Volume Two
May 2014

Appendix 15

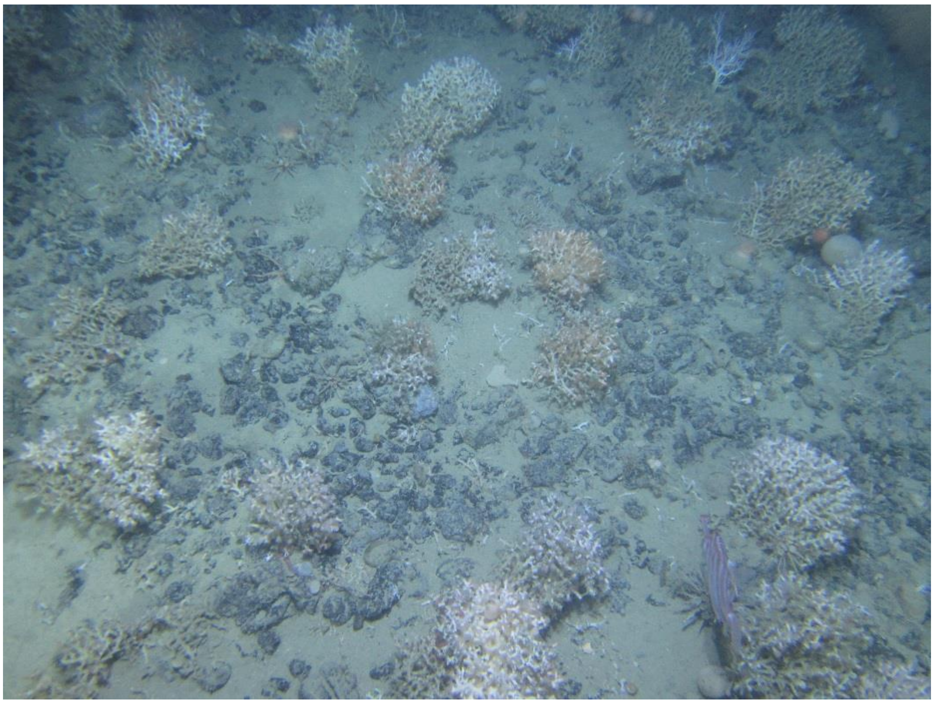
Benthic communities on MPL area 50270 on the Chatham Rise (Rowden et al. 2013)

Chatham Rock Phosphate Ltd

Benthic communities of MPL area 50270 on the Chatham Rise

Prepared for Chatham Rock Phosphate Ltd

May 2013



Authors/Contributors:
Ashley Rowden, Daniel Leduc, Leigh Torres, David Bowden, Alan Hart, Caroline Chin, Nikki Davey, Jonathan Wright, Megan Carter, Braden Crocker, Jane Halliday, Anne-Nina Loerz, Geoff Read, Sadie Mills, Owen Anderson, Kate Neill, Michelle Kelly, Di Tracey, Steffi Kaiser, Dennis Gordon, Serena Wilkins, Peter Horn, Arne Pallentin, Scott Nodder, Kevin Mackay, Lisa Northcote

For any information regarding this report please contact:

Dr Ashley A Rowden
Principal Scientist
Benthic Ecology
+64-4-386 0334
a.rowden@niwa.co.nz

National Institute of Water & Atmospheric Research Ltd
301 Evans Bay Parade, Greta Point
Wellington 6021
Private Bag 14901, Kilbirnie
Wellington 6241
New Zealand

Phone +64-4-386 0300
Fax +64-4-386 0574

NIWA Client Report No: WLG2012-25
Report date: May 2013
NIWA Project: CRP12302

Cover photo: Coral-dominated benthic community on the Chatham Rise [CRP Limited]

Contents

Tables

Figures

Reviewed by

AB MacDiarmid

Dr Alison MacDiarmid

Approved for release by

Julie Hall

Dr Julie Hall

Executive summary

The mineral prospecting licence area 50270 of Chatham Rock Phosphate Limited (CRP) covers an area of 4726 km^2 on the Chatham Rise. CRP proposes to mine part of this area, and in support of the ‘marine consent’ to undertake mining, information regarding the benthic communities in the licence area is required. This information will be used to assess the implications of the proposed mining activities on benthic communities, and to design measures to mitigate, and monitor, potential environmental effects.

The objectives of the present project were to: Determine the benthic community structure within the licence area, and the environmental drivers of any patterns observed; use these data to produce predictive models of the distribution of benthic communities within the licence area; and compare the structure and distribution of benthic communities within the licence area with benthic communities previously sampled elsewhere on the Chatham Rise.

An Environmental Survey of 13 survey areas was carried out in the north-western part of the licence area in March 2012. A remotely operated vehicle (ROV) was used to conduct photographic transects above the seafloor, and a box-corer was used to directly sample the seabed. Images of the seafloor from the ROV and samples from the box-cores were used to obtain data on benthic epifauna and infauna, respectively. The seafloor habitat was also characterised using the same images and samples, as well as topographic metrics from multi-beam echo sounder data collected during the survey.

Multivariate statistics analyses identified 12 epifauna and 5 infauna communities, their characterising taxa, and distributions. The potential extent of suitable habitat for each of these communities in the study area was then predicted by modelling. The environmental variables that explain the overall community structure and the distribution of the individual communities were also identified by these analyses. The predicted distribution of suitable habitat for all but one community was explained in part by the distribution density of phosphorite nodules in the study area.

The structure and distribution of two epifauna communities and one infauna community are closely related to the distribution of high density patches of phosphorite nodules. The two epifauna communities are dominated by the stony coral *Goniocorella dumosa* and show a patchy distribution in the east of the study area. The infauna community that exhibits a positive relationship with nodule density is characterised mainly by amphipod and polychaete species. Suitable habitat for this community extends over the study area, but occurs predominantly in the west.

Comparison of the benthic communities identified by the survey and communities described from previous sampling on the Chatham Rise indicates that epifauna communities within the licence area have not been found elsewhere on the Rise to date. In particular, the communities dominated by high abundances of *Goniocorella dumosa* have only been observed within the licence area. The nodule-associated amphipod-dominated community also appears not to have been observed before.

To assess the potential uniqueness of some of the benthic communities in the licence area it is recommended that additional analysis is undertaken. This analysis could include data from sampling elsewhere on the Chatham Rise using techniques comparable to those used in the Environmental Survey, and raw data from the Chatham Rise OS20/20 survey.

1 Introduction

1.1 Proposed phosphorite nodule mining on the Chatham Rise

Phosphorite deposits are potentially the most important economic marine mineral resource around New Zealand, and the main deposits are on the Chatham Rise (Glasby & Wright 1990). The distribution and characteristics of these deposits has been well studied since 1975 (e.g. Pasho 1976, Cullen 1980, Kudrass & Cullen 1982, Kudrass & von Rad 1984a, von Rad & Kudrass 1987), and the results of these studies have been reviewed by Glasby & Wright (1990).

Phosphorite deposits are formed by the phosphatization of limestone, which was followed by the fragmentation of this chalk hardground on the Chatham Rise, in a process that began in the mid-Miocene. Phosphorite occurs as “nodules” (2 to > 150 mm diameter, maximum frequency 10 - 40 mm diameter) in a matrix of glauconitic sand, and can extend beneath the seafloor sediment surface to 0.7 m. Nodules are found in water depths of about 400 m along approximately 400 km of the crest of the Chatham Rise. Nodule distribution is very patchy at a number of spatial scales as a result of biological and physical processes that took place during and after phosphatization (e.g. upwelling, bioturbation, iceberg scouring). The region with the highest concentration of nodules is between longitudes 179° and 180° East. Here combined nodule weight averages 66 kg/m^2, which represents a total of about 100 million tonnes (Glasby & Wright 1990). Nodules contain minerals that can be used as a component of agricultural fertilizer, which is why there has been a long interest in mining these deposits.

Mineral Prospecting Licences (MPL), pursuant to the Continental Shelf Act 1964, have been issued to Chatham Phosphate Limited (MPL 50297) and Chatham Rock Phosphate Limited (MPL 50270). The area of the Chatham Rise covered by these licences is 15,640 km^2 and 4726 km^2, respectively (Figure 1-1). The Mineral Prospecting Licence provides mining companies with the right to undertake sampling and other activities that allow them to evaluate the economic worth of phosphorite deposits within their licence area, and to gather information that will inform any future mining operations (e.g. practical operation of mining tools), before they submit an application for a mining licence to New Zealand Petroleum and Minerals. Mining companies also need to seek a ‘marine consent’, pursuant to the Exclusive Economic Zone and Continental Shelf (Environmental Effects) Act 2012, before mining operations can commence on the Chatham Rise. Chatham Rock Phosphate Limited (CRP) is seeking such a consent, and in support of their application they are producing an Environmental Impact Assessment (EIA). The EIA includes information that has been used to design spatial planning measures that aim to mitigate, and monitor, the environment effects of the proposed mining activities. Knowledge of the structure and distribution of benthic communities on the Chatham Rise is essential information for the EIA.

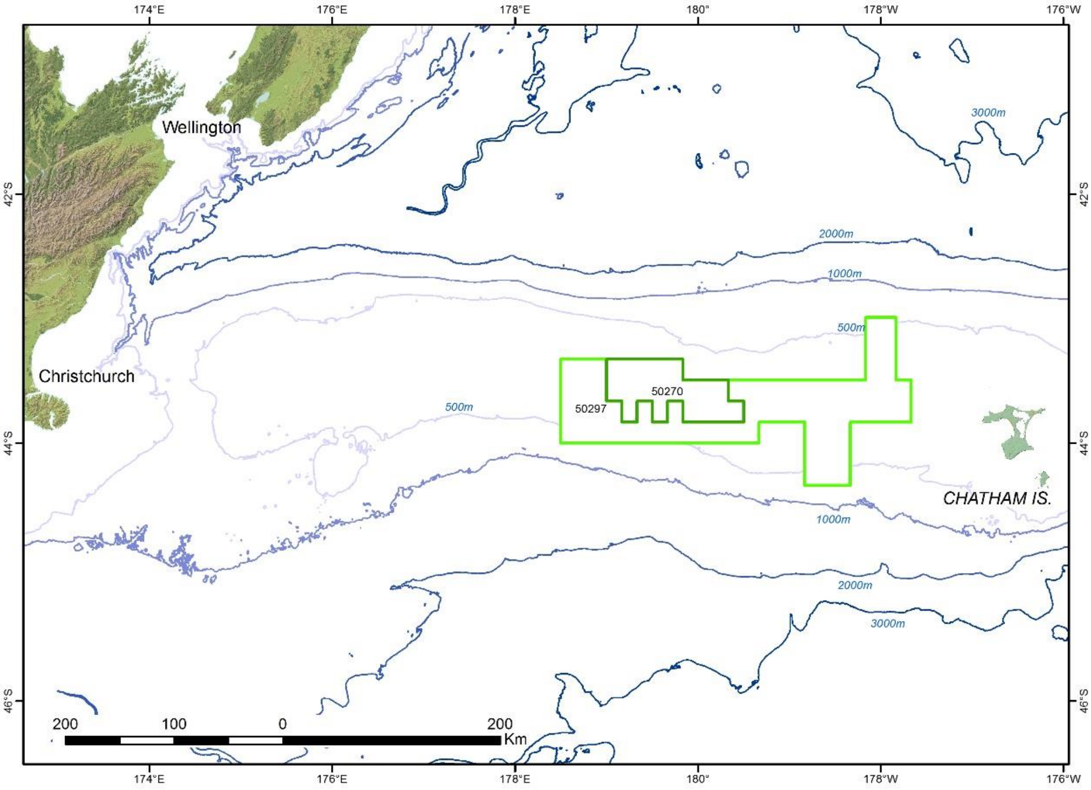


Figure 1-1: Map showing the Chatham Rise and the location of Chatham Rock Phosphate's Mineral Prospecting License area (area with dark green border, 50270; the area marked by light green border is licence area of another mining company).

1.2 Benthic Communities of the Chatham Rise

The Chatham Rise is a prominent submarine feature that extends 100 km from Banks Peninsula eastwards for 1400 km. Five areas with depths less than 200 m occur across the rise: Mernoo, Veryan, Reserve and Wharekauri Banks and the Chatham Islands. West of the Chatham Islands, the Rise is generally flat topped at 200-400 m, whilst east, north and south of the feature the water depths increase to over 2000 m (MacKay et al. 2005). Surface sediments on the Rise are predominantly fine-grained sands and muds with occasional outcrops of coarser material. Below 150 m the calcareous organic fraction of the sediment is composed mostly of foraminiferan tests, whereas molluscan fragments are more common above 150 m and may dominate the sediments at shallower depth (e.g. the biogenic sediments of the Mernoo and Veryan Banks) (Norris 1964).

Of the prominent banks on the Chatham Rise shallower than 300 m, only the benthic fauna of the Mernoo Bank has been partially described, and only then for molluscs occurring at three shallow (77-104 m) essentially shelf stations (Dell 1951). Descriptions of the slope/bathyal fauna began with a brief report by Hurley (1961) who examined six stations from depths of 403-604 m from sandy mud on the Chatham Rise. Hurley (1961) described a "*Serolis bromleyana* [*Brucerolis hurleyi*]-*Spatangus multispinus* community" and considered this community to be "sufficiently distinct from any sublittoral communities previously described to warrant distinctive recognition." Probert and co-workers began (from 1989) to examine in a systematic way the composition and distribution of benthic fauna across the rise, which became incorporated into a wider study led by Nodder (from 1997) to understand the influence of the Subtropical Front (STF), an oceanographic feature that overlies and characterises the Chatham Rise ecosystem (Sutton 2001).

Studies of the macrofauna (animals retained on sieve mesh >300 µm) have used different sampling gears to sample the two main components of the benthic community. Anchor-box dredges, box-corers and multi-corers to sample the fauna mainly residing within the sediment (infauna), and small trawls, benthic sleds and towed cameras to sample the fauna of the seafloor surface (epifauna).

There have also been studies of the supra- or hyper-benthos (animals of the benthic boundary layer ~1 m above the seafloor surface) (Lörz 2010, Knox et al. 2012), and those that have focussed on the meiofauna (animals retained on sieve mesh >45 µm but <300 µm) of the Chatham Rise (e.g., Grove et al. 2006, Leduc et al. 2012), but these are not considered further here.

1.2.1 Infauna communities

Probert and McKnight (1993) sampled stations on three north-south transects across the rise (244-1394 m) using an anchor-box dredge, and reported that the infauna was dominated numerically by polychaetes and peracarid crustaceans and that biomass of the sediment macroinvertebrate assemblages was greater on the south side than on the north side of the rise. Biomass on the north side declined logarithmically with depth, whilst on the south side biomass was unrelated to bathymetry, which Probert & McKnight (1993) attributed to differences in surface primary productivity and the resulting organic flux to the seabed across the STF. Probert et al. (1996) described the polychaete fauna in greater detail, and using multivariate analysis identified two main polychaete communities, one occurring mainly on the crest of the rise (244-663 m) and a deeper one (802-1394 m) on the slopes of the rise. Community composition also differed between the north and south of the rise (south of the rise the station assemblages were more homogeneous in composition). Probert et al. (1996) considered the faunal differences to reflect differences in the quantity and quality of the food supplied to the seabed controlled by the spatial and temporal dynamics of the STF.

In a subsequent study, Probert et al. (2009) examined the polychaete fauna from eight sites along a north-south transect across the central Chatham Rise from water depths of c. 2300 to 350 m. Multivariate analysis grouped the shallowest sites, at c.350–453 m, and samples from sites at c. 1000 m and 2300 m north and south of the Rise which were more disparate in their faunal composition. A distinct assemblage was recorded from a site at c. 750 m on the southern flank of the rise. As in the earlier study (Probert et al. 1996), faunal composition differed between the northern and southern flanks of the rise, and faunal density again appeared to be highest on the southern side of the rise.

1.2.2 Epifauna communities

McKnight & Probert (1997) described the epifaunal component of the Chatham Rise macrobenthos from samples taken with a small Agassiz trawl at generally the same stations as previous dredging for infauna (Probert & McKnight 1993, Probert et al. 1996), augmented with samples taken in 1993 from a further 16 stations on the central sampling transect. Using multivariate analyses, McKnight & Probert (1997) identified three benthic “community groups”; the shallowest community was characterised mainly by crustaceans and two deeper water communities characterised mainly by echinoderms. Group A was found on mainly sandy sediments on the crest and shallower flanks of the rise at 237-602 m; Group B at 462-1693 m was associated with muddy sediments; Group C on muddy sediments at 799-2039 m. McKnight & Probert (1997) considered community “A” to be similar to the *Serolis bromleyana* [*Brucerolis hurleyi*]-*Spatangus multispinus* community described by Hurley (1961), and commented that whilst some species of this community and of communities “B” and “C” were found elsewhere in New Zealand (and some globally) at bathyal depths, the extent of their respective distributions was poorly known. It was also noted that the bathymetric range of assemblages on the north and south flanks of the Chatham Rise appeared to be asymmetric, presumably because of temperature differences caused by the vertical displacement of the Antarctic Intermediate water on the north flank (McKnight & Probert 1997).

In 2007 an Ocean Survey 20/20 (OS20/20) survey was conducted on the Challenger Plateau and Chatham Rise, which included sampling of the epifauna using a benthic sled, trawl, and taking of video and still images using a towed camera (Bowden 2011). Floerl et al. (2012), using multivariate analysis, identified 9 main “biological groups” (represented by >2 sites) of which 8 were observed on the Chatham Rise, and three of them only on the rise. The distribution of these groups showed a marked across-rise pattern, that these authors presumed to be driven by depth, slope and productivity (Floerl et al. 2012).

1.2.3 Environmental drivers

As is noted above, environmental factors such as substrate type and depth were first related to the patterns of benthic community structure and distribution on the Chatham Rise. It was also speculated early on that patterns were most likely related to food availability as controlled by oceanographic processes. A multidisciplinary study to understand benthic-pelagic coupling processes associated with the STF on the Chatham Rise (that confirmed some of the benthic patterns observed by Probert and co-workers), clearly established that the spatial pattern in the make-up of benthic communities across the rise that reflects variability in the transportation of organic matter to the seabed (Nodder et al. 2003). This variability was related to both the position of STF, where surface waters have seasonally high levels of plankton biomass, and the influence of currents that advect particles of sinking organic matter that result from the death of planktonic organisms (Nodder et al. 2003). A spring deposition event of phytodetritus on the southern flank of the rise recorded in a subsequent study by (Nodder et al. 2007) was coincident with a region of current convergence, and with elevated benthic biomass and sediment community respiration rates. A study by Berkenbusch et al. (2011), that included data for meiofauna, reiterated the importance of phytodetritus flux in structuring benthic assemblages in the Chatham Rise/Subtropical Front region.

While it is evident that significant sampling of benthic communities has taken place on the Chatham Rise, and a broad understanding of community structure and distribution has been developed in the context of the main environmental drivers of these patterns – studies to date have been restricted to relatively few sites, particularly on the crest of the rise, and there has been very little information generated to date for the MPL area 50270 of Chatham Rock Phosphate Limited (CRP) (Beaumont et al. 2010).

1.2.4 Benthic communities of the MPL area 50270

Dawson (1984) summarised the taxon-focused studies which were published in the 1960s and 1970s, as well as geologically-focused sampling (grabs and photo/video images) undertaken by NZ-German collaborative studies (in 1978 and 1981 using the RV *Valdivia* and RV *Sonne*, respectively), when qualitatively describing the benthic fauna and assessing possible effects of phosphorite nodule mining on the rise. The wide expanse of sediments that make up much of the surface of the rise where mining is proposed were deemed to be characterised by large echinoids (*Paramaretia* and *Spatangus*), asteroids (*Zoroaster, Astropecten, Plutonaster, Mediaster*), conical sponges (*Hyalascus*.), crabs (*Carcinoplax victoriensis*, *Trichopeltarion fantasticum*), galatheids (*Munida*), gastropods (*Cymatona* and *Fusitriton*), and smaller burrowing polychaetes, bivalves, isopods, amphipods, cumaceans (Dawson 1984). Polychaetes were the dominant group in terms of frequency of occurrence (by station). In places where there was hard substratum suitable for colonisation by sessile fauna, Dawson (1984) noted that a "quite extensive epifauna" of corals (such as *Goniocoralla dumosa*), bryozoans, cnidarians, bivalves and brachiopods developed. Dawson considered the "*Goniocorella* clumps" as "epifaunal oases" which "undoubtedly attract small fish as feeding areas and may well be more the centre of energy dispersal than the smoother parts of the Rise".

Dawson's (1984) summary was in part based on the observations recorded by Kudrass & von Rad (1984b) from underwater imagery taken during the RV *Sonne* survey. Analysis of this imagery led these authors to note a series of correlations between the distribution of phosphorite nodules and macrobenthic fauna. In particular they noted that "colonies of branching corals (e.g. *Goniocorella dumosa*) and gorgonian corals form patches of dense growth, especially in areas where large phosphorite nodules cover the seafloor in Area 4 [eastern part of their study area].". They also remarked that "those corals are much less frequent in Areas 1 and 2 [western part of their study area] where phosphorite nodules are smaller.". Other positive correlations with nodules were noted for small burrowing crabs, molluscs, brachiopods, asteroids, and cidarid echinoids. Other types of echinoid were observed to show a negative correlation with visible phosphorite nodules (Kudrass & von Rad 1984b).

Between the survey described in this report and the surveys by RV *Valdivia* and RV *Sonne*, no samples have been taken that can be used to provide a better appreciation of the benthic communities of the licence area than that summarised by Dawson (1984), and detailed in part by Kudrass & von Rad (1984b). However, data from the 2007 OS20/20 survey of the Challenger Plateau and Chatham Rise has been used to make predictions of the distribution of benthic communities across the slope areas off central New Zealand (Compton et al. 2012), that includes the licence area. Model predictions are a useful way to provide an indication of the structure of benthic communities in unsampled areas, and are particularly useful for spatial management planning (Guisam & Thuiller 2005). At the large spatial scale of the OS20/20 survey models, there was little in the way of predicted change in assemblage composition across the licence area (Compton et al. 2012). This result is not surprising, given the spatial scale at which the models were operating and the fact that the models did not include any data from within the licence area.

Thus it is important to obtain information on the structure and distribution of the benthic communities within the licence area, and for these data to be used to generate predictive maps that can inform the management of the environmental effects of the proposed mining of phosphorite nodules on the Chatham Rise. It is also important to place information on the benthic communities within the licence area in the context of what is known about communities elsewhere on the rise.

1.3 Objectives

The project reported here had three objectives:

1. Determine the benthic community structure within the licence area, and the environmental drivers of any patterns observed.
2. Use these data to produce predictive models of the distribution of benthic communities within the licence area.
3. Compare the structure and distribution of benthic communities in the licence area with benthic communities previously sampled elsewhere on the Chatham Rise.

2 Methods

2.1 Environmental Survey design

2.1.1 Rationale for survey design

The main aim of the Environmental Survey was to characterise the benthic habitats and communities within the licence area, and to provide CRP with additional geotechnical information about their licence area.

CRP designated eight areas for geotechnical investigation within the licence area, with the expectation that these areas will be the first sites of any future mining. These mining target areas span the shallower, central part of north-western region of the licence area. Each area occupies approximately 15 km^2.

As the potential site of future mining, it is important that the benthic communities of these targets areas are known so the direct physical impact of mining activities can be assessed. It is also important to know what benthic communities exist in other parts of the licence area, and outside of the licence area, in order to be able to assess the indirect impacts of future mining activities (e.g. from the dispersal of suspended sediment). In addition, wider sampling gives a more robust understanding of the regional biodiversity in order to assess the particular biotic characteristics within the licence area.

Knowledge of the character and distribution of benthic communities will also provide information that can be used to plan future management strategies. For example, to identify areas with benthic communities similar to those areas that will be directly impacted, which could be ‘set aside’ as ‘reserve’ areas to provide potential sources of colonising fauna to aid recovery of the disturbed areas.

2.1.2 Survey planning

All available information about the benthic habitats and communities of the licence area, and its vicinity (Beaumont & Baird 2011), were compiled and where possible converted into data layers for use in GIS. Subsidiary data that could be useful for planning purposes were also converted to layers. Data layers included: bathymetry (including multi-beam echo-sounder and side scan data from an exploratory survey conducted by CRP), sediment composition, benthic invertebrates (phylum level), phosphorite nodule density, seismic facies, commercial fishing tows, research survey fish catch rates (hoki, hake, ling), sample data from RV *Valdavia* and RV *Sonne* (including video transects), and sample data held in NIWA databases (for different gear types and target sample type, and specifically for an OS20/20 survey of the Chatham Rise that was undertaken in 2007).

Relatively few data were available for benthic invertebrates in the licence area, and in the absence of time to analyse all data in great detail or with sophisticated methods, ‘expert knowledge’ was used to review the data layers. This review aimed to determine the likely distribution of different benthic habitats, and thus the scale at which faunal communities are likely to vary among, and within, the mining target areas, and the broader licence area.

The multi-beam echo-sounder (MBES) data gathered by the earlier exploratory survey were deemed the most useful data for this purpose because it illustrated the scale at which seabed depth and topography varied across the region of the licence area that is likely to be the focus of the proposed mining. Depth and topography are important habitat characteristics known to be correlated with the distribution and composition of benthic communities (e.g., Kostylev 2001).

Based on the initial bathymetric data, the eight mining target areas appeared to represent a range of different habitats, although areas 1 and 2 appeared to be similar to one another. A further six areas (covering a similar areal extent to the mining target areas) were selected to represent areas of both similar and dissimilar habitat within the region of the licence area where the target areas are located. Two further areas (areas 9 and 13) were selected that represent ‘far-field’ sites at the western and eastern extremes of the licence area. The western far-field area (area 9) was located outside of the area of MPL 50270 (in the licence area of another mining company) in order to be some distance from its neighbouring target area (Figure 2-1).

Additional far-field sites, are in effect, provided by sampling conducted in 2007 during the OS20/20 research survey outside of the licence area in deeper waters to the north and south, and to the west and east. Sampling at OS20/20 sites was not exactly the same as undertaken for the Environmental Survey, but were deemed similar enough in character to provide useful comparative data.

The video and still images taken by a remotely operated vehicle (ROV) when used to determine the structure (composition and relative abundance) of mega-and macro-epifauna communities, and the *lebensspuren* (life traces) of infauna communities, while direct samples of the seafloor taken by a box-corer were used to determine the structure of infauna communities. Together these sampling methods provide good information about the seabed habitat and benthic communities.

The depth and topography within the designated areas are used to assess the orientation of the proposed ROV transects and the number of box-core stations that would be required to adequately capture the habitat heterogeneity within each area. Within the 16 survey areas, the locations of 3 ROV transects and 2 box-core stations per transect were planned prior to the survey.

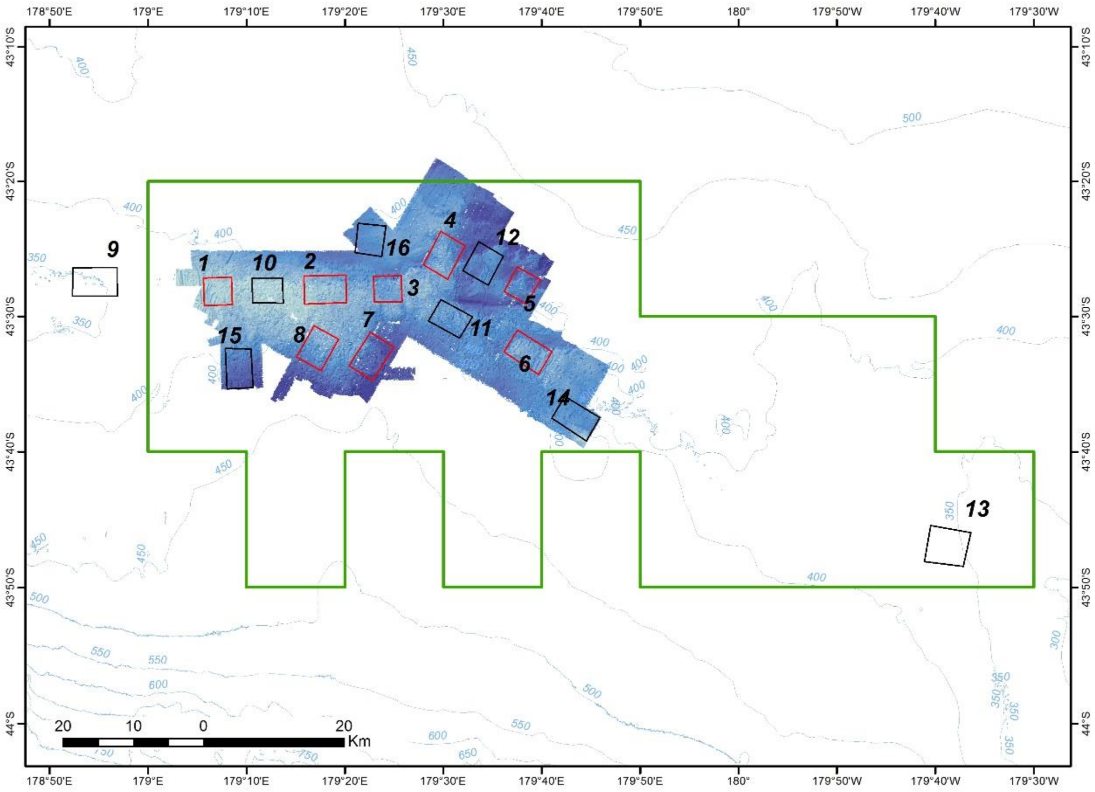


Figure 2-1: Map showing the location of the survey areas within the licence areas (red boxes are mining target areas; MPL 50270 is outlined in green).

2.2 The Survey

The Environmental Survey was conducted from the RV *Dorado Discovery*, operated by Odyssey Marine Explorations. The survey was undertaken at the CRP licence area between 17th and 31st March 2012.

2.2.1 Biological Sampling

Prior to the survey it was estimated that it would take 12 hours to complete the ROV transects in each survey area, and a further 12 hours to sample using the box-corer. Thus, if one survey area was completed per 24 hours, and with minimal on-site transit times, it was predicted that it would take approximately 16 days to complete the entire benthic survey (not including bad weather days). Sixteen days was the proposed duration of the survey voyage. With the risk that it may not be possible to complete the survey as planned so sampling was prioritised.

The highest priority was placed on sampling the mining target areas (1-8). Areas 1 and 2 were likely to be similar habitats and thus area 2 was the lowest mining target area priority. Area 7 was in deeper water and had less potential mining interest and was to be sampled after area 8. Priority order for mining target areas was therefore: 1, 3, 4, 5, 6, 8, 7, 2. Of the other sample areas (9-16), the areas within the main focus region that represent habitats different from the mining target areas were to be sampled next (14, 15, 16). Thereafter, areas that had habitats that were likely to be similar to one of the mining target areas were to be sampled (11, 12, 10), before finally sampling areas outside of the focus area (13, 9). Priority order for remaining sample areas was 14, 15, 16, 11, 12, 10, 13, 9.

Weather conditions and gear performance issues during the survey meant that survey areas 10, 13 and 9 were not sampled (which include the two ‘far-field’ sites). The remaining areas were all sampled with 3 ROV transects, and most areas were sampled with 2 box-core stations per transect (i.e. 6 stations). Exceptions were areas 3, 16 (5 stations), and area 12 (4 stations) (Figure 2-2).

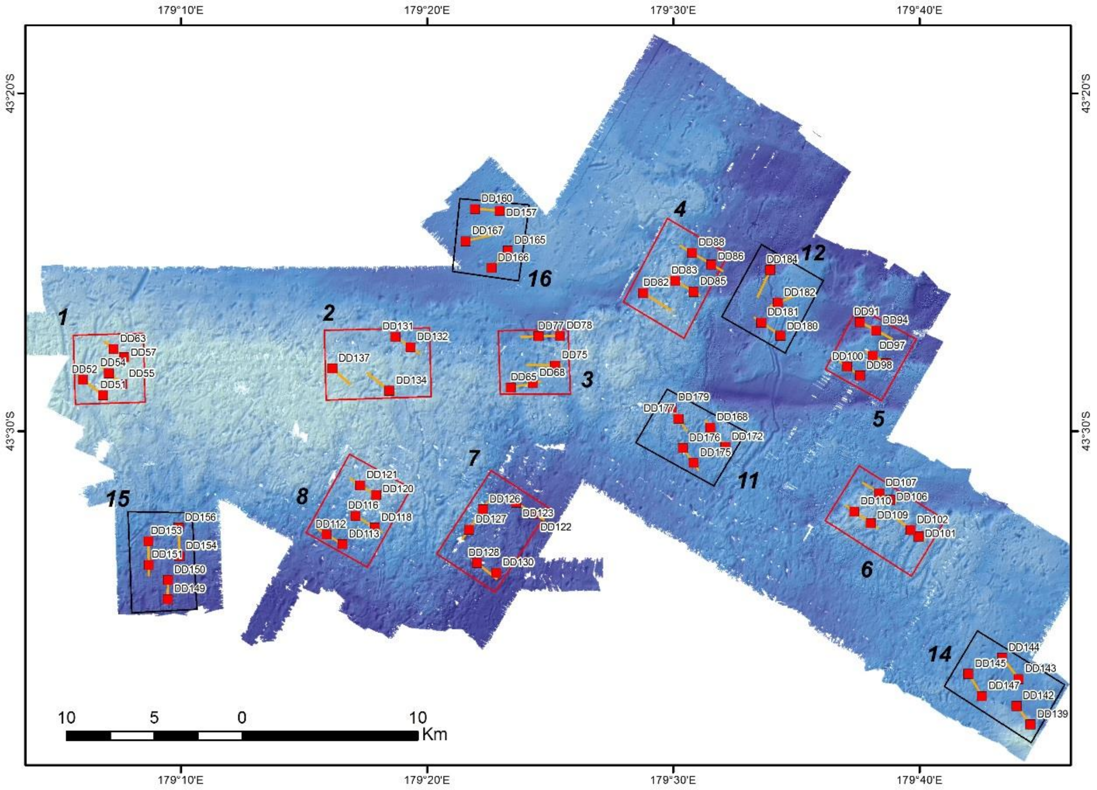


Figure 2-2: Map showing the location of the ROV transects (orange lines) and box-core stations (red squares with station numbers) within the survey areas (red boxes are mining target areas).

2.2.2 Multi-beam echo-sounder survey

Multi-beam Echo-sounder (MBES) data were collected from the wider survey area using a ship-board Reson 8160 (50 kHz), as well as high-resolution MBES data from transects with the survey areas using a Reson 7125 (400 kHz) mounted on a remotely operated vehicle (see below). MBES bathymetry data were edited and gridded with PDS2000 software by Odyssey Marine Exploration during the survey.

Data from the MBES survey was collected in part to provide data for use in the benthic community analysis and for habitat suitability modelling (see below).

2.3 Biological sampling methods

2.3.1 Seafloor imaging

Video and still images taken by cameras on a remotely operated vehicle (ROV) were used to characterise benthic habitat and to sample mega- and macro-benthic communities. The ROV, *Zeus* II (Figure 2-3), was 'flown' at a target height of 2 m above the seafloor and at a speed of 0.5 knot along transects of approximately 1 nautical mile. Transects were initially completed in order of priority, then later in the most operationally efficient sequence. The ROV's video and still cameras were inclined towards the seafloor at an angle of 45º. Still images were triggered manually at least every 15 seconds. The seabed position, depth and altitude of the ROV was continuously logged.

The live video feed from the ROV was viewed on-board the research vessel by two biologists who logged their observations of benthic and pelagic organisms to the lowest taxonomic level possible in a hierarchical Access database. The biologists also logged observations of 'lebensspuren' (animal live traces) as they occurred on soft sediments. A geologist simultaneously logged seafloor features and bottom type in another Access database. If the biologists wanted to take video and still photographs at closer range or recover a sample, then progress along the transect was suspended while the ROV manoeuvred to complete the task. The ROV resumed the transect when the task was completed, and all camera settings were returned to transect defaults.

The manipulator arms of the ROV were used to sample animals where the identification of particular taxa was uncertain, and of small rocks or coral heads that provided habitat for biota that were unlikely to be observable in video and still images. Some use was made of net attachments in retrieving the specimens but most were collected directly using the ROV manipulator arm. Time of capture was recorded along with video and still images of the collection process. Retrieved samples were preserved on-board for later processing. Stopping the ROV during transects to obtain these samples was time consuming and therefore this type of sampling was infrequent.

During the ROV transect, the biologists assessed the suitability of box coring sites chosen prior to the voyage to determine whether they were representative of the benthic habitats imaged along the transect, and identified alternative sites nearby if necessary.

Figure 2-3: Remotely operated vehicle (ROV) *Zeus II* used to take images of the seafloor and obtain multi-beam echo sounder data. [photo: Emily Jones, Golder Associates].

2.3.2 Box-coring

Upon completion of the ROV transects, two box core stations were occupied on each transect. A Reineck type box-corer with a core of 200 (w) x 300 (l) x 450 (d) mm was used to sample the macro-benthic communities and to characterise the habitat (Figure 2-4). On recovery of the box-core sample, the quality of the sample was categorised as ‘good’, ‘fair’ or ‘poor’. A good quality sample showed surface features such as burrow openings, pits and mounds, had a relatively horizontal surface (i.e., not slumped in one direction), and evenly distributed surface fauna if present (i.e., not piled in one corner). A poor quality sample had slumping, large holes that clearly drained away to the base of the sample, no intact surface features or a ‘washed out’ look. A fair quality sample showed most of the features of a good quality box sample, with a few of the poor quality indicators (i.e., a small part of the core surface was ‘washed out’ but the majority was intact).

Where large nodules and hardground fragments were observed on the seafloor by the ROV video prior to the box-corer deployment, box-core samples were seldom undisturbed. This disturbance was primarily due to the large rocks catching between the box and the spade, which disrupted the seal at the base of the sample. In these instances ‘fair’ samples were often retained for processing as the frequency of ‘good’ samples recovered in areas other than soft sediment was very low. As the voyage progressed, time constraints dictated that repeat sampling to obtain good or fair quality samples was only possible once per site.

After the sample quality assessment, the surface of the sample was labelled and photographed and biological observations noted. Macrofauna observed on the surface, e.g. polychete worms or small urchins, were removed and preserved separately. When possible, a 10 cm diameter plastic core up to 40 cm long was inserted into the sample to recover a sub-sample for later sediment characterisation analysis. If the box-core sample was more than 15 cm thick it was further processed in two parts. The upper 15 cm was removed from the box using a small plastic trowel. This sediment was gently homogenised using filtered seawater (100 µm) and washed through a 300 µm sieve. The material (fauna and sediment) retained on the sieve was preserved in 10% buffered formalin solution. The portion of the sample below 15 cm was washed on a 1 mm sieve and the retained material preserved as above. For ease of processing and to prevent damage to the fauna, the larger phosphorite nodules in the sample were separated by hand and retained in a labelled bag. These nodules were preserved with the respective sieved sample. Often the samples that were unsuitable for biological processing, i.e., those categorised as ‘poor’, were kept as geological samples. Potentially interesting fauna among these rejected samples were sometimes retained. These samples were photographed and described on board.

