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The Storm Bay Observing System

An evaluation of the sampling parameters and design for assessing the performance of salmon aquaculture

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1. Summary

The current FRDC project "2018-131: Storm Bay Observing System: Assessing the Performance of Aquaculture Development" has implemented an environmental monitoring program, which consists of local scale lease-specific monitoring and broadscale monitoring (BEMP) of Storm Bay. This has been augmented with additional research and sampling measurements at both local and broad scales. The local scale lease monitoring and research was undertaken at various sites <1.5 km from active leases in Storm Bay during peak biomass and focuses on measuring variables in the surrounding water column and soft sediment habitats. The BEMP monitoring and research focusing on sampling sites at varying distances from active leases in Storm Bay throughout the year and measures parameters in the water column, soft sediment, seagrass, and surrounding reef habitats. This report reviews both the local scale lease and BEMP monitoring being undertaken in Storm Bay for each habitat and makes recommendations about what parameters and sites should be monitored to detect any interactions between salmon farming and the receiving environment into the future. The key findings and recommendations for monitoring of each habitat are presented below.

Water column

Local-scale

- Comparison of three different sampling approaches (i.e. inline, discrete, and temporal sampling) highlighted the immense spatial and temporal variability in the key physicochemical and biological properties of the water column.
- Traditional discrete sampling (without very high levels of replication in space and time) will provide little power for detecting and assessing nutrient emissions from a lease and the potential biological response.
- Inline sampling is the most informative technique for mapping the spatial footprint of nutrients released by farming, particularly ammonium (NH_4).
- Inline sampling should be considered in the following circumstances:
    - to document the spatial footprint of ammonium and nitrate + nitrite (NO_x) during peak biomass at new leases,
    - when there are major changes to production levels,
    - when further investigation of the water column is required due to exceedances of water quality trigger levels at compliance and near-scale sites.

Broad scale (BEMP)

- Indicators for assessing water column performance be informed by the local and broad scale sampling reported here. These surveys captured the spatial and temporal variation in key physicochemical and biological properties of the water column and allowed us to recommend which parameters and depths should be prioritised for future monitoring. Notably, several parameters were found to be of low importance for assessing salmon farm effects and sampling at 10 m provided little additional insight beyond that from surface and bottom samples.

- The current Environmental Licences stipulate how water quality should be measured and assessed at a single compliance site. If the monthly or annual rolling median trigger levels are exceeded the license holder is required to undertake additional investigations and analysis of the monitoring data to determine to what extent the exceedances are caused by marine farming operations. Further guidance should be considered that describes how monitoring data from the other BEMP sites can be used to help determine attribution and the magnitude and extent of change from the licenced lease.
- Further guidance and clarity be provided on the intent of the BEMP water quality monitoring program, notably the intended scale(s) that ecosystem performance is detected, assessed, and managed (e.g. individual leases, leases collectively in a DGV region, leases collectively in Storm Bay or a combination thereof). The intent has direct implications for what is required for a robust water quality monitoring program.
- For the purposes of this report, we have considered three management scales of interest for water quality: (1) lease, (2) DGV region and (3) entire system and we have assessed the power to detect significant differences at each scale for different sampling designs.
- The power to detect significant change varied between management scales, sampling designs, parameters, depths, and effect sizes.
- Of the three management scales tested, the greatest power to detect significant change was at the entire system scale, followed by DGV regions. Detecting lease specific effects with a single compliance site had the lowest power and required the highest number of reference sites. For all scales, power was improved when a balanced design was implemented (i.e., equal numbers of sites at each distance category). For detecting the effects of farming 'collectively' at the system scale, 80% power was achieved for all parameters when 6 sites are sampled at each distance. At the regional (DGV) and local (lease) scales 6 sites at each distance also provided 80% power for all variables in DGV region 80, but in DGV region 93 more sites are required for TAN (19) and chlorophyll *a* (23). This is because the trigger levels for TAN and chlorophyll *a* are lower in DGV region 93. To monitor local (lease) scale effects the sites must be placed in locations that avoid overlap with the potential influence of other leases in the region.
- The parameter with the lowest power to detect significant change was chlorophyll *a*. In the current Environmental Licence where the focus is on lease specific effects and a single compliance site, >100 reference sites are required to achieve 80% power for the annual rolling median. The power for detecting lease specific effects improves with a balanced sampling design. Power was also greater for detecting change with monthly compared with annual rolling median chlorophyll *a* trigger levels.
- Increasing the number of sites improved the power to detect change substantially more than an increase in sample frequency (i.e. from monthly to fortnightly). The application of seasonal triggers did not improve power for NOx for any of the management scales or sampling designs, but there was some evidence of an improvement in power for TAN, depending on the season, at the regional scale. We

recommend that seasonal triggers for TAN be considered further given that nutrient emissions from salmon farming is likely to vary seasonally depending on the timing of peak production.

- The modelling results suggest that depending on the management scenario implemented and the biomass of salmon farmed, further consideration about the location of farfield sites is required. Under the 2ktN expansion scenario the current farfield sites are predicted to be influenced by salmon farming activities. CSIRO's TASSE model provides a powerful tool for informing decisions on potential modifications to the spatial arrangement of sites in the BEMP.
- Overall, the major recommendations for future monitoring of the water column would see a consolidation in the number of parameters and depths sampled. The power analysis highlighted that the number of sites rather than sample frequency has the greatest influence on the power to detect and assess change in the water column due to farming activities. It is also clear that a balanced sampling design provided the greatest power for detecting change. However, before specific recommendations can be made on the number of sites and their location, greater clarity is required on the intended scale(s) that ecosystem performance is detected, assessed, and managed.
- We suggest further work is required on the application and utility of remote sensing and automated monitoring platforms as techniques to monitor the interactions between salmon farming and the surrounding water column in Storm Bay.
- We also highlight that further work is required to more fully understand how phytoplankton community composition and the presence of specific phytoplankton taxa can be better used to identify environmental change at both local and broad scales.

Soft sediments

Local-scale

The requirements for local (lease) scale benthic surveys are well established, however, we recommend several modifications to the sampling design and assessment criteria to improve the power and utility of these surveys for detecting and managing salmon farm effects:

- The establishment of robust baseline conditions and ongoing monitoring of reference conditions remains critical for assessing environmental performance, we recommend:
    - The number of control (reference) sites sampled in baseline and ongoing performance assessments needs to be increased (≥4[1]) to better capture background variation. This is imperative to ensure there is adequate statistical power to assess environmental performance and compliance.
    - To ensure that both the direction and magnitude of the footprint can be determined with sufficient statistical power, at least 4 compliance sites be

[1] This is consistent with the original recommendations of Crawford et al. (2002)

sampled on the boundary/s of interest (e.g., proximity to production and direction of predominant current flow).
    - Sampling of cage sites be included in benthic compliance surveys. This provides an 'upper end' of current impact, and in turn gives important context when interpreting the degree of change at compliance sites relative to reference conditions.
- The Environmental Standards should primarily focus on change relative to reference conditions (baseline and control sites) rather than a suite of standardised parameter thresholds.
- The technical standards that accompany the new Environmental Standard should provide detailed guidance on the required analysis and presentation of benthic compliance conditions, along with the survey design required to achieve robust results.
- Macrofauna continue to be the most reliable indicator of sediment conditions, with sediment chemistry such as redox and sulphide providing location dependent measures of the enrichment footprint. Other parameters, such as the various measures of C and N in the sediments and sediment particle size analysis are informative when establishing the background environmental conditions and provide context when describing monitoring results at a given site but are not reliable indictors of farm impacts. We suggest that beyond the baseline assessment, sediment 'archive' samples be collected for particle size and C and N and that these are only processed to help explain unexpected change in the other condition metrics and/or non-compliance.
- Consideration should be given to the inclusion of the benthic health index, AMBI, in lease performance assessments. It can provide a single, easily understandable metric for community data that has traditionally required expert knowledge to interpret.
- The application of environmental DNA metabarcoding at the Yellow Bluff lease suggests that the bacterial community (16S rRNA) provides a sensitive measure of enrichment, and similarly, the eDNA analogue of AMBI, microgAMBI. We suggest this approach be tested at other leases/environments.

Broad-scale

Further clarity needs to be provided on the purpose of the broad-scale sediment surveys and how it relates to management. The current environmental licences require a written interpretation of site-specific temporal change and any "unusual" results, but otherwise don't stipulate any conditions on the health of the benthos at far-field sites.. From this we interpret that the far-field surveys are not required to attribute lease specific change at the broad scale, rather to provide broader system context for local (lease) scale surveys and any potential warning signs of system wide deterioration. Other findings and recommendations include.

- Benthic indicators for assessing performance should be based on the results of the first three broadscale surveys reported here. These three surveys capture the spatial and temporal variation of the sediment environment and the key biotic and abiotic conditions. There is no evidence of farm effects on the broadscale sediment

environment from these initial surveys, and as such, we suggest they serve as the reference condition for assessing performance as the industry develops.

- We also agree with Thompson et al. (2008) that the level of risk and the need for further investigation is scaled based on the number of affected sites.
- Further, we suggest the assessment of change is based on different regions in Storm Bay identified through the cluster analysis of macrofaunal communities. This will help constrain natural variation evident across the whole system and improve the power to detect change.
- The use of video as a monitoring tool for broad-scale sites should be explored further. Initial findings indicate that it can provide additional utility by way of increasing site scale and the ability to capture potential impact responses not currently considered, i.e., epiphyte/drift algae, large mobile epifauna and physical characteristics.
- Given the relatively consistent grouping of sites which represent different environmental conditions (habitat regions) across Storm Bay we suggest that annual surveys focus on a subset of sites representative of the different habitats across Storm Bay. These sites will effectively act as "sentinel" sites that indicate when the ecology of each habitat region may be changing.
- The full suite of 23 sites should be surveyed every 5 years and/or prior to any significant increase in farmed biomass across Storm Bay.
- During the annual surveys, if any of the sentinel sites in a habitat region show clear signs of change relative to reference conditions (i.e. first 3 surveys) that is consistent with increased organic enrichment, then we recommend follow up surveys be undertaken at all other sites in the region/s. We also suggest this be accompanied by video surveys at sites to capture the potential for broader epibenthic change.
- The community metrics of change could include typical multivariate ordination techniques and/or a global benthic health index such AMBI which is regarded as sensitive to minor disturbances.
- A range of taxa that respond to lower levels of organic enrichment were documented. These species will provide a more sensitive measure of broad-scale change. Although their presence is characteristic of background conditions, their increased presence, from reference conditions (captured during the first three surveys), will likely provide an early indication of broadscale change. We note however, that a concomitant shift in benthic community composition is typically a more robust and reliable indicator of change than change in any individual species abundance.

Inshore Reefs

Biodiversity surveys combined with Rapid Visual Assessments (RVA) is recommended for future monitoring of inshore reef ecosystems in Storm Bay. The RVA is a simple cost effective and sensitive method for detecting nutrient enrichment on reefs and biodiversity surveys provide information on the consequences of this nutrient enrichment to the species

assemblages associated with these habitats. We recommend several modifications to the sampling design for consideration:

- A decrease in the number of sites that are monitored regularly. 30 sites across Storm Bay have provided a robust baseline, but our analysis has indicated that there is redundancy between sites, particularly regarding ecosystem function. A list of 14 sites is proposed that are representative of all significant groupings found through the analysis of macroalgae biodiversity, along with ecosystem function through RVA. The recommended site list is balanced between western, eastern, and northern areas of Storm Bay, within the limits of where inshore reef habitat occurs. We suggest the full suite of 30 sites be resurveyed once every 5 years.
- Summer and winter monitoring is retained for the immediate future. Notably, the dataset for eastern Storm Bay is much smaller and appears far more variable in terms of biodiversity and function than western Storm Bay; the additional monitoring will aid a better understanding of natural variability and what constitutes significant change.

We suggest the inshore reef program be reviewed again after five years (the next biodiversity survey) with summer only RVA surveys considered if the data indicates broadscale stability across seasons. The number of sites for Edgar-Barrett biodiversity surveys could also be reviewed at this point. However we also note that any proposed major increase in biomass or change in lease area (or location) in Storm Bay should prompt an immediate review of the sampling design (e.g. number and location of sites and survey frequency).

Should the RVA surveys indicate significant change to key ecosystem parameters, such as a decrease in macroalgal canopy, changes to canopy composition, or increases in nutrient indicator parameters (i.e. epiphytic, filamentous or nuisance algae) compared to baseline conditions at any given site, then we recommend the following:

- Biodiversity surveys to assess potential effects on reef ecology (e.g. abundance and diversity of all fish, invertebrates and algae)
- Surveys using remote platforms (e.g. ROV, AUV, towed camera systems) to cover a greater spatial area to better understand the spatial extent of any change.
- If reduced to summer only, RVA surveys to be resumed at twice-yearly to ascertain temporal nature of the change.
- Other lines of evidence for the attribution of change be considered e.g. connectivity modelling, biochemical tracers, gradient sampling.

Deep Reefs

This work has documented the high biodiversity present in the deep reef ecosystems of Storm Bay. However, our understanding of the dynamics of these systems remains limited, including how they might respond to nutrient enrichment, both at a community and species level. Further data on these systems is needed to make detailed recommendations around a simplified monitoring protocol that is robust enough to detect change. Given this, we

recommend a precautionary approach be adopted for the monitoring of deep reefs until further data is collated and analysed.

An approach that combines frequent qualitative assessments with less regular quantitative biodiversity surveys is recommended in the short-medium term. More specifically:

- Annual qualitative monitoring, as per the current Environmental Licences, be extended to encompass six sites, with the addition of Betsey West and North Bruny. Further suggested refinements include:
    - All depth strata should be captured at each site. This may require transects to extend beyond 200m in length where substrate is present to capture the full depth range of the site. Both forward-facing and downward-facing video footage on all transects for a more robust assessment of fish and benthic communities. Where possible this should be done in HD or greater and with adequate lighting so imagery can be used in quantitative assessment if needed.
    - Use of a georeferencing system (USBL if possible), such that image location can be ground-truthed against bathymetry.
    - Clearly defined guidelines for image analysis and scoring (i.e. start and end times, field of view etc.) to ensure reproducibility and comparability across years, for example:
        - Footage is scored using the CATAMI classification system for benthic assemblages.
    - Specialised video/imagery scoring software program (i.e. EventMeasure or TransectMeasure) is adopted for both qualitative and quantitative sampling.
- Quantitative surveys that capture biodiversity (fish and benthic assemblages) using NESP methods be undertaken every five years on the eight reefs surveyed as part of this project.
- Following three quantitative surveys (including the one undertaken through this project), the spatial and temporal dynamics of these systems should be assessed and documented. An aim of this evaluation will be to produce a protocol for monitoring of these systems using a simplified indicator/functional approach.
- Targeted research on the mesophotic algal communities to establish the link between nutrient enrichment and potential indicator species. This will assist both the interpretation of monitoring data and the development of a more targeted monitoring approach.

Seagrass

The monitoring program for seagrass should be scaled to the ecological importance of the seagrass in that system. Seagrass will always have inherent value in an ecosystem for the services this habitat provides, along with the capacity of seagrass to act as a sentinel for environment change. However, the monitoring effort where ecological significance is high might be different to where the spatial extent of the beds is limited, such as in the case of Storm Bay.

Given this, a simple approach assessing bed extent is recommended for the future monitoring of seagrass beds in Storm Bay. For a dynamic seagrass species such as *Zostera* spp., monitoring l variation in bed extent and composition is a more appropriate measure for indicating longer-term fluctuations in health of the bed than measuring condition alone. When combined with a method that allows for a quantitative assessment of the condition of the seagrass and ecology of the associated flora and fauna, this becomes an appropriate seagrass monitoring program for Storm Bay.

For the monitoring of bed extent and composition, the following process is recommended:

- Between 3-5 long transects (≥ 200 m) are established at each site extending from adjacent soft sediments and spanning the entire seagrass bed/area of interest.
- Along these transects a drop camera with a 1 m^2 frame is lowered to the substrate every 10 m and a benthic image is captured. The vessel used for this process should be equipped with a DGPS and each image georeferenced.
- Images are scored into one of six categories from the original SeaMap assessments depending on the dominant vegetation: seagrass, sparse seagrass, patchy seagrass, mixed bed, macroalgae or sand. All images should be archived for more detailed scoring either as outlined below, or where the need arises.
- These categories can then be matched with the waypoint collected for each photo-quadrat and subsequently mapped using ArcGIS or a similar program.
- These surveys should be repeated once every two years, with survey frequency reviewed after five years e.g. if beds are stable and there have been no major increases in farmed biomass or lease locations, biennial assessments could be considered.
- If large shifts are detected in the extent of the seagrass or composition of the beds, then images should be scored quantitatively to provide ecological information around these changes.
- If there are any significant changes to biomass or lease area in Storm Bay, it is recommended that images are scored quantitatively prior to this occurring.

In the case that change is detected and/or a quantitative assessment is required, we recommend that the methods adopted for this are the point-count assessments outlined in Section 7.1.3:

- At each site within the transects used for assessing extent and composition, a 200 m subsection should be demarcated for the condition assessment.
- Where possible, this 200 m section should be within the main bed or include as much of the main bed as possible.
- Quantitative assessments should be undertaken using a software package such as Coral Point Count with Excel extension (CPCe) or TransectMeasure that provides capacity for 50-point count within the image.
- Photo-quadrats should be scored for seagrass and epiphyte cover, as well as sessile invertebrates and macroalgae associated with seagrass beds (see Appendix 7-1 for the table of parameters used in this study).

- Surveys should always be undertaken at the same time of year to avoid any confounding temporal effects.

The data collected through quantitatively scoring of photo-quadrats can be used to capture the general ecology of seagrass beds and help to inform any changes observed in the bed extent and composition mapping. Regardless of whether change is observed, we recommend that images are processed quantitatively once every five years to track the ecology of the seagrass beds in Storm Bay. This program should be reviewed after five years, with frequency of bed extent mapping and quantitative surveys reviewed at this point.

General considerations for future monitoring

A recurring theme across all receiving habitats was the need for greater clarity on the purpose of the monitoring program and how it relates to management. This is fundamental to the design of an effective monitoring program – one that can detect and assess, with some confidence, whether an activity is causing unacceptable change to the environment. There can be little doubt that the current monitoring program in Storm Bay is very comprehensive with respect to the habitats sampled, the parameters measured and the spatial and temporal scales it encompasses, but ultimately, for it to be effective and efficient it needs to be designed to answer specific management questions and priorities. This includes being scalable to the level of development. For the Storm Bay monitoring program, there are three basic aims that might be considered: 1) to assess ecological health of the major receiving habitats, 2) to assess whether regulated performance criteria have been exceeded and 3) to detect and assess the impacts of salmon farm inputs. Whilst the ultimate purpose of the monitoring program might be to detect and attribute change to salmon farming, this is less straightforward for some habitats because of the challenges in establishing robust reference conditions that provide the necessary inferential strength. For example, the patchy distribution of both seagrass and reef habitats in Storm Bay does not lend itself to having control and impact locations or locations along a predicted gradient of exposure. Similarly, for assessing impacts at the scale of the entire system (Storm Bay) we don't have the luxury of reference (control) systems. In these examples, assessing ecosystem health and change relative to baseline conditions should be the priority, and inferences about the likely cause of change will depend on other lines of evidence (e.g., model outputs, indicator specificity, timing, proximity, tracers). In contrast, soft sediments and the water column allow for a more robust sampling design and greater inferential strength. The challenge here is ensuring the sampling design has the required replication and power to detect meaningful change against the background variability inherent in these systems.

These are important considerations that need to be made more explicit when describing the purpose and intent of the Storm Bay monitoring program and how it relates to management. This will underpin an effective and robust design and public confidence in its application.

Future research priorities

Several research priorities have been identified that have the potential to further improve both the effectiveness and efficiency of the monitoring program into the future, these include:

- Development of the benthic health index, AMBI, for lease performance assessments as an easily understandable metric for benthic community health.
- Further investigation on the value of using environmental DNA metabarcoding as monitoring tool.
- Improved understanding of phytoplankton community composition in Storm Bay as a measure of environmental change.
- Further development of remote platforms (e.g. ROV, AUV, towed camera systems) for monitoring ecosystem health of benthic habitats (e.g. inshore and deep reefs, seagrass, sediments).
- Targeted research on the mesophotic reef habitats to better understand their dynamics and potential response to nutrient enrichment and potential indicator species.
- Further work is required on the application and utility of remote sensing and automated monitoring platforms as techniques to monitor the interactions between salmon farming and the surrounding water column in Storm Bay.
- The CSIRO TASSE biogeochemical model predicts changes in water quality for Storm Bay based on different scenarios of salmon farming expansion. This provides a powerful tool for evaluating future scenarios against the current spatial arrangement of sites in the BEMP and informing potential modifications.

Abbreviations

AUV	Autonomous Underwater Vehicles
ANZECC	Australian and New Zealand Environment and Conservation Council
AST	Analytical Services Tasmania
BEMP	Broadscale Environmental Monitoring Program
CATAMI	Collaborative and Automated Tools for Analysis of Marine Imagery
CPCe	Coral Point Count with Excel Extensions
CONNIE	Connectivity Interface; open access online modelling and visualisation tool
CSIRO	Commonwealth Scientific and Industrial Research Organisation
CTD	Conductivity Temperature Depth
DGPS	Differential Global Positioning System
DGV	Default Guideline Value
DNRET	Department of Natural Resources and Environment Tasmania
EAC	East Australian Current
EIS	Environmental Impact Statement
ELs	Environmental Licences
EPA	The Environment Protection Authority Tasmania
FRDC	Fisheries Research and Development Corporation
IMAS	Institute for Marine and Antarctic Studies
IMOS	Integrated Marine Observing System
IP	Internet Protocol
MFDP	Marine Farm Development Plan
NESP	National Environmental Science Program
OSRA	Oil Spill Response Atlas
PA	Planning Authority
ROV	Remote Operated Vehicle
RVA	Rapid Visual Assessment

2. General background

In Tasmania, the salmon industry has developed rapidly since the first trials in 1985 and has grown progressively to a total production in 2020-21 of 83,033 tonnes, equating to an estimated production value of $1.01 billion (DNRET, 2022). To achieve further growth, the salmon industry will need to consider a suite of alternate production approaches including improvements in farming practices, innovations in technology and expansion of the industry into deeper and more exposed areas such as Storm Bay.

Salmon farming in open sea cages produces organic and inorganic wastes which have the potential to impact surrounding habitats (Edgar et al., 2009, Macleod and Forbes, 2004, Oh et al., 2015). Waste products consist of faecal material, uneaten feed pellets and metabolic waste products in dissolved inorganic forms (Strain et al., 2020). When the particulate matter sinks to the seabed it has the potential to change the structure and function of the surrounding soft sediment (Macleod et al., 2003), seagrass and reef communities (White et al., 2021, White et al., 2022). Dissolved wastes may enhance ambient nutrient levels in the water column (Ross et al., 2022), influencing primary and secondary production (Da Silva et al., 2022).

Maintaining high environmental performance, through the development of a robust scientific monitoring program is a high priority for both the salmon industry and its regulators. The development of a Storm Bay broadscale monitoring program is central to environmental management, good farm health and maintaining public confidence in the industry. The program must be able to detect ecosystem change and the influence of salmon farming at multiple spatial and temporal scales. Specifically, the program must identify and monitor the relevant components of ecosystems that could be affected by salmon farming using an appropriate sampling design. Based on the data collected and research conducted though FRDC project “2018-131: Storm Bay Observing System: Assessing the Performance of Aquaculture Development” this report will conduct a review of the monitoring program that was developed by the Environment Protection Authority (EPA)/Planning Authority (PA) for Storm Bay, assess its efficacy in detecting the interactions between salmon farming and the surrounding habitats, and make recommendations for potential refinement based on the findings.

2.1. Overview of the monitoring program in Storm Bay

Storm Bay is an inlet of the Tasman Sea bounded by Bruny Island (west) and the Tasman Peninsula (east). The bay is in southeast Tasmania and approximately 500 km^2 in area. Historical and current monitoring has demonstrated the water column dynamics in the bay are strongly influenced by oceanic currents: Leeuwin, Sub Antarctic and East Australian and freshwater inputs from the River Derwent, the Huon River via the D'Entrecasteaux Channel and runoff from land (Harris et al., 1991, Swadling et al., 2017, Wild-Allen et al., 2021).

Storm Bay was identified as a potential area for the expansion of salmon farming in the Tasmanian Governments Sustainable Industry Growth Plan (DPIPWE 2017). Currently two major salmonid producers: Tassal Operations Pty Ltd and Huon Aquaculture Company Pty Ltd farm in the Storm Bay region, with Petuna Pty Ltd also engaged in the planning process

with an approved site in the north-central area of Storm Bay. The approval process allowed for staggered development, with an initial limit of 30,000 tonnes of salmon production, the implementation of a comprehensive environmental monitoring program, and the development of a biogeochemical model (Wild-Allen et al., 2021).

The current FRDC project "2018-131: Storm Bay Observing System: Assessing the Performance of Aquaculture Development" has implemented the broad scale (BEMP) and local scale lease-specific monitoring programs that were developed by the Environment Protection Authority Tasmania (EPA) and the Marine Farming Branch within the Department of Primary Industries, Parks, Water and Environment (now the Aquaculture Branch of DNRET). This has been augmented with additional research and sampling measurements at both local and broad scales. The local scale monitoring and research is focused on measurements of the key chemical, physical and biological indicators of ecosystem condition in the water column and soft sediments at various sites in the immediate vicinity (<1.5 km) of active leases in Storm Bay, typically during peak biomass. This research has been focused on MF281 East of Yellow Bluff and MF279 West of Wedge Island leases. The broad scale component of the research is designed to monitor and measure parameters in the water column, soft sediment, seagrass, and surrounding reef systems, across a range of sites and throughout the year (Figure 2-1). This report will review both the local scale lease and BEMP monitoring being undertaken in Storm Bay for each habitat and make recommendations about what parameters and sites should be monitored to detect any interactions between salmon farming and the receiving environment into the future.

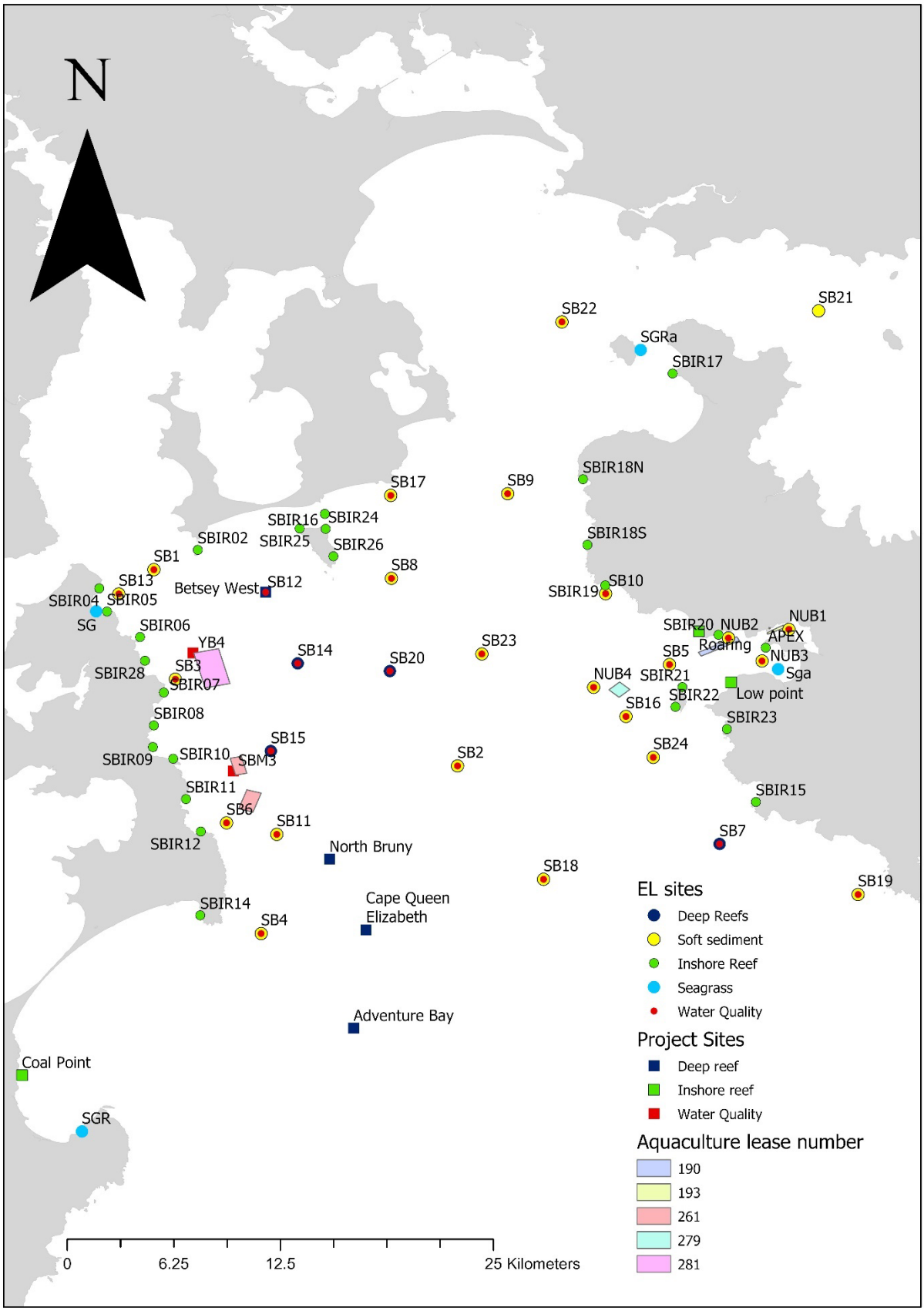

Figure 2-1: Map of the BEMP sites surveyed in each habitat and the active leases in Storm Bay.

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3 Water column monitoring

Environmental monitoring programs designed to assess the influence of organic and inorganic nutrients released by salmon farming into the water column have produced varied results both globally (Sara 2007, Price et al. 2015) and in Tasmania (Ross & MacLeod 2013, Ross et al. 2022). Some studies have reported increases in the concentration of ammonia, chlorophyll *a* biomass, abundances of key phytoplankton taxa and declines in dissolved oxygen at the local scale (i.e. near the cage) during peak production while others have reported minimal or no differences (see review by Price et al. 2015). Studies at the regional or broadscale, are limited but have similarly, found varied evidence for the influence of salmon farming on the water column (Pitta et al. 2006, Ross & MacLeod 2013). Collectively these studies have highlighted the need for carefully designed monitoring programs to determine whether any changes in the water column are linked to salmon aquaculture activities and to understand the role of other major sources of nutrients and influences.

In this chapter we aimed to:

1. Describe the potential interactions between salmon farming and the water column, based on a) local scale monitoring and b) broadscale (BEMP) monitoring.
2. Undertake power analyses to determine the sensitivity of the current BEMP sampling design in detecting both lease and broader ecosystem level changes in the water column.
3. Recommend key variables, sample frequency and sampling design(s) for future water column monitoring efforts.
4. Discuss the application of automated monitoring techniques for monitoring the interactions between salmon farming and the water column.

3.1 Local-scale water column monitoring

Open-cage salmon farming contributes excess nutrients to the surrounding water column environment, with fish excreting up to 45% of the nitrogen in the form of dissolved inorganic nitrogen (DIN), and ammonia (NH_4), or ammonium (TAN) (Wang et al. 2012). Despite this, it is difficult to consistently detect a nutrient footprint from salmon farming. This is because NH_4 is a highly bio-reactive form of inorganic nitrogen that is rapidly consumed by marine phytoplankton, algae, and bacteria (Pitta et al. 2009). This high lability means that the effects of salmon farming on the water column are often highly variable and therefore hard to detect using traditional monitoring techniques. An investigation into local scale water quality using both auto-analysers and discrete samples was conducted to better understanding nutrient dynamics in the proximity to salmon cages during peak biomass. These results were also used to inform the broadscale (BEMP) water column monitoring.

3.1.1 Nutrient mapping using discrete and continuous sampling approaches.

Discrete samples capture nutrients from a patch of water at a particular point in time and space and are often used to monitor salmon farming activities. However, discrete samples can be affected by other environmental factors such as the form of the nutrient input stream (i.e. pulse vs continuous), local hydrodynamics (current flow, presence of infrastructure) and biophysical characteristics of the receiving environment. In the case of

highly labile compounds such as NH_3 and NH_4, methodological decisions such as whether the sample is filtered or frozen prior to analysis, along with the lag time between collection and laboratory analysis of the sample can also influence the monitoring outcomes.

The issues associated with discrete sampling can be addressed by using automated monitoring techniques, such as in-line or portable auto-analysers that are deployed on a platform or used in conjunction with a vessel. In collaboration with CSIRO, we trialled the use of an automated inline sampling system that captures point measurements of both NH_4 and nitrogen oxides (NO_x) every four minutes. This technology allowed us to explore local scale nutrient dynamics, particularly for highly labile forms of inorganic nitrogen. This sampling was paired with complementary discrete sampling of NH_4, NO_x, nitrite (NO_2), phosphate (PO_4), silicate (Si), chlorophyll *a* and phytoplankton abundance and composition to better understand the spatial scale of influence of an active salmon lease during peak biomass.

Design

Sampling was conducted in March and December 2021 to coincide with peak biomass on the MF281 (East of Yellow Bluff) lease. Over an eight-hour period, 3 subsets of data were collected (Table 3-1), each with different objectives. Dataset 1 was captured using the CSIRO high spatial resolution nutrient instrument along with an underway sensor system (also referred to as the DUDES sampling system) installed on board the vessel South Cape. The underway sensor system ran for the duration of the survey and captured continuous measurements of conductivity, temperature, and fluorescence. The water intake for this system is approximately 2 m in depth and runs over the instrumentation (sensors) at a flow rate of approximately 3 L/minute. The water flow from this system was linked to a modified Seal AA100 nutrient instrument which analysed water for NH_4 and NO_x concentrations. Calibration samples were taken regularly throughout the day and analysed on the AA3 nutrient auto-analyser at the CSIRO laboratories upon return from the field. In March 2021 sampling was undertaken in a series of expanding circles around the lease, while in December 2021 a more haphazard 'zig-zag' pattern across the sampling area was followed (see Section 3-1-4). The primary aim of this dataset was to capture high resolution spatial data for NH_4 and NO_x at varying distances from the lease.

Dataset 2 was a series of discrete samples at 5 distances from the cage (0, 50, 100, 500 and 1000 m) in 4 different directions from the farm (NW, N, NE & E) (Figure 3-1). These directions were sampled as most of the cages were in the northern part of the lease. At each of these stations 3 depths were sampled (1 m, 10 m & 1 m from the bottom) (Table 3-1). In March 2021, all 20 sampling stations were sampled, while in December 2021 stations 16, 17, 18 and 19 were missed due to unfavourable weather conditions. At each station, a CTD (Seabird SBE 19 or a Yeokal) was initially deployed to profile the salinity, temperature, dissolved oxygen (DO) and turbidity throughout the water column. Following this, water was captured from each of the 3 depth strata using a 5 L Niskin. From the Niskin, three x 10 mL samples were passed through a 0.45 µm PES filter and placed in the dark on ice for subsequent nutrient analysis (NH_4, NOx, nitrite, PO_4, Si) at the CSIRO laboratories. Samples were analysed using an AA3 auto-analyser and processed within 6 hours of collection. A 1 L sample was collected for bacteria and passed through a 0.2µm sterivex filter using a peristaltic pump, with the volume recorded. Filters were snap frozen using liquid nitrogen and stored at -80°C for subsequent analysis. A 1 L sample was collected for

phytoplankton, fixed immediately using Lugols solution, and analysed at Analytical Services Tasmania (AST). Two litres of water were collected for chlorophyll *a* analysis, with a known volume of sample passed through a GF/F Whatman filter on return to the lab. These filters were subsequently analysed for the chlorophyll *a* concentration by AST. Samples for chlorophyll *a* were only collected in December 2021. The primary aim was to provide a depth profile to complement the high-resolution surface sampling obtained through the inline systems (Dataset 1).

Table 3-1: Summary of the sampling parameters collected as part of the local scale water quality sampling events in March and December 2021.

Dataset	Scale	Type of variability measured	Sampling type	Sampling depths	Samples analysed for:
1	Local scale	Spatial *	Inline sampling	Surface	Nutrients (NH_4, NOx, NO_2)
2	Local scale	Spatial*	Discrete samples	1 m, 10 m & 1 m from bottom	Nutrients (NH_4, NOx, NO_2 phosphate, Si) Environmental (temperature, salinity fluorescence) Phytoplankton (Bacteria Phytoplankton Chlorophyll *a* biomass**)
3	Local scale	Temporal	Discrete samples	1 m, 10 m & 1 m from bottom	Nutrients (NH_4, NOx, nitrite, PO_4, Si) Environmental (temperature, salinity fluorescence) Phytoplankton (Bacteria Phytoplankton, Chlorophyll *a* biomass**)

* Given that these datasets take much of the sampling period (8 hour), the spatial patterns will inevitably encompass a component of temporal variation.

**Chlorophyll *a* samples were only collected during sampling in December 2021.

Dataset 3 assessed temporal variation in nutrient concentrations throughout the sampling period (approximately 8 hrs) at a single sampling station located at the feed barge in the centre of the lease (Figure 3-1) across three depth strata (1 m, 10 m, & 1 m from the bottom), which are hereafter referred to as surface, 10 m or bottom (Table 3-1). Samples at this station were collected 5 and 4 times within the March and December sample periods respectively (every 2-3 hrs, with samples collected and processed for nutrients, bacteria, phytoplankton, and chlorophyll *a* as per the methods outlined above). Note that for this report, bacteria data are not presented.

Data analyses

Differences in the physical environment between March and December 2021 were examined in PRIMER using normalised data with Euclidean distance matrices. Data were visualised using principal components analysis (PCA) and non-metric multidimensional scaling (nMDS) plots with eigenvectors used to show key parameters contributing to the differences between groups. Based on differences in the physiochemical environment

between the two surveys, the relationships between distance to the lease and environmental parameters, including nutrients, were examined separately for each survey.

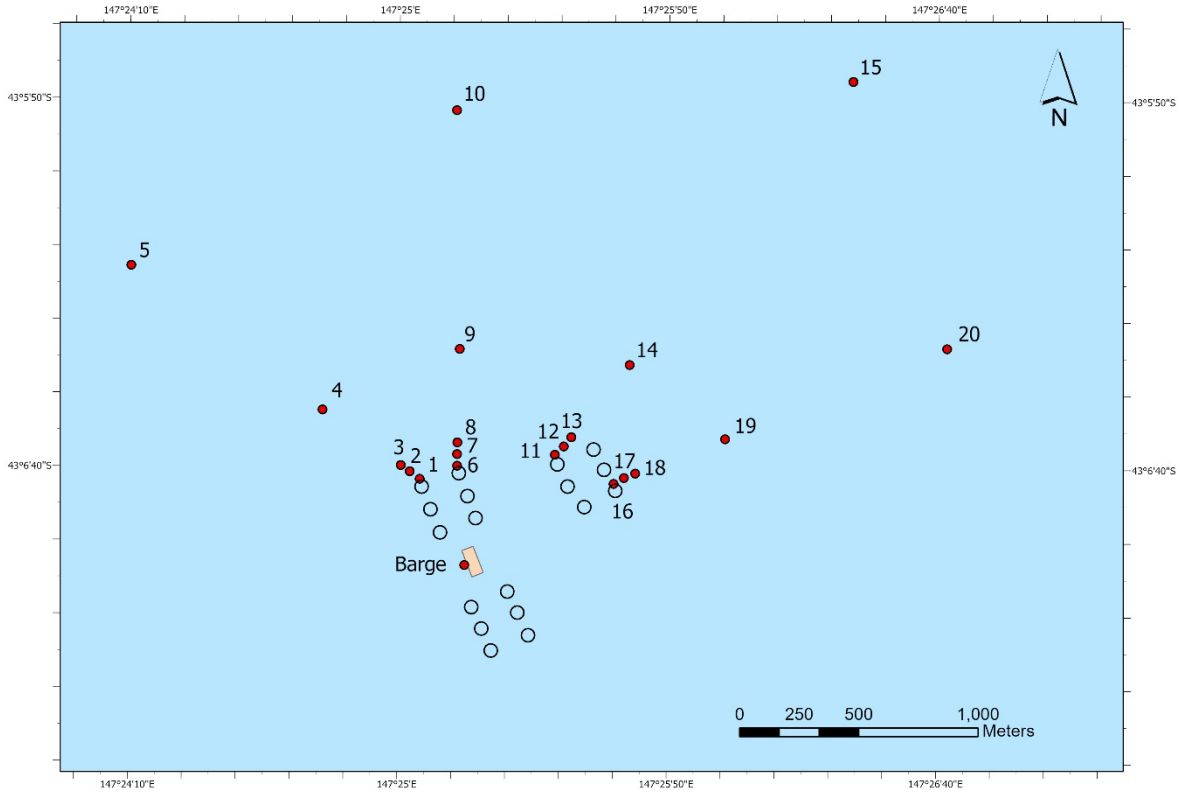


Figure 3-1: Locations of the discrete samples (red circles) collected during local scale water quality monitoring in March and December 2021. The open circles show the active pen locations.

3.1.2 Spatial patterns in key water column parameters – discrete samples

The physical variables in the water column differed between the March and December 2021 surveys (Figure 3-2). Principal components analysis highlights that the water column in March was warmer, particularly at the surface, but the concentrations of most nutrients were higher in bottom waters in December compared to March (Figure 3-2). In December, the water column was more stratified, as evidenced by a more distinct depth gradient for both temperature and salinity, relative to March (Figure 3-3).

Of all parameters, there was some evidence that DO (Figure 3-4), NH_4 (Figure 3-5) and PO_4 (Figure 3-6) varied with distance to the lease. For DO, this trend was particularly evident in the bottom water in December 2021 (Figure 3-5), where sites 0 m and 50 m from the cage had DO concentrations that were 1-2 mg/L lower than sites at 1500 m. PO_4 concentrations also appeared higher in proximity to the lease in bottom waters in December 2021. Although quite variable between transects, the highest NH_4 concentrations were observed in proximity to the lease in the surface waters in both surveys, and at 10 m depth in December (Figure 3-5). In contrast, there was no clear effect of distance on NO_x. Across both surveys, NO_x was higher in the bottom waters with the trend stronger in December than in March 2021 (Figure 3-5).

Total phytoplankton cell counts were highest on the surface across both March and December 2021 surveys, with concentrations approximately double in the December survey compared to March (Figure 3-7). In contrast, fluorescence was highest at 10 m stations and

comparable across both surveys (Figure 3-7). There were no strong patterns observed with proximity to the lease in total abundances of phytoplankton cells and fluorescence. Although there was also no clear pattern with distance for chlorophyll *a* biomass, concentrations were greater at depth and at site to the NE at 10 m (Figure 3-8).

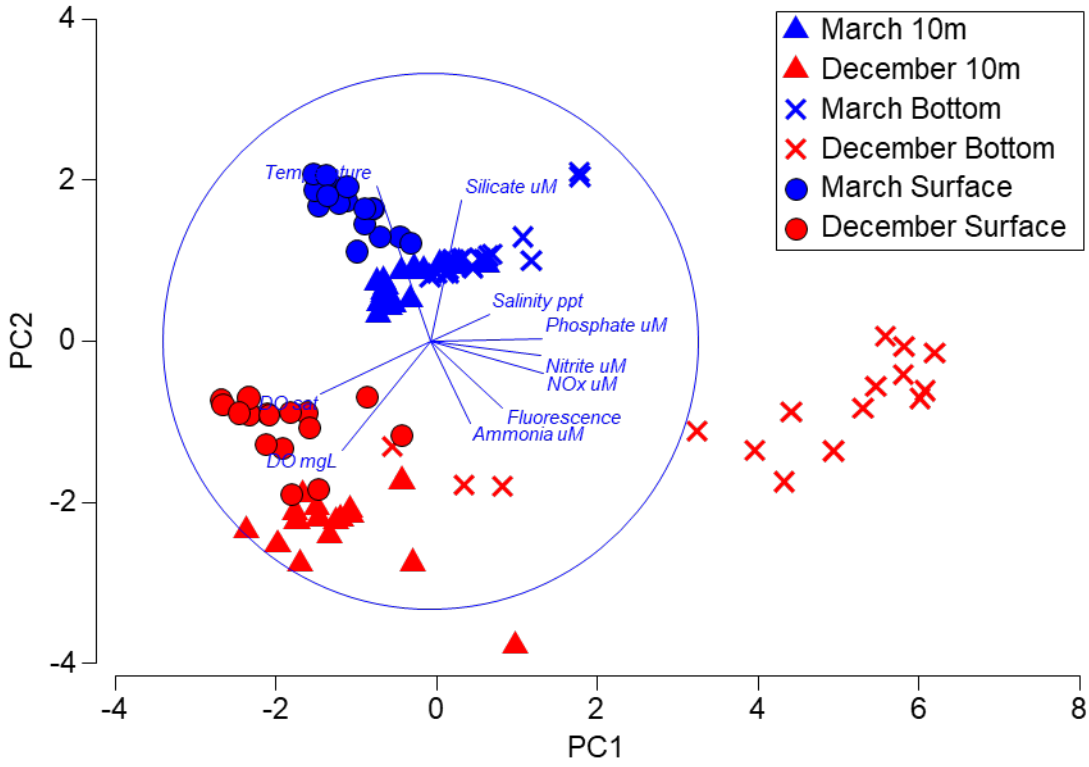


Figure 3-2: PCA plot of physiochemical parameters associated with the water column at the MF281 (East of Yellow Bluff) lease in March (blue) and December (red) 2021. Vectors correspond to eigenvectors from the PCA analysis, with coefficients in the linear combinations making up the principal components.

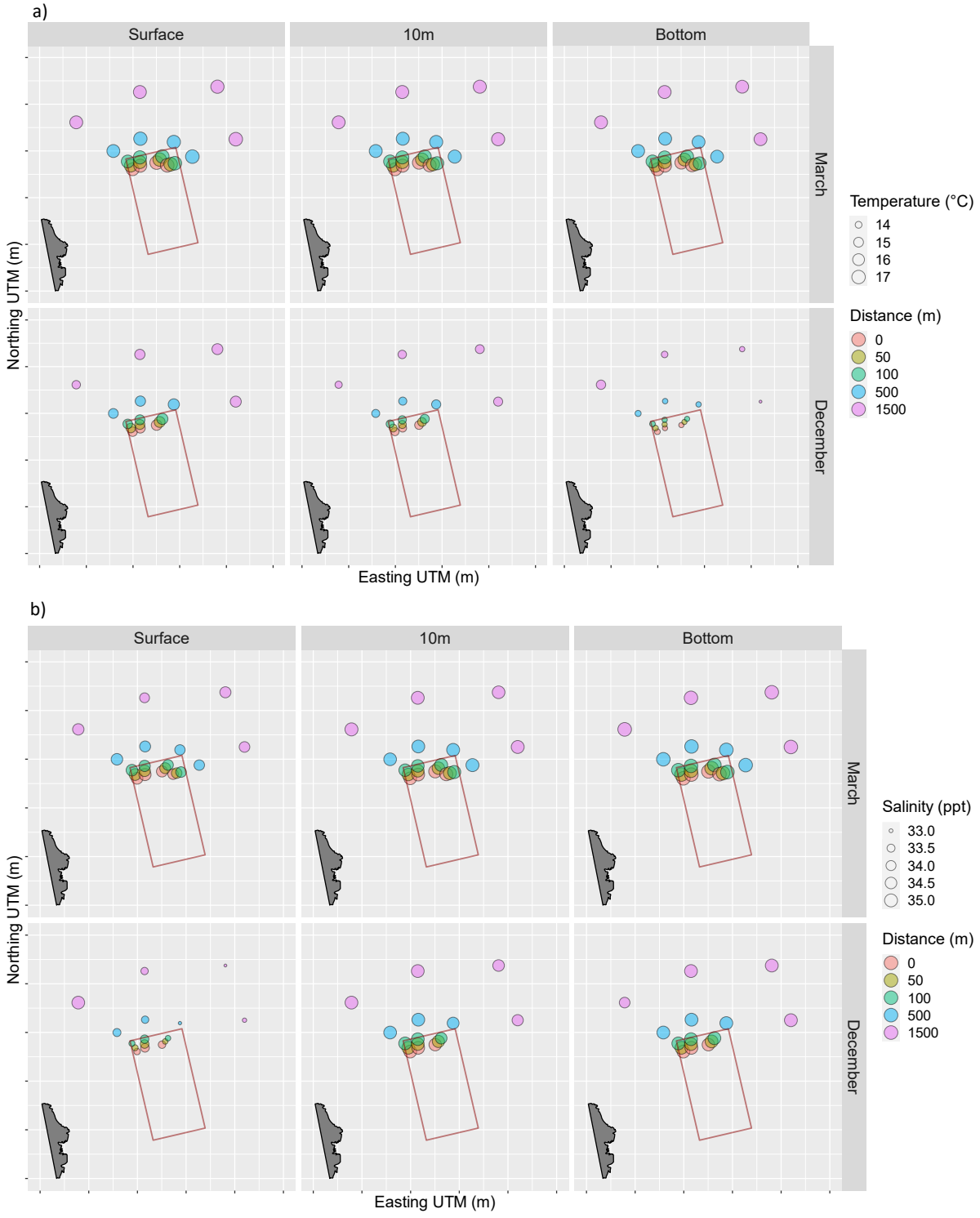


Figure 3-3: Bubble plots showing the relative a) temperatures (°C) and b) salinities (ppt) across three depth strata in both March and December 2021 at the 20 sampling stations surrounding the MF281 (East of Yellow Bluff) lease. Note that sampling was not conducted at stations 15-19 in December 2021.

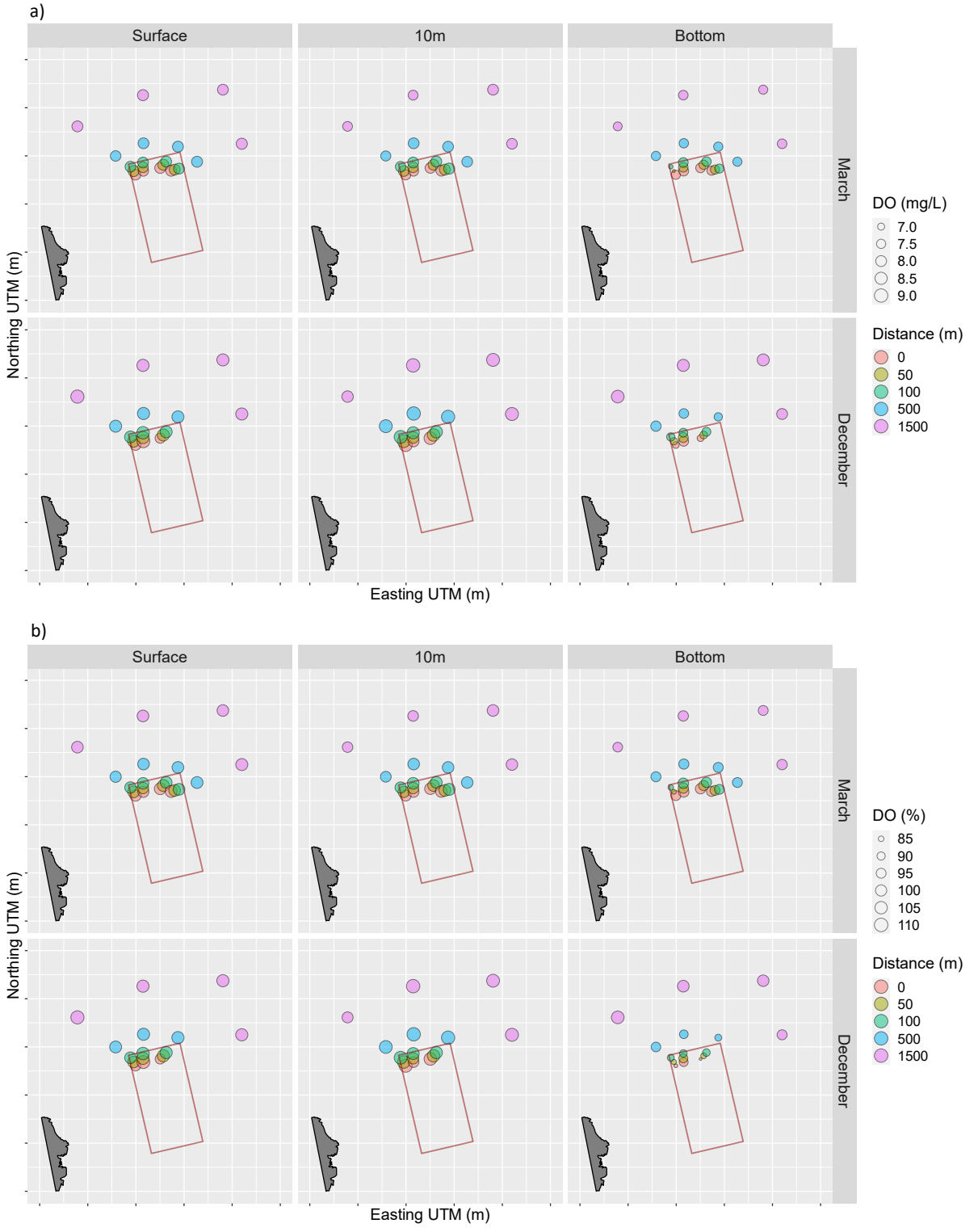


Figure 3-4: Bubble plots showing the relative concentrations of DO in a) mg/L and b) percentage saturation across three depth strata in both March and December 2021 at the 20 sampling stations surrounding the MF281 (East of Yellow Bluff) lease. Note that stations 15-19 were not sampled in December 2021.

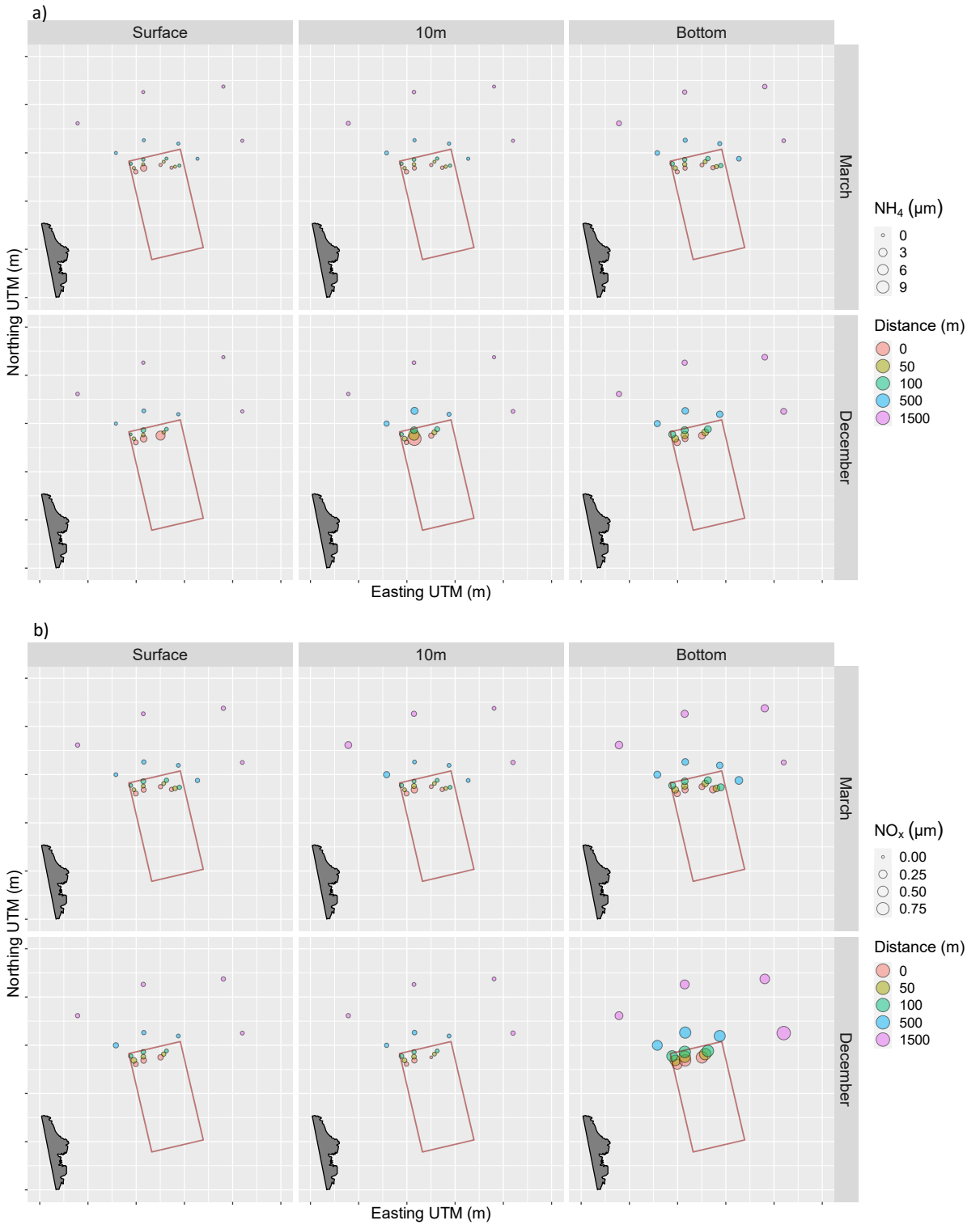


Figure 3-5: Bubble plots showing the relative concentrations of a) NH_4 (uM) and b) NO_x (uM) across three depth strata in both March and December 2021 at the 20 sampling stations surrounding the MF281 (East of Yellow Bluff) lease. Note that stations 15-19 were not surveyed in December 2021.

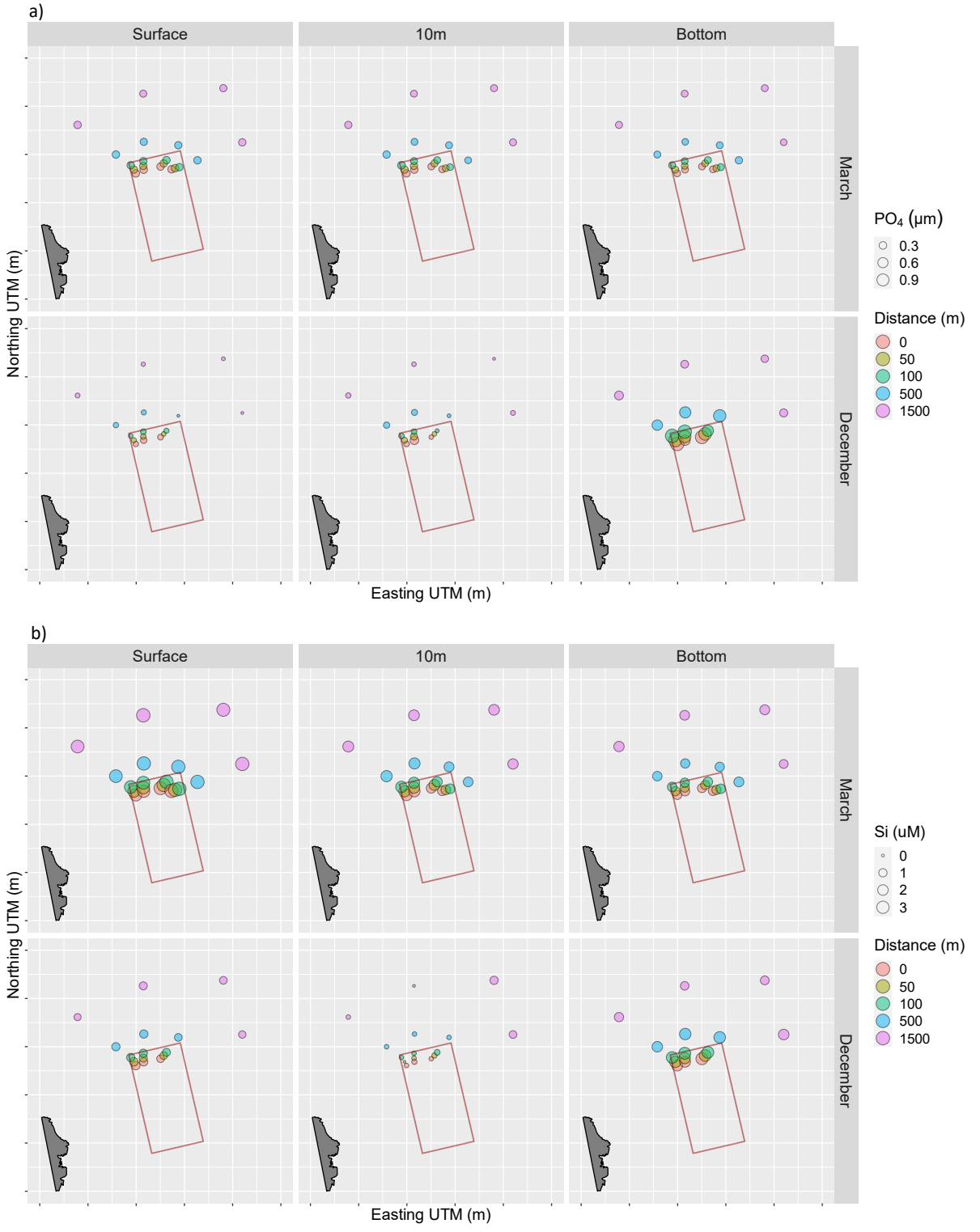


Figure 3-6: Bubble plots showing the relative concentrations of a) PO_4 (uM) and b) SiO_4 across three depth strata in both March and December 2021 at the 20 sampling stations surrounding the MF281 (East of Yellow Bluff) lease. Note that stations 15-19 were not surveyed in December 2021.

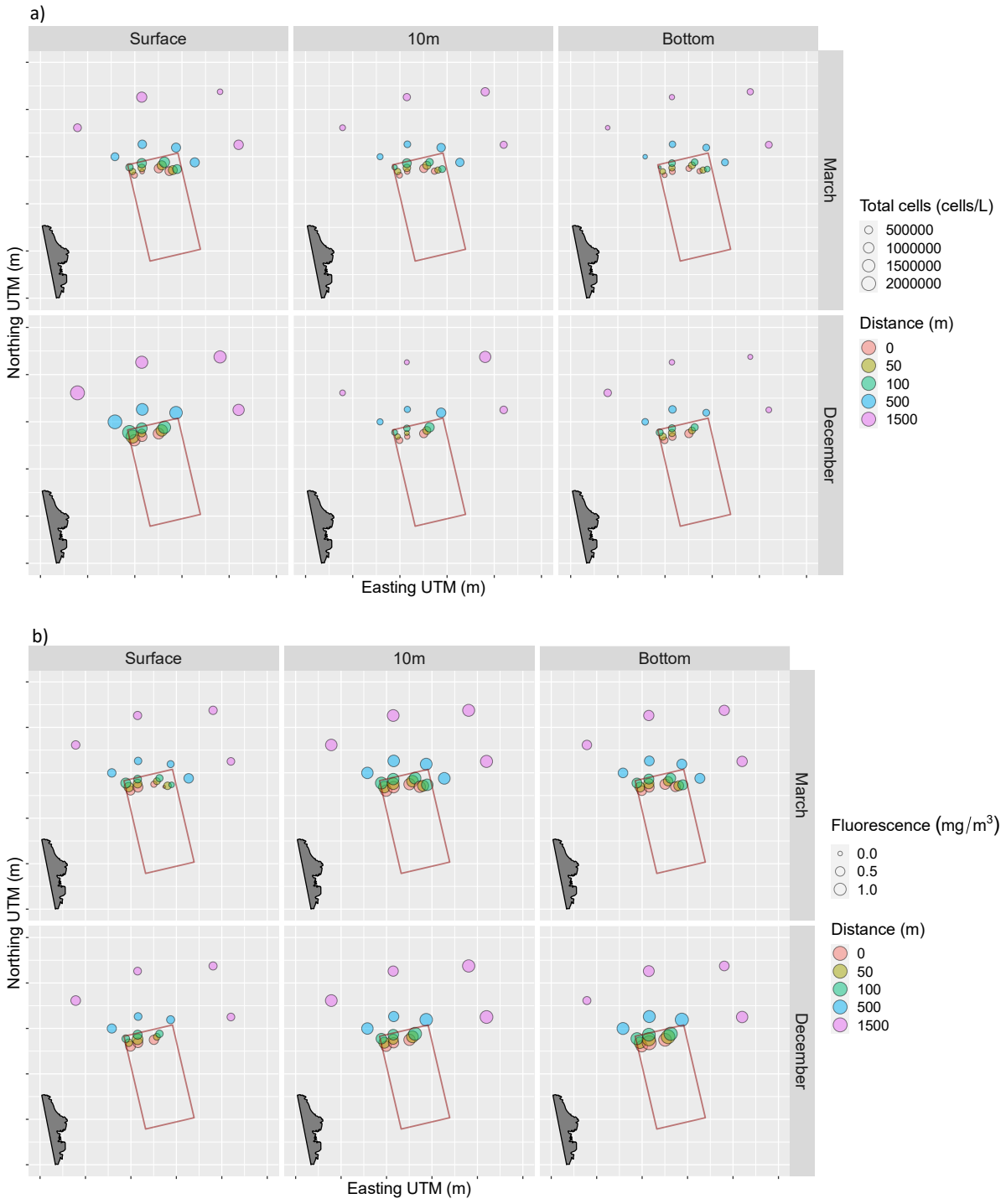


Figure 3-7: Bubble plots showing the relative concentrations of a) phytoplankton (cells/L) and b) fluorescence (mg/m^3) across three depth strata in both March and December 2021 at the 20 sampling stations surrounding the MF281 (East of Yellow Bluff) lease. Note that stations 15-19 were not surveyed in December 2021.

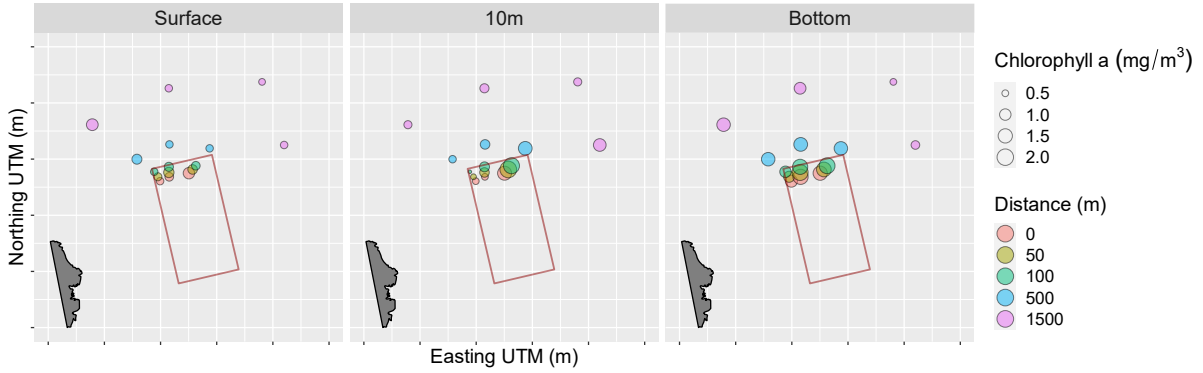


Figure 3-8: Bubble plots showing the relative biomass of chlorophyll a (mg/m^3) across three depth strata in December 2021 at sampling stations surrounding the MF281 (East of Yellow Bluff) lease. Note that chlorophyll *a* was only collected in December 2021 and stations 15-19 were not surveyed in December 2021.

3.1.3 Spatial patterns in phytoplankton communities – discrete samples

Like the physiochemical parameters, there was a clear difference in the phytoplankton community between the March and December 2021 surveys, and in both surveys the community changed with depth (Figure 3-9). The change with depth for the phytoplankton community was most evident in December which aligns with the greater stratification observed in physiochemical parameters in this survey (Figure 3-3). Vector analysis indicated that the March survey was characterised by a greater concentration of unidentified pennant diatoms, *Cerataulina pelagica* (centric diatom) and *Cylindrotheca* sp (pennate diatom) (Figure 3-9).

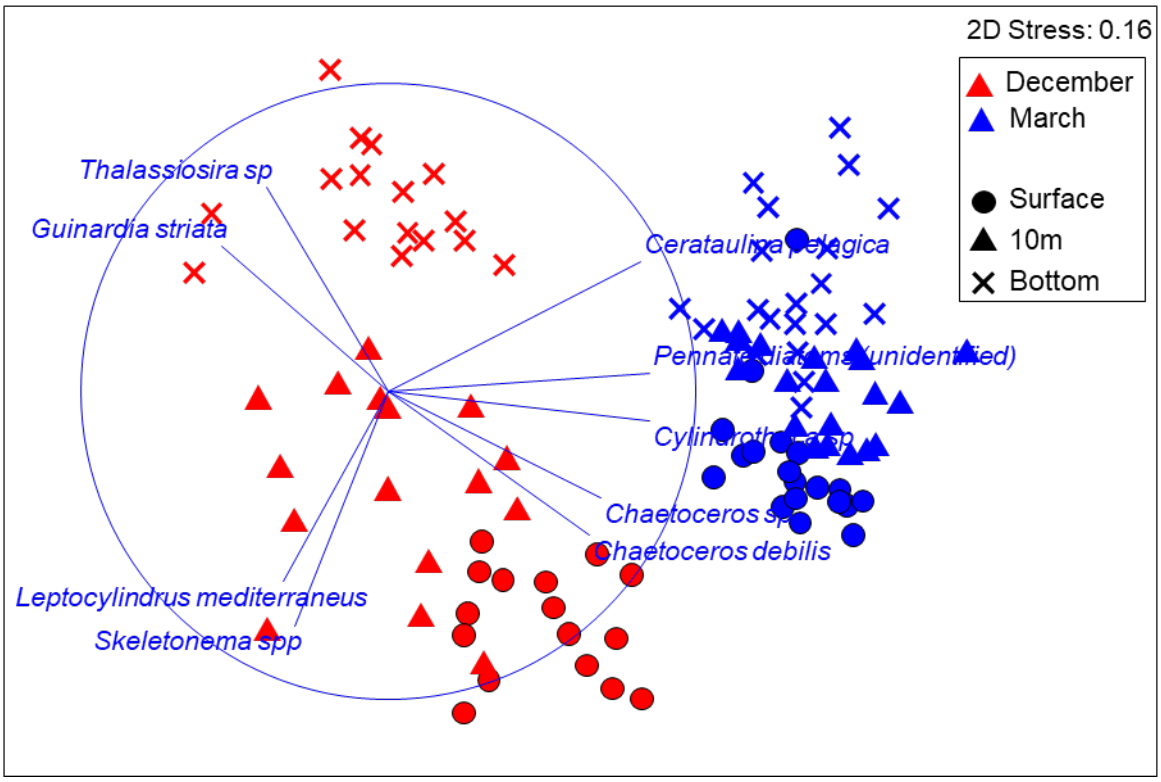


Figure 3-9: nMDS examining phytoplankton communities (all species) from the March and December 2021 sampling events. Labels indicate sampling event and symbols indicate depth of sampling. Data have been fourth-root transformed with a Bray-Curtis similarity matrix. Pearson's vector overlays contributing to ordination with a base variable comparison of >0.7 are included

When the March and December 2021 surveys were examined separately, there appeared to be a spatial pattern associated with direction in March 2021. The ordination suggests that the phytoplankton to the NW differed from the other direction, but this needs to be treated with some caution given the relatively high stress (0.22) (Figure 3-10). Regardless, depth stratification was the dominant determinant of phytoplankton community composition in both surveys and there was no evidence of communities changing with distance from the cages (Figure 3-10). Vector analysis indicated that different species were driving community trends observed with depth in December compared to March 2021, and this was mainly due to shifts in the diatom species present (Figure 3-10). When the phytoplankton community was separated into diatoms and dinoflagellates/flagellates, depth stratification was reflected in the diatom communities in both March and December. In contrast, dinoflagellate/flagellate communities showed no clear distribution with depth (Figure 3-11) and again, there was no evidence of a distance effect for either diatoms or dinoflagellates/flagellates.

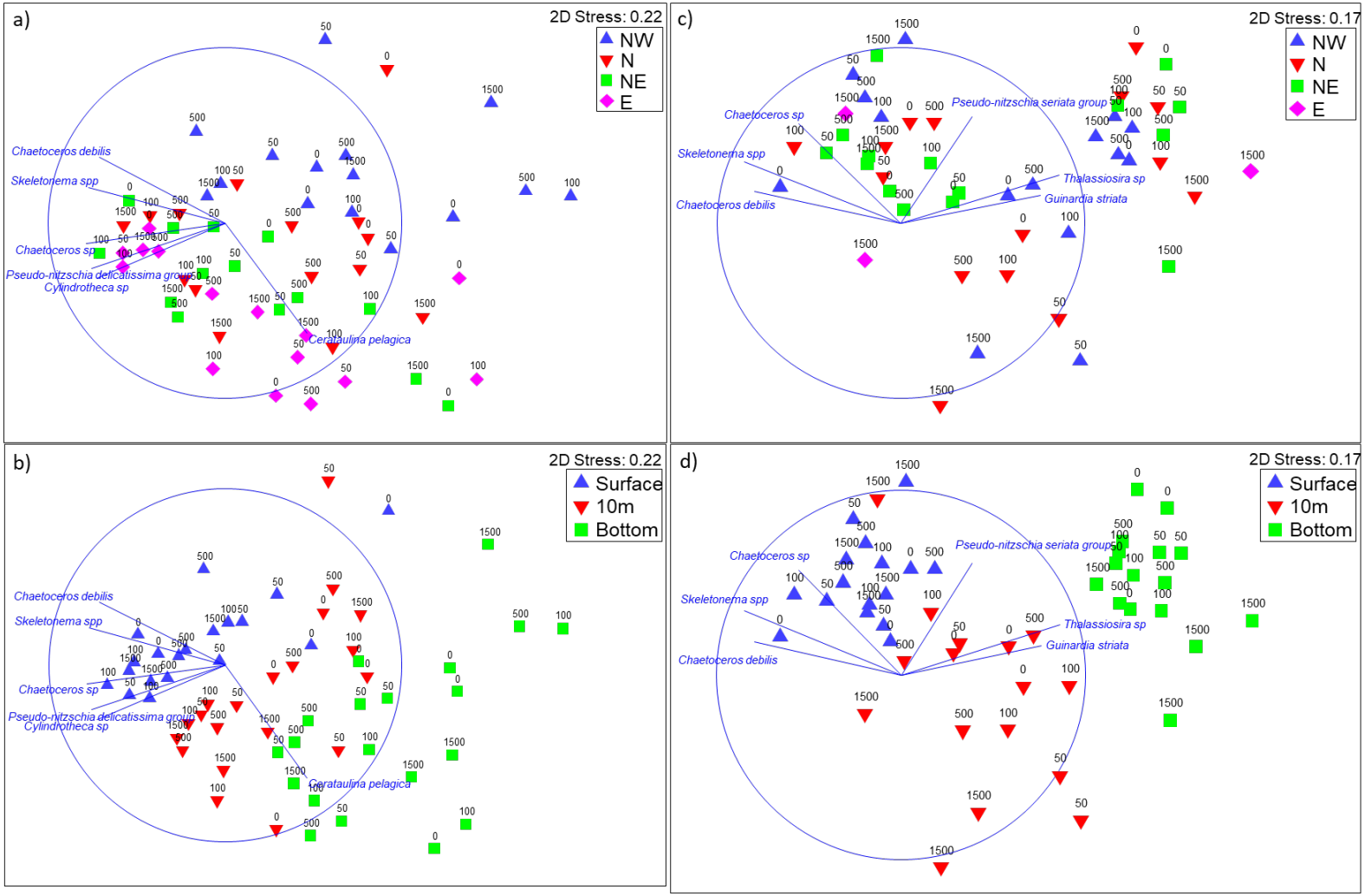


Figure 3-10: nMDS based on Bray-Curtis similarity examining phytoplankton communities across both the March (a -b) and December (c-d) 2021 sampling events. Data are shown grouped by both sampling direction (a, c) and sampling depth (b, d). Labels indicate distance from the nearest stocked cage. Pearson's vector overlays contributing to ordination with a base variable comparison of >0.7 are included.

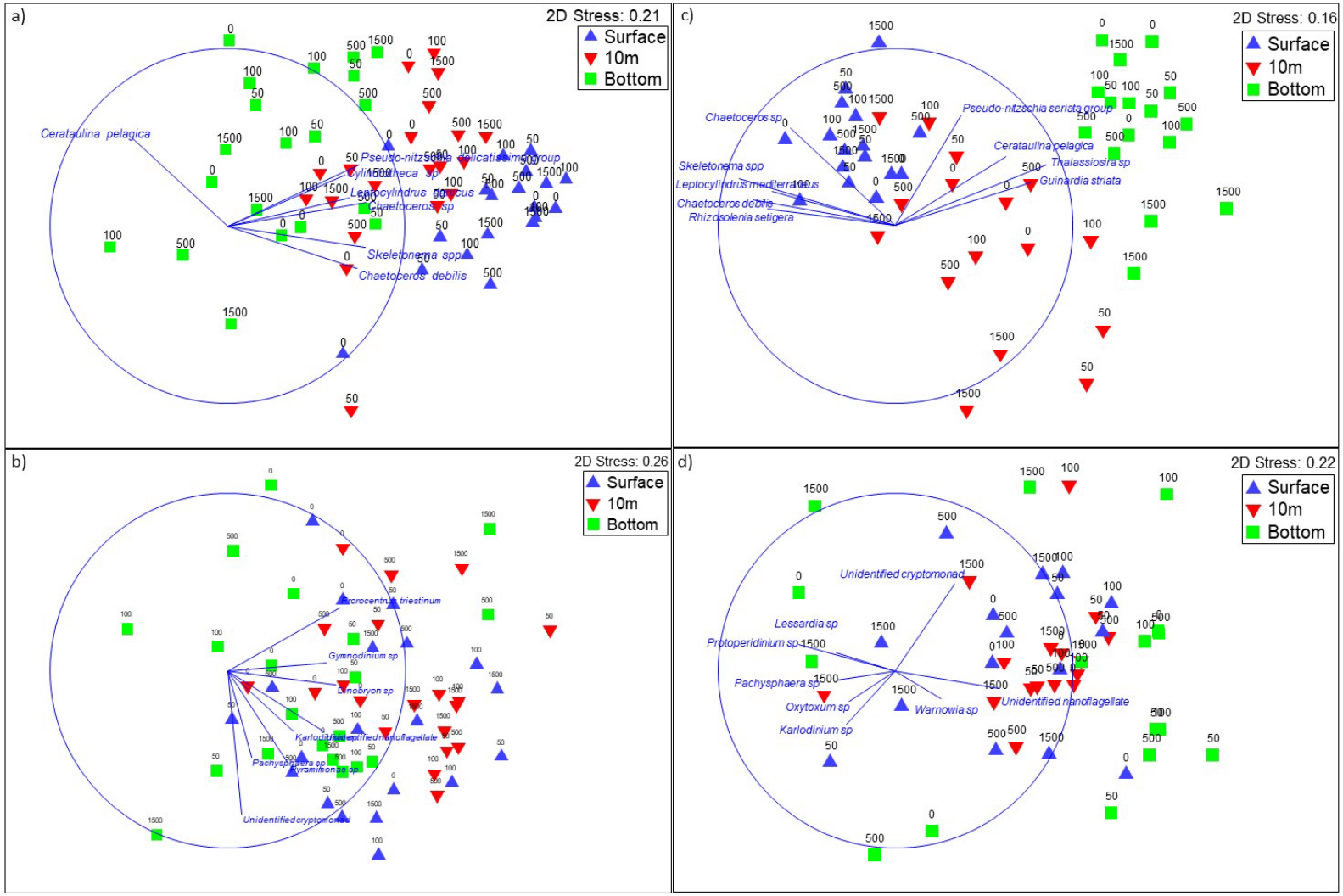


Figure 3-11: nMDS based on Bray-Curtis similarity examining phytoplankton communities across both the March and December 2021 sampling events and depths by diatoms (a, c) and dinoflagellates & flagellates (b, d) from the March (a-b) and December (c-d). Labels indicate distance from the nearest stocked cage. Pearson's vector overlays contributing to ordination with a base variable comparison of >0.7 are included.

3.1.4 High resolution mapping of key physicochemical parameters

Similar to the pattern observed from the discrete samples, the continuous sampling captured the physiochemical differences between March and December 2021, with warmer and more saline surface waters in March compared with December (Figure 3-12). The continuous sampling revealed a north-south gradient in salinity across the survey area in both surveys, highlighting the influence of Derwent estuary waters in the region (Figure 3-12).

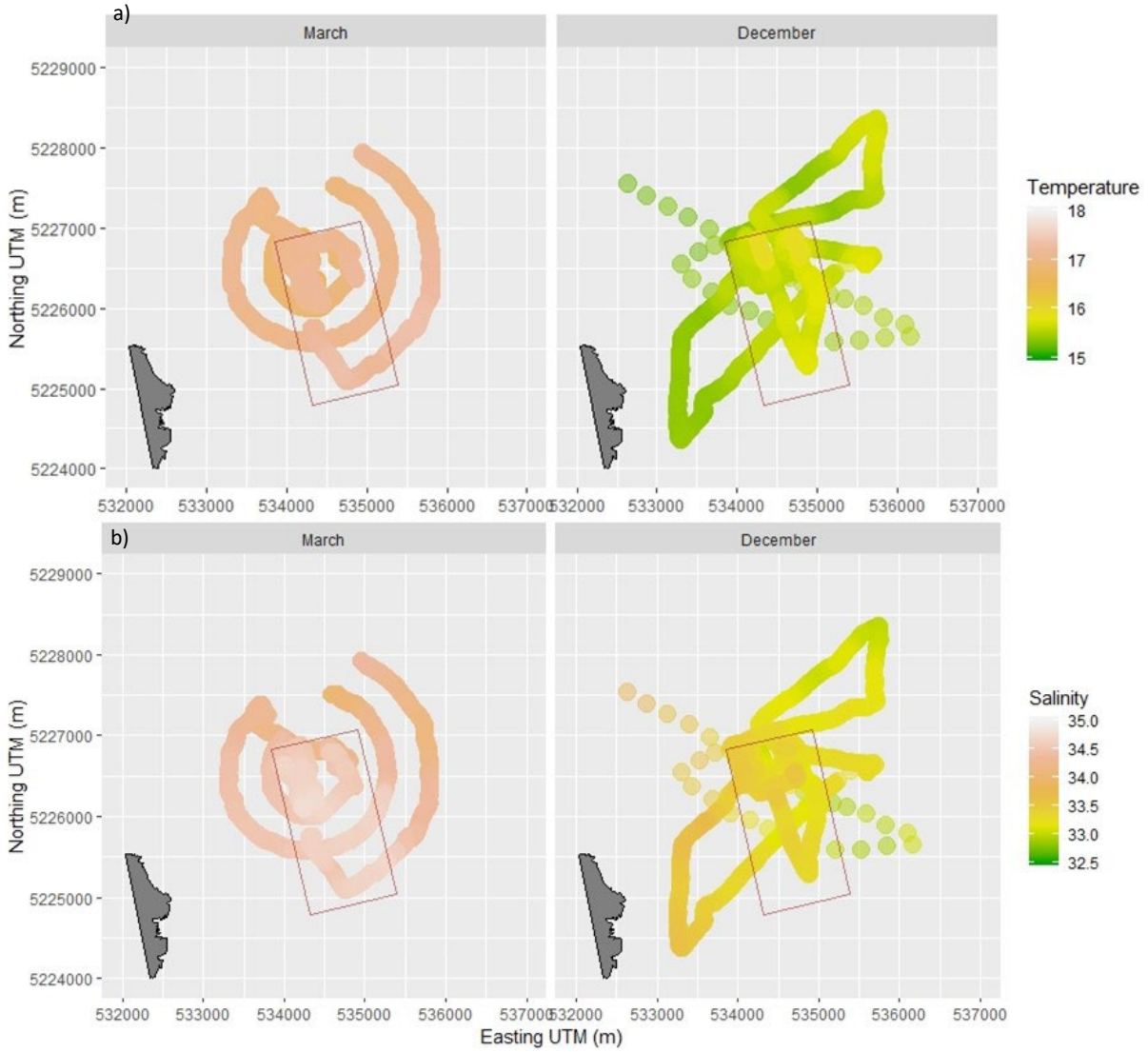


Figure 3-12: Heat maps produced from continuous sampling of surface water column for a) temperature C and b) salinity (ppt) by the DUDES sampling system in both March and December 2021.

Continuous sampling of NH_4 near the lease demonstrated the patchy distribution of this variable across both space and time (Figure 3-13), however concentrations were clearly more elevated on the lease. NH_4 reached up to 5 uM in patches within the lease, but concentrations were typically much lower beyond the lease boundary (Figure 3-13). Concentrations of NH_4 were relatively consistent between March and December 2021 surveys. In contrast, there were clear differences between surveys in surface NO_x, with higher values recorded in March compared to December 2021. Unlike NH_4, there was no clear pattern in relation to proximity to the lease for NO_x (Figure 3-13).

The pattern for fluorescence also highlighted patchiness in the surface water column across both space and time (Figure 3-14). Although there is some indication that fluorescence was often more elevated at the lease, the pattern was more difficult to discern than NH_4 (Figure 3-13, Figure 3-14). There also appeared to be more of a temporal trend in fluorescence, with values generally increasing throughout the day (see section 3.1.5), which further complicates the interpretation.

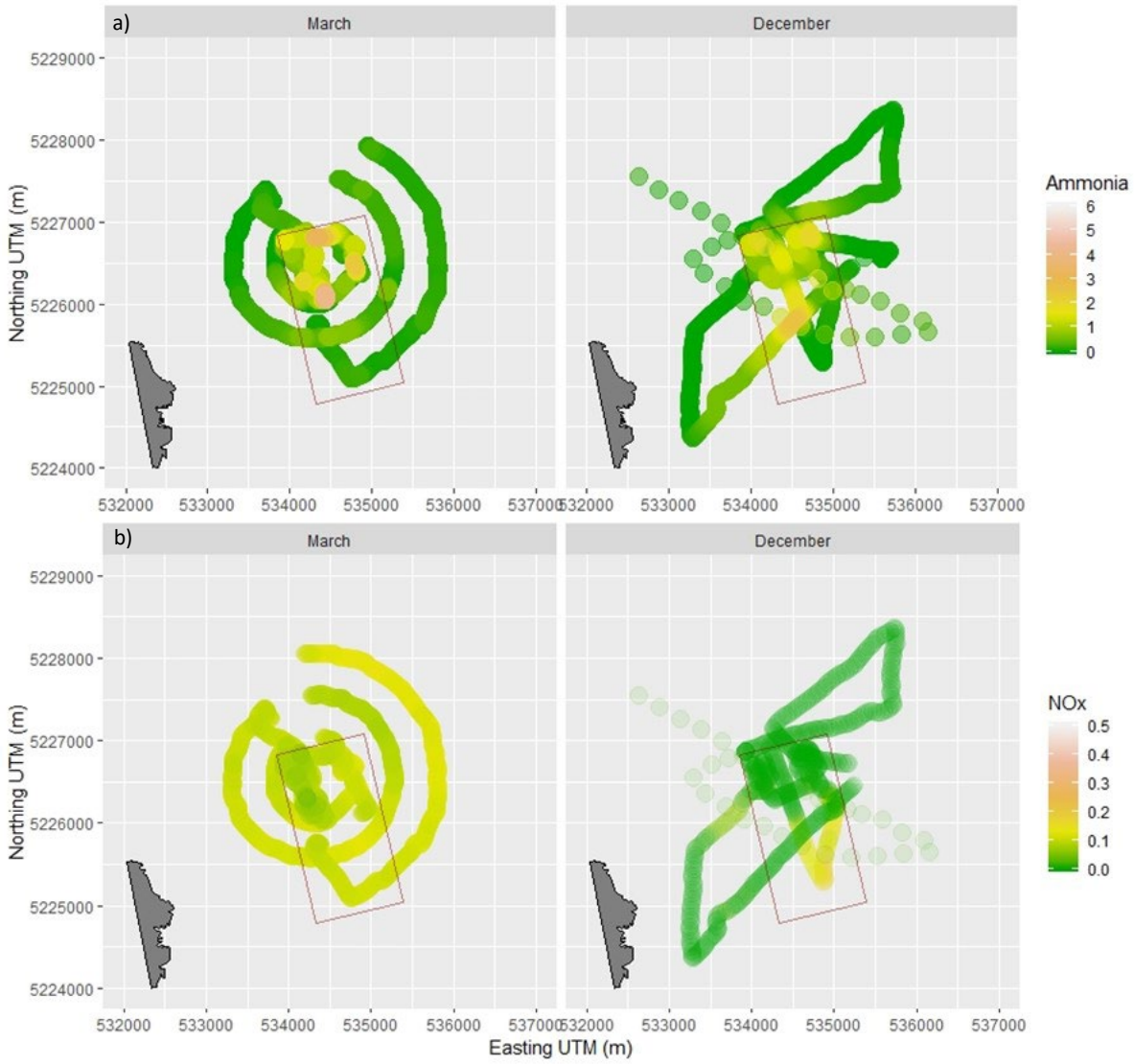


Figure 3-13: Heat maps produced from continuous sampling of surface water column for a) NH_4 (uM) and b) NO_x (uM) by the DUDES sampling system coupled with a Seal AA100 in both March and December 2021.

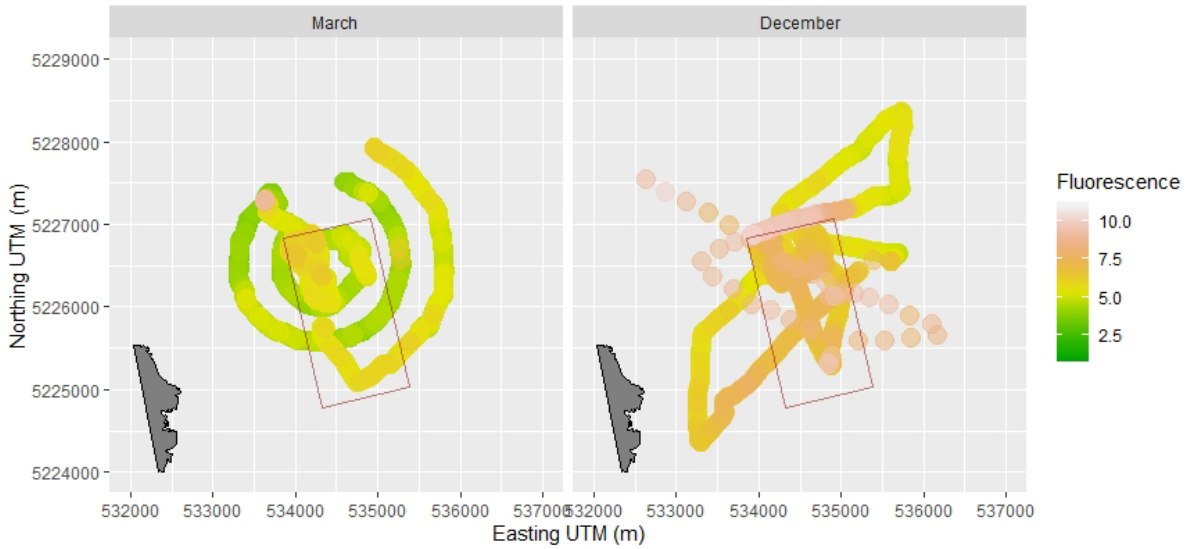


Figure 3-14: Heat maps produced from continuous sampling of surface water column for fluorescence (mg/m^3) collected by the DUDES sampling system in both March and December 2021.

3.1.5 Temporal variability of water column parameters

Sampling at the feed barge (see Figure 3-1) showed variation in water column parameters throughout the day, and the patterns varied between March and December 2021 surveys and with sampling depth (Figure 3-15, Figure 3-17). For example, in December NH_4 concentrations varied significantly throughout the day with concentrations highest in the morning at 10m and the bottom, and in the early afternoon at the surface. In March 2021, NH_4 concentrations were lower, but they also varied through the day with surface concentrations increasing throughout the day. Stratification in dissolved oxygen concentrations and percent saturation was also more evident in December (Figure 3-16). Results for NO_x, NO_2, PO_4 and Si also highlight differences between surveys, depth, and time of day. Notably, concentrations were typically highest in bottom waters in December, but in March PO_4 and Si concentrations were highest in the surface. A decrease in surface fluorescence across the 8-hour sampling period was observed at the barge in March (Figure 3-17), which is opposite to the trend suggested by the continuous sampler (Figure 3-14). Total phytoplankton cell counts from surface samples also declined throughout the day in March but were higher and more variable across the day in December (Figure 3-17).

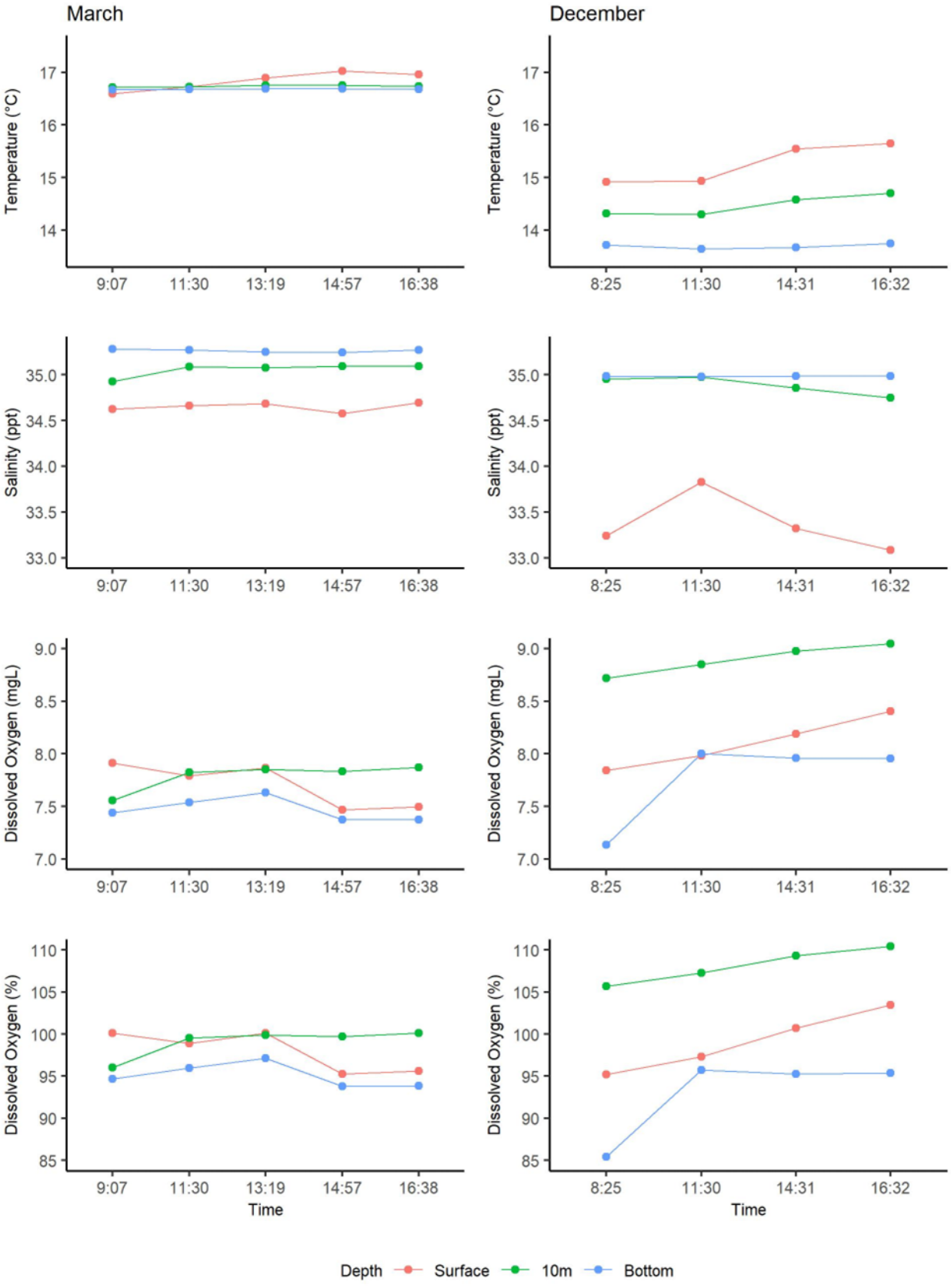


Figure 3-15: Variation in temperature (°C), salinity (ppt) and DO (mg/L and % saturation) at the barge survey site across an eight-hour period in March and December 2021.

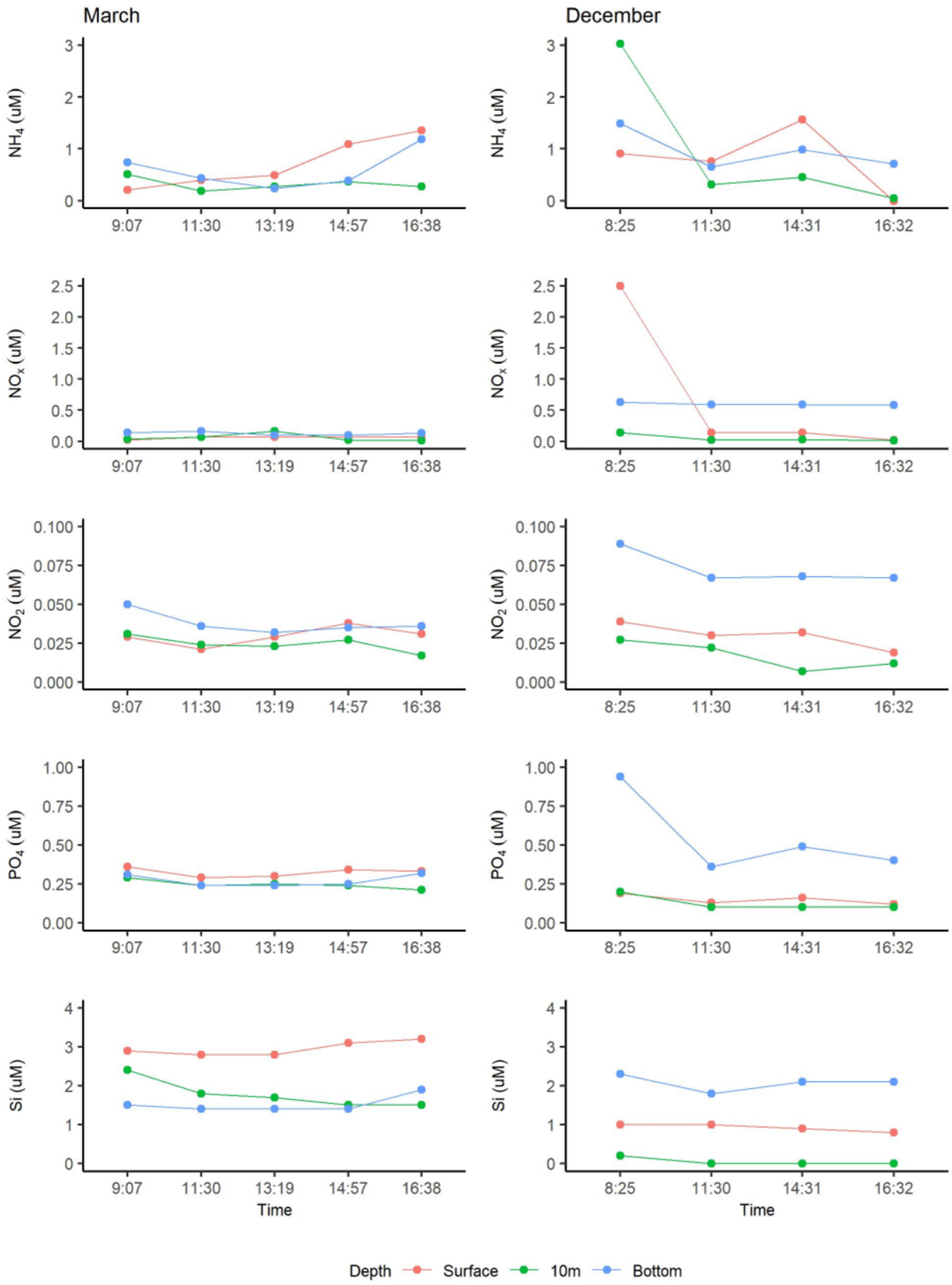


Figure 3-16: Variation in NH_4 (uM), NO_x (uM), NO_2 (uM), PO_4 (uM) and Si (uM) at the barge survey site across an eight-hour period in March and December 2021.

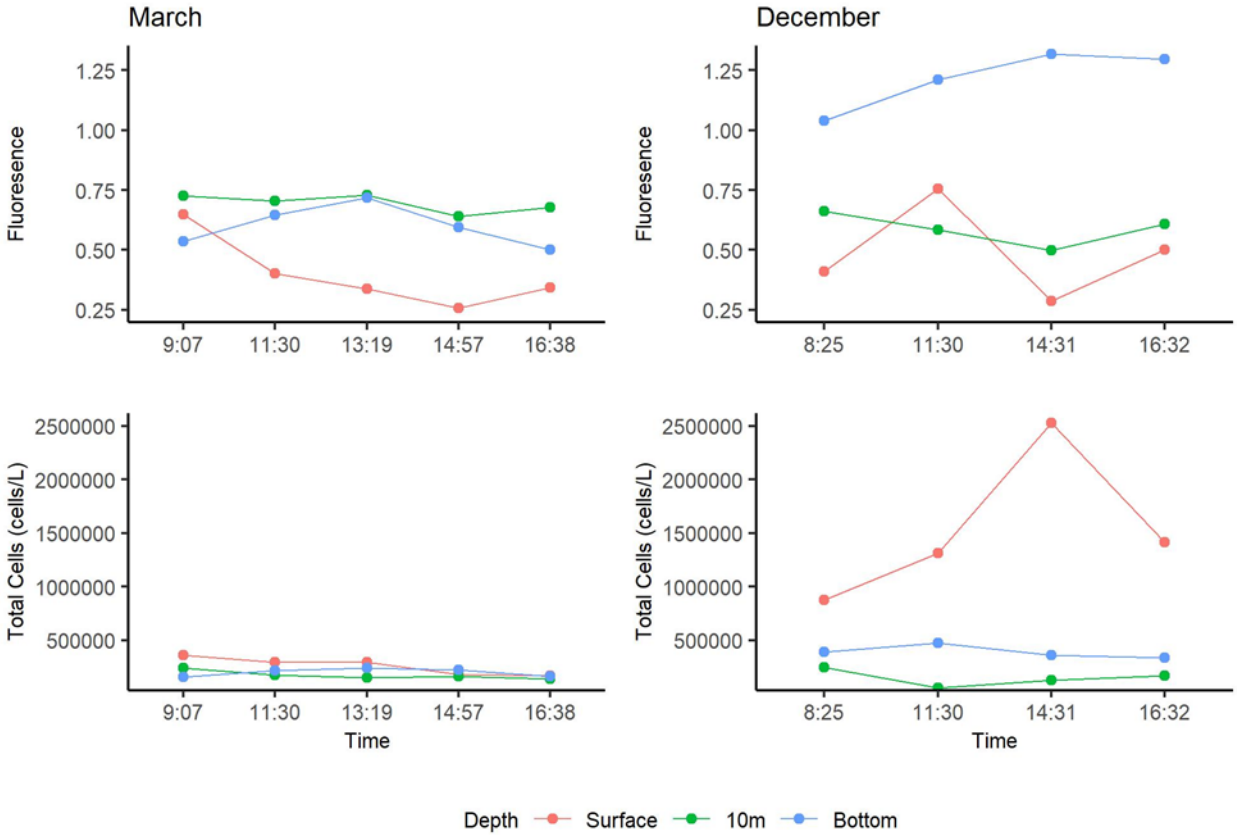


Figure 3-17: Variation in fluorescence (mg/m^3) and total phytoplankton cells (cells/L) at the barge survey site across an eight-hour period in March and December 2021.

3.1.6 Summary and learnings for broadscale monitoring of Storm Bay

The local scale sampling and the comparison of three different sampling approaches (i.e. inline, discrete and temporal sampling) highlighted the immense spatial and temporal variability in the key physicochemical and biological properties of the water column. This presents a challenge for detecting farm related effects at local and broad scales, particularly effects that are indirect, more subtle, and incremental through time. Nonetheless, the application of a continuous inline system did capture the local footprint of NH_4 in surface waters produced via fish excretion. Similarly, the discrete sampling provided evidence of local scale effects on DO and PO_4 in bottom waters. The local scale changes in bottom waters most likely result from the mineralisation from the solid waste (faeces and feed) footprint on the seabed (see section 4 for a description of the benthic footprint). There were also patterns evident with both direction and depth for chlorophyll *a*, phytoplankton community composition and abundance, but a clear relationship with proximity to the lease was more difficult to discern against background variation. From a broad scale perspective this sampling has highlighted the utility of some key response parameters that will more readily reveal farm related effects on water quality, particularly in the vicinity of leases, but most critically, it shows the importance of a robust design that has sufficient power to detect meaningful change given the spatial and temporal variability inherent in the water column.

Further, environmental performance in water quality is assessed against trigger levels (see below section for further details) at a compliance site for each lease. If the annual rolling median or monthly (chlorophyll *a* biomass only) values at the compliance site exceed these

trigger levels the Licence holder is required to undertake additional investigations and analysis of other environmental data to determine to what extent the exceedances are caused by marine farming operations. We suggest that the additional investigation could include a local scale monitoring exercise through inline sampling as outlined above if the exceedance is persistent. This sampling is invaluable for monitoring because it provides a more comprehensive and informative snapshot of the spatial footprint of a specific salmon lease. However, caution must be exercised if the results of nutrient monitoring from different laboratories are compared, as differences in sampling methods and instrumentation can impact the results (Ross & MacLeod 2013) e.g. CSIRO process the nutrient samples for NH_4, whereas AST process for total ammoniacal nitrogen (TAN). Ideally the samples from local and broadscale monitoring should be processed through the same laboratory or if this is not possible, duplicate samples should be compared across laboratories.

3.2 Water column monitoring - Broadscale

3.2.1 BEMP

The Broadscale Environmental Monitoring Program (BEMP) for Storm Bay was initiated in August 2019 to provide knowledge and information about the surrounding water quality. The objective of the sampling is to document spatial and temporal trends in key parameters, allowing assessment of the interactions between salmon farming and the water column, in the context of other key drivers of environmental change.

Design

In the Storm Bay project, twenty-seven BEMP sites and two project sites were sampled monthly. The BEMP sites were selected by the PA and EPA, with the intention of monitoring the interactions between salmon farming and the water column at varying spatial and temporal scales, with the potential to detect localised effects at individual sites and cumulative effects at multiple sites. IMAS added the two project sites to capture the near scale at multiple leases. Collectively, the monitoring sites extended over three spatial scales (near-scale, [< 500 m from a lease], intermediate [< 5 km] and far-field [> 5 km]).

The sampling details for the sites are summarized in Table 2. Sampling commenced at various time points during the project based on environmental licence and project requirements. At each site, dissolved oxygen, temperature, salinity, turbidity, fluorescence, and pH were measured (full water column profile) using a CTD (Seabird SBE 19 or a Yeokal). The CTD measurements are reported on at 0.5 – 1 m below the surface, at 10 m depth, and within 1 m of the seabed.

At each of these depths, discrete water samples were collected using Teflon sampling bottle (surface samples only) or Niskin bottles for the analysis of total nitrogen (TN), total nitrogen Kjeldahl (TKN), total phosphorus (TP), total ammoniacal nitrogen (TAN), nitrate + nitrite (NOx), nitrate (NO_3), nitrite (NO_2), dissolved organic carbon (DOC), dissolved reactive phosphorus (DRP) and silica (SiO_2). Integrated water column samples for chlorophyll *a* and phytoplankton counts were collected from the surface to 12 m depth in Storm Bay and on the surface in the Derwent Estuary using a weighted Lund tube. All samples were processed by AST.

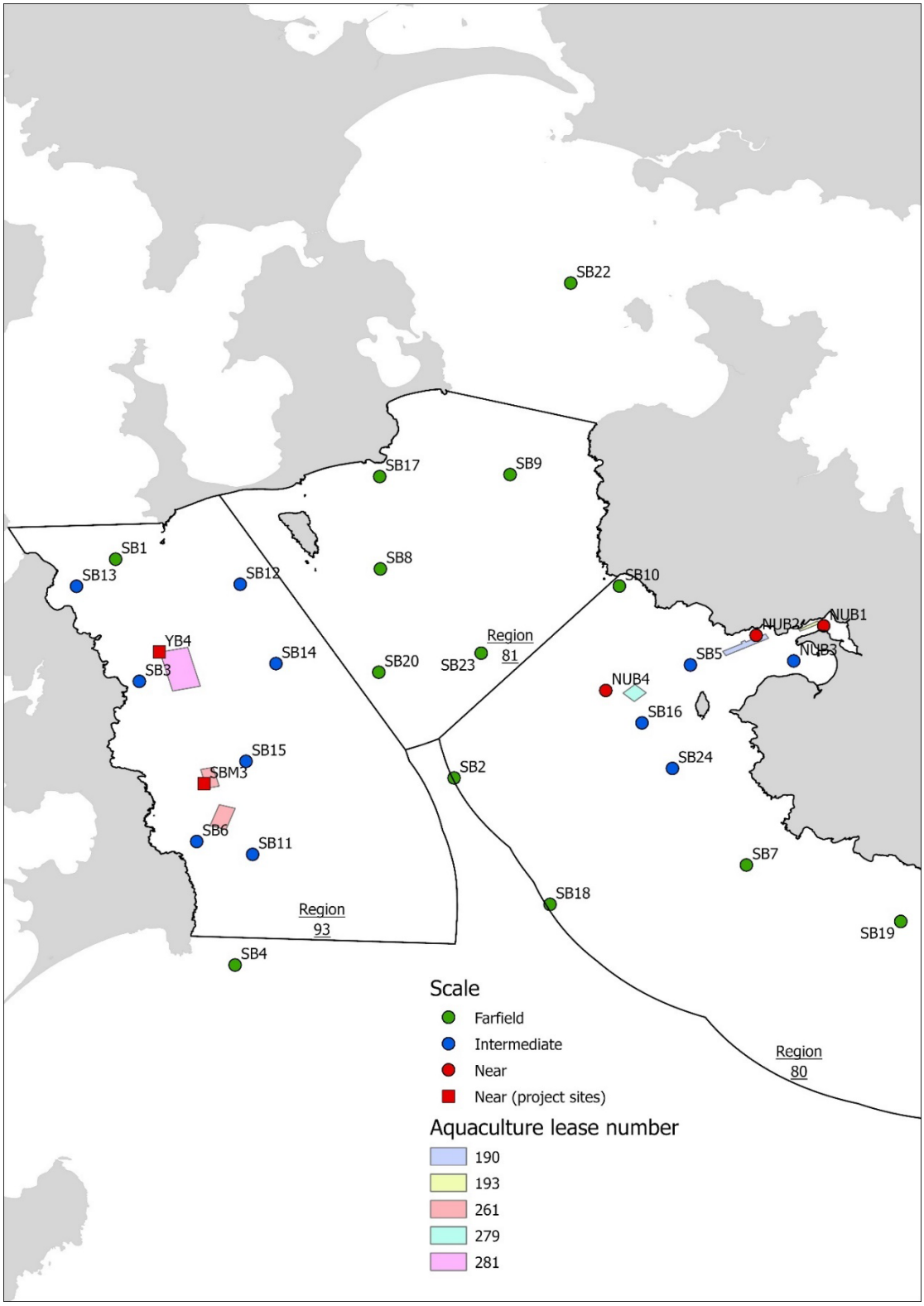


Figure 3-18: Map showing the location of the water column monitoring sites (circle = BEMP monitoring sites and square = project sites) in Storm Bay and their classification as near, intermediate and far-field.[1]

[1] Note: Sites SB11, SB16, NUB4, SB4 SB8, SB20 and SB23 were reclassified from what was proposed in the ELs as intermediate, intermediate, near scale, far-field, far-field, far-field, far-field, respectively, based on their distances to current active leases.

Table 3-2**:** The current Storm Bay broad-scale sampling sites, categorisation (near scale, intermediate or far-field).* Denotes project sites and + compliance sites.[1]

Site	Scale	Date commenced
YB4*	Near	Feb-20
SMB3*	Near	Feb-20
BEMP-SB1	Far-field	Aug-19
BEMP-SB2	Far-field	Aug-19
BEMP-SB3+	Intermediate	Aug-19
BEMP-SB4	Far-field	Aug-19
BEMP-SB5+	Intermediate	Aug-19
BEMP-SB6	Intermediate	Aug-19
BEMP-SB7	Far-field	Aug-19
BEMP-SB8	Far-field	Aug-19
BEMP-SB9	Far-field	Aug-19
BEMP-SB10	Far-field	Aug-19
BEMP-SB11	Intermediate	Aug-19
BEMP-SB12	Intermediate	Aug-19
BEMP-SB13	Intermediate	Aug-19
BEMP-SB14	Intermediate	Aug-19
BEMP-SB15	Intermediate	Aug-19
BEMP-SB16	Intermediate	Feb-20
BEMP-SB17	Far-field	Jun-21
BEMP-SB18	Far-field	Jun-21
BEMP-SB19	Far-field	Jun-21
BEMP-SB20	Far-field	Jun-21
BEMP-SB22	Far-field	Jun-21
BEMP-SB23	Far-field	Jun-21
BEMP-SB24	Intermediate	Feb-20
NUB1	Near scale	Aug-19
NUB2	Near scale	Aug-19
NUB3	Intermediate	Aug-19
NUB4	Near	Aug-19

3.2.2 Spatial and temporal variation in key parameters

Storm Bay is a complex system with considerable inter and intra-annual variation in water properties, which are driven by global and local forcings (Harris et al. 1991, Swadling et al. 2017, Wild-Allen et al. 2021). Across almost 3 years of monitoring (i.e. August 2019 to April 2022), there were distinct trends in key variables for surface and bottom waters samples (IMAS 2021, 2022). The trends in the mid water (10 m) samples were often similar to either surface or bottom waters, depending on the variable measured (IMAS 2020a, 2021, 2022). Hereafter, we focus on presenting the results from the surface and bottom water samples.

Throughout the monitoring period, there was an annual increase in the mean summer and winter seawater temperatures (Figure 3-19), and a decrease in the mean summer DO levels (Figure 3-20). The sites with the highest surface seawater temperatures were in the SE region of Storm Bay while the sites with the lowest DO were found in the NW corner of Storm Bay. By contrast, in the bottom waters the temperature was more homogeneous with the lowest values recorded in Fredrick Henry Bay. The lowest values of DO were recorded at the bottom waters at some sites close to salmon farms (i.e. SBM3, NUB1, YB4 and NUB4).

Salinity in the bottom waters varied little through time but in the surface waters there were consistently lower values of salinity recorded in winter than summer (Figure 3-21). The salinity in the surface waters were higher and lower, respectively in summer-autumn 2020-2021 than 2019 particularly in the oceanic sites, which could reflect stronger influence of the EAC eddies during these periods. The lowest values of salinity were recorded in the surface waters of SB1, SB12, SB14 (Figure 3-21), during strong La Niña years when rainfall was higher (Figure 3-22). Plots of temperature versus salinity, based on CTD profiles throughout the water column show that fresher surface waters were also common at sites SB12, SB3, SB14, SB8, SB9 and YB4 and to a lesser extent SB6 and SB15 (Figure 3-23). This reflects circulation in Storm Bay, where fresh surface waters flow from NE and S from the Derwent Estuary. SiO_2 in the surface waters was highest in winter – spring (Figure 3-24), particularly at sites SB1, SB22, and NUB1 when freshwater inputs were highest.

At most sites, the NO_x (Figure 3-25), NO_3 (Figure 3-26) and DRP (Figure 3-27) showed clear seasonal trends, with higher concentrations through the winter – spring compared to summer – autumn. There were also higher values of these nutrients in the bottom waters compared with the surface waters. The spatial and temporal variation in nutrient concentrations and temperature could be linked to the varying influence of the three dominant currents in Storm Bay (Buchanan et al. 2013) and changes in the flow from the Derwent Estuary. The increase in nutrients during winter – spring are linked to the strengthening of the sub-Antarctic current resulting in higher values of NO_x and NO_3 at the oceanographic sites of SB4, SB18 and SB19 (Figure 3-25, 3-27) while the increased flow from the Derwent Estuary (Figure 3-28) during winter - spring was accompanied by higher values of DRP at sites along the western side of Storm Bay (Figure 3-27). The decline in these nutrients during summer – autumn relates to the retraction of the sub-Antarctic current, presence of the Leeuwin current or presence of EAC eddies during some years and declines in the flow of the Derwent River (Figure 3-28).

By contrast, the concentrations of TN (Figure 3-29), TKN (Figure 3-30), TP (Figure 3-31), TAN (Figure 3-32), NPOC (Figure 3-34), NPOC dissolved (Figure 3-35) varied interannually with weak or unclear seasonal trends. There is some indication that the values of TN, TKN, NPOC,

NPOC dissolved have increased through time but with high variability between seasons and sites. For TN and TKN summer and autumn show an increasing trend but winter a decreasing trend. TN (Figure 3-29) was higher at sites on the E than the W side of Storm Bay, whilst TKN (Figure 3-30), NPOC (Figure 3-34), and NPOC dissolved (Figure 3-35) were higher at the coastal than oceanic sites. The values of TP decreased throughout the sampling and were much higher at the coastal than oceanic sites (Figure 3-31). TAN showed no distinct temporal trend with higher values recorded in the top and bottom waters at some sites close to salmon farms (i.e., SBM3, NUB1 and NUB2) but not others (i.e., YB4 and NUB4), (Figure 3-32). The values of NPOC and NPOC dissolved increased between spring – summer of 2019/20 and 2020/21 but remained the same between 2020/21 and 2021/22. These trends were consistent across all sites, irrespective of the sampling design but the causes remain unknown (Appendix Figures 1-2).

Plots of TAN versus salinity, show that there were riverine sources at sites SB1, 12, 13, and YB4 while all the other sites were more marine dominated (Figure 3-33). These results are likely explained by differing sources of nutrient inputs into Storm Bay (i.e., coastal runoff, riverine inputs vs. salmon farming).

The biomass of chlorophyll *a* (Figure 3-36), fluorescence (Figure 3-37), total abundance of phytoplankton (Figure 3-38), diatoms (Figure 3-39) and dinoflagellates (Figure 3-40) showed weak seasonal trends, with blooms recorded in winter – spring of 2020 but not 2019 or 2021. These phytoplankton blooms were potentially linked to increased concentrations of NO_x (Figure 3-25) and lower westerly wind strength (Figure 3-42). There was a weak positive relationship between the biomass of chlorophyll *a* and fluorescence (Figure 3-43). However, the relationship was influenced by the amount of freshwater, with river influenced sites showing a weaker relationship than oceanic sites (Figure 3-43). This may be due to coloured dissolved organic matter (CDOM) in freshwater interfering with the fluorescence measurements. Throughout the sampling, there was a slight increase in the abundances of harmful phytoplankton through time that could be linked to rising sea surface temperatures (Figure 3-19). The highest biomass of chlorophyll a were recorded at sites closest to the Derwent Estuary (SB1, SB3, SB8, SB12, SB13 and SB14) and Nubeena (NUB1-3) whereas the highest abundances of phytoplankton (SB13, SB18, and SBM3) dinoflagellates (YB4, NUB1, SBM3, SB13), diatoms (SBM3, SB13, SB5), and harmful algae (YB4) were recorded at some sites close to salmon farms but not others.

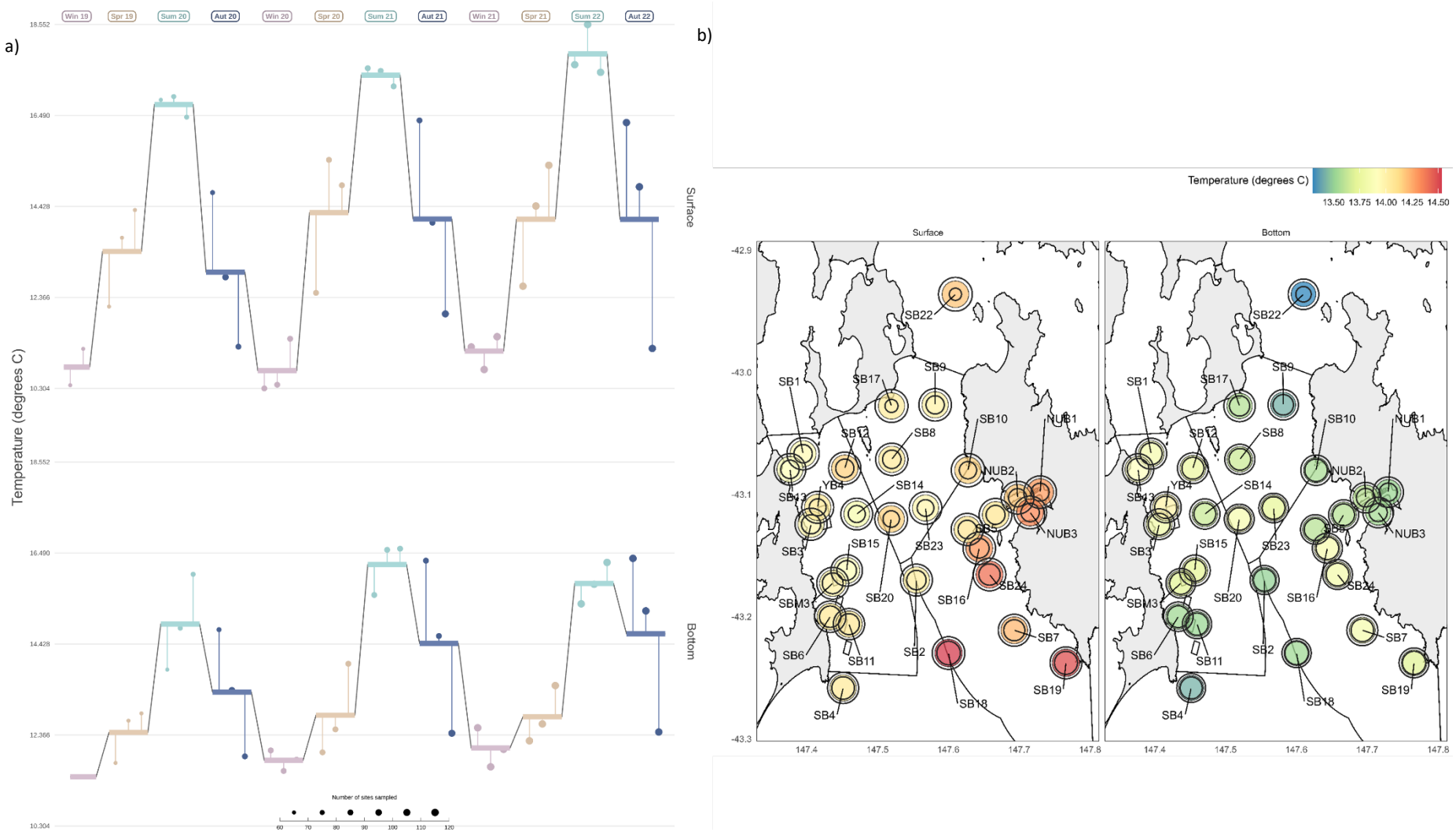


Figure 3-19: Temporal and spatial variation in seawater temperature (°C). A) lollipop plot showing seasonal means (coloured lines) and survey means (dots) in the surface and bottom waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). B) map showing the mean (coloured circle), 20th percentile (small black circle) and 80th percentile (large black circle) at all sites and active leases (black squares) for each DGV region (black lines) from August 2019 to April 2022

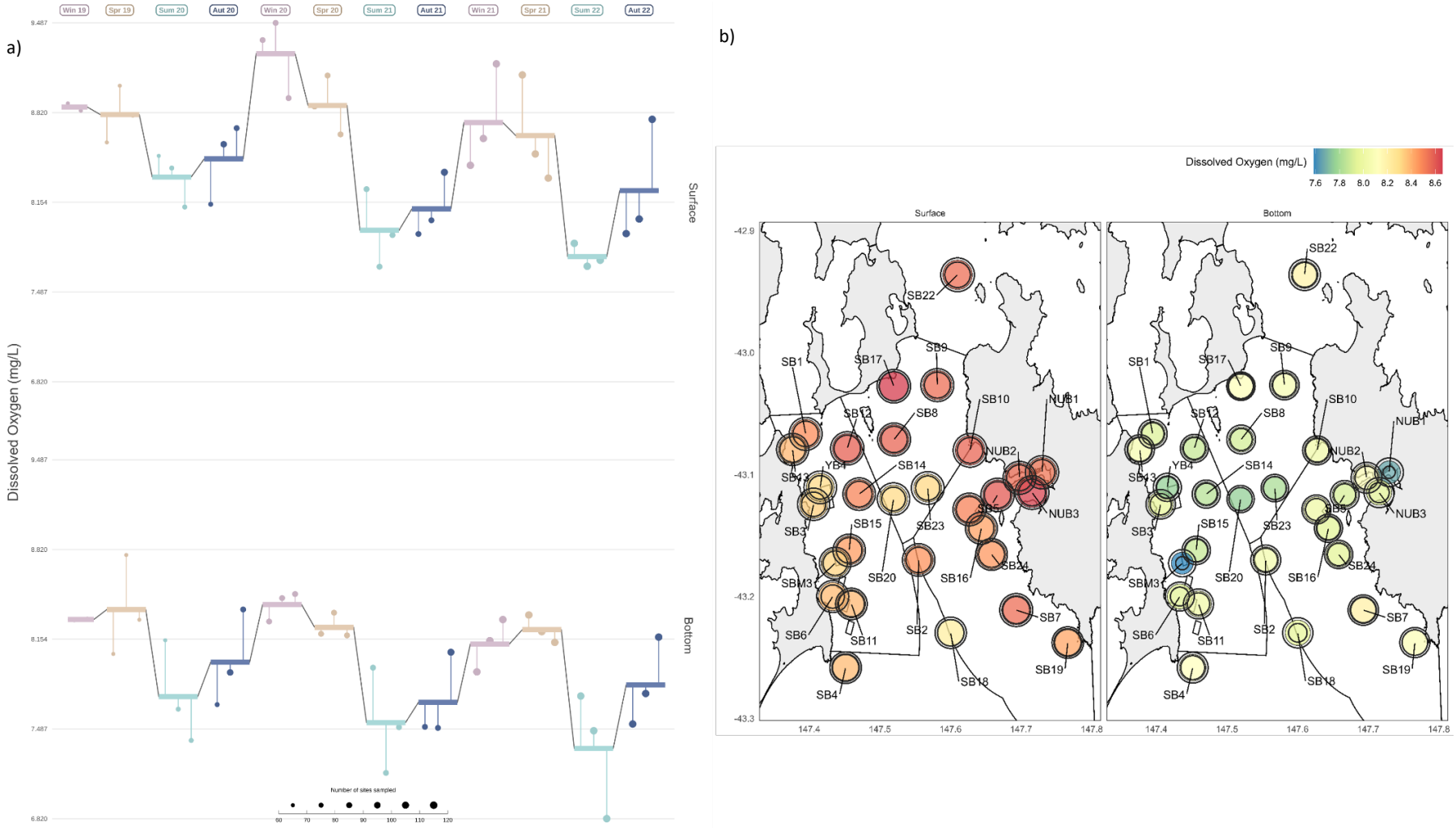


Figure 3-20: Temporal and spatial variation in seawater DO (mg/L, dissolved oxygen). A) lollipop plot showing seasonal means (coloured lines) and survey means (dots) in the surface and bottom waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). B) map showing the mean (coloured circle), 20th percentile (small black circle) and 80th percentile (large black circle) at all sites and active leases (black squares) for each DGV region (black lines) from August 2019 to April 2022.

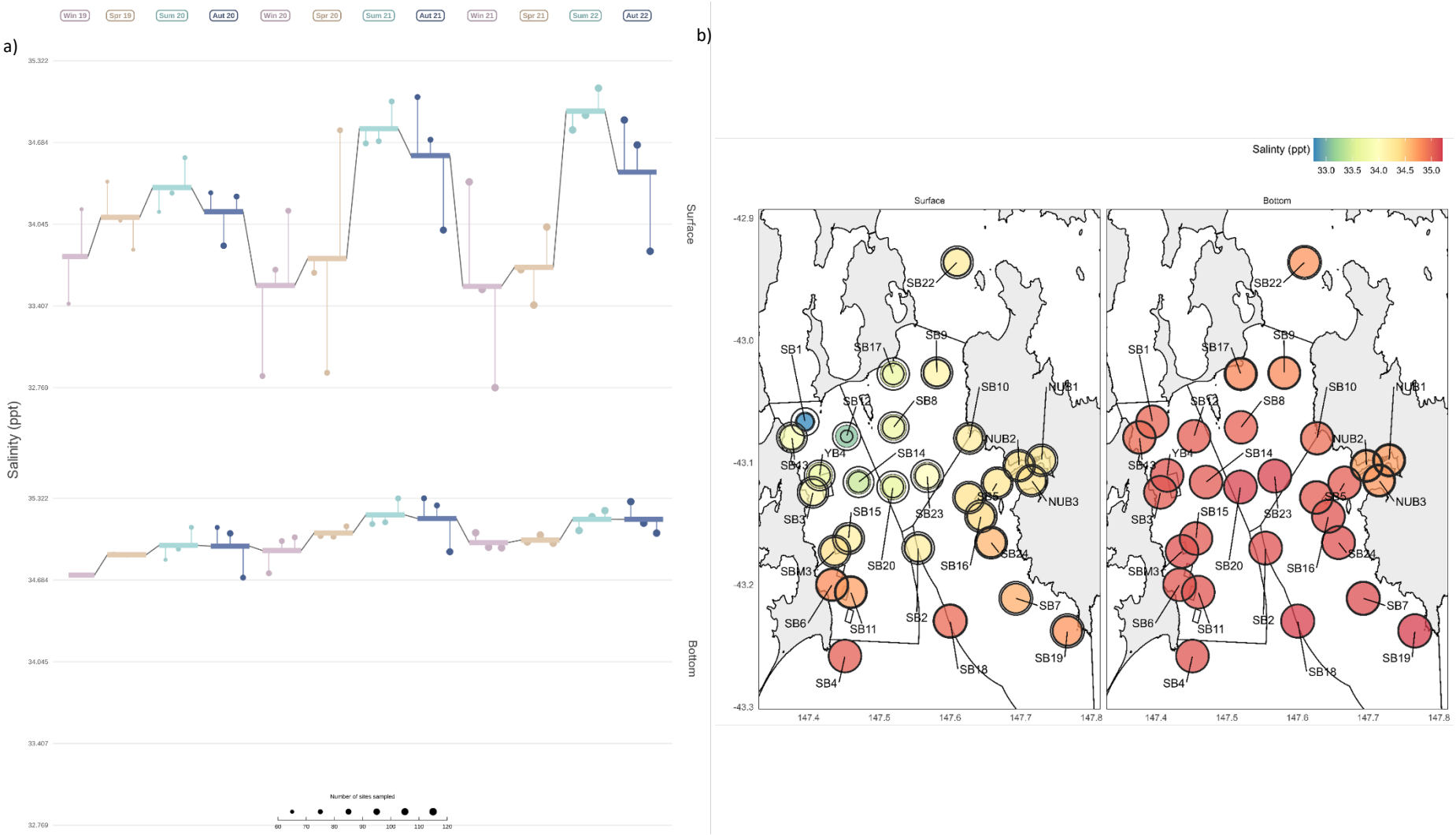


Figure 3-21: Temporal and spatial variation in seawater salinity (ppt). A) lollipop plot showing seasonal means (coloured lines) and survey means (dots) in the surface and bottom waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). B) map showing the mean (coloured circle), 20th percentile (small black circle) and 80th percentile (large black circle) at all sites and active leases (black squares) for each DGV region (black lines) from August 2019 to April 2022.

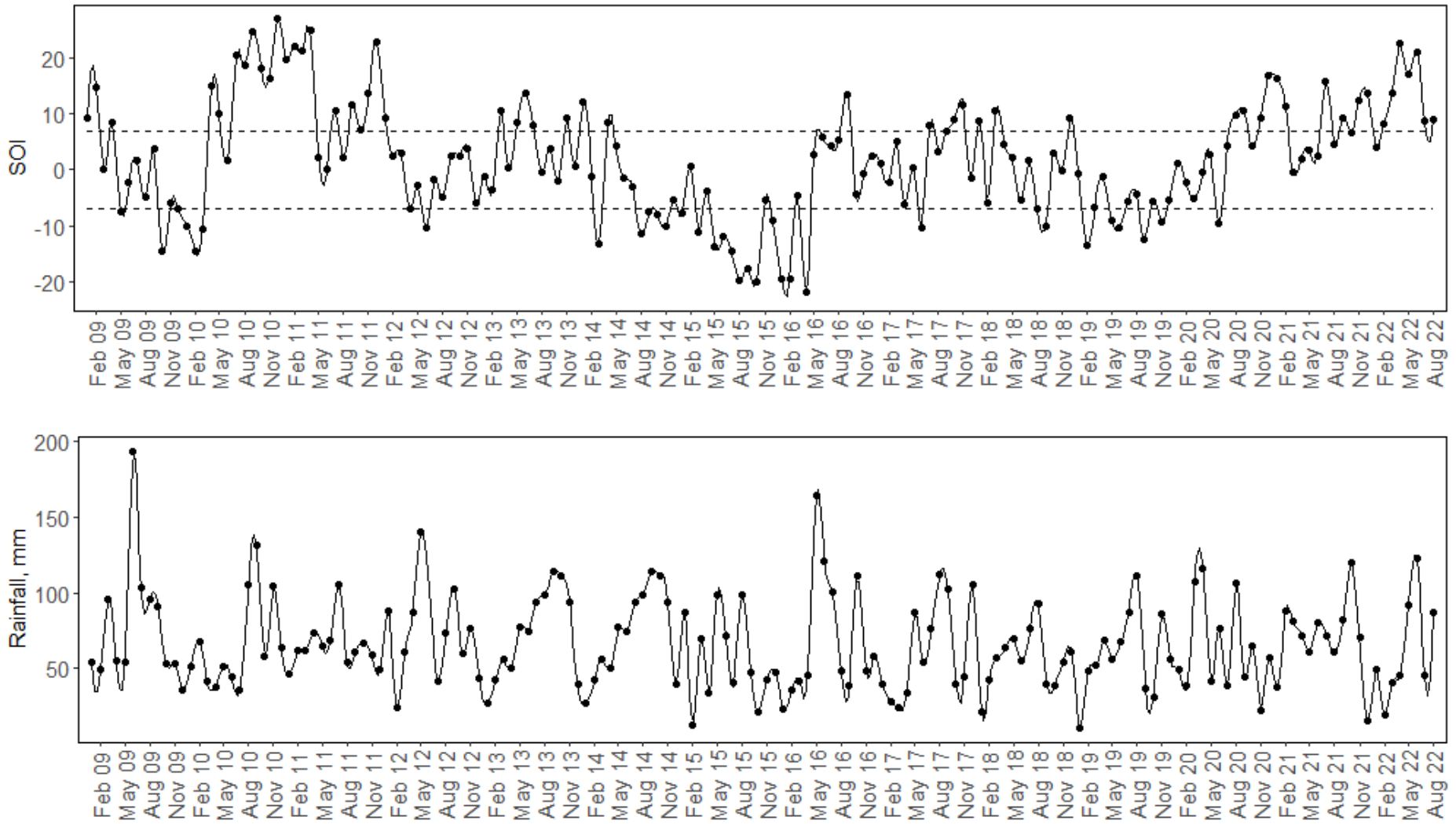


Figure 3-22: Top panel: Southern Ocean Index (SOI), 2010 – 2022, dashed lines show +7 and -7; Bottom panel: Average rainfall (black line) measured at the Bruny Island BoM site, January 2009- August 2022 (Data from Bureau of Meteorology).

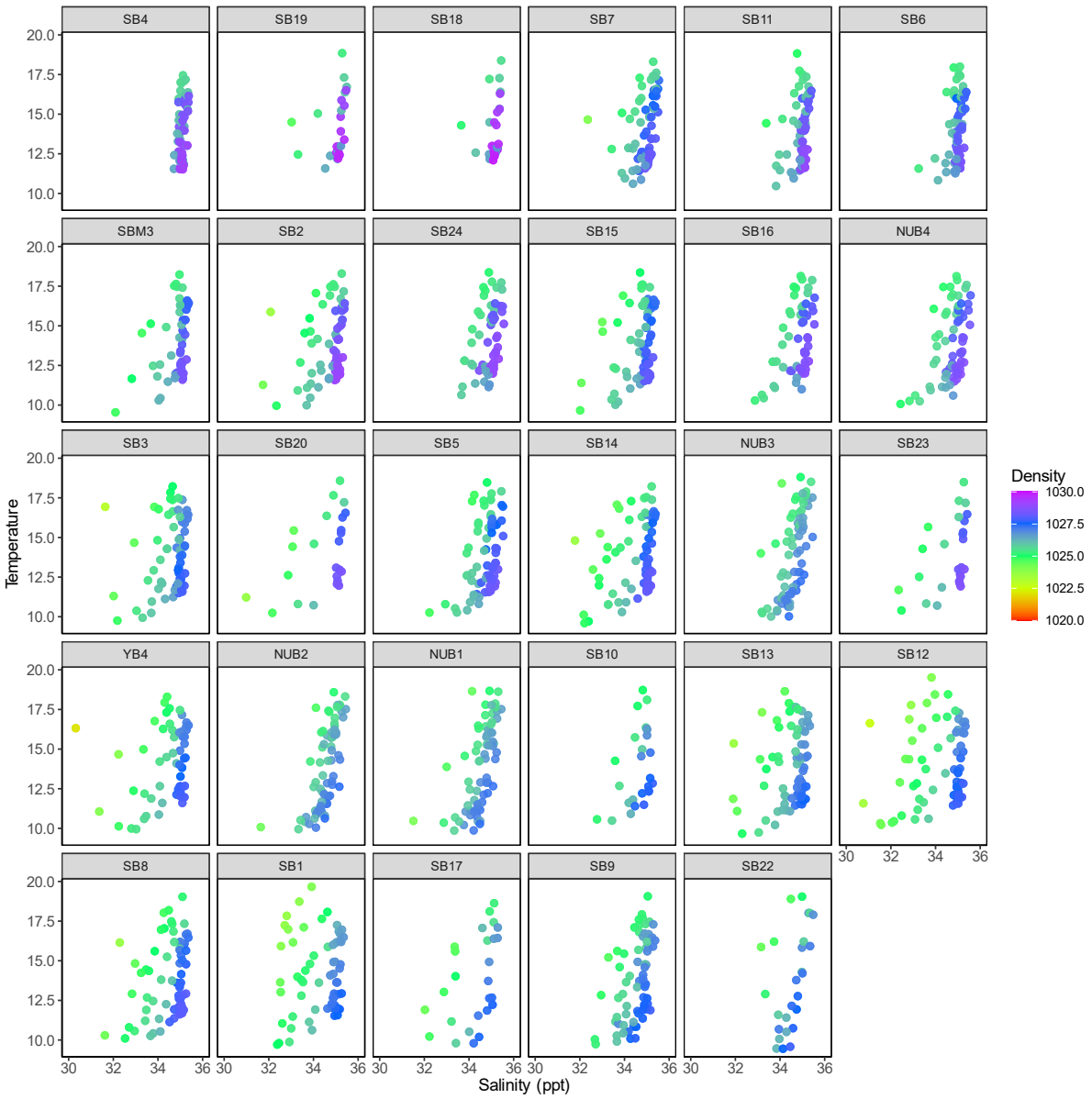


Figure 3-23: Temperature (ºC)-salinity (ppt) plots. Points show data from each CTD deployment on every sampling date from August 2019 to April 2022, for each site. Colour bar is seawater density, with less dense water layers showing to the left of each plot.

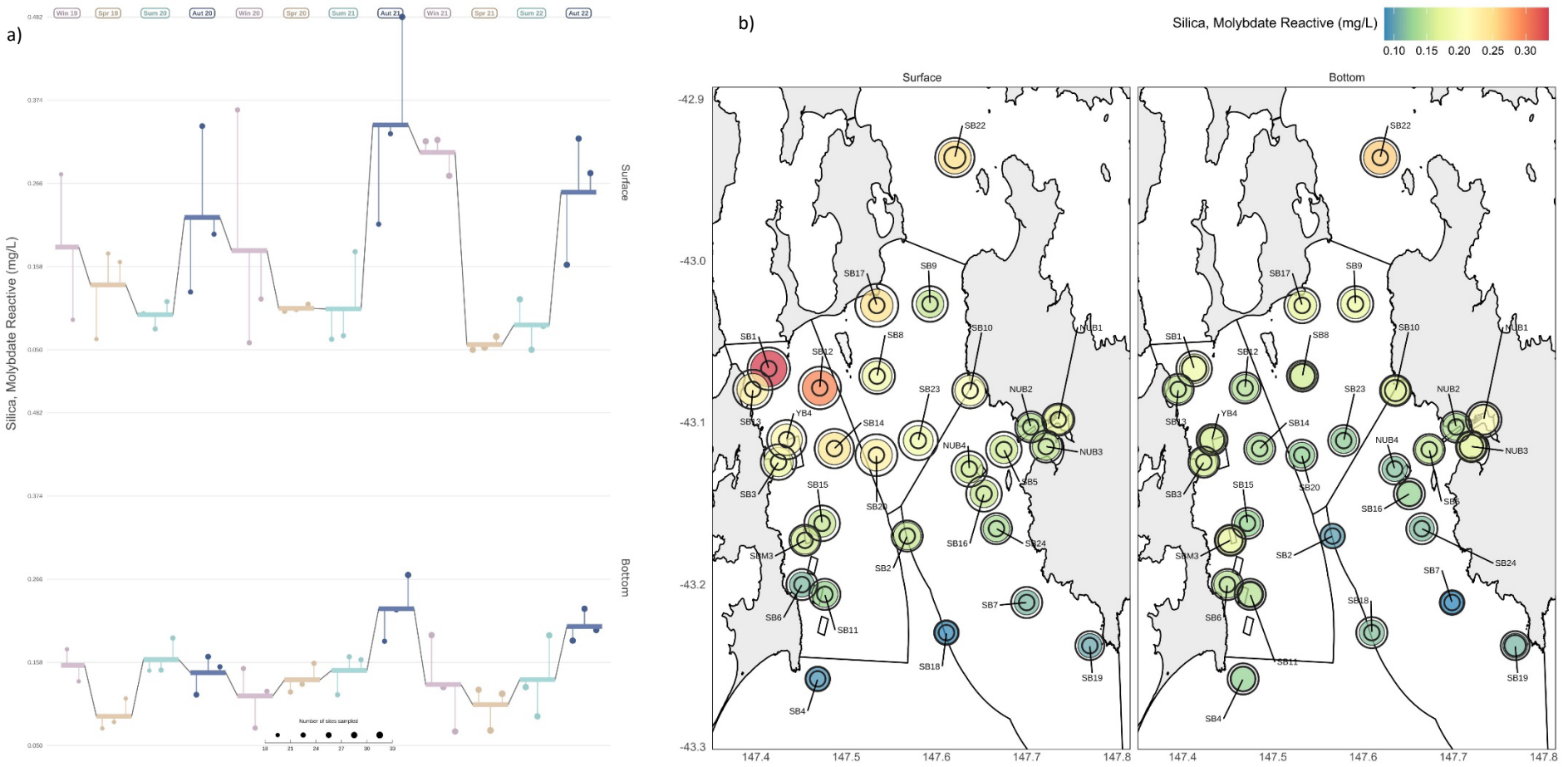


Figure 3-24: Temporal and spatial variation in seawater SiO2 (mg/L, silica). A) lollipop plot showing seasonal means (coloured lines) and survey means (dots) in the surface and bottom waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). B) map showing the mean (coloured circle), 20th percentile (small black circle) and 80th percentile (large black circle) at all sites and active leases (black squares) for each DGV region (black lines) from August 2019 to 2022.

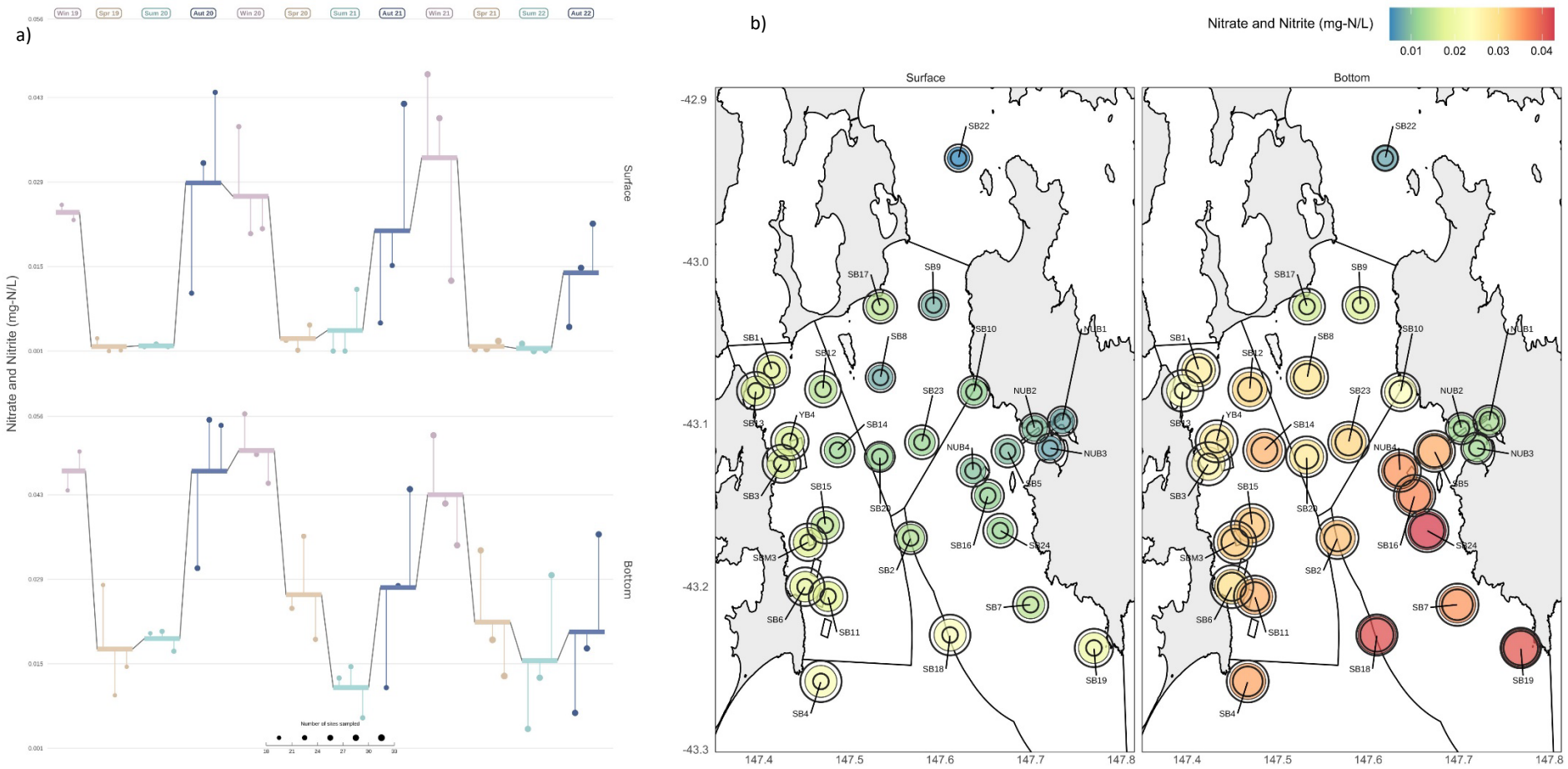


Figure 3-25: Temporal and spatial variation in seawater NO_x (mg/L). A) lollipop plot showing seasonal means (coloured lines) and survey means (dots) in the surface and bottom waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). B) map showing the mean (coloured circle), 20th percentile (inner black circle) and 80th percentile (outer black circle) at all sites and active leases (black squares) for each default guideline (DGV) region (black lines) from August 2019 to April 2022.

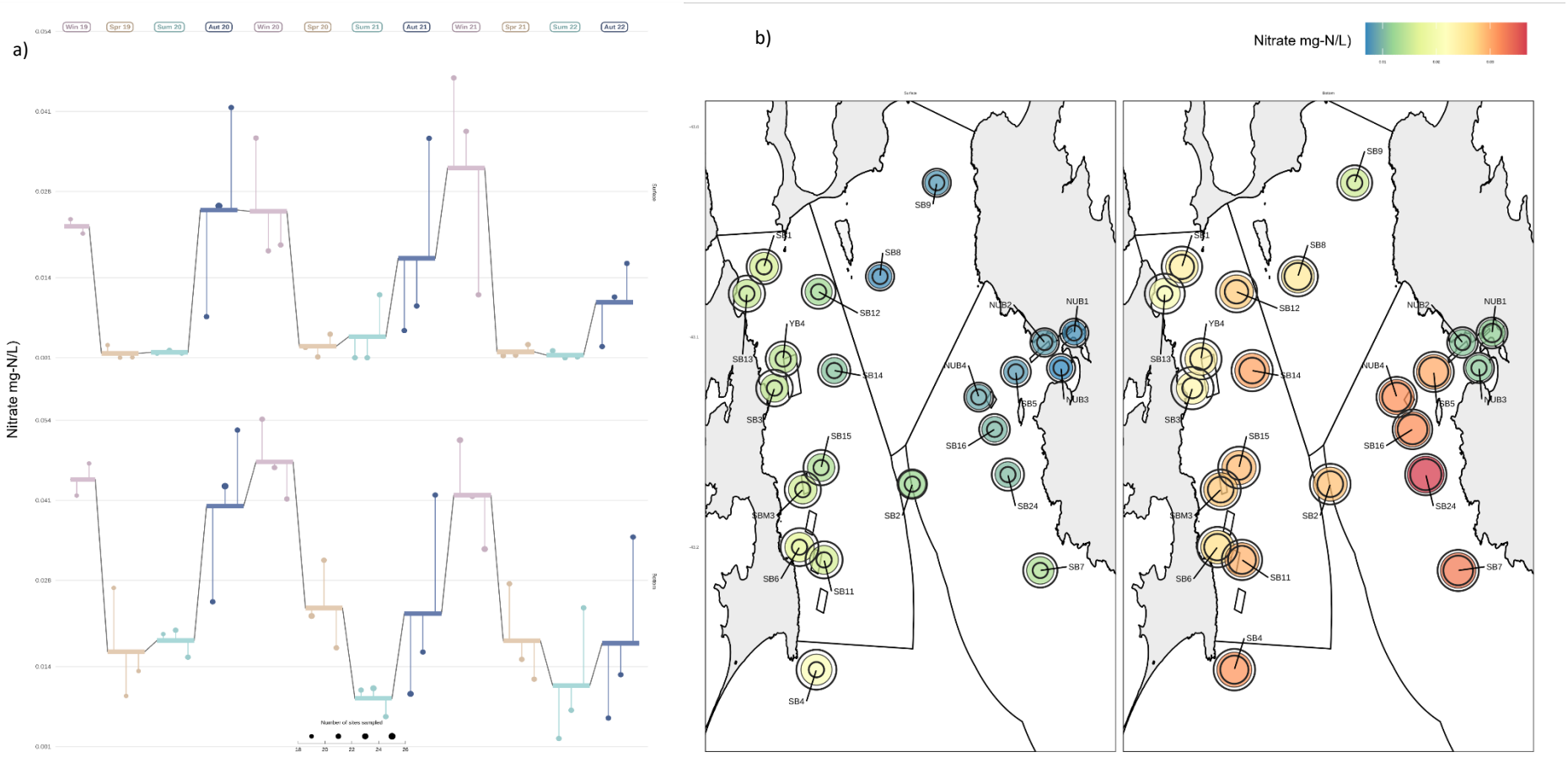


Figure 3-26: Temporal and spatial variation in seawater NO_3 (mg/L, nitrate). A) lollipop plot showing seasonal means (coloured lines) and survey means (dots) in the surface and bottom waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). B) map showing the mean (coloured circle), 20th percentile (inner black circle) and 80th percentile (outer black circle) at all sites and active leases (black squares) for each default guideline (DGV) region (black lines) from August 2019 to April 2022.

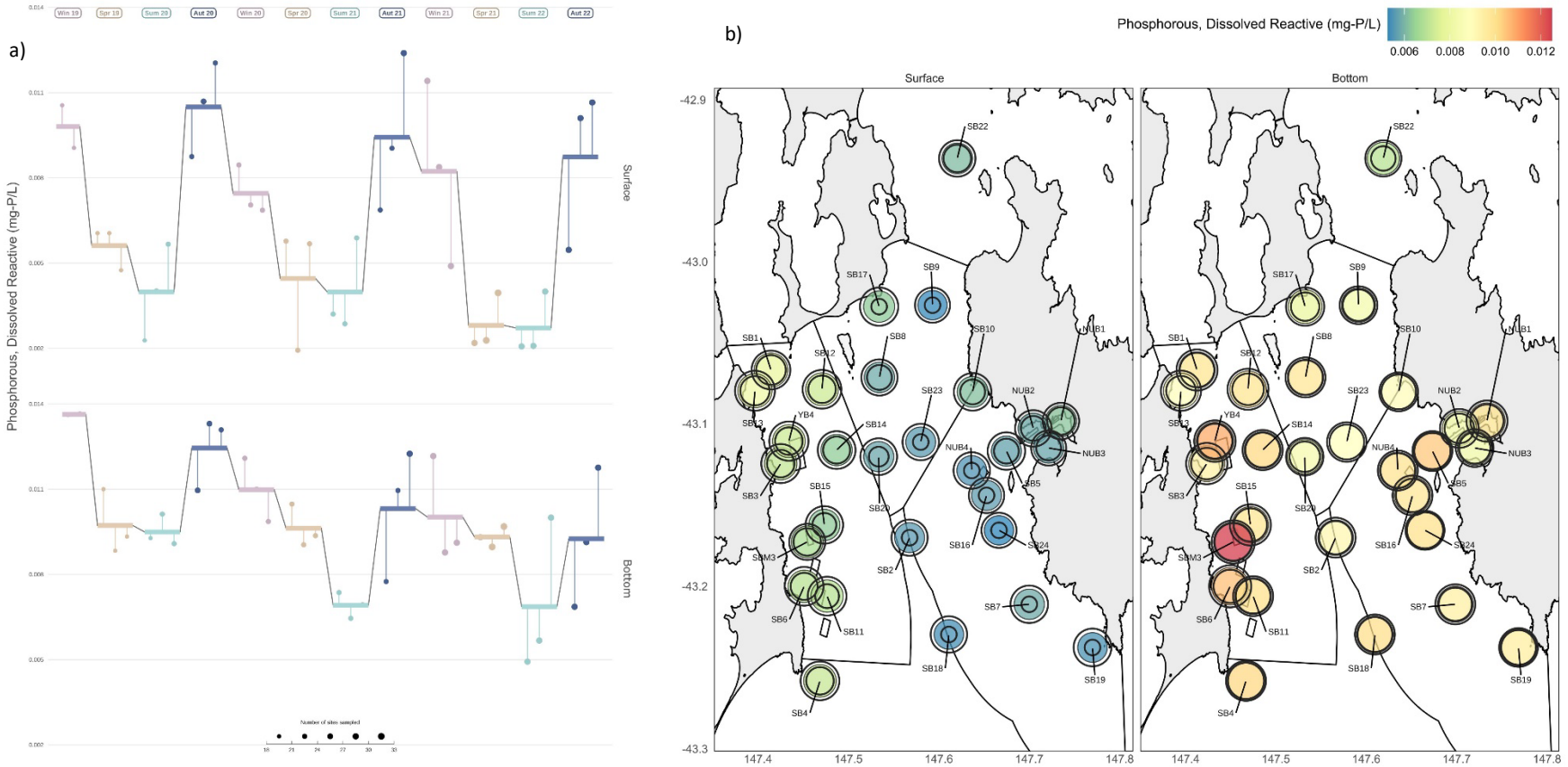


Figure 3-27: Temporal and spatial variation in seawater DRP (mg-P/L, dissolved reactive phosphorous). A) lollipop plot showing seasonal means (coloured lines) and survey means (dots) in the surface and bottom waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). B) map showing the mean (coloured circle), 20th percentile (inner black circle) and 80th percentile (outer black circle) at all sites and active leases (black squares) for each default guideline (DGV) region (black lines) from August 2019 to April 2022.

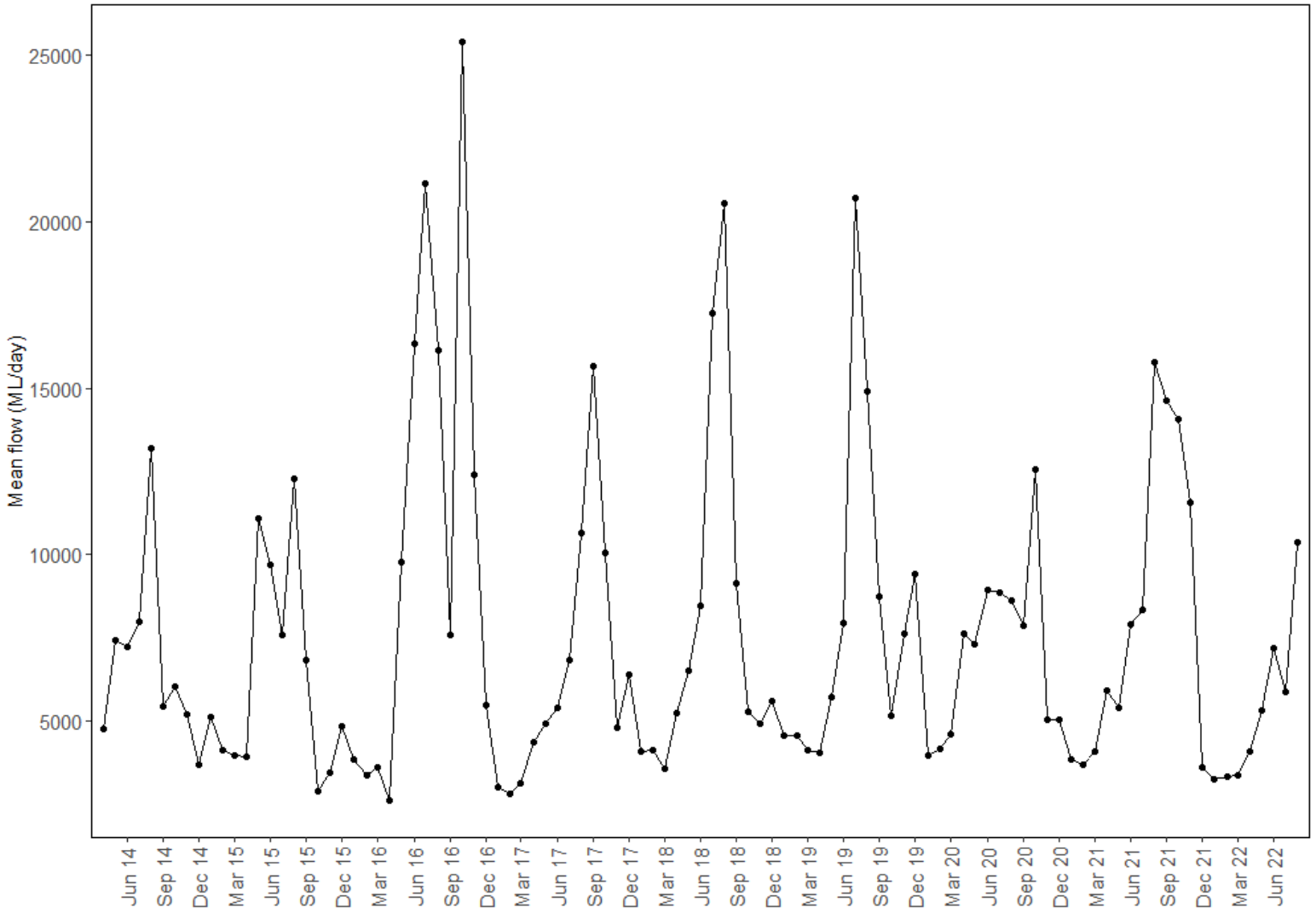


Figure 3-28: Mean monthly flow (ML/day) from Derwent Estuary between June 2014 to August 2022.

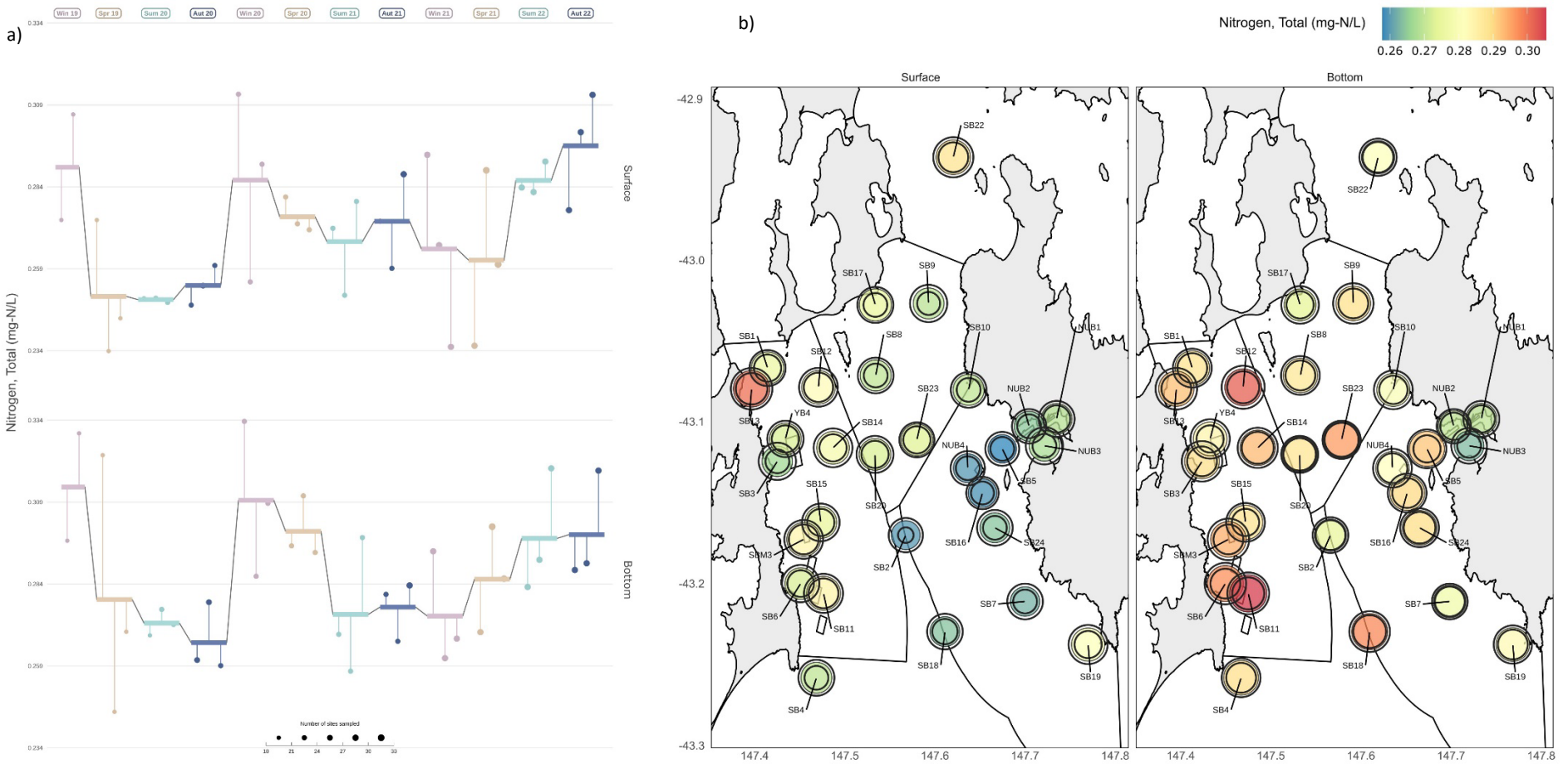


Figure 3-29: Temporal and spatial variation in seawater total nitrogen (mg-N/L). A) lollipop plot showing seasonal means (coloured lines) and survey means (dots) in the surface and bottom waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). B) map showing the mean (coloured circle), 20th percentile (inner black circle) and 80th percentile (outer black circle) at all sites and active leases (black squares) for each default guideline (DGV) region (black lines) from August 2019 to April 2022.

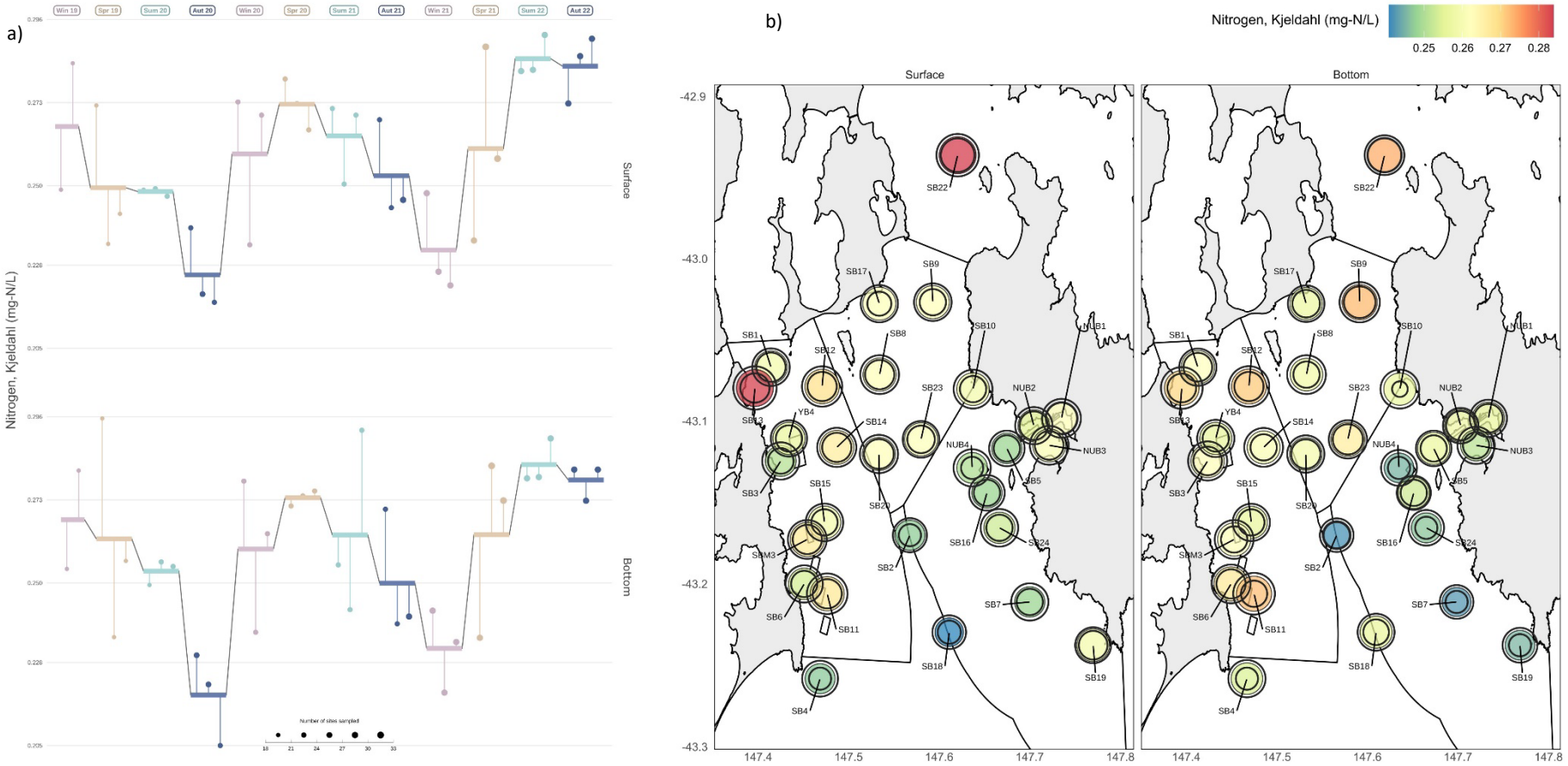


Figure 3-30: Temporal and spatial variation in seawater TKN (mg-N/L, total nitrogen Kjeldahl). A) lollipop plot showing seasonal means (coloured lines) and survey means (dots) in the surface and bottom waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). B) map showing the mean (coloured circle), 20th percentile (inner black circle) and 80th percentile (outer black circle) at all sites and active leases (black squares) for each default guideline (DGV) region (black lines) from August 2019 to April 2022.

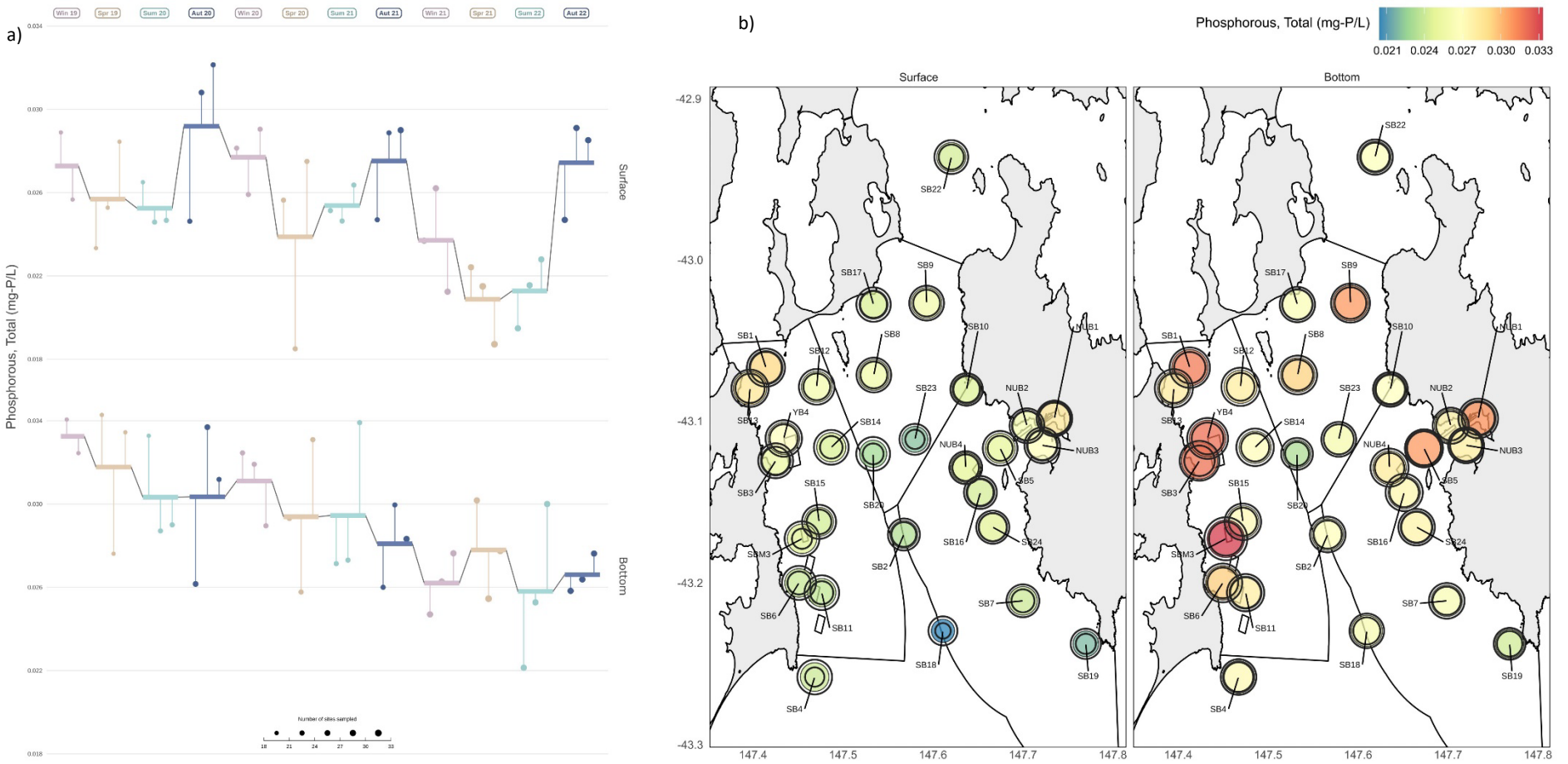


Figure 3-31: Temporal and spatial variation in seawater TP (mg-P/L, total phosphorous). A) lollipop plot showing seasonal means (coloured lines) and survey means (dots) in the surface and bottom waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). B) map showing the mean (coloured circle), 20th percentile (inner black circle) and 80th percentile (outer black circle) at all sites and active leases (black squares) for each default guideline (DGV) region (black lines) from August 2019 to April 2022.

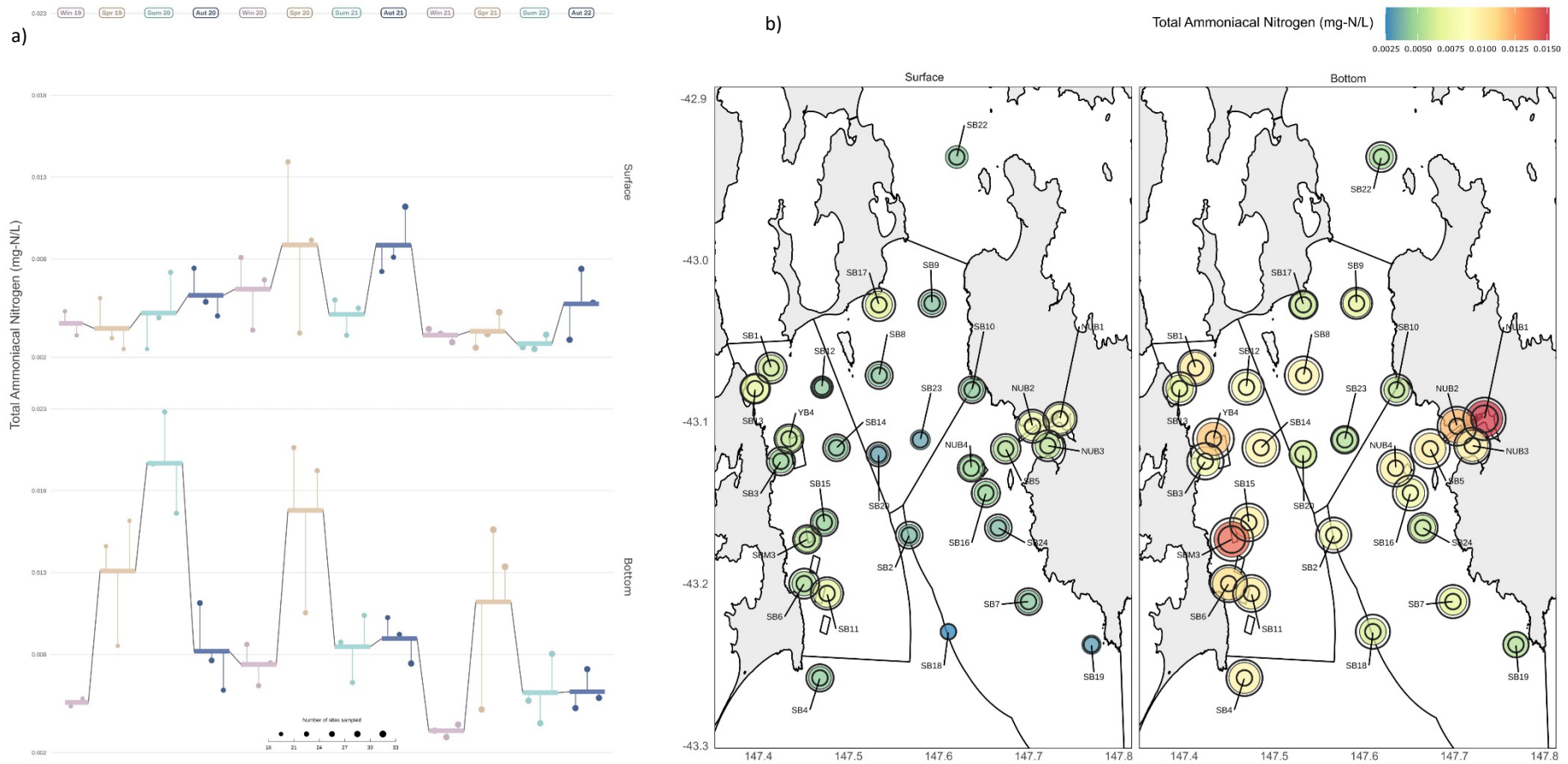


Figure 3-32: Temporal and spatial variation in seawater TAN (mg-N/L, total ammoniacal nitrogen). A) lollipop plot showing seasonal means (coloured lines) and survey means (dots) in the surface and bottom waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). B) map showing the mean (coloured circle), 20th percentile (inner black circle) and 80th percentile (outer black circle) at all sites and active leases (black squares) for each default guideline (DGV) region (black lines) from August 2019 to April 2022.

Figure 3-33: TAN (mg-N/L, total ammoniacal nitrogen) - salinity (ppt) plots. Points show data from each deployment on every sampling date for each site. Colour bar is water density (kg/m^3).

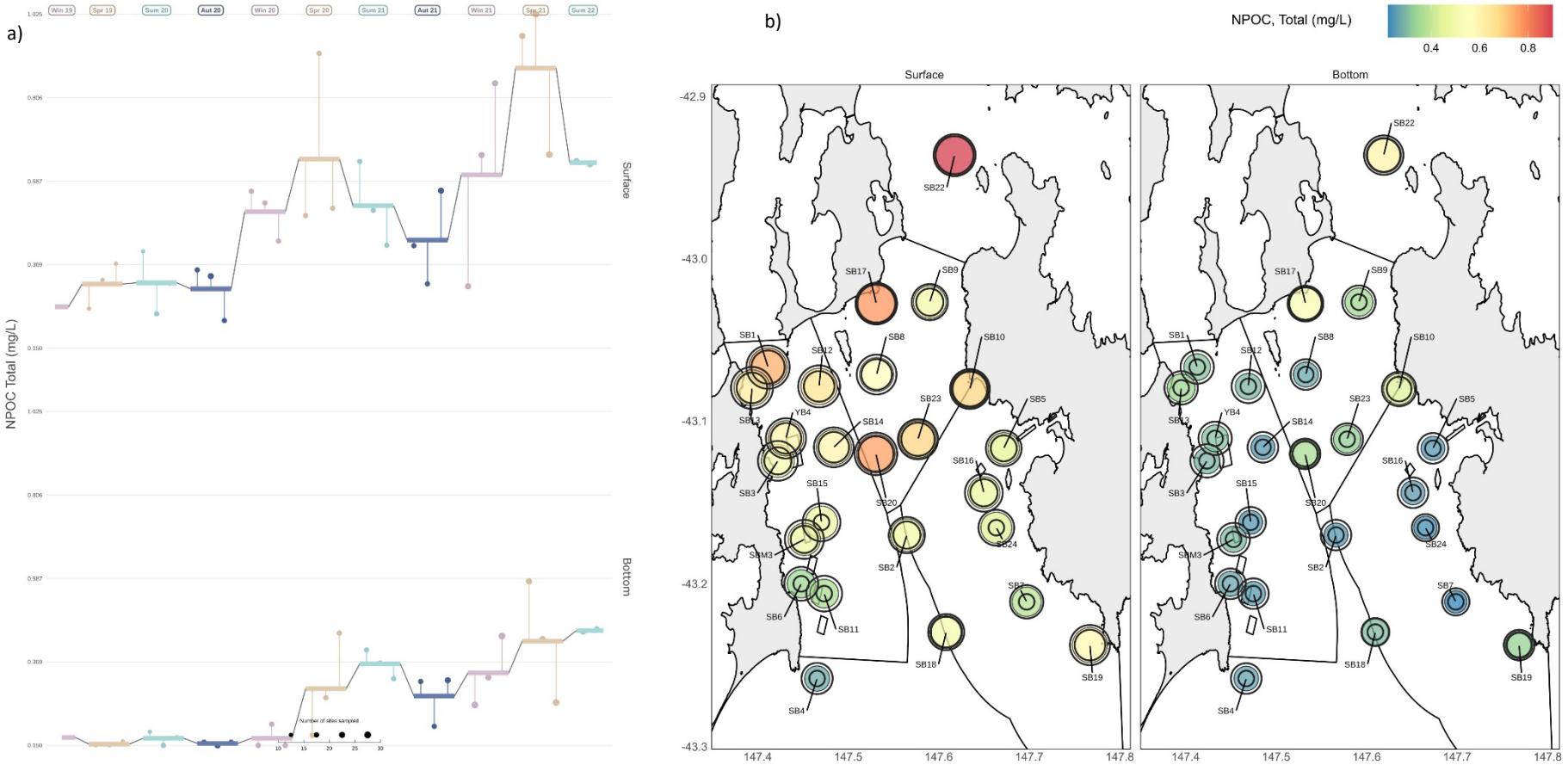


Figure 3-34: Temporal and spatial variation in seawater NPOC (mg/L, non-purgeable organic carbon). A) lollipop plot showing seasonal means (coloured lines) and survey means (dots) in the surface and bottom waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). B) map showing the mean (coloured circle), 20th percentile (inner black circle) and 80th percentile (outer black circle) at all sites and active leases (black squares) for each default guideline (DGV) region (black lines) from August 2019 to February 2022. Note: Sampling for NPOC total ceased in summer 2022.

