Forecasting future habitat suitability of marine taxa to advance climate-smart marine spatial planning in Aotearoa New Zealand

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Executive summary

Forecasting the future distribution of marine species using habitat suitability models (HSMs) is a fundamental component of climate-smart marine spatial planning, allowing a range of scenarios to be developed to meet specific objectives around future-proofing the sustainable management and protection of biodiversity and resource use. HSMs can also be used to predict the likely response of species distributions to changing environmental conditions and can therefore help determine the vulnerability of species to climate change. However, forecasting future distribution using these tools relies on several critical assumptions, uncertainties and limitations that require careful consideration. To help address these issues, NIWA (Earth Sciences New Zealand after July 1st, 2025) has developed an expert-informed framework for the development of HSMs to predict the future distribution of marine taxa and has applied this framework to three case study taxonomic groups: sponges, kelps and dolphins. Te Papa Atawhai - the Department of Conservation (DOC) also has a substantial interest in utilising predicted future distribution of marine taxa for appraising vulnerability and to inform climate-smart marine protected area design and climate change adaptation actions. In this study, DOC contracted NIWA to expand the application of the future forecasting framework to additional marine taxa, including: biogenic habitat-forming benthic invertebrates; fish species of high recreational, commercial and/or cultural importance; threatened and at risk macroalgae; and whales. Specifically, this project aimed to pool outputs of HSMs for all species groups (new HSMs from this study, and prior HSMs) and contained specific objectives to:

- Map the present-day and future distribution of species in broad benthic invertebrate, macroalgae, fish and marine mammal taxonomic groups, considering two future time periods (mid-century and end-of century) and under two future emissions scenarios (i.e., shared socioeconomic pathways, SSPs).
- Quantify the predicted change in extent and overlap of core habitat between present-day and future scenarios to determine species vulnerability to climate change impacts.
- Identify and map potential refugia, areas of range contraction and expansion for each species.
- Using a selected set of species, develop and apply methods to examine the overlap of present-day and future-distributions with areas of high intensity of non-climate related stressors to guide decision-making with respect to both climate and non-climate impacts.

Across all species groups, HSMs were fit for 73 marine species and species complexes, with all models performing well by standard model evaluation metrics. Spatial cross-validation showed some variability in model predictive performance among geographic regions. Expert evaluation of inputs suggested that, generally, occurrence data was accurate with few spatial biases and environmental variables used to predict distribution were ecologically relevant. Expert evaluation of model predictive performance suggested that most model predictions (85%) were either ‘highly accurate’ or ‘accurate’; fewer model predictions (14%) were assessed as ‘somewhat accurate’ or ‘largely inaccurate’ (1 species). While changes in thermal conditions contributed strongly to most models, a range of other environmental variables were important drivers of future distribution including, changes in salinity, oxygen concentration (especially for macroalgae), current velocity and mixed layer depth.

As expected, there were often large differences in the predicted distribution of species under the four future climate scenarios, with the largest departures from present-day distribution typically observed for the most extreme scenario (end of century under SSP3-7.5). There were significant differences in forecasted changes in distributions both within and between species groups; invertebrate groups and kelps had the greatest predicted decreases in the extent of core habitat (e.g., HSI > 0.75). Biogenic habitat-forming taxa with the greatest predicted decreases included the dog cockle (*Tucetona spp.*), horse mussel (*Atrina spp.*) and bryozoan (*Cellaporina spp.*). Of the kelps, two species of *Marginariella* and *Cystophora, Xiphophora gladiata,* bull kelp (*Durvillaea spp*.) and the giant bladder kelp (*Macrocystis pyrifera*) had the largest predicted range contractions. The distributions of fish species showed a range of responses with several species exhibiting large increases in the extent of core habitat (e.g., kingfish, snapper, pilchard). Several coastal and deepwater fish were predicted to experience range contraction, with blue cod, hapuku, hoki and southern blue whiting predicted to be the most vulnerable to changes in habitat suitability. Similarly, the distribution patterns of marine mammal species showed diverse responses with coastal bottlenose dolphin and common dolphin having predicted increases in range and Hector’s dolphin and Bryde’s whale having significant contractions of core areas. Across all species there was regional variability in locations of potential refugia; however, areas in the south and east of the South Island regularly featured as refugia for many taxa.

Threatened/at risk macroalgae had a high overlap between potential refugia and areas of high stressor intensity from suspended particulate matter that compromises light conditions at the seafloor. Areas of overlap between non-climate related stressors and refugia for these taxa were located mostly in the northern half of the North Island. Some biogenic habitat-forming invertebrate taxa including *Callyspongia*, *Crella incrustans* and *Dactylia* had over 30% overlap between potential refugia and areas with high trawling intensity, with these overlapping areas typically occurring off the east and north coasts of the South Island.

A range of decision points, considerations and solutions to address the uncertainty inherent in forecasting future distribution using HSMs are identified and discussed along with recommendations for future work to improve the outputs generated by this study. Outputs from the project include spatial layers representing present-day and future distributions for 73 taxa, statistical and expert evaluation scores and further information that may be useful in appraising the utility of these predictions. Spatial layers of predicted habitat suitability index are publicly available via the DOC marine data portal along with the aforementioned metadata. Together, the outputs generated by this study provide an important repository of information to guide climate-smart marine spatial planning for New Zealand.

1 Background

Understanding the future distributions of marine species is essential for making informed decisions on the management of climate and non-climate related stressors to biodiversity. Spatially explicit layers on the distribution of biodiversity under various climate change scenarios are the key components to climate-smart marine spatial planning (MSP) (Queirós et al. 2021; Frazão Santos et al. 2024). Combined with information on the distributions of resource uses and other anthropogenic stressors, uncertainty, and environmental conditions, such information allows for the development of spatial planning scenarios that can guide the establishment of networks of spatial management zones that enhance climate resilience and adaptation in marine socio-ecological systems (Frazão Santos et al. 2020; Queirós et al. 2021; Queirós et al. 2025).

While a broad range of methods exists for mapping the distribution of marine species, forecasting distributions into the future is typically undertaken using spatial models that characterise species relationships with environmental conditions and forecast changes in habitat suitability (inferring potential distributions) based on predicted changes in those conditions (Elith & Leathwick 2009; Elith et al. 2010; Porfirio et al. 2014). Early models were driven largely by thermal conditions (Howard et al. 2014; Peters et al. 2022b), however recent studies show the importance of considering a wide range of biophysical variables that may change under future climate change scenarios (Elith et al. 2010; Robinson et al. 2011; Porfirio et al. 2014). Such correlative models (often termed habitat suitability models, HSMs) have been developed across the full range of marine species phylogeny (Jensen et al. 2017; Simon-Nutbrown et al. 2020; Peters et al. 2022a; Musimwa et al. 2025), and across global, national and regional scales (Kleisner et al. 2017; Martínez et al. 2018; Fragkopoulou et al. 2021; Anderson et al. 2022b). Most often, future-focussed HSMs are generated using presence-only (also called presence-background) or presence-absence data (Robinson et al. 2017), where presence represents the spatiotemporal occurrence of the species of interest and background/absence data is used to characterise locations where the species does not occur or to provide a meaningful sample of the environmental space (in the case of background data). However, models are also commonly developed using data that can approximate the relative abundance and/or density of species, which can provide rich and more nuanced predictions based on density dependent factors (Chang et al. 2021; Rullens et al. 2021; Cruz et al. 2024; Stephenson et al. 2024; Bennion et al. 2025; Hadiyanto et al. 2025).

In addition to mapping changes in habitat suitability and potential refugia (Anderson et al. 2022; Kavousi et al. 2018; Carroll et al. 2015), future forecasting HSMs can also be used to quantify vulnerability of species to climate change impacts based on metrics that reflect change in area occupied, or aerial overlap of highly suitable habitats (Stephenson et al. 2023c). Predictions from HSMs are also used to appraise the exposure of species to non-climate related stressors which may further threaten species viability and adaptability and is thus another important component of climate-smart MSP (Ramírez et al. 2018; Fragkopoulou et al. 2021; Stephenson et al. 2023b; Zelli et al. 2025a).

While HSMs are powerful tools for climate-smart MSP, the process of forecasting distributions into poorly sampled future environmental space is associated with important assumptions, uncertainties and limitations (Elith et al. 2010; Bridges et al. 2023).

Foremost among these are assumptions around the accurate characterisation of a species' present-day niche, which may be heavily influenced by factors including spatial biases in occurrence data, inaccurate data on environmental conditions, mismatches in scale and spatiotemporal resolution and model misspecification (Wiens et al. 2009; Elith et al. 2010; Porfirio et al. 2014). Additionally, significant variation in future predictions can be attributed to the use of different modelling frameworks, variation in conditions between climate change scenarios (i.e., shared socioeconomic pathways, SSPs), the source of data on current and future environmental variables (e.g., Earth System Models/General Circulation Models), and approaches used (when necessary) to classify continuous predictions of habitat suitability into areas most likely to be occupied (i.e., thresholding), among other factors (Wiens et al. 2009; Beale & Lennon 2012; Porfirio et al. 2014; Goberville et al. 2015; Hellegers et al. 2025a). It is crucial for the potential impact of such assumptions and uncertainties on model predictions to be well documented and incorporated into decision making.

In Aotearoa New Zealand (NZ), a range of studies have recently been undertaken to map the present-day distribution of a broad range of marine species and habitats at the national scale (Stephenson et al. 2022b; Stephenson et al. 2023a; Stephenson et al. 2023b; Brough et al. 2025). A comparatively limited number of studies have predicted the future distribution of species. Currently, there are robust predictions of future distributions for vulnerable marine ecosystem taxa such as deep sea corals (Anderson et al. 2022, Zelli et al. 2025) and two species of cetacean (Peters et al. 2022). Additionally, recent work contracted by the Department of Conservation (DOC) expanded the approach to predict present day distributions of over 600 marine taxa (the NZ atlas of seafloor biodiversity) to forecast future distributions (Anderson 2022). While attractive as a cost-effective option, this approach uses an 'automated' model fitting framework with limited appraisal of the key model inputs and outputs and upholding of model assumptions. Given the availability of well-maintained databases on the occurrence of marine species (e.g., museum and online open-source data repositories) and the recent development of an Earth System Model specific to the New Zealand region (Williams et al. 2016; Behrens et al. 2020c), there are ample opportunities to generate robust predictions of future distributions.

The National Institute of Water and Atmospheric Research (NIWA) has recently adapted a framework for developing expert-informed HSMs for the forecasting of future distribution. The framework has been applied to three case study groups – sponge taxa, large brown macroalgae (i.e., kelp) and dolphins. The DOC 2020 Climate Change Adaptation Action Plan (CCAAP) includes actions for a range of DOC functions, including biodiversity conservation and management, and is intended to prioritise climate change research including determining the marine sites, species, habitats and ecosystems that are most at risk from climate change. In this study, DOC has contracted NIWA to expand the application of the expert-informed framework to an additional four species groups including fish, macroalgae, benthic invertebrates and additional cetacean taxa. Outputs from these four groups will be combined with the initial three case study groups to generate a single repository of predicted future climate distributions for a broad range of species. In addition, using data from each group we will calculate metrics that can be used to determine the vulnerability of species distributions to climate change impacts, identify potential refugia, and showcase simple methods to consider potential impacts of non-climate related stressors in a climate-smart MSP context. In addition, we aim to compare outputs generated by the automated forecasting approach (Anderson 2022) to those generated in this study to determine the utility of the automated framework.

The key outputs of this study include:

- Spatially explicit layers for the present-day and future distribution of seven species groups, with associated statistical validation and expert-appraisal scores.
- Ranking of species based on vulnerability to climate change impacts on distribution via calculation of percentage change in areal extent and overlap of core habitats between the present-day and future scenarios.
- Maps of potential ‘refugia’, areas of range contraction and expansion for each species.
- Quantification of the overlap of present day and future distribution with areas with high non-climate related stressors for two priority groups and mapping areas of overlap.

Together, these outputs provide a publicly available repository that can guide climate-smart MSP for a range of important marine species.

2 Methods

2.1 Selection of taxa

Under previous work by NIWA and within this study, HSM approaches were applied to four broad taxonomic groups: fish, benthic invertebrates, macroalgae and marine mammals. Each broad group contains two discrete species sub-groups: fish - coastal and deepwater species; benthic invertebrates - sponges and biogenic habitat-forming species; macroalgae - kelps and threatened/at risk macroalgae; marine mammals - whales and dolphins (Table 2-1). The number of species within each group varied, with species prioritised for inclusion based on perceived impact of climate change, threatened status, ecosystem service provision or recreational/commercial/cultural importance (Table 2-1). For fish and macroalgae, taxa were modelled at the species level. For marine mammals, taxa were modelled at the species level, or for some taxa (e.g., orca, bottlenose dolphin, blue whale) at the species complex or ecotype level. Several forms of orca and bottlenose dolphin occur in NZ waters. In this study, we prioritised 'coastal' ecotypes of both species, with occurrence data for other, more offshore ecotypes being removed. Occurrence records for the two blue whale species (*Balaenoptera musculus intermedia* and *Balaenoptera musculus brevicausa*) were inconsistently identified to species level and thus records were merged to represent a single blue whale species complex (*Balaenoptera musculus spp.)*

For invertebrates, models were developed at the lowest taxonomic level possible (i.e., prioritising species level), however lower resolution groupings were required for taxa that did not meet minimum requirements for the number of occurrence data (50 unique locations). Thus, as per Stephenson et al. 2023a, invertebrate records were often aggregated to genus or in the case of the bamboo corals (*Keratoisididae*) family, based on the grouping that achieved greater than 50 occurrence records and/or based on expert advice on appropriate groupings. Initial NIWA modelling focused on sponges as a case study, which included all genera included in the NZ species atlas. Under this study, a new case study was developed to focus on biogenic habitat forming invertebrate taxa and this included four sponges – two of which were run in the initial NIWA case study. For these genera (*Callyspongia spp., Dactylia spp*.), we used outputs from models developed under the biogenic habitat forming case study, as they include updated occurrence records and expert evaluation. Thus, all biogenic habitat forming sponges are reported along with the biogenic habitat forming invertebrate case study, with the remaining genera (i.e., non-habitat forming) being presented in the 'sponge' case study.

Table 2-1: Species list. List of species that were the focus of forecasting future distribution in this study and by NIWA. The wider taxonomic group, species group, datasets used for pooling occurrence data and the number of occurrence records for each species is provided in the table. * indicates taxa not included or included as a different taxonomic resolution in the NZ atlas of seabed biodiversity (Stephenson et al. 2023).

Species/taxa	Scientific name	Species group	Datasets used	No. Occurrence records
Fish				
Blue cod	*Parapercis colias*	Coastal fish	TRAWL	13 558
Gurnard (red)	*Chelidonichthys kumu*	Coastal fish	TRAWL	7 678
Kahawai	*Arripis trutta*	Coastal fish	TRAWL	1 176
Kingfish	*Seriola lalandi*	Coastal fish	TRAWL	571

Species/taxa	Scientific name	Species group	Datasets used	No. Occurrence records
Pilchard	*Sardinops neopilchardus**	Coastal fish	TRAWL	423
Red cod	*Pseudophycis bachus*	Coastal fish	TRAWL	8 079
Snapper	*Chrysophrys [Pagrus] auratus*	Coastal fish	TRAWL	4 985
Tarakihi	*Nemadactylus macropterus**	Coastal fish	TRAWL	6 555
Bluenose	*Hyperoglyphe antarctica*	Deepwater fish	TRAWL	928
Hake	*Merluccius australis*	Deepwater fish	TRAWL	9 445
Hapuku	*Polyprion oxygeneios*	Deepwater fish	TRAWL	3 293
Hoki	*Macruronus novaezelandiae*	Deepwater fish	TRAWL	18 629
Ling	*Genypterus blacodes*	Deepwater fish	TRAWL	13 982
Orange roughy	*Hoplostethus atlanticus*	Deepwater fish	TRAWL	11 612
Southern blue whiting	*Micromesistius australis*	Deepwater fish	TRAWL	2 134
Benthic invertebrates				
Bivalve	*Atrina zelandica*	Biogenic habitat formers	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	172
Sponge	*Callyspongia* spp.	Biogenic habitat formers	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	222
Bryozoan	*Celleporina* spp.	Biogenic habitat formers	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	149
Bryozoan	*Cinctipora elegans**	Biogenic habitat formers	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	58
Sponge	*Crella incrustans**	Biogenic habitat formers	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	80
Sponge	*Dactylia* spp.	Biogenic habitat formers	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	150
Bryozoan	*Hornera* spp.	Biogenic habitat formers	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	155
Sponge	*Iophon* spp.*	Biogenic habitat formers	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	182
Crustacean	*Jasus edwardsii*	Biogenic habitat formers	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	206 889
Cnidarian (bamboo coral)	Keratoisididae	Biogenic habitat formers	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	430
Bivalve	*Ostrea* spp.*	Biogenic habitat formers	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	250
Cnidarian (bubblegum coral)	*Paragorgia* spp.	Biogenic habitat formers	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	93
Bivalve	*Tucetona* spp.*	Biogenic habitat formers	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	288

Species/taxa	Scientific name	Species group	Datasets used	No. Occurrence records
Sponge	*Aphrocallistes* spp.	Sponges	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	119
Sponge	*Ecionemia* spp.	Sponges	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	131
Sponge	*Farrea* spp.	Sponges	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	114
Sponge	*Geodia* spp.	Sponges	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	226
Sponge	*Haliclona* spp.	Sponges	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	98
Sponge	*Hyalascus* spp.	Sponges	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	413
Sponge	*Lissodendoryx* spp.	Sponges	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	73
Sponge	*Poecillastra* spp.	Sponges	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	112
Sponge	*Stelletta* spp.	Sponges	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	240
Sponge	*Suberites* spp.	Sponges	NiwaInverts, Te Papa and Auckland Museum invertebrate collections	263
Macroalgae				
Macroalgae	*Carpophyllum angustifolium*	Kelp	Niwaalgae	103
Macroalgae	*Carpophyllum flexuosum*	Kelp	Niwaalgae	346
Macroalgae	*Carpophyllum maschalocarpum*	Kelp	Niwaalgae	396
Macroalgae	*Carpophyllum plumosum*	Kelp	Niwaalgae	234
Macroalgae	*Cystophora scalaris*	Kelp	Niwaalgae	137
Macroalgae	*Cystophora torulosa*	Kelp	Niwaalgae	125
Macroalgae	*Desmarestia ligulata*	Kelp	Niwaalgae	95
Bull kelp	*Durvillaea antarctica*	Kelp	Niwaalgae	115
Macroalgae	*Ecklonia radiata*	Kelp	Niwaalgae	474
Macroalgae	*Landsburgia quercifolia*	Kelp	Niwaalgae	183
Giant kelp	*Macrocystis pyrifera*	Kelp	Niwaalgae	152
Macroalgae	*Marginariella boryana*	Kelp	Niwaalgae	77
Macroalgae	*Marginariella urvilliana*	Kelp	Niwaalgae	106
Macroalgae	*Xiphophora chondrophylla*	Kelp	Niwaalgae	162
Macroalgae	*Xiphophora gladiata*	Kelp	Niwaalgae	146
Macroalgae	*Aeodes nitidissima*	Threatened/at risk	Niwaalgae	113
Macroalgae	*Gigartina macrocarpa*	Threatened/at risk	Niwaalgae	95

Species/taxa	Scientific name	Species group	Datasets used	No. Occurrence records
Macroalgae	*Grateloupia urvilleana*	Threatened/at risk	Niwaalgae	74
Macroalgae	*Microdictyon mutabile*	Threatened/at risk	Niwaalgae	63
Macroalgae	*Myriogloea intestinalis*	Threatened/at risk	Niwaalgae	90
Macroalgae	*Pachymenia dichotoma*	Threatened/at risk	Niwaalgae	65
Macroalgae	*Pachymenia lusoria*	Threatened/at risk	Niwaalgae	68
Macroalgae	*Petalonia binghamiae*	Threatened/at risk	Niwaalgae	105
Marine mammals				
Bottlenose dolphin (coastal ecotype only)	*Tursiops truncatus*	Dolphins	NZ Marine Mammal Sighting Database (DOC) and MPI observer databases	191
Common dolphin	*Delphinus delphis*	Dolphins	NZ Marine Mammal Sighting Database (DOC) and MPI observer databases	1 862
Dusky dolphin	*Lagenorhynchus obscurus*	Dolphins	NZ Marine Mammal Sighting Database (DOC) and MPI observer databases	458
Hector's dolphin	*Cephalorhynchus hectori hectori*	Dolphins	NZ Marine Mammal Sighting Database (DOC) and MPI observer databases	2 862
Māui dolphin	*Cephalorhynchus hectori maui*	Dolphins	NZ Marine Mammal Sighting Database (DOC) and MPI observer databases	1 596
Orca (coastal ecotype only)	*Orcinus orca*	Dolphins	NZ Marine Mammal Sighting Database (DOC) and MPI observer databases	830
Blue whale (species complex)	*Balaenoptera musculus spp.*	Whales	NZ Marine Mammal Sighting Database (DOC) and MPI observer databases	317
Bryde's whale	*Balaenoptera edeni brydei*	Whales	NZ Marine Mammal Sighting Database (DOC) and MPI observer databases	340
Humpback whale	*Megaptera novaeangliae*	Whales	NZ Marine Mammal Sighting Database (DOC) and MPI observer databases	104
Long-finned pilot whale	*Globicephala melas*	Whales	NZ Marine Mammal Sighting Database (DOC) and MPI observer databases	194
Southern right whale	*Eubalaena australis*	Whales	NZ Marine Mammal Sighting Database (DOC) and MPI observer databases	72
Sperm whale	*Physeter macrocephalus*	Whales	NZ Marine Mammal Sighting Database (DOC) and MPI observer databases	157

2.2 Modelling framework

This study utilised an established, expert-informed framework for the development of species distribution models with the capacity of forecasting distributions under different future climate change scenarios.

Within the framework, steps are identified where the contribution from species experts are invited, and include the review of inputs (e.g., occurrence data, environmental variables) to the modelling approach, and appraisal of the outputs (e.g., environmental drivers, predicted distributions; Figure 2-1). Both the expert appraisal and statistical modelling approach have been adapted from similar studies used to predict a broad suite of species distributions in New Zealand (e.g., Stephenson et al. 2023a) and is highly adaptable while considering a range of uncertainties that contribute to predicting future species distributions.

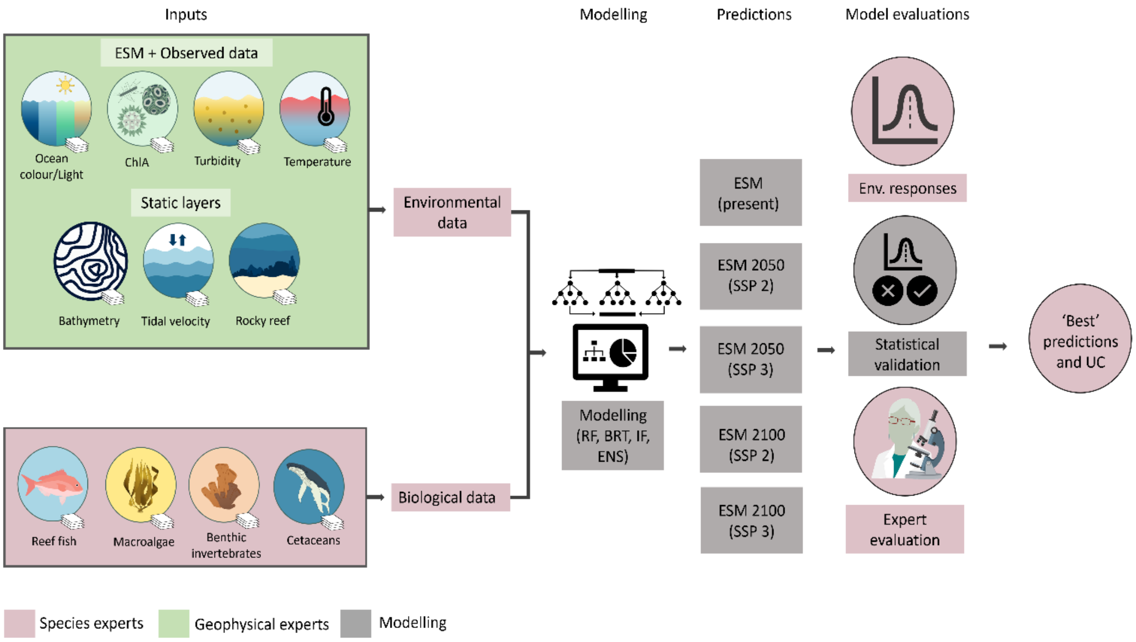

Figure 2-1: Expert-informed framework. The framework used to develop expert-informed predictions of future species distributions, with key steps identified for input and appraisal by species and geophysical experts.

The core inputs to the HSMs are data on the occurrence/absence of the species of interest and data on the environmental conditions at each observation that can be used to characterise a species niche (Elith & Leathwick 2009). In this study, species occurrence data were pooled from a broad range of sources, with different data repositories being used for the taxonomic groups that were the focus of this study (Table 2-1). The distribution of occurrence (and absence/background) data can have a considerable influence on predicted distributions, with sampling bias often resulting in over or under predictions that may not always be apparent in typical model evaluation statistics and uncertainty calculations (Phillips et al. 2009). In general, it is assumed that the distribution of occurrence records represents a realistic approximation of the species niche in geographic space. However, for studies spanning broad scales (e.g., New Zealand waters), it is rare to have occurrence data sets available that have been developed for the purpose of modelling distribution and thus most studies utilise databases that contain observations pooled from a broad range of surveys that may or may not include comprehensive coverage of the species range. Such datasets require careful appraisal to ensure the distribution of the data conforms with expert understanding of the present geographical distribution of a species. To accurately predict species distribution in the future, it is essential to robustly characterise the relationships between species and their environment in the present day (Wiens et al. 2009; Elith et al. 2010), and spatial biases in occurrence data can impact such characterisations. In this study, appraisal of occurrence data was undertaken by species experts who were provided with high resolution maps of plotted occurrence data for each species. Experts were asked to critically appraise the distribution and clustering of occurrence data according to their understanding of species distribution and habitat use requirements. Experts then scored how well the distribution of occurrence data conformed with their expert opinion using predefined criteria listed in Appendix A.

A broad range of environmental data can be used for modelling species distributions based on the relationships between species occurrence and the environmental variables that characterise a species niche. Typically, environmental data are either considered static (i.e., do not change through time), for example, characteristics of the seafloor including depth, slope, and aspect, or are considered dynamic (i.e., are expected to change through time), for example, seawater characteristics and chemistry. Both types of environmental data make important contributions to the models. However, for forecasting future distributions, dynamic variables are critical as these are the data upon which predicted change is based.

In this study, we draw from existing databases of environmental data at the national scale that have been used extensively for modelling species distributions (Stephenson et al. 2022a; Stephenson et al. 2023a), and were developed with input from geophysical experts (Figure 2-1). The database contains both static and dynamic variables. However, not all variables that are expected to change in the future are available to be forecasted, as the Earth System Models (ESM) used to predict future ocean conditions do not contain the full suite of biologically meaningful variables that can drive distributions. In this study, we term dynamic variables for which we can obtain future predictions ‘dynamic – forecastable’, and those that have no available future projection ‘dynamic – non forecastable (Table 2-2). The NZ Earth System Model (Williams et al. 2016; Behrens et al. 2020) was used to generate a range of physical and biogeochemical variables for inclusion as forecastable dynamic variables. The NZ ESM is an ensemble model that integrates outputs of global-scale numerical models for ocean chemistry, physical processes and biogeochemistry with a high-resolution regional ocean model developed for the NZ marine environment (Williams et al. 2016; Behrens et al. 2020). The inclusion of NZ specific drivers of ocean conditions has been shown to reduce biases when compared to its parent model (Sellar et al. 2019; Behrens et al. 2020).

Due to the availability of a multitude of both static, dynamic – not forecastable, and dynamic – forecastable environmental variables, the decision of which variables to include for each species was decided by respective species experts, drawing on the most ecologically relevant variables as a priority. Experts were provided with a full list of available variables and asked to rank these into three groups according to their relevance for a particular species. Variables in the top ranked group were retained for the initial checking of collinearity (see Section 2.3) and inclusion within each species model. While prioritisation based on ecological importance rather than the ability to forecast dynamic variables means that some relationships are unable to be forecasted, this approach is considered best practise (see Elith et al. 2010 and references therein).

Table 2-2: Environmental variables. Environmental variables used to predict species distribution for the present day and into the future. The variable type (static, dynamic - non forecastable, dynamic - forecastable), is given along with list of the species groups for which the variable was selected by species experts.