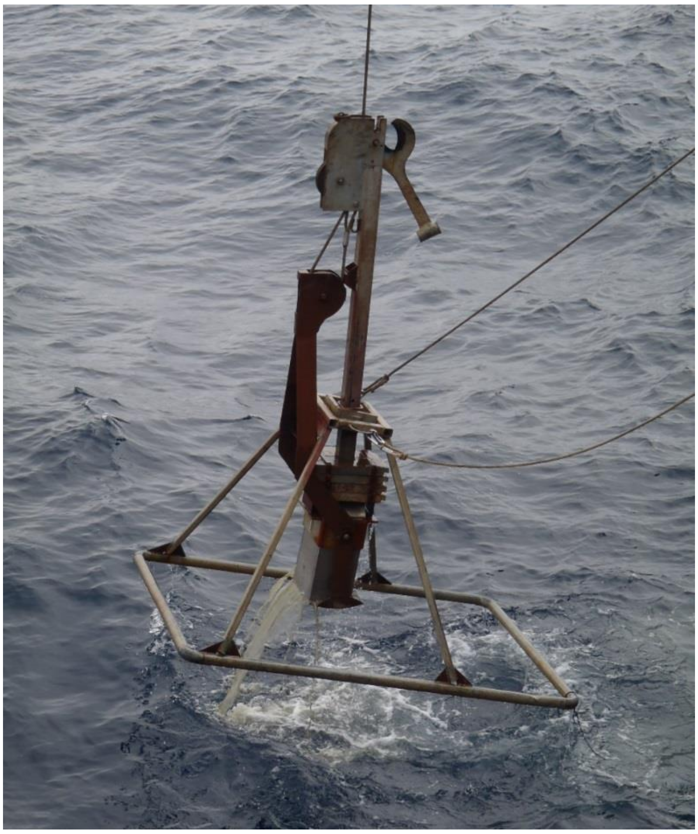


Figure 2-4: Reineck-type box-corer used to take samples of infauna and sediment. [photo: Emily Jones, Golder Associates].

2.4 Laboratory sample treatment

2.4.1 Seafloor images

While the video was of sufficient quality to make qualitative shipboard observations of benthic organisms (Beaumont & Rowden 2013) and broad-scale habitat descriptions (see companion report by Nodder et al. 2013), it was not adequate to provided faunal data for the quantitative analysis of benthic community structure. The still images were used instead.

More images were taken than could be practically analysed (a total of 16,822 images were taken during the survey). Typically, at the frequency at which images were taken on the survey (every 15 seconds), NIWA would analyse every 4th image (an unpublished NIWA study has shown that this level of analysis is sufficient to identify >50% of the total number of taxa identified by the analysis of all images on a transect), however, CRP were only willing to analyse the number of images that equates to every 8th image. In order to determine if this frequency was likely to lead to a poor understanding of the fauna in the survey areas, a trial analysis of all images from a single survey transect was conducted. The trial indicated that at a frequency of every 8th image the analyses would identify only ~40% of the total number of taxa identified by the analysis of all images on a transect (a result similar to the unpublished study). This issue arises because of the patchy nature of the seafloor habitat (i.e. substrate) and the high likelihood that images of small patches of habitat would not be analysed, and therefore species that might be particular to these habitats would go unrecorded. In order to overcome this issue, rather than analyse images on a strictly regular frequency of every 8th image, images were selected for analysis with respect to substrate type (i.e. stratified sampling).

A substrate descriptor was recorded for each image as a string of descriptions of all the substrate categories observed, without information about the proportions in each category (because there was insufficient time to calculate these data). Substrate categories were based on the basic substrate type descriptors typically used for habitat characterisation (mud/sand, cobbles/pebbles, boulders) with the addition of categories specific to the location (nodules, chalk patches, chalk hard-ground, scour, ledges, ‘dark patches’ (interpreted as recently exposed sub-surface layer of small-sized nodules, exposed through an unknown form of disturbance, Kudrass & von Rad 1984b)).

After each image had been analysed to characterise the substrate, this information was used to select images for the faunal analysis based on a simple stratification. Images were identified from each transect that were taken of broadly soft (mud/sand, dark patches, chalk patches, scour) or hard (cobbles/pebbles, nodules, chalk hard-ground) seafloor habitat, and also small and distinct habitat types that are likely to be under represented if images were selected at regular intervals of every 8th image. These latter habitats were the substrate categories boulder and ledges.

All images within the strata boulders and ledges were selected for identification of fauna. Typically, only one or two images were taken of each occurrence of these habitats on a transect. For the hard substrate strata, the 2nd image was selected at the start of each habitat patch and every subsequent image taken at intervals of 2 minutes (i.e. every 8th image) until the end of the habitat patch. A similar selection process was used for the soft substrata, except that the first image to be selected was the 3rd image in the habitat patch and the subsequent frequency of selection was an image every 3 minutes (i.e. every 12th image) until the end of the habitat patch. This selection process meant that small patches of soft or hard habitat were not sampled (i.e. where < 10 images in total were taken). The use of the 2nd/3rd image, rather than the 1st image, to begin the selection process reflects the desire to avoid including images at the boundary of habitat patches (which are more indeterminate for soft than hard substrate, hence 3rd compared to 2nd image). The difference in the sampling frequency for images in the hard and soft strata reflects the relative homogeneity of the latter habitat, and therefore fewer images were deemed necessary to capture the biodiversity of this substrate.

Counts of fauna observed on the selected images were made using the software package ImageJ (http://rsbweb.nih.gov/ij/). Images were initially colour balanced and adjusted for contrast and brightness where necessary. The upper fifth of the image area was not analysed because the 45 degree camera angle caused loss of image illumination at the top of the image frame, depending on the ROV height and pitch. To econmise on analysis time, image area was not calculated. However, the images analysed were taken at a relatively consistent height above the seabed (2.01 ±0.14 m, n=3,033) and, therefore, the observable area of the seafloor was very similar across all images (approximately 6 m^2 total area, 4 m^2 analysed area).

Faunal identifications (to lowest possible taxonomic level) and counts were made by three experienced observers who analysed images from separate transects. Identification of the fauna observed was standardised between observers by maintaining a common working ‘pick-list’ of fauna names. This list was based on identifications from NIWA’s ‘working guide’ to identifying fauna from seafloor images (which is supported by a ‘library’ of example images of fauna) and published identification resources. Unknown or unidentifiable animals were initially tagged with a placeholder identification on the faunal pick-list, and representative images were sent to taxonomic experts for identification. The faunal pick-list and working guide/library was updated during the analysis by adding names for fauna newly encountered during the analysis. These names were based on a consensus among observers or as advised by taxonomic experts.

An audit of the faunal identifications among observers was undertaken, including a formal annotated review by one observer of all the images identified by the other two observers for one transect. After fauna on all images were identified, a meeting among observers was held to discuss the resulting data and any potential identification issues and to carry out any necessary identification reconciliation.

2.4.2 Box-core samples

On return to the laboratory, the box-core samples were sieved on two stacked sieves (1 mm and 300 µm mesh) and the remaining material stained with 0.2 % Rose Bengal (to aid the visual recognition of macrofauna among the retained material). Material retained on the 1 mm sieve was sorted by eye on a white tray. Macrofauna were removed, separated into major taxonomic groups and preserved in 80% ethanol. The coarse sediment fraction (> 1 mm) was retained for separate analysis (see below). The material retained on the 300 µm sieve was also sorted by eye in a white tray. The macrofauna from this fraction were removed, separated into major taxonomic groups using a dissecting microscope, added to those collected from the 1 mm sieve and preserved in 80% ethanol. Some of the box core samples contained a large amount of fine sediment (300 µm – 1 mm). For these samples an elutrification process was used to first separate the macrofauna and lighter material prior to sorting in a white tray. The elutrification process was repeated three times. The remaining sediment of the first 10 samples processed in this manner were checked for any remaining macrofauna. This check revealed that more than 90% of the macrofauna was retained in the elutriate and no major taxonomic bias was noted. The fine sediment fraction (300 µm – 1 mm) was not retained for any additional analysis.

The macrofauna sorting was carried out by three trained technicians and a quality assurance check was carried out by another technician (the most experienced sorting technician on site) on 10% of the samples sorted. No sorting inconsistency or macrofauna recovery issues were identified by this audit.

Sorted macrofauna were then identified to the lowest possible/practical taxonomic level by taxonomists or parataxonomists, counted and stored in 80% ethanol.

Sediment retained on the 1 mm sieve (i.e. > very coarse sand particle size) from each box-core sample was first sorted into chalk and non-chalk material, and then wet weighed separately on a balance (± 0.001 g). The non-chalk material was predominantly phosphorite nodules, and the weight of this fraction was considered to equate to the weight of nodules in a sample.

Sediment sub-cores taken from the box-cores during the survey were processed by Royal Boskalis and Hill Laboratories on behalf of CRP, and resulting data were used in the benthic community analysis and for characterising the habitat (see below).

2.5 Habitat characterisation

About 3 km^2 of ROV-mounted 7125 system MBES data and more than 500 km^2 of ship-mounted 8160 system MBES data were collected during the survey. The former data were gridded at 10 cm and the latter data were gridded at 25 m resolution. Data were exported from the PDS2000 software as ASCII files prior to laboratory processing.

The intention was to re-process all the MBES backscatter data using SonarScope, a processing software developed by the French research organisation IFREMER (L'Institut Français de Recherche pour l'Exploitation de la Mer), with which NIWA has close links. However, the quality of the backscatter data was unsuitable for this form of re-processing, these data were not re-processed and have not been used in subsequent analyses. The absence of the backscatter data was a significant impediment to deriving robust estimates of the spatial variation in benthic habitat, and for use in benthic community analysis and subsequent habitat suitability modelling. As a consequence, effort was focused on characterising the habitats using seafloor morphology derivatives from the MBES bathymetry data.

These metrics were: depth, slope (steepest gradient to any neighbouring cell); aspect (direction of slope); curvature (change of slope); plan curvature (curvature of the surface perpendicular to the slope direction); profile curvature (curvature of the surface in the direction of slope). In addition a further set of derivatives were calculated for the standard deviation of depth, depth range, standard deviation of the slope, terrain rugosity, based on a 3, 5, 7 and 15 grid cell focal mean.

The methodology for determining these metrics from the MBES bathymetric data are provided in the companion report by Nodder et al. (2013). This report also details how data from the sediment samples, and sediment samples from previous sampling, were used to generate further information on the habitat characteristics of the study area (including %mud, %sand, %gravel, nodule density).

2.6 Benthic community analysis

2.6.1 Pre-analysis treatment

In order to construct datasets suitable for the final analysis, data were first subjected to modification and assessment.

Some taxa from the image data records were removed prior to analysis. Fish species respond differently to the presence of a ROV and its lights (e.g. avoidance response), and therefore a complete record of the demersal or benthic fish community is not reliably obtained by just using this method of data capture. Thus, fish taxa records were not included in the final dataset (32 taxa), leaving the focus of the analysis on the invertebrate communities alone. Some invertebrate taxa were also removed from the data for the following reasons: (1) their abundance was too low to provide useful information about variation in community structure ($n < 7$), (2) they were infaunal taxa (e.g., echiurans), and (3) they were ill-defined and/or could be confused with other taxa. Several taxa were also combined due to possible uncertainties about their identity.

Data for lebenspurren (life traces of animals) were also not included in the datasets to be analysed because records that relate to infauna were too sparse to allow for a meaningful community analysis. Originally it was intended for these data to be analysed separately as another means to characterise the infauna community, particularly those animals not well-sampled by a box-corer (i.e. large animals that exist in low densities and/or live in deep burrows). However, CRP requested that data for scampi (*Metanephrops challengeri*) burrows (and visible scampi) be examined, and a brief commentrary on these data appear in Appendix A. Lebenspurren records that related to epifauna were never intended to be analysed, and so they too were excluded from the image dataset used in the final analysis.

Appendix B, which details all taxa observed on the analysed seafloor images indicates which taxa were not included in the image dataset used in the final analysis.

Appendix C details all infauna taxa that were sampled by the box-corer. Twenty-four taxa were removed from the dataset prior to analyses for one or more of the following reasons: (1) too few individuals were recorded to provide useful information on community structure ($n < 6$), (2) taxon was not well defined because specimens were either immature or damaged, and could therefore have been confused with other taxa, and (3) the lower mesh size used (300 µm) too coarse to provide reliable estimate of abundance (e.g., nematodes).

Box-core samples differed both in the degree of disturbance incurred during sample retrieval (sample quality), and in the volume of sediment they contained (sample quantity). Sample quality was assessed on-board ship immediately after sample retrieval, and each box-core was assigned to one of three categories (good, fair, or poor) (see section 2.3.2). Prior to the final analysis, box-core data was subjected to some statistical tests to determine if sample quality and quantity would influence patterns of benthic community structure revealed by the analysis. There was no significant difference in infauna abundance between good, fair, and poor box-cores (PERMANOVA, $P > 0.05$), and no relationship was found between sample volume and infauna abundance (DistLM, $P < 0.05$) (see below for details about these statistical techniques). All box-core samples were therefore included in the final analyses.

2.6.2 Datasets

Analyses were conducted on two main datasets: epifauna (image data from ROV) and infauna (box-core data). The epifaunal image dataset comprised a large number of images (2844), a substantial proportion of which (25%) contained no observable fauna. Analyses of the epifauna dataset were therefore conducted at the level of both individual images and transects (i.e., pooling all images within each transect). Transect-level analyses helped avoid problems associated with the large number of faunal observations with low (or no) abundance, and enabled the investigation of patterns at larger spatial scales (~6000 m^2 at transect level vs ~6 m^2 at image level).

2.6.3 Statistical approach

Analyses of community structure were conducted using statistical routines in the multivariate software package PRIMER v6 (Clarke & Gorley 2006). Analyses were based on similarity matrices built using Bray-Curtis similarity (Clarke et al. 2006) of square root-transformed abundance data. The square root transformation was used to decrease the influence of highly abundant taxa on community patterns (Clarke & Warwick 2001).

The following procedure was used for the analysis of each dataset: first, natural group structure in the samples was identified using a similarity profile test, and the results of the analysis were superimposed on a map of the study area for graphical representation and description of spatial patterns in community distribution. The taxa contributing most to within-group similarity were also identified using a similarity percentage routine. The contribution of the different spatial scales to variation in community structure were compared using a multivariate version of ANOVA. Finally, the relationship between three sets of predictor variables and benthic community structure were investigated using a form of multivariate multiple-regression. The three sets of predictor variables were (1) spatial variables, (2) substrate variables, and (3) topographical variables. The nature and number of variables differed between each dataset and details of analyses conducted are given below.

2.6.4 Epifauna (image-level)

A total of 2844 images were analysed for epifauna community structure from 39 transects across 13 survey areas (Appendix D). Spatial patterns in community structure were described using group-average hierarchical cluster analysis in the routine CLUSTER (Clarke & Warwick 2001). A similarity profile test (SIMPROF) was performed to identify natural group structure in the samples, i.e. communities (Clarke et al. 2008). The SIMPROF routine conducts a series of permutation tests to find clusters of samples with statistically significant internal structure (P set at 0.01; Clarke & Warwick 2001). SIMPROF could not be performed directly on the epifaunal image data because of the high number of samples and associated high computing power required. Instead, a first classification of the still images was conducted based on the epifauna data and using k-means grouping with the Calinski-Harabasz stopping statistic (Milligan & Cooper 1985, Calinski & Harabasz 1974). This process classified all images into 108 classes. Fauna abundances across all images in each of those classes were then averaged and SIMPROF was performed on those values (P set at 0.01). The SIMPER routine was used to identify the five taxa contributing most to within-group similarity for each SIMPROF group (Clarke and Warwick 2001).

The PERMANOVA routine in PRIMER was used to compare the effects of different spatial scales (i.e., survey area and transect) on benthic community structure (Anderson et al. 2008). PERMANOVA is a semi-parametric, permutation-based routine for analysis of variance based on any similarity measure (e.g., Bray-Curtis). Analyses were conducted using the fixed factor Survey Area and random factor Transect nested within Survey Area (Quinn & Keough 2009). P-values for individual predictor variables were obtained using 9999 permutations. Because PERMANOVA is sensitive to differences in multivariate dispersion among groups, the PERMDISP routine in PRIMER was used to test for homogeneity of dispersion when significant factor effects were found (Anderson et al. 2008). The square root of estimates of components of variation was used for comparing the amount of variation attributable to the two factors (i.e., Survey Area and Transect) in the multivariate PERMANOVA models (Anderson et al. 2008).

Because many of the images (25%) contained no faunal data (i.e., no fauna were observed) the similarity matrix for PERMANOVA (and DistLM, see below) was built by adding a “dummy” taxon to avoid undefined similarities between pairs of images (Clarke & Warwick 2001). This procedure assumes that images without any fauna are 100% similar to each other, which in the case of epifauna is a reasonable assumption.

Relationships between epifauna community structure and predictor variables were investigated using Distance-based Linear Models (DistLMs) in PERMANOVA+ (Anderson et al. 2008). The DistLM routine is based on an approach called distance-based redundancy analysis (dbRDA) first developed by Legendre & Anderson (1999). It is a semi-parametric, permutation-based method that does not rely on the assumption of normally distributed data, and is a form of multivariate multiple regression that can be performed directly on a distance or dissimilarity matrix of choice (Anderson et al. 2008). The analyses conducted in DistLM are based on the individual samples, thereby allowing straight-forward interpretation of partial regression tests (Anderson et al. 2008). In contrast, other approaches, which treat the individual distances as a single univariate response, are problematic for the interpretation of multiple regression analyses (e.g., the Mantel approach, Dutilleul et al. 2000, Legendre et al. 2005, Anderson et al. 2011).

Variability in benthic community structure was partitioned according to three sets of predictor variables in DistLM, i.e., spatial (latitude, longitude, and water depth), substrate (visual observations of sediment physical characteristics derived from ROV images, see section 2.4.1; i.e. the substrate variables mud/sand, nodules, chalk, dark patches, boulders, cobbles, scour, and ledge, and an additional substrate variable (habitat diversity) was derived by adding substrate observations for each image), and topography variables (210 bathymetry-derived variables derived from ROV and ship-based MBES data; see section 2.5 and Nodder et al. (2013)). Because the image dataset was so large, and because the DistLM routine has high computing power requirements, not all 210 bathymetry-derived topography variables could be entered in the DistLM models. In addition, only variables derived from ship data could be used because there were large gaps in the data obtained by the ROV. Some data were missing from the ship data, but only for 83 images (which represent < 3% of all images); these images were therefore removed from the dataset prior to DistLM analyses. DistLM analyses were conducted using a set of nine bathymetry-derived variables (one for each derivative), using either the smallest or largest spatial scale. The smallest scale consisted of the smallest neighbourhood size (1 grid cell of size 25×25 m), whereas the largest spatial scale consisted of the largest neighbourhood size (15x15 grid cells of size 25×25 m). The set of variables providing the strongest overall correlations (R^2) was selected.

Relationships between predictor variables and benthic community structure were initially examined by analysing each variable in marginal tests. Sequential tests using a step-wise selection procedure and using the Akaike Information Criterion (AIC) as selection criterion were then used to determine which set of variables were most strongly correlated with benthic community structure (Quinn & Keough 2009). P-values for individual predictor variables were obtained using 999 permutations of raw data.

2.6.5 Epifauna (transect-level)

Faunal data from all analysed images were pooled for each of the 39 transects prior to analyses (n = 34-99 images per transect). The SIMPROF routine was used to identify natural groupings (P set at 0.01). Variability in community structure was partitioned according to three main sets of predictor variables in DistLM, i.e., spatial (latitude, longitude, and water depth), substrate (mud/sand, nodules, chalk, dark patches, boulders, cobbles, scour, ledge, and habitat diversity (calculated using the Shannon–Wiener diversity index (Etter & Grassle, 1992)), and topography variables (210 bathymetry-derived variables based on ROV and ship-based MBES data; see section 2.5 and Nodder et al. (2013)). For each transect, substrate observations from all analysed ROV images were added, and the mean and standard deviation of each spatial and topography variable were used as predictor variables in the DistLM analysis (see above).

2.6.6 Infauna

Data were available from a total of 77 box-cores for infauna community analyses (Appendix E). Preliminary cluster analysis showed five highly divergent box-core stations (DD74, 80, 81, 136, and 163), which showed low similarity with other stations (<30%). These stations had the lowest abundance of all the box-core stations (n < 20). These box-core stations were omitted from subsequent analyses to avoid the overriding influence of these low abundance samples in analyses of infauna community structure.

SIMPROF, SIMPER, PERMANOVA and PERMDISP analyses were conducted as for the epifauna analyses. Variability in infauna community structure was partitioned according to three sets of predictor variables in DistLM, i.e., spatial (latitude, longitude, and water depth), substrate (sediment physical characteristics measured from sediment sub-cores taken from the bx-cores - % mud, % sand, % gravel, median particle diameter, sorting, and nodule weight; see section 2.4.2 and Nodder et al. (2013)), and topography (210 bathymetry-derived variables derived from ROV and ship-based MBES data; see section 2.5 and Nodder et al. (2013)). Sediment parameter data were missing for 11 of the 72 box-core samples analysed, except for nodule weight, for which no data were missing. Initial DistLM analyses showed that benthic community structure was significantly but weakly correlated with most sediment parameters, with % gravel and nodule weight as the two variables showing the strongest correlations (R^2 = 0.05-0.06, P = 0.001). When either variable was fitted first into the regression models, correlations with all the other sediment parameters became non-significant (P > 0.05). Thus it was decided to use nodule weight as the only sediment variable in the final DistLM analyses of infauna because (1) there were no missing data for this variable, (2) % gravel largely reflects the amount of nodules present in the sediment, and (3) the same procedure was used to derive all nodule weight data, whereas other variables were derived using different methods and in different laboratories (see Nodder et al. 2013).

2.7 Habitat suitability modelling

2.7.1 Datasets

The results of the benthic community analysis provided the location of eipfauna and infauna communities in the study area (see sections 3.2.1 and 3.2.3).

Data for the predictor variables were provided by the habitat characterisation layers generated by Nodder et al. (2013).

Separate data layers for longitude and latitude (spatial variables that act as proxies for unmeasured environmental variables) were also generated. The layers for these spatial variables (that act also as proxies for unmeasured environmental variables) used the latitude/longitude for the centroid of each 25 x 25 m grid cell across the area covered by the other environmental data layers.

2.7.2 Modelling approach

Boosted regression tree (BRT) models were generated to interpret the distribution of benthic communities relative to environmental variability, and to predict the distribution of benthic communities across the study area.

BRT is an ensemble method that interprets complex relationships between species (or groups of species/communities) and their environment by partitioning similar observations into groups based on many simple classification or regression trees (Elith et al. 2006, Leathwick et al. 2006). The first of two algorithms implemented in BRT partitions the response variable (species or groups of species/communities) into groups with similar characteristics using regression or classification trees. Boosting is the second algorithm and stems from machine learning where trees are fitted iteratively, emphasizing observations that poorly fit the existing collection of trees (Friedman et al. 2000). Boosting combines these trees to minimize misclassification errors and improve predictive performance over a single tree model (Leathwick et al. 2006). Additional advantages to BRT are its ability to include continuous and categorical data, handle missing and outlying data, cope with irrelevant and correlated predictor (environmental) variables, and automatically fit interactions between predictors.

Boosting is optimized by the learning rate (lr) that considers residual variation during tree building, and tree complexity (tc) that estimates interactions between predictor variables. Model fit and predictive performance are balanced to reduce overfitting by jointly optimizing the number of trees (nt), lr, and tc (Elith et al. 2008).

The relative importance of predictor variables in a model is determined by its contribution to the model as measured by the number of times it is selected for tree splitting. The contribution of each variable is scaled so that the sum equals 100, with higher numbers reflecting stronger influence on the response variable (Elith et al. 2008). Fitted-functions are produced by BRT that show the effect of a focal predictor on the response while controlling for the average effect of all other variables in the model (Buston & Elith 2011).

BRT models of species distribution have been shown to be an effective method to understand the ecological drivers of species distribution patterns, and a reliable approach to generate predictions of species distributions across many scales (Buston & Elith 2011, Elith et al. 2006, Leathwick et al. 2006, Torres et al. 2013), including benthic communities (Compton et al. 2012).

2.7.3 Model analysis

The ‘gbm’ package version 1.6-3.1 (Ridgeway 2007) implemented in R (R Development Core Team 2011), plus custom code available online (Elith et al. 2008), was used to generate BRT models of the epifauna and infauna benthic communities.

Models were not generated for communities for which there were insufficient data to make robust models. This meant that no models were made for the six less observed epifauna communities at the image-level scale (n = < 40 images), and two infauna communities (n = < 10 box-core samples). Models of epifauna communities at the transect-level scale were also not generated due to insufficient explanatory capacity of the predictor variables. BRT models for these communities could not be generated without error, likely due to the high environmental variation along single transects which could not be used to describe communities based on averaged data.

Binomial (presence/absence) BRT models were generated, using a bernoulli distribution, for the remaining benthic communities: the three main infauna communities (Communities *d*, *g*, *h*) and six epifauna communities (Communities *c, g, h, l, k, l*). Additionally, an abundance model (using a poisson distribution) for the stony coral *Gonicorella dumosa* was generated.

For each community and the *Goniocorella dumosa* model, five initial models were generated with the response variable, either presence/absence or abundance, related to a suite of environmental predictor variables at one of five different spatial scales: sampling point, 3 grid cell focal mean, 5 grid cell focal mean, 7 grid cell focal mean, and 15 grid cell focal mean. Predictor variable values of longitude, latitude, depth, nodule density, %mud, %gravel and %sand at the sampling point were included in all models. The other scale appropriate predictor environmental variables in each model were aspect, curvature, plan curvature, profile curvature, depth range, standard deviation of depth, slope, standard deviation of slope, and rugosity.

The predictive performance of these five scale models were compared based on area under the receiver operating curve (AUC), and cross-validation per cent deviance explained (CVdev). AUC is widely used to evaluate binomial models (Fawcett 2006) by measuring the ability to discriminate between areas with species/community presence or absence. AUC ranges from 0 to 1: 1 = perfect discrimination, < 0.5 = worse than random, > 0.7 is considered ‘‘useful’’ (Swets 1988). Although AUC has limitations for measuring model performance (Austin 2007, Lobo et al. 2008), it can be used as a relative metric of model performance because it provides a single value that is easy to interpret. CVdev is estimated by a cross-validation procedure run during the modelling process that withholds a subset of data at each tree. CVdev is a measure of the goodness of fit between the predicted and raw values and indicates how well the model predicted the subsets of withheld data (Buston & Elith 2011).

Once the appropriate scale for each model was determined, each model was optimized based on the above described performance metrics (AUC and CVdev) by varying the tree complexity (number of interactions allowed between variables) and only including predictor variables that contributed more than 5% to the model (Buston & Elith 2011). Fitted-functions of the optimized models were produced to show the effect of each predictor variable in the model on the response while controlling for the average effect of all other variables in the model (Buston & Elith 2011).

2.7.4 Predictive mapping

Predictive maps were made for the habitat suitability (scaled low (0) to high (1)) of each benthic infauna and epifauna community. A predictive map of *Goniocorella dumosa* probability of occurrence was also derived from the optimal model of abundance. Mapped predictions were produced using the function predict.gbm (Ridgeway 2007) and the package Raster (Hijmans 2010) in R (R Development Core Team 2011). The output prediction ascii file was converted to a raster in ArcGIS (version 10, ESRI) and projected into UTM 60S for display. Due to the highly skewed nature of the raster data (many more low values of community presence), map illustration was optimised using a two-standard deviation 'stretch' (the default setting in ArcGIS for raster datasets that have statistics). This approach is used to brighten raster datasets that normally appear dark, by preventing pixel values being stretched to the extremes, and overemphasising the areas of low values. This form of illustration was chosen to, in effect, highlight those areas that have a greater proportion of individual pixels with relatively high habitat suitability. With the colour ramp used, these areas appear as conspicuous red patches on the output maps and thereby aid the visual appreciation of where generally in the study area suitable habitat is more likely to be found. It must be noted that within these areas, there are individual pixels that are not predicted to be suitable habitat (see Appendix F for a more detailed explantion and illustration).

As well as the individual prediction maps of each community, composite maps were made of the six epifauna communities with predicted habitat suitability greater than 0.5, and two infauna communities with predicted habitat suitability greater than 0.75.

3 Results

3.1 Habitat characterisation

The results of the analysis of MBES bathymetric data, and substrate data compiled from sediment samples taken during the survey and previous surveys in the study area, are described by Nodder et al. (2013) in a companion report.

3.2 Benthic community analysis

3.2.1 Epifauna (image-level)

A total of 16,090 individuals belonging to 97 epifauna taxa were identified from the ROV images (Appendix B). The most diverse groups was the echinoderms (32 taxa), followed by cnidarians (25), sponges (16), and molluscs (7). The most abundant taxon was the stony coral *Goniocorella dumosa* (3621 counts), followed by brachiopods (lamp shells, 2628), "*Gracilechinus multidentatus*/juvenile *Paramaretia peloria"* (sea urchins/heart urchins, 2628 counts), "branching bryozoans/hydroids/other" (2080), and "*Paramaretia peloria*/*Spatangus multispinus*/Tam O'Shanter" (heart urchins/sea urchins, 1414).

The 2844 analysed images were classified into twelve communities by k means followed by SIMPROF (Figure 3-1); six of these community groups comprised at least 40 images, and the following focuses on these six communities. Spatangidae (heart urchins) accounted for most (96%) of the similarity of the largest community (Community *c*, n = 1114). Branching "bryozoans/hydroids/other" accounted for a significant proportion of within-group similarity of all six community groups except Community *h*. Galatheidae (squat lobsters) and Didemnidae (ascidians) accounted for much of the similarity of Community *k*, whereas "*Paramaretia peloria*/*Spatangus multispinus*/Tam O'Shanter" (heart urchins/sea urchins) and brachiopods (lamp shells) accounted for most of the similarity of community groups *l* and *i*, respectively. *Goniocorella dumosa* (stony coral) accounted for most of the similarity of Community *h*; Stylasteridae (hydrocoral) were also a substantial contributor for this community group (Figure 3-2). The highest mean dissimilarity between pairs of communities were observed between Communities *c* and *g*, and between *c* and *h*. Communities *g* and *h* showed the lowest mean dissimilarity (Table 3-2).

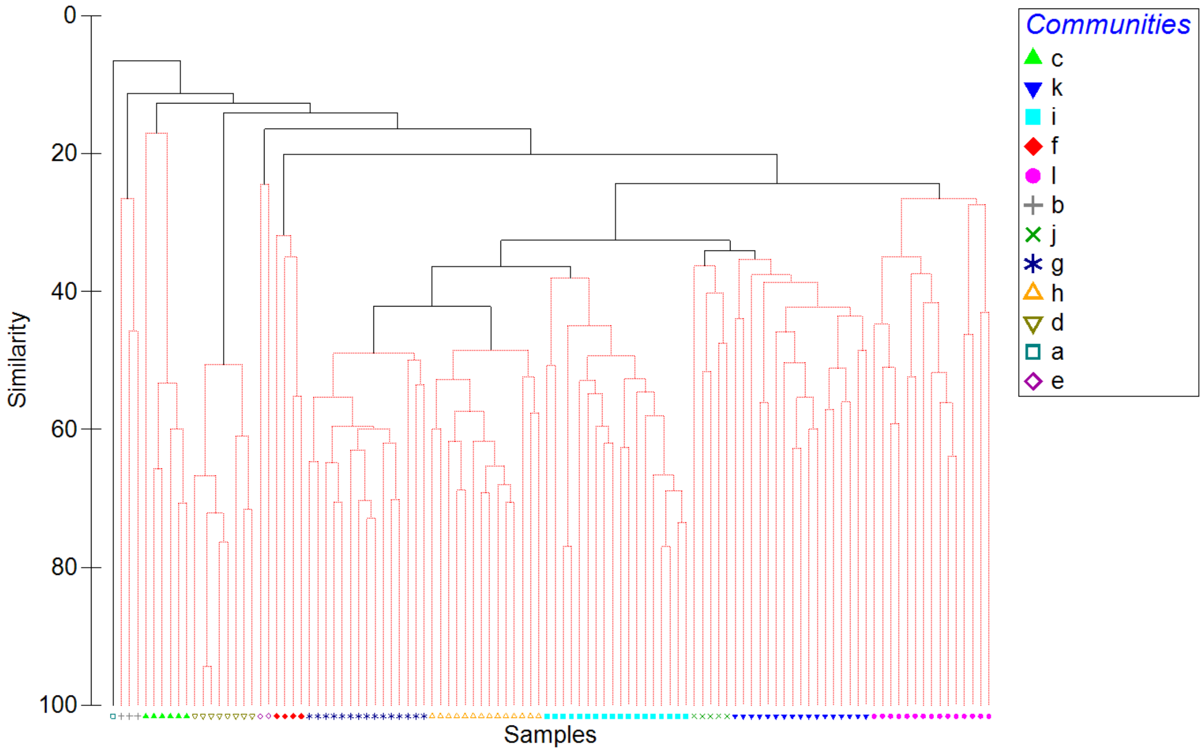


Figure 3-1: Dendrogram showing groups of samples identified as epifauna communities (image-level) by SIMPROF (after initial k means classification).

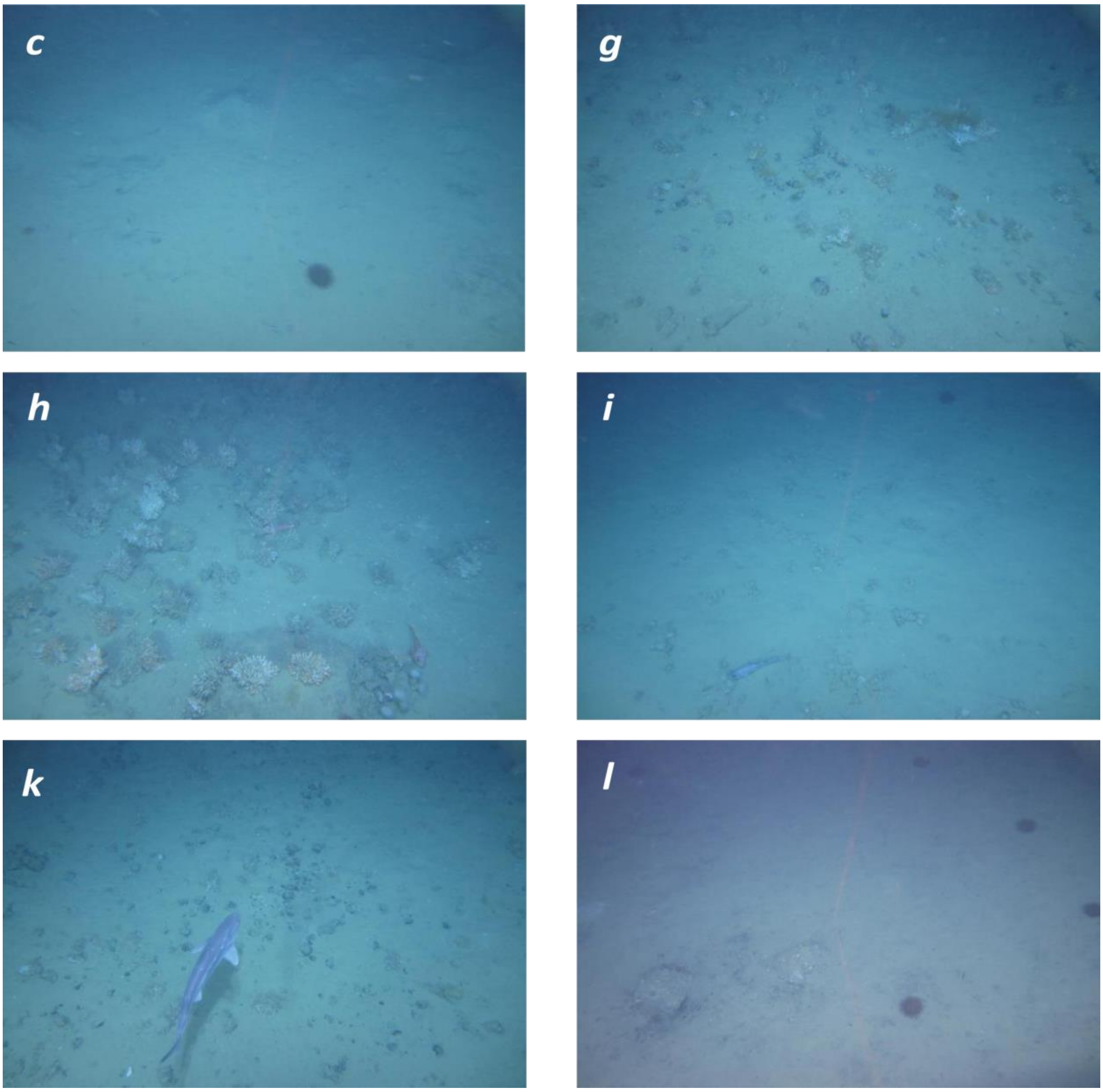


Figure 3-2: Seafloor images representative of the epifauna communities (image-level) identified by SIMPROF (Communities *c, g, h, I, k* and *l*).

Table 3-1: Results of the SIMPER analysis showing the five taxa contributing most to the within group similarity for the epifauna communities (image-level) identified by SIMPROF. [Only community groups with > 40 images are shown. Av. Abund = Average abundance, Av. Sim = Average similarity, Sim/SD = Similarity/Standard Deviation, Contrib% = % contribution to overall similarity, Cum% = % cumulative similarity].

