Marine Biodiversity Framework for Aotearoa New Zealand

Biological Diversity Mapping

Prepared for Department of Conservation

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Executive summary

The Oceans Secretariat was established in Aotearoa New Zealand in 2021 to take a multi-agency approach to ensure the long-term health and resilience of coastal and marine ecosystems. Officials from the Department of Conservation (DOC), Ministry for Primary Industries (MPI) and the Ministry of the Environment (MfE) developed a work plan which included the development of a shared agency view of national priorities for marine biodiversity. A key priority is a consistent approach to identifying areas of importance for biodiversity. Such areas are regularly integrated into decision-making and management across a range of marine policy including planning for marine protected areas, aquaculture, and renewable energy.

Agencies have agreed to adapt the Key Ecological Areas (KEA) framework developed by the Marine Protected Areas Science Advisory Group to build a standardised mapping methodology for each criterion. The KEA framework describes nine criteria that can be used to identify areas of high conservation value. These criteria include: 1) Vulnerability, Fragility, Sensitivity or Slow Recovery; (2) Uniqueness / Rarity / Endemism; (3) Special Importance for Life History Stages; (4) Importance for Threatened / Declining Species and Habitats; (5) Biological Primary Productivity; (6) Biological Diversity; (7) Naturalness; (8) Ecological Function; and (9) Ecological Services. In this study, we develop a framework to map criterion 6, Biological Diversity. A KEA under the Biological Diversity criterion is an area that “contains comparatively higher diversity of ecosystems, habitats, communities or species, or has higher genetic diversity”.

We developed a framework for mapping Biological Diversity using three different methodologies and illustrated its application for five high-level taxa (and disaggregated functional and taxonomic groupings) including macroalgae (two disaggregated functional groups), seabirds (six taxonomic groups), demersal fish (six functional groups), seafloor invertebrates (four functional groups), and cetaceans (two taxonomic groups) across Aotearoa New Zealand's waters. Three methodologies were applied to existing spatial distribution layers for species and species complexes within each grouping to map biodiversity across space: 1) Stacked richness, 2) Zonation prioritisation and 3) Macroecological modelling. The methodologies incorporated model uncertainties for the spatial layers, with an additional consideration of seafloor condition for seafloor invertebrates. Example layers for top 5% and 10% areas are identified for seafloor invertebrates, to demonstrate how the maps could be used to identify priority areas for management.

Output maps for each approach and each grouping are presented in the report. The spatial areas of high diversity are consistent across approaches for some groupings (e.g., central Chatham Rise for seafloor invertebrates) yet this for other groupings areas of high diversity are inconsistent between approaches reflecting that the methodological approaches capture different aspects of biodiversity. For example, the stacked approach captures areas of high richness, but does not capture potential critical habitat for rare species. In contrast, the Zonation approach ensures the top priority areas are representative across all species regardless of rarity (provided an input layer is available). Providing multiple methodological approaches within the mapping framework allows for the tailored application of the most appropriate approach depending on the management situation. When the appropriate approach is selected, thresholds that identify high biodiversity areas can be used. The sensitivity of these thresholds can be adjusted based on the management decisions or needs of the end user. The framework developed here allows systematic mapping of biodiversity, with multiple options to adapt the outputs for particular management objectives. This framework could be further developed to incorporate maps for additional KEA criteria, with overlapping high value areas defined as priority areas for conservation.

1 Introduction

1.1 Background

Our marine environment is affected by a significant range of stressors, including land use, climate change, extractive uses, and pollution. To minimise risks to biodiversity, it is critical that use of the ocean and its resources is sustainably managed, allowing mixed resource use, whilst protecting high biodiversity areas (Edgar et al. 2014; Halpern 2014).

In Aotearoa New Zealand, the Oceans Secretariat (comprising of officials from the Department of Conservation, Ministry for Primary Industries and Ministry for the Environment) was established in 2021, to support achievement of the vision of the Oceans and Fisheries portfolio which is to "ensure the long-term health and resilience of ocean and coastal ecosystems, including the role of fisheries".

As a step towards achieving the vision of the Oceans and Fisheries portfolio, the Oceans Secretariat intends to develop a shared agency view of national priorities for marine biodiversity. Currently, government agencies that develop marine policy/legislation and management strategies relating to activities such as MPA planning, aquaculture, fishing, and infrastructure in the marine environment do not have a consistent approach to identifying areas of importance for biodiversity. A consistent and agreed approach is required so that the decision-making process for identifying important areas across sectors is transparent and defensible.

Marine directors from across the Oceans agencies agreed that relevant existing work by the Marine Protected Areas Science Advisory Group (MSAG) would form a good basis to work from. Criteria to identify Key Ecological Areas (KEA), largely based on EBSA criteria, were developed by the MSAG (Freeman et al. 2017). The KEA criteria are: 1) Vulnerability, Fragility, Sensitivity or Slow Recovery; (2) Uniqueness / Rarity / Endemism; (3) Special Importance for Life History Stages; (4) Importance for Threatened / Declining Species and Habitats; (5) Biological Primary Productivity; (6) Biological Diversity; (7) Naturalness; (8) Ecological Function; and (9) Ecological Services (Freeman et al. 2017). Oceans agencies are adapting these criteria for the purpose of identifying areas of importance for biodiversity, and seeking to develop methodologies to map areas of importance against the criteria.

1.2 Project context

A cross-agency working group (with members from each Oceans agency) agreed that the sixth KEA criterion, Biological Diversity, would be the first criterion to focus on as it was generally acceptable to all agencies, feasible with relevant data available including species richness information held on a range of taxa, and it will be relevant for multiple work programmes (e.g., resource management reform, MPA planning, aquaculture, offshore renewable energy).

KEAs under the Biological Diversity criterion are areas that "contain comparatively higher diversity of ecosystems, habitats, communities or species, or have higher genetic diversity". This study investigated various methodologies for defining important areas of Biological Diversity for several taxa, including macroalgae, seabirds, demersal fish, seafloor invertebrates, and cetaceans. The output of this work is a portfolio of maps depicting areas important for diversity and some guidance on how these could be refined and used in marine spatial planning processes.

Prior DOC contracts to NIWA have compiled ecological datasets to describe nine KEA criteria (DOC investigation number 4735), which were then evaluated for comprehensiveness and uncertainty (DOC investigation number 4759). The KEA criteria were then compared to the IUCN's framework (Key Biological Areas) to determine if international methodologies for defining marine protected areas could be adapted to the KEA framework (DOC investigation number BIO205). These projects are built upon here to develop a framework for mapping marine biodiversity. In addition, this report considers the influence of other KEA criteria on Biological Diversity (i.e., criterion 3: Special Importance for Life History Stages, and criterion 7: Naturalness). Outside of this project, the working group will consider the policy implications of this work to incorporate the methodologies developed here into marine spatial planning in Aotearoa New Zealand.

2 Methods

Throughout the results and discussion, reference is made to depth classes and seafloor features in Aotearoa New Zealand's Exclusive Economic Zone (EEZ). For reference see Figure 2-1 for a map showing the bathymetry of Aotearoa-New Zealand's EEZ. Major seafloor features referred to throughout this report are labelled.

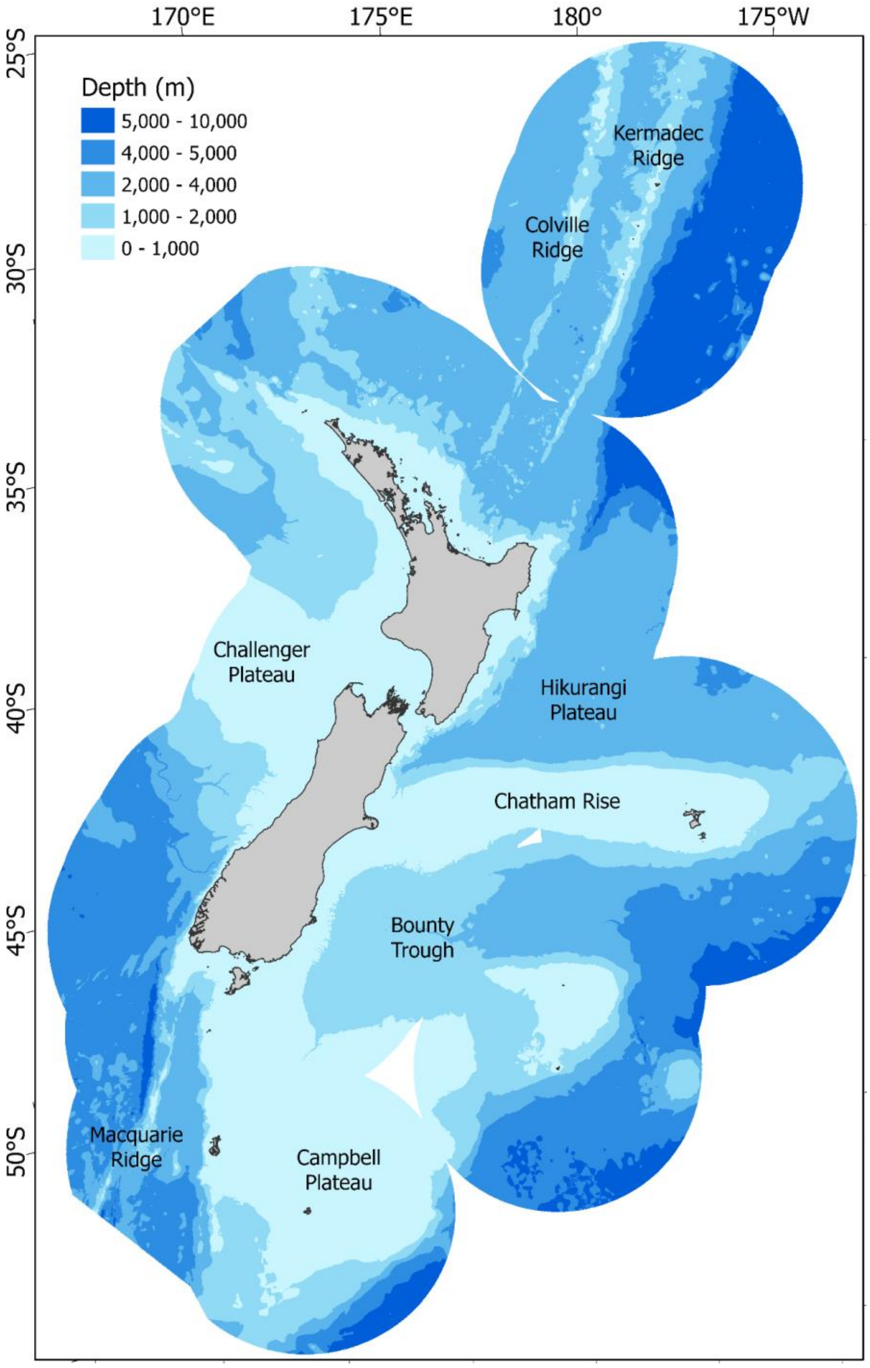

Figure 2-1: Depth (m) and major seafloor features in Aotearoa New Zealand's economic exclusion zone (EEZ).

2.1 Data

The Aotearoa New Zealand government holds many datasets that can be used to inform the delineation of KEAs (Lundquist et al. 2020b). The layers used to map Biological Diversity are outputs (predictions) from spatial models (e.g., species distribution models) for various taxa groupings (e.g., individual species, species complexes and genera) across five high-level taxa groups:

- Seafloor invertebrates (205 genera)
- Demersal fish (234 species and grouped species complexes)
- Macroalgae (82 species)
- Seabirds (73 species)
- Cetaceans (12 species and grouped species complexes)

The layers used to map biodiversity for demersal fish, macroalgae, cetaceans and seafloor invertebrates are modelled layers of habitat suitability. Habitat suitability models (often referred to as species distribution models and environmental niche models, interchangeably) are correlative models that predict the distribution of suitable environmental ranges for species (Guisan and Zimmermann 2000; Guisan et al. 2013; Stephenson et al. 2021b) using information on species occurrence and spatially explicit environmental data. Throughout this report, these modelled layers will be referred to as habitat suitability models.

Most habitat suitability models used in this project are available from the DOC marine portal (https://doc-marine-data-deptconservation.hub.arcgis.com/), with the exception of cetacean and seabird layers. The demersal fish, cetaceans and seafloor invertebrate layers have a resolution of 1 km x 1 km and macroalgae layers have a resolution of 250 m x 250 m. Several layers in each taxa group were not carried through to analyses, these taxa have therefore been omitted from lists of layers used here (Appendix A). These included: 1) layers that failed an expert evaluation process or internal model fit evaluation (see Stephenson et al. (2023a) for details); 2) layers that represented invasive species (as these may be considered when mapping the Naturalness criterion); and 3) layers that were not deemed robust, i.e., did not undertake routine model validation. For example, a total of 30 cetacean layers are available (Stephenson et al. 2020), however only 12 of these layers included sufficient data to allow a bootstrapped approach to estimating the model fit and uncertainty. The exception to these 'rules' were the seabird distribution layers which were not developed using a spatial modelling approach (see below).

The seabird spatial distributions used for this project were developed by Birdlife (2015) and are annual averages of breeding, and non-breeding, at-sea distributions for 73 species, including 3 species that were not split by breeding and non-breeding distributions (Birdlife 2015; Richard et al. 2017). The seabird distribution layers have a resolution of 1 km x 1 km and were created using several sources and data types including: annual distribution maps from NABIS (a hot spot layer, the 90% and the 100% of the population distributions), BirdLife International global range maps, presence layers, at-sea observations, observer data, telemetry, and the positions of main colonies (Richard and Abraham 2013). These data were combined using several weighting strategies with the density of breeding seabirds assumed to decrease exponentially with increasing distance from colonies. Information of colony size, location, and the exponential rate of decrease were obtained from the literature (Richard and Abraham 2013; Richard et al. 2017). As these layers were not produced using typical species distribution modelling tools, there are no validation metrics or estimates of uncertainty associated with these spatial predictions (Stephenson et al. 2018). However, in the absence of specific model predictions, the layers likely represent the best available information for seabird distribution at the national scale.

2.2 Biodiversity groups

The broad taxa groups used in this study (demersal fish, macroalgae, seabirds, seafloor invertebrates, and cetaceans) were selected based on data availability. See Stephenson et al. (2018) and Lundquist et al. (2020b) for a review of datasets collated to inform the identification of KEAs. Biological diversity was mapped for each of these broad taxa groups, and also for further disaggregated groups within each broad taxonomic group. Following discussion with the cross agency working group, 20 disaggregated groups were agreed based on their relevance for management (e.g., a group representing 'taxa that form key biogenic habitat') (Table 2-1). For fish and seafloor invertebrates, disaggregated groups were established based on functional zones (i.e., pelagic) or life-history traits (i.e., mobile, sessile). Given the limited number of layers available, the cetacean group was disaggregated into two groups (as more groups would result in very few taxa contributing to biodiversity layers): whales (toothed and baleen) and dolphins (i.e., Delphinidae spp.). Several groupings were informed by expert opinion (taxonomists and ecologists) which was obtained for previous projects contracted to NIWA by FNZ and DOC (Bennion et al. 2023; Stephenson et al. 2023a). Examples include the placement of seafloor invertebrates into the 'key biogenic habitat-forming taxa' group which was informed by experts with a background in the ecology of habitat-forming benthic taxa. The macroalgal groupings were informed by Neill et al. (2016) and split into canopy-forming macroalgae and other macroalgae. Full lists of taxa that comprise each mapped biodiversity group are provided in Table A-1 to Table A-5 in Appendix A. An overview of the sub-groups within each higher-level taxonomic group is provided in Table 2-1 below.

Table 2-1: Broad and disaggregated biodiversity groups mapped, and number of taxa (species, species complexes or genera layers) included in analyses to map each biodiversity group.

Broad taxa group and number of taxa	Disaggregated group	Number of taxa in disaggregated group
Seafloor invertebrates (n=205)	Key biogenic habitat forming	33
Seafloor invertebrates (n=205)	Mobile	125
Seafloor invertebrates (n=205)	Sessile	37
Seafloor invertebrates (n=205)	Pelagic	10
Macroalgae (n=82)	Canopy-forming	14
Macroalgae (n=82)	Other macroalgae	68
Demersal Fish (n=234)	Benthic	45
Demersal Fish (n=234)	Pelagic	22
Demersal Fish (n=234)	Bentho-pelagic	39
Demersal Fish (n=234)	Bathyal-pelagic	39

Demersal Fish (n=234)	Bathyal-demersal	82
Demersal Fish (n=234)	Reef associated	7
Cetaceans (n=12)	Whales	5
Cetaceans (n=12)	Delphinidae	7
Seabirds (n=73)	Shags	11
Seabirds (n=73)	Albatrosses	12
Seabirds (n=73)	Penguins	9
Seabirds (n=73)	Shearwaters	8
Seabirds (n=73)	Petrels	28
Seabirds (n=73)	Other seabirds	5

2.3 Data pre-processing

Single spatial layers that represent the biodiversity of each group were developed using three methods: (1) stacked richness; (2) Zonation decision-support tool; and (3) a macro-ecological model (MEM). For the first two approaches, layers from habitat suitability models previously developed for demersal fish, cetaceans, macroalgae and seafloor invertebrates (Lundquist et al. 2020b; Stephenson et al. 2023a), and spatial layers of seabird densities were used. For habitat suitability model layers, several data processing steps were taken which varied among taxa, depending on the availability of associated uncertainty and environmental coverage layers (Table 2-2).

2.3.1 Incorporating model uncertainty

For the stacked approach, where an uncertainty layer was available (demersal fish, cetaceans, macroalgae, and seafloor invertebrates) (Table 2-2), it was weighted by 0.2 and subtracted from habitat suitability layers. This weighting was chosen to ensure consistency with other spatial planning exercises in Aotearoa New Zealand (Bennion et al. 2023), and past studies which determined that 0.2 provided an optimal weighting for balancing the discounting of low habitat suitability areas, while not resulting in their complete removal (Rowden et al. 2019; Lundquist et al. 2020a). Essentially, this process reduces the importance of grid cells with high uncertainty (standard deviation, SD or coefficient of variation, CV). For the Zonation approach, the layers were not pre-adjusted to consider uncertainty, but associated uncertainty layers were included within the Zonation prioritisation.

2.3.2 Considering environmental coverage

Cetacean layers were clipped to areas of high environmental coverage when such data layers were available (Table 2-2). Environmental coverage is a representation of how well the training data used to create the models is distributed across the total the environmental space. The layer ranges from 0 to 1 where 0 indicates very low sampling of the environmental space and 1 a very high level of sampling (see Stephenson et al. (2020) and Stephenson et al. (2021b) for details. A cut-off was used based on the value (0.075) applied in Stephenson et al. (2020) to exclude poorly sampled areas for cetaceans within Aotearoa New Zealand’s EEZ. The generation of biodiversity layers for cetaceans was undertaken both with and without this restriction to give users the option of using the ‘clipped’ and ‘unclipped’ extents. A restriction of the modelled spatial extent based on environmental coverage was not used for demersal fish, seafloor invertebrates and macroalgae. For demersal fish and seafloor invertebrates, habitat suitability was clipped to a maximum depth of 2000 m based on the very low coverage of occurrence data beyond 2000 m for these taxa (Lundquist et al. 2020a). No further clipping to environment coverage was performed, as there was strong overlap between low environmental coverage and the 2000 m depth contour, with <0.01 environmental coverage below 2000 m for both demersal fish and seafloor invertebrates. Surveys for several groups (e.g., seafloor invertebrates) likely do not include representative inshore communities. The extent of inshore sampling is regionally variable, and thus a minimum depth was not included as this would remove some areas that are well sampled. Caution is therefore advised for the interpretation of shallow water biodiversity for seafloor invertebrates in particular (Table C-2).

The macroalgae layers have been generated for the spatial extent of rocky reefs in Aotearoa New Zealand to a maximum of 40m depth, based on DOC's national rocky reef layer (Lundquist et al. 2020b; Stephenson et al. 2023a). There is reasonable coverage of macroalgae across the environmental gradients within the extent of the rocky reef spatial layer. Further, given that the predicted distributions have been restricted to rocky reef habitat, it was decided that no additional reduction of the spatial extent was necessary.

2.3.3 Considering historical trawl impact

For seafloor invertebrates, a ‘condition’ layer to account for the impact of historical fisheries-related stressors on seafloor invertebrate communities has been recently used for spatial planning exercises in Aotearoa New Zealand (Bennion et al. 2023). Habitat suitability models only consider environmental variables, with predicted high suitability in areas that have been altered by fishing. Considering habitat condition allows for a more accurate prediction of the relative probability of presence. A condition layer for seafloor invertebrates has been produced based on the number of trawls conducted within a grid cell and the unique responses of functional assemblages to such disturbance (Rowden et al. in review, FNZ project BEN2019-04). The method used to develop this condition layer is detailed by Mormede et al. (2017), often referred to as ‘MSRP’ (Mormede, Sharp, Roux, and Parker) naturalness. For seafloor invertebrates, these three fishing impact layers (large, erect hard sessile taxa, small, fragile and encrusting taxa, and deep burrowing infauna) have been applied to the respective taxa spatial distribution (Table A-1). The condition layers are scaled 0-1 and are subtracted from predicted habitat suitability layers to reduce the relative probability of presence in grid cells that have been highly impacted (e.g., contain a high number of trawls). In this way, relative habitat suitability is weighted by the scale of historical disturbance. The creation of biodiversity layers for seafloor invertebrates was undertaken with and without condition applied to illustrate the outcomes of this data-processing step and the subsequent implications for the mapping of biodiversity.

2.3.4 Habitat suitability threshold

In the final data preparation step, a ROC (Receiver Operating Characteristic) derived cut-off was applied to the individual habitat suitability layers (i.e., all layers except the seabird distribution layers). The ROC cut-off is used to remove spatial predictions in areas where the probability of taxa occurrence is unlikely. Cell values below the ROC cut-off are set to zero to remove the contribution of these cells for calculating biodiversity. This method for removing the contribution of areas with low likelihood of occurrence is often applied in Aotearoa-NZ marine spatial planning exercises (Bennion et al. 2023). For the Zonation approach, the values above the ROC cut-off are retained (i.e., ROC-linear). For the stacked approach, all values above the cut-off are given a value of one, indicating that the taxon is present within a cell (i.e., ROC-binary). This distinction between methods is to aid interpretability of the stacked richness approach, where the aim was to have an alpha diversity-based richness layer output which would essentially contain alpha diversity (counts) of taxa in each grid cell. To achieve this, the input layers needed to be binary. For the Zonation approach, the cell removal algorithm performs better with raster layers with on a continuous scale (0-1), though binary layers can be used as inputs. A continuous (0-1) rank priority layer is the core zonation output regardless of whether the input layers are binary or continuous, however binary inputs reduce valuable information that could be used to inform the cell removal algorithm.

2.3.5 Seabird layers

Much of the processing discussed above does not apply to the seabird layers, as they are not ‘species distribution models’, and thus do not have associated uncertainty, environmental coverage, or a ROC derived cut-off. For most of the seabird taxa, there are breeding and non-breeding spatial layers at the spatial extent of the EEZ. Further, the maximum values in the spatial layers differ greatly among taxa. As these layers are density estimates, this difference is expected given some taxa will be more abundant than others within the spatial extent of Aotearoa New Zealand’s EEZ. To use these layers in the Zonation and stacked approaches, two processing steps were taken, 1) breeding and non-breeding density layers were combined (added) to produce a single layer for each taxon to represent non-seasonal distributions, and 2) each layer was scaled (0-1). This rescaling allowed layers to be equally weighted when used in the stacked approach and is comparable with the Zonation approach where rescaling is conducted within Zonation so that the magnitude of values within a given spatial layer does not skew prioritisations.

Table 2-2: Summary information on the approaches used to map marine biodiversity here. Information on data availability, methodologies and outputs have been included.

	Stacked richness	Zonation	Macroecological model
Taxa groups	Seafloor invertebrates Demersal fish Macroalgae Cetaceans Seabirds*	Seafloor invertebrates Demersal fish Macroalgae Cetaceans Seabirds*	Seafloor invertebrates
Disaggregation possible?	✓	✓	✗
Disaggregation groups	Broad taxa: **5** Disaggregated: **20**	Broad taxa: **5** Disaggregated: **20**	Broad taxa: **1** Disaggregated: **0**
Environmental coverage	✓	✓	✓

Condition (fishing impact)	✓	✓	✗
ROC-threshold application	ROC-binary	ROC-linear	na
Output	Maps of stacked richness	Zonation rank priority maps	Macroecological model output map

*Seabird distribution layers are not HSI layers, do not have probability of occurrence values; no uncertainty layers; naturalness or environmental coverage layer associated with them.

2.4 Method 1 – Stacked richness

The stacked approach makes use of binary presence-absence (demersal fish, seafloor invertebrates, macroalgae, and cetaceans), and scaled (seabirds) layers to estimate alpha diversity (richness) at a variety of spatial extents depending on the taxa group. Alpha diversity is a term used to describe the "within-sample" diversity (Magurran 2021). In essence, it is a measure of how diverse a single sample is (in this case a grid cell), based on the number of different species observed. In this way, the stacked approach used here aims to derive a richness value within each grid cell within respective spatial extents. In other words, richness here refers to the sum of species which are present/likely to be present within a grid cell (Bennion et al. 2022; Stewart-Sinclair and Lundquist 2022; Bennion et al. 2023).

For the stacked approach, binary processed layers for each disaggregated taxa group were summed in R (R-Core-Team 2022), using the *raster* package (Hijmans et al. 2022). The value of the overlapping grid cells was summed, such that areas with higher numbers of overlapping predicted taxa presences will have higher species richness. The approach was repeated for combined 'higher level' taxa groups to produce 33 layers of marine biodiversity (Table 2-3).

2.5 Method 2 – Zonation

Zonation is a decision support-tool which uses an iterative cell removal algorithm to identify priority areas for conservation purposes. Zonation is akin to other well-known spatial prioritisation tools like Marxan and prioritizr (prioritizr is implemented in R). When using Zonation to explore spatial planning scenarios, various settings can be used, such as the inclusion of a resistance layer that represents the connectivity between habitats. For example, in the marine environment this could be marine protected areas or impact layers that represent barriers between fragmented habitats. Zonation is routinely used to inform spatial planning in marine environments in Aotearoa New Zealand (Rowden et al. 2019; Lundquist et al. 2020a; Tablada et al. 2022; Bennion et al. 2023). For the development of biodiversity layers here, Zonation's standard core-area removal algorithm with minimal settings was used, and no additional cost or value options or boundary smoothing algorithms were included (Moilanen et al. 2014).

In the core-area removal algorithm, the cell removal process aims to minimise biological marginal loss by iteratively picking a cell *i* that has the lowest value of occurrence over all biodiversity features in the cell. Therefore, if even one species has a high proportion of its relative occurrence found there, the cell gets a high value. Removal is then carried out by calculating a removal index δ_i for each of the cells using the following equation:

$$\delta_i = \max_j \frac{q_{ij} w_j}{c_i},$$

where w_j is the weight of species j and c_i is the cost of adding cell i to the reserve network. When running the analysis, the programme analyses all cells and calculates a δ_i value for each cell based on the feature that has the highest weighted proportion of distribution remaining in that specific cell. The cell which has the lowest δ_i value will then be removed (Moilanen 2005; Moilanen et al. 2014), i.e., given a low priority ranking. For development of Zonation biodiversity layers here, no additional weighting was used for individual taxa. If weightings were used, this could allow for upweighting protected species, so they have a higher influence on the removal rule i.e., they are retained in the solution longer and will therefore have a proportionally higher influence on where Zonation identifies priority areas.

Whereas the stacked approach involves adding values in each cell, the Zonation core-area removal approach considers how well the value of each layer is represented in the priority ranking (i.e., considering representation of all taxon groups as well as species richness). For instance, if a taxon has a comparatively different distribution to other taxa, it will strongly influence priority ranking as the core-area cell removal algorithm will strive to retain high value cells for this taxon even in areas where other taxa may not have high-value distribution. The Zonation prioritisation tool was used to identify high priority biodiversity areas for combined 'higher level' and disaggregated taxa groups to produce 33 layers of marine biodiversity (Table 2-3).

2.6 Method 3 – Macroecological models

Macroecological models (MEM) are grounded in macro-ecological theory (i.e., that the fundamental characteristics of the environment shape the distribution of biodiversity facets) and fit counts of observed taxa (e.g., observed richness) within defined spatial units as a response to the environmental characteristics of each unit (Moser et al. 2005; Leathwick et al. 2006; Dubuis et al. 2011; Bacheler et al. 2016). Based on the observed relationship between environmental conditions and richness, richness is predicted to a grid of known environmental characteristics. MEM have been used extensively across diverse marine, terrestrial and freshwater systems at a range of scales (Leathwick et al. 2006; Rosset et al. 2010; Dubuis et al. 2011). MEMs provide useful information on the environmental variables and/or habitat characteristics that result in areas of high biodiversity. However, as MEM models count the numbers of species/taxa rather than the distribution of taxa themselves, information on the contribution of individual taxa to diversity is lost.

A MEM was generated for seafloor invertebrate taxa by Brough et al. (in review) using the same dataset used to develop the individual models that underpin the stacked richness layer for seafloor invertebrates (i.e., the occurrence of 205 invertebrate taxa). Taxa identity was summarised to genus level and the number of genera per 1 km cell was summed for each location where some sampling had occurred, throughout Aotearoa New Zealand waters. To account for variation among sampling methods, the number of taxa sampled using four unique gear classes was summarised. The gear classes report the catchability and area sampled of a diverse assemblage of sampling methods (see Stephenson et al. 2021a for more details). The number of unique sampling occurrences was calculated for each cell, for each gear class and was used as an offset to account for variability in sampling effort across cells. The environmental characteristics of each 1 km cell were extracted from a suite of high-resolution environmental datasets including physical seafloor and oceanographic variables (Stephenson et al., 2020). MEMs were generated for each gear class separately using ensemble models of boosted regression trees, random forests, and generalised additive models (see Stephenson et al. (2023a) for details). A final MEM that represents seafloor invertebrate alpha diversity using all gear classes was generated by summing the four individual gear class MEMs. Individual genera were included in a single gear class MEM (the gear class that had the highest number of occurrences), to prevent counting taxa more than once when the final MEM was generated.

As the MEM was developed for seafloor invertebrates as an entire group, not discrete functional groups, it was not possible to apply a fishing condition layer to the group as a whole. The relevant functional group fishing condition layer could not be applied to species within these groups as the condition layers were developed for application at the level of an individual species prediction. The MEM uses counts of species (not presence/absence of individual species) as a response variable, so the condition layers do not hold relevant information for the scaling of the predictions.

2.7 Identifying important areas

Outputs from the three mapping methods (stacked richness, Zonation and macroecological models) provide continuous estimates of biological diversity across all evaluated cells in the analysis. Thresholds can be applied to these values to identify top value areas (or conversely low value areas) for informing management decisions (Bennion et al. 2022; Stewart-Sinclair and Lundquist 2022). Importantly, the sensitivity of thresholds can be tailored depending on the management question or context. Less sensitive (lower) thresholds will identify larger spatial areas as being important, whereas more sensitive (higher) thresholds will identify smaller spatial areas as being important. The selection of thresholds should be both a science and policy decision, based on conservation objectives or specific management goals. To explore how thresholds could be applied, a percentiles approach was used to extract top value areas in biodiversity layers. To demonstrate the application of thresholds, areas with the top 5% and 10% of values were identified and mapped. An example is provided based on the stacked and Zonation approaches, using the high-level biodiversity group seafloor invertebrates with condition (fishing impact) applied, as well as an example for the macroecological model for the same group, without the application of condition.

2.8 Evaluation of layers

As a final step, the high level and disaggregated group biodiversity maps were assessed qualitatively by NIWA ecologists on the project team (Table C-2). Maps were scored either 1 (accurate), 2 (somewhat accurate) or 3 (largely inaccurate) based upon how well mapped biodiversity patterns represented known areas of high and low biodiversity for each group (for detailed descriptions of the categories see Table C-1). Maps with a score 3 were deemed too inaccurate for future management use. Additionally, for each group, specific geographical areas were highlighted that were thought to be accurately or inaccurately representing biodiversity (Table C-2).

Table 2-3: Biodiversity layers developed using the stacked, Zonation and MEM approaches. Spatial extent of biodiversity layers is provided.

Approach used	High-level biodiversity group	Disaggregated biodiversity group	Spatial extent
Stacked richness	Macroalgae	All combined	Rocky reef
	Macroalgae	Canopy forming	Rocky reef
	Macroalgae	Others	Rocky reef

Approach used	High-level biodiversity group	Disaggregated biodiversity group	Spatial extent
	Seafloor invertebrates	All combined	EEZ to 2000 m depth
	Seafloor invertebrates	All combined, no condition applied	EEZ to 2000 m depth
	Seafloor invertebrates	Key biogenic habitat formers	EEZ to 2000 m depth
	Seafloor invertebrates	Key biogenic habitat formers, no condition applied	EEZ to 2000 m depth
	Seafloor invertebrates	Mobile	EEZ to 2000 m depth
	Seafloor invertebrates	Mobile, no condition applied	EEZ to 2000 m depth
	Seafloor invertebrates	Pelagic	EEZ to 2000 m depth
	Seafloor invertebrates	Pelagic, no condition applied	EEZ to 2000 m depth
	Seafloor invertebrates	Sessile	EEZ to 2000 m depth
	Seafloor invertebrates	Sessile, no condition applied	EEZ to 2000 m depth
	Cetaceans	All combined	Area of sufficient data coverage
	Cetaceans	All combined	EEZ
	Cetaceans	Dolphins	Area of sufficient data coverage
	Cetaceans	Dolphins	EEZ
	Cetaceans	Whales	Area of sufficient data coverage
	Cetaceans	Whales	EEZ
	Demersal fish	All combined	EEZ to 2000 m depth
	Demersal fish	Bathyal-demersal	EEZ to 2000 m depth
	Demersal fish	Bathyal-pelagic	EEZ to 2000 m depth
	Demersal fish	Benthic	EEZ to 2000 m depth
	Demersal fish	Benthopelagic	EEZ to 2000 m depth
	Demersal fish	Pelagic	EEZ to 2000 m depth

Approach used	High-level biodiversity group	Disaggregated biodiversity group	Spatial extent
	Demersal fish	Reef	EEZ to 2000 m depth
	Seabirds	All combined	EEZ
	Seabirds	Albatrosses	EEZ
	Seabirds	Others	EEZ
	Seabirds	Penguins	EEZ
	Seabirds	Petrels	EEZ
	Seabirds	Shags	EEZ
	Seabirds	Shearwater	EEZ
Zonation	Macroalgae	All combined	Rocky reef
	Macroalgae	Canopy forming	Rocky reef
	Macroalgae	Others	Rocky reef
	Seafloor invertebrates	All combined	EEZ to 2000 m depth
	Seafloor invertebrates	All combined, no condition applied	EEZ to 2000 m depth
	Seafloor invertebrates	Key biogenic habitat formers	EEZ to 2000 m depth
	Seafloor invertebrates	Key biogenic habitat formers, no condition applied	EEZ to 2000 m depth
	Seafloor invertebrates	Mobile	EEZ to 2000 m depth
	Seafloor invertebrates	Mobile, no condition applied	EEZ to 2000 m depth
	Seafloor invertebrates	Pelagic	EEZ to 2000 m depth
	Seafloor invertebrates	Pelagic, no condition applied	EEZ to 2000 m depth
	Seafloor invertebrates	Sessile	EEZ to 2000 m depth
	Seafloor invertebrates	Sessile, no condition applied	EEZ to 2000 m depth
	Cetaceans	All combined	Area of sufficient data coverage
	Cetaceans	All combined	EEZ

Approach used	High-level biodiversity group	Disaggregated biodiversity group	Spatial extent
	Cetaceans	Dolphins	Area of sufficient data coverage
	Cetaceans	Dolphins	EEZ
	Cetaceans	Whales	Area of sufficient data coverage
	Cetaceans	Whales	EEZ
	Demersal fish	All combined	EEZ to 2000 m depth
	Demersal fish	Bathyal-demersal	EEZ to 2000 m depth
	Demersal fish	Bathyal-pelagic	EEZ to 2000 m depth
	Demersal fish	Benthic	EEZ to 2000 m depth
	Demersal fish	Benthopelagic	EEZ to 2000 m depth
	Demersal fish	Pelagic	EEZ to 2000 m depth
	Demersal fish	Reef	EEZ to 2000 m depth
	Seabirds	All combined	EEZ
	Seabirds	Albatrosses	EEZ
	Seabirds	Others	EEZ
	Seabirds	Penguins	EEZ
	Seabirds	Petrels	EEZ
	Seabirds	Shags	EEZ
MEM approach	Seafloor invertebrates	All combined	EEZ to 2000 m depth

3 Results

3.1 Results - Method 1 - Stacked Richness

The stacked richness approach overlaps the predicted spatial distributions of taxa included in analyses. For this method, each grid cell contains either a 1 (presence) or 0 (absence). When stacked, areas where multiple taxa are considered present are summed. The result of the stacking process is a single biodiversity layer for each taxa group and sub-groups where the highest numbers in the output layer indicate areas with high species richness (overlapping high habitat suitability and areas with low values indicate low richness (overlapping areas of low habitat suitability).

High-level mapped biodiversity groups (e.g., seafloor invertebrates or cetaceans) are shown in the main report along with examples of a sub-group for each high-level biodiversity group e.g., (key biogenic habitat formers or Delphinidae. All other mapped biodiversity layers for the stacked approach are shown in Appendix B.

3.1.1 Taxa 1 – Seafloor invertebrates

Areas of high species richness for all seafloor invertebrates combined (high-level biodiversity group) are predicted along the Chatham Rise (Figure 3-1). The highest species richness (>~65 genera) is mapped on the central area of the Chatham Rise (Figure 3-1). Low species richness (~7 genera) is predicted inshore, typically in areas where water depth is <200 m (Figure 3-1). See Table C-2 for comments on the degree of accuracy associated with inshore versus offshore seafloor invertebrate diversity.

An example of a seafloor invertebrate sub-group (‘key biogenic habitat forming taxa’) further emphasises that this method predicts low species richness for ‘shallow’ areas in coastal Aotearoa New Zealand (Figure 3-2). For instance, the Hauraki Gulf contains almost no cells with species richness values greater than 0-5 genera (Figure 3-2). Areas of comparatively high richness (>10 genera) are mapped on the Kermadec Ridge (Figure 3-2B) and Macquarie Ridge (Figure 3-2).

For seafloor invertebrates, the analysis was undertaken with and without a condition layer (bottom-fishing impact) to allow comparison of the impact of applying this layer for biodiversity mapping. When condition was not applied, the high-level seafloor invertebrates layer contained fewer cells with high richness in the central area of the Chatham Rise (Figure B-1). Instead, high richness areas were present on the northern edge of central Chatham Rise, where the Graveyard Seamounts are present (Figure B-1). In the biodiversity layer for key biogenic habitat groups, low richness (<5 genera) is again mapped in much of Aotearoa New Zealand’s inshore areas (Figure B-4), and areas of high richness are predicted in many of the same areas as the layer in which condition was applied. However, there is comparably higher richness mapped in areas to the northeast and southeast of the Chatham Islands (Figure B-4E).

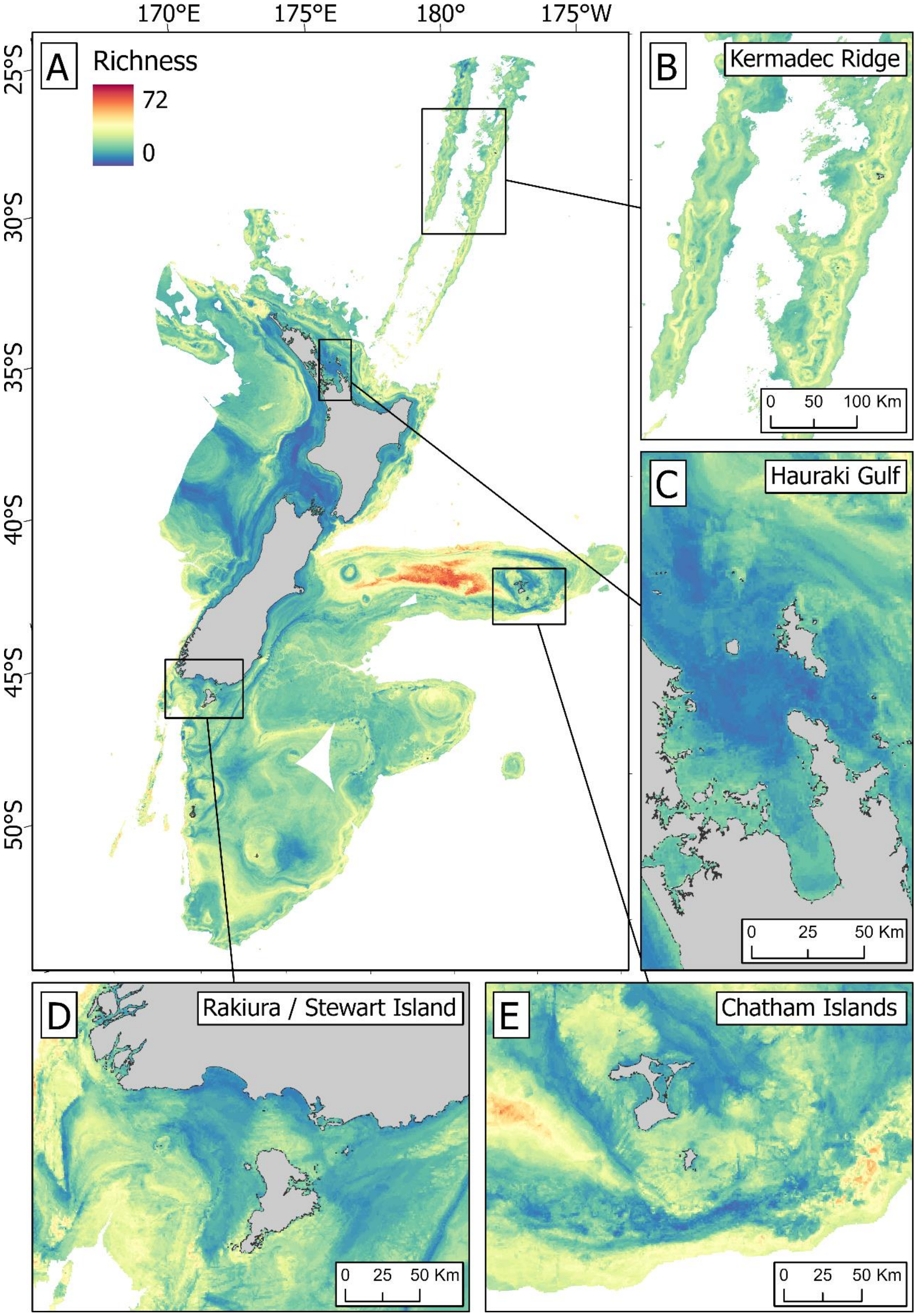

Figure 3-1: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for all seafloor invertebrate taxa (205 genera combined). Condition (fishing impact layer) has been applied. Low richness areas shown in blue, high richness shown in red. Cut-off of mapped extent is 2000 m depth.

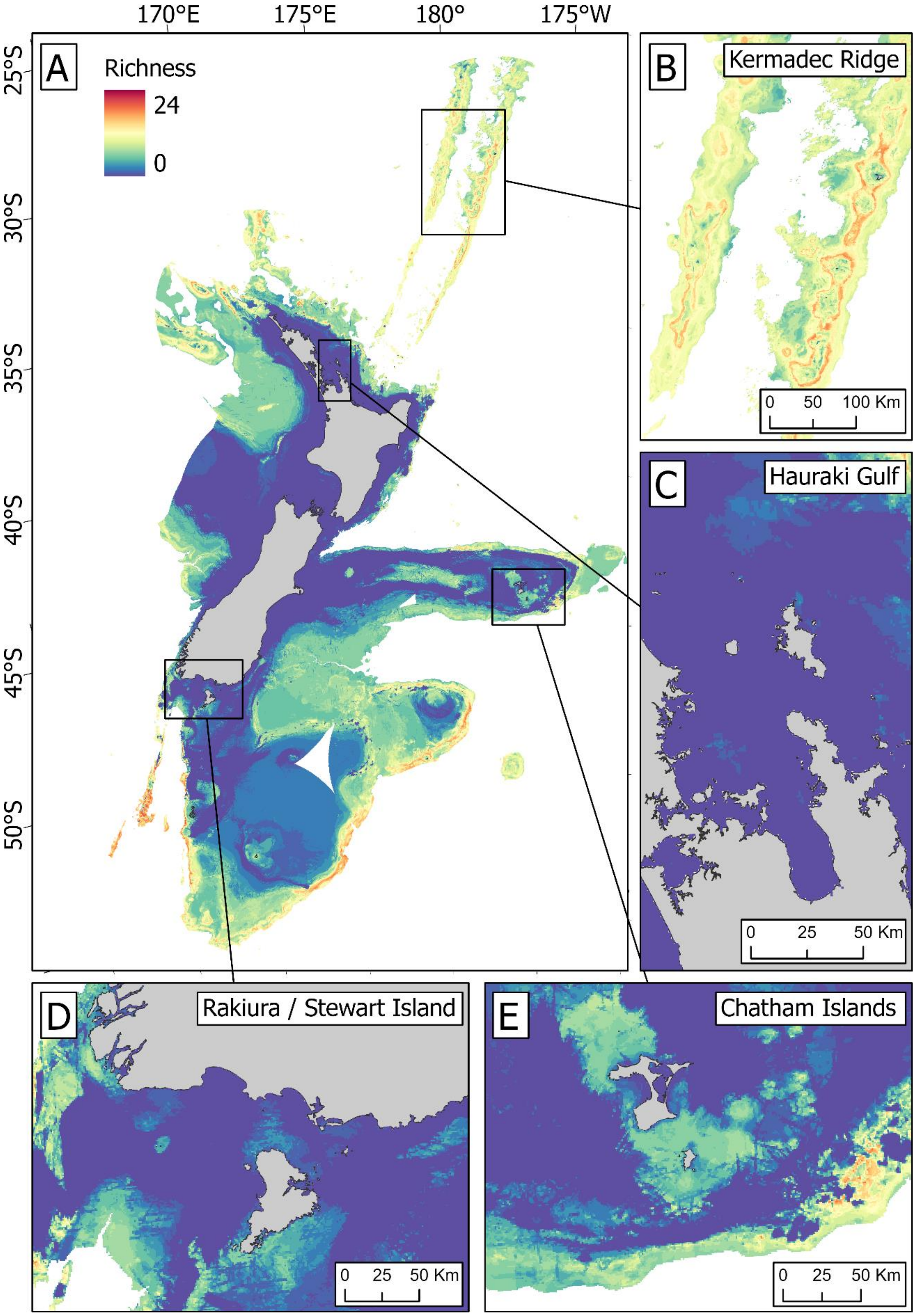

Figure 3-2: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for key biogenic habitat-forming taxa (33 genera). Condition (fishing impact layer) has been applied. Low richness areas shown in blue, high richness shown in red. Cut-off of mapped extent is 2000 m depth.

3.1.2 Taxa 2 – Demersal fish

The high-level biodiversity group (234 species combined) map for demersal fish is shown in Figure 3-3. Mapped richness values are between 30 and 45 in much of the northern areas of the mapped area (i.e., depths shallower than 2000 m). Areas of particularly high richness (>~65 species) are mapped along the northern edge of the Chatham Rise, and eastern edge of the Chatham Rise (east of the Chatham Islands) (Figure 3-3). Very few areas of the lowest richness class (~7 species) are mapped, though some of these areas can be seen inshore around Rakiura/Stewart and the Chatham Islands (Figure 3-3D, E), and Auckland Islands (see blue area South of Aotearoa New Zealand, Figure 3-3).

Bentho-pelagic taxa are provided as an example of a demersal fish sub-group. Bentho-pelagic refers to the functional zone in the water column close to the seafloor where species belonging to this group are found. For this group, low richness is mapped in many of the deeper areas - for example in the Bounty Trough (Figure 3-4). High richness is mapped on the eastern and western sides of central Chatham Rise (Figure 3-4). The highest richness (>13 species) is mapped south of Murihiku/Southland Aotearoa New Zealand (Figure 3-4D) and surrounding the Chatham Islands (Figure 3-4E).

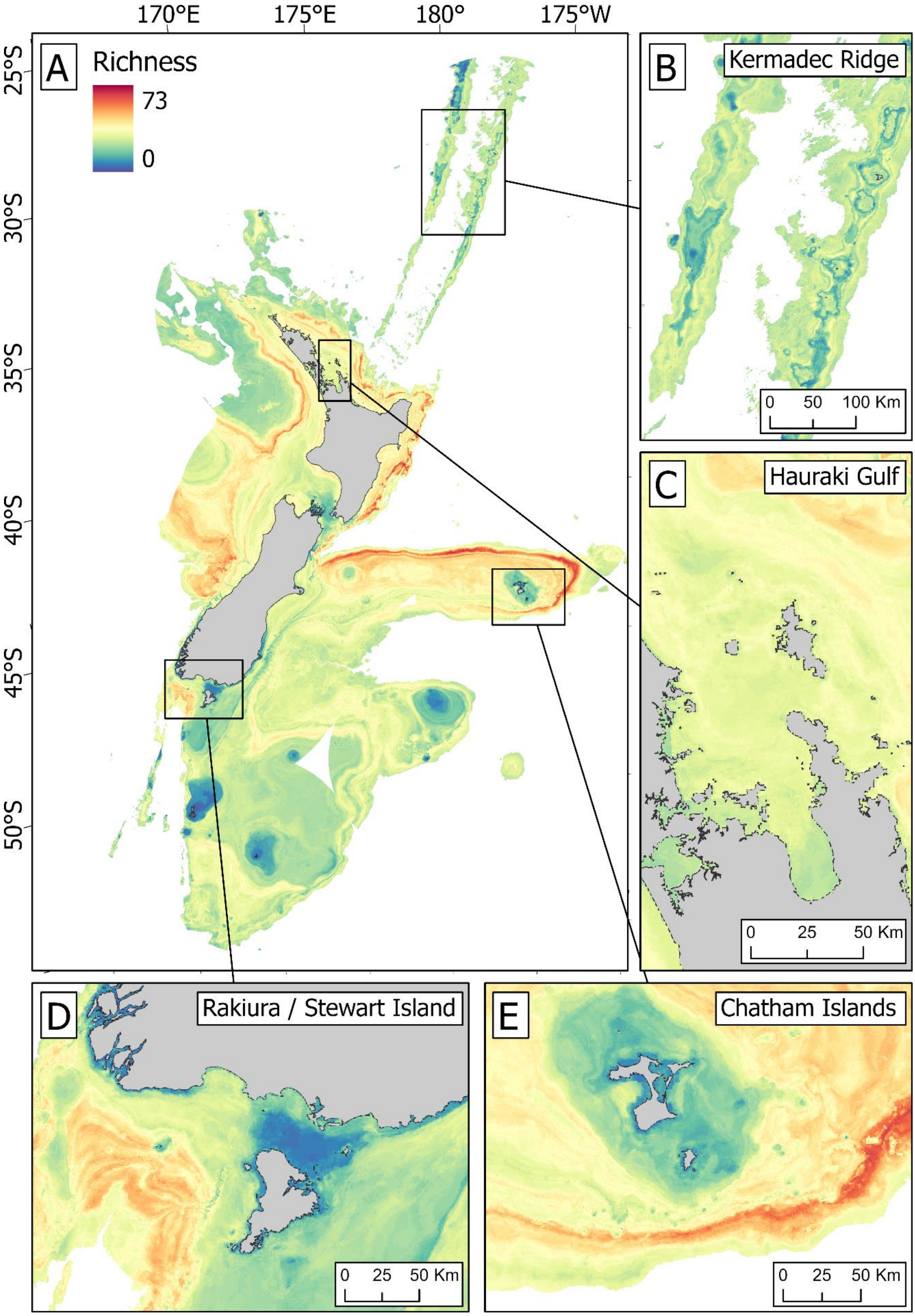

Figure 3-3: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for all demersal fish taxa combined (234 species). Low richness areas shown in blue, high richness shown in red. Cut-off of mapped extent is 2000 m depth.