Environmental variable	Description	Type	Fish	Benthic invertebrates	Macroalgae	Marine mammal
Bathy	Depth of the seafloor (m)	Static	✓	✓	✓	✓
BedDist	Benthic sediment disturbance (ms^{-1})	Static		✓	✓	✓
BEN_SI	Bottom silicon (mmol SI m^{-2})	Dynamic - forecastable		✓		

Environmental variable	Description	Type	Fish	Benthic invertebrates	Macroalgae	Marine mammal
BotPhos	Bottom phosphate (µmol l^{-1})	Dynamic - non-forecastable				
Bottom_Salt	Salinity at depth (PSU)	Dynamic - forecastable		✓		
Bottom_Temp	Temperature at depth (°C)	Dynamic - forecastable	✓	✓		
Bottom_pH	pH of seawater at depth (pH)	Dynamic - forecastable		✓		
BPI_broad	Bathymetric position index (broad) (m)	Static	✓			✓
BPI_fine	Bathymetric position index (fine) (m)	Static	✓	✓		✓
CHD	Diatomic chlorophyll-*a* concentration (mg m^{-3})	Dynamic - forecastable				
Chl-a.Grad	Chlorophyll-*a* concentration spatial gradient (mg m^{-3} km^{-1})	Dynamic - non-forecastable		✓		✓
DET_bottom	Detritus concentration at the seafloor (mmol m^{-3})	Dynamic - forecastable				
DIN_bottom	Bottom nitrate concentration (mmol m^{-3})	Dynamic - forecastable		✓		
Ebed	Seabed incident irradiance (E m^{-2} d^{-1})	Dynamic - non-forecastable	✓		✓	
epC100	export production at 100-m depth (C m^{-2} yr^{-1})	Dynamic - forecastable		✓		✓
Gravel	Percent gravel (%)	Static	✓	✓		
MED_QSR	Sea surface radiation (W m^{-2})	Dynamic - forecastable		✓	✓	
MED_XZE	Euphotic depth (m)	Dynamic - forecastable		✓		
MLD	Mixed layer depth (m)	Dynamic - forecastable	✓	✓		✓
Mud	Percent mud (%)	Static	✓	✓	✓	✓
OM_ARG	Omega aragonite averaged across water column	Dynamic - forecastable				
OM_CAL_bottom	Omega calcite at the seafloor	Dynamic - forecastable		✓		

Environmental variable	Description	Type	Fish	Benthic invertebrates	Macroalgae	Marine mammal
OXY_bottom	Dissolved oxygen at depth (mmol O_2 m^{-3})	Dynamic - forecastable	✓	✓	✓	
PB555nm	Particulate backscatter at 555 nm (previously used to generate 'turbidity') (m^{-1})	Dynamic - non-forecastable		✓	✓	
Rough	Roughness (m)	Static		✓		✓
Sand	Percent sand (%)	Static	✓	✓		✓
Slope	Slope of the seafloor (°)	Static	✓	✓		✓
SSS	Sea surface salinity (PSU)	Dynamic - forecastable			✓	✓
SST	Sea surface temperature (°C)	Dynamic - forecastable	✓	✓	✓	✓
SSTGrad	Sea surface temperature gradient (°C km^{-1})	Dynamic - forecastable			✓	✓
TC	Tidal Current speed (ms^{-1})	Dynamic - non-forecastable	✓	✓	✓	✓
TempRes	Temperature residuals (°C)	Dynamic - forecastable	✓	✓		
TPP3	Net primary production by the vertically-generalised production model (mmol N m^{-3} d^{-1})	Dynamic - forecastable	✓	✓		✓
TPP3_bottom	Net primary production by the vertically-generalised production model (mmol N m^{-3} d^{-1})	Dynamic - forecastable				✓
Velo_bottom	Current velocity at the seafloor (ms^{-1})	Dynamic - forecastable	✓	✓		✓
Velo_surface	Current velocity surface (ms^{-1})	Dynamic - forecastable				✓
CHL_MLD	MLD averaged Chlorophyll	Dynamic - forecastable		✓		✓
BBP443	Particulate backscatter at 443 nm (m^{-1})	Dynamic – non-forecastable				✓

2.3 Modelling methods

Our expert informed framework utilised a well-established method for developing habitat suitability models (HSM) to forecast the present day and future distribution of species. The approach was initially developed for predicting present day distribution for over 600 marine species in the 'Atlas of Seafloor Biodiversity for New Zealand' (Stephenson et al. 2023a). Changes to the approach used here includes: (a) more stringent removal of correlated environmental variables, which can have an amplified influence on forecasting future distribution (Braunisch et al. 2013), (b) spatial cross validation of the ensemble prediction, and (c) generation of partial dependence plots. All modelling and subsequent spatial analyses were undertaken within R studio (R Core Team 2023; Posit team 2025) using the packages *raster* (Hijmans 2023), *dismo* (Hijmans et al. 2023), *gbm* (Ridgeway & GBM Developers 2024), *extendedForest* (Breiman et al. 2023), *rasterVis* (Perpinan et al. 2023), *rgeos* (Bivand & Rundel 2023), *ggplot2* (Wickam 2024), *ggpattern* (FC & Davis 2025), and *latticeExtra* (Sarkar & Andrews 2022).

Detailed methods on the statistical approach can be found in Anderson et al. (2022a) and Stephenson et al. (2023a) with the key steps briefly summarised here:

1. Check collinearity among environmental variables. Variables with a pairwise Pearson correlation coefficient > 0.75 are considered highly correlated. The variable to retain in each correlated pair was based on the highest relative importance score generated by a random forest model fit with conditional permutation and thus not strongly influenced by collinearity (Dormann et al. 2013).

2. Boosted regression trees (BRT) and random forest (RF) models were independently developed for each species using the full suite of occurrence data available. Background (absence) data was generated using the target group background approach, with the occurrence data from species from within the same taxonomic group sampled under the same circumstances being used as background data points. BRTs and RFs were trained iteratively, using a randomly selected training data set consisting of two thirds of the occurrence data and an equal number of background data points[1]. The remaining one third occurrence data and an equal number of background data points were used as a withheld evaluation data set. This process was repeated 100 times for each species in a bootstrapping process with randomly selected training and evaluation data generated for each iteration.

3. Five spatial predictions of habitat suitability index (HSI) were generated for each bootstrapped iteration. Predictions for present day conditions used dynamic variables averaged between the years 2002 and 2020. Predictions for future time periods were based on greenhouse gas concentration trajectories under two shared socioeconomic pathways (SSPs, emission scenarios), with SSP2-4.5 representing a moderate increase in emissions, and SSP3-7.0 representing a strong increase in emissions. Future predictions for each SSP were generated for two future time periods, mid-century (2040 – 2069) and end of the century (2080 – 2099). The only exception to this is for the initial sponge case study undertaken previously by NIWA, where predictions were made under SSP3 7.5 only. The future predictions are hereafter termed 'future scenarios'. The five predictions for each of the 100 bootstrapped iterations were

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[1] For several data-poor benthic invertebrates, repeated-random sampling with replacement was used instead due to models fitting poorly.

averaged to generate mean BRT and RF predictions. Spatially-explicit uncertainty (standard deviation of the HSI) was calculated based on bootstrapped data.

4. Spatial predictions and associated uncertainty were generated for NZ waters to a maximum depth of 2000 m at 1 x 1 km cell resolution. Due to the lack of accurate date on substrate type for macroalgae, the prediction extent was confined to the 'rocky-reef habitat' as defined by DOC's national rocky reef GIS polygon layer (Figure 2-2). Thus, spatial predictions represent the suitability of habitat given the presence of appropriate substrate type. Predictions for marine mammals were generated for a slightly wider area than the maximum 2000 m depth cut-off used for invertebrates and fish, as there were some well-sampled areas beyond this limit. Thus, we included a buffer around the full extent of the occurrence data for marine mammals which was added to the prediction extent defined by the 2000 m depth contour.

5. Area under the curve (AUC) and True Skill Statistic (TSS) were generated for each bootstrap iteration using the withheld evaluation data set. These model evaluation statistics were averaged for each species across the 100 bootstraps.

6. The relative importance of the environmental variables for each model iteration was calculated using built in approaches for the RF (Ellis et al. 2012) and BRT (Friedman & Meulman 2003) models. Each relative importance score, for each model type was scaled such that they represent the percentage contribution to the HSM for each species. Partial dependence plots were similarly generated at each model iteration for each model type using the function *partial* in the R Package *pdp* (Greenwell 2024).

7. An ensemble (ENS) prediction was generated for each of the five predictions for each species, generated using the weighted average (based on model AUC scores) of the HSI predictions and spatially explicit uncertainty (SD). See Stephenson et al. (2023a) and Anderson et al. (2022a) for the ensemble model formulae. Scores for the importance of environmental variables and partial dependence plots were similarly averaged for each species.

8. Spatial cross validation was used as a final model evaluation step for the ensemble prediction. Species occurrence and target group background data was apportioned to eight discrete zones within NZ waters that represented bioregions developed by Stephenson et al. (2023d). AUC and TSS scores were calculated for each zone separately and thus this approach takes into consideration any spatial variability in the performance of the model prediction.

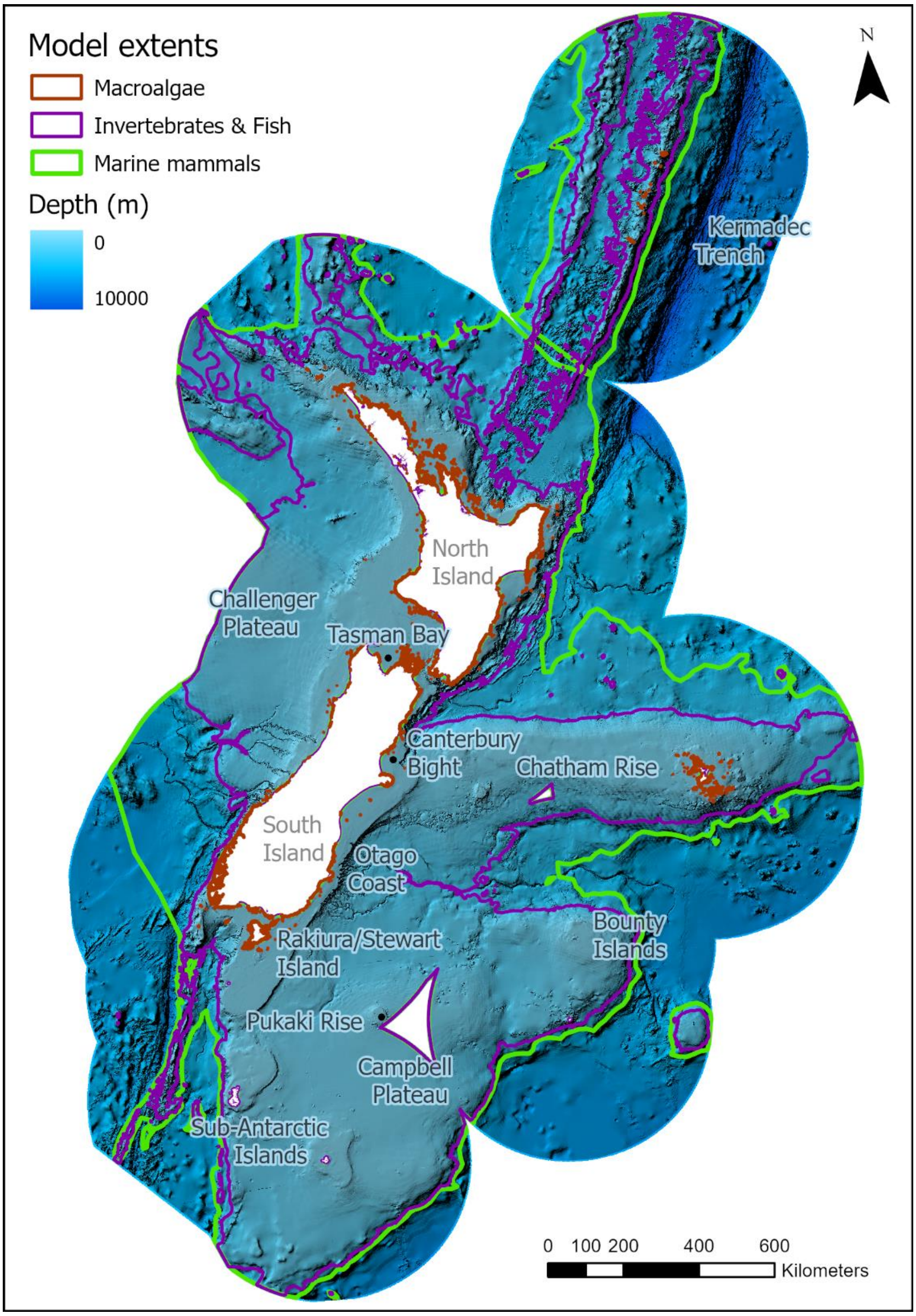

Figure 2-2: **Study area.** New Zealand Exclusive Economic Zone (blue shaded background), with outlines of prediction extents used for the different taxa.

2.4 Expert appraisal

Our framework for the development of expert-informed HSMs adapted an expert-appraisal method developed initially by Stephenson et al. (2023a) for the development of the NZ Atlas of Seafloor Biodiversity and utilised for additional biodiversity mapping projects for NZ government agencies (Bennion et al. 2023; Bennion et al. 2024b). In addition to the review of the model inputs discussed above, experts also appraised the key outputs from the HSMs, i.e., the importance of the environmental drivers of distribution and the spatial predictions of species distribution. Experts were provided with detailed instructions to guide their appraisal and a set of criteria by which to score their knowledge of species ecology, the accuracy of occurrence data and the model outputs (Appendix A).

The evaluation of environmental drivers was used to determine how well the models approximated experts' understanding of the environmental forces that shape species distribution and was based on the relative importance scores generated for each ensemble prediction. Scoring criteria ranged from 1 (environmental drivers closely matched experts understanding of species' niche) to 4 (environmental drivers do not match experts' understanding of species' niche). These scores can be used to identify where there may be issues with the model spatial predictions and can be used to troubleshoot models with spurious predictions (Appendix A).

Experts provided critical appraisal of the accuracy of spatial predictions for species present-day distribution, based on the alignment between the prediction and experts' view of where the species are currently distributed in NZ waters. Scoring criteria ranged from 1 - very accurate (predicted distribution reflects expert view, >80% agreement) to 5 - inaccurate (predicted distribution does not match species experts view, <20% agreement). Due to the known difficulty in appraising the spatial distribution of a continuous variable (i.e., HSI) (Santini et al. 2021), following Stephenson et al. (2023a) this appraisal was based on a binarisation of the present-day spatial prediction using a threshold derived from the receiver operating characteristic (ROC) curve. This threshold determines the HSI value that maximises the sensitivity (true positive rate) and sensitivity (true negative rate) (i.e., max TSS) and allows each prediction to be classified into areas where a species has the greatest probability of being present. MaxTSS is one of the most widely used and accurate thresholds for binarising predictions from HSMs (Liu et al. 2013), though see discussion for considerations around thresholding approaches.

Predictions for the four future scenarios were not appraised using specific scoring criteria due to the fact that species future distributions are largely unknown and are subject to a range of conditions that are likely outside of the knowledge base of species experts. For example, species experts cannot be expected to have a detailed understanding of the biophysical changes experienced by marine habitats throughout NZ waters and under the various climate change scenarios. However, it was still considered relevant to provide experts with the opportunity to comment of future distributions and thus a final expert-appraisal field was supplied that allowed experts to provide insight on these future scenarios. Experts were asked to comment on how feasible the predictions seem, and if there were certain locations/species where experts expected greater or reduced change in distributional patterns. It is expected that these comments will provide useful insight for future users of these spatial layers and may encourage further refinement of the predictions where necessary.

2.5 Determining climate change impacts on distribution

The impact of climate change on species distribution patterns was summarised using several approaches that allow quantification and visualisation of how species occurrence may change under the four future scenarios compared with their present-day distribution. There are a range of decision-points associated with these approaches (see section 4.2), with the foremost being decisions around how best to represent 'where' a species is distributed within predictions of continuous HSI (i.e., to identify a threshold above which the species is likely to occur).

A significant amount of research has focussed on reviewing thresholding approaches for determining climate change impacts on distribution (Liu et al. 2013; Muscatello et al. 2021; Hellegers et al. 2025a), with some studies arguing that thresholding results in a loss of information that undermines accurate predictions (Guillera-Arroita et al. 2015; Santini et al. 2021). However, some thresholding is required to quantify absolute changes in distribution and the most recent studies argue for the calculation of multiple thresholds that can be adapted to suit the spatial planning needs of managers (Hellegers et al. 2025). Thus, following the approach of Hellegers et al. (2025) and using the ensemble model for each species, we calculate four data-driven thresholds and have made these available with the continuous predictions of HSI for each species. In addition, we utilised a 'fixed HSI' threshold of 0.75[2] to represent areas of core (or important) habitat for each species following Westmeijer et al. (2019); Stephenson et al. (2023b); Musimwa et al. (2025). The fixed threshold for core habitat is used to approximate areas where habitat quality is high (i.e., not just where species are likely to occur). In this study, the representation of the impacts of climate change on species distributions utilised the fixed HSI threshold to quantify changes in distributions. However, see section 4.3 for discussion around caveats to this approach.

For each species group (Table 2-1) we generated the following outputs:

- Maps showing the distribution of core habitat (HSI > 0.75) for the present-day and alongside maps for the four future scenarios for each species.
- Graphical representation of the percent change in extent (in km^2) of core habitat between the present day and the four future scenarios. This calculation summarises the extent of range contraction/expansion for each species. The total area (in km^2) of a species present-day core area is overlaid upon these figures to indicate species with more restricted present-day distributions which is an important consideration when appraising vulnerability climate change.
- Graphical representation of the percent overlap between present day distributions and the four future scenarios. This calculation describes the degree to which present-day core areas remain core areas under the future scenarios, which can be independent from the percentage change in extent. For example, a species with predicted range expansion (i.e., increase in core area extent) may show both high (i.e., expands from a base that remains occupied) or low (i.e., full range shift) overlap with existing core habitat areas.

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[2] MaxTSS thresholds were used to represent core habitat for the macroalgae HSMs given the distribution of HSI values in present-day and future predictions meant that a large amount of information was being lost by applying the 0.75 HSI threshold (i.e., most HSI values were <0.75 in spatial predictions). This artifact was also present in present-day predictions developed by Stephenson et al. (2023a) and it likely due to clipped predictions to the arbitrary 'rocky reef' layer (Figure 2-1).

- Calculation and mapping of potential refugia following definitions by Zelli et al. (2025) including: 1) *Internal refugia* – areas of present-day core habitat that remain core habitat in the future, 2) *External refugia* – areas of future core habitat that are not considered core habitat in the present-day distribution (i.e., range expansion), 3) *Areas of range contraction* – areas of present day core habitat that are not considered core habitat in the future. These calculations were based on the most extreme future scenario – end of the century under SSP3-7.0 (see section 4.2).

2.6 Considering impacts of non-climate related stressors

Climate-smart MSP does not consider the impacts of climate change in isolation, and recognises the importance of successfully managing existing non-climate related stressors for improving ecosystem resilience (Queirós et al. 2021; Frazão Santos et al. 2024). To this end, using the outputs generated by the HSMs described in this study, we demonstrate simple analysis routines that can be used to identify species with heightened vulnerability to climate change impacts, given their exposure to existing stressors that may compromise resilience. These approaches form the basis of recommendations to DOC for the future use of the outputs generated by this study. The analyses are based on the overlap of species predicted distribution with areas currently impacted by stressors, which lower their resilience to climate change impacts. Here, 'currently impacted' areas are where the intensity of particular stressors is sufficiently high to compromise the suitability of habitats (also known as the stressor-response footprint).

The key inputs for the analyses are:

- Spatially explicit predictions of habitat suitability index for the species/group of interest for the present day and under future scenarios.
- Spatially explicit layers representing the intensity of stressors (or a proxy thereof) with known impacts on the species/group.
- Information on species responses to the stressor that can be used to calculate a 'stressor response footprint' (Low et al. 2023). This footprint is a spatial representation of the area over which the stressor is likely to negatively impact the species/group. See section 4.3 for situations when this information is not available which may be the case for poorly studied species/groups.

The steps to this analysis include:

1. Create a layer representing the 'stressor response footprint' by thresholding the spatially explicit stressor layer to represent areas where stressor intensity is likely to have a negative impact on species. This involves determining a cut-off value for stressor intensity above which raster cell values are set to 1 and below which cell values are set to 0 (i.e., binarisation). The cut-off value should be determined based on studies (e.g., published literature) on species responses across a gradient of stressor intensity.
2. Predicted species present-day and future distributions layers should be binarised (e.g., by the fixed HSI threshold for 'core' distribution).
3. Intersect layers for binary (0-1) species present-day and future core distributions with the stressor response layer. Sum the total area contained within the intersecting area

and calculate the percentage of a species distribution that overlaps the stressor response footprint. Species with higher overlap can be considered more vulnerable to non-climate related stressors.

4. Undertake the same intersection analysis to calculate the percentage overlap of *refugia* and the stressor response footprint, which could include internal refugia, external refugia or both.

5. Map the overlap of stressor response footprint and areas of importance for the species (e.g., core areas/refugia) to provide a spatial representation of areas where management intervention may be required to reduce existing stressors and build climate resilience.

We demonstrate the approach with two species-groups with well-known impacts from non-climate related stressors, biogenic habitat-forming benthic invertebrates and threatened/at risk macroalgae. For the invertebrates, we use a spatially explicit representation of the distribution and intensity of bottom contact fishing, recently updated by Rowden et al. (2024). The stressor layer represents the mean swept area ratio (MeanSAR) – an estimate of the ratio between uncontacted and contacted (i.e., swept) seafloor habitat in each 1 x 1 km grid cell (Rowden et al. 2024). Many studies have demonstrated the negative relationship between bottom-contact fishing intensity and seafloor biodiversity (Lambert et al. 2017). In this study, we used information generated by González-Irusta et al. (2018) that determined even relatively low levels of trawling intensity ($SAR < 0.2$) can have a negative impact on the biomass of sensitive species, such as biogenic habitat-forming invertebrates. Thus, we used a cutoff value of for MeanSAR of 0.2 to determine a stressor response layer for these species.

For threatened/at risk macroalgae, the effect of suspended sediments and other particulate matter on the attenuation of light is a significant stressor (Tait et al. 2021; Thoral et al. 2023). There are few studies demonstrating clear links between marine macroalgae and easily mapped footprints for suspended particulates (e.g., remotely sensed data products). However recent work in NZ has shown that kelp forests below a critical light level of 1.0 mol m^{-2} day^{-1} have compromised ecological resilience, this is likely a useful threshold for the management of stressors affecting water clarity (e.g., sedimentation) (Tait 2019). Thus in this study, we use spatially explicit mean estimate of light availability at the seafloor (EBED), which considers both the depth of the seafloor, photosynthetically active radiation at the surface and downwelling light attenuation (KPAR) that accounts for absorption due to suspended particulate material (Thoral et al. 2023). EBED values below 1.0 mol m^{-2} day^{-1} were used as a cutoff for to characterise a generalised stressor response footprint for macroalgae using and EBED layer at 250 m x 250 m resolution (Stephenson et al. 2022a).

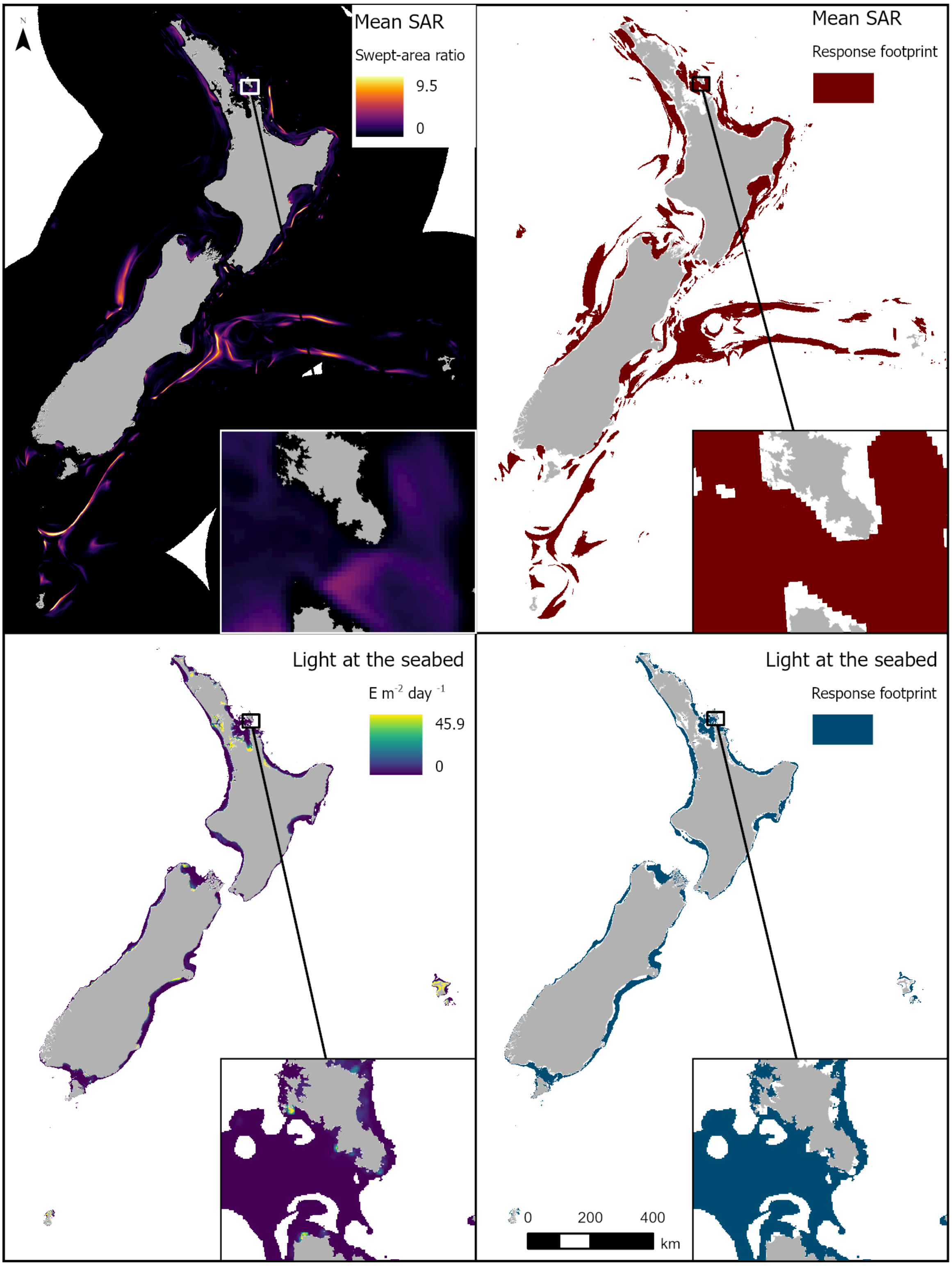

Figure 2-3: Stressors and response footprints. Top row: Mean swept-area ratio of trawling (left) and corresponding response footprint (right) of all cells > 0.2. Bottom row: Light at the seabed (left) and corresponding response footprint (right) of all cells < 1.0 mol m^{-2} day$^{-1.}$

2.7 Comparison with ‘automated’ approach

To determine the utility of utilising an ‘automated’ approach to generating HSMs for forecasting future species distribution, we compared the results generated by this study (i.e., using the expert-informed framework) with those generated by Anderson (2022). The outputs of each study were compared at the level of individual species for three taxonomic groups (fish, sponges, and kelps) using two approaches:

- For each species and for each study, we calculated the percentage change in aerial extent (in km^2) of core areas (HSI > 0.75) between predictions for the present day and for 2090 under SSP3-7.0. The percentage change in core area calculated from each study was plotted by species to visualise the variation in this key metric used to demonstrate vulnerability to climate change between the studies. The total area of present-day core habitat for each species, by study, was plotted alongside this to determine if any of the variability between studies stemmed from predictions for the present day.
- The distribution of core habitat (HSI > 0.75) for each species at the end of the century and under SSP3-7.0 was mapped for each species (Appendix B), with colour coding used to indicate where the predictions from both studies agreed (overlapping core area), or where core area was predicted from a single study only.

Together, these two approaches provide useful information on the compatibility of the approaches and may shed light on the utility of using an automated approach for forecasting species future distributions.

3 Results

3.1 Species distribution under climate change scenarios

The following sections summarise the outputs of HSMs to predict species future distribution and to characterise species vulnerability to climate change. Each section contains the key outputs listed in Section 2.3 and a summary of the key results for each species group (Table 3-1).

Maps for the spatial distribution of species for the present day and for the four future scenarios are provided in each section. However, it was not possible to generate large, high-resolution maps for the 70+ species covered in this study which would enable detailed visualisation of fine-scale changes in distribution. To provide users with the opportunity to interrogate these results at fine scale, spatial layers for the distribution of each species for the present day and the four future scenarios have been uploaded to DOC's Marine Data Portal[3] and are available for viewing and download.

3.1.1 Coastal fish

HSMs for coastal fish all performed well, with AUC score above 0.9 and TSS scores above 0.6 for all species – indicating 'excellent' model performance (Table 3-1). The species with the lowest performance was red cod (mean BRT AUC = 0.877) and the highest performing model was generated for snapper (mean RF AUC = 0.988). Standard deviation around the model fit metrics was uniformly low for each HSM indicating consistent high model performance. Spatial cross validation scores for the ensemble prediction indicated model performance was generally high across all bioregions where a species was found. Models for some species (e.g., gurnard, pilchard, red cod) showed variability in predictive performance across bioregions, however all cross-validation scores (AUC) were above thresholds for adequate performance (AUC > 0.7).

Table 3-1: Model evaluation - coastal fish. Summary of model performance for HSMs used to predict future distribution of coastal fish. Mean AUC/TSS scores along with their standard deviation were generated across the 100 bootstrap iterations for each species and for each BRT and RF model. Spatial cross validation scores (minimum and maximum AUC across bioregions) for the ensemble prediction are also provided. AUC > 0.7 and TSS > 0.6 indicate good predictive performance.

Species	RF AUC (SD)	RF TSS (SD)	BRT AUC (SD)	BRT TSS (SD)	ENS spatial CV (AUC min/max)
Blue cod	0.975 (0.003)	0.837 (0.012)	0.971 (0.003)	0.827 (0.012)	0.97/0.99
Gurnard	0.959 (0.003)	0.813 (0.008)	0.95 (0.004)	0.807 (0.008)	0.805/0.997
Kahawai	0.944 (0.009)	0.801 (0.022)	0.942 (0.009)	0.792 (0.022)	0.899/0.999
Kingfish	0.935 (0.012)	0.769 (0.031)	0.93 (0.013)	0.774 (0.03)	0.949/0.943
Pilchard	0.954 (0.012)	0.826 (0.035)	0.952 (0.013)	0.825 (0.032)	0.779/0.947
Red cod	0.891 (0.004)	0.629 (0.009)	0.877 (0.005)	0.616 (0.012)	0.751/0.936
Snapper	0.988 (0.002)	0.911 (0.007)	0.987 (0.002)	0.91 (0.007)	0.911/0.988
Tarakihi	0.914 (0.004)	0.699 (0.01)	0.896 (0.006)	0.681 (0.011)	0.819/0.983

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[3] https://doc-marine-data-deptconservation.hub.arcgis.com/

Expert appraisal for coastal fish provided useful insight into the accuracy of the inputs and outputs of the HSMs for coastal fish (Table 3-2). Experts ranked their own knowledge as very high (1, for snapper), low (4, for pilchard) and moderate (3) for all other species.

The accuracy of the species occurrence data was accurate (2) or very accurate (1) for all species except hapuku (somewhat accurate, 3). The experts had difficulty in appraising the environmental drivers of the HSMs for three species (kahawai, kingfish, pilchard) given their lower knowledge base for these species. The contribution of the environmental variables to the HSMs were listed as 'somewhat accurate (3)' for all other species except blue cod and red cod. Experts found species present-day distribution to be 'very accurate' (1) or 'accurate' (2) for all coastal fish. See Appendix B for the full expert review including commentary of the future predictions.

Table 3-2: Expert appraisal - coastal fish. Summary of expert appraisal of the inputs (occurrence records) and outputs (environmental drivers, present-day distribution) of HSMs for coastal fish. Scores range for 1 (highest) to 5 (lowest) - see Appendix A for scoring criteria and Appendix B for the full review including commentary on future predictions. For some species, experts were unable to provide accurate appraisal of the environmental drivers (-).