Taxa	*Av.Abund*	*Av.Sim*	*Sim/SD*	*Contrib%*	*Cum.%*
Community *c* (n = 1114)					
Spatangidae	5.03	38.00	1.34	96.22	96.22
Branching bryozoan/hydroid/other	0.03	0.30	0.46	0.76	97.94
Paramaretia peloria/ *Spatangus multispinus*/ Tam O'Shanter	0.09	0.23	0.42	0.59	98.53
Flabellum	0.01	0.15	0.45	0.37	98.90
Zoroasteridae/Asteriidae	0.03	0.10	0.43	0.26	99.16
Community *k* (n = 590)					
Galatheidae	0.61	4.39	0.77	19.43	19.43
Branching bryozoan/hydroid/other	0.69	4.27	0.60	18.88	38.31
Didemnidae	0.47	3.14	0.57	13.90	52.22
Goniocorella dumosa	1.00	1.48	0.25	6.54	58.75
Gracilechinus multidentatus/ juvenile *Paramaretia peloria*	0.29	1.33	0.45	5.87	64.62
Community *l* (n = 520)					
Paramaretia peloria/ *Spatangus multispinus*/ Tam O'Shanter	6.84	14.91	0.90	68.43	68.43
Branching bryozoan/hydroid/other	0.51	2.04	0.50	9.38	77.82
Galatheidae	0.16	0.78	0.64	3.57	81.39
Cup corals (stalked)	0.44	0.70	0.20	3.23	84.62
Zoroasteridae/Asteriidae	0.20	0.69	0.17	3.16	87.78
Community *i* (n = 272)					
Brachiopoda	10.34	30.26	1.76	74.77	74.77
Branching bryozoan/hydroid/other	1.51	3.19	0.63	7.88	82.65
Galatheidae	0.66	2.50	1.48	6.18	88.83
Cidaridae	0.33	1.16	1.23	2.87	91.69
Didemnidae	0.77	0.92	0.72	2.28	93.97
Community *g* (n = 149)					
Branching bryozoan/hydroid/other	7.02	20.49	1.73	44.53	44.53
Goniocorella dumosa	6.98	13.89	1.14	30.20	74.73
Cidaridae	0.63	2.27	1.58	4.94	79.66
Didemnidae	0.55	1.85	1.58	4.03	83.69
Galatheidae	0.46	1.73	1.30	3.76	87.45
Community *h* (n = 103)					
Goniocorella dumosa	27.73	35.90	1.86	69.96	69.96
Brachiopoda	8.15	8.31	0.82	16.20	86.16
Galatheidae	1.48	2.16	1.31	4.22	90.37
Stylasteridae (white)	0.75	0.89	0.84	1.73	92.10
Didemnidae	0.74	0.80	1.03	1.57	93.67

Table 3-2: Mean dissimilarity (%) between epifauna community groups (image-level) identified by SIMPROF.

Community	*c*	*g*	*h*	*k*	*l*
g	91.69				
h	93.18	57.87			
k	81.56	64.92	73.13		
l	83.02	77.53	83.53	70.50	
i	85.77	63.68	63.77	65.90	74.06

Each transect comprised images classified as belonging to several community groups (i.e., the level of heterogeneity was high along transects). Images belonging to Community *c* were common in most transects and survey areas (Appendix G), but others, such as Community *h*, were more common in some transects than others (e.g., survey area 12 versus 2, Figure 3-3).

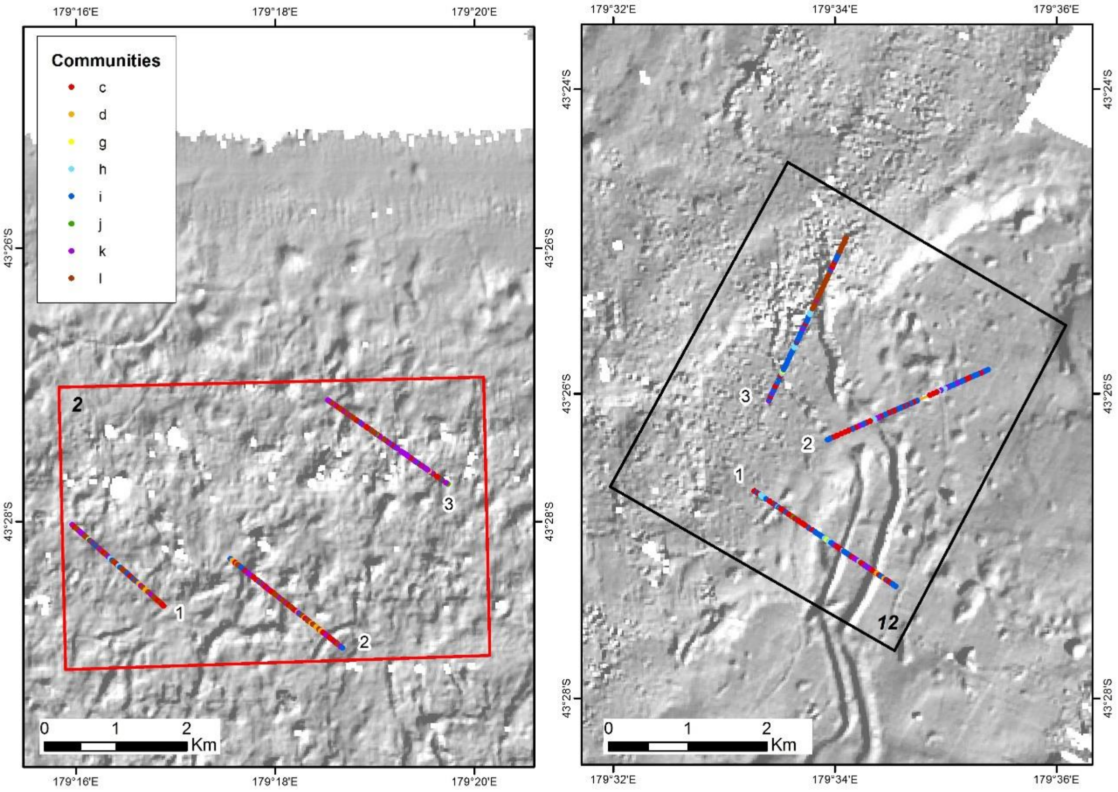


Figure 3-3: Maps showing the heterogeneous distribution of epifauna communities (image-level) within transects, and among survey areas (e.g. survey areas 2 and 12).

There were significant effects of the factors Survey Area and Transect on epifauna community structure (PERMANOVA, P = 0.001). There was a significant difference in multivariate dispersion between survey areas (PERMDISP, P = 0.001), indicating that among-survey area differences in community structure may be due to differences in multivariate dispersion. Survey areas 4, 5 and 6 (located in eastern half of the study area) were characterised by the highest mean multivariate dispersion (43.2 - 44.7), whereas survey areas 8, 15 and 16 (western half of the study area) were characterised by the lowest mean multivariate dispersion (31.6 - 32.1). Comparison of the square root of estimates of components of variation shows that the factor

Survey Area (13.54) explained about 30% more of the variation in community structure than the factor Transect (9.97), meaning that among-survey area (~5 - 50 km scale) variability was greater than within-transect (~1 - 5 km) variability .

DistLM results based on the bathymetry-derived topography variables at small and large spatial scales were very similar, with bathymetry-derived predictor variables only very weakly correlated ($R^2 < 0.01$) with community structure. Therefore, only the results of DistLM models based on the bathymetry-derived topography variables at the smallest spatial scale are shown. Epifaunal community structure was most strongly correlated with the substrate variables mud/sand and nodules in marginal tests ($P = 0.001$, $R^2 = 0.09$ and 0.07, respectively; Table 3-3). In sequential tests, the variables mud/sand, followed by longitude and latitude, were selected as the main predictors, and together explained 12% of the variability in epifauna community structure (image-level).

Table 3-3: Results of DistLM analyssi showing correlations between predictor variables and epifauna community structure (image-level). Only variables that are significantly correlated (<0.05) and with an $R^2 > 0.01$ are shown. AIC = Aikaike Information Criterion, SS = Sum of Squares, Pseudo-F = Pseudo-F Statistic, P = probablity, R^2 = proportion of explained variation attributable to each variable, R^2 (cumul.) = cumulative proportion of variation, res.df = residual degrees of freedom].

Variable	*AIC*	*SS*	*Pseudo-F*	*P*	*R^2*	*R^2 (cumul.)*	*res.df*
Marginal							
Mud/sand	-	479000	277.24	0.001	0.09	-	-
Nodules	-	380000	215.25	0.001	0.07	-	-
Dark patch	-	156000	84.792	0.001	0.03	-	-
Longitude	-	109000	58.732	0.001	0.02	-	-
Boulders	-	103000	55.281	0.001	0.02	-	-
Latitude	-	51377	27.294	0.001	0.01	-	-
Sequential							
Mud/sand	20576	479000	277.24	0.001	0.09	0.09	2758
Longitude	20517	103000	61.075	0.001	0.02	0.11	2757
Latitude	20489	51802	30.976	0.001	0.01	0.12	2756

3.2.2 Epifauna (transect-level)

SIMPROF analysis of the transect-level data classified the 39 transects into 5 communities (each comprising 5-10 transects), except for three transects that were left unclassified (Figure 3-4). Community *h* was the largest group and was characterised by high abundance of Spatangidae (heart urchins) and Brachipoda (lamp shells). "*Paramaretia peloria*/*Spatangus multispinus*/Tam O'Shanter" (heart urchins/sea urchins) and brachiopods (lamp shells) accounted for a substantial proportion of the similarity of Communities *e*, *f*, and *g*. *Goniocorella dumosa* (stony coral) accounted for much of the similarity of Community *e* and, to a lesser extent, Community *c* (, Figure 3-5). Communities *e* and *f* showed the highest mean dissimilarity, whereas communities e and c showed the lowest mean dissimilarity (Table 3-5).

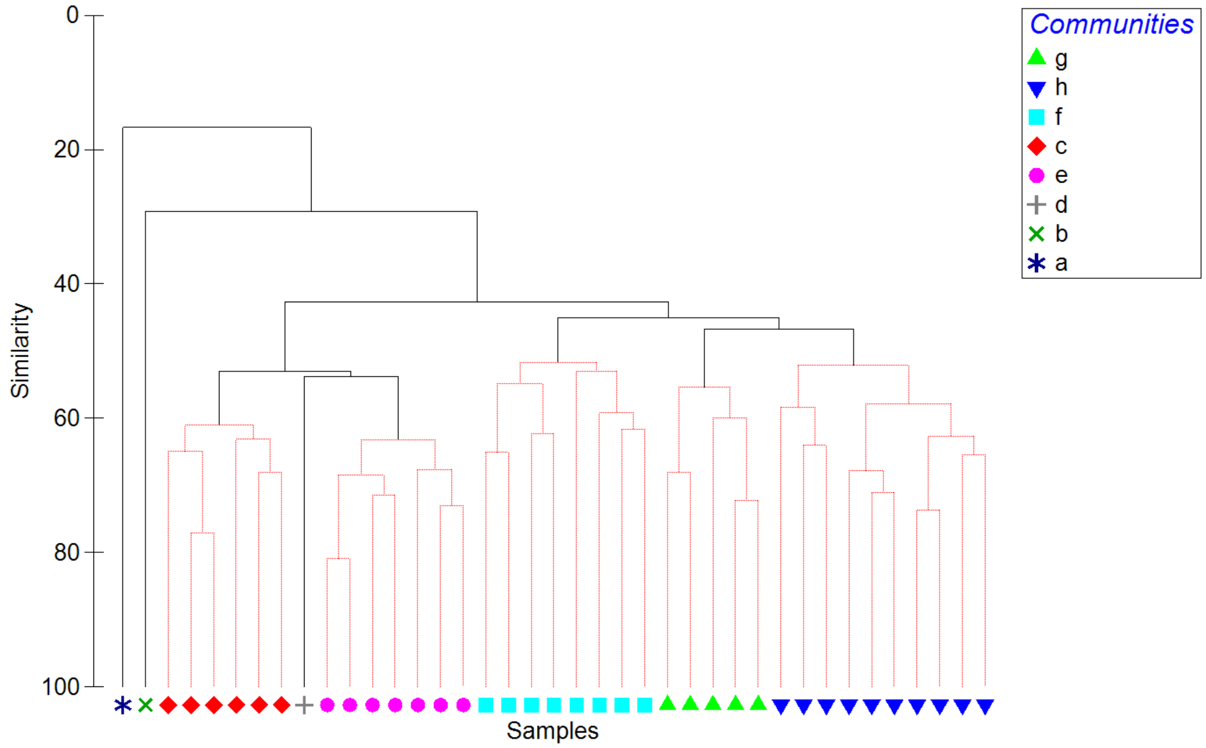


Figure 3-4: Dendrogram showing groups of samples identified as epifauna communities (transect-level) by SIMPROF.

Table 3-4: Results of the SIMPER analysis showing the five taxa contributing most to the within group similarity for the epifauna communities (transect-level) identified by SIMPROF. [Av.Abund = Average abundance, Av.Sim = Average similarity, Sim/SD = Similarity/Standard Deviation, Contrib% = % contribution to overall similarity, Cum% = % cumulative similarity].

Taxa	*Av.Abund*	*Av.Sim*	*Sim/SD*	*Contrib%*	*Cum.%*
Community *h* (n = 10)					
Spatangidae	38.80	9.42	0.78	23.09	23.09
Brachiopoda	46.00	8.40	1.43	20.59	43.68
Paramaretia peloria/ *Spatangus multispinus*/ Tam O'Shanter	40.40	8.02	1.11	19.64	63.32
Gracilechinus multidentatus/ juvenile *Paramaretia peloria*	85.80	4.11	0.58	10.06	73.39
Galatheidae	13.50	3.46	1.84	8.47	81.85
Community *f* (n = 8)					
Paramaretia peloria/ *Spatangus multispinus*/ Tam O'Shanter	53.25	17.12	1.65	35.10	35.10
Branching bryozoan/hydroid/other	30.63	11.79	1.82	24.18	59.28
Galatheidae	11.38	4.86	3.10	9.97	69.25
Didemnidae	10.50	3.60	1.72	7.38	76.63
Brachiapoda	11.88	1.99	0.70	4.07	80.71
Community *e* (n = 7)					
Goniocorella dumosa	313.00	26.77	2.68	45.21	45.21
Brachiopoda	187.57	14.30	1.10	24.16	69.37
Gracilechinus multidentatus/ juvenile *Paramaretia peloria*	59.71	3.31	1.10	5.59	74.96
Galatheidae	28.43	2.59	1.60	4.37	79.33
Paramaretia peloria/ *Spatangus multispinus*/ Tam O'Shanter	49.43	2.46	0.75	4.15	83.48
Community *c* (n = 6)					
Branching bryozoan/hydroid/other	186.00	22.20	3.38	40.25	40.25
Goniocorella dumosa	192.83	12.69	2.04	23.01	63.25
Brachiopoda	56.33	5.63	1.22	10.21	73.47
Gracilechinus multidentatus/ juvenile *Paramaretia peloria*	119.33	3.40	0.97	6.17	79.63
Didemnidae	22.33	2.48	2.53	4.50	84.13
Community *g* (n = 5)					
Brachiopoda	93.60	8.82	0.59	20.10	20.10
Paramaretia peloria/ *Spatangus multispinus*/ Tam O'Shanter	39.20	7.44	1.86	16.95	37.05
Suberites n. sp. 1	11.60	4.07	1.94	9.28	46.33
Cup corals (stalked)	13.60	4.05	1.70	9.23	55.56
Branching bryozoan/hydroid/other	17.20	3.72	1.18	8.47	64.03

Table 3-5: Mean dissimilarity (%) between epifauna community groups (transect-level) identified by SIMPROF.

Community	*c*	*e*	*f*	*g*
e	46.71			
f	57.45	62.80		
g	54.78	51.88	53.88	
h	58.74	52.36	55.57	53.30

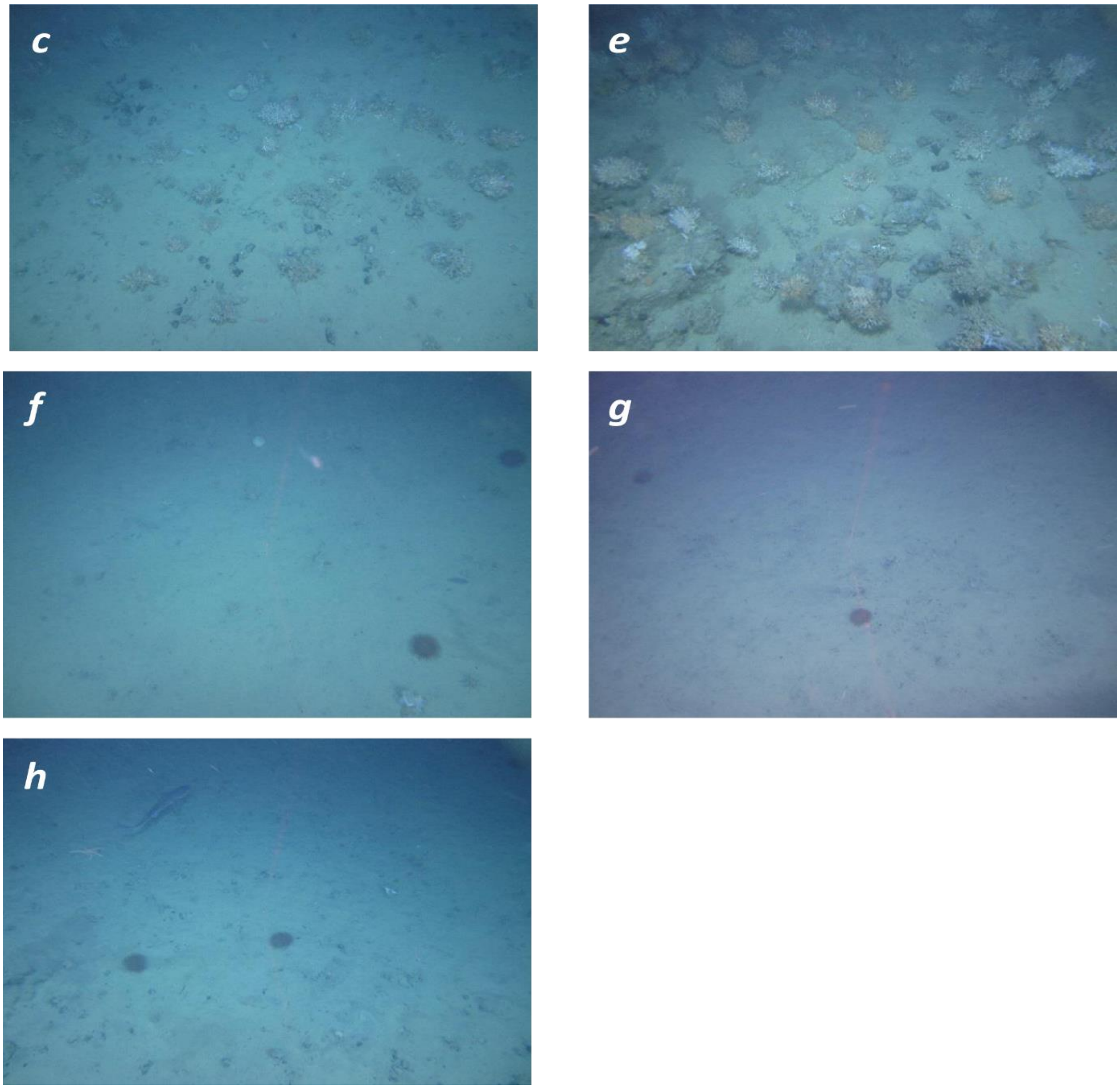


Figure 3-5: Seafloor images representative of the epifauna communities (transect-level) identified by SIMPROF (Communities *c, e, f, g*, and *h*).

The stony coral *Goniocorella dumosa* was much more abundant in the eastern half of the study area (Figure 3-6). Similarly, Community *e* (which was dominated by *Goniocorella dumosa*) was restricted to the eastern half of the study area. Community *c* comprised transects situated in the central and eastern portions of the study area. Community *f* was restricted to the central and western side of the study area, whereas Community *h* was distributed over the entire study area (Figure 3-7).

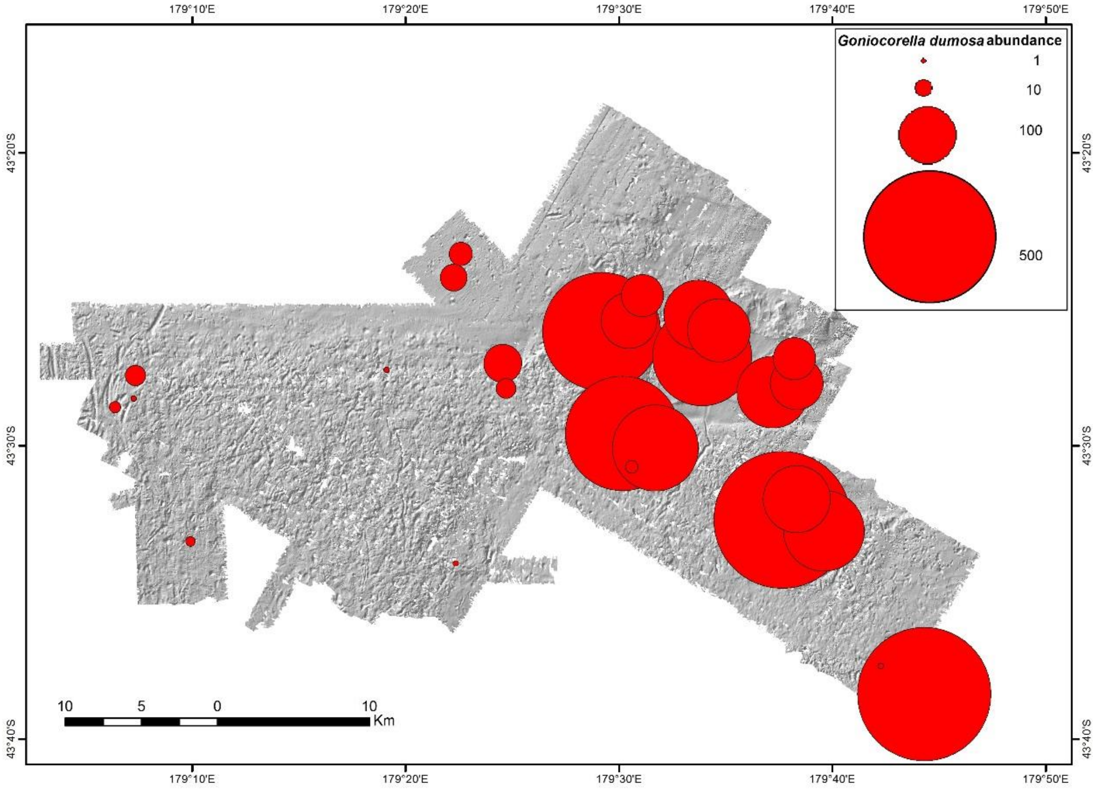


Figure 3-6: Distribution of the relative abundance of the stony coral *Goniocorella dumosa* in the study area. [abundance equals number of colonies imaged per transect]

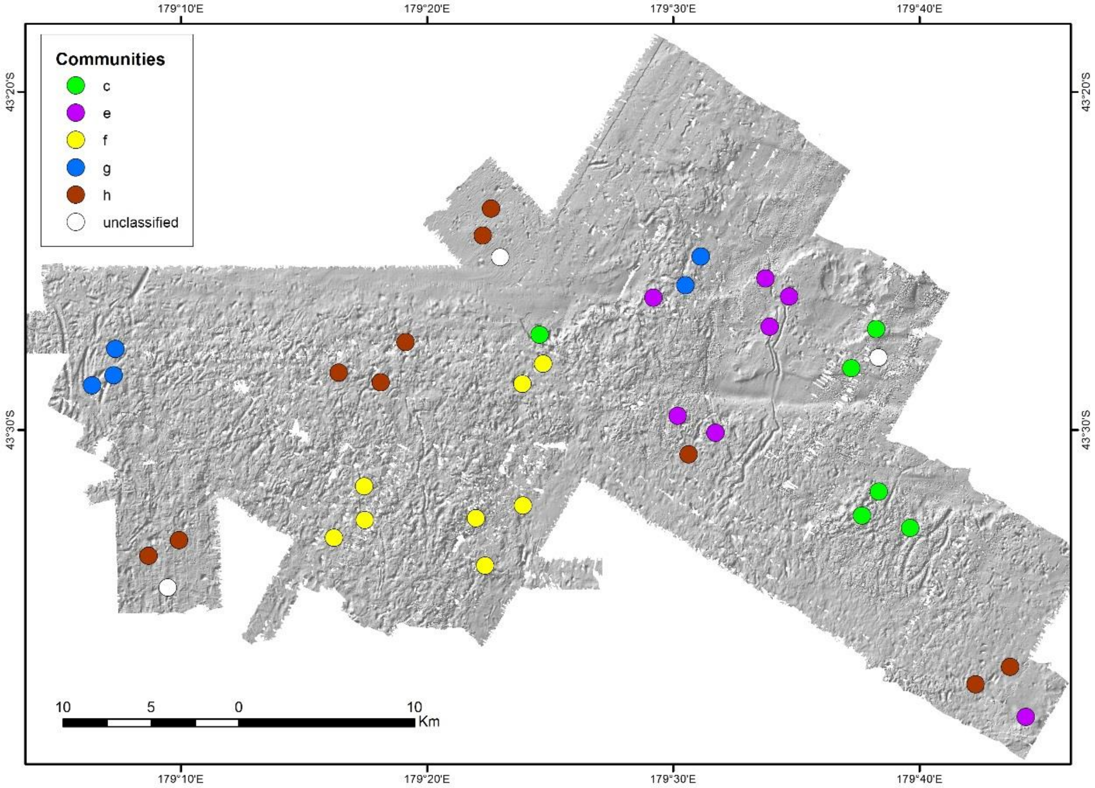


Figure 3-7: Distribution of epifauna communities (transect-level) in the study area.

Because image data were pooled by transect (i.e., no replication at the level of Transect), it was not possible to conduct a formal PERMANOVA test comparing variation at the scale of Survey Area and Transect. However, transects from the same survey area were generally more similar to each other than transects from different survey areas (e.g., survey areas 6, 8 and 12); there were some exceptions, however, with transects from some survey areas showing high dissimilarity from each other (e.g., survey areas 4, 14, and 16).

Epifauna community structure at the transect-level was significantly correlated with 162 out of the 225 predictor variables entered in the DistLM model. For the sake of brevity, only the results of the sequential tests are shown (Table 3-6). Community structure was most strongly correlated with substrate variables (dark patches, habitat diversity, nodules), followed by range of water depth (at 15 grid cell focal mean scale), and spatial variables (latitude, longitude, and water depth). Together, the substrate variables listed above explained about one quarter of the variability in community structure (R^2 = 0.26), whereas spatial variables explained about one fifth of the variability (R^2 = 0.18).

Table 3-6: Results of the DistLM analysis showing correlations (sequential tests only) between predictor variables and epifauna community structure (transect-level). [Only variables that are significantly correlated (P <0.05) are shown. AIC = Aikaike Information Criterion, SS = Sum of Squares, Pseudo-F = Pseudo-F Statistic, P = probablity, R^2 = proportion of explained variation attributable to each variable, R^2 (cumul.) = cumulative proportion of variation, res.df = residual degrees of freedom, gcfm = grid cell focal mean, SD = standard deviation].

Variable	*AIC*	*SS*	*Pseudo-F*	*P*	*R^2*	*R^2 (cumul.)*	*res.df*
Dark patch	286.54	6761.3	4.58	0.001	0.11	0.11	37
Habitat diversity	284.38	5531.5	4.0564	0.001	0.09	0.20	36
Depth range (15x gcfm)	283.03	4034.8	3.1343	0.001	0.07	0.27	35
Nodules	281.91	3466.0	2.8335	0.001	0.06	0.32	34
Latitude	280.92	3072.7	2.6326	0.002	0.05	0.37	33
Longitude	279.85	2912.2	2.6174	0.003	0.05	0.42	32
Longitude (SD)	279.36	2201.8	2.0434	0.015	0.04	0.46	31
Water depth	278.75	2163.5	2.0777	0.011	0.04	0.49	30
Curvature	278.19	1980.6	1.9631	0.015	0.03	0.52	29

3.2.3 Infauna

A total of 5248 individuals belonging to 307 infauna taxa were identified from the box-core samples and used in the final analyses (Appendix C). Arthropods and annelids were the most diverse phyla (87 and 80 taxa, respectively), followed by bryozoans (60), molluscs (36), echinoderms (27), and cnidarians (8). Annelids were the most abundant taxon (51% of total abundance), followed by arthropods (26%), echinoderms (7%), bryozoans (6%), molluscs (3%), and cnidarians (2%)

SIMPROF divided the box-core samples into 5 infauna community groups, except for 4 box-core samples that were left unclassified (Figure 3-8). Most of the box-core stations (88%) were classified within one of three main communities (Communities *d*, *g*, and *h*). Community *i* is not included in the following group comparisons because it comprised only samples from two box-core stations. Phoxocephalid amphipods were among the five species contributing most to within-group similarity of all groups except Community *e*. Lumbrinerid and cirratulid polychaetes were among the taxa contributing most to similarity of the largest community group (Community *g*, n = 41), whereas lysianassoid amphipods and capitellid polychaetes were among the highest contributors to Community *d* (n = 12). *Kinbergonuphis* sp. and Syllids (polychaetes) characterised Community *h* (n = 10) and *Escharella spinosissima* (a bryozoan), nephtydid polychaetes, and cirratulid polychaetes characterised Community *e* (n = 3) (). Pairs of communities showing the highest mean dissimilarity were Communities *e* and *i*, and *e* and *h*. The groups with the lowest mean dissimilarity were Communities *g* and *h* (Table 3-8).

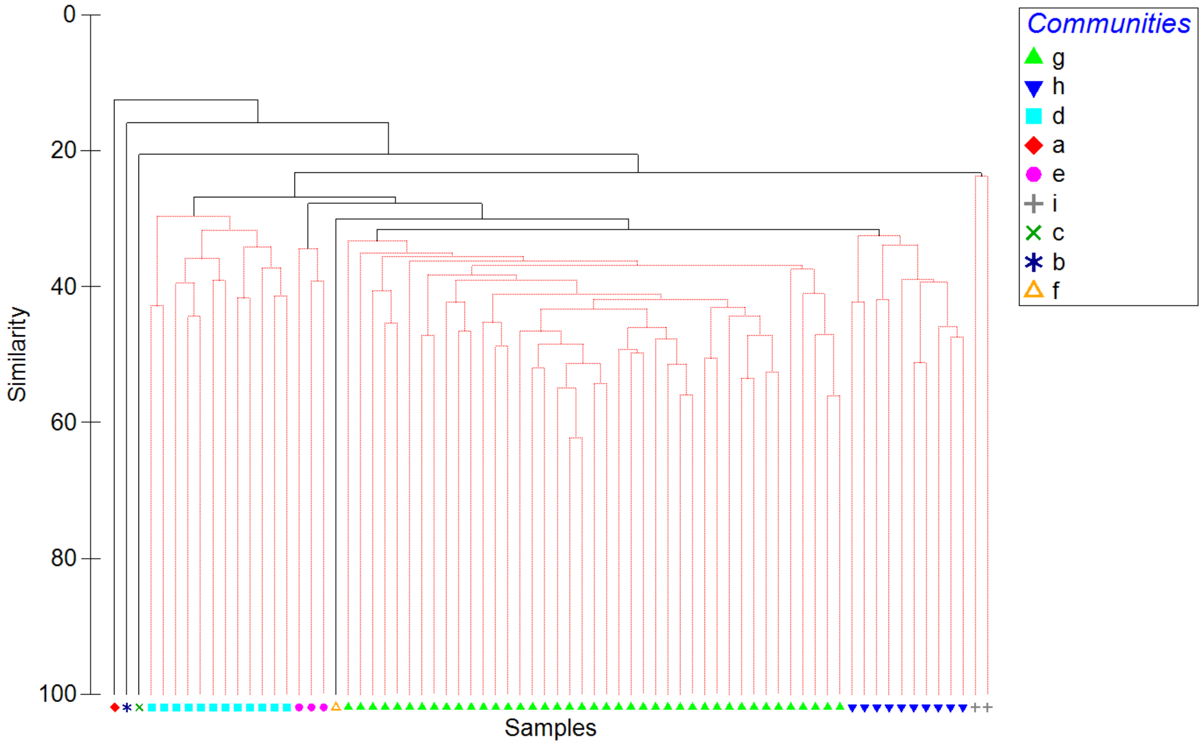


Figure 3-8: Dendrogram showing groups identified as infauna communities by SIMPROF.

Table 3-7: Results of SIMPER analysis showing the five taxa contributing most to the within group similarity of the infauna communities identified by SIMPROF. [Av. Abund = Average abundance, Av. Sim = Average similarity, Sim/SD = Similarity/Standard Deviation, Contrib% = % contribution to overall similarity, Cum% = % cumulative similarity].

Taxa	*Av.Abund*	*Av.Sim*	*Sim/SD*	*Contrib%*	*Cum.%*
Community *g* (n = 41)					
Lumbrineridae spp.	4.49	3.47	1.52	10.24	10.24
Phoxocephalidae sp. 1	4.22	3.03	1.10	8.93	19.17
Cirratulidae spp.	4.46	2.94	1.45	8.66	27.82
Urohaustoroidea sp.	4.34	2.54	1.00	7.49	35.31
Nephtyidae sp.	3.24	2.16	0.96	6.36	41.67
Community *d* (n = 12)					
Lysianassoidea sp.	7.67	2.98	0.98	10.72	10.72
Phoxocephalidae sp. 1	2.83	2.88	1.34	10.36	21.08
Eunice cf. *Eunice*-Seamounts-1	4.08	2.24	0.75	8.04	29.13
Capitellidae spp.	3.25	2.06	1.49	7.40	36.53
Lumbrineridae spp.	2.33	1.66	1.06	5.95	42.48
Community *h* (n = 10)					
Phoxocephalidae sp. 1	2.30	4.29	2.10	13.10	13.10
Kinbergonuphis sp.	2.40	3.48	1.35	10.61	23.71
Syllidae Eusyllinae/Syllinae	2.30	3.47	1.45	10.57	34.28
Lumbrineridae spp.	2.50	3.11	1.11	9.47	43.76
Nephtyidae sp.	1.50	2.33	0.97	7.12	50.88
Community *e* (n = 3)					
Escharella spinosissima	5.33	4.82	10.75	14.13	14.13
Nephtyidae sp.	5.67	3.68	1.15	10.79	24.92
Cirratulidae spp.	4.67	2.89	1.72	8.48	33.40
Chaperia sp.	3.00	2.89	10.75	8.48	41.88
Fenestrulina n. sp.	3.33	2.89	10.75	8.48	50.35
Community *i* (n = 2)					
Phoxocephalidae sp. 1	1.00	1.96	N/A	14.29	14.29
Cirratulidae spp.	2.00	1.96	N/A	14.29	28.57
Eunice sp.	2.50	1.96	N/A	14.29	42.86
Lumbrineridae spp.	1.50	1.96	N/A	14.29	57.14
Paraprionospio coora	1.00	1.96	N/A	14.29	71.43

Table 3-8: Mean dissimilarity (%) between infauna communities identified by SIMPROF.

Community	***d***	***e***	***g***	***h***
e	76.97			
g	72.40	70.58		
h	74.47	78.52	68.46	
i	77.52	83.75	76.38	75.62

Community *g* was distributed over the entire study area, as was Community *d,* although this community was more common in the west. Community *h* was restricted to the western side of the study area. Communities *e* and *i* were found in the north-east (Figure 3-9).

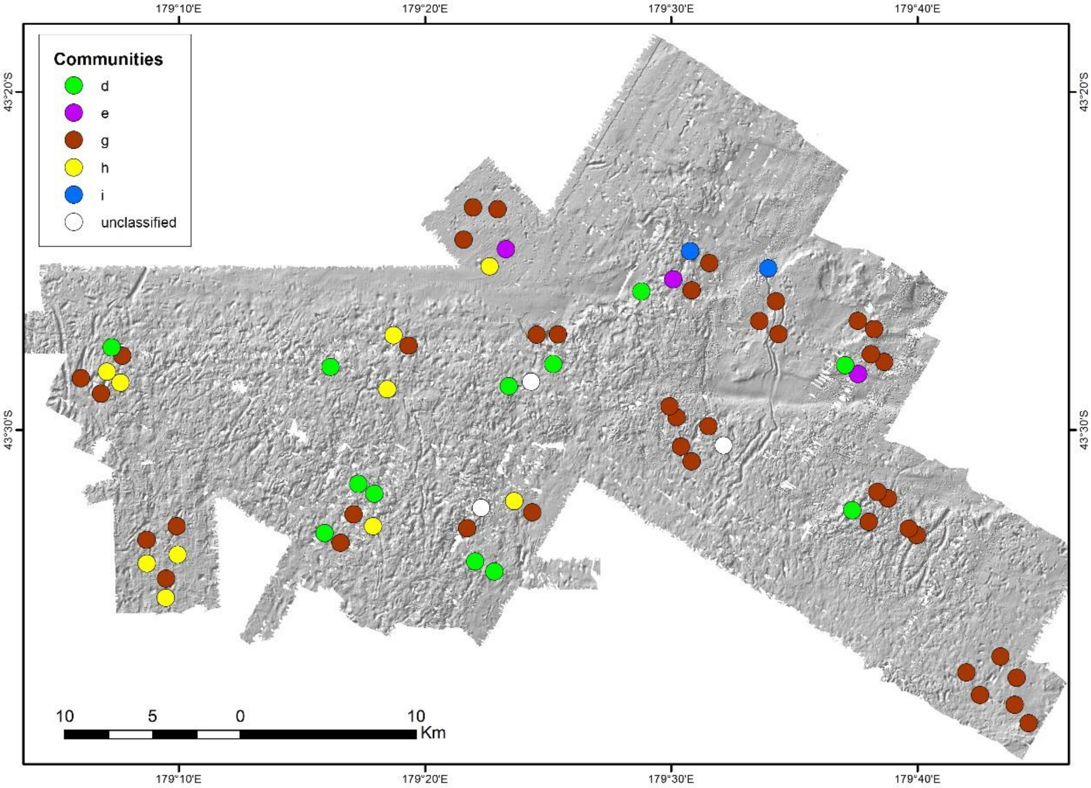


Figure 3-9: Distribution of infauna communities in the study area.

There were significant effects of Survey Area and Transect on infaunal community structure (PERMANOVA, $P < 0.05$). There was no difference in multivariate dispersion among survey areas (PERMDISP, $P > 0.05$). Comparison of the square root of estimates of components of variation suggests that factors Survey Area (12.19) and Transect (12.91) explained a similar proportion of the variation in infaunal community structure. These results suggest a similar levels of heterogeneity at the survey area (~5-50 km) and within-survey area (~1-5 km) scales.

Infauna community structure was significantly correlated with four of the 214 predictor variables entered in the DistLM regression analyses, and the correlations were weak ($R^2 < 0.05$). Nodule weight and longitude were selected in sequential tests as the most strongly correlated variables, and together explain 8% of the variability in infaunal community structure. Some bathymetry-derived topographic variables (i.e., curvature, rugosity) were also significantly correlated with community structure, but relationships were weaker than for the variables mentioned above ($R^2 = 0.02$).

Table 3-9: Results of the DistLM analysis showing correlation between predictor variables and infauna community structure. [Only variables that are significantly correlated ($P < 0.05$) are shown. AIC = Aikaike Information Criterion, SS = Sum of Squares, Pseudo-F = Pseudo-F Statistic, P = probablity, R^2 = proportion of explained variation attributable to each variable, R^2 (cumul.) = cumulative proportion of variation, res.df = residual degrees of freedom, gcfm = grid cell focal mean].

Variable	*AIC*	*SS*	*Pseudo-F*	*P*	*R^2*	*R^2 (cumul.)*	*res.df*
Marginal tests							
Nodule weight	-	8923.9	3.8166	0.001	0.05	-	-
Longitude	-	6278.9	2.6427	0.001	0.04	-	-
Profile curvature (15x gcfm)	-	4188.4	1.7409	0.013	0.02	-	-
Curvature (15x gcfm)	-	3867.4	1.6045	0.015	0.02	-	-
Sequential tests							
Nodule weight	551.86	8537.1	3.6962	0.001	0.05	0.05	69
Longitude	551.43	5363.8	2.3684	0.001	0.03	0.08	68

3.3 Habitat suitability modelling

3.3.1 Overall model performance

The final BRT model for each community or species abundance were at different scales (sampling point, and 3, 5 and 7 grid cell focal means), included different predictor variables, and had varying learning rates (range: 0.0009-0.008) and tree complexities (range: 2-4). The epifauna community models had a mean CVdev of 0.183 and an AUC of 0.789, with all models but one (Community *k*) having an AUC value greater than 0.72 (Table 3-10). Community *k* also had the lowest CVdev value (0.042) and for these reasons the model results are the least reliable, which is likely due to insufficient explanatory capacity of the predictor variables included in the model. An AUC value for the *Goniocorella dumosa* abundance model cannot be calculated, but the CVdev value for this model was 0.47, the highest of all models generated. The infauna community models had a mean CVdev of 0.204 and mean AUC of 0.848, with all models having AUC values greater than 0.77 (Table 3-11).

Appendix H provides the fitted functions for the BRT models of the epifauna and infauna communities.

Table 3-10: Model parameters and performance metrics of epifauna community (image-level) and *Goniocorella dumosa* boosted regression tree models. [tc = tree complexity, lr = learning rate, Cvdev = cross-validation per cent deviance explained, AUC = area under receiver operating curve, gcfm = grid cell focal mean].

Community	*Scale*	*Parameters (contribution %)*	*tc*	*lr*	*# of trees*	*CVdev*	*AUC*
c	Sampling point	Nodule density (19.70) Depth (12.64) Gravel (12.52) Rugosity [15x gcfm] (12.40) Aspect (11.41) Latitude (11.05) Longitude (10.91) Slope SD [3x gcfm] (9.38)	3	0.0075	1050	0.117	0.721
g	7x gcfm	Longitude (49.42) Depth (13.82) Profile curvature (13.40) Nodule density (12.42) Latitude (10.94)	3	0.004	1450	0.289	0.881
h	5x gcfm	Latitude (21.13) Longitude (19.59) Plan curvature (15.24) Depth (14.22) Curvature (13.84) Nodule density (8.48) Mud (7.41)	4	0.008	1250	0.291	0.906
i	3x gcfm	Latitude (32.39) Mud (18.97) Depth SD [15x gcfm] (12.47) Depth (12.37) Longitude (11.16) Rugosity [15x gcfm] (6.42) Curvature (6.22)	3	0.004	1300	0.173	0.789
k	5x gcfm	Latitude (18.51) Depth range [15x gcfm] (14.51) Longitude (14.23) Nodule density (13.56) Curvature (12.24) Gravel (9.27) Mud (9.10) Sand (8.58)	4	0.002	1400	0.042	0.639
l	5x gcfm	Longitude (29.40) Depth (15.42) Latitude (15.33) Nodule density (11.50) Depth SD [15x gcfm] (9.86) Aspect (9.55) Gravel (8.93)	3	0.0075	1200	0.187	0.799
Goniocorella dumosa	3x gcfm	Longitude (17.70) Rugosity [3x gcfm] (14.56) Depth (14.44) Aspect (12.77) Mud (11.64) Latitude (11.45) Depth range [3x gcfm] (10.40) Profile curvature (7.04)	4	0.0075	1100	0.47	NA

Table 3-11: Model parameters and performance metrics of infauna community binomial boosted regression tree models. [tc = tree complexity, lr = learning rate, Cvdev = cross-validation per cent deviance explained, AUC = area under receiver operating curve, gcfm = grid cell focal mean].

Community	*Scale*	*Parameters (contribution %)*	*tc*	*lr*	*# of trees*	*CVdev*	*AUC*
d	Sampling point	Nodule density (30.61) Depth range (13.84) Depth (13.68) Depth SD [7x gcfm] (10.13) Plan curvature (9.44) Slope SD [3x gcfm] (9.31) Aspect (6.86) Rugosity [5x gcfm] (6.12)	3	0.0009	1100	0.114	0.767
g	3x gcfm	Slope (26.11) Longitude (17.63) Nodule density (11.42) Depth (9.05) Slope SD [3x gcfm] (8.51) Plan curvature (7.23) Depth range [5x gcfm] (6.95) Aspect (6.58) Profile curvature (6.52)	3	0.002	1100	0.271	0.892
h	3x gcfm	Longitude (34.14) Plan curvature (27.97) Depth range [15x gcfm] (13.59) Curvature (8.53) Depth SD [7x gcfm] (8.47) Nodule density (7.30)	2	0.002	1050	0.228	0.886

3.3.2 Epifauna (image-level)

All models for the six main epifauna communities are considered ‘useful’ (i.e. AUC > 0.7), except the model for Community *k* (AUC = 0.639). Models for Communities *g* and *h* are particularly good (i.e. highest CvDev and AUC values).

Because the model for Community *k* (characterised by a range of non-related taxa/functional types) is not particularly robust, the results should be treated with some caution. Suitable habitat for Community *k* is predicted to be highest in two latitudinal bands in the northern and southern parts of the study area, with small patches of suitable habitat in between (Figure 3-10). Apart from spatial variables (latitude, longitude, depth range), the distribution of suitable habitat for this community is related to relatively high values for nodule density and seafloor curvature, and is also related to the proportions of gravel, mud and sand (Table 3-10, Appendix H).

It should be noted here that if the variables latitude and longitude were included in the best model for any community, and particularly if one of these variables is important (i.e. high % contribution), then the predictive maps tend to show areas of suitable habitat described by sharp vertical and horizontal boundaries.

Suitable habitat for Community *l* (characterised by urchins typical of soft sediment, and to a lesser extent epifauna taxa found on isolated hardground) is predicted to occur primarily in the shallower and western part of the study area, and a part of the north-eastern section of the study area (Figure 3-11). Apart from depth and the other spatial variables (longitude and latitude), the distribution of suitable habitat for this community is related to nodule density (but not a simple relationship) and relatively high values for variation (SD) in depth at the scale of 3.52 km^2 (i.e. 15x gcfm around a cell of 5x 25m), and a north-east aspect (Table 3-10, Appendix H).

Community *c* (dominated by spatangid urchins typical of soft sediments) is predicted to be found at suitable habitat in relatively deeper water, primarily in the periphery of the study area (Figure 3-12). Apart from depth, the two other spatial variables (latitude and longitude) included in the best model also explain the distribution of suitable habitat for this community. Suitable habitat is generally related to low values for rugosity, nodule density, and gravel content of the substrate.

The habitat suitability model for Community *i* (dominated by brachiopods that require some hard substrate for attachment) is strongly influenced by latitude, and to a lesser extent longitude, and as such suitable habitat is predicted to mostly occur in relatively large areas across the northern (primarily north-eastern) section of the study area (Figure 3-13). The other spatial variable, depth, also contributes to the best model, and the patches of suitable habitat in the study area tend to be in shallower water. Topographic variables (depth variation, rugosity, seafloor curvature) and mud content of the substrate also explain some of the habitat suitability, although in a non-linear manner (Table 3-10, Appendix H).

Community *g* (characterised by sessile epifauna taxa such as bryozoans and hydroids, as well as the stony coral *Goniocorella dumosa*) is predicted to be found at suitable habitat in the eastern part of the study area, in areas where depths are shallower (Figure 3-14). This distribution is mainly related to the importance of the spatial variables longtitude and depth in the best model (and to a lesser extent, latitude). The profile curvature of the seafloor and the nodule density are positively related to suitable habitat for this community (Table 3-10, Appendix H).

Suitable habitat for Community *h* (dominated by the stony coral *Goniocorella dumosa*) is predicted to occur in patches primarily in the eastern side of the study area, although there are some other areas of suitable habitat in the north-western section of the area (Figure 3-15). These areas of most suitable habitat for community *h* are in relatively shallow water. This distribution of suitable habitat reflects the importance of the spatial variables (latitude, longitude and depth) in the best model. Topographic variables that described the curvature of the seafloor (curvature and plan curvature) at the scale of 0.016 km^2 are important for identifying suitable habitat for this community (when the values for either curvature metric are relatively high in a positive or negative direction). Relatively low values for nodule density and high values for the mud content of the substrate are also related to habitat suitability for Community *h* (Table 3-10, Appendix H)

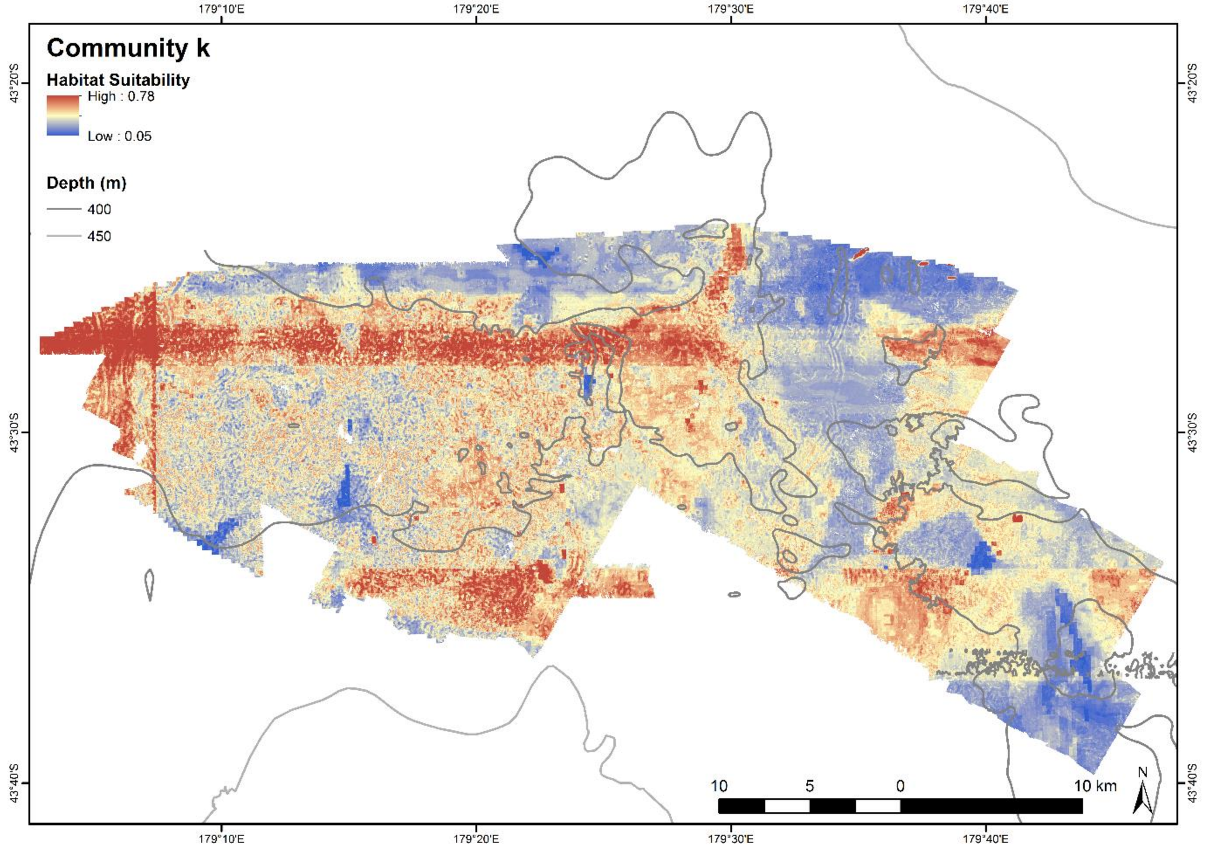


Figure 3-10:Predicted habitat suitability for epifauna Community *k* (image-level) in the study area.

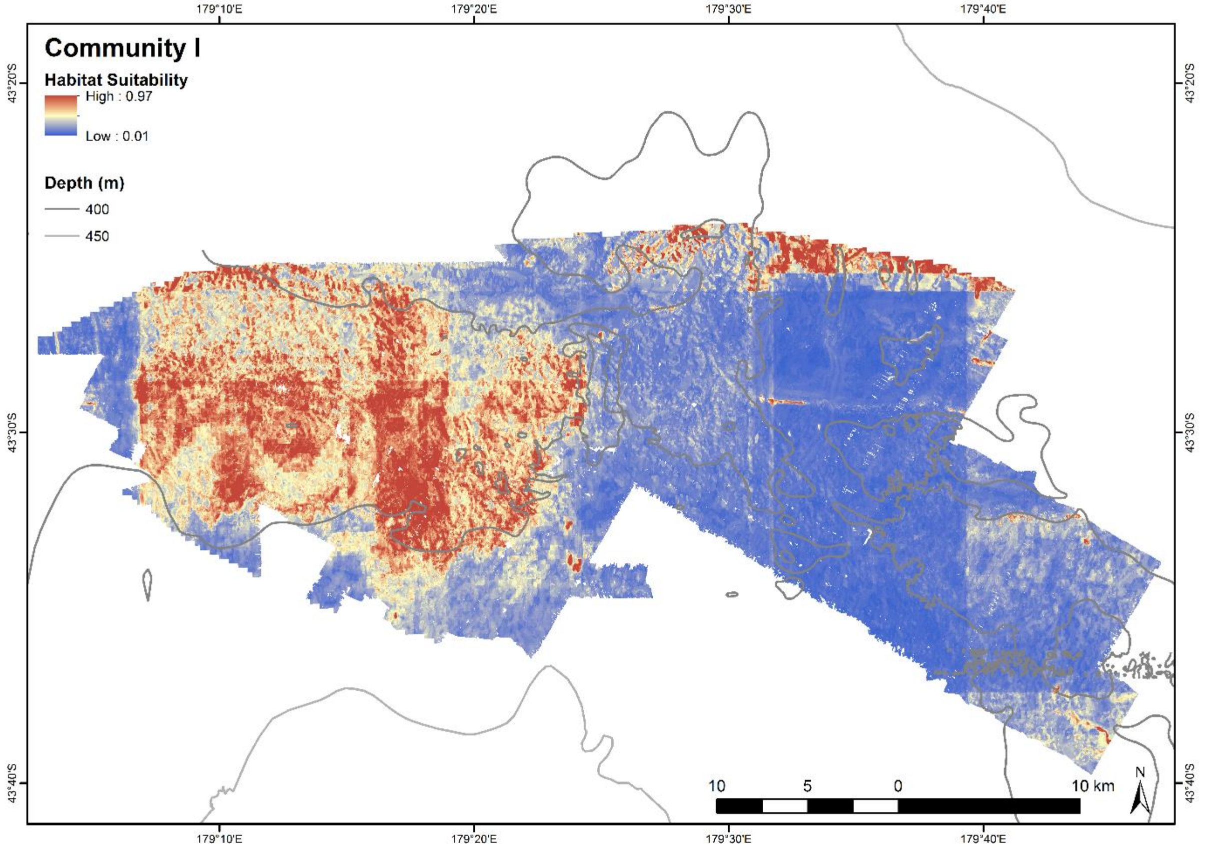


Figure 3-11:Predicted habitat suitability for epifauna Community *I* (image-level) in the study area.

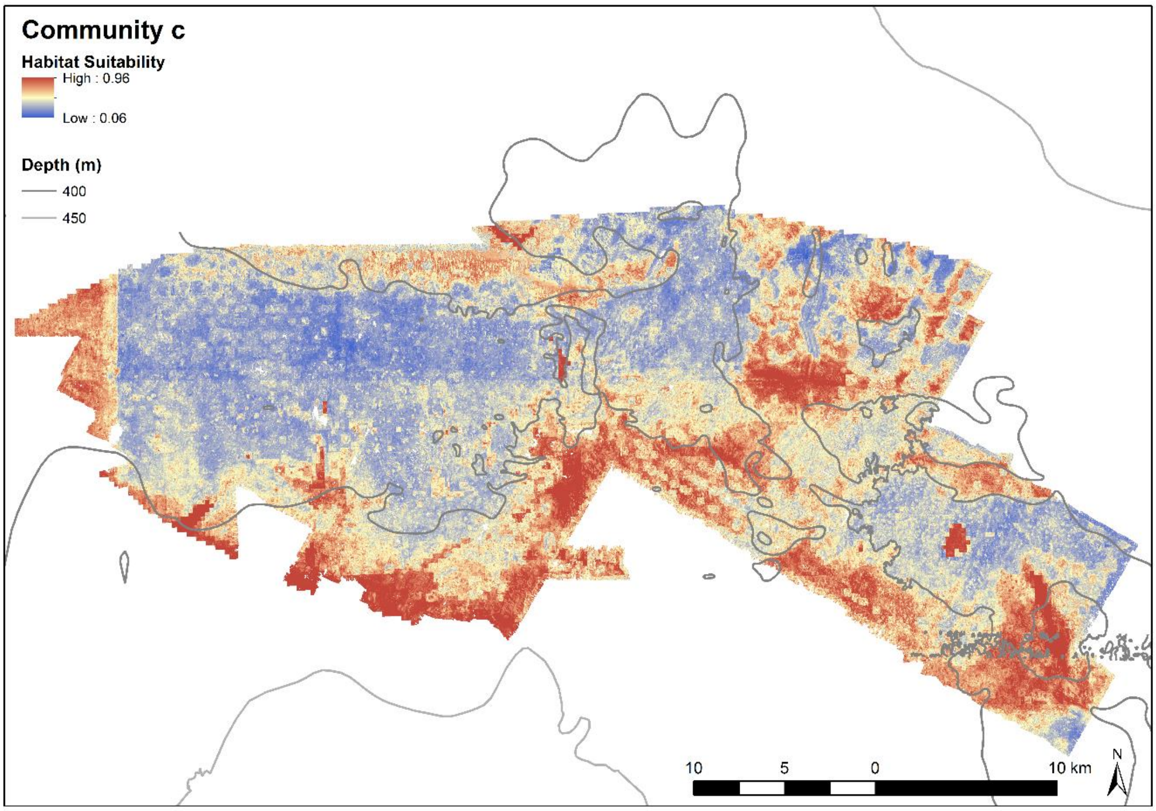


Figure 3-12:Predicted habitat suitability for epifauna Community *c* (image-level) in the study area.

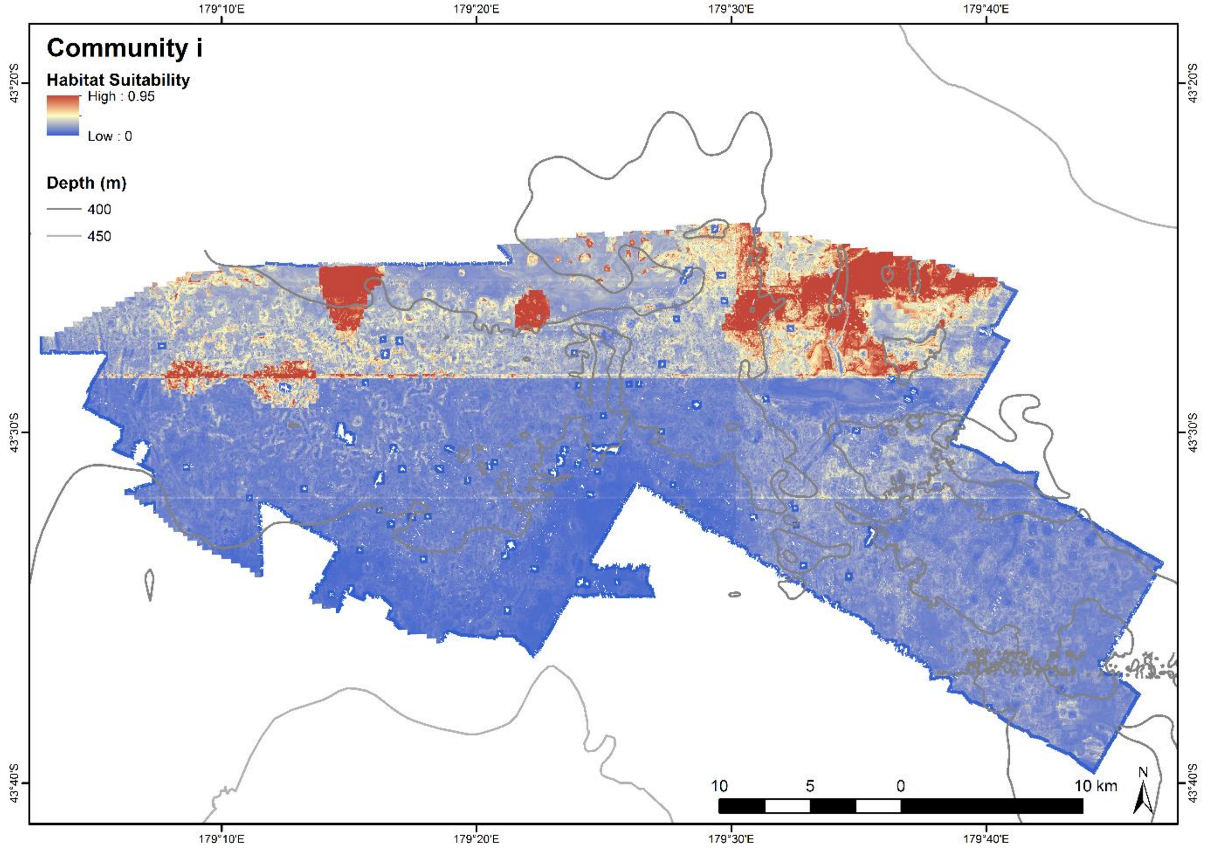


Figure 3-13: Predicted habitat suitability for epifauna Community i (image-level) in the study area.

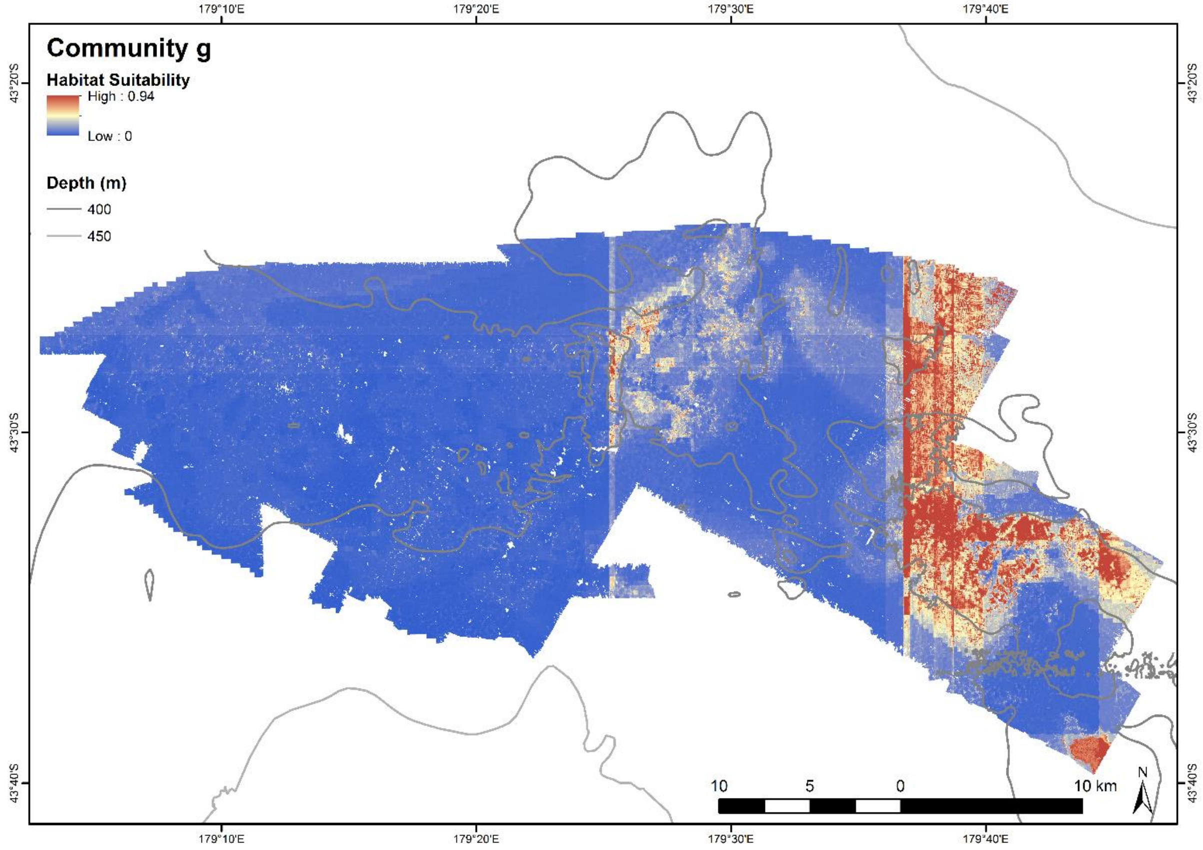


Figure 3-14:Predicted habitat suitability for epifauna Community g (image-level) in the study area.

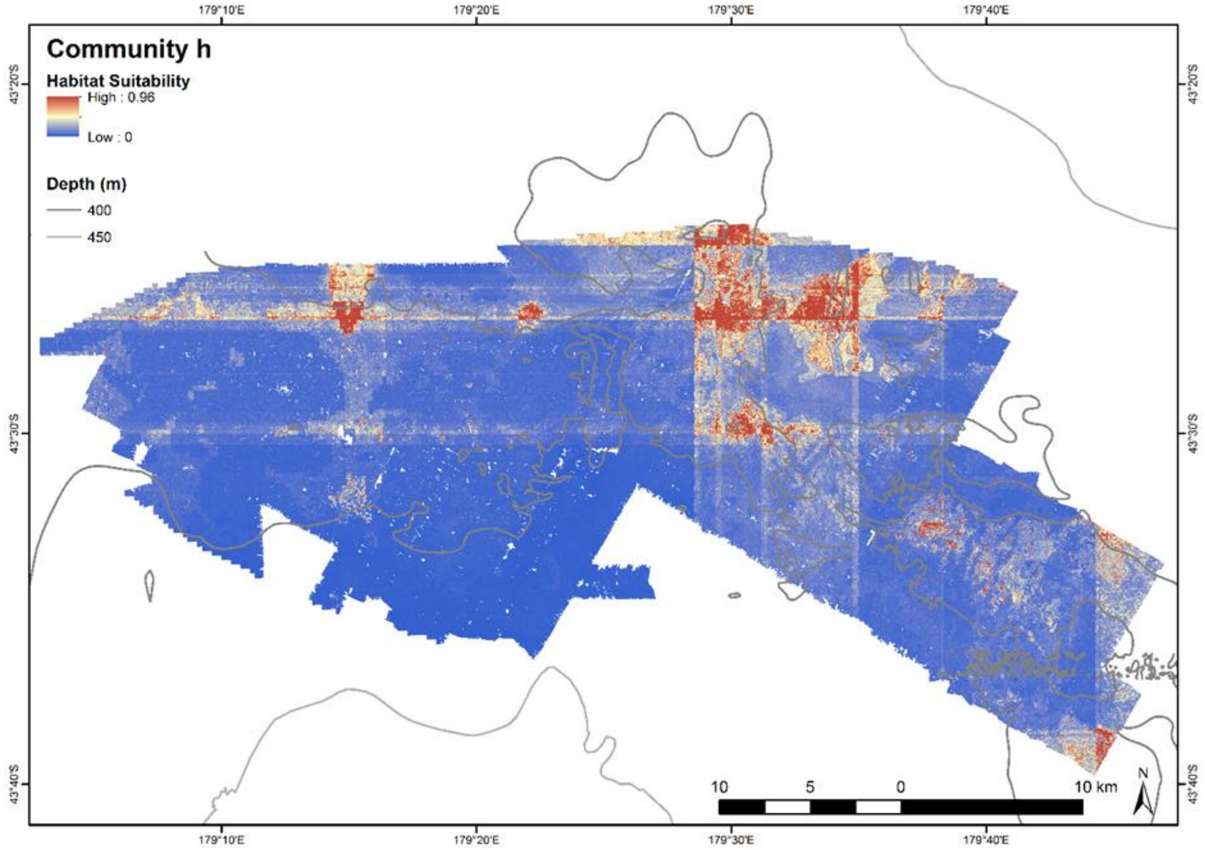


Figure 3-15:Predicted habitat suitability for epifauna Community *h* (image-level) in the study area.

Figure 3-16 shows a composite of the predicted suitable habitat (suitability >0.5) for each epifauna community. This map, in effect, summarises the contrasting predicted distributions of the six main epifauna communities in the study area, and illustrates their relative dominance in terms of areal coverage. Communities *c* and *l* (those characterised mainly by urchins typically associated with soft sediment) are together predicted to occupy the majority of the study area, with habitat for Community *l* predicted to have a distinct western distribution. Suitable habitat for the remainder of the epifauna communities is patchy, with Communities i and k occurring mainly in patches in the northern section of the study area, and Communities *g* and *h* in the eastern section. These communities are characterised by epifauna taxa that are sessile and require the presence of hard substratum for attachment. Substrate and topographic variables and relatively important in predicting suitable habitat for these communities.

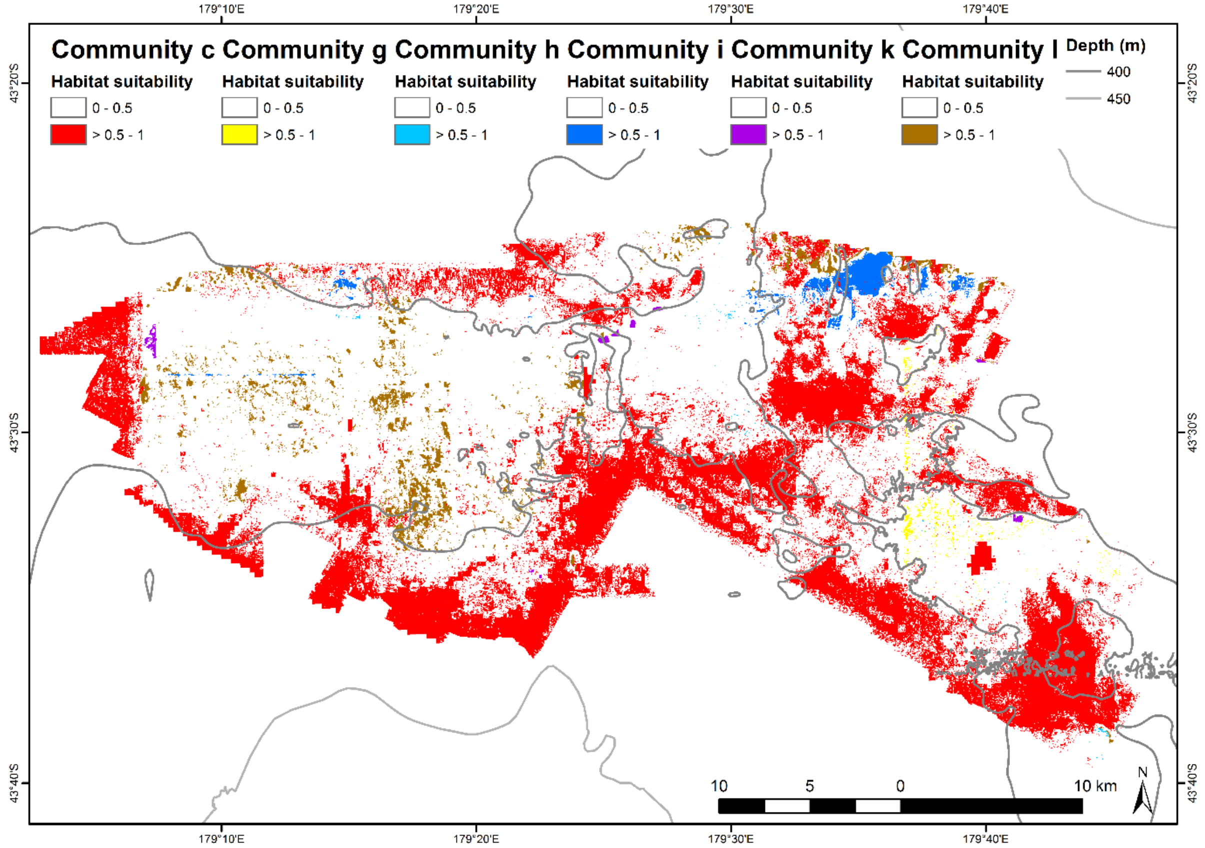


Figure 3-16:Composite of predicted habitat suitability (>0.5) for epifauna Communities *c, g, h, I, k* and *l* (image-level) in the study area.

3.3.3 *Goniocorella dumosa*

The stony coral *Goniocorella dumosa* is predicted to be more abundant in the eastern region of the study area (Figure 3-17). Within this region, the coral is predicted to have a patchy distribution, with both small (~0.25 km^2) and relatively large (~5 -20 km^2) patches of abundant coral (>20 colonies per image) occurring at relatively shallow water depths. Apart from being related to spatial variables (longitude, depth, latitude), this pattern of predicted distribution of coral abundance is explained by topographic variables (aspect, profile curvature), and in particular a positive relationship with the rugosity of the seafloor (Table 3-10, Appendix H). The predicted distribution of abundant *Goniocorella dumosa* is similar to the combined predicted suitable habitat for Communities *g* and *h* (see above), which are both characterised by this stony coral.

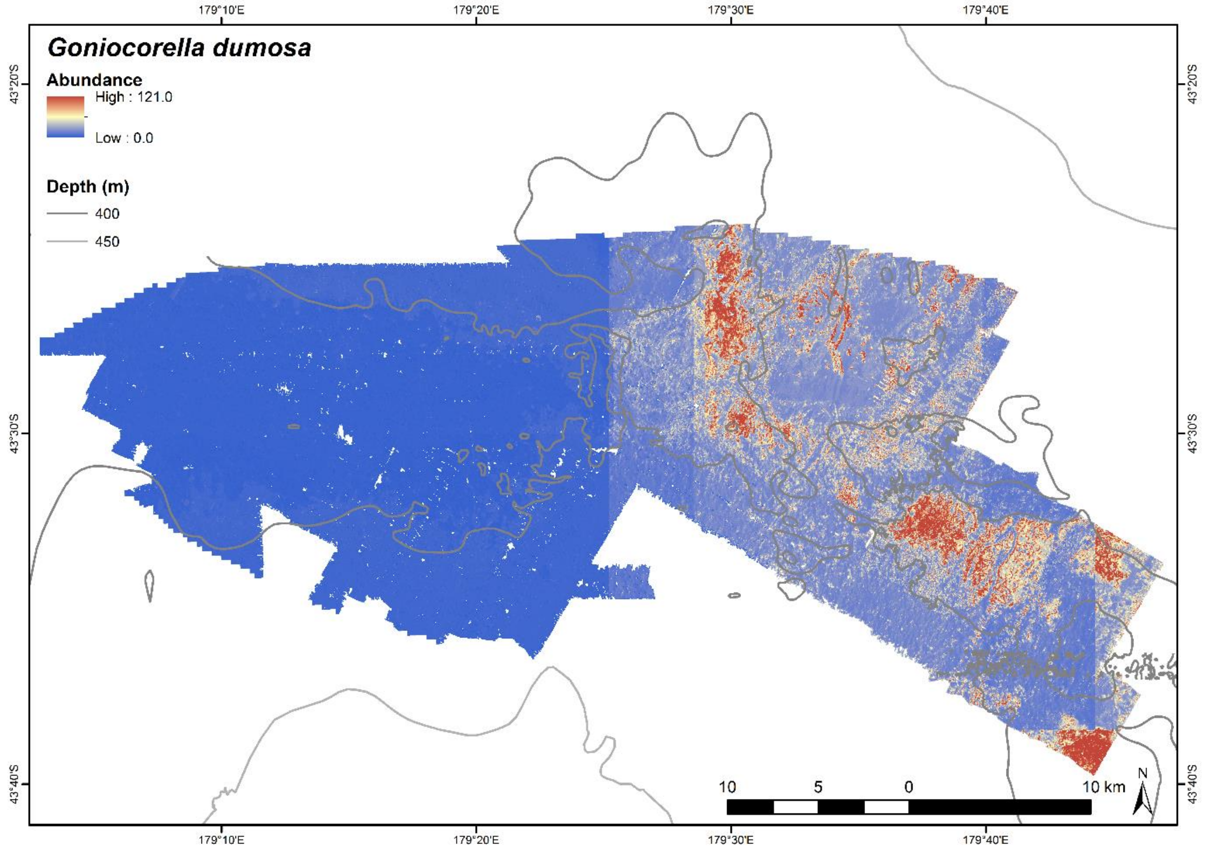


Figure 3-17:Predicted probability of occurrence for the stony coral *Goniocorella dumosa* in the study area.

3.3.4 Infauna

All models for the three main infauna communities are considered ‘useful’ (i.e. AUC > 0.7), although the model for Community *d* is not particularly robust, having a relatively weak CvDev (0.114) and an AUC of 0.767.

Suitable habitat for Community *d* (dominated by two species of amphipod) is predicted to occur mainly in the western part of the study area, although there are also smaller areas of suitable habitat in the east (Figure 3-18). Areas of suitable habitat are generally shallow, and occur over a narrow depth range (and with little variation in depth within this range). Habitat suitability for this community is strongly and positively related to nodule density and topographic measures of the seafloor (plan curvature, variation in depth and slope, aspect (north-west) and rugosity) (Table 3-11, Appendix H).

Community *h* (characterised by an amphipod and a number of polychaete taxa) has a distinctly western distribution of predicted suitable habitat (Figure 3-19), reflecting the importance of the variable longitude for the best model (Table 3-11, Appendix H). In this western region of the study area the most suitable habitat occurs in relatively small patches with a narrow depth range (and with little variation in depth within this range). The other variables that contribute to the best model and are responsible for the spatial patterns of predicted habitat suitability are plan curvature (positive in and along slope direction), curvature of the seafloor (when flat or slightly negative), and nodule density (when around 20 - 25 kg/m^2) (Table 3-11, Appendix H).

The habitat suitability model for Community *g* (characterised by a mix of polychaete and amphipod species) predicts that suitable habitat for this infauna community widespread throughout the study area, although there is greater amount of habitat in the east than in the west (Figure 3-20). Highly suitable habitat generally occurs in relatively small areas that align with the slope of seafloor depressions, troughs or iceberg furrows. This pattern reflects that not only is suitable habitat related to the spatial variable longitude, but also to the topographic variables slope, variation in the slope, and plan and profile curvature (when negative). Nodule density is typically low for suitable habitat, and the variables depth (relatively deep), depth range (relatively high), and aspect (north-west) also contribute to the best model for this community (Table 3-11, Appendix H).

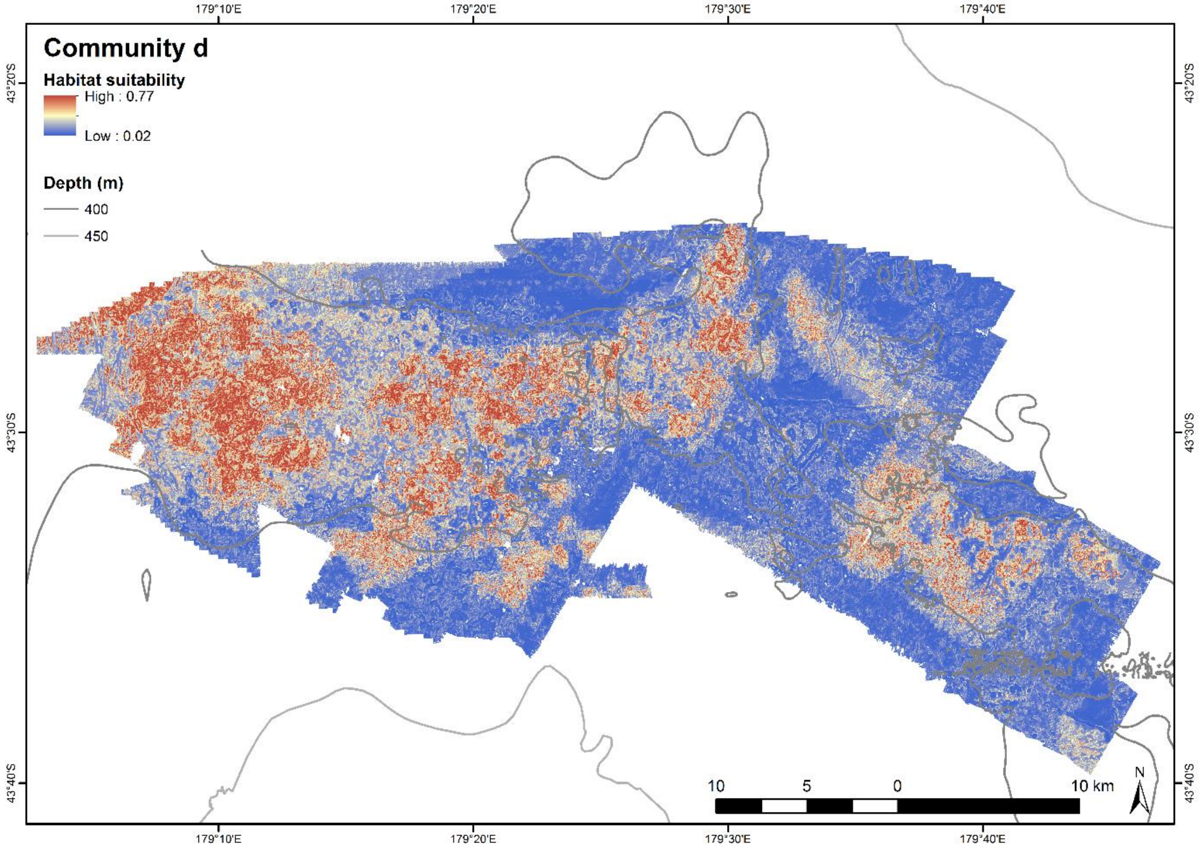


Figure 3-18:Predicted habitat suitability for infauna Community *d* in the study area.

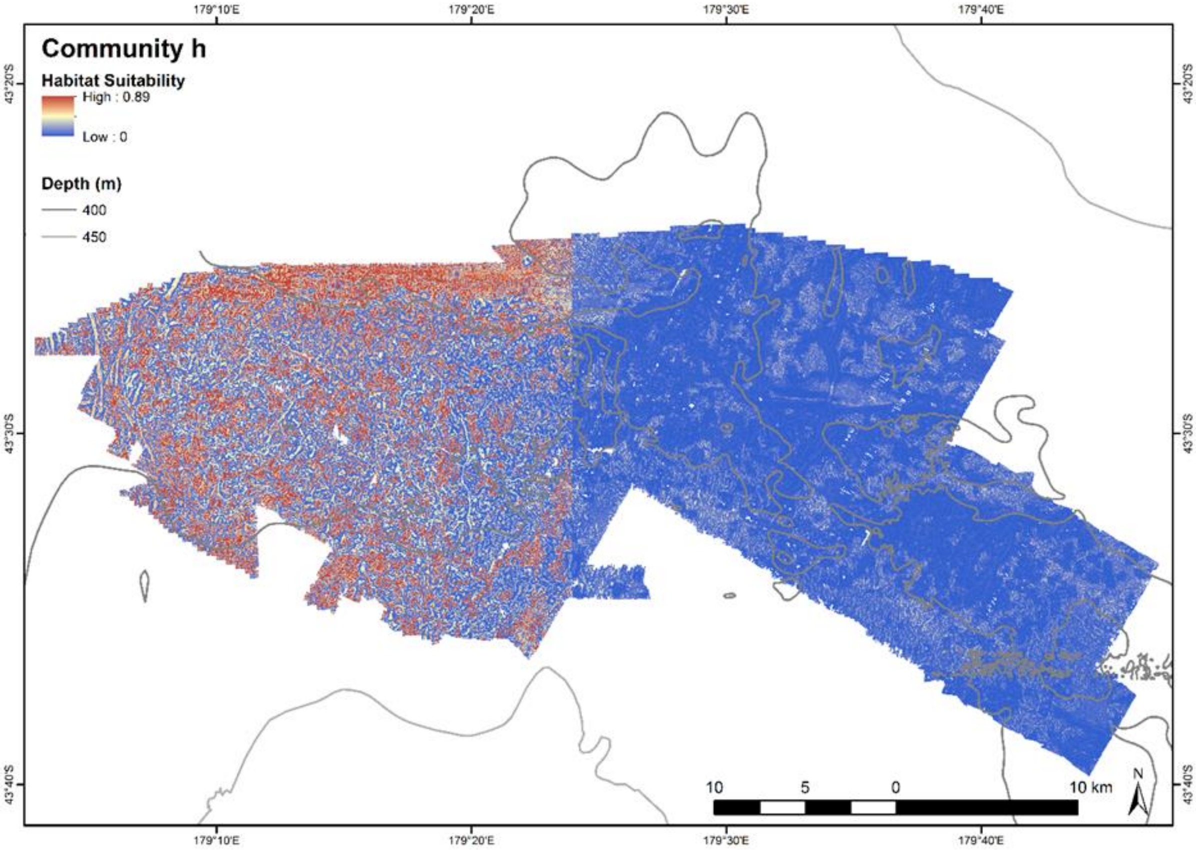


Figure 3-19:Predicted habitat suitability of infauna Community *h* in the study area.

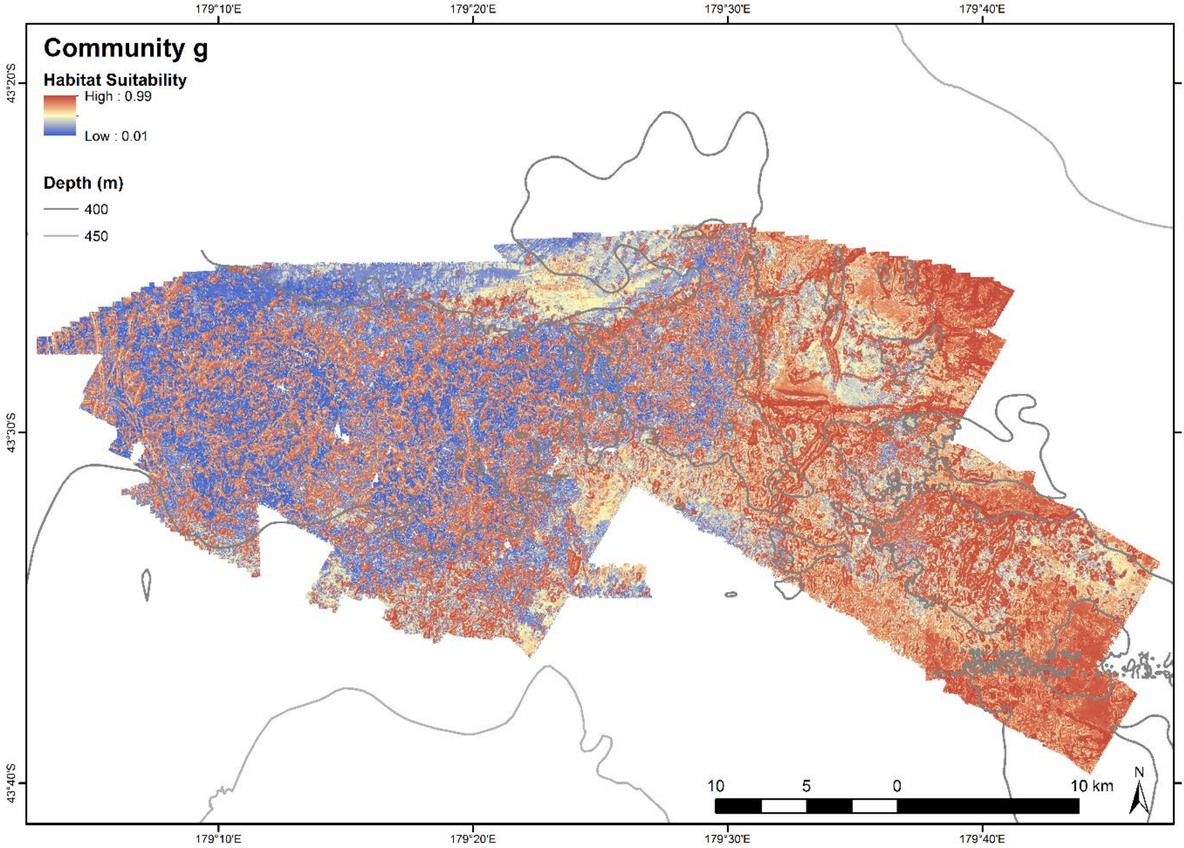


Figure 3-20:Predicted habitat suitability of infauna Community *g* in the study area.

The models for the three infauna communities predict contrasting patterns of suitable habitat in the study area, particularly for Communities *g* and *h*. Figure 3-21 hows a composite of the predicted suitable habitat (>0.75) for these two communities. What is notable is that the small scale patches of suitable habitat for Community *g* in the western half of the study area are surrounded by similarly small scale patches of suitable habitat for Community *h*. Suitable habitat (>0.75) for Community *d* was not included on this composite map, because including suitable habitat for all three communities in the western area of the study area would make it difficult for the eye to distinguish obvious patterns. However, comparing the map for Community *d* (Figure 3-18) with the composite map (Figure 3-21) shows that in the eastern region of the study area predicted habitat for Community *d* occupies approximately those areas not predicted to be suitable by the model for Community *g*.

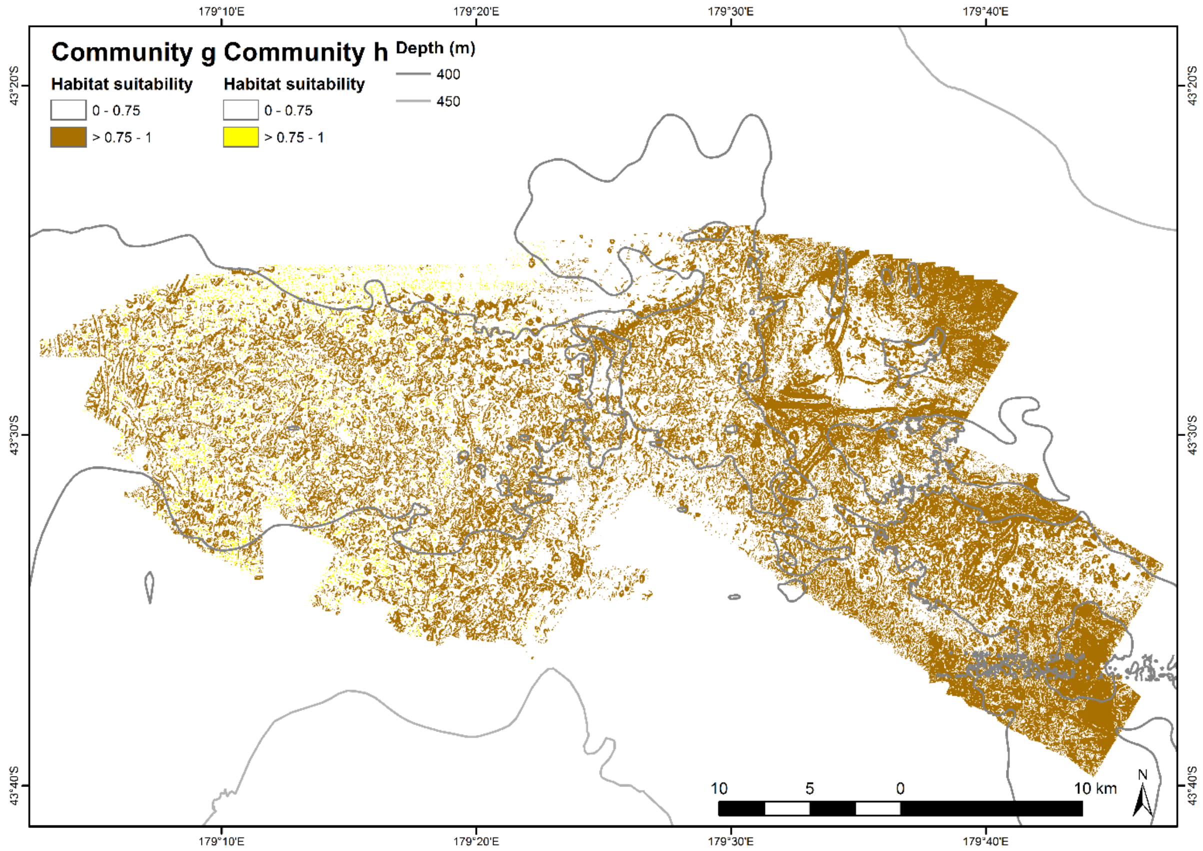


Figure 3-21: Composite of predicted habitat suitability (>0.75) for infauna Communities *g* and *h* in the study area.

4 Discussion

The Environmental Survey conducted by CRP was largely successful in obtaining data to characterise the benthic communities and habitats of a portion of the licence area MPL 50270 on the Chatham Rise. ROV photographic transects and box-core sampling obtained images and samples that were used to identify epifauna and infauna communities across the study area. Data were also recovered that could be used to explain the structure and distribution of these communities, and to predict the distribution of suitable habitat for these communities across the entire study area. The survey was designed to provide this information in support of CRP's Environmental Impact Assessment. The main results are summarised below and then discussed in the context of what is known about benthic community structure elsewhere on the Chatham Rise.

4.1 Benthic community structure and distribution in the study area

Taken together the results of the benthic community analysis and the habitat suitability modelling allow for a good appreciation of the structure of the benthic communities in the study area, the patterns of their distribution and likely wider distribution, and the reasons for these patterns.

4.1.1 Epifauna communities

Twelve epifauna communities were identified by the analysis of the individual still images of the seafloor obtained by the ROV. Community structure varied at both the among-survey area scale (~5 – 50 km) and within-survey area scale (~1 – 5 km), although the former scale accounted for more of the observed variability in structure. Overall, benthic community structure was explained (though weakly) by the contrasting distribution of mud/sand (i.e. soft sediment) and phosphorite nodules (i.e. hard substrate). The overall weak association with environmental variables is probably a consequence of the diverse nature of the communities, and their contrasting environmental drivers. Habitat suitability modelling allowed for a better appreciation of the environmental forces that account for the structure and distribution of each of the identified epifauna communities.

The most common community type, Community *c,* was found, and was predicted to be found, across much of the study area, particularly in the deeper waters of the periphery of the study area. This community was dominated by spatangid urchins that occurred on soft sediments with low gravel content, low rugosity, and low nodule density. Spatangid urchins move on and through soft sediment when feeding, and a fairly uniform, flat sand/mud substrate with few large particles to impede their mobility is ideal habitat (Schinner 1993). The next most common epifauna community, Community *l*, was also characterised by urchins and to a lesser extent by sessile taxa such as bryozoans and hydroids that require hard substrates to colonise. This community was found and predicted to occur in a fairly extensive area of the western side of the study area (and a smaller area in the north-east). Suitable habitat for this community was relatively shallow, predominantly soft sediment but with some surface nodules to provide sites of attachment for sessile epifauna taxa. Nodules are widespread in relatively low densities on the shallow western parts of the study area (Nodder et al. 2013).

In addition to these two main communities (in terms of areal extent), the other epifauna communities identified were predicted to have patchy distributions. Suitable habitat for Community *i* was predicted to be found in relatively large patches in the north of the study area, particularly the north-east. Here water depths are relatively shallow and various topographic variables also play a part in providing suitable habitat for this community. Community *i* is dominated by brachiopods which require hard substrates for attachment, and images of the seafloor show that this substrate is provided by pebble-sized rocks and phosphorite nodules. Rocks and nodules are patchily distributed in the study area (Nodder et al. 2013), which understandably accounts for the patchy distribution of this community. Communities *g* and *h* were also predicted to have a patchy distribution, they were the two most similar epifauna communities identified during the survey, and both were found mainly in the eastern section of the study area. Within this eastern area, Community *h* was predicted to have a more northern distribution than Community *g*. Community *h* was dominated by the stony coral *Goniocorella domosa*, and while this coral was also a characterising species for Community *g*, this community was almost equally characterised by other sessile taxa such as bryozoans and hydroids. Suitable habitat for both these communities was relatively shallow, and topographic variables that relate to seafloor curvature are important for explaining their distribution. Measures of curvature are indicative of small-scale elevations in the seafloor, and these would be beneficial for the sessile taxa that characterise these two communities by raising them into faster water flows that contain food material (Tong et al. 2012). These taxa also require hard substrates for attachment, and seafloor photographs indicate that these are provided by relatively large phosphorite nodules as well as rocks of other material. Phosphorite nodule density was identified as an important variable in the habitat suitability model for Community *g,* and nodules have a patchy distribution in the eastern side of the study area (Nodder et al. 2013) which would account patchy distribution of these coral-based communties. Not surprisingly, the distribution and predicted distribution of *Goniocorella dumosa* abundance matches the predicted distribution of suitable habitat for Communities *g* and *h*.

The remaining epifauna communities (at the image-level) were not found at many locations, and the habitat suitability model for one of these communities, Community *k*, indicates that they are likely to occur in relatively small patches. This model was not particularly robust (probably because it is characterised by a range of different taxa and functional types), but the predictive map for Community *k* indicates that this community is restricted to two narrow latitudinal bands in the north and south of the study area. Considering the reliability of the model, no attempt is made here to explain this distribution pattern. No attempt was made to generate models for the remaining six epifauna communities because of the small number of images in which they were observed. Thus, the possible reasons for the structure and likely distribution of these relatively rare epifauna communities in the study area are not known.

Analysis of the image data at the transect-level identified five epifauna communities. By pooling images for each transect, communities that may exist at a large spatial scale can be identified or alternatively the scale-independent constancy of particular communities. An examination of the taxa that characterised the five identified communities, and the patterns of their distribution, revealed that the transect-level communities are equivalent to five of the six main communities identified at the image-level. That is, image-level epifauna Communities *c, l, i, g* and *h* are re-identified at the transect-level by Communities *h, f, g, c* and *e* (respectively). Unfortunately it was not possible to produce robust habitat suitability models for the transect-level communities, but because of the observed scale-independence, the image-level predictive maps provide a suitable means to appreciate the likely distribution of the main and consistent epifauna communities in the study area.

In summary, epifauna community structure in the portion of the licence area surveyed was observed to vary at two scales, but predominantly at the larger among-survey area scale. This pattern of spatial variation reflects the observation that the main epifauna communities are distributed with respect to soft sediment (Communities *c* and *l*), and within the general area occupied by this substrate, the relatively large-scale patchy distribution of hard substrate (Communities *i, g* and *h*) (even if the hard substrate within these patches was small in size). Variation in seafloor topography also plays a part in generating suitable habitat for epifauna communities, and by undefined variables that change with longitude, depth and latitude. These variables could include differences that relate to the availability of food – e.g., particulate organic carbon (POC) flux and current speed – both of which vary in some way with these spatial variables on the Chatham Rise (Nodder et al. 2007). Notable is the association between the patchy distribution of hard substrate, particularly phosphorite nodules, and Communities *g* and *h* in the eastern part of the study area, and the abundance of the stony coral *Goniocorella dumosa* which characterises these communities. Community *h*, in particular, has abundances of *Goniocorella dumosa* that allow areas where this community is found to be termed “coral thickets” (Macdiarmid et al. 2013). Coral dominated communities found elsewhere in the world have been observed to be highly diverse in terms of their invertebrate fauna (e.g. Henry & Roberts 2007) and can also provide important habitat for juvenile or larval fish (D’Onghia et al. 2010, Baillon et al. 2012). As such these particular epifauna communities have a notable significance for ecosystem function (Dawson 1984).

4.1.2 Infauna communities

Five communities were identified by the analysis of the sample data obtained by the box-coring. Community structure varied at both the among-survey area scale (~5 – 50 km) and within-survey area scale (~1 – 5 km), and these two spatial scales explain a similar proportion of the observed variability in structure. Overall, benthic community structure was explained (though weakly) by the longitude (or rather some unknown environmental characteristics that change with longitude) and the weight of phosphorite nodules. Topographic variables (e.g. curvature and rugosity) were also correlated with infauna community structure but even more weakly than the aforementioned variables. The overall weak association with environmental variables in the analysis is probably a consequence of the scale difference between most of the measures of environmental variability (which were derived from MBES data – 625 m^2) and the box-core samples (0.06 m^2). Habitat suitability modelling allowed for a better appreciation of the environmental forces that account for the structure and distribution of each of the identified infauna communities.

The three main infauna communities were Communities *g, d* and *h*. Community *g* was found, and was predicted to occur across much of the study area, although there was a greater amount of suitable habitat predicted in the east than in the west. This community is characterised by polychaetes and amphipods (mainly lumbrinerids and phoxocephalids, respectively) that are predicted to be found on the slopes of seafloor depressions, troughs and ancient iceberg furrows. These taxa may benefit directly or indirectly from the particular sediment and/or hydrological conditions that occur on the slopes of such topographic features (e.g. relatively coarser sediments, topographically entrained currents; e.g. Conway et al. 1991). However, it is hard to describe any particular ecological reasons for the association when little is known about the life habits of these characterising taxa. Another community predicted to be fairly widespread, at least in relatively shallow water, was Community *d*. The two most dominant taxa of Community *d* were amphipods (lysianassid and phoxocephalid species). Suitable habitat for this community was defined by having relatively high phosphorite nodule density, as well as a topographic variables that describe a ‘bumpy’ seafloor (plan curvature, variation in slope, rugosity). Because the characterising species of this community (which also include a number of polychaete species) were unidentified and belong to taxa that exhibit a wide array of ecologies, it is unwise to speculate too much here as to the reason why this community appears to have such a close association with the distribution of nodules. However, the relative density of nodules may significantly affect basic sediment parameters (e.g. median grain size, sorting etc) of the sand/mud matrix. Such parameters are known to be related to infaunal community structure (Snelgrove & Butman 1994). Community *h*, characterised by a phoxocephalid amphipod and otherwise by polychaete species, was found and was predicted to have suitable habitat in the western section of the study area. Within this distinct western distribution, suitable habitat was predicted to occur in small patches with a fairly even distribution. The habitat suitability model identified these areas to have a relatively flat topography. Again, because the ecology of the unidentified characterising species is unknown, it is not immediately clear why this community appears to prefer habitat that is different from that of the other two main infauna communities. Despite not being able to describe the ecological niches of these communities it is clear that they occupy separate habitats; one is found on the slopes of depression-type topographic features that vary in spatial scale, another is associated with bumpy topography and nodules, and the third with relatively flat habitat.

The remaining two infauna communities, Communities *i* and *e*, were not often encountered by the box-core sampling. Each was only sampled twice in the north-eastern section of the study area. Because of the small sample size, no habitat suitability models could be generated for these communities. Thus, the possible reasons for the structure and likely distribution of these relatively rare infauna communities in the study area is not known.

In summary, infauna community structure varies equally at two spatial scales in the study area. This pattern of spatial variation reflects the observation that while environmental characteristics varied broadly across the study site, particularly longitudinally, within any one area there were distinct differences in habitat type as a result of small-scale variations in the seafloor topography. The three main communities (Communities *d, g* and *h*) occurred in distinct topographic habitats in the western side of the study area, while only two of them (Communities *d* and *g*) are found in the eastern side. As for the epifauna communities, undefined variables that change with longitude, depth and latitude also influence the distribution of infauna communities in the study area. These variables could include differences that relate to the availability of food – e.g., particulate organic carbon (POC) flux and current speed – both of which vary in some way with these spatial variables on the Chatham Rise (Nodder et al. 2007). Notable is the association between phosphorite nodule density and the structure and distribution of infauna Community *d*. What particular ecological relationship exist between this community, dominated by lysianassid and phoxocephalid amphipods, and the relatively high and patchy abundance of nodules is not known, but it could represent a ‘nodule-specific community’. Nodule-based communities have been observed at abyssal depths in the Pacific where managanese nodules dominate the seafloor surface (Veillette et al. 2007).

Finally, it is worth noting that the location of box-core samples identified as belonging to infauna Communties *g* and *h*, and images identified as illustrating soft-sediment epifauna Communities *c* and *l* (and their predicted habitat suitability distribution) are commensurate enough to suggest that these communities are approximately synonymous – just identified using different sampling techniques. That is, one is the infauna component of the respective epifauna component of the other. Parallels between other epifauna and infauna components are not so obvious. Such complete synonymy is not to be expected where box-coring was not possible in patches of substrate that contained a high density of hard ground on the seafloor surface, but which was sampled by means of ROV imagery.

4.2 Comparison with benthic communities elsewhere on the Chatham Rise

The information about benthic community structure and distribution within the licence area provided by the Environmental Survey needs to be viewed alongside available information about benthic communities elsewhere on the Chatham Rise. It is important to make this comparison, principally, to determine if the communities identified by the survey are found elsewhere in the region or whether they are unique communities (or not yet known from elsewhere). However, it is important before attempting to make such a comparison to understand the limitations of any such assessment. Comparisons are impacted principally by differences in the data collection method (e.g., type of sampling gear, scale of sampling) as well as by the analysis method (e.g. different classification or ordination techniques, and subjective or objective means for identifying communities). Obviously, the ideal comparison is made using results derived from both the same sampling and analysis method, but this is not always possible (e.g. given time constraints or the availability of raw data). Reasonable comparisons can be made even if different, yet functional similar, sampling techniques have been used (e.g., grab and box-core sampling, or ROV and towed camera), particularly if there is time to first standardise the different datasets as much as possible and then analyse the standardised data by the same method. If the same sampling gear has been used it is possible to make reasonable qualitative comparisons even if different analytical techniques have been used to identify communities, at least when the 'family' of analysis techniques is similar (e.g., classification). Any other sort of comparison is far from ideal and should be made with appropriate caution. Below, qualitative comparisons are made between the results of this study and those of previous published studies on the benthic communities of the Chatham Rise, but in the context of the limitations expressed above.

4.2.1 Epifauna communities

McKnight & Probert (1997) described a single epifauna community found at sites in water depths of 237-602 m, a range that includes the depth range of the study area (370-420 m). Their sites were ~10-165 km to the west, and ~135 km east, of the study area. Sites were sampled using a small trawl, and sampling for their survey was over a larger-spatial scale that the present survey. While McKnight & Probert (1997) used broadly similar analytical techniques to the present study to define community identity and structure, the sampling method they used limits the meaningfulness of any comparison between the results of the two studies. The community identified by McKnight & Probert (1997) on sandy sediments of the crest of the rise was characterised by *Munida gracilis, Phylladiorhynchus pusillus*, *Campylonotus rathbunae*, *Philocheras acutirostratus* and *Brucerolis hurleyi* (Crustacea), *Amphiura lanceolata* (Ophiuroidea), *Cuspidaria fairchildi* and *Euciroa galatheae* (Bivalvia). Not surprisingly, given the difference in sampling gear (trawl versus images from ROV transects) the characteristic species of this community are not comparable to any characterising taxa for communities identified by the CRP Environmental Survey. However, that is not to say that the same community was not sampled by the two studies, because the definition of the communities by the two studies is sampling method (gear/sampling scale) dependent.

The epifauna "groups" described by Floerl et al (2012) were sampled and identified using similar techniques (video from a towed camera, multivariate classification) as those used in the present study. However, the OS20/20 survey encompassed a much larger area, sampling density was much lower, and did not include the central portion of the rise that includes the licence area. Nonetheless a qualitative comparison between the results of the two studies is worthwhile making, particularly because the occurrence of these epifauna groups was predicted to occur in unsampled regions of the Chatham Rise by Hewitt et al. (2011). First it must be noted that the biological groups identified by Floerl et al (2012) were slightly modified by Hewitt et al (2011), before their distribution was interpolated into unsampled space. Hewitt et al. (2011), beginning with the biological groups identified by Floerl et al (2012), used information on the location of the sample sites, species composition, and environmental gradients to re-allocate some sites to different groups – which they then termed “biotic habitats”. For the sake of this comparison, biotic habitats can be considered to be broadly equivalent to communities because on the Chatham Rise only 1 site was re-allocated to another group. Hewitt et al. (2011) made a map showing the distribution of these biotic habitats based on the distinctive environmental characteristics specific to the biotic habitats and spatial continuity of habitats. Their map predicts 2 biotic habitats in the licence area: “B7” and “B5”. Biotic habitat “B7”, which covers most of the study area, can be found elsewhere on the crest of the Chatham Rise and on the Challenger Plateau between water depths of 249-587 m, and is characterised (in video and still images) by the decapods *Munida gracilis* and *Notopandalus magnoculus.* Biotic habitat “B5”, is predicted to occur in the southern part of CRP’s licence area, and over a large area of the Chatham Rise, but not on the Challenger Plateau. This biotic habitat is found between 210-682 m water depths where there are muddy sediments, and is characterised (in video and still images) by *Sympagurus dimorphus* (pagurid crustacean), *Hyalinoecia longibranchiata* (polychaete) and taxa belonging to the Cladhorizidae (sponges) (Hewitt et al. 2011, Floerl et al. 2012). None of the epifauna communities identified by the present study correspond, in terms of characterising species, to these two biotic habitats identified by the OS20/20 survey.

That the two biotic habitats predicted to occur in the licence area do not correspond to the communities identified by the Environmental Survey is perhaps not surprising given the high level of uncertainty that must be placed on the predictive map because of the interpolation method used by Hewitt et al. (2011). What is notable, however, is that none of the epifauna communities identified by the present study are similar to any of the 8 biotic habitats identified on the Chatham Rise when the sampling and analysis techniques used are broadly comparable (Floerl et al. 2012, Hewitt et al. 2011). What this comparison suggests is either, that the identification of communities is strongly influenced by the scale of the sampling, or that the licence area contains epifauna communities that are not found elsewhere on the rise (or Challenger Plateau). While variation in sampling scale can influence the identity of communities, it is interesting to note that a change in sampling scale between image-level and transect-level in the present analysis did not alter the identity of the epifauna communities. Thus it is certainly possible, given that the licence area is located within a large area where no samples were taken during the OS20/20 survey, that the epifauna communities identified by the Environmental Survey could indeed be unique to the study area.

Some support is provided for this speculation by the distinct nature of the habitat provided by, or modified by, phosphorite nodules. For example, epifauna Communities *g* and *h* are dominated by the stony coral *Goniocorella dumosa,* the relative abundance of which relates in part to the presence of nodules on which they can live and grow. Thus these two communities are only likely to develop where nodules are in relatively high density. While *Goniocorella dumosa* can be found outside the licence area elsewhere on the Chatham Rise (Tracey et al. 2011), it was not recorded in any of the 2007 OS20/20 samples (David Bowden pers. comm.) and communities dominated by this coral have not been recorded from anywhere other than where nodules exist in relatively high densities within the licence area (Kudrass & von Rad 1984b, Dawson 1984).

4.2.2 Infauna communities

Probert & McKnight (1993) sampled the infauna across the rise (244-1394 m), and reported that the infauna was dominated numerically by polychaetes and peracarid crustaceans. Sampling of the infauna using a box-corer in the present study also revealed the dominance of polychaetes and crustaceans (mainly amphipods). The study by Probert & McKnight (1993) concentrated upon presenting biomass data, rather than community structure. Later Probert et al. (1996) described the polychaete fauna in greater detail, recording at least 126 species from the same stations/three transects as Probert & McKnight (1993). Their multivariate analysis of these data identified two main polychaete communities, one of which occurred mainly on the crest of the rise, at depths (244-663 m) that includes the depth range of the study area (370-420 m). The sites were this community was found were ~10-165 km to the west, and ~135 km east, of the present study area. Species characteristic of this crest community were *Aglaophamus verrilli* (Nephtyidae), *Laonice* sp. (Spionidae), *Kinbergonuphis ?proalopus* (Onuphidae), *Notomastus* sp. (Capitellidae), *Labiosthenolepis laevis* (Sigalionidae) and *Euchone* sp. (Sabellidae) (Probert et al. 1996). In a subsequent study, Probert et al. (2009) examined only the polychaete infauna from eight sites along a north-south transect (350 – 2300 m) across the central Chatham Rise (178° 30' E longitude). A total of 169 putative species were identified and used for multivariate analysis, which identified a community at the shallowest sites (350–453 m), where numerical dominants included *Lumbrineris* sp. (Lumbrineridae), *Linopherus minuta* (Amphinomidae), *Dipolydora* cf. *socialis* (Spionidae), *Aglaophamus verrilli* (Nephtyidae), *Prionospio ?ehlersi* (Spionidae), Syllinae sp. (Syllidae), *Monticellina* sp. (Umagillidae), and *Cossura* sp. (Cossuridae) (Probert et al. 2009). The sites where this community was found are ~50-100 km west of the study area.

The sampling of infauna communities described above was performed using an anchor-box dredge, but Probert (1984) found that there was no significant differences in terms of quantitative estimates between the anchor box dredge and the box-corer used in the present study. The studies by Probert et al. (1996, 2009) used very similar multivariate analysis techniques to those used in the present study. As such it is, in principal, reasonable to qualitatively compare the results across all three studies. However, Probert and co-workers only examined the polychaete component of the fauna rather than all taxonomic groups, and they also identified the taxa to species or putative species level. In the present study, identification included multiple taxonomic groups (including the other dominant group, the amphipod crustaceans) but was mainly to family level. These differences make a comparison somewhat limited but nonetheless worth attempting.

The characterising taxa for all five of the infauna communities identified in the study area included polychaetes. Of the three main infauna communities, two (Communities *g* and *h*) were mainly characterised by polychaete taxa, and some of these taxa are shared with the characterising taxa (at least at the family level, and one species) of the shallow rise communities identified by Probert et al (1996, 2009). That is, one of the three characterising polychaete taxa of Community *g* was shared with the taxa characterising the community identified by Probert et al. (1996), and two with the community described by Probert et al. (2009); and two of the four characterising polychaete taxa of Commuinity *h* were shared with the taxa characterising the community identified by Probert et al. (1996), and three with the community described by Probert et al. (2009). Without knowing the species identity of the polychaetes identified by the present study, it not possible to conclude with any confidence whether infauna Community *g* and *h* are synonymous with the communities identified elsewhere on the Chatham Rise by Probert et al. (1996, 2009). However, the overlap in taxa at the family level indicates that this might be possible. The two primary characterising taxa of the third main community, Community *d*, were amphipods. Although at the family level one and all three characterising polychaete taxa of this community were among the characterising taxa of the communities identified by Probert et al. (1996, 2009 - respectively), it is unlikely that this infauna community is synonymous with any sampled previously. The reason for this conclusion relates to the finding by the present study that areas of most suitable habitat for Community *d* are strongly related to high nodule density. As already noted in section 4.1.2, the presence of a lot of nodules in the soft substrate will affect the basic parameters of the sediment, possibly providing a distinct habitat that could be responsible for developing a specialised infauna community. As such it is not unreasonable to suggest that infauna Community *d* could be unique to soft sediments with high phosphorite nodule content on the Chatham Rise.

5 Conclusion and Recommendations

Analysis of data recovered by the Environmental Survey provided for the identification of 12 epifauna and 5 infauna communities within the north-west portion of Chatham Rock Phosphate’s mineral prospecting licence area. The structure, characterising taxa, and distribution of these communities was determined by statistical analysis, and suitable habitat for these communities in the study area was predicted by modelling. The environmental variables that explain the overall community structure and the distribution of the individual communities were also identified. The structure and distribution of two epifauna communities and one infauna community are closely related to the density of phosphorite nodules.

The two epifauna communities, both of which show a patchy distribution in the east of the licence area, are dominated by the stony coral *Goniocorella dumosa*. This coral relies upon hard substrate, such as that provided by relatively large nodules, for attachment. Similar corals, particularly when in high abundance, are known to provide habitat for a diverse community of other invertebrates and, potentially, larval or juvenile fish.

The one infauna community that exhibits a relationship with nodule density is characterised mainly by amphipod and polychaete species. Suitable habitat for this community extends over the entire study area, predominantly in the west, but the nature of the ecological association between its characterising species and the nodules is not known. However, the presence of nodules in the sediment could result in a phosphorite ‘nodule-specific community’, as has been found or manganese nodule habitats at abyssal depths elsewhere in the Pacific.

Comparison of the benthic communities identified by this study and communities described from previous sampling on the Chatham Rise indicates that some epifauna communities within the licence area have not been found elsewhere on the rise. Although the coral *Goniocorella dumosa* is widely distributed in New Zealand waters, it has previously been recorded as low densities of isolated colonies. The communities dominated by high abundance of *Goniocorella dumosa* identified here in the licence area have not been recorded in previous surveys; either on the Chatham Rise or elsewhere in New Zealand waters. From published reports, it is possible that at least two of the main infauna communities have been sampled before on the crest of the Chatham Rise, but the nodule-associated amphipod-dominated community identified here does not appear to have been recorded before.

To assess the potential uniqueness of some of the benthic communities in the licence area, it is recommended that further sampling and analysis be undertaken. This can be achieved by conducting additional sampling elsewhere on the Chatham Rise using techniques comparable with those used in the CRP Environmental Survey. This sampling would be within the areas included in the original survey design, but which were not sampled. In addition, raw data and images from the sampling conducted during the Chatham Rise OS20/20 survey, could be examined using the techniques used in the present study to develop a more widespread picture of communities on the Chatham Rise. The results of this sampling would serve to field validate the habitat suitability models presented here, and to construct new habitat suitability models for the entire Chatham Rise.

Information presented in this report, together with knowledge of the proposed nodule mining activities, can be used to help assess the implications of mining for benthic communities in the licence area, and to design measures to mitigate and monitor any environmental effects.

6 Acknowledgements

Thanks are owed to the following people for their valuable and essential role in this project:

Malcolm Clark (NIWA) for his contribution to the design of the environmental survey.

The voyage leader Ray Wood (Geological and Nuclear Sciences, now Chatham Rock Phosphate Limited) and other members of the environmental survey team on-board the RV *Dorado Discovery,* including the ship's crew, ROV operators, and data managers and loggers. Particular thanks are owed to Emily Jones (Golders Associates Ltd) and Adrian Hellman (Odyssey Marine Explorations) for assisting with biological sampling during the survey, and Simon Nielsen (Kenex) for geological context setting.

Bruce Marshall (Museum of New Zealand - Te Papa Tongarewa) for identifying mollusc specimens recovered by the box-coring.

Julie Hall (NIWA) for managing the project efficiently and effectively.

Alison Macdiarmid (NIWA) for reviewing the report and providing constructive comment.