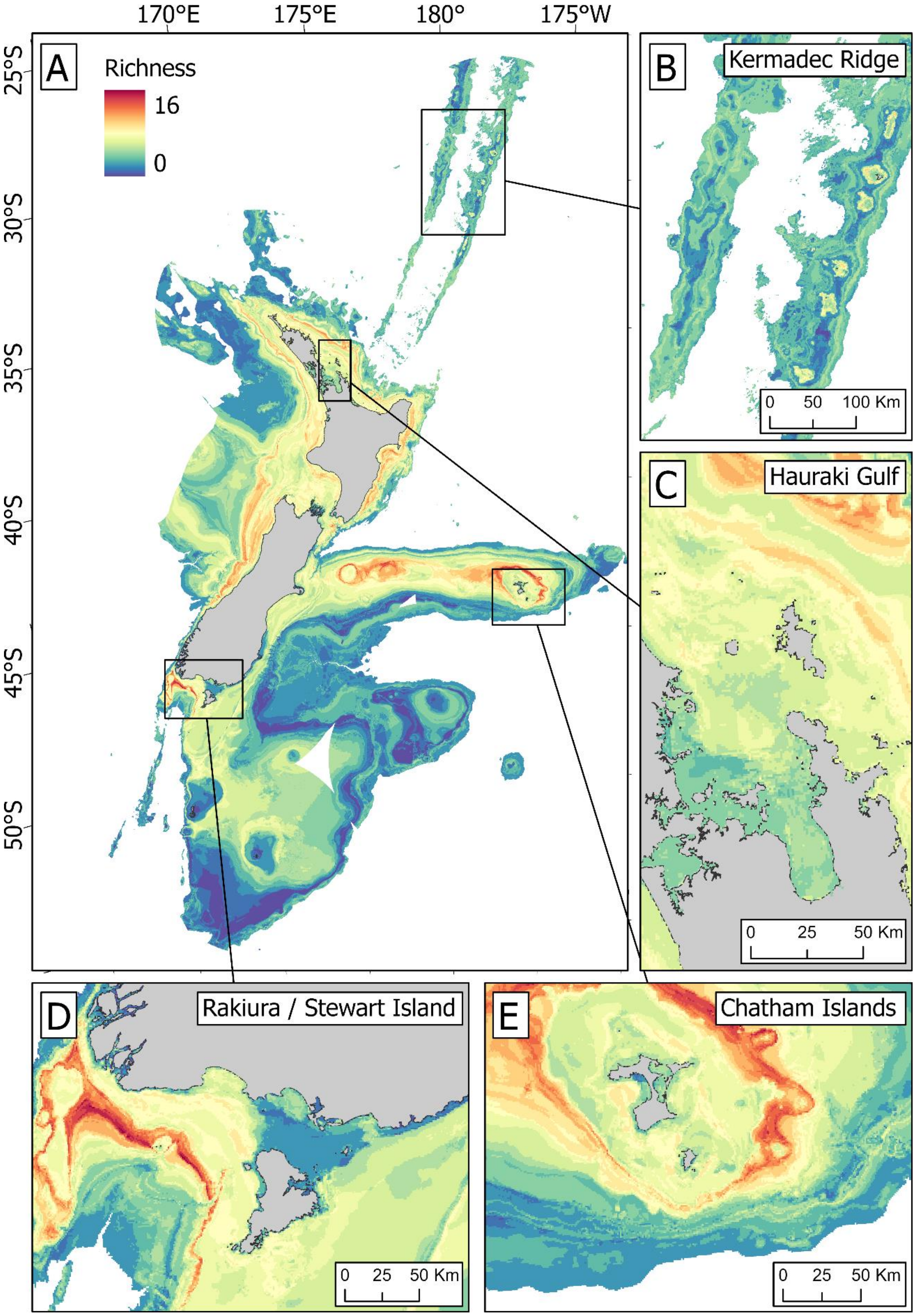

Figure 3-4: **Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for bentho-pelagic taxa (39 species). Low richness areas shown in blue, high richness shown in red. Cut-off of mapped extent is 2000 m depth.**

3.1.3 Taxa 3 – Macroalgae

The macroalgae layers used for biodiversity mapping have been predicted to the distribution of rocky reef habitat around the coast of Aotearoa New Zealand (Lundquist et al. 2020b). The high-level richness map shows areas of high richness (~32 species) predicted in the Wellington region (Figure 3-5E). Comparatively low richness (~7 species) was mapped in Banks Peninsula (Figure 3-5D) and the Mercury Islands, east of the Coromandel Peninsula (Figure 3-5C).

Similar spatial patterns in stacked species richness were observed for the macroalgae sub-group, canopy-forming macroalgae (Figure 3-6). Areas of high stacked richness (>7 species) are in the Wellington region (Figure 3-7E), and surrounding Rakiura/Stewart Island (Figure 3-7D). The other sub-group for macroalgae, i.e., all other macroalgae layers available for mapping, can be found in Appendix B. Areas of high richness (>18 species) are in the Wellington region and surrounds (Figure B-3E), and in several bays throughout Northland. Similar to the canopy-forming macroalgae biodiversity group, areas of low richness have been mapped at Banks Peninsula (Figure B-3D) and the Mercury Islands (Figure B-3C).

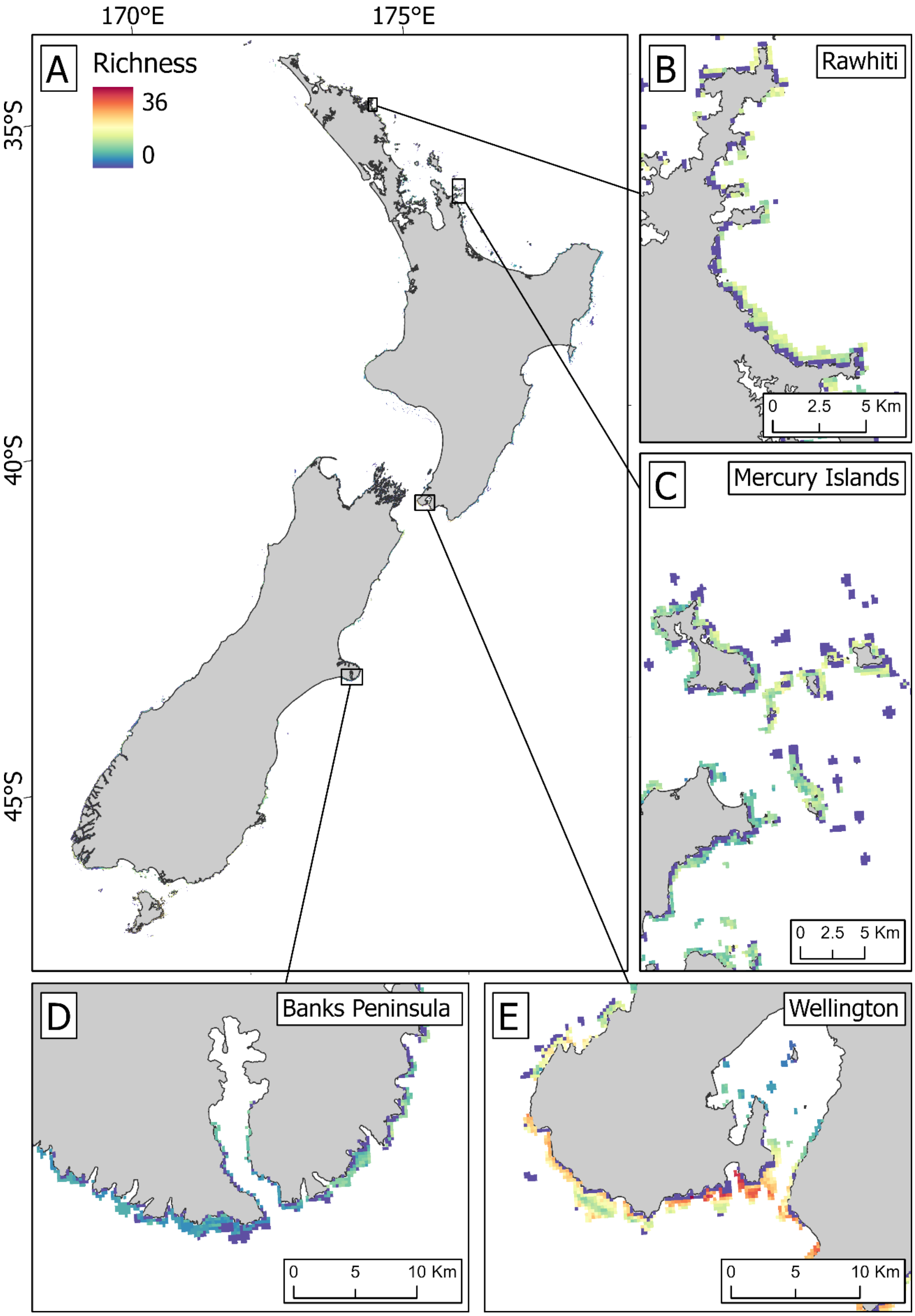

Figure 3-5: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for all macroalgae taxa combined (82 species). Low richness areas shown in blue, high richness shown in red. Mapped extent is restricted to coastal rocky reef.

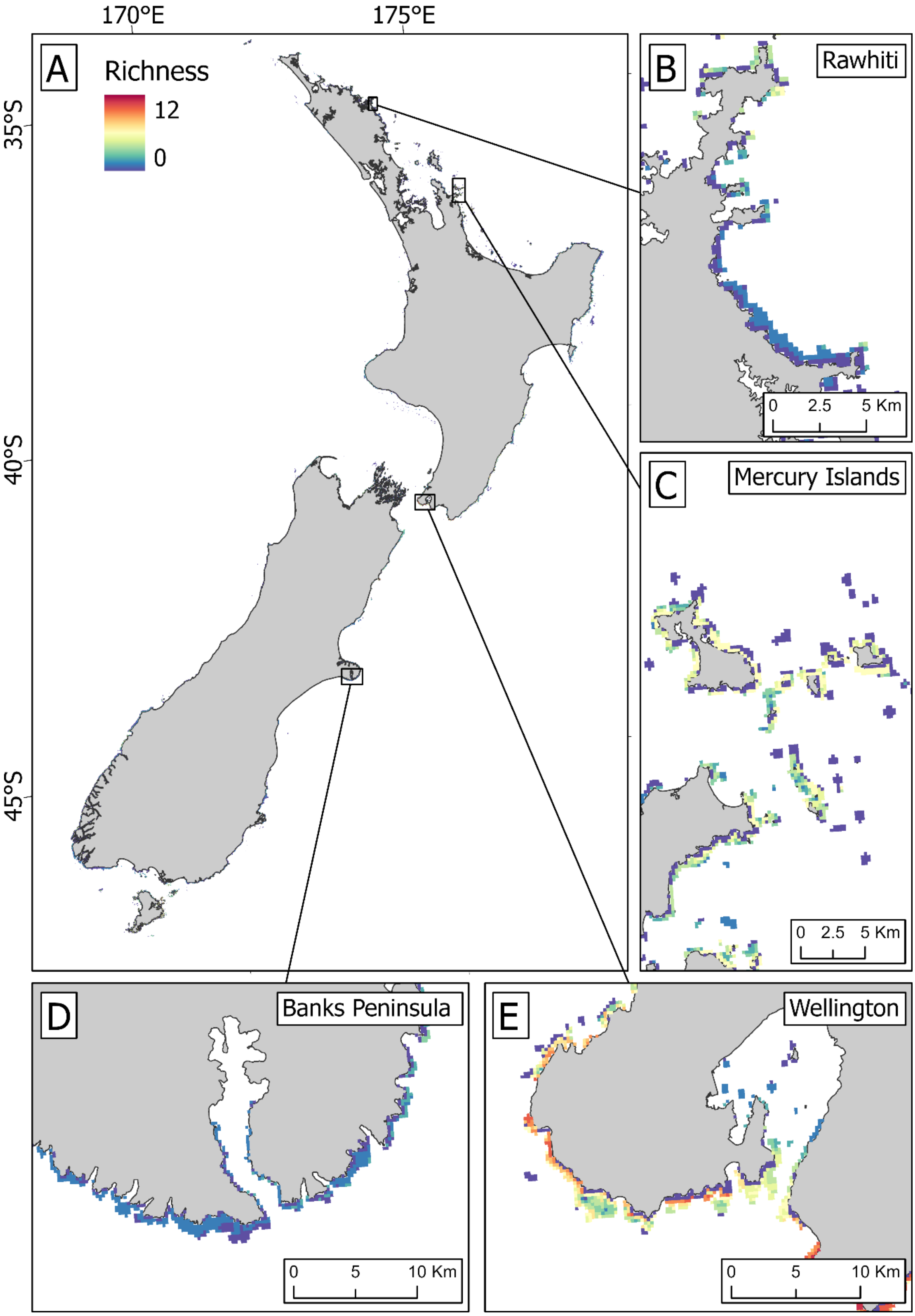

Figure 3-6: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for canopy-forming macroalgae (14 species). Low richness areas shown in blue, high richness shown in red. Mapped extent is restricted to coastal rocky reef.

3.1.4 Taxa 4 – Seabirds

The seabird data available for this biodiversity mapping work were produced using a combination of data sources and were not species distribution models. Thus, in contrast to the biodiversity layers output for other taxa groups, the seabird stacked richness layers were not created with binary (presence-absence) input layers. Instead, density estimates were normalised (linear, 0-1). As with other stacked approaches, the high-level seabird biodiversity group (all species) (Figure 3-7), and an example of one of the biodiversity sub-groups (albatrosses - 12 species) (Figure 3-8) is presented below.

In the combined, high-level seabird layer, highest richness (>21) is located around the coast, over waters shallower than c. 100 m (Figure 3-7). Areas of lowest mapped species richness (<11) are found in the northernmost and easternmost areas of Aotearoa-New Zealand's EEZ (Figure 3-7). For the sub-group example, albatrosses, areas of highest richness (c. 6) are found around the Chatham Islands and Campbell Island (Figure 3-8). Areas of lowest richness (<1) are present in the northern regions of Aotearoa New Zealand's EEZ (Figure 3-8).

It is important to note that there is a significant sampling bias in the seabird datasets, which is evident in the mapped richness layers. The layers are density based, where point samples of species presence are centred around colony locations due to targeted sampling in these areas. Evidence of this bias towards colony locations can be seen in the albatross (Figure 3-8) and petrels (Figure B-12) sub-group layers.

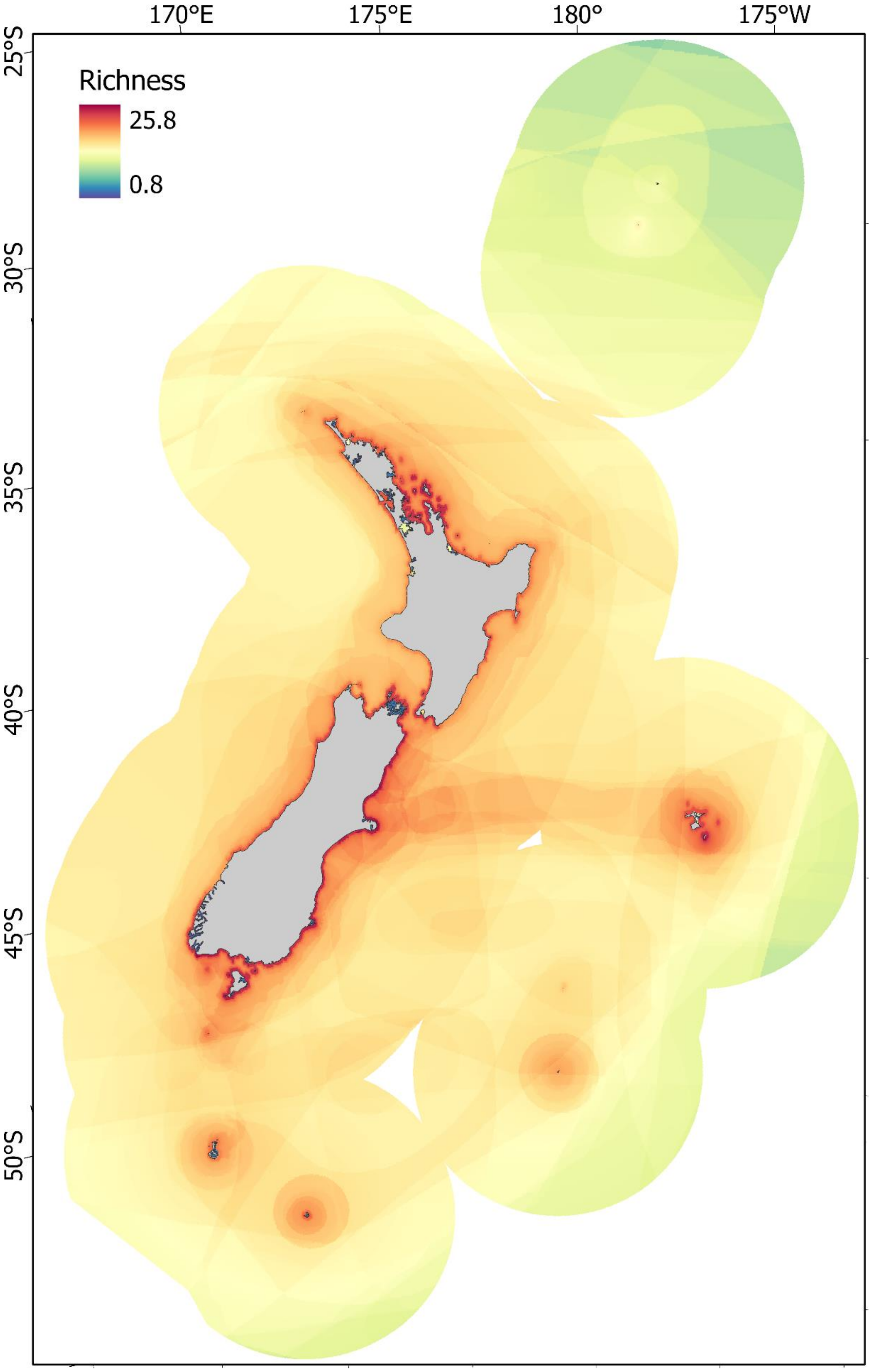

Figure 3-7: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for all seabird taxa (73 species combined). Low richness areas shown in blue, high richness shown in red.

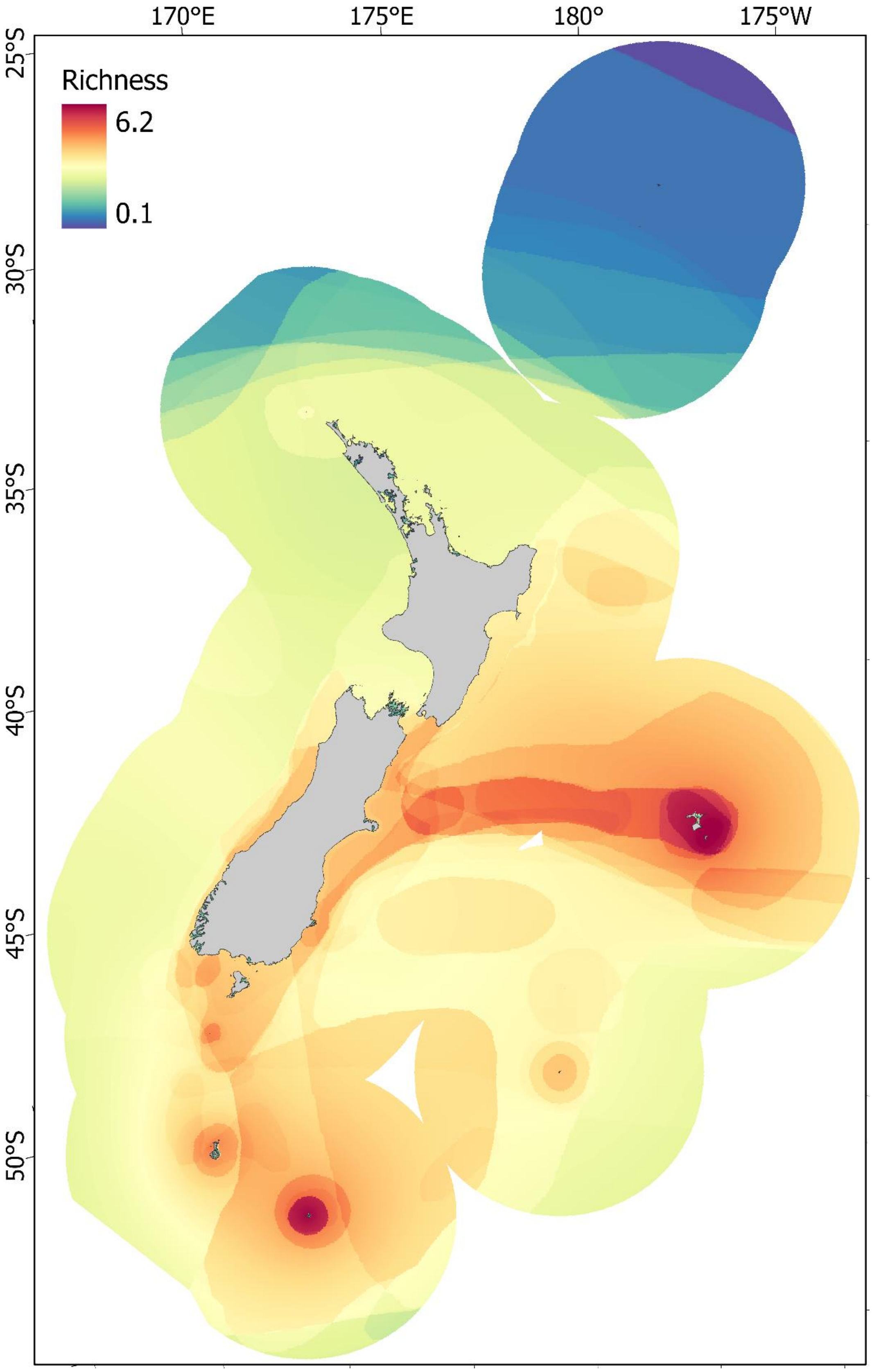

Figure 3-8: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for albatross taxa (12 species). Low richness areas shown in blue, high richness shown in red.

3.1.5 Taxa 5 – Cetaceans

The high-level biodiversity layer for cetaceans (12 species and species complexes combined) is shown in Figure 3-9. Cetacean biodiversity layers presented in-text were clipped to areas greater than 0.075 in the cetacean environmental coverage layer (Stephenson et al. 2020). Unclipped cetacean biodiversity maps, at the scale of the EEZ are provided in Appendix B (Figure B-2, Figure B-17, and Figure B-18). Areas of high richness (>5) are mapped in the southeast of the Chatham Islands, and south of Southland/Murihiku (Figure 3-9). Comparatively low areas of richness (<1) are mapped in the Canterbury Bight south of Banks Peninsula (Figure 3-9D) and north of the Hauraki Gulf (Figure 3-9C).

The cetacean sub-groups show contrasting spatial patterns in stacked species richness (e.g., Delphinidae; Figure 3-10). Areas of high richness are mapped to the east and southeast of the Chatham Islands, and south of Southland/Murihiku Aotearoa New Zealand. In contrast to the high-level cetacean map, the Delphinidae sub-group map shows comparatively high richness (>3) north of the Hauraki Gulf (Figure 3-10C). Low areas of richness (<1) are mapped south of Banks Peninsula (Figure 3-10D), north of the Hauraki Gulf (Figure 3-9C), and east and west of the Far North (Figure 3-10B).

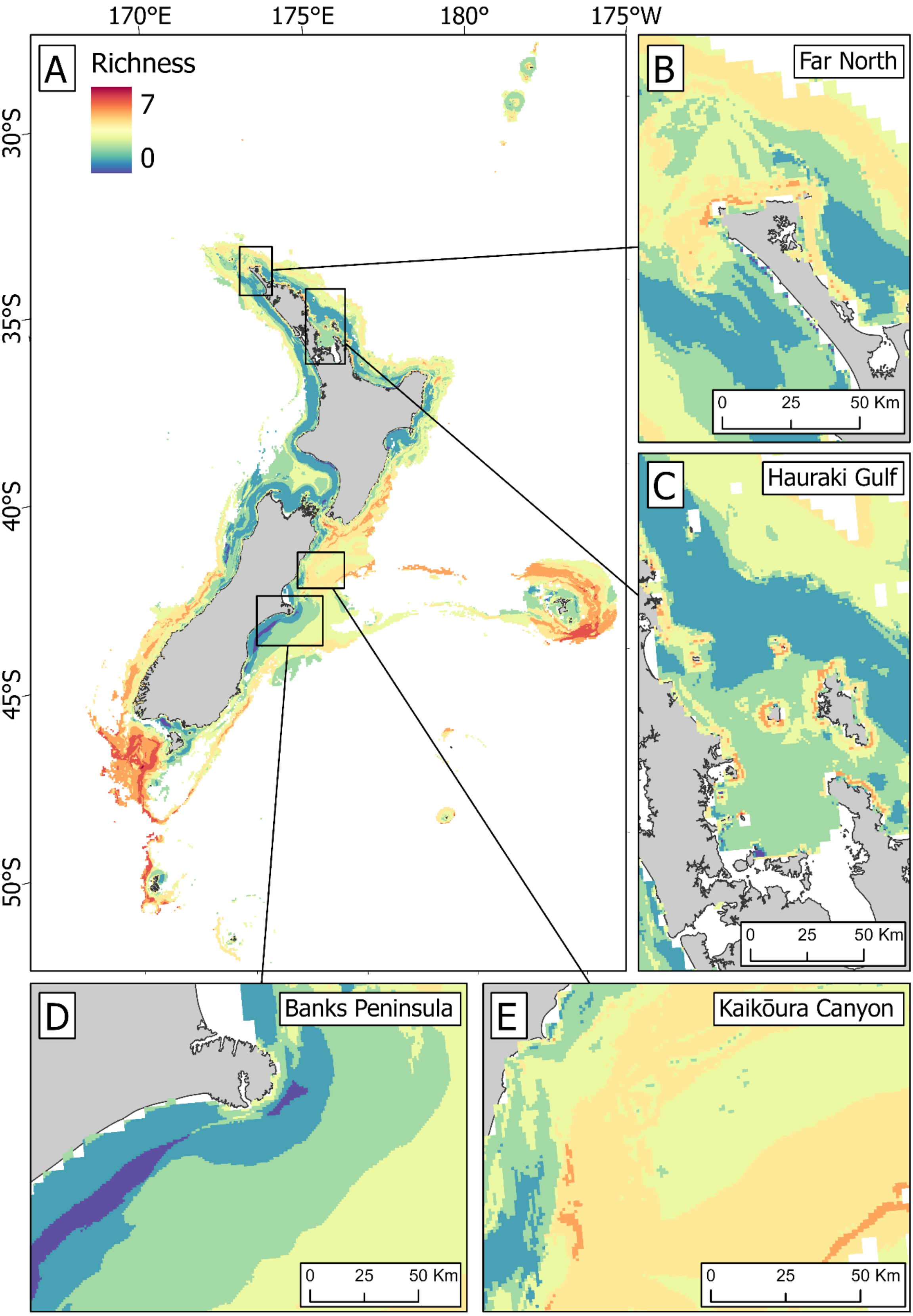

Figure 3-9: **Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for all cetacean taxa combined (12 species). Low richness areas shown in blue, high richness shown in red. Cut-off of mapped extent is areas with environmental coverage values <0.075.**

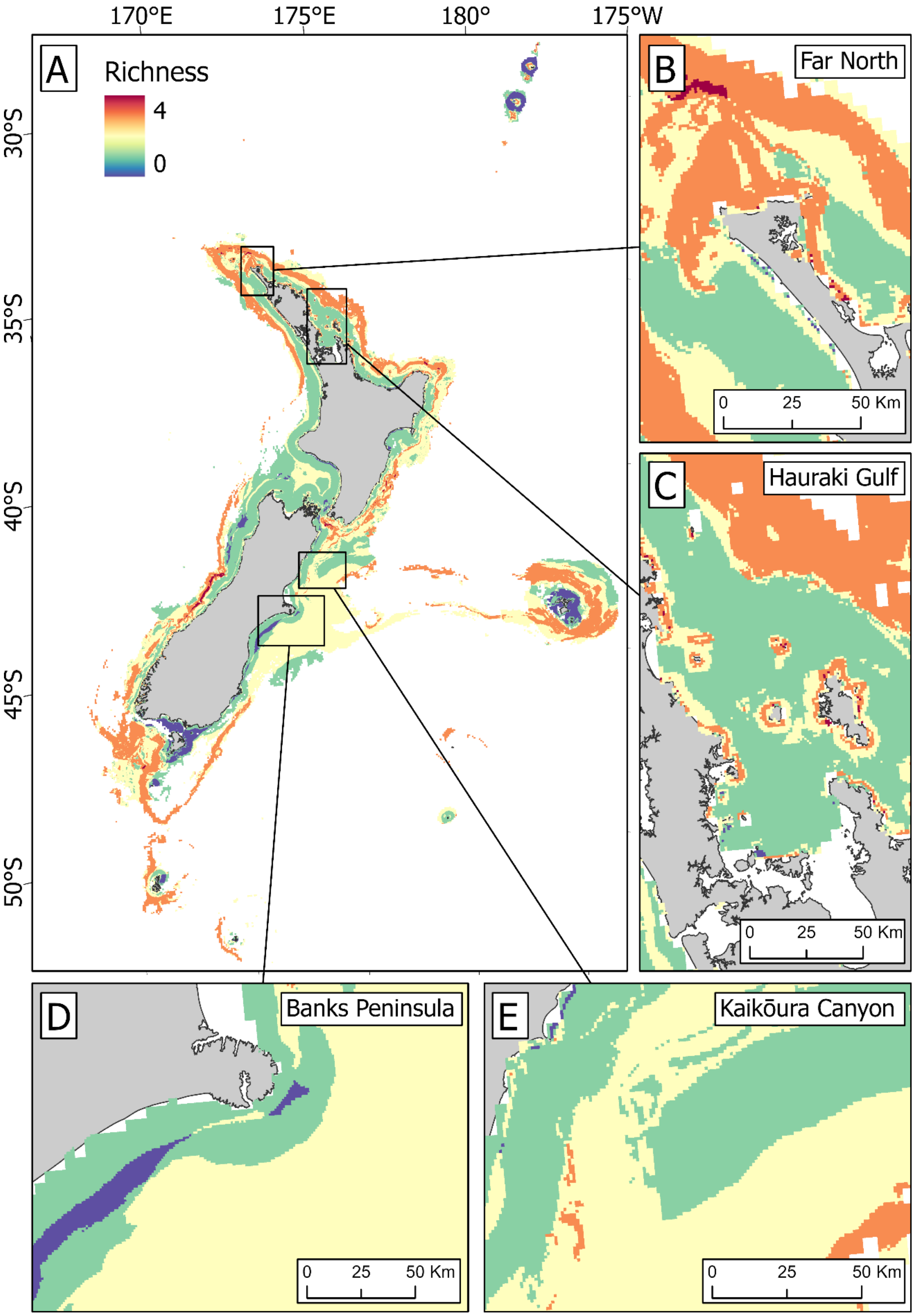

Figure 3-10: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for delphinid taxa (7 species) masked to the area of sufficient environmental cover. Low richness areas shown in blue, high richness shown in red. Cut-off of mapped extent is areas with environmental coverage values <0.075.

3.2 Results - Method 2 - Zonation

The Zonation approach uses the predicted spatial distributions of taxa, and their associated uncertainty, to rank the importance of areas for biodiversity. For this work, the predicted distributions were presence-absence layers for each taxon (except for the seabird taxa group). Input layers were continuous (seabird layers) or ROC-linear. Standard Zonation classes and colour schemes are typically used to present the results of Zonation rank priority maps (see also Lundquist et al. (2020a) and Bennion et al. (2023)). As the output here is being used as a biodiversity output, to align the outputs with the stacked approach, and to allow for comparisons to be drawn, a continuous scale (between 0-1) was used to map output biodiversity layers.

The rank priority map produced by the Zonation approach gives cells a higher value i.e., a value close to one where multiple taxa are considered present, or where key areas are identified based on Zonation core-area cell removal. As with the stacked approach, high-level mapped biodiversity groups (seafloor invertebrates or cetaceans) using the Zonation approach are presented in the main body of the report, along with an example of a sub-group for each high-level biodiversity group (key biogenic habitat formers or Delphinidae). All other mapped biodiversity layers for the stacked approach are shown in Appendix B.

3.2.1 Taxa 1 - Seafloor invertebrates

The high-level Zonation approach map for seafloor invertebrates is shown in Figure 3-11. Areas of high Zonation rank priority are mapped in the inner Hauraki Gulf (Figure 3-11C), surrounding the Chatham Islands (Figure 3-11E), and in the centre of the Chatham Rise (Figure 3-11). Comparatively low areas of Zonation rank priority are mapped in the Bounty Trough, and west of northern Aotearoa New Zealand (Figure 3-11).

The biodiversity sub-group for seafloor invertebrates, key biogenic habitat forming taxa, is shown in Figure 3-12. In general, many areas inshore, c. 100-200 m depth, are mapped with low Zonation rank priority (Figure 3-12). In contrast, high Zonation rank priority areas are mapped in the outer Hauraki Gulf (Figure 3-12C), south of Rakiura/Stewart Island (Figure 3-12), on the central Chatham Rise (Figure 3-12), and along the Kermadec Ridge (Figure 3-12B). All other seafloor invertebrate sub-groups mapped using the Zonation approach are shown in Appendix B (see Figure B-24 and Figure B-27 to Figure B-33).

The maps for seafloor invertebrate biodiversity shown in-text have a condition layer (fishing impact) applied before Zonation prioritisation analyses. Maps without condition applied for the are included in Appendix B. Comparing the outputs, more of the inshore c. 100-200 m area is mapped as high Zonation rank priority when condition is not applied (compare Figure 3-12 and Figure B-27). Additionally, when condition is not applied, a larger extent of the Chatham Rise is mapped with higher Zonation rank priority (Figure B-27).

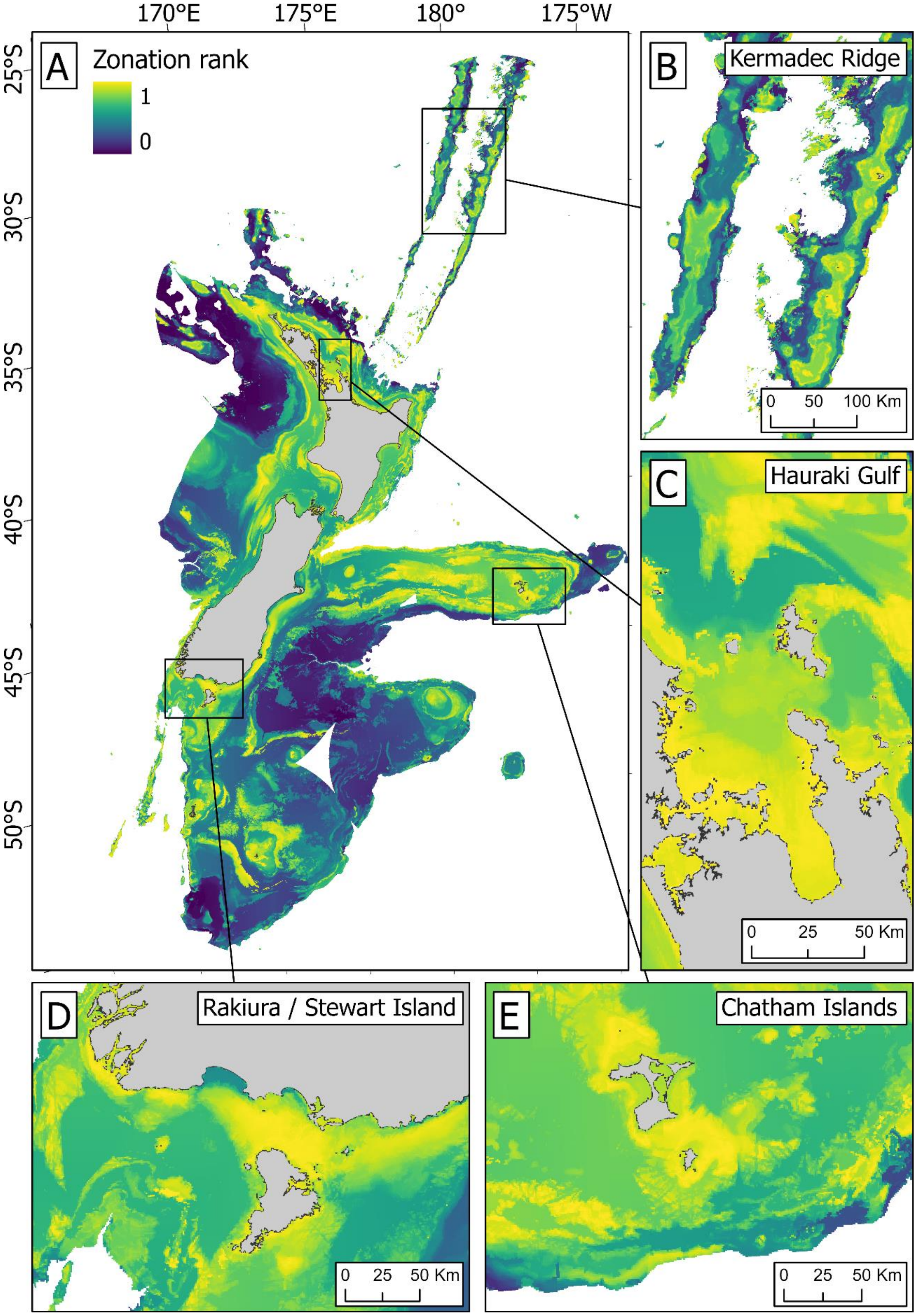

Figure 3-11: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for all seafloor invertebrate taxa (205 genera combined). Condition (fishing impact layer) has been applied. Low rank priority is shown in dark blue, high rank priority is shown in yellow. Cut-off of mapped extent is 2000 m depth.

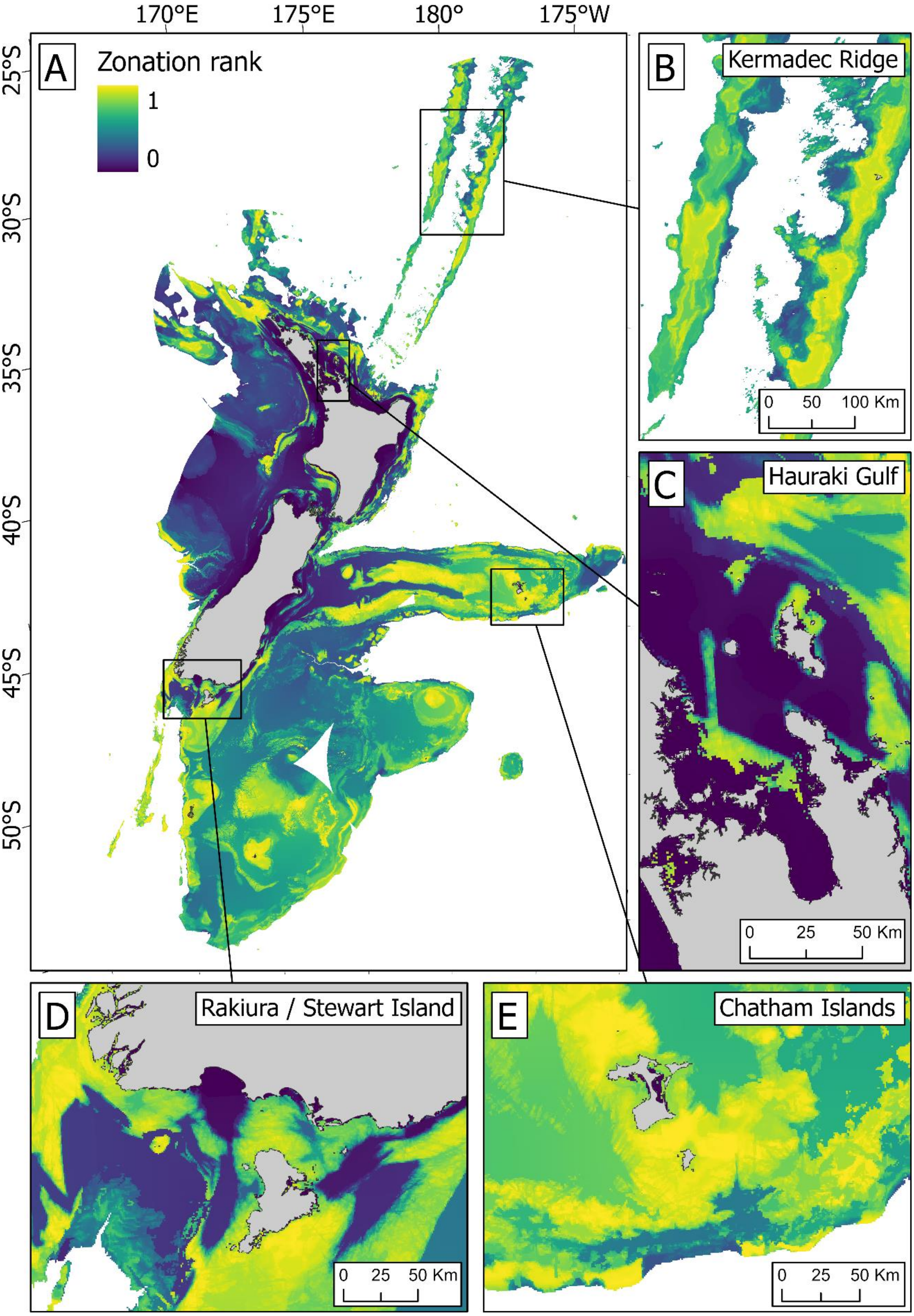

Figure 3-12: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for key biogenic habitat-forming taxa (33 genera). Cut-off of mapped extent is 2000 m depth. Condition (fishing impact layer) has been applied. Low rank priority is shown in dark blue, high rank priority is shown in yellow.

3.2.2 Taxa 2 – Demersal fish

The map for high-level demersal fish biodiversity created using the Zonation approach is shown in Figure 3-13. Areas of high Zonation rank priority are visible around much of Aotearoa New Zealand (Figure 3-13), typically at depths <1000 m. Much of the inner, and outer Hauraki Gulf has been mapped as high Zonation rank priority (Figure 3-13C). In contrast, deeper areas like the Bounty Trough (Figure 3-13) and Kermadec Ridge (Figure 3-13B) have a comparatively low Zonation rank priority. The stacked approach for all demersal fish combined (234 species), showed highest richness on the northern edge of the Chatham Rise and to the east and southeast of the Chatham Islands (Figure 3-3E). However, high Zonation rank priority occurs in different areas (compare Figure 3-3 and Figure 3-13). There is some overlap between the two approaches on several areas on the Chatham Rise, though generally high Zonation rank priority is more evenly distributed across the study area (Figure 3-13).

An example of a demersal fish biodiversity sub-group is shown in Figure 3-14. Areas of high Zonation rank priority are mapped throughout much of the Hauraki Gulf (Figure 3-14C) and in shallow waters around the coast of Aotearoa New Zealand and the southwest Chatham Rise (Figure 3-14). Low Zonation rank priority is mapped along the Kermadec Ridge (Figure 3-14B) and Bounty Trough (Figure 3-14), similar to the high-level demersal fish biodiversity group (Figure 3-13). All other mapped biodiversity sub-groups for demersal fish are included in Appendix B (see Figure B-42 to Figure B-46).

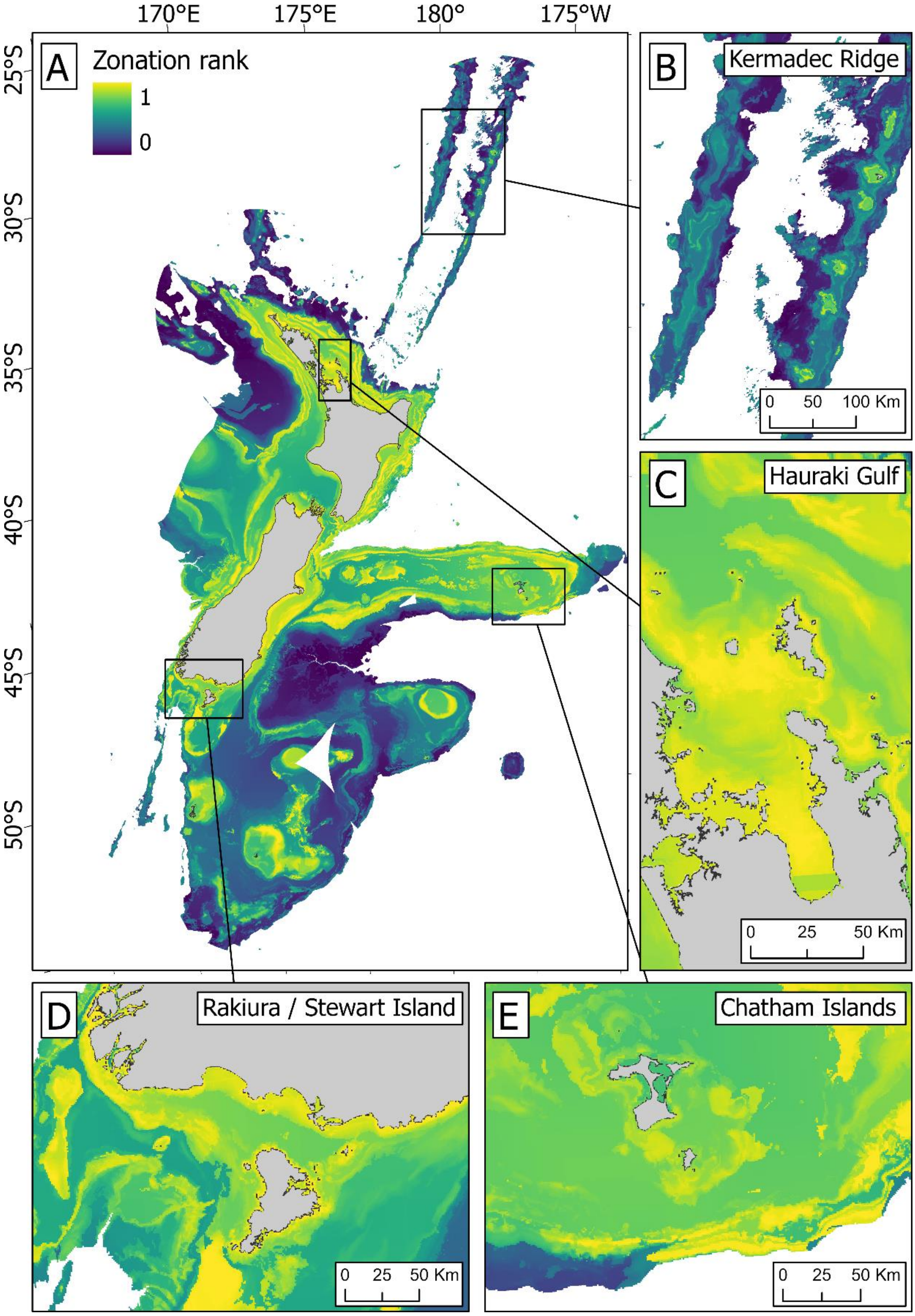

Figure 3-13: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for all demersal fish taxa combined (234 species). Low rank priority is shown in dark blue, high rank priority is shown in yellow. Cut-off of mapped extent is 2000 m depth.

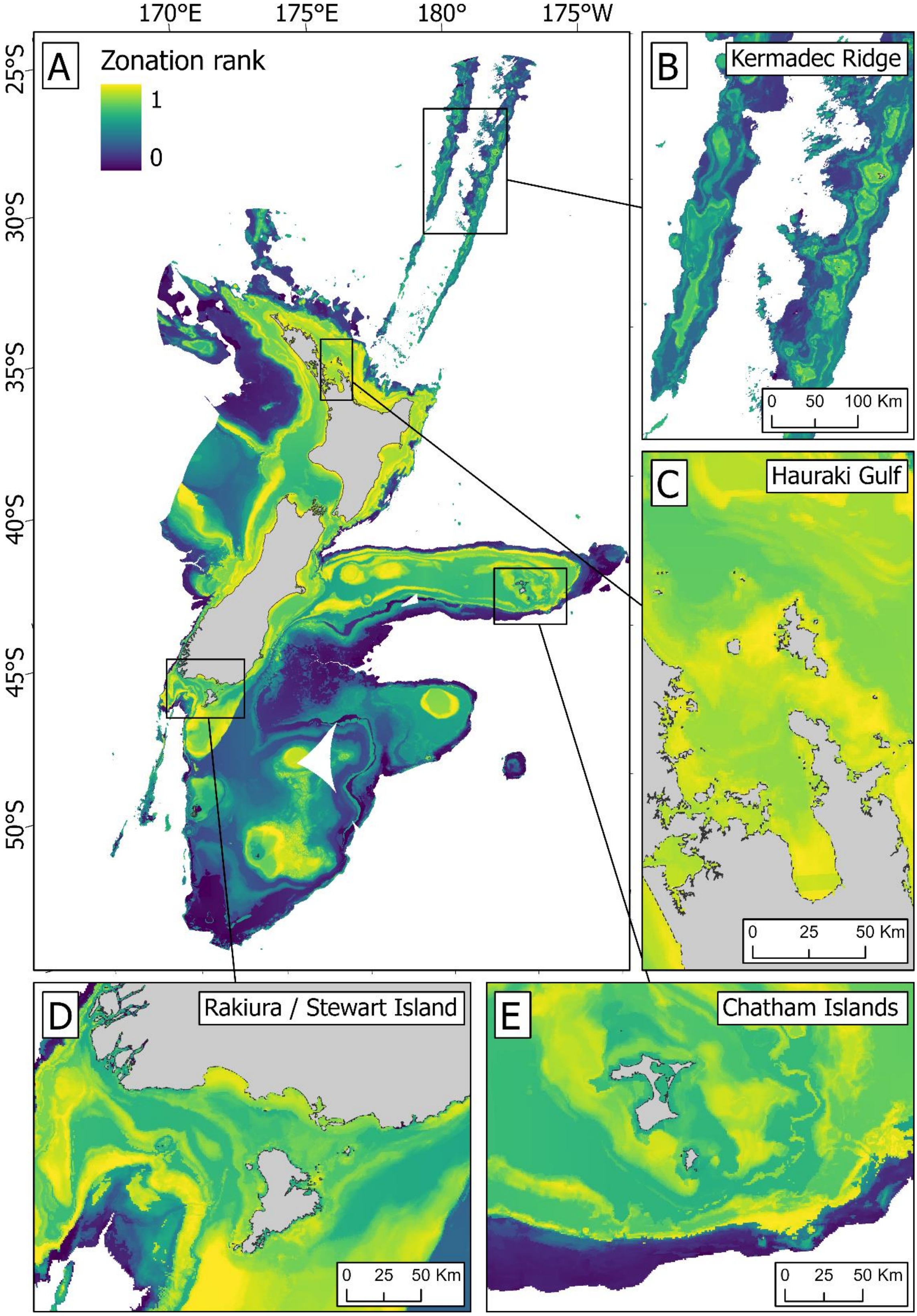

Figure 3-14: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for bentho-pelagic taxa (39 species). Low rank priority is shown in dark blue, high rank priority is shown in yellow. Cut-off of mapped extent is 2000 m depth.

3.2.3 Taxa 3 – Macroalgae

The high-level biodiversity map for all modelled macroalgae taxa (82 species in total) produced using the Zonation approach is shown in Figure 3-15. The macroalgae spatial distributions used to create macroalgae biodiversity maps have been predicted to a rocky reef spatial layer, thus spatial predictions are restricted to shallow, coastal rocky areas. The higher resolution of the data (250 m x 250 m) and the small patches of coastal reef area make it challenging to view the outputs at the national scale. Areas of high Zonation rank priority are at Cape Brett (Figure 3-15B), in several areas surrounding the Mercury Islands (Figure 3-15C), and throughout the Wellington Region (Figure 3-15E). Areas of low Zonation rank priority are mapped at Banks Peninsula (Figure 3-15D).

An example of one of the two macroalgae biodiversity sub-groups (canopy-forming macroalgae, 14 genera) is shown in Figure 3-16. Many of the high Zonation rank priority areas for canopy-forming macroalgae are in the same areas as for the high-level macroalgae group (i.e., Mercury Islands, Wellington Region, and Cape Brett, Figure 3-16). Again, this approach maps Banks Peninsula as having comparatively low Zonation rank priority (Figure 3-16D). The other macroalgae sub-group is shown mapped in Figure B-26 in Appendix B.

Compared to the stacked approach, the Zonation approach shows comparatively higher rank priority in the Mercury Islands and Cape Brett (compare Figure 3-5 and Figure 3-15). Additionally, Banks Peninsula is mapped with low richness using the stacked approach (Figure 3-5D) and low Zonation rank priority using the Zonation approach (Figure 3-15D). In both the stacked and Zonation approaches, the Wellington Region is identified as a high priority area for macroalgae (high richness and high Zonation rank priority. For example, see panel E in Figure 3-5, Figure 3-6, Figure 3-15, and Figure 3-16.

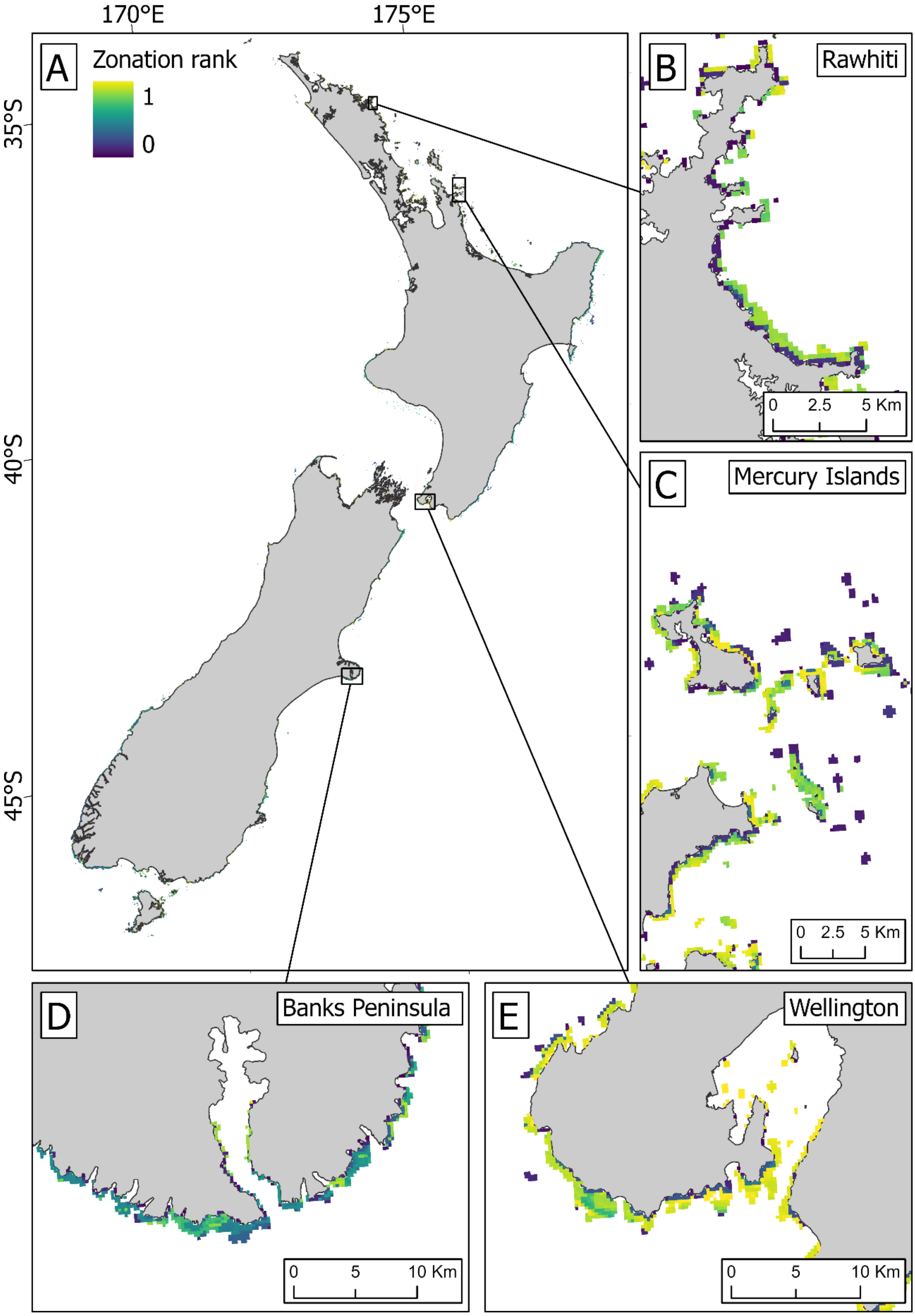

Figure 3-15: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for all macroalgae taxa combined (82 species). Low rank priority is shown in dark blue, high rank priority is shown in yellow. Mapped extent is restricted to coastal rocky reef.

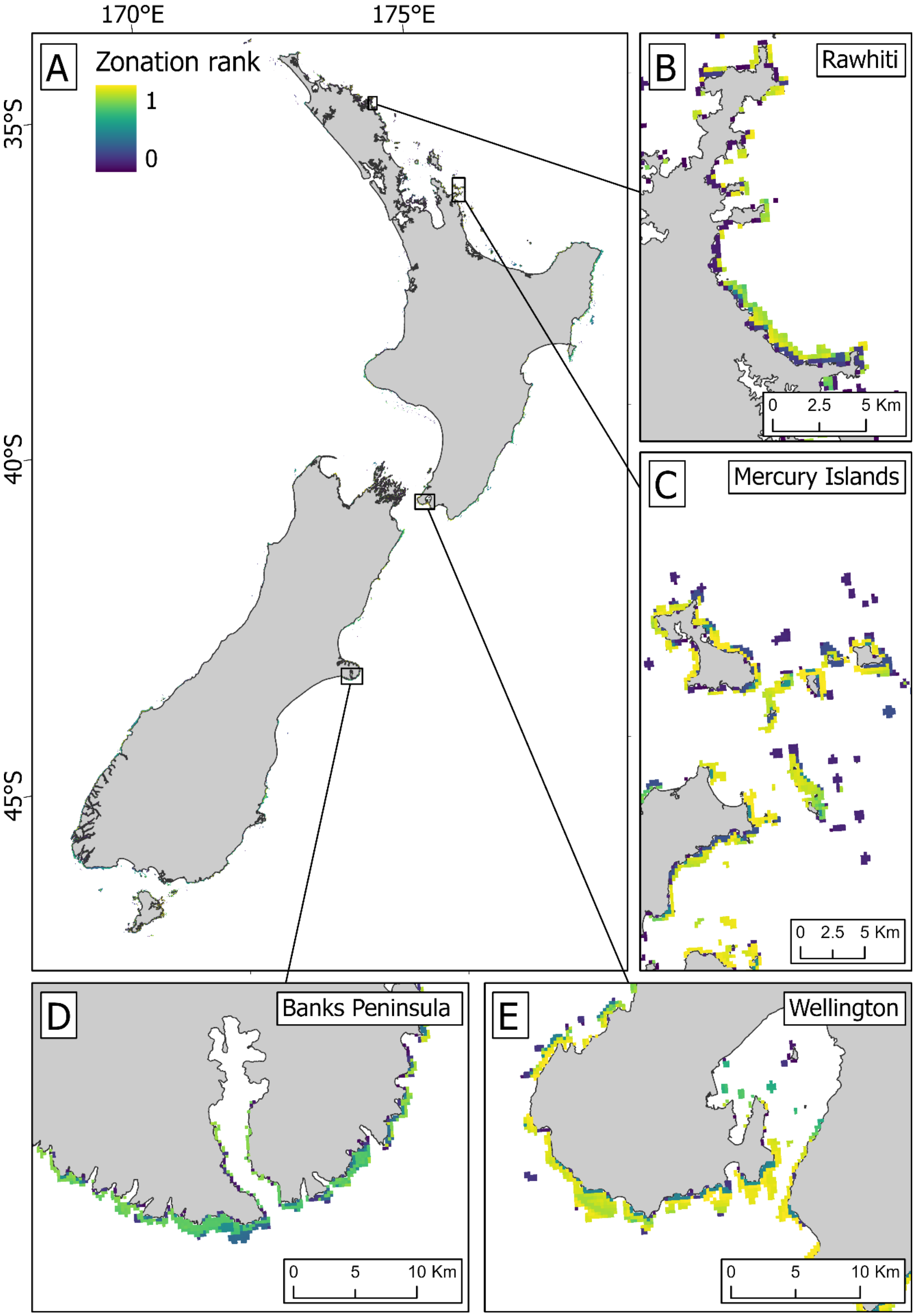

Figure 3-16: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for canopy-forming macroalgae (14 species). Generic Zonation output colours are used. Low rank priority is shown in black, high rank priority is shown in red. Mapped extent is restricted to rocky reef.

3.2.4 Taxa 4 – Seabirds

The seabird biodiversity group at the highest level (73 taxa) is shown mapped in Figure 3-17 using the Zonation approach. The seabird input layers differ from the previous mapped groups as they are not habitat suitability index (modelled) spatial distributions, and instead are normalised (0-1) density maps. The Zonation approach identified areas of high and low rank priority. For seabirds, high Zonation rank priority is mapped throughout coastal mainland Aotearoa-NZ, and the surrounding coastlines of several offshore islands, for example the Chatham Islands Figure 3-17). Generally, the only areas of Aotearoa-NZ's waters with low Zonation rank priority for the high-level seabird group are areas that are considerably far from land masses, for example, the westernmost area of Aotearoa New Zealand's EEZ (Figure 3-17).

An example of a seabird biodiversity sub-group (albatrosses - 12 species) is shown in Figure 3-18. Key areas of high Zonation rank priority are mapped around the South Island of Aotearoa New Zealand, the Chatham Islands, and Auckland and Campbell Islands (Figure 3-17). All other biodiversity sub-groups for seabird taxa are shown in Appendix B (see Figure B-34 to Figure B-38).

Comparing the stacked and Zonation output maps for the high-level seabird biodiversity group, the maps identify similar areas of higher biodiversity. Areas of high richness are mapped in the Chatham Islands, much of coastal Aotearoa New Zealand and close to several offshore sub-Antarctic islands (compare Figure 3-7 and Figure 3-17). Few obvious dissimilarities exist when comparing the two approaches (Figure 3-7 and Figure 3-17), though for the stacked approach there is higher richness mapped across the central area of the Chatham Rise (Figure 3-7) compared to the Zonation approach (Figure 3-17).

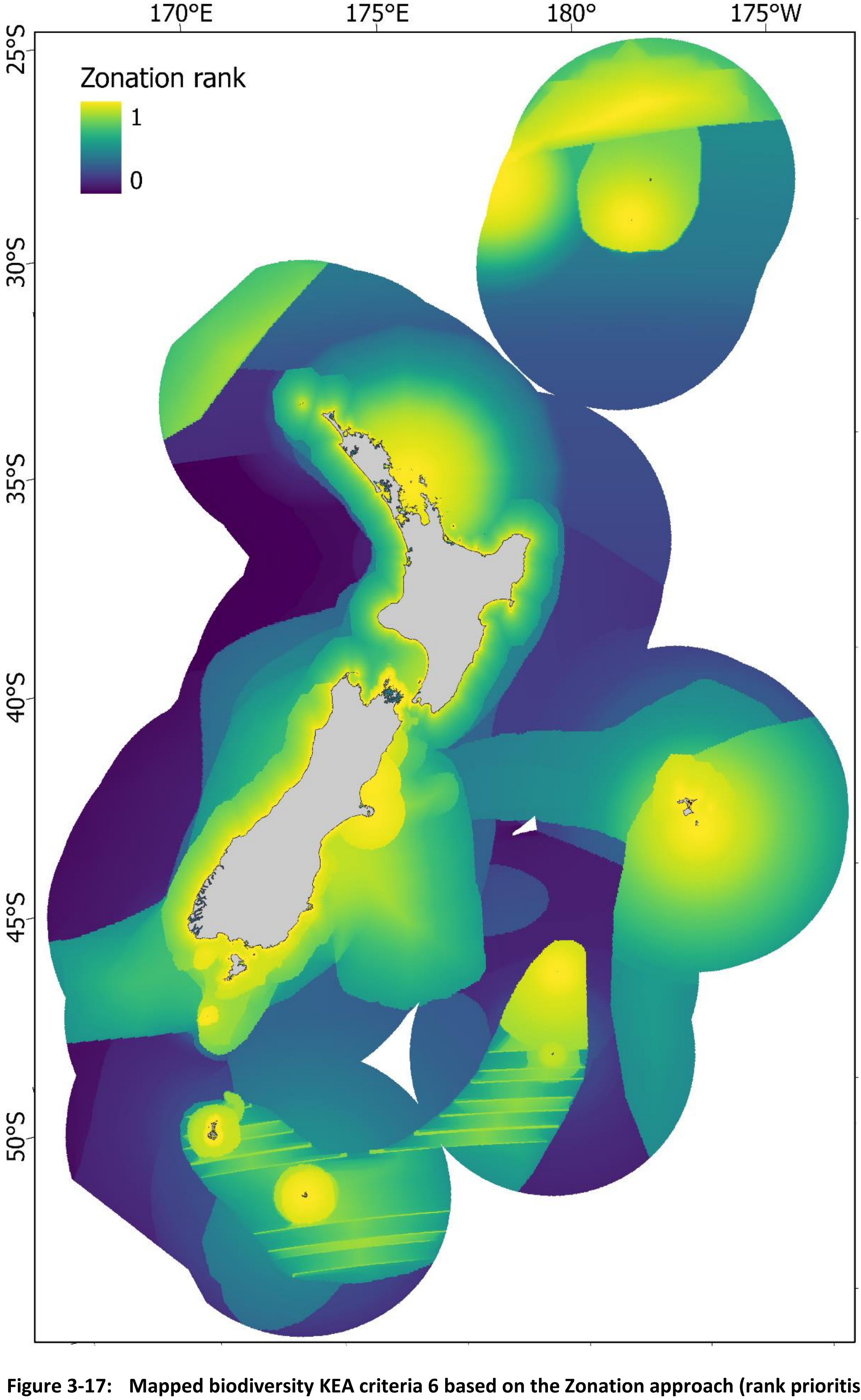

Figure 3-17: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for all seabird taxa (73 species combined). Low rank priority is shown in dark blue, high rank priority is shown in yellow.

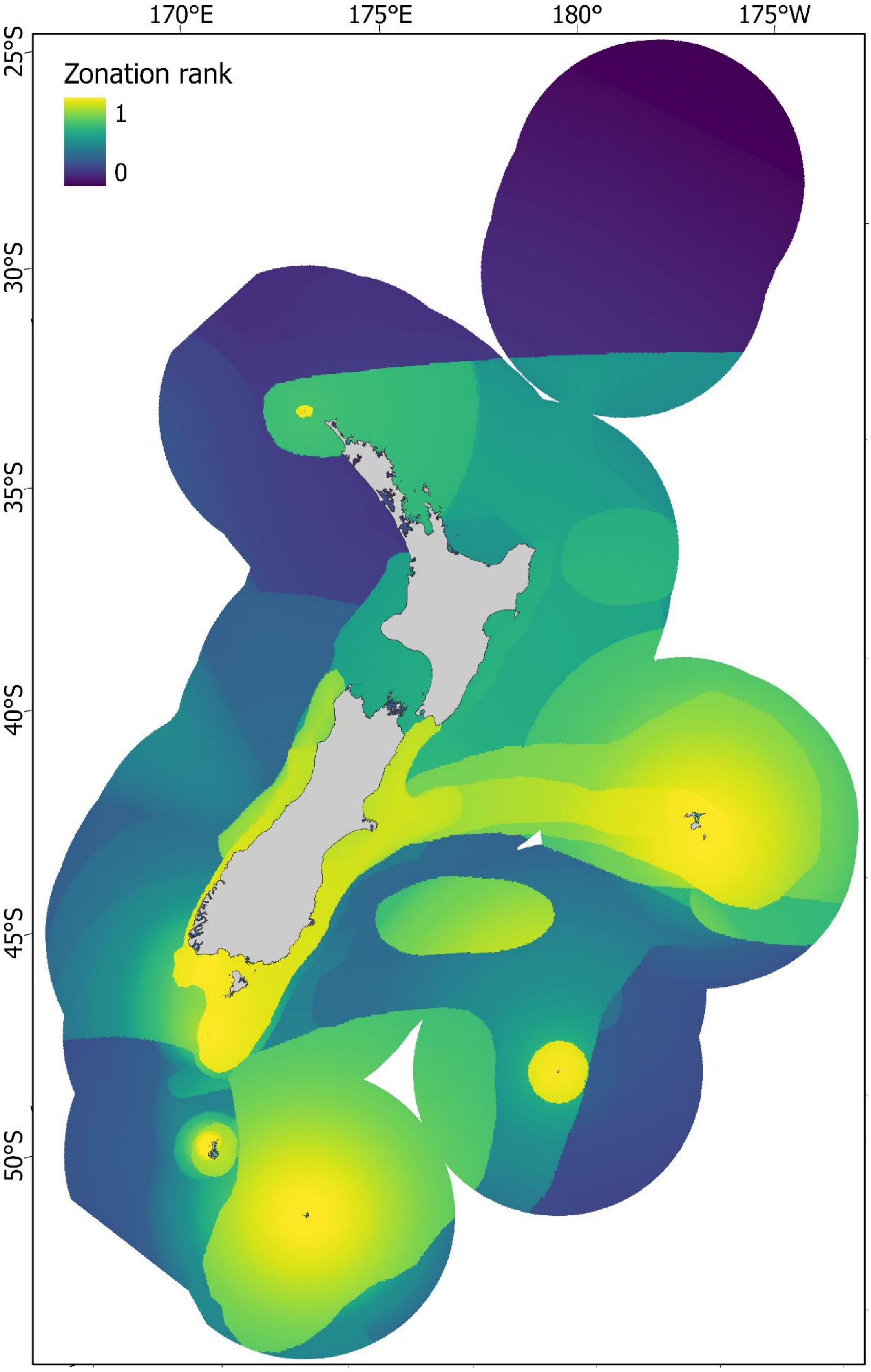

Figure 3-18: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for albatross taxa (12 species). Low rank priority is shown in dark blue, high rank priority is shown in yellow.

3.2.5 Taxa 5 – Cetaceans

Both Delphinidae and whale taxa are combined in the high-level biodiversity group for cetaceans (12 taxa using the Zonation approach (Figure 3-19). Areas of high Zonation rank priority are mapped in the inner Hauraki Gulf (Figure 3-19B), inshore north and south of Banks Peninsula (Figure 3-19D), and in several areas of the Kaikōura Canyon (Figure 3-19E). Areas of low Zonation rank priority are mapped surrounding the Chatham Islands (Figure 3-19) and in deeper areas offshore (the extent clipped by environmental coverage) (e.g., east of the Far North, Figure 3-19B).

An example of one of the Zonation biodiversity sub-groups (Delphinidae) is provided in Figure 3-20. Areas of high Zonation rank priority for Delphinidae are mapped on the east coast of the Far North (Figure 3-20B), north and south of Banks Peninsula (Figure 3-20D), and in the shallower areas of the Kaikōura Canyon (Figure 3-20E). Low areas of Zonation rank priority are mapped around the Chatham Islands and in the deeper areas of the Kaikōura Canyon (Figure 3-20E). The whale biodiversity sub-group is shown in Figure B-39 in Appendix B. In-text, the cetacean maps provided have been clipped to areas of 'acceptable' environmental coverage (Stephenson et al. 2020). The cetacean biodiversity layers have been provided at the spatial extent of the whole EEZ in the Appendix (Figure B-2, Figure B-40, and Figure B-41).

There are several differences between the stacked and Zonation rank priority outputs for cetaceans. For the Zonation approach, key areas of high Zonation rank priority are mapped in the inner Hauraki Gulf, and inshore Banks Peninsula (Figure 3-19C, D). However, for the stacked approach, areas of high species richness are mapped off the south of the South Island of Aotearoa New Zealand and to the southeast of the Chatham Rise (Figure 3-9). For both approaches, the Kaikōura Canyon is mapped as high richness (Figure 3-9E) or high Zonation rank priority (Figure 3-19), though for the Zonation approach the area is mapped with comparatively high priority.

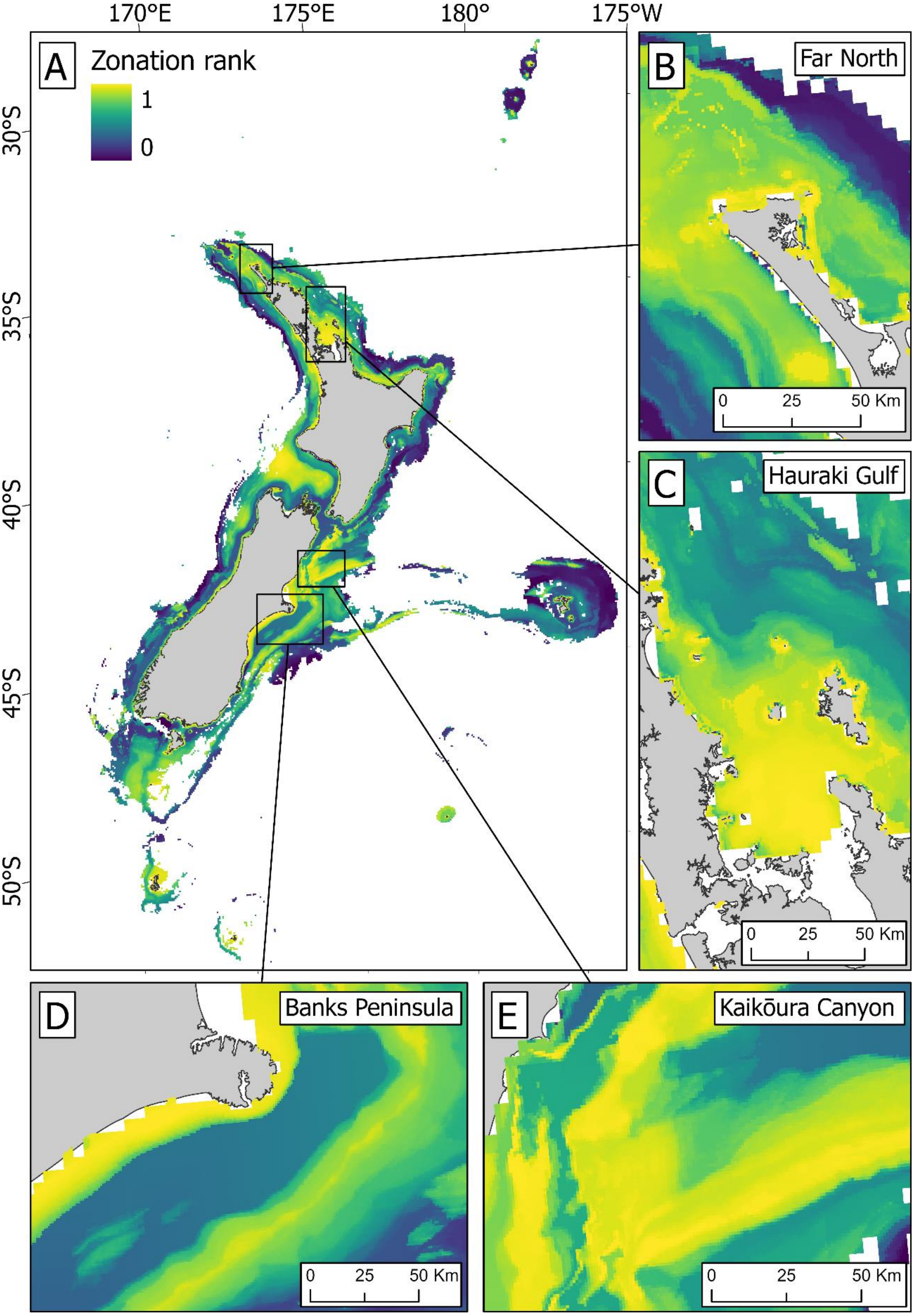

Figure 3-19: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for all cetacean taxa (12 species combined). Low rank priority is shown in dark blue, high rank priority is shown in yellow. Cut-off of mapped extent is areas with environmental coverage values <0.075.

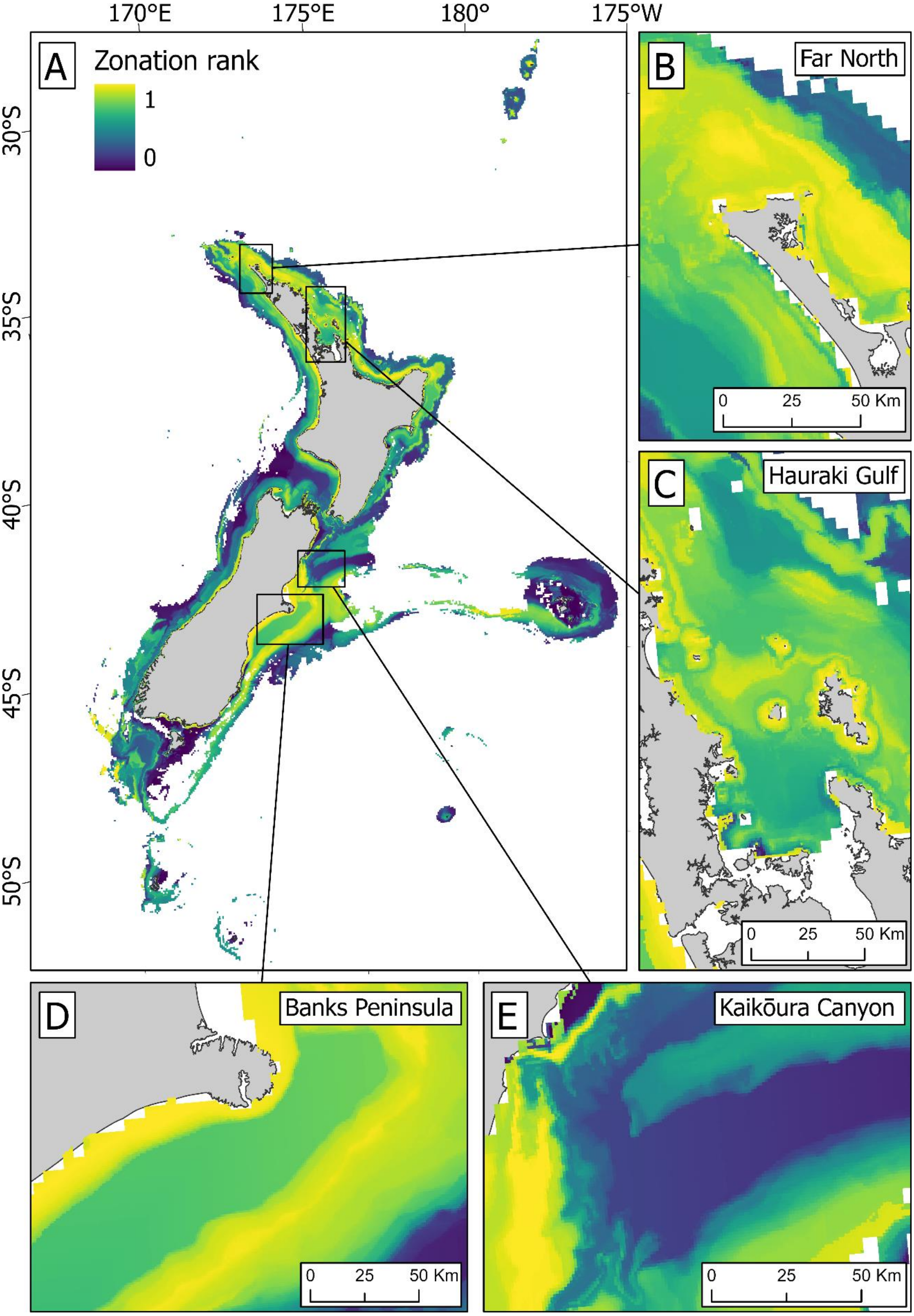

Figure 3-20: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for delphinid taxa (7 species), masked to the area of sufficient environmental coverage. Low rank priority is shown in dark blue, high rank priority is shown in yellow. Cut-off of mapped extent is areas with environmental coverage values <0.075.

3.3 Results - Method 3 - Macroecological models

The MEM approach varies from the previous methods in that it does not use individual predictions of species distribution to represent the distribution of biodiversity. In contrast, it predicts the distribution of alpha diversity (i.e., richness) based on the relationship between richness and environmental variables. In order to be comparable, the same dataset of seafloor invertebrate genera occurrence (i.e., 205 genera), was used to generate the MEM (see Brough et al. (in review) for more details).

3.3.1 Taxa 1 – Seafloor invertebrates

The macroecological modelled layer for the high-level seafloor invertebrate biodiversity group (205 genera) is shown in Figure 3-21. Areas of high mapped richness (>28) can be found in Fiordland and along the Macquarie Ridge (Figure 3-21D). Moderate richness is mapped throughout much of Aotearoa New Zealand's EEZ at depths ranging from 0-1000 m (Figure 3-21, see Figure 2-1 for reference depths). Moderate to high richness is mapped across large areas of the Campbell Plateau (Figure 3-21) and near islands throughout the Hauraki Gulf (Figure 3-21C). Moderate richness can be found across much of the 0-1000 m depth range. Low richness is mapped in many of the areas deeper than 1000 m such as to the west of Aotearoa New Zealand near the Challenger Plateau and throughout the Bounty Trough (Figure 3-21).

Mapped macroecological richness differs quite substantially between the stacked and Zonation approach outputs. In contrast to the high-level biodiversity groups shown for other approaches, the macroecological approach did not have condition (fishing impact) applied. Therefore, for a more accurate comparison of methodologies, the mapped macroecological approach is compared to the stacked and Zonation approach maps for the high-level seafloor invertebrate biodiversity group without condition applied as shown in Appendix B (Figure B-1, Figure B-24). Whereas the stacked and Zonation approaches (Figure B-1, Figure B-24) show high mapped value (richness and rank priority) across much of the Chatham Rise, the macroecological approach shows moderate richness in this area (Figure 3-21). Broadly, the Zonation approach and the macroecological approach identified lower priority areas or species richness at depths deeper than 1000 m, whereas the stacked approach resulted in areas of moderate richness throughout these deeper areas (Figure B-1). For the Zonation approach, high rank priority areas are mapped in the inner Hauraki Gulf (Figure B-24C). In contrast, the stacked and macroecological model approaches show moderate to low richness throughout the Hauraki Gulf area (Figure B-1C and Figure 3-21C).

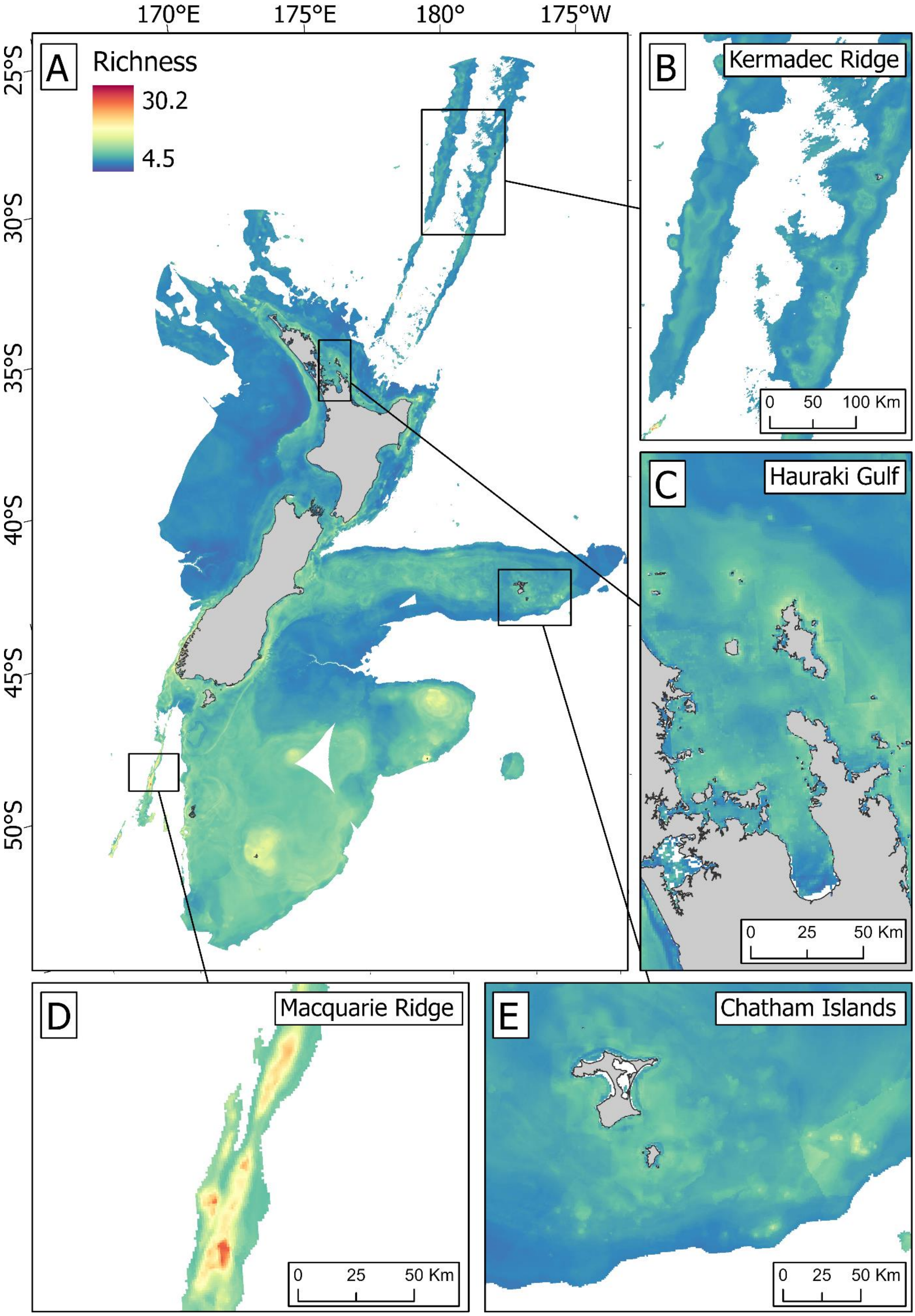

Figure 3-21: Mapped biodiversity KEA criteria 6 based on the macroecological modelling approach for all seafloor invertebrate taxa (205 genera combined). Low richness areas shown in blue, high richness shown in red. Cut-off of mapped extent is 2000 m depth.

3.4 Results – Delineating high value areas

Areas of high biodiversity are often used to inform management decisions. Three examples are provided based on the application of thresholds to identify high biodiversity areas using the stacked richness (Figure 3-22), Zonation (Figure 3-23), and MEM (Figure 3-24) approaches, where the top 5% and 10% of cells have been identified as high priority areas. The examples given are for the same biodiversity group: seafloor invertebrates (205 genera combined).

Comparing the stacked and Zonation approaches, both maps show high biodiversity areas on the Kermadec Ridge and along the Chatham Rise (Figure 3-22 and Figure 3-23). However, the stacked approach identifies a larger area as high priority on the Chatham Rise compared to the Zonation approach (Figure 3-22 and Figure 3-23). The Zonation approach has mapped much of the Hauraki Gulf as high value (Figure 3-23C), but the stacked approach shows no top value (5% or 10%) within the Hauraki Gulf (Figure 3-22).

There is comparably more high value area identified on the Campbell Plateau in the MEM output (Figure 3-24) compared to the stacked and Zonation approaches (Figure 3-23). Furthermore, there are comparably few top areas identified on the Chatham Rise when using the MEM approach (Figure 3-24). All three approaches identify top areas on the Macquarie Ridge (Figure 3-22, Figure 3-23, and Figure 3-24) and the MEM and Zonation approaches both identify top areas on the east coast of the South Island and off the coast of Southland (Murihiku) (Figure 3-23D, Figure 3-24D).

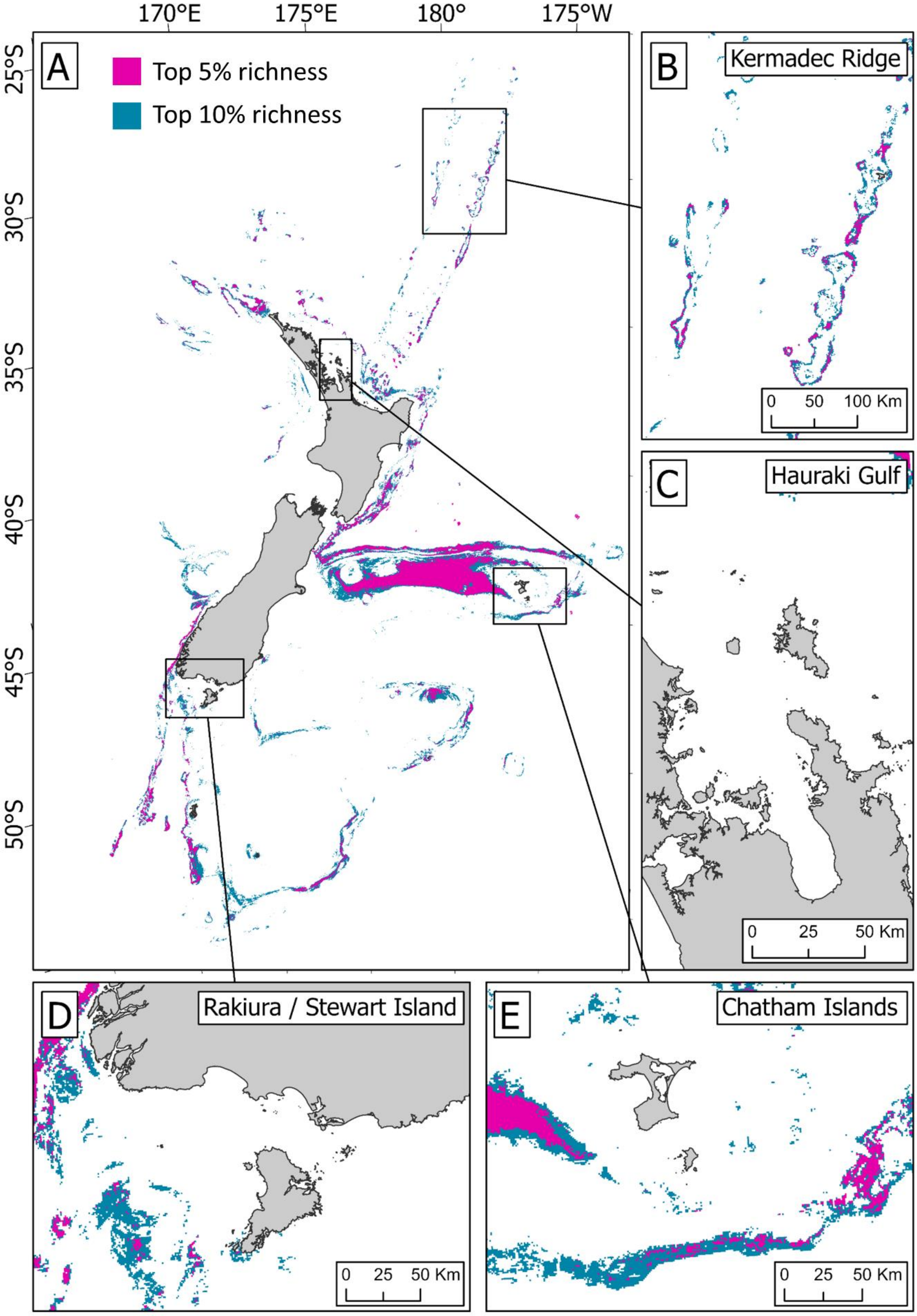

Figure 3-22: High value areas (top 5% and 10%) of stacked richness value for seafloor invertebrates (205 genera) with condition (fishing impact) applied. Cut-off of mapped extent is 2000 m depth.

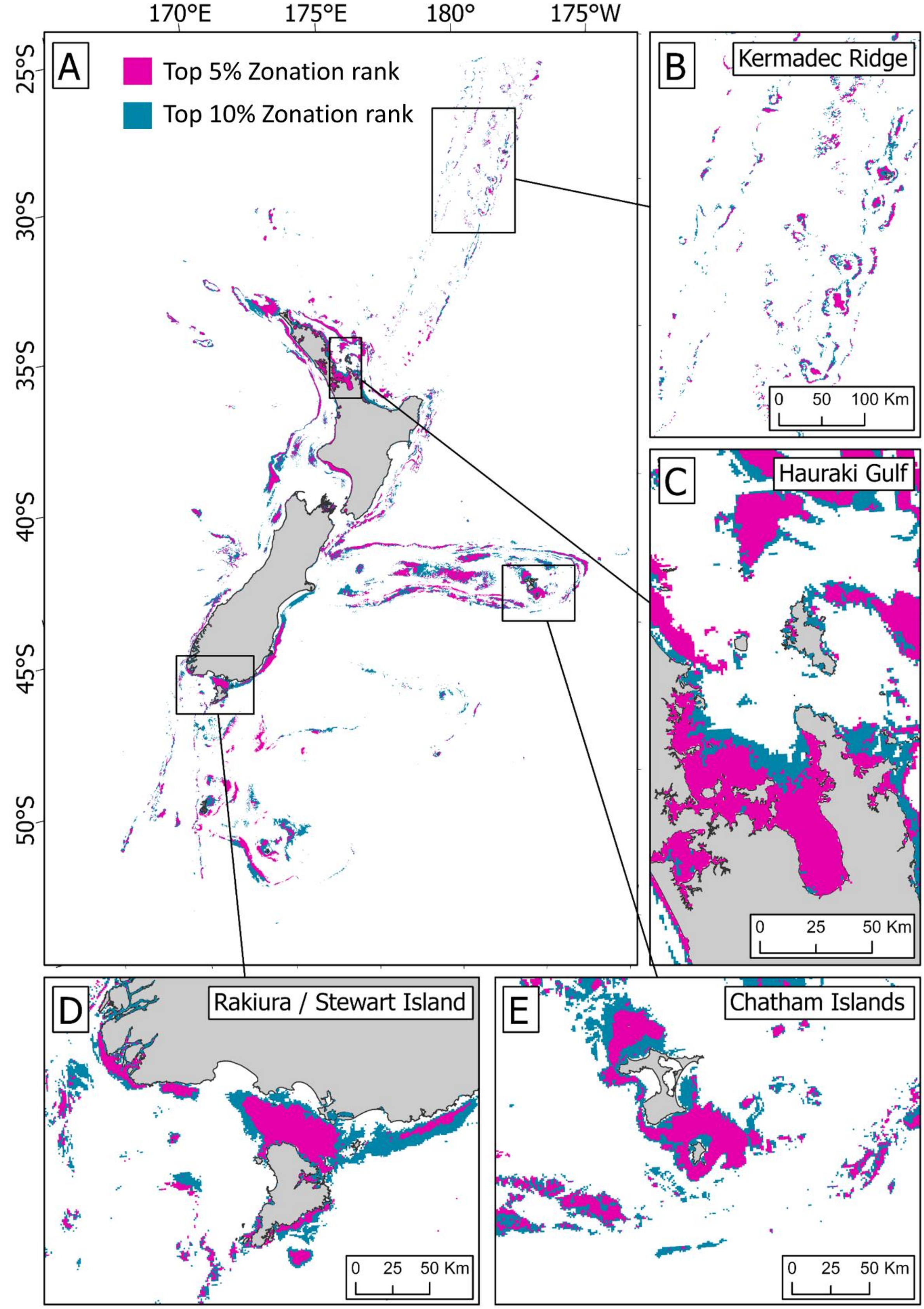

Figure 3-23: High value areas (top 5% and 10%) of Zonation rank priority for seafloor invertebrates (205 genera) with condition (fishing impact) applied. Cut-off of mapped extent is 2000 m depth.

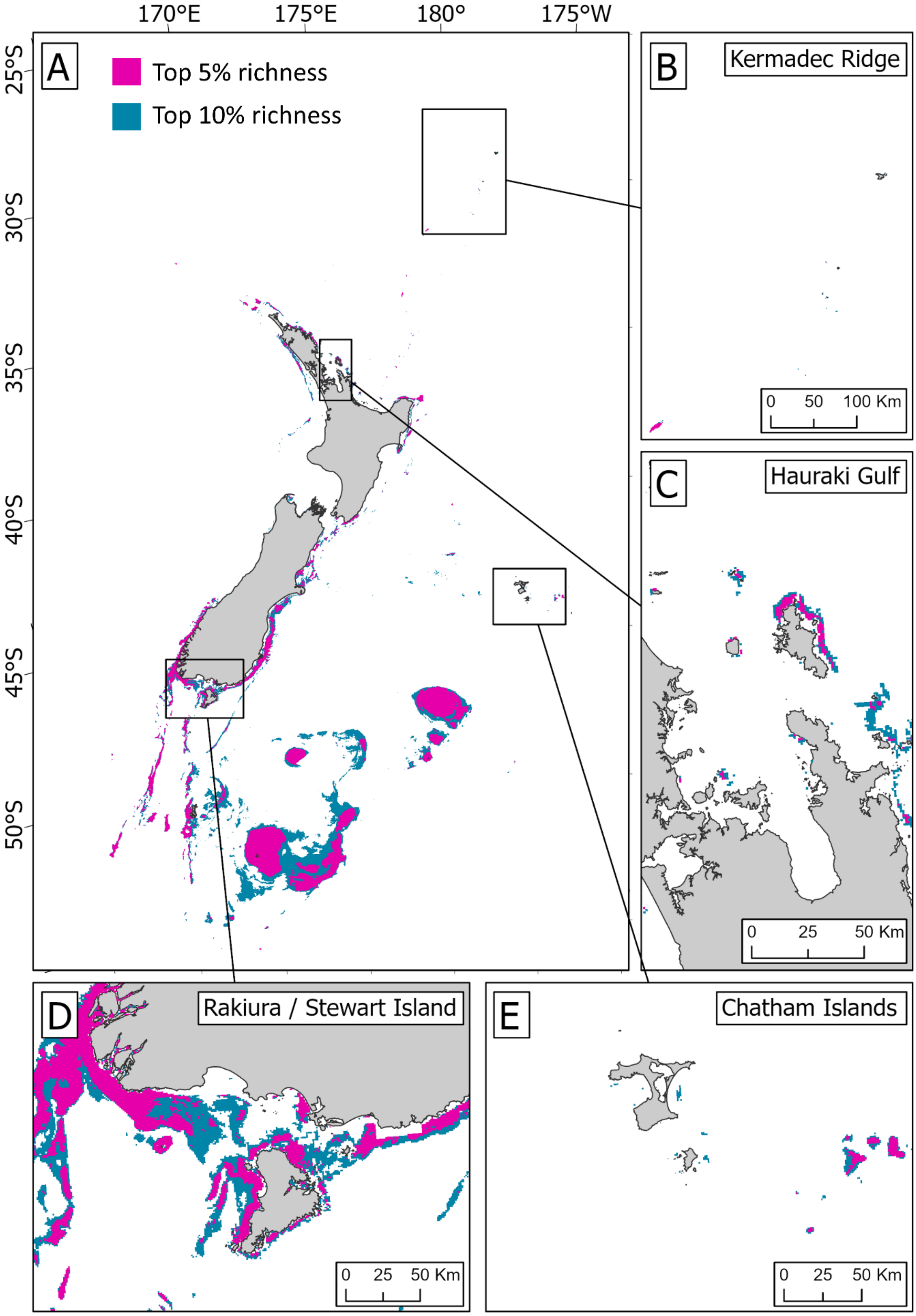

Figure 3-24: High value areas (top 5% and 10%) of MEM richness for seafloor invertebrate (205 genera) without condition (fishing impact) applied. Cut-off of mapped extent is 2000 m depth.

4 Discussion

4.1 General

The aim of this project was to develop a standardised, adaptable framework to identify important areas for biological diversity, and to generate maps of biodiversity for use in marine spatial planning across different government agencies. Methodologies were developed for three separate approaches - each resulting in spatial biodiversity layers.

The marine biodiversity outputs presented here from each methodology can have different thresholds applied to show, for example, the top 5% of areas that are most diverse are located. The selection thresholds is flexible and may be based on considerations for planning priorities and locations and taxa (Bennion et al. 2022; Stewart-Sinclair and Lundquist 2022). This allows resource managers to refine and adapt the maps to be used in decision making and marine spatial planning, whilst keeping a standardised approach. For example, once areas that are important for Biological Diversity have been identified (following one or more of the methodologies used here) other objectives and layers could be used to refine these maps into management units. For example, managers might be interested in identifying areas that are important for multiple taxa groups and could thus include inputs for various taxa to identify where top areas overlap to further refine these maps. Another possibility is that managers might be interested in protecting areas that are adjacent or close to areas already under protection (for connectivity) and these layers could be combined with maps of current protected areas in order to prioritise areas with the highest connectivity. Additionally, managers may want to explore how areas of high mapped diversity are distributed around Aotearoa New Zealand, for example where top areas overlap with bioregions.

Some of the biodiversity outputs produced here incorporate principles related to other KEA criteria. For example, the seafloor invertebrate biodiversity group incorporates condition (fishing impact), which is related to KEA criterion 7, Naturalness. Further, output layers for key biogenic habitat forming taxa could be used as a starting point for producing spatial layers for KEA criterion 3, Special Importance for Life History Stages, given the role of biogenic habitats as nurseries for linked species assemblages (Morrison et al. 2014; Anderson et al. 2019).

Mapping KEA criteria individually for different taxonomic or functional groups provides flexibility in how output layers are used to inform management decisions, with managers and decision-makers able to consider subsets of layers that are most applicable to the decision-making process (e.g., spatial layers related to the biodiversity of seafloor communities may be more relevant than cetacean layers when managing the impacts of bottom contact fishing). However, the individual layers developed here could also be combined with layers for other KEA criteria to define areas that have broad ecological relevance. For example, biodiversity layers could be combined with layers for Naturalness (criterion 7), Rarity (Criterion 2), or Special Importance for Life History Stages (criterion 3). Following this approach, managers could identify areas that are important for multiple KEA criteria.

4.2 Comparison of methodologies

Providing multiple methodological approaches within the mapping framework allows for the tailored application of the most appropriate approach depending on the management situation. The benefits, limitations and additional recommendations for each approach are outlined in Table 4-1 and discussed below.

Broadly, the stacking approach has the benefit of being the most straightforward and therefore repeatable of the three approaches applied here (Table 4-1). It can be easily replicated by managers and decision makers who may not have the technical background or software necessary for the Zonation or macroecological model approaches. If data layers are updated, then the stacked approach can easily be re-applied. Further, due to the simplicity of the stacked approach, the results are easily understandable for stakeholders/end-users. However, the approach only considers areas with a high number of taxa as high value areas (i.e., alpha diversity or species richness), and high value areas may not overlap with the predicted distributions of rarer or range restricted species. If outputs are applied for management without the addition of other mapped KEA criteria such as Criterion 2, Rarity/ Uniqueness / Endemism, important habitat areas of rare species could be lost due to destructive activities or excluded from protection depending on the planning action.

On the contrary, provided a spatial layer is available, the Zonation approach ensures that the high biodiversity areas selected are representative of all species regardless of rarity, though Zonation is contingent on spatial layers being available for all taxa to be input. While Zonation typically uses raster or gridded spatial layers and thus is suited to continuous modelled distribution layers, Zonation can also include point records for rare species in the prioritisation. Zonation internally converts point records into raster layers normalised to a scale of 0-1, assuming the point record distribution is representative of the taxon's distribution. In the analyses here, most species with available habitat suitable layers would be 'common' species due to the minimum number of point records required for robust models – although rarer species may be hidden somewhat in the genus-level analyses. Thus, while the Zonation approach does provide for representation of all groups, the layers presented here are unlikely to adequately represent Criterion 2, Rarity/ Uniqueness / Endemism due to lack of inclusion of rare taxa within the available modelled layers.

The Zonation approach does, however, ensure representation of all species in its outputs. Zonation's core-area cell removal algorithm iteratively removes 'low value' cells until areas of high value across several taxa included in the analyses are identified. Importantly, Zonation considers the total value of a given layer, i.e., extent of distribution and values (probability of occurrence or abundance), in grid cells. In this way, areas of overlapping distributions of many taxa are identified as high rank priority. However, Zonation strives to capture high value areas for all layers included. So, if a given taxa has a comparatively different spatial distribution to the other taxa included in the analyses, areas could be identified as high priority that only contain high value for one, or few taxa. As Zonation will identify areas as priority even if few taxa have distribution there, it can capture the distribution of rare taxa with comparatively different spatial distributions. This is both a benefit and limitation of Zonation for use for creating biodiversity layers as areas of high Zonation rank priority may not necessarily represent high value for many taxa. Whereas other areas in the same rank priority maps, may have high rank priority due overlapping distributions of multiple taxa.

The Zonation analyses and methodology are more complex than the stacking approach, potentially making it harder to communicate outputs to stakeholders. However, in Aotearoa New Zealand, Zonation is the primary decision-support tool used on several occasions to inform marine spatial planning activities (Rowden et al. 2019; Lundquist et al. 2020a; Tablada et al. 2022; Bennion et al. 2023). Many decision makers and stakeholders are thus familiar with spatial planning software and its outputs (rank priority layers).

MEMs have several advantages over stacked and Zonation approaches. Computationally, they are less demanding as one model is created with richness as a response variable, instead of dozens, or even hundreds of individual species models which are then stacked. In this way, rare and/or range restricted species are included in this approach, meaning a taxon with few occurrence records can still be included in an MEM (Biber et al. 2020). The same taxon could not be included in a stacked approach as there would be too few occurrences to train individual species models. However, this distinction also highlights a key limitation of the MEM approach in that species-specific models are not created (Biber et al. 2020), and therefore the taxonomic resolution is limited to the modelled biodiversity group (i.e., disaggregation of high-level biodiversity groups is not possible unless MEMs are rerun). For this reason, MEM outputs are less flexible than stacked approach outputs, where richness estimates are produced post-hoc. Further, as the distribution of biodiversity is reliant on a single model, the preparation of the data that underpins the MEM requires special consideration to minimise the models' sensitivities to catchability and uneven sampling effort by including sampling effort associated with gear class (per cell) as an offset in the model. An additional advantage of the MEM approach is that the key environmental factors that contribute to high biodiversity are identified as part of the modelling framework. This information can be useful for the preservation of the ecological processes that result in high biodiversity (e.g., primary production) and the identification of threats to diversity (e.g., variation in temperature).

When comparing each approach with the qualitative map scores (Table C-1, Table C-2) each of the approaches had one output map scored 1-Accurate, which included the only output map for the MEM approach. The Zonation approach had 24 maps scored a 2-Somewhat accurate and eight maps scored 3-Largely inaccurate. The stacked approach had 19 maps scored 2-Somewhat accurate, and 13 maps scored 3-Largely inaccurate. Thus, the Zonation approach performed marginally better using when assessing the qualitative scorings, with the development of further MEMs required to be able to compare how well this approach performs.

4.3 Data limitations and considerations

The modelled layers of taxon spatial distributions used in this project have a variety of associated limitations which are discussed at length in previous KEA reports (Lundquist et al. 2020a; Lundquist et al. 2020b; Bennion et al. 2022). Some of these limitations, which have implications for biodiversity layer development, are mentioned here.

There are several data limitations that either 1) prevented the inclusion of taxa groups in this project or 2) should be noted as groups were included that may be incomplete or have specific biases. Previous projects for the collation and creation of KEA datasets pooled much of the data that was used for this biodiversity mapping project (Stephenson et al. 2018; Lundquist et al. 2020b). Few data were available on reptiles, for example, and thus no reptile biodiversity group has been mapped here. Furthermore, though there are some pelagic groups mapped here (included within demersal fish and seafloor invertebrates databases, Table 2-1), the occurrence records used to train the models that produced these layers were based largely on demersal trawls (Lundquist et al. 2020b), which is not a reliable sampling method for pelagic species. The DOC Marine Data Portal also includes modelled habitat suitability layers for reef fish, but this group was not included as the models were predicted to the extent of the rocky reef layer used for coastal macroalgae prediction, but many of the reef fish are known to exist across broader extents. Additionally, some species included in the reef fish layer are included in the demersal fish broad taxonomic grouping.

A significant number of taxa were not able to be included in the biodiversity mapping exercises due to a lack of data (i.e., models of habitat suitability have been developed for ~600 species or genera, whereas Aotearoa New Zealand's marine biodiversity is estimated to be more than 17,000 species). Additionally, data used to create the models (both the input habitat suitability models and the MEM) were collected throughout the year, and seasonality was not included in the model development. Thus, the distribution of biodiversity presented in this report represent relative static richness only (not explicit estimates for the number of taxa within each cell). These maps are based on the assumption that the distribution of relative richness is a good proxy for the distribution of true richness. However, this framework could be further developed with the inclusion of seasonal distributions such as existing monthly seabird distributions (Richard et al. 2017) and seasonal cetacean distributions (Stephenson et al. 2023b). Seasonal distributions specific to life history stages such as fish spawning sites would be best captured when mapping the Special Importance for Life History Stages criterion.

Sampling biases are inherent issues of spatial modelling. Areas that are sampled more often can influence spatial predictions, particularly in unsampled space. Overlapping predictive layers in the stacked richness and Zonation approaches risks the accumulation of spatial biases. Such biases may also be taxon dependent and thus require careful interpretation. For example, key algal specialists are based at Te Papa Tongarewa Museum of New Zealand and NIWA Wellington, thus the coastal area around the Wellington region is disproportionately sampled. Similarly, demersal fish research trawls occur the most frequently on the Chatham Rise, increasing the likelihood that species with enough samples to create models have high habitat suitability in these areas. When combining multiple layers with such biases, this could imply greater species richness in such areas. Many of the biodiversity layers produced here show evidence of additive spatial bias, where swathes of Aotearoa-New Zealand's inshore habitats which are known to contain high biodiversity e.g., species richness (Hewitt et al. 2005; Morrison 2021), contain low predicted species richness (Figure 3-1).

The seabird distribution layers have several unique characteristics compared to the species distribution modelled layers used for other biodiversity groups. Limited data records were available to develop the seabird spatial distribution layers. The data available was primarily based on bycatch observer records showing bias with respect to reporting within proximity of fishing vessels, or land-based or knowledge of land-based colonies, nesting or roosting sites. There was limited information of the at-sea distribution of seabirds when not associated with fishing vessels (Stephenson et al. 2018). As these are not species distribution modelled layers, they have not been validated with typical fit metrics, and do not have uncertainty estimates linked to them. Additionally, the seabird biodiversity layers here are based on point data that are often collected in areas that are important for breeding (i.e., colonies) and so are biased towards these areas (Lundquist et al. 2020b). These point data could be used instead of (or in addition to) seabird distribution layers to map KEA (3) Special Importance for Life History Stages.

Here we applied a fishing impact condition layer to seafloor invertebrate biodiversity layers, and while the inverse of this could be used to map Naturalness (KEA criterion 7), it is important to note that the lack of fishing impact is not the only indicator for habitat naturalness (Lundquist et al. 2020b). It is also important to note that the taxa used to develop the specific functional responses to fishing that underpin these layers may be specific to the typical depths of the invertebrate taxa modelled here, as these MSRP layers are based on taxa found at depths typical of Aotearoa New Zealand's offshore fishing fleet rather than for nearshore, coastal or estuarine species. Since we focused on biological diversity here, it was beyond the scope of this report to investigate condition (naturalness) layers, but future work could explore this aspect further. The need for impact layers to down weight areas that have been considerably impacted has been raised in previous studies

(Bennion et al. 2022; Bennion et al. 2023). In the coastal zone, a condition layer for sedimentation impact would significantly improve our ability to consider condition and down weight areas that might otherwise be identified as high priority, despite historic and ongoing impact. However, if the management objective is to consider areas for restoration, then down weighting such areas might not be desirable.

Most data used here were based on binomial models (presence-absence) that predict the occurrence of species in response to a suite of environmental variables. The resultant layers are probability of occurrence (0-1), as point records available in national databases that include abundance data (weights or counts) are insufficient to model abundance for most taxa. Furthermore, catchability of different taxa may vary by gear type, by sampling season, and with other factors that vary between surveys, also influencing measured abundance at a location. While habitat suitability model outputs are used to infer abundance, habitat suitability (or relative probability of occurrence) is not necessarily correlated with modelled abundance (Weber et al. 2017; Jiménez-Valverde et al. 2021). Rather it is important to consider that the biodiversity layers produced may indicate where high priority areas are based on occurrence, but high priority areas may have relatively low abundance for some species. Certain biodiversity metrics incorporate the abundance of taxa (i.e., evenness). If data on abundance become available for taxa, it will be important to consider how priority areas based on abundance might differ to those based on presence (richness). For example, see Gros et al. (2023), where high priority areas for vulnerable marine ecosystem (VME) indicator taxa are concurrently mapped.

A final, important consideration is that apart from the MEM output, the mapped biodiversity output layers presented in this report have not been statistically validated (input habitat suitability model layers have undergone statistical and expert evaluation). Typically, statistical validation of layers for richness is undertaken by determining the correlation between predicted and observed richness (Dubuis et al. 2011; Calabrese et al. 2014). Brough et al. (in review), explored the correlation between observed richness and both the stacked-SDM and MEM models for seafloor invertebrates presented in this study. The MEM was shown to be a robust prediction of seafloor invertebrate richness, yet the stacked SDM performed poorly. It was suggested the biases in both sampling method and distribution that underpin the stacked SDM estimate of richness strongly influenced its robustness. Such biases are not as pronounced within the other taxa groups; however, validation of their biodiversity layers is strongly recommended and is achievable with existing datasets.

Table 4-1: Benefits, limitations, and recommendations for each of the methods used herein to develop spatial layers of marine biodiversity.

Method	Benefits	Limitations	Recommendations
Stacked approach	Easily applied and communicated to stakeholders. Based on fundamental principles of alpha diversity (richness). Tried and tested method for identifying biodiversity priority areas.	When applied using presence-absence modelled layers, potentially skewed by sampling bias. Underlying biases can be amplified, spatial extent of taxa distributions not considered and taxa with comparatively different distributions are not well captured.	Vulnerability weighting strategies could be applied to individual taxa or taxa groups when applying the stacked approach.

Method	Benefits	Limitations	Recommendations
Zonation approach	Decision-support tool Zonation is often applied to spatial planning tasks in Aotearoa-NZ; therefore, stakeholders are broadly familiar with outputs. Rare or range restricted taxa are captured in priority area identification. Several settings can be applied to assist identification of priority areas.	Zonation strives to capture priority areas for all taxa (if equally weighted). Generally, biodiversity metrics like alpha diversity (richness) are based on simple concepts that a site with more taxa present is more biodiverse. The rank priority output from Zonation is different in the way that it considers the spatial extent of taxa distributions and makes effort to capture high priority areas for all taxa.	There are many Zonation settings that have not been used in this work. For example, smoothing algorithms and weighting. When mapping protected, rare or threatened taxa, weighting strategies could be applied to influence core-area cell removal based on relative vulnerability of certain taxa.
Macroecological approach	Richness is modelled as the response variable. In this way, the development of biodiversity layers is not performed post-modelling. This minimises the amplification of spatial biases which are more likely with the stacked approach.	Disaggregation into sub-groups is not possible when a macroecological model is created. Sub-group models could be developed too but this needs to be done at the time of modelling and information cannot be disaggregated afterwards.	Models should be developed for more taxa groups.

4.4 Future steps and conclusions

1. **Conduct independent ground-truthing to validate predicted biodiversity**
   Depending on the methodology used, different areas have been identified as high priority areas. For example, for seafloor invertebrates, the stacked approach identifies several large areas on the Chatham Rise, the Zonation approach identifies large areas of the Hauraki Gulf, and the macroecological approach identifies areas within Fiordland and the Macquarie Ridge. Whatever the method used for identifying priority areas, independent ground-truthing to validate predicted biodiversity value would allow for robust evaluation of their usefulness for spatial planning and could be undertaken in future to validate the biodiversity outputs presented here. In the absence of targeted independent surveys, preliminary evaluation could be carried out using the datasets that were utilised here. Additionally, future work could investigate why biodiversity areas differ between groups, and if particular species and groups are driving spatial biodiversity patterns.

2. **Prioritise the development of MEMs**
   MEMs, stacked, and Zonation approaches have their pros and cons. In this report, our inability to fully represent biodiversity was linked to data limitations. One key advantage of the MEM approach is the ability to include range restricted and rare species in models of biodiversity. While disaggregation of biodiversity groups is not possible once MEMs have been produced, developing MEMs with certain biodiversity groups can be executed with ease. For example, Leathwick et al. (2006) developed an MEM for demersal fish. Considerably more data exists now that could be used to update the model, and biodiversity sub-groups based on demersal fish functional zones could be developed concurrently. Future work could prioritise the development of MEMs that include taxonomic groups with limited coverage with existing species-specific models (Table 2-1).

3. **Investigate the inclusion of additional condition layers**
   As mentioned in the limitations (Section 4.3), we have included a condition layer for fishing impact for seafloor invertebrate taxa. While this could be considered an overlap with KEA Criterion 7: Naturalness, where possible, other condition layers could be included such as sediment impacts and climate change stressors. While there was no scope for creation of new condition/impact layers in this report, future work could develop KEA criterion 7 further and could investigate a variety of condition layers that could be combined with the biodiversity layers developed here, as appropriate to the taxa considered.

4. **Include abundance data when available**
   Areas of high mapped richness will not necessarily correlate with areas of high abundance. Biodiversity metrics that consider taxa abundance would greatly improve the usefulness of output biodiversity layers for identifying priority areas. Abundance data at the scale needed for the spatial extents mapped here is not available for most groups apart from demersal fish from the FNZ research trawl database, and abundance layers are currently being developed for these taxa (Brough et al, unpublished data). National databases for other groups (e.g., seafloor invertebrates, macroalgae) are often more opportunistic rather than based on systematically sampling with comparable gear methods, and often lack information on abundance. If available in future, the use of abundance-based biodiversity metrics in combination with the methods described here will lead to more robust estimates of marine biodiversity for spatial planning.

5. **Include seasonal data where appropriate**
   For highly mobile species such as seabirds and cetaceans, the modelled distributions may cover large areas across the whole of the EEZ, making it difficult to identify priority areas. However, seasonal patterns of annual ocean productivity cycles and seasonal plankton blooms could drive seasonally important priority areas. This framework could be replicated inputting seasonally specific data (if available) to develop monthly or seasonal biodiversity maps.

6. **Map other biodiversity metrics such as beta and gamma diversity**
   The biodiversity maps produced here are based primarily on the species diversity metric of alpha diversity (richness within a particular area). Other biodiversity metrics like beta and gamma diversity could be mapped to provide additional, and complementary information for spatial planning that may be more suitable for certain tasks. For this work, the spatial scales used were based on the extent of the modelled distributions available. Other species diversity metrics like beta and gamma diversity require consideration of spatial scales before they can be applied. Future work could focus on mapping biodiversity between certain areas to assess beta diversity (i.e., comparing different habitats) or at different spatial scales to assess gamma diversity (i.e., total across different habitats).

7. **Map other KEA criteria, and combine maps to identify important areas**
   A combination of the biodiversity maps created here could be used in concert to identify KEAs for Biological Diversity across all taxa groups. Additionally, while the approaches used here focused on the Biological Diversity KEA criterion, similar methodologies could be applied to map other criterion, i.e., areas important for life history stages. KEAs could be refined by stacking maps for multiple criteria, and identifying overlapping high value areas across criteria to aid the identification of priority areas.

5 Acknowledgements

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6 References

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Appendix A Biodiversity groups – Taxa lists

Table A-1: Lists of taxa that comprises the seafloor invertebrate biodiversity group. Specific condition (fishing impact) layers were applied to each seafloor invertebrate taxon based on their morpho-characteristics (LEHS- large, erect, hard, sessile, SFE- small, fragile, encrusting, DBI- deep burrowing infauna). Some taxa were not assigned a category as they were less likely to be affected by bottom-impact trawling (e.g., pelagic taxa).

Phylum	Order	Family	Genus	Common name	Biodiversity group	Fishing impact layer category
Cnidaria	Alcyonacea	Isididae	*Acanella*	Bamboo coral	Key biogenic habitat formers	LEHS
Cnidaria	Alcyonacea	Acanthogorgiidae	*Acanthogorgia*	Soft coral	Key biogenic habitat formers	LEHS
Cnidaria	Pennatulacea	Anthoptilidae	*Anthoptilum*	Sea pen	Key biogenic habitat formers	LEHS
Porifera	Sceptrulophora	Aphrocallistidae	*Aphrocallistes*	Sponge	Key biogenic habitat formers	LEHS
Cnidaria	Antipatharia	Schizopathidae	*Bathypathes*	Black coral	Key biogenic habitat formers	LEHS
Bryozoa	Cheilostomatida	Candidae	*Caberea*	Bryozoan	Key biogenic habitat formers	LEHS
Porifera	Haplosclerida	Callyspongiidae	*Callyspongia*	Sponge	Key biogenic habitat formers	LEHS
Bryozoa	Cheilostomata	Cellariidae	*Cellaria*	Bryozoan	Key biogenic habitat formers	LEHS
Cnidaria	Alcyonacea	Chrysogorgiidae	*Chrysogorgia*	Soft coral	Key biogenic habitat formers	LEHS
Cnidaria	Anthoathecata	Stylasteridae	*Conopora*	Red coral	Key biogenic habitat formers	LEHS
Porifera	Haplosclerida	Callyspongiidae	*Dactylia*	Sponge	Key biogenic habitat formers	LEHS
Cnidaria	Scleractinia	Caryophylliidae	*Desmophyllum*	Stony coral	Key biogenic habitat formers	LEHS
Porifera	Tetractinellida	Ancorinidae	*Ecionemia*	Sponge	Key biogenic habitat formers	LEHS
Cnidaria	Scleractinia	Dendrophylliidae	*Enallopsammia*	Stony coral	Key biogenic habitat formers	LEHS
Cnidaria	Anthoathecata	Stylasteridae	*Errina*	Red coral	Key biogenic habitat formers	LEHS
Porifera	Sceptrulophora	Farreidae	*Farrea*	Sponge	Key biogenic habitat formers	LEHS
Bryozoa	Cheilostomata	Celleporidae	*Galeopsis*	Bryozoan	Key biogenic habitat formers	LEHS
Porifera	Tetractinellida	Geodiidae	*Geodia*	Sponge	Key biogenic habitat formers	LEHS
Cnidaria	Scleractinia	Caryophylliidae	*Goniocorella*	Stony coral	Key biogenic habitat formers	LEHS
Bryozoa	Cyclostomata	Horneridae	*Hornera*	Bryozoan	Key biogenic habitat formers	LEHS

Porifera	Lyssacinosida	Rossellidae	*Hyalascus*	Sponge	Key biogenic habitat formers	LEHS
Cnidaria	Alcyonacea	Isididae	*Keratoisis*	Bamboo coral	Key biogenic habitat formers	LEHS
Cnidaria	Scleractinia	Oculinidae	*Madrepora*	Coral	Key biogenic habitat formers	LEHS
Cnidaria	Alcyonacea	Primnoidae	*Metafannyella*	Soft coral	Key biogenic habitat formers	LEHS
Cnidaria	Alcyonacea	Primnoidae	*Narella*	Soft coral	Key biogenic habitat formers	LEHS
Cnidaria	Alcyonacea	Paragorgiidae	*Paragorgia*	Bubblegum coral	Key biogenic habitat formers	LEHS
Porifera	Tetractinellida	Vulcanellidae	*Poecillastra*	Sponge	Key biogenic habitat formers	LEHS
Cnidaria	Scleractinia	Caryophylliidae	*Solenosmilia*	Stony coral	Key biogenic habitat formers	LEHS
Porifera	Tetractinellida	Ancorinidae	*Stelletta*	Sponge	Key biogenic habitat formers	SFE
Cnidaria	Anthoathecata	Stylasteridae	*Stylaster*	Red coral	Key biogenic habitat formers	LEHS
Porifera	Suberitida	Suberitidae	*Suberites*	Sponge	Key biogenic habitat formers	LEHS
Cnidaria	Alcyonacea	Clavulariidae	*Telesto*	Soft coral	Key biogenic habitat formers	LEHS
Cnidaria	Alcyonacea	Primnoidae	*Thouarella*	Soft coral	Key biogenic habitat formers	LEHS
Arthropoda	Decapoda	Acanthephyridae	*Acanthephyra*	Shrimp	Mobile	DBI
Mollusca	Neogastropoda	Buccinulidae	*Aeneator*	Whelk	Mobile	-
Annelida	Phyllodocida	Nephtyidae	*Aglaophamus*	Polychaete	Mobile	DBI
Mollusca	Neogastropoda	Volutidae	*Alcithoe*	Volute	Mobile	-
Mollusca	Neogastropoda	Ancillariidae	*Amalda*	Snail	Mobile	-
Echinodermata	Ophiurida	Ophiopyrgidae	*Amphiophiura*	Brittle star	Mobile	-
Echinodermata	Amphilepidida	Amphiuridae	*Amphioplus*	Brittle star	Mobile	-
Echinodermata	Amphilepidida	Amphiuridae	*Amphiura*	Brittle star	Mobile	-
Annelida	Phyllodocida	Aphroditidae	*Aphrodita*	Sea mouse	Mobile	-
Echinodermata	Echinothurioida	Echinothuriidae	*Araeosoma*	Sea urchin	Mobile	SFE
Arthropoda	Decapoda	Aristeidae	*Aristaeomorpha*	Shrimp	Mobile	DBI
Arthropoda	Decapoda	Aristeidae	*Aristaeopsis*	Shrimp	Mobile	DBI
Arthropoda	Decapoda	Aristeidae	*Aristeus*	Shrimp	Mobile	DBI
Echinodermata	Paxillosida	Astropectinidae	*Astromesites*	Sea star	Mobile	-
Echinodermata	Aspidochirotida	Stichopodidae	*Australostichopus*	Sea cucumber	Mobile	-
Mollusca	Neogastropoda	Buccinidae	*Austrofusus*	Whelk	Mobile	-
Echinodermata	Aspidochirotida	Synallactidae	*Bathyplotes*	Sea cucumber	Mobile	-
Echinodermata	Notomyotida	Benthopectinidae	*Benthopecten*	Sea star	Mobile	-
Echinodermata	Spatangoida	Brissidae	*Brissopsis*	Sea urchin	Mobile	SFE
Arthropoda	Isopoda	Serolidae	*Brucerolis*	Isopod	Mobile	-
Echinodermata	Pedinoida	Pedinidae	*Caenopedina*	Sea urchin	Mobile	SFE
Arthropoda	Decapoda	Campylonotidae	*Campylonotus*	Shrimp	Mobile	DBI

Echinodermata	Valvatida	Goniasteridae	*Ceramaster*	Sea star	Mobile	-
Echinodermata	Notomyotida	Benthopectinidae	*Cheiraster*	Sea star	Mobile	-
Mollusca	Neogastropoda	Turbinellidae	*Coluzea*	Snail	Mobile	-
Mollusca	Neogastropoda	Buccinulidae	*Cominella*	Whelk	Mobile	-
Echinodermata	Forcipulatida	Stichasteridae	*Cosmasterias*	Sea star	Mobile	-
Echinodermata	Valvatida	Solasteridae	*Crossaster*	Sea star	Mobile	-
Arthropoda	Decapoda	Homolidae	*Dagnaudus*	Carrier crab	Mobile	-
Echinodermata	Camarodonta	Echinidae	*Dermechinus*	Sea urchin	Mobile	-
Arthropoda	Decapoda	Paguridae	*Diacanthurus*	Hermit crab	Mobile	-
Echinodermata	Paxillosida	Astropectinidae	*Dipsacaster*	Sea star	Mobile	-
Arthropoda	Decapoda	Leucosiidae	*Dittosa*	Crab	Mobile	-
Echinodermata	Spatangoida	Loveniidae	*Echinocardium*	Sea urchin	Mobile	SFE
Echinodermata	Camarodonta	Echinidae	*Echinus*	Sea urchin	Mobile	SFE
Mollusca	Littorinimorpha	Naticidae	*Falsilunatia*	Snail	Mobile	-
Mollusca	Littorinimorpha	Ranellidae	*Fusitriton*	Snail	Mobile	-
Annelida	Phyllodocida	Glyceridae	*Glycera*	Polychaete	Mobile	-
Arthropoda	Lophogastrida	Lophogastridae	*Gnathophausia*	Shrimp	Mobile	DBI
Echinodermata	Cidaroida	Cidaridae	*Goniocidaris*	Sea urchin	Mobile	SFE
Echinodermata	Euryalida	Gorgonocephalidae	*Gorgonocephalus*	Basket starfish	Mobile	SFE
Echinodermata	Camarodonta	Echinidae	*Gracilechinus*	Sea urchin	Mobile	SFE
Mollusca	Octopoda	Megaleledonidae	*Graneledone*	Octopus	Mobile	-
Arthropoda	Decapoda	Solenoceridae	*Haliporoides*	Shrimp	Mobile	DBI
Annelida	Phyllodocida	Polynoidae	*Harmothoe*	Polychaete	Mobile	-
Echinodermata	Spinulosida	Echinasteridae	*Henricia*	Sea star	Mobile	-
Echinodermata	Molpadiida	Molpadiidae	*Heteromolpadia*	Sea cucumber	Mobile	-
Echinodermata	Dendrochirotida	Heterothyonidae	*Heterothyone*	Sea cucumber	Mobile	-
Echinodermata	Valvatida	Goniasteridae	*Hippasteria*	Sea star	Mobile	-
Annelida	Eunicida	Onuphidae	*Hyalinoecia*	Polychaete	Mobile	-
Echinodermata	Echinothurioida	Echinothuriidae	*Hygrosoma*	Sea urchin	Mobile	SFE
Arthropoda	Decapoda	Scyllaridae	*Ibacus*	Slipper lobster	Mobile	DBI
Arthropoda	Decapoda	Majidae	*Jacquinotia*	Crab	Mobile	-
Arthropoda	Decapoda	Palinuridae	*Jasus*	Spiny lobster	Mobile	-
Echinodermata	Elasipodida	Laetmogonidae	*Laetmogone*	Sea cucumber	Mobile	-
Arthropoda	Decapoda	Majidae	*Leptomithrax*	Crab	Mobile	-
Arthropoda	Decapoda	Nematocarcinidae	*Lipkius*	Shrimp	Mobile	DBI
Arthropoda	Decapoda	Lithodidae	*Lithodes*	King crab	Mobile	-
Echinodermata	Valvatida	Goniasteridae	*Lithosoma*	Sea star	Mobile	-
Arthropoda	Decapoda	Paguridae	*Lophopagurus*	Hermit crab	Mobile	-
Echinodermata	Paxillosida	Luidiidae	*Luidia*	Sea star	Mobile	-
Arthropoda	Decapoda	Raninidae	*Lyreidus*	Crab	Mobile	-
Mollusca	Trochida	Calliostomatidae	*Maurea*	Snail	Mobile	-
Echinodermata	Valvatida	Goniasteridae	*Mediaster*	Sea star	Mobile	-

Arthropoda	Decapoda	Nephropidae	*Metanephrops*	Lobster	Mobile	DBI
Echinodermata	Molpadiida	Molpadiidae	*Molpadia*	Sea cucumber	Mobile	-
Arthropoda	Decapoda	Munididae	*Munida*	Squat lobster	Mobile	DBI
Arthropoda	Decapoda	Munidopsidae	*Munidopsis*	Squat lobster	Mobile	DBI
Arthropoda	Isopoda	Cirolanidae	*Natatolana*	Isopod	Mobile	-
Arthropoda	Decapoda	Ovalipidae	*Nectocarcinus*	Crab	Mobile	-
Arthropoda	Decapoda	Lithodidae	*Neolithodes*	King crab	Mobile	-
Arthropoda	Decapoda	Pandalidae	*Notopandalus*	Shrimp	Mobile	-
Mollusca	Octopoda	Octopodidae	*Octopus*	Octopus	Mobile	-
Echinodermata	Valvatida	Odontasteridae	*Odontaster*	Sea star	Mobile	-
Echinodermata	Cidaroida	Cidaridae	*Ogmocidaris*	Sea urchin	Mobile	SFE
Echinodermata	Ophiacanthida	Ophiacanthidae	*Ophiacantha*	Sea star	Mobile	-
Echinodermata	Amphilepidida	Ophiactidae	*Ophiactis*	Brittle star	Mobile	-
Echinodermata	Euryalida	Asteroschematidae	*Ophiocreas*	Brittle star	Mobile	-
Echinodermata	Ophiurida	Ophiomusaidae	*Ophiomusa*	Brittle star	Mobile	-
Echinodermata	Ophiacanthida	Ophiomyxidae	*Ophiomyxa*	Sea star	Mobile	-
Echinodermata	Amphilepidida	Ophionereididae	*Ophionereis*	Brittle star	Mobile	-
Echinodermata	Ophiacanthida	Ophiacanthidae	*Ophiophthalmus*	Sea star	Mobile	-
Echinodermata	Ophiacanthida	Ophiodermatidae	*Ophiopsammus*	Sea star	Mobile	-
Echinodermata	Amphilepidida	Hemieuryalidae	*Ophiozonella*	Brittle star	Mobile	-
Echinodermata	Ophiurida	Ophiuridae	*Ophiura*	Brittle star	Mobile	-
Mollusca	Octopoda	Opisthoteuthidae	*Opisthoteuthis*	Octopus	Mobile	-
Arthropoda	Decapoda	Oplophoridae	*Oplophorus*	Shrimp	Mobile	-
Arthropoda	Decapoda	Ovalipidae	*Ovalipes*	Crab	Mobile	-
Echinodermata	Elasipodida	Laetmogonidae	*Pannychia*	Sea cucumber	Mobile	-
Echinodermata	Molpadiida	Caudinidae	*Paracaudina*	Sea cucumber	Mobile	-
Arthropoda	Decapoda	Lithodidae	*Paralomis*	King crab	Mobile	-
Echinodermata	Spatangoida	Eurypatagidae	*Paramaretia*	Sea urchin	Mobile	SFE
Arthropoda	Decapoda	Pasiphaeidae	*Pasiphaea*	Shrimp	Mobile	DBI
Mollusca	Pectinida	Pectinidae	*Pecten*	Scallop	Mobile	SFE
Mollusca	Neogastropoda	Buccinulidae	*Penion*	Whelk	Mobile	-
Echinodermata	Clypeasteroida	Laganidae	*Peronella*	Sand dollar	Mobile	SFE
Echinodermata	Echinothurioida	Phormosomatidae	*Phormosoma*	Sea urchin	Mobile	SFE
Arthropoda	Decapoda	Galatheidae	*Phylladiorhynchus*	Squat lobster	Mobile	DBI
Echinodermata	Valvatida	Goniasteridae	*Pillsburiaster*	Sea star	Mobile	-
Mollusca	Octopoda	Octopodidae	*Pinnoctopus*	Octopus	Mobile	-
Arthropoda	Decapoda	Pandalidae	*Plesionika*	Shrimp	Mobile	DBI
Echinodermata	Paxillosida	Astropectinidae	*Plutonaster*	Sea star	Mobile	-
Arthropoda	Decapoda	Polychelidae	*Polycheles*	Blind lobster	Mobile	DBI
Echinodermata	Paxillosida	Astropectinidae	*Proserpinaster*	Sea star	Mobile	-
Mollusca	Neogastropoda	Volutidae	*Provocator*	Volute	Mobile	-

Echinodermata	Paxillosida	Pseudarchasteridae	*Pseudarchaster*	Sea star	Mobile	-
Echinodermata	Forcipulatida	Stichasteridae	*Pseudechinaster*	Sea star	Mobile	-
Echinodermata	Camarodonta	Temnopleuridae	*Pseudechinus*	Sea urchin	Mobile	SFE
Echinodermata	Aspidochirotida	Synallactidae	*Pseudostichopus*	Sea cucumber	Mobile	-
Echinodermata	Paxillosida	Astropectinidae	*Psilaster*	Sea star	Mobile	-
Arthropoda	Decapoda	Goneplacidae	*Pycnoplax*	Crab	Mobile	-
Mollusca	Cephalaspidea	Scaphandridae	*Scaphander*	Snail	Mobile	-
Echinodermata	Forcipulatida	Asteriidae	*Sclerasterias*	Sea star	Mobile	-
Echinodermata	Valvatida	Solasteridae	*Solaster*	Sea star	Mobile	-
Echinodermata	Spatangoida	Spatangidae	*Spatangus*	Sea urchin	Mobile	SFE
Arthropoda	Decapoda	Polychelidae	*Stereomastis*	Blind lobster	Mobile	DBI
Arthropoda	Decapoda	Parapaguridae	*Sympagurus*	Hermit crab	Mobile	-
Mollusca	Pectinida	Pectinidae	*Talochlamys*	Scallop	Mobile	SFE
Arthropoda	Decapoda	Majidae	*Teratomaia*	Crab	Mobile	-
Arthropoda	Decapoda	Trichopeltariidae	*Trichopeltarion*	Crab	Mobile	-
Mollusca	Neogastropoda	Nassariidae	*Tritia*	Whelk	Mobile	-
Arthropoda	Decapoda	Chirostylidae	*Uroptychus*	Crab	Mobile	-
Arthropoda	Decapoda	Inachidae	*Vitjazmaia*	Crab	Mobile	-
Echinodermata	Forcipulatida	Zoroasteridae	*Zoroaster*	Sea star	Mobile	-
Mollusca	Pectinida	Pectinidae	*Zygochlamys*	Scallop	Mobile	-
Echinodermata	Elasipodida	Pelagothuriidae	*Enypniastes*	Sea cucumber	Pelagic	-
Mollusca	Oegopsida	Histioteuthidae	*Histioteuthis*	Squid	Pelagic	-
Arthropoda	Decapoda	Nematocarcinidae	*Nematocarcinus*	Shrimp	Pelagic	-
Mollusca	Oegopsida	Ommastrephidae	*Nototodarus*	Squid	Pelagic	-
Mollusca	Oegopsida	Onychoteuthidae	*Onykia*	Squid	Pelagic	-
Chordata	Pyrosomatida	Pyrosomatidae	*Pyrosoma*	Tunicate	Pelagic	-
Mollusca	Myopsida	Loliginidae	*Sepioteuthis*	Squid	Pelagic	-
Arthropoda	Decapoda	Sergestidae	*Sergestes*	Prawn	Pelagic	-
Mollusca	Oegopsida	Cranchiidae	*Teuthowenia*	Squid	Pelagic	-
Mollusca	Oegopsida	Ommastrephidae	*Todarodes*	Squid	Pelagic	-
Mollusca	Limida	Limidae	*Acesta*	Bivalve	Sessile	SFE
Cnidaria	Leptothecata	Lafoeidae	*Acryptolaria*	Hydroid	Sessile	LEHS
Cnidaria	Leptothecata	Aglaopheniidae	*Aglaophenia*	Hydroid	Sessile	LEHS
Arthropoda	Amphipoda	Ampeliscidae	*Ampelisca*	Amphipod	Sessile	SFE
Cnidaria	Alcyonacea	Alcyoniidae	*Anthomastus*	Soft coral	Sessile	LEHS
Annelida	Scolecida	Maldanidae	*Asychis*	Bamboo worm	Sessile	-
Cnidaria	Actiniaria	Actiniidae	*Bolocera*	Sea anemone	Sessile	LEHS
Brachiopoda	Terebratulida	Terebratellidae	*Calloria*	Brachiopod	Sessile	SFE
Cnidaria	Scleractinia	Caryophylliidae	*Caryophyllia*	Stony coral	Sessile	LEHS
Bryozoa	Cheilostomata	Celleporidae	*Celleporina*	Bryozoan	Sessile	LEHS
Cnidaria	Leptothecata	Zygophylacidae	*Cryptolaria*	Hydroid	Sessile	LEHS
Bryozoa	Cyclostomata	Lichenoporidae	*Disporella*	Bryozoan	Sessile	SFE

Cnidaria	Zoantharia	Epizoanthidae	*Epizoanthus*	Anemone like coral	Sessile	LEHS
Annelida	Eunicida	Eunicidae	*Eunice*	Bristle worm, bobbit worm	Sessile	-
Bryozoa	Cheilostomata	Microporellidae	*Fenestrulina*	Bryozoan	Sessile	SFE
Cnidaria	Scleractinia	Flabellidae	*Flabellum*	Coral	Sessile	LEHS
Brachiopoda	Terebratulida	Terebratellidae	*Gyrothyris*	Brachiopoda	Sessile	SFE
Porifera	Haplosclerida	Chalinidae	*Haliclona*	Sponge	Sessile	SFE
Cnidaria	Alcyonacea	Alcyoniidae	*Heteropolypus*	Soft coral	Sessile	LEHS
Brachiopoda	Terebratulida	Terebratulidae	*Liothyrella*	Brachiopod	Sessile	LEHS
Porifera	Poecilosclerida	Coelosphaeridae	*Lissodendoryx*	Sponge	Sessile	SFE
Cnidaria	Leptothecata	Aglaopheniidae	*Lytocarpia*	Hydroid	Sessile	LEHS
Brachiopoda	Terebratulida	Terebratellidae	*Magasella*	Brachiopod	Sessile	SFE
Annelida	Scolecida	Maldanidae	*Maldane*	Bamboo worm	Sessile	DBI
Bryozoa	Cheilostomata	Microporidae	*Micropora*	Bryozoan	Sessile	SFE
Cnidaria	Scleractinia	Flabellidae	*Monomyces*	Coral	Sessile	LEHS
Cnidaria	Leptothecata	Plumulariidae	*Nemertesia*	Hydroid	Sessile	LEHS
Brachiopoda	Terebratulida	Terebratellidae	*Neothyris*	Brachiopod	Sessile	SFE
Mollusca	Carditida	Carditidae	*Pleuromeris*	Clam	Sessile	-
Mollusca	Cardiida	Cardiidae	*Pratulum*	Clam	Sessile	DBI
Mollusca	Carditida	Carditidae	*Purpurocardia*	Clam	Sessile	DBI
Bryozoa	Cheilostomata	Smittinidae	*Smittina*	Bryozoan	Sessile	LEHS
Annelida	Sabellida	Serpulidae	*Spirobranchus*	Polychaete	Sessile	SFE
Cnidaria	Scleractinia	Caryophylliidae	*Stephanocyathus*	Stony coral	Sessile	LEHS
Cnidaria	Leptothecata	Sertulariidae	*Symplectoscyphus*	Hydroid	Sessile	SFE
Mollusca	Venerida	Veneridae	*Tawera*	Clam	Sessile	-
Bryozoa	Cyclostomata	Cerioporidae	*Telopora*	Bryozoan	Sessile	SFE

Table A-2: Lists of taxa that comprises demersal fish biodiversity group.

Common name	Family name	Scientific name	Biodiversity group
Bigscale brown slickhead, largescaled brown slickhead	Alepocephalidae	*Alepocephalus australis*	Bathyal-demersal
Alert Pigfish	Congiopodidae	*Alertichthys blacki*	Bathyal-demersal
Thresher shark	Alopiidae	*Alopias vulpinus*	Bathyal-demersal
Deepwater spiny skate, Thorny skate	Rajidae	*Amblyraja hyperborea*	Bathyal-demersal
Giant hatchetfish	Sternoptychidae	*Argyropelecus gigas*	Bathyal-demersal
Longtail skate, Softnose skate	Arhynchobatidae	*Arhynchobatis asperrimus*	Bathyal-demersal
Hairy conger	Congridae	*Bassanago hirsutus*	Bathyal-demersal
Longnose deepsea skate	Arhynchobatidae	*Bathyraja shuntovi*	Bathyal-demersal
Deepsea lizardfish	Bathysauridae	*Bathysaurus ferox*	Bathyal-demersal

Smooth deepsea skate	Arhynchobatidae	*Brochiraja asperula*	Bathyal-demersal
Prickly deepsea skate	Arhynchobatidae	*Brochiraja spinifera*	Bathyal-demersal
Dawson's cat shark	Scyliorhinidae	*Bythaelurus dawsoni*	Bathyal-demersal
Banded bellowsfish, Redbanded bellowsfish	Macroramphosidae	*Centriscops humerosus*	Bathyal-demersal
Leafscale gulper shark	Centrophoridae	*Centrophorus squamosus*	Bathyal-demersal
Potuguese dogfish	Somniosidae	*Centroscymnus coelolepis*	Bathyal-demersal
Owston'sdogfish	Somniosidae	*Centroscymnus owstonii*	Bathyal-demersal
Longnose velvet dogfish, Golden dogfish (Aus.)	Somniosidae	*Centroselachus crepidater*	Bathyal-demersal
Pink frogmouth, Coffinfish, red frogmouth	Chaunacidae	*Chaunax spp.*	Bathyal-demersal
Carpenter's chimaera, Purple chimaera	Chimaeridae	*Chimaera lignaria*	Bathyal-demersal
Frill shark	Chlamydoselachidae	*Chlamydoselachus anguineus*	Bathyal-demersal
Spottyface rattail	Macrouridae	*Coelorinchus acanthiger*	Bathyal-demersal
Blacklip rattail	Macrouridae	*Coelorinchus celaenostomus*	Bathyal-demersal
Banded rattail	Macrouridae	*Coelorinchus fasciatus*	Bathyal-demersal
Notable rattail	Macrouridae	*Coelorinchus innotabilis*	Bathyal-demersal
Kaiyomaru rattail	Macrouridae	*Coelorinchus kaiyomaru*	Bathyal-demersal
Mahia rattail	Macrouridae	*Coelorinchus matamua*	Bathyal-demersal
Darkbanded rattail	Macrouridae	*Coelorinchus maurofasciatus*	Bathyal-demersal
Upturned-snout rattail	Macrouridae	*Coelorinchus mycterismus*	Bathyal-demersal
Oliver's rattail	Macrouridae	*Coelorinchus oliverianus*	Bathyal-demersal
Smallbanded rattail	Macrouridae	*Coelorinchus parvifasciatus*	Bathyal-demersal
Roughhead rattail	Macrouridae	*Coelorinchus trachycarus*	Bathyal-demersal
Deepsea pigfish	Congiopodidae	*Congiopodus coriaceus*	Bathyal-demersal
Humpback rattail	Macrouridae	*Coryphaenoides dossenus*	Bathyal-demersal
Serrulate rattail	Macrouridae	*Coryphaenoides serrulatus*	Bathyal-demersal
Four-ray rattail	Macrouridae	*Coryphaenoides subserrulatus*	Bathyal-demersal
Lookdown dory, King dory (Australia)	Cyttidae	*Cyttus traversi*	Bathyal-demersal
Seal shark, Black shark	Dalatiidae	*Dalatias licha*	Bathyal-demersal
Shovelnosed dogfish, Brier shark (Aus.)	Centrophoridae	*Deania calcea*	Bathyal-demersal
Basketwork eel	Synaphobranchidae	*Diastobranchus capensis*	Bathyal-demersal
Common messmate	Carapidae	*Echiodon cryomargarites*	Bathyal-demersal
Redbait, Red baitfish	Emmelichthyidae	*Emmelichthys nitidus*	Bathyal-demersal
White cardinalfish, White deepsea cardinal	Epigonidae	*Epigonus denticulatus*	Bathyal-demersal
Bigeye cardinalfish, Bigeye deepsea cardinal	Epigonidae	*Epigonus lenimen*	Bathyal-demersal
Robust cardinalfish, Robust deepsea cardinal	Epigonidae	*Epigonus robustus*	Bathyal-demersal
Deepsea cardinalfish, Black deepsea cardinal	Epigonidae	*Epigonus telescopus*	Bathyal-demersal
Smooth lanternshark, Slender lanternshark (Aus.)	Etmopteridae	*Etmopterus pusillus*	Bathyal-demersal
Eucla cod	Euclichthyidae	*Euclichthys polynemus*	Bathyal-demersal
Ling	Ophidiidae	*Genypterus blacodes*	Bathyal-demersal
Slender smooth-hound	Pseudotriakidae	*Gollum attenuatus*	Bathyal-demersal
Black halosaur, Abyssal halosaur	Halosauridae	*Halosauropsis macrochir*	Bathyal-demersal
Common halosaur	Halosauridae	*Halosaurus pectoralis*	Bathyal-demersal

Longnose spookfish, Longnose chimaera	Rhinochimaeridae	*Harriotta raleighana*	Bathyal-demersal
Sharpnose sevengill shark	Hexanchidae	*Heptranchias perlo*	Bathyal-demersal
Deepsea flathead, Deepsea ghostflathead	Hoplichthyidae	*Hoplichthys haswelli*	Bathyal-demersal
Pale ghost shark, Brown ghostshark	Chimaeridae	*Hydrolagus bemisi*	Bathyal-demersal
Black ghostshark, Little black ghostshark	Chimaeridae	*Hydrolagus homonycteris*	Bathyal-demersal
Dark ghost shark (ghost shark), Mottled ghostshark	Chimaeridae	*Hydrolagus novaezealandiae*	Bathyal-demersal
Pointynose blue ghost shark, Purple ghostshark	Chimaeridae	*Hydrolagus trolli*	Bathyal-demersal
Pineapple rattail	Trachyrincidae	*Idiolophorhynchus andriashevi*	Bathyal-demersal
Smallhead cod	Moridae	*Lepidion microcephalus*	Bathyal-demersal
Schmidt's cod, Giant lepidion	Moridae	*Lepidion schmidti*	Bathyal-demersal
Orange perch	Serranidae	*Lepidoperca aurantia*	Bathyal-demersal
Javelinfish	Macrouridae	*Lepidorhynchus denticulatus*	Bathyal-demersal
Blackspot rattail	Macrouridae	*Lucigadus nigromaculatus*	Bathyal-demersal
Carinate rattail, Ridge scaled rattail	Macrouridae	*Macrourus carinatus*	Bathyal-demersal
Spiky oreo	Oreosomatidae	*Neocyttus rhomboidalis*	Bathyal-demersal
Squashed face marlinspike	Macrouridae	*Nezumia namatahi*	Bathyal-demersal
Spineback	Notacanthidae	*Notacanthus sexspinis*	Bathyal-demersal
Prickly dogfish	Oxynotidae	*Oxynotus bruniensis*	Bathyal-demersal
Yellow boarfish, Bigspine boarfish	Pentacerotidae	*Pentaceros decacanthus*	Bathyal-demersal
Rubyfish	Emmelichthyidae	*Plagiogeneion rubiginosum*	Bathyal-demersal
Smooth oreo	Oreosomatidae	*Pseudocyttus maculatus*	Bathyal-demersal
Blobfish	Psychrolutidae	*Psychrolutes microporos*	Bathyal-demersal
Japanese gurnard	Triglidae	*Pterygotrigla andertoni*	Bathyal-demersal
Snubnosed eel	Synaphobranchidae	*Simenchelys parasitica*	Bathyal-demersal
Northern spiny dogfish, Green-eyed dogfish	Squalidae	*Squalus griffini*	Bathyal-demersal
New Zealand torpedo	Torpedinidae	*Tetronarce nobiliana*	Bathyal-demersal
Velvet rattail	Macrouridae	*Trachonurus gagates*	Bathyal-demersal
White rattail	Trachyrincidae	*Trachyrincus aphyodes*	Bathyal-demersal
Unicorn rattail	Trachyrincidae	*Trachyrincus longirostris*	Bathyal-demersal
Cape scorpionfish, Sea perches	Sebastidae	*Trachyscorpia eschmeyeri*	Bathyal-demersal
Grenadier cod	Moridae	*Tripterophycis gilchristi*	Bathyal-demersal
Shortsnout lancetfish	Alepisauridae	*Alepisaurus brevirostris*	Bathyal-pelagic
Smallscale brown slickhead	Alepocephalidae	*Alepocephalus antipodianus*	Bathyal-pelagic
Black oreo	Oreosomatidae	*Allocyttus niger*	Bathyal-pelagic
Warty oreo	Oreosomatidae	*Allocyttus verrucosus*	Bathyal-pelagic
Pale toadfish	Psychrolutidae	*Ambophthalmos angustus*	Bathyal-pelagic
Fangtooth	Anoplogastridae	*Anoplogaster cornuta*	Bathyal-pelagic
Silverside	Argentinidae	*Argentina elongata*	Bathyal-pelagic
Dark cusk	Ophidiidae	*Brotulotaenia nigra*	Bathyal-pelagic
Rudderfish	Centrolophidae	*Centrolophus niger*	Bathyal-pelagic
Viperfish	Stomiidae	*Chauliodus sloani*	Bathyal-pelagic
McMillan's rattail	Macrouridae	*Coryphaenoides mcmillani*	Bathyal-pelagic

Abyssal rattail	Macrouridae	*Coryphaenoides murrayi*	Bathyal-pelagic
Striate rattail	Macrouridae	*Coryphaenoides striaturus*	Bathyal-pelagic
Warty seadevil	Ceratiidae	*Cryptopsaras couesii*	Bathyal-pelagic
Spinyfin, Black roughy, black discfish	Diretmidae	*Diretmichthys parini*	Bathyal-pelagic
Discfish, Silver discfish	Diretmidae	*Diretmus argenteus*	Bathyal-pelagic
Johnson's cod, Johnson's slender cod	Moridae	*Halargyreus johnsonii*	Bathyal-pelagic
Orange roughy	Trachichthyidae	*Hoplostethus atlanticus*	Bathyal-pelagic
Giant barracudina, Barracudinas	Paralepididae	*Magnisudis prionosa*	Bathyal-pelagic
Pearlside, Pennant pearlside	Sternoptychidae	*Maurolicus australis*	Bathyal-pelagic
Smalltooth pelagic cod, Pelagic cods	Melanonidae	*Melanonus gracilis*	Bathyal-pelagic
Largetooth pelagic cod, Arrowtail pelagic cod	Melanonidae	*Melanonus zugmayeri*	Bathyal-pelagic
Limp eelpout	Zoarcidae	*Melanostigma gelatinosum*	Bathyal-pelagic
Black javelinfish, Black whiptail (Aus.)	Macrouridae	*Mesobius antipodum*	Bathyal-pelagic
Ribaldo	Moridae	*Mora moro*	Bathyal-pelagic
Snipe eel, Blackspot snipe eel	Nemichthyidae	*Nemichthys scolopaceus*	Bathyal-pelagic
Finless flounder	Achiropsettidae	*Neoachiropsetta milfordi*	Bathyal-pelagic
Giant black dragonfish, Speckled dragonfish	Stomiidae	*Opostomias micripnus*	Bathyal-pelagic
Common roughy	Trachichthyidae	*Paratrachichthys trailli*	Bathyal-pelagic
Lighthousefish, Silver lighthousefish	Phosichthyidae	*Phosichthys argenteus*	Bathyal-pelagic
Robust pelagic basslet, Rotund cardinalfish	Howellidae	*Rosenblattia robusta*	Bathyal-pelagic
Slender ragfish	Centrolophidae	*Schedophilus huttoni*	Bathyal-pelagic
Elongated bristlemouth fish	Gonostomatidae	*Sigmops spp.*	Bathyal-pelagic
Talismania longifilis, Threadfin slickhead	Alepocephalidae	*Talismania longifilis*	Bathyal-pelagic
Squaretail	Tetragonuridae	*Tetragonurus cuvieri*	Bathyal-pelagic
Dealfish, Peregrin dealfish	Trachipteridae	*Trachipterus trachypterus*	Bathyal-pelagic
Furry whiptail	Macrouridae	*Trachonurus villosus*	Bathyal-pelagic
Tasmanian ruffe	Centrolophidae	*Tubbia spp.*	Bathyal-pelagic
Elongate dory	Zeniontidae	*Zenion sp*	Bathyal-pelagic
Hagfish, Common hagfish	Myxinidae	*Eptatreus spp.*	Benthic
Violet cod	Moridae	*Antimora rostrata*	Benthic
Pink cod	Moridae	*Auchenoceros punctatus*	Benthic
Spotted flounder	Rhombosoleidae	*Azygopus flemingi*	Benthic
Swollenhead conger	Congridae	*Bassanago bulbiceps*	Benthic
Elephant fish	Callorhinchidae	*Callorhinchus milii*	Benthic
Red Gurnard, Gurnard	Triglidae	*Chelidonichthys kumu*	Benthic
Snapper	Sparidae	*Chrysophrys auratus*	Benthic
Brill	Rhombosoleidae	*Colistium guntheri*	Benthic
Turbot	Rhombosoleidae	*Colistium nudipinnis*	Benthic
Pigfish, Southern pigfish	Congiopodidae	*Congiopodus leucopaecilus*	Benthic
Globefish	Tetraodontidae	*Contusus richei*	Benthic
Bonyskull toadfish	Psychrolutidae	*Cottunculus nudus*	Benthic
Sand stargazer	Leptoscopidae	*Crapatalus novaezelandiae*	Benthic
Silver dory, Pink dory	Cyttidae	*Cyttus novaezealandiae*	Benthic

Long-tailed stingray	Dasyatidae	*Dasyatis thetidis*	Benthic
Smooth Skate	Rajidae	*Dipturus innominatus*	Benthic
Spotted stargazer	Uranoscopidae	*Genyagnus monopterygius*	Benthic
Sandfish, Beaked salmon, sand eel	Gonorynchidae	*Gonorynchus forsteri*	Benthic
Giant stargazer, Monkfish	Uranoscopidae	*Kathetostoma giganteum*	Benthic
Scaly gurnard	Triglidae	*Lepidotrigla brachyoptera*	Benthic
Crested flounder	Bothidae	*Lophonectes mongonuiensis*	Benthic
Snipefish	Macroramphosidae	*Macroramphosus scolopax*	Benthic
Rig	Triakidae	*Mustelus lenticulatus*	Benthic
Porae	Cheilodactylidae	*Nemadactylus douglasii*	Benthic
Tarakihi	Cheilodactylidae	*Nemadactylus macropterus*	Benthic
Dark toadfish	Psychrolutidae	*Neophrynichthys latus*	Benthic
Crested Bellowfish	Macroramphosidae	*Notopogon lilliei*	Benthic
Blue cod	Pinguipedidae	*Parapercis colias*	Benthic
Yellow cod, Yellow weever	Pinguipedidae	*Parapercis gilliesii*	Benthic
Cucumber fish	Paraulopidae	*Paraulopus spp.*	Benthic
Sowfish, Giant boarfish	Pentacerotidae	*Paristiopterus labiosus*	Benthic
Lemon sole	Rhombosoleidae	*Pelotretis flavilatus*	Benthic
Sole (complex)	Rhombosoleidae	*Peltorhamphus spp.*	Benthic
Bass	Polyprionidae	*Polyprion americanus*	Benthic
Red cod	Moridae	*Pseudophycis bachus*	Benthic
Yellowbelly flounder	Rhombosoleidae	*Rhombosolea leporina*	Benthic
Sand flounder	Rhombosoleidae	*Rhombosolea plebeia*	Benthic
Greenback flounder	Rhombosoleidae	*Rhombosolea tapirina*	Benthic
Spiny seadragon	Syngnathidae	*Solegnathus spinosissimus*	Benthic
Red mullet, goatfish	Mullidae	*Upeneichthys porosus*	Benthic
Brown stargazer	Uranoscopidae	*Xenocephalus armatus*	Benthic
Longfin boarfish	Pentacerotidae	*Zanclistius elevatus*	Benthic
Rough skate	Rajidae	*Zearaja nasuta*	Benthic
Carpet Shark	Scyliorhinidae	*Cephaloscyllium isabellum*	Benthic
Butterfly perch	Serranidae	*Caesioperca lepidoptera*	Bentho-pelagic
Moki, Blue moki	Latridae	*Latridopsis ciliaris*	Bentho-pelagic
Leatherjacket	Monacanthidae	*Meuschenia scaber*	Bentho-pelagic
Broadnose sevengill shark	Hexanchidae	*Notorynchus cepedianus*	Bentho-pelagic
Hapuku, Groper	Polyprionidae	*Polyprion oxygeneios*	Bentho-pelagic
Longsnout lancetfish	Alepisauridae	*Alepisaurus ferox*	Bentho-pelagic
Longfinned beryx, Imperador (Australia)	Berycidae	*Beryx decadactylus*	Bentho-pelagic
Capro dory	Zeniontidae	*Capromimus abbreviatus*	Bentho-pelagic
Thickhead Rattail	Macrouridae	*Cetonurus crassiceps*	Bentho-pelagic
Oblique-banded rattail	Macrouridae	*Coelorinchus aspercephalus*	Bentho-pelagic
Two saddle rattail	Macrouridae	*Coelorinchus biclinozonalis*	Bentho-pelagic
Bollons' rattail	Macrouridae	*Coelorinchus bollonsi*	Bentho-pelagic
Cook's rattail	Macrouridae	*Coelorinchus cookianus*	Bentho-pelagic

Kermadec rattail	Macrouridae	*Coelorinchus kermadecus*	Bentho-pelagic
Short-tailed black ray	Dasyatidae	*Dasyatis brevicaudata*	Bentho-pelagic
Filamentous rattail	Bathygadidae	*Gadomus aoteanus*	Bentho-pelagic
School shark, Grey boy, tope	Triakidae	*Galeorhinus galeus*	Bentho-pelagic
Silver conger	Congridae	*Gnathophis habenatus*	Bentho-pelagic
Silver roughy	Trachichthyidae	*Hoplostethus mediterraneus*	Bentho-pelagic
Bluenose	Centrolophidae	*Hyperoglyphe antarctica*	Bentho-pelagic
Banded stargazer	Uranoscopidae	*Kathetostoma binigrasella*	Bentho-pelagic
Bulbos rattail	Macrouridae	*Kuronezumia bubonis*	Bentho-pelagic
Starnose black rat	Macrouridae	*Kuronezumia leonis*	Bentho-pelagic
Frostfish	Trichiuridae	*Lepidopus caudatus*	Bentho-pelagic
Hoki, Blue grenadier (Aus.)	Merlucciidae	*Macruronus novaezelandiae*	Bentho-pelagic
Hake, Southern hake	Merlucciidae	*Merluccius australis*	Bentho-pelagic
Southern blue whiting	Gadidae	*Micromesistius australis*	Bentho-pelagic
Eagle ray	Myliobatidae	*Myliobatis tenuicaudatus*	Bentho-pelagic
Dwarf cod	Moridae	*Notophycis marginata*	Bentho-pelagic
Smallscale cod	Nototheniidae	*Notothenia microlepidota*	Bentho-pelagic
Gemfish	Gempylidae	*Rexea solandri*	Bentho-pelagic
Pacific spookfish, Widenose chimaera	Rhinochimaeridae	*Rhinochimaera pacifica*	Bentho-pelagic
Common warehou, Blue warehou	Centrolophidae	*Seriolella brama*	Bentho-pelagic
Silver warehou	Centrolophidae	*Seriolella punctata*	Bentho-pelagic
Blunthead puffer	Tetraodontidae	*Sphoeroides pachygaster*	Bentho-pelagic
Spiny dogfish	Squalidae	*Squalus acanthias*	Bentho-pelagic
Mirror dory	Zeidae	*Zenopsis nebulosa*	Bentho-pelagic
John dory	Zeidae	*Zeus faber*	Bentho-pelagic
Largespine velvet dogfish	Somniosidae	*Scymnodon macracanthus*	Bentho-pelagic
Barracouta	Gempylidae	*Thyrsites atun*	Pelagic
Greenback jack mackerel, Horse mackerel	Carangidae	*Trachurus declivis*	Pelagic
Yelloweye mullet, Herring, sprat	Mugilidae	*Aldrichetta forsteri*	Pelagic
Deepwater burrfish	Diodontidae	*Allomycterus pilatus*	Pelagic
Witch	Bothidae	*Arnoglossus scapha*	Pelagic
Kahawai	Arripidae	*Arripis trutta*	Pelagic
Alfonsino, Splendid alfonsino	Berycidae	*Beryx splendens*	Pelagic
Ray's bream	Bramidae	*Brama spp.*	Pelagic
Anchovy	Engraulidae	*Engraulis australis*	Pelagic
Southern lanternshark	Etmopteridae	*Etmopterus granulosus*	Pelagic
Lucifer dogfish, Blackbelly lanternshark (Aus)	Etmopteridae	*Etmopterus lucifer*	Pelagic
Ragfish	Centrolophidae	*Pseudoicichthys australis*	Pelagic
Hector's lanternfish	Myctophidae	*Lampanyctodes hectoris*	Pelagic
Common tubeshoulder	Platytroctidae	*Persparsia kopua*	Pelagic
Pilchard, Sardine	Clupeidae	*Sardinops sagax*	Pelagic
Blue mackerel, English mackerel, Pacific	Scombridae	*Scomber australasicus*	Pelagic
Kingfish, Yellowtail kingfish	Carangidae	*Seriola lalandi*	Pelagic

White warehou	Centrolophidae	*Seriolella caerulea*	Pelagic
Hammerhead shark, Smooth hammerhead shark	Sphyrnidae	*Sphyrna zygaena*	Pelagic
Sprat (complex)	Clupeidae	*Sprattus spp.*	Pelagic
Slender jack mackerel, Chilean jack mackerel	Carangidae	*Trachurus murphyi*	Pelagic
Yellowtail jack mackerel, Horse mackerel	Carangidae	*Trachurus novaezelandiae*	Pelagic
Girdled wrasse	Labridae	*Notolabrus cinctus*	Reef
Trumpeter	Latridae	*Latris lineata*	Reef
Spotty	Labridae	*Notolabrus celidotus*	Reef
Banded wrasse	Labridae	*Notolabrus fucicola*	Reef
Silver trevally	Carangidae	*Pseudocaranx georgianus*	Reef
Scarlet wrasse, Red soldierfish	Labridae	*Pseudolabrus miles*	Reef
Bigscale brown slickhead, largescaled brown slickhead	Alepocephalidae	*Alepocephalus australis*	Bathyal-demersal

Table A-3: Lists of taxa that comprises the macroalgae biodiversity group.

Phylum	Order	Family	Species	Biodiversity group
Ochrophyta	Fucales	Sargassaceae	*Carpophyllum angustifolium*	Canopy-forming algae
Ochrophyta	Fucales	Sargassaceae	*Carpophyllum flexuosum*	Canopy-forming algae
Ochrophyta	Fucales	Sargassaceae	*Carpophyllum maschalocarpum*	Canopy-forming algae
Ochrophyta	Fucales	Sargassaceae	*Carpophyllum plumosum*	Canopy-forming algae
Ochrophyta	Fucales	Sargassaceae	*Cystophora retroflexa*	Canopy-forming algae
Ochrophyta	Fucales	Sargassaceae	*Cystophora scalaris*	Canopy-forming algae
Ochrophyta	Fucales	Sargassaceae	*Cystophora torulosa*	Canopy-forming algae
Ochrophyta	Fucales	Durvillaeaceae	*Durvillaea antarctica*	Canopy-forming algae
Ochrophyta	Laminariales	Lessoniaceae	*Ecklonia radiata*	Canopy-forming algae
Ochrophyta	Laminariales	Laminariaceae	*Macrocystis pyrifera*	Canopy-forming algae
Ochrophyta	Fucales	Seirococcaceae	*Marginariella boryana*	Canopy-forming algae
Ochrophyta	Fucales	Seirococcaceae	*Marginariella urvilliana*	Canopy-forming algae
Ochrophyta	Fucales	Sargassaceae	*Sargassum sinclairii*	Canopy-forming algae
Ochrophyta	Fucales	Sargassaceae	*Landsburgia quercifolia*	Canopy-forming algae
Ochrophyta	Ectocarpales	Adenocystaceae	*Adenocystis utricularis*	Other algae
Rhodophyta	Halymeniales	Halymeniaceae	*Aeodes nitidissima*	Other algae
Rhodophyta	Gracilariales	Gracilariaceae	*Agarophyton chilense*	Other algae
Rhodophyta	Ceramiales	Wrangeliaceae	*Anotrichium crinitum*	Other algae
Rhodophyta	Bonnemaisoniales	Bonnemaisoniaceae	*Asparagopsis armata*	Other algae
Ochrophyta	Scytothamnales	Bachelotiaceae	*Bachelotia antillarum*	Other algae
Rhodophyta	Balliales	Balliaceae	*Ballia callitricha*	Other algae
Rhodophyta	Gelidiales	Gelidiaceae	*Capreolia implexa*	Other algae
Ochrophyta	Sporochnales	Sporochnaceae	*Carpomitra costata*	Other algae
Rhodophyta	Gigartinales	Caulacanthaceae	*Caulacanthus ustulatus*	Other algae
Chlorophyta	Bryopsidales	Caulerpaceae	*Caulerpa brownii*	Other algae
Chlorophyta	Bryopsidales	Caulerpaceae	*Caulerpa flexilis*	Other algae
Chlorophyta	Bryopsidales	Caulerpaceae	*Caulerpa geminata*	Other algae
Rhodophyta	Ceramiales	Ceramiaceae	*Centroceras clavulatum*	Other algae
Chlorophyta	Cladophorales	Cladophoraceae	*Chaetomorpha aerea*	Other algae
Rhodophyta	Rhodymeniales	Champiaceae	*Champia novae-zelandiae*	Other algae
Rhodophyta	Gigartinales	Gigartinaceae	*Chondracanthus chapmanii*	Other algae
Rhodophyta	Ceramiales	Rhodomelaceae	*Chondria macrocarpa*	Other algae
Rhodophyta	Ceramiales	Rhodomelaceae	*Cladhymenia oblongifolia*	Other algae
Rhodophyta	Bangiales	Bangiaceae	*Clymene coleana*	Other algae
Chlorophyta	Bryopsidales	Codiaceae	*Codium convolutum*	Other algae
Chlorophyta	Bryopsidales	Codiaceae	*Codium fragile*	Other algae
Chlorophyta	Bryopsidales	Codiaceae	*Codium gracile*	Other algae
Ochrophyta	Ectocarpales	Scytosiphonaceae	*Colpomenia sinuosa*	Other algae
Rhodophyta	Corallinales	Corallinaceae	*Corallina aff ferreyrae*	Other algae

Rhodophyta	Gracilariales	Gracilariaceae	*Crassiphycus proliferus*	Other algae
Rhodophyta	Ceramiales	Rhodomelaceae	*Dasyclonium incisum*	Other algae
Ochrophyta	Desmarestiales	Desmarestiaceae	*Desmarestia ligulata*	Other algae
Ochrophyta	Ectocarpales	Ectocarpaceae	*Ectocarpus siliculosus*	Other algae
Rhodophyta	Ceramiales	Callithamniaceae	*Euptilota formosissima*	Other algae
Rhodophyta	Gelidiales	Gelidiaceae	*Gelidium caulacantheum*	Other algae
Rhodophyta	Gigartinales	Gigartinaceae	*Gigartina atropurpurea*	Other algae
Rhodophyta	Gigartinales	Gigartinaceae	*Gigartina macrocarpa*	Other algae
Rhodophyta	Halymeniales	Halymeniaceae	*Grateloupia urvilleana*	Other algae
Rhodophyta	Gigartinales	Phyllophoraceae	*Gymnogongrus furcatus*	Other algae
Rhodophyta	Gigartinales	Phyllophoraceae	*Gymnogongrus torulosus*	Other algae
Ochrophyta	Sphacelariales	Stypocaulaceae	*Halopteris funicularis*	Other algae
Ochrophyta	Sphacelariales	Stypocaulaceae	*Halopteris virgata*	Other algae
Rhodophyta	Ceramiales	Delesseriaceae	*Haraldiophyllum crispatum*	Other algae
Rhodophyta	Ceramiales	Delesseriaceae	*Hymenena variolosa*	Other algae
Rhodophyta	Ceramiales	Rhodomelaceae	*Laurencia distichophylla*	Other algae
Rhodophyta	Ceramiales	Rhodomelaceae	*Laurencia thyrsifera*	Other algae
Rhodophyta	Ceramiales	Wrangeliaceae	*Lophothamnion hirtum*	Other algae
Rhodophyta	Ceramiales	Rhodomelaceae	*Lophurella hookeriana*	Other algae
Chlorophyta	Cladophorales	Cladophoraceae	*Lychaete herpestica*	Other algae
Rhodophyta	Gracilariales	Gracilariaceae	*Melanthalia abscissa*	Other algae
Chlorophyta	Cladophorales	Siphonocladus clade	*Microdictyon mutabile*	Other algae
Ochrophyta	Syringodermatales	Syringodermataceae	*Microzonia velutina*	Other algae
Ochrophyta	Ectocarpales	Chordariaceae	*Myriogloea intestinalis*	Other algae
Rhodophyta	Halymeniales	Halymeniaceae	*Pachymenia dichotoma*	Other algae
Rhodophyta	Halymeniales	Halymeniaceae	*Pachymenia lusoria*	Other algae
Ochrophyta	Ectocarpales	Scytosiphonaceae	*Petalonia binghamiae*	Other algae
Rhodophyta	Plocamiales	Plocamiaceae	*Plocamium angustum*	Other algae
Rhodophyta	Plocamiales	Plocamiaceae	*Plocamium cartilagineum*	Other algae
Rhodophyta	Plocamiales	Plocamiaceae	*Plocamium cirrhosum*	Other algae
Rhodophyta	Gigartinales	Kallymeniaceae	*Psaromenia berggrenii*	Other algae
Rhodophyta	Gigartinales	Gigartinaceae	*Psilophycus alveatus*	Other algae
Rhodophyta	Gelidiales	Gelidiaceae	*Pterocladiella capillacea*	Other algae
Rhodophyta	Bangiales	Bangiaceae	*Pyropia plicata*	Other algae
Rhodophyta	Gigartinales	Cystocloniaceae	*Rhodophyllis membranacea*	Other algae
Rhodophyta	Gigartinales	Gigartinaceae	*Sarcothalia decipiens*	Other algae
Rhodophyta	Ceramiales	Delesseriaceae	*Schizoseris dichotoma*	Other algae
Ochrophyta	Ectocarpales	Scytosiphonaceae	*Scytosiphon lomentaria*	Other algae
Rhodophyta	Gigartinales	Phyllophoraceae	*Stenogramma interruptum*	Other algae
Rhodophyta	Ceramiales	Rhodomelaceae	*Vidalia colensoi*	Other algae
Ochrophyta	Fucales	Xiphophoraceae	*Xiphophora chondrophylla*	Other algae
Ochrophyta	Fucales	Xiphophoraceae	*Xiphophora gladiata*	Other algae
Ochrophyta	Dictyotales	Dictyotaceae	*Zonaria turneriana*	Other algae

Table A-4: Lists of taxa that comprises the seabird biodiversity group.

Common name	Species Name	KEA group
Antipodean Wandering Albatross	*Diomedea antipodensis*	Albatross
Campbell Island Mollymawk	*Thalassarche impavida*	Albatross
Chatham Island Mollymawk	*Thalassarche eremita*	Albatross
Gibson’s Wandering Albatross	*Diomedea antipodensis gibsoni*	Albatross
Grey Headed Mollymawk	*Thalassarche chrysostoma*	Albatross
Light Mantled Sooty Albatross	*Phoebetria palpebrata*	Albatross
Northern Buller’s Mollymawk	*Diomedea bulleri platei*	Albatross
Northern Royal Albatross	*Diomedea sanfordi*	Albatross
White Capped Mollymawk	*Thalassarche steadi*	Albatross
Salvin’s Mollymawk	*Thalassarche salvini*	Albatross
Southern Buller’s Mollymawk	*Thalassarche bulleri*	Albatross
Southern Royal Albatross	*Diomedea epomophora*	Albatross
Australasian Gannet	*Morus serrator*	Other
Brown Skua	*Stercorarius antarcticus*	Other
Caspian Tern	*Hydroprogne caspia*	Other
Masked Booby	*Sula dactylatra*	Other
Pacific White Tern	*Gygis alba*	Other
Chatham Island Blue Penguin	*Eudyptula minor chathamensis*	Penguin
Eastern Rockhopper Penguin	*Eudyptes chrysocome filholi*	Penguin
Erect Crested Penguin	*Eudyptes sclateri*	Penguin
Fiordland Crested Penguin	*Sternula nereis*	Penguin
Northern Blue Penguin	*Eudyptula minor iredalei*	Penguin
Snares Crested Penguin	*Eudyptes robustus*	Penguin
Southern Blue Penguin	*Eudyptula minor minor*	Penguin
White Flippered Blue Penguin	*Eudyptula minor albosignata*	Penguin
Yellow Eyed Penguin	*Megadyptes antipodes*	Penguin
Antarctic Prion	*Pachyptila desolata*	Petrels
Black Bellied Storm Petrel	*Fregetta tropica*	Petrels
Black Petrel	*Procellaria parkinsoni*	Petrels
Broad Billed Prion	*Pachyptila vittata*	Petrels
Chatham Island Petrel	*Pterodroma axillaris*	Petrels
Chatham Island Taiko	*Pterodroma magentae*	Petrels
Codfish Island Diving Petrel	*Pelecanoides georgicus whenuahouensis*	Petrels
Cooks Petrel	*Pterodroma cookii*	Petrels
Fairy Prion	*Pachyptila turtur*	Petrels
Grey Faced Petrel	*Pterodroma gouldi*	Petrels
Grey Petrel	*Procellaria cinerea*	Petrels
Kermadec Petrel	*Pterodroma neglecta*	Petrels
Kermadec Storm Petrel	*Pelagodroma albiclunis*	Petrels
Mottled Petrel	*Pterodroma inexpectata*	Petrels

Northern Diving Petrel	*Pelecanoides urinatrix urinatrix*	Petrels
Northern Giant Petrel	*Macronectes halli*	Petrels
NZ Storm Petrel	*Fregetta maoriana*	Petrels
NZ White Faced Storm Petrel	*Pelagodroma marina*	Petrels
Pycroft's Petrel	*Diomedea sanfordi*	Petrels
Snares Cape pigeon	*Daption capense*	Petrels
Soft Plumaged Petrel	*Pterodroma mollis*	Petrels
Southern Diving Petrel	*Pelecanoides urinatrix*	Petrels
Subantarctic Diving Petrel	*Pelecanoides urinatrix exsul*	Petrels
Westland Petrel	*Procellaria westlandica*	Petrels
White Bellied Storm Petrel	*Fregetta grallaria*	Petrels
White Chinned Petrel	*Procellaria aequinoctialis*	Petrels
White Headed Petrel	*Pterodroma lessonii*	Petrels
White Naped Petrel	*Pterodroma cervicalis*	Petrels
Auckland Island Shag	*Leucocarbo colensoi*	Shags
Blue Shag	*Mergus australis oliveri*	Shags
Bounty Island Shag	*Leucocarbo ranfurlyi*	Shags
Campbell Island Shag	*Leucocarbo campbelli*	Shags
Chatham Island Shag	*Leucocarbo onslowi*	Shags
King Shag	*Leucocarbo carunculatus*	Shags
Little Black Shag	*Phalacrocorax sulcirostris*	Shags
Pied Shag	*Phalacrocorax varius varius*	Shags
Pitt Island Shag	*Phalacrocorax featherstoni*	Shags
Spotted Shag	*Stictocarbo punctatus*	Shags
Stewart Island Shag	*Leucocarbo chalconotus*	Shags
Bullers Shearwater	*Ardenna bulleri*	Shearwater
Flesh Footed Shearwater	*Puffinus carneipes*	Shearwater
Fluttering Shearwater	*Sternula nereis*	Shearwater
Huttons Shearwater	*Puffinus huttoni*	Shearwater
Kermadec Little Shearwater	*Puffinus gavia kermadecensis*	Shearwater
North Island Little Shearwater	*Puffinus assimilis*	Shearwater
Sooty Shearwater	*Ardenna grisea*	Shearwater
Wedge Tailed Shearwater	*Ardenna pacifica*	Shearwater

Table A-5: Lists of taxa that comprises the cetacean biodiversity group. 'Complex' denotes that multiple species or sub-species were included in the model. See Stephenson et al. (2020) for details.

Common name	Species	Family	KEA group
Hector's dolphin	*Cephalorhynchus hectori hectori*	Delphinidae	Delphinidae
Māui dolphin	*Cephalorhynchus hectori maui*	Delphinidae	Delphinidae
Common dolphin	*Delphinus delphis*	Delphinidae	Delphinidae
Dusky dolphin	*Lagenorhynchus obscurus*	Delphinidae	Delphinidae
Bottlenose dolphin	*Tursiops truncatus*	Delphinidae	Delphinidae
Pilot whale	*Globicephala* spp. (complex)	Delphinidae	Delphinidae
Orca, killer whale	*Orcinus orca* (complex)	Delphinidae	Delphinidae
Bryde's whale	*Balaenoptera edeni brydei*	Balaenopteridae	Whale
Southern right whale	*Eubalaena australis*	Balaenidae	Whale
Humpback whale	*Megaptera novaeangliae*	Balaenopteridae	Whale
Sperm whale	*Physeter macrocephalus*	Physeteridae	Whale
Blue whale	*Balaenoptera musculus* (complex)	Balaenopteridae	Whale

Appendix B Supplementary figures

B. 1. Stacked Richness

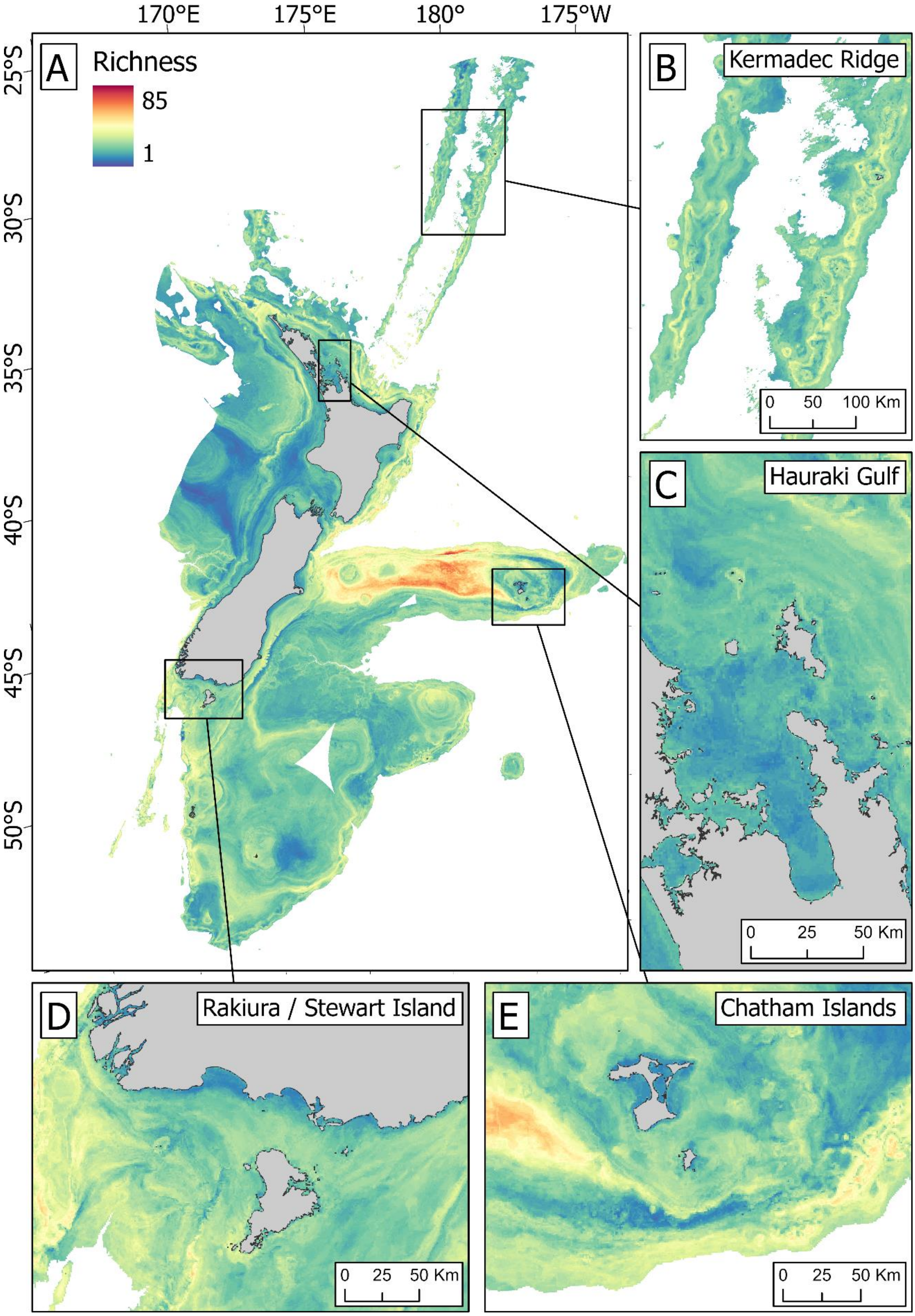

Figure B-1: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for all seafloor invertebrate taxa (205 genera combined). Condition (fishing impact layer) has not been applied. Low richness areas shown in blue, high richness shown in red. Cut-off of mapped extent is 2000 m depth.

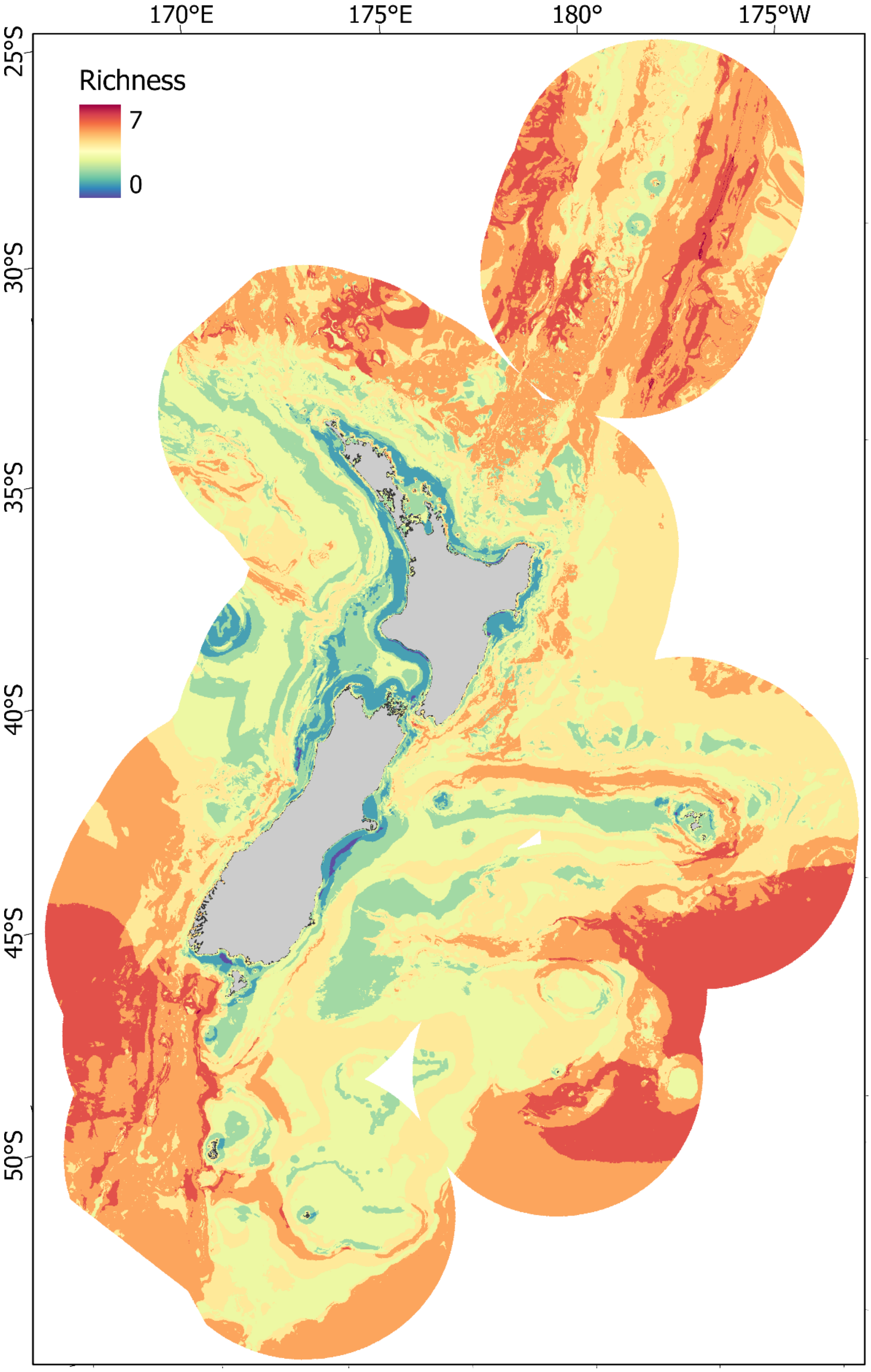

Figure B-2: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for all cetacean taxa (12 genera combined). Low richness areas shown in blue, high richness shown in red.

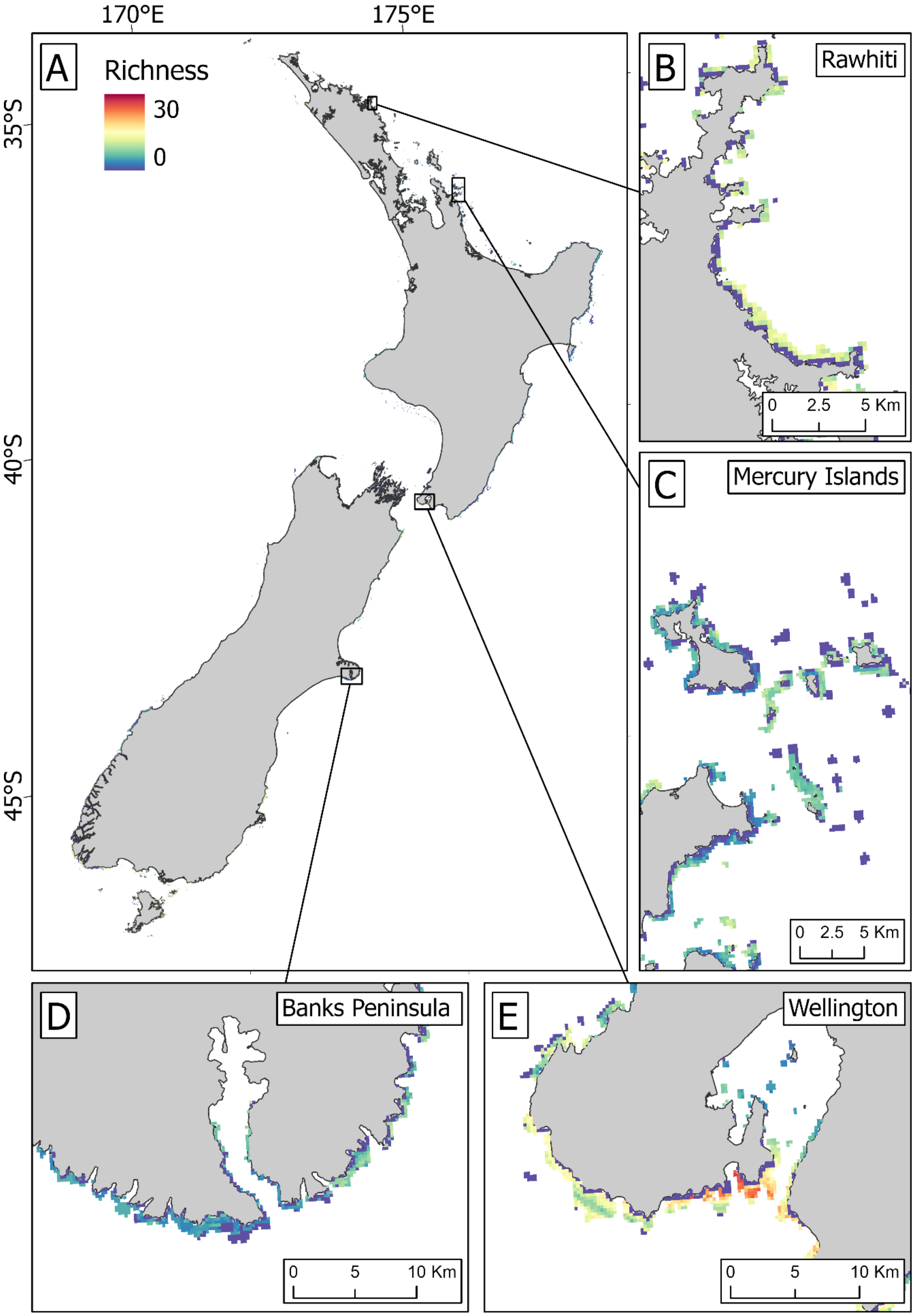

Figure B-3: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for non-canopy-forming macroalgae taxa (68 genera). Low richness areas shown in blue, high richness shown in red. Mapped extent is restricted to rocky reef.

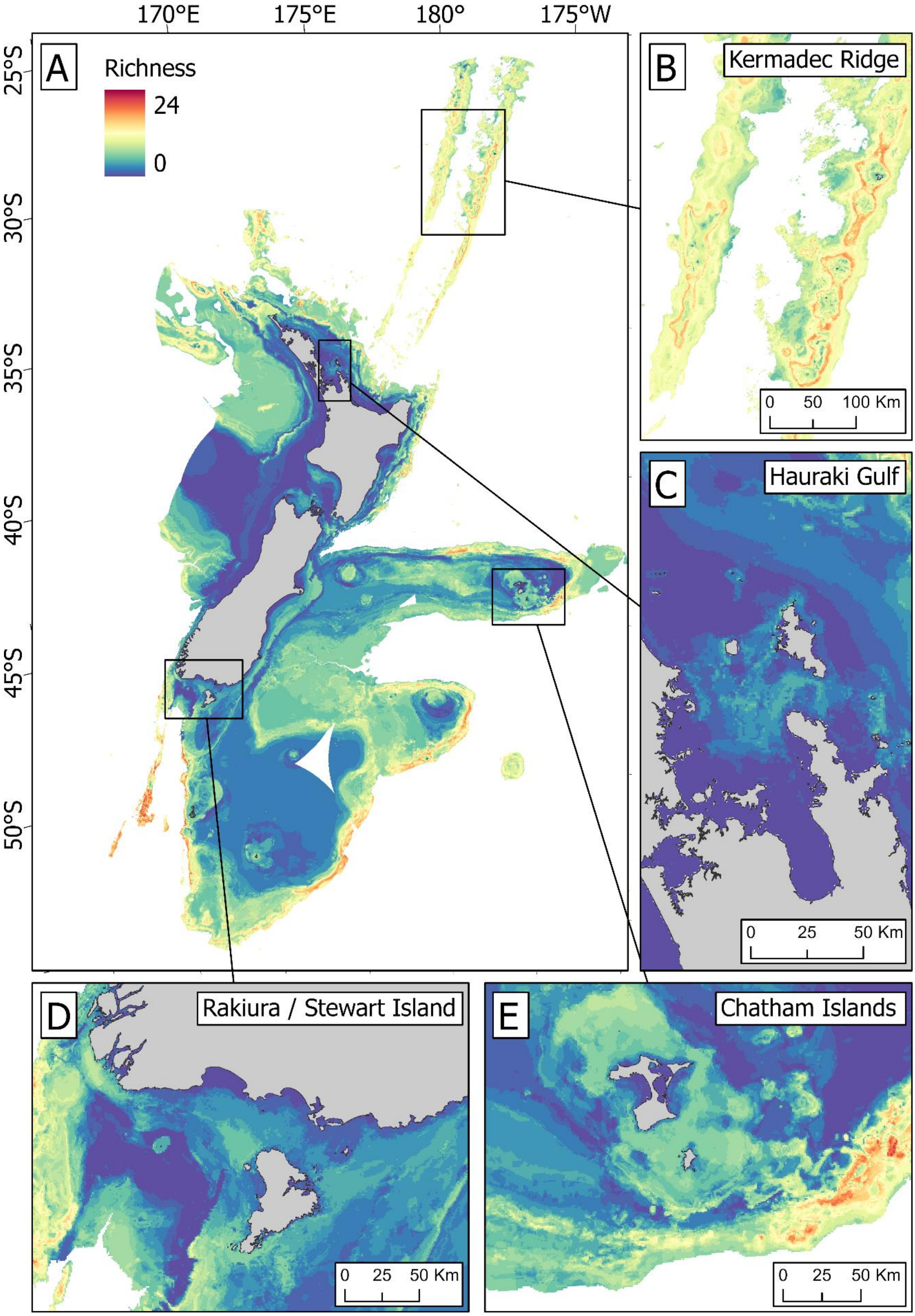

Figure B-4: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for all combined seafloor invertebrates (205 genera). Condition (fishing impact layer) has not been applied. Low richness areas shown in blue, high richness shown in red. Cut-off of mapped extent is 2000 m depth.

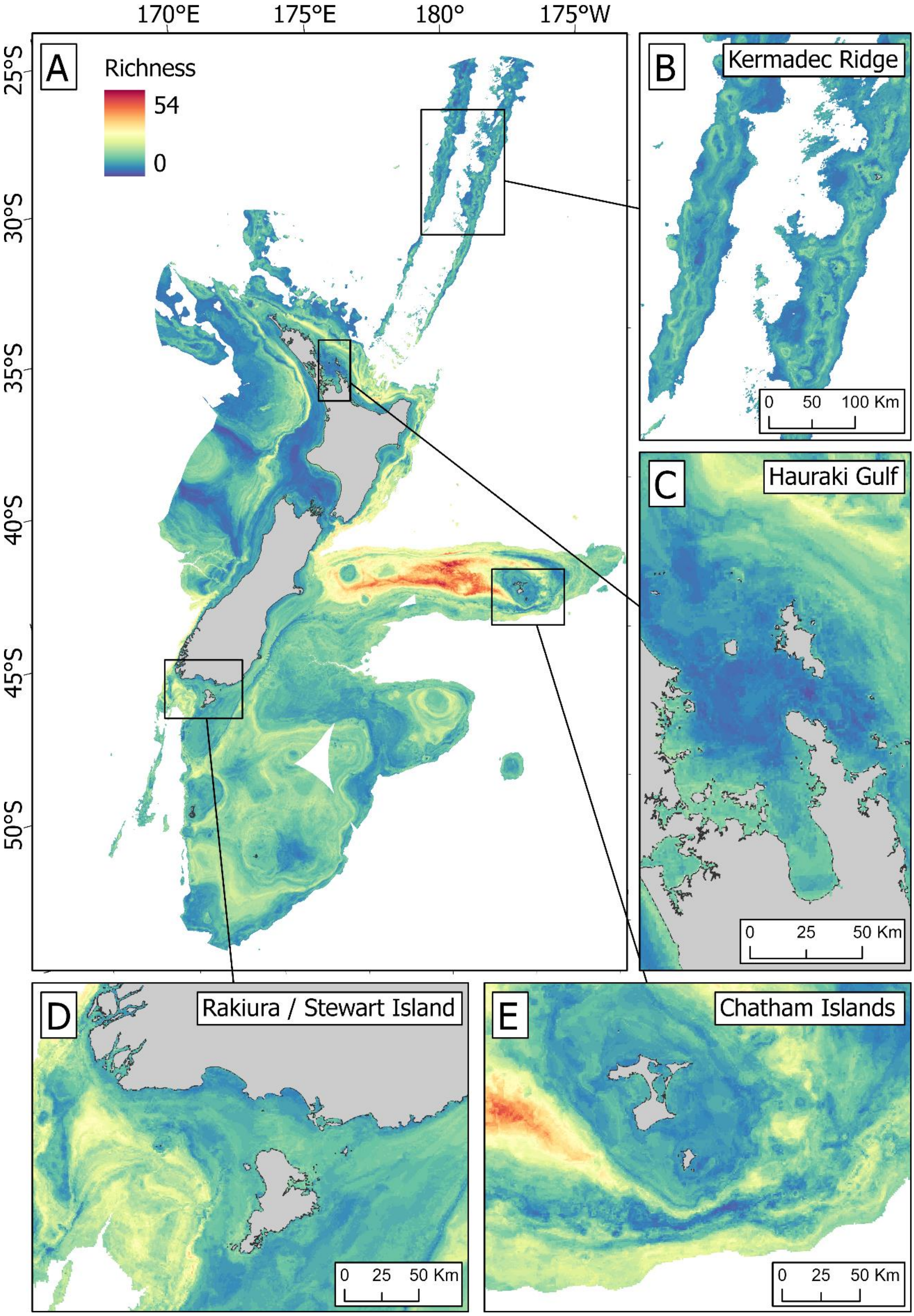

Figure B-5: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for mobile seafloor invertebrate taxa (125 genera). Condition (fishing impact layer) has been applied. Low richness areas shown in blue, high richness shown in red. Cut-off of mapped extent is 2000 m depth.

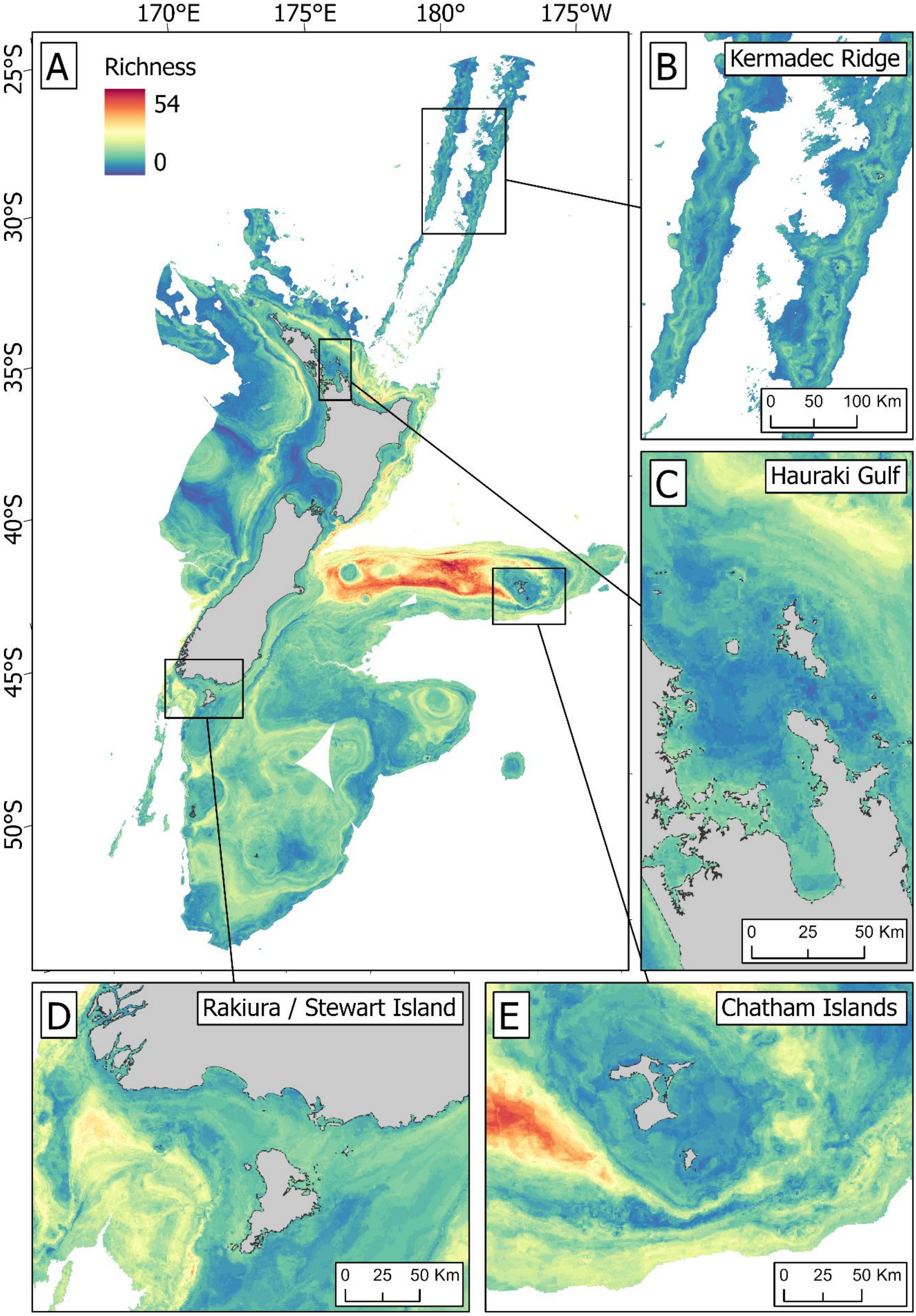

Figure B-6: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for mobile seafloor invertebrate taxa (125 genera). Condition (fishing impact layer) has not been applied. Low richness areas shown in blue, high richness shown in red.Cut-off of mapped extent is 2000 m depth.

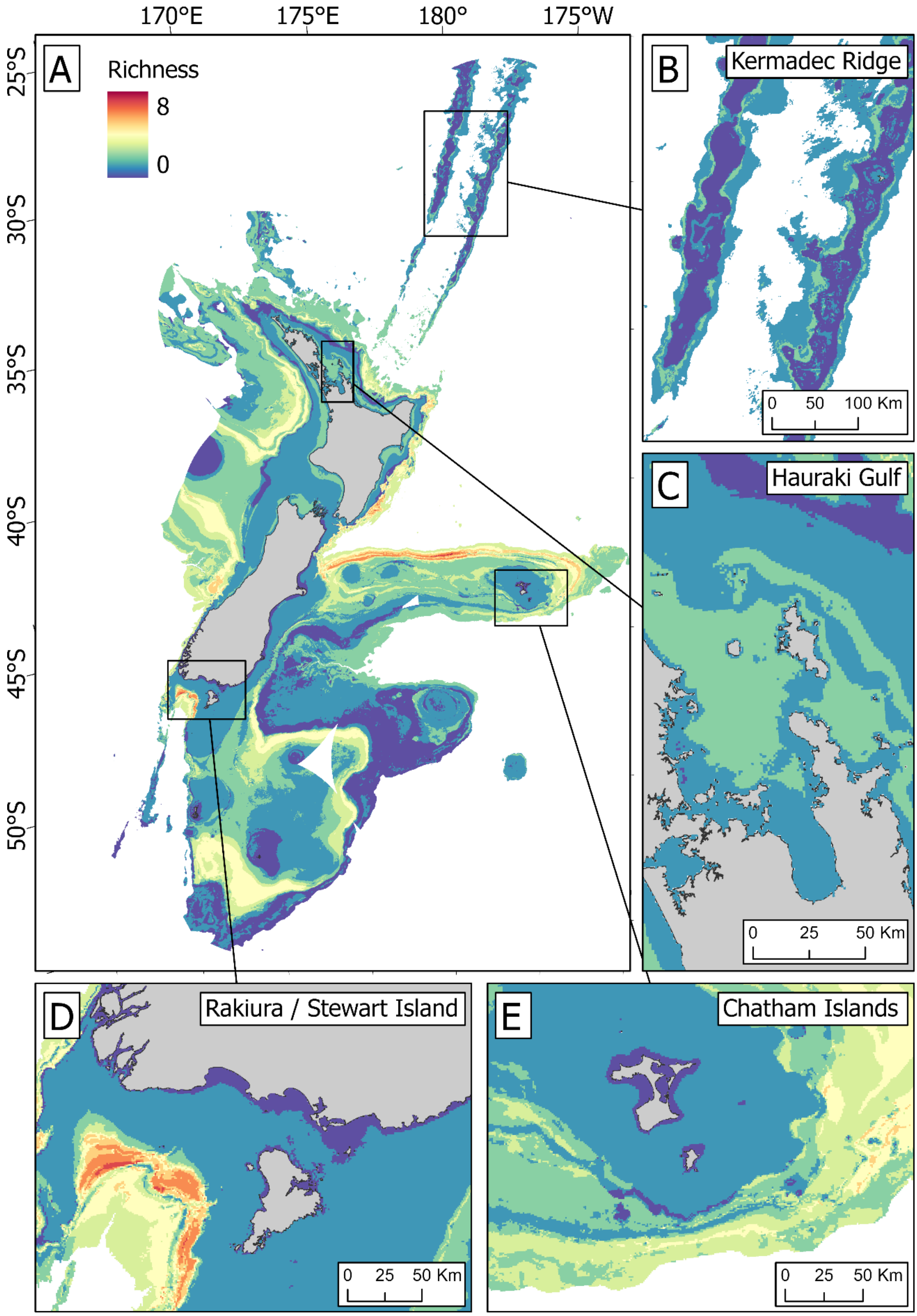

Figure B-7: **Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for pelagic invertebrate taxa (10 genera). Condition (fishing impact layer) has been applied. Low richness areas shown in blue, high richness shown in red. Cut-off of mapped extent is 2000 m depth.**

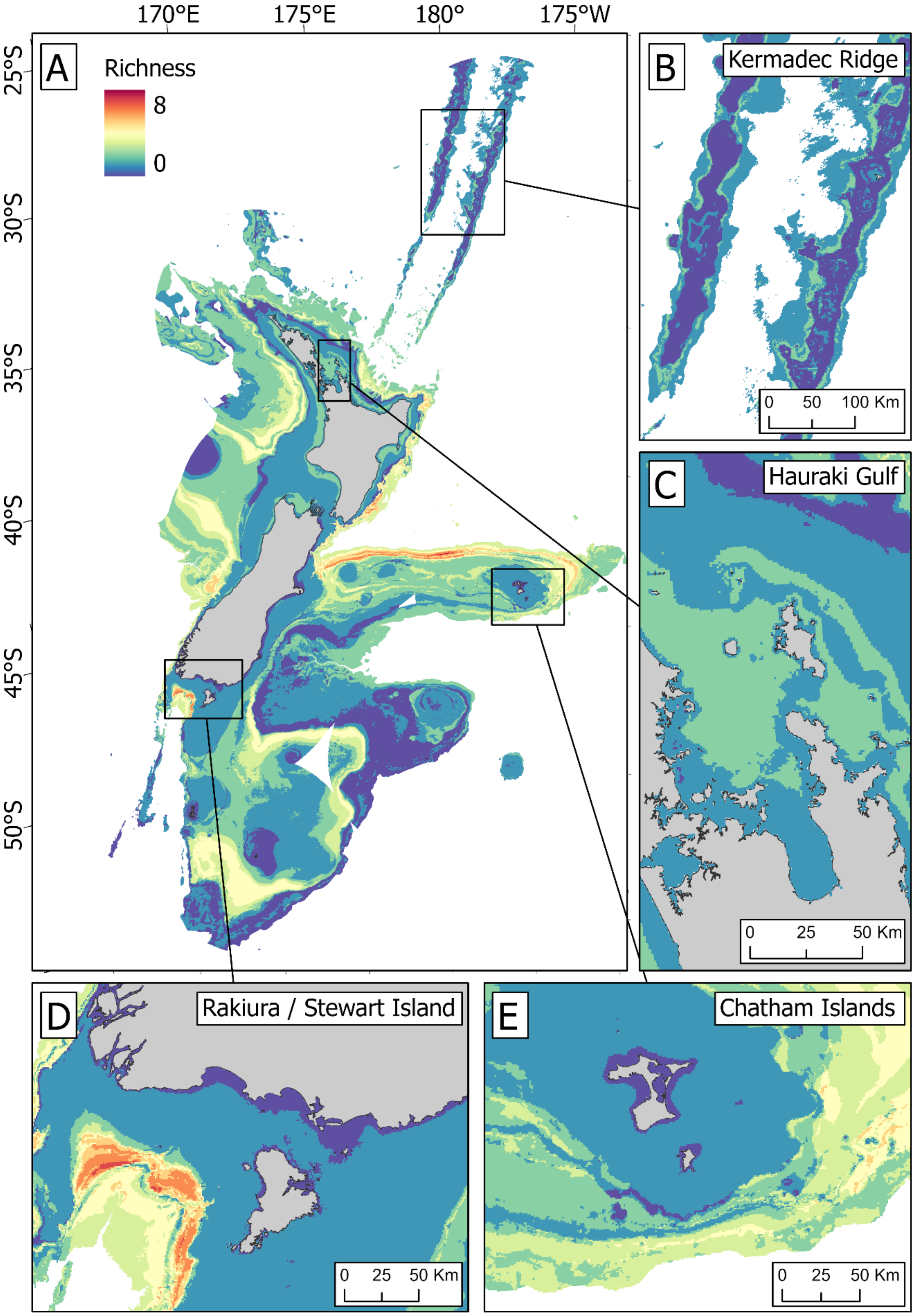

Figure B-8: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for pelagic invertebrate taxa (10 genera). Condition (fishing impact layer) has not been applied. Low richness areas shown in blue, high richness shown in red. Cut-off of mapped extent is 2000 m depth.

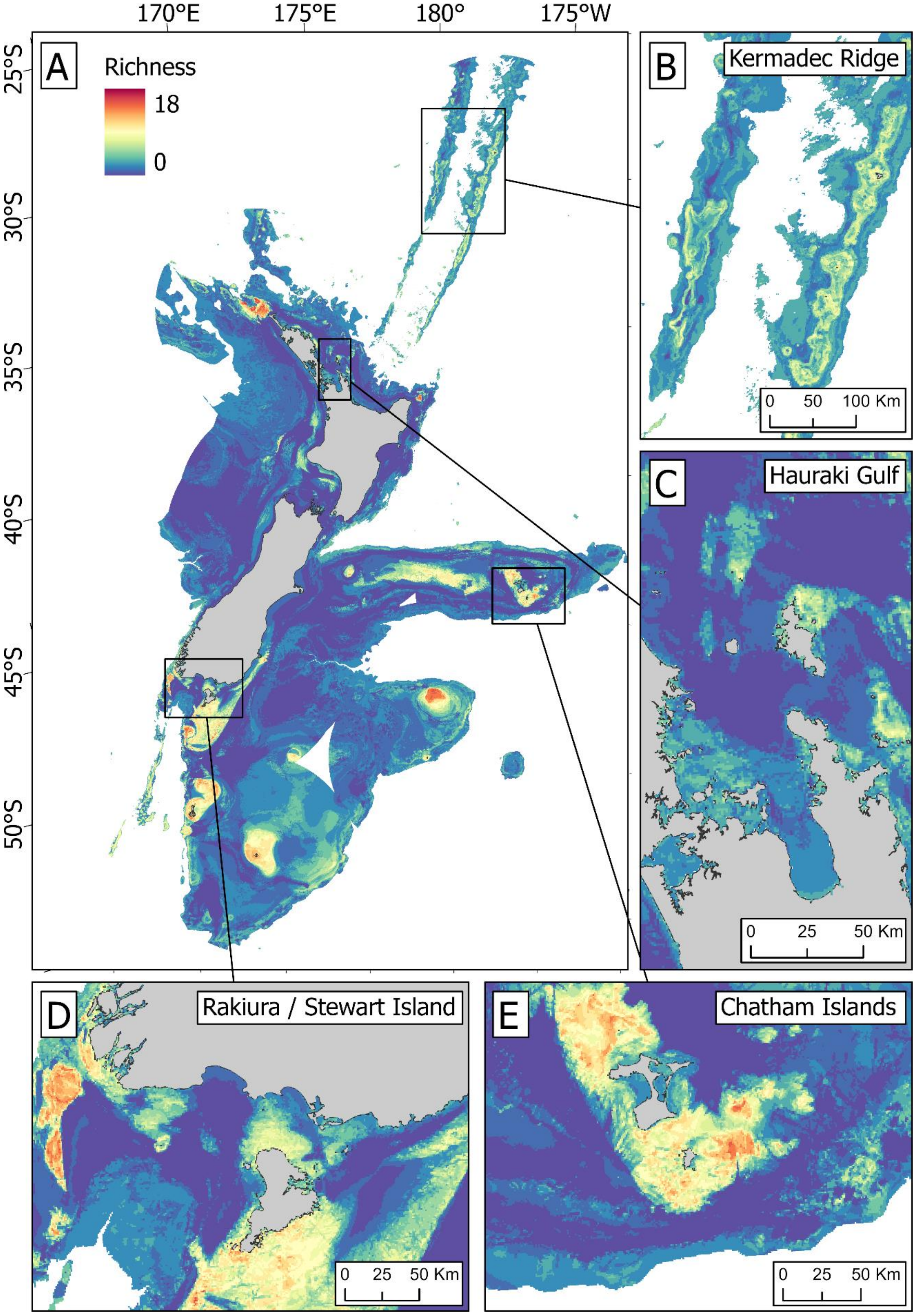

Figure B-9: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for sessile seafloor invertebrate taxa (37 genera). Condition (fishing impact layer) has been applied. Low richness areas shown in blue, high richness shown in red. Cut-off of mapped extent is 2000 m depth.

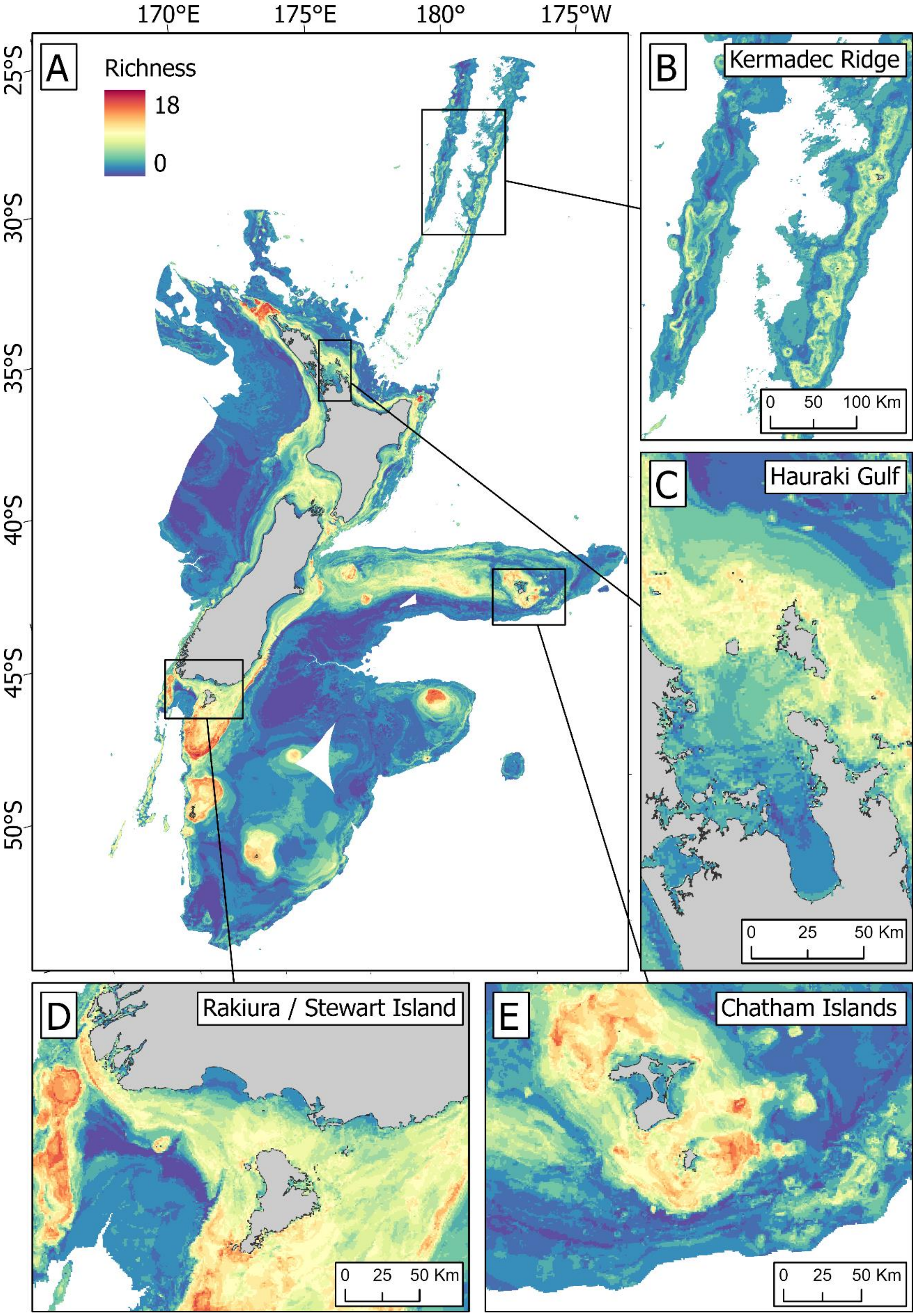

Figure B-10: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for sessile seafloor invertebrate taxa (37 genera). Condition (fishing impact layer) has not been applied. Low richness areas shown in blue, high richness shown in red. Cut-off of mapped extent is 2000 m depth.

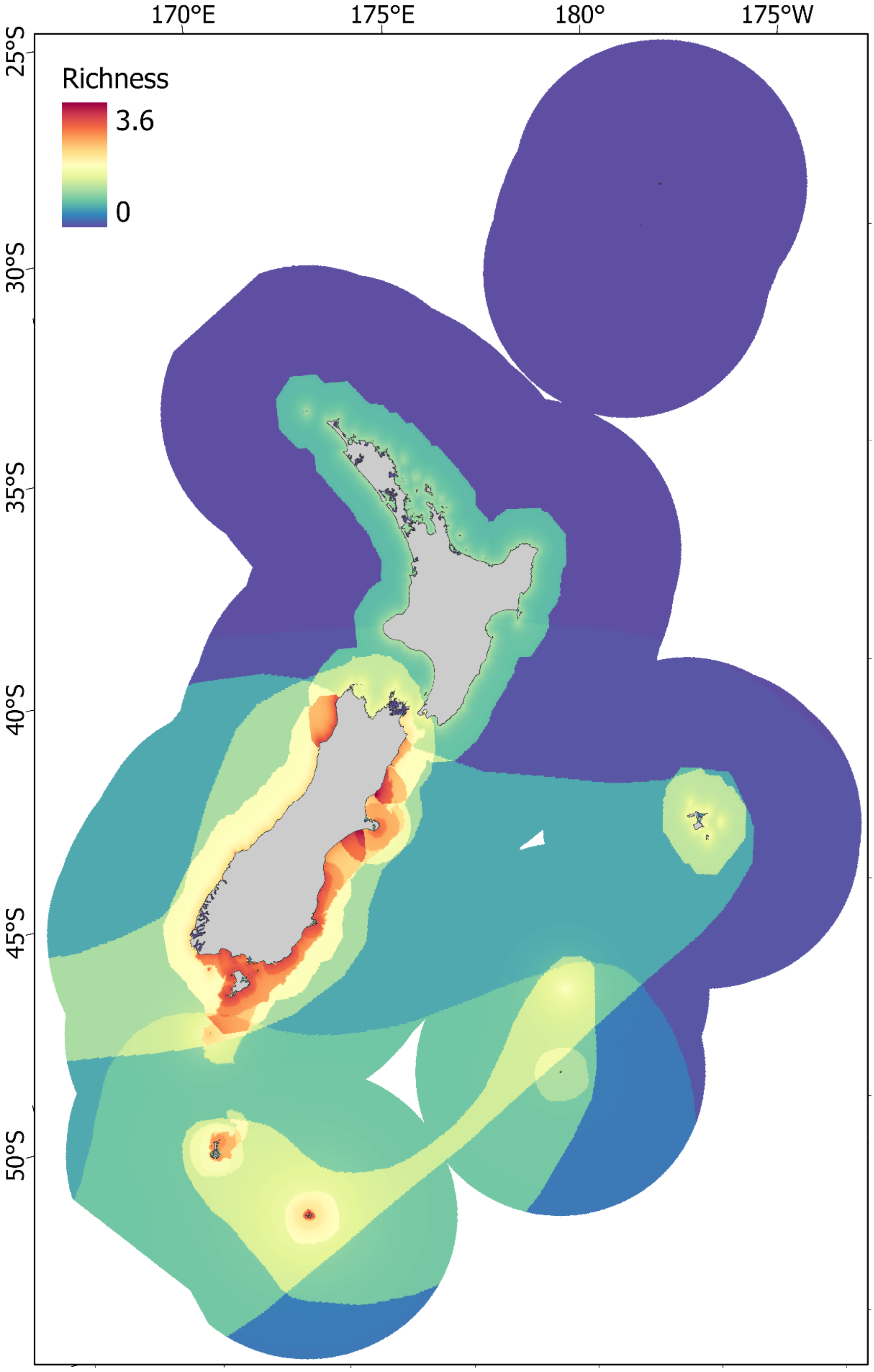

Figure B-11: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for penguin taxa (9 genera). Low richness areas shown in blue, high richness shown in red.

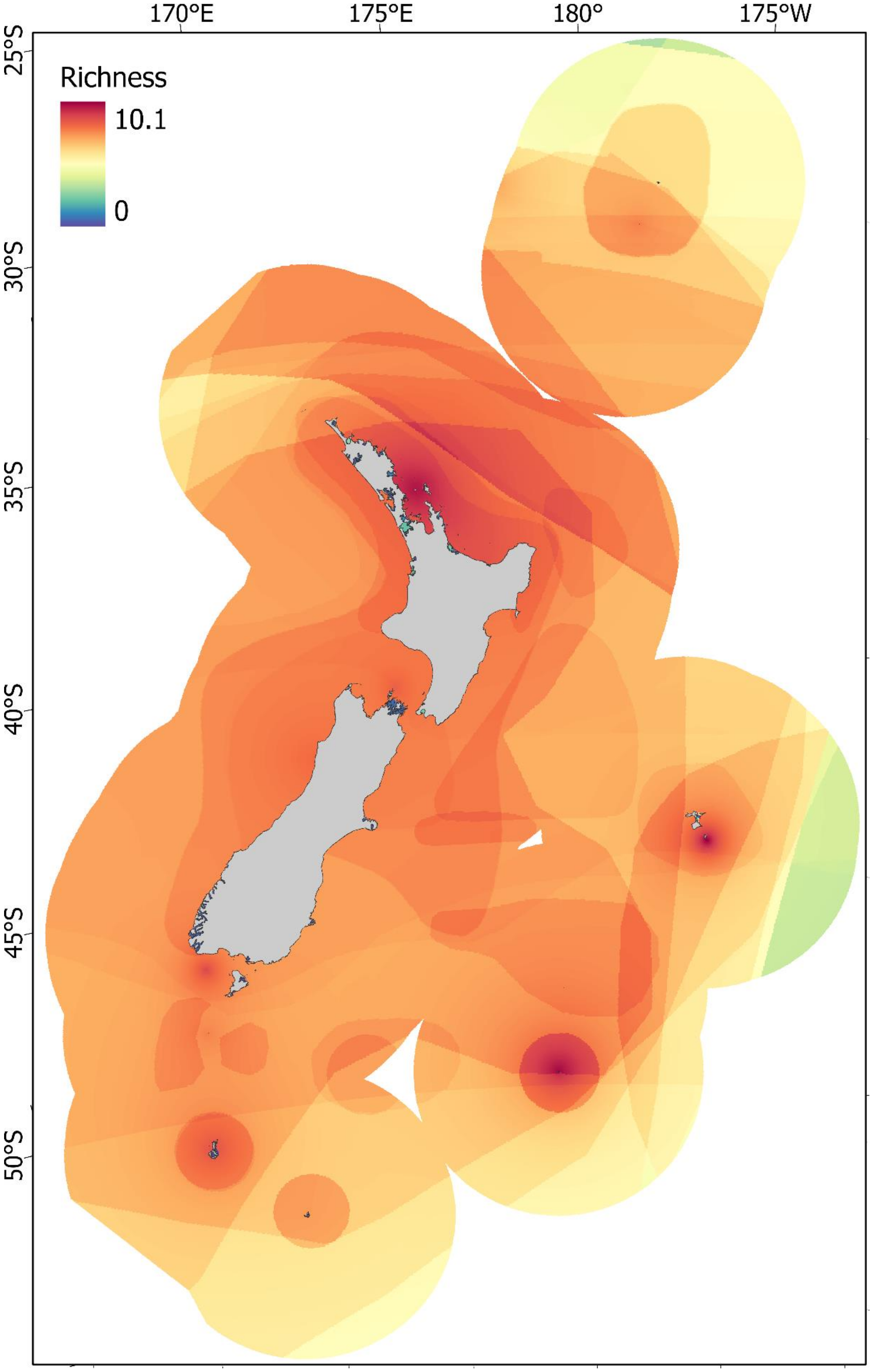

Figure B-12: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for petrel taxa (28 genera). Low richness areas shown in blue, high richness shown in red.

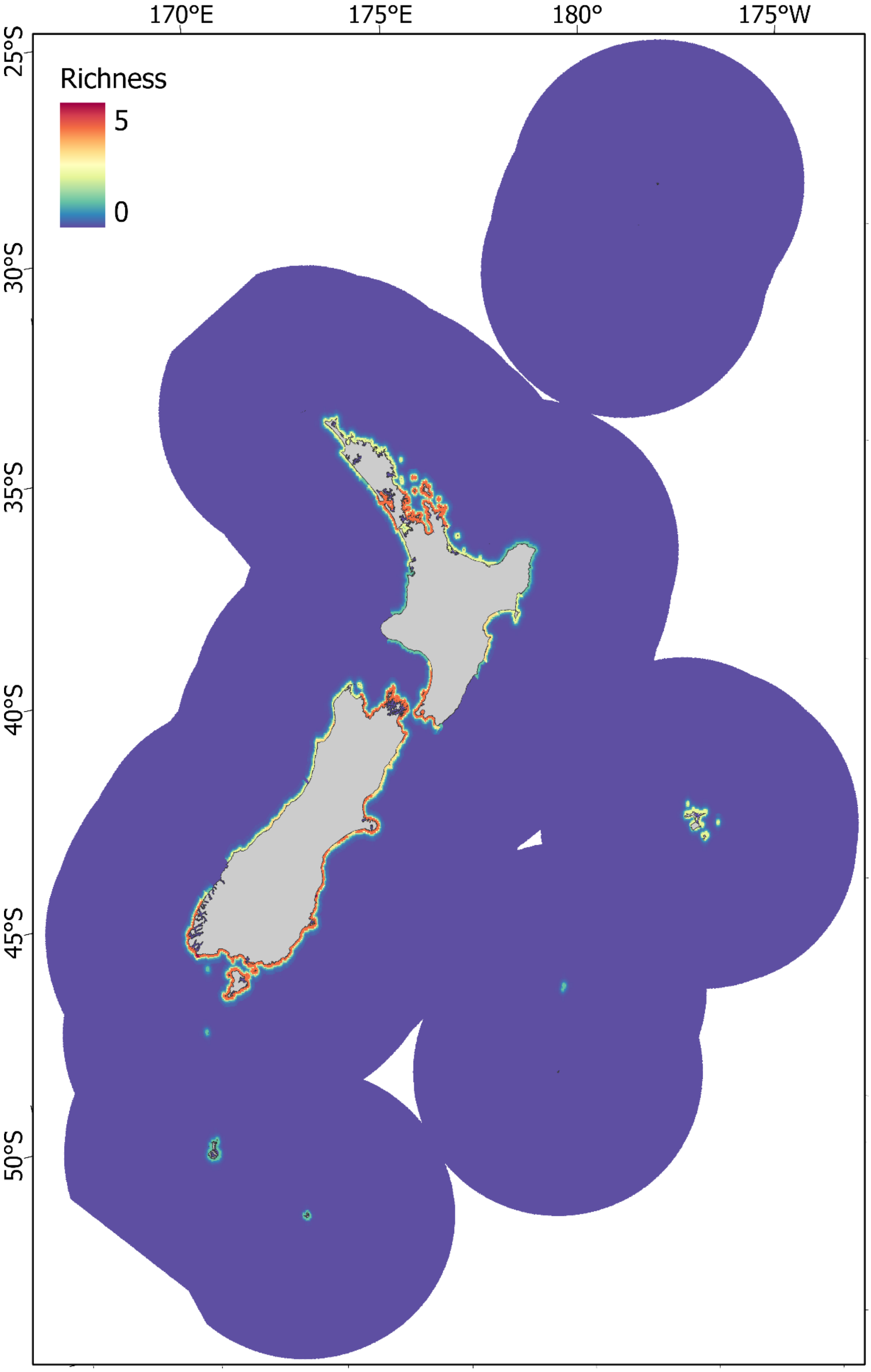

Figure B-13: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for shag taxa (11 genera). Low richness areas shown in blue, high richness shown in red.

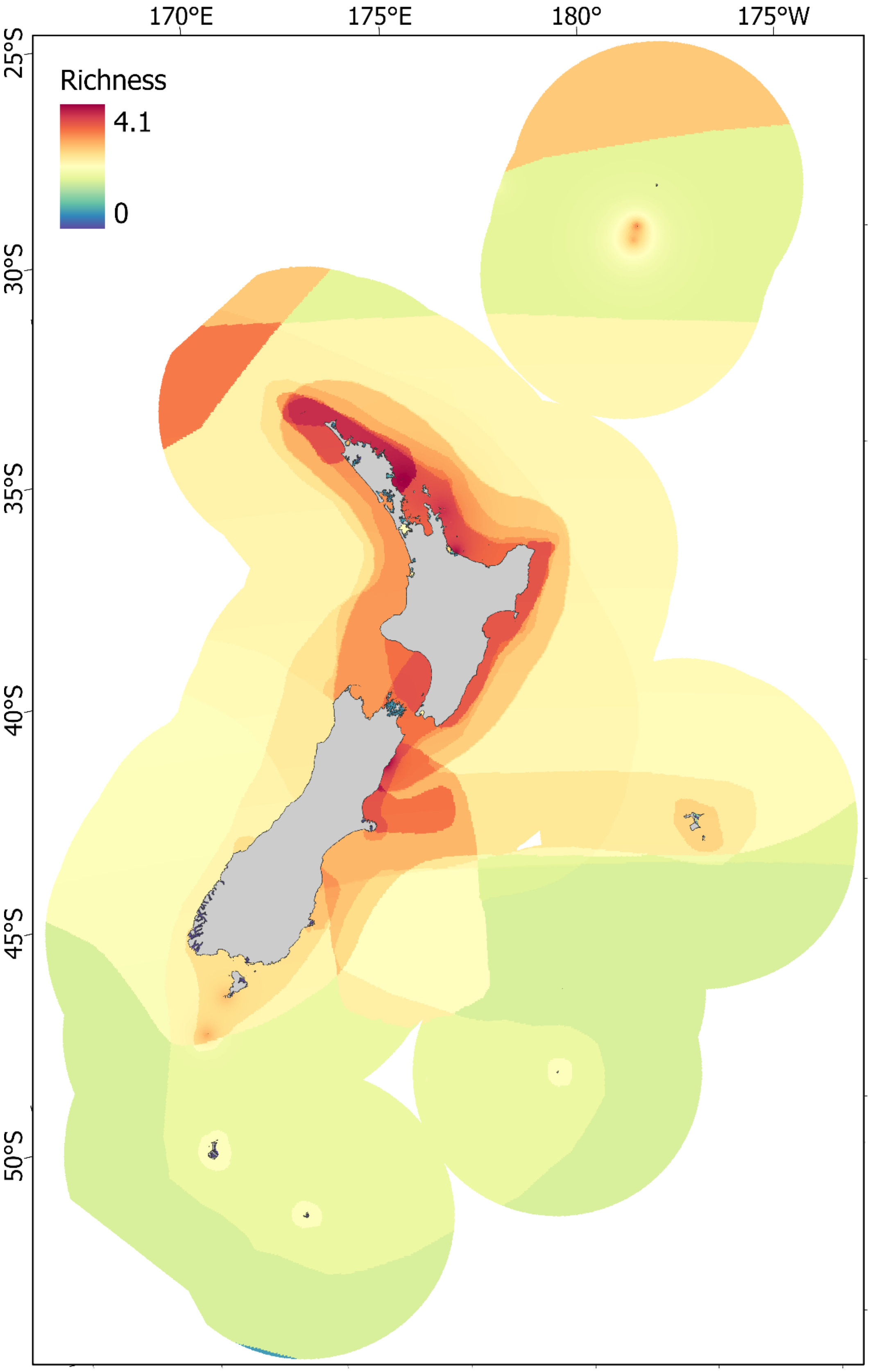

Figure B-14: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for shearwater taxa (8 genera). Low richness areas shown in blue, high richness shown in red.

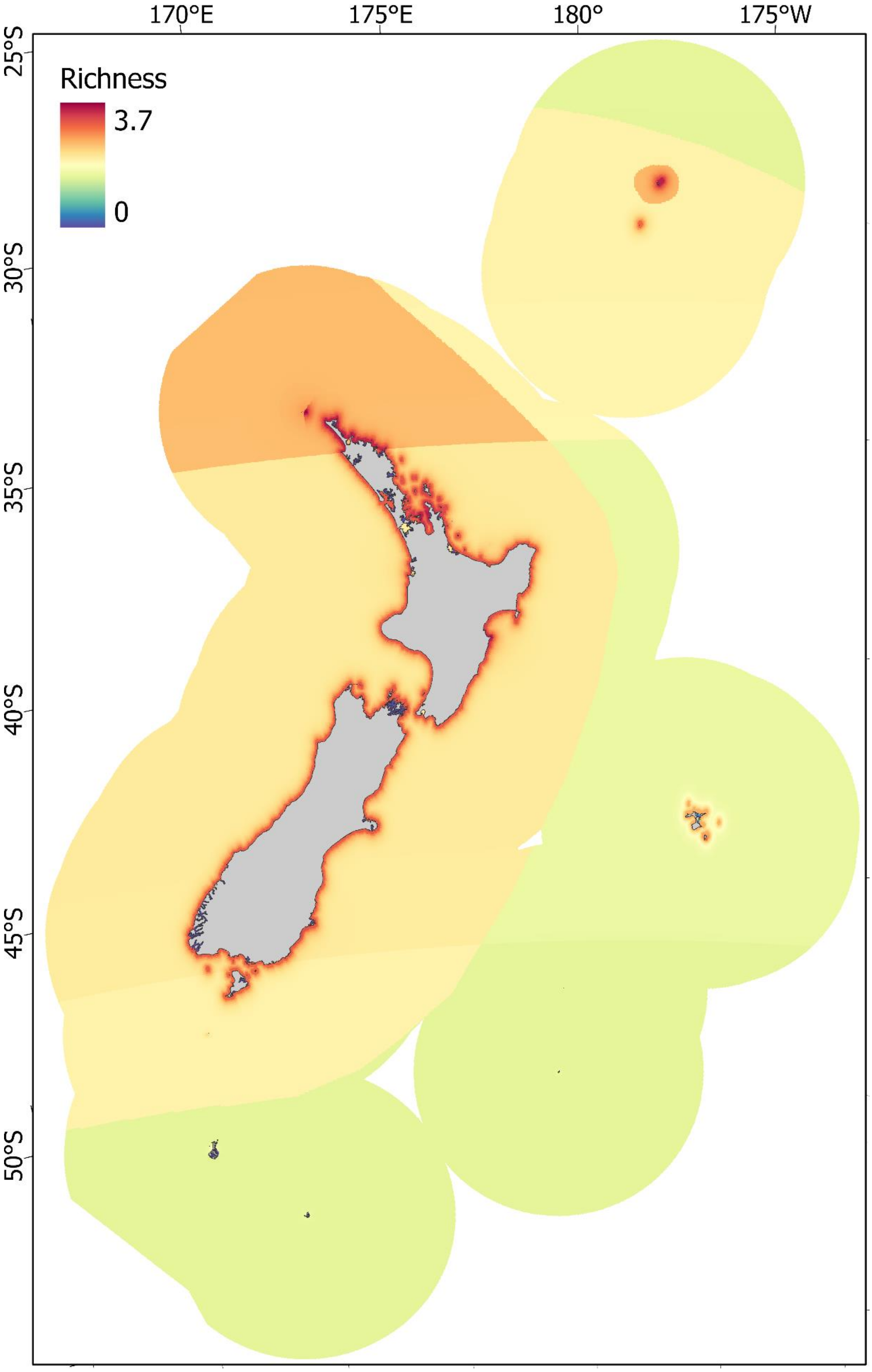

Figure B-15: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for other seabird taxa (5 genera) besides albatross, penguins, petrels, shags and shearwaters. Low richness areas shown in blue, high richness shown in red.

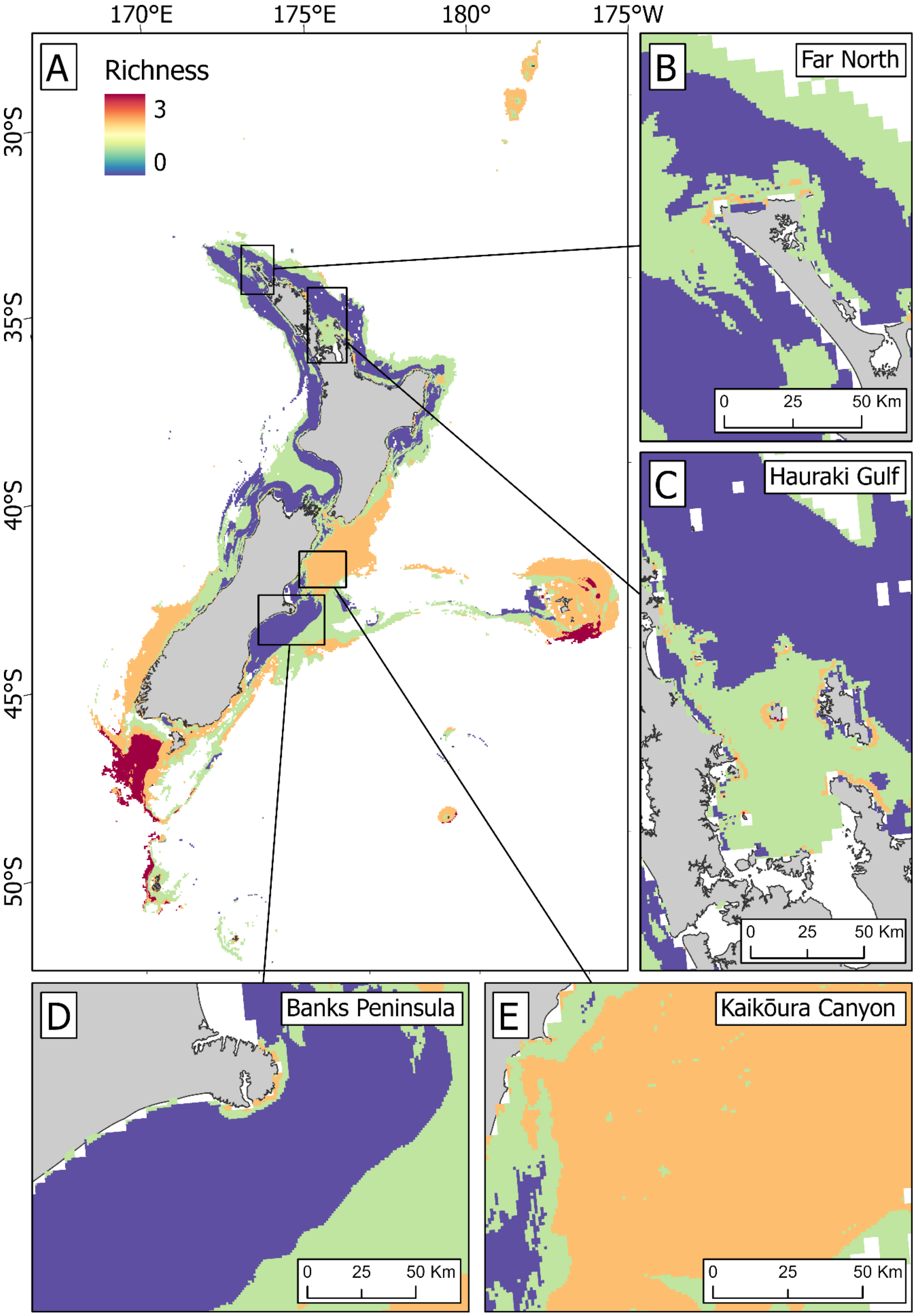

Figure B-16: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for whale taxa (5 genera), masked to the area of sufficient environmental cover. Low richness areas shown in blue, high richness shown in red. Cut-off of mapped extent is areas with environmental coverage values <0.075.

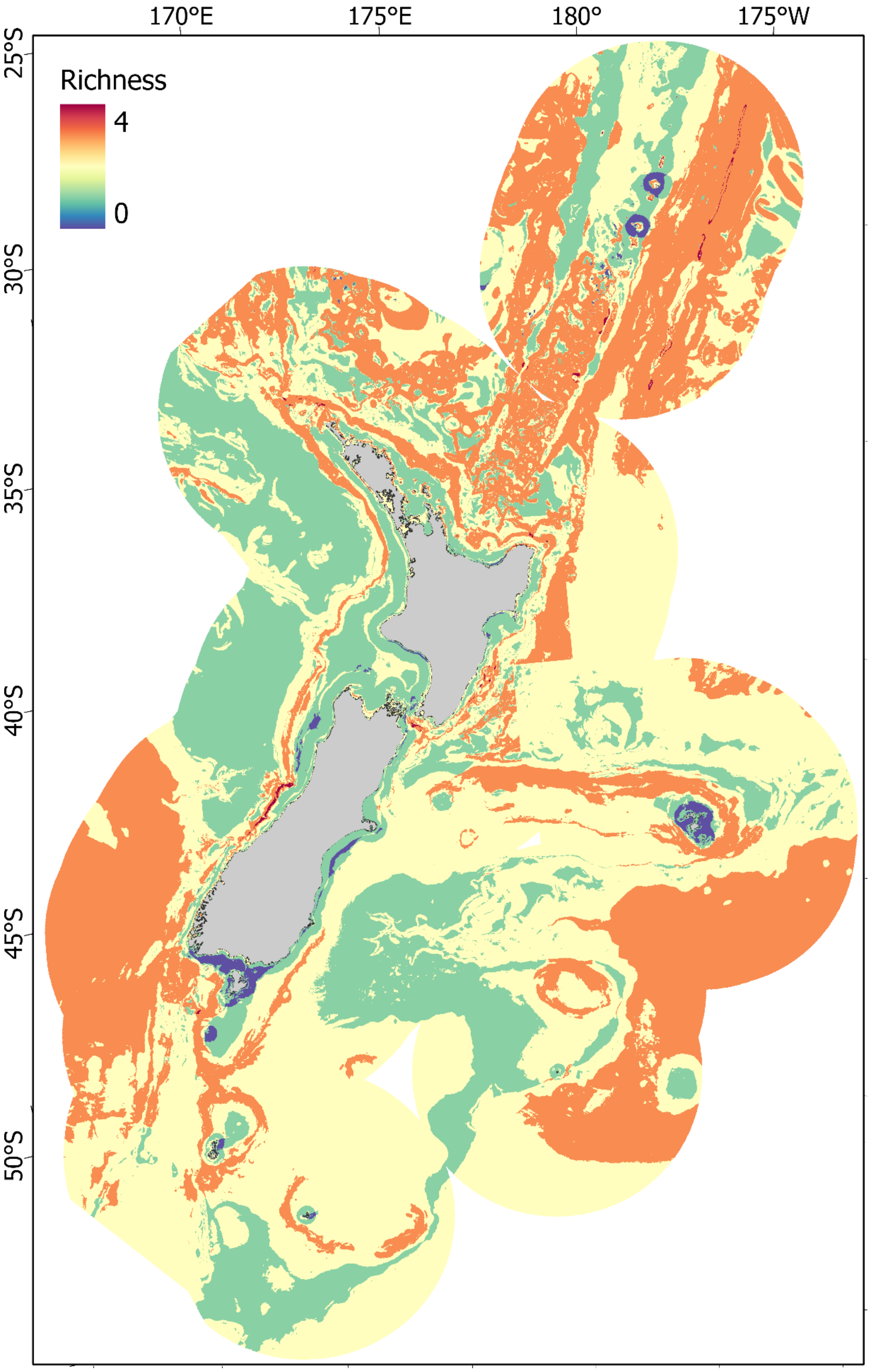

Figure B-17: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for delphinid taxa (7 genera). Low richness areas shown in blue, high richness shown in red. The artifact to the east and southeast of the North Island is attributed to the bottlenose dolphin modelled layer and is due to the underlying turbidity environmental layer, which was not available at the EEZ scale for modelling.

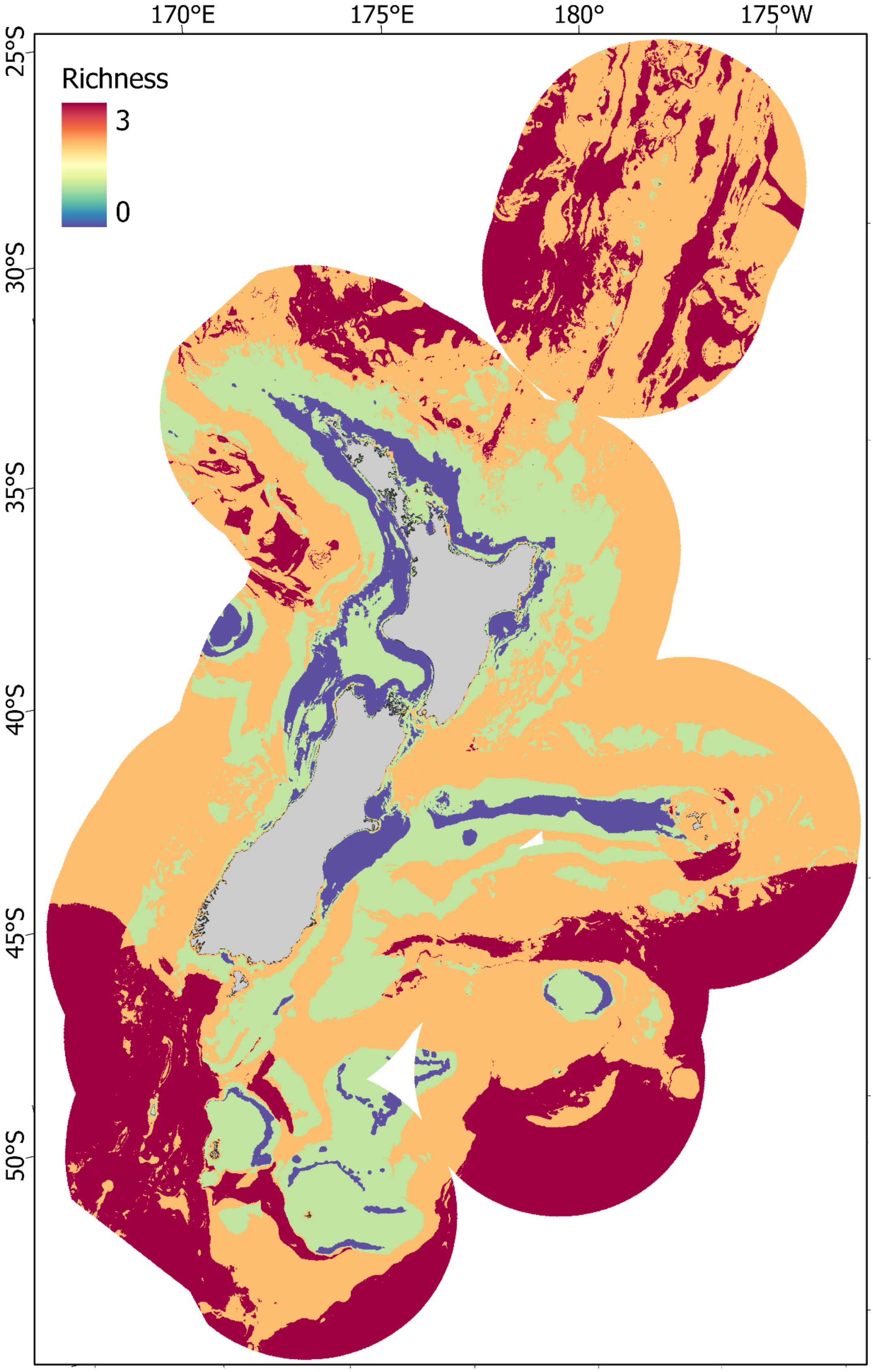

Figure B-18: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for whale taxa (5 genera). Low richness areas shown in blue, high richness shown in red.

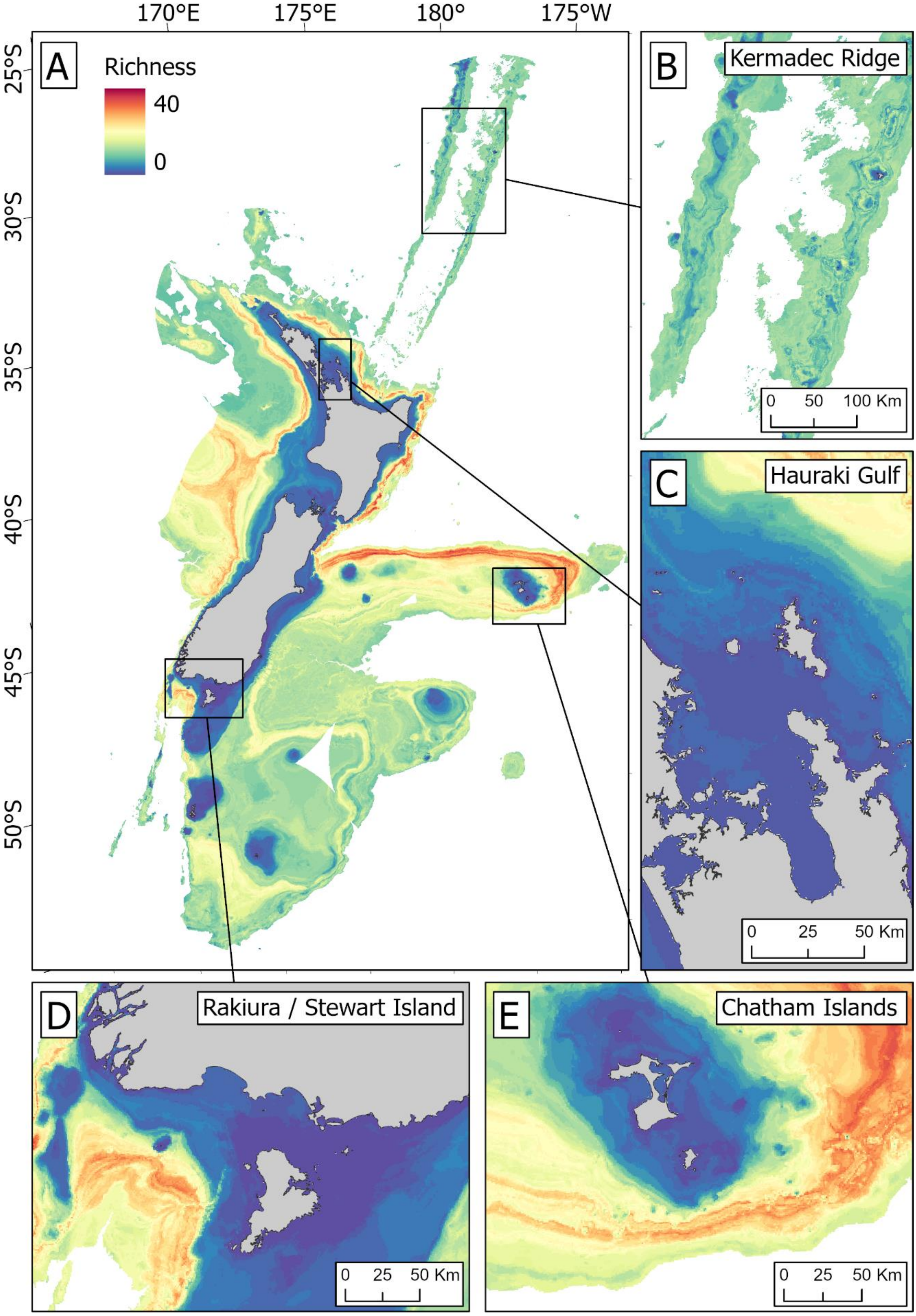

Figure B-19: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for bathyal-demersal fish taxa (82 genera). Low richness areas shown in blue, high richness shown in red. Cut-off of mapped extent is 2000 m depth.

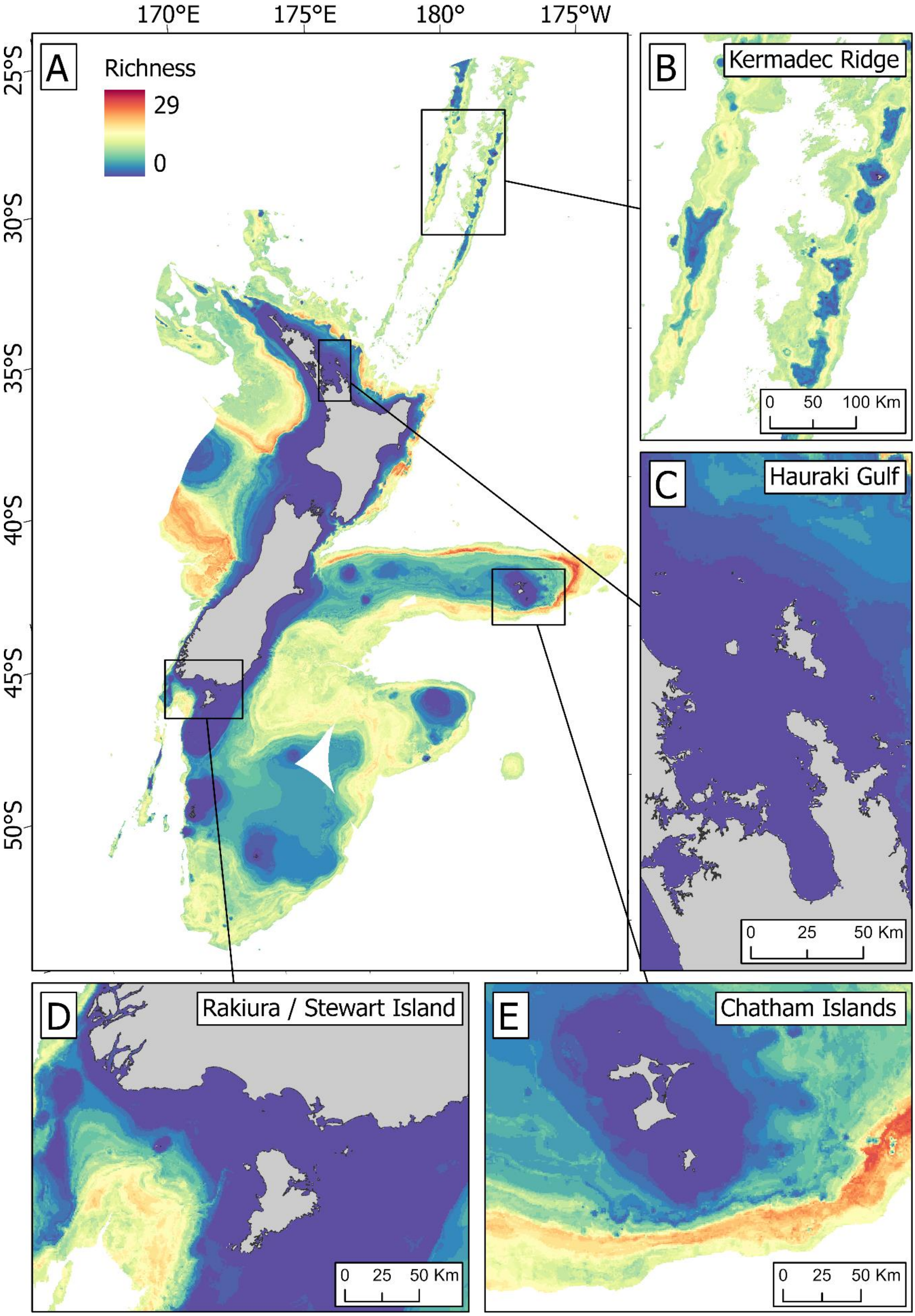

Figure B-20: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for bentho-pelagic demersal fish taxa (39 genera). Low richness areas shown in blue, high richness shown in red. Cut-off of mapped extent is 2000 m depth.

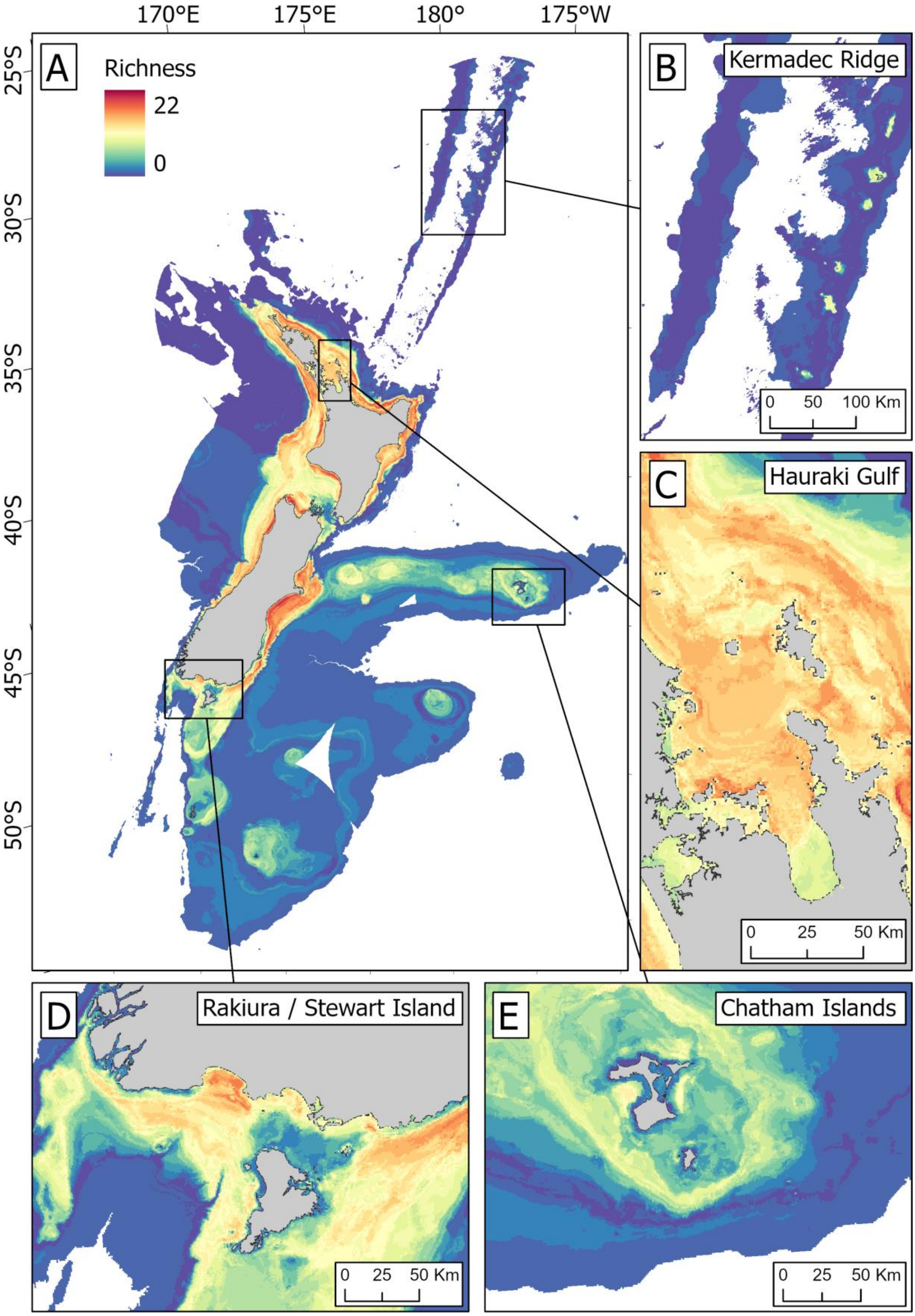

Figure B-21: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for benthic fish taxa (45 genera). Low richness areas shown in blue, high richness shown in red. Cut-off of mapped extent is 2000 m depth.

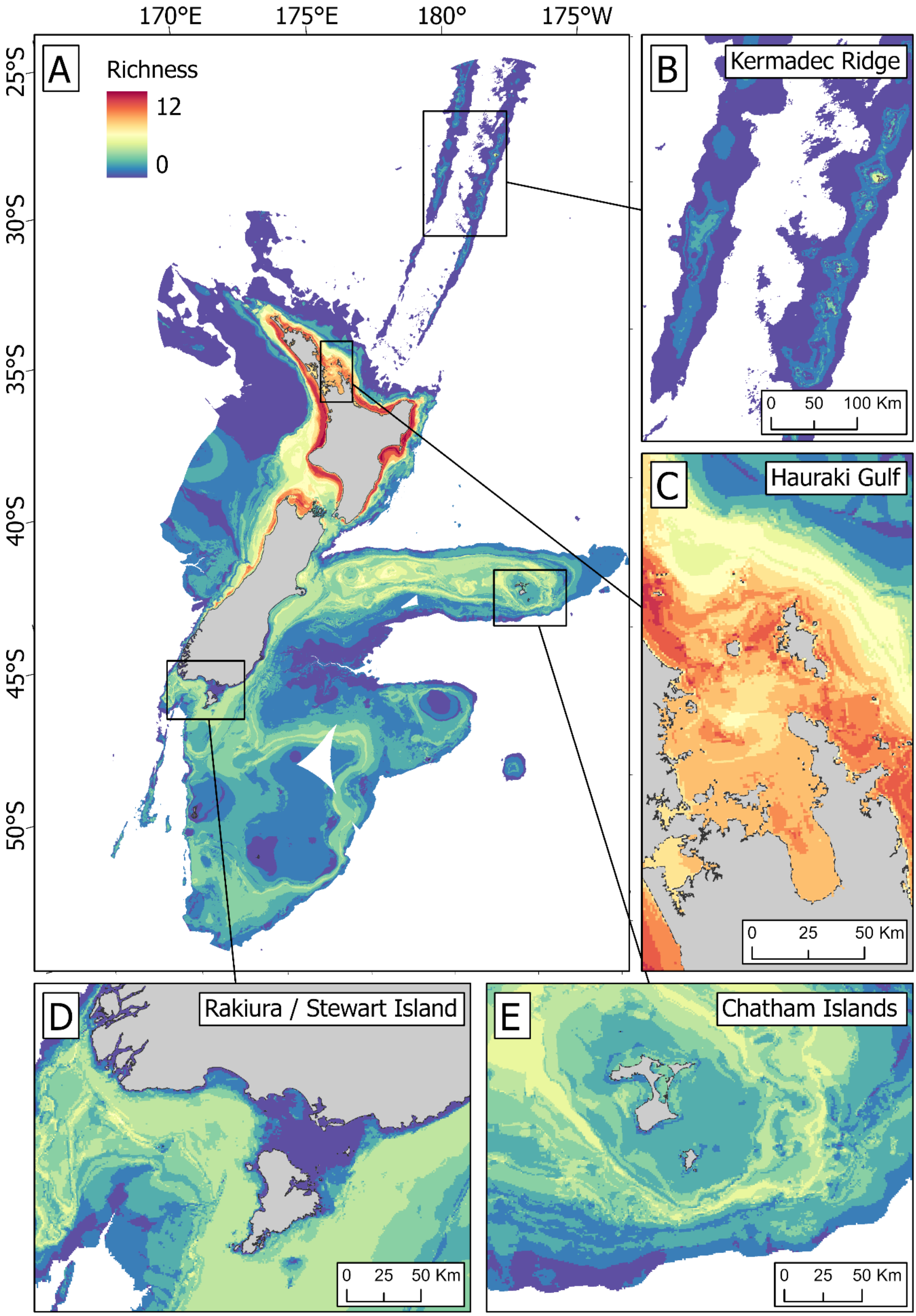

Figure B-22: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for pelagic fish taxa (22 genera). Low richness areas shown in blue, high richness shown in red. Cut-off of mapped extent is 2000 m depth.

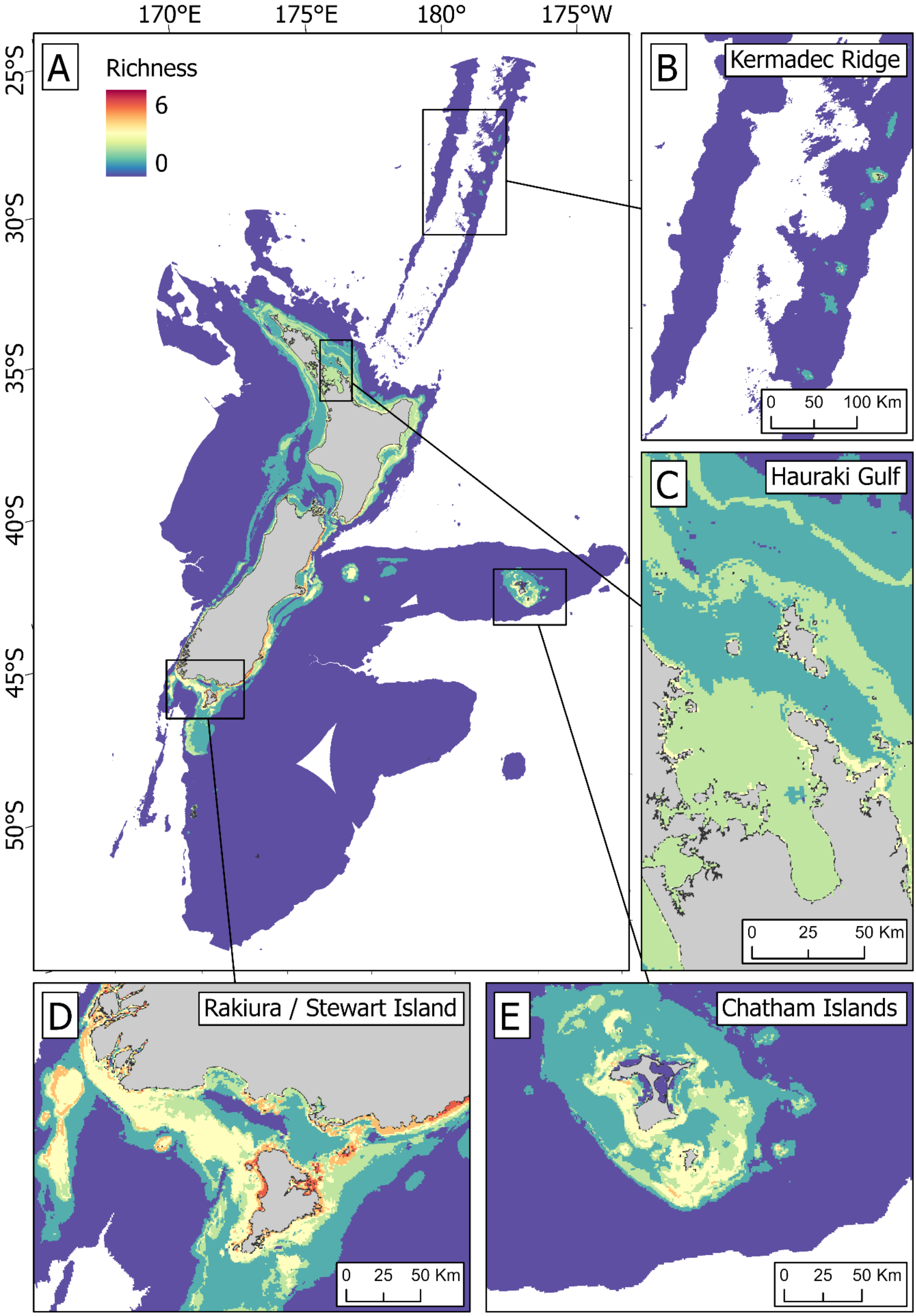

Figure B-23: Mapped biodiversity KEA criteria 6 based on the stacked approach (alpha diversity; species richness) for reef-associated demersal fish taxa (7 genera). Low richness areas shown in blue, high richness shown in red. Cut-off of mapped extent is 2000 m depth.

B. 2. Zonation

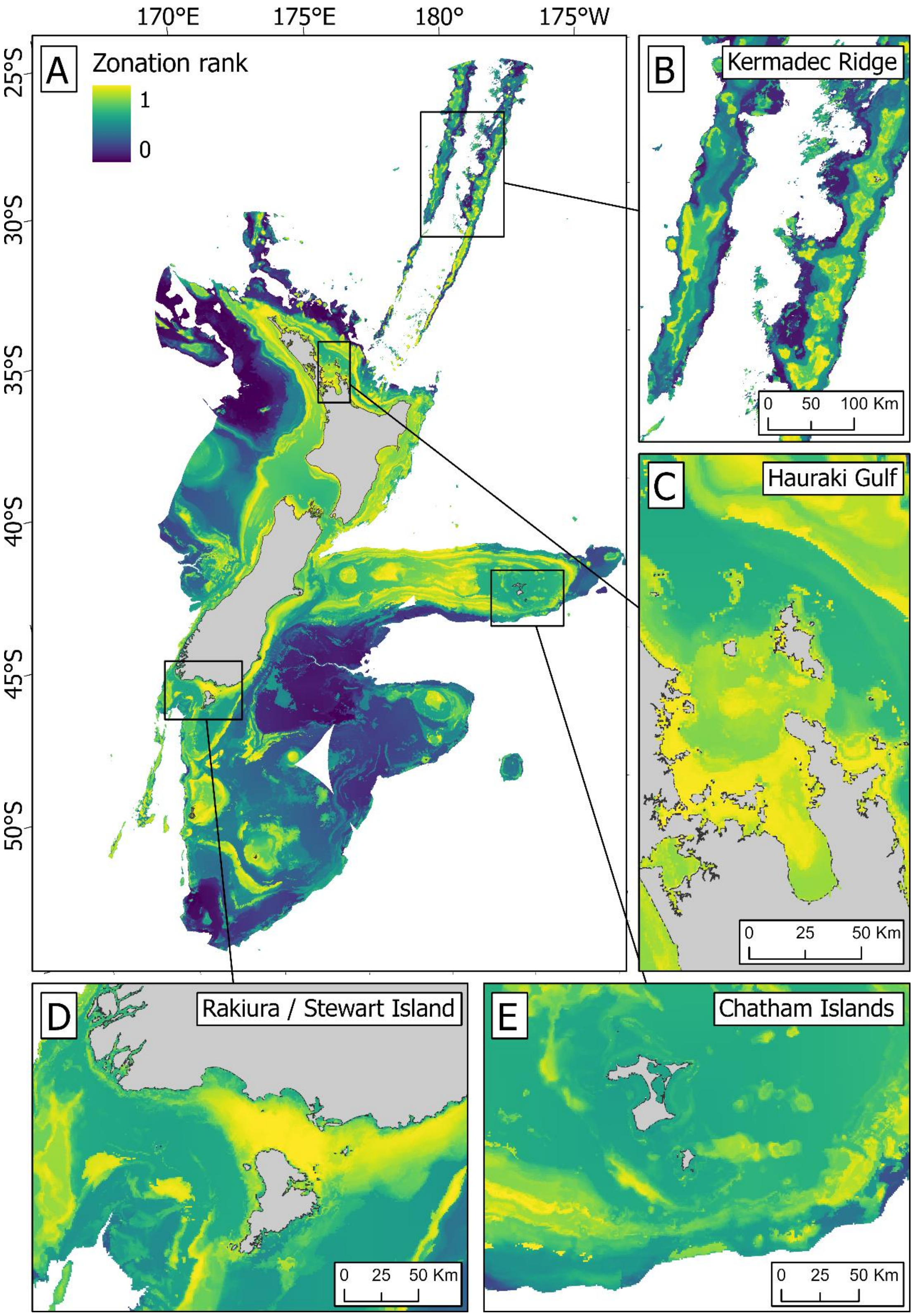

Figure B-24: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for all seafloor invertebrate taxa (205 genera combined). Condition (fishing impact layer) has not been applied. Low rank priority is shown in dark blue, high rank priority is shown in yellow. Cut-off of mapped extent is 2000 m depth.

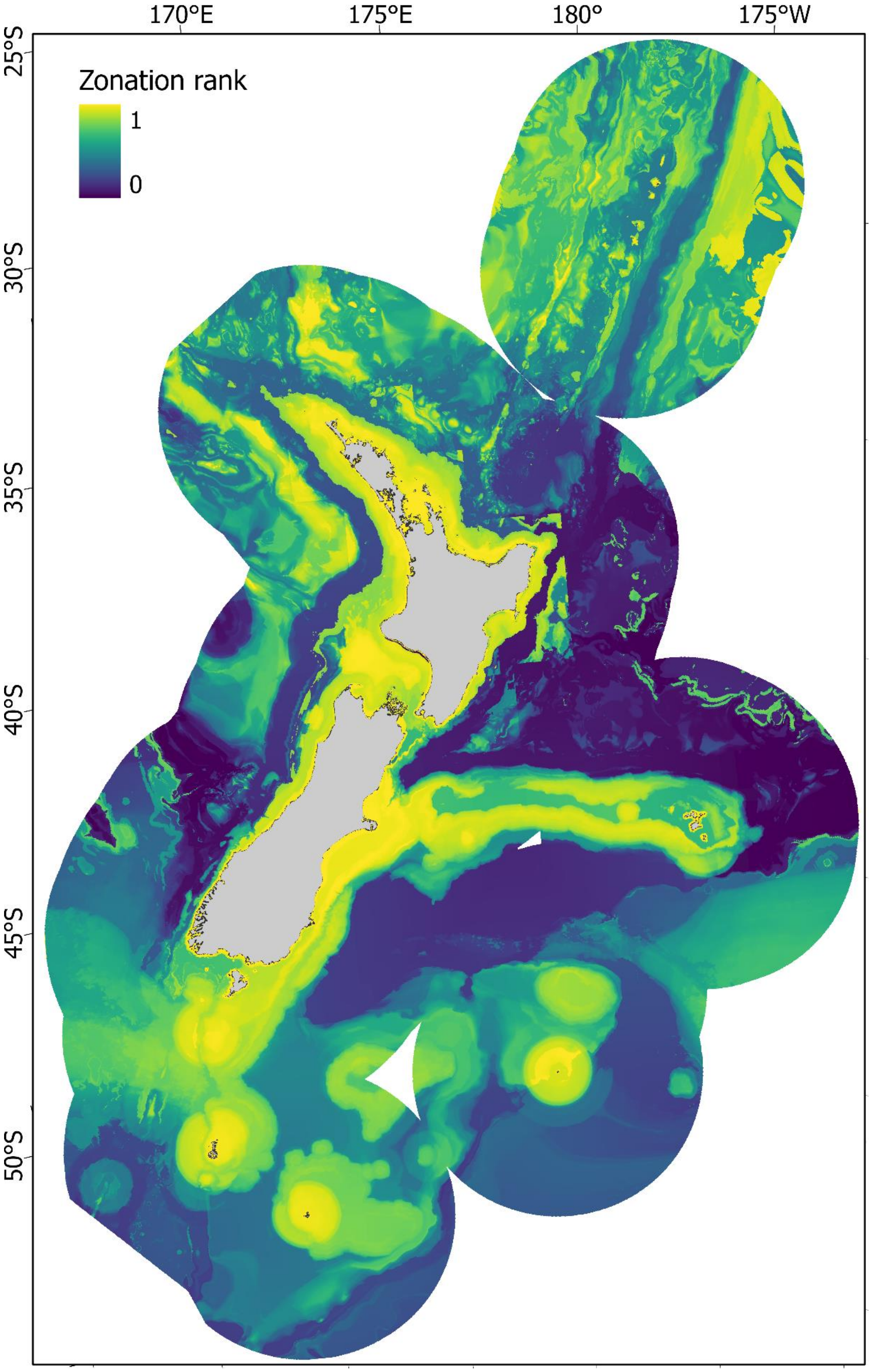

Figure B-25: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for all cetacean taxa (12 genera combined). Low rank priority is shown in dark blue, high rank priority is shown in yellow. Cut-off of mapped extent is 2000 m depth.

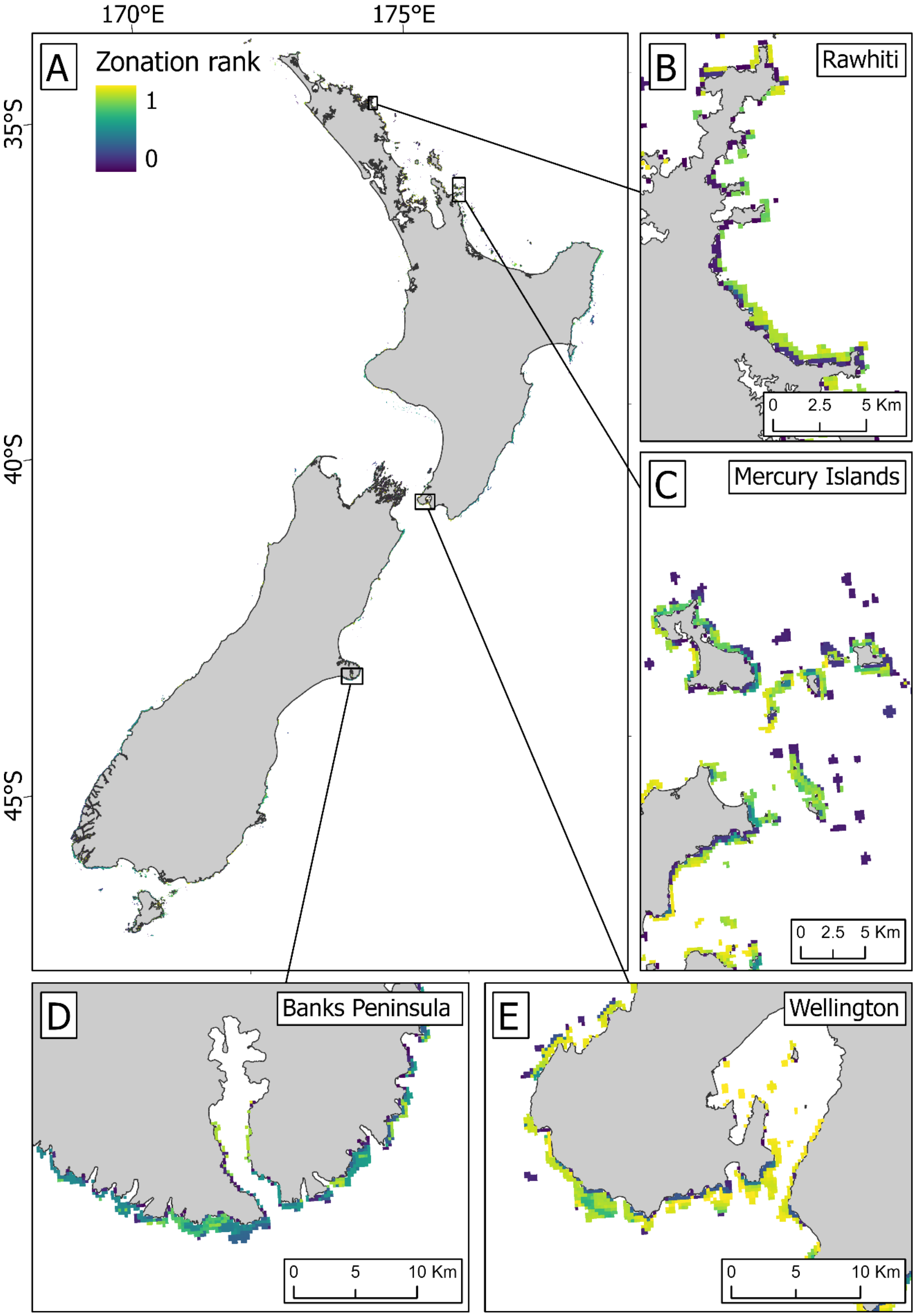

Figure B-26: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for non-canopy-forming macroalgae taxa (68 genera). Low rank priority is shown in dark blue, high rank priority is shown in yellow. Mapped extent is restricted to rocky reef.

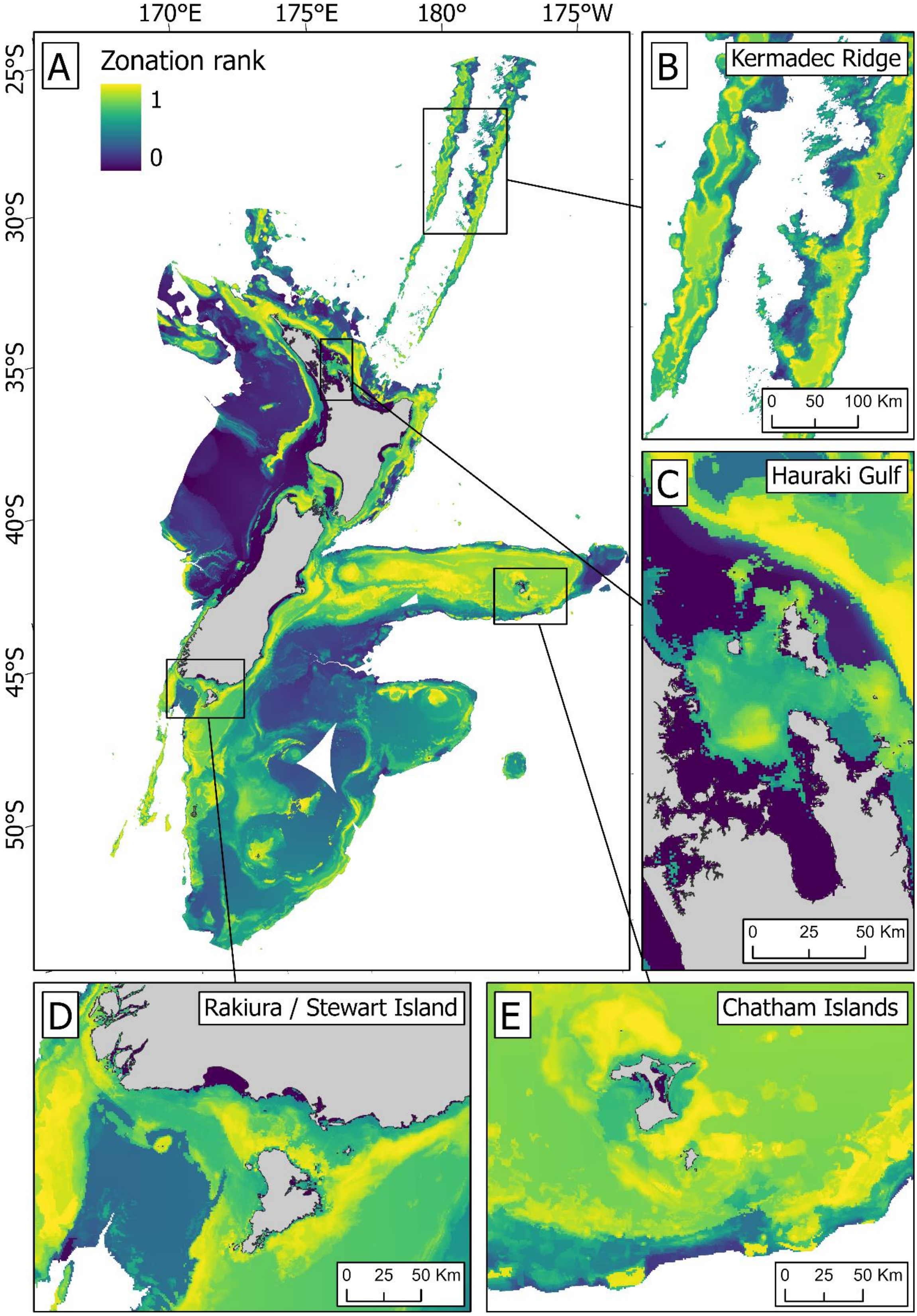

Figure B-27: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for key biogenic habitat-forming invertebrate taxa (33 genera). Condition (fishing impact layer) has not been applied. Low rank priority is shown in dark blue, high rank priority is shown in yellow. Cut-off of mapped extent is 2000 m depth.

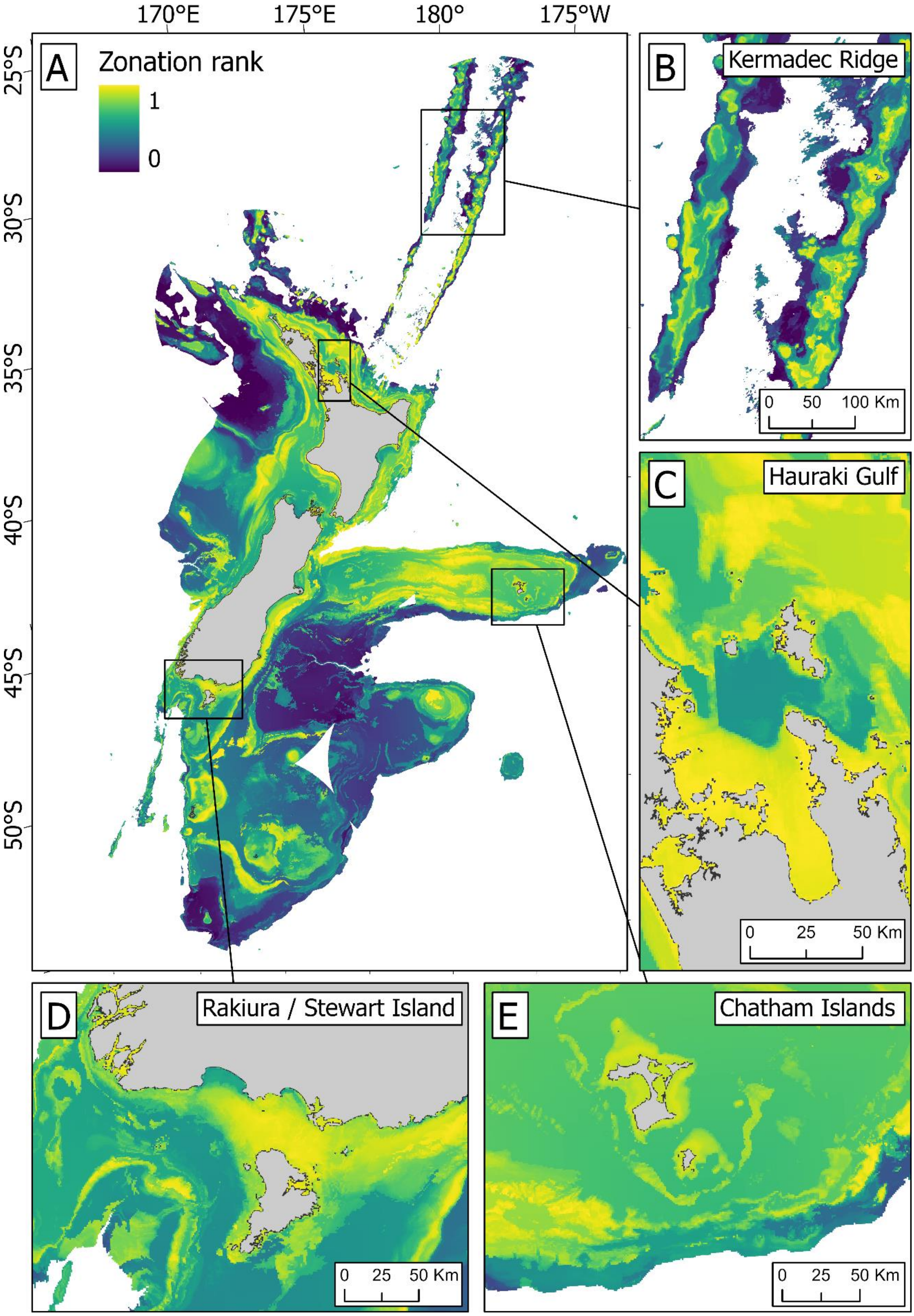

Figure B-28: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for mobile invertebrate taxa (125 genera). Condition (fishing impact layer) has been applied. Low rank priority is shown in dark blue, high rank priority is shown in yellow. Cut-off of mapped extent is 2000 m depth.

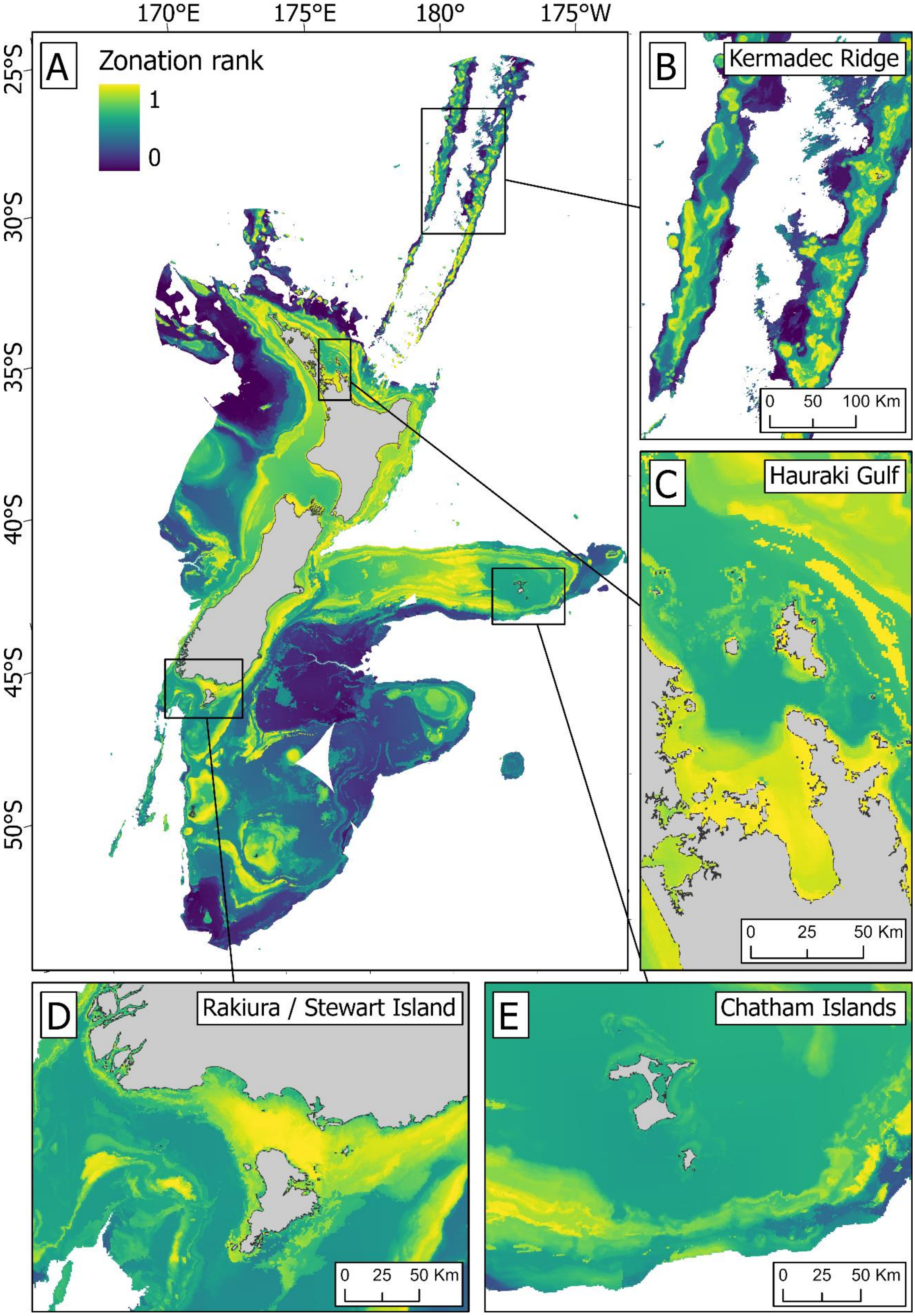

Figure B-29: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for mobile seafloor invertebrate taxa (125 genera). Condition (fishing impact layer) has not been applied. Low rank priority is shown in dark blue, high rank priority is shown in yellow. Cut-off of mapped extent is 2000 m depth.

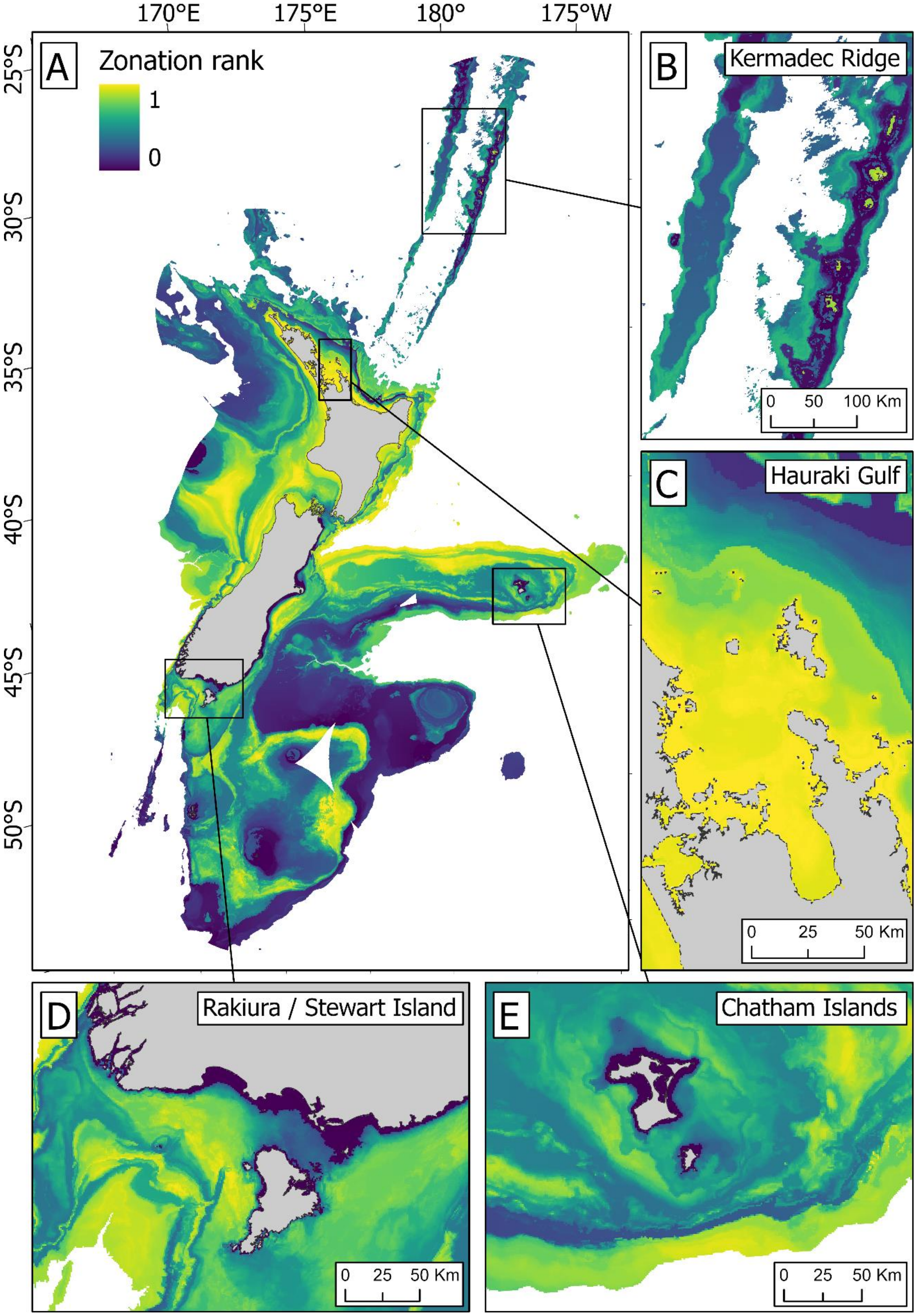

Figure B-30: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for pelagic invertebrate taxa (10 genera). Condition (fishing impact layer) has been applied. Low rank priority is shown in dark blue, high rank priority is shown in yellow. Cut-off of mapped extent is 2000 m depth.

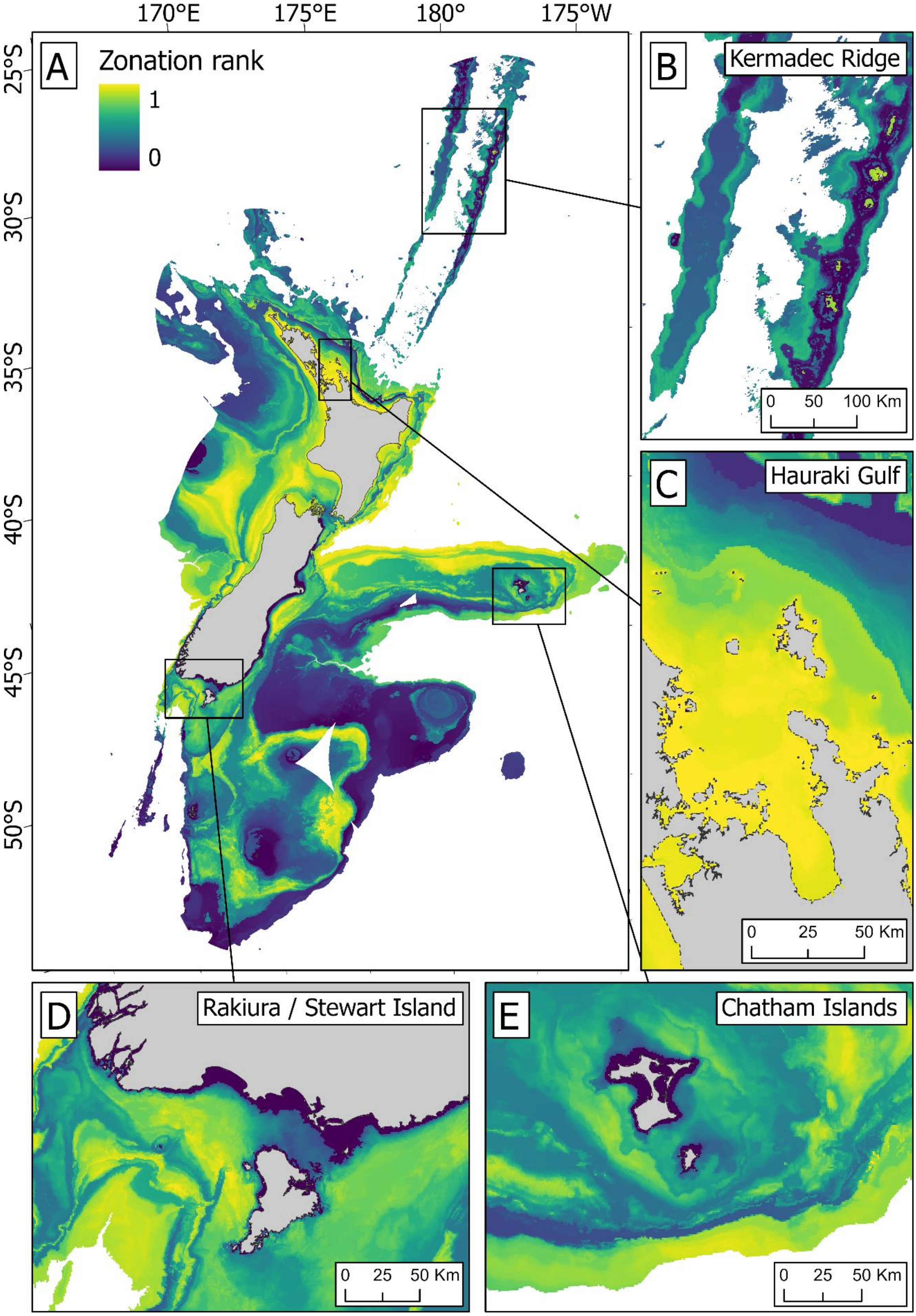

Figure B-31: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for pelagic invertebrate taxa (10 genera). Condition (fishing impact layer) has not been applied. Low rank priority is shown in dark blue, high rank priority is shown in yellow. Cut-off of mapped extent is 2000 m depth.

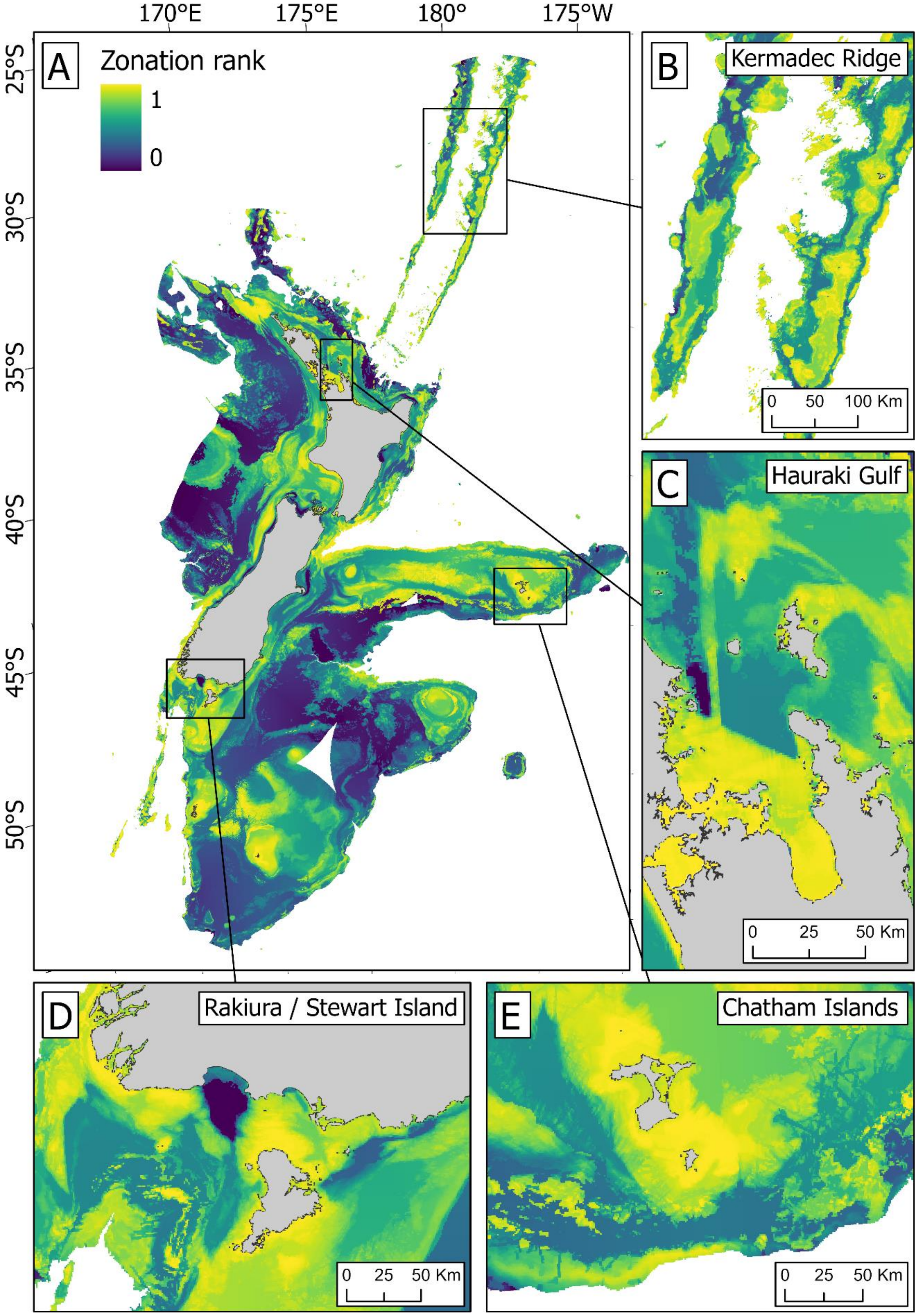

Figure B-32: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for sessile seafloor invertebrate taxa (37 genera). Condition (fishing impact layer) has been applied. Low rank priority is shown in dark blue, high rank priority is shown in yellow. Cut-off of mapped extent is 2000 m depth.

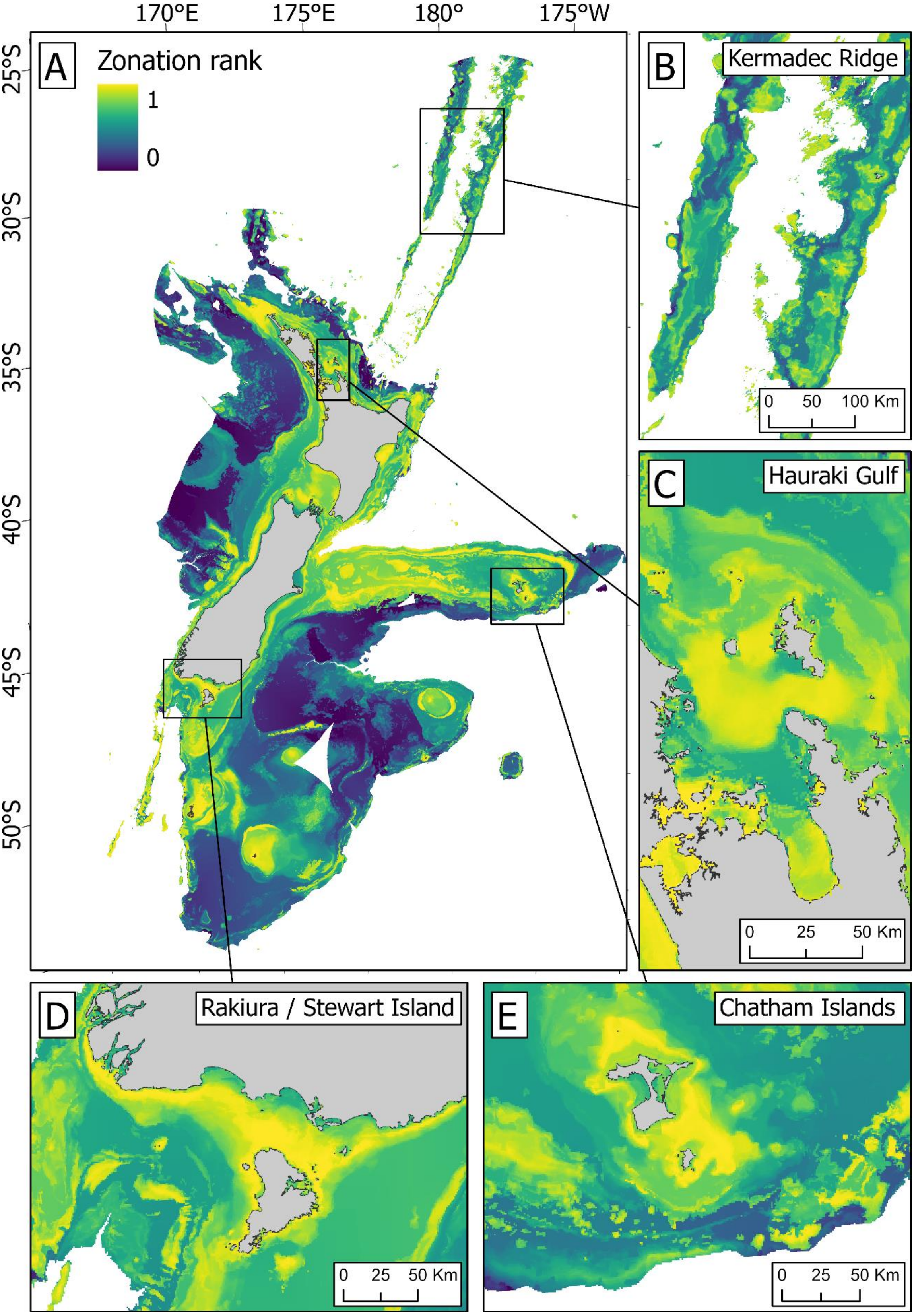

Figure B-33: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for sessile seafloor invertebrate taxa (37 genera). Condition (fishing impact layer) has not been applied. Low rank priority is shown in dark blue, high rank priority is shown in yellow. Cut-off of mapped extent is 2000 m depth.

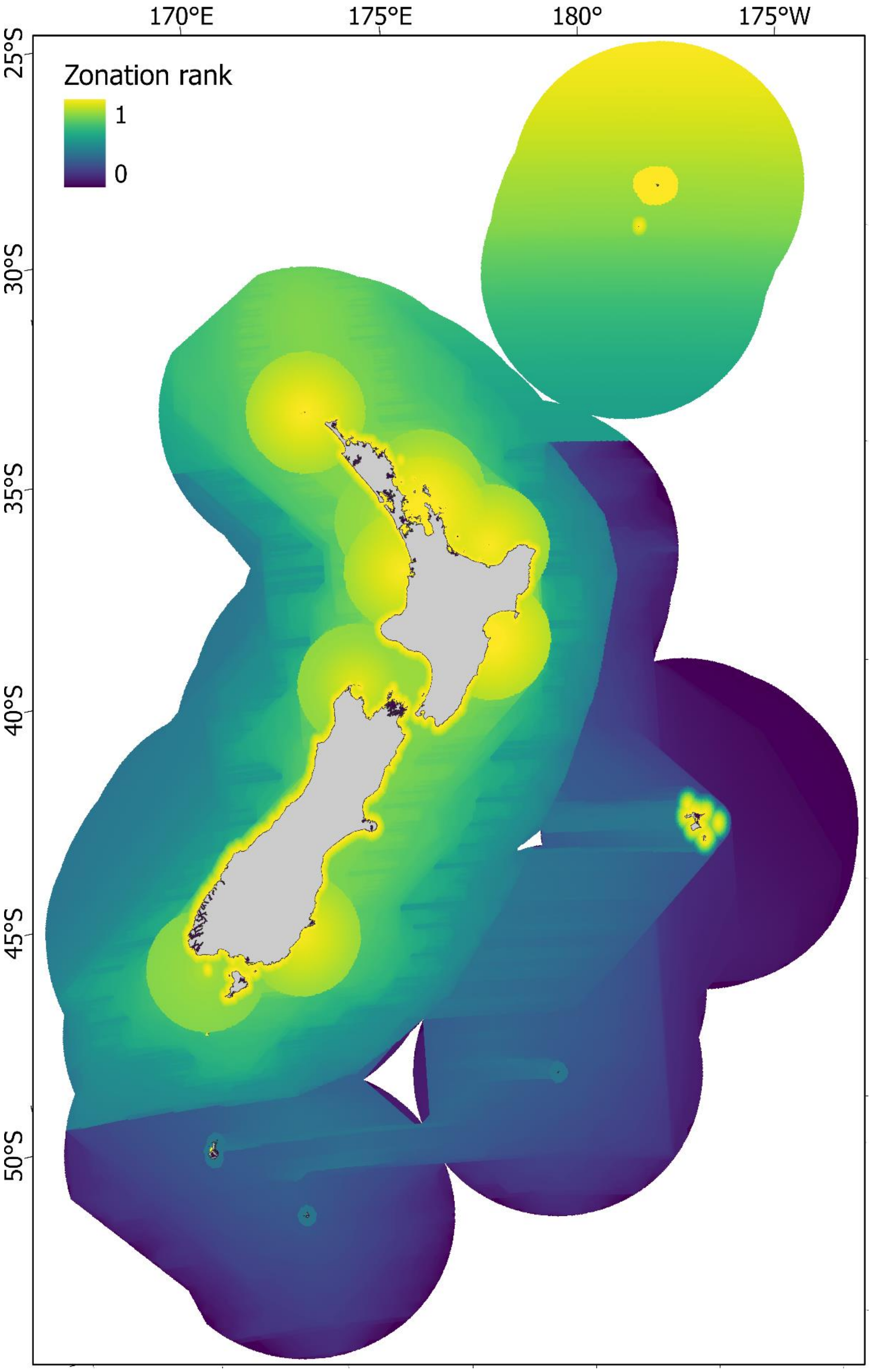

Figure B-34: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for other seabird taxa (5 genera), besides albatross, penguins, petrels, shags, and shearwaters. Low rank priority is shown in dark blue, high rank priority is shown in yellow.

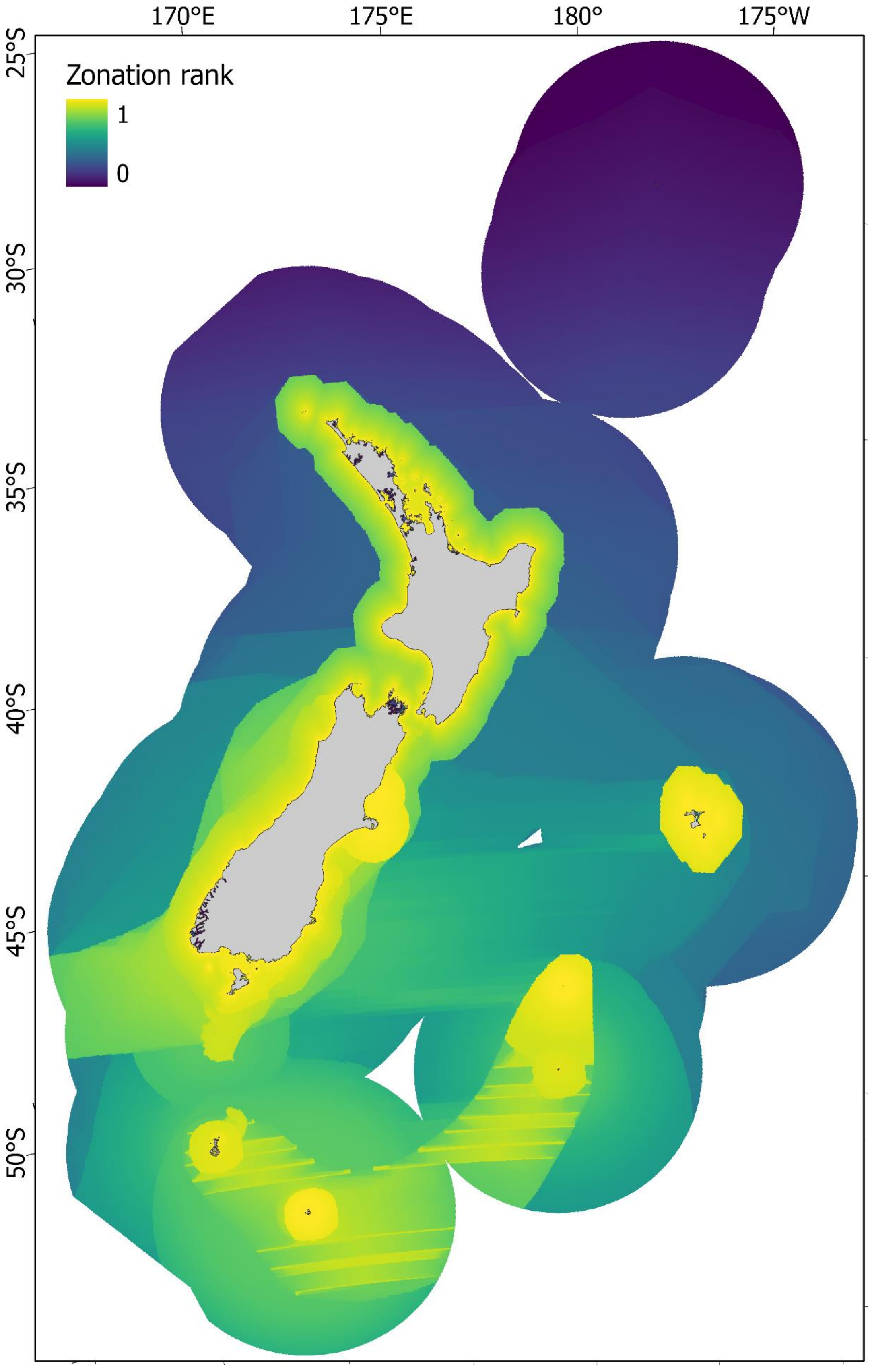

Figure B-35: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for penguin taxa (9 genera). Low rank priority is shown in dark blue, high rank priority is shown in yellow.

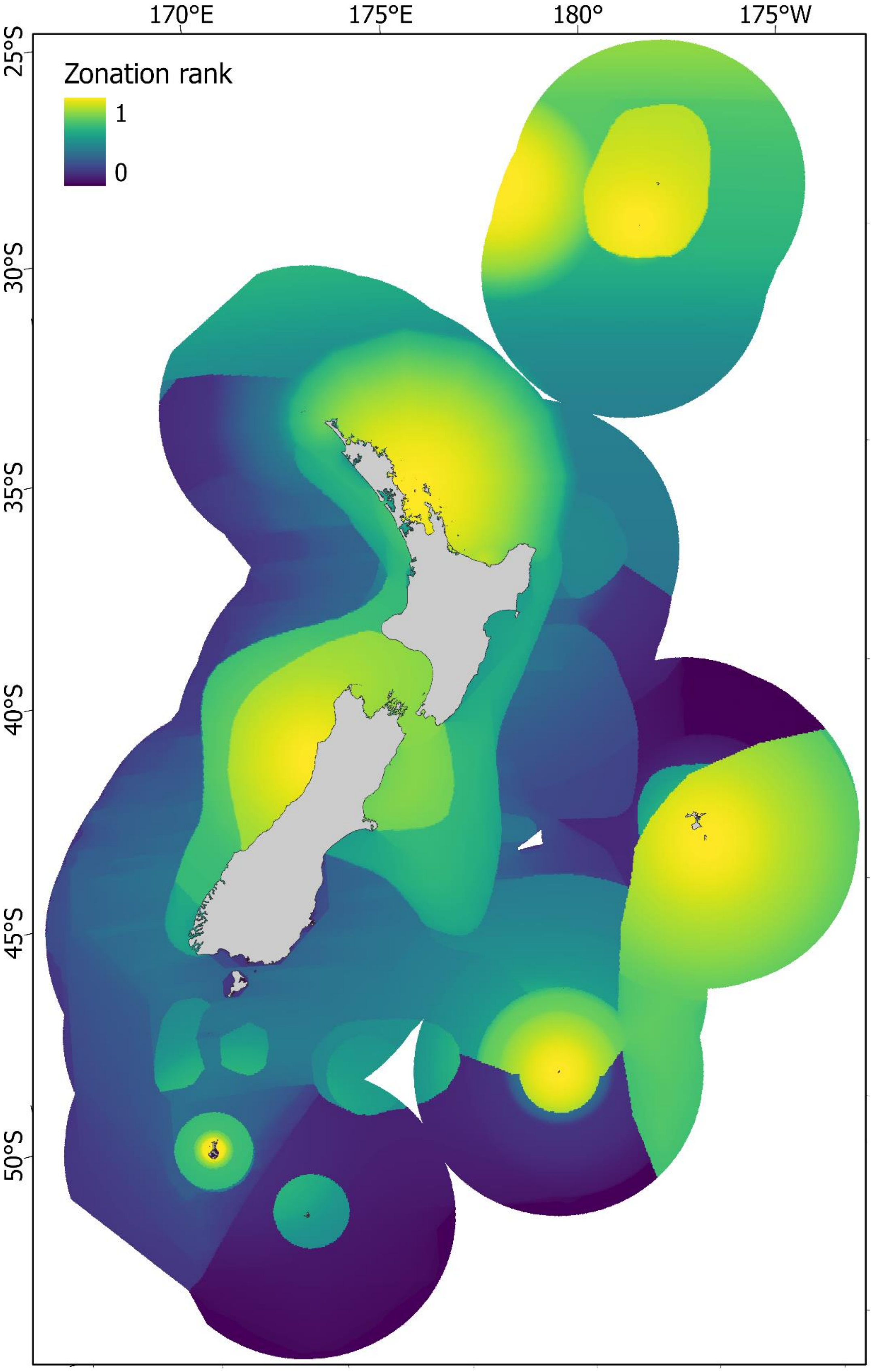

Figure B-36: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for petrel taxa (28 genera). Low rank priority is shown in dark blue, high rank priority is shown in yellow.

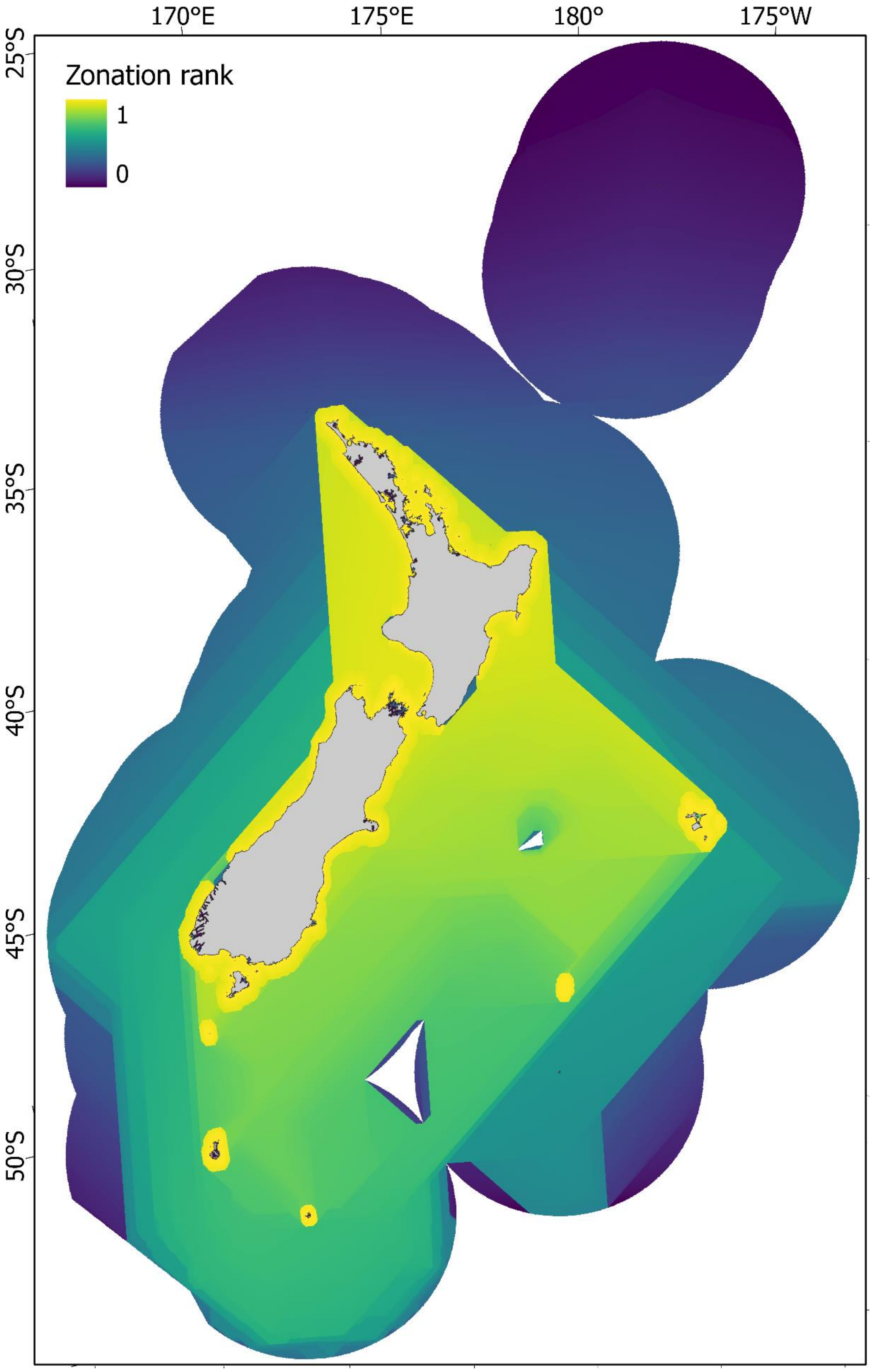

Figure B-37: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for shag taxa (11 genera). Low rank priority is shown in dark blue, high rank priority is shown in yellow.

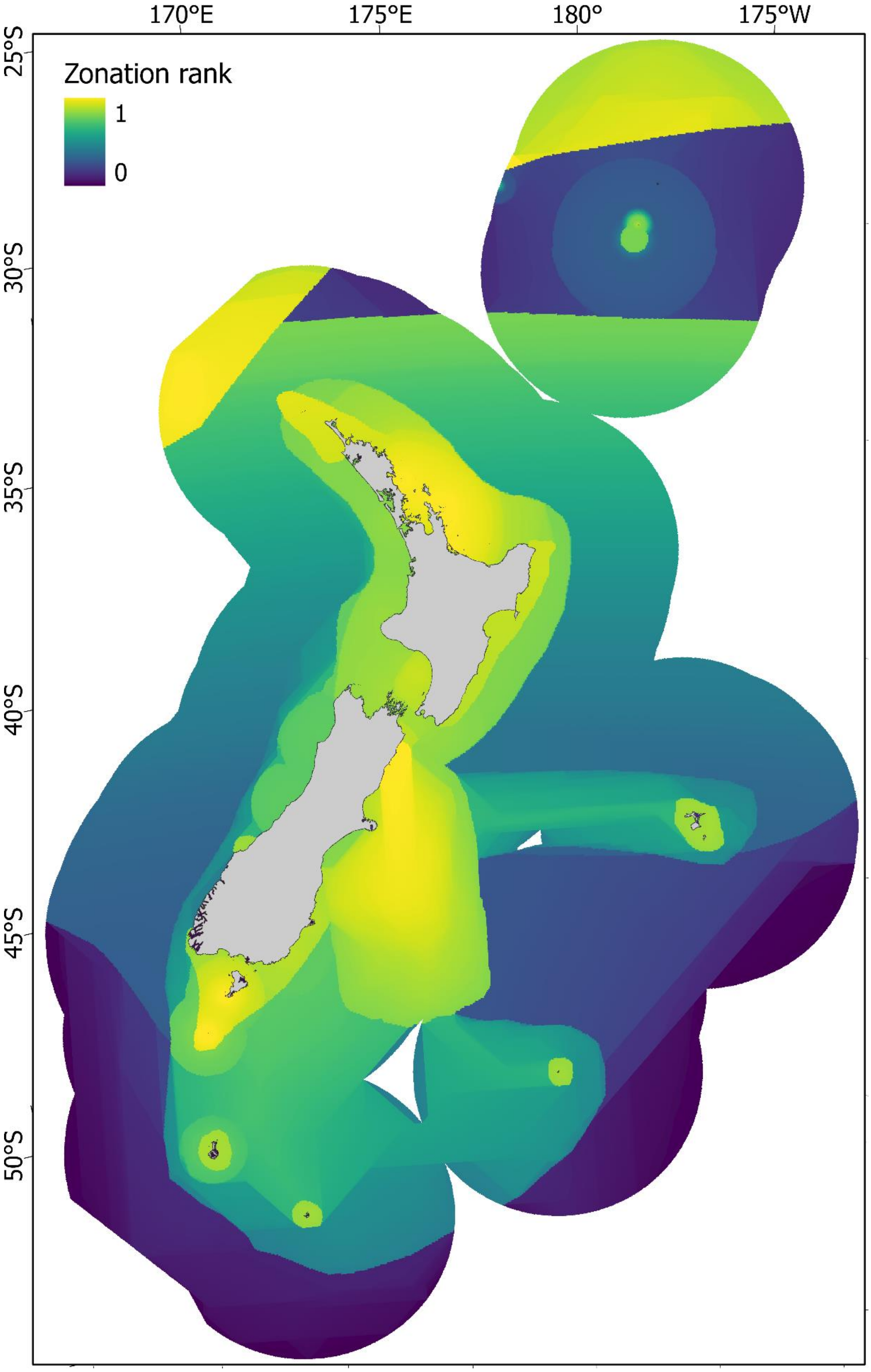

Figure B-38: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for shearwater taxa (8 genera). Low rank priority is shown in dark blue, high rank priority is shown in yellow.

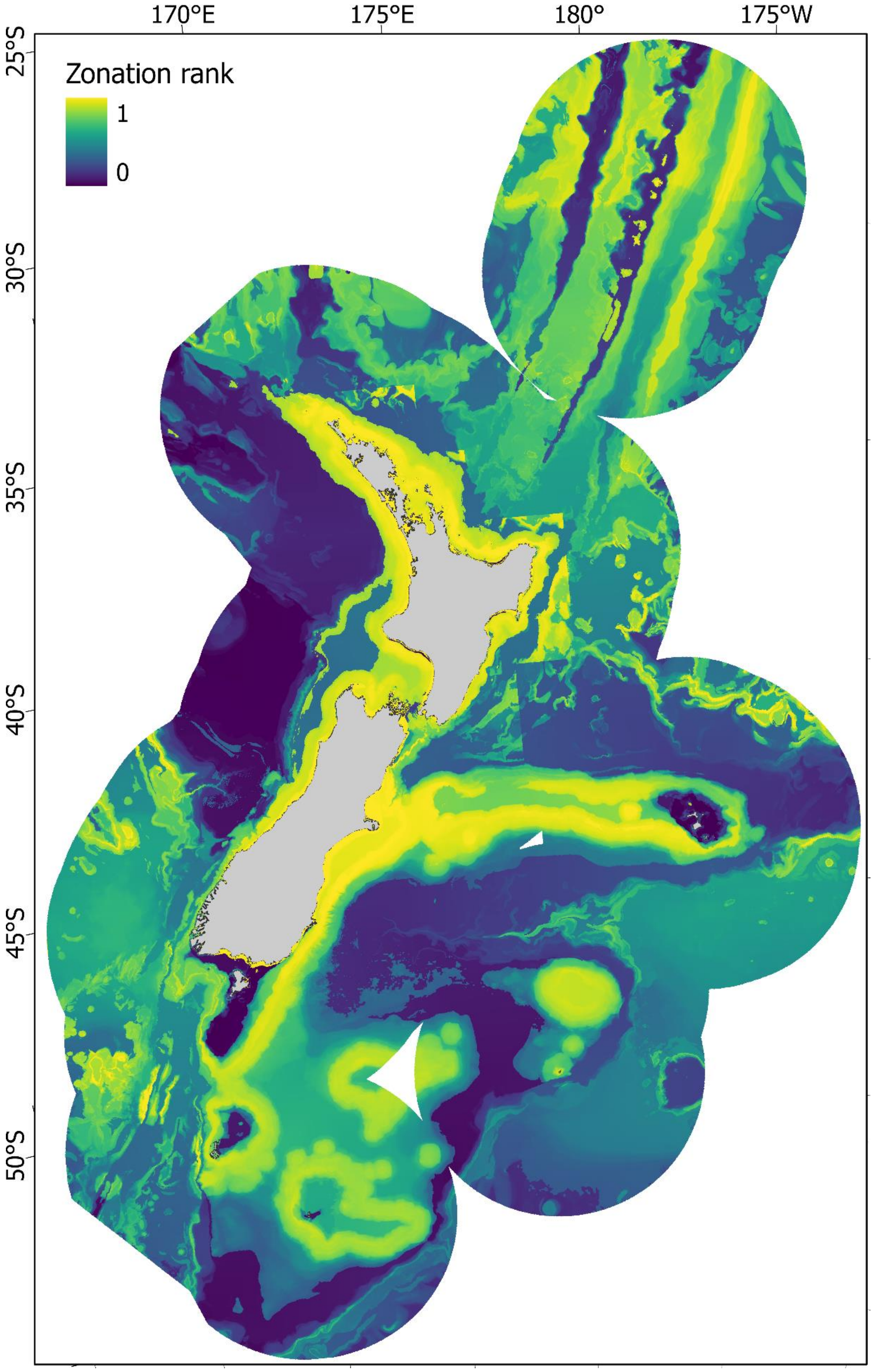

Figure B-39: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for delphinid taxa (7 genera). Low rank priority is shown in dark blue, high rank priority is shown in yellow. The artifact to the east and southeast of the North Island is attributed to the bottlenose dolphin modelled layer and is due to the underlying turbidity environmental layer, which was not available at the EEZ scale for modelling.

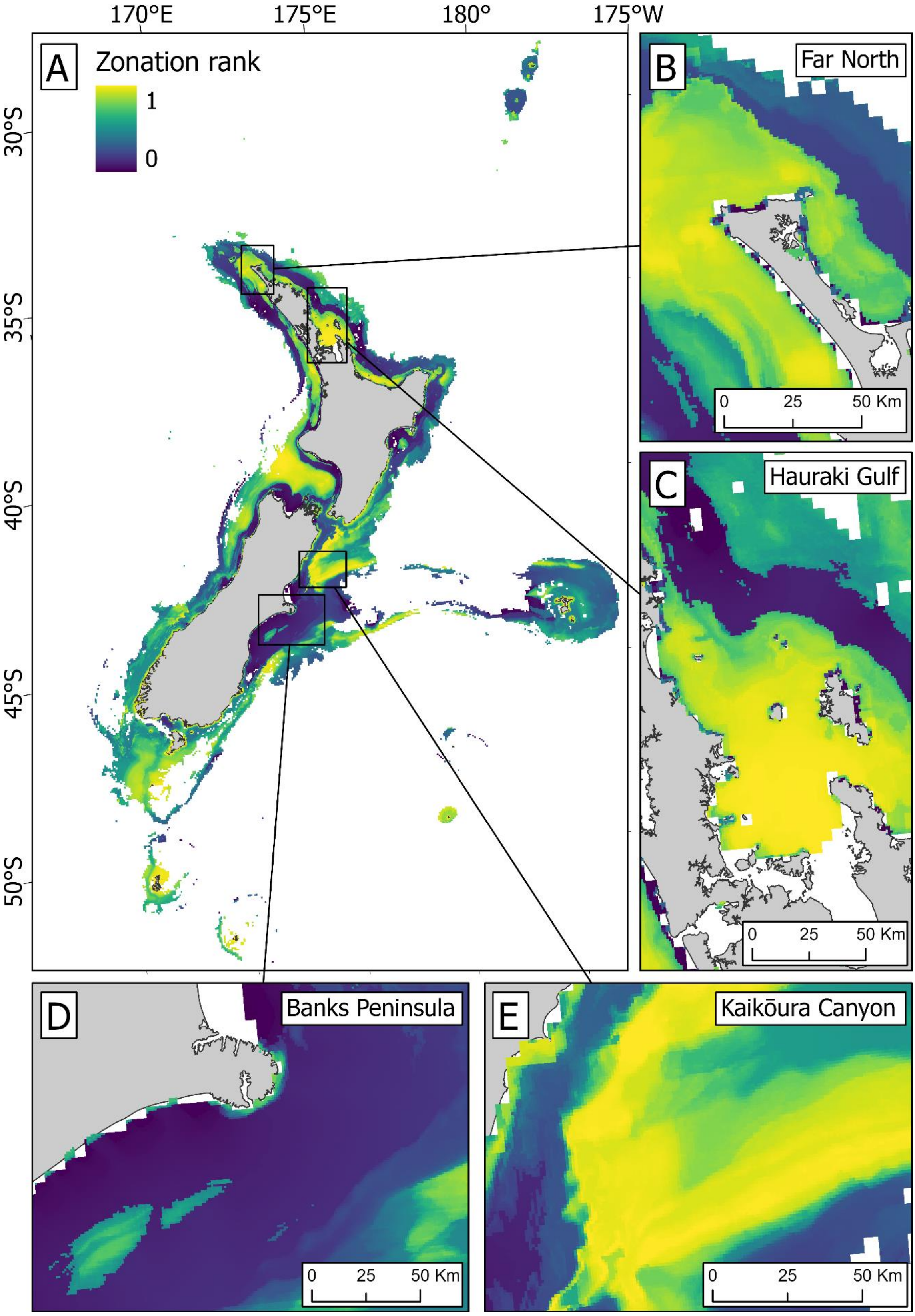

Figure B-40: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for whale taxa (5 genera), masked to the area of sufficient environmental coverage. Low rank priority is shown in dark blue, high rank priority is shown in yellow. Cut-off of mapped extent is areas with environmental coverage values <0.075.

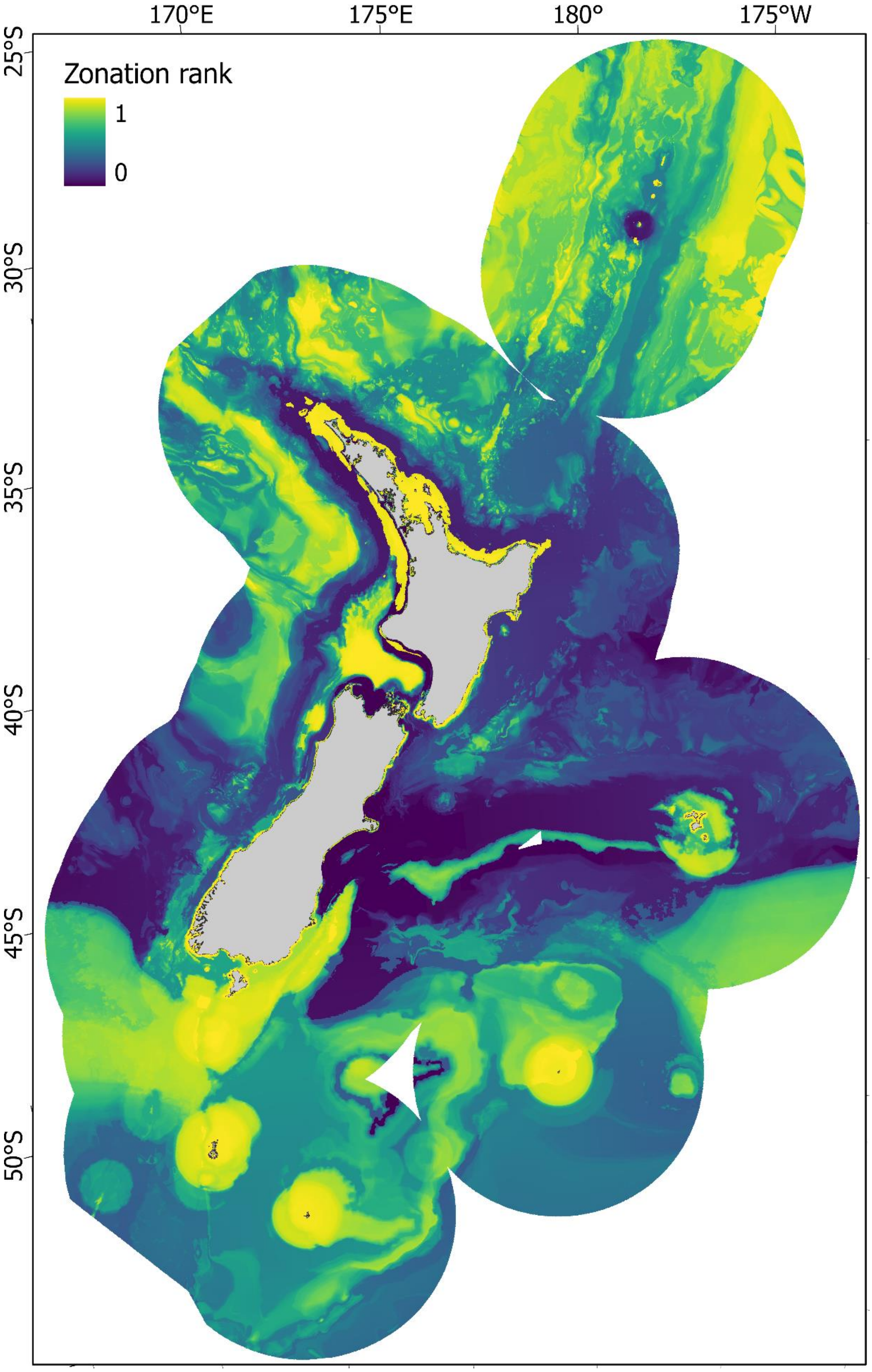

Figure B-41: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for whale taxa (5 genera). Low rank priority is shown in dark blue, high rank priority is shown in yellow.

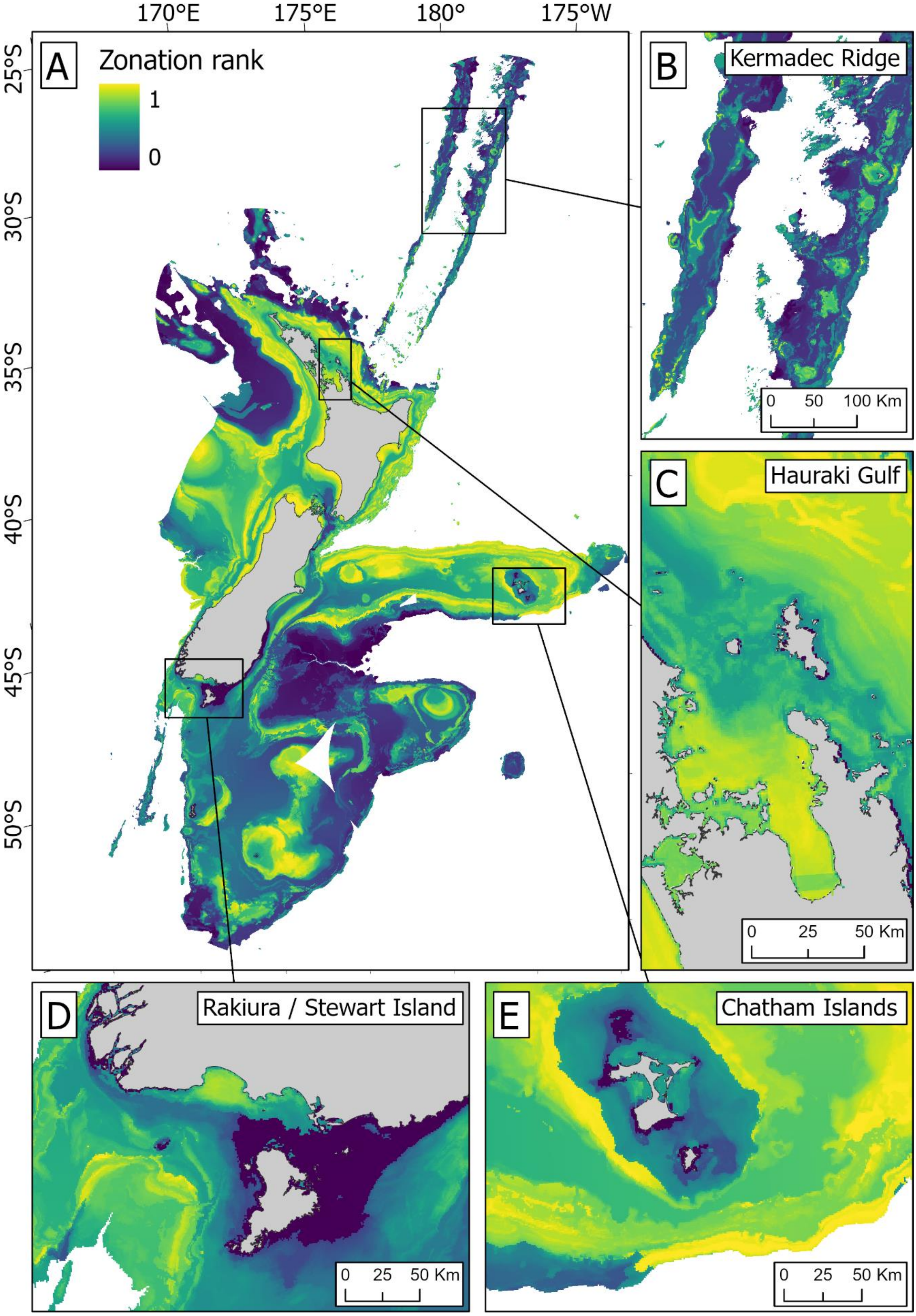

Figure B-42: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for bathyal-demersal fish taxa (82 genera). Low rank priority is shown in dark blue, high rank priority is shown in yellow. Cut-off of mapped extent is 2000 m depth.

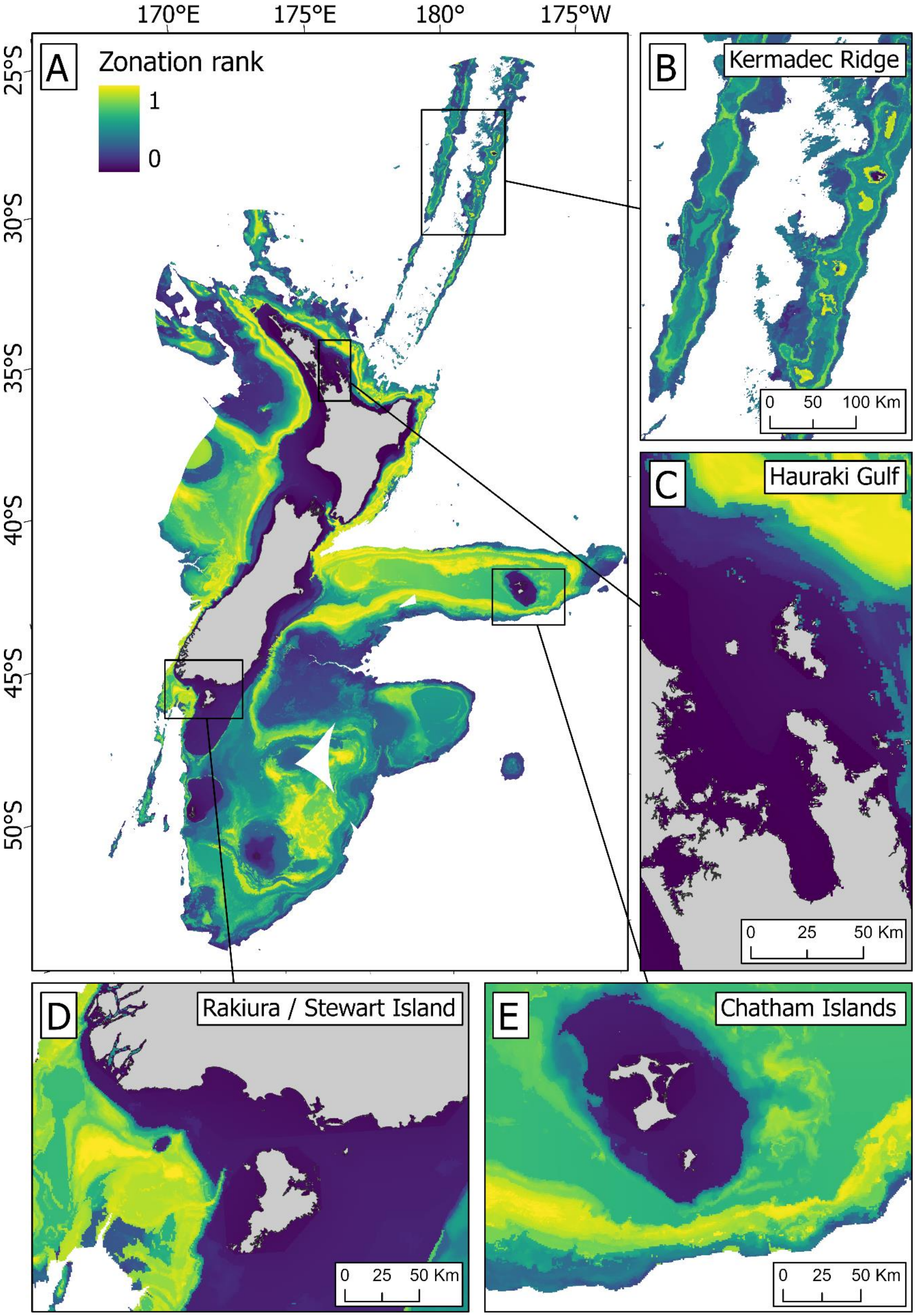

Figure B-43: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for bathyal-pelagic fish taxa (39 genera). Low rank priority is shown in dark blue, high rank priority is shown in yellow. Cut-off of mapped extent is 2000 m depth.

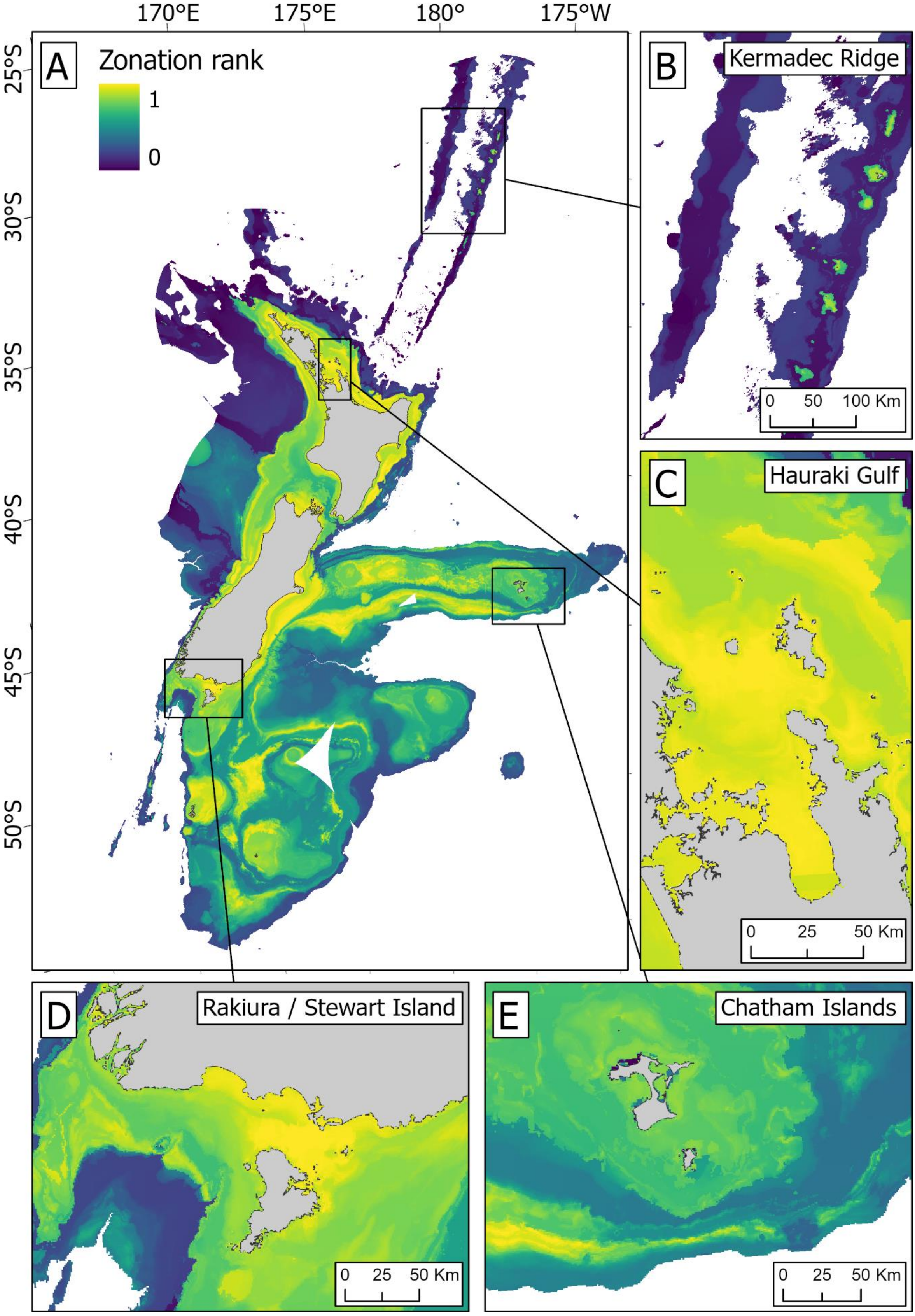

Figure B-44: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for benthic fish taxa (45 genera). Low rank priority is shown in dark blue, high rank priority is shown in yellow. Cut-off of mapped extent is 2000 m depth.

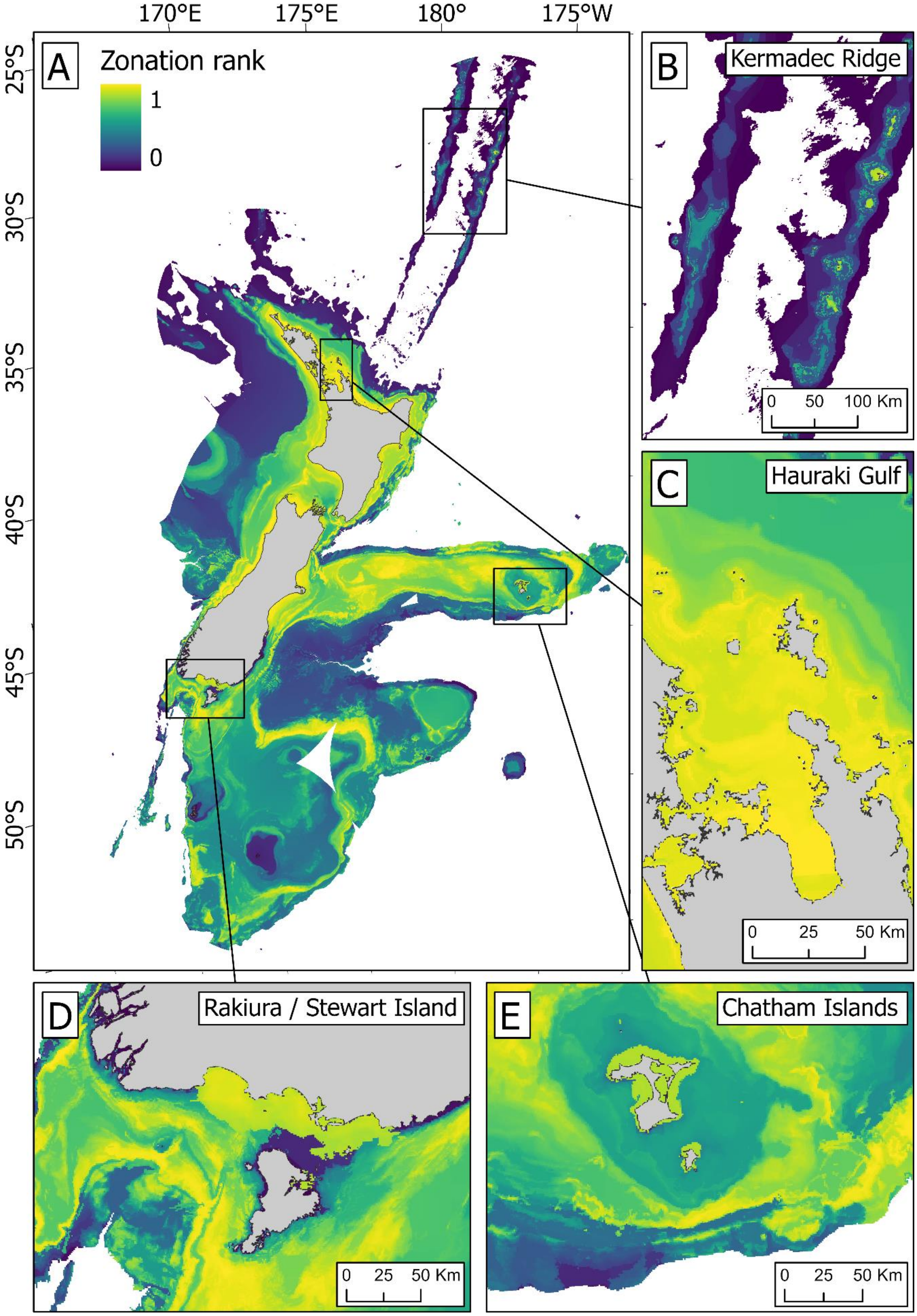

Figure B-45: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for pelagic fish taxa (22 genera). Low rank priority is shown in dark blue, high rank priority is shown in yellow. Cut-off of mapped extent is 2000 m depth.

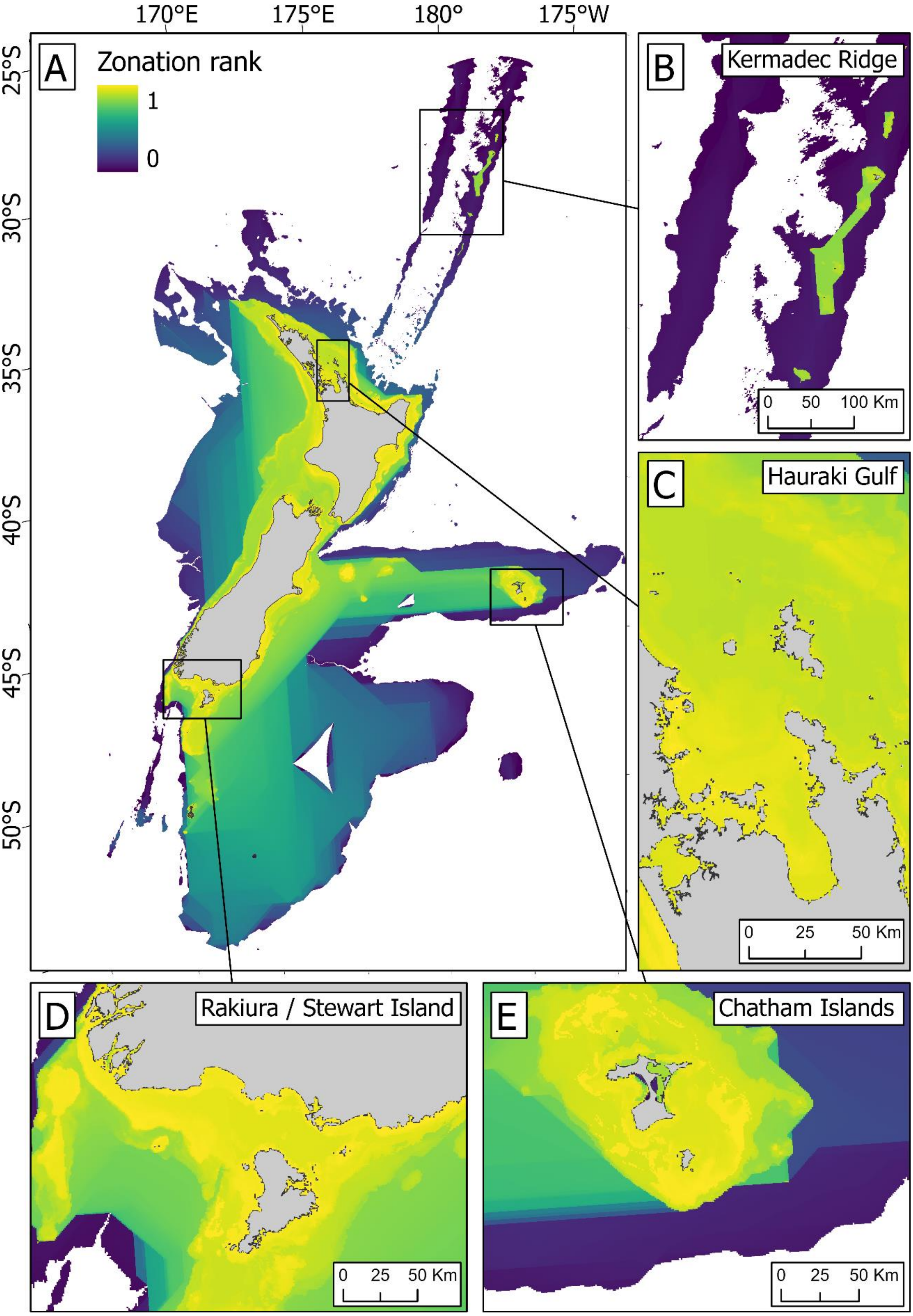

Figure B-46: Mapped biodiversity KEA criteria 6 based on the Zonation approach (rank prioritisation) for reef-associated fish taxa (7 genera). Low rank priority is shown in dark blue, high rank priority is shown in yellow. Cut-off of mapped extent is 2000 m depth.

Appendix C Qualitative map assessments

Table C-1: Evaluation score categories for the qualitative output biodiversity map evaluations conducted by the NIWA project team ecologists.

Evaluation score	Description
1 – Accurate	Biodiversity map reflects ecologist view of areas containing high and low marine biodiversity, but some areas may not be correct
2 – Somewhat accurate	Biodiversity map somewhat reflects ecologist view of areas containing high and low marine biodiversity, but there are considerable areas that are considered incorrect
3 – Largely inaccurate	Biodiversity map contains large inconsistencies with ecologist view of areas containing high and low marine biodiversity. Advise against using map for management

Table C-2: Qualitative scores assigned by NIWA ecologists to each biodiversity map (1- Accurate, 2- Somewhat accurate and 3- Largely inaccurate) (Table C-1), for high level taxa groups, and disaggregated groups across the stacked, Zonation and macroecological model approaches. Comments consider how biodiversity maps reflects known patterns of biodiversity whilst identifying areas of high and low map accuracy.

Approach	Biodiversity group (high level)	Disaggregated biodiversity group	Qualitative assessment	Comments – NIWA ecologists
Stacked approach	Macroalgae	All combined	2	Wellington bias, likely due to sampling bias. Chatham Islands are potentially overpredicted. Banks peninsular is low, probably correct. Otago coastline - shows up high to north, reasonable. Stewart Island, known hotspot.
	Macroalgae	Canopy forming	2	Picked up known high biodiversity areas in the Otago region. Wellington high bias still apparent, likely sampling effort bias.
	Macroalgae	Others	2	Generally ok, with significant Wellington sampling effort bias. Stewart Island showing high importance.

Approach	Biodiversity group (high level)	Disaggregated biodiversity group	Qualitative assessment	Comments – NIWA ecologists
	Seafloor Invertebrates	All combined	3	Strong bias towards Chatham Rise, hotspot is expected but inflated importance and makes it difficult to differentiate richness in other areas. Missing expected high richness areas around Kermadec Ridge and Hauraki Gulf, Fiordland, outer offshore islands around northeast coast (Aotea Great Barrier Island, Poor Knights), headlands along coast (Cape Brett, tip of Coromandel Peninsula). Identifies hotspots around the North Cape.
	Seafloor Invertebrates	All combined, no condition applied	3	Strong bias towards Chatham Rise, hotspot is expected but inflated importance and makes it difficult to differentiate richness in other areas. Missing expected high richness areas around Kermadec Ridge and Hauraki Gulf, Fiordland, outer offshore islands around northeast coast (Aotea Great Barrier Island, Poor Knights), headlands along coast (Cape Brett, tip of Coromandel Peninsula). Identifies hotspots around the North Cape.
	Seafloor Invertebrates	Key biogenic habitat formers	2	Inshore hotspots not identified and no differentiation across inshore areas. At the 200 m depth ridge line expected high richness areas are identified. Deepwater coral hotspots are also largely identified quite well, as well as high richness areas und seamounts and the Macquarie Ridge. Off the South coast, the outer edge of the slope is picked up well, but the continuation of richness along the slope around the Otago coast is potentially not accurate, and no expected high in The Foveaux Strait.
	Seafloor Invertebrates	Key biogenic habitat formers, no condition applied	2	Inshore hotspots not identified and no differentiation across inshore areas. At the 200 m depth ridge line expected high richness areas are identified. Deepwater coral hotspots are also largely identified quite well, as well as high richness areas und seamounts and the Macquarie Ridge. Off the South coast, the outer edge of the slope is picked up well, but the continuation of richness along the slope around the Otago coast is potentially not accurate, and no expected high in The Foveaux Strait.
	Seafloor Invertebrates	Mobile	3	Hotspots (and potentially overprediction) at Chatham Rise are potentially obscuring patterns elsewhere. Too heavily biased to the Chatham Rise.

Approach	Biodiversity group (high level)	Disaggregated biodiversity group	Qualitative assessment	Comments – NIWA ecologists
	Seafloor Invertebrates	Mobile, no condition applied	3	Hotspots (and potentially overprediction) at Chatham Rise are potentially obscuring patterns elsewhere. Too heavily biased to the Chatham Rise.
	Seafloor Invertebrates	Pelagic	2	The southern South Island shelf is picked up well, but high Subantarctic hotspots missing, and there should be more differentiation inshore. Squid hotspots are the Auckland and Campbell Islands shelves which are missing. Expected high areas on the Otago shelf are also missing. The Northern Chatham Rise is unlikely to be a hotspot for squid. Expected hotspots on the Kaikōura and Pegasus canyons are picked up quite well.
	Seafloor Invertebrates	Pelagic, no condition applied	2	The southern South Island shelf is picked up well, but high Subantarctic hotspots missing, and there should be more differentiation inshore. Squid hotspots are the Auckland and Campbell Islands shelves which are missing. Expected high areas on the Otago shelf are also missing. The Northern Chatham Rise is unlikely to be a hotspot for squid. Expected hotspots on the Kaikōura and Pegasus canyons are picked up quite well.
	Seafloor Invertebrates	Sessile	2	Hotspot around the Far North and East Cape are as expected. The Hauraki Gulf seems to be represented ok, and the South is generally ok except the Foveaux Strait is underrepresented.
	Seafloor Invertebrates	Sessile, no condition applied	2	Hotspot around the Far North and East Cape are as expected. The Hauraki Gulf seems to be represented ok, and the South is generally ok except the Foveaux Strait is underrepresented.
	Cetaceans	All combined	3	Lots that don't appear realistic, particularly model hotspots SE and SW, Kermadec Ridge where very few data points exist. Diversity quite skewed to pelagic waters rather than transitional waters where we would expect high diversity
	Cetaceans	All combined	2	Kaikōura and Pegasus canyon should be more important, eastern Chatham Rise shows and important hotspot and we don’t know if this is correct. In the big hotspot west of Stewart Island we would expect it to be good but high uncertainty.

Approach	Biodiversity group (high level)	Disaggregated biodiversity group	Qualitative assessment	Comments – NIWA ecologists
	Cetaceans	Dolphins - EEZ	3	Large offshore hotspots that are very uncertain, but generally ok in shallower areas as per clipped version.
	Cetaceans	Dolphins - clipped	2	Generally, aligns with areas of importance for these taxa. Hauraki Gulf - ok in representation, wider areas are probably where dolphins are found, then shelf break well picked out as well as the offshore islands Aotea Great Barrier, Hauturu. Far North - coastal margin as well as shelf break are showing up well. Three Kings also picked up, which is a known high diversity spot. Otago shelf break also picked up around the Otago Canyons. However, Kaikōura - picks up the shelf hotspots but misses the canyon, which is a key feeding spot, showcasing we don't have these features showing up in models. West of Stewart Island, possibly realistic, but lack of data records to confirm this.
	Cetaceans	Whales - EEZ	3	Lacking sufficient species to identify patterns.
	Cetaceans	Whales - clipped	3	Kaikōura for example, should be a dozen species there, but insufficient models to do this. Stewart Island region should not be higher than Kaikōura
	Demersal Fish	All combined	2	Generally good, important areas on shelf break, Chatham Rise highlighted. Differentiation within Chatham Rise. Inshore differentiation is not good, for example Hauraki Gulf and Hawke's Bay. Marlborough Sounds and Kaikōura noticeable low predicted diversity, likely due to fewer shallow species, with bias toward models of species found 200m and deeper.
	Demersal Fish	Bathyal-demersal	2	Predicting highest abundance on shelf break/slope, makes general sense. Very little background knowledge of the team on this group.
	Demersal Fish	Bathyal-pelagic	2	Likely ok, a bit more differentiation on shelf break/continental slope that might co-locate with variations in productivity. Very little background knowledge of the team on this group. Picks up low diversity area on shelf near subantarctic.

Approach	Biodiversity group (high level)	Disaggregated biodiversity group	Qualitative assessment	Comments – NIWA ecologists
	Demersal Fish	Benthic	2	Capturing more shelf species, but not showing expected higher diversity northern than southern. Good for Campbell Plateau, lower diversity. Foveaux Strait unexpectedly low, though it is picking up southland current/jet that might influence diversity from Stewart Island up to Otago. Lots of data in southern area to support models.
	Demersal Fish	Benthopelagic	3	Doesn't match known areas e.g., hoki, hake, ling - unclear where Chatham Rise features are coming from. Low expertise of project team on these groups.
	Demersal Fish	Pelagic	2	East coast North Island, believe generally ok. Possibly overexaggerates importance of west coast Northland.
	Demersal Fish	Reef	3	Poor inshore differentiation should be a gradient from north to south. Missing most reef species, as reef-clipped layers (e.g., triplefins) not included, only 2000m scale SDMs.
	Seabirds	All combined	3	Heavily biased toward breeding colonies and foraging distance. Missing known high diversity at sea foraging off Otago Coast, Chatham Rise, Foveaux Strait. Hauraki Gulf Islands probably ok, though would anticipate full gulf rather than solely adjacent to offshore islands. Expected hotspots around the Three Kings islands and Cook Strait missing.
	Seabirds	Albatrosses	2	Broadly represents important areas in the EEZ for albatross. Subantarctics, Otago, east coast South Island, but somewhat confined to island breeding colonies and not capturing true foraging range. North and Kermadec Ridge not important, captured correctly.
	Seabirds	Others	3	Includes Terns, Gannets and Boobies - Terns make sense, general coastal. Missing any coastal differentiation, e.g., Muriwai, Cape Kidnappers etc. of known hotspots.

Approach	Biodiversity group (high level)	Disaggregated biodiversity group	Qualitative assessment	Comments – NIWA ecologists
	Seabirds	Penguins	3	Subantarctic islands should be more important. Correct in picking up South Island as important. Should be pulling out Foveaux Strait, Stewart Island and Fiordland. Missing Fiords which should be important. West coast South Island poorly identified. Northern half of South Island suggest many high biodiversity areas that should not be there, very few hoiho e.g., on Banks Peninsula.
	Seabirds	Petrels	2	Picked up known Hauraki Gulf hotspot, high diversity most everywhere. Colony bias in information that is suggesting easterly is less important.
	Seabirds	Shags	1	Generally, the nearshore coastal areas are good. Hauraki Gulf should be hotspot. Might expect Northland/Bay of Islands also to be high. Top of the South important for shags and south of South Island.
	Seabirds	Shearwater	2	Generally ok, wide range of shearwaters on northwest coasts. However missing other high diversity areas in south especially around the Foveaux Strait. Picks up Hutton's shearwater habitat around Banks. Unclear why Lord Howe area to NW is getting picked up as well as north of Kermadec Ridge.
Zonation approach	Macroalgae	All combined	2	Wellington bias, likely due to sampling bias. Chatham Rise potentially overpredicted. Banks Peninsula is low which is probably correct. Otago area shows up high to north which is expected. Stewart Island is a known hotspot.
	Macroalgae	Canopy forming	1 or high 2	Wellington bias less noticeable in Zonation canopy formers. Exposed coastlines generally coming up higher than sheltered locations as expected. Generally, Zonation map a bit better than Stacked.
	Macroalgae	Others	2	Like canopy forming.
	Seafloor Invertebrates	All combined	2	Chatham Rise has nuanced hotspots. Expected high areas are identified around the Otago coast, Foveaux strait, Hauraki Gulf, Kermadec Ridge, Macquarie Ridge, North Cape and sea mounts. In general, the inshore areas look ok.

Approach	Biodiversity group (high level)	Disaggregated biodiversity group	Qualitative assessment	Comments – NIWA ecologists
	Seafloor Invertebrates	All combined, no condition applied	2	Chatham Rise has nuanced hotspots. Expected high areas are identified around the Otago coast, Foveaux strait, Hauraki Gulf, Kermadec Ridge, Macquarie Ridge, North Cape, and sea mounts. In general, the inshore areas look ok.
	Seafloor Invertebrates	Key biogenic habitat formers	2	Expected high areas identified around the Hauraki Gulf, North Cape hotspots identified well, (but with the really inshore areas missing), Foveaux Strait and Otago inshore. High areas on the Chatham rise are identified quite well.
	Seafloor Invertebrates	Key biogenic habitat formers, no condition applied	2	Expected high areas identified around the Hauraki Gulf, North Cape hotspots identified well, (but with the really inshore areas missing), Foveaux Strait and Otago inshore. High areas on the Chatham rise are identified quite well.
	Seafloor Invertebrates	Mobile	2	Potentially too high in the inner-Hauraki Gulf, looks ok elsewhere
	Seafloor Invertebrates	Mobile, no condition applied	2	Potentially too high in the inner-Hauraki Gulf, looks ok elsewhere
	Seafloor Invertebrates	Pelagic	2	Expected inshore areas high areas are picked up in the Far North, Kaikōura area, west coast of the South Island and Tasman Golden Bay. Potentially too high in the Hauraki Gulf and expected high areas around the Auckland and Campbell Islands shelves are missing.
	Seafloor Invertebrates	Pelagic, no condition applied	2	Expected inshore areas high areas are picked up in the Far North, Kaikōura area, west coast of the South Island and Tasman Golden Bay. Potentially too high in the Hauraki Gulf and expected high areas around the Auckland and Campbell Islands shelves are missing.
	Seafloor Invertebrates	Sessile	2	Far North and East Cape hotspots seem realistic. Hotspots in the Hauraki Gulf and Hawkes Bay are likely overrepresenting (inshore areas too high), Foveaux Strait maybe underrepresented, but the rest of the South seems ok.
	Seafloor Invertebrates	Sessile, no condition applied	2	Far North and East Cape hotspots seem realistic. Hotspots in the Hauraki Gulf and Hawkes Bay are likely overrepresenting (inshore areas too high), Foveaux Strait maybe underrepresented, but the rest of the South seems ok.

Approach	Biodiversity group (high level)	Disaggregated biodiversity group	Qualitative assessment	Comments – NIWA ecologists
	Cetaceans	All combined - EEZ	2	A lot of expected offshore areas removed in Zonation where there is high model uncertainty. Suggests mostly the shelf system is important, so again missing transitional zones with high diversity. E Coast South Island suggests whole of shelf important but should be a margin around the coastal shelf break where both coastal and offshore species are found in this transitional zone. In the coastal zone, it does not distinguish known hotspots such as the Hauraki Gulf and Northland, rather suggests all inshore is important. A bit better than stacked approach.
	Cetaceans	All combined - clipped	2	At a fine scale at Kaikōura it identifies less diverse areas (e.g. canyon area) which are known are actually highly diverse, east coast South Island is high, but likely a bias as Hector's dolphin is the only species there. Hauraki Gulf ok, Northland high inshore but really diversity is around the shelf break.
	Cetaceans	Dolphins - EEZ	3	EEZ East coast South Island - pulling out inshore margin when only one species there. Similar in Kaikōura. Shallow waters picked out, but missing canyons in prioritisation, Pegasus Canyon for example should be high priority, missing a lot of this fine scale detail.
	Cetaceans	Dolphins - clipped	2	No differentiation among shelf, not identifying transition zones, or high productivity canyon zones of known high diversity. South Taranaki bight also not showing up
	Cetaceans	Whales - EEZ	3	Lack of differentiation on the shelf, similar to others where inshore shown as important, but not showing the transition zones at the shelf break. Hauraki Gulf should stand out. Kaikōura and Pegasus Canyon noticeably missing here. Otago ok, but not distinguishing known features and canyon systems, subtropical front.
	Cetaceans	Whales - clipped	2	Identifies main areas of high biodiversity we know about including the Hauraki Gulf, South Taranaki Bight, offshore Canterbury canyon systems and general Northland coast. West coast of Northland the offshore areas appear unimportant, which does not match high level of strandings recorded in this area.

Approach	Biodiversity group (high level)	Disaggregated biodiversity group	Qualitative assessment	Comments – NIWA ecologists
	Demersal Fish	All combined	2	Mixed compared to stacked, putting higher emphasis on southern Chatham Rise rather than northern. A bit more inshore differentiation than stacked. Otago/South - nearshore suggested is more important than shelf break/transitional zones.
	Demersal Fish	Bathyal-demersal	2	Predicting highest abundance on the shelf break/slope which makes general sense. Very little background knowledge of the team on this group. Unexpectedly high in inshore Hauraki Gulf (<200 m deep).
	Demersal Fish	Bathyal-pelagic	2	Likely ok, a bit more differentiation on shelf break/continental slope that might co-locate with variations in productivity. Very little background knowledge of the team on this group. Picks up expected low diversity area on shelf near subantarctic.
	Demersal Fish	Benthic	2	Capturing more shelf species, but not showing expected higher diversity in the north compared to south. Not as good as the stacked approach for Campbell Plateau. Foveaux Strait high and picking up current from Steward Island up the Otago coast that is likely to influence diversity. Lots of data in southern area to support models.
	Demersal Fish	Benthopelagic	3	Doesn't match known areas e.g., hoki, hake, ling - unclear where Chatham Rise features are coming from. Low expertise of project team on these groups.
	Demersal Fish	Pelagic	2	Zonation output looks a bit better than the stacked approach. High diversity areas associated with known areas of pelagic productivity on the northeast coast. No midwater trawls off Otago coast, so possibly under-reported as low diversity.
	Demersal Fish	Reef	3	Poor inshore differentiation should be a decreasing richness gradient from north to south. Missing most reef species, as reef-clipped layers (e.g., triplefins) not included, only 2000m scale SDMs.

Approach	Biodiversity group (high level)	Disaggregated biodiversity group	Qualitative assessment	Comments – NIWA ecologists
	Seabirds	All combined	3	Heavily biased toward breeding colonies and foraging distance. Missing known high diversity at sea foraging, should not just be constrained to shelf. Otago coast and other areas not differentiated, though Hauraki Gulf as a whole is highlighted.
	Seabirds	Albatrosses	2	Broadly represents important areas in the EEZ for albatross. Subantarctics, Otago, east coast South Island, but somewhat confined to island breeding colonies and not capturing true foraging range. North and Kermadec Ridge not important, captured correctly.
	Seabirds	Others	3	Generally, not good, lumping together species with quite different habitats, and are not important in Aotearoa New Zealand like Pacific white term and booby.
	Seabirds	Penguins	3	Worse than stacked penguin diversity. Picking up all coastal areas including North Island.
	Seabirds	Petrels	2	Hauraki Gulf well represented. West coast of South Island also good, noting however that inputted shape layers result in strange patterns. Generally ok.
	Seabirds	Shags	3	Some identification of shallow areas on South Island, but generally overpredicting into deeper areas.
	Seabirds	Shearwater	2	Generally similar to Stacked output but does a better of picking up south of Stewart Island. Wide range of shearwaters on northwest coasts. However missing other high diversity areas in south/ Foveaux Strait. Picks up Hutton's shearwater habitat around Banks. Unclear why Lord Howe area to NW is getting picked up as well as north of Kermadec Ridge.
MEM approach	Benthic Inverts	All combined	1	Highlights areas of known high richness - Northland coast, Otago coast, Foveaux Strait and canyon systems, seamounts and ridges. Areas of lower richness also seem accurate (e.g., challenger plateau). Very high richness of Campbell and Bounty Island shelves may be overprediction but accounted for by uncertainty. Score also based on cross-validation with observed richness.