Species	Assessment of expert knowledge	Accuracy of occurrence records	Environmental drivers	Accuracy of predicted present-day distribution
Blue cod	3	2	2	2
Gurnard	3	1	3	1
Kahawai	3	2	-	2
Kingfish	3	1	-	1
Pilchard	4	1	-	2
Red cod	3	1	2	2
Snapper	1	1	3	1
Tarakihi	3	1	3	1

Across all coastal fish, twenty environmental variables contributed to the HSMs, including six 'forecastable' dynamic variables derived from the NZ ESM (Table 3-3). However, for any given species, between eight and twelve non-correlated variables were used to predict distribution. The environmental variables contributing to each species HSM varied across species, but there were consistently high contributions (between 31.8% and 52.5% importance) from bathymetry for all species except snapper. Seawater temperature at the seafloor (Bottom_Temp) was highly correlated with bathymetry but was a better predictor of snapper distribution and thus was retained in the snapper model only, contributing 61.3%. Along with Bottom_Temp (for snapper), sea surface temperature (SST) was typically the most important forecastable (ESM-derived) variable indicating SST is responsible for most changes in future fish distribution. However, other ESM-derived variables also made meaningful contributions for some species including vertically integrated productivity (TPP3), mixed layer depth (MLD) and temperature residual (TempRes) for snapper and measures of current velocity at the surface (Velo_surface) or at the seafloor (Velo_bottom). Horizontal gradient in SST made small contributions to pelagic species including kahawai, kingfish and pilchard. Static (non-ESM) variables of importance including swell exposure at the seafloor (BedDist), turbidity (BBP443) and slope of the seafloor (Slope).

There were substantial differences among both coastal and deepwater fish species with respect to changes in distribution between the present day and four future scenarios. As expected, changes in both percent change and overlap in core habitat were more pronounced for the most extreme future scenario (2090 under SSP3-7.0) compared to 2050 under SSP2-4.5 (Figure 3-1). A contraction in the extent of core habitat was predicted for ten species, with the largest contractions exhibited under the most extreme future scenario (2090 under SSP3-7.0). Blue cod, hake, hapuku and southern blue whiting exhibited the largest decrease in core habitat under all future scenarios (between 35 and 55% reduction under SSP3-7.0). Along with bluenose, blue cod and hapuku occupy a relatively small extent of core habitat, and thus these species may be particularly vulnerable to climate change impacts. Five species were predicted to increase the extent of core habitat, with gurnard, kingfish and snapper exhibiting the greatest increases (up to 28, 42 and 27% under SSP3, respectively). The spatial overlap of core habitat largely mirrored changes in extent, with reduced overlap for those species showing larger decreases in extent. However, for species predicted to experience an increase in core habitats, some species (e.g., snapper) retained relatively high (~80%) overlap in core areas, while others (e.g., kingfish) had less overlap (~60%).

Table 3-3: Environmental variable importance - coastal fish. Relative importance scores (RIS) for the twenty predictor variables retained for the development of habitat suitability models for coastal. The values represent the percentage contribution of each predictor to the ensemble model prediction for each species. Variables available to forecast future conditions (ESM variables) are noted. Variable names and abbreviations are listed in Table 2-2. Green shading is used to distinguish the variable with the highest contribution (dark green) and the lowest contribution (white), with colour between the highest and lowest contributions being established based on linear interpolation based on the relative position of a variable between the highest and lowest contributor.

	ESM variable	BCO	GUR	KAH	KIN	PIL	RCO	SNA	TAR
Bathy		43.10	45.18	44.26	31.80	38.90	42.09	0.00	52.50
BedDist		7.53	19.74	9.54	12.84	7.52	7.69	6.98	12.13
Bottom_Temp	✓	0.00	0.00	0.00	0.00	0.00	0.00	61.34	0.00
BPI_broad		0.00	0.00	0.00	0.00	0.00	3.62	0.00	0.00
BPI_fine		1.64	0.00	0.00	1.98	0.00	2.98	1.23	2.71
Chl-a.Grad		0.00	0.00	5.19	4.45	4.78	0.00	0.00	0.00
Ebed		0.00	9.91	0.00	0.00	0.00	0.00	0.00	0.00
Gravel		5.67	0.00	0.00	0.00	0.00	4.32	0.00	3.59
MLD		0.00	0.00	0.00	0.00	0.00	0.00	4.34	0.00
Mud		2.60	2.64	0.00	0.00	0.00	5.22	0.00	0.00
Rough		4.90	7.48	0.00	0.00	0.00	0.00	0.00	0.00
Slope		0.00	0.00	0.00	3.74	4.43	5.26	3.05	5.92
SST	✓	9.40	5.92	14.21	27.39	19.51	5.10	0.00	5.42
SSTGrad		0.00	0.00	2.30	2.38	2.54	0.00	0.00	0.00
TC		3.31	0.00	0.00	1.91	0.00	0.00	1.19	0.00
TempRes	✓	4.48	0.00	0.00	0.00	0.00	6.20	13.07	0.00
TPP3	✓	5.94	5.75	3.71	3.07	5.46	6.84	4.25	5.58
Velo_bottom	✓	4.32	3.38	0.00	0.00	0.00	4.63	1.15	4.24
Velo_surface	✓	0.00	0.00	3.55	4.06	3.76	0.00	0.00	0.00
BBP443		7.09	0.00	17.25	6.39	13.11	6.05	3.39	7.89

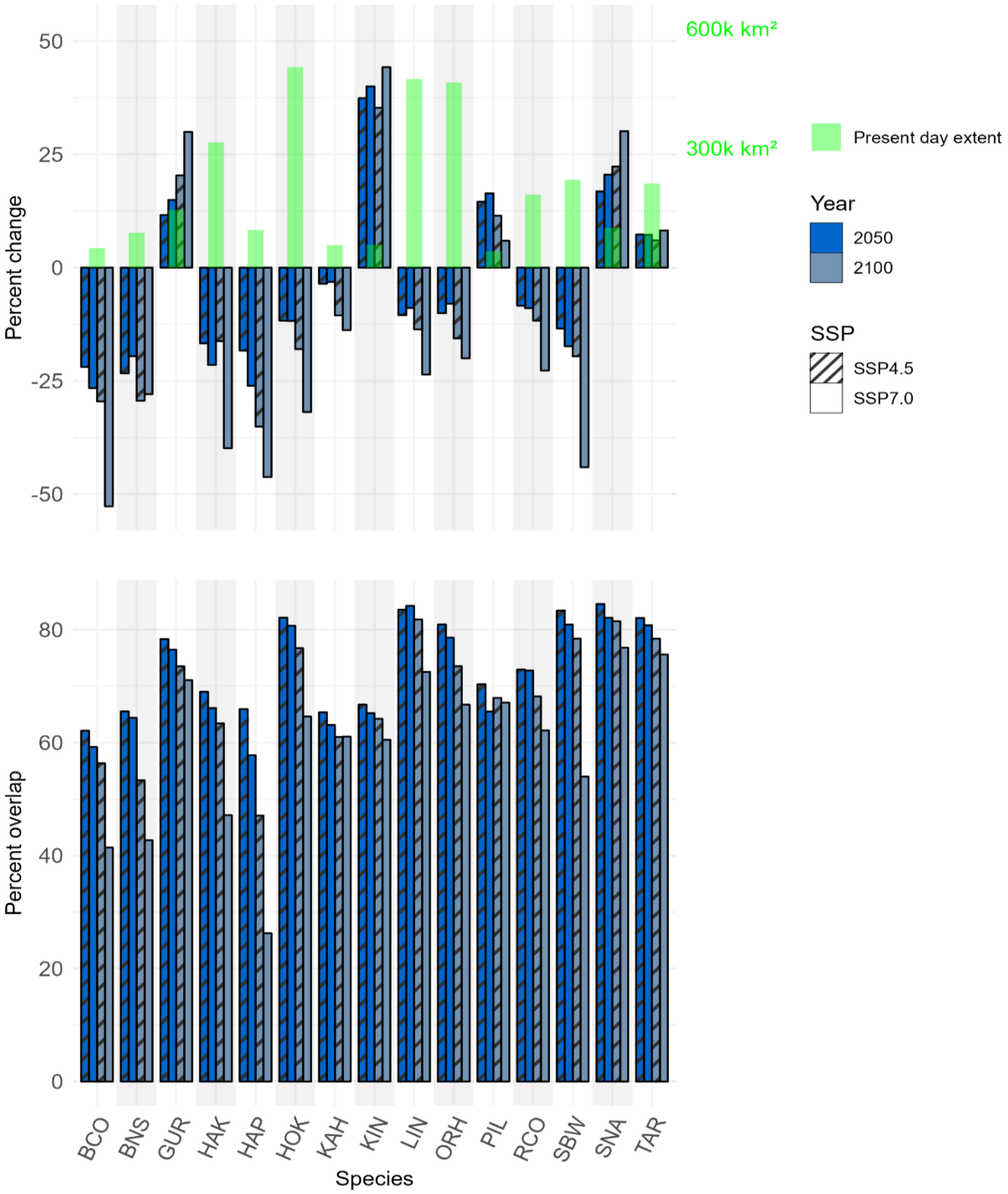

Figure 3-1: Change in core habitat - all fish. Graphical representation of the spatial overlap (bottom) and percentage change (top) in the extent of core habitat (HSI > 0.75) between the present day and the four future scenarios. The total extent of core habitat for the present day is overlaid on the top panel to indicate species with more restricted present-day range. Species codes are blue cod (BCO), bluenose (BNS), gurnard (GUR), hapuku (HAP), hoki (HOK), kahawai (KAH), kingfish (KIN), ling (LIN), orange roughy (ORH), pilchard (PIL), red cod (RCO), southern blue whiting (SBW), snapper (SNA) and tarakihi (TAH).

Spatial predictions of the distribution of core habitat for the present day and under future climate scenarios revealed some significant changes for some coastal fish (Table 3-2). Core habitat for blue cod was predicted to contract to the south and south-east of the South Island/Rakiura in all future scenarios (Figure 3-2). The extent of core habitat for kahawai was predicted to expand, particularly in the offshore extent in the South Island and contract in the North Island. Core habitat for kingfish was predicted to increase significantly in the South Island and in the Chatham Islands under all future scenarios and a similar effect was predicted for pilchard. Snapper was predicted to have increased extent of core habitat in the north and west of the South Island and core habitat for red cod was predicted to decrease on the east coast of the North Island and to become patchier around the South Island (Figure 3-2).

The distribution of potential refugia for coastal fish shows areas that will remain (internal refugia) and may become (external refugia/range expansion) important for each species under the most extreme future scenario (2090 – SSP3) and provides visualisation of areas where species may experience range contraction. Snapper, kingfish and pilchard all show broad areas of external refugia in the South Island that is representative of range expansion of these more northern species. As identified in Figure 3-4, core habitat for blue cod is predicted to contract from most areas under SSP3 by 2090, with the remaining internal refugia being present in the south of the South Island and around Stewart Island. Blue cod show limited external refugia apart from a narrow band of habitat south of Stewart Island. Gurnard exhibit broad areas of internal refugia with some range contraction in the south-east of the South Island and external refugia off Taranaki and the west coast of the South Island. Internal refugia for pilchard, kingfish and kahawai are located mostly in the North Island with external refugia in the South, with kahawai exhibiting range contraction in the northern North Island. Tarakihi are predicted to experience range contraction in Tasman/Golden Bay and in discrete areas around the both the North and South Islands with external refugia mainly in the south of the South Island and on the Chatham Rise. Snapper showed limited range contraction throughout core habitat, while red cod experienced contraction throughout both the North and South Island with key internal refugia being located on the Chatham Rise, west coast of the South Island, Canterbury Bight and around the sub-Antarctic Islands.

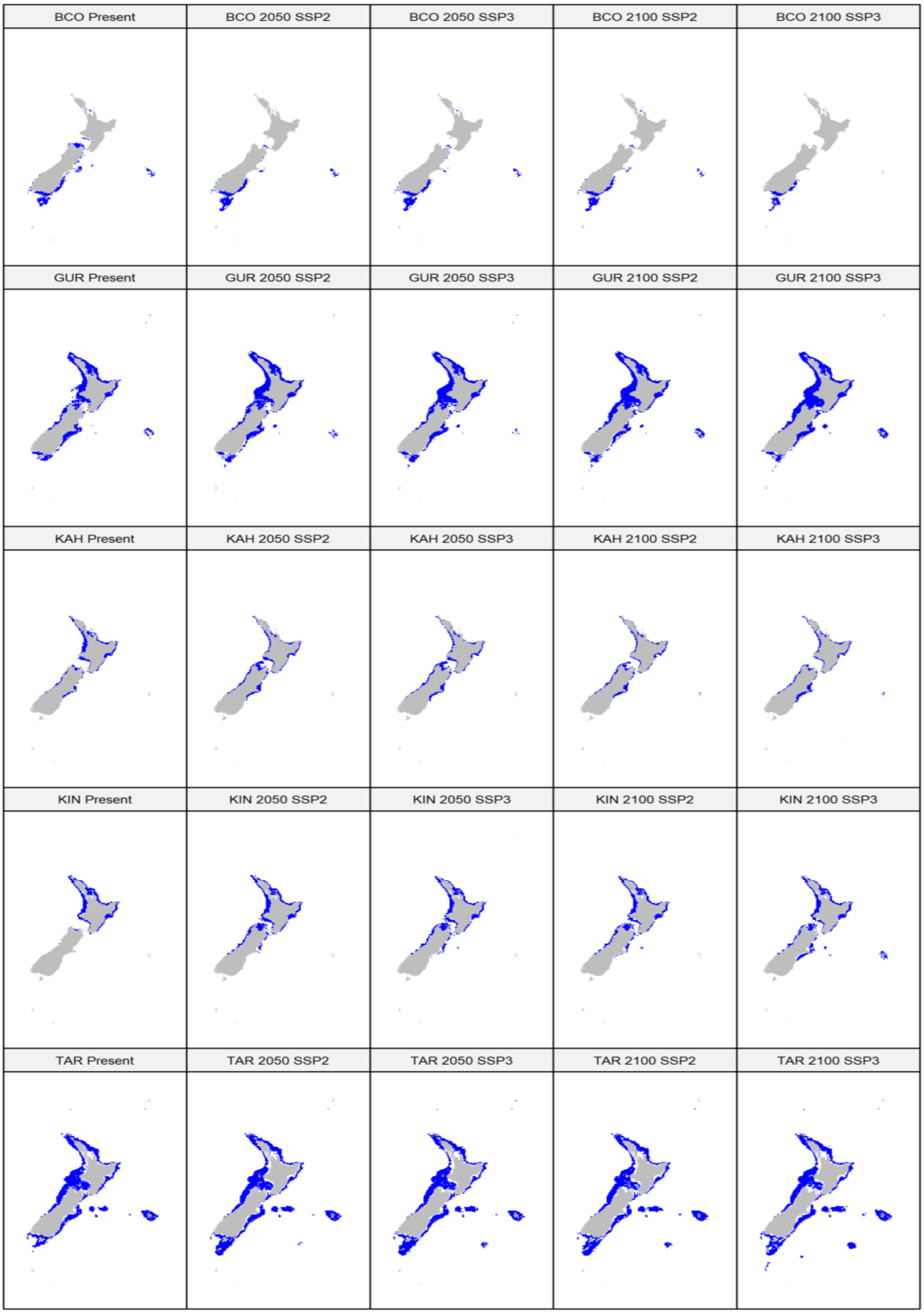

Figure 3-2: Core habitat distribution - coastal fish. The predicted distribution of core habitat (HSI > 0.75) for coastal fish species for the present day (left) and four future scenarios; mid-century (2050) and end-of century (2090) under SSP2 and SSP3 emissions scenarios. Species are blue cod (BCO), gurnard (GUR), kahawai (KAH), kingfish (KIN), pilchard (PIL), snapper (SNA), red cod (RCO), tarakihi (TAR). Figure continued on next page.

Figure 3-3: Core habitat distribution - coastal fish (cont.). The predicted distribution of core habitat (HSI > 0.75) for coastal fish species for the present day (left) and four future scenarios; mid-century (2050) and end-of century (2090) under SSP2 and SSP3 emissions scenarios. Species are blue cod (BCO), gurnard (GUR), kahawai (KAH), kingfish (KIN), pilchard (PIL), snapper (SNA), red cod (RCO), tarakihi (TAR).

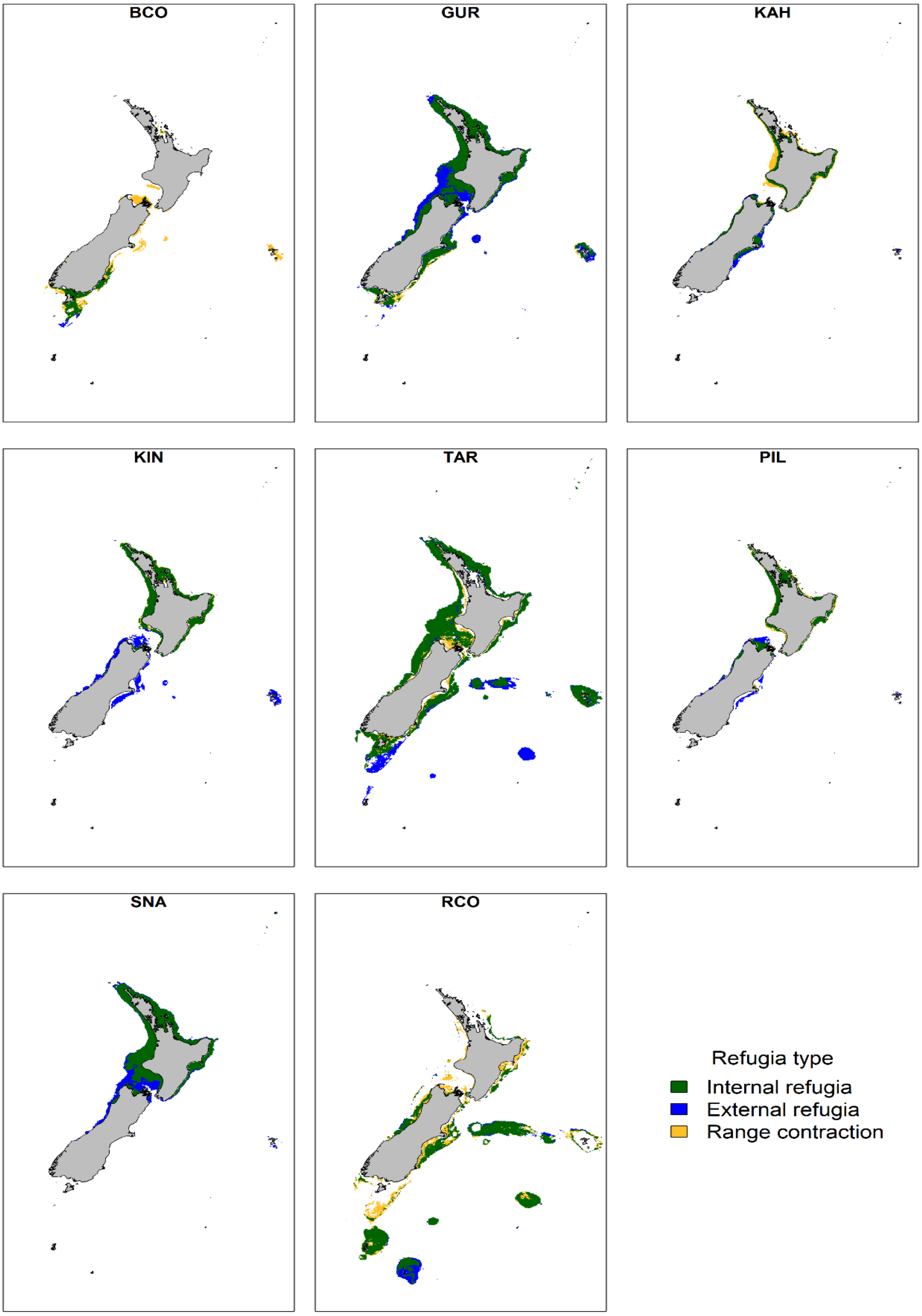

Figure 3-4: Potential refugia (SSP3) - coastal fish. The distribution of two types of potential climate refugia for coastal fish. Internal refugia are areas considered core habitat (HSI > 0.75) in both present day and the most extreme future scenario (2090, SSP3-7.0). External refugia (i.e., range expansion) are areas considered core habitat in the future but not for the present day. Areas showing range contraction (present day core habitat that is not considered core habitat in the future) are also shown. Species are blue cod (BCO), gurnard (GUR), kahawai (KAH), kingfish (KIN), pilchard (PIL), snapper (SNA), red cod (RCO), and tarakihi (TAR).

3.1.2 Deepwater fish

HSMs for deepwater fish all performed well, with AUC score above 0.9 and TSS scores above 0.6 for all species (except hake) – indicating 'excellent' model performance Table 3-4). The species with the lowest performance was hake (mean BRT AUC = 0.864 and the highest performing model was generated for orange roughy (mean RF AUC = 0.992) with all AUC values well above the standard for acceptable performance (AUC = 0.7). Standard deviation around the model fit metrics was uniformly low for each HSM indicating consistent high model performance. Spatial cross validation scores for the ensemble predictions indicated model performance was high across all bioregions where a species is found, with some variability among bioregions for hake, hoki, and hapuku.

Table 3-4: Model evaluation - deepwater fish. Summary of model performance for HSMs used to predict future distribution of coastal fish. Mean AUC/TSS scores along with their standard deviation were generated across the 100 bootstrap iterations for each species and for each BRT and RF model. Spatial cross validation scores (minimum and maximum AUC across bioregions) for the ensemble predictions are also provided AUC > 0.7 and TSS > 0.6 indicate good predictive performance.

Species	RF AUC (SD)	RF TSS (SD)	BRT AUC (SD)	BRT TSS (SD)	ENS spatial CV (AUC min/max)
Bluenose	0.923 (0.011)	0.736 (0.023)	0.917 (0.01)	0.727 (0.026)	0.921/0.956
Hake	0.873 (0.004)	0.597 (0.009)	0.864 (0.005)	0.59 (0.01)	0.872/0.965
Hapuku	0.927 (0.006)	0.723 (0.016)	0.922 (0.006)	0.709 (0.016)	0.923/0.999
Hoki	0.931 (0.002)	0.71 (0.005)	0.931 (0.002)	0.715 (0.005)	0.870/0.949
Ling	0.915 (0.002)	0.672 (0.005)	0.914 (0.002)	0.671 (0.007)	0.928/0.987
Orange roughy	0.992 (0.001)	0.933 (0.004)	0.99 (0.001)	0.933 (0.004)	0.991/0.994
Southern blue whiting	0.984 (0.002)	0.884 (0.011)	0.981 (0.003)	0.871 (0.011)	0.982/0.988

Expert appraisal for deepwater fish provided useful insight into the accuracy of the inputs and outputs of the HSMs for these species (Table 3-5). Experts ranked their own knowledge as high (2), for all species except bluenose and hake for which experts considered they had a moderate (3) level of knowledge. The accuracy of the species occurrence data was very accurate (1) or accurate (2) for all species except orange roughy (somewhat accurate, 3). The contribution of the environmental variables to the HSMs were listed as 'accurate (2)' for all bluenose, hake and hoki, very accurate (1) for ling and southern blue whiting and somewhat accurate (3) for orange roughy. Experts found species present-day distribution to be 'very accurate' (1) or 'accurate' (2) for all deepwater fish species. See Appendix B for the full expert review including commentary of the future predictions.

Table 3-5: Expert appraisal - deepwater fish. Summary of expert appraisal of the inputs (occurrence records) and outputs (environmental drivers, present-day distribution) of HSMs for deepwater fish. Scores range for 1 (highest) to 5 (lowest) - see Appendix A for scoring criteria and Appendix B for the full review including commentary on future predictions.

Species	Assessment of expert knowledge	Accuracy of occurrence records	Environmental drivers	Accuracy of predicted present-day distribution
Bluenose	3	1	2	1
Hake	3	2	2	2
Hapuku	3	3	3	2
Hoki	2	1	2	1
Ling	2	1	1	1
Orange roughy	2	3	3	1
Southern blue whiting	2	1	1	1

Across all deepwater fish, sixteen environmental variables contributed to the HSMs, including five 'forecastable' dynamic variables derived from the NZ ESM Table 3-6). However, for any given species, between nine and thirteen non-correlated variables were used to predict distribution. The environmental variables contributing to each species HSM varied across species, but there were consistently high contributions (between 30.53 and 67.15% importance) from bathymetry for all species except bluenose and southern blue whiting. Seawater temperature at the seafloor (Bottom_Temp) was highly correlated with bathymetry but was a better predictor of distribution for these two species and thus was retained for these models only, contributing 35.20% and 10.69% respectively. Along with Bottom_Temp, a range of other forecastable (ESM derived) variables were important, with SST being the most important for hapuku and ling, MLD for hake and oxygen concentration at the seafloor (OXY_bottom) making important contributions to orange roughy, bluenose and hake. Vertically integrated productivity (TPP3) was the most important predictor for southern blue whiting and made moderate contributions to most other species. In addition to bathymetry, other static variables that ranked highly for some species included metrics for terrain complexity (BPI), light at the seafloor (EBED) and slope (for bluenose only).

Table 3-6: Environmental importance - deepwater fish. Relative importance scores (RIS) for the sixteen predictor variables retained for the development of habitat suitability models for deepwater fish. The values represent the percentage contribution of each predictor to the ensemble model prediction for each species. Variables available to forecast future conditions (ESM variables) are noted. Variable names and abbreviations are listed in Table 2-2. Green shading is used to distinguish the variable with the highest contribution (dark green) and the lowest contribution (white), with colour between the highest and lowest contributions being established based on linear interpolation based on the relative position of a variable between the highest and lowest contributor.

	ESM variable	BNS	HAK	HAP	HOK	LIN	ORH	SBW
Bathy		0.00	30.53	52.37	50.93	40.84	67.15	0.00
Bottom_Temp	✓	35.20	0.00	0.00	0.00	0.00	0.00	10.69
BPI_broad		4.13	9.62	0.00	5.22	4.67	1.70	1.75
BPI_fine		3.64	6.75	3.30	4.19	4.02	0.91	1.97
Ebed		11.44	3.63	0.00	5.67	10.90	0.00	0.00
Gravel		2.31	0.00	3.76	0.00	0.00	1.96	0.00
MLD	✓	5.18	13.18	0.00	6.63	6.89	0.00	9.17
Mud		0.00	0.00	3.86	0.00	0.00	1.78	0.00
OXY_bottom	✓	10.18	8.78	0.00	6.49	6.38	9.72	6.22
Sand		2.88	0.00	0.00	0.00	0.00	0.00	0.00
Slope		11.52	0.00	3.76	0.00	0.00	3.10	0.00
SST	✓	0.00	0.00	17.44	6.03	8.28	3.79	0.00
TC		0.00	0.00	5.46	0.00	0.00	0.00	0.00
TempRes	✓	5.03	10.82	0.00	5.45	7.68	2.20	20.10
TPP3	✓	4.39	9.39	6.59	5.57	6.07	6.44	48.50
Velo_bottom	✓	4.10	7.30	3.46	3.83	4.27	1.24	1.59

Spatial predictions of the distribution of core habitat for the present day and under future climate scenarios revealed changes for some deepwater fish (Figure 3-5). Present-day core habitat for bluenose was predicted to occur in shelf-break habitat throughout NZ waters north of Stewart Island and this remained consistent in future scenarios except for decreases off the Otago coast and on the Challenger Plateau. Core habitat for hapuku was predicted to undergo the most significant change of the deepwater species, with a strong contraction to areas in the south of the South Island and the sub-Antarctic. The distribution of core habitat also contracted for hoki and ling under all future scenarios, with key habitat being lost around the North Island and of the west coast of the South Island in the most extreme future scenario (2090 under SSP3-7.0). Similarly, orange roughy core habitat around the North Island was significantly reduced in each future scenario along with areas of the south-east coast of the South Island. Southern blue whiting was predicted to experience a reduction and fragmentation of core sub-Antarctic habitat with increasing severity of future scenarios.

Potential refugia and areas of range contraction of core habitat for deepwater fish were broadly distributed in NZ waters (Figure 3-7). Internal refugia for bluenose occurred in deeper shelf break habitat around the North Island and northern slopes of the Chatham Rise, with some external refugia on the southern Chatham Rise and south-west of Stewart Island. For hake, internal refugia were interspersed with areas of range contraction on the Chatham Rise and on the Cambell Plateau. Hapuku exhibited significant range contraction of core habitat with remaining internal refugia on in the south-east of the South Island and some external refugia around Auckland and Bounty Islands and the Pukaki Rise. Internal refugia for ling and hoki occurred broadly on the Chatham Rise and Campbell Plateau, with range contractions exhibited around the North Island an off the west coast of the South Island. Orange roughy showed similar range contraction around the North Island and had internal refugia on the slopes of the Chatham Rise and Campbell Plateau and the southern Challenger Plateau. Fragmented internal refugia were evident for southern blue whiting within their existing core habitat on the Campbell Plateau (Figure 3-7).