7 References

Anderson MJ, Gorley RN, Clarke KR (2008) PERMANOVA+ for PRIMER: guide to software and statistical methods. PRIMER-E, Plymouth.

Anderson MJ, Crist TO, Chase JM, Vellend M, Inouye BD, Freestone AL, Sanders NJ, Cornell HV, Comita LS, Davies KF, Harrison SP, Kraft NJB, Stegen JC, Swenson NG (2011) Navigating the multiple meanings of β diversity: a roadmap for the practicing ecologist. Ecology Letters 14:19–28

Austin M (2007) Species distribution models and ecological theory: A critical assessment and some possible new approaches. Ecological Modelling 200(1–2): 1-19.

Baillon S, Hamel J-F, Wareham VE, Mercier A (2012) Deep cold-water corals as nurseries for fish larvae. Frontiers in Ecology and the Environment; doi:10.1890/120022

Beaumont J, Baird S. (2011) Biological and commercial fishing data within the Minerals Prospecting Licence 50270 area on the Chatham Rise. NIWA Client Report No. WLG2011-10. 36 p.

Beaumont J, Rowden AA (2013) Potential for recolonisation and recovery by benthic communities following mining disturbance on the Chatham Rise. NIWA Client Report Prepared for Chatham Rock Phosphate. 34p

Berkenbusch K, Probert PK, Nodder SD (2011) Comparative biomass of sediment benthos across a depth transect, Chatham Rise, Southwest Pacific Ocean. Marine Ecology Progress Series 425: 79–90.

Bowden DA (2011) Benthic invertebrate samples and data from the Ocean Survey 20/20 voyages to Chatham Rise and Challenger Plateau, 2007. Aquatic Environment and Biodiversity Report No. 65, Ministry of Fisheries, Wellington, New Zealand.

Buston PM, Elith J (2011) Determinants of reproductive success in dominant pairs of clownfish: a boosted regression tree analysis. Journal of Animal Ecology 80(3): 528-538.

Calinski T, Harabasz J (1974) A dendrite method for cluster analysis. Communications in Statistics 3:1-27.

Clarke KR, Gorley RN (2006) PRIMER v6: User Manual/Tutorial. PRIMER-E Ltd, Plymouth.

Clarke KR, Warwick RM (2001) Change in marine communities: an approach to statistical analysis and interpretation, 2nd edn. PRIMER-E Ltd, Plymouth.

Clarke KR, Somerfield PJ, Chapman MG (2006) On resemblance measures for ecological studies, including taxonomic dissimilarities and a zero-adjusted Bray–Curtis coefficient for denuded assemblages. Journal of Experminental Marine Biology and Ecology 330: 55–80.

Clarke KR, Somerfield PJ, Gorley RN (2008) Testing of null hypotheses in exploratory community analyses: similarity profiles and biota-environment linkage. Journal of Experimental Marine Biology and Ecology 366:56–69.

Conway KW, Barrie JV, Austin WC, Luternauer JL (1991) Holocene sponge bioherms on the western Canadian continental shelf. Continental Shelf Research 11: 771–790.

Compton TJ, Bowden DA., Pitcher R, Hewitt JE, Ellis N (2013) Biophysical patterns in benthic assemblage composition across contrasting continental margins off New Zealand. Journal of Biogeography 40: 75-89.

Cullen DJ (1980) Distribution, composition and age of submarine phosphorites on Chatham Rise, East of New Zealand. Society of Economic Paleontologists and Mineralogists Special Publication 29: 139-148

Dawson E (1984) The benthic fauna of the Chatham Rise: An assessment relative to possible effects of phosphorite mining. Geologisches Jahrbuch D65: 209-231.

Dell RK (1951) A molluscan fauna from the Mernoo Bank, New Zealand. New Zealand Journal of Science and Technology ?: 15-18.

D'Onghia G, Maiorano P, Sion L, Giove A, Capezzuto F, Carlucci R, Tursi A (2010) Effects of deep-water coral banks on the abundance and size structure of the megafauna in the Mediterranean Sea. Deep-Sea Research II 57: 397-411.

Dutilleul P, Stockwell JD, Frigon D, Legendre P (2000) The Mantel test versus Pearson's correlation analysis: assessment of the differences for biological and environmental studies. Journal of Agricultural, Biological, and Environmental Statistics 5:131–150.

Elith J, Graham CH, Anderson RP, Dudik M, Ferrier S, Guisan A, Hijmans RJ, Huettmann F, Leathwick JR, Lehmann A, Li J, Lohmann LG, Loiselle BA, Manion G, Moritz C, Nakamura M, Nakazawa Y, Overton JM, Peterson AT, Phillips SJ, Richardson K, Scachetti-Pereira R, Schapire RE, Soberon J, Williams S, Wisz MS, Zimmermann NE (2006) Novel methods improve prediction of species' distributions from occurrence data. Ecography 29(2): 129-151.

Elith J, Leathwick JR, Hastie T (2008) A working guide to boosted regression trees. Journal of Animal Ecology 77(4): 802-813.

Etter RJ, Grassle JF (1992) Patterns of species diversity in the deep sea as a function of sediment particle size diversity. Nature 360: 576−578.

Fawcett T (2006) An introduction to ROC analysis. Pattern Recognition Letters 27(8): 861-874.

Floerl O, Hewitt J, Bowden D (2012) Chatham-Challenger Ocean Survey 20/20 Post Voyage analyses: Objective 9 – Patterns in Species Composition. New Zealand Aquatic Environment and Biodiversity Report No. 97, 40p.

Friedman J, Hastie T, Tibshirani R (2000) Additive logistic regression: A statistical view of boosting. Annals of Statistics 28(2): 337-374.

Glasby GP, Wright IC (1990) Marine mineral potential in New Zealand's Exclusive Economic Zone. Marine Mining 9: 403-427.

Grove SL, Probert PK, Berkenbusch K, Nodder SD (2006) Distribution of bathyal meiofauna in the region of the Subtropical Front, Chatham Rise, south-west Pacific. Journal of Experimental Marine Biology and Ecology 330: 342–355.

Guisan A, Thuiller W (2005) Predicting species distribution: offering more than simple habitat models. Ecology Letters 8(9): 993-1009.

Henry L-A, Roberts JM (2007) Biodiversity and ecological composition of macrobenthos on cold-water coral mounds and adjacent off-mound habitat in the bathyal Porcupine Seabight, NE Atlantic. Deep-Sea Research I 54: 654–672.

Hewitt J, Julian K, Bone EK (2011) Chatham–Challenger Ocean Survey 20/20 Post-Voyage Analyses: Objective 10 – Biotic habitats and their sensitivity to physical disturbance. New Zealand Aquatic Environment and Biodiversity Report No. 81, 36p.

Hijmans RJ (2010) Package raster. Available at: http://cran.r-project.org/web/packages/raster/, p.

Hurley DE 1961. The distribution of the isopod crustacean Serolis bromleyana Suhm with a discussion of an associated deepwater community. New Zealand Oceanographic Institute Memoir 13: 225-233.

Knox MA, Hogg ID, Pilditch CA, Lörz A-N, Nodder SD (2012) Abundance and diversity of epibenthic amphipods (Crustacea) from contrasting bathyal habitats. Deep-Sea Research I 62:1–9.

Kudrass H-R, Cullen DJ (1980) Submarine phosphorite nodules from the central Chatham Rise off New Zealand – composition, distribution, and reserves – (Valdivia-Cruise 1978). Geologisches Jahrbuch D51: 3-41.

Kudrass H-R, von Rad U (1984a) Geology and some mining aspects of the Chatham Rise phosphorite: a synthesis of SONNE-17 results. Geologisches Jahrbuch D65: 233-252.

Kudrass H-R, Von Rad U (1984b). Underwater television and photpgraphy observations, side-scan sonar and acoustic reflectivity measurements of phosphorite-rich areas of the Chaham Rise (New Zealand). Geologisches Jahrbuch D65: 69-89.

Leathwick JR, Elith J, Francis MP, Hastie T, Taylor P (2006) Variation in demersal fish species richness in the oceans surrounding New Zealand: an analysis using boosted regression trees. Marine Ecology-Progress Series 321: 267-281.

Leduc D, Rowden AA, Probert PK, Pilditch CA, Nodder S, Bowden DA, Duineveld GCA, Witbaard R (2012). Nematode beta diversity on the continental slope of New Zealand: spatial patterns and environmental drivers. Marine Ecology Progress Series 545: 37-52.

Legendre P, Anderson MJ (1999) Distance-based redundancy analysis: testing multispecies hypotheses responses in multifactorial ecological experiments. Ecological Monographs 69: 1−24.

Legendre P, Borcard D, Peres-Neto PR (2005) Beta diversity: partitioning the spatial variation of community composition data. Ecological Monographs 75:435–450.

Lobo JM, Jiménez-Valverde A, Real R (2008) AUC: a misleading measure of the performance of predictive distribution models. Global Ecology and Biogeography 17(2): 145-151.

Lörz A-N (2010) Biodiversity of an unknown New Zealand habitat: bathyal invertebrate assemblages in the benthic boundary layer. Marine Biodiversity DOI 10.1007/s12526-010-0064-x

MacDiarmid A, Bowden D, Cummings V, Morrison M, Jones E, Kelly M, Neil H, Nelson W, Rowden A (2013) Sensitive marine benthic habitats defined. NIWA Client Report prepared for Ministry for the Environment. 72p.

MacKay KA, Wood BA, Clark MR (2005) Chatham Rise Bathymetry. NIWA Miscellaneous Chart Series 82. NIWA.

McKnight DG, Probert PK (1997) Epibenthic communities on the Chatham Rise, New Zealand. New Zealand Journal of Marine and Freshwater Research 31:505-513.

Milligan GW, Cooper MC (1985) An examination of procedures for determining the number of clusters in a data set. Psychometrika 50: 159–179.

Nodder SD, Pilditch CA, Probert PK, Hall JA (2003) Variability in benthic biomass and activity beneath the Subtropical Front, Chatham Rise, SW Pacific Ocean. Deep-Sea Research I 50: 959-985.

Nodder SD, Duineveld GCA, Pilditch CA, Sutton PJ, Probert PK, Lavaleye MSS, Witbaard R, Chang FH, Hall JA, Richardson KM (2007) Physical focusing of phytodetritus deposition beneath a deep-ocean front, Chatham Rise, New Zealand. Limnology and Oceanography 52: 299-314.

Nodder S, Pallentin A, Mackay K, Bowden D (2013) Seafloor morphology and substrate characterisation on Chatham Rise. NIWA Client Report prepared for Chatham Rock Phosphate Ltd. 38p.

Norris RM (1964) Sediments of Chatham Rise. New Zealand Oceanographic Institute Memoir No. 26.

Quinn PQ, Keough MJ (2009) Experimental Design and Data Analysis for Biologists, 1st edn. Cambridge University Press, Cambridge.

Pasho DW (1976) Distribution and morphology of Chatham Rise phosphorites. Memior of the New Zealand Oceanographic Institute 77: 27p.

Probert PK (1984) A comparison of macrofaunal samples taken by a box corer and anchor-box dredge. New Zealand Oceanographic Institute Records 4 (13): 149-157.

Probert PK, McKnight DG (1993) Biomass of bathyal macrobenthos in the region of the Subtropical Convergence, Chatham Rise, New Zealand. Deep-Sea Research I 40: 1003-1007.

Probert PK, Grove SL, McKnight DG, Read GB (1996) Polychaete distribution on the Chatham Rise, Southwest Pacific. Internationale Revue der Gesamten Hydrobiologie 81: 577-588.

Probert PK, Glasby CJ, Grove SL, Paavo BL (2009) Bathyal polychaete assemblages in the region of the Subtropical Front, Chatham Rise, New Zealand. New Zealand Journal of Marine and Freshwater Research 43: 1121–1135.

von Rad & Kudrass (1987) Exploration and genesis of submarine phosphorite deposits from the Chatham Rise, New Zealand – a review. In: Marine minerals advances in research and resource assessment, ed. Teleki P et al. Dordrecht: Reidel, 157-175.

R Development Core Team (2011) R: A language and environment for statistical computing. Vienna, Austria, R Foundation for Statistical Computing. p.

Ridgeway G (2007) Generalized Boosted Regression Models. p.

Schinner GO (1993) Burrowing Behavior, Substratum Preference, and Distribution of Schizaster canaliferus (Echinoidea: Spatangoida) in the Northern Adriatic Sea. Marine Ecology 14: 129–145.

Snelgrove PVR, Butman CA (1994) Animal-sediment relationships revisited: cause versus effect. Oceanography and Marine Biology Annual Review 32: 111-177.

Sutton P (2001). Detailed structure of the Subtropical front over Chatham Rise, east of New Zealand. Journal of Geophysical Research. C. Oceans 106(C12): 31,045-031,056.

Swets JA (1988) Measuring the accuracy of diagnostic systems. Science 240: 1285-1293.

Tong R, Purser A, Unnithan V, Guinan J (2012) Multivariate Statistical Analysis of Distribution of Deep-Water Gorgonian Corals in Relation to Seabed Topography on the Norwegian Margin. PLoS ONE 7(8): e43534. doi:10.1371/journal.pone.0043534

Torres LG, Smith TD, Sutton P, MacDiarmid A, Bannister J, Miyashita T (2013) From exploitation to conservation: habitat models using whaling data predict distribution patterns and threat exposure of an endangered whale. Diversity and Distributions: n/a-n/a. <http://dx.doi.org/10.1111/ddi.12069>

Tracey DM, Rowden AA, Mackay KA, Compton T (2011) Habitat-forming cold-water corals show affinity for seamounts in the New Zealand region. Marine Ecology Progress Series 430: 1-22.

Tuck I, Hartill B, Parkinson D, Smith M, Armiger H, Rush N, Drury J (2011) Estimating the abundance of scampi, Metanephrops challengeri, from photographic surveys in SCI 3 (2009 & 2010). NIWA Final Research Report prepared for Ministry of Fisheries. 29p.

Veillettea J, Sarrazin J, Gooday AJ, Gale´ron J, Caprais J-C, Vangriesheim A, Etoubleau J, Christian JR, Juniper SK (2007) Ferromanganese nodule fauna in the Tropical North Pacific Ocean: species richness, faunal cover and spatial distribution. Deep-Sea Research I 54: 1912–1935.

Appendix A Scampi (*Metanephrops challengeri*) density

Data for scampi (*Metanephrops challengeri*) and scampi burrows observed in the analysed images were used to estimate the density of this fishery species in the study area. It is important to note that observation protocols and analysis methods did not follow those used in surveys used for scampi stock assessment. In addition, the images analysed were taken at 2 m above the seafloor rather than the stock assessment standard of 4 m (e.g., see Tuck et al. 2011). The density estimates made from data obtained by the present study were compared to estimates made for the most important scampi fishery area (SCI 3) on the Chatham Rise. This fishery area is >100 km west of the study area and in water depths of 300-500 m, a depth range that encompasses the water depths of the study area (370-420 m). Within the SCI 3 fishery area commercial trawling for scampi is concentrated between the Mernoo Bank and the Reserve Bank, and immediately north of the Reserve Bank (Tuck et al. 2011).

Only three observations of scampi outside of (or visible in) their burrows, and 47 scampi burrows were recorded from the images that were analysed during the Environmental Survey (n = 3281). Where scampi and/or their burrows were observed in seafloor images, counts ranged from 1-10 per image, but Figure A-1 shows that scampi and/or their burrows were rarely observed in images taken along the ROV transects in all of the survey areas. The overall mean density of scampi was 0.0002 m^{-2} and for scampi burrows was 0.0036 m^{-2}. These densities are much lower than those observed in the 2010 scampi stock assessment of the SCI 3 fishery area; 0.0172 m^{-2} and 0.0653 m^{-2}, for visible scampi and major burrow openings respectively (Tuck et al. 2011). Scampi and burrow densities in the study area are also much lower than for previous years in SCI 3, and compared to other scampi fishery areas (Tuck et al. 2011).

As already noted, there are differences between the present study and the 2010 stock assessment survey in how seafloor images of scampi and their burrows were obtained and counts made. These dissimilarities could affect the reliability of the density estimates of the present study, and could explain in-part the difference between the stock assessment survey estimates. However, when assessing the possible survey technique-related reasons for different density estimates (between stock assessment and OS20/20 Survey techniques), Tuck et al (2011) noted that there was no discernable effect of making counts from images taken closer to the seafloor and when images were of relatively low resolution (the case in the present study). They also noted that where counting protocols were standardised they attributed the greatest amount of uncertainty to the location of the survey. That is, where photographic surveys are undertaken inside known scampi grounds the probability of a counted burrow being a scampi burrow is likely to be greater than for counts made outside of recognised scampi grounds – because other species are known to excavate burrows that are similar in appearance to scampi burrows in the latter. The study area is not a recognised scampi ground and therefore density estimates are more likely to be over estimates rather than under estimates.

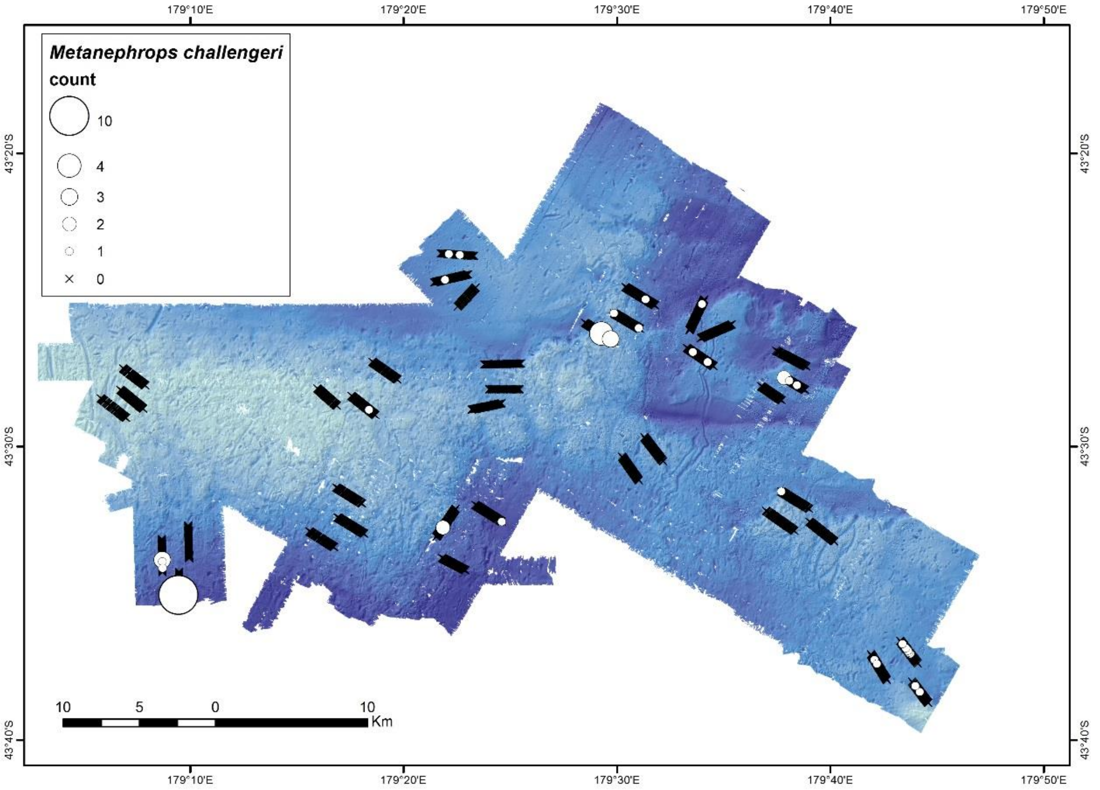


Figure A-1: Map showing the number of scampi (*Metanephrops challengeri*) and/or scampi burrows observed in seafloor images (analysed area of image = $4m^2$).

Appendix B Epifauna taxa identified from seafloor images

Taxa followed by one or more asterisk(s) were not included in final analyses.

* Taxon not well defined, could have been confused with other taxa in list; and/or low abundance

** Infauna taxon

*** Mobile taxa that can avoid ROV - fish/shark/cephlapod

Phylum	Class	Order	Family	Genus	Taxa name
Annelida	Polychaeta	-	-	-	Polychaeta *
Annelida	Polychaeta	-	-	-	quill worm/ tube worm/scaphopod *
Annelida	Polychaeta	-	-	-	Tube worm (generic) *
Annelida	Polychaeta	Canalipalpata	Sabellidae	-	Sabellid
Annelida	Polychaeta	Eunicida	Onuphidae	*Hyalinoecia*	*Hyalinoecia* sp
Annelida	Polychaeta	Terebellida	Terebellidae	-	Terebellidae (mass of thin tentacles) **
Arthropoda	Malacostraca	Decapoda	Polychelidae	-	Polychelidae
Arthropoda	Malacostraca	Pericarida	-	-	Amphipoda *
Athropoda	Malacostraca	Decapoda	-	-	Decapoda (crabs) *
Athropoda	Malacostraca	Decapoda	-	-	Decapoda (natant)
Athropoda	Malacostraca	Decapoda	-	-	Decapoda (shrimps) *
Athropoda	Malacostraca	Decapoda	Atelecyclidae	*Trichopeltarion*	*Trichopeltarion fantasticum*
Athropoda	Malacostraca	Decapoda	Galatheidae	-	Galatheidae
Athropoda	Malacostraca	Decapoda	Nephropidae	*Metanephrops*	*Metanephrops challengeri*
Athropoda	Malacostraca	Decapoda	Paguridae	-	Pagurid
Brachiopoda	-	-	-	-	Brachiopoda
Bryozoa	-	-	-	-	Bryozoan - Antler *(Onchoporoides moseleyi?)*
Bryozoa	-	-	-	-	Bryozoan - Bushy form *
Bryozoa	-	-	-	-	Bryozoan - Yellow lacey *
Bryozoa	-	-	-	-	Bryzoan - Branched coral-like form *
Bryozoa	-	-	-	-	Bryzoan - Encrusting form
Bryozoa	-	-	-	-	Bryzoan - Lacy fan forms *
Bryozoa	-	-	-	-	Bryzoan - Stylasterid look-alikes
Bryozoa	Gymnolaemata	Cheilostomatida	Bitectiporidae	*Bitectipora*	*Bitectipora retepora*
Bryozoa	Gymnolaemata	Cheilostomatida	Celleporidae	*Celleporina*	*Celleporina grandis*
Chordata	Actinopterygii	-	-	-	Unidentified fish ***
Chordata	Actinopterygii	Beryciformes	Berycidae	*Beryx*	*Beryx splendens* ***
Chordata	Actinopterygii	Gadiformes	Macrouridae	*Coelorinchus*	*Coelorinchus acpercephalus* ***
Chordata	Actinopterygii	Gadiformes	Macrouridae	*Coelorinchus*	*Coelorinchus bollonsi* ***
Chordata	Actinopterygii	Gadiformes	Macrouridae	*Coelorinchus*	*Coelorinchus cookianus* ***
Chordata	Actinopterygii	Gadiformes	Macrouridae	*Coelorinchus*	*Coelorinchus fasciatus* ***
Chordata	Actinopterygii	Gadiformes	Macrouridae	*Coelorinchus*	*Coelorinchus oliveranus* ***
Chordata	Actinopterygii	Gadiformes	Macrouridae	*Coelorinchus*	Unidentified rattail ***
Chordata	Actinopterygii	Gadiformes	Macrouridae	*Lepidorhynchus*	*Lepidorhynchus denticulatus****
Chordata	Actinopterygii	Gadiformes	Merlucciidae	*Macruronus*	*Macruronus novaezelandiae* ***

Chordata	Actinopterygii	Gadiformes	Moridae	*Pseudophycis*	*Pseudophycis bachus* ***
Chordata	Actinopterygii	Gadiformes	Moridae	*Pseudophycis*	*Pseudophycis* spp ***
Chordata	Actinopterygii	Gadiformes	Moridae	*Notophycis*	*Notophycis marginata* ***
Chordata	Actinopterygii	Myctophiformes	Myctophidae	-	Myctophid ***
Chordata	Actinopterygii	Ophidiiformes	-	-	Unidentified eel ***
Chordata	Actinopterygii	Ophidiiformes	Ophidiidae	*Genypterus*	*Genypterus blacodes* ***
Chordata	Actinopterygii	Osmeriformes	Argentinidae	*Argentina*	*Argentina elongata* ***
Chordata	Actinopterygii	Perciformes	Centrolophidae	*Seriolella*	*Seriolella brama* ***
Chordata	Actinopterygii	Perciformes	Centrolophidae	*Seriolella*	*Seriolella caerulea* ***
Chordata	Actinopterygii	Perciformes	Centrolophidae	*Seriolella*	*Seriolella punctata* ***
Chordata	Actinopterygii	Perciformes	Epigonidae	*Epigonus*	*Epigonus telescopus* ***
Chordata	Actinopterygii	Perciformes	Percophidae	*Bembrops*	*Bembrops morelandi* ***
Chordata	Actinopterygii	Pleuronectiformes	-	-	Unidentified flatfish ***
Chordata	Actinopterygii	Pleuronectiformes	Pleuronectidae	*Azygopus*	*Azygopus pinnifasciatus* ***
Chordata	Actinopterygii	Scorpaeniformes	Sebastidae	*Helicolenus*	*Helicolenus* spp ***
Chordata	Actinopterygii	Syngnathiformes	Centriscidae	*Centriscops*	*Centriscops humerosus* ***
Chordata	Actinopterygii	Zeiformes	Cyttidae	*Cyttus*	*Cyttus traversi* ***
Chordata	Ascidiacea	-	-	-	Ascidian *
Chordata	Ascidiacea	Aplousobranchia	Didemnidae	-	Didemnid
Chordata	Ascidiacea	Aplousobranchia	Polyclinidae	*Synoicum*	*Synoicum otagoensis*
Chordata	Elasmobranchii	-	-	-	Unidentified shark***
Chordata	Elasmobranchii	Carcharhiniformes	Scyliorhinidae	*Halaelurus*	*Halaelurus dawsoni* ***
Chordata	Elasmobranchii	Squaliformes	Squalidae	*Squalus*	*Squalus acanthias* ***
Chordata	Holocephali	Chimaeriformes	Chimaeridae	*Hydrolagus*	*Hydrolagus novaezelandiae* ***
Cnidaria	Anthozoa	Actiniaria	-	-	Anemones *
Cnidaria	Anthozoa	Actiniaria	-	-	Anenome uni 6
Cnidaria	Anthozoa	Actiniaria	-	-	Anenome uni 7
Cnidaria	Anthozoa	Actiniaria	-	-	Actinaria (indent) *
Cnidaria	Anthozoa	Actiniaria	-	-	Anenome - deep deep red *
Cnidaria	Anthozoa	Actiniaria	-	-	Anenome - uni large/light purple *
Cnidaria	Anthozoa	Actiniaria	Actiniidae	-	Actiniidae
Cnidaria	Anthozoa	Actiniaria	Actinostolidae	-	Actinostolidae
Cnidaria	Anthozoa	Actiniaria	Actinostolidae	-	Actinostolidae
Cnidaria	Anthozoa	Actiniaria	Edwardsiidae	-	Edwardsid
Cnidaria	Anthozoa	Actiniaria	Hormathiidae	-	Hormathiidae
Cnidaria	Anthozoa	Alcyonacea	-	-	Gorgonian (indent)
Cnidaria	Anthozoa	Alcyonacea	Alcyoniidae	-	Alcyoniidae
Cnidaria	Anthozoa	Alcyonacea	Alcyoniidae	*Anthomastus*	*Anthomastus* sp.
Cnidaria	Anthozoa	Alcyonacea	Primnoidae	-	Primnoidae
Cnidaria	Anthozoa	Alcyonacea	Primnoidae	*Callogorgia*	*Callogorgia* spp
Cnidaria	Anthozoa	Antipatharia	Leiopathidae	*Leiopathes*	*Leiopathes*
Cnidaria	Anthozoa	Ceriantharia	-	-	Ceriantharia spp
Cnidaria	Anthozoa	Corallimorpharia	-	-	Corallimorpharia 2
Cnidaria	Anthozoa	Scleractinia	Caryophylliidae	-	cup corals (stalked)
Cnidaria	Anthozoa	Scleractinia	Caryophylliidae	Desmophyllum/Caryophyllia	Desmophyllum/Caryophyllia *
Cnidaria	Anthozoa	Scleractinia	Caryophylliidae	Goniocorella	*Goniocorella dumosa*
Cnidaria	Anthozoa	Scleractinia	Caryophylliidae	*Stephanocyathus*	*Stephanocyathus* spp.

Cnidaria	Anthozoa	Scleractinia	Flabellidae	*Flabellum*	*Flabellum*
Cnidaria	Anthozoa	Scleractinia	Flabellidae	*Flabellum*	*Flabellum* 1
Cnidaria	Anthozoa	Scleractinia	Flabellidae	*Flabellum*	*Flabellum* 3
Cnidaria	Anthozoa	Scleractinia	Flabellidae	*Flabellum*	*Flabellum rubrum*
Cnidaria	Hydrozoa	Anthoathecatae	Stylasteridae	-	Stylasteridae (white)
Cnidaria	Hydrozoa	Anthoathecatae	Stylasteridae	*Calyptopora*	*Calyptopora* spp
Cnidaria	Hydrozoa	Anthoathecatae	Stylasteridae	*Lepidotheca*	*Lepidotheca* spp
Cnidaria	Hydrozoa	Leptothecatae	-	-	Hydroid *
Echinodermata	Asteroidea	-	-	-	Asteroid - 6 arm *
Echinodermata	Asteroidea	-	-	-	Asteroids *
Echinodermata	Asteroidea	Brisingida	Brisingidae	-	Brisingid 1
Echinodermata	Asteroidea	Brisingida	Brisingidae	-	Brisingidae
Echinodermata	Asteroidea	Forcipulatida	Asteriidae	-	Asteriidae
Echinodermata	Asteroidea	Forcipulatida	Asteriidae	*Sclerasterias*	*Sclerasterias mollis*
Echinodermata	Asteroidea	Forcipulatida	Zoroasteridae	-	Zoroasteridae
Echinodermata	Asteroidea	Forcipulatida	Zoroasteridae	*Zoroaster*	*Zoroaster* sp
Echinodermata	Asteroidea	Forcipulatida	Zoroasteridae/Asteriidae	-	Zoroasteridae/Asteriidae
Echinodermata	Asteroidea	Notomyotida	Benthopectinidae	*Benthopecten*	*Benthopecten* sp
Echinodermata	Asteroidea	Paxillosida	Astropectinidae	-	Astropectinidae
Echinodermata	Asteroidea	Paxillosida	Astropectinidae	*Astromesites/Psilaster/Proserpinaster*	*Astromesites/Psilaster/Proserpinaster*
Echinodermata	Asteroidea	Paxillosida	Astropectinidae	*Dipsacaster*	*Dipsacaster magnificus*
Echinodermata	Asteroidea	Paxillosida	Astropectinidae	*Dipsacaster*	*Dipsacaster* sp
Echinodermata	Asteroidea	Paxillosida	Astropectinidae	*Plutonaster/Dytaster*	*Plutonaster/Dytaster*
Echinodermata	Asteroidea	Spinulosida	Echinasteridae	-	Echinasteridae
Echinodermata	Asteroidea	Spinulosida	Pterasteridae	-	Pterasteridae
Echinodermata	Asteroidea	Spinulosida	Solasteridae	*Solaster*	*Solaster torulatus*
Echinodermata	Asteroidea	Valvatida	Goniasteridae	*Lithosoma*	*Lithosoma novazealandiae*
Echinodermata	Asteroidea	Valvatida	Goniasteridae	*Mediaster*	*Mediaster* sp
Echinodermata	Asteroidea	Valvatida	Goniasteridae	*Plinthaster/Ceramaster*	*Plinthaster/Ceramaster*
Echinodermata	Crinoidea	-	-	-	Crinoidea
Echinodermata	Crinoidea	-	-	-	Crinoidea (motile) *
Echinodermata	Echinoidea	Camarodonta/Spatangoida	Echinidae/Spatangidae	*Gracilechinus/Paramaretia*	*Gracilechinus multidentatus*/juvenile *Paramaretia peloria*
Echinodermata	Echinoidea	Cidaroida	-	-	Cidaroida
Echinodermata	Echinoidea	Cidaroida	Cidaridae	-	Cidaridae
Echinodermata	Echinoidea	Cidaroida	Cidaridae	*Goniocidaris*	*Goniocidaris parasol* *
Echinodermata	Echinoidea	Cidaroida	Cidaridae	*Goniocidaris*	*Goniocidaris* sp *
Echinodermata	Echinoidea	Echinoida	-	-	Echinoida
Echinodermata	Echinoidea	Echinoida	Echinidae	-	Echinidae
Echinodermata	Echinoidea	Echinoida	Echinidae	*Dermechinus*	*Dermechinus horridus*
Echinodermata	Echinoidea	Echinoida	Echinidae	*Gracilechinus*	*Gracilechinus multidentatus* *
Echinodermata	Echinoidea	Echinothurioida/Spatangoida	Echinothuriidae/Spatangidae	*Hygrosoma/Paramaretia*	*Hygrosoma luculentum*/*Paramaretia peloria* *
Echinodermata	Echinoidea	Spatangoida	Spatangidae	-	Spatangidae
Echinodermata	Echinoidea	Spatangoida	Spatangidae	*Paramaretia*	*Paramaretia peloria*/ *Spatangus multispinus*/ Tam O Shanter
Echinodermata	Echinoidea	Temnopleuroida	Temnopleuridae	*Pseudechinus*	*Pseudechinus flemingi*
Echinodermata	Holothuroidea	-	-	-	Holothurian *
Echinodermata	Holothuroidea	Elasipodida	Laetmogonidae	*Laetmogone*	*Laetmogone* sp
Echinodermata	Holothuroidea	Dendrochirotida	Psolidae	*Psolus*	*Psolus sp*

Echinodermata	Ophiuroidea	-	-	-	Ophiuroid *
Echinodermata	Ophiuroidea	Ophiurida	-	-	Ophiurida *
Echiura	-	-	-	-	Echiuran **
Mollusca	Bivalvia	-	-	-	Bivalve *
Mollusca	Bivalvia	Limoida	Limidae	*Acesta*	*Acesta maui*
Mollusca	Cephalopoda	Octopoda	Octopodidae	*Enteroctopus*	*Enteroctopus zealandicus* ***
Mollusca	Gastropoda	-	-	-	Gastropod *
Mollusca	Gastropoda	Archaeogastropoda	Calliostomatidae	-	Callostomatidae
Mollusca	Gastropoda	Neogastropoda	Buccinidae	-	Buccinidae
Mollusca	Gastropoda	Neogastropoda	Buccinidae	*Austrofusus*	*Austrofusus glans*
Mollusca	Gastropoda	Neogastropoda	Buccinidae	*Penion*	*Penion* sp
Mollusca	Gastropoda	Neogastropoda	Olividae	-	Olividae
Mollusca	Gastropoda	Neogastropoda	Volutidae	-	Volutidae*
Mollusca	Gastropoda	Neotaenioglossa	Ranellidae	*Fusitriton*	*Fusitriton magellanicus*
Multiple	-	-	-	-	Branching bryozoan/hydroid/other
Multiple	-	-	-	-	Unidentified *
Multiple	-	-	-	-	Unidentified encrusting organisms *
Multiple	-	-	-	-	Unidentified white object *
Porifera	Calcarea	-	-	-	Calcarea *
Porifera	Demospongiae	-	-	-	Demospongiae (encrusting) *
Porifera	Demospongiae	-	-	-	Sponges (demo)
Porifera	Demospongiae	Astrophorida	-	-	Astrophorid - black
Porifera	Demospongiae	Astrophorida	Geodiidae	*Penares*	*Penares palmatoclada ? **
Porifera	Demospongiae	Astrophorida	Pachastrellidae	-	Pachastrellidae
Porifera	Demospongiae	Astrophorida	Vulcanellidae	*Poecillastra*	*Poecillastra laminaris*
Porifera	Demospongiae	Hadromerida	Suberitidae	*Suberites*	*Suberites* n. sp. 1
Porifera	Demospongiae	Hadromerida	Suberitidae	*Suberites*	*Suberites* sp 2
Porifera	Demospongiae	Hadromerida	Polymastiidae	Tentorium	*Tentorium papillatum*
Porifera	Demospongiae	Halichondrida	Axinella/Pararaphoxya	-	Axinella/Pararaphoxya
Porifera	Demospongiae	Lithistida	Corallistidae	*Awhiowhio*	*Awhiowhio sepulchrum*
Porifera	Demospongiae	Poecilosclerida	Cladorhizidae	-	Cladorhizidae (tri carnie sponge)
Porifera	Demospongiae	Poecilosclerida	Hymedesmiidae	*Hymedesmia (Stylopus)*	*Hymedesmia* (*Stylopus*) n. sp. 1
Porifera	Demospongiae	Poecilosclerida	Coelosphaeridae	*Lissodendoryx (Ectyodoryx)*	*Lissodendoryx (Ectyodoryx)* n. sp 1?
Porifera	Demospongiae	Poecilosclerida	Dendoricellidae	*Pyloderma*	*Pyloderma demonstrans*
Porifera	Demospongiae	Spirophorida	Tetillidae	*Craniella*	*Craniella* cf *metaclada* *
Porifera	Hexactinellida	-	-	-	Hexactinellida
Porifera	Hexactinellida	Hexactinosida	-	-	Hexactinosida *
Porifera	Hexactinellida	Hexactinosida	Farreidae	-	Farreidae *
Porifera	Hexactinellida	Lyssacinosida	Rossellidae	*Hyalascus*	*Hyalascus* n. sp

Appendix C Infauna taxa identified from box-core samples

Taxa followed by one or more asterisk(s) were not included in final analyses.

