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Development of a bioregionalisation for VME indicator taxa

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Development of a bioregionalisation for VME indicator taxa

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Summary

Bioregions are large areas of relatively similar environmental conditions that can support similar communities of species. Using occurrence information for Vulnerable Marine Ecosystem (VME) indicator taxa and environmental data, a VME-specific bioregionalisation was produced for the Evaluated Area of the SPRFMO Convention Area and adjacent waters. Various bioregionalisation methodologies were explored, and a hierarchical classification approach was carried forward, drawing from the results of a genus-level gradient forest model. Bioregions may provide an additional spatial scale to assess the performance of spatial conservation measures to prevent Significant Adverse Impacts to VMEs.

1. Purpose

The purpose of this paper is to update the Scientific Committee on the development of a bioregionalisation for Vulnerable Marine Ecosystem (VME) indicator taxa. This work has been undertaken in response to the 2022 Intersessional Working Group on Bottom Fishing identifying that technical work developing ecologically relevant bioregions for the SPRFMO Convention Area could be useful in the future to improve evaluations of the effectiveness of the spatial management areas (COMM11-Doc07, para 209).

2. Background

The Conservation and Management Measure for the Management of Bottom Fishing in the SPRFMO Convention Area (CMM03-2023) includes a spatial management approach that aims to ensure the long-term conservation and sustainable use of deep-sea fishery resources. The CMM seeks to prevent Significant Adverse Impacts (SAIs) on VMEs by protecting a large proportion of the predicted distribution of VME indicator taxa (Table 2-1; SC11-DW01_rev1). Currently, paragraph 39 of CMM03-2023 requires that "From 2023, the Scientific Committee shall adopt the Fishery Management Area as the appropriate scale of management for assessing the performance of the VME spatial management scenarios" to prevent SAIs to VMEs. However, the FMAs were designed for orange roughy (*Hoplostethus atlanticus*) stock assessments and have been informed by an array of orange roughy genetics, life-history characteristics, and habitat use information (Clark et al. 2016). In this way, the boundaries are tailored to specifically support stock assessments and while they may be relevant for that purpose, they are unlikely to represent an ecological spatial scale relevant to VMEs. That is, the distribution of distinct populations, communities or habitats of sessile VMEs will be controlled by different environmental factors, operating at different spatial scales, than for mobile fish. As such, the FMAs are unlikely to be the ideal ecological spatial scale for assessing the performance of the spatial management measures in preventing SAIs to VMEs.

Biogeographic regionalisation or 'bioregionalisation' is a process where the physical and/or biological variability in the environment is analysed, classified, and mapped into spatial units, each with distinct biological, ecological, and physical properties (Dunstan et al. 2018). Bioregions represent large-scale biodiversity patterns that result from historical and present-day environmental factors (Spalding et al. 2007). As such, bioregions describe areas of homogenous environmental conditions which can be characterized by distinct communities (Woolley et al. 2019). Bioregions are a central component to spatial and ecosystem-based management (Stephenson et al. 2023). Within a SPRFMO context, protection of each VME indicator taxon within each biogeographic region, and adequate overall representation of bioregions within areas closed to bottom fishing, could be an important consideration for determining the performance of the spatial management measures.

While the 2023 BFIA (SC11-DW01_rev1) evaluated the performance of spatial management measures at the scale of each FMA, the 2020 BFIA (SC8-DW07 rev 1) assessed performance at four different spatial scales: the whole SPRFMO Evaluated Area; bioregions as proposed by Costello et al. (2017); broad fisheries administrative units; and orange roughy FMAs. Existing bioregions defined using broad (global) schemes, such as those proposed by Costello et al. (2017) may be based on limited biological data within a given region (i.e., New Zealand's Exclusive Economic Zone (EEZ) and SPRFMO Evaluated Area) or may have used surrogate environmental data at a very coarse spatial resolution (e.g., 5° grid

cells). When identifying bioregions for the purposes of assessing representativity or for impact assessments (like the BFIA) at regional scales, Berger et al. (2020) consider that bioregionalisations should be regionally derived because spatially dynamic environmental regimes, e.g., in the South Pacific, likely drive biodiversity patterns at smaller scales than that of ocean basins typically recorded by global bioregionalisations. Global bioregions (e.g., Costello et al. 2017) may therefore be less relevant for regional biota and existing regional bioregions for the South Pacific (e.g., Dunstan et al. 2018) are not specific to VME indicator taxa.

Other Regional Fisheries Management Organisations/Agreements (hereafter referred to as RFMOs), such as Northwest Atlantic Fisheries Organisation (NAFO) and South Indian Ocean Fisheries Agreement (SIOFA) have tested bioregionalisation methodologies and delineated bioregions specifically for RFMOs (Pepin et al. 2013, Ramiro-Sánchez et al. 2023; but noting that these have yet to be applied for management purposes). Delineation of bioregional boundaries can be informed by the distribution of all benthic taxa data (Costello et al. 2017) or a subset of taxa (for example, VME indicator taxa) only as in the bioregional approach developed for SIOFA (Ramiro-Sánchez et al. 2023). Depending on data availability, it may be possible to produce VME indicator taxa (combined), or VME indicator (individual e.g., Bryozoa) specific bioregionalisations. A combined VME indicator taxa bioregionalisation is potentially a more ecologically relevant scale for managing VME communities and habitats (e.g., SIOFA approach). Individual VME indicator bioregions may be a more ecologically relevant scale for managing VME indicator populations e.g., The North Pacific Fisheries Commission (NPFC), following methods of Summers and Watling (2021) and Watling and Lapointe (2022).

The delineation of bioregional boundaries is often a trade-off between ecological classification detail and management requirements. There is therefore no prescribed 'bioregional scale', though typically bioregions are the lowest level of environmental/ecological classification detail possible, while still being ecologically meaningful and useful for management. Nested classification detail within 'bioregions' is referred to differently as this nested detail represents a different ecological scale. For example, "community classes" are nested in the bioregions of Stephenson et al. (2023), while bioregions produced for NAFO, contain two smaller nested spatial scales referred to as "Ecosystem Production Units" and "Ecoregions" (Pepin et al. 2013). Delineation of bioregions is typically data-driven, but given the subjective nature of bioregionalisations, often the optimal number of bioregions and/or the delineation of bioregional boundaries is in part expert-informed, and may incorporate some input from policy-makers and marine spatial planners (Dunstan et al. 2018, Stephenson et al. 2023).

Recognising the limitations of bioregionalisations previously used for estimating the performance of spatial measures in the SPRFMO Evaluated Area, and in particular their scale, the 12th Meeting of the SPRFMO Commission directed that "*the Scientific Committee to adopt Fishery Management Areas as the appropriate scale of management for assessing the performance of spatial management areas"* (Para 39; CMM 03-2023). Nevertheless, in the 2019 BFIA Standard (BFIS 2019) Appendix B referring to scale, definitions, and distribution of VMEs, it is noted that *"as more information becomes available (such as the location of known VMEs or VME indicator taxa) it may be more appropriate to undertake impact assessments for particular benthic communities, assemblages or at a bioregional level".* Recognising that additional data has become available that could facilitate the development of a bioregionalisation for VME indicator taxa in the SPRFMO Evaluated Area, which could potentially have some future utility in assessing the performance of the spatial management areas at ecologically

relevant spatial scales, the New Zealand Government added the exploratory development of a bioregionalisation for VME indicator taxa to the scope of works for the 2024 calendar year.

Table 2-1 | VME indicator taxa identified in CMM03-2023 and Fisheries New Zealand (FNZ) and Food and Agriculture Organization (FAO) codes.

Phylum	Lower taxonomic group	Qualifying taxa	FNZ Code	FAO Code
Porifera (sponges)	Demospongiae and Hexactinellida		DEM & HEX	PFR
Cnidaria	Scleractinia (Stony corals)	All taxa within the following genera: *Solenosmilia*; *Goniocorella*; *Enallopsammia*; *Madrepora*; *Oculina; Lophelia*	SVA, GDU, ERO, MOC	CSS
	Antipatharia (Black corals)		COB	AQZ
	Alcyonacea* (Soft corals)	All taxa excluding Gorgonian Alcyonacea	ALCY	ALZ
	Gorgonian Alcyonacea* (tree-like forms, sea fans, sea whips, bottlebrush corals)	All taxa within the following suborders: Holaxonia; Calaxonia; Scleraxonia	GOC	GGW
	Pennatulacea* (Sea pens)	All taxa	PTU	NTW
	Actiniaria (Anemones)	All taxa	ANT	ATX
	Zoantharia (Hexacorals)	All taxa	ZAH	ZOT
	Hydrozoa (Hydroids)		HDR	HQZ
	Stylasteridae (Hydrocorals)	All taxa	COR	AXT
Bryozoa (Bryozoans)			COZ	BZN
Habitat indicators				
Echinodermata	Brisingida ('Armless' stars)	All taxa	BRG	BHZ
	Crinoidea (Sea lillies and feather stars)	All taxa	CRI	CWD

**Note: systematics of Octocorallia (i.e., Alcyonacea) has since been revised using phylogenetics methods. See McFadden et al. (2022) for further details.*

Here, we present the exploratory development of a bioregionalisation for VME indicator taxa in the SPRFMO Evaluated Area (i.e., see SC11-DW01_rev1 for definition of Evaluated Area, and see Figure 1 in SC10-DW05 showing Evaluated Area relative to SPRFMO Convention Area) and adjacent waters (see Figure 3-1). Various modelling approaches, and subsequent classifications, that estimate bioregional boundaries within the area are presented. The use of differing taxonomic levels of species data used to train models, was also tested (i.e., VME indicator taxa level and genus level). Tested methodologies are discussed in brief, while gradient forest (Ellis et al. 2012) modelling, the methodology taken forward, is described in detail. The bioregionalisation considered to be optimal is also shown and described in detail, while results for the bioregionalisations at higher levels are included in the Annex for comparison.

3. Methods

3.1 Initial testing of bioregionalisation approaches

A variety of bioregionalisation approaches were considered for this study. Woolley et al. (2019) consider that modelling approaches that can be used for bioregionalisations can be categorised into four main types:

1. **Predict first, then group**. A two-stage approach is used to (1) predict each species distribution and then (2) cluster predictions. For example, environmental variables can be incorporated through Species Distribution Models (SDMs). SDMs are then used as inputs into a spatial clustering analysis in the second step (e.g., k-means or another clustering algorithm), for instance, the approach detailed in Ramiro-Sánchez et al. (2023), for the Southern Indian Ocean Fisheries Agreement (SIOFA) using networks. Another example of this approach is gradient forests (Stephenson et al. 2022, Stephenson et al. 2023).

2. **Jointly predict, then group.** An extension of the above approach but using joint Species Distribution Models i.e., jSDMs (Ovaskainen et al. 2016, Stephenson et al. 2021a). Following production of jSDMs, outputs are clustered. The classification is referred to as Regions of Common Profiles (RCPs) by the authors of the R package used to implement jSDMs; *hmsc* (Ovaskainen et al. 2016). This should not be confused with the approach with the same name included below under 'analyse simultaneously'.

3. **Group first, then predict.** Another two-stage approach that involves (1) clustering biological data to "represent groups of relatively homogenous species composition" (Woolley et al. 2019) and (2) predicting the clusters into unsampled locations using a variant of species distribution modelling (Rubidge et al. 2016, Ramiro-Sánchez et al. 2023).

4. **Analyse simultaneously (one-step approach).** Perform both clustering and spatial predictions within a single model that defines the bioregions and produces uncertainty measures (e.g., RCPs). For example, see Foster et al. (2013).

After due consideration, three bioregionalisation approaches were tested that were relatively simple to implement given the time and data available. A type 1 approach, where habitat suitability models for 17 VME indicator taxa produced by Bennion et al. (2024) and Stephenson et al. (2021b) were used in a way similar to that described in Ramiro-Sánchez et al. (2023). That is, habitat suitability index (HSI) within 1 km x 1 km grid cells was used as an abundance proxy [following receiver operating characteristic (ROC) cut-off transformation; see BFIA; SC8-DW07 rev 1]. Gridded format data were converted into an abundance-absence matrix, whereby columns denoted VME indicator taxa, and rows were sites (i.e., unique grid cells). A k-means algorithm was then used to cluster the matrix information (a range of k values was used; k = 2 to 75). The elbow method was then used to infer an optimal number of clusters (k), whereby the lowest number of clusters (k) with the lowest within sum of square error was deemed 'optimal'. In this case, k = 5 was deemed optimal. Given the computationally demanding nature of this method, the clustering algorithm was applied at an aggregated cell size (resolution) of 10 km x 10 km, while the elbow method was applied at a resolution of 20 km x 20 km. Ultimately, the approach was deemed inflexible for the desired uses, and the computationally demanding nature of the approach made further explorations challenging. However,

it should be noted that the despite the large cell size, and limited testing of the approach, the outputs were deemed somewhat promising.

Another approach tested was the 'analyse simultaneously' type 4 one-step approach, in the form of RCPs. This approach was previously tested using occurrence information for 10 VME indicator taxa in the study area, but the work was not progressed (O. Anderson, unpublished). The RCP models are a type of 'Mixture-of-Experts Models' and try to describe how homogeneous groups of sites vary with the environment. This is done by grouping sites based on the biological content (taxa observed at each site) and assessing how these groups vary across environmental or physical gradients (Foster et al. 2013). The methods used followed the methods described in Hill et al. (2017) Briefly, an occurrence data matrix (presence-absence) was generated using the same datasets used to train the models in Bennion et al. (2024) and Stephenson et al. (2021b). The occurrence matrix was therefore at the 'VME indicator taxa' level, and contained 11,428 rows (i.e., unique gird cells with presence or absence information). The environmental data used were many of the same used to develop the more recent additional set of habitat suitability models for VME indicator taxa (Bennion et al. 2024) and included bathymetric position index-broad (BPI-broad), dissolved oxygen, particulate organic carbon export to the seafloor (POC), standard deviation of the slope (slope SD), temperature at depth, ruggedness, percent gravel, percent mud, seamounts (presence-absence). Several RCP models were produced, with a varying number of RCPs (1 to 8). Following production of RCP models, the Bayesian Information Criterion (BIC) was used to infer what the optimal number of RCPs (i.e., bioregions) might be. Unexplained variation in the dependent variable and the number of explanatory variables (in this case RCPs) increase the value of BIC. Therefore, akin to the elbow method, an optimal number of RCPs is considered to be the lowest number of RCPs with low BIC (i.e., the point where the curve flattens). When tested here, the optimal number of RCPs was determined to be RCPs = 5. Like the k-means approach detailed above, the RCP approach was computationally demanding. The model spatial prediction for the optimal RCPs (i.e., 5) was not deemed to be useful as little classification detail was present in the Evaluated Area, therefore the approach was not carried forward.

The final approach tested, another type 1 approach, was gradient forest (GF) modelling. Gradient forest (Pitcher 2011, Ellis et al. 2012) models use species distribution data (abundance or presence-absence) to control the selection, weighting, and transformation of environmental predictors to maximise their correlation with species compositional turnover and establish where along the range of environmental gradients important compositional changes occur (Ellis et al. 2012). Transformed environmental variables (representing compositional turnover) can then be classified to define spatial groups that capture variation in species composition and turnover (Pitcher 2011, Stephenson et al. 2018, Stephenson et al. 2020b). In New Zealand's EEZ, GF models have been used for a combination of macroalgae, reef/demersal fish, and seafloor invertebrate data to generate the New Zealand Seafloor Community Classification (Stephenson et al. 2022). This classification was subsequently reduced to a bioregionalisation (75 classes reduced to 9 bioregions), referred to as the Seafloor Bioregionalisation for New Zealand (Stephenson et al. 2023). Ultimately, the GF approach was considered as the most appropriate of the three approaches tested (the nested nature of the approach was deemed useful too), and so was the approach taken forward for the final analyses.

3.2 Biological data used for GF modelling

Occurrence records for VME indicator taxa at respective levels (n = 17) e.g., Phylum Bryozoa, Order Actiniaria were extracted (Geange et al. 2020, Stephenson et al. 2021b). Occurrence records were

filtered to depths between 200–3,000 m (i.e., study area; as per Stephenson et al. (2021b) and Bennion et al. (2024); see Figure 3-1 and Figure 3-2). Occurrence (presence-only) data used to train the models were compiled for previously produced habitat suitability models (Stephenson et al. 2021b, Bennion et al. 2024), and SC papers (SC8-DW11), from New Zealand and Australian museum/collection records, fisheries research databases, and online biodiversity databases. Data were groomed by checking for positional errors, crosschecking recorded depths against the best available bathymetry estimates for the region (Mackay et al. 2015), removing duplicate records, and removing records outside of the study area and modelled depth range (i.e., shallower than 200 m and deeper than 3,000 m water depth). Presence records were spatially aggregated to a 1 km x 1 km grid resolution, i.e., a taxon was considered present in given 1 km cell if there was any presence record from within that cell.

Sampling gear/methods were manually assessed. All records collected with gear/methods that are static, highly selective (e.g., grabs) were omitted by tagging all mobile gear/methods (trawl, dredge, and towed video) to be retained (i.e., those gear that take a sample most commensurate with a 1 km grid cell). The total number of sampling methods prior to filtering was 188, while the number retained for modelling was 163.[1] Taxonomic information was extracted and compared to WoRMS – (World Register of Marine Species) to check and, where applicable, correct nomenclature (Chamberlain and Vanhoorne 2023). Where possible, all genera level records for VME indicator taxa were retained, but unknown, unsure/missing, or higher-level classifications within 'genera' level spaces, were removed. The total number of genera prior to data grooming was 863. Following taxonomic filtering, and filtering for <10 unique location occurrences per genera (Stephenson et al. 2022), there were 182 genera remaining for modelling. In the final data grooming step, rows (i.e., unique locations, 1 km x 1 km grid cells) were removed if there were no presence records within them. Following removal of non-modelled taxa presences, an occurrence matrix (presence-absence) with 3,341 unique locations remained (7,205 instances of taxon presence), for 182 genera of VME indicator taxa. A breakdown of the number of genera included in the GF model for each VME indicator is shown in Table 3-1.

To estimate compositional turnover, GF models require an occurrence matrix of locations with presence-absence information. As in Stephenson et al. (2022) and Stephenson et al. (2020b), systematically collected absence records were not widely available across the study area or consistently available across sampling methods. Instead, where a taxon has not been recorded at the same site as another, it is assumed to be absent from that location. This approach is somewhat similar to the use of "target-group background" data (Phillips et al. 2009) for species distribution modelling i.e., grid cells within which any of the taxa not being modelled had been previously recorded as present (Stephenson et al. 2021b). Previous GF models produced for the New Zealand EEZ generated separate models for 'catchability' classes based on sampling gear (Stephenson et al. 2022). This approach was explored here, but it was determined that there were too few data to develop separate GF models in this manner. Instead, it is assumed that by retaining only data sampled using towed gears, different catchabilities are managed as best as possible given the data available at present. The distribution of records (sites or 'unique locations') for the GF modelled VME indicator taxa are shown in Figure 3-1. Accounting of the data, including numbers of unique sites with occurrence information in the

[1] *This total does not represent 163 distinct gear classes, instead, it represents unique labels for sampling methods, where minor changes to reporting style or cases (e.g., capital letters) are used, labels will be counted as separate sampling methods.*

Evaluated area, EEZs, and the entire study area is shown in Table 3-2 (counts also provided across 500 m depth intervals).

Table 3-1 | Number of genera included in gradient forest models for each VME indicator taxa, as well as the number of genera in the SPRFMO Evaluated Area within the dataset compiled for SC8-DW11.

VME indicator taxon	Number of genera modelled (EEZs and Evaluated Area)	Number genera in the SPRFMO Evaluated Area (SC8-DW11)
Actiniaria	7	17
Octocorallia (sea pens: 8, true soft corals: 7, sea fans: 17)	32	8 (soft corals); 38 (gorgonians); 10 (sea pens); 56 (total)
Antipatharia	8	20
Brisingida	4	6
Bryozoa	59	67
Crinoidea	10	22
Porifera (Demospongiae: 20; Hexactinellida: 13)	33	81 (total for Porifera)
Hydrozoa	17	30
Scleractinia	4	5
Stylasteridae	7	14
Zoantharia	1	3
Total	**182**	**321**

Table 3-2 | Number of unique locations (1 km x 1 km grid cells with occurrence records VME indicator presence information) in Exclusive Economic Zones (EEZs) and the SPRFMO Evaluated Area provided across depth intervals.