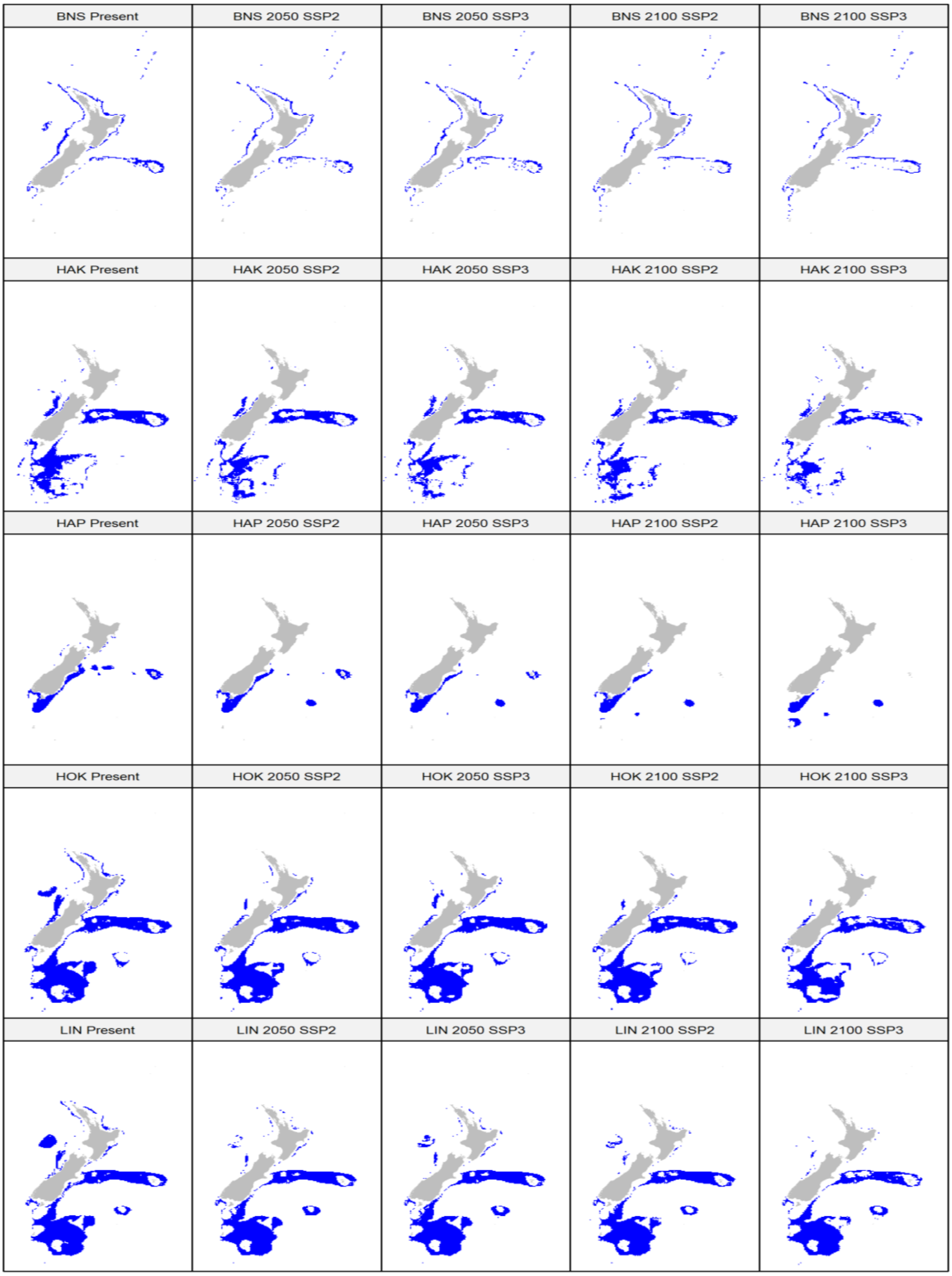

Figure 3-5: Core habitat distribution - deepwater fish. The predicted distribution of core habitat (HSI > 0.75) for deepwater fish species for the present day (left) and four future scenarios; mid-century (2050) and end-of century (2090) under SSP2 and SSP3 emissions scenarios. Species are bluenose (BNS), hake (HAK), hapuku (HAP), hoki (HOK), Ling (LIN), orange roughy (ORH), and southern blue whiting (SBW). Figure continued on the next page.

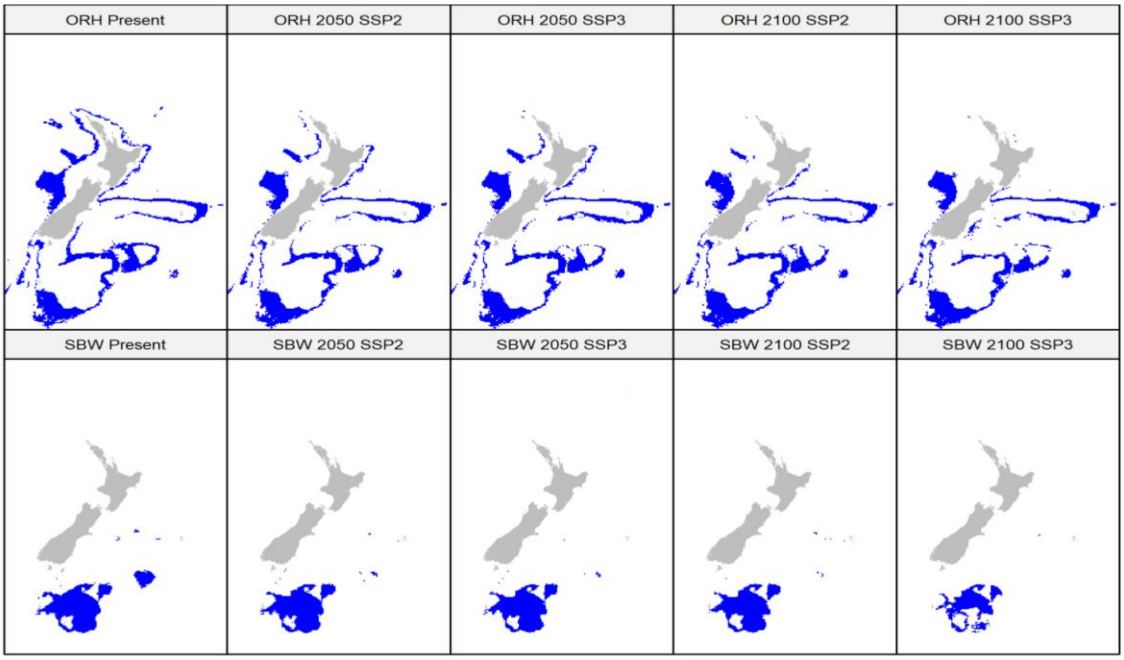

Figure 3-6: Core habitat distribution - deepwater fish (cont.). The predicted distribution of core habitat (HSI > 0.75) for deepwater fish species for the present day (left) and four future scenarios; mid-century (2050) and end-of century (2090) under SSP2 and SSP3 emissions scenarios. Species are bluenose (BNS), hake (HAK), hapuku (HAP), hoki (HOK), Ling (LIN), orange roughy (ORH), and southern blue whiting (SBW).

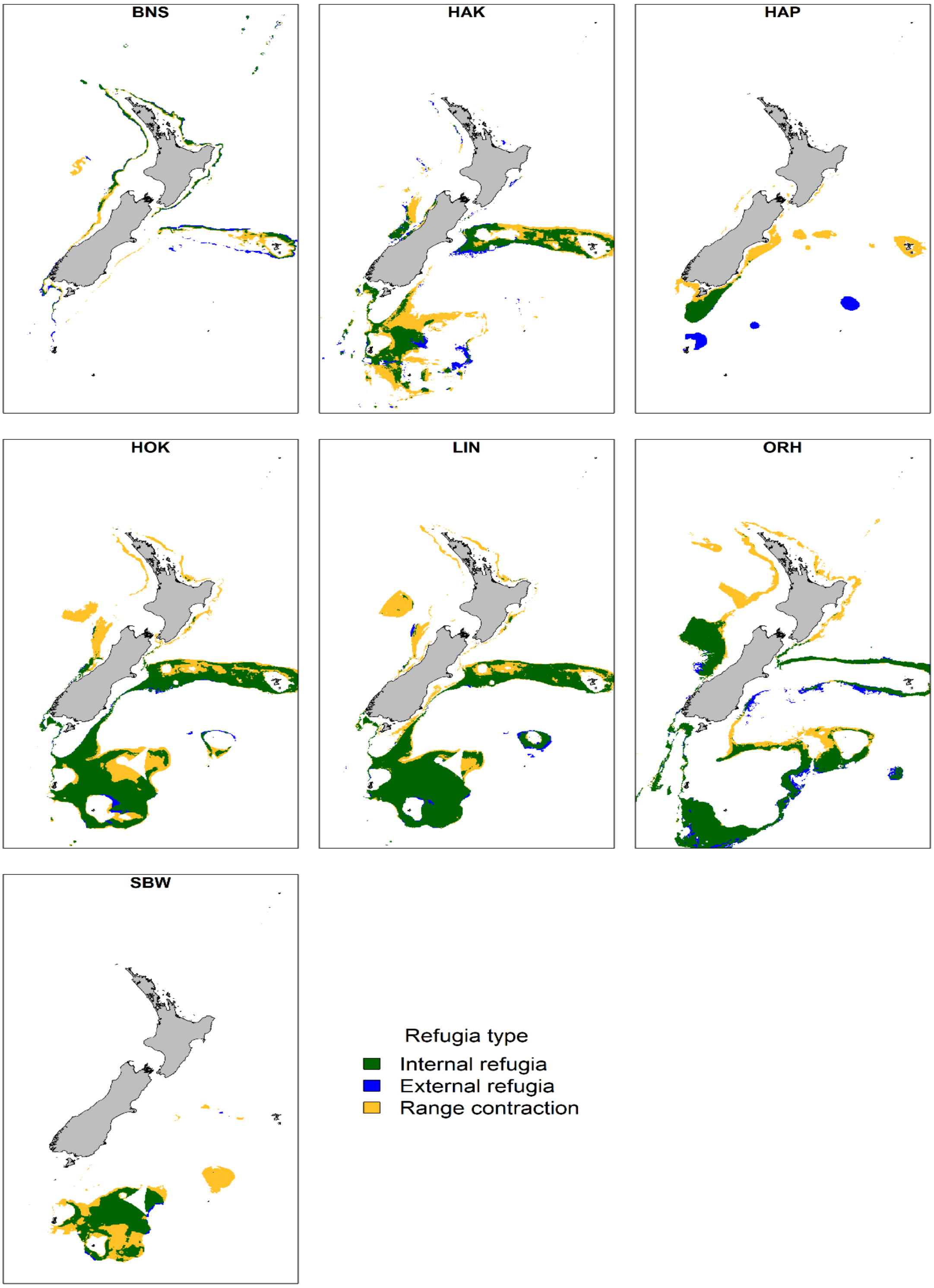

Figure 3-7: Potential refugia (SSP3) - deepwater fish. The distribution of two types of potential climate refugia for coastal fish. Internal refugia are areas considered core habitat (HSI > 0.75) in both present day and the most extreme future scenario (2090 under SSP3-7.0), external refugia (i.e., range expansion) are areas considered core habitat in the future but not for the present day. Areas showing range contraction (present day core habitat that is not considered core habitat in the future) are also shown. Species are bluenose (BNS), hake (HAK), hapuku (HAP), hoki (HOK), Ling (LIN), orange roughy (ORH) and southern blue whiting (SBW).

3.1.3 Benthic invertebrates - Biogenic habitat-forming taxa

HSMs for biogenic invertebrate species all performed moderately well, with AUC scores above 0.8 and TSS scores above 0.6 for most species – indicating ‘good’ model performance overall (Table 3-7). The species with the lowest performance was for *Celleporina* (mean BRT AUC = 0.682) and the highest performing model was generated for *Paragorgia* (mean RF AUC = 0.955) with almost all AUC values well above the standard for acceptable performance (AUC = 0.7), apart for the mean BRT AUC for *Celleporina*. Standard deviation around the model fit metrics was low for most HSM indicating consistent model performance. Model performance for some of the HSMs fluctuated by >~0.1 SD, for example, the models for *Cinctipora elegans* and *Crella incrustans* (Table 3-7). Spatial cross validation scores for the ensemble prediction indicated model performance was generally high across all bioregions (most min AUC >0.7) where each given taxon is found (or where enough occurrence records were available to calculate the AUC metric).

Table 3-7: Model evaluation – biogenic habitat-forming taxa. Summary of model performance for HSMs used to predict future distribution of biogenic habitat-forming taxa. Mean AUC/TSS scores along with their standard deviation were generated across the 100 bootstrap iterations for each species and for each BRT and RF model. Spatial cross validation scores (minimum and maximum AUC across bioregions) for the ensemble prediction are also provided. AUC > 0.7 and TSS > 0.6 indicate good predictive performance.

Taxa	RF AUC (SD)	RF TSS (SD)	BRT AUC (SD)	BRT TSS (SD)	ENS spatial CV (AUC min/max)*
Atrina	0.900 (0.048)	0.730 (0.097)	0.892 (0.052)	0.717 (0.097)	0.727/0.952
Callyspongia spp.	0.770 (0.063)	0.501 (0.103)	0.716 (0.082)	0.418 (0.119)	0.727/0.973
Celleporina spp.	0.713 (0.086)	0.454 (0.122)	0.682 (0.089)	0.411 (0.133)	0.817/0.923
Cinctipora elegans	0.883 (0.092)	0.766 (0.151)	0.860 (0.105)	0.731 (0.160)	0.921/0.944
Crella incrustans	0.847 (0.092)	0.682 (0.152)	0.812 (0.098)	0.629 (0.157)	0.875/1.000
Dactylia spp.	0.871 (0.059)	0.684 (0.113)	0.819 (0.072)	0.603 (0.129)	0.832/0.929
Hornera spp.	0.765 (0.085)	0.513 (0.136)	0.710 (0.093)	0.436 (0.134)	0.780/0.948
Iophon spp.	0.825 (0.061)	0.603 (0.114)	0.816 (0.061)	0.580 (0.106)	0.704/0.904
Jasus edwardsii[4]	0.963 (0.002)	0.829 (0.008)	0.940 (0.002)	0.759 (0.008)	0.919/0.962
Keratoisididae spp.	0.891 (0.033)	0.676 (0.067)	0.886 (0.038)	0.683 (0.073)	0.595/0.915
Ostrea spp.	0.873 (0.046)	0.663 (0.086)	0.859 (0.049)	0.648 (0.086)	0.813/1.000
Paragorgia spp.	0.955 (0.037)	0.854 (0.093)	0.927 (0.061)	0.809 (0.112)	0.925/0.982
Tucetona spp.	0.831 (0.046)	0.576 (0.082)	0.815 (0.051)	0.560 (0.089)	0.768/0.922

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[4] *Jasus edwardsii* was included within the group benthic invertebrate biogenic habitat-forming taxa. Though not a biogenic habitat former, the same biological occurrence datasets were used to develop this set of HSMs. As the only other ‘benthic invertebrate’ section is sponge-specific, this section was deemed the most appropriate location to report results for this HSM.

Expert appraisal for biogenic habitat-forming taxa provided useful insight into the accuracy of the inputs and outputs of the HSMs (Table 3-8). Experts ranked their own knowledge as very high (1, for sponges and bryozoans), low (4-5, for *Tucetona* and *Ostrea*), good (2, for Keratoisididae and *Paragorgia*) and moderate (3) for *Atrina*. The accuracy of the species occurrence data was accurate (2) or very accurate (1) for all species except *Paragorgia* (somewhat accurate, 3). The contribution of the environmental variables to the HSMs were listed as 'somewhat accurate (3)' for most species, while for molluscs the drivers were listed as 'accurate (2)'. Experts found species present-day distribution to be 'very accurate' (1) or 'accurate' (2) for all biogenic habitat-forming taxa (Table 3-8). See Appendix B for the full expert review including commentary of the future predictions.

Table 3-8: Expert appraisal – biogenic habitat-forming taxa. Summary of expert appraisal of the inputs (occurrence records) and outputs (environmental drivers, present-day distribution) of HSMs for biogenic habitat-forming taxa. Scores range for 1 (highest) to 5 (lowest) - see Appendix A for scoring criteria and Appendix B for the full review including commentary on future predictions.

Taxa	Assessment of expert knowledge	Accuracy of occurrence records	Environmental drivers	Accuracy of predicted present-day distribution
Atrina	3	2	2	2
Callyspongia	1-2	1	4	3
Celleporina	1	2	3	2
Cinctipora elegans	1	2	3	2
Crella incrustans	1-2	2-3	3-4	3
Dactylia	1-2	2-3	2	2
Hornera	1	2	3	2
Iophon	1-2	2-3	3-4	3
Jasus edwardsii	2	2	2	2
Keratoisididae	2	2	3	1
Ostrea	5	2	2	2
Paragorgia	2	3	3	2
Tucetona	4	2	2	2

Across all biogenic habitat-forming taxa, twenty-three environmental variables contributed to the HSMs, including twelve dynamic variables derived from the NZ ESM (Table 3-9). For any given species, between nine and eleven non-correlated variables were used to generate HSM predictions. The environmental variables contributing to each species HSM varied across species, but there were consistently moderate-high contributions from OXY bottom (bottom oxygen concentration) for all species. Two other environmental variables were included in for all HSMs: mud (percent mud) and velo bottom (water velocity at the seafloor), with ≥5% importance for each HSM. Bottom oxygen concentration (OXY bottom), bathymetry and swell exposure at the seafloor (BedDist) were some of the most important variables for each HSM. Bottom oxygen represents the most important forecastable (ESM-derived) variable across taxa, indicating it is responsible for most changes in future distribution. However, other ESM-derived variables also made meaningful contributions for some taxa including bottom pH for *Atrina*, bottom nitrate concentration (DIN_bottom) for *Callyspongia,* sea surface radiation (MED QSR) for *Cinctipora elegans* and omega calcite at the seafloor (OM CAL bottom) for *Celleporina*.

Table 3-9: Environmental importance – biogenic habitat-forming taxa. Relative importance scores (RIS) for the twenty-three predictor variables used for the development of habitat suitability models for biogenic habitat-forming taxa. The values represent the percentage contribution of each predictor to the ensemble model prediction for each species. Variables available to forecast future conditions (ESM variables) are noted. Variable names and abbreviations are listed in Table 2-2. Green shading is used to distinguish the variable with the highest contribution (dark green) and the lowest contribution (white), with colour between the highest and lowest contributions being established based on linear interpolation based on the relative position of a variable between the highest and lowest contributor.

	ESM variable	*Atrina*	*Callyspongia*	*Celleporina*	*Cinctipora.elegans*	*Crella.incrustans*	*Dactylia*	*Hornera*	*Iophon*	*Jasus edwardsii*	Keratoisididae	*Ostrea*	*Paragorgia*	*Tucetona*
Bathy		0.00	0.00	0.00	0.00	21.86	0.00	0.00	0.00	0.00	48.04	22.35	37.29	11.00
BedDist		3.96	8.31	0.00	0.00	10.59	24.37	0.00	22.76	39.46	0.00	3.75	0.00	23.59
BEN_SI	✓	0.00	0.00	0.00	0.00	0.00	6.36	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bottom_pH	✓	20.87	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7.44	8.51	12.82	14.33
Bottom_Salt	✓	3.99	8.93	0.00	0.00	8.29	7.07	0.00	14.26	16.39	7.47	7.12	4.90	0.00
Bottom_Temp	✓	15.37	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
BPI_fine		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	14.51	0.00	0.00	0.00	0.00
CHL_MLD		14.45	6.68	7.40	0.00	7.58	0.00	6.46	4.61	0.00	0.00	18.11	0.00	4.45
ChlAGrad		0.00	0.00	13.13	6.47	0.00	0.00	7.27	0.00	0.00	0.00	0.00	0.00	0.00
DIN_bottom	✓	0.00	25.70	0.00	0.00	0.00	16.45	0.00	12.52	0.00	0.00	0.00	0.00	0.00
Gravel		4.81	0.00	8.70	8.83	0.00	0.00	17.90	0.00	0.00	0.00	3.00	0.00	7.54
MED_QSR	✓	0.00	5.67	7.29	20.77	6.13	5.48	8.25	8.42	0.00	0.00	0.00	0.00	0.00
MLD	✓	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7.56	0.00	4.46
Mud		4.82	7.56	7.44	6.66	10.46	4.98	13.90	9.13	0.00	4.79	3.05	4.54	6.45
OM_CAL_bottom	✓	0.00	0.00	19.99	10.39	0.00	0.00	8.49	0.00	0.00	0.00	0.00	0.00	0.00
OXY_bottom	✓	25.13	8.15	11.77	18.20	10.15	6.64	9.51	6.40	8.00	8.88	19.12	5.42	7.68
PB555nm		0.00	12.73	5.98	5.63	8.96	15.30	7.27	9.25	3.95	0.00	0.00	0.00	0.00
Roughness		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.25	6.56	0.00	4.51	0.00
Slope		0.00	7.43	0.00	0.00	7.01	6.52	0.00	4.73	0.00	0.00	0.00	0.00	0.00
SST	✓	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.46	0.00	8.36	8.46
TC		3.13	0.00	11.50	11.33	0.00	0.00	10.01	0.00	0.00	0.00	3.21	0.00	5.77
TPP3_surface	✓	0.00	0.00	0.00	6.65	0.00	0.00	0.00	0.00	3.64	7.89	0.00	17.87	0.00
Velo_bottom	✓	3.47	8.83	6.82	5.06	8.96	6.84	10.95	7.91	7.79	4.47	4.21	4.29	6.25

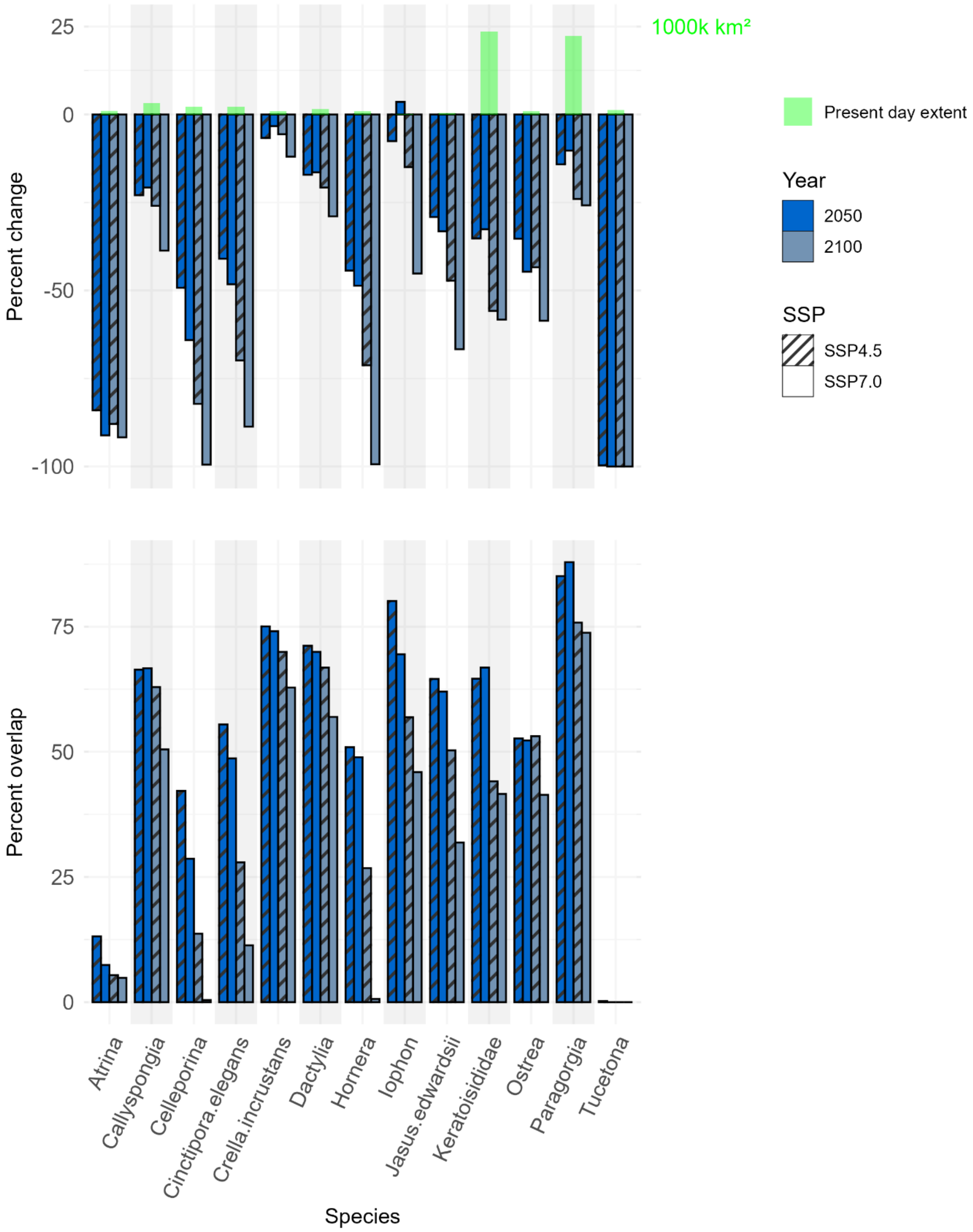

Figure 3-8: Change in core habitat – biogenic habitat-forming taxa. Graphical representation of the spatial overlap (bottom) and percentage change (top) in the extent of core habitat (HSI > 0.75) between the present day and the four future scenarios. The total extent of core habitat for the present day is overlaid on the top panel to indicate species with more restricted present-day range.

There were substantial differences among biogenic habitat-forming taxa in terms of changes in distribution between the present day and four future scenarios. Changes in both percent change in extent and overlap in core habitat were more pronounced for the most extreme future scenario (2090 under SSP3-7.0) compared to 2050 under SSP2-4.5 (Figure 3-8), for most taxa. A contraction in the extent of core habitat was predicted for all taxa, with one exception in the 2050 SSP3-7.0 scenario for *Iophon* (Figure 3-8). *Celleporina*, *Cinctipora elegans*, *Hornera, Atrina* and *Tucetona* exhibited the largest decrease in core habitat under all future scenarios (between 50-100% reduction under SSP3-7.0 for 2090). Most taxa occupy a relatively small core habitat extent, but *Atrina* and *Tucetona* may be particularly vulnerable to climate change impacts given the large decrease in core habitat under all future scenarios and the comparatively small extent of their core habitat. The spatial overlap of core habitat largely mirrored changes in extent, with reduced overlap for those taxa showing larger decreases in extent (particularly for *Atrina* and *Tucetona*).

Spatial predictions of the distribution of core habitat for the present day and under future climate scenarios revealed changes for some biogenic habitat-forming taxa (Figure 3-9 to Figure 3-11). For some taxa, including *Callyspongia*, *Dactylia*, *Crella incrustans*, *Ostrea*, Keratoisididae, and *Paragorgia,* core habitat around the South Island was predicted to remain largely consistent, with decreases in the North. Present-day core habitat for *Atrina* was predicted to occur around the coast of the North and South Islands of NZ, while core habitat was heavily reduced around the North Island in future scenarios, with a comparatively small area in the southeast of the South Island remaining consistent across the future scenarios. Core habitats for *Cinctipora elegans*, *Celleporina*, and *Hornera* were predicted in similar areas, for example, Snares Shelf, Stewart Island, Auckland Islands, Chatham Islands, and Bollon's Seamount (Figure 3-9 to Figure 3-11). The core habitats for these taxa undergo contractions under future scenarios, with strong contraction to areas in the south of the South Island and the sub-Antarctic. Core habitat contraction for *Tucetona* was the most dramatic, with large contractions of core habitat in all future scenarios compared to the present-day prediction of core habitat.

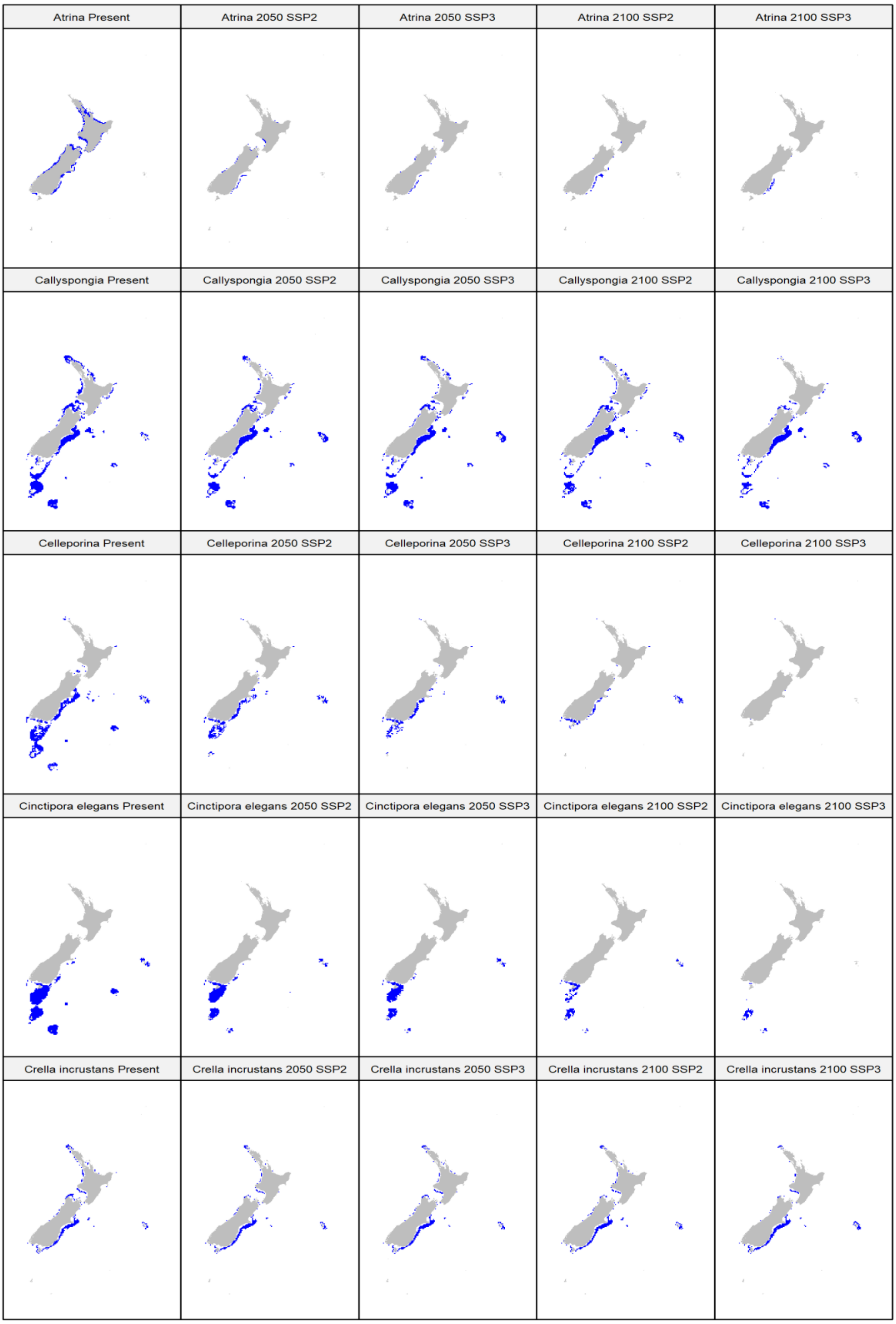

Figure 3-9: Core habitat distribution – biogenic habitat-forming taxa. The predicted distribution of core habitat (HSI > 0.75) for biogenic habitat-forming taxa for the present day (left) and four future scenarios; mid-century (2050) and end-of century (2090) under SSP2-4.5 and SSP3-7.0 emissions scenarios.

