

## Marine Environment & Ecology

# A preliminary assessment of the deepwater benthic communities of the Great Australian Bight Marine Park



**David R. Currie and Shirley J. Sorokin**

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**SARDI Aquatic Sciences  
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**December 2011**

**Report to the South Australian Department of Environment and Natural Resources and the Commonwealth Department of Sustainability, Environment, Water, Population and Communities**



**Government  
of South Australia**

Department of Environment  
and Natural Resources



**Australian Government**

Department of Sustainability, Environment, Water, Population and Communities

Director of National Parks

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## EXECUTIVE SUMMARY

1. This report describes the composition and distribution of benthic macrofauna collected from the deep, offshore, waters of the Great Australian Bight Marine Park (GABMP) during RV *Southern Surveyor* voyage SS2010\_T02 in August 2010.
2. Quantitative samples of infauna and epifauna were collected from three depth stratified sampling stations (500 m, 1000 m, and 2000 m) on the continental slope of the Benthic Protection Zone (BPZ) using a 0.1 m<sup>2</sup> Smith-McIntyre grab and 4 m-wide beam trawl.
3. A total of 57 putative infaunal species representing eight phyla were collected. Less than 4% of these taxa (2/57) could be confidently assigned to existing species, and it appears that a large proportion of the infauna is undescribed.
4. Motile organisms (mostly annelids, arthropods and molluscs) dominated the infauna, and collectively comprised over 73% of the total abundance and 74% of the total species richness.
5. Infaunal abundance declined with increasing depth and was highest in the upper-slope sediments (which also supported the highest concentrations of nitrogen and organic carbon). Infaunal diversity did not vary directly with depth and was highest at the 1000 m sampling station (31 spp.) and lowest at the 2000 m station (5 spp.).
6. Cluster analyses of the infaunal species abundance data revealed a strong environmental gradient on the BPZ slope, and highlighted marked shifts in species representation and the presence of three distinct infaunal communities (upper-slope, mid-slope and lower-slope) that were closely allied with changes in depth and sediment sorting.
7. A species accumulation model developed with contemporary grab data suggests that the deep-water infaunal communities of the BPZ slope are considerably more diverse than those found on the shallower waters of the adjacent continental shelf.
8. A total of 84 putative epifaunal species representing ten phyla were also collected during the survey. As for the infauna, most epifaunal taxa (51/84) could not be confidently assigned to existing species, and it appears that a large proportion of the epifauna (61%) is also undescribed.
9. Motile scavenging and predatory organisms (mainly arthropods, chordates and echinoderms) were the dominant epifauna, and collectively comprised over 63% of the total biomass and 58% of the total species richness.

10. Epifaunal richness and biomass were positively correlated, and both metrics were highest on the mid-slope (1000 m depth) where the sediments were muddy and poorly sorted, and lowest on the lower-slope (2000 m depth) where the sediments were bimodal in structure and composed of very-fine sand and silt.
11. Cluster analyses of the epifaunal species composition was similar to that of infauna and confirmed a strong environmental gradient on the BPZ slope and the presence of three distinct communities (upper-slope, mid-slope and lower-slope) that are closely related to changes in depth and sediment sorting.
12. Spatial patterns in epifaunal and infaunal community structure were broadly consistent with depth-related discontinuities in water circulation along Australia's southern continental margin.
13. A species accumulation model developed using contemporary sled data suggests that the deep-water epifaunal communities of the BPZ slope are marginally more diverse than those found in the shallower waters of the adjacent continental shelf. However, the reliability of this estimate is uncertain due to gear differences between surveys.
14. The discovery of a volcanic pinnacle *Anna's Pimple* inside the BPZ was a noteworthy feature of the voyage. This cone-shaped igneous structure, rising almost 200 m from the surrounding soft-sediment, was located at a depth of 2000 m in the middle of BPZ by the vessels swath acoustics. Due to its extreme age (~45 Ma) and geographical isolation, this pinnacle is significant, as it may support benthic organisms and communities that have evolved on and are unique to the rocky structure.
15. This preliminary research has provided novel insights into the composition and distribution of benthic fauna from the deep-water bedforms of the BPZ. However, with little comparable data available outside the BPZ it remains uncertain if the BPZ effectively represents and preserves the benthic habitats and assemblages of the continental slope.
16. A sustained commitment to data collection is required to address these data insufficiencies. As four petroleum exploration tenements straddling the BPZ are scheduled to be drilled for hydrocarbons in 2013/14 (PIRSA, 2011), it is imperative that the composition, distribution and ecological significance of the region's benthic fauna and habitats are comprehensively audited as a matter of priority.

# 1 INTRODUCTION

## 1.1 Background

The Benthic Protection Zone (BPZ) of the Great Australian Bight Marine Park (GABMP) was proclaimed in 1998, and consists of a 20 nautical-mile-wide strip orientated north to south and extending from three nautical miles from the coast to the edge of Australia's Exclusive Economic Zone (EEZ), 200 nautical miles offshore (Figure 1). Within this zone, the benthic communities are protected from demersal trawling and other potentially destructive human activities.

The location of the BPZ was not established on the basis of any quantitative ecological data. In the absence of such information, the BPZ was located with the goal of preserving the benthic assemblages from a cross-shelf (and slope) transect near the widest part of the continental margin. As a result, the suitability of the BPZ for representing the region's benthic biodiversity was, and has remained to a large extent, unknown. In 2002, several important advances in our understanding of the benthic biodiversity of the eastern Great Australian Bight (GAB) shelf were made, when the first quantitative epibenthic survey of the region was undertaken (Sorokin et al., 2005; Ward et al., 2003). This exploratory seafloor study demonstrated that the BPZ was effective in representing the epifaunal biodiversity of the eastern GAB shelf (Ward et al., 2006). Furthermore, it established that the macrofaunal communities of the eastern GAB shelf are among the world's most diverse (with almost 800 invertebrate species being identified from 65 individual sled tows of 5-minutes duration).

Follow-up surveys conducted on the eastern shelf during 2006 (Currie et al., 2007, 2008, 2009), have provided additional insights into patterns of faunal distribution on the shelf and their relationships to environmental factors. In particular, these surveys have confirmed that species richness and biomass generally decline with increasing depth and distance offshore. Moreover, these surveys have served to highlight the patchwork in sedimentary habitats and associated faunas on the shelf, and the role that recurrent oceanographic conditions have in mitigating these. While different benthic communities are also likely to inhabit the different sedimentary facies that blanket the deeper water bedforms of the continental slope, this remote environment remains poorly studied.

Almost half of the seafloor in the BPZ is located in waters between 200 m and 5,000 m depth, and remains un-surveyed for benthos. Accordingly, it is unclear if the BPZ effectively represents and preserves the benthic habitats and assemblages of the continental slope. The continental slope and deep-water reaches of the BPZ present significant sampling challenges,

and few vessels in Australia (e.g. RV *Southern Surveyor*) are presently equipped to undertake such work. The close proximity of the *Southern Surveyor* to the BPZ during a transit from Fremantle to Hobart (Voyage No. SS010\_T02) in August 2010, provided an opportunity to sample the deep-water benthos of the GABBPZ, and to quantify, for the first time, the areas benthic biodiversity (Currie, 2010a). This report details the benthic sampling undertaken during the transit voyage to evaluate infaunal and epifaunal biodiversity on the continental slope of the BPZ.

## 1.2 Objectives

The BPZ is currently one of 14 temperate Commonwealth Marine Protected Areas (MPAs) in Australia (DSEWPac, 2011). These MPAs form part of an integrated strategy for marine conservation and management through the National Representative System of Marine Protected Areas. While conservation of marine biological diversity is the overarching goal of the strategy, it remains to be determined what biological diversity is being conserved offshore on the seafloor of the BPZ slope. This study aims to address this knowledge gap and provide quantitative information on the distribution and diversity of the deep-water faunal communities of the BPZ.

While this report concentrates on describing the infaunal and epifaunal assemblages collected from targeted sampling of the seafloor in the BPZ, three additional objectives were pursued during the *Southern Surveyor* voyage. These included operations to: 1) investigate water mass structure and interactions along the southern margin of Australia (Figure 2a), and particularly the chemical properties and isotopic signatures of the westward flowing Flinders Current; 2) characterise and map previously unsurveyed sections of Australia's upper-slope seabed to support bio-regional planning and management; and 3) deploy autonomous profiling floats to characterise the changing state of the upper ocean and patterns of ocean climate variability (Figure 2b). Further information on these piggy-back surveys can be found in Currie (2010b).

## 2 METHODS

### 2.1 Field sampling and laboratory processing

Six depth-stratified stations inside the BPZ (at 200 m, 500 m, 1000 m, 1500 m, 2000 m and 4000 m depth) were initially identified as prospective sampling locations for benthos (Figure 1). However, poor weather conditions during the transit meant that only half these stations could be sampled safely (i.e. 500 m, 1000 m, 2000 m). Prior to sampling these three stations, a broad-scale mapping survey was conducted using the vessels multi-beam sonar (Kongsberg-Simrad EM300). This provided high-resolution bathymetry of the target stations, and subsequently guided our gear deployments in each area.

Benthic infauna were quantified from a single 0.1 m<sup>2</sup> Smith-McIntyre grab sample at each station (Figure 2c). These grabs were sieved through a 1 mm mesh screen, and the fauna retained preserved in 5% formaldehyde solution. The fauna was later sorted in the laboratory to the lowest taxonomic level (generally species) before being counted and photographed. Voucher specimens and a database were subsequently lodged at the South Australian Museum, Adelaide.

Two sediment sub-samples (70 ml and 10 ml) were retained from each grab prior to sieving to determine the composition and structure of the seabed at each sampling station. These were collected from each grab by scraping an open vial across the top of each sample, and were subsequently snap-frozen and stored at -20 °C before being analysed. The larger of the two sediment sub-samples was wet-sieved through an agitated stack of Endecotts sieves to determine the grain-size structure and sorting coefficients of the sediments. The smaller sample was freeze dried, sieved, and then ground to a talcum-powder consistency before being processed in an elemental analyser (LECO TruSpec CN) to determine the organic carbon and total nitrogen content.

Quantitative samples of epifauna were collected using a 4 m wide beam trawl fitted with a 1 cm mesh bag (Figure 2d). This trawl gear was towed once over a 1000 m distance at each sampling station. On retrieval the catch was emptied on deck and a photograph taken. The collective weight of each shot was then determined, and the catch transferred to labelled plastic bags before being snap-frozen. Samples were later stored at -20 °C prior to laboratory analysis.

Trawl samples were defrosted and sorted in the laboratory to the lowest taxonomic level (species level where possible) before being counted and weighed. During this process, all broken shells and rocks were discarded, while fragments of the same non-unitary organism

(e.g. colonial ascidians) were consolidated and collectively weighed and counted as a single entity. Voucher specimens of all species collected were photographed before being preserved in 70% ethanol. All voucher specimens have been lodged at the South Australian Museum, Adelaide

## **2.2 Statistical analyses**

### **2.2.1 Univariate patterns in infauna and epifauna**

One-way analysis of variance (ANOVA) was used to test differences in total species richness and abundance of infauna among the different depth strata. Similar tests were also applied separately for differences in total species richness and biomass of epifauna between the different depth strata. Prior to conducting all ANOVAs, homogeneity of variance was examined using Levene's test and heterogeneity removed where necessary using a  $\log_{10}(n+1)$  transformation.

### **2.2.2 Environmental parameters**

Spatial trends in benthic abundance, biomass and species richness were examined in relation to the physical and chemical attributes at each sampling station. The relative strength of each environmental relationship was assessed independently for both infauna and epifauna using Spearman's rank correlation coefficients.

### **2.2.3 Multivariate patterns**

Depth-related differences in community structure were examined using Bray-Curtis (B-C) dissimilarity measures (Bray and Curtis, 1957). A single square-root transformation was applied to the data before calculating the B-C dissimilarity measures. This transformation was necessary to prevent a small number of large or abundant species unduly influencing the B-C dissimilarity measures (Clarke, 1993).

The computer package PRIMER (Primer-E Ltd., Plymouth) was used to generate B-C dissimilarities and to undertake all multivariate analyses (Clarke and Gorley, 2001). Spatial patterns in dissimilarity were initially assessed using hierarchical agglomerative clustering. A similarity percentages (SIMPER) routine was then applied to identify those species contributing most to observed differences. The extent to which measured environmental variables

accounted for any community differences was subsequently tested using the biological environmental (BIOENV) routine (Clarke and Ainsworth, 1993).

#### **2.2.4 Biodiversity**

To assess relative biodiversity of the BPZ slope fauna, randomised species accumulation curves were constructed using the grab and trawl data. The increasing number of different species observed as samples are successively pooled (*Sobs*), was determined using the (Species-Area) plot routine in PRIMER (Clarke and Gorley, 2001). A second order polynomial model was fitted to the *Sobs* means using SPSS software (SPSS, 2007), and the equation used to estimate the numbers of species collected with increasing levels of sampling (i.e. up to 65 grabs or trawls). These were then compared to the species accumulation curves of 65 epifaunal sled samples taken from the eastern GAB shelf during 2002 (Ward et al., 2006), and 65 infaunal grab samples taken from the same shelf locations during 2006 (Currie et al., 2009).

## 3 RESULTS

### 3.1 Environmental characteristics

#### 3.1.1 Sediment composition and structure

Sediments taken from the three depth-stratified sampling stations inside the BPZ (500 m, 1000 m and 2000 m) were variable in structure and ranged from very-fine sand to very-fine silt (Table 1). These sediments were found to be composed almost entirely of biogenic material, including fragments of sponges, bryozoans, scaphopods, pteropods and foraminifera. Spatial patterns in grain-size were broadly consistent with patterns in bathymetry, with sediments being coarsest at the shallowest station (500 m) and finer in the deeper waters offshore (1000 m and 2000 m). Sediment sorting, by comparison, was less clearly related to depth, and was lowest (least variable is size structure) at the 1000 m station (Table 1).

The organic carbon content of the sediments ranged between 0.765 and 1.285%, and broadly reflected trends in sediment size structure (Table 1). Notably, organic carbon content was found to be almost twice as high in the coarser sediments of the upper slope (500 m) than in the finer sediments of the lower slope (1000 m and 2000 m). Similar trends were also observed for concentrations of sedimentary nitrogen and sulphur (Table 1).

### 3.2 Infauna

#### 3.2.1 Species composition

A total of 57 infaunal species representing eight phyla were collected from grab samples at the three depth-stratified sampling stations (Appendices 1-3). Annelida (bristle worms) were the dominant phyla in terms of abundance and accounted for 37.6% of the total number of individuals collected (93) (Figure 3a). Mollusca (shellfish), Arthropoda (mostly crabs and shrimps) and Sipuncula (peanut worms) were also relatively well represented, and comprised approximately 19.4%, 16.1% and 12.9% of the total abundance. All other phyla collected, including Cnidaria (hydroids), Echinodermata (brittle stars), Nematoda (round worms) and Porifera (sponges) were much less common, and individually comprised less than 8% of the total abundance.

Annelids were also the best represented phylum in terms of species richness, and accounted for 48.3% (28) of all infaunal species collected (Figure 3b). Sipunculids, arthropods, and

molluscs were also well represented, and accounted for 15.5% (9), 13.8% (8) and 12.1% (7) of the total species richness. Most other phyla collected, including cnidarians, echinoderms, nematodes and poriferans were relatively less diverse and represented by fewer than 4% (2) of the total species collected.

Annelids, arthropods and molluscs were the most widely distributed phyla, and occurred at all three of the depth-stratified sampling stations (Figure 3c). Nematodes and sipunculids, by comparison, had much more restricted distributions and were only encountered at the two shallower stations surveyed (500 m and 1000 m). All other phyla collected were limited to just a single depth stratum, with echinoderms and poriferans only being collected from the 1000 m station and the cnidarians only being collected from the 2000 m station.