Depth (m) intervals	Number of unique locations (EEZs)	Number of unique locations in the SPRFMO Evaluated Area
200–500	821	17
500–1,000	1,277	89
1,000–1,500	784	114
1,500–2,000	137	8
2,000–2,500	55	2
2,500–3,000	35	2
Total	**3,109**	**232**

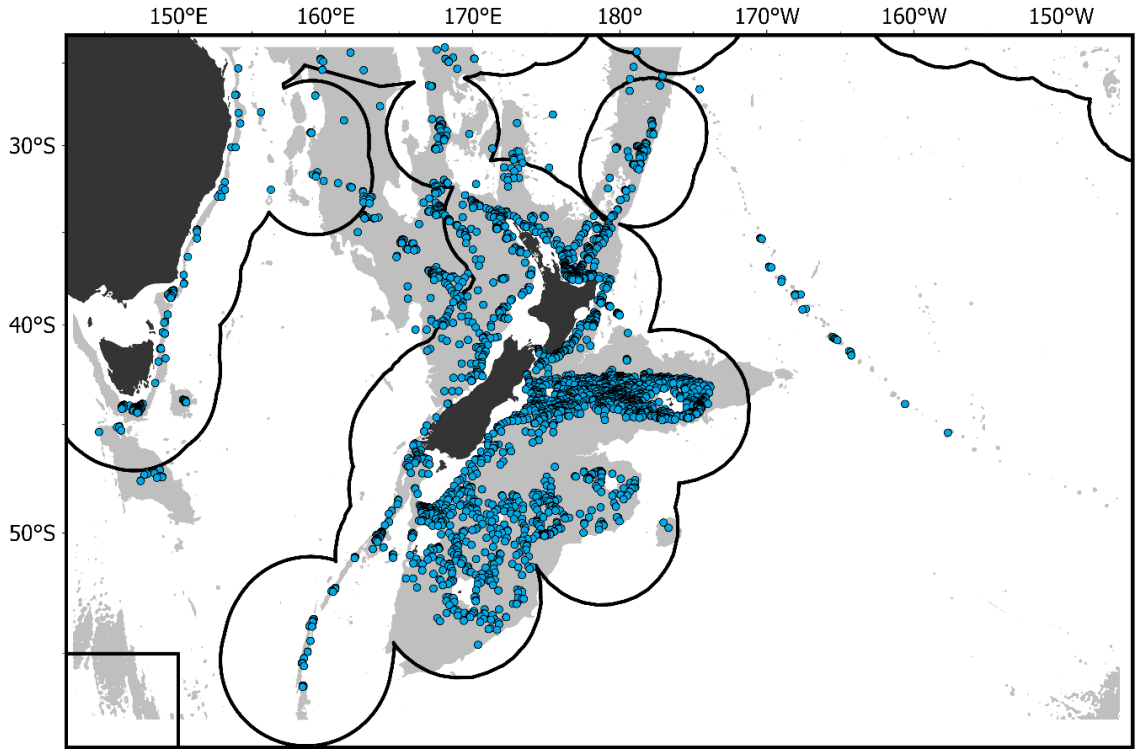

Figure 3-1 | Sites (blue points, 3,341 in total) that provided information of VME indicator taxa presence-absence for gradient forest model development. Black lines indicate the boundaries between the SPRFMO Evaluated Area and the multiple Exclusive Economic Zones (EEZs). Grey area shows the 'study area' bound between depths of 200 to 3,000 m.[2]

3.3 Environmental data

The environmental variable datasets used as predictors in the GF models are the same as those used previously for the habitat suitability models of VME indicator taxa. For further details, see open-access peer-reviewed publications from Stephenson et al. (2021b) and Bennion et al. (2024).

The environmental variables included in GF models were BPI-broad, slope SD, ruggedness, dissolved oxygen, aragonite saturation state at depth, temperature at depth, POC, depth, salinity, and silicate concentration (see Stephenson et al. 2021b for the ecological reasoning behind the selection of these variables). It should be noted that substrate variables (percent mud and gravel) were used in some initial GF models, however, they were removed from model development in the testing phase due to artifacts (e.g., large clusters of cells with the same value, which created erroneous spatial patterns) noticed in spatial predictions attributable to these layers. This removal is similar to past work, where for abundance models for some VME indicator taxa, the substrate variables were removed following the detection of artifacts in some of the spatial predictions (SC11-DW07_rev1). However, it should be noted that some of the included variables can act as coarse-scale proxies for substrate type; i.e., BPI-broad, slope SD, ruggedness (Georgian et al. 2019, Stephenson et al. 2021b).

[2] The term 'study area' refers to the model area which includes areas within the EEZs of several countries and areas in the high seas of the SPRFMO Evaluated Area between depths of 200–3,000 m.

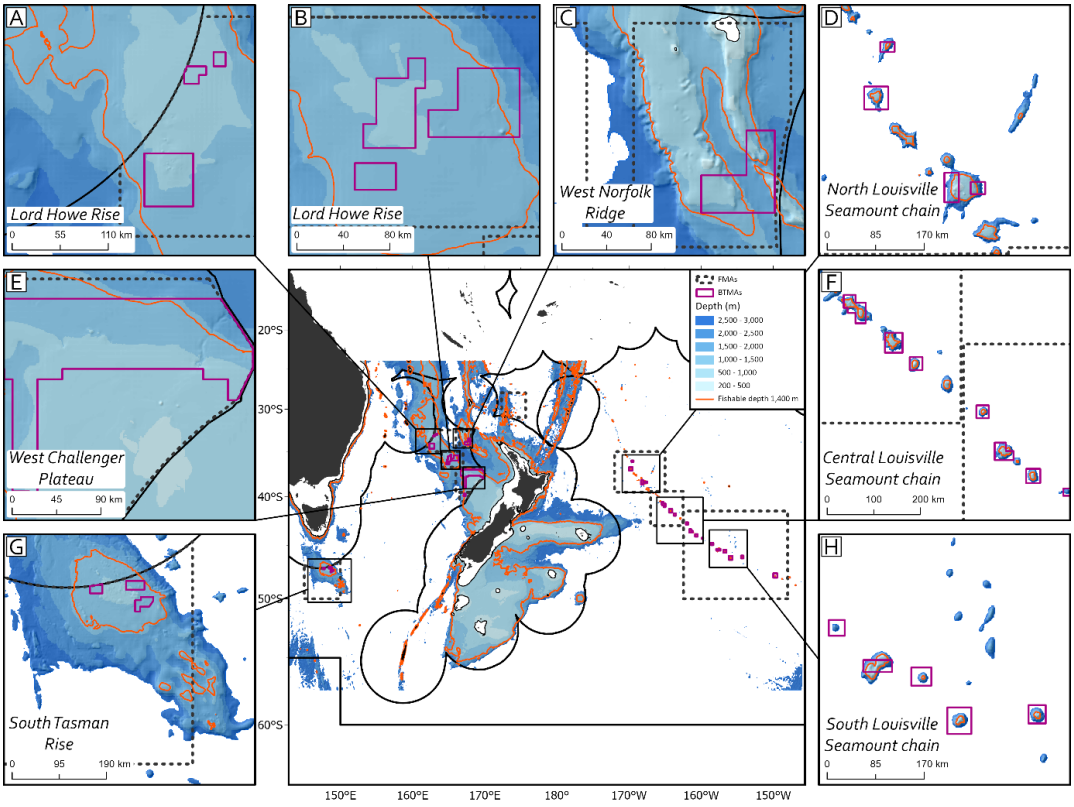

Figure 3-2 | Map of water depth (bathymetry) across the study area (200 m to 3,000 m). Depth is shown in metres (m), with hillshade relief. An orange contour line is used to show 'fishable depth' at 1,400 m (SC11-DW01). Black lines indicate the boundaries between the SPRFMO Evaluated Area and the multiple Exclusive Economic Zones (EEZs), dotted lines show Fishery Management Area (FMA) boundaries, and pink lines show Bottom Trawl Management Area (BTMA) boundaries. A thin black contour line is used to show 200 m depth (the minimum depth of the study area, seen as white areas on continental shelves).

3.4 Gradient forest modelling

Gradient forest modelling is an extension of the Random Forest (RF; Breiman 2001) approach, whereby the values of the tree-splits from the RF models for all taxon models with positive fits ($R^2_f > 0$) are aggregated to develop empirical distributions that represent taxa compositional turnover along each environmental gradient (Pitcher 2011, Ellis et al. 2012). The turnover function is measured in dimensionless R^2 units, where taxa with highly predictive random forest models (high R^2_f values) have greater influence on the turnover functions than those with low predictive power (lower R^2_f). The use of the dimensionless R^2 to quantify compositional turnover enables information from multiple taxa to be combined, even if that information comes from different sampling devices, surveys or regions (Ellis et al. 2012).[3]

In this study, gradient forest models were initially developed at two taxonomic resolutions: genus and VME indicator taxa level. Of these two resolutions, genus level data were considered more likely to produce bioregions with more general ecological relevance, while bioregionalisation from VME indicator taxa level data may be more directly relevant to understanding representativeness of the

[3] *The dimensionless R^2 used in GF models is not to be confused with the commonly employed R-squared (R^2) i.e., the coefficient of determination.*

spatial measures (because these were designed based partly on VME indicator taxa habitat suitability models). The R package *worrms* (Chamberlain and Vanhoorne 2023), which links to WoRMs, was used to check, and where required, update, nomenclature. The VME indicator taxa level GF models were fitted with 17 taxa at 11,428 unique locations. The genus level GF models were fitted with 182 genera at 3,341 unique locations, together with the 10 environmental variables discussed in the previous section.

GF models were applied using the R package *gradientforest* (Ellis et al. 2012) and follow closely the methods detailed in Pitcher (2011) and Stephenson et al. (2022). GF models were fitted with 250 trees and default settings for the correlation threshold (0.5) used in the conditional importance calculation of environmental variables. The GF model was bootstrapped (100 times), meaning that transformed environmental variables are means across said bootstraps. Therefore, uncertainty estimates (e.g., standard deviation, SD) could be developed too, if required. The bootstrapping process involved generating GF models for the 182 genera 100 times, with randomly sampled sites (with replacement) equal in number to the total number of sites (e.g., 3,341 for the genus level GF models). Additional estimates of uncertainty were produced in the form of 'environmental coverage', detailed below and discussed in SC papers SC10-DW05 and SC11-DW07_rev1, as well as Stephenson et al. (2021b).

The compositional turnover functions for each genus (shapes of the turnover curves) were used to transform the gridded environmental layers (1 km x 1 km grid), creating a "transformed environmental space" representing compositional turnover (Pitcher 2011, Ellis et al. 2012). From the 100 bootstrapped iterations, transformed environmental layers were used to produce mean compositional turnover (hereafter 'compositional turnover'). Compositional turnover was visualized using principal components analysis (PCA), and by mapping, using the colour scheme derived from their respective PCA analyses. Compositional turnover was then used to produce biotic groups via hierarchical clustering. Clustering in a hierarchical manner means that if clustering is carried out for e.g., 50 groups, but bioregions are selected at a 7–9 group level, the higher-level biotic group classifications are nested within the delineated bioregions. The mean spatial estimate of compositional turnover from the GF model (i.e., the bootstrapped GF model) was classified using a two-stage approach (Stephenson et al. 2020b) using the R package *cluster* (Maechler 2019). In the first stage, mean spatial estimates of compositional turnover were clustered to form 50 initial biotic groups using non-hierarchical, k-medoids clustering. For the second stage, a hierarchical clustering approach was employed via a flexible unweighted pair group method with arithmetic mean (UPGMA) using the Manhattan distance metric (Stephenson et al. 2018, Stephenson et al. 2022). This second classification step was undertaken at various levels of classification detail ranging from 3 to 50-group levels at increments of 1.

Following Stephenson et al. (2023), Analysis of Similarities (ANOSIM) was used to assess the within- and between-group variation depending on classification detail. The ANOSIM R value indicates whether the difference between groups (i.e., classes) is larger than within groups. Typically, low R values with fewer groups would be expected, as this means the variability within groups is larger than between them, with R increasing with increasing classification detail. The 'optimal' number of classes or groups for a bioregionalisation depends on a variety of factors, but ANOSIM can assist with this choice. For example, lowest number of classes with highest R can be deemed most useful (as per Stephenson et al. 2023). This approach echoes the elbow and BIC methods detailed in the sections regarding the k-means and RCP approaches above. Occurrence information (either VME indicator or

genus level occurrence matrix) was tagged with classification information. ANOSIM R was used to assess differences between clusters (from 3 classes to 50 classes with a step of 1). Drawing from the classification, in depth descriptions were produced for 7–9 class levels (hereafter 7–9 group bioregionalisations). Dendrograms were constructed to evaluate differences between the different bioregional groups.

3.5 Environmental coverage

Potential concentration of biological samples (i.e., occurrence records) in a given portion of the 'environmental space' (defined as the multidimensional space when considering each of the environmental variables as a dimension) is likely to result in high levels of confidence associated with the predicted results. On the other hand, predictions in areas of environmental space where occurrence sampling is low need to be carefully and cautiously interpreted. To account for the lack of biological data used to predict compositional turnover in some of the modelled areas, a measure of "coverage of environmental space" (Pinkerton et al. 2010, Smith et al. 2013, Stephenson et al. 2020a) (hereafter termed environmental coverage) was calculated, using the methodology outlined by Stephenson et al. (2021b). Briefly, VME indicator taxa occurrence data were used to inform variation in sampling density within the environmental space by combining all presence-data locations (i.e., unique grid cells with occurrence information) with the same number of randomly selected sample cells from the environmental space (where there were no biological samples). A boosted regression tree (BRT) model was used to model the relationship between these "present" (true) samples and "absent" (unsampled) samples for the 10 environmental variables used in the GF models. The predicted distribution of the coverage of the environmental space yield estimates between 0–1. Estimates of 0 indicate very low sampling of the environmental space, whereas estimates of 1 indicate a very high level of sampling.

3.6 Characterising the bioregions

Following interpretation of the classification dendrogram and ANOSIM results, descriptions were produced for the bioregionalisations. Descriptions were based on:

1) Summary statistics of the environmental conditions present in each of the bioregions (median, and interquartile range, i.e., IQR1 and IQR3).

2) Descriptive statistics of the percentage of habitat suitability (Stephenson et al. 2021b, Bennion et al. 2024) for VME indicator taxa contained within the bioregions.

3) Similarity Percentage (SIMPER) analysis to describe the contribution of modelled genera to within bioregion similarity and between bioregion dissimilarity.

Similarity percentages were calculated using the statistical software Primer-e v.7 (Clarke and Gorley 2006) based on the Bray-Curtis dissimilarity statistic. Percentage (%) contributions to within bioregion similarity are provided, as well as pairwise (%) comparisons of contributions to between group (i.e., bioregion) dissimilarity. SIMPER was run only for taxa with >20 unique locations to reduce the influence of genera with very few presences on interpretation of results. That is, rare or simply poorly sampled genera could disproportionately contribute to dissimilarity (e.g., if all the presences for one genus were present in one bioregion this one genus would contribute significantly to between group dissimilarity when in fact it may be poorly represented in the dataset). It should be noted that this could limit the influence that rare species have on the analyses. The occurrence matrix used to

generate the GF model was used for the analyses, however, after filtering for >20 unique locations, an occurrence matrix containing 108 genera and 3,273 unique locations was therefore used for the analyses at the genus level. A threshold of 60% contribution was used for the analyses. Reporting of within group similarity was restricted to genera that contributed ≥7% to similarity, whereas pairwise comparisons are only provided for the 7-group bioregionalisation and only the top 4 contributors to dissimilarity are shown. These reporting thresholds are arbitrary and used to reduce the quantity of information for the sake of parsimony.

Distribution maps of the bioregionalisations were produced, which allowed for a visual assessment of the bioregions within FMAs.[4] Furthermore, the area occupied by each bioregion within the study area (Figure 3-1) was calculated, as were fragmentation metrics. For fragmentation metric production, the R package *landscapemetrics* (Hesselbarth et al. 2019) was used to produce a variety of metrics that describe fragmentation e.g., number of fragmented bioregion patches and patch area (km^2), as well as calculation of the coefficient of variation of the Euclidean distance (nearest neighbour edge-to-edge) distance between patches. A comparison between the area of the individual bioregion patches and the area of FMAs was also made (i.e., to compare the scale of these two potential areas used for management assessment). For the 7-group bioregionalisation only, text descriptions of the bioregions were also produced. To develop these text descriptions, the relative importance of environmental variable contributions to the GF model was considered, with focus placed on depth and the top five variable contributors. This description method closely follows the approach detailed by Stephenson et al. (2023).

4. Results

Across 100 bootstraps, successful models were generated for all 182 genera. The proportion of out-of-bag variance explained was generally high for the genera included in the GF models, with a minimum R^2_f of 0.77 for *Schizosmittina* (Bryozoa) and a maximum R^2_f of 0.83 for *Cryptolaria* (Hydrozoa)[5]. Conditional importance of environmental variables (R^2 weighted importance) indicates the influence of each of the 10 environmental variables on the compositional turnover functions. Weighted importance of environmental variables ranged from 0.003 for seafloor ruggedness to 0.005 for salinity (Figure 4-1). Mean predicted compositional turnover in geographic and PCA space is shown in Figure 4-2.

Environmental coverage was high in shallower areas, for example on the Chatham Rise and Campbell plateau in New Zealand's EEZ and on the Norfolk Ridge, Challenger Plateau, and on seamounts along the Louisville Seamount Chain in the Evaluated Area (Figure 4-3). In contrast, environmental coverage was lower primarily in deeper areas (deeper than fishable depths, 1,400 m; as per SC11-DW01). For example, low coverage of the environmental space was estimated in the Bounty Trough (in New Zealand's EEZ) and in the deeper areas across the Louisville Seamount Chain, Norfolk Ridge, and South Tasman Rise (Figure 4-3).

[4] *All maps included in this paper were produced at a high pixel resolution. For greater detail the zoom function can be used, while image quality is maintained.*

[5] *Values are mean across bootstraps; overall mean variance explained was 80%.*

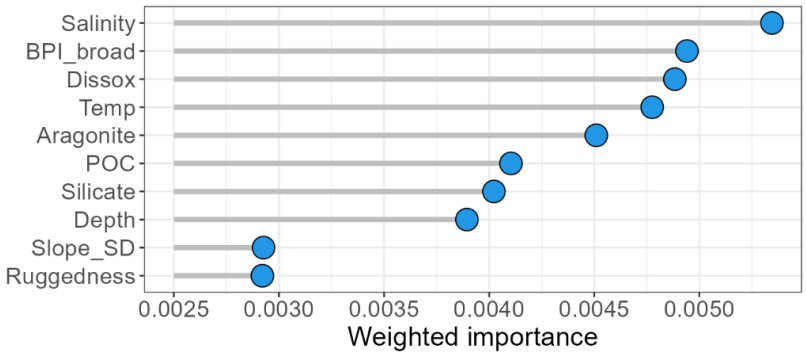

Figure 4-1 | Mean R^2 weighted importance across 100 bootstrapped gradient forest (GF) models of the 10 environmental variables used to generate the GF models. BPI: bathymetric position index-broad; Dissox: dissolved oxygen at depth; Temp: temperature at depth; POC: particulate organic carbon export to the seafloor; Slope SD: standard deviation of the slope.

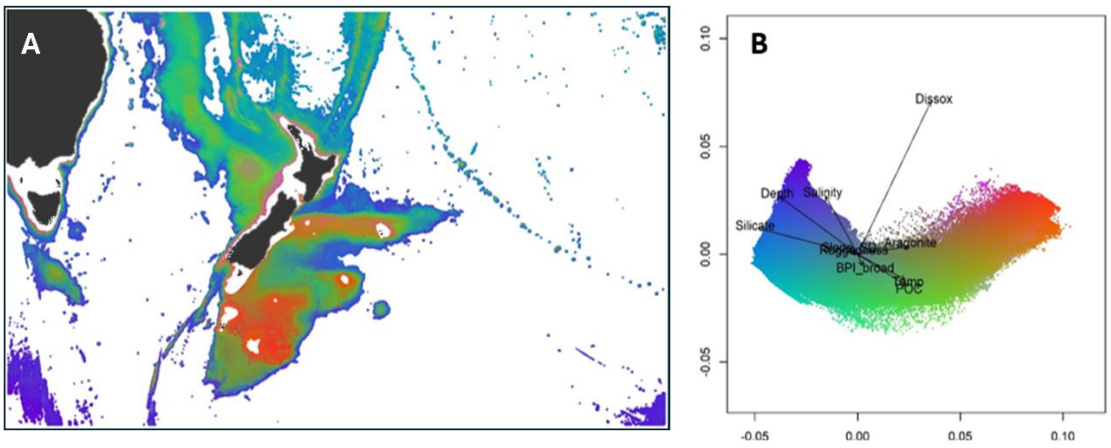

Figure 4-2 | Mean predicted taxa compositional turnover (across 100 bootstraps) in geographic (A) and principal components analysis (PCA) space (B) derived from gradient forest models. Colours are based on the first three axes of a PCA analysis so that similarities/differences in colour correspond broadly to similarities/differences in mean predicted compositional turnover. Vectors in the PCA space (B) indicate correlations for the environmental predictors.

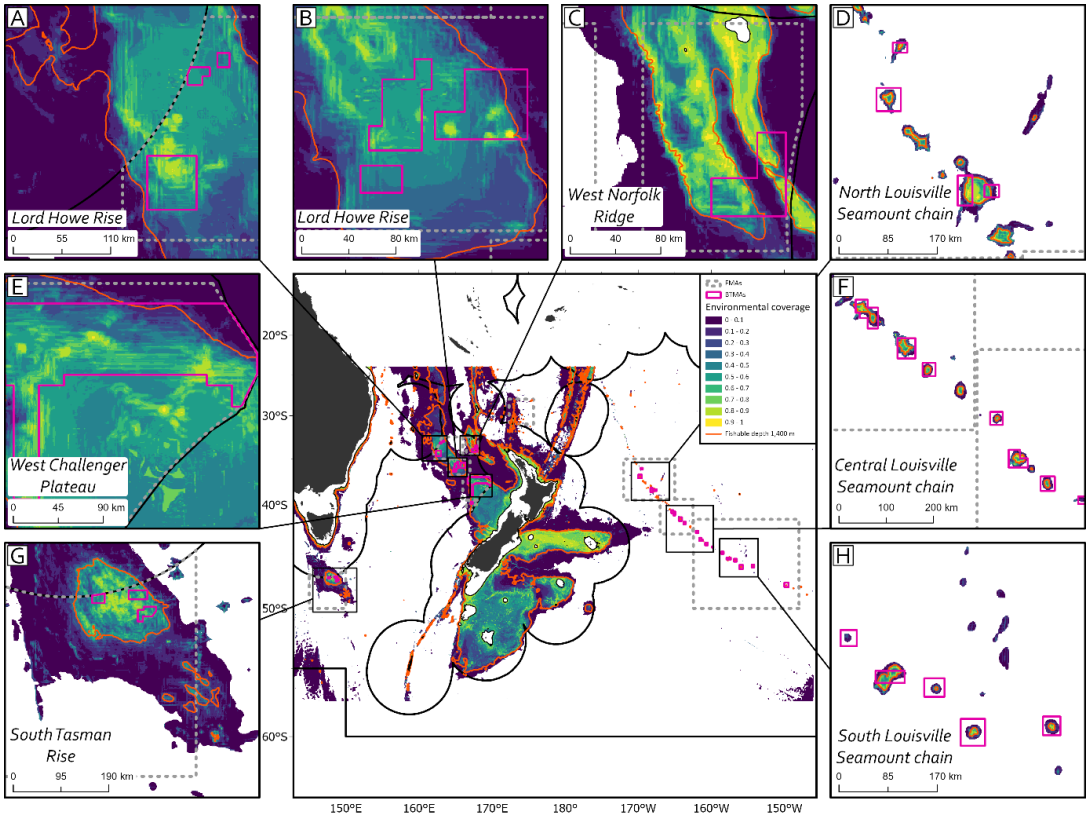

Figure 4-3 | Environmental coverage (0–1) between 200 and 3,000 m depth. Low values of environmental coverage (dark blue) indicate parts of the environmental space that contained few samples, meaning greater caution should be placed on the predictions in these areas. Environmental coverage is generated using the unique locations (sites) used to train the gradient forest models. An orange contour line is used to show 'fishable depth' at 1,400 m (SC11-DW01). Black lines indicate the boundaries between the SPRFMO Evaluated Area and the multiple Exclusive Economic Zones (EEZs), dotted lines show Fishery Management Area (FMA) boundaries, and pink lines show Bottom Trawl Management Area (BTMA) boundaries.

The hierarchical structure of the 7, 8, and 9-group bioregionalisations was visualised using hierarchical dendrograms showing bioregion similarity (Figure 4-4). Dendrograms represent the hierarchical structure of the classification, becoming more complex (more branches) as the number of classification groups increases. As such, they can not only be used to understand the structure of classification within any one group level, but also the sequentially changes in the structural distinction of the classification with increasing group level. For the 7-group bioregionalisation (Figure 4-4, A), bioregions 1, 2, and 3 were more similar than the other bioregions, while bioregions 4 and 5 are more similar to each other than the other bioregions, the same can be said for the bioregions (6 and 7) which were more similar than all other bioregions.

The 8-group bioregionalisation dendrogram was expectedly similar given the nested nature of the classification scheme used, with the 8th bioregion most similar to bioregion 7, branching at just over 0.1 similarity (Figure 4-4, B).

The 9-group bioregionalisation dendrogram splits in a different area, with the 9th bioregion added becoming bioregion 1. Bioregion 1 was most like bioregion 3, also branching at just over 0.1 similarity

(Figure 4-4, C). In general, very little bioregional distinction was added to the 7-group bioregionalisation by the 8- and 9-group bioregionalisations.

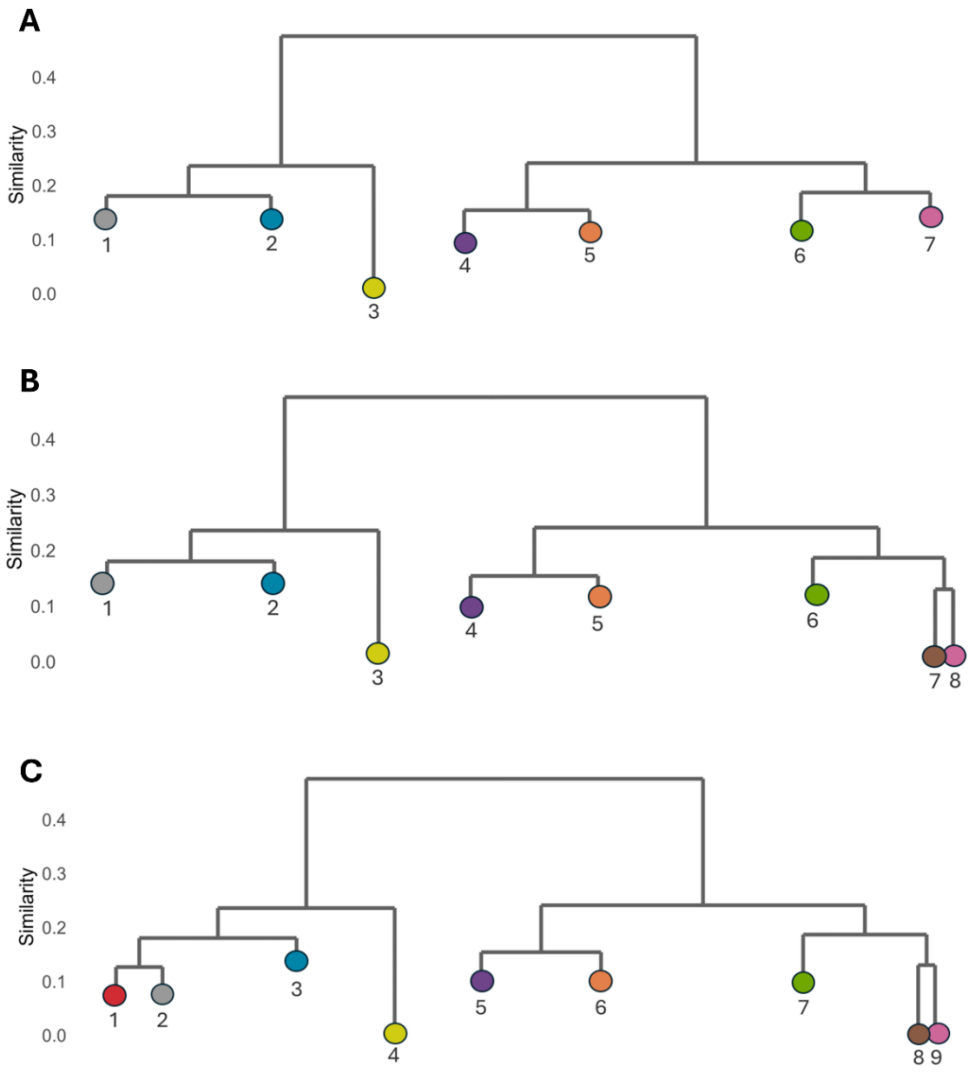

Figure 4-4 | Dendrogram (hierarchical tree) describing similarities (derived from the Manhattan distance metric) among the 7, 8, and 9-group bioregionalisations. Leaf colour for the 7-group (A) matched to Figure 4-, colour for the 8-group (B) matched to Figure 9-8, and colour matched to Figure 9-13, for the 9-group (C) bioregionalisation.

Global R values generally increased as the classification detail was increased (Figure 4-5).[6] The Global R values were higher for the VME indicator taxa level assessment compared to the genus-level ANOSIM. Nevertheless, the classification strength became more gradual once the number of

[6] *During testing phases, ANOSIM was also conducted at VME indicator taxa level occurrence matrix data. A decreasing R value was found as the classification detail was increased. A decreasing global R value with increasing numbers of classes is counter to what would be expected (Stephenson et al. 2022). Following tests, it was determined that the decreasing R value with increasing classes for the VME indicator level ANOSIM was attributable to the comparatively high number of Actiniaria records (62% of the unique locations in the occurrence matrix contained information for Actiniaria only).*

classification groups reached 9 groups. As already noted, when developing bioregionalisations, it is generally desirable to delineate a fewer number of bioregions, while maintaining classification strength. Therefore, the 7-group bioregionalisation was considered optimal. Nonetheless, descriptions were produced for 7, 8, and 9 group bioregionalisations, though emphasis was placed on the 7-group bioregionalisation in the main text. The 8- and 9-group bioregionalisations were described in the Annex in greater detail (Figure 9-8, onwards for the 9-group bioregionalisation and Figure 9-13 for the 9-group bioregionalisation). Furthermore, an example of a VME indicator taxa classification with a higher level of classification detail (28 classes) is shown in the Annex (Figure 9-18).

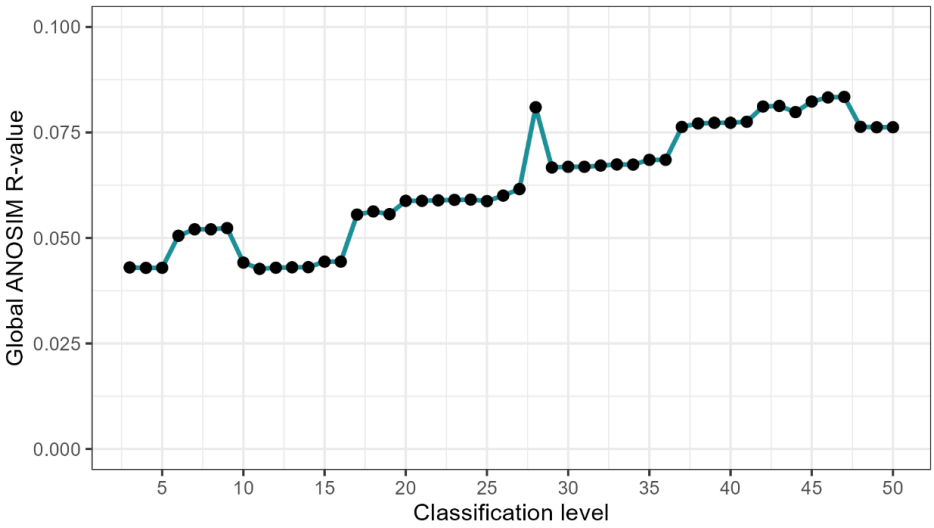

Figure 4-5 | Global ANOSIM R-value at varying levels of classification detail (3–50-group classification).

For the 7-group bioregionalisation, median and interquartile range values of environmental conditions within each bioregion are shown in Table 4-1. The highest values for aragonite saturation, POC export to the seafloor, salinity, and temperature at depth are present in bioregion 1 (Table 4-1). The highest ruggedness and slope SD was contained within bioregion 6, and the highest values for BPI-broad, and dissolved oxygen are contained within bioregion 7, while the deepest bioregion was bioregion 5 (with the highest silicate concentration also). The same descriptive statistics of environmental conditions within bioregions are provided for the 8 and 9-group bioregionalisations in the Annex. See Table 9-2 and Table 9-6. Bioregion text descriptions for the 7-group bioregionalisation are presented in Table 4-2.

Table 4-1 | Bioregion number (colour matched to Figure 4-), descriptions, and median and interquartile range (IQ range: 25–75 quantile) of environmental conditions for the 7-group bioregionalisation. Cell colours highlight the highest (orange) and lowest (green) median values for each environmental condition.

Bioregion	Aragonite saturation	BPI-broad	Depth	Dissolved oxygen	POC export to the seafloor
1	1.8 (1.7, 2)	1005 (223, 1249)	-515 (-750, -493)	4.5 (4.4, 4.6)	23.4 (19.8, 25.2)
2	1.5 (1.4, 1.6)	287 (217, 440)	-648 (-714, -586)	4.4 (4.4, 4.6)	22.9 (21.6, 24.2)
3	1.1 (1.1, 1.2)	437 (305, 620)	-1015 (-1109, -941)	4.2 (4.1, 4.3)	18.1 (16.8, 19)
4	0.9 (0.9, 1)	325 (147, 536)	-1440 (-1613, -1270)	3.8 (3.6, 4)	12.7 (11.4, 14.4)
5	0.8 (0.7, 0.8)	162 (-117, 536)	-2594 (-2834, -2246)	3.9 (3.5, 4.6)	5.5 (3.2, 7.2)
6	0.8 (0.7, 0.9)	3451.5 (3202, 3735)	-1586.5 (-2001.8, -1297)	3.6 (3.5, 3.9)	4.1 (1.8, 6.9)
7	1.4 (1.3, 1.5)	3759 (3485, 3996)	-778 (-927, -627)	5.2 (5, 5.5)	9.5 (1.5, 17.5)
Bioregion	**Ruggedness**	**Salinity**	**Silicate concentration**	**Slope SD**	**Temperature at depth**
1	0.00001 (0.0000002, 0.0003)	34.9 (34.8, 35.1)	9 (6.6, 9.7)	0.4 (0.1, 1.6)	10.5 (10.2, 12.1)
2	0.0000004 (0.0000001, 0.000002)	34.7 (34.6, 34.7)	14.3 (12.3, 16.4)	0.1 (0, 0.2)	8.8 (8.3, 9.3)
3	0.000002 (0.00000042, 0.00001)	34.5 (34.5, 34.5)	38 (30.7, 44.9)	0.1 (0.1, 0.3)	5.4 (4.9, 6.1)
4	0.000004 (0.0000007, 0.00003)	34.5 (34.5, 34.6)	75.9 (64.2, 85.3)	0.2 (0.1, 0.5)	3.4 (2.9, 4)
5	0.000032 (0.000006, 0.0002)	34.7 (34.7, 34.7)	112.5 (104.2, 121.2)	0.5 (0.2, 1.2)	1.9 (1.4, 2.2)
6	0.008 (0.004, 0.018)	34.6 (34.5, 34.7)	106.1 (84, 117.8)	6.6 (5.2, 8)	2.4 (2.1, 2.9)
7	0.0007 (0.0001, 0.0032)	34.4 (34.4, 34.4)	14.3 (10.8, 20.2)	2.7 (1.1, 5.3)	6.8 (6.2, 7.3)

Table 4-2 | Description of bioregions for the 7-group bioregionalisation (bioregion colour matched to Figure 4-). Text developed using the environmental contribution statistics in Table 4-1, while considering the variables which contributed more to the gradient forest models (Figure 4-1). Upper bathyal water depths: 300–800 m, lower bathyal water depths: 800–3,500 m.

Bioregion	Text description of the environmental conditions within bioregions
1	Upper bathyal water depths, characterized by relatively high salinity, temperature, dissolved oxygen, aragonite, and organic matter flux to the seafloor.
2	Upper bathyal water depths, characterized by relatively high salinity, temperature, dissolved oxygen, and organic matter flux to a relatively flat seafloor.
3	Lower bathyal water depths, characterized by relatively intermediate salinity and temperature, and relatively high organic matter flux to a relatively flat seafloor.
4	Lower bathyal water depths, characterized by relatively intermediate salinity and low temperature, and intermediate organic matter flux to a relatively flat seafloor.
5	Lower bathyal water depths, characterized by relatively intermediate salinity and very low temperature, low aragonite and high silicate, and relatively low organic matter flux to the seafloor.
6	Lower bathyal water depths, characterized by relatively intermediate salinity and low temperature, low oxygen, and relatively low organic matter flux to a relatively rugged seafloor with highly variable slope.
7	Upper bathyal water depths, characterized by relatively low salinity and intermediate temperature, high dissolved oxygen, and intermediate organic matter flux to a relatively rugged seafloor.

Percentage of habitat suitability for VME indicator taxa contained within the bioregions of the 7-group regionalisation is shown in Figure 4-6 for the Evaluated Area (area within the 'study area' excluding EEZs). The habitat suitability index (0–1) outputs from the habitat suitability models were transformed using the ROC cut-off (hereafter referred to ROC-linear transformed suitable habitat). This transformation was used to reflect relative abundance of VME indicator taxa, as per SC8-DW07 rev 1, in each bioregion. For most VME indicator taxa, the majority of ROC-linear transformed suitable habitat was contained within bioregion 5 (the largest bioregion), however, for the stony coral taxa, the amount was more variable across other bioregions. For instance, 100% of ROC-linear transformed suitable habitat for *Goniocorella dumosa* was contained within bioregion 7, almost 50% of ROC-linear transformed suitable habitat for *Solenosmilia variabilis* was contained within bioregions 6 and 7, while >70% of ROC-linear transformed suitable habitat for *Enallopsammia rostrata* contained within bioregion 3. ROC-linear transformed suitable habitat for all VME indicator taxa was summed within bioregions, and the percentage contribution of each VME indicator taxon is also shown in Figure 4-6. Hydrozoa and Bryozoa contribute ~10% of ROC-linear transformed suitable habitat to most of the bioregions, while other VME indicators, like Stylasteridae contribute ~10% ROC-linear transformed suitable habitat to the sum value in bioregions 6 and 7. Actiniaria contributed surprisingly little ROC-linear transformed suitable habitat to the sum value in bioregions. Following interrogation of the datasets this result was found to be attributed to the ROC-linear transformation of the raw habitat suitability values, where most of the suitable habitat in the Evaluated Area fell below the ROC cut-off and was therefore zero value (i.e., HSI = 0). The same statistics produced for the 8 and 9-group bioregionalisations are shown in the Annex (Figure 9-7 and Figure 9-12).

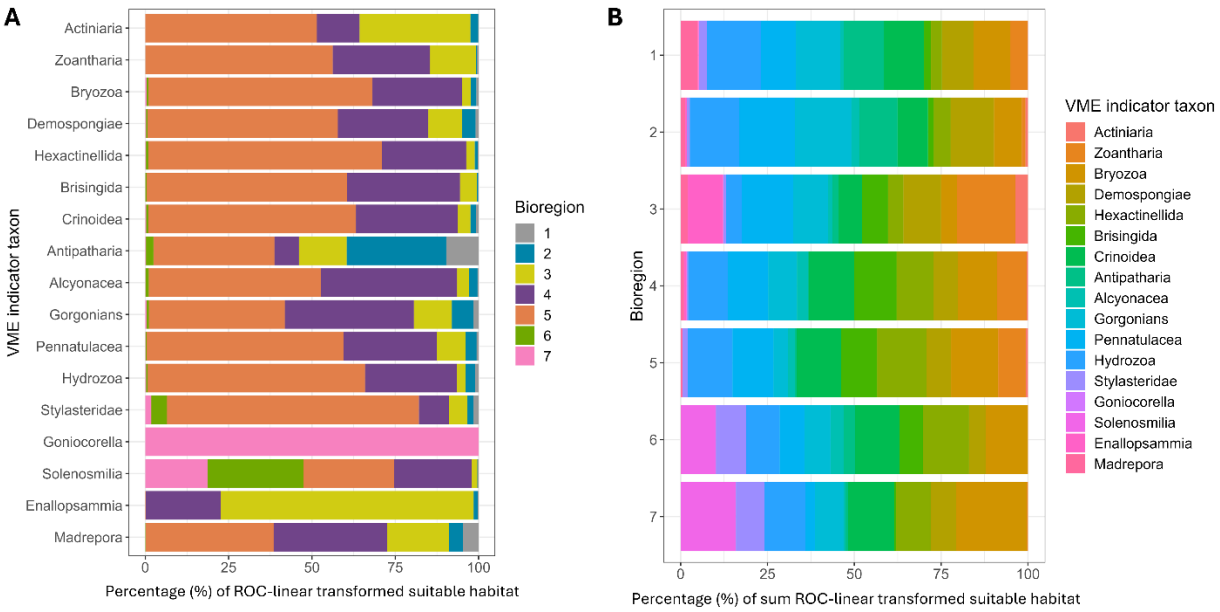

Figure 4-6 | Stacked bar charts show the percentage (%) of ROC-linear transformed suitable habitat for VME indicator taxa in bioregions for the 7-group bioregionalisation. A) Shows the percentage of ROC-linear transformed suitable habitat for each VME indicator contained within each bioregion (each bar represents 100% ROC-linear transformed suitable habitat for each VME indicator). Colours are matched to Figure 4-. B) shows the percentage (%) contribution of each VME indicator to the sum of ROC-linear transformed suitable habitat within each bioregion (each bar represents 100% of the summed ROC-linear transformed suitable habitat for all VME indicator taxa). Note: values in these charts were calculated for the SPRFMO Evaluated Area only**.**

Finally, bioregions are described with ecological information derived from the SIMPER analysis. Within bioregion similarity percentages indicate how similar the assemblages of VME genera are within bioregions, as well as the percentage contribution of each genus to within bioregion similarity (Table 4-3). Within bioregion similarity percentages were relatively low (<10%, for all bioregions 1-7), which is as expected given the high-level of classification (i.e., low level of classification detail). Higher within bioregion similarities (%) would be expected as the classification detail increases, this is because classification detail would increase within group homogeneity. For bioregionalisations, which are typically high-level, the SIMPER analysis is therefore more useful for providing an insight into the fauna that contribute to within group similarity. For example, for bioregion 2 *Hyalascus* (Hexactinellida), contributes 66% to the observed within bioregion similarity, whereas for bioregion 6 *Solenosmilia variabilis* (Scleractinia) contributes 83% to observed within bioregion similarity. For other bioregions, taxa representing multiple genera contributed to the majority of the within bioregion similarity.

Pairwise comparisons of dissimilarity between bioregions are shown in Table 4-4. Dissimilarity percentages were high for all between bioregion comparisons (>90%). As above, lower between group dissimilarities (%) would be expected as the classification detail increases, this is because classification detail would increase between group heterogeneity. For bioregionalisations, which are typically high-level, the SIMPER analysis is therefore more useful for providing an insight into the fauna that contribute to between group dissimilarity. Average dissimilarity was highest between bioregions 1 and 6, and lowest between bioregions 4 and 6. No single taxon contributed more than 13% to between

bioregion dissimilarity. For example, *Solenosmilia* (Scleractinia) and *Conopora* (Stylasteridae) contributed the most to the between bioregion dissimilarity for bioregions 1 and 6, 11% and 4% respectively). While *Hyalascus* (Hexactinellida) and *Goniocorella* (Scleractinia) contributed the most to between bioregion dissimilarity for bioregions 1 and 2, at 10% and 6% respectively. SIMPER analyses were carried out at the genus and VME indicator level, and for bioregionalisations at the 7, 8 and 9 group levels. See Table 9-1 and Table 9-5 in the Annex.[7]

Table 4-3 | Within group similarity Percentage (SIMPER) results for the 7-group bioregionalisation. SIMPER was calculated using genus-level information. Bioregions (colours matched to Figure 4-), average percentage similarity (within bioregions), and the top VME indicator contributors to similarity (arbitrary ≥6% cut-off used for reporting) are shown. Refer to Table 2-1 for taxon code detail.

Bioregion	Average similarity (%)	Top VME indicator contributors to similarity (≥6%)
1	3.98	*Epizoanthus* (ZAH; 16%); *Anthoptilum* (PTU; 15%); *Conopora* (COR; 13%); *Lytocarpia* (HDR; 8%); *Goniocorella* (GDU; 8%)
2	8.13	*Hyalascus* (HEX; 66%)
3	3.83	*Epizoanthus* (ZAH; 20%); *Solenosmilia* (SVA; 20%); *Keratoisis* (ALCY; 9%); *Enallopsammia* (ERO; 9%)
4	4.67	*Solenosmilia* (SVA; 46%); *Keratoisis* (ALCY; 8%); *Anthomastus* (ALCY; 6%)
5	2.89	*Umbellula* (PTU; 22%); *Keratoisis* (ALCY; 13%); *Farrea* (HEX; 13%); *Epizoanthus* (ZAH; 8%)
6	8.27	*Solenosmilia* (SVA; 83%)
7	7.93	*Keratoisis* (ALCY; 22%); *Symplectoscyphus* (HDR; 9%); *Acryptolaria* (HDR; 8%); *Solenosmilia* (SVA; 8%); *Chiastosella* (COZ; 7%); *Escharella* (COZ; 7%)

[7] *More than 100 genera were included in the SIMPER analyses; community dissimilarity is therefore comprised of contributions of all taxa included. Variability among taxa that contribute comparatively little to dissimilarity (e.g., <1%) will comprise a lot of missing detail. Therefore, caution should be taken when interpreting the results of SIMPER herein where focus has been placed on the top-contributors to dissimilarity only.*

Table 4-4 | Between group similarity Percentage (SIMPER) results for the 7-group bioregionalisation. SIMPER was calculated using genus-level information. Bioregions, average percentage dissimilarity (pairwise between bioregions), and the top VME indicator contributors to similarity (arbitrary top four contributors cut-off used for reporting) are shown. Refer to Table 2-1 for taxon code detail.

Comparison	Average dissimilarity (%)	Top four VME indicator contributors to dissimilarity (%)
1 & 2	98.07	*Hyalascus* (HEX; 10%); *Goniocorella* (GDU; 6%); *Epizoanthus* (ZAH; 4%); *Lytocarpia* (HDR; 4%)
1 & 3	97.83	*Epizoanthus* (ZAH; 6%); *Conopora* (COR; 4%); *Anthoptilum* (PTU; 4%); *Solenosmilia* (SVA; 4%)
2 &3	97.71	*Hyalascus* (HEX; 11%); *Goniocorella* (GDU; 5%); *Epizoanthus* (ZAH; 4%); *Solenosmilia* (SVA; 4%)
1 & 4	98.27	*Solenosmilia* (SVA; 6%); *Epizoanthus* (ZAH; 4%); *Anthoptilum* (PTU; 4%); *Conopora* (COR; 3%)
2 & 4	98.66	*Hyalascus* (HEX; 9%); *Solenosmilia* (SVA; 6%); *Goniocorella* (GDU; 4%); *Suberites* (DEM; 4%)
3 & 4	96.41	*Solenosmilia* (SVA; 8%); *Keratoisis* (ALCY; 5%); *Epizoanthus* (ZAH; 5%); *Enallopsammia* (ERO; 3%)
1 & 5	98.17	*Epizoanthus* (ZAH; 5%); *Anthoptilum* (PTU; 4%); *Conopora* (COR; 4%); *Umbellula* (PTU; 4%)
2 & 5	98.7	*Hyalascus* (HEX; 10%); *Goniocorella* (GDU; 4%); *Suberites* (DEM; 4%); *Umbellula* (PTU; 4%)
3 & 5	97.53	*Epizoanthus* (ZAH; 5%); *Solenosmilia* (SVA; 5%); *Keratoisis* (ALCY; 5%); *Umbellula* (PTU; 4%)
4 & 5	97.06	*Solenosmilia* (SVA; 7%); *Keratoisis* (ALCY; 5%); *Farrea* (HEX; 4%); *Umbellula* (PTU; 3%)
1 & 6	98.22	*Solenosmilia* (SVA; 11%); *Conopora* (COR; 4%); *Bathypathes* (COB; 4%); *Epizoanthus* (ZAH; 4%)
2 & 6	98.72	*Solenosmilia* (SVA; 12%); *Hyalascus* (HEX; 8%); *Goniocorella* (GDU; 4%); *Bathypathes* (4%)
3 & 6	96.1	*Solenosmilia* (SVA; 13%); *Bathypathes* (COB; 4%); *Epizoanthus* (ZAH; 4%); *Narella* (GOC; 3%)
4 & 6	93.96	*Solenosmilia* (SVA; 13%); *Bathypathes* (COB; 4%); *Narella* (GOC; 3%); *Acryptolaria* (HDR; 3%)
5 & 6	96.98	*Solenosmilia* (SVA; 12%); *Bathypathes* (COB; 5%); *Narella* (GOC; 4%); *Acryptolaria* (HDR; 4%)
1 & 7	97.88	*Keratoisis* (ALCY; 7%); *Solenosmilia* (SVA; 5%); *Acryptolaria* (HDR; 5%); *Symplectoscyphus* (HDR; 5%)
2 & 7	97.92	*Hyalascus* (HEX; 7%); *Keratoisis* (ALCY; 7%); *Goniocorella* (GDU; 5%); *Solenosmilia* (SVA; 5%)
3 & 7	96.63	*Keratoisis* (ALCY; 8%); *Solenosmilia* (SVA; 7%); *Acryptolaria* (HDR; 5%); *Symplectoscyphus* (HDR; 4%)
4 & 7	95.63	*Solenosmilia* (SVA; 7%); *Keratoisis* (ALCY; 7%); *Acryptolaria* (HDR; 5%); *Symplectoscyphus* (HDR; 4%)
5 & 7	97.11	*Keratoisis* (ALCY; 8%); *Solenosmilia* (SVA; 6%); *Acryptolaria* (HDR; 5%); *Symplectoscyphus* (HDR; 5%)
6 & 7	94.37	*Solenosmilia* (SVA; 10%); *Keratoisis* (ALCY; 6%); *Acryptolaria* (HDR; 5%); *Errina* (COR; 5%)

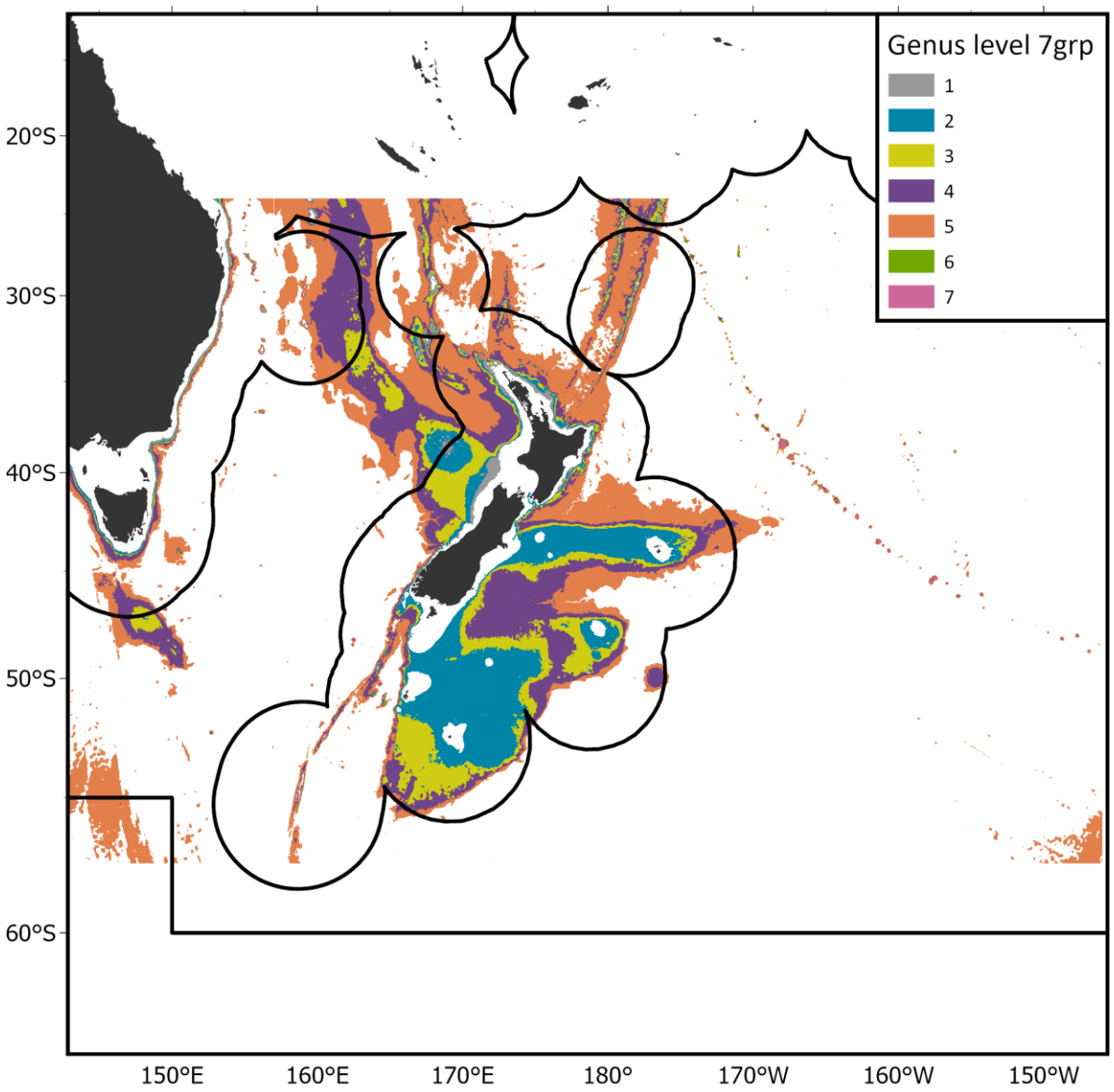

Figure 4-7 | Geographic distribution of the 7-group bioregionalisation derived from the bootstrapped gradient forest model fitted with genus-level VME indicator occurrence information. Black lines indicate the boundaries between the SPRFMO Evaluated Area and the multiple Exclusive Economic Zones (EEZs). A thin black contour line is used to show 200 m depth (the minimum depth of the study area, seen as white areas on continental shelves).

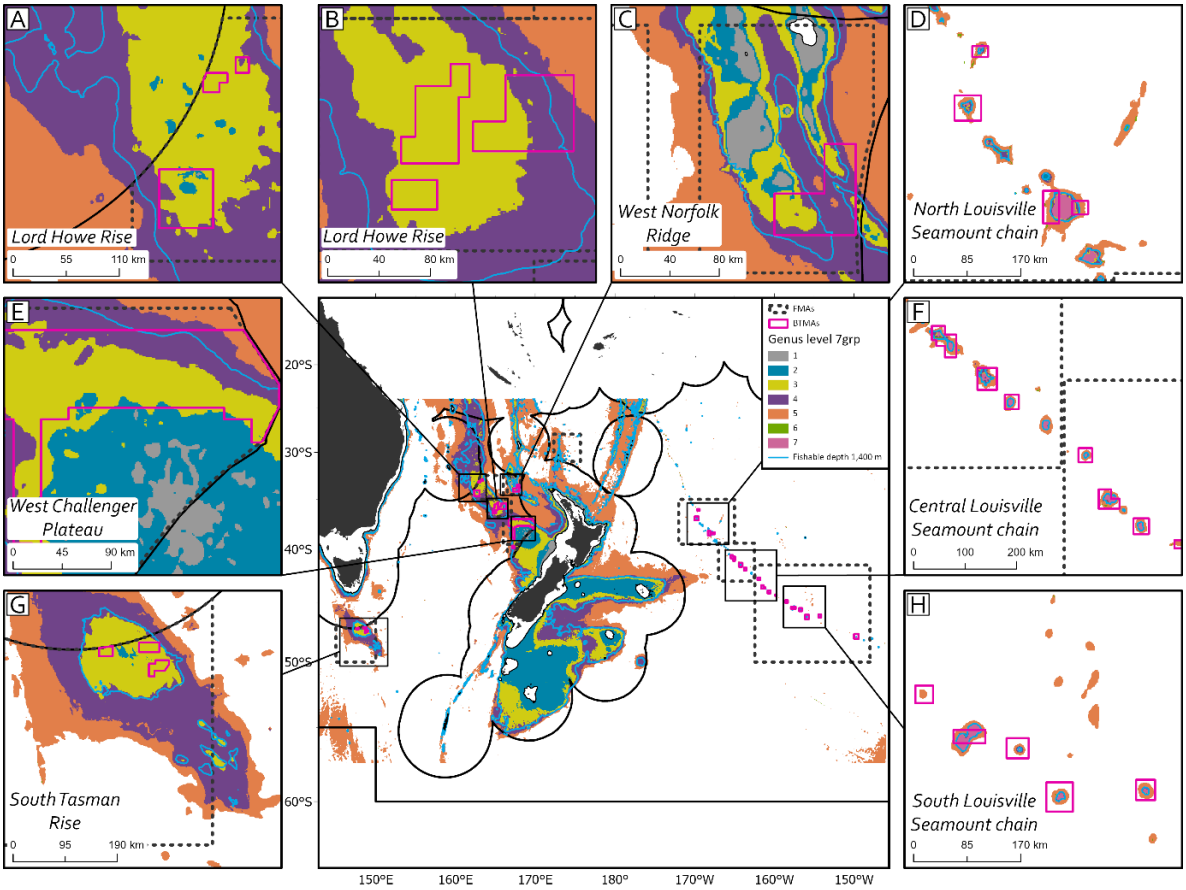

Figure 4-8 | Geographic distribution of the 7-group bioregionalisation derived from the bootstrapped gradient forest model fitted with genus-level VME indicator occurrence information. Black lines indicate the boundaries between the SPRFMO Evaluated Area and the multiple Exclusive Economic Zones (EEZs), dotted lines show Fishery Management Area (FMA) boundaries, and pink lines show Bottom Trawl Management Area (BTMA) boundaries. A thin black contour line is used to show 200 m depth (the minimum depth of the study area, seen as white areas on continental shelves).

The 7-group bioregionalisation is shown in Figure 4-7 and Figure 4-8. Bioregion 1 can be seen in shallower areas; for example, on the Challenger Plateau and West Norfolk Ridge (Figure 4-8); bioregion 2 was also shallow, occurring primarily within New Zealand's EEZ on the top of plateaus; bioregion 3 follows continental shelf boundaries; bioregions 4 and 5 occur throughout deeper waters of the study area, while bioregions 6 and 7 were associated with elevated topography, including seamounts (Figure 4-8). Maps in the same format as Figure 4-8 are shown for the 8 and 9-group bioregionalisations in the Annex (Figure 9-8 and Figure 9-13). Also shown in the Annex are 'close up' maps showing bioregions (7, 8 and 9- group levels) in each FMA (7-group: Figure 9-5 and Figure 9-6, 8-group: Figure 9-10 and Figure 9-11, 9-group: Figure 9-15 and Figure 9-16).

Further descriptive statistics for the 7-group bioregionalisation, including area of the bioregions and patches of bioregions, as well as fragmentation metrics, are summarized in Table 4-5 and Table 4-6. Bioregion 5 was the largest in area, while bioregion 7 was the smallest. While 58% and 67% of the area of bioregions 6 and 7 are contained within the Evaluated Area, <10% of bioregions 1 and 2 are contained within the Evaluated Area portion of the study area (see Table 4-5 for further details).

Fragmentation information is shown in Table 4-6, showing that some bioregions are more fragmented than others. For instance, there were >1,000 patches of bioregions 4 and 5 (though it should be noted that these were also the largest bioregions), while there were 134 patches of bioregion 7. The size (log transformed area km^2) of bioregion patches is summarised using boxplots (Figure 4-9), highlighting the variability of patch size for different bioregions. For example, there was greater bioregion patch size and variation for bioregions 2–5 compared to bioregions 1, 6, and 7 (Figure 4-9). Coefficient of variation of Euclidean distance between patches (Table 4-6) provide an estimate of patch-patch distance variability. The greatest Euclidean distance CV was obtained for bioregion 3 (405.8) while the lowest was for bioregion 5 (194.6). The same metrics are provided in the Annex for the 8-group and 9-group bioregionalisations (8-group: Table 9-3, Table 9-4, and Figure 9-9; 9-group: Table 9-7, Table 9-8 and Figure 9-14).

Table 4-5 | Area metrics for the 7-group bioregionalisation (colour matched to Figure 4-). Area (km^2) of each bioregion is shown within Exclusive Economic Zones (EEZs), the SPRFMO Evaluated Area, and the entire study area (total). The percentage of the area contained within the Evaluated Area is also shown.

Bioregion	EEZs	Evaluated Area	Entire study area	Percentage (%) in Evaluated Area
1	71,167	7,003	78,170	9.0
2	689,378	25,483	714,861	3.6
3	531,743	88,269	620,012	14.2
4	869,955	238,783	1,108,738	21.5
5	1,395,930	517,737	1,913,667	27.1
6	2,144	4,290	6,434	66.7
7	2,546	3,565	6,111	58.3

Table 4-6 | Patch and fragmentation metrics for the 7-group bioregionalisation (colour matched to Figure 4-). The total bioregion area (km^2) is shown as well as the number of geographically separated patches for each bioregion, the mean and standard deviation (SD) of patch area, and the coefficient of variation (CV) of the Euclidean distance between patches.

Bioregion	Total bioregion area (km^2)	No. of patches	Mean patch area (km^2)	SD patch area (km^2)	Euclidean distance CV*
1	78,170	496	157.6	1,540.8	278.5
2	714,861	799	894.7	20,723.7	248.9
3	620,012	876	707.8	10,577.6	405.8
4	1,108,738	1,016	1,091.3	17,059.1	285.8
5	1,913,667	1,248	1,533.4	32,485.8	194.6
6	6,434	486	13.2	28.7	223.0
7	6,111	134	45.6	122.4	267.8

**Coefficient of variation of Euclidean nearest-neighbour distance (edge-to-edge).*

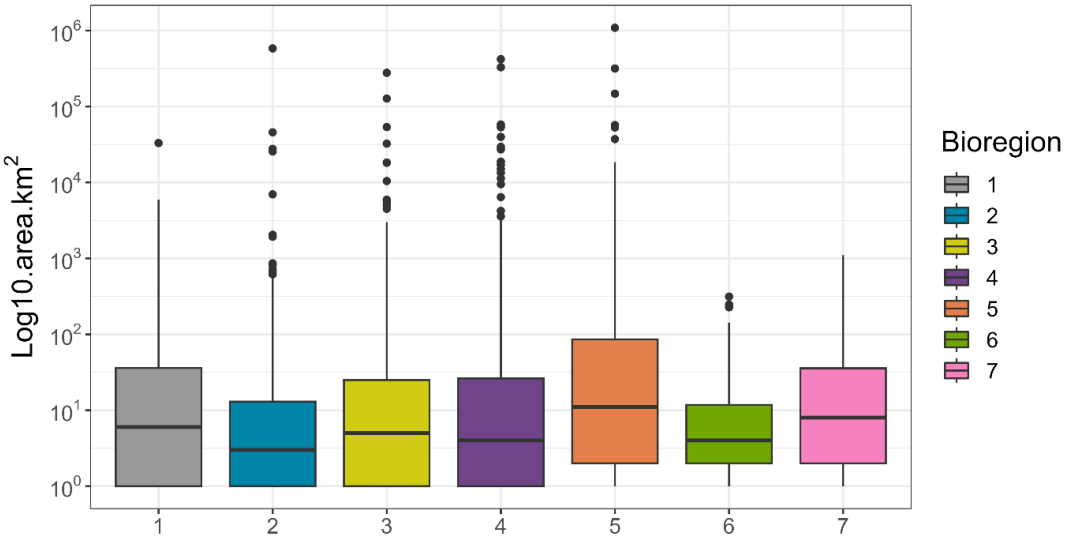

Figure 4-9 | Boxplot shows the area (km^2 log transformed) of each patch for each bioregion in the 7-group bioregionalisation. Each box shows the interquartile range, horizontal lines show the median, whiskers show the min -max (e.g., Q1 – 1.5*IQR), and dots indicate outliers. Box colour is matched to Figure 4-.

In 2023, the SC agreed that "*although the appropriate scale to assess and manage impacts on VMEs has not been defined in SPRFMO, the smaller scale of the Fishery Management Areas is likely to be a more biologically appropriate scale at which to assess and manage these impacts than larger scales*" (para 73 of SC8 Report). We therefore compared the spatial scale of bioregions for the 7-group bioregionalisation was compared to FMA scale by constructing boxplots of the spatial extent of groups within the 7-group bioregionalisation and FMAs (in km^2). Two versions were produced, the first based on EEZs and Evaluated Area (entire study area), and the second including the Evaluated Area only. Across the entire study area, the bioregions were highly variable in size and many times larger than the FMAs (Table 4-7); however, when the Evaluated Area only was considered, the scale was more similar, and even more similar when the extent of FMAs was reduced to the depth range of the study area (i.e., maximum depth of 3000 m; Figure 4-10; see also Table 4-7). The same comparisons are shown for the 8 and 9-group bioregionalisations in the Annex (Figure 9-17).

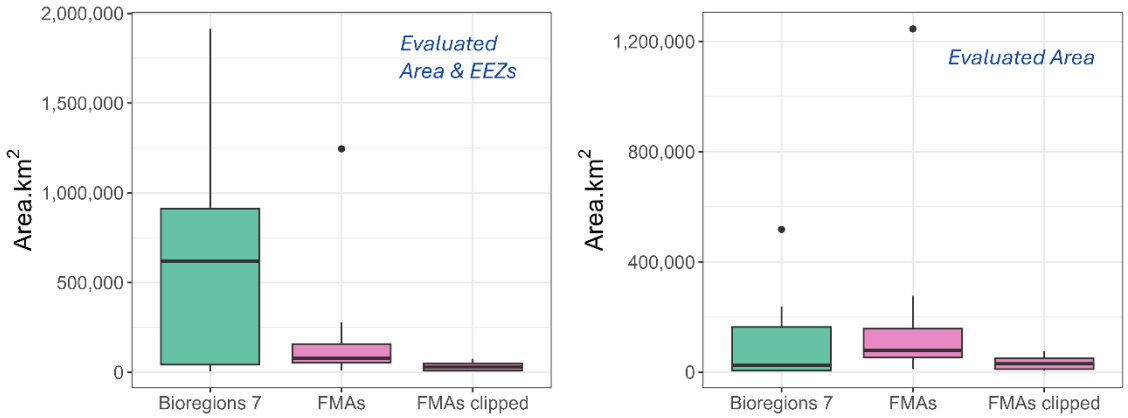

Figure 4-10 | Area (km^2) of bioregions for the 7-group bioregionalisation is compared to the area of FMAs. On the x-axis, 'FMAs' refers to the full extent of the FMAs, whereas 'FMAs clipped' refers to the extent of the FMAs clipped to the maximum depth of the study area; 3000 m. The boxplot on the left shows the total area of the bioregions across the entire study area (SPRFMO Evaluated Area and Exclusive Economic Zones (EEZs) compared to Fishery Management Areas (FMAs). The boxplot on the right shows the area of each bioregion in the Evaluated Area only, compared to the area of FMAs.

Table 4-7 | Area (to nearest km^2) of each Fishery Management Area and bioregion for the 7-group bioregionalisation (colour matched to Figure 4-). Areas for FMAs are presented including and excluding Bottom Trawl Management Areas (BTMAs), while areas for bioregions are presented within Exclusive Economic Zones (EEZs) and the Evaluated Area only.

FMA	Area	Area excluding BTMA		Bioregion	EEZs	Evaluated Area
West Norfolk	27,134	23,898		1	71,167	7,003
North Lord Howe	74,689	70,649		2	689,378	25,483
Central Lord Howe	45,612	38,469		3	531,743	88,269
NW Challenger	78,220	54,474		4	869,955	238,783
North Louisville	277,338	273,351		5	1,395,930	517,737
Central Louisville	151,578	147,326		6	2,144	4,290
South Tasman Rise	159,597	157,837		7	2,546	3,565
South Louisville	1,245,375	1,233,964				
Westpac Bank	11,060	10,404				

5. Discussion

The availability of ecologically relevant bioregionalisations provide a variety of opportunities for management and conservation of marine biodiversity, given that representativeness of habitat type or bioregion is a primary design criterion for designing effective marine protected areas (Grorud-Colvert et al. 2021). For example, ensuring that there is adequate spatial protection within each bioregion can help increase the likelihood that spatial management measures protect the full range of different groups and distinct assemblages of VME indicator taxa. Additionally, protecting an adequate proportion of all bioregions can help manage the uncertainty associated with information

on the distribution of VME indicator taxa (Foster et al. 2017). This is particularly important when the distributions of these taxa are inferred from models predicting the distribution of suitable habitat, and which underpin the design of the spatial management measures in the SPRFMO Evaluated Area.

5.1 VME indicator taxa-specific bioregionalisation

Various bioregionalisation approaches were explored for this study. Analysis indicated that the gradient forest (GF) model approach was most suitable for this project, not only due to the promising results from initial model tests, but also because of the hierarchical nature of the classification procedure. That is, where higher level of classification detail is nested within the bioregions, it could be useful for future applications. For example, a higher group classification could be used to represent 'VME communities' nested within 'VME bioregions', as per the New Zealand Seafloor Community Classification and Bioregions (Stephenson et al. 2022, Stephenson et al. 2023). An example of a higher 28-group classification from the analysis presented here, that could be used to represent 'VME communities' within the 7-group 'VME bioregions', is provided in the Annex (Figure 9-18). While the VME bioregions produced here represent a more ecologically relevant large spatial scale than FMAs, higher group classifications, such as that developed for 'VME communities' here, could be used in addition to assess the performance of the spatial management measures to prevent SAIs to VMEs (i.e., in a multi-spatial scale assessment process; SC12 DWXX).

The GF models were also tested at different taxonomic levels (VME indicator level i.e., as per Table 2-1, and genus level). GF models developed with genus level data were deemed to be more robust, given that compositional turnover would not be derived from a mixture of taxonomic resolutions, i.e., some VME indicators are at phyla level like Bryozoa, while separate turnover functions would be derived for each coral taxon, represented at species to order level. Furthermore, during development of this work concerns were raised about the influence of the comparatively high number of sites containing Actiniaria records only when models were run at VME indicator level, and the repercussions this could have during bootstrapping procedures. The SIMPER analysis also highlighted the impact of Actiniaria on the production of a VME indicator level bioregionalisation, whereby Actiniaria was the key contributor to within group similarity and between group dissimilarity for many of the bioregions. Therefore, a GF model, using genus level occurrence information was the final selected modelling approach.

The results from the ANOSIM analysis primarily guided the selection of the appropriate classification detail of the model to denote VME specific bioregions. While it is often suggested that the lowest number of groups for the highest classification detail is preferrable (Stephenson et al. 2023), descriptions and maps were produced for bioregion group levels 7 to 9. Producing this information provided the opportunity to carry out an informed assessment of the bioregionalisations and consider what level of detail might be most useful. Several facets of the larger number bioregionalisations were considered with respect to finally choosing the 7-group bioregionalisation. Firstly, the relatedness of 'extra' bioregions was considered via examination of classification dendrograms indicating similarities, whereby additional bioregions were found not to be particularly dissimilar. Furthermore, the small area of 'extra' delineated bioregions in the 8- and 9-group bioregionalisations (e.g., bioregion 6 is relatively small ~2,000 km^2, but is comprised of 385 fragmented patches) and their similarity in environmental conditions is inconsistent with the general concept of bioregions, i.e., that they should be relatively large-scale representations of environmental and biological homogeneity. Therefore, it was established that while the one or two extra bioregions did provide some additional classification

detail, it was not enough to warrant their inclusion in a bioregionalisation, and the 7-group bioregionalisation was carried forward.

5.2 Limitations & uncertainty

Nevertheless, limitations to bioregionalisations exist, mainly linked to the use of predictive models to delineate bioregion boundaries. Ultimately, the quantity and quality of data used to train models is the principal limitation. The models developed in this study were trained with occurrence information, while absences have been assumed in an approach akin to target-group background absence generation. True absence (and abundance) information from systematic surveys, with consistent sampling gear, would greatly reduce uncertainty associated with the presence-absence occurrence matrix.[8] Furthermore, the GF model was generated with environmental datasets, which in some cases, were at a coarser native resolution and reduced to the 1 km x 1 km grid used here. While some substrate type information was available for model development, mud and gravel were excluding in the testing phase. The presence and abundance of benthic communities is often linked to substrate type, and therefore high-resolution substrate information would greatly improve the quality of information available for model development. The availability and use of other environmental data layers (e.g., variation in sea surface temperature as a proxy for the location of oceanic fronts) would also likely improve the models. The GF model was trained with information for 182 VME indicator genera, but many more genera comprising VME indicator taxa are present in the Evaluated Area (estimates from available data are presented in Table 3-1). Representation of more VME indicator genera in the GF model would improve the determination of the taxa compositional turnover, and therefore the bioregionalisation. Finally, the occurrence information used to train the GF model captures some areas of the environmental space of the study area better than others. This difference is primary linked to sampling effort, where in this study, most of the available data comes from New Zealand's EEZ, particularly the Chatham Rise. Environmental coverage indicates the spaces where we can be more and less certain in model predictions. The results highlight that in most cases, areas deeper than fishable depth (1,400 m) are less well represented by training data, and therefore caution should be placed on the bioregional predictions in these spaces.

Despite the limitations noted above, approaches could be developed to use the 7-group bioregionalisation produced here, with two spatially explicit measures of uncertainty (environmental coverage and SD of compositional turnover), to assess the effectiveness of spatial management measures. Until enough data is available to demonstrably improve the bioregionalisation, independent statistical validation of the bioregionalisation could be conducted to inform its utility for management (for example, see the validation approach applied by Stephenson et al. 2024). Presence-absence and abundance information for VME indicator taxa is currently available from imagery surveys carried out in the study area (Deep-Towed Imaging System, DTIS; SC11-DW07_rev1) which could be used to validate the bioregionalisation. It should be noted, that in most cases the species information derived from DTIS imagery is not available at genus level, and thus validation would therefore likely have to be conducted at the taxonomic levels as which VME indicator taxa are designated (as per Table 2-1).

[8] *Some of this uncertainty will be captured in the standard deviation of species compositional turnover that can be produced via bootstrapping.*

6. Recommendations

It is recommended that the Scientific Committee:

- **Notes** that a hierarchical approach has been used to develop a bioregionalisation for VME indicator taxa in the Evaluated Area portion of the SPRFMO Convention Area, and 7-, 8- and 9-group classifications have been described.
- **Agrees** that the approach used to develop the VME indicator taxa bioregionalisation is appropriate.
- **Agrees** that the 7-group classification delineates the fewest number of bioregions, while maintaining classification strength.
- **Agrees** that bioregions may provide an additional spatial scale for evaluating the performance of spatial management measures and represent a more ecologically relevant large spatial scale than FMAs.
- **Recommends** that until enough data is available to demonstrably improve the bioregionalisation, independent statistical validation of the bioregionalisation should be conducted to inform its utility for management**.**
- **Recommends** to the Commission that, if the bioregionalisation is assessed as having utility for management, a task is added to the SC's multi-annual workplan to use the VME indicator taxa bioregionalisation to evaluate the performance of the bottom fishing spatial management measures.
- **Recommends** that further development and validation of abundance models for VME indicator taxa be undertaken so that they can be used for future development the bioregionalisation.

7. Acknowledgements

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9. Annex

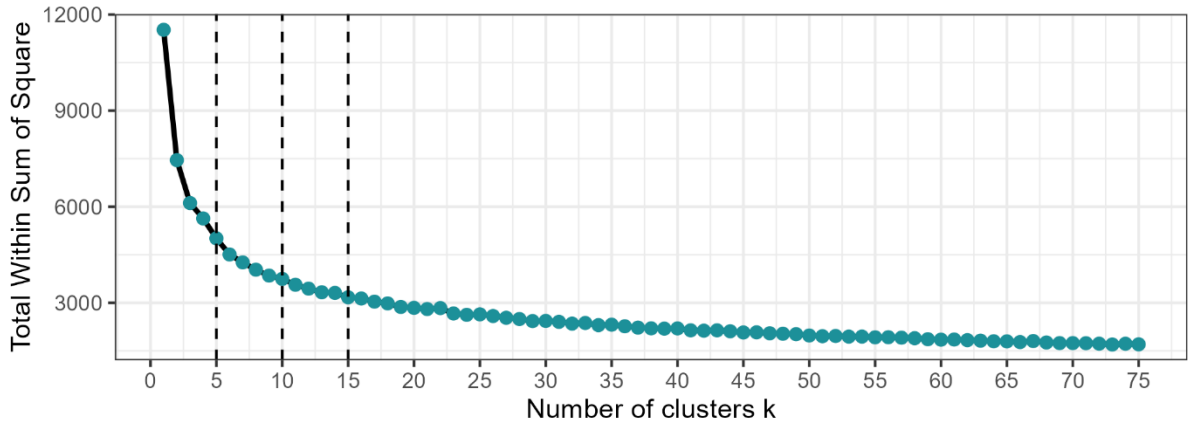

Figure 9-1 | Elbow plot showing the total within sum of squares compared to number of clusters (k = 1–75) i.e., increased classification detail. Dotted lines show multiple subjectively defined turning points (elbows).

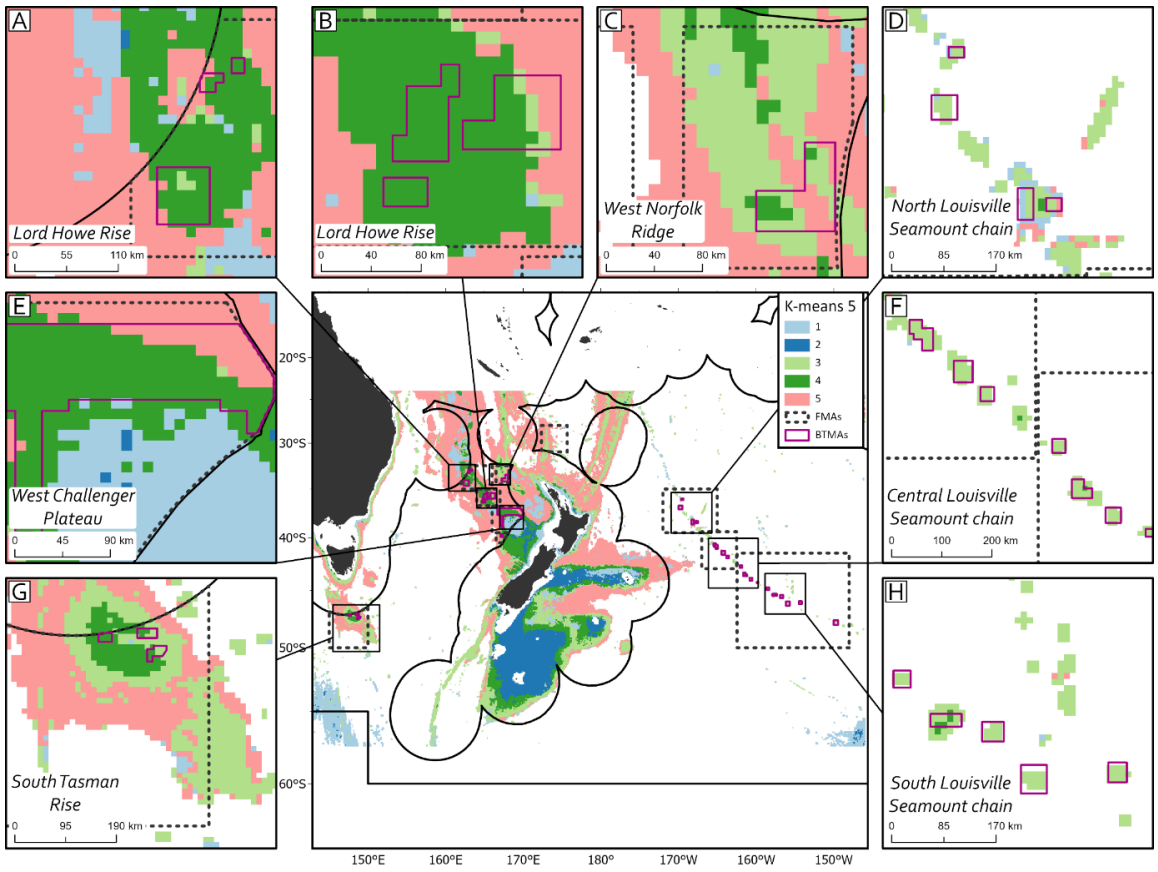

Figure 9-2 | k-means generated classification (k = 5) using habitat suitability models for 17 VME indicators (Stephenson et al. 2021b, Bennion et al. 2024). Black lines indicate the boundaries between the SPRFMO Evaluated Area and the multiple Exclusive Economic Zones (EEZs), dotted lines show Fishery Management Area (FMA) boundaries, and pink lines show Bottom Trawl Management Area (BTMA) boundaries.

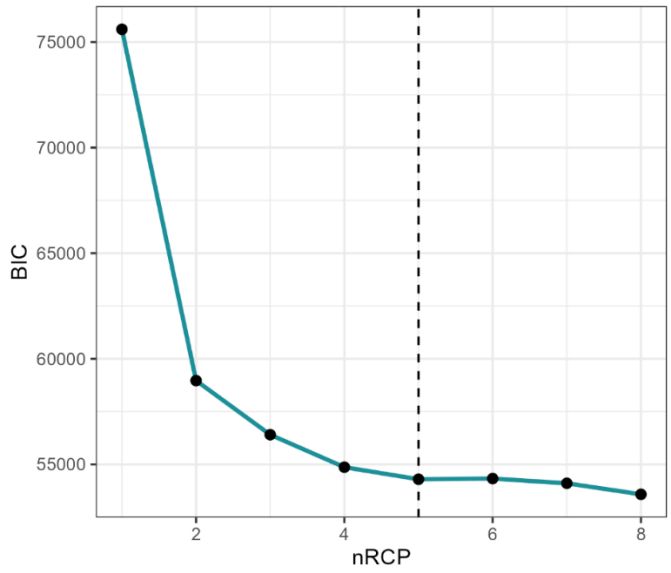

Figure 9-3 | Bayesian information criterion (BIC) shown for different numbers of Regions of Common Profiles (RCPs). Dotted line shows the subjectively defined number of RCPs (nRCP) at 5.

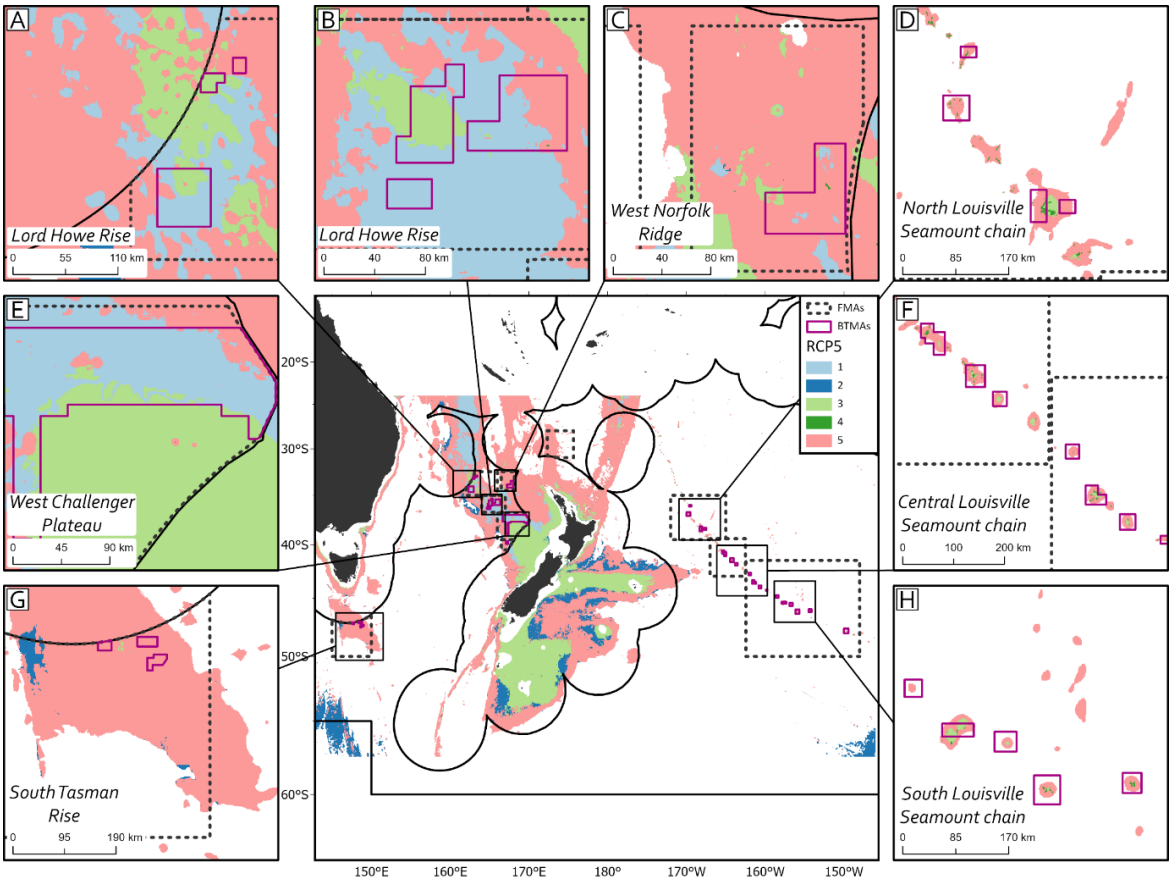

Figure 9-4 | Regions of Common Profiles (RCP) model generated classification VME indicator taxa level occurrence information (for 17 VME indicators). Black lines indicate the boundaries between the SPRFMO Evaluated Area and the multiple Exclusive Economic Zones (EEZs), dotted lines show Fishery Management Area (FMA) boundaries, and pink lines show Bottom Trawl Management Area (BTMA) boundaries.

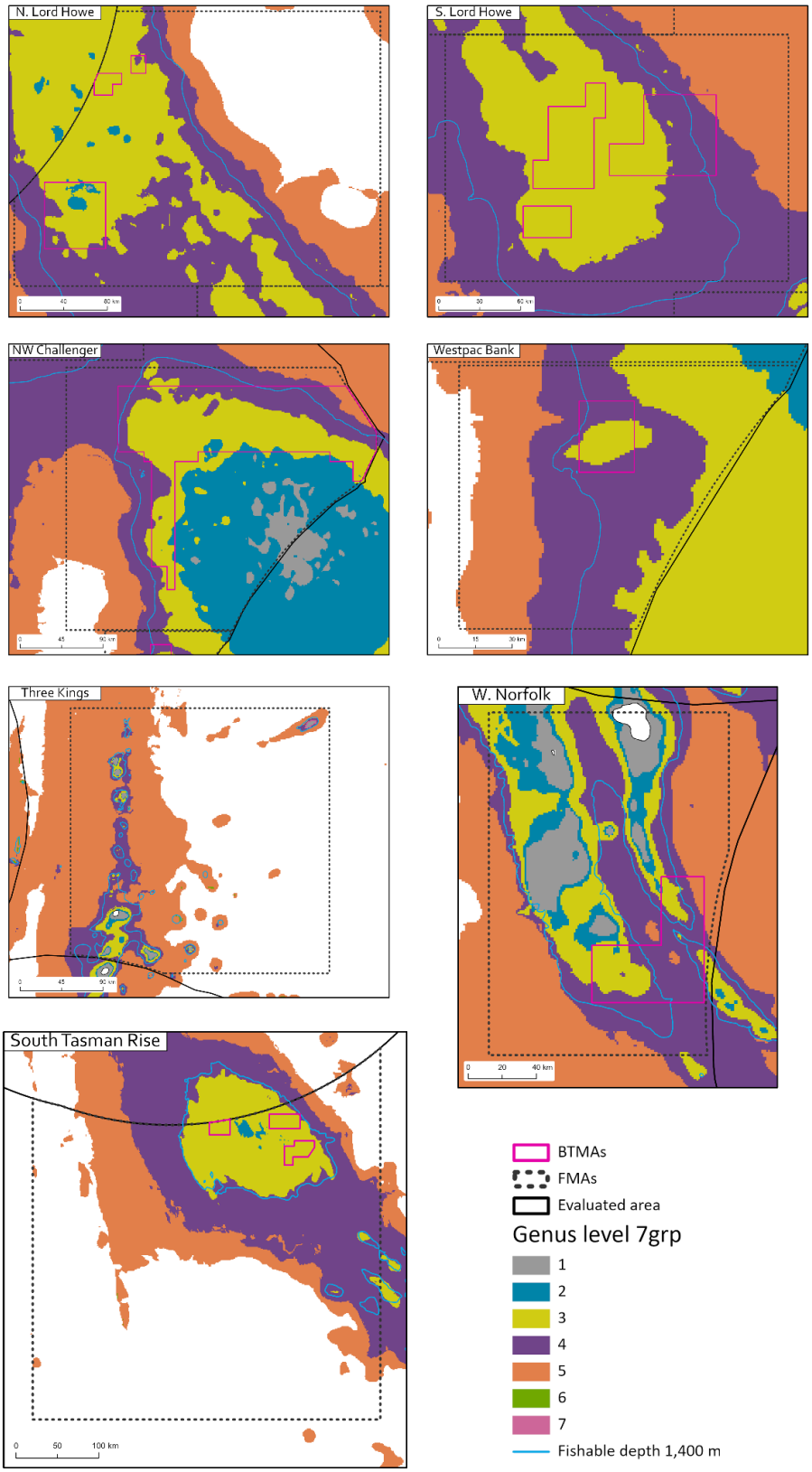

Figure 9-5 | Geographic distribution of the 7-group bioregionalisation derived from the bootstrapped gradient forest model fitted with genus-level VME indicator occurrence information shown for each Fishery Management Area (FMA) (excluding Louisville Seamount Chain). Black lines indicate the boundaries between the SPRFMO Evaluated Area and the multiple Exclusive Economic Zones (EEZs), dotted lines show FMA boundaries, and pink lines show Bottom Trawl Management Area (BTMA) boundaries.

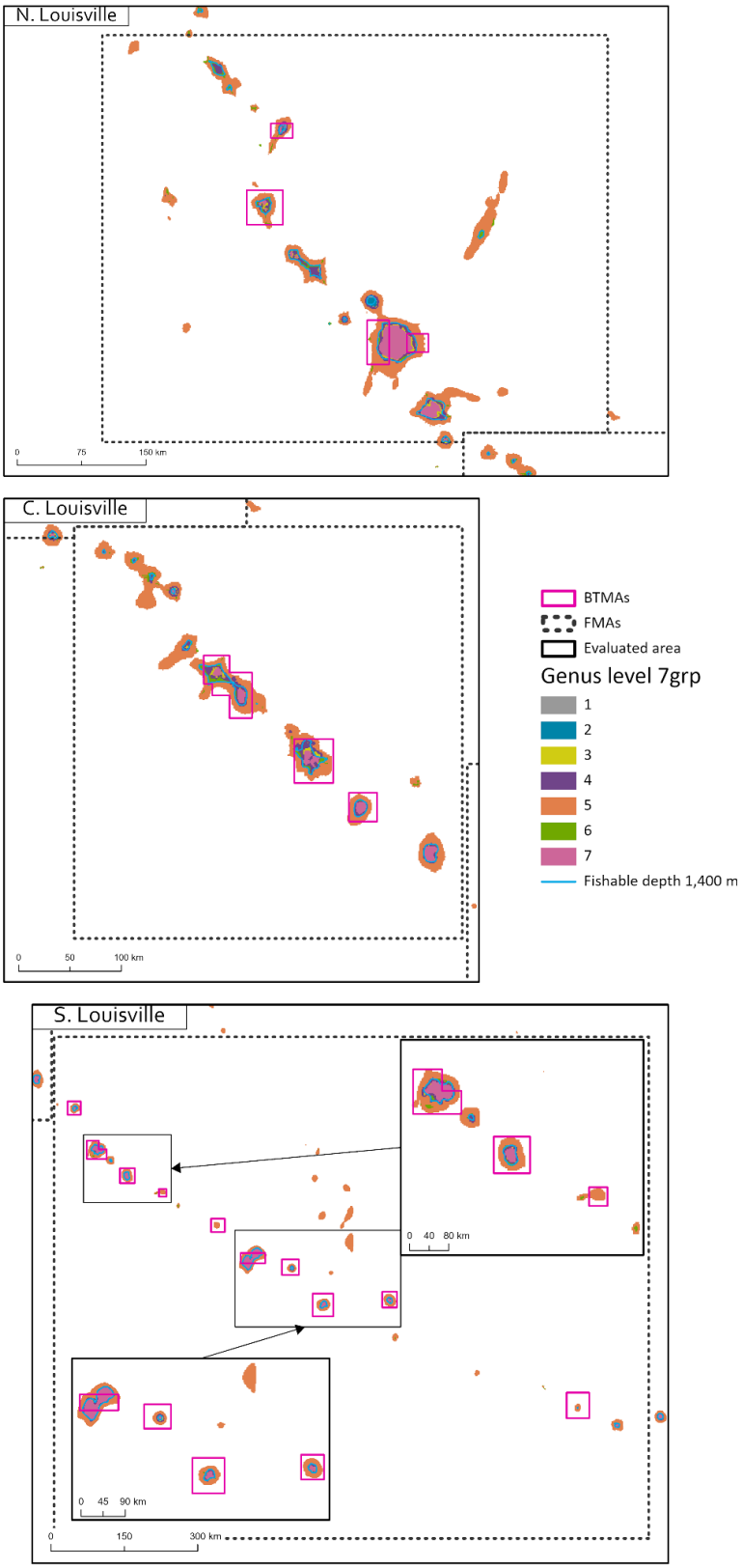

Figure 9-6 | Geographic distribution of the 7-group bioregionalisation derived from the bootstrapped gradient forest model fitted with genus-level VME indicator occurrence information shown for Fishery Management Areas (FMAs) on the Louisville Seamount Chain. Dotted lines show FMA boundaries, and pink lines show Bottom Trawl Management Area (BTMA) boundaries.

8-group bioregionalisation

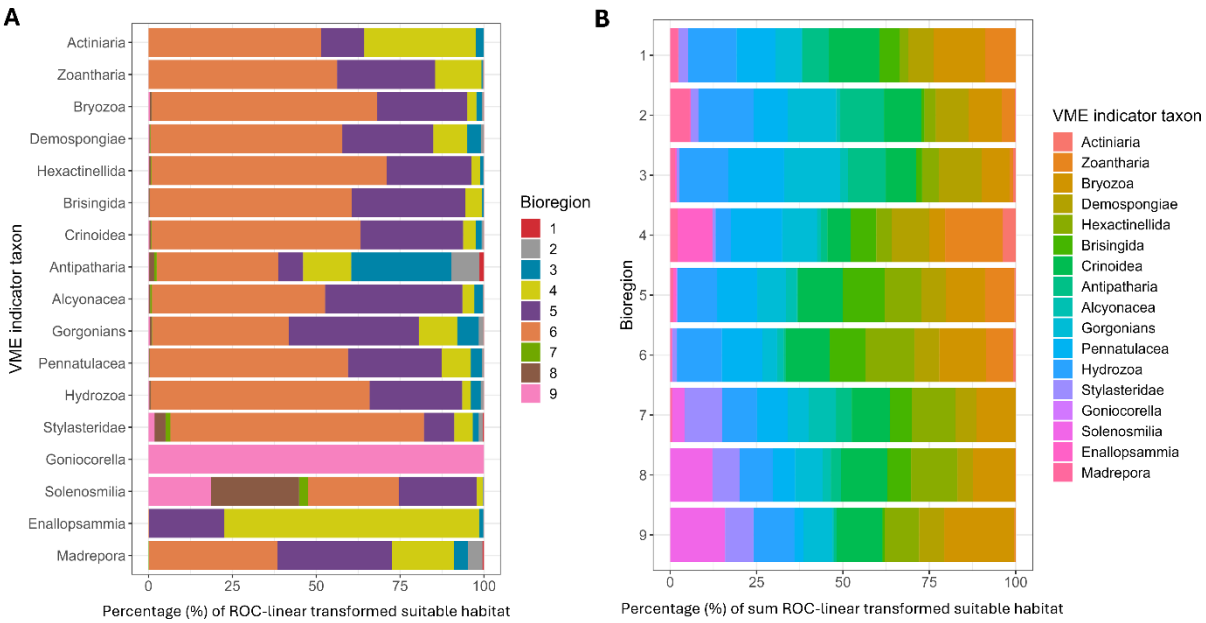

Figure 9-7 | Stacked bar charts show the percentage (%) of ROC-linear transformed suitable habitat for VME indicators in bioregions for the 8-group bioregionalisation. A) Shows the percentage of ROC-linear transformed suitable habitat for each VME indicator contained within each bioregion (each bar represents 100% ROC-linear transformed suitable habitat for each VME indicator). Colours are matched to Figure 9-8. B) shows the percentage (%) contribution of each VME indicator to the sum of ROC-linear transformed suitable habitat within each bioregion (each bar represents 100% of the summed ROC-linear transformed suitable habitat for all VME indicators). Note: values in these charts were calculated for the SPRFMO Evaluated Area only.

Table 9-1 | Similarity Percentage (SIMPER) results for the 8-group bioregionalisation. SIMPER was calculated using genus-level community information. Bioregions (colours matched to Figure 9-8), average percentage similarity (within bioregions), and the top VME indicator contributors to similarity (arbitrary ≥6% cut-off used for reporting) are shown. Refer to Table 2-1 for taxon code detail.

Bioregion	Average similarity (%)	Top VME indicator contributors to similarity (≥6%)
1	3.98	*Epizoanthus* (ZAH; 16%); *Anthoptilum* (PTU; 15%); *Conopora* (COR; 13%); *Lytocarpia* (HDR; 8%); *Goniocorella* (GDU; 8%)
2	8.13	*Hyalascus* (HEX; 66%)
3	3.83	*Epizoanthus* (ZAH; 20%); *Solenosmilia* (SVA: 19%); Keratoisis (ALCY; 9%); *Enallopsammia* (ERO; 9%)
4	4.67	*Solenosmilia* (SVA; 46%); *Keratoisis* (ALCY; 8%)
5	2.89	*Umbellula* (PTU; 22%); *Keratoisis* (ALCY; 13%); *Farrea* (HEX; 9%); *Epizoanthus* (ZAH; 8%)
6	5.79	*Solenosmilia* (SVA; 38%); *Novodinia* (BRG; 33%)
7	9.73	*Solenosmilia* (SVA; 91%)
8	7.93	*Keratoisis* (ALCY; 22%); *Symplectoscyphus* (HDR; 9%); *Acryptolaria* (HDR; 8%); *Solenosmilia* (SVA; 8%); *Chiastosella* (COZ; 7%); *Escharella* (COZ; 7%)

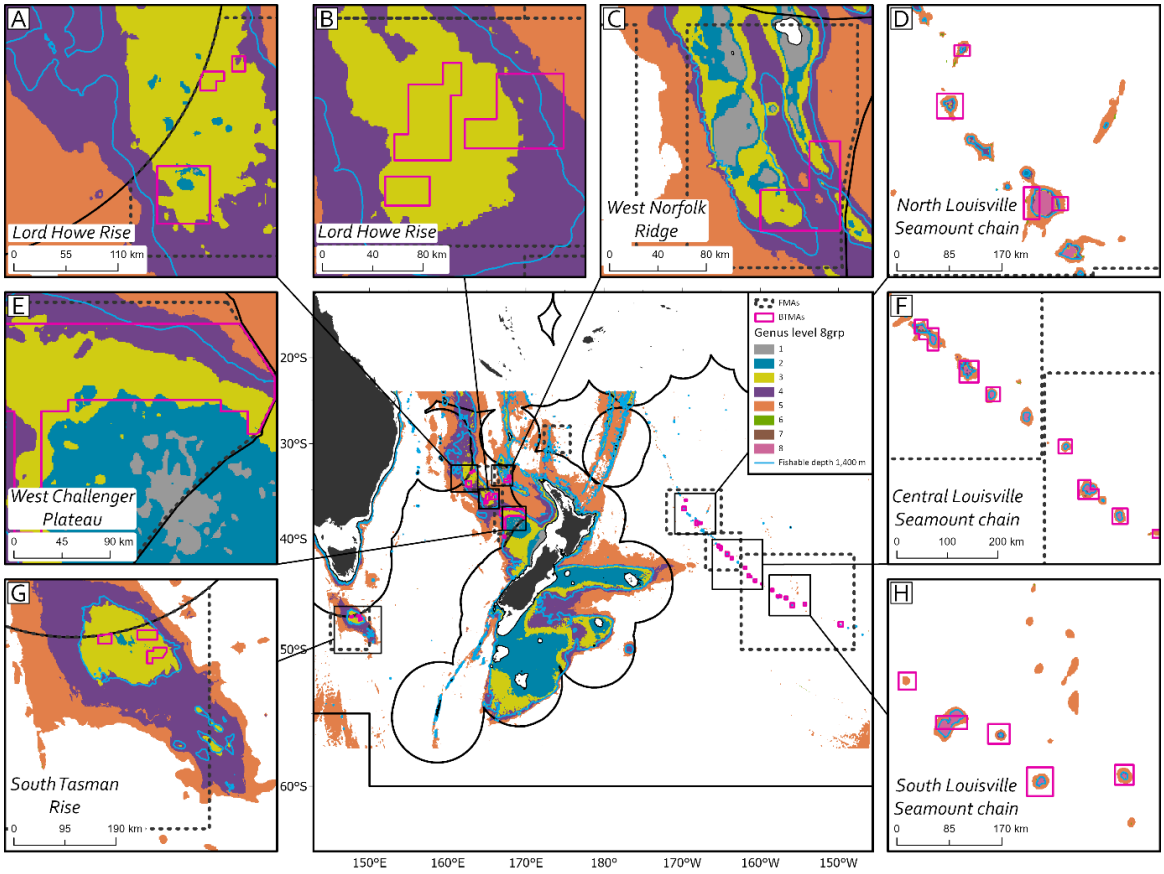

Figure 9-8 | Geographic distribution of the 8-group bioregionalisation derived from the bootstrapped gradient forest model fitted with genus-level VME indicator occurrence information. Black lines indicate the boundaries between the SPRFMO Evaluated Area and the multiple Exclusive Economic Zones (EEZs), dotted lines show Fishery Management Area (FMA) boundaries, and pink lines show Bottom Trawl Management Area (BTMA) boundaries.

Table 9-2 | Bioregion number (colour matched to Figure 9-8), descriptions, and median and interquartile range (IQ range: 25–75 quantile) of environmental conditions for the 8-group bioregionalisation. Cell colours highlight the highest (orange) and lowest (green) median values for each environmental condition.

Bioregion	Aragonite saturation	BPI-broad	Depth	Dissolved oxygen	POC export to the seafloor
1	1.8 (1.7, 2)	1005 (223, 1249)	-515 (-750, -493)	4.5 (4.4, 4.6)	23.4 (19.8, 25.2)
2	1.5 (1.4, 1.6)	287 (217, 440)	-648 (-714, -586)	4.4 (4.4, 4.6)	22.9 (21.6, 24.2)
3	1.1 (1.1, 1.2)	437 (305, 620)	-1015 (-1109, -941)	4.2 (4.1, 4.3)	18.1 (16.8, 19)
4	0.9 (0.9, 1)	325 (147, 536)	-1440 (-1613, -1270)	3.8 (3.6, 4)	12.7 (11.4, 14.4)
5	0.8 (0.7, 0.8)	162 (-117, 536)	-2594 (-2834, -2246)	3.9 (3.5, 4.6)	5.5 (3.2, 7.2)
6	0.7 (0.7, 0.8)	2035 (1428, 2816)	-2384 (-2763, -1976)	3.8 (3.5, 4.5)	2.2 (1.5, 4.3)
7	0.8 (0.8, 0.9)	3561 (3380, 3817)	-1461 (-1770, -1238)	3.6 (3.4, 3.8)	4.8 (2.6, 7.7)
8	1.4 (1.3, 1.5)	3759 (3485, 3996)	-778 (-927, -627)	5.2 (5, 5.5)	9.5 (1.5, 17.5)

Bioregion	Ruggedness	Salinity	Silicate concentration	Slope SD	Temperature at depth
1	0.00001 (0.0000002, 0.0003)	34.9 (34.8, 35.1)	9 (6.6, 9.7)	0.4 (0.1, 1.6)	10.5 (10.2, 12.1)
2	0.0000004 (0.0000001, 0.000002)	34.7 (34.6, 34.7)	14.3 (12.3, 16.4)	0.1 (0, 0.2)	8.8 (8.3, 9.3)
3	0.000002 (0.00000042, 0.00001)	34.5 (34.5, 34.5)	38 (30.7, 44.9)	0.1 (0.1, 0.3)	5.4 (4.9, 6.1)
4	0.000004 (0.0000007, 0.00003)	34.5 (34.5, 34.6)	75.9 (64.2, 85.3)	0.2 (0.1, 0.5)	3.4 (2.9, 4)
5	0.00003 (0.000006, 0.0002)	34.7 (34.7, 34.7)	112.5 (104.2, 121.2)	0.5 (0.2, 1.2)	1.9 (1.4, 2.2)
6	0.03 (0.02, 0.04)	34.7 (34.6, 34.7)	111.2 (105.5, 119.6)	7.8 (6.1, 9.3)	2 (1.8, 2.3)
7	0.006 (0.004, 0.01)	34.6 (34.5, 34.6)	100.6 (78.8, 117.2)	6.3 (5, 7.7)	2.5 (2.2, 3)
8	0.00072 (0.0001, 0.00321)	34.4 (34.4, 34.4)	14.3 (10.8, 20.2)	2.7 (1.1, 5.3)	6.8 (6.2, 7.3)

Table 9-3 | Accounting metrics for the 8-group bioregionalisation (colour matched to Figure 9-8). Area (km^2) of each bioregion is shown within Exclusive Economic Zones (EEZs), the SPRFMO Evaluated Area, and the entire study area (total). The percentage of the area contained within the Evaluated Area is also shown.

Bioregion	EEZs	Evaluated Area	Entire study area	Percentage (%) in Evaluated Area
1	71,167	7,003	78,170	9
2	689,378	25,483	714,861	3.6
3	531,743	88,269	620,012	14.2
4	869,955	238,783	1,108,738	21.5
5	1,395,930	517,737	1,913,667	27.1
6	1,317	977	2,294	42.6
7	827	3,313	4,140	80
8	2,546	3,565	6,111	58.3

Table 9-4 | Fragmentation metrics for the 8-group bioregionalisation (colour matched to Figure 9-8). The total bioregion area (km^2) is shown as well as the number of geographically separated patches for each bioregion, the mean and standard deviation (SD) of patch area, and the coefficient of variation (CV) of the Euclidean distance between patches.

Bioregion	Total bioregion area (km^2)	No. of patches	Mean patch area (km^2)	SD patch area (km^2)	Euclidean distance CV*
1	78,170	496	157.6	1,540.8	278.5
2	714,861	799	894.7	20,723.7	248.9
3	620,012	876	707.8	10,577.6	405.8
4	1,108,738	1,016	1,091.3	17,059.1	285.8
5	1,913,667	1,248	1,533.4	32,485.8	194.6
6	2,294	385	6	8.2	213.7
7	4,140	176	23.5	42.6	247
8	6,111	134	45.6	122.4	267.8

**Coefficient of variation of Euclidean nearest-neighbour distance (edge-to-edge).*

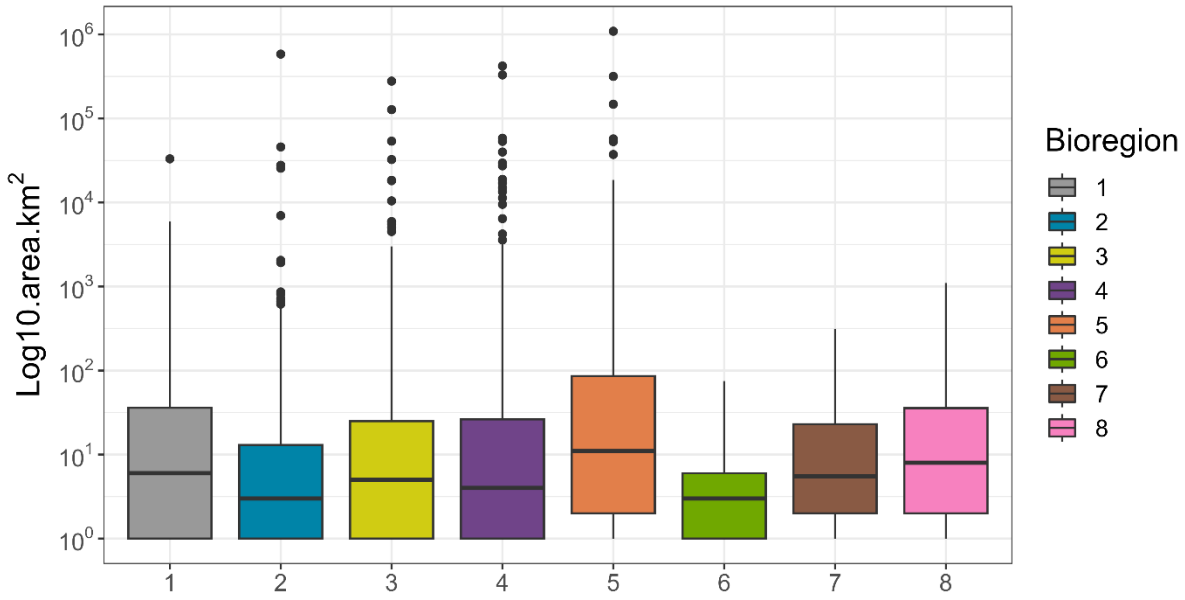

Figure 9-9 | Boxplot shows the area (km^2 log transformed) of each patch for each bioregion in the 8-group bioregionalisation. Each box shows the interquartile range, horizontal lines show the median, whiskers show the min -max (e.g., Q1 – 1.5*IQR), and dots indicate outliers. Box colour is matched to Figure 9-8.

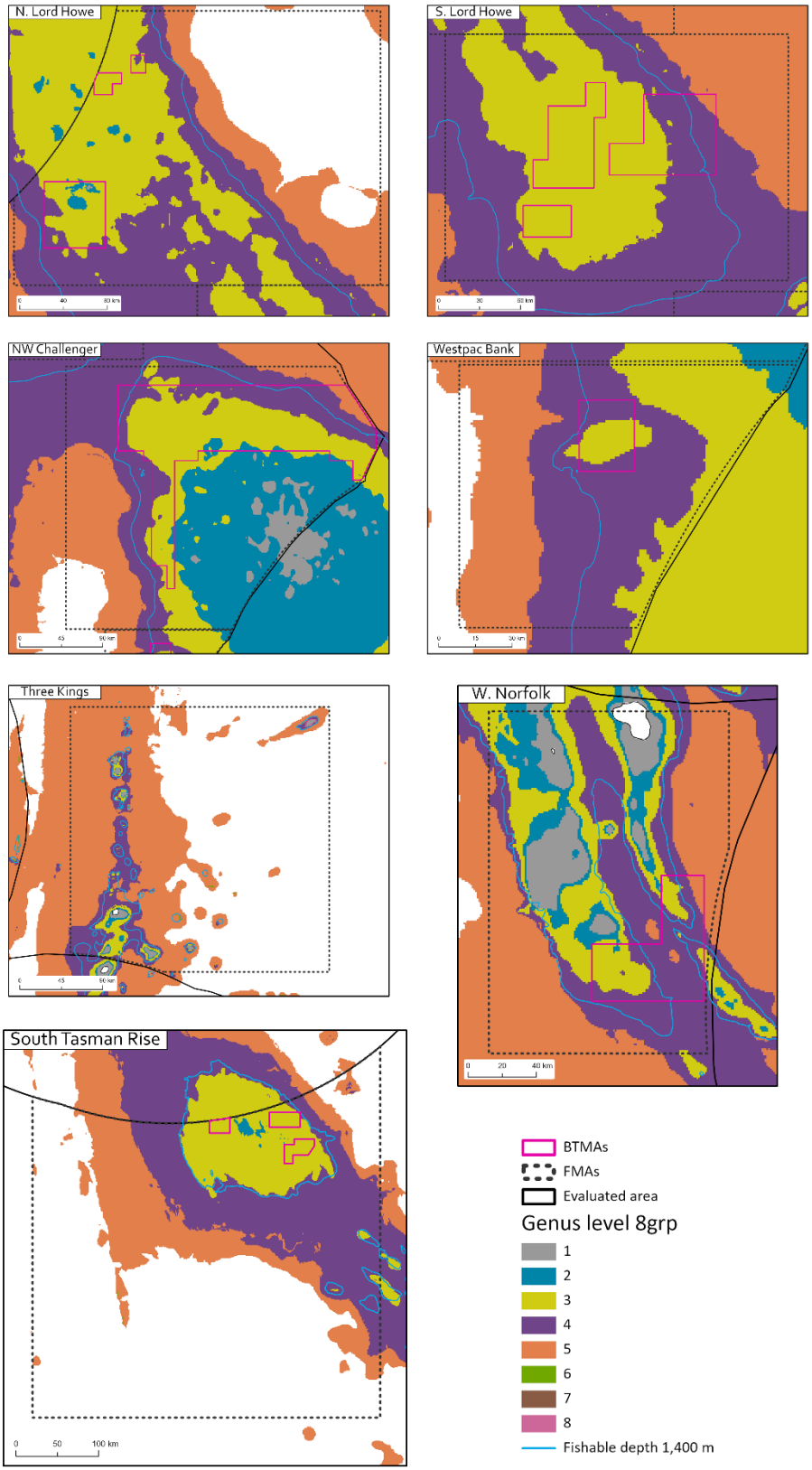

Figure 9-10 | Geographic distribution of the 8-group bioregionalisation derived from the bootstrapped gradient forest model fitted with genus-level VME indicator occurrence information shown for each Fishery Management Area (FMA) (excluding Louisville Seamount Chain). Black lines indicate the boundaries between the SPRFMO Evaluated Area and the multiple Exclusive Economic Zones (EEZs), dotted lines show FMA boundaries, and pink lines show Bottom Trawl Management Area (BTMA) boundaries.

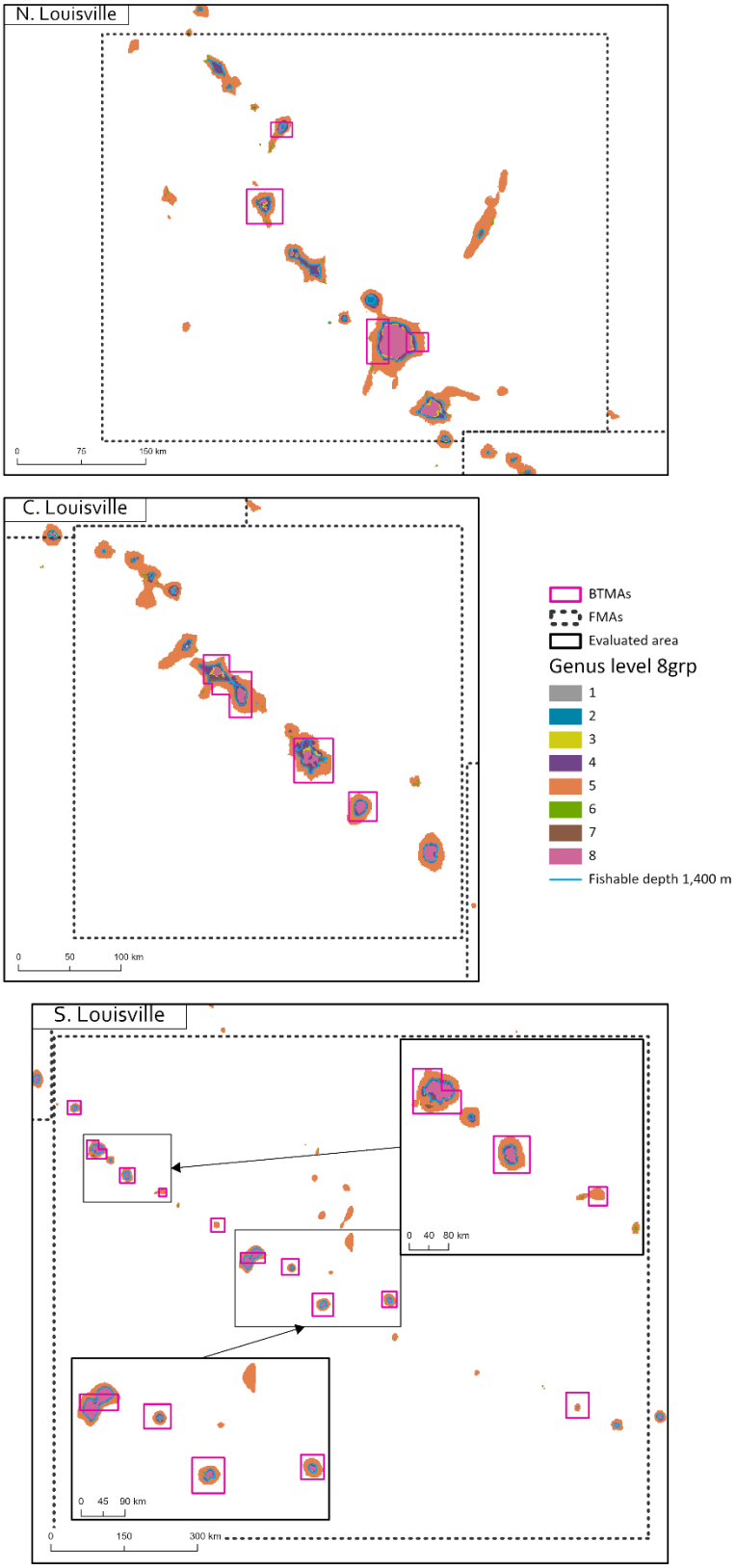

Figure 9-11 | Geographic distribution of the 8-group bioregionalisation derived from the bootstrapped gradient forest model fitted with genus-level VME indicator occurrence information shown for Fishery Management Areas (FMAs) on the Louisville Seamount Chain. Dotted lines show FMA boundaries, and pink lines show Bottom Trawl Management Area (BTMA) boundaries.

9-group Bioregionalisation

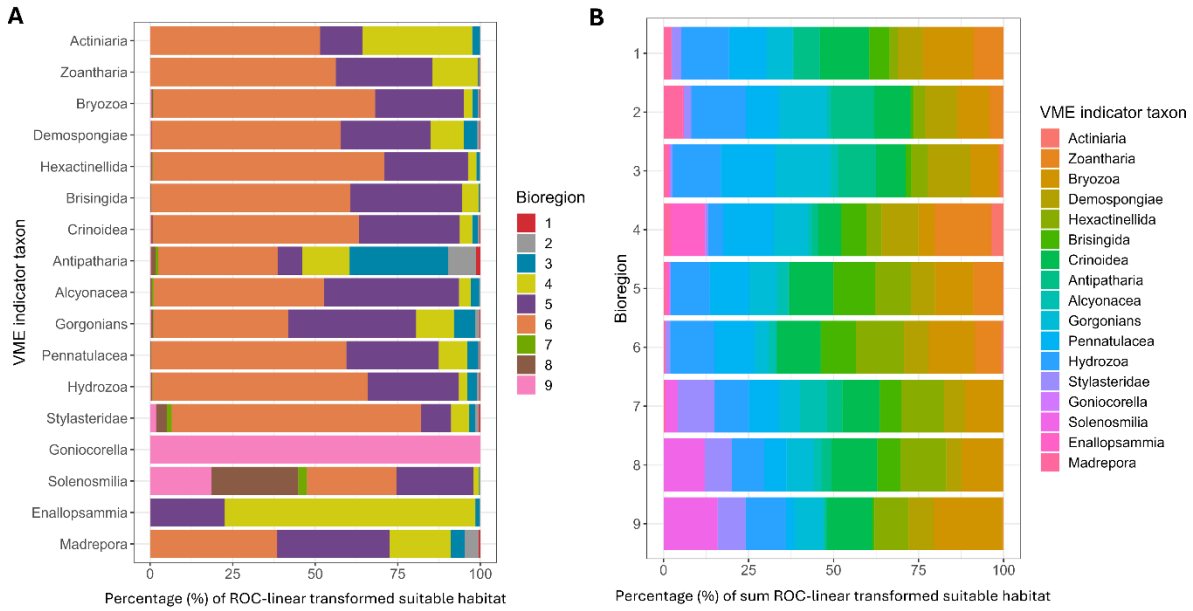

Figure 9-12 | Stacked bar charts show the percentage (%) of ROC-linear transformed suitable habitat for VME indicators in bioregions for the 9-group bioregionalisation. A) Shows the percentage of ROC-linear transformed suitable habitat for each VME indicator contained within each bioregion (each bar represents 100% ROC-linear transformed suitable habitat for each VME indicator). Colours are matched to Figure 9-13. B) shows the percentage (%) contribution of each VME indicator to the sum of ROC-linear transformed suitable habitat within each bioregion (each bar represents 100% of the summed ROC-linear transformed suitable habitat for all VME indicators). Note: values in these charts were calculated for the SPRFMO Evaluated Area only.

Table 9-5 | Similarity Percentage (SIMPER) results for the 9-group bioregionalisation. SIMPER was calculated using genus-level community information. Bioregions (colours matched to Figure 9-13), average percentage similarity (within bioregions), and the top VME indicator contributors to similarity (arbitrary ≥6% cut-off used for reporting) are shown. Refer to Table 2-1 for taxon code detail.

Bioregion	Average similarity (%)	Top VME indicator contributors to similarity (≥6%)
1	3.46	*Epizoanthus* (ZAH; 16%); *Anthoptilum* (PTU; 15%); *Conopora* (COR; 13%); *Lytocarpia* (HDR; 8%); *Goniocorella* (GDU; 8%)
2	4.96	*Hyalascus* (HEX; 66%)
3	8.13	*Epizoanthus* (ZAH; 20%); *Solenosmilia* (SVA: 19%); *Keratoisis* (ALCY; 9%); *Enallopsammia* (ERO; 9%)
4	3.83	*Solenosmilia* (SVA; 46%); *Keratoisis* (ALCY; 8%)
5	4.67	*Umbellula* (PTU; 22%); *Keratoisis* (ALCY; 13%); *Farrea* (HEX; 9%); *Epizoanthus* (ZAH; 8%)
6	2.89	*Solenosmilia* (SVA; 38%); *Novodinia* (BRG; 33%)
7	5.79	*Solenosmilia* (SVA; 91%)
8	9.73	*Keratoisis* (ALCY; 22%); *Symplectoscyphus* (HDR; 9%); *Acryptolaria* (HDR; 8%); *Solenosmilia* (SVA; 8%); *Chiastosella* (COZ; 7%); *Escharella* (COZ; 7%)
9	7.93	*Epizoanthus* (ZAH; 16%); *Anthoptilum* (PTU; 15%); *Conopora* (COR; 13%); *Lytocarpia* (HDR; 8%); *Goniocorella* (GDU; 8%)

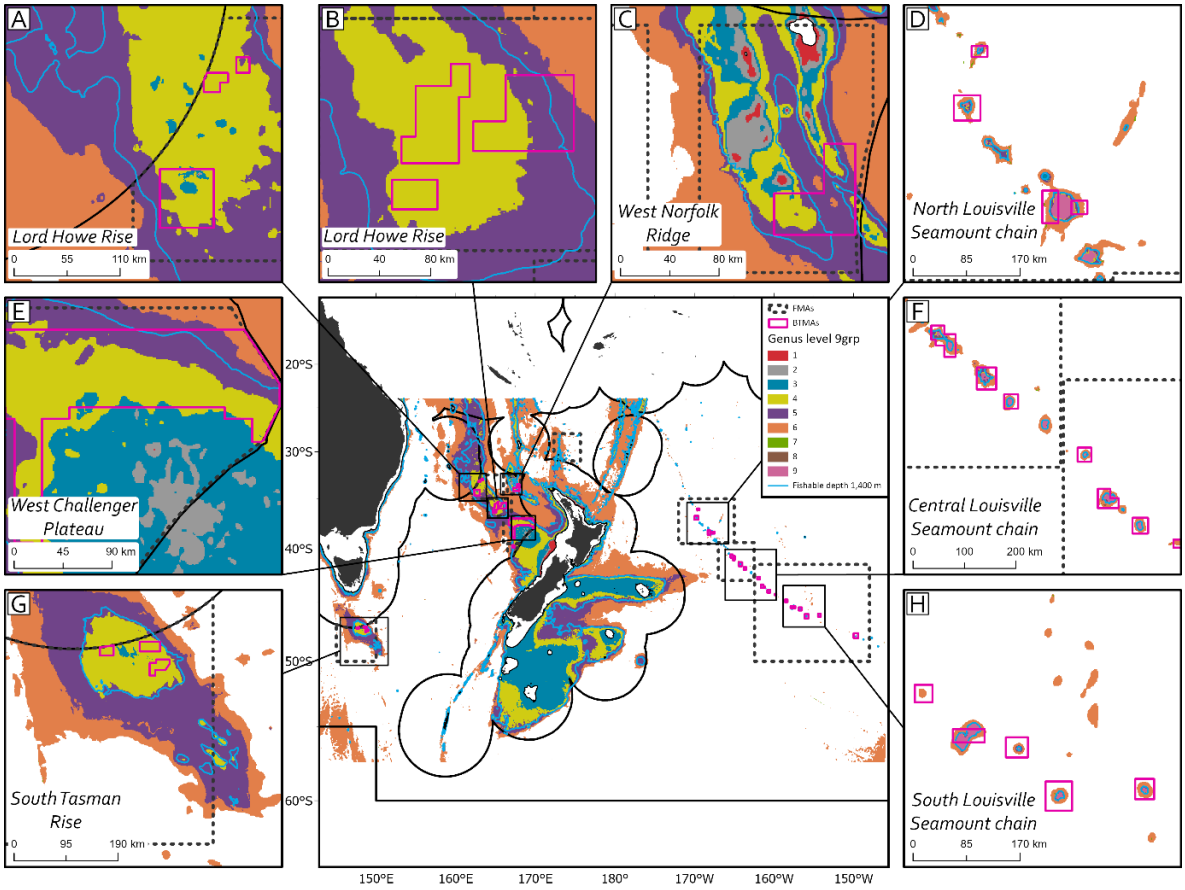

Figure 9-13 | Geographic distribution of the 9-group bioregionalisation derived from the bootstrapped gradient forest model fitted with genus-level VME indicator occurrence information. Black lines indicate the boundaries between the SPRFMO Evaluated Area and the multiple Exclusive Economic Zones (EEZs), dotted lines show Fishery Management Area boundaries (FMAs), and pink lines show Bottom Trawl Management Area (BTMA) boundaries.

Table 9-6 | Bioregion number (colour matched to Figure 9-13), descriptions, and median and interquartile range (IQ range: 25–75 quantile) of environmental conditions for the 9-group bioregionalisation. Cell colours highlight the highest (orange) and lowest (green) median values for each environmental condition.

Bioregion	Aragonite saturation	BPI-broad	Depth	Dissolved oxygen	POC export to the seafloor
1	2.4 (2.2, 2.6)	1536 (1145.5, 1882)	-332 (-500.8, -249.3)	4.5 (4.3, 4.6)	21.7 (20.3, 27.9)
2	1.7 (1.7, 1.8)	922 (194, 1171)	-547 (-754, -497)	4.5 (4.4, 4.6)	23.6 (19.2, 25.2)
3	1.5 (1.4, 1.6)	287 (217, 440)	-648 (-714, -586)	4.4 (4.4, 4.6)	22.9 (21.6, 24.2)
4	1.1 (1.1, 1.2)	437 (305, 620)	-1015 (-1109, -941)	4.2 (4.1, 4.3)	18.1 (16.8, 19)
5	0.9 (0.9, 1)	325 (147, 536)	-1440 (-1613, -1270)	3.8 (3.6, 4)	12.7 (11.4, 14.4)
6	0.8 (0.7, 0.8)	162 (-117, 536)	-2594 (-2834, -2246)	3.9 (3.5, 4.6)	5.5 (3.2, 7.2)
7	0.7 (0.7, 0.8)	2035 (1428, 2816)	-2384 (-2763, -1976)	3.8 (3.5, 4.5)	2.2 (1.5, 4.3)
8	0.8 (0.8, 0.9)	3561 (3380, 3817)	-1461 (-1770, -1238)	3.6 (3.4, 3.8)	4.8 (2.6, 7.7)
9	1.4 (1.3, 1.5)	3759 (3485, 3996)	-778 (-927, -627)	5.2 (5, 5.5)	9.5 (1.5, 17.5)

Bioregion	Ruggedness	Salinity	Silicate concentration	Slope SD	Temperature at depth
1	0.00022 (0.00003, 0.00081)	35.4 (35.2, 35.5)	3.3 (2.5, 5.3)	1.5 (0.6, 2.8)	15.3 (13.5, 17.6)
2	0.000006 (0.0000001, 0.0001)	34.8 (34.8, 34.9)	9.6 (8.3, 9.8)	0.2 (0, 1.2)	10.4 (10.2, 11)
3	0.0000004 (0.0000001, 0.000002)	34.7 (34.6, 34.7)	14.3 (12.3, 16.4)	0.1 (0, 0.2)	8.8 (8.3, 9.3)
4	0.000002 (0.00000042, 0.00001)	34.5 (34.5, 34.5)	38 (30.7, 44.9)	0.1 (0.1, 0.3)	5.4 (4.9, 6.1)
5	0.000004 (0.0000007, 0.00003)	34.5 (34.5, 34.6)	75.9 (64.2, 85.3)	0.2 (0.1, 0.5)	3.4 (2.9, 4)
6	0.000032 (0.000006, 0.0002)	34.7 (34.7, 34.7)	112.5 (104.2, 121.2)	0.5 (0.2, 1.2)	1.9 (1.4, 2.2)
7	0.03 (0.02, 0.04)	34.7 (34.6, 34.7)	111.2 (105.5, 119.6)	7.8 (6.1, 9.3)	2 (1.8, 2.3)
8	0.006 (0.004, 0.01)	34.6 (34.5, 34.6)	100.6 (78.8, 117.2)	6.3 (5, 7.7)	2.5 (2.2, 3)
9	0.0007 (0.0001, 0.0032)	34.4 (34.4, 34.4)	14.3 (10.8, 20.2)	2.7 (1.1, 5.3)	6.8 (6.2, 7.3)

Table 9-7 | Accounting metrics for the 9-group bioregionalisation (colour matched to Figure 9-13). Area (km^2) of each bioregion is shown within Exclusive Economic Zones (EEZs), the SPRFMO Evaluated Area, and the entire study area (total). The percentage of the area contained within the Evaluated Area is also shown.

Bioregion	EEZs	Evaluated Area	Entire study area	Percentage (%) in Evaluated Area
1	40,584	1,294	41,878	3.1
2	30,583	5,709	36,292	15.7
3	689,378	25,483	714,861	3.6
4	531,743	88,269	620,012	14.2
5	869,955	238,783	1,108,738	21.5
6	1,395,930	517,737	1,913,667	27.1
7	1,317	977	2,294	42.6
8	827	3,313	4,140	80
9	2,546	3,565	6,111	58.3

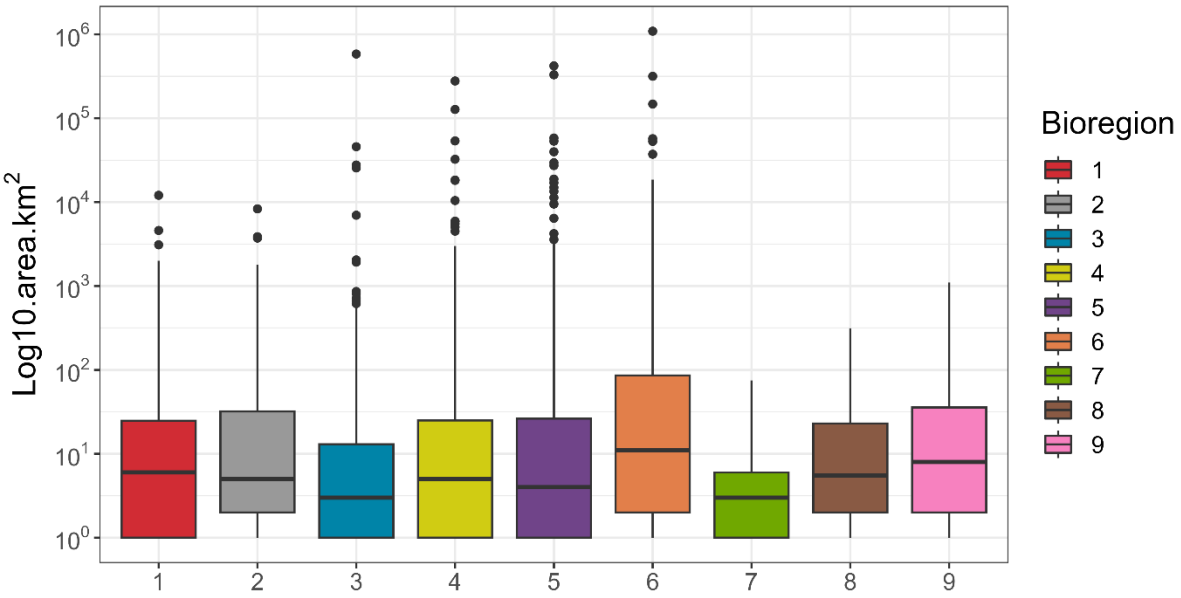

Figure 9-14 | Boxplot shows the area (km^2 log transformed) of each patch for each bioregion in the 9-group bioregionalisation. Each box shows the interquartile range, horizontal lines show the median, whiskers show the min -max (e.g., Q1 – 1.5*IQR), and dots indicate outliers. Box colour is matched to Figure 9-13.

Table 9-8 | Fragmentation metrics for the 9-group bioregionalisation (colour matched to Figure 9-13). The total bioregion area (km^2) is shown as well as the number of geographically separated patches for each bioregion, the mean and standard deviation (SD) of patch area, and the coefficient of variation (CV) of the Euclidean distance between patches.

Bioregion	Total bioregion area (km^2)	No. of patches	Mean patch area (km^2)	SD patch area (km^2)	Euclidean distance CV*
1	41,878	478	87.6	631.1	649.9
2	36,292	433	83.8	492.1	291.5
3	714,861	799	894.7	20,723.7	248.9
4	620,012	876	707.8	10,577.6	405.8
5	1,108,738	1,016	1,091.3	17,059.1	285.8
6	1,913,667	1,248	1,533.4	32,485.8	194.6
7	2,294	385	6	8.2	213.7
8	4,140	176	23.5	42.6	247
9	6,111	134	45.6	122.4	267.8

**Coefficient of variation of Euclidean nearest-neighbour distance (edge-to-edge).*

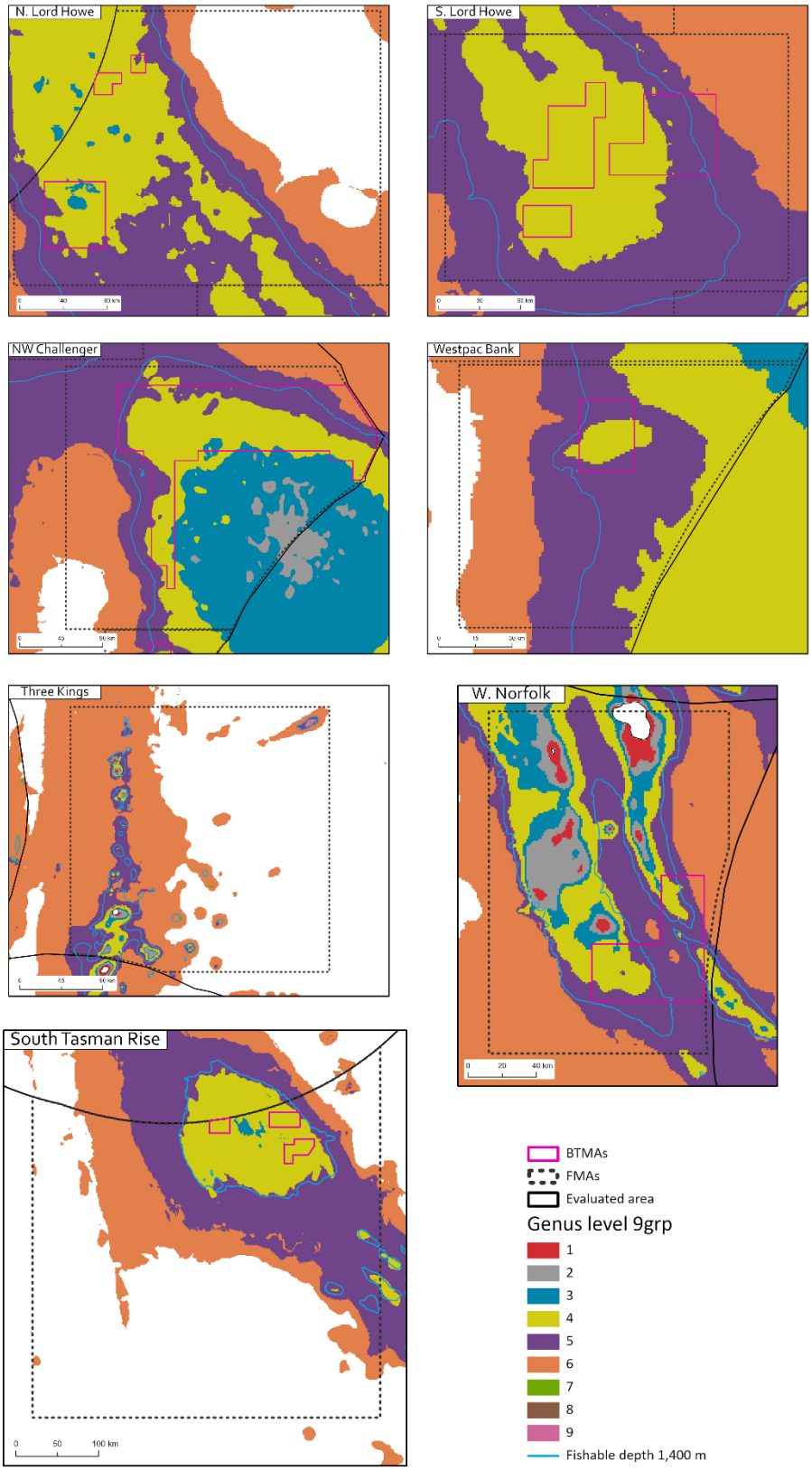

Figure 9-15 | Geographic distribution of the 9-group bioregionalisation derived from the bootstrapped gradient forest model fitted with genus-level VME indicator occurrence information shown for each Fishery Management Area (FMA) (excluding Louisville Seamount Chain). Black lines indicate the boundaries between the SPRFMO Evaluated Area and the multiple Exclusive Economic Zones (EEZs), dotted lines show FMA boundaries, and pink lines show Bottom Trawl Management Area (BTMA) boundaries.

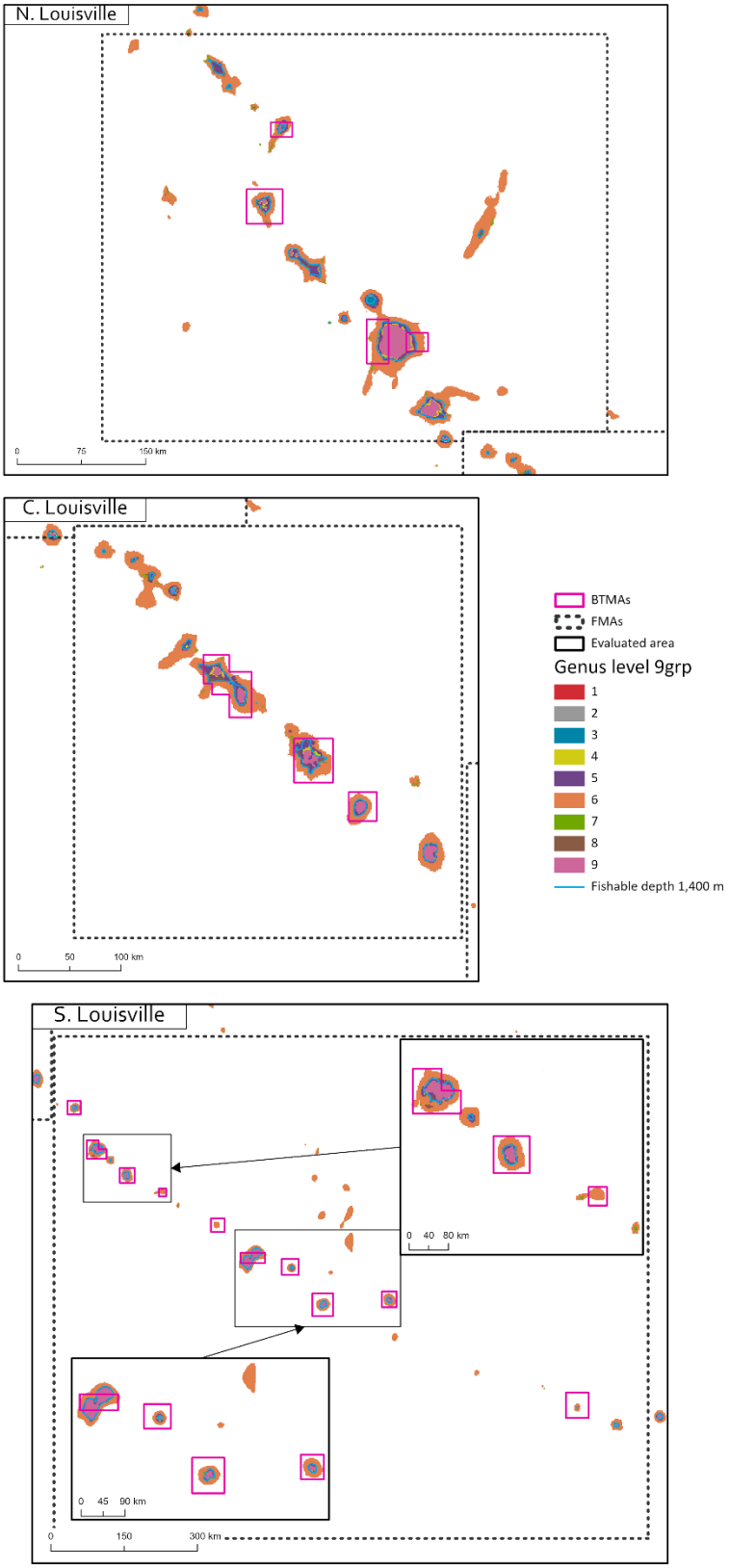

Figure 9-16 | Geographic distribution of the 9-group bioregionalisation derived from the bootstrapped gradient forest model fitted with genus-level VME indicator occurrence information shown for Fishery Management Areas (FMAs) on the Louisville Seamount Chain. Dotted lines show FMA boundaries, and pink lines show Bottom Trawl Management Area (BTMA) boundaries.

Bioregion and FMA scale comparison

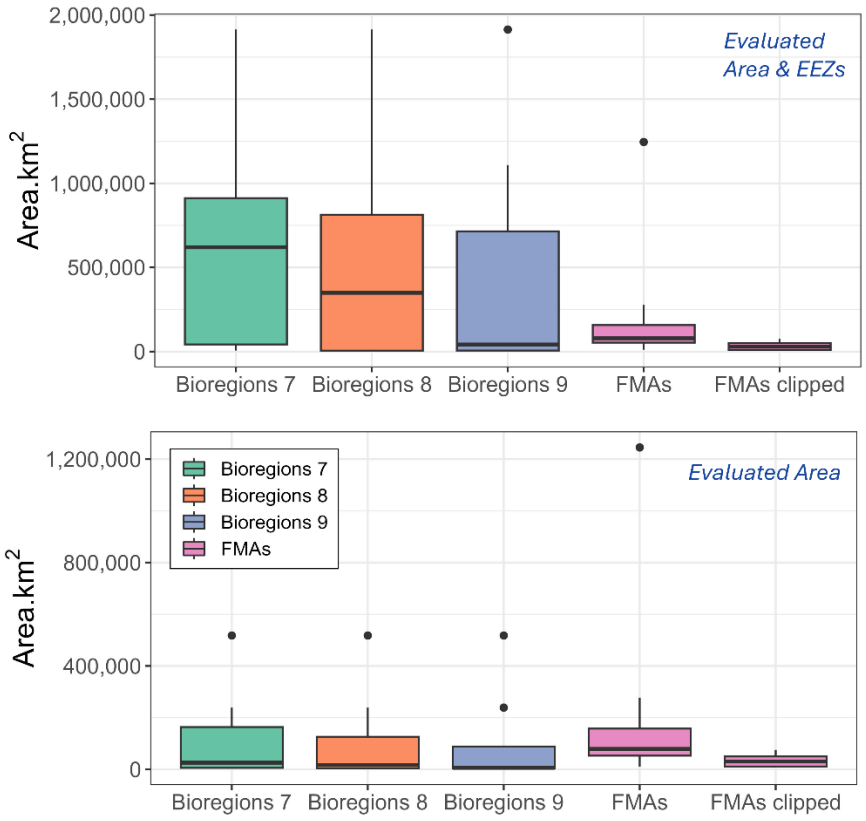

Figure 9-17 | Area (km^2) of bioregions for the 7, 8, and 9 group bioregionalisations is compared to the area of FMAs. On the x-axis, 'FMAs' refers to the full extent of the FMAs, whereas 'FMAs clipped' refers to the extent of the FMAs clipped to the maximum depth of the study area; 3000 m. The top boxplot shows the total area of the bioregions across the entire study area (SPRFMO Evaluated Area and Exclusive Economic Zones (EEZs) compared to Fishery Management Areas (FMAs). The bottom boxplot shows the area of each bioregion in the Evaluated Area only, compared to the area of FMAs.

28-group Classification

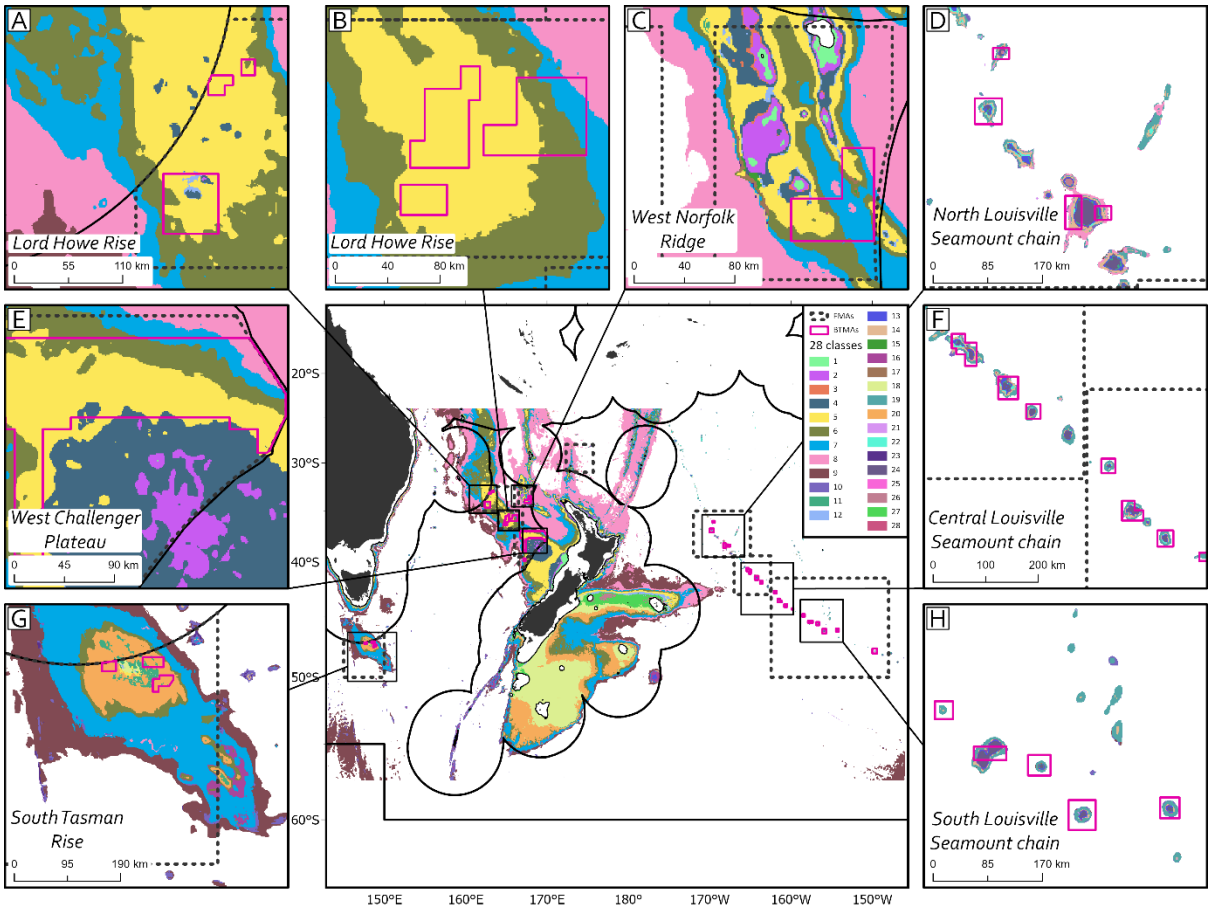

Figure 9-18 | Geographic distribution of the 28-group classification derived from the bootstrapped gradient forest model fitted with genus-level VME indicator occurrence information. Black lines indicate the boundaries between the SPRFMO Evaluated Area and the multiple Exclusive Economic Zones (EEZs), dotted lines show Fishery Management Area (FMA) boundaries, and pink lines show Bottom Trawl Management Area (BTMA) boundaries.