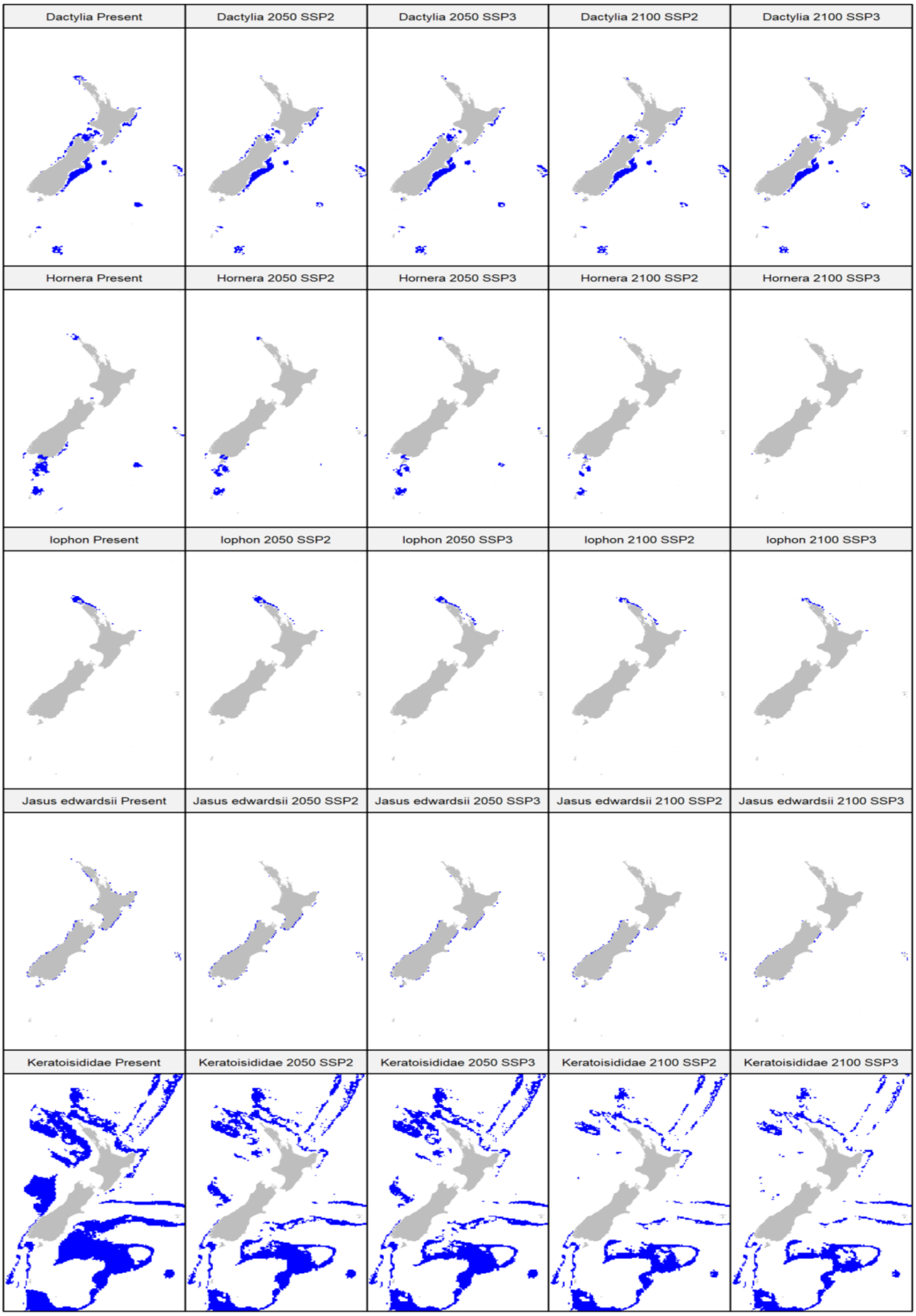

Figure 3-10: Core habitat distribution – biogenic habitat-forming taxa (cont.). The predicted distribution of core habitat (HSI > 0.75) for biogenic habitat-forming taxa for the present day (left) and four future scenarios; mid-century (2050) and end-of century (2090) under SSP2-4.5 and SSP3-7.0 emissions scenarios.

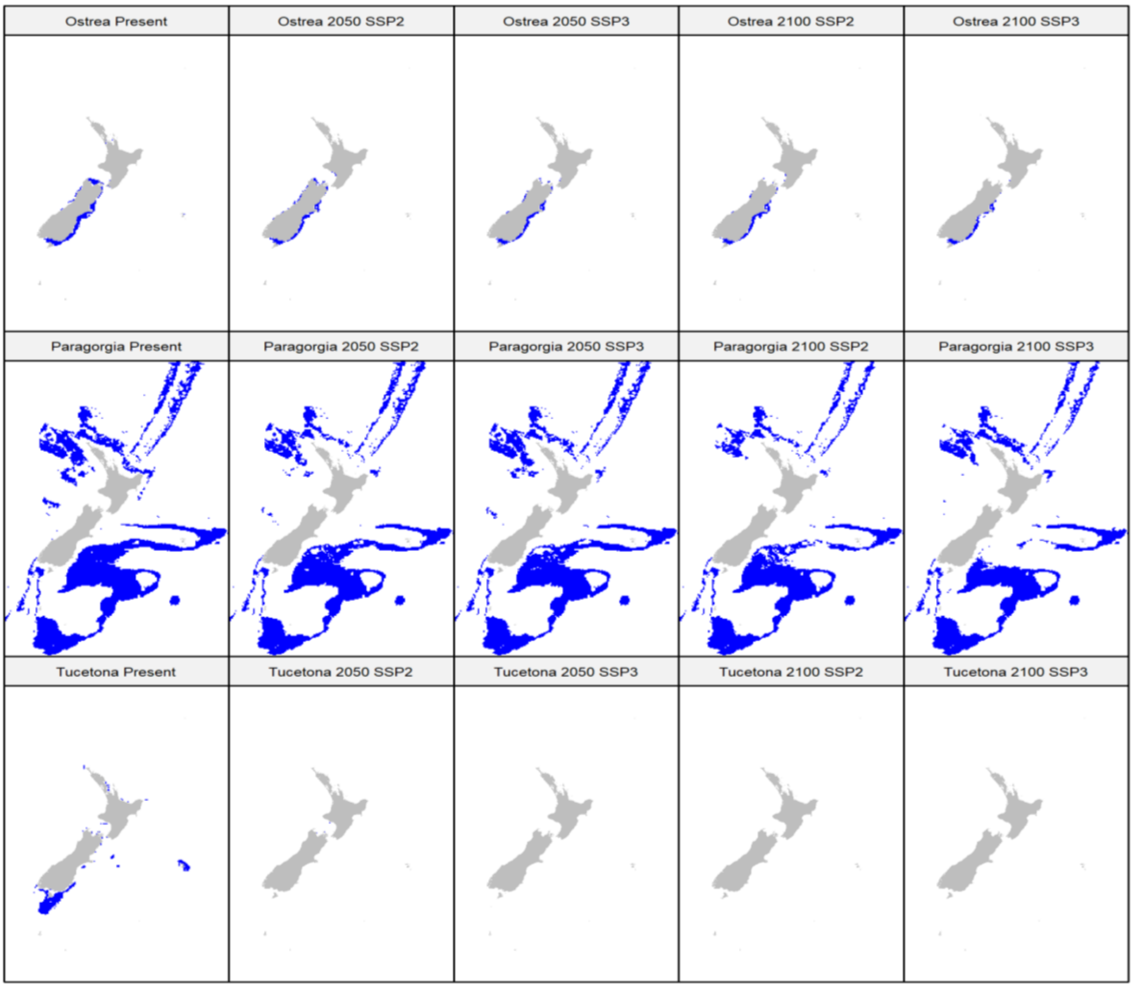

Figure 3-11: Core habitat distribution – biogenic habitat-forming taxa (cont.). The predicted distribution of core habitat (HSI > 0.75) for biogenic habitat-forming taxa for the present day (left) and four future scenarios; mid-century (2050) and end-of century (2090) under SSP2-4.5 and SSP3-7.0 emissions scenarios.

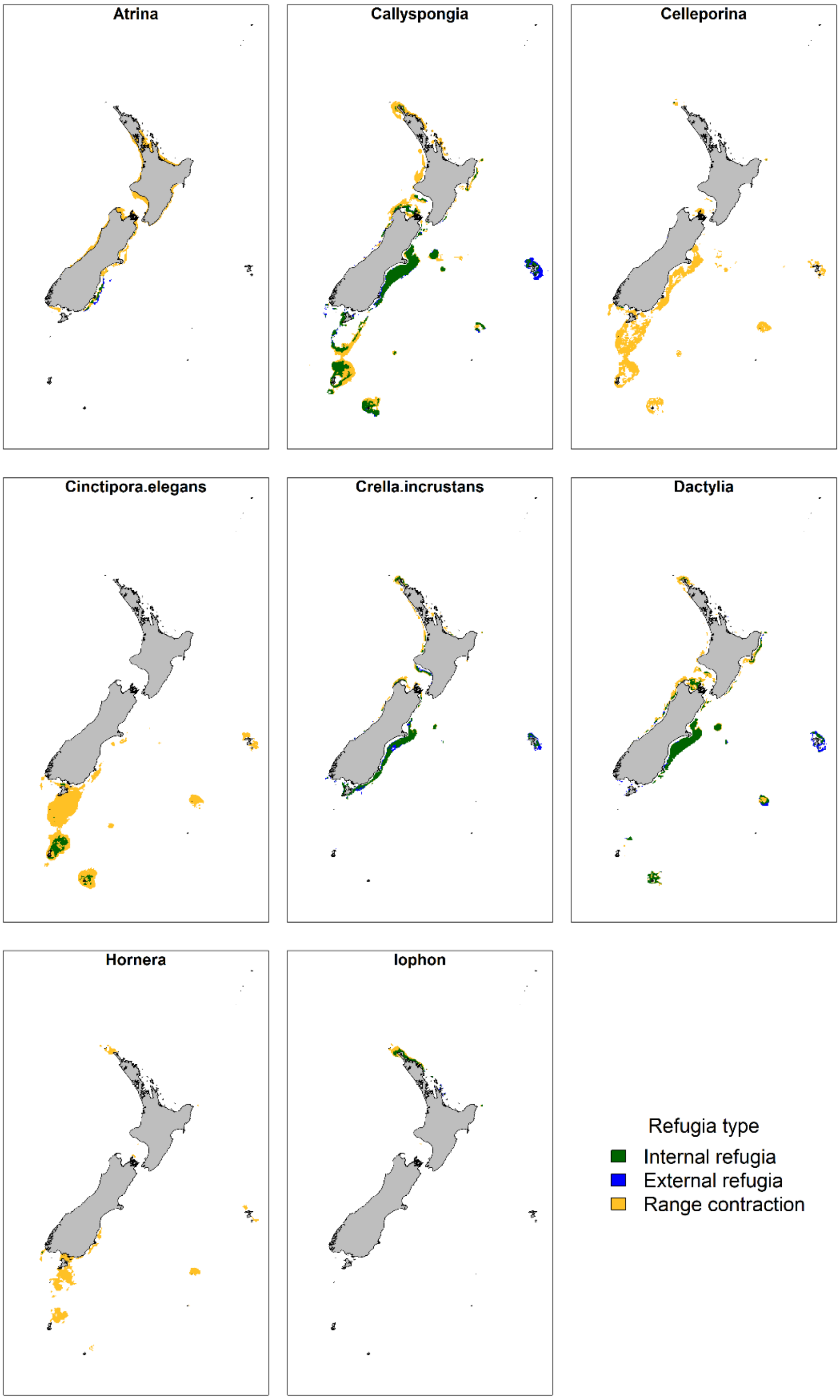

Figure 3-12: Potential refugia (SSP3) – biogenic habitat-forming taxa. The distribution of two types of potential climate refugia for biogenic habitat-forming taxa. Internal refugia are areas considered core habitat (HSI > 0.75) in both present day and the most extreme future scenario (2090, SSP3-7.0). External refugia (i.e., range expansion) are areas considered core habitat in the future but not for the present day. Area's showing range contraction (present day core habitat that is not considered core habitat in the future) are also shown.

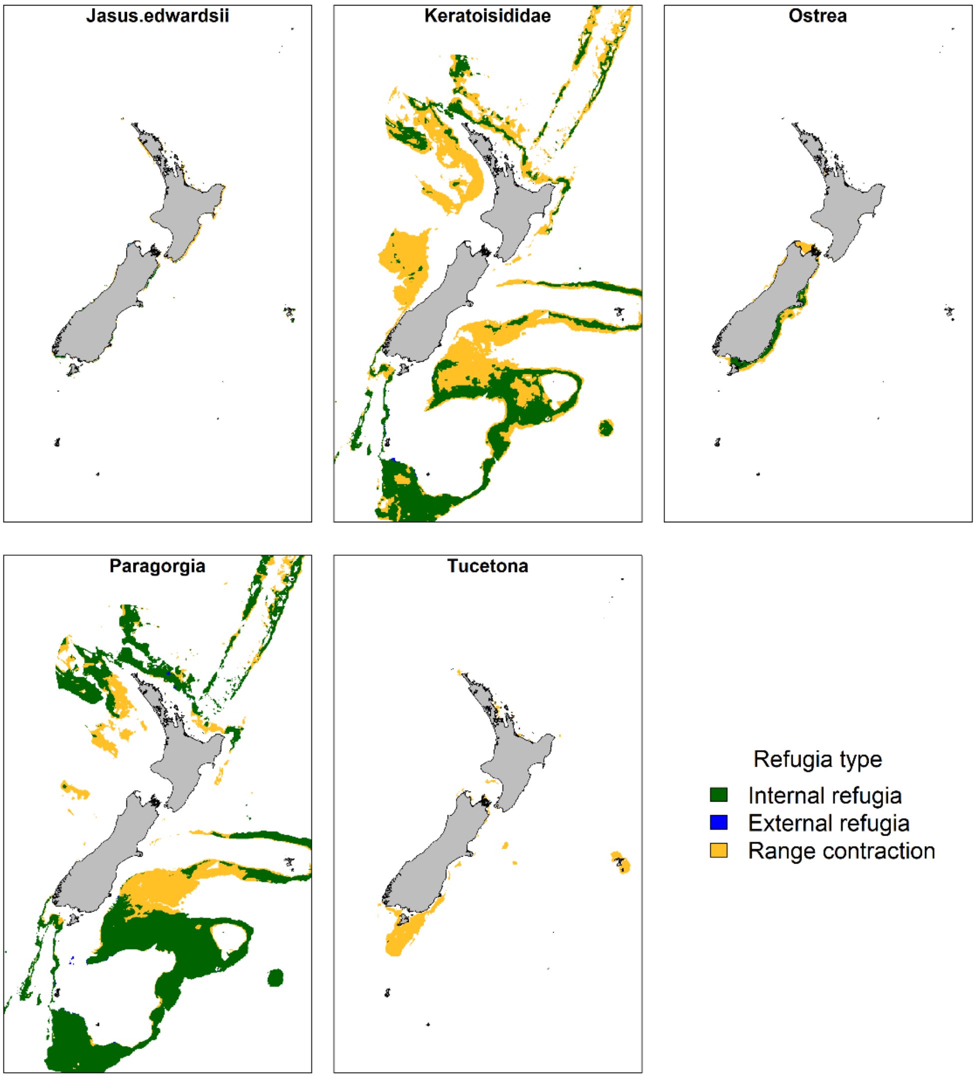

Figure 3-13: Potential refugia (SSP3) – biogenic habitat-forming taxa (cont.).

Potential refugia and areas of range contraction of core habitat for biogenic habitat-forming taxa were broadly distributed throughout NZ waters (Figure 3-12 and Figure 3-13). Internal refugia for *Ostrea*, *Crella incrustans*, *Dactylia*, and *Callyspongia* were distributed in similar areas off the southeast coast of the South Island. In contrast, for Keratoisididae and *Paragorgia*, large slope areas around the Chatham Rise (north and south) and the Campbell Plateau were identified as internal refugia. Relatively few areas of external refugia were identified, however external refugia were present around the Chatham Islands for three sponge taxa, including *Callyspongia*, *Dactylia*, and *Crella incrustans.* Range contractions were evident in many coastal areas of the North Island for *Atrina*, *Callyspongia*, *Dactlyia*, while in the coastal South Island, there were range contractions for *Ostrea*, *Callyspongia*, *Celleporina*, *Cinctipora elegans*, and *Hornera* (with considerable range contraction on Snares Shelf for bryozoan taxa, *Celleporina*, *Cinctipora elegans*, and *Hornera,* in particular). Similarly for *Tucetona*, range contraction was predicted south of the South Island (Snares Shelf) and around the Chatham Islands. Range contraction for Keratoisididae and *Paragorgia* was present in the Bounty Trough, Hokitika Canyon, west of the North Island of New Zealand and along the Kermadec Ridges (Figure 3-12 and Figure 3-13).

3.1.4 Benthic invertebrates - Sponges

HSMs for sponges all performed well, with AUC scores above 0.8 and TSS scores above 0.5 for most taxa – indicating 'moderate' to 'good' model performance (Table 3-10). The HSM with the lowest performance was for *Lissodendoryx* (mean BRT AUC = 0.695) and the highest performing model was generated for *Farrea* (mean BRT AUC = 0.959). Standard deviation around the model fit metrics was, for most HSMs, uniformly low indicating consistent model performance. Exceptions, where SD was ~0.1 or higher, include *Lissodendoryx*, *Haliclona*, and *Poecillastra* for TSS scores. Spatial cross validation scores for the ensemble prediction indicated model performance was generally high across all bioregions (AUC > 0.8) where each given taxa are found (or where enough occurrence records were available).

Table 3-10: Model evaluation – sponges. Summary of model performance for HSMs used to predict future distribution of sponges. Mean AUC/TSS scores along with their standard deviation were generated across the 100 bootstrap iterations for each species and for each BRT and RF model. Spatial cross validation scores (minimum and maximum AUC across bioregions) for the ensemble prediction are also provided. AUC > 0.7 and TSS > 0.6 indicate good predictive performance.

Taxa	RF AUC (SD)	RF TSS (SD)	BRT AUC (SD)	BRT TSS (SD)	ENS spatial CV (AUC min/max)*
Aphrocallistes	0.91 (0.052)	0.74 (0.106)	0.905 (0.059)	0.735 (0.121)	0.972/1.00
Ecionemia	0.9 (0.034)	0.725 (0.067)	0.887 (0.037)	0.69 (0.078)	0.904/1.00
Lissodendoryx	0.732 (0.069)	0.436 (0.107)	0.695 (0.075)	0.395 (0.113)	0.929/1.00
Farrea	0.964 (0.021)	0.868 (0.062)	0.959 (0.023)	0.853 (0.064)	0.985/1.00
Geodia	0.844 (0.042)	0.596 (0.083)	0.818 (0.042)	0.548 (0.08)	0.959/0.98
Haliclona	0.831 (0.073)	0.611 (0.115)	0.774 (0.08)	0.526 (0.119)	0.961/1.00
Hyalascus	0.882 (0.018)	0.646 (0.04)	0.872 (0.02)	0.639 (0.044)	0.856/1.00
Poecillastra	0.834 (0.063)	0.612 (0.107)	0.828 (0.065)	0.592 (0.111)	0.961/1.00
Stelletta	0.862 (0.041)	0.624 (0.078)	0.845 (0.044)	0.597 (0.078)	0.987/0.999
Suberites	0.842 (0.029)	0.588 (0.052)	0.813 (0.033)	0.545 (0.059)	0.932/0.974

Expert appraisal for sponge taxa provided insight into the accuracy of the inputs and outputs of the HSMs (Table 3-11). The sponge expert ranked their own knowledge as very high (1) for almost all taxa, except for *Lissodendoryx* (2, high). For most taxa, the accuracy of the species occurrence data was accurate (2), though for *Haliclona* the accuracy of species occurrence data was somewhat accurate (3). For *Hyalascus,* the distribution of species occurrence data was deemed very accurate (1). For sponge taxa, the expert provided appraisal of both partial dependence of environmental variables, as well as environmental variable drivers. For most sponge HSMs, the contribution of environmental variables to the HSMs were ranked as accurate (2) to somewhat accurate (3). For *Haliclona* the contribution of environmental variables was deemed very accurate (1) to accurate (2), while for *Stelletta* environmental variable partial dependence and contribution was listed as very accurate (1). Five taxa were given a score of very accurate (1) for present-day distributions, while two received a score of accurate (2, *Stelletta* and *Lissodendoryx*) and the rest received a score of accurate or less (3, somewhat accurate). See Appendix B for the full expert review.

Table 3-11: Expert appraisal – sponges. Summary of expert appraisal of the inputs (occurrence records) and outputs (environmental drivers, present-day distribution) of HSMs for sponges. Scores range for 1 (highest) to 5 (lowest) - see Appendix A for scoring criteria and Appendix B for the full review including commentary on future predictions.

Taxa	Assessment of expert knowledge	Accuracy of occurrence records	Environmental drivers*	Accuracy of predicted present-day distribution
Aphrocallistes	1	2	2	3
Ecionemia	1	2	2-3	1
Lissodendoryx	2	2	2-3	2
Farrea	1	2	2-3	1
Geodia	1	2	2-3	1
Haliclona	1	3	1-2	3
Hyalascus	1	1	2	1
Poecillastra	1	2	2-3	2-3
Stelletta	1	2	1	1
Suberites	1	2	2-3	2

**Note: for sponge models, environmental drivers were assessed based on expert appraisal of relative importance of environmental variables used, as well as visual assessment of partial dependence plots.*

Across all sponge taxa, twelve environmental variables contributed to the HSMs, including seven ‘forecastable’ dynamic variables derived from the NZ ESM (Table 3-12). The environmental variables contributing to each species HSM varied across taxa, but there were consistent contributions (13% importance) from Bottom_Temp (seawater temperature at the seafloor) and OXY bottom (oxygen concentration on the seafloor). Along with these variables, silicate concentration at the seafloor (BEN SI) were the three most commonly selected forecastable (ESM-derived) variables indicating that they are likely drivers of change in future distributions. The relative importance of these three variables differed between taxa. For *Ecionemia*, *Farrea* and *Hyalascus*, bottom temperature was the most important variable, whereas silicate concentration at the seafloor was most important for *Lissodendoryx* and *Poecillastra.*

Table 3-12: Environmental importance – sponges. Relative importance scores (RIS) for the twelve predictor variables retained for the development of habitat suitability models for sponge taxa. The values represent the percentage contribution of each predictor to the ensemble model prediction for each species. Variables available to forecast future conditions (ESM variables) are noted. Variable names and abbreviations are listed in Table 2-2. Green shading is used to distinguish the variable with the highest contribution (dark green) and the lowest contribution (white), with colour between the highest and lowest contributions being established based on linear interpolation based on the relative position of a variable between the highest and lowest contributor.

	ESM variable	*Aphrocallistes*	*Ecionemia*	*Farrea*	*Geodia*	*Haliclona*	*Hyalascus*	*Lissodendoryx*	*Poecillastra*	*Stelletta*	*Suberites*
BEN_SI	✓	10.36	9.84	15.17	6.27	9.06	8.54	11.42	14.78	7.01	10.27
Bottom_Salt	✓	14.45	6.64	3	5.16	8.27	10.12	10.84	7.69	5.43	13.03
Bottom_Temp	✓	10.21	21.37	17.65	11.42	10.37	23.06	8.91	12.43	6.76	11.73
epC100	✓	5.1	7.7	3.96	5.65	9.29	4.51	6.4	4.42	7.26	4.95
MED_XZE	✓	4.73	5.16	7.29	5.58	7.11	5.23	8.49	4.82	11.97	6.09
Mud		7.68	8.15	4.3	10.69	7.29	4.48	6.94	7.05	5.31	5.66
OXY_bottom	✓	14.66	18.46	12.79	12.61	7.21	15.89	10.27	8.85	12.44	14.17
PB555nm		5.24	5.19	4.58	12.67	13.44	5.06	6.23	11.25	7.89	6.46
Rough		13.51	4.2	14.65	8.37	9.96	5.09	8.54	12.34	13.8	6.79
Sand		2.69	4.86	3.69	6.04	6.4	3.28	8.22	4.24	5.65	5.39
Slope		9.1	3.06	10.02	7.07	5.77	7.2	5.81	8.69	6.06	6.82
TempRes	✓	2.2	5.3	2.83	8.4	5.76	7.51	7.88	3.38	10.35	8.57

There were substantial differences among sponge taxa with respect to changes in distribution between the present day and two future scenarios (sponge HSMs were predicted for SSP3-7.0 only). As expected, changes in both percent change and overlap in core habitat were more pronounced for the end of century scenario (i.e., 2090) compared to 2050 (Figure 3-14). A contraction in the extent of core habitat was predicted for nine taxa, with the largest contractions exhibited for *Ecionemia*, *Haliclona* and *Lissodendoryx* (between 25 and 75% reduction). Most sponge taxa modelled for this project occupy a relatively small extent of core habitat (with the exception of *Hyalascus* and *Suberites*). Thus, these species may be particularly vulnerable to climate change impacts. Interestingly for *Aphrocallistes*, a small range contraction was predicted for 2050, while a range extension was predicted for 2090 (c. 15% increase). The trend in spatial overlap of core habitat between current and future distributions showed reduced overlap for those species showing larger decreases in extent. However low overlap was also seen for species that were predicted to experience an increase in core habitats (e.g., *Aphrocallistes*, ~40% in 2090).

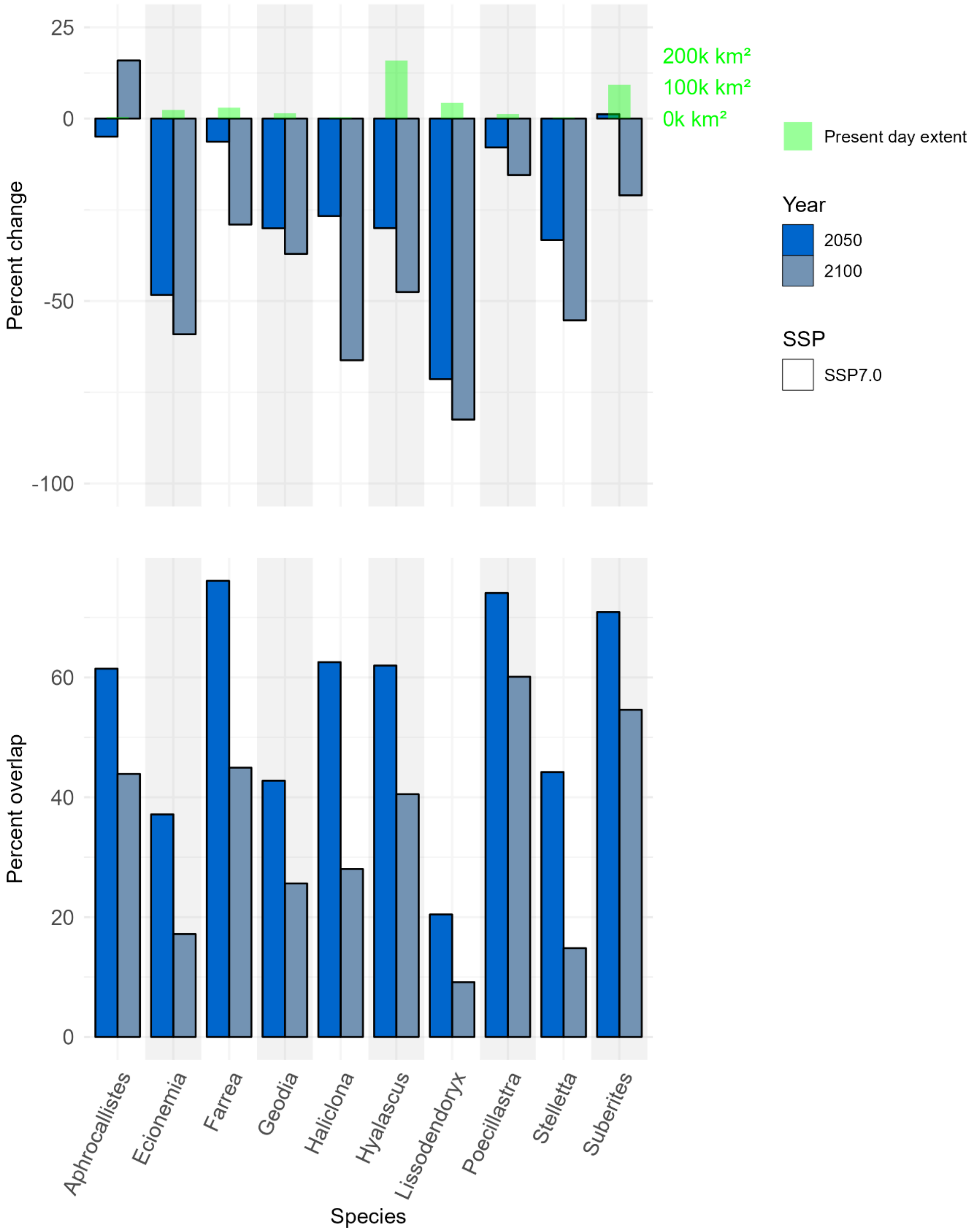

Figure 3-14: Change in core habitat – sponges. Graphical representation of the spatial overlap (bottom) and percentage change (top) in the extent of core habitat (HSI > 0.75) between the present day and the two future scenarios. The total extent of core habitat for the present day is overlaid on the top panel to indicate species with more restricted present-day range. Note only a single SSP scenario (SSP3 7.5) was used in the initial case study of sponge taxa under the NIWA model development.