### **3.2.2 Spatial patterns in species richness and abundance**

Infauna species richness varied inconsistently with depth, and was highest at the 1000 m sampling station (31 spp.) and lowest at the 2000 m station (5 spp.), with an intermediate number (22 spp.) being collected from the shallowest station surveyed (500 m) (Figure 4a). This pattern in species richness followed general trends in sediment sorting across the BPZ slope (as indicated by the significant inverse correlation between these parameters (Table 2)) and suggests that infaunal diversity is elevated in the more homogeneous (poorly-sorted) sediments.

Infaunal abundance, by comparison, varied directly with depth and was more than 91% lower at the 2000 m sampling station than at the 500 m sampling station (Figure 4b). The strength of this relationship between abundance and depth is further verified by a significant inverse correlation between these parameters (Table 2). Because depth also co-varied with the nitrogen and organic carbon contents of the sediments, significant rank correlations between these chemical elements and infaunal abundance are also apparent. Most notably, infaunal abundances are highest in the shallow upper-slope sediments that support the highest concentrations of nitrogen and organic carbon.

### **3.2.3 Community structure**

Three discrete communities were separated at the 10% B-C similarity level (Figure 5). These included an “upper slope” community (comprising the one and only grab sample take at 500 m depth), a “mid slope” community (comprising the 1000 m grab sample), and a “lower slope” community (comprising the 2000 m grab sample). Annelids dominated all three communities

and accounted for more than 40%, 36% and 33% of the total faunal abundance on the “upper slope”, “mid slope” and “lower slope”, respectively. All other phyla varied markedly in abundance across the three communities (0-33%).

SIMPER analysis was undertaken to determine which species contributed most to differences between the three communities. Abundances of the 15 species contributing  $\geq 3\%$  to the between-sample dissimilarity are given in Table 3. Results from the SIMPER analysis confirm that the three communities are characterised by small subsets of species with restricted distributions.

The “upper slope” community (i.e. BPZ\_500) was primarily separated from all other communities by nine relatively abundant species representing four phyla. These included the pteropod *Limacina* sp.1, the bristle worm Maldanidae 4, the bivalve mollusc *Cuna* sp.1 and the peanut worm *Sipuncula* 3; all of which were unique to the “upper slope”. Notably, only one of the 22 species represented in this community (i.e. the round worm Chromadoridae 1) had a wider distribution, and was also recorded from the “mid slope” (i.e. BPZ\_1000).

The “mid slope” community, although the most diverse (31 spp.), was also characterised and differentiated by a small number of relatively common species that were not found elsewhere on the BPZ slope. These included the tanaid *Cyathura* sp. 1, the amphipods *Birubius* sp. 1 and *Metaphoxus* sp.1, and the sponge Demospongiae 5. The presence of the round worm Chromadoridae 1 in this community (i.e. a species which was also encountered in the “upper slope”), accounted for all of the B-C similarity between these communities, and was a primary discriminator in separating these from the “lower slope”.

The “lower slope” community (i.e. BPZ\_2000) comprised the least diverse collection of species and also displayed the highest level of local endemism, with none of the five infaunal species comprising the community being found elsewhere on the slope. This deep-water community was typified by just a single species of cnidarian (i.e. Hydroid 1), on account of its relatively higher abundance.

### **3.2.4 Environmental linkages - community structure**

The PRIMER routine BIOENV was used to assess the correspondence and significance of environmental data from the seafloor to the three communities identified from the infaunal cluster analyses. Measures of organic carbon and nitrogen in the sediments were excluded from these analyses as they are highly correlated and co-vary with depth. Depth and sediment sorting both provided equivalent solutions and independently correlated most closely with the

infaunal community structure ( $\rho w = 0.87$ ). The other primary variables (sediment % <63  $\mu\text{m}$  and sedimentary sulphur) were much more weakly correlated ( $\rho w < 0.01$ ), and failed to provide an improved explanation for the biological pattern when combined with either depth of sediment sorting.

### 3.2.5 Biodiversity

By extrapolating the species accumulation curve using the polynomial model (Equation 1) it is estimated that an equivalent number of random grab samples undertaken on the BPZ slope will collect higher numbers of infaunal species than has previously been recorded on the shelf (Figure 6).

$$S = -0.1386n^2 + 19.409n \quad \text{Equation 1}$$

Where

$S$  = number of species predicted, and  
 $n$  = number of grab samples

During 2006, a total of 240 species of infauna were collected from 65 replicate 0.1 m<sup>2</sup> Smith-McIntyre grabs taken across a 700 km section of the eastern GAB shelf (Currie et al., 2007). In comparison, an equal number of grab samples (65) taken across the BPZ slope is predicted to return more than twice this number of species (i.e. ~676 spp.). This result suggests that the infauna inhabiting the deep-water bedforms of the continental slope of the BPZ is considerably more diverse than the infauna of the adjacent continental shelf.

## 3.3 Epifauna

### 3.3.1 Species composition

A total of 84 epifaunal species representing ten phyla were collected from beam-trawl samples at the three depth-stratified sampling stations (Appendices 1-3). Chordata (fish) were the dominant phyla in terms of biomass, and accounted for 41.2% (8186 g) of the total catch (Figure 7a). Porifera (sponges), Echinodermata (mostly brittle stars and sea cucumbers) and Cnidaria (corals and anemones) were also relatively well represented, and comprised 24.6% (4891 g), 20.9% (4157 g) and 10.6% (2106 g) of the total biomass sampled, respectively. All other phyla collected, including Annelida (bristle worms), Arthropoda (mostly crabs and

shrimps), Mollusca (shellfish), Priapulida (penis worms), Sipuncula (peanut worms) and Urochordata (Tunicates), were much less common and individually comprised less than 2% (259 g) of the total epifaunal biomass.

While arthropods represented only a small proportion (1.1%) of the overall epifaunal biomass, this taxonomic grouping was the most speciose, and contained 23.8% (20) of all species collected in the beam-trawl shots (Figure 7b). Chordates were the next most diverse phylum collected (21.4%, 18), followed by molluscs (14.3%, 12) and echinoderms (13.1%, 11). All other epifaunal phyla collected, including annelids, cnidarians, poriferans, priapulids sipunculids and urochordates had much lower diversities, and individually compromised less than 9.5% (8) of the total species richness.

Arthropods, chordates, cnidarians and echinoderms were the most widely distributed taxa, and were encountered at all three depth-stratified sampling stations (Figure 7c). Annelids, molluscs, poriferans and sipunculids had much more restrictive distributions, with the two former phyla occurring only at the 500 m and 1000 m stations, and the two latter phyla being collected only at the 1000 m and 2000 m stations. All other phyla sampled were limited to just a single depth stratum; with urochordates only being collected from the 1000 m station, and priapulids only being collected from the 2000 m station.

### **3.3.2 Spatial patterns in species richness and biomass**

The spatial distribution of epifaunal species among the three depth-stratified sampling stations in the BPZ was broadly consistent with the infauna. Species richness was, for example, highest at the 1000 m station (42 spp.), lowest at the 2000 m station (12 spp.), and intermediate at the 500 m station (30 spp.) (Figure 8a). As for the infauna, this distribution pattern followed trends in sediment size-structure, and hence epifaunal richness was negatively correlated with sediment sorting (Table 4). This result furthermore indicates that epifaunal diversity on the slope bedforms may be enhanced by progressively more homogeneous sediments.

Depth-related trends in epifaunal biomass closely follow those of richness (Figure 8b), and accordingly richness and biomass are significantly correlated (Table 4). Epifaunal biomass was highest at the 1000 m station (10,317 g), marginally smaller at the 500 m station (9519 g), and markedly lower at the 2000 m station (42 g). This trend in epifaunal biomass parallels that of sediment sorting (Table 4), and indicates that the more homogeneous sediments support the highest epibenthic standing-stocks.

### 3.3.3 Community structure

As for the infauna, three discrete communities were separated at the 10% B-C similarity level (Figure 9). These are an “upper slope” community (comprising the single trawl shot undertaken at 500 m depth), a “mid slope” community (containing the 1000 m trawl sample), and a “lower slope” community (comprising the 2000 m trawl sample). The higher order taxonomy and associated trophic structure varied markedly between these communities. Predatory and scavenging chordates (fish) dominated the “upper slope” communities (62% of total biomass), while filter-feeding poriferans (sponges) and cnidarians (sea pens) dominated the “mid slope” and “lower slope” communities, respectively (47% and 48% of biomass).

SIMPER analysis was undertaken to evaluate which species contributed most to differences between the three communities. Biomasses of the 20 species contributing  $\geq 3\%$  to the between-sample dissimilarity are given in Table 5. This SIMPER analysis is generally consistent with the results obtained for infauna, and shows that the three communities are characterised by small subsets of epifaunal species with very limited distributions.

The “upper slope” community (i.e. BPZ\_500) is characterised and principally separated from the other communities by nine species with relatively high biomasses. These mostly include fish (pink ling *Genypterus blacodes*, blacktip cucumberfish *Paraulopus nigripinnis*, little whiptail *Coelorinchus gormani*, banded-fin flounder *Azygopus pinnifasciatus* and three-spined cardinal fish *Apogonops anomalus*), sea cucumbers (*Holothuria* sp. 1 and 2), and cup corals (*Desmophyllum dianthus*); all of which are unique to the upper slope. The community also contains a large (>70 mm height) and abundant anemone species (*Hormathia lacunifera*), that appears to have a much wider range on the slope, and is also encountered on the “mid slope”.

The glass sponge *Rosella* sp. 1, was recognised by SIMPER as a primary discriminator for the “mid slope” community (i.e. BPZ\_1000). This small, globular species (<30 mm diameter) accounted for almost half of the total biomass sampled at this location. Moreover, this same species was also the most commonly encountered organism during the survey, with 1345 individuals collected from the single trawl shot undertaken at this location. Eight other species unique to the location, including the brittle star *Ophioplinthus accomodata*, cut-throat eel *Synaphobranchus oregoni*, warty oreo *Allocyttus verrucosus*, spotty-faced whiptail *Coelorinchus acanthiger*, basketwork eel *Diastobranchus capensis*, globehead whiptail *Cetonurus globiceps*, and pteropod *Cavolina* sp. 1, typified and distinguished the “mid slope” community on account of their relatively high biomasses. The anemone *Hormathia lacunifera*, which was also found in the “upper slope”, accounted for all of the B-C similarity between these communities, and was the principal species separating the “upper slope” and “mid slope” communities from those of the “lower slope”.

As was the case for infauna, the “lower slope” community (i.e. BPZ\_2000) contained the least diverse collection of species, and also displayed the highest level of local endemism, with none of the 12 epifaunal species from the community being found elsewhere on the slope. This community was characterised by just two species on account of their relatively high biomasses. These included the delicate sea pen *Umbellula* sp. 1 (>300 mm length), and the strawberry prawn Sergestidae 1 (<30 mm carapace length).

### 3.3.4 Environmental linkages - community structure

The PRIMER routine BIOENV was used to assess the correspondence and significance of environmental data from the seafloor to the three communities identified from the epifaunal cluster analyses. As was the case for the infaunal analysis, measures of organic carbon and nitrogen in the sediments were excluded from these analyses as they are highly correlated and co-vary with depth. Depth and sediment sorting both provided equivalent solutions and independently correlated most closely with the epifaunal community structure ( $\rho_w = 0.87$ ). The other primary variables (sediment % <63  $\mu\text{m}$  and sedimentary sulphur) were much more weakly correlated ( $\rho_w < 0.01$ ), and failed to provide an improved explanation for the biological pattern when combined with either depth or sediment sorting.

### 3.3.5 Biodiversity

As no other beam-trawl data exist for the GAB, this assessment of epifaunal diversity on the BPZ slope relies on comparisons with benthic sled collections undertaken across the eastern GAB shelf during 2002 (Ward et al., 2006). While gear differences between surveys mean that these comparisons are less than perfect (i.e. swept area beam-trawl  $\approx 4X$  swept area sled tow), they presently represent the only viable option for gauging regional differences in epifaunal biodiversity.

During the Ward et al. survey of the GAB shelf in 2002, a total of 797 species were obtained from 65 replicate 500 m sled tows (1.8 m wide) spanning a 700 km section of the eastern continental shelf. The randomised mean species accumulation curve for this sled sampling is presented in Figure 10, together with the species curve predicted for beam-trawl sampling by the polynomial model (Equation 2)

$$S = -0.19n^2 + 27.57n$$

Equation 2

Where

$S$  = number of species predicted, and  
 $n$  = number of beam-trawl tows

Under this simulation, an estimated 989 epibenthic species could be collected if an equivalent number of beam-trawl samples (65) were randomly undertaken on the BPZ slope. Based on this comparison, it appears that the deep-water epifaunal communities of the BPZ slope are marginally more diverse than those encountered on the adjacent continental shelf.

## 4 DISCUSSION

### 4.1 Faunal patterns

Almost all of the seafloor beyond the State water limits (3 nm) out to the edge of the Australian Exclusive Economic Zone (200 nm) is composed of soft sediments, but despite the prevalence of this habitat very little is known about the diversity and distribution of the associated biota. Few systematic surveys of benthic infauna and epifauna have been undertaken on the slope waters surrounding Australia (Poore, 1995), and patterns and drivers of faunal composition are only now beginning to emerge for this deep-water ecosystem as the Commonwealth Government seeks to implement a network of Marine Protected Areas in south-western Australia to better manage biodiversity and resources (DEWHA, 2007; Williams et al., 2010).

The sediments of the BPZ slope can be characterised as muddy oozes containing large quantities of skeletal organic fragments. Due largely to variations in the quantities of the skeletal remnants, the sediment size-structure varies markedly between locations. In the current study, we observed strong correlations between sediment sorting and the number of infaunal and epifaunal species, and it appears that the least variable sediments support the most diverse faunas. They also appear to support the highest biomasses of epifauna. Similar relationships have been demonstrated for many coastal and shelf environment (Bergen et al., 2001; Coleman et al., 1997; Snelgrove, 1999), but these associations do not infer causality. Faunal correlations with sediment are complex, and may in part reflect the influences of other factors such as hydrodynamic and sediment transport processes which affect the distribution of both sediment and fauna (Snelgrove and Butman, 1994).

Strong correlations were also observed in this study between infaunal abundance and depth, with the number of infaunal organisms declining progressively with increasing depth and distance offshore. This faunal pattern is not replicated in the adjacent GAB shelf, where hotspots of infaunal abundance coincide with areas of recurrent seasonal upwelling (Currie et al., 2009). In spite of such discrepancies, depth-related faunal gradients are a general feature of the GAB shelf (Currie et al., 2009; Ward et al., 2006), and also appear to be a characteristic of the BPZ slope.

Marked shifts in community structure were observed across the BPZ slope in relation to depth. Such changes in community structure are widely reported on shelf and slope habitats (Cartes et al., 2009; Kroncke et al., 2003; Louzao et al., 2010), but geographical differences between studies, as well as variations in the range of depths considered or the classification procedures employed, mean that patterns are frequently contradictory. In this study spanning water depths

of 500 to 2000 m on the continental slope off southern Australia, three distinct infaunal and epifaunal communities were identified. In respect of the taxonomically better known group, the epifauna, these include: a moderately diverse upper slope community (500 m) characterised by several species endemic to Australasia (e.g. the blacktip cucumberfish *Paraulopus nigripinnis* and three-spined cardinal fish *Apogonops anomalus*), a highly diverse mid slope community (1000 m) typified by more widely ranging southern temperate species (e.g. the brittle star *Ophioplinthus accomodata* and basketwork eel *Diastobranchus capensis*) and a low-diversity lower slope community (2000 m) that includes species with circumglobal distributions (e.g. the sea spider *Colossendeis antarctica*). These results appear to be broadly consistent with faunal breaks in demersal fish data from a narrower depth range (500-1200 m) off southern Australia (Koslow et al., 1994); where distinct assemblages are evident in the upper (500 m) and mid-slope (800-1200 m).

Similarities in fish community structure between the southeast Australian mid slope and the North Atlantic, prompted Koslow et al. (1994) to suggest that the biogeographic patterns were consistent with ocean circulation at intermediate depths. They observed that their mid slope community resided within the core depth range (800-1200 m) of the Antarctic Intermediate Water mass, which extends around the northern rim of the Southern Ocean (Fine, 1993). Like Koslow et al. (1994), our mid slope infaunal and epifaunal communities also corresponded with the Antarctic Intermediate Water, but a faunal break on the upper slope also corresponds with the core depth range (400-900 m) of the westward moving Flinders Current (Middleton and Bye, 2007). While these relationships are not necessarily causative, they are of considerable interest, as they suggest that ocean circulation patterns play a key role in structuring benthos at regional scales (10-1000 km).

## 4.2 Conservation significance

Due to the remote and generally inaccessible nature of the coastline, the marine ecosystems of the GAB have received considerably less research attention than other areas of temperate Australia. Despite this, there is increasing evidence that the shelf waters spanning the GAB support a benthic marine biodiversity that is globally significant (Edyvane, 1999; Sorokin et al., 2005; Ward et al., 2006). High levels of species richness on the shelf have been attributed to a lack of mass extinction events over the recent geological past (McGowran et al., 1997), while high levels of endemism are attributed to Australia's long period of isolation as a continent (~80 Ma) (Phillips, 2001). High levels of benthic biodiversity and endemism have also been

postulated for the adjacent GAB slope (Currie and Kendrick, 2006), but remain unproven in this poorly studied region.

During the present study, 57 species of infauna and 84 species of epifauna were collected from the deep-water section of the BPZ. While these collections represent only a small component of Australia's marine macrofaunal biodiversity (>250,000 species (Butler et al., 2010)), the low levels of sampling effort applied during the survey infer that the BPZ slope is remarkably diverse. Indeed, our preliminary species accumulation models suggested that the benthic assemblages of the continental slope are comparatively more diverse than those found on the adjacent continental shelf. This finding is consistent with a number of other cross shelf-slope studies (Levin et al., 2001; Rex, 1981). However, geographical variations in substrate heterogeneity mean that such patterns in diversity do not always hold true (Danovaro et al., 2009; Gray et al., 1997). Unfortunately, the reliability of our estimates of diversity in this study are constrained to a large degree by a very small sample size. Differences in sampling methodologies between surveys add further uncertainty in respect of our hypotheses on epifauna diversity. An increase in sampling effort and the application of a consistent sampling technique would certainly support more robust and equitable estimates of diversity, and should promote a better understanding of their distribution patterns and the factors underpinning them.

At present, it is hard to comment on the conservation values of many of the benthic fauna sampled in the BPZ, as their identities have either yet to be confirmed, or because no data have been published on their distribution. Almost 96% of infauna and 61% of epifauna collected could not be confidently assigned to existing species and appears that a large proportion of these organisms may be undescribed. Voucher material for each taxon collected in this study has been lodged in the South Australian Museum, and will be a valuable reference source for future bio-geographical assessments once their identities are accurately verified.

### **4.3 *Anna's Pimple*: the discovery of an enigmatic volcano in the BPZ**

Bathymetric maps defining the distribution of seafloor features and the benthic communities that colonise them are essential to our understanding of marine ecosystems and our ability to manage them responsibly. Seabed maps provide a geographical basis for evaluating the quality and quantity of benthic resources and can aid the sustainable use of seafloor resources and focus monitoring efforts. As part of a national habitat mapping project, swath data are currently being collected around Australia's continental margin, with a major focus on the upper-slope and mid-slope seabed (200 m to 1500 m depth range). Benthic habitat mapping was a key objective during *Southern Surveyor* voyage SS2010\_T02, and available transit time was

used to target unmapped sections of the upper-slope and mid-slope seabed between Fremantle and Hobart.

One of the most remarkable findings during this mapping process was the discovery of a cone-shaped volcanic pinnacle at a depth of 2000 m inside the BPZ (Figures 11 and 12). This 800 m diameter structure, rising almost 200 m above the surrounding soft-sediments, was undocumented when the Benthic Protection Zone was first proclaimed in 1998. Australia's southern margin had previously been considered a non-volcanic rifted margin, however over the last two decades numerous volcanic bodies have been reported as scattered across the GAB slope (Schofield and Totterdell, 2008). These intrusive bodies have been collectively referred to as the "Bight Basin Igneous Complex" by Schofield and Totterdell (2008), and are believed to have been formed during the middle Eocene (~45 Ma), when seafloor spreading rates along Australia's southern margin were accelerating.

Similar volcanic features off southern Tasmania and New Zealand's north-east coast have been shown to support extremely diverse and unique benthic faunas (Clark and Rowden, 2009; Koslow et al., 2001), and it seems likely that *Anna's Pimple* in the BPZ also supports a diverse collection of faunal elements, including some species that may be unique to the structure. Seamounts exert strong influences on the patchiness of deep-sea benthos by providing habitat for sessile suspension-feeding organisms in an environment otherwise dominated by fine-grained sediments (Probert et al., 1997). With larval connectivity in the deep-sea controlled to a large degree by water circulation patterns, low species overlap and high levels of endemism may be expressed by seamounts separated by small geographical distances when current flows are unfavourable (Richer de Forges et al., 2000).

While the biology and life histories of most seamount species is poorly known, some species appear to be extremely long-lived and slow growing (Grigg, 1993). These characteristics mean that seamount faunas are particularly vulnerable to direct human impacts from activities such as bottom trawling and mining (Clark et al., 2010). As yet, the relative vulnerabilities of any faunal communities associated with *Anna's Pimple* in the BPZ are unknown, as the feature remains unsurveyed for benthos.

#### **4.4 Future research**

Conservation of benthos in the BPZ is a fundamental objective of the current marine park management plan (DEH, 2005). However, it is largely uncertain what levels of benthic biodiversity and endemism are currently being protected in the BPZ, particularly in the deeper

offshore waters. The location of the BPZ was not determined on the basis of any quantitative ecological data. In the absence of any baseline data, the BPZ was located with the aim of conserving a representative strip of seafloor at the widest part of the continental margin. As a result, the suitability of the BPZ for representing the region's benthic biodiversity was, and has remained to a large extent, unknown.

Benthic surveys undertaken in and around the BPZ over the last decade have made significant contributions to our understanding of the regional benthos, and in particular have provided a quantitative basis for evaluating the effectiveness of the BPZ in representing the infaunal and epifaunal biodiversity of the continental shelf (Currie et al., 2007; Ward et al., 2006). Most notably, these studies have demonstrated that the BPZ is well-placed to represent and conserve the benthic infaunal and epifaunal communities of the eastern shelf. However, these same studies have also served to highlight inadequacies in our understanding of benthic biodiversity on the western and inner shelves, and particularly our knowledge of the deep offshore waters of the GAB slope. Moreover, these studies have emphasised gaps in our understanding of other key benthic faunal groups, most notably demersal fish.

Documenting the composition and distribution of the central GAB benthos has gained considerable relevance in recent years, as the deep offshore area is thought to support significant oil and gas reserves, and is currently the subject of an extensive 3D seismic survey (PIRSA, 2011). Before a need arises to manage hydrocarbon extraction in or around the BPZ, it is imperative that the environmental values of the region are adequately assessed.

In the present study, a small number of infaunal and epifaunal samples were collected using grabs and beam-trawls inside the deep-water section of the BPZ. These samples are providing novel insights into the region's seafloor biodiversity, but the restricted spatial coverage precludes any robust assessment of the geographical uniqueness of the faunal elements collected. If the representativeness of the slope fauna potentially impacted by hydrocarbon exploration activities is to be established, then a dedicated survey of the area needs to be undertaken as a matter of priority.

The exploratory drilling programme currently proposed for the central GAB slope (PIRSA, 2011), will have both direct and indirect effects on the benthos. The spatial extent, magnitude and persistence of these impacts, being dependent on a wide variety of factors including the location of the wells and the volume and composition of the drill cuttings discharged, as well as the vulnerabilities of the species themselves. A robust assessment of these impacts will require a Before After Control Impact (BACI) survey design, and will need to embrace sufficient time-series sampling before exploratory drilling commences, to evaluate natural variations in the composition and population structures of the faunal elements. Given that an exploratory drilling

programme has been proposed for 2013-14, the need to initiate baseline sampling in the very near future is highlighted.

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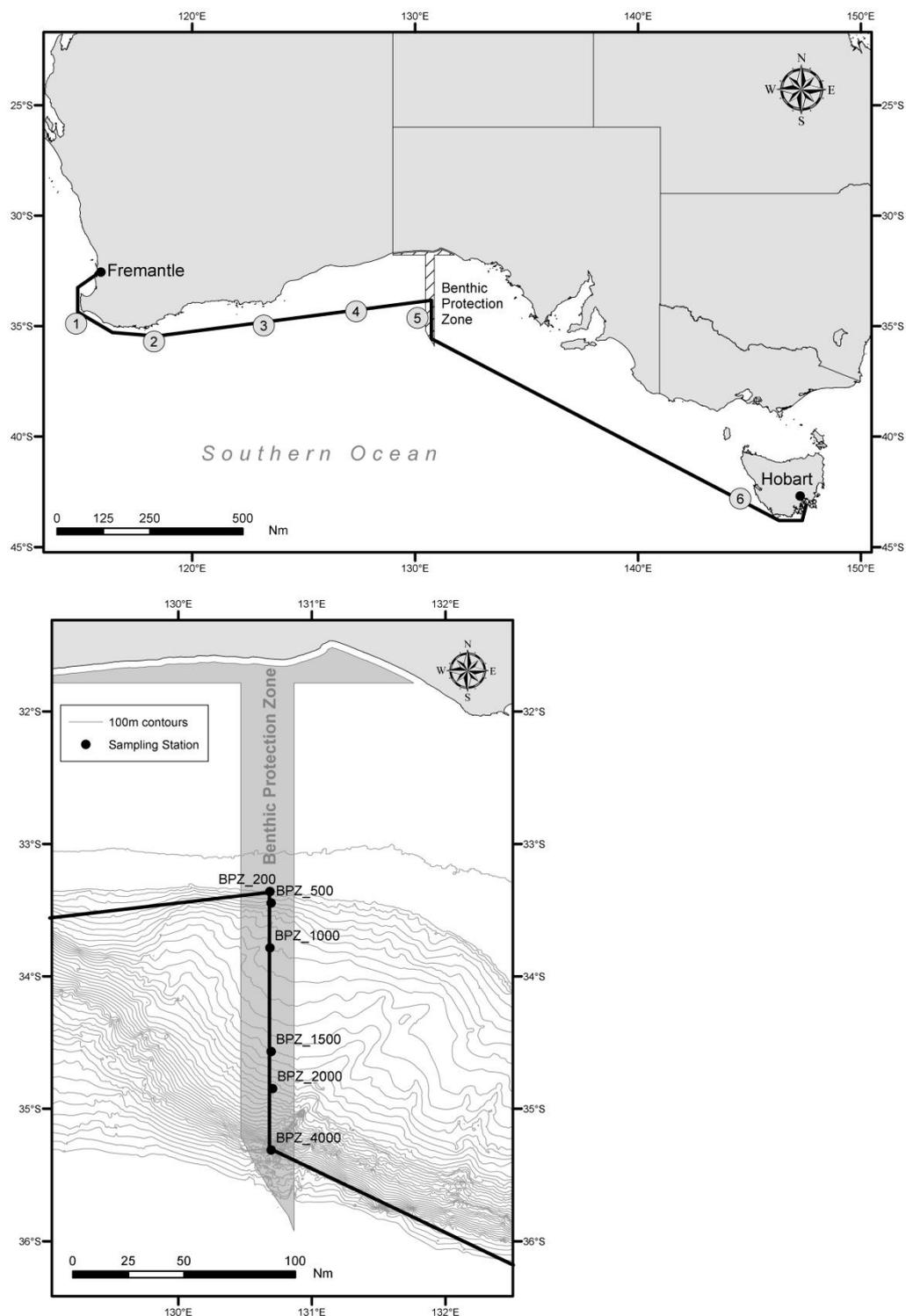
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## ACKNOWLEDGEMENTS

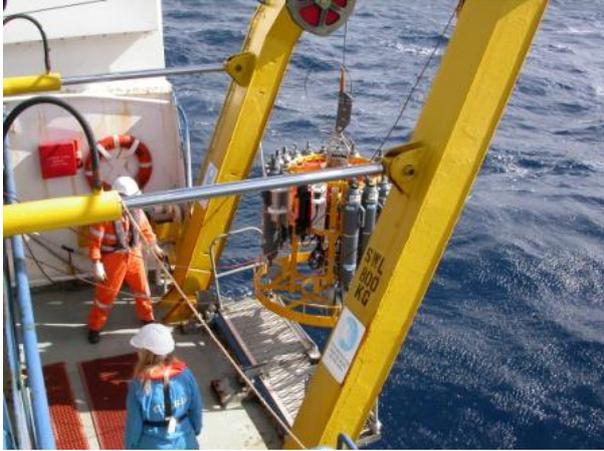
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**Figure 1.** Maps showing the transit route of *Southern Surveyor* during research voyage SS2010\_T02 (Fremantle-Hobart, 11-20 August 2010), and the locations of 6 proposed deep-water benthic sampling stations on the continental slope of the Great Australian Bight Marine Park – Benthic Protection Zone. Numerals circled in the upper map denote the locations of stations sampled for water column properties.



**Figure 2.** Images of sampling gear deployed during *Southern Surveyor* transit voyage SS2010\_T02 including: a) Niskin rosette with Conductivity Temperature Depth (CTD) sensor, b) Argo float (yellow cylinder), c).Smith-McIntyre grab and d) beam trawl.

a)



c)



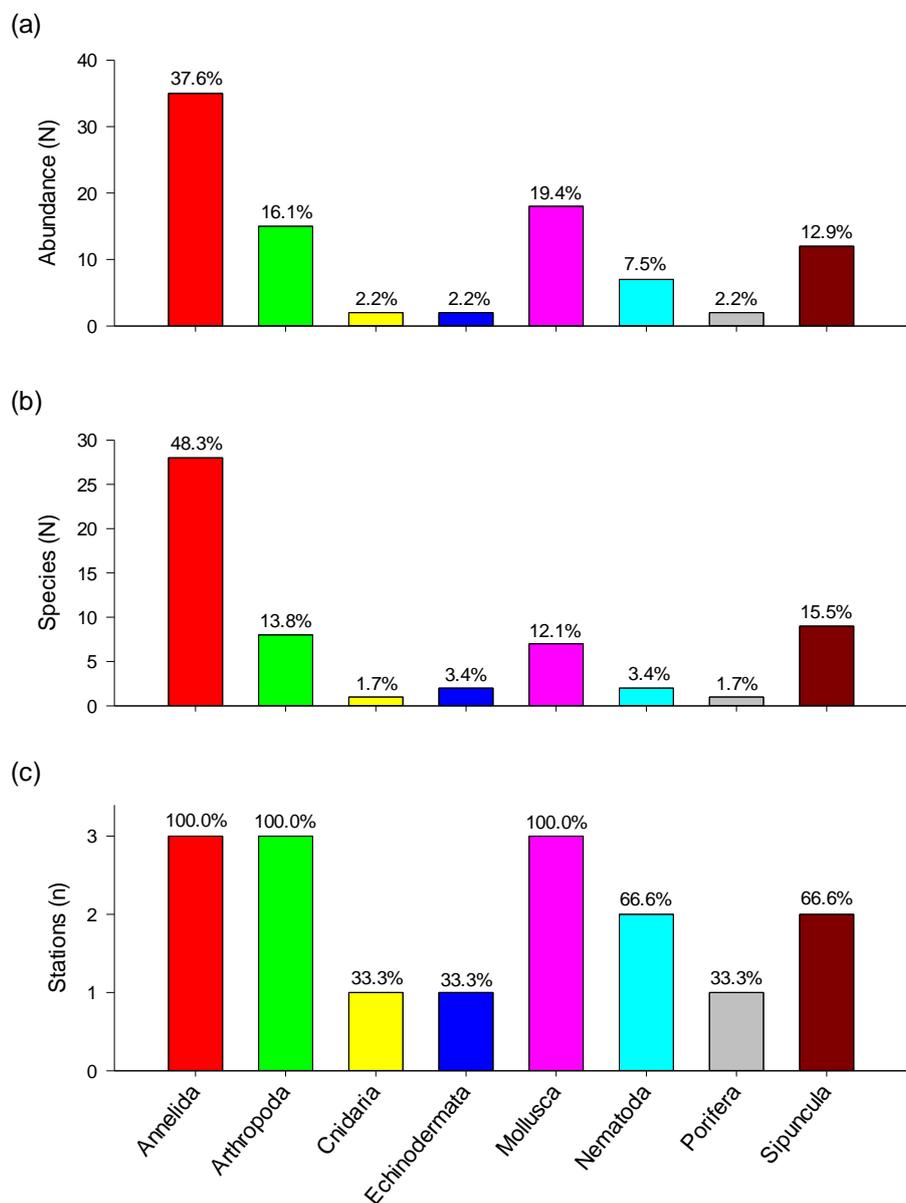
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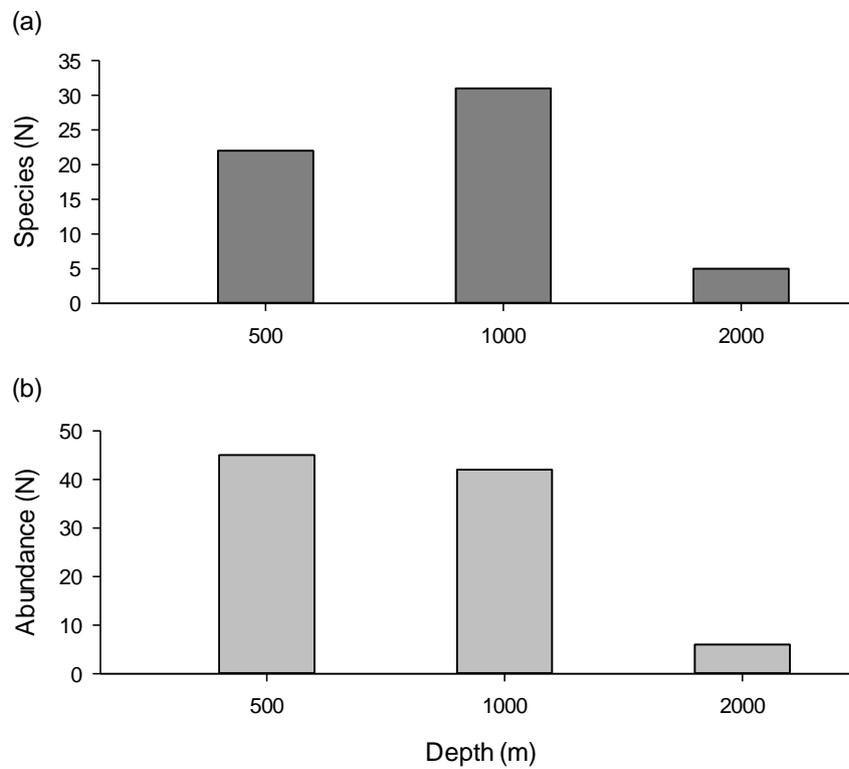
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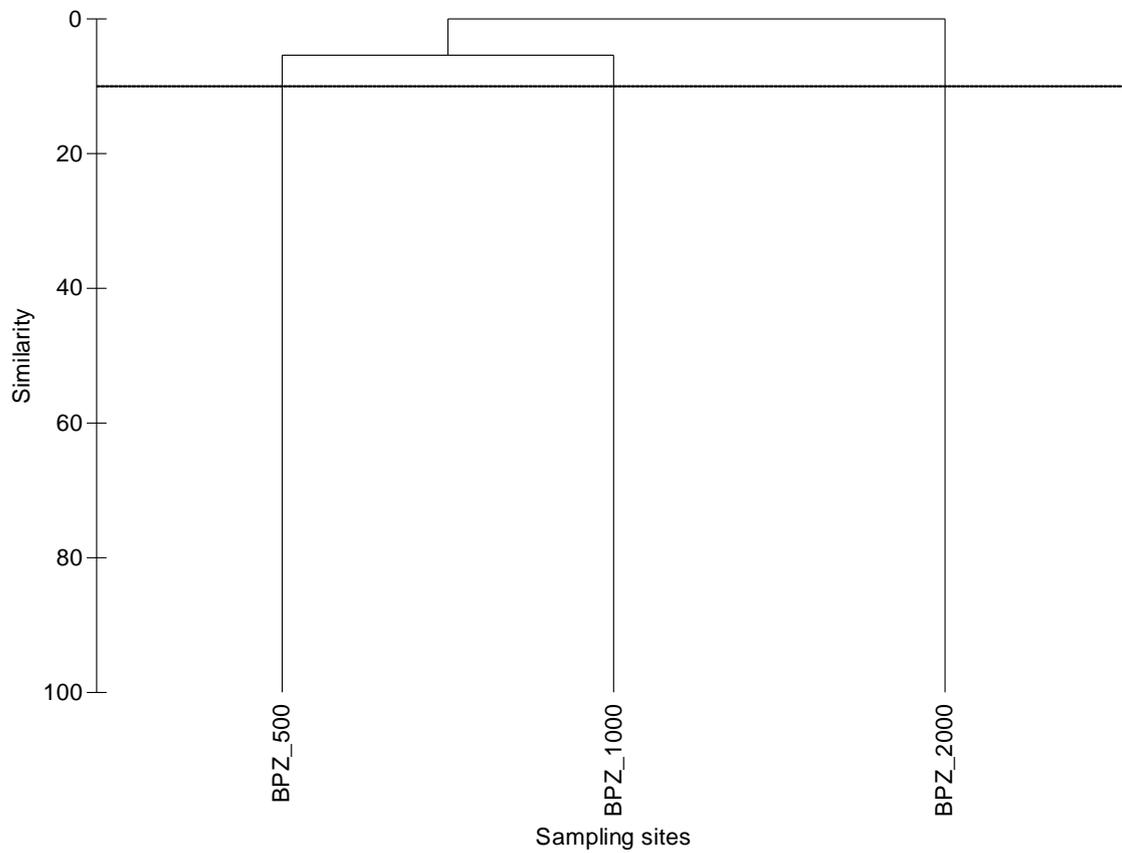
**Figure 3.** Plots of (a) total abundance, (b) total species richness, and (c) total occurrence (out of three sampling stations) of each major infaunal phyla collected during grab sampling in the BPZ. Values for each variable are shown as percentages above each bar.



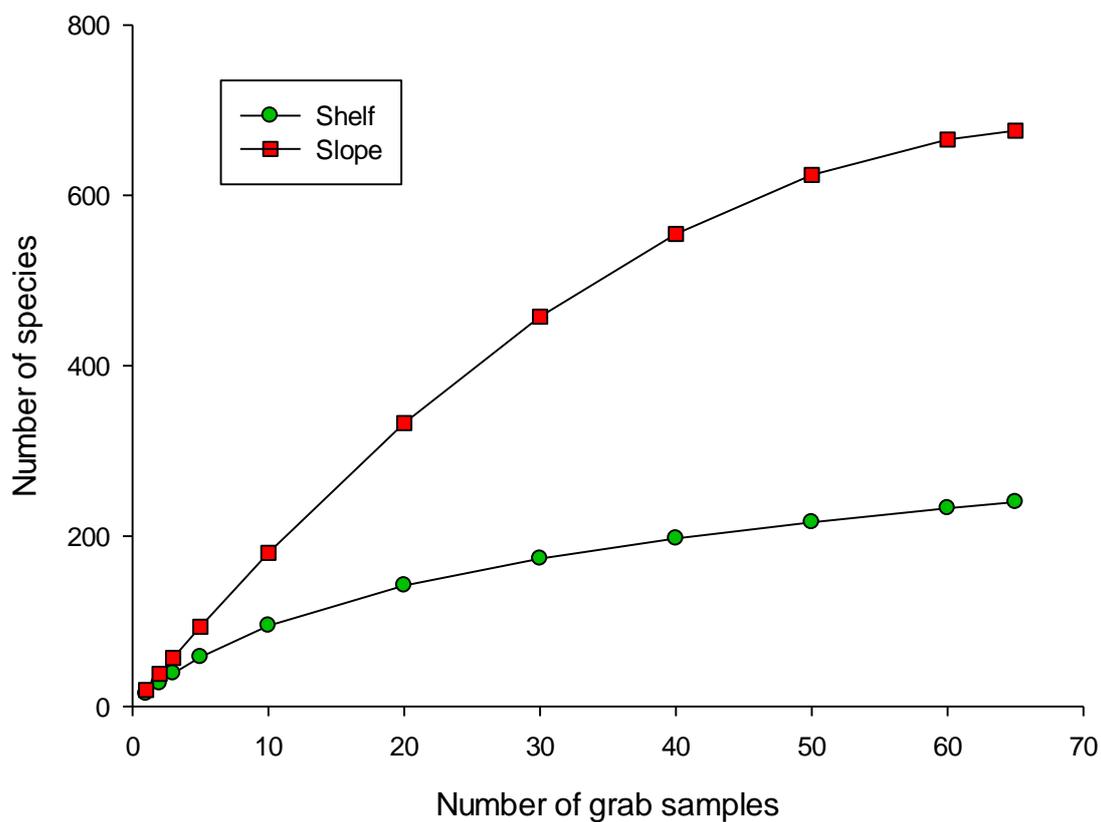
**Figure 4.** Total number of (a) infaunal species, and (b) infaunal organisms collected from grab samples taken at three depth-stratified sampling stations inside the BPZ.



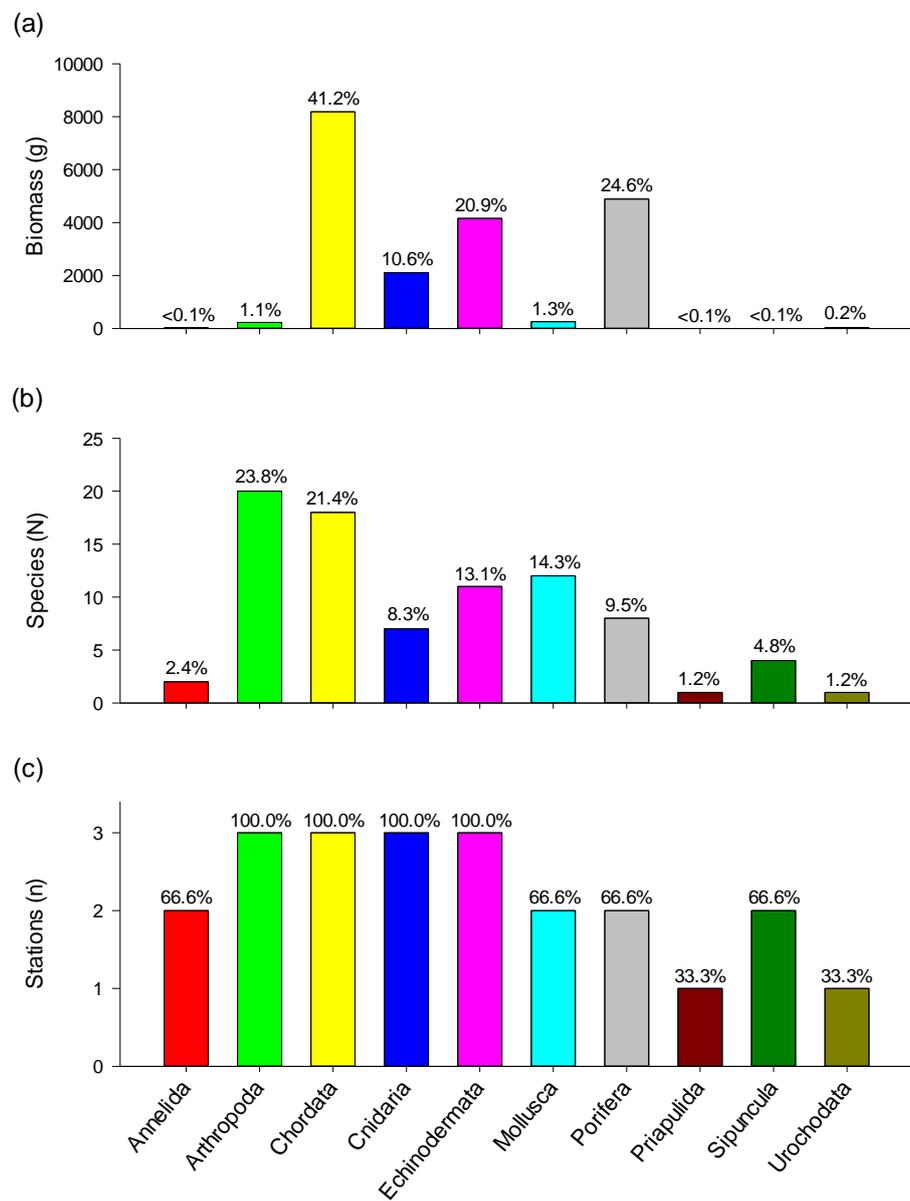
**Figure 5.** Dendrogram of infaunal community structure at three depth-stratified sampling stations inside the BPZ. Three discrete communities are identified at the 10% Bray-Curtis similarity level (horizontal line): upper slope (BPZ\_500), mid slope (BPZ\_1000) and lower slope (BPZ\_2000).



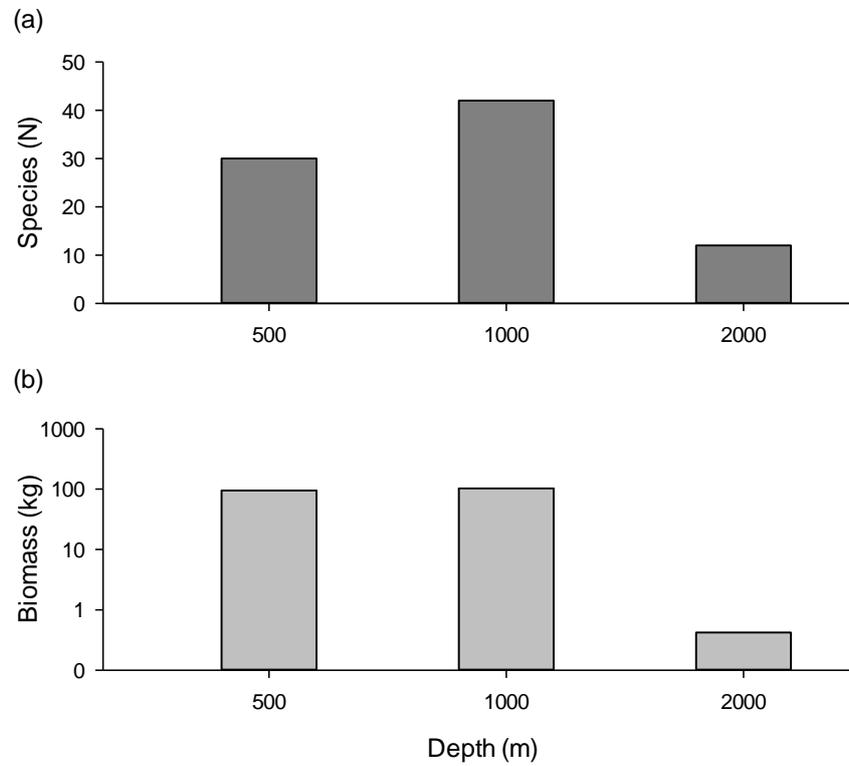
**Figure 6.** Cumulative species curves displaying the observed randomised accumulation of infaunal organisms from 65 grab samples on the eastern GAB shelf (green circles), and the predicted mean number of infaunal organisms from replicate grab samples on the BPZ slope (red squares). Note shelf data presented are from a 2006 survey (Currie et al., 2007).



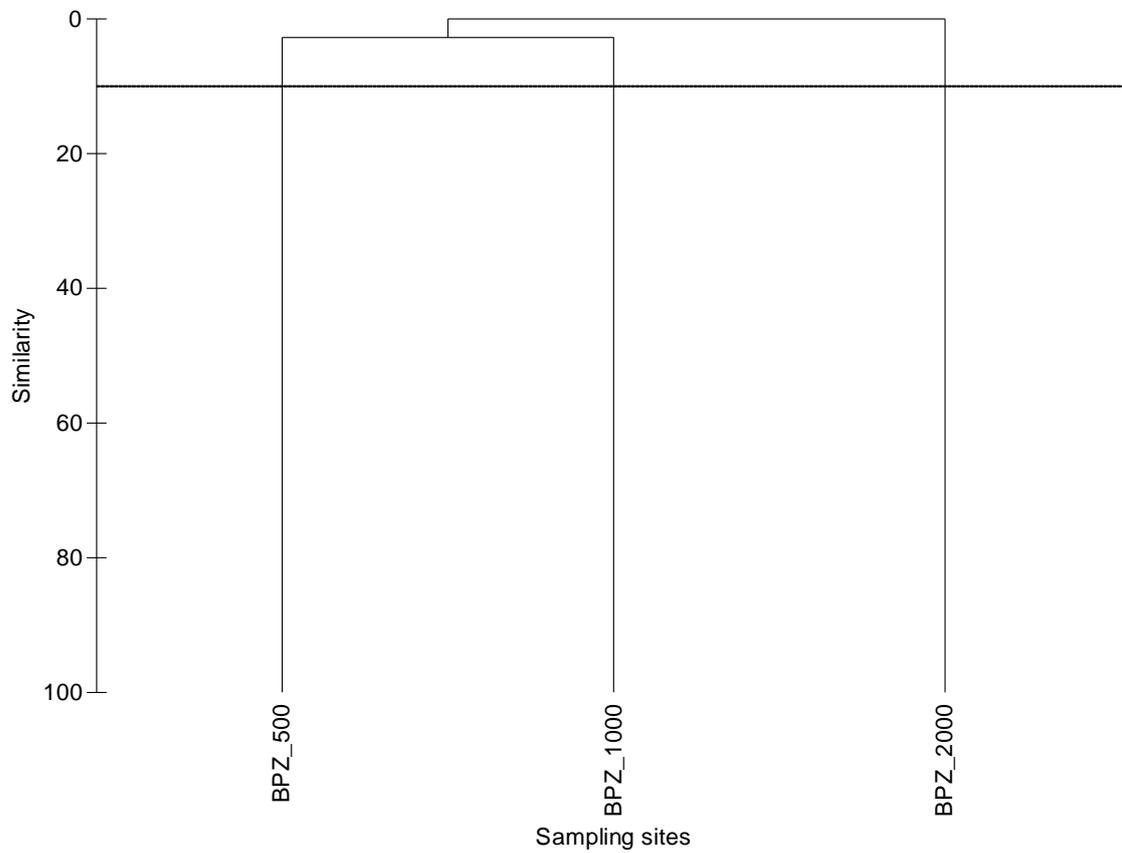
**Figure 7.** Plots of (a) total biomass (grams wet weight), (b) total species richness, and (c) total occurrence (out of three sampling stations) of each major epifaunal phyla collected during trawl sampling in the BPZ. Values for each variable are shown as percentages above each bar.



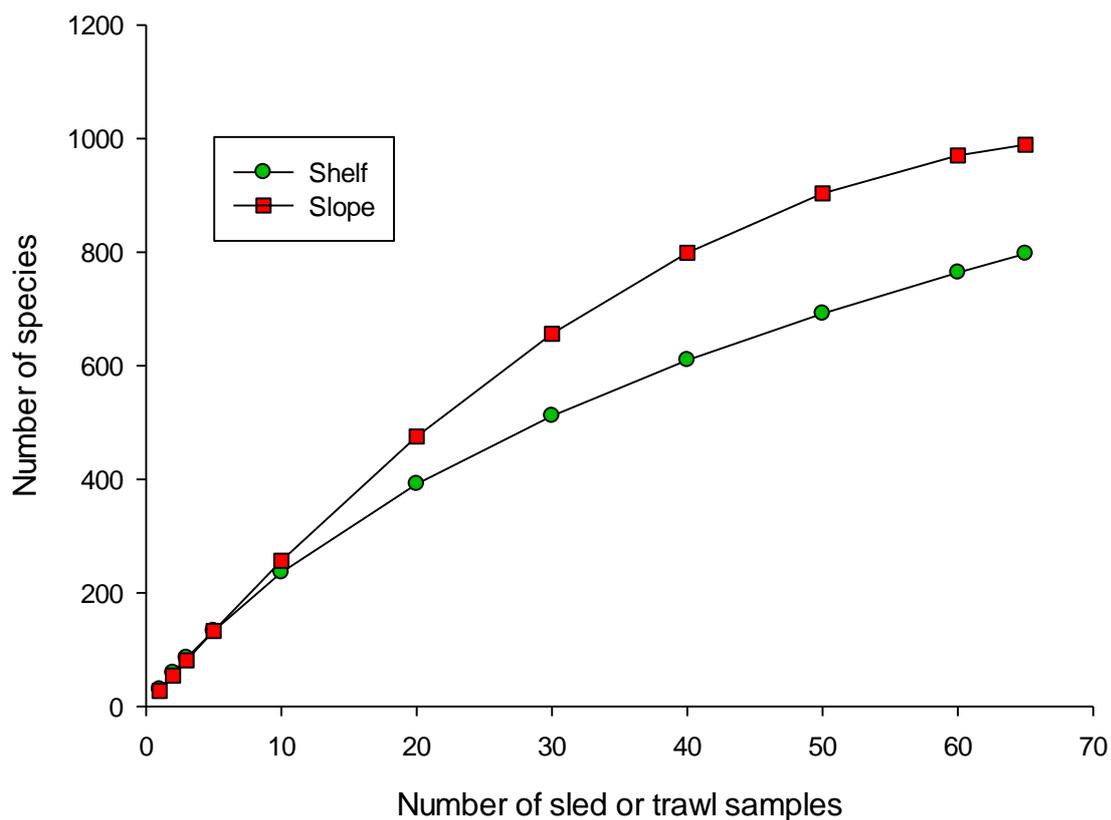
**Figure 8.** Total (a) number of epifaunal species, and (b) wet-weights of epifaunal organisms collected from beam-trawl samples taken at three depth-stratified sampling stations inside the BPZ.



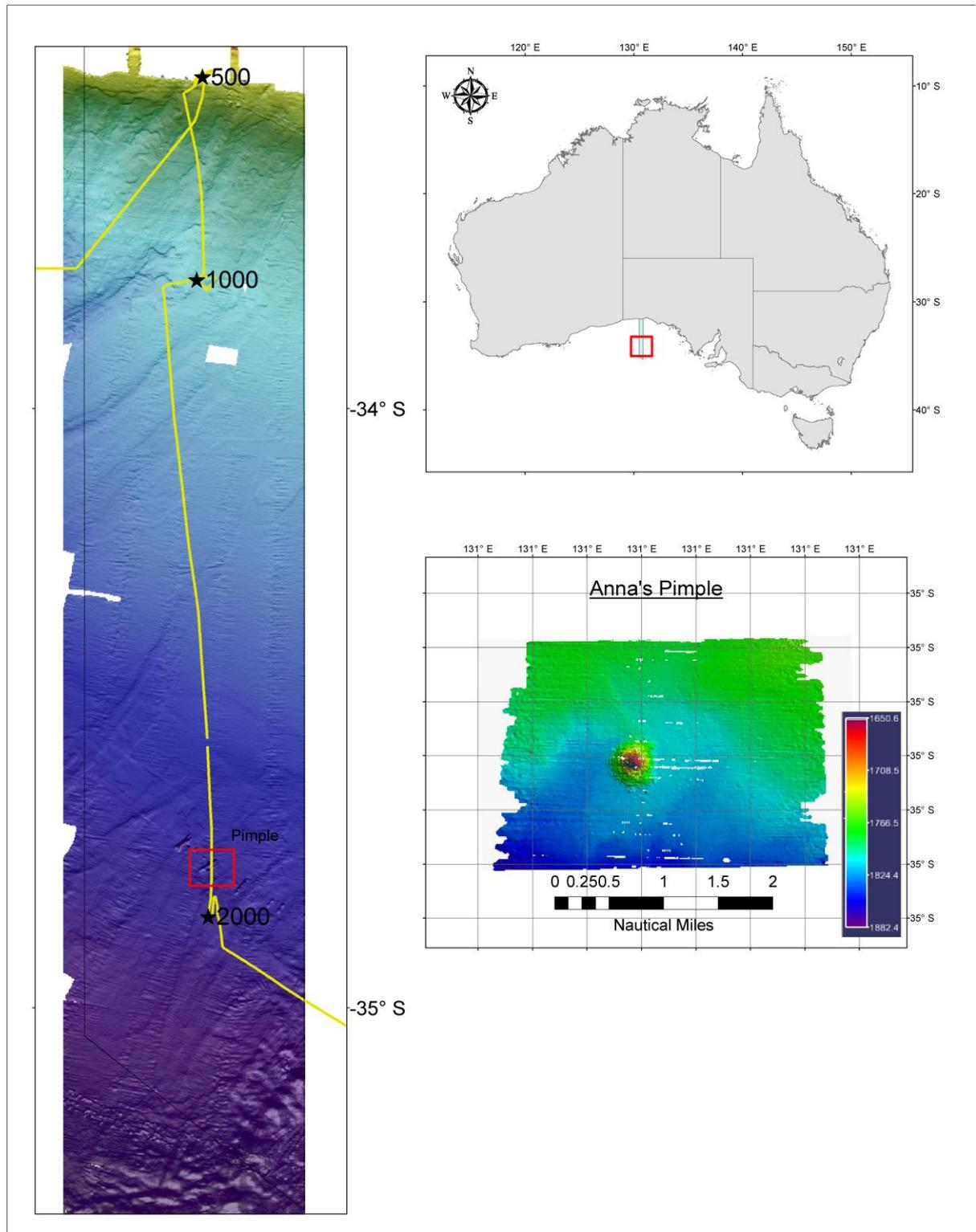
**Figure 9.** Dendrogram of epifaunal community structure at three depth-stratified sampling stations inside the BPZ. Three discrete communities are identified at the 10% Bray-Curtis similarity level (horizontal line): upper slope (BPZ\_500), mid slope (BPZ\_1000) and lower slope (BPZ\_2000).



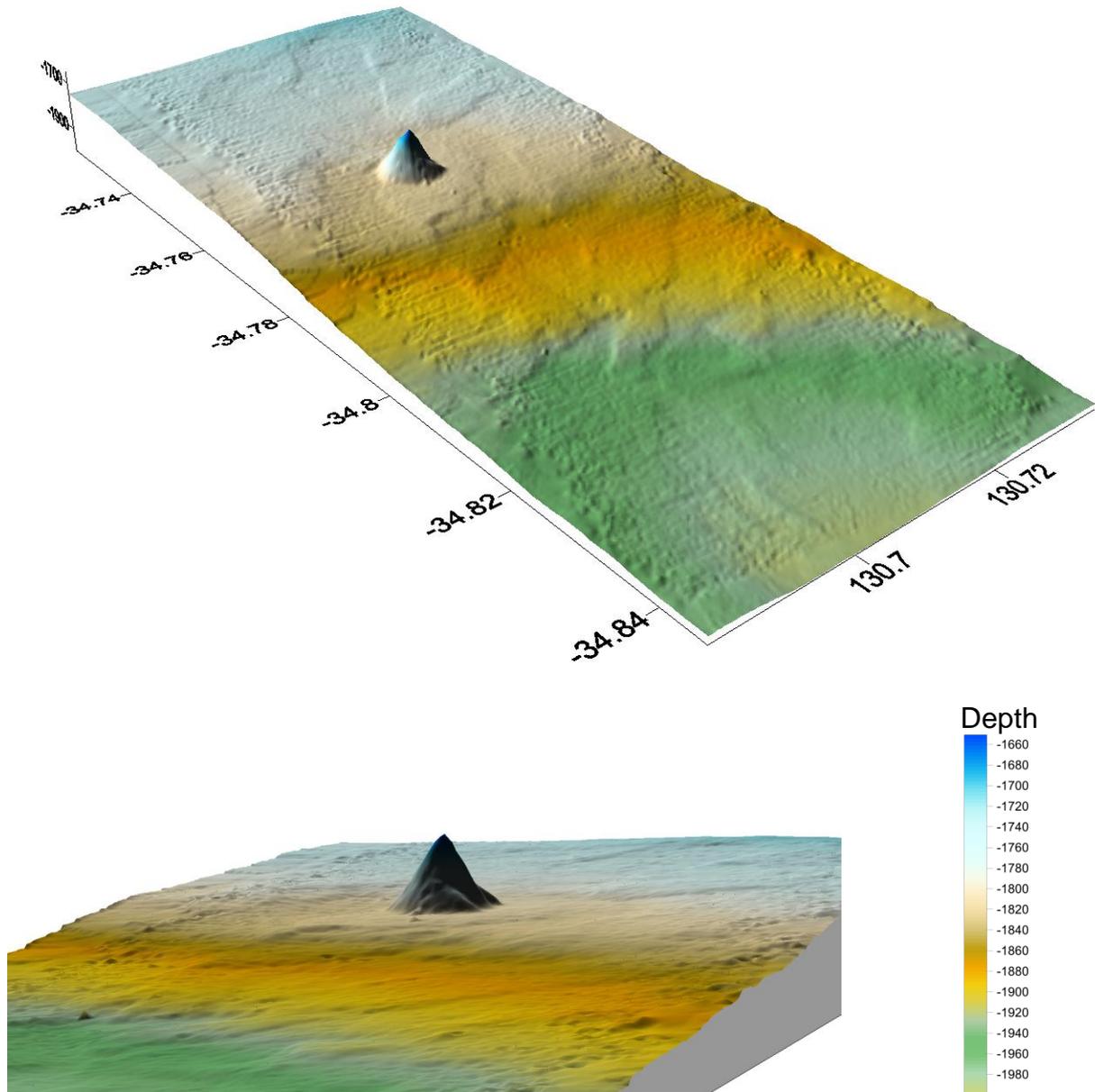
**Figure 10.** Cumulative species curves displaying the observed randomised accumulation of epifaunal organisms from 65 sled shots on the eastern GAB shelf (green circles), and the predicted mean number of epifaunal organisms for replicate beam-trawl shots on the BPZ slope (red squares). Note shelf data presented are from a 2002 survey (Ward et al., 2006).



**Figure 11.** Swath bathymetric image of the Benthic Protection Zone of the Great Australian Bight Marine Park showing the voyage path (yellow line), benthic sampling stations (stars), and the location of *Anna's Pimple* (a 200m high volcanic pinnacle) identified from EM300 multi-beam soundings collected during *Southern Surveyor* transit voyage SS2010\_T02.



**Figure 12.** 3D renderings of Anna's Pimple developed from EM300 multi-beam soundings collected during Southern Surveyor transit voyage SS2010\_T02. Note all depths in metres.



**Table 1.** Summary of environmental factors at three depth-stratified sampling stations in the Benthic Protection Zone of the Great Australian Bight Marine Park.

Station	Latitude (°S)	Longitude (°E)	Depth (m)	Sediment size (%<63µm)	Sediment sorting (Phi)	Sediment carbon (% organic)	Sediment nitrogen (%)	Sediment sulphur (%)
BPZ_500	33.4516	130.6865	500	62.53	2.100	1.285	0.099	0.179
BPZ_1000	33.8022	130.7043	1000	81.70	1.990	0.769	0.089	0.108
BPZ_2000	34.8481	130.7064	2000	76.10	2.285	0.765	0.086	0.112

**Table 2.** Spearman's rank correlation coefficients between infaunal abundance and richness and adjacent environmental conditions at three depth-stratified sampling stations inside the BPZ. Significant positive (+) and negative (-) correlations are denoted at the \*\* 1% level.

	Depth	% Mud	Sediment sorting	Sediment carbon	Sediment nitrogen	Sediment sulphur	Abundance
Depth	.	.	.	.	.	.	.
% Mud	ns	.	.	.	.	.	.
Sediment sorting	ns	ns	.	.	.	.	.
Sediment carbon	(-)**	ns	ns	.	.	.	.
Sediment nitrogen	(-)**	ns	ns	(+)**	.	.	.
Sediment sulphur	ns	(-)**	ns	ns	ns	.	.
Abundance	(-)**	ns	ns	(+)**	(+)**	ns	.
Richness	ns	ns	(-)**	ns	ns	ns	ns

**Table 3.** Total abundance (N per 0.1 m<sup>2</sup>) of infauna in three communities identified from cluster analysis. Species listed were identified as contributing 3% or more to the dissimilarity between samples. Species are ranked in order of decreasing abundance across all samples.

Phylum	Scientific Name	BPZ_500	BPZ_1000	BPZ_2000
Mollusca	<i>Limacina</i> sp. 1	8		
Nematoda	Chromadoroidae 1	3	4	
Annelida	Maldanidae 4	6		
Mollusca	<i>Cuna</i> sp. 1	4		
Arthropoda	<i>Cyathura</i> sp. 1		4	
Arthropoda	<i>Birubius</i> sp. 1		3	
Arthropoda	<i>Metaphoxus</i> sp. 1		3	
Sipuncula	Sipuncula 3	3		
Annelida	Ampharetidae 1	2		
Porifera	Demospongiae 5		2	
Mollusca	<i>Dentalium</i> sp. 1	2		
Cnidaria	Hydroid 1			2
Annelida	Magelonidae 1	2		
Sipuncula	Sipuncula 1	2		

**Table 4.** Spearman's rank correlation coefficients between epifaunal biomass and richness and adjacent environmental conditions at three depth-stratified sampling stations inside the BPZ. Significant positive (+) and negative (-) correlations are denoted at the \*\* 1% level.

	Depth	% Mud	Sediment sorting	Sediment carbon	Sediment nitrogen	Sediment sulphur	Biomass
Depth	.	.	.	.	.	.	.
% Mud	ns	.	.	.	.	.	.
Sediment sorting	ns	ns	.	.	.	.	.
Sediment carbon	(-)**	ns	ns	.	.	.	.
Sediment nitrogen	(-)**	ns	ns	(+)**	.	.	.
Sediment sulphur	ns	(-)**	ns	ns	ns	.	.
Biomass	ns	ns	(-)**	ns	ns	ns	.
Richness	ns	ns	(-)**	ns	ns	ns	(+)**

**Table 5.** Total biomass (g per 4000 m<sup>2</sup>) of epifauna in three communities identified from cluster analysis. Species listed were identified as contributing 3% or more to the dissimilarity between samples. Species are ranked in order of decreasing biomass across all samples.

Phylum	Scientific Name	BPZ_500	BPZ_1000	BPZ_2000
Chordata	<i>Genypterus blacodes</i>	4900		
Porifera	<i>Rosella</i> sp. 1		4883	
Echinodermata	<i>Ophioplinthus accomodata</i>		2822	
Cnidaria	<i>Hormathia lacunifera</i>	1191	14	
Echinodermata	<i>Holothuria</i> sp. 1	1006		
Cnidaria	<i>Desmophyllum dianthus</i>	870		
Chordata	<i>Synaphobranchus oregoni</i>		757	
Chordata	<i>Allocyttus verrucosus</i>		438	
Chordata	<i>Coelorinchus acanthiger</i>		405	
Chordata	<i>Paraulopus nigripinnis</i>	385		
Chordata	<i>Coelorinchus gormani</i>	299		
Chordata	<i>Diastobranchus capensis</i>		267	
Chordata	<i>Coelorinchus fasciatus</i>		236	
Mollusca	<i>Cavolina</i> sp. 1		159	
Echinodermata	<i>Holothuria</i> sp. 2	144		
Chordata	<i>Azygopus pinnifasciatus</i>	140		
Chordata	<i>Apogonops anomalus</i>	121		
Chordata	<i>Cetonurus globiceps</i>		101	
Cnidaria	<i>Umbellula</i> sp. 1			14
Arthropoda	Sergestidae 1			8

**Appendix 1.** Taxonomic and functional classification of 138 benthic species collected from three grab and three trawl shots at three depth-stratified sampling stations (500 m, 1000 m, 2000 m) inside the Benthic Protection Zone (BPZ) of the Great Australian Bight Marine Park (GABMP).

Phylum	Class	Family	Species	Common Name	Code
Porifera	Demospongiae	Undefined	Demospongiae 1	Sponge	S001
Porifera	Demospongiae	Undefined	Demospongiae 2	Sponge	S006
Porifera	Demospongiae	Undefined	Demospongiae 3	Sponge	S007
Porifera	Demospongiae	Undefined	Demospongiae 4	Sponge	S008
Porifera	Demospongiae	Undefined	Demospongiae 5	Sponge	INF_38
Porifera	Hexactinellida	Euplectellidae	Euplectella sp. 1	Sponge	S005
Porifera	Hexactinellida	Rosellidae	<i>Rosella</i> sp. 1	Sponge	S003
Porifera	Hexactinellida	Undefined	Hexactinellida 1	Sponge	S004
Porifera	Hexactinellida	Undefined	Hexactinellida 2	Sponge	S002
Cnidaria	Anthozoa	Antipathidae	Antipathidae 1	Coral	H001
Cnidaria	Anthozoa	Caryophylliidae	<i>Desmophyllum dianthus</i>	Coral	O004
Cnidaria	Anthozoa	Caryophylliidae	<i>Stephanocyathus</i> sp. 1	Coral	O005
Cnidaria	Anthozoa	Hormathidae	<i>Hormathia lacunifera</i>	Anemone	O002
Cnidaria	Anthozoa	Umbellulidae	<i>Umbellula</i> sp. 1	Sea Pen	O001
Cnidaria	Hydrozoa	Stylasteridae	Stylasteridae 1	Hydrocoral	O003
Cnidaria	Hydrozoa	Undefined	Hydroid 1	Hydroid	INF_05
Nematoda	Chromadorea	Chromadoroidea	Chromadoroidea 1	Round Worm	INF_24
Annelida	Polychaeta	Ampharetidae	Ampharetidae 1	Bristle Worm	INF_12
Annelida	Polychaeta	Aphroditidae	Aphrodita sp. 1	Bristle Worm	P002
Annelida	Polychaeta	Capitellidae	Capitellidae 1	Bristle Worm	INF_51
Annelida	Polychaeta	Chaetopteridae	Chaetopteridae 1	Bristle Worm	INF_14
Annelida	Polychaeta	Chaetopteridae	Chaetopteridae 2	Bristle Worm	INF_20
Annelida	Polychaeta	Cirratulidae	Cirratulidae 1	Bristle Worm	INF_13
Annelida	Polychaeta	Eulepethidae	<i>Grubeulepis kurnai</i>	Bristle Worm	INF_11
Annelida	Polychaeta	Flabelligeridae	Flabelligeridae 1	Bristle Worm	INF_45
Annelida	Polychaeta	Goniadidae	Goniadidae 1	Bristle Worm	INF_54
Annelida	Polychaeta	Lumbrineridae	Lumbrineridae 1	Bristle Worm	INF_50
Annelida	Polychaeta	Lumbrineridae	<i>Lumbrineris</i> sp. 1	Bristle Worm	INF_15
Annelida	Polychaeta	Magelonidae	Magelonidae 1	Bristle Worm	INF_19
Annelida	Polychaeta	Maldanidae	Maldanidae 1	Bristle Worm	INF_01
Annelida	Polychaeta	Maldanidae	Maldanidae 2	Bristle Worm	INF_02
Annelida	Polychaeta	Maldanidae	Maldanidae 3	Bristle Worm	INF_17
Annelida	Polychaeta	Maldanidae	Maldanidae 4	Bristle Worm	INF_18
Annelida	Polychaeta	Nereidae	Nereidae 1	Bristle Worm	INF_47
Annelida	Polychaeta	Opheliidae	<i>Armandia</i> sp. 1	Bristle Worm	INF_41
Annelida	Polychaeta	Orbiniidae	Orbiniidae 1	Bristle Worm	INF_16
Annelida	Polychaeta	Paraonidae	Paraonidae 1	Bristle Worm	INF_48
Annelida	Polychaeta	Poecilochaetidae	<i>Poecilochaetus</i> sp. 1	Bristle Worm	INF_61
Annelida	Polychaeta	Polygordiidae	Polygordiidae 1	Bristle Worm	INF_59
Annelida	Polychaeta	Polynoidae	<i>Harmothoe</i> sp. 1	Bristle Worm	P001
Annelida	Polychaeta	Sabellidae	Sabellidae 1	Bristle Worm	INF_25
Annelida	Polychaeta	Spionidae	<i>Prionospio</i> sp. 1	Bristle Worm	INF_56

Phylum	Class	Family	Species	Common Name	Code
Annelida	Polychaeta	Spionidae	Spionidae 1	Bristle Worm	INF_44
Annelida	Polychaeta	Spionidae	Spionidae 2	Bristle Worm	INF_46
Annelida	Polychaeta	Spionidae	Spionidae 3	Bristle Worm	INF_58
Annelida	Polychaeta	Syllidae	Syllidae 1	Bristle Worm	INF_55
Annelida	Polychaeta	Terebellidae	Terebellidae 1	Bristle Worm	INF_53
Sipuncula	Sipuncula	Undefined	Sipuncula 1	Peanut Worm	INF_21
Sipuncula	Sipuncula	Undefined	Sipuncula 2	Peanut Worm	INF_22
Sipuncula	Sipuncula	Undefined	Sipuncula 3	Peanut Worm	INF_23
Sipuncula	Sipuncula	Undefined	Sipuncula 4	Peanut Worm	INF_27
Sipuncula	Sipuncula	Undefined	Sipuncula 5	Peanut Worm	INF_28
Sipuncula	Sipuncula	Undefined	Sipuncula 6	Peanut Worm	INF_39
Sipuncula	Sipuncula	Undefined	Sipuncula 7	Peanut Worm	INF_40
Sipuncula	Sipuncula	Undefined	Sipuncula 8	Peanut Worm	INF_42
Sipuncula	Sipuncula	Undefined	Sipuncula 9	Peanut Worm	INF_60
Sipuncula	Undefined	Undefined	Sipuncula 10	Peanut Worm	I001
Sipuncula	Undefined	Undefined	Sipuncula 11	Peanut Worm	I003
Sipuncula	Undefined	Undefined	Sipuncula 12	Peanut Worm	I005
Sipuncula	Undefined	Undefined	Sipuncula 13	Peanut Worm	I006
Priapulida	Undefined	Undefined	Priapulida 1	Penis Worm	I002
Arthropoda	Cirripedia	Scalpellidae	<i>Arcoscalpellum</i> sp. 1	Goose Barnacle	C008
Arthropoda	Malacostraca	Anthuridae	<i>Cyathura</i> sp. 1	Tanaid	INF_32
Arthropoda	Malacostraca	Aristeidae	<i>Austropenaeus nitidus</i>	Prawn	C004
Arthropoda	Malacostraca	Campylonotidae	<i>Campylonotus rathbunae</i>	Shrimp	C013
Arthropoda	Malacostraca	Cerolidae	<i>Brucerolis victoriensis</i>	Isopod	C001
Arthropoda	Malacostraca	Crangonidae	Crangonidae 1	Shrimp	C005
Arthropoda	Malacostraca	Crangonidae	<i>Metacrangon</i> sp. 1	Shrimp	C017
Arthropoda	Malacostraca	Cyonomidae	<i>Cyonomus</i> sp. 1	Crab	C016
Arthropoda	Malacostraca	Galatheididae	<i>Agononida procera</i>	Squat Lobster	C011
Arthropoda	Malacostraca	Glyphocrangonidae	<i>Glyphocrangon</i> sp. 1	Shrimp	C014
Arthropoda	Malacostraca	Goneplacidae	<i>Carcinoplax meridionalis</i>	Crab	C009
Arthropoda	Malacostraca	Idoteidae	<i>Idotea</i> sp. 1	Idoteid	INF_36
Arthropoda	Malacostraca	Majidae	Majidae 1	Spider Crab	C015
Arthropoda	Malacostraca	Neotanaisidae	<i>Neotanais giganteus</i>	Tanaid	INF_31
Arthropoda	Malacostraca	Oplophoridae	<i>Acantheephyra quadrispinosa</i>	Shrimp	C003
Arthropoda	Malacostraca	Paguridae	Paguridae 1	Hermit Crab	C006
Arthropoda	Malacostraca	Paguridae	Paguridae 2	Hermit Crab	C007
Arthropoda	Malacostraca	Paguridae	<i>Propagurus deprofundus</i>	Hermit Crab	C010
Arthropoda	Malacostraca	Pandalidae	Pandalidae 1	Shrimp	C018
Arthropoda	Malacostraca	Paratanaisidae	Paratanaisidae 1	Tanaid	INF_35
Arthropoda	Malacostraca	Phoxocephalidae	<i>Birubius</i> sp. 1	Amphipod	INF_33
Arthropoda	Malacostraca	Phoxocephalidae	<i>Metaphoxus</i> sp. 1	Amphipod	INF_34
Arthropoda	Malacostraca	Polychelidae	<i>Polycheles suhmi</i>	Deep-sea Lobster	C012
Arthropoda	Malacostraca	Sergestidae	Sergestidae 1	Prawn	C002
Arthropoda	Malacostraca	Urohaustoridae	<i>Urohaustorius</i> sp. 1	Amphipod	INF_06
Arthropoda	Maxillopoda	Calanidae	Calanidae 1	Copepod	INF_03

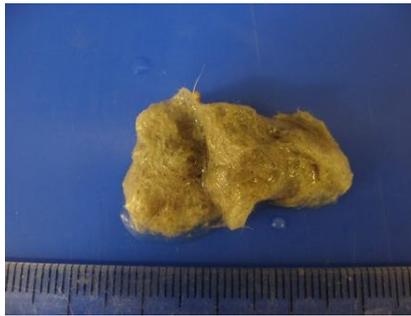
Phylum	Class	Family	Species	Common Name	Code
Arthropoda	Pycnogonida	Colossendeidae	Colossendeidae 1	Sea Spider	PY002
Arthropoda	Pycnogonida	Colossendeidae	<i>Colossendeis antarctica</i>	Sea Spider	PY001
Mollusca	Bivalvia	Condylocardiidae	<i>Cuna</i> sp. 1	Cardita	INF_08
Mollusca	Bivalvia	Tellinidae	Tellina 1	Tellin	INF_04
Mollusca	Gastropoda	Bullidae	<i>Bulla</i> sp. 1	Bubble Shell	M005
Mollusca	Gastropoda	Cavolinidae	<i>Cavolina</i> sp. 1	Pteropod	M001
Mollusca	Gastropoda	Cavoliniidae	<i>Cavolina</i> sp. 2	Pteropod	INF_07
Mollusca	Gastropoda	Cerithiidae	<i>Cerithium</i> sp. 1	Cerithid	INF_30
Mollusca	Gastropoda	Janthinidae	<i>Janthina</i> sp. 1	Purple Shell	M008
Mollusca	Gastropoda	Limacinidae	<i>Limacina</i> sp. 1	Pteropod	INF_10
Mollusca	Gastropoda	Muricidae	<i>Enixotrophon obtusiliratum</i>	Murex Shell	M002
Mollusca	Gastropoda	Naticidae	Naticidae 1	Moon Shell	M011
Mollusca	Gastropoda	Philinidae	<i>Philine</i> sp. 1	Sea Slug	M009
Mollusca	Gastropoda	Rissoidea	<i>Pusillina</i> sp. 1	Rissoid	INF_29
Mollusca	Gastropoda	Trochidae	<i>Clanculus</i> sp. 1	Top Shell	M004
Mollusca	Gastropoda	Turbinellidae	<i>Columbarium</i> sp. 1	Pagoda Shell	M010
Mollusca	Gastropoda	Turridae	<i>Comitas</i> sp. 1	Turrid	M006
Mollusca	Gastropoda	Turridae	<i>Fusinus novaehollandiae</i>	Turrid	M007
Mollusca	Scaphopoda	Dentaliidae	<i>Dentalium francisense</i>	Tusk Shell	M003
Mollusca	Scaphopoda	Dentaliidae	<i>Dentalium</i> sp. 1	Tusk Shell	INF_09
Echinodermata	Asterozoa	Astropectinidae	<i>Astropecten</i> sp. 1	Sea Star	E006
Echinodermata	Asterozoa	Astropectinidae	<i>Astropecten</i> sp. 2	Sea Star	E005
Echinodermata	Echinozoa	Cidaridae	<i>Histiocidaridaris</i> sp. 1	Urchin	E004
Echinodermata	Echinozoa	Echinothuriidae	<i>Phomosoma bursarium</i>	Pancake Urchin	E011
Echinodermata	Holothurozoa	Chiridotidae	Chiridotidae 1	Sea Cucumber	INF_43
Echinodermata	Holothurozoa	Chiridotidae	<i>Trochodota</i> sp. 1	Sea Cucumber	E007
Echinodermata	Holothurozoa	Holothuriidae	<i>Holothuria</i> sp. 1	Sea Cucumber	E008
Echinodermata	Holothurozoa	Holothuriidae	<i>Holothuria</i> sp. 2	Sea Cucumber	E009
Echinodermata	Holothurozoa	Holothuriidae	<i>Holothuria</i> sp. 3	Sea Cucumber	E010
Echinodermata	Ophiurozoa	Ophiuridae	<i>Ophioplinthus accomodata</i>	Brittle Star	E002
Echinodermata	Ophiurozoa	Ophiuridae	<i>Ophiura</i> sp. 1	Brittle Star	E001
Echinodermata	Ophiurozoa	Ophiuridae	Ophiuridae 1	Brittle Star	INF_37
Urochordata	Urochordata	Urochordata	Urochordata 1	Tunicate	I007
Chordata	Actinopterygii	Acropomatidae	<i>Apogonops anomalus</i>	Three-spined Cardinal Fish	F003
Chordata	Actinopterygii	Bathygadidae	<i>Bathygadus cottoides</i>	Rat-tail	F012
Chordata	Actinopterygii	Callionymidae	<i>Foetonepus phasis</i>	Stinkfish	F004
Chordata	Actinopterygii	Callionymidae	<i>Foetorepus apricus</i>	Stinkfish	F011
Chordata	Actinopterygii	Hoplichthyidae	<i>Hoplichthys haswelli</i>	Deep-sea Flathead	F002
Chordata	Actinopterygii	Macrouridae	<i>Cetonurus globiceps</i>	Whiptail	F008
Chordata	Actinopterygii	Macrouridae	<i>Coelorinchus acanthiger</i>	Whiptail	F015
Chordata	Actinopterygii	Macrouridae	<i>Coelorinchus fasciatus</i>	Whiptail	F016
Chordata	Actinopterygii	Macrouridae	<i>Coelorinchus gormani</i>	Whiptail	F006
Chordata	Actinopterygii	Moridae	<i>Antimora rostrata</i>	Violet cod	F017
Chordata	Actinopterygii	Myctophidae	Myctophidae 1	Lantern Fish	F001
Chordata	Actinopterygii	Ophidiidae	<i>Genypterus blacodes</i>	Pink Ling	F018

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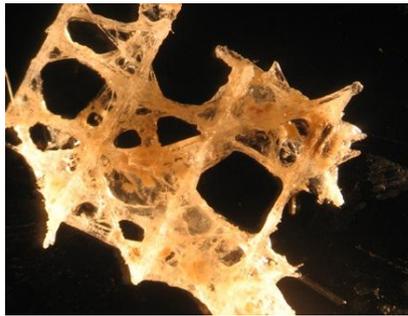
<b>Phylum</b>	<b>Class</b>	<b>Family</b>	<b>Species</b>	<b>Common Name</b>	<b>Code</b>
Chordata	Actinopterygii	Oreosomatidae	<i>Alloctytus verrucosus</i>	Warty Oreo	F009
Chordata	Actinopterygii	Paraulopidae	<i>Paraulopus nigripinnis</i>	Blacktip Cucumberfish	F007
Chordata	Actinopterygii	Rhombosoleidae	<i>Azygopus pinnifasciatus</i>	Banded-fin Flounder	F005
Chordata	Actinopterygii	Stomiidae	<i>Chauliodus sloani</i>	Viperfish	F010
Chordata	Actinopterygii	Synaphobranchidae	<i>Diastobranchus capensis</i>	Eel	F014
Chordata	Actinopterygii	Synaphobranchidae	<i>Synaphobranchus oregoni</i>	Eel	F013

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**Appendix 2.** Photographic plates depicting 138 species collected in grab and trawl shots at three depth-stratified sampling stations inside the Benthic Protection Zone of the Great Australian Bight Marine Park.



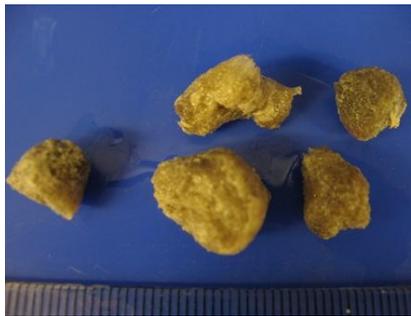
S001 - Demospongiae 1



S005 - *Euplectella* sp. 1



O004 - *Desmophyllum dianthus*



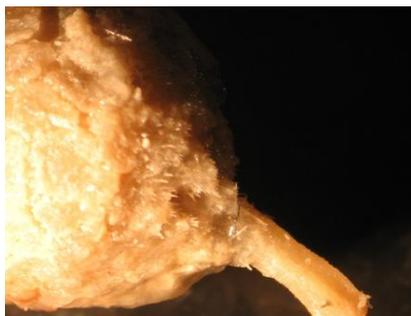
S006 - Demospongiae 2



S003 - *Rosella* sp. 1



O005 - *Stephanocyathus* sp. 1



S007 - Demospongiae 3



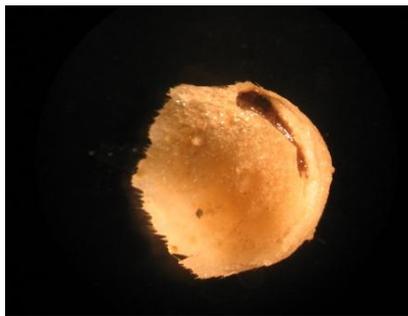
S004 - Hexactinellida 1



O002 - *Hornathia lacunifera*



S008 - Demospongiae 4



S002 - Hexactinellida 2



O001 - *Umbellula* sp. 1



INF\_38 - Demospongiae 5



H001 - Antipathidae 1



O003 - Stylasteridae 1



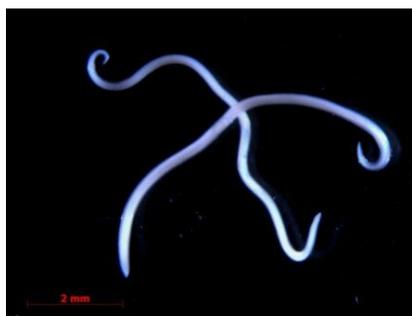
INF\_05 - Hydroid 1



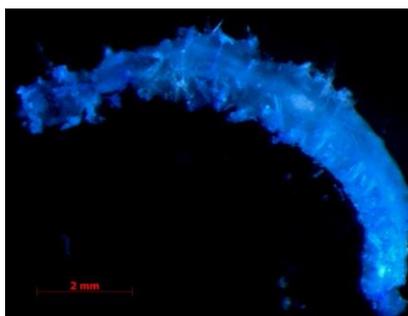
INF\_14 - Chaetopteridae 1



INF\_54 - Goniadidae 1



INF\_24 - Chromadoridae 1



INF\_20 - Chaetopteridae 2



INF\_50 - Lumbrineridae 1



INF\_12 - Ampharetidae 1



INF\_13 - Cirratulidae 1



INF\_15 - *Lumbrineris* sp. 1



P002 - *Aphrodita* sp. 1



INF\_11 - *Grubeulepis kurnai*



INF\_19 - Magelonidae 1



INF\_51 - Capitellidae 1



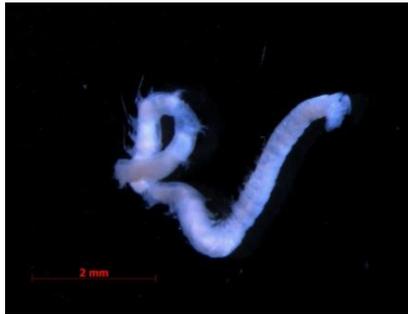
INF\_45 - Flabelligeridae 1



INF\_01 - Maldanidae 1



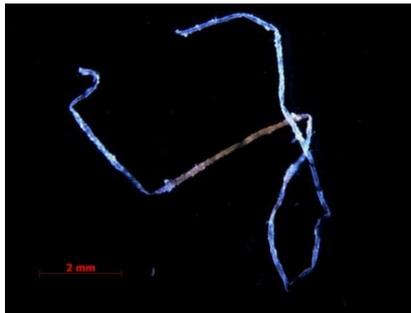
INF\_02 - Maldanidae 2



INF\_16 - Orbiniidae 1



INF\_25 - Sabellidae 1



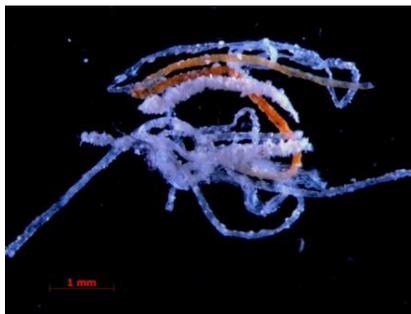
INF\_17 - Maldanidae 3



INF\_48 - Paraonidae 1



INF\_56 - *Prionospio* sp. 1



INF\_18 - Maldanidae 4



INF\_61 - *Poecilochaetus* sp. 1



INF\_44 - Spionidae 1



INF\_47 - Nereidae 1



INF\_59 - Polygordiidae 1



INF\_46 - Spionidae 2



INF\_41 - *Armandia* sp. 1



P001 - *Harmothoe* sp. 1



INF\_58 - Spionidae 3



INF\_55 - Syllidae 1



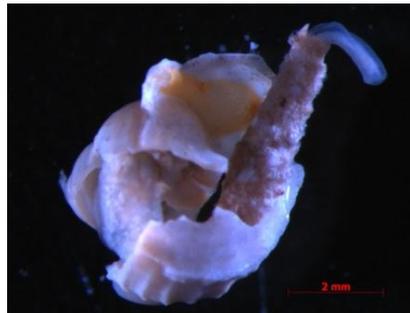
INF\_27 - Sipuncula 4



INF\_60 - Sipuncula 9



INF\_53 - Terebellidae 1



INF\_28 - Sipuncula 5



I001 - Sipuncula 10



INF\_21 - Sipuncula 1



INF\_39 - Sipuncula 6



I003 - Sipuncula 11



INF\_22 - Sipuncula 2



INF\_40 - Sipuncula 7



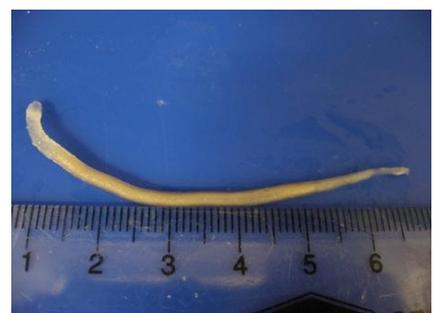
I005 - Sipuncula 12



INF\_23 - Sipuncula 3



INF\_42 - Sipuncula 8



I006 - Sipuncula 13



I002 - Priapulida 1



C001 - *Brucerolis victoriensis*



C014 - *Glyphocrangon* sp. 1



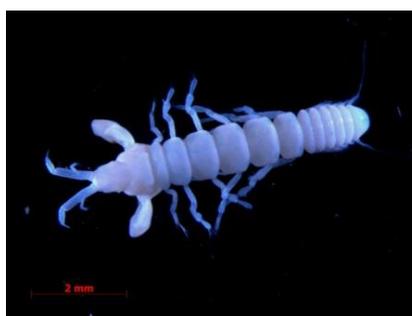
C008 - *Arcoscalpellum* sp. 1



C005 - Cragonidae 1



C009 - *Carcinoplax meridionalis*



INF\_32 - *Cyathura* sp. 1



C017 - *Metacrangon* sp. 1



INF\_36 - *Idotea* sp. 1



C004 - *Austropenaeus nitidus*



C016 - *Cymonimus* sp. 1



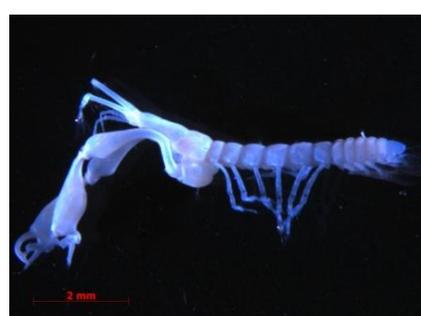
C015 - Majidae 1



C013 - *Campylonotus rathbunae*



C011 - *Agononida procera*



INF\_31 - *Neotanais giganteus*



C003 - *A. quadrispinosa*



INF\_35 - Paratanaidae 1



INF\_06 - *Urohaustorius* sp. 1



C006 - Paguridae 1



INF\_33 - *Birubius* sp. 1



INF\_03 - Calanidae 1



C007 - Paguridae 2



INF\_34 - *Metaphoxus* sp. 1



PY002 - Colossendeidae 1



C010 - *Propagurus deprofundus*



C012 - *Polycheles suhmi*



PY001 - *Colossendeis antarctica*



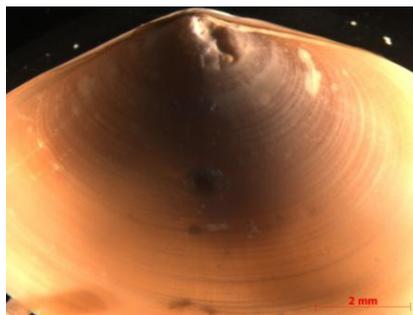
C018 - Pandalidae 1



C002 - Sergestidae 1



INF\_08 - *Cuna* sp. 1



INF\_04 - *Tellina* 1



M008 - *Janthina* sp. 1



INF\_29 - *Pusillina* sp. 1



M005 - *Bulla* sp. 1



INF\_10 - *Limacina* sp. 1



M004 - *Clanculus* sp. 1



M001 - *Cavolina* sp. 1



M002 - *E. obtusiliratum*



M010 - *Columbarium* sp. 1



INF\_07 - *Cavolina* sp. 2



M011 - Naticidae 1



M006 - *Comitas* sp. 1



INF\_30 - *Cerithium* sp. 1



M009 - *Philine* sp. 1



M007 - *Fusinus novaehollandiae*



M003 - *Dentalium francisense*



E011 - *Phomosoma bursarium*



E010 - *Holothuria* sp. 3



INF\_09 - *Dentalium* sp. 1



INF\_43 - Chiridotidae 1



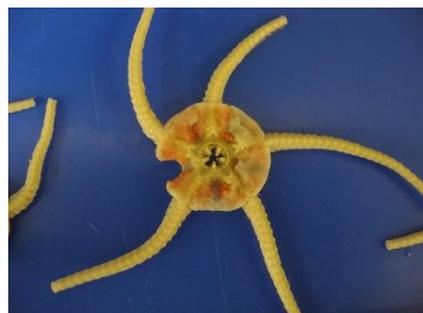
E002 - *Ophioplithus accomodata*



E006 - *Astropecten* sp. 1



E007 - *Trochodota* sp. 1



E001 - *Ophiura* sp. 1



E005 - *Astropecten* sp. 2



E008 - *Holothuria* sp. 1



INF\_37 - Ophiuridae 1



E004 - *Histiocidaris* sp. 1



E009 - *Holothuria* sp. 2



I007 - Urochordata 1



F003 - *Apogonops anomalus*



F008 - *Cetonurus globiceps*



F001 - Myctophidae 1



F012 - *Bathygadus cottoides*



F015 - *Coelorinchus acanthiger*



F018 - *Genypterus blacodes*



F004 - *Foetonepus phasis*



F016 - *Coelorinchus fasciatus*



F009 - *Allocyttus verrucosus* (centre)



F011 - *Foetorepus apricus*



F006 - *Coelorinchus gormani*



F007 - *Paraulopus nigripinnis* (centre)



F002 - *Hoplichthys haswelli*



F017 - *Antimora rostrata*



F005 - *Azygopus pinnifasciatus*



F010 - *Chauliodus sloani*



F014 - *Diastobranthus capensis*



F013 - *Synaphobranchus oregoni*

**Appendix 3.** Summary list of species abundances (N) and biomasses (weight in grams - trawls only) collected from three grabs (0.1 m<sup>2</sup>) and three beam-trawl shots (4000 m<sup>2</sup>) at three depth-stratified sampling stations (500 m, 1000 m, 2000 m) inside the Benthic Protection Zone (BPZ) of the Great Australian Bight Marine Park (GABMP).

Station	Method	Weight	Abundance	Code	Species	Phylum
BPZ_500	Grab	-	2	INF_12	Ampharetidae 1	Annelida
BPZ_500	Grab	-	1	INF_14	Chaetopteridae 1	Annelida
BPZ_500	Grab	-	1	INF_20	Chaetopteridae 2	Annelida
BPZ_500	Grab	-	1	INF_13	Cirratulidae 1	Annelida
BPZ_500	Grab	-	1	INF_11	<i>Grubeulepis kurnai</i>	Annelida
BPZ_500	Grab	-	1	INF_15	<i>Lumbrineris</i> sp. 1	Annelida
BPZ_500	Grab	-	2	INF_19	Magelonidae 1	Annelida
BPZ_500	Grab	-	1	INF_17	Maldanidae 3	Annelida
BPZ_500	Grab	-	6	INF_18	Maldanidae 4	Annelida
BPZ_500	Grab	-	1	INF_16	Orbiniidae 1	Annelida
BPZ_500	Grab	-	1	INF_25	Sabellidae 1	Annelida
BPZ_500	Grab	-	1	INF_06	<i>Urohaustorius</i> sp. 1	Arthropoda
BPZ_500	Grab	-	1	INF_07	<i>Cavolina</i> sp. 2	Mollusca
BPZ_500	Grab	-	4	INF_08	<i>Cuna</i> sp. 1	Mollusca
BPZ_500	Grab	-	2	INF_09	<i>Dentalium</i> sp. 1	Mollusca
BPZ_500	Grab	-	8	INF_10	<i>Limacina</i> sp. 1	Mollusca
BPZ_500	Grab	-	3	INF_24	Chromadoroidea 1	Nematoda
BPZ_500	Grab	-	2	INF_21	Sipuncula 1	Sipuncula
BPZ_500	Grab	-	1	INF_22	Sipuncula 2	Sipuncula
BPZ_500	Grab	-	3	INF_23	Sipuncula 3	Sipuncula
BPZ_500	Grab	-	1	INF_27	Sipuncula 4	Sipuncula
BPZ_500	Grab	-	1	INF_28	Sipuncula 5	Sipuncula
BPZ_500	Trawl	16	4	P002	<i>Aphrodita</i> sp. 1	Annelida
BPZ_500	Trawl	6	2	C011	<i>Agononida procera</i>	Arthropoda
BPZ_500	Trawl	10	1	C013	<i>Campylonotus rathbunae</i>	Arthropoda
BPZ_500	Trawl	72	33	C009	<i>Carcinoplax meridionalis</i>	Arthropoda
BPZ_500	Trawl	1	1	C016	<i>Cymonomus</i> sp. 1	Arthropoda
BPZ_500	Trawl	1	2	C014	<i>Glyphocrangon</i> sp. 1	Arthropoda
BPZ_500	Trawl	2	1	C015	Majidae 1	Arthropoda
BPZ_500	Trawl	0.5	1	C017	<i>Metacrangon</i> sp. 1	Arthropoda
BPZ_500	Trawl	47	23	C018	Pandalidae 1	Arthropoda
BPZ_500	Trawl	2	1	C012	<i>Polycheles suhmi</i>	Arthropoda
BPZ_500	Trawl	39	2	C010	<i>Propagurus deprofundus</i>	Arthropoda
BPZ_500	Trawl	121	4	F003	<i>Apogonops anomalus</i>	Chordata
BPZ_500	Trawl	140	25	F005	<i>Azygopus pinnifasciatus</i>	Chordata
BPZ_500	Trawl	299	9	F006	<i>Coelorinchus gormani</i>	Chordata
BPZ_500	Trawl	39	7	F004	<i>Foetonepus phasis</i>	Chordata
BPZ_500	Trawl	4900	1	F018	<i>Genypterus blacodes</i>	Chordata
BPZ_500	Trawl	3	1	F002	<i>Hoplichthys haswelli</i>	Chordata
BPZ_500	Trawl	385	3	F007	<i>Paraulopus nigripinnis</i>	Chordata

Station	Method	Weight	Abundance	Code	Species	Phylum
BPZ_500	Trawl	870	132	O004	<i>Desmophyllum dianthus</i>	Cnidaria
BPZ_500	Trawl	1191	34	O002	<i>Hormathia lacunifera</i>	Cnidaria
BPZ_500	Trawl	11	1	O005	<i>Stephanocyathus</i> sp. 1	Cnidaria
BPZ_500	Trawl	13	2	E006	<i>Astropecten</i> sp. 1	Echinodermata
BPZ_500	Trawl	92	3	E005	<i>Astropecten</i> sp. 2	Echinodermata
BPZ_500	Trawl	11	3	E004	<i>Histiocidaridaris</i> sp. 1	Echinodermata
BPZ_500	Trawl	1006	125	E008	<i>Holothuria</i> sp. 1	Echinodermata
BPZ_500	Trawl	144	3	E009	<i>Holothuria</i> sp. 2	Echinodermata
BPZ_500	Trawl	25	11	E010	<i>Holothuria</i> sp. 3	Echinodermata
BPZ_500	Trawl	11	4	M010	<i>Columbarium</i> sp. 1	Mollusca
BPZ_500	Trawl	23	7	M007	<i>Fusinus novaehollandiae</i>	Mollusca
BPZ_500	Trawl	38	26	M009	<i>Philine</i> sp. 1	Mollusca
BPZ_1000	Grab	-	1	INF_41	<i>Armandia</i> sp. 1	Annelida
BPZ_1000	Grab	-	1	INF_51	Capitellidae 1	Annelida
BPZ_1000	Grab	-	1	INF_45	Flabelligeridae 1	Annelida
BPZ_1000	Grab	-	1	INF_54	Goniadidae 1	Annelida
BPZ_1000	Grab	-	1	INF_50	Lumbrineridae 1	Annelida
BPZ_1000	Grab	-	1	INF_47	Nereidae 1	Annelida
BPZ_1000	Grab	-	1	INF_48	Paraonidae 1	Annelida
BPZ_1000	Grab	-	1	INF_61	<i>Poecilochaetus</i> sp. 1	Annelida
BPZ_1000	Grab	-	1	INF_59	Polygordiidae 1	Annelida
BPZ_1000	Grab	-	1	INF_56	<i>Prionospio</i> sp. 1	Annelida
BPZ_1000	Grab	-	1	INF_44	Spionidae 1	Annelida
BPZ_1000	Grab	-	1	INF_46	Spionidae 2	Annelida
BPZ_1000	Grab	-	1	INF_58	Spionidae 3	Annelida
BPZ_1000	Grab	-	1	INF_55	Syllidae 1	Annelida
BPZ_1000	Grab	-	1	INF_53	Terebellidae 1	Annelida
BPZ_1000	Grab	-	3	INF_33	<i>Birubius</i> sp. 1	Arthropoda
BPZ_1000	Grab	-	4	INF_32	<i>Cyathura</i> sp. 1	Arthropoda
BPZ_1000	Grab	-	1	INF_36	<i>Idotea</i> sp. 1	Arthropoda
BPZ_1000	Grab	-	3	INF_34	<i>Metaphoxus</i> sp. 1	Arthropoda
BPZ_1000	Grab	-	1	INF_31	<i>Neotanais giganteus</i>	Arthropoda
BPZ_1000	Grab	-	1	INF_35	Paratanaidae 1	Arthropoda
BPZ_1000	Grab	-	1	INF_43	Chiridotidae 1	Echinodermata
BPZ_1000	Grab	-	1	INF_37	Ophiuridae 1	Echinodermata
BPZ_1000	Grab	-	1	INF_30	<i>Cerithium</i> sp. 1	Mollusca
BPZ_1000	Grab	-	1	INF_29	<i>Pusillina</i> sp. 1	Mollusca
BPZ_1000	Grab	-	4	INF_24	Chromadoroidae 1	Nematoda
BPZ_1000	Grab	-	2	INF_38	Demospongiae 5	Porifera
BPZ_1000	Grab	-	1	INF_39	Sipuncula 6	Sipuncula
BPZ_1000	Grab	-	1	INF_40	Sipuncula 7	Sipuncula
BPZ_1000	Grab	-	1	INF_42	Sipuncula 8	Sipuncula
BPZ_1000	Grab	-	1	INF_60	Sipuncula 9	Sipuncula
BPZ_1000	Trawl	0.5	1	P001	<i>Harmothoe</i> sp. 1	Annelida
BPZ_1000	Trawl	8	2	C003	<i>Acanthephyra quadrispinosa</i>	Arthropoda
BPZ_1000	Trawl	1	1	C008	<i>Arcoscalpellum</i> sp. 1	Arthropoda

Station	Method	Weight	Abundance	Code	Species	Phylum
BPZ_1000	Trawl	19	4	C004	<i>Austropenaeus nitidus</i>	Arthropoda
BPZ_1000	Trawl	5	2	C005	Crangonidae 1	Arthropoda
BPZ_1000	Trawl	0.5	1	C006	Paguridae 1	Arthropoda
BPZ_1000	Trawl	1.5	5	C007	Paguridae 2	Arthropoda
BPZ_1000	Trawl	438	1	F009	<i>Allocyttus verrucosus</i>	Chordata
BPZ_1000	Trawl	54	2	F017	<i>Antimora rostrata</i>	Chordata
BPZ_1000	Trawl	1	1	F012	<i>Bathygadus cottoides</i>	Chordata
BPZ_1000	Trawl	101	1	F008	<i>Cetonurus globiceps</i>	Chordata
BPZ_1000	Trawl	36	1	F010	<i>Chauliodus sloani</i>	Chordata
BPZ_1000	Trawl	405	2	F015	<i>Coelorinchus acanthiger</i>	Chordata
BPZ_1000	Trawl	236	1	F016	<i>Coelorinchus fasciatus</i>	Chordata
BPZ_1000	Trawl	267	1	F014	<i>Diastobranthus capensis</i>	Chordata
BPZ_1000	Trawl	3	2	F011	<i>Foetorepus apricus</i>	Chordata
BPZ_1000	Trawl	757	1	F013	<i>Synaphobranchus oregoni</i>	Chordata
BPZ_1000	Trawl	14	1	O002	<i>Hormathia lacunifera</i>	Cnidaria
BPZ_1000	Trawl	24	1	E004	<i>Histiocidarid</i> sp. 1	Echinodermata
BPZ_1000	Trawl	2822	648	E002	<i>Ophioplithus accomodata</i>	Echinodermata
BPZ_1000	Trawl	13	2	E011	<i>Phomosoma bursarium</i>	Echinodermata
BPZ_1000	Trawl	1	1	E007	<i>Trochodota</i> sp. 1	Echinodermata
BPZ_1000	Trawl	9	20	M005	<i>Bulla</i> sp. 1	Mollusca
BPZ_1000	Trawl	159	270	M001	<i>Cavolina</i> sp. 1	Mollusca
BPZ_1000	Trawl	1	2	M004	<i>Clanculus</i> sp. 1	Mollusca
BPZ_1000	Trawl	2	1	M006	<i>Comitas</i> sp. 1	Mollusca
BPZ_1000	Trawl	2	3	M003	<i>Dentalium francisense</i>	Mollusca
BPZ_1000	Trawl	10	1	M002	<i>Enixotrophon obtusiliratum</i>	Mollusca
BPZ_1000	Trawl	3	3	M007	<i>Fusinus novaehollandiae</i>	Mollusca
BPZ_1000	Trawl	0.5	1	M008	<i>Janthina</i> sp. 1	Mollusca
BPZ_1000	Trawl	0.5	9	M011	Naticidae 1	Mollusca
BPZ_1000	Trawl	1	1	S006	Demospongiae 2	Porifera
BPZ_1000	Trawl	0.5	1	S007	Demospongiae 3	Porifera
BPZ_1000	Trawl	1	3	S008	Demospongiae 4	Porifera
BPZ_1000	Trawl	0.5	1	S005	<i>Euplectella</i> sp. 1	Porifera
BPZ_1000	Trawl	0.5	1	S004	Hexactinellida 1	Porifera
BPZ_1000	Trawl	1	2	S002	Hexactinellida 2	Porifera
BPZ_1000	Trawl	4883	1345	S003	<i>Rosella</i> sp. 1	Porifera
BPZ_1000	Trawl	3	3	I003	Sipuncula 11	Sipuncula
BPZ_1000	Trawl	0.5	10	I005	Sipuncula 12	Sipuncula
BPZ_1000	Trawl	0.5	1	I006	Sipuncula 13	Sipuncula
BPZ_1000	Trawl	31	3	I007	Urochordata 1	Urochordata
BPZ_2000	Grab	-	1	INF_01	Maldanidae 1	Annelida
BPZ_2000	Grab	-	1	INF_02	Maldanidae 2	Annelida
BPZ_2000	Grab	-	1	INF_03	Calanidae 1	Arthropoda
BPZ_2000	Grab	-	2	INF_05	Hydroid 1	Cnidaria
BPZ_2000	Grab	-	1	INF_04	Tellina 1	Mollusca
BPZ_2000	Trawl	1	2	C001	<i>Brucerolis victoriensis</i>	Arthropoda
BPZ_2000	Trawl	0.5	1	PY002	Colossendeidae 1	Arthropoda

Station	Method	Weight	Abundance	Code	Species	Phylum
BPZ_2000	Trawl	0.5	1	PY001	<i>Colossendeis antarctica</i>	Arthropoda
BPZ_2000	Trawl	8	2	C002	Sergestidae 1	Arthropoda
BPZ_2000	Trawl	1	6	F001	Myctophidae 1	Chordata
BPZ_2000	Trawl	1	1	H001	Antipathidae 1	Cnidaria
BPZ_2000	Trawl	5	1	O003	Stylasteridae 1	Cnidaria
BPZ_2000	Trawl	14	13	O001	<i>Umbellula</i> sp. 1	Cnidaria
BPZ_2000	Trawl	6	9	E001	<i>Ophiura</i> sp. 1	Echinodermata
BPZ_2000	Trawl	3	1	S001	Demospongiae 1	Porifera
BPZ_2000	Trawl	1	1	I002	Priapulida 1	Priapulida
BPZ_2000	Trawl	1	1	I001	Sipuncula 10	Sipuncula