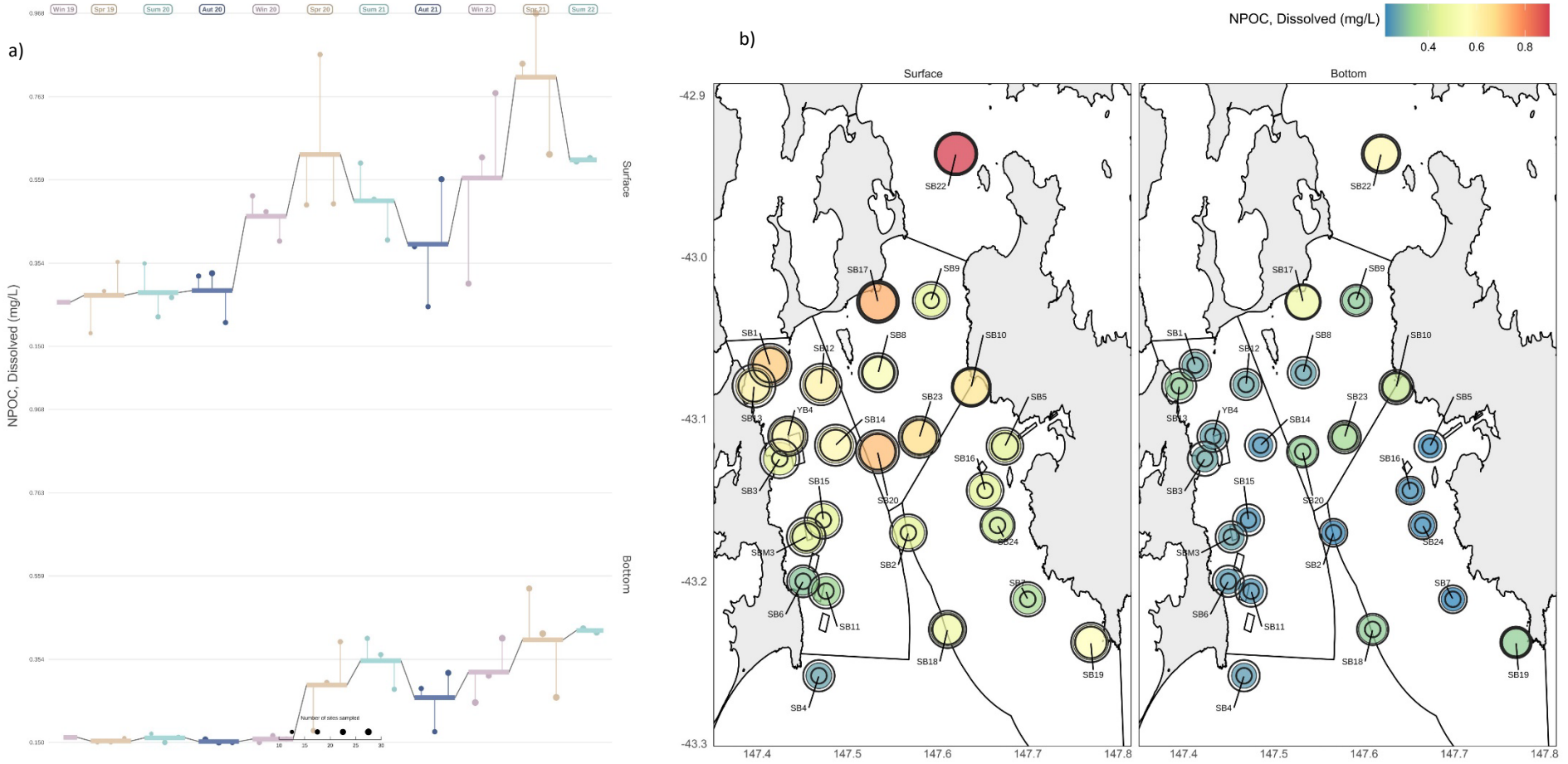


Figure 3-35: Temporal and spatial variation in seawater NPOC dissolved (mg/L, non-purgeable organic carbon dissolved). A) lollipop plot showing seasonal means (coloured lines) and survey means (dots) in the surface and bottom waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). B) map showing the mean (coloured circle), 20th percentile (inner black circle) and 80th percentile (outer black circle) at all sites and active leases (black squares) for each default guideline (DGV) region (black lines) from August 2019 to February 2022. Note: Sampling for NPOC dissolved total ceased in summer 2022.

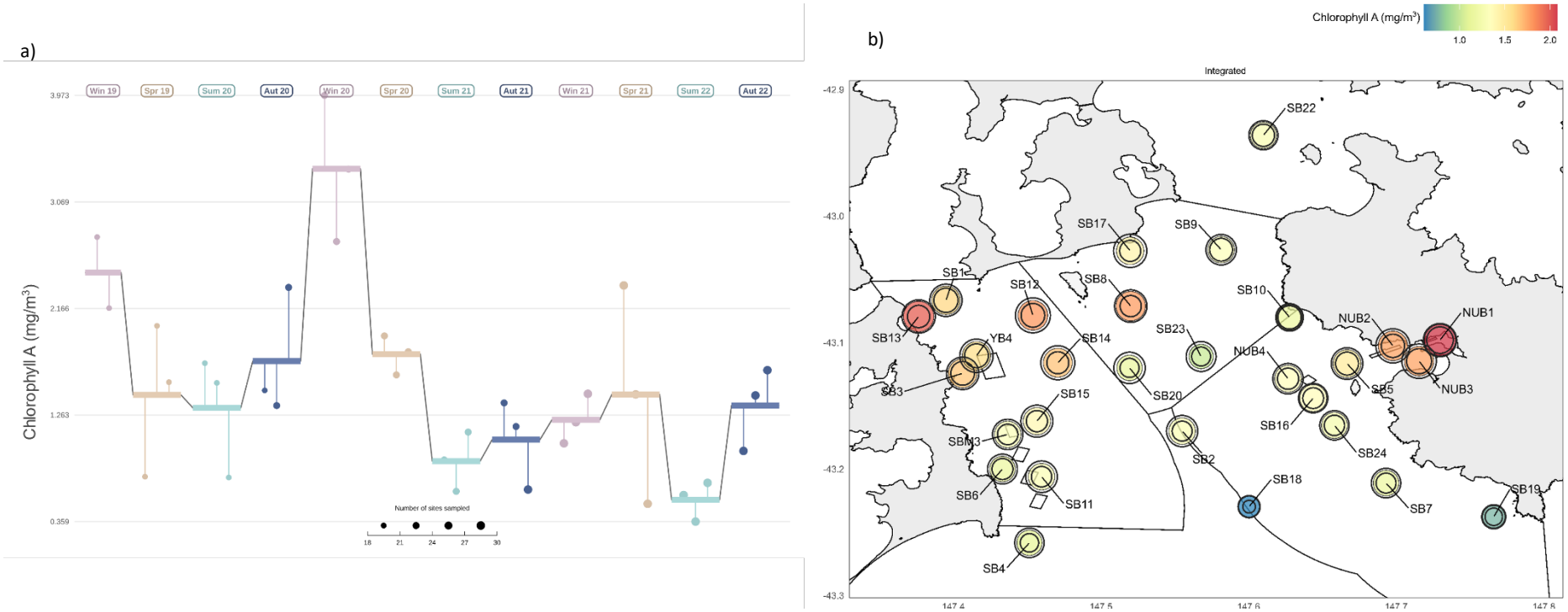


Figure 3-36: Temporal and spatial variation in seawater biomass of chlorophyll *a* (mg/m^3). A) lollipop plot showing seasonal means (coloured lines) and survey means (dots) in the 0-12 m waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). B) map showing the mean (coloured circle), 20th percentile (inner black circle) and 80th percentile (outer black circle) at all sites and active leases (black squares) for each default guideline (DGV) region (black lines) from August 2019 to April 2022.

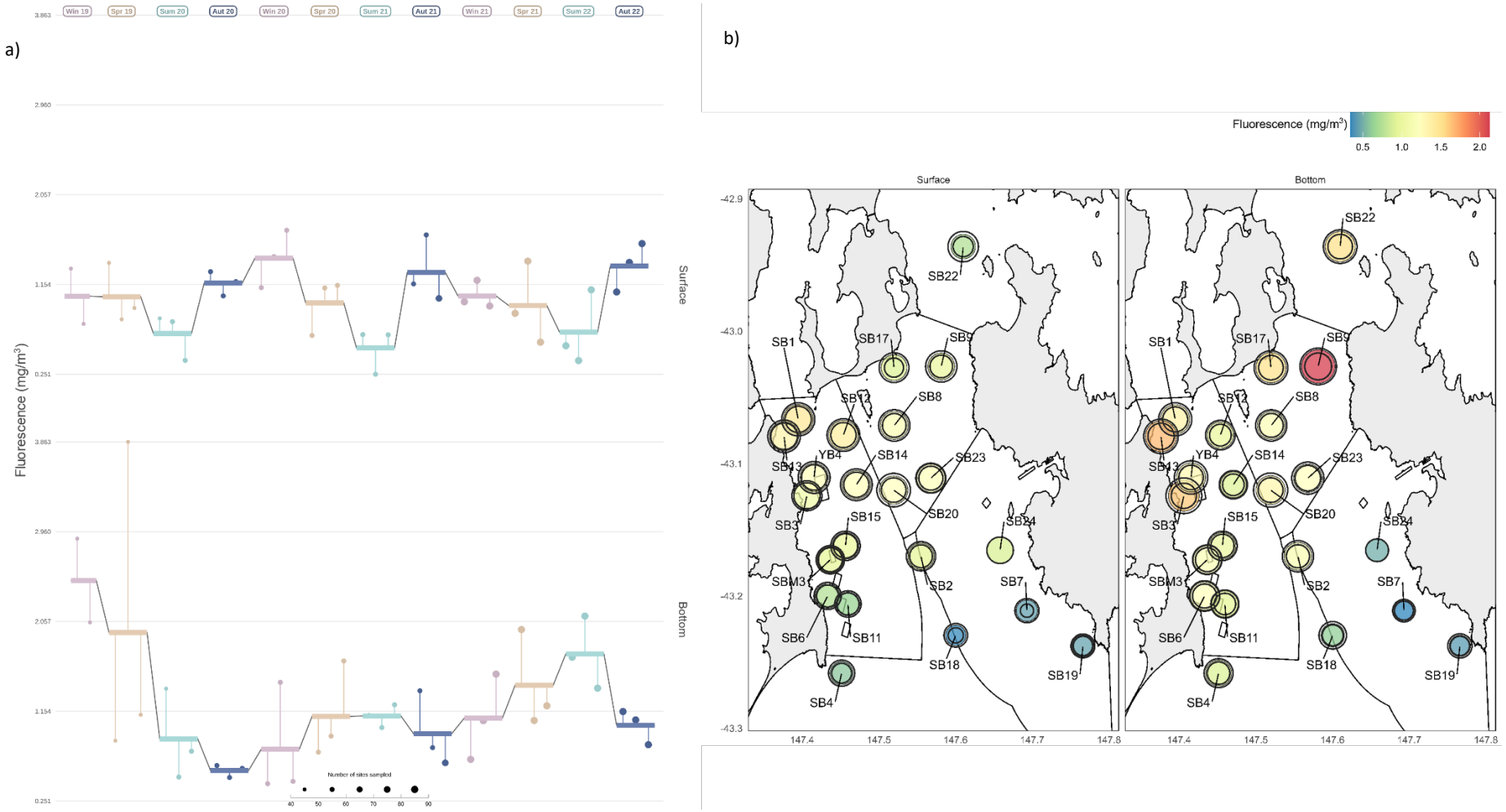


Figure 3-37: Temporal and spatial variation in seawater fluorescence (mg/m^3). A) lollipop plot showing seasonal means (coloured lines) and survey means (dots) in the 0-12 m surface and bottom waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). B) map showing the mean (coloured circle), 20th percentile (inner black circle) and 80th percentile (outer black circle) at all sites and active leases (black squares) for each default guideline (DGV) region (black lines) from August 2019 to April 2022.

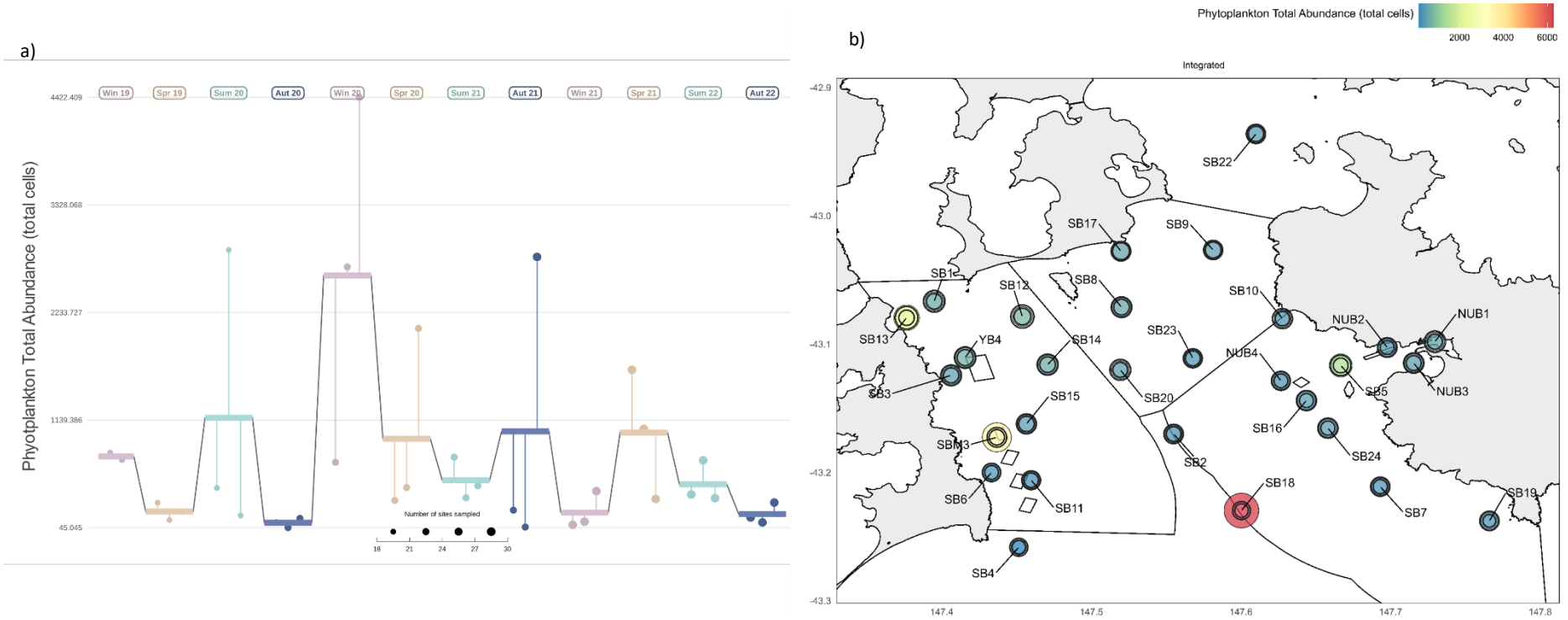


Figure 3-38: Temporal and spatial variation in total abundance of phytoplankton (total cells/0.5L). A) lollipop plot showing seasonal means (coloured lines) and survey means (dots) in the 0-12 m waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). B) map showing the mean (coloured circle), 20th percentile (inner black circle) and 80th percentile (outer black circle) at all sites and active leases (black squares) for each default guideline (DGV) region (black lines) from August 2019 to April 2022.

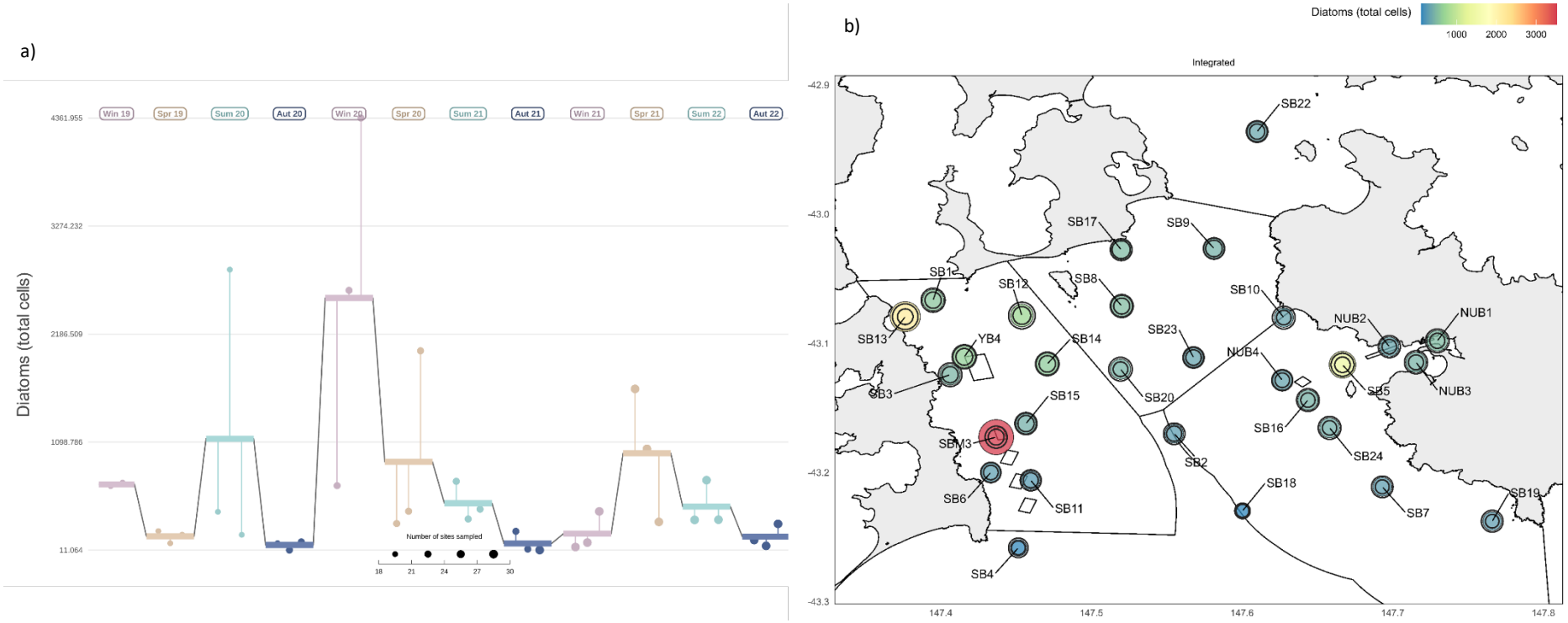


Figure 3-39: Temporal and spatial variation in total abundance (total cells/0.5 L) of diatoms. A) lollipop plot showing seasonal means (coloured lines) and survey means (dots) in the 0-12 m waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). B) map showing the mean (coloured circle), 20th percentile (inner black circle) and 80th percentile (outer black circle) at all sites and active leases (black squares) for each default guideline (DGV) region (black lines) from August 2019 to April 2022.

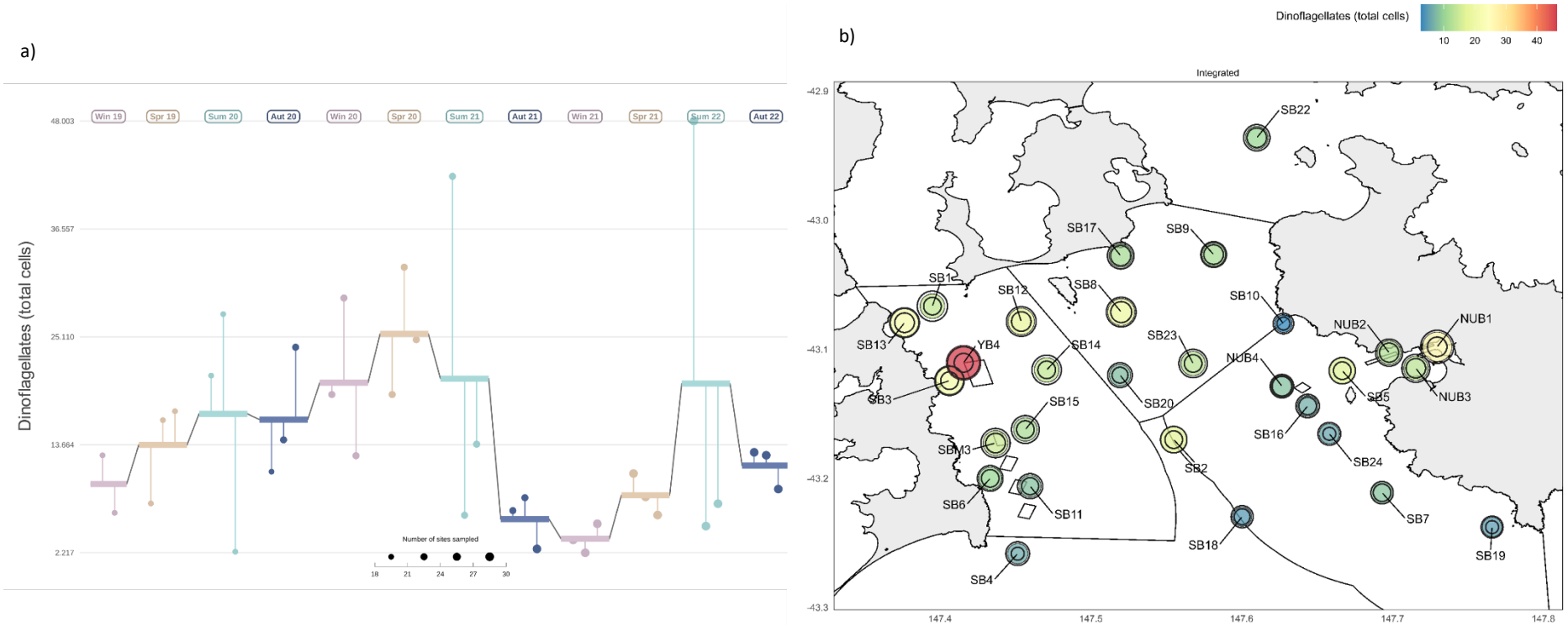


Figure 3-40: Temporal and spatial variation in total abundance (total cells/ 0.5 L) of dinoflagellates. A) lollipop plot showing seasonal means (coloured lines) and survey means (dots) in 0-12 m waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). B) map showing the mean (coloured circle), 20th percentile (inner black circle) and 80th percentile (outer black circle) at all sites and active leases (black squares) for each default guideline (DGV) region (black lines) from August 2019 to April 2022.

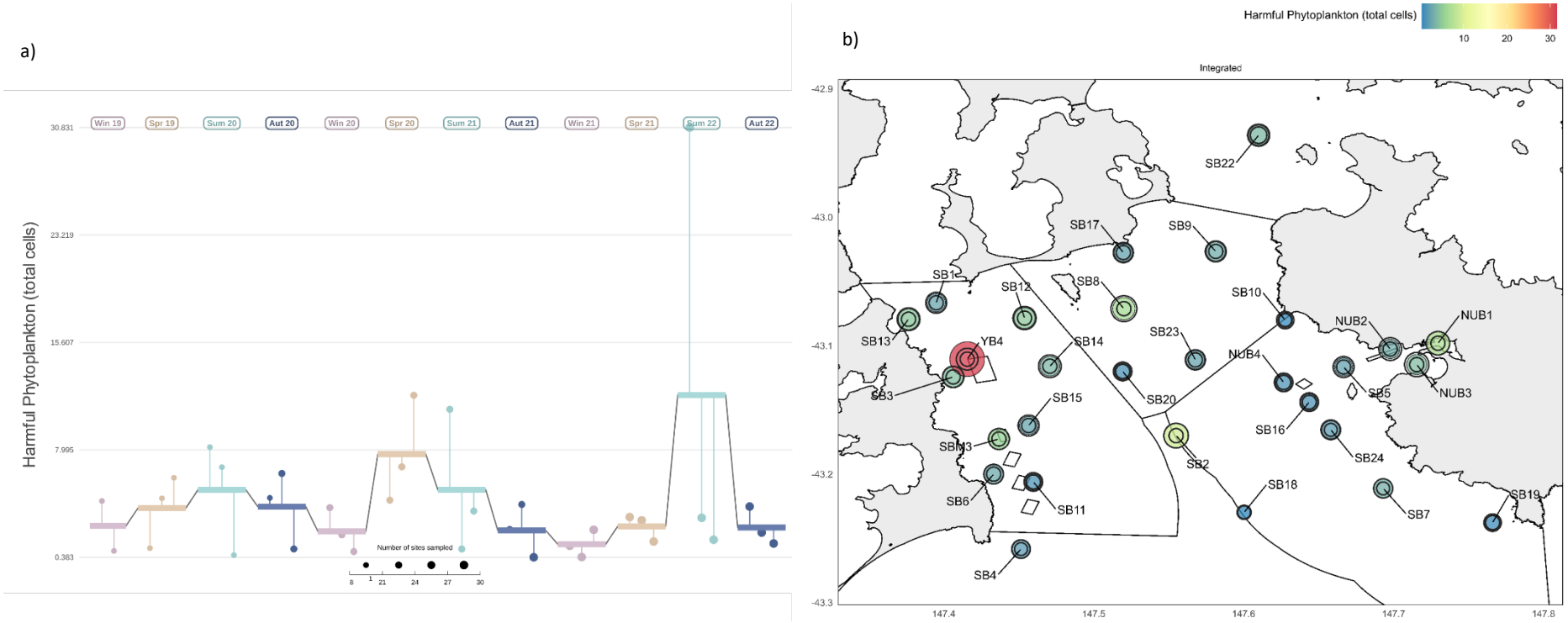


Figure 3-41: Temporal and spatial variation in total abundance (total cells/ 0.5 L) of harmful phytoplankton. A) lollipop plot showing seasonal means (coloured lines) and survey means (dots) in 0-12 m waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). B) map showing the mean (coloured circle), 20th percentile (inner black circle) and 80th percentile (outer black circle) at all sites and active leases (black squares) for each default guideline (DGV) region (black lines) from August 2019 to April 2022.

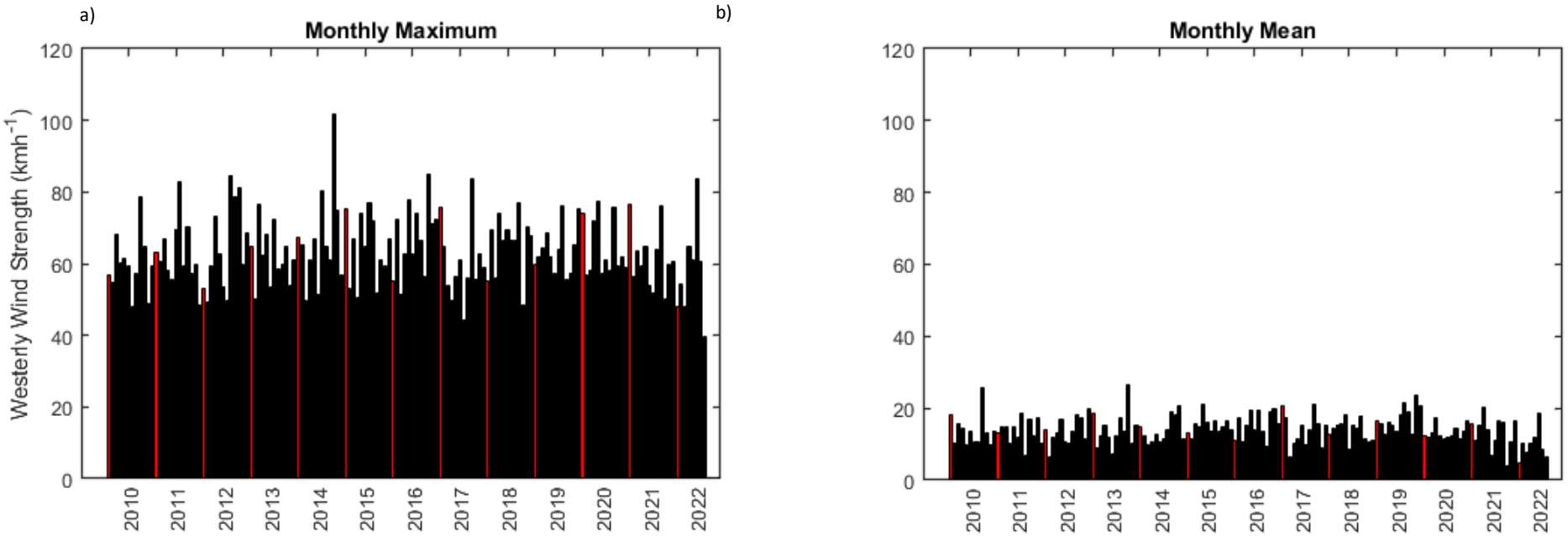


Figure 3-42: A) Maximum westerly wind strength (kmh^{-1}) and B) Mean westerly wind strength (kmh^{-1}) in Storm Bay by month. Wind speed and direction was measured at the Cape Bruny BoM site, from January 2009- August 2022. Vertical red lines depict January of each year.

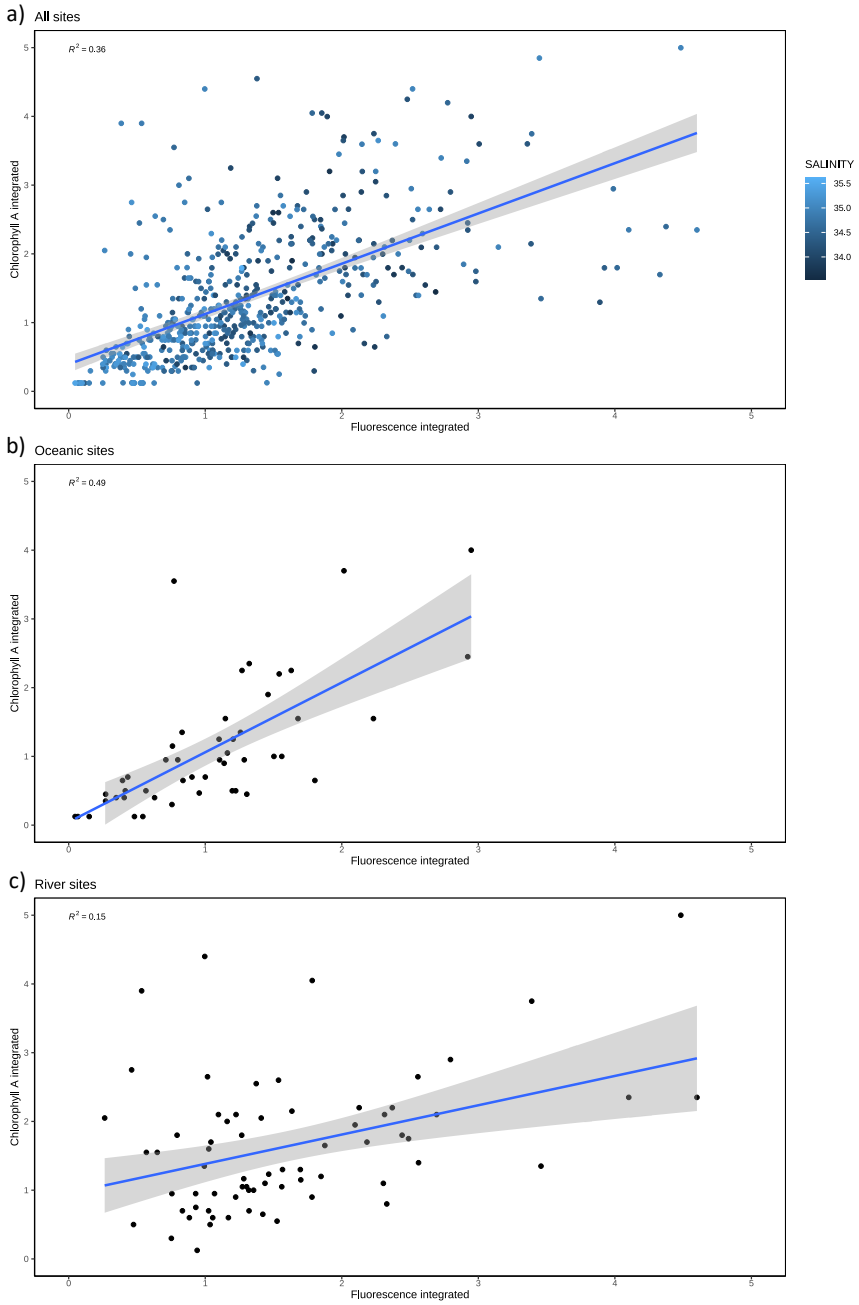


Figure 3-43: Relationship between chlorophyll a (mg/m^3) and fluorescence (mg/m^3) across a) all sites, b) oceanic sites and c) river influenced sites in Storm Bay, from August 2019 – August 2022. The data points in a) are coloured in relation to salinity (ppt).

3.3 Sensitivity of the current broadscale sampling design to detect environmental change.

3.3.1 Environmental performance assessment

The EPA has developed lease specific triggers and default guideline values (DGVs) for assessing water quality and associated aquatic ecosystem protection, which provides a reference point for assessing the potential influence of salmon farming or other inputs on water quality in Storm Bay (Table 3-1). The DGVs have been developed in accordance with the National Water Quality Management Strategy (https://www.waterquality.gov.au/anz-guidelines) for regions around Tasmania. In Storm Bay DGVs have been developed for 3 subregions (80, 81 and 90; Figure 3-18) and the entire Storm Bay.

The lease specific triggers and DGVs are based on the 80th or 20th percentile, depending on the parameter of interest. For MF279 (West of Wedge Island) and region 80 which also contains the MF190 (Creeses Mistake) and MF193 (Badgers Cove) leases the trigger levels and DGVs were calculated based on data from seven sites (SB5, NUB3, NUB4, SB2, SB7, NUB1, NUB2) collected between February 2014 to June 2019. For region 81 which does not contain any salmon leases at present the DGVs were calculated based on data from four sites (SB8, SB9, PET-SB1 and PET-SB2) collected between October 2016 to October 2020. For MF281 (East of Yellow Bluff) and region 90 which also contains the MF261 (Storm Bay 1 and Storm Bay 2) leases the trigger levels and DGVs were calculated based on data from three sites (SB1, SB3 and SB6) collected between January 2018 and June 2019. For the entire Storm Bay the DGVs were calculated based on data from 14 sites (SB1, SB2, SB3, SB5, SB6, SB7, SB8, SB9, NUB1, NUB2, NUB3, NUB4, PET-SB1, and PET-SB2) collected from February 2014 to October 2020.

Performance of the compliance site and sites within the DGV regions is currently assessed using the rolling annual median value (i.e., the middle value of 12 monthly measurements) for each of the parameters measured. If the rolling annual median of any of the parameters exceed the trigger levels at the compliance sites (i.e. SB3 for MF281 and SB5 for MF279), the Licence holder is required to undertake additional investigations and analysis of other environmental data to determine to what extent the exceedances are caused by marine farming operations.

This framework has several challenges in monitoring the interactions between salmon farming and the surrounding water column. The lease specific trigger levels currently focus on monitoring compliance at specific sites (i.e. SB3 and SB5) but don't provide clear guidance around how to monitor for regional or ecosystem changes. The focus on monitoring a single site for compliance means exceedances may be missed due to random chance or wrongly attributed to salmon farming when other sources of nutrients are not considered. Similarly, the trigger levels for the DGVs do not provide guidance on how to interpret changes at sites at varying distances from salmon leases.

To address these challenges, Strain et al. (2020) proposed that any changes/exceedance at the compliance site or sites within the DGV regions should be interpreted in the context of other sites at varying spatial scales from salmon leases. For example, if exceedances were recorded at the compliance site in region 93 (i.e. SB3) the first step would be to compare the compliance site to other sites within (< 5 km) of the lease/s of interest; in this case SB3

(~1.2km from the lease) would be compared with sites YB4, SMB3, SB6, SB11, SB12, SB13, SB14 and SB15 (all < 5 km from the lease within the same DGV region; Figure 3-18). If the pattern is only observed at the compliance site or sites close to the lease, it suggests a localised effect that may be lease or farm related. Additional gradient sampling on a transect and/or dispersion modelling (e.g. CONNIE) is then recommended to identify the likely cause and the spatial extent of change. If additional sampling is required, we suggest that the the inline sampling methodology demonstrated above is considered given that it provides a comprehensive snapshot of the spatial footprint.

If a similar pattern is observed in the < 5 km sites, then the next step would be to compare these sites against sites > 5 km from the lease for that DGV region: in this case sites SB1, SB2 and SB4. If the pattern is seen at sites < 5 km from the lease/s but is not observed at the > 5 km sites, then this would suggest that the change may also be farm related. Higher resolution sampling and modelling would be required to understand the cause of the change. If the pattern is shared with the far-field sites this could indicate a regional or even broader system change. In this case, other data sources (e.g. sites monitored by the Derwent Estuary Program, Channel/Huon BEMP and the Oil Spill Response Atlas (OSRA) regions 80 and 81), and the Storm Bay BGC model nested in the SE Australia regional model will be pivotal in interpreting the drivers and scale of change.

A similar logic is applied to assess changes in the entire DGV region. For example, in region 93, sites near (< 500 m) active leases (i.e. YB4, SMB3) are compared to sites at intermediate distances (< 5 km) from active leases (i.e. SB3, SB11, SB12, SB13, SB14, SB15) and far-field (> 5 km) from active leases (i.e. SB1, SB2 and SB4) to understand the scale and causes of any changes in the water column.

However, it is important to recognise that by using an annual rolling median to monitor compliance only sustained high (or low for parameters like DO) values will lead to exceedance of the investigative trigger levels. As (Goudey 1999) noted, multiple months can be higher or lower than the trigger level, but the site may still be compliant. This is implicit in deciding to use a rolling annual median and ensures that investigations are not unnecessarily triggered due to occasional low-level spikes in the data, which could be linked to external influences. However, the influence of salmon farming on the water column and surrounding habitats is also likely to vary seasonally depending on the timing of peak production. Trigger limits based on the annual rolling median may not detect these seasonal changes. Hence, the ANZECC recommend the development of seasonal trigger values for indicators that exhibit seasonal variation. While seasonal trigger levels for some DGV regions and the entire Storm Bay have been calculated, these values have not been implemented in a management context.

3.3.2. Performance of the compliance sites and DGV regions against the triggers

Throughout the monitoring period, both the annual rolling median at the compliance sites: SB3 for the MF281 East of Yellow Bluff lease exceeded the trigger levels for chlorophyll *a* (4 occasions in 2020/21 sampling for the monthly and annual investigative trigger levels, 1 occasion in 2021/22 sampling for the annual investigative trigger level) and for TAN in the surface waters (2 occasions in 2020/21). SB5 for the MF279 West of Wedge Island lease exceeded the trigger levels for chlorophyll *a* (2 occasions in 2020/21 for the monthly trigger level), for TAN in 10 m of water (5 occasions in 2020/21) and for NOx in the bottom water

(10 occasions in 2020/21 and 1 occasion in 2021/22). These exceedences were accompanied by higher values of chlorophyll *a* and TAN in the surface waters in the near and intermediate sites for region 93 during the 2020/21 and 2021/22 monitoring which contains the leases MF281 and MF261. There were higher values of chlorophyll *a* in the near and intermediate scale sites for region 80 during the 2020/21 monitoring which contains the leases MF279, MF190, and MF193. By contrast the values of TAN for SB5 and other near scale sites in region 80 were lower than the intermediate but similar to the farfield sites and the values of NOx were similar in all sites for the 2020/21 monitoring. These results suggest that there were potentially localised interactions between salmon farming and the surrounding water column which resulted in higher values of chlorophyll *a* biomass and TAN in the surface waters, but that the effects were temporally variable and difficult to separate from other influences (i.e., inputs from the Derwent Estuary and Parsons Creek), whereas the higher values of NOx were likely linked to regional scale influences (IMAS 2020a, 2021, 2022).

3.3.3. Power analysis

Given the inherent variability in background conditions it is important to ensure that the monitoring program can detect meaningful change. The number of sites and frequency of monitoring are key factors that can influence the sensitivity of a sampling design to detect change. Storm Bay is currently managed through 2 compliance sites and 3 DGV regions. Using the data collected in the Storm Bay project from August 2019 to April 2022 we undertook power analyses to assess the number of sites and frequency of monitoring required to detect change at sites based on annual, seasonal and monthly (chlorophyll *a* only) trigger levels for compliance sites, regions 93 and 80 and the entire Storm Bay for TAN, TN, NO_x, TP, DRP, DO and chlorophyll *a* at surface and bottom waters (Table 3-3, 3-4).

Table 3-3: Annual and seasonal (for regions 93 and 80 only) default guideline values (determined from historical data) for regions in Storm Bay.

Parameter (mg/L) or (mg/m3 for chlorophyll *a* only)	Region 93 – Annual	Region 93 - Summer	Region 93 - Autumn	Region 93 – Winter	Region 93 – Spring
TAN (surface)	0.006	0.007	0.012	0.010	0.008
TAN (bottom)	0.010	0.015	0.015	0.010	0.017
TN (surface)	0.31	0.29	0.31	0.30	0.28
TN (bottom)	0.33	0.31	0.33	0.32	0.29
NOx (surface)	0.039	0.002	0.034	0.051	0.002
NOx (bottom)	0.042	0.010	0.043	0.052	0.020
TP (surface)	0.05	0.034	0.035	0.040	0.026
TP (bottom)	0.04	0.040	0.045	0.040	0.028
DRP (surface)	0.013	0.008	0.011	0.013	0.006
DRP (bottom)	0.014	0.010	0.012	0.014	0.009
DO (surface) (lower limit)	7.7	7.202	6.540	8.090	7.808
DO (bottom) (lower limit)	7.0	6.630	6.164	7.779	7.725
Chlorophyll *a* (integrated)	1.5	0.500	0.772	0.605	0.706

Parameter (mg/L) or (mg/m3 for chlorophyll *a* only)	Region 80 - Annual	Region 80 - Summer	Region 80 - Autumn	Region 80 – Winter	Region 80 – Spring
TAN (surface)	0.009	0.006	0.010	0.015	0.008
TAN (bottom)	0.017	0.014	0.014	0.019	0.019
TN (surface)	0.33	0.32	0.33	0.34	0.31
TN (bottom)	0.34	0.33	0.33	0.34	0.34
NOx (surface)	0.015	0.003	0.006	0.041	0.004
NOx (bottom)	0.035	0.011	0.025	0.046	0.041
TP (surface)	0.04	0.03	0.04	0.04	0.03
TP (bottom)	0.04	0.04	0.04	0.04	0.04
DRP (surface)	0.008	0.006	0.008	0.012	0.007
DRP (bottom)	0.012	0.009	0.01	0.013	0.013
DO (surface) (lower limit)	7.8	7.7	7.7	8.3	8.4
DO (bottom) (lower limit)	7.5	7.4	7.2	7.7	8.0
Chlorophyll *a* (integrated)	2.2	1.9	1.7	3.9	2.4

Table 3-4**:** Annual and seasonal default guideline values (determined from historical data) for Storm Bay. ND = insufficient data collected.

Parameter (mg/L) or (mg/m3)	Annual	Summer	Autumn	Winter	Spring
TAN (surface)	0.009	0.009	0.009	0.009	0.008
TAN (bottom)	0.014	0.009	0.011	0.008	0.016
TN (surface)	0.32	0.31	0.32	0.34	0.30
TN (bottom)	0.34	0.31	0.34	0.36	0.37
NOx (surface)	0.020	0.002	0.007	0.047	0.009
NOx (bottom)	0.044	0.002	0.031	0.048	0.044
TP (surface)	0.040	0.040	0.030	0.040	0.030
TP (bottom)	0.040	0.040	0.040	0.040	0.040
DRP (surface)	0.010	0.007	0.008	0.013	0.009
DRP (bottom)	0.013	0.007	0.012	0.014	0.014
DO (surface) (lower limit)	7.8	7.7	7.7	8.6	8.5
DO (bottom) (lower limit)	7.4	7.7	7.7	ND	ND
Chlorophyll *a* (integrated)	2.0	1.5	1.6	3.7	1.8

3.3.4 Methods

To measure the level of variation in the environmental monitoring variables within and between a site and a month, we fitted linear mixed effects regression models to the far-field sites. We used a Box Cox transformation method on each of the selected variables, as many were highly skewed (Table 3-5). Some values were consistently below the detection level (i.e. TAN and NO_x). To retain variation in these values, a value was imputed between zero and the detection level value, based on a transformed normal distribution. The linear mixed effects regression models were seasonally adjusted, and month and site were treated as random effects. Separate models were fitted for surface and bottom measures, for regions

80 and 93 and for all of Storm Bay. We did not detect significant temporal auto correlation over and above the seasonal variation, and so it was not accounted for in the regression models.

Table 3-5: λ represents the best Box Cox transformation ($y' = {y^\lambda}/{\lambda}$) that renders the data closest to a normal distribution.

Parameter (mg/L) or (mg/m3)	λ	Detectable level	% of data that is not detected
TAN	-1	0.005	55%
TN	0.24	0	0%
NOx	0.03	0.002	33%
TP	0.03	0	0%
DRP	0.39	0.003	11%
DO	1.12	0	0%
Chlorophyll *a*	0.06	0.5	4%

To measure the power to detect significant changes in the variables, between sites at different distances from salmon leases, we simulated data using the level of variation as measured in the above-mentioned models. The effect size was set at 50%, 100% and 200%, where an effect size of 100% is equivalent to when the mean of the environmental variable has decreased to the 20th (DO only) or increased to the 80th percentile (i.e., the trigger levels) (Table 3-4). This effect size was assumed to be consistent across seasons, although fish biomass and nitrogen emissions in Storm Bay are slightly higher in spring than other seasons.

The power to detect change was examined for all variables, for the compliance sites, regions 80, 93 and for the entire Storm Bay, for 4 different scenarios. These scenarios were (1) compliance site vs. sites < 5 km from the lease, (2) compliance and sites < 5 km from the lease vs. sites > 5 km from the lease, (3) near scale sites vs. intermediate scale sites, and (4) near and intermediate scale sites vs. far field sites. Power was estimated as the proportion of 200 simulations that showed a significant difference between categories of sites, for data collected once a month for one year, using a seasonally adjusted linear mixed effects regression model and a Box Cox transformation (Table 3-5). We also estimated power, if data were only collected in one season, using the 80th percentile for each season, (i.e., the seasonal trigger levels) for TAN and NOx. To determine the number of sites needed to detect significant differences, power was estimated when the number of sites varied between 1 and 100 (for each distance) and when samples were collected once or twice a month.

Table 3-6: The classification of each site by DGV region and across the entire Storm Bay for the four scenarios tested in the power analysis.

Sites	Region 93: Scenarios 1 & 2	Region 93: Scenario 3 & 4	Region 80: Scenarios 1 & 2	Region 80: Scenario 3 & 4	Storm Bay: Scenarios 1 & 2	Storm Bay: Scenarios 3 & 4
SB1	> 5 km	Far			> 5 km	Far
SB2	> 5 km	Far	> 5 km	Far	> 5 km	Far
SB3	Compliance	Intermediate			Compliance	Intermediate
SB4	> 5 km	Far			> 5 km	Far
SB5			Compliance	Intermediate	Compliance	Intermediate
SB6	< 5 km	Intermediate			< 5 km	Intermediate
SB7			> 5 km	Far	> 5 km	Far
SB10			> 5 km	Far	> 5 km	Far
SB11	< 5 km	Intermediate			< 5 km	Intermediate
SB12	< 5 km	Intermediate			< 5 km	Intermediate
SB13	< 5 km	Intermediate			< 5 km	Intermediate
SB14	< 5 km	Intermediate			< 5 km	Intermediate
SB15	< 5 km	Intermediate			< 5 km	Intermediate
SB16			< 5 km	Intermediate	< 5 km	Intermediate
SB17			> 5 km	Far	> 5 km	Far
SB18			> 5 km	Far	> 5 km	Far
SB19			> 5 km	Far	> 5km	Far
SB24			< 5 km	Intermediate	< 5 km	Intermediate
NUB1			< 5 km	Near	< 5 km	Near
NUB2			< 5 km	Near	< 5 km	Near
NUB3			< 5 km	Intermediate	< 5 km	Intermediate
NUB4			< 5 km	Near	< 5 km	Near
SBM3	< 5 km	Near			< 5 km	Near
YB4	< 5 km	Near			< 5 km	Near

3.3.5 Results

For most parameters, the variation between month was higher than between (farfield) sites (Table 3-7). The results from the linear model showed there were significant seasonal differences in TP in the surface waters, TAN in the bottom waters, and DRP, NOx and DO at both depths (Table 3-7). Throughout the sampling period, the maximum values for TP in the surface waters and DRP and NOx at both depths were recorded in winter, while the maximum values for TAN in the surface waters and the minimum values for DO at both depths were recorded in late summer (Table 3-7). There was more variation between months (after adjusting for seasonal effects) than there was between sites for all parameters, at all depths, except NOx in the bottom waters (Table 3-7). The parameters shown here were used as the basis for simulating the data in the power analyses (Table 3-7).

The power to detect significant differences between categories of sites differed between

scenarios, regions, depths, and effect sizes. For the lease-specific management scenarios, (i.e., (1) compliance site vs. sites < 5 km of the lease and (2) compliance and sites < 5 km of the lease vs. sites > 5 km from the lease) the simulations for MF279 (West of Wedge Island) suggested there was 80% power to detect differences in TP in the surface and bottom waters and TAN, DO and TN in the surface waters for an effect size equivalent to the trigger levels (i.e., 100%). However, for TAN, DO and TN in the bottom waters, only effect sizes that were 1.2 to 1.5 times greater than the trigger levels could be detected with 80% power in scenario 1 (Figure 3-44) while effect sizes that were equivalent to the trigger levels (i.e. 100%) could be detected in scenario 2. By contrast, for NOx in the bottom waters and chlorophyll *a* biomass, 80% power to detect changes was only achieved with very large effect sizes (i.e., > 200%) for scenario 1, but smaller effect sizes (~150%) could be detected for both variables for scenario 2.

Table 3-7: Results of the linear mixed effects model on the farfield sites. Seasonal adjustment was made by including the fixed effects $cos(2\pi t\ /12)$ and $sin(2\pi t/12)$, where t is the month. An asterisk (*) is shown for variables/depths that have significant seasonal variation, using a χ^2 likelihood ratio test and a Bonferroni adjustment for 13 tests.

Parameter (mg/L) or (mg/m3)	Depth	Variation between months	Variation between sites	Variation within a site and month	Seasonal min	Seasonal max	Month when the minimum value is recorded	Month when maximum value is recorded	p-value for seasonal effect
TAN	S	32%	3%	65%	0.0048	0.0052	9	3	0.53
TAN	B	44%	1%	55%	0.0045	0.011	6	12	< 0.0001 *
TN	S	35%	2%	63%	0.25	0.28	12	6	0.016
TN	B	42%	3%	56%	0.27	0.29	2	8	0.42
NOx	S	18%	8%	74%	0.00083	0.034	12	6	< 0.0001 *
NOx	B	10%	23%	67%	0.0081	0.052	1	7	< 0.0001 *
TP	S	23%	19%	59%	0.022	0.027	12	6	0.0017 *
TP	B	24%	9%	67%	0.026	0.028	3	9	0.25
DRP	S	37%	11%	53%	0.003	0.0098	12	6	< 0.0001 *
DRP	B	15%	2%	84%	0.0071	0.012	1	7	< 0.0001 *
DO	S	19%	5%	76%	8	9	2	8	< 0.0001 *
DO	B	33%	5%	62%	7.6	8.5	3	9	< 0.0001 *
Chlorophyll *a*	I	41%	18%	41%	0.71	1.5	2	8	0.01

For the DGV management scenarios (i.e., (3) near scale sites vs. intermediate scale sites, and (4) near and intermediate scale sites vs. far field scale sites) the simulations for region 80, showed that 80% power was achieved with an effect size equivalent to the trigger levels (i.e., 100%) for all variables excluding nitrate + nitrate in the bottom waters, DRP in the surface waters and integrated samples of chlorophyll *a* (Figure 3-44). For these variables 80% power to detect changes was only achieved with larger effect sizes (~ 150%) for scenario 3 while effect sizes that were equivalent to the trigger levels (i.e. 100%) could be detected by scenario 4. By contrast, for chlorophyll *a* biomass, 80% power to detect changes was only achieved with effect sizes >100%, but for both variables scenario 4 could detect smaller effect sizes (<150%) compared with scenario 3 (>150%).

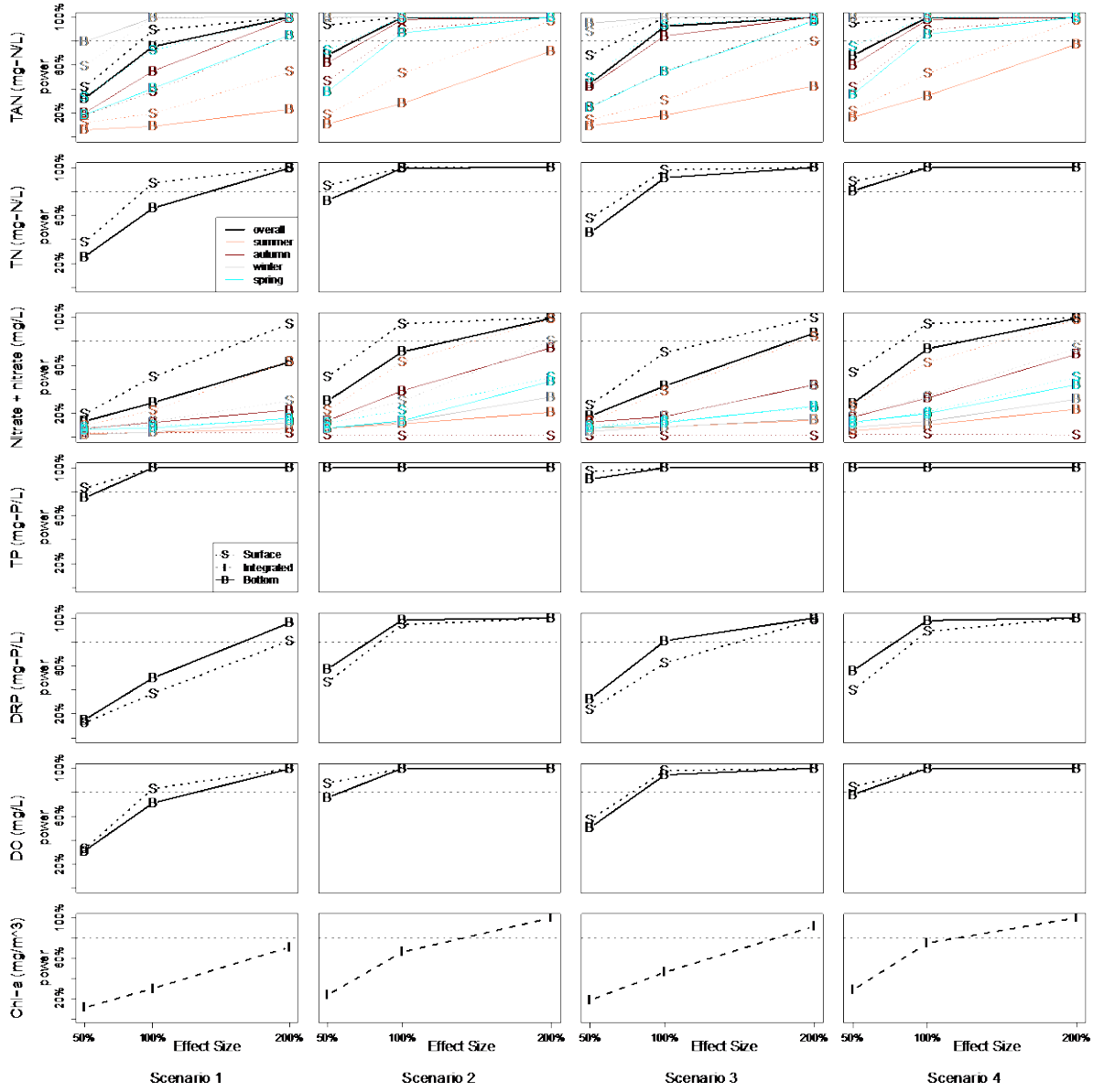


Figure 3-44: Power to detect significant differences at region 80, for each parameter (mg/L) or (mg/m3), across four different scenarios: (1) compliance site (n = 1) vs. sites < 5km from the lease (n = 6), (2) compliance and sites < 5 km from the lease (n = 7) vs. sites > 5 km from the lease (n = 6), (3) near scale sites (n = 3) vs. intermediate scale sites (n = 4), and (4) near and intermediate scale sites (n = 7) vs. far field sites (n = 6), and 3 different effect sizes (50%, 100% and 200% of the trigger levels). Solid lines represent bottom measures and dotted lines represent surface measures. For NOx and TAN, power is also shown if data were only collected in one season. The horizontal dashed line represents 80% power.

For MF281 (East of Yellow Bluff), the simulations for the lease-specific scenarios, ((1) compliance site vs. sites < 5 km from the lease and (2) compliance and sites < 5 km from the lease vs. sites > 5 km from the lease), suggested there was at least 80% power to detect differences in all parameters except for TAN and TN the surface and bottom waters for scenario 1, and chlorophyll *a* biomass in both scenarios for an effect size equivalent to the trigger levels (i.e., 100%) (Figure 3-45). There was 80% power to detect differences in TN and TAN (surface only) for effect sizes slightly greater than the trigger levels (~ 120%) in scenario 2, but for scenario 1 only very large effect sizes (i.e., 200%) could be detected for both variables. For chlorophyll *a* biomass, effect sizes that were double the trigger levels

(i.e., 200%) were still not sufficient to obtain 80% power to detect changes, but the power in scenario 2 was clearly greater than scenario 1(Figure 3-45).

For the DGV management scenarios (i.e., (3) near scale sites vs. intermediate scale sites, and (4) near and intermediate scale sites vs. far field scale sites) the simulations for region 93, showed that 80% power was achieved for all variables excluding TN, TAN in the surface and bottom waters and integrated samples of chlorophyll *a* biomass (Figure 3-45). 80% power to detect changes in TN was achieved at an effect size of approximately 120% in scenario 2 and 150% in scenario 1, and for TAN closer to 200% for both scenarios. Effect sizes of double the trigger levels (i.e., 200%) were still not sufficient to obtain 80% power to detect changes

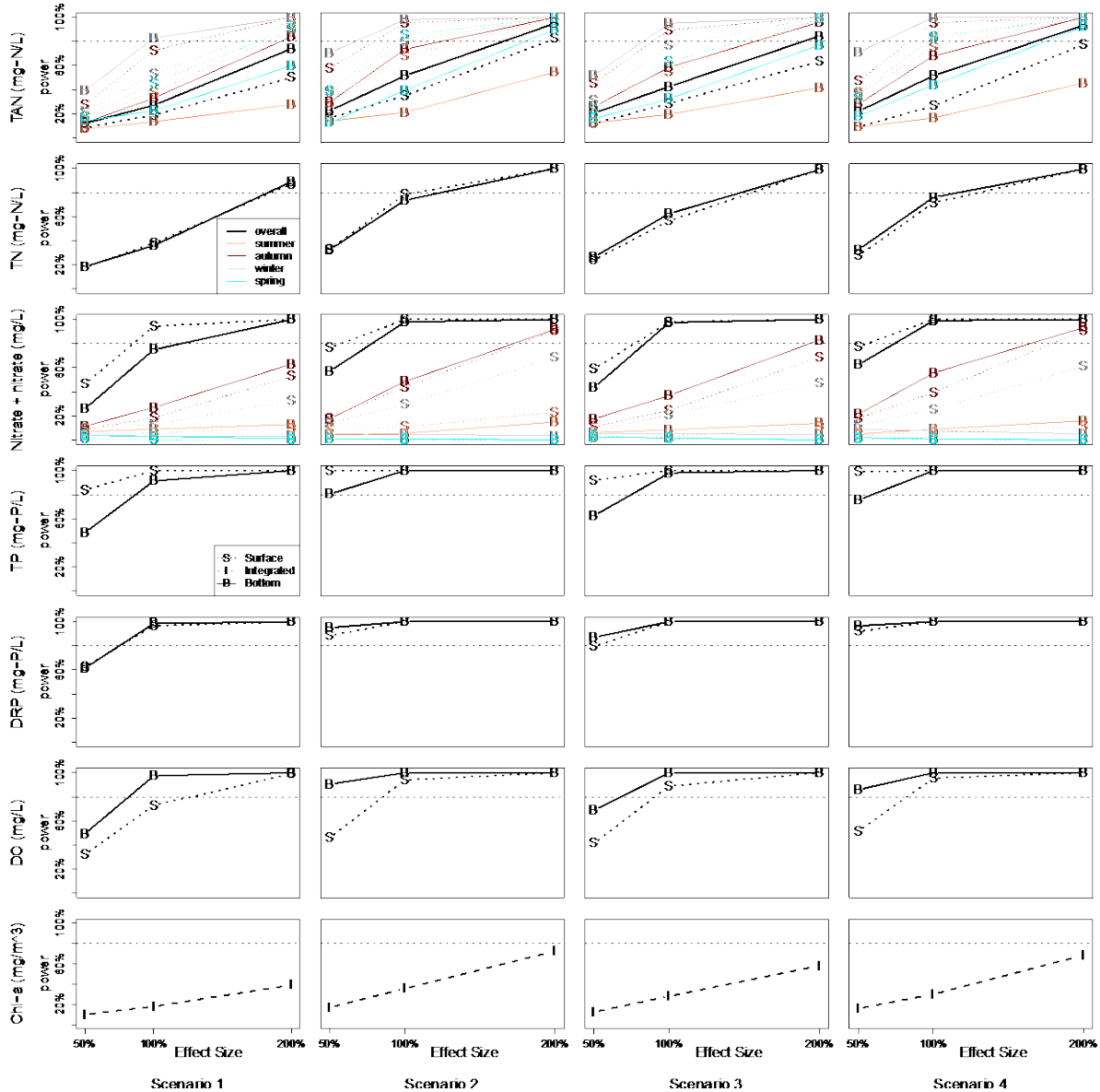


Figure 3-45: Power to detect significant differences at region 93, for each parameter (mg/L) or (mg/m3), across four different scenarios: (1) compliance site (n = 1) vs. sites < 5km from the lease (n = 8), (2) compliance and sites < 5 km from the lease (n = 9) vs. sites > 5 km from the lease (n = 3), (3) near scale sites (n = 2) vs. intermediate scale sites (n = 7), and (4) near and intermediate scale sites (n = 9) vs. far field sites (n = 3), and 3 different effect sizes (50%, 100% and 200% of the trigger levels). Solid lines represent bottom measures and dotted lines represent surface measures. For nitrate + nitrite and TAN, power is also shown if data were only collected in one season. The horizontal dashed line represents 80% power.

for TAN in surface samples or chlorophyll *a* biomass for integrated samples (Figure 3-45), irrespective of the scenario.

For the entire Storm Bay, there was 80% power to detect change in all parameters excluding chlorophyll *a* biomass in scenario 1 (compliance sites vs. sites < 5km from the lease) and scenario 3 (near scale sites vs. intermediate scale sites) (Figure 3-46). For these two scenarios, 80% power for chlorophyll a biomass was achieved at effect sizes of ~200% and 150%, respectively (Figure 3-46).

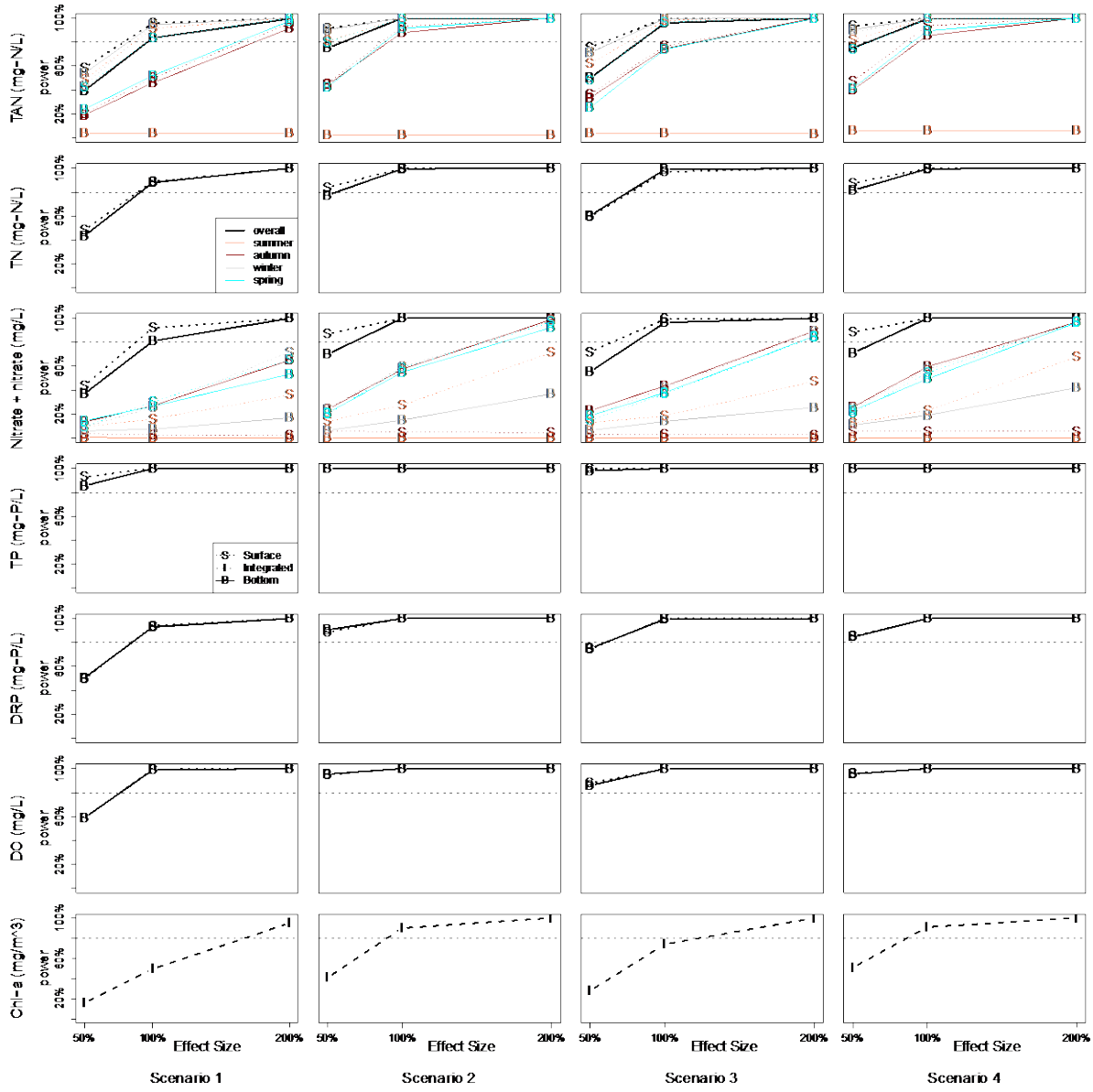


Figure 3-46: Power to detect significant differences for the entire Storm Bay, for each parameter (mg/L or mg/m3), across four different scenarios of sampling: (1) compliance site (n = 2) vs. < 5km (n = 14); (2) < 5km (n = 16) vs. < 5km (n = 8); (3) near scale (n = 5) vs. intermediate sites (n = 11); (4) near and intermediate scale sites (n = 16) vs. far scale sites (n = 8), and 3 different effect sizes (50%, 100% and 200% of the trigger levels). Solid lines represent bottom measures and dotted lines represent surface measures. For NOx and TAN, power is also shown if data were only collected in one season. The horizontal dashed represents 80% power.

Effect sizes that were based on seasonal triggers did not improve power to detect changes in NOx for either of the DGV regions or across Storm Bay, irrespective of the scenario

(Figures 3 44, 45 & 46). There was, however, some evidence to suggest that the power for detecting changes in TAN in surface and bottom waters in winter was improved when seasonal triggers were applied to region 80 and 93 but not the entire Storm Bay (Figures 3 44, 45 & 46).

Figure 3-47 shows the effect of increasing the number of sites (n 1 = distance 1 and n 2 = distance 2) and sampling frequency (1 time per month and 2 times per month), on the power to detect changes in the parameters, irrespective of scenario, across all of Storm Bay. Across all variables and depths, the power to detect change was improved substantially by increasing the number of sites, but only negligibly when increasing the frequency of samples (i.e. from 1 to 2 per month) (Figure 3-47). For all parameters, 80% power was achieved by sampling at least 12 sites, (6 at each distance) (Figure 3-47).

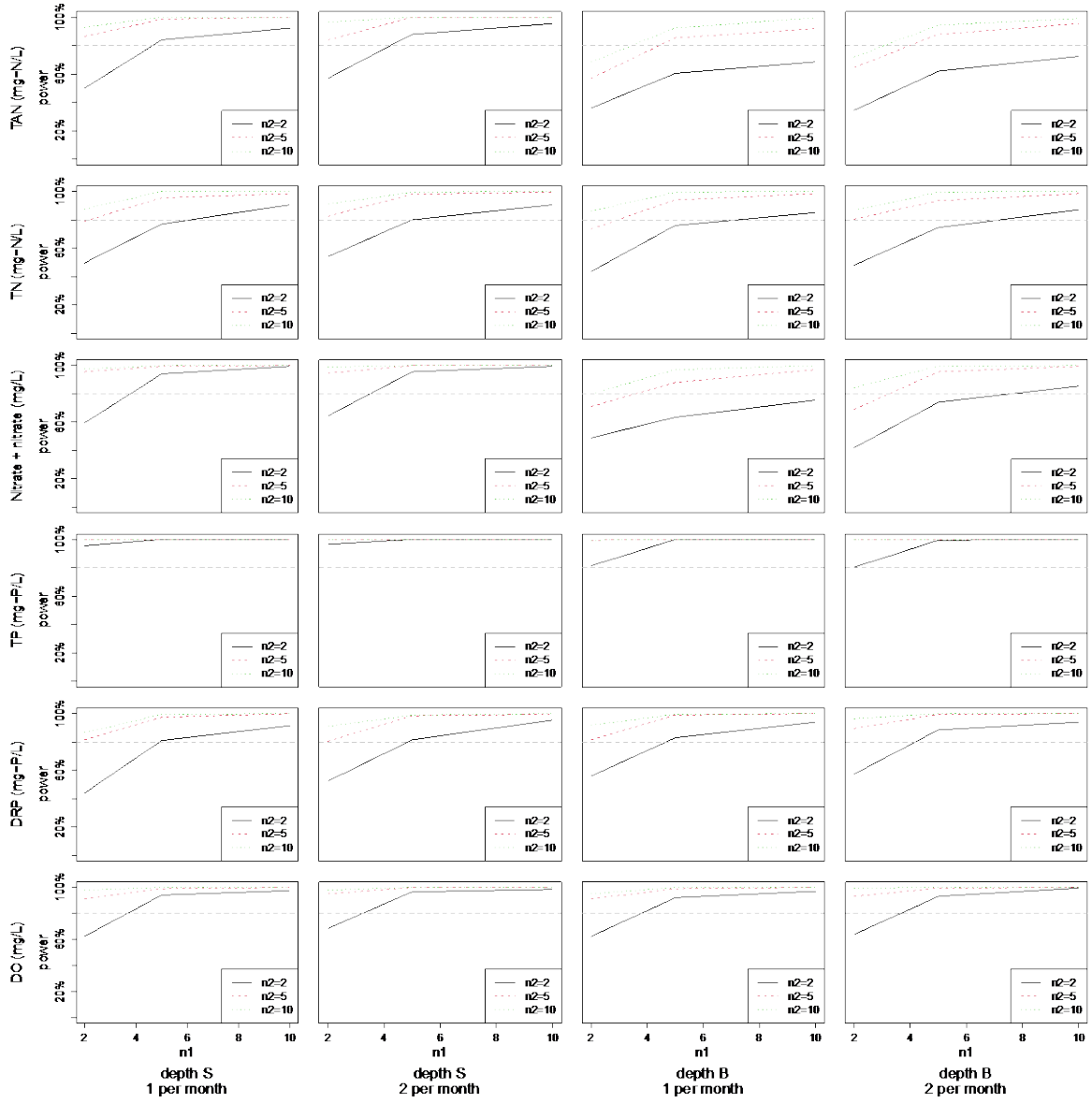


Figure 3-47: Power for each parameter (mg/L), to detect significant differences across Storm Bay for different numbers of sites (n 1 = distance 1 and n 2 = distance 2) and samples per month (1 or 2 times per month). The horizontal dashed line represents 80% power.

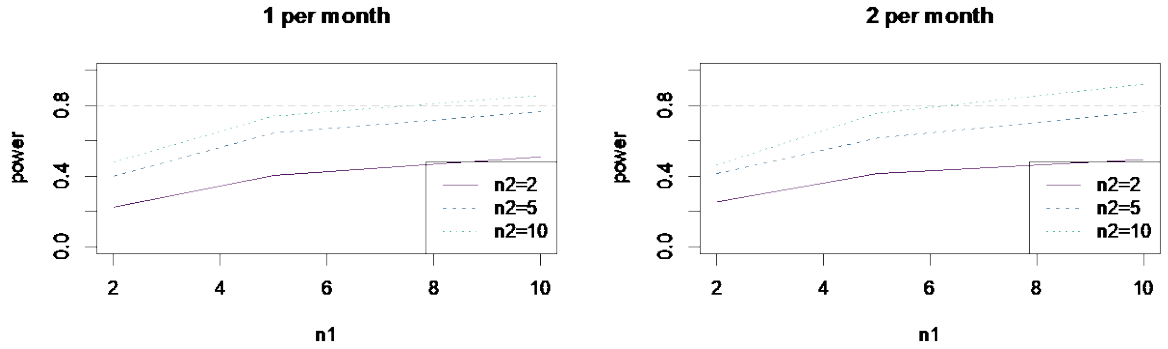


Figure 3-48: Power to detect significant differences in chlorophyll a biomass (mg/m^3) across the entire Storm Bay, for different numbers of sites (n 1 = distance 1 and n 2 = distance 2) and samples per month (1 or 2 times per month). The horizontal dashed line represents 80% power.

The power to detect significant differences in chlorophyll *a* between sites in different categories (i.e., scenarios 1- 4) for the monthly trigger levels (i.e., 3.3 mg/m^3 for region 93 East of Yellow Bluff and 4.6 mg/m^3 for region 80 West of Wedge Island) was estimated based on two independent sample T-tests. The minimum number of sites needed to obtain 80% power was 10 sites for region 93, 5 sites at each distance (e.g., compliance vs. > 5 km or <5 km vs. >5km, near vs. intermediate scale) and 6 sites for region 80, 3 sites at each distance (e.g., <5 km vs. >5km, near vs. intermediate scale). The number of sites required to capture the variation in chlorophyll *a* biomass was higher in region 93 than region 80, because the monthly trigger level assigned to this region was lower.

3.4 Water column monitoring – Overview

3.4.1 Sampling parameters

Based on the results from local and broadscale monitoring of Storm Bay we recommend that the following parameters, frequency and depths be sampled to monitor the interactions between salmon farming, other nutrient sources and the surrounding water column (Table 3-8). The parameters with high importance for monitoring the interactions between salmon farming and the water column are TAN, TN, chlorophyll *a* biomass, phytoplankton abundances, and DO. Parameters of medium importance for interpreting environmental changes in Storm Bay are TP, DRP, NOx, temperature, salinity and SiO_2 and lowest priority are NO_3, TKN, NPOC, NPOC dissolved, fluorescence and pH.

Salmon farming releases carbon (C), nitrogen (N) and phosphorus (P) into the water column. Dissolved inorganic N (i.e., NH3+) and P (i.e., PO4 3−) (DIN and DIP, respectively) are released through excretion, and inorganic C as CO2 is released through respiration (Wang et al. 2012). Particulate organic C, N and P (POC, PON and POP, respectively) are released through defecation and loss of feed (Wang et al. 2012). Dissolved organic C, N and P (DOC, DON, and DOP, respectively) are generated through dissolution of particulate organic fractions (Olsen et al. 2008). The DIN and DIP can be readily taken up by phytoplankton resulting in blooms of phytoplankton and particularly diatoms and harmful algae species (Reed et al. 2016).

Depletion of DO in the surface waters can occur because of fish respiration and bacterial processing of waste products (Hook et al. 2021). If the seabed beneath a salmon farm becomes enriched by particulate wastes, biological activity of bacteria can cause a reduction in bottom water DO (Ross et al. 2022). Monitoring in Tasmania suggests that salmon farming

activities can cause changes in water column NH_4, TAN, TN, abundances of phytoplankton and DO at sites within 500 m of the lease in exposed locations such as Storm Bay (IMAS 2020a, 2021, 2022) and DO throughout the ecosystem in sheltered locations such as Macquarie Harbour (Ross et al. 2022). These parameters are therefore considered the highest priority for future monitoring efforts.

By contrast, there was little evidence to suggest that salmon farming activities in Storm Bay and elsewhere have resulted in higher concentrations of NOx, TP, DRP or SiO2. Instead, many of these parameters, along with temperature and salinity, showed clear seasonal trends and were influenced by external forcings including the influence of the sub-Antarctic and Leeuwin Currents, EAC eddies and flow of the Derwent River (see above section for further details). Monitoring of these parameters along with the dominant current flow and direction provides important information about the background variation in Storm Bay and will help to interpret changes in the parameters which are linked to salmon farming activities.

The parameters of lower importance for future monitoring showed overlapping trends with other variables (i.e. NOx and NO_3, chlorophyll *a* biomass and fluorescence), site specific trends (i.e. NPOC, NPOC dissolved, TKN) or high variation between instruments (i.e. pH). Because of these considerations, these parameters are considered less important in future monitoring of the interactions between salmon farming and the surrounding water column. Finally we suggest that monitoring of key parameters should focus on sampling the surface and bottom waters as sampling at 10 m did not provide any additional information.

Table 3-8: Proposed monitoring parameters for Storm Bay, depth, frequency, and importance (High, Medium, or Low).

Parameter (mg/L) or (mg/m3)	Depth	Frequency	Importance (Low/Medium/High)
Nutrients		1 per month	
TAN	Surface/1 m above bottom		H
TN			H
Nitrite + Nitrate			M
NO_3			L
TKN			L
TP			M
DRP			M
NPOC			L
NPOC (Dissolved)			L
Phytoplankton			
Chlorophyll *a*	12 m integrated	1 per month	H
Abundance total, diatoms, dinoflagellates, harmful species			H
Environmental parameters			
Current flow and direction	Throughout the water column	1 per month	M
DO			H
Fluorescence			L
pH			L
Temperature			M
Salinity			M
SiO2			M

3.4.2 Sampling design

The results of the power analyses showed there was high variability in most parameters between months. This high variability meant that monitoring based on 12 months of sampling was more likely to detect significant differences between sites at different distances from the lease than seasonal monitoring which is only based on three samples. Because of this, the use of seasonal trigger levels did not improve power of the monitoring program to detect significant differences between categories of sites.

The power analyses also showed that increasing the number of samples in a month from one to two did not increase the power of the design to detect change. Instead, the results suggested that implementing a balanced design (i.e., equal numbers of sites for each distance category) would improve power. Based on the annual rolling median effect size (100%), the highest number of sites was required to monitor changes in chlorophyll *a* biomass. A minimum of 6 sites in each distance category (e.g., distance 1 vs. distance 2) were required to improve the power of the monitoring program to detect significant changes in this parameter across the entire Storm Bay.

The scenario testing showed that monitoring which focused on detecting the local (lease) scale effects of salmon farming for chlorophyll *a* biomass with only a single compliance site required the largest number of sites (n > 100 at another distance) to achieve 80% power (Table 3-9). Monitoring which focused on detecting the effects of salmon farming on chlorophyll *a* biomass at the lease or DGV region scale with a balanced design (e.g. distance 1 vs. distance 2) required approximately half as many sites (n = 46, 23 at each distance) (Table 3-9). Monitoring which focused on detecting ecosystem level effects of salmon farming for chlorophyll *a* biomass and implemented a balanced design (i.e. equal number of samples at 2 distances) required the smallest number of sites to achieve 80% power (n = 12, 6 at each distance) (Table 3-9).

3.4.3 Site selection

The spatial arrangement of sites in the current BEMP program was informed by CONNIE nutrient dispersion modelling and the desire to sample and monitor potential interactions at near, intermediate, and far field scales. As described above, these categories are based on distance from the nearest active lease. The CSIRO TASSE biogeochemical model that predicts changes in water quality for Storm Bay based on an increase in nutrient loads associated with the expansion of salmon farming scenarios (Table 3-10) provides an opportunity to further evaluate and prioritise site selection for each category based on predicted change. Here, we assess and contrast change for the current sites based on the difference between scenario 4 that predicted water quality conditions with an additional fish farm nitrogen load of approximately 2k tonnes in Storm Bay and scenario 3 that predicted water quality conditions pre-Storm Bay development (Table 3-10).

CSIRO provided IMAS with model output for a suite of water quality parameters, evaluated at monitoring site locations in Storm Bay. Not all sites, which make up the Storm Bay BEMP monitoring program were included in the output. This was because the model runs finished mid-2020 and new sites were added to the Storm Bay monitoring program after that time, based on environmental licence requirements. The modelled data had a temporal resolution of 2 hours and encompassed a range of discrete depth layers including surface, mid and bottom waters. In this analysis we used both mean monthly surface dissolved inorganic

nitrogen (DIN i.e., NOx + TAN) and total ammoniacal nitrogen (TAN) to examine change from a proposed 2kt tonne expansion. TAN is the major form of DIN output from farms; however, it is rapidly nitrified into nitrite and nitrate. Including both variables provides a more complete characterisation of the waste nutrient footprint extending from the farms.

Table 3-9: The minimum number of sites required to sample differences the key parameters to obtain 80% power when the effect size is based on annual trigger levels.

Parameter (mg/L or mg/m3)	Depth	Minimum number of sites (< 5 km from the lease, > 5 km from the lease, intermediate or far-field) for 80% power with 1 compliance site, region 93	Minimum number of sites (< 5 km from the lease, > 5 km from the lease, intermediate or far-field) for 80% power with 1 compliance site, region 80	Minimum number of sites (< 5 km from the lease, > 5 km from the lease, intermediate or far-field) for 80% power with 2 compliance sites, entire Storm Bay	Minimum total number of sites at each of two distances for 80% power with a balanced design region 93	Minimum total number of sites at each of two distances for 80% power with a balanced design region 80	Minimum total number of sites at each of two distances for 80% power with a balanced design entire Storm Bay
TAN	S	>100	16	4	19 and 19	2 and 2	2 and 2
TN	S	>100	12	7	4 and 4	2 and 2	3 and 3
NOx	S	42	>100	5	2 and 2	3 and 3	3 and 3
TP	S	4	4	3	2 and 2	2 and 2	2 and 2
DRP	S	6	>100	4	2 and 2	4 and 4	2 and 2
DO	S	75	14	3	2 and 2	2 and 2	2 and 2
TAN	B	>100	49	18	7 and 7	2 and 2	3 and 3
TN	B	>100	43	8	4 and 4	2 and 2	3 and 3
NOx	B	16	>100	13	2 and 2	5 and 5	3 and 3
TP	B	10	4	2	2 and 2	2 and 2	2 and 2
DRP	B	4	>100	2	2 and 2	3 and 3	2 and 2
DO	B	7	27	3	2 and 2	2 and 2	2 and 2
Chlorophyll *a*	I	>100	>100	>100	23 and 23	6 and 6	6 and 6

3.4.4 Modelled change at the broadscale monitoring sites – 2ktN scenario.

Predicted change in mean annual surface DIN and TAN under a 2ktN scenario is shown in Figure 3-50 and Figure 3-51 respectively. Mean annual surface DIN increased across all the Storm Bay monitoring sites modelled, based on the 6-year average. Given STP, industry and salmon farm loads were similar for scenarios 3 and 4, except for a substantial increase in salmon production in Storm Bay (Figure 3-49), this result is due to the increased production in that region. Actual values for predicted mean monthly and annual change in surface DIN

are shown in Table 3-11. Sites have been ranked in descending order based on annual percentage change, which is the average of monthly values for each site. This ranking has near-scale sites most impacted followed by intermediate and then far field, preserving the original categorisation of these sites in the monitoring program.

Table 3-10: Summary of model runs and scenarios to characterise historical and projected water quality in Storm Bay under various management regimes. Scenario numbering is kept the same as in the TASSE model report (Wild-Allen et al 2021).

Scenario	River Load	STP + Industry load	Farm Load	Purpose
3. Pre-Storm Bay Development	2015-20	2015 load repeated each year	2013 loads repeated each year (farms in Huon, D'Entrecasteaux Channel & Nubeena)	Quantify impact of anthropogenic load (circa 2013) on WQ in Storm Bay
4. Post-Storm Bay development 2020 + 2ktN in SB)	2015-20	2020 load repeated each year	Projected loads in SB[2] + 2020 loads elsewhere, repeated each year	Predict plausible future impacts of anthropogenic loads on WQ in Storm Bay

Results in Table 3-11 indicate a shift in surface DIN at near-scale sites from 80 - 240%, intermediate sites from 20 – 60% and far field from 10-20%. We expect similar shifts in the near-scale, intermediate and far field monitoring sites added during 2020 and not analysed here, based on the maps of simulated change for this scenario comparison in Wild-Allen et. al. (2021) and shown here (Figure 3-52).

Change (%) in mean annual surface TAN, based on the 2ktN expansion scenario, showed similar results to DIN. However, sites SB1, SB8 and SB12 to the north of Storm Bay alternated in their ranked position with southern sites SB7, SB2 and SB4 respectively, when comparing change in annual surface DIN and TAN (Table 3-11, Table 3-12). Results in Table 3-12 indicate a shift in surface TAN at near-scale sites from 52 - 220%, intermediate sites from 13 – 50% and far field from 3 - 15%.

The categorisation of near-scale, intermediate and far field categorisations were based on distances from leases; the TASSE model results are consistent with this categorisation. Although this captures a gradient of exposure, we would recommend that additional sites that more reliably capture background reference conditions are included.

A biogeochemical model was similarly constructed to examine impacts of salmon aquaculture in the D'Entrecasteaux Channel and Huon Estuary (Wild-Allen et al. 2010). That model was used to design a monitoring program for the region based on change in WQ parameters including labile nutrients (N, P), chlorophyll *a* and bottom water DO (Wild-Allen et al. 2011). Every grid cell was ranked in order (depth averaged reducing the grid to 2D) of

[2] Assuming 2ktN model scenario results in a load of 2295 tNy^{-1} discharged in Storm Bay over an annual cycle where Nov load is 2 x Jan load and distributed across leases as 668.5 tNy^{-1} Tassal (includes Nubeena); 1147.5 tNy^{-1} HAC; 459.0 tNy^{-1} Petuna

impact. Here we have only used the monitoring site locations, but a similar process can be followed using TASSE in Storm Bay whereby every grid cell is simulated.

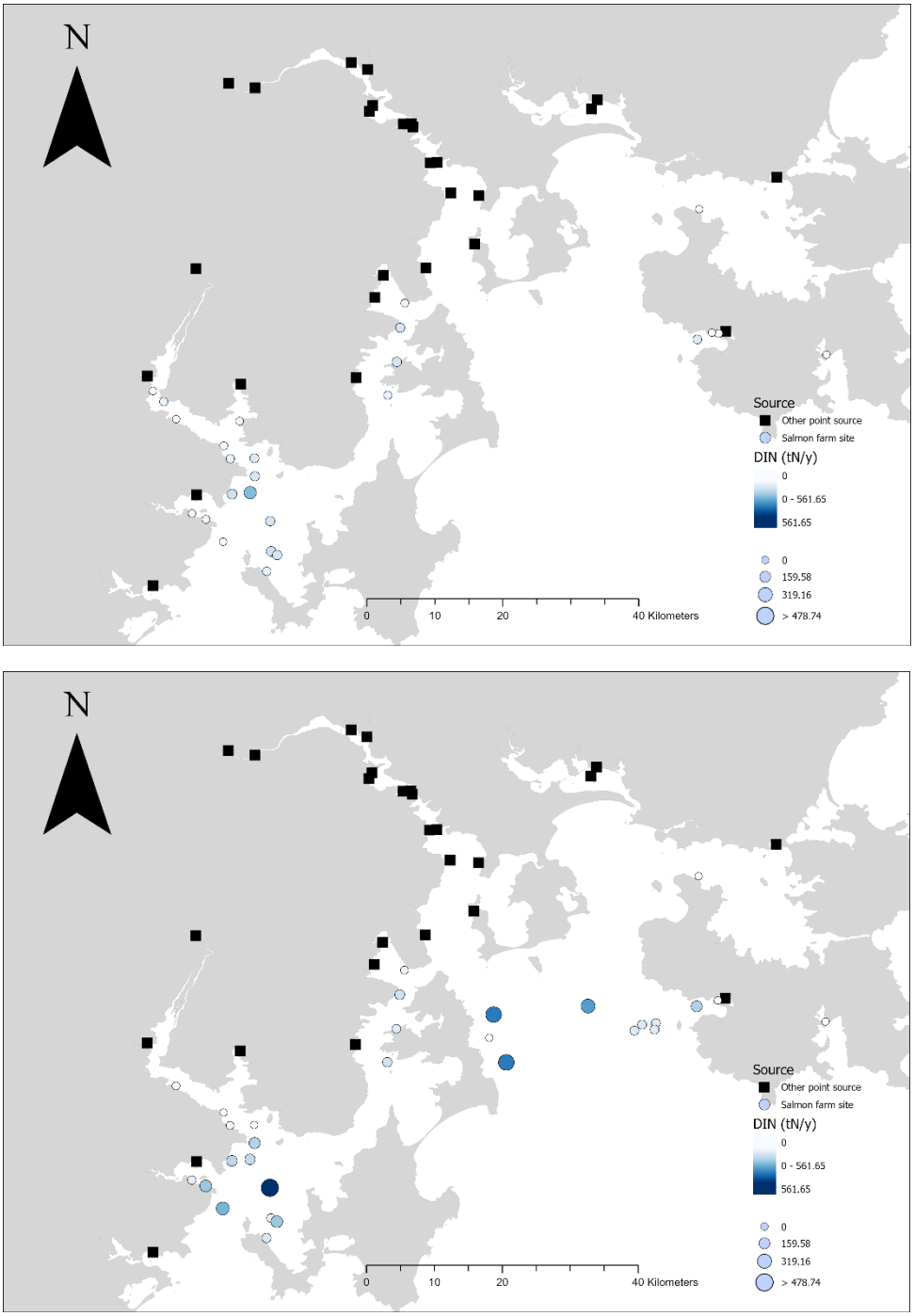


Figure 3-49: DIN (tNy-1) output from STP's, industry (squares) and salmon farms (circles) in pre-Storm Bay development (scenario 3, top) and 40 k tonne expansion (scenario 4, bottom). A significant increase in DIN is apparent in Storm Bay, solely derived from farm loads under the proposed expansion.

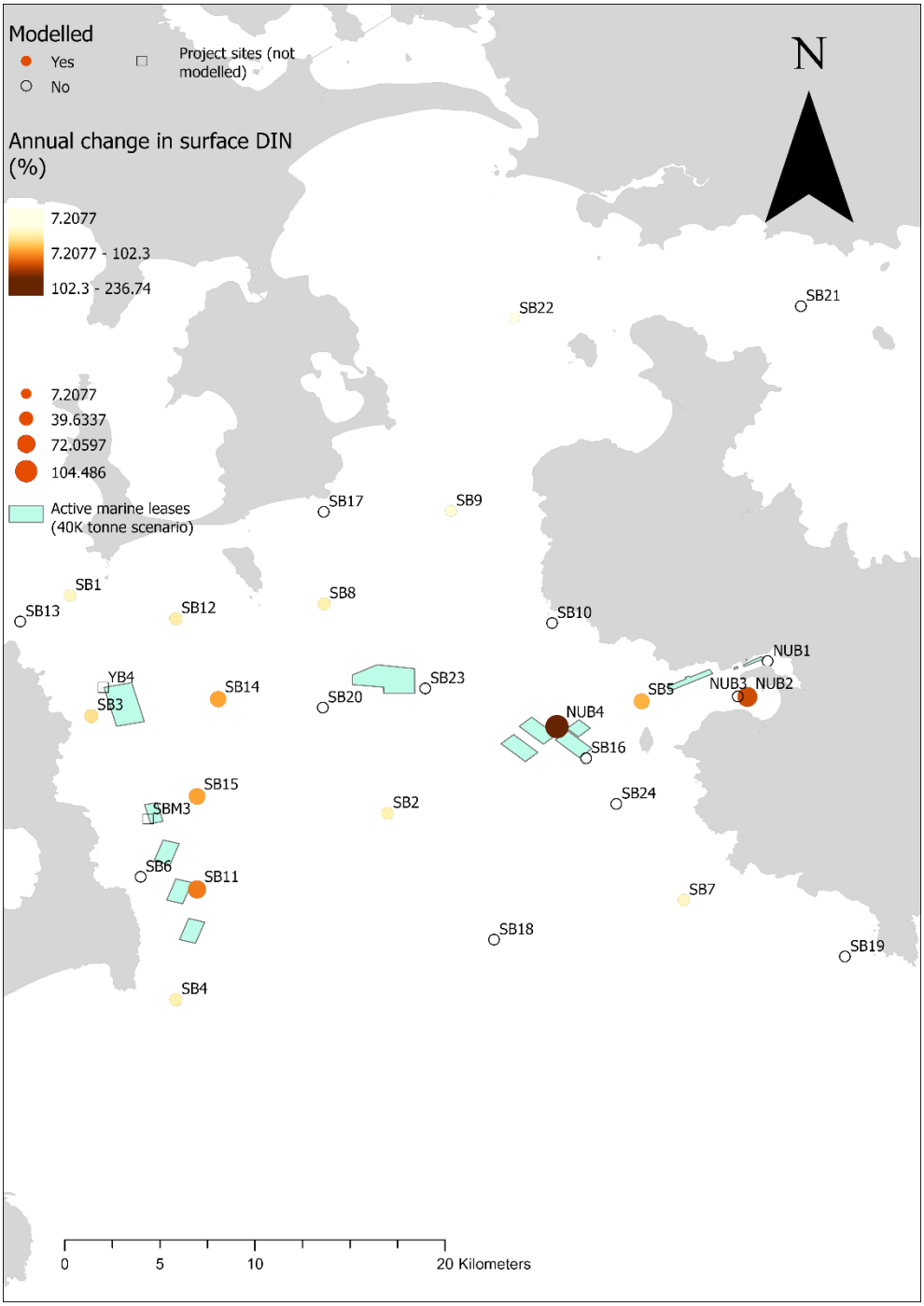


Figure 3-50: Percentage change in annual surface DIN for Storm Bay monitoring locations 2015-2020. Change is difference in surface DIN between the 40k tonnes farming in Storm Bay and pre-Storm Bay development.

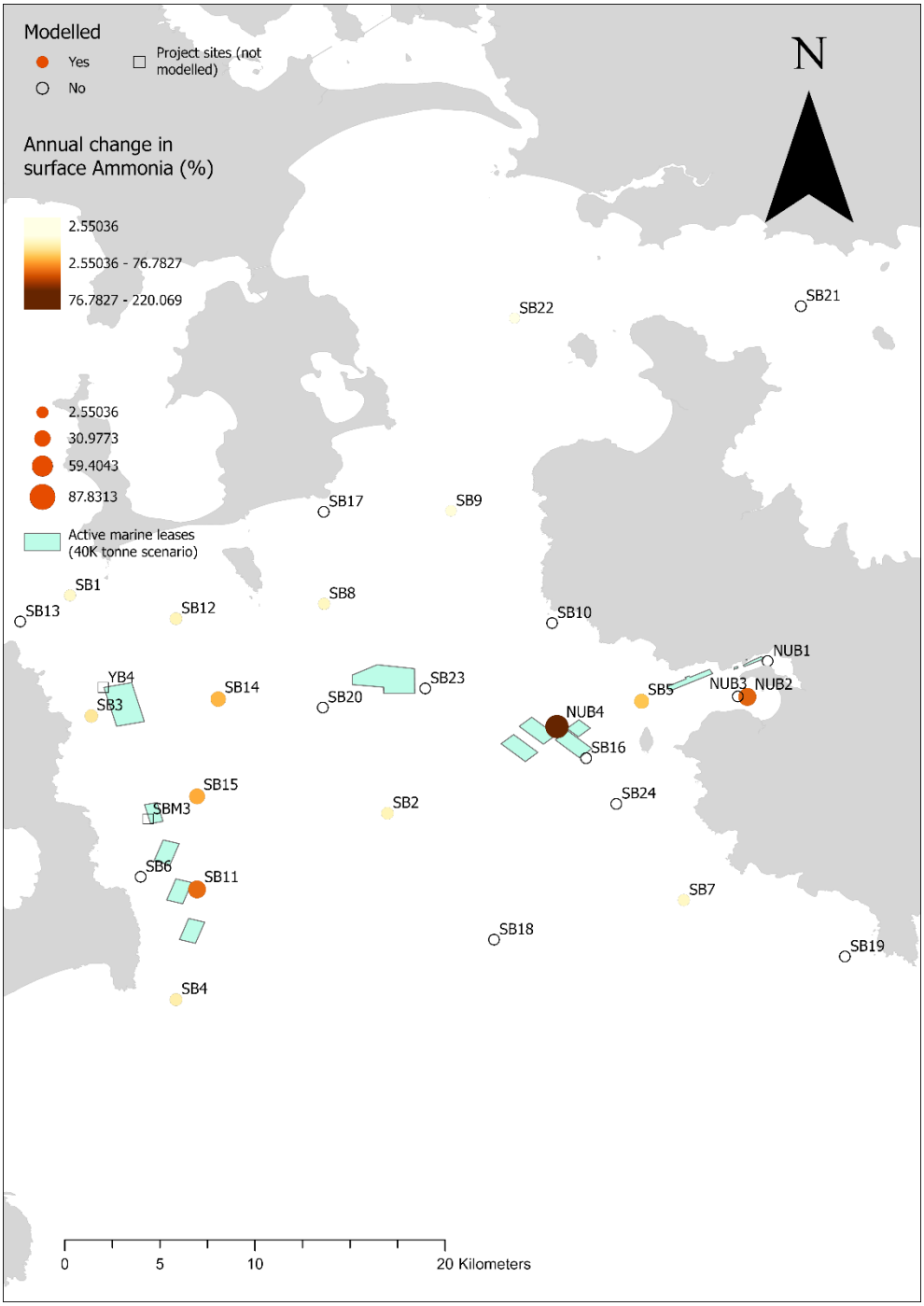


Figure 3-51: Percentage change in annual surface TAN for Storm Bay monitoring locations 2015-2020. Change is the difference in surface DIN between the 40k tonnes farming in Storm Bay and pre-Storm Bay development.

Table 3-11: Percentage change in surface DIN for Storm Bay sites based on monthly means in January, April, July and October from 2015-2020. Change is between scenarios 4 and 3.

Mean monthly change (%) in surface DIN between scenarios 3 and 4								
Site	**Type**	**Longitude**	**Latitude**	**Jan**	**Apr**	**July**	**Oct**	**Annual**
NUB4	Near Scale	147.63	-43.129	56	86	44	760	237
NUB2	Near Scale	147.72	-43.115	46	114	135	17	78
SB11	Intermediate	147.46	-43.206	67	59	49	81	64
SB15	Intermediate	147.46	-43.162	51	52	38	69	53
SB14	Intermediate	147.47	-43.116	45	53	24	83	51
SB5	Intermediate	147.67	-43.117	39	56	56	38	47
SB3	Intermediate	147.41	-43.124	34	40	22	31	32
SB12	Intermediate	147.45	-43.078	26	38	12	21	24
SB4	Far Field	147.45	-43.258	26	23	22	21	23
SB8	Far Field	147.52	-43.071	23	29	18	21	23
SB2	Far Field	147.55	-43.17	24	13	29	22	22
SB1	Far Field	147.4	-43.067	19	26	10	19	19
SB7	Far Field	147.69	-43.211	11	11	28	17	17
SB9	Far Field	147.58	-43.027	10	7	19	12	12
SB22	Far Field	147.61	-42.936	6	4	10	9	7

Table 3-12: Percentage change in surface TAN for Storm Bay sites based on monthly means in January, April, July and October from 2015-2020. Change is between scenarios 4 and 3.

Mean monthly change (%) in surface TAN between scenarios 3 and 4								
Site	**Type**	**Longitude**	**Latitude**	**Jan**	**Apr**	**July**	**Oct**	**Annual**
NUB4	Near Scale	147.63	-43.129	36	67	38	739	220
NUB2	Near Scale	147.72	-43.115	22	56	122	8	52
SB11	Intermediate	147.46	-43.206	41	45	44	71	50
SB15	Intermediate	147.46	-43.162	22	33	32	56	36
SB14	Intermediate	147.47	-43.116	18	28	18	69	33
SB5	Intermediate	147.67	-43.117	21	33	49	17	30
SB3	Intermediate	147.41	-43.124	18	22	17	21	20
SB4	Far Field	147.45	-43.258	13	14	18	17	15
SB12	Intermediate	147.45	-43.078	12	21	7	12	13
SB2	Far Field	147.55	-43.17	6	6	24	15	13
SB8	Far Field	147.52	-43.071	10	12	12	9	11
SB7	Far Field	147.69	-43.211	6	5	23	6	10
SB1	Far Field	147.4	-43.067	7	13	6	11	9
SB9	Far Field	147.58	-43.027	2	2	13	3	5
SB22	Far Field	147.61	-42.936	1	2	5	3	3

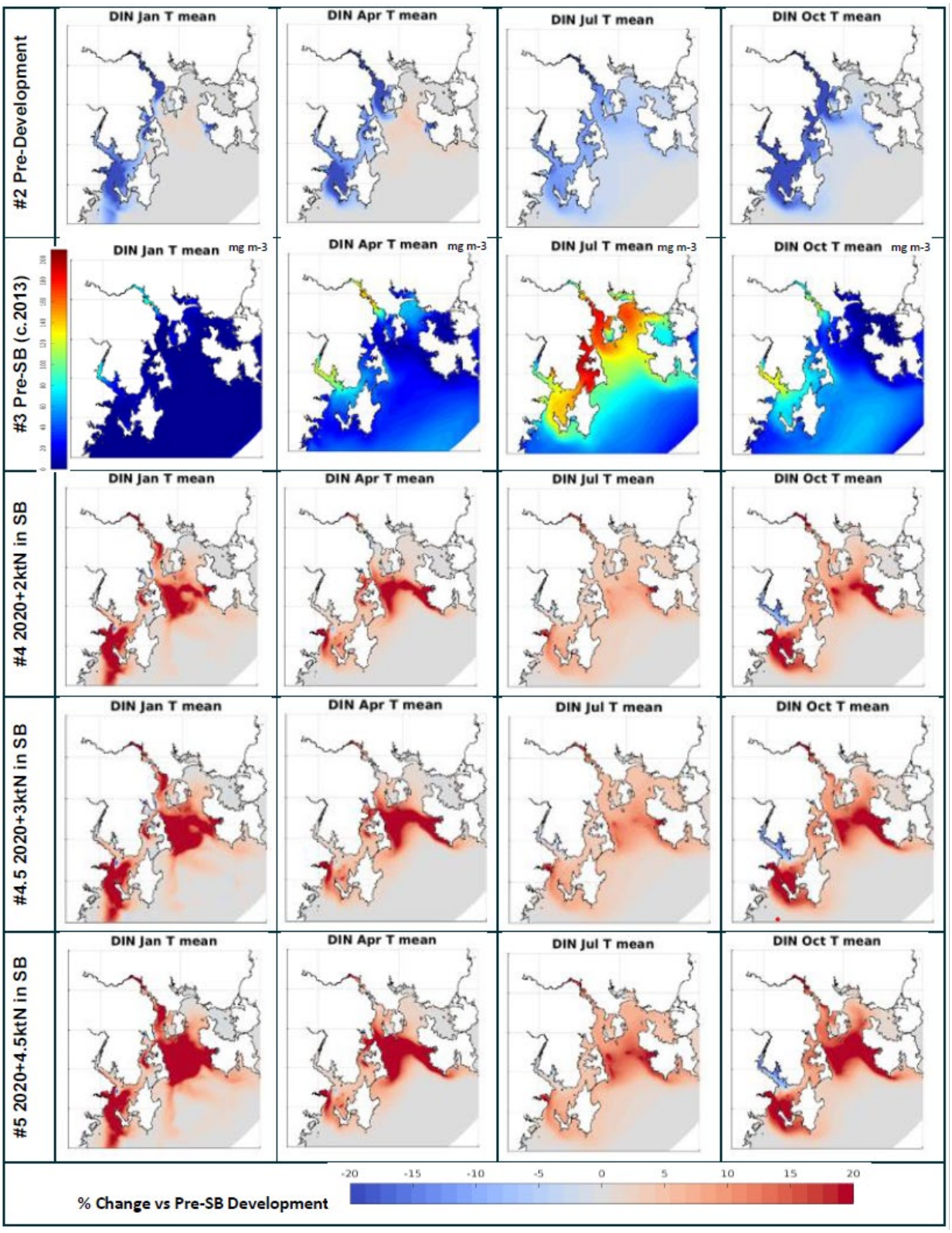


Figure 3-52: Change in simulated monthly mean surface dissolved nitrogen for each scenario relative to #3 Pre-Storm Bay (circa 2013 loads) in summer, autumn, winter and spring (Jan, Apr, Jul, Oct). Figure sourced with permission from Wild Allen et al., (2023).

3.5 Future monitoring techniques

3.5.1 Remote sensing

Remotely sensed spectrally resolved light can be used to estimate water quality parameters. The light exiting a water mass defines its 'colour' giving the name to the study of ocean colour. There has been significant effort in the development of algorithms to derive marine biogeochemical and optical quantities from satellite measurements of ocean colour. With these algorithms, ocean colour data records provide invaluable resources to study regional phenomena such as chlorophyll *a* biomass and phytoplankton dynamics. Moreover, this approach derives information about the water column on finer spatial and temporal scales than other traditional methods of sampling. Given that data collected by low Earth orbit (LEO) satellites have been ongoing for 20 years, interest in using satellite data records to support coupled hydrodynamic-biological modelling efforts (Gnanadesikan et al. 2010, Dutkiewicz et al. 2015, Rousseaux & Gregg 2015, Mannino et al. 2016) and management and decision-making activities (Schaeffer et al. 2015) has also grown.

Inherent Optical Properties (IOP's) are the light scattering and absorption characteristics of particulate and dissolved materials in natural waters. These can be used to characterise the underwater light field from a known light field entering at the surface. Optically active particles in coastal waters include phytoplankton, coloured dissolved organic matter (CDOM) and total suspended matter (TSM). Fresh water influx from rivers and terrestrial run-off enriched with organic matter serves as an important source of CDOM to coastal waters. The absorption coefficient of a material determines how far light of a particular wavelength can penetrate before it is absorbed. For phytoplankton this coefficient is a suitable parameter for assessing community composition in terms of size structure and pigment composition (Sathyendranath et al. 2005, Bracher et al. 2017). Similarly, spectral absorption coefficients of CDOM provide biogeochemically useful proxies of aquatic dissolved organic carbon (DOC) (Vodacek et al. 1997, Mannino et al. 2008, Fichot & Benner 2011, Matsuoka et al. 2012, Vantrepotte et al. 2015), allowing the estimation of this carbon pool from optical measurements in some aquatic environments. Phytoplankton debris contributes significantly to the CDOM pool in coastal and estuarine waters (Parida et al. 2019). In general, absorption of blue light by CDOM overlaps the phytoplankton absorption peak near 440 nm, resulting in a competition between CDOM and phytoplankton for light in this region of the visible spectrum (Twardowski & Donaghay 2001). Light leaving the water at this frequency could have resulted from interaction with either OAP making interpretation difficult.

Spectrally resolved light signals leaving the ocean surface are detected by sensors mounted on satellites orbiting the earth. Spectrally resolved reflectance is calculated from the ratio of light entering and exiting the water surface at each specific frequency. Reflectance is an apparent optical property (AOP) of the water which depends on the geometry (e.g., angle light exited the water) of the light field. IOPs of the water can be calculated from the AOPs, using an inverse solution method. However, there are issues with this approach. Different combinations of IOPs can result in the same reflectance if the ratio of independent observations compared to the number of unknown IOP variables is low or the uncertainty in the reflectance data is high. This makes the inverse problem ill-posed mathematically and determining IOPs intractable. Using advanced machine learning methods to derive IOPs is

another method being explored to deal with uncertainty and unknowns (Doerffer & Schiller 2007, D'Alimonte et al. 2012). Artificial neural networks (ANNs) have shown promise for retrieving constituent matter concentrations (D'Alimonte et al. 2012, Chen et al. 2014a). ANN approaches also exist solely for deriving IOPs (Ioannou et al. 2011, 2013, Chen et al. 2014b). Like all empirical approaches, however, machine learning methods require a large Reflectance/IOP training dataset (Doerffer & Schiller 2007, Ioannou et al. 2011) that spans a wide range of optical conditions. Accordingly, ANN approaches are often tuned and applied regionally (Doerffer & Schiller 2007, D'Alimonte et al. 2012). These methods all benefit from data collected *in situ* in coastal regions which can be used to calibrate and validate results.

3.5.2. Calibration of remote sensor measurements

Comparison of remotely sensed observations against empirical data must account for the fact that the coastal marine environment is dynamic, and sampling is across multiple scales of variability. Firstly, *in situ* observations are measured simultaneously with remote measurements. Thus, the time scales of environmental change must be considered to address how conditions will change between the timing of the two events. Similarly, water samples may be taken at point locations on the order of square metres at or near the surface only, whereas satellite imagery is a vertically integrated value averaged laterally across square kilometres. Measurements taken at only a few depths in the upper layers prevents a true representation of the signal observed by satellite, so validation benefits from continuous depth resolved data. In coastal regions, reflectance is heavily influenced by nonliving, organic and inorganic particles. Temporal scales of variability in these biological and optical properties are typically minutes to hours as the result of advection by changing tidal currents, suspension of bottom sediments by waves and currents, and land-ocean exchanges of optically important materials (Werdell et al. 2018). This further inhibits the process of remotely sensing phytoplankton in the shallow locations. However, despite all this, using ocean colour to monitor ecosystem health in shallow shelf waters has steadily increased.

There are also many complex issues that must be addressed in applying algorithms to process these data. Most remote sensing algorithms were designed for deeper waters where light does not reflect from the seafloor. This assumption does not hold in optically shallow waters, greatly reducing the accuracy of existing algorithms in those areas. Another issue is that shallow coastal water only makes up a fraction of the overall pixels calculated through satellite imagery. Determining the location of these pixels across the entire data set is a difficult task for routine daily processing. Similarly, coastal waters are often optically heterogeneous, as opposed to open oceans, making validation of algorithms difficult. This is compounded in optically shallow regions where within-pixel seafloor and bathymetric variability and stray light from adjacent features (e.g. sand cays and breaking waves) further complicate algorithm validation efforts (Werdell et al. 2018). Not only are appropriate sampling protocols and methodologies required, but also a publicly accessible archive of in situ AOP/IOP data for algorithm development and validation. To that end, it is likely that the recently initiated NASA-funded Coral Reef Airborne Laboratory (CORAL; https://coral.jpl.nasa.gov/) project will contribute greatly to the afore-mentioned knowledge gaps.

3.5.3 Remote sensing in SE Tasmania

There are currently many algorithms used to determine chlorophyll *a* biomass from satellite born sensors in Southeast Tasmanian waters such as MODIS, SeaWIFS and GlobColor. Furthermore, these algorithms have been calibrated to work at higher latitudes and encompass Tasmanian waters. As previously mentioned, these algorithms are not currently suitable for detecting the biomass chlorophyll *a* or the relatively abundances of phytoplankton in Storm Bay. This is largely due to the abundance of coloured dissolved organic matter (CDOM) and total suspended matter (TSM) in this region (Wild-Allen et al. 2021). Another major caveat for remote sensing data is that it is much more accurate in detecting small species of phytoplankton than it is in larger species (package-effect) (Soja-Woźniak et al. 2020). Empirical studies in Storm Bay have shown that the phytoplankton that respond to enrichment from farms are larger species, which has implications for this approach.

CSIRO's TASSE model, developed as part of Storm Bay project, calculates the surface reflectance based on predicted particle concentrations in the water. This model uses the same algorithms as popular global remote sensing products (e.g., OC3M, MODIS etc.) to calculate these AOP's. However, the spectrally resolved optical model developed by CSIRO was calibrated for Great Barrier Reef (Baird et al. 2020). Work is continuing to be done to calibrate the optical model for CDOM, TSM and phytoplankton species in SE Tasmania. The optical model can be validated against new satellite products such as Secchi depth and Fluorescence Line Height (FLH) which are useful IOPs in CDOM rich waters (Wild-Allen et al. 2021). The aim here is to have TASSE reproduce signals being observed by satellites and describe (accurately) the composition of the water in terms of IOPs.

Fluorescence Line Height (FLH) is calculated for some satellite sensors and MODIS has appropriate bands for this calculation. This essentially uses a narrow band of light at which phytoplankton passively fluoresces. It is a case of comparing how the 'satellite product' compares to in situ measurements for the same period. This method is mostly useful for detecting phytoplankton blooms in surface water. CSIRO is currently working to calibrate FLH algorithms in shallow coastal waters in SE Tasmania. If successful, this approach could be applied to monitor the biomass of chlorophyll *a* in Storm Bay.

3.5.4 Automated monitoring techniques

Salmon farming can influence the nutrient dynamics and phytoplankton assemblages of the surrounding water column through changes in hydrodynamics and the input of excess nutrients. The greatest impacts are generally observed close to the lease and in the dominant direction of current flow (IMAS 2020b). Traditional monitoring relies on taking discrete water samples and measurements of the physical and chemical properties to track these changes. Deploying real-time water quality monitoring instruments (e.g., on a buoy or mooring) can, however, allow the high frequency measurements of environmental parameters at key locations (e.g., Schmidt et al. 2018, Ross et al. 2022).

For example, acoustic environmental sensor strings have been used to collect information on biological production (via dissolved oxygen measurements) and water column stratification (via temperature and salinity measurements) since 2016 at three sites close to salmon farms in the centre of Macquarie Harbour (Ross et al. 2022). Analyses of discrete water column samples and the environmental string data showed that the real-time

measurements provided valuable insights into the evolution of DO levels through time. The data from these strings will be further informed by delayed mode loggers which have been deployed at two additional sites north and south of the centre loggers to monitor the influence of the Gordon River and the ocean (Ross et al. 2022).

In Storm Bay, one acoustic environmental sensor string has been deployed at the MF281 East of Yellow Bluff Lease to assess the interactions between this lease and the surrounding water column. The string provides real time data on DO, temperature, depth, and fluorescence (as a proxy for chlorophyll *a* biomass) at the lease. However, these sensors have been damaged by stormy weather conditions and are subject to biofouling and marine growth, which can influence the measurement outcomes. The relationship between fluorescence and chlorophyll *a* biomass (Figure 4-26), which was weaker at river influenced sites, holds promise at more oceanic sites, but further research is required to determine how these measurements can be used for monitoring in a local context. Finally, any conclusions are currently limited to one specific location, i.e., the MF281 East of Yellow Bluff Lease, and cannot be used to determine the effects of salmon farming on the surrounding water column.

3.6 Water column monitoring – Summary

3.6.1 Local scale monitoring

The local scale sampling and the comparison of three different sampling approaches (i.e inline, discrete, and temporal sampling) highlighted the immense spatial and temporal variability in the key physicochemical and biological properties of the water column. The application of a continuous inline system did capture the local footprint of NH_3 in surface waters produced via fish excretion. Similarly, the discrete sampling provided evidence of local scale effects on DO and PO_4 in bottom waters. There were also patterns evident with both direction and depth for chlorophyll *a* biomass, phytoplankton community composition and abundance, but a clear relationship with proximity to the lease was more difficult to discern against background variation. Given these limitations and the high cost of sampling we suggest inline sampling should only be used to provide a one-off snapshot of the spatial footprint of a specific salmon lease during peak biomass or when there are substantial changes in the amount of salmon biomass farmed.

3.6.2 Broad scale monitoring

Across almost 3 years of monitoring (i.e., August 2019 to April 2022), there were distinct trends in key variables for surface and bottom waters samples. The trends in the mid water (10 m) samples were often like surface or bottom waters, depending on the variable measured. Throughout the monitoring, there was an annual increase in the mean summer and winter seawater temperatures and a decrease in the mean summer DO levels.

For surface waters, there were consistently lower values of salinity recorded in winter than summer, particularly at sites close to the Derwent Estuary. The NO_x, NO_3 and DRP showed clear seasonal trends, with higher concentrations through the winter – spring compared to summer – autumn. There were also higher values of these nutrients in the bottom waters compared with the surface waters. The spatial and temporal variation in nutrient concentrations and temperature could be linked to the varying influence of the three dominant currents in Storm Bay and changes in the flow from the Derwent Estuary.

By contrast, the concentrations of TN, TKN, TP, TAN, biomass of chlorophyll *a*, fluorescence, total abundance of phytoplankton, diatoms and dinoflagellates varied interannually with weak or unclear seasonal trends. NPOC and NPOC dissolved increased between 2019 and 2020-2021 but the reasons remain unclear. Phytoplankton blooms were recorded during winter – spring of 2020 but not during 2019 or 2021; these blooms were potentially linked to increased values of NOx and lower westerly wind strength. The lowest values of DO and the highest abundances of phytoplankton were recorded at sites closest to salmon farms.

3.6.3 Recommendations for monitoring

Based on the results from local and broadscale monitoring of Storm Bay we recommend that the following parameters are of high importance for future monitoring efforts focused on detecting the interactions between salmon farming and the water column: TAN, TN, chlorophyll *a* biomass, phytoplankton abundances, and DO. TP, DRP, NOx, temperature, salinity and SiO_2 are of moderate importance for interpreting these results and interpreting the changes in the context of other environmental forcings and NO_3, TKN, NPOC, NPOC dissolved, fluorescence and pH are of lower importance. Monitoring of these key parameters should focus on sampling the surface and bottom waters as sampling 10 m did not provide any additional information. The results of the power analyses showed there was high variability in most parameters between months. This high variability meant that monitoring based on 12 months of sampling was more likely to detect significant differences between sites at different distances than seasonal monitoring which is only based on three samples. Because of this, monitoring should focus primarily on the use of annual rolling medians and associated trigger levels. The power analyses also suggested that implementing a balanced design (i.e. equal numbers of sites for each distance category) would improve the ability of the monitoring program to detect change, particularly in chlorophyll *a* biomass. If a balanced design was implemented: monitoring for local (lease) scale would require the highest number of new sites to be implemented in the near scale to avoid overlapping with other active leases in the DGV region, followed by DGV regions, with the fewest number of sites required to monitor the entire Storm Bay. The monitoring design also considered the predicted spatial extent of influence from salmon farming under different scenarios of production. The results from the CSIRO TASSE biogeochemical model suggest that with the expansion of salmon farming in Storm Bay more far field sites are required to monitor change.

3.6.4 Future directions

An assessment of remote sensing techniques and automated monitoring platforms suggest that further work is required to implement these techniques to monitor the interactions between salmon farming and the surrounding water column in Storm Bay. This research should prioritise deploying environmental sensor strings (or profilers) within the active salmon leases in Storm Bay. These strings along with discrete samples of nutrients, chlorophyll *a* biomass, DO, fluorescence and depth resolved optically active particles at sites > 500 m of the lease could help to calibrate remote sensing products. The sensor environmental strings and inline sampling of NH_4, NOx, NO_2, and fluorescence are complementary techniques that could also help to provide further information about the interactions between salmon farming and the surrounding water column through time and space.

4 Sediment Monitoring

Salmon farms are mostly situated above soft-sediment (sand, silt, and mud) and therefore environmental monitoring programs have primarily focused on assessing any changes in the chemistry and/or benthic fauna of these habitats. Organic enrichment and increased sedimentation derived from salmon farming can alter benthic community assemblage (Wildish et al. 2003, Hargrave 2010) and enhance anaerobic activity, resulting in the accumulation of sulphides with adverse effects on aerobic bacteria and other organisms due to progressive oxygen depletion (Hamoutene 2014). In addition, salmon farming has the potential to act as a vector for the spread of non-indigenous species into new areas and could alter the distribution and abundances of mobile invertebrate predators and scavengers attracted to waste (Woodcock et al. 2018, Bannister et al. 2019).

An important element of managing the benthic response to farming is to ensure that conditions immediately under cages facilitate the efficient break down and assimilation of waste. In Tasmania, a feature of these conditions is the dominance of opportunistic animals such as capitellid worms and nebaliid crustaceans (Macleod et al. 2007). The rotation of cages within fish farm leases and the subsequent fallowing of areas of the seabed is a commonly used technique which allows for the recovery of infauna communities. This in turn ensures that sediment conditions do not deteriorate to a point that ecological function is significantly impaired, thereby threatening the viability of farming operations. However, environmental management controls require that these conditions do not extend beyond the lease boundary, or more specifically, “there must be no significant visual, physico-chemical or biological impacts at or extending beyond 35 metres from the boundary of the Lease Area.”

The responses of soft-sediment environments to salmon farming will vary depending on the production levels and the hydrographic and sedimentological conditions (Macleod et al. 2006, Macleod et al. 2007). A state-wide meta-analysis of benthic monitoring data associated with salmon farms in Tasmania found that subtle effects on macrofaunal communities were evident to at least 50-150 m from the cage (Edgar et al. 2010), and more recent research at farms in more dispersive environments, including Storm Bay, in southern Tasmania (Ross et al. 2022) found evidence of a larger spatial footprint (at least 200 m). However, at a broader regional scale there has been no evidence of effects on soft sediment environments (Pitta et al. 2009, Ross & MacLeod 2013).

The focus of this component of the study was to assess the potential interactions of salmon farming with soft-sediment habitats at the two scales identified in the environmental monitoring program.

More specifically in this chapter we aimed to:

1. Determine the extent of the benthic footprint at active leases in Storm Bay.
2. Assess environmental performance at the 35 m from the lease boundary compliance sites relative to reference sites and baseline conditions.
3. Assess the broad-scale spatial and temporal dynamics of Storm Bay soft sediment habitats and their potential interactions with farming.
4. Recommend modifications to the local and broad-scale monitoring programs (e.g., design, variables and analysis).

4.1 Local-scale

The local (lease) scale sediment survey requirements for marine farms are defined in the environmental licences and include samples collected at external compliance (35 m from lease boundary) and control sites. Sediment conditions at each site are assessed visually via remotely operated vehicle (ROV) with video, and from grab sample measurements of sediment chemistry and faunal communities. Performance was assessed against environmental standards for visual, physico-chemical and biological impacts (Table 4-1). The objective of the sampling in this study was to provide a more detailed assessment of the benthic footprint at the Yellow Bluff and West of Wedge leases, allowing for an evaluation of the prescribed monitoring design and assessment criteria.

Table 4-1: Trigger limits for the Storm Bay Environmental Licences (10211/1, 10180/1)

There must be no significant visual, physico-chemical or biological impacts at or extending beyond 35 metres from the boundary of the Lease Area. The following impacts may be regarded as significant:

Visual impacts:

- Presence of fish feed pellets;
- Presence of bacterial mats (e.g., *Beggiatoa* spp.);
- Presence of gas bubbling arising from the sediment, either with or without disturbance of the sediment;
- Presence of numerous opportunistic polychaetes (e.g., *Capitella* spp., *Dorvilleid* spp.) on the sediment surface.

Physico-chemical

Redox

- A corrected redox value which differs significantly from the reference site(s) or is < 0 mV at a depth of 3 cm within a core sample.

Sulphide

- A corrected sulphide level which differs significantly from the reference site(s) or is > 250 μM at a depth of 3 cm within a core sample.

Biological:

- A 20 times increase in the total abundance of any individual taxonomic family relative to reference sites;
- An increase at any compliance site of greater than 50 times the total Annelid abundance at reference sites;
- A reduction in the number of families by 50 per cent or more relative to reference sites;
- Complete absence of fauna.
- As natural environmental variation renders some locations more susceptible to significant changes in parameter values, the above thresholds will be considered in addition to baseline environmental information for determining the presence/absence of a significant impact.

4.1.1 Design and parameters

Benthic sediment surveys were conducted annually or in accordance with the stocking and fallowing regime and within 30 days of lease peak production. The benthic sediment survey requirements are outlined in section 3V1 of the respective Environmental Licence, and the

sites, methodologies and reporting guidelines are described in 3V10, 3V11 and 3V12, respectively.

The Environmental Licence states that "samples must be collected at sites to be co-located with video survey external (compliance) sites and control sites established in the baseline environmental survey report."

For the Yellow Bluff lease (MF281), surveys to fulfil the requirements of the Environmental Licence (EL 10180/1) were completed in March 2020 and March 2022 and an additional survey was conducted in March 2021 when biomass was also reasonably high to better understand temporal variability (Table 4-2). The results of all three surveys are contrasted against the baseline survey that was conducted in February 2019. In addition to the required control and compliance sites, sites at increasing distances from cages (0, 10, 35, 50 and 100 m) were sampled on three transects (N, W, and E) in the March 2020 survey (Table 4-3; Figure 4-1). In the subsequent surveys, the number of distances sampled on each transect was reduced (March 2021: 0 & 35 m, March 2022: 0, 35, 100 m). Feed input for the three-month period leading into each survey, relative to the mean at active cages across all three survey periods is shown in Figure 4-2.

At the West of Wedge lease (MF279), surveys to fulfil the requirements of the Environmental Licence (EL 10211/1) were completed in January 2021 and December 2021 and contrasted against the baseline survey completed in March 2019 (Table 4-2). In addition to the required control and compliance sites in the EL, two of the broad-scale survey sites (SB-16 and NUB-4) were included as additional control sites and samples were also collected at sites directly adjacent to the active cages in each survey (Table 4-4; Figure 4-3). Given the relatively low biomass trialled at the West of Wedge lease, additional distances from the cages were not sampled. Feed input for the three-month period leading into each survey, relative to the mean at active cages across the two survey periods is shown in Figure 4-4.

At each site, the benthic sediment survey components included, benthic biota (infauna and bacteria/algal mat identification), sediment chemistry (redox potential, sulphide concentration and stable isotope analysis), sediment core descriptions (Munsell chart) and particle size analysis. Benthic macrofauna were sampled in triplicate using a Van Veen Grab (surface area 0.0675 m^2). All samples were sieved to 1 mm and the fauna identified to the lowest possible taxonomic resolution and counted**.** Sediment cores (250 mm long, 45 mm internal diameter) were collected to evaluate sediment sulphide, redox, particle size, organic carbon and nitrogen content and their isotopic composition ($\delta^{15}N$, $\delta^{13}C$). A visual assessment was also made of each core, including measurement of core length, sediment colour (using a Munsell soil chart), assessment of plant/animal life and assessment for gas vesicles and smell (indicating presence/absence of hydrogen sulphide). The methods of collection and analysis were as per those outlined in the environmental licence conditions and Macleod and Forbes (2004).

Table 4-2: Summary of the sampling parameters for the local (lease) scale surveys conducted at Yellow Bluff and West of Wedge between 2019 and 2022 (including baseline surveys).

Lease	Date	Survey type	Samples analysed for:
Yellow Bluff	Feb 2019	Baseline	**Biota:** benthic infauna **Chemistry:** redox, heavy metals, sulphides, particle size, organic matter **Visual**: description of physical characteristics
Yellow Bluff	Mar 2020	Environmental Licence*	**Biota:** benthic infauna **Chemistry:** redox, stable isotopes, sulphides, particle size, organic matter **Visual**: description of physical characteristics
Yellow Bluff	Mar 2021	Research only	**Biota:** benthic infauna **Chemistry:** redox, stable isotopes, sulphides, particle size, organic matter **Visual**: description of physical characteristics
Yellow Bluff	Mar 2022	Environmental Licence*	**Biota:** benthic infauna **Chemistry:** redox, stable isotopes, sulphides, particle size, organic matter **Visual**: description of physical characteristics
West of Wedge	Nov 2019	Baseline	**Biota:** benthic infauna **Chemistry:** redox, heavy metals, sulphides, particle size, organic matter **Visual**: description of physical characteristics
West of Wedge	Jan 2021	Environmental Licence	**Biota:** benthic infauna **Chemistry:** redox, stable isotopes, sulphides, particle size, organic matter **Visual**: description of physical characteristics
West of Wedge	Dec 2021	Environmental Licence	**Biota:** benthic infauna **Chemistry:** redox, stable isotopes, sulphides, particle size, organic matter **Visual**: description of physical characteristics

* Additional research sites

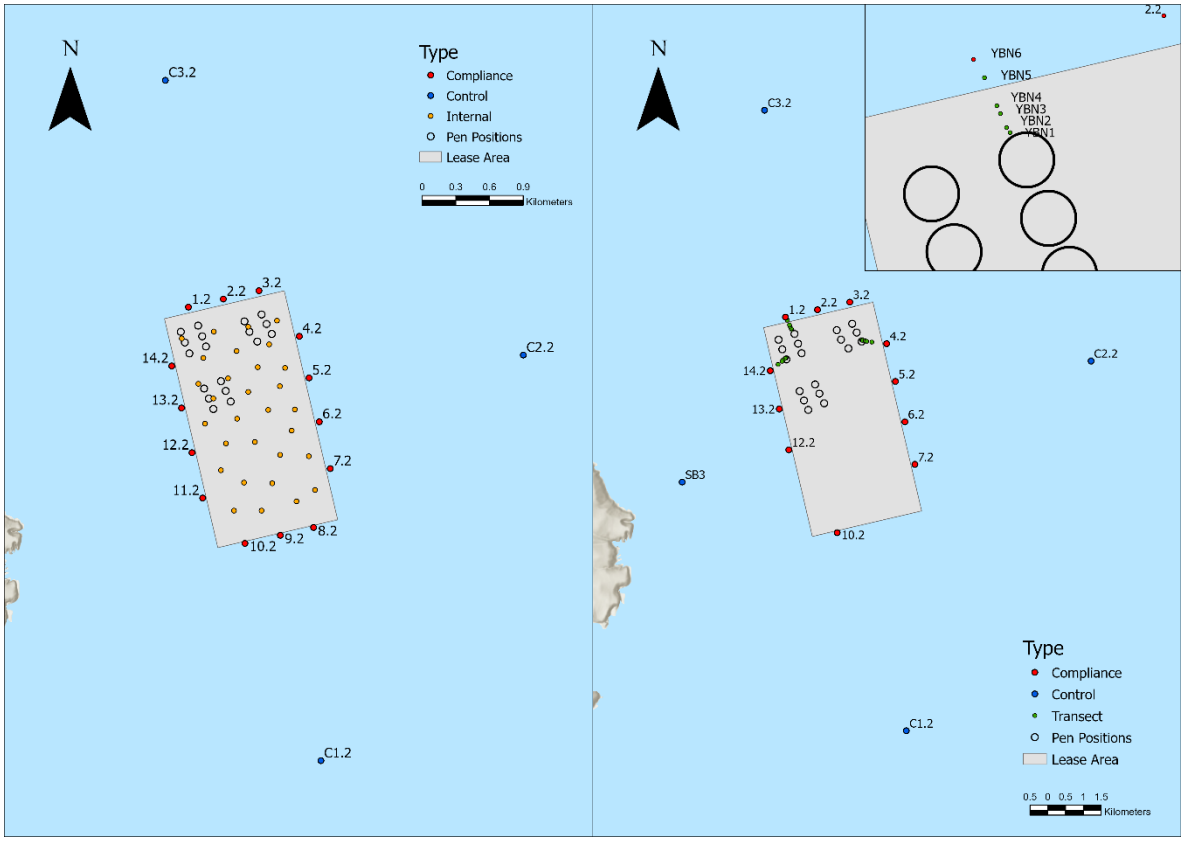


Figure 4-1: Maps showing (left) compliance, control and internal farm sites, sampled as part of the requirements for the Environmental Licence baseline, (right) all sites sampled in IMAS surveys, including position of transects (YBW, YBN & YBE) that were sampled for FRDC 2018-131. The inset shows positions on the transect that was sampled on the North side of the lease.

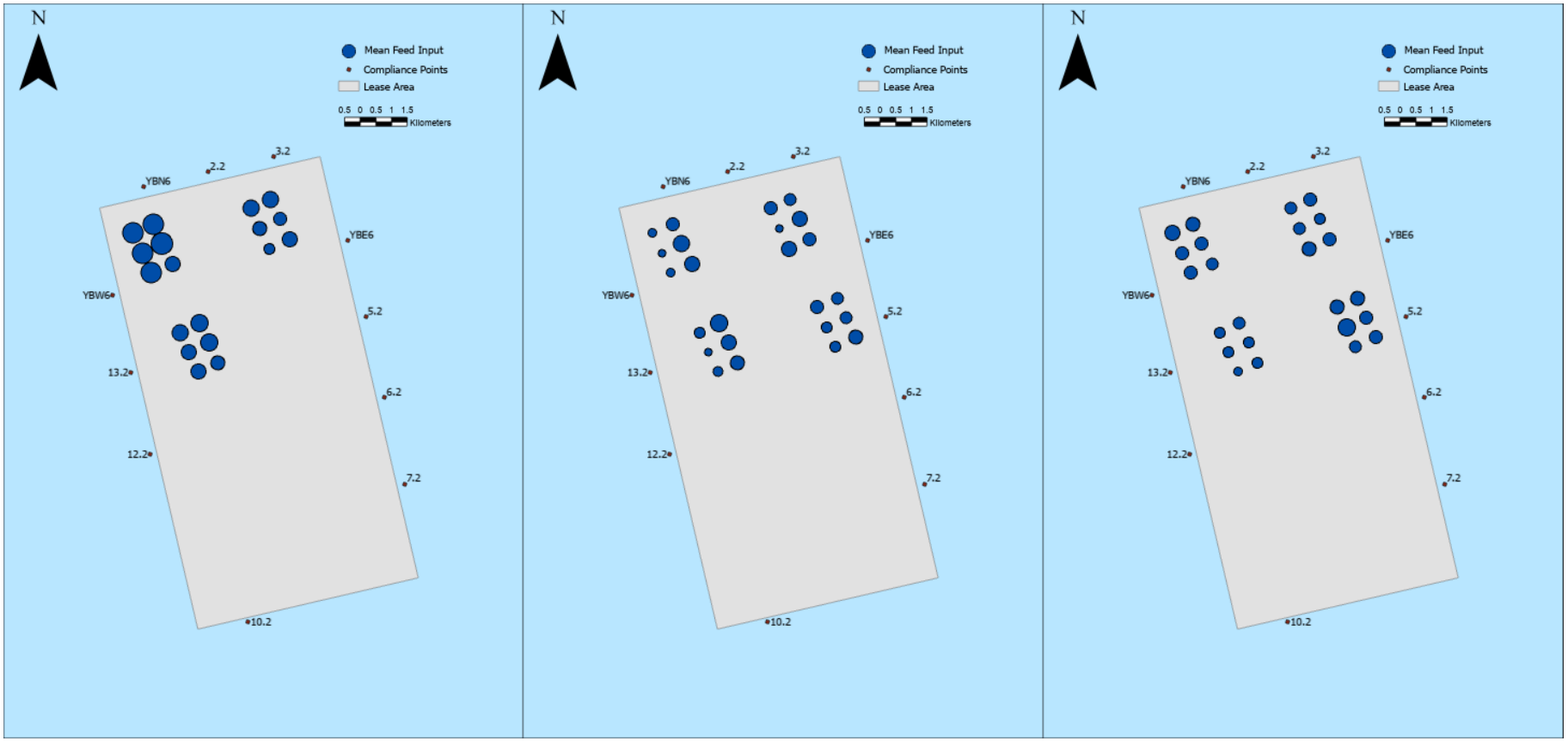


Figure 4-2: Proportional symbols showing feed input for the three-month period leading into the benthic survey, relative to the mean at active cages across all three periods at Yellow Bluff. From L-R: 2020, 2021 & 2022.

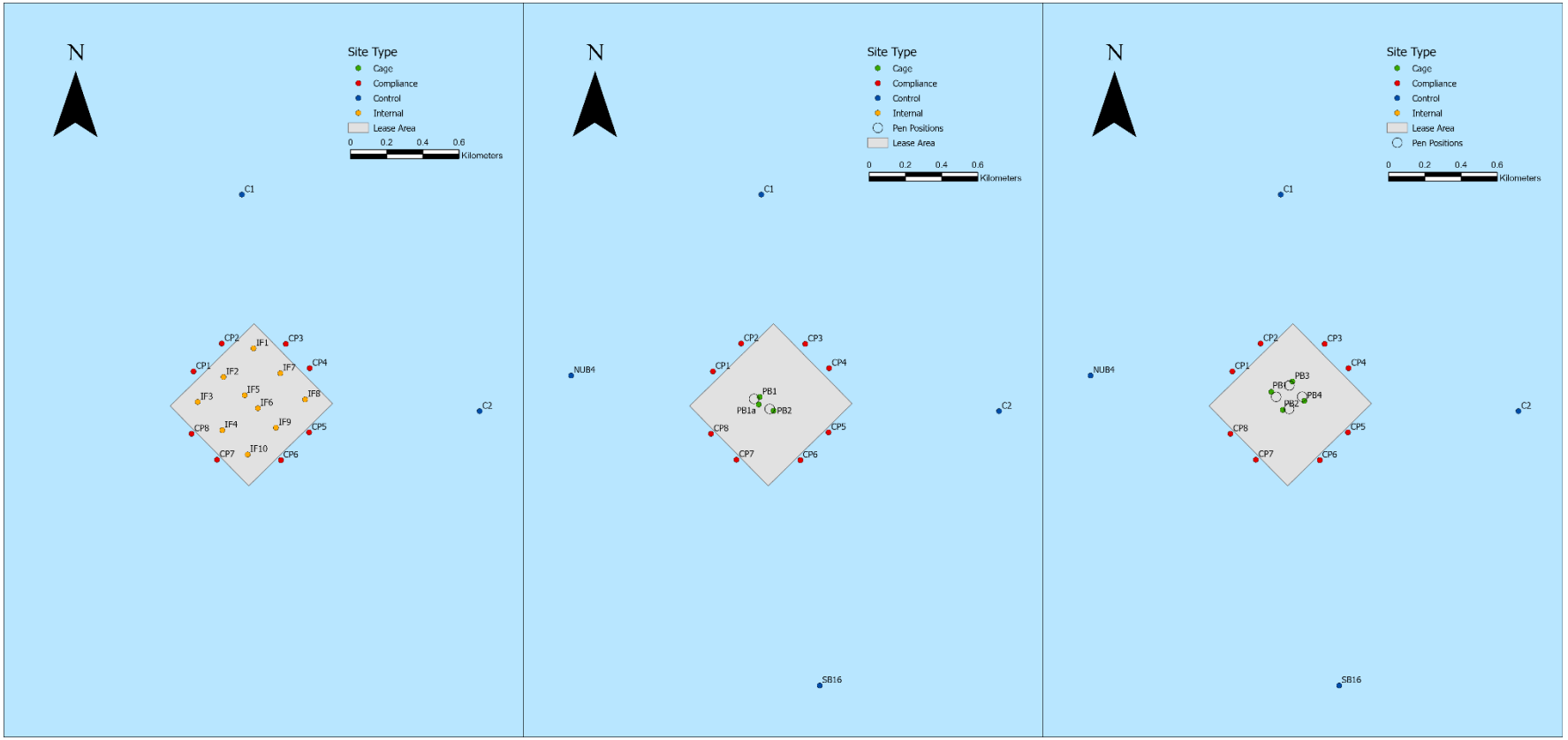


Figure 4-3: Map showing the location of sites sampled at MF279 as part of the baseline survey in March 2019 (left), compliance monitoring in January 2021 (middle) and compliance monitoring in December 2021 (right).

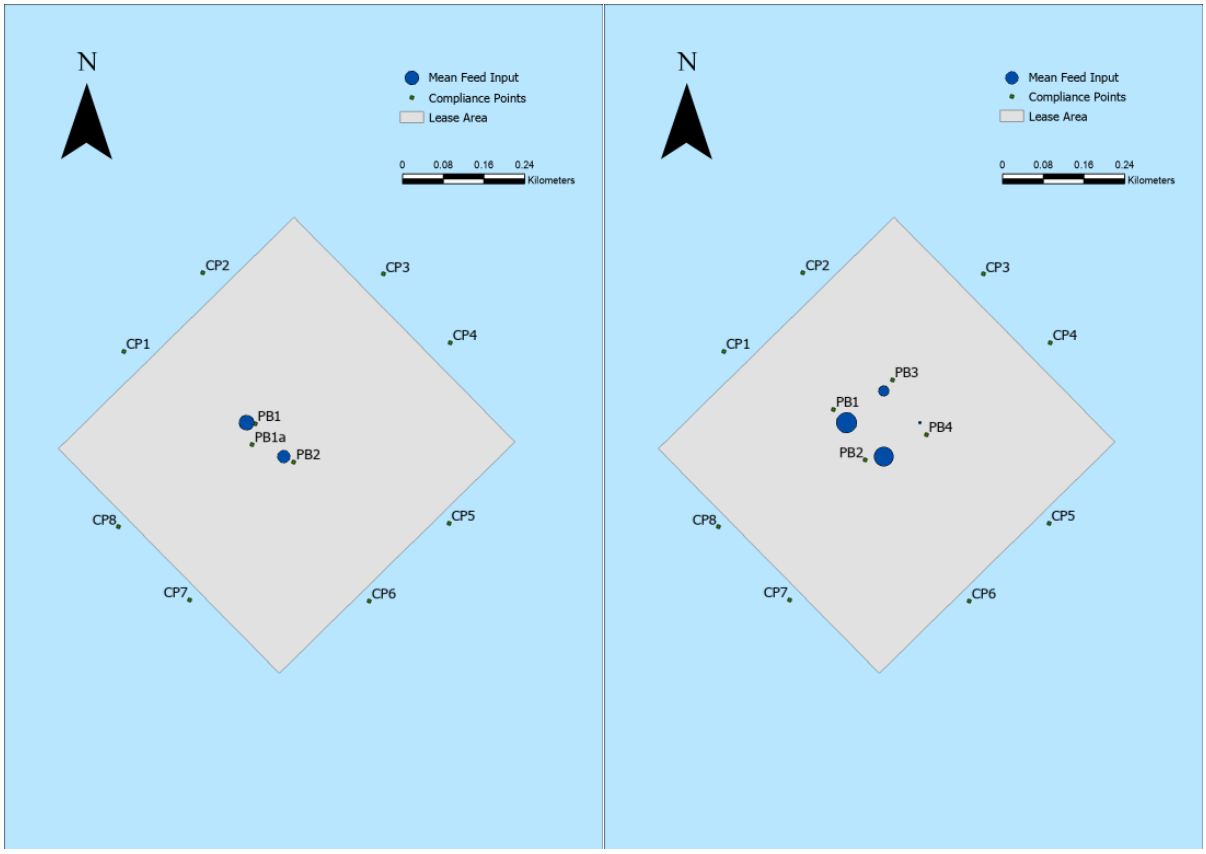


Figure 4-4: Proportional symbols showing feed input for the three-month period leading into the benthic survey relative to the mean at active cages across both periods at West of Wedge. From L-R: January 2021 and December 2021.

Table 4-3: Summary of the survey design for sampling at Yellow Bluff across February 2019 (baseline), March 2020, 2021, and 2022. The shaded boxes were sampled as a requirement under the Environmental Licence 10180/1. *Only macrofaunal samples collected.

Baseline/EL site name	IMAS site name	Distance from nearest pen (m)	Distance from lease edge (m)	Depth (m)	February 2019 (baseline)	March 2020	March 2021	March 2022	Site Category
	YBN1	0	internal	27		yes	yes	yes	Cage
	YBN2	10	internal	27		yes			
	YBN3	35	internal	27		yes	yes	yes	35 m from cage
	YBN4	50	internal	27		yes			
	YBN5	100	internal	27		yes		yes	
1.2	YBN6	135	35	27	yes	yes	yes	yes	Compliance
C3.2	YBN7	2155	2050	23	yes	yes	yes	yes	Control
	YBE1	0	internal	28		yes	yes	yes	Cage
	YBE2	10	internal	28		yes			
	YBE3	35	internal	28		yes	yes	yes	35 m from cage
	YBE4	50	internal	28		yes			
	YBE5	100	internal	29		yes		yes	
4.2	YBE6	250	35	29	yes	yes	yes	yes	Compliance
C2.2	YBE7	2250	1940	33	yes	yes	yes	yes	Control
	YBW1	0	internal	27		yes	yes	yes	Cage
	YBW2	10	internal	27		yes			
	YBW3	35	internal	27		yes	yes	yes	35 m from cage
	YBW4	50	internal	27		yes			

	YBW5	100	internal	26		yes		yes	
14.2	YBW6	200	35	26	yes	yes	yes	yes	Compliance
SB3	YBW7	1585	1123	23	yes	yes	yes	yes	Control
C1.2	YBS7	3295	2075	35	yes	yes		yes	Control
2.2	YB2.2	262	35	27	yes	yes*		yes	Compliance
3.2	YB3.2	212	35	28	yes			yes	Compliance
5.2	YB5.2	165	35	30	yes			yes	Compliance
6.2	YB6.2	391	35	31	yes			yes	Compliance
7.2	YB7.2	1078	35	32	yes	yes*			Compliance
10.2	YB10.2	1248	35	30	yes	yes*	yes		Compliance
12.2	YB12.2	447	35	27	yes	yes*		yes	Compliance
13.2	YB13.2	261	35	27	yes	yes*		yes	Compliance

Table 4-4: Summary of the survey design for sampling at West of Wedge across March 2019 (baseline), January 2021 and December 2021. The shaded boxes were sampled as a requirement under the Environmental Licence 10211/1. * The exact coordinates of the pen sites varied between surveys but the pen they were sampled adjacent to remained the same. ** Not collected as part of the baseline survey, but they are part of the broad-scale sediment survey, and we consider good control sites.

Baseline/EL name	Depth (m)	March 2019	January 2021	Distance to nearest pen January (m)	December 2021	Distance to nearest Pen December (m)	Site Category
CP1	39	yes	yes	274	yes	280	Compliance
CP2	39	yes	yes	315	yes	281	Compliance
CP3	38	yes	yes	415	yes	301	Compliance
CP4	38	yes	yes	398	yes	301	Compliance
CP5	39	yes	yes	350	yes	321	Compliance
CP6	40	yes	yes	330	yes	330	Compliance
CP7	41	yes	yes	335	yes	336	Compliance
CP8	41	yes	yes	306	yes	325	Compliance
C1	38	yes	yes	1131	yes	1057	Control
C2	35	yes	yes	1268	yes	1198	Control
SB-16**	43		yes	1555	yes	1555	Control
NUB-4**	41		yes	1019	yes	1032	Control
PB1	40		yes	0	yes*	0	Cage
PB1a	40		yes	0			Cage
PB2	40		yes	0	yes*	0	Cage
PB3	40				yes*	0	Cage
PB4	40				yes	0	Cage

Box 4.1 Application of the AZTI Marine Biotic Index (AMBI)

Many biological indicators and indices have been developed to characterise anthropogenic effects on soft sediment habitats, most of which are based on the foundational work of Pearson and Rosenberg (1978) who described the community response to gradients of organic pollution or disturbance (Keeley et al. 2012a). The AZTI Marine Biotic Index (AMBI) is one such benthic quality index that has been widely adopted. Originally developed by Borja et al. (2000) for European estuaries and coastal environments, it has been adapted for local conditions around the world (Muniz et al. 2005, Callier et al. 2008, Teixeira et al. 2012).

AMBI is often used to characterise the impacts of organic enrichment from aquaculture. In one such case, Keeley et al. (2012a) compared a suite of benthic indices for assessing impacts from finfish aquaculture in New Zealand. They found that AMBI and the closely related multivariate version M-AMBI were among the most versatile indices out of the 15 investigated.

AMBI indicates the level of impact at a site based on the weighted proportion of species (or families) that are known to be tolerant of or sensitive to disturbed conditions, with the most tolerant given an ecological grouping (EG) of V through to I for the most sensitive (see Table 1).

Table 1: Adapted from Grall and Glemarac (1997) with local context based on the descriptions of Macleod & Forbes (2004).

Group I	*S*pecies very sensitive to organic enrichment and present in normal conditions. They include the specialist carnivores and some deposit feeding tubicolous polychaetes. Ampelicsa sp, Apseudes sp., higher numbers of crustaceans.
Group II	Species indifferent to enrichment, always present in low densities with non-significant variations in time. These include suspension feeders, less selective carnivores and scavengers.
Group III	Species tolerant of excess organic matter enrichment. These species may occur in normal conditions but their populations are stimulated by organic enrichment. These are only some of the surface-deposit-feeding species, for example tubicolous spionids, which ingest the superficial film of organic matter deposited at the surface.
Group IV	Second-order opportunistic species. These are the small species with a short life cycle, adapted to a life in reduced sediment where they can proliferate. They are the subsurface deposit feeders essentially related to the cirratulids.
Group V	First-order opportunistic species. These are the deposit feeders that proliferate in sediments reduced up to the surface. *Capitella* sp. *Malacoceros tripartitus, Nebalia* sp. Some nematodes and oligochaetes may also be present

Since it was first established, the AMBI species database has increased substantially to include a wider range of species from around the globe. However, its application in regions outside of Europe has required the development of locally applicable species databases. Ross et al. (2015) successfully applied AMBI in the unique Macquarie Harbour on the west coast of Tasmania. However, until now, it has not been developed and tested in other regions of Tasmania where benthic macrofaunal communities are far more diverse.

Keeley et al. (Keeley et al. 2012a, Keeley et al. 2012b), Muniz et al. (2005) and Gillett et al. (2015) provide guidance on developing EGs for local AMBI analyses in the absence of sufficient species coverage in the original database. Typically, this includes a combination of quantitative analysis and best professional judgement (BPJ) based on a prior knowledge of impacts levels. For the purposes of this study the allocation of species to different species groupings was based on prior knowledge of impact stages in Tasmania (Macleod & Forbes 2004, Edgar et al. 2010) and a calibration exercise using a range of response parameters (physico-chemical, visual and biological) measured at varying distances from the source of enrichment at the Trumpeter Bay salmon lease off north Bruny Island in Storm Bay, over successive surveys. This approach resulted in a simple classification of EG based on family abundances at sites along an enrichment (impact) gradient (Table 2).

Table 2: Ecological groupings allocated based on the enrichment gradient

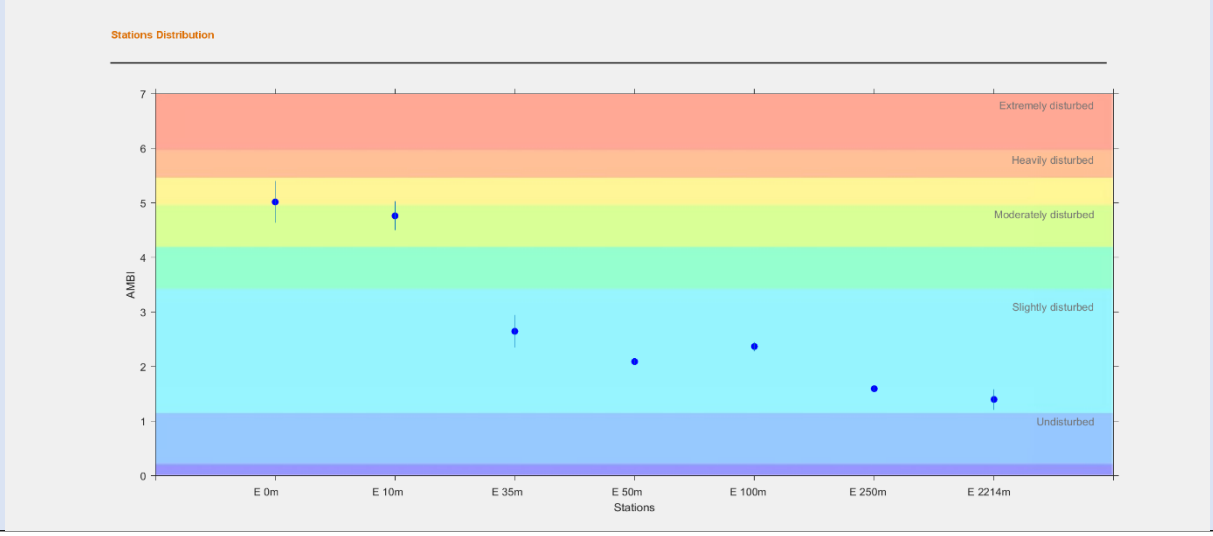
Ecological grouping	Distance	Site
V	0 m	1
IV	35 m	2
III	100 m	3
II	200 m	4
I	500 m,1000 m, Control Outer	5,6, CO

Families were assigned to an EG based on where they were most abundant. Table 3 shows the families that were characteristics of the most heavily impacted sites (i.e., 0 m) and assigned to group V, i.e., the most tolerant families. These groupings are consistent with local knowledge and literature and include classic enrichment tolerant families such as Capitellidae and Nebaliidae, along with several families that are associated with net fouling.

Table 3: Group V families

Code - Family	EG
APP-Phoxichilidiidae	V
APP-Phoxichilidiidae	V
CAJ-Ischyroceridae	V
CBH-Hymenosomatidae	V
CC-Caprellidae	V
CDP-Palaemonidae	V
CIA-Janiridae	V
CN-Nebaliidae	V
CTL-Leptocheliidae	V
MGWM-Pleurobranchidae	V
MPM-Mytilidae	V
MPXH-Hiatellidae	V
WPC-Capitellidae	V

The efficacy of the new index (AMBI-TAS) was then tested using the dataset from Yellow Bluff. The AMBI-TAS classification of sites correlated well with other response parameters. In the example below on the eastern transect, macrofaunal communities were classified as heavily disturbed at 0 m, moderately disturbed 10 m and generally improved with increasing distance from the cage (Figure 1). Further refinement including additional group I families will refine the index and reduce the tendency to score control sites as slightly disturbed.



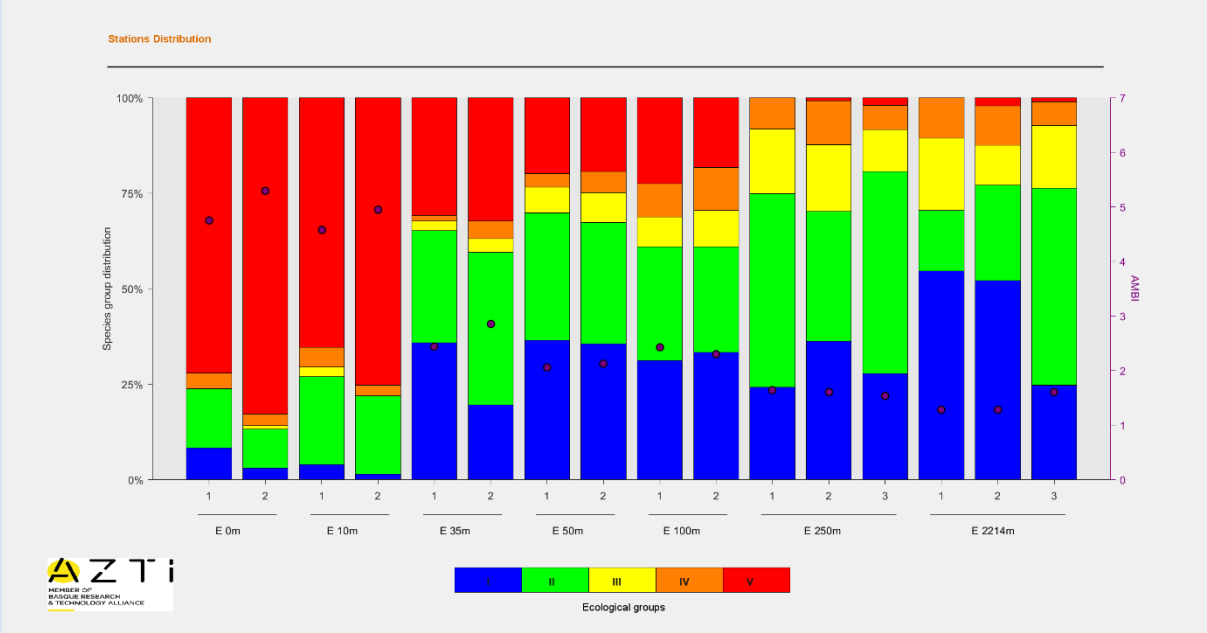


Figure 1: AMBI output for the eastern transect at Yellow Bluff in March 2020. The top panel shows the AMBI score at increasing distances from the cage and the bottom panel shows the relative proportion of each ecological group that contributed to the score. Sites are from L to R: YBE1-7.

M-AMBI - Following from AMBI, a multivariate version (M-AMBI) was developed that incorporates measures of richness and diversity (Muxika et al. 2007). M-AMBI has proven useful at distinguishing and characterising extremely impacted sites where conditions are azoic. For the conditions encountered in this study we found very good agreement between both versions and for simplicity we only present AMBI results.

4.1.2 Spatial and temporal variation in key parameters

The cornerstone of the local (lease) scale benthic sediment survey and the associated performance assessment is the characterisation of reference conditions. This comes in two parts: first, a baseline assessment to establish the environmental conditions (visual, physicochemical, and biological) of the sedimentary habitat across lease, compliance, and control areas prior to the commencement of farming. Given that these conditions may vary in time independent of farming, the second part requires monitoring of environmental conditions through time, and more specifically at the control sites. Any changes at the lease compliance sites can be assessed in the context of temporal change in reference conditions, as observed at the control sites.

Yellow Bluff

The baseline assessment at Yellow Bluff in February 2019 (Aquenal 2019c) revealed no clear spatial patterns in sediment chemistry across compliance, control, or internal lease sites (Figure 4-6, plot on left). Observed redox values were high (average 325 mV at 3 cm; all >200 mv) and indicative of well oxygenated sediments and most sites recorded sulphide levels near zero (average 1.58 uM; all <20 µM). Sediments across the area were dominated

by medium to fine sand, contained a low proportion of silts and were home to a diverse and abundant benthic fauna (~170 ind. Per grab &155 families total). Crustaceans dominated the faunal community (65.0% of individuals), followed by molluscs (16%), polychaetes (14.4%) and echinoderms (0.8%). The most common families were Photidae and Maeridae amphipods, Philomedidae ostracods, and Galeommatidae and Veneridae bivalves. Notably, Capitellidae polychaetes were recorded in low densities across the survey area but the species recorded are not considered indicative of organic enrichment. Given the relatively uniform patterns in physico-chemical parameters and the high taxonomic diversity across the area in the baseline, potential impacts such as an increase in species dominance patterns or a decline in taxonomic diversity should be readily discernible.

The first (March 2020) benthic sediment survey after farming had commenced provided clear evidence of the expected impacts of farm derived organic enrichment. Despite significant variation between transects and distances from the cage, there was a clear gradient of effect for both redox potential and sulphide concentration (Figure 4-5).

All three transects show a clear gradient of effect with redox potential increasing from the cage out to 50-100 m (Figure 4-5). However, lower values were observed on the northern transect relative to the east and west. Beyond 100 m from the cage, there was significant variation between sites and the pattern with distance was not always evident. On the northern transect, redox at the compliance site N6 (135 m) was considerably lower than both the site closer, N5 (100 m) and the more distant control site N7 (2225 m). On the eastern transect, a similar pattern was seen at E5 (100 m) which had a markedly lower redox than both the closer and more distant sites. On the western transect, potential increased to over 200 mV at 100 m (W5) from the cage, but readings at the two more distant sites were much lower. A gradient effect from the cage out was also evident for sulphide, but again with variability within and between transects. Sulphide concentrations were generally higher on the western and northern transects relative to the east. Site E5 was again an outlier with both high sulphide and low redox relative to adjacent sites on the transect. The maps provided in Figure 4-6 help further visualise the spatial response in redox and sulphide to the addition of farming between the baseline survey and the first peak production survey in March 2020.

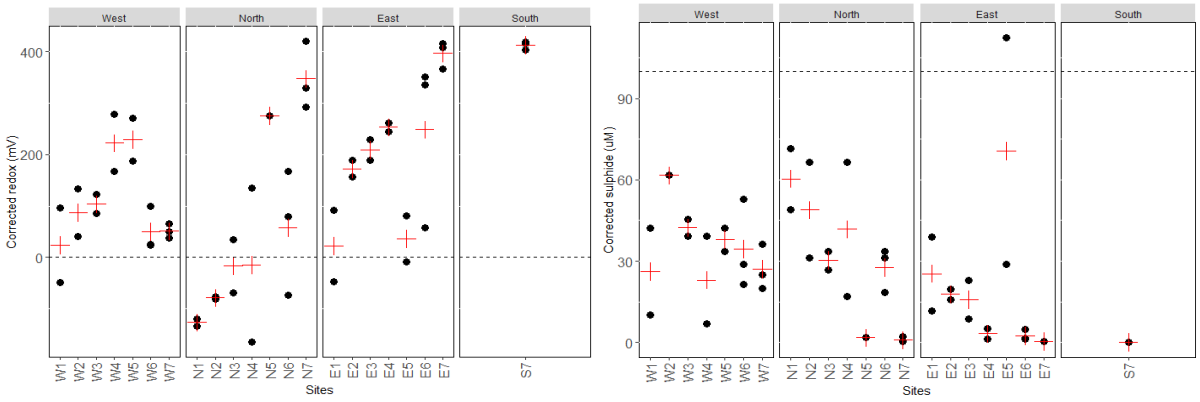


Figure 4-5: Corrected redox values (mV) and sulphide concentration (µM) at 3cm depth for sediments collected at control, compliance and farm sites in March 2020. Black points represent individual core readings while red crosses represent the site mean.

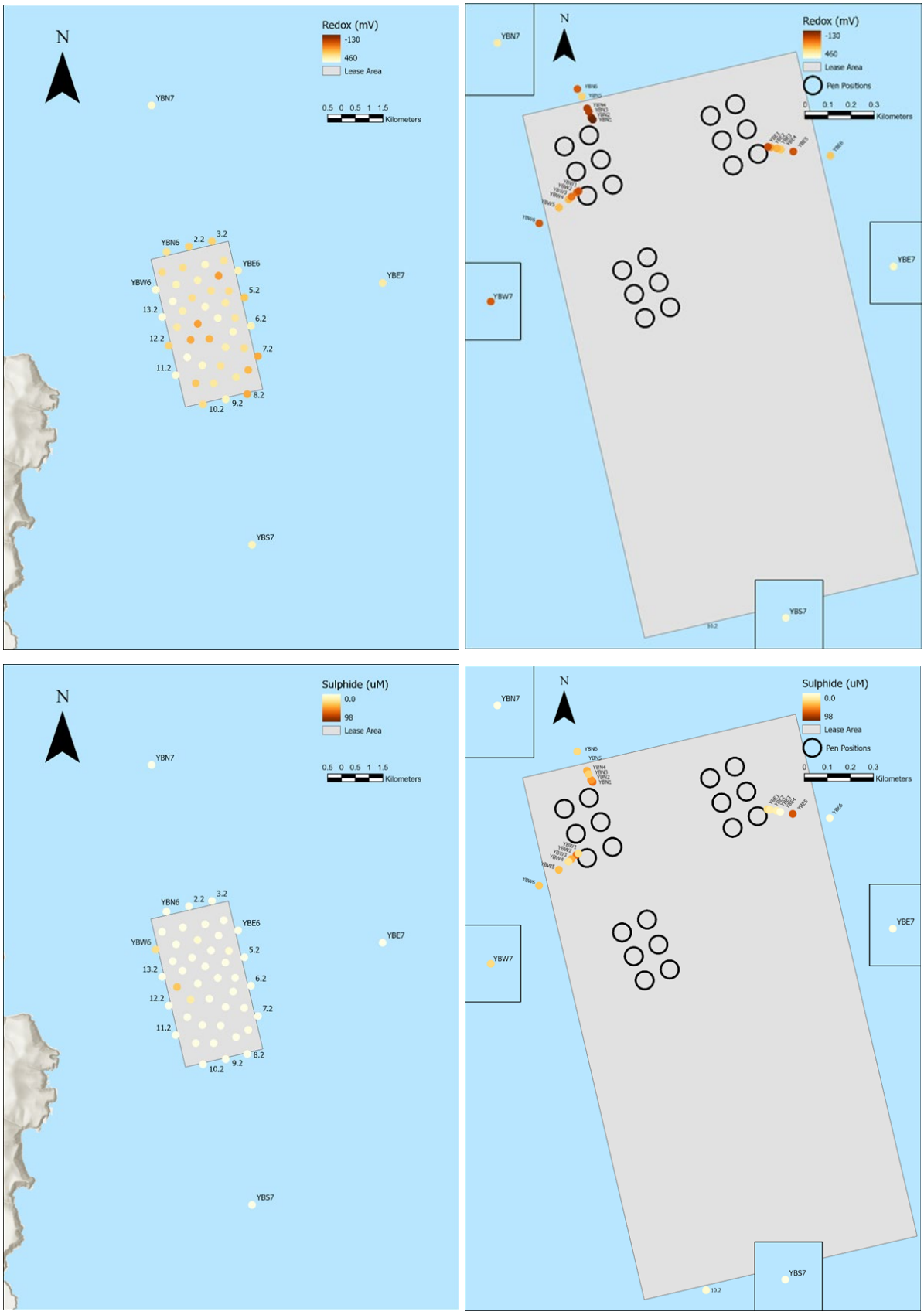


Figure 4-6: Map showing redox (mV; top panels) and sulphide (uM; bottom panels) at the control, compliance and farm sites during the baseline (left) and at the control, compliance and transect sites in March 2020 (right).

The patterns for sediment carbon and nitrogen content also revealed an enrichment signal from the cages, but again there was significant variation between transects (Figure 4-7). There was a clear enrichment gradient with distance on both the eastern and northern transects, but the results suggested that enrichment was greater and extended further from the cage on the northern transect.

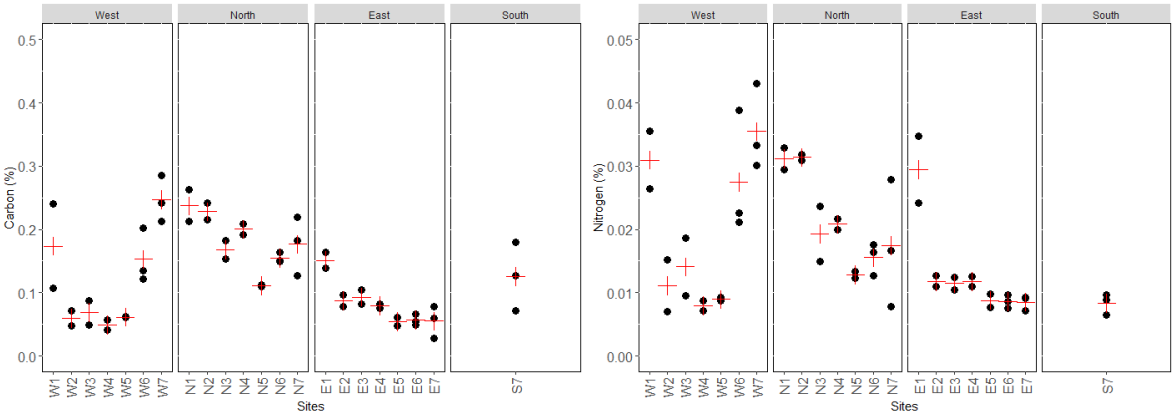


Figure 4-7: Sediment carbon (%; left) and nitrogen (%; right) collected at control, compliance and farm sites in March 2020. Black points represent values from individual replicates while red crosses represent the site mean.

Consistent with the enrichment gradient evident from the physico-chemical variables, family richness was reduced near the cages (Figure 4-8). On the transects to the west and east, family richness was variable, but relatively similar from site 3 (35 m from the cage) and beyond. Family richness at these sites was similar at the control site to the south and the additional compliance sites. On the transect to the north there was a very clear gradient of increasing family richness with distance from the cage along the entire transect. In contrast, the spatial pattern with distance from the cage was far less evident for total faunal abundance (Figure 4-9). Total abundance was lower at the two sites closest to the cage on the eastern transect and there was some evidence of abundance increasing with distance from the cage on the northern transect, but the large variability with and between sites obscured these trends.

Greater insight into the biological response can be gained by a more detailed community analysis and a focus on the known enrichment indicator species (or families). Annelids are considered a key group in this regard because many of the taxa are indicators of organic enrichment (Macleod & Forbes 2004, Dean 2008). The transect data highlight significant within (i.e., between grabs) and between site variability (Figure 4-10). Overall, annelid abundance appears higher at sites closer to cages, and this was most evident on the eastern transect. Capitellidae was the most common family in this survey, with many of the species in this family known indicators of pollution; in south-eastern Tasmania, species of the genus *Capitella* are recognised as indicators of organic enrichment associated with marine farming (Macleod & Forbes 2004). *Capitella sp.* abundance was greater in proximity to cages and consistent with the response of physico-chemical parameters. They were in higher abundances further from the cage on the northern transect compared to the east and west (Figure 4-11).

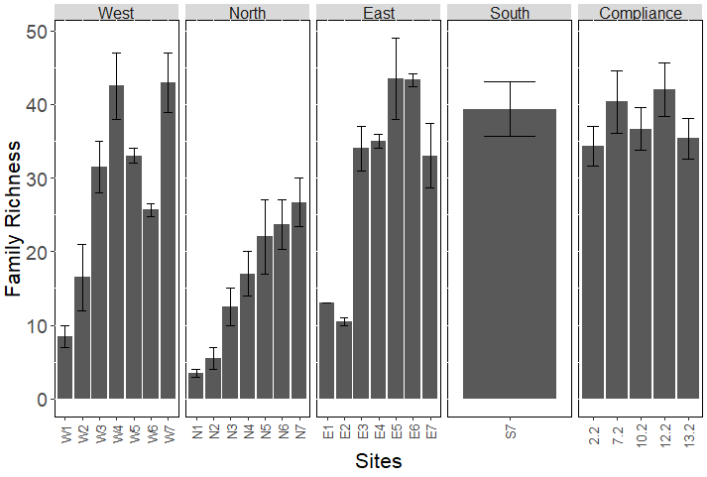


Figure 4-8: Mean number of families per grab collected at control, compliance and farm sites in March 2020. Two replicates were collected at positions 1-5 and three replicates at positions 6-7.

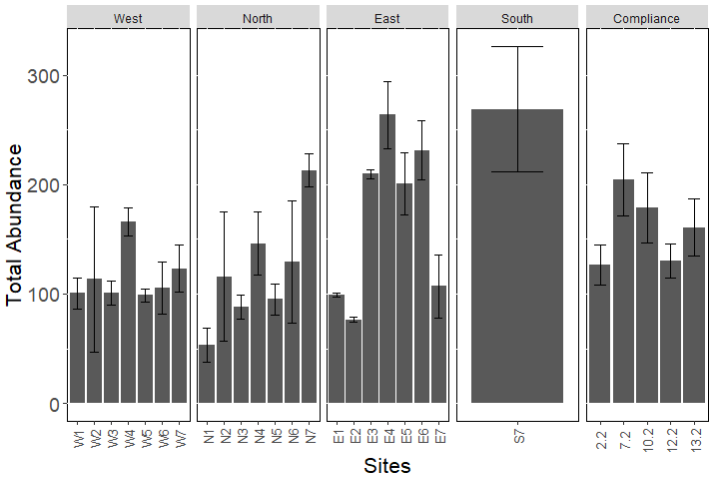


Figure 4-9: Mean number of benthic invertebrates per grab collected at control, compliance and farm sites in March 2020. Two replicates were collected at positions 1-5 and three replicates at positions 6-7.

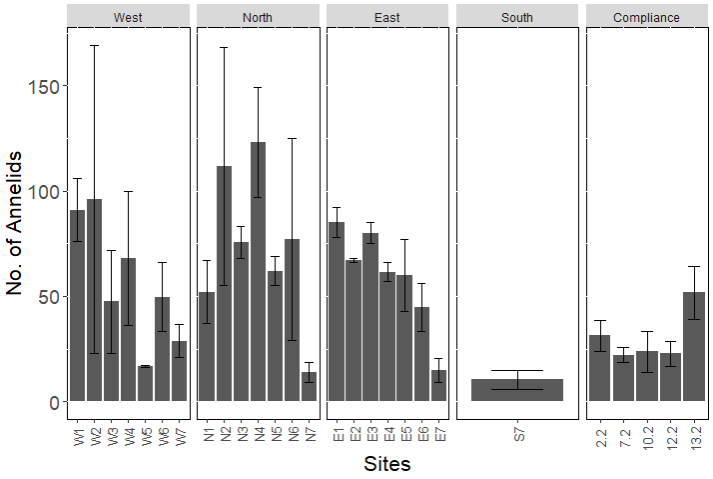


Figure 4-10: Mean number of annelids per grab collected at control, compliance and farm sites in March 2020. Two replicates were collected at positions 1-5 and three replicates at positions 6-7.

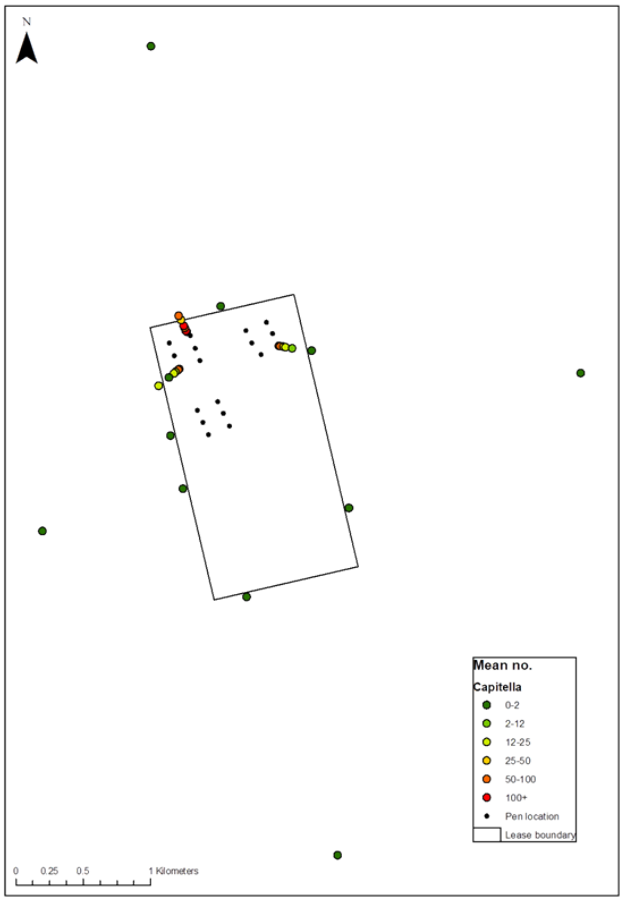


Figure 4-11: Map showing the relative abundance of *Capitella* sp. at the control, compliance and transect sites in March 2020.

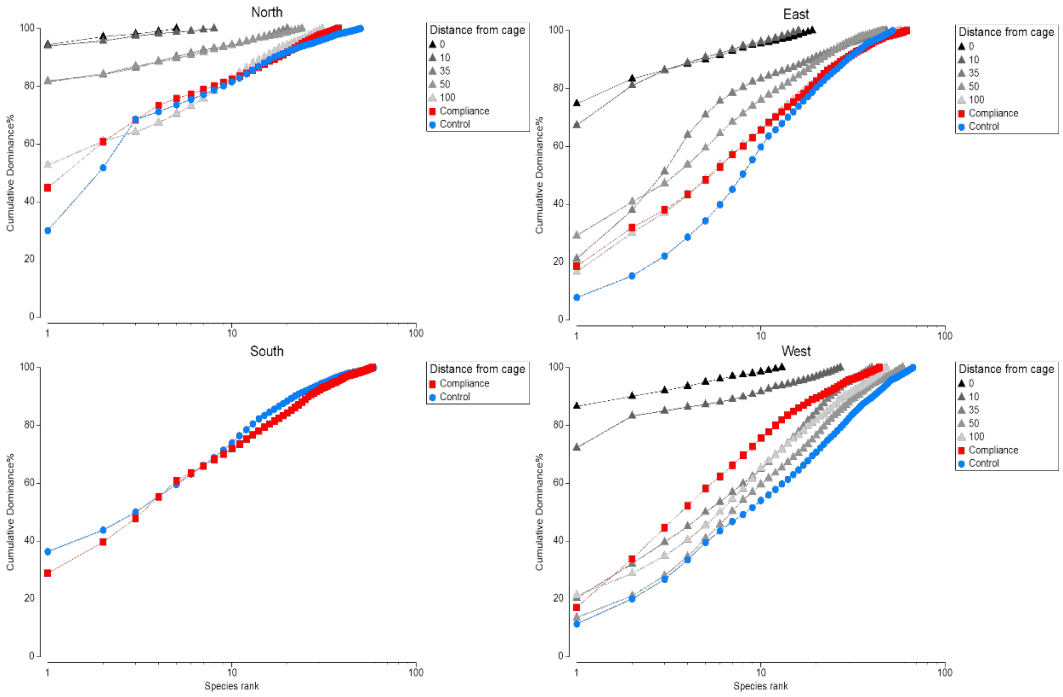


Figure 4-12: K-dominance plots from transect sites to the north, east, south and west of the lease in March 2020. Red squares represent compliance sites and blue circles represent control sites while graduated grey triangles represent research transect sites where a darker grey indicates a site closer to the cage. Site averaged family data was used.

K- dominance plots also provide insight into the level of impact in sediment communities. They show the cumulative percentage of abundance made up by individual families, starting with the most dominant; a large percentage of the total abundance shared amongst a small number of species is often an indication of an impacted site. Here, the K-dominance analysis showed a clear trend of high single-family dominance near the cage and lower dominance when moving further away (Figure 4-12). The footprint of higher single-family dominance near cages was largest on the northern transect sites from 0-35 m from the cage, while dominance patterns at the 100 m and compliance site (135 m from the cage) could be considered moderately impacted. On the western transect, sites 0-10 m from the cage were similarly highly impacted; however, all sites beyond this showed a normal level of family diversity. On the eastern transect, there was a clear but smaller impact at 0-10 m sites, while all further sites had a relatively normal level of diversity.

In Figure 4-13 the multidimensional scaling (MDS) ordination highlights the separation of sites closer to the cage to the upper left; sites (N1-5) to the north from 0-100 m, sites (W1-2) to the west from 0-10 m, and sites (E1-2) to the east from 0-10 m. The vector overlay shows the contribution of families to patterns in the ordination. Abundance of the enrichment indicator family Capitellidae is the correlate on the main axis of separation for these sites; this likely depicts the enrichment footprint and impact on benthic communities. Figure 4-14 illustrates the gradient of enrichment along transects using trajectories from site 1 to site 7. There is a distinct pattern in dissimilarity along the north transect with near cage sites to the top-left and far-field sites to the bottom-right. The western transect follows a similar pattern however it starts lower than the north transect and transitions more rapidly to the region of compliance and controls sites, suggesting a more localised region of impact in that direction. The eastern transect starts closest to the region of compliance and controls sites, suggesting a localised and lower level of impact to the east.

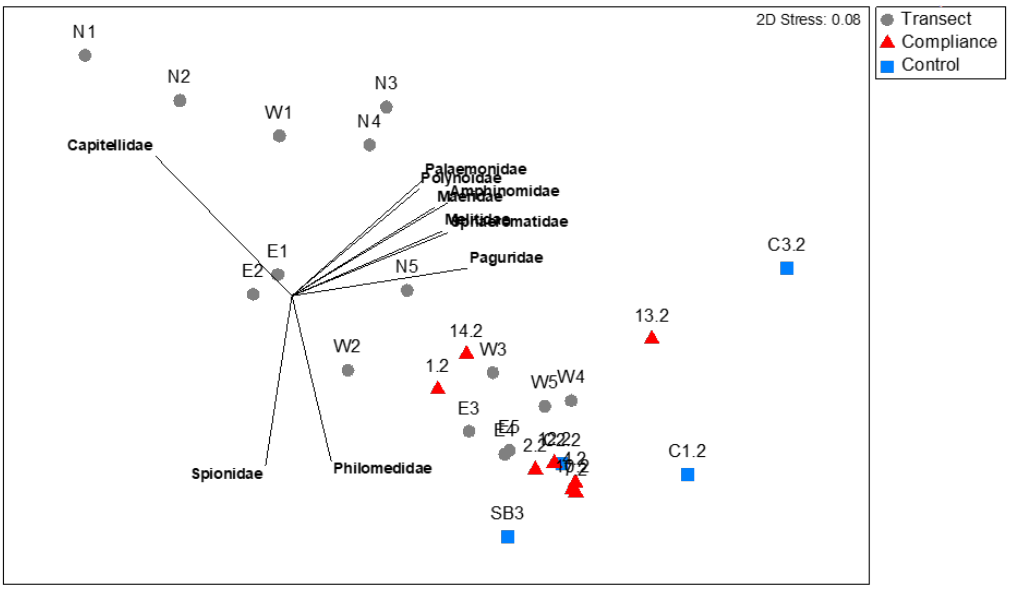


Figure 4-13: Results of non-metric multidimensional scaling analysis (nMDS; 2D stress = 0.08) using benthic infauna data collected from eight compliance sites (red triangles), four control sites (blue squares), and fifteen transect sites (grey circles). Vectors indicate key families with a high correlation (>0.7) with ordination space and represent families driving the separation of sites in two dimensions.

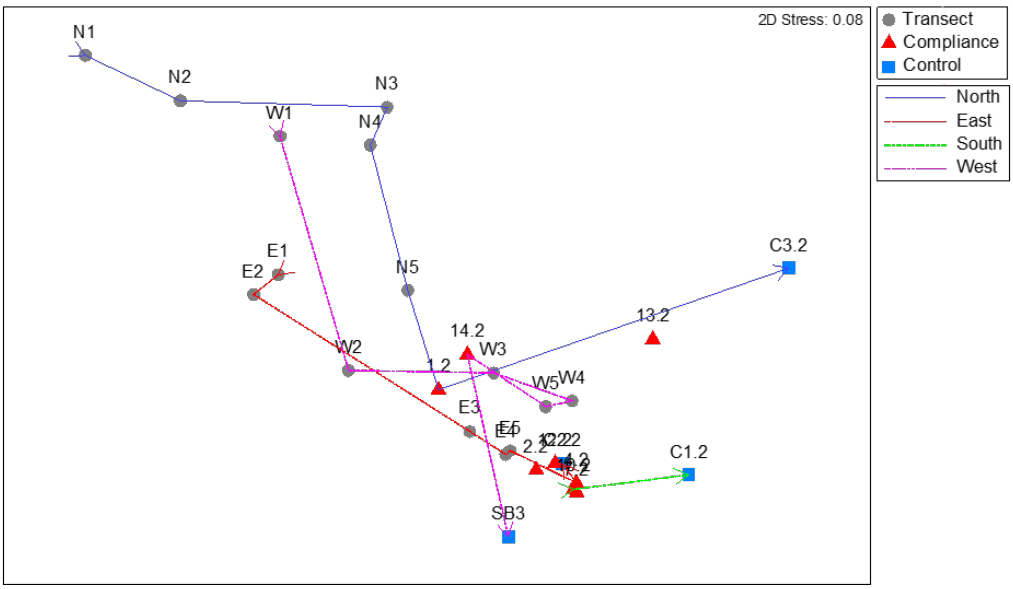


Figure 4-14: Results of non-metric multidimensional scaling analysis (nMDS; 2D stress = 0.08) using benthic infauna data collected from eight compliance sites (red triangles), four control sites (blue squares), and fifteen transect sites (grey circles). Trajectories start at the site closest to pen and finish at the most distant.

AMBI (see Box 4.1 for background) generally categorised sites as heavily disturbed at the cages, decreasing in impact to slightly disturbed by the end of the transect; all compliance and control sites were considered slightly disturbed (Figure 4-15). The presence of species such as *Capitella* sp. and *Nebalia* sp., and copepods which proliferate in highly enriched environments contribute to the heavily disturbed classification at the cage sites in the AMBI. The index also highlights the variability between transects. On the eastern transect, AMBI was high (>4.2) at 0 – 10 m from the cage but dropped substantially from 35-100 m (2-3), and it was lower again (<2) at the more distant compliance and control sites. In contrast, on the northern transect, AMBI was indicative of heavily disturbed conditions (>5.5) out to 50 m, and moderate disturbance at 100 m before improving further at the compliance and control sites. However, it was notable that conditions at the compliance site to the north (N6/1.2) were variable across the slight to moderate disturbance boundary; this is consistent with the increased presence of *Capitella* sp. at this site[1] and the more extended footprint of enrichment on the northern transect seen for other parameters. On the western transect, conditions were more variable (1.5 – 4) indicative of slightly to moderately disturbed conditions at sites between 10-50 m before improving (<2) at the 100 m and control sites.