Figure 3-15: Core habitat distribution – sponges. The predicted distribution of core habitat (HSI > 0.75) for sponge genera for the present day (left) and two future scenarios; mid-century (2050) and end-of century (2090) under SSP3 emissions scenario. Note only a single SSP scenario (SSP3 7.5) was used in the initial case study of sponge taxa under the NIWA model development

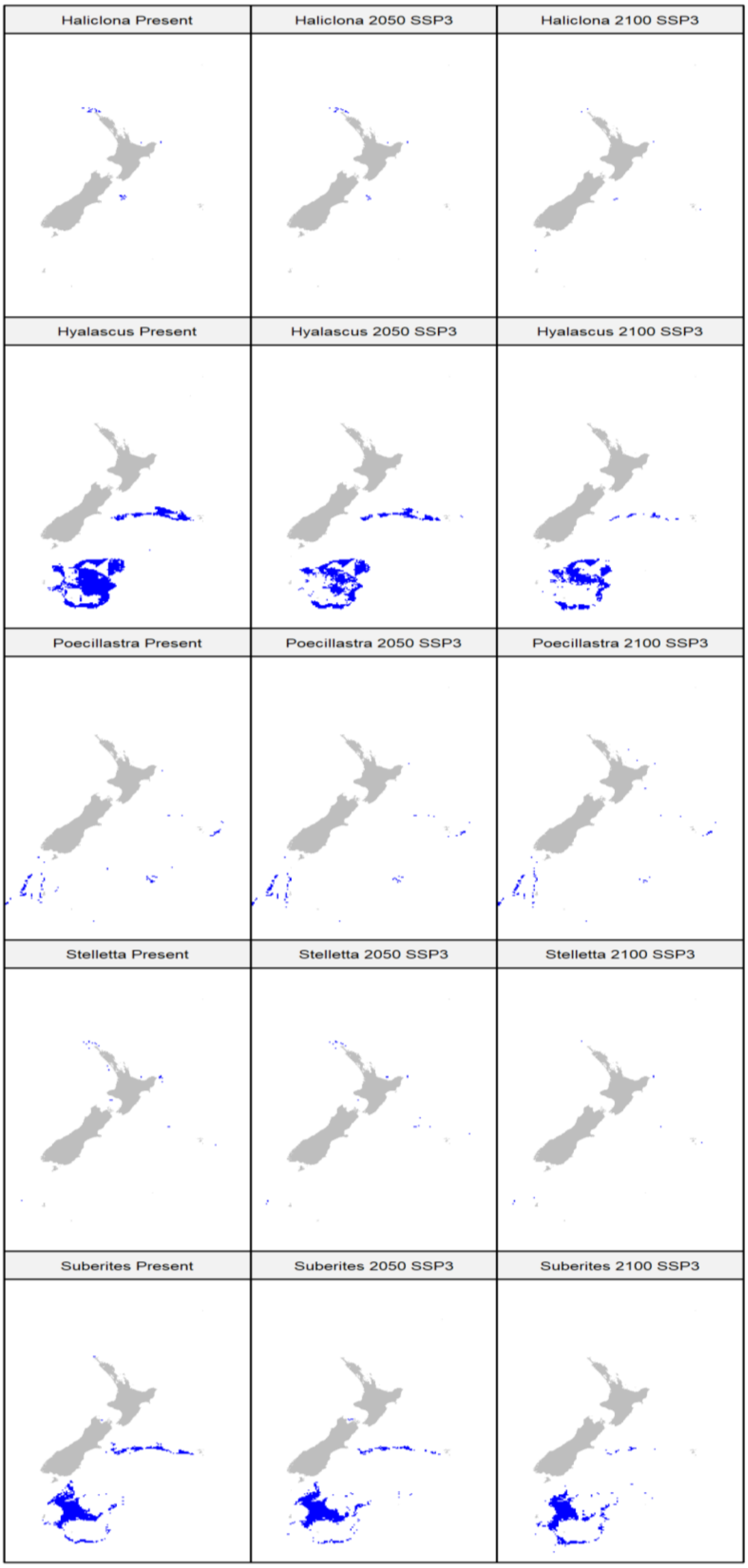

Figure 3-16: Core habitat distribution – sponges (cont.). The predicted distribution of core habitat (HSI > 0.75) for sponge genera for the present day (left) and two future scenarios; mid-century (2050) and end-of century (2090) under SSP3 emissions scenario. Note only a single SSP scenario (SSP3 7.5) was used in the initial case study of sponge taxa under the NIWA model development

Spatial predictions of the distribution of core habitat for the present day and under future climate scenarios revealed changes for some sponge taxa (Figure 3-15 and Figure 3-16). Present-day core habitat for *Ecionemia* was predicted to occur off North Cape, along the central Chatham Rise, and around the Chatham Islands including the Andes Knolls. This spatial pattern remained somewhat consistent across future scenarios, though a decrease in core habitat was predicted along the Chatham Rise, and North Cape core habitat was predicted to be absent in 2090. For *Lissodendoryx*, core habitat was predicted on slopes northeast of the Chatham Rise, and to the south of the Campbell Plateau. In future scenarios these areas remained consistent but with strong contractions on the Campbell Plateau. Present-day predictions for *Geodia* core habitat included small patches around the northern half of the North Island of NZ, and to the south of the South Island (near Puysegur Trench). Large areas of core habitat were predicted on the central Chatham Rise and surrounding Chatham Islands. In future predictions, *Geodia* exhibited contraction of the Chatham Rise core habitat, and loss of core habitat around the North Island. In the 2090 prediction, there was increased core habitat predicted in the Puysegur Trench area to the south of the South Island. Large areas of the Campbell Plateau and northern Chatham Rise were predicted to be core habitat for *Hyalascus*, with some range contraction across the core habitat areas in future scenarios, though their locations remained largely consistent. Present day predictions for *Haliclona, Aphrocallistes* and *Stelletta* were small and patchy. Areas predicted to be core habitat for all three taxa included patches around the North Island and on the Chatham Rise. In future scenarios, *Haliclona* and *Stelletta* were predicted to decrease in core habitat, while for *Aphrocallistes* in 2090, range expansion was predicted to occur in areas to the east of East Cape. For other taxa, including *Farrea*, *Poecillastra* and *Suberites,* changes were less evident under future scenarios.

Potential refugia and areas of range contraction of core habitat for sponge taxa were broadly distributed (Figure 3-17). Internal refugia for *Suberites* and *Hyalascus* were predicted to occur in the southern area of the Campbell Plateau and south Chatham Rise, whereas for *Poecillastra* internal refugia were predicted on the Macquarie Ridge. For *Farrea*, internal refugia were broadly distributed on underwater topographical features to the north and northeast of the North Island. External refugia were predicted for *Hyalascus* and *Suberites* in the middle and south of the Campbell Plateau, respectively, while for *Geodia*, external refugia was predicted in the Puysegur Trench area. For *Farrea* and *Aphrocallistes*, external refugia were predicted to the northeast of the North Island. Range contraction was predicted on the Chatham Rise for *Hyalascus, Suberites, Geodia* and *Ecionemia*. For several taxa (*Lissodendoryx, Hyalascus,* and *Suberites*), significant range contraction was predicted to occur on the Campbell Plateau. Finally, for *Stelletta, Ecionemia* and *Stelletta*, range contraction under future scenarios was predicted off North Cape.

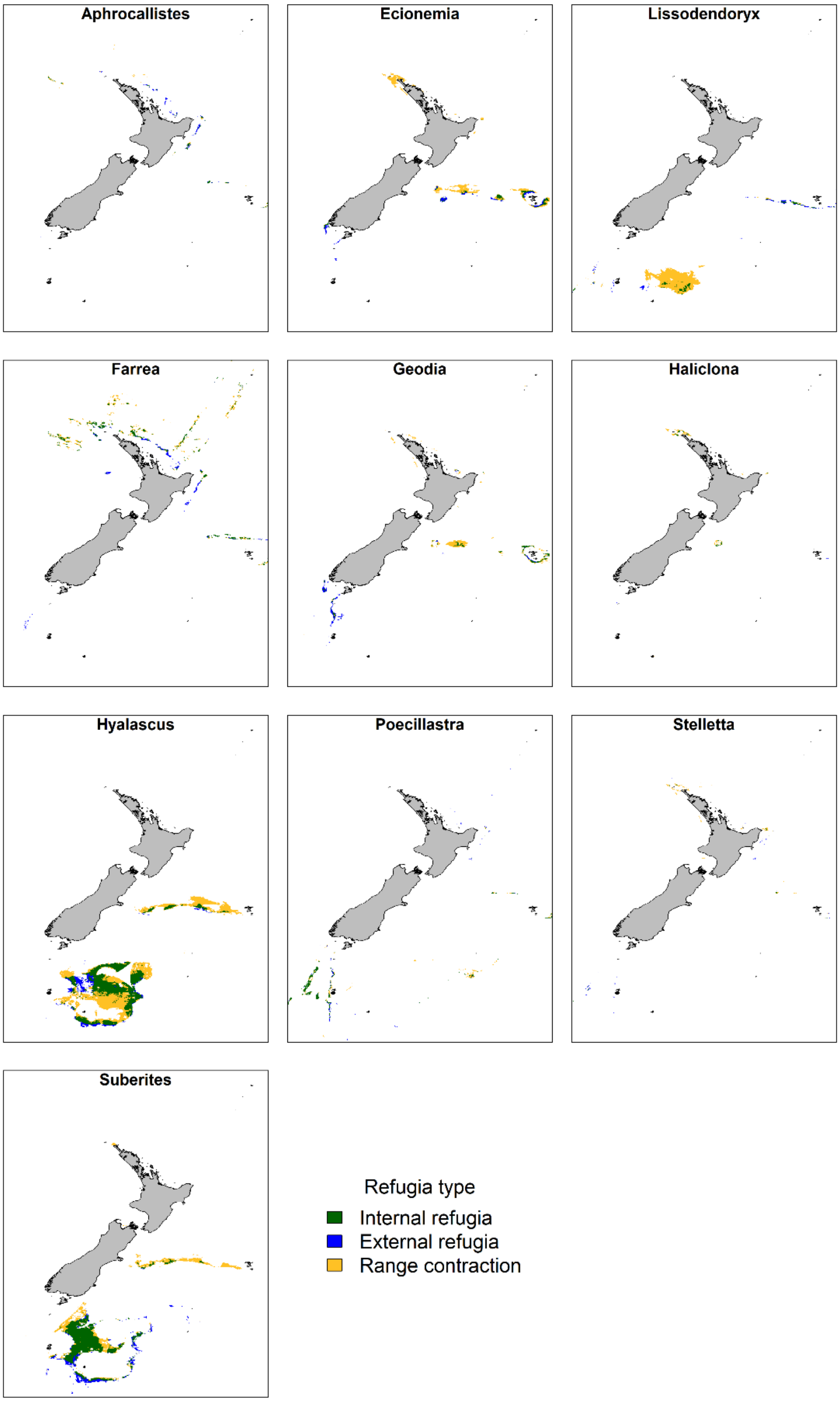

Figure 3-17: Potential refugia (SSP3) – sponges. The distribution of two types of potential climate refugia for sponge taxa. Internal refugia are areas considered core habitat (HSI > 0.75) in both present day and the most extreme future scenario (2090, SSP3). External refugia are areas considered core habitat in the future but not for the present day (i.e., range expansion). Areas showing range contraction (present day core habitat that is not considered core habitat in the future) are also shown.

3.1.5 Macroalgae – Kelp

HSMs for kelp species performed moderately well, with AUC score above 0.7 and TSS scores above 0.5 for most species (Table 3-13). The species with the lowest performance was *Cystophora torulosa* (mean BRT AUC = 0.698) and the highest performing model was generated for *Carpophyllum angustifolium* (mean BRT AUC = 0.899). Standard deviation around the model fit metrics was uniformly low (<0.1 SD) for each HSM indicating consistent model performance. Spatial cross validation scores for the ensemble prediction indicated model performance was generally high across all bioregions where a species was found. Models for some species (e.g., *Cystophora torulosa* and *Desmarestia ligulata*) showed variability in predictive performance across bioregions, however most cross-validation scores (AUC) were above 0.7.

Table 3-13: Model evaluation – kelps. Summary of model performance for HSMs used to predict future distribution of kelp species. Mean AUC/TSS scores along with their standard deviation were generated across the 100 bootstrap iterations for each species and for each BRT and RF model. Spatial cross validation scores (minimum and maximum AUC across bioregions) for the ensemble prediction are also provided. AUC > 0.7 and TSS > 0.6 indicate good predictive performance. For some species there was insufficient data to undertake spatial CV (na), while for others there were sufficient data in a single bioregion only (single spatial CV value).

Taxa	RF AUC (SD)	RF TSS (SD)	BRT AUC (SD)	BRT TSS (SD)	ENS spatial CV (AUC min/max)*
Carpophyllum angustifolium	0.911 (0.027)	0.761 (0.059)	0.899 (0.03)	0.732 (0.062)	na
Carpophyllum flexuosum	0.745 (0.03)	0.404 (0.057)	0.72 (0.032)	0.359 (0.056)	0.783/0.848
Carpophyllum maschalocarpum	0.779 (0.023)	0.444 (0.047)	0.757 (0.024)	0.423 (0.047)	0.669
Carpophyllum plumosum	0.821 (0.029)	0.583 (0.052)	0.808 (0.033)	0.577 (0.055)	0.763/0.931
Cystophora scalaris	0.827 (0.037)	0.56 (0.064)	0.815 (0.034)	0.546 (0.063)	0.751/0.90
Cystophora torulosa	0.716 (0.052)	0.385 (0.08)	0.698 (0.055)	0.373 (0.085)	0.641/0.859
Desmarestia ligulata	0.816 (0.051)	0.565 (0.089)	0.812 (0.057)	0.574 (0.085)	0.650/1.00
Durvillaea spp.	0.834 (0.043)	0.579 (0.074)	0.821 (0.046)	0.562 (0.077)	0.744/0.937
Ecklonia radiata	0.753 (0.024)	0.405 (0.044)	0.727 (0.025)	0.367 (0.041)	0.922
Landsburgia quercifolia	0.769 (0.042)	0.458 (0.07)	0.739 (0.043)	0.416 (0.073)	0.795/0.910
Macrocystis pyrifera	0.829 (0.046)	0.562 (0.072)	0.814 (0.043)	0.558 (0.076)	0.80
Marginariella boryana	0.858 (0.048)	0.623 (0.089)	0.838 (0.05)	0.593 (0.088)	0.805/0.892
Marginariella urvilliana	0.866 (0.036)	0.635 (0.074)	0.85 (0.04)	0.628 (0.076)	0.748/0.901
Xiphophora chondrophylla	0.88 (0.028)	0.674 (0.05)	0.876 (0.025)	0.667 (0.053)	na
Xiphophora gladiata	0.892 (0.03)	0.705 (0.057)	0.891 (0.03)	0.701 (0.055)	0.882

**Note: for some taxa, not enough data was available within a given bioregion to calculate spatial CV model fits.*

Expert appraisal for kelp species provided useful insight into the accuracy of the inputs and outputs of the HSMs (Table 3-14). Experts ranked their own knowledge as very high (2) for all except two species, *Desmarestia ligulate* and *Durvillaea spp.*, where the experts listed their knowledge as moderate (3). The accuracy of the species occurrence data was assessed as being very accurate (1) for all species. For most species, the experts provided a score of accurate (2) for the environmental drivers of the HSMs. For *Carpophyllum angustifolium*, *Carpophyllum flexuosum*, *Cystophora torulosa* and *Durvillaea spp.*, the contribution of the environmental variables to the HSMs were listed as ‘somewhat accurate (3)’. Experts found species present-day distribution to vary in accuracy. For *Carpophyllum angustifolium, Marginariella boryana, Marginariella urvilliana* and *Xiphophora gladiata*, present-day predictions obtained a score of ‘very accurate’ (1). However, experts found the present-day prediction for *Durvillaea antarctica* to be ‘somewhat accurate (3)’, while the present-day prediction for *Cystophora scalaris* received the lowest score of all kelp HSMs of ‘largely inaccurate (4)’. See Appendix B for the full expert review including commentary.

Table 3-14: Expert appraisal – kelps. Summary of expert appraisal of the inputs (occurrence records) and outputs (environmental drivers, present-day distribution) of HSMs for kelp species. Scores range for 1 (highest) to 5 (lowest) - see Appendix A for scoring criteria and Appendix B for the full review including commentary on future predictions.

Taxa	Assessment of expert knowledge	Accuracy of occurrence records	Environmental drivers*	Accuracy of predicted present-day distribution
Carpophyllum angustifolium	2	1	3	1
Carpophyllum flexuosum	2	1	3	2
Carpophyllum maschalocarpum	2	1	2	2
Carpophyllum plumosum	2	1	2	2
Cystophora scalaris	2	1	2	4
Cystophora torulosa	2	1	3	2
Desmarestia ligulata	3	1	2	2
Durvillaea spp.	3	1	3	3
Ecklonia radiata	2	1	2	2
Landsburgia quercifolia	2	1	2	2
Macrocystis pyrifera	2	1	2	2
Marginariella boryana	2	1	2	1
Marginariella urvilliana	2	1	2	1
Xiphophora chondrophylla	2	1	2	2
Xiphophora gladiata	2	1	2	1

**Note: for kelp models, environmental drivers were assessed based on expert appraisal of relative importance of environmental variables used, as well as visual assessment of partial dependence plots.*

Across all kelp species, eleven environmental variables contributed to the HSMs, including five ‘forecastable’ dynamic variables derived from the NZ ESM (Table 3-15). The importance of environmental variables contributing to each species HSM varied across species, but there were high contributions from bottom oxygen concentration (OXY bottom) and slope for most species. Along with oxygen concentration at the seafloor (OXY bottom), nitrate concentration at the seafloor (DIN bottom), closely followed by euphotic depth (MED XZE), were typically the most important forecastable (ESM derived) variable indicating they are responsible for most changes in future distributions of kelp species. Static (non-ESM) variables of importance included slope of the seafloor for most species, and bathymetric position index-fine (BPI-fine) for *Durvillaea spp.* and *Landsburgia quercifolia*.

Table 3-15: Environmental importance – kelps. Relative importance scores (RIS) for the twelve predictor variables retained for the development of habitat suitability models for kelps. The values represent the percentage contribution of each predictor to the ensemble model prediction for each species. Variables available to forecast future conditions (ESM variables) are noted. Variable names and abbreviations are listed in Table 2-2. Green shading is used to distinguish the variable with the highest contribution (dark green) and the lowest contribution (white), with colour between the highest and lowest contributions being established based on linear interpolation based on the relative position of a variable between the highest and lowest contributor.

	ESM variable	***Carpophyllum angustifolium***	***Carpophyllum flexuosum***	***Carpophyllum maschalocarpum***	***Carpophyllum plumosum***	***Cystophora scalaris***	***Cystophora torulosa***	***Desmarestia ligulata***	***Durvillaea antarctica***	***Ecklonia radiata***	***Landsburgia quercifolia***	***Macrocystis pyrifera***	***Marginariella boryana***	***Marginariella urvilliana***	***Xiphophora chondrophylla***	***Xiphophora gladiata***
Bathy		3.90	8.30	6.10	5.30	4.10	7.90	4.80	5.70	8.20	6.90	4.20	4.80	4.20	4.30	3.50
BPI_fine		7.00	7.50	7.00	8.20	8.50	6.60	5.20	15.80	9.80	16.90	4.50	10.40	10.20	6.90	6.30
CHD	✓	5.70	9.70	6.10	7.70	7.10	10.00	5.40	8.20	7.80	6.60	7.30	6.90	7.20	4.60	6.90
DIN_bottom	✓	4.40	10.40	8.10	9.50	7.60	7.70	7.30	10.40	10.00	7.60	10.80	7.90	9.90	6.50	16.40
MED_XZE	✓	4.90	12.10	7.70	9.10	8.40	10.50	5.30	6.60	9.10	12.10	7.90	9.70	8.30	5.80	8.20
Mud		2.30	5.20	4.10	3.60	3.40	6.00	4.20	5.80	4.80	6.70	3.30	3.40	4.70	2.10	3.40
OXY_bottom	✓	36.90	12.40	11.00	15.60	21.60	6.60	26.40	14.60	15.50	9.20	18.90	14.60	12.10	30.00	8.70
PB555nm		5.80	9.60	11.00	8.90	5.40	13.20	7.40	6.20	8.80	8.10	4.30	6.50	4.70	5.10	5.90
Rough		6.40	9.20	11.30	8.70	7.00	8.90	9.30	8.60	8.60	8.60	5.40	5.80	5.00	4.70	4.10
SST	✓	5.70	8.70	9.20	5.80	5.40	14.30	5.70	6.30	8.00	6.80	5.80	5.10	4.30	5.70	3.60
Slope		16.90	6.90	18.30	17.40	21.40	8.30	18.90	11.70	9.50	10.40	27.70	24.80	29.50	24.40	33.00

There were substantial differences among kelp species with respect to changes in distribution between the present day and four future scenarios. As expected, changes in both percent change and overlap in core habitat were more pronounced for the most extreme future scenario (i.e., 2090 SSP3-7.0) compared to 2050 under SSP2-4.5 (Figure 3-18). A contraction in the extent of core habitat was predicted for ten species, with the largest contractions exhibited under the most extreme future scenario (2090 under SSP3-7.0). For three species, contractions were predicted under SSP2-4.5, but extensions were predicted for the same species under SSP3-7.0. *Carpophyllum flexuosum, Cystophora scalaris, Durvillaea antarctica, Macrocystis pyrifera*, and *Marginariella boryana* exhibited the largest decrease in core habitat under all future scenarios.

All species occupy a relatively small extent of core habitat and thus may be particularly vulnerable to climate change impacts on habitats. Several species were predicted to increase in extent of core habitat, though the magnitude of increase varied between future scenarios. *Carpophyllum angustifolium*, *Carpophyllum maschalocarpum*, *Carpophyllum plumosum* and *Cystophora torulosa* exhibited increases (up to 25% for certain future scenarios). However, by far the greatest increase (nearly 200% increase in core habitat extent) was predicted for *Xiphophora chondrophylla* under future scenario 2090 SSP3-7.0. The spatial overlap of core habitat largely mirrored changes in aerial extent, with reduced overlap for those species showing larger decreases in extent. However, some predicted to experience an increase in core habitats (e.g., *Carpophyllum plumosum*) retained relatively high (~80%) overlap in core areas, while others (e.g., *Carpophyllum flexuosum*) had less overlap (~60%).

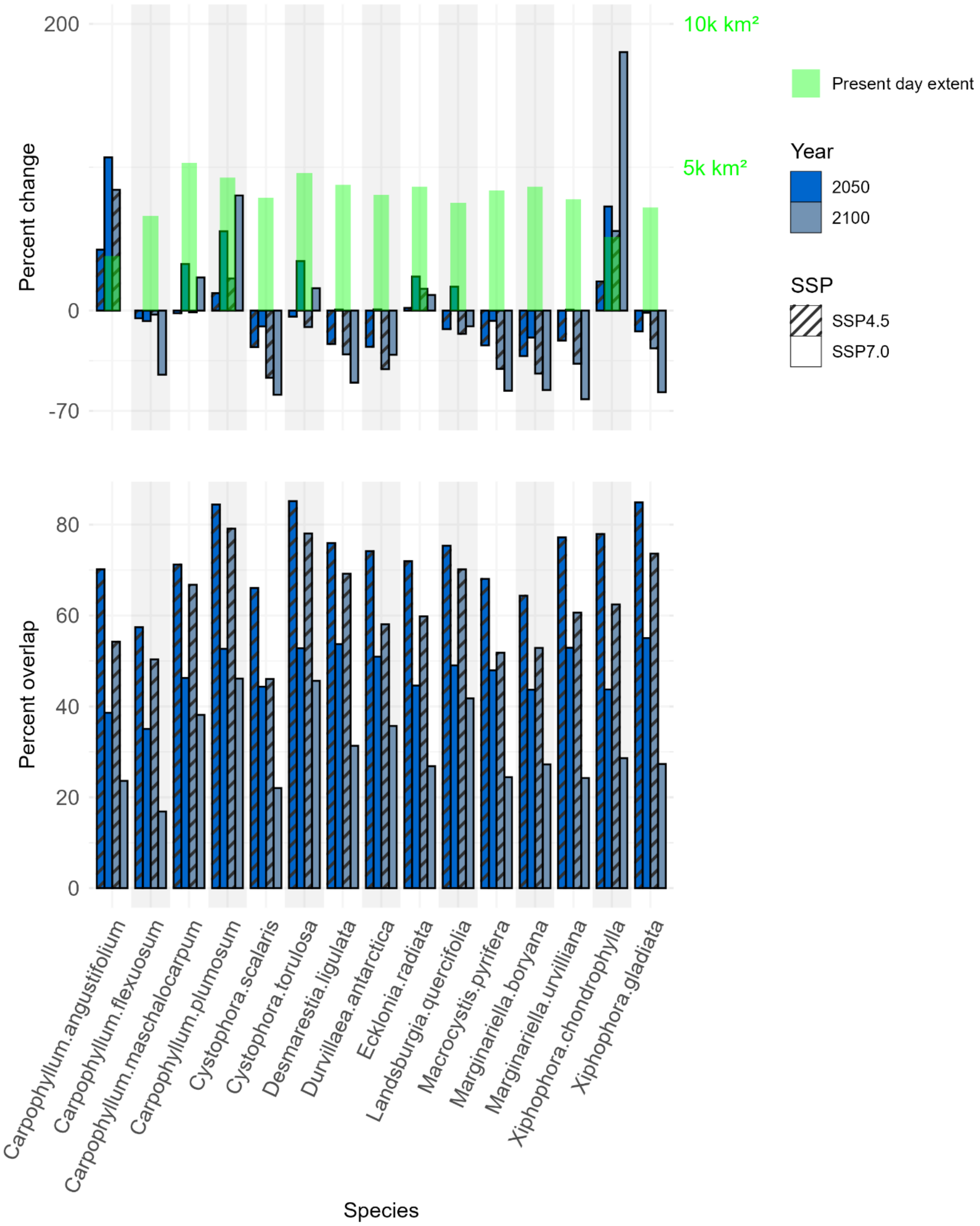

Figure 3-18: Change in core habitat – kelps. Graphical representation of the spatial overlap (bottom) and percentage change (top) in the aerial extent of ROC threshold core habitat (HSI > MaxTSS cut-off) between the present day and the two future scenarios. The total aerial extent of core habitat for the present day is overlaid on the top panel to indicate species with more restricted present-day range.

Spatial predictions of the distribution of core habitat (based on MaxTSS thresholds) for the present day and under future climate scenarios revealed changes for most kelp species (Figure 3-19 to Figure 3-21). Present-day predictions of core habitat were distributed in three areas (species dependent); including the northeast North Island, Marlborough Sounds/top of the South Island, and east coast South Island/bottom of the South Island. Present-day core habitat was predicted to occur in the northeast North Island for *Carpophyllum angustifolium, Carpophyllum flexuosum, Carpophyllum maschalocarpum, Carpophyllum plumosum, Cystophora torulosa, Ecklonia radiata* and *Xiphophora chondrophylla*. Decreases and increases in core habitat in this area was species-specific, but for *Xiphophora chondrophylla*, increased core habitat was predicted in future scenarios, as opposed to *Ecklonia radiata*, where decreases were predicted (for 2090, SSP3). Present-day core habitat was predicted to occur in the Marlborough Sounds/top of the South Island for *Carpophyllum flexuosum, Carpophyllum maschalocarpum, Cystophora torulosa* and *Marginariella boryana*. Decreased core habitat in this area was predicted for *Carpophyllum flexuosum* and *Marginariella boryana* in future scenarios, while the core habitat of *Carpophyllum maschalocarpum* increased in some future scenarios compared to present-day, but in 2090 under SSP3-7.0 the core habitat area was similar to the present-day extent. Relatively little change was predicted for *Cystophora torulosa* in this area. Core habitat (ROC thresholded) was predicted in the east coast South Island/bottom of the South Island area for *Cystophora scalaris, Desmarestia ligulate, Durvillaea antarctica*, *Marginariella boryana, Marginariella urvilliana,* and *Xiphophora gladiata*. For most of these species, core habitat remained largely consistent across future scenarios, with some localised species-specific core habitat contraction (Figure 3-19 to Figure 3-21).

Figure 3-19: Core habitat distribution – kelps. The predicted distribution of ROC-thresholded core habitat (HSI > MaxTSS cut-off) for kelp species for the present day (left) and four future scenarios; mid-century (2050) and end-of century (2090) under SSP3-7.0 emissions scenario.

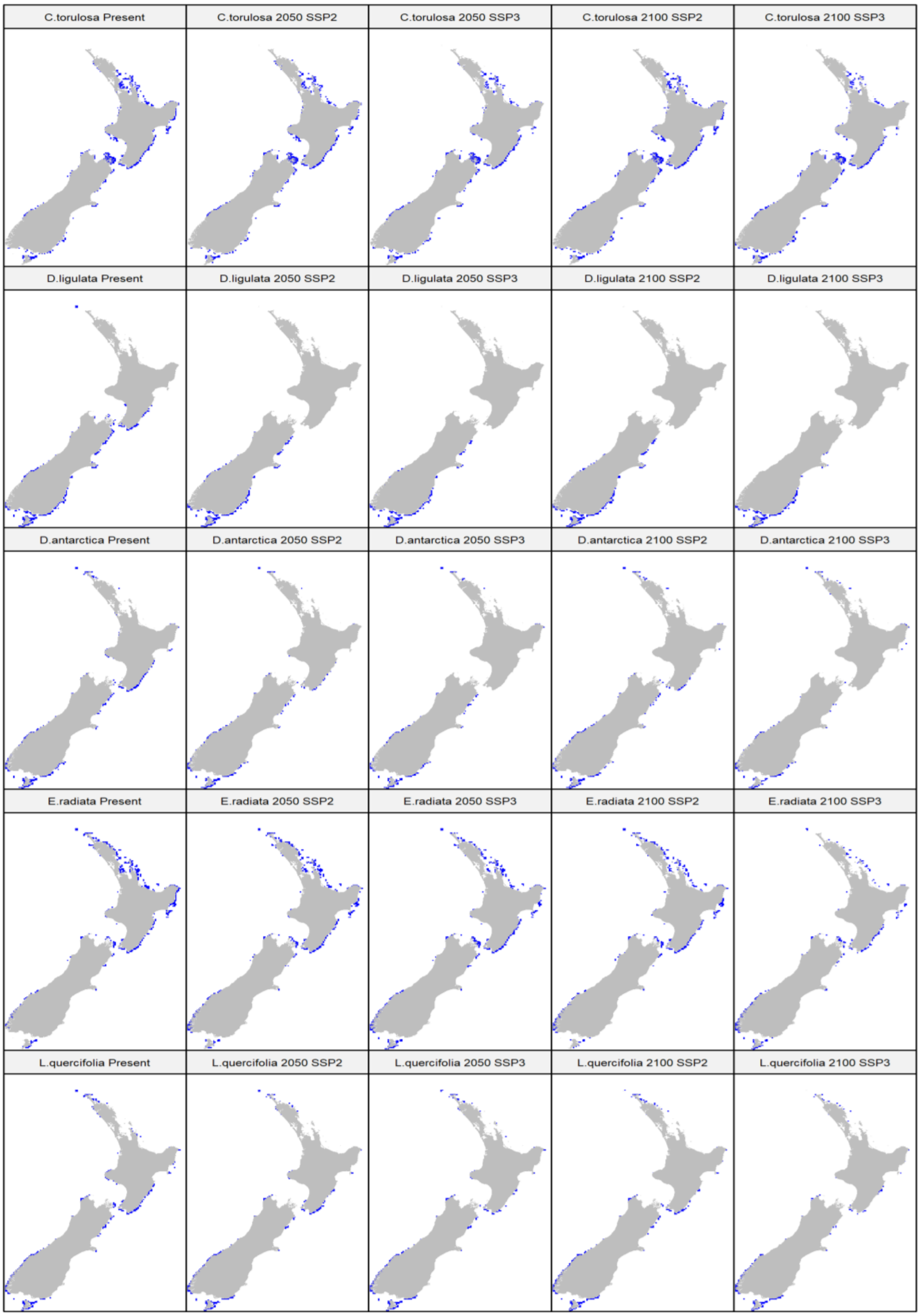

Figure 3-20: Core habitat distribution – kelps (cont.). The predicted distribution of ROC-thresholded core habitat (HSI > MaxTSS cut-off) for kelp species for the present day (left) and four future scenarios; mid-century (2050) and end-of century (2090) under SSP3-7.0 emissions scenario.