* Too few individuals (n < 6)

** Taxon not well defined, could have been confused with other taxa in list

*** Mesh size too coarse to provide reliable estimate of abundance

Phylum	Class	Order	Family	Genus	Final ID
Annelida	-	-	-	-	Annelida sp.
Annelida	Oligochaeta	Haplotaxida	Naididae	-	Naididae sp.
Annelida	Polychaeta	Amphinomida	Amphinomidae	*Chloeia*	*Chloeia inermis*
Annelida	Polychaeta	Amphinomida	Amphinomidae	*Linopherus*	*Linopherus minuta*
Annelida	Polychaeta	Aphroditiformia	Acoetidae	*Panthalis*	*Panthalis novaezealandiae*
Annelida	Polychaeta	Aphroditiformia	Polynoidae	*Harmothoe*	*Harmothoe* sp.
Annelida	Polychaeta	Aphroditiformia	Polynoidae	-	Polynoidae spp.**
Annelida	Polychaeta	Aphroditiformia	Sigalionidae	*Labiosthenolepis*	*Labiosthenolepis laevis*
Annelida	Polychaeta	Aphroditiformia	Sigalionidae	-	Sigalionidae sp.
Annelida	Polychaeta	Eunicida	Dorvilleidae	-	Dorvilleidae sp. 1
Annelida	Polychaeta	Eunicida	Eunicidae	*Eunice*	*Eunice* cf. *Eunice*-Seamounts-1
Annelida	Polychaeta	Eunicida	Eunicidae	Eunice	*Eunice* sp.
Annelida	Polychaeta	Eunicida	Lumbrineridae	-	Lumbrineridae spp.
Annelida	Polychaeta	Eunicida	Oenonidae	-	Oenonidae sp.
Annelida	Polychaeta	Eunicida	Onuphidae	*Kinbergonuphis*	*Kinbergonuphis* sp.
Annelida	Polychaeta	Eunicida	Onuphidae	-	Onuphidae sp.
Annelida	Polychaeta	Eunicida	Onuphidae	*Rhamphobrachium*	*Rhamphobrachium averincevi*
Annelida	Polychaeta	Phyllodocida	Chrysopetalidae	-	Chrysopetalidae sp. 1
Annelida	Polychaeta	Phyllodocida	Glyceridae	*Glycera*	*Glycera knoxi*
Annelida	Polychaeta	Phyllodocida	Glyceridae	*Glycera*	*Glycera lamelliformis*
Annelida	Polychaeta	Phyllodocida	Glyceridae	*Glycera*	*Glycera* sp.
Annelida	Polychaeta	Phyllodocida	Goniadidae	*Goniada*	*Goniada* sp.
Annelida	Polychaeta	Phyllodocida	Goniadidae	-	Goniadidae sp.
Annelida	Polychaeta	Phyllodocida	Hesionidae	*Oxydromus*	*Oxydromus* sp.
Annelida	Polychaeta	Phyllodocida	Nephtyidae	*Aglaophamus*	*Aglaophamus verrilli*
Annelida	Polychaeta	Phyllodocida	Nephtyidae	-	Nephtyidae sp.
Annelida	Polychaeta	Phyllodocida	Nephtyidae	*Nephtys*	*Nephtys* sp.
Annelida	Polychaeta	Phyllodocida	Phyllodocidae	*Eulalia*	*Eulalia* sp.
Annelida	Polychaeta	Phyllodocida	Phyllodocidae	-	Phyllodocidae spp.**
Annelida	Polychaeta	Phyllodocida	Pilargidae	*Ancistrosyllis*	*Ancistrosyllis ancistrosyllis*-A
Annelida	Polychaeta	Phyllodocida	Sphaerodoridae	-	Sphaerodoridae sp.
Annelida	Polychaeta	Phyllodocida	Syllidae Eusyllinae/Syllinae	-	Syllidae Eusyllinae/Syllinae
Annelida	Polychaeta	Phyllodocida	Syllidae Exogoninae	-	Syllidae Exogoninae
Annelida	Polychaeta	Phyllodocida	Unknown	-	Phyllodocida sp.A66:G337
Annelida	Polychaeta	Sabellida	Oweniidae	*Myriochele*	*Myriochele* sp.

Annelida	Polychaeta	Sabellida	Oweniidae	*Myriowenia*	*Myriowenia myriowenia*-A
Annelida	Polychaeta	Sabellida	Sabellidae	*Euchone*	*Euchone euchone*-A
Annelida	Polychaeta	Sabellida	Sabellidae	-	Sabellidae spp.**
Annelida	Polychaeta	Sabellida	Serpulidae	-	Serpulidae sp
Annelida	Polychaeta	Sabellida	Serpulidae	*Serpula*	*Serpula* sp.
Annelida	Polychaeta	Sabellida	Siboglinidae	-	Siboglinidae sp.
Annelida	Polychaeta	Scolecida	Capitellidae	-	Capitellidae spp.
Annelida	Polychaeta	Scolecida	Cossuridae	*Cossura*	*Cossura consimilis*
Annelida	Polychaeta	Scolecida	Maldanidae	*Asychis*	*Asychis trifilosus*
Annelida	Polychaeta	Scolecida	Maldanidae	*Euclymene*	*Euclymene euclymene*-A
Annelida	Polychaeta	Scolecida	Maldanidae	*Euclymenin*	*Euclymenin* sp.
Annelida	Polychaeta	Scolecida	Maldanidae	*Lumbriclymene*	*Lumbriclymene* cf. *cylindricauda*
Annelida	Polychaeta	Scolecida	Maldanidae	*Maldane*	*Maldane theodori*
Annelida	Polychaeta	Scolecida	Maldanidae	-	Maldanidae sp.
Annelida	Polychaeta	Scolecida	Maldanidae	*Rhodine*	*Rhodine intermedia*
Annelida	Polychaeta	Scolecida	Opheliidae	*Ophelina*	*Ophelina ophelina*-B
Annelida	Polychaeta	Scolecida	Orbiniidae	-	Orbiniidae sp.
Annelida	Polychaeta	Scolecida	Paraonidae	*Aricidea*	*Aricidea aricidea*-3
Annelida	Polychaeta	Scolecida	Paraonidae	*Aricidea*	*Aricidea aricidea*-A
Annelida	Polychaeta	Scolecida	Paraonidae	*Levinsenia*	*Levinsenia gracilis*
Annelida	Polychaeta	Scolecida	Scalibregmatidae	-	Scalibregmatidae sp.
Annelida	Polychaeta	Spionida	Chaetopteridae	-	Chaetopteridae sp. 1
Annelida	Polychaeta	Spionida	Chaetopteridae	*Spiochaetopterus*	*Spiochaetopterus* sp. 1
Annelida	Polychaeta	Spionida	Spionidae	?*Malacoceros*	?*Malacoceros*
Annelida	Polychaeta	Spionida	Spionidae	*Laonice*	*Laonice laonice*-A
Annelida	Polychaeta	Spionida	Spionidae	*Laonice*	*Laonice* sp.
Annelida	Polychaeta	Spionida	Spionidae	*Paraprionospio*	*Paraprionospio coora*
Annelida	Polychaeta	Spionida	Spionidae	*Polydora*	*Polydora* sp.
Annelida	Polychaeta	Spionida	Spionidae	*Prionospio*	*Spionidae* spp.**
Annelida	Polychaeta	Spionida	Spionidae	*Scolelepis*	*Scolelepis scolelepis*-3
Annelida	Polychaeta	Spionida	Spionidae	*Spiophanes*	*Spiophanes japonicum*
Annelida	Polychaeta	Spionida	Spionidae	*Spiophanes*	*Spiophanes modestus*
Annelida	Polychaeta	Spionida	Trochochaetidae	*Trochochaeta*	*Trochochaeta* aff. *japonica*
Annelida	Polychaeta	Terebellida	Acrocirridae	*Acrocirrus*	*Acrocirrus acrocirrus*-A
Annelida	Polychaeta	Terebellida	Ampharetidae	*Ampharete*	*Ampharete kerguelensis*
Annelida	Polychaeta	Terebellida	Ampharetidae	*Amphicteis*	*Amphicteis amphicteis*-A
Annelida	Polychaeta	Terebellida	Ampharetidae	*Melinna*	*Melinna armandi*
Annelida	Polychaeta	Terebellida	Ampharetidae	-	Ampharetidae sp. 1
Annelida	Polychaeta	Terebellida	Cirratulidae	-	Cirratulidae spp.
Annelida	Polychaeta	Terebellida	Fauveliopsidae	*Fauveliopsis*	*Fauveliopsis* sp.
Annelida	Polychaeta	Terebellida	Flabelligeridae	-	Flabelligeridae sp. 1
Annelida	Polychaeta	Terebellida	Flabelligeridae	-	Flabelligeridae sp. 2
Annelida	Polychaeta	Terebellida	Flabelligeridae	-	Flabelligeridae sp. 3
Annelida	Polychaeta	Terebellida	Terebellidae	*Artacama*	*Artacama artacama*-A
Annelida	Polychaeta	Terebellida	Terebellidae	-	Terebellidae sp.
Annelida	Polychaeta	Terebellida	Terebellidae	*Pista*	Pista sp.
Annelida	Polychaeta	Terebellida	Terebellidae	*Pseudopista*	*Pseudopista pseudopista*-01

Annelida	Polychaeta	Terebellida	Terebellidae Polycirrinae	-	Terebellidae Polycirrinae
Annelida	Polychaeta	Terebellida	Trichobranchidae	*Terebellides*	*Terebellides narribri*
Arthropoda	Copepoda	-	-	-	Copepoda spp.
Arthropoda	Malacostraca	Amphipoda	-	-	Amphipoda sp. Damaged*
Arthropoda	Malacostraca	Amphipoda	-	-	Amphipoda sp. Unidentifed*
Arthropoda	Malacostraca	Amphipoda	Ampeliscidae	-	Ampeliscidae sp.
Arthropoda	Malacostraca	Amphipoda	Aoridae	-	Aoridae sp.
Arthropoda	Malacostraca	Amphipoda	Corophioidea	-	Corophioidea sp.
Arthropoda	Malacostraca	Amphipoda	Eusiridae	-	Eusiridae sp.
Arthropoda	Malacostraca	Amphipoda	Iphimediidae	-	Iphimediidae sp.
Arthropoda	Malacostraca	Amphipoda	Lepechinellidae	-	Lepechinellidae sp.
Arthropoda	Malacostraca	Amphipoda	Liljeborgiidae	*Liljeborgia*	*Liljeborgia hansoni*
Arthropoda	Malacostraca	Amphipoda	Lysianassoidea	-	Lysianassoidea sp.
Arthropoda	Malacostraca	Amphipoda	Lysianassoidea	-	Lysianassoidea sp.
Arthropoda	Malacostraca	Amphipoda	Oedicerotidae	-	Oedicerotidae sp.
Arthropoda	Malacostraca	Amphipoda	Pardaliscidae	cf *Alcufia*	cf *Alcufia* sp.
Arthropoda	Malacostraca	Amphipoda	Photidae	-	Photidae sp.
Arthropoda	Malacostraca	Amphipoda	Phoxocephalidae	-	Phoxocephalidae sp. 1
Arthropoda	Malacostraca	Amphipoda	Phoxocephalidae	-	Phoxocephalidae sp. 2
Arthropoda	Malacostraca	Amphipoda	Phoxocephalidae	-	Phoxocephalidae sp. 3
Arthropoda	Malacostraca	Amphipoda	Phoxocephalidae	-	Phoxocephalidae sp. 4
Arthropoda	Malacostraca	Amphipoda	Platyschnopiidae	-	Platyschnopiidae sp.
Arthropoda	Malacostraca	Amphipoda	Stenothoidae	-	Stenothoidae sp.
Arthropoda	Malacostraca	Amphipoda	Synopiidae	-	Synopiidae sp.
Arthropoda	Malacostraca	Amphipoda	Urohaustoroidea	-	Urohaustoroidea sp.
Arthropoda	Malacostraca	Cumacea	-	-	Cumacea damaged *
Arthropoda	Malacostraca	Cumacea	-	-	Cumacea sp.12
Arthropoda	Malacostraca	Cumacea	Bodotriidae	-	Bodotriidae sp. 3
Arthropoda	Malacostraca	Cumacea	Diastylidae	-	Diastylidae sp. 1
Arthropoda	Malacostraca	Cumacea	Diastylidae	-	Diastylidae sp. 13
Arthropoda	Malacostraca	Cumacea	Diastylidae	-	Diastylidae sp. 9
Arthropoda	Malacostraca	Cumacea	Lampropidae	-	Lampropidae sp. 10
Arthropoda	Malacostraca	Cumacea	Lampropidae	-	Lampropidae sp. 11
Arthropoda	Malacostraca	Cumacea	Lampropidae	-	Lampropidae sp. 2
Arthropoda	Malacostraca	Cumacea	Lampropidae	-	Lampropidae sp. 5
Arthropoda	Malacostraca	Cumacea	Lampropidae	-	Lampropidae sp. 6
Arthropoda	Malacostraca	Cumacea	Leuconidae	-	Leuconidae sp. 7
Arthropoda	Malacostraca	Cumacea	Nannastacidae	-	Nannastacidae sp. 4
Arthropoda	Malacostraca	Cumacea	Nannastacidae	*Campylaspis*	*Campylaspis rex* sp. 8
Arthropoda	Malacostraca	Eucarida	-	-	Eucarida spp.*
Arthropoda	Malacostraca	Isopoda	Acanthaspidiidae	*Ianthopsis*	*Ianthopsis* sp. 1
Arthropoda	Malacostraca	Isopoda	Acanthaspidiidae	*Ianthopsis*	*Ianthopsis* sp. 2
Arthropoda	Malacostraca	Isopoda	Anthuridea	-	Anthuridea indet.**
Arthropoda	Malacostraca	Isopoda	Anthuridea	-	Anthuridea sp. 1
Arthropoda	Malacostraca	Isopoda	Anthuridea	-	Anthuridea sp. 2
Arthropoda	Malacostraca	Isopoda	Anthuridea	-	Anthuridea sp. 3
Arthropoda	Malacostraca	Isopoda	Anthuridea	-	Anthuridea sp. 4

Arthropoda	Malacostraca	Isopoda	Anthuridea	-	Anthuridea sp. 5
Arthropoda	Malacostraca	Isopoda	Anthuridea	-	Anthuridea sp. 6
Arthropoda	Malacostraca	Isopoda	Cirolanidae	-	Cirolanidae indet.**
Arthropoda	Malacostraca	Isopoda	Cirolanidae	-	Cirolanidae sp. 1
Arthropoda	Malacostraca	Isopoda	Cirolanidae	-	Cirolanidae sp. 2
Arthropoda	Malacostraca	Isopoda	Cirolanidae	-	Cirolanidae sp. 3
Arthropoda	Malacostraca	Isopoda	Dendrotionidae	*Dendrotion*	*Dendrotion* sp. 1
Arthropoda	Malacostraca	Isopoda	Dendrotionidae	*Dendrotion*	*Dendrotion* sp. 2
Arthropoda	Malacostraca	Isopoda	Desmosomatidae	-	Desmosomatidae indet.**
Arthropoda	Malacostraca	Isopoda	Desmosomatidae	*Chelator*	*Chelator* indet.**
Arthropoda	Malacostraca	Isopoda	Desmosomatidae	*Chelator*	*Chelator* sp. 1
Arthropoda	Malacostraca	Isopoda	Desmosomatidae	*Chelator*	*Chelator* sp. 2
Arthropoda	Malacostraca	Isopoda	Desmosomatidae	*Chelator*	*Chelator* sp. 3
Arthropoda	Malacostraca	Isopoda	Desmosomatidae	*Chelator*	*Chelator* sp. 4
Arthropoda	Malacostraca	Isopoda	Desmosomatidae	*Desmosoma*	*Desmosoma* sp. 1
Arthropoda	Malacostraca	Isopoda	Desmosomatidae	*Desmosoma*	*Desmosoma* sp. 2
Arthropoda	Malacostraca	Isopoda	Desmosomatidae	*Eugerda*	*Eugerda* sp. 1
Arthropoda	Malacostraca	Isopoda	Desmosomatidae	*Eugerda*	*Eugerda* sp. 2
Arthropoda	Malacostraca	Isopoda	Desmosomatidae	*Eugerdella*	*Eugerdella* sp. 1
Arthropoda	Malacostraca	Isopoda	Desmosomatidae	*Mirabilicoxa*	*Mirabilicoxa* sp. 1
Arthropoda	Malacostraca	Isopoda	Desmosomatidae	*Mirabilicoxa*	*Mirabilicoxa* sp. 2
Arthropoda	Malacostraca	Isopoda	Desmosomatidae	*Mirabilicoxa*	*Mirabilicoxa* sp. 3
Arthropoda	Malacostraca	Isopoda	Desmosomatidae	*Mirabilicoxa*	*Mirabilicoxa* sp. 4
Arthropoda	Malacostraca	Isopoda	Desmosomatidae	*Paradesmosoma*	*Paradesmosoma* sp. 1
Arthropoda	Malacostraca	Isopoda	Desmosomatidae	*Prochelator*	*Prochelator* sp. 1
Arthropoda	Malacostraca	Isopoda	Desmosomatidae	*Pseudogerda*	*Pseudogerda* sp. 1
Arthropoda	Malacostraca	Isopoda	Janiridae	-	Janiridae sp. 1
Arthropoda	Malacostraca	Isopoda	Janiridae	-	Janiridae sp. 2
Arthropoda	Malacostraca	Isopoda	Munnidae	-	Munnidae sp. 1
Arthropoda	Malacostraca	Isopoda	Munnopsidae	-	Munnopsidae indet.**
Arthropoda	Malacostraca	Isopoda	Munnopsidae	-	Munnopsidae sp. 1
Arthropoda	Malacostraca	Isopoda	Munnopsidae	-	Munnopsidae sp. 2
Arthropoda	Malacostraca	Isopoda	Nannoniscidae	*Exiliniscus*	*Exiliniscus* sp. 1
Arthropoda	Malacostraca	Isopoda	Nannoniscidae	*Exiliniscus*	*Exiliniscus* sp. 2
Arthropoda	Malacostraca	Isopoda	Nannoniscidae	*Nannoniscus*	*Nannoniscus* sp. 1
Arthropoda	Malacostraca	Isopoda	Paramunnidae	*Pentaceration*	*Pentaceration* sp. 1
Arthropoda	Malacostraca	Isopoda	Paramunnidae	*Pentaceration*	*Pentaceration* sp. 2
Arthropoda	Malacostraca	Isopoda	Serolidae	-	Serolidae sp. 1
Arthropoda	Malacostraca	Isopoda	Sphaeromatidae	-	Sphaeromatidae sp. 1
Arthropoda	Malacostraca	Isopoda	Thambematidae	cf. *Thambema*	cf. *Thambema* sp. 1
Arthropoda	Malacostraca	Isopoda	Valvifera	-	Valvifera sp. 1
Arthropoda	Malacostraca	Isopoda	Valvifera	-	Valvifera sp. 2
Arthropoda	Malacostraca	Isopoda	Valvifera	-	Valvifera sp. 3
Arthropoda	Malacostraca	Isopoda	Valvifera	-	Valvifera sp. 4
Arthropoda	Malacostraca	Isopoda	Valvifera	-	Valvifera sp. 5
Arthropoda	Malacostraca	Leptostraca	-	-	Leptostraca sp.
Arthropoda	Malacostraca	Leptostraca	Paranebaliidae	*Levinebalia*	*Levinebalia cf fortunata*

Arthropoda	Malacostraca	Tanaidacea	-	-	Tanaidacea spp.
Arthropoda	Maxillopoda	Scalpelliformes	Calanticidae	*Calantica*	*Calantica* sp.
Arthropoda	Maxillopoda	Scalpelliformes	Scalpellidae	*Arcoscalpellum*	*Arcoscalpellum* sp.
Arthropoda	Ostracoda	-	-	-	Ostracoda spp.
Brachiopoda	-	-	-	-	Brachiopoda spp.
Bryozoa	Gymnolaemata	Cheilostomata	Aeteidae	*Aetea*	*Aetea ligulata*
Bryozoa	Gymnolaemata	Cheilostomata	Arachnopusiidae	*Arachnopusia*	*Arachnopusia perforata*
Bryozoa	Gymnolaemata	Cheilostomata	Aspidostomatidae	cf. *Aspidostoma*	cf. *Aspidostoma* sp.
Bryozoa	Gymnolaemata	Cheilostomata	Beaniidae	*Beania*	*Beania* n. sp.
Bryozoa	Gymnolaemata	Cheilostomata	Bitectiporidae	*Bitectipora*	*Bitectipora retepora*
Bryozoa	Gymnolaemata	Cheilostomata	Bitectiporidae	*Parkermavella*	*Parkermavella virago*
Bryozoa	Gymnolaemata	Cheilostomata	Bitectiporidae	*Schizosmittina*	*Schizosmittina cinctipora*
Bryozoa	Gymnolaemata	Cheilostomata	Bitectiporidae	*Schizosmittina*	*Schizosmittina melanobater*
Bryozoa	Gymnolaemata	Cheilostomata	Buffonellodidae	*Aimulosia*	*Aimulosia marsupium*
Bryozoa	Gymnolaemata	Cheilostomata	Buffonellodidae	*Bugula*	*Bugula* sp.
Bryozoa	Gymnolaemata	Cheilostomata	Buffonellodidae	*Ipsibuffonella*	*Ipsibuffonella* sp.
Bryozoa	Gymnolaemata	Cheilostomata	Calloporidae	"*Pelikopyxis*"	"*Pelikopyxis*" n. sp.
Bryozoa	Gymnolaemata	Cheilostomata	Calloporidae	*Amphiblestrum*	*Amphiblestrum* sp.
Bryozoa	Gymnolaemata	Cheilostomata	Calloporidae	*Ellisina*	*Ellisina* sp.
Bryozoa	Gymnolaemata	Cheilostomata	Calwelliidae	*Malakosaria*	*Malakosaria* sp.
Bryozoa	Gymnolaemata	Cheilostomata	Candidae	*Caberea*	*Caberea* sp.
Bryozoa	Gymnolaemata	Cheilostomata	Cellariidae	*Melicerita*	*Melicerita knoxi*
Bryozoa	Gymnolaemata	Cheilostomata	Cellariidae	*Melicerita*	*Melicerita* sp.
Bryozoa	Gymnolaemata	Cheilostomata	Celleporidae	*Celleporina*	*Celleporina grandis*
Bryozoa	Gymnolaemata	Cheilostomata	Celleporidae	*Galeopsis*	*Galeopsis* n. sp.
Bryozoa	Gymnolaemata	Cheilostomata	Celleporidae	*Galeopsis*	*Galeopsis polyporus*
Bryozoa	Gymnolaemata	Cheilostomata	Celleporidae	*Galeopsis*	*Galeopsis* sp.
Bryozoa	Gymnolaemata	Cheilostomata	Celleporidae	Genus i-et.	Genus indet. n. sp.
Bryozoa	Gymnolaemata	Cheilostomata	Celleporidae	*Lagenipora*	*Lagenipora* cf. *pinnacula*
Bryozoa	Gymnolaemata	Cheilostomata	Celleporidae	*Osthimosia*	*Osthimosia* sp.
Bryozoa	Gymnolaemata	Cheilostomata	Chaperiidae	*Chaperia*	*Chaperia* sp.
Bryozoa	Gymnolaemata	Cheilostomata	Chaperiidae	*Chaperiopsis*	*Chaperiopsis lanceola*
Bryozoa	Gymnolaemata	Cheilostomata	Chaperiidae	*Chaperiopsis*	*Chaperiopsis* sp.
Bryozoa	Gymnolaemata	Cheilostomata	Chaperiidae	*Chaperiopsis*	*Chaperiopsis splendida*
Bryozoa	Gymnolaemata	Cheilostomata	Chaperiidae	*Patsyella*	*Patsyella acanthodes*
Bryozoa	Gymnolaemata	Cheilostomata	Cribrilinidae	*Figularia*	*Figularia pelmatifera*
Bryozoa	Gymnolaemata	Cheilostomata	Escharinidae	*Chiastosella*	*Chiastosella grandis*
Bryozoa	Gymnolaemata	Cheilostomata	Euthyroididae	*Euthyroides*	*Euthyroides* n. sp.
Bryozoa	Gymnolaemata	Cheilostomata	Foveolariidae	*Foveolaria*	*Foveolaria elliptica*
Bryozoa	Gymnolaemata	Cheilostomata	Lanceoporidae	*Calyptotheca*	*Calyptotheca janua*
Bryozoa	Gymnolaemata	Cheilostomata	Microporellidae	*Fenestrulina*	*Fenestrulina* n. sp.
Bryozoa	Gymnolaemata	Cheilostomata	Microporidae	*Opaeophora*	*Opaeophora monopia*
Bryozoa	Gymnolaemata	Cheilostomata	Phidoloporidae	*Reteporella*	*Reteporella* sp.
Bryozoa	Gymnolaemata	Cheilostomata	Phidoloporidae	*Stephanollona*	*Stephanollona scintillans*
Bryozoa	Gymnolaemata	Cheilostomata	Porinidae	*Haswelliporina*	*Haswelliporina* sp.
Bryozoa	Gymnolaemata	Cheilostomata	Porinidae	*Semihaswellia*	*Semihaswellia* sp.
Bryozoa	Gymnolaemata	Cheilostomata	Romancheinidae	*Escharella*	*Escharella* sp.

Bryozoa	Gymnolaemata	Cheilostomata	Romancheinidae	*Escharella*	*Escharella spinosissima*
Bryozoa	Gymnolaemata	Cheilostomata	Smittinidae	*Parasmittina*	*Parasmittina aotea*
Bryozoa	Gymnolaemata	Cheilostomata	Smittinidae	*Parasmittina*	*Parasmittina* n. sp. 1
Bryozoa	Gymnolaemata	Cheilostomata	Smittinidae	*Smittina*	*Smittina* n. sp. ("*obliqua*")
Bryozoa	Gymnolaemata	Cheilostomata	Smittinidae	*Smittina*	*Smittina* sp.
Bryozoa	Gymnolaemata	Cheilostomata	Smittinidae	*Smittoidea*	*Smittoidea* sp.
Bryozoa	Gymnolaemata	Ctenostomata	Arachnidiidae	*Arachnidium*	*Arachnidium* n. sp.
Bryozoa	Stenolaemata	Cyclostomata	Annectocymidae	*Entalophoroecia*	*Entalophoroecia* sp.
Bryozoa	Stenolaemata	Cyclostomata	Diaperoeciidae	*Diaperoecia*	*Diaperoecia purpurascens*
Bryozoa	Stenolaemata	Cyclostomata	Fascigeridae	*Filifascigera*	*Filifascigera* cf. *pluripora*
Bryozoa	Stenolaemata	Cyclostomata	Horneridae	*Hornera*	*Hornera* sp.
Bryozoa	Stenolaemata	Cyclostomata	Incertae sedis	*Telopora*	*Telopora* sp.
Bryozoa	Stenolaemata	Cyclostomata	Lichenoporidae	*Disporella*	*Disporella pristis*
Bryozoa	Stenolaemata	Cyclostomata	Lichenoporidae	*Disporella*	*Disporella* sp.
Bryozoa	Stenolaemata	Cyclostomata	Plagioeciidae	*Plagioecia*	*Plagioecia* sp.
Bryozoa	Stenolaemata	Cyclostomata	Plagioeciidae	-	*Plagioeciidae* sp.
Bryozoa	Stenolaemata	Cyclostomata	Stomatoporidae	*Stomatopora*	*Stomatopora* sp.
Bryozoa	Stenolaemata	Cyclostomata	Tubuliporidae	*Tubulipora*	*Tubulipora* sp.
Cercozoa	Gromiidea	Gromiida	Gromiidae	*Gromia*	*Gromia* n. sp.?
Cnidaria	Anthozoa	Actiniaria	-	-	Actiniaria sp.
Cnidaria	Anthozoa	Actiniaria	-	-	Actiniaria sp. 'flat'
Cnidaria	Anthozoa	Actiniaria	Edwardsiidae	-	Edwardsiidae spp.
Cnidaria	Anthozoa	Alcyonacea	-	-	Alcyonacea spp.*
Cnidaria	Anthozoa	Pennatulacea	-	-	Pennatulacea sp.*
Cnidaria	Anthozoa	Scleractinia	-	*Caryophyllia*	*Caryophyllia* sp.
Cnidaria	Anthozoa	Scleractinia	-	*Scleractinia*	*Scleractinia* sp.
Cnidaria	Hydrozoa	Anthoathecata	Stylasteridae	*Conopora*	*Conopora laevis*
Cnidaria	Hydrozoa	Leptothecata	-	-	Leptothecata sp.
Cnidaria	Hydrozoa	Leptothecata	Campanulariidae	*Clytia*?	*Clytia*? sp.
Cnidaria	Scyphozoa	Coronatae	Nausithoidae	*Nausithoe*	*Nausithoe punctata*
Echinodermata	Asteroidea	-	-	-	Asteroidea sp. 1
Echinodermata	Asteroidea	Notomyotida	Benthopectinidae	*Cheiraster*	*Cheiraster* sp. 1
Echinodermata	Echinoidea	Spatangoida	-	Spatangoida?	Spatangoida? **
Echinodermata	Echinoidea	Spatangoida	Brissidae	*Brissopsis*	*Brissopsis oldhami*
Echinodermata	Echinoidea	Spatangoida	Loveniidae	?*Echinocardium*	?*Echinocardium lymani***
Echinodermata	Echinoidea	Spatangoida	Loveniidae	*Echinocardium*	*Echinocardium lymani*
Echinodermata	Echinoidea	Spatangoida	Spatangidae	*Spatangus*	*Spatangus* sp.
Echinodermata	Holothuroidea	-	-	-	Holothuroidea spp.*
Echinodermata	Holothuroidea	Dendrochirotida	Heterothyonidae	*Heterothyone*	*Heterothyone alba*
Echinodermata	Holothuroidea	Dendrochirotida	Placothuriidae	*Placothuria*	*Placothuria huttoni*
Echinodermata	Holothuroidea	Molpadiida	Caudinidae	*Paracaudina*	*Paracaudina chilensis*
Echinodermata	Holothuroidea	Molpadiida	Caudinidae	*Paracaudina*	Paracaudina sp.
Echinodermata	Ophiuroidea	Ophiurida	-	-	Ophiurida sp. 1
Echinodermata	Ophiuroidea	Ophiurida	-	-	Ophiurida sp. 2
Echinodermata	Ophiuroidea	Ophiurida	Amphiuridae	*Amphioplus*	*Amphioplus ctenacantha*
Echinodermata	Ophiuroidea	Ophiurida	Amphiuridae	*Amphioplus*	*Amphioplus dikellacantha*
Echinodermata	Ophiuroidea	Ophiurida	Amphiuridae	*Amphiura*	*Amphiura ?micra*

Echinodermata	Ophiuroidea	Ophiurida	Amphiuridae	*Amphiura*	*Amphiura* cf. *hinemoae*
Echinodermata	Ophiuroidea	Ophiurida	Amphiuridae	*Amphiura*	*Amphiura* cf. *psilopora*
Echinodermata	Ophiuroidea	Ophiurida	Amphiuridae	*Amphiura*	*Amphiura correcta*
Echinodermata	Ophiuroidea	Ophiurida	Amphiuridae	*Amphiura*	*Amphiura* indeterminate/juvenile*
Echinodermata	Ophiuroidea	Ophiurida	Amphiuridae	*Amphiura*	*Amphiura latisquama*
Echinodermata	Ophiuroidea	Ophiurida	Amphiuridae	*Amphiura*	*Amphiura magellanica*
Echinodermata	Ophiuroidea	Ophiurida	Amphiuridae	*Amphiura*	*Amphiura tutanekai*
Echinodermata	Ophiuroidea	Ophiurida	Ophiacanthidae	*Ophiacantha*	*Ophiacantha ?pentagona*
Echinodermata	Ophiuroidea	Ophiurida	Ophiacanthidae	*Ophiacantha*	*Ophiacantha* juvenile*
Echinodermata	Ophiuroidea	Ophiurida	Ophiacanthidae	*Ophiacantha*	*Ophiacantha otagoensis*
Echinodermata	Ophiuroidea	Ophiurida	Ophiactidae	*Ophiactis*	*Ophiactis hirta*
Echinodermata	Ophiuroidea	Ophiurida	Ophiuridae	?*Ophiomastus*	?*Ophiomastus*
Echinodermata	Ophiuroidea	Ophiurida	Ophiuridae	cf. *Actinozonella/ Ophiomastus*	cf. *Actinozonella/ Ophiomastus* -
Echinodermata	Ophiuroidea	Ophiurida	Ophiuridae	*Ophiomisidium*	*Ophiomisidium irene*
Echinodermata	Ophiuroidea	Ophiurida	Ophiuridae	*Ophiura*	*Ophiura irrorata*
Mollusca	Aplacophora	-	-	-	Aplacophora spp.
Mollusca	Aplacophora			*Solenogastre*	Solenogastre sp. 1
Mollusca	Aplacophora			*Solenogastre*	Solenogastre sp. 2
Mollusca	Bivalvia		-	-	Bivalvia sp.
Mollusca	Bivalvia		Condylocardiidae	*Cuna*	*Cuna mendica*
Mollusca	Bivalvia		Cuspidariidae	*Cuspidaria*	*Cuspidaria* sp.
Mollusca	Bivalvia		Galeommatidae	*Scintillona*	*Scintillona benthicola*
Mollusca	Bivalvia		Limidae	*Limatula*	*Limatula suteri*
Mollusca	Bivalvia		Malletiidae	*Austrotindaria*	*Austrotindaria benthicola*
Mollusca	Bivalvia		Malletiidae	*Austrotindaria*	*Austrotindaria flemingi*
Mollusca	Bivalvia		Manzanillidae	*Nucinella*	*Nucinella maoriana*
Mollusca	Bivalvia		Neoleptonidae	*Neolepton*	*Neolepton* sp.
Mollusca	Bivalvia		Nuculanidae	*Poroleda*	*Poroleda lanceolata*
Mollusca	Bivalvia		Nuculanidae	*Saccella*	*Saccella hedleyi*
Mollusca	Bivalvia		Nuculidae	*Ennucula*	*Ennucula strangeiformis*
Mollusca	Bivalvia		Nuculidae	*Linucula*	*Linucula recens*
Mollusca	Bivalvia		Periplomatidae	*Pe-aloma*	*Pendaloma micans*
Mollusca	Bivalvia		Solemyidae	*Solemya*	*Solemya parkinsonii*
Mollusca	Bivalvia		Thraciidae	*Parvithracia*	*Parvithracia suteri*
Mollusca	Bivalvia		Thyasiridae	*Genaxinus*	*Genaxinus* sp.
Mollusca	Bivalvia		Thyasiridae	*Leptaxinus*	*Leptaxinus* sp.
Mollusca	Bivalvia		Thyasiridae	*Parathyasira*	*Parathyasira neozelanica*
Mollusca	Bivalvia		Verticordiidae	*Policordia*	*Policordia* sp.
Mollusca	Bivalvia		Yoldiidae	*Yoldiella*	*Yoldiella* sp. 1
Mollusca	Gastropoda		-	-	Gastropoda sp.
Mollusca	Gastropoda		-	-	Gastropoda sp. 'slug'
Mollusca	Gastropoda		Mitromorphidae	*Mitromorpha*	*Mitromorpha* sp.
Mollusca	Gastropoda		Nassariidae	*Nassarius*	*Nassarius ephamillus*
Mollusca	Gastropoda		Naticidae	*Uberella*	*Uberella vitrea*
Mollusca	Gastropoda		Philinidae	*Philine*	*Philine* sp. 1
Mollusca	Gastropoda		Philinidae	*Philine*	*Philine* sp. 2
Mollusca	Gastropoda		Pseudomelatomidae	*Comitas*	*Comitas onokeana vivens*

Mollusca	Gastropoda		Retusidae	*Volvulella*	*Volvulella truncata*
Mollusca	Polyplacophora	Ischnochitonina	Schizochitonidae	*Loricella*	*Loricella profundior*
Mollusca	Polyplacophora	Lepidopleurina	Leptochitonidae	*Parachiton*	*Parachiton* ?
Mollusca	Scaphopoda		Dentaliidae	*Antalis*	*Antalis nana*
Nematoda	-	-	-	-	Nematoda spp.***
Nemertea	-	-	-	-	Nemertea sp. micro
Nemertea	-	-	-	-	Nemertea spp.**
Platyhelminthes	-	-	-	-	Platyhelminthes sp.
Porifera	-	-	-	-	Porifera spp.**
Porifera	Hexactinellida	Lyssacinosida	Rossellidae	*Rossella*	*Rossella* sp.
Sipuncula	-	-	-	-	Sipuncula spp.
Tunicata	Ascidiacea	-	-	-	Ascidiacea spp.*
Tunicata	Ascidiacea	Enterogona	Didemnidae	-	Didemnidae sp.
Tunicata	Ascidiacea	Enterogona	Polyclinidae	*Aplidium*	*Aplidium* sp.

Appendix D Station data for ROV transects

Survey area	Transect	Longitude - start (decimal degrees E)	Latitude – start (decimal degrees S)	Longitude - finish (decimal degrees E)	Latitude - finish (decimal degrees S)	Mean depth (m)
1	1	179.09680	43.47262	179.11682	43.48388	378.2
1	2	179.13017	43.47858	179.11216	43.46782	372.2
1	3	179.11416	43.45556	179.13172	43.46536	375.2
2	1	179.26606	43.46708	179.28135	43.47692	373.5
2	2	179.29253	43.47122	179.29253	43.47122	380.4
2	3	179.32890	43.46208	179.30886	43.45189	390.0
3	1	179.38650	43.47909	179.41022	43.47552	393.8
3	2	179.42424	43.46756	179.40025	43.46755	394.7
3	3	179.39645	43.45344	179.42515	43.45299	403.6
4	1	179.47500	43.42969	179.49799	43.44036	392.4
4	2	179.51812	43.43318	179.49762	43.42430	395.1
4	3	179.50659	43.40936	179.52998	43.41981	403.6
5	1	179.62877	43.47380	179.61259	43.46580	401.8
5	2	179.62997	43.46067	179.64712	43.46793	404.3
5	3	179.64831	43.45465	179.62418	43.44551	409.8
6	1	179.65040	43.54273	179.66993	43.55399	393.0
6	2	179.63875	43.54794	179.61634	43.53646	387.8
6	3	179.62818	43.52550	179.65035	43.53546	395.1
7	1	179.38189	43.57034	179.36421	43.56364	414.6
7	2	179.35899	43.55148	179.37412	43.53538	401.9
7	3	179.38946	43.53321	179.41007	43.54266	420.2
8	1	179.27913	43.55712	179.25978	43.54823	405.4
8	2	179.28182	43.54024	179.30271	43.54954	399.0
8	3	179.28084	43.52330	179.30103	43.53244	387.8
11	1	179.50411	43.50585	179.51723	43.51933	399.6
11	2	179.49702	43.48639	179.50906	43.49995	394.5
11	3	179.53619	43.50856	179.52148	43.49475	393.9
12	1	179.55451	43.44400	179.57579	43.45444	404.2
12	2	179.58973	43.43073	179.56555	43.43840	401.4
12	3	179.55671	43.43413	179.56834	43.41633	410.7
14	1	179.69849	43.61786	179.71088	43.63271	398.0
14	2	179.74325	43.64566	179.73044	43.63344	392.3
14	3	179.73510	43.62327	179.72119	43.61021	399.2
15	1	179.14472	43.55253	179.14512	43.57148	410.5
15	2	179.15767	43.58512	179.15808	43.57109	417.4
15	3	179.16593	43.56357	179.16517	43.54496	407.2
16	1	179.37571	43.42057	179.38983	43.40965	401.3
16	2	179.38402	43.40221	179.35714	43.40671	399.2
16	3	179.36259	43.39026	179.38871	43.39169	399.7

Appendix E Station data for box-cores

Box-core Station	Latitude (decimal degrees S)	Longitude (decimal degrees E)	Water depth (m)
DD51	43.48228	179.11406	384.7
DD52	43.47466	179.10044	383.5
DD54	43.47140	179.11811	372.0
DD55	43.47677	179.12715	371.1
DD57	43.46350	179.12842	376.9
DD63	43.45952	179.12132	374.5
DD65	43.47854	179.39013	388.0
DD68	43.47633	179.40495	393.0
DD75	43.46759	179.42013	390.1
DD77	43.45325	179.40882	400.7
DD78	43.45300	179.42334	405.9
DD82	43.43185	179.47965	398.4
DD83	43.42591	179.50136	392.7
DD85	43.43133	179.51378	399.5
DD86	43.41797	179.52581	408.2
DD88	43.41205	179.51267	401.7
DD91	43.44632	179.62630	424.1
DD94	43.45047	179.63714	402.5
DD95	43.46664	179.64412	413.2
DD97	43.46284	179.63506	398.5
DD98	43.47262	179.62633	406.0
DD100	43.46825	179.61756	397.2
DD101	43.55181	179.66608	387.7
DD102	43.54866	179.66066	396.7
DD106	43.53379	179.64666	397.9
DD107	43.53052	179.63936	391.1
DD109	43.54526	179.63359	386.4
DD110	43.53955	179.62240	382.1
DD112	43.55083	179.26537	402.4
DD113	43.55570	179.27606	406.6
DD116	43.54165	179.28499	402.2
DD118	43.54751	179.29818	397.0
DD120	43.53151	179.29898	385.2
DD121	43.52660	179.28815	390.7
DD122	43.54069	179.40577	422.8
DD123	43.53514	179.39362	417.7
DD126	43.53850	179.37123	397.6
DD127	43.54847	179.36181	400.2
DD128	43.56481	179.36722	414.0
DD130	43.56970	179.38019	420.3

DD131	43.45347	179.31200	393.9
DD132	43.45861	179.32209	389.7
DD134	43.48006	179.30782	378.0
DD137	43.46913	179.26927	367.6
DD139	43.64426	179.74181	386.9
DD142	43.63515	179.73225	399.8
DD143	43.62197	179.73376	400.8
DD144	43.61152	179.72262	399.9
DD145	43.61941	179.69973	397.2
DD147	43.63039	179.70894	399.1
DD149	43.58267	179.15778	421.5
DD150	43.57331	179.15803	417.2
DD151	43.56580	179.14496	413.2
DD153	43.55411	179.14475	413.2
DD154	43.56148	179.16585	411.2
DD156	43.54754	179.16525	404.6
DD157	43.39135	179.38240	398.4
DD160	43.39041	179.36576	401.0
DD165	43.41100	179.38807	400.2
DD166	43.41958	179.37696	401.1
DD167	43.40632	179.35947	401.9
DD168	43.49818	179.52509	393.2
DD172	43.50778	179.53534	395.1
DD175	43.51563	179.51365	398.8
DD176	43.50833	179.50649	399.3
DD177	43.49381	179.50358	402.4
DD179	43.48844	179.49880	399.0
DD180	43.45288	179.57254	406.7
DD181	43.44649	179.55947	408.3
DD182	43.43676	179.57079	404.0
DD184	43.42047	179.56564	423.6

Appendix F Displaying predicted habitat suitability

Maps of predicted habitat suitability for benthic communities in the study area were made using a two-standard deviation 'stretch' colour scale to highlight areas that contain a greater proportion of pixels of relatively high habitat suitability. Figure F-1 shows a portion of the predicted habitat suitability map for epifauna (image–level) Community *h* (see Figure 3-15). In this map, the red pixels delineate an area (the central patch) where pixels of relatively high habitat suitability are more likely to be found than in areas delineated by blue pixels. This figure also shows where seafloor images were located, from which data were used to identify epifauna communities and to generate habitat suitability models for the epifauna communities.

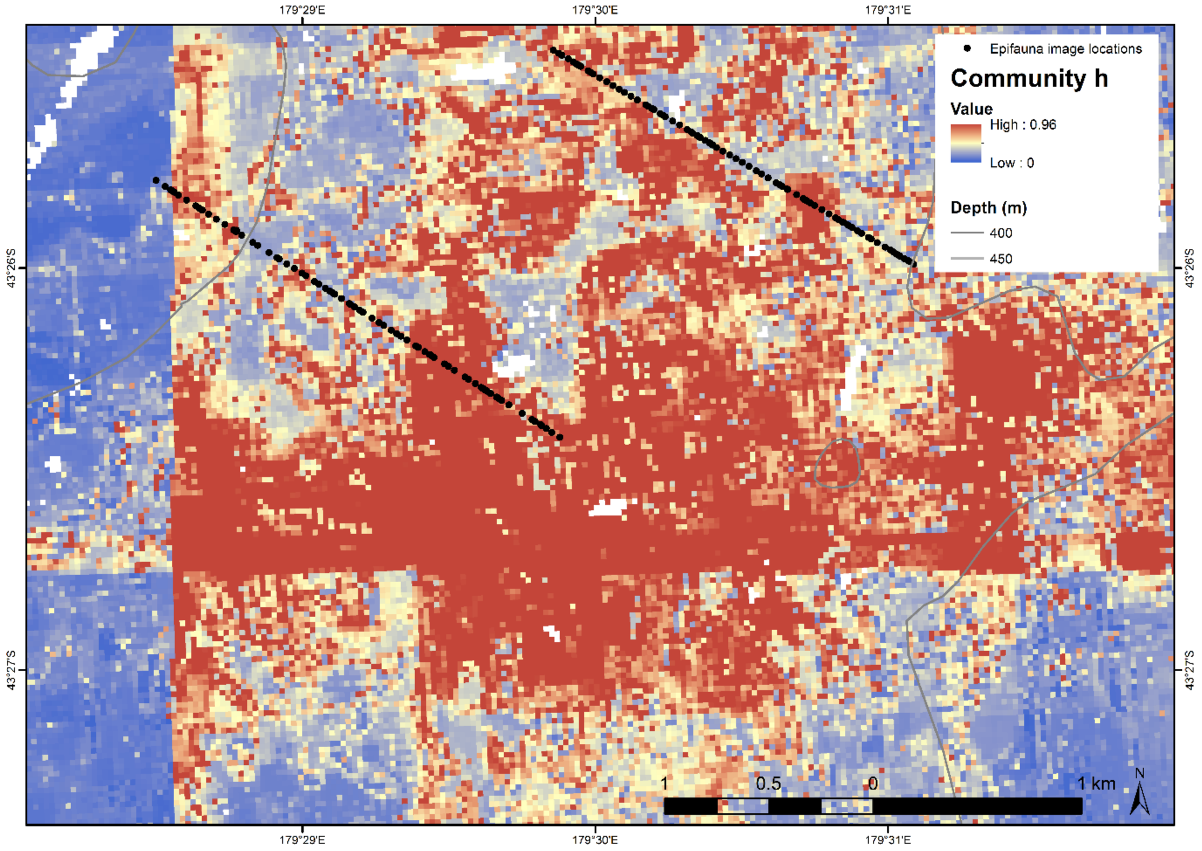


Figure F-1: Predicted habitat suitability for epifauna Community h (image-level) in a portion of the study area illustrated using a two-standard devistion 'stretch' scale. [also shown are the locations of seafloor images where epifauna were observed]

Figure F-2 illustrates the same spatial area as Figure F-1 but with habitat suitability classed into three groups. This figure shows that pixels of habitat suitability >0.5 (i.e. a pixel is more likely to be suitable habitat than not) are concentrated towards the centre of the red patch (of Figure F-1), but are also dispersed across the entire area delineated by the red patch using the ‘stretch’ scale. Furthermore this figure shows that Community *h* was directly observed at locations where the predicted habitat suitability, within the red patch, was generally <0.3.

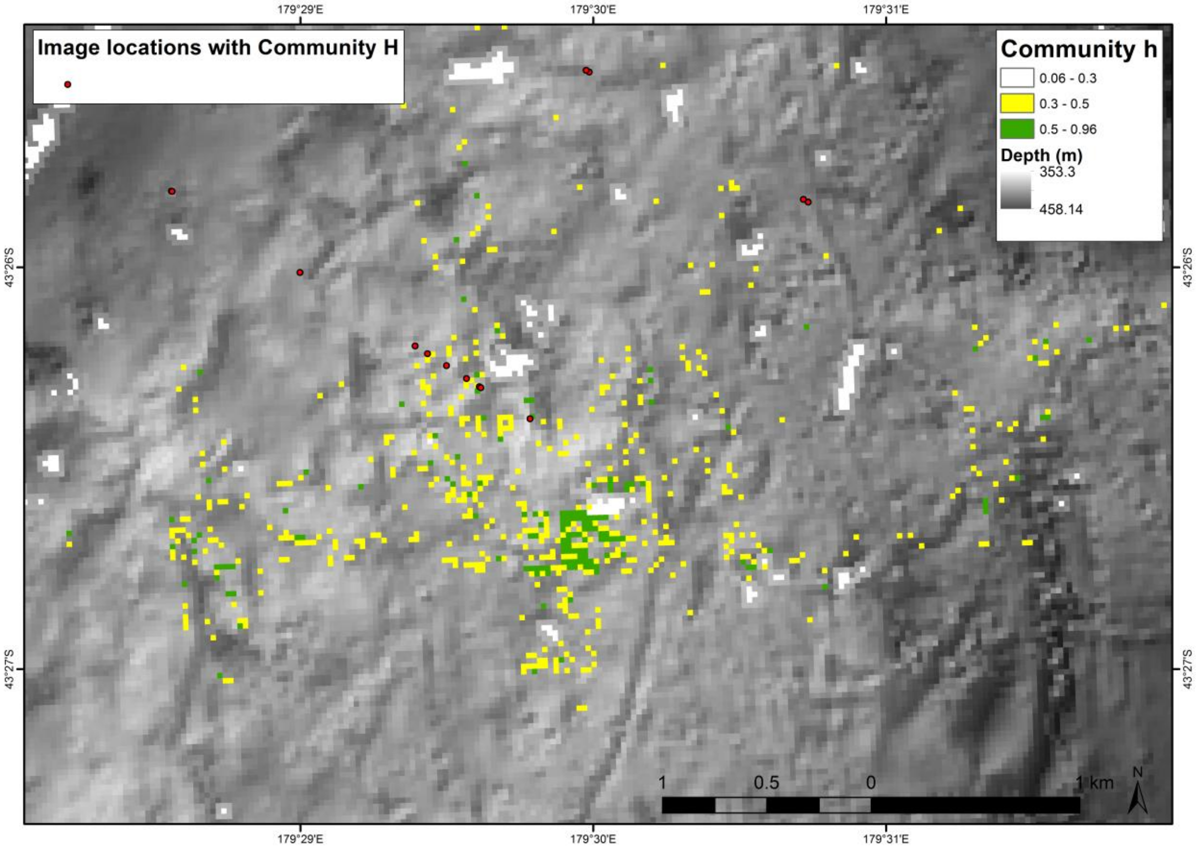
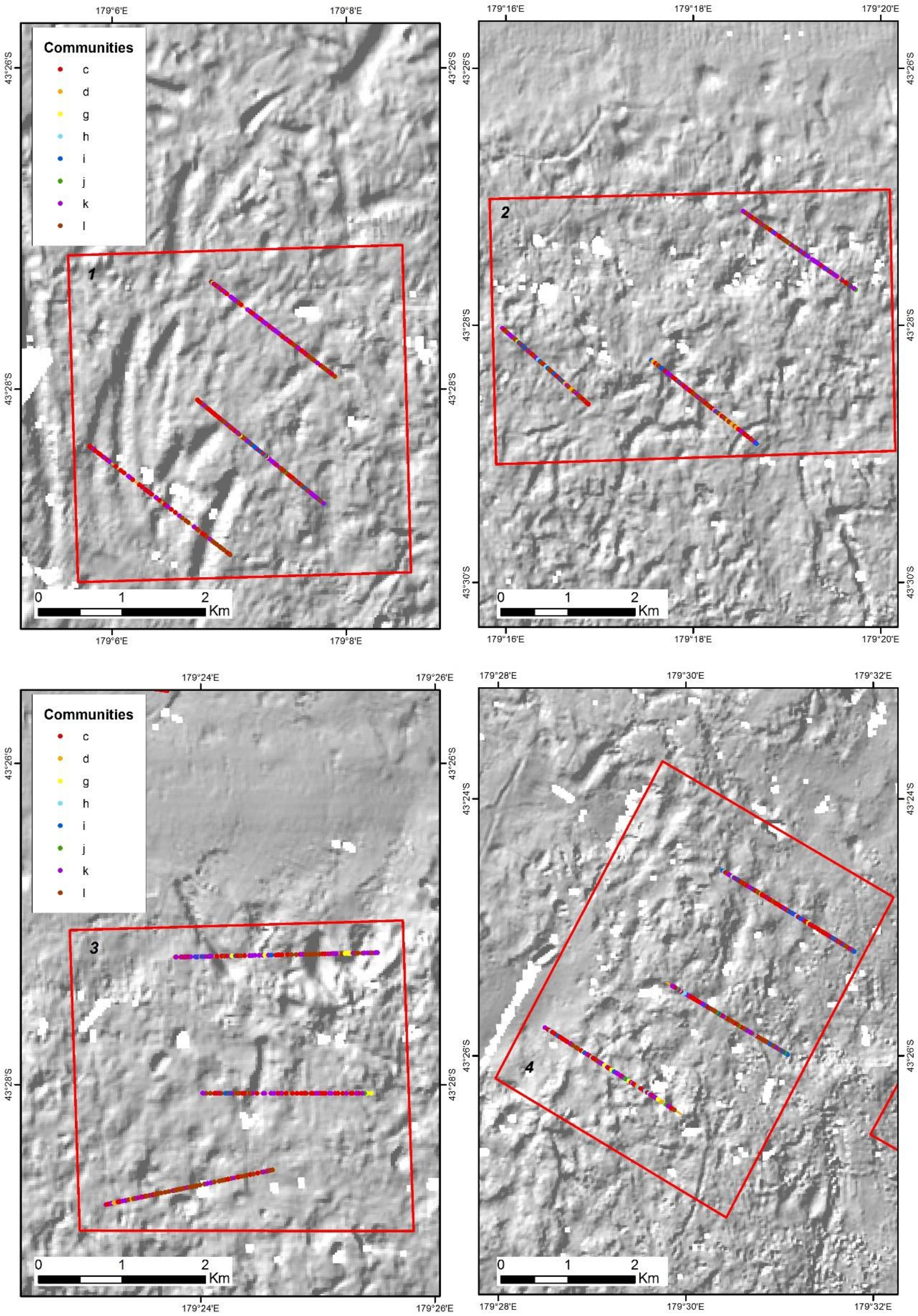
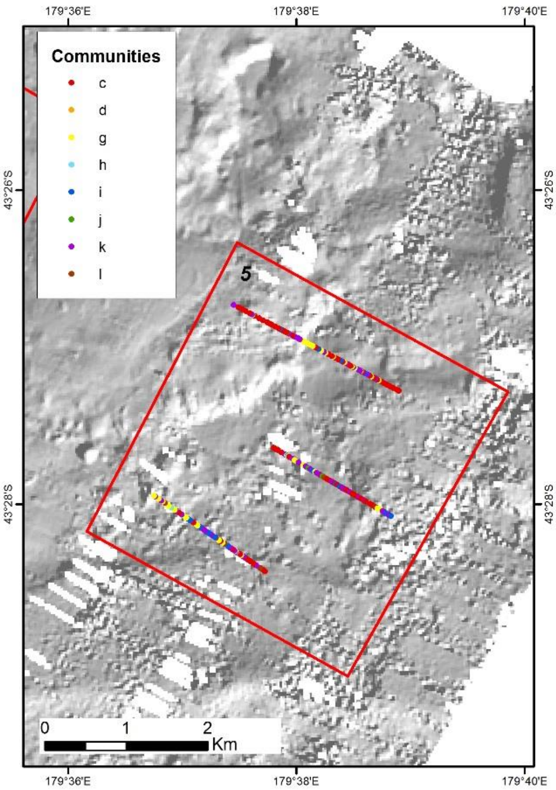


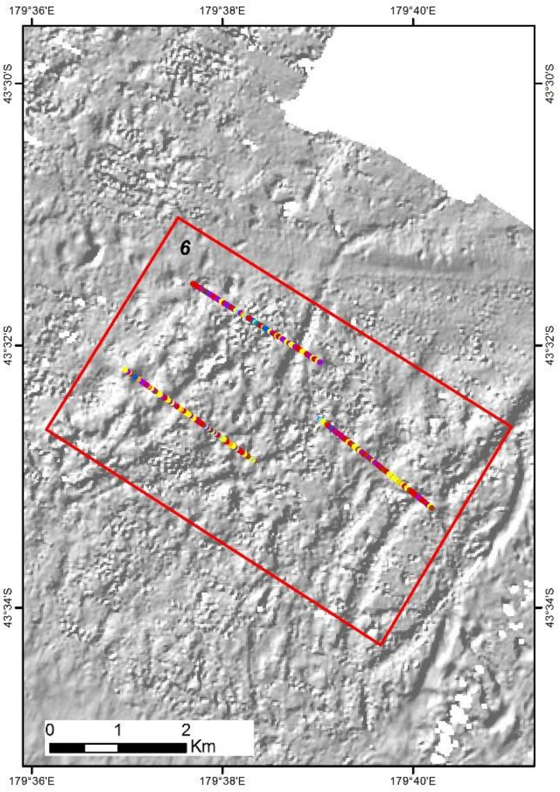
Figure F-2: Predicted habitat suitability for epifauna Community *h* (image-level) in the study area illustrated using a three class scale (values <0.06 are not shown) overlain on a bathymetric terrain model. [also shown are the locations where Community *h* was directly observed in seafloor images]

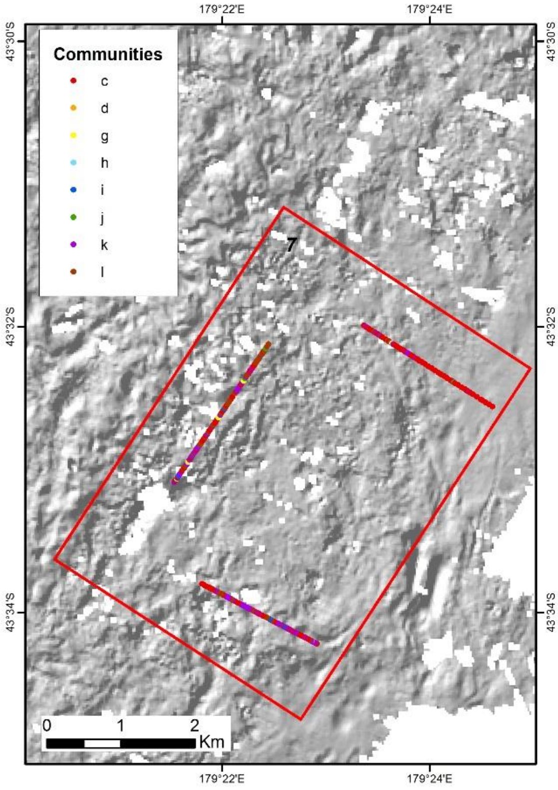
Overall, these two figures provide an example which shows that: (1) the colour scale method adopted to illustrate the habitat suitability models in this report is useful for identifying general areas where locations of relatively high habitat suitability can be found (e.g., an area of ~15 km^2 in the northeastern part of the study area); (2) that within these areas, habitat of relatively high habitat suitability may be restricted to small patches (e.g., < 0.01 km^2), but thesenumerous small patches may be distributed widely across the larger general area (e.g., 25m – 400m apart); and (3) communities can occur at locations within the general area that are predicted to have relatively low habitat suitability (e.g., <0.3). Together these two figures provide an indication of the likelihood of encountering a particular community if mining occurs (depending on the scale of mining) within the general areas of suitable habitat (i.e. the red patches on the model output maps).

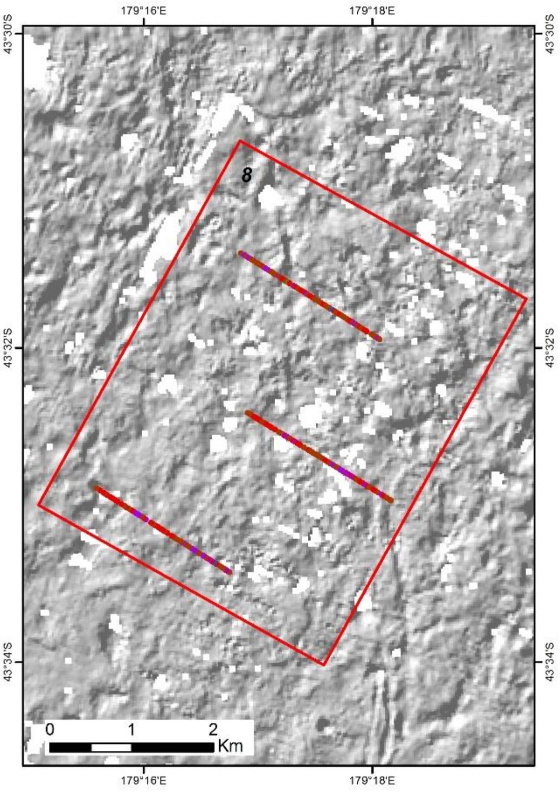
Appendix G Maps of survey areas showing distribution of epifauna communities (image-level) along ROV transects

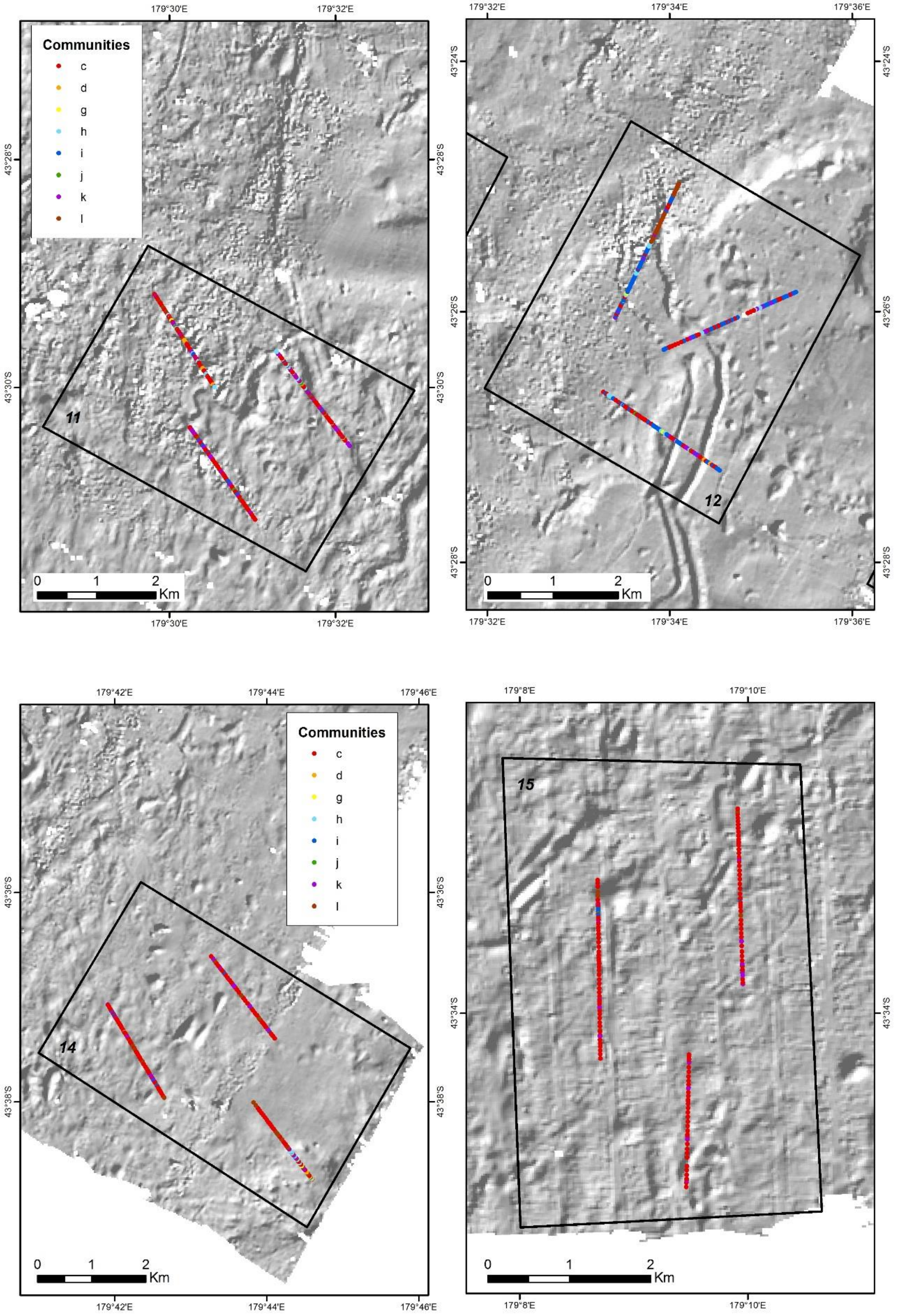


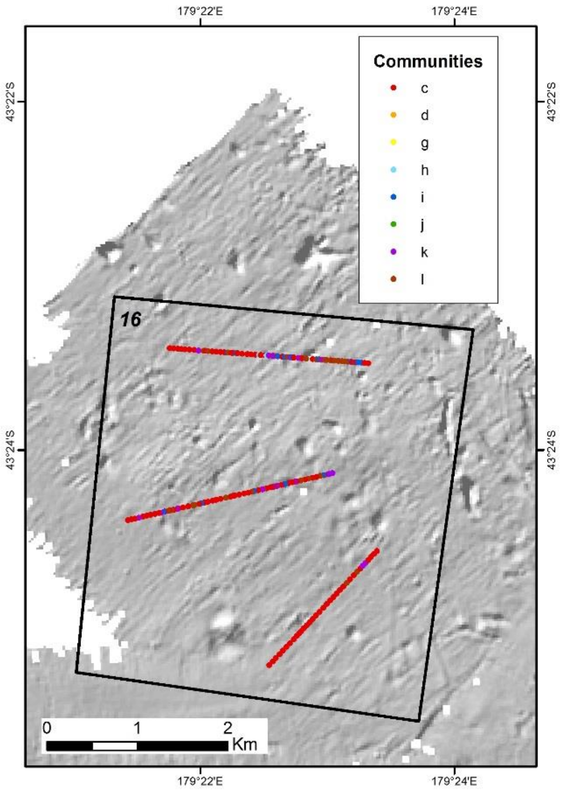

179°36'E
179°38'E
179°40'E
43°26'S
43°28'S
Communities
c
d
g
h
i
j
k
l
5
0
1
2
Km


179°36'E
179°38'E
179°40'E
43°30'S
43°32'S
43°34'S
6
0
1
2
Km


179°22'E
179°24'E
43°30'S
43°32'S
43°34'S
Communities
c
d
g
h
i
j
k
l
7
0
1
2
Km

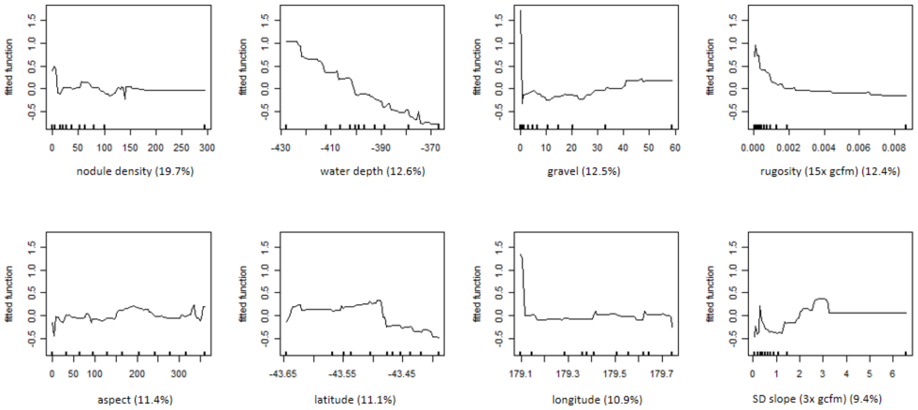

179°16'E
179°18'E
43°30'S
43°32'S
43°34'S
8
0
1
2
Km


Communities
c
d
g
h
i
j
k
l
11
12
14
15
179°30'E
179°32'E
179°34'E
179°36'E
179°42'E
179°44'E
179°46'E
179°8'E
179°10'E
43°24'S
43°26'S
43°28'S
43°30'S
43°34'S
43°36'S
43°38'S
0 1 2 Km

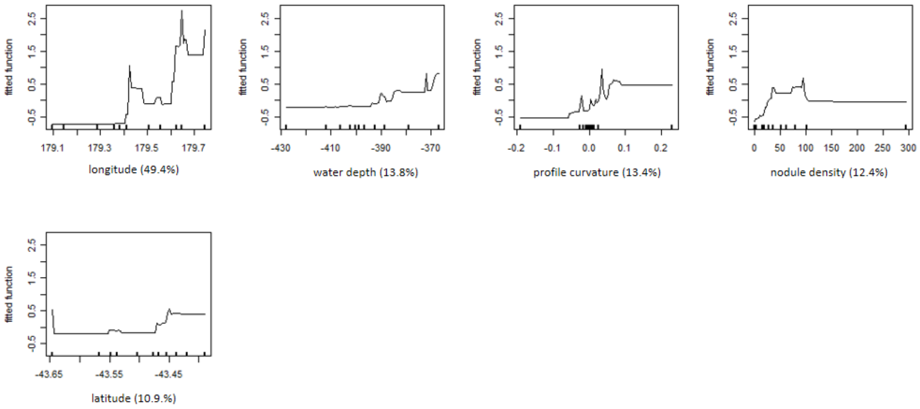

179°22'E
179°24'E
43°22'S
43°24'S
Communities
c
d
g
h
i
j
k
l
16
0
1
2
Km

Appendix H Fitted functions for BRT models of habitat suitability

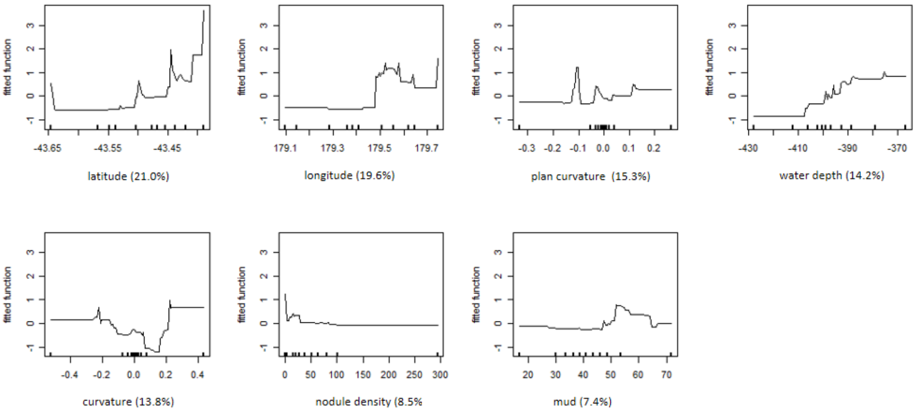
Epifauna – Community *c*



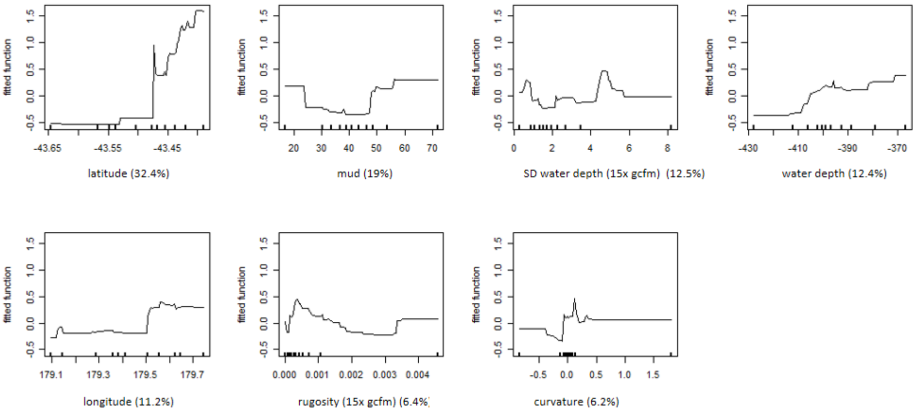
Epifauna – Community *g*



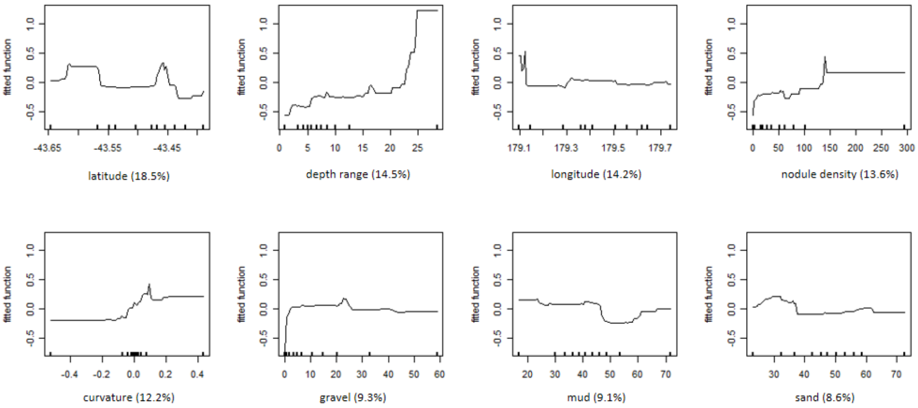
Epifauna – Community *h*



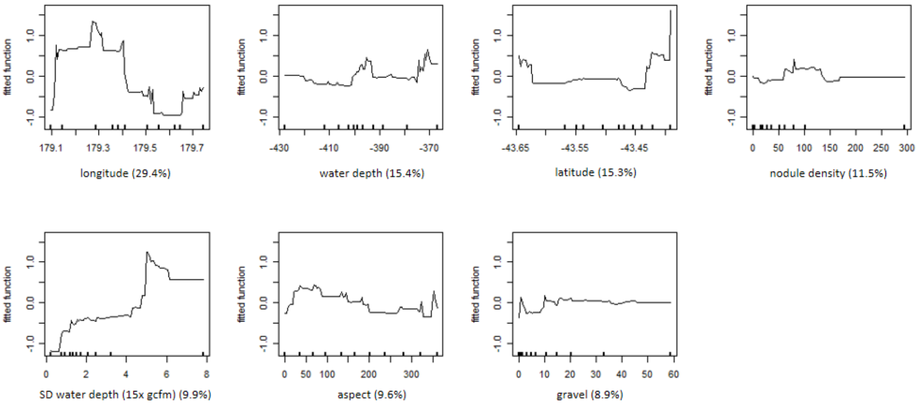
Epifauna – Community *i*



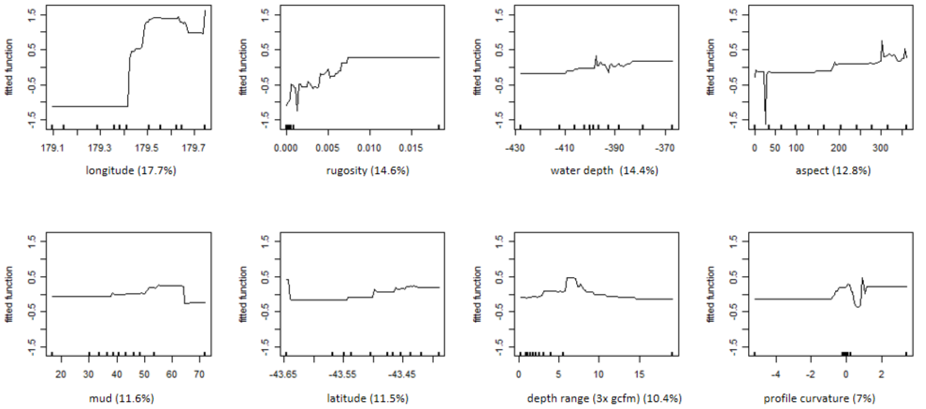
Epifauna – Community *k*



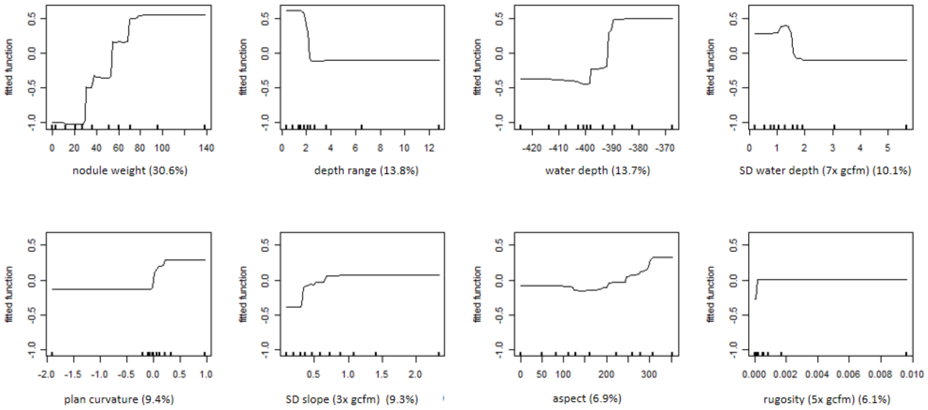
Epifauna – Community *l*



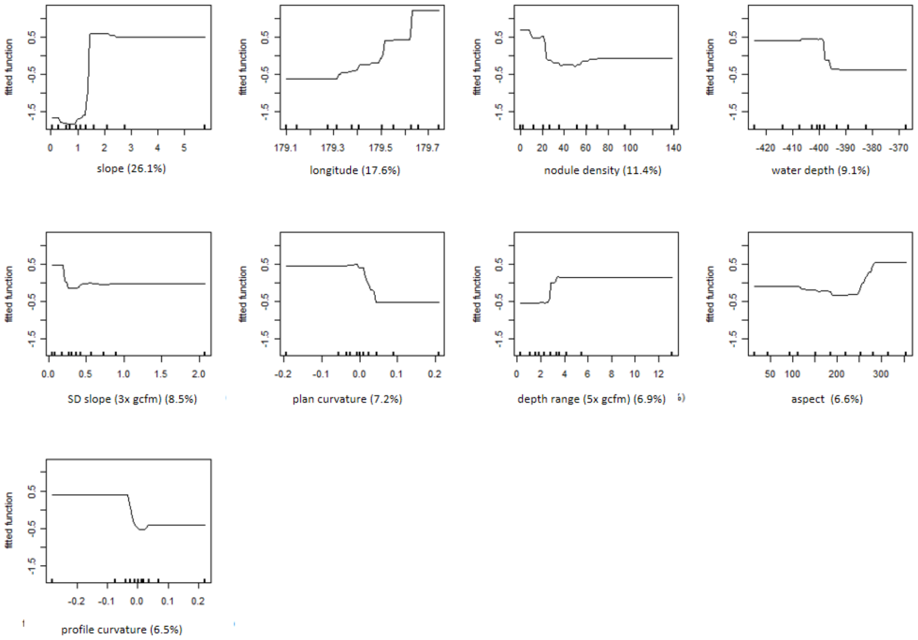
***Goniocorella dumosa* (abundance)**



Infauna - Community *d*



Infauna – Community *g*



Infauna – Community *h*