



# Application of KEA Criteria at National and Regional level: a Proof-of-Concept

*Prepared for Department of Conservation*

*September 2022*

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NIWA CLIENT REPORT No: 2022276HN  
Report date: September 2022  
NIWA Project: DOC22212

Quality Assurance Statement		
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	Approved for release by:	Michael Bruce

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## Executive summary

Research and management organisations create, collect, and manage various types of marine geospatial data with singular and sometimes differing outcomes or goals in mind (e.g., environmental, scientific, economic, or commercial). Often, data is lost or not used to its fullest potential following the completion of a certain set of goals. Key challenges are in the creation of ‘silos’ of data, where datasets are not easily accessible and not readily available on-request. These silos or lost data can increase costs of tasks downstream, limit collaboration across projects and institutions, and reduce transparency, all of which can foster mistrust among mana whenua, stakeholders, and the wider public. Recognising this disconnect, the Department of Internal Affairs (DIA) is funding the Enabling Integrated Marine Management initiative under the Digital Government Partnership Innovation Fund (DGPIF).

As part of the Enabling Integrated Marine Management initiative, Toitū Te Whenua - Land Information New Zealand (LINZ), Manatū Ahu Matua - Ministry of Primary Industries (MPI), Te Papa Atawhai - Department of Conservation (DOC), and Te Arawhiti each developed a use case to test the feasibility of a cloud-based data-sharing technology (i.e., a data mesh) to increase data sharing across institutions and to reduce the ‘silo’ effect. The Datamesh, developed by Oceanum Limited, provides a means to discover and interrogate spatial data stored on various online platforms and systems from a single port-of-call. The DOC use case aimed to demonstrate the feasibility of the Datamesh to source spatial marine biodiversity data from a variety of data-portals. As an output of the DOC use case, a web-based prototype application (hereafter referred to as the ‘KEA App’) was developed to showcase the strengths of a cloud-based data mesh for sharing standardised marine spatial data and performing targeted analyses.

DOC is required under the Conservation Act 1987 to conserve Aotearoa New Zealand’s biodiversity. To aid with this, a Key Ecological Area (KEA) framework has been proposed as a methodology to identify important areas for marine biodiversity. The KEA framework defines nine criteria under which a KEA could be proposed. These 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 productivity, 6) Biological diversity, 7) Naturalness, 8) Ecological function, and 9) Ecosystem services.

As proof-of-concept for the DOC use case, practical KEA boundaries were delineated using data sourced from the Datamesh and a prototype web-based application (‘the KEA App’) was developed. Habitat suitability index (HSI) models, located on the DOC Marine Data Portal, and fish spawning areas, located on the MPI Open Data Portal, were sourced via the Datamesh and a standardised approach to delineate KEA criteria 1, 3, and 6 was tested at national and regional scales. The aims of this project were to: 1) test the Datamesh platform, 2) develop preliminary standardised approaches to KEA delineation, 3) explore the impact of threshold selection on KEA boundary delineation, and 4) consider the implications of KEA delineation at national and regional scales.

The DOC use case provided a robust test of the Datamesh and its capacity for development of applications (‘Apps’) to standardise and automate targeted analyses, such as the delineation of KEAs. Key strengths and limitations of the Datamesh, in its current form, identified by our team during this work are discussed. Delineation of KEAs at national and regional scales, under a variety of thresholds, showcased the complexity and limitations of a standardised national approach to KEA delineation. Recommendations from our team for further development of the Datamesh and the KEA App to support a standardised approach to KEA delineation are provided to inform the proof-of-concept.

# 1 Introduction

## 1.1 Background

Marine ecosystems have been degraded due to anthropogenic stressors including pollution, overfishing, sedimentation, and climate change (Halpern et al. 2008). As a result, these habitats need to be protected or restored to conserve biodiversity and delivery of ecosystem services. Te Papa Atawhai Department of Conservation (DOC) is required under the Conservation Act 1987 to conserve the biodiversity of Aotearoa New Zealand, in both marine and terrestrial realms. To help guide DOC work programmes, in 2020 DOC released the Climate Change Adaptation Action Plan<sup>1</sup> and Te Mana o Te Taiao - the Aotearoa New Zealand Biodiversity Strategy<sup>2</sup>.

One tool for achieving DOC's goals under the Conservation Act 1987 is implementation of Marine Protected Areas (MPAs). With good design and effective enforcement of no-take areas, MPAs have been shown to be successful in protecting marine habitats and biodiversity (Edgar et al. 2014, Halpern 2014). The first step in designing a network of MPAs is to identify areas that maximize biodiversity returns, so that we can prioritise establishment of MPAs in line with biodiversity value.

In Aotearoa New Zealand, the Key Ecological Areas (KEA) framework is being developed to delineate areas that have high conservation value. High value is determined with reference to nine KEA criteria: 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). These criteria were adapted from the Convention on Biological Diversity's (CBD) "Ecologically and Biologically Significant Areas"<sup>3</sup> (Clark et al. 2014).

The delineation of KEAs requires the application of thresholds to identify areas that best represent KEA criteria, however, these have not yet been fully developed and agreed for the KEA criteria. The IUCN's (International Union for Conservation of Nature) Key Biological Area (KBA) framework (IUCN 2016) includes criteria with considerable overlap with the KEA criteria and associated thresholds that could be adapted to illustrate the delineation of KEAs in Aotearoa New Zealand. KBAs are sites that contribute significantly to global persistence of different aspects of biodiversity - importantly the thresholds used to delineate globally important sites can be downscaled and used at a national scale.

The Aotearoa New Zealand government holds many datasets that can be used to inform the delineation of KEAs, with > 600 modelled habitat suitability layers for cetaceans, fish, invertebrates, seabirds, and macroalgae. There are also polygon and point data for biogenic habitats, habitat distributions, and species ranges (Lundquist et al. 2020b). These datasets will form the foundation for identifying and delineating KEAs.

## 1.2 Project context

Organisations collect, manage, and produce various types of marine geospatial data, often with a specific goal in mind. Institutional silos of data are frequently inaccessible to outside users, or not easily shared to enable informed decision-making. Further, a lack of transparency around data

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<sup>1</sup> <https://www.doc.govt.nz/our-work/climate-change-and-conservation/adapting-to-climate-change/>

<sup>2</sup> <https://www.doc.govt.nz/nature/biodiversity/aotearoa-new-zealand-biodiversity-strategy/>

<sup>3</sup> <https://www.cbd.int/ebsa/about>

ownership can lead to mistrust between stakeholders and iwi partners. Recognising the disconnect between data production, data management, and sharing, the Department of Internal Affairs (DIA) has granted funding from the Digital Government Partnership Innovation Fund (DGPIF) to Toitū Te Whenua Land Information New Zealand (LINZ), Manatū Ahu Matua - Ministry of Primary Industries (MPI), Te Papa Atawhai - Department of Conservation (DOC), and Te Arawhiti to undertake its Enabling Integrated Marine Management initiative via a 'proof-of-concept'. This initiative involves testing the feasibility of a cloud-based data mesh to enable better integration and transparency of marine spatial data in Aotearoa New Zealand. It is hoped that a data mesh will improve access, discovery, reuse, and integration of marine spatial datasets from a variety of sources (held in various portals and platforms). Under the initiative, a proof-of-concept will be delivered that tests the feasibility and performance of a cloud-based platform, which has been developed by Oceanum Limited (the Datamesh). As part of this overarching proof-of-concept, the four partner agencies each developed a specific use case to test the performance and benefits of the Datamesh (while also acknowledging the risks and benefits) to inform a further business case. The DOC's use case related to marine and coastal planning - specifically, mapping marine Key Ecological Areas (KEAs).

### 1.3 Aims and objectives

Previous DOC contracts to NIWA have assembled datasets that could be used to inform the boundaries of KEAs (Stephenson et al. 2018, Lundquist et al. 2020a, Lundquist et al. 2020b). More recently, NIWA evaluated the potential to apply thresholds from the IUCN Key Biological Area framework to KEA databases to delineate Key Ecological Areas in Aotearoa New Zealand's marine environment (DOC contract #BIO-205, Stewart-Sinclair and Lundquist 2022). As part of that contract, a case study (using data for protected deepwater coral taxa) was used to work through the process of identifying and delineating KEAs under criteria 2 (Uniqueness / Rarity / Endemism) and 4 (Importance for Threatened / Declining Species and Habitats).

Here, NIWA was contracted by DOC to build upon these prior contracts and develop comprehensive examples of the KEA delineation process with a concurrent aim to test the Datamesh. The outputs of this contract formed part of DOC's use case, and included testing the methodology for the delineation of practical KEA boundaries using previously identified datasets (Lundquist et al. 2020b), from multiple online sources (MPI and DOC) that could be linked into the Datamesh. The practicalities and benefits of a data mesh were investigated by:

1. exploring the graphical user interface of the Datamesh,
2. searching for and downloading data from multiple sources,
3. testing an application that sources datasets through to the Datamesh to delineate KEA boundaries, and
4. illustrating the practicalities of the Datamesh for achieving KEA delineation to feed into the proof-of-concept project.

This project aims to align with outcomes from Te Mana o Te Taiao - the Aotearoa New Zealand Biodiversity Strategy, including: Goal 10.4.1 "Significant progress has been made in identifying, mapping and protecting coastal ecosystems and identifying and mapping marine ecosystems of high biodiversity value", Goal 4.2 "National, agreed common data standards and open data agreements are ensuring everyone has access to a federated repository of biodiversity information", and Goal 4.3 "A framework for identifying and prioritising high biodiversity value areas has been developed and agreed on".

## 2 Methods for delineating KEA criteria and thresholds

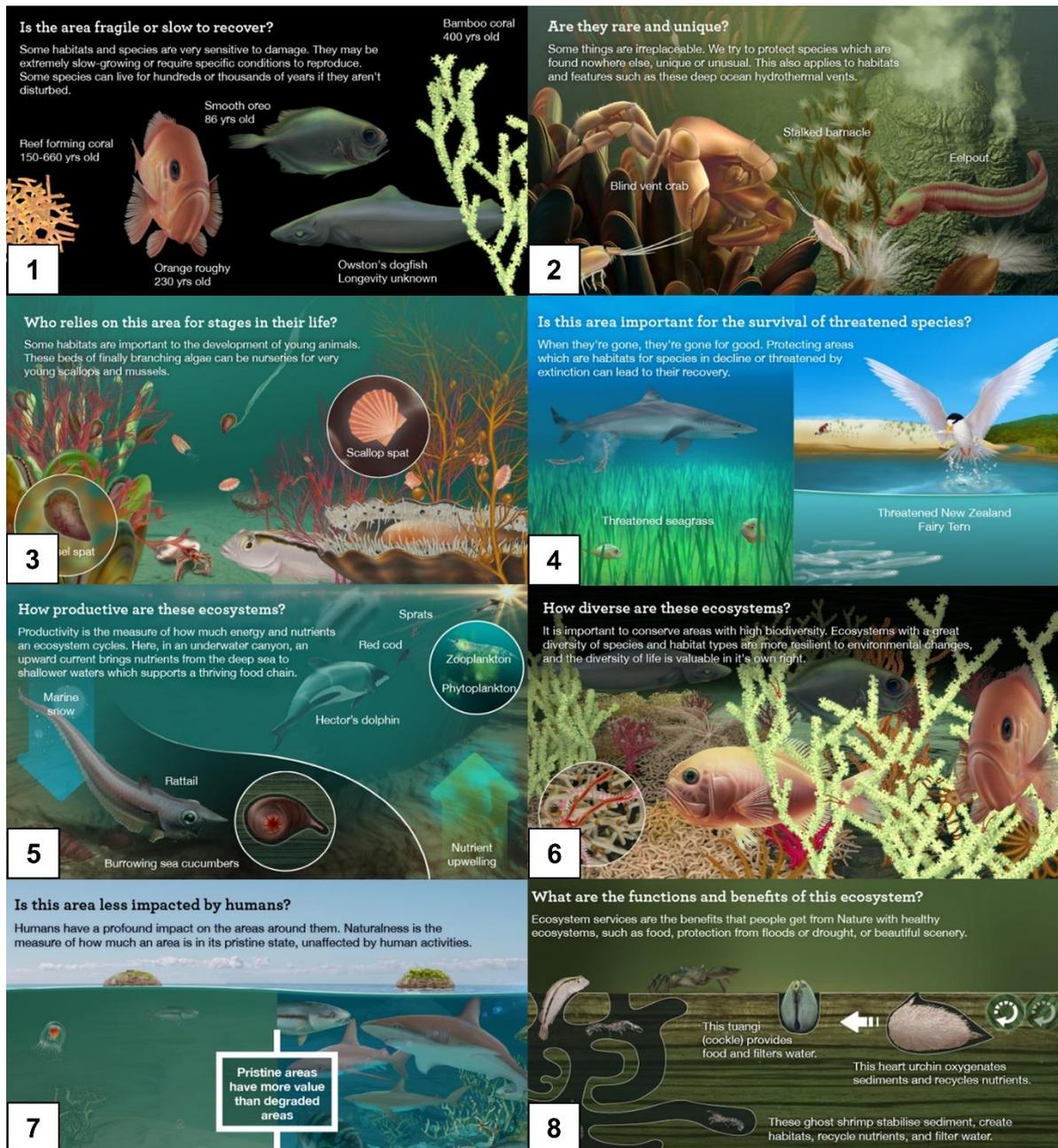
### 2.1 Selection of KEA criteria and associated case studies

In this analysis, we delineated KEAs under criteria 1, 3, and 6 (Figure 2-1), which were chosen to complement criteria developed in prior DOC contracts to NIWA (criteria 2 and 4 in (Stewart-Sinclair and Lundquist 2022)) and informed by data availability. KEA criteria 1, 3, and 6 were selected because the datasets available were already in a suitable format for analyses and to be linked to the Datamesh.

Criterion 1 (Vulnerability, fragility, sensitivity, or slow recovery) is defined as “areas that contain a relatively high proportion of sensitive habitats, biotopes or species that are functionally fragile or with slow recovery” (Freeman et al. 2017, Lundquist et al. 2020b). Examples of habitats that fit this criterion include biogenic habitats like sponge gardens and bryozoan beds (Wood et al. 2012). For criterion 1, datasets for Porifera (sponges) and Bryozoa were used.

Criterion 3 (Special importance for life history stages) is defined as “areas that are required for a population to survive and thrive” (Freeman et al. 2017, Lundquist et al. 2020b). Examples of habitats that could be applied to criterion 3 are fish spawning or nursery grounds, marine areas around pinniped and seabird breeding colonies, migratory corridors, and sites where animals aggregate for feeding. For criterion 3, datasets of fish spawning areas were used.

Criterion 6 (Biological diversity) is defined as “areas containing species, populations, or communities with comparatively higher natural biological productivity” (Freeman et al. 2017, Lundquist et al. 2020b). Examples of habitats that fit criterion 6 are structurally complex communities such as deepwater sponge and coral communities or areas with high diversity of fish and invertebrate species. For criterion 6, macroalgae and reef fish datasets were used.



**Figure 2-1: Key ecological area (KEA) infographics.** Note: KEA criteria 8 & 9: Ecosystem function and services are shown in the same figure [8]. Images obtained from the Department of Conservation ([www.doc.govt.nz](http://www.doc.govt.nz)).

## 2.2 Data sources

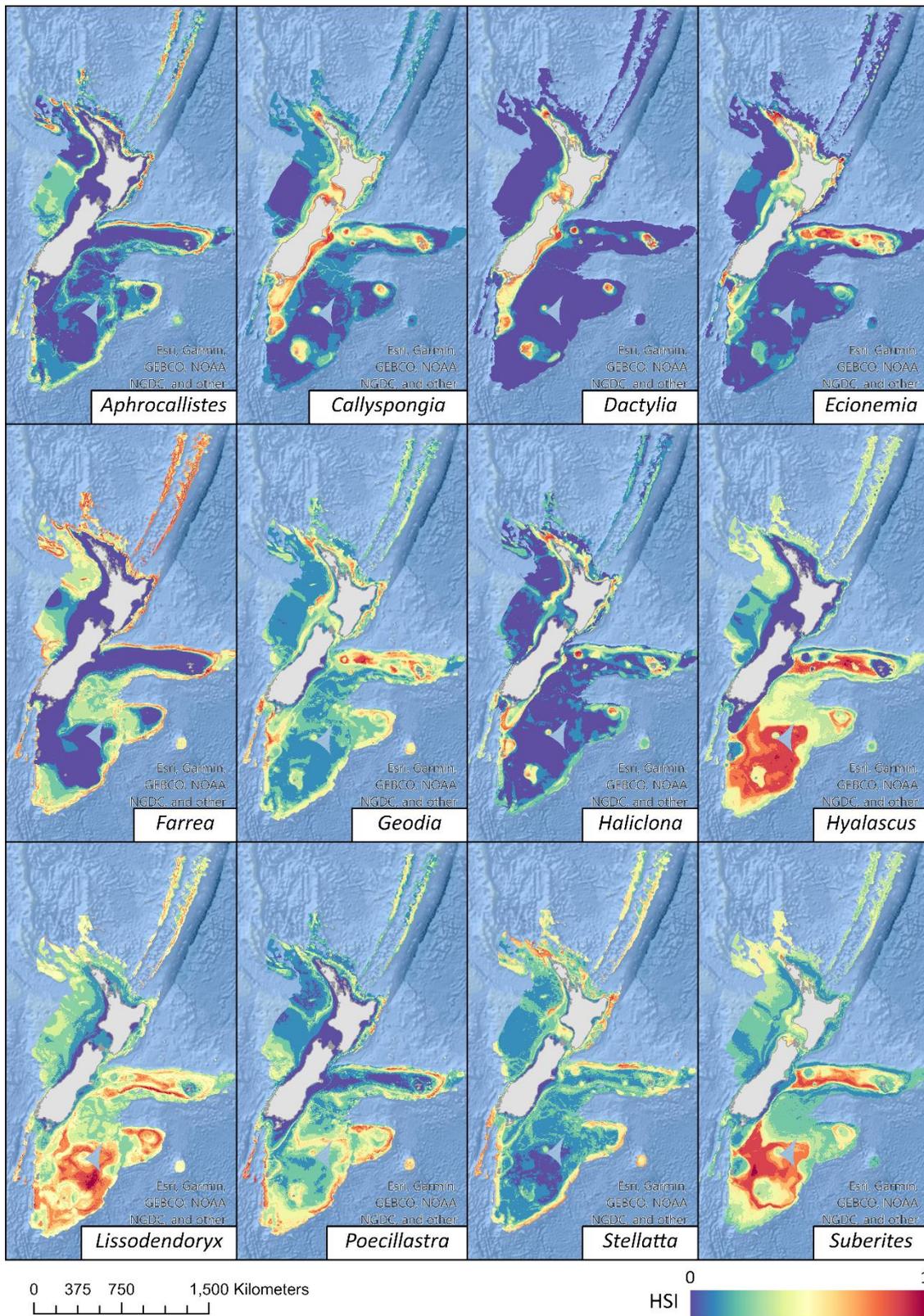
### 2.2.1 Habitat suitability models

Previous NIWA client reports contracted by DOC involved the compilation of datasets to assist in KEA delineation (Stephenson et al. 2018, Lundquist et al. 2020b), but also the development of habitat suitability models of a range of taxa including invertebrates (e.g., sponges, Figure 2-2), demersal and reef fishes and macroalgae (Lundquist et al. 2020b). For this use case, these habitat suitability models were identified as primary datasets for delineating KEAs under criteria 1 and 6.

Habitat suitability index (HSI) models are spatial predictions of species distributions created using a correlative approach that predicts species distribution patterns by relating known species locations (point records) to a set of spatially explicit environmental parameters (Elith and Leathwick 2009). HSI models are spatially integrated tools that can extrapolate from typically limited, and often spatially biased, point records to continuous modelled spatial distributions (Porfirio et al. 2014, Rullens et al. 2022). Having comprehensive spatial layers for marine biodiversity is crucial for conservation and spatial management, which has led to a rise in the development and application of HSI models. HSI modelled layers are particularly useful for the marine environment given the scarcity of species occurrence and abundance records, and spatial biases in data collection in the oceans (Robinson et al. 2017).

While modelling species distributions, it is important to consider uncertainty in predictions. This can be achieved using model fit metrics (where model performance is assessed), but also the variance in spatial predictions. The modelled layers used here were developed using a bootstrapping approach, thus model output layers are mean values over 100 bootstraps (Stephenson et al. 2021), with associated uncertainty (standard deviation) layers. These uncertainty layers can be used in spatial planning processes to weight information based on how certain it is (Lundquist et al. 2020a) and inform decision-making.

HSI model layers used for this use case include: 12 sponge genera, 11 bryozoan genera, 86 macroalgae species and 50 reef fish species (listed in Table A-1). All models are produced at the national scale, the sponge and bryozoan models were predicted to the EEZ scale (<2000 m depth) at a resolution (grid size) of 1 km. The macroalgae and reef fish layers were predicted to a rocky reef layer (<40 m depth) to territorial sea scale at a resolution of 250 m.



**Figure 2-2: Habitat suitability index (HSI) predictions for 12 Porifera (sponge) genera.** HSI values shown on equal interval scale between 0 and 1.

### 2.2.2 Finfish spawning areas

The finfish spawning layers were available on the Fisheries New Zealand (FNZ) NABIS database and were compiled as part of the KEA database (Stephenson et al. 2018). The finfish spawning layers are the extents of known annual spawning distributions for 39 species (see Table A-2) (NABIS 2012). The layers are based on expert knowledge of spawning distributions of a selection of commercially important finfish, and are provided as expert-drawn polygons (Stephenson et al. 2018). Here, all 39 finfish spawning distribution layers were used to delineate KEAs. The extent of the spawning areas varied between taxa, for example, the spawning area for porbeagle shark covers the entire EEZ and is 2,000 times greater than the spawning area for blue moki. To account for variation in spawning area extent, layers were weighted based on their size relative to the other 38 layers.

## 2.3 KEA delineation process for criterion 1: Vulnerability, fragility and slow recovery and criterion 6: Biological diversity

In this use case, delineation of KEAs required the application of a series of thresholds to transition from HSI models to practical KEA boundaries. To delineate KEAs under criterion 1 using HSI model layers, several steps were involved in a spatial analysis. Broadly, these steps involved applying three separate thresholds: 1) HSI threshold, 2) top value threshold, 3) proportion of total extent threshold, and consideration of uncertainty layers across HSI models.

The first step transformed HSI model layers to exclude all values below a minimum HSI value. This process involved reclassifying HSI layers from a continuous layer of HSI values between 0 and 1 to a binary presence/absence layer (0/1) representing areas where each taxon is likely to occur. For this use case, two thresholds were used to investigate the impact of selecting HSI values as thresholds (0.5 and 0.7). Here, every value below the selected threshold (0.5 or 0.7) was reclassified to 0 and all values above were reclassified to 1. This approach was used for this use case, but other methods (based on model sensitivity and specificity) could be used to inform HSI threshold selection.

Following application of the HSI threshold, the resultant layers were assumed to represent predicted presence/absence of each taxon. Layers for each taxon were overlapped and normalised (between 0 and 1) by the number of layers used, producing a single hotspot layer for that feature (e.g., sponges: Figure 2-3A). Hotspots are described as consistent, high-density aggregations of a species or multiple species. The hotspot layer created in this process is based on assumed presence of a taxon given a higher probability of occurrence (i.e., higher HSI value). Under this assumption, areas where multiple species distributions overlap are described as hotspots.

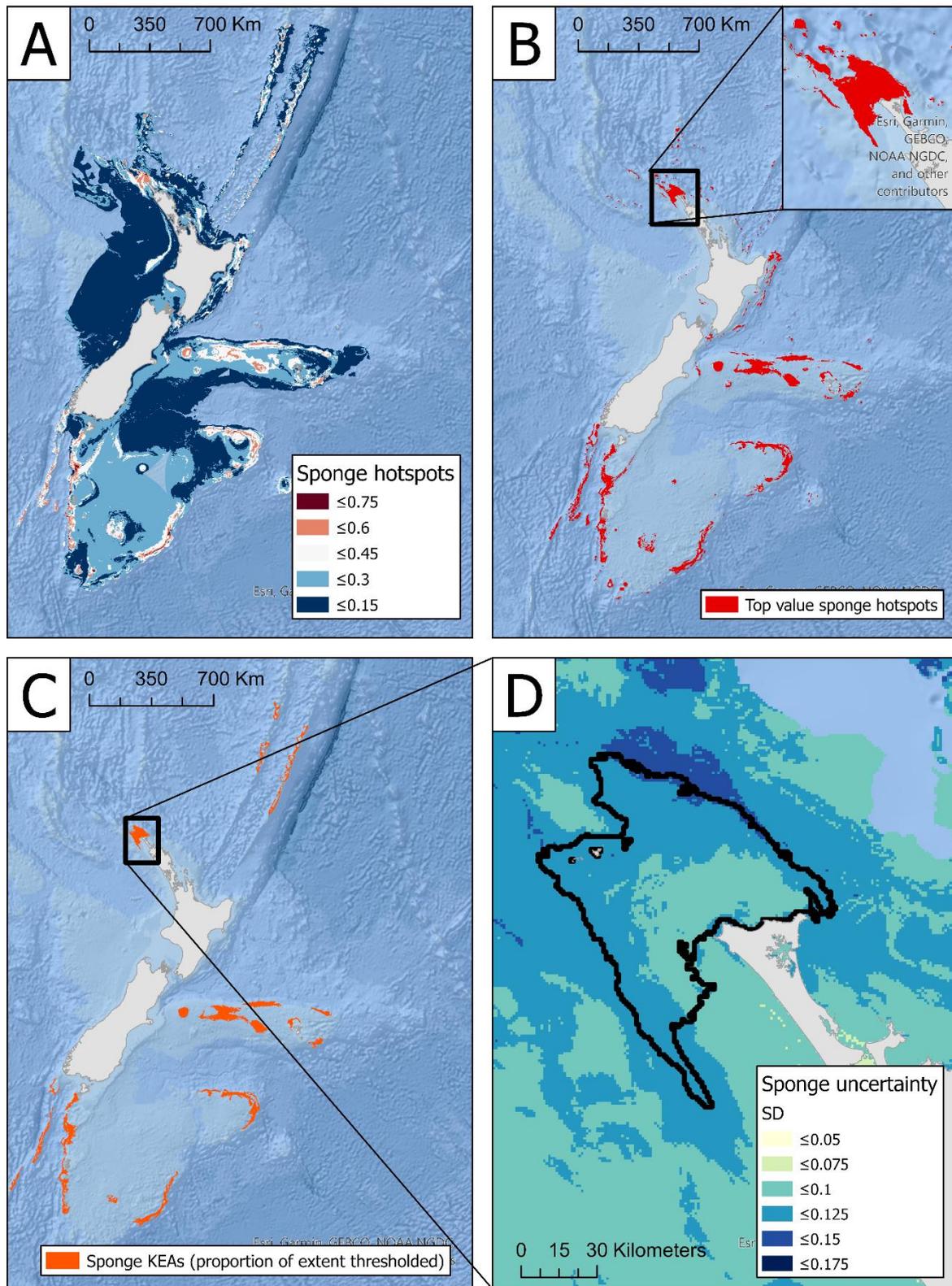
The second step involved application of a 'top value' threshold (Figure 2-3B, illustrating a 10% top value threshold). If the data used was abundance or density data, this top value would represent the highest densities of a species or aggregation of species. In this analysis because HSI model layers rather than abundance predictions are used, the top value relates to the highest number of overlapping taxa once HSI thresholds have been applied. The top value was calculated using a percentile approach where the distribution of values in the entire 'hotspot' raster layer is considered. Top value thresholds of 1, 5 and 10% were explored to assess the impact of this choice on KEA delineation.

The third step involved applying an 'proportion of extent threshold', which is directly aligned with the KBA approach (Stewart-Sinclair and Lundquist 2022). Following determination of high value areas through step one and step two, in this third step, continuous areas of high values were delineated based on the proportion of high value area compared to the total extent of the area remaining, following application of the top value threshold to the combined hotspot layer).

This process removes high value areas that may be too small to be considered a 'key' ecological area. Essentially, high value areas are filtered for continuous areas greater than the proportion of extent threshold ( $\geq$ % of the total extent) so smaller areas are not delineated as KEAs (Figure 2-3C).

In the final step, uncertainty layers which accompany all the HSI layers used for this analysis were overlapped resulting in a mean uncertainty layer for the species group (e.g., sponges: Figure 2-3D). In this format, a higher uncertainty value (i.e., standard deviation) can be interpreted as higher uncertainty in spatial predictions and therefore delineated KEAs.

The delineation process was repeated at national and regional extents for all criteria and taxa examples. The 'national' extent is shown in Figure 2-2, which is the native extent of the raster layers sourced through the Datamesh from the DOC Marine Portal. Spatial predictions were generated for all geographic areas within the EEZ to depths of 2000 m (areas considered to have adequate sample coverage). The Northland Regional Council (NRC) administrative boundary was selected to illustrate an example using a regional extent following the same steps illustrated above (Figures 2-5, 2-6). All analyses were performed in R (R Core Team 2013) using base R and the package 'raster' (Hijmans et al. 2015).

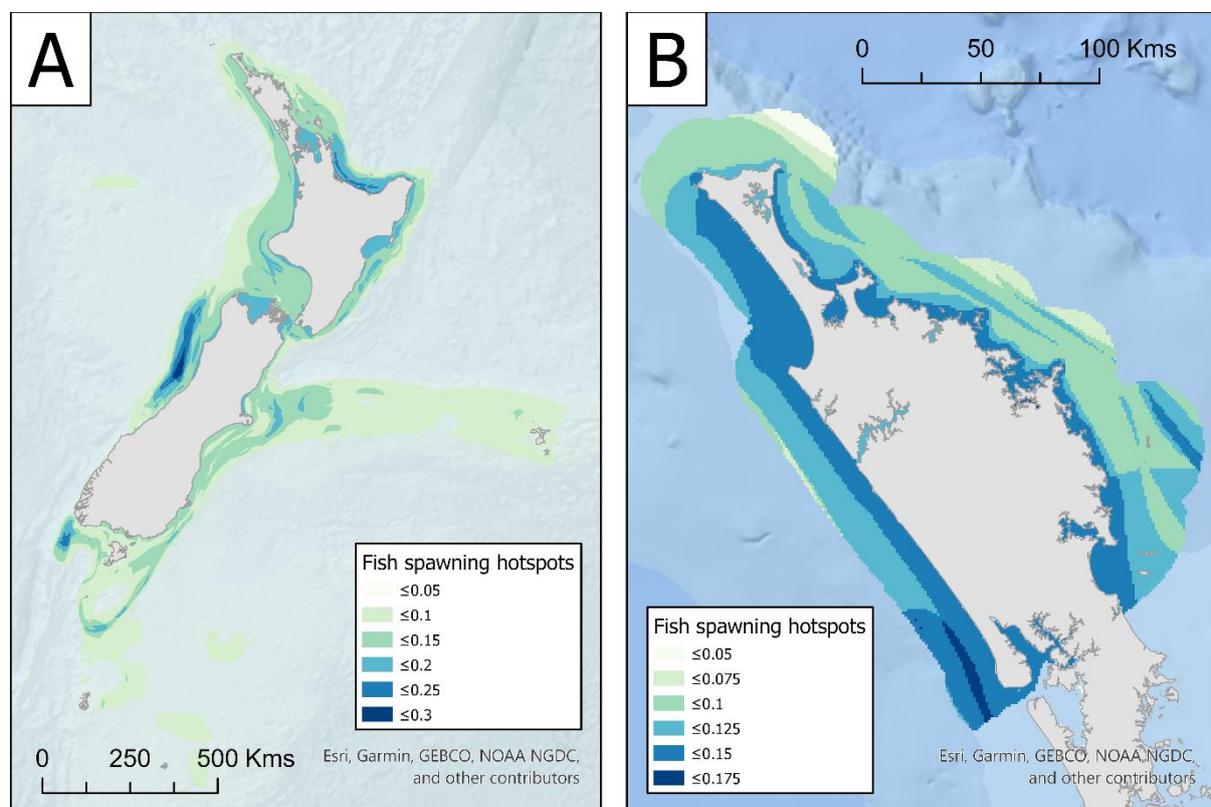


**Figure 2-3: Process for KEA delineation for criteria 1 for sponge biogenic habitats.** A) Sponge hotspots derived by overlapping sponge distributions (12 genera), applying 0.5 habitat suitability index threshold, and normalising by the number of layers ( $n = 12$ ), B) Top value sponge hotspots, in this case the top value is all values >90th percentile (i.e., top 10%), C) Continuous areas following application of proportion of total extent threshold, D) Example of delineated KEA (black outline) used to sample the uncertainty layer (standard deviation, average of 12 sponge uncertainty layers) shown.

## 2.4 KEA delineation process for criterion 3: Special importance for life history stages

All finfish spawning areas (polygons) were rasterised, and each cell was given a value of 1. Each species layer was then weighted based on the size of spawning area, relative to all other finfish spawning area layers (determined via quantiles). For example, if a layer was greater than 75% of the other layers, it was given a weighting of 0.25. For layers between 50-75%, it was given a weighting of 0.50. For layers between 25-50%, it was given a weighting of 0.75. Finally, for layers between 0-25%, it was given a weighting of 1. This weighting process reduced the influence of broad spawning polygons that covered large areas of the EEZ. The finfish spawning area datasets contains different polygons for individual species for 'core' and or 'wider' spawning grounds. For this use case, all polygons were incorporated into the analysis i.e., the full spawning grounds including core and wider spawning areas.

Finfish spawning hotspots were identified by overlapping finfish spawning areas. From this hotspot layer (Figure 2-4), higher value areas, that is areas where greater numbers of finfish spawning grounds overlap, were extracted using a percentile approach. Percentiles are based on the distribution of values within a multispecies layer, 'top value' areas were identified based on top value percentiles (e.g., 0.01%, 0.05%, 1% or 5%). Finally, a 'proportion of extent threshold' was used (as described above for criteria 1), to remove areas too small to be considered 'key' ecological areas. As with criteria 1, the KEA delineation process was repeated at national and regional extents. As the finfish spawning layers used in this analysis were not modelled layers, there are no accompanying uncertainty layers (e.g., standard deviation) to include in the analysis.



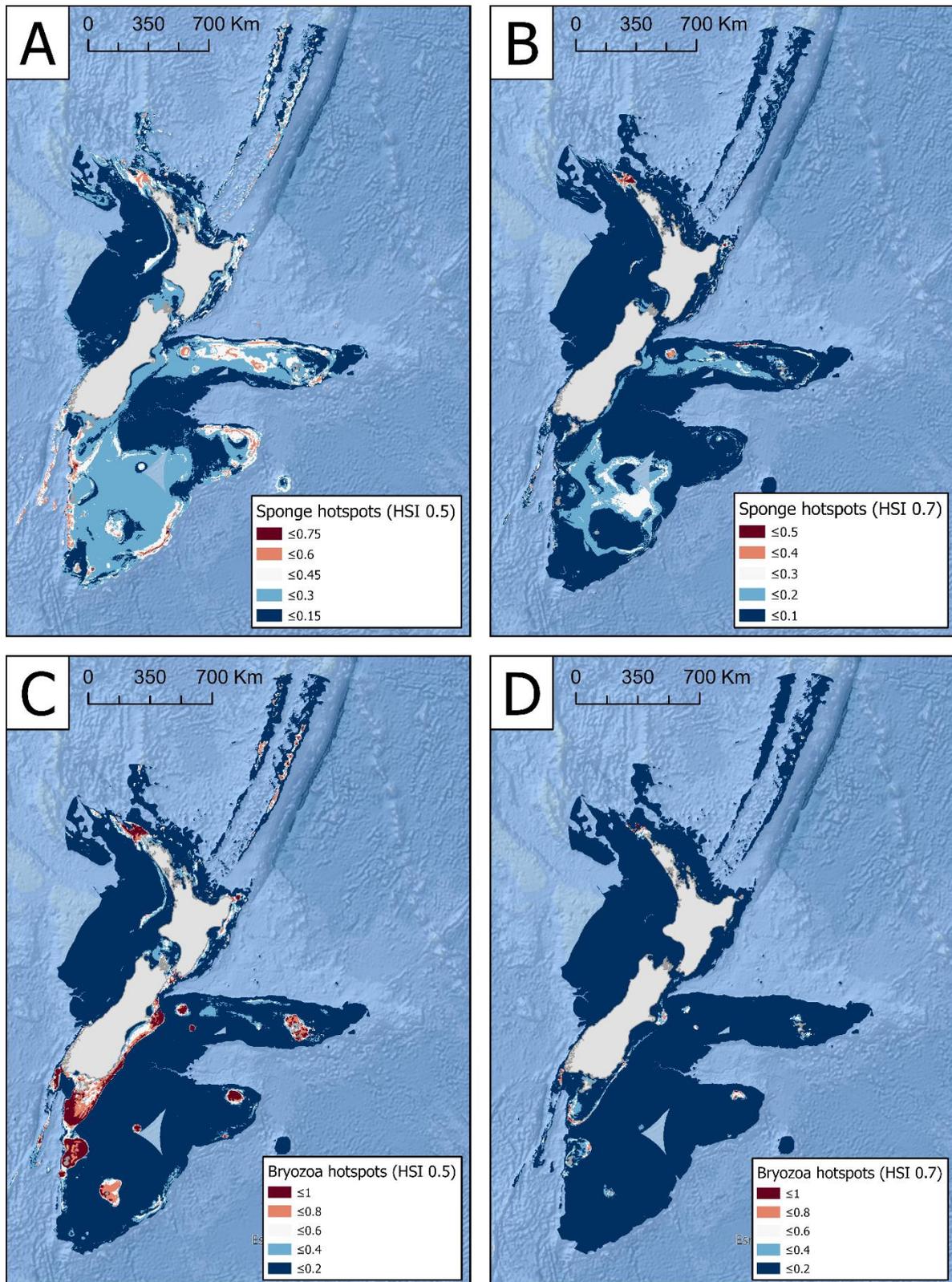
**Figure 2-4: Fish spawning area hotspots.** Dark blue indicates high value areas comprising multiple overlapping finfish spawning layers. Finfish spawning layers were normalised by the number of layers included in the analysis. A) national extent. B) regional extent.

## 3 Delineation of KEAs

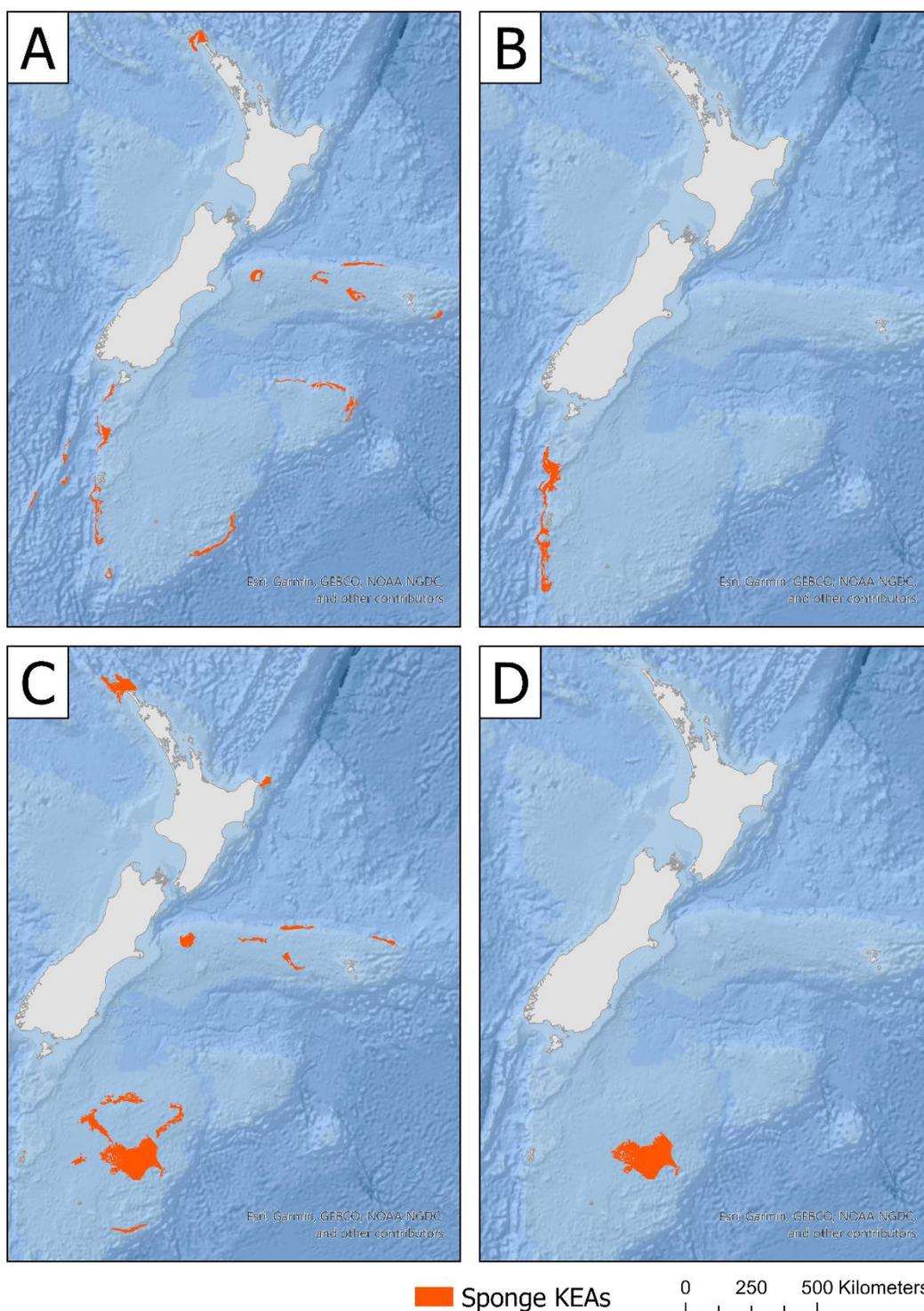
### 3.1 Criterion 1: Vulnerability, fragility, sensitivity, or slow recovery for sponge biogenic habitats

Under KEA criterion 1, KEAs were delineated using Porifera (sponge) taxa and Bryozoa taxa HSI model layers (Figure 3-1). Thresholds tested (HSI, top value and proportion of extent) heavily influenced the size and placement of KEA boundaries. For example, for sponges, a lower HSI threshold (0.5), a lower top value threshold and a lower 'proportion of total extent' threshold increased the number of KEAs delineated. The proportion of extent threshold resulted in the largest differences between KEAs in the scenarios, as it results in the removal of smaller (potentially impractical) KEA boundaries, and retention of only larger, continuous areas. For example, for sponges (Table 3-1, Figure 3-2), with a HSI cut-off of 0.7, a top value threshold of 1% and proportion of extent threshold of 1%, eight KEAs were delineated. When a 10% proportion of total extent threshold was used instead, the number of KEAs decreased to 2 but the summed area of KEAs delineated only decreased by ~25% (Table 3-1).

For testing the impact of KEA delineation at national and regional scales, input datasets were clipped to the Northland Regional Council administrative boundary and analyses were repeated under the same threshold settings as the national analysis (Table 3-2, Figure 3-3). At a regional scale, the implications of threshold selection are more pronounced, with top value thresholds of 1% resulting in no KEAs being delineated. With lower thresholds, KEAs are consistently delineated in the northern portion of the NRC regional boundary, off the coast of Cape Reinga. At the regional scale, the number of taxa included in the 'hotspot' analysis step was lower, as fewer taxa ( $n = 10$ ) were present in the region after applying a HSI threshold of 0.5, and only 8 taxa were present at a threshold of 0.7.



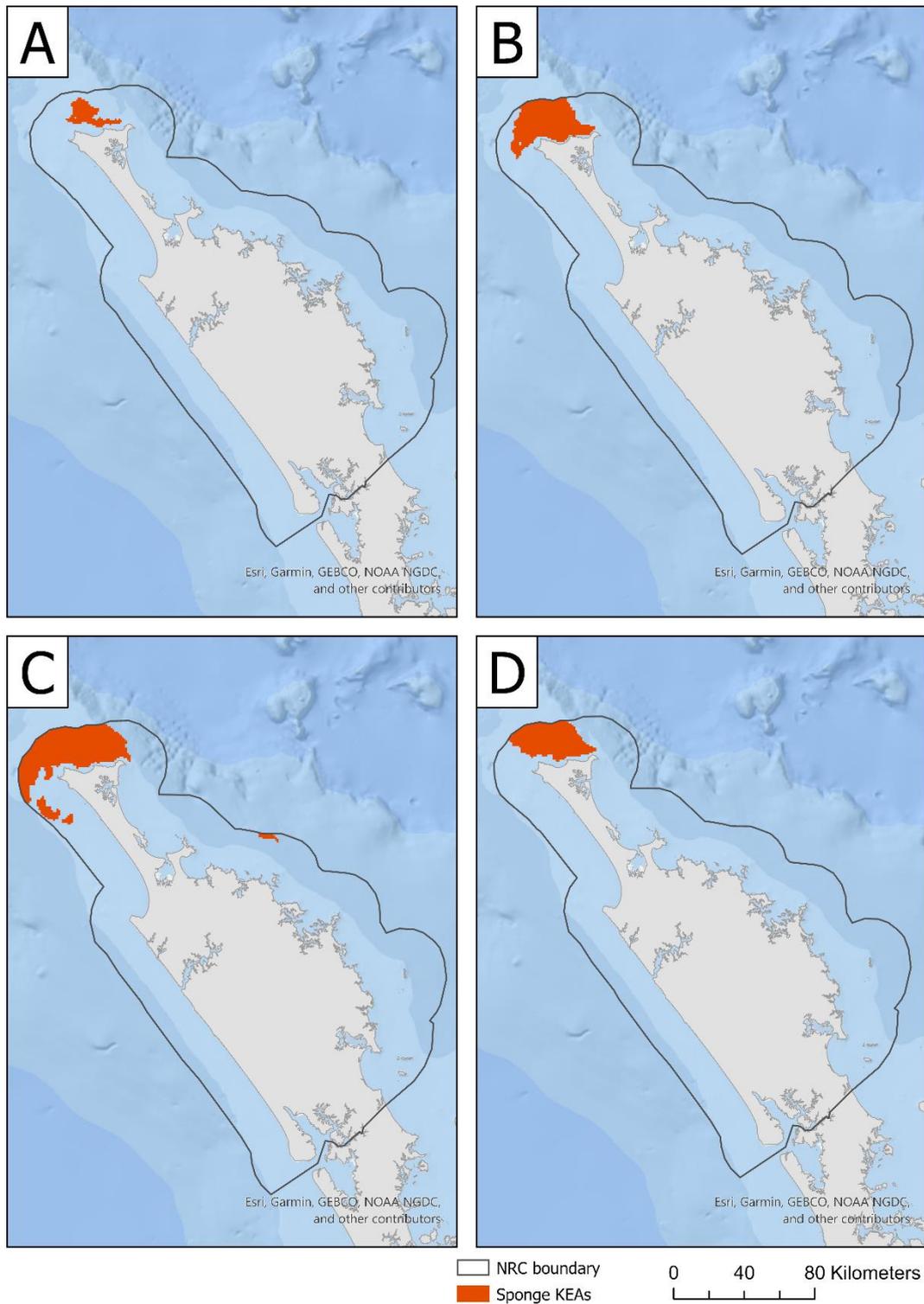
**Figure 3-1: Sponge and Bryozoa hotspot (species richness) examples.** A) Sponge hotspots resulting from combined estimated of species richness for 12 sponge genera using only values above a HSI threshold value of 0.5, B) Sponge hotspots resulting from a HSI threshold value of 0.7, C) Bryozoa hotspots resulting from combined estimated of species richness for 11 bryozoa genera using only values above a HSI threshold of 0.5, D) Bryozoa hotspots resulting from a HSI threshold of 0.7.



**Figure 3-2: Delineated KEAs for criterion 1 for sponge taxa at national scale.** KEA criterion 1: Vulnerability, fragility, sensitivity, or slow recovery, developed using 12 sponge genera (HSI layers). A) HSI threshold: 0.5, top value threshold: 5%, proportion threshold: 1%, B) HSI threshold: 0.5, top value threshold: 10%, proportion threshold: 10%, C) HSI threshold: 0.7, top value threshold: 10%, proportion threshold: 1%, D) HSI threshold: 0.7, top value threshold: 10%, proportion threshold: 10%.

**Table 3-1: National scale area calculations to trigger KEA criterion 1 for sponge taxa.** KEA criterion 1: Vulnerability, fragility, sensitivity, or slow recovery using 12 sponge genera (HSI layers). Threshold combinations (HSI, top value of hotspots, and proportion thresholds) are shown for each scenario. Total area of top value hotspots for 12 Porifera (sponge) taxa, the proportion required to trigger a KEA under criteria 1 at  $\geq 1\%$  or  $\geq 10\%$  of the total 'top value' extent, and the number of sites within NZ that reach this threshold are also shown. All area values in hectares (ha).

HSI cut-off	Top value (top % value)	Proportion of extent (% of total)	Number of KEAs	Top value extent (ha)	Minimum Proportion threshold (ha)	Sum Area (ha) of delineated KEAs
0.5	1	1	18	1,116,500	11,165	624,700
0.7	1	1	8	1,084,600	10,846	723,000
0.5	5	1	21	4,856,700	48,567	2,772,800
0.7	5	1	13	7,629,100	76,291	5,086,300
0.5	10	1	21	13,035,400	130,354	8,947,300
0.7	10	1	13	7,629,100	76,291	5,086,300
0.5	1	10	2	1,116,500	111,650	233,300
0.7	1	10	2	1,084,600	108,460	548,700
0.5	5	10	0	4,856,700	485,670	-
0.7	5	10	1	7,629,100	762,910	2,333,400
0.5	10	10	1	13,035,400	1,303,540	1,322,200
0.7	10	10	1	7,629,100	762,910	2,333,400



**Figure 3-3: Delineated KEAs for criterion 1 for Porifera (sponges) in Te Tai Tokereu (Northland).** KEA criterion 1: Vulnerability, fragility, sensitivity, or slow recovery using 12 sponge genera (HSI layers). A) HSI threshold: 0.5, top value threshold: 5%, proportion threshold: 1%, B) HSI threshold: 0.5, top value threshold: 10%, proportion threshold: 10%, C) HSI threshold: 0.7, top value threshold: 10%, proportion threshold: 1%, D) HSI threshold: 0.7, top value threshold: 5%, proportion threshold: 10%.

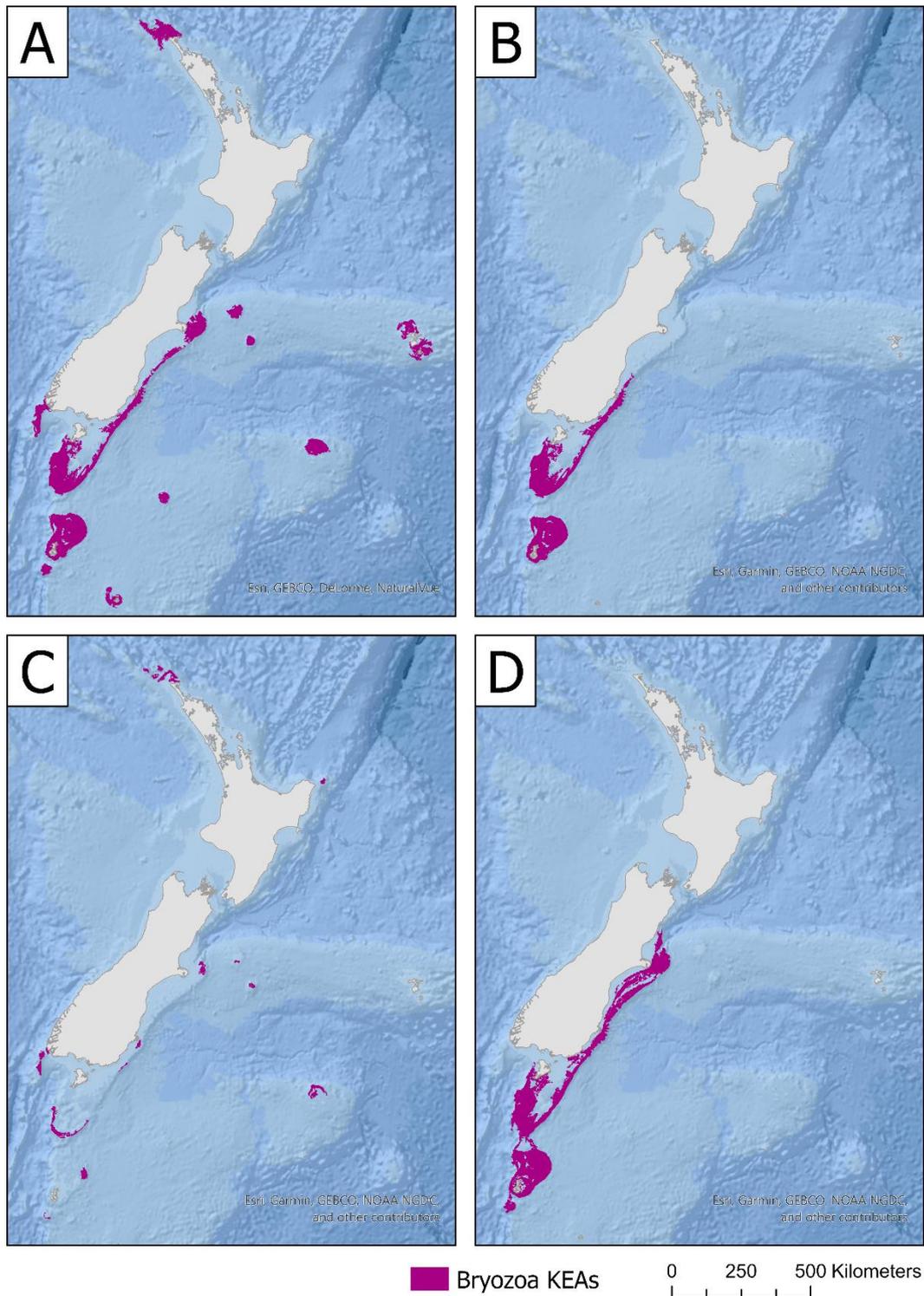
**Table 3-2: Regional scale area calculations to trigger KEA criterion 1 for sponge taxa.** KEA criterion 1: Vulnerability, fragility, sensitivity, or slow recovery using 12 sponge genera (HSI layers). Threshold combinations (HSI, top value of hotspots, and proportion thresholds) are shown for each scenario. Total area of top value hotspots for Porifera (sponge) taxa, the proportion required to trigger a KEA under criteria 1 at  $\geq 1\%$  or  $\geq 10\%$  of the total ‘top value’ extent, and the number of sites within Te Tai Tokerau (Northland) that reach this threshold are also shown. All area values in hectares (ha). For some threshold combinations, no KEAs were delineated (blanks).

HSI cut-off	Top value (top % value)	Proportion of extent (% of total)	Number of KEAs	Top value extent (ha)	Minimum Proportion threshold (ha)	Sum Area (ha) of delineated KEAs
0.5	1	1	0	-	-	-
0.7	1	1	0	-	-	-
0.5	5	1	1	22,222	222	22,222
0.7	5	1	1	74,505	745	74,405
0.5	10	1	2	93,056	931	92,560
0.7	10	1	4	138,791	1,388	137,601
0.5	1	10	0	-	-	-
0.7	1	10	0	-	-	-
0.5	5	10	1	22,222	2,222	22,222
0.7	5	10	1	74,505	7,451	73,017
0.5	10	10	1	93,056	9,306	85,715
0.7	10	10	1	138,791	13,879	124,307

### 3.2 Criterion 1: Vulnerability, fragility, sensitivity, or slow recovery for bryozoan biogenic habitats

The analysis for KEA criterion 1 was repeated for bryozoan biogenic habitats at national (Figure 3-4, Table 3-3) and regional (Figure 3-5, Table 3-4) scales using HSI model layers of 11 Bryozoa taxa. For bryozoan biogenic habitats, a lower HSI threshold (0.5), a lower top value threshold and a lower ‘proportion of total extent’ threshold, increased the number of KEAs delineated (Table 3-3). For instance, using a HSI cut-off of 0.7, a top value threshold of 1% and proportion of extent threshold of 1%, 16 KEAs were delineated. When a 10% proportion of total extent threshold was used instead, the number of KEAs decreased to 3. Similarly, when a 0.5 HSI cut-off was used with a top value threshold of 10 and a proportion of extent threshold of 1%, 14 KEAs were delineated, but using stricter thresholds (1%, 10%, respectively) decreased the number of KEAs to 1.

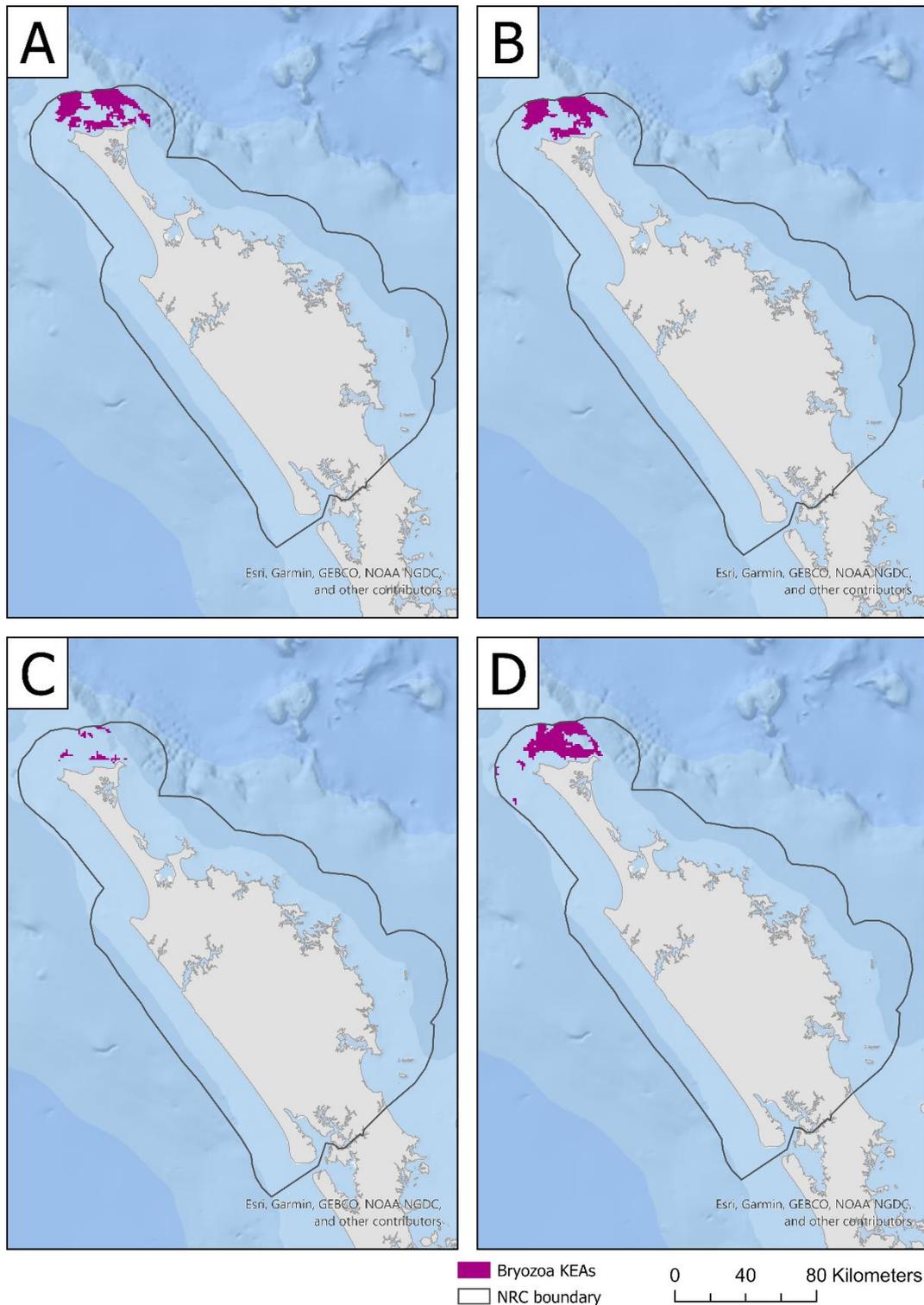
For testing the impact of KEA delineation at national and regional scales, input datasets were clipped to the Northland Regional Council administrative boundary and analyses were repeated under the same threshold settings as the national analysis (Table 3-4). At a regional scale, KEAs are consistently delineated in the northern portion of the NRC regional boundary (like for sponges, see Figure 3-3 and Figure 3-5), off the coast of Cape Reinga. At the regional scale, the number of taxa included in the ‘hotspot’ analysis step was lower ( $n = 10$ ) after applying a HSI threshold of 0.7.



**Figure 3-4: Delineated KEAs for criterion 1 for Bryozoa taxa at national scale.** KEA criterion 1: Vulnerability, fragility, sensitivity, or slow recovery, developed using 11 Bryozoa genera (HSI layers). A) HSI threshold: 0.5, top value threshold: 5%, proportion threshold: 1%, B) HSI threshold: 0.5, top value threshold: 5%, proportion threshold: 10%, C) HSI threshold: 0.7, top value threshold: 1%, proportion threshold: 1%, D) HSI threshold: 0.7, top value threshold: 10%, proportion threshold: 10%.

**Table 3-3: National scale area calculations to trigger KEA criterion 1 for bryozoan taxa.** KEA criterion 1: Vulnerability, fragility, sensitivity, or slow recovery, developed using 11 Bryozoa genera (HSI layers). Threshold combinations (his, top value of hotspots, and proportion thresholds) are shown for each scenario. Total area of top value hotspots for 11 Bryozoan taxa, the proportion required to trigger a KEA under criteria 1 at  $\geq 1\%$  or  $\geq 10\%$  of the total 'top value' extent, and the number of sites within NZ that reach this threshold are also shown. All area values in hectares (ha).

HSI cut-off	Top value (top % value)	Proportion of extent (% of total)	Number of KEAs	Top value extent (ha)	Minimum Proportion threshold (ha)	Sum Area (ha) of delineated KEAs
0.5	1	1	16	1,411,000	14,110	1,158,800
0.7	1	1	16	1,261,300	12,613	1,004,700
0.5	5	1	14	8,654,000	86,540	7,395,800
0.7	5	1	17	8,226,300	82,263	6,409,400
0.5	10	1	14	8,654,000	86,540	7,395,800
0.7	10	1	14	13,438,300	134,383	11,006,600
0.5	1	10	1	1,411,000	141,100	581,300
0.7	1	10	3	1,261,300	126,130	502,100
0.5	5	10	2	8,654,000	865,400	3,994,000
0.7	5	10	2	8,226,300	822,630	3,066,800
0.5	10	10	2	8,654,000	865,400	3,994,000
0.7	10	10	1	13,438,300	1,343,830	6,194,100



**Figure 3-5: Delineated KEAs for criterion 1 for Bryozoa in Te Tai Tokereu (Northland)** KEA criterion 1: Vulnerability, fragility, sensitivity, or slow recovery, developed using 11 Bryozoa genera (HSI layers). A) HSI threshold: 0.5, top value threshold: 5%, proportion threshold: 1%, B) HSI threshold: 0.5, top value threshold: 5%, proportion threshold: 10%, C) HSI threshold: 0.7, top value threshold: 1%, proportion threshold: 1%, D) HSI threshold: 0.7, top value threshold: 5%, proportion threshold: 10%.

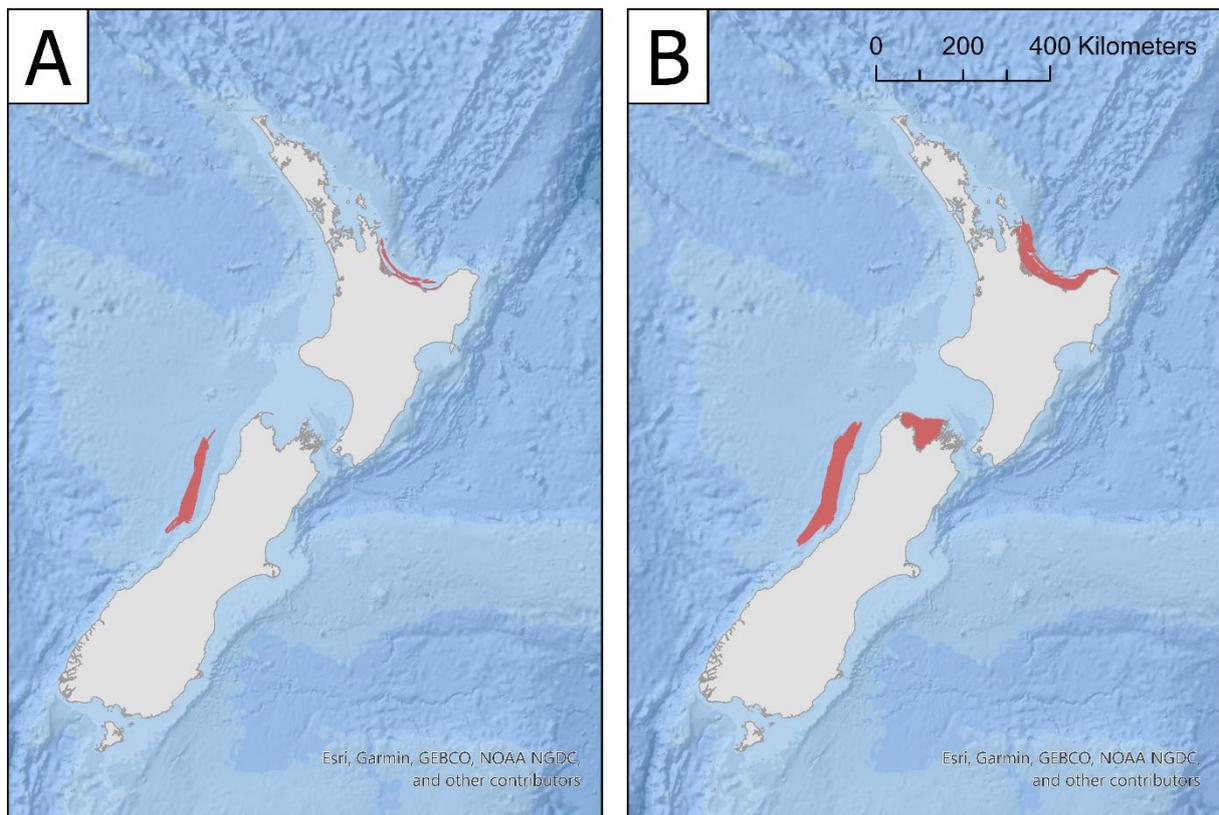
**Table 3-4: Regional scale area calculations to trigger KEA criterion 1 for bryozoan taxa.** KEA criterion 1: Vulnerability, fragility, sensitivity, or slow recovery, developed using 11 Bryozoa genera (HSI layers). Thresholds (HSI, top value of hotspots, and proportion thresholds) are shown for each scenario. Total area of top value hotspots for 11 Bryozoa genera, the proportion required to trigger a KEA under criteria 1 at  $\geq 1\%$  or  $\geq 10\%$  of the total ‘top value’ extent, and the number of sites within Te Tai Tokerau (Northland) that reach this threshold are also shown. All area values in hectares (ha).

HSI cut-off	Top value (top % value)	Proportion of extent (% of total)	Number of KEAs	Top value extent (ha)	Minimum Proportion threshold (ha)	Sum Area (ha) of delineated KEAs
0.5	1	1	4	16,667	167	16,171
0.7	1	1	11	7,738	77	7,738
0.5	5	1	5	61,707	617	60,219
0.7	5	1	4	56,548	565	55,159
0.5	10	1	3	165,478	1,655	162,898
0.7	10	1	1	172,323	1,723	172,224
0.5	1	10	2	16,667	1,667	15,278
0.7	1	10	4	7,738	774	5,456
0.5	5	10	2	61,707	6,171	51,389
0.7	5	10	1	56,548	5,655	52,679
0.5	10	10	1	165,478	16,548	158,037
0.7	10	10	1	172,323	17,232	172,224

### 3.3 Criterion 3: Special importance for life history stages for finfish spawning

KEAs of special importance for life history stages were delineated using polygon shapefiles of finfish spawning areas for 39 taxa (Figure 3-6). A series of thresholds were explored to assess their impact on KEA boundary delineation (Table 3-5). A series of top value and proportion of extent thresholds were used. Stricter thresholds reduced the number of KEAs delineated with the proportion of extent threshold having the greatest impact on the number of KEAs delineated, whereas the top value threshold had the greatest impact on sum area of KEAs delineated. At the national scale, large KEAs were consistently delineated in the Marlborough and Bay of Plenty regions, as well as the west coast of the South Island (Te Waipounamu) (Figure 3-6).

For the regional comparison, lower thresholds were required to ensure KEA delineation (Figure 3-7, Table 3-6). The need for lower thresholds was due to the difference in extents between the full area assessed (extent of the largest fish spawning area polygon) and the NRC administrative region used for the regional assessment. As a result, KEAs were delineated in the NRC region that were not delineated when using the full extent of the input layers (Figure 3-7).

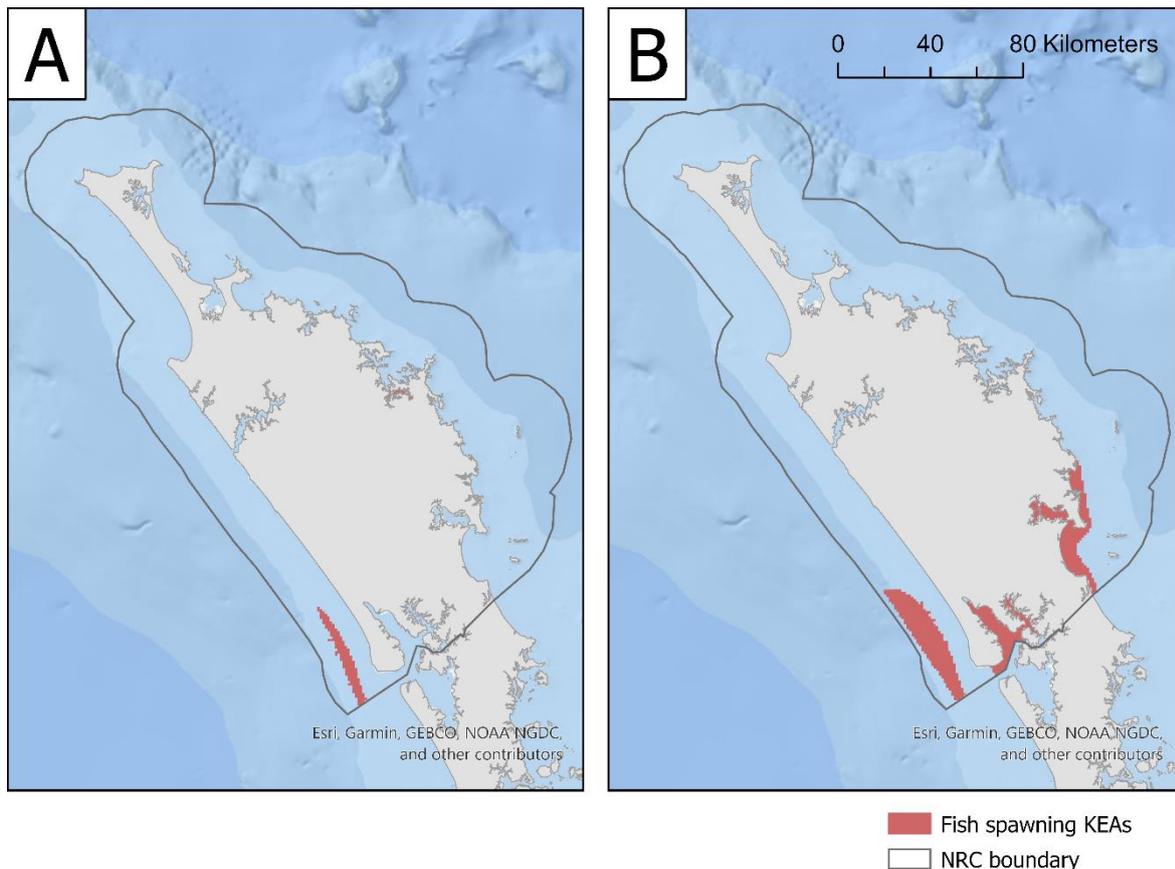


■ Fish spawning KEAs

**Figure 3-6: Delineated KEAs for criterion 3 for national finfish spawning at national scale.** KEA criterion 3: Special importance for life history stages, developed using finfish spawning layers (polygons) for 39 taxa. A) Top value threshold: 0.1%, proportion threshold: 10%, B) top value threshold: 0.5%, proportion threshold: 10%.

**Table 3-5: National scale area calculations to trigger KEA criterion 3 for finfish spawning layers.** KEA criterion 3: Special importance for life history stages, developed using finfish spawning layers (polygons) for 39 taxa. Threshold combinations (Top value of hotspots, and proportion thresholds) are shown for each scenario. Total area of top value hotspots for fish spawning areas, the proportion required to trigger a KEA under criterion 3 at  $\geq 1\%$ ,  $\geq 2\%$  or  $\geq 10\%$  of the total 'top value' extent, and the number of sites within NZ that reach this threshold are also shown. All area values in hectares (ha).

Top value (top % value)	Proportion of extent (% of total)	Number of KEAs	Top value extent (ha)	Minimum Proportion threshold (ha)	Sum Area (ha) of delineated KEAs
0.01	1	3	943,300	9,433	912,600
0.01	2	3	943,300	18,866	912,600
0.01	10	2	943,300	94,330	819,300
0.05	1	15	4,674,100	46,741	4,422,100
0.05	2	9	4,674,100	93,482	4,023,400
0.05	10	3	4,674,100	467,410	2,698,900
1	1	12	8,441,600	84,416	7,795,500
1	2	8	8,441,600	168,832	7,330,000
1	10	3	8,441,600	844,160	5,798,300



**Figure 3-7: Delineated KEAs for criterion 3 for finfish spawning in Te Tai Tokereu (Northland).** KEA criterion 3: Special importance for life history stages, developed using finfish spawning layers (polygons) for 39 taxa. A) Top value threshold: 5%, proportion threshold: 2%, B) top value threshold: 10%, proportion threshold: 10%.

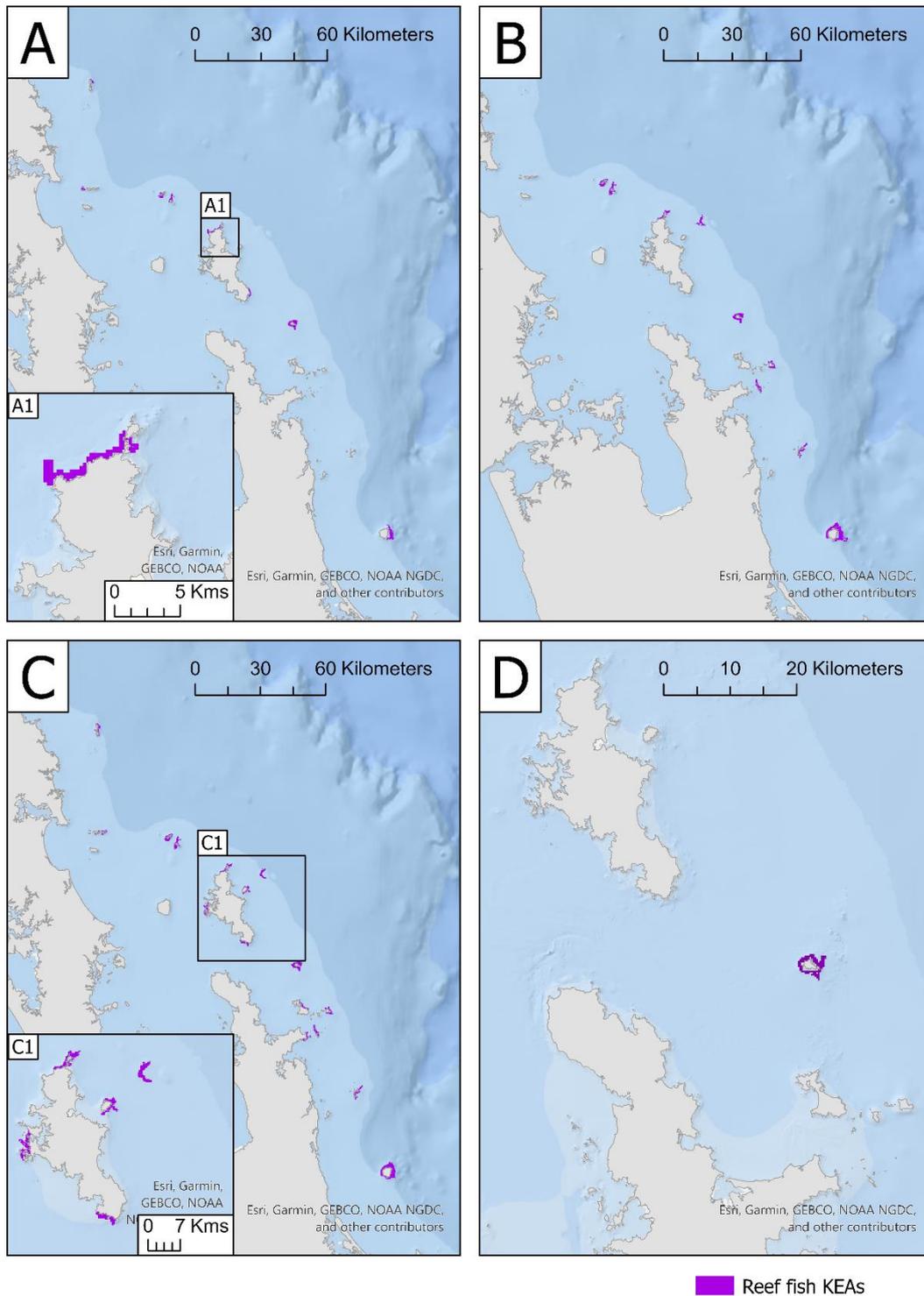
**Table 3-6: Regional area calculations to trigger KEA criterion 3 for finfish spawning in Te Tai Tokerau (Northland).** KEA criterion 3: Special importance for life history stages, developed using finfish spawning layers (polygons) for 39 taxa. Threshold combinations (Top value of hotspots, and proportion thresholds) are shown for each scenario. Total area of top value hotspots for fish spawning areas, the proportion required to trigger a KEA under criteria 3 at  $\geq 1\%$ ,  $\geq 2\%$  or  $\geq 10\%$  of the total 'top value' extent, and the number of sites within Te Tai Tokerau (Northland) that reach this threshold are also shown. All area values in hectares (ha).

Top value (top % value)	Proportion of extent (% of total)	Number of KEAs	Top value extent (ha)	Minimum Proportion threshold (ha)	Sum Area (ha) of delineated KEAs
10	10	2	123,600	12,360	111,000
10	2	3	123,600	2,472	111,000
10	1	3	123,600	1,236	115,800
5	10	1	25,900	2,590	18,900
5	2	2	25,900	518	18,900
5	1	2	25,900	259	16,500

### 3.4 Criterion 6: Biological diversity for reef fish

The process of delineating KEAs under criterion 6 was identical to the methodology used for criterion 1, though this criterion used a different set of habitat suitability index models. Under KEA criterion 1, KEAs were delineated using reef fish HSI models ( $n = 50$ ), with spatial predictions (and the resulting KEAs) restricted to a rocky reef layer. As with criterion 1, stricter thresholds resulted in fewer, or no, KEAs delineated. On a national scale, the proportion of extent threshold (i.e., 1 or 10%) had the biggest impact on the number of KEAs delineated (Figure 3-8, Table 3-7). Only one KEA was delineated when the proportion of extent threshold was 10%. The threshold approach is used to eliminate small, fragmented areas from being delineated as KEAs, with the 10% threshold dropping most initial KEAs attributed to the typical shape of these modelled layers, i.e., as rocky reef areas tend to be narrow and limited in size with very few areas greater than 10% of the top value layer. At a national scale, KEAs were often delineated within the outer Hauraki Gulf region.

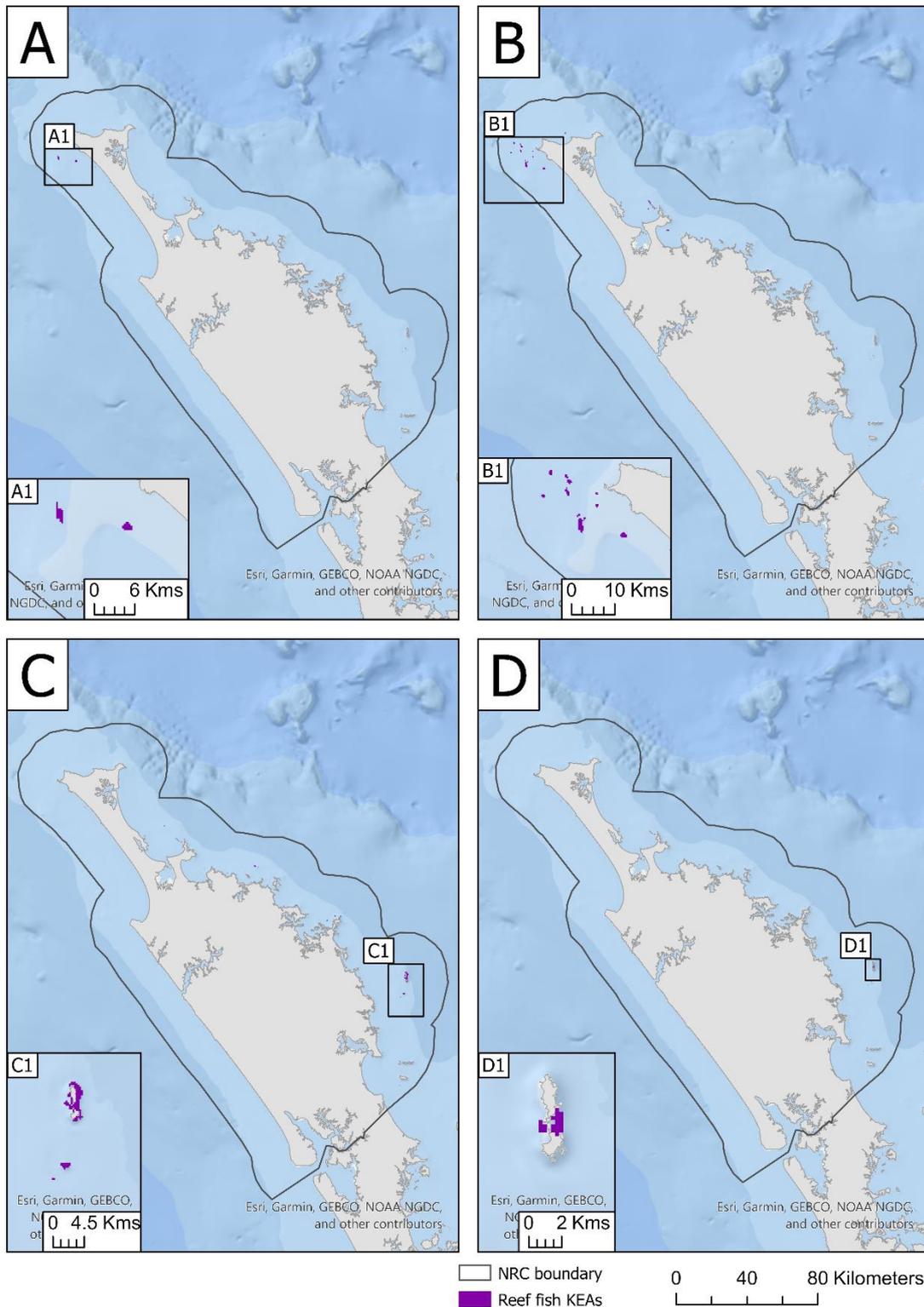
When the analysis was repeated at a regional scale (NRC), the same impact of threshold selection is apparent, with stricter thresholds resulting in fewer KEAs (Figure 3-9, Table 3-8). At the regional scale (Northland), a top value threshold of 10% resulted in  $>20$  KEAs delineated, whereas less than 10 KEAs were delineated when the threshold was 5% or lower.



**Figure 3-8: Delineated KEAs for criterion 6 for reef fish at national scale.** KEA criterion 6: Biological diversity, developed using 50 reef fish species (HSI layers). A) HSI threshold: 0.5, top value threshold: 5%, proportion threshold: 1%, B) HSI threshold: 0.5, top value threshold: 10%, proportion threshold: 1%, C) HSI threshold: 0.7, top value threshold: 10%, proportion threshold: 1%, D) HSI threshold: 0.7, top value threshold: 1%, proportion threshold: 10%.

**Table 3-7: Area calculations to trigger KEA criterion 6 for reef fish at national scale.** KEA criterion 6: Biological diversity, developed using 50 reef fish species (HSI layers). Threshold combinations (HSI, top value of hotspots, and proportion thresholds) are shown for each scenario. Total area of top value hotspots for reef fish taxa, the proportion required to trigger a KEA under criteria 6 at  $\geq 1\%$  or  $\geq 10\%$  of the total 'top value' extent, and the number of sites within NZ that reach this threshold are also shown. All area values in hectares (ha). For some threshold combinations, no KEAs were delineated (blanks).

HSI cut-off	Top value (top % value)	Proportion of extent (% of total)	Number of KEAs	Top value extent (ha)	Minimum Proportion threshold (ha)	Sum Area (ha) of delineated KEAs
0.5	1	1	21	4,570	46	2,506
0.7	1	1	5	3,590	36	2,725
0.5	5	1	13	25,150	252	6,006
0.7	5	1	17	25,850	259	10,356
0.5	10	1	15	46,230	462	12,737
0.7	10	1	18	42,410	424	13,237
0.5	1	10	1	4,569	457	656
0.7	1	10	1	3,594	359	650
0.5	5	10	0	25,150	2515	-
0.7	5	10	0	25,850	2585	-
0.5	10	10	0	46,231	4623	-
0.7	10	10	0	42,413	4241	-



**Figure 3-9: Delineated KEAs for criterion 6 for reef fish in Te Tai Tokerou (Northland).** KEA criterion 6: Biological diversity, developed using 50 reef fish species (HSI layers). A) HSI threshold: 0.5, top value threshold: 5%, proportion threshold: 10%, B) HSI threshold: 0.5, top value threshold: 10%, proportion threshold: 1%, C) HSI threshold: 0.7, top value threshold: 5%, proportion threshold: 1%, D) HSI threshold: 0.7, top value threshold: 1%, proportion threshold: 10%.

**Table 3-8: Regional scale area calculations to trigger KEA criterion 6 (Biological diversity) for reef fish.** Threshold combinations (HSI, top value of hotspots, and proportion thresholds) are shown for each scenario. Total area of top value hotspots for reef fish taxa, the area required to trigger a KEA under criteria 6 at  $\geq 1\%$  or  $\geq 10\%$  of the total 'top value' extent, and the number of sites within Te Tai Tokerau (Northland) that reach this threshold are also shown. All area values in hectares (ha).

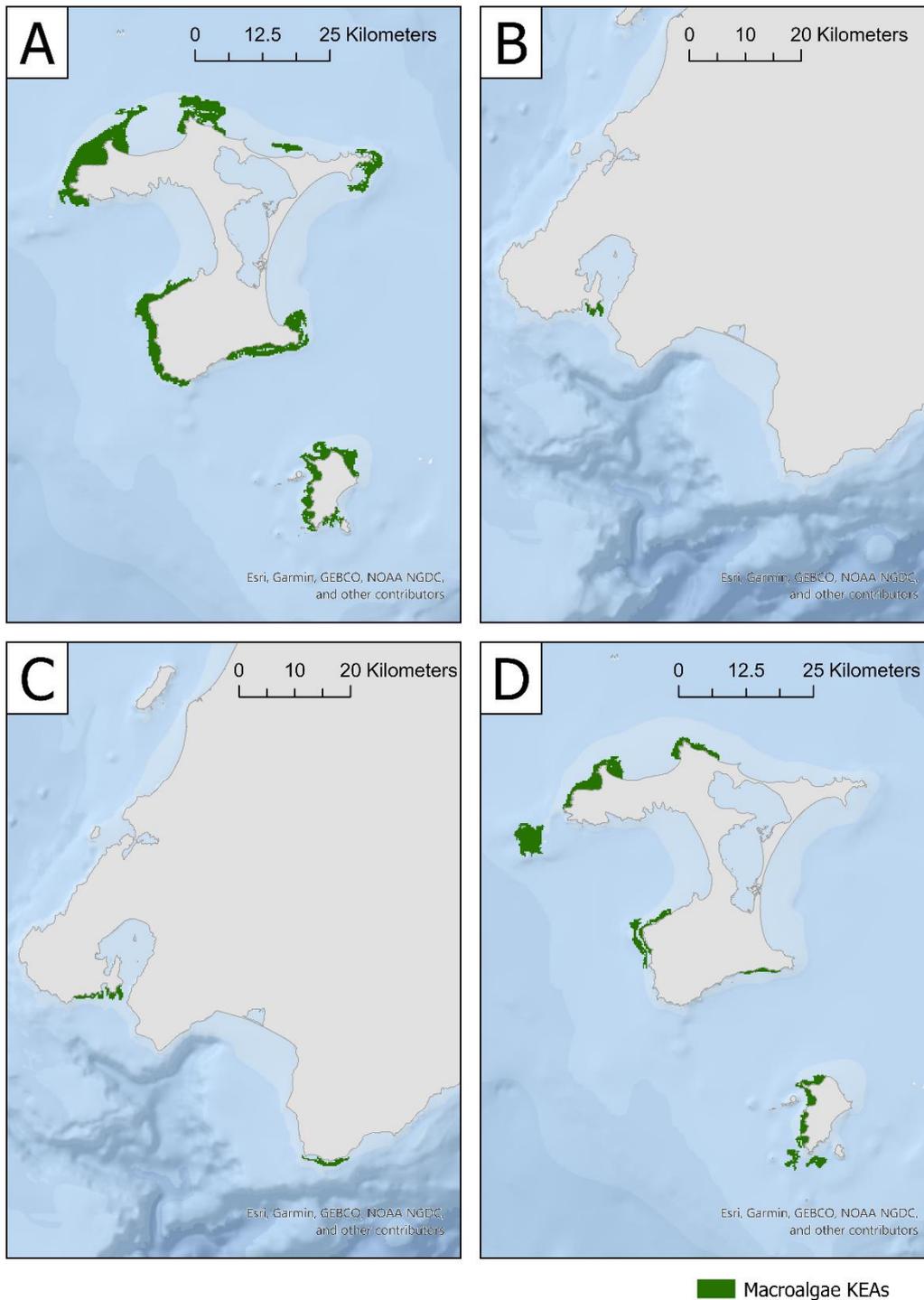
HSI cut-off	Top value (top % value)	Proportion of extent (% of total)	Number of KEAs	Top value extent (ha)	Minimum Proportion threshold (ha)	Sum Area (ha) of delineated KEAs
0.5	1	1	19	2,581	26	1,388
0.7	1	1	13	244	2	244
0.5	5	1	16	938	9	831
0.7	5	1	18	1,113	11	1,038
0.5	10	1	23	2,106	21	1,575
0.7	10	1	20	2,313	23	1,594
0.5	1	10	0	2,581	258	-
0.7	1	10	2	244	24	125
0.5	5	10	2	938	94	344
0.7	5	10	1	1,113	111	513
0.5	10	10	1	2,106	211	331
0.7	10	10	1	2,313	231	544

### 3.5 Criterion 6: Biological diversity for macroalgae

The analysis for KEA criterion 6 was repeated for macroalgae at national (Figure 3-10, Table 3-9) and regional (Figure 3-11, Table 3-10) scales using modelled distribution layers of 86 macroalgae species.

At a national scale, the proportion of extent threshold (i.e., 1 or 10%) had the biggest impact on the number of macroalgae KEAs delineated (Table 3-9). Few KEAs were delineated when the proportion of extent threshold was 10% (max: 2, min: 0). When the proportion of extent threshold was 10% most initial KEAs were dropped. This can be attributed to the typical shape of these modelled layers (rocky reef habitat <40 m in depth), which results in very few areas greater than 10% of the resultant top value layer. At a national scale, KEAs were often delineated in the Wellington and Chatham Islands Rēkohu / Wharekauri areas (Figure 3-10).

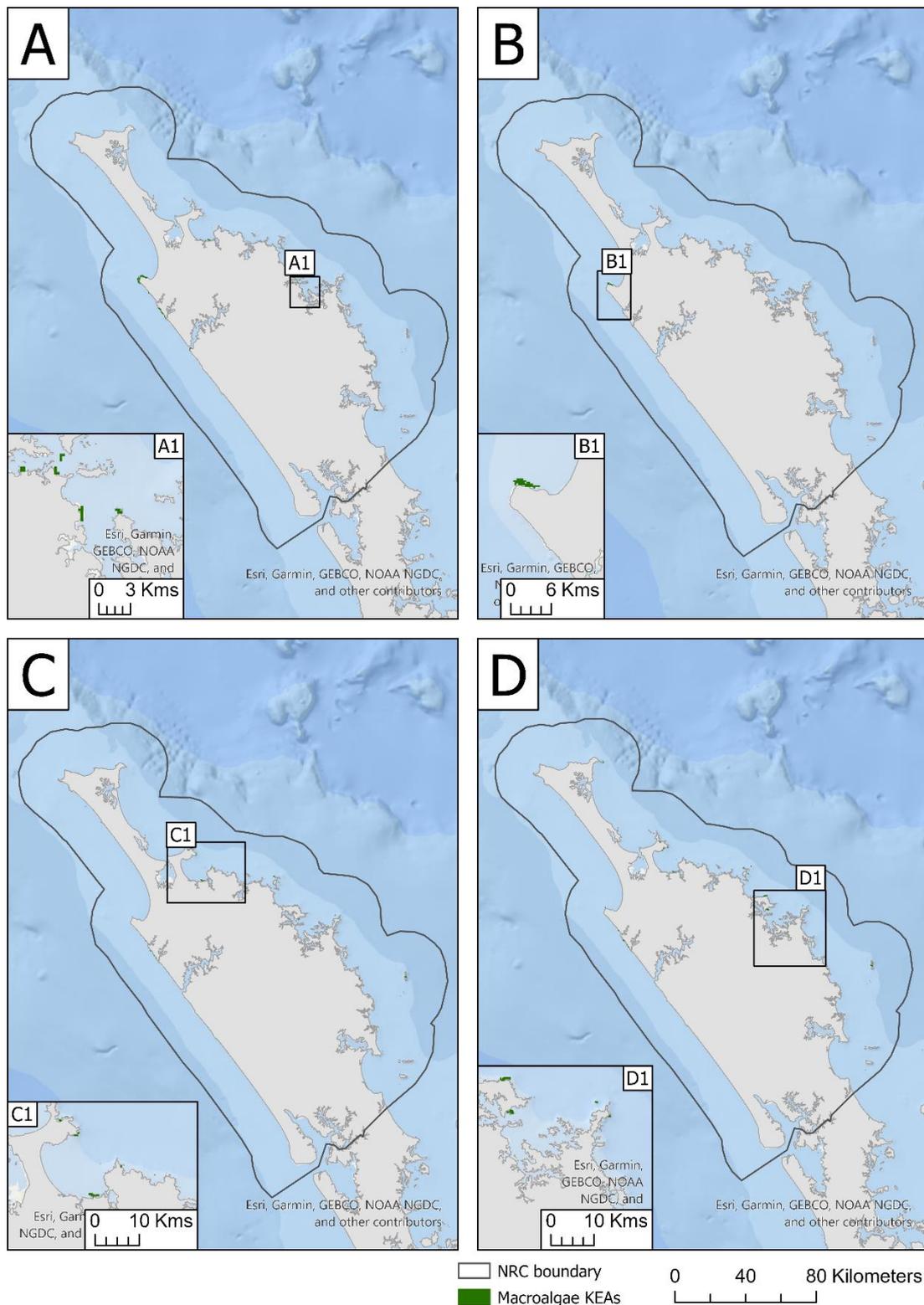
When the analysis was repeated at a regional scale (NRC), the same impact of threshold selection is apparent, with stricter thresholds resulting in fewer KEAs (Table 3-10). Often, small KEAs were delineated close to Ahipara, Doubtless Bay, and Bay of Islands areas (Figure 3-11).



**Figure 3-10: Delineated KEAs for criterion 6 for macroalgae at national scale.** Regional insets for EEZ scale analysis for Wellington region (B, C) and Chatham Islands/Rēkohu/Wharekauri (A, D). KEA criterion 6: Biological diversity, developed using 86 macroalgal species (HSI layers). A) HSI threshold: 0.5, top value threshold: 5%, proportion threshold: 1%, B) HSI threshold: 0.5, top value threshold: 1%, proportion threshold: 1%, C) HSI threshold: 0.7, top value threshold: 10%, proportion threshold: 1%, D) HSI threshold: 0.7, top value threshold: 1%, proportion threshold: 1%.

**Table 3-9: National scale area calculations to trigger KEA criterion 6 for macroalgae.** KEA criterion 6: Biological diversity, developed using 86 macroalgal species (HSI layers). Threshold combinations (HSI, top value of hotspots, and proportion thresholds) are shown for each scenario. Total area of top value hotspots for macroalgal taxa, the proportion required to trigger a KEA under criteria 6 at  $\geq 1\%$  or  $\geq 10\%$  of the total 'top value' extent, and the number of sites within NZ that reach this threshold are also shown. All area values in hectares (ha).

HSI cut-off	Top value (top % value)	Proportion of extent (% of total)	Number of KEAs	Top value extent (ha)	Minimum Proportion threshold (ha)	Sum Area (ha) of delineated KEAs
0.5	1	1	20	4,460	45	2,956
0.7	1	1	19	3,480	35	1,937
0.5	5	1	19	20,730	207	15,050
0.7	5	1	15	21,560	216	8,856
0.5	10	1	15	44,830	448	29,156
0.7	10	1	17	34,900	349	14,925
0.5	1	10	1	4,460	446	462
0.7	1	10	0	3,480	348	-
0.5	5	10	2	20,730	2,073	7,681
0.7	5	10	1	21,560	2,156	2,281
0.5	10	10	1	44,830	4,483	7,106
0.7	10	10	0	34,900	3,490	-



**Figure 3-11: Delineated KEAs for criterion 6 for macroalgae in Te Tai Tokerou (Northland).** KEA criterion 6: Biological diversity, developed using 86 macroalgal species (HSI layers). A) HSI threshold: 0.5, top value threshold: 10%, proportion threshold: 1%, B) HSI threshold: 0.5, top value threshold: 5%, proportion threshold: 10%, C) HSI threshold: 0.7, top value threshold: 5%, proportion threshold: 1%, D) HSI threshold: 0.7, top value threshold: 10%, proportion threshold: 1%.

**Table 3-10: Regional area calculations to trigger KEA criterion 6 (for macroalgae.** KEA criterion 6: Biological diversity, developed using 86 macroalgal species (HSI layers). Threshold combinations (HSI, top value of hotspots, and proportion thresholds) are shown for each scenario. Total area of top value hotspots for macroalgal taxa, the proportion required to trigger a KEA under criteria 6 at  $\geq 1\%$  or  $\geq 10\%$  of the total 'top value' extent, and the number of sites within Te Tai Tokerau (Northland) that reach this threshold are also shown. All area values in hectares (ha).

HSI cut-off	Top value (top % value)	Proportion of extent (% of total)	Number of KEAs	Top value extent (ha)	Minimum Proportion threshold (ha)	Sum Area (ha) of delineated KEAs
0.5	1	1	15	131	1	131
0.7	1	1	12	200	2	200
0.5	5	1	17	1,319	13	888
0.7	5	1	20	1,275	13	675
0.5	10	1	18	2,475	25	1,750
0.7	10	1	19	2,581	26	1,388
0.5	1	10	2	131	13	38
0.7	1	10	1	200	20	131
0.5	5	10	1	1,319	132	250
0.7	5	10	1	1,275	128	138
0.5	10	10	3	2,475	248	1,044
0.7	10	10	0	2,581	258	-

## 4 KEA delineation and future steps

In this use case KEA delineation was tested for three criteria, using different taxa and thresholds at different scales (national and regional). Threshold combinations had significant impact on the placement, number, and size of KEAs delineated. The proportion of extent threshold (1 or 10%) had the biggest impact on the size and number of KEAs delineated, whereas the HSI threshold (0.5 or 0.7) had a greater impact on KEA location (e.g., Figure 2-1 and Figure 3-2). In some cases, KEA placement was consistent between taxa in similar taxonomic groups, across different threshold combinations and analysis scale (e.g., north of Cape Regina for Bryozoa and sponges, Figure 3-3 & Figure 3-5).

### Thresholds

Defining specific thresholds for individual taxa or habitats was beyond the scope of this project, but we explore them here for test purposes. The defining of thresholds for habitat suitability or 'probability of occurrence' models requires careful consideration. Here, we showed examples using thresholds of 0.5 and 0.7 - values that are likely to represent occurrences of a taxa, whereas lower HSI values (e.g., 0.3) are unlikely to be useful in delineating KEAs, as a habitat suitability index value <0.3 indicates low likelihood that a taxon will be present at a given location. The actual threshold values used are for illustrative purposes only, as the primary objective of this project was to develop a KEA delineation methodology that links to data from the DOC geodata portal and other sources (and to test the functionality of the Datamesh and develop a prototype KEA App). Consequently, KEAs delineated here and by the KEA App as part of the use case should not be used to inform management.

Another approach to applying a threshold to HSI model layers is the use of a receiver operating characteristic (ROC) cut-off values. ROC cut-off values represent the point at which both sensitivity (true positive rate) and specificity (true negative rate) are at their maximum (closest to 1). In future, it is recommended that set thresholds for HSI values for KEA delineation are used, a ROC cut-off threshold could be explored as another possible threshold to designate areas of higher probability of occurrence.

Given thresholds used have considerable impact on the size of KEAs delineated, top value thresholds could incorporate ecological targets (e.g., 50% distribution protected), proportion of area thresholds could be informed by management needs/logistics, and connectivity (see e.g., Brough et al. 2021) could be incorporated into analyses using thresholds/buffers that encompass delineated KEAs.

### Selection of taxa

Selection of taxa for inclusion in KEA delineation is important. Consultation with taxonomists can assist in identifying key species or genera that best represent a particular KEA criterion, as well as provide assessment of robustness of spatial maps based on expert ecological knowledge. For example, for KEA criterion 1 (Vulnerability, fragility, sensitivity, or slow recovery), some sponge species, i.e., glass sponges, may be more fragile and therefore more vulnerable to disturbance, whereas encrusting sponges may be more resilient to certain disturbance impacts. Additionally, there are clear patterns in the predicted distribution of sponge taxa included in this use case (Figure 2-2), which illustrates the importance of considering taxa groups included in analyses. Similarly, all the fish spawning layers in Table A-2 were included in the analysis for KEA criterion 3, but a nuanced approach might be applicable where overlapping life-history stages of taxa included in the analysis are evaluated prior to delineation.

Many other datasets currently exist which could have been included in the spatial analysis described in this use case. For an overview of some of the datasets available see 'Appendix A Summary of Key Ecological Areas, Stage 2 Workshop' in Lundquist et al. (2020).

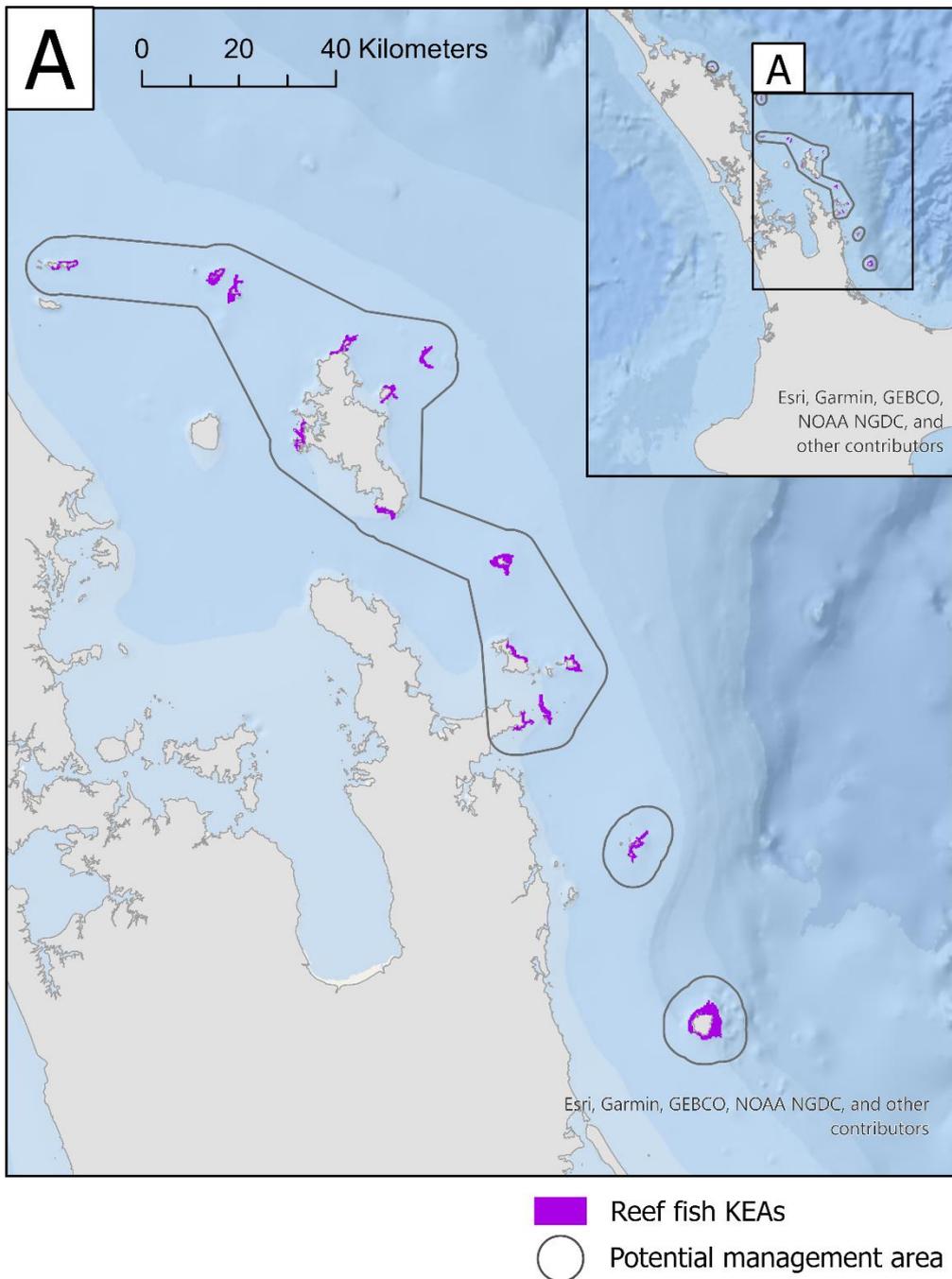
## Recommendations

- In this use case, all HSI model layers available for species that fitted under the KEA criteria 1 and 6 were included, given the purely illustrative purpose of this project (i.e., testing the Datamesh). Model performance metrics exist for all the modelled layers used herein, which should be considered before these layers are used in real world application. These metrics include commonly used model fit metrics and an 'expert evaluation' score based on advice from taxonomic/ecological experts.
- HSI models are available at national scales, but these often extrapolate into unsampled space. Thus, we recommend that for a regional analysis, uncertainty and environmental coverage (poorly sampled areas based on environmental variables) layers are incorporated into analyses.
- Predictive species abundance models would be preferable instead of predictive HSI models, so that areas of highest value align with areas that have greatest species abundance rather than highest habitat suitability.
- Stressor layers could be used to identify if delineated KEAs are vulnerable to impact (e.g., bottom trawling footprint layer). Conversely, MPA layers (current protected areas) or similar could be used to identify if KEAs are currently afforded any protection.
- Spatial prioritisation software like Marxan, Zonation, or prioritizr could be incorporated into the KEA delineation methodology.

### 4.1 Management considerations

Practical boundaries are important for MPA design and implementation. Delineation of KEAs under criterion 6 in this project highlights where 'practical' boundaries might need to be considered. Several, small KEAs were delineated within the outer Hauraki Gulf region, even under different threshold values (north and south of Aotea, Great Barrier Island, Figure 3-8). KEAs delineated within a certain distance of each other may want to be considered in union to avoid impractical placement of many small, nearby protected areas. Standardised delineation of practical KEA boundaries may therefore require a smoothing step, as well as consideration of buffers and practical management boundaries.

To illustrate what this might look like in practice, boundaries were created surrounding delineated KEAs with a distance threshold of 30 km and a buffer of 5 km (Figure 4-1). This produced large areas that encompassed nearby KEAs. However, these 'management areas' contain areas that are outside of original delineated KEA boundaries. For example, the reef fish layers used in this analysis are clipped to rocky reef habitat, and the area encompassed within the 'management area' includes substrates outside of this classification. A similar methodology has been incorporated into the prototype KEA App via a smoothing step.



**Figure 4-1: Delineated KEAs for reef fish for criterion 6 with potential broader scale management areas shown.** KEA criterion 6: Biological diversity, developed using 50 reef fish species (HSI layers) and the following thresholds: HSI threshold: 0.7, top value threshold: 10%, proportion threshold: 1%. Potential management areas are also shown (polygon outline). In this scenario the management area was created based on a maximum distance of 30 km between delineated KEAs in addition to a 5 km buffer.

## 5 Datamesh and the KEA App testing and recommendations

### 5.1 Datamesh benefits and limitations for accessing marine geospatial data

As part of the overall proof-of-concept for a data mesh, Oceanum Ltd. were contracted to provide a cloud-based data mesh as a hub for marine spatial data that would link governmental institute data from various sources (and for various uses) in one place. As part of DOC's use case, the functionality of the Datamesh was tested.

The Datamesh provides a platform to locate, interrogate, analyse, and download data from multiple portals housing geospatial data. The platform has the potential to greatly increase data use, transparency, and connectivity between organisations. Importantly, for end-users, the platform can mean less time and cost investment in data procurement. The Datamesh in its current form has the potential to decrease the silo effect by increasing data accessibility. There are key successes of the Datamesh in its present form, however, there are also areas where the Datamesh could be improved.

#### Key successes

- The Datamesh is a hub for data connectivity, integration, and transparency between multiple institutions and sources. A key attribute of the Datamesh is that data is not held by the Datamesh. It is not a repository and, thus, not constrained by the inflexibility that comes with standardising input data. Instead, the Datamesh connects to multiple sources at once, without copying the data from the original sources, allowing users to select multiple datasets, bundle them, and download them all at once.
- The Datamesh protects data custodianship and allows data owners to manage version control within a single authoritative dataset. Additionally, confidential data can be shared with restricted access (limiting access via password). As data is not copied to the Datamesh, source data is retained on host platforms and systems, ensuring its security.
- Projects can be created where a user can select and bundle datasets without downloading them, allowing the user to return from where they left off on a previous visit. Applications can also be created which allow users to analyse/process data linked to the Datamesh platform without having to download any data.
- The Datamesh front end is a GUI (graphical user interface) which has benefits for the user. For example, the spatial extent of datasets can be visualised and specified by the user. Also, hovering over selected data provides the user with available metadata of layers selected.

#### Potential improvements

- Dataset extents can be visualised on the Datamesh, but as the Datamesh does not copy the datasets to the platform, layers cannot be visualised in detail. While beneficial for speed and data security, it does mean that datasets cannot be interrogated in detail (e.g., exploration of attribute tables of vector datasets) before downloading them onto the end-user's system.

- Geographic projections cannot be chosen when data is bundled and downloaded. Datasets remain in their native projections. Reprojection of spatial datasets (e.g., rasters) can be a time-consuming pre-processing step for spatial analyses. Being able to pre-select geographic projections prior to bringing data onto a local system could both increase productivity and reduce the risk of error.
- In its present form, the Datamesh does not retain all metadata from host portals. For example, the HSI layers from the DOC Marine Data Portal are accompanied by metadata which details their source, attribution information, and limitations. Guaranteeing that all metadata held on host portals remains attached to datasets is vital in ensuring that end-users have all relevant information required to guide and interpret their analyses.

## 5.2 KEA App

This DOC use case included the development of a prototype ‘KEA App’. The KEA App provides a means for users to delineate KEAs without spatial analysis expertise. The KEA App links to datasets via the Datamesh. In this way, a user could conduct an analysis with data from multiple sources and export delineated KEAs, without having to download, format, and process the data on the user’s machine. Within the KEA App, the user first selects the KEA criterion they wish to explore. Next, the user chooses the taxa group they want to incorporate into the analysis and selects an analysis area. The user can then select a single species or multiple species, and vary the HSI threshold, the top value threshold, and the proportion of total extent threshold (referred to as the ‘polygon area threshold’ in the current version of the KEA App), each using a sliding scale. The output layers are polygons representing the KEAs for the selected criterion taxa, and threshold combination.

A selection of thresholds was tested for the use case (section 3), and the KEA App allows users to toggle thresholds and explore what these thresholds mean for the size and placement of delineated KEAs. Since scientifically informed thresholds have not yet been defined for taxa and habitats, the KEA App should not be used to inform management at this stage, although this is planned as part of ongoing work.

The KEA App uses R code written by NIWA and translated into Python by Oceanum Ltd. to delineate KEAs. Some differences were noted when comparing the results of our desktop analysis presented here (R-based) with the results from the KEA App (Python-based). For example, the KEA App converts zero value cells into blank (non-value) cells, that has flow-on effects for the size and number of KEAs delineated. This issue can be resolved by editing the Python code to ensure consistency between the original R code and the KEA App.

## 6 Conclusion

This project contributed to the DOC use case, as part of an overall proof-of-concept to test the feasibility of a data mesh, by (1) developing a methodology to delineate KEAs for three KEA criteria and testing the approach at the national and regional scales, and by (2) testing the functionality and applications of the Datamesh and the prototype KEA App. However, KEAs delineated here and by the KEA App should not be used to inform management, as scientifically informed thresholds have not yet been defined. We identify a series of recommended improvements to the KEA delineation methodology and the KEA App, as well as suggestions for improving Datamesh operability.

The Datamesh is designed to be a one-stop shop for accessing marine-related geospatial data in various formats. Our testing demonstrated the usefulness of the platform for facilitating access to geospatial data from multiple sources to inform marine management in Aotearoa New Zealand.

User-friendly tools, such as the KEA App, offer users the ability to run analyses without having to download data onto their work system. Tools of this kind would be a valuable add-on for end-users to perform analyses, saving time and informing national, regional, local, and rohe moana scale management of marine ecosystems.

## 7 Acknowledgements

We thank the Department of Conservation (particularly Amélie Augé, Enrique Pardo, and Shane Geange) for input into the development of this project, and Oceanum Ltd. (David Johnson, Peter McComb) for providing access to the Datamesh, development of the KEA App, and input on the project. We thank Tom Brough for advice on dataset processing and spatial analyses and for providing input on recommendations to improve the Datamesh and KEA App for future spatial analysis. We also thank Eva Leunissen for input at the testing phase (Datamesh and KEA app). We thank Katie Cook and Michael Bruce for reviewing this report.

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## Appendix A

**Table A-1: List of modelled spatial distributions (i.e., taxa) used in each use-case.** KEA criterion tested, group and list of taxa within each group are shown.

KEA criterion	Group	No.	Taxon
1: Vulnerability, fragility, sensitivity, or slow recovery	Bryozoa	1	<i>Caberea</i>
		2	<i>Cellaria</i>
		3	<i>Celleporina</i>
		4	<i>Disporella</i>
		5	<i>Fenestrulina</i>
		6	<i>Figularia</i>
		7	<i>Galeopsis</i>
		8	<i>Hornera</i>
		9	<i>Micropora</i>
		10	<i>Smittina</i>
		11	<i>Telopora</i>
	Porifera (sponge)	1	<i>Aphrocallistes</i>
		2	<i>Callyspongia</i>
		3	<i>Dactylia</i>
		4	<i>Ecionemia</i>
		5	<i>Farrea</i>
		6	<i>Geodia</i>
		7	<i>Haliclona</i>
		8	<i>Hyalascus</i>
		9	<i>Lissodendoryx</i>
		10	<i>Poecillastra</i>
		11	<i>Stelletta</i>
6: Biological diversity	Reef fish	12	<i>Suberites</i>
		1	<i>Aldrichetta forsteri</i>
		2	<i>Aplodactylus arctidens</i>
		3	<i>Arripis trutta</i>
		4	<i>Bodianus vulpinus</i>
		5	<i>Caesioperca lepidoptera</i>
		6	<i>Cheilodactylus spectabilis</i>
		7	<i>Chironemus marmoratus</i>
		8	<i>Chromis dispilus</i>
		9	<i>Conger verreauxi</i>
		10	<i>Coris sandageri</i>
		11	<i>Decapterus koheru</i>
		12	<i>Forsterygion flavonigrum</i>
		13	<i>Forsterygion lapillum</i>
		14	<i>Forsterygion malcolmi</i>
		15	<i>Forsterygion maryannae</i>
16	<i>Forsterygion varium</i>		

KEA criterion	Group	No.	Taxon
		17	<i>Helicolenus percoides</i>
		18	<i>Hypoplectrodes huntii</i>
		19	<i>Hypoplectrodes sp B</i>
		20	<i>Karalepis stewarti</i>
		21	<i>Latridopsis ciliaris</i>
		22	<i>Lotella rhacinus</i>
		23	<i>Meuschenia scaber</i>
		24	<i>Nemadactylus douglasii</i>
		25	<i>Nemadactylus macropterus</i>
		26	<i>Notoclinops caerulepunctus</i>
		27	<i>Notoclinops segmentatus</i>
		28	<i>Notoclinops yaldwyni</i>
		29	<i>Notolabrus celidotus</i>
		30	<i>Notolabrus cinctus</i>
		31	<i>Notolabrus fucicola</i>
		32	<i>Odax pullus</i>
		33	<i>Optivus elongatus</i>
		34	<i>Parablennius laticlavus</i>
		35	<i>Parapercis colias</i>
		36	<i>Paratrachichthys trailli</i>
		37	<i>Parma alboscapularis</i>
		38	<i>Pempheris adspersa</i>
		39	<i>Pseudocaranx dentex</i>
		40	<i>Pseudolabrus luculentus</i>
		41	<i>Pseudolabrus miles</i>
		42	<i>Ruanoho decemdigitatus</i>
		43	<i>Ruanoho whero</i>
		44	<i>Scorpaena papillosus</i>
		45	<i>Scorpis lineolatus</i>
		46	<i>Scorpis violaceus</i>
		47	<i>Seriola lalandi</i>
		48	<i>Suezichthys aylingi</i>
		49	<i>Trachurus sp</i>
		50	<i>Upeneichthys lineatus</i>
	Macroalgae	1	<i>Adenocystis utricularis</i>
		2	<i>Aeodes nitidissima</i>
		3	<i>Agarophyton chilense</i>
		4	<i>Anotrichium crinitum</i>
		5	<i>Asparagopsis armata</i>
		6	<i>Bachelotia antillarum</i>
		7	<i>Ballia callitricha</i>
		8	<i>Capreolia implexa</i>
		9	<i>Carpomitra costata</i>

KEA criterion	Group	No.	Taxon
		10	<i>Carpophyllum angustifolium</i>
		11	<i>Carpophyllum flexuosum</i>
		12	<i>Carpophyllum maschalocarpum</i>
		13	<i>Carpophyllum plumosum</i>
		14	<i>Caulacanthus ustulatus</i>
		15	<i>Caulerpa brownii</i>
		16	<i>Caulerpa flexilis</i>
		17	<i>Caulerpa geminata</i>
		18	<i>Centroceras clavulatum</i>
		19	<i>Chaetomorpha aerea</i>
		20	<i>Champia novae-zelandiae</i>
		21	<i>Chondracanthus chapmanii</i>
		22	<i>Chondria macrocarpa</i>
		23	<i>Cladhymenia oblongifolia</i>
		24	<i>Clymene coleana</i>
		25	<i>Codium convolutum</i>
		26	<i>Codium fragile</i>
		27	<i>Codium gracile</i>
		28	<i>Colpomenia peregrina</i>
		29	<i>Colpomenia sinuosa</i>
		30	<i>Corallina aff ferreyrae</i>
		31	<i>Crassiphycus proliferus</i>
		32	<i>Cystophora retroflexa</i>
		33	<i>Cystophora scalaris</i>
		34	<i>Cystophora torulosa</i>
		35	<i>Dasyclonium incisum</i>
		36	<i>Desmarestia ligulata</i>
		37	<i>Durvillaea antarctica</i>
		38	<i>Ecklonia radiata</i>
		39	<i>Ectocarpus siliculosus</i>
		40	<i>Euptilota formosissima</i>
		41	<i>Gelidium caulacanthum</i>
		42	<i>Gigartina atropurpurea</i>
		43	<i>Gigartina macrocarpa</i>
		44	<i>Grateloupia urvilleana</i>
		45	<i>Gymnogongrus furcatus</i>
		46	<i>Gymnogongrus torulosus</i>
		47	<i>Halopteris funicularis</i>
		48	<i>Halopteris virgata</i>
		49	<i>Haraldiophyllum crispatum</i>
		50	<i>Hymenena variolosa</i>
		51	<i>Landsburgia quercifolia</i>
		52	<i>Laurencia distichophylla</i>

KEA criterion	Group	No.	Taxon
		53	<i>Laurencia thysifera</i>
		54	<i>Lophothamnion hirtum</i>
		55	<i>Lophurella hookeriana</i>
		56	<i>Lychaete herpestica</i>
		57	<i>Macrocystis pyrifera</i>
		58	<i>Marginariella boryana</i>
		59	<i>Marginariella urvilliana</i>
		60	<i>Melanthalia abscissa</i>
		61	<i>Microdictyon mutabile</i>
		62	<i>Microzonia velutina</i>
		63	<i>Myriogloea intestinalis</i>
		64	<i>Pachymenia dichotoma</i>
		65	<i>Pachymenia lusoria</i>
		66	<i>Petalonia binghamiae</i>
		67	<i>Plocamium angustum</i>
		68	<i>Plocamium cartilagineum</i>
		69	<i>Plocamium cirrhosum</i>
		70	<i>Psaromenia berggrenii</i>
		71	<i>Psilophycus alveatus</i>
		72	<i>Pterocладиella capillacea</i>
		73	<i>Pyropia plicata</i>
		74	<i>Rhodophyllis membranacea</i>
		75	<i>Sarcothalia decipiens</i>
		76	<i>Sargassum sinclairii</i>
		77	<i>Schizoseris dichotoma</i>
		78	<i>Scytosiphon lomentaria</i>
		79	<i>Stenogramma interruptum</i>
		80	<i>Ulva australis</i>
		81	<i>Ulva compressa</i>
		82	<i>Undaria pinnatifida</i>
		83	<i>Vidalia colensoi</i>
		84	<i>Xiphophora chondrophylla</i>
		85	<i>Xiphophora gladiata</i>
		86	<i>Zonaria turneriana</i>

**Table A-2: List of fish taxa used for use-case for KEA criterion 3: special importance for life history stages.** The area (Ha) of each fish spawning area layer is shown, as well as the weighting that was applied to each fish spawning layer based on its size respective to all other layers i.e., smaller areas have higher weighting (between 0 and 1).

No.	ID	Fish spawning layer	Fish spawning area (Ha)	Weight
1	SBG	Spotted black groper	71600	1
2	MOK	Blue moki	401800	1
3	SPO	Rig	623500	1
4	BGZ	Banded stargazer	1225300	1
5	ELE	Elephant fish	1444100	1
6	BAS	Bass	2337800	1
7	SKI	Gem fish	2398400	1
8	ANC	Anchovy	3109400	1
9	FRO	Frostfish	4352000	1
10	WAR	Blue warehouse	5179100	1
11	TAR	Tarakihi	5560200	0.75
12	WWA	White warehouse	6035400	0.75
13	BUT	Butterfish	6451900	0.75
14	SPA   SPM   SPR	Sprats	6524000	0.75
15	JDO	John dory	6596000	0.75
16	GUR	Gurnard	7316200	0.75
17	SBW	Southern blue whiting	9083300	0.75
18	SNA	Snapper	9338500	0.75
19	HAP	Hapuku	9795200	0.75
20	SWA	Silver warehouse	10381300	0.75
21	TRE	Trevally	10462000	0.5
22	EPT	Black cardinal	10805600	0.5
23	YBF	Yellow belly flounder	11696700	0.5
24	BAR	Barroua	12587200	0.5
25	JMN	Jack mackerel, <i>Trachurus novaezelandiae</i>	14136900	0.5
26	EMA	Blue mackerel	15015900	0.5
27	HAK	Hake	19299400	0.5
28	SPE	Sea perch	20009500	0.5
29	KAH	Kahawai	23909400	0.5
30	JMD	Jack mackerel, <i>Trachurus declivis</i>	34282500	0.5
31	ORH	Orange roughy	38073600	0.25
32	JMM	Jack mackerel, <i>Trachurus murphyi</i>	42447200	0.25
33	RCO	Red cod	49312500	0.25
34	LIN	Ling	52660800	0.25
35	RIB	Ribaldo	61782200	0.25
36	STA	Giant stargazer	67092100	0.25
37	HOK	Hoki	79011500	0.25
38	BWS	Blueshark	674848000	0.25
39	POS	Porbeagle shark	782247600	0.25