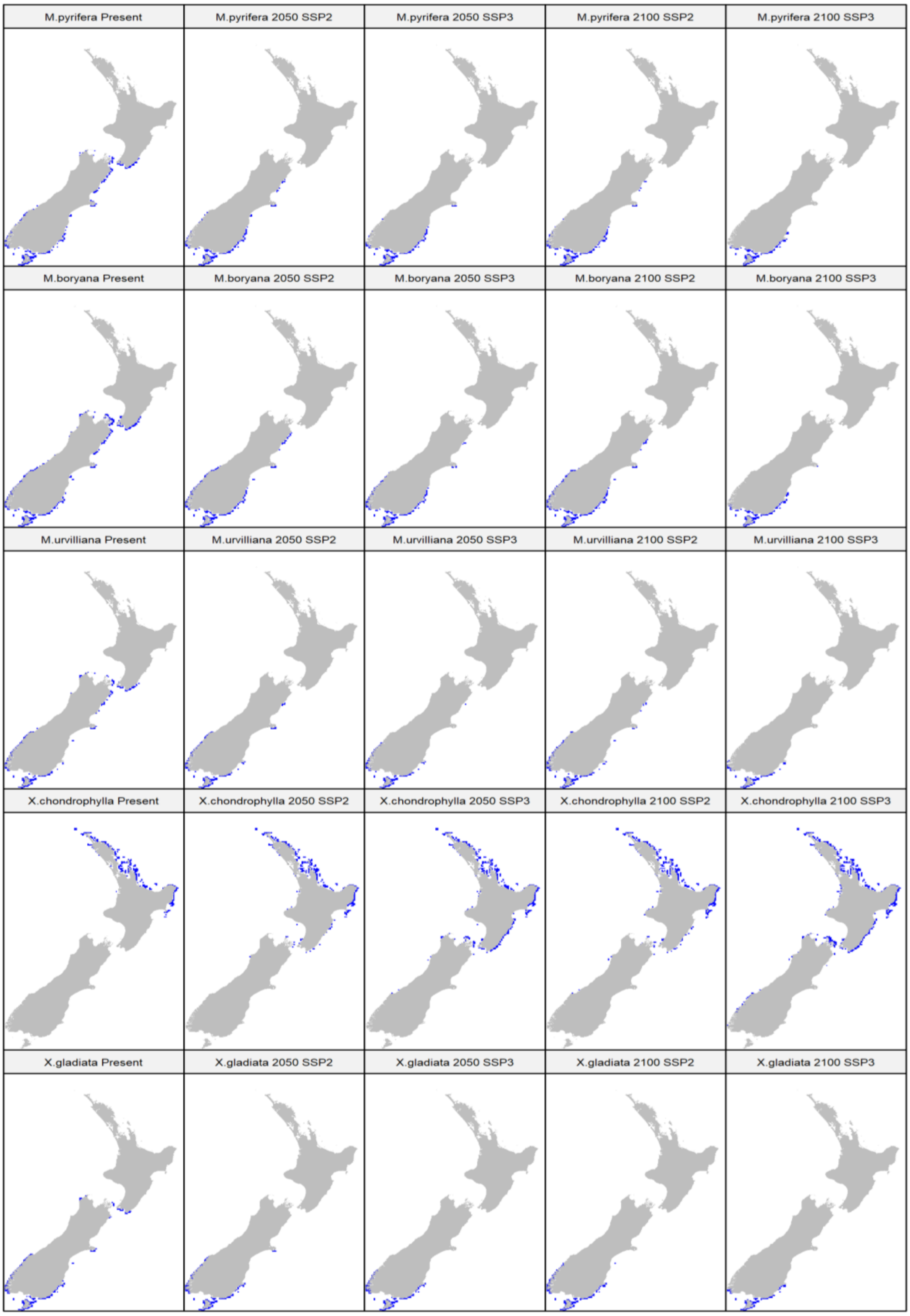

Figure 3-21: Core habitat distribution – kelps (cont.). The predicted distribution of ROC-thresholded core habitat (HSI > MaxTSS cut-off) for kelp species for the present day (left) and four future scenarios; mid-century (2050) and end-of century (2090) under SSP3-7.0 emissions scenario.

Potential refugia and areas of range contraction of core habitat for kelp species were broadly distributed around New Zealand's coastline (Figure 3-22 and Figure 3-23). Internal refugia occurred for *Carpophyllum angustifolium, Carpophyllum maschalocarpum* and *Carpophyllum plumosum* in the northeast/east of the North Island (e.g., Hauraki Gulf and Bay of Plenty). For *Cystophora torulosa* and *Carpophyllum maschalocarpum*, internal refugia occurred in the Marlborough Sounds area. The bottom of the South Island (east coast and Stewart Island) hosts internal refugia for *Cystophora torulosa, Desmarestia ligulate, Macrocystis pyrifera* and *Durvillaea antarctica*. External refugia were inconsistent across species (Figure 3-22 and Figure 3-23). For example, external refugia occurred around the North Island coast for *Carpophyllum maschalocarpum,* but for *Carpophyllum plumosum* areas of the South Island coast (southwest and northeast) were predicted to host external refugia. Areas around Stewart Island had external refugia for *Marginariella urvilliana*, *Xiphophora gladiata*, *Carpophyllum maschalocarpum, Carpophyllum flexuosum* and *Carpophyllum plumosum*. Fragmented external refugia were evident for *Marginariella urvilliana, Xiphophora gladiata, Ecklonia radiata, Landsburgia quercifolia and Macrocystis pyrifera* (Figure 3-22 and Figure 3-23). Finally, range contraction was predicted broadly around the NZ coastline for different taxa. For eight species (*Marginariella urvilliana*, *Marginariella boryana*, *Macrocystis pyrifera, Carpophyllum flexuosum, Cystophora scalaris, Desmarestia ligulate, Durvillaea antarctica* and *Xiphophora gladiata*), range contraction was evident towards the south of the North Island (Wellington region) and at the top of the South Island (including Marlborough Sounds) (Figure 3-22 and Figure 3-23).

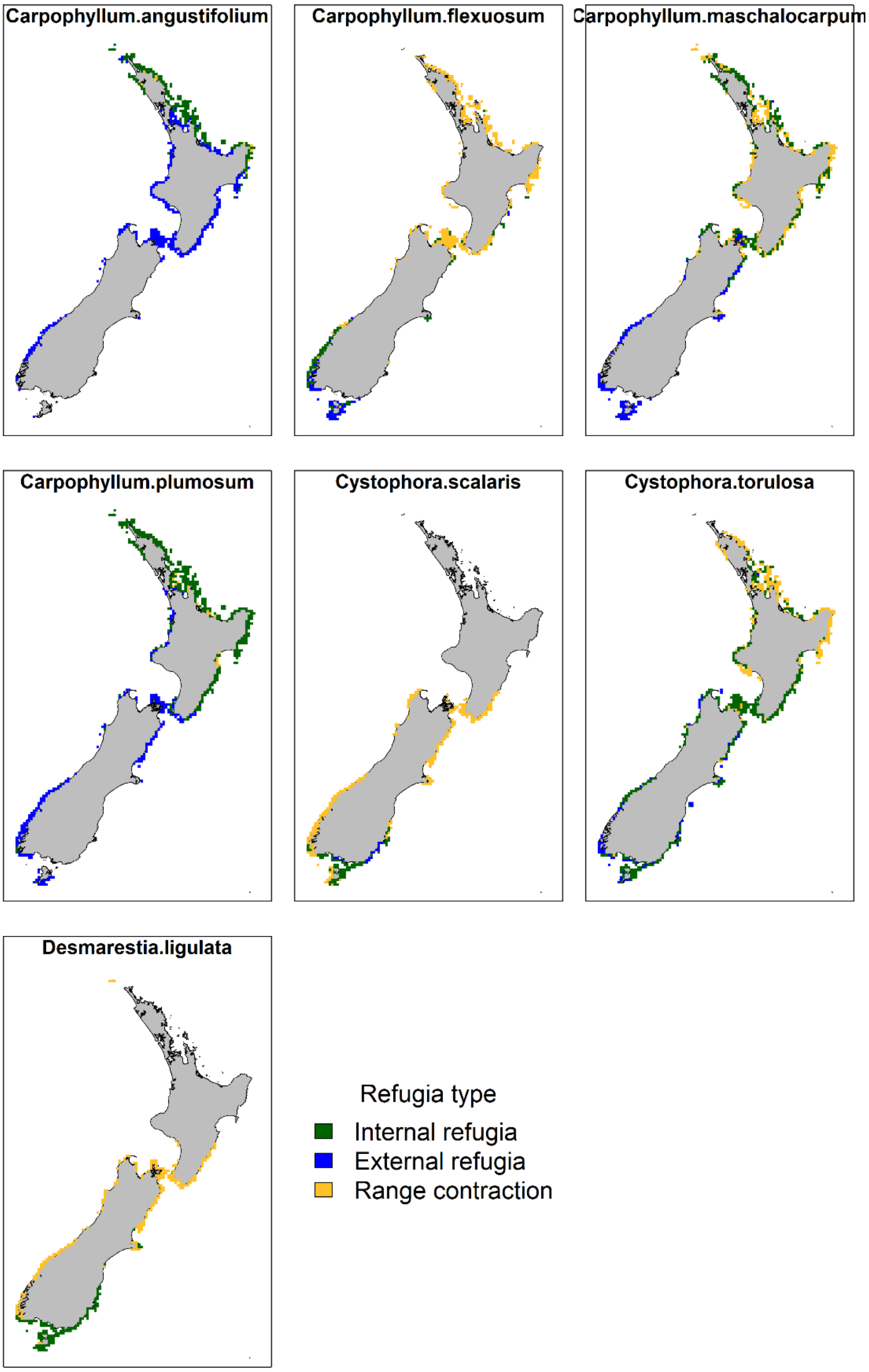

Figure 3-22: Potential refugia (SSP3) – kelps. The distribution of two types of potential climate refugia for kelp species. Internal refugia are areas considered ROC-thresholded core habitat (HSI > MaxTSS) in both present day and the most extreme future scenario (2090, SSP3). External refugia are areas considered core habitat in the future but not for the present day. Areas showing range contraction (present day core habitat that is not considered core habitat in the future) are also shown. Grid cell size aggregated to 10 km x 10 km for visualisation.

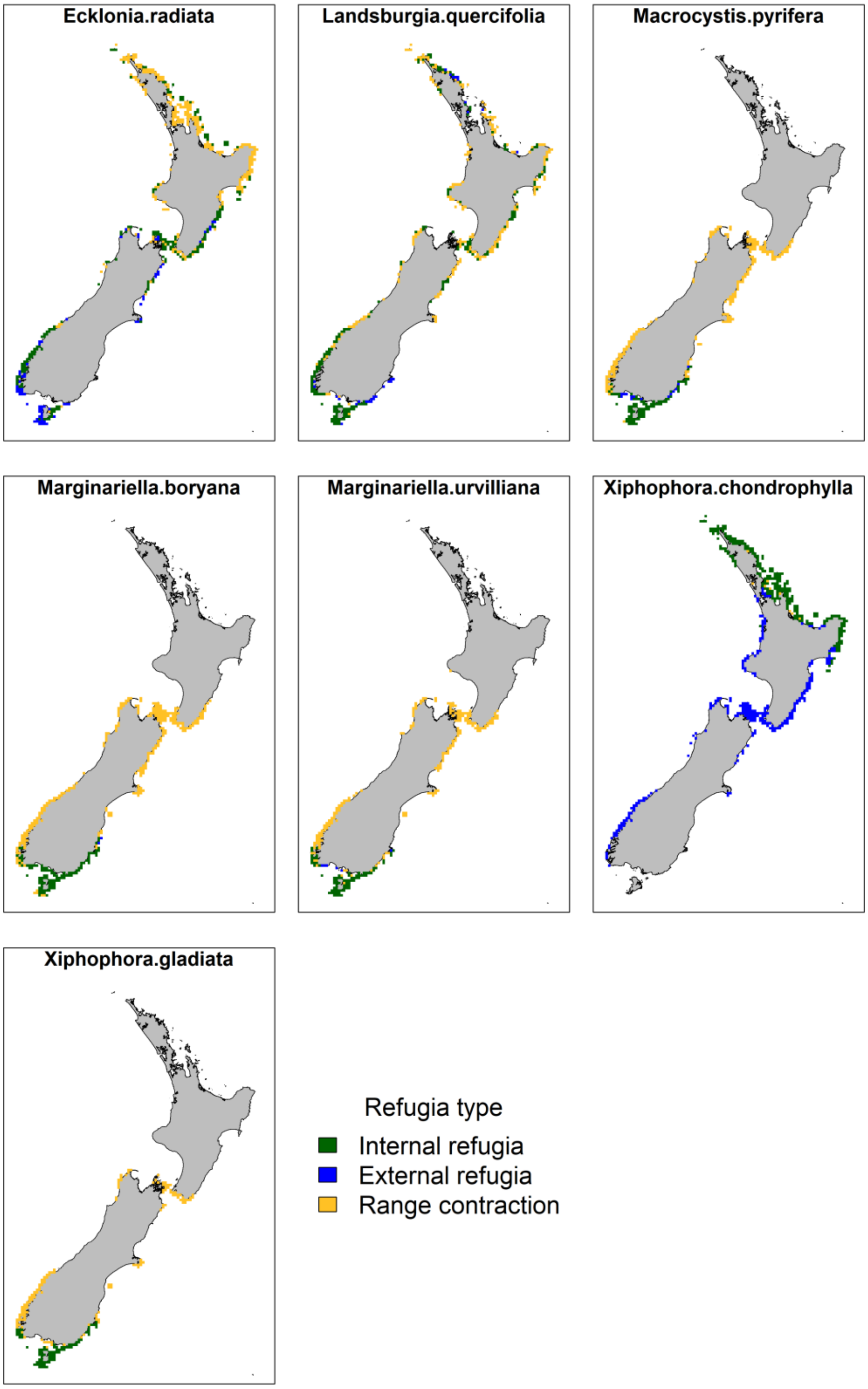

Figure 3-23: Potential refugia (SSP3) – kelps (cont.). The distribution of two types of potential climate refugia for kelp species. Internal refugia are areas considered ROC-thresholded core habitat (HSI > MaxTSS cut-off) in both present day and the most extreme future scenario (2090, SSP3). External refugia are areas considered core habitat in the future but not for the present day (i.e., range expansion). Areas showing range contraction (present day core habitat that is not considered core habitat in the future) are also shown. Grid cell size aggregated to 10 km x 10 km for visualisation.

3.1.6 Macroalgae – Threatened/at risk species

HSMs for threatened macroalgae all performed well, with AUC score above 0.7 and TSS scores 0.5 for most species – indicating 'moderate' to 'good' model performance overall (Table 3-16). The species with the lowest performance was *Myriogloea intestinalis* (mean BRT AUC = 0.701) and the highest performing model was generated for *Pachymenia lusoria* (mean BRT AUC = 0.913). Standard deviation around the model fit metrics was mostly low for each HSM indicating consistent model performance (<0.1 for most HSMs). Spatial cross validation scores for the ensemble prediction indicated model performance was generally high across all bioregions where a species was found. Models for some species (e.g., *Myriogloea intestinalis* and *Pachymenia lusoria*) showed variability in predictive performance across bioregions, however all cross-validation scores (AUC) were above thresholds for adequate performance (AUC ≥0.7).

Table 3-16: Model evaluation – threatened macroalgae. Summary of model performance for HSMs used to predict future distribution of threatened macroalgae species. Mean AUC/TSS scores along with their standard deviation were generated across the 100 bootstrap iterations for each species and for each BRT and RF model. Spatial cross validation scores (minimum and maximum AUC across bioregions) for the ensemble prediction are also provided. AUC > 0.7 and TSS > 0.6 indicate good predictive performance. For some species there was insufficient data to undertake spatial CV (na), while for others there were sufficient data in a single bioregion only (single spatial CV value).

Taxa	RF AUC (SD)	RF TSS (SD)	BRT AUC (SD)	BRT TSS (SD)	ENS spatial CV (AUC min/max)*
Aeodes nitidissima	0.837 (0.034)	0.589 (0.068)	0.831 (0.037)	0.586 (0.065)	0.905
Gigartina macrocarpa	0.818 (0.043)	0.572 (0.081)	0.816 (0.045)	0.579 (0.083)	0.787/0.90
Grateloupia urvilleana	0.782 (0.066)	0.502 (0.108)	0.734 (0.064)	0.425 (0.106)	0.914/1.00
Microdictyon mutabile	0.911 (0.048)	0.75 (0.097)	0.897 (0.05)	0.734 (0.09)	na
Myriogloea intestinalis	0.736 (0.063)	0.441 (0.102)	0.701 (0.076)	0.396 (0.111)	0.678/0.947
Petalonia binghamiae	0.767 (0.05)	0.483 (0.085)	0.769 (0.049)	0.477 (0.085)	0.726/0.866
Pachymenia dichotoma	0.882 (0.047)	0.698 (0.084)	0.87 (0.05)	0.701 (0.087)	0.860/0.967
Pachymenia lusoria	0.923 (0.041)	0.773 (0.096)	0.913 (0.044)	0.756 (0.096)	0.793/1.00

**Note: for some taxa, not enough data was available within a given bioregion to calculate spatial CV model fits.*

Expert appraisal for threatened macroalgae provided useful insight into the accuracy of the inputs and outputs of the HSMs (Table 3-17). Experts ranked their own knowledge as high (2) for most species, though experts ranked their knowledge for *Microdictyon mutabile* and *Myriogloea intestinalis* as moderate (3). The experts assessed the accuracy of the species occurrence data as very accurate (1) for all species. Similarly, experts gave the contribution of environmental variables to the HSMs the same score of 'accurate (2)' for every species. Experts found species present-day distribution to be 'very accurate' (1) or 'accurate' (2) for all threatened macroalgae species. See Appendix B for the full expert review including commentary on the present-day predictions.

Table 3-17: Expert appraisal – threatened macroalgae. Summary of expert appraisal of the inputs (occurrence records) and outputs (environmental drivers, present-day distribution) of HSMs for threatened macroalgae species. Scores range for 1 (highest) to 5 (lowest) - see Appendix A for scoring criteria and Appendix B for the full review including commentary on future predictions.

Taxa	Assessment of expert knowledge	Accuracy of occurrence records	Environmental drivers*	Accuracy of predicted present-day distribution
Aeodes nitidissima	2	1	2	2
Gigartina macrocarpa	2	1	2	1
Grateloupia urvilleana	2	1	2	1
Microdictyon mutabile	3	1	2	1
Myriogloea intestinalis	3	1	2	2
Petalonia binghamiae	2	1	2	2
Pachymenia dichotoma	2	1	2	2
Pachymenia lusoria	2	1	2	1

Across all threatened macroalgae, ten environmental variables contributed to the HSMs, including four ‘forecastable’ dynamic variables derived from the NZ ESM (Table 3-18). However, for any given species, nine non-correlated variables were used to predict species’ distributions. The environmental variables contributing to each species HSM varied across species, but there were consistently high contributions (between 16.8 and 45.45% importance) from SST for all but two species (*Myriogloea intestinalis,* and *Pachymenia lusoria*). Sea surface temperature was highly correlated with sea surface radiation (MED QSR), but sea surface radiation was a better predictor of the distributions for the two aforementioned taxa, thus it was retained for these HSMs in place of sea surface temperature. Along with sea surface radiation, sea surface temperature (SST) was typically the most important forecastable (ESM-derived) variable indicating SST is responsible for most changes in future distributions of threatened macroalgae. However, other ESM-derived variable also made meaningful contributions for some species including sea surface salinity (SSS), and sea surface temperature gradient (SSTGrad). Static (non-ESM) variables of importance for some species including swell exposure at the seafloor (BedDist), bathymetry (Bathy), seabed incident irradiance (Ebed) and percent mud (Mud).

Table 3-18: Environmental importance – threatened macroalgae. Relative importance scores (RIS) for the twelve predictor variables retained for the development of habitat suitability models for threatened macroalgae species. The values represent the percentage contribution of each predictor to the ensemble model prediction for each species. Variables available to forecast future conditions (ESM variables) are noted. Variable names and abbreviations are listed in Table 2-2. Green shading is used to distinguish the variable with the highest contribution (dark green) and the lowest contribution (white), with colour between the highest and lowest contributions being established based on linear interpolation based on the relative position of a variable between the highest and lowest contributor.

	ESM variable	***Aeodes nitidissima***	***Gigartina macrocarpa***	***Grateloupia urvilleana***	***Microdictyon mutabile***	***Myriogloea intestinalis***	***Pachymenia dichotoma***	***Pachymenia lusoria***	***Petalonia binghamiae***
Bathy		10.73	9.77	14.66	8.23	23.14	4.51	4.86	11.93
BedDist		8.00	10.48	11.50	5.19	11.35	6.30	16.00	12.55
Ebed		8.43	6.76	7.58	5.74	16.86	5.13	11.25	8.06
MED_QSR	✓	0.00	0.00	0.00	0.00	8.03	0.00	25.68	0.00
Mud		6.32	7.32	9.26	11.97	7.69	7.49	8.47	7.44
PB555nm		8.73	7.76	10.02	5.50	8.09	8.49	4.25	9.92
SSS	✓	9.87	15.68	10.91	12.36	8.18	13.78	16.57	10.27
SST	✓	37.06	30.49	16.88	40.67	0.00	45.45	0.00	22.78
SSTGrad	✓	5.34	5.44	10.00	4.29	7.94	4.99	5.06	10.06
TC		5.52	6.28	9.20	6.07	8.73	3.86	7.85	6.98

There were substantial differences among threatened macroalgae species with respect to changes in core habitat extent between the present day and four future scenarios. As expected, changes in both percent change and overlap in core habitat were more pronounced for the most extreme future scenario (i.e., 2090 SSP3-7.0) (Figure 3-24). A contraction in the extent of core habitat was predicted for two species. *Grateloupia urvilleana* and *Pachymenia dichotoma* exhibited decreases in core habitat under all future scenarios (mostly <50% reduction under SSP2-4.5 and SSP3-7.0). *Grateloupia urvilleana* occupies a relatively small areal extent of core habitat, and thus this species may be particularly vulnerable to climate change impacts. Five species were predicted to increase in extent of core habitat (not including *Myriogloea intestinalis*, which responded variably under future scenarios), with *Aeodes nitidissima* and *Microdictyon mutabile* exhibiting the greatest increases (up to 275 and 175% under 2090 SSP3-7.0, respectively). The spatial overlap of core habitat largely mirrored changes in extent, with reduced overlap for those species showing larger changes in extent. Some species were predicted to experience a decrease in core habitats (e.g., *Pachymenia lusoria*) but retained relatively high (up to >75% under both SSP2-4.5 and SSP3-7.0 in 2050) overlap in core areas, while others (e.g., *Aeodes nitidissima*) had less overlap (~25-40%) despite increasing core habitat extent.

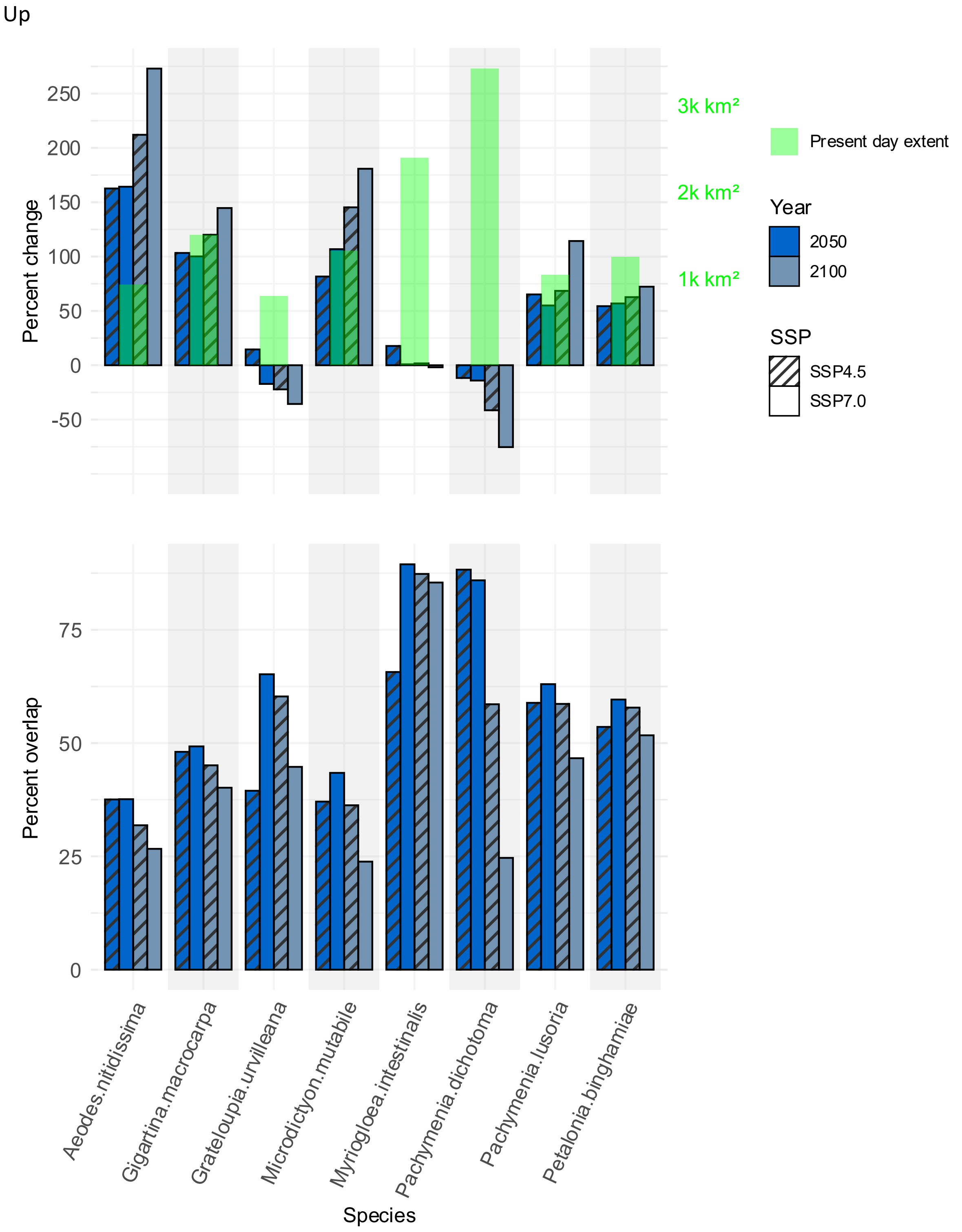

Figure 3-24: Change in occupied habitat – threatened macroalgae. Graphical representation of the spatial overlap (bottom) and percentage change (top) in the aerial extent of ROC threshold core habitat (HSI > MaxTSS cut-off) between the present day and the two future scenarios. The total aerial extent of core habitat for the present day is overlaid on the top panel to indicate species with more restricted present-day range.

Figure 3-25: Occupied habitat distribution – threatened macroalgae. The predicted distribution of ROC-thresholded occupied habitat (HSI > MaxTSS cut-off) for threatened macroalgae species for the present day (left) and four future scenarios; mid-century (2050) and end-of century (2090) under SSP3-7.0 emissions scenario.

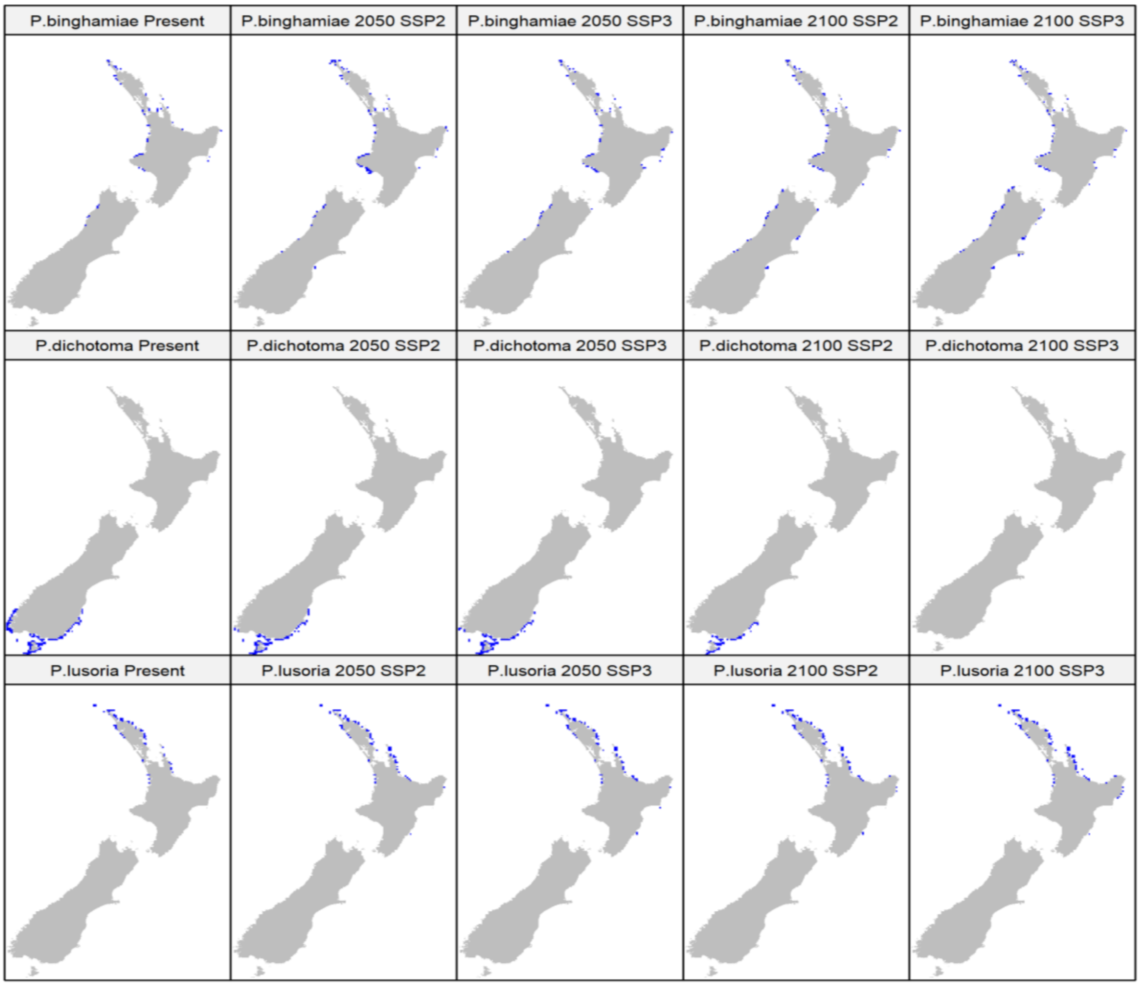

Figure 3-26: Core habitat distribution – threatened macroalgae (cont.). The predicted distribution of ROC-thresholded core habitat (HSI > MaxTSS cut-off) for threatened macroalgae species for the present day (left) and four future scenarios; mid-century (2050) and end-of century (2090) under SSP3-7.0 emissions scenario.