In the March 2021 and 2022 surveys the full transects were not sampled and we have restricted temporal comparisons to the sites and distances that were sampled in all three surveys; cage (0 m), 35 m from cage, compliance and control sites.

In March 2021 redox levels were similar at the cage (0 m) sites but were higher at the 35 m from cage, compliance and control sites, relative to March 2020 (Figure 4-16). In March

[1] It is important to note that the compliance site on the northern transect is closer to the cages (135 m) compared the compliance sites on the western (200 m) and eastern transects (235 m).

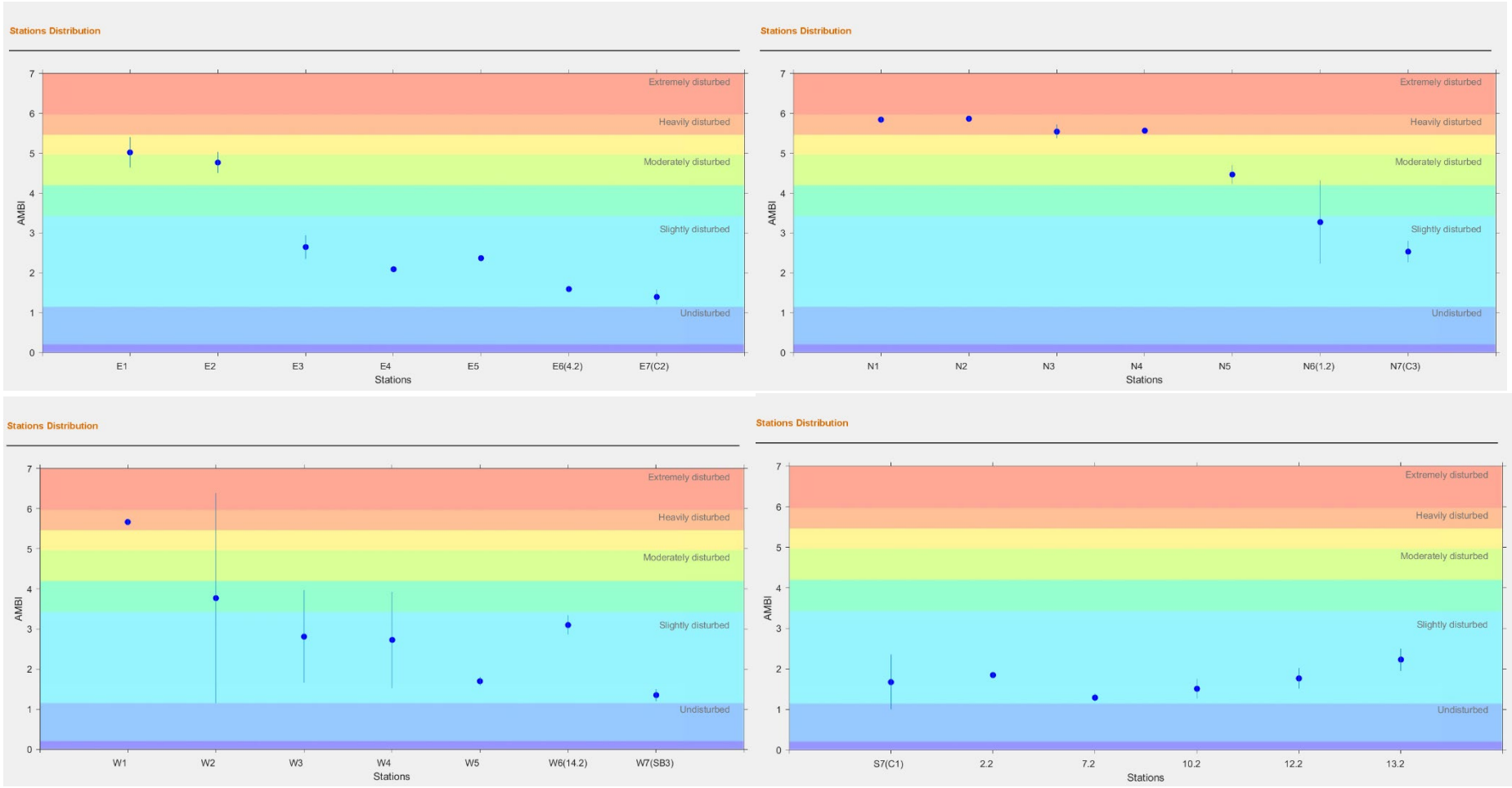


Figure 4-15: AMBI at sites on the eastern (top left), northern (top right) and western (bottom left) transects, and the additional compliance and control sites (bottom right).

2022, redox was again lower at the 35 m from cage and compliance sites, but higher at the cage sites. In contrast, sulphide levels showed a similar pattern across all three surveys, with the exception of higher values at the cage (0 m) sites in March 2021 (Figure 4-16). For family richness, there was a clear trend of increasing richness with distance from the cage, although in 2021 the 35 m site was slightly lower than under the cage. In 2020, total abundance was lowest at the cage and increased with distance; however, in 2021 and 2022, a spike was observed at the cage, a trough at 35 m and then an increase with distance from the cage. Interestingly, the number of annelids remained higher at the cage (0 m; mostly capitelids) sites in March 2021 and 2022, but abundances at the 35 m from cage and compliance sites were lower relative to March 2020.

AMBI in all three surveys highlighted a clear gradient of effect, with major to moderate effects in closer proximity to the cages (0 – 35 m; Figure 4-18). Notably conditions at the compliance sites improved across the three surveys, and in March 2022 the index was similar (<2) across the compliance and control sites. The community response to enrichment through time is further illustrated in the nMDS ordination in Figure 4-19, showing the community trajectories from the cage, 35 m from cage, compliance, and control sites in each survey. In the 2019 baseline, variability in community structure between the compliance and control sites pre farming is evident and in the three surveys conducted during production, the distinct communities in closer proximity to cages are evident. Community structure was more variable in closer proximity to the enrichment source, which is to be expected given changes in stocking and feed inputs through time.

Overall, the local-scale benthic sampling at Yellow Bluff documented the spatial footprint and gradient of enrichment with distance from the cage. These results are consistent with recent work conducted at the nearby Storm Bay 1 and Trumpeter[2] leases (Ross et al. 2022). It was also notable that the footprint was not uniform and extended further to the north-west; it is unclear if this reflects current direction and subsequent deposition patterns and/or the greater stocking of the cage grid in the northwest corner during the initial stage of the study. Although, the picture from the different response parameters did vary somewhat, collectively they all converged to describe a similar pattern in space and time (Figure 4-16, Figure 4-17, Figure 4-18).

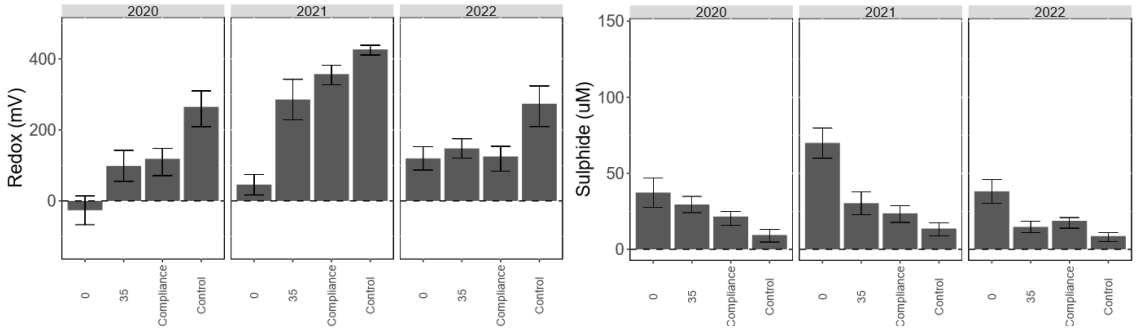


Figure 4-16: Corrected redox values (mV; mean ± SE) and sulphide concentration (µM; mean ± SE) at 3 cm depth for sediments collected at cage, 35 m from cage, compliance, and control sites in March 2020, 2021, and 2022.

[2] The Trumpeter lease is no longer in production and was destocked in 2019

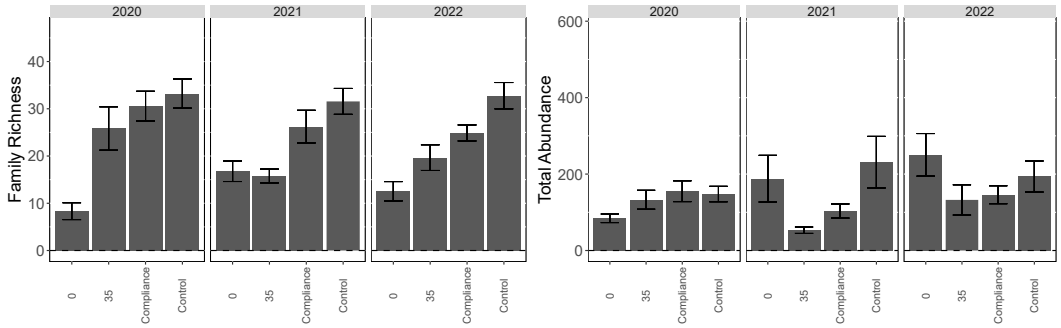


Figure 4-17: Family richness and total abundance per grab (mean ± SE) at cage, 35 m from cage, compliance, and control sites in March 2020, 2021, and 2022.

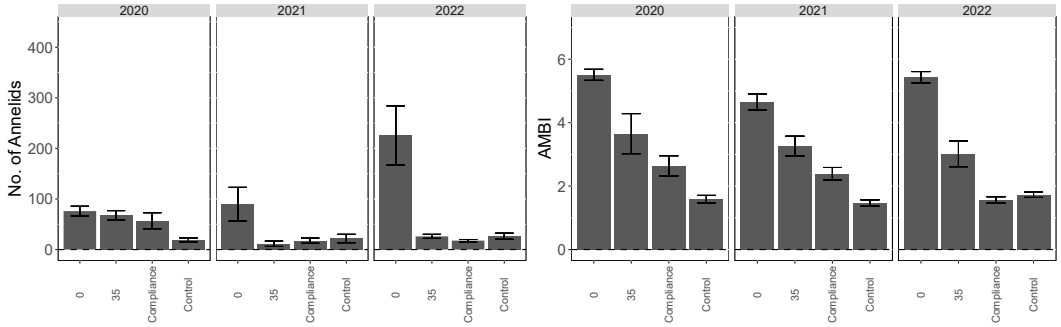


Figure 4-18: Number of Annelids and AMBI (mean ± SE) at cage, 35 m from cage, compliance, and control sites in March 2020, 2021, and 2022.

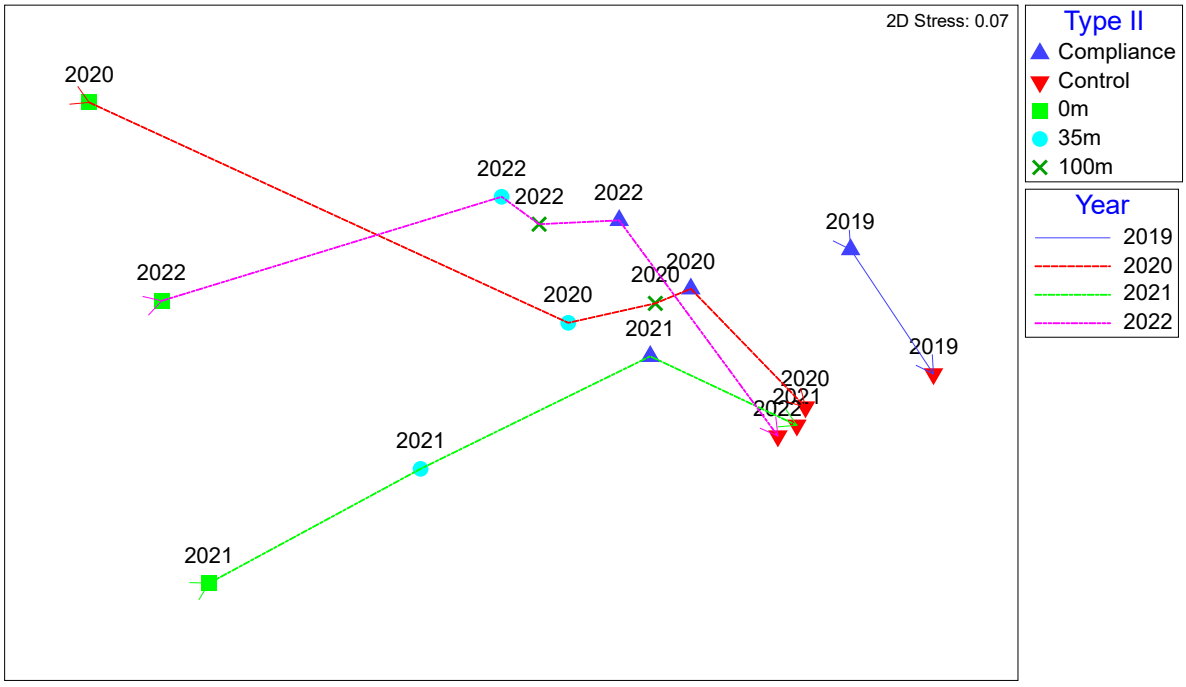


Figure 4-19: Results of non-metric multidimensional scaling analysis (nMDS; 2D stress = 0.07) using benthic infauna data collected from cage, 35 m, 100 m, compliance and control sites in the March 2020, 2021, and 2022 surveys. Compliance and control sites from the 2019 baseline survey are also included for context. Trajectories start at the cages site and finish at the most distant site (controls).

West of Wedge

The West of Wedge Lease (MF279) is located on the eastern side of Storm Bay in an area with water depths between 37-40 m. Farming at the West of Wedge lease began with one cage in April 2020 (Figure 4-4). At the time of the January 2021 survey, two cages were stocked. These cages were fallowed from February 2021 to June 2021 and then four cages were stocked from November 2021 until beyond the December 2021 survey (Figure 4-4). Because of this, the number of farm sites and their location varied between surveys (Table 4-4).

The baseline assessment in March 2019 revealed no clear spatial patterns in sediment characteristics and chemistry across compliance, control, or internal lease sites (Aquenal 2019b). Observed redox values were high (average 314 mV at 3 cm; all >250 mV) and indicative of well oxygenated sediments. Most sites recorded sulphide levels near zero (<1 µM); the exception was control site C1 (average 43.56 uM) where sulphide was highly variable between replicates (i.e., 114.36, 16.27 and 0.05 uM for each of the three replicates).

Sediments across the area were dominated by medium to fine sand, contained a low proportion of silt and had very low organic content (average 1.0%; range 0.7-1.5%). Benthic faunal analysis revealed typically abundant and diverse fauna (~125 individuals per grab & 115 families total). Crustaceans dominated the faunal community (83% of individuals), followed by molluscs (7.2%), polychaetes (7.1%) and echinoderms (1.3%). The most common families were Diastylidae and Bodotriidae cumaceans, Lysianassidae, Eusiridae, Isaeidae and Phoxocephalidae amphipods and Cypridinidae ostracods.

The only Capitellidae observed were in very low densities across the survey area and none of the species present were considered indicative of organic enrichment. Based on the relatively uniform patterns in physico-chemical parameters, high taxonomic diversity and dominance of crustaceans in the baseline, potential impacts such as an increase in species dominance patterns, particularly for deposit feeders (e.g., polychaetes) should be readily discernible.

As previously mentioned, more detailed transect sampling was not conducted at West of Wedge because of the low biomass (i.e., only 2-4 stocked cages) at the lease over the course of the study. To provide important insight on expected responses to organic enrichment at this lease should the farm footprint extend to the compliance sites, cage sites were sampled, and with only 2 control sites prescribed by the EL, two of the broad-scale survey sites (SB-16 and NUB-4) were included as additional control sites.

At the time of the first survey in January 2021, two cages had been stocked at the lease since July 2020 and one of the cages since April 2020. Unsurprisingly, there was no evidence of benthic effects at the compliance sites for any of the physico-chemical or biological parameters. Redox potential was higher at the control (450 ± 2 mV) and compliance (444 ± 5 mV) sites compared to the two cage sites (377 ± 27 mV; Figure 4-20) and sulphide was lower at the control (3.3 ± 0.3 µM) and compliance (3.3 ± 0.3 µM) sites relative to the cages (15.1 ± 5.1 µM; Figure 4-21). The results for both sediment carbon and nitrogen content were far

more variable between sites (Figure 4-22 & 23) with no clear pattern between control, compliance, and cage sites. Sediment carbon content tended to be more elevated at the compliance and control (C1) sites to the north, and only one cage site replicate was clearly elevated. For nitrogen there were no clear spatial patterns, although cage site PB1 had one replicate with elevated sediment nitrogen.

The patterns observed for the key biological patterns told a similar story to the physico-chemical parameters with no evidence of any enrichment effects at the compliance sites and some evidence, as expected, at the cage sites. Family richness was similar across compliance sites (34 ± 1 families per grab), control sites (32 ± 1 families per grab) and farm sites (32 ± 2 families per grab). Total abundance was also similar across compliance sites (128 ± 8 ind. per grab) and control sites (114 ± 7 ind. per grab), but higher and more variable at the cage sites (211 ± 77 ind. per grab). A similar pattern was observed for annelid numbers. Their abundance at the cage sites (77.8 ± 55.8 annelids per grab) was higher than at compliance (14.1 ± 1.5 annelids per grab) and control sites (9.5 ± 1.4 annelids per grab). The pattern was largely attributable to the larger number of annelids in two of the replicates at cage site PB1a.

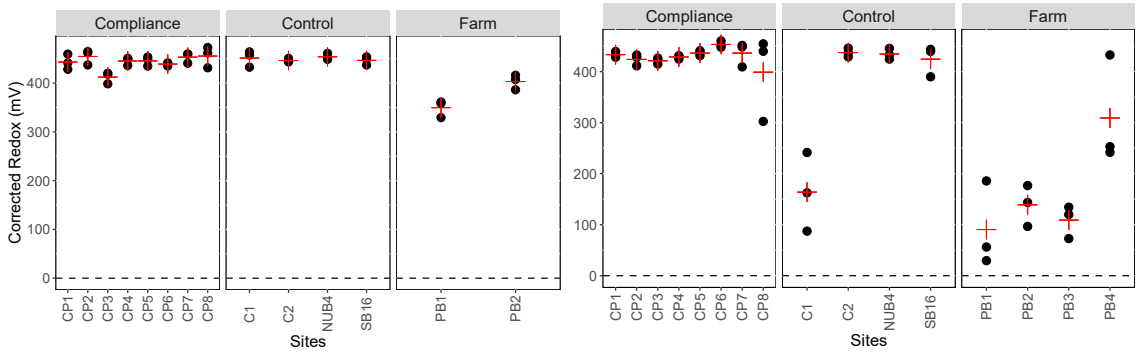


Figure 4-20: Corrected redox values (mV) at 3 cm depth for sediments collected at compliance, control and farm sites at MF279 in January 2021 (left) and December 2021 (right).

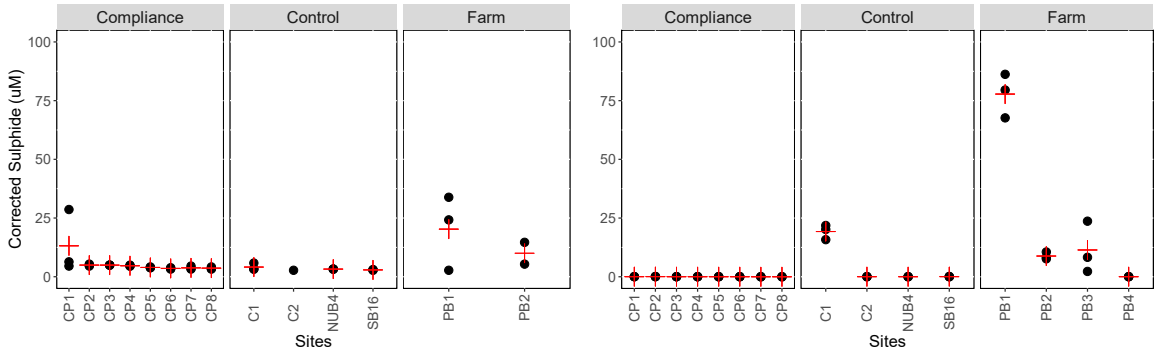


Figure 4-21: Corrected sulphide values (uM) at 3 cm depth for sediments collected at compliance, control and farm sites at MF279 in January 2021 (left) and December 2021 (right).

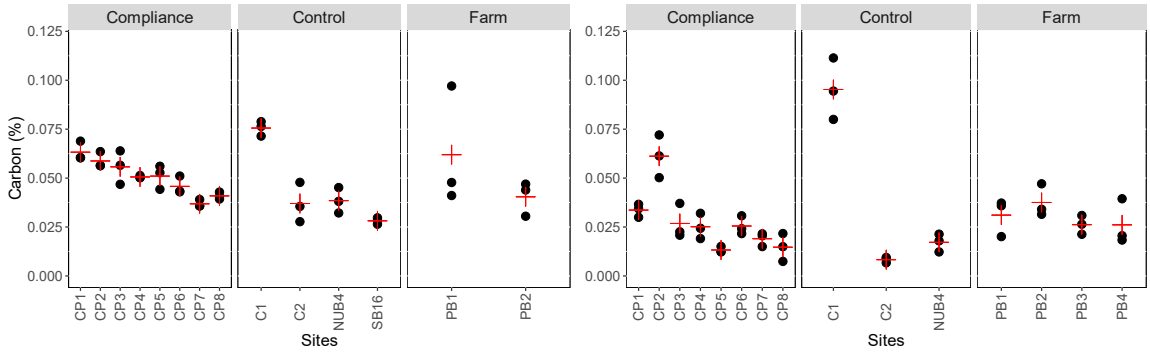


Figure 4-22: Sediment carbon content (%) at compliance, control, and farm sites at MF279 in January 2021 (left) and December 2021 (right).

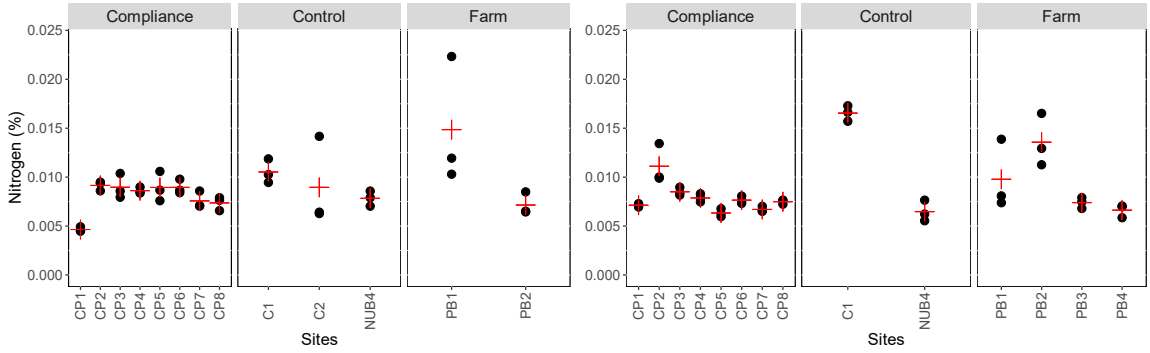


Figure 4-23: Sediment nitrogen content (%) at compliance, control, and farm sites at MF279 in January 2021 (left) and December 2021 (right).

The multidimensional scaling (nMDS) plot revealed more subtle differences in benthic community composition between the sites (Figure 4-25). Sites with more similar communities are placed closer together in the ordination space and those with greater differences are further apart. The three farm sites PB1, PB1a and PB2 clearly separated to the right of the plot from all other sites, suggesting these sites possess a distinct faunal community. The remainder of the control and compliance sites formed a group at 60% similarity to the left of the plot. This pattern would seem to represent small scale spatial differences in macrofauna communities whilst the separation of the farm sites is more likely to be indicative of organic enrichment. This level of sensitivity in detecting changes given the low level of farming is a positive reflection of the monitoring programme. The AMBI benthic quality index further highlights the capacity of the monitoring program to reveal more subtle impacts on benthic assemblages (Figure 4-26).

At the time of the second survey in December 2021, four cages were stocked. The lease was fallowed soon after the January 2021 survey and two cages were stocked from June 2021 and a third and fourth cage stocked in October and November respectively. As illustrated in Figure 4-4, feed inputs over the three months prior to the December 2021 survey were much higher for cages 1 and 2 (i.e., at sites PB1 and PB2). Relative to the same two cages in January 2021 redox values at PB1 and PB2 declined in December and sulphide concentrations increased at PB1 but not PB2 (Figure 4-20 and 21). Redox and sulphide remained high and low respectively at PB4, but at PB3 redox was lower and sulphide higher relative to most of the control and compliance sites. The pattern across the four cage sites

appears to be consistent with their relative feed inputs. Amongst the control and compliance sites, control site C1 is a clear outlier. In the December 2021 survey, sulphide and redox levels, and carbon and nitrogen content (Figure 4-22) at C1 were indicative of localised enrichment. Sediment carbon was also elevated at C1 in the January 2021 survey and a high sulphide reading in a single core at C1 was reported from the 2019 baseline. With only two control sites (C1 & C2) prescribed in the environmental licence for the West of Wedge lease (MF279) these results, and the inclusion of broadscale sites SB-16 and NUB-4 as additional controls, highlight the importance of having a minimum of three control sites.

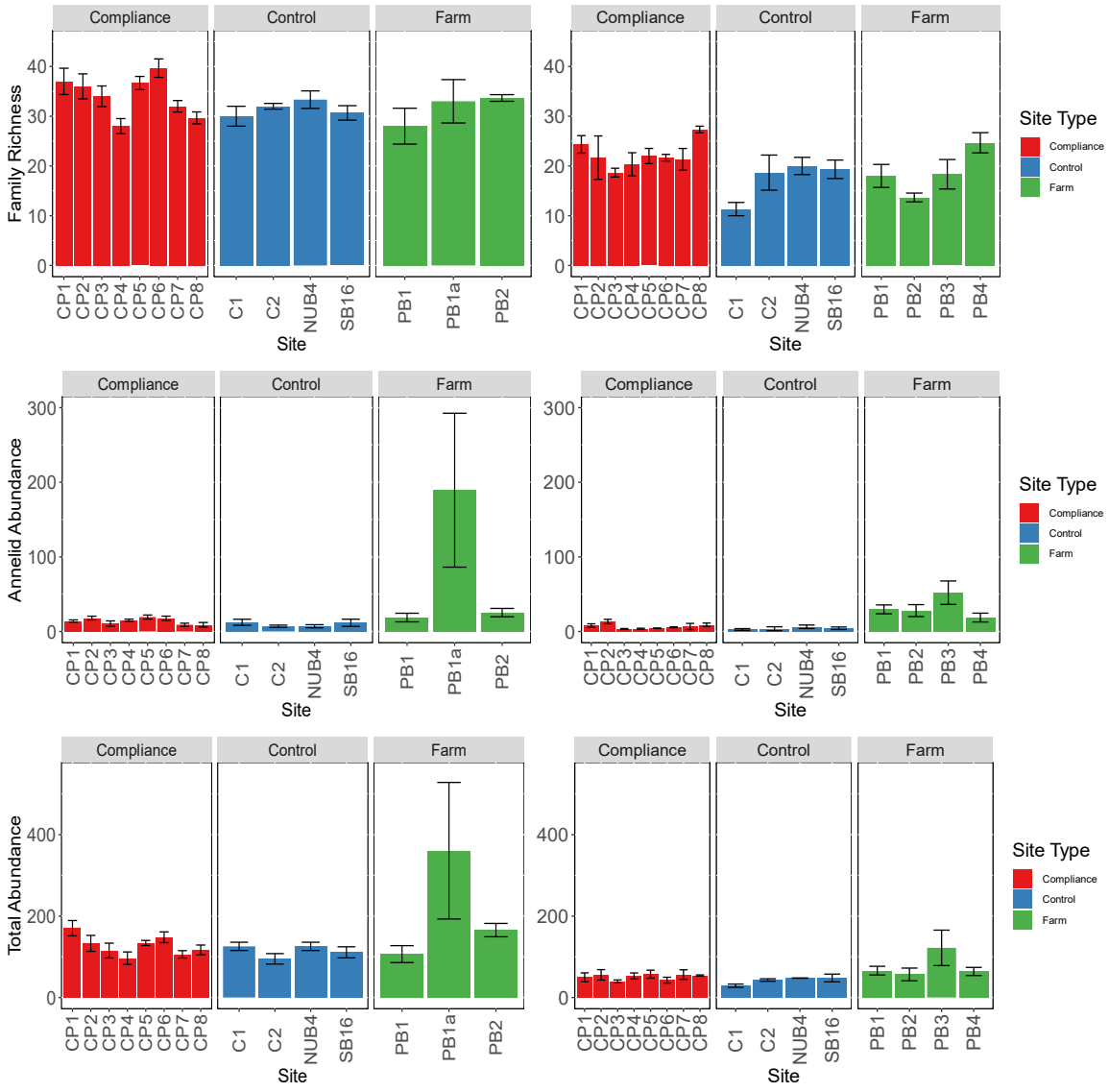


Figure 4-24: Family richness (top), annelid abundance (middle) and total abundance (bottom) (mean ± SE per grab) at compliance, control and farm sites at MF279 in January 2021 (left) and December 2021 (right).

For the biological parameters in December 2021, family richness was similar across compliance, control and cage sites, but total abundance was greater at the cage sites relative to the control and compliance sites (Figure 4-24). This is largely attributable to the higher annelid abundance at the cage compared to control and compliance sites (Figure

4-24). This is consistent with the conclusion from the baseline report that the expected increase in annelids in response to enrichment would be easily identifiable against the crustacean dominated benthic community in the region.

The MDS ordination (Figure 4-25) shows the relationship between sites based on the benthic community composition. One large group containing all compliance sites, control site C2 and farm site PB4 is defined to the bottom left of the plot at 60% similarity. This suggests these sites possess a macrofaunal community typical of the area. Farm sites PB3 and PB2 form a group removed to the right, while PB1 is isolated further to the right, demonstrating that changes in macrofaunal communities due to farm enrichment are represented in this direction. Macrofauna at control site C1 is the most dissimilar, although, in a different direction, indicating that differences seen at this site are likely not associated with farm enrichment.

The second multidimensional scaling (nMDS) plot in Figure 4-25 reveals the changes in benthic communities between surveys and in response to farming. Although benthic community composition varies across surveys, the communities at the compliance and control sites overlap and are close together in each survey, with the major exception at control site C1. This is consistent with the other response parameters which highlight C1 as an outlier relative to the other control and compliance sites; site C1 appears be in an area of localised enrichment independent of farming. All the cage sites in each survey separate to the right of the plot, with the sites most distant typically corresponding to sites with the greater feed inputs. The AMBI benthic quality index further highlights the capacity of the monitoring program to reveal more subtle impacts on benthic assemblages (Figure 4-26); cage sites PB1, PB2 and PB3 have AMBI scores ranging from 3 – 4 at the boundary of slightly to moderately disturbed conditions and all of the control and compliance sites have scores <2 which is at the lower end of the slightly disturbed category.

Overall, the combined analysis indicates that the communities at the West of Wedge lease are diverse and relatively unimpacted. Without the spatial resolution gained by the application of a transect design, the size of the farm impact footprint is hard to determine. However, the magnitude of the impact directly under the cages has remained minor to moderate throughout the survey period. This is to be expected considering the low levels of farm production at this lease to date.

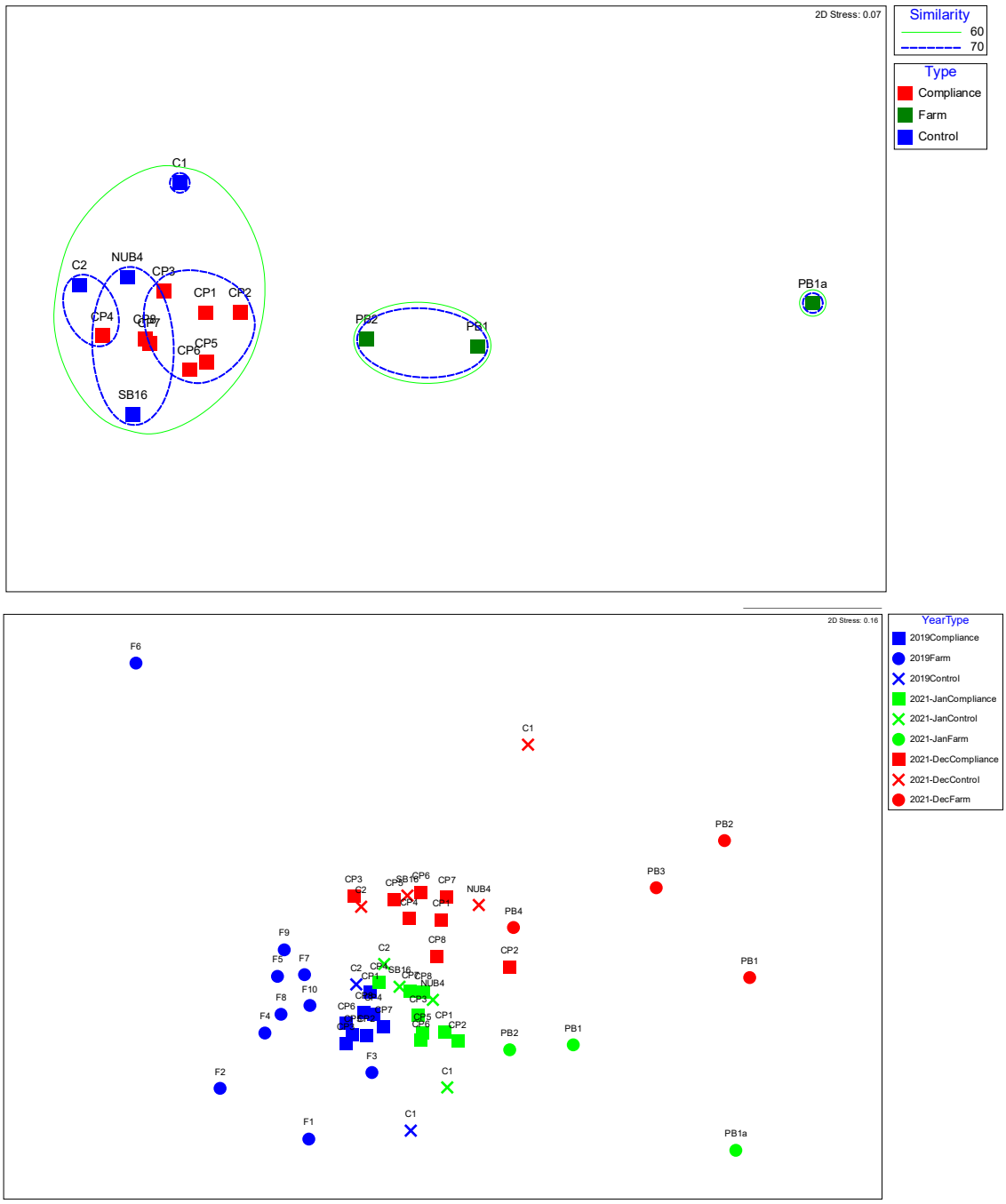


Figure 4-25: nMDS plots of the benthic invertebrate communities at compliance (red squares), control (blue squares), and farm sites (green squares) in January 2021 (top panel) and together with the February 2019 baseline and December 2021 surveys (bottom panel). Points represent pooled abundances of three replicates at each site. In the top panel the ellipses represent community similarity at 60% and 70% based on cluster analysis.

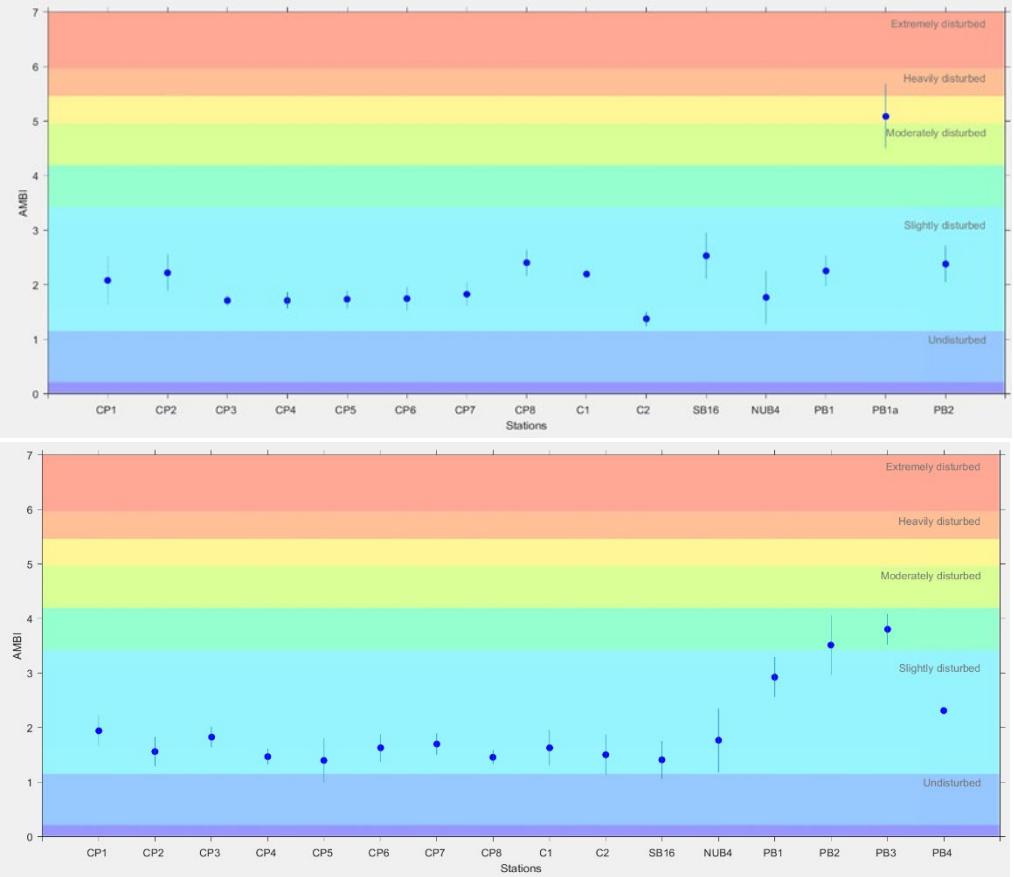


Figure 4-26: Plot showing mean AMBI in sediments at MF279 compliance, control and farm sites in the January 2021 (top panel) and December 2021 (bottom panel) surveys. Coloured bands represent disturbance categories as prescribed by AZTI's AMBI software.

4.1.3 Environmental performance assessment

The Environmental Licence to operate a marine lease stipulates standards for the assessment of the benthic conditions and significant visual, physico-chemical or biological impacts (Table 4-1). However, there is ambiguity in their interpretation evident across published benthic sediment survey reports[3], particularly in relation to the temporal and spatial scales that are intended (e.g. see Aquenal 2019b, IMAS 2020c). More clarity needs to be provided on how to relate changes at compliance sites to reference sites, and whether reference sites are referring to control sites or baseline conditions at the same sites. For the biological criteria which require an assessment of change against baseline conditions, differences in the sampling design also need to be considered when interpreting change. In the Baseline Survey, single sediment samples were taken from three locations 20 m apart at each site (e.g., 1.1, 1.2, 1.3) and for monitoring under the Environmental Licence, three replicate samples were taken from the central site from the Baseline Environmental Survey (i.e., 1.2, 2.2……11.2). For the purposes of this assessment, we have used data from all samples collected.

Here, we assess performance of the key sediment parameters across surveys at the Yellow Bluff and West of Wedge leases consistent with the approach outlined by Crawford et al.

[3] The new Environmental Standards will address this through accompanying technical standards

(2002) in their evaluation of techniques for environmental monitoring of salmon farming in Tasmania. In the first instance, sediment conditions at the compliance sites (i.e. 35 m from lease boundary) are compared against conditions observed prior to farming (the baseline) at the same sites. The change at compliance sites is then contrasted against that observed at more distant reference sites over the same period to identify if conditions have changed independent of farming. We also provide assessment against the criteria for a significant impact outlined in The Environmental Licence and provide context for our interpretation.

Yellow Bluff

Physico-chemical parameters

There was evidence across the 3 surveys conducted during farm production that both sediment redox and sulphide at compliance sites were affected by farming. Redox and sulphide measured directly adjacent to the cages where impacts are likely to be the greatest provide important context on the magnitude of effect (Figure 4-27 & 28).

Relative to baseline reference conditions, sediment redox was lower at the compliance sites but comparable (or higher) at the control sites in March 2020 and 2022, and it was notably lower again at the cage sites. In March 2021 the difference between the compliance and control sites was comparable to that observed in the baseline. Although sulphide was higher at the controls in the production surveys relative to the baseline, the increase at compliance sites was comparatively higher in each survey. Relative to the compliance sites, sulphide levels were higher again at the cage sites.

For redox and sulphide, the Environmental Licence conditions stipulates a significant impact as:

- A corrected redox value which differs significantly from the reference site(s) or is <0 mV at a depth of 3 cm within a core sample.
- A corrected sulphide level which differs significantly from the reference site(s) or is >250 μM at a depth of 3 cm within a core sample.

We interpret the first part of the condition as a comparison of the mean of compliance and control sites for each survey[4]. The difference was significant for redox in 2020 ($p=0.0178$) and 2022 ($p=0.032$) and for sulphide in 2020 only ($p=0.022$). For the second condition, there was a single core with a redox <0 in surveys 1 and 3 at compliance site CP1, but all other redox sulphide and values for individual cores were above or below the thresholds respectively. A weakness in this test for the evidence of farm effects is that the compliance and controls sites may be different due to the influence of sources external to the farm. A more powerful test is to compare change observed at the compliance sites from the baseline with the change observed at the control sites from the baseline. If the change at the compliance sites is significantly greater than observed at the controls, then there is evidence of a farm effect at the compliance sites, and if not, the change at the compliance sites is explainable as being due to sources independent of the farm. In 2020, this test found

[4] Note, data was transformed when necessary to meet the assumptions of a normal distribution for the statistical tests.

that on average, redox at compliance sites decreased by 212 mV since the baseline survey, while control sites increased by 26 mV over the same period. The difference between these groups was statistically significant (p=0.041). It was also found that sulphide concentration increased by an average of 13 µM at compliance sites and 0.12 µM at control sites. However, the difference between these groups was not significant (p=0.08). In 2022, this test found that on average, redox at compliance sites decreased by 124 mV since the baseline survey, while control sites increased by 48 mV over the same period. The difference between these groups was statistically significant (p=0.001).

It is important to note that on their own, the physico-chemical measures of organic enrichment are often not considered to be as reliable or sensitive as the response of benthic macrofauna communities. As such, we suggest it is important to assess the changes observed in sulphide and redox in the context of the biological parameters.

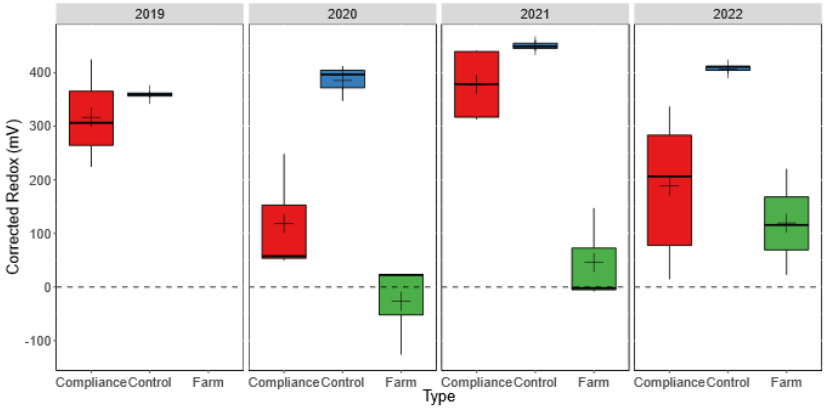


Figure 4-27: Boxplots comparing corrected redox (mV) at Yellow Bluff compliance, control and farm sites in the February 2019 (baseline) and during production in March 2020, 2021, and 2022. Boxes represent the interquartile range (IQR; 25th - 75th percentile), the median (internal line) and the mean (cross). Whiskers (vertical lines) extend to the maximum and minimum values closest to 1.5 times IQR and points beyond this are considered outliers and plotted with site labels.

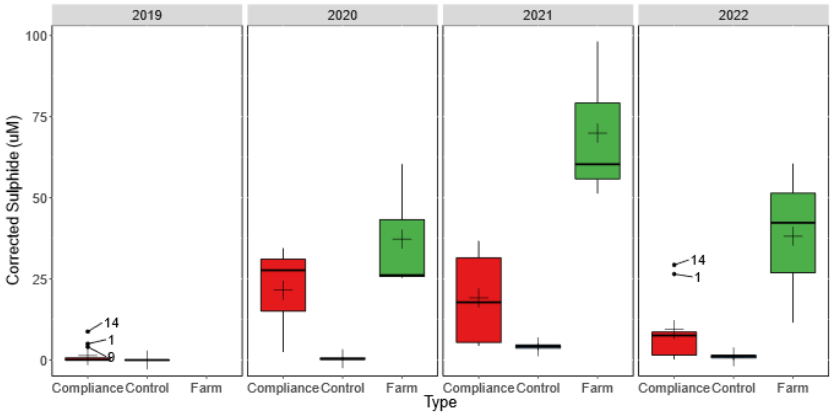


Figure 4-28: Boxplots comparing sulphide (uM) at Yellow Bluff compliance, control and farm sites in the February 2019 (baseline) and during production in March 2020, 2021, and 2022. Boxes represent the interquartile range (IQR; 25th - 75th percentile), the median (internal line) and the mean (cross). Whiskers (vertical lines) extend to the maximum and minimum values closest to 1.5 times IQR and points beyond this are considered outliers and plotted with site labels.

Biological parameters

There was no evidence that the number of families was affected by farming in the 2020 and 2021 surveys; conversely, the decrease in family richness observed at the cage sites reveals the expected response to farm enrichment (Figure 4-29). Relative to baseline reference conditions, the number of families was similar at both the compliance and control sites in 2020, and in 2021 the number of families decreased by a similar amount at control and compliance sites. In March 2022, there was a bigger decrease at the compliance sites relative to the controls, but the outliers in Figure 4-29 highlight that the pattern was not consistent across sites. Notably, low family richness was observed at compliance site 1 (northern transect) in both 2021 and 2022.

The figures for total abundance highlight the variability between control sites in the baseline survey. Interestingly, despite a change in community composition at the cage sites (see below), total abundance at the enriched cage sites did not increase relative to compliance and control sites as expected. This highlights that total abundance pooled across all taxa is not necessarily a reliable indicator of impact.

Total annelid abundances provided evidence of a farm affect at the compliance sites in March 2020, but not March 2021 or 2022. In March 2020 there was an increase in the number of annelids at the compliance but not the control sites relative to the baseline. The increase at the compliance sites was largely attributable the presence of the enrichment indicator species, *Capitella* sp., particularly at sites on the northeast boundary of the lease (Figure 4-11).

For the biological parameters, the Environmental Licence conditions stipulate a significant impact as:

- A 20 times increase in the total abundance of any individual taxonomic family relative to reference sites;
- An increase at any compliance site of greater than 50 times the total Annelid abundance at reference sites;
- A reduction in the number of families by 50 per cent or more relative to reference sites;
- A complete absence of fauna.
- As natural environmental variation renders some locations more susceptible to significant changes in parameter values, the above thresholds will be considered in addition to baseline environmental information for determining the presence/absence of a significant impact.

We interpret the first condition as a 20 times greater increase in the total abundance of any family at compliance sites than at control sites relative to baseline conditions. A change of 20 times or greater should first be observed when comparing compliance sites to baseline conditions before the change over the same period at control sites is considered. In the March 2020 survey, Ophiuridae (brittle stars) was the only family that increased (126 times) by greater than 20 times at the compliance sites relative to the baseline (Appendix 4-3). This compared to an increase at control sites of 5.5 times, relative to the baseline. As such, the change at the compliance sites equates to a 23 times increase relative to the change at the control sites. In March 2021, Nassariidae (gastropods) increased (26 times) by greater than

20 times at the compliance sites relative to the baseline. At the controls, there were only 2 individuals recorded in the baseline and none in March 2021. In March 2022, Loveniidae (heart urchin) increased (53 times) by greater than 20 times at compliance sites relative to the baseline. At the controls, there were no individuals recorded in the baseline and two in March 2022. Instances where a family was not observed in one of the surveys makes calculating change problematic. For simplicity we have considered the change in Nassariidae and Loveniidae at control sites as a 2 times decrease and increase respectively. As such, the change at the compliance sites would equate to a 52 and 26.5 times increase for Nassariidae and Loveniidae respectively relative to the change at the control (reference) sites.

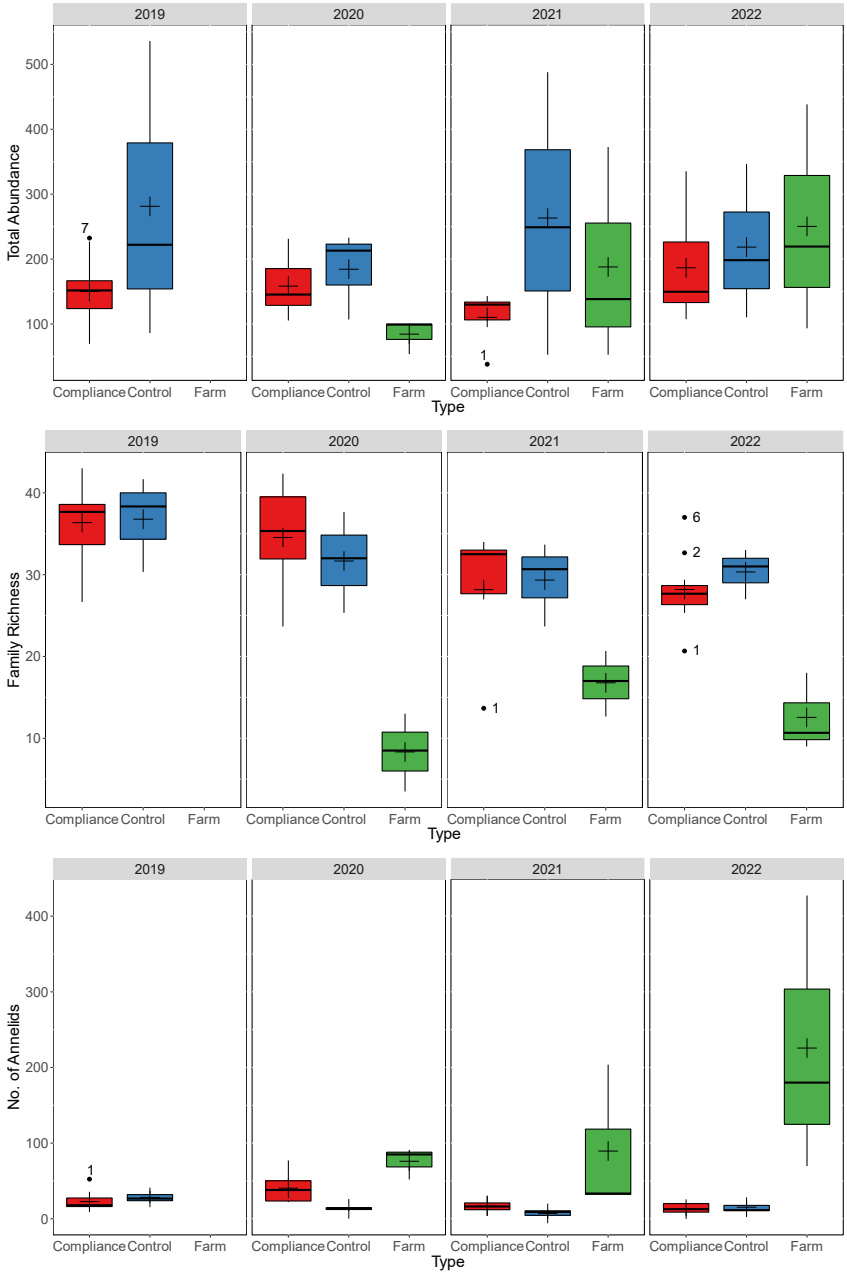


Figure 4-29: Boxplots comparing total abundance (top panel), family richness (middle panel) and number of annelids (bottom panel) in grab samples at Yellow Bluff compliance, control and farm sites in the February 2019 (baseline) and during production in March 2020, 2021, and 2022. Boxes represent the interquartile range (IQR; 25th - 75th percentile), the median (internal line) and the mean (cross). Whiskers (vertical lines)

extend to the maximum and minimum values closest to 1.5 times IQR and points beyond this are considered outliers and plotted with site labels.

The second condition clearly refers to individual site effects. There were no cases of a 50 times or greater increase in the abundance of Annelids at a compliance site than at control sites relative to baseline conditions. We interpret the third condition as a 50 per cent or greater decrease in the number of families at compliance than control sites relative to baseline conditions. In both 2021 and 2022 there was a reduction in the number of families relative to the baseline at both compliance and control sites. In 2021 the decrease was greater at the controls than the compliance sites and in 2022 the opposite pattern was observed; in neither case was change at the compliance sites 50% greater than observed at the controls. For the final condition, an abundant and diverse fauna was observed at all compliance sites, where the number of families ranged from 24-52 per site and abundance ranged from 105-488 indiv. per grab. At control sites the number of families ranged from 38-61 per site and total abundance ranged from 56-347 indiv. per grab.

To help further contextualise the responses observed at the compliance sites, notably in redox and sulphide, we explored the macrofaunal community data in more detail using multidimensional scaling (MDS) plots, K dominance plots and the AMBI benthic index.

The multidimensional scaling (MDS) plot shows the relationship between sites based on benthic community composition across the 2019 baseline, and three subsequent surveys conducted during farm production (Figure 4-30). Most of the compliance sites and several control sites across all surveys form a tight cluster at 60% similarity. A few of the baseline compliance sites and control site C1 from 2019 and 2020 sit just outside this group. Compliance site 1 and control site C2 from the 2021 survey are further removed, while control site C3 is dissimilar in each year; the different sediment particle size at this site

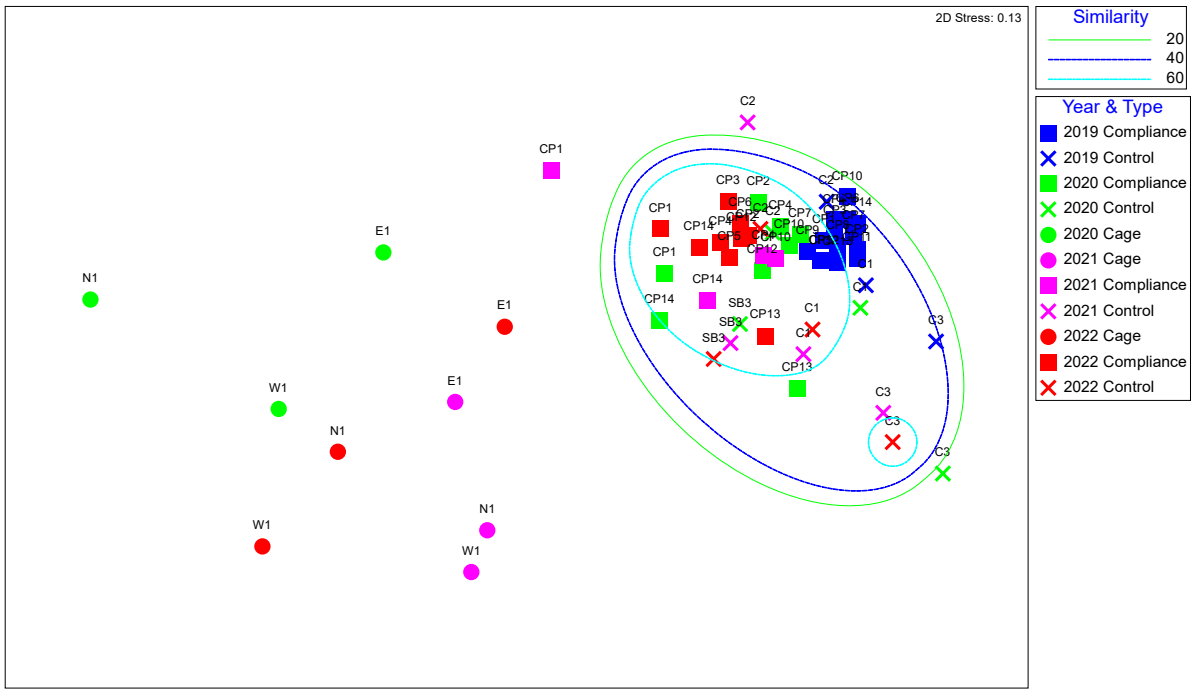


Figure 4-30: Results of non-metric multidimensional scaling analysis (nMDS; 2D stress = 0.13) using benthic infauna data collected at compliance, control, and cage sites in February 2019 (baseline) and during

production In March 2020, 2021, and 2022. Points represent averaged abundances three replicates at each site. The ellipses represent community similarity at levels of 20%, 40% and 60% based on cluster analysis.

suggests a somewhat different habitat may drive this dissimilarity (Appendix 4-1). An overall temporal trend is present, with a progressive shift seen at most compliance and control sites. Cage sites are the most dissimilar when compared to baseline conditions and are also home to the most variable communities between surveys.

Faunal dominance patterns as shown by K-dominance plots can be seen in Figure 4-31, comparing pooled family level data from comparable sites in the 2019 baseline, 2020, 2021 and 2022 surveys. Dominance was low at all sites in the baseline but ~70% of the community at control site C3 was made up of the three most abundant families and was a clear outlier. The homogeneity of dominance in the baseline allowed for change in this metric to be easily visualised. As expected, the cage sites in 2020 and 2022, and to a lesser extent in 2021 had high single-family dominance, owing to the large numbers of Capitellidae. In 2022, single family dominance increased at several of the compliance sites, notably those to the north of the lease (sites 1, 2 & 3). The levels of dominance (>55%) at these sites could be considered moderately impacted relative to baseline conditions (Clarke & Gorley 2015).

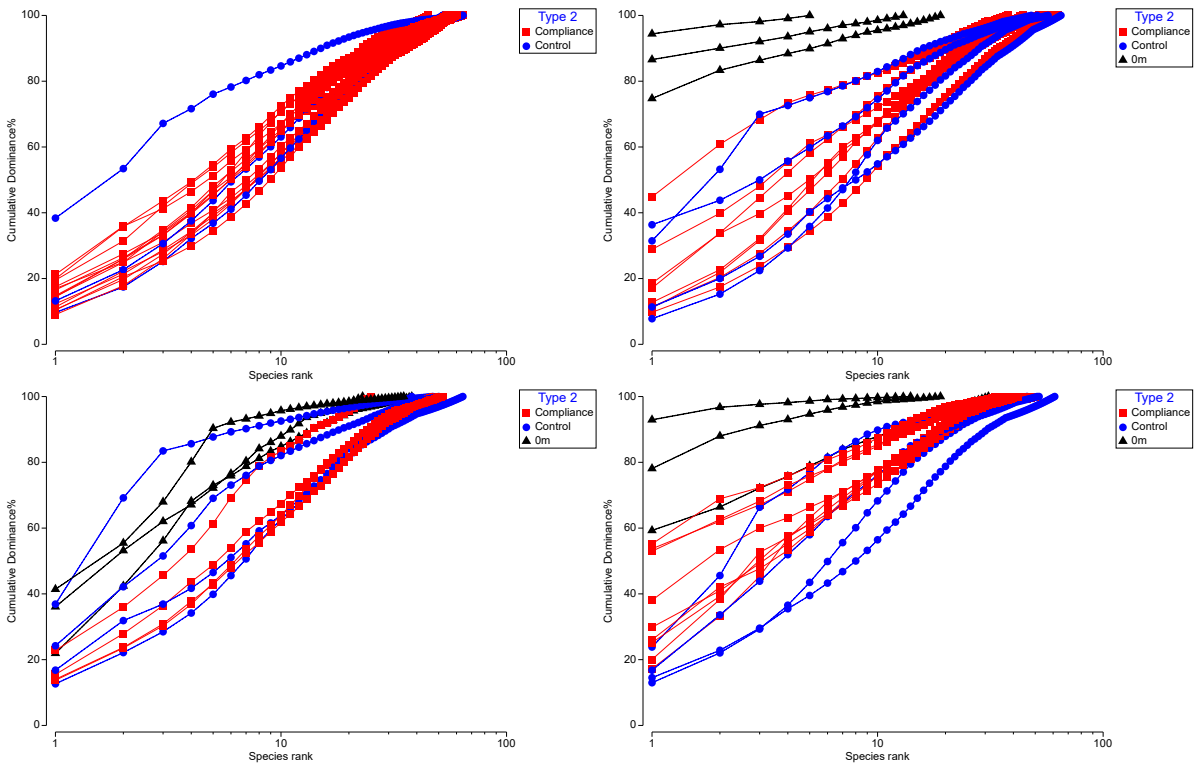


Figure 4-31: Results of k-dominance analysis at MF281 from all compliance, control, and cage sites in February 2019 (top left) and during production in March 2020 (top right), 2021(bottom left), and 2022 (bottom right).

AMBI classified all sites in the baseline survey as slightly disturbed (Figure 4-32). The mean AMBI score was greater at the compliance sites compared to the control sites in each of the three peak production surveys yet remained in the slightly disturbed classification (Figure 4-32). Mean AMBI at control sites remained relatively unchanged across all four surveys and

were all slightly disturbed. Cage sites were the most disturbed (moderate – heavily disturbed) in all three surveys, although this was not as pronounced in 2021.

The additional community analysis outlined above supports the evidence provided by redox and sulphide data that there has been an impact since farming began, albeit relatively minor, at some compliance sites (particularly to the north of the lease) at Yellow Bluff.

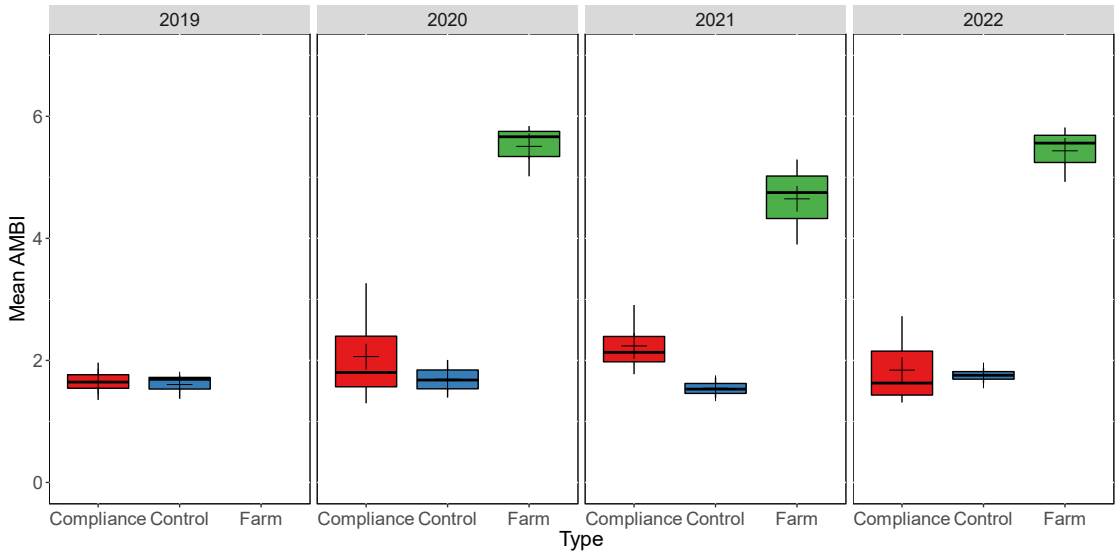


Figure 4-32: Boxplots comparing AMBI in grab samples at compliance, control and farm sites in February 2019 (baseline) and during production In March 2020, 2021, and 2022. Boxes represent the interquartile range (IQR; 25th - 75th percentile), the median (internal line) and the mean (cross). Whiskers (vertical lines) extend to the maximum and minimum values closest to 1.5 times IQR and points beyond this are considered outliers and plotted with site labels.

West of Wedge

Physico-chemical parameters

There was no evidence across the two surveys conducted around peak production that either sediment redox or sulphide at compliance sites was affected by farming. Redox and sulphide measured directly adjacent to the cages where impacts are likely to be the greatest provide important context.

Relative to baseline reference conditions, sediment redox was higher at both compliance and control sites in January and December 2021 (Figure 4-33). It was also higher at cage sites in January 2021 before decreasing notably in December. The difference between compliance and control site redox was negligible in the 2019 baseline survey, a trend repeated in January 2021 but not in December, where low redox values at control site C1 brought the control group average down. When extra experimental control sites NUB-4 and SB-16 were included, the variance created by C1 was reduced and comparisons between compliance and control sites can be more readily made (Figure 4-34). Redox at farm sites in January was only slightly lower than compliance and control sites. However, in December, redox at cage sites was much lower than at compliance and control sites, an expected result considering the increased intensity of farming over this period.

Sulphides at compliance sites increased between 2019 and January 2021 but decreased again by December 2021 (Figure 4-34). The inverse pattern was observed at control sites; however, this does not appear to be an indication of a farm effect, more so large variability at control sites between years. As with redox measurements, sulphide concentration at control site C1 was high in 2019 and December 2021, inflating the group average. This occurrence highlights the problems of a small set of control sites (two in this instance), particularly when large amounts of natural variation are observed. When extra experimental control sites NUB-4 and SB-16 are included, the variance created by C1 in December 2021 is reduced and comparisons between compliance and control sites can be more readily made (Figure 4-34). The highest sulphide levels were observed at farm sites in both January and December 2021.

With respect to the Environmental Licence conditions[5] for redox and sulphide, no significant differences were observed between control and compliance sites in either survey and there were no individual cores at compliance sites with a redox <0 mV or sulphide >250 µM.

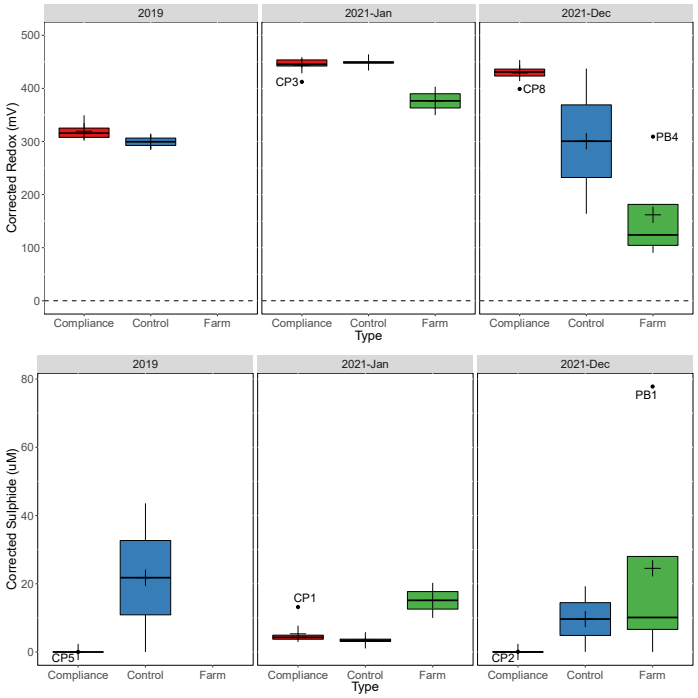


Figure 4-33: Boxplots comparing corrected redox (mV) and sulphide (uM) at West of Wedge compliance, control and farm sites in the March 2019 (baseline) and during production in January and December 2021. Boxes represent the interquartile range (IQR; 25th - 75th percentile), the median (internal line) and the mean (cross). Whiskers (vertical lines) extend to the maximum and minimum values closest to 1.5 times IQR and points beyond this are considered outliers and plotted with site labels.

[5] The same interpretations outlined above for Yellow Bluff are applied for West of Wedge

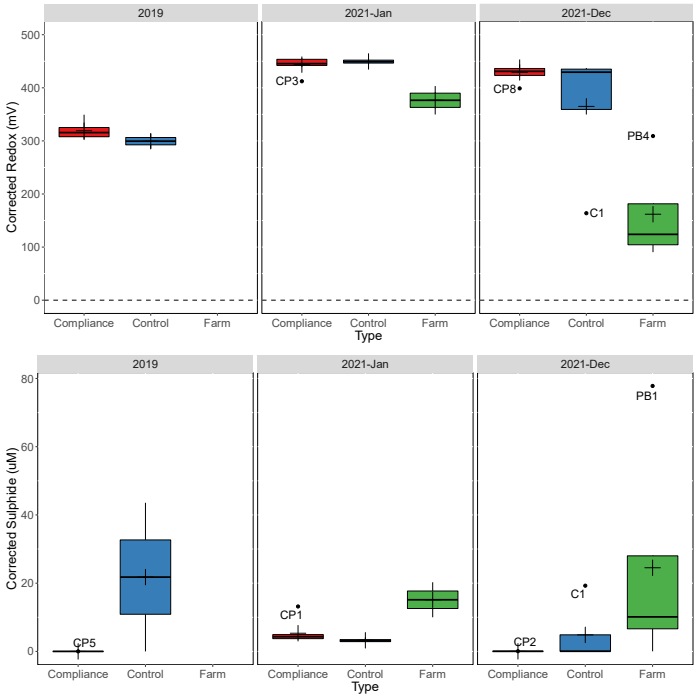


Figure 4-34: Boxplots comparing corrected redox (mV) and sulphide (uM) at West of Wedge compliance, control and farm sites in the March 2019 (baseline) and during production in January and December 2021. These plots include experimental control sites NUB-4 and SB-16. Boxes represent the interquartile range (IQR; 25th - 75th percentile), the median (internal line) and the mean (cross). Whiskers (vertical lines) extend to the maximum and minimum values closest to 1.5 times IQR and points beyond this are considered outliers and plotted with site labels.

Biological parameters

There was no evidence that the number of families at compliance sites was affected by farming in the January and December 2021 surveys; for context, there was also no decrease in family richness observed at the cage sites. Relative to baseline reference conditions, the number of families was similar at the compliance sites and slightly higher at control sites in January 2021. In December 2021, it appears regional level change occurred (see section 4.2), with the number of families decreasing across all sites, including under cages.

Total abundance and the number of annelids followed a similar trend to the number of families. However, they were both higher at cage sites than compliance and controls in January 2021 and December 2021. Increased abundance in *Capitella sp.* at a single cage site (PB1a) was responsible for the large variance in January 2021. No increase in *Capitella sp.* on this scale was seen in December 2021, highlighting inconsistent spatial impacts of farming, particularly early in the life of a new lease.

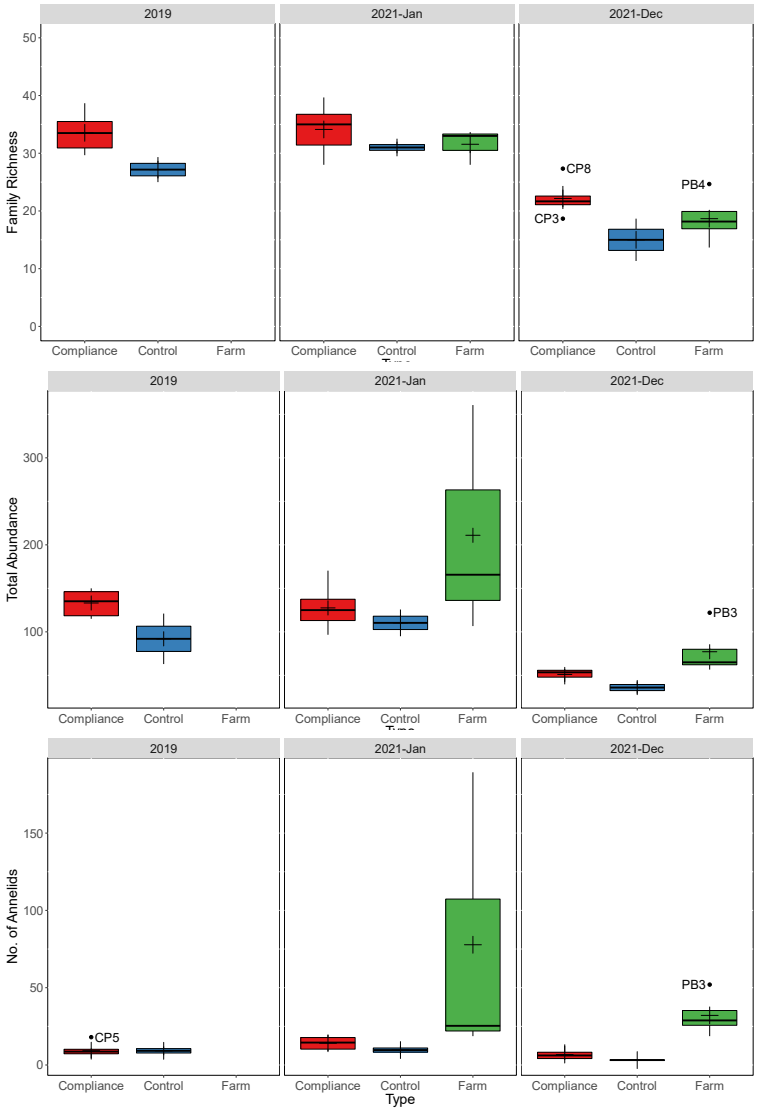


Figure 4-35: Boxplots comparing the family richness (top panel), total abundance (middle panel) and number of annelids (bottom panel) in grab samples at West of Wedge compliance, control and farm sites in the March 2019 (baseline) and during production In January and December 2021. Boxes represent the interquartile range (IQR; 25th - 75th percentile), the median (internal line) and the mean (cross). Whiskers (vertical lines) extend to the maximum and minimum values closest to 1.5 times IQR and points beyond this are considered outliers and plotted with site labels.

With respect to the Environmental Licence conditions for biological parameters there was no evidence that any of the conditions that stipulate a significant impact were met. Importantly, an abundant and diverse fauna was observed at all compliance sites, where the number of families ranged from 30-62 per site and total abundance ranged from 29-208 indiv. per grab. At control sites the number of families ranged from 22-54 per site and total abundance ranged from 21-142 indiv. per grab.

4.2 Broad-scale

The broad-scale sediment survey requirements are defined in the Environmental Licences. Collectively, the Environmental Licences include sites spanning the entire Storm Bay region (Figure 4-36). Sediment conditions at each site were assessed from grab sample measurements of sediment chemistry and faunal communities. At present there are no defined performance measures for the broad-scale soft sediment environment. For the purposes of this study,, we have assessed performance more generally based on the extensive knowledge in Tasmania gained from local-scale assessments of benthic responses to enrichment. Importantly, this includes knowledge gained for the Storm Bay environment in the current study (section 4.1) and the recently completely FRDC report (Ross et al. 2021).

The objective of the sampling was to assess the broad-scale spatial and temporal dynamics of Storm Bay soft sediment habitats and potential interactions with farming, allowing for an evaluation of the prescribed monitoring design and assessment criteria.

4.2.1 Design

The broadscale benthic sediment surveys are conducted annually in spring at the 23 sites across Storm Bay (Table 4-5) identified in the current Environmental Licences; most of these sites overlap with the water column sampling sites. The survey requirements including the sites, methodologies and reporting guidelines are described in section 3F2 of the respective Environmental Licences.

At each site, the benthic sediment survey components included benthic biota (infauna and bacteria/algal mat identification), sediment chemistry (redox potential, sulphide concentration and stable isotope analysis), sediment core descriptions (Munsell chart) and particle size analysis. Benthic macrofauna were sampled in triplicate using a Van Veen Grab (surface area 0.0675 m2). All samples were sieved to 1 mm, and the fauna identified to the lowest possible taxonomic resolution and counted. Sediment cores (250 mm long, 45 mm internal diameter) were collected to evaluate sediment sulphide, redox, particle size, organic carbon and nitrogen content and their isotopic composition (δ15N, δ13C). A visual assessment was also made of each core, including measurement of core length, sediment colour (using a Munsell soil chart), assessment of plant/animal life, gas vesicles and smell (indicating presence/absence of hydrogen sulphide). The methods of collection and analysis were as per those outlined in the environmental licence conditions and MacLeod and Forbes (2004). At each site, dissolved oxygen, temperature, salinity, turbidity, florescence, and pH were also measured within 1 m of the seabed (at each site using a SONDE [YSI EXO2])

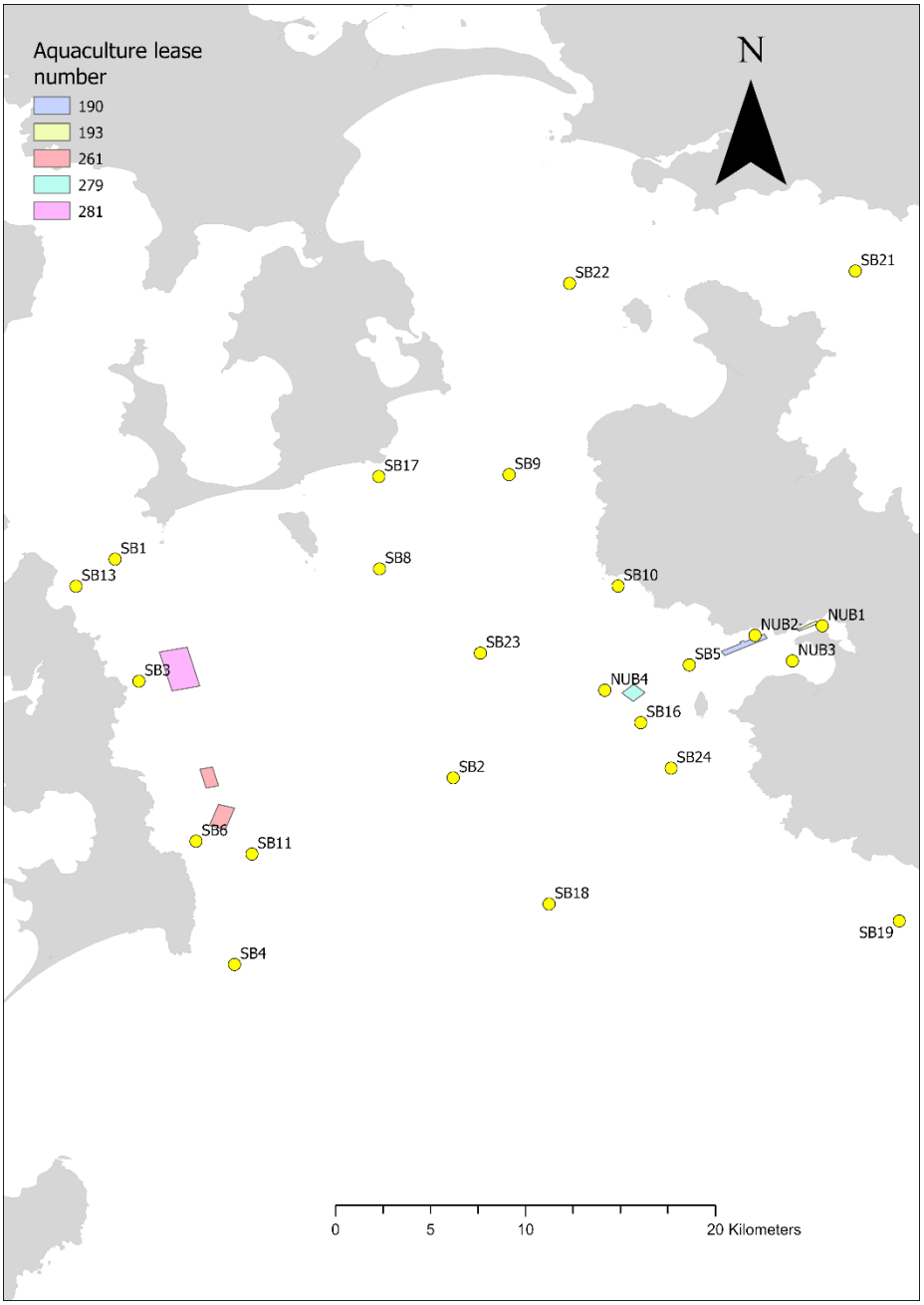


Figure 4-36: Map showing locations of the broad-scale soft-sediment sites surveyed in Spring 2019, 2020 and 2021. Active marine farm leases are depicted as coloured rectangles.

Table 4-5: Details of sites surveyed in Storm Bay in Spring 2019, 2020 and 2021. Samples at all sites were analysed for benthic infauna, redox potential, sulphide concentration, particle size distribution, organic matter content (LOI), elemental carbon and nitrogen content, stable isotopes. A description of visual characteristics using ROV/drop camera and core descriptions was also undertaken.

Site	Location	Depth (m)	Dates
SB-1	South West of Iron Pot	17	Spring 2019, 2020, 2021
SB-2	Mid Storm Bay	49	Spring 2019, 2020, 2021
SB-3	Near Yellow Bluff	23	Spring 2019, 2020, 2021
SB-4	South East of Cape Queen Elizabeth	51	Spring 2019, 2020, 2021
SB-5	North of Wedge Island	33	Spring 2019, 2020, 2021
SB-6	East of Variety Bay	37	Spring 2019, 2020, 2021
SB-8	South East of Betsey Island	30	Spring 2019, 2020, 2021
SB-9	South West of North West Head	22	Spring 2019, 2020, 2021
SB-10	South of Outer North Head	22	Spring 2019, 2020, 2021
SB-11	East of Variety Point	44	Spring 2019, 2020, 2021
SB-13	off Bull Bay	17	Spring 2019, 2020, 2021
SB-16	South east corner of west of Wedge zone	45	Spring 2019, 2020, 2021
SB-17	South of Cape Contrariety	19	Spring 2019, 2020, 2021
SB-18	Mid southern Storm Bay	65	Spring 2019, 2020, 2021
SB-19	West of cape Raoul	64	Spring 2019, 2020, 2021
SB-21	Norfolk Bay	10	Spring 2019, 2020, 2021
SB-22	Fredrick Henry Bay	23	Spring 2019, 2020, 2021
SB-23	East of Petuna lease	39	Spring 2019, 2020, 2021
SB-24	West of Tumbledown point	50	Spring 2019, 2020, 2021
NUB-1	Nubeena (NUB 1)	17	Spring 2019, 2020, 2021
NUB-2	Nubeena (NUB 2)	17	Spring 2019, 2020, 2021
NUB-3	Nubeena (NUB 3)	18	Spring 2019, 2020, 2021
NUB-4	Nubeena (NUB 4)	43	Spring 2019, 2020, 2021

4.2.2 Spatial and temporal variation in key parameters

Storm Bay is a complex and large system that is home to a wide variety of soft sediment habitats. The influence of ocean currents, waves, river flows and other terrestrial inputs on the sediment environment varies across the different geographical areas of the bay. Local characteristics such as depth, sediment particle size composition (e.g., silt content) and organic matter availability, in turn influence the unique macrofaunal communities. Because of this natural variation, identifying system-wide trends in benthic communities and sediment chemistry is inherently difficult.

Sediment properties

Sites sampled in Storm Bay cover a wide variety of depths (10-65 m). Fine sand is the dominant sediment type with small amounts of coarse sand, silt, and gravel present (Figure 4-37). Sites in the south-east region of Storm Bay (SB-2, SB-16, SB-18, SB-23 & SB-24) have higher proportions of coarse sand which likely reflects greater exposure, while the two shallower and more sheltered sites, SB-21 & NUB-1 contained more silt than others. Over the three years of surveys there was very little change in particle size distribution.

Redox potential of the sediments across Storm Bay was on average high (>350 mV) across all three surveys, and similarly sulphide concentrations were low (<10 µM; Figure 4-39). However, significant spatial and, to a much lesser extent, temporal variability is also evident (Figure 4-38Figure 4-41). This appears to reflect differences in hydrography and the concomitant changes in the physical sediment characteristics. Lower redox and higher sulphide values were typically measured at sites which were in shallower, more sheltered areas with higher silt content (e.g., NUB 1-3 and SB-21), a phenomenon seen in similar large systems such as the D'Entrecasteaux Channel (Aquenal 2011). Interestingly, two of the shallower coastal sites that were near inshore reefs, SB-3 and SB-17 also had relatively low redox. Variability between replicate cores for both redox and sulphide was also notable, and this was often at the more coastal or sheltered sites. Variability at this scale is not uncommon and it likely reflects the patchy distribution and breakdown of organic matter that has accumulated in the sediment, often observed as small black sand patches in visual assessments. Because of this variability, replication at this scale is important.

Organic carbon and nitrogen content in sediments was low and typical of a more oceanic and sandier sediment environment (Figure 4-39 & 42). Consistent with the patterns observed for sediment particle size, redox and sulphide, the two shallower and more sheltered sites with a higher silt content, SB-21 & NUB-1, had the highest sediment carbon and nitrogen content, and to a lesser extent, NUB-2 and NUB-3. Sediment nitrogen and, to a lesser extent, carbon also appear to be marginally higher at the sites on the western side of Storm Bay along the Bruny coastline.

On a system-wide level, no clear and significant temporal trends were observed in redox, sulphide, or sediment carbon and nitrogen content. However, the carbon and nitrogen isotopic signatures varied across the three years, most notably in 2021 (Figure 4-40). The mean $\delta^{15}N$ signature of the sediments for all sites combined was lower in 2021 compared to 2020 and 2019 (4.7, 6.5 and 7.2‰, respectively) and the mean $\delta^{13}C$ signature was greater in 2021 compared to 2020 and 2019 (-20.5, -21.3 and -21.5‰, respectively). Both trends indicate a stronger marine origin in 2021 as the source of organic material to the sediments, the only exception being NUB-1 (close to Nubeena township), where $\delta^{13}C$ became depleted over time, suggesting a greater terrestrial influence.

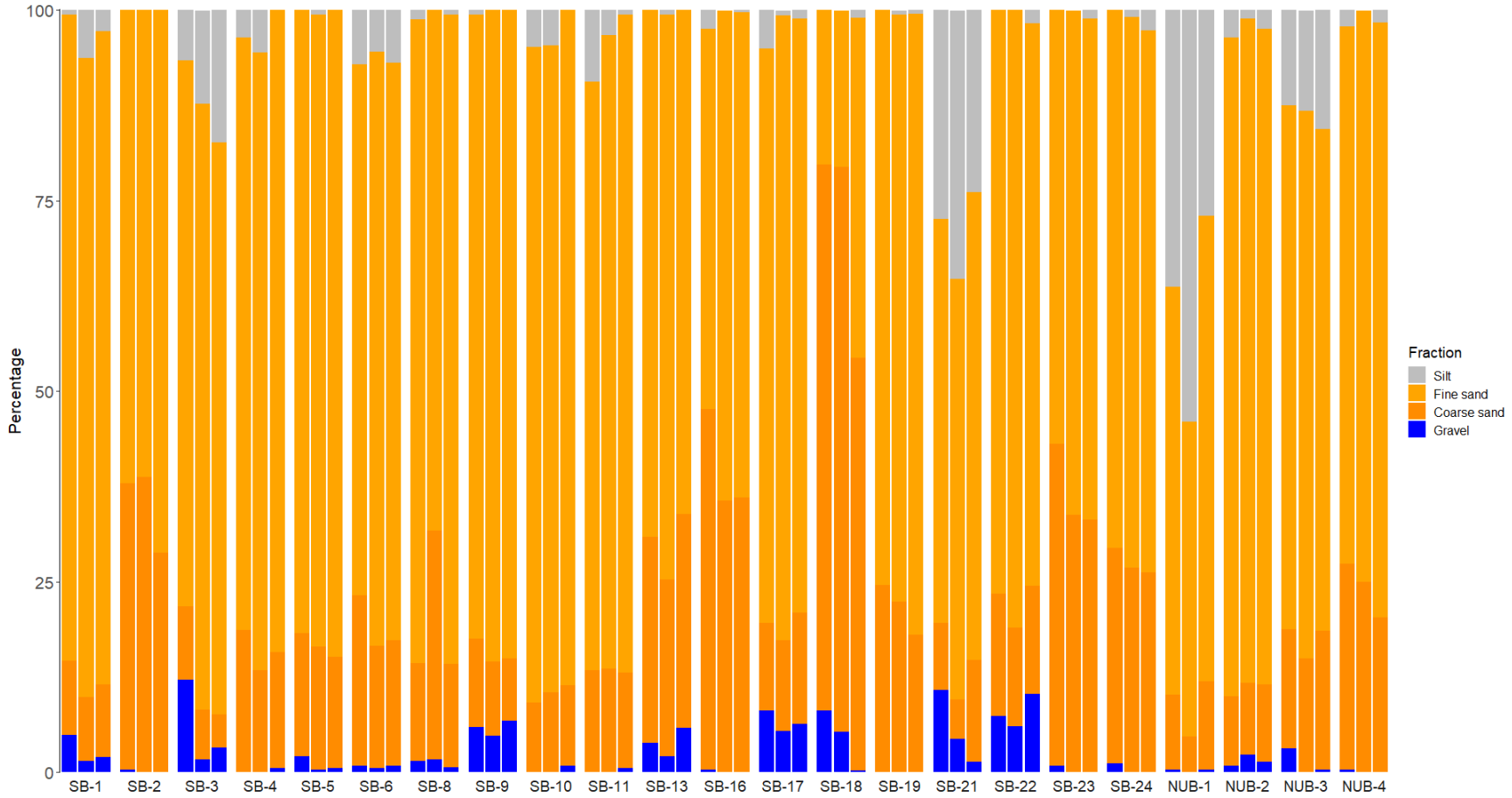


Figure 4-37: Spatial and temporal variation in the percentage (mean) of gravel (>2 mm), coarse sand (<2 mm to >0.25 mm), fine sand (<0.25 to 0.063 mm) and silt (<0.063 mm) for 23 sites in Storm Bay for sediments collected in 2019 (left bar for each site), 2020 (middle bar for each site) and 2021 (right bar for each site).

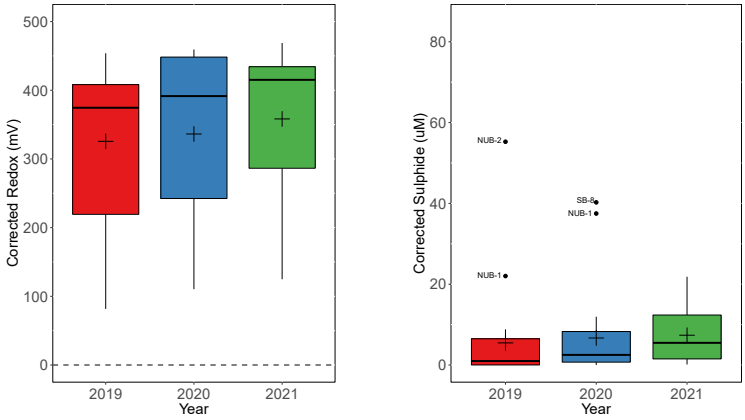


Figure 4-38: Boxplots comparing corrected redox (mV) and sulphide (uM) in Storm Bay sediments across 2019, 2020 and 2021 broadscale surveys. Boxes represent the interquartile range (IQR; 25th - 75th percentile), the median (internal line) and the mean (cross). Whiskers (vertical lines) extend to the maximum and minimum values closest to 1.5 times IQR and points beyond this are considered outliers and plotted with site labels.

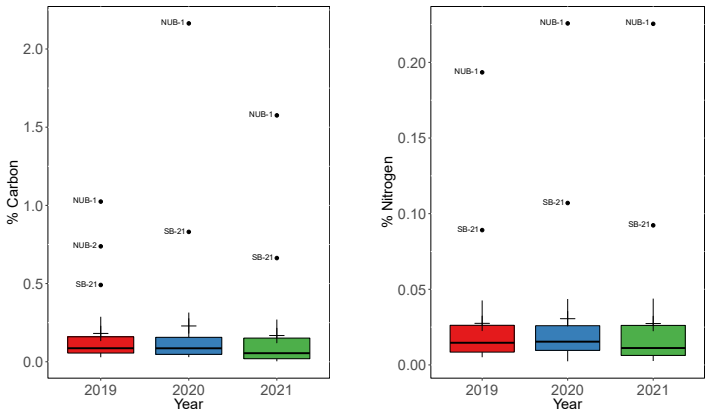


Figure 4-39: Boxplots comparing sediment organic carbon and nitrogen content (%) in Storm Bay sediments across 2019, 2020 and 2021 broadscale surveys. Boxes represent the interquartile range (IQR; 25th - 75th percentile), the median (internal line) and the mean (cross). Whiskers (vertical lines) extend to the maximum and minimum values closest to 1.5 times IQR and points beyond this are considered outliers and plotted with site labels.

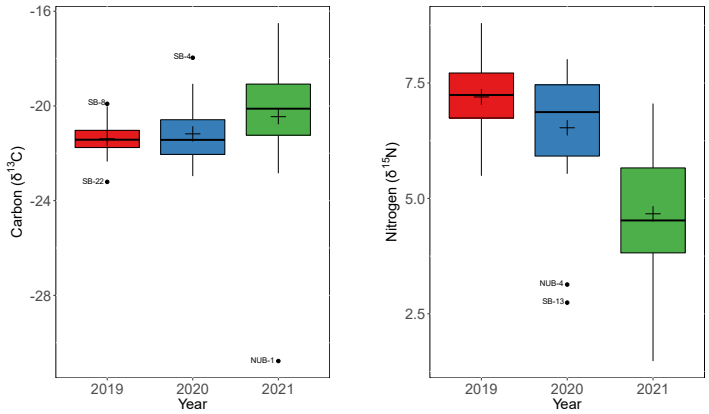


Figure 4-40: Boxplots comparing carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) stable isotope values sediment organic carbon and nitrogen content (%) in Storm Bay sediments across 2019, 2020 and 2021 broadscale surveys. Boxes represent the interquartile range (IQR; 25th – 75th percentile), the median (internal line) and the mean (cross). Whiskers (vertical lines) extend to the maximum and minimum values closest to 1.5 times IQR and points beyond this are considered outliers and plotted with site labels.

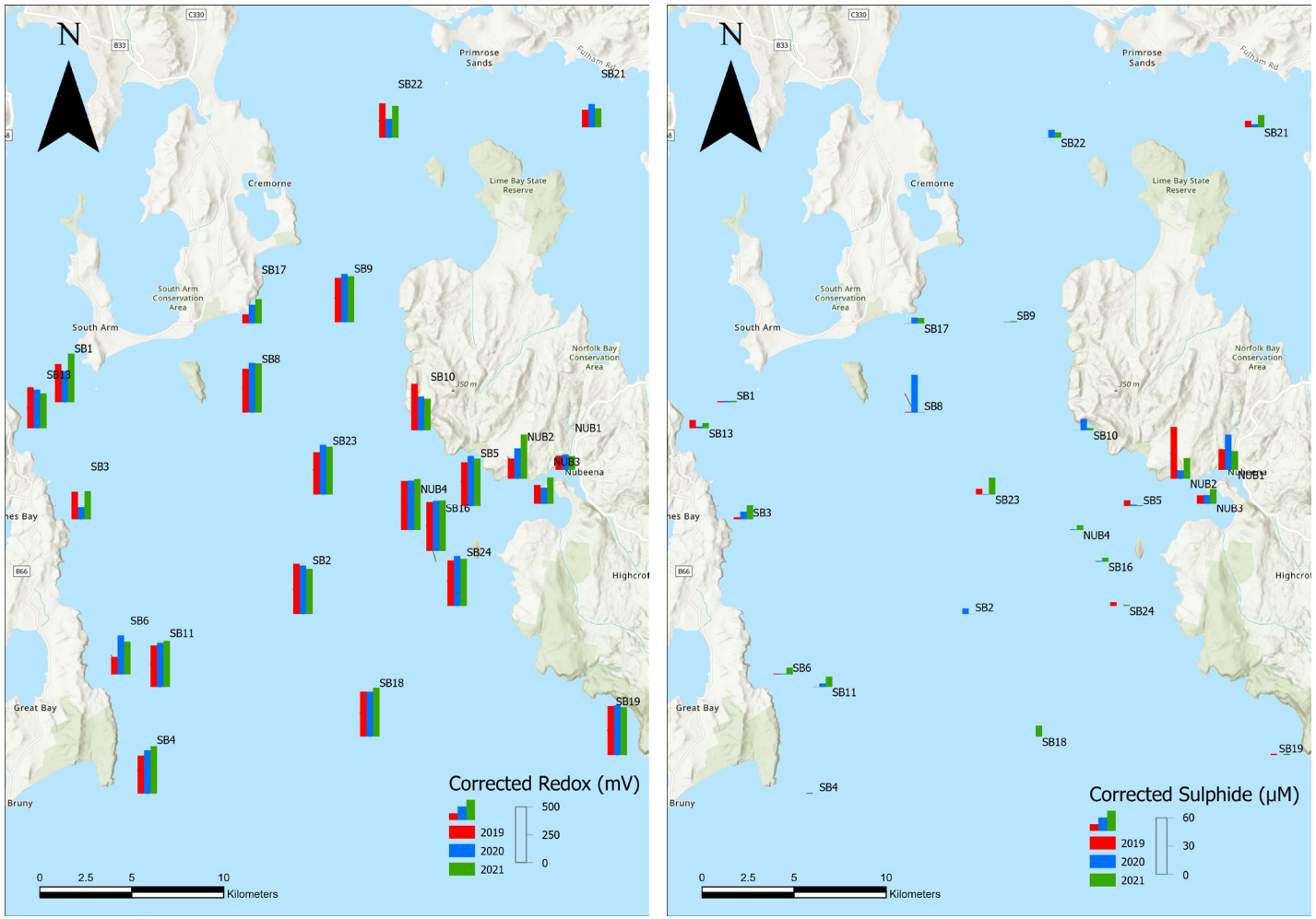


Figure 4-41: Maps showing the spatial and temporal variation in sediment redox (mV) and sulphide (uM) by survey across Storm Bay. Red bars represent 2019, blue bars represent 2020 and green bars represent 2021.

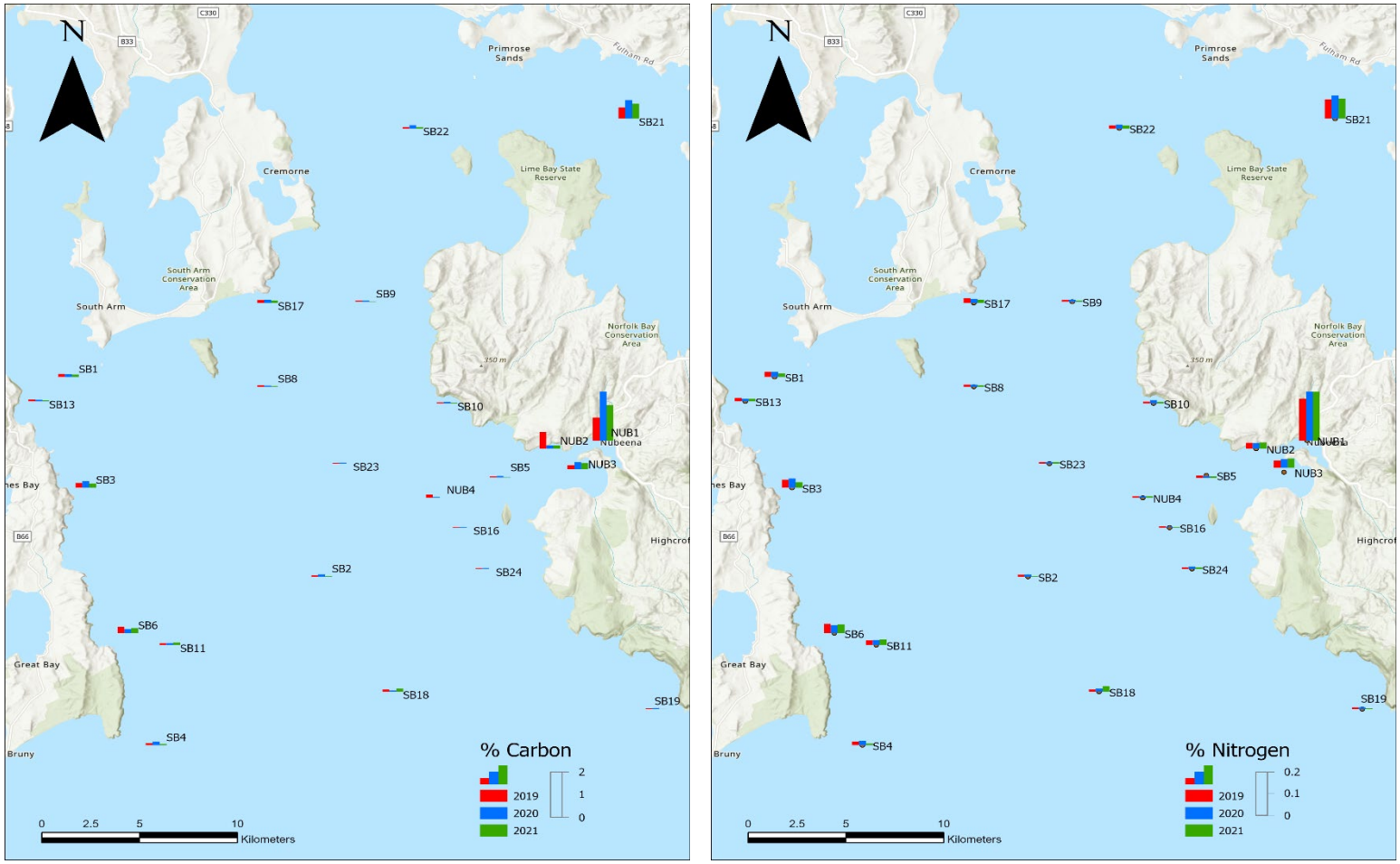


Figure 4-42: Maps showing the spatial and temporal variation in the carbon and nitrogen content (%) in sediments by survey across Storm Bay. Red bars represent 2019, blue bars represent 2020 and green bars represent 2021

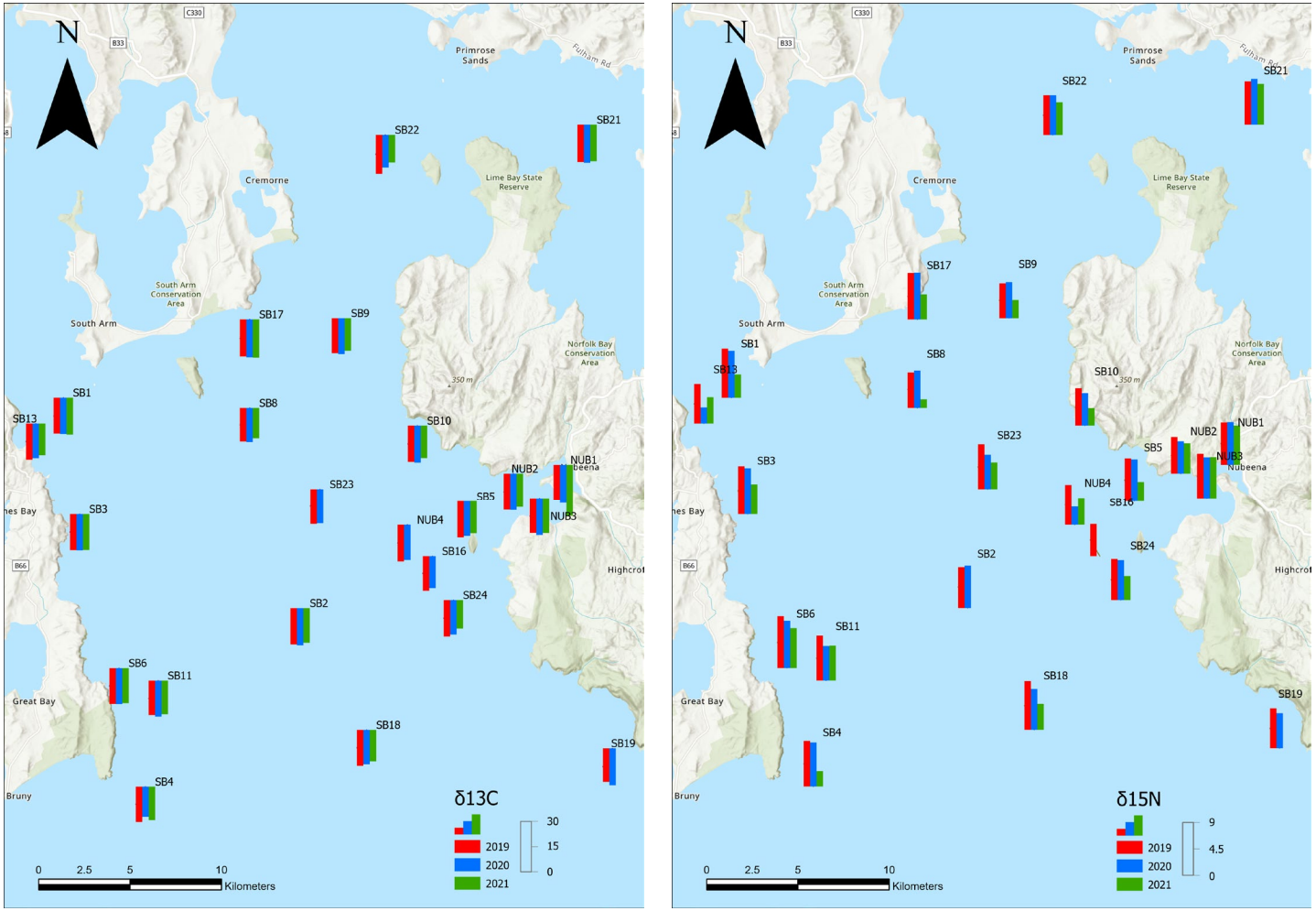


Figure 4-43:Maps showing the spatial and temporal variation in the carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) stable isotopes in sediments by survey across Storm Bay. Red bars represent 2019, blue bars represent 2020 and green bars represent 2021.

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Benthic communities

Across the three surveys, 20,312 individuals, comprising 438 species among 193 families, were collected from 207 grab samples. Crustaceans were the most abundant group making up 61% of samples. Annelids were the second most abundant group (25%), then molluscs (9%), echinoderms (3%) and other taxa (2%, e.g., nemerteans, sipunculan worms and tunicates). Sediments were dominated by the arthropod families Aoridae, Bodotriidae, Phoxocephalidae and Philomedidae, the annelid families Spionidae, Lumbrineridae and Trichobranchidae, the molluscan families Cardiidae, Verneridae and Anabathridae, and the echinoderm families Ophiuridae and Loveniidae.

Benthic communities appeared relatively similar across 2019 and 2020 but changed markedly in 2021. A decrease in total abundance, family richness and species diversity were observed at most sites (Figure 4-44, 45 & 46). Sites in areas less exposed to the oceanic influence from the south-west appeared more insulated from this change, particularly those in embayments such as SB-21 in Norfolk Bay and some sites in the northern portion of Storm Bay such as SB-3, SB-8, SB-9 and SB-13. Sites that changed the most were in the relatively exposed, deep and sandy regions of Storm Bay, particularly in the south-east quadrant. In 2021, sediment carbon and nitrogen content and $\delta^{15}N$ were depleted relative to the previous two years, and $\delta^{13}C$ was more elevated. This suggests that a change in the source and/or amount of organic matter may help explain the shift in benthic community in 2021 and the decline in abundance and richness.

There were fewer annelids in 2021 compared to the 2020 and 2019 surveys (21, 36 and 29 indiv. per grab respectively; Figure 4-45). In 2021, annelids were most abundant at SB-21 and NUB-1 (121 and 116 ind. per grab respectively) and least abundant at SB-1 and SB-19 (0.7 ind. per grab; Figure 4-47). In 2021, the decrease in annelid abundance varied between sites; however, at a few sites (SB-4, SB-6, SB-11, SB-21 and SB-22) there was an increase (dependent on site and year).

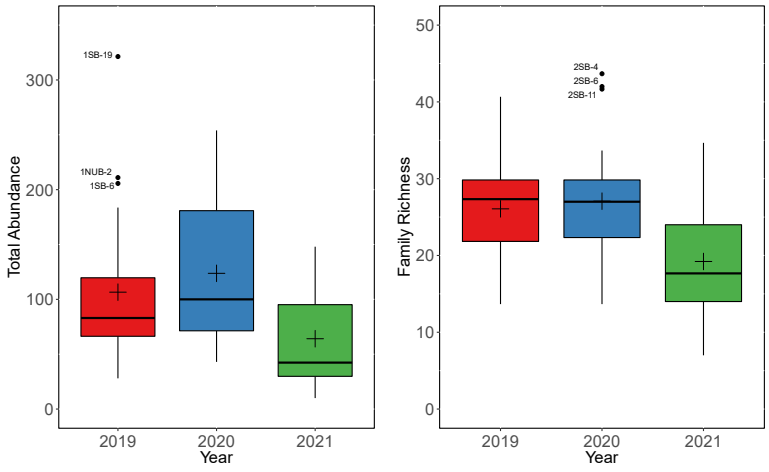

Figure 4-44: Boxplots comparing total abundance and family richness for Storm Bay across 2019, 2020 and 2021 broadscale surveys. Boxes represent the interquartile range (IQR; 25th - 75th percentile), the median (internal line) and the mean (cross). Whiskers (vertical lines) extend to the maximum and minimum values closest to 1.5 times IQR and points beyond this are considered outliers and plotted with site labels.

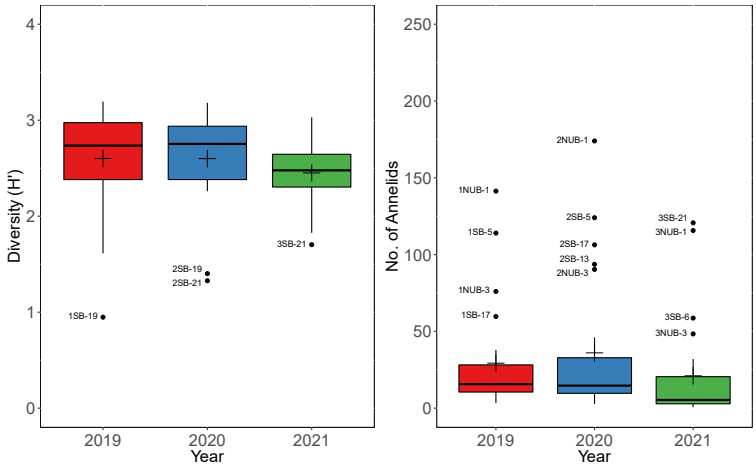

Figure 4-45: Boxplots comparing species diversity and the number of annelids for Storm Bay across 2019, 2020 and 2021 broadscale surveys. Boxes represent the interquartile range (IQR; 25th - 75th percentile), the median (internal line) and the mean (cross). Whiskers (vertical lines) extend to the maximum and minimum values closest to 1.5 times IQR and points beyond this are considered outliers and plotted with site labels.

The MDS plot shows several potential groupings of sites with similar macrofaunal assemblages based on their location in Storm Bay. The most distinct group includes site SB-21 in Norfolk Bay, and NUB-1 and NUB-3 in Nubeena, which are situated on the right of the plot (Figure 4-48). These sites are in more sheltered locations where the sediments are typically finer (e.g., a higher proportion of silt [<0.063 mm]) and more organically enriched (%C and %N) relative to the other, more exposed, sandier sites. The assemblages at these sites were categorised by higher abundances of annelids from the families Lumbrineridae, Eunicidae, Flabelligeridae, Polynoidae, Nephtyidae, Terebellidae, Trichobranchidae and Pectinariidae, the arthropod families Callianassida and Litocheiridae, and the ascidian family Ascidiidae (Figure 4-48).

The reduction in the number of families and total abundances in 2021 is highlighted in the MDS plot. Sites located in the central and eastern side of Storm Bay (SB-2, SB-5, SB-16, SB-17, SB-18, SB-19, SB-23, SB-24 and NUB-4), which had the greatest reductions in the number of families and abundances are positioned more to the left in the MDS in comparison to the 2020 and 2019 surveys (Figure 4-48). Although the greatest changes occurred in this region of Storm Bay, a reduction in the number of families and abundances was seen across the entire Bay except for a few coastal sites, which remained the same or had a slight increase. Regardless, temporal change is small relative to spatial variability and separation of sites, with site groupings remaining similar across the three years.

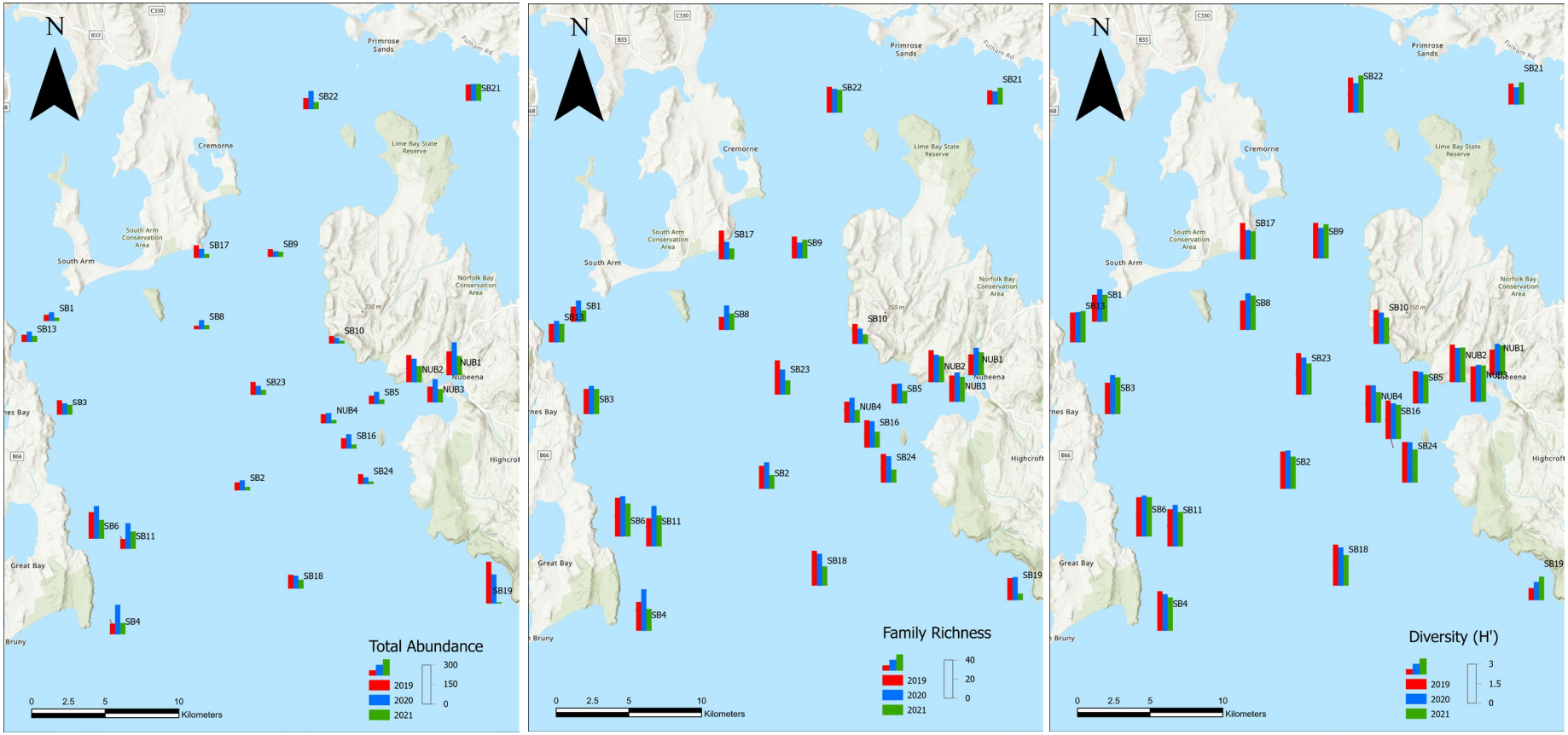

Figure 4-46: Maps showing the spatial and temporal variation in mean total abundance, family richness and diversity per grab by survey across Storm Bay. Red bars represent 2019, blue bars represent 2020 and green bars represent 2021.

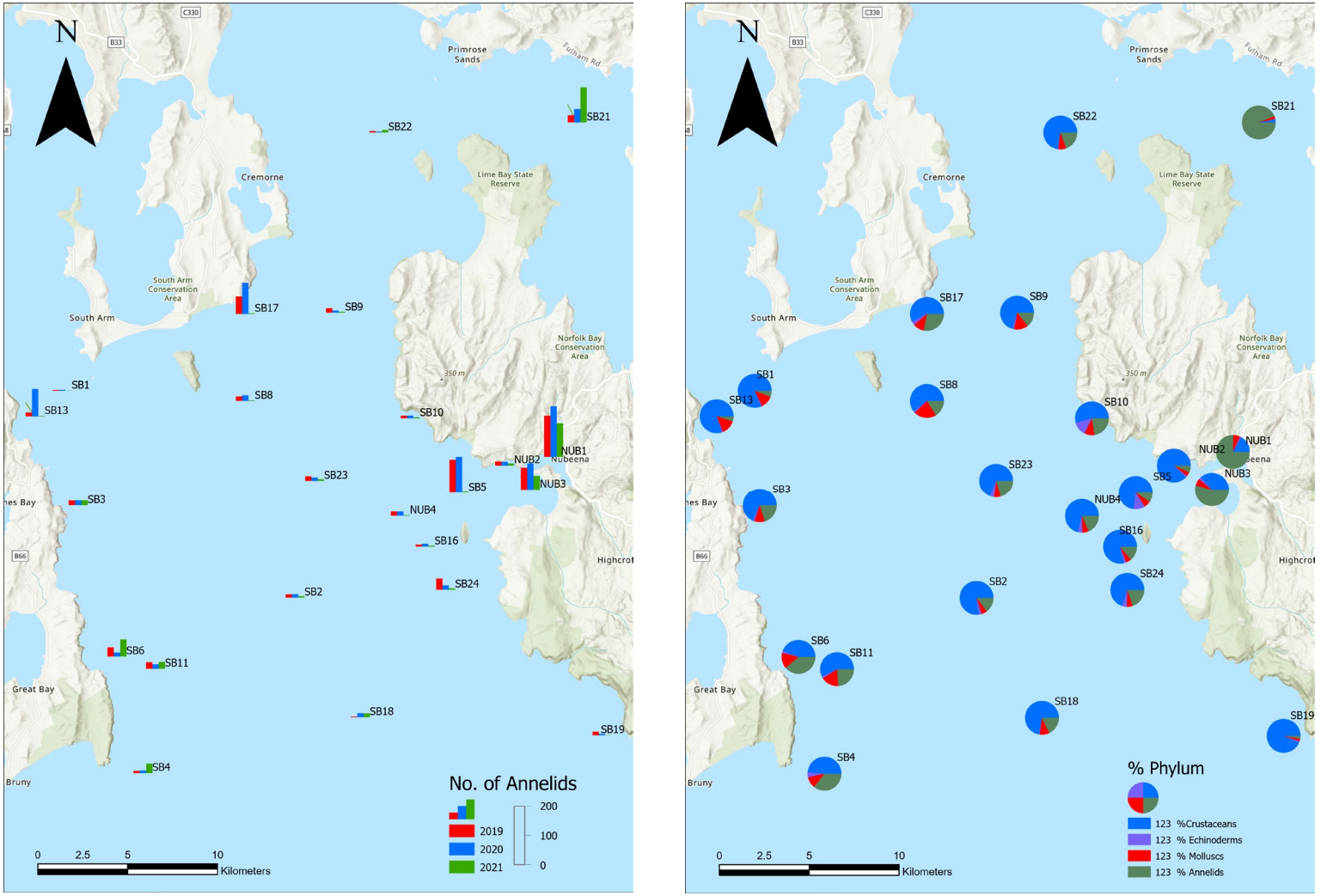

Figure 4-47: Maps showing the spatial variation in the composition of major phyla across Storm Bay. The left plot shows number of annelids and red bars represent 2019, blue bars represent 2020 and green bars represent 2021. The right plot shows pie charts representing percentage compositions of major phyla, crustaceans (blue), echinoderms (purple), molluscs (red) and annelids (green).

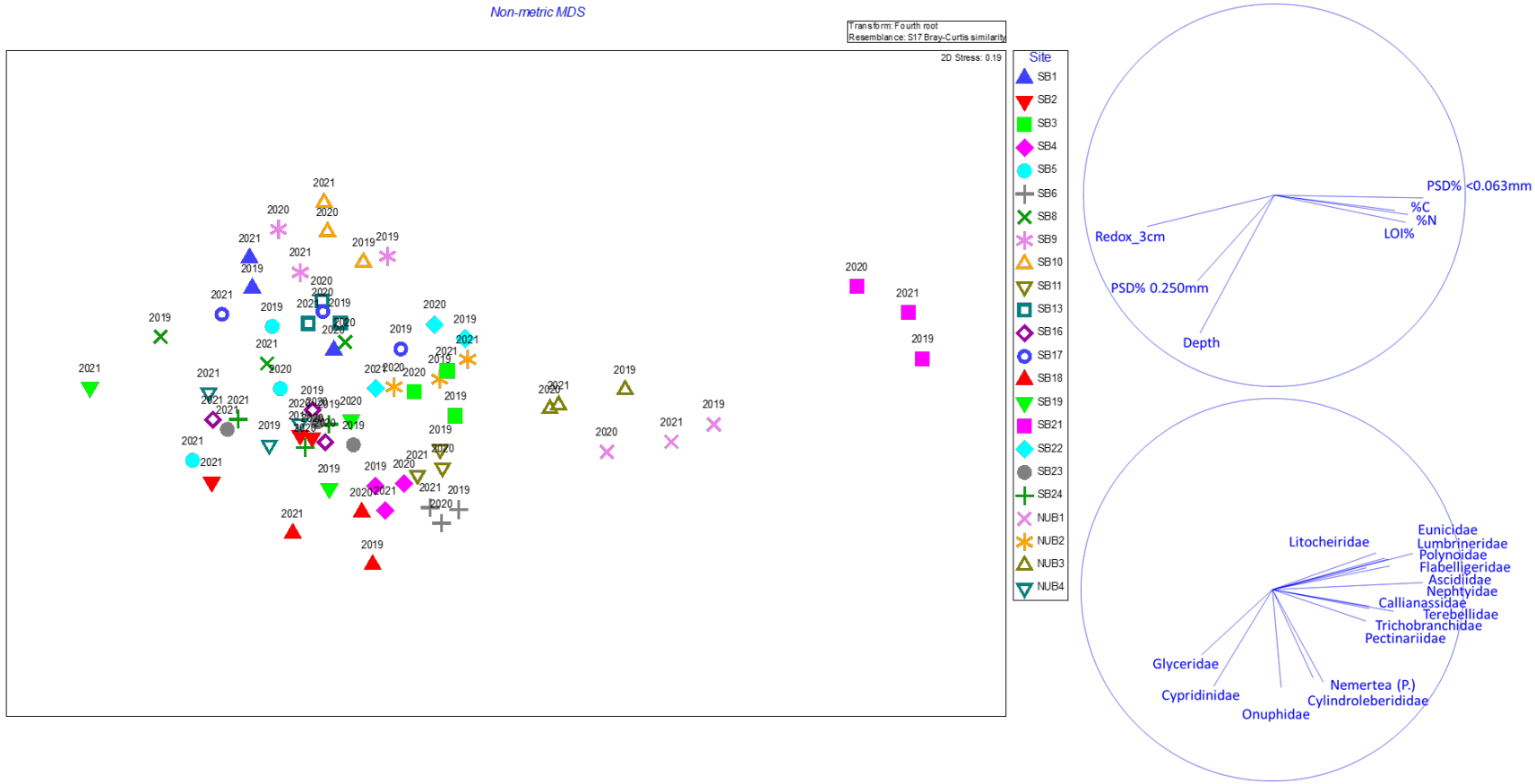

Figure 4-48: nMDS plot of the benthic invertebrate families (average per site) from the 23 sites in Storm Bay sampled in 2019, 2020 and 2021. Vectors indicate key families and environmental variables with a high correlation (>0.55) driving the separation of sites in two dimensions.

To further identify groups of sites that may represent different habitat regions in Storm Bay, two clustering methods were used. These groupings will help inform any potential recommendations to the spatial design of the broadscale sediment program. For example, groups based on macrofaunal communities could aid in the selection of a subset of sites representative of the different habitats across Storm Bay. Cluster analysis of macrofauna data averaged over the three surveys indicates the presence of 9-11 distinct communities. Non-hierarchical clustering by kR means resulted in 11 groups (SIMPROF = 0.002; Figure 4-49) and hierarchical clustering resulted in 9 groups (SIMPROF = 0.002; Figure 4-49). Although the significance values can be considered quite conservative, higher p values resulted in larger numbers of groupings that made less sense ecologically. Importantly, there was a high degree of consensus between the two clustering methods, with the only difference being kR clustering classified sites SB-9 and SB-22 as distinct communities, while hierarchical clustering grouped these sites with a larger northern group (i.e., with SB-1, SB-13 and SB-17). CAP analysis demonstrated both methods had correct classification of sites into groups of over 85%.

The largest of the groups, possessing six sites (red dots) was in the central and south-eastern region of Storm Bay (Figure 4-51). These sites are in a relatively deep, more exposed region of Storm Bay where the sediments are sandier, well oxygenated (i.e., higher redox) with low organic matter content (Figure 4-50). On the western side of Storm Bay, adjacent to northern Bruny Island, there was another distinct group of sites (green dots). These sites are in a region that is less exposed compared to the central and south-eastern group and tend to have a higher organic matter content, greater fine sand and silt fractions and less oxygenated sediments (Figure 4-50). The northern group (blue dots) was classified differently by the two clustering methods (SB-1, SB-13, SB-17 + (SB-9 and SB-22)) and these sites are all likely to be slightly more protected and less oceanic.

The group/s (orange symbols) which were the most distinct from the rest of the sites included sites in Nubeena (NUB-1 and NUB-3) and Norfolk Bay (SB-21; Figure 4-49). These sites are the most protected sites and are characterised by a high percentage of silt (particles <0.063 mm in size), increased organic enrichment (%N, %C and LOI) and low redox potential, and a higher proportion of annelids, compared to the rest of the sampling sites (Figure 4-50). Site NUB-2, which clusters on its own, is in a similar environment but is slightly less protected with a lower silt organic matter content and far fewer annelids in the macrofaunal community. Sites SB-5 and SB-10 are also quite distinct but are more like the oceanic sites in the central and south-eastern group. Interestingly there are far more echinoderms at these two sites relative to adjacent inshore and offshore groupings (Figure 4-47). The remaining two sites SB-18 and SB-19 were distinct from each other and all other groupings in both clustering methods. These are the furthest to the southeast and the deepest of all the sites (~64-65 m). Site SB-18 had the highest fraction of coarse sands and SB-19 had the most crustacean dominated community of all sites.

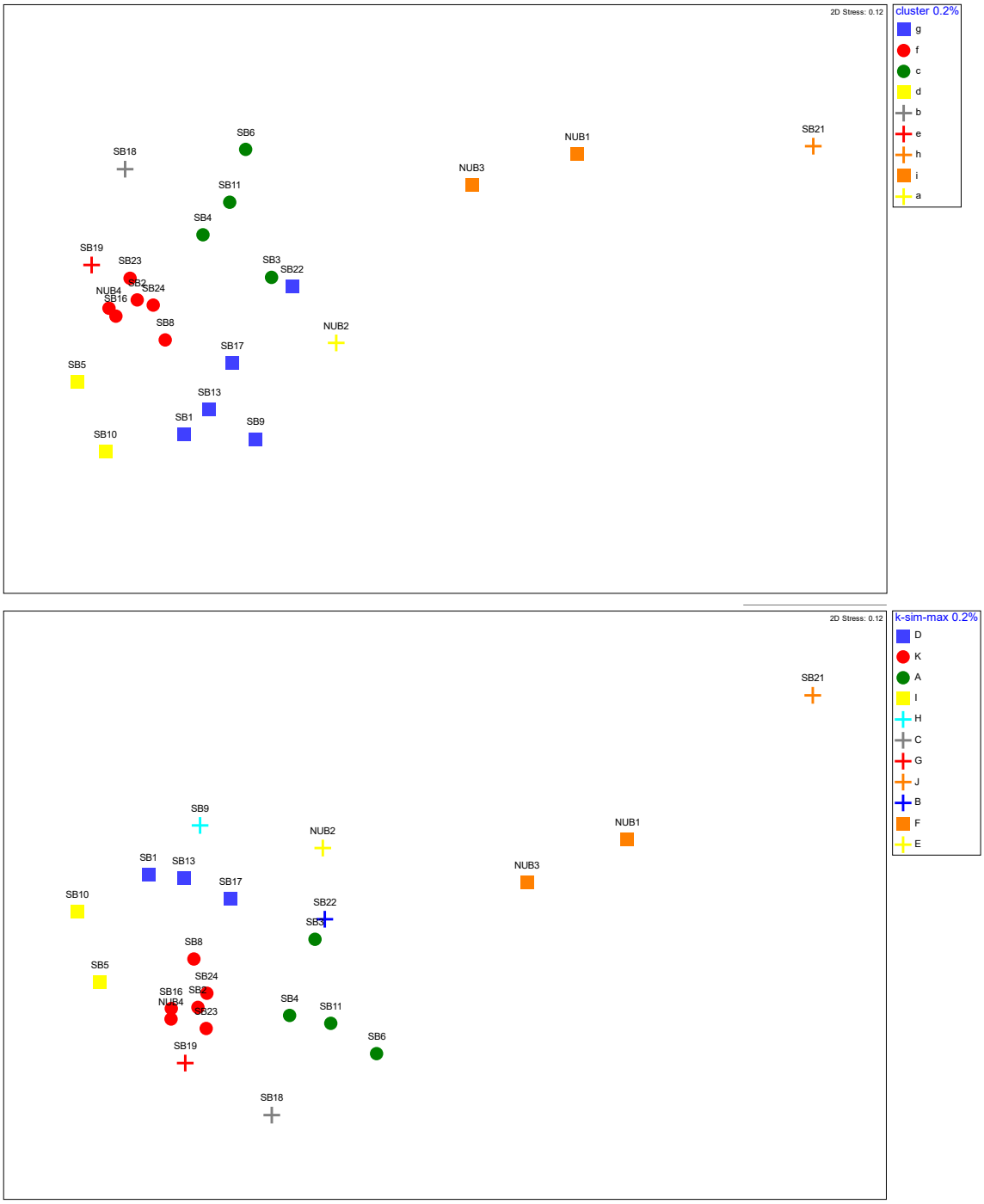

Figure 4-49: nMDS plot of the benthic invertebrate families (average per site) from the 23 sites in Storm Bay sampled in 2019, 2020 and 2021. Groupings represent hierarchical clusters (top panel) and kRClusters (bottom panel) both with a SIMPROF value of 0.002. Point colours/shapes represent unique sample groups.

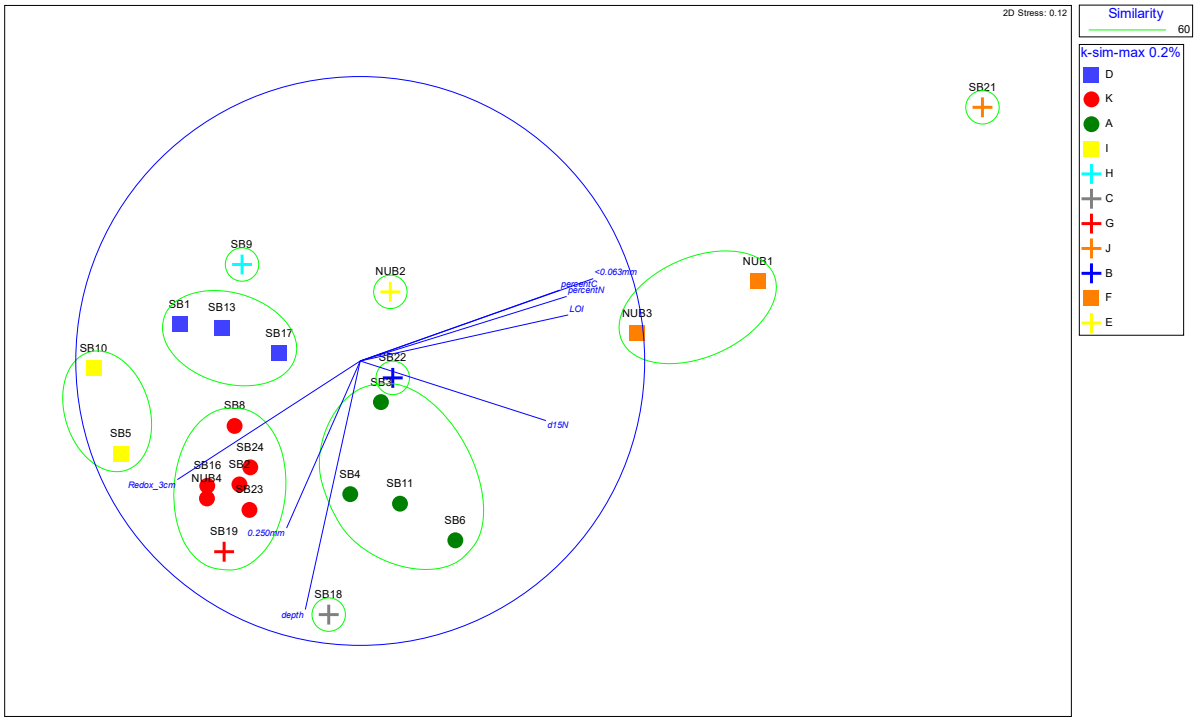

Figure 4-50: nMDS plot of the benthic invertebrate families (average per site) from the 23 sites in Storm Bay sampled in 2019, 2020 and 2021. Groupings represent kRClusters with a SIMPROF value of 0.002. The ellipses represent community similarity at 60% based on cluster analysis. Pearson's vector overlays of environmental variable contributing to ordination with a base variable comparison of >0.6 are included. The length of the vectors indicates the strength of the correlation

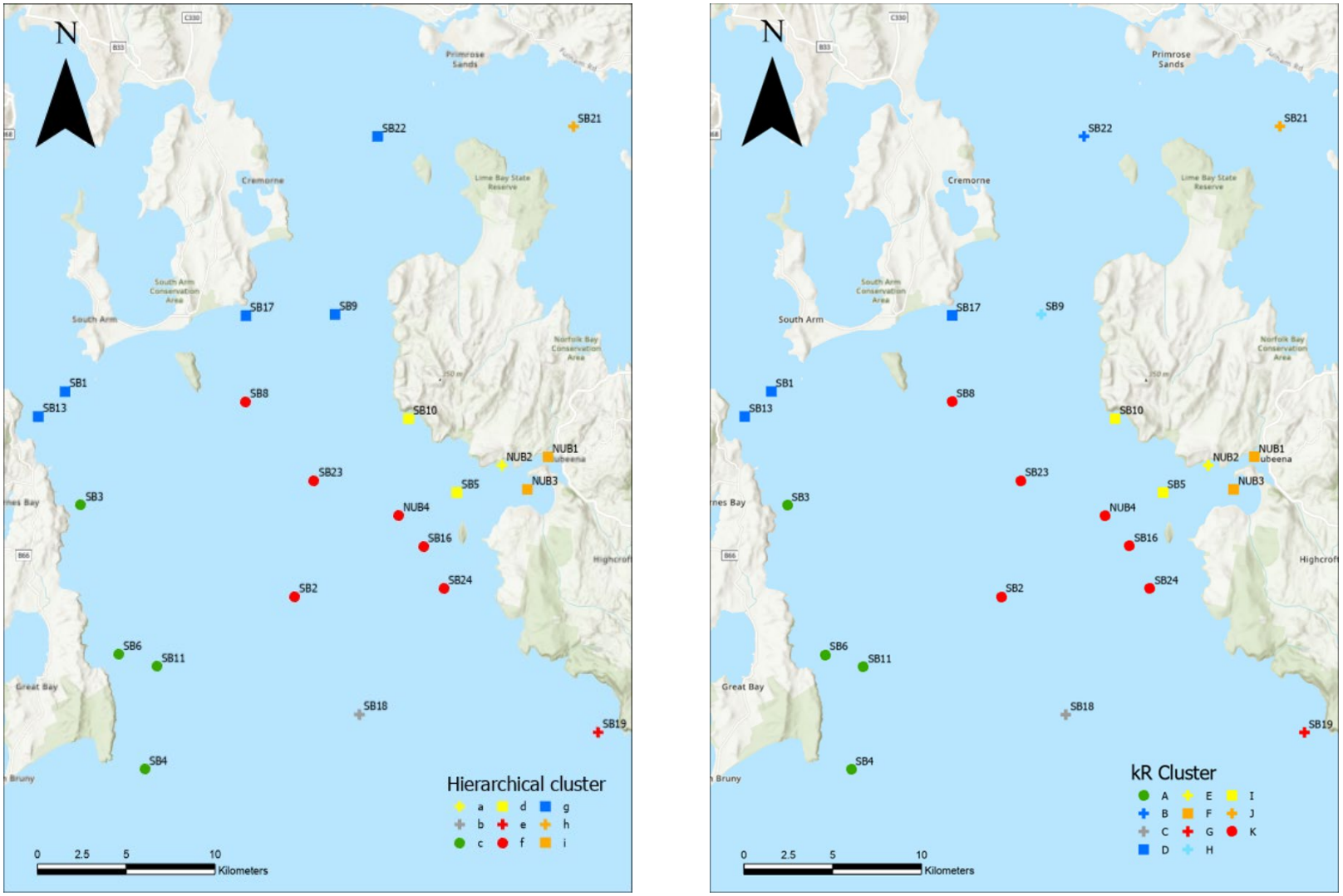

Figure 4-51: Maps showing the location of 23 soft sediment monitoring sites where macrofaunal samples were collected in 2019, 2020 and 2021. Colours represent site groupings based on hierarchical clusters (left) and kRClusters (right) between site and survey averaged macrofaunal community data.

4.2.3 Environmental performance assessment

Detection of far-field benthic effects of aquaculture has been limited to distances up to 2km from a lease (Weitzman et al. 2019). Further field effects have been hypothesised but attribution to aquaculture remains a challenge (Price et al. 2015). Theoretically, such effects may be directly related to dispersion of nutrients and particulates or indirectly, when water column primary production is stimulated, leading to nutrient export to the benthos. Impacts may therefore be delayed or cumulative, appearing minor at first. As such, assessing far-field benthic habitats using the same criteria and thresholds as at the local-scale may not be suitable for detecting more subtle and incremental system-wide change.

Thompson et al. (2008) found that this was the case when assessing broad-scale benthic health in the Huon Estuary and D'Entrecasteaux Channel because of the considerable natural spatial variation at the system scale and the subsequent effects on statistical power when attributing change. They proposed preliminary performance measures that were scaled (low, medium, and high-risk levels) according to the number of sites and parameters for which there was 'significant change' over time, i.e., a) one site = low risk; (b) two sites in $\geq$ 2 indicators = moderate risk; or (c) $\geq$ 3 sites in $\geq$ 2 indicators = high risk. The parameters and indicators proposed included both sediment chemistry (redox and sulphide) and biota (community structure and indicator species). The proposed response was similarly scaled to the level of exceedance, but always included a requirement for immediate sampling of the affected site/s to determine the extent and magnitude of change and the likely cause. Ultimately, they recommended that suitable benthic indicators or a suite of indicators should be developed based on benthic sediment samples collected as part of the initial Huon Estuary and D'Entrecasteaux Channel BEMP sediment surveys. To date, a set of robust benthic indicators have not yet been developed for the Huon Estuary and D'Entrecasteaux Channel BEMP (Aquenal 2021), although the Tasmanian EPA intends to undertake a review of baseline trigger levels as part of the Environmental Standards (ES) project. In the interim, Aquenal assessed benthic performance against the preliminary measures proposed by Thompson et al (2008), with key literature for the region used to provide context to observed trends (Butler et al. 2000, Macleod & Forbes 2004, Thompson et al. 2008).

For Storm Bay, we also recommend that the benthic indicators for assessing performance are based on the results of the first three broadscale surveys reported here. These three surveys capture the spatial and temporal variation of the sediment environment and the key biotic and abiotic conditions. As described below, there is no evidence of farm effects on the broadscale sediment environment from these initial surveys, and as such, we suggest they serve as the references for assessing performance as the industry develops.

In the absence of clearly defined indicators and thresholds for the broadscale sediment environment, we provide a generalised assessment of benthic health using the biotic and abiotic indicators proposed by Macleod and Forbes (2004) for local (lease) scale assessments in more exposed sandy locations in south-eastern Tasmania. Importantly, these indicators and thresholds were recently tested and validated for Storm Bay leases by Ross et al. (2021).

Table 4-6: Macleod and Forbes (2004) summary table of the key features of impact/recovery categories at exposed/sandy site. (NB. For the key biotic indictor category: organisms identified with * are considered collectively to reflect different effect categories rather than individually).

Impact Stage	I	II	III	IV	V	VII	VIII	IX
Effect Category	**No evidence of impact**	**Minor effects (Degrading)**	**Moderate effects (Degrading)**	**Major effects 1. (Degrading)**	**Major effects 2. (Degrading)**	**Major effects (Recovering)**	**Moderate effects (Recovering)**	**Minor effects (Recovering)**
Description		Small scale community change; Sediment chemistry unaffected or with only very minor effects	Significant community change; Sediment chemistry affected	Major community change; Monospecific dominance; major sediment chemistry changes	As in Stage IV; Beggiatoa/ outgassing on disturbance	Fauna returns to monospecific dominance; major sediment chemistry effects	Fauna re-establishing (zone of enhancement); Sediment chemistry still affected	Community largely recovered; Sediment chemistry recovered
Generalised Benthic Categories	Unimpacted indicator species present	Larger, long lived species & pristine indicators absent. Diversity may be greater than pristine (zone of enhancement)	Rapid change in community mix; deposit feeding polychaetes/ opportunists dominate. Filter/suspension feeders absent.	Opportunists (esp. Capitellids) characterise community	Infaunal opportunists (esp Capitellids) dominate. Patchy beggiatoa/ outgassing may be evident.	Opportunists (Capitellids) still dominate but no.s dropping & other species colonising.	Transitional species prevalent - notable increase in epibenthic opportunists.	Diversification of community but absence of climax/long lived species.
Key Biotic Indicators	*Apseudes, Ampelisca*	**Lyssianassidae, *Euphilomedes, *Polydora cf socialis,* *Phoxocephalidae	*Capitella* (dominant); *Neanthes, *Corophium, *Polydora cf socialis, *Tethygenia, *Cumacea*, *Phoxocephalidae)	*Capitella* (dominant); **Neanthes,* *Phoxocephalidae, **Dimorphostylis*	*Capitella* (greatly dominant); **Neanthes,* *Phoxocephalidae	*Capitella* (dominant), **Neanthes, *Corophium, *Nebalia*, *Phoxocephalidae	*Capitella* (lower no's), **Euphilomedes, *Polydora cf socialis, *Euchone*	Mix of species with increasing crustacea and decreasing annelids. **Apseudes, *Polydora cf socialis, *Euphilomedes, *Nephtys*
Shannon Index	>2	>2	>1<2; No. spp. >50% of ref	<1; No. spp. <50% of ref		<1; No. spp. <50% of ref	>1<2; No. spp. >50% of ref	>2
Total Abundance	Same as ref		x3 ref	x6-9 ref		x6-9 ref	x3 ref	
Redox Potential (mV)	>100mV	0-100mV (or >50% ref)	0-100mV (or >50% ref)	<0mV		<0mV	0-100mV (or >50% ref)	0-100mV (or >50% ref)
Sulphide Conc. (uM)	Below detection	Below detection	>50uM	>100uM		>100uM	>50uM	Below detection
Benthic Photo Score	Pos've	0 to -3	-4 to -3	<-4		<-4	-4 to -3	0 to -3
Video Score	>5	2.5-5	<2.5	Neg've		Neg've	<2.5	2.5-5
Video Features	Algae, Echiurans/ Sipunculans	Prevalence of burrow/ faunal track/ tubes; Echiurans/ Sipunculans	Sea slugs (Pleurobranchia)	Any evidence of Beggiatoa, Gas bubbles, Black sediments;		Any evidence of Beggiatoa, Gas bubbles, Black sediments;	Sea slugs (Pleurobranchia)	Point at which sea slugs are displaced (temporal)

The authors reported broad alignment with the recommendations for more exposed sandy sites, but again highlighted the inherent variability both within and between regions and the concomitant importance of assessing change relative to baseline and refence conditions rather than fixed parameter ranges.

For sediment chemistry, redox potential values <0 mV and sulphide concentrations >100 µM are indicative of highly enriched conditions. Conversely, redox potential values >100 mV and sulphide concentrations below detection levels are considered indicative of sites not influenced by organic enrichment (Table 4-6). The mean redox potential across all sites was >300 mV for each survey and the only site redox <100 mV was at site SB-17 in 2019 (82 mV). Mean sulphide concentration across all sites was <10 µM for each survey; however, moderate sulphide concentrations (~10 – 50 µM) were consistently detected at the three inshore Nubeena sites and at several other sites (2020 – SB-8, 10; 2021 SB-3, 11, 18, 21, 23) in one of the three surveys. Although both redox and sulphide have proven reliable at detecting major to moderate effects, both parameters (particularly sulphide) are considered

less reliable at discerning temporal change and more subtle effects (Macleod & Forbes 2004, Ross et al. 2021).

It is well documented that faunal assemblages at impacted sites are less diverse but more abundant due to the dominance of a few opportunistic species (Pearson & Rosenberg 1978, Macleod & Forbes 2004, Keeley et al. 2015). Macleod and Forbes (2004) considered a Shannon diversity index (H') of <2 to be indicative of moderate - high enrichment, and >2 unimpacted conditions (Table 4-7). Mean diversity across all sites was >2 for each survey and a diversity index of <2 was only observed at SB-19 and SB-21 in all years and NUB-1 in 2019. At SB-19 and SB-21, the macrofaunal communities were dominated by a single family (Bodotriidae and Lumbrineridae respectively) and neither are known indicators of organic enrichment. The community at NUB-1 was dominated by two families of polychaete (Cirratulidae and Trichobranchidae) and likewise, neither are known to respond to organic enrichment. This suggests dominance in these instances is due to localised environmental conditions that suit these families' preferences.

Mean total abundance and family richness across all sites was also high (i.e., >100 indiv. and >25 families per grab) across both the 2019 and 2020 surveys, consistent with healthy and unimpacted benthic communities. However, as previously described, there was a system wide decrease in both abundance and richness in 2021. Closer inspection revealed that much of this change occurred at sites in the relatively exposed, deep, and sandy regions of Storm Bay, particularly in the south-east quadrant. The more depleted sediment carbon and nitrogen content and $\delta^{15}N$, and elevated $\delta^{13}C$ relative to the previous two years, suggests that a change in the source and/or amount of organic matter may help explain the shift in benthic community. These changes are not consistent with the response we would anticipate in the presence of farm derived organic matter, i.e., more enriched sediments and an increase in faunal abundance.

Both MacLeod and Forbes (2004) and the more recent study by Ross et al. (2021) highlight that changes in community composition and the functional characteristics of the species present provide the most sensitive measure of organic enrichment. Annelids are known to become more prevalent in farm enriched sediments, and in 2021, there were in fact, fewer annelids compared to the 2020 and 2019 surveys (21, 36 and 29 ind. per grab respectively). Of the species known to respond to highly enriched conditions (e.g., *Capitella* spp., *Dorvilleid* sp. and *Nebalia* sp.) only *Nebalia* sp.1 was common at a small number of sites across the three surveys, notably at NUB-2, and to a lesser extent at SB-6 and SB-11 (Table 4-7); all of these sites are in closer proximity to leases. However, it is the species that are less tolerant of the reduced sediments often found under cages but respond opportunistically to lower levels of organic enrichment that will provide a more sensitive measure of broad-scale change. For Storm Bay, Ross et al. (2021) found certain taxa, notably the polychaetes *Pectinaria antipoda, Pectinaria cf. dodeka, Mediomastus* sp. And *Perinereis* sp.*,* heart urchin *Echinocardium cordatum*, amphipods from the family Phoxocephalidae, the dogwhelk *Nassarius nigellus* and the two introduced bivalves *Corbula gibba* and *Theora lubrica* were more abundant closer to the cage (e.g., 35 m) or at the cage during fallowing, taking advantage of low to moderate levels of enrichment. These are species that would be considered 'moderate – impact' indicator species in the application of the Macleod and Forbes (2004) effects table (Table 4-6) to Storm Bay. Further from the cage (35 – 200 m),

there was a transition to several more sensitive species, mostly sessile suspension feeders or surface deposit feeders, that were in greater abundances than they are typically found at background (reference) conditions, taking advantage of lower levels of enrichment. These are the species that would be described as characteristic of "minor – impact" indicators by Macleod and Forbes (2004) and included the spionid polychaetes *Spionid* sp.4 and *Dipolydora giardi,* onuphid polychaete *Hirsutonuphis intermedia*, amphipods *Tipimegus cf. thalerus* and *Hippomedon cf. hippolyte,* ostracod *Euphilomedes* sp., brittle star *Ophiura cf. kinbergi* and anemone *Edwardsii* sp.

Although the presence of these species is characteristic of background conditions, their increased presence, from reference conditions captured during the first three surveys, will likely provide an early indication of broadscale change. However, we suggest that a concomitant shift in benthic community composition will be a more robust and reliable indicator of change than individual species change. We also agree with Thompson et al. (2008) that the level of risk and the need for further investigation is scaled based on the number of affected sites. Further, we suggest the assessment of change is based on different regions in Storm Bay identified through the cluster analysis of macrofaunal communities. This will help constrain natural variation evident across the whole system and improve the power to detect change. The community metrics of change could include typical multivariate ordination techniques and/or a global benthic health index such AMBI which is regarded as sensitive to minor disturbances (see Box 4-1) (Keeley et al. 2012a, Keeley et al. 2012b).

Table 4-7: Summed abundances of organic enrichment indicator species in sediments at 23 Storm Bay sites in 2019, 2020 and 2021.

Phylum	Arthropoda			Annelida			Annelida		
Family	Nebaliidae			Dorvilleidae			Dorvilleidae		
Species	*Nebalia* sp. 1			*Schistomeringos loveni*			*Ophryotrocha sp.1*		
Year	2019	2020	2021	2019	2020	2021	2019	2020	2021
SB-1	0	0	0	0	0	0	0	0	0
SB-2	0	0	0	0	0	0	0	0	0
SB-3	**1**	0	0	0	0	0	0	0	0
SB-4	0	**3**	**2**	0	0	0	0	0	0
SB-5	0	**2**	0	0	0	0	0	0	0
SB-6	**7**	**8**	**11**	0	0	0	0	0	0
SB-8	0	0	0	0	0	0	0	0	0
SB-9	0	0	0	0	0	0	0	0	0
SB-10	0	0	0	0	0	0	0	0	0
SB-11	**2**	**7**	**1**	0	0	0	0	0	0
SB-13	**1**	0	**1**	0	0	0	0	0	0
SB-16	0	**1**	0	**1**	0	0	0	0	0
SB-17	0	0	0	0	0	0	0	0	0
SB-18	0	0	0	0	0	0	0	0	0
SB-19	0	0	0	0	0	0	0	0	0
SB-21	0	0	0	**3**	**1**	**1**	0	0	0
SB-22	0	0	0	0	0	0	0	0	0
SB-23	0	0	0	0	0	0	**2**	0	0
SB-24	0	0	0	0	0	0	0	0	0
NUB-1	0	0	0	**2**	**2**	**8**	0	0	0
NUB-2	**59**	**62**	**75**	0	0	0	0	0	0
NUB-3	0	0	0	**1**	0	0	0	0	0
NUB-4	0	0	0	0	0	0	0	0	0
Total	**70**	**83**	**90**	**7**	**3**	**9**	**2**	**0**	**0**

Visual assessment of benthic environments via remotely operated vehicles (ROVs) is a technique already employed for local-scale impact assessments (Crawford et al. 2001). Applying this technique to the broad-scale surveys has the capacity to provide important context and scale when interpreting change from the more quantitative biotic and abiotic performance measures derived from grab and core samples. A recent project assessed the utility of ROV visual assessment for characterising soft sediment environments at the broad-scale in Storm Bay (Graham 2022). The study identified the added utility that the visual assessment can provide to the broadscale sediment monitoring program. The technique was able to quantitatively assess epibiotic (e.g., algal cover, and the presence and abundance of larger invertebrates such as sea stars and scallops) and physical (e.g., sediment ripple size) site characteristics and in turn differentiate sites based on such characteristics. Thus, the addition of ROV visual assessment and its much broader survey footprint at each site facilitates the sampling and assessment of important features such as algal cover, large mobile fauna, and physical site characteristics. These features also provide context for the interpretation of spatial and temporal patterns in the benthic community and physico-chemical data.

4.3 Other Monitoring Techniques – Environmental DNA (eDNA)

Environmental DNA (eDNA) metabarcoding involves identification of biological communities based on genetic material extracted from environmental samples (e.g., sediment or water) (Taberlet et al. 2012). Nucleic acids extracted from marine sediments contain taxonomic and functional information originating from a broad range of nearby organisms including animals, algae, bacteria, and fungi. Metabarcoding methods allow scientists to survey taxa from all kingdoms including environmentally sensitive microscopic organisms that cannot be surveyed by traditional methods (Thomsen & Willerslev 2015). To survey specific groups of organisms, taxonomically informative genes are amplified using PCR. The PCR products are then sequenced using Next Generation Sequencing (NGS) technologies and the resulting sequence reads are combined based on similarity into discrete groups or “taxonomic units,” most commonly operational taxonomic units (OTUs) or amplicon sequence variants (ASVs). These units can be compared to databases holding taxonomic information for known sequences of the gene of interest, to identify the taxa from which the DNA originated (Ruppert et al. 2019). Unlike visual methods for surveying biological communities, the data obtained from metabarcoding experiments cannot be accurately related to the absolute abundance of an organism in the original samples, or even to the number of occurrences of the target DNA from that organism. This is because PCR amplification alters the relative proportions of different sequences in the sample and because sampling depth cannot be held constant across samples during the sequencing process (Gloor et al. 2017). Regardless, sequences that are more abundant in the original samples are generally more likely to be sequenced more often and thus a rough estimate of relative abundance for different features (ASVs/OTUs/taxa) in eDNA metabarcoding datasets can be made (Skelton et al. 2022).

Metabarcoding of DNA extracted from soft sediments has been highly scrutinised globally as a potentially powerful and cost-effective addition to the salmon aquaculture environmental

monitoring toolkit (Rector et al. 2018). Studies applying metabarcoding methods to salmon farm case studies have focussed on both bacterial communities and eukaryote communities including animals, foraminifera, ciliates, and other microalgae (Lejzerowicz et al. 2015, Pochon et al. 2015, Dowle et al. 2016, Keeley et al. 2018, Stoeck et al. 2018, Frühe et al. 2021). Implementation of eDNA based methods into legislated monitoring programs remains a challenge globally due to the need for standardised sampling and data processing protocols. However, several recent eDNA metabarcoding projects in the salmon farming context have developed biotic indices for environmental impact assessment (Aylagas et al. 2014, Aylagas et al. 2017, Keeley et al. 2018) and tested the effects of methodological decisions on results (Dully et al. 2021, Laroche et al. 2021) with the vision of moving towards standardised, robust, sensitive, and easily interpreted methods for uptake by managers. The eDNA metabarcoding method is often claimed to be a cost and time effective alternative to traditional approaches to monitoring soft sediment biological communities. Empirical evidence to date suggests eDNA methods give the greatest cost/time advantage when implemented on a large scale (Aylagas et al. 2018). However, case specific validation of both the utility and cost effectiveness of eDNA metabarcoding methods will be vital to allow managers to make informed decisions on the use of these methods in monitoring programs.

In Tasmania, the interaction between macrofauna and salmon aquaculture is well understood (Macleod et al. 2004, Edgar et al. 2005, Macleod et al. 2008); however, less is known about how taxa that could be targeted by eDNA metabarcoding such as bacteria and non-animal eukaryotes may respond. To date eukaryotes such as microalgae and foraminifera have not been surveyed in sediments near to Tasmanian salmon farms. Bacterial communities at salmon farms in the D'Entrecasteaux channel and at Nubeena have been investigated in the past but never using eDNA metabarcoding (Bissett et al. 2006, Bissett et al. 2007). These studies showed that bacterial diversity decreased, and taxonomic composition of the community changed in response to salmon farming. However, they highlighted that there was a large amount of random variation in bacterial community diversity and composition and further research is needed to identify predictable responses to salmon farm disturbance (Bissett et al. 2006, Bissett et al. 2007).

Recent advances in DNA sequence technology and taxonomic databases allow bacterial communities to be sampled more comprehensively with greater taxonomic resolution, which may allow more confidence in the data and conclusions in relation to bacterial community monitoring (Pawlowski et al. 2022). Applying eDNA metabarcoding to soft sediments may allow a more holistic view of the sediment biota, extending the scope of future salmon aquaculture monitoring programs beyond macrofauna alone to a broad range of macroscopic and microscopic taxa.

4.3.1 Case study and sampling design

As part of the Storm Bay Observing System, we trialled 16S rRNA (bacteria) and 18S rRNA (eukaryote) eDNA metabarcoding on a subset of the sediment samples collected for macrofauna and sediment analyses (Table 4-3 & Table 4-5). The samples used for eDNA analysis were from the first local (lease) scale survey at Yellow Bluff in March 2020 and from the first two broad-scale (BEMP) surveys of Storm Bay in October 2019 and October 2020.

Here we present a summary of the data collected in these case studies, with the following aims:

- Identify potential eDNA metabarcoding derived indicator metrics that could be applied to future salmon farm environmental monitoring, including indicator taxa, diversity, and a bacterial community marine biotic index.
- Compare 18S rRNA and traditional visual methods in their ability to survey soft sediment macrofauna communities and their response to salmon farm derived organic enrichment.
- Outline the spatial and temporal variation in metabarcoding derived biological communities in Storm Bay to provide context for future assessments of farm interactions with these communities.
- Conduct a cost-benefit analysis to compare the cost of the eDNA metabarcoding method to traditional methods.

For the local-scale survey, duplicate sediment cores at six distances (0 m, 10 m, 35 m, 50 m, 100 m and reference) along three transects were analysed (total of 36 samples). For the broad-scale surveys, triplicate cores from all 23 soft sediment sites for both years were analysed (a total of 138 samples).

4.3.2 Methods

Sampling, molecular analysis, bioinformatics, and cost-benefit analysis

Cores were collected in an identical manner to those collected for sediment physical and chemical analysis (see section 3.1.1) except that the perspex core was soaked in a 20% bleach solution between samples. Approximately 5 g of sediment was sampled from the top 5 cm of each core and stored in 10 mL cryovials. The cryovials were immediately frozen with liquid nitrogen. Upon return to the laboratory all samples were stored at -80°C until processing. DNA was extracted from all samples using the Qiagen DNeasy PowerSoil Pro kit following the manufacturers protocol. Genomic DNA was sent to the Ramaciotti Centre for Genomics where the V1-V3 region of the 16S rRNA gene (bacteria) and V9 region of 18S rRNA gene (eukaryotes) were amplified and sequenced following the protocols presented in Australian Microbiome Scientific Manual (Lawrence & van de Kamp 2022). Sequence data were processed separately for each gene (16S rRNA or 18S rRNA) and group of samples (local-scale or broad-scale). All sequence data was filtered, merged, and clustered into ASVs using DADA2 (Callahan et al. 2016) and following the methods of Frühe et al. (2021). Chimera removal was completed with DADA2 using the “consensus” method and taxonomy was assigned with the *assignTaxonomy* function in DADA2. We used the Silva version 138.2 SSU reference database (Quast et al. 2013) for bacteria and the PR2 version 4.13.0 18S rRNA reference database (Vaulot 2019) for eukaryotes. Family level taxonomic information for metazoa (animals) was not available in the PR2 database.

To allow a direct comparison between the macrofauna and metabarcoding datasets, the lowest taxonomic rank assigned to each ASV using the PR2 database was used to query the WoRMS database (Costello et al. 2013); when a match occurred taxonomic data for higher taxonomic levels were extracted. ASVs that could not be assigned to the appropriate

domain (Eukarya or Bacteria) were removed along with ASVs that were assigned to chloroplasts or mitochondria and ASVs that were sequenced less than 10 times or appeared in only a single sample. The bacteria-based benthic health index microGAMBI was calculated as per the methods described by Aylagas et al. (2017) using the taxa list provided in a subsequent study (Borja 2018). This taxa list was updated for the 16S rRNA datasets using taxon-specific information extracted from the literature following the guidelines provided by the original authors (Borja 2018). For the microGAMBI calculation the 16S rRNA dataset was summed at the genus level and all taxa that made up less than 1% of the total dataset were removed.

A cost-benefit analysis based on the methods used by Aylagas et al. (2018) was conducted to compare the time and monetary cost of processing sediment samples via a combined 18S rRNA and 16S rRNA metabarcoding approach to the traditional visual macrofauna approach. Only sample processing and bioinformatics costs were considered as field sampling and data analysis costs were similar for the two methods. Time cost was calculated based on systematic recording of the time taken to process samples by experts during the Yellow Bluff survey in March 2020. Monetary cost was based on the UTAS award rates, known costs of consumables, and costs of sequencing services at the Ramaciotti Centre for Genomics from the same survey.

Statistical Analyses

To evaluate the effects of distance and direction from the salmon farm on 18S rRNA diversity, 16S rRNA diversity and microgAMBI, we fitted a linear model with a Gaussian distribution and the following formula: response = Distance + Direction + Distance * Direction. We conducted ANOVA to test for significant effects.

To identify potential bacterial indicator taxa, we used ALDEx2 (an R package designed for identifying differentially abundant features in high throughput sequencing datasets) (Fernandes et al. 2013) to identify bacterial families that had significantly different sequence abundances between the cage sites and reference sites. We used the default t-test function, and as suggested by the authors, deemed families with an effect size greater than 2 or less than -2 as significant.

Multivariate analysis of metabarcoding communities from the broad-scale surveys was conducted in PRIMER7 (Clarke & Gorley 2015) following a compositional approach as recommended by Gloor et al. (2017). Aitchison distance between sample averages for each combination of survey (2019 or 2020) and site was used as the similarity measure and ordinations were by PCA. Averaging was conducted after applying the centred log ratio (CLR) transformation. We chose hierarchical clustering using the UPGMA method in PRIMER 7 as the clustering method for the broad-scale analysis of both the 18S and 16S rRNA datasets. With the goal of identifying groups of samples that may correspond to different habitat regions in Storm Bay, we tested similarity thresholds that corresponded to 3 – 10 sample clusters. From these eight scenarios we selected the final clusters by choosing the scenario that yielded the lowest misclassification percentage in a CAP analysis using the clusters as the grouping factor.

4.3.3 Results and Interpretation

Local-scale (16S rRNA Metabarcoding)

Changes in alpha diversity and turnover in community composition along gradients of impact are vital requisites for the use of biological communities in environmental monitoring. Generally, a reduction in diversity and dominance of specific indicator taxa is indicative of disturbed sediment biological communities (Pearson & Rosenberg 1978) and this trend has been observed for eDNA metabarcoding derived bacterial communities near to salmon farms (Stoeck et al. 2018, Dully et al. 2021). At Yellow Bluff, bacterial Shannon diversity was lower close to the farm compared to sites further away (Figure 4-52, Table 4-8); however, the response of Shannon diversity to distance depended on the transect. Specifically, bacterial Shannon diversity remained low for a further distance from the farm on the north transect compared to the other transects (Figure 4-52, Table 4-8), which was reflective of other signs of disturbance (lower redox, lower macrofauna family richness and higher macrofauna AMBI values) on this transect (Figure 4-5, Figure 4-6, Figure 4-8, Figure 4-15).

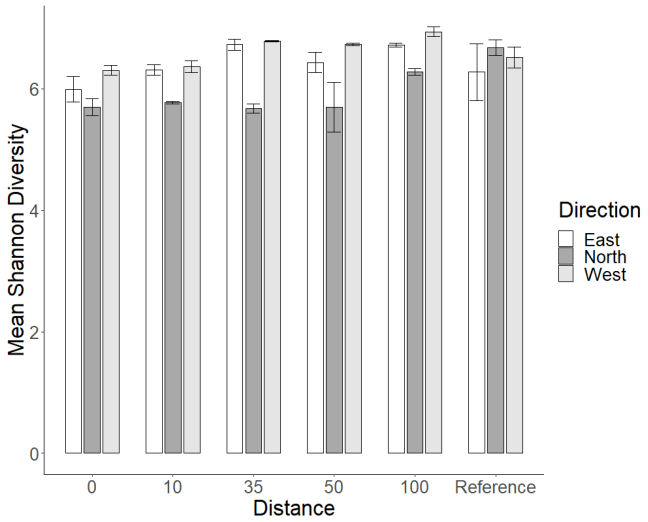

Figure 4-52: Average (± SD) bacterial Shannon diversity from 16S rRNA metabarcoding of 36 sediment samples collected at 6 distances along three transects radiating from a salmon farm at Yellow Bluff, Tasmania in March 2020.

Table 4-8: Results from linear modelling and ANOVA testing for the effect of distance and direction on Shannon diversity and microGAMBI values measured in soft sediment samples (n = 36) by eDNA metabarcoding of the 16S (bacteria) and 18S rRNA (eukaryotes) genes at Yellow Bluff in March 2020. Significant effects (p<0.05) are shown in bold.

Parameter	Factor	Df	Deviance	Residual Df	Residual deviance	F	P
Eukaryote Shannon Diversity	**Distance**	**1**	**2.70**	**34**	**11.28**	**7.89**	**0.009**
	Direction	2	0.61	32	10.77	0.89	0.42
	Distance x Direction	2	0.49	30	10.28	0.71	0.50
	Distance	1	0.21	34	6.10	2.65	0.11

Bacterial Shannon Diversity	**Direction**	**2**	**2.64**	**32**	**3.46**	**16.25**	**0.00002**
	Distance x Direction	**2**	**1.03**	**30**	**2.43**	**6.34**	**0.01**
microGAMBI	**Distance**	**1**	**30.16**	**34**	**19.65**	**96.12**	**<0.00001**
	Direction	**2**	**9.26**	**32**	**10.39**	**14.75**	**0.00005**
	Distance x Direction	2	0.97	30	9.41	1.55	0.23

There were clear trends in bacterial community composition at the Phylum level that occurred over the distance gradient. For example, the Campylobacterota made up a large proportion of sequences in the 0 metre and 10 metre samples but were gradually replaced along the distance gradient by the Proteobacterota which had their highest relative abundances in the reference samples (Figure 4-53). Phylum Bacteroidota and Desulfobacterota relative abundance was relatively consistent across all distances but dropped in the reference site samples (Figure 4-53).

We chose the family rank for identifying specific bacterial indicator taxa as it was shown in a global study to be the most powerful taxonomic rank for differentiating sites in different salmon aquaculture related disturbance categories based on 16S rRNA data (Frühe et al. 2021). There were 10 bacterial families identified as significantly more abundant at the cage sites than the reference sites (Table 4-9). Many of these families shared similar functional traits, suggesting their presence in salmon cage sediments is driven by specific environmental conditions under the salmon cage favouring certain functional groups. For example, the Sulfurovaceae, Desulfobacteraceae, Sulfurimonadaceae and Rhodobactereaceae are all involved in metabolism of sulphur compounds (Pujalte et al. 2014, Jeon et al. 2017, Wang et al. 2022), while the Flavobacteriaceae and Spirochaetacea are known members of the salmon gut microbiome (Fogarty et al. 2019). These results show the potential for 16S rRNA metabarcoding to differentiate sites with differing levels of aquaculture-related disturbance based on bacterial community composition, thus providing potential indicator taxa that could characterise disturbed soft sediments in Tasmania. Families that were more abundant in the reference site samples (Table 4-9) are further discussed in the broad-scale section where we investigate whether they are specific to local-scale reference sites or are part of the broader Storm Bay sediment microbiome.

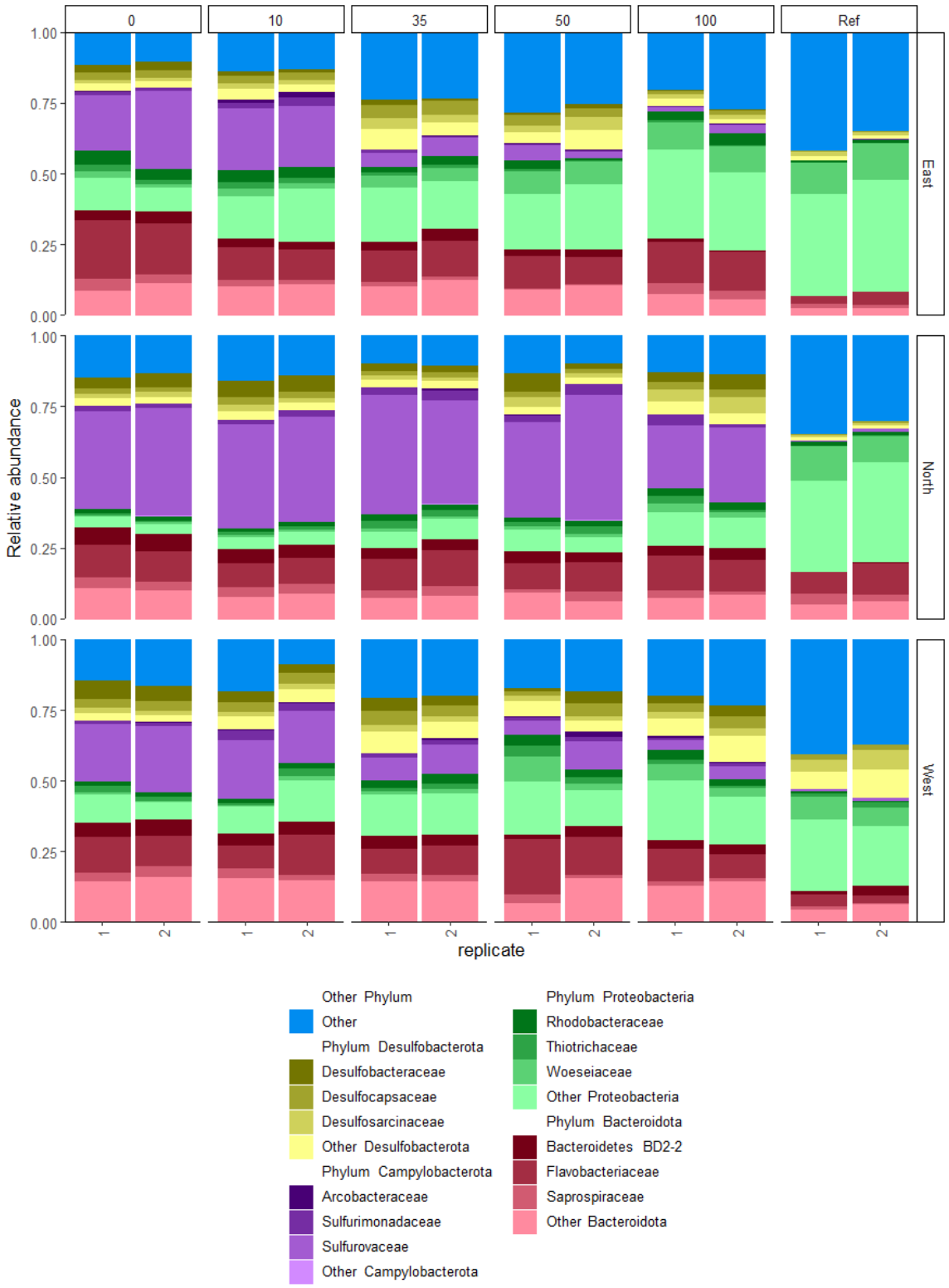

Figure 4-53: Relative sequence abundances of the top 3 most sequenced bacterial families within each of the top 4 most sequenced bacterial phyla. Relative abundances are calculated from results of 16S rRNA metabarcoding of 36 sediment samples collected at 6 distances along three transects radiating from a salmon farm at Yellow Bluff, Tasmania in March 2020.

Table 4-9: Results from ALDEx2 testing for differences in bacterial family sequence abundance between cage sites (n = 6) and reference sites (n = 6) at Yellow Bluff in March 2020.

Family	Effect size	Mean % relative abundance (control sites)	Mean % relative abundance (0 metre sites)
Sulfurovaceae	3.97	0.53	27.26
Flavobacteriaceae	2.99	5.54	14.04
Woeseiaceae	-2.84	10.06	1.01
Desulfobacteraceae	2.61	0.05	4.48
Spirochaetaceae	2.30	0.31	3.54
Saprospiraceae	2.88	1.74	3.59
Rhodobacteraceae	2.32	0.96	2.42
Pirellulaceae	-2.57	3.65	0.11
Marinifilaceae	2.18	0.04	1.84
Sulfurimonadaceae	5.30	0.09	1.28
Prolixibacteraceae	2.47	0.23	2.09
Marinilabiliaceae	3.98	0.04	1.95
Sandaracinaceae	-3.25	3.53	0.06
Nitrosococcaceae	-2.22	2.73	0.14

In a monitoring framework context, consideration of individual analyses for many indicator taxa may be inefficient for informing management, especially where many taxa are involved as is the case in metabarcoding datasets. Instead, metrics that summarise biological communities and give an estimate of the health of an environment may be preferred. For this reason, indices such as the AZTI Marine Biotic Index (AMBI) (Borja et al. 2000) have been developed for summarising macrofauna community datasets. AMBI provides a single metric which characterises sediment samples into different levels of disturbance from undisturbed to extremely disturbed based on prior ecological knowledge of the surveyed taxa. More recently, a similar index known as microgAMBI has been developed for metabarcoding based bacterial datasets (Aylagas et al. 2017). MicrogAMBI categorises bacterial taxa into two groups (EGI: not associated with pollution and EGIII: associated with pollution) and a 1 – 6 index is calculated based on the relative abundance of these groups where 1 indicates high ecological status, 6 indicates bad ecological status and in between values are classed as good, moderate, or poor. At Yellow Bluff in March 2020 average microgAMBI values for each sampling station were correlated with macrofauna AMBI values from the same samples (Figure 4-54). MicrogAMBI showed a significant reduction along the distance gradient from bad or poor ecological status at the cage sites to good at the reference sites (Figure 4-54, Table 4-8). Each transect displayed a similar pattern but the northern transect displayed higher microgAMBI values (worse ecological status) than the east and west transects. As mentioned in relation to bacterial Shannon diversity, this was reflective of other signs of disturbance (lower redox, lower macrofauna family richness and higher macrofauna AMBI values) on this transect in March 2020 (Figure 4-27, Figure 4-29, Figure 4-32).

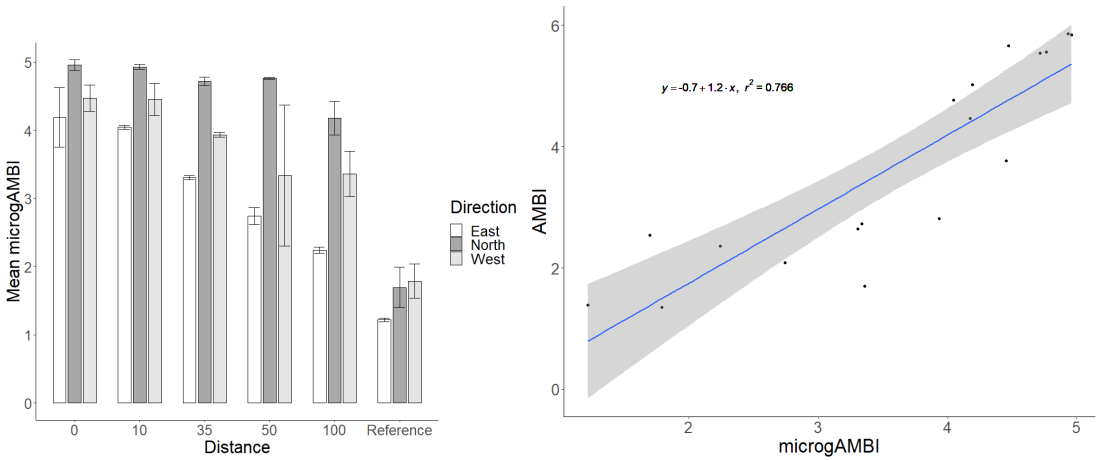

Figure 4-54: Average (± SD) microgAMBI (left) and linear correlation between microgAMBI and AMBI (right). Data are calculated from 16S rRNA metabarcoding of 36 sediment samples collected at 6 distances along three transects radiating from a salmon farm at Yellow Bluff, Tasmania in March 2020.

Local-scale (18S rRNA Metabarcoding)

Metazoa (animals), Ciliophora, Dinoflagellata and Apicomplexa were the most sequenced eukaryote divisions in the 18S rRNA dataset from Yellow Bluff in March 2020. Diversity and relative abundances of eukaryote taxa were investigated to identify whether there were shifts in community structure and composition at different sites that may be used to assess the level of aquaculture influence at sediment monitoring sites. Eukaryote Shannon diversity in the local-scale 18S rRNA dataset was significantly lower at the cage sites compared to more distant sites; however, it was not influenced by direction from the farm (Figure 4-55, Table 4-8). We interpret this as an indication that 18S rRNA alpha diversity was less sensitive than the other metrics (macrofauna family richness, 16S rRNA Shannon diversity, AMBI and microgAMBI) which had stronger relationships with distance and were lower on the north transect compared the other transects.

Turnover in the eukaryote community along the distance gradient at Yellow Bluff in March 2020 appeared to be mostly attributed to protistan taxa. For example, relative abundance of Ciliate sequences was highest at the 0 and 10 metre sites and was consistently lower in the 100 metre and reference samples (Figure 4-56). In contrast the dinoflagellates had their highest relative abundance in the 100 metre and reference sites and their lowest relative abundance in the 0 and 10 metre sites. Metazoan (animal) sequences made up a significant proportion of 18S rRNA sequences at all sites, however there were no obvious trends in metazoan relative abundance along the distance from farm gradient or between transects. We chose to investigate the relative abundances of metazoa in the 18S rRNA dataset at lower taxonomic ranks (Phylum and Family) because a key question for the utility of 18S rRNA metabarcoding in environmental monitoring is whether it can perform similarly to traditional methods for surveying macrofauna taxa. Macrofauna serve as a good benchmark for new monitoring tools as their responses to aquaculture derived disturbance are already well known.

The metazoan community revealed at Yellow Bluff in March 2020 by 18S rRNA metabarcoding had some key differences to the community revealed by the traditional

macrofauna surveys. The gradient of Annelid dominance in highly disturbed sites to Arthropod dominance in undisturbed sites characteristic of macrofauna communities (Figure 4-29, Figure 4-35) was not observed in the metabarcoding data (Figure 4-56). The Platyhelminthes and Nematodes were dominant groups in the metabarcoding derived metazoan community but were completely absent or extremely rare in the macrofauna analysis of the same samples. This discrepancy has also been noted at a salmon farm in Scotland (Lejzerowicz et al. 2015) and is likely due to these meiofaunal animals being damaged or passing through the sieves during macrofauna analysis. Of the 121 animal families detected by metabarcoding only 20 also appeared in the macrofauna dataset. Of these 20 families only one made up at least 1% of 18S rRNA sequences, this was Capitellidae, solely represented by the genus Capitella in the 18S rRNA dataset. Capitella is a known indicator of disturbed soft sediment environments in Tasmania (Macleod et al. 2007) and the macrofauna analysis at Yellow Bluff in March 2020 showed high abundances of capitella at the 0 and 10 metre sites compared to the more distant sites (Figure 4-11). This trend was not reflected in the metabarcoding data where capitella relative abundance was high in a few single samples but showed no consistent elevation at sites close to the farm (Figure 4-57).

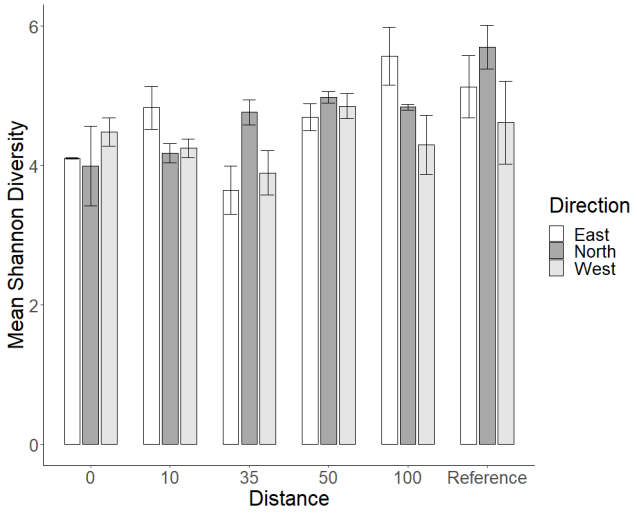

Figure 4-55: Average (± SD) eukaryote Shannon diversity from 18S rRNA metabarcoding of 36 sediment samples collected at 6 distances along three transects radiating from a salmon farm at Yellow Bluff, Tasmania in March 2020.

Overall, the 18S rRNA method employed in the Storm Bay Observing System showed promise in detecting local-scale changes in eukaryote alpha diversity related to aquaculture impacts, however it was not as sensitive as macrofauna and 16S rRNA diversity or microgAMBI (Table 4-8). Compared to traditional visual methods the 18S rRNA method appeared to be less informative for discerning changes in macrofauna community composition that could be related to salmon aquaculture. The protistan component of the community (e.g., ciliates and dinoflagellates) showed more potential for differentiating sites experiencing distinct levels of aquaculture related disturbance at Yellow Bluff in March 2020. Further investigation into these protistan communities could reveal useful aquaculture impact indicator taxa and allow implementation of eukaryote metabarcoding derived benthic health indices.

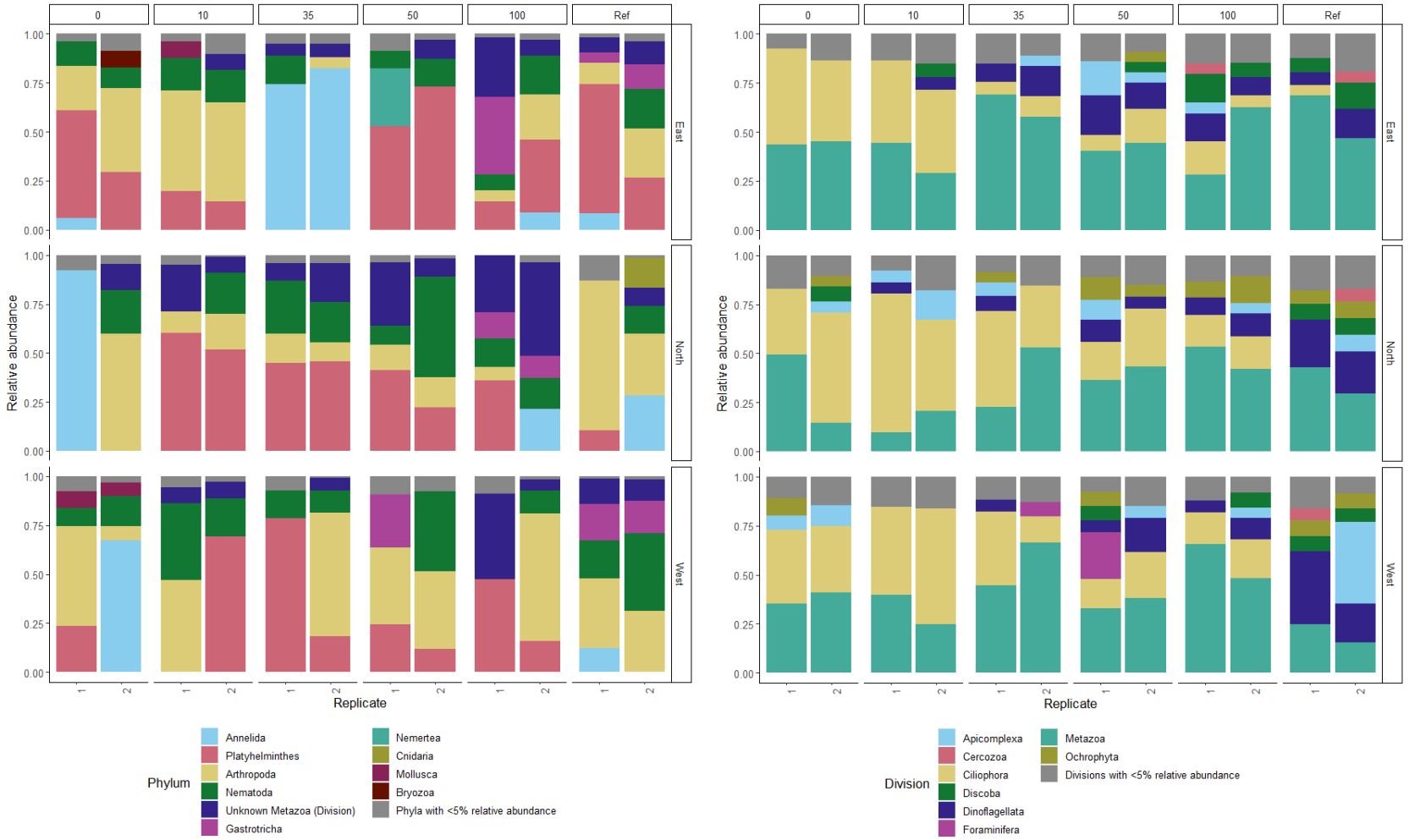

Figure 4-56: Relative sequence abundance of eukaryote divisions (left) and metazoan phyla (right). Each column shows one sample. Data are from 18S rRNA metabarcoding of 36 sediment samples collected at 6 distances along three transects radiating from a salmon farm at Yellow Bluff, Tasmania in March 2020.

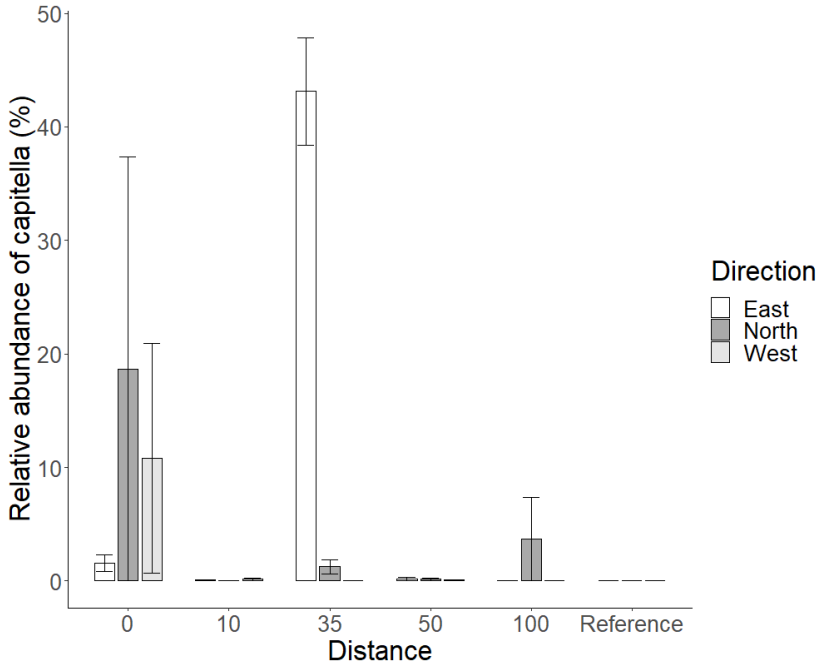

Figure 4-57: Average (± SD) relative sequence abundance of the genus capitella from 18S rRNA metabarcoding of 36 sediment samples collected at 6 distances along three transects radiating from a salmon farm at Yellow Bluff, Tasmania in March 2020.

At the local-scale, the 16S rRNA metabarcoding showed greater promise than the 18S rRNA method for differentiating sites with differing levels of aquaculture disturbance based on alpha diversity and community taxonomic composition. Thus, for the purpose of this summary we decided to focus on the 16S rRNA datasets to investigate potential metabarcoding derived indicator taxa and benthic health indices and did not further investigate these parameters in the 18S rRNA dataset.

Broad-scale (16S rRNA Metabarcoding)

Principle component analysis (PCA) allows the viewing of datasets with many variables (taxa in the case of metabarcoding datasets) in a two-dimensional plot (Figure 4-58,). Each point on the plot represents the averaged bacterial or eukaryote community of a site in a particular year. Communities positioned close to each other on the PCA plot are more similar to each other than communities positioned further away from each other. Blue vector lines represent correlations of environmental variables with the communities that they point towards.

PCA and hierarchical cluster analysis of 16S rRNA metabarcoding data from Storm Bay in 2019 and 2020 separated the 23 sites surveyed into six groups based on differences in the bacterial communities (Figure 4-58, Figure 4-59). The group which was most dissimilar from the rest of the sites was group b which included sites in Nubeena (NUB-1 and NUB-2) and Norfolk Bay (SB-21). These are the most sheltered sites and as shown by the environmental vectors on the PCA plot, are characterised by a high percentage of silt (particles <0.063 mm in size), increased organic enrichment (%N, %C and LOI%) and low redox potential, compared to the rest of the sampling stations. Group a is represented by site NUB-2 which is

in a similar environment to the group b sites but is slightly less sheltered and as such there is less silt and organic matter. Group d is also quite distinct from the other samples and represents more oceanic sites in the central and south-eastern regions of Storm Bay, which are deeper sites characterised by more sandy sediments with higher redox potential. The remaining groups (c, e, f, and g) are more similar to each other, with most appearing to represent a gradient of estuarine influence. Specifically, the group e sites are located close to the Derwent estuary, group c slightly further south and group f represented by oceanic sites in the south-west of Storm Bay. Group g is represented by coastal sites on Bruny Island, located near to the salmon farms at leases 281 and 261. There were no cases where bacterial communities from different years at the same site were grouped separately, indicating there is far greater spatial variation in bacterial communities in Storm Bay than temporal variation.

Groupings which represent different environmental conditions (habitat regions) across Storm Bay could inform the spatial design of future bacterial monitoring programs (also see section 4.4.2). Site groups based on 16S rRNA metabarcoding derived bacterial communities could aid in the selection of a subset of sites representative of the different habitats across Storm Bay, which may act as "sentinel" sites that indicate when the ecology of each habitat region may be changing in response to salmon aquaculture inputs.

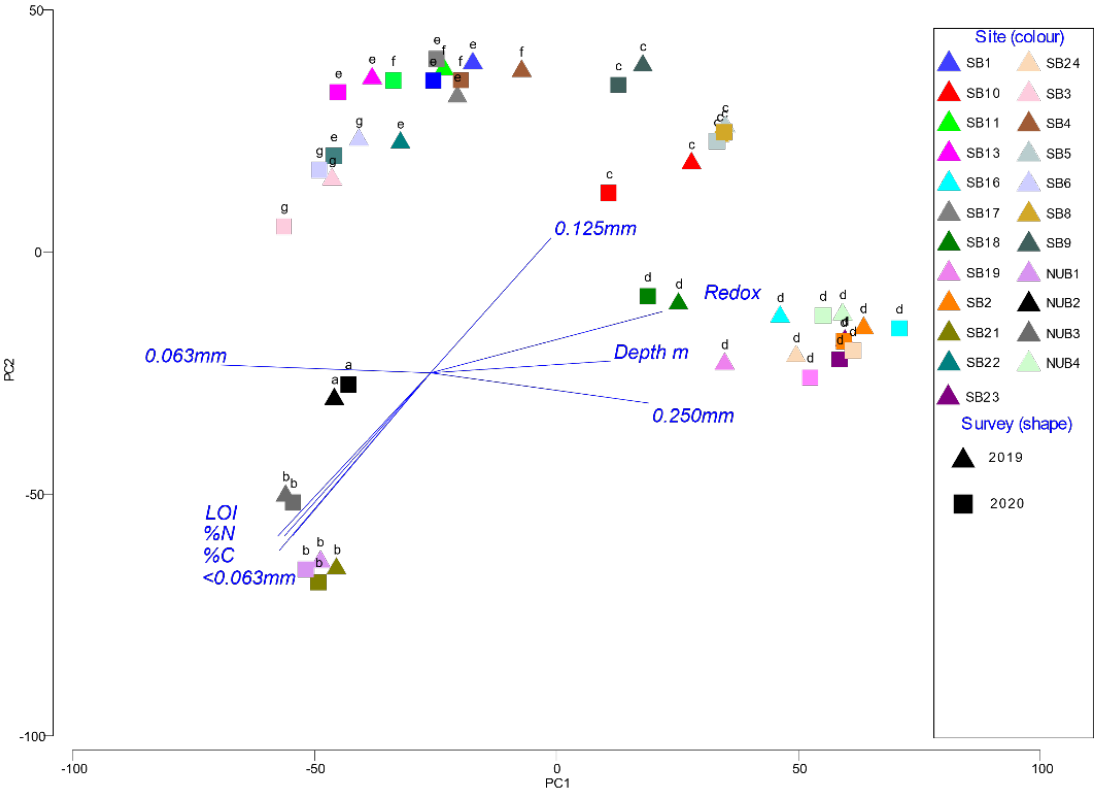

Figure 4-58: PCA ordination displaying Euclidean distances between 16S rRNA metabarcoding derived bacterial communities at 23 sediment monitoring sites across 2 years. Distances were calculated between averaged CLR transformed data for each combination of site and survey. Labels for each point display the sample groups based on hierarchical clustering. Vectors show Pearson correlations with a coefficient of at least 0.5 between PCA axes and normalised environmental variables.

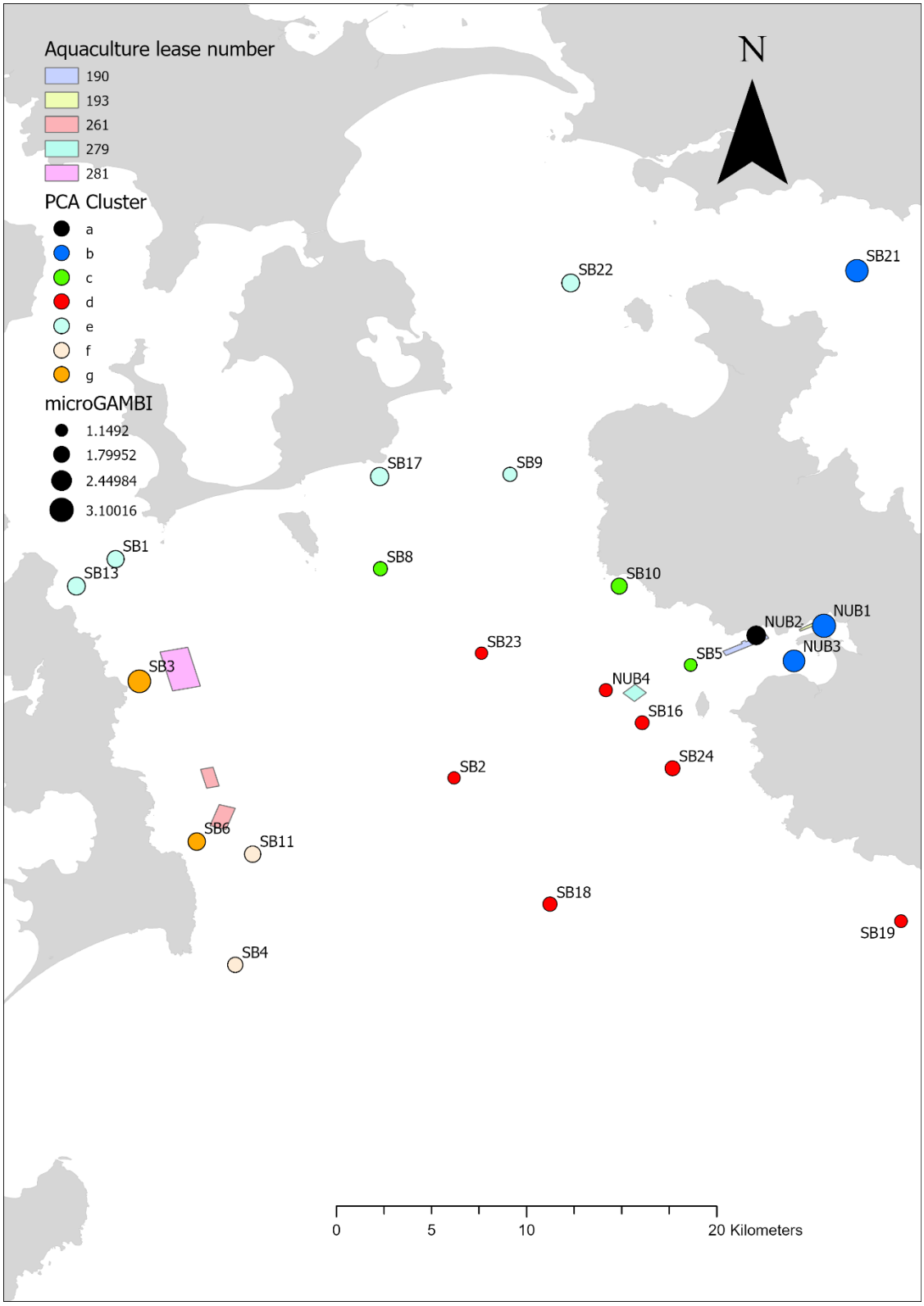

Figure 4-59: Map showing the location of 23 soft sediment monitoring sites where eDNA samples were collected in 2019 and 2020. The colour shows site groupings based on hierarchical clustering of Euclidean distances between site and survey averaged 16S rRNA bacterial community data. Size of the dots shows the two year (2019 and 2020) average microgAMBI for each site.

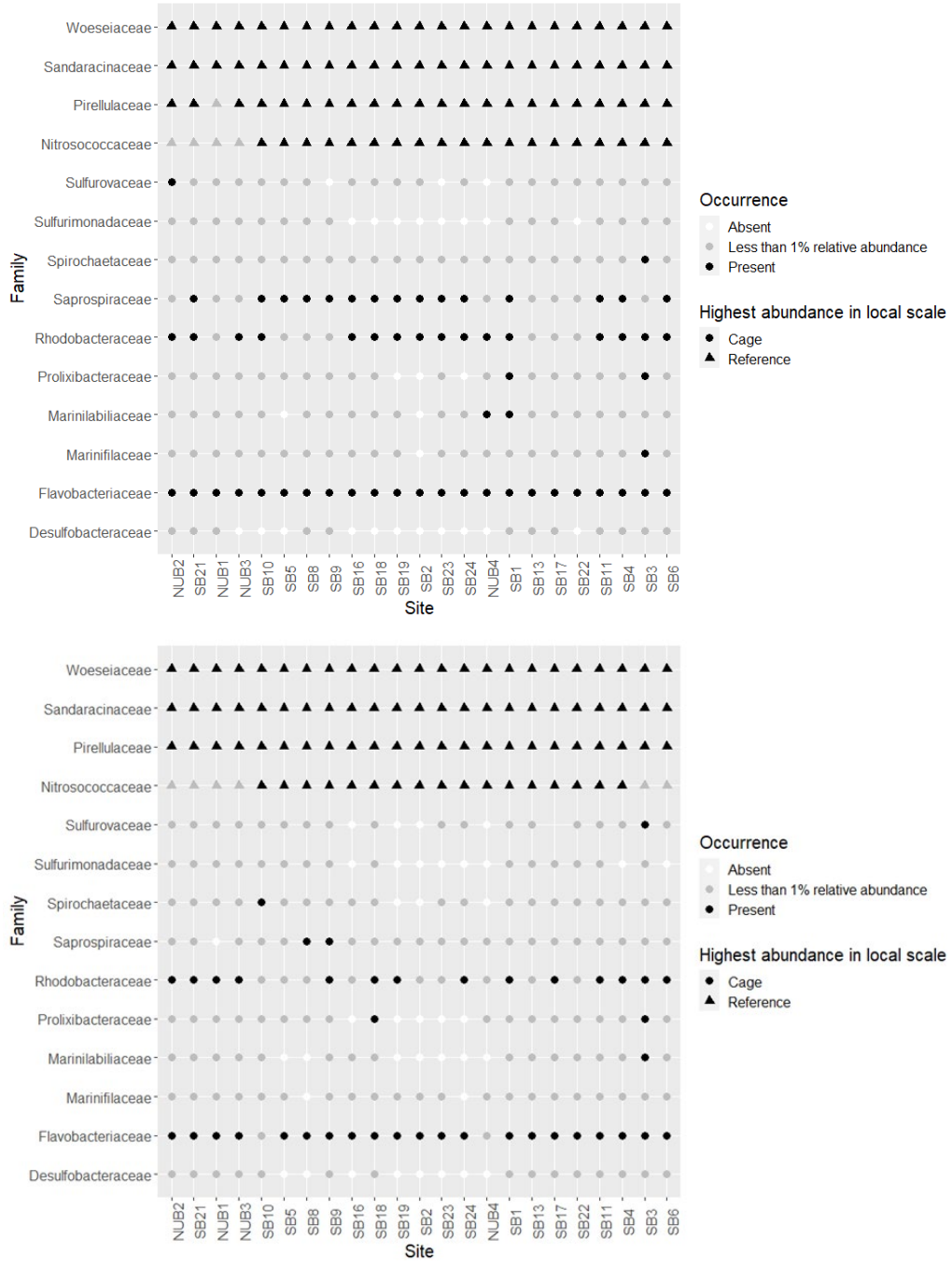

Figure 4-60: Occurrence of bacterial families in the 23 broadscale sites surveyed in 2019 (top) and 2020 (bottom). Bacterial families shown are those identified as differentially abundant between cage sites and reference sites in the local (lease) scale survey at Yellow Bluff in March 2020.

While PCA provides useful information about biological community datasets, the results are not easily interpreted in the context of a legislated monitoring program because no discrete thresholds indicating unacceptable change can be easily set. A future broad-scale monitoring program involving eDNA metabarcoding of bacterial communities will require robust and easily interpreted metrics. As such, we chose to investigate variation in microGAMBI values and occurrence of select indicator bacterial families (identified in the local-scale Yellow Bluff survey in March 2020) at the broad-scale monitoring sites in the

2019 and 2020 surveys. We chose these metrics as they were the most sensitive from the local-scale eDNA metabarcoding sampling at Yellow Bluff in March 2020.

Two-year average microGAMBI values were below 2.5 (high or good ecological status) for all except four sites (Figure 4-59). These were the group b, sheltered sites in Nubeena and Norfolk Bay (SB-21, NUB-1 and NUB-3) and SB-3 which is located on the Bruny Island coast near the Yellow Bluff salmon farm lease (MF281), which all had moderate ecological status (2.5<microgAMBI≤3.6; Figure 4-59; Aylagas et al. 2017). This result is unsurprising as these are the sites closest to sources of organic enrichment. These were also sites where bacterial families that had higher relative abundance in the reference sites than the cage sites (bacterial indicators of undisturbed sediments) during the Yellow Bluff March 2020 survey were rare or absent (relative abundance below 1%) (Figure 4-60). Most notably, the Nitrosococcaceae were rare or absent at NUB-1, NUB-2, NUB-3 and SB-21 in both 2019 and 2020. Generally bacterial families that that had higher relative abundance in the cage sites than the reference sites during the Yellow Bluff March 2020 survey (bacterial indicators of disturbed sediments) were rare or absent at the broad-scale monitoring sites. The most notable exceptions to this were the Flavobacteriaceae, Rhodobacteraceae and Saprospiraceae which appeared in higher relative abundances at a range of sites in both the 2019 and 2020 broad-scale surveys (Figure 4-60).

These results suggest that the proposed bacterial indicators of disturbed sediments likely exist in low abundances throughout Storm Bay sediments but only thrive in disturbed sediments such as those underneath salmon farm cages. The proposed bacterial indicators of undisturbed sediments were almost ubiquitous in the broad-scale sites (Figure 4-60), suggesting that their low abundance in sediments under salmon cages may be driven by sensitivity to aquaculture-related disturbance. MicroGAMBI showed promise as a broad-scale monitoring metric as it only indicated environmental disturbance at sites close to sources of organic enrichment.

Broad-scale (18S rRNA Metabarcoding)

The environmental drivers of 18S rRNA derived eukaryote community structure were similar to the drivers of the bacterial communities in Storm Bay. Percent carbon and nitrogen, organic carbon content (LOI%) and the proportion of silt (<0.063 mm) were positively correlated with eukaryote communities in the sheltered sites located in Nubeena and Norfolk Bay (SB-21, NUB-1, NUB-3) (Figure 4-61). Depth, redox potential, and proportion of sand particles (0.125 mm and 0.250 mm) were most strongly positively correlated with eukaryote communities in the centre and southeast of Storm Bay experiencing greater oceanic influence (SB-19, SB-18, SB-24, SB-16, NUB-4, SB-2, SB-23, SB-11 and SB-4) (Figure 4-61).

While there were similarities in Storm Bay eukaryotic and bacterial community relationships with environmental variables, the eukaryote community was the less powerful tool for differentiating sites in different habitats. Cluster analysis identified four groups of samples based on the eukaryotic communities in Storm Bay compared to seven for the bacterial communities (Figure 4-59, Figure 4-61), as a result the eukaryotic community groupings were coarser than the bacterial groupings. For example, the eukaryote communities did not

differentiate sites in the north of Storm Bay (SB-13, SB-1, SB-17, SB-9 and SB-22) from those in Nubeena (NUB-1 NUB-2 and NUB-3) (Figure 4-62). Eukaryote communities from each site did not differ in their group assignment between years, indicating minimal temporal variation compared to spatial variation (Figure 4-61). Because 16S rRNA metabarcoding appeared to be the more sensitive broad-scale monitoring method, for the purpose of this summary we did not investigate the relationship between eukaryote taxonomic composition and spatial, temporal, or environmental variation across the Storm Bay broad-scale monitoring sites.

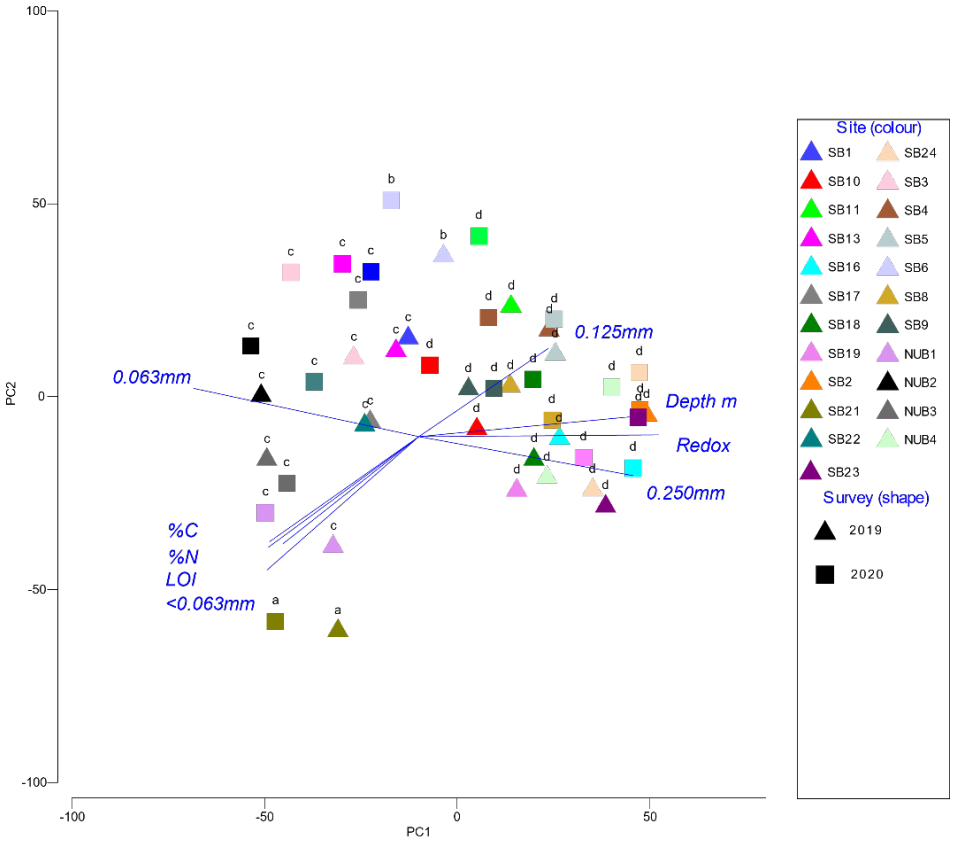

Figure 4-61: PCA ordination displaying Euclidean distances between 18S rRNA metabarcoding derived eukaryote communities at 23 sediment monitoring sites across 2 years. Distances were calculated between averaged CLR transformed data for each combination of site and survey. Labels for each point display the sample groups based on hierarchical clustering. Vectors show Pearson correlations with a coefficient of at least 0.5 between PCA axes and normalised environmental variables.

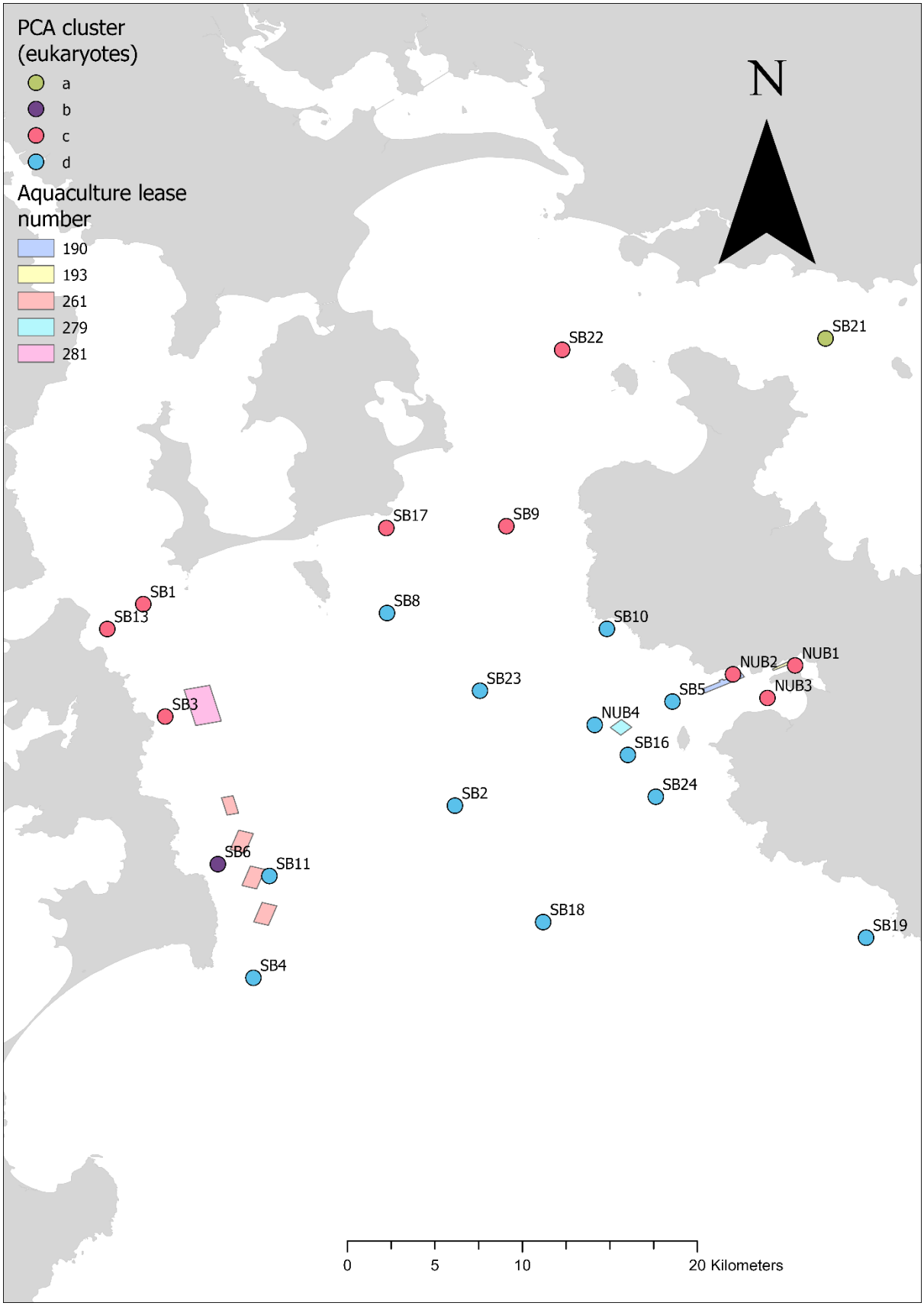

Figure 4-62: Map showing the location of 23 soft sediment monitoring sites where eDNA samples were collected in 2019 and 2020. The colour shows site groupings based on hierarchical clustering of Euclidean distances between site and survey averaged 18S rRNA eukaryote community data.

4.3.4 Cost-Benefit analysis

The cost-benefit analysis showed that a combined 16S and 18S rRNA eDNA metabarcoding approach to analysing sediment biological communities is more costly and time consuming compared to the macrofauna approach for smaller sample numbers but the eDNA method's cost and time efficiency increase dramatically when larger sample numbers are involved (Figure 4-63). We estimate that the combined eDNA method is more time efficient than the macrofauna approach if more than 14 samples are processed and more cost efficient if more than 96 samples are processed.

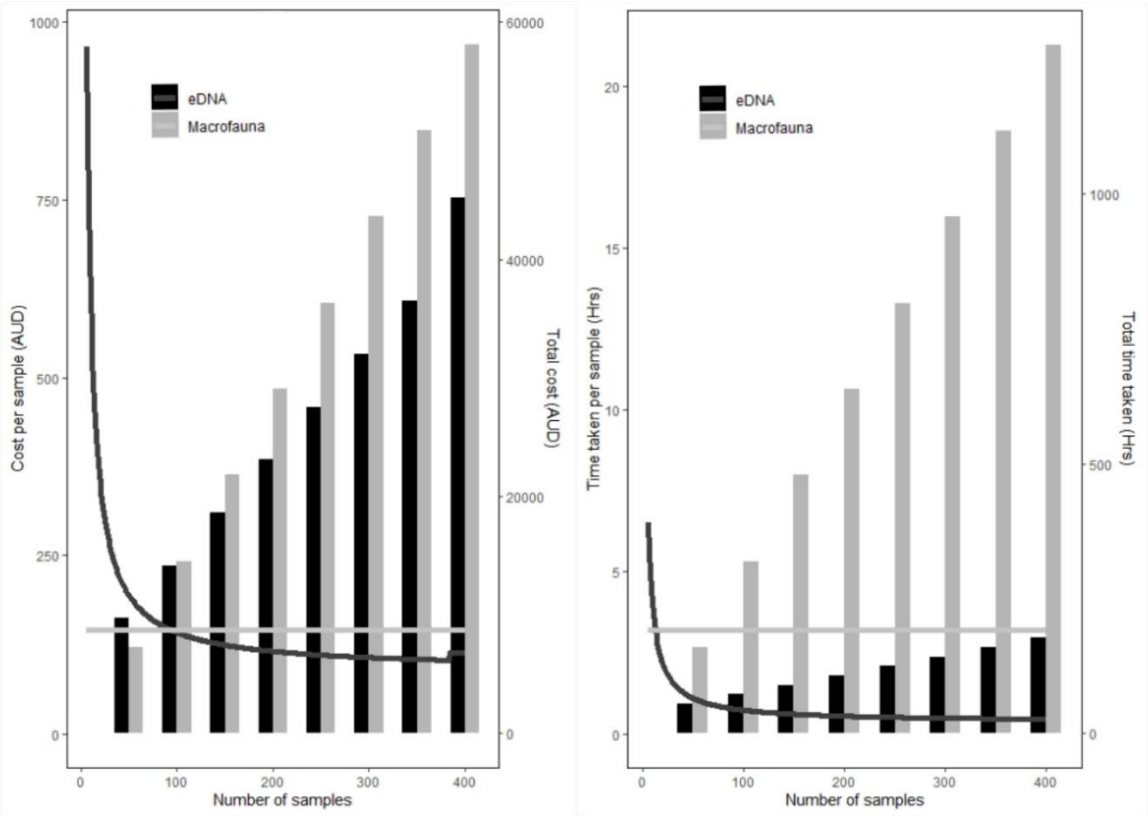

Figure 4-63: Results of the cost benefit analysis comparing a combined 16S rRNA and 18S rRNA metabarcoding method to traditional visual analysis of macrofauna for the same samples. The left plot shows the total monetary cost (bars) and cost per sample (lines) for both methods. The right plot shows total time taken (bars) and time per sample (lines) for both methods.

4.4 Sediment Monitoring – Summary

4.4.1 Local-scale

The local (lease) scale responses at both Yellow Bluff and West of Wedge (WoW) were consistent with expectations based on production levels and recent research documenting the spatial footprint of farms at more dispersive environments, including the Trumpeter and Storm Bay One leases (Ross et al. 2021). At the Yellow Bluff lease, the results of the more detailed initial peak production survey revealed a clear gradient of effect, but the difference between the transects revealed asymmetry in the footprint. Major to moderate effects for key biotic and abiotic response parameters typically occurred in closer proximity to the

cages (0 – 35 m) on the transects to the east and west, but to the north, moderate effects were evident out to 100 – 150 m from the cage. This pattern likely reflects a combination of current flow and particle dispersion to the north-west and greater stocking in proximity to the northern transect. In agreeance with previous research, benthic community composition appeared the most reliable, sensitive, and informative measure of sediment condition.

The application of the benthic health index, AMBI, that summarises the macrofaunal community data set into a single metric to characterises different levels of disturbance, also performed extremely well. Similarly, the application of environmental DNA metabarcoding showed that bacterial and eukaryote communities in Tasmania do exhibit a response to salmon aquaculture related disturbance, and that the bacterial community (16S rRNA) provides a more sensitive measure of enrichment. The eDNA analogue of AMBI, microgAMBI developed for bacterial datasets, correlated well with our macrofaunal based AMBI. MicrogAMBI described a similar disturbance gradient, from poor ecological status at the cage sites to good at the reference site, and poorer scores extending further from the cage on the northern transect.

There were very low levels of fish production at the WoW lease during the study period and this was reflected in the benthic response. There was no evidence of enrichment effects at the compliance and control sites, but as expected, enrichment effects were evident for the key biological measures and physico-chemical parameters at the cage sites. The hydrological conditions (e.g., greater bottom currents and significant wave height) at the West of Wedge lease are quite different to the Yellow Bluff and other leases on the western side of Storm Bay. As such, sampling should be repeated when the lease/s on the eastern side of Storm Bay (including West of Wedge) are much closer to peak production to fully understand the spatial extent and magnitude of the enrichment footprint.

At both leases, the assessment of performance at the compliance points (35 m from the lease boundary) highlighted the importance of assessing change relative to reference conditions, both prior to farming (the baseline) and at reference sites (i.e., to capture temporal change in reference conditions independent of farming). Similarly, we highlight the value of cage site sampling in providing context with regard to the expected response to farm enrichment. However, as discussed, ambiguity in the intended spatial and temporal scales in the current licence conditions and benthic criteria has led to a range of different interpretations; this needs to be addressed in the new Environmental Standards. At the Yellow Bluff lease, there were some occasions when the criteria, based on our interpretation, for significant physico-chemical impacts were met at the compliance sites. We argue that these measures of organic enrichment should be considered in the context of the more sensitive and reliable biological parameters. In March 2020, the increase in annelids and single-family dominance at compliance sites, largely attributable to the presence of the enrichment indicator species *Capitella* sp., and particularly at sites on the north-east boundary of the lease, confirms that the enrichment footprint extended over the lease boundary. However, an abundant and diverse community remained across all compliance sites in all surveys. Whilst confirming that the enrichment footprint could be detected at compliance points, AMBI showed that the level of disturbance at the more

affected sites remained in the upper range of the slightly disturbed classification. For context, cages sites were classified as moderate to heavily disturbed in all three surveys.

4.4.2 Broad-scale

The system-wide surveys captured the range of soft sediment habitats across the different geographical areas of Storm Bay. These habitats and the macrofaunal communities they support are shaped by physical oceanography (e.g., waves, currents and tides) and local characteristics such as depth, sediment particle size composition (e.g., silt content) and the availability of organic matter.

Fine sand was the dominant sediment type with small amounts of coarse sand, silt, and gravel. Sites in the south-east region had higher proportions of coarse sand which likely reflects greater exposure, while the shallower and more sheltered sites in Nubeena and Norfolk Bay contained more silt than others. Sediment redox potential across Storm Bay was on average high across all three surveys, and similarly sulphide concentrations were low. However, significant spatial and to a much lesser extent, temporal variability was also evident, which appears to reflect differences in hydrography and the concomitant changes in the physical sediment characteristics, i.e., lower redox and higher sulphide values were typically measured at sites that were in shallower, more sheltered areas with higher silt content. Although no clear and significant temporal trends were observed in redox, sulphide, or sediment C and N content, the mean $\delta^{15}N$ signature was lower and $\delta^{13}C$ signature higher in 2021 compared to 2020 and 2019. Both trends indicate a stronger marine origin in 2021 as the source of organic material to the sediments.

The benthic communities were rich and diverse across Storm Bay with crustaceans the most dominant group, making up 61% of samples. The exception was at the more sheltered locations (Nubeena and Norfolk Bay) where the sediments are typically finer, more organically enriched and annelids are the dominant taxa. Cluster analysis based on the macrofaunal communities was also used to identify groups of sites that may correspond to different habitat (environment) regions in Storm Bay. There were 4-5 major groupings of sites representative of the different habitats across Storm Bay, and there was a high degree of overlap with the groupings identified based on the eDNA bacterial community data. Although the spatial patterns and groupings remained relatively stable across the three years, there was a marked shift in benthic communities at most sites in 2021 relative to 2020 and 2019. The change appeared greatest at sites in the more exposed, deep and sandy regions of Storm Bay. Sediment isotope data suggest that a change in the source and/or amount of organic matter may help explain the shift in benthic community in 2021. Importantly, these changes are not consistent with the response we would anticipate due to the input of farm derived organic matter, i.e., more enriched sediments and an increase in faunal abundance.

In the absence of clearly defined indicators and thresholds for the broad-scale sediment environment, we provided a generalised assessment of benthic health using the biotic and abiotic indicators developed by Macleod and Forbes (2004) and recently validated for Storm Bay leases by Ross et al. (2021). There was no evidence of farm effects based on sediment chemistry or the more sensitive macrofaunal community measures. As such, we recommend

that the benthic indicators for assessing performance in the future are based on the results of the first three broadscale surveys reported here. These three surveys capture the spatial and temporal variation of the sediment environment and the key biotic and abiotic conditions. Further, we suggest the assessment of change is based on different regions in Storm Bay identified through the cluster analysis of macrofaunal communities. This will help constrain natural variation evident across the whole system and improve the power to detect change.

4.5 Recommendations

4.5.1 Local-scale

The requirements for local (lease) scale benthic surveys are well established, however, we recommend several modifications to the sampling design and assessment criteria to improve the power and utility of these surveys for detecting and managing salmon farm effects:

- The establishment of robust baseline conditions and ongoing monitoring of reference conditions remains critical for assessing environmental performance, we recommend:
    - The number of control (reference) sites sampled in baseline and ongoing performance assessments needs to be increased (≥4) to better capture background variation[6]. This is imperative to ensure there is adequate statistical power to assess environmental performance and compliance.
    - To ensure that both the direction and magnitude of the footprint can be determined with sufficient statistical power, at least 4 compliance sites should be sampled on the boundary/s of interest (e.g., proximity to production and direction of predominant current flow).
    - Sampling of cage sites should be included in benthic compliance surveys. This provides an 'upper end' of current impact, and in turn gives important context when interpreting the degree of change at compliance sites relative to reference conditions.
- The Environmental Standards should focus on change relative to baseline and reference conditions rather than a suite of standardised parameter thresholds.
- The technical standards that accompany the new Environmental Standard should provide detailed guidance on the required analysis and presentation of benthic compliance conditions, along with the survey design required to achieve robust results.
- Macrofauna continue to be the most reliable indicator of sediment conditions, with the sediment chemistry such as redox and sulphide providing location dependent measures of the enrichment footprint. Other parameters, such as the various measures of C and N in the sediments and sediment particle size analysis are

[6] This is consistent with the original recommendations of Crawford et al. (2002)

informative when establishing the background environmental conditions and provide context when describing monitoring results at a given site but are not reliable indictors of farm impacts. We suggest that beyond the baseline assessment, sediment 'archive' samples be collected for particle size and C and N and that these are only processed to help explain unexpected change in the other condition metrics and/or non-compliance.

- Consideration should be given to the inclusion of the benthic health index, AMBI, in lease performance assessments. It can provide a single, easily understandable metric for community data that has traditionally required expert knowledge to interpret.
- The application of environmental DNA metabarcoding at the Yellow Bluff lease suggests that the bacterial community (16S rRNA) provides a sensitive measure of enrichment, and similarly, the eDNA analogue of AMBI, microgAMBI. We suggest this approach be tested at other leases/environments.

4.5.2 Broad-scale

Further clarity needs to be provided on the purpose of the broad-scale sediment surveys and how it relates to management. The current environmental licences do not stipulate any conditions on the health of the benthos at far-field sites, but that a written interpretation of site-specific temporal change and any "unusual" results is required. From this we interpret that the far-field surveys are not required to identify lease specific change (i.e. attribution to a specific leases), rather to provide broader system context for local-scale surveys and any potential warning signs of system wide deterioration. Other findings and recommendations include.

- Benthic indicators for assessing performance should be based on the results of the first three broadscale surveys reported here. These three surveys capture the spatial and temporal variation of the sediment environment and the key biotic and abiotic conditions. There is no evidence of farm effects on the broadscale sediment environment from these initial surveys, and as such, we suggest they serve as the reference condition for assessing performance as the industry develops.
- We also agree with Thompson et al. (2008) that the level of risk and the need for further investigation is scaled based on the number of affected sites.
- Further, we suggest the assessment of change is based on different regions in Storm Bay identified through the cluster analysis of macrofaunal communities. This will help constrain natural variation evident across the whole system and improve the power to detect change.
- We suggest further exploration around the use of video as a monitoring tool for broad-scale sites. Initial findings indicate that it can provide additional utility by way of increasing site scale and the ability to capture potential impact responses not currently considered, i.e., epiphyte/drift algae, large mobile epifauna and physical characteristics.

- Given the relatively consistent grouping of sites which represent different environmental conditions (habitat regions) across Storm Bay (e.g. Figure 4-64) we suggest that annual surveys focus on a subset of sites representative of the different habitats across Storm Bay. These sites will effectively act as "sentinel" sites that indicate when the ecology of each habitat region may be changing.
- The full suite of 23 sites should be surveyed every 5 years and/or prior to any significant increase in farmed biomass across Storm Bay
- During the annual surveys, if any of the sentinel sites in a habitat region show clear signs of change relative to reference conditions (i.e. first 3 surveys) that is consistent with increased organic enrichment, then we recommend follow up surveys be undertaken at all other sites in the region/s. We also suggest this be accompanied by video surveys at sites to capture the potential for broader epibenthic change. The community metrics of change could include typical multivariate ordination techniques and/or a global benthic health index such AMBI which is regarded as sensitive to minor disturbances.
- A range of taxa that respond to lower levels of organic enrichment were documented. These species will provide a more sensitive measure of broad-scale change. Although their presence is characteristic of background conditions, their increased presence, from reference conditions (captured during the first three surveys), will likely provide an early indication of broadscale change. We note however, that a concomitant shift in benthic community composition is typically a more robust and reliable indicator of change than change in any individual species abundance.

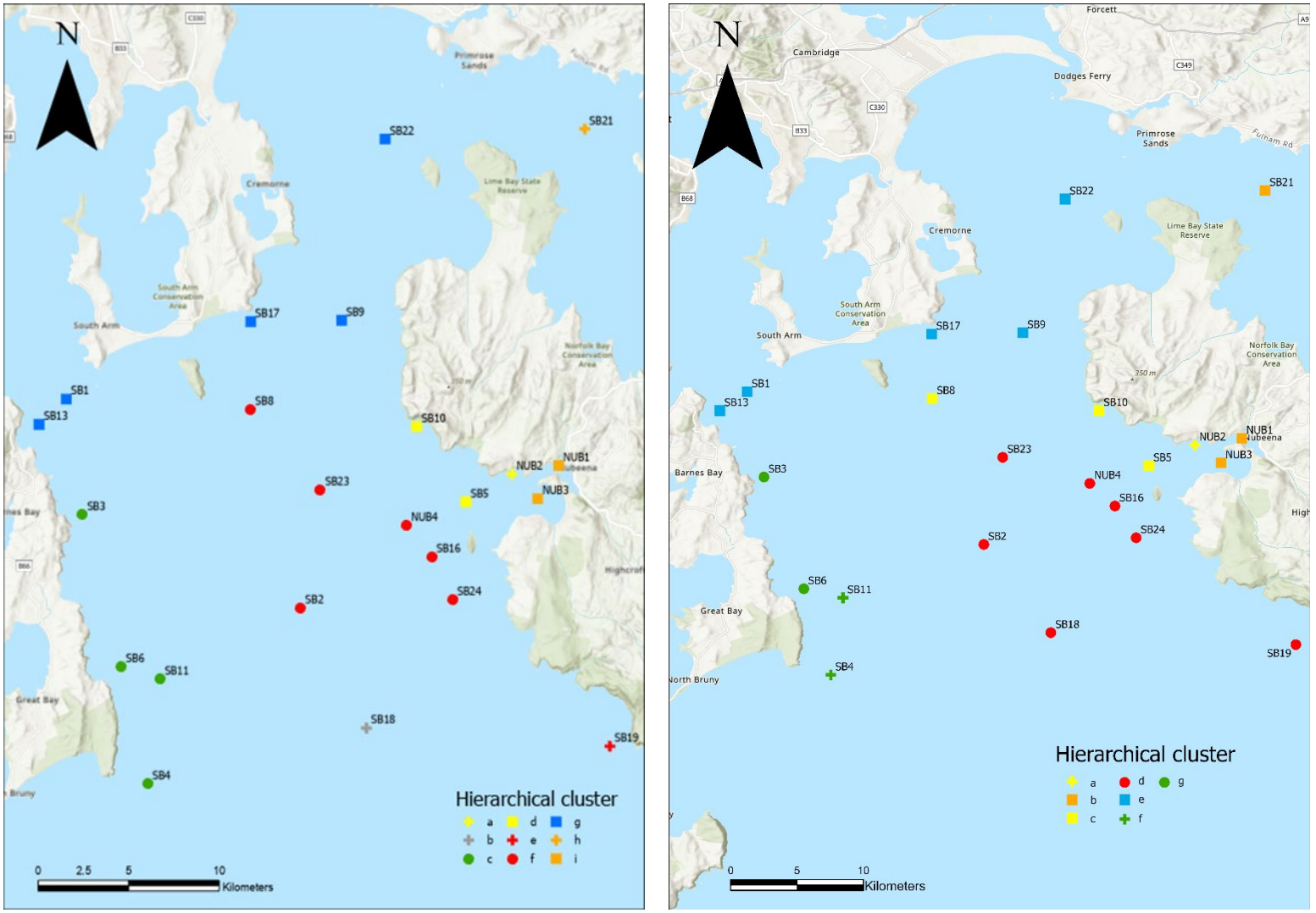

Figure 4-64: Maps showing the location of 23 soft sediment monitoring sites where macrofaunal samples (left map) were collected in 2019, 2020 and 2021 and eDNA samples (right map) in 2019 and 2020. The colour shows site groupings based on hierarchical clustering of Euclidean distances between site and survey averaged macrofaunal and 16S rRNA bacterial community data.

5 Inshore Reefs

As the industry has expanded in Tasmanian coastal waters, the need to better understand the interaction between salmon farming and inshore reef systems has been increasingly recognised (Oh et al. 2015, Ross et al. 2021). Monitoring of inshore rocky reefs is now an environmental licence requirement of both the Okehampton Bay and the Storm Bay BEMP programs. Nutrients and organic matter enrichment, regardless of the source, can affect inshore reefs via several pathways, both direct and indirect (see Figure 5-1). Excess nutrients can be taken up directly by algae but can also lead to increased sedimentation onto the reef through increasing water column productivity. Increased sedimentation can also occur directly through inputs of particulate organic matter (White et al. 2022b; Figure 5-1). In some cases, sustained nutrient enrichment can cause a phase shift in the reef ecosystem, with broadscale loss of the canopy-forming macroalgae (Eriksson et al. 2002, Connell et al. 2008). Loss of canopy-forming species can potentially have significant impact on reef biodiversity and function. Unfortunately, a management response often only occurs after widespread canopy loss, which is generally too late (Campbell et al. 2014). Therefore, methods for monitoring the potential effects of salmon farm inputs on inshore temperate reefs need to be sensitive enough to detect a loss of resilience or impact of organic enrichment prior to canopy loss occurring.

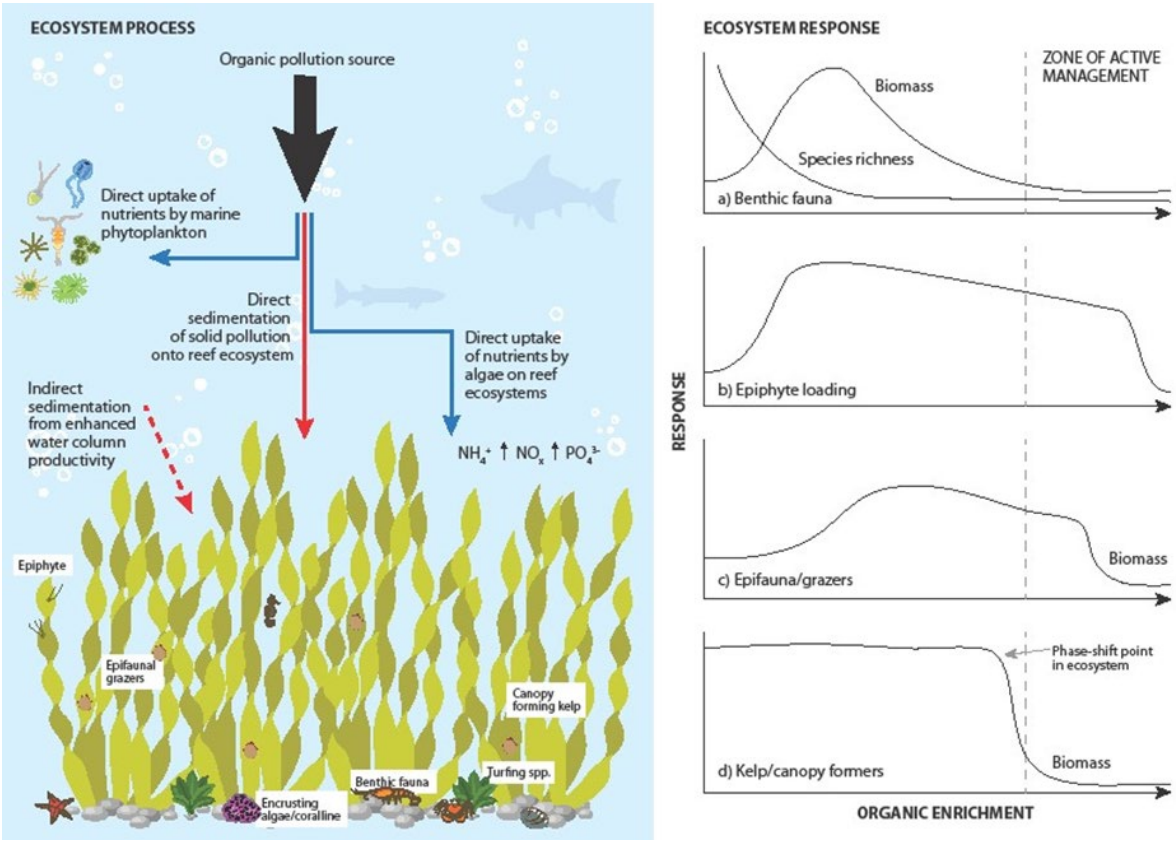

Figure 5-1: Schematic of potential pathways for impacts on temperate reef ecosystems through organic enrichment (White et al. 2022b, *in review*).

To ensure that monitoring can capture early warning signs of nutrient enrichment, but also document broader ecological condition and change of reef ecosystems, two survey techniques have been adopted in the Storm Bay BEMP. The "Edgar-Barrett" method provides a full census of all fish, invertebrate and algae species at a given site, whilst the Rapid Visual Assessment (RVA) method targets functional groups and indicator species that have relevance to organic enrichment, thereby providing an early indication of organic enrichment on temperate reef ecosystems.

The biodiversity surveys operate primarily as an important baseline for the region, documenting the abundance and diversity of all fish, invertebrates and algae. This survey method is designed to maximise the ability to detect i) changes in population numbers and size-structure, ii) cascading ecosystems effects associated with disturbance and iii) long-term change and variability in temperate reef assemblages (Edgar & Barrett 1997, Edgar & Barrett 1999). To track ecosystem shifts through time, Edgar-Barrett surveys are generally revisited at sites every 5-10 years. Because the method has been consistently implemented across both Tasmania (including at sites in Storm Bay) and southern Australia for over 25 years, it is also possible to compare local results to a broader database and separate out local impacts (e.g. salmon farming) from more regional or broad-scale changes (i.e. climate change). While the value of Edgar-Barrett biodiversity surveys is without question, their ability to detect a loss of resilience or impact of organic enrichment prior to canopy loss is limited. While they will certainly detect when a phase-shift has occurred, they may be less sensitive to a loss in resilience, specifically to nutrient enrichment from salmon farming. A review of these methods in Valentine et al. (2016) concluded that a more targeted approach would be useful in assessing the impacts of salmon farming on temperate reef ecosystems in south-eastern Tasmania.

To that end, FRDC project 2015-024 developed a Rapid Visual Assessment (RVA) survey that would detect change in ecosystem function due to organic enrichment (Ross et al. 2021). The RVA was designed to be complementary to the Edgar-Barrett surveys and provide the means to rapidly assess functional change and loss of resilience due to organic enrichment. This survey method was designed to be undertaken biannually, so prolonged growth of enrichment associated species could be separated from acute ecosystem responses to pulse nutrient that occur seasonally, or with rainfall events. While FRDC project 2015-024 has demonstrated the utility of the RVA to detect change on reef systems relating to nutrient enrichment, there is still a need to refine the most suitable indicator suite and its relevant thresholds to inform management. A critical element of this refinement will come through the collection of survey data across multiple years and sites in Storm Bay, after which the project will make recommendations for ongoing monitoring.

The focus of this component of the study was to implement these methods in Storm Bay with the following objectives:

1. Document the broad scale spatial and temporal dynamics of Storm Bay inshore rocky reef habitats.
2. Assess the capacity of the inshore reef monitoring program to measure reef health and the interactions with salmon farming.

3. Recommend any potential modifications to the inshore rocky reef monitoring program (e.g. design, variables, analysis).

5.1 Design & Survey Methods

Surveys were conducted at 30 inshore reef sites in Storm Bay between 2019 and 2022 (Figure 5-2). Each site was surveyed using the two different survey methods: the biodiversity (or 'Edgar-Barrett') method and rapid visual assessment (RVA). For each site, biodiversity surveys were conducted initially during late summer/early autumn, followed by biannual RVA surveys, during late summer and late winter each subsequent year.

A summary of when biodiversity surveys were undertaken at each site is shown in Table 5-1. Originally, all sites were to be surveyed across 2019 and 2020, however, COVID delays resulted in this timeframe extending into 2021. Following initial biodiversity surveys, rapid visual assessment (RVA) surveys were undertaken biannually (during winter and summer) at each of the Storm Bay inshore reef sites (Table 5-2). RVA surveys were undertaken biannually at the western sites since winter 2019. For six of the eastern sites, biannual RVA surveys commenced following biodiversity surveys in winter 2020, and for the remaining 10 sites, biannual RVA surveys were undertaken since winter 2021.

5.1.1 Biodiversity surveys

The method involves surveying 4 x 50 m transects per site split over 200 m along a continuous depth contour. The survey method utilised three census techniques to record descriptive information on reef biodiversity along the transects at different spatial scales:

- Fish abundance and size were surveyed in two 5 m-wide blocks on either side of the transect line by a diver swimming parallel to the transect line.
- Mobile invertebrates and cryptic fish were surveyed in a 1 m block by a diver swimming adjacent to the transect line.
- The abundance of macroalgal species and sessile invertebrates was recorded by placing 0.25 m^2 quadrats at 10 m intervals along the transect line (i.e., 5 quadrats per 50 m transect) and quantifying the percentage cover of these species within each quadrat. The quadrat was divided into a grid of 7 x 7 perpendicular wires, giving 50 points (including one corner). Cover was estimated by counting the number of times each species occurred directly under the 50 points within the quadrat (1.25 m^2 total area for each of the 50 m transects). Taxa that could not be reliably identified to the species level were recorded and included in the dataset at the genus level or as a functional group e.g. 'filamentous brown algae.' These taxa were excluded from species richness counts.

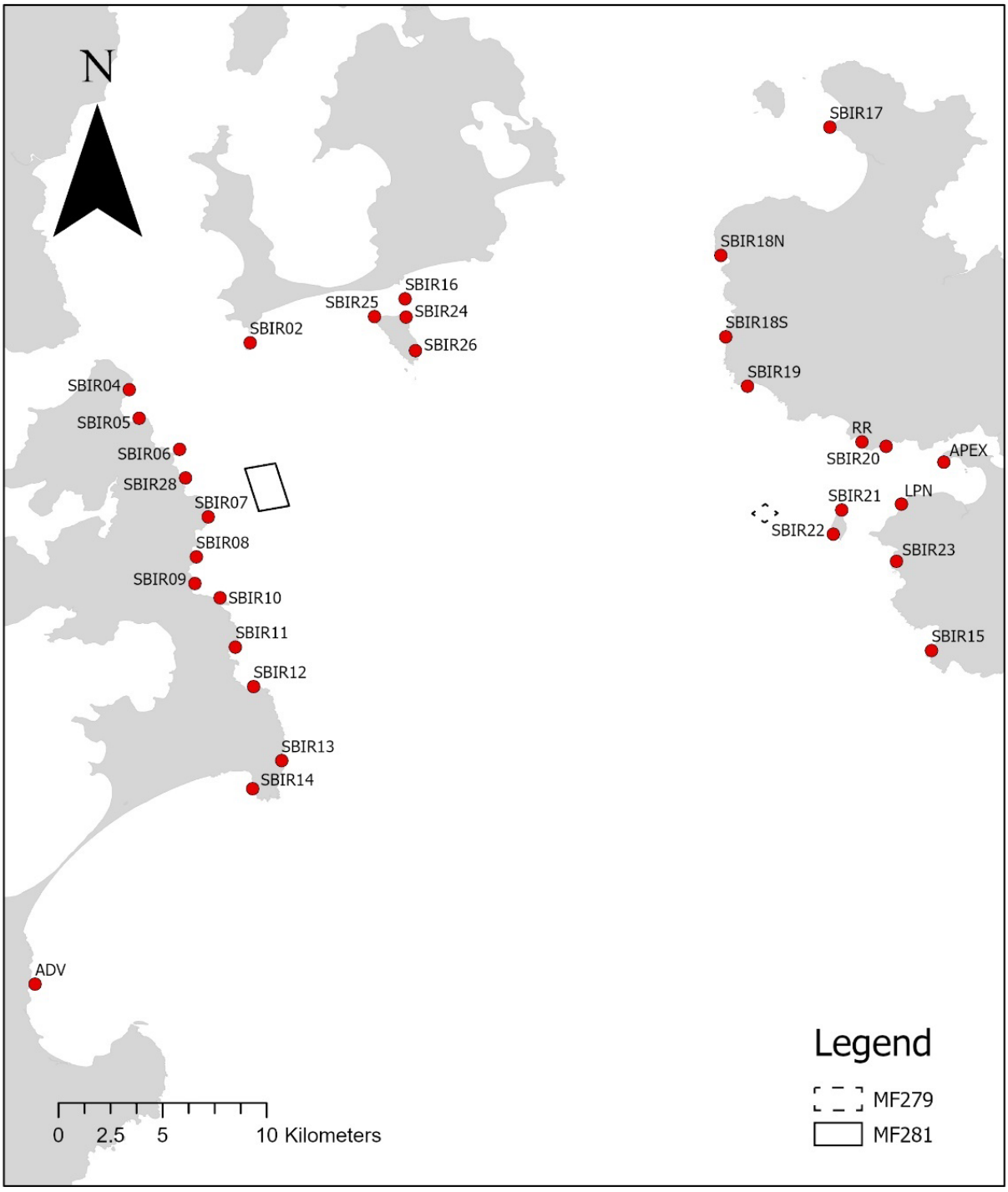

Figure 5-2: Map showing the locations of the inshore reef sites at which biodiversity surveys and RVAs were undertaken from 2019-2022.

Table 5-1: Summary of the timeline of biodiversity surveys conducted at the Storm Bay inshore reef sites. Shaded cells indicate that a survey was conducted at that site during that survey event.

	Biodiversity surveys		
Site code	Summer 2019	Summer 2020	Summer 2021
SBIR02			
SBIR04			
SBIR05			
SBIR06			
SBIR28			
SBIR07			
SBIR08			
SBIR09			
SBIR10			
SBIR11			
SBIR12			
SBIR13			
SBIR14			
ADV			
SBIR25			
SBIR24			
SBIR26			
SBIR16			
SBIR17			
SBIR18N			
SBIR18S			
SBIR19			
RR			
SBIR20			
APEX			
LPN			
SBIR21			
SBIR22			
SBIR23			
SBIR15			

Table 5-2: Summary of the timeline of RVA surveys conducted at the Storm Bay inshore reef sites. Shaded cells indicate that a survey was conducted at that site during that survey event.

Site code	RVA surveys						
	Winter 2019	Summer 2020	Winter 2020	Summer 2021	Winter 2021	Summer 2022	Winter 2022
SBIR02							
SBIR04							
SBIR05							
SBIR06							
SBIR28							
SBIR07							
SBIR08							
SBIR09							
SBIR10							
SBIR11							
SBIR12							
SBIR13^							
SBIR14							
ADV							
SBIR25							
SBIR24							
SBIR26							
SBIR16							
SBIR17							
SBIR18N							
SBIR18S							
SBIR19							
RR							
SBIR20							
APEX							
LPN							
SBIR21							
SBIR22							
SBIR23							
SBIR15							

^An initial biodiversity survey was undertaken at SBIR13, however, conditions at this site were deemed unsuitable for regular monitoring. As a result, this site was excluded from the reef survey program.

5.1.2 Rapid Visual Assessment (RVA) surveys

This method uses 15 functional parameters as a proxy for ecosystem health. Of these, 10 are broad structural parameters associated with ecosystem function, while five relate solely to enrichment response, as follows:

- Macroalgae (e.g., canopy algae, understorey brown/green/red algae)
- Substrate type (e.g., encrusting coralline algae, encrusting red algae, turfing algae, sponge cover)
- Trophic effects (e.g., dominant mobile invertebrates, encrusting fauna on algae)
- Enrichment indicators (e.g., epiphytic algae, filamentous algae, nuisance algal species [green: *Ulva*/*Chaetomorpha*, red: *Asparagopsis*] and dust on algae)

As canopy-forming algae have a disproportionate influence on the function of reef systems, canopy cover was also assessed at the species level as part of these surveys. Sites were assessed through diver surveys using 1 m^2 quadrats at 12 fixed locations at any given site. All 15 functional parameters were scored in each quadrat, with the quadrat also photographed for archival purposes.

5.1.3 Data analysis

For each of the three techniques, patterns in abundance and species richness (total number of species across transects), along with patterns in abundances of key species, were visualised using bubble plots developed in ArcGIS Pro. As *Trachinops caudimaculatus* (southern hulafish) were often present in excess of 1000 individuals, they were found to dominate trends in the data disproportionate to their ecological influence. Similar trends were found for *Cenolia trichoptera* and *Meridiastra calcar* in the invertebrate data. To lessen their influence, and following an initial examination of the data, these three species were square root transformed prior to any subsequent community analysis. For multivariate analyses, fish and invertebrate datasets were also log transformed, to account for the large number of species present in low abundances. No transformation was applied to the algae dataset. Multivariate analyses included non-metric multidimensional scaling (nMDS) in the PRIMER v7 software package (Clarke et al. 2014). Pearson's vector overlays were used to determine which taxa were driving dissimilarities between sites. Spatial and temporal variability in reef function was first examined with both agglomerative hierarchical (cluster analysis) and non-hierarchical (kRCluster) routines employed. Both routines used SIMPROF with a probability cut-off of $p \leq 0.1$ to determine significant groupings in data.

Diversity metrics were calculated for each of the three techniques, using the "vegan" package in R. The following calculations were used for each of the key metrics, as per Oksanen (2013):

Shannon Diversity Index:

$$H = -\sum_{i=1}^{S} p_i \, log_b \, p_i$$

Where p_i is the proportion of species i, and S is the number of species so that $\Sigma_{i=1}^{S} p_i = 1$, and b is the base of the logarithm.

Alpha diversity $(\boldsymbol{\alpha})$**:** mean species richness per site.

Gamma diversity $(\boldsymbol{S})$**:** total number of species across all sites.

Beta diversity:

$$\beta = \frac{S}{\alpha} - 1$$

RVA data were examined using non-metric multidimensional scaling (nMDS) in the PRIMER v7 software package (Clarke et al. 2014). For nMDS analyses, the percentage cover of each functional parameter for each site was converted to a Bray-Curtis similarity matrix index

(Clarke et al. 2014). This analysis was used to produce a graphical depiction of the similarity/dissimilarity in the 15 functional parameters between sites and surveys. Pearson's vector overlays were used to determine which of the 15 parameters were driving the dissimilarity between surveys and sites. Cluster analyses, including both hierarchical and non-hierarchical (kRCluster) approaches, were also used to examine similarities between sites and surveys. For both agglomerative hierarchical and non-hierarchical techniques, a SIMPROF of $p \leq 0.1$ was applied to examine consistent groups within the data. For all sites, interannual trends in individual parameters were examined across all RVA survey events to date.

5.2 Results

5.2.1 Spatial variability in biodiversity

From 30 sites across Storm Bay, we observed a total of 78 fish species (11,703 individuals in total), 54 invertebrate species (12,383 individuals in total) and 121 species of macroalgae and sessile invertebrates (Appendix 5-1). Patterns in abundance and diversity varied between each of these groups across Storm Bay. Fish communities were generally dominated by species from the families Labridae, Monacanthidae and Odacidae. Where *Trachinops caudimaculatus* (southern hulafish) was present, it was numerically dominant, with a total of 5525 individuals observed across all sites (Appendix 5-1). Other schooling fish that were observed included *Dinolestes lewini* (long-fin pike), *Pempheris multiradiata* (common bullseye), *Arripis trutta* (Australian salmon) and *Trachurus declivis* (jack mackerel) (Appendix 5-1). Of these, *A. trutta* and *T. declivis* are planktivorous and transient, whereas *D. lewini* and *P. multiradiata* are likely to be reef resident. Numerically, feather stars (namely *Cenolia trichoptera*) were the dominant invertebrate group recorded, although consistent numbers of *Jasus edwardsii* (southern rock lobster), *Heliocidaris erythrogramma* (short-spined urchin) and *Haliotis rubra* (blacklip abalone) were found across Storm Bay (Appendix 5-1). Canopy-forming macroalgae was the dominant functional group across benthic communities on inshore reefs in Storm Bay, with most sites dominated by either *Phyllospora comosa* (crayweed) or *Ecklonia radiata* (common kelp; Appendix 5-1). Red algae were the most diverse functional group, often accounting for over half of the algal species richness observed at any given site (Appendix 5-1).

When trends in abundance of fish and invertebrates are examined at a bay-wide scale, the highest abundance of fish were recorded at SBIR02, SBIR26, SBIR17, Apex, SBIR22 and SBIR28 (≥ 80 individuals per transect; Figure 5-3). Higher abundances at these sites were due to elevated numbers of the common species listed above (Appendix 5-1). SBIR25 and SBIR21 recorded high mobile invertebrate abundance (≥ 110 individuals per transect), with SBIR17 and Apex also elevated (Figure 5-4). Comparatively higher numbers of *H. erythrogramma* were recorded at these sites (≥ 100 individuals per transect) and contributed to a large proportion of the total abundance observed (Appendix 5-1).

Diversity was examined using a range of metrics for fish, invertebrates and macroalgae across Storm Bay (Appendix 5-2). Shannon diversity values for fish were generally highest on the western side of Storm Bay, with Adventure Bay, SBIR14, SBIR07, SBIR06 and SBIR04 higher than all other sites (Figure 5-5). While SBIR02, SBIR26 and SBIR17 all recorded higher

fish abundance, the Shannon diversity was particularly low at these sites, suggesting fish populations at these sites were dominated by only a few species in high abundance (Figure 5-3, Figure 5-5). Diversity metrics for mobile invertebrates indicated a much more even distribution of species across Storm Bay (Figure 5-6), although SBIR14, SBIR21, SBIR22 and Apex were comparatively lower in terms of Shannon diversity. At these sites, *C. trichoptera* and/or *H. erythrogramma* were present in large numbers, often in tandem with lower species richness. In contrast to fish, the algal and sessile invertebrate diversity was generally higher in eastern Storm Bay, with all sites north of Creeses Mistake recording relatively high Shannon diversity values (Figure 5-7). SBIR04 and SBIR28 in the west were also comparatively diverse, with SBIR28 having a particularly high number of canopy-forming species present (Figure 5-7, Appendix 5-2).

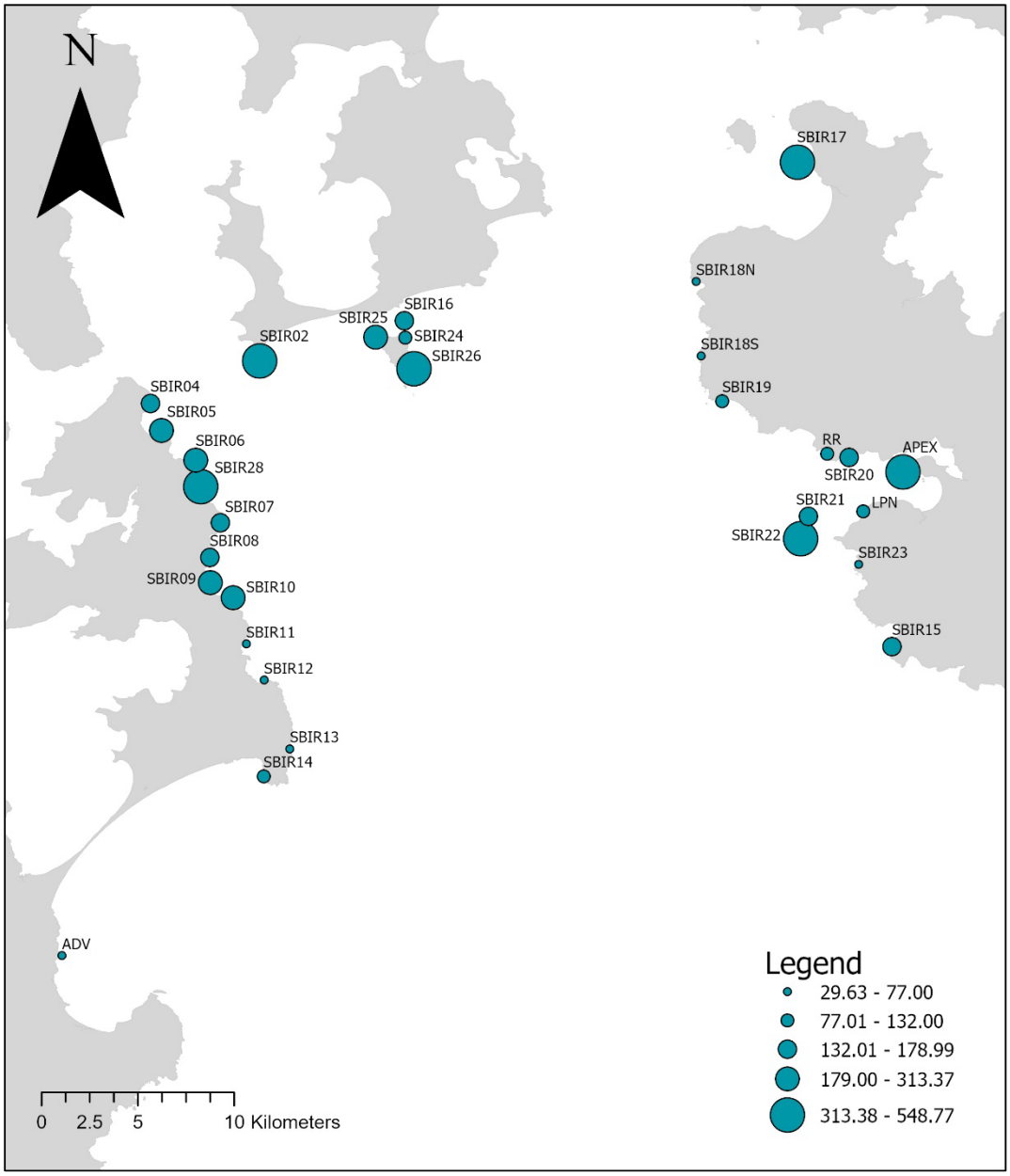

Figure 5-3: Storm Bay reef biodiversity sites with the size of the bubbles indicating the total abundance of fish at each site (abundance of all species summed across transects).

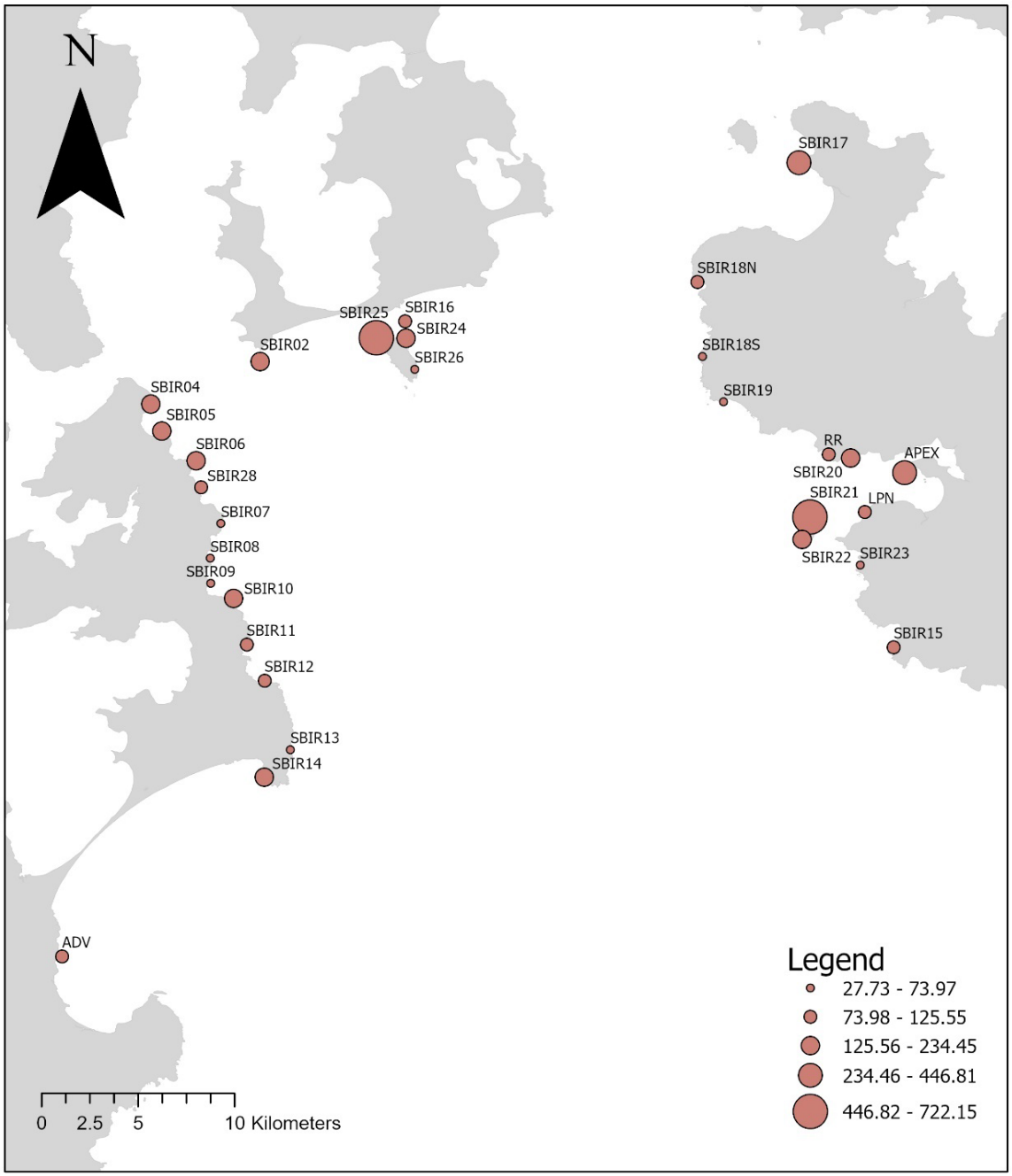

Figure 5-4: Storm Bay reef biodiversity sites with the size of the bubbles indicating the total abundance of invertebrates at each site (abundance of all species summed across transects).

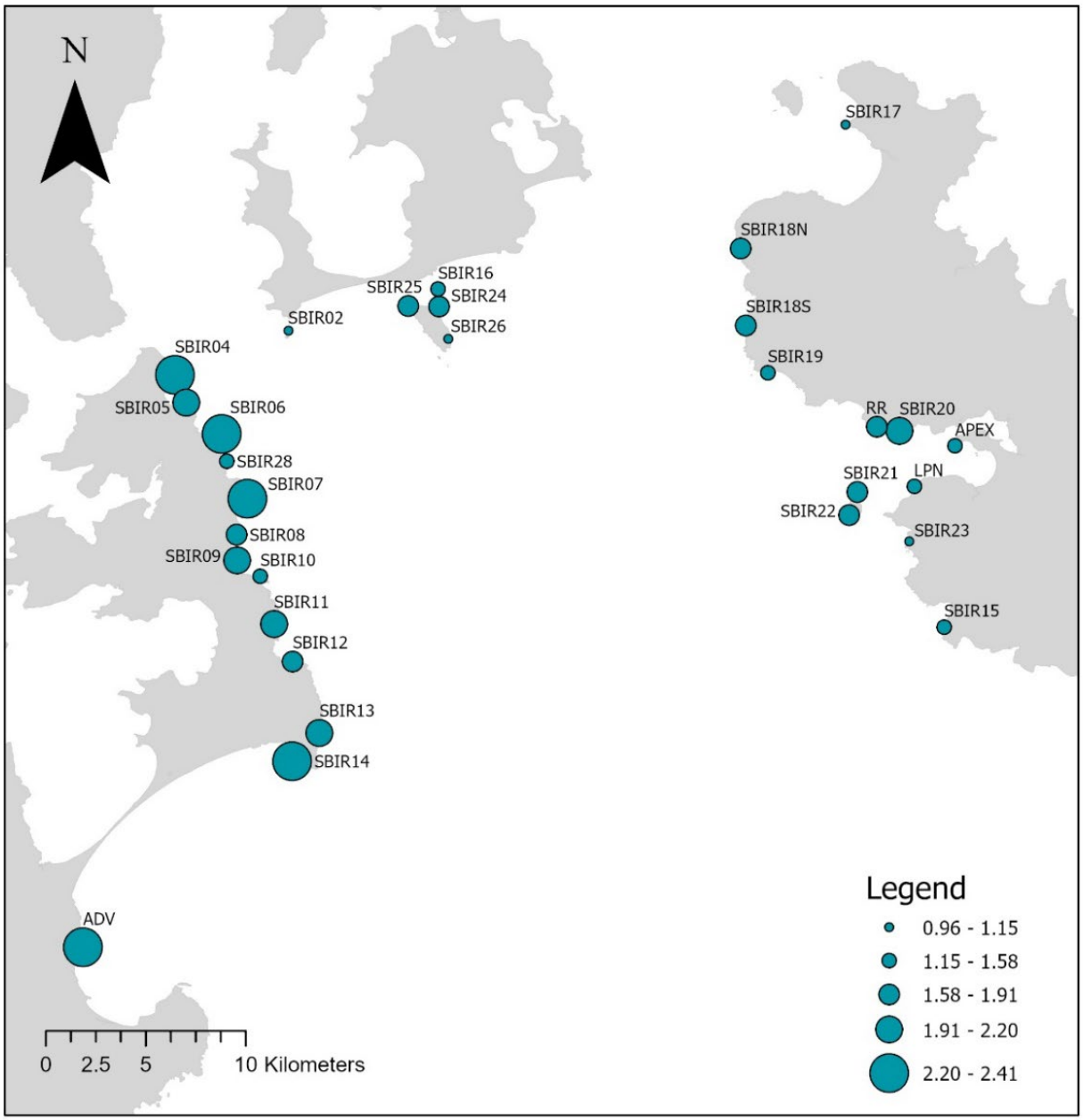

Figure 5-5: Storm Bay reef biodiversity sites with the size of the bubbles indicating the Shannon diversity values for the fish communities at each site.

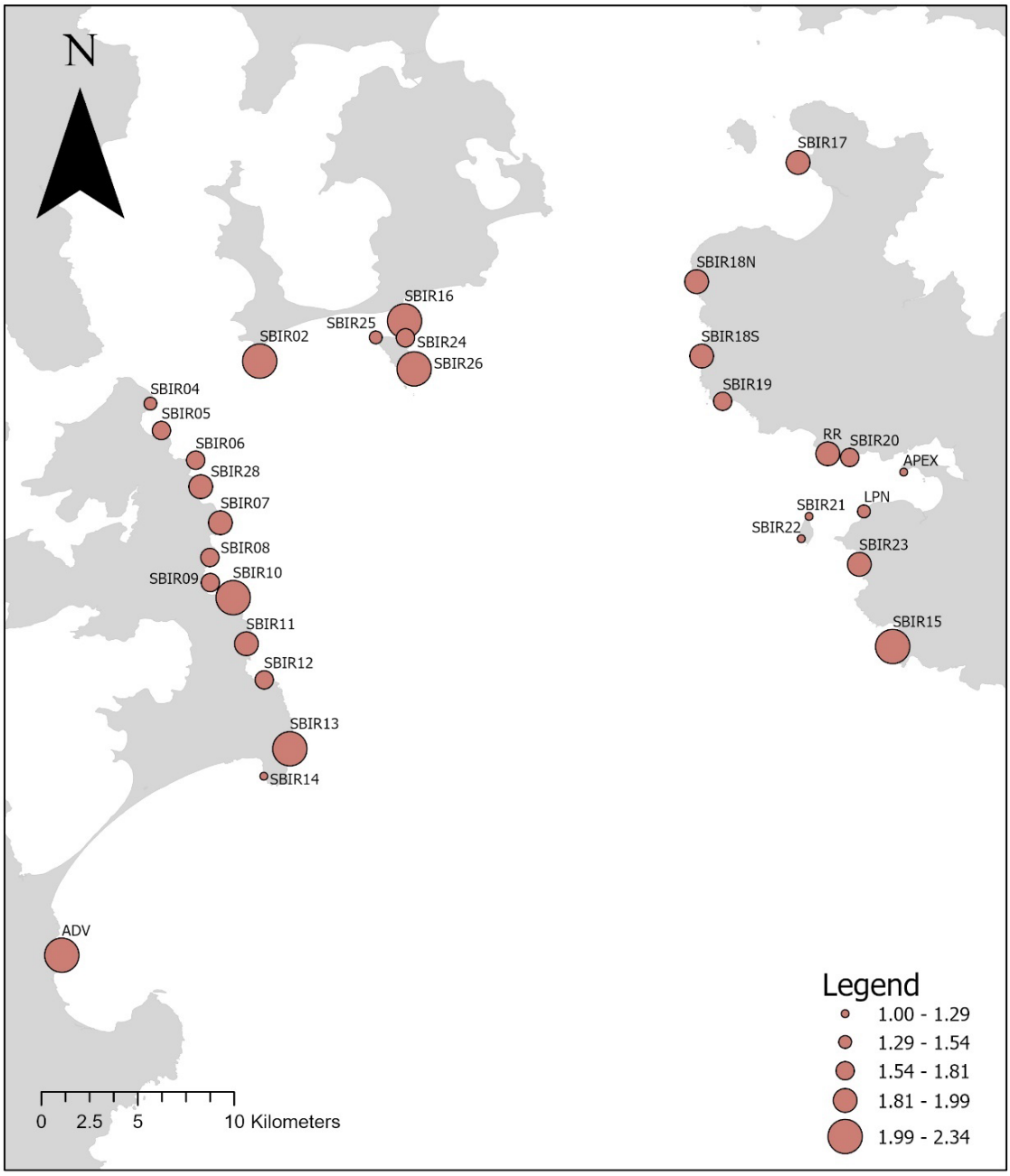

Figure 5-6: Storm Bay reef biodiversity sites with the size of the bubbles indicating Shannon diversity values for the mobile invertebrate communities at each site.

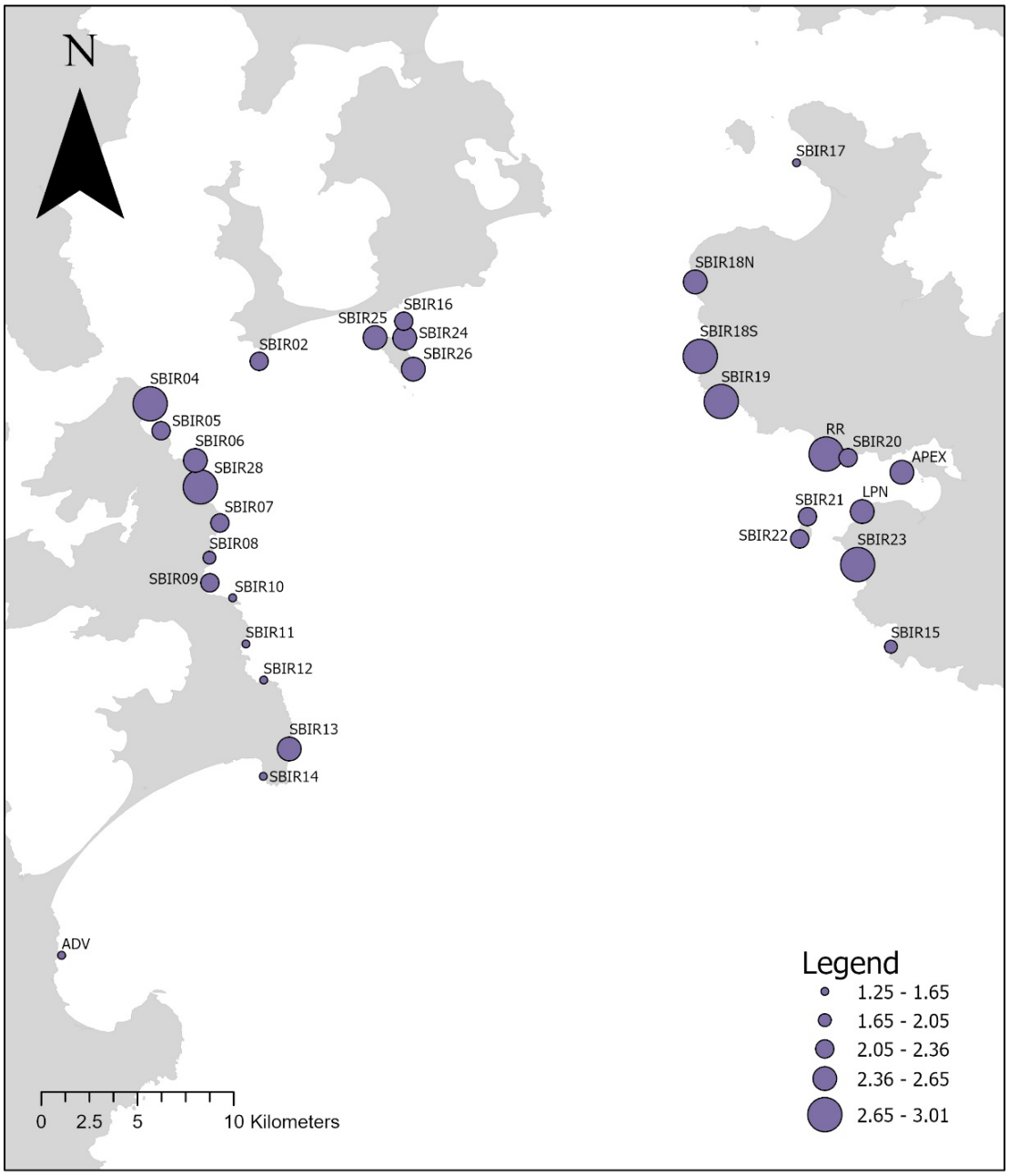

Figure 5-7: Storm Bay reef biodiversity sites with the size of the bubbles indicating Shannon diversity values for the algae and sessile invertebrate communities at each site. Note, only taxa which represent unique species were included in Shannon diversity calculations.

When fish, invertebrate and algal communities are examined at a community level, it is apparent that fish and invertebrate communities are more homogeneous across Storm Bay than macroalgal communities. Cluster analysis and kRCluster indicated four and three significant groupings within fish communities respectively, with groupings relatively similar between these two analyses (Figure 5-8, Figure 5-9). The largest cluster from both analyses was comprised of sites that tended to be lower in wave exposure from North Bruny, Betsey Island and within Nubeena (Figure 5-8, Figure 5-9). In contrast, invertebrate communities had only two significant clusters, with only SBIR13 changing groups between analysis methods (Figure 5-10, Figure 5-11).

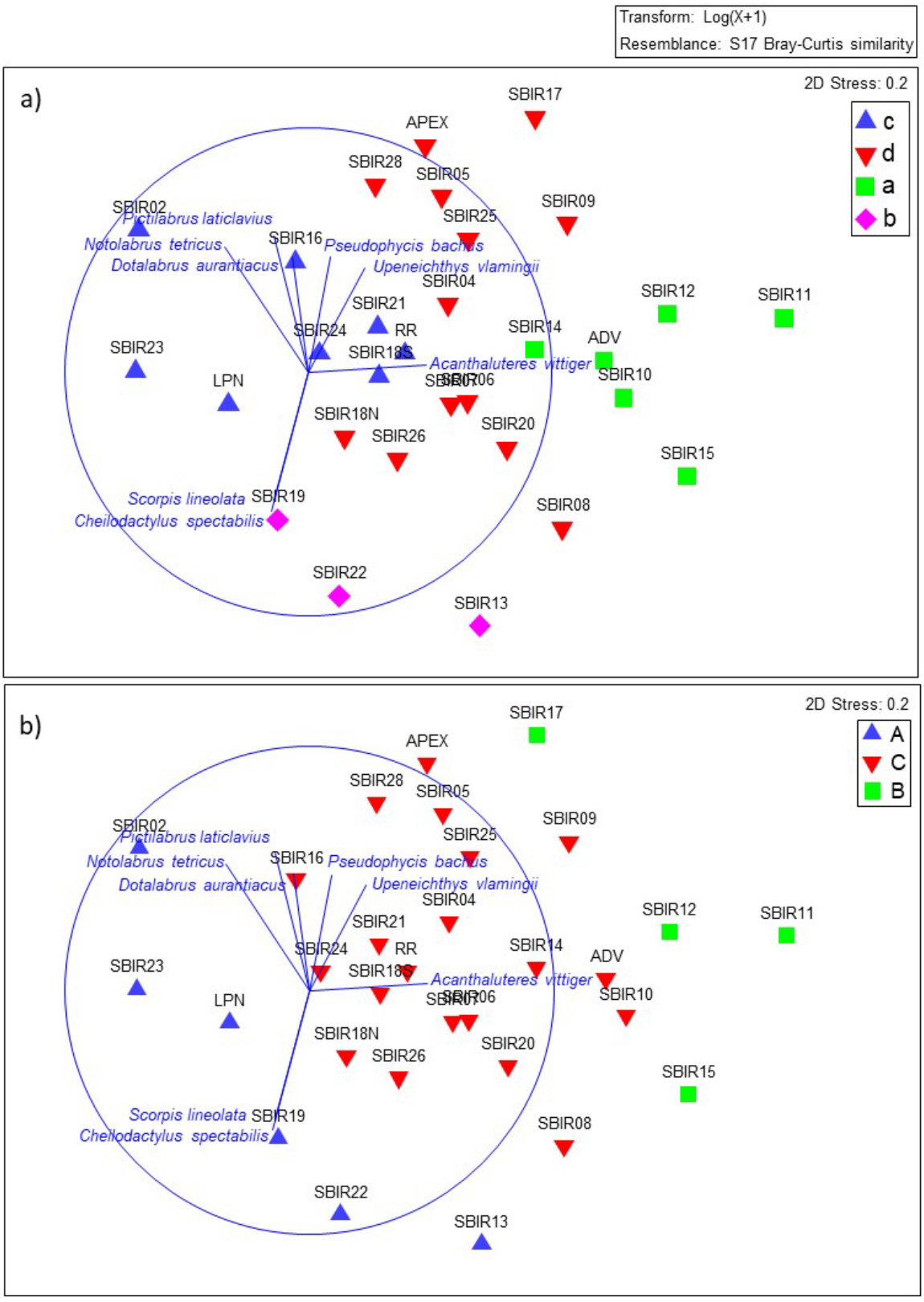

Figure 5-8: nMDS on fish community assemblages across Storm Bay, with data averaged at a site level across the four transects. Groupings represent a) hierarchical cluster analysis and b) kRClusters both with a SIMPROF value of 0.01. Pearson's vector overlays contributing to ordination with a base variable comparison of >0.5 are included. The length of the vectors indicates the strength of the correlation.

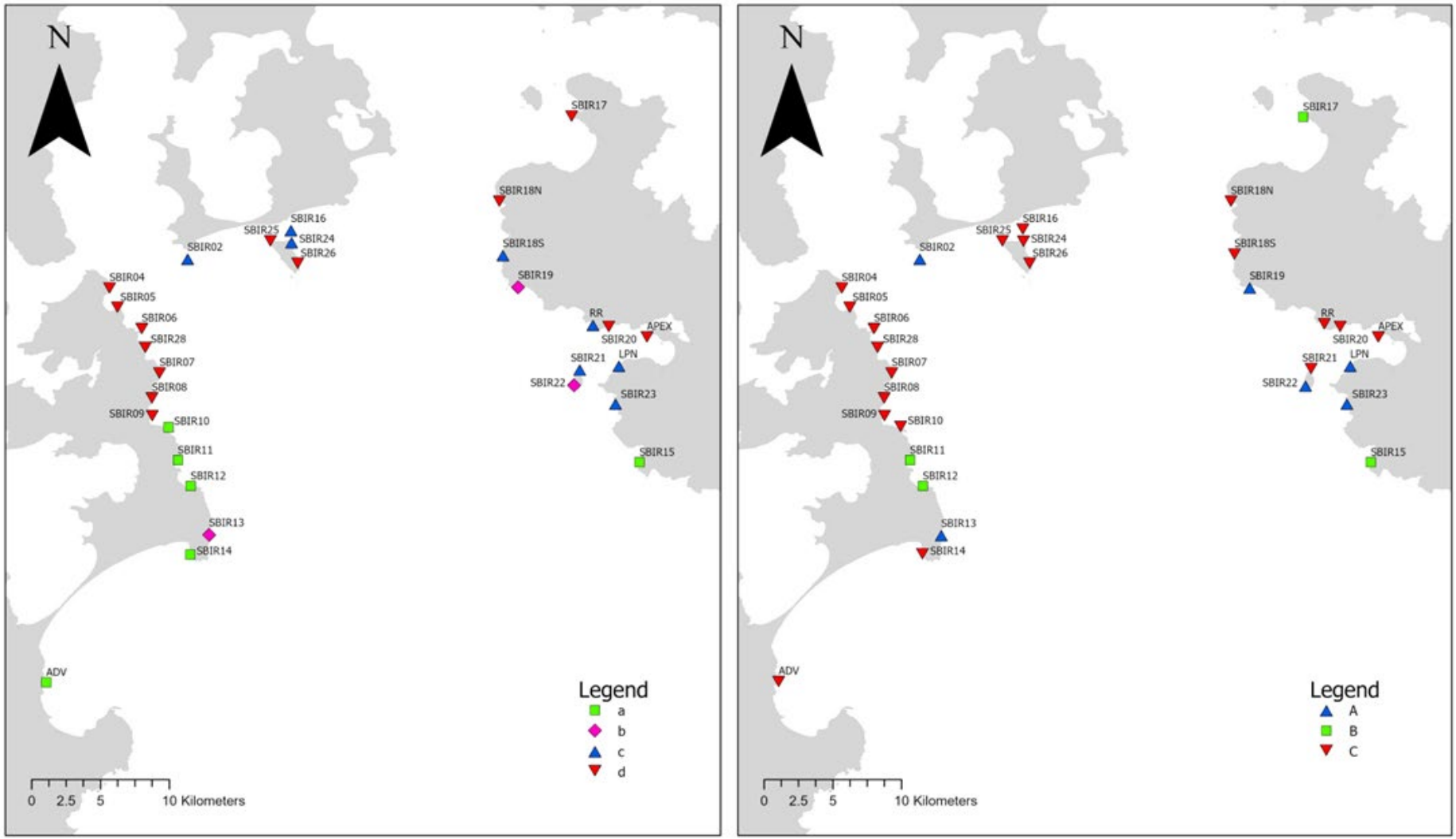

Figure 5-9: Storm Bay reef biodiversity sites, with symbols indicating groupings of fish community assemblages as determined through hierarchical cluster analysis (left) and kRCluster analysis (right), both with a SIMPROF significance measure of 0.01.

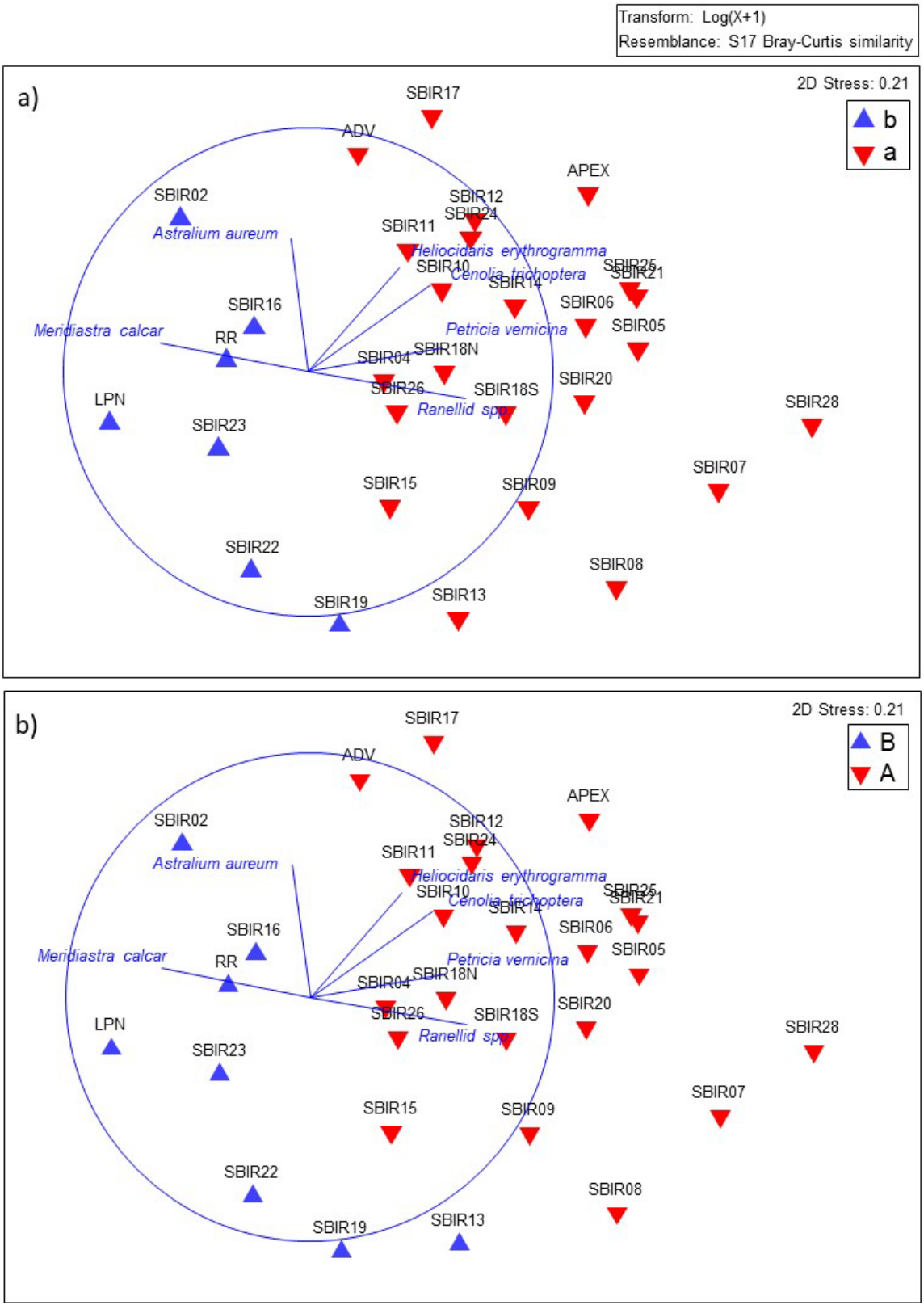

Figure 5-10: nMDS on mobile invertebrate assemblages across Storm Bay, with data averaged at a site level across the four transects. Groupings represent a) non-hierarchical clusters and b) kRClusters both with a SIMPROF value of 0.01. Pearson's vector overlays contributing to ordination with a base variable comparison of >0.6 are included. The length of the vectors indicates the strength of the correlation.

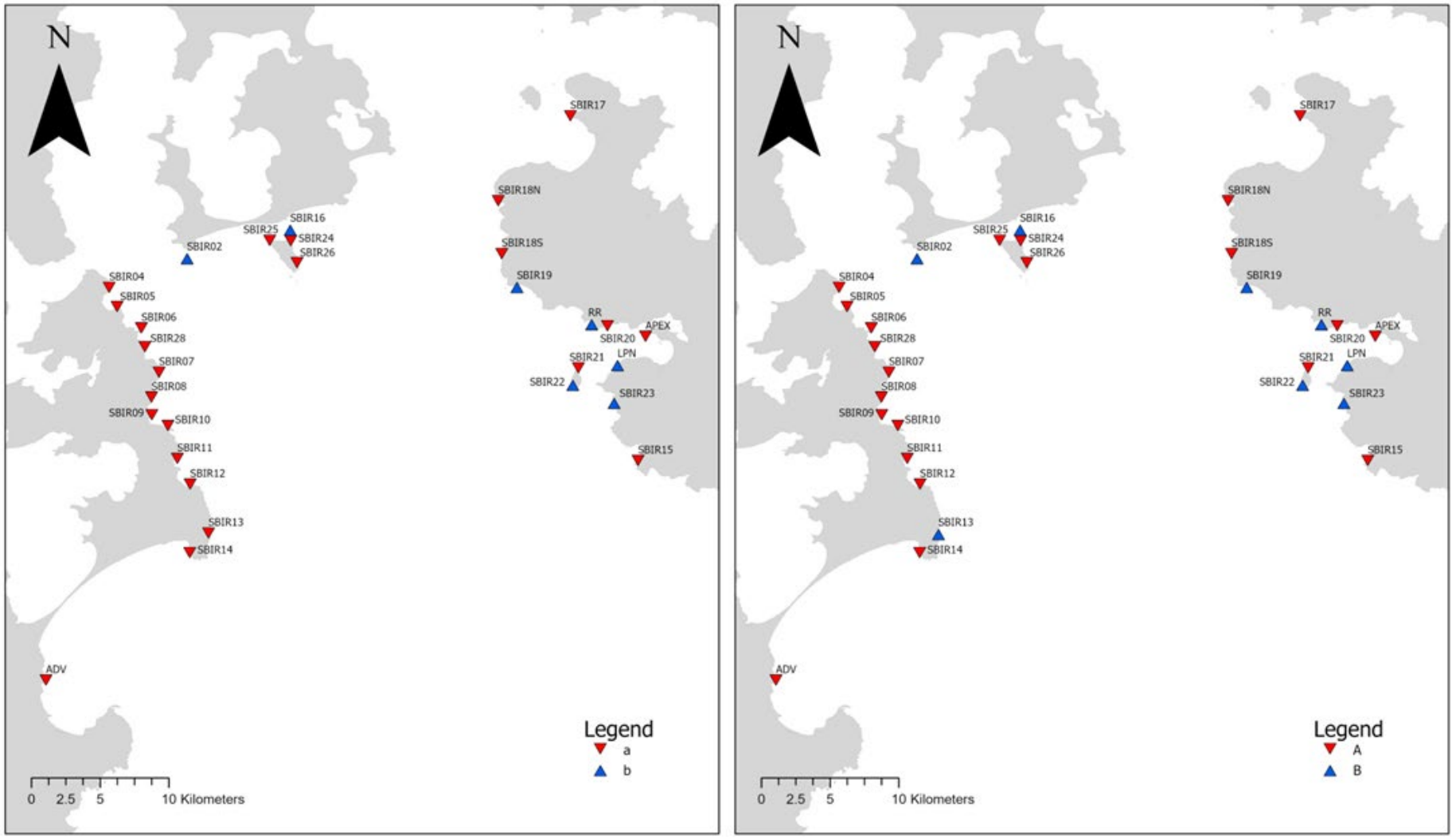

Figure 5-11: Storm Bay reef biodiversity sites, with symbols indicating groupings of invertebrate community assemblages as determined through non-hierarchical cluster analysis (left) and kRCluster analysis (right), both with a SIMPROF significance measure of 0.01.

Macroalgae communities had the most complex grouping patterns, suggesting a higher degree of spatial variability in biodiversity across Storm Bay than either fish or invertebrate communities. Both hierarchical cluster analysis and kRCluster indicated seven significant groupings in the data, with clustering between the two analyses consistent across most sites (Figure 5-12). Two main clusters dominated the data with the first representing sites largely dominated by *P. comosa* and found along the southern part of north Bruny Island and SBIR20 and SBIR15 in the east (Figure 5-12, Figure 5-13). The second main cluster was comprised of sites where *E. radiata* was dominant; these sites were along the northern section of north Bruny Island, around Betsey Island and SBIR21 in Nubeena (Figure 5-12, Figure 5-13). Hierarchical cluster analysis also included Apex Point in this group of sites, but kRCluster analysis indicated Apex was in a separate group with SBIR17.

All other significant groupings had far fewer sites and clustered based on either the high abundance of one or two unique species, and/or the low abundance of *P. comosa* and/or *E. radiata*. These clusters tended to be more variable between sites, as indicated by the greater spread on the nMDS plots (Figure 5-12, Figure 5-13, Appendix 5-1).

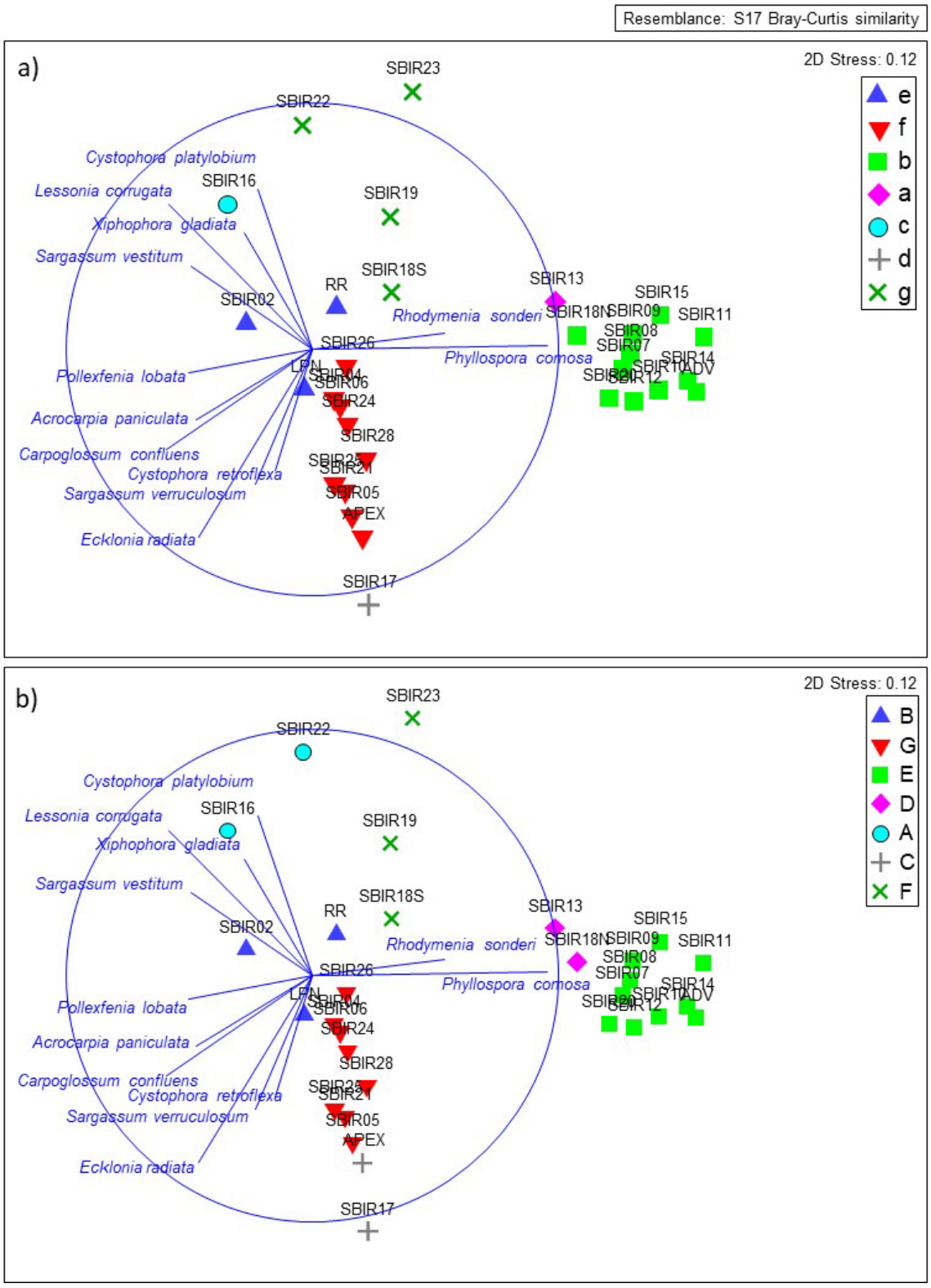

Figure 5-12: nMDS on algal communities across Storm Bay, with data averaged at a site level across the four transects. Groupings represent a) hierarchical cluster analysis and b) kRCluster analysis both with a SIMPROF value of 0.01. Pearson's vector overlays contributing to ordination with a base variable comparison of >0.5 are included. The length of the vectors indicates the strength of the correlation.

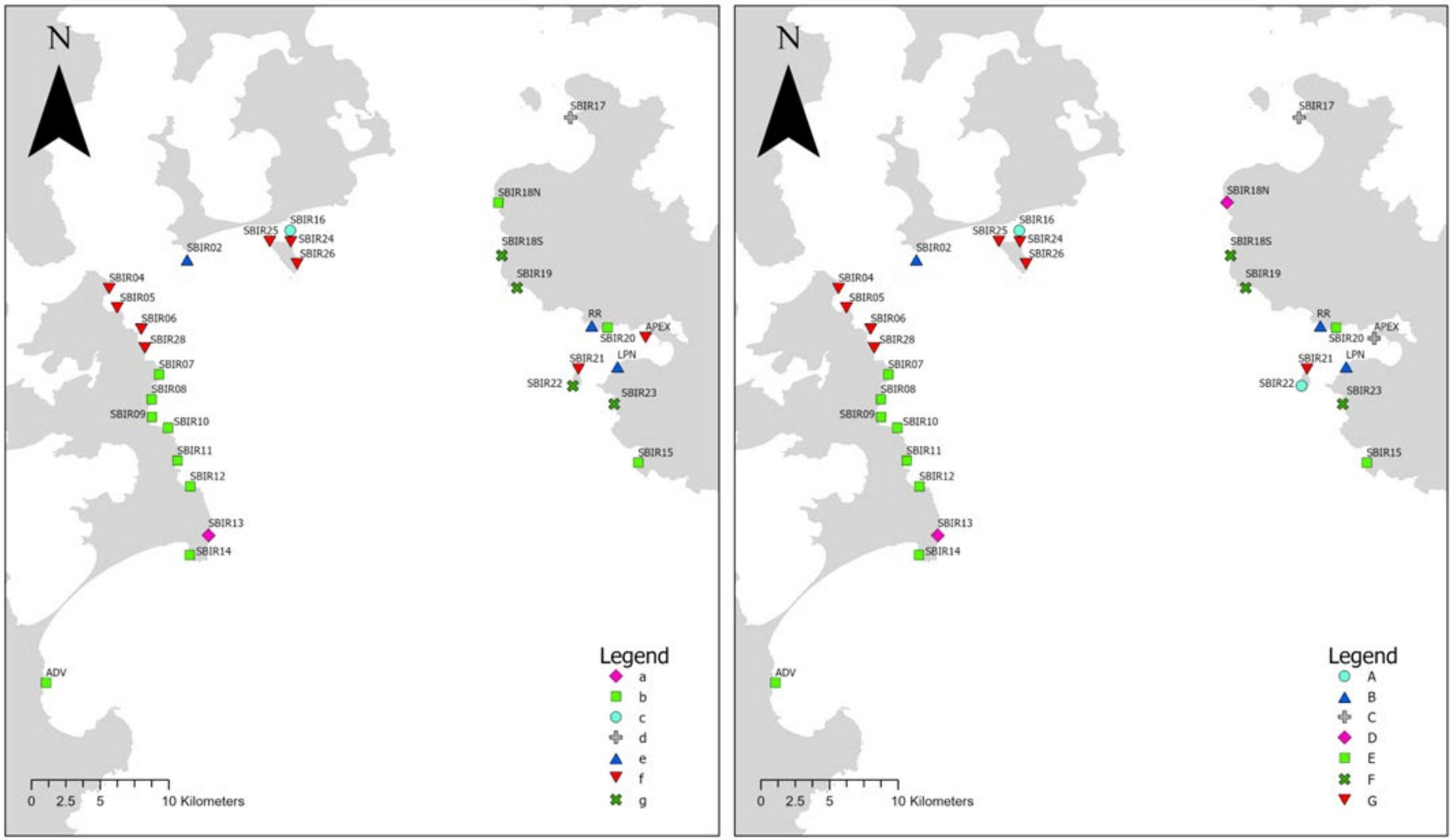

Figure 5-13: Storm Bay reef biodiversity sites, with symbols indicating groupings of algae and sessile invertebrate community assemblages as determined through non-hierarchical cluster analysis (left) and kRCluster analysis (right), both with a SIMPROF significance measure of 0.01.

5.2.2 Distribution of ecologically or commercially important species in Storm Bay

There were only two fish species with strong commercial interest found in consistent abundance across Storm Bay within our survey period. *Latridopsis forsteri* (bastard trumpeter) is a popular commercial and recreational species that was present at 12 sites. It was generally seen in small schools (i.e. 8-10 individuals), although one large school was observed at SBIR22 (Figure 5-14, Appendix 5-1). As this is a highly mobile species, the significance of this site in terms of *L. forsteri* abundance is unclear without time-series data. *Chirodactylus spectabilis* (banded morwong) are commercially harvested by a small-scale coastal gillnet fishery and are classified as transitional depleting (Moore et al. 2018). *C. spectabilis* were found at 22 sites across Storm Bay, with numbers generally in the range of 2-10 individuals in total across the site, although 24 individuals were recorded at SBIR22 (Figure 5-14, Appendix 5-1).

For mobile invertebrates with commercial significance, both *Jasus edwardsii* (southern rock lobster) and *Haliotis rubra* (black-lipped abalone) were regularly recorded at sites within Storm Bay. *J. edwardsii* was found at every site except SBIR11 and Roaring, whereas *H. rubra* was recorded from all sites except Low Point North and SBIR28 (Figure 5-15). Particularly high abundances (≥ 20 individuals across the site) of *J. edwardsii* were observed at SBIR04, SBIR06 and SBIR17, whereas higher abundances (≥ 30 individuals across the site) of *H. rubra* were recorded at SBIR10, SBIR22 and SBIR24 (Figure 5-15, Appendix 5-1). Given both these species utilise cryptic habitat, relatively higher abundances are likely to be reflective of habitat availability along the 200 m surveyed.

In terms of ecological importance, *Olisthops cyanomelas* (herring cale) have increased in abundance over the past decade in SE Tasmania and are a warm-water indicator species (Barrett et al. 2014). *O. cyanomelas* was present at 25 sites across Storm Bay, generally with 2-10 individuals recorded at each site. *Heliocidaris erythrogramma* (short-spined urchin) also has ecological significance, due to its ability to drive ecosystem-level change through the formation of barrens habitat through overgrazing (Pederson & Johnson 2007). While patchier in its distribution across Storm Bay than *J. edwardsii* and *H. rubra*, *H. erythrogramma* was found at six sites (SBIR06, SBIR14, SBIR17, SBIR21, SBIR25 and Apex) in abundances close to or exceeding 100 individuals across the site (Figure 5-16). At two sites (SBIR21 and Apex) total abundance exceeded 300 individuals, which equates to 6 urchins/m^2 across the site (Figure 5-16). As there was no evidence of barren formation at any reef site within Storm Bay, it is likely these densities are within the carrying capacity of the reef systems. Of note, the range-extending long-spined urchin *Centrostephanus rodgersii* was found at two sites (SBIR10 and SBIR12; Appendix 5-1), with a total abundance of 1 individual per site, and is not currently having a discernible impact on the ecology of macroalgal communities in Storm Bay.

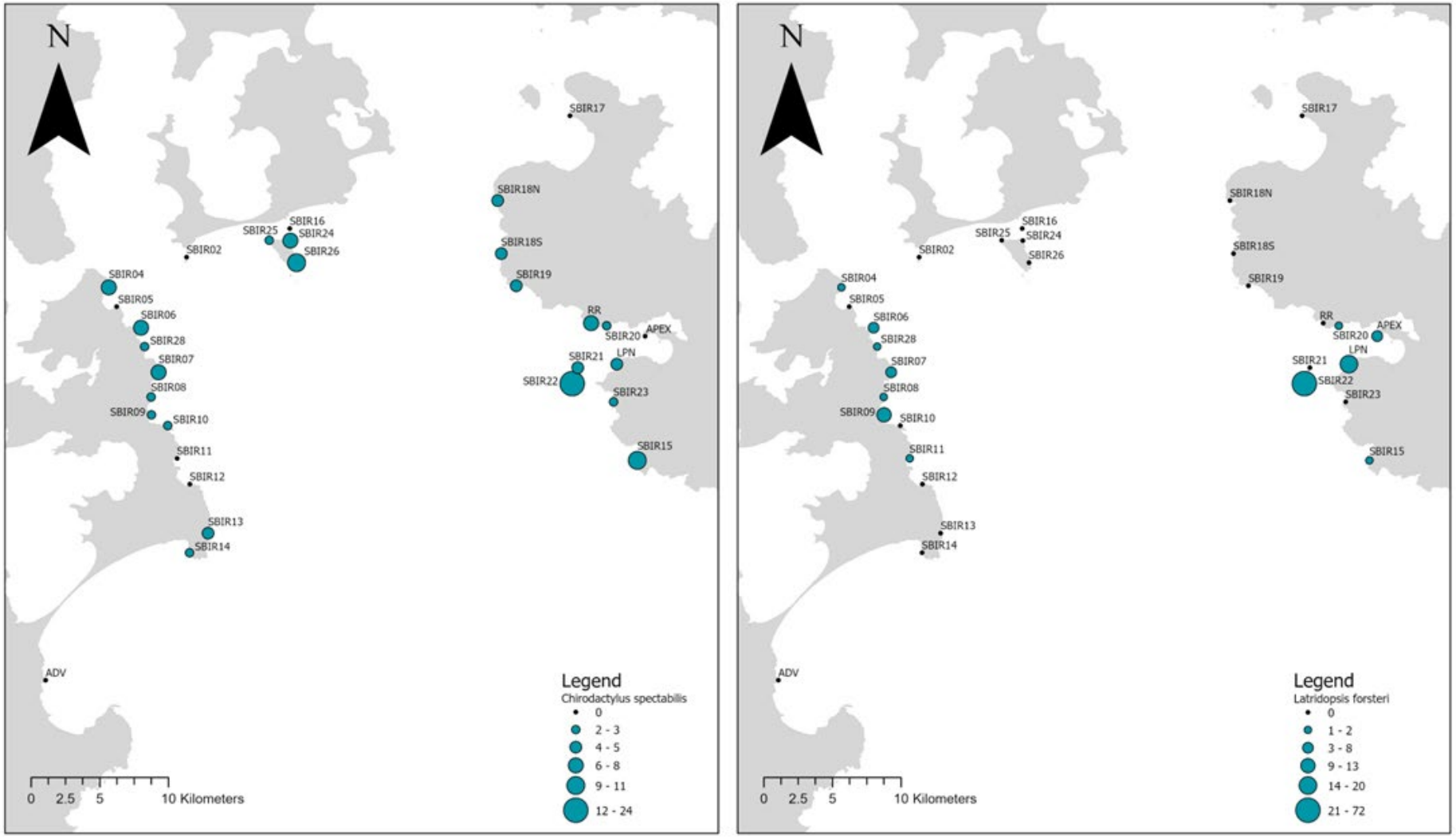

Figure 5-14: Storm Bay reef biodiversity sites, with the size of the bubbles indicating the total abundance (summed across transects) of key fish species, *Chirodactylus spectabilis* (left) and *Latridopsis forsteri* (right), at each site.

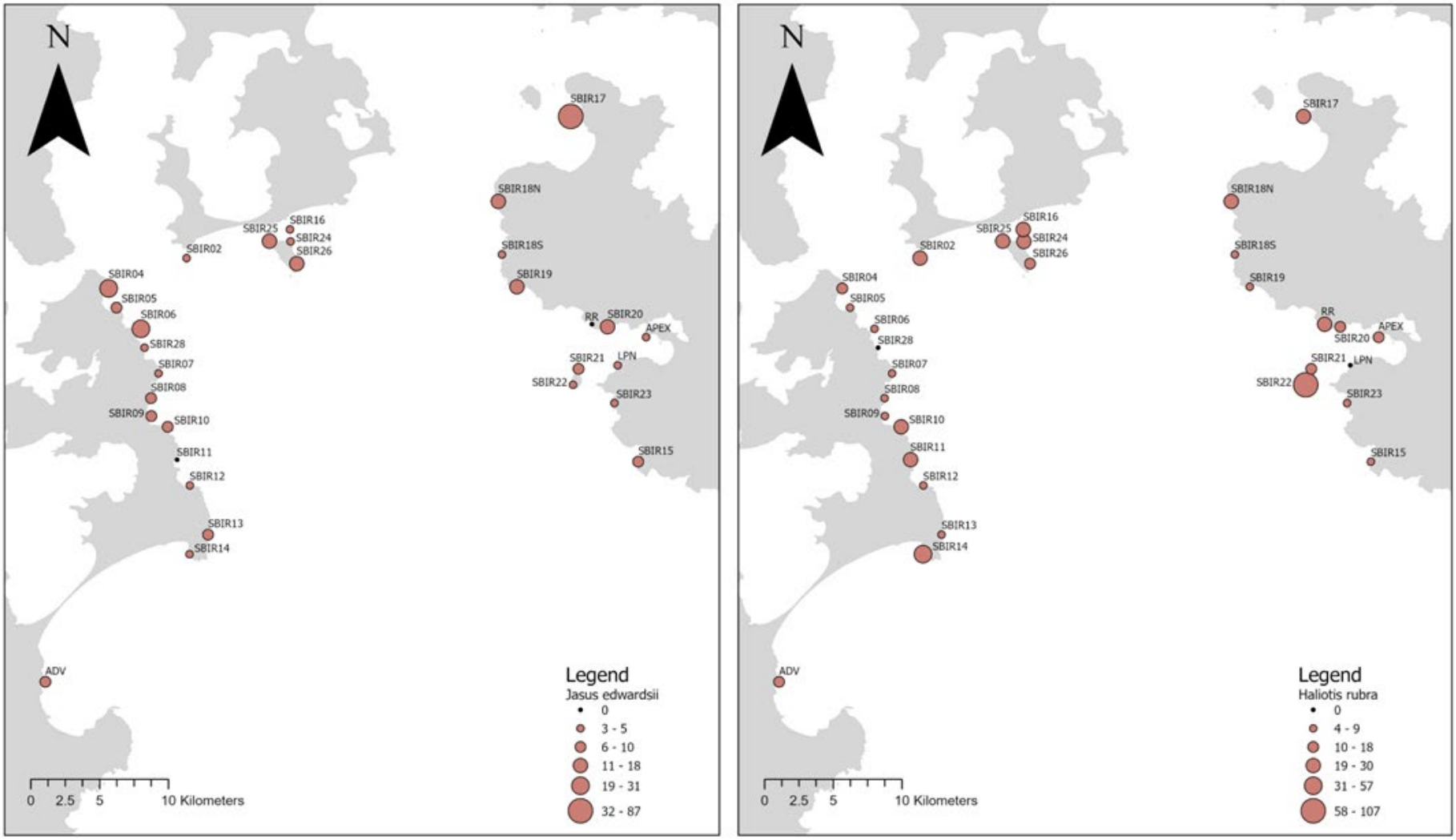

Figure 5-15: Storm Bay reef biodiversity sites, with the size of the bubbles indicating the total abundance (summed across transects) of key invertebrate species, *Jasus edwardsii* (left) and *Haliotis rubra* (right), at each site.

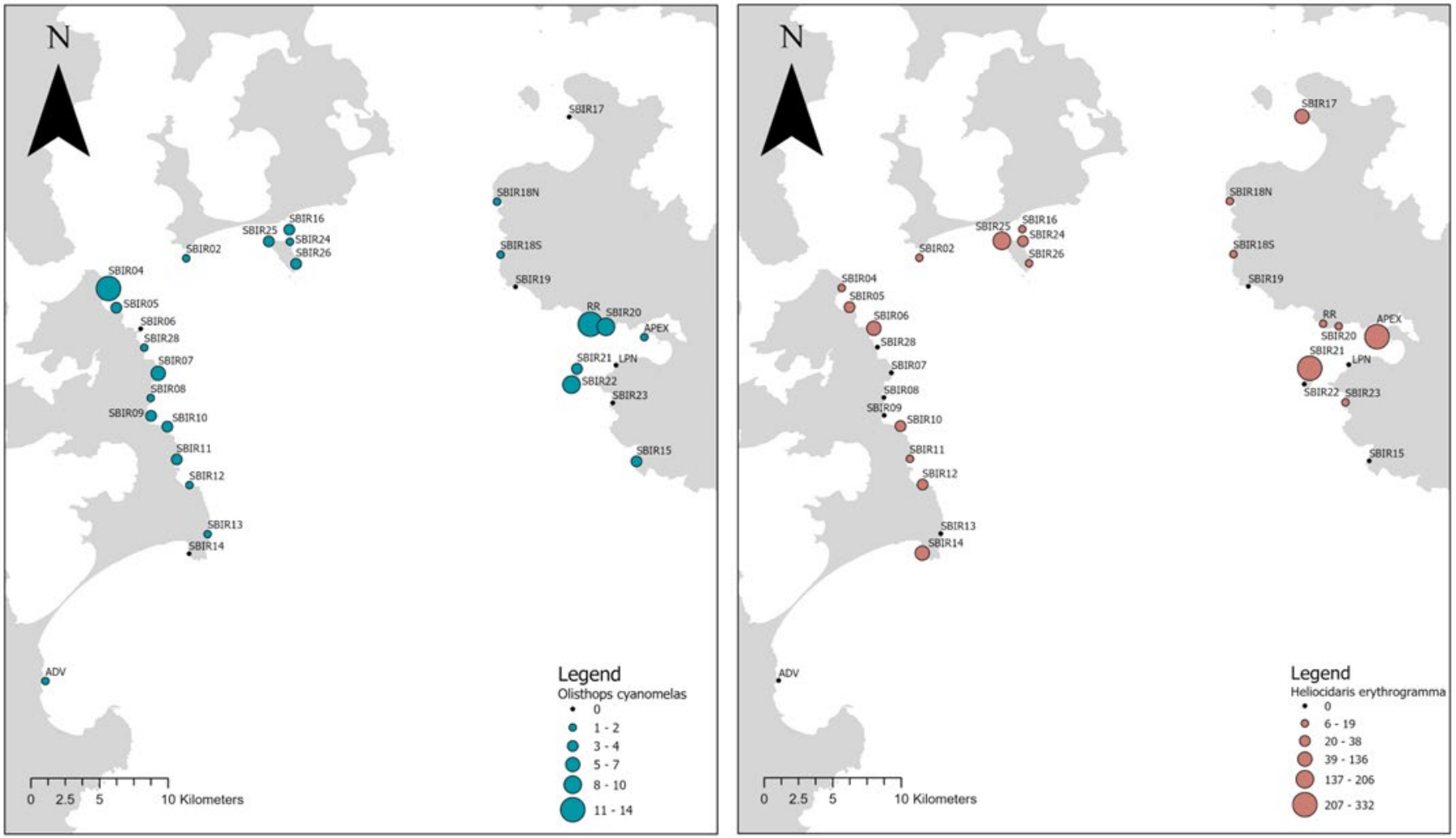

Figure 5-16: Storm Bay reef biodiversity sites, with the size of the bubbles indicating the total abundance (summed across transects) of key fish and invertebrate species, *Olisthops cyanomelas* (left) and *Heliocidaris erythrogramma* (right), at each site.

Four species of canopy-forming macroalgae were regularly recorded on biodiversity transects in Storm Bay (Figure 5-17). *Phyllospora comosa* (crayweed) and *Ecklonia radiata* (common kelp) were the most abundant canopy-forming species, with one or both of these species present at all sites except SBIR23. Where *P. comosa* was present, it tended to dominate assemblages, with a distribution that was associated with more exposed sites further away from the influence of the Derwent estuary (Figure 5-17). *E. radiata* was more cosmopolitan in range and tended to dominate where *P. comosa* was absent. The exception to this was SBIR22, where *Lessonia corrugata* (strapweed) was dominant instead (Figure 5-17). While the Edgar-Barrett method will underestimate the abundance of *Macrocystis pyrifera* (giant kelp), this species was still recorded at three locations in Storm Bay; SBIR02, SBIR24 and Low Point North (Figure 5-17).

Figure 5-17: Storm Bay reef biodiversity sites, with the size of the bubbles indicating the average percentage cover of key algae species at each site (percentage cover averaged across quadrats and transects). Species are (in a clockwise order from the top left pane): a) *Phyllospora comosa*, b) *Ecklonia radiata*, c) *Macrocystis pyrifera* and d) *Lessonia corrugata*.

5.2.3 Spatial variability in reef function

The function of reefs in Storm Bay was examined through Rapid Visual Assessment (RVA), with cluster analysis indicating a relatively homogenous ecosystem function across Storm Bay throughout the survey period. Agglomerative hierarchical and kRCluster analysis indicated three and four significant groupings respectively (Figure 5-18, Figure 5-19). The formation of these clusters was variable between hierarchical and kRCluster analysis. Hierarchical cluster analysis suggested there was one large cluster containing the majority of the sites, whereas kRCluster analysis split this grouping (Figure 5-18), with one cluster ("B") containing sites with higher canopy and pink crustose coralline algae cover, another cluster with a higher abundance of brown understory algae ("A") and two smaller, more variable clusters ("D" and "C"; Figure 5-18).

This analysis indicated that from a functional perspective, reef sites across north Bruny Island were similar, with only SBIR04, SBIR28 and SBIR07 grouping separately across both cluster analyses (Figure 5-19). Sites around Betsey Island were functionally similar and grouped with SBIR18S, SBIR22, SBIR23 and Roaring across both analyses, along with SBIR04 and SBIR28 from the western side of Storm Bay (Figure 5-19). All other sites were variable in their groupings between analyses, indicating that eastern Storm Bay is much more variable in terms of ecosystem function than western Storm Bay (Figure 5-19).

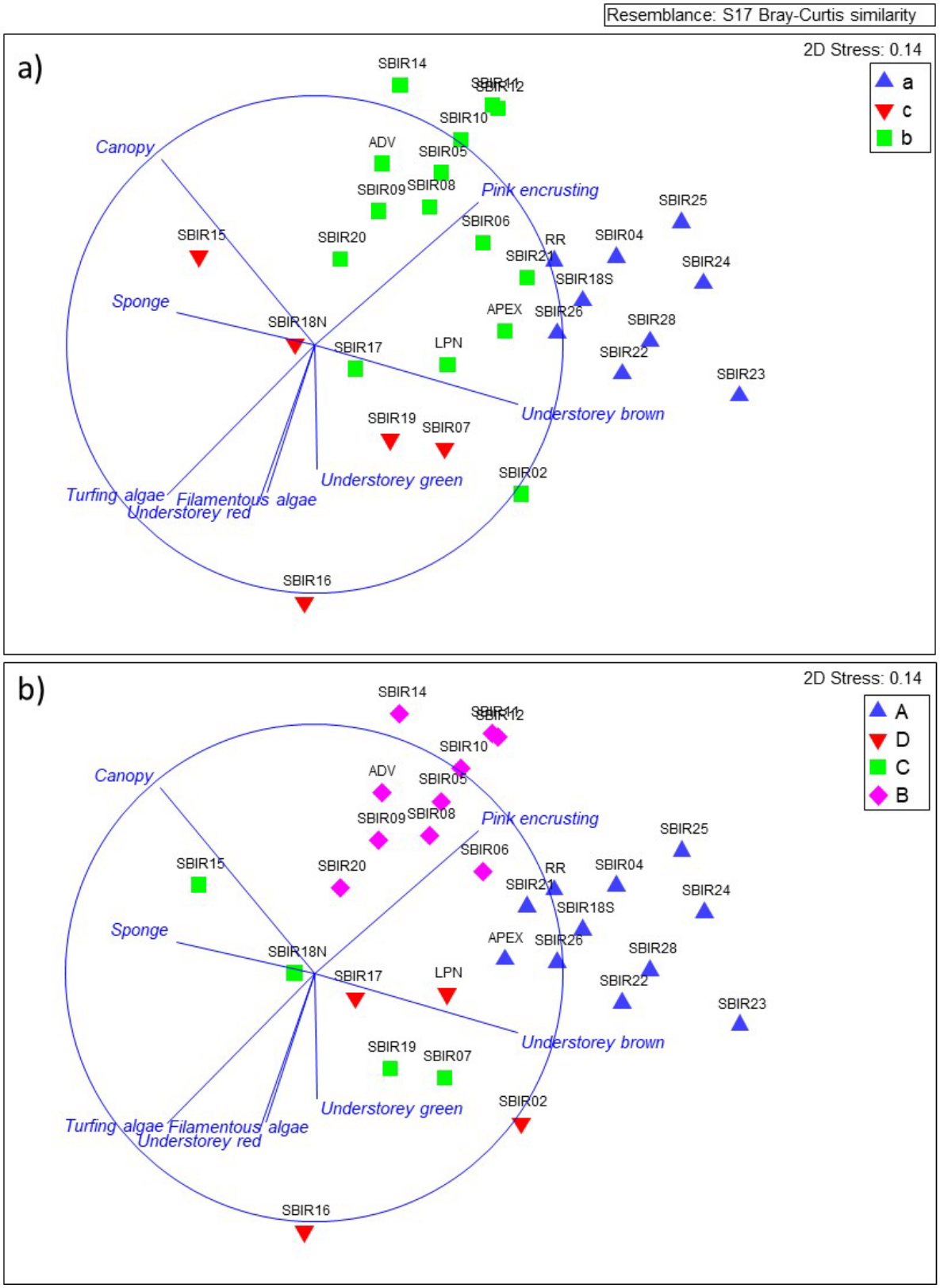

Figure 5-18: nMDS on functional parameters representing reef communities across Storm Bay. Groupings represent a) non-hierarchical clusters and b) kRClusters both with a SIMPROF value of 0.01. Pearson's vector overlays contributing to ordination with a base variable comparison of 0.5 are included.

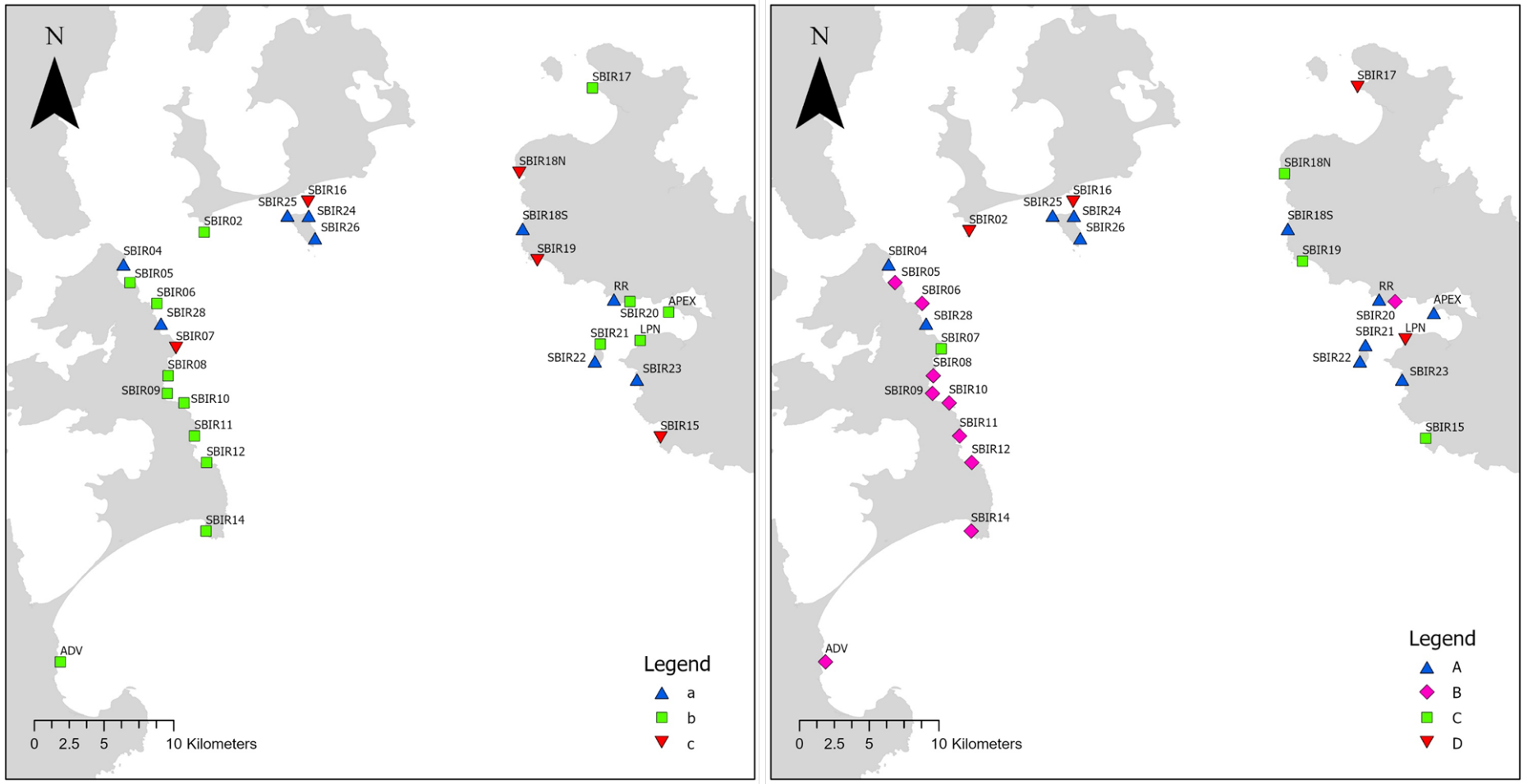

Figure 5-19: Storm Bay RVA sites, with symbols showing site groupings as determined through non-hierarchical cluster analysis (left) and kRCluster analysis (right) on RVA community data (averaged across surveys and years). A SIMPROF significance measure of 0.01 has been used for both analyses.

5.2.4 Temporal variability in reef function

Temporal variability in reef function was first compared between summer and winter, using data averaged across the survey period (2019-2022; Figure 5-20). For most sites, the variation in functional parameters between summer and winter was less than the variation between sites (Figure 5-20). However, results indicate that seasonal variation is high for SBIR02, SBIR16, SBIR17, SBIR26, SBIR28 and Low Point North (Figure 5-20). These sites tended to have lower canopy cover (<50%) and were dominated by turfing or understorey brown algae instead (Figure 5-20, Appendix 5-3).

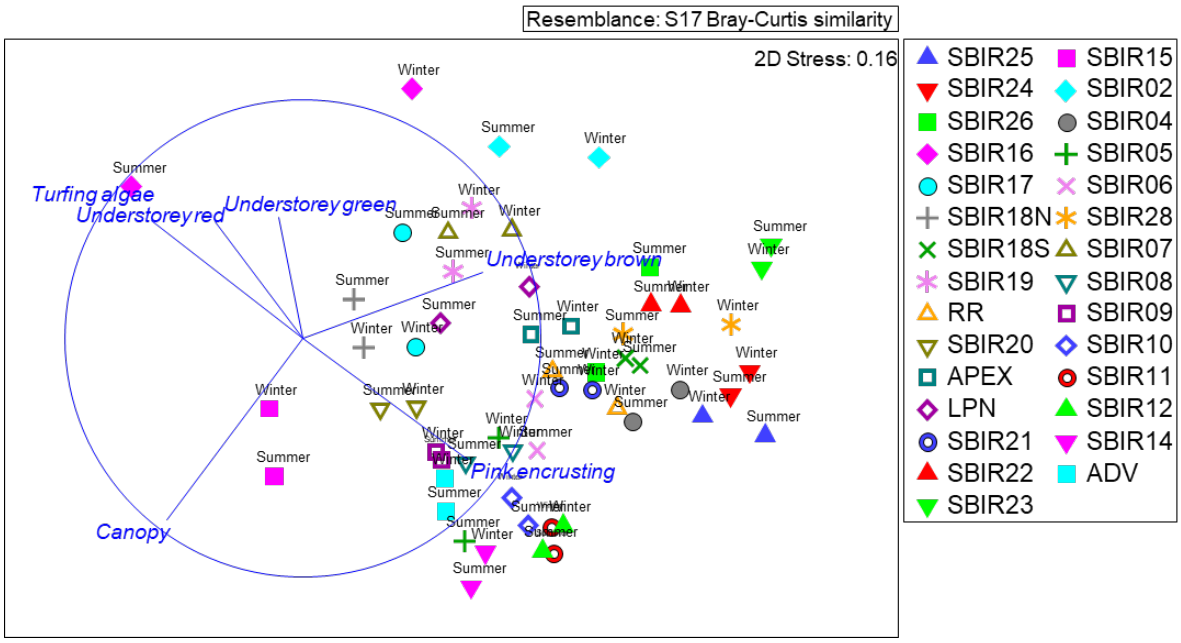

Figure 5-20: nMDS examining RVA parameters across all survey sites in Storm Bay on data averaged across the survey period (2019-2022) but separated by season. Pearson's vector overlays contributing to ordination with a base variable comparison of 0.5 are included.

Seasonal versus site-level variability was explored further using cluster analysis across the survey period, with agglomerative hierarchical cluster and kRCluster analysis indicating eight and seven significant groups of sites respectively (Figure 5-21, Table 5-3). SIMPROF analysis on hierarchical cluster groups found the majority of sites fell into one of two major groupings: either "g" which was loosely the majority of sites from northern and eastern Storm Bay, or "f" which represented most of the sites from north Bruny Island (Figure 5-21, Table 5-3). While most sites were relatively stable in terms of the designated cluster across year and season, there were several sites (i.e. SBIR02 – Iron Pot, SBIR05 – Bull Bay Sth, SBIR08 – Trumpeter Bay Nth, SBIR20 – Creeses Mistake) that fell into three or more clusters depending on the year and season, indicating variability in ecosystem function across the survey period. Analysis suggested that SBIR02 (Iron Pot) and SBIR16 (Black Jack Reef) were relatively distinct in terms of ecosystem function compared to other sites across both year and season (Figure 5-21, Table 5-3).

Major clusters indicated by kRCluster analysis were similar to those found in the hierarchical cluster analysis, with the majority of western Storm Bay sites falling into one group ("G") (Figure 5-21, Table 5-3). While "F" was still the dominant group across eastern sites, there

was much more variability, both spatially and temporally, than observed in hierarchical cluster analysis (Table 5-3). SBIR17 (Lobster Point), APEX (Apex Point) and LPN (Low Point North) were consistently group “E”; SBIR18N (Black Jack Bight), SBIR20 (Creeses Mistake) and SBIR15 (Curio Bay) were group “D” and SBIR19 (Outer North Head) was group “C”. Similarly, kRCluster analysis indicated that SBIR02 (Iron Pot) and SBIR16 (Black Jack Reef) were distinct in terms of ecosystem function across Storm Bay, and that SBIR02 in particular was highly variable in terms of groupings across both years and seasons.

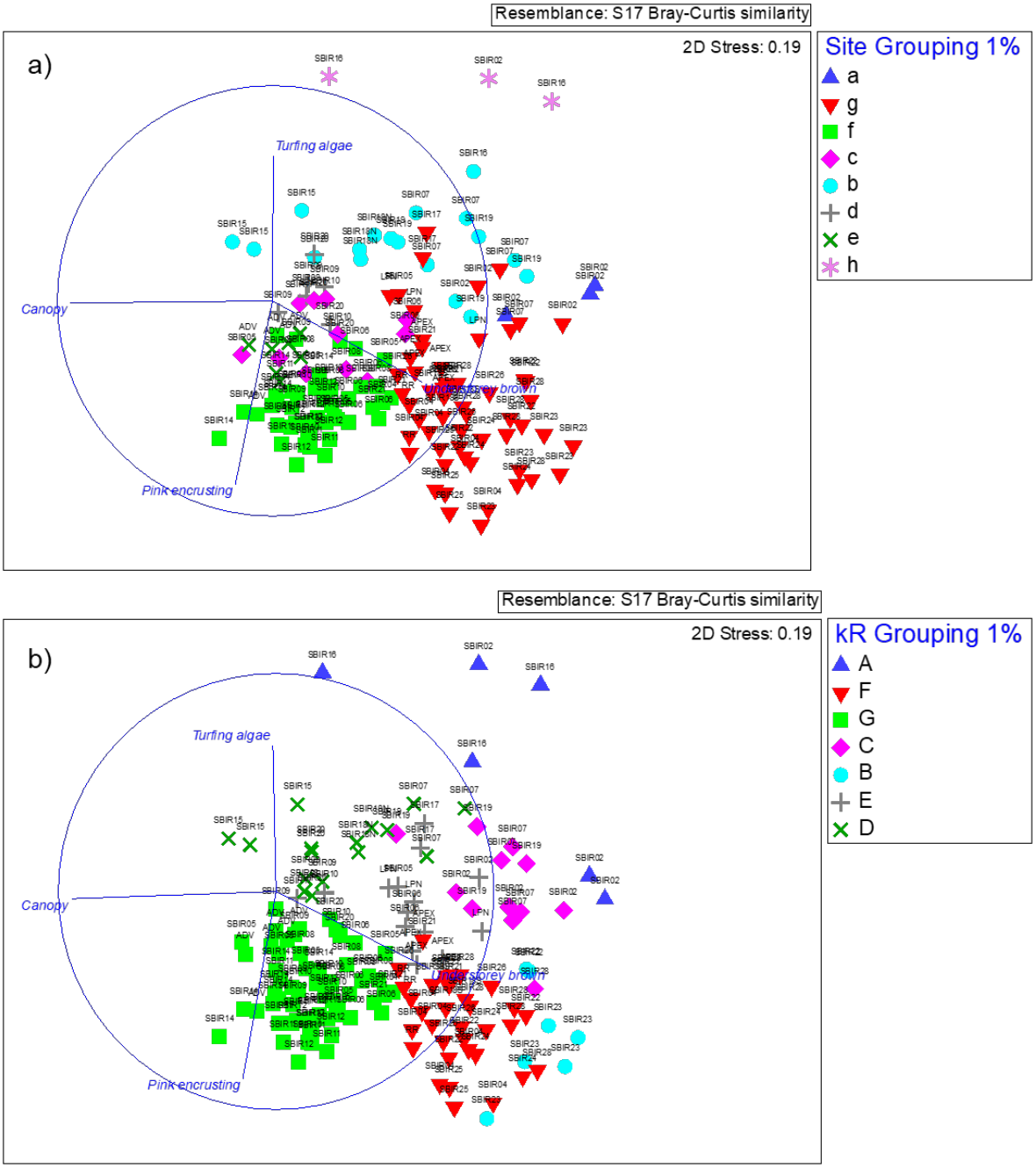

Figure 5-21: nMDS on the site average data from all 30 sites for the period Winter 2019 – Winter 2022. Symbols indicate the groups found by SIMPROF tests for both clustering techniques: a) hierarchical agglomerative (8 groups) and b) kRCluster non-hierarchical (7 groups). Pearson’s vector overlays contributing to ordination with base variable comparison of >0.5 are included.

Table 5-3: Unconstrained data groupings from hierarchical cluster analysis and kRCluster analysis with SIMPROF significance level set at 1%. Colours and letters denote different groupings, with lower-case letters indicating the groupings from the cluster analysis and capital letters indicating the groupings from the kRCluster analysis.

	Winter Cluster				Summer Cluster			Winter kRCluster				Summer kRCluster		
Site	**2019**	**2020**	**2021**	**2022**	**2020**	**2021**	**2022**	**2019**	**2020**	**2021**	**2022**	**2020**	**2021**	**2022**
SBIR02	a	a	g	a	b	g	h	A	C	E	A	C	C	A
SBIR04	g	g	g	g	f	g	g	F	F	F	F	G	F	F
SBIR05	f	f	g	c	f	c	c	G	G	E	G	G	G	G
SBIR06	c	f	c	c	f	f	f	G	G	E	E	G	G	G
SBIR28	g	g	g	g	g	g	g	F	C	F	F	F	F	F
SBIR07	g	g	b	g	b	b	b	C	C	D	C	C	D	D
SBIR08	f	f	e	c	f	f	d	G	G	G	G	G	G	D
SBIR09		f	d	d	f	f	d		G	D	G	G	G	D
SBIR10	f	f	c	c	f	f	f	G	G	G	E	G	G	G
SBIR11	f	f	e	f	f	f	f	G	G	G	G	G	G	G
SBIR12	f	f	f	f	f	f	f	G	G	G	G	G	G	G
SBIR14	f	f	f	f	f	f	e	G	G	G	G	G	G	G
ADV		f	e	e	f	e	e		G	G	G	G	G	G
SBIR16			b	h			h			A	A			A
SBIR24			g	g			g			F	F			F
SBIR25			g	g			g			F	F			F
SBIR26			g	g			g			F	F			F
SBIR17			c	g			g			E	E			E
SBIR18N			b	b			b			D	D			D
SBIR18S			g	g			g			F	F			F
SBIR19		b	b	b		b	b		C	C	C		C	D
RR			g	g			g			F	F			F
SBIR20		f	b	c		d	d		G	D	D		G	D
APEX		g	g	g		g	g		F	E	E		E	E
LPN			g	g			g			E	E			E
SBIR21		f	g	g		f	g		G	F	F		G	F
SBIR22		g	g	g		g	g		F	B	F		F	B
SBIR23		g	g	g		g	g		B	B	B		B	B
SBIR15			b	b			b			D	D			D

Vector analysis suggested that the main factors driving groupings were differences between canopy, turfing algae, understorey brown, understorey red, red encrusting and sponge covers (Figure 5-20, Figure 5-21). With the exception of SBIR28 and SBIR02, canopy cover was highest at sites in the western side of Storm Bay and this was consistent throughout both year and survey (Figure 5-22). In the east of Storm Bay, only SBIR15 and SBIR20 regularly recorded canopy above 75% cover. At sites with high canopy cover, there was a consistent seasonal pattern observed, where canopy was slightly lower in winter compared to summer. Understorey brown algae tended to have an inverse relationship with canopy cover. Sites where canopy was consistently above 75% cover generally had comparatively low abundance of understorey brown algae (Figure 5-22, Figure 5-23).

Understorey green algae were consistently low across both year and season and only slightly elevated at a small number of sites (Apex, Low Point North, SBIR17, SBIR07; Figure 5-24). In contrast, understorey red algae were much more variable across both year and season, reflecting the ephemeral nature of many species of red algae (Figure 5-25). Sites in the east of Storm Bay tended to have higher abundance of red algae (>25%), particularly those situated within or close to Wedge Bay (SBIR19, SBIR20, Roaring, Apex), although SBIR07 in the west also recorded higher abundance of red algae (Figure 5-25).

Substrate parameters (pink and red encrusting algae, turfing algae and sponge) were highly variable between sites, although temporal variation depended on the parameter. For example, pink and red encrusting algae, along with sponge tended to have quite low variability between surveys, with limited seasonal variation (Figure 5-26, Figure 5-27, Figure 5-28). Sites with high pink encrusting algal cover tended to be associated with either high canopy cover or low turfing algal cover. In contrast turfing algae were highly variable and, where recorded in high abundance, could fluctuate by more than 30% (Figure 5-29). Sites with high abundance of turfing algae included SBIR02, SBIR16, SBIR07, SBIR08, SBIR09 and SBIR20, with SBIR16 particularly high (>60%, Summer 2022; Figure 5-29).

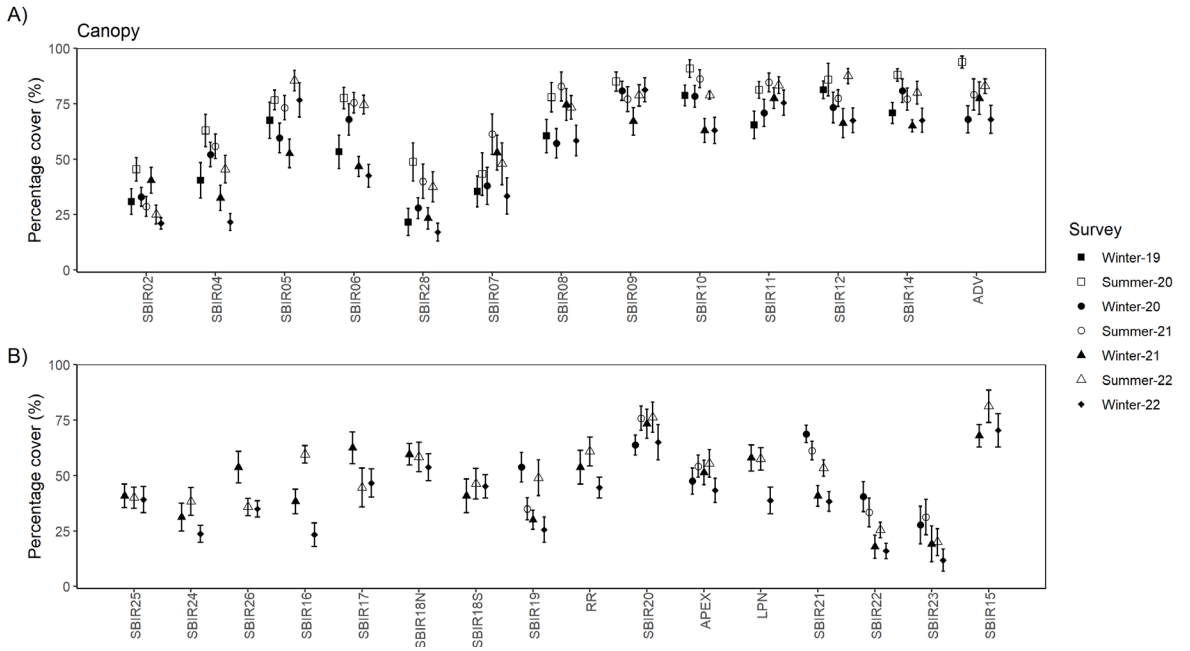

Figure 5-22: Mean (± SE) cover of canopy algae observed at all RVA surveys across Storm Bay. Different survey events are marked by different symbols.

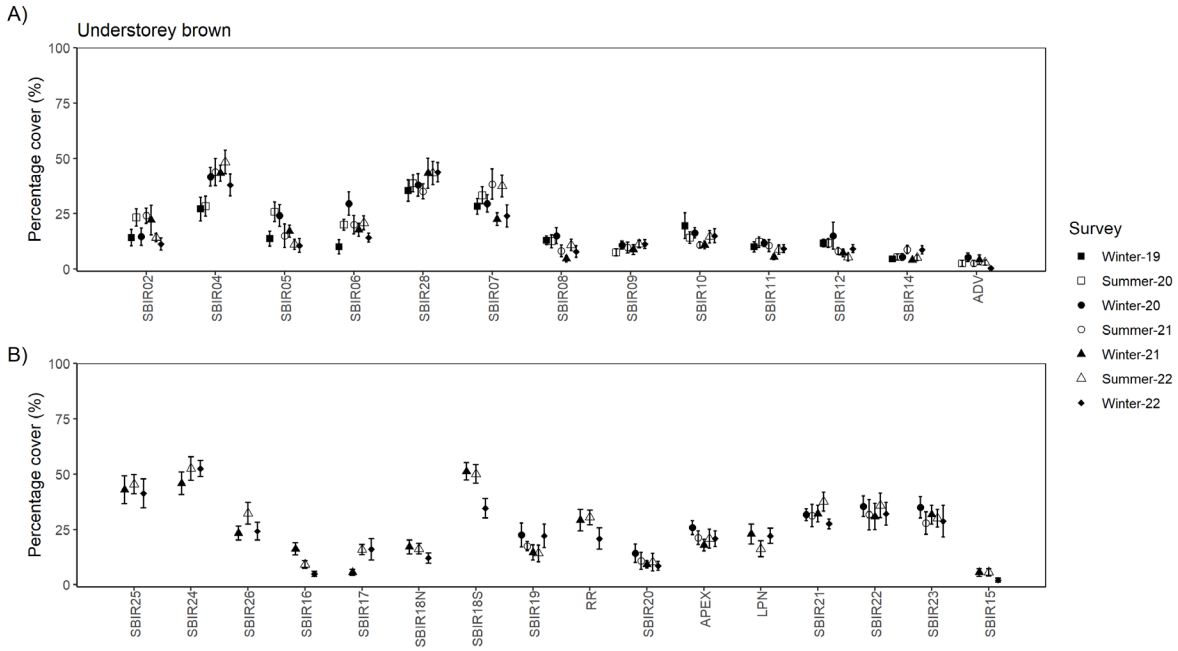

Figure 5-23: Mean (± SE) cover of understorey brown algae observed at all RVA surveys across Storm Bay. Different survey events are marked by different symbols.

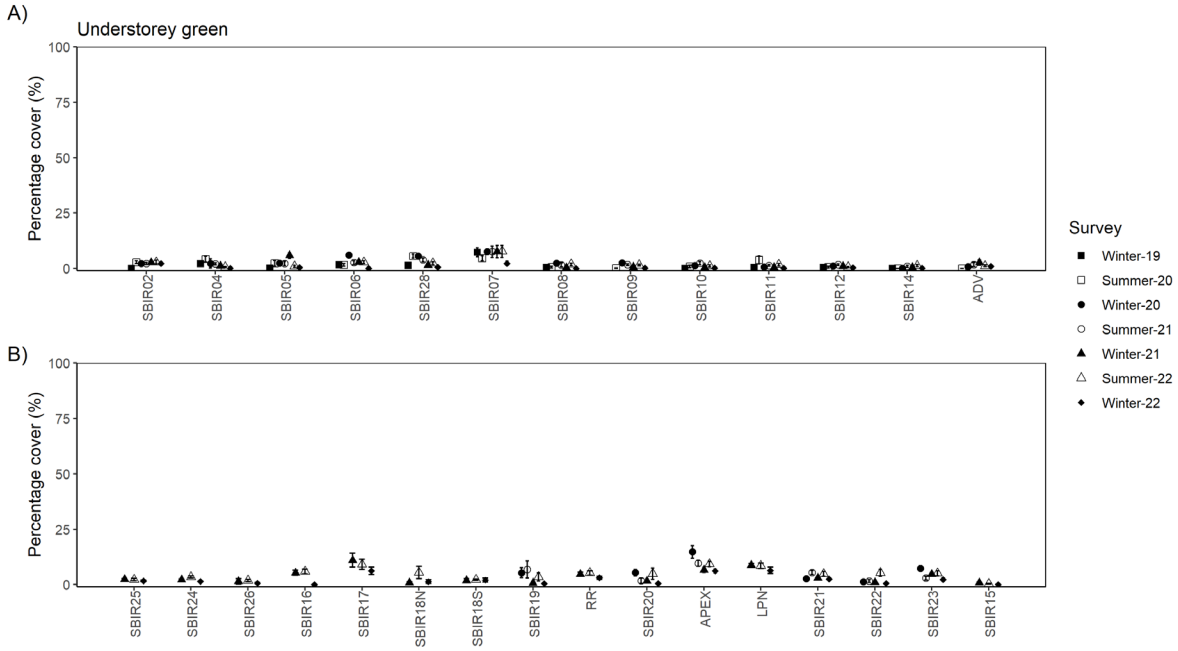

Figure 5-24: Mean (± SE) cover of understorey green algae observed at all RVA surveys across Storm Bay. Different survey events are marked by different symbols.

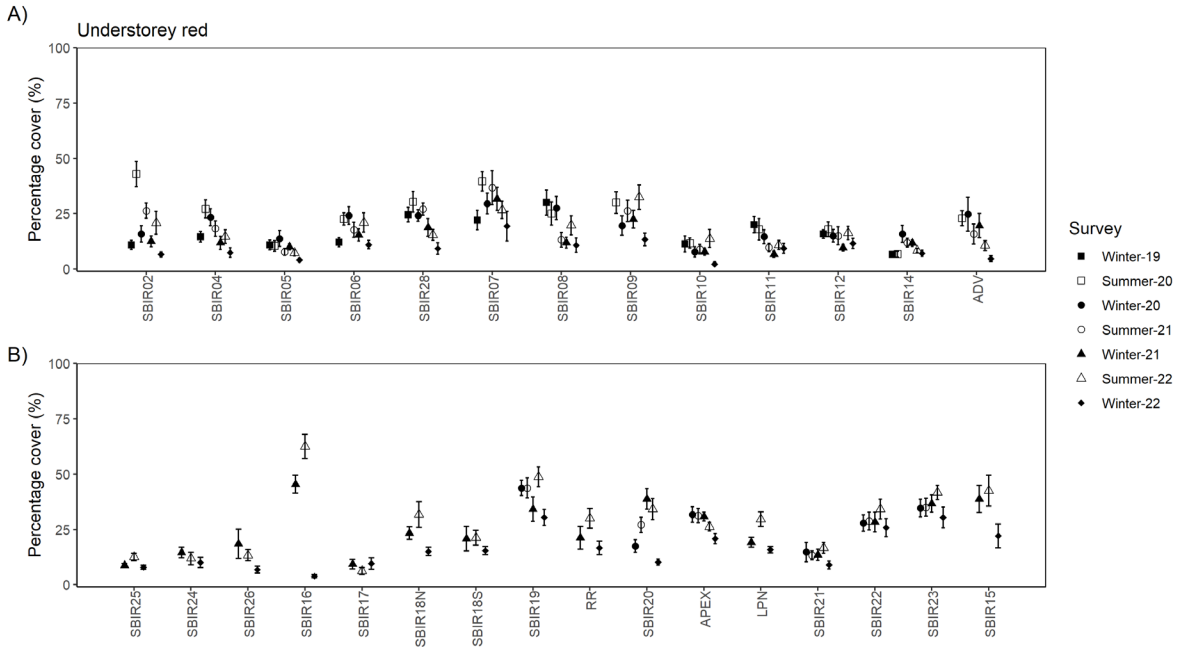

Figure 5-25**:** Mean (± SE) cover of understorey red algae observed at all RVA surveys across Storm Bay. Different survey events are marked by different symbols.

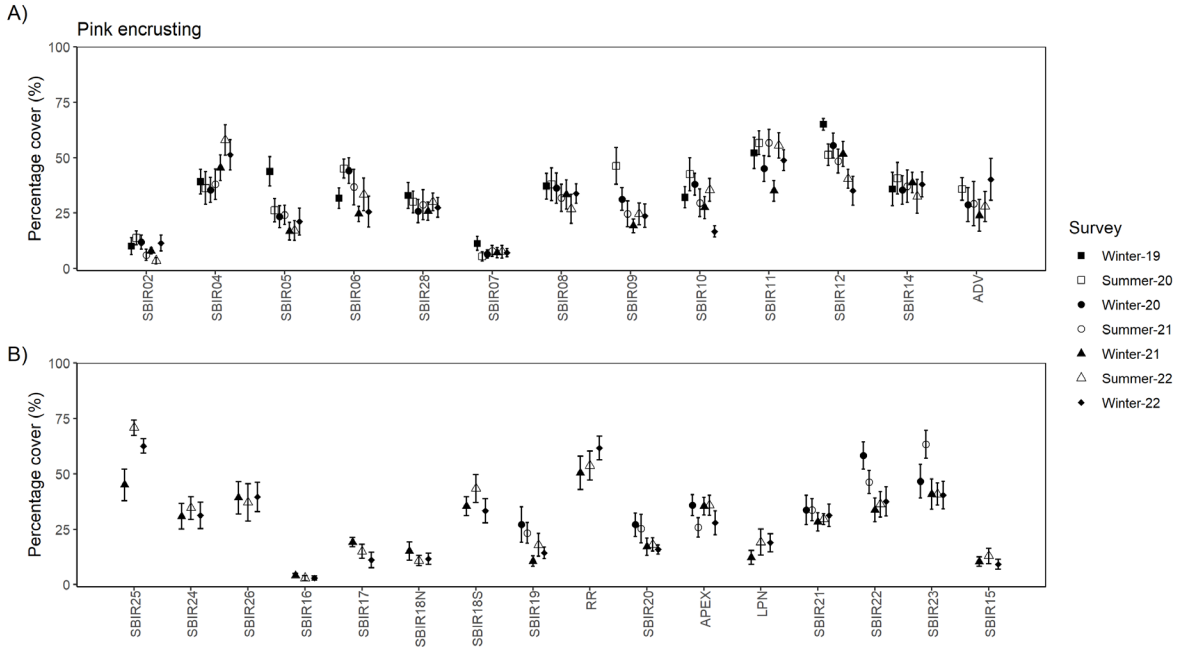

Figure 5-26: Mean (± SE) cover of pink encrusting algae observed at all RVA surveys across Storm Bay. Different survey events are marked by different symbols.

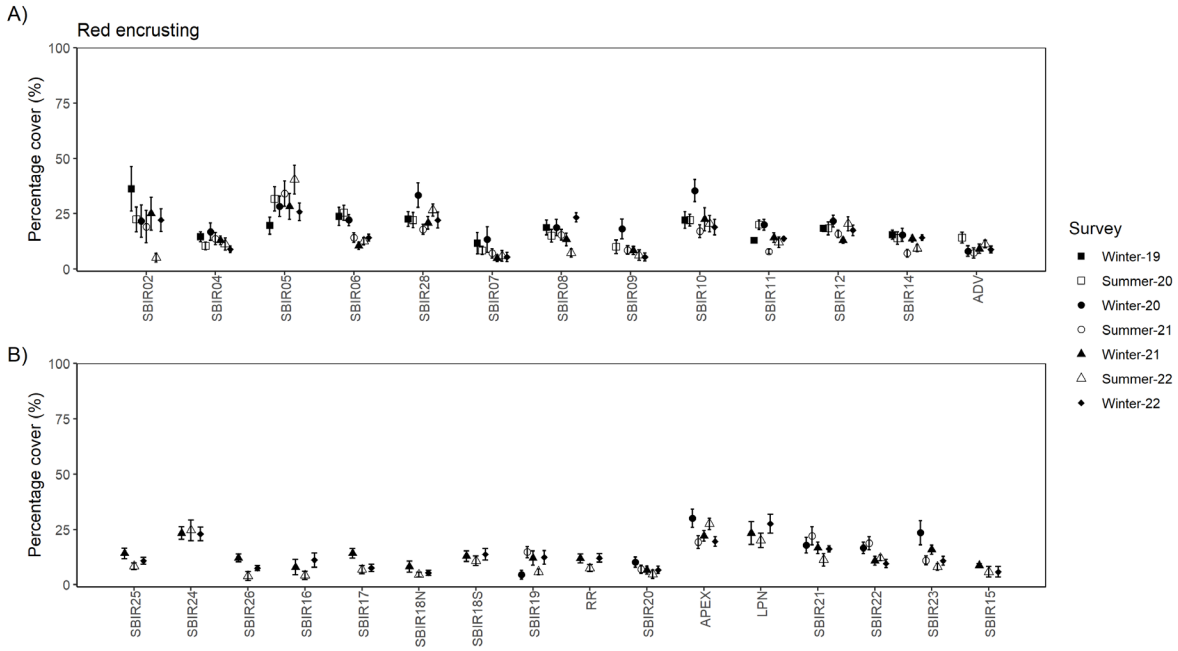

Figure 5-27: Mean (± SE) cover of red encrusting algae observed at all RVA surveys across Storm Bay. Different survey events are marked by different symbols.

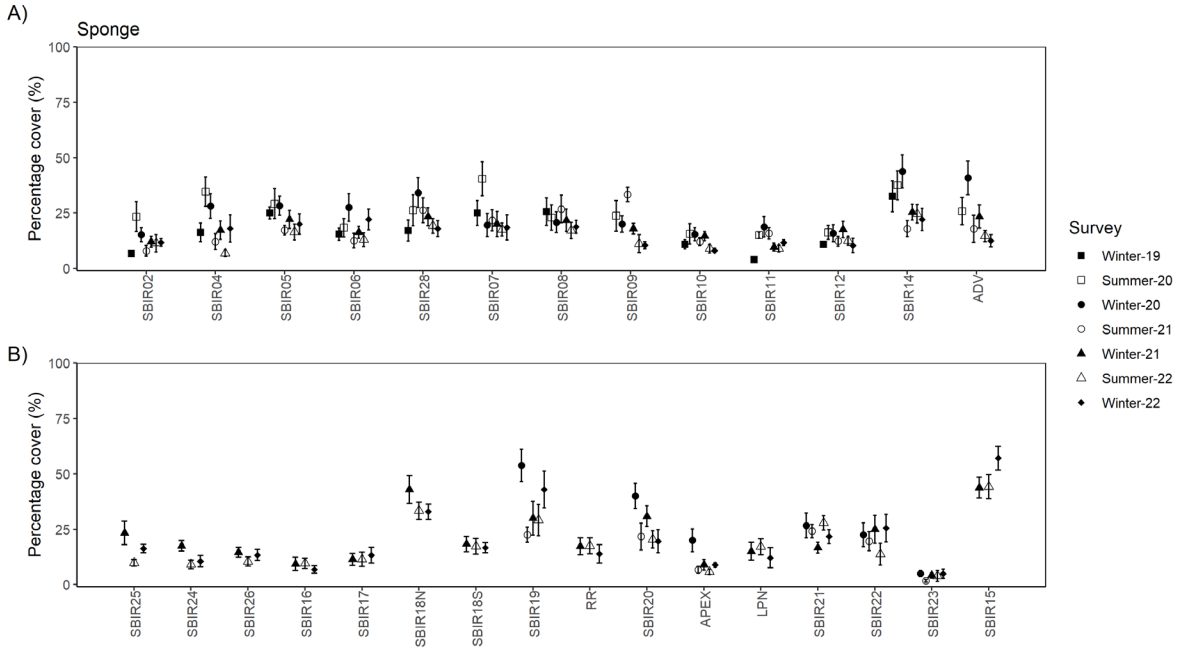

Figure 5-28: Mean (± SE) cover of sponge observed at all RVA surveys across Storm Bay. Different survey events are marked by different symbols.

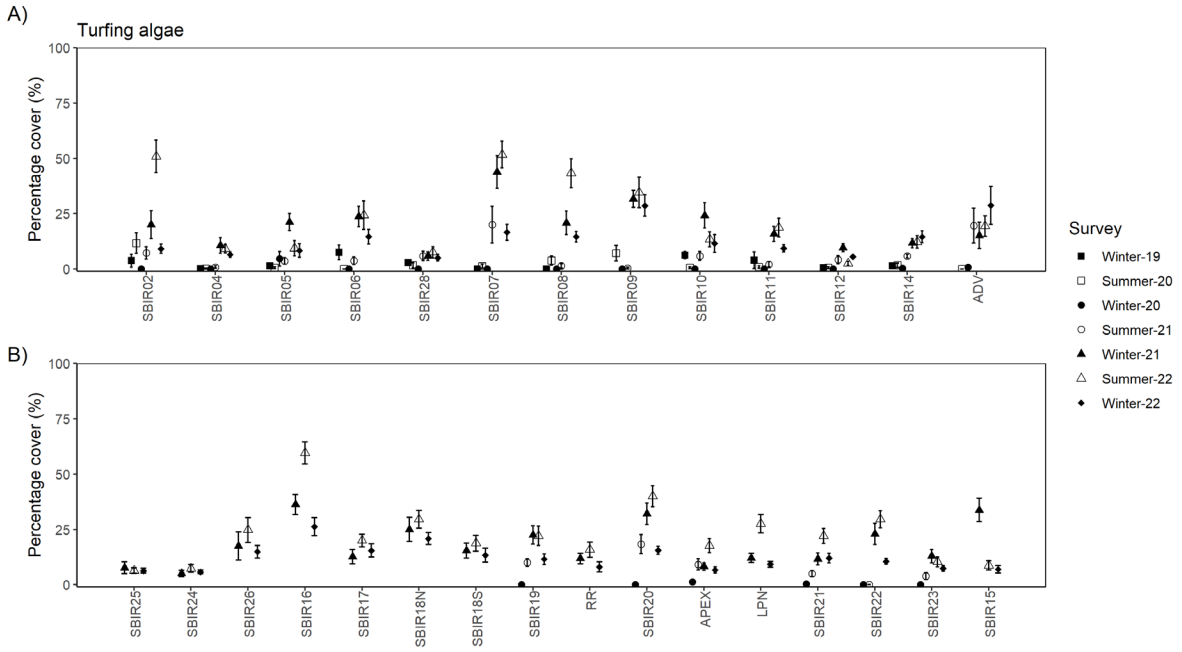

Figure 5-29: Mean (± SE) cover of turfing algae observed at all RVA surveys across Storm Bay. Different survey events are marked by different symbols.

5.2.5 Indicators of nutrient enrichment

Overall, there were very few indicators of nutrient enrichment present at the survey sites across Storm Bay. Vector analysis indicated that sites and groupings were defined largely through differences in structural parameters (i.e. canopy cover), rather than the presence or absence of nutrient indicators. Epiphytic algae were the most abundant nutrient enrichment indicator but covers remained low (<10%) at all but a few sites (Figure 5-30). SBIR14 (Cape Queen Elizabeth) regularly recorded the highest abundance of epiphytic algae (>25%), most likely to due to the proximity of this site to a gannet colony. Filamentous algae were generally absent from all sites, except at SBIR02 and SBIR16 (Figure 5-31). These sites both recorded high values in summer 2022 (>25%), although filamentous algae were absent in the subsequent winter survey (Figure 5-31). Nuisance green and red algae were also largely absent from Storm Bay throughout the survey period, although SBIR16 and Low Point North recorded low but consistent presence of nuisance green (<5%) throughout the survey period (Figure 5-32, Figure 5-33).

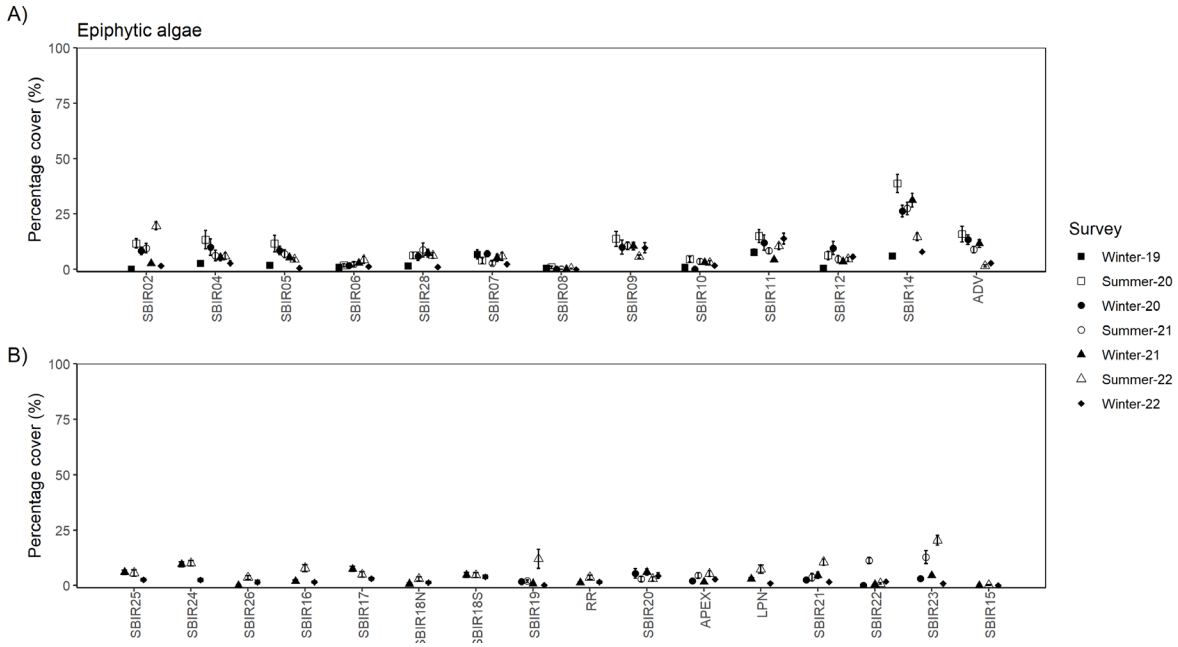

Figure 5-30: Mean (± SE) cover of epiphytic algae observed at all RVA surveys across Storm Bay. Different survey events are marked by different symbols.

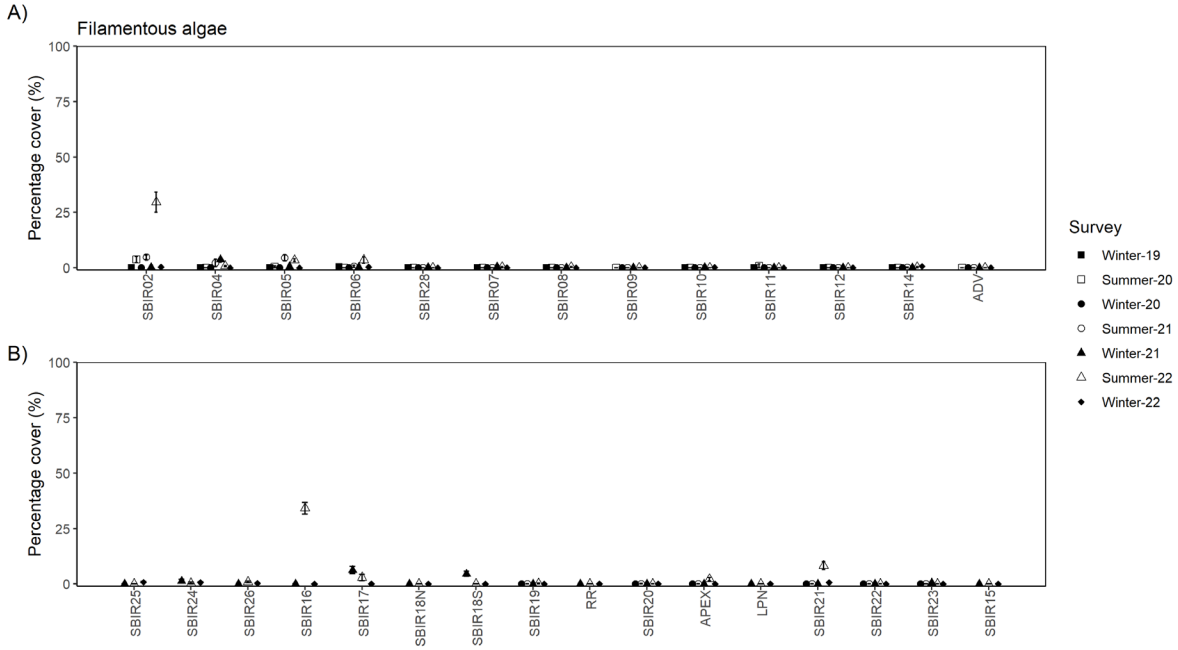

Figure 5-31: Mean (± SE) cover of filamentous algae observed at all RVA surveys across Storm Bay. Different survey events are marked by different symbols.

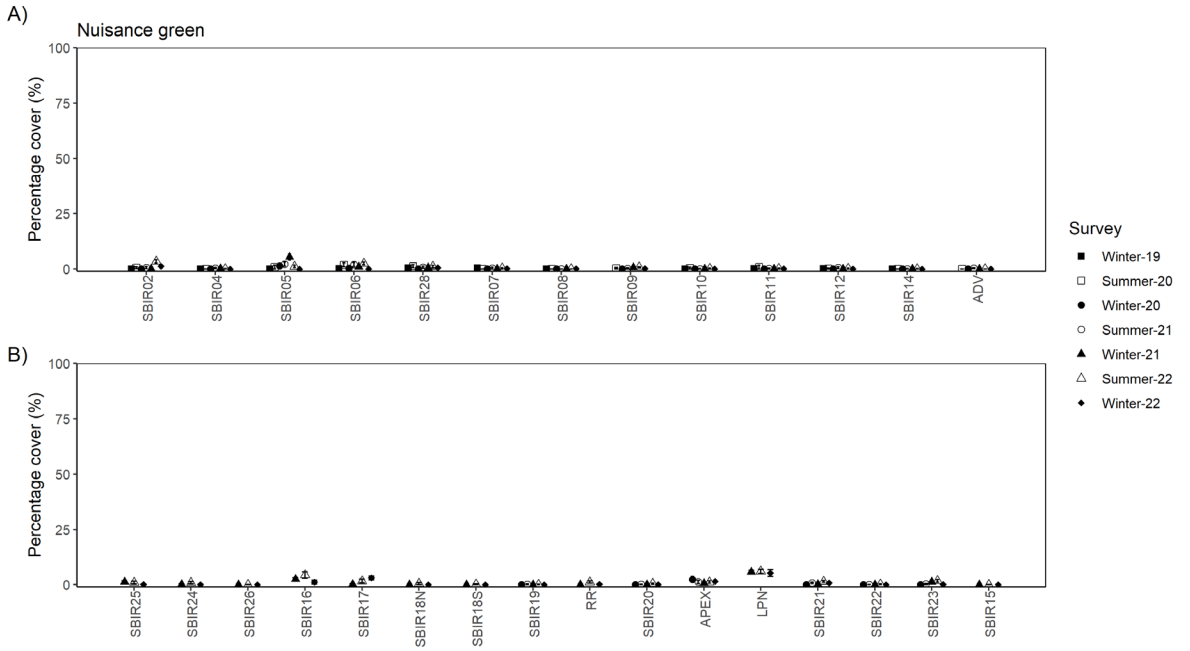

Figure 5-32: Mean (± SE) cover of nuisance green algae observed at all RVA surveys across Storm Bay. Different survey events are marked by different symbols.

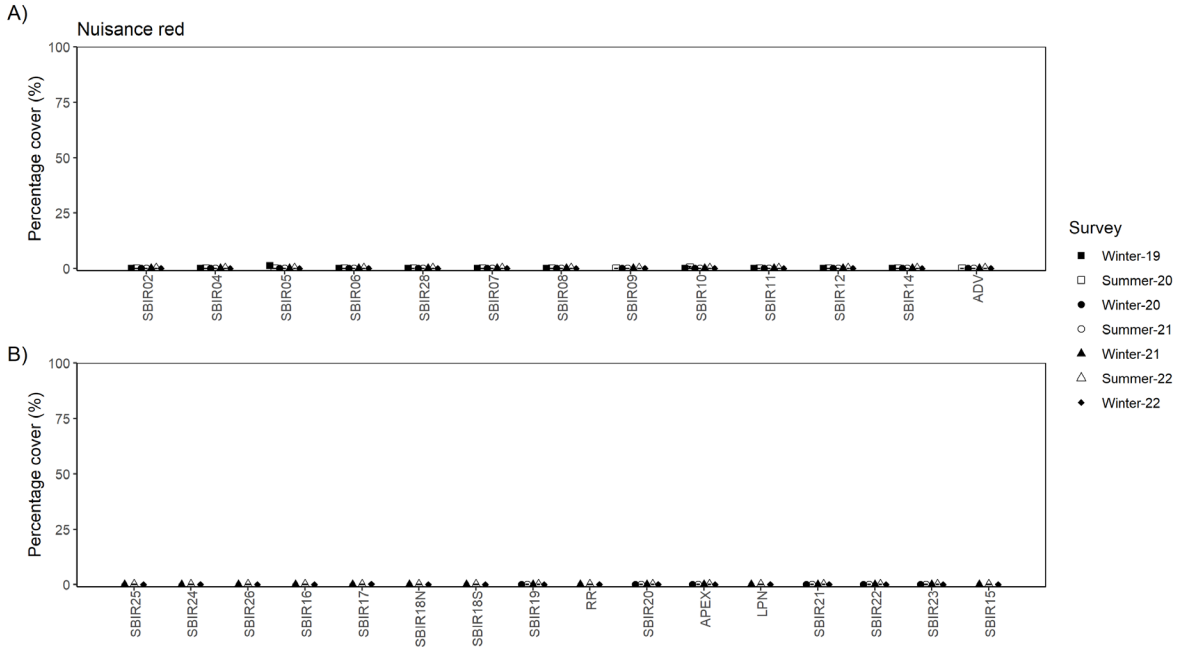

Figure 5-33: Mean (± SE) cover of nuisance red algae observed at all RVA surveys across Storm Bay. Different survey events are marked by different symbols.

5.3 Synthesis

Overall, data collected on inshore reefs as part of this project has allowed the development of a detailed and comprehensive baseline. This baseline suggests that the inshore reefs observed in Storm Bay are generally healthy, with diversity of fish, invertebrate and algal

communities as expected for south-east Tasmania, and reef function indicating minimal nutrient enrichment. This baseline provides the capacity to detect and evaluate any broadscale ecological changes that may occur on inshore reef systems into the future. The two survey techniques used, underwater visual census (i.e. biodiversity surveys) and functional analysis (i.e. RVA), provided complementary information on the health and ecology of the inshore reef systems in Storm Bay.

Across 30 inshore reef survey sites, biodiversity surveys have provided a comprehensive census of marine life associated with these habitats within Storm Bay. This census data can be used to assess shifts in the species assemblages associated with these habitats over time and to better understand broadscale changes, while allowing for the opportunity to examine unforeseen or cumulative impacts on rocky reef habitats (Valentine et al. 2016). Diversity was typical of shallow reef assemblages found throughout south-eastern Tasmania (Reef Life Survey Foundation 2023), with western Storm Bay having higher diversity in fish and eastern Storm Bay higher diversity in algae. No sites stood out as being particular hotspots for biodiversity, although certain sites (e.g. SBIR22, SBIR17, SBIR14) clearly provided better habitat for commercial species such as abalone and rock lobster.

This study found that biodiversity in fish and mobile invertebrate assemblages could be considered at a regional level, rather than the site level. Analysis of data suggested that fish assemblages were similar around the northern part of Storm Bay and more variable in the south and east. Similarly, invertebrate assemblages were relatively homogenous across Storm Bay, with only 7 sites separating from the main group, and most of these found in the east. In contrast, species assemblages of macroalgae varied considerably across Storm Bay. Following the models developed by Edgar (1984) and Hill et al. (2010), variation in macroalgal species assemblages appears to be largely related to wave exposure in western Storm Bay. However, distribution of species assemblages is more variable in eastern Storm Bay, with all significant groupings present within a relatively small area. While exposure is likely to be influencing the observed spatial variability in macroalgal assemblages in this part of Storm Bay, other environmental factors, such as nutrient availability, proximity to freshwater inputs (and consistency thereof), light availability, site aspect, substrate composition and geomorphology have the potential to influence macroalgae assemblages (Schiel 1990, Pinho et al. 2015, Ramos et al. 2016, Smale et al. 2020, Mora-Soto et al. 2021). Many of these parameters were observed to be more variable in the east compared to the west and therefore are likely to be driving the high diversity noted in macroalgal assemblages across a small spatial scale.

While the biodiversity data has provided an invaluable part of the baseline in Storm Bay, previous studies have indicated that it is not necessarily fit for purpose in terms of detecting low-level nutrient enrichment on rocky reef systems (Valentine et al. 2016, Ross et al. 2021). The RVA method evaluates benthic communities through multiple functional parameters with an emphasis on macroalgae and has been demonstrated to be capable of detecting low to moderate levels of nutrient enrichment on rocky reef habitat (Ross et al. 2021, White & Brasier 2021, White et al. 2021b). It is therefore a valuable tool in monitoring for effects of salmon aquaculture in these environments (White et al. 2021b, White et al. 2022a). In Storm Bay, RVA indicated minimal enrichment with no sites showing a sustained, elevated

presence of nutrient indicators. Instead, ecosystem function appears largely driven by dynamics associated with macroalgal canopy. This is reflected in the cluster analysis, with groupings generally reflecting the dynamic between macroalgae canopy and relative abundance of understorey and substrate composition. As the RVA is a functional assessment, it is therefore far more simplistic in its assessment of an ecosystem than a biodiversity survey; this is reflected in the number of significant groups indicated by RVA (3-4 groupings) versus biodiversity assessments (7 groupings).

As RVA surveys are more simplistic, they are inherently less labour-intensive regarding dive time and data processing. This provided the capacity to assess temporal variability in ecosystem function over the lifespan of this project, through repeat surveys in every year for both summer and winter. We found that some sites were very stable across time (i.e. SBIR10-SBIR14, Adventure Bay, SBIR24-26), whereas others were more variable (i.e. SBIR02, SBIR05, SBIR07, SBIR08, SBIR20). The capacity to assess variability over time was limited in the eastern region of Storm Bay. As RVA surveys did not commence on the eastern side of Storm Bay until the West of Wedge lease was stocked in 2021, most sites in this area of Storm Bay only have three data points. Understanding long term variability is critical in detecting significant change in ecosystem function. Reef monitoring with regard to salmon aquaculture interactions is still in a developmental phase and understanding natural variability is a critical component for developing appropriate tools to inform management of these systems.

While the data collected through this project provides an invaluable baseline, the design was largely constrained by where suitable reef habitat could be found for surveys. As inshore reefs in close proximity to salmon leases are largely absent within Storm Bay, the monitoring of these systems was assessed at a broadscale only. Given the broadscale nature of the design, changes that may occur in reef systems are unlikely to be attributed to one factor alone. To attribute change (or a portion thereof) to salmon farming, multiple lines of evidence will be needed. This may include targeted studies that use tools such as modelling, biochemical and molecular profiling of macroalgae, and gradient experiments. When used in conjunction with ecology-based surveys, these tools have capacity to provide more confidence in examining any possible link between salmon aquaculture and broadscale change in inshore reef systems.

5.4 Recommendations for monitoring

The approach of biodiversity surveys combined with RVA is recommended for future monitoring on inshore reef ecosystems in Storm Bay. While RVA can be used as a sensitive method to detect nutrient enrichment on reefs, biodiversity surveys can provide information on the consequences of this nutrient enrichment to the species assemblages associated with these habitats. Inherently, biodiversity is good, with high species richness associated with functional redundancy and stable ecosystem function and a loss of biodiversity indicating a decrease in ecosystem resilience (Duffy 2002, Steneck et al. 2002, Stachowicz et al. 2007, Halpern & Floeter 2008, Tilman et al. 2014). While RVA provides a robust and simple method of understanding whether change has occurred in the system

particularly due to nutrient enrichment, the biodiversity surveys provide information regarding the ecosystem-level consequences of this change.

Given the relative stability and similarity of several sites, combined with an overall healthy ecosystem across Storm Bay with relatively few signs of nutrient enrichment, a decrease in the number of sites that are monitored regularly is recommended. While examining 30 sites across Storm Bay was invaluable in informing a robust baseline, our analysis has indicated that there was redundancy between sites, particularly regarding ecosystem function. Analysis of the data above has informed the recommended site list for monitoring into the future, which suggests approximately 14 sites; SBIR02, SBIR05, SBIR28, SBIR07, SBIR10, SBIR14, SBIR26, SBIR17, SBIR19, SBIR20, Apex Point, SBIR21, SBIR22 and SBIR23 (Figure 5-34). This site list was developed to be representative of all significant groupings found through the analysis of macroalgae biodiversity (see Sections 5.2.1 and 5.2.2), along with ecosystem function through RVA (see Sections 5.2.3 and 5.2.4). The recommended site list is balanced between western, eastern, and northern areas of Storm Bay, within the limits of where inshore reef habitat occurs.

We recommend that summer and winter monitoring is retained for the immediate future. Our data suggests that the evaluation of reef health goes beyond the simple presence or absence of a parameter such as nuisance algae. Seasonal variation in the structure of reef systems, such as the fluctuation in canopy cover or nuisance algae between winter and summer, is an attribute of a healthy reef ecosystem. Enriched systems appear to lose seasonal variability, with enrichment parameters sustained throughout summer and winter and variation in canopy inconsistent with season. Capturing both seasons through monitoring, at least in the short term, is an important part of the assessment process. Notably, the dataset for eastern Storm Bay is much smaller and appears far more variable in terms of biodiversity and function than western Storm Bay; the additional monitoring will aid a better understanding of natural variability and what constitutes significant change.

Overall, we recommend that a robust monitoring program capable of detecting broadscale change be developed based on:

- Underwater visual census following Edgar-Barrett biodiversity (ATRC) methods at 30 sites once every five years.
- RVA surveys following the IMAS method at a reduced number of sites (~14) in summer and winter annually.
- Biodiversity and RVA surveys across the full suite of 30 sites conducted prior to any significant increases in biomass or lease area in Storm Bay.

Note that after five years this program should be re-evaluated, with the option of reducing RVA surveys to summer only if the data indicates broadscale stability. The number of sites for Edgar-Barrett biodiversity surveys could also be reviewed at this point. However, if surveys are reduced to summer only, it is recommended that they return to twice-yearly following any significant increase in biomass or lease area in Storm Bay.

If RVA surveys indicate significant change to key ecosystem parameters, such as a decrease in macroalgal canopy, changes to canopy composition, or increases in nutrient indicator

parameters (i.e. epiphytic, filamentous or nuisance algae) compared to baseline conditions at any given site, then we recommend follow up surveys be undertaken:

- Biodiversity surveys to assess the ecosystem-level impact that any changes to canopy or nutrient indicators may have.
- Surveys using remote platforms (e.g. ROV, AUV, towed camera systems) to cover a greater spatial area to better understand the spatial extent of any change.
- If reduced to summer only, RVA surveys to be resumed at twice-yearly to ascertain temporal nature of the change.

Over time, the development of remote tools (i.e. ROV or towed camera) could be considered for compliance monitoring on inshore reef ecosystems, which is likely to focus on canopy cover and nuisance algae. However, for a BEMP program, where the aim of monitoring should be to evaluate broadscale ecosystem health a more holistic understanding of the ecosystem is required. As demonstrated through FRDC 2015-024, remote techniques can only accurately capture data on two parameters; canopy cover and epiphytic algae (Ross et al. 2021). While fluctuations in these parameters are solid triggers for further investigation, measurements of these two parameters alone is not enough to fully evaluate the overall health of the ecosystem. For this, diver-based surveys are still the best way to fully assess reef ecosystems, given the 3-dimensional structure of these habitats.

If attribution is of interest, then targeted research should be considered. Depending on the change observed, multiple techniques may be used to examine how salmon aquaculture might contribute to any observed change. This could include the application of tools such as modelling (connectivity and biogeochemical), biochemical techniques and deployment of indicator species along a gradient, depending on the overall aim of the monitoring or research question.

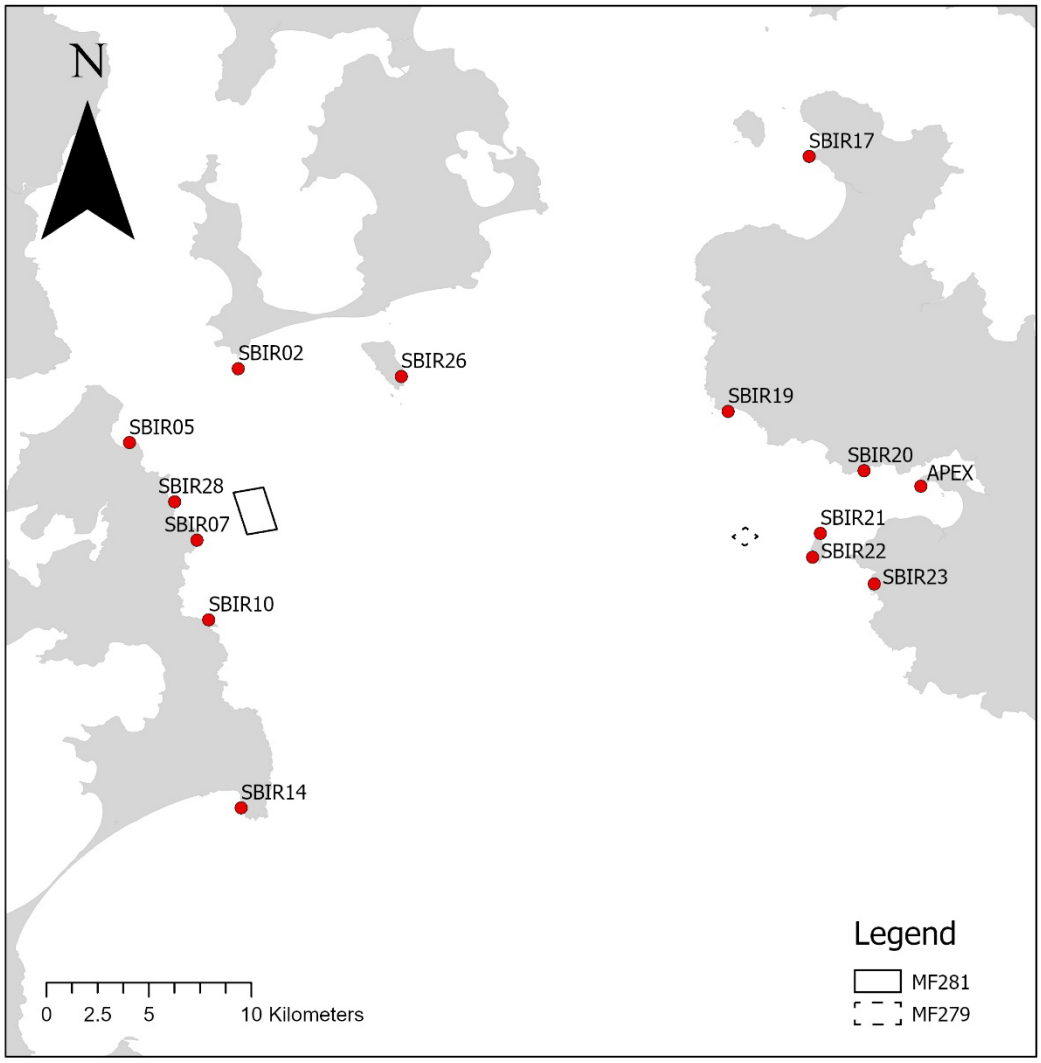

Figure 5-34: Map of proposed sites for reduced program for broadscale inshore reef monitoring. Sites are SBIR02, SBIR05, SBIR28, SBIR07, SBIR10, SBIR14, SBIR26, SBIR17, SBIR19, SBIR20, Apex Point, SBIR21, SBIR22 and SBIR23.

6 Deep Reefs

Deep reefs or temperate mesophotic ecosystems typically occur from approximately 30-150 m (the limit of photosynthesis) on rocky substrate and support a diverse array of fish, mobile fauna and benthic assemblages (Bell et al. 2022). The deep reefs in Storm Bay are nominally defined as "shallow mesophotic", meaning they are light-limited systems extending from 25-50 m in depth. Shallower sites are dominated by diverse green and red macroalgal assemblages, while in deeper locations, sponges and sessile invertebrates are the dominant biota (Bastiaansen 2020). Although the interactions between deep reefs and anthropogenic activities are largely unstudied, the release of nutrients and organic matter into the environment could have complex, direct and indirect effects on the assemblage of the deep reefs (Figure 6-1). As these reefs occur at depths where many species may be light-limited, any changes to the light regime may drive community level change in these systems. Directly, the release of nutrients can favour the growth of green (i.e. *Caulerpa*), red (various species) and turf algal species (Burfeind & Udy 2009, Liu et al. 2016), but excess nutrients can also induce phytoplankton blooms that reduce the availability of light to the benthos (Downing et al. 1999, Xu et al. 2014). This can result in declines in the growth and survival of algae (Strain et al. 2014) and negative impacts on the survival of phototrophic sponges e.g. cup sponges (Bell et al. 2015).

Sedimentation, both directly from aquaculture and indirectly from increased water column productivity, can have both positive and negative effects on sponges, corals and other sessile invertebrates, depending on the sensitivity of any given species (Figure 6-1; Bell et al. 2015). Increased sedimentation, through the deposition of organic matter, will also affect the deep reef assemblages via a number of mechanisms (Bell et al. 2015). At low levels, the deposition of organic matter may increase the supply of food for specific sessile invertebrate groups (i.e. erect and massive sponges, mussels, ascidians; Bell et al. 2015). At higher levels, sedimentation can smother the gametophytes or small juveniles of foliose brown algae (Airoldi 2003, Strain et al. 2015) and clog the filtration apparatus of sponges, with potential to inflict at least partial mortality on some sponge taxa (i.e. cup sponges), corals and other sessile invertebrates (Bell et al. 2015). Indirectly, the loss of erect sessile invertebrates and brown algae could have flow on effects on other trophic groups which include species of commercial value, such as rock lobsters and abalone, which rely on these taxa for habitat and/or food.

In a system such as Storm Bay, salmon aquaculture represents a source of nutrients, but inputs from the Derwent estuary and other catchments also contribute significantly to nutrient loadings (Wild-Allen et al. 2010). It is important to understand the proportional influence of salmon aquaculture in the context of region-wide drivers. Understanding the pathways of interaction is complex, with little existing research on nutrient enrichment and temperate mesophotic reefs and very little known about the deep reef communities of Storm Bay.

In more recent years, the BEMP programs for new Atlantic salmon growing regions have been expanded to include other potential receiving habitats, including deep reefs. Protocols

for monitoring inshore reefs have been developed, with FRDC 2015-024 being the first project to establish performance indicators and monitoring protocols for inshore reef habitats (Ross et al. 2021). In contrast, understanding how to monitor the condition of deep reef habitats for interactions with salmon aquaculture is limited and there is a need for methods to be developed.

The BEMP in Storm Bay was initiated in August 2019, with the aim of improving the understanding of the deep reef systems in Storm Bay. To provide regional level context, techniques for monitoring mesophotic systems developed through the National Environmental Science Program (NESP) Hub (Monk et al. 2020, Barrett & Monk 2021, Perkins et al. 2022) were used and tested for suitability in these systems. The aim of this research program was twofold: a) to establish a thorough baseline understanding of the biota associated with the deep reef systems in Storm Bay and b) to develop monitoring techniques that can determine significant change to these systems. This understanding will be used to make recommendations on how to monitor deep reef systems into the future.

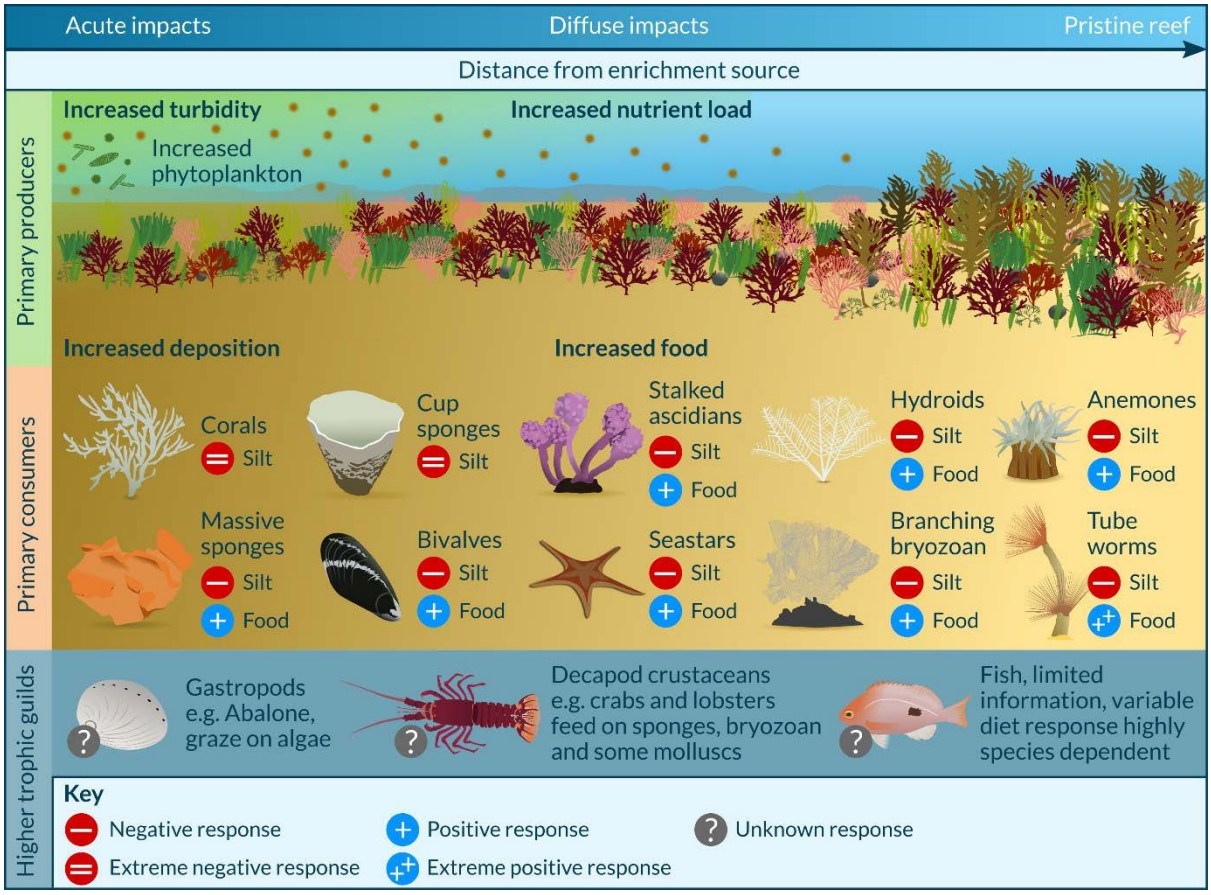

Figure 6-1: Schematic of potential pathways for impacts on deep reef ecosystems in Storm Bay through organic enrichment.

6.1 Design & survey methods

The deep reefs in Storm Bay follow a gradient from the south-west of Betsey Island in the north to adjacent to Adventure Bay on Bruny Island in the south. They are mainly located on the western side of Storm Bay, although Dart Bank is a significant system in the east (Figure 6-2). In 2022, surveys were undertaken at eight sites to capture the biodiversity of the

Storm Bay deep reef systems (Figure 6-2, Table 6-1). At each site, between one and five 200 m transects were surveyed using a remotely operated vehicle (Falcon ROV), with start and end coordinates recorded for each transect. The number of transects recorded from each reef was dictated by the spatial extent of the reef and the conditions (i.e. visibility) on the day of the survey. Footage was collected for two different purposes; qualitative assessments were performed at transect DR1 from Dart Bank, Horseshoe Reef, Variety Reef and Crayfish Rock to satisfy environmental license conditions, and a quantitative analysis was undertaken at all sites in 2022 to better understand the ecology of the deep reef systems in Storm Bay (Table 6-1).

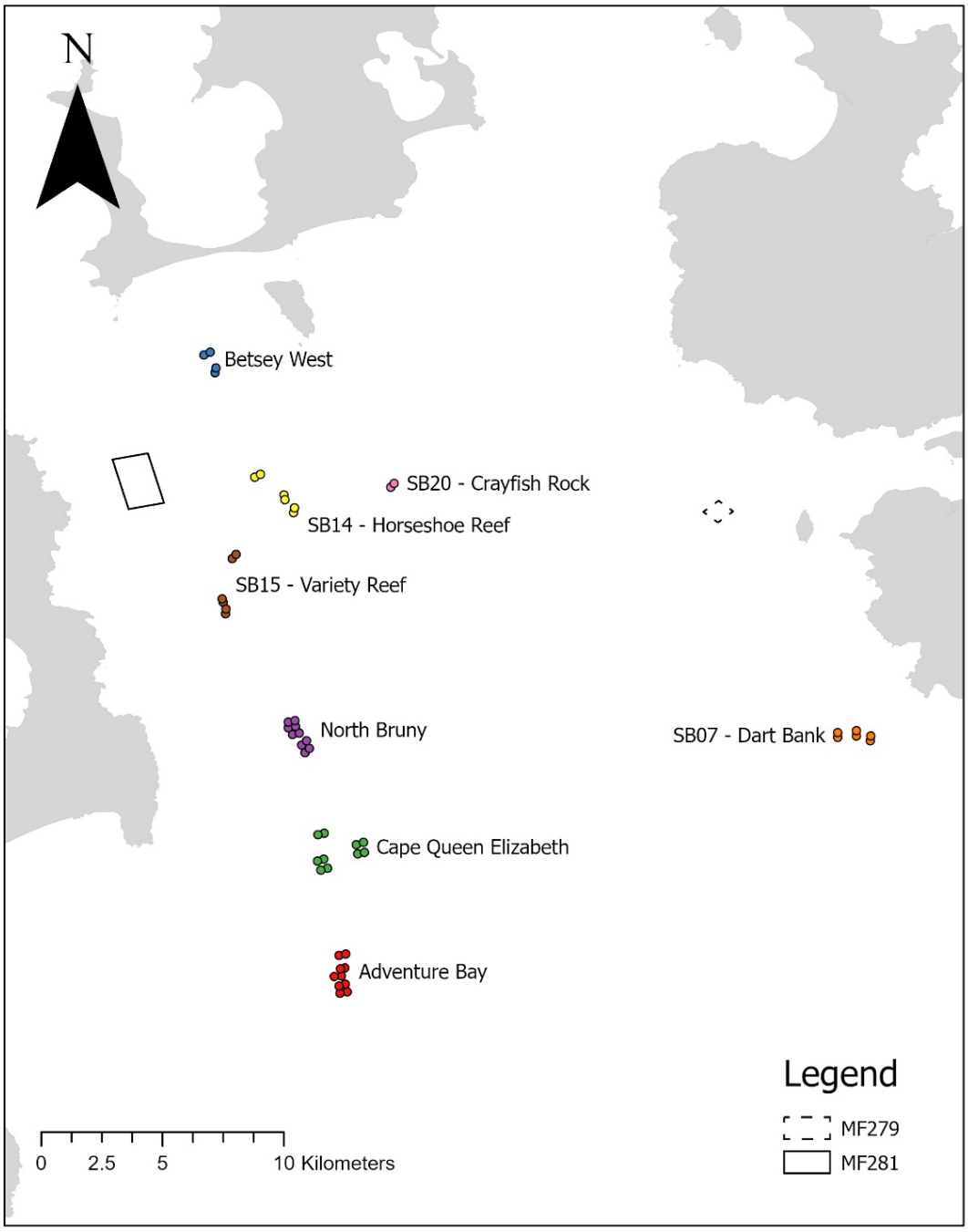

Figure 6-2: Map showing the locations of the deep reef sites with points indicating the 200 m transect start and end locations at each site.

Table 6-1: Summary of deep reef surveys, indicating which transects had qualitative assessments of fish and benthic communities (via forward-facing video), quantitative assessments of fish communities (via forward-facing video) and quantitative assessments of benthic communities (via benthic stills) undertaken across a three-year period in Storm Bay.

Site	Transect	Qualitative (fish & benthic communities)	Quantitative (fish)	Quantitative (benthic communities)
Dart Bank - SB07	DR1*	X	X	X
	DR2		X	X
	DR3		X	
Horseshoe Reef - SB14	DR1*	X		
	DR4		X	X
	DR5		X	X
Variety Reef - SB15	DR1*	X		
	DR2			X
	DR5		X	X
Crayfish Rock - SB20	DR1*	X	X	X
North Bruny	DR1		X	X
	DR2		X	
	DR3		X	X
	DR4		X	
	DR5		X	
Betsey West	DR1		X	X
	DR5		X	X
Cape Queen Elizabeth	DR1		X	X
	DR2		X	
	DR3		X	X
	DR4		X	
	DR5		X	X
Adventure Bay	DR1		X	X
	DR2		X	
	DR3		X	X
	DR4		X	
	DR5			X

*Indicates the transects surveyed annually as part of environmental license conditions, as specified by the EPA.

6.1.1 Qualitative assessment

Video for qualitative assessments was collected using a Saab Seaeye Falcon ROV for transect DR1 at Dart Bank, Horseshoe Reef, Variety Reef and Crayfish Rock, with all footage captured in 1080k with 60 frames per second. Dominant fish, algae and invertebrates were recorded and tabulated. Where species identification was indeterminate, the established and accepted classification scheme of the Collaborative and Automated Tools for Analysis of Marine Imagery (CATAMI) was used to categorise observed biota (Althaus et al. 2015). This scheme, widely used in Australia for benthic surveys, was established to provide a consistent set of identifiers for a wide variety of marine environments, whereby a defined descriptor is assigned to specific biota.

6.1.2 Quantitative assessment

For quantitative assessments, a Saab Seaeye Falcon ROV was used to house two forward-facing Sony FDR-X3000 stereo cameras which recorded underwater footage in 1080p and 60 frames per second. In addition, a bottom-mounted GoPro Hero9 camera enabled capture of 20MP benthic stills at a rate of one frame per second. Lasers set at a distance of 10 cm were mounted on the bottom of the ROV to quantify all benthic imagery collected by the downward-facing camera. Location of the transect was recorded using LinkQuest's TrackLink 1500LC USBL system, with a pole-mounted transceiver located just below the hull of the vessel and a transponder mounted on the ROV. The ROV was flown at approximately 0.5 m/second along the transect length, remaining at a constant altitude of approximately 1 m above the substrate where possible.

Due to either poor visibility or issues with lasers, forward-facing footage and benthic imagery were not collected consistently at each site (Table 6-1). Thus, a subset of transects were selected for quantitative assessment of footage and imagery. A minimum of two transects were assessed at each site, with the exception of Crayfish Rock, where only one transect was collected due to the small size of the reef.

Fish community structure was assessed by analysing stereo video footage from the forward-facing cameras using the EventMeasure image annotation software (https://www.seagis.com.au/event.html). Using this software, all fish within a consistent field of view (5 m in front of the cameras and ~2.5 m either side of the cameras) were identified to species level. They were counted and body length measurements were taken. This field of view was used to limit bias associated with varying visibility at different sites.

Benthic images were annotated to quantify the percentage cover of benthic biota and substrata. A subsample of every 10th image was taken for each transect to avoid spatial overlap of images. Of this subsample, a further subset of 50 images was randomly selected for annotation. These images were then screened for image quality, and any images that were unsuitable for annotation (i.e. too blurry or too close/far away from the bottom) were removed and replaced with suitable images from the original subsample. TransectMeasure software (https://www.seagis.com.au/transect.html) was then used to annotate the subsample of 50 images per transect. Twenty-five random points were overlaid over each image and each point was allocated an identity according to the Australian Morphospecies Catalogue (AMC), which is an extension of the CATAMI (Collaborative and Automated Tools for Analysis of Marine Imagery) classification scheme for scoring marine biota and substrata (Althaus et al. 2015).

6.1.3 Data analysis

Patterns in fish and benthic community structure were investigated using the multivariate software package PRIMER v7 (Plymouth Routines in Multivariate Research; Clarke et al. 2014). Average abundance (for fish) and average percentage cover (for benthic data) were calculated. The fish community data were log transformed prior to multivariate analyses, while no transformation was applied to the benthic community data. A Bray-Curtis dissimilarity matrix was calculated, and non-metric multidimensional scaling (nMDS) was

undertaken to visualise patterns in the data. Vector overlays using Pearson's correlation were employed to identify key species and taxa driving trends in the data across both sites and depth bands. For the benthic data, nMDS were undertaken both for the complete list of taxa recorded and for taxa in functional groups.

Patterns in the distribution of average fish abundance and Shannon diversity for fish and benthic invertebrates was examined in ArcGIS. Trophic groups (for the fish data) and functional groups (for the benthic data) across the Storm Bay deep reef sites were visualised using pie charts developed in ArcGIS Pro.

Diversity metrics were calculated for both the fish and benthic community datasets, using the "vegan" package in R. All matrix, substrate and 'unscorable' categories were removed from the benthic dataset prior to the calculation of diversity metrics. Due to an uneven survey design with varying numbers of transects per site, all diversity metrics were calculated per transect and then averaged across transects within a site. For the benthic data, as the majority of taxa represent morphospecies or functional groups (e.g. 'membranous red algae') rather than species, all taxa apart from biological matrix, substrate and 'unscorable' categories were included in taxa richness calculations. The calculations used for each of the key diversity metrics are outlined in Chapter 5.1.3 of this report.

The suitability of the sampling design for adequately capturing biodiversity at each site was assessed on sites where the greatest number of transects were completed. For fish communities, performance of survey design was evaluated at North Bruny and Cape Queen Elizabeth (both with 5 transects), while for benthic communities, data from Cape Queen Elizabeth and Adventure Bay (both with 3 transects) were evaluated. Species accumulation across the number of images per transect (for the benthic data), distance along the transect (for the fish data) and the number of transects per site (for both the fish and the benthic data) were examined using the "vegan" package in R. An iterative approach using random permutations was used when examining benthic species accumulation across increasing numbers of images per transect, while the "collector" method (which adds transects in the order they appear in the dataset) was used when examining fish and benthic species accumulation across increasing numbers of transects, due to the small number of transects per site.

A comparison of the datasets produced by both the qualitative and quantitative assessments of the deep reef benthic communities was also conducted, to compare the number of taxa recorded by both methods.

6.2 Results

6.2.1 Biodiversity & function of deep reef fish assemblages

From the eight sites surveyed in Storm Bay, a total of 35 fish species was observed across 31 genera, with an average abundance of 1030 individuals per 200 m transect. Communities were dominated by planktivorous species from the family Serranidae, with *Caesioperca lepidoptera* (butterfly perch) and *Caesioperca rasor* (barber perch) accounting for 84% of the total fish abundance across all sites. Species from the families Labridae (wrasses) and Monacanthidae (leatherjackets), along with *Dinolestes lewini* (long-fin pike) and

Pseudophycis bachus (red cod), were also common. Commercial species such as jackass morwong (*Nemadactylus macropterus*), grey morwong (*Nemadactylus douglasii*) and long-snout boarfish (*Pentaceropsis recurvirostris*) were also observed on the deeper reef systems (Appendix 6-1).

Spatial heterogeneity was observed in the fish communities across Storm Bay. In terms of total abundance, the highest numbers of fish were found in the southern sites, with Cape Queen Elizabeth and Adventure Bay recording 7471 and 5707 individuals per transect respectively (Figure 6-3, Appendix 6-1). These sites had higher abundances of *C. lepidoptera* (4703 and 3444 individuals per transect) and *Helicolenus percoides* (red gurnard perch; 18 and 28 individuals per transect) than the more northern sites. Betsey West in the north and Dart Bank in the east also appeared to be distinct. More diverse assemblages of Monacanthids and Labrids were observed on these transects, along with an absence of *Parequula melbournensis* (silverbelly), *Scorpis lineolata* (silver sweep) and *Pempheris multiradiata* (common bullseye), and much lower numbers of *Nemadactylus macropterus* (jackass morwong; Figure 6-4, Appendix 6-1). Transect depth corresponded to these patterns, with transects at Adventure Bay and Cape Queen Elizabeth occurring in depths >40 m, whereas Betsey West and Dart Bank transects were typically in the 20-30 m depth band (Figure 6-4).

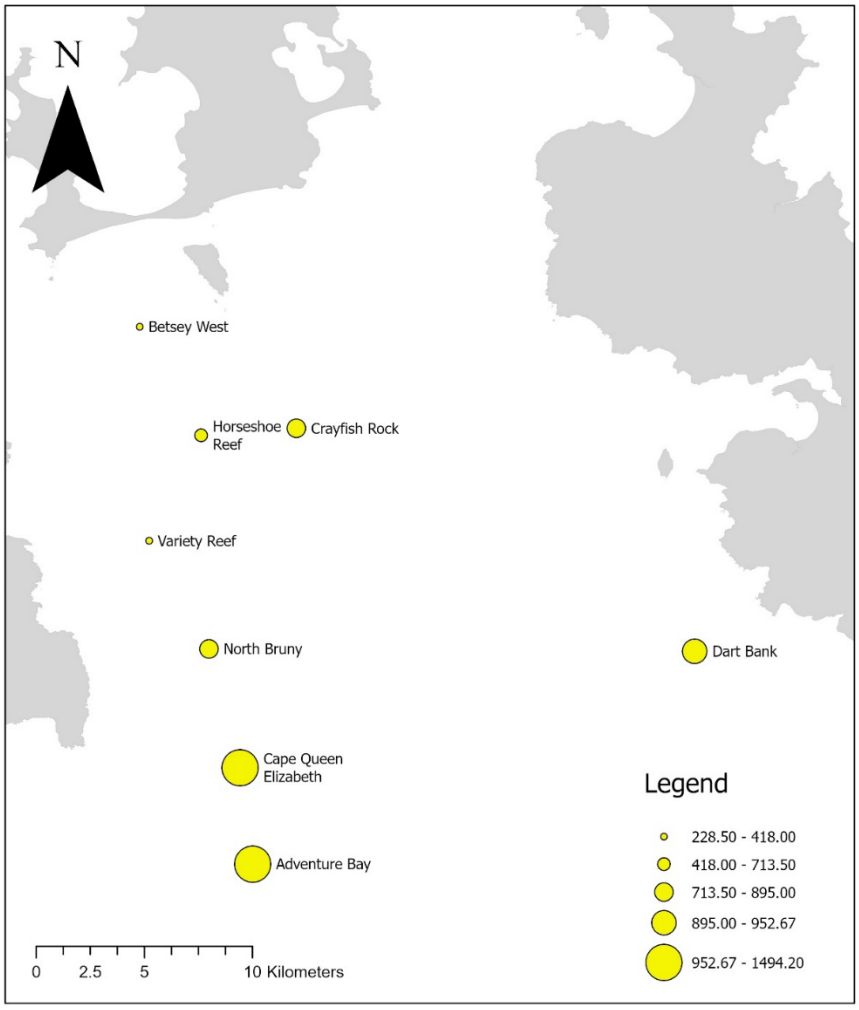

Figure 6-3: Storm Bay deep reef sites, with the size of the bubbles indicating the average abundance of fish species at each site (total abundance averaged across all transects at a site).

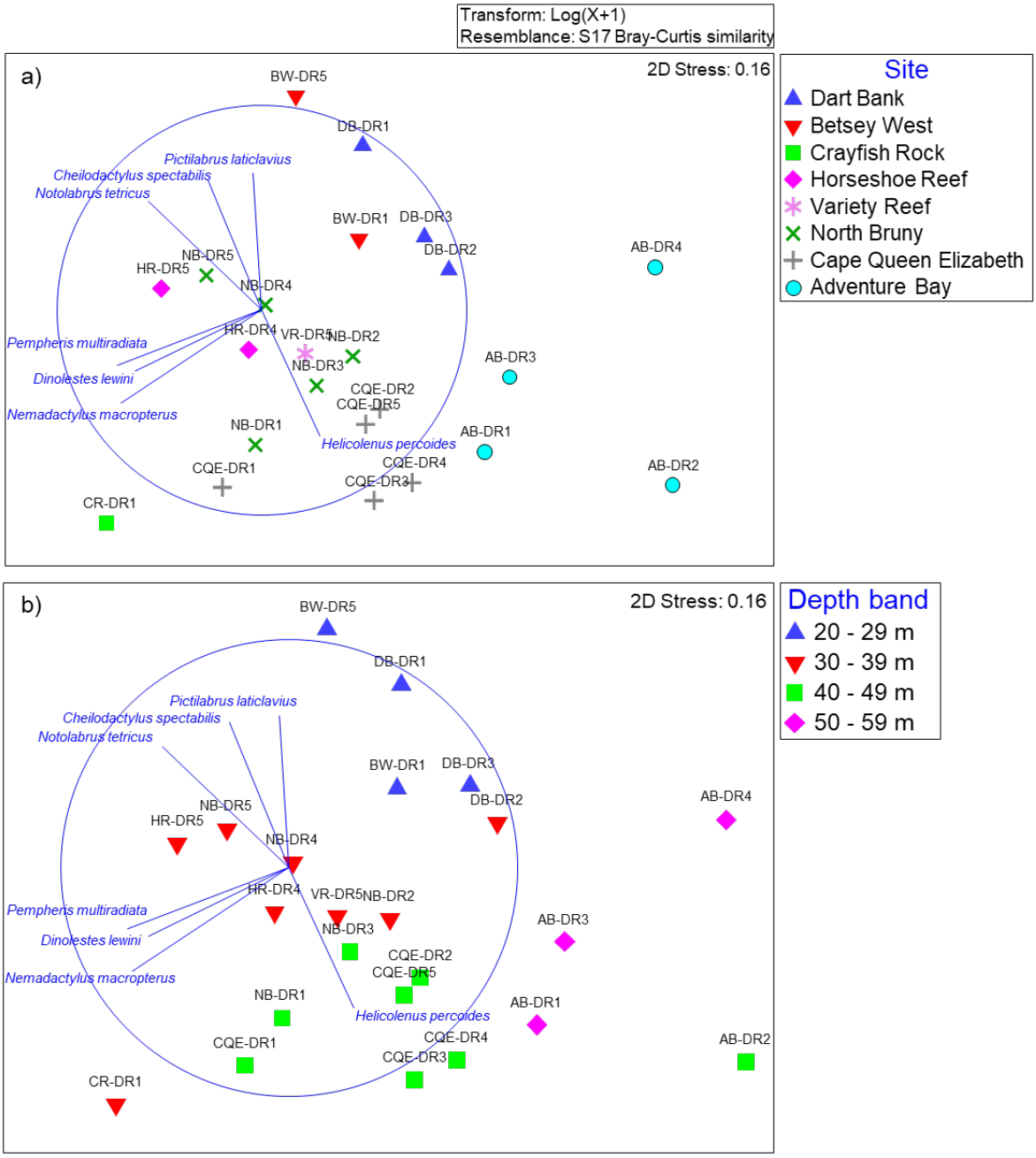

Figure 6-4: nMDS on deep reef fish community data, with symbols indicating a) site and b) depth band. Pearson's vector overlays contributing to ordination with a base variable comparison of >0.6 are included. The length of the vectors indicates the strength of the correlation.

Diversity was examined using a range of metrics for fish on the deep reef systems in Storm Bay (Appendix 6-2). Shannon diversity values were highest at Crayfish Rock and Betsey West and lowest at Adventure Bay (Figure 6-5). However, the highest abundance of fish was recorded at Adventure Bay, indicating that assemblages are dominated by only a small number of species (Figure 6-5, Appendix 6-2). While site-level differences were observed, overall variation in Shannon diversity was low (~ 1) across the whole of Storm Bay. Our analysis indicates that while species assemblages shifted between sites, the diversity within these sites remained largely consistent.

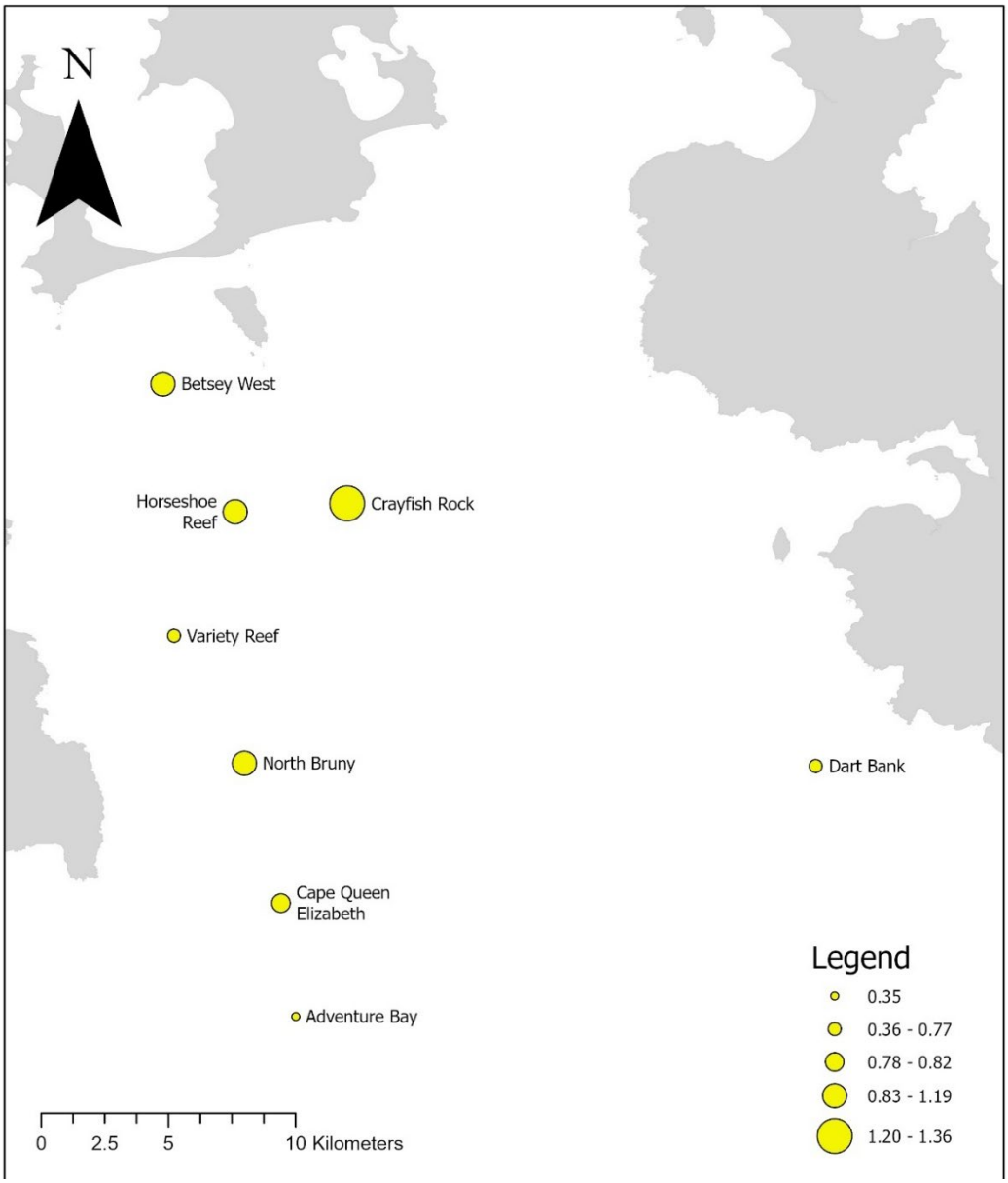

Figure 6-5: Storm Bay deep reef sites, with the size of the bubbles indicating average Shannon diversity values for the fish communities at each site. Only taxa which were identified to the species level have been included in diversity calculations. Baitfish (Clupeidae & Pristigasteridae) have been excluded.

Analysis of trophic groups indicate that fish communities in Storm Bay are dominated numerically by planktivorous species (Figure 6-6). Functional diversity in fish assemblages decreased with latitude, with over 90% of all fish recorded at Adventure Bay being planktivorous (Figure 6-6). This corresponds to increases in depth in the more southerly reefs, but also proximity to the Southern Ocean. Benthic invertivores were the other most common trophic group and tended to decrease with latitude, comprising almost 25% at Betsey West, compared with <10% at Adventure Bay (Figure 6-6). Browsing herbivores only had a strong presence at the shallower sites, Betsey West and Dart Bank, whereas higher carnivores comprised nearly a third of the population at Crayfish Rock (Figure 6-6). As the "higher carnivore" classification includes *D. lewini*, which is a schooling fish, it is likely that only having one transect at Crayfish Rock inflated the importance of this trophic group at this site.

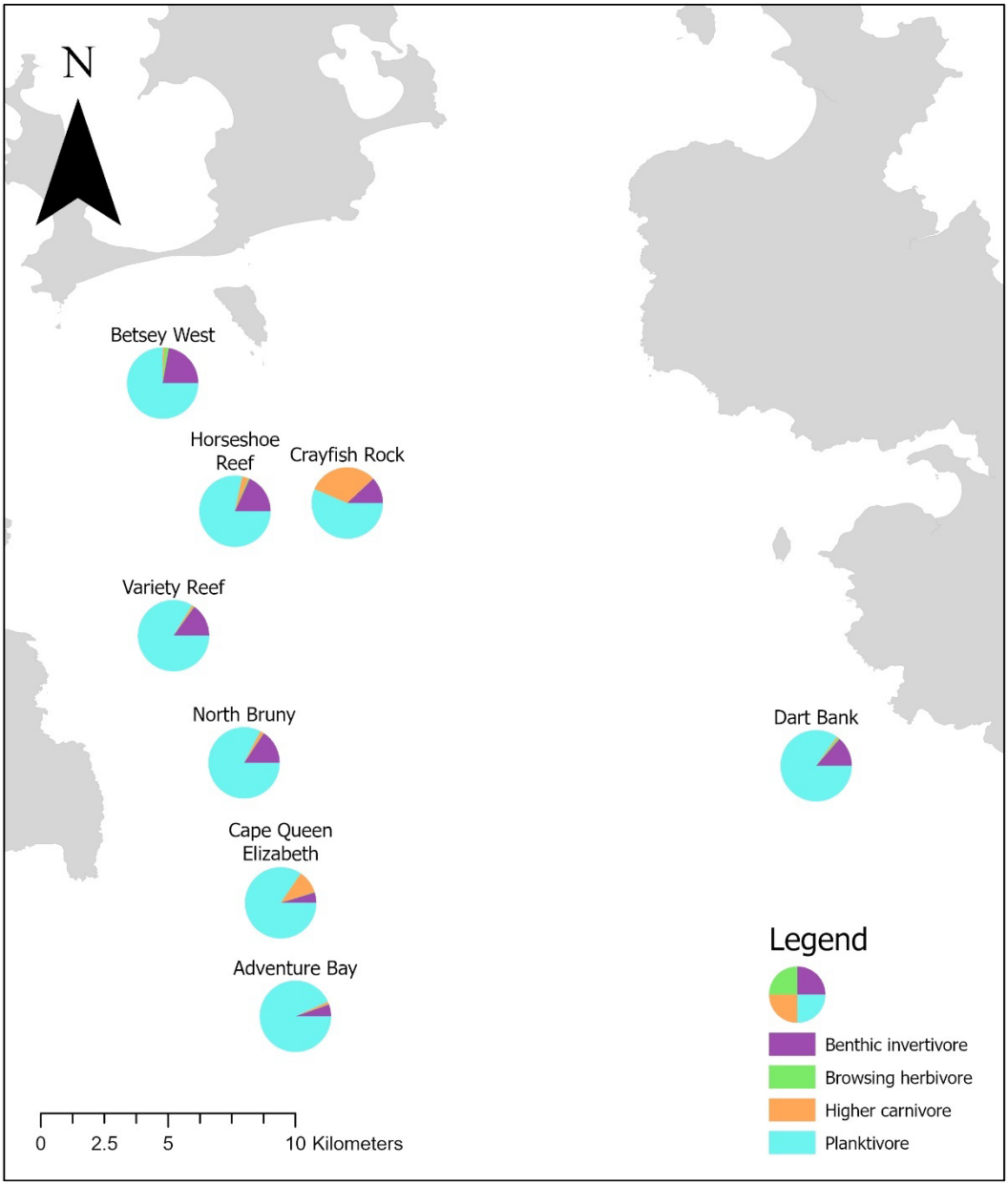

Figure 6-6: Map of Storm Bay deep reef sites with pie chart symbols indicating fish community composition at each site by trophic group. Total fish abundances at each site have been averaged across transects.

6.2.2 Biodiversity of deep reef benthic assemblages

Benthic assemblages on the deep reefs of Storm Bay were highly diverse, with over 220 species and morphospecies identified across the eight sites (Appendix 6-1). Dominant groups included green and red macroalgae, biological matrices and cnidarians (Appendix 6-1). Sponges were also an important group and were present on all transects. While generally not occurring in high abundances, the majority of the observed deep reef biodiversity is accounted for by this group, with 187 individual sponge morphospecies recorded (Appendix 6-1).

Both within-site and between-site variation in distribution of benthic assemblages were observed, likely to be driven by the depth of the reefs (Figure 6-7). The presence of *Caulerpa* spp. and red foliose macroalgae were typical of shallower transects (20-29 m) captured from

Betsey West and Dart Bank (Figure 6-7, Appendix 6-1). The presence of unconsolidated substrate and bryozoan/cnidarian matrix increased with transect depth, with large portions of these substrate types observed at Adventure Bay, Cape Queen Elizabeth and North Bruny, which are >40 m in depth (Figure 6-7). The different taxonomic groupings present in the matrix conglomerates were a factor in driving variation between transects and sites. Factors influencing matrix variation include depth and all of the associated covariates with depth, including light, wave exposure, nutrient availability and proximity to nutrient sources such as the Derwent estuary and the Southern Ocean.

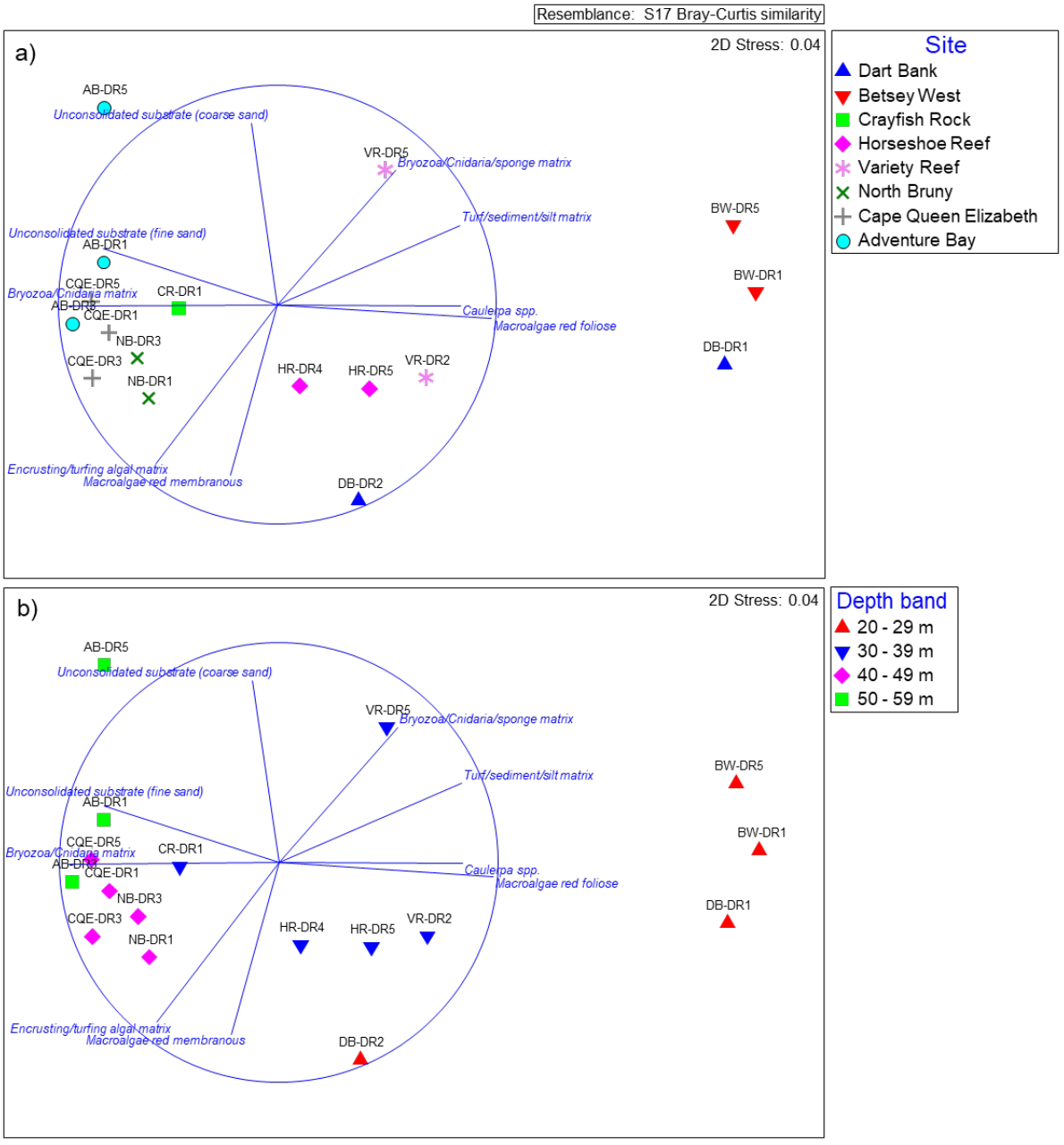

Figure 6-7: nMDS on deep reef benthic community data, with symbols indicating a) Site and b) Depth band. Pearson's vector overlays contributing to ordination with a base variable comparison of >0.8 are included. The length of the vector indicates the strength of the correlation.

Diversity was examined using a range of metrics for benthic communities on the deep reef systems in Storm Bay (Appendix 6-2). As matrix was grouped at a much higher taxonomic level than all other morphospecies, this component was excluded from diversity analyses, despite its relative importance in overall percentage cover. In general, the more southerly sites (North Bruny, Cape Queen Elizabeth, Adventure Bay) had higher average Shannon diversities than the northern sites (Figure 6-8). This result reflects the higher proportion of sponge, which was a highly diverse group in terms of morphospecies present in these communities (Appendix 6-1).

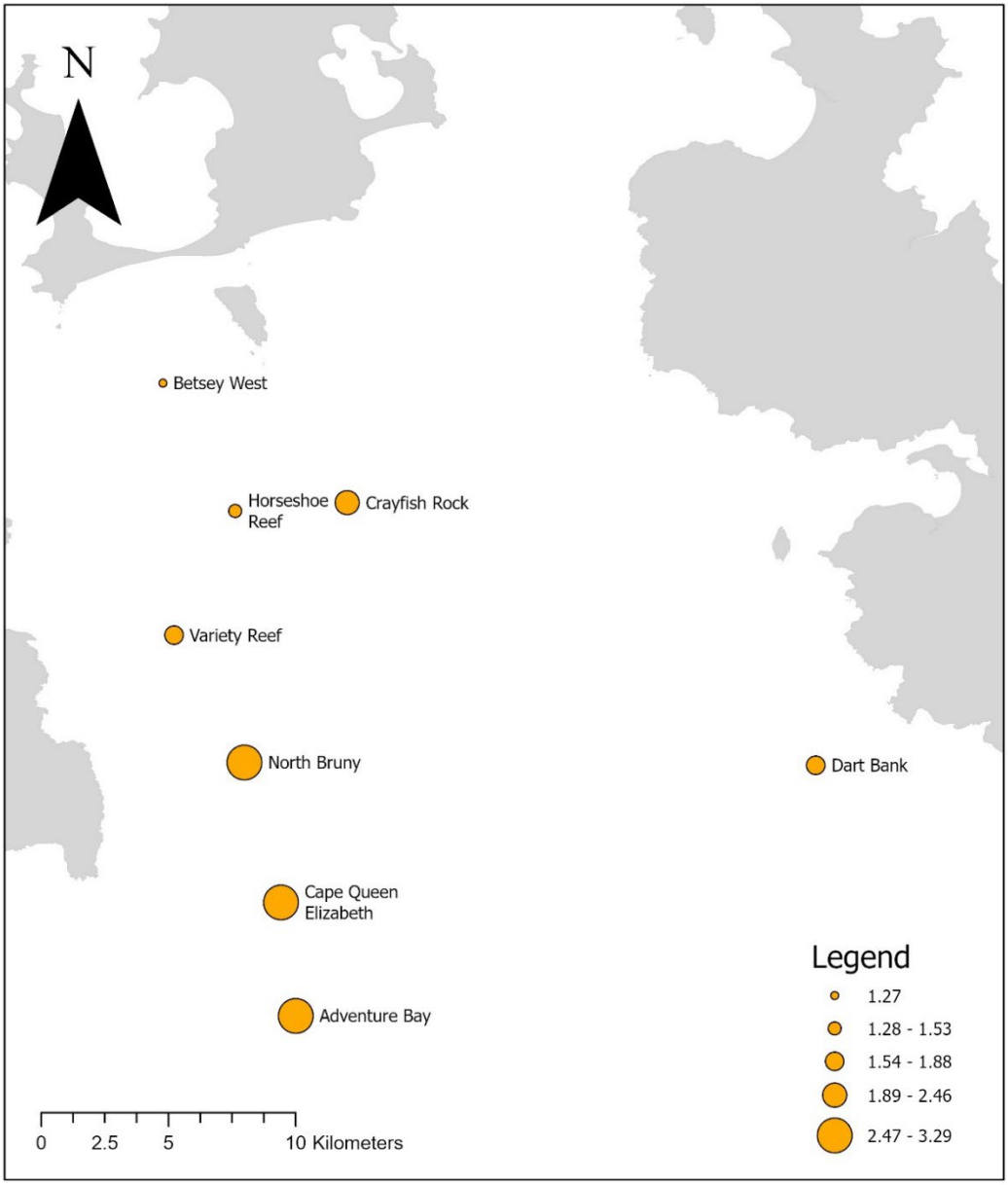

Figure 6-8: Storm Bay deep reef sites, with the size of the bubbles indicating average Shannon diversity values for the benthic communities at each site. Matrix, substrate and 'unscorable' categories have been excluded from diversity calculations.

Analysis of broad functional groups within benthic communities demonstrates a clear north-south gradient in communities corresponding also to a gradient in site depth (Figure 6-9, Figure 6-10). The shallower sites (Betsey West and Dart Bank) had a higher proportion of red

and green macroalgae, with nMDS analysis indicating that these groups are key in distinguishing the shallower transects (Figure 6-9, Figure 6-10). In contrast, at the deeper sites (North Bruny, Cape Queen Elizabeth, Adventure Bay) the proportion of matrix increased, with unconsolidated substrate also increasing with depth (Figure 6-9). Sites with intermediate depth (Horseshoe Reef, Variety Reef) recorded a large proportion of red macroalgae, but minimal green macroalgae was observed (Figure 6-9). When sponges were broken down into broad functional categories for nMDS analysis, encrusting and barrel morphologies were more likely to occur at the deeper sites, whereas erect palmate sponges were more likely to feature at shallow sites (Figure 6-10). Of note, brown macroalgae was not a significant component of deep reef benthic communities at any site surveyed (Appendix 6-1).

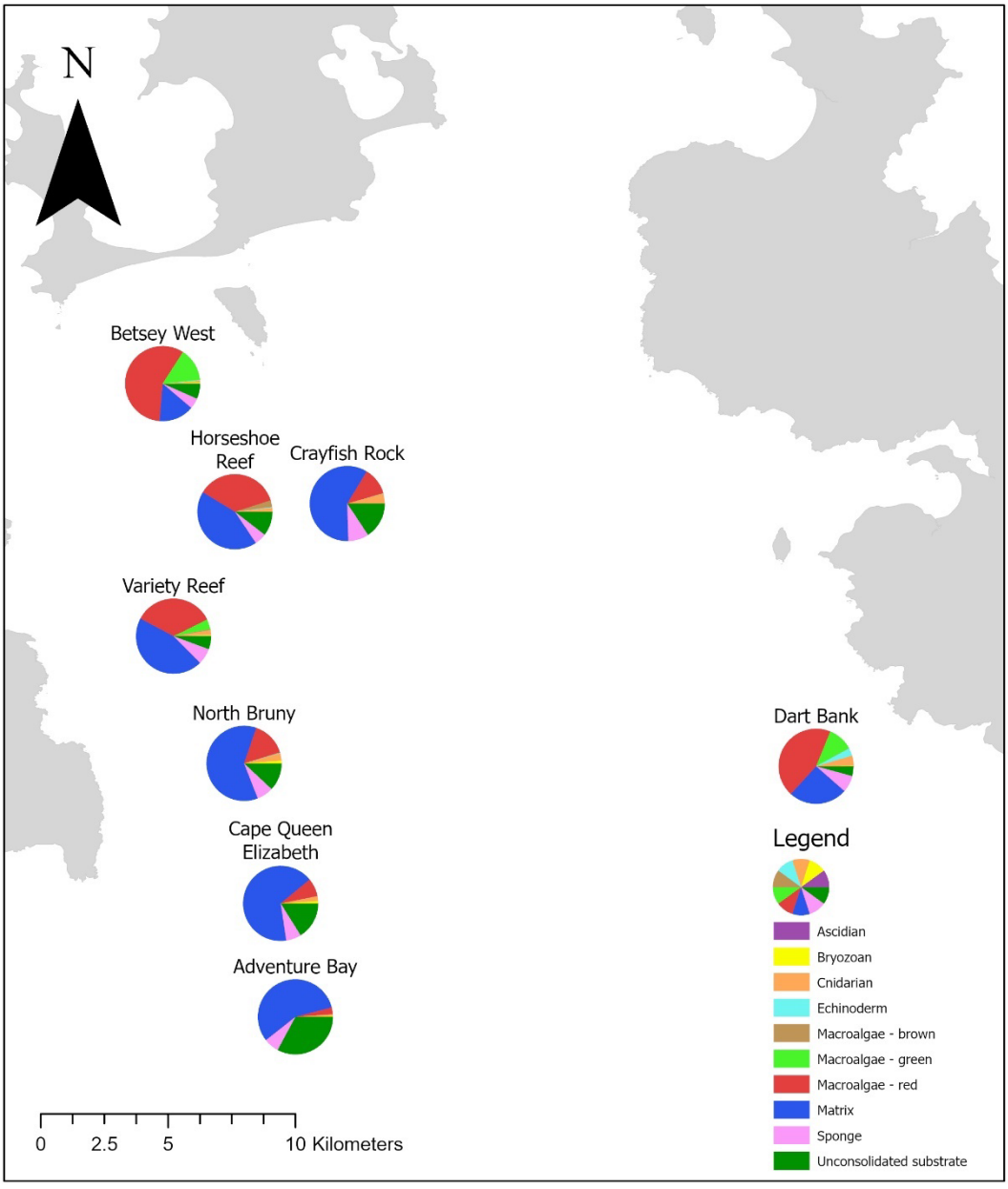

Figure 6-9: Map of Storm Bay deep reef sites with pie chart symbols indicating benthic community composition at each site by functional group (all sponge morphotypes have been grouped together). Percentage covers at each site have been averaged across transects.

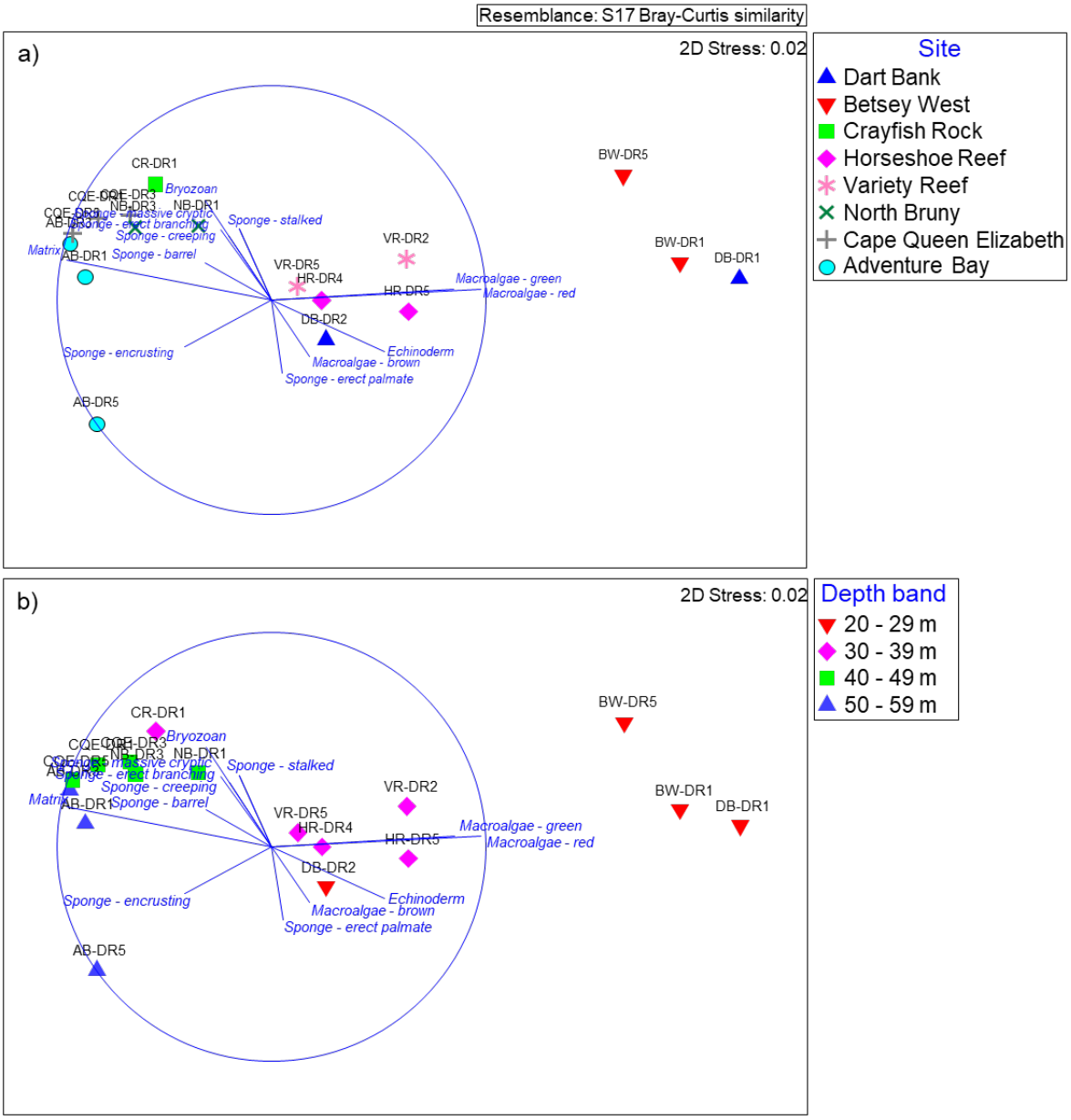

Figure 6-10: nMDS on deep reef benthic community data, with symbols indicating a) site and b) depth band. Taxa have been combined into functional groups. Pearson's vector overlays contributing to ordination with a base variable comparison of >0.3 are included. The length of the vector indicates the strength of the correlation.

6.2.3 Assessment of survey design

Survey design for assessing deep reef fish communities was evaluated at North Bruny and Cape Queen Elizabeth, the two sites where five transects were captured and analysed. At both sites, the first transect captured a large portion (approximately 70%) of the total number of species observed across the five transects (Figure 6-11). While there were novel species still being recorded on transect five, the accumulation curve began to plateau at this point (Figure 6-11).

When the accumulation of species within each transect is examined, the number of novel species detected at North Bruny generally began to plateau at approximately 150 m into the

transect, with the notable exception of DR4 (Figure 6-12). Greater variability between transects was observed at Cape Queen Elizabeth, where no novel species were observed beyond 100 m at DR4. DR1-3 still accumulated novel species at 200 m (Figure 6-12). At both sites, there was variation in the total proportion of species each transect was able to capture. Individual transects at North Bruny captured between 33% (DR2) and 70% (DR1, DR5) of the total number of species observed at that site, whereas Cape Queen Elizabeth ranged between 33% (DR4) and 73% (DR1) (Figure 6-11, Figure 6-12).

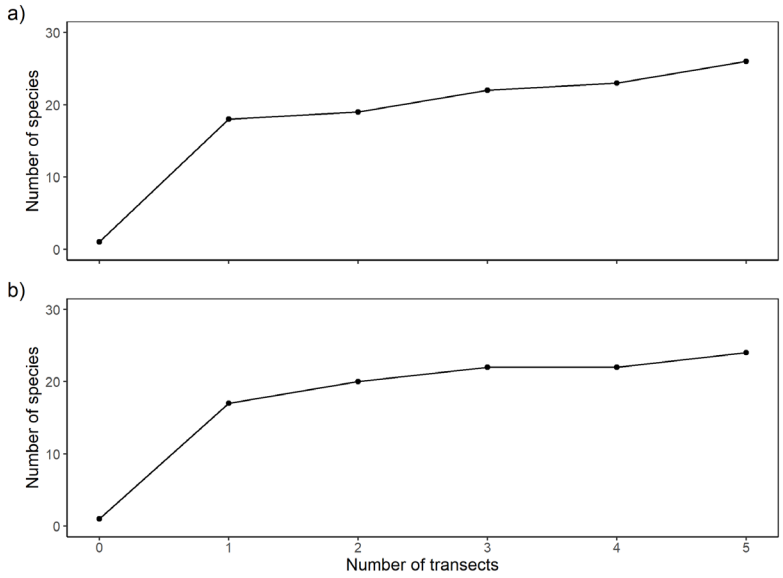

Figure 6-11: Species accumulation curve for fish communities on deep reefs with the number of novel species summed across transects (collector method) for the fish community at a) North Bruny and b) Cape Queen Elizabeth.

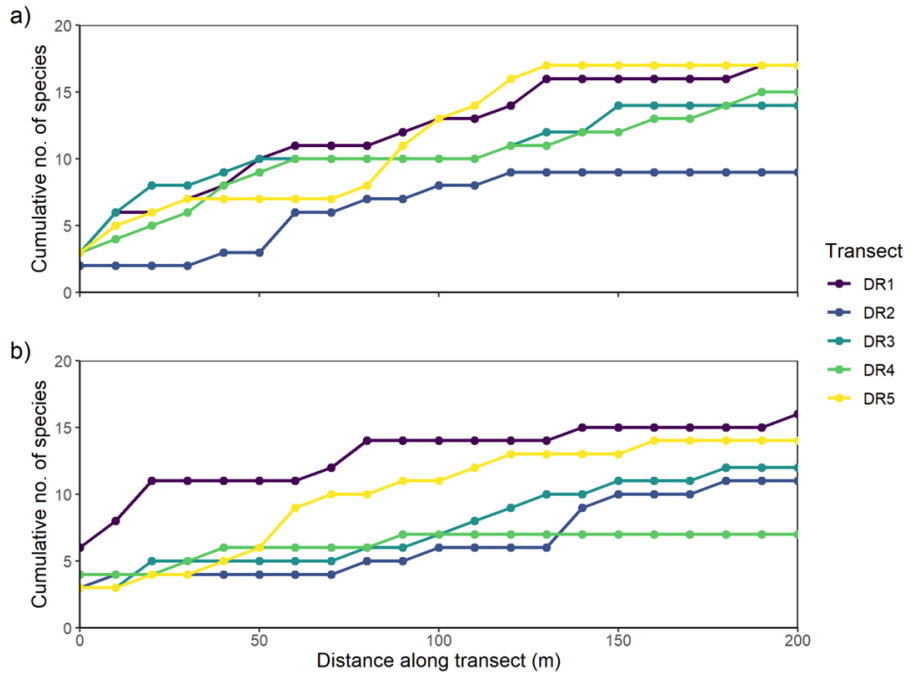

Figure 6-12: Cumulative fish species count by distance along the transect for the five deep reef transects at a) North Bruny and b) Cape Queen Elizabeth.

Survey design for assessing deep reef benthic communities was evaluated at Cape Queen Elizabeth and Adventure Bay, the two sites where three transects were captured and analysed. At neither site was an asymptote observed and it is therefore evident that more than three transects are required before the cumulation of morphospecies begins to plateau (Figure 6-13). This was tested both with sponges at the morphospecies level and sponges collapsed at the functional level. While the curve began to flatten with sponges at functional groups, particularly at Cape Queen Elizabeth, there was still an accumulation of taxa between transects 2 and 3 (Figure 6-13). Biodiversity captured within transects was subsequently examined using nMDS with data presence/absence transformed. At Cape Queen Elizabeth, there is considerable overlap in community composition between the three transects analysed (Figure 6-14). In contrast, at Adventure Bay, the community at DR5 is different to that observed in DR1 and DR3 (Figure 6-14), with very little overlap between photo-quadrats. At sites where there is high between-transect variability, it is expected that a greater number of transects is likely to be needed to adequately capture overall biodiversity at that site.

When the accumulation of morphospecies within each transect was examined it was found that the accumulation curve was still in the exponential phase at 50 quadrats at both sites (Figure 6-15a-c, Figure 6-16a-c). When sponges were reduced to functional groups, curves began to flatten at 50 quadrats, but no asymptote was observed in any iteration (Figure 6-15d-f, Figure 6-16d-f). These trends were consistent across both site and transect.

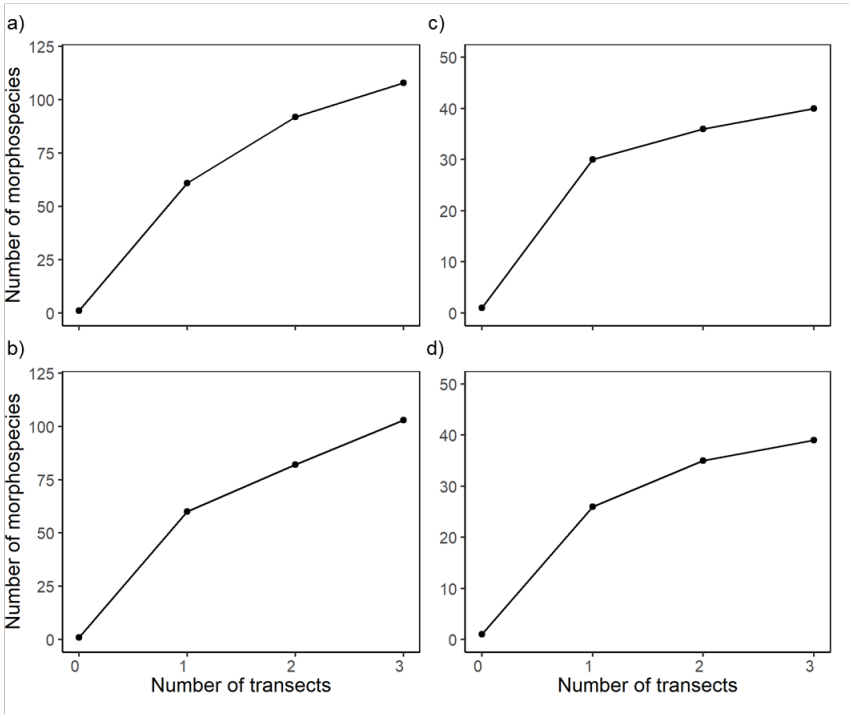

Figure 6-13: Species accumulation curve on deep reefs with the number of novel species summed across transects (collector method) for the benthic communities at a & c) Cape Queen Elizabeth and b & d) Adventure Bay. Species accumulation with sponges collapsed to functional group are represented by c & d.

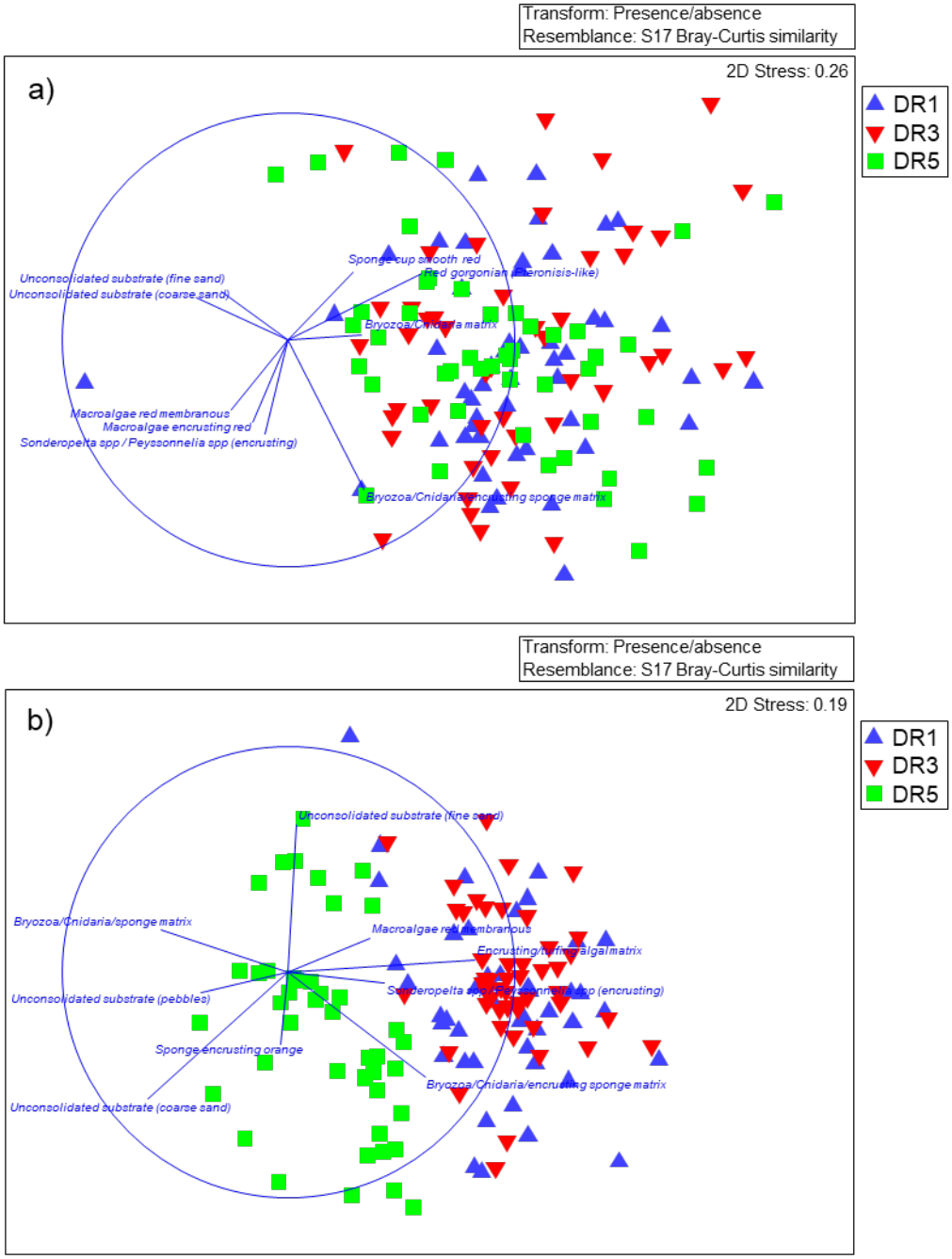

Figure 6-14: nMDS plots on deep reef benthic community data from a) Cape Queen Elizabeth and b) Adventure Bay. Data have been presence/absence transformed with each data point representing an individual photo-quadrat.

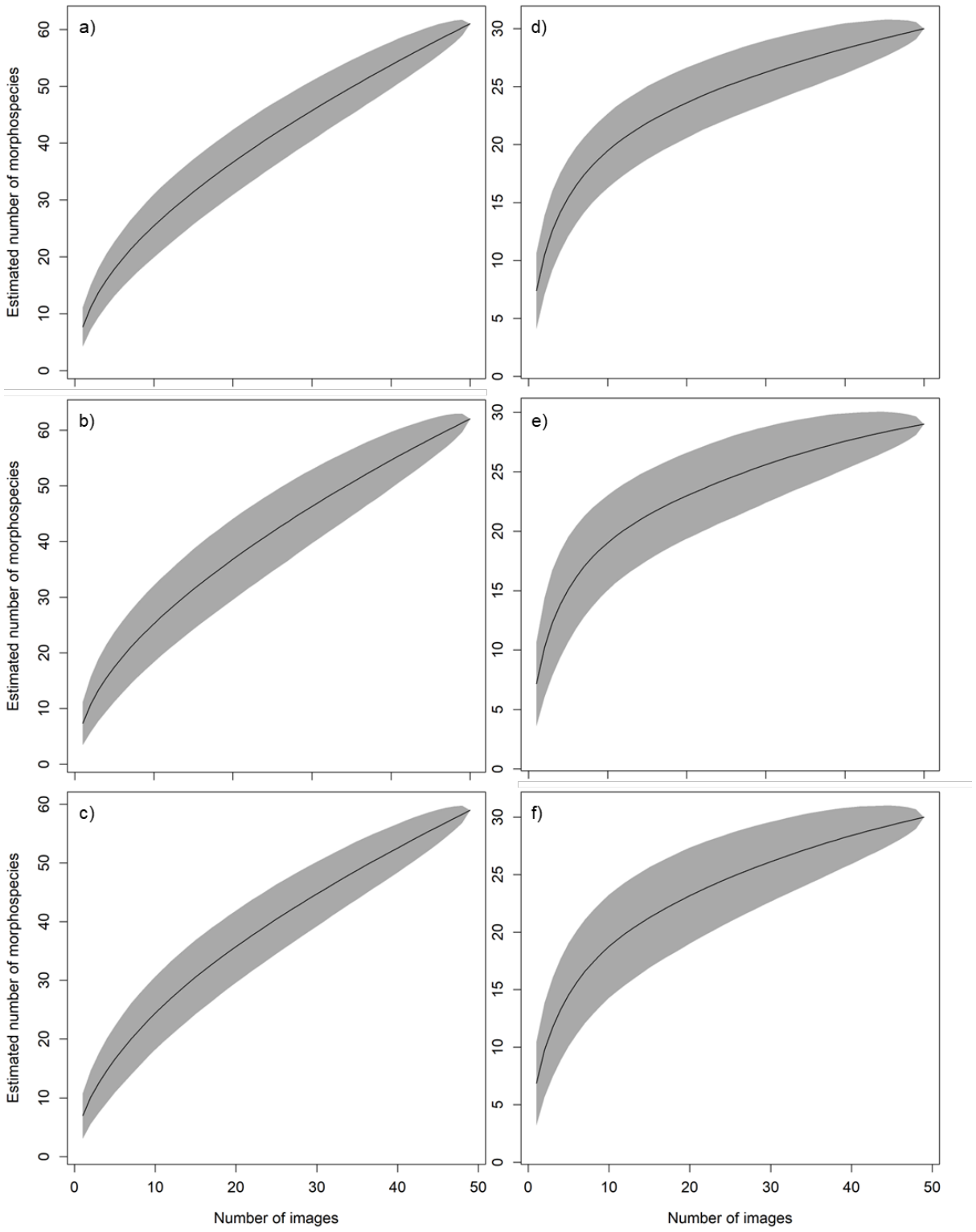

Figure 6-15: Species accumulation curves for the benthic community at Cape Queen Elizabeth, with a)-c) showing DR1, DR3 and DR5 with all taxa, and d)-f) showing DR1, DR3 and DR5 with sponge taxa collapsed to functional group.

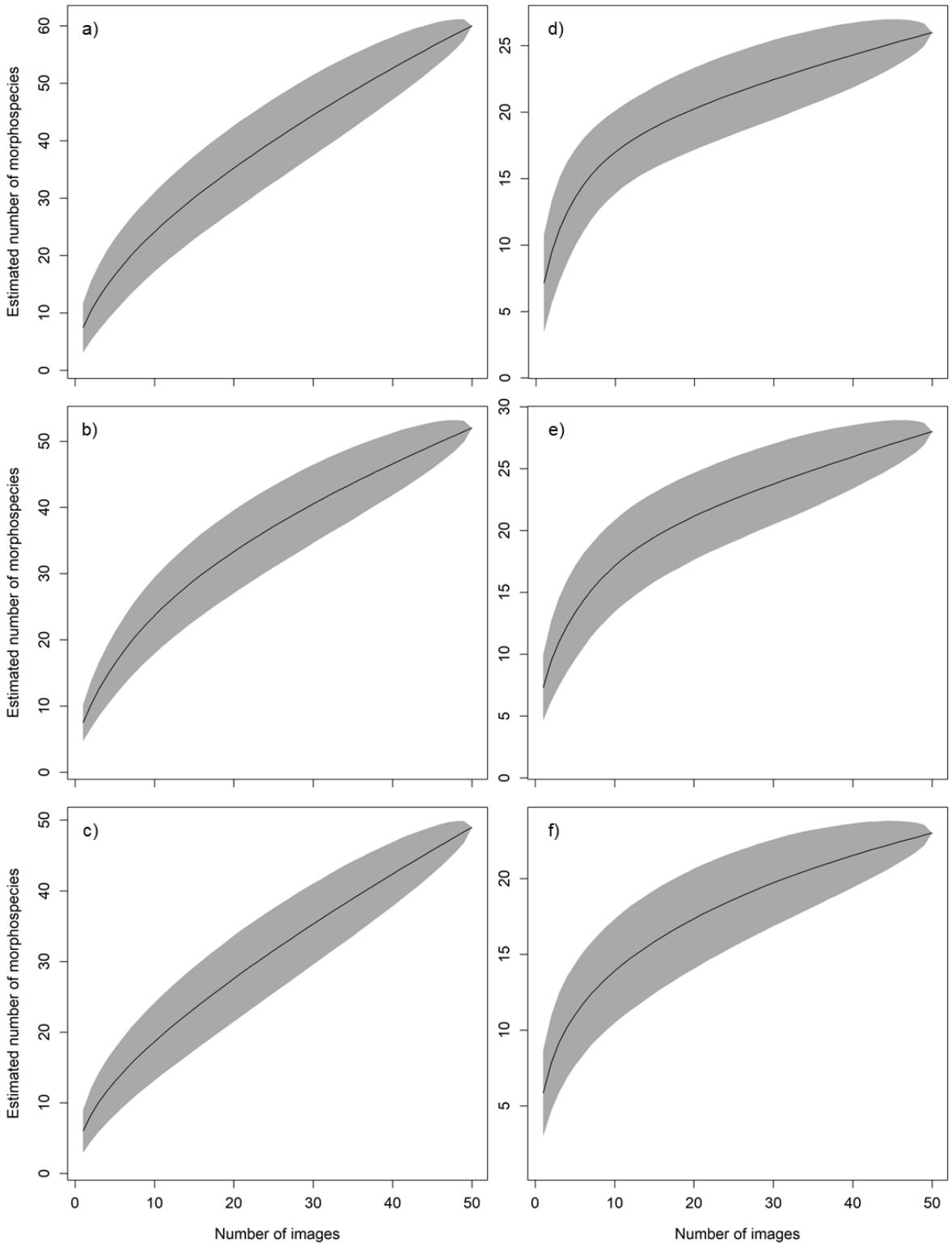

Figure 6-16: Species accumulation curves for the benthic community at Adventure Bay, with a)-c) showing DR1, DR3 and DR5 with all taxa and d)-f) showing DR1, DR3 and DR5 with sponge taxa collapsed to functional group.

6.2.4 Comparison between benthic qualitative and quantitative assessment techniques

When qualitative and quantitative assessment techniques were compared for benthic communities, it was found that the quantitative scoring system consistently detected a greater number of taxa/morphospecies than the qualitative system and at much lower taxonomic/morphotaxa levels (Table 6-2). Overall, the quantitative scoring system was much more powerful in characterising the matrix and identifying sessile invertebrates, with this trend consistent across the two sites examined (Table 6-2). Matrix was not characterised through qualitative surveys; this method only detected 21% of the sessile invertebrate morphotaxa that the quantitative surveys were able to capture. In contrast, both methods had similar results for mobile invertebrate taxa. The contrast between the two methods was also smaller for algae, with only 20% of the diversity lost between methods (Table 6-2).

Table 6-2: Comparison of the number of benthic taxa or substrate categories recorded at each level of the CATAMI or AMC classification schemes, for both the qualitative and quantitative benthic community assessments at Dart Bank, DR1 and Crayfish Rock, DR1.

			Matrix		**Substrate**		**Algae**		**Sessile invertebrates**		**Mobile invertebrates**	
Site	**Transect**	**Classification level**	Qualitative	Quantitative	Qualitative	Quantitative	Qualitative	Quantitative	Qualitative	Quantitative	Qualitative	Quantitative
Dart Bank	DR1	CATAMI_L2_L3	-	3	-	-	-	-	-	-	-	-
		CATAMI_L4	-	-	-	-	2	1	9	-	-	-
		CATAMI_L5	-	-	1	2	2	3	-	-	-	-
		CATAMI_L6_L7	-	-	-	-	-	-	-	-	-	-
		AMC	-	-	-	-	2	3	-	44	1	1
Crayfish Rock	DR1	CATAMI_L2_L3	-	4	-	-	-	-	1	-	-	-
		CATAMI_L4	-	-	-	-	2	2	9	-	-	-
		CATAMI_L5	-	-	1	2	-	2	-	-	-	-
		CATAMI_L6_L7	-	-	-	-	-	-	1	-	-	-
		AMC	-	-	-	-	-	-	-	49	1	1
Total			**0**	**7**	**2**	**4**	**8**	**11**	**20**	**93**	**2**	**2**

6.3 Synthesis

This project is the first comprehensive evaluation of the biota on the deep reef systems in Storm Bay. Data collected through this project can be used as a baseline from which to benchmark future change, as well as provide opportunity to better understand the ecology of these important systems.

The fish communities observed on the Storm Bay deep reefs were similar to those reported from the mesophotic reefs in the south-east Marine Parks network (Monk et al. 2016, Perkins et al. 2023b). Communities in both systems were largely dominated numerically by schooling planktivorous species such as *C. lepidoptera* (butterfly perch), although in terms of sub-dominant species, there were differences in the perch assemblages observed between Storm Bay and the Huon and Freycinet marine parks (Perkins et al. 2023a). Deep reefs in Storm Bay also recorded more diverse wrasse and leatherjacket assemblages, with several of these species more strongly associated with the shallow sites where macroalgae dominated benthic assemblages. One limitation of the Storm Bay project was that deep reef fish assemblages were only surveyed using ROV, whereas Marine Park surveys use a combination of Baited Remote Underwater Video (BRUV) and ROV. As such, Marine Park datasets record larger numbers of carnivores (Monk et al. 2016, Perkins et al. 2023b). Given the commercial and ecological significance of these higher order species, the deployment of BRUVs should be considered in future assessments of fish assemblages of deep reefs in Storm Bay.

The biodiversity observed in benthic communities on the deeper reef systems in Storm Bay was generally higher than that reported from mesophotic reefs in the nearby south-east Marine Parks network (Monk et al. 2016, Perkins et al. 2021). Similar to the south-east Marine Parks, the majority of diversity in Storm Bay was recorded within the sponge assemblages, with many singletons (i.e. only seen once) observed, suggesting the benthic communities are dominated by species that are highly diverse and spatially rare (Monk et al. 2016). However, the deep reef system in Storm Bay is also unique in the region in that it is truly “shallow mesophotic”, with the deepest reefs in Storm Bay (i.e. Adventure Bay – 40-49 m) only slightly deeper than the shallowest systems observed in the south-east Marine Parks (Perkins et al. 2021). For example, the shallowest areas of the Huon Marine Park are 35 m, which is approximately the observed transition depth from macroalgae to sponges in Storm Bay (Perkins et al. 2023a). As there is a marked transition in light availability in the depth range of deep reefs in Storm Bay (i.e. 20-50 m), there was a clear depth gradient observed in benthic communities. The shallower sites such as Betsey West and Dart Bank were dominated by red and green macroalgae, whereas at the deeper sites (Adventure Bay) an assemblage more typical of a mesophotic system dominated by sessile invertebrates was found (Magalhães et al. 2015, Heyns et al. 2016). This transition from shallow to deep communities will contribute to the higher diversity observed in Storm Bay, relative to deeper mesophotic systems from the south-east Marine Parks.

An Autonomous Underwater Vehicle (AUV) previously surveyed Variety Reef, North Bruny and Cape Queen Elizabeth in 2015, and then Variety Reef and North Bruny again in 2020, which allows an examination of temporal change in these systems (Bastiaansen 2020).

Trends captured were relatively similar, with the depth gradient outlined by Bastiaansen (2020) also evident in this study. A similar richness in morphospecies was also observed in early AUV surveys compared to the current project. However, survey design varied between the two projects, so data need further manipulation before direct comparison is possible. Despite this, initial analysis would suggest relatively similar results across time in comparable depth strata on similar reefs. For example, on Variety Reef across both surveys, red algae were dominant in the 30-39 m depth band, with biological matrix increasing at 40-49 m (Bastiaansen 2020). Further analysis of both datasets is required to better understand the more subtle variation over time. Evaluation of more shallow transects collected on Variety Reef in 2022 through the Storm Bay project will also facilitate the comparison.

While the surveys undertaken in 2022 have increased our understanding of the deep reef systems in Storm Bay, due to logistical constraints and ongoing issues with poor visibility throughout 2022 a full survey was unable to be completed. While there were sufficient data captured to evaluate fish assemblages, analysis of data suggested that sampling effort was insufficient to capture the full biodiversity of the benthic communities. Benthic diversity on deep reef systems was examined using standard methods developed by the National Environmental Science Program (NESP; Monk et al. 2020, Barrett & Monk 2021, Perkins et al. 2022). This allowed a consistent approach, with the Storm Bay dataset directly comparable with surveys undertaken through the NESP in the south-east Marine Parks. While diversity in the benthic community of Storm Bay was high relative to regional diversity, the morphospecies approach is likely to be under-representative of the true species diversity present in these systems. The biological matrix observed regularly in quadrat images is grouped into broad categories based on the dominant functional taxa; however, this matrix is likely to be a conglomerate of a wide range of species, with the true species diversity of biological matrix relatively unknown (Connell et al. 2014, Bell et al. 2022). Likewise, a morphospecies approach does not allow for the speciation of algae on the shallower reefs, nor does it capture the true genetic variability of the sponge populations. However, the morphospecies approach does allow for a repeatable and replicable dataset to be collected at depths where diver surveys are impossible and specimens are difficult to obtain.

While the ROV transects allowed for robust capture of the fish assemblages (forward-facing video footage) and benthic assemblages (downward-facing still images), mobile invertebrates were a group that were not well captured. For example, downward-facing video footage captured in pilot surveys suggested a much higher number of southern rock lobster than what was recorded using a photo-quadrat approach. While our pilot suggested benthic video transects may be used to capture mobile invertebrates, downward-facing still-images are needed to quantitatively assess benthic communities. As mobile invertebrates also include commercially and ecologically important species of molluscs and echinoderms, building a more robust assessment method targeting mobile invertebrates into future surveys is worth considering. This could include downward-facing video, along with targeted techniques such as crayfish potting used to survey populations of rock lobster in the Tasman Fracture Marine Park (Perkins et al. 2022, Perkins et al. 2023b).

This study suggests that the overall sampling effort required to capture robust quantitative data that accurately represents biodiversity of fish assemblages was met through our sampling design. Results here indicate that five 200 m transects capture the fish biodiversity at each site with confidence. In contrast, three 200 m transects did not adequately capture biodiversity of benthic communities, and a much greater number of transects and/or quadrats within transects may be required. Due to the time taken to process benthic images, only two sites had three transects completed; all other sites were less than this, with only 50 images on each transect. Our analysis suggests that this effort is not enough to robustly capture biodiversity and that sampling effort needs to be higher. This is similar to previous studies, with Perkins et al. (2022) suggesting that up to 200 images could be required per transect to adequately capture biodiversity using the 30-point count method adopted in this study. Bastiaansen (2020) found similar results, suggesting that over 175 images would be necessary to detect a 50% change in more common groups detected. Thus, a far larger sampling effort is required if benthic biodiversity is to be a key metric. While fish assemblages on deep reefs are easier to monitor, benthic communities are likely to be more sensitive to nutrient enrichment. Algae and sessile invertebrates interact directly with dissolved and particulate waste streams, and they respond to changes in light availability that may occur through nutrient enrichment in the water column (Strain et al. 2020). Thus, the monitoring of benthic assemblages should be included in a holistic monitoring framework for these systems. The effort involved in processing benthic imagery for biodiversity is a common bottleneck for monitoring. While biodiversity surveys have intrinsic value as a baseline, a move to indicator morphospecies or functional groups may be a more pragmatic and sensitive approach for ongoing monitoring (Perkins et al. 2016, Perkins et al. 2017, Perkins et al. 2022).

There are several approaches involving key species or functional groups that are worth further investigation. Both this study and the earlier work by Bastiaansen (2020) suggest there is very strong depth stratification of benthic communities. By characterising communities typical of depth strata at different sites across Storm Bay, upwards or downwards shifts of these communities at particular sites may indicate changes in water clarity and therefore light availability, a factor linked to nutrient enrichment (Wahl et al. 2015, Heyns et al. 2016, Bell et al. 2022). This may be as simple as changes to the ratios of several key indicators at high functional levels (i.e. the brown:green:red ratio of macroalgae, the macroalgae:matrix ratio or macroalgae:sponge ratio). In terms of individual species indicators, Bastiaansen (2020) proposed a series of potential indicator morphospecies that could be used to detect change on Variety and North Bruny reefs, based on a comparison between the 2015 and the 2020 AUV data. These potential morphospecies included *Caulerpa* spp., erect fine branching red algae, calcareous encrusting algae, simple white rough sponge, red cup sponges, filamentous red algae and turf/sand/sediment matrix. While *Caulerpa* spp. will respond to nutrient enrichment, as well as have sensitivity to changes in the light regime (Henríquez Antipa 2015), there is little current understanding of the environmental factors that may drive change in the other morphospecies, and whether this may be linked to changes in the nutrient regime in Storm Bay. Further work needs to be undertaken, both on the dataset collected in the present project as well as on time-series

data, with the aim of establishing key indicator species and functional groups that can be used in ongoing monitoring for responses to nutrient enrichment in these systems.

6.4 Recommendations for monitoring

This work has highlighted the high biodiversity present on the deep reef systems in Storm Bay, with these systems unique for the depth range that they cover in south-east Tasmania. They are a prominent feature of the Storm Bay seafloor and are relatively difficult to monitor compared to other systems. The project has also highlighted our limited knowledge regarding the complexity of these systems and how they respond to nutrient enrichment, both at a community and species level. Further data on these systems is needed to make detailed recommendations around a simplified monitoring protocol that is robust enough to detect change. Given this, we recommend a precautionary approach be adopted for the monitoring of deep reefs until further data is collated and analysed.

An approach that combines frequent qualitative assessments with less regular quantitative biodiversity surveys is recommended in the short-medium term. The approach recognises the difficulties in monitoring these systems, along with the need to better understand the diversity and variability of these systems in order to detect change.

More specifically, the following is recommended:

- Annual monitoring, be extended from four to six sites, with the addition of Betsey West and North Bruny. Further suggested refinements include:
    - All depth strata should be captured at each site. This may require transects to extend beyond 200m in length where substrate is present to capture the full depth range of the site. If 200 m is sufficient to capture all depth strata, then that is all that is required.
    - Use of both forward-facing and downward-facing video footage to provide a more robust assessment of fish and benthic communities. Where possible this should be done in HD or greater and with adequate lighting so imagery can be used in quantitative assessment if needed.
    - Use of a georeferencing system (USBL if possible), such that image location can be ground-truthed against bathymetry.
    - Guidelines for image analysis and scoring (i.e. start and end times, field of view etc.) to ensure reproducibility and comparability across years, for example:
        - footage is scored using the CATAMI classification system for benthic assemblages.
        - specialised video/imagery scoring software program (i.e. EventMeasure or TransectMeasure) is adopted for both qualitative and quantitative sampling.
- Quantitative surveys that capture biodiversity (fish and benthic assemblages) using NESP methods be undertaken every five years on the eight reefs surveyed as part of this project, and any additional “deep” reefs uncovered through additional mapping.

- Following three quantitative surveys (including the one undertaken through this project), the spatial and temporal dynamics of these systems should be assessed and documented. An aim of this evaluation will be to produce a protocol for monitoring of these systems using a simplified indicator/functional approach.

Our data suggests that deep reef communities are strongly influenced by depth. To compare sites and gain better understanding of broadscale versus localised changes, the comparison of similar depth strata between sites is necessary. This can be achieved through capturing a transect that covers a greater range of depth strata, but also including Betsey West and North Bruny, into regular monitoring, which will extend the array of depth strata covered and provide additional information on response of reefs to factors such as depth, proximity to salmon farming and proximity to the Derwent. The number of sites surveyed could be re-evaluated at five years.

While we are recommending that footage collected only needs to be analysed quantitatively every five years, given the limited knowledge of these systems, it would seem prudent to collect this footage in a way that could be analysed quantitatively should the need arise. This includes forward and downward facing camera systems, along with USBL if footage is being collected via an ROV, which allows us to accurately assign location and therefore to each image.

Given the gaps in knowledge identified by this project, further research is recommended to support the further development of monitoring:

- Further investigation of the current dataset, along with any future time-series data to establish key indicator species and functional groups.
- Further investigation on the current dataset to determine the number of transects, quadrats and points within quadrats that need to be analysed to consistently detect change in benthic systems.
- Building of a more robust assessment method targeting mobile invertebrates, particularly ecologically and commercial important species of crustaceans, molluscs and echinoderms.
- Targeted research on the mesophotic algal communities to establish the link between nutrient enrichment and potential indicator species. This will assist both the interpretation of monitoring data and the development of a more targeted monitoring approach.

7 Seagrass

Seagrass beds are amongst the most highly productive coastal marine ecosystems and are widely considered to be a sink for carbon and nutrients such as nitrogen and phosphorus. These ecosystems are common in shallow waters, typically down to 20 m depth, where there is sufficient substrate and light to grow. The high primary productivity of seagrass beds in turn supports a large biomass of primary consumers, with these communities providing critical ecosystem services, such as the removal and recycling of nutrients, filtering of the water column and stabilisation of the seabed. Globally, seagrass beds are recognised as important habitats for carbon sequestration (McKenzie et al. 2020) and nutrient cycling, particularly of nitrogen and phosphorus (Burkholder et al. 2006, Apostolaki et al. 2009), and can support a great diversity of species by providing food, shelter and nursery areas for fish and invertebrates (Heck et al. 2003). Seagrass beds are known to be sensitive to environmental change, particularly changes in water quality through alterations to nutrient and light regimes, with numerous seagrass species on the decline in coastal areas subject to increased urbanisation (Burkholder et al. 2007).

Increased nutrient loading can produce variable responses to seagrass health and bed condition depending on the receiving environment (Mutchler & Hoffman 2017, Connolly et al. 2018). Areas that are subject to nutrient limitation may have an initial positive response to nutrient enrichment, which can stimulate seagrass growth (Williams & Ruckelshaus 1993, Wear et al. 1999). However, nutrient enrichment can also stimulate water column productivity and the growth of epiphytic algae. Decreased light availability is one of the most widely cited causes of seagrass decline, whether through increased shading due to enhanced epiphytic algal growth, or increased turbidity of the water column (Burkholder et al. 2007). Different species of seagrass have different light requirements and the response to nutrient enrichment, among other forms of disturbance, will depend on the species' life history traits (O'Brien et al. 2018, Sherman et al. 2018). Therefore, understanding the interactions between a potential nutrient source and nearby seagrass beds is critical for management of these systems.

There are numerous potential pathways for interactions with salmon farming on seagrass beds, both acute and diffuse. Alterations to the light regime is one of the better studied pathways and can include direct effects such as shading from cages and farm infrastructure to more diffuse effects related to increased nutrients from farm outputs. These diffuse effects include the smothering of seagrass and competition for light from faster growing epiphytic algal species, as well as lower light penetration through the water column due to increased primary productivity in pelagic systems (Apostolaki et al. 2009). There are also potential pathways for interaction between seagrass beds and solid components of fish farm waste. Increased inputs of waste organic matter into the sediments can enable sulphide invasion in the roots and rhizomes leading to mortality in plants (Frederiksen et al. 2007).

Most research on the interaction between fish farms and seagrass beds has been undertaken on beds dominated by *Posidonia oceanica* around sea bream and sea bass cages in the Mediterranean. In contrast, seagrass beds in Storm Bay are dominated by species from the *Zostera tasmanica/nigricaulis* complex. While the pathways of potential interaction are the same, the ecology of this species and therefore the potential response

may be different. In general, *Posidonia* produces only 1-2 leaves per year and has very slow rhizome elongation rates, with individual plants relatively persistent over a large temporal scale. In contrast, species from the *Zostera tasmanica/nigricaulis* complex show higher growth rates across leaves, roots and rhizomes, produce seeds in higher densities, and turnover at a higher rate than *Posidonia* (Waycott et al. 2014, Sherman et al. 2018). These biological and ecological factors may influence the resilience of *Zostera tasmanica/nigricaulis* to nutrient enrichment; however there has been little research to date examining this directly.

Monitoring of seagrass habitats as part of the BEMP programs was first introduced in Okehampton Bay in 2017. The BEMP in Storm Bay was initiated in August 2019, with seagrass monitoring included at four sites around Storm Bay – Bull Bay, Adventure Bay, Sloping Island and Wedge Bay. Of these sites, Bull Bay, Adventure Bay and Sloping Island contain seagrass beds dominated by the *Zostera tasmanica/nigricaulis* complex (also referred to as "*Heterozostera tasmanica/nigricaulis,*" hereafter "*Zostera* spp."), whereas Wedge Bay contains beds of green macroalgae. However, the SeaMap Tasmania data collected in 2001 suggest that, historically, Wedge Bay was also the location of a *Zostera tasmanica/nigricaulis* bed (Barrett et al. 2001).

Seagrass is regularly monitored in other jurisdictions, both within Australia and globally, with a range of methods used depending on the research question of interest. The Environmental Licenses for the Storm Bay salmon leases focused on seagrass health and epiphyte cover, although did not specify exact methodology. Seagrass transects conducted by Tassal and Huon Aquaculture as part of their environmental baseline surveys used ROV and were qualitative in their assessment. In this project we trialled a variety of methods to map seagrass extent and to assess the health and ecological status of the seagrass beds in Storm Bay. Methods included ROV transects as well as drop camera images, using both qualitative and quantitative scoring techniques. Stable isotopes were also collected to characterise the nitrogen status of study sites. Increased tissue nitrogen as a result of nutrient enrichment has commonly been reported in seagrass species, with alterations to the C:N ratio reflecting changes in nutrient regime (Duarte 1990). Changes to δ^{15}N values can also be used to characterise the enrichment status of a seagrass bed, particularly when normalised for morphological characteristics such as leaf mass (Lee et al. 2004).

The seagrass sampling in this project was broken into two major components addressing a) the spatial dynamics of the major seagrass beds in Storm Bay, and b) the relative health of the seagrass within those beds. The survey design was that outlined in the Environmental Licenses, with power analysis conducted to evaluate this design. There are no major seagrass beds within the immediate vicinity of any salmon aquaculture lease in Storm Bay and therefore the objective of the monitoring was to assess the health and distribution of seagrass beds within the broadscale environmental context. The overall aims of this project were to a) form a baseline for both seagrass bed extent and condition from which to benchmark future change, b) understand the capacity of the survey design used to detect change and c) evaluate methods tested to provide recommendations for future monitoring of seagrass beds in Storm Bay.

7.1 Design & survey methods

7.1.1 Study sites

Seagrass surveys were conducted at four sites within the Storm Bay region in association with two marine farming leases. The two western sites, Bull Bay and Adventure Bay, were associated with BEMP monitoring for MF281 Yellow Bluff, and East of Sloping Island and Wedge Bay were associated with BEMP monitoring for MF279 West of Wedge (Figure 7-1). While some transects were lengthened (Bull Bay) or added (Adventure Bay) to capture the full extent of the seagrass bed, the design implemented was that outlined in the Environmental Licenses for the Storm Bay salmon leases.

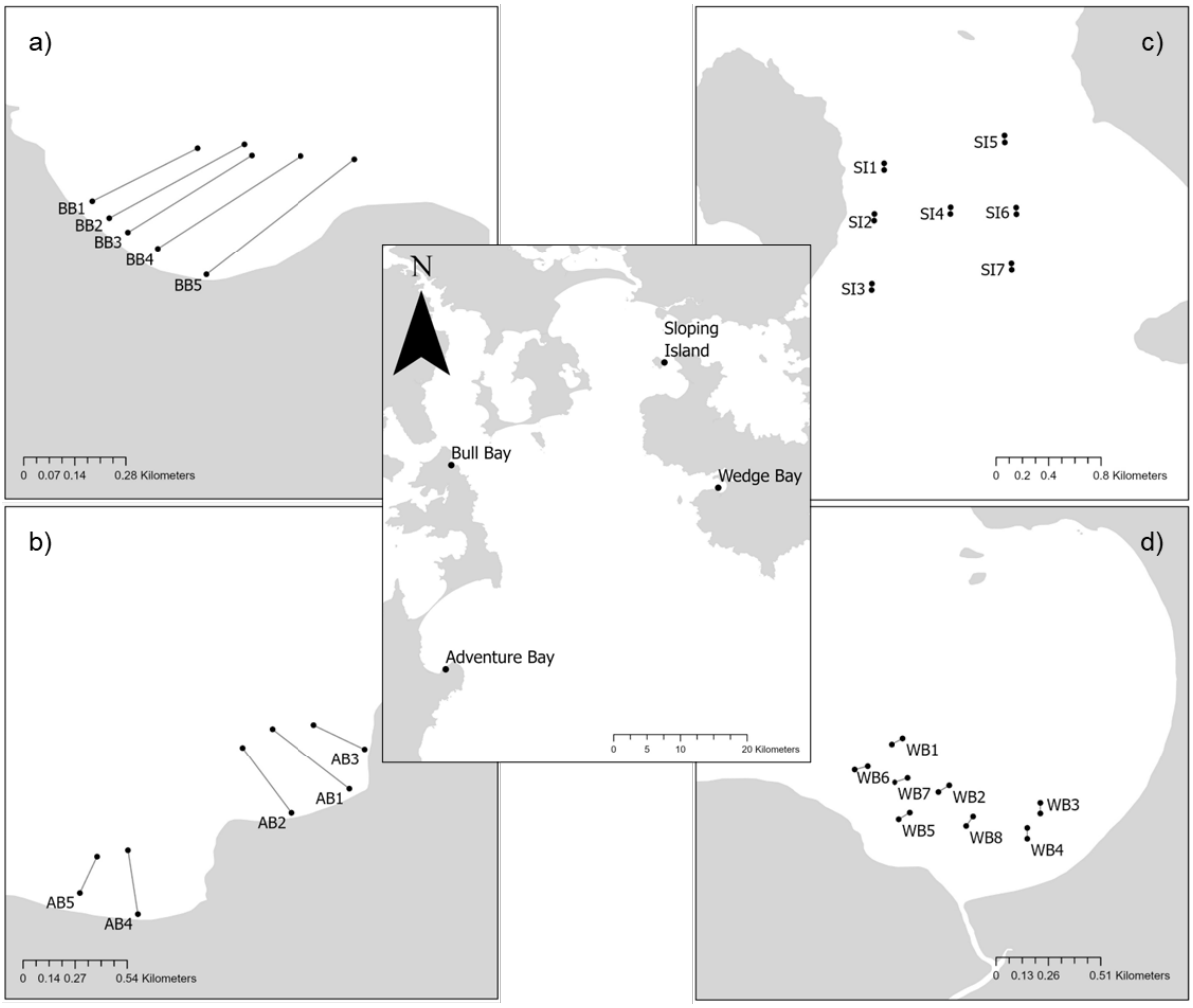

Figure 7-1: Location of seagrass transects surveyed at a) Bull Bay, b) Adventure Bay, c) East of Sloping Island and d) Wedge Bay. Transects are labelled with a site code where BB = Bull Bay, AB = Adventure Bay, SI = Sloping Island and WB = Wedge Bay.

7.1.2 Image capture

Seagrass beds were surveyed along transects in November, with Bull Bay and Adventure Bay surveyed from 2019-2021 and East of Sloping Island and Wedge Bay surveyed from 2020-2021. Transects were used for video capture using an ROV, as well as the collection of a series of photo-quadrat images using a drop camera. Drop camera images were used for both bed extent mapping and quantitative scoring. Initially, all transects followed locations

stipulated in the Environmental Licenses; however, transects were extended at Bull Bay and Adventure Bay following the 2019 survey to capture the full extent of the seagrass beds at these sites.

For video footage, a lead-core rope marked with cattle-ear tags at 10 m intervals was deployed between two predetermined GPS locations at each site. A BlueROV2 was then piloted along the transect line, at a maximum speed of 0.3 m/s and care was taken to keep the dominant substrate type (e.g. seagrass or epiphytic algae) in field of view. A single forward-facing camera was used, tilted so the field of view was approximately 60% substrate and 40% water column at any given point in time. Video footage (HD or UHD) was captured using Delta ROV's OceanVault recorder and data server, allowing overlay of NMEA DGPS strings obtained from the vessel's GPS system on the images.

Photo-quadrats were captured from the same transects, with a downward-facing camera mounted to a 0.25 m^2 stainless steel quadrat frame, that ensured images were captured from a standard area approximately 1 m from the bottom. Photos were captured every 10 m across the entire transect length, regardless of whether the substrate was sand, seagrass or macroalgae. The unit was lowered directly out of the dive door, with the line kept vertical to ensure that the photo-quadrats could be consistently georeferenced by the vessel's DGPS system.

To examine seasonal variability, photo-quadrats were also collected from seagrass beds in March, June and September of 2021. As the aim of this sampling was to examine fluctuations in seagrass condition throughout the year, photo-quadrats were captured from only the portion of the transect where the main seagrass bed occurred, with a minimum of four quadrats collected from each transect. It should be noted that this was only necessary in Bull Bay and Adventure Bay, as the transects at Sloping Island and Wedge Bay were much shorter and only encompassed seagrass or macroalgal beds.

7.1.3 Image processing

As outlined above, image processing occurred for three purposes: a) an estimation of bed extent, b) a qualitative assessment of the seagrass beds and c) a quantitative assessment of the beds.

Seagrass bed extent was estimated using the photo-quadrats obtained from the full transects collected in November each year. Each photo-quadrat was assigned one of five seabed categories: sand, sparse seagrass, patchy seagrass, seagrass and seagrass/macroalgae (Table 7-1). These data were used to estimate fluctuations in seagrass bed extent on an annual basis.

ROV video footage was scored qualitatively for seagrass and epiphytic algal cover using a categorical system based on percentage cover (Table 7-2). Data from the baseline surveys, conducted in summer 2019 by Aquenal (2019a), were also collated for comparison.

Table 7-1: Seabed categories designated to photo-quadrat images to determine bed extent across surveys.

Seabed category	Definition
Sand	Totally bare substrate, no bed forming species present
Sparse seagrass	Low seagrass cover <33% (as defined at the SeaMAP convention).
Patchy seagrass	Dense seagrass cover (>33%) with bare substrate patches in image
Seagrass	Seagrass cover (>33%) evenly distributed throughout the quadrat
Seagrass/macroalgae	Two bed forming taxa present, e.g., seagrass and *Caulerpa,* neither appears to be dominant.
Macroalgae	Macroalgae is the dominant bed forming species (e.g., *Caulerpa)*

Table 7-2: Qualitative scores used to determine seagrass and epiphytic algae cover from ROV videos and the estimated percentages that corresponded to each score (White et al. 2021a).

Qualitative score	Seagrass cover description	Epiphytic cover description	Estimated percentage cover
0	No seagrass cover	No epiphytic growth	0%
1	Very low seagrass cover	Very low; virtually clean plants	1-5%
2	Low seagrass cover	Low; minimal epiphytic growth	5-20%
3	Medium seagrass cover	Medium; obvious epiphytic growth	20-60%
4	High seagrass cover	High; most plants covered	60-90%
5	Very high seagrass cover	Very high; plants completely covered	90-100%

All photo-quadrat images were analysed quantitatively in the Windows-based software Coral Point Count Version 4.1 with Excel extension (CPCe). A 50-point grid was randomly overlaid on each quadrat image and each point was scored. Where possible, all biota beneath each point was identified to the lowest taxonomic level, including seagrass, macroalgae, benthic and mobile invertebrates (Appendix 7-1). Where bare substrate (e.g., sand or sediment) was present, this was also scored. Scores were doubled for each quadrat to calculate percentage cover.

7.1.4 Stable isotope sampling

Plants were collected by snorkellers for stable isotope analysis at each of the four survey sites in November 2021. To assess any seasonal variation in biochemical parameters, additional samples were collected from Bull Bay in November 2020 and June and September 2021. On each sampling occasion, between 10-20 plants were collected (rhizome to grass tip) from each transect, with as much epiphytic growth removed as possible in situ. Plants were stored on ice and subsequently frozen on return to the laboratory.

For analysis, samples were defrosted, with the rhizome separated from the sample and any remaining epiphytic algae scraped from the seagrass blades using a scalpel. Individual seagrass plants were then dissected by leaf age, with the first five leaves (1 being newest and 5 being oldest, Figure 7-2) from approximately 20 plants per transect placed in individual zip lock bags by leaf number. All samples were refrozen prior to freeze drying.

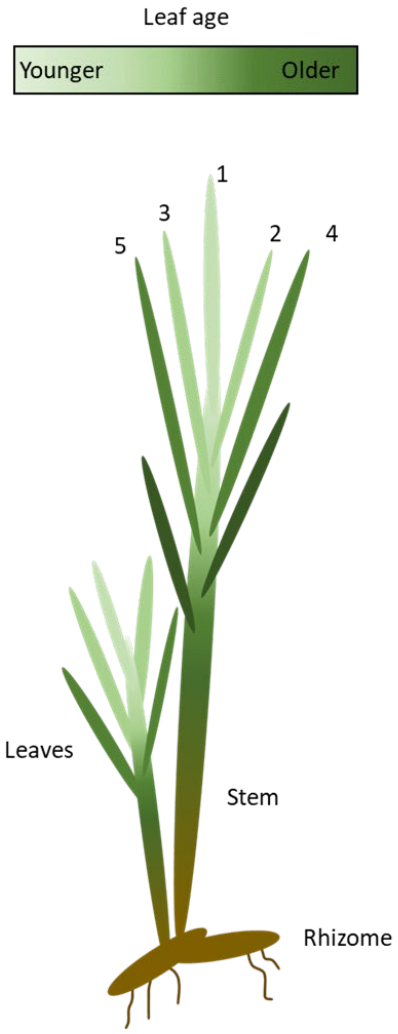

Figure 7-2: Schematic of seagrass plant for leaf dissection, showing the youngest leaf (number 1) to the oldest leaf (number 5) used for stable isotope analysis.

All rhizomes and dissected leaves were freeze dried until a constant weight was reached, usually within 48-72 hours. Dried samples were removed from zip lock bags using forceps, ground using a Retsch MM200 laboratory ball mill for 1 minute at 25/s, and transferred into a glass sample tube with the aid of a stainless-steel spatula and aluminium foil funnel. For quality assurance, all materials were cleaned in a sonicator for five minutes, rinsed with ethanol and dried using Kimwipes between each sample. In addition, aluminium foil was placed over the bench top to prevent cross contamination.

The ground seagrass tissues were sent to the Stable Isotope Facility within the School of Chemistry at Monash University for total nitrogen, total carbon, δ13C and δ15N analyses.

Elemental composition was calculated as total nitrogen (TN) and total carbon (TC) as a percentage:

$$X\ (\%) = Elemental\ weight / total\ sample\ weight \times 100$$

where X is Total Nitrogen or Total Carbon.

Isotopic values are presented on a delta scale (δ) which indicates the deviation in parts per thousand ($^{0}/_{00}$) of the isotopic composition of a sample from an internationally accepted standard:

$$\delta X = [(Rsample/Rstandard)-1]x10^{3}$$

Where X is $\delta^{13}C$ or $\delta^{15}N$ and R is the corresponding ratio of $^{13}C/^{12}C$ or $^{15}N/^{14}N$ respectively (Peterson & Fry 1987). As such, the lower the δ value relative to the standard, the more depleted in the heavier isotope the sample is and the higher the δ value relative to the standard, the more enriched in the heavier isotope the sample is.

7.1.5 Data analysis

Seagrass bed extent was mapped in ArcGIS Pro using the seabed categories determined for each of the photo-quadrats taken across all transects by site and year. Percentage cover data was used to investigate spatial and temporal variability in seagrass beds within Storm Bay via the multivariate software package PRIMER v7 (Plymouth Routines in Multivariate Research; Clarke et al. 2014). As we were only interested in parameters within the bed, photo-quadrat images at the beginning or end of the seagrass bed containing bare substrate (e.g. photo-quadrats scored as 100% sand cover, no bed-forming species present) were removed from the dataset prior to analysis. To determine broadscale differences between sites, the transect-average for each taxonomic group from the November surveys (2019, 2020 and 2021) were used. No transformation was applied to the photo-quadrat percentage cover data including seagrass, algae and invertebrate groups. A Bray-Curtis dissimilarity matrix was calculated, and non-metric multidimensional scaling (nMDS) was undertaken to visualise patterns in the data. Vector overlays using Pearson's correlation were employed to identify key species and taxa driving the observed trends in the data across sites or survey period.

Bar plots were produced for key taxonomic groups (*Zostera* spp., total green macroalgae, *Chaetomorpha billardierii* and filamentous algae) to observe the quantitative differences between sites and survey periods. These data were plotted by site, transect and year.

Power to detect change was conducted on two levels: a) the number of photo-quadrats needed to detect a certain level of change to *Zostera* spp. cover within a transect, and b) the number of transects required to detect a certain level of change to *Zostera* spp. cover within a site. Given that the length and number of transects vary between sites within the Environmental Licenses, this approach will allow recommendations around appropriate transect length and number of photo-quadrats for a more uniform design to be implemented across Storm Bay. Power analysis was done using a paired t-test within the R package "pwr". The effect size and percentage detectable change (effect size/mean *Zostera* spp. cover * 100) was determined for each transect, calculated using the number of photo-quadrats per transect (*n*) and standard deviation in seagrass cover to a power level of 0.8. In all instances, *n* was rounded up to a whole value as only complete photo-quadrats can be taken in field surveys. A paired t-test was then used to determine the number of quadrats (*n*) required to detect a 25, 50, 75 and 100% change in seagrass cover per transect. This was done by adjusting the effect size to obtain the desired percentage detectable change and

resolving for *n* at a power level of c. 0.8. The same two-step method was used to calculate the number of transects required to detect a 25, 50, 75 and 100% change in seagrass cover per site. In all instances *n* was rounded up to a whole value as only a complete transect should be conducted in field surveys. Mean values used at a transect level were based on the number of quadrats collected within those transects and therefore were not necessarily consistent within each transect.

Mean values of seagrass cover was compared between quantitative and qualitative methods. For this comparison, it was assumed that the quantitative data were the 'true' value, compared to the qualitative ROV assessment.

7.2 Results

7.2.1 Ecology of seagrass beds in Storm Bay

Seagrass bed extent

Bed extent and the dominant bed-forming species varied between sites (Figure 7-3, Figure 7-4). At Bull Bay 'sparse seagrass' was the dominant bed type, with denser 'seagrass' patches on the easternmost transects (BB4 and BB5) and deeper sections of the westernmost transects (BB1 and BB2; Figure 7-3). This was consistent across all three surveys (2019, 2020 & 2021), with clear change in bed extent or cover evident. At Adventure Bay, a well-defined bed edge was observed at the shallow and deeper ends of the transects in 2019 (Figure 7-3). When these transects were extended in 2020, a transition from seagrass to macroalgae was evident at depth on transects AB1-AB4. In 2021, macroalgae appears to extend further into the seagrass bed with an increased number of mixed bed photo-quadrats recorded (Figure 7-3).

The bed edge was not captured at Sloping Island; this is likely a result of transect position and length as well as the sparse nature of the seagrass bed at this site. Some variation in the density of seagrass within transects was observed between 2020 and 2021 (Figure 7-4). The bed at Wedge Bay was dominated by macroalgae across the survey period, with some variation in cover of macroalgae and bare substrate within transects between 2020 and 2021 (Figure 7-4).

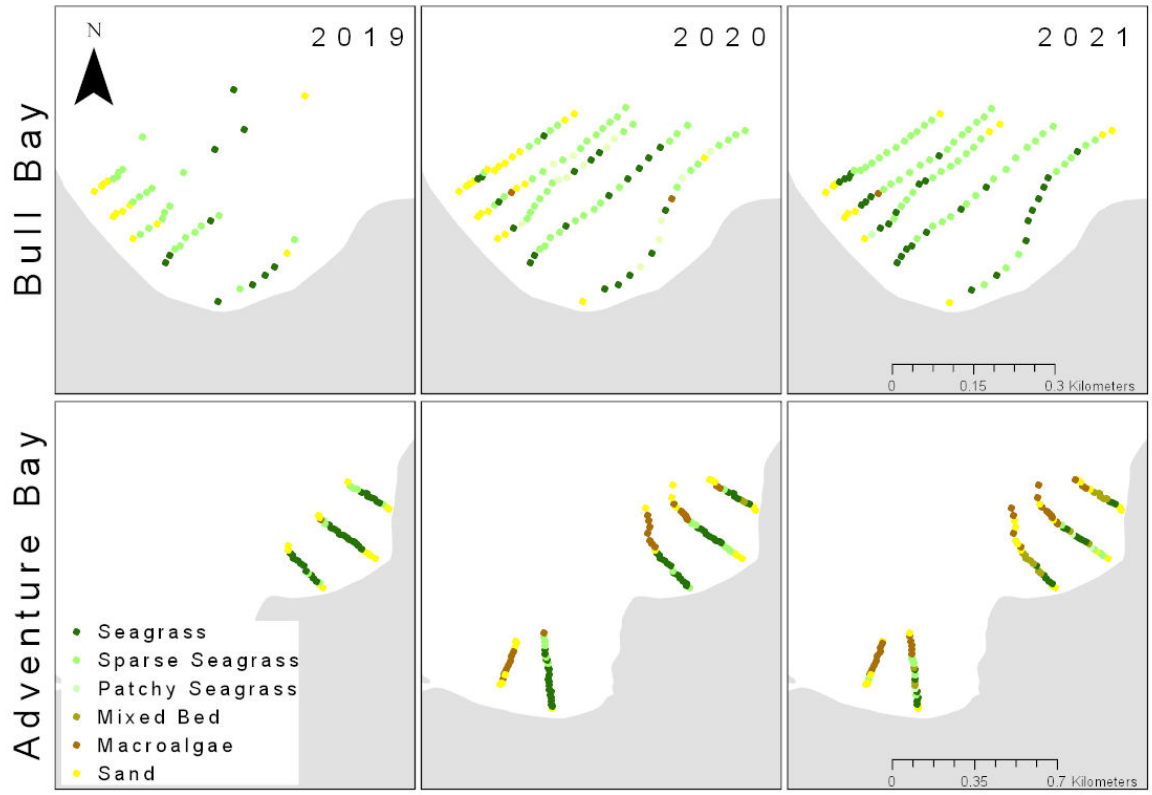

Figure 7-3: Seagrass extent mapping at Adventure Bay and Bull Bay in November 2019, 2020 and 2021. Each dot is coloured by substrate type as determined from photo-quadrat images. Note that the southernmost transects at Adventure Bay were not surveyed in 2019.

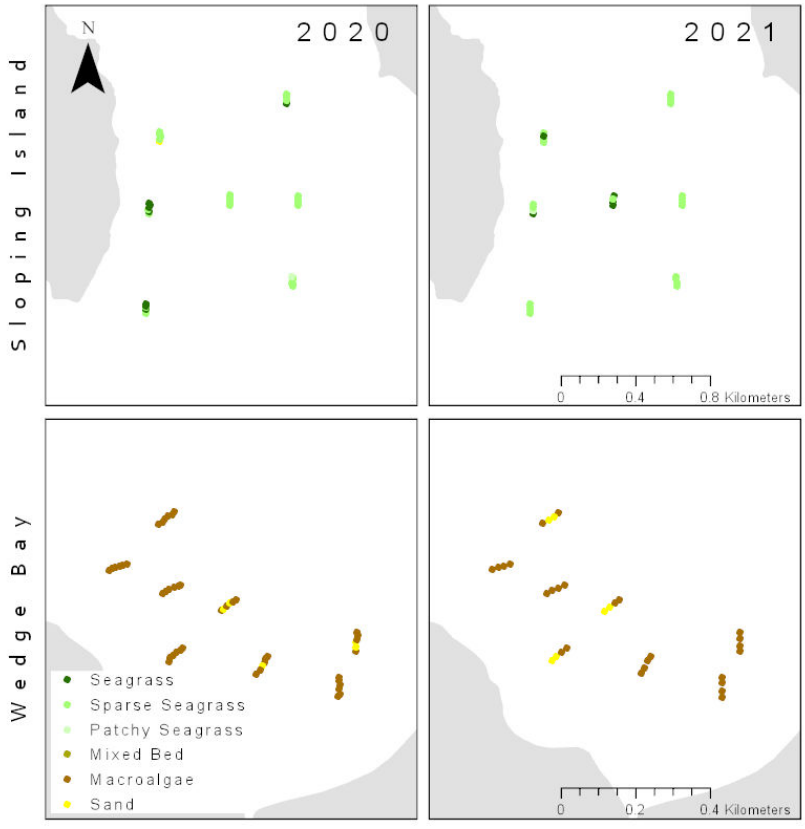

Figure 7-4: Seagrass extent mapping at Sloping Island and Wedge Bay in November 2019 to 2021. Each dot is coloured by substrate type as determined from photo-quadrat images.

Spatial variability of seagrass in Storm Bay

There was variability observed in seagrass along with associated flora and fauna between sites in Storm Bay (Figure 7-5). There were clear differences between Wedge Bay and the other three sites. Throughout the study period, Wedge Bay was dominated by macroalgae (mainly *Caulerpa* spp.) and very small amounts of *Halophila*, compared to beds dominated by *Zostera* spp. at all other sites (Figure 7-5, Appendix 7-1). Transect AB5 in Adventure Bay, also dominated by green macroalgae rather than *Zostera* spp., clustered with the Wedge Bay transects. The ordination also indicated that Adventure Bay, Bull Bay and Sloping Island were distinct from each other (Figure 7-5). Although *Zostera* spp. was present at all these sites, analysis suggests that each site had distinct algal and faunal assemblages. For example, *Caulerpa longifolia* and *Ostrea angasi* were generally present in higher abundances at Bull Bay, whereas Adventure Bay transects typically had higher abundance of filamentous green algae and *Chaetomorpha billardierii* (Figure 7-5). While there was variation between transects, *Zostera* spp. cover was generally less at Sloping Island and Bull Bay, compared to Adventure Bay, with more patches of bare substrate (i.e. sand) present (Figure 7-5).

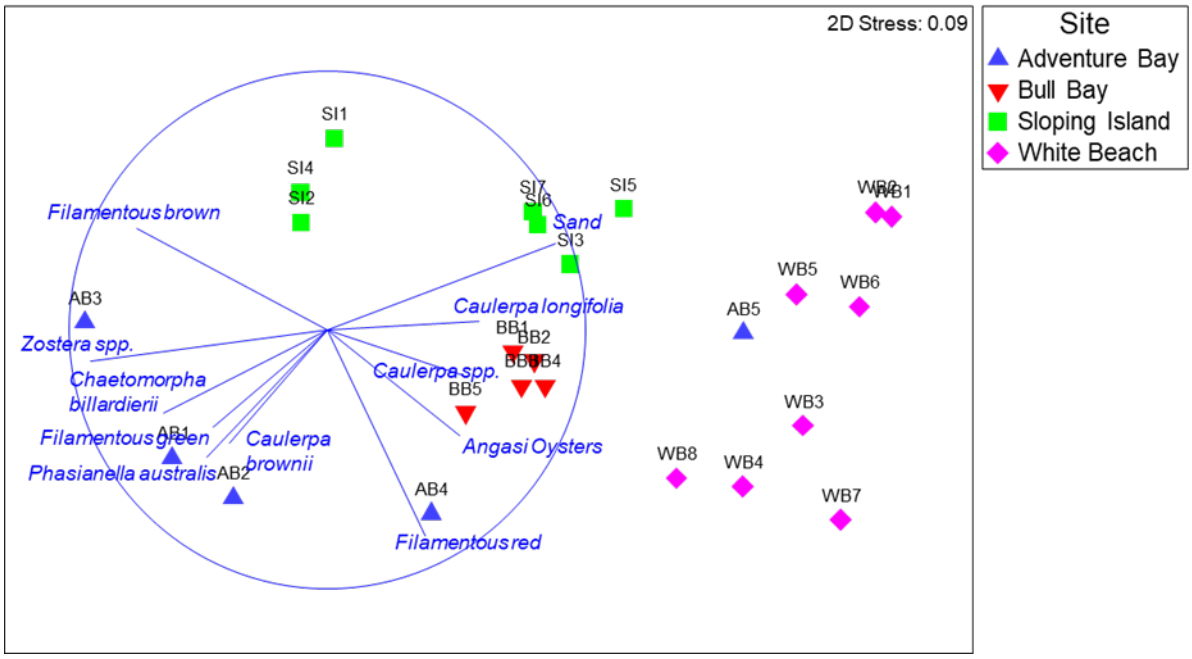

Figure 7-5: nMDS plot on photo-quadrat data averaged across all years surveyed. Pearson's vector overlays contributing to ordination with base variable comparison of > 0.55 are included.

Within sites, Adventure Bay transects were the most variable, ranging in *Zostera* spp. cover from 41.9% (AB2) to 58.8% (AB1) per transect, with more diverse macroalgae (both attached and drift) observed at this site. Sloping Island also had high between transect variability, with SI1, SI2 & SI4 all with much higher cover of *Zostera* spp. and filamentous algae than the other transects (Figure 7-5, Appendix 7-1).

Temporal variability of seagrass beds

Temporal variability in seagrass beds was examined across both years and seasons at a site level, with variation in seagrass along with associated flora and fauna observed at each site.

At Adventure Bay, seagrass and associated biota were generally more similar in the earlier surveys (November 2019, November 2020, March 2021), with a shift occurring before the June 2021 survey (Figure 7-6). Vector analysis suggests that this shift was due to changes in the abundance of *Cheatomorpha billardierii*, filamentous brown algae and *Zostera* spp. (Figure 7-6). While there were temporal shifts in AB5, analysis suggests that this transect was distinct throughout the study period. Different trends were observed in Bull Bay, where composition of seagrass and associated flora and fauna was relatively similar between November 2019 and November 2020 (Figure 7-6). Vector analysis indicated that *Zostera* spp. was the dominant feature of the bed in March 2021; however, the abundance of filamentous red algae increased across June 2021 to November 2021, with vector analysis also indicating an increased presence of sand in photo-quadrats (Figure 7-6).

At Sloping Island, the seagrass and associated flora and fauna were similar in November 2020 and March 2021, before a shift in community composition was observed across June and September 2021 (Figure 7-7). Analysis indicates the seagrass and associated biota in November 2021 were again more similar to November 2020 and March 2021. Temporal variation at Wedge Bay was less clear, although November 2020 and March 2021 generally had high abundance of *Caulerpa* species present, particularly *C. longifolia*, as well as epiphytic and filamentous algal groups (Figure 7-7). Sand tended to be present in higher abundance from June 2021 to November 2021.

Spatial and temporal variability in key parameters

Key parameters indicated by vector analysis were subsequently examined in more detail, with trends generally supportive of what was observed through nMDS analysis. For example, highest values of *Zostera* spp. cover at Bull Bay (44.4% to 86.8%) were recorded in March 2021 (Figure 7-8), whereas the temporal variability in *Zostera* spp. cover at Adventure Bay was less consistent across transects (Figure 7-8). Despite this, AB5 had the lowest *Zostera* spp. cover across all surveys. At Sloping Island, *Zostera* spp. cover across transects was highly variable, with between transect variability higher than any observable temporal trend (Figure 7-8). As expected, the abundance of *Zostera* spp. was negligible across all transects in Wedge Bay.

Green macroalgae were regularly recorded at Wedge Bay, where they were the dominant bed-forming taxa, and were also present at both Adventure Bay and Bull Bay (Figure 7-9). Green macroalgae cover (mostly *Caulerpa* spp.) at Wedge Bay varied with survey month, declining on transects WB1 and WB4-WB7 across the survey period (Figure 7-9). Cover varied on the other transects at Wedge Bay (WB2, WB3 and WB8), but there was no clear temporal pattern. At Adventure Bay (AB1-AB4), green macroalgae become more common in September 2021 and November 2021, while at Bull Bay they were present across all surveys.

Filamentous algae were present at all sites, and at Adventure Bay and Sloping Island they often represented over 50% cover (Figure 7-10). At three of the study sites (Adventure Bay, Bull Bay and Wedge Bay) the type of filamentous algae transitioned from brown/green to red over the study period (Figure 7-10). This transition was also observed at Sloping Island; however, filamentous brown increased again in the final survey in November 2021. Across all sites the lowest cover of filamentous algae was observed in June 2021. Filamentous

green algae was relatively rare or absent across most sites and surveys, except for transects AB1 and AB2 in November 2019, and SI5 between March and September 2021. *Chaetomorpha billardierii* was most prevalent at Adventure Bay, notably in the November surveys and March 2021. Overall, the presence of filamentous algae at Adventure Bay and Bull Bay was more predictable in space and time relative to Sloping Island and Wedge Bay, where it was far more variable (Figure 7-10).

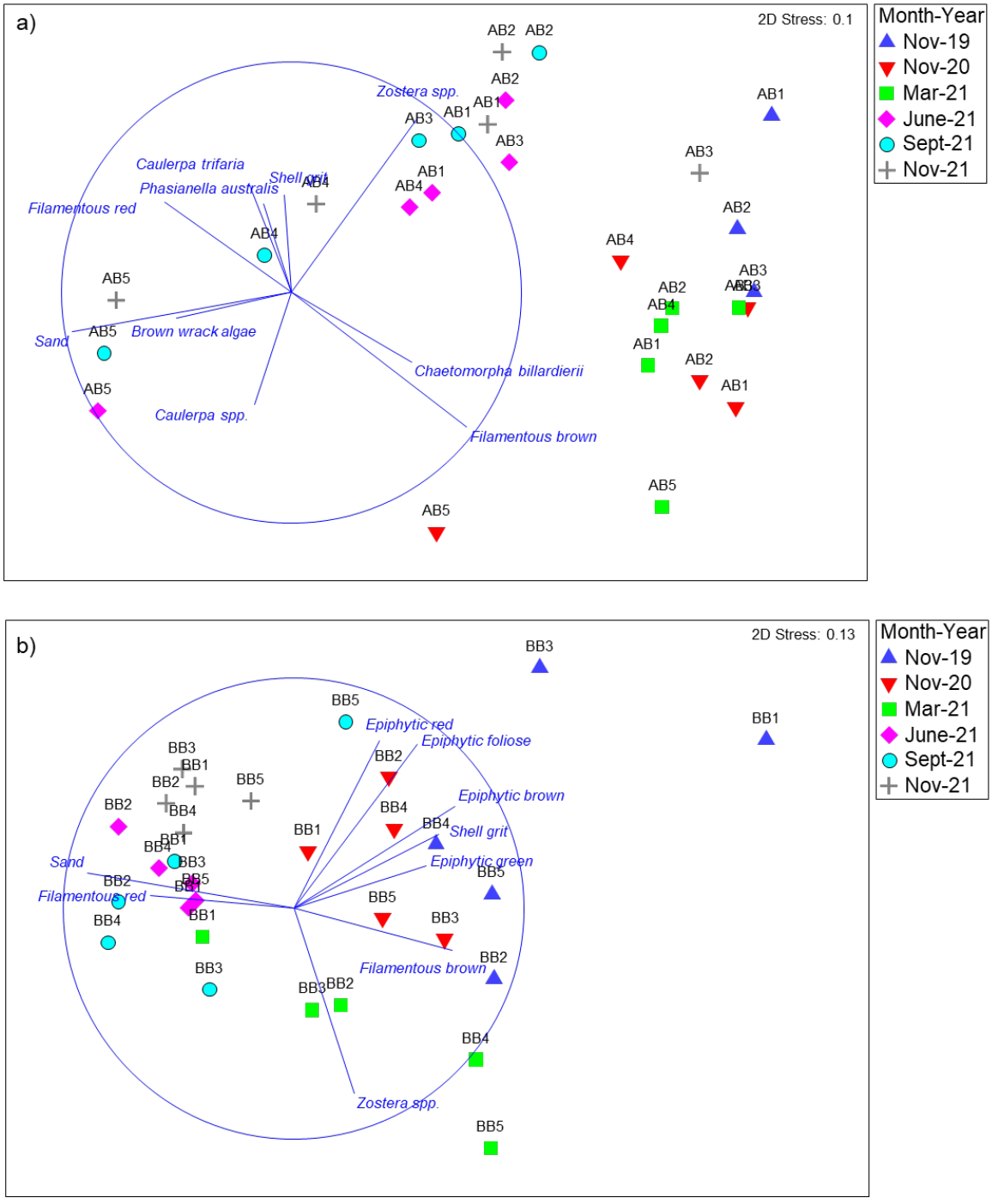

Figure 7-6: nMDS plot examining temporal trends on photo-quadrat data for a) Adventure Bay and b) Bull Bay. Data were averaged at a transect level. Pearson's vector overlays contributing to ordination with a base variable comparison of >0.4 for Adventure Bay and >0.3 for Bull Bay are included.

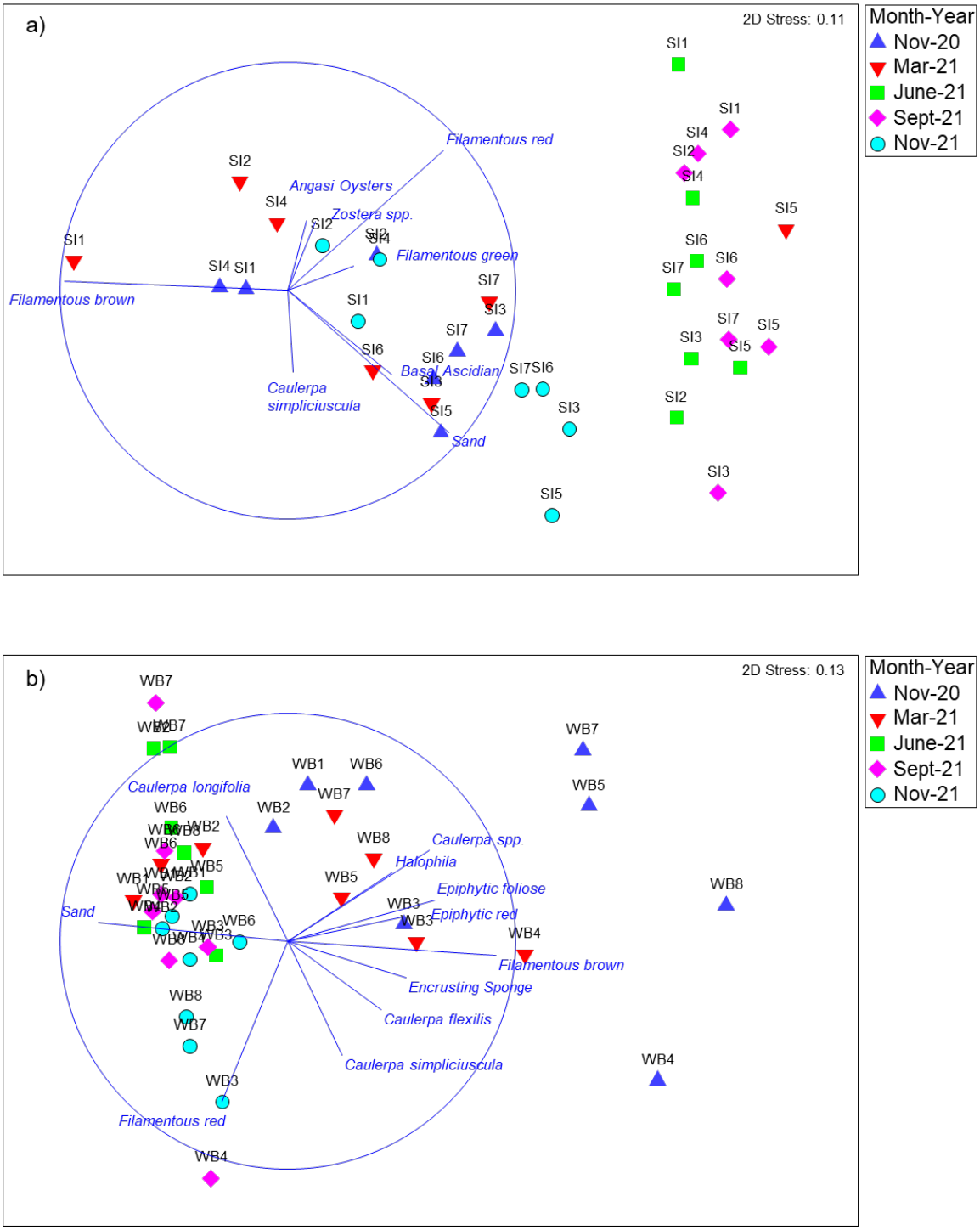

Figure 7-7: nMDS plot on photo-quadrat data examining temporal trends from a) Sloping Island and b) Wedge Bay. Data were averaged at a transect level. Pearson's vector overlays contributing to ordination with a base variable comparison of >0.3 are included.

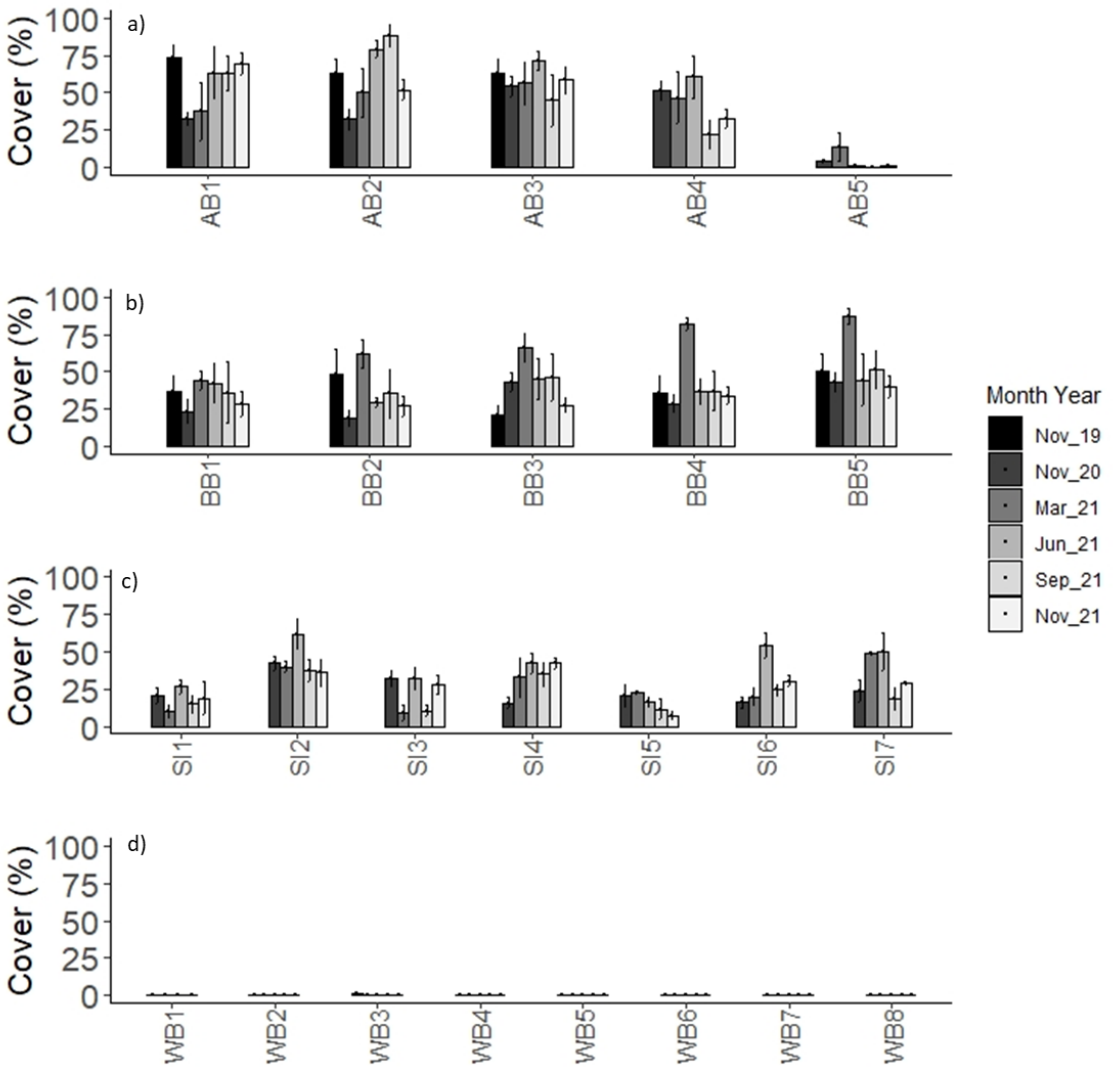

Figure 7-8: Mean (+/- SE) seagrass (*Zostera* spp.) cover for transects at a) Adventure Bay, b) Bull Bay c) Sloping Island and d) Wedge Bay from November 2019 to November 2021. Note that, in 2019, photo-quadrats were only collected at Adventure Bay and Bull Bay.

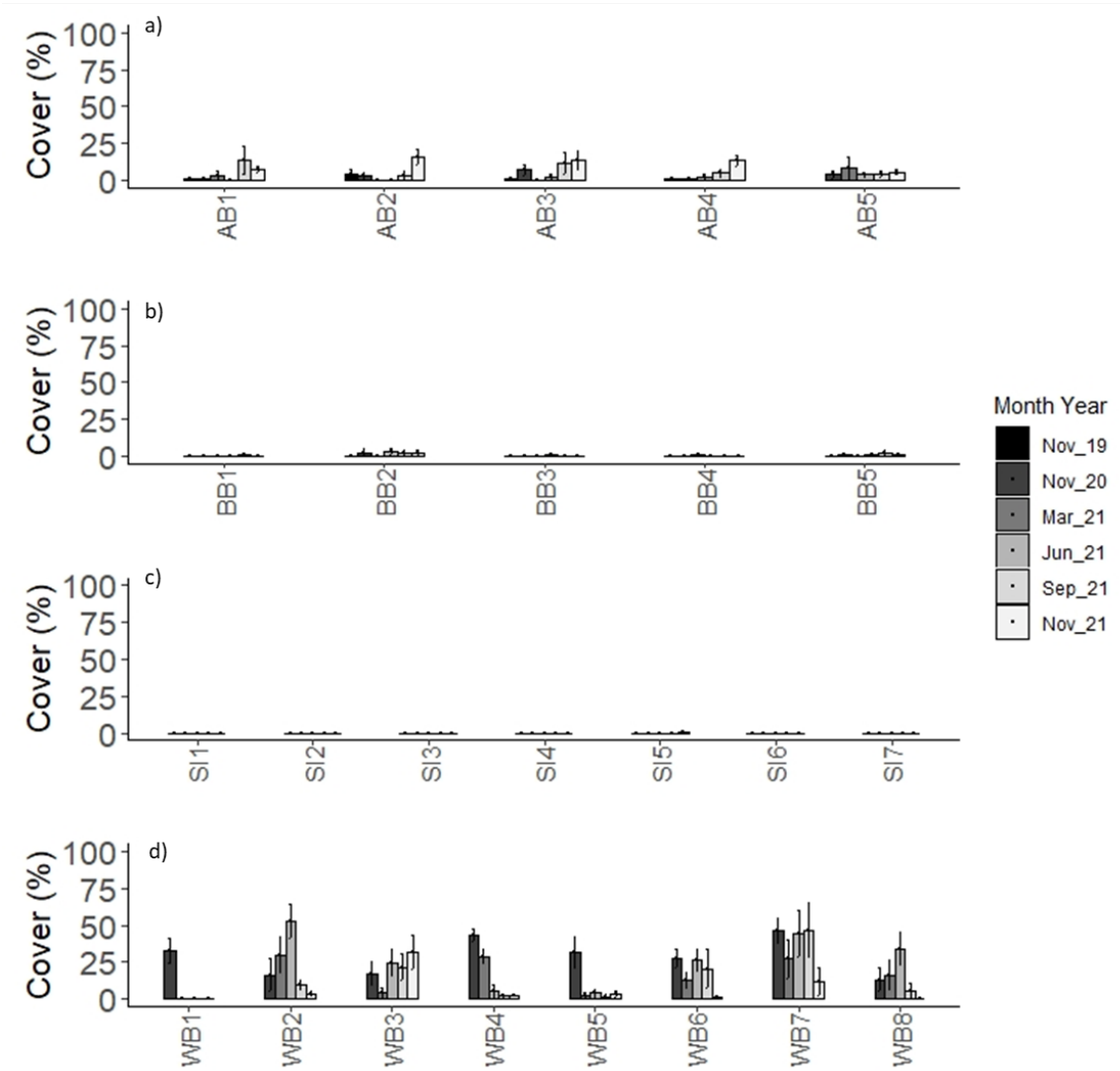

Figure 7-9: Mean (+/- SE) total green macroalgae cover for transects at a) Adventure Bay, b) Bull Bay c) Sloping Island and d) Wedge Bay from November 2019 to November 2021. Note that, in 2019, photo-quadrats were only collected from Adventure Bay and Bull Bay.

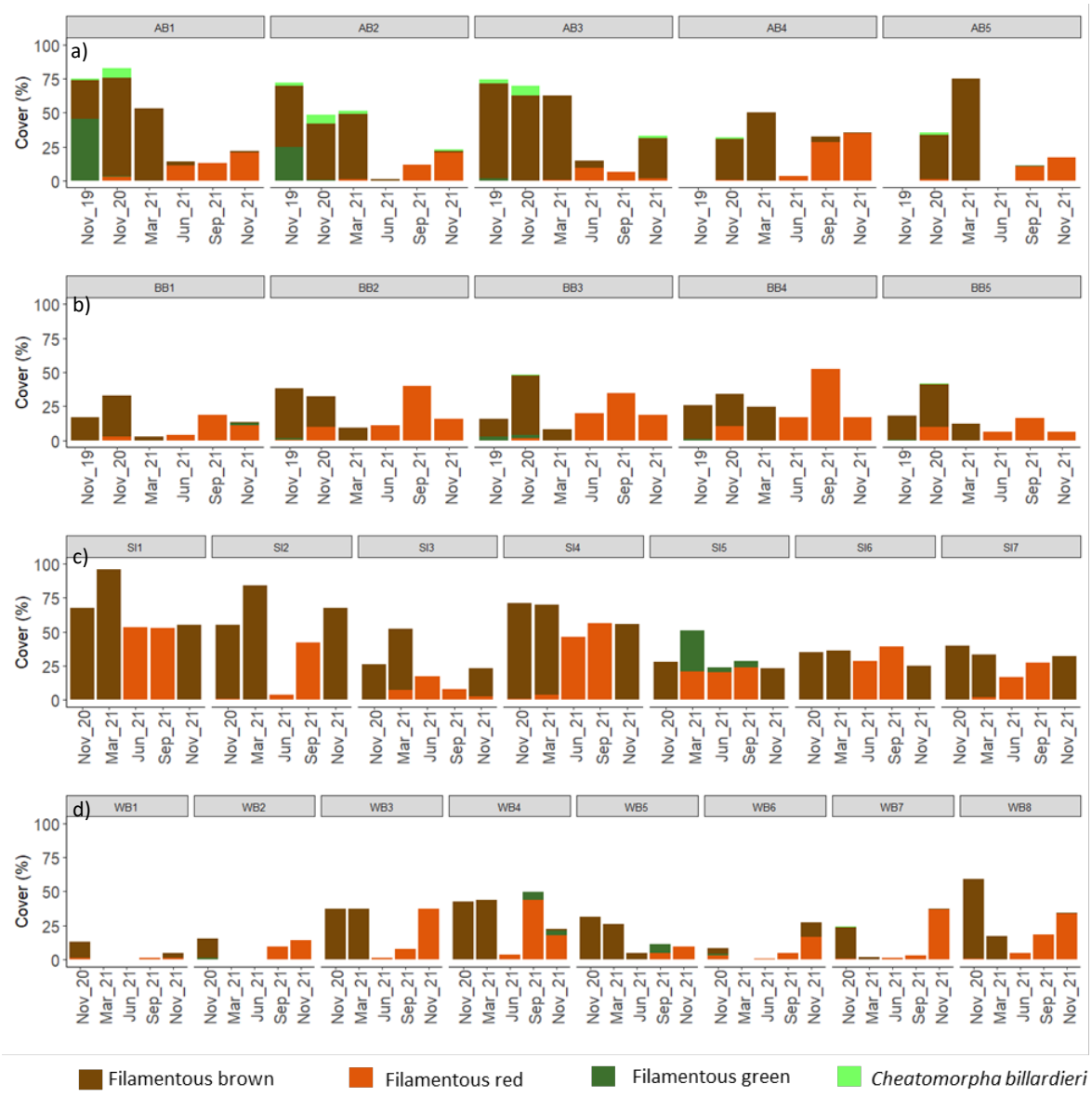

Figure 7-10: Mean cover of filamentous algae for transects at a) Adventure Bay, b) Bull Bay, c) Sloping Island and d) Wedge Bay from November 2019 to November 2021. Note that, in November 2019, photo-quadrats were only recorded at Adventure Bay and Bull Bay.

7.2.2 Stable isotope ratios of seagrass beds in Storm Bay

Site comparison

Total carbon content of rhizomes was approximately 10% lower compared to leaf samples across all sites, with no observable trend with age in total carbon observed in leaf samples across sites (Figure 7-11). In contrast, rhizomes recorded similar $\delta^{13}C$ signatures to leaves, with variation between sites (Figure 7-11). Rhizomes from Bull Bay tended to be relatively depleted in $\delta^{13}C$ (-13.8‰ ±0.3) compared to Adventure Bay (-9.6‰ ±0.2) and Sloping Island (-11.8‰ ±0.4). Consistent trends in the $\delta^{13}C$ isotope in leaves between sites were harder to discern.

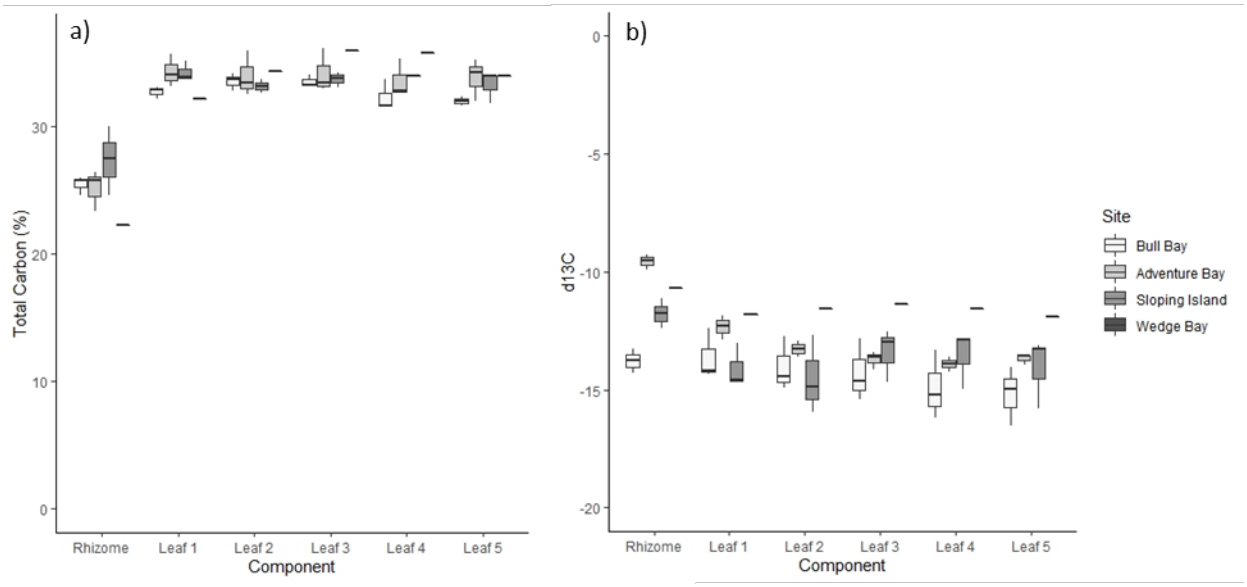

Figure 7-11: Total carbon (a) and δ^{13}C (b) of the seagrass collected at Bull Bay, Adventure Bay, Sloping Island and Wedge Bay in November 2021. Boxes represent the first and third quartiles, and the median value is highlighted by the line within each box. Whiskers indicate the minimum and maximum values recorded.

Total nitrogen was approximately 2% lower in rhizomes than leaves, consistent across all sites (Figure 7-12). There was also a general trend of decreasing nitrogen in leaf tissue associated with age, consistent across Bull Bay (Leaf 1: 2.7% ±0.3, Leaf 5: 2.0% ±0.2), Adventure Bay (Leaf 1: 2.8% ±0.1, Leaf 5: 2.2% ±0.1) and Sloping Island (Leaf 1: 2.1% ±0.2, Leaf 5: 1.6% ±0.1). Generally, Sloping Island recorded lower nitrogen content in leaf tissue than Bull Bay or Adventure Bay. δ^{15}N in rhizomes also tended to be more depleted than leaves (Figure 7-12). The difference between rhizomes and leaves depended on site; Bull Bay rhizomes were relatively enriched (6.28‰) in comparison to Adventure Bay (4.51‰) and Sloping Island (3.86‰) and therefore a smaller difference in δ^{15}N between the two tissues was evident at Bull Bay compared to the other sites (Figure 7-12). δ^{15}N values in leaves were more enriched at Sloping Island compared to Bull Bay and Adventure Bay.

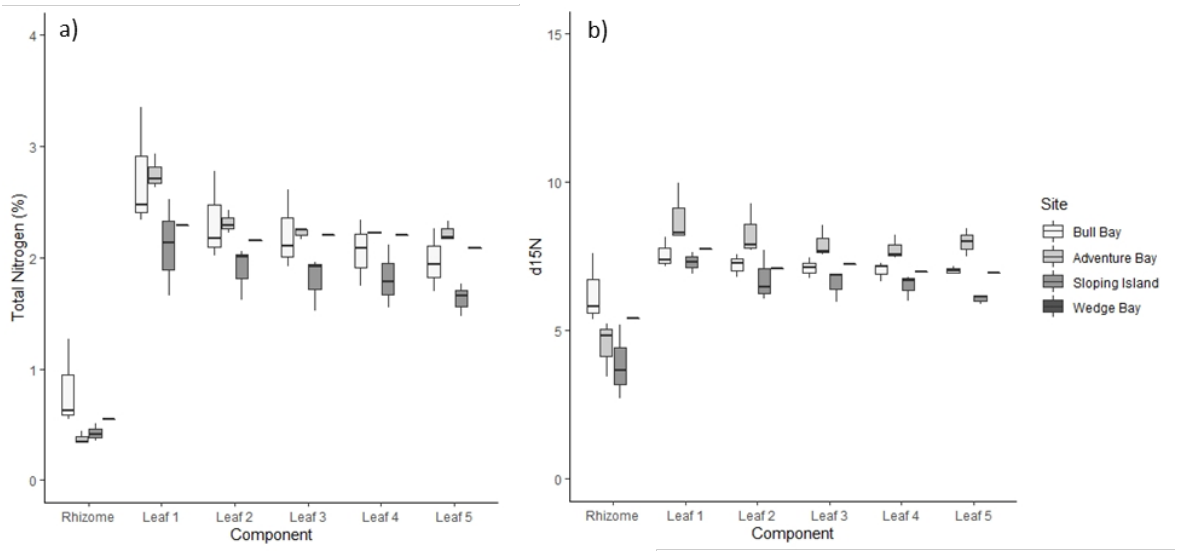

Figure 7-12: Total nitrogen (a) and δ^{15}N (b) of the seagrass collected at Bull Bay, Adventure Bay, Sloping Island and Wedge Bay in November 2021.

Seasonal comparison

There were no strong seasonal patterns in total percentage carbon in rhizome or leaves of seagrass sampled from Bull Bay (Figure 7-13). In contrast, seasonal trends were observed in δ^{13}C, which was dependent on leaf age (Figure 7-13). δ^{13}C values from seagrass collected in both November 2020 and November 2021 tended to have higher values in Leaf 1 (-12.8‰ ±1.0 and -13.6‰ ±0.6, respectively) and Leaf 2 (-13.7‰ ±1.2 and -14.02‰ ±0.6, respectively) compared to both June (Leaf 1: -16.2‰ ±0.9, Leaf 2: -16.3‰ ±0.9) and September (Leaf 1: -15.2‰ ±1.3, Leaf 2: -15.45‰ ±1.4). In samples taken from leaves 3-5, differences between month of sampling were negligible (Figure 7-13).

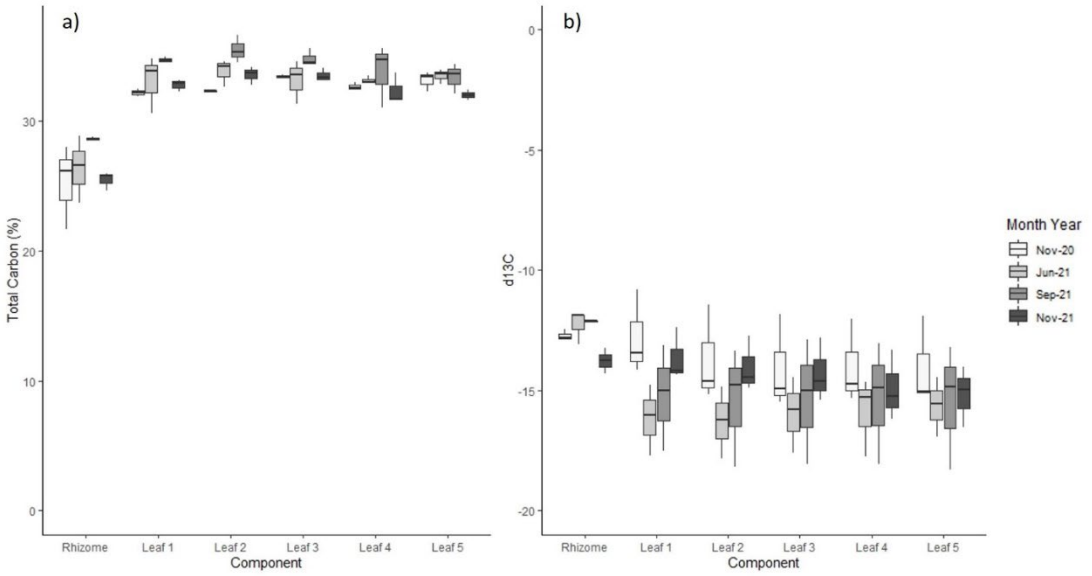

Figure 7-13: Total carbon (a) and δ^{13}C (b) of the seagrass collected at Bull Bay between November 2020 and 2021.

There were clear differences between sampling months observed in the total percentage nitrogen of seagrass, as well as differences between November 2020 and November 2021 (Figure 7-14). In rhizomes, samples collected in June had the highest proportion of nitrogen in tissues, with an average value 1.5 to 2.3% higher than all other months sampled. There was a general decreasing trend of total percent N in tissue with leaf age across samples collected in June (Leaf 1: 2.9% ±0.2 to Leaf 5: 2.3% ±0.1), September (Leaf 1: 3.1% ±0.1 to Leaf 5: 2.3% ±0.2) and November 2021 (Leaf 1: 2.7% ±0.3 to Leaf 5: 2.0% ±0.2). In contrast, total percent N remained relatively stable with leaf age in November 2020 (Leaf 1: 2.1% ±0.2 to Leaf 5: 1.9% ±0.2). As such, differences between sampling month were more pronounced in Leaf 1 than they were in Leaf 5. However, differences observed in nitrogen content between sampling month were not necessarily reflected in the stable isotope values (Figure 7-14). More depleted δ^{15}N values were recorded in rhizomes collected in November 2020 (6.4‰ ±0.3) and November 2021 (6.3‰ ±0.7) compared with those collected in June (8.3‰ ±0.1) or September (9.0‰ ±1.5), although there were no observable trends between sampling month and seagrass leaves (Figure 7-14).

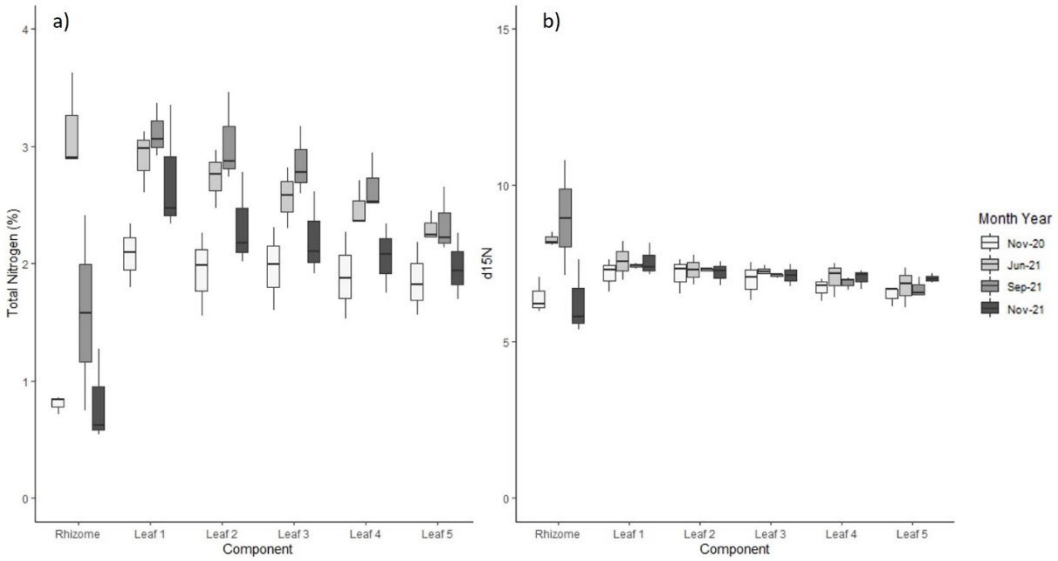

Figure 7-14: Total nitrogen (a) and δ^{15}N (b) of the seagrass collected at Bull Bay between November 2020 and 2021.

7.2.3 Detecting change in seagrass beds

Given the length and number of transects vary between sites within the Environmental Licenses, power to detect change was conducted on two levels: a) the number of photo-quadrats needed to detect a certain level of change to *Zostera* spp. cover within a transect, and b) the number of transects required to detect a certain level of change to *Zostera* spp. cover within a site. The estimated number of photo-quadrats within transects required to detect a 25% change in *Zostera* spp. cover was lower at Adventure Bay (20-70) than Sloping Island (3-160) and Bull Bay (51-212) across all years and transects (Figure 7-15). To detect a 50% change in *Zostera* spp. cover at Adventure Bay, where seagrass cover was relatively high, power analyses suggest that 9-20 photo-quadrats per transect would be required. This range reduces to 5-10 and 4-7 photo-quadrats to detect a 75% and 100% change respectively (Figure 7-15). At Bull Bay, where seagrass cover was more variable than Adventure Bay, the estimated number of photo-quadrats were slightly higher at 17-55, 8-25 and 6-16 photo-quadrats per transect to detect a 50%, 75% and 100% change in *Zostera* spp. cover, respectively (Figure 7-15). For Sloping Island, where *Zostera* spp. cover was sparser and less variable, the estimated number of photo-quadrats required to detect a 50%, 75% and 100% change in *Zostera* spp. cover was 5-42, 2-20 and 2-12 photo-quadrats per transect, respectively (Figure 7-15).

At the site level (where *n* = number of transects), the number of transects per site required to detect a 25, 50, 75 or 100% change were investigated. To detect a 25% change in *Zostera* spp. cover at the site level, an estimated 4-12 transects would be required at Adventure Bay, 7-18 transects at Bull Bay and 22-24 transects at Sloping Island (Figure 7-16). Far fewer transects are needed to detect a 50%, 75% or 100% change, with 3-8, 3-5 and 2-4 transects adequate across all sites to capture these levels of change in the percentage cover of *Zostera* spp. The number of transects required is dependent on the number of photo-quadrats within transects, with Sloping Island, where there were shorter transects with fewer photo-quadrats, requiring a greater number of transects to detect similar levels of change.

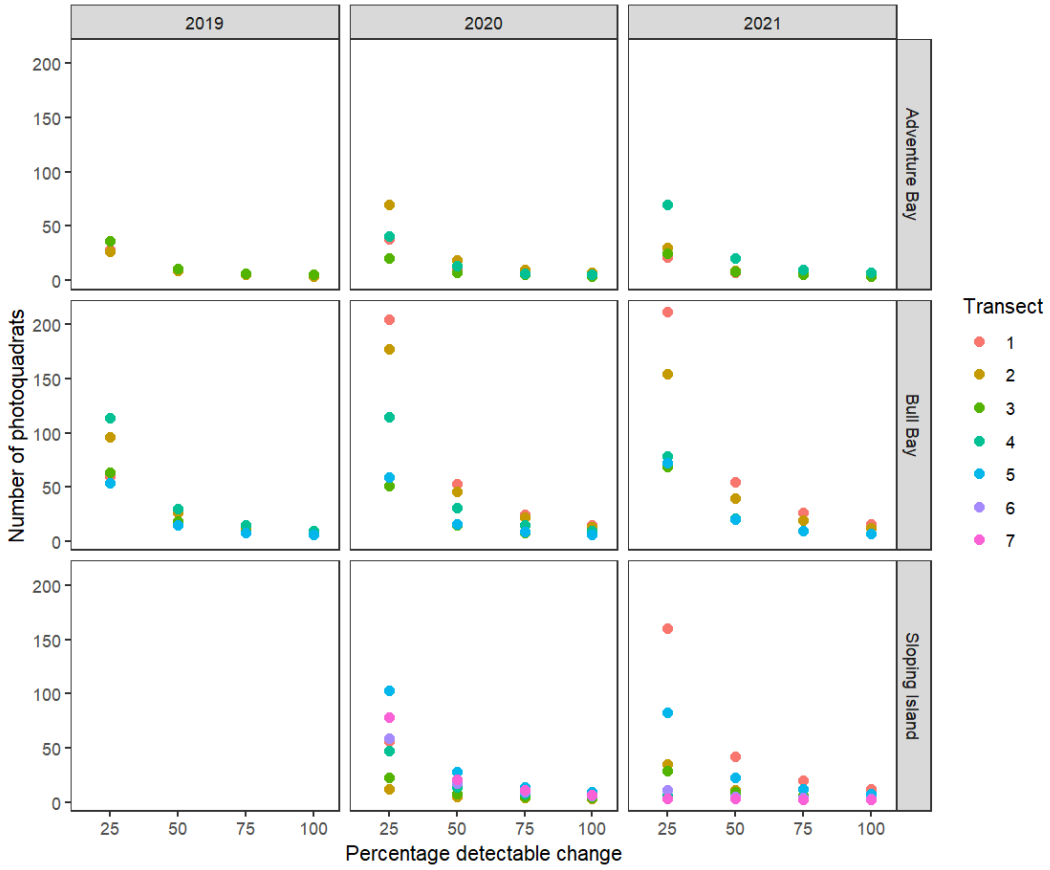

Figure 7-15: Number of photo-quadrats required per transect to detect a 25, 50, 75 and 100% change in *Zostera* spp. cover at Adventure Bay, Bull Bay and Sloping Island based on the average cover and standard deviation recorded in previous years. Note, there is no data for Sloping Island in 2019 as no surveys were conducted that year.

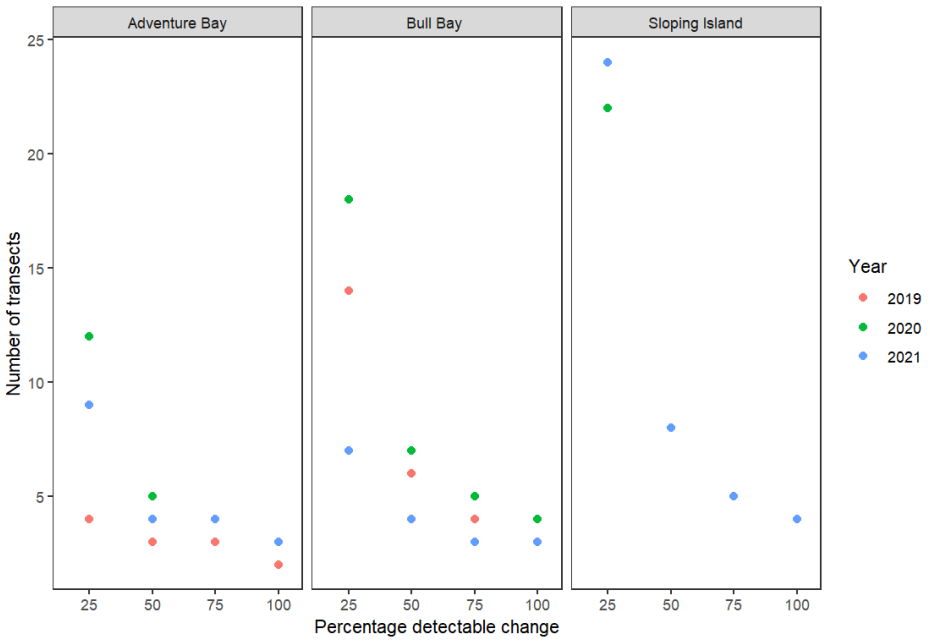

Figure 7-16: Number of transects required per site to detect a 25, 50, 75 and 100% change in *Zostera* spp. cover at Adventure Bay, Bull Bay and Sloping Island based on the average cover and standard deviation recorded in previous years.

7.2.4 Comparison of methods for monitoring

Across all categories, there were 19 instances in which *Zostera* spp. cover was overestimated; 15 of these were overestimated by one qualitative score (i.e. a qualitative score of 4 with a corresponding percentage cover representative of a qualitative score of 3, e.g. transect BB2, 2019) and four instances were overestimated by two categories (e.g. transect BB5, 2020; Table 7-3). There were only two instances in which *Zostera* spp. cover was underestimated by the qualitative scores. Both of these were scored as 'none', but their corresponding percentages recorded very small amounts of *Zostera* spp. cover (1-5%). For *Zostera* spp. cover, the qualitative ROV scores were most accurate for 'none' to 'medium' (scores 0 to 3) cover, ranging from 77 to 100% accuracy across these scores (Table 7-4). 'High' and 'very high' (scores of 4 and 5, respectively) *Zostera* spp. cover recorded from the ROV video was generally an overestimation, with only 1 out of 17 instances accurately scored (Table 7-4).

Table 7-3: Comparison between qualitative seagrass scores from ROV transects and the average total seagrass percentage cover from the photo-quadrat (PQ) surveys conducted in November 2019, 2020, and 2021. Cells are colour coded by ROV score and associated percentage cover (photo-quadrat data).

Site	Transect	ROV 2019	PQ 2019	ROV 2020	PQ 2020	ROV 2021	PQ 2021
Bull Bay	BB1	4	22	3	16	3	22
	BB2	4	26	3	16	3	23
	BB3	3	15	4	40	3	23
	BB4	3	36	4	29	3	34
	BB5	-	50	5	41	4	34
Adventure Bay	AB1	4	60	4	19	3	30
	AB2	4	48	4	17	4	27
	AB3	4	50	4	31	4	29
	AB4	-	-	5	45	3	29
	AB5	-	-	1	4	1	1
East of Sloping Island	SI1	-	-	3	21	3	19
	SI2	-	-	3	42	3	36
	SI3	-	-	3	32	3	28
	SI4	-	-	2	16	3	43
	SI5	-	-	3	21	2	8
	SI6	-	-	3	16	3	31
	SI7	-	-	3	23	3	30
Wedge Bay	WB1	-	-	0	5	0	0
	WB2	-	-	0	0	0	0
	WB3	-	-	0	1	0	0
	WB4	-	-	0	0	0	0
	WB5	-	-	0	0	0	0
	WB6	-	-	0	0	0	0
	WB7	-	-	0	0	0	0
	WB8	-	-	0	0	0	0

*Colour key for score comparison:

Qualitative score	Cover description	% cover	Colour
0	None	0%	
1	Very low	1-5%	
2	Low	5-20%	
3	Medium	20-60%	
4	High	60-90%	
5	Very high	90-100%	

Table 7-4: The occurrence (count) of the qualitative scores of *Zostera* spp. cover during the 2019-2021 November ROV surveys (Table 7-3) and the number and accuracy (percentage) of each score given that were correct, underestimated, or overestimated in comparison.

Qualitative score	Cover description	Count of score	Correct occurrences	Underestimated occurrences	Overestimated occurrences
0	None	16	14 (88%)	2 (13%)	0
1	Very low	2	1 (50%)	0	1 (50%)
2	Low	2	2 (100%)	0	0
3	Medium	22	17 (77%)	0	5 (23%)
4	High	13	1 (8%)	0	12 (92%)
5	Very high	2	0	0	2 (100%)

Overall, the qualitative ROV scores for total epiphytic cover were less accurate than those for *Zostera* spp. cover (Table 7-6). Thirteen out of 15 'high' scores were overestimated by one category, but for the 'very high' scores, 7 out of the 9 instances were overestimated by two categories (Table 7-6). The 'medium' epiphytic cover (score of 3) was the most accurate with 68% of these scores reflecting the corresponding percentage cover. 'Low' epiphytic cover scores were generally an underestimation (67%) and 'high' to 'very high' cover was most often an overestimation (88 and 100% of scores respectively; Table 7-5).

Table 7-5: The occurrence (count) of the qualitative scores of epiphytic cover during the 2019-2021 November ROV surveys (Table 7-5) and the number and accuracy (percentage) of each score given that were correct, underestimated, or overestimated in comparison with the associated percentage.

Qualitative score	Cover description Cover	Count of score	Correct occurrences	Underestimated occurrences	Overestimated occurrences
0	None	0	N/A	N/A	N/A
1	Very low	0	N/A	N/A	N/A
2	Low	6	2 (33%)	4 (67%)	0
3	Medium	25	17 (68%)	1 (4%)	7 (28%)
4	High	17	2 (12%)	0	15 (88%)
5	Very high	9	0	N/A	9 (100%)

Table 7-6: Comparison between qualitative epiphytic cover scores from ROV transects and the average total epiphyte percentage cover from the photo-quadrat (PQ) surveys conducted in November 2019, 2020 & 2021. Cells are colour coded by score (ROV data) and associated percentage cover (photo-quadrat data).

Site	Transect	ROV 2019	PQ 2019	ROV 2020	PQ 2020	ROV 2021	PQ 2021
Bull Bay	BB1	3	27	2	24	3	16
	BB2	4	22	2	32	3	16
	BB3	4	29	3	47	3	26
	BB4	4	36	3	38	3	20
	BB5	-	28	2	40	3	19
Adventure Bay	AB1	5	65	5	55	4	14
	AB2	5	58	5	43	4	20
	AB3	5	59	5	42	5	28
	AB4	-	-	4	35	3	31
	AB5	-	-	5	56	3	17
East of Sloping Island	SI1	-	-	4	72	4	55
	SI2	-	-	4	56	3	68
	SI3	-	-	3	31	3	24
	SI4	-	-	5	74	3	56
	SI5	-	-	3	34	2	24
	SI6	-	-	3	40	3	25
	SI7	-	-	4	40	3	32
Wedge Bay	WB1	-	-	2	14	2	8
	WB2	-	-	3	17	3	15
	WB3	-	-	4	39	3	38
	WB4	-	-	4	47	4	25
	WB5	-	-	4	39	4	13
	WB6	-	-	3	16	3	28
	WB7	-	-	3	26	3	37
	WB8	-	-	4	71	4	35

*Colour key for score comparison:

Qualitative score	Cover description	% cover	Colour
0	None	0%	
1	Very low	1-5%	
2	Low	5-20%	
3	Medium	20-60%	
4	High	60-90%	
5	Very high	90-100%	

7.3 Synthesis

Overall, these results present an insight into the health, spatial extent and ecology of seagrass beds in Storm Bay, providing a comprehensive baseline for these habitats into the future. As there are no seagrass beds within close proximity (<5 km) to aquaculture operations, our sampling program focused on broadscale seagrass health. As seagrass can be a sensitive indicator of declining environmental conditions, long-term monitoring of this habitat may provide early warning of a loss in ecosystem health across Storm Bay (Connolly et al. 2018).

In terms of broadscale patterns, results indicate that the ecology of each of the four sites was different. While Adventure Bay had the densest seagrass cover across the largest spatial area, this changed over the course of the study, with macroalgae (predominantly species of *Caulerpa*) an increasingly prominent feature on transects. In contrast, the cover of seagrass at Bull Bay was sparser than Adventure Bay, although the bed appeared to increase in size across the study period. Of note, the area of seagrass cover within Bull Bay was much larger than indicated by previous SeaMap data (Barrett et al. 2001). Seagrass at Sloping Island was sparse and patchy, although the bed covered a wide spatial area, which was stable within the two years of sampling at this site. At Wedge Bay, the site was a green macroalgal bed, with only very sparse *Halophila* present. While SeaMap data from 2001 indicates that Wedge Bay was once a *Zostera* spp. bed, the transects surveyed for the West of Wedge salmon lease collected in 2019 indicated that the bed was predominantly green macroalgae prior to the commencement of this study (Aquenal 2019b). Green macroalgae can replace seagrass beds for a variety of reasons, including nutrient enrichment, physical disturbance and changes to physiochemical parameters in the water column (Hendriks et al. 2010, Schmidt et al. 2012). Given the time interval between the SeaMap survey and the baseline survey in 2019, it is not possible to establish causality for the shift in bed composition. However, given the green macroalgae bed is now well established, re-establishment of a *Zostera* spp. bed in Wedge Bay is unlikely to occur in the near future and will depend on long-term prevailing environmental conditions that favour *Zostera* spp. over green macroalgae.

Zostera spp. is a dynamic, fast-growing species with capacity for both vegetative and sexual reproduction (Sherman et al. 2018). Evidence for this can be seen in Bull Bay, where the bed has increased in size over the past 20 years and appears to have expanded even within the study period (Barrett et al. 2001). In contrast, Adventure Bay appears to be in a phase of retraction. Transects that were dominated by seagrass in 2019 now have a much higher portion of green macroalgae. While small fluctuations between seagrass and macroalgae are reasonably common depending on environmental factors, particularly for a species such as *Zostera* spp., tipping points for where the dominant species in the bed shifts are unknown. Green macroalgae are likely to outcompete seagrass under high nutrient, low light scenarios (Hendriks et al. 2010); however, the exact environmental conditions for this scenario to occur will vary depending on site and a number of environmental factors acting synergistically. Furthermore, with fast-growth patterns and high fecundity, *Zostera* as a genus tends to proliferate in higher nutrient environments than most other seagrass species

(Sherman et al. 2018), so nutrient stimulation alone is unlikely to lead to propagation of green macroalgae on seagrass beds.

Overall, the variation observed between sites in expansion and retraction of the *Zostera* spp. beds is typical for this genus, with *Zostera* known to be dynamic in distribution and persistence. This small scale variability often leads to difficulty understanding factors that influence seagrass cover, which inhibits effective management (Sherman et al. 2018). For example, *Zostera nigricaulis* was monitored for 70 years in Port Phillip Bay, with no consistent pattern in variation of cover (Ball et al. 2014). Based on this, Jenkins et al. (2015) developed a model relating resilience of seagrass to nutrient stress, where populations living in sandy, nutrient-limited environments were likely to be far more ephemeral than those in sheltered, muddy environments with more persistent nutrients. Given the seagrass sites within Storm Bay are located on sandy sediments that are likely to be nutrient-limited, a large amount of variation in bed extent is expected to occur over relatively short time intervals. Thus, a multi-metric approach, combining bed extent with shifts in bed composition, and a biochemical measure such as stable isotopes will provide power for understanding the influence of the environment on seagrass bed dynamics.

The flora and fauna that were observed in photo-quadrats were used to better understand the ecology at each of the four study sites. This method allowed us to track presence and abundance of seagrass, epiphytic algae and larger mobile and sessile invertebrates, and was found to be an effective method of characterising ecology at sites. All four sites were distinct, with multivariate analysis sensitive enough to detect temporal shifts in the beds across the study period. Despite site-level differences, November was likely to capture the heaviest epiphyte loadings; winter was when plants were likely to be their cleanest. This trend is similar to that reported in other locations across a wide range of seagrass species (e.g. Moore & Wetzel 2000, Prado et al. 2008, Prado et al. 2010, Castejón-Silvo et al. 2012, Piazzi et al. 2016). To provide further information on seagrass ecology in Storm Bay, an Honours project complementary to this study examined biodiversity of infauna and epifauna existing within seagrass beds, by sampling using sediment cores and identifying all taxa to the species level using microscopy. This research found that biodiversity of infauna was particularly high in Adventure Bay and Bull Bay, along with Fulham Island (a site within Norfolk Bay), compared with other sites in Norfolk Bay and the Derwent Estuary (Wise 2022). However, infauna assemblages were also distinct at a site level, which was attributed to variation in seagrass structural complexity, with site-specific environmental factors also influencing species abundance and diversity (Wise 2022). Seagrass community assemblage along with associated functional traits were found to be sensitive indicators of nutrient stimulation (Wise 2022). Overall, we found that photo-quadrats provide a robust method to rapidly quantify ecology at a site level; however, taxonomic studies provide an additional level of detail, with changes at community and functional levels likely to be indicators of nutrient enrichment.

Stable isotopes and nitrogen content provided valuable insight into nitrogen dynamics at a site level, along with how to sample the seagrass to reduce variability in results. For instance, as the leaf ages, nitrogen content declines and the $\delta^{15}N$ of leaves becomes more depleted. Therefore, it is important to be consistent with the section of the plant that is

sampled. Seasonal variation in nitrogen content of seagrass leaves and rhizomes was also evident, suggesting this parameter is sensitive enough to reflect fluctuations in ambient nitrogen availability. Similar results have been reported for *Posidonia oceanica* and *Zostera marina*, with nitrogen content declining with age of the leaf (Invers et al. 2002) and enhanced environmental nitrogen generally reflected in the nitrogen content of seagrass leaves (Burkholder et al. 1994, Prado et al. 2010, Castejón-Silvo et al. 2012). While nitrogen content and isotope results provide a good baseline regarding nitrogen loading at each of the sites, biochemical sampling for ongoing broadscale monitoring is unlikely to be necessary in the context of Storm Bay, where seagrass is a relatively minor habitat. However, if a change is detected in the ecology and attribution to a particular environmental perturbation is of interest, re-sampling beds for nitrogen content and isotopes in seagrass will provide insight into the nitrogen dynamics of the site. Likewise, into the future, if there is salmon development at sites where seagrass is a dominant habitat, parameters such as tissue nitrogen content and stable isotopes will provide time-integrated signals that have the potential to act as an early warning for ecosystem decline.

While the photo-quadrat method provided a robust method of assessing seagrass beds, it was also found to be limited under certain scenarios. Variability in seagrass cover increased as the cover of epiphyte increased, with high epiphyte loadings obscuring the seagrass below. Thus, seagrass cover is potentially underscored where epiphyte cover is high, with care needed in interpretation of data under these scenarios. While in-situ scoring may help to overcome this, it is a far more time-consuming method. Instead, regular QA/QC to ensure consistency between photo-quadrat scorers, along with a set of clear scoring guidelines should be considered essential to ensure a robust and comparable time-series of data, overcoming some of the limitations of sampling through photo-quadrats. In terms of overall power of sampling design, our study indicates Sloping Island was more variable than either Adventure Bay or Bull Bay. At Sloping Island, the transects were short (50 m) compared to the longer transects in both Bull Bay and Adventure Bay (approximately 200 m), which is the likely source of this variation. Power analysis suggested that the current design will not detect a 100% change in seagrass cover at Sloping Island. While tipping points in seagrass beds have not been explored as part of this study, it is reasonable to assume that a monitoring program should have the power to detect a 50% change in abundance of a foundation species, in this case seagrass, to be robust. Our power analysis at the quadrat level suggested that 15-20 quadrats per transect provided this level of power at sites within Storm Bay. For sites with longer transects, generally between 3-5 long transects was adequate to detect 50% change in seagrass cover across the site.

The other method trialled as part of this study was a qualitative assessment using ROV transects. In comparison to the quantitative photo-quadrat method, the ROV method tended to provide higher estimates for seagrass and epiphyte cover, particularly when epiphyte cover was high. There was also difficulty comparing between both years and scorers, with QA/QC on data being more difficult. While problematic in obtaining robust assessments, this method can cover a large spatial area quickly. With the addition of a USBL system to ensure accurate geolocation and a downward facing camera to enable replicable and repeatable scoring, this technique could become a valuable tool for future monitoring.

However, for the system and scoring method that was tested as part of this project, only catastrophic change could be determined with any level of confidence.

In terms of site selection, there is very little seagrass remaining in the subtidal areas within Wedge Bay. While the Wedge Bay site was historically a seagrass bed, it has been dominated almost entirely by green macroalgae since 2019 (Barrett et al. 2001, Aquenal 2019b). While continued monitoring would allow any potential seagrass recovery to be tracked, it may not be necessary to monitor this site every year while it exists as a green macroalgal bed. Similarly, while Norfolk Bay was considered beyond the scope of this research program, Honours research examining biodiversity of infauna associated with the seagrass beds in Norfolk Bay suggested this area could have biological interest (Wise 2022). Depending on the overall aim of future broadscale monitoring programs within Storm Bay, an additional monitoring site around the entrance of Norfolk Bay (e.g. Fulham Island) might be considered.

More generally, it is recommended that any monitoring program focused on seagrass should be scaled based on the ecological significance of the area of interest. Seagrass is an inherent indicator of system health that can also provide significant habitat for associated flora and fauna. While some regions within Tasmania have seagrass with high ecological significance (i.e., far north-west), the ecological values associated with seagrass habitat in Storm Bay is less well understood. In areas where seagrass beds are thought to have low ecological significance, an annual monitoring program could be limited to bed extent mapping using photo-quadrats across a series of predetermined transects. Photo-quadrats could be kept in archive and analysed if bed extent mapping suggests there is substantial decline in seagrass cover. However, where beds are considered to be highly significant ecologically, full biodiversity surveys using methods such as those outlined in Wise (2022) should be considered as part of a baseline, but also as part of an additional ongoing monitoring program along with more frequent quantitative photo-quadrat assessments and potentially biochemical analyses. Overall, the aim of the monitoring program and the significance of the habitat within a region should determine the effort invested in monitoring seagrass. There are numerous methods and techniques that have the capacity to assess seagrass health and condition; choosing the appropriate approach is dependent on the data required and how important the habitat is within the context of the broader ecosystem.

7.4 Recommendations for future monitoring

As discussed above, any monitoring program for seagrass should be scaled to the ecological importance of the seagrass in that system. Seagrass will always have inherent value in an ecosystem for the services this habitat provides, along with the capacity of seagrass to act as a sentinel for environmental change. However, the monitoring effort where ecological significance is high might be different to where the spatial extent of the beds is limited, such as in the case of Storm Bay. Likewise, there are no seagrass beds in close proximity to farm sites in Storm Bay. Therefore monitoring of seagrass beds in this region is only likely to occur as an indicator of broadscale ecosystem health.

Given this, a simple approach assessing bed extent is recommended for the future monitoring of seagrass beds in Storm Bay. For a dynamic seagrass species such as *Zostera* spp., monitoring variation in bed extent and composition is a more appropriate measure for indicating longer-term fluctuations in health of the bed than measuring condition alone. If collected in a manner that allows for a quantitative assessment of the condition of the seagrass and ecology of the associated flora and fauna, should the need for further information arise, this becomes an appropriate seagrass monitoring program for Storm Bay.

For the monitoring of bed extent and composition, the following process is recommended:

- Between 3-5 long transects (≥ 200 m) are established at each site extending from adjacent soft sediments and spanning the entire seagrass bed/area of interest.
- Along these transects a drop camera with a 1 m^2 frame is lowered to the substrate every 10 m and a benthic image is captured. The vessel used for this process should be equipped with a DGPS and each image georeferenced.
- Images are scored into one of six categories from the original SeaMap assessments depending on the dominant vegetation: seagrass, sparse seagrass, patchy seagrass, mixed bed, macroalgae or sand. All images should be archived for more detailed scoring either as outlined below, or where the need arises.
- These categories can then be matched with the waypoint collected for each photo-quadrat and subsequently mapped using ArcGIS or a similar program.
- These surveys should be repeated once every two years, with survey frequency reviewed after five years e.g. if beds are stable and there have been no major increases in farmed biomass or lease locations, longer periods between monitoring could be considered.
- If large shifts in the extent of the seagrass or composition of the beds is observed, then images should be scored quantitatively to provide ecological information around these changes.
- If there are any significant changes to biomass or lease area in Storm Bay, it is recommended that images are scored quantitatively prior to this occurring.

In the case that change is detected and/or a quantitative assessment is required, we recommend that the methods adopted for this are the point-count assessments outlined in Section 7.1.3:

- At each site within the transects used for assessing extent and composition, a 200 m subsection should be demarcated for the condition assessment.
- Where possible, this 200 m section should be within the main bed or include as much of the main bed as possible.
- Quantitative assessments should be undertaken using a software package such as Coral Point Count with Excel extension (CPCe) or TransectMeasure that provides capacity for 50-point count within the image.

- Photo-quadrats should be scored for seagrass and epiphyte cover, as well as sessile invertebrates and macroalgae associated with seagrass beds (see Appendix 7-1 for the table of parameters used in this study).
- Surveys should always be undertaken at the same time of year to avoid any confounding temporal effects.

The data collected through quantitatively scoring of photo-quadrats can be used to capture the general ecology of seagrass beds and help to inform any changes observed in the bed extent and composition mapping. Regardless of whether change is observed, we recommend that images are processed quantitatively once every five years to track the ecology of the seagrass beds in Storm Bay. This program should be reviewed after five years, with frequency of bed extent mapping and quantitative surveys reviewed at this point.

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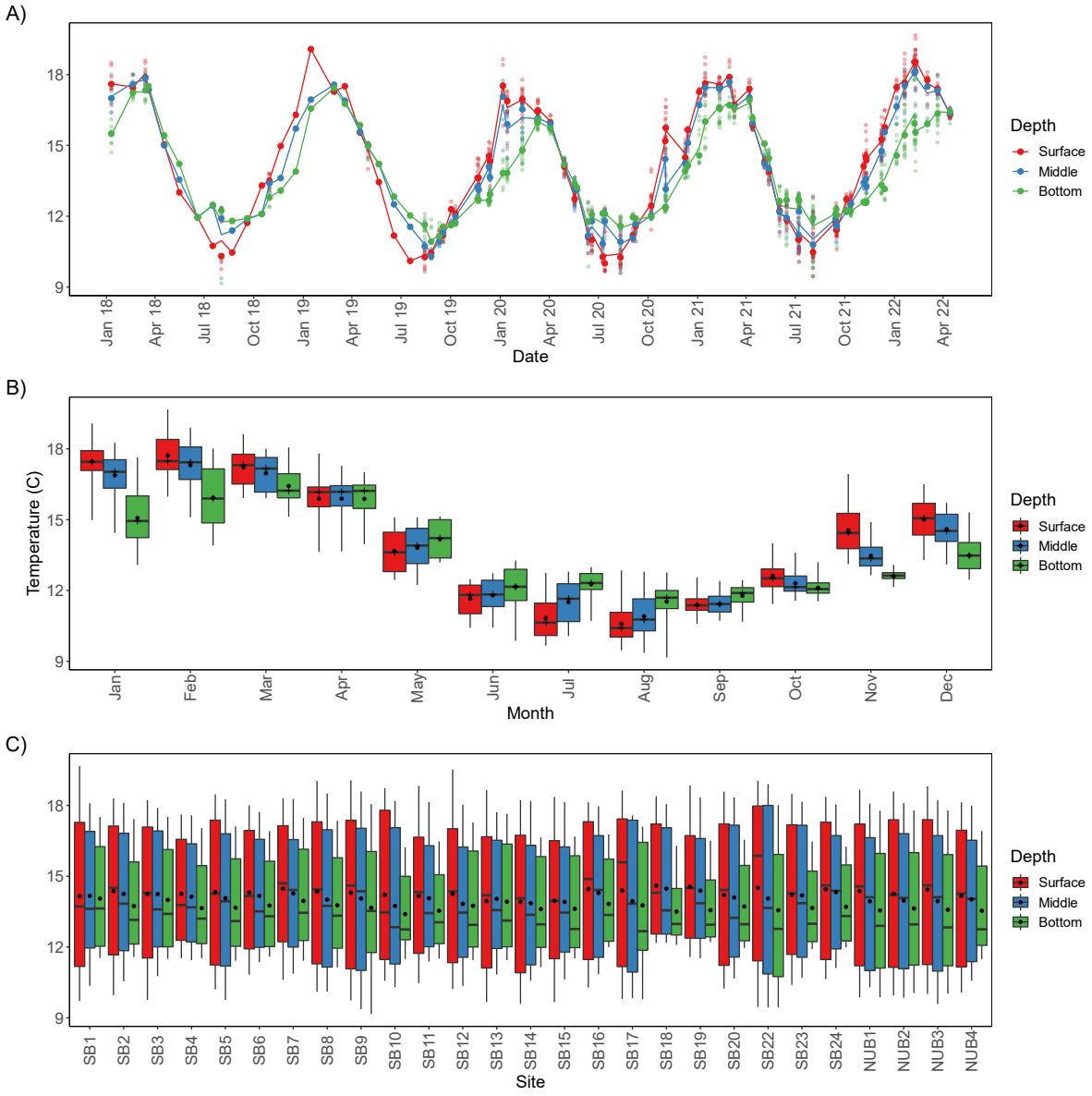
9 Appendices

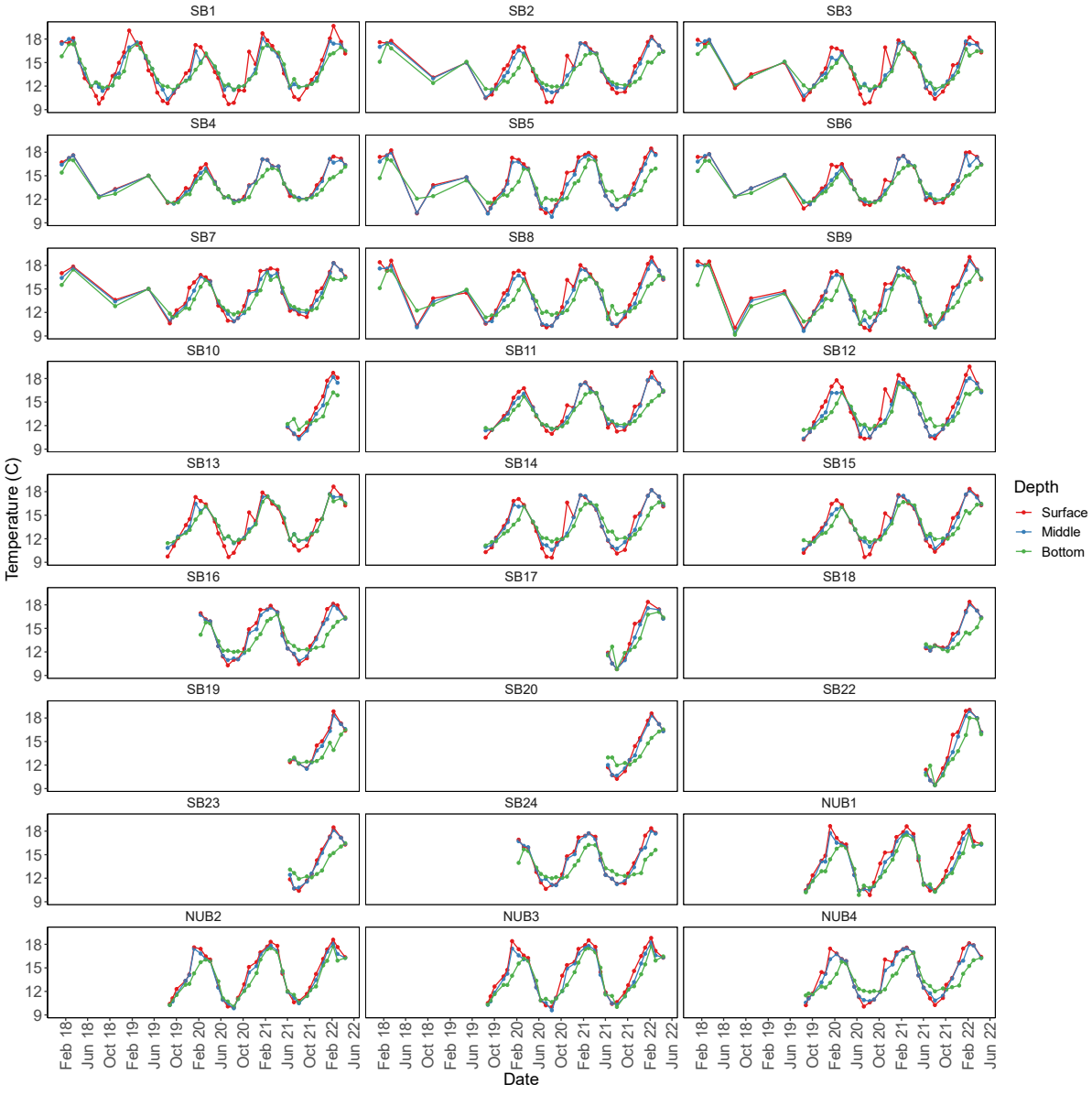
The following figures and table are not cited in the main report, but are provided as relevant additional information for each of the labelled chapters and sections within

Appendix 3-1: Water column – physico-chemical parameters

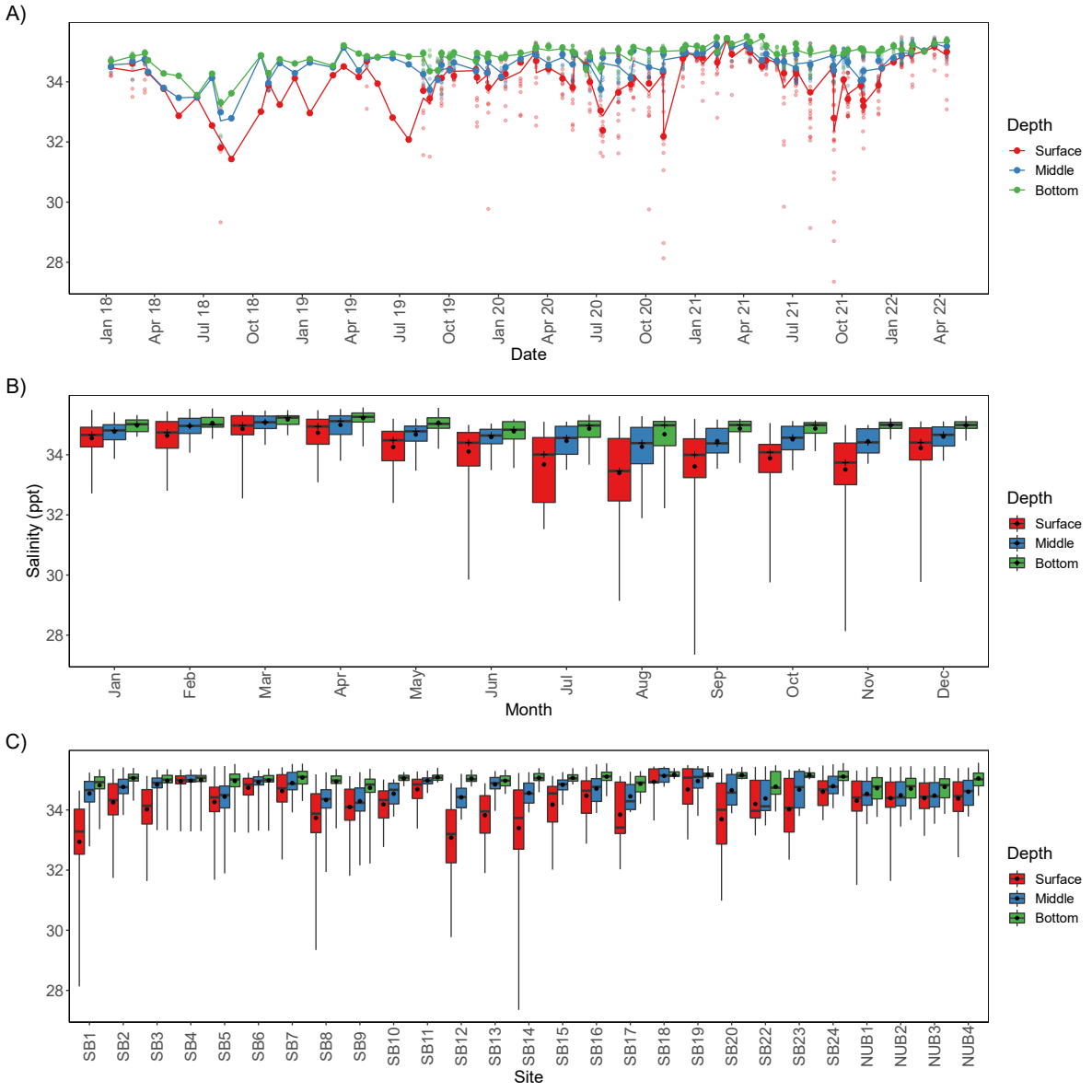
Spatial and temporal variation in temperature (°C) values for surface, middle and bottom samples collected across Storm Bay. A) monthly temperature for all sites through time with the means for surface, middle (10 m, excluding NUB1-4) and bottom plotted as lines. B) variation in temperature across the year with all data from every site pooled for each month and C) variation in temperature for each site pooled over time. In B) and C) the boxplots show the mean, median and the 25th and 75th percentiles.



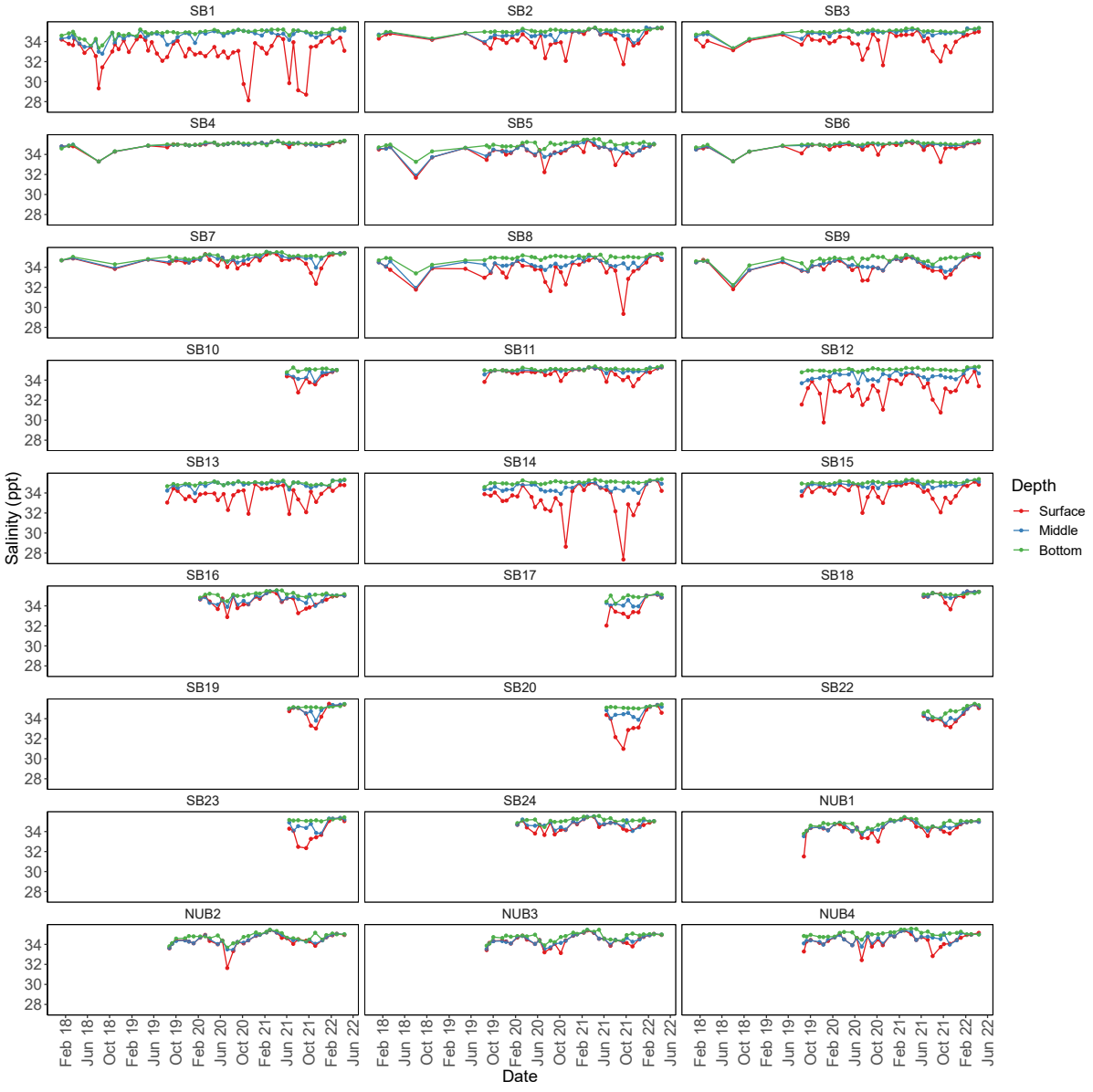
Spatial and temporal variation in temperature (°C) values for surface, middle (10 m, excluding NUB1-4) and bottom samples across Storm Bay.



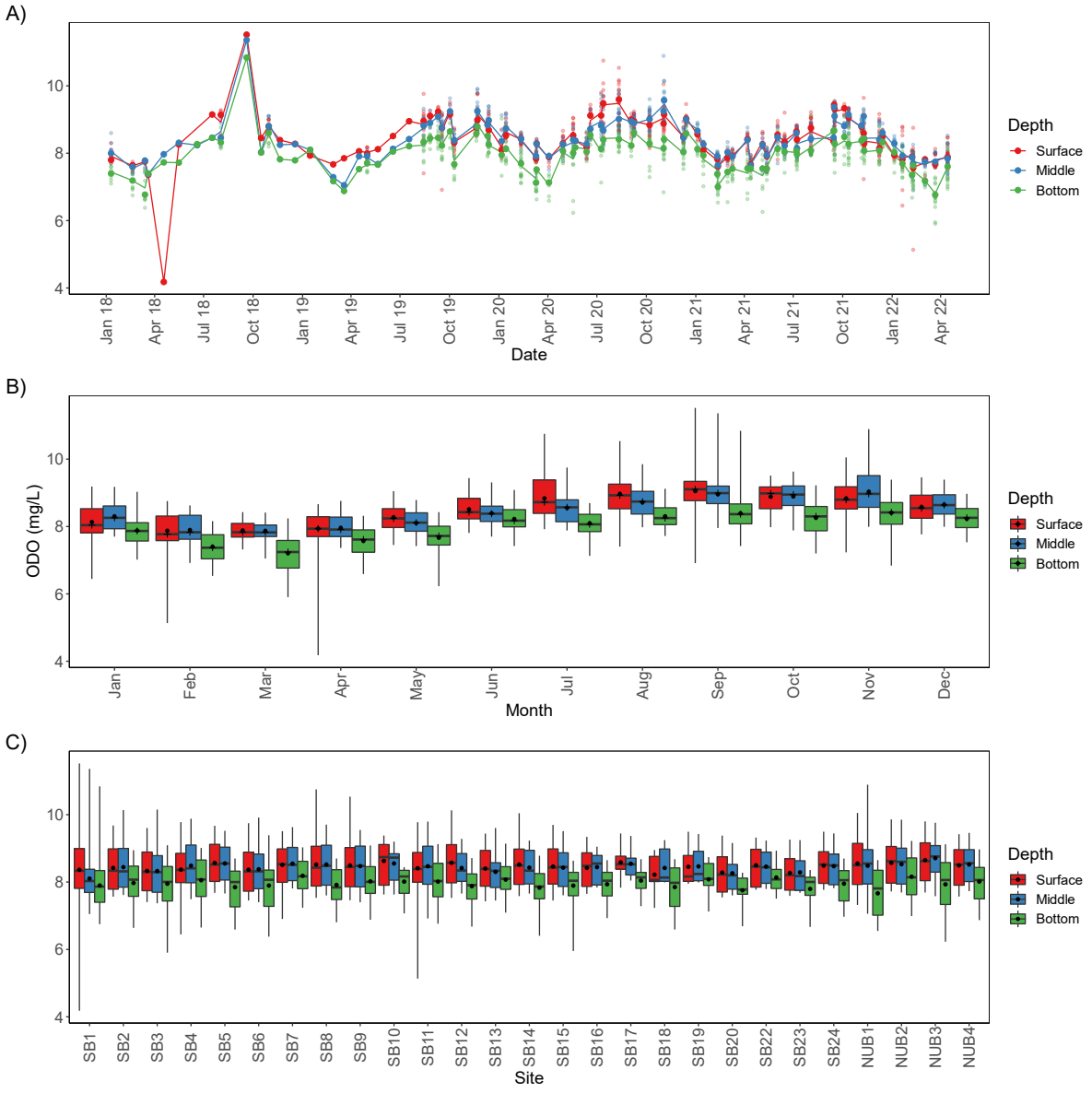
Spatial and temporal variation in salinity (ppt) values for surface, middle and bottom samples collected across Storm Bay. A) monthly salinity for all sites through time with the means for surface, middle (10 m, excluding NUB1-4) and bottom plotted as lines. B) variation in salinity across the year, with all data from every site pooled for each month, C) variation in salinity for each site pooled over time. In b) and c) the boxplots show the mean, median and the 25th and 75th percentiles.



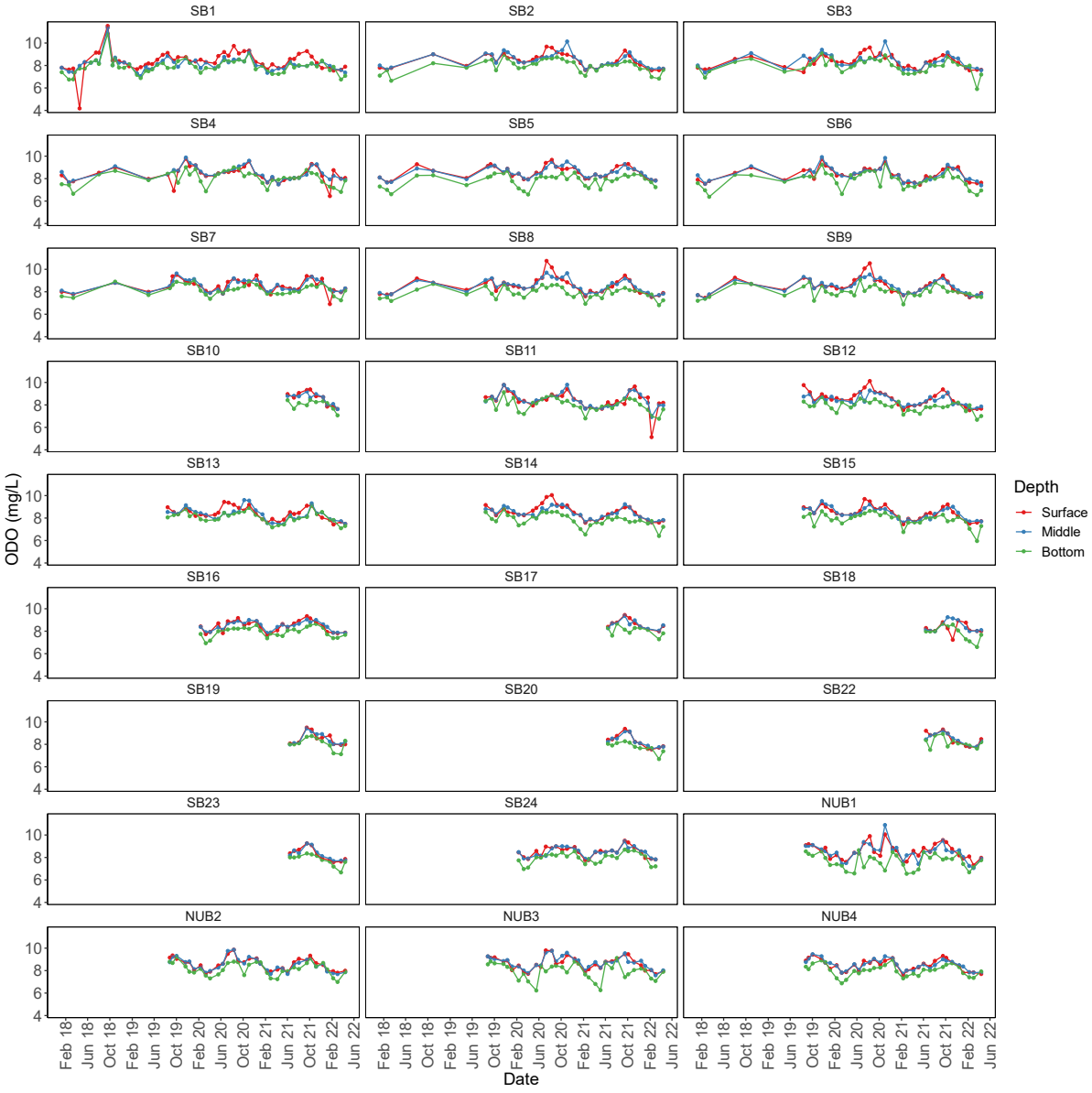
Spatial and temporal variation in salinity (ppt) values for surface, middle (10 m, excluding NUB1-4) and bottom samples across Storm Bay.



Spatial and temporal variation in dissolved oxygen (mg/L) values for surface, middle and bottom samples collected across Storm Bay. A) monthly dissolved oxygen for all sites through time with the means for surface, middle (10 m, excluding NUB1-4) and bottom plotted as lines. b) variation in dissolved oxygen across the year, with all data from every site pooled for each month, c) variation in dissolved oxygen for each site pooled over time. In B) and C) the boxplots show the mean, median and the 25th and 75th percentiles.



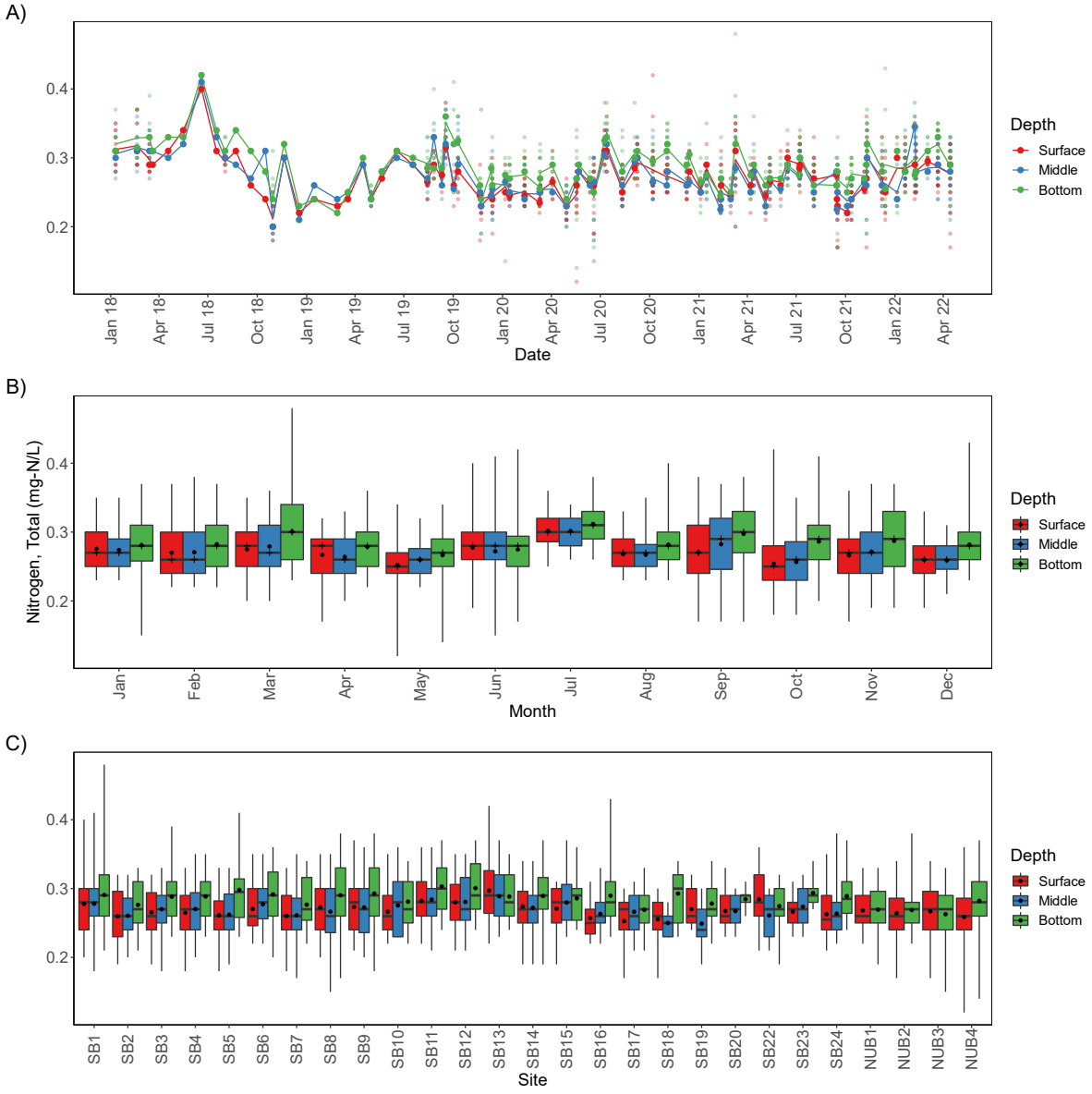
Spatial and temporal variation in dissolved oxygen (mg/L) values for surface, middle (10 m, excluding NUB1-4) and bottom samples collected across Storm Bay[1].



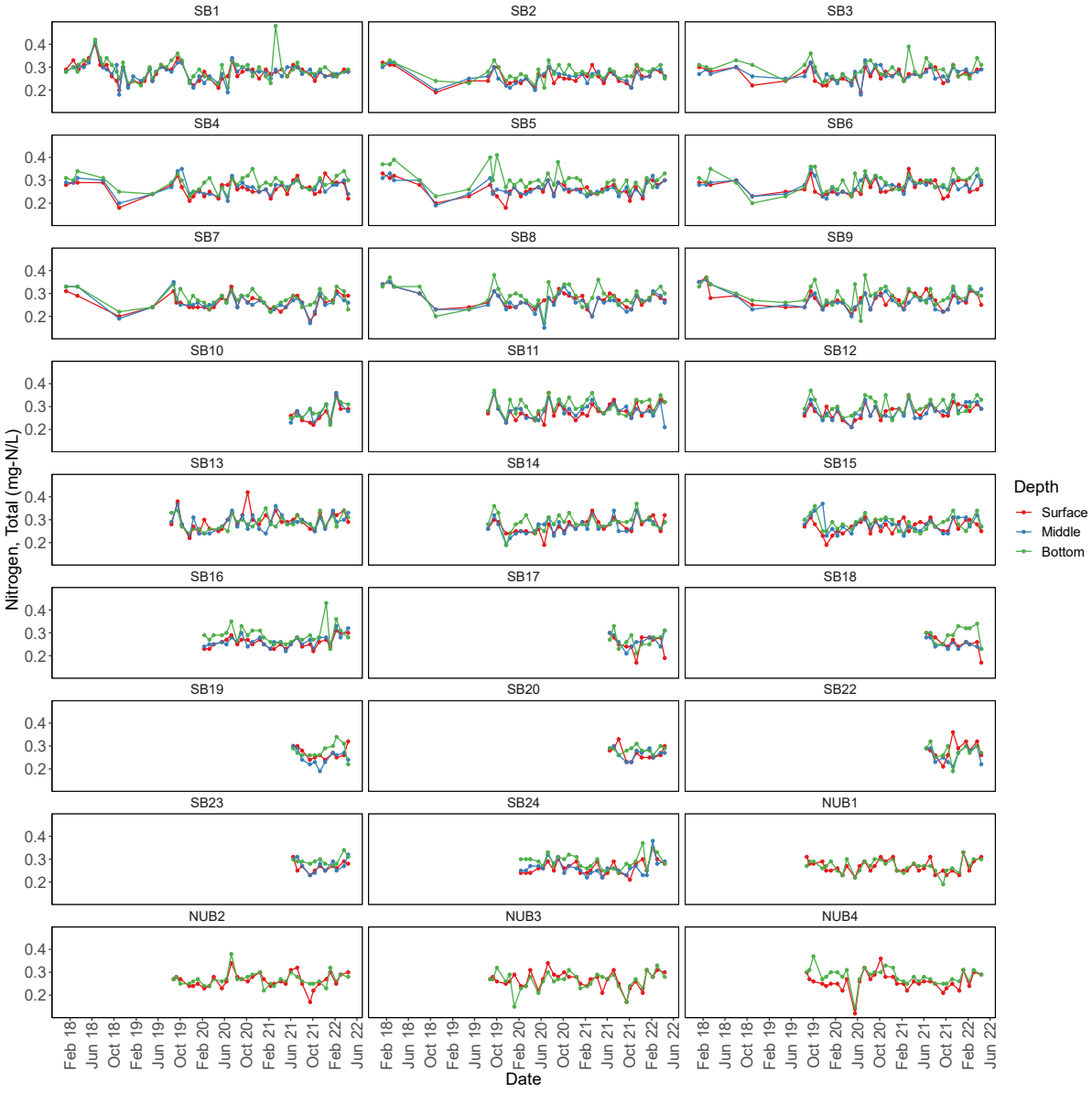
[1] Extremely low and high values of dissolved oxygen were observed at SB1 in May 2018 in the surface waters and September 2018 at all depths, respectively.

Appendix 3-2: Water column – nutrients

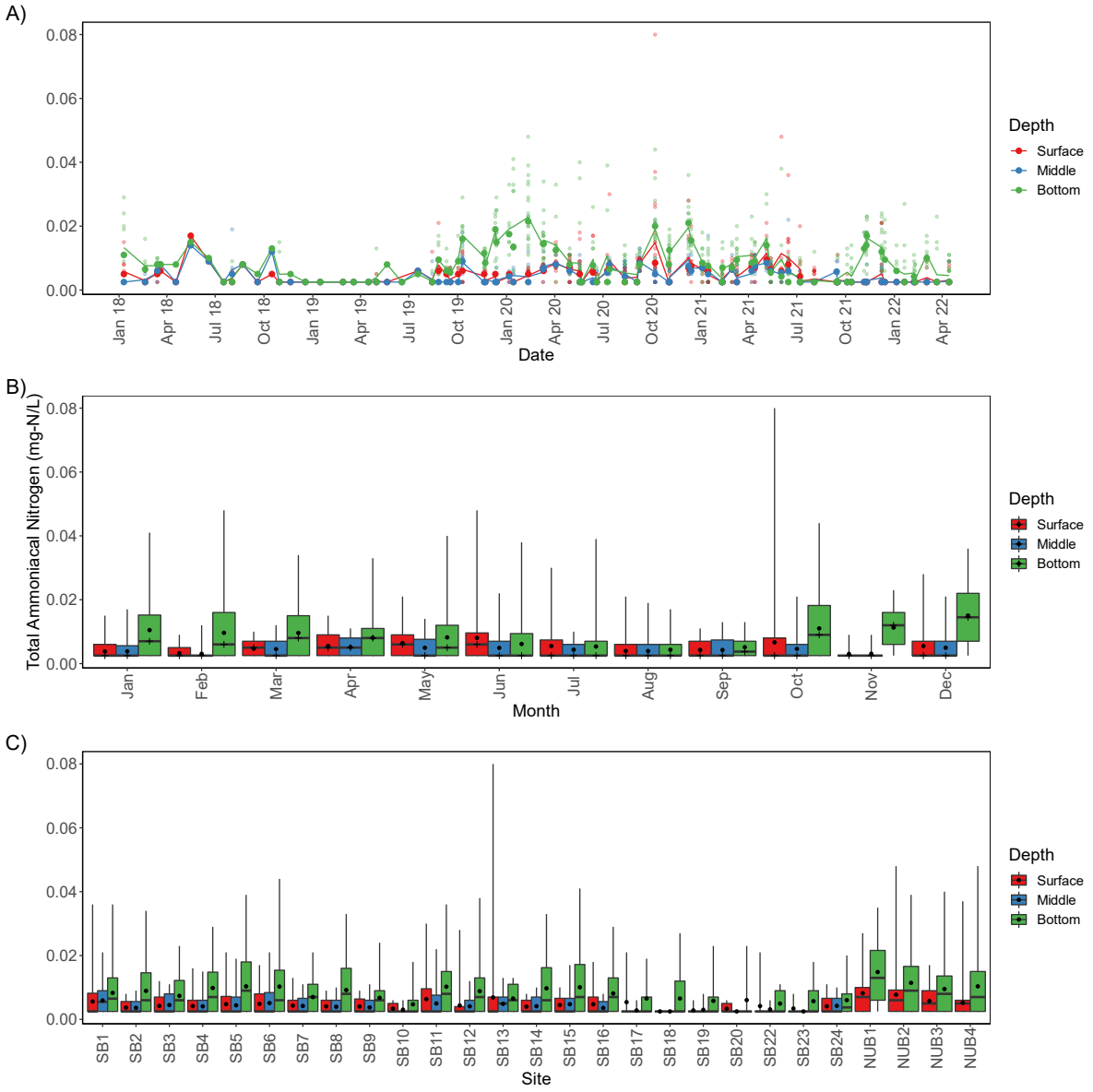
Spatial and temporal variation in total nitrogen (mg-N/L) values for surface, middle and bottom samples collected across Storm Bay. A) monthly total nitrogen for all sites through time with the means for surface, middle (10 m, excluding NUB1-4) and bottom plotted as lines. B) variation in total nitrogen across the year, with all data from every site pooled for each month. C) variation in total nitrogen for each site pooled over time. In B) and C) the boxplots show the mean, median and the 25th and 75th percentiles.



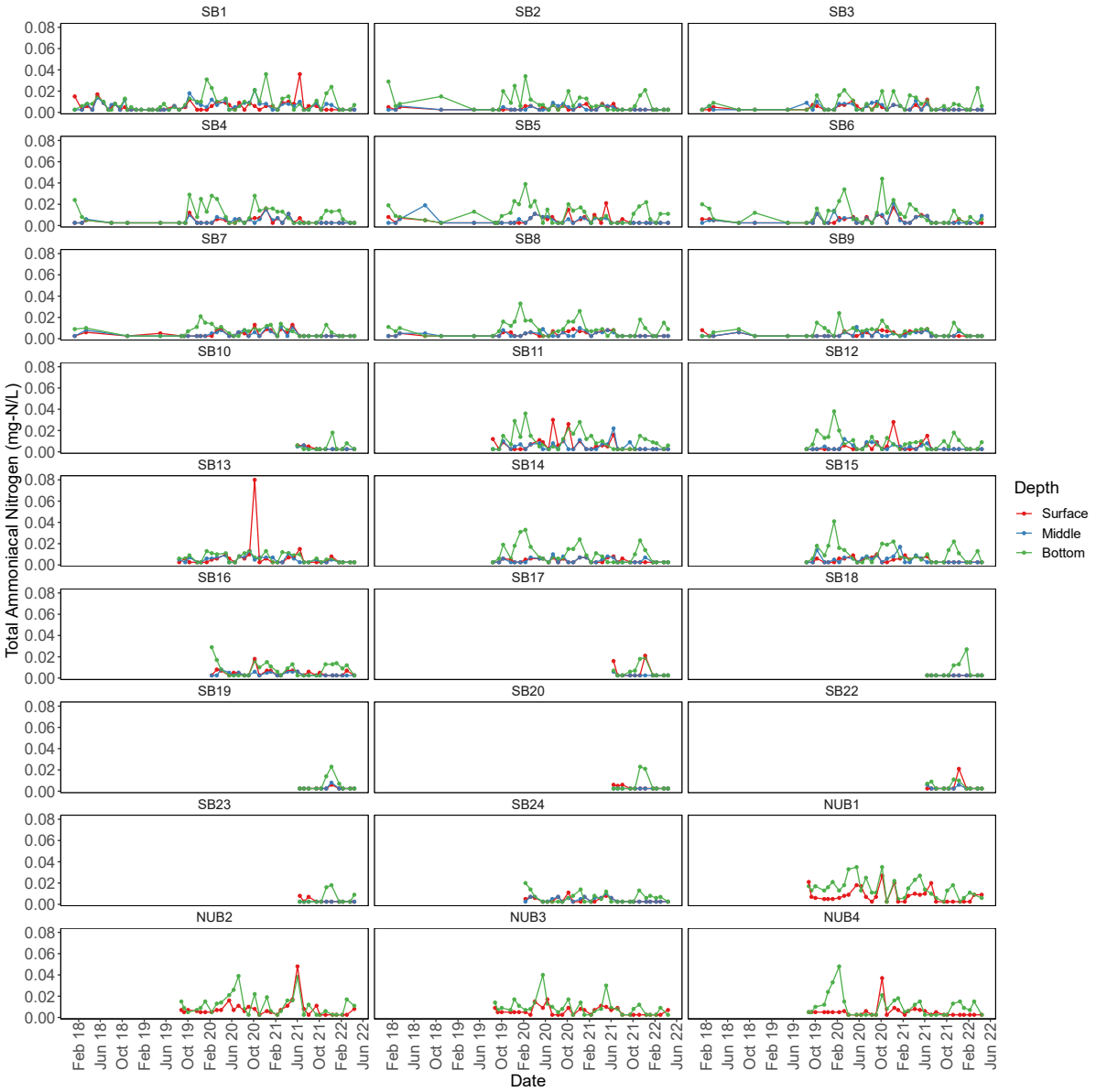
Spatial and temporal variation in total nitrogen (mg-N/L) values for surface, middle (10 m, excluding NUB1-4) and bottom samples collected across Storm Bay through time.



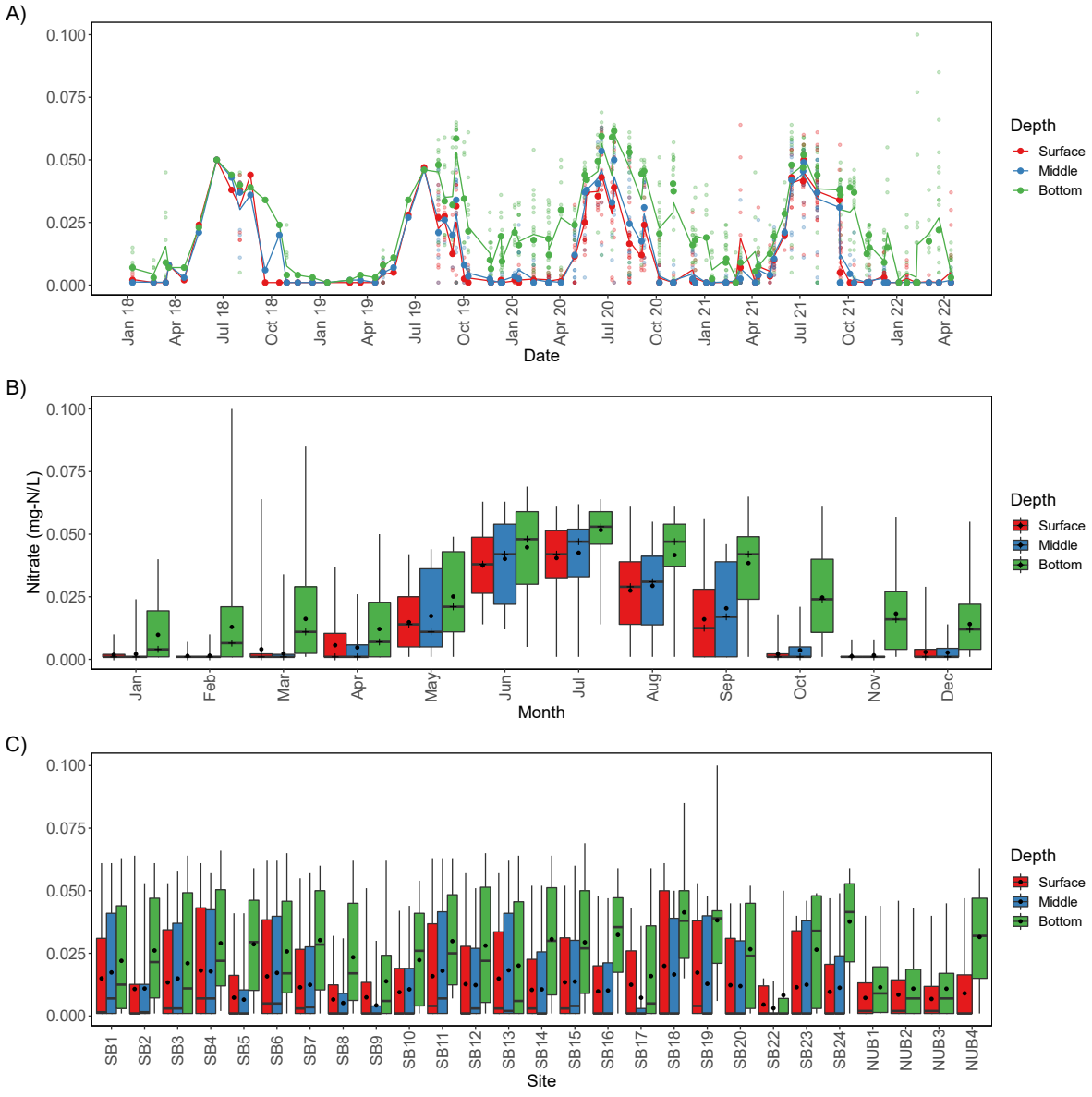
Spatial and temporal variation in total ammoniacal nitrogen (mg-N/L) values for surface, middle and bottom samples collected across Storm Bay. A) monthly ammonia for all sites through time with the means for surface, middle (10 m, excluding NUB1-4) and bottom plotted as lines. B) variation in ammonia across the year, with all data from every site pooled for each month. C) variation in ammonia for each site pooled over time. In b) and c) the boxplots show the mean, median and the 25th and 75th percentiles.



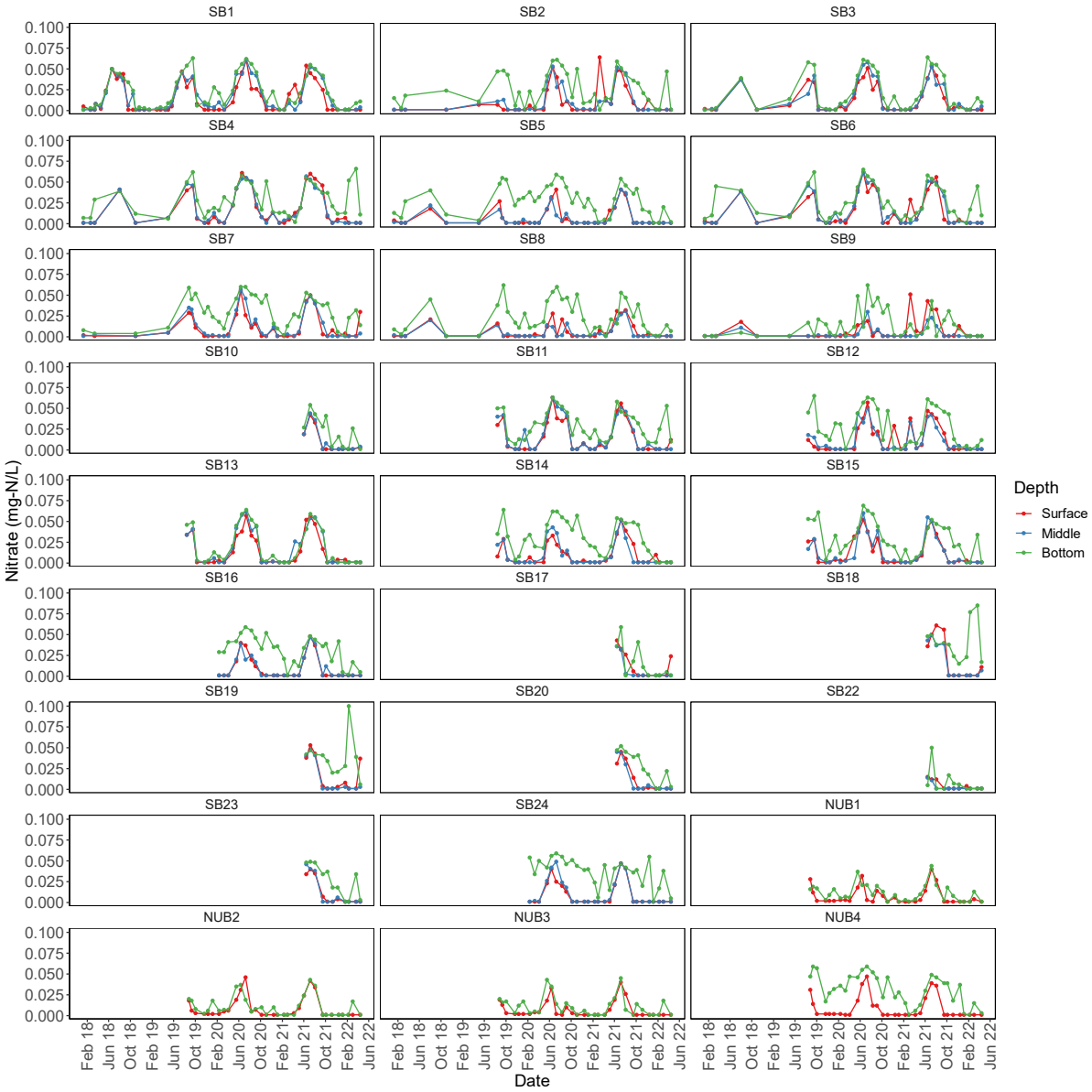
Spatial and temporal variation in total ammoniacal nitrogen (mg-N/L) values for surface, middle (10 m, excluding NUB1-4) and bottom samples collected across Storm Bay.



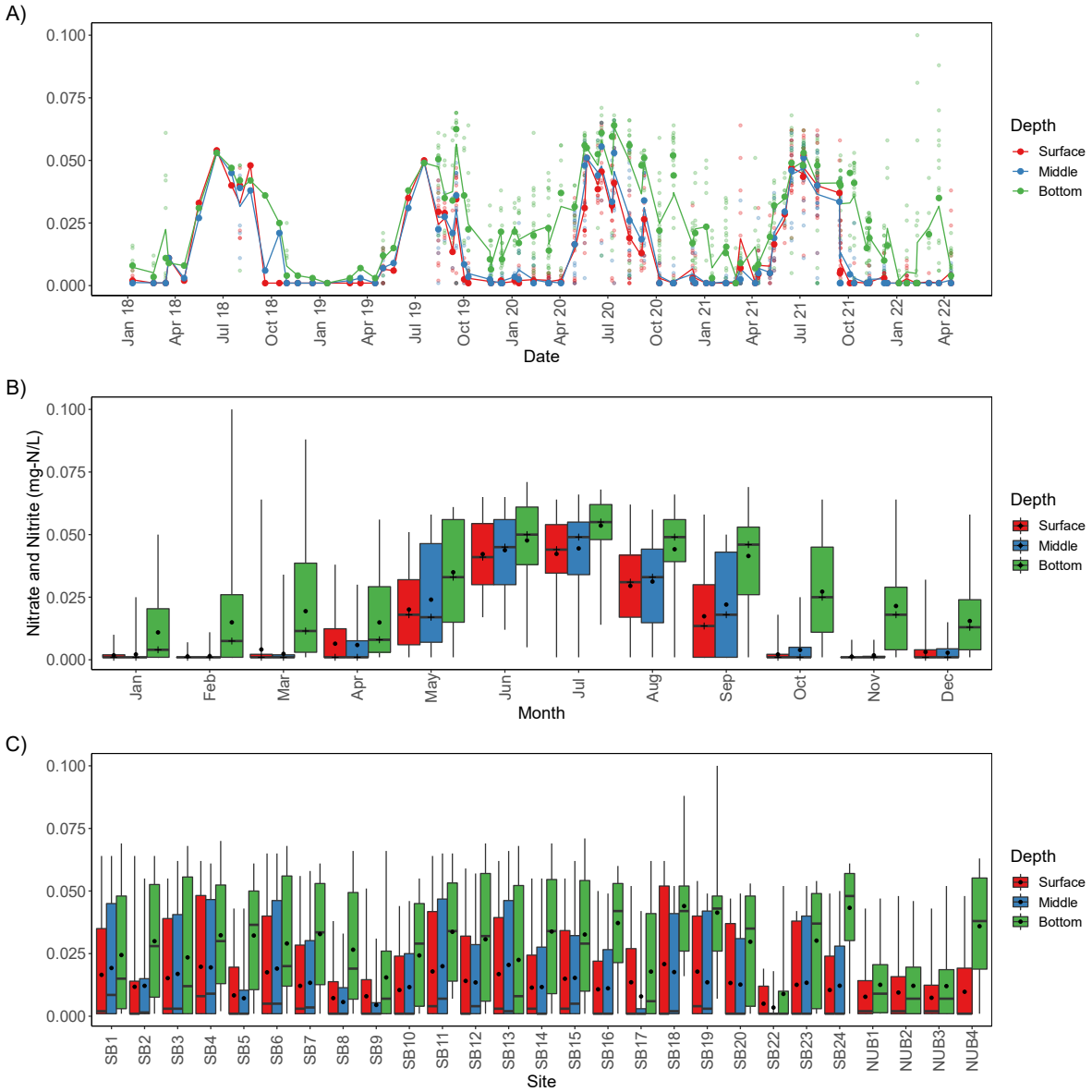
Spatial and temporal variation in nitrate (mg-N/L) values for surface, middle (10 m, excluding NUB1-4) and bottom samples collected across Storm Bay. A) monthly nitrate for all sites through time with the means for surface, middle and bottom plotted as lines. B) variation in nitrate across the year, with all data from every site pooled for each month. C) variation in nitrate for each site pooled over time. In B) and C) the boxplots show the mean, median and the 25th and 75th percentiles.



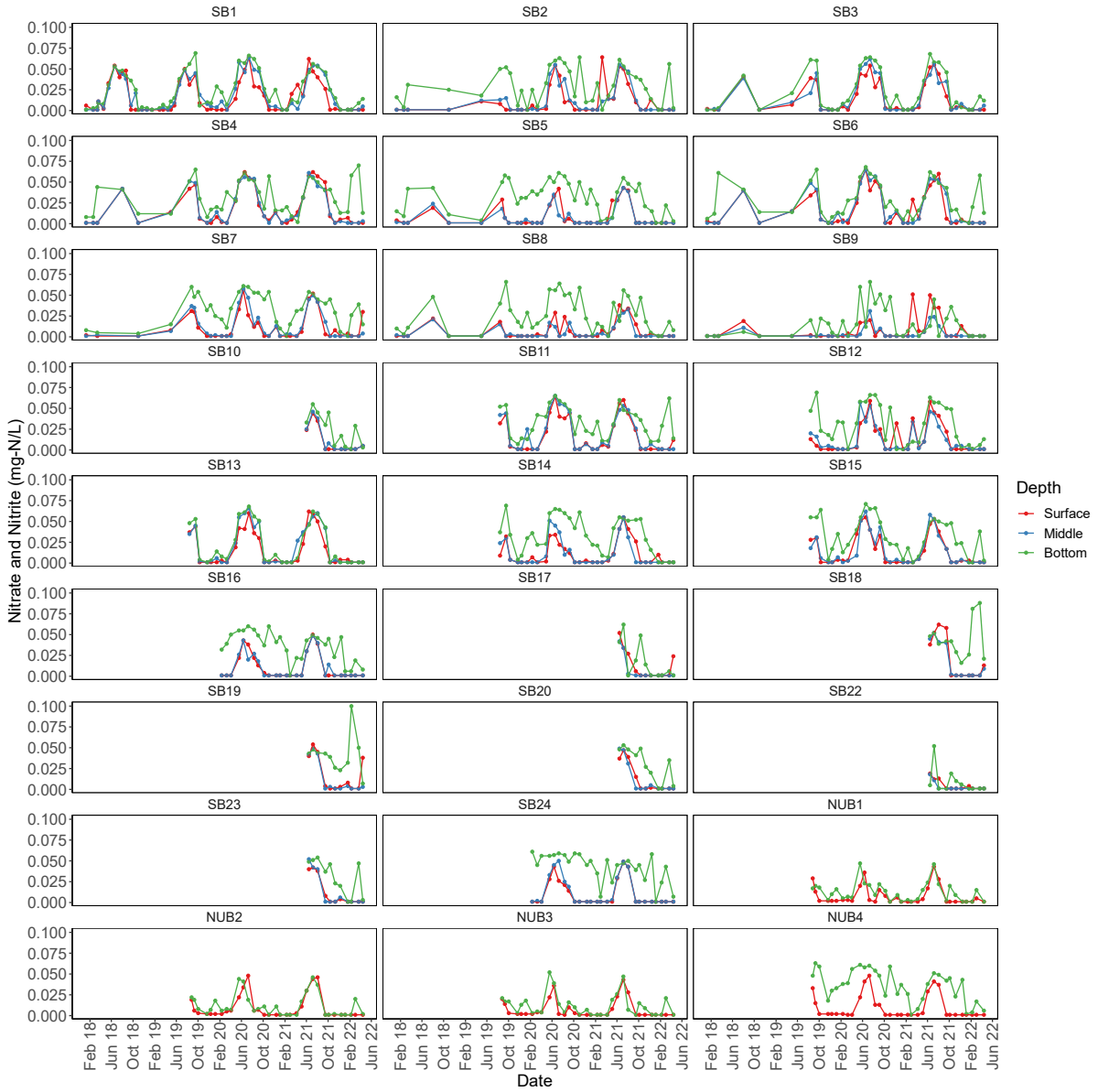
Spatial and temporal variation in nitrate (mg-N/L) values for surface, middle (10 m, excluding NUB1-4) and bottom samples collected across Storm Bay.



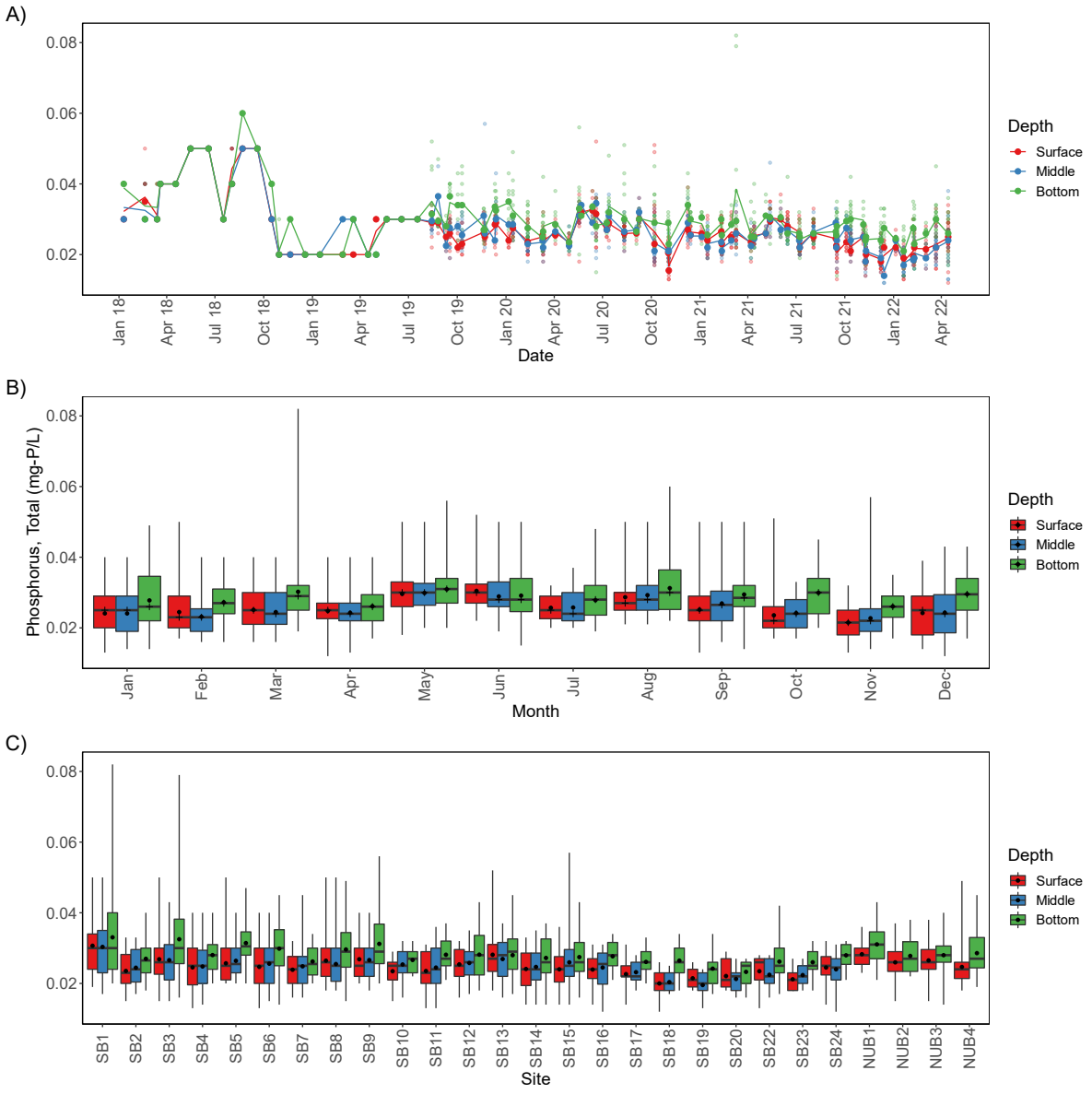
Spatial and temporal variation in nitrate and nitrite (mg-N/L) values for surface, middle (10 m, excluding NUB1-4) and bottom samples collected across Storm Bay. A) monthly nitrate and nitrite for all sites through time with the means for surface, middle and bottom plotted as lines, B) variation in nitrate and nitrite across the year, with all data from every site pooled for each month. C) variation in nitrate and nitrite for each site pooled over time, and D) variation in nitrate and nitrite at each site through time. In b) and c) the boxplots show the mean, median and the 25th and 75th percentiles.



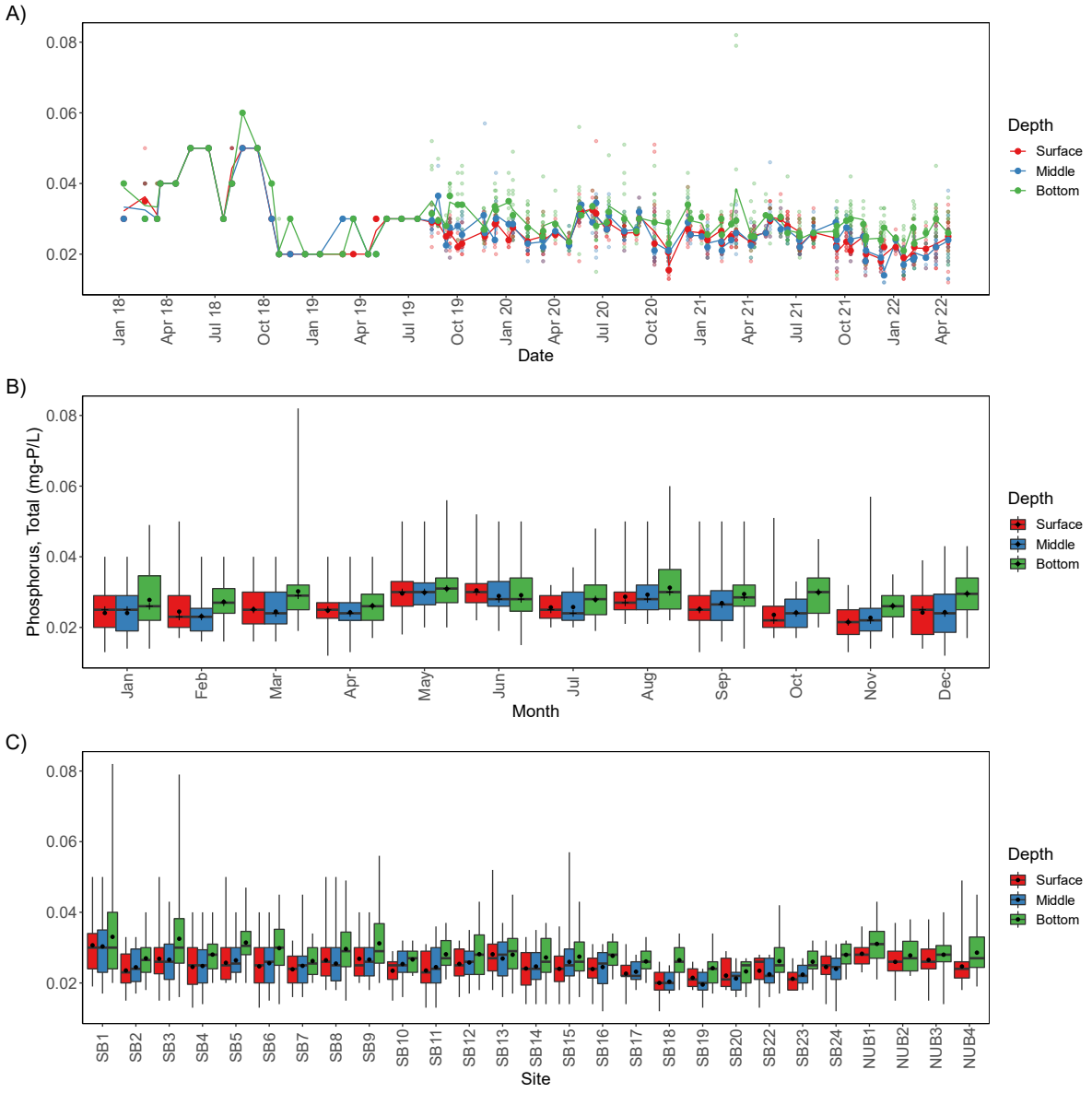
Spatial and temporal variation in nitrate and nitrite (mg-N/L) values for surface, middle (10 m, excluding NUB1-4) and bottom samples collected across Storm Bay.



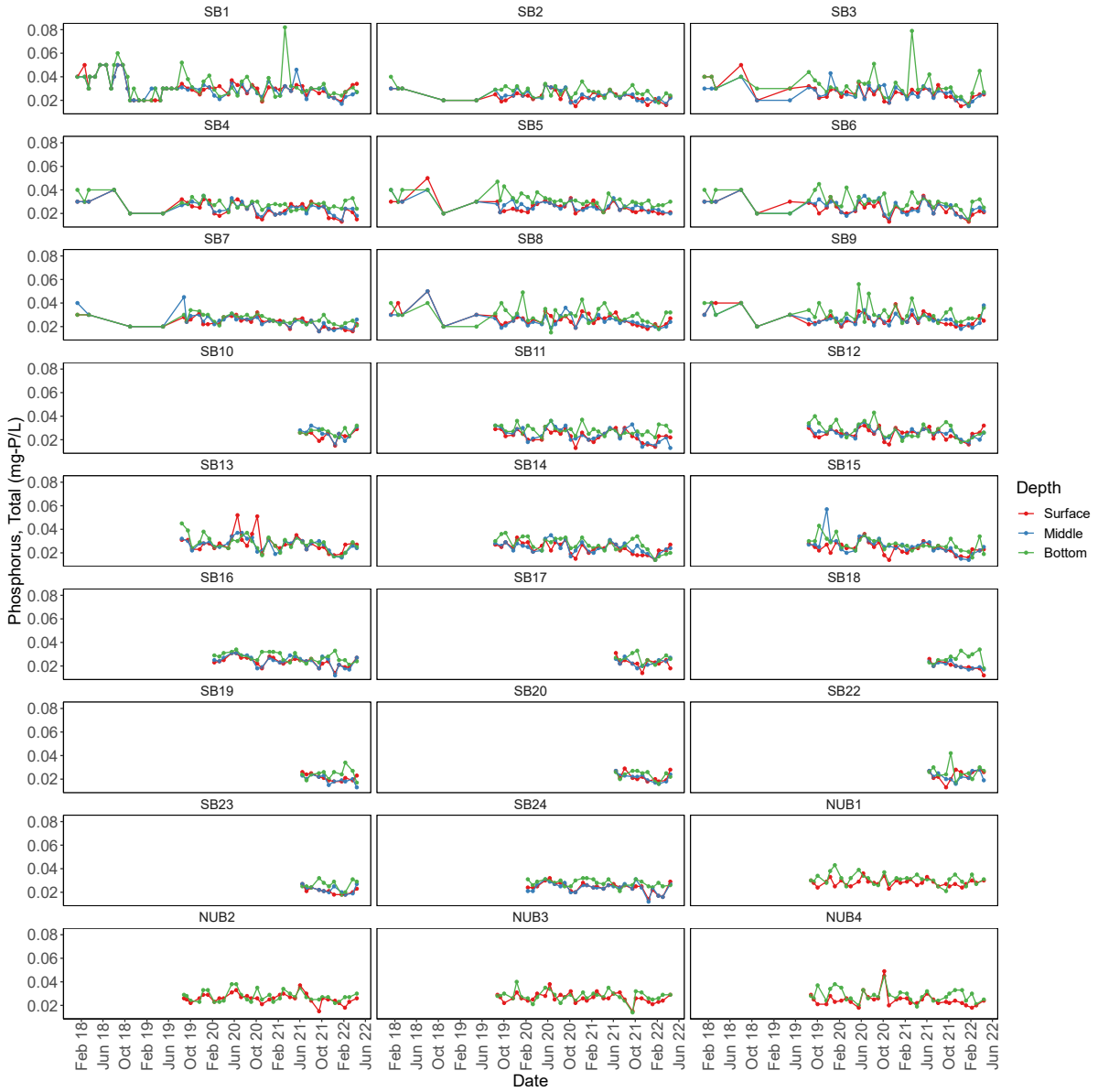
Spatial and temporal variation in total phosphorus (mg-P/L) values for surface, middle (10 m, excluding NUB1-4) and bottom samples collected across Storm Bay. A) monthly total phosphorus for all sites through time with the means for surface, middle (10 m, excluding NUB1-4) and bottom plotted as lines B) variation in total phosphorus across the year, with all data from every site pooled for each month. C) variation in total phosphorus for each site pooled over time, and D) variation in total phosphorus at each site through time. In b) and c) the boxplots show the mean, median and the 25th and 75th percentiles.



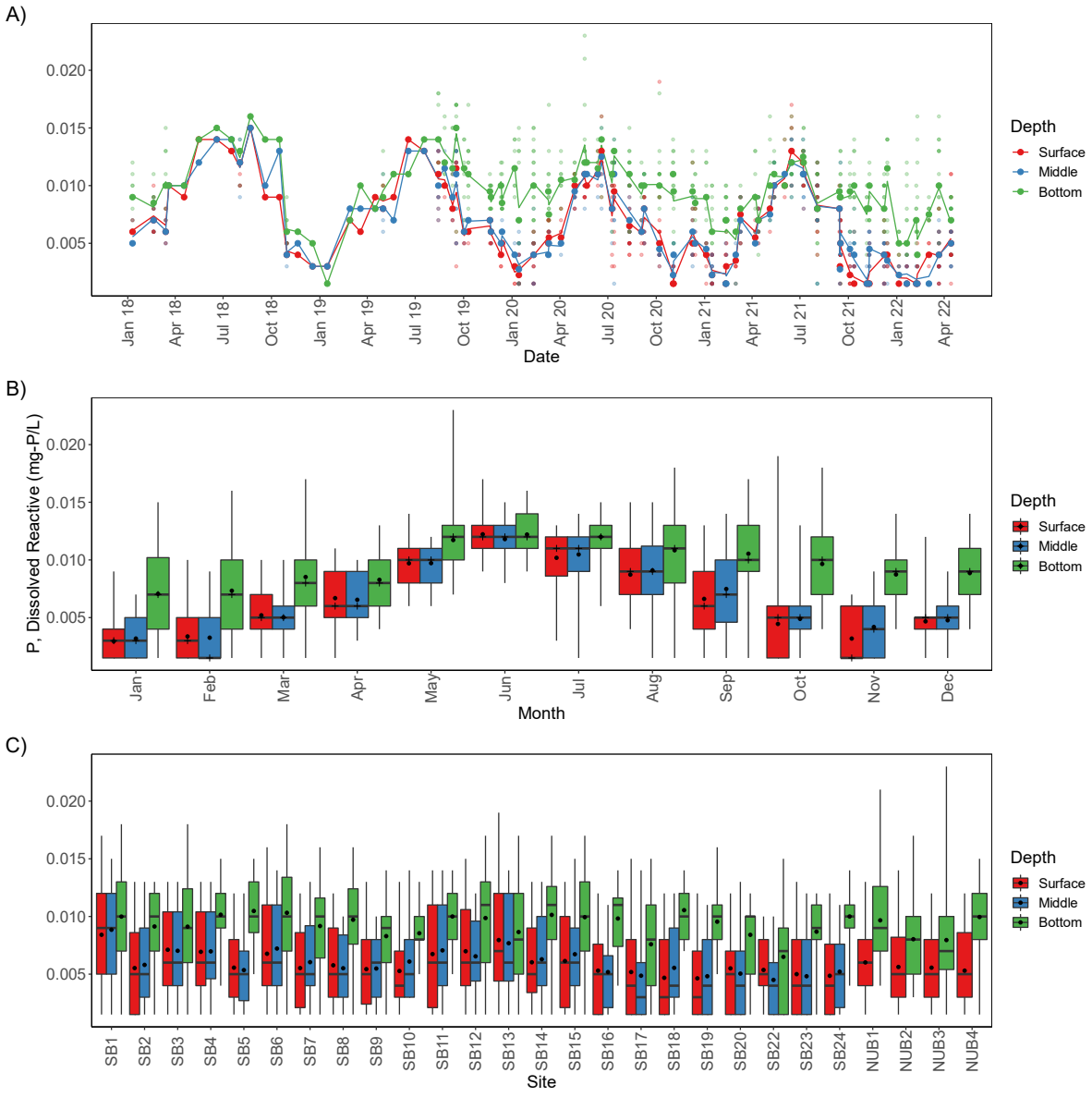
Spatial and temporal variation in total phosphorus (mg-P/L) values for surface, middle (10 m, excluding NUB1-4) and bottom samples collected across Storm Bay. A) monthly total phosphorus for all sites through time with the means for surface, middle (10 m, excluding NUB1-4) and bottom plotted as lines B) variation in total phosphorus across the year, with all data from every site pooled for each month. C) variation in total phosphorus for each site pooled over time, and D) variation in total phosphorus at each site through time. In b) and c) the boxplots show the mean, median and the 25th and 75th percentiles.



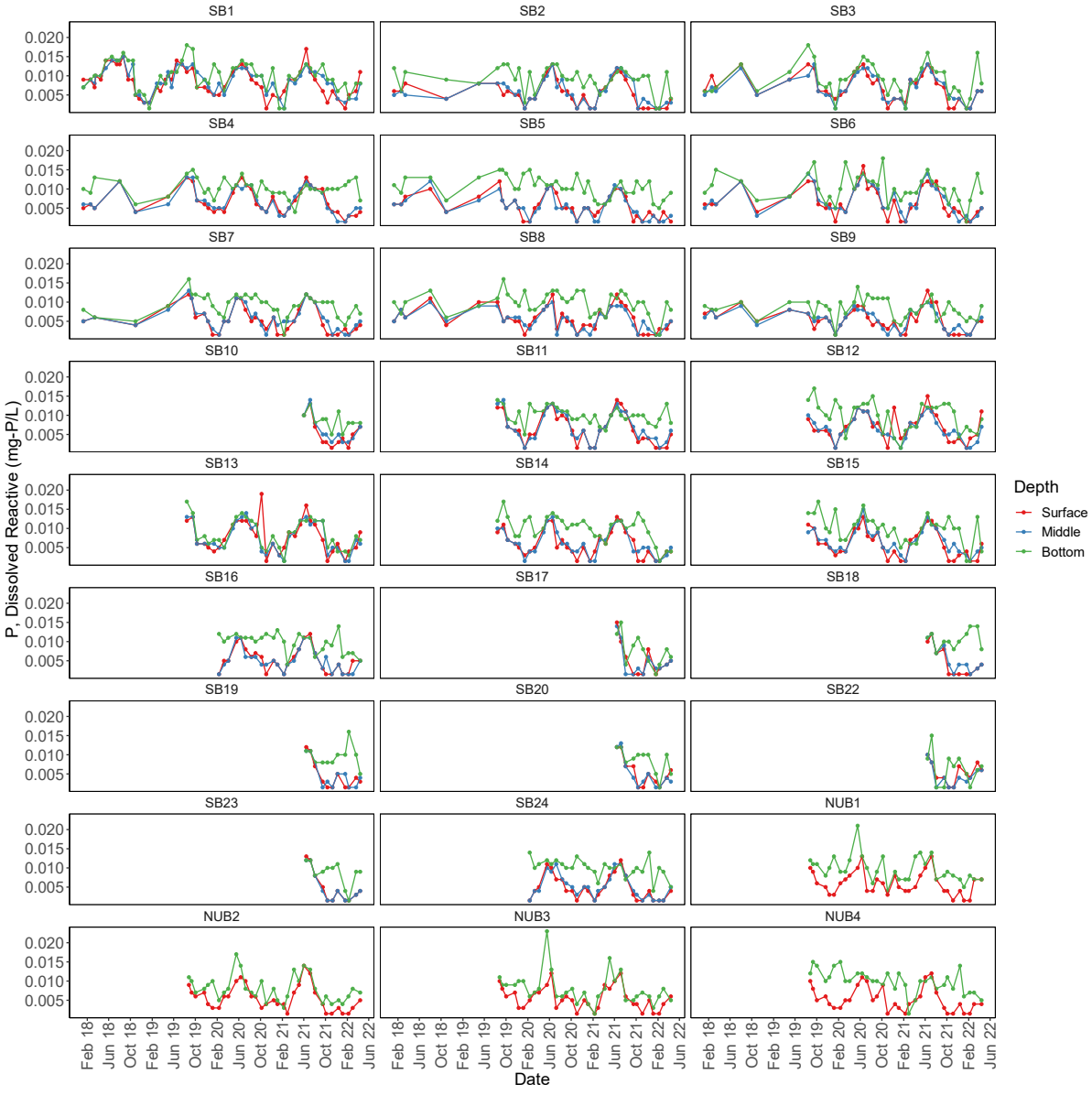
Spatial and temporal variation in total phosphorus (mg-P/L) values for surface, middle (10 m, excluding NUB1-4) and bottom samples collected across Storm Bay.



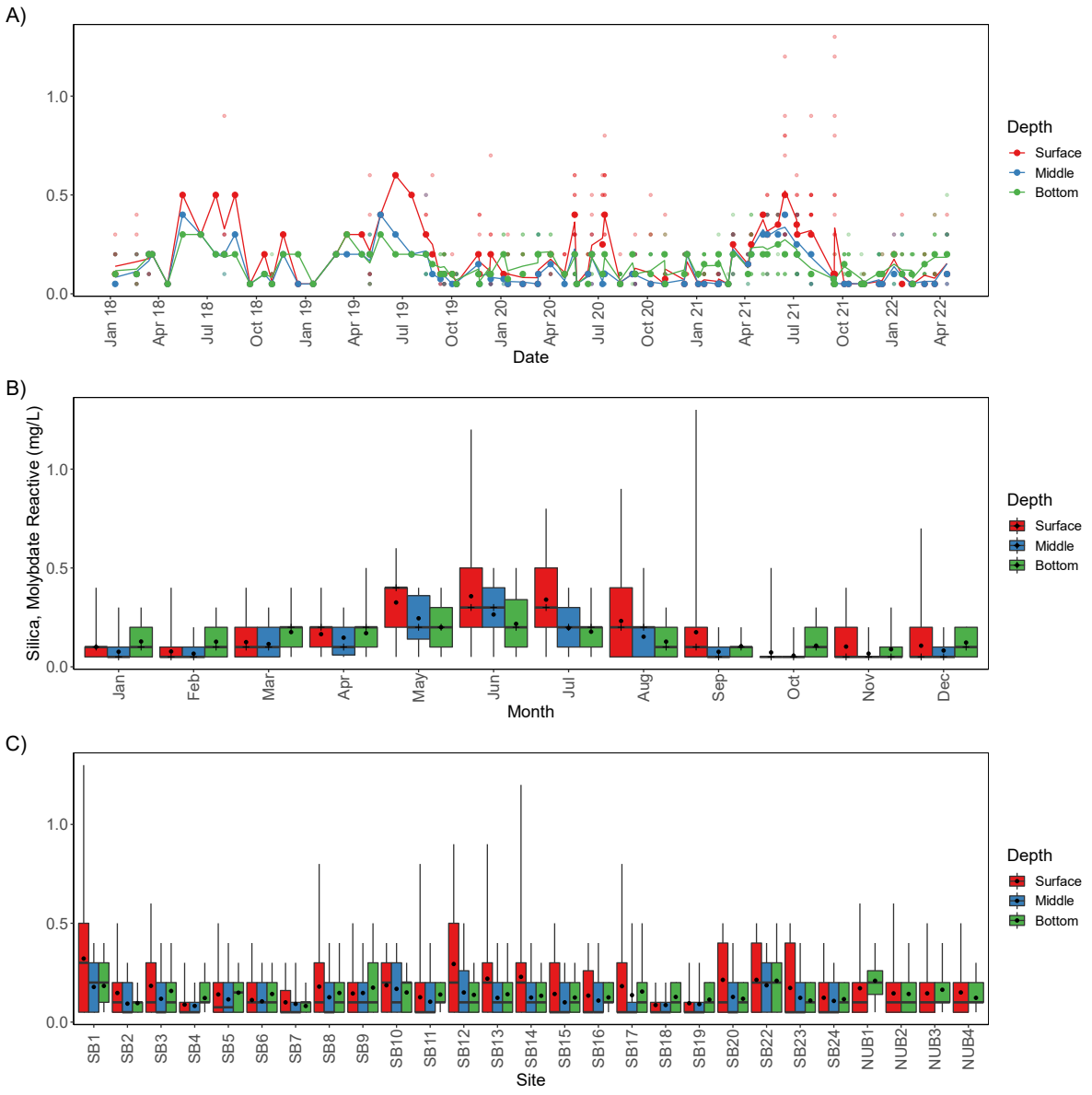
Spatial and temporal variation in dissolved reactive phosphorus (mg-P/L, DRP) values for surface, middle (10 m, excluding NUB1-4) and bottom samples collected across Storm Bay. A) monthly DRP for all sites through time with the means for surface, middle and bottom plotted as lines. B) variation in DRP across the year, with all data from every site pooled for each month. C) variation in DRP for each site pooled over time, and D) variation in DRP at each site through time. In B) and C) the boxplots show the mean, median and the 25th and 75th percentiles.



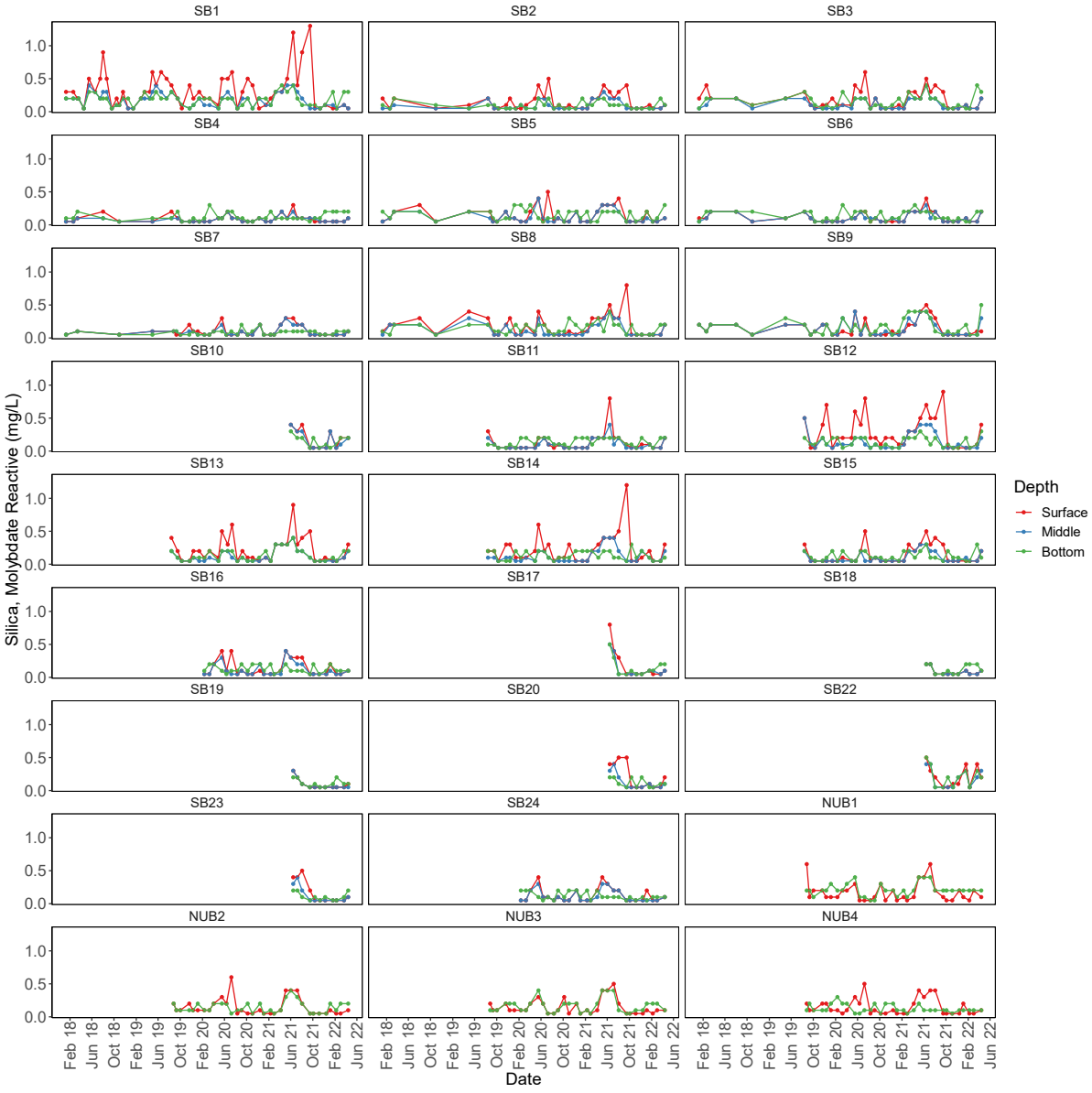
Spatial and temporal variation in dissolved reactive phosphorus (mg-P/L, DRP) values for surface, middle (10 m, excluding NUB1-4) and bottom samples collected across Storm Bay.



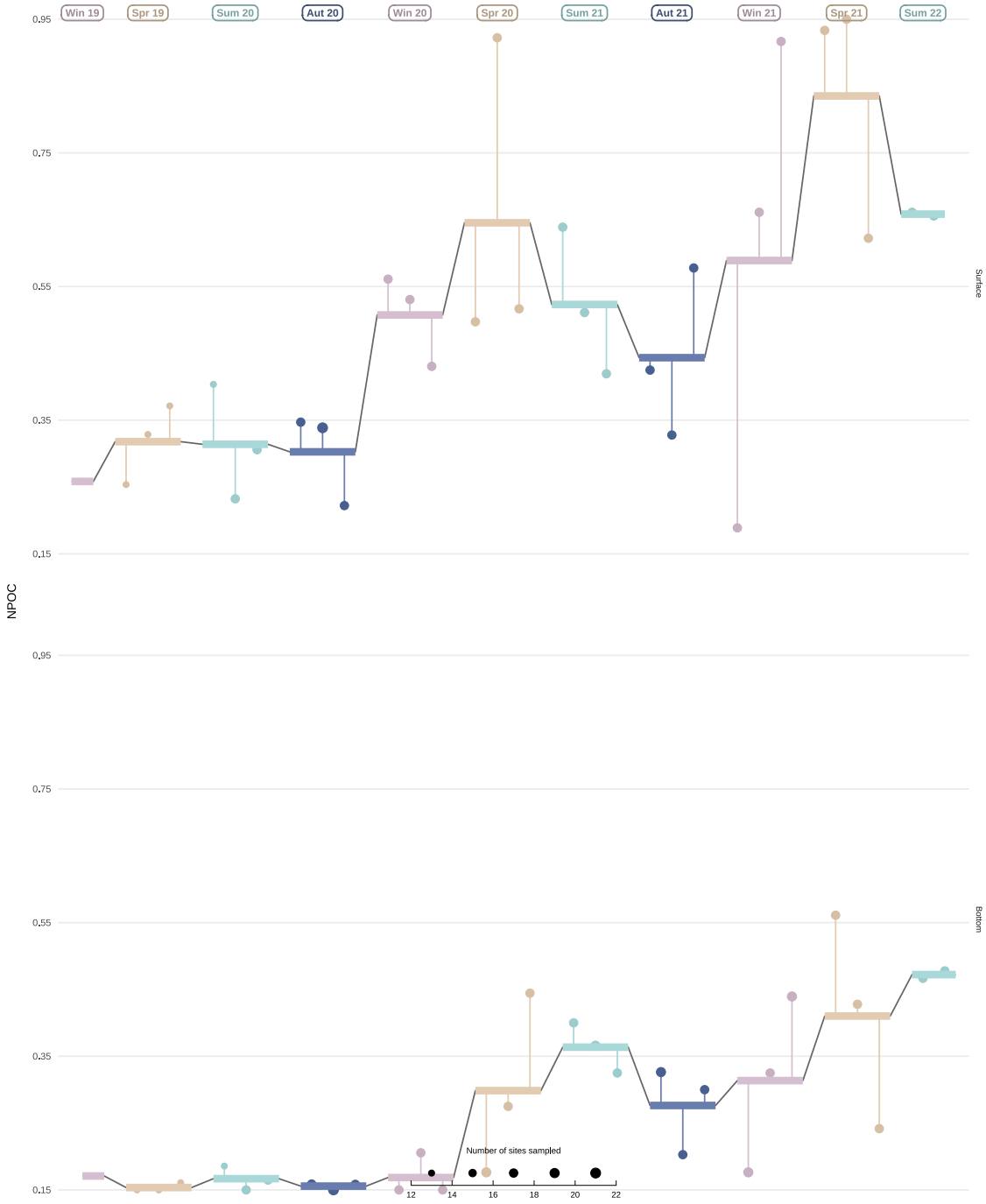
Spatial and temporal variation in silica molybdate reactive (mg/L) values for surface, middle (10 m, excluding NUB1-4) and bottom samples collected across Storm Bay. A) monthly silica for all sites through time with the means for surface, middle and bottom plotted as lines. B) variation in silica across the year, with all data from every site pooled for each month. C) variation in silica for each site pooled over time. In B) and C) the boxplots show the mean, median and the 25th and 75th percentiles.



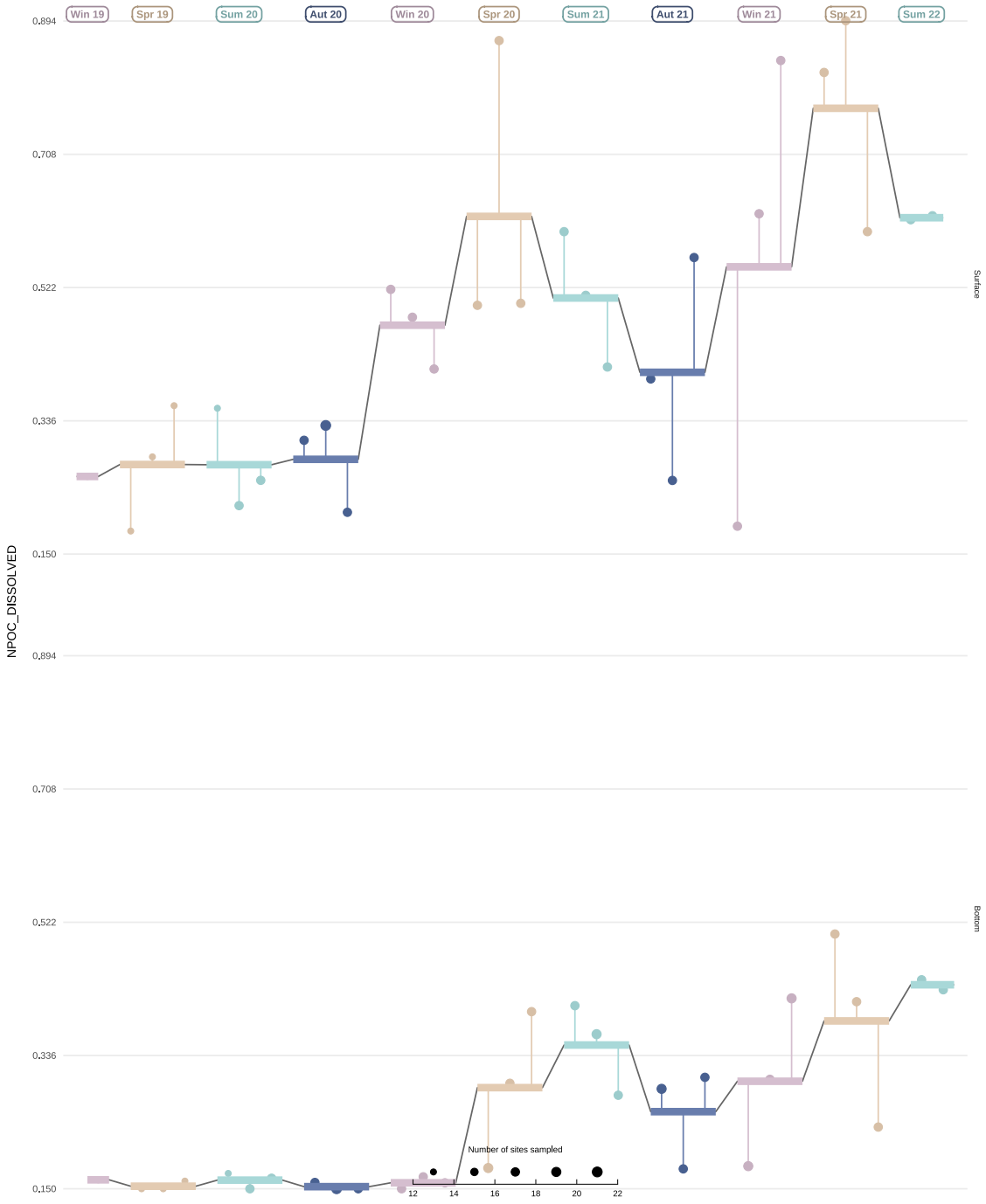
Spatial and temporal variation in silica molybdate reactive (mg/L) values for surface, middle (10 m, excluding NUB1-4) and bottom samples collected across Storm Bay.



Temporal variation in seawater NPOC (mg/L, non-purgeable organic carbon) at the consistently monitored sites through time (SB1, SB2, SB3, SB4, SB5, SB6, SB7, SB8, SB9, SB11, SB12, SB13, SB14, SB15, SB16, SB24, NUB1, NUB2, NUB3, NUB4, YB4, SBM4). Lollipop plot showing seasonal means (coloured lines) and survey means (dots) in the i) surface and ii) bottom waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). Note: Sampling for NPOC dissolved total ceased in summer 2022.

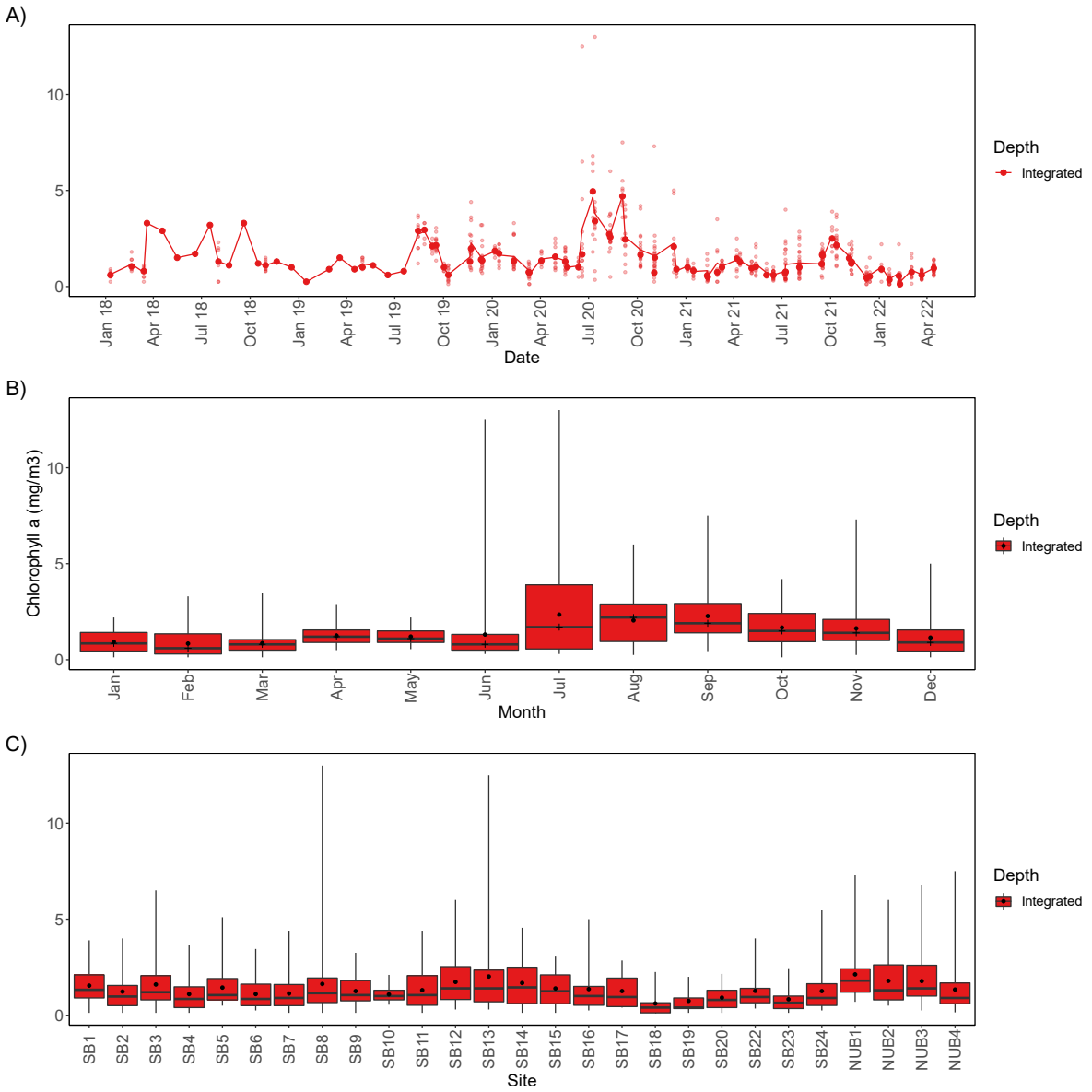


Temporal variation in seawater NPOC dissolved (mg/L, non-purgeable organic carbon dissolved) at the consistently monitored sites through time (SB1, SB2, SB3, SB4, SB5, SB6, SB7, SB8, SB9, SB11, SB12, SB13, SB14, SB15, SB16, SB24, NUB1, NUB2, NUB3, NUB4, YB4, SBM4). Lollipop plot showing seasonal means (coloured lines) and survey means (dots) in the i) surface and ii) bottom waters of Storm Bay across all sites (size of the circle indicates the number of sites sampled). Note: Sampling for NPOC dissolved total ceased in summer 2022.

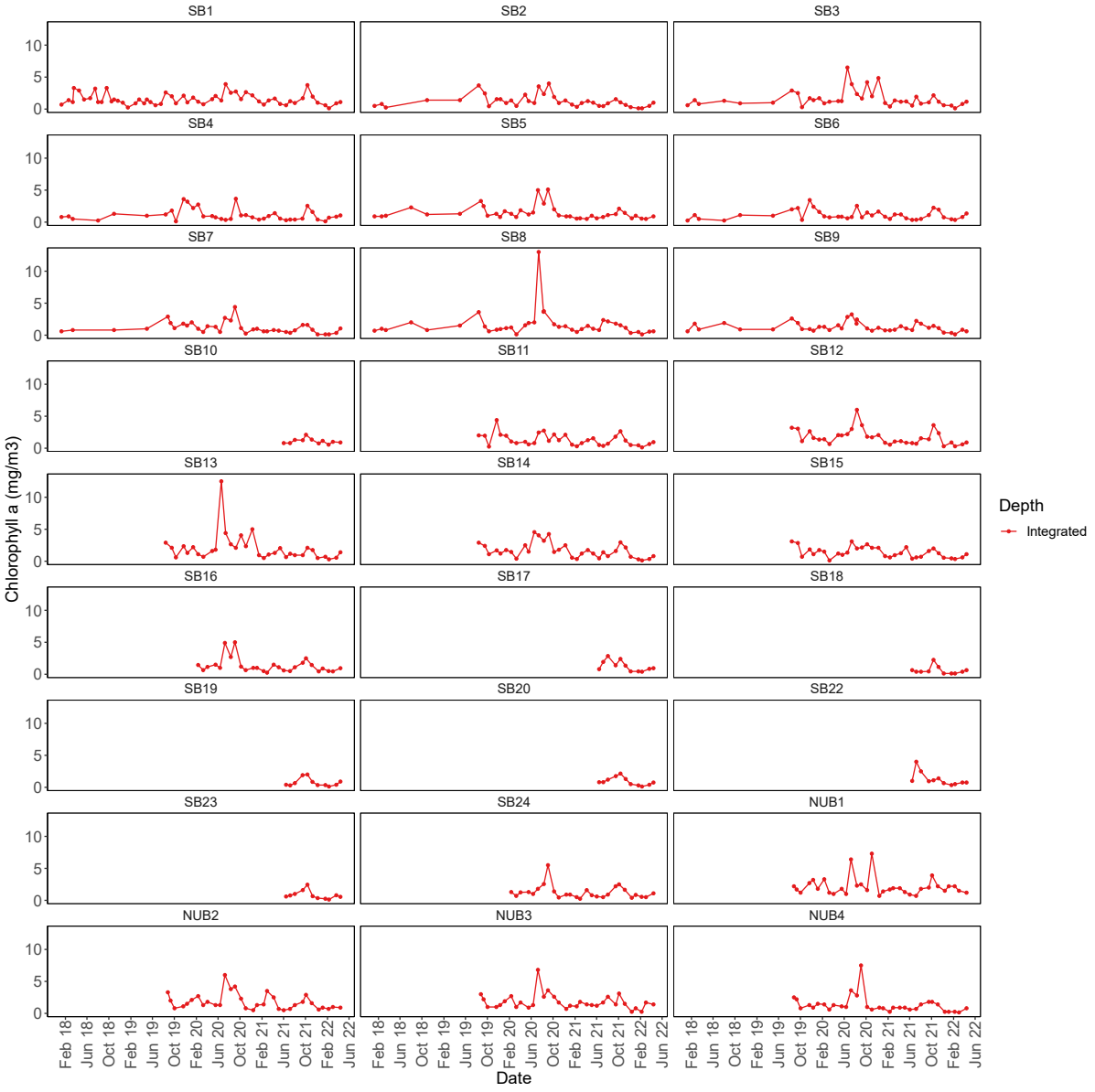


Appendix 3-3: Water column – phytoplankton biomass and communities

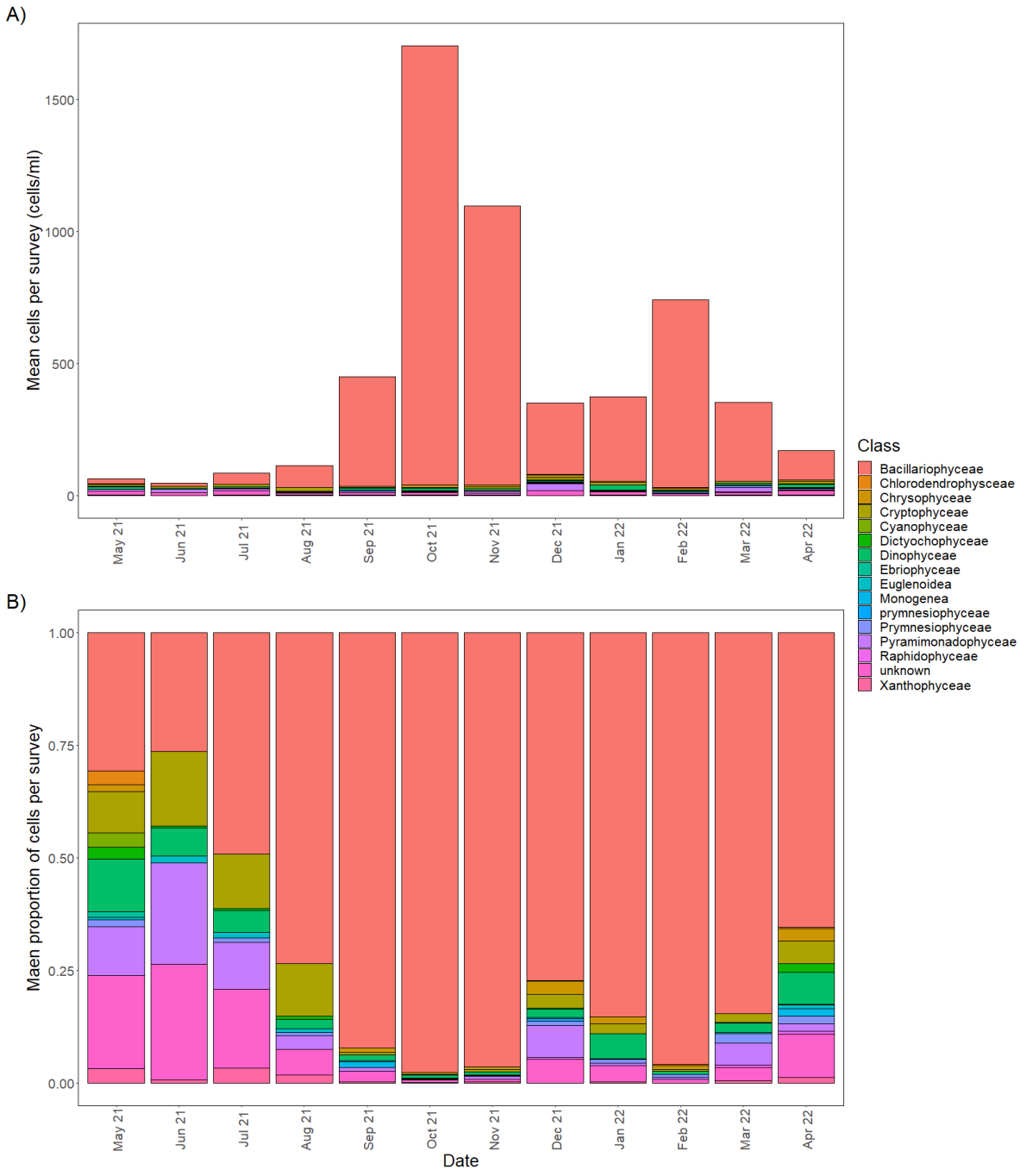
Spatial and temporal variation in chlorophyll *a* (mg/L) values for integrated samples collected across Storm Bay. A) monthly chlorophyll *a* for all sites through time with the means plotted as lines. B) variation in chlorophyll *a* across the year, with all data from every site pooled for each month. C) variation in chlorophyll *a* for each site pooled over time. In B) and C) the boxplots show the mean, median and the 25th and 75th percentiles.



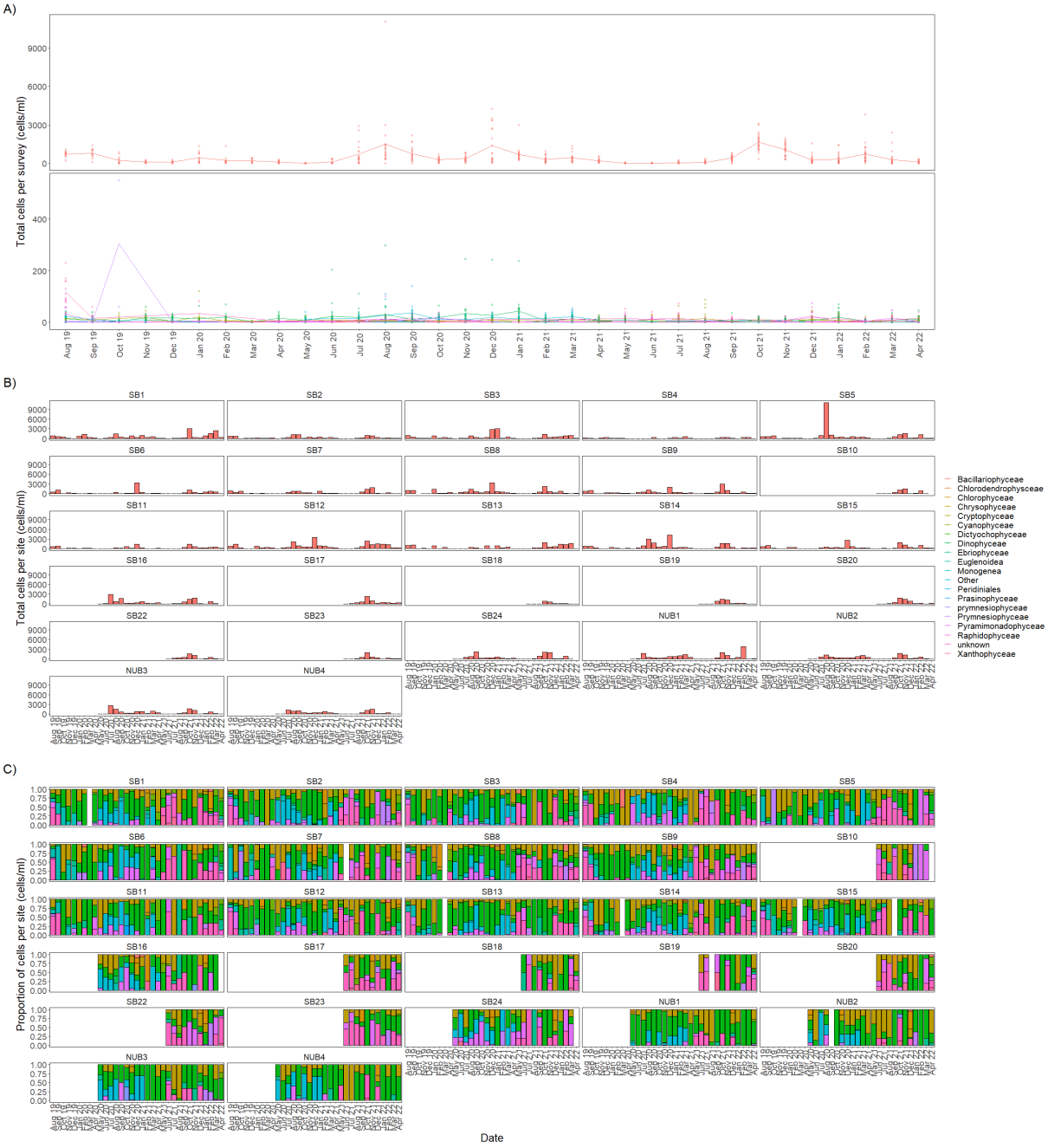
Spatial and temporal variation in chlorophyll *a* (mg/L) values for integrated samples collected across Storm Bay.



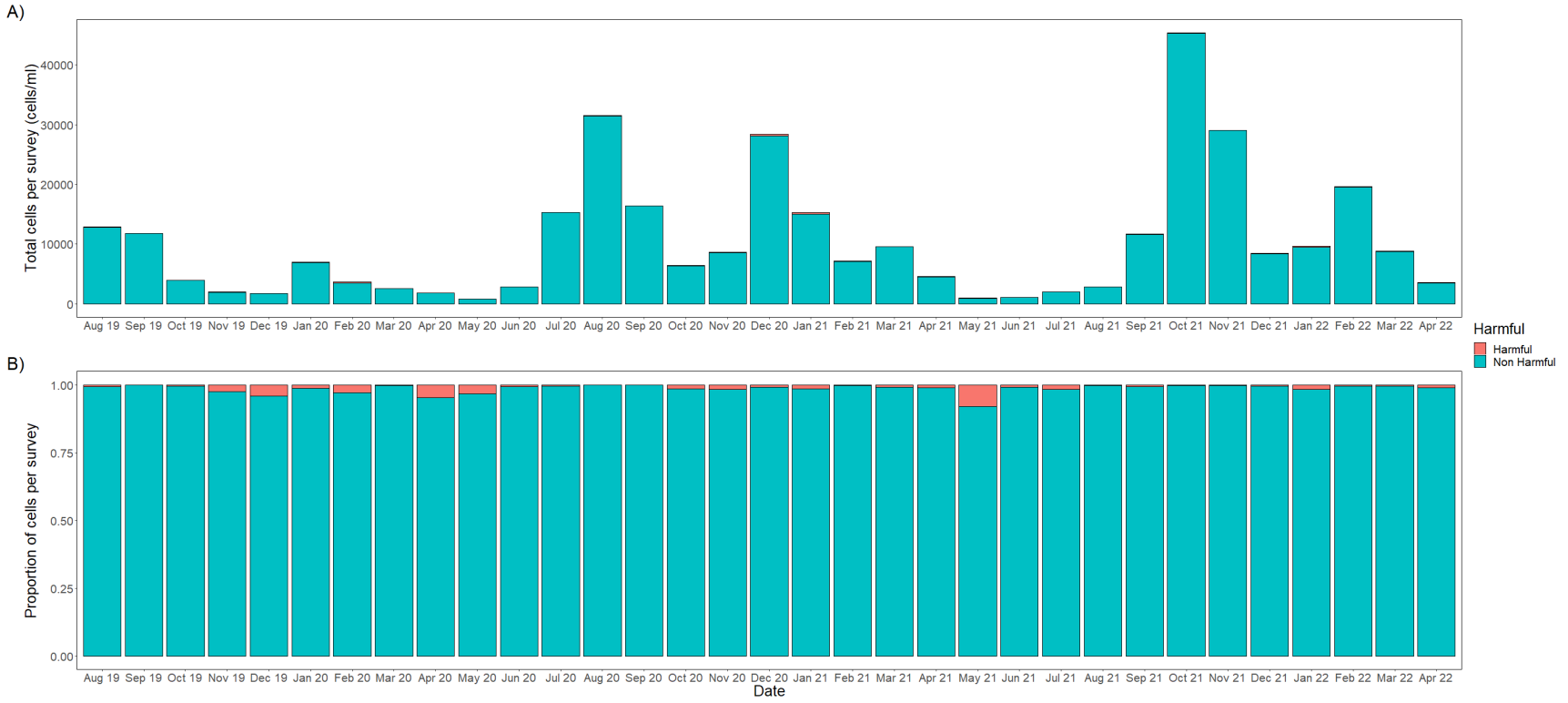
The A) mean densities of phytoplankton (cells/mL per site for each survey event) by class, and B) the relative proportion of phytoplankton (cells/mL per site for each date) by class for samples collected across Storm Bay.



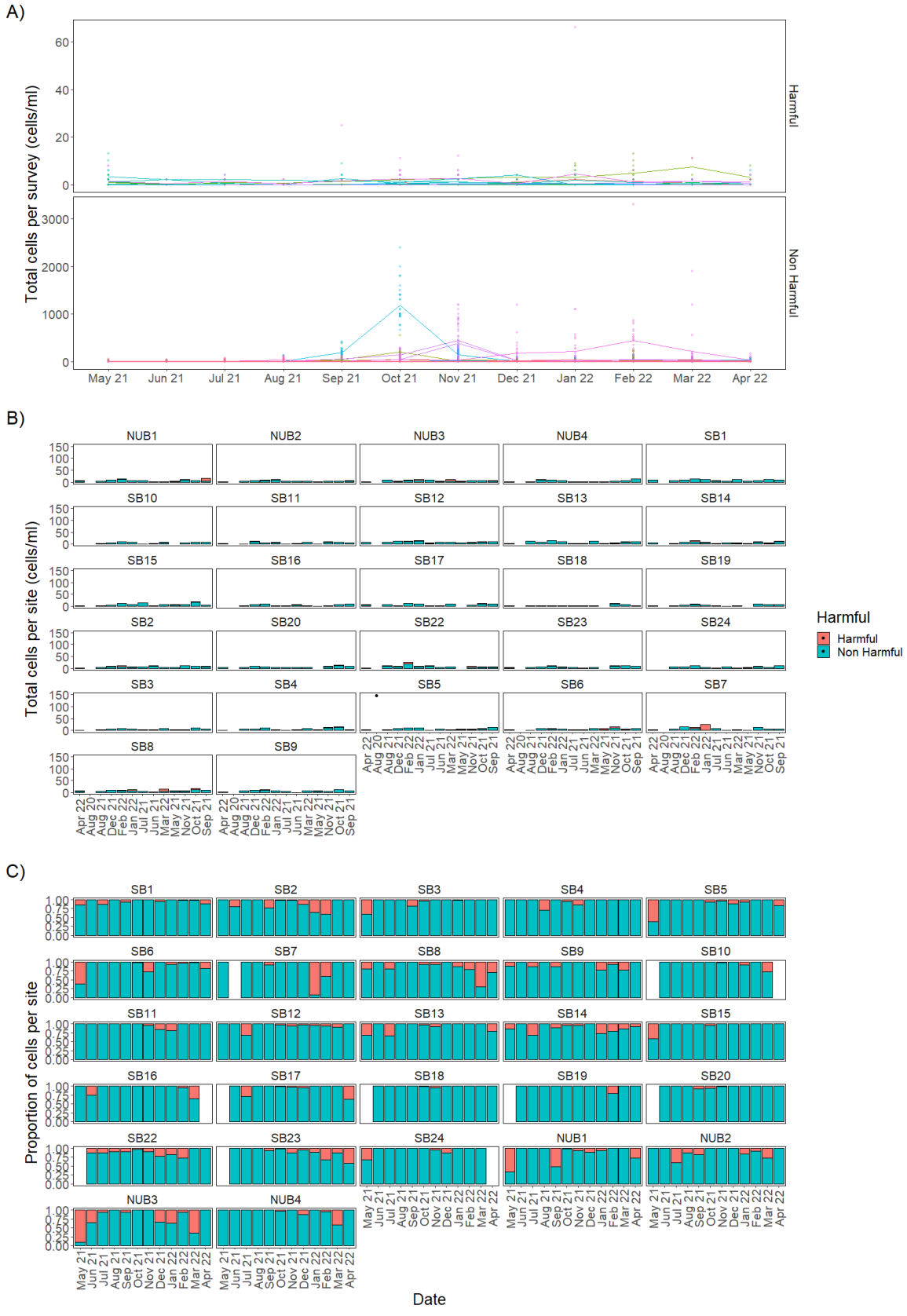
Spatial and temporal variation in the density (cells/mL per site for each month) of phytoplankton collected across Storm Bay. A) densities per month for all sites through time with the means plotted as lines for Bacillariophyceae and all other classes, B) total density for each site through time, and C) relative proportion of all classes excluding Bacillariophyceae at each site through time.



The A) mean densities of phytoplankton (cells/mL per site for each month) and the B) relative abundance of phytoplankton (cells/mL per site for each month) of harmful and non-harmful phytoplankton, for samples across Storm Bay.



Spatial and temporal variation in the densities of harmful and non-harmful phytoplankton (cells/mL per site for each month) across Storm Bay. A) density of harmful species only, integrated across all sites through time with the means plotted as lines, B) density at each site through time, and C) relative proportion at each site through time.



Appendix 3-4: Water quality power analysis results

Power analysis results for the different scenarios, for three different effect sizes (50%, 100% and 200% of the trigger levels) and across the two regions and for all of Storm Bay. These results were used to generate Figures 3-44 – 3-46.

Environmental Variables	Depth	Region	Effect Size (%)	Power (%)	Scenario
TAN (mg-N/L)	Surface	80	50	8.5	1
TAN (mg-N/L)	Bottom	80	50	12	1
TN (mg-N/L)	Surface	80	50	18	1
TN (mg-N/L)	Bottom	80	50	18.5	1
Nitrate + nitrate (mg/L)	Surface	80	50	46.5	1
Nitrate + nitrate (mg/L)	Bottom	80	50	26	1
TP (mg-P/L)	Surface	80	50	84	1
TP (mg-P/L)	Bottom	80	50	48.5	1
DRP (mg-P/L)	Surface	80	50	62.5	1
DRP (mg-P/L)	Bottom	80	50	61.5	1
DO (mg/L)	Surface	80	50	32	1
DO (mg/L)	Bottom	80	50	49.5	1
Chl-a (mg/m^3)	Integrated	80	50	10	1
TAN (mg-N/L)	Surface	80	50	41.5	1
TAN (mg-N/L)	Bottom	80	50	32	1
TN (mg-N/L)	Surface	80	50	37.5	1
TN (mg-N/L)	Bottom	80	50	25.5	1
Nitrate + nitrate (mg/L)	Surface	80	50	19.5	1
Nitrate + nitrate (mg/L)	Bottom	80	50	13.5	1
TP (mg-P/L)	Surface	80	50	83	1
TP (mg-P/L)	Bottom	80	50	75	1
DRP (mg-P/L)	Surface	80	50	12.5	1
DRP (mg-P/L)	Bottom	80	50	15	1
DO (mg/L)	Surface	80	50	32.5	1
DO (mg/L)	Bottom	80	50	31	1
Chl-a (mg/m^3)	Integrated	80	50	11	1
TAN (mg-N/L)	Surface	80	50	16.5	2
TAN (mg-N/L)	Bottom	80	50	22.5	2
TN (mg-N/L)	Surface	80	50	33	2
TN (mg-N/L)	Bottom	80	50	32.5	2
Nitrate + nitrate (mg/L)	Surface	80	50	76.5	2
Nitrate + nitrate (mg/L)	Bottom	80	50	57	2
TP (mg-P/L)	Surface	80	50	100	2
TP (mg-P/L)	Bottom	80	50	80.5	2
DRP (mg-P/L)	Surface	80	50	88.5	2
DRP (mg-P/L)	Bottom	80	50	95	2
DO (mg/L)	Surface	80	50	46	2
DO (mg/L)	Bottom	80	50	90.5	2
Chl-a (mg/m^3)	Integrated	80	50	17	2
TAN (mg-N/L)	Surface	80	50	93.5	2
TAN (mg-N/L)	Bottom	80	50	68.5	2
TN (mg-N/L)	Surface	80	50	85	2
TN (mg-N/L)	Bottom	80	50	72.5	2
Nitrate + nitrate (mg/L)	Surface	80	50	50.5	2
Nitrate + nitrate (mg/L)	Bottom	80	50	30.5	2
TP (mg-P/L)	Surface	80	50	100	2

Environmental Variables	Depth	Region	Effect Size (%)	Power (%)	Scenario
TP (mg-P/L)	Bottom	80	50	100	2
DRP (mg-P/L)	Surface	80	50	46.5	2
DRP (mg-P/L)	Bottom	80	50	57.5	2
DO (mg/L)	Surface	80	50	87.5	2
DO (mg/L)	Bottom	80	50	75.5	2
Chl-a (mg/m^3)	Integrated	80	50	23.5	2
TAN (mg-N/L)	Surface	80	50	12	3
TAN (mg-N/L)	Bottom	80	50	20.5	3
TN (mg-N/L)	Surface	80	50	24	3
TN (mg-N/L)	Bottom	80	50	26.5	3
Nitrate + nitrate (mg/L)	Surface	80	50	59	3
Nitrate + nitrate (mg/L)	Bottom	80	50	43.5	3
TP (mg-P/L)	Surface	80	50	92	3
TP (mg-P/L)	Bottom	80	50	62.5	3
DRP (mg-P/L)	Surface	80	50	79.5	3
DRP (mg-P/L)	Bottom	80	50	87	3
DO (mg/L)	Surface	80	50	41.5	3
DO (mg/L)	Bottom	80	50	69	3
Chl-a (mg/m^3)	Integrated	80	50	12.5	3
TAN (mg-N/L)	Surface	80	50	68	3
TAN (mg-N/L)	Bottom	80	50	44.5	3
TN (mg-N/L)	Surface	80	50	57.5	3
TN (mg-N/L)	Bottom	80	50	45.5	3
Nitrate + nitrate (mg/L)	Surface	80	50	27	3
Nitrate + nitrate (mg/L)	Bottom	80	50	18	3
TP (mg-P/L)	Surface	80	50	97	3
TP (mg-P/L)	Bottom	80	50	90.5	3
DRP (mg-P/L)	Surface	80	50	23.5	3
DRP (mg-P/L)	Bottom	80	50	32.5	3
DO (mg/L)	Surface	80	50	57	3
DO (mg/L)	Bottom	80	50	50.5	3
Chl-a (mg/m^3)	Integrated	80	50	18.5	3
TAN (mg-N/L)	Surface	80	50	9	4
TAN (mg-N/L)	Bottom	80	50	22	4
TN (mg-N/L)	Surface	80	50	27.5	4
TN (mg-N/L)	Bottom	80	50	32.5	4
Nitrate + nitrate (mg/L)	Surface	80	50	77.5	4
Nitrate + nitrate (mg/L)	Bottom	80	50	62.5	4
TP (mg-P/L)	Surface	80	50	99	4
TP (mg-P/L)	Bottom	80	50	75.5	4
DRP (mg-P/L)	Surface	80	50	92	4
DRP (mg-P/L)	Bottom	80	50	96.5	4
DO (mg/L)	Surface	80	50	51.5	4
DO (mg/L)	Bottom	80	50	86	4
Chl-a (mg/m^3)	Integrated	80	50	16	4
TAN (mg-N/L)	Surface	80	50	95	4
TAN (mg-N/L)	Bottom	80	50	68	4
TN (mg-N/L)	Surface	80	50	88.5	4
TN (mg-N/L)	Bottom	80	50	80.5	4
Nitrate + nitrate (mg/L)	Surface	80	50	54	4
Nitrate + nitrate (mg/L)	Bottom	80	50	28.5	4

Environmental Variables	Depth	Region	Effect Size (%)	Power (%)	Scenario
TP (mg-P/L)	Surface	80	50	100	4
TP (mg-P/L)	Bottom	80	50	100	4
DRP (mg-P/L)	Surface	80	50	39.5	4
DRP (mg-P/L)	Bottom	80	50	56	4
DO (mg/L)	Surface	80	50	84.5	4
DO (mg/L)	Bottom	80	50	78	4
Chl-a (mg/m^3)	Integrated	80	50	28.5	4
TAN (mg-N/L)	Surface	93	100	19	1
TAN (mg-N/L)	Bottom	93	100	27	1
TN (mg-N/L)	Surface	93	100	38	1
TN (mg-N/L)	Bottom	93	100	36	1
Nitrate + nitrate (mg/L)	Surface	93	100	94.5	1
Nitrate + nitrate (mg/L)	Bottom	93	100	75	1
TP (mg-P/L)	Surface	93	100	100	1
TP (mg-P/L)	Bottom	93	100	91.5	1
DRP (mg-P/L)	Surface	93	100	96.5	1
DRP (mg-P/L)	Bottom	93	100	98.5	1
DO (mg/L)	Surface	93	100	73	1
DO (mg/L)	Bottom	93	100	97.5	1
Chl-a (mg/m^3)	Integrated	93	100	18	1
TAN (mg-N/L)	Surface	93	100	89	1
TAN (mg-N/L)	Bottom	93	100	75.5	1
TN (mg-N/L)	Surface	93	100	87	1
TN (mg-N/L)	Bottom	93	100	66	1
Nitrate + nitrate (mg/L)	Surface	93	100	50.5	1
Nitrate + nitrate (mg/L)	Bottom	93	100	29	1
TP (mg-P/L)	Surface	93	100	100	1
TP (mg-P/L)	Bottom	93	100	100	1
DRP (mg-P/L)	Surface	93	100	37	1
DRP (mg-P/L)	Bottom	93	100	50	1
DO (mg/L)	Surface	93	100	83	1
DO (mg/L)	Bottom	93	100	71	1
Chl-a (mg/m^3)	Integrated	93	100	30	1
TAN (mg-N/L)	Surface	93	100	35	2
TAN (mg-N/L)	Bottom	93	100	51.5	2
TN (mg-N/L)	Surface	93	100	78.5	2
TN (mg-N/L)	Bottom	93	100	73.5	2
Nitrate + nitrate (mg/L)	Surface	93	100	100	2
Nitrate + nitrate (mg/L)	Bottom	93	100	98	2
TP (mg-P/L)	Surface	93	100	100	2
TP (mg-P/L)	Bottom	93	100	100	2
DRP (mg-P/L)	Surface	93	100	100	2
DRP (mg-P/L)	Bottom	93	100	100	2
DO (mg/L)	Surface	93	100	94	2
DO (mg/L)	Bottom	93	100	100	2
Chl-a (mg/m^3)	Integrated	93	100	35.5	2
TAN (mg-N/L)	Surface	93	100	100	2
TAN (mg-N/L)	Bottom	93	100	100	2
TN (mg-N/L)	Surface	93	100	100	2
TN (mg-N/L)	Bottom	93	100	99.5	2
Nitrate + nitrate (mg/L)	Surface	93	100	95	2

Environmental Variables	Depth	Region	Effect Size (%)	Power (%)	Scenario
Nitrate + nitrate (mg/L)	Bottom	93	100	71.5	2
TP (mg-P/L)	Surface	93	100	100	2
TP (mg-P/L)	Bottom	93	100	100	2
DRP (mg-P/L)	Surface	93	100	94.5	2
DRP (mg-P/L)	Bottom	93	100	98.5	2
DO (mg/L)	Surface	93	100	100	2
DO (mg/L)	Bottom	93	100	100	2
Chl-a (mg/m^3)	Integrated	93	100	66	2
TAN (mg-N/L)	Surface	93	100	28.5	3
TAN (mg-N/L)	Bottom	93	100	42.5	3
TN (mg-N/L)	Surface	93	100	56.5	3
TN (mg-N/L)	Bottom	93	100	62.5	3
Nitrate + nitrate (mg/L)	Surface	93	100	98	3
Nitrate + nitrate (mg/L)	Bottom	93	100	97.5	3
TP (mg-P/L)	Surface	93	100	100	3
TP (mg-P/L)	Bottom	93	100	98	3
DRP (mg-P/L)	Surface	93	100	100	3
DRP (mg-P/L)	Bottom	93	100	100	3
DO (mg/L)	Surface	93	100	89	3
DO (mg/L)	Bottom	93	100	100	3
Chl-a (mg/m^3)	Integrated	93	100	28	3
TAN (mg-N/L)	Surface	93	100	100	3
TAN (mg-N/L)	Bottom	93	100	92.5	3
TN (mg-N/L)	Surface	93	100	98	3
TN (mg-N/L)	Bottom	93	100	91.5	3
Nitrate + nitrate (mg/L)	Surface	93	100	71	3
Nitrate + nitrate (mg/L)	Bottom	93	100	43	3
TP (mg-P/L)	Surface	93	100	100	3
TP (mg-P/L)	Bottom	93	100	100	3
DRP (mg-P/L)	Surface	93	100	62.5	3
DRP (mg-P/L)	Bottom	93	100	81	3
DO (mg/L)	Surface	93	100	98	3
DO (mg/L)	Bottom	93	100	94.5	3
Chl-a (mg/m^3)	Integrated	93	100	46	3
TAN (mg-N/L)	Surface	93	100	26.5	4
TAN (mg-N/L)	Bottom	93	100	51.5	4
TN (mg-N/L)	Surface	93	100	71.5	4
TN (mg-N/L)	Bottom	93	100	76	4
Nitrate + nitrate (mg/L)	Surface	93	100	100	4
Nitrate + nitrate (mg/L)	Bottom	93	100	99	4
TP (mg-P/L)	Surface	93	100	100	4
TP (mg-P/L)	Bottom	93	100	100	4
DRP (mg-P/L)	Surface	93	100	100	4
DRP (mg-P/L)	Bottom	93	100	100	4
DO (mg/L)	Surface	93	100	95.5	4
DO (mg/L)	Bottom	93	100	100	4
Chl-a (mg/m^3)	Integrated	93	100	30	4
TAN (mg-N/L)	Surface	93	100	100	4
TAN (mg-N/L)	Bottom	93	100	100	4
TN (mg-N/L)	Surface	93	100	100	4
TN (mg-N/L)	Bottom	93	100	100	4

Environmental Variables	Depth	Region	Effect Size (%)	Power (%)	Scenario
Nitrate + nitrate (mg/L)	Surface	93	100	95	4
Nitrate + nitrate (mg/L)	Bottom	93	100	74	4
TP (mg-P/L)	Surface	93	100	100	4
TP (mg-P/L)	Bottom	93	100	100	4
DRP (mg-P/L)	Surface	93	100	89	4
DRP (mg-P/L)	Bottom	93	100	98	4
DO (mg/L)	Surface	93	100	100	4
DO (mg/L)	Bottom	93	100	100	4
Chl-a (mg/m^3)	Integrated	93	100	75	4
TAN (mg-N/L)	Surface	SB	200	50	1
TAN (mg-N/L)	Bottom	SB	200	74	1
TN (mg-N/L)	Surface	SB	200	87	1
TN (mg-N/L)	Bottom	SB	200	89	1
Nitrate + nitrate (mg/L)	Surface	SB	200	100	1
Nitrate + nitrate (mg/L)	Bottom	SB	200	100	1
TP (mg-P/L)	Surface	SB	200	100	1
TP (mg-P/L)	Bottom	SB	200	100	1
DRP (mg-P/L)	Surface	SB	200	100	1
DRP (mg-P/L)	Bottom	SB	200	100	1
DO (mg/L)	Surface	SB	200	99	1
DO (mg/L)	Bottom	SB	200	100	1
Chl-a (mg/m^3)	Integrated	SB	200	39	1
TAN (mg-N/L)	Surface	SB	200	100	1
TAN (mg-N/L)	Bottom	SB	200	100	1
TN (mg-N/L)	Surface	SB	200	100	1
TN (mg-N/L)	Bottom	SB	200	99.5	1
Nitrate + nitrate (mg/L)	Surface	SB	200	95	1
Nitrate + nitrate (mg/L)	Bottom	SB	200	63	1
TP (mg-P/L)	Surface	SB	200	100	1
TP (mg-P/L)	Bottom	SB	200	100	1
DRP (mg-P/L)	Surface	SB	200	81	1
DRP (mg-P/L)	Bottom	SB	200	96	1
DO (mg/L)	Surface	SB	200	100	1
DO (mg/L)	Bottom	SB	200	99.5	1
Chl-a (mg/m^3)	Integrated	SB	200	71	1
TAN (mg-N/L)	Surface	SB	200	82.5	2
TAN (mg-N/L)	Bottom	SB	200	95	2
TN (mg-N/L)	Surface	SB	200	100	2
TN (mg-N/L)	Bottom	SB	200	100	2
Nitrate + nitrate (mg/L)	Surface	SB	200	100	2
Nitrate + nitrate (mg/L)	Bottom	SB	200	100	2
TP (mg-P/L)	Surface	SB	200	100	2
TP (mg-P/L)	Bottom	SB	200	100	2
DRP (mg-P/L)	Surface	SB	200	100	2
DRP (mg-P/L)	Bottom	SB	200	100	2
DO (mg/L)	Surface	SB	200	100	2
DO (mg/L)	Bottom	SB	200	100	2
Chl-a (mg/m^3)	Integrated	SB	200	72.5	2
TAN (mg-N/L)	Surface	SB	200	100	2
TAN (mg-N/L)	Bottom	SB	200	100	2
TN (mg-N/L)	Surface	SB	200	100	2

Environmental Variables	Depth	Region	Effect Size (%)	Power (%)	Scenario
TN (mg-N/L)	Bottom	SB	200	100	2
Nitrate + nitrate (mg/L)	Surface	SB	200	100	2
Nitrate + nitrate (mg/L)	Bottom	SB	200	99.5	2
TP (mg-P/L)	Surface	SB	200	100	2
TP (mg-P/L)	Bottom	SB	200	100	2
DRP (mg-P/L)	Surface	SB	200	100	2
DRP (mg-P/L)	Bottom	SB	200	100	2
DO (mg/L)	Surface	SB	200	100	2
DO (mg/L)	Bottom	SB	200	100	2
Chl-a (mg/m^3)	Integrated	SB	200	100	2
TAN (mg-N/L)	Surface	SB	200	63.5	3
TAN (mg-N/L)	Bottom	SB	200	84.5	3
TN (mg-N/L)	Surface	SB	200	99	3
TN (mg-N/L)	Bottom	SB	200	99	3
Nitrate + nitrate (mg/L)	Surface	SB	200	100	3
Nitrate + nitrate (mg/L)	Bottom	SB	200	100	3
TP (mg-P/L)	Surface	SB	200	100	3
TP (mg-P/L)	Bottom	SB	200	100	3
DRP (mg-P/L)	Surface	SB	200	100	3
DRP (mg-P/L)	Bottom	SB	200	100	3
DO (mg/L)	Surface	SB	200	100	3
DO (mg/L)	Bottom	SB	200	100	3
Chl-a (mg/m^3)	Integrated	SB	200	58	3
TAN (mg-N/L)	Surface	SB	200	100	3
TAN (mg-N/L)	Bottom	SB	200	100	3
TN (mg-N/L)	Surface	SB	200	100	3
TN (mg-N/L)	Bottom	SB	200	100	3
Nitrate + nitrate (mg/L)	Surface	SB	200	100	3
Nitrate + nitrate (mg/L)	Bottom	SB	200	87	3
TP (mg-P/L)	Surface	SB	200	100	3
TP (mg-P/L)	Bottom	SB	200	100	3
DRP (mg-P/L)	Surface	SB	200	98.5	3
DRP (mg-P/L)	Bottom	SB	200	100	3
DO (mg/L)	Surface	SB	200	100	3
DO (mg/L)	Bottom	SB	200	100	3
Chl-a (mg/m^3)	Integrated	SB	200	91.5	3
TAN (mg-N/L)	Surface	SB	200	77.5	4
TAN (mg-N/L)	Bottom	SB	200	93.5	4
TN (mg-N/L)	Surface	SB	200	99.5	4
TN (mg-N/L)	Bottom	SB	200	99.5	4
Nitrate + nitrate (mg/L)	Surface	SB	200	100	4
Nitrate + nitrate (mg/L)	Bottom	SB	200	100	4
TP (mg-P/L)	Surface	SB	200	100	4
TP (mg-P/L)	Bottom	SB	200	100	4
DRP (mg-P/L)	Surface	SB	200	100	4
DRP (mg-P/L)	Bottom	SB	200	100	4
DO (mg/L)	Surface	SB	200	100	4
DO (mg/L)	Bottom	SB	200	100	4
Chl-a (mg/m^3)	Integrated	SB	200	68.5	4
TAN (mg-N/L)	Surface	SB	200	100	4
TAN (mg-N/L)	Bottom	SB	200	100	4

Environmental Variables	Depth	Region	Effect Size (%)	Power (%)	Scenario
TN (mg-N/L)	Surface	SB	200	100	4
TN (mg-N/L)	Bottom	SB	200	100	4
Nitrate + nitrate (mg/L)	Surface	SB	200	100	4
Nitrate + nitrate (mg/L)	Bottom	SB	200	99.5	4
TP (mg-P/L)	Surface	SB	200	100	4
TP (mg-P/L)	Bottom	SB	200	100	4
DRP (mg-P/L)	Surface	SB	200	100	4
DRP (mg-P/L)	Bottom	SB	200	100	4
DO (mg/L)	Surface	SB	200	100	4
DO (mg/L)	Bottom	SB	200	100	4
Chl-a (mg/m^3)	Integrated	SB	200	100	4
TAN (mg-N/L)	Surface	Storm Bay	50	58.5	1
TAN (mg-N/L)	Surface	Storm Bay	100	96	1
TAN (mg-N/L)	Surface	Storm Bay	200	100	1
TAN (mg-N/L)	Bottom	Storm Bay	50	39.5	1
TAN (mg-N/L)	Bottom	Storm Bay	100	83.5	1
TAN (mg-N/L)	Bottom	Storm Bay	200	99.5	1
TN (mg-N/L)	Surface	Storm Bay	50	48.5	1
TN (mg-N/L)	Surface	Storm Bay	100	89	1
TN (mg-N/L)	Surface	Storm Bay	200	100	1
TN (mg-N/L)	Bottom	Storm Bay	50	43.5	1
TN (mg-N/L)	Bottom	Storm Bay	100	88	1
TN (mg-N/L)	Bottom	Storm Bay	200	100	1
Nitrate + nitrate (mg/L)	Surface	Storm Bay	50	44	1
Nitrate + nitrate (mg/L)	Surface	Storm Bay	100	92	1
Nitrate + nitrate (mg/L)	Surface	Storm Bay	200	100	1
Nitrate + nitrate (mg/L)	Bottom	Storm Bay	50	37	1
Nitrate + nitrate (mg/L)	Bottom	Storm Bay	100	81	1
Nitrate + nitrate (mg/L)	Bottom	Storm Bay	200	100	1
TP (mg-P/L)	Surface	Storm Bay	50	93	1
TP (mg-P/L)	Surface	Storm Bay	100	100	1
TP (mg-P/L)	Surface	Storm Bay	200	100	1
TP (mg-P/L)	Bottom	Storm Bay	50	85.5	1
TP (mg-P/L)	Bottom	Storm Bay	100	100	1
TP (mg-P/L)	Bottom	Storm Bay	200	100	1
DRP (mg-P/L)	Surface	Storm Bay	50	49.5	1
DRP (mg-P/L)	Surface	Storm Bay	100	94	1
DRP (mg-P/L)	Surface	Storm Bay	200	100	1
DRP (mg-P/L)	Bottom	Storm Bay	50	50.5	1
DRP (mg-P/L)	Bottom	Storm Bay	100	93	1
DRP (mg-P/L)	Bottom	Storm Bay	200	100	1
DO (mg/L)	Surface	Storm Bay	50	59	1
DO (mg/L)	Surface	Storm Bay	100	99.5	1
DO (mg/L)	Surface	Storm Bay	200	100	1
DO (mg/L)	Bottom	Storm Bay	50	59	1
DO (mg/L)	Bottom	Storm Bay	100	99	1
DO (mg/L)	Bottom	Storm Bay	200	100	1
Chl-a (mg/m^3)	Integrated	Storm Bay	50	16	1
Chl-a (mg/m^3)	Integrated	Storm Bay	100	49.5	1
Chl-a (mg/m^3)	Integrated	Storm Bay	200	95	1
TAN (mg-N/L)	Surface	Storm Bay	50	91.5	2

Environmental Variables	Depth	Region	Effect Size (%)	Power (%)	Scenario
TAN (mg-N/L)	Surface	Storm Bay	100	100	2
TAN (mg-N/L)	Surface	Storm Bay	200	100	2
TAN (mg-N/L)	Bottom	Storm Bay	50	75	2
TAN (mg-N/L)	Bottom	Storm Bay	100	100	2
TAN (mg-N/L)	Bottom	Storm Bay	200	100	2
TN (mg-N/L)	Surface	Storm Bay	50	84	2
TN (mg-N/L)	Surface	Storm Bay	100	100	2
TN (mg-N/L)	Surface	Storm Bay	200	100	2
TN (mg-N/L)	Bottom	Storm Bay	50	77.5	2
TN (mg-N/L)	Bottom	Storm Bay	100	99.5	2
TN (mg-N/L)	Bottom	Storm Bay	200	100	2
Nitrate + nitrate (mg/L)	Surface	Storm Bay	50	87	2
Nitrate + nitrate (mg/L)	Surface	Storm Bay	100	100	2
Nitrate + nitrate (mg/L)	Surface	Storm Bay	200	100	2
Nitrate + nitrate (mg/L)	Bottom	Storm Bay	50	70	2
Nitrate + nitrate (mg/L)	Bottom	Storm Bay	100	100	2
Nitrate + nitrate (mg/L)	Bottom	Storm Bay	200	100	2
TP (mg-P/L)	Surface	Storm Bay	50	100	2
TP (mg-P/L)	Surface	Storm Bay	100	100	2
TP (mg-P/L)	Surface	Storm Bay	200	100	2
TP (mg-P/L)	Bottom	Storm Bay	50	100	2
TP (mg-P/L)	Bottom	Storm Bay	100	100	2
TP (mg-P/L)	Bottom	Storm Bay	200	100	2
DRP (mg-P/L)	Surface	Storm Bay	50	88.5	2
DRP (mg-P/L)	Surface	Storm Bay	100	100	2
DRP (mg-P/L)	Surface	Storm Bay	200	100	2
DRP (mg-P/L)	Bottom	Storm Bay	50	90.5	2
DRP (mg-P/L)	Bottom	Storm Bay	100	100	2
DRP (mg-P/L)	Bottom	Storm Bay	200	100	2
DO (mg/L)	Surface	Storm Bay	50	95	2
DO (mg/L)	Surface	Storm Bay	100	100	2
DO (mg/L)	Surface	Storm Bay	200	100	2
DO (mg/L)	Bottom	Storm Bay	50	95.5	2
DO (mg/L)	Bottom	Storm Bay	100	100	2
DO (mg/L)	Bottom	Storm Bay	200	100	2
Chl-a (mg/m^3)	Integrated	Storm Bay	50	41	2
Chl-a (mg/m^3)	Integrated	Storm Bay	100	90	2
Chl-a (mg/m^3)	Integrated	Storm Bay	200	100	2
TAN (mg-N/L)	Surface	Storm Bay	50	75.5	3
TAN (mg-N/L)	Surface	Storm Bay	100	100	3
TAN (mg-N/L)	Surface	Storm Bay	200	100	3
TAN (mg-N/L)	Bottom	Storm Bay	50	50	3
TAN (mg-N/L)	Bottom	Storm Bay	100	96	3
TAN (mg-N/L)	Bottom	Storm Bay	200	100	3
TN (mg-N/L)	Surface	Storm Bay	50	59.5	3
TN (mg-N/L)	Surface	Storm Bay	100	97	3
TN (mg-N/L)	Surface	Storm Bay	200	100	3
TN (mg-N/L)	Bottom	Storm Bay	50	60.5	3
TN (mg-N/L)	Bottom	Storm Bay	100	99	3
TN (mg-N/L)	Bottom	Storm Bay	200	100	3
Nitrate + nitrate (mg/L)	Surface	Storm Bay	50	72	3

Environmental Variables	Depth	Region	Effect Size (%)	Power (%)	Scenario
Nitrate + nitrate (mg/L)	Surface	Storm Bay	100	99.5	3
Nitrate + nitrate (mg/L)	Surface	Storm Bay	200	100	3
Nitrate + nitrate (mg/L)	Bottom	Storm Bay	50	55.5	3
Nitrate + nitrate (mg/L)	Bottom	Storm Bay	100	96.5	3
Nitrate + nitrate (mg/L)	Bottom	Storm Bay	200	100	3
TP (mg-P/L)	Surface	Storm Bay	50	100	3
TP (mg-P/L)	Surface	Storm Bay	100	100	3
TP (mg-P/L)	Surface	Storm Bay	200	100	3
TP (mg-P/L)	Bottom	Storm Bay	50	98	3
TP (mg-P/L)	Bottom	Storm Bay	100	100	3
TP (mg-P/L)	Bottom	Storm Bay	200	100	3
DRP (mg-P/L)	Surface	Storm Bay	50	74.5	3
DRP (mg-P/L)	Surface	Storm Bay	100	100	3
DRP (mg-P/L)	Surface	Storm Bay	200	100	3
DRP (mg-P/L)	Bottom	Storm Bay	50	75	3
DRP (mg-P/L)	Bottom	Storm Bay	100	99.5	3
DRP (mg-P/L)	Bottom	Storm Bay	200	100	3
DO (mg/L)	Surface	Storm Bay	50	88	3
DO (mg/L)	Surface	Storm Bay	100	100	3
DO (mg/L)	Surface	Storm Bay	200	100	3
DO (mg/L)	Bottom	Storm Bay	50	86	3
DO (mg/L)	Bottom	Storm Bay	100	100	3
DO (mg/L)	Bottom	Storm Bay	200	100	3
Chl-a (mg/m^3)	Integrated	Storm Bay	50	28	3
Chl-a (mg/m^3)	Integrated	Storm Bay	100	74	3
Chl-a (mg/m^3)	Integrated	Storm Bay	200	100	3
TAN (mg-N/L)	Surface	Storm Bay	50	93.5	4
TAN (mg-N/L)	Surface	Storm Bay	100	100	4
TAN (mg-N/L)	Surface	Storm Bay	200	100	4
TAN (mg-N/L)	Bottom	Storm Bay	50	75	4
TAN (mg-N/L)	Bottom	Storm Bay	100	99.5	4
TAN (mg-N/L)	Bottom	Storm Bay	200	100	4
TN (mg-N/L)	Surface	Storm Bay	50	87.5	4
TN (mg-N/L)	Surface	Storm Bay	100	100	4
TN (mg-N/L)	Surface	Storm Bay	200	100	4
TN (mg-N/L)	Bottom	Storm Bay	50	81.5	4
TN (mg-N/L)	Bottom	Storm Bay	100	99.5	4
TN (mg-N/L)	Bottom	Storm Bay	200	100	4
Nitrate + nitrate (mg/L)	Surface	Storm Bay	50	88.5	4
Nitrate + nitrate (mg/L)	Surface	Storm Bay	100	100	4
Nitrate + nitrate (mg/L)	Surface	Storm Bay	200	100	4
Nitrate + nitrate (mg/L)	Bottom	Storm Bay	50	71	4
Nitrate + nitrate (mg/L)	Bottom	Storm Bay	100	100	4
Nitrate + nitrate (mg/L)	Bottom	Storm Bay	200	100	4
TP (mg-P/L)	Surface	Storm Bay	50	100	4
TP (mg-P/L)	Surface	Storm Bay	100	100	4
TP (mg-P/L)	Surface	Storm Bay	200	100	4
TP (mg-P/L)	Bottom	Storm Bay	50	100	4
TP (mg-P/L)	Bottom	Storm Bay	100	100	4
TP (mg-P/L)	Bottom	Storm Bay	200	100	4
DRP (mg-P/L)	Surface	Storm Bay	50	85.5	4

Environmental Variables	Depth	Region	Effect Size (%)	Power (%)	Scenario
DRP (mg-P/L)	Surface	Storm Bay	100	100	4
DRP (mg-P/L)	Surface	Storm Bay	200	100	4
DRP (mg-P/L)	Bottom	Storm Bay	50	84.5	4
DRP (mg-P/L)	Bottom	Storm Bay	100	100	4
DRP (mg-P/L)	Bottom	Storm Bay	200	100	4
DO (mg/L)	Surface	Storm Bay	50	96	4
DO (mg/L)	Surface	Storm Bay	100	100	4
DO (mg/L)	Surface	Storm Bay	200	100	4
DO (mg/L)	Bottom	Storm Bay	50	95.5	4
DO (mg/L)	Bottom	Storm Bay	100	100	4
DO (mg/L)	Bottom	Storm Bay	200	100	4
Chl-a (mg/m^3)	Integrated	Storm Bay	50	51	4
Chl-a (mg/m^3)	Integrated	Storm Bay	100	91	4
Chl-a (mg/m^3)	Integrated	Storm Bay	200	100	4

Power analysis results for different numbers of sites at the two distances (n1 and n2), for different numbers of samples per month. Balance is calculated as min(n1,n2)/(n1+n2). These results were used to generate Figures 3-47 – 3-48.

Environmental Variables	Depth	Samples per month	n1	n2	Total Number of Sites	Balance	Power (%)
TAN (mg-N/L)	Surface	1	2	2	4	0.5	50
TAN (mg-N/L)	Bottom	1	2	2	4	0.5	36
TN (mg-N/L)	Surface	1	2	2	4	0.5	49.5
TN (mg-N/L)	Bottom	1	2	2	4	0.5	43.5
Nitrate + nitrate (mg/L)	Surface	1	2	2	4	0.5	59.5
Nitrate + nitrate (mg/L)	Bottom	1	2	2	4	0.5	49
TP (mg-P/L)	Surface	1	2	2	4	0.5	95.5
TP (mg-P/L)	Bottom	1	2	2	4	0.5	81.5
DRP (mg-P/L)	Surface	1	2	2	4	0.5	44
DRP (mg-P/L)	Bottom	1	2	2	4	0.5	56
DO (mg/L)	Surface	1	2	2	4	0.5	62.5
DO (mg/L)	Bottom	1	2	2	4	0.5	62.5
Chl-a (mg/m^3)	Integrated	1	2	2	4	0.5	22.5
TAN (mg-N/L)	Surface	1	5	2	7	0.29	84
TAN (mg-N/L)	Bottom	1	5	2	7	0.29	60.5
TN (mg-N/L)	Surface	1	5	2	7	0.29	77
TN (mg-N/L)	Bottom	1	5	2	7	0.29	76
Nitrate + nitrate (mg/L)	Surface	1	5	2	7	0.29	94
Nitrate + nitrate (mg/L)	Bottom	1	5	2	7	0.29	63.5
TP (mg-P/L)	Surface	1	5	2	7	0.29	100
TP (mg-P/L)	Bottom	1	5	2	7	0.29	100
DRP (mg-P/L)	Surface	1	5	2	7	0.29	81
DRP (mg-P/L)	Bottom	1	5	2	7	0.29	83
DO (mg/L)	Surface	1	5	2	7	0.29	94
DO (mg/L)	Bottom	1	5	2	7	0.29	92
Chl-a (mg/m^3)	Integrated	1	5	2	7	0.29	40.5
TAN (mg-N/L)	Surface	1	10	2	12	0.17	92.5
TAN (mg-N/L)	Bottom	1	10	2	12	0.17	68.5
TN (mg-N/L)	Surface	1	10	2	12	0.17	90.5
TN (mg-N/L)	Bottom	1	10	2	12	0.17	85
Nitrate + nitrate (mg/L)	Surface	1	10	2	12	0.17	99.5

Environmental Variables	Depth	Samples per month	n1	n2	Total Number of Sites	Balance	Power (%)
Nitrate + nitrate (mg/L)	Bottom	1	10	2	12	0.17	75.5
TP (mg-P/L)	Surface	1	10	2	12	0.17	100
TP (mg-P/L)	Bottom	1	10	2	12	0.17	100
DRP (mg-P/L)	Surface	1	10	2	12	0.17	91.5
DRP (mg-P/L)	Bottom	1	10	2	12	0.17	94
DO (mg/L)	Surface	1	10	2	12	0.17	97.5
DO (mg/L)	Bottom	1	10	2	12	0.17	97
Chl-a (mg/m^3)	Integrated	1	10	2	12	0.17	51
TAN (mg-N/L)	Surface	1	2	5	7	0.29	86.5
TAN (mg-N/L)	Bottom	1	2	5	7	0.29	57
TN (mg-N/L)	Surface	1	2	5	7	0.29	79
TN (mg-N/L)	Bottom	1	2	5	7	0.29	73.5
Nitrate + nitrate (mg/L)	Surface	1	2	5	7	0.29	95.5
Nitrate + nitrate (mg/L)	Bottom	1	2	5	7	0.29	71
TP (mg-P/L)	Surface	1	2	5	7	0.29	100
TP (mg-P/L)	Bottom	1	2	5	7	0.29	99.5
DRP (mg-P/L)	Surface	1	2	5	7	0.29	81.5
DRP (mg-P/L)	Bottom	1	2	5	7	0.29	81.5
DO (mg/L)	Surface	1	2	5	7	0.29	91
DO (mg/L)	Bottom	1	2	5	7	0.29	91
Chl-a (mg/m^3)	Integrated	1	2	5	7	0.29	40
TAN (mg-N/L)	Surface	1	5	5	10	0.5	98.5
TAN (mg-N/L)	Bottom	1	5	5	10	0.5	85.5
TN (mg-N/L)	Surface	1	5	5	10	0.5	95.5
TN (mg-N/L)	Bottom	1	5	5	10	0.5	94
Nitrate + nitrate (mg/L)	Surface	1	5	5	10	0.5	99.5
Nitrate + nitrate (mg/L)	Bottom	1	5	5	10	0.5	88
TP (mg-P/L)	Surface	1	5	5	10	0.5	100
TP (mg-P/L)	Bottom	1	5	5	10	0.5	100
DRP (mg-P/L)	Surface	1	5	5	10	0.5	97.5
DRP (mg-P/L)	Bottom	1	5	5	10	0.5	99
DO (mg/L)	Surface	1	5	5	10	0.5	99
DO (mg/L)	Bottom	1	5	5	10	0.5	99
Chl-a (mg/m^3)	Integrated	1	5	5	10	0.5	64.5
TAN (mg-N/L)	Surface	1	10	5	15	0.33	100
TAN (mg-N/L)	Bottom	1	10	5	15	0.33	92
TN (mg-N/L)	Surface	1	10	5	15	0.33	98.5
TN (mg-N/L)	Bottom	1	10	5	15	0.33	98.5
Nitrate + nitrate (mg/L)	Surface	1	10	5	15	0.33	100
Nitrate + nitrate (mg/L)	Bottom	1	10	5	15	0.33	97
TP (mg-P/L)	Surface	1	10	5	15	0.33	100
TP (mg-P/L)	Bottom	1	10	5	15	0.33	100
DRP (mg-P/L)	Surface	1	10	5	15	0.33	100
DRP (mg-P/L)	Bottom	1	10	5	15	0.33	100
DO (mg/L)	Surface	1	10	5	15	0.33	100
DO (mg/L)	Bottom	1	10	5	15	0.33	100
Chl-a (mg/m^3)	Integrated	1	10	5	15	0.33	76.5
TAN (mg-N/L)	Surface	1	2	10	12	0.17	93
TAN (mg-N/L)	Bottom	1	2	10	12	0.17	68.5
TN (mg-N/L)	Surface	1	2	10	12	0.17	87.5
TN (mg-N/L)	Bottom	1	2	10	12	0.17	86

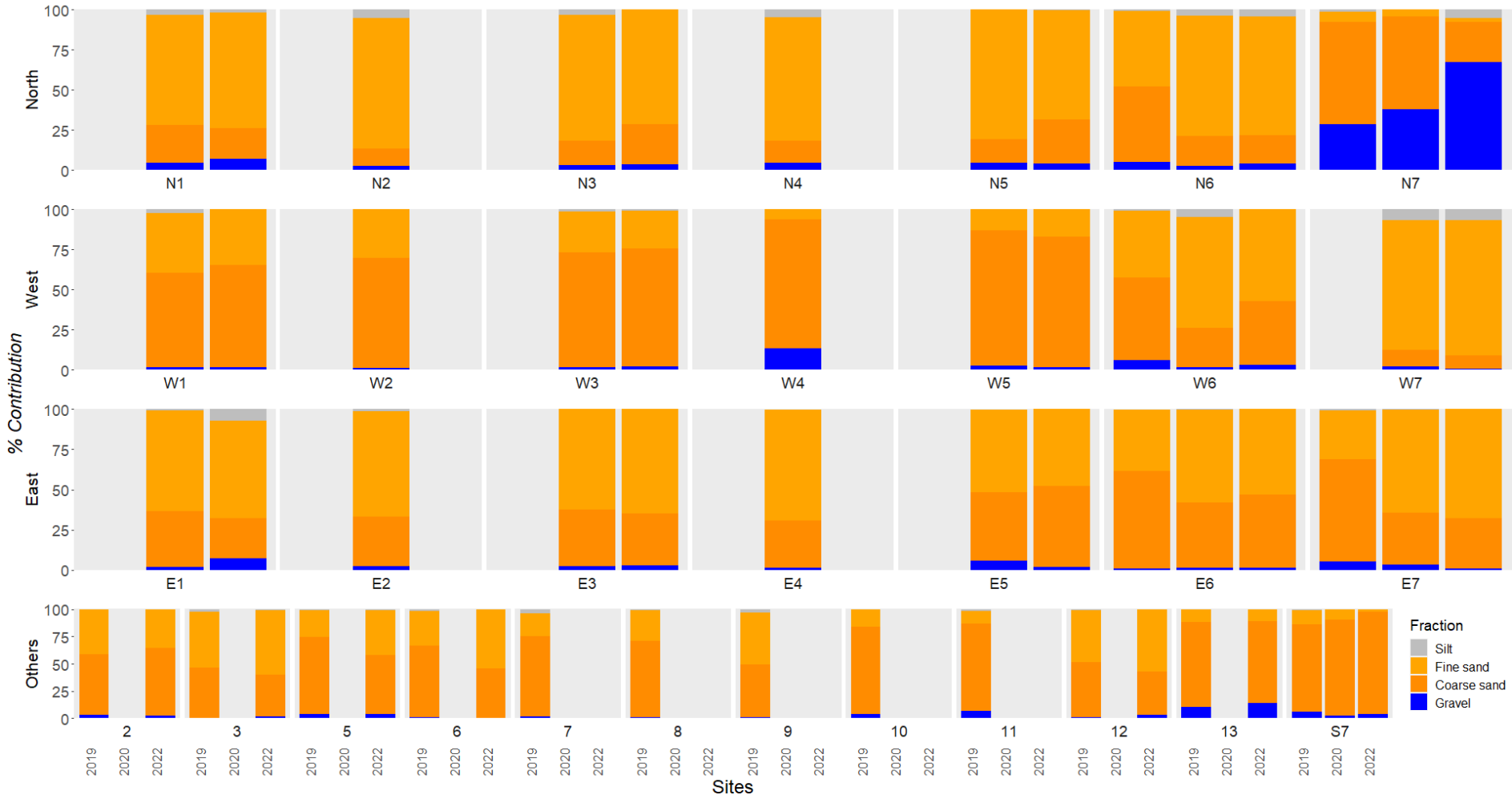
Environmental Variables	Depth	Samples per month	n1	n2	Total Number of Sites	Balance	Power (%)
Nitrate + nitrate (mg/L)	Surface	1	2	10	12	0.17	97.5
Nitrate + nitrate (mg/L)	Bottom	1	2	10	12	0.17	80
TP (mg-P/L)	Surface	1	2	10	12	0.17	100
TP (mg-P/L)	Bottom	1	2	10	12	0.17	99.5
DRP (mg-P/L)	Surface	1	2	10	12	0.17	86.5
DRP (mg-P/L)	Bottom	1	2	10	12	0.17	92
DO (mg/L)	Surface	1	2	10	12	0.17	98
DO (mg/L)	Bottom	1	2	10	12	0.17	95
Chl-a (mg/m^3)	Integrated	1	2	10	12	0.17	48
TAN (mg-N/L)	Surface	1	5	10	15	0.33	100
TAN (mg-N/L)	Bottom	1	5	10	15	0.33	92.5
TN (mg-N/L)	Surface	1	5	10	15	0.33	100
TN (mg-N/L)	Bottom	1	5	10	15	0.33	99.5
Nitrate + nitrate (mg/L)	Surface	1	5	10	15	0.33	100
Nitrate + nitrate (mg/L)	Bottom	1	5	10	15	0.33	97
TP (mg-P/L)	Surface	1	5	10	15	0.33	100
TP (mg-P/L)	Bottom	1	5	10	15	0.33	100
DRP (mg-P/L)	Surface	1	5	10	15	0.33	99.5
DRP (mg-P/L)	Bottom	1	5	10	15	0.33	99.5
DO (mg/L)	Surface	1	5	10	15	0.33	100
DO (mg/L)	Bottom	1	5	10	15	0.33	100
Chl-a (mg/m^3)	Integrated	1	5	10	15	0.33	74
TAN (mg-N/L)	Surface	1	10	10	20	0.5	100
TAN (mg-N/L)	Bottom	1	10	10	20	0.5	99.5
TN (mg-N/L)	Surface	1	10	10	20	0.5	100
TN (mg-N/L)	Bottom	1	10	10	20	0.5	100
Nitrate + nitrate (mg/L)	Surface	1	10	10	20	0.5	100
Nitrate + nitrate (mg/L)	Bottom	1	10	10	20	0.5	100
TP (mg-P/L)	Surface	1	10	10	20	0.5	100
TP (mg-P/L)	Bottom	1	10	10	20	0.5	100
DRP (mg-P/L)	Surface	1	10	10	20	0.5	100
DRP (mg-P/L)	Bottom	1	10	10	20	0.5	100
DO (mg/L)	Surface	1	10	10	20	0.5	100
DO (mg/L)	Bottom	1	10	10	20	0.5	100
Chl-a (mg/m^3)	Integrated	1	10	10	20	0.5	85.5
TAN (mg-N/L)	Surface	2	2	2	4	0.5	57
TAN (mg-N/L)	Bottom	2	2	2	4	0.5	34.5
TN (mg-N/L)	Surface	2	2	2	4	0.5	54
TN (mg-N/L)	Bottom	2	2	2	4	0.5	48
Nitrate + nitrate (mg/L)	Surface	2	2	2	4	0.5	64.5
Nitrate + nitrate (mg/L)	Bottom	2	2	2	4	0.5	42
TP (mg-P/L)	Surface	2	2	2	4	0.5	96.5
TP (mg-P/L)	Bottom	2	2	2	4	0.5	80.5
DRP (mg-P/L)	Surface	2	2	2	4	0.5	52.5
DRP (mg-P/L)	Bottom	2	2	2	4	0.5	57.5
DO (mg/L)	Surface	2	2	2	4	0.5	68.5
DO (mg/L)	Bottom	2	2	2	4	0.5	64
Chl-a (mg/m^3)	Integrated	2	2	2	4	0.5	25.5
TAN (mg-N/L)	Surface	2	5	2	7	0.29	88
TAN (mg-N/L)	Bottom	2	5	2	7	0.29	62
TN (mg-N/L)	Surface	2	5	2	7	0.29	80

Environmental Variables	Depth	Samples per month	n1	n2	Total Number of Sites	Balance	Power (%)
TN (mg-N/L)	Bottom	2	5	2	7	0.29	74.5
Nitrate + nitrate (mg/L)	Surface	2	5	2	7	0.29	95.5
Nitrate + nitrate (mg/L)	Bottom	2	5	2	7	0.29	74
TP (mg-P/L)	Surface	2	5	2	7	0.29	100
TP (mg-P/L)	Bottom	2	5	2	7	0.29	99.5
DRP (mg-P/L)	Surface	2	5	2	7	0.29	81.5
DRP (mg-P/L)	Bottom	2	5	2	7	0.29	88.5
DO (mg/L)	Surface	2	5	2	7	0.29	96.5
DO (mg/L)	Bottom	2	5	2	7	0.29	93
Chl-a (mg/m^3)	Integrated	2	5	2	7	0.29	41.5
TAN (mg-N/L)	Surface	2	10	2	12	0.17	95.5
TAN (mg-N/L)	Bottom	2	10	2	12	0.17	72.5
TN (mg-N/L)	Surface	2	10	2	12	0.17	90.5
TN (mg-N/L)	Bottom	2	10	2	12	0.17	87
Nitrate + nitrate (mg/L)	Surface	2	10	2	12	0.17	99.5
Nitrate + nitrate (mg/L)	Bottom	2	10	2	12	0.17	85.5
TP (mg-P/L)	Surface	2	10	2	12	0.17	100
TP (mg-P/L)	Bottom	2	10	2	12	0.17	100
DRP (mg-P/L)	Surface	2	10	2	12	0.17	95.5
DRP (mg-P/L)	Bottom	2	10	2	12	0.17	94
DO (mg/L)	Surface	2	10	2	12	0.17	98.5
DO (mg/L)	Bottom	2	10	2	12	0.17	99.5
Chl-a (mg/m^3)	Integrated	2	10	2	12	0.17	49.5
TAN (mg-N/L)	Surface	2	2	5	7	0.29	84
TAN (mg-N/L)	Bottom	2	2	5	7	0.29	64.5
TN (mg-N/L)	Surface	2	2	5	7	0.29	82.5
TN (mg-N/L)	Bottom	2	2	5	7	0.29	80.5
Nitrate + nitrate (mg/L)	Surface	2	2	5	7	0.29	94.5
Nitrate + nitrate (mg/L)	Bottom	2	2	5	7	0.29	69
TP (mg-P/L)	Surface	2	2	5	7	0.29	100
TP (mg-P/L)	Bottom	2	2	5	7	0.29	100
DRP (mg-P/L)	Surface	2	2	5	7	0.29	80.5
DRP (mg-P/L)	Bottom	2	2	5	7	0.29	89.5
DO (mg/L)	Surface	2	2	5	7	0.29	95
DO (mg/L)	Bottom	2	2	5	7	0.29	93
Chl-a (mg/m^3)	Integrated	2	2	5	7	0.29	41.5
TAN (mg-N/L)	Surface	2	5	5	10	0.5	100
TAN (mg-N/L)	Bottom	2	5	5	10	0.5	88
TN (mg-N/L)	Surface	2	5	5	10	0.5	98
TN (mg-N/L)	Bottom	2	5	5	10	0.5	93.5
Nitrate + nitrate (mg/L)	Surface	2	5	5	10	0.5	100
Nitrate + nitrate (mg/L)	Bottom	2	5	5	10	0.5	95.5
TP (mg-P/L)	Surface	2	5	5	10	0.5	100
TP (mg-P/L)	Bottom	2	5	5	10	0.5	100
DRP (mg-P/L)	Surface	2	5	5	10	0.5	98.5
DRP (mg-P/L)	Bottom	2	5	5	10	0.5	99.5
DO (mg/L)	Surface	2	5	5	10	0.5	100
DO (mg/L)	Bottom	2	5	5	10	0.5	99.5
Chl-a (mg/m^3)	Integrated	2	5	5	10	0.5	61.5
TAN (mg-N/L)	Surface	2	10	5	15	0.33	100
TAN (mg-N/L)	Bottom	2	10	5	15	0.33	95.5

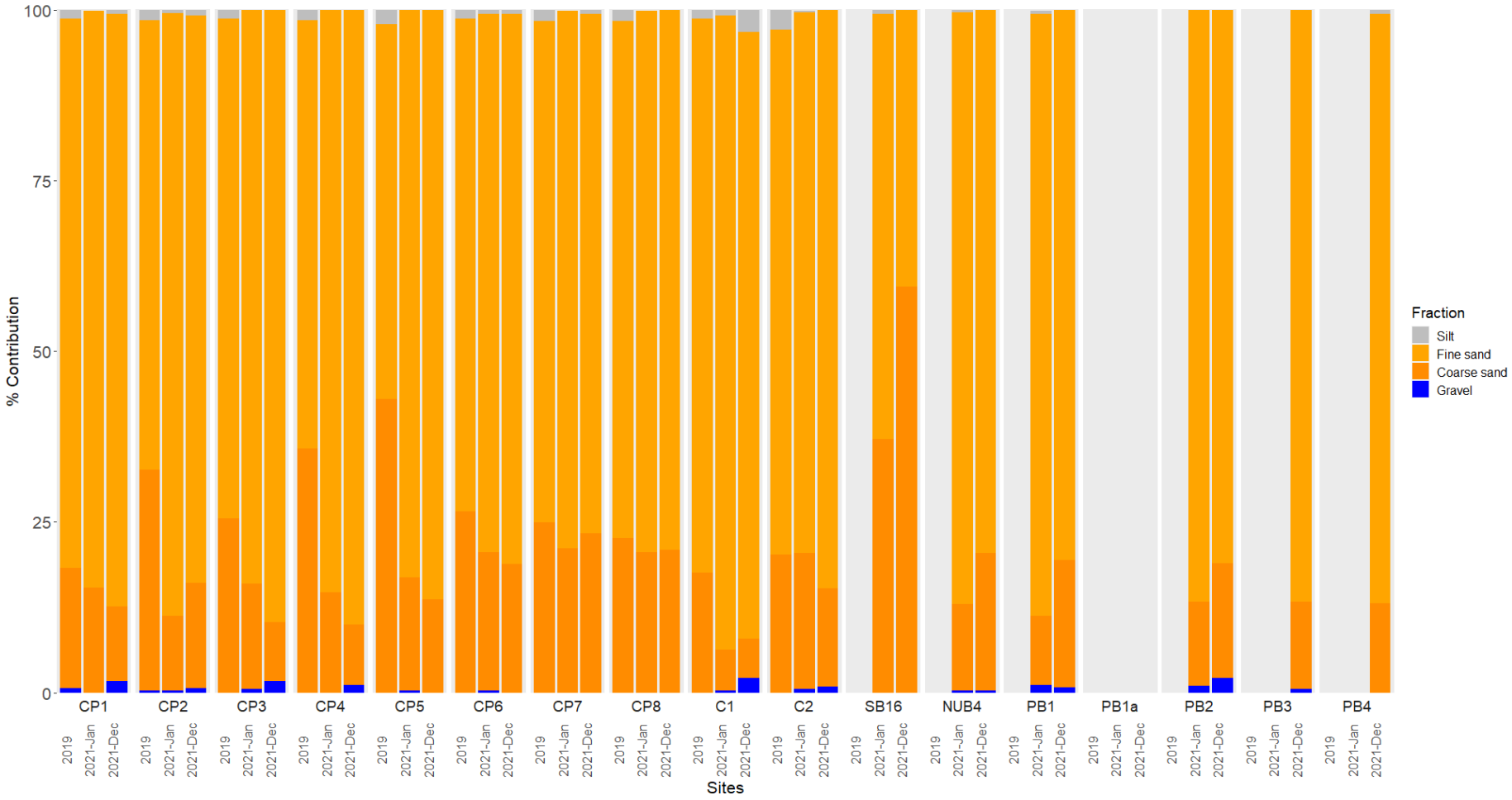
Environmental Variables	Depth	Samples per month	n1	n2	Total Number of Sites	Balance	Power (%)
TN (mg-N/L)	Surface	2	10	5	15	0.33	99.5
TN (mg-N/L)	Bottom	2	10	5	15	0.33	98.5
Nitrate + nitrate (mg/L)	Surface	2	10	5	15	0.33	100
Nitrate + nitrate (mg/L)	Bottom	2	10	5	15	0.33	99.5
TP (mg-P/L)	Surface	2	10	5	15	0.33	100
TP (mg-P/L)	Bottom	2	10	5	15	0.33	100
DRP (mg-P/L)	Surface	2	10	5	15	0.33	99.5
DRP (mg-P/L)	Bottom	2	10	5	15	0.33	100
DO (mg/L)	Surface	2	10	5	15	0.33	100
DO (mg/L)	Bottom	2	10	5	15	0.33	100
Chl-a (mg/m^3)	Integrated	2	10	5	15	0.33	76.5
TAN (mg-N/L)	Surface	2	2	10	12	0.17	96.5
TAN (mg-N/L)	Bottom	2	2	10	12	0.17	72
TN (mg-N/L)	Surface	2	2	10	12	0.17	91
TN (mg-N/L)	Bottom	2	2	10	12	0.17	86.5
Nitrate + nitrate (mg/L)	Surface	2	2	10	12	0.17	99
Nitrate + nitrate (mg/L)	Bottom	2	2	10	12	0.17	84.5
TP (mg-P/L)	Surface	2	2	10	12	0.17	100
TP (mg-P/L)	Bottom	2	2	10	12	0.17	100
DRP (mg-P/L)	Surface	2	2	10	12	0.17	91
DRP (mg-P/L)	Bottom	2	2	10	12	0.17	96.5
DO (mg/L)	Surface	2	2	10	12	0.17	98
DO (mg/L)	Bottom	2	2	10	12	0.17	99.5
Chl-a (mg/m^3)	Integrated	2	2	10	12	0.17	46.5
TAN (mg-N/L)	Surface	2	5	10	15	0.33	100
TAN (mg-N/L)	Bottom	2	5	10	15	0.33	94.5
TN (mg-N/L)	Surface	2	5	10	15	0.33	99.5
TN (mg-N/L)	Bottom	2	5	10	15	0.33	99.5
Nitrate + nitrate (mg/L)	Surface	2	5	10	15	0.33	100
Nitrate + nitrate (mg/L)	Bottom	2	5	10	15	0.33	99.5
TP (mg-P/L)	Surface	2	5	10	15	0.33	100
TP (mg-P/L)	Bottom	2	5	10	15	0.33	100
DRP (mg-P/L)	Surface	2	5	10	15	0.33	99
DRP (mg-P/L)	Bottom	2	5	10	15	0.33	100
DO (mg/L)	Surface	2	5	10	15	0.33	100
DO (mg/L)	Bottom	2	5	10	15	0.33	100
Chl-a (mg/m^3)	Integrated	2	5	10	15	0.33	75.5
TAN (mg-N/L)	Surface	2	10	10	20	0.5	100
TAN (mg-N/L)	Bottom	2	10	10	20	0.5	99
TN (mg-N/L)	Surface	2	10	10	20	0.5	100
TN (mg-N/L)	Bottom	2	10	10	20	0.5	100
Nitrate + nitrate (mg/L)	Surface	2	10	10	20	0.5	100
Nitrate + nitrate (mg/L)	Bottom	2	10	10	20	0.5	100
TP (mg-P/L)	Surface	2	10	10	20	0.5	100
TP (mg-P/L)	Bottom	2	10	10	20	0.5	100
DRP (mg-P/L)	Surface	2	10	10	20	0.5	100
DRP (mg-P/L)	Bottom	2	10	10	20	0.5	100
DO (mg/L)	Surface	2	10	10	20	0.5	100
DO (mg/L)	Bottom	2	10	10	20	0.5	100
Chl-a (mg/m^3)	Integrated	2	10	10	20	0.5	92

Appendix 4-1: Particle size distribution plots

Particle size distribution at Yellow Bluff in 2019, 2020 and 2022. No particle size data was collected in 2021. Light grey columns represent data that was not collected at that site for that survey.



Particle size distribution at West of Wedge in 2019, January 2021 and December 2021. Light grey columns represent data that was not collected at that site for that survey.



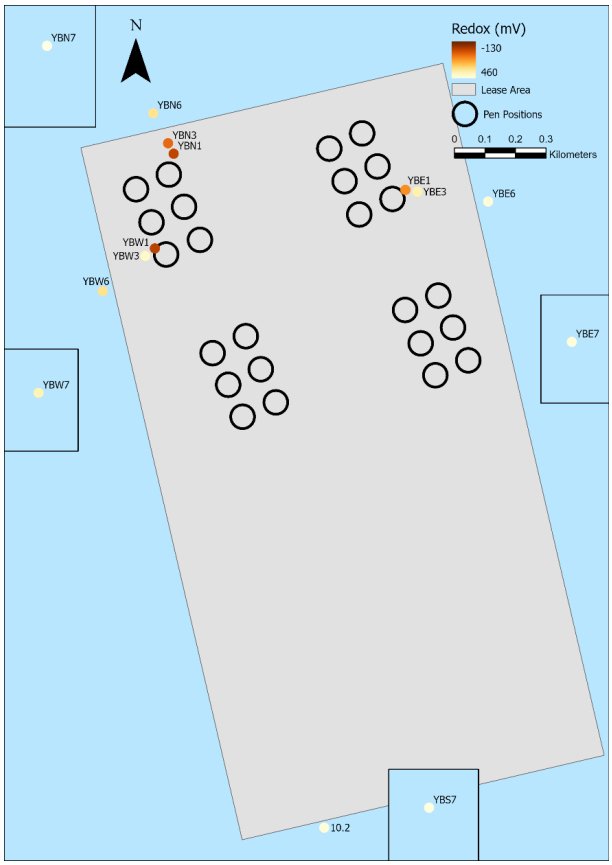
Appendix 4-2: Change in family abundance of macrofauna

Change in macrofauna family abundance at Yellow Bluff in 2020, 2021 and 2022 compared to the baseline survey in 2019. Only families which had a relative change of greater than 20 times are displayed.

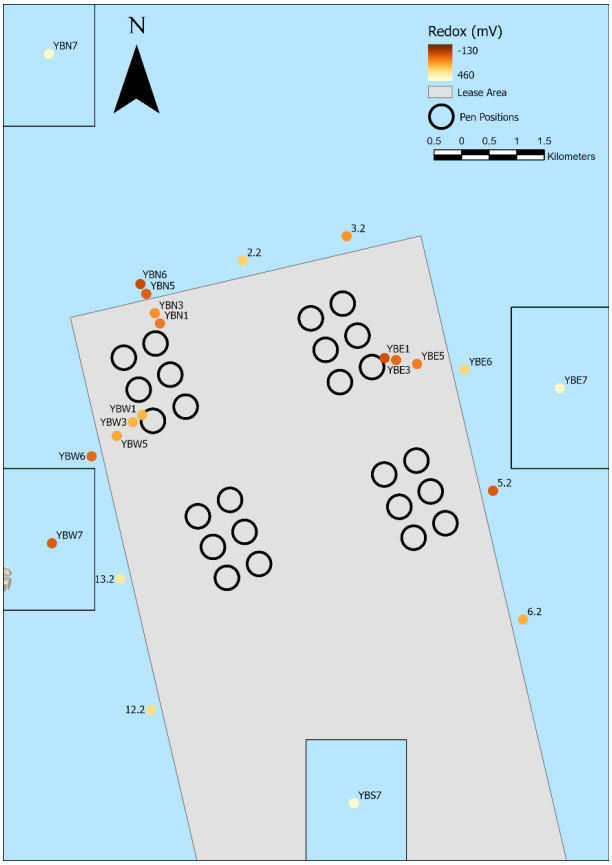
	Change at control sites (times)			Change at compliance sites (times)			Relative change (times)		
Family	2020	2021	2022	2020	2021	2022	2020	2021	2022
Loveniidae	NA	NA	2	NA	NA	53	NA	NA	26.5
Ophiuridae	5.5	2	2	126	NA	15.6	22.9	NA	7.8
Nassariidae	7	0.5	1	5	26	0.3	0.7	52	0.7

Appendix 4-3:

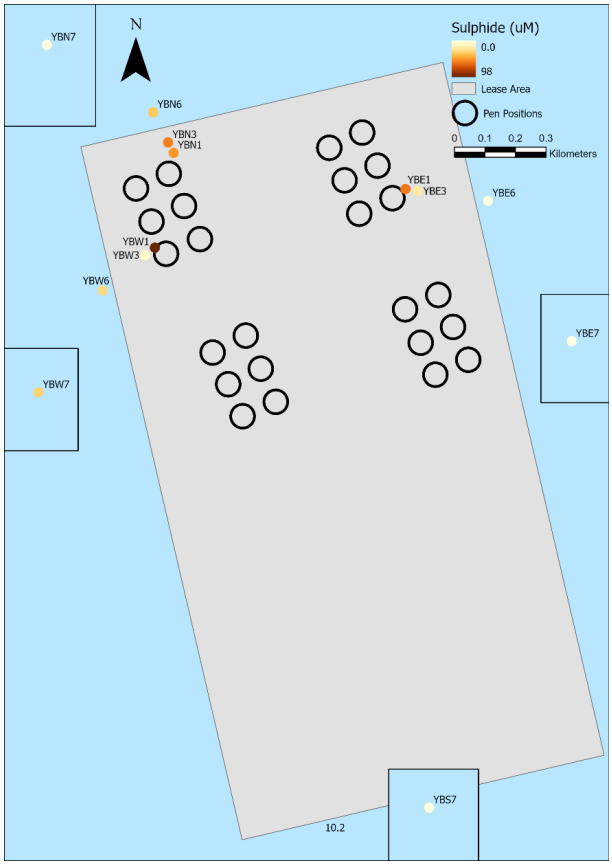
2021 (2YB)



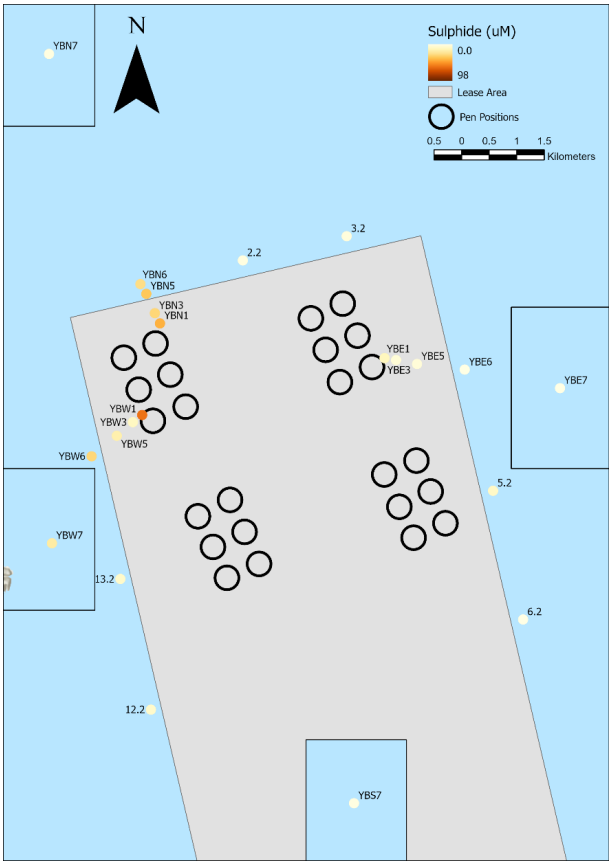
2022 (3YB)



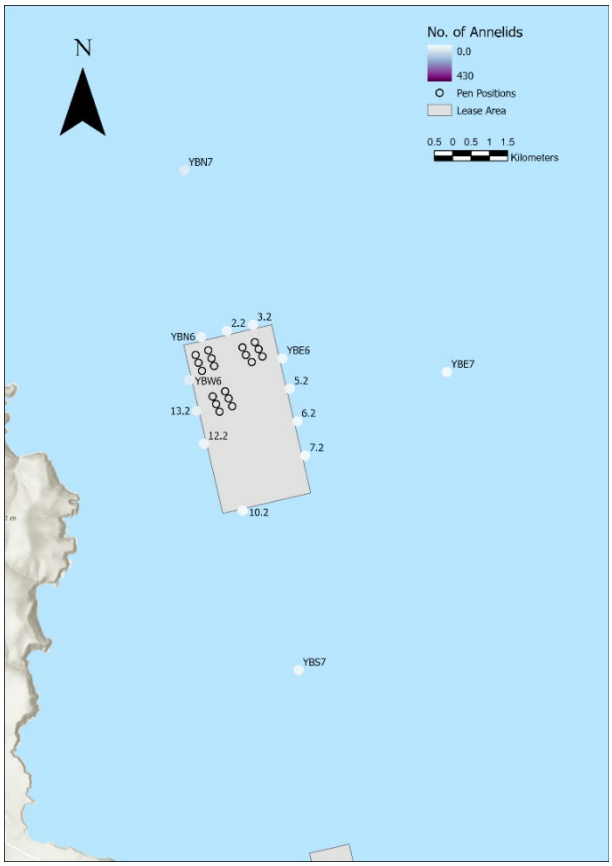
2021 (2YB)



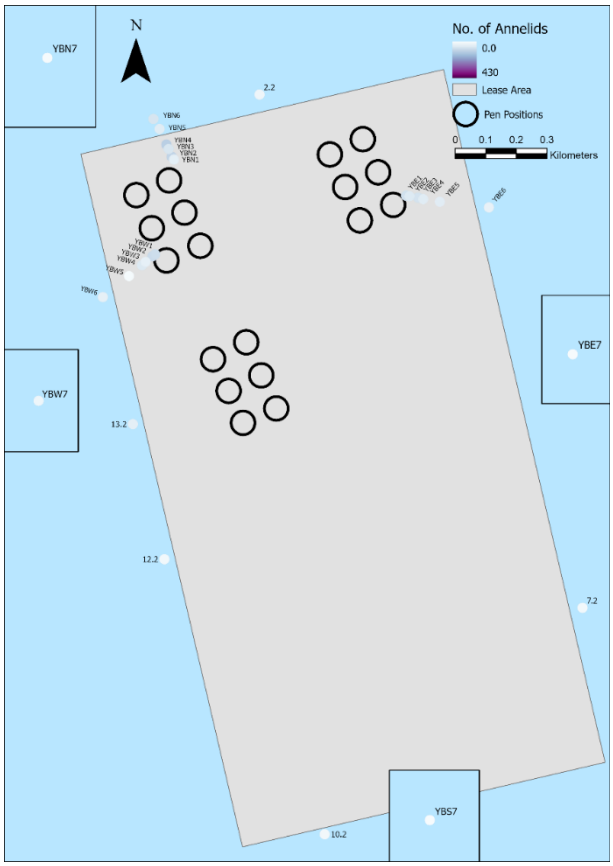
2022 (3YB)



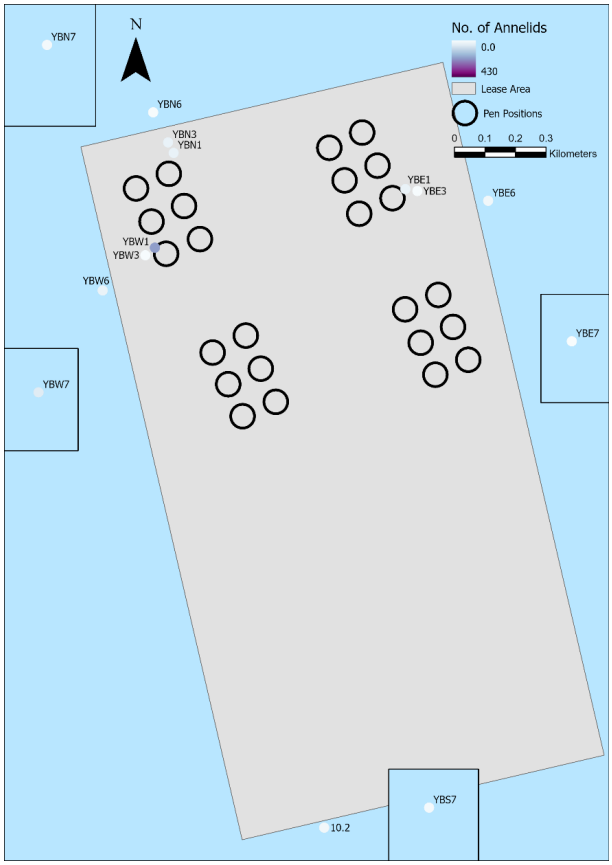
2019 (Baseline)



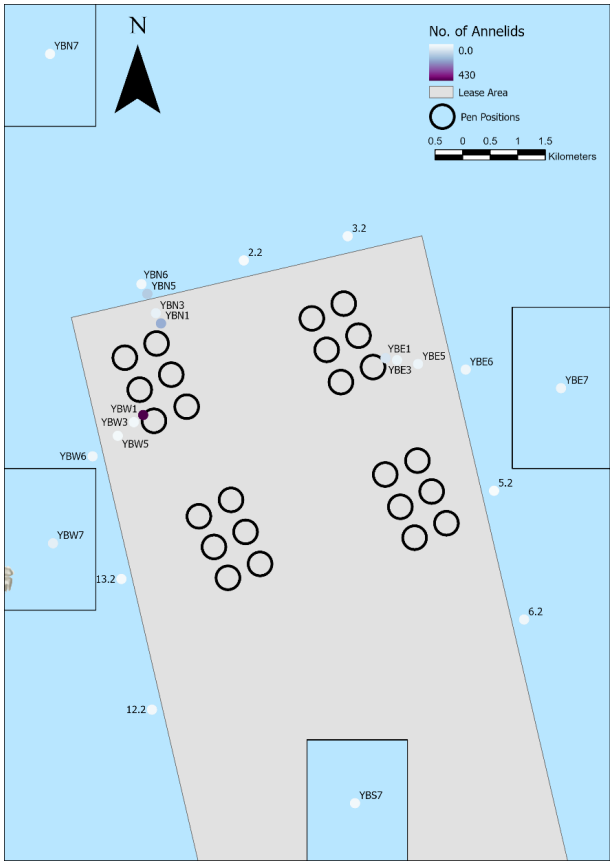
2020 (1YB)



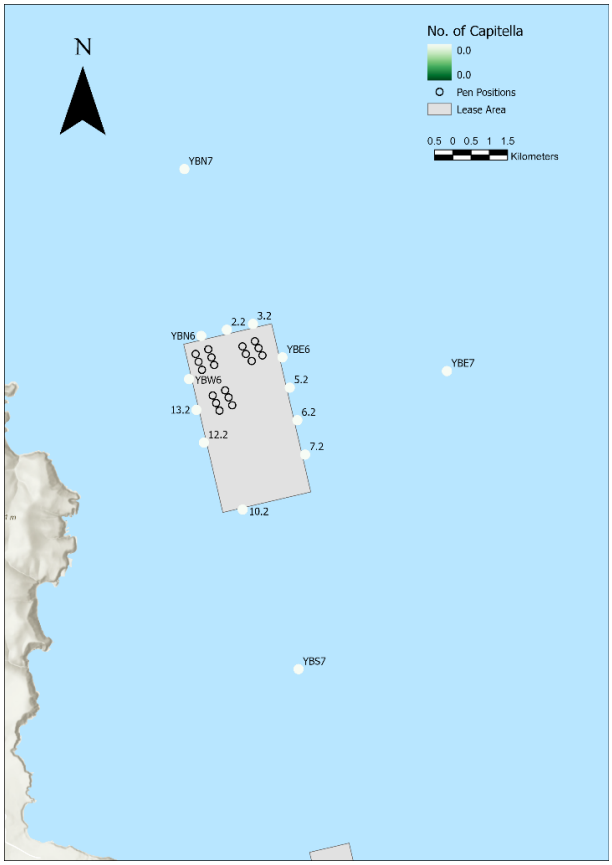
2021 (2YB)



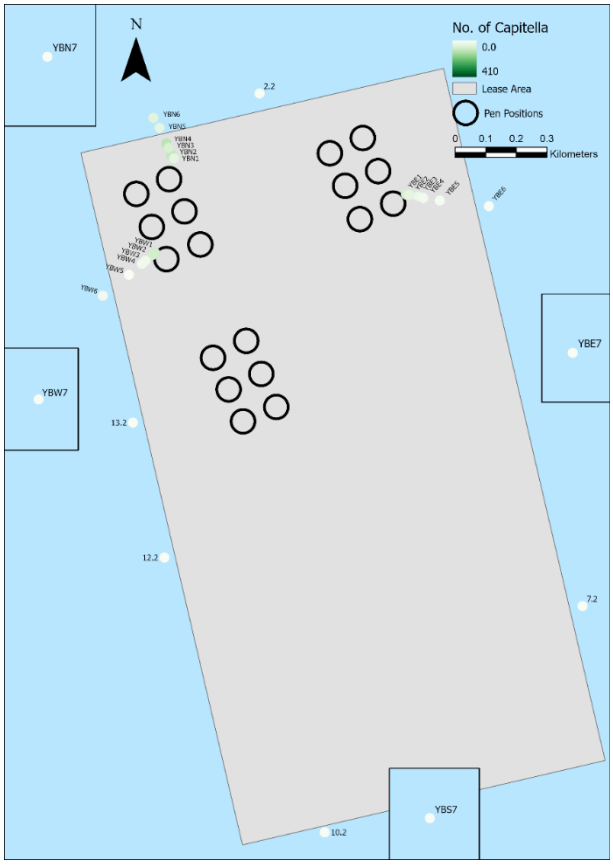
2022 (3YB)



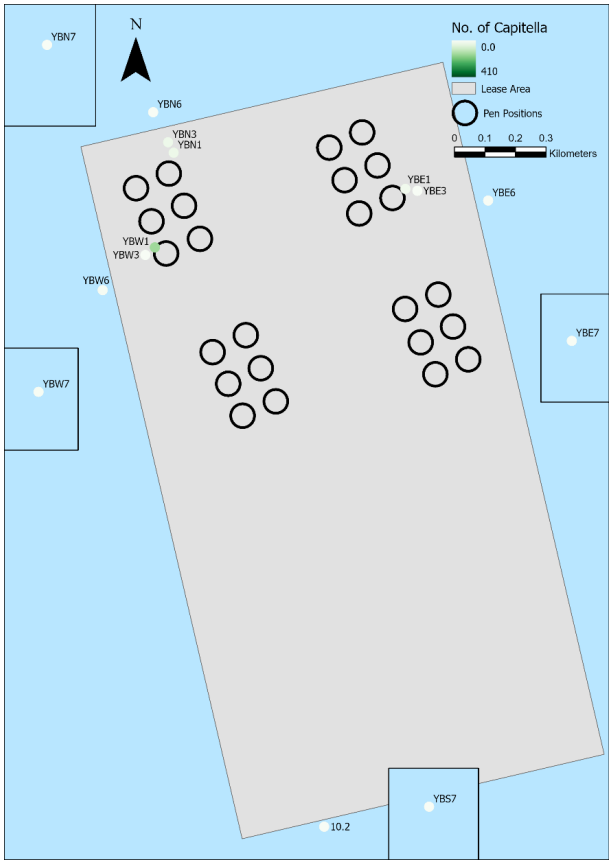
2019 (Baseline)



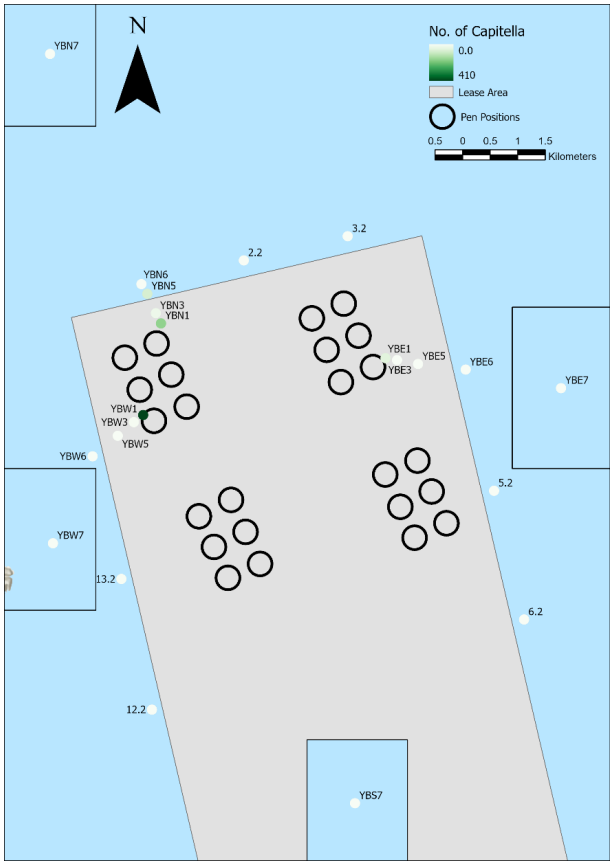
2020 (1YB)



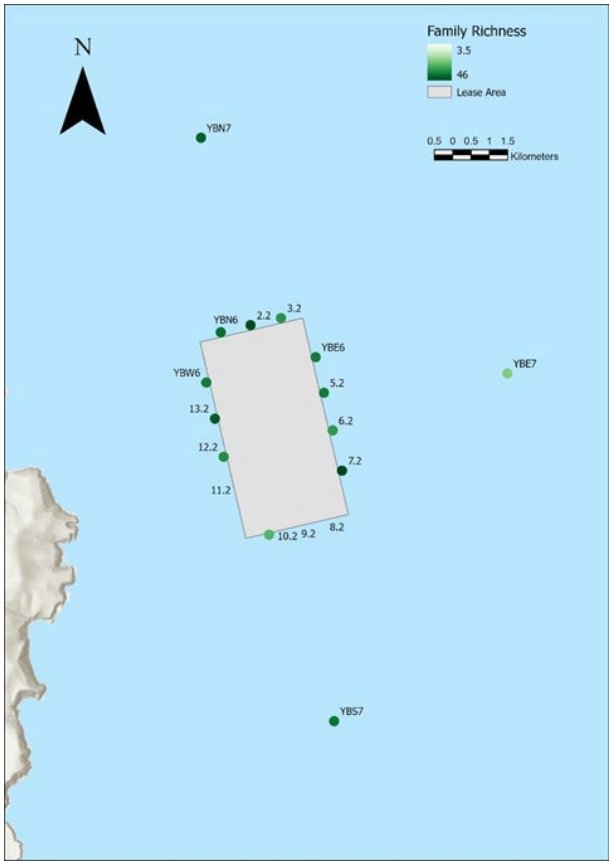
2021 (2YB)



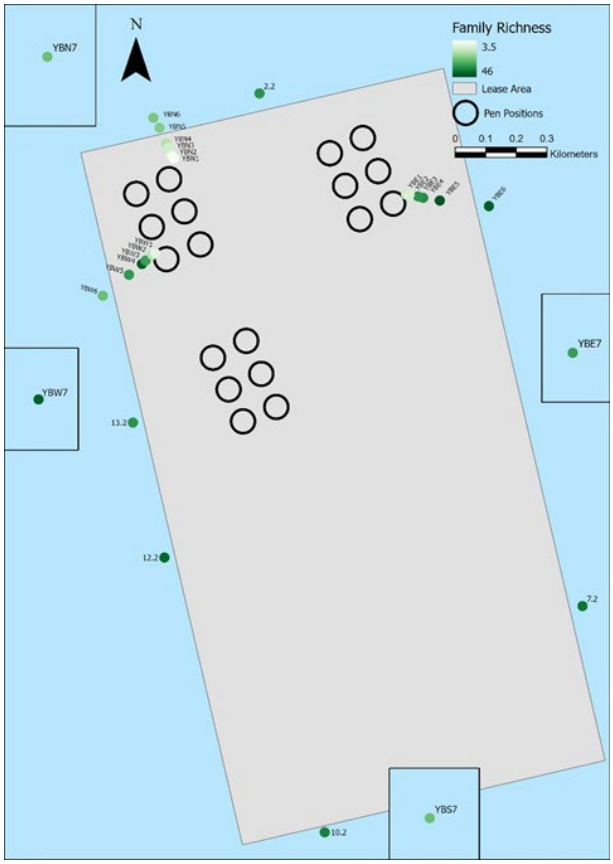
2022 (3YB)



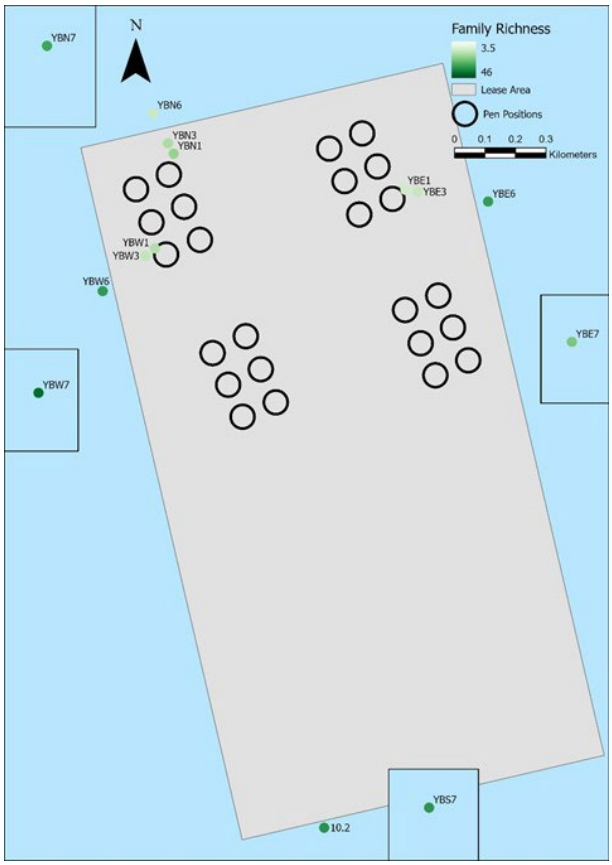
2019 (Baseline)



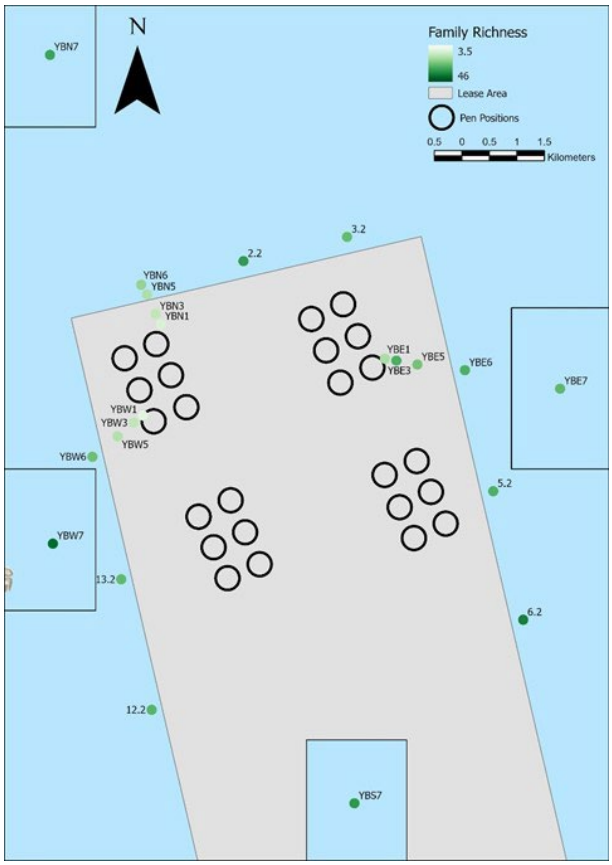
2020 (1YB)



2021 (2YB)



2022 (3YB)



Appendix 4-4: Mean values for sediment parameters across all years

Mean values for sediment parameters for broadscale sites across all years.

	Redox (mv)			Sulphide (uM)			LOI (%)			Carbon (%)			Nitrogen (%)			δ 13C			δ 15N		
Site	2019	2020	2021	2019	2020	2021	2019	2020	2021	2019	2020	2021	2019	2020	2021	2019	2020	2021	2019	2020	2021
SB-1	344	280	438	1.1	1.4	1.6	1.44	0.92	1.62	0.14	0.12	0.11	0.024	0.025	0.017	-21.45	-21.68	-21.99	8.39	7.99	3.98
SB-2	454	437	408	0.0	6.0	0.1	0.96	0.91	1.29	0.06	0.11	0.03	0.009	0.011	0.003	-21.66	-22.12	-20.63	6.97	7.23	NA
SB-3	257	110	261	2.2	8.3	14.7	1.46	1.88	2.09	0.21	0.30	0.18	0.037	0.044	0.026	-21.43	-21.61	-21.36	8.26	7.92	5.18
SB-4	345	392	429	0.0	1.1	0.1	1.25	1.20	1.31	0.10	0.16	0.05	0.017	0.020	0.008	-21.03	-17.96	-19.85	7.77	7.51	2.62
SB-5	403	459	436	7.1	2.5	1.7	0.88	0.82	1.10	0.06	0.07	0.03	0.013	0.009	0.008	-21.80	-20.84	-19.33	7.38	7.20	3.34
SB-6	157	350	294	0.8	0.7	7.3	1.54	1.79	2.08	0.29	0.19	0.23	0.043	0.038	0.041	-21.37	-21.43	-20.87	8.80	8.02	6.79
SB-8	395	449	445	1.0	40.3	0.4	0.78	0.79	0.75	0.07	0.05	0.02	0.009	0.009	0.006	-19.91	-20.23	-18.09	6.08	6.38	1.48
SB-9	400	437	417	0.0	0.5	1.1	0.77	0.84	0.92	0.06	0.05	0.02	0.008	0.010	0.006	-20.87	-21.43	-19.42	5.94	6.15	3.11
SB-10	419	305	286	0.1	11.9	2.5	0.85	1.29	1.03	0.05	0.07	0.02	0.009	0.015	0.006	-21.64	-22.08	-19.38	6.35	5.54	2.98
SB-11	375	398	415	0.2	3.6	11.1	1.67	1.52	2.06	0.09	0.09	0.12	0.022	0.023	0.026	-20.56	-21.49	-20.12	7.62	5.88	5.94
SB-13	371	350	314	8.8	1.8	5.5	1.12	0.77	1.13	0.08	0.07	0.05	0.016	0.013	0.011	-21.65	-20.67	-18.82	6.72	2.74	4.48
SB-16	449	459	463	0.0	0.7	4.3	0.78	0.63	1.03	0.04	0.03	0.00	0.005	0.002	0.003	-20.61	-19.07	NA	5.49	NA	NA
SB-17	82	168	219	0.2	6.3	5.6	1.09	0.84	1.15	0.12	0.13	0.10	0.021	0.018	0.015	-22.06	-22.53	-22.84	7.90	7.95	4.25
SB-18	406	405	440	0.0	0.0	11.7	1.54	1.72	1.38	0.09	0.05	0.14	0.010	0.014	0.026	-21.32	-20.46	-18.65	8.33	6.96	4.42
SB-19	441	448	433	1.4	0.0	1.4	0.76	0.73	0.75	0.03	0.04	0.00	0.008	0.008	0.003	-20.02	-22.01	NA	6.78	5.96	NA
SB-21	160	210	172	7.0	3.4	13.1	3.22	2.90	3.29	0.49	0.83	0.66	0.089	0.107	0.092	-22.35	-22.74	-21.77	7.37	7.81	6.94
SB-22	309	169	287	0.0	8.3	5.6	0.90	0.78	0.73	0.06	0.14	0.06	0.015	0.018	0.014	-23.21	-19.46	-16.50	6.76	6.76	5.57
SB-23	381	449	432	6.0	0.4	18.1	0.79	0.76	0.71	0.03	0.04	0.00	0.008	0.008	0.006	-21.03	-20.66	NA	7.67	5.90	4.56
SB-24	410	448	423	4.0	0.0	1.2	1.03	0.90	0.95	0.03	0.05	0.01	0.008	0.010	0.008	-21.71	-20.51	-16.89	6.97	6.78	4.09
NUB-1	130	139	125	22.0	37.5	20.1	5.93	6.24	6.24	1.02	2.16	1.58	0.193	0.226	0.226	-21.34	-22.96	-30.77	7.24	7.31	6.70
NUB-2	182	275	398	55.3	9.0	21.8	1.44	1.25	1.36	0.74	0.16	0.16	0.028	0.027	0.029	-21.88	-22.02	-20.20	6.26	5.53	5.18
NUB-3	169	145	237	8.8	9.2	15.4	1.65	1.50	1.67	0.18	0.31	0.27	0.034	0.041	0.044	-21.07	-22.15	-21.11	7.61	7.01	7.05
NUB-4	451	453	469	0.0	0.9	5.0	0.73	0.81	0.91	0.14	0.04	0.00	0.007	0.007	0.007	-21.90	-21.01	NA	6.91	3.13	4.65

Mean values for sediment parameters for East of Yellow Bluff sites across all years.

	Redox (mv)			Sulphide (uM)			LOI (%)			Carbon (%)			Nitrogen (%)			δ 13C			δ 15N		
Site	2020	2021	2022	2020	2021	2022	2020	2021	2022	2020	2021	2022	2020	2021	2022	2020	2021	2022	2020	2021	2022
W1	24	-8	220	26.2	98.2	60.5	0.9	1.18	1.0	0.18	-	0.14	0.035	-	0.025	-23.0	-	-24.0	5.8	-	4.3
W2	87	-	-	61.6	-	-	0.8	-	-	0.06	-	-	0.015	-	-	-22.2	-	-	5.5	-	-
W3	103	409	212	42.4	11.0	10.4	0.9	0.80	0.8	0.07	-	0.04	0.015	-	0.008	-21.7	-	-23.6	5.5	-	2.7
W4	222	-	-	23.0	-	-	1.2	-	-	0.05	-	-	0.010	-	-	-21.2	-	-	4.8	-	-
W5	229	-	191	38.0	-	16.4	1.0	-	1.2	0.06	-	0.07	0.010	-	0.015	-22.0	-	-23.8	5.1	-	5.5
W6	50	312	78	34.5	29.8	29.3	1.7	1.24	1.6	0.15	-	0.20	0.027	-	0.041	-21.5	-	-21.9	6.9	-	6.9
W7	51	378	54	27.0	33.0	19.1	1.8	1.91	2.0	0.25	-	0.30	0.033	-	0.044	-22.2	-	-23.5	7.7	-	7.8
E1	22	147	23	25.4	60.3	11.5	1.1	1.24	2.2	0.15	-	0.63	0.025	-	0.112	-22.3	-	-23.1	6.4	-	5.1
E2	172	-	-	17.8	-	-	1.1	-	-	0.09	-	-	0.010	-	-	-21.9	-	-	4.9	-	-
E3	209	369	77	15.8	21.9	4.6	1.0	0.95	0.9	0.09	-	0.06	0.010	-	0.012	-22.0	-	-22.3	4.6	-	3.1
E4	253	-	-	3.2	-	-	1.0	-	-	0.08	-	-	0.010	-	-	-21.5	-	-	5.4	-	-
E5	36	-	123	70.6	-	4.0	1.0	-	1.1	0.06	-	0.08	0.010	-	0.014	-21.9	-	-22.7	6.5	-	4.1
E6	248	441	283	2.5	4.4	0.3	1.0	0.78	1.0	0.06	-	0.05	0.010	-	0.010	-21.4	-	-22.6	6.6	-	2.6
E7	396	441	397	0.4	3.0	0.1	1.0	0.92	0.9	0.06	-	0.06	0.010	-	0.012	-20.9	-	-22.3	7.6	-	5.4
N1	-126	-2	116	60.4	51.3	42.3	1.4	1.35	1.4	0.24	-	0.32	0.030	-	0.048	-21.8		-23.1	5.6	-	4.8
N2	-79	-	-	48.9	-	-	1.5	-	-	0.23	-	-	0.030	-	-	-21.9	-	-	5.4	-	-
N3	-16	78	154	30.3	58.2	29.2	1.4	1.30	1.4	0.17	-	0.21	0.015	-	0.033	-21.2	-	-23.1	5.5	-	4.5
N4	-15	-	-	41.8	-	-	1.2	-	-	0.20	-	-	0.020	-	-	-22.6	-	-	5.3	-	-
N5	NA	-	56	NA	-	35.1	1.1	-	1.2	0.11	-	0.18	0.010	-	0.024	-21.0	-	-22.9	6.8	-	5.2
N6	58	318	14	27.7	36.7	26.5	1.4	0.86	1.3	0.15	-	0.14	0.017	-	0.020	-21.6	-	-22.6	6.2	-	5.4
N7	347	461	411	0.9	5.0	1.7	1.8	1.27	1.9	0.18	-	0.14	0.020	-	0.057	-20.9	-	-22.0	6.5	-	9.5
S7	412	449	413	0.1	4.3	1.3	1.9	1.73	2.1	0.13	-	0.13	0.010	-	0.019	-22.1	-	-22.2	6.9	-	7.5
2	-	-	272	-	-	1.6	-	-	1.2	-	-	0.09	-	-	0.012	-	-	-22.3	-	-	5.4
3	-	-	158	-	-	2.5	-	-	1.0	-	-	0.05	-	-	0.008	-	-	-22.3	-	-	3.4
5	-	-	43	-	-	8.7	-	-	1.2	-	-	0.10	-	-	0.012	-	-	-22.2	-	-	4.3
6	-	-	206	-	-	0.2	-	-	1.0	-	-	0.08	-	-	0.016	-	-	-21.9	-	-	5.6
10	-	439	-	-	5.8	-	-	1.07	-	-	-	-	-	-	-	-	-	-	-	-	-
12	-	-	304	-	-	7.6	-	-	0.9	-	-	0.06	-	-	0.008	-	-	-22.8	-	-	4.5
13	**-**	**-**	**337**	**-**	**-**	**8.1**	**-**	**-**	**1.3**	**-**	**-**	**0.11**	**-**	**-**	**0.013**	**-**	**-**	**-20.9**	**-**	**-**	**5.3**

Mean values for sediment parameters for West of Wedge sites across all years.

	Redox (mv)			Sulphide (uM)			LOI (%)			Carbon (%)			Nitrogen (%)			δ 13C			δ 15N		
Site	2019	2021-Jan	2021-Dec	2019	2021-Jan	2021-Dec	2019	2021-Jan	2021-Dec	2019	2021-Jan	2021-Dec	2019	2021-Jan	2021-Dec	2019	2021-Jan	2021-Dec	2019	2021-Jan	2021-Dec
CP1	305	443	433	0.0	13.2	0.0	1.17	0.60	0.90	-	0.06	0.03	-	0.005	0.007	-	-22.2	-24.6	-	<LOD*	3.2
CP2	336	455	424	0.0	4.9	0.1	1.13	0.73	1.07	-	0.06	0.06	-	0.009	0.011	-	-21.0	-23.5	-	5.9	3.8
CP3	302	412	421	0.0	4.9	0.0	1.13	0.74	0.96	-	0.06	0.03	-	0.009	0.009	-	-20.6	-22.4	-	7.3	3.9
CP4	322	445	429	0.0	4.7	0.0	1.03	0.74	0.95	-	0.05	0.03	-	0.009	0.008	-	-20.5	-22.9	-	6.5	3.8
CP5	320	446	436	0.0	3.9	0.0	0.93	0.73	0.87	-	0.05	0.01	-	0.009	0.006	-	-20.4	-22.8	-	4.9	3.5
CP6	312	439	453	0.0	3.5	0.0	0.93	0.74	0.84	-	0.05	0.03	-	0.009	0.008	-	-20.2	-23.5	-	5.4	3.7
CP7	349	453	436	0.0	3.8	0.0	0.97	0.66	0.90	-	0.04	0.02	-	0.008	0.007	-	-19.9	-23.3	-	4.5	3.8
CP8	309	456	399	0.0	3.6	0.0	0.93	0.75	0.89	-	0.04	0.01	-	0.007	0.007	-	-20.1	-22.5	-	5.8	4.1
C1	286	451	164	43.6	4.1	19.3	1.23	0.89	1.08	-	0.08	0.10	-	0.011	0.017	-	-21.0	-22.0	-	4.9	5.2
C2	313	446	437	0.0	NA	0.0	0.70	0.65	0.76	-	0.04	0.01	-	0.009	<LOD*	-	-20.0	-21.7	-	7.0	<LOD*
NUB4	-	454	434	-	3.2	0.0	-	0.82	0.86	-	0.04	0.02	-	0.008	0.006	-	-20.1	-20.9	-	4.2	3.8
SB16	-	447	424	-	2.9	0.1	-	0.73	0.97	-	0.03	<LOD*	-	<LOD*	<LOD*	-	-20.1	<LOD*	-	<LOD*	<LOD*
PB1	-	350	90	-	20.3	77.8	-	0.94	0.92	-	0.06	0.03	-	0.015	0.010	-	-21.3	-22.6	-	3.3	2.8
PB1a	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PB2	-	403	139	-	10.0	8.8	-	0.80	0.85	-	0.04	0.04	-	0.007	0.014	-	-20.5	-22.2	-	1.7	3.7
PB3	-	-	109	-	-	11.4	-	-	0.95	-	-	0.03	-	-	0.007	-	-	-21.7	-	-	4.4
PB4	-	-	309	-	-	0.0	-	-	0.89	-	-	0.03	-	-	0.007	-	-	-21.8	-	-	4.5

*<LOD = Lower than limit of detection

Appendix 4-5: Mean values for macrofaunal community data across all years

Mean values for macrofaunal communities at the broadscale sites.

	Mean Abundance			Mean Family Richness			Mean Diversity (H')			Mean Annelids			Mean AMBI		
Site	2019	2020	2021	2019	2020	2021	2019	2020	2021	2019	2020	2021	2019	2020	2021
SB-1	48.7	67.7	26.0	16.0	22.3	12.0	2.1	2.5	2.1	3.3	4.0	0.7	1.141	1.379	1.155
SB-2	63.0	78.7	28.7	24.3	28.0	14.7	2.9	2.9	2.5	11.7	12.3	5.3	1.655	0.94	1.893
SB-3	118.0	86.7	76.3	27.3	30.7	27.3	2.5	3.1	2.9	17.0	17.3	17.3	0.949	1.271	1.443
SB-4	83.0	228.3	88.3	30.0	43.7	23.0	3.0	2.8	2.6	7.3	8.7	32.0	1.217	0.93	1.101
SB-5	71.3	101.3	42.3	21.7	22.0	14.3	2.6	2.5	2.3	114.0	124.0	3.0	1.623	1.926	2.203
SB-6	205.7	252.7	145.7	40.7	42.0	34.7	3.0	3.1	3.0	31.7	13.7	58.7	1.443	1.874	2.094
SB-8	28.0	72.3	32.7	13.7	25.0	17.3	2.3	2.8	2.6	16.0	19.7	2.7	2.186	2.554	1.758
SB-9	60.7	44.0	40.3	23.0	16.7	19.7	2.7	2.3	2.6	16.0	7.7	3.3	1.379	1.195	1.307
SB-10	58.3	43.0	21.3	21.0	16.0	10.0	2.6	2.4	2.0	9.3	9.3	3.3	2.477	1.719	2.275
SB-11	76.3	198.3	134.0	29.3	41.7	32.7	2.9	3.2	2.6	22.7	15.0	23.7	1.342	1.403	1.197
SB-13	54.7	80.0	47.3	19.3	22.3	19.3	2.3	2.3	2.4	13.3	93.7	1.7	1.138	0.786	1.413
SB-16	80.0	110.7	32.3	28.7	27.7	16.7	3.0	2.8	2.6	6.7	10.0	3.3	1.819	2.639	1.942
SB-17	97.7	70.0	31.0	30.3	18.3	11.7	2.8	2.3	2.2	59.7	106.3	2.3	1.923	1.971	2.128
SB-18	108.0	100.0	70.0	36.7	33.7	20.3	3.2	3.0	2.3	3.3	14.7	14.0	2.042	1.466	1.395
SB-19	321.3	223.7	10.0	23.3	24.3	7.0	0.9	1.4	1.8	12.3	4.7	0.7	2.826	2.431	1.471
SB-21	127.0	130.3	132.0	15.0	13.7	17.7	1.6	1.3	1.7	24.7	46.0	120.7	2.721	2.804	2.682
SB-22	87.0	141.0	55.0	27.3	25.0	24.0	2.7	2.3	2.9	4.7	2.7	9.0	1.194	1.154	1.61
SB-23	100.3	70.3	38.7	36.0	26.3	15.0	3.2	2.9	2.4	15.7	11.7	6.0	1.129	1.335	2.098
SB-24	76.0	50.7	20.0	29.7	27.3	13.7	3.1	3.1	2.5	38.0	14.7	4.3	1.747	1.438	1.838
NUB-1	183.7	254.0	148.0	22.0	29.0	24.0	2.0	2.4	2.3	141.3	174.0	115.7	1.559	1.542	1.922
NUB-2	211.0	183.3	125.0	33.7	29.0	27.3	2.9	2.6	2.7	14.0	13.0	7.0	2.159	2.21	2.33
NUB-3	121.3	178.3	102.0	27.7	31.0	26.3	2.7	2.9	2.8	76.0	90.3	48.3	1.265	1.987	1.915
NUB-4	69.7	80.3	27.3	23.0	27.0	13.3	2.9	2.9	2.4	15.0	15.0	1.7	1.537	1.908	2.578

Mean values for macrofaunal communities at the East of Yellow Bluff sites.

	Mean Abundance			Mean Family Richness			Mean Diversity (H')			Mean Annelids			Mean AMBI		
Site	2020	2021	2022	2020	2021	2022	2020	2021	2022	2020	2021	2022	2020	2021	2022
W1	100.5	372.7	438.3	8.5	17.0	9.0	0.6	1.5	0.4	91.0	203.7	427.3	5.7	5.3	5.8
W2	113.5	-	-	16.5	-	-	1.5	-	-	96.0	-	-	3.8	-	-
W3	101.0	63.7	51.0	31.5	15.0	15.0	2.9	2.0	2.3	47.5	1.0	15.7	2.8	3.2	2.8
W4	166.0	-	-	42.5	-	-	3.2	-	-	68.0	-	-	2.7	-	-
W5	99.0	-	58.3	33.0	-	16.7	3.0	-	2.5	16.5	-	10.0	1.7	-	1.9
W6	105.3	143.0	110.3	25.7	32.7	25.3	2.7	3.0	2.6	49.7	30.7	20.0	3.1	2.2	1.4
W7	123.3	152.7	124.0	42.3	40.3	40.3	3.3	3.1	3.2	28.7	53.3	44.3	1.4	1.3	1.7
E1	99.0	52.7	93.3	13.0	12.7	18.0	1.1	2.1	1.7	85.0	33.3	69.7	5.0	3.9	4.9
E2	76.5	-	-	10.5	-	-	1.2	-	-	67.0	-	-	4.8	-	-
E3	209.5	26.7	289.3	34.0	14.3	29.0	2.5	2.4	1.7	80.0	1.7	27.3	2.6	2.4	1.9
E4	263.5	-	-	35.0	-	-	2.8	-	-	61.5	-	-	2.1	-	-
E5	200.5	-	182.7	43.5	-	24.7	3.1	-	2.2	60.0	-	25.0	2.4	-	1.5
E6	231.3	129.0	220.7	42.3	32.3	28.7	3.0	2.9	2.4	44.7	17.7	20.3	1.6	2.0	1.3
E7	107.0	52.7	110.3	32.0	23.7	27.0	3.0	2.9	2.8	15.0	0.0	24.0	1.4	1.4	1.6
N1	53.5	138.3	219.3	3.5	20.7	10.7	0.3	2.0	1.1	52.0	31.3	180.0	5.8	4.8	5.6
N2	116.0	-	-	5.5	-	-	0.3	-	-	111.5	-	-	5.9	-	-
N3	88.0	68.7	57.0	12.0	18.0	15.0	0.9	2.1	2.0	75.5	32.3	35.0	5.5	4.2	4.4
N4	146.0	-	-	16.5	-	-	0.9	-	-	123.0	-	-	5.6	-	-
N5	95.0	-	160.3	22.5	-	17.3	2.0	-	1.8	62.0	-	123.3	4.4	-	3.7
N6	129.3	38.0	107.3	23.7	13.7	20.7	2.3	2.3	1.9	77.0	3.7	12.7	3.3	2.9	1.9
N7	213.0	488.0	346.7	25.3	30.7	31.0	2.0	1.8	2.2	14.0	12.0	10.3	2.0	1.7	1.9
S7	233.0	249.0	198.3	37.7	33.7	33.0	2.6	2.4	2.7	10.3	9.0	11.3	1.7	1.5	1.8
2	126.7	-	335.3	34.0	-	32.7	3.0	-	2.0	31.3	-	4.3	1.8	-	1.6
3	-	-	253.0	-	-	26.3	-	-	1.9	-	-	8.7	-	-	1.4
5	-	-	133.0	-	-	28.7	-	-	2.6	-	-	3.3	-	-	2.2
6	-	-	226.3	-	-	37.0	-	-	2.8	-	-	20.7	-	-	1.5
7	204.3	-	-	39.0	-	-	3.0	-	-	22.0	-	-	1.3	-	-
10	179.0	130.7	-	36.7	34.0	-	2.7	3.0	-	23.7	14.7	-	1.5	1.8	-

12	130.0	-	144.0	41.0	-	27.7	3.3	-	2.6	22.7	-	15.0	1.8	-	2.7
13	160.7	-	149.7	34.0	-	26.7	3.0	-	2.6	51.7	-	9.3	2.2	-	2.5

Mean values for macrofaunal communities at the West of Wedge sites.

	Mean Abundance			**Mean Family Richness**			**Mean Diversity (H')**			**Mean Annelids**			**Mean AMBI**		
Site	2019	2021-Jan	2021-Dec	2019	2021-Jan	2021-Dec	2019	2021-Jan	2021-Dec	2019	2021-Jan	2021-Dec	2019	2021-Jan	2021-Dec
CP1	130.0	170.3	49.7	30.7	37.0	24.3	2.8	2.9	3.0	10.0	14.0	8.0	1.4	2.1	1.9
CP2	150.0	133.0	55.7	36.0	36.0	21.7	3.0	3.0	2.6	9.7	18.0	13.3	1.4	2.2	1.6
CP3	115.0	115.3	39.7	29.7	34.0	18.7	2.8	3.0	2.7	6.0	10.7	3.3	1.1	1.7	1.8
CP4	116.0	96.7	53.0	32.0	28.0	20.3	2.9	3.0	2.7	7.7	15.0	3.7	1.0	1.7	1.5
CP5	145.0	134.0	57.3	38.7	36.7	22.0	3.1	3.0	2.7	18.0	19.3	4.3	1.1	1.7	1.4
CP6	149.7	148.0	42.7	35.0	39.7	21.7	2.9	3.2	2.9	7.7	17.7	5.7	1.4	1.7	1.6
CP7	140.3	106.0	56.3	35.3	32.0	21.3	3.0	3.0	2.8	10.7	9.0	6.7	1.4	1.8	1.7
CP8	119.3	117.0	54.0	31.0	29.7	27.3	2.9	2.8	3.1	4.3	9.0	9.0	1.5	2.4	1.5
C1	63.0	125.7	29.0	25.0	30.0	11.3	2.9	3.0	2.0	6.3	12.3	2.7	1.7	2.2	1.6
C2	121.0	95.0	43.0	29.3	32.0	18.7	2.9	3.0	2.6	12.0	7.0	3.7	0.9	1.4	1.5
NUB4	-	125.7	47.7	-	33.3	20.0	-	3.0	2.7	-	7.0	6.3	-	1.8	1.8
SB16	-	111.0	48.0	-	30.7	19.3	-	2.9	2.6	-	11.7	4.3	-	2.5	1.4
PB1	-	106.7	66.0	-	28.0	18.0	-	2.9	2.4	-	18.7	29.7	-	2.3	2.9
PB1a	-	360.7	-	-	33.0		-	2.1	-	-	189.3	-	-	5.1	-
PB2	-	165.7	56.7	-	33.7	13.7	-	2.9	2.3	-	25.3	28.0	-	2.4	3.5
PB3	-	-	122.0	-	-	18.3	-	-	2.2	-	-	52.0	-	-	3.8
PB4	-	-	64.0	-	-	24.7	-	-	2.8	-	-	18.7	-	-	2.3

Appendix 4-6: Macrofauna raw data for Yellow Bluff in March 2020, March 2021 and March 2022

Macrofauna raw data for Yellow Bluff in March 2020 (data is pooled by site).

Family name	N1	N2	N3	N4	N5	N6	N7	E1	E2	E3	E4	E5	E6	E7	S7	W1	W2	W3	W4	W5	W6	W7	2	7	10	12	13
Ampeliscidae	0	0	0	0	0	4	1	0	0	1	0	2	3	0	8	0	1	1	3	1	0	42	0	4	9	19	0
Ampharetidae	0	0	0	0	0	3	1	0	0	3	1	3	0	0	0	0	0	0	0	0	0	7	0	0	0	0	1
Amphinomidae	0	0	0	0	0	0	7	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	3
Amphipoda (O.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	0	0	0	0	0	0	0	0	0
Amphiuridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Anabathridae	0	0	0	0	4	6	1	0	0	4	6	5	4	5	2	0	0	1	0	0	0	5	1	15	6	5	0
Anthuridae	0	0	0	0	2	0	2	1	0	0	1	1	1	0	4	0	1	4	3	0	1	7	2	7	5	8	6
Aoridae	1	2	4	8	3	1	0	1	0	2	2	2	11	18	50	0	0	5	13	3	0	6	9	12	5	16	22
Apistobranchidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Apseudidae	0	0	0	0	0	3	107	0	0	1	1	1	10	17	293	0	0	0	15	0	2	9	1	16	10	1	2
Arcturidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
Asteriidae	1	1	1	3	4	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0
Austrarcturellidae	0	0	0	0	0	0	0	0	0	1	3	0	5	6	0	0	0	0	0	1	0	2	0	9	2	0	0
Axiidae	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bodotriidae	0	0	0	2	4	9	10	0	2	2	5	2	31	14	20	1	4	4	6	9	4	5	18	29	13	14	10
Bopyridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
Brachyura (iO)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Branchiostomatidae	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Callipallenidae	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Calyptraeidae	0	0	0	0	0	0	9	0	0	0	0	0	0	0	4	0	0	0	0	0	0	2	0	0	0	1	0
Cancridae	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Capitellidae	101	218	144	238	100	174	2	148	103	70	30	20	2	1	0	174	164	41	45	1	54	2	0	1	2	4	55
Caprellidae	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cardiidae	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	1	0	1	1	0	5	0	0	2	4	0
Carditidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	2	0	0	0	0	0	0	0	1
Cerithiopsidae	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chaetiliidae	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Cingulopsidae	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0	0	0	0
Cirolanidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	1	1	0
Cirratulidae	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	1	5	0	0	2	1	0	0	0	0
Columbellidae	0	0	0	0	0	0	0	0	0	0	0	0	10	5	0	0	0	0	0	0	0	4	1	4	5	9	0
Condylocardiidae	0	0	0	0	0	1	9	0	0	3	0	1	0	0	1	0	1	3	6	11	5	1	0	58	10	4	27

Family name	N1	N2	N3	N4	N5	N6	N7	E1	E2	E3	E4	E5	E6	E7	S7	W1	W2	W3	W4	W5	W6	W7	2	7	10	12	13
Copepoda (sCl.)3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Copepoda (sCl.)4	0	0	0	0	0	0	0	0	0	2	0	1	1	0	0	0	0	0	0	0	0	0	1	0	3	0	0
Corbulidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
Corophiidae	0	0	0	0	0	0	3	0	0	56	61	54	129	22	20	0	0	0	1	1	0	2	24	61	155	8	10
Crangonidae	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	1	0	0
Cucumariidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Cylindroleberididae	0	0	1	0	0	0	0	0	0	1	2	0	18	6	4	0	0	4	6	2	0	1	3	5	2	14	2
Cypridinidae	0	0	0	0	0	0	0	0	0	0	0	3	0	1	3	0	0	0	0	0	0	2	0	3	7	0	1
Dexaminidae	0	0	0	1	2	2	0	0	0	0	1	0	3	1	16	0	0	3	1	0	1	0	1	6	1	1	6
Diastylidae	0	0	3	3	5	5	0	0	1	3	15	9	19	21	0	1	2	6	9	7	2	3	6	14	5	6	2
Dogielinotinae	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dorvilleidae	0	0	1	0	0	0	0	0	0	0	1	0	6	1	1	0	0	4	23	1	0	0	3	0	0	1	8
Edwardsiidae	0	0	0	0	0	0	0	0	0	20	4	1	1	1	1	0	0	1	5	3	1	0	6	0	0	5	14
Enteropneusta (Cl.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
Eusiridae	0	0	0	1	0	2	9	4	1	3	4	0	4	12	24	0	1	2	2	2	3	9	4	15	9	16	22
Galatheidae	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Galeommatidae	0	0	1	0	1	3	0	0	0	0	0	0	0	0	4	0	0	0	0	0	1	2	1	1	2	0	0
Glyceridae	0	0	0	0	0	0	1	0	0	0	4	7	5	3	3	0	0	0	3	2	0	0	6	4	5	3	5
Glycymerididae	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	2	0	0	1
Gnathiidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0
Gynodiastylidae	0	0	0	0	1	1	0	0	0	2	2	1	2	6	1	0	3	1	1	0	2	1	4	4	2	3	0
Hesionidae	0	0	0	0	0	0	4	0	0	0	0	0	0	0	1	0	0	0	5	0	0	0	0	0	0	0	17
Hexapodidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1
Hiatellidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Holozoidae	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	1	0	0	0	0
Hymenosomatidae	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Inachoididae	0	0	0	0	0	1	0	1	0	0	3	1	0	0	0	0	0	0	0	0	0	0	1	0	1	1	0
Isaeidae	0	0	1	1	6	62	1	1	8	89	154	67	93	16	2	0	1	7	7	12	24	22	41	52	58	36	1
Ischyroceridae	0	0	1	2	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
Janiridae	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Kalliapseudidae	0	0	0	0	0	0	3	0	0	0	0	0	0	0	8	0	0	0	0	0	0	3	0	0	0	0	0
Lepetidae	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Leptocheliidae	0	0	0	2	0	0	0	3	0	0	0	0	0	0	1	1	0	0	9	0	0	7	0	0	0	0	1
Leucosiidae	0	0	0	0	0	0	0	0	0	1	3	4	0	1	0	0	0	0	1	0	0	1	1	1	0	1	0

Family name	N1	N2	N3	N4	N5	N6	N7	E1	E2	E3	E4	E5	E6	E7	S7	W1	W2	W3	W4	W5	W6	W7	2	7	10	12	13
Leucothoidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0
Liljeborgiidae	0	0	1	0	1	2	0	0	0	1	7	2	2	1	0	0	0	4	3	1	7	4	2	5	0	1	18
Limidae	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Loveniidae	0	0	4	0	0	0	0	2	1	0	1	0	2	1	0	0	2	10	4	7	34	6	10	0	4	6	0
Luciferidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Lucinidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Lumbrineridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	7
Lysianassidae	0	0	0	1	0	3	0	0	0	3	21	22	12	3	33	0	0	0	2	2	1	1	12	12	5	9	0
Mactridae	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Maeridae	0	0	0	0	0	0	192	0	0	0	0	0	0	0	14	0	0	0	0	0	0	0	0	1	0	0	15
Majidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Maldanidae	0	0	0	0	0	1	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	6	0	1	1	0	1
Mangeliidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	4	0	0	0	0	0
Marginellidae	0	0	0	0	0	0	0	0	0	0	0	0	4	2	0	0	0	0	0	0	0	0	1	0	1	0	0
Melitidae	0	0	0	0	0	0	9	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	2	1	2
Melphidippidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	0	0	0	2	0	0	4	0	4	1	0	0
Muricidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0
Myochamidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Myodocopa (SCl.)	0	0	0	0	0	0	0	0	0	1	0	0	10	1	0	0	0	0	1	2	0	0	8	4	5	2	0
Mysidae	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0
Mytilidae	0	1	0	0	1	0	0	0	0	0	0	0	1	0	1	2	0	1	0	0	0	0	0	0	0	0	0
Nassariidae	0	4	1	3	2	4	6	2	0	1	2	4	0	7	0	7	2	0	0	1	4	4	1	0	0	2	3
Naticidae	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	1	1	1	4	0
Nebaliidae	0	0	0	0	0	1	0	0	0	2	2	0	0	1	0	0	0	0	0	0	2	1	1	0	1	4	0
Nematoda (P.)	0	0	0	0	1	0	0	0	0	0	0	9	3	4	1	0	0	0	5	4	0	0	18	7	2	25	3
Nemertea (P.)	0	0	0	0	6	2	8	0	0	3	0	9	5	3	6	0	2	7	16	7	7	4	7	3	6	6	33
Nephtyidae	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0
Nereididae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	2	0	0	1	0	2	2
Nuculanidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Nuculidae	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Oedicerotidae	0	0	1	0	0	4	0	0	0	1	4	3	4	5	17	0	2	2	2	0	0	9	1	2	2	1	0
Oenonidae	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Oligochaeta (sCl)	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Olivellidae	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Family name	N1	N2	N3	N4	N5	N6	N7	E1	E2	E3	E4	E5	E6	E7	S7	W1	W2	W3	W4	W5	W6	W7	2	7	10	12	13
Onuphidae	0	0	0	0	1	6	0	3	2	12	9	15	20	4	3	1	1	11	5	9	11	3	20	4	12	8	1
Opheliidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	0	0	0	0	0	0	0	0	0	0	0	1
Ophiuridae	0	1	0	1	5	20	2	3	3	8	27	10	42	17	3	0	2	15	25	42	19	0	37	78	30	13	13
Orbiniidae	0	0	0	0	3	4	0	0	1	3	1	1	1	0	0	0	1	0	3	0	0	6	0	0	0	0	1
Ostracoda (Cl.)1	0	0	0	0	0	0	0	0	0	2	8	1	1	3	7	0	1	0	1	1	1	0	6	3	0	2	0
Ovalipidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Oweniidae	0	0	0	0	1	3	4	1	4	4	5	4	10	3	1	0	0	5	4	5	12	0	12	5	1	9	5
Paguridae	0	0	0	0	0	0	17	0	0	1	0	2	2	0	9	0	0	2	5	1	6	6	0	1	7	5	18
Palaemonidae	0	0	1	1	0	0	8	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Paramunnidae	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Paraonidae	0	0	0	1	0	0	2	0	0	0	0	0	0	1	1	0	0	0	6	1	1	0	0	0	1	0	28
Pasiphaeididae	0	0	0	0	0	0	0	0	0	0	0	0	3	1	0	0	0	0	1	0	1	4	1	0	0	2	1
Pectinariidae	0	1	2	4	2	3	0	1	2	8	14	6	1	0	0	2	0	2	3	1	10	2	2	0	0	2	0
Philinidae	0	0	0	8	5	4	0	1	0	2	0	5	0	0	0	3	1	2	1	1	0	0	1	1	0	0	0
Philomedidae	0	0	0	0	1	5	0	6	0	29	34	24	37	18	22	0	1	5	2	15	3	25	34	47	44	22	0
Phoronida (P.)	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
Photidae	0	0	0	0	0	0	2	0	0	0	6	2	12	7	44	0	1	1	0	2	0	4	1	4	1	2	9
Phoxichilidiidae	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phoxocephalidae	0	0	0	0	1	3	15	1	0	4	6	4	10	3	21	0	1	5	5	4	13	25	5	1	8	17	19
Phyllodocidae	0	0	0	0	0	4	0	0	1	2	6	4	4	2	0	0	0	3	1	1	2	2	2	2	2	0	0
Pilumnidae	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pinnotheridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	2
Platyischnopidae	0	0	0	0	0	0	1	0	0	0	0	0	4	2	2	0	0	0	0	2	0	0	0	2	3	2	0
Pleurobranchidae	0	0	4	4	6	0	1	0	1	1	0	3	0	0	0	1	2	1	0	0	1	0	0	0	0	0	0
Poecilochaetidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	2	0
Polygordiidae	0	0	0	0	0	0	0	0	0	0	0	0	3	0	2	0	0	1	0	0	0	0	1	0	1	0	3
Polynoidae	0	0	1	1	0	0	4	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
Psammobiidae	0	0	0	0	0	1	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	0	1	0	0	0	1
Pseudocumatidae	0	0	0	0	0	0	0	0	0	0	1	0	1	2	0	0	0	0	1	0	0	0	0	0	1	0	3
Pyramidellidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0
Retusidae	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	2	0
Rutidermatidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0
Sabellidae	0	0	0	0	0	0	0	0	0	1	7	10	30	4	2	0	1	0	0	1	1	5	2	7	2	4	0
Sarsiellidae	0	0	0	0	0	0	0	0	0	0	6	2	3	0	0	0	0	3	1	0	0	2	2	6	5	6	1

Family name	N1	N2	N3	N4	N5	N6	N7	E1	E2	E3	E4	E5	E6	E7	S7	W1	W2	W3	W4	W5	W6	W7	2	7	10	12	13
Sebidae	0	0	0	0	0	0	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Serolidae	0	0	0	0	0	0	2	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0
Serpulidae	0	0	0	0	0	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sigalionidae	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0	0	0	0	0	0	2	0	0	0	1	0
Solenidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Sphaeromatidae	0	0	0	0	0	3	139	0	0	2	7	8	20	2	29	0	0	0	1	2	0	1	8	6	14	1	10
Spionidae	3	4	2	1	16	29	0	17	21	53	34	28	35	25	6	4	25	24	22	10	53	32	41	38	40	30	12
Syllidae	0	0	1	1	1	4	12	0	0	3	11	13	13	1	1	1	0	3	5	1	1	15	3	1	3	1	4
Synaptidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Synopiidae	0	0	0	0	1	2	8	0	0	0	2	2	8	3	60	3	2	4	21	4	1	12	0	11	5	1	43
Talitridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Temnopleuridae	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Terebellidae	0	0	0	0	0	0	2	0	0	0	0	3	0	0	0	0	0	0	2	0	0	0	0	0	0	0	1
Terebridae	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Thraciidae	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	3	3	0	0	0	0	0
Trochidae	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Turritellidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Urohaustoriidae	0	0	0	0	0	0	0	0	0	0	0	1	7	2	0	0	0	0	2	3	0	0	0	7	0	2	0
Veneridae	0	0	1	2	1	0	0	0	0	2	0	2	0	7	3	0	0	0	0	3	9	6	0	1	0	1	0
Whiteleggiidae	0	0	0	0	0	0	0	0	0	0	1	5	11	24	2	0	0	0	0	0	0	0	0	18	0	4	0
Total Abundance	**107**	**232**	**176**	**292**	**190**	**388**	**639**	**198**	**153**	**419**	**527**	**401**	**694**	**321**	**806**	**201**	**227**	**202**	**332**	**198**	**316**	**370**	**380**	**613**	**537**	**390**	**482**
Total Families	**5**	**8**	**20**	**24**	**31**	**38**	**50**	**19**	**16**	**48**	**46**	**57**	**62**	**52**	**59**	**13**	**27**	**40**	**59**	**48**	**44**	**67**	**54**	**59**	**58**	**65**	**55**

Macrofauna raw data for Yellow Bluff in March 2021 (data is pooled by site).

Family	N1	N3	N6	N7	E1	E3	E6	E7	S7	W1	W3	W6	W7	10
Alpheidae	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Ampeliscidae	0	0	1	0	0	1	2	0	11	0	1	2	69	6
Ampharetidae	0	1	0	0	0	0	1	0	1	0	0	0	2	1
Amphilochidae	1	0	0	0	0	0	0	0	0	5	0	0	0	0
Amphinomidae	0	0	0	4	0	0	0	0	0	0	0	0	0	0
Anabathridae	0	0	1	8	0	0	1	3	0	0	1	0	1	7
Anthozoa (Cl.)	3	0	0	0	0	0	0	0	0	0	0	0	0	0
Anthuridae	0	0	0	3	0	3	2	0	8	1	1	0	9	10
Aoridae	0	1	1	13	0	0	20	3	70	0	0	6	6	20
Apistobranchidae	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Apseudidae	0	1	0	209	0	1	4	4	134	1	1	11	11	7
Arcturidae	0	0	0	0	0	0	1	2	0	0	0	0	0	2
Ascidiidae	0	0	0	0	0	0	0	0	0	3	0	0	0	0
Asteriidae	9	0	0	0	0	0	0	0	0	4	0	0	1	0
Austrarcturellidae	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Balanidae	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Bodotriidae	3	4	15	8	8	3	33	8	9	1	9	8	11	11
Brachyura (iO)	0	0	0	0	0	0	0	0	1	1	0	0	0	0
Calyptraeidae	0	0	0	0	0	0	0	0	0	0	0	0	3	0
Capitellidae	85	82	1	1	57	1	0	0	2	463	0	13	6	0
Caprellidae	10	0	0	0	0	0	0	0	1	21	0	0	0	0
Cardiidae	0	0	0	0	0	0	0	0	0	0	0	0	2	1
Chaetiliidae	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Chitonidae	0	0	0	3	0	0	0	0	0	0	0	0	0	0
Chrysopetalidae	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Cirratulidae	1	0	0	0	0	0	0	0	1	1	0	0	0	1
Columbellidae	3	1	0	0	0	0	1	2	0	3	0	0	3	4
Condylocardiidae	0	0	0	8	0	0	0	1	0	0	4	1	0	7
Copepoda (sCl.)	0	0	0	0	0	0	1	2	0	0	0	0	0	0
Corbulidae	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Corophiidae	2	3	0	0	0	0	1	2	3	0	0	3	0	0
Crangonidae	0	0	0	0	0	0	0	0	0	0	0	0	1	0

Family	N1	N3	N6	N7	E1	E3	E6	E7	S7	W1	W3	W6	W7	10
Cucumariidae	0	0	0	2	0	0	0	0	0	0	0	0	0	0
Cylindroleberididae	5	1	6	0	3	6	11	1	7	0	2	21	5	13
Cypridinidae	0	0	0	0	0	0	10	20	4	0	0	0	0	9
Dexaminidae	1	0	0	0	0	0	2	3	7	1	0	0	0	2
Diastylidae	3	3	2	5	1	1	7	8	0	0	4	1	8	9
Dorvilleidae	0	0	0	0	0	0	1	0	0	0	0	1	0	0
Edwardsiidae	0	0	0	0	0	1	0	0	0	0	0	14	7	0
Enteropneusta (Cl.)	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Eunicidae	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Eusiridae	0	0	0	3	0	0	0	0	0	0	0	0	0	0
Galeommatidae	0	2	1	0	0	2	1	0	1	1	0	1	0	0
Gastropod (Cl.)	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Gastropoda (Cl.)	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Glyceridae	0	0	0	2	1	0	2	0	4	0	1	0	0	4
Glycymerididae	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Gnathiidae	0	0	0	0	0	0	0	0	2	0	0	0	0	0
Goniadidae	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Gynodiastylidae	0	0	0	0	0	0	0	2	3	0	0	3	0	0
Haylidae	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Hesionidae	0	0	0	3	0	0	0	0	1	0	0	0	0	0
Hexapodidae	0	1	1	2	0	0	1	0	1	0	1	1	1	7
Hymenosomatidae	4	3	0	0	0	0	0	0	0	2	0	0	0	0
Inachoididae	12	2	0	0	1	0	0	1	0	11	1	0	3	0
Isaeidae	0	0	0	0	0	0	0	0	8	0	0	0	1	0
Ischyroceridae	57	0	0	0	3	0	48	9	62	140	1	0	0	27
Janiridae	1	0	0	1	0	0	0	0	0	0	0	0	0	0
Kalliapseudidae	0	0	0	30	0	0	0	0	4	0	0	0	8	0
Lepetidae	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Leptocheliidae	3	0	0	0	0	0	0	0	0	5	0	0	1	0
Leucosiidae	0	0	0	1	0	0	0	1	0	0	0	5	2	0
Leucosoleniidae	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Leucothoidae	1	0	0	1	0	0	0	0	0	0	0	0	0	0
Liljeborgiidae	15	4	1	5	7	0	2	0	1	2	0	4	3	0
Loveniidae	0	1	0	0	0	0	9	1	0	0	0	13	2	0

Family	N1	N3	N6	N7	E1	E3	E6	E7	S7	W1	W3	W6	W7	10
Luciferidae	4	1	2	0	0	1	0	0	6	1	1	4	0	0
Lucinidae	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Lysianassidae	0	5	1	4	0	0	20	3	22	0	1	12	9	9
Maeridae	34	6	10	461	0	0	0	0	1	0	0	0	0	0
Maldanidae	0	0	0	0	0	0	0	0	0	0	0	1	2	1
Marginellidae	1	0	0	0	0	0	0	2	0	0	0	0	0	1
Melitidae	1	0	0	6	0	0	0	4	1	0	0	0	0	4
Melphidippidae	0	1	0	0	0	0	0	0	2	0	0	0	3	0
Molgulidae	0	0	0	0	0	0	0	2	0	0	0	0	0	0
Myochamidae	0	0	0	0	0	0	0	1	1	0	0	0	0	0
Myodocopida (O.)	0	1	0	0	0	2	2	0	0	0	0	1	0	0
Mysidae	0	1	0	0	0	0	0	0	0	2	0	1	1	0
Mytilidae	6	1	0	0	8	0	0	0	0	157	0	0	0	0
Nassariidae	0	36	9	0	0	7	0	0	0	3	63	17	2	0
Naticidae	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Nebaliidae	91	1	2	0	3	2	2	0	0	114	1	1	0	2
Nematoda (P.)	0	0	0	1	0	0	19	0	0	0	0	0	0	0
Nemertea (P.)	0	0	26	5	0	17	2	0	4	0	55	42	1	6
Nephtyidae	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Nereididae	1	6	9	0	14	1	0	0	0	9	1	23	0	0
Nuculidae	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Nuuanuidae	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Oedicerotidae	1	3	1	0	0	1	6	9	2	0	0	6	3	5
Oenonidae	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Oligochaeta (sCl)	0	0	0	1	0	0	0	0	0	0	0	1	0	0
Olividae	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Onuphidae	0	0	0	0	0	0	28	0	2	0	1	5	22	20
Opheliidae	0	0	0	0	0	0	0	0	4	0	0	0	1	0
Ophiuridae	0	0	1	6	0	0	1	1	1	0	0	0	0	2
Orbiniidae	0	0	1	1	0	0	0	0	0	0	0	1	6	0
Ostracoda (Cl.)	0	0	0	0	0	0	2	5	4	0	3	5	2	2
Oweniidae	0	0	0	2	0	0	4	0	0	0	0	7	3	2
Paguridae	0	0	0	32	0	0	12	0	6	1	0	4	3	2
Palaemonidae	20	1	0	0	1	0	0	0	0	0	0	0	0	0

Family	N1	N3	N6	N7	E1	E3	E6	E7	S7	W1	W3	W6	W7	10
Paramunnidae	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Paraonidae	0	1	0	3	0	0	0	0	3	0	0	2	0	0
Pasiphaeidae	5	1	3	2	3	4	1	0	2	2	7	12	10	2
Pectinariidae	0	0	0	0	0	0	2	0	0	0	0	5	3	0
Philomedidae	1	3	0	2	1	11	60	15	69	0	6	59	22	55
Photidae	1	15	9	4	3	2	5	6	5	0	2	28	17	38
Phoxichilidiidae	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Phoxocephalidae	0	2	2	8	1	5	6	10	21	0	4	28	21	5
Phyllodocidae	0	0	0	0	0	0	4	0	0	0	0	1	7	2
Pilumnidae	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Pinnotheridae	1	0	0	0	0	0	0	0	0	9	1	0	0	0
Platyhelminthes (P.)	1	0	0	0	0	0	0	0	0	2	0	0	0	0
Platyischnopidae	0	0	0	4	0	0	2	0	2	0	0	0	0	4
Pleurobranchidae	6	2	0	0	6	0	0	0	0	2	0	0	0	0
Polygordiidae	0	0	0	0	0	0	0	0	2	0	0	0	0	0
Polynoidae	1	0	0	0	1	0	0	0	0	0	0	1	1	0
Pontogeneiidae	12	0	5	23	6	3	4	9	3	10	16	12	23	4
Psammobiidae	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Pseudocumatidae	0	1	0	0	0	0	1	1	0	0	0	1	1	0
Pyramidellidae	0	0	0	0	0	0	0	0	0	0	0	1	1	0
Retusidae	0	0	1	0	0	0	0	0	0	0	1	0	0	1
Sabellidae	0	0	0	0	0	0	0	0	0	0	0	0	4	0
Sarsiellidae	0	0	0	0	0	0	4	1	0	0	0	0	1	17
Scalibregmatidae	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Sebidae	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Serolidae	0	0	0	9	0	0	2	1	10	0	0	0	0	0
Serpulidae	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Sigalionidae	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Sipuncula (P.)	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Solenidae	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Sphaeromatidae	0	0	0	540	0	0	7	4	30	0	0	3	1	28
Spionidae	6	7	0	2	27	1	6	0	3	136	0	29	77	13
Stegocephalidae	0	0	0	0	0	0	0	0	4	0	0	0	0	0
Syllidae	0	0	0	12	0	1	5	0	1	1	0	1	19	0

Family	N1	N3	N6	N7	E1	E3	E6	E7	S7	W1	W3	W6	W7	10
Synaptidae	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Synopiidae	0	0	2	14	1	0	6	3	181	1	1	4	11	7
Terebellidae	0	0	0	2	0	0	0	0	0	0	0	0	2	0
Trichobranchidae	0	0	0	2	0	0	0	0	3	0	0	0	0	0
Turritellidae	0	0	0	0	0	0	0	0	0	0	0	0	2	0
Urohaustoriidae	0	0	0	0	0	0	1	3	0	0	0	0	0	5
Veneridae	0	0	0	0	0	1	1	0	0	0	0	1	0	2
Whiteleggiidae	0	0	0	0	0	0	10	4	5	0	0	0	0	2
Total Abundance	**415**	**206**	**114**	**1464**	**158**	**80**	**387**	**158**	**747**	**1118**	**191**	**429**	**458**	**392**
Total Families	**40**	**36**	**26**	**50**	**23**	**26**	**52**	**38**	**54**	**35**	**28**	**51**	**66**	**48**

Macrofauna raw data for Yellow Bluff in March 2022 (data is pooled by site).

Family	N1	N3	N5	N6	N7	E1	E3	E5	E6	E7	S7	W1	W3	W5	W6	W7	2	3	5	6	12	13
Ampeliscidae	0	0	0	0	1	0	0	0	4	4	14	0	0	0	1	31	0	0	1	4	0	1
Ampharetidae	0	0	0	0	3	0	0	0	0	0	0	0	0	0	2	3	0	0	2	0	1	2
Amphinomidae	0	0	0	0	13	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	3
Amphiuridae	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anabathridae	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Anthuridae	0	0	0	0	6	0	0	5	3	1	11	0	0	0	2	15	0	1	3	8	6	4
Aoridae	0	0	1	1	2	0	0	11	43	15	100	0	0	1	21	3	5	16	17	74	48	6
Apseudidae	0	0	1	1	248	2	0	2	0	43	100	0	0	10	7	9	2	0	3	6	4	117
Arcturidae	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	1	1	0
Ascidiidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Asteriidae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Austrarcturellidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
Bivalvia (Cl.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Bodotriidae	0	2	2	10	5	2	4	8	16	15	2	0	5	6	10	8	22	14	12	14	19	5
Callipallenidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Calyptraeidae	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
Cancridae	4	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Capitellidae	514	80	224	2	2	166	3	2	2	2	1	1222	18	1	3	1	2	1	0	0	0	6
Caprellidae	6	1	0	0	1	3	3	0	2	0	0	0	0	0	0	0	0	0	0	1	0	0
Cardiidae	0	2	0	0	0	1	0	0	0	3	0	0	0	0	0	0	3	0	0	0	0	0
Carditidae	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chitonidae	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cirolanidae	0	0	0	0	1	0	0	0	0	0	4	0	0	0	0	0	0	0	0	2	7	0
Condylocardiidae	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	10	2	0	0	1	8
Copepoda (sCl.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0
Corbulidae	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Corophiidae	0	0	0	0	0	0	2	1	12	0	0	0	0	0	0	0	14	8	7	7	5	6
Crangonidae	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0
Cylindroleberididae	1	2	2	4	0	1	12	4	6	2	3	0	9	10	5	12	4	7	9	6	7	7
Cypridinidae	0	0	0	1	0	0	3	1	3	6	2	0	0	1	0	0	8	2	8	14	7	0
Dexaminidae	0	4	2	0	1	0	1	0	2	1	3	0	0	1	2	0	4	1	0	0	5	14
Diastylidae	1	6	10	13	0	2	2	5	21	24	2	0	8	9	7	22	16	6	6	4	12	3

Family	N1	N3	N5	N6	N7	E1	E3	E5	E6	E7	S7	W1	W3	W5	W6	W7	2	3	5	6	12	13
Dogielinotinae	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dorvilleidae	0	0	0	0	0	0	0	0	2	1	2	0	0	0	0	0	1	0	0	2	0	1
Edwardsiidae	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0
Enteropneusta (Cl.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0	0	0	0	0
Eusiridae	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0
Galeommatidae	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	5	1	0	0	0	0	0
Glyceridae	0	0	0	0	1	0	0	0	1	2	3	0	0	0	1	0	0	0	1	2	1	1
Gnathiidae	0	0	0	0	2	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0	2	0
Goniadidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Gynodiastylidae	0	0	1	1	0	0	1	1	0	1	2	0	0	2	4	0	1	0	1	0	0	0
Hesionidae	0	0	0	0	1	0	0	0	0	0	3	1	0	0	0	0	0	0	0	0	0	2
Hexapodidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Hiatellidae	0	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
Hymenosomatidae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Inachoididae	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	3	0	0	0	2	0	0
Ischyroceridae	65	5	1	0	23	9	37	13	15	19	61	7	0	2	0	1	56	26	73	51	129	72
Janiridae	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Joeropsidae	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Kalliapseudidae	0	0	0	0	48	0	0	0	0	0	36	0	0	0	0	2	0	0	0	0	0	0
Leptocheliidae	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0
Leucosiidae	0	0	0	0	0	0	1	0	0	1	0	0	0	0	1	1	2	1	1	0	0	0
Leucothoidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Limidae	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Loveniidae	0	4	4	27	0	4	20	13	5	2	0	0	3	0	2	2	7	6	1	1	2	2
Luciferidae	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Lumbrineridae	0	0	0	0	1	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0
Lysianassidae	0	0	1	4	6	2	3	6	15	4	14	1	2	0	16	12	8	12	17	17	14	6
Mactridae	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Maldanidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13	0	0	0	0	0	2
Marginellidae	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0
Melitidae complex	0	7	8	4	216	1	2	1	2	1	5	0	3	1	6	3	1	1	3	4	2	25
Myodocopida (O.)	0	0	0	0	0	0	4	2	0	0	1	0	0	0	0	0	0	1	1	3	0	0
Mysidae	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Mytilidae	2	0	0	0	0	1	0	0	0	0	0	6	1	0	0	0	1	0	0	0	0	0

Family	N1	N3	N5	N6	N7	E1	E3	E5	E6	E7	S7	W1	W3	W5	W6	W7	2	3	5	6	12	13
Nassariidae	1	0	1	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Naticidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Nebaliidae	8	0	0	1	0	3	1	1	1	0	0	2	0	0	3	1	2	2	2	1	0	0
Nematoda (P.)	0	0	0	0	1	0	0	2	0	1	0	0	0	0	0	0	7	1	0	6	0	0
Nemertea (P.)	0	0	5	5	5	0	9	10	7	5	6	0	11	16	4	7	11	5	6	2	9	13
Nephtyidae	0	0	0	0	0	0	7	3	1	0	0	0	0	0	1	4	0	0	0	0	0	0
Nereididae	4	6	15	1	0	16	9	2	1	0	0	6	18	17	5	0	0	0	1	1	0	2
Nuculanidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Oedicerotidae	0	0	0	4	0	2	3	3	6	8	0	0	2	4	5	4	7	4	2	11	5	0
Oligochaeta (sCl)	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Onuphidae	0	0	0	4	0	0	16	23	11	23	3	0	0	1	4	54	4	12	1	23	18	0
Opheliidae	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
Ophiuridae	1	0	1	12	0	2	15	16	9	3	5	0	9	8	8	1	29	22	12	10	2	5
Orbiniidae	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	11	0	0	0	0	0	0
Ostracoda (Cl.)	1	0	0	1	0	3	13	12	12	3	16	0	6	8	5	1	8	12	6	17	9	4
Oweniidae	0	0	1	3	0	0	8	0	0	9	0	0	2	0	0	0	2	0	0	0	1	0
Paguridae	0	0	0	0	54	1	0	1	0	1	15	0	1	2	1	9	0	0	6	1	0	23
Palaemonidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Paramunnidae	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Paraonidae	0	0	0	0	1	0	0	0	0	0	2	0	0	3	0	0	0	0	0	0	0	2
Pasiphaeidae	0	0	1	0	0	2	1	0	0	0	0	0	0	0	0	4	1	0	0	0	2	1
Pectinariidae	0	11	11	6	0	7	10	2	1	0	0	2	0	0	1	9	1	0	1	2	3	0
Philinidae	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Philomedidae	11	0	2	9	3	4	84	123	102	21	33	0	17	28	53	9	97	104	80	96	36	19
Phoronida (P.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Photidae	0	12	48	173	24	10	525	190	252	30	19	0	9	7	57	25	533	419	57	171	26	25
Phoxocephalidae	0	2	6	4	11	2	9	14	15	4	14	0	12	17	40	14	21	9	14	12	12	15
Phyllodocidae	0	0	0	2	0	0	2	1	1	1	2	0	0	0	0	1	1	0	0	0	1	0
Pinnotheridae	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
Platyhelminthes (P.)	0	0	0	0	26	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Platyischnopidae	0	0	0	0	3	0	1	0	1	5	2	0	1	0	0	0	2	1	3	2	1	3
Pleurobranchidae	12	9	5	0	0	7	11	9	1	0	0	12	0	0	0	2	0	0	1	0	0	0
Polygordiidae	0	0	0	0	2	0	0	0	11	0	2	0	0	8	0	0	0	0	1	2	1	2
Polynoidae	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0	0	0	0

Family	N1	N3	N5	N6	N7	E1	E3	E5	E6	E7	S7	W1	W3	W5	W6	W7	2	3	5	6	12	13
Pontogeneiidae	1	1	3	0	4	1	1	2	0	0	1	0	2	0	0	1	2	0	5	3	1	1
Psammobiidae	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	1	1	0	0	0	0
Pseudocumatidae	0	0	2	2	0	0	3	5	11	10	1	0	2	3	4	0	1	4	3	13	1	1
Ranellidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Retusidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Sabellidae	0	0	0	3	2	0	3	2	8	10	6	0	0	0	3	12	1	3	1	7	5	4
Sarsiellidae	0	0	0	0	0	0	8	2	6	3	0	0	0	2	1	0	18	12	2	7	3	1
Schizasteridae	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sebidae	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Serolidae	0	0	0	0	7	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
Sigalionidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Sipuncula (P.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Solenidae	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0
Sphaeromatidae	0	1	0	1	226	0	1	3	12	2	48	0	0	0	0	1	48	26	18	13	5	8
Spionidae	21	8	119	16	0	20	24	40	21	24	2	50	9	0	38	9	1	10	2	22	14	1
Stegocephalidae	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0
Stenothoidae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Syllidae	1	0	0	0	2	0	0	0	1	0	1	0	0	0	0	6	0	0	0	0	0	0
Synaptidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
Synopiidae	0	4	1	2	56	0	3	2	4	2	25	0	0	4	3	3	13	2	4	13	1	25
Terebellidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0	0	0	0	0
Trichobranchidae	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0
Trochidae	0	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Upogebiidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Urohaustoriidae	0	1	0	0	0	0	2	2	2	1	1	0	0	0	0	0	2	2	0	1	1	0
Veneridae	0	0	0	0	1	0	0	0	0	1	4	0	0	0	0	0	10	1	1	1	0	0
Whiteleggiidae	0	0	0	0	0	0	0	0	9	12	2	0	0	0	0	0	14	0	0	12	0	1
Total Abundance	**658**	**171**	**481**	**322**	**1040**	**280**	**868**	**548**	**662**	**331**	**595**	**1315**	**153**	**175**	**331**	**372**	**1006**	**759**	**399**	**679**	**432**	**449**
Total Families	**19**	**23**	**30**	**33**	**52**	**31**	**41**	**42**	**44**	**46**	**51**	**14**	**25**	**29**	**39**	**61**	**47**	**38**	**44**	**50**	**42**	**41**

Appendix 4-7: Macrofauna raw data for West of Wedge in 2019, January 2021 and December 2021

Macrofauna raw data for West of Wedge during the baseline survey in 2019 (data is pooled by site).

Family	Phylum	CP1	CP2	CP3	CP4	CP5	CP6	CP7	CP8	C1	C2
Cryptoporidae	Brachiopoda	1	0	0	0	0	0	0	1	0	0
Ampeliscidae	Arthropoda	0	0	1	0	1	1	0	0	0	1
Dexaminidae	Arthropoda	1	0	0	1	0	0	0	0	0	1
Eusiridae	Arthropoda	14	18	40	36	9	17	13	14	14	66
Ischyroceridae	Arthropoda	5	13	2	4	0	2	6	16	0	4
Lysianassidae	Arthropoda	51	63	51	32	49	60	61	34	3	20
Melitidae	Arthropoda	6	8	5	3	8	4	9	3	1	10
Oedicerotidae	Arthropoda	4	1	0	4	8	8	12	4	2	10
Phoxocephalidae	Arthropoda	24	25	19	18	20	27	25	12	31	11
Platyischnopidae	Arthropoda	4	1	1	3	3	6	3	5	3	3
Aoridae	Arthropoda	20	37	21	27	38	39	26	21	8	28
Urohaustoriidae	Arthropoda	5	10	9	9	6	8	5	5	9	6
Amphilochidae	Arthropoda	0	0	0	1	0	0	1	0	0	0
Podoceridae	Arthropoda	0	1	0	0	0	0	0	0	0	0
Synopiidae	Arthropoda	8	7	12	13	13	8	5	6	1	8
Leucosiidae	Arthropoda	0	0	1	1	0	0	1	0	1	0
Inachoididae	Arthropoda	0	0	1	2	0	0	0	2	1	0
Hexapodidae	Arthropoda	0	0	0	0	0	1	0	0	0	0
Phtisicidae	Arthropoda	1	0	0	0	1	0	0	0	0	0
Pasiphaeidae	Arthropoda	5	6	5	8	7	5	6	1	5	3
Galatheidae	Arthropoda	0	1	0	0	1	0	0	0	0	0
Palaemonidae	Arthropoda	0	0	0	1	0	0	0	0	0	0
Copepoda (sCl.)	Arthropoda	0	0	0	0	1	0	1	0	0	0
Cirolanidae	Arthropoda	1	2	0	1	4	1	2	2	0	4
Chaetiliidae	Arthropoda	1	2	1	0	1	4	0	1	0	0
Gnathiidae	Arthropoda	1	2	2	4	3	1	2	1	0	4
Arcturidae	Arthropoda	9	5	4	15	2	18	7	8	0	5
Paramunnidae	Arthropoda	0	4	4	0	1	0	0	0	0	0
Anthuridae	Arthropoda	1	1	1	2	0	10	4	0	3	1
Sphaeromatidae	Arthropoda	1	2	2	2	3	0	0	1	5	0
Mysidae	Arthropoda	0	1	1	1	3	1	0	1	1	4
Nebaliidae	Arthropoda	0	0	0	0	0	0	0	0	1	0

Family	Phylum	CP1	CP2	CP3	CP4	CP5	CP6	CP7	CP8	C1	C2
Sarsiellidae	Arthropoda	0	0	1	0	0	1	0	0	0	0
Cypridinidae	Arthropoda	20	10	12	10	19	15	20	21	0	15
Philomedidae	Arthropoda	11	5	5	8	6	10	10	14	1	9
Cylindroleberididae	Arthropoda	2	1	0	2	3	2	2	1	7	1
Paguridae	Arthropoda	5	2	1	0	0	1	1	0	0	0
Whiteleggiidae	Arthropoda	16	32	13	6	19	30	27	16	0	7
Bodotriidae	Arthropoda	50	29	10	11	9	43	30	50	9	29
Diastylidae	Arthropoda	69	72	66	67	80	61	61	62	11	51
Lampropidae	Arthropoda	0	0	0	0	0	1	0	0	0	0
Gynodiastylidae	Arthropoda	2	3	0	0	7	0	13	6	0	7
Pseudocumatidae	Arthropoda	1	6	2	2	3	7	1	1	1	3
Loveniidae	Echinodermata	0	2	2	1	2	1	2	0	2	0
Amphiuridae	Echinodermata	0	0	1	1	3	1	3	1	0	0
Ophiuridae	Echinodermata	4	3	0	1	2	3	0	1	0	2
Columbellidae	Mollusca	0	6	0	0	0	0	0	1	3	0
Anabathridae	Mollusca	0	4	8	4	9	6	3	6	6	0
Eatoniellidae	Mollusca	3	2	4	1	1	2	0	0	0	1
Marginellidae	Mollusca	1	3	1	0	6	1	3	3	3	1
Muricidae	Mollusca	0	1	0	0	0	1	1	0	0	0
Nassariidae	Mollusca	0	0	1	0	0	0	0	0	0	0
Pyramidellidae	Mollusca	2	1	2	1	2	1	1	2	3	0
Retusidae	Mollusca	3	0	1	1	0	3	1	3	0	0
Litiopidae	Mollusca	0	1	0	0	1	0	0	0	0	0
Mangeliidae	Mollusca	0	1	0	0	0	0	0	2	3	0
Olividae	Mollusca	0	1	0	0	0	0	0	0	0	0
Pleurobranchidae	Mollusca	0	0	0	0	0	0	0	0	1	0
Philinidae	Mollusca	0	0	0	1	0	0	0	0	0	0
Terebridae	Mollusca	1	4	1	1	1	1	0	0	0	0
Naticidae	Mollusca	0	2	0	1	0	0	0	1	0	0
Turritellidae	Mollusca	1	0	0	2	0	2	2	1	0	3
Psammobiidae	Mollusca	0	0	0	0	2	0	0	0	0	1
Veneridae	Mollusca	0	4	1	3	8	4	4	4	6	3
Cardiidae	Mollusca	1	3	0	0	5	1	3	1	0	0
Condylocardiidae	Mollusca	0	0	0	0	0	1	0	0	0	0

Family	Phylum	CP1	CP2	CP3	CP4	CP5	CP6	CP7	CP8	C1	C2
Galeommatidae	Mollusca	0	0	1	1	2	1	1	1	9	0
Trigoniidae	Mollusca	0	1	0	1	0	0	1	0	0	0
Limidae	Mollusca	0	0	0	0	0	0	1	1	0	0
Corbulidae	Mollusca	0	1	0	0	0	0	0	0	0	0
Glycymerididae	Mollusca	1	1	5	5	1	0	1	1	13	2
Solenidae	Mollusca	0	0	0	0	1	1	1	1	0	1
Myochamidae	Mollusca	0	2	0	0	2	0	0	0	0	0
Thraciidae	Mollusca	0	0	0	0	0	1	0	0	0	0
Phoronida (P.)	Phoronida	0	0	1	0	0	0	0	0	0	0
Sipuncula (P.)	Sipuncula	0	3	0	0	0	0	0	0	0	0
Edwardsiidae	Cnidaria	1	1	0	1	0	0	2	2	0	0
Ophichthidae	Chordata	0	0	0	1	0	0	0	0	0	0
Gobiidae	Chordata	0	0	0	1	0	0	0	0	0	0
Nemertea (P.)	Nemertea	2	3	2	1	2	0	3	1	2	1
Nematoda (P.)	Nematoda	1	1	3	2	3	3	2	3	1	1
Opheliidae	Annelida	0	0	0	5	2	0	0	0	2	1
Phyllodocidae	Annelida	1	3	0	0	4	0	1	0	0	1
Capitellidae	Annelida	0	1	0	1	2	1	2	1	1	2
Glyceridae	Annelida	2	1	1	1	6	4	1	2	0	4
Sabellidae	Annelida	8	5	6	5	6	1	5	1	5	2
Onuphidae	Annelida	1	0	0	0	1	0	0	1	0	0
Maldanidae	Annelida	0	1	0	0	0	0	0	0	0	5
Orbiniidae	Annelida	5	10	1	4	9	2	4	0	0	5
Spionidae	Annelida	10	7	6	6	21	10	11	7	4	15
Paraonidae	Annelida	0	0	1	0	0	0	1	0	0	0
Cirratulidae	Annelida	0	0	0	0	1	1	1	0	0	0
Syllidae	Annelida	0	0	0	0	0	0	0	1	0	0
Terebellidae	Annelida	0	0	0	0	0	0	3	0	0	1
Ampharetidae	Annelida	0	0	1	0	1	0	0	0	0	0
Pectinariidae	Annelida	1	0	2	0	1	2	1	0	5	0
Sigalionidae	Annelida	0	1	0	0	0	0	1	0	1	0
Oweniidae	Annelida	2	0	0	1	0	2	1	0	1	0
Total Abundance		**390**	**450**	**345**	**348**	**435**	**449**	**421**	**358**	**189**	**363**
Total Families		**49**	**61**	**50**	**56**	**58**	**55**	**57**	**52**	**40**	**45**

Macrofauna raw data for West of Wedge for the January 2021 survey (data is pooled by site).

Family	Phylum	CP1	CP2	CP3	CP4	CP5	CP6	CP7	CP8	C1	C2	PB1	PB2
Cryptoporidae	Brachiopoda	0	0	0	0	0	0	0	0	0	0	0	0
Phoxichilidiidae	Arthropoda	0	2	3	0	1	0	0	0	1	0	0	0
Amphipoda (O.)	Arthropoda	0	0	0	0	0	0	0	0	1	0	0	1
Ampeliscidae	Arthropoda	2	0	1	0	0	1	1	3	3	1	0	0
Corophiidae	Arthropoda	0	0	0	0	0	0	0	0	0	2	0	0
Dexaminidae	Arthropoda	2	0	6	0	2	2	7	7	2	5	0	0
Eusiridae	Arthropoda	5	1	2	0	2	1	3	3	5	20	1	1
Ischyroceridae	Arthropoda	36	20	13	8	3	13	17	64	5	16	13	9
Lysianassidae	Arthropoda	77	77	51	29	78	40	23	14	38	17	24	48
Melitidae	Arthropoda	1	1	5	4	6	8	2	1	7	6	0	2
Oedicerotidae	Arthropoda	1	3	12	11	7	4	7	5	5	6	0	1
Phoxocephalidae	Arthropoda	13	30	27	26	25	26	17	8	15	19	1	27
Platyischnopidae	Arthropoda	2	2	2	4	2	1	0	0	0	3	0	0
Aoridae	Arthropoda	74	47	39	29	49	34	42	48	35	40	55	27
Urohaustoriidae	Arthropoda	12	10	13	4	4	8	6	4	9	6	3	4
Amphilochidae	Arthropoda	1	0	0	0	0	0	0	0	0	0	1	0
Leucothoidae	Arthropoda	0	0	0	0	0	1	0	0	1	0	0	0
Podoceridae	Arthropoda	1	0	0	1	0	3	0	0	3	0	0	1
Synopiidae	Arthropoda	1	2	1	0	1	1	1	1	1	0	2	1
Cancridae	Arthropoda	0	0	0	0	0	0	0	0	0	0	1	0
Leucosiidae	Arthropoda	1	2	1	0	1	2	0	0	0	0	5	4
Inachoididae	Arthropoda	0	1	1	0	1	1	1	0	0	0	0	1
Hexapodidae	Arthropoda	0	0	0	0	0	0	0	0	0	0	0	0
Pinnotheridae	Arthropoda	0	0	0	0	1	0	0	0	0	0	0	0
Caprellidae	Arthropoda	0	2	1	0	0	1	0	0	4	1	0	0
Phtisicidae	Arthropoda	0	0	0	0	0	0	0	0	0	0	0	0
Pasiphaeididae	Arthropoda	0	0	0	0	0	0	0	1	0	0	0	0
Callianassidae	Arthropoda	0	0	0	0	0	0	0	0	0	0	0	1
Galatheidae	Arthropoda	0	0	0	0	1	0	0	0	0	0	0	0
Palaemonidae	Arthropoda	0	0	0	0	0	0	0	0	0	0	0	0
Copepoda (sCl.)	Arthropoda	0	0	0	1	2	0	0	1	0	0	0	0
Cirolanidae	Arthropoda	2	0	4	4	1	1	0	0	1	6	0	0

Chaetiliidae	Arthropoda	0	1	0	0	0	0	2	1	0	1	0	0
Gnathiidae	Arthropoda	4	1	4	9	2	4	7	3	3	6	0	0
Arcturidae	Arthropoda	10	10	2	6	2	7	5	3	5	16	0	1
Paramunnidae	Arthropoda	0	0	0	0	0	3	1	0	0	0	0	0
Anthuridae	Arthropoda	8	7	8	4	6	7	2	5	19	4	4	4
Serolidae	Arthropoda	1	2	0	0	2	0	0	1	0	1	0	0
Sphaeromatidae	Arthropoda	0	1	0	0	1	1	0	0	0	0	0	0
Mysidae	Arthropoda	0	0	1	0	1	0	0	0	2	5	1	0
Nebaliidae	Arthropoda	0	0	0	0	0	1	0	0	0	0	1	2
Sarsiellidae	Arthropoda	1	0	0	0	0	0	0	0	0	0	0	0
Cypridinidae	Arthropoda	55	22	25	30	20	34	57	42	3	13	3	2
Ostracoda (Cl.)	Arthropoda	1	1	0	0	0	0	0	0	1	1	7	10
Philomedidae	Arthropoda	17	13	2	2	4	3	7	11	17	3	35	81
Cylindroleberididae	Arthropoda	8	3	3	0	1	6	6	3	1	2	1	6
Paguridae	Arthropoda	1	1	4	0	1	2	0	1	1	0	0	0
Leptocheliidae	Arthropoda	0	1	0	0	0	3	0	0	0	0	1	0
Whiteleggiidae	Arthropoda	5	1	8	6	27	48	3	1	0	3	0	1
Bodotriidae	Arthropoda	53	12	14	18	20	26	15	30	72	8	12	15
Diastylidae	Arthropoda	23	7	23	19	16	31	14	31	26	11	4	6
Lampropidae	Arthropoda	0	0	0	0	0	0	1	0	1	0	0	0
Gynodiastylidae	Arthropoda	6	1	2	1	0	2	4	3	1	2	0	1
Pseudocumatidae	Arthropoda	1	10	1	4	1	0	2	1	1	3	0	10
Asteriidae	Echinodermata	0	0	0	0	3	1	0	0	0	0	2	2
Echinidea (iCl.)	Echinodermata	0	1	0	0	0	0	0	0	1	0	0	0
Loveniidae	Echinodermata	5	10	1	1	2	4	1	1	4	2	2	13
Cucumariidae	Echinodermata	0	1	0	0	0	0	0	0	0	0	0	0
Synaptidae	Echinodermata	0	0	0	0	0	0	0	0	0	0	1	1
Amphiuridae	Echinodermata	0	0	0	0	0	1	2	1	0	0	0	0
Ophiuridae	Echinodermata	1	3	5	1	4	8	1	1	3	6	5	7
Columbellidae	Mollusca	0	4	3	0	3	0	0	0	15	0	1	0
Anabathridae	Mollusca	0	3	3	6	9	3	4	5	24	0	1	1
Eatoniellidae	Mollusca	0	0	0	0	0	0	0	0	0	0	0	0
Marginellidae	Mollusca	7	10	5	5	6	3	7	7	1	3	7	2
Muricidae	Mollusca	0	0	0	0	0	0	0	0	0	0	0	0
Nassariidae	Mollusca	5	2	0	0	0	0	2	0	0	0	20	38

Pyramidellidae	Mollusca	1	1	0	2	3	0	1	0	7	0	2	0
Acteocinidae	Mollusca	1	0	2	0	0	0	0	0	0	0	0	1
Retusidae	Mollusca	0	2	0	0	0	0	0	0	0	0	0	0
Litiopidae	Mollusca	0	0	0	0	0	0	0	0	0	0	0	0
Mangeliidae	Mollusca	0	0	1	0	1	2	0	1	0	0	0	0
Olividae	Mollusca	0	0	0	0	0	0	0	0	0	0	0	0
Pleurobranchaeidae	Mollusca	0	0	0	0	1	3	0	0	0	0	1	0
Philinidae	Mollusca	1	0	0	0	0	0	0	0	0	0	4	0
Terebridae	Mollusca	0	0	0	1	1	0	0	0	1	0	0	0
Naticidae	Mollusca	0	0	1	1	1	1	2	3	1	1	0	1
Turritellidae	Mollusca	0	0	2	1	0	0	1	0	2	1	0	1
Cingulopsidae	Mollusca	1	0	1	0	0	0	0	0	1	0	0	0
Mytilidae	Mollusca	0	0	0	0	0	0	0	0	0	0	4	24
Psammobiidae	Mollusca	0	1	0	0	0	1	0	0	0	0	0	0
Carditidae	Mollusca	0	0	0	0	0	0	0	0	1	0	0	0
Veneridae	Mollusca	2	0	0	1	1	1	1	0	0	0	3	2
Cardiidae	Mollusca	2	3	3	1	2	4	2	2	1	3	1	1
Condylocardiidae	Mollusca	0	0	0	0	0	0	0	0	0	1	0	0
Galeommatidae	Mollusca	1	1	0	0	2	0	0	0	0	0	1	0
Hiatellidae	Mollusca	0	0	0	0	0	0	0	0	0	0	0	1
Trigoniidae	Mollusca	1	0	1	0	0	1	0	0	0	1	0	0
Limidae	Mollusca	0	0	0	0	0	0	0	0	0	0	0	0
Corbulidae	Mollusca	0	0	0	0	0	0	0	0	0	0	0	0
Glycymerididae	Mollusca	0	0	0	0	3	1	0	1	2	0	0	0
Solenidae	Mollusca	0	0	0	0	0	0	0	0	0	0	0	0
Myochamidae	Mollusca	1	0	0	0	0	3	3	0	0	1	0	0
Thraciidae	Mollusca	0	0	0	0	0	0	0	0	0	0	0	0
Scaphopoda (Cl.)	Mollusca	0	0	0	0	0	0	0	0	3	0	0	0
Phoronida (P.)	Phoronida	1	1	0	0	1	0	0	0	0	0	0	0
Platyhelminthes (P.)	Platyhelminthes	0	0	1	0	0	0	0	0	0	0	0	0
Sipuncula (P.)	Sipuncula	0	0	0	0	0	0	1	0	0	0	0	0
Edwardsiidae	Cnidaria	3	5	1	0	1	0	6	1	0	0	28	44
Ophichthidae	Chordata	0	0	0	0	0	0	0	0	0	0	0	0
Gobiidae	Chordata	0	0	0	0	0	0	0	0	0	0	0	0
Nemertea (P.)	Nemertea	3	3	1	3	3	3	3	5	0	1	6	15

Nematoda (P.)	Nematoda	8	0	4	2	6	25	1	0	0	1	0	0
Opheliidae	Annelida	0	0	0	0	0	0	1	0	0	0	0	0
Phyllodocidae	Annelida	3	2	0	0	2	2	0	1	4	1	4	1
Capitellidae	Annelida	0	0	0	0	0	0	0	1	0	0	6	0
Dorvilleidae	Annelida	1	0	0	0	0	0	0	0	0	0	0	0
Glyceridae	Annelida	3	3	2	4	4	5	4	3	4	1	1	2
Sabellidae	Annelida	3	2	4	8	1	3	3	5	0	1	0	1
Onuphidae	Annelida	5	6	1	0	8	14	5	2	1	0	2	6
Maldanidae	Annelida	0	1	0	1	0	0	0	0	0	10	0	0
Nereididae	Annelida	1	0	0	0	0	0	0	0	0	0	2	3
Orbiniidae	Annelida	4	3	3	6	3	4	3	1	0	0	1	0
Spionidae	Annelida	12	14	18	17	10	6	5	7	8	22	14	25
Paraonidae	Annelida	0	0	0	0	0	0	0	0	0	0	0	0
Cirratulidae	Annelida	0	0	0	0	0	0	0	1	0	1	0	0
Syllidae	Annelida	1	0	0	1	0	2	0	0	0	0	0	0
Terebellidae	Annelida	1	1	1	2	15	7	0	0	1	0	0	0
Ampharetidae	Annelida	2	2	1	1	5	1	0	1	1	1	0	2
Polynoidae	Annelida	0	0	1	0	0	0	0	0	0	0	0	0
Amphinomidae	Annelida	0	1	0	0	1	0	0	0	1	0	0	0
Pectinariidae	Annelida	0	0	0	0	1	1	0	0	0	0	13	6
Sigalionidae	Annelida	1	0	1	0	0	0	0	0	1	0	0	3
Oweniidae	Annelida	5	16	0	5	8	8	6	5	0	0	13	27
Polygordiidae	Annelida	0	3	0	0	0	0	0	0	0	0	0	0
	Total abundance	**511**	**399**	**346**	**290**	**402**	**444**	**318**	**351**	**377**	**285**	**320**	**497**
	Total Families	**63**	**61**	**57**	**45**	**65**	**65**	**50**	**50**	**56**	**50**	**47**	**53**

Macrofauna raw data for West of Wedge for the December 2021 survey (data is pooled by site).

Family	Phylum	CP1	CP2	CP3	CP4	CP5	CP6	CP7	CP8	C1	C2	PB4	PB5	PB6	PB7
Ampeliscidae	Arthropoda	3	2	0	1	0	1	0	3	0	0	0	0	0	0
Corophiidae	Arthropoda	1	1	0	0	0	0	0	1	0	1	0	0	0	0
Dexaminidae	Arthropoda	3	2	0	10	4	3	4	2	1	1	5	2	1	0
Eusiridae	Arthropoda	0	1	0	0	1	0	0	2	0	1	0	0	0	0
Ischyroceridae	Arthropoda	9	5	3	3	2	5	11	4	0	6	0	28	15	5
Lysianassidae	Arthropoda	9	9	13	20	12	6	16	15	2	13	1	11	13	6
Melitidae	Arthropoda	0	0	1	5	1	0	3	1	0	0	0	0	1	0
Oedicerotidae	Arthropoda	1	2	2	3	5	10	6	6	0	6	0	0	2	0
Phoxocephalidae	Arthropoda	8	13	15	20	17	4	8	5	31	15	2	3	13	9
Platyischnopidae	Arthropoda	2	2	1	1	1	0	0	1	0	3	0	0	1	1
Aoridae	Arthropoda	10	24	15	16	7	11	18	19	8	5	3	11	16	1
Urohaustoriidae	Arthropoda	5	7	7	7	10	9	8	7	6	4	0	3	5	0
Amphilochidae	Arthropoda	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Synopiidae	Arthropoda	0	0	0	0	0	0	1	0	0	0	1	1	1	1
Leucosiidae	Arthropoda	0	1	0	0	0	0	0	1	0	0	0	0	0	0
Brachyura (iO)	Arthropoda	0	0	0	0	0	0	0	0	0	0	0	1	1	0
Caprellidae	Arthropoda	0	0	1	0	0	0	1	1	0	0	5	24	2	0
Pasiphaeidae	Arthropoda	0	0	0	1	0	0	3	0	0	0	0	0	0	1
Crangonidae	Arthropoda	1	1	0	0	0	0	0	1	0	1	0	0	1	0
Axiidae	Arthropoda	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Copepoda (sCl.)	Arthropoda	1	0	0	0	2	0	0	0	0	0	0	0	1	0
Cirolanidae	Arthropoda	0	0	0	0	2	0	0	1	0	0	0	0	0	0
Chaetiliidae	Arthropoda	1	0	1	0	2	0	0	0	0	0	0	0	0	0
Gnathiidae	Arthropoda	3	0	4	5	1	1	0	3	0	0	0	1	1	0
Arcturidae	Arthropoda	2	0	1	5	0	1	1	3	0	2	0	0	0	0
Paramunnidae	Arthropoda	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Anthuridae	Arthropoda	4	3	0	2	6	1	1	2	4	1	0	3	4	2
Serolidae	Arthropoda	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Sphaeromatidae	Arthropoda	1	2	1	0	2	0	0	0	0	2	0	1	0	0
Mysidae	Arthropoda	0	0	0	1	1	1	0	0	0	0	0	0	0	0
Nebaliidae	Arthropoda	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Cypridinidae	Arthropoda	6	2	6	4	7	9	8	8	0	6	0	2	2	0

Family	Phylum	CP1	CP2	CP3	CP4	CP5	CP6	CP7	CP8	C1	C2	PB4	PB5	PB6	PB7
Ostracoda (Cl.)	Arthropoda	0	0	0	1	0	0	0	1	0	0	0	0	0	0
Philomedidae	Arthropoda	6	18	2	1	5	4	1	9	4	2	37	62	19	23
Cylindroleberididae	Arthropoda	0	0	0	0	2	1	1	2	3	0	0	2	5	0
Paguridae	Arthropoda	1	0	0	0	0	5	0	1	0	0	0	0	0	0
Whiteleggiidae	Arthropoda	2	0	4	9	33	0	17	2	0	21	0	0	0	0
Bodotriidae	Arthropoda	11	2	10	12	8	10	5	6	2	3	2	0	5	0
Diastylidae	Arthropoda	4	7	7	10	4	6	11	9	2	4	0	1	2	1
Gynodiastylidae	Arthropoda	3	0	1	1	1	0	2	5	0	0	0	0	2	0
Pseudocumatidae	Arthropoda	6	2	3	2	4	7	0	1	1	1	1	0	3	0
Asteriidae	Echinodermata	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Echinidea (iCl.)	Echinodermata	0	0	0	0	0	0	0	0	1	0	0	0	1	0
Loveniidae	Echinodermata	1	1	0	0	1	0	1	1	0	1	4	15	3	14
Phyllophoridae	Echinodermata	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Amphiuridae	Echinodermata	0	0	0	0	0	5	0	0	0	2	0	0	0	0
Ophiuridae	Echinodermata	4	4	2	5	2	2	9	2	0	5	0	0	5	1
Columbellidae	Mollusca	0	1	1	0	0	0	0	0	1	0	0	0	0	0
Anabathridae	Mollusca	0	1	0	0	0	0	0	0	4	1	1	0	0	0
Marginellidae	Mollusca	1	2	2	0	0	1	0	0	0	1	0	0	0	0
Nassariidae	Mollusca	0	0	0	0	0	0	0	0	0	0	29	2	0	2
Pyramidellidae	Mollusca	5	1	0	0	0	0	0	0	1	0	0	0	0	0
Tornatinidae	Mollusca	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Retusidae	Mollusca	1	0	0	0	0	0	0	0	0	0	1	0	0	0
Olividae	Mollusca	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Pleurobranchidae	Mollusca	0	1	0	0	0	0	1	0	0	0	4	3	2	0
Philinidae	Mollusca	0	0	0	0	0	0	0	1	0	0	0	2	0	0
Terebridae	Mollusca	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Naticidae	Mollusca	0	1	0	0	0	0	0	2	0	0	0	1	0	0
Turritellidae	Mollusca	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Mytilidae	Mollusca	0	1	0	0	0	0	0	0	0	0	3	22	0	8
Psammobiidae	Mollusca	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Veneridae	Mollusca	0	0	0	0	0	0	0	0	1	1	0	1	0	0
Cardiidae	Mollusca	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Condylocardiidae	Mollusca	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Galeommatidae	Mollusca	0	0	0	0	0	0	0	0	2	0	5	0	2	0

Family	Phylum	CP1	CP2	CP3	CP4	CP5	CP6	CP7	CP8	C1	C2	PB4	PB5	PB6	PB7
Glycymerididae	Mollusca	0	2	0	0	0	1	0	1	3	0	0	0	0	0
Solenidae	Mollusca	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Myochamidae	Mollusca	0	0	0	0	0	2	0	0	0	0	0	0	0	0
Thraciidae	Mollusca	0	0	0	0	0	1	1	0	0	0	0	0	0	0
Anthozoa(Cl.)	Cnidaria	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Edwardsiidae	Cnidaria	4	4	0	1	5	1	2	4	1	0	2	2	4	4
Nemertea (P.)	Nemertea	1	0	3	2	3	3	4	0	1	2	2	6	0	5
Nematoda (P.)	Nematoda	2	1	2	0	6	0	2	1	0	5	0	0	2	0
Phyllodocidae	Annelida	1	0	0	0	0	0	0	0	0	0	1	0	0	0
Capitellidae	Annelida	1	2	2	0	1	0	0	2	0	0	13	107	10	19
Dorvilleidae	Annelida	0	0	0	0	1	0	0	0	0	0	0	0	1	0
Glyceridae	Annelida	0	1	1	1	0	3	2	1	1	2	4	0	0	0
Sabellidae	Annelida	0	0	0	0	1	0	1	5	0	0	0	0	1	0
Onuphidae	Annelida	2	1	0	1	0	0	1	2	0	0	6	1	4	2
Lumbrineridae	Annelida	1	0	0	0	0	0	0	1	0	0	0	0	0	0
Nereididae	Annelida	0	0	0	0	1	0	0	0	0	0	2	0	0	0
Orbiniidae	Annelida	4	1	3	2	0	2	5	5	0	2	1	0	3	0
Spionidae	Annelida	12	29	4	6	8	8	10	9	7	7	35	38	31	20
Cirratulidae	Annelida	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Syllidae	Annelida	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Ampharetidae	Annelida	0	1	0	0	0	1	0	0	0	0	0	0	0	0
Polynoidae	Annelida	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Amphinomidae	Annelida	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Pectinariidae	Annelida	0	0	0	0	0	0	0	0	0	0	23	9	3	42
Sigalionidae	Annelida	0	2	0	0	0	0	0	0	0	0	1	0	0	0
Oweniidae	Annelida	2	3	0	1	0	3	0	1	0	0	1	0	2	0
Polygordiidae	Annelida	0	0	0	0	0	0	1	1	0	0	0	1	1	0
Total Abundance		**149**	**167**	**119**	**159**	**172**	**128**	**169**	**162**	**87**	**129**	**198**	**366**	**192**	**170**
Total Families		**44**	**41**	**30**	**31**	**38**	**32**	**36**	**46**	**22**	**33**	**31**	**30**	**40**	**23**

Appendix 4-8: Macrofauna raw data for Storm Bay broadscale surveys 2019, 2020 and 2021

Macrofauna raw data for Storm Bay for the 2019 survey (data is pooled by site).

	SB1	SB2	SB3	SB4	SB5	SB6	SB8	SB9	SB10	SB11	SB13	SB16	SB17	SB18	SB19	SB21	SB22	SB23	SB24	NUB1	NUB2	NUB3	NUB4
Callipallenidae	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Phoxichilidiidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Ascidiidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0
Molgulidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pyuridae	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Holozoidae	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cryptoporidae	0	0	0	8	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
Ampeliscidae	1	0	13	5	0	22	0	0	0	4	2	0	23	5	0	1	7	0	0	0	45	11	0
Corophiidae	0	0	0	0	0	0	0	0	0	0	0	0	0	5	1	0	0	0	0	0	0	0	0
Dexaminidae	0	1	3	0	0	0	0	4	0	0	0	1	0	0	1	0	0	4	2	1	1	1	0
Eusiridae	0	1	0	5	0	0	0	0	1	2	0	0	0	2	0	0	0	0	3	0	0	0	0
Pontogeneiidae	6	1	12	2	3	0	0	1	8	1	2	4	6	0	0	0	0	23	3	0	2	0	4
Haylidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Isaeidae	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	1	0	0
Photidae	1	4	0	0	2	14	4	24	2	3	9	4	9	5	12	0	23	12	8	0	13	2	8
Ischyroceridae	3	16	5	0	2	0	15	1	1	0	3	12	1	0	1	0	1	9	11	0	26	0	7
Amaryllidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lysianassidae	5	6	2	15	8	7	0	2	1	7	2	22	11	0	2	0	4	4	7	0	34	0	10
Liljeborgiidae	0	0	2	0	0	1	0	3	0	1	0	0	2	0	0	0	5	1	0	0	11	1	0
Melitidae	0	0	0	0	1	0	0	1	0	0	0	2	0	0	0	0	0	1	1	0	0	0	1
Maeridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Melphidippidae	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
Oedicerotidae	0	5	2	2	2	9	0	0	1	5	0	2	0	1	4	0	1	9	12	1	20	9	3
Phoxocephalidae	8	4	20	7	21	6	0	4	18	11	3	18	8	16	20	0	2	15	17	2	101	4	12
Platyischnopidae	0	1	0	1	0	4	0	0	0	2	0	1	0	2	2	0	0	2	1	0	0	0	0

Aoridae	64	20	8	29	38	19	6	19	0	7	71	10	8	5	2	0	63	8	7	1	49	0	17
Urohaustoriidae	5	5	0	2	33	0	3	0	12	0	2	8	4	4	5	0	2	2	4	0	2	0	12
Amphilochidae	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Leucothoidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Podoceridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Synopiidae	0	1	1	3	1	5	0	0	1	1	4	0	0	10	2	0	4	3	1	0	12	0	2
Stegocephalidae	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hymenosomatidae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	2	0
Leucosiidae	0	0	2	0	0	3	0	0	1	1	2	0	1	0	1	0	1	2	0	0	0	1	0
Inachoididae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0
Majidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Pinnotheridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ovalipidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hexapodidae	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Litocheiridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Brachyura (iO)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Caprellidae	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Alpheidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pasiphaeidae	0	1	5	0	0	1	0	4	0	0	0	1	3	0	1	0	0	0	0	0	3	0	0
Callianassidae	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	2	0	0	0	3	1	0	0
Crangonidae	0	0	0	0	1	0	0	1	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0
Galatheidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Palaemonidae	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Copepoda (sCl.)	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	2	0	0	2	0
Janiridae	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
Cirolanidae	0	0	0	0	4	1	0	2	2	0	0	0	1	7	0	1	0	2	1	0	1	0	1
Chaetiliidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Gnathiidae	0	0	0	0	0	0	0	0	0	0	0	0	0	8	3	0	0	4	2	0	0	0	0
Arcturidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0

Austrarcturellidae	0	2	0	6	0	3	0	0	0	1	0	6	0	0	0	0	0	2	4	0	0	0	1
Paramunnidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anthuridae	2	2	5	2	4	23	2	1	8	8	4	1	11	7	1	0	2	2	5	5	5	0	7
Serolidae	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0
Sphaeromatidae	4	1	4	0	3	0	2	0	0	0	4	0	2	53	0	0	0	0	1	0	2	0	0
Mysidae	0	1	0	0	2	0	0	0	1	0	0	2	0	0	0	1	1	1	1	0	0	0	1
Nebaliidae	0	0	1	0	0	8	0	0	1	2	1	1	0	0	0	0	0	0	0	0	60	0	0
Sarsiellidae	0	1	0	3	0	3	0	0	0	2	1	0	0	0	1	0	0	0	1	0	0	0	0
Cypridinidae	0	4	1	8	0	5	1	0	0	1	0	4	0	3	3	0	0	8	3	0	0	0	4
Ostracoda (Cl.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Philomedidae	2	15	16	31	2	0	0	0	1	48	2	9	5	8	8	0	0	15	4	45	0	18	0
Rutidermatidae	0	0	0	2	0	3	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
Myodocopida (O.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cylindroleberididae	0	4	3	3	0	4	0	1	0	4	0	2	0	7	3	0	0	1	5	2	7	1	0
Paguridae	3	4	151	2	0	31	10	5	0	0	0	0	0	5	0	0	0	2	6	0	7	0	1
Apseudidae	0	0	0	3	1	49	0	0	0	2	1	0	1	31	0	0	8	0	0	0	5	0	0
Kalliapseudidae	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Leptocheliidae	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	2	0	4	0
Tanaidacea (O.)	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Whiteleggiidae	0	21	0	0	0	0	1	0	0	0	0	27	0	4	3	0	0	31	11	0	0	0	10
Bodotriidae	3	4	1	4	1	7	5	10	7	1	6	9	10	24	815	0	2	2	11	0	74	19	4
Diastylidae	0	4	0	4	3	4	0	18	8	0	2	6	3	1	1	0	18	38	3	2	40	12	9
Lampropidae	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nannastacidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Gynodiastylidae	0	15	0	0	0	0	1	2	4	1	1	17	5	1	3	0	0	9	11	0	23	0	15
Pseudocumatidae	1	0	0	6	18	2	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
Crustacea (sPh.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Leucosoleniidae	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Astropectinidae	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0

Asteriidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Echinidea (iCl.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Loveniidae	0	8	3	8	13	0	1	7	36	5	0	8	11	0	20	4	2	6	13	7	14	1	10
Schizasteridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6
Cucumariidae	0	0	1	0	0	4	0	0	2	2	0	0	0	0	0	0	0	0	1	0	0	0	0
Chiridotidae	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Phyllophoridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Synaptidae	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0
Amphiuridae	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	1	2	0	0	0
Ophionereididae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0
Ophiuridae	0	1	1	17	0	20	1	0	0	3	0	0	1	2	0	0	0	2	0	0	3	2	0
Chitonidae	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Chaetodermatidae	0	0	0	2	0	6	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Lepetidae	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Columbellidae	11	0	0	0	0	0	0	0	3	0	8	1	3	0	0	0	2	0	0	0	0	2	0
Anabathridae	0	0	0	0	10	9	0	0	0	4	0	0	0	0	0	0	0	6	0	0	1	0	0
Rastodentidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Marginellidae	0	0	0	0	0	0	0	1	2	0	2	0	0	4	0	0	0	3	0	0	0	0	0
Muricidae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nassariidae	0	1	0	0	0	1	0	0	0	0	1	0	2	0	6	0	2	0	0	1	5	5	0
Pyramidellidae	0	0	0	0	2	1	0	0	7	0	0	0	2	0	0	0	0	0	0	0	1	0	0
Tornatinidae	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Retusidae	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0
Trochidae	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0
Mangeliidae	0	0	0	0	0	5	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0
Olividae	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Aeolidioidea (S.F.)	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pleurobranchidae	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Philinidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2	1	0	0

Calyptraeidae	1	0	1	0	0	0	1	4	0	0	1	0	1	0	0	0	0	0	0	0	1	0	0
Terebridae	0	0	0	0	1	0	0	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Epitoniidae	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fasciolariidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cassidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cerithiopsidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Naticidae	0	0	0	0	0	0	0	0	0	0	2	1	4	0	3	0	1	0	0	0	0	0	0
Pseudomelatomidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Turritellidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	4	7	0
Cingulopsidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bivalvia (Cl.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lucinidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nuculanidae	1	0	0	0	0	7	1	0	0	3	1	0	8	0	0	0	7	0	0	0	0	0	0
Nuculidae	0	0	0	0	0	1	0	0	0	1	0	0	1	0	1	0	0	0	0	3	0	0	0
Ostreidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0
Psammobiidae	0	0	0	0	0	0	1	6	0	0	3	1	1	0	0	0	3	1	1	0	0	0	0
Solemyidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0
Tellinidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0
Carditidae	0	0	0	0	0	0	0	0	0	0	0	0	0	13	0	0	0	0	0	0	0	0	0
Mactridae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Veneridae	4	0	6	0	1	1	4	12	2	4	5	2	10	2	0	16	1	2	2	2	0	1	0
Cardiidae	0	0	0	13	0	119	0	0	0	3	0	0	0	1	2	1	0	1	0	1	0	12	1
Condylocardiidae	1	0	2	1	2	0	0	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	0
Galeommatidae	0	0	0	0	0	2	1	0	1	0	0	0	9	8	0	0	1	0	1	0	1	0	0
Hiatellidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
Trigoniidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
Limidae	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Semelidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	28	0	1	0
Corbulidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	4	0

Pectinidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Glycymeridae	0	0	0	2	0	0	12	0	0	2	0	3	1	0	0	0	0	1	1	0	0	0	0
Solenidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Myochamidae	0	0	0	3	0	4	0	0	0	1	0	0	0	1	1	0	0	1	1	0	0	0	1
Thraciidae	0	0	1	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	2	0
Scaphopoda (Cl.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phoronida (P.)	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	3	0	0	0
Platyhelminthes (P.)	0	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0
Phascolionidae	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sipuncula (P.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anthozoa (Cl.)	6	0	5	1	11	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Edwardsiidae	0	1	3	0	0	8	0	0	0	0	0	1	0	1	5	0	0	5	2	0	0	0	12
Ophichthidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pleuronectidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Enteropneusta (Cl.)	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Nemertea (P.)	3	3	1	6	1	9	2	1	0	3	1	2	3	5	1	5	0	2	5	5	2	3	0
Nematoda (P.)	0	0	0	0	0	0	0	1	0	0	1	1	0	5	1	0	1	3	0	0	0	0	2
Oligochaeta (sCl)	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	1	0	0	0	0	0
Opheliidae	0	0	0	3	0	3	1	1	0	0	0	0	1	7	0	0	2	0	0	0	0	0	0
Phyllodocidae	0	0	1	0	0	0	0	0	0	3	1	0	0	2	0	0	3	0	0	2	2	0	0
Capitellidae	0	0	5	0	0	18	0	0	0	1	0	2	16	1	0	6	6	1	0	12	0	0	0
Dorvilleidae	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	3	0	2	0	2	0	1	0
Nephtyidae	0	0	1	2	0	4	0	0	0	1	0	0	1	0	0	30	2	0	0	13	2	23	0
Flabelligeridae	0	0	2	0	0	0	0	0	0	2	0	0	0	0	0	10	0	0	0	0	0	0	0
Glyceridae	0	3	0	0	2	0	1	0	1	0	0	3	0	4	1	0	0	2	1	0	0	0	4
Goniadidae	0	0	0	0	0	1	0	0	0	0	0	0	1	2	0	0	0	0	0	1	0	3	0
Hesionidae	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	1	3	0	0	2	0	0	0
Serpulidae	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Sabellidae	0	0	1	0	0	6	1	3	0	1	0	4	0	1	4	0	10	7	16	0	0	5	16

Eunicidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	20	0	0	0	3	0	3	0
Onuphidae	0	2	12	4	0	12	0	1	0	13	1	7	2	0	5	0	4	3	5	0	4	0	6
Lumbrineridae	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	219	0	0	1	1	1	54	0
Oenonidae	0	0	0	0	0	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Maldanidae	0	1	3	1	0	11	0	2	0	2	0	0	1	0	0	1	1	1	0	0	0	0	0
Nereididae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Orbiniidae	2	1	3	3	4	0	0	0	5	3	0	4	0	0	0	1	2	6	2	0	3	8	1
Apistobranchidae	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spionidae	4	14	23	22	14	87	6	26	25	38	6	24	84	4	9	0	43	17	20	2	15	6	17
Paraonidae	0	0	0	0	0	10	0	0	0	0	0	0	0	6	0	0	2	0	0	0	0	0	0
Cirratulidae	1	0	1	0	0	2	1	0	0	1	0	0	1	0	0	0	0	0	2	161	1	6	0
Syllidae	3	0	5	0	0	3	0	0	0	2	4	0	3	3	0	0	3	0	0	0	1	1	0
Terebellidae	0	0	4	0	0	0	0	0	1	2	0	0	0	3	2	11	3	1	0	34	1	40	1
Trichobranchidae	0	0	0	2	0	6	0	0	0	1	1	0	0	2	0	36	5	0	0	186	0	8	0
Ampharetidae	0	0	5	0	0	10	0	0	0	1	0	0	0	0	0	0	3	0	0	1	3	63	0
Polynoidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0
Amphinomidae	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0
Chaetopteridae	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Magelonidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0
Pectinariidae	0	0	0	1	0	0	0	0	1	1	0	0	0	1	0	3	0	0	0	3	1	0	0
Sigalionidae	0	0	1	1	0	1	0	0	0	2	1	0	2	0	0	0	2	1	0	0	0	0	0
Oweniidae	0	0	0	0	0	1	0	3	2	0	0	1	1	0	0	0	0	5	0	0	7	3	0
Polygordiidae	0	2	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	1	0	0	0	0
Scalibregmatidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
Total abundance	**146**	**189**	**354**	**249**	**214**	**617**	**84**	**182**	**175**	**229**	**164**	**240**	**293**	**324**	**964**	**381**	**261**	**301**	**228**	**551**	**633**	**364**	**209**
Total families	**26**	**41**	**50**	**45**	**33**	**61**	**25**	**39**	**37**	**55**	**38**	**44**	**50**	**61**	**42**	**25**	**44**	**59**	**51**	**39**	**54**	**48**	**34**

Macrofauna raw data for Storm Bay for the 2020 survey (data is pooled by site).

	SB1	SB2	SB3	SB4	SB5	SB6	SB8	SB9	SB10	SB11	SB13	SB16	SB17	SB18	SB19	SB21	SB22	SB23	SB24	NUB1	NUB2	NUB3	NUB4
Callipallenidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phoxichilidiidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascidiidae	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Molgulidae	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pyuridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Holozoidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cryptoporidae	0	0	0	4	0	0	0	0	0	17	0	0	0	0	0	0	0	0	1	0	0	0	0
Ampeliscidae	6	1	11	5	1	19	0	0	0	17	3	0	0	1	4	1	23	0	0	1	45	32	0
Corophiidae	0	0	0	1	0	0	0	0	7	0	0	0	0	0	1	0	13	0	0	0	4	0	1
Dexaminidae	1	0	1	1	0	1	3	2	0	0	1	3	0	0	2	0	0	3	0	0	4	0	2
Eusiridae	0	0	0	5	1	2	2	0	1	7	0	0	0	4	5	0	0	0	1	0	0	0	0
Pontogeneiidae	5	8	9	0	1	3	4	3	0	4	9	5	1	0	0	0	0	1	6	0	2	0	3
Haylidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Isaeidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Photidae	6	10	20	16	2	42	6	37	6	16	10	6	7	7	15	1	150	4	6	1	82	16	8
Ischyroceridae	7	2	2	1	1	0	34	4	0	0	8	84	0	0	3	0	5	2	4	0	35	1	16
Amaryllidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lysianassidae	2	2	2	18	62	19	5	2	4	15	1	21	66	5	2	0	6	6	4	1	5	1	24
Liljeborgiidae	2	0	0	1	0	0	2	1	0	2	1	2	5	0	1	0	2	1	4	0	5	1	1
Melitidae	0	0	0	0	0	0	1	0	0	0	0	0	7	2	1	0	0	0	0	0	0	0	1
Maeridae	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Melphidippidae	0	0	0	0	0	0	0	0	0	0	2	0	0	4	0	0	1	0	0	0	5	0	0
Oedicerotidae	0	9	0	0	3	5	3	1	8	3	0	1	0	5	7	1	0	3	13	2	4	22	0
Phoxocephalidae	22	8	26	10	20	12	7	4	9	23	20	10	7	11	5	0	7	13	7	3	40	6	7
Platyischnopidae	1	1	0	0	0	6	0	0	0	3	3	4	4	0	1	0	1	1	1	0	0	0	2
Aoridae	66	14	11	63	20	32	3	19	0	31	94	14	11	5	2	0	89	6	3	1	57	0	35

Urohaustoriidae	7	5	0	0	18	2	7	0	2	0	5	12	1	9	4	0	0	2	6	0	1	0	3
Amphilochidae	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Leucothoidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Podoceridae	0	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Synopiidae	3	8	16	3	2	0	0	0	0	0	3	2	0	20	2	0	3	3	1	0	5	0	0
Stegocephalidae	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Hymenosomatidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	2	0
Leucosiidae	0	0	1	0	0	1	0	0	0	3	0	0	1	0	0	0	1	0	0	0	0	0	0
Inachoididae	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Majidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pinnotheridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ovalipidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hexapodidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	2	0
Litocheiridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
Brachyura (iO)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Caprellidae	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	1
Alpheidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pasiphaeidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	0
Callianassidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
Crangonidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Galatheidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Palaemonidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Copepoda (sCl.)	0	0	0	0	0	0	3	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0
Janiridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cirolanidae	0	0	1	0	4	0	1	0	1	1	0	1	1	1	0	0	0	0	2	0	0	7	1
Chaetiliidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Gnathiidae	0	2	0	1	1	0	1	0	0	0	0	1	0	2	0	0	0	1	1	0	0	0	6
Arcturidae	0	0	3	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0
Austrarcturellidae	0	0	0	14	1	1	2	0	0	1	0	1	0	2	0	0	0	1	2	0	0	0	1

Paramunnidae	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0
Anthuridae	4	8	7	8	10	72	3	0	17	21	4	4	3	3	2	0	3	1	3	8	2	1	7
Serolidae	0	0	1	2	0	0	0	0	0	0	0	2	0	0	1	0	4	0	0	0	0	1	0
Sphaeromatidae	4	0	2	0	2	0	2	2	1	0	6	0	2	47	3	0	0	0	0	1	0	0	0
Mysidae	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Nebaliidae	0	0	0	3	2	8	0	0	0	7	0	1	0	1	0	0	0	0	0	0	62	0	0
Sarsiellidae	0	0	2	9	0	1	0	0	0	6	0	0	0	1	0	0	1	0	1	1	1	0	0
Cypridinidae	0	11	0	9	3	3	0	0	0	12	0	11	0	6	16	0	0	4	10	2	3	0	10
Ostracoda (Cl.)	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0
Philomedidae	2	11	32	29	2	6	0	0	0	85	28	13	7	20	6	0	2	5	2	114	1	47	2
Rutidermatidae	0	0	0	4	0	6	0	0	0	7	0	0	0	1	0	0	0	0	0	0	0	0	0
Myodocopida (O.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	6	0
Cylindroleberididae	1	0	2	4	0	3	4	0	2	2	0	2	0	2	2	0	2	1	0	6	2	3	1
Paguridae	2	1	0	52	0	0	0	6	0	21	1	12	0	2	0	0	0	4	3	0	1	0	5
Apseudidae	2	0	0	1	3	65	0	1	0	12	1	1	1	15	0	0	7	0	0	0	4	0	0
Kalliapseudidae	0	0	0	0	0	4	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Leptocheliidae	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tanaidacea (O.)	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
Whiteleggiidae	0	48	0	4	0	0	0	0	0	0	0	26	0	0	11	0	0	34	1	0	0	0	0
Bodotriidae	14	15	3	3	20	15	13	10	7	2	3	17	18	21	521	0	11	13	12	1	59	31	13
Diastylidae	5	6	5	6	19	7	9	13	7	4	3	10	2	1	1	1	16	5	6	3	56	34	8
Lampropidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0
Nannastacidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Gynodiastylidae	1	2	3	2	0	2	0	0	0	0	0	1	0	1	0	0	0	1	0	0	2	0	3
Pseudocumatidae	0	1	0	0	3	0	8	0	0	0	0	5	0	0	0	0	0	0	0	0	2	0	9
Crustacea (sPh.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Leucosoleniidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Astropectinidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Asteriidae	0	0	2	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Echinidea (iCl.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Loveniidae	0	1	0	0	1	0	1	0	0	2	0	0	1	0	0	0	1	0	0	7	3	7	0
Schizasteridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cucumariidae	0	0	0	0	0	1	1	0	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Chiridotidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phyllophoridae	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Synaptidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Amphiuridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	1	0
Ophionereididae	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ophiuridae	0	2	2	21	54	2	0	0	7	7	0	3	4	0	0	0	0	2	2	0	1	4	2
Chitonidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chaetodermatidae	0	0	0	2	0	6	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
Lepetidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Columbellidae	13	0	4	4	2	0	5	0	0	2	3	0	3	0	0	0	1	1	0	0	0	0	0
Anabathridae	0	1	9	53	7	25	3	0	0	55	0	3	0	5	0	0	0	4	0	0	0	0	6
Rastodentidae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Marginellidae	1	3	0	0	0	0	2	0	1	6	3	5	1	2	2	0	1	0	2	0	0	0	5
Muricidae	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nassariidae	0	1	0	1	0	0	1	0	0	0	2	0	1	0	4	0	4	0	0	2	1	16	0
Pyramidellidae	2	0	5	1	2	0	7	0	1	0	0	0	0	0	0	0	0	0	1	0	3	1	2
Tornatinidae	0	0	0	0	0	0	0	0	1	0	0	0	0	2	1	0	0	2	0	0	0	0	1
Retusidae	1	1	1	1	0	0	0	0	0	2	1	0	1	0	0	0	0	0	2	0	0	1	1
Trochidae	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0
Mangeliidae	1	1	2	0	0	0	0	0	0	2	0	1	0	1	0	0	0	0	0	0	0	0	0
Olividae	2	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Aeolidioidea (S.F.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Pleurobranchidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Philinidae	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	1	1	0	0

Calyptraeidae	0	0	3	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Terebridae	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0	1	0	1	0	0	0	0
Epitoniidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fasciolariidae	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Cassidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cerithiopsidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Naticidae	0	1	0	0	0	0	1	0	1	0	0	4	0	1	3	0	0	1	1	0	0	1	4
Pseudomelatomidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Turritellidae	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0	0
Cingulopsidae	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
Bivalvia (Cl.)	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Lucinidae	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
Nuculanidae	0	0	3	1	0	11	0	0	0	20	0	0	6	1	0	0	14	0	0	0	0	0	0
Nuculidae	0	0	0	1	1	5	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	3	0
Ostreidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Psammobiidae	1	0	0	0	0	0	1	2	1	0	3	0	1	0	0	0	8	1	1	0	0	0	0
Solemyidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tellinidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	1	0
Carditidae	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
Mactridae	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0
Veneridae	1	1	3	1	0	0	10	4	1	4	4	0	2	6	5	1	1	2	1	0	0	1	0
Cardiidae	0	2	2	7	1	1	0	0	0	1	0	0	0	1	1	0	0	0	0	1	3	1	0
Condylocardiidae	3	0	3	1	1	0	0	0	2	2	4	0	0	2	0	0	0	0	0	0	3	0	0
Galeommatidae	0	0	1	3	0	0	0	0	0	5	0	0	0	5	0	0	0	0	1	0	0	1	0
Hiatellidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trigoniidae	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Limidae	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
Semelidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	39	0	0	0

Corbulidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
Pectinidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Glycymerididae	0	0	0	8	2	0	8	1	0	3	2	0	1	2	0	0	0	3	1	0	0	0	1
Solenidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Myochamidae	0	0	1	0	0	10	0	0	0	0	0	0	0	0	2	0	0	0	2	0	0	0	0
Thraciidae	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0
Scaphopoda (Cl.)	0	0	0	0	0	4	0	0	0	5	0	0	0	1	0	0	0	0	0	0	0	0	0
Phoronida (P.)	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	0	16	0	2	1
Platyhelminthes (P.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phascolionidae	1	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Sipuncula (P.)	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anthozoa (Cl.)	0	0	5	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Edwardsiidae	0	0	0	0	0	9	0	0	0	3	0	2	0	1	0	2	0	0	3	0	0	2	0
Ophichthidae	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Pleuronectidae	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Enteropneusta (Cl.)	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Nemertea (P.)	1	2	4	6	0	21	3	0	0	7	0	4	0	4	1	2	0	7	3	4	1	4	1
Nematoda (P.)	0	4	0	1	0	0	4	0	0	0	0	0	0	3	0	0	0	7	1	0	0	0	1
Oligochaeta (sCl)	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
Opheliidae	0	0	0	0	0	3	1	2	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
Phyllodocidae	1	2	2	0	0	1	0	0	0	1	3	1	0	0	1	0	0	0	0	0	0	0	1
Capitellidae	1	0	0	0	0	24	1	0	0	3	0	2	0	0	0	0	1	0	0	30	0	1	0
Dorvilleidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	2	0	0	1
Nephtyidae	0	0	0	0	0	0	0	0	0	5	1	0	0	0	0	40	0	0	0	37	0	44	0
Flabelligeridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0	0	0	0	0	0
Glyceridae	0	2	0	2	1	0	0	0	0	0	0	2	0	0	2	0	0	2	1	0	0	0	5
Goniadidae	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
Hesionidae	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0

Serpulidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sabellidae	0	19	0	9	0	9	4	0	0	3	0	3	1	1	3	0	3	14	6	4	0	0	13
Eunicidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	19	0	0	0	0	0	0	0
Onuphidae	2	0	4	15	0	16	0	0	0	31	0	7	0	9	2	0	0	4	1	0	0	0	1
Lumbrineridae	2	2	0	0	0	0	0	0	1	1	0	1	1	1	1	261	0	0	0	2	0	56	0
Oenonidae	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Maldanidae	0	0	2	187	0	16	0	0	1	4	0	0	1	0	0	0	2	0	0	1	0	1	0
Nereididae	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0
Orbiniidae	0	0	1	1	0	4	0	1	2	4	0	2	0	1	1	2	0	2	0	0	0	6	2
Apistobranchidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
Spionidae	5	2	22	33	28	125	33	7	32	66	3	15	40	2	4	2	23	32	10	32	11	13	18
Paraonidae	0	0	0	0	0	25	0	0	0	0	0	0	0	2	0	0	0	0	0	1	0	0	0
Cirratulidae	0	0	0	1	0	4	0	0	0	0	1	2	0	6	1	2	0	0	1	163	1	1	0
Syllidae	1	0	8	0	0	12	2	1	0	3	0	0	1	12	0	0	0	0	0	0	1	0	0
Terebellidae	0	0	2	7	0	0	0	0	0	10	0	0	0	1	11	8	3	1	0	46	0	17	0
Trichobranchidae	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	27	0	0	0	169	0	9	0
Ampharetidae	0	0	3	9	0	63	0	1	0	0	0	0	0	1	0	0	2	0	1	19	2	45	0
Polynoidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	1	1	0	0
Amphinomidae	0	0	0	0	0	0	0	0	0	1	0	0	0	5	0	0	0	0	0	0	0	0	0
Chaetopteridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Magelonidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pectinariidae	0	0	0	0	1	2	1	0	0	2	0	0	0	0	0	0	2	1	0	1	0	1	1
Sigalionidae	0	0	0	3	0	5	2	2	0	3	0	0	0	0	0	0	3	0	1	0	0	0	1
Oweniidae	0	1	1	11	0	2	0	0	1	0	0	0	0	1	0	0	2	2	1	14	23	75	1
Polygordiidae	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	1
Scalibregmatidae	0	0	0	0	0	6	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Total abundance	**203**	**236**	**260**	**685**	**304**	**758**	**217**	**132**	**129**	**595**	**240**	**332**	**210**	**300**	**671**	**391**	**423**	**211**	**152**	**762**	**550**	**535**	**241**
Total families	**39**	**48**	**51**	**64**	**37**	**59**	**45**	**28**	**29**	**63**	**36**	**46**	**33**	**67**	**45**	**23**	**41**	**49**	**53**	**47**	**44**	**49**	**48**

Macrofauna raw data for Storm Bay for the 2021 survey (data is pooled by site).

	SB1	SB2	SB3	SB4	SB5	SB6	SB8	SB9	SB10	SB11	SB13	SB16	SB17	SB18	SB19	SB21	SB22	SB23	SB24	NUB1	NUB2	NUB3	NUB4
Callipallenidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
Phoxichilidiidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascidiidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	0	0	0	3	0	0	0
Molgulidae	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Pyuridae	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Holozoidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cryptoporidae	0	0	0	3	0	0	0	0	0	8	0	0	0	0	0	0	0	0	0	0	0	0	0
Ampeliscidae	2	0	22	2	0	30	3	0	1	12	1	0	1	2	0	1	8	4	1	5	35	14	0
Corophiidae	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Dexaminidae	0	0	0	4	0	0	2	2	0	0	0	3	0	0	0	3	0	0	1	1	2	2	0
Eusiridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pontogeneiidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Haylidae	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Isaeidae	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Photidae	0	0	5	1	0	3	6	7	0	1	5	1	1	0	1	1	4	4	0	0	21	1	0
Ischyroceridae	0	1	1	0	0	0	6	1	0	0	8	6	0	0	1	0	10	10	4	0	8	0	13
Amaryllidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
Lysianassidae	3	10	2	12	29	9	4	0	2	15	1	8	19	10	1	0	3	3	4	0	17	0	11
Liljeborgiidae	0	1	2	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0
Melitidae	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Maeridae	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Melphidippidae	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2	0	0
Oedicerotidae	0	0	1	1	0	4	3	1	1	4	1	3	1	2	0	0	1	3	1	2	4	13	1
Phoxocephalidae	17	7	24	5	15	3	6	5	12	12	4	7	11	9	5	0	9	5	5	2	25	14	6
Platyischnopidae	1	0	0	1	2	1	0	0	0	4	2	0	0	4	0	0	1	0	0	0	0	0	0
Aoridae	24	7	4	24	14	19	14	29	0	6	50	2	15	10	2	0	34	2	3	0	61	0	8

Urohaustoriidae	2	0	0	0	17	0	1	2	5	1	8	3	2	2	1	0	1	1	3	0	0	0	2
Amphilochidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Leucothoidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
Podoceridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Synopiidae	0	0	4	1	0	0	0	0	0	0	1	0	0	7	0	0	5	0	0	0	2	0	0
Stegocephalidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hymenosomatidae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Leucosiidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Inachoididae	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Majidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pinnotheridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Ovalipidae	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hexapodidae	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	2	0
Litocheiridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
Brachyura (iO)	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Caprellidae	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0
Alpheidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pasiphaeidae	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Callianassidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	3	0
Crangonidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Galatheidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Palaemonidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Copepoda (sCl.)	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0
Janiridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cirolanidae	0	0	0	4	0	1	1	1	1	2	0	0	0	1	0	0	1	0	0	0	0	4	0
Chaetiliidae	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Gnathiidae	0	1	0	0	0	0	0	0	0	0	0	2	0	2	0	0	0	0	0	0	0	0	0
Arcturidae	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Austrarcturellidae	0	0	0	38	0	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0

Paramunnidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anthuridae	2	0	10	1	8	47	0	4	12	8	7	3	8	2	1	0	3	0	1	3	6	1	3
Serolidae	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0	0	2	1	0	0	1	0	0
Sphaeromatidae	2	0	1	0	6	0	2	0	0	0	1	0	1	66	0	1	0	0	0	0	0	0	0
Mysidae	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nebaliidae	0	0	0	3	1	11	0	0	0	1	1	0	3	0	0	0	1	0	0	0	75	0	0
Sarsiellidae	0	0	0	8	0	2	0	0	0	3	3	0	0	0	0	0	1	0	0	0	1	0	0
Cypridinidae	0	7	0	7	4	3	4	2	0	3	0	9	0	3	5	0	0	20	4	0	0	0	5
Ostracoda (Cl.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
Philomedidae	1	10	39	17	3	4	4	0	0	66	2	11	1	10	4	0	3	1	6	33	1	28	1
Rutidermatidae	0	0	0	0	0	2	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0
Myodocopida (O.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3	0
Cylindroleberididae	1	0	2	2	2	3	0	0	1	2	0	0	0	0	0	0	1	0	0	4	0	3	1
Paguridae	1	2	7	7	0	1	0	2	3	91	2	0	0	7	1	0	2	0	2	0	1	0	0
Apseudidae	0	0	5	0	0	41	0	0	0	9	2	0	0	3	0	0	15	0	0	0	13	0	0
Kalliapseudidae	0	0	1	0	0	3	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0
Leptocheliidae	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
Tanaidacea (O.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Whiteleggiidae	0	1	0	0	0	0	0	0	0	0	0	2	0	2	0	0	0	4	1	0	0	0	2
Bodotriidae	1	3	2	0	3	5	5	10	4	3	2	7	14	12	3	0	5	18	5	1	23	24	6
Diastylidae	2	4	0	1	0	3	1	7	1	0	2	1	2	0	0	0	5	6	1	1	13	16	2
Lampropidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Nannastacidae	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Gynodiastylidae	0	0	0	1	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	0
Pseudocumatidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0
Crustacea (sPh.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Leucosoleniidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Astropectinidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Asteriidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Echinidea (iCl.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Loveniidae	3	0	3	0	0	0	0	0	2	1	5	0	0	0	0	0	1	0	0	3	3	11	0
Schizasteridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cucumariidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chiridotidae	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Phyllophoridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Synaptidae	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Amphiuridae	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	4	3	1	0
Ophionereididae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ophiuridae	1	2	0	9	1	6	1	0	0	0	0	4	0	0	0	0	1	11	2	0	0	2	4
Chitonidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Chaetodermatidae	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Lepetidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Columbellidae	0	0	4	1	0	1	2	0	4	0	1	1	0	0	0	0	0	0	0	0	0	0	0
Anabathridae	0	2	4	11	6	18	9	0	0	38	1	4	0	1	0	0	0	0	0	0	0	0	0
Rastodentidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Marginellidae	2	3	0	0	0	1	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0
Muricidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nassariidae	0	0	5	0	0	0	0	1	1	0	1	0	0	0	0	0	0	0	0	3	5	7	0
Pyramidellidae	0	1	6	1	0	0	4	1	1	4	2	0	0	1	0	0	0	0	0	0	0	0	0
Tornatinidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Retusidae	0	0	1	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trochidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mangeliidae	0	0	2	0	0	2	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
Olividae	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Aeolidioidea (S.F.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pleurobranchidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Philinidae	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Calyptraeidae	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Terebridae	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Epitoniidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fasciolariidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
Cassidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Cerithiopsidae	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Naticidae	0	2	0	0	2	0	0	2	0	0	0	1	0	1	0	0	0	0	0	1	0	0	0
Pseudomelatomidae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Turritellidae	0	0	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	6	0	0
Cingulopsidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bivalvia (Cl.)	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
Lucinidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nuculanidae	0	0	0	0	0	1	0	0	0	5	0	0	2	0	0	0	10	0	0	0	0	0	0
Nuculidae	0	0	0	0	0	3	0	0	0	0	1	0	0	0	0	0	0	0	0	1	3	3	0
Ostreidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Psammobiidae	0	0	0	0	0	0	0	2	0	0	2	0	0	0	0	0	5	0	0	0	0	0	0
Solemyidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tellinidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Carditidae	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	3	0	0	0	0	0
Mactridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Veneridae	1	0	1	0	0	0	7	12	2	1	5	1	0	0	0	1	2	1	0	0	0	1	4
Cardiidae	0	1	3	1	0	4	0	1	0	2	0	0	0	0	0	0	0	0	0	0	1	1	1
Condylocardiidae	3	0	0	0	0	0	0	1	0	0	10	0	0	0	0	0	0	0	0	0	7	0	0
Galeommatidae	0	0	0	0	0	0	0	0	0	4	0	0	0	1	0	0	0	0	0	0	0	1	0
Hiatellidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trigoniidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Limidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Semelidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	5	0	0	0
Corbulidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	4	1	0	0
Pectinidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Glycymeridae	0	1	0	0	0	0	2	1	0	5	2	2	0	0	1	0	0	0	0	0	0	0	2
Solenidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Myochamidae	0	0	0	0	0	7	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
Thraciidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Scaphopoda (Cl.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phoronida (P.)	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	3	0	0	0
Platyhelminthes (P.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phascolionidae	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Sipuncula (P.)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Anthozoa (Cl.)	1	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Edwardsiidae	0	1	0	0	0	6	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
Ophichthidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pleuronectidae	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Enteropneusta (Cl.)	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Nemertea (P.)	3	2	2	1	3	12	0	3	0	3	0	0	2	2	0	3	2	0	1	7	0	1	2
Nematoda (P.)	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Oligochaeta (sCl)	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
Opheliidae	0	0	1	0	0	1	1	2	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
Phyllodocidae	0	0	1	3	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	2	0
Capitellidae	0	0	0	3	0	12	0	0	0	4	0	0	0	0	0	2	1	0	0	22	0	0	0
Dorvilleidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	1	0	8	0	0	0
Nephtyidae	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	35	1	0	0	30	0	33	0
Flabelligeridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
Glyceridae	0	2	0	2	1	0	1	0	0	0	0	2	1	0	0	0	1	4	3	0	0	0	1
Goniadidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Hesionidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0
Serpulidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sabellidae	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	2	3	1	1	6	0	0	0
Eunicidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78	0	0	0	0	3	0	0

Onuphidae	0	0	14	9	0	19	1	1	0	25	0	4	0	15	1	0	5	3	0	0	1	1	0
Lumbrineridae	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	199	0	0	1	0	1	49	0
Oenonidae	0	0	0	0	1	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
Maldanidae	0	0	0	61	0	11	1	0	0	3	0	0	0	1	0	2	0	0	0	0	0	1	0
Nereididae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Orbiniidae	1	0	2	0	1	9	0	0	1	1	0	0	0	0	0	0	0	0	1	3	0	4	0
Apistobranchidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spionidae	0	8	21	5	4	41	2	7	8	12	0	4	5	1	1	0	3	7	4	5	9	4	3
Paraonidae	0	0	0	0	0	52	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Cirratulidae	0	0	0	0	0	3	0	0	0	0	0	0	0	4	0	0	0	0	1	124	1	0	0
Syllidae	1	0	9	0	0	8	0	0	0	15	3	0	0	2	0	2	4	0	0	0	2	0	0
Terebellidae	0	1	2	0	0	0	1	0	0	7	0	0	0	0	0	16	0	1	0	27	1	9	0
Trichobranchidae	0	0	0	6	0	0	0	0	0	2	0	0	0	0	0	19	0	0	0	112	0	5	0
Ampharetidae	0	0	1	2	0	14	0	0	0	0	0	0	0	0	0	0	1	0	0	6	1	20	0
Polynoidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0
Amphinomidae	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
Chaetopteridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Magelonidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pectinariidae	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0
Sigalionidae	0	1	0	2	0	0	0	0	0	0	0	0	0	1	0	0	2	0	1	0	0	0	0
Oweniidae	0	4	0	3	1	1	1	0	1	0	1	0	0	1	0	0	0	1	1	3	1	17	1
Polygordiidae	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
Scalibregmatidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Total abundance	**78**	**86**	**229**	**265**	**127**	**437**	**98**	**121**	**64**	**402**	**142**	**97**	**93**	**210**	**30**	**396**	**165**	**116**	**60**	**444**	**375**	**306**	**82**
Total families	**25**	**27**	**48**	**39**	**24**	**50**	**31**	**38**	**20**	**47**	**36**	**30**	**21**	**43**	**16**	**30**	**42**	**25**	**27**	**38**	**47**	**38**	**24**

Appendix 5-1: Summary tables from inshore reef biodiversity baseline for fish, invertebrate & algal species

Summary of fish survey results for the western Storm Bay sites. Data represent total abundance of fish species for the 2000 m^2 survey area at each site (summed across blocks and transects within a site).

		Site													
Family	**Species**	**SBIR02**	**SBIR04**	**SBIR05**	**SBIR06**	**SBIR28**	**SBIR07**	**SBIR08**	**SBIR09**	**SBIR10**	**SBIR11**	**SBIR12**	**SBIR13**	**SBIR14**	**ADV**
Aplodactylidae	*Aplodactylus arctidens* (Marblefish)	0	0	0	1	0	1	1	1	1	0	1	3	8	1
Apogonidae	*Vincentia conspersa* (Southern cardinalfish)	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Arripidae	*Arripis trutta* (Australian salmon)	250	0	0	0	0	0	0	0	0	0	0	0	0	0
Bovichtidae	*Bovichtus angustifrons* (Dragonet)	0	0	0	0	0	0	0	1	0	0	0	0	0	1
Carangidae	*Trachurus novaezelandiae* (Yellow-tail scad)	0	0	0	0	0	0	0	20	0	0	0	0	0	0
Cheilodactylidae	*Chirodactylus spectabilis* (Banded morwong)	0	8	0	7	2	8	1	2	1	0	0	4	3	0
Dasyatidae	*Bathytoshia brevicaudata* (Smooth stingray)	0	1	0	1	0	0	0	0	0	0	0	0	0	0
Dinolestidae	*Dinolestes lewini* (Long-fin pike)	0	0	15	61	0	5	19	1	11	0	0	8	3	6
Diodontidae	*Diodon nicthemerus* (Globe fish)	0	1	0	1	0	1	0	0	0	4	1	0	1	0
Gnathanacanthidae	*Gnathanacanthus goetzeei* (Red velvetfish)	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Kyphosidae	*Atypichthys strigatus* (Mado sweep)	0	0	1	0	0	0	1	0	0	0	0	0	0	0
	Girella tricuspidata (Luderick)	0	0	0	0	0	0	0	0	0	0	0	1	0	0
	Girella zebra (Zebra fish)	0	0	0	0	0	0	0	0	0	0	0	0	0	1
	Scorpis aequipinnis (Sea sweep)	0	0	0	0	0	0	0	0	0	0	0	4	10	7
	Scorpis lineolata (Silver sweep)	0	6	0	35	0	23	19	0	0	0	0	14	0	0
Labridae	*Dotalabrus aurantiacus* (Castelnaus wrasse)	0	1	5	4	1	0	0	4	0	0	0	0	0	0
	Notolabrus fucicola (Purple wrasse)	38	28	3	12	25	15	4	9	9	3	7	11	29	7
	Notolabrus tetricus (Blue-throat wrasse)	74	33	59	56	106	30	9	45	10	2	8	5	7	8
	Pictilabrus laticlavius (Senator wrasse)	7	1	16	14	12	5	1	1	0	1	1	0	5	3
	Pseudolabrus rubicundus (Rosy wrasse)	0	3	0	1	4	3	0	2	0	0	0	0	0	0
Latridae	*Latridopsis forsteri* (Bastard trumpeter)	0	2	0	5	1	8	2	13	0	1	0	0	0	0
	Pseudogoniistius nigripes (Magpie perch)	0	0	0	1	0	0	0	0	0	0	0	3	0	2
Monacanthidae	*Acanthaluteres vittiger* (Toothbrush leatherjacket)	0	3	3	16	1	22	39	83	121	2	29	5	4	14
	Brachaluteres jacksonianus (Pygmy leatherjacket)	0	0	0	0	0	0	0	1	0	0	0	0	0	0
	Meuschenia australis (Brown-striped leatherjacket)	0	1	0	3	0	0	1	7	1	0	0	0	4	2
	Meuschenia flavolineata (Yellow-stripe leatherjacket)	0	0	0	0	0	0	0	0	0	1	0	0	0	0

		Site													
Family	**Species**	**SBIR02**	**SBIR04**	**SBIR05**	**SBIR06**	**SBIR28**	**SBIR07**	**SBIR08**	**SBIR09**	**SBIR10**	**SBIR11**	**SBIR12**	**SBIR13**	**SBIR14**	**ADV**
Monacanthidae	*Meuschenia freycineti* (Six-spine leatherjacket)	0	0	0	0	0	0	0	0	0	0	0	0	1	0
	Scobinichthys granulatus (Rough leatherjacket)	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Moridae	*Pseudophycis bachus* (Red cod)	0	0	1	0	2	0	0	0	0	0	1	0	0	0
	Pseudophycis barbata (Bearded cod)	0	0	0	1	0	1	0	1	0	0	0	0	0	0
Mullidae	*Upeneichthys vlamingii* (Southern goatfish)	0	0	0	0	0	0	0	2	0	0	1	0	0	0
Octopodidae	*Macroctopus maorum* (Maori octopus)	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Odacidae	*Heteroscarus acroptilus* (Rainbow cale)	0	0	0	0	0	0	0	3	0	0	0	0	0	0
	Neoodax balteatus (Little rock whiting)	0	11	14	1	16	1	0	4	0	0	2	0	0	0
	Olisthops cyanomelas (Herring cale)	1	14	3	0	1	7	1	3	4	4	1	1	0	1
	Siphonognathus beddomei (Pencil weed whiting)	0	24	21	11	21	22	2	0	2	1	0	0	5	4
Ostraciidae	*Aracana aurita* (Shaws cowfish)	0	3	1	0	0	0	0	4	0	1	0	1	3	0
Pempheridae	*Pempheris multiradiata* (Common bullseye)	0	14	58	3	189	0	55	92	0	0	0	0	0	0
Pentacerotidae	*Pentaceropsis recurvirostris* (Long-snouted boarfish)	0	1	0	0	0	0	1	0	1	0	0	0	0	0
Plesiopidae	*Trachinops caudimaculatus* (Hulafish)	0	33	249	77	25	3	3	66	764	34	65	0	50	89
Pomacentridae	*Parma microlepis* (White-ear)	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Rajidae	*Dentiraja lemprieri* (Thornback skate)	0	0	1	0	0	0	0	0	0	0	0	0	0	0
	Spiniraja whitleyi (Melbourne skate)	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Scyliorhinidae	*Cephaloscyllium laticeps* (Draughtboard shark)	2	0	0	0	0	0	0	0	0	0	2	0	1	0
Tetraodontidae	*Tetractenos glaber* (Smooth toadfish)	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trachichthyidae	*Paratrachichthys trailli* (Sandpaperfish)	0	0	0	0	4	0	0	0	0	0	0	0	0	0
Tripterygiidae	*Forsterygion varium* (Many-rayed threefin)	0	0	0	0	1	0	0	0	0	0	0	0	1	0
Urolophidae	*Urolophus cruciatus* (Banded stingaree)	0	0	0	0	0	0	0	2	0	0	0	0	0	0
Total Abundance		**373**	**189**	**450**	**312**	**413**	**155**	**159**	**367**	**925**	**54**	**119**	**60**	**135**	**146**
Species Richness		**7**	**20**	**15**	**21**	**18**	**16**	**16**	**23**	**11**	**11**	**12**	**12**	**16**	**14**

Summary of fish survey results for the eastern Storm Bay sites. Data represent total abundance of fish species for the 2000 m^2 survey area at each site (summed across blocks and transects within a site).

		Site															
Family	**Species**	**SBIR25**	**SBIR24**	**SBIR26**	**SBIR16**	**SBIR17**	**SBIR18N**	**SBIR18S**	**SBIR19**	**RR**	**SBIR20**	**APEX**	**LPN**	**SBIR21**	**SBIR22**	**SBIR23**	**SBIR15**
Aplodactylidae	*Aplodactylus arctidens* (Marblefish)	0	2	0	0	2	1	1	1	2	5	0	0	1	6	0	1
Apogonidae	*Vincentia conspersa* (Southern cardinalfish)	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Carangidae	*Trachurus declivis* (Jack mackerel)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
Cheilodactylidae	*Chirodactylus spectabilis* (Banded morwong)	1	6	11	0	0	5	4	4	6	3	0	4	5	24	2	10
Dasyatidae	*Bathytoshia brevicaudata* (Smooth stingray)	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Dinolestidae	*Dinolestes lewini* (Long-fin pike)	0	9	361	0	0	2	4	0	1	9	5	0	7	19	4	0
Diodontidae	*Diodon nicthemerus* (Globe fish)	0	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0
Kyphosidae	*Girella elevata* (Rock blackfish)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
	Scorpis aequipinnis (Sea sweep)	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0
	Scorpis lineolata (Silver sweep)	0	0	2	0	0	0	0	49	0	26	0	0	0	153	0	0
Labridae	*Dotalabrus aurantiacus* (Castelnaus wrasse)	1	0	0	0	2	0	0	2	0	0	6	2	1	0	1	0
	Notolabrus fucicola (Purple wrasse)	9	20	13	33	3	4	15	8	48	11	8	37	63	31	0	14
	Notolabrus tetricus (Blue-throat wrasse)	54	70	35	57	43	21	37	39	34	13	244	31	50	56	34	4
	Pictilabrus laticlavius (Senator wrasse)	25	7	11	7	14	5	4	2	2	5	48	1	7	0	8	0
	Pseudolabrus rubicundus (Rosy wrasse)	5	0	0	1	1	2	2	0	0	2	0	0	1	0	0	0
Latridae	*Latridopsis forsteri* (Bastard trumpeter)	0	0	0	0	0	0	0	0	0	2	5	20	0	72	0	1
	Pseudogoniistius nigripes (Magpie perch)	0	4	1	0	1	0	0	0	0	0	0	0	0	1	0	0
Monacanthidae	*Acanthaluteres spilomelanurus* (Bridled leatherjacket)	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
	Acanthaluteres vittiger (Toothbrush leatherjacket)	18	1	1	2	24	0	0	0	2	3	0	1	0	0	0	30
	Meuschenia australis (Brown-striped leatherjacket)	4	0	2	0	1	0	1	3	1	2	1	0	0	3	0	0
	Meuschenia freycineti (Six-spine leatherjacket)	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Moridae	*Pseudophycis bachus* (Red cod)	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Mullidae	*Upeneichthys vlamingii* (Southern goatfish)	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0
Odacidae	*Neoodax balteatus* (Little rock whiting)	5	2	0	0	390	0	0	0	0	2	47	0	7	0	0	1
	Olisthops cyanomelas (Herring cale)	3	1	3	3	0	1	2	0	13	10	2	0	4	10	0	4

		Site															
Family	**Species**	**SBIR25**	**SBIR24**	**SBIR26**	**SBIR16**	**SBIR17**	**SBIR18N**	**SBIR18S**	**SBIR19**	**RR**	**SBIR20**	**APEX**	**LPN**	**SBIR21**	**SBIR22**	**SBIR23**	**SBIR15**
Odacidae	*Siphonognathus beddomei* (Pencil weed whiting)	95	8	1	28	0	0	1	0	0	0	9	1	3	0	0	0
Ostraciidae	*Aracana aurita* (Shaws cowfish)	2	1	1	4	5	1	0	1	0	0	0	0	0	1	2	1
	Aracana ornata (Ornate cowfish)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Pempheridae	*Pempheris multiradiata* (Common bullseye)	4	0	41	0	0	16	0	0	0	20	0	0	0	0	0	0
Pentacerotidae	*Pentaceropsis recurvirostris* (Long-snouted boarfish)	0	0	0	0	0	1	0	0	0	2	0	0	0	1	0	0
Plesiopidae	*Trachinops caudimaculatus* (Hulafish)	104	0	13	0	974	3	17	0	40	1063	1808	0	18	0	0	27
Pomacentridae	*Parma microlepis* (White-ear)	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Scyliorhinidae	*Cephaloscyllium laticeps* (Draughtboard shark)	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0
Serranidae	*Caesioperca rasor* (Barber perch)	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Tripterygiidae	*Trinorfolkia clarkei* (Common threefin)	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
Total Abundance		**330**	**132**	**497**	**139**	**1470**	**62**	**89**	**109**	**151**	**1178**	**2185**	**97**	**167**	**378**	**51**	**195**
Species Richness		**14**	**13**	**15**	**10**	**18**	**12**	**12**	**9**	**11**	**16**	**12**	**8**	**12**	**13**	**6**	**13**

Summary of invertebrate and cryptic fish survey results for the western Storm Bay sites. Data represent total abundance for the 200 m^2 survey area at each site (summed across transects within a site).

		Site													
Taxonomic group	**Species**	**SBIR02**	**SBIR04**	**SBIR05**	**SBIR06**	**SBIR28**	**SBIR07**	**SBIR08**	**SBIR09**	**SBIR10**	**SBIR11**	**SBIR12**	**SBIR13**	**SBIR14**	**ADV**
Arthropod - sea spider	*Pseudopallene ambigua* (Yellow sea spider)	0	0	0	0	0	0	0	0	1	2	0	0	0	0
Cnidarian - anemone	*Phlyctenactis tuberculosa* (Swimming anemone)	1	0	0	0	0	0	0	0	0	1	0	0	0	0
Crustacean - crab	*Nectocarcinus tuberculosus* (Velvet crab)	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Pagurid spp. (Hermit crab)	0	0	1	0	0	0	0	0	0	0	0	0	0	0
	Pagurixus handrecki (Handrecks hermit crab)	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Plagusia chabrus (Red bait crab)	1	24	4	4	0	0	0	5	9	6	3	3	7	5
	Strigopagurus strigimanus (Rasping hermit crab)	11	0	0	5	1	5	1	0	6	2	4	0	5	4
Crustacean - lobster	*Jasus edwardsii* (Southern rock lobster)	1	31	10	29	3	5	7	7	10	0	2	8	5	7
Echinoderm - feather star	*Antedon loveni* (Lovens feather star)	0	1	0	0	0	0	0	0	0	0	0	0	0	0
	Cenolia trichoptera (Feather star)	4	40	566	258	107	127	55	98	373	371	486	3	92	12
	Comanthus tasmaniae (Feather star)	1	0	34	20	18	11	0	1	0	3	1	2	0	0
Echinoderm - sea star	*Asterias amurensis* (Northern Pacific seastar)	7	0	0	0	0	0	0	0	0	0	0	0	0	0
	Coscinasterias muricata (Eleven-arm star)	1	0	0	0	0	0	0	0	0	0	0	0	0	0
	Fromia polypora (Many-spotted seastar)	0	0	0	0	1	0	2	0	1	0	0	0	0	0
	Meridiastra calcar (Eight-armed seastar)	1113	0	0	0	0	0	0	0	0	0	0	0	0	0
	Nectria ocellata (Ocellate seastar)	0	0	0	0	1	1	7	0	0	1	0	0	0	0
	Petricia vernicina (Velvet star)	0	0	0	0	3	1	0	2	1	0	0	0	1	0
	Tosia australis (Southern biscuit star)	4	3	0	0	4	1	0	0	0	1	0	0	0	0
	Tosia magnifica (Magnificent biscuit star)	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Echinoderm - urchin	*Centrostephanus rodgersii* (Long-spine urchin)	0	0	0	0	0	0	0	0	1	0	1	0	0	0
	Goniocidaris impressa (Pencil urchin)	1	2	0	0	0	0	0	0	0	0	0	0	0	0
	Goniocidaris tubaria (Pencil urchin)	0	0	10	2	0	0	0	0	0	0	0	0	0	0
	Heliocidaris erythrogramma (Short-spined urchin)	4	7	38	71	0	0	0	0	28	1	27	0	136	0

		Site													
Taxonomic group	**Species**	**SBIR02**	**SBIR04**	**SBIR05**	**SBIR06**	**SBIR28**	**SBIR07**	**SBIR08**	**SBIR09**	**SBIR10**	**SBIR11**	**SBIR12**	**SBIR13**	**SBIR14**	**ADV**
Echinoderm - urchin	*Holopneustes inflatus* (Inflated egg urchin)	1	0	0	0	0	0	0	0	0	0	0	0	0	4
Echinoderm - sea cucumber	*Australostichopus mollis* (Sea cucumber)	1	0	0	1	0	0	0	0	0	1	1	0	0	0
Mollusc - gastropod	*Agnewia tritoniformis* (Murex shell)	5	0	1	0	0	1	0	0	11	4	13	1	0	0
	Aplysia parvula (Black-lined sea hare)	0	0	0	0	1	0	0	0	0	0	0	0	0	0
	Argobuccinum pustulosum (Swollen triton)	0	0	0	0	0	0	0	0	1	1	0	0	0	0
	Astralium aureum (Star shell)	7	0	0	0	0	0	0	0	7	11	21	0	0	41
	Cabestana spengleri (Triton shell)	5	0	0	0	0	0	0	0	2	0	0	2	0	0
	Cabestana tabulata (Fringed triton)	0	0	0	0	0	0	0	0	0	0	0	0	0	2
	Ceratosoma brevicaudatum (Short tailed nudibranch)	0	0	0	0	0	0	0	0	0	1	0	0	0	0
	Charonia lampas (Red triton shell)	0	0	0	0	0	0	0	0	0	0	0	0	1	0
	Clanculus flagellatus (Top shell)	0	0	0	0	0	9	0	3	0	0	0	0	0	6
	Clanculus undatus (Wavy top shell)	0	0	0	8	31	1	0	0	0	0	0	0	2	13
	Dicathais orbita (Dog whelk)	2	0	0	0	0	1	0	0	3	0	0	1	1	0
	Haliotis rubra (Blacklip abalone)	22	17	5	8	0	1	5	5	30	27	9	3	57	11
	Maoricolpus roseus (New Zealand screw shell)	1	0	0	0	0	0	0	0	1	1	0	0	0	0
	Mitra glabra (Black mitre)	0	0	0	0	0	0	0	0	4	0	0	0	0	0
	Notocypraea comptoni (Brown cowrie)	0	0	0	0	1	0	0	0	0	0	0	0	0	0
	Nudibranchia spp. (Nudibranch)	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Phasianotrochus eximius (Giant kelp shell)	0	0	0	0	0	0	0	0	0	0	0	0	0	2
	Pleurobranchaea maculata (Grey side-gilled slug)	3	0	0	0	0	0	0	0	0	0	0	0	0	0
	Pleuroploca australasia (Tulip shell)	0	3	1	0	1	0	0	0	0	0	0	0	0	0
	Ranella australasia (Australian rock whelk)	0	0	0	0	0	0	1	0	0	1	0	2	0	0
	Ranellid spp. (Triton shell)	0	0	1	1	5	3	1	0	0	0	0	0	2	0
	Turbo undulatus (Turban shell)	45	112	1	0	2	0	0	2	1	0	0	4	0	10
Mollusc - bivalve	*Mimachlamys asperrima* (Doughboy scallop)	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Cryptic fish	*Bovichtus angustifrons* (Dragonet)	0	0	0	0	0	0	0	0	0	0	0	2	0	0

		Site													
Taxonomic group	**Species**	**SBIR02**	**SBIR04**	**SBIR05**	**SBIR06**	**SBIR28**	**SBIR07**	**SBIR08**	**SBIR09**	**SBIR10**	**SBIR11**	**SBIR12**	**SBIR13**	**SBIR14**	**ADV**
Cryptic fish	*Cephaloscyllium laticeps* (Draughtboard shark)	0	0	1	0	0	0	0	0	0	0	0	0	1	0
	Diodon nicthemerus (Globe fish)	0	2	1	1	0	0	1	0	0	0	0	0	0	0
	Eocallionymus papilio (Painted stinkfish)	0	3	0	0	0	0	0	0	0	0	0	0	0	0
	Forsterygion varium (Many-rayed threefin)	10	7	1	1	0	1	1	2	7	4	7	0	0	2
	Heteroclinus johnstoni (Johnstons weedfish)	0	2	1	0	0	0	0	0	0	0	1	0	0	0
	Heteroclinus perspicillatus (Common weedfish)	0	0	0	0	0	1	0	0	0	0	0	0	0	0
	Heteroclinus spp. (Weedfish)	0	0	0	0	0	0	0	0	0	1	0	0	0	0
	Pempheris multiradiata (Common bullseye)	0	58	4	4	80	0	0	85	0	0	0	17	1	0
	Phyllopteryx taeniolatus (Weedy seadragon)	0	0	0	0	1	0	0	0	0	0	0	0	0	0
	Pseudophycis bachus (Red cod)	0	0	0	0	0	0	0	0	1	0	0	0	0	0
	Pseudophycis barbata (Bearded cod)	0	0	0	0	0	0	0	1	0	0	0	0	1	1
	Scorpaena papillosa (Southern rock cod)	2	0	5	4	1	3	0	2	0	2	3	0	0	1
	Trinorfolkia clarkei (Common threefin)	0	5	4	2	0	0	0	0	4	0	1	0	1	0
	Urolophus cruciatus (Banded stingaree)	0	0	0	0	0	0	0	1	0	0	0	0	0	0
	Vincentia conspersa (Southern cardinalfish)	0	0	0	0	0	0	0	14	0	0	0	0	0	1
Invertebrate total abundance		**1241**	**240**	**672**	**407**	**179**	**167**	**80**	**124**	**490**	**435**	**568**	**29**	**309**	**117**
Cryptic fish total abundance		**12**	**77**	**17**	**12**	**82**	**5**	**2**	**105**	**12**	**7**	**12**	**19**	**4**	**5**
Invertebrate species richness		**22**	**10**	**12**	**11**	**14**	**13**	**9**	**9**	**18**	**17**	**11**	**10**	**11**	**12**
Cryptic fish species richness		**2**	**6**	**7**	**5**	**3**	**3**	**2**	**6**	**3**	**3**	**4**	**2**	**4**	**4**

Summary of invertebrate and cryptic fish survey results for the eastern Storm Bay sites. Data represent total abundance for the 200 m^2 survey area at each site (summed across transects within a site).

		Site															
Taxonomic group	**Species**	**SBIR25**	**SBIR24**	**SBIR26**	**SBIR16**	**SBIR17**	**SBIR18N**	**SBIR18S**	**SBIR19**	**RR**	**SBIR20**	**APEX**	**LPN**	**SBIR21**	**SBIR22**	**SBIR23**	**SBIR15**
Cnidarian - anemone	*Phlyctenactis tuberculosa* (Swimming anemone)	0	0	0	0	0	0	0	2	0	0	0	0	1	1	4	1
Crustacean - crab	*Metacarcinus novaezelandiae* (Piecrust crab)	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
	Plagusia chabrus (Red bait crab)	5	3	9	6	3	7	5	13	6	24	2	11	11	20	3	9
	Strigopagurus strigimanus (Rasping hermit crab)	1	2	0	4	4	0	0	0	0	0	0	9	0	0	0	6
Crustacean - lobster	*Jasus edwardsii* (Southern rock lobster)	17	3	16	1	87	13	4	18	0	17	3	2	7	2	2	6
Echinoderm - feather star	*Cenolia trichoptera* (Feather star)	467	153	13	23	5	38	121	5	30	296	529	16	1020	5	14	136
	Comanthus tasmaniae (Feather star)	289	2	0	1	0	0	0	0	1	81	0	0	298	0	0	1
Echinoderm - sea star	*Coscinasterias muricata* (Eleven-arm star)	0	0	0	8	0	0	0	0	1	1	0	0	0	0	0	1
	Fromia polypora (Many-spotted seastar)	0	1	0	0	0	0	0	0	0	3	0	0	1	0	0	0
	Meridiastra calcar (Eight-armed seastar)	0	3	0	141	0	0	0	2	293	0	0	795	0	0	256	1
	Nectria ocellata (Ocellate seastar)	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Pentagonaster dubeni (Fire-brick star)	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
	Petricia vernicina (Velvet star)	6	1	0	0	0	0	0	0	0	3	1	0	3	0	0	0
	Tosia australis (Southern biscuit star)	0	0	0	5	34	12	1	0	6	3	5	15	0	0	0	0
	Tosia magnifica (Magnificent biscuit star)	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0
Echinoderm - sea urchin	*Goniocidaris impressa* (Pencil urchin)	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0

		Site															
Taxonomic group	**Species**	**SBIR25**	**SBIR24**	**SBIR26**	**SBIR16**	**SBIR17**	**SBIR18N**	**SBIR18S**	**SBIR19**	**RR**	**SBIR20**	**APEX**	**LPN**	**SBIR21**	**SBIR22**	**SBIR23**	**SBIR15**
Echinoderm sea urchin	*Goniocidaris tubaria* (Pencil urchin)	1	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
	Heliocidaris erythrogramma (Short-spined urchin)	206	38	9	1	96	19	15	0	1	5	332	0	308	0	1	0
	Holopneustes inflatus (Inflated egg urchin)	1	0	0	0	0	0	1	0	0	0	2	0	0	0	3	0
Echinoderm - sea cucumber	*Australostichopus mollis* (Sea cucumber)	0	0	1	0	0	0	1	0	0	0	0	0	8	0	0	4
Mollusc - gastropod	*Agnewia tritoniformis* (Murex shell)	0	0	0	8	0	0	0	0	15	0	0	0	1	0	0	13
	Aplysia parvula (Black-lined sea hare)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
	Argobuccinum pustulosum (Swollen triton)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
	Astralium aureum (Star shell)	0	76	0	1	48	0	0	0	1	0	0	0	0	0	0	0
	Cabestana spengleri (Triton shell)	0	0	0	1	0	0	0	2	3	0	0	0	1	5	0	13
	Cabestana tabulata (Fringed triton)	1	0	4	0	0	0	0	0	0	0	0	0	0	0	0	1
	Ceratosoma brevicaudatum (Short tailed nudibranch)	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
	Charonia lampas (Red triton shell)	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Clanculus undatus (Wavy top shell)	1	0	0	0	0	0	2	0	0	0	33	0	1	0	4	0
	Dicathais orbita (Dog whelk)	1	1	4	1	1	0	0	1	3	1	0	4	1	31	0	0
Mollusc - gastropod	*Haliotis rubra* (Blacklip abalone)	25	30	18	24	28	28	5	3	26	12	15	0	12	107	9	6
	Lepsiella vinosa (Oyster drill)	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
	Maoricolpus roseus (New Zealand screw shell)	0	0	0	2	0	0	0	0	0	0	4	0	0	0	0	3
	Patelloida insignis (Maltese-cross limpet)	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
	Patelloida victoriana (Victorian limpet)	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0

		Site															
Taxonomic group	**Species**	**SBIR25**	**SBIR24**	**SBIR26**	**SBIR16**	**SBIR17**	**SBIR18N**	**SBIR18S**	**SBIR19**	**RR**	**SBIR20**	**APEX**	**LPN**	**SBIR21**	**SBIR22**	**SBIR23**	**SBIR15**
Mollusc - gastropod	*Penion maximus* (Giant whelk)	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Phasianotrochus eximius (Giant kelp shell)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Pleurobranchaea maculata (Grey side-gilled slug)	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
	Pleuroploca australasia (Tulip shell)	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
	Ranella australasia (Australian rock whelk)	2	1	0	0	0	9	2	0	0	2	0	0	3	1	0	0
	Ranellid spp. (Triton shell)	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Sassia verrucosa (Verrucose triton)	0	0	3	0	0	1	1	16	0	0	4	0	1	1	3	0
	Scutus antipodes (Elephant snail)	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
	Turbo undulatus (Turban shell)	0	0	3	0	24	0	0	0	0	0	0	0	0	0	2	0
Mollusc - cephalopod	*Macroctopus maorum* (Maori octopus)	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Cryptic fish	*Aetapcus maculatus* (Warty prowfish)	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
	Bovichtus angustifrons (Dragonet)	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	1
	Cephaloscyllium laticeps (Draughtboard shark)	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
	Chironemus maculosus (Silver spot)	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
	Diodon nicthemerus (Globe fish)	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
	Forsterygion varium (Many-rayed threefin)	0	0	1	5	1	3	2	5	0	32	11	3	4	3	3	0
	Genypterus tigerinus (Rock ling)	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
	Heteroclinus johnstoni (Johnstons weedfish)	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0
	Pempheris multiradiata (Common bullseye)	0	0	9	0	24	9	1	14	0	24	0	0	0	0	0	0
	Pseudophycis bachus (Red cod)	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0
	Pseudophycis barbata (Bearded cod)	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0

		Site															
Taxonomic group	**Species**	**SBIR25**	**SBIR24**	**SBIR26**	**SBIR16**	**SBIR17**	**SBIR18N**	**SBIR18S**	**SBIR19**	**RR**	**SBIR20**	**APEX**	**LPN**	**SBIR21**	**SBIR22**	**SBIR23**	**SBIR15**
Cryptic fish	*Scorpaena papillosa* (Southern rock cod)	2	0	0	4	10	0	0	1	0	2	2	1	1	0	0	2
	Trinorfolkia clarkei (Common threefin)	2	0	0	3	2	0	0	2	0	0	0	8	1	0	0	9
	Vincentia conspersa (Southern cardinalfish)	0	0	0	0	21	0	0	0	0	0	0	0	0	0	0	1
Invertebrate total abundance		**1028**	**320**	**81**	**227**	**335**	**129**	**159**	**62**	**386**	**452**	**931**	**853**	**1679**	**176**	**302**	**205**
Cryptic fish total abundance		**5**	**0**	**11**	**12**	**68**	**13**	**4**	**22**	**0**	**59**	**13**	**12**	**7**	**3**	**3**	**13**
Invertebrate species richness		**18**	**17**	**11**	**15**	**14**	**10**	**12**	**9**	**12**	**14**	**12**	**8**	**17**	**10**	**12**	**17**
Cryptic fish species richness		**3**	**0**	**3**	**3**	**10**	**3**	**3**	**4**	**0**	**4**	**2**	**3**	**4**	**1**	**1**	**4**

Macroalgal survey results for the western Storm Bay sites. Data represent mean % cover across 20 replicate 0.25 m^2 quadrats per site. The column FG% represents the total % cover for each functional group. For each site, the species richness across all quadrats has been summed to produce a total species richness for each algal functional group and for all algal functional groups combined. Sites are ordered in a north-south direction. Note: only taxa which represent unique species have been included in species richness counts.

		Site																											
Taxonomic group	**Species**	**SBIR02**	**FG%**	**SBIR04**	**FG%**	**SBIR05**	**FG%**	**SBIR06**	**FG%**	**SBIR28**	**FG%**	**SBIR07**	**FG%**	**SBIR08**	**FG%**	**SBIR09**	**FG%**	**SBIR10**	**FG%**	**SBIR11**	**FG%**	**SBIR12**	**FG%**	**SBIR13**	**FG%**	**SBIR14**	**FG%**	**ADV**	**FG%**
Canopy-forming algae	*Caulocystis cephalornithos*	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.8		0.0		0.0		0.0		0.0		0.0		0.0	
	Cystophora moniliformis	0.0		1.6		1.6		0.0		1.8		1.5		0.0		2.5		0.8		0.0		0.0		0.0		0.0		0.0	
	Cystophora platylobium	0.0		6.5		0.0		1.4		0.0		0.0		0.0		6.1		0.0		0.0		0.0		0.0		0.0		0.0	
	Cystophora retroflexa	0.0		0.0		0.0		0.0		0.2		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Durvillaea potatorum	0.0		0.0		0.0		0.0		0.0		0.0		3.0		1.0		0.0		9.4		0.0		19.8		0.0		0.0	
	Ecklonia radiata	11.3		48.8		56.2		43.0		28.2		9.3		9.2		3.6		14.1		5.5		19.7		16.2		12.1		10.0	
	Lessonia corrugata	17.7	41.6	16.8	78.1	0.0	70.0	21.7	70.3	0.6	36.0	0.0	88.1	1.5	81.9	0.0	82.6	0.0	84.8	0.0	80.8	0.0	93.5	4.5	72.9	0.0	93.2	0.0	99.2
	Macrocystis pyrifera	4.4		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Phyllospora comosa	0.0		0.0		0.0		0.0		0.0		69.5		66.3		68.2		69.5		65.7		73.8		30.4		78.9		83.4	
	Sargassum fallax	0.0		0.0		1.7		0.0		0.4		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Sargassum spp.	0.0		1.7		3.2		0.4		1.7		3.0		0.0		0.0		0.0		0.0		0.0		0.5		0.8		5.2	
	Sargassum verruculosum	0.0		0.0		3.3		0.5		0.4		0.7		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Sargassum vestitum	8.2		2.7		4.0		3.3		2.7		4.1		1.9		0.4		0.4		0.2		0.0		1.5		1.4		0.6	
Encrusting algae	Brown algae (encrusting)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.5		0.5		0.0		0.0		0.0		0.0	
	Crustose coralline algae	14.8	21.0	41.6	61.9	15.2	54.6	22.1	37.1	14.5	28.6	16.2	25.2	43.6	52.5	32.8	48.6	40.4	53.3	44.1	55.0	42.8	55.9	22.4	34.4	35.6	44.6	23.9	31.9
	Peyssonnelia spp. (encrusting)	6.2		20.3		39.4		15.0		14.1		9.0		8.9		15.8		12.4		10.4		13.1		12.0		9.0		8.0	
Encrusting invertebrate	*Galeolaria caespitosa*	0.0		0.0		0.4		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Mytilidae	47.1	55.5	2.7	11.5	0.0	19.5	0.0	29.9	0.0	10.1	0.3	22.1	0.0	5.9	0.0	9.9	0.0	15.9	0.0	10.2	0.0	10.6	0.0	6.0	0.0	11.1	0.0	11.3
	Porifera (encrusting)	5.9		8.8		19.1		29.9		10.1		21.8		5.9		9.9		13.8		10.2		10.6		6.0		11.1		11.3	
	Sessilia	2.5		0.0		0.0		0.0		0.0		0.0		0.0		0.0		2.1		0.0		0.0		0.0		0.0		0.0	
Epiphytic algae	Filamentous brown algae	0.0		0.0		5.4		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Filamentous red algae	1.4	1.4	4.6	4.6	12.9	19.6	10.5	10.5	14.9	14.9	5.0	5.0	0.0	0.0	0.6	2.7	0.5	0.5	0.0	0.0	0.5	0.5	0.4	0.4	5.6	5.6	3.0	3.0
	Hypnea ramentacea	0.0		0.0		1.3		0.0		0.0		0.0		0.0		2.1		0.0		0.0		0.0		0.0		0.0		0.0	
Sessile invertebrate	*Amathia wilsoni*	0.0	2.6	0.1	1.2	1.8	9.9	0.3	19.6	0.5	5.4	3.2	11.4	1.0	6.9	0.2	10.5	0.0	8.1	0.0	3.9	0.0	5.6	0.4	6.3	0.8	18.5	2.6	12.8
	Ascidiacea	0.1		0.0		0.0		1.4		0.0		0.0		0.1		3.3		0.0		0.0		0.1		1.2		3.9		2.0	

		Site																											
Taxonomic group	**Species**	**SBIR02**	**FG%**	**SBIR04**	**FG%**	**SBIR05**	**FG%**	**SBIR06**	**FG%**	**SBIR28**	**FG%**	**SBIR07**	**FG%**	**SBIR08**	**FG%**	**SBIR09**	**FG%**	**SBIR10**	**FG%**	**SBIR11**	**FG%**	**SBIR12**	**FG%**	**SBIR13**	**FG%**	**SBIR14**	**FG%**	**ADV**	**FG%**
Sessile invertebrate	Ascidiacea (encrusting)	0.0	2.6	0.0	1.2	0.0	9.9	0.0	19.6	0.0	5.4	0.0	11.4	0.0	6.9	0.0	10.5	0.0	8.1	0.0	3.9	0.4	5.6	0.0	6.3	0.0	18.5	0.0	12.8
	Bivalvia	0.4		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Bryozoa	0.0		0.0		3.9		4.6		1.8		2.8		4.2		4.9		4.0		2.9		3.0		1.9		4.6		6.7	
	Bryozoa (encrusting)	0.0		0.0		0.0		0.0		0.0		1.5		1.2		0.2		0.9		0.2		0.7		0.0		0.0		0.0	
	Clavelina spp.	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.2		0.0		0.0		0.0		0.0		0.0	
	Corynactis australis	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.2		0.0		0.2		1.8		1.9		0.0	
	Gymnangium superbum	0.0		0.4		0.0		5.0		0.8		0.3		0.0		0.1		0.0		0.0		0.0		0.3		0.0		0.2	
	Hydroida	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.3		0.0		0.0		0.0		0.0		0.0	
	Phlyctenanthus australis	1.1		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.2		0.0	
	Porifera	0.3		0.0		3.8		8.3		2.3		3.6		0.3		1.5		1.4		0.6		0.9		0.6		7.0		1.3	
	Pyura australis	0.7		0.4		0.4		0.0		0.0		0.0		0.1		0.3		1.1		0.2		0.3		0.1		0.1		0.0	
	Tethya spp.	0.0		0.3		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
Substrate	Bare rock	1.1	24.1	0.0	13.4	0.0	13.8	0.0	10.9	0.0	29.4	0.0	25.7	3.0	4.1	1.8	11.2	1.1	14.2	4.5	22.7	4.6	14.0	4.5	14.1	0.2	27.3	0.0	35.2
	Cobble	0.0		0.6		0.0		0.0		6.6		2.6		0.4		0.0		0.0		5.0		0.3		1.8		0.6		0.0	
	Gravel	2.9		0.0		0.0		0.0		0.0		0.0		0.0		0.0		3.1		0.0		0.0		0.0		0.0		0.0	
	Pebbles	0.0		0.0		0.0		0.0		0.0		0.0		0.7		0.0		0.0		3.0		1.9		0.0		0.0		0.0	
	Sand	0.0		8.4		6.5		4.0		15.8		7.8		0.0		4.3		1.7		0.0		6.7		0.0		3.2		0.5	
	Shell	4.4		1.2		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.5		0.0		0.0		0.0	
	Turf/sand/sediment matrix	15.7		3.2		7.3		6.9		7.0		15.3		0.0		5.1		8.3		10.2		0.0		7.8		23.3		34.7	
Turf algae	Turf algae	0.0	30.4	0.0	4.4	0.0	16.2	0.0	17.3	0.0	11.1	0.0	17.0	25.9	26.9	11.3	17.2	0.0	1.0	0.0	1.4	3.5	4.7	0.0	31.6	0.0	4.4	0.0	13.5
	Turf algae (brown)	21.6		0.6		2.0		2.0		1.6		1.4		0.0		0.0		1.0		0.0		0.0		3.0		0.0		0.0	
	Turf algae (green)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.2		0.0		0.0	
	Turf algae (red)	8.8		3.8		14.2		15.3		9.5		15.6		1.0		5.9		0.0		1.4		1.2		28.4		4.4		13.5	
Understorey brown algae	*Acrocarpia paniculata*	0.1	13.9	8.3	35.2	13.3	35.0	11.5	28.4	17.6	47.3	0.4	12.2	1.1	8.7	2.4	21.2	0.0	6.1	0.0	0.4	0.0	6.6	1.6	13.9	0.0	4.4	0.0	2.0
	Carpoglossum confluens	13.7		12.9		9.9		14.0		8.5		3.6		1.4		6.8		2.4		0.2		3.5		0.0		0.0		0.0	
	Carpomitra costata	0.0		0.5		0.0		0.2		0.0		0.8		0.0		0.2		0.0		0.0		0.0		0.4		2.3		0.2	
	Cladostephus spongiosus	0.0		0.0		0.0		0.0		0.0		0.0		0.1		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Dictyopteris muelleri	0.1		0.5		0.2		0.3		0.0		0.0		0.4		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Dictyota dichotoma	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.1		0.0		0.0		0.0	
	Halopteris paniculata	0.0		7.5		1.2		1.8		7.9		3.3		0.6		3.6		0.1		0.0		0.1		2.4		0.0		0.4	

		Site																											
Taxonomic group	**Species**	**SBIR02**	**FG%**	**SBIR04**	**FG%**	**SBIR05**	**FG%**	**SBIR06**	**FG%**	**SBIR28**	**FG%**	**SBIR07**	**FG%**	**SBIR08**	**FG%**	**SBIR09**	**FG%**	**SBIR10**	**FG%**	**SBIR11**	**FG%**	**SBIR12**	**FG%**	**SBIR13**	**FG%**	**SBIR14**	**FG%**	**ADV**	**FG%**
Understorey brown algae	*Lobophora variegata*	0.0	13.9	0.5	35.2	0.5	35.0	0.2	28.4	0.0	47.3	0.5	12.2	0.0	8.7	1.6	21.2	0.0	6.1	0.0	0.4	0.0	6.6	0.0	13.9	0.3	4.4	0.0	2.0
	Perithalia caudata	0.0		4.1		1.7		0.0		3.8		0.0		1.9		3.0		0.0		0.0		1.2		3.2		0.0		0.0	
	Xiphophora gladiata	0.0		0.5		0.0		0.0		1.8		0.0		0.6		1.4		0.0		0.0		0.0		1.1		0.0		0.0	
	Zonaria spp.	0.0		0.4		8.2		0.4		7.7		3.6		2.6		2.2		3.6		0.2		1.7		5.2		1.8		1.4	
Understorey green algae	*Bryopsis gemellipara*	0.1	1.7	0.0	4.3	0.0	0.1	0.0	0.8	0.0	6.5	0.0	0.3	0.0	0.3	0.0	0.7	0.0	1.5	0.0	1.1	0.0	1.9	0.0	0.0	0.0	0.6	0.0	0.4
	Caulerpa hodgkinsoniae	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.1		0.0	
	Caulerpa longifolia	0.0		0.4		0.0		0.0		0.5		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Caulerpa scalpelliformis	0.0		0.0		0.0		0.0		1.5		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Caulerpa spp. (rhizomes)	0.0		0.4		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Caulerpa trifaria	0.0		0.0		0.0		0.0		2.1		0.1		0.0		0.6		0.0		0.0		0.0		0.0		0.0		0.0	
	Chaetomorpha coliformis	0.0		1.4		0.0		0.0		0.0		0.0		0.0		0.0		0.3		0.0		0.0		0.0		0.0		0.1	
	Chaetomorpha spp.	0.0		0.0		0.0		0.0		0.3		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Cladophora spp.	1.3		0.0		0.0		0.0		0.0		0.0		0.1		0.0		1.1		1.1		1.9		0.0		0.0		0.0	
	Codium fragile	0.0		0.2		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.3		0.0	
	Codium harveyi	0.0		0.0		0.0		0.0		0.0		0.0		0.2		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Codium pomoides	0.0		0.0		0.0		0.0		0.0		0.1		0.0		0.0		0.0		0.0		0.0		0.0		0.2		0.0	
	Codium spp.	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.1		0.0		0.0		0.0		0.0		0.0	
	Ulva spp.	0.3		1.9		0.1		0.8		2.1		0.1		0.0		0.1		0.0		0.0		0.0		0.0		0.0		0.3	
Understorey red algae	*Acrosorium ciliolatum*	0.0	15.3	0.0	51.2	0.0	21.9	0.0	45.9	0.0	45.1	0.0	34.9	0.0	23.4	0.4	19.9	0.0	9.9	0.0	14.7	0.0	14.8	0.0	42.8	0.0	11.3	0.0	30.3
	Areschougia spp.	0.0		0.1		0.3		0.0		0.0		0.5		0.0		0.3		0.0		0.0		0.0		0.0		0.0		0.0	
	Arthrocardia wardii	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.3	
	Ballia callitricha	0.0		7.1		1.2		4.3		2.5		3.7		4.1		1.8		3.5		2.8		2.3		1.7		1.1		4.6	
	Callophyllis lambertii	0.0		1.5		0.2		0.1		0.5		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.2	
	Callophyllis rangiferina	1.1		4.2		6.1		3.5		5.0		0.2		0.0		0.5		0.0		0.0		0.0		0.0		0.0		1.2	
	Camontagnea oxyclada	0.0		1.9		0.0		0.2		0.0		1.3		0.3		1.1		0.2		1.3		1.3		0.7		0.0		0.0	
	Champia spp.	0.0		0.0		0.3		0.3		1.0		0.6		0.0		0.2		0.0		0.0		0.0		0.0		0.0		0.0	
	Cheilosporum sagittatum	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.2		0.1		0.1	
	Corallina officinalis	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.1		1.0		2.4		4.4	
	Delisea plumosa	0.0		0.0		1.2		0.7		0.4		0.3		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Delisea pulchra	0.0		0.1		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.3		0.1	

		Site																									
Taxonomic group	**Species**	**SBIR02**	**FG%**	**SBIR04**	**FG%**	**SBIR05**	**FG%**	**SBIR06**	**FG%**	**SBIR28**	**FG%**	**SBIR07**	**FG%**	**SBIR08**	**FG%**	**SBIR09**	**FG%**	**SBIR10**	**FG%**	**SBIR11**	**FG%**	**SBIR12**	**FG%**	**SBIR13**	**FG%**	**SBIR14**	**FG%**	**ADV**	**FG%**
Understorey red algae	*Dictyomenia harveyana*	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.1		0.0		0.0		0.0		0.0		0.0		0.0	
	Echinothamnion hystrix	0.4		0.6		0.0		1.8		6.6		1.2		0.0		1.7		0.0		0.0		0.0		0.0		0.0		0.0	
	Erythrymenia minuta	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.3		0.0		0.0		0.0		0.2		0.0		0.2	
	Euptilota articulata	0.0		0.4		0.0		0.9		0.2		3.9		0.2		0.0		0.0		0.0		0.6		0.0		0.0		0.1	
	Foliose red algae	0.9		0.0		1.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.2		0.9		0.5		0.0	
	Gelidium australe	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.2		0.0		0.0	
	Gelidium spp.	0.0		0.0		0.0		0.0		0.0		0.3		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Haliptilon roseum	0.0		3.7		0.0		0.0		0.0		0.0		1.2		0.1		0.1		0.3		0.0		7.5		1.8		11.6	
	Hemineura frondosa	0.0		0.5		0.5		0.7		0.7		0.5		0.1		0.1		0.0		0.0		0.0		0.1		0.0		2.7	
	Hymenena spp.	0.0		0.0		0.0		0.0		0.0		0.0		0.1		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Laurencia elata	0.0		0.0		0.0		0.5		0.4		0.0		0.0		0.3		0.0		0.0		0.0		0.0		0.0		0.0	
	Laurencia spp.	0.0		0.0		0.8		0.4		0.5		0.1		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Lenormandia marginata	0.3		1.4		1.2		3.7		2.6		7.8		1.9		1.2		0.0		0.0		0.1		0.4		0.7		2.2	
	Melanthalia obtusata	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.3		0.4		0.0		0.0		0.0	
	Mychodea acanthymenia	0.0	15.3	0.6	51.2	0.0	21.9	0.0	45.9	0.0	45.1	0.2	34.9	0.0	23.4	0.1	19.9	0.0	9.9	0.0	14.7	0.0	14.8	0.0	42.8	0.0	11.3	0.0	30.3
	Mychodea aciculare	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.5		0.0		0.6		0.0		0.0		0.0		0.0	
	Nitospinosa tasmanica	1.3		0.0		0.4		2.8		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.2	
	Nizymenia conferta	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.1		0.0		0.0		0.0		0.0	
	Peyssonnelia novaehollandiae	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.5		0.0		0.0		0.4		0.0		0.6		0.0	
	Phacelocarpus apodus	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		5.2		0.0		0.0	
	Phacelocarpus peperocarpos	0.0		0.7		1.1		3.8		0.8		2.9		3.2		1.6		0.2		3.0		0.5		2.8		0.2		0.0	
	Plocamium angustum	0.2		7.8		5.2		4.8		6.6		2.5		5.2		2.0		0.0		1.0		1.9		9.9		0.2		0.6	
	Plocamium dilatatum	0.0		0.8		0.0		1.0		0.6		0.6		0.0		1.8		0.0		0.0		0.2		0.2		1.8		0.0	
	Plocamium mertensii	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.3		0.0		0.0		0.0	
	Plocamium patagiatum	0.0		0.0		0.0		0.0		0.0		0.0		0.4		0.0		0.3		0.0		0.0		0.0		0.0		0.0	
	Pollexfenia lobata	8.2		9.3		1.8		0.8		11.2		0.5		0.0		0.4		0.0		0.0		0.0		0.0		0.0		0.4	
	Polyopes constrictus	0.2		7.9		0.2		5.2		3.1		2.2		1.7		3.3		0.3		1.3		1.3		10.1		0.6		0.3	
	Ptilonia australasica	0.0		0.0		0.0		0.0		0.0		1.1		0.1		0.0		0.0		0.0		0.0		0.9		0.0		0.0	

		Site																													
Taxonomic group	**Species**	**SBIR02**	**FG%**	**SBIR04**	**FG%**	**SBIR05**	**FG%**	**SBIR06**	**FG%**	**SBIR28**	**FG%**	**SBIR07**	**FG%**	**SBIR08**	**FG%**	**SBIR09**	**FG%**	**SBIR10**	**FG%**	**SBIR11**	**FG%**	**SBIR12**	**FG%**	**SBIR13**	**FG%**	**SBIR14**	**FG%**	**ADV**	**FG%**
Understorey red algae	*Rhodymenia sonderi*	0.0		0.0		0.0		0.0		0.0		0.0		1.3		0.6		0.6		2.0		0.4		0.0		0.0		0.0	
	Rhodymenia spp.	0.5		1.8		0.0		4.4		1.8		3.2		2.3		0.5		4.6		0.3		2.3		0.3		1.0		0.7	
	Rhodymenia wilsonis	1.2		0.8		0.0		6.0		0.2		1.3		0.5		0.0		0.0		0.0		0.4		0.5		0.0		0.4	
	Sonderopelta/Peyssonnelia	0.0		0.0		0.4		0.0		0.4		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Sonderophycus coriaceus	0.0	15.3	0.0	51.2	0.0	21.9	0.0	45.9	0.0	45.1	0.0	34.9	0.8	23.4	0.2	19.9	0.0	9.9	1.0	14.7	2.1	14.8	0.0	42.8	0.0	11.3	0.0	30.3
	Synarthrophyton patena	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.1		0.7		0.0		0.0		0.0		0.0	
	Thamnoclonium dichotomum	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.3		0.0		0.0		0.0		0.0		0.0		0.0	
	Tsengia feredayae	1.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
Canopy-forming algae species richness		**4**	**-**	**5**	**-**	**5**	**-**	**5**	**-**	**7**	**-**	**5**	**-**	**5**	**-**	**7**	**-**	**4**	**-**	**4**	**-**	**2**	**-**	**5**	**-**	**3**	**-**	**3**	**-**
Understorey brown algae species richness		**3**	**-**	**9**	**-**	**7**	**-**	**7**	**-**	**6**	**-**	**6**	**-**	**8**	**-**	**8**	**-**	**3**	**-**	**2**	**-**	**5**	**-**	**6**	**-**	**3**	**-**	**3**	**-**
Understorey green algae species richness		**2**	**-**	**4**	**-**	**1**	**-**	**1**	**-**	**4**	**-**	**3**	**-**	**1**	**-**	**2**	**-**	**1**	**-**	**0**	**-**	**0**	**-**	**0**	**-**	**3**	**-**	**2**	**-**
Understorey red algae species richness		**9**	**-**	**18**	**-**	**13**	**-**	**17**	**-**	**16**	**-**	**17**	**-**	**15**	**-**	**23**	**-**	**8**	**-**	**12**	**-**	**15**	**-**	**16**	**-**	**11**	**-**	**17**	**-**
Total algae species richness		**18**	**-**	**36**	**-**	**26**	**-**	**30**	**-**	**33**	**-**	**31**	**-**	**29**	**-**	**40**	**-**	**16**	**-**	**18**	**-**	**22**	**-**	**27**	**-**	**20**	**-**	**25**	**-**

Macroalgal survey results for the eastern Storm Bay sites. Data represent mean % cover across 20 replicate 0.25 m^2 quadrats per site. The column FG% represents the total % cover for each functional group. For each site, the species richness across all quadrats has been summed to produce a total species richness for each algal functional group and for all algal functional groups combined. Sites are ordered in a clockwise direction from Betsey Island around to Tasman Peninsula, and then from north to south down the Peninsula. Note: only taxa which represent unique species have been included in species richness counts.

		Site															
Taxonomic group	**Species**	**SBIR25**	**FG%**	**SBIR24**	**FG%**	**SBIR26**	**FG%**	**SBIR16**	**FG%**	**SBIR17**	**FG%**	**SBIR18N**	**FG%**	**SBIR18S**	**FG%**	**SBIR19**	**FG%**
Canopy-forming algae	*Caulocystis cephalornithos*	0.0		0.0		0.0		0.0		0.8		0.0		0.0		0.0	
	Cystophora monilifera	0.2		1.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Cystophora moniliformis	0.0		1.0		3.2		3.6		0.8		0.0		0.0		0.0	
	Cystophora platylobium	0.4		0.0		0.0		1.2		0.0		0.0		12.3		6.3	
	Cystophora retroflexa	0.0		0.0		0.0		0.0		3.0		0.0		0.0		0.0	
	Durvillaea potatorum	0.0		0.0		4.0		0.0		0.0		0.0		0.0		0.0	
	Ecklonia radiata	39.9	44.4	35.1	51.7	24.1	53.7	5.1	61.3	43.6	50.9	9.6	48.1	16.0	46.0	8.0	40.1
	Lessonia corrugata	0.0		11.4		5.8		36.8		0.0		2.0		11.7		20.4	
	Macrocystis pyrifera	0.0		0.2		0.0		0.0		0.0		0.0		0.0		0.0	
	Phyllospora comosa	0.0		0.0		0.4		0.0		0.0		31.1		5.0		4.0	
	Sargassum spp.	1.1		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Sargassum verruculosum	0.0		0.3		0.0		0.0		1.9		0.0		0.0		0.0	
	Sargassum vestitum	2.8		2.7		16.2		14.6		0.8		5.4		1.0		1.4	
Drift algae	Drift algae	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	8.5	8.5	0.0	0.0	0.0	0.0	0.0	0.0
Encrusting algae	Crustose coralline algae	35.7	56.1	38.0	58.5	36.3	39.6	5.6	16.6	16.1	41.0	14.8	17.2	37.7	42.1	34.2	38.8
	Peyssonnelia spp. (encrusting)	20.4		20.5		3.3		11.0		24.9		2.4		4.4		4.6	
Encrusting invertebrate	*Galeolaria caespitosa*	0.0		0.3		0.0		0.0		0.0		0.0		0.0		0.0	
	Mytilidae	0.0	12.0	0.4	9.2	0.0	26.4	18.3	70.2	0.0	18.0	0.0	34.5	0.0	14.3	0.0	12.1
	Mytilus galloprovincialis	0.0		0.0		12.4		38.1		0.0		0.0		0.0		0.0	
	Porifera (encrusting)	12.0		8.5		14.0		13.8		18.0		34.5		14.3		12.1	
Epiphytic algae	Filamentous green algae	0.0		0.0		0.0		0.0		0.1		0.0		0.0		0.0	
	Filamentous red algae	1.8	5.3	0.0	0.0	0.0	0.2	3.1	3.1	0.0	0.1	0.0	0.0	0.0	0.9	0.0	7.9
	Hypnea ramentacea	3.5		0.0		0.2		0.0		0.0		0.0		0.9		7.9	
Sessile invertebrate	*Amathia wilsoni*	0.4		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Anthothoe albocincta	0.3	13.2	0.0	6.1	0.0	1.7	0.1	6.1	0.3	6.1	0.1	14.2	0.0	5.6	0.0	3.7
	Anthozoa	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.1	

		Site															
Taxonomic group	**Species**	**SBIR25**	**FG%**	**SBIR24**	**FG%**	**SBIR26**	**FG%**	**SBIR16**	**FG%**	**SBIR17**	**FG%**	**SBIR18N**	**FG%**	**SBIR18S**	**FG%**	**SBIR19**	**FG%**
Sessile invertebrate	Ascidiacea	2.1		0.0		0.1		0.0		0.5		0.1		0.0		0.0	
	Ascidiacea (encrusting)	0.0		0.0		0.0		0.0		0.0		0.8		0.5		0.0	
	Bivalvia	0.0		0.0		0.0		0.3		0.0		0.0		0.0		0.0	
	Botrylloides spp.	0.0		0.0		0.0		0.0		0.4		0.0		0.0		0.0	
	Bryozoa	4.3		4.5		0.3		3.5		1.8		4.6		2.9		0.4	
	Bryozoa (encrusting)	0.0		0.2		0.0		0.0		0.0		0.6		0.0		0.4	
	Corynactis australis	0.0		0.0		0.1		0.0		0.0		1.3		0.0		0.0	
	Erythropodium hicksoni	0.0		0.0		0.0		0.0		0.0		0.0		0.2		0.0	
	Gymnangium superbum	0.0	13.2	0.0	6.1	0.0	1.7	0.0	6.1	0.4	6.1	0.0	14.2	0.0	5.6	0.0	3.7
	Herdmania grandis	0.4		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Hydroida	0.3		0.0		0.6		0.0		0.0		1.3		0.2		0.9	
	Phlyctenanthus australis	0.0		0.0		0.0		0.0		0.0		0.1		0.0		0.0	
	Porifera	4.9		0.7		0.4		0.4		2.4		2.8		1.5		0.6	
	Pyura australis	0.4		0.4		0.2		1.0		0.3		2.3		0.3		1.3	
	Pyura gibbosa	0.0		0.0		0.0		0.8		0.0		0.0		0.0		0.0	
	Pyura stolonifera	0.0		0.0		0.0		0.0		0.0		0.2		0.0		0.0	
	Serpulidae	0.1		0.3		0.0		0.0		0.0		0.0		0.0		0.0	
Substrate	Bare rock	1.4		1.3		0.6		0.4		0.8		0.4		1.2		1.3	
	Cobble	1.4		0.8		0.0		0.0		0.0		0.0		0.2		0.0	
	Gravel	0.0		2.7		0.0		0.0		0.2		0.0		0.0		0.0	
	Pebbles	0.0	6.9	0.0	8.9	0.0	19.4	0.0	8.4	0.0	27.3	0.0	27.7	0.0	32.5	5.0	9.3
	Sand	1.1		2.5		1.2		0.0		4.0		2.0		1.7		3.0	
	Shell	0.0		0.8		0.8		0.8		0.0		0.4		0.2		0.0	
	Turf/sand/sediment matrix	3.0		0.8		16.8		7.2		22.3		24.9		29.2		0.0	
Turf algae	Turf algae	3.6		5.9		11.0		0.0		4.5		0.0		0.0		16.5	
	Turf algae (brown)	0.0	8.4	0.0	12.7	0.0	13.9	29.9	53.6	0.0	12.9	0.0	1.2	0.0	0.0	0.0	16.5
	Turf algae (green)	0.0		1.0		0.0		1.4		1.6		0.0		0.0		0.0	
	Turf algae (red)	4.8		5.8		2.9		22.3		6.8		1.2		0.0		0.0	
Understorey brown algae	*Acrocarpia paniculata*	12.0		9.0		11.4		0.0		0.1		0.0		2.5		7.7	
	Carpoglossum confluens	21.4	49.4	10.6	32.8	5.7	26.9	5.8	8.8	0.0	9.2	4.0	5.0	8.5	31.7	0.4	12.2
	Carpomitra costata	0.7		0.0		0.0		0.0		0.0		0.0		0.0		0.0	

		Site															
Taxonomic group	**Species**	**SBIR25**	**FG%**	**SBIR24**	**FG%**	**SBIR26**	**FG%**	**SBIR16**	**FG%**	**SBIR17**	**FG%**	**SBIR18N**	**FG%**	**SBIR18S**	**FG%**	**SBIR19**	**FG%**
Understorey brown algae	*Dictyopteris muelleri*	0.7	49.4	0.1	32.8	0.0	26.9	0.6	8.8	0.1	9.2	0.0	5.0	0.0	31.7	0.0	12.2
	Dictyota dichotoma	0.0		0.0		0.0		0.1		0.0		0.0		0.0		0.0	
	Dilophus spp.	0.0		0.0		0.0		0.0		0.1		0.0		0.0		0.0	
	Halopteris paniculata	3.4		0.9		1.0		0.0		0.0		0.0		0.0		1.6	
	Lobophora variegata	0.1		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Perithalia caudata	7.7		4.5		3.9		0.2		0.0		1.0		19.6		1.9	
	Sargassum decipiens	0.0		0.0		0.0		0.0		7.7		0.0		0.0		0.0	
	Xiphophora gladiata	1.9		5.6		3.3		1.8		0.0		0.0		1.1		0.4	
	Zonaria spp.	1.5		2.1		1.6		0.3		1.2		0.0		0.0		0.2	
Understorey green algae	*Apjohnia laetevirens*	0.6	6.0	0.0	6.4	0.0	2.2	0.0	3.2	0.0	4.3	0.0	3.7	0.0	4.6	0.0	7.7
	Bryopsis gemellipara	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.1	
	Caulerpa brownii	0.0		0.1		0.0		0.0		0.0		0.0		0.0		0.0	
	Caulerpa flexilis	0.0		0.0		0.0		0.0		0.0		1.8		3.8		0.0	
	Caulerpa geminata	0.0		0.0		0.0		0.0		0.5		0.0		0.0		0.0	
	Caulerpa longifolia	0.0		0.0		0.1		0.0		0.2		0.0		0.0		0.8	
	Caulerpa simpliciuscula	0.0		0.2		0.0		0.0		0.4		0.0		0.0		0.0	
	Caulerpa spp. (rhizomes)	2.0		1.4		0.0		0.0		0.0		0.0		0.8		0.0	
	Caulerpa trifaria	0.0		0.0		0.0		0.0		0.7		1.6		0.0		5.6	
	Chaetomorpha coliformis	0.2		1.4		0.2		0.0		0.0		0.0		0.0		1.2	
	Cladophora feredayi	0.0		0.0		0.0		0.5		0.0		0.0		0.0		0.0	
	Cladophora spp.	0.0		3.3		1.9		0.8		1.2		0.3		0.0		0.0	
	Codium fragile	2.5		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Ulva spp.	0.7		0.0		0.0		1.9		1.3		0.0		0.0		0.0	
Understorey red algae	*Areschougia* spp.	0.0	24.6	0.1	27.1	0.0	18.8	0.0	15.8	0.2	7.4	0.0	37.9	0.0	38.5	0.0	40.4
	Ballia callitricha	1.5		3.0		2.7		0.0		0.2		1.4		3.3		2.3	
	Callophyllis lambertii	0.0		0.0		0.0		0.4		0.0		0.2		0.0		0.0	
	Callophyllis rangiferina	9.0		0.3		0.0		2.0		0.0		8.8		1.7		0.2	
	Camontagnea oxyclada	0.0		0.3		0.0		0.0		0.0		0.0		1.0		3.8	
	Champia viridis	0.0		0.1		0.0		0.0		0.0		0.0		0.0		0.0	
	Dasythamniella plumigera	0.0		0.0		0.0		0.3		0.0		0.0		0.0		0.0	
	Delisea pulchra	0.0		0.0		0.0		0.0		0.0		5.8		0.4		2.7	

		Site															
Taxonomic group	**Species**	**SBIR25**	**FG%**	**SBIR24**	**FG%**	**SBIR26**	**FG%**	**SBIR16**	**FG%**	**SBIR17**	**FG%**	**SBIR18N**	**FG%**	**SBIR18S**	**FG%**	**SBIR19**	**FG%**
Understorey red algae	*Echinothamnion hystrix*	1.9		1.8		1.5		0.2		0.0		0.0		0.0		0.1	
	Euptilota articulata	0.2		0.1		1.4		2.7		0.0		0.4		0.2		0.3	
	Foliose red algae	0.2		0.0		0.0		0.2		0.3		0.0		0.0		0.0	
	Gelidium australe	0.0		0.0		0.6		0.0		0.0		0.0		0.0		0.1	
	Gelinaria ulvoidea	0.3		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Gigartina spp.	0.0		0.0		0.0		1.0		0.0		0.0		0.0		0.0	
	Gloiocladia spp.	0.0		0.0		0.0		0.4		0.0		0.0		0.0		0.0	
	Haliptilon roseum	0.0		0.0		0.9		0.0		0.0		0.0		0.0		0.0	
	Hemineura frondosa	0.4		3.0		0.3		0.9		0.0		0.0		0.1		0.8	
	Kallymenia spp.	0.0		0.0		0.0		1.2		0.0		0.0		0.0		0.0	
	Laurencia elata	0.0		0.2		0.0		0.0		0.0		0.0		2.1		1.6	
	Laurencia majuscula	0.0		0.0		0.0		0.0		0.0		0.3		1.1		0.0	
	Laurencia spp.	0.0		0.0		0.0		0.0		0.2		0.0		0.0		0.0	
	Lenormandia marginata	0.9		0.9		0.6		0.9		0.0		2.0		0.0		0.0	
	Mychodea acanthymenia	1.3		0.0		0.0		0.0		0.0		0.2		0.0		0.0	
	Mychodea aciculare	0.0	24.6	0.0	27.1	0.0	18.8	0.0	15.8	4.5	7.4	0.0	37.9	0.0	38.5	0.0	40.4
	Nitospinosa tasmanica	0.0		0.0		0.0		1.0		0.0		0.0		0.0		0.0	
	Nizymenia australis	0.0		0.0		0.0		0.0		0.0		0.0		0.2		2.9	
	Nizymenia spp.	0.0		0.3		0.0		0.0		0.0		0.0		0.0		0.0	
	Peyssonnelia novaehollandiae	0.1		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Phacelocarpus apodus	0.0		0.0		0.3		0.0		0.0		0.0		0.0		0.0	
	Phacelocarpus peperocarpos	0.0		0.4		0.0		0.0		0.0		2.2		5.2		5.7	
	Phacelocarpus sessilis	0.0		0.0		0.0		0.0		0.0		0.2		0.0		0.0	
	Plocamium angustum	2.0		4.8		3.4		0.0		0.8		1.8		5.1		2.2	
	Plocamium costatum	1.9		0.0		0.0		0.0		0.0		0.0		0.3		0.3	
	Plocamium dilatatum	2.8		4.8		0.1		0.0		0.0		0.0		0.0		0.0	
	Plocamium mertensii	0.0		0.6		0.0		0.0		0.0		0.8		6.3		2.6	
	Plocamium patagiatum	0.0		0.0		0.0		0.0		0.0		2.2		0.4		0.0	
	Pollexfenia lobata	0.8		3.0		0.0		2.9		0.0		0.0		0.0		0.2	
	Polyopes constrictus	0.8		1.6		5.5		0.0		0.0		2.7		4.8		6.1	
	Pterocladiella capillacea	0.0		0.0		0.0		0.1		0.0		0.0		0.0		0.0	

		Site															
Taxonomic group	**Species**	**SBIR25**	**FG%**	**SBIR24**	**FG%**	**SBIR26**	**FG%**	**SBIR16**	**FG%**	**SBIR17**	**FG%**	**SBIR18N**	**FG%**	**SBIR18S**	**FG%**	**SBIR19**	**FG%**
Understorey red algae	*Ptilonia australasica*	0.0		0.7		0.2		0.0		0.0		0.0		0.6		2.4	
	Rhodymenia sonderi	0.0		0.0		0.3		0.0		0.0		0.0		0.0		0.0	
	Rhodymenia spp.	0.5	24.6	1.1	27.1	1.0	18.8	1.5	15.8	1.1	7.4	4.0	37.9	3.9	38.5	2.1	40.4
	Rhodymenia wilsonis	0.0		0.0		0.0		0.1		0.0		4.9		1.8		4.0	
	Stenogramme interrupta	0.0		0.0		0.0		0.0		0.1		0.0		0.0		0.0	
Canopy-forming algae species richness		**4**	**-**	**7**	**-**	**6**	**-**	**5**	**-**	**6**	**-**	**4**	**-**	**5**	**-**	**5**	**-**
Understorey brown algae species richness		**9**	**-**	**7**	**-**	**6**	**-**	**6**	**-**	**5**	**-**	**2**	**-**	**4**	**-**	**6**	**-**
Understorey green algae species richness		**4**	**-**	**3**	**-**	**2**	**-**	**2**	**-**	**5**	**-**	**2**	**-**	**1**	**-**	**4**	**-**
Understorey red algae species richness		**14**	**-**	**17**	**-**	**13**	**-**	**13**	**-**	**5**	**-**	**15**	**-**	**17**	**-**	**18**	**-**
Total algae species richness		**31**	**-**	**34**	**-**	**27**	**-**	**26**	**-**	**21**	**-**	**23**	**-**	**27**	**-**	**33**	**-**

Macroalgal survey results for the eastern Storm Bay sites. Data represent mean % cover across 20 replicate 0.25 m^2 quadrats per site. The column FG% represents the total % cover for each functional group. For each site, the species richness across all quadrats has been summed to produce a total species richness for each algal functional group and for all algal functional groups combined. Sites are ordered in a clockwise direction from Betsey Island around to Tasman Peninsula, and then from north to south down the Peninsula. only taxa which represent unique species have been included in species richness counts.

		Site															
Taxonomic group	**Species**	**RR**	**FG%**	**SBIR20**	**FG%**	**APEX**	**FG%**	**LPN**	**FG%**	**SBIR21**	**FG%**	**SBIR22**	**FG%**	**SBIR23**	**FG%**	**SBIR15**	**FG%**
Canopy-forming algae	*Cystophora monilifera*	0.0	61.3	0.0	74.1	0.7	50.4	0.0	35.3	0.0	62.4	0.0	67.8	0.0	39.2	0.0	70.4
	Cystophora moniliformis	0.0		0.0		0.0		0.0		0.0		0.0		3.6		0.0	
	Cystophora platylobium	3.0		0.5		0.0		0.0		2.8		10.9		20.1		0.5	
	Cystophora retroflexa	0.0		0.0		1.0		0.0		0.0		0.0		0.0		0.0	
	Durvillaea potatorum	0.0		0.0		0.0		0.0		0.0		0.0		7.4		0.0	
	Ecklonia radiata	21.2		15.0		37.3		22.6		56.7		1.3		0.0		4.7	
	Lessonia corrugata	30.9		1.1		0.0		6.3		0.0		43.5		7.2		2.0	
	Macrocystis pyrifera	0.0		0.0		0.0		3.1		0.0		0.0		0.0		0.0	
	Phyllospora comosa	0.0		54.5		0.0		0.0		0.0		0.0		0.0		59.7	
	Sargassum fallax	0.0		0.0		9.7		0.0		0.0		0.0		0.0		0.0	
	Sargassum verruculosum	0.5		0.0		1.7		0.0		0.0		0.0		0.0		0.0	
	Sargassum vestitum	5.7		3.0		0.0		3.3		2.9		12.1		0.9		3.5	
Encrusting algae	Crustose coralline algae	42.7	47.0	16.7	19.4	22.2	36.3	11.8	28.5	31.8	45.7	40.6	44.9	37.2	47.4	24.5	29.2
	Peyssonnelia spp. (encrusting)	4.3		2.7		14.1		16.7		13.9		4.3		10.2		4.7	
Encrusting invertebrate	Mytilidae	0.2	14.7	0.0	21.9	0.0	8.1	0.1	4.7	0.0	23.9	0.0	14.5	0.0	1.4	0.0	20.4
	Mytilus galloprovincialis	0.4		0.0		0.0		0.0		0.0		0.7		0.0		5.3	
	Porifera (encrusting)	14.1		21.9		8.1		4.5		23.9		13.8		1.4		15.0	
	Sessilia	0.0		0.0		0.0		0.1		0.0		0.0		0.0		0.1	
Epiphytic algae	*Asparagopsis armata*	0.0	0.4	0.0	0.0	0.7	1.3	0.0	1.7	0.0	1.7	0.0	0.0	1.3	22.5	0.0	0.0
	Filamentous brown algae	0.0		0.0		0.0		0.1		0.0		0.0		0.0		0.0	
	Filamentous red algae	0.0		0.0		0.0		1.6		1.7		0.0		0.0		0.0	
	Hypnea ramentacea	0.4		0.0		0.6		0.0		0.0		0.0		21.2		0.0	
Sessile invertebrate	*Amathia wilsoni*	0.0	6.4	0.8	12.5	2.6	18.4	0.0	3.1	4.9	24.0	0.0	21.9	0.0	0.4	0.0	12.2
	Anthothoe albocincta	0.0		0.0		0.0		0.4		0.3		0.0		0.0		0.0	
	Anthozoa	0.5		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Ascidiacea	0.0		0.1		1.2		0.0		0.3		0.6		0.0		0.2	
	Ascidiacea (encrusting)	0.0		0.0		0.0		0.0		0.6		0.0		0.0		0.1	

		Site															
Taxonomic group	**Species**	**RR**	**FG%**	**SBIR20**	**FG%**	**APEX**	**FG%**	**LPN**	**FG%**	**SBIR21**	**FG%**	**SBIR22**	**FG%**	**SBIR23**	**FG%**	**SBIR15**	**FG%**
Sessile invertebrate	Bryozoa	0.0	6.4	4.3	12.5	7.0	18.4	1.1	3.1	9.0	24.0	0.6	21.9	0.3	0.4	0.7	12.2
	Bryozoa (encrusting)	1.7		0.0		1.7		0.0		0.0		0.2		0.0		0.0	
	Capnella spp.	0.0		0.0		0.0		0.0		0.0		0.1		0.0		0.0	
	Clavelina spp.	0.0		0.1		0.0		0.0		0.5		0.0		0.0		0.0	
	Corynactis australis	0.1		2.3		1.0		0.0		0.0		3.7		0.0		1.1	
	Erythropodium hicksoni	0.0		0.0		1.1		0.0		0.3		0.0		0.0		0.0	
	Gymnangium superbum	1.8		0.0		0.0		0.0		0.3		0.0		0.0		0.0	
	Hydroida	0.0		1.0		1.6		0.0		1.2		2.3		0.0		0.9	
	Phlyctenactis tuberculosa	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.3	
	Porifera	0.8		2.5		1.5		0.4		4.9		0.0		0.1		1.8	
	Pyura australis	1.5		1.1		0.7		1.2		1.7		14.4		0.0		7.1	
	Zoanthidea	0.0		0.3		0.0		0.0		0.0		0.0		0.0		0.0	
Substrate	Bare rock	2.1	12.9	0.5	3.7	0.4	4.3	0.0	45.4	0.2	10.9	1.4	1.4	1.5	31.7	1.5	30.6
	Cobble	2.3		0.0		1.8		1.0		0.5		0.0		0.9		0.0	
	Sand	0.0		3.2		2.1		15.0		4.7		0.0		29.3		0.2	
	Shell	0.4		0.0		0.0		0.4		0.0		0.0		0.0		0.0	
	Turf/sand/sediment matrix	8.1		0.0		0.0		29.0		5.5		0.0		0.0		28.9	
Turf algae	Turf algae	0.0	11.6	36.8	36.8	24.7	24.7	0.0	0.0	6.6	11.0	11.2	17.2	9.6	9.6	0.0	0.0
	Turf algae (green)	0.3		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Turf algae (red)	11.3		0.0		0.0		0.0		4.4		6.0		0.0		0.0	
Understorey brown algae	*Acrocarpia paniculata*	0.9	12.2	0.0	4.6	3.7	17.8	0.0	21.2	9.9	30.5	0.5	18.0	6.7	23.6	0.0	1.5
	Carpoglossum confluens	4.3		4.4		9.8		14.1		14.1		0.0		1.0		0.0	
	Carpomitra costata	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.5	
	Dictyopteris muelleri	0.0		0.0		0.0		0.0		0.0		0.0		0.2		0.0	
	Dilophus spp.	0.0		0.0		0.0		0.0		0.0		1.2		0.0		0.3	
	Halopteris paniculata	1.8		0.0		0.0		0.0		0.6		0.3		1.9		0.0	
	Perithalia caudata	3.6		0.0		2.2		0.0		5.1		13.0		0.0		0.0	
	Sargassum decipiens	0.0		0.0		0.3		2.5		0.0		0.0		0.0		0.0	
	Xiphophora gladiata	0.7		0.0		0.0		4.6		0.0		3.0		13.8		0.0	
	Zonaria spp.	0.9		0.2		1.8		0.0		0.8		0.0		0.0		0.7	
Understorey green algae	*Caulerpa brownii*	0.0	6.6	0.0	4.8	0.3	24.6	0.0	12.2	0.0	2.1	0.0	2.6	0.0	12.0	0.0	1.0

		Site															
Taxonomic group	**Species**	**RR**	**FG%**	**SBIR20**	**FG%**	**APEX**	**FG%**	**LPN**	**FG%**	**SBIR21**	**FG%**	**SBIR22**	**FG%**	**SBIR23**	**FG%**	**SBIR15**	**FG%**
Understorey green algae	*Caulerpa flexilis*	0.0	6.6	1.9	4.8	15.3	24.6	0.0	12.2	0.5	2.1	0.0	2.6	2.3	12.0	0.0	1.0
	Caulerpa longifolia	0.0		2.9		0.0		0.0		0.0		0.0		0.0		0.0	
	Caulerpa simpliciuscula	0.0		0.0		3.4		0.0		0.0		0.0		1.4		0.0	
	Caulerpa spp. (rhizomes)	0.0		0.0		0.9		0.0		0.0		0.0		0.0		0.0	
	Chaetomorpha coliformis	2.9		0.0		2.7		3.5		1.0		0.0		4.0		0.0	
	Cladophora feredayi	1.3		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Cladophora spp.	1.8		0.0		1.7		3.1		0.6		2.6		4.0		1.0	
	Ulva spp.	0.6		0.0		0.3		5.6		0.0		0.0		0.3		0.0	
Understorey red algae	*Areschougia* spp.	0.0	40.0	0.2	28.4	0.0	24.4	0.0	23.5	0.0	26.6	0.0	25.5	0.3	37.1	0.0	30.1
	Ballia callitricha	3.5		1.0		0.2		5.5		0.5		1.2		1.6		2.0	
	Callophyllis lambertii	0.1		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Callophyllis rangiferina	0.4		4.4		2.6		0.0		0.3		0.0		0.2		0.0	
	Camontagnea oxyclada	0.2		0.0		0.0		0.0		0.4		0.0		3.9		0.0	
	Champia spp.	0.0		0.0		0.0		0.0		0.1		0.0		0.0		0.0	
	Champia viridis	0.0		0.0		0.6		0.0		0.0		0.0		0.0		0.0	
	Delisea pulchra	0.0		0.0		0.0		0.0		0.0		0.0		1.2		0.0	
	Dictyomenia harveyana	0.0		0.0		0.0		0.1		0.0		0.0		0.0		0.0	
	Echinothamnion hystrix	0.3		0.0		0.0		0.5		0.0		0.0		0.9		0.0	
	Erythrymenia minuta	0.0		0.0		0.0		0.0		0.0		0.1		0.0		0.0	
	Euptilota articulata	0.2		1.3		1.0		0.0		1.7		0.0		0.1		0.7	
	Gelidium australe	0.0		0.0		0.6		0.5		0.0		0.0		4.0		0.0	
	Gloiocladia halymenioides	0.0		0.0		0.1		0.0		0.0		0.0		0.0		0.0	
	Haliptilon roseum	0.0		0.0		0.0		0.0		0.0		0.0		0.7		0.0	
	Hemineura frondosa	1.4		4.6		2.8		0.0		2.4		0.1		1.0		0.0	
	Hypnea pannosa	0.0		0.0		0.0		0.0		0.0		0.0		0.4		0.0	
	Laurencia elata	0.2		0.2		0.0		0.1		1.4		3.1		0.0		1.3	
	Laurencia majuscula	0.0		0.0		0.5		0.0		0.0		0.0		0.3		0.0	
	Laurencia spp.	0.1		0.0		0.0		0.0		0.2		0.0		0.0		0.0	
	Lenormandia marginata	0.4		1.1		1.2		0.0		1.1		0.0		0.2		0.1	
	Mychodea acanthymenia	0.4		0.0		0.0		0.0		0.0		0.0		1.3		0.0	
	Mychodea aciculare	0.0		2.8		0.0		0.0		0.0		0.0		0.0		0.0	

		Site															
Taxonomic group	**Species**	**RR**	**FG%**	**SBIR20**	**FG%**	**APEX**	**FG%**	**LPN**	**FG%**	**SBIR21**	**FG%**	**SBIR22**	**FG%**	**SBIR23**	**FG%**	**SBIR15**	**FG%**
Understorey red algae	*Nizymenia australis*	0.0		0.0		0.0		0.0		0.0		0.0		0.6		0.0	
	Nizymenia conferta	0.6		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Peyssonnelia novaehollandiae	0.0		0.0		0.1		0.0		0.1		0.0		0.0		0.0	
	Phacelocarpus apodus	0.8		0.0		0.0		0.0		0.4		0.0		0.0		0.0	
	Phacelocarpus peperocarpos	3.5		0.2		8.5		0.0		0.9		4.1		2.3		7.7	
	Phacelocarpus sessilis	0.0		0.0		0.0		0.4		0.0		0.0		0.0		0.6	
	Phacelocarpus spp.	0.3		0.0		0.0		0.0		0.1		0.3		0.0		0.0	
	Plocamium angustum	1.3		0.4		3.2		2.3		0.3		0.4		6.9		1.7	
	Plocamium cartilagineum	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.4	
	Plocamium costatum	0.0		0.0		0.3		0.0		1.1		0.0		0.0		0.0	
	Plocamium dilatatum	0.7		1.4		0.0		0.1		0.0		1.0		2.7		2.0	
	Plocamium mertensii	0.0		0.6		0.5		0.0		5.3		0.0		0.6		0.0	
	Plocamium patagiatum	0.4	40.0	0.0	28.4	0.0	24.4	0.0	23.5	0.0	26.6	0.7	25.5	0.0	37.1	0.5	30.1
	Plocamium preissianum	0.0		0.0		0.0		0.0		0.6		0.8		0.0		0.0	
	Pollexfenia lobata	5.8		0.0		1.5		4.4		1.5		0.0		1.4		0.0	
	Polyopes constrictus	9.9		0.7		0.0		7.8		1.7		6.2		4.9		4.3	
	Pterocladia spp.	0.0		0.0		0.0		0.0		0.0		1.0		0.0		0.0	
	Pterocladiella capillacea	0.8		0.0		0.0		0.4		0.0		0.0		0.0		0.9	
	Ptilonia australasica	0.4		0.2		0.0		0.0		0.0		0.8		0.0		0.0	
	Rhodymenia sonderi	0.8		1.3		0.2		0.1		0.0		0.0		0.1		1.2	
	Rhodymenia spp.	1.2		5.1		0.5		1.2		3.8		1.1		0.6		5.7	
	Rhodymenia wilsonis	5.4		1.5		0.0		0.1		2.7		4.6		0.0		1.0	
	Sonderophycus coriaceus	0.0		0.4		0.0		0.0		0.0		0.0		0.0		0.0	
	Stenogramme interrupta	0.0		1.0		0.0		0.0		0.0		0.0		0.7		0.0	
	Synarthrophyton patena	0.9		0.0		0.0		0.0		0.0		0.0		0.2		0.0	
Canopy-forming algae species richness		**5**	**-**	**5**	**-**	**5**	**-**	**4**	**-**	**3**	**-**	**4**	**-**	**5**	**-**	**5**	**-**
Understorey brown algae species richness		**6**	**-**	**2**	**-**	**5**	**-**	**3**	**-**	**5**	**-**	**5**	**-**	**5**	**-**	**3**	**-**
Understorey green algae species richness		**3**	**-**	**2**	**-**	**5**	**-**	**2**	**-**	**2**	**-**	**0**	**-**	**4**	**-**	**0**	**-**
Understorey red algae species richness		**23**	**-**	**18**	**-**	**16**	**-**	**13**	**-**	**17**	**-**	**12**	**-**	**24**	**-**	**14**	**-**
Total algae species richness		**37**	**-**	**27**	**-**	**31**	**-**	**22**	**-**	**27**	**-**	**21**	**-**	**38**	**-**	**22**	**-**

Appendix 5-2: Diversity metrics from inshore reef biodiversity baseline for fish, invertebrate and algal species

Key diversity metrics for the fish community data across the Storm Bay inshore reef sites.

Site	Species richness	Shannon diversity	Alpha diversity	Gamma diversity	Beta diversity
SBIR02	7	0.96	4.00	52	12.00
SBIR04	20	2.41	10.00	52	4.20
SBIR05	15	2.06	9.50	52	4.47
SBIR06	21	2.27	10.50	52	3.95
SBIR28	18	1.58	8.50	52	5.12
SBIR07	16	2.32	8.25	52	5.30
SBIR08	16	1.87	7.00	52	6.43
SBIR09	23	2.11	10.50	52	3.95
SBIR10	11	1.32	6.50	52	7.00
SBIR11	11	2.07	4.50	52	10.56
SBIR12	12	1.76	6.50	52	7.00
SBIR13	12	2.20	6.00	52	7.67
SBIR14	16	2.33	8.50	52	5.12
ADV	14	2.30	7.50	52	5.93
SBIR25	14	1.87	8.75	52	4.94
SBIR24	13	1.65	6.50	52	7.00
SBIR26	15	1.07	7.25	52	6.17
SBIR16	10	1.58	5.75	52	8.04
SBIR17	18	1.15	9.25	52	4.62
SBIR18N	12	1.91	4.75	52	9.95
SBIR18S	12	1.72	6.00	52	7.67
SBIR19	9	1.37	5.00	52	9.40
RR	11	1.64	5.25	52	8.90
SBIR20	16	2.15	9.25	52	4.62
APEX	12	1.48	8.25	52	5.30
LPN	8	1.41	4.25	52	11.24
SBIR21	12	1.66	7.00	52	6.43
SBIR22	13	1.76	7.50	52	5.93
SBIR23	6	1.09	3.50	52	13.86
SBIR15	13	1.45	5.50	52	8.45

Key diversity metrics for the invertebrate community data across the Storm Bay inshore reef sites.

Site	Species richness	Shannon diversity	Alpha diversity	Gamma diversity	Beta diversity
SBIR02	22	2.15	10.75	54	4.02
SBIR04	10	1.54	6.75	54	7.00
SBIR05	12	1.77	6.75	54	7.00
SBIR06	11	1.78	7.00	54	6.71
SBIR28	14	1.93	6.50	54	7.31
SBIR07	13	1.99	6.75	54	7.00
SBIR08	9	1.76	4.50	54	11.00
SBIR09	9	1.79	4.75	54	10.37
SBIR10	18	2.22	9.25	54	4.84
SBIR11	17	1.92	7.25	54	6.45
SBIR12	11	1.80	5.50	54	8.82
SBIR13	10	2.10	3.75	54	13.40
SBIR14	11	1.27	6.25	54	7.64

ADV	12	2.07	6.50	54	7.31
SBIR25	18	1.35	8.75	54	5.17
SBIR24	17	1.77	8.00	54	5.75
SBIR26	11	2.08	5.50	54	8.82
SBIR16	15	2.16	7.75	54	5.97
SBIR17	14	1.85	7.50	54	6.20
SBIR18N	10	1.96	6.50	54	7.31
SBIR18S	12	1.88	6.00	54	8.00
SBIR19	9	1.74	5.00	54	9.80
RR	12	1.89	6.75	54	7.00
SBIR20	14	1.81	7.50	54	6.20
APEX	12	1.00	7.00	54	6.71
LPN	8	1.51	6.25	54	7.64
SBIR21	17	1.29	9.00	54	5.00
SBIR22	10	1.22	4.75	54	10.37
SBIR23	12	1.89	6.75	54	7.00
SBIR15	17	2.34	8.00	54	5.75

Key diversity metrics for the macroalgae community data across the Storm Bay inshore reef sites. Only taxa which represent unique species have been included in diversity metric calculations.

Site	Species richness	Shannon diversity	Alpha diversity	Gamma diversity	Beta diversity
SBIR02	21	2.16	13.00	119	8.15
SBIR04	41	2.74	25.50	119	3.67
SBIR05	29	2.17	17.00	119	6.00
SBIR06	33	2.59	20.50	119	4.80
SBIR28	35	2.82	21.75	119	4.47
SBIR07	34	2.15	20.75	119	4.73
SBIR08	32	1.92	17.75	119	5.70
SBIR09	45	2.20	20.75	119	4.73
SBIR10	20	1.25	11.25	119	9.58
SBIR11	20	1.33	11.00	119	9.82
SBIR12	25	1.41	13.50	119	7.81
SBIR13	32	2.57	16.25	119	6.32
SBIR14	25	1.30	11.50	119	9.35
ADV	28	1.50	14.00	119	7.50
SBIR25	37	2.50	20.75	119	4.73
SBIR24	38	2.63	21.25	119	4.60
SBIR26	32	2.65	17.50	119	5.80
SBIR16	32	2.20	15.50	119	6.68
SBIR17	26	1.65	11.75	119	9.13
SBIR18N	29	2.58	17.50	119	5.80
SBIR18S	31	2.81	21.50	119	4.53
SBIR19	36	3.01	22.50	119	4.29
RR	43	2.79	21.75	119	4.47
SBIR20	32	2.19	19.25	119	5.18
APEX	38	2.64	23.00	119	4.17
LPN	25	2.51	16.00	119	6.44
SBIR21	34	2.30	23.25	119	4.12
SBIR22	27	2.36	16.50	119	6.21
SBIR23	41	2.95	23.75	119	4.01
SBIR15	27	2.05	17.50	119	5.80

Appendix 5-3: Summary tables for inshore reef RVA data

Mean ± SE percentage covers of major RVA parameters for each survey (summer and winter) at each site, averaged across years. Sites marked with an asterisk were only surveyed once during that season, so values shown are site averages for that single survey event.

	Canopy	Understorey brown	Understorey green	Understorey red	Epiphytic algae	Filamentous algae	Nuisance green	Nuisance red	Pink encrusting	Red encrusting	Sponge	Turfing algae
Summer												
SBIR02	33 ± 6.3	20.5 ± 3.2	2.6 ± 0.2	30 ± 6.6	13.6 ± 3.1	12.7 ± 8.5	1.5 ± 0.9	0 ± 0	7.8 ± 3.1	15.5 ± 5.3	14.2 ± 4.7	23.3 ± 13.8
SBIR04	54.7 ± 5.1	40.1 ± 6	2.3 ± 1	20 ± 3.7	8.5 ± 2.4	1 ± 0.6	0.2 ± 0.1	0 ± 0	44 ± 7	11.8 ± 1	17.8 ± 8.5	3.4 ± 2.9
SBIR05	78.4 ± 3.6	17.3 ± 4.4	1.8 ± 0.4	8.5 ± 1	7.7 ± 2.1	2.8 ± 1.2	1.4 ± 0.4	0 ± 0	22.5 ± 2.8	35.4 ± 2.6	21 ± 4.1	4.5 ± 2.6
SBIR06	75.8 ± 0.9	20.3 ± 0.3	2.3 ± 0.4	20.4 ± 1.4	2.8 ± 0.7	1.4 ± 1.1	2.1 ± 0.2	0 ± 0	38.3 ± 3.5	17.4 ± 4.1	14.6 ± 1.9	9.4 ± 7.6
SBIR28	42.1 ± 3.4	39 ± 2.4	3.9 ± 0.9	24.3 ± 4.5	7.1 ± 0.8	0 ± 0	1.1 ± 0.1	0 ± 0	29.6 ± 0.4	22.2 ± 2.5	23.9 ± 2.4	5 ± 1.7
SBIR07	50.8 ± 5.4	36.4 ± 1.5	6.6 ± 1	34.3 ± 3.9	4.2 ± 0.9	0.1 ± 0.1	0.3 ± 0.1	0 ± 0	6.9 ± 0.8	7.1 ± 0.7	26.5 ± 7	24.3 ± 14.7
SBIR08	78 ± 2.7	10.5 ± 1.3	1.3 ± 0.4	19.3 ± 3.4	0.4 ± 0.2	0.1 ± 0.1	0 ± 0	0 ± 0	32.2 ± 3.2	12.6 ± 2.7	22.3 ± 2.8	16.1 ± 13.6
SBIR09	80.3 ± 2.4	9.5 ± 1.1	1.1 ± 0.5	29.6 ± 1.8	10 ± 2.3	0 ± 0	0.4 ± 0.2	0 ± 0	31.8 ± 7.2	8.3 ± 1.1	22.8 ± 6.4	14 ± 10.5
SBIR10	85.3 ± 3.5	13.2 ± 1.2	1.4 ± 0.5	11.4 ± 1.4	3.7 ± 0.5	0 ± 0	0.2 ± 0.1	0.1 ± 0.1	35.8 ± 3.7	19.9 ± 1.5	12.2 ± 1.9	6.6 ± 3.7
SBIR11	83.1 ± 1	10.5 ± 1	2.3 ± 0.8	12.8 ± 2.6	11.3 ± 2	0.3 ± 0.3	0.4 ± 0.2	0 ± 0	56.3 ± 0.4	13.3 ± 3.5	13.3 ± 2.2	7.2 ± 5.8
SBIR12	83.6 ± 3.1	8.4 ± 1.8	0.9 ± 0.4	16.4 ± 0.8	5.1 ± 0.6	0 ± 0	0.3 ± 0.1	0 ± 0	46.7 ± 3.2	18.2 ± 1.3	13.7 ± 1.3	2.4 ± 1
SBIR14	81.7 ± 3.2	6.4 ± 1.2	0.7 ± 0.4	8.9 ± 1.5	26.9 ± 7	0.2 ± 0.1	0.1 ± 0	0 ± 0	36.8 ± 2.4	10.1 ± 2	26.7 ± 5.7	6.6 ± 3.1
ADV	85.3 ± 4.4	2.6 ± 0.1	1 ± 0.5	16.4 ± 3.6	8.8 ± 4.1	0 ± 0	0.1 ± 0.1	0 ± 0	31 ± 2.5	10.9 ± 2	19.4 ± 3.3	13 ± 6.5
SBIR25*	40.0	45.4	2.3	12.5	5.7	0.0	1.0	0.0	70.8	8.3	9.8	6.4
SBIR24*	38.3	52.5	3.5	11.8	10.0	0.4	0.9	0.0	34.6	24.6	9.1	7.3
SBIR26*	35.8	32.3	1.8	13.3	3.6	0.9	0.0	0.0	37.1	3.9	10.4	24.8
SBIR16*	59.6	9.2	5.9	62.5	7.8	34.2	4.4	0.0	2.9	4.2	9.6	59.6
SBIR17*	44.6	15.8	9.1	6.3	5.0	2.9	1.7	0.0	15.0	6.8	11.4	20
SBIR18N*	58.3	16.3	5.4	31.7	3.0	0.0	0.6	0.0	10.8	4.5	33.3	29.6
SBIR18S*	46.3	50.0	2.3	21.3	4.7	0.0	0.2	0.0	43.3	10.8	17.3	18.8
SBIR19	42 ± 7	15.8 ± 1.7	5.2 ± 1.7	46.3 ± 2.5	7 ± 5	0.1 ± 0.1	0.1 ± 0	0 ± 0	20.6 ± 2.7	10.3 ± 4.5	25.8 ± 3.3	16 ± 6
RR*	60.8	30.4	5.3	30.0	3.7	0.0	1.2	0.0	53.8	7.5	17.5	15.8
SBIR20	76 ± 0.2	10.5 ± 0.3	3.4 ± 1.5	30.6 ± 3.5	3 ± 0	0 ± 0	0.3 ± 0.2	0 ± 0	21.7 ± 3.6	5.9 ± 1.1	21 ± 0.6	29.2 ± 10.8
APEX	54.8 ± 0.6	21 ± 0.2	9.5 ± 0.1	28.8 ± 2.5	5 ± 0.4	1.1 ± 1.1	1.2 ± 0	0 ± 0	30.8 ± 5	23.4 ± 4.1	6.2 ± 0.5	13.4 ± 4.3
LPN*	57.5	16.3	8.5	29.6	7.3	0.0	6.0	0.0	19.2	20.0	17.1	27.5
SBIR21	57.3 ± 4	34.4 ± 3.1	5.1 ± 0.3	15 ± 1.7	7.2 ± 3.4	4.1 ± 4.1	1.2 ± 0.3	0 ± 0	31.7 ± 2.1	16.7 ± 5.4	26 ± 1.9	13.5 ± 8.5

	Canopy	Understorey brown	Understorey green	Understorey red	Epiphytic algae	Filamentous algae	Nuisance green	Nuisance red	Pink encrusting	Red encrusting	Sponge	Turfing algae
SBIR22	29.4 ± 4	33.8 ± 2.1	3.5 ± 1.9	31.5 ± 2.7	6.1 ± 5.2	0 ± 0	0.1 ± 0.1	0 ± 0	41.3 ± 5	15.4 ± 3.3	16.7 ± 2.9	14.8 ± 14.8
SBIR23	25.6 ± 5.6	29 ± 1	4 ± 1.1	38.3 ± 3.3	16.6 ± 3.8	0 ± 0	1 ± 0.7	0 ± 0	52.1 ± 11.3	9.5 ± 1.5	2.8 ± 1.1	7.1 ± 3.2
SBIR15*	81.3	5.6	0.4	42.5	0.2	0.0	0.0	0.0	12.9	5.8	44.2	8.8
Winter												
SBIR02	31.3 ± 4	15.5 ± 2.3	1.8 ± 0.6	11.4 ± 1.9	3.1 ± 1.8	0.1 ± 0.1	0.3 ± 0.3	0 ± 0	10.3 ± 0.9	26.3 ± 3.4	11.4 ± 1.7	8.2 ± 4.4
SBIR04	36.7 ± 6.4	37.5 ± 3.7	1.4 ± 0.5	14.3 ± 3.4	5.2 ± 1.7	0.9 ± 0.9	0 ± 0	0 ± 0	42.8 ± 3.5	13.3 ± 1.7	19.9 ± 2.8	4.3 ± 2.6
SBIR05	64.1 ± 5.2	16.4 ± 2.9	2.2 ± 1.3	9.7 ± 2	4.1 ± 1.8	0.1 ± 0.1	1.7 ± 1.3	0.3 ± 0.3	26.3 ± 6	25.5 ± 2.1	23.9 ± 1.8	8.9 ± 4.4
SBIR06	52.6 ± 5.6	17.9 ± 4.2	2.6 ± 1.3	15.7 ± 3	1.6 ± 0.4	0.3 ± 0.1	0.4 ± 0.2	0 ± 0	31.5 ± 4.5	17.6 ± 3.2	20.3 ± 2.8	11.5 ± 5.1
SBIR28	22.5 ± 2.2	40.1 ± 2.1	2.2 ± 1.1	19.2 ± 3.6	3.9 ± 1.6	0 ± 0	0.4 ± 0.1	0 ± 0	28 ± 1.7	24.7 ± 2.9	23.1 ± 3.9	3.5 ± 1.3
SBIR07	39.9 ± 4.4	26.1 ± 1.7	6.1 ± 1.3	25.7 ± 2.9	5.3 ± 1.1	0.1 ± 0.1	0.1 ± 0.1	0 ± 0	8 ± 1.1	8.8 ± 2.2	20.8 ± 1.4	15.1 ± 10.3
SBIR08	62.6 ± 4	10.1 ± 2.4	0.8 ± 0.5	20 ± 5.1	0.1 ± 0.1	0 ± 0	0 ± 0	0 ± 0	35.1 ± 0.9	18.5 ± 2	21.7 ± 1.4	8.9 ± 5.3
SBIR09	76.4 ± 4.7	10.3 ± 0.8	1.1 ± 0.7	18.5 ± 2.7	10.1 ± 0.2	0 ± 0	0.3 ± 0.2	0 ± 0	24.7 ± 3.5	10.6 ± 3.8	16.1 ± 2.9	20.1 ± 10.1
SBIR10	70.7 ± 4.5	15.4 ± 1.8	0.5 ± 0.3	7.2 ± 1.9	1.4 ± 0.7	0.1 ± 0	0 ± 0	0 ± 0	28.5 ± 4.5	24.7 ± 3.7	12.2 ± 1.7	10.5 ± 5.1
SBIR11	72.3 ± 2.7	9.1 ± 1.3	0.4 ± 0.1	12.6 ± 3	9.5 ± 2.2	0 ± 0	0 ± 0	0 ± 0	45.2 ± 3.7	15.2 ± 1.6	11 ± 3.1	7.3 ± 3.4
SBIR12	72.1 ± 3.4	10.8 ± 1.7	0.7 ± 0.2	13 ± 1.5	4.8 ± 1.9	0 ± 0	0 ± 0	0 ± 0	51.8 ± 6.3	17.6 ± 1.8	13.6 ± 1.8	3.9 ± 2.3
SBIR14	71 ± 3.5	5.6 ± 1	0.1 ± 0.1	10.3 ± 2.2	17.8 ± 6.4	0.2 ± 0.2	0 ± 0	0 ± 0	37 ± 0.8	14.7 ± 0.4	30.9 ± 4.8	7 ± 3.6
ADV	71.1 ± 3.2	3.3 ± 1.5	1.5 ± 0.6	16.3 ± 6	9.3 ± 3.3	0 ± 0	0 ± 0	0 ± 0	30.9 ± 4.8	8.7 ± 0.3	25.6 ± 8.3	14.9 ± 8.1
SBIR25	40 ± 0.8	42.1 ± 0.8	2 ± 0.3	8.3 ± 0.4	4.3 ± 1.7	0.4 ± 0.4	0.8 ± 0.6	0 ± 0	53.8 ± 8.8	12.5 ± 1.7	19.8 ± 3.5	7 ± 0.7
SBIR24	27.5 ± 3.8	49.2 ± 3.3	1.8 ± 0.4	12.3 ± 2.3	6 ± 3.5	1 ± 0.3	0.2 ± 0.1	0 ± 0	31 ± 0.2	23.1 ± 0.2	14 ± 3.5	5.5 ± 0.4
SBIR26	44.4 ± 9.4	23.8 ± 0.4	1 ± 0.4	12.7 ± 5.8	0.8 ± 0.8	0.2 ± 0.2	0 ± 0	0 ± 0	39.4 ± 0.2	9.8 ± 2.3	14 ± 0.6	16.2 ± 1.3
SBIR16	30.8 ± 7.5	10.6 ± 5.7	2.7 ± 2.7	24.7 ± 20.8	1.8 ± 0.2	0 ± 0	1.9 ± 0.6	0 ± 0	3.5 ± 0.5	9.5 ± 1.6	8.1 ± 1.3	31.3 ± 5
SBIR17	54.6 ± 7.9	10.8 ± 5.2	8.6 ± 2.4	9.5 ± 0.1	5.3 ± 2.2	3.1 ± 3.1	1.7 ± 1.4	0.1 ± 0.1	15.2 ± 4	10.9 ± 3.3	12.4 ± 1	14.1 ± 1.4
SBIR18N	56.7 ± 2.9	14.6 ± 2.5	1.1 ± 0.3	19.2 ± 4.2	1 ± 0.3	0 ± 0	0 ± 0	0 ± 0	13.4 ± 1.8	6.8 ± 1.4	37.9 ± 5	22.9 ± 2.1
SBIR18S	43 ± 2.2	42.9 ± 8.3	2 ± 0.1	18.1 ± 2.7	4.3 ± 0.4	2.3 ± 2.3	0 ± 0	0 ± 0	34.4 ± 1	13.3 ± 0.4	17.5 ± 0.8	14.4 ± 1
SBIR19	36.4 ± 8.7	19.7 ± 2.6	2.2 ± 1.6	36.1 ± 4	1 ± 0.5	0 ± 0	0 ± 0	0 ± 0	17.3 ± 5	9.7 ± 2.6	42.2 ± 6.9	11.4 ± 6.5
RR	49.2 ± 4.6	25 ± 4.2	3.9 ± 0.8	19 ± 2.3	1.5 ± 0.1	0 ± 0	0.1 ± 0.1	0 ± 0	56 ± 5.6	12 ± 0.1	15.5 ± 1.7	10 ± 1.9
SBIR20	67.4 ± 3	10.6 ± 1.8	2.6 ± 1.5	22.1 ± 8.6	5.3 ± 0.5	0 ± 0	0 ± 0	0 ± 0	20 ± 3.6	7.8 ± 1.2	30.1 ± 5.9	15.9 ± 9.3
APEX	47.4 ± 2.3	21.5 ± 2.3	9.2 ± 2.8	27.8 ± 3.5	2.2 ± 0.3	0 ± 0	1.6 ± 0.5	0 ± 0	33.1 ± 2.6	23.9 ± 3.1	12.6 ± 3.7	5.4 ± 2.1
LPN	48.3 ± 9.6	22.5 ± 0.4	7.6 ± 1.2	17.5 ± 1.7	2 ± 1	0 ± 0	5.5 ± 0.2	0 ± 0	15.6 ± 3.3	25.4 ± 2.1	13.5 ± 1.5	10.7 ± 1.4
SBIR21	49.3 ± 9.7	30.4 ± 1.5	2.8 ± 0.1	12.4 ± 1.8	2.9 ± 0.9	0.2 ± 0.2	0.3 ± 0.3	0 ± 0	31.1 ± 1.6	16.9 ± 0.5	21.7 ± 2.9	8.1 ± 3.8
SBIR22	24.8 ± 7.8	32.8 ± 1.4	0.9 ± 0.2	27.4 ± 0.8	0.8 ± 0.5	0 ± 0	0 ± 0	0 ± 0	43.2 ± 7.6	12.4 ± 2.2	24.3 ± 0.9	11.2 ± 6.6

	Canopy	Understorey brown	Understorey green	Understorey red	Epiphytic algae	Filamentous algae	Nuisance green	Nuisance red	Pink encrusting	Red encrusting	Sponge	Turfing algae
SBIR23	19.6 ± 4.6	31.8 ± 1.8	4.7 ± 1.4	33.9 ± 1.8	2.9 ± 1.1	0.2 ± 0.2	0.5 ± 0.4	0 ± 0	42.6 ± 2	16.7 ± 3.7	4.7 ± 0.3	6.8 ± 3.7
SBIR15	69.2 ± 1.3	3.8 ± 1.8	0.4 ± 0.4	30.4 ± 8.3	0 ± 0	0 ± 0	0 ± 0	0 ± 0	9.8 ± 0.6	7.3 ± 1.5	50.4 ± 6.7	20.4 ± 13.4

Mean ± SE percentage covers of major canopy-forming species for each survey (summer and winter) at each site, averaged across years. Sites marked with an asterisk were only surveyed once during that season, so values shown are site averages for that single survey event.

	Phyllospora comosa	*Ecklonia radiata*	*Lessonia corrugata*	*Sargassum* spp.	*Durvillaea potatorum*	*Macrocystis pyrifera*	*Cystophora* spp.
Summer							
SBIR02	0 ± 0	17.6 ± 3.7	8.5 ± 1.5	2.1 ± 1.1	0 ± 0	4 ± 0.8	0 ± 0
SBIR04	0 ± 0	42.6 ± 3.7	11.9 ± 1.3	0.1 ± 0.1	0 ± 0	0 ± 0	0 ± 0
SBIR05	0 ± 0	75.2 ± 3.1	0 ± 0	2.6 ± 1.3	0 ± 0	0 ± 0	0.6 ± 0.6
SBIR06	0 ± 0	58.9 ± 2.8	15 ± 1	1.3 ± 1.3	0 ± 0	0 ± 0	0.7 ± 0.4
SBIR28	0 ± 0	35.7 ± 2.1	4 ± 1	2.1 ± 1	0 ± 0	0 ± 0	0 ± 0
SBIR07	20.3 ± 4.3	15.3 ± 2.6	10.1 ± 1.3	0 ± 0	0 ± 0	0 ± 0	5.1 ± 5.1
SBIR08	60.8 ± 2.1	3 ± 1.5	0.9 ± 0.5	0 ± 0	13.4 ± 1.6	0 ± 0	0 ± 0
SBIR09	66.4 ± 2.4	12.1 ± 1.8	0 ± 0	0 ± 0	1.8 ± 0.4	0 ± 0	0 ± 0
SBIR10	64.3 ± 8.5	20.7 ± 5.3	0 ± 0	0.3 ± 0.3	0 ± 0	0 ± 0	0 ± 0
SBIR11	52.5 ± 6	15 ± 3.5	0 ± 0	1.5 ± 1.5	14 ± 0.8	0 ± 0	0 ± 0
SBIR12	64.1 ± 6.2	22 ± 3.5	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
SBIR14	63.9 ± 6	17.8 ± 5.4	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
ADV	67.1 ± 2.9	9.3 ± 4.2	0 ± 0	0.3 ± 0.3	8.3 ± 3.3	0 ± 0	0 ± 0
SBIR25*	0.0	37.9	0.0	2.1	0.0	0.0	0.0
SBIR24*	0.0	38.3	0.0	0.0	0.0	0.0	0.0
SBIR26*	0.0	34.2	0.0	1.7	0.0	0.0	0.0
SBIR16*	0.8	5.0	36.7	12.1	0.0	0.0	5.0
SBIR17*	0.0	44.6	0.0	0.0	0.0	0.0	0.0
SBIR18N*	36.7	14.2	7.1	0.0	0.4	0.0	0.0
SBIR18S*	15.8	10.4	19.6	0.0	0.4	0.0	0.0
SBIR19	0 ± 0	17 ± 0.3	24.6 ± 6.3	0.4 ± 0.4	0 ± 0	0 ± 0	0 ± 0

	Phyllospora comosa	*Ecklonia radiata*	*Lessonia corrugata*	*Sargassum* spp.	*Durvillaea potatorum*	*Macrocystis pyrifera*	*Cystophora* spp.
RR*	0.0	24.6	36.3	0.0	0.0	0.0	0.0
SBIR20	50 ± 0.4	21.9 ± 0.6	4.2 ± 0.4	0 ± 0	0 ± 0	0 ± 0	0 ± 0
APEX	0 ± 0	47.3 ± 0.2	0 ± 0	6 ± 1	0 ± 0	1.3 ± 1.3	0.2 ± 0.2
LPN*	0.0	30.0	8.8	2.9	0.0	15.8	0.0
SBIR21	0.4 ± 0.4	55.4 ± 3.8	0 ± 0	1.7 ± 0.4	0 ± 0	0 ± 0	0 ± 0
SBIR22	0 ± 0	5.6 ± 1.9	17.7 ± 8.1	4.4 ± 4.4	0 ± 0	0 ± 0	1.7 ± 1.7
SBIR23	0 ± 0	0 ± 0	18.5 ± 3.1	0 ± 0	7.1 ± 2.5	0 ± 0	0 ± 0
SBIR15*	71.7	5.8	2.1	0.0	1.7	0.0	0.0
Winter							
SBIR02	0 ± 0	12 ± 1.8	4.4 ± 2.1	7.4 ± 0.5	0 ± 0	7.5 ± 2.6	0 ± 0
SBIR04	0 ± 0	33.4 ± 6.2	2.8 ± 0.5	0.4 ± 0.4	0 ± 0	0 ± 0	0 ± 0
SBIR05	0 ± 0	62.1 ± 6.4	0 ± 0	1.3 ± 0.7	0 ± 0	0 ± 0	0.7 ± 0.7
SBIR06	0 ± 0	42.8 ± 6.3	6.6 ± 1.3	3.4 ± 1.9	0 ± 0	0 ± 0	0 ± 0
SBIR28	0 ± 0	20.8 ± 2.1	1.6 ± 0.2	0.1 ± 0.1	0 ± 0	0 ± 0	0 ± 0
SBIR07	16.9 ± 1.8	13.1 ± 1.9	2.7 ± 1.2	3.2 ± 0.9	0 ± 0	0 ± 0	3.8 ± 3.8
SBIR08	50.1 ± 5.1	2.3 ± 0.5	1.4 ± 0.5	0.1 ± 0.1	8.7 ± 2.4	0 ± 0	0 ± 0
SBIR09	57.6 ± 3.9	11.2 ± 2.9	0 ± 0	0.8 ± 0.8	6.7 ± 1.9	0 ± 0	0 ± 0
SBIR10	56 ± 4.6	14.5 ± 1.3	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
SBIR11	50.2 ± 3.1	11 ± 2.5	0 ± 0	1.1 ± 0.7	9.3 ± 0.9	0 ± 0	0 ± 0
SBIR12	51.7 ± 5.1	20.4 ± 1.7	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
SBIR14	56.9 ± 4	13.9 ± 0.5	0 ± 0	0.3 ± 0.2	0 ± 0	0 ± 0	0 ± 0
ADV	53.9 ± 4.5	2.9 ± 0.4	0.1 ± 0.1	0.6 ± 0.4	13.6 ± 2.2	0 ± 0	0 ± 0
SBIR25	0 ± 0	35.6 ± 1.5	0 ± 0	4.4 ± 0.6	0 ± 0	0 ± 0	0 ± 0
SBIR24	0 ± 0	25 ± 3.3	0.6 ± 0.6	1.7 ± 0	0 ± 0	0.2 ± 0.2	0 ± 0
SBIR26	0 ± 0	24.4 ± 6.5	0.2 ± 0.2	19.8 ± 2.7	0 ± 0	0 ± 0	0 ± 0
SBIR16	0 ± 0	0.5 ± 0.5	16.5 ± 3.5	13.8 ± 4.5	0 ± 0	0 ± 0	0 ± 0
SBIR17	0 ± 0	34.4 ± 6	0 ± 0	16 ± 2.3	0 ± 0	0 ± 0	4.2 ± 4.2
SBIR18N	44 ± 0.2	7.3 ± 2.7	5.4 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
SBIR18S	13.3 ± 4.2	4.6 ± 2.1	22.1 ± 4.2	1.5 ± 1.5	1.5 ± 1.5	0 ± 0	0 ± 0
SBIR19	0.8 ± 0.5	11 ± 1.6	24.4 ± 7	0.3 ± 0.1	0 ± 0	0 ± 0	0 ± 0
RR	0.4 ± 0.4	21.5 ± 5.6	19.8 ± 0.2	7.5 ± 0.8	0 ± 0	0 ± 0	0 ± 0
SBIR20	40.8 ± 8.3	20.7 ± 6.2	4 ± 1.5	1.8 ± 1	0 ± 0	0 ± 0	0 ± 0
APEX	0 ± 0	38.2 ± 2.2	0 ± 0	8.8 ± 1.3	0 ± 0	0.4 ± 0.2	0 ± 0

	Phyllospora comosa	***Ecklonia radiata***	***Lessonia corrugata***	***Sargassum* spp.**	***Durvillaea potatorum***	***Macrocystis pyrifera***	***Cystophora* spp.**
LPN	0 ± 0	23.8 ± 2.5	3.8 ± 1.7	3.3 ± 0.8	0 ± 0	17.5 ± 9.6	0 ± 0
SBIR21	0 ± 0	42.4 ± 11.8	0 ± 0	6.9 ± 2	0 ± 0	0 ± 0	0 ± 0
SBIR22	0 ± 0	3.3 ± 0.4	17.9 ± 9.5	3.5 ± 2	0 ± 0	0 ± 0	0 ± 0
SBIR23	0 ± 0	0.1 ± 0.1	11.9 ± 2.7	0.3 ± 0.1	6.8 ± 2.4	0.4 ± 0.2	0 ± 0
SBIR15	56 ± 4.8	7.3 ± 2.7	2.3 ± 1.5	0.4 ± 0.4	3.1 ± 1	0 ± 0	0 ± 0

Appendix 6-1: Summary tables for deep reef fish and benthic community data

Summary of quantitative survey results for the fish communities at each of the Storm Bay deep reef sites. Data represent average abundance of fish species across all transects at each site.

Trophic group	Family	Site name / Site abbreviation	Dart Bank DB	Betsey West BW	Crayfish Rock CR	Horseshoe Reef HR	Variety Reef VR	North Bruny NB	Cape Queen Elizabeth CQE	Adventure Bay AB
Browsing herbivore	Aplodactylidae	*Aplodactylus arctidens* (Marblefish)	0.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Benthic invertivore	Cheilodactylidae	*Chirodactylus spectabilis* (Banded morwong)	6.3	1.5	0.0	1.5	0.0	2.8	0.0	0.0
Benthic invertivore	Cheilodactylidae	*Nemadactylus douglasii* (Grey morwong)	0.0	0.0	2.0	0.0	0.0	0.0	0.0	0.0
Benthic invertivore	Cheilodactylidae	*Nemadactylus macropterus* (Jackass morwong)	1.0	3.0	35.0	11.0	17.0	25.2	10.4	0.5
Higher carnivore	Dinolestidae	*Dinolestes lewini* (Long-fin pike)	0.7	0.0	152.0	17.0	0.0	1.4	120.2	0.0
Benthic invertivore	Diodontidae	*Diodon nicthemerus* (Globe fish)	0.0	2.0	0.0	0.0	0.0	0.0	0.0	0.0
Benthic invertivore	Gerreidae	*Parequula melbournensis* (Silverbelly)	0.0	0.0	2.0	0.0	0.0	0.2	0.6	0.0
Planktivore	Kyphosidae	*Scorpis lineolata* (Silver sweep)	0.0	0.0	0.0	0.0	0.0	0.6	0.2	0.0
Benthic invertivore	Labridae	*Dotalabrus aurantiacus* (Castelnaus wrasse)	0.0	0.0	0.0	0.0	0.0	0.2	0.0	0.0
Benthic invertivore	Labridae	*Notolabrus tetricus* (Blue-throat wrasse)	18.0	12.5	8.0	11.0	4.0	14.2	4.4	1.0
Benthic invertivore	Labridae	*Pictilabrus laticlavius* (Senator wrasse)	2.0	2.0	0.0	0.0	0.0	0.0	0.0	0.0
Benthic invertivore	Labridae	*Pseudolabrus rubicundus* (Rosy wrasse)	95.7	27.5	27.0	25.0	30.0	83.2	42.4	40.0
Benthic invertivore	Labridae	*Suezichthys aylingi* (Crimson cleaner fish)	0.0	0.0	0.0	0.0	0.0	0.2	0.0	0.0
Benthic invertivore	Latridae	*Latridopsis forsteri* (Bastard trumpeter)	0.0	0.0	0.0	0.0	0.0	0.8	0.0	0.0
Benthic invertivore	Latridae	*Pseudogoniistius nigripes* (Magpie perch)	0.3	0.5	0.0	0.5	0.0	1.0	0.4	0.0
Browsing herbivore	Monacanthidae	*Acanthaluteres vittiger* (Toothbrush leatherjacket)	5.7	0.5	0.0	1.5	0.0	1.0	0.4	0.3
Browsing herbivore	Monacanthidae	*Eubalichthys gunnii* (Gunns leatherjacket)	1.0	2.0	0.0	3.0	0.0	0.0	0.8	0.8
Browsing herbivore	Monacanthidae	*Meuschenia australis* (Brown-striped leatherjacket)	0.0	1.5	1.0	0.0	1.0	0.2	1.0	0.0
Benthic invertivore	Monacanthidae	*Meuschenia scaber* (Velvet leatherjacket)	4.7	0.5	0.0	1.0	1.0	3.8	6.6	5.0
Benthic invertivore	Monacanthidae	*Thamnaconus degeni* (Degens leatherjacket)	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.0
Higher carnivore	Moridae	*Pseudophycis bachus* (Red cod)	6.3	0.5	124.0	3.0	3.0	12.0	4.4	3.8
Benthic invertivore	Mullidae	*Upeneichthys vlamingii* (Southern goatfish)	0.3	1.5	1.0	1.0	0.0	0.0	0.4	0.0
Higher carnivore	Ophidiidae	*Genypterus tigerinus* (Rock ling)	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.0
Benthic invertivore	Ostraciidae	*Aracana aurita* (Shaws cowfish)	0.3	0.0	1.0	0.0	0.0	0.4	1.6	1.0
Benthic invertivore	Pempheridae	*Pempheris multiradiata* (Common bullseye)	0.0	0.0	30.0	4.0	11.0	3.6	4.0	0.0
Benthic invertivore	Pentacerotidae	*Pentaceropsis recurvirostris* (Long-snouted boarfish)	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0

Trophic group	Family	Site name / Site abbreviation	Dart Bank DB	Betsey West BW	Crayfish Rock CR	Horseshoe Reef HR	Variety Reef VR	North Bruny NB	Cape Queen Elizabeth CQE	Adventure Bay AB
Benthic invertivore	Pinguipedidae	*Parapercis allporti* (Barred grubfish)	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.3
Benthic invertivore	Plesiopidae	*Trachinops caudimaculatus* (Hulafish)	0.0	0.0	0.0	75.0	0.0	3.2	0.0	0.0
Browsing herbivore	Pomacentridae	*Parma microlepis* (White-ear)	0.0	0.0	0.0	0.0	0.0	0.2	0.4	0.0
Higher carnivore	Scorpaenidae	*Helicolenus percoides* (Red gurnard perch)	0.0	0.5	2.0	0.5	1.0	1.2	3.6	7.0
Benthic invertivore	Scorpaenidae	*Neosebastes scorpaenoides* (Common gurnard perch)	0.0	0.0	0.0	0.0	0.0	0.4	0.0	0.0
Planktivore	Serranidae	*Caesioperca lepidoptera* (Butterfly perch)	804.0	160.5	498.0	503.0	342.0	555.0	940.6	861.0
Planktivore	Serranidae	*Caesioperca rasor* (Barber perch)	5.0	12.0	0.0	55.5	8.0	183.4	350.2	4.0
Benthic invertivore	Serranidae	*Hypoplectrodes maccullochi* (Half-banded seaperch)	0.0	0.0	0.0	0.0	0.0	0.6	1.0	0.8
Benthic invertivore	Trachichthyidae	*Paratrachichthys macleayi* (Sandpaperfish)	0.3	0.0	0.0	0.0	0.0	0.2	0.2	1.5
		Clupeidae & Pristigasteridae	0.0	0.0	0.0	0.0	0.0	0.0	0.0	500.0
Species richness			**18**	**16**	**13**	**16**	**10**	**25**	**23**	**14**

Mean percentage cover of benthic taxa and substrate categories across all photoquadrats and transects at each Storm Bay deep reef site. The column FG% represents the total percentage cover for each functional group. For each site, a count of all taxa has been used to produce a total taxa richness across all functional groups. Note, taxa that have zero values across all sites were present in the data, but at an average percentage cover of <0.1%.

Functional group	Site name / Site abbreviation	Dart Bank DB	FG%	Betsey West BW	FG%	Crayfish Rock CR	FG%	Horseshoe Reef HR	FG%	Variety Reef VR	FG%	North Bruny NB	FG%	Cape Queen Elizabeth CQE	FG%	Adventure Bay AB	FG%
Ascidian	Colonial ascidian (apricot)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Colonial ascidian (white *Clavelina*-like)	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0
	Colonial ascidian (white translucent)	0.0		0.0		0.0		0.0		0.1		0.0		0.0		0.0	
Bryozoan	Bryozoa hard branching (*Hornera robusta*-like)	0.0		0.0		0.0		0.0		0.0		0.1		0.1		0.0	
	Bryozoa hard fenestrate (*Celleporaria*-like)	0.0		0.0		0.0		0.0		0.0		0.0		0.3		0.2	
	Bryozoa hard fenestrate (lace)	0.1	0.2	0.0	0.6	0.0	0.0	0.0	0.0	0.0	0.4	0.7	1.2	0.5	1.0	0.1	0.3
	Bryozoa soft foliaceous (fluffy beige)	0.0		0.2		0.0		0.0		0.2		0.1		0.0		0.0	
	Bryozoa soft foliaceous (orange)	0.0		0.3		0.0		0.0		0.2		0.4		0.1		0.1	

	Site name	Dart Bank		Betsey West		Crayfish Rock		Horseshoe Reef		Variety Reef		North Bruny		Cape Queen Elizabeth		Adventure Bay	
Functional group	**Site abbreviation**	**DB**	**FG%**	**BW**	**FG%**	**CR**	**FG%**	**HR**	**FG%**	**VR**	**FG%**	**NB**	**FG%**	**CQE**	**FG%**	**AB**	**FG%**
Cnidarian	Blue soft coral	0.0		0.0		0.0		0.0		0.4		0.2		0.0		0.0	
	Bramble coral (*Acabaria* sp.)	0.0		0.0		0.0		0.0		0.0		0.1		0.0		0.1	
	Bramble coral (*Asperaxis karenae*)	0.0		0.0		0.2		0.0		0.0		0.0		0.1		0.0	
	Colonial zoanthids	2.1		0.0		0.4		0.2		0.1		0.2		0.1		0.0	
	Erythropodium hicksoni	0.9		0.7		0.0		0.2		0.0		0.0		0.0		0.0	
	Pale orange gorgonian	0.0	4.4	0.0	0.7	0.0	4.3	0.0	1.7	0.0	2.1	0.0	3.2	0.0	2.1	0.0	0.9
	Pink gorgonian	0.0		0.0		0.0		0.0		0.8		0.0		0.0		0.1	
	Pink gorgonian (*Pteronisis*-like)	0.8		0.0		0.0		0.6		0.0		0.1		0.2		0.0	
	Primnoella australasiae	0.0		0.0		0.2		0.0		0.0		0.0		0.0		0.0	
	Red gorgonian (*Pteronisis*-like)	0.5		0.0		3.6		0.7		0.6		2.5		1.7		0.7	
	Soft coral (*Capnella*-like)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
Echinoderm	*Cenolia trichoptera*	3.3	3.3	0.3	0.3	0.1	0.1	0.3	0.3	0.0	0.0	0.2	0.2	0.1	0.1	0.0	0.0
Gastropod	Gastropod (unidentified volute)	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Macroalgae - brown	Erect coarse-branching brown algae	0.0		0.0		0.0		0.1		0.2		0.0		0.0		0.0	
	Lobophora spp.	0.0	0.1	0.0	0.0	0.0	0.1	0.0	2.9	0.1	0.4	0.1	0.2	0.0	0.0	0.0	0.0
	Membranous brown algae	0.1		0.0		0.1		2.8		0.2		0.1		0.0		0.0	
Macroalgae - green	*Caulerpa* spp.	10.8	10.8	14.2	14.3	0.0	0.0	0.0	0.0	4.2	4.2	0.0	0.0	0.0	0.0	0.0	0.0
	Ulva spp.	0.0		0.1		0.0		0.0		0.0		0.0		0.0		0.0	
Macroalgae - red	Encrusting red algae	0.8		1.5		0.0		0.4		1.9		2.6		1.6		0.8	
	Foliose red algae	37.0		52.5		11.0		29.8		30.8		4.5		0.1		0.1	
	Laminate red algae	0.0		0.1		0.0		0.0		0.0		0.0		0.0		0.0	
	Membranous red algae	5.9	44.2	0.0	57.8	0.8	11.8	5.3	36.3	0.1	34.8	5.8	14.9	3.7	7.8	0.7	2.9
	Sonderopelta spp. / *Peyssonnelia* spp. (encrusting)	0.4		1.5		0.0		0.3		1.4		1.5		1.3		1.0	
	Sonderopelta spp. / *Peyssonnelia* spp. (laminate)	0.1		2.2		0.1		0.4		0.5		0.6		1.1		0.2	
	Thamnoclonium dichotomum	0.0		0.0		0.0		0.0		0.0		0.0		0.1		0.0	
Matrix	Bryozoa/Cnidaria matrix	10.6		0.6		44.3		27.8		30.4		44.0		48.8		40.0	
	Bryozoa/Cnidaria/creeping sponge matrix	0.0		0.0		1.4		0.1		0.1		0.1		0.1		0.0	
	Bryozoa/Cnidaria/encrusting sponge matrix	2.0	25.3	0.5	15.1	3.8	59.1	2.4	43.0	4.9	45.1	3.4	61.2	5.0	66.4	6.2	56.7
	Bryozoa/Cnidaria/sponge matrix	0.0		5.0		0.0		0.0		0.9		0.0		0.0		1.1	
	Encrusting/turfing algal matrix	10.8		0.5		9.5		12.8		6.5		13.7		12.5		9.3	

	Site name	Dart Bank		Betsey West		Crayfish Rock		Horseshoe Reef		Variety Reef		North Bruny		Cape Queen Elizabeth		Adventure Bay	
Functional group	**Site abbreviation**	**DB**	**FG%**	**BW**	**FG%**	**CR**	**FG%**	**HR**	**FG%**	**VR**	**FG%**	**NB**	**FG%**	**CQE**	**FG%**	**AB**	**FG%**
Matrix	Turf/sediment/silt matrix	1.8		8.6		0.0		0.0		2.2		0.0		0.0		0.0	
Sponge - barrel	Black barrel sponge	0.0		0.0		0.0		0.0		0.0		0.0		0.1		0.0	
	Brown barrel sponge	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.1	0.0	0.1	0.0	0.0
	Pink barrel sponge (lumpy)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Yellow barrel sponge (thick)	0.0		0.0		0.0		0.0		0.0		0.1		0.0		0.0	
Sponge - chimney	Grey chimney sponge (rough, small oscula)	0.0		0.0		0.0		0.0		0.1		0.0		0.0		0.0	
	White chimney sponge (round)	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0
	Yellow chimney sponge (rough)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
Sponge - creeping	Brown creeping ramose sponge	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Cream creeping ramose sponge	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Grey creeping ramose sponge (shapeless)	0.0		0.0		0.1		0.0		0.0		0.0		0.1		0.0	
	Orange creeping ramose sponge	0.0	0.2	0.0	0.0	0.2	1.1	0.0	0.3	0.0	0.1	0.0	0.2	0.0	0.2	0.0	0.1
	Purple creeping ramose sponge	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	White creeping ramose sponge (fat)	0.2		0.0		0.8		0.2		0.0		0.0		0.1		0.0	
	White creeping ramose sponge (shapeless)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Yellow creeping ramose sponge	0.0		0.0		0.1		0.0		0.0		0.1		0.0		0.1	
Sponge - cup	Beige cup sponge (shallow, irregular)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Beige cup sponge (thick)	0.0		0.1		0.0		0.0		0.0		0.0		0.0		0.0	
	Black cup sponge (smooth)	0.0		0.0		0.1		0.0		0.0		0.2		0.5		0.2	
	Blue cup sponge	0.0		0.0		0.0		0.1		0.0		0.1		0.0		0.0	
	Blue cup sponge (thick)	0.0		0.1		0.0		0.0		0.0		0.0		0.0		0.0	
	Light pink cup sponge (flat, thick)	0.1		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Pink cup sponge (thick)	0.1	0.5	0.1	0.4	0.0	0.2	0.0	2.2	0.0	1.4	0.0	1.1	0.0	1.2	0.0	0.6
	Red cup sponge	0.0		0.0		0.0		0.0		0.2		0.0		0.0		0.0	
	Red cup sponge (smooth)	0.2		0.0		0.2		2.1		1.2		0.7		0.6		0.2	
	Red cup sponge (thick)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	White cup sponge	0.0		0.1		0.0		0.0		0.0		0.0		0.0		0.0	
	White cup sponge (frilly)	0.0		0.0		0.0		0.1		0.0		0.0		0.0		0.0	
	Yellow cup sponge	0.0		0.0		0.0		0.0		0.0		0.0		0.1		0.1	
	Yellow cup sponge (thick)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	

	Site name	Dart Bank		Betsey West		Crayfish Rock		Horseshoe Reef		Variety Reef		North Bruny		Cape Queen Elizabeth		Adventure Bay	
Functional group	**Site abbreviation**	**DB**	**FG%**	**BW**	**FG%**	**CR**	**FG%**	**HR**	**FG%**	**VR**	**FG%**	**NB**	**FG%**	**CQE**	**FG%**	**AB**	**FG%**
Sponge - encrusting	Beige encrusting sponge (oscula)	0.0	0.9	0.0	1.6	0.0	0.0	0.0	0.6	0.0	1.2	0.0	1.4	0.0	1.6	0.1	3.2
	Beige encrusting sponge (smooth)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.1	
	Black encrusting sponge	0.0		0.0		0.0		0.0		0.0		0.0		0.1		0.1	
	Black encrusting sponge (papillate)	0.0		0.0		0.0		0.1		0.0		0.0		0.0		0.0	
	Black encrusting sponge (thick)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Blue encrusting sponge	0.0		0.0		0.0		0.0		0.2		0.1		0.0		0.0	
	Brown encrusting sponge	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Green encrusting sponge	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Grey encrusting sponge (rugose)	0.0		0.0		0.0		0.1		0.0		0.0		0.0		0.0	
	Grey encrusting sponge (smooth)	0.0		0.0		0.0		0.0		0.0		0.0		0.1		0.0	
	Light orange encrusting sponge	0.0		0.1		0.0		0.1		0.1		0.2		0.2		0.7	
	Orange beige encrusting sponge	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.1	
	Orange encrusting sponge	0.2		0.2		0.0		0.0		0.2		0.5		0.5		0.6	
	Orange encrusting sponge (lumpy)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.1	
	Pink white encrusting sponge (papillate)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	White encrusting sponge	0.0		0.2		0.0		0.0		0.0		0.0		0.2		0.0	
	White encrusting sponge (granular)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	White encrusting sponge (lumpy)	0.3		0.8		0.0		0.1		0.5		0.2		0.3		0.6	
	Yellow encrusting sponge (rough)	0.1		0.1		0.0		0.0		0.0		0.0		0.0		0.0	
	Yellow encrusting sponge (smooth)	0.0		0.1		0.0		0.0		0.0		0.2		0.2		0.5	
	Yellow encrusting sponge (thick)	0.1		0.0		0.0		0.0		0.0		0.0		0.0		0.2	
	Yellow orange encrusting sponge (thick)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
Sponge - erect branching	Beige erect branching sponge (fine)	0.0	1.5	0.0	0.4	0.0	3.8	0.0	1.0	0.0	1.6	0.0	1.9	0.0	1.0	0.0	0.7
	Beige erect branching sponge (spindles)	0.1		0.0		0.3		0.1		0.1		0.0		0.0		0.1	
	Beige erect branching sponge (stumpy)	0.1		0.0		0.0		0.0		0.1		0.2		0.1		0.0	
	Cream erect branching sponge	0.0		0.0		0.0		0.0		0.0		0.1		0.0		0.0	
	Cream erect branching sponge (thick)	0.1		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Grey arborescent sponge	0.9		0.0		1.8		0.1		0.2		0.3		0.1		0.0	
	Grey arborescent sponge (stumpy)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Grey erect branching sponge (fine)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	

	Site name	Dart Bank		Betsey West		Crayfish Rock		Horseshoe Reef		Variety Reef		North Bruny		Cape Queen Elizabeth		Adventure Bay	
Functional group	**Site abbreviation**	**DB**	**FG%**	**BW**	**FG%**	**CR**	**FG%**	**HR**	**FG%**	**VR**	**FG%**	**NB**	**FG%**	**CQE**	**FG%**	**AB**	**FG%**
Sponge - erect branching	Grey erect branching sponge (ramose)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Grey erect branching sponge (stumpy)	0.0		0.0		0.3		0.0		0.2		0.0		0.1		0.0	
	Grey erect branching sponge (thorny)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Orange arborescent sponge	0.0		0.0		0.5		0.0		0.0		0.2		0.2		0.1	
	Orange arborescent sponge (thin)	0.0		0.0		0.0		0.0		0.0		0.0		0.1		0.0	
	Orange brown arborescent sponge (fingers)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Orange erect branching sponge (finger)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Orange erect branching sponge (lumpy)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Purple arborescent sponge	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Purple arborescent sponge (irregular)	0.0		0.0		0.2		0.0		0.0		0.0		0.0		0.0	
	Purple arborescent sponge (thin)	0.0		0.0		0.1		0.0		0.0		0.0		0.0		0.0	
	Purple erect branching sponge (prostrate)	0.0		0.0		0.0		0.2		0.3		0.9		0.1		0.2	
	Purple erect branching sponge (ramose)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Purple erect branching sponge (stumps)	0.0	1.5	0.0	0.4	0.1	3.8	0.0	1.0	0.0	1.6	0.0	1.9	0.0	1.0	0.0	0.7
	Purple erect branching sponge (stumpy)	0.0		0.0		0.2		0.0		0.2		0.0		0.0		0.2	
	White arborescent sponge	0.1		0.1		0.2		0.0		0.1		0.0		0.0		0.0	
	White arborescent sponge (short)	0.0		0.1		0.1		0.2		0.2		0.0		0.1		0.1	
	White erect branching sponge (fine)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	White erect branching sponge (pointed)	0.0		0.0		0.2		0.0		0.0		0.0		0.0		0.0	
	White erect branching sponge (stubby)	0.1		0.0		0.0		0.0		0.1		0.0		0.0		0.0	
	White erect branching sponge (thorny lumps)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Yellow arborescent sponge	0.0		0.0		0.0		0.1		0.0		0.0		0.0		0.0	
	Yellow arborescent sponge (flat)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Yellow erect branching sponge (french fries)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Yellow erect branching sponge (stumpy)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Yellow erect branching sponge (thick, pointed)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Yellow erect branching sponge (thorny)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
Sponge - erect fan	Blue erect fan sponge (thick)	0.0		0.0		0.1		0.0		0.0		0.0		0.0		0.0	
	Brown erect fan sponge (thin blade)	0.0	0.1	0.0	0.2	0.1	0.5	0.0	0.1	0.0	0.6	0.0	0.3	0.0	0.2	0.0	0.1
	Brown erect fan sponge (thin)	0.0		0.0		0.2		0.0		0.1		0.0		0.0		0.0	

	Site name	Dart Bank		Betsey West		Crayfish Rock		Horseshoe Reef		Variety Reef		North Bruny		Cape Queen Elizabeth		Adventure Bay	
Functional group	**Site abbreviation**	**DB**	**FG%**	**BW**	**FG%**	**CR**	**FG%**	**HR**	**FG%**	**VR**	**FG%**	**NB**	**FG%**	**CQE**	**FG%**	**AB**	**FG%**
Sponge - erect fan	Cream erect fan sponge	0.0		0.0		0.1		0.0		0.0		0.0		0.0		0.0	
	Light pink erect fan sponge (lumpy)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Orange erect fan sponge (flat)	0.0		0.0		0.0		0.0		0.1		0.0		0.0		0.0	
	Orange erect fan sponge (thick)	0.0		0.0		0.0		0.0		0.0		0.0		0.1		0.0	
	Orange erect fan sponge (thorny)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Pink erect fan sponge (thick)	0.0	0.1	0.0	0.2	0.0	0.5	0.0	0.1	0.1	0.6	0.0	0.3	0.0	0.2	0.0	0.1
	White erect fan sponge (frilly)	0.0		0.0		0.0		0.0		0.1		0.0		0.0		0.0	
	White erect fan sponge (thick)	0.0		0.0		0.1		0.0		0.1		0.2		0.0		0.0	
	White erect fan sponge (thin)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Yellow erect fan sponge	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Yellow erect fan sponge (thick)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
Sponge - erect palmate	Grey erect palmate sponge	0.4		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Orange erect arborescent fan sponge	0.0		0.1		0.0		0.0		0.0		0.0		0.0		0.1	
	Orange erect arborescent fan sponge (flat)	0.0	0.4	0.0	0.1	0.2	0.2	0.0	0.0	0.0	0.0	0.1	0.2	0.0	0.1	0.0	0.4
	Orange erect palmate sponge (flat, pronghorn)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.1	
	Orange erect palmate sponge (simple)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
Sponge - fan	Orange fan sponge (frilly)	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.0	0.0	0.0	0.1
	Pink fan sponge	0.1		0.0		0.0		0.0		0.0		0.2		0.0		0.0	
Sponge - laminar	Apricot laminar sponge (stalked)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Grey laminar sponge (fungi)	0.1		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Grey laminar sponge (rough)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Grey laminar sponge (thin, folded)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Orange laminar sponge (irregular)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Orange laminar sponge (surface pores)	0.0	0.2	0.0	0.0	0.0	0.1	0.0	0.2	0.0	0.2	0.0	0.0	0.0	0.2	0.0	0.1
	Peach laminar sponge (irregular)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	White laminar sponge (irregular)	0.1		0.0		0.1		0.1		0.0		0.0		0.1		0.0	
	White laminar sponge (small)	0.0		0.0		0.0		0.0		0.1		0.0		0.0		0.0	
	Yellow laminar sponge (fine)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Yellow laminar sponge (foam)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Yellow laminar sponge (irregular)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	

Functional group	Site name / Site abbreviation	Dart Bank DB	Dart Bank FG%	Betsey West BW	Betsey West FG%	Crayfish Rock CR	Crayfish Rock FG%	Horseshoe Reef HR	Horseshoe Reef FG%	Variety Reef VR	Variety Reef FG%	North Bruny NB	North Bruny FG%	Cape Queen Elizabeth CQE	Cape Queen Elizabeth FG%	Adventure Bay AB	Adventure Bay FG%
Sponge - massive ball	Black ball sponge (papillate)	0.0	0.1	0.0	0.1	0.0	0.2	0.0	0.1	0.0	0.0	0.0	0.1	0.0	0.2	0.0	0.0
	Yellow ball sponge (knobby)	0.0		0.0		0.0		0.1		0.0		0.0		0.1		0.0	
	Yellow ball sponge (papillate, irregular)	0.0		0.0		0.2		0.0		0.0		0.0		0.0		0.0	
	Yellow ball sponge (smooth)	0.0		0.0		0.0		0.0		0.0		0.1		0.1		0.0	
Sponge - massive cryptic	White massive cryptic sponge (spiky)	0.0	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Sponge - massive globular	Blue globular sponge	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1
	Orange globular sponge	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Orange globular sponge (Tethya-like)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Pink globular sponge (Tethya-like)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
Sponge - massive simple	Beige massive simple sponge (brain)	0.0	3.0	0.0	1.5	0.0	2.4	0.0	0.6	0.0	1.5	0.0	1.5	0.0	1.7	0.0	1.1
	Beige massive simple sponge (honeycomb)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Beige massive simple sponge (laminar-like)	0.0		0.0		0.1		0.0		0.0		0.0		0.0		0.0	
	Beige massive simple sponge (lumpy)	0.1		0.1		0.0		0.0		0.0		0.0		0.1		0.1	
	Beige massive simple sponge (lumpy, shapeless)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Beige massive simple sponge (shapeless)	0.1		0.1		0.1		0.0		0.1		0.1		0.1		0.1	
	Beige massive simple sponge (small)	0.0		0.0		0.0		0.1		0.2		0.1		0.1		0.0	
	Black massive simple sponge (oscula, papillate)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Black massive simple sponge (smooth)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Blue massive simple sponge (lumpy)	0.1		0.0		0.1		0.0		0.0		0.1		0.0		0.0	
	Blue massive simple sponge (shapeless)	0.2		0.3		0.0		0.0		0.1		0.0		0.1		0.0	
	Cream massive simple sponge (papillate)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Dark grey massive simple sponge	0.0		0.0		0.1		0.0		0.0		0.0		0.0		0.0	
	Grey massive simple sponge (brain)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Grey massive simple sponge (creep)	0.2		0.0		0.2		0.0		0.0		0.0		0.3		0.1	
	Grey massive simple sponge (laminar-like)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.1	
	Grey massive simple sponge (smooth globes)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Massive simple sponge (shapeless)	0.1		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Massive simple sponge (unidentifiable)	0.0		0.1		0.0		0.0		0.0		0.0		0.0		0.0	
	Orange massive simple sponge (holey)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	

	Site name	Dart Bank		Betsey West		Crayfish Rock		Horseshoe Reef		Variety Reef		North Bruny		Cape Queen Elizabeth		Adventure Bay	
Functional group	**Site abbreviation**	**DB**	**FG%**	**BW**	**FG%**	**CR**	**FG%**	**HR**	**FG%**	**VR**	**FG%**	**NB**	**FG%**	**CQE**	**FG%**	**AB**	**FG%**
Sponge - massive simple	Orange massive simple sponge (lumpy)	0.1		0.0		0.0		0.0		0.0		0.1		0.1		0.0	
	Orange massive simple sponge (rough)	0.1		0.1		0.0		0.0		0.0		0.0		0.0		0.0	
	Orange massive simple sponge (smooth)	0.0		0.0		0.0		0.0		0.0		0.1		0.0		0.1	
	Pink massive simple sponge	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Pink massive simple sponge (irregular)	0.1		0.1		0.1		0.0		0.0		0.0		0.1		0.0	
	Pink massive simple sponge (oscula)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Purple massive simple sponge	0.1		0.0		0.1		0.0		0.0		0.0		0.1		0.1	
	Purple massive simple sponge (irregular)	0.0		0.1		0.0		0.0		0.0		0.0		0.1		0.0	
	Purple massive simple sponge (laminar, oscula)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Purple massive simple sponge (shapeless)	0.0		0.0		0.1		0.0		0.0		0.1		0.0		0.0	
	Red massive simple sponge	0.1		0.1		0.0		0.0		0.1		0.1		0.0		0.0	
	Red massive simple sponge (irregular)	0.0		0.0		0.0		0.0		0.0		0.1		0.0		0.0	
	Red/white massive simple sponge (shapeless)	0.0		0.0		0.0		0.0		0.0		0.1		0.0		0.0	
	Velvet massive simple sponge	0.0		0.0		0.0		0.0		0.0		0.0		0.1		0.0	
	White massive simple sponge	0.0	3.0	0.0	1.5	0.0	2.4	0.0	0.6	0.0	1.5	0.0	1.5	0.0	1.7	0.0	1.1
	White massive simple sponge (holey)	0.0		0.0		0.1		0.0		0.0		0.0		0.0		0.0	
	White massive simple sponge (labyrinth)	0.0		0.0		0.1		0.0		0.0		0.0		0.0		0.0	
	White massive simple sponge (lumpy)	0.4		0.0		0.4		0.1		0.1		0.0		0.1		0.1	
	White massive simple sponge (papillate)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	White massive simple sponge (rough)	0.0		0.1		0.1		0.0		0.0		0.0		0.0		0.1	
	White massive simple sponge (shapeless)	0.6		0.1		0.6		0.3		0.5		0.2		0.4		0.1	
	Yellow massive simple sponge (frilly)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Yellow massive simple sponge (holey)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Yellow massive simple sponge (irregular ball)	0.0		0.0		0.1		0.0		0.0		0.0		0.0		0.1	
	Yellow massive simple sponge (knobby)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Yellow massive simple sponge (lumpy wave)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Yellow massive simple sponge (lumpy)	0.2		0.2		0.3		0.0		0.0		0.0		0.0		0.1	
	Yellow massive simple sponge (papillate)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	Yellow massive simple sponge (shapeless)	0.0		0.0		0.0		0.0		0.0		0.1		0.0		0.1	
	Yellow massive simple sponge (shapeless, smooth)	0.3		0.0		0.1		0.0		0.0		0.2		0.0		0.1	

Functional group	Site name / Site abbreviation	Dart Bank DB	FG%	Betsey West BW	FG%	Crayfish Rock CR	FG%	Horseshoe Reef HR	FG%	Variety Reef VR	FG%	North Bruny NB	FG%	Cape Queen Elizabeth CQE	FG%	Adventure Bay AB	FG%
Sponge - stalked	White stalked sponge (lumpy)	0.0	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Sponge - tube	Beige tube sponge (prostrate)	0.0		0.1		0.0		0.0		0.0		0.0		0.0		0.0	
	White tube sponge (thorny)	0.0		0.0		0.1		0.0		0.0		0.0		0.0		0.0	
	Orange tube sponge (white tips)	0.0	0.0	0.0	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.1
	White tube sponge (cluster)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	White tube sponge (colony)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
	White tube sponge (large oscula)	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
Sponge - tubular	Blue tubular sponge	0.0	0.1	0.0	0.0	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Pink tubular sponge	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
Substrate - unconsolidated	Coarse sand	1.4		5.5		2.6		2.3		4.9		0.2		4.6		10.9	
	Fine sand	2.9		0.1		13.0		8.2		0.7		11.7		11.1		20.9	
	Gravel	0.0	4.2	1.0	6.6	0.0	15.7	0.0	10.5	0.0	5.6	0.0	12.0	0.4	16.1	0.3	32.9
	Pebbles	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.8	
	Silt	0.0		0.0		0.0		0.0		0.0		0.0		0.0		0.0	
Taxa diversity (includes all categories)		**93**	**-**	**77**	**-**	**60**	**-**	**61**	**-**	**89**	**-**	**91**	**-**	**107**	**-**	**102**	-

Appendix 6-2: Diversity metrics for deep reef fish and benthic community data

Key diversity metrics for the fish community data across the Storm Bay deep reef sites.

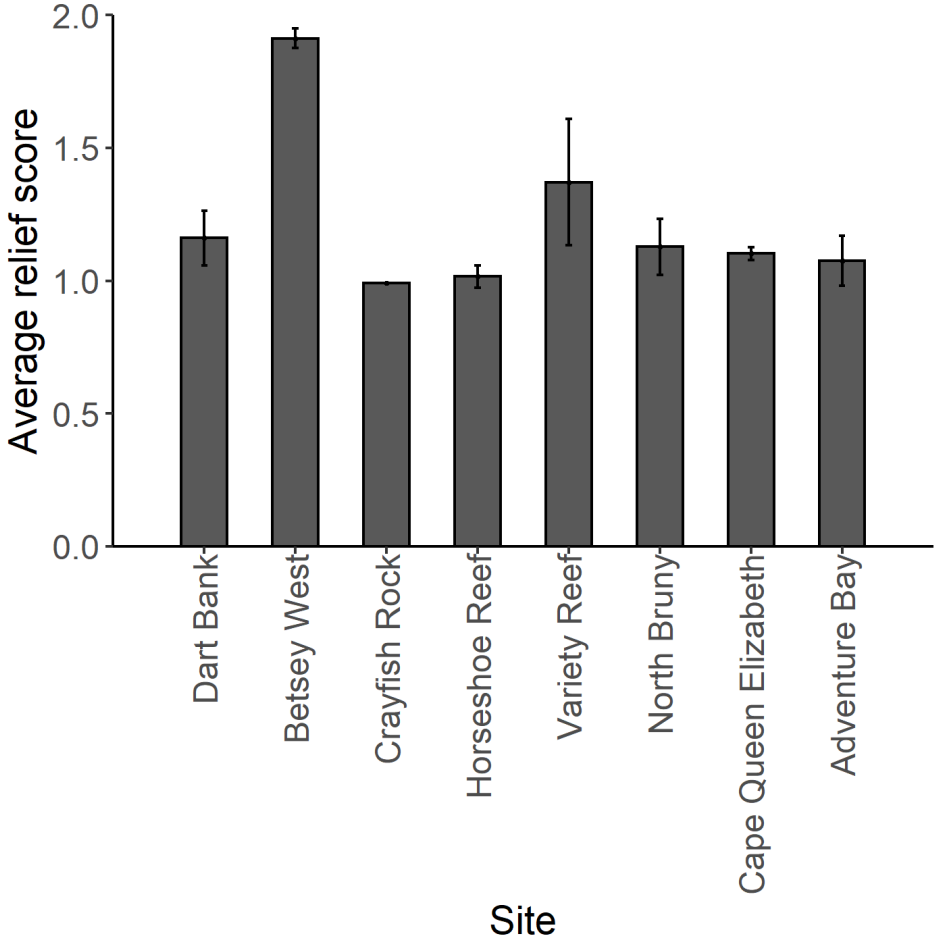
Site	Average species richness	Average Shannon diversity	Alpha diversity	Gamma diversity	Beta diversity
Dart Bank	12	0.74	12.0	35	1.92
Betsey West	13	1.19	12.0	35	1.80
Crayfish Rock	13	1.36	13.0	35	1.69
Horseshoe Reef	14	1.02	14.0	35	1.50
Variety Reef	10	0.78	10.0	35	2.50
North Bruny	14	1.09	14.4	35	1.43
Cape Queen Elizabeth	12	0.83	12.0	35	1.92
Adventure Bay	9	0.35	8.75	35	3.00

Key diversity metrics for the benthic community data across the Storm Bay deep reef sites.

Site	Average taxa richness	Average Shannon diversity	Alpha diversity	Gamma diversity	Beta diversity
Dart Bank	55.00	1.88	4.73	219	45.30
Betsey West	42.00	1.28	3.46	219	62.29
Crayfish Rock	54.00	2.46	3.40	219	63.41
Horseshoe Reef	37.00	1.54	3.73	219	57.71
Variety Reef	50.00	1.74	3.66	219	58.84
North Bruny	56.50	2.93	4.08	219	52.68
Cape Queen Elizabeth	53.33	3.14	3.08	219	70.09
Adventure Bay	44.67	3.29	2.14	219	101.34

Appendix 6-3: Relief scores for deep reef transects

Average relief scores across transects for each deep reef site. A relief score was assigned to each of the 25 points scored per image, and averages were taken across points, images and transects within sites. The scoring system is as follows: 0 = Flat substrate, sandy, rubble with few features, ~0 substrate slope; 1 = Some relief features amongst mostly flat substrate/sand/rubble, <45 degree substrate slope; 2 = Mostly relief features amongst some flat substrate or rubble, ~45 substrate slope; 3 = Good relief structure with some overhangs, >45 substrate slope; 4 = High structural complexity, fissures and caves, vertical wall, ~90 substrate slope; 5 = Exceptional structural complexity, numerous large holes and caves, vertical wall, ~90 substrate slope.



Appendix 7-1: Summary tables from seagrass photo-quadrats

Average percentage cover per transect for seagrass, algae and faunal categories scored >0 at Adventure Bay for all surveys between November 2020 and November 2021.

	Nov-19			Nov-20					Mar-21				
Category	**AB1**	**AB2**	**AB3**	**AB1**	**AB2**	**AB3**	**AB4**	**AB5**	**AB1**	**AB2**	**AB3**	**AB4**	**AB5**
Zostera spp.	73.8	63.1	63.1	33.0	32.5	54.2	51.0	4.0	37.5	50.0	56.4	46.8	13.3
Filamentous brown	28.1	44.5	69.6	72.0	41.3	62.7	29.8	32.2	53.0	48.0	62.0	50.4	74.7
Filamentous green	45.4	24.8	1.6	0.6	0.3	0.0	0.3	0.0	0.0	0.0	0.0	0.0	0.0
Filamentous red	0.0	0.2	0.0	3.0	0.0	0.0	0.5	1.2	0.0	1.0	0.4	0.0	0.0
Epiphytic brown	0.0	0.0	0.0	0.0	0.0	0.2	0.0	11.5	0.0	0.0	0.0	0.0	0.0
Epiphytic green	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0
Epiphytic red	1.9	3.2	0.7	1.1	5.7	1.1	0.1	11.2	1.5	0.0	0.8	0.0	0.0
Chaetomorpha billardierii	1.5	2.5	2.9	6.9	6.5	7.1	1.2	1.7	0.0	2.5	0.0	0.0	0.0
Ulva/Enteromorpha	0.4	0.0	0.0	0.8	2.5	0.0	0.0	1.7	0.0	0.0	0.0	0.0	0.0
Epiphytic foliose	1.9	3.2	0.7	1.1	5.7	1.3	0.2	22.8	1.5	0.0	0.8	0.0	0.0
Caulerpa brownii	0.0	0.0	0.0	0.0	3.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0
Caulerpa scalpelliformis	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Caulerpa trifaria	0.7	4.6	0.7	0.4	0.0	6.2	0.0	3.8	0.0	0.0	0.0	0.0	0.0
Caulerpa spp.	0.0	0.0	0.0	0.5	0.0	0.9	0.0	0.2	3.0	0.0	0.0	0.8	8.0
Brown wrack algae	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0
Red wrack algae	0.0	0.2	0.0	0.0	0.0	0.0	0.0	1.4	0.0	0.0	0.0	0.0	0.0
Brown algae	0.0	0.0	0.0	0.0	0.0	0.0	2.1	0.0	0.0	0.0	0.0	0.0	0.0
Green algae	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.0	0.0	0.0	0.0
Red algae	1.3	0.6	0.0	0.0	0.0	0.0	2.4	0.0	0.0	0.0	0.0	0.0	0.0
Dead algae	0.0	0.0	0.0	0.0	0.0	0.0	1.6	0.8	0.0	0.0	0.0	0.0	0.0
Sand	4.2	6.9	4.5	8.6	12.2	3.6	22.3	38.6	23.5	15.0	5.6	18.4	24.7
Shell grit	0.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Encrusting sponge	0.4	0.0	0.0	0.3	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0
Free standing sponge	1.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.0	0.0	0.0	0.0
Phasianella australis	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Angasi oysters	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0
Commercial scallop	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Total filamentous	**73.5**	**69.5**	**71.2**	**75.6**	**41.7**	**62.7**	**30.6**	**33.4**	**53.0**	**49.0**	**62.4**	**50.4**	**74.7**
Total *Caulerpa* spp.	**0.7**	**4.6**	**0.7**	**1.0**	**3.0**	**7.1**	**1.0**	**4.0**	**3.0**	**0.0**	**0.0**	**0.8**	**8.0**
Total wrack	**0.0**	**0.2**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**1.4**	**0.0**	**1.0**	**0.0**	**0.0**	**0.0**
Total substrate	**4.6**	**6.9**	**4.5**	**8.6**	**12.2**	**3.6**	**22.3**	**38.6**	**23.5**	**15.0**	**5.6**	**18.4**	**24.7**

Average percentage cover per transect for seagrass, algae and faunal categories scored >0 at Adventure Bay for all surveys between November 2020 and November 2021 (continued).

	June-21					Sept-21					Nov-21				
Category	**AB1**	**AB2**	**AB3**	**AB4**	**AB5**	**AB1**	**AB2**	**AB3**	**AB4**	**AB5**	**AB1**	**AB2**	**AB3**	**AB4**	**AB5**
Zostera spp.	63.6	79.2	71.6	60.8	1.2	63.3	88.7	44.8	22.0	0.0	69.5	52.0	58.5	32.7	0.6
Filamentous brown	2.8	0.8	5.2	0.0	0.0	0.0	0.0	0.0	4.0	0.0	1.7	0.7	30.0	0.6	0.0
Filamentous green	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0
Filamentous red	11.2	0.0	9.2	3.2	0.0	12.7	12.0	6.4	28.3	10.3	20.3	20.8	1.5	35.0	16.8
Epiphytic brown	0.0	0.4	1.2	0.0	0.0	0.0	4.7	0.0	0.0	0.0	0.0	0.2	0.3	0.0	0.0
Epiphytic green	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Epiphytic red	0.0	7.2	0.0	0.4	0.0	0.7	4.0	9.2	0.0	0.0	0.2	12.2	10.8	0.1	0.5
Chaetomorpha billardierii	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.2	1.5	0.0	0.0
Ulva/Enteromorpha	0.0	0.0	0.0	0.0	0.0	0.7	2.0	4.0	0.3	0.0	0.0	0.2	0.0	0.0	0.0
Epiphytic foliose	0.0	7.6	1.2	0.4	0.0	0.7	8.7	9.2	0.0	0.0	0.2	12.3	11.0	0.1	0.5
Caulerpa brownii	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.7	0.3	0.0	0.0	0.0
Caulerpa scalpelliformis	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0
Caulerpa trifaria	0.0	0.0	2.4	0.0	0.0	14.0	3.3	11.6	4.3	2.7	6.0	15.3	13.3	11.2	5.5
Caulerpa spp.	0.0	0.0	0.0	2.0	4.0	0.0	0.0	0.0	0.7	1.7	0.5	0.5	0.3	2.4	0.2
Brown wrack algae	0.0	0.0	0.0	0.0	2.4	0.0	0.0	0.0	5.0	1.0	0.0	0.0	0.0	1.7	0.0
Red wrack algae	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	12.3	0.0	0.0	0.0	0.0	0.0	0.0
Brown algae	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Green algae	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Red algae	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Dead algae	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Sand	47.6	36.0	29.2	58.0	97.2	32.0	19.3	36.8	50.0	93.3	23.7	16.7	2.8	46.2	86.3
Shell grit	0.0	0.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.2	0.0	0.1	0.2
Encrusting sponge	0.0	0.0	0.0	0.0	0.0	0.7	0.0	0.0	0.0	0.0	0.8	0.2	0.5	0.0	0.0
Free standing sponge	1.2	0.0	0.0	0.0	0.0	0.7	0.7	0.4	0.0	0.0	0.5	0.0	0.0	0.1	0.0
Phasianella australis	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.2	0.0	0.1	0.0
Angasi oysters	0.0	0.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.0	0.0	0.0	0.3
Commercial scallop	0.0	0.0	0.0	0.0	0.0	0.7	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0
Total filamentous	**14.0**	**0.8**	**14.4**	**3.2**	**0.0**	**12.7**	**12.0**	**6.4**	**32.3**	**11.3**	**22.0**	**21.5**	**31.5**	**35.5**	**16.8**
Total *Caulerpa* spp.	**0.0**	**0.0**	**2.4**	**2.0**	**4.0**	**14.0**	**3.3**	**11.6**	**5.0**	**4.3**	**7.2**	**16.2**	**13.8**	**13.6**	**5.7**
Total wrack	**0.0**	**0.0**	**0.0**	**0.0**	**2.4**	**0.0**	**0.0**	**0.0**	**17.3**	**1.0**	**0.0**	**0.0**	**0.0**	**1.7**	**0.0**
Total substrate	**47.6**	**36.8**	**29.2**	**58.0**	**97.2**	**32.0**	**19.3**	**36.8**	**50.0**	**93.3**	**24.0**	**16.8**	**2.8**	**46.3**	**86.5**

Average percentage cover per transect for seagrass, algae and faunal categories scored >0 at Bull Bay for all surveys between November 2020 and November 2021.

	Nov-19					Nov-20					Mar-21				
Category	**BB1**	**BB2**	**BB3**	**BB4**	**BB5**	**BB1**	**BB2**	**BB3**	**BB4**	**BB5**	**BB1**	**BB2**	**BB3**	**BB4**	**BB5**
Zostera spp.	37.0	48.3	20.8	35.8	50.0	23.1	19.1	42.7	28.8	42.8	44.4	62.0	66.3	82.0	86.8
Filamentous brown	16.7	36.3	12.8	24.9	17.4	29.7	22.2	43.3	23.6	31.5	2.8	9.0	8.0	24.3	12.0
Filamentous green	0.0	1.3	2.8	0.7	0.6	0.0	0.2	2.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Epiphytic red	0.0	0.3	0.0	0.0	0.0	2.9	9.7	1.8	10.5	9.9	0.0	0.0	0.0	0.0	0.0
Epiphytic brown	8.0	0.0	6.8	0.0	6.3	0.7	2.1	2.7	1.1	0.7	0.0	0.0	0.0	0.0	0.0
Epiphytic green	1.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.0
Epiphytic red	11.3	1.0	18.8	10.2	3.7	0.0	3.0	0.1	2.9	0.1	0.0	0.0	0.0	0.0	0.0
Chaetomorpha billardierii	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.9	0.0	0.3	0.0	0.0	0.0	0.0	0.0
Chaetomorpha coliformis	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Ulva/Enteromorpha	0.0	1.0	0.0	0.0	0.0	1.1	0.1	0.1	0.0	0.5	0.0	0.0	0.0	0.3	0.0
Epiphytic foliose	21.0	1.0	25.6	10.2	10.0	0.7	5.1	2.8	4.0	0.8	0.0	0.0	0.0	0.3	0.0
Caulerpa scalpelliformis	0.0	0.0	0.0	0.0	0.0	0.0	2.4	0.2	0.0	0.8	0.0	0.0	0.3	0.0	0.0
Caulerpa spp.	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.7	0.0
Brown wrack algae	0.0	0.0	0.4	1.3	0.0	0.6	0.0	0.2	0.0	0.0	2.0	0.0	0.0	0.0	0.4
Red wrack algae	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Brown algae	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.6	0.0	0.0	0.0	0.0	0.0
Red algae	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.9	1.9	0.0	0.0	0.0	0.0	0.0
Sand	2.3	25.3	32.0	39.6	30.3	64.9	44.2	37.7	36.8	39.7	82.8	44.7	50.7	28.3	17.2
Shell grit	42.0	2.0	8.8	0.9	5.4	0.0	0.4	0.0	0.3	1.9	0.0	0.0	0.0	0.0	0.0
Encrusting sponge	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Free standing sponge	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Maoricolpus roseus	0.0	0.0	0.0	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.0
Angasi oysters	0.7	0.0	0.8	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.8	0.7	0.3	0.3	0.0
Commercial scallop	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.0	0.0	0.0	0.3	0.0
Total filamentous	**16.7**	**38.0**	**15.6**	**25.6**	**18.0**	**32.6**	**32.1**	**47.3**	**34.1**	**41.4**	**2.8**	**9.0**	**8.0**	**24.3**	**12.0**
Total *Caulerpa* spp.	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**2.4**	**0.2**	**0.0**	**0.8**	**0.0**	**0.0**	**0.3**	**0.7**	**0.0**
Total wrack	**0.0**	**0.0**	**0.4**	**1.3**	**0.0**	**0.6**	**0.1**	**0.2**	**0.0**	**0.0**	**2.0**	**0.0**	**0.0**	**0.0**	**0.4**
Total substrate	**44.3**	**27.3**	**40.8**	**40.4**	**35.7**	**64.9**	**44.7**	**37.7**	**37.1**	**41.6**	**82.8**	**44.7**	**50.7**	**28.3**	**17.2**

Average percentage cover per transect for seagrass, algae and faunal categories scored >0 at Bull Bay for all surveys between November 2020 and November 2021 (continued).

	June-21					Sept-21					Nov-21				
Category	**BB1**	**BB2**	**BB3**	**BB4**	**BB5**	**BB1**	**BB2**	**BB3**	**BB4**	**BB5**	**BB1**	**BB2**	**BB3**	**BB4**	**BB5**
Zostera spp.	42.3	29.3	45.2	36.3	44.4	36.0	35.5	46.4	36.8	51.5	28.0	27.1	27.5	33.9	39.6
Filamentous brown	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.0	0.0
Filamentous green	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.0	0.0	0.0	0.0	0.0
Epiphytic red	3.7	11.0	19.6	16.9	6.4	18.5	40.0	34.4	52.4	16.0	11.0	15.8	18.7	16.9	6.4
Epiphytic brown	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	2.0
Epiphytic green	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Epiphytic red	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.8	0.0	16.5	6.5	3.1	11.1	3.2	10.1
Chaetomorpha billardierii	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Chaetomorpha coliformis	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.9
Ulva/Enteromorpha	0.0	0.0	0.0	0.0	0.0	0.5	0.0	1.6	0.0	1.5	0.8	0.1	0.5	0.2	2.8
Epiphytic foliose	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.8	0.0	17.5	6.5	3.1	11.1	3.2	12.1
Caulerpa scalpelliformis	0.3	3.0	1.2	0.0	0.8	0.5	2.0	0.0	0.0	2.0	0.0	2.1	0.2	0.2	0.8
Caulerpa spp.	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Brown wrack algae	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.8	0.0	0.0	0.3	0.0	0.0	0.0	0.0
Red wrack algae	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0
Brown algae	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Red algae	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Sand	79.0	87.3	66.0	77.4	75.6	67.5	59.5	44.4	54.8	33.5	69.8	70.2	71.1	70.5	61.4
Shell grit	0.0	0.0	0.0	0.3	0.0	0.0	0.0	0.8	0.4	0.0	0.8	0.3	0.5	0.6	0.2
Encrusting sponge	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0
Free standing sponge	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0
Maoricolpus roseus	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.4	0.2	0.0
Angasi oysters	0.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.2	0.0
Commercial scallop	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0
Total filamentous	**3.7**	**11.0**	**19.6**	**16.9**	**6.4**	**18.5**	**40.0**	**34.4**	**52.4**	**16.0**	**13.3**	**15.8**	**18.7**	**16.9**	**6.4**
Total *Caulerpa* spp.	**0.3**	**3.0**	**1.2**	**0.0**	**0.8**	**0.5**	**2.5**	**0.0**	**0.0**	**2.0**	**0.0**	**2.1**	**0.2**	**0.2**	**0.8**
Total wrack	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.8**	**0.0**	**0.0**	**0.4**	**0.0**	**0.0**	**0.0**	**0.0**
Total substrate	**79.0**	**87.3**	**66.0**	**77.7**	**75.6**	**67.5**	**59.5**	**45.2**	**55.2**	**33.5**	**70.5**	**70.6**	**71.5**	**71.1**	**61.6**

Average percentage cover per transect for seagrass, algae and faunal categories scored >0 at Sloping Island for all surveys between November 2020 and November 2021.

	Nov-20							Mar-21							June-21						
Category	**SI1**	**SI2**	**SI3**	**SI4**	**SI5**	**SI6**	**SI7**	**SI1**	**SI2**	**SI3**	**SI4**	**SI5**	**SI6**	**SI7**	**SI1**	**SI2**	**SI3**	**SI4**	**SI5**	**SI6**	**SI7**
Zostera spp.	20.7	42.3	32.0	15.7	20.6	16.0	23.3	10.0	40.0	9.0	33.0	23.0	20.0	49.0	26.5	62.0	32.0	42.5	16.5	54.5	50.5
Filamentous brown	67.7	54.7	26.0	70.3	28.0	35.3	39.7	96.0	84.0	45.0	66.0	0.0	36.0	31.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Filamentous green	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	30.0	0.0	0.0	0.0	0.0	0.0	0.0	3.5	0.0	0.0
Filamentous red	0.0	0.7	0.0	0.7	0.0	0.0	0.3	0.0	0.0	7.0	4.0	21.0	0.0	2.0	53.5	4.0	17.5	46.5	20.5	28.5	16.5
Epiphytic brown	3.0	0.0	5.0	0.0	8.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	6.5	0.0	4.5	0.0	0.0	0.0	0.0
Epiphytic green	1.0	1.0	0.0	0.0	0.0	1.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Epiphytic red	0.0	0.0	0.0	2.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Ulva/Enteromorpha	0.0	0.0	0.0	0.0	0.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Epiphytic foliose	4.0	1.0	5.0	2.7	8.3	1.7	0.0	0.0	0.0	0.0	0.0	2.0	0.0	0.0	6.5	0.0	4.5	0.0	0.0	0.0	0.0
Caulerpa simpliciuscula	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Sand	20.0	35.7	50.0	18.7	45.0	48.3	56.0	3.0	13.0	54.0	17.0	42.0	35.0	52.0	30.5	68.5	75.0	52.0	66.0	58.5	57.0
Shell grit	5.0	0.0	1.0	0.0	5.3	0.0	0.0	2.0	0.0	0.0	5.0	0.0	9.0	0.0	2.5	0.0	0.0	1.5	0.5	0.0	0.0
Encrusting sponge	0.0	0.0	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Free standing sponge	0.0	0.0	0.0	0.0	0.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.5
Total filamentous	**67.7**	**55.3**	**26.0**	**71.0**	**28.0**	**35.3**	**40.0**	**96.0**	**84.0**	**52.0**	**70.0**	**51.0**	**36.0**	**33.0**	**53.5**	**4.0**	**17.5**	**46.5**	**24.0**	**28.5**	**16.5**
Total *Caulerpa* spp.	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**
Total wrack	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**
Total substrate	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**

Average percentage cover per transect for seagrass, algae and faunal categories scored >0 at Sloping Island for all surveys between November 2020 and November 2021 (continued).

	Sept-21							Nov-21						
Category	**SI1**	**SI2**	**SI3**	**SI4**	**SI5**	**SI6**	**SI7**	**SI1**	**SI2**	**SI3**	**SI4**	**SI5**	**SI6**	**SI7**
Zostera spp.	15.0	37.5	10.5	35.0	11.5	24.5	18.5	19.0	36.0	28.0	42.5	7.5	30.5	29.5
Filamentous brown	0.0	0.0	0.0	0.0	0.0	0.0	0.0	55.0	67.5	20.5	56.0	23.5	25.0	32.0
Filamentous green	0.0	0.0	0.0	0.0	4.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Filamentous red	53.0	42.0	8.0	56.5	24.0	39.0	27.5	0.0	0.0	2.5	0.0	0.0	0.0	0.0
Epiphytic brown	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Epiphytic green	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Epiphytic red	0.0	0.0	2.0	0.0	0.0	2.5	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0
Ulva/Enteromorpha	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Epiphytic foliose	0.0	0.0	2.0	0.0	0.0	2.5	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0
Caulerpa simpliciuscula	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0
Sand	46.5	42.0	85.0	45.0	60.0	63.0	70.5	40.5	28.5	80.0	36.5	80.5	69.5	72.0
Shell grit	9.5	0.5	0.0	0.5	0.0	0.0	0.5	3.5	0.0	0.0	1.0	2.0	1.0	0.0
Encrusting sponge	0.0	0.0	0.0	0.0	0.5	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Free standing sponge	0.0	0.0	0.0	0.0	0.0	0.5	1.0	0.0	0.0	0.0	1.0	0.0	0.5	0.5
Total filamentous	**53.0**	**42.0**	**8.0**	**56.5**	**28.5**	**39.0**	**27.5**	**55.0**	**67.5**	**23.0**	**56.0**	**23.5**	**25.0**	**32.0**
Total *Caulerpa* spp.	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.5**	**0.0**	**0.0**
Total wrack	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**
Total substrate	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**

Average percentage cover per transect for seagrass, algae and faunal categories scored >0 at Wedge Bay for all surveys between November 2020 and November 2021. Note, no data was collected from transect WB1 in June 2021.

	Nov-20								Mar-21								June-21			
Category	**WB1**	**WB2**	**WB3**	**WB4**	**WB5**	**WB6**	**WB7**	**WB8**	**WB1**	**WB2**	**WB3**	**WB4**	**WB5**	**WB6**	**WB7**	**WB8**	**WB1**	**WB2**	**WB3**	**WB4**
Zostera spp.	0.7	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0
Halophila spp.	0.3	0.0	0.0	0.0	3.3	0.0	6.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0
Filamentous brown	11.7	14.7	37.3	42.3	31.3	4.0	23.0	58.7	0.0	0.0	37.0	44.0	26.0	0.0	2.0	17.0		0.0	0.0	0.0
Filamentous green	0.0	1.0	0.0	0.0	0.0	1.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0
Filamentous red	1.3	0.0	0.0	0.0	0.0	3.0	0.7	0.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	1.5	3.5
Epiphytic brown	0.0	0.0	1.0	0.0	7.7	0.0	0.0	0.0	0.0	0.0	2.0	0.0	8.0	0.0	5.0	0.0		0.0	0.0	0.0
Epiphytic green	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0
Epiphytic red	1.0	1.7	0.7	4.3	0.3	7.7	2.7	11.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	4.0		1.0	0.0	0.0
Chaetomorpha billardierii	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0
Ulva/Enteromorpha	0.0	0.0	0.0	0.0	2.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0
Epiphytic foliose	1.0	1.7	1.7	4.3	8.0	7.7	2.7	11.7	0.0	0.0	2.0	0.0	8.0	0.0	5.0	4.0		1.0	0.0	0.0
Caulerpa flexilis	0.0	0.0	0.0	0.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0
Caulerpa longifolia	16.0	16.3	0.0	10.7	0.0	2.0	2.0	0.0	0.0	14.0	0.0	0.0	2.0	13.0	0.0	0.0		52.5	0.0	0.0
Caulerpa simpliciuscula	0.0	0.0	4.7	31.7	1.7	0.0	0.0	0.0	0.0	0.0	4.0	17.0	0.0	0.0	0.0	0.0		0.0	22.5	5.0
Caulerpa trifaria	5.0	0.0	12.7	0.0	0.0	0.0	13.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	2.0	0.0
Caulerpa spp.	11.7	0.0	0.0	0.0	29.7	25.3	31.7	13.0	0.0	6.0	0.0	12.0	0.0	0.0	27.0	16.0		0.0	0.0	0.0
Brown wrack	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.0	0.7	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0
Green wrack	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.0	0.0		0.0	0.0	0.0
Sand	59.7	67.0	64.3	20.3	38.7	58.0	34.7	19.7	96.0	76.7	56.0	47.0	74.0	88.0	71.0	62.0		68.0	76.0	83.5
Shell grit	0.0	0.0	0.0	0.0	0.0	2.0	0.0	0.0	0.0	0.0	0.0	3.0	0.0	0.0	0.0	0.0		0.0	0.5	1.5
Encrusting sponge	0.0	0.0	0.0	0.7	0.0	0.0	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0
Free standing sponge	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.5
Maoricolpus roseus	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0
Angasi oysters	0.7	0.0	0.3	0.0	0.0	0.0	1.0	0.0	4.0	1.3	3.0	0.0	0.0	0.0	0.0	5.0		0.0	3.0	13.0
Commercial scallop	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0
Total filamentous	**13.0**	**15.7**	**37.3**	**42.3**	**31.3**	**8.3**	**23.7**	**59.3**	**0.0**	**0.0**	**37.0**	**44.0**	**26.0**	**0.0**	**2.0**	**17.0**		**0.0**	**1.5**	**3.5**
Total *Caulerpa* spp.	**32.7**	**16.3**	**17.3**	**43.0**	**31.3**	**27.3**	**46.7**	**13.0**	**0.0**	**20.0**	**4.0**	**29.0**	**2.0**	**13.0**	**27.0**	**16.0**		**52.5**	**24.5**	**5.0**
Total wrack	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**2.0**	**0.7**	**0.0**	**0.0**	**0.0**	**0.0**	**2.0**	**0.0**		**0.0**	**0.0**	**0.0**
Total substrate	**59.7**	**67.0**	**64.3**	**20.3**	**38.7**	**60.0**	**34.7**	**19.7**	**96.0**	**76.7**	**56.0**	**50.0**	**74.0**	**88.0**	**71.0**	**62.0**		**68.0**	**76.5**	**85.0**

Average percentage cover per transect for seagrass, algae and faunal categories scored >0 at Wedge Bay for all surveys between November 2020 and November 2021 (continued).

	June-21				Sept-21								Nov-21							
Category	**WB5**	**WB6**	**WB7**	**WB8**	**WB1**	**WB2**	**WB3**	**WB4**	**WB5**	**WB6**	**WB7**	**WB8**	**WB1**	**WB2**	**WB3**	**WB4**	**WB5**	**WB6**	**WB7**	**WB8**
Zostera spp.	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Halophila spp.	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Filamentous brown	5.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	3.5	0.5	0.0	1.0	0.0	11.0	0.5	0.5
Filamentous green	0.0	0.0	0.0	0.0	0.0	0.0	0.0	6.0	7.0	0.0	0.0	0.0	0.0	0.0	0.0	4.0	0.0	0.0	0.0	0.0
Filamentous red	0.0	0.5	1.5	4.5	1.5	9.5	7.5	43.5	4.5	4.5	3.0	18.5	1.5	14.0	37.5	17.5	9.5	16.5	36.5	34.0
Epiphytic brown	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0
Epiphytic green	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Epiphytic red	2.5	2.5	0.0	0.0	3.0	4.5	1.0	0.0	0.0	0.0	0.0	0.0	2.0	0.0	0.0	1.5	3.5	0.0	0.0	0.0
Chaetomorpha billardierii	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Ulva/Enteromorpha	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Epiphytic foliose	2.5	2.5	0.0	0.0	3.0	4.5	1.0	0.0	0.0	0.0	0.0	0.0	3.0	0.0	0.0	2.5	3.5	0.0	0.0	0.0
Caulerpa flexilis	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Caulerpa longifolia	2.5	26.0	42.5	16.5	0.0	10.0	0.0	0.0	0.0	20.0	46.0	0.0	0.0	3.0	0.0	0.0	1.5	0.5	11.0	0.0
Caulerpa simpliciuscula	1.0	0.0	0.0	13.5	0.0	0.0	15.5	2.0	0.0	0.0	0.0	5.5	0.0	0.0	30.5	2.5	1.5	0.0	0.5	0.0
Caulerpa trifaria	0.0	0.0	2.0	3.5	0.0	0.0	4.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Caulerpa spp.	0.5	0.0	0.0	0.0	0.0	0.0	1.5	0.0	1.5	0.5	0.5	0.0	0.0	0.0	1.0	0.0	0.0	0.5	0.0	0.0
Brown wrack	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.0
Green wrack	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Sand	93.5	80.0	62.5	75.5	93.0	84.5	76.0	46.0	88.5	82.5	54.5	79.0	93.0	89.0	61.0	74.5	87.5	73.5	59.5	70.0
Shell grit	0.0	0.5	0.0	0.0	0.0	0.0	0.0	3.0	0.0	0.0	2.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Encrusting sponge	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Free standing sponge	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	2.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0
Maoricolpus roseus	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0
Angasi oysters	0.0	1.5	0.0	0.5	0.5	0.5	0.5	3.5	0.0	0.0	0.0	0.0	0.5	0.0	0.0	1.5	0.0	1.0	2.0	1.0
Commercial scallop	0.0	0.0	0.5	0.0	0.5	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Total filamentous	**5.0**	**0.5**	**1.5**	**4.5**	**1.5**	**9.5**	**7.5**	**49.5**	**11.5**	**4.5**	**3.0**	**18.5**	**5.0**	**14.5**	**37.5**	**22.5**	**9.5**	**27.5**	**37.0**	**34.5**
Total *Caulerpa* spp.	**4.0**	**26.0**	**44.5**	**33.5**	**0.0**	**10.0**	**21.5**	**2.0**	**1.5**	**20.5**	**46.5**	**5.5**	**0.0**	**3.0**	**31.5**	**2.5**	**3.0**	**1.0**	**11.5**	**0.0**
Total wrack	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	**1.5**	**0.0**	**0.0**
Total substrate	**93.5**	**80.5**	**62.5**	**75.5**	**93.0**	**84.5**	**76.0**	**49.0**	**88.5**	**82.5**	**57.0**	**79.0**	**93.0**	**89.0**	**61.0**	**74.5**	**87.5**	**73.5**	**59.5**	**70.0**

Appendix 7-2: Seagrass power analysis

Effect size and percentage detectable change of *Zostera* spp. cover, based on results of a paired t-test, where sample size (n) is the number of photo-quadrats per transect and power = 0.8.

Site	Year	Transect	Number of photo-quadrats	*Zostera* % cover (± SD)	Effect size	Percentage detectable change
Adventure Bay	2019	AB1	17	73.8 ± 33.0	23.89	32
		AB2	12	67.5 ± 29.7	26.39	39
		AB3	11	63.1 ± 32.9	30.9	49
	2020	AB1	16	33.0 ± 17.5	13.12	40
		AB2	12	32.5 ± 23.5	20.9	64
		AB3	9	54.2 ± 20.3	21.66	40
		AB4	21	51.0 ± 28.8	18.5	36
	2021	AB1	12	69.5 ± 26.4	23.46	34
		AB2	12	52.0 ± 24.3	21.59	42
		AB3	8	58.5 ± 24.8	28.67	49
		AB4	17	39.5 ± 29.3	21.2	54
Bull Bay	2019	BB1	6	37.00 ± 25.45	36.44	75
		BB2	6	48.33 ± 41.50	59.53	123
		BB3	5	20.80 ± 14.60	24.56	118
		BB4	9	35.78 ± 33.95	36.22	101
		BB5	7	50.00 ± 32.08	40.82	82
	2020	BB1	14	23.14 ± 29.47	23.90	103
		BB2	18	19.10 ± 22.40	15.70	82
		BB3	18	42.67 ± 26.63	18.66	44
		BB4	20	28.80 ± 27.71	18.30	64
		BB5	19	42.84 ± 28.10	19.10	45
	2021	BB1	16	28.00 ± 33.59	25.17	90
		BB2	18	27.10 ± 29.40	20.60	76
		BB3	17	27.53 ± 20.38	14.75	54
		BB4	20	33.90 ± 26.41	17.44	51
		BB5	17	39.65 ± 29.80	21.57	54
Sloping Island	2020	SI1	6	20.7 ± 13.4	19.3	93
		SI2	6	42.3 ± 11.4	16.4	39
		SI3	6	32.0 ± 12.9	18.5	58
		SI4	6	15.7 ± 9.3	13.4	85
		SI5	7	20.6 ± 18.4	23.4	114
		SI6	8	16.0 ± 10.7	12.4	77
		SI7	6	23.3 ± 18.1	25.9	111
	2021	SI1	4	19.0 ± 21.3	45.2	238
		SI2	4	36.0 ± 18.3	38.9	108
		SI3	4	28.0 ± 12.8	27.1	97
		SI4	4	42.5 ± 7.2	15.3	36
		SI5	4	7.5 ± 6.0	12.7	169
		SI6	4	30.5 ± 7.7	16.4	54
		SI7	4	29.5 ± 1.9	4.1	14

Number of photo-quadrats required per transect to detect 25, 50, 75 and 100% change in *Zostera* spp. cover based on the average values collected during 2019, 2020 and 2021 surveys at Adventure Bay, Bull Bay and Wedge Bay. To a power of 0.8.

Site	Year	Transect	*Zostera* % cover (± SD)	Percentage detectable change			
				25	50	75	100
Adventure Bay	2019	AB1	73.8 ± 33.0	28	9	6	4
		AB2	67.5 ± 29.7	27	9	5	4
		AB3	63.1 ± 32.9	36	11	6	5
	2020	AB1	33.0 ± 17.5	38	11	7	5
		AB2	32.5 ± 23.5	70	19	10	7
		AB3	54.2 ± 20.3	20	7	5	4
		AB4	51.0 ± 28.8	41	13	6	5
	2021	AB1	69.5 ± 26.4	21	7	5	4
		AB2	52.0 ± 24.3	30	9	6	4
		AB3	58.5 ± 24.8	25	8	5	4
		AB4	39.5 ± 29.3	70	20	10	7
Bull Bay	2019	BB1	37.00 ± 25.45	60	17	9	6
		BB2	48.33 ± 41.50	96	26	13	8
		BB3	20.80 ± 14.60	63	18	9	7
		BB4	35.78 ± 33.95	114	30	15	10
		BB5	50.00 ± 32.08	54	15	8	6
	2020	BB1	23.14 ± 29.47	205	53	25	15
		BB2	19.10 ± 22.40	177	46	22	13
		BB3	42.67 ± 26.63	51	15	8	6
		BB4	28.80 ± 27.71	115	31	15	10
		BB5	42.84 ± 28.10	59	16	9	6
	2021	BB1	28.00 ± 33.59	212	55	26	16
		BB2	27.10 ± 29.40	154	40	19	12
		BB3	27.53 ± 20.38	69	20	10	7
		BB4	33.90 ± 26.41	78	21	10	7
		BB5	39.65 ± 29.80	72	20	10	7
Sloping Island	2020	SI1	20.7 ± 13.4	56	16	9	6
		SI2	42.3 ± 11.4	12	5	4	3
		SI3	32.0 ± 12.9	23	8	5	4
		SI4	15.7 ± 9.3	47	14	8	6
		SI5	20.6 ± 18.4	103	28	14	9
		SI6	16.0 ± 10.7	59	17	9	6
		SI7	23.3 ± 18.1	78	21	11	7
	2021	SI1	19.0 ± 21.3	160	42	20	12
		SI2	36.0 ± 18.3	35	11	6	5
		SI3	28.0 ± 12.8	29	9	6	4
		SI4	42.5 ± 7.2	6	4	3	3
		SI5	7.5 ± 6.0	83	23	12	8
		SI6	30.5 ± 7.7	11	5	4	3
		SI7	29.5 ± 1.9	3	3	2	2

Effect size and percentage detectable change of *Zostera* spp. cover, based on results of a paired t-test, where sample size (n) is the number of transects per site and power = 0.8.

Site	Year	Number of transects (n)	*Zostera* % cover (± SD)	Effect size	Percentage detectable change
Adventure Bay	2019	3	68.1 ± 5.4	17.63	25.88
	2020	4	42.7 ± 11.6	24.68	57.82
	2021	4	54.9 ± 12.5	26.60	48.47
Bull Bay	2019	5	38.4 ± 11.7	19.68	51.27
	2020	5	31.3 ± 11.0	18.50	59.09
	2021	5	31.2 ± 5.5	9.25	29.62
Sloping Island	2020	7	24.4 ± 9.6	12.22	50.14
	2021	7	27.6 ± 11.4	14.51	52.62

Number of transects required per site to detect 25, 50, 75 and 100% change in *Zostera* spp. cover based on the average values collected during 2019, 2020 and 2021 surveys at Adventure Bay, Bull Bay and Wedge Bay. To a power of 0.8.

Site	Year	*Zostera* % cover (± SD)	Percentage detectable change			
			25	50	75	100
Adventure Bay	2019	68.1 ± 5.4	4	3	3	2
	2020	42.7 ± 11.6	12	5	4	3
	2021	54.9 ± 12.5	9	4	4	3
Bull Bay	2019	38.4 ± 11.7	14	6	4	3
	2020	31.3 ± 11.0	18	7	5	4
	2021	31.2 ± 5.5	7	4	3	3
Sloping Island	2020	24.4 ± 9.6	22	8	5	4
	2021	27.6 ± 11.4	24	8	5	4

Appendix 7-3: Seagrass stable isotope analysis

Site average (± standard error) for total nitrogen (TN), total carbon (TC), δ15N and δd13C from seasonal surveys in Bull Bay between November 2020 and 2021, and Adventure Bay, Sloping Island and Wedge Bay in November 2021. No standard error values are shown for Wedge Bay as only one sample was analysed for each component from this site.

Site	Year	Month	Component	TN (%)	δ^{15}N (‰)	TC (%)	δ^{13}C (‰)
Bull Bay	2020	Nov	Leaf 1	2.1 ± 0.2	7.2 ± 0.3	32.1 ± 0.2	-12.8 ± 1.0
	2020	Nov	Leaf 2	1.9 ± 0.2	7.2 ± 0.3	32.3 ± 0.1	-13.7 ± 1.2
	2020	Nov	Leaf 3	2.0 ± 0.2	7.0 ± 0.4	33.4 ± 0.1	-14.1 ± 1.1
	2020	Nov	Leaf 4	1.9 ± 0.2	6.7 ± 0.2	32.6 ± 0.2	-14.0 ± 1.0
	2020	Nov	Leaf 5	1.9 ± 0.2	6.5 ± 0.2	33.1 ± 0.5	-14.0 ± 1.1
	2020	Nov	Rhizome	0.8 ± 0.0	6.4 ± 0.3	25.2 ± 1.9	-12.7 ± 0.1
	2021	June	Leaf 1	2.9 ± 0.2	7.6 ± 0.4	33.0 ± 1.3	-16.2 ± 0.9
	2021	June	Leaf 2	2.7 ± 0.1	7.3 ± 0.3	33.8 ± 0.6	-16.3 ± 0.9
	2021	June	Leaf 3	2.6 ± 0.1	7.3 ± 0.1	33.1 ± 1.0	-15.9 ± 0.9
	2021	June	Leaf 4	2.5 ± 0.1	7.0 ± 0.3	33.1 ± 0.2	-15.9 ± 0.9
	2021	June	Leaf 5	2.3 ± 0.1	6.8 ± 0.4	33.4 ± 0.3	-15.6 ± 0.7
	2021	June	Rhizome	3.1 ± 0.2	8.3 ± 0.1	26.3 ± 1.5	-12.3 ± 0.4
	2021	Sept	Leaf 1	3.1 ± 0.1	7.4 ± 0.1	34.7 ± 0.1	-15.2 ± 1.3
	2021	Sept	Leaf 2	3.0 ± 0.2	7.3 ± 0.0	35.5 ± 0.6	-15.4 ± 1.4
	2021	Sept	Leaf 3	2.9 ± 0.2	7.1 ± 0.0	34.8 ± 0.4	-15.3 ± 1.5
	2021	Sept	Leaf 4	2.7 ± 0.1	6.9 ± 0.1	33.8 ± 1.4	-15.3 ± 1.5
	2021	Sept	Leaf 5	2.3 ± 0.2	6.7 ± 0.2	33.3 ± 0.7	-15.5 ± 1.5
	2021	Sept	Rhizome	1.6 ± 0.7	9.0 ± 1.5	28.6 ± 0.1	-12.1 ± 0.0
	2021	Nov	Leaf 1	2.7 ± 0.3	7.6 ± 0.3	32.7 ± 0.3	-13.6 ± 0.6
	2021	Nov	Leaf 2	2.3 ± 0.2	7.2 ± 0.2	33.5 ± 0.4	-14.0 ± 0.7
	2021	Nov	Leaf 3	2.2 ± 0.2	7.1 ± 0.2	33.5 ± 0.3	-14.3 ± 0.8
	2021	Nov	Leaf 4	2.1 ± 0.2	7.0 ± 0.2	32.3 ± 0.7	-14.9 ± 0.8
	2021	Nov	Leaf 5	2.0 ± 0.2	7.0 ± 0.1	32.0 ± 0.2	-15.2 ± 0.7
	2021	Nov	Rhizome	0.8 ± 0.2	6.3 ± 0.7	25.4 ± 0.4	-13.8 ± 0.3
Adventure Bay	2021	Nov	Leaf 1	2.8 ± 0.1	8.8 ± 0.6	34.3 ± 0.8	-12.3 ± 0.3
	2021	Nov	Leaf 2	2.3 ± 0.1	8.3 ± 0.5	34.0 ± 1.0	-13.3 ± 0.2
	2021	Nov	Leaf 3	2.2 ± 0.0	7.9 ± 0.3	34.2 ± 1.0	-13.7 ± 0.2
	2021	Nov	Leaf 4	2.2 ± 0.0	7.7 ± 0.2	33.6 ± 0.9	-13.9 ± 0.2
	2021	Nov	Leaf 5	2.2 ± 0.1	8.0 ± 0.3	33.8 ± 0.9	-13.7 ± 0.1
	2021	Nov	Rhizome	0.4 ± 0.0	4.5 ± 0.5	25.2 ± 0.9	-9.6 ± 0.2
Sloping Island	2021	Nov	Leaf 1	2.1 ± 0.2	7.3 ± 0.2	34.2 ± 0.5	-14.1 ± 0.5
	2021	Nov	Leaf 2	1.9 ± 0.1	6.7 ± 0.5	34.6 ± 1.4	-14.5 ± 1.0
	2021	Nov	Leaf 3	1.8 ± 0.1	6.6 ± 0.3	33.7 ± 0.4	-13.4 ± 0.7
	2021	Nov	Leaf 4	1.8 ± 0.2	6.5 ± 0.2	35.4 ± 1.4	-13.5 ± 0.7
	2021	Nov	Leaf 5	1.6 ± 0.1	6.1 ± 0.1	33.3 ± 0.7	-14.1 ± 0.9
	2021	Nov	Rhizome	0.4 ± 0.0	3.9 ± 0.7	27.4 ± 1.6	-11.8 ± 0.4
Wedge Bay	2021	Nov	Leaf 1	2.3	7.7	32.2	-11.8
	2021	Nov	Leaf 2	2.2	7.1	34.3	-11.6
	2021	Nov	Leaf 3	2.2	7.2	35.9	-11.4
	2021	Nov	Leaf 4	2.2	7.0	35.8	-11.6
	2021	Nov	Leaf 5	2.1	7.0	34.0	-11.9
	2021	Nov	Rhizome	0.5	5.4	22.3	-10.7