtr <- anco.quad %>% tukey_hsd(macro.taxa.richness ~ site)
pwc.mtr
```

```
## # A tibble: 1 x 9
##   term  group1  group2 null.value estimate conf.low conf.high p.adj
p.adj.signif
## * <chr> <chr>   <chr>       <dbl>    <dbl>    <dbl>     <dbl> <dbl> <chr>
## 1 site  Milne ~ Refer~          0    0.847   -0.789      2.48 0.287 ns
```

```
## Macroalgae SDI + Fines
res.aov.masdi <- anco.quad %>% anova_test(macro.sdi ~ fines + site)
```

```
## Coefficient covariances computed by hccm()
```

```
get_anova_table(res.aov.masdi)
```

```
## ANOVA Table (type II tests)
##
##   Effect DFn DFd     F     p p<.05   ges
## 1  fines   1  14 8.936 0.010     * 0.390
## 2   site   1  14 0.964 0.343       0.064
```

```
masdi <- anco.quad %>%
  emmeans_test(
    macro.sdi~ site, covariate = fines,
    p.adjust.method = "bonferroni"
  )
masdi
```

```
## # A tibble: 1 x 9
##   term       .y.       group1    group2    df statistic     p p.adj
p.adj.signif
## * <chr>      <chr>     <chr>     <chr>  <dbl>     <dbl> <dbl> <dbl> <chr>
## 1 fines*site macro.sdi Milne Po~ Refer~    14     0.982 0.343 0.343 ns
```

```
get_emmeans(masdi)
```

```
## # A tibble: 2 x 8
##   fines site           emmean     se    df conf.low conf.high method
##   <dbl> <fct>           <dbl>  <dbl> <dbl>    <dbl>     <dbl> <chr>
## 1  58.0 Milne Port      0.556 0.0556    14    0.437     0.675 Emmeans test
## 2  58.0 Reference Area  0.469 0.0596    14    0.342     0.597 Emmeans test
```

```
## Sessile Taxa Richness + Fines
res.aov.str <- anco.quad %>% anova_test(sessile.taxa.richness ~ fines + site)
```

```
## Coefficient covariances computed by hccm()

get_anova_table(res.aov.str)

## ANOVA Table (type II tests)
##
##   Effect DFn DFd     F     p p<.05   ges
## 1  fines   1  14 2.507 0.136       0.152
## 2   site   1  14 1.194 0.293       0.079

str <- anco.quad %>%
  emmeans_test(
    sessile.taxa.richness ~ site, covariate = fines,
    p.adjust.method = "bonferroni"
  )
str

## # A tibble: 1 x 9
##   term       .y.          group1 group2    df statistic     p p.adj
p.adj.signif
## * <chr>      <chr>        <chr>  <chr>  <dbl>     <dbl> <dbl> <dbl> <chr>
## 1 fines*site sessile.tax~ Milne~ Refer~    14     -1.09 0.293 0.293 ns

get_emmeans(str)

## # A tibble: 2 x 8
##   fines site           emmean    se    df conf.low conf.high method
##   <dbl> <fct>           <dbl> <dbl> <dbl>    <dbl>     <dbl> <chr>
## 1  58.0 Milne Port       4.64 0.654    14     3.24      6.05 Emmeans test
## 2  58.0 Reference Area   5.78 0.701    14     4.27      7.28 Emmeans test

## Sessile Total Cover
res.aov.stc <- anco.quad %>% anova_test(sessile.total.cover ~ site)

## Coefficient covariances computed by hccm()

res.aov.stc

## ANOVA Table (type II tests)
##
##   Effect DFn DFd     F     p p<.05   ges
## 1   site   1  15 0.664 0.428       0.042

pwc.stc <- anco.quad %>% tukey_hsd(sessile.total.cover ~ site)
pwc.stc

## # A tibble: 1 x 9
##   term  group1  group2 null.value estimate conf.low conf.high p.adj
p.adj.signif
## * <chr> <chr>   <chr>       <dbl>    <dbl>    <dbl>     <dbl> <dbl> <chr>
## 1 site  Milne ~ Refer~          0    -4.86    -17.6      7.85 0.428 ns
```

```r
## Sessile SDI
res.aov.ssdi <- anco.quad %>% anova_test(sessile.sdi ~ site)

## Coefficient covariances computed by hccm()

res.aov.ssdi

## ANOVA Table (type II tests)
##
##   Effect DFn DFd     F     p p<.05  ges
## 1   site   1  15 0.951 0.345       0.06

pwc.ssdi <- anco.quad %>% tukey_hsd(sessile.sdi ~ site)
pwc.ssdi

## # A tibble: 1 x 9
##   term  group1  group2 null.value estimate conf.low conf.high p.adj
p.adj.signif
## * <chr> <chr>   <chr>       <dbl>    <dbl>    <dbl>     <dbl> <dbl> <chr>
## 1 site  Milne ~ Refer~          0    0.101   -0.120     0.323 0.345 ns

## Motile Taxa Richness + Depth
res.aov.motr <- anco.quad %>% anova_test(motile.taxa.richness ~ fines + site)

## Coefficient covariances computed by hccm()

get_anova_table(res.aov.motr)

## ANOVA Table (type II tests)
##
##   Effect DFn DFd     F     p p<.05      ges
## 1  fines   1  14 2.314 0.150       1.42e-01
## 2   site   1  14 0.001 0.974       8.12e-05

motr <- anco.quad %>%
  emmeans_test(
    motile.taxa.richness ~ site, covariate = fines,
    p.adjust.method = "bonferroni"
  )
motr

## # A tibble: 1 x 9
##   term       .y.          group1 group2    df statistic     p p.adj
p.adj.signif
## * <chr>      <chr>        <chr>  <chr>  <dbl>     <dbl> <dbl> <dbl> <chr>
## 1 fines*site motile.taxa~ Milne~ Refer~    14    0.0337 0.974 0.974 ns

get_emmeans(motr)

## # A tibble: 2 x 8
##   fines site           emmean    se    df conf.low conf.high method
##   <dbl> <fct>           <dbl> <dbl> <dbl>    <dbl>     <dbl> <chr>
```

```
## 1  58.0 Milne Port       2.37 0.596    14    1.09       3.65 Emmeans test
## 2  58.0 Reference Area   2.34 0.638    14    0.967      3.70 Emmeans test
```

```
### Motile Density + Depth
res.aov.md <- anco.quad %>% anova_test(motile.density ~ depth + site)

## Coefficient covariances computed by hccm()

get_anova_table(res.aov.md)

## ANOVA Table (type II tests)
##
##   Effect DFn DFd      F        p p<.05   ges
## 1  depth   1  14 22.784 0.000297     * 0.619
## 2   site   1  14  0.094 0.763000       0.007

md <- anco.quad %>%
  emmeans_test(
    motile.density ~ site, covariate = depth,
    p.adjust.method = "bonferroni"
  )
md

## # A tibble: 1 x 9
##   term       .y.          group1 group2    df statistic     p p.adj
p.adj.signif
## * <chr>      <chr>        <chr>  <chr>  <dbl>     <dbl> <dbl> <dbl> <chr>
## 1 depth*site motile.dens~ Milne~ Refer~    14    -0.307 0.763 0.763 ns

get_emmeans(md)

## # A tibble: 2 x 8
##   depth site           emmean    se    df conf.low conf.high method
##   <dbl> <fct>           <dbl> <dbl> <dbl>    <dbl>     <dbl> <chr>
## 1 -9.45 Milne Port       8.83  3.86    14    0.553      17.1 Emmeans test
## 2 -9.45 Reference Area  10.6   4.10    14    1.78       19.4 Emmeans test
```

```
## Motile SDI + Fines
res.aov.msdi <- anco.quad %>% anova_test(motile.sdi ~ fines + site)

## Coefficient covariances computed by hccm()

get_anova_table(res.aov.msdi)

## ANOVA Table (type II tests)
##
##   Effect DFn DFd     F     p p<.05   ges
## 1  fines   1  14 1.340 0.266       0.087
## 2   site   1  14 0.376 0.550       0.026

msdi <- anco.quad %>%
  emmeans_test(
    motile.sdi ~ site, covariate = depth,
```

```
    p.adjust.method = "bonferroni"
  )
msdi

## # A tibble: 1 x 9
##   term       .y.        group1   group2    df statistic     p p.adj
p.adj.signif
## * <chr>      <chr>      <chr>    <chr>  <dbl>     <dbl> <dbl> <dbl> <chr>
## 1 depth*site motile.sdi Milne P~ Refer~    14     -1.28 0.220 0.220 ns

get_emmeans(msdi)

## # A tibble: 2 x 8
##   depth site           emmean     se    df conf.low conf.high method
##   <dbl> <fct>           <dbl>  <dbl> <dbl>    <dbl>     <dbl> <chr>
## 1 -9.45 Milne Port      0.224 0.0970    14   0.0157     0.432 Emmeans test
## 2 -9.45 Reference Area  0.407 0.103     14   0.186      0.628 Emmeans test
```

APPENDIX 5E

Power Analysis

POWER ANALYSIS – BENTHIC EPIFAUNA AND MACROFLORA

This section presents the results of a power analysis undertaken for the 2021 benthic epifauna and macroflora monitoring data at Milne Port.

METHODS

A Type I error is concluding there is a significant effect when none exists (i.e., a false positive). Alpha (α) is the probability of committing a Type I error. A Type II error is the probability of concluding there is no significant effect when there is a real effect of some specified magnitude (i.e., a false negative). Beta (β) is the probability of committing a Type II error. The power of a statistical test (1 - β) is the probability of detecting a real effect. In this analysis, the Type I error-rate (α), also referred to as the significance level, was set to 0.05. The desired minimum statistical power was 80%, which corresponds to a type II error-rate of 0.2. Power analyses were conducted to assess the power of statistical tests under multiple effect sizes. For each model, a set of effect sizes was created, based on preliminary power analyses, so that power >80% was achieved at the largest absolute values of effect sizes, but also so that power is assessed at a range of effect sizes. Both negative and positive effect sizes were used, to assess the power of detecting either a reduction or an increase in values of the response variables. Since the analysis focused on assessment of changes to statistical power at different effect sizes, the power analysis used the observed samples sizes from the collected data.

Data Simulation following Effect Size Application

The power to detect statistically significant effects was estimated using residual bootstrapping in R v. 4.0.4 (R 2021), following the approach of Fox and Weisberg (2018). The general approach was to simulate data based on the model selected for interpretation, the observed sample size (or the sample size of choice), and the residuals, and re-run the models that were used for the original analysis using the simulated data. The data simulation and analysis were repeated 1,000 times, and the proportion of repetitions where the *P*-values of interest were significant ($P<0.05$) was interpreted as the statistical power of the test.

To produce simulated data, the original model was used to predict values of the response variable, and the raw residuals (i.e. the difference between the predicted and observed value for each observation) from the original model were calculated and retained. The predicted values were then adjusted according to the effect size, depending on analysis (see below for details). For each iteration of the simulation, the residuals from the original analysis were sampled with replacement, and then summed with effect size-adjusted model predictions, to produce a set of simulated data. Adding the residuals to the effect size-adjusted predictions was done to create a level of variability in the simulated data that was similar to the observed data. The simulated data were then analyzed using the same model structure as the original analysis.

In the analysis of 2021 data, where the question of interest was the detection of change in response variables between exposure and the reference area, the effect was applied as percentage relative to the values predicted for the reference area. That is, an increasing effect size resulted in a larger difference between exposure and reference area samples (Figure 1). The simulated data were analyzed using the same model as the original analysis described in the main report, and the *P*-values for the site on the response variable were retained, which included both the main effect of site and an interaction with site (for ANCOVAs where a significant interaction between site and the covariate was found). If any of these *P*-values were less than 0.05, it was considered a significant overall effect of site. The proportion of repetitions with *P*-values less than 0.05 was interpreted as the statistical power of the overall regression for that effect size. The power analysis was performed on a range of effect sizes - 20%, 30%, and 40%, and a range of sample sizes – from the collected 17 quadrats (8 in the

reference and 9 in exposure area) up to 60 samples total (30 quadrats at each site), in increments of 1 quadrat per site. Since the modeling used a normal distribution of the errors, the power to detect an effect size applies to either negative or positive effect size. That is, the 20%, 30%, and 40% effect sizes represent either a decrease or an increase of the relevant magnitude.

Power Analysis – Reporting of Results

Power curves were produced, showing statistical power as a function of sample size and effect size in percentages. Horizontal lines were added to visualize statistical power values of 0.8 (hereafter sufficient power) and 0.9 (hereafter high power), and the observed effect size was provided in the results.

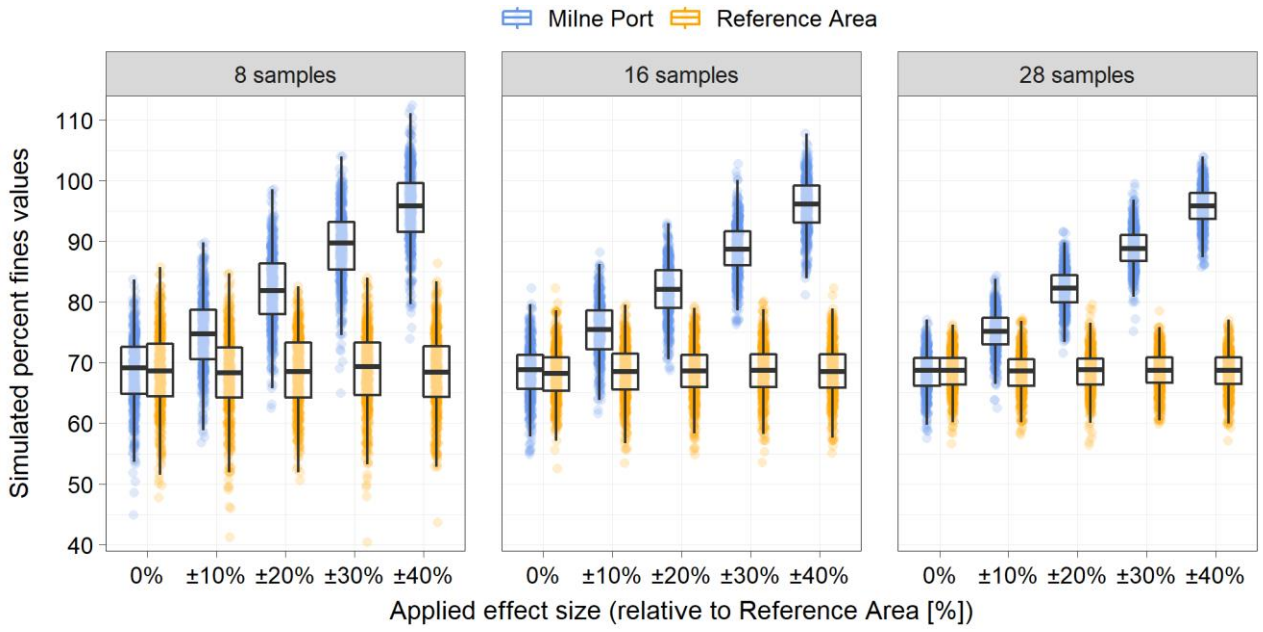


Figure 1 Application of effect sizes and simulation of increasing sample sizes to assess statistical power of detecting a difference between the reference and exposure area (2021 percent fines model).

RESULTS

The power analysis indicated that the data collected as part of the substrate, macroflora, and benthic epifauna sampling had low power to detect a ±20% effect size at the collected sample size for all examined variables (Figure 2). An increase in sample size would only result in sufficient power to detect a ±20% effect size for fines (at 12 samples taken at each of the two areas), for macroflora total percent cover (at 22 samples per area), and for sessile epifauna taxa richness (at 30 samples per area). This level of effort is prohibitive, especially given that it would still not achieve sufficient power for the remaining variables.

For an effect size of ±40%, sufficient power would be achieved for the following combinations of variables and effect sizes:

- Detrital veneer – at 18 samples per area

- Percent fines – 8 samples per area
- Macroflora:
  - SDI – 11 samples per area
  - taxa richness – 11 samples per area
  - percent cover – 9 samples per area
- Sessile epifauna:
  - SDI – at 20 samples per area
  - Taxa richness – at 8 samples per area
- Motile epifauna:
  - Density – at 13 samples per area
  - Taxa richness – at 10 samples per area
- Sufficient power was not achieved even at ±40% effect size and 30 samples per area for detrital algae, motile epifauna SDI, and sessile epifauna percent cover.

The observed effect sizes for the analyzed summary variables were as follows: 39% for detrital veneer, -24% for percent fines, 7% for detrital algae, -18% for macroflora taxa richness, -15% for macroflora total percent cover, 16% for macroflora SDI, -33% sessile epifauna taxa richness, 27% for sessile epifauna percent cover, -21% for sessile epifauna SDI, -20% for motile epifauna taxa richness, -8% for motile epifauna density, and -49% for motile epifauna SDI. This is consistent with the only significant effect found in the original analyses (given the observed effect size and sample size) being the significant difference in fines. For all other variables, either a large effect size or a large sample size would be required to detect a significant difference between the reference and exposure area.

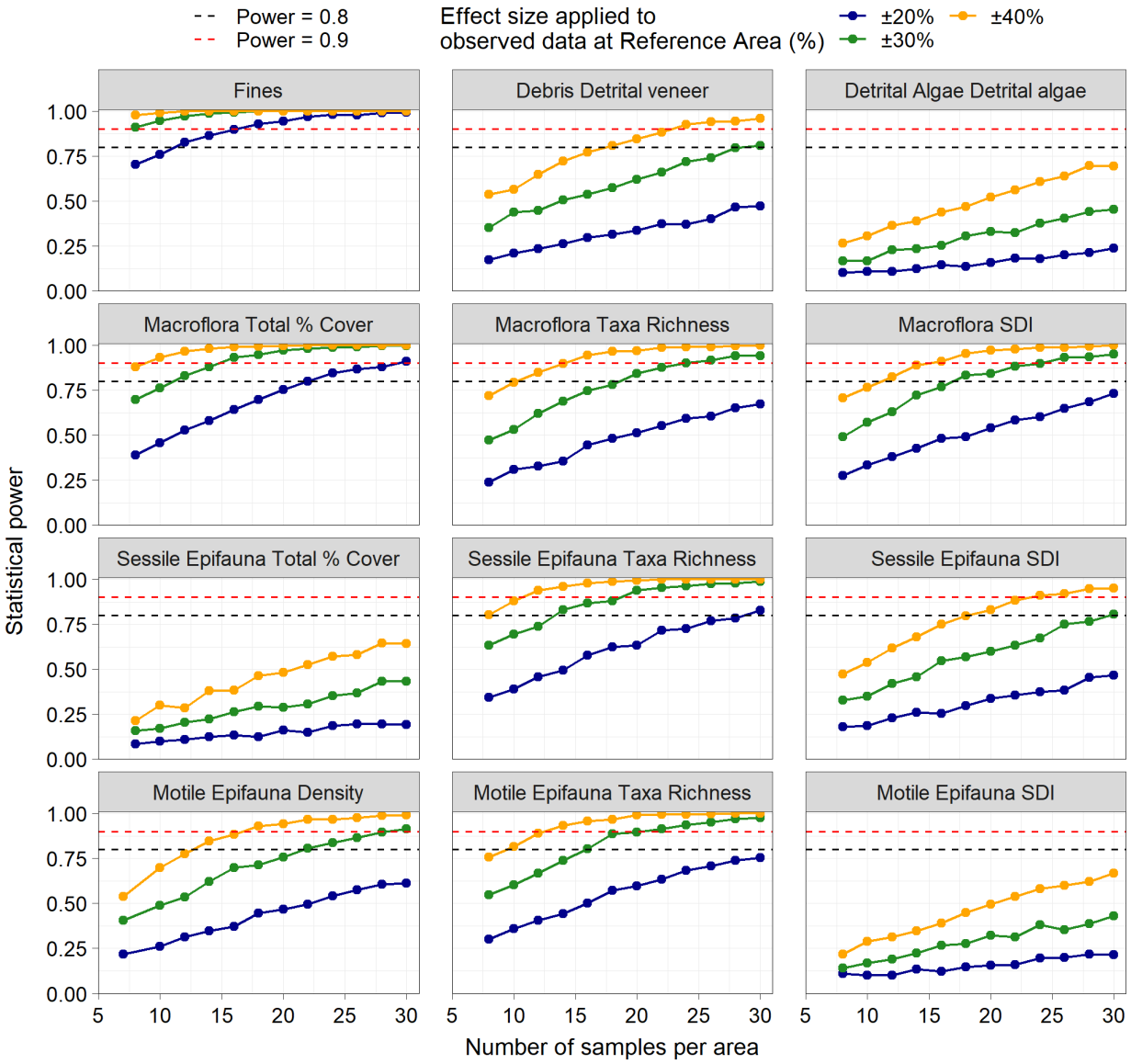


Figure 2 Statistical power of the models of summary indices detect a significant effect between the reference and exposure area based on quadrat data collected in 2021.

SUMMARY

Overall, statistical power was low to detect a ±20% effect size relative to the reference area even if sample sizes increased. For some variables, such as sessile epifauna total percent cover, motile epifauna SDI, and detrital algae, none of the assessed sample sizes and effect sizes resulted in sufficient power.

An increase in sample size to 25 quadrats per site (i.e., total of 50 quadrats) would result in sufficient power (>0.8) to detect a ±40% effect size for most variables, except for detrital algae (power of 0.64), motile epifauna SDI (power of 0.6) and sessile epifauna total percent cover (power of 0.58).

Implications of Power Analysis Results

The results indicated that none of the summary variables had sufficient power to detect a ±20% effect size given the 2021 sample size. Due to the variability in the data, either a large effect size or a large sample size (or both) would be required to consistently be able to detect a difference between the two areas. An increase to 25 quadrats per site (from the current 9 quadrats) would still not achieve sufficient power to detect a ±20% for most variables, except for percent fines and macroflora total cover. The increase in sample size, combined with setting ±40% effect sizes as the desired difference to detect would achieve sufficient power for most, but not all summary variables. This sample size would require a substantial increase in field effort.

REFERENCES

Fox, J. and Weisberg, S. 2018. Bootstrapping Regression Models in R. An Appendix to An R Companion to Applied Regression, third edition, https://socialsciences.mcmaster.ca/jfox/Books/Companion/appendices/Appendix-Bootstrapping.pdf.

R Core Team. 2021. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/.

APPENDIX 5F

Taxa List

APPENDIX 5F
Taxa Identified During 2021
Quadrat Surveys in Milne Port, NU

Marine Invertebrates	
Common Name	**Scientific Name**
Cone worm	*Cistenides granulata*
Sabellid worm spp. 1	Sabellidae indet.
Sabellid worm spp. 2	Sabellidae indet.
Flat worm	Platyhelminthes indet.
Brittle star	Ophiuridae indet.
Green sea urchin	*Strongylocentrotus droebachiensis*
Burrowing Anemone	Ceriantharia indet.
Margarite snail	*Margarites* spp.
Snail	Vetigastropoda indet.
Greenland scallop	*Similipecten greenlandicus*
Icelandic scallop	*Chlamys islandica*
Wrinkled rock-borer	*Hiatella arctica*
Blunt gaper	*Mya* spp.
Northern Astarte	*Astarte borealis*
Astarte clam	Astarte spp.
Macoma clam	*Macoma* spp.
	Bivalvia indet.
Limpet	Lottiidae indet.
Mussel	Mytilida indet.
Green mussel spp. 1	Mytilida indet.
Pandalus shrimp	*Pandalus* spp.
Sculptured shrimp	*Sclerocrangon boreas*
Barnacle	Balanomorpha indet.
Amphipod	Amphipoda Indet.
Orange tunicate	*Polycarpa* spp.
Tunicate	Tunicata indet.
Macroflora	
Common Name	**Scientific Name**
Sugar kelp	*Saccharina latissima*
Sieve kelp	*Agarum clathratum*
Rockweed	*Fucus distichus*
Pylaiella	*Pylaiella* spp.
	Halosiphon tomentosus
Acid weed	*Desmarestia* spp.
Brown filamentous 1	cf. *Coelocladia arctica*
Brown filamentous algae	Phaeophyceae indet.
	Chaetomorpha melagonium
Green filamentous tuft 1	Chlorophyta indet.
	Savoiea arctica
	Coccotylus truncatus
Dilsea	*Dilsea socialis*
Red filamentous algae	Rhodophyta indet.
Encrusting coralline algae	Corallinales indet.
Fish	
Common Name	**Scientific Name**
Pout	cf. *Gymnelus* spp.
Sculpin	Family Cottidae
Unidentified juvenile fish	Pisces indet.

GOLDER
MEMBER OF WSP

golder.com