Spatial predictions of the distribution of core habitat for the present day and under future climate scenarios revealed changes for some threatened macroalgae species (Figure 3-25 and Figure 3-26). Present-day core habitat (ROC thresholded) for threatened macroalgae species were predicted to occur in several consistent areas across all species. For instance, core habitat for *Aeodes nitidissima, Gigartina macrocarpa*, *Microdictyon mutabile* and *Pachymenia lusoria* was predicted around the coast of the North Island, particularly in the northeast region. Core habitat was predicted to occur in the south of the South Island (east coast South Island) for few species, including *Myriogloea intestinalis* and *Pachymenia dichotoma*. Reductions in core habitat extent were predicted to occur for several species in future scenarios. Decreases in core habitat extent was most severe under the most extreme future scenario (SSP3-7.0, e.g., *Pachymenia dichotoma*). However, increases were evident for some species under the same scenario, for example *Aeodes nitidissima*.

Potential refugia and areas of range contraction of core habitat for threatened macroalgae were fragmented for most species and broadly distributed around the NZ coastline (Figure 3-37). Internal refugia occurred in the upper North Island (Northland region) for *Gigartina macrocarpa* and *Pachymenia lusoria*. Limited, fragmented areas of external refugia were predicted for some species, for example around the North Island coastline for *Pachymenia lusoria, Aeodes nitidissima* and *Gigartina macrocarpa*, and on the west coast of the South Island for *Petalonia binghamiae*.

For *Pachymenia lusoria, Aeodes nitidissima* and *Gigartina macrocarpa*, range contraction was predicted to occur in the north of the North Island, while considerable range contraction was predicted to occur for *Pachymenia dichotoma* along the bottom of the South Island of NZ, including Stewart Island.

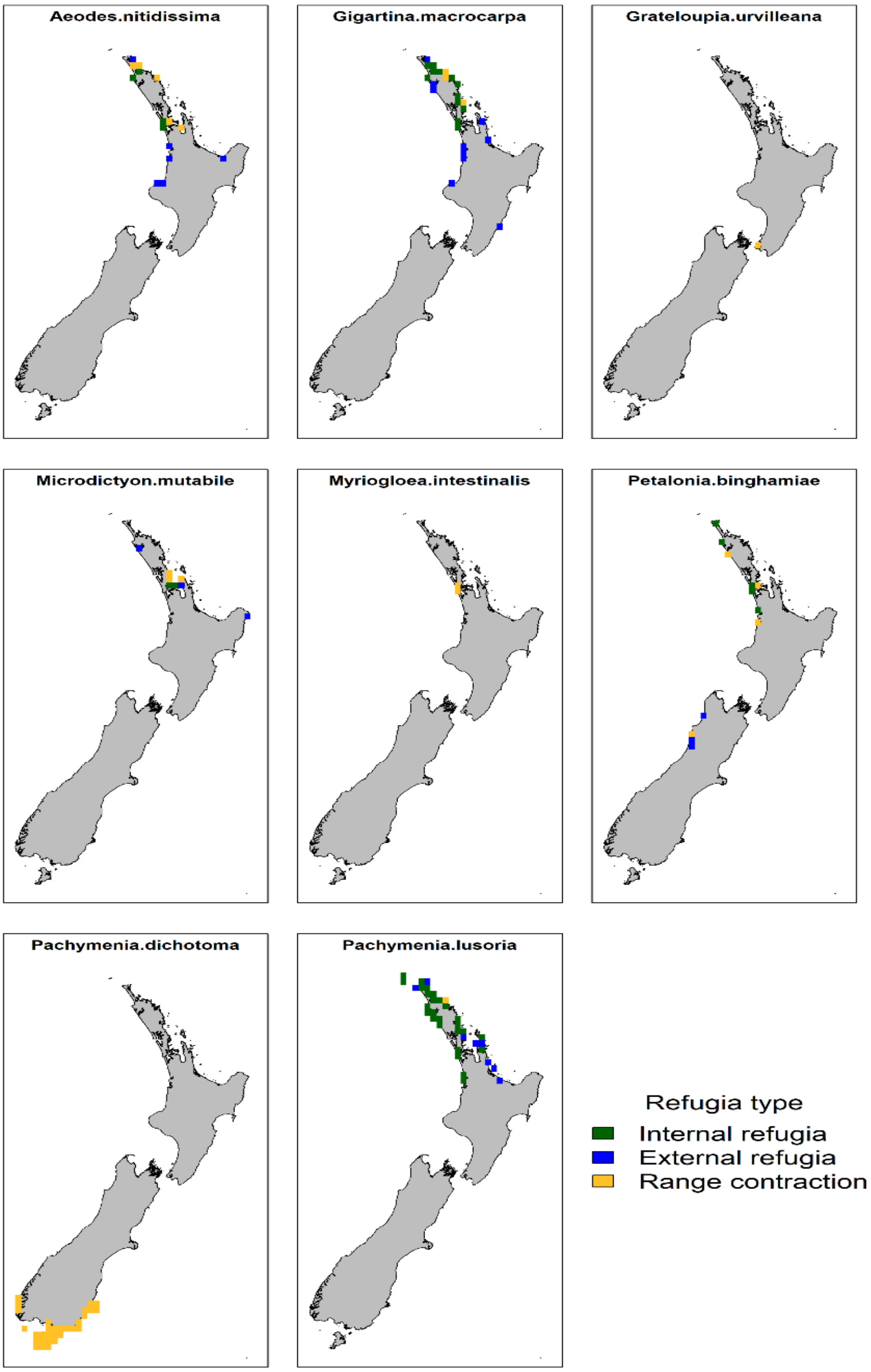

Figure 3-27: Potential refugia (SSP3) –threatened macroalgae. The distribution of two types of potential climate refugia for threatened macroalgae species. Internal refugia are areas considered ROC-thresholded core habitat (HSI > MaxTSS cutoff) in both present day and the most extreme future scenario (2090, SSP3). External refugia are areas considered core habitat in the future but not for the present day (i.e., range expansion). Areas showing range contraction (present day core habitat that is not considered core habitat in the future) are also shown. Grid cell size aggregated to 20 km x 20 km for visualisation.

3.1.7 Marine mammals

HSMs for marine mammal species all performed well, with AUC scores above 0.9 and TSS scores above 0.6 for the most species – indicating 'excellent' model performance (Table 3-19). The species with the lowest performance was humpback whale (mean BRT AUC = 0.825) and the highest performing model was generated for Māui dolphin (mean RF AUC = 0.996) with all AUC values well above the standard for acceptable performance (AUC = 0.7). Standard deviation around the model fit metrics was uniformly low for each HSM indicating consistent high model performance.

Table 3-19: Model evaluation – marine mammals. Summary of model performance for HSMs used to predict future distribution of marine mammal species. Mean AUC/TSS scores along with their standard deviation were generated across the 100 bootstrap iterations for each species and for each BRT and RF model. AUC > 0.7 and TSS > 0.6 indicate good predictive performance.

Species	RF AUC (SD)	RF TSS (SD)	BRT AUC (SD)	BRT TSS (SD)	ENS spatial CV (AUC min/max)
Bottlenose dolphin	0.902 (0.016)	0.690 (0.040)	0.895 (0.017)	0.679 (0.039)	0.780/0.990
Common dolphin	0.907 (0.005)	0.676 (0.013)	0.900 (0.005)	0.660 (0.013)	0.839/0.933
Dusky dolphin	0.871 (0.017)	0.590 (0.035)	0.852 (0.018)	0.568 (0.033)	0.844/0.943
Hector's dolphin	0.980 (0.004)	0.897 (0.013)	0.977 (0.005)	0.890 (0.012)	0.865/0.988
Māui dolphin	0.996 (0.003)	0.954 (0.017)	0.995 (0.003)	0.950 (0.018)	0.961/0.995
Orca	0.908 (0.012)	0.662 (0.032)	0.902 (0.013)	0.658 (0.031)	0.778/0.931
Blue whale	0.944 (0.010)	0.762 (0.026)	0.930 (0.011)	0.738 (0.031)	0.895/0.978
Bryde's whale	0.961 (0.009)	0.847 (0.022)	0.961 (0.008)	0.842 (0.021)	0.938/0.965
Humpback whale	0.843 (0.015)	0.554 (0.033)	0.825 (0.020)	0.525 (0.036)	0.813/0.920
Long-finned pilot whale	0.870 (0.020)	0.612 (0.045)	0.855 (0.020)	0.598 (0.042)	0.764/0.913
Southern right whale	0.894 (0.016)	0.664 (0.036)	0.873 (0.018)	0.624 (0.034)	0.762/0.982
Sperm whale	0.910 (0.016)	0.694 (0.042)	0.888 (0.019)	0.673 (0.039)	0.791/0.954

Expert appraisal for marine mammals provided useful insight into the accuracy of the inputs and outputs of the HSMs for these species (Table 3-5). Experts ranked their own knowledge as high (2) or very high (1), for all species except blue whales for which experts considered they had a moderate (3) level of knowledge. The accuracy of the species occurrence data was very accurate (1) or accurate (2) for all species except humpback whale and long-finned pilot whale ('somewhat accurate (3)'). The contribution of the environmental variables to the HSMs were listed as 'accurate (2)' for all species except common dolphin and Orca ('very accurate (1)') and humpback whale ('somewhat accurate (3)'). Experts found species present-day distribution to be 'very accurate' (1) or 'accurate' (2) for all species except blue whale, humpback whale, southern right whale and sperm whale (3). See Appendix B for the full expert review including commentary of the future predictions.

Table 3-20: Expert appraisal – marine mammals. Summary of expert appraisal of the inputs (occurrence records) and outputs (environmental drivers, present-day distribution) of HSMs for delphinid species. Scores range for 1 (highest) to 5 (lowest) - see Appendix A for scoring criteria and Appendix B for the full review including commentary on future predictions.

Species	Assessment of expert knowledge	Accuracy of occurrence records	Environmental drivers	Accuracy of predicted present-day distribution
Bottlenose dolphin	1	1	2	1
Common dolphin	2	1	1	1
Dusky dolphin	2	1	2	2
Hector's dolphin	1	1	2	2
Māui dolphin	1	1	2	2
Orca	2	2	1	1
Blue whale	3	2	2	3
Bryde's whale	1	2	2	2
Humpback whale	1	3	3	3
Long-finned pilot whale	2	3	2	2
Southern right whale	1	1	2	3
Sperm whale	1	2	2	3

Across all marine mammals, nineteen environmental variables contributed to the HSMs, including eight ‘forecastable’ dynamic variables derived from the NZ ESM (Table 3-21). However, for any given species, between eight or nine non-correlated variables were used to predict distributions. The environmental variables contributing to each species HSM varied among species, but there were consistently moderate to high contributions (between 7.59% and 42.29% importance) from bathymetry for all species. SST was the most important dynamic variable for all marine mammal species modelled here except pilot whale, Māui dolphin and sperm whale. Other important dynamic variables included mixed layer depth (MLD), which was the most important variable for pilot and sperm whale and salinity which was most important for Māui dolphin. Vertically integrated productivity (TPP3) also made significant contributions for some species (blue whale, dusky dolphin, pilot whale) along with surface current velocity (dusky dolphin, humpback whale). Static variables that ranked high for some species included turbidity (particular for Hector’s/Māui dolphin), slope, chlorophyll-a gradient, bathymetric position index and seabed swell exposure (BedDist).

There were substantial differences among marine mammal species with respect to changes in distribution between the present day and four future scenarios. As expected, changes in both percent change and overlap in core habitat were more pronounced for the most extreme future scenario (i.e., 2090 under SSP3-7.0) compared to 2050 under SSP2-4.5 (Figure 3-28). A contraction in the extent of core habitat was predicted under all future scenarios for five species (Bryde’s and southern right whales and dusky, Hector’s and Māui dolphin), while reduced extent of core habitat was apparent for blue whales, humpback whales, pilot whales and sperm whales under only some future scenarios. Under the most extreme future scenario, Bryde’s whale was predicted to experience over 62% reduction in core habitat and showed a greater reduction for mid-century under SSP2-4.5 (the more moderate emissions scenario) than the more extreme scenario.

Core habitat for Hector’s dolphins was predicted to undergo greater than 50% decline in extent in all future scenarios except mid-century under SSP2-4.5, with a greater than 80% reduction under the most extreme future scenario. Due to the relatively restricted present-day extent of core habitat and large projected declines in extent for Bryde’s whales and Hector’s dolphins, these species are likely the most vulnerable marine mammal species investigated by this study. Dusky dolphin, Māui dolphin and southern right whale are also likely to be vulnerable due to the same factors. Bottlenose dolphins, orca and common dolphins were predicted to undergo increases in the extent of core habitat under all future scenarios, with core habitat for bottlenose dolphins predicted to increase by over 70% (Figure 3-28) by 2090 under SSP3. Common dolphin were predicted to increase their core extent by up to 45% by 2090 under SSP3 and core area for Orca was predicted to increase by ~25% across all future scenarios.

Change in the overlap among present day and future core habitat typically mirrored changes in extent, with those species experiencing both large positive and negative changes in extent also exhibiting the greatest reduction in overlap (Figure 3-28). However, some species with minimal change in extent also showed reduced overlap among present-day and future core areas (e.g., blue whale, humpback whale), which suggests the locations of core habitat for these species is changing, while the extent remains relatively similar over time.

Table 3-21: Environmental variable importance - marine mammals. Relative importance scores (RIS) for the sixteen predictor variables retained for the development of habitat suitability models for marine mammals. The values represent the percentage contribution of each predictor to the ensemble model prediction for each species. Variables available to forecast future conditions (ESM variables) are noted. Variable names and abbreviations are listed in Table 2-2. Species codes are Bryde's whale (BdW), blue whale (Blw), coastal bottlenose dolphin (BnD), common dolphin (CmD), dusky dolphin (DuskD), humpback whale (HbW), Hector's dolphin (HectD), long-finned pilot whale (LfpW), Māui dolphin (Māui), coastal Orca (Orca), sperm whale (SpW), southern right whale (SrW). Green shading is used to distinguish the variable with the highest contribution (dark green) and the lowest contribution (white), with colour between the highest and lowest contributions being established based on linear interpolation based on the relative position of a variable between the highest and lowest contributor.

	ESM variable	Blw	BnD	BdW	CmD	DuskD	HectD	HbW	LfpW	Māui	Orca	SrW	SpW
Bathy		12.44	31.24	7.59	13.82	9.86	20.34	14.80	31.95	9.21	34.20	22.63	42.29
BedDist		0.00	7.93	0.00	0.00	0.00	4.37	0.00	0.00	9.77	6.69	27.34	0.00
BPI_broad		7.52	0.00	2.92	4.35	9.65	0.00	7.47	4.35	0.00	0.00	4.16	3.97
BPI_fine		5.46	3.06	0.00	0.00	0.00	1.41	16.79	0.00	1.35	6.06	0.00	4.04
Chl-a.Grad		10.03	0.00	2.45	6.58	5.52	0.00	5.58	11.64	0.00	0.00	4.41	4.85
MLD	✓	0.00	0.00	0.00	0.00	0.00	0.00	0.00	14.14	0.00	0.00	0.00	13.80
Mud		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.17	0.00	0.00	0.00
Rough		0.00	12.95	0.00	0.00	0.00	0.00	0.00	0.00	1.52	0.00	0.00	0.00
Sand		0.00	3.68	0.00	0.00	0.00	1.61	0.00	0.00	0.00	3.62	0.00	0.00
Slope		13.37	0.00	0.00	5.04	7.77	0.00	0.00	6.64	0.00	6.98	11.65	9.01
SSS	✓	0.00	0.00	9.77	0.00	0.00	0.00	0.00	0.00	15.28	0.00	0.00	8.58
SST	✓	28.24	15.24	56.74	46.29	31.17	21.33	19.02	0.00	0.00	9.59	7.40	0.00
SSTGrad	✓	4.71	2.94	1.76	3.76	5.27	2.80	5.56	4.25	0.75	2.83	3.30	3.97
TC		0.00	4.52	5.36	0.00	0.00	1.54	16.90	0.00	0.96	3.10	4.44	0.00
TPP3	✓	12.54	5.50	3.94	7.33	13.65	0.00	6.80	12.75	4.12	4.67	4.07	5.50
Velo_bottom	✓	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.99
Velo_surface	✓	5.69	4.43	4.11	4.25	9.40	2.14	7.06	4.33	7.72	3.17	5.00	0.00
CHL_MLD	✓	0.00	0.00	0.00	0.00	0.00	7.42	0.00	0.00	0.00	0.00	0.00	0.00
BBP443		0.00	8.52	5.35	8.59	7.72	37.04	0.00	9.95	45.16	19.09	5.59	0.00

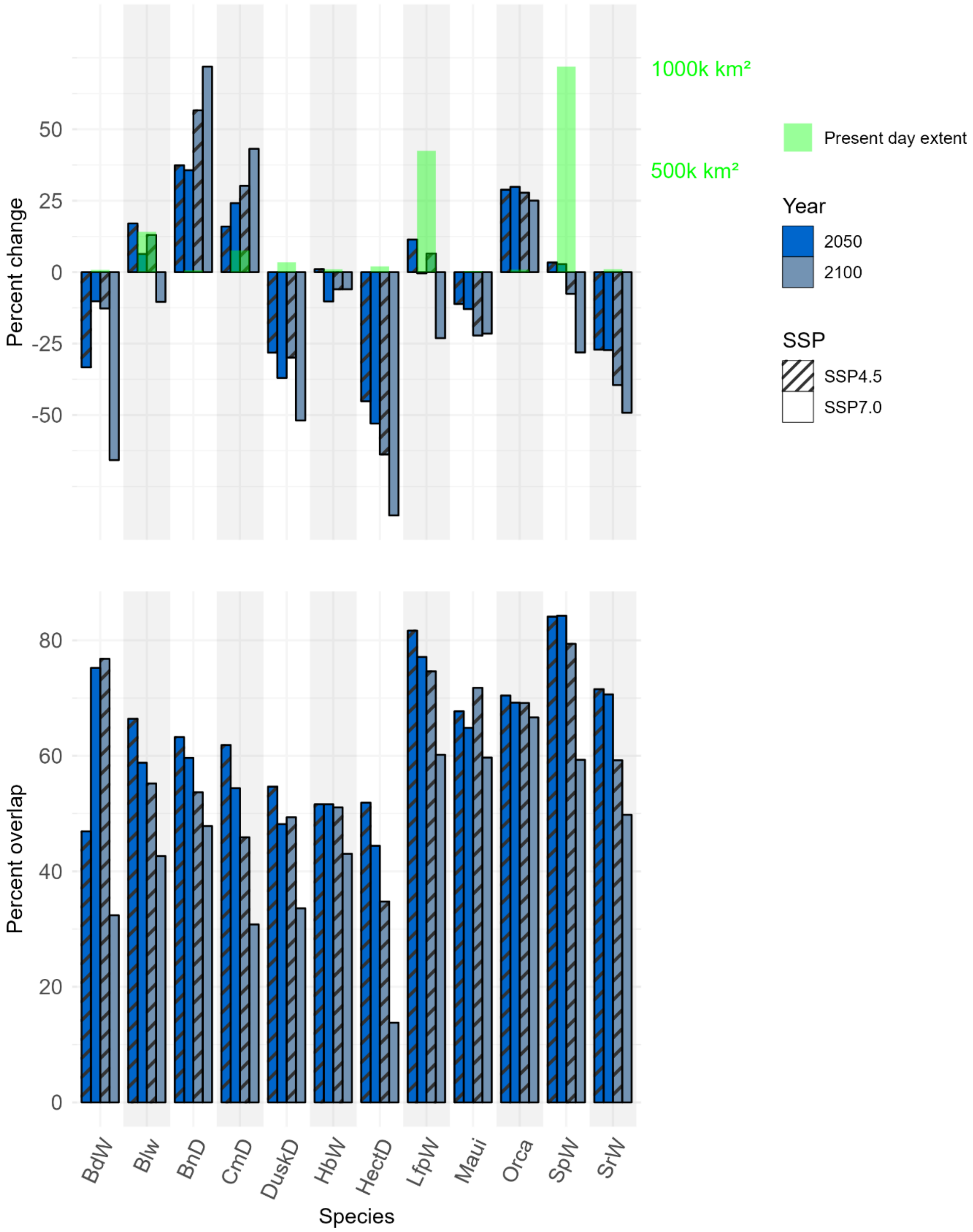

Figure 3-28: Changes in core habitat - all marine mammals. Graphical representation of the spatial overlap (bottom) and percentage change (top) in the extent of core habitat (HSI > 0.75) between the present day and the four future scenarios. The total extent of core habitat for the present day is overlaid on the top panel to indicate species with more restricted present-day range. Species codes are Bryde's whale (BdW), blue whale (Blw), coastal bottlenose dolphin (BnD), common dolphin (CmD), dusky dolphin (DuskD), humpback whale (HbW), Hector's dolphin (HectD), long-finned pilot whale (LfpW), Māui dolphin (Māui), coastal Orca (Orca), sperm whale (SpW), southern right whale (SrW).

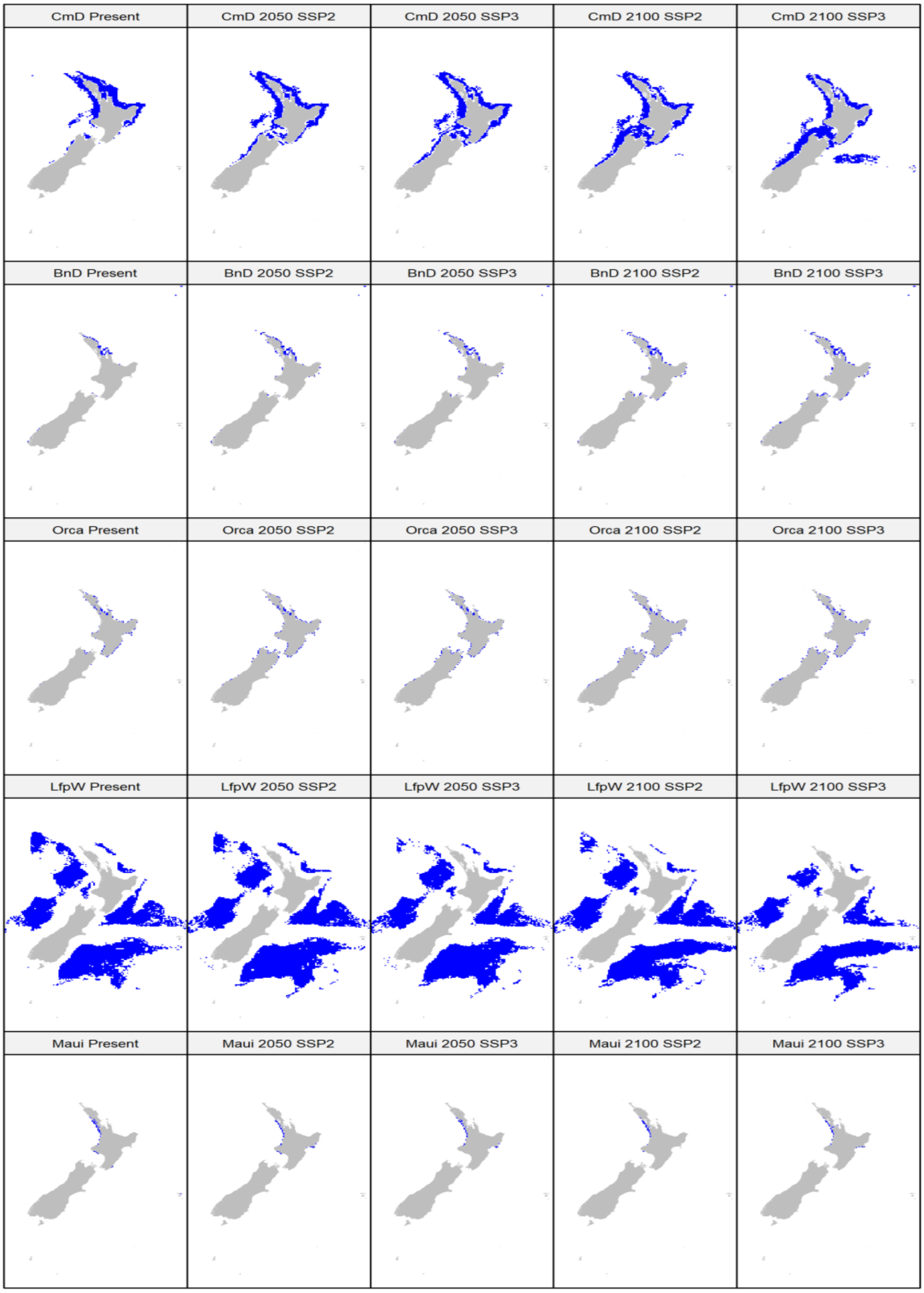

Figure 3-29: Core habitat distribution - dolphins. The predicted distribution of core habitat (HSI > 0.75) for dolphin species for the present day (left) and four future scenarios; mid-century (2050) and end-of century (2090) under SSP2-4.5 and SSP3-7.0 /emissions scenarios. Species are common dolphin (CmD), bottlenose dolphin (BnD), Orca (Orca), long-finned pilot whale (LfpW), Māui dolphin (Māui), Hector's dolphin (HectD), dusky dolphin (DuskD). Figure continued on the next page.

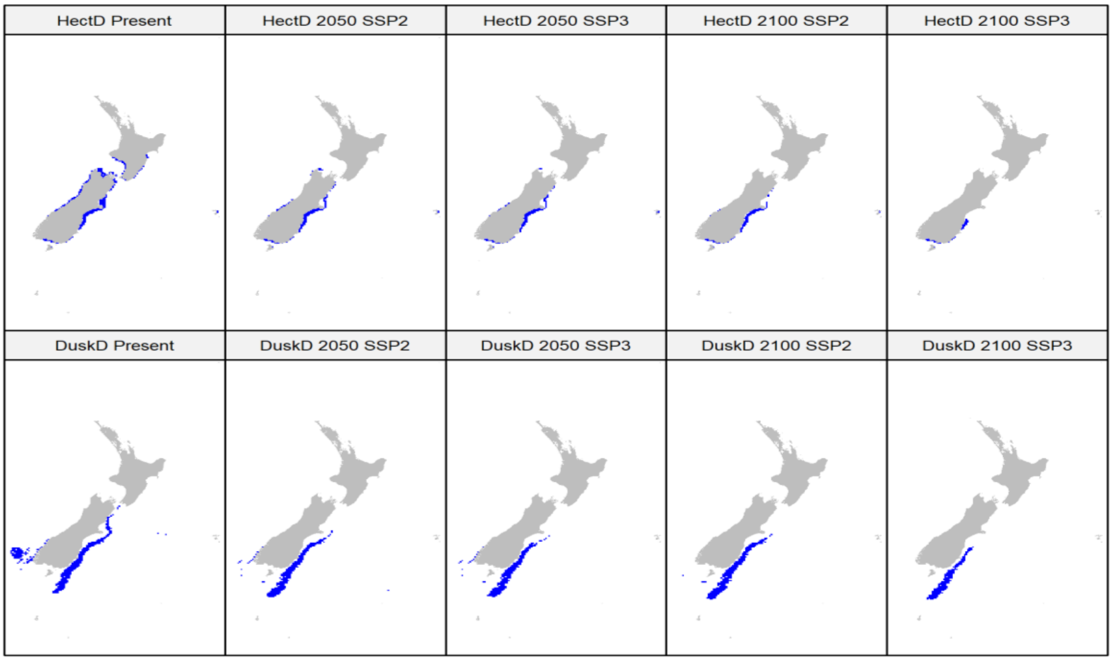

Figure 3-30: Core habitat distribution - dolphins (cont.). The predicted distribution of core habitat (HSI > 0.75) for dolphin species for the present day (left) and four future scenarios; mid-century (2050) and end-of century (2090) under SSP2-4.5 and SSP3-7.0 /emissions scenarios. Species are common dolphin (CmD), bottlenose dolphin (BnD), Orca (Orca), long-finned pilot whale (LfpW), Māui dolphin (Māui), Hector's dolphin (HectD), dusky dolphin (DuskD). Figure continued on next page.

Spatial predictions of the distribution of core habitat for the present day and under future climate scenarios revealed diverse responses for the various dolphin species (Figure 3-29). Core habitat for common dolphin was predicted to expand from current core habitat in northern half of the North Island to the lower North Island and the west coast of the South Island under all future scenarios and to the Chatham Rise by the end of the century under SSP3-7.0. Similarly, core coastal habitat for bottlenose dolphins is predicted to expand outside to areas in the lower North Island, into Tasman/Golden Bay and to the west coast of the South Island by 2090 under both SSP scenarios. Orca were predicted to have a greater extent of core area around the South Island by 2090 with limited change to existing core habitat in the North Island. Core habitat for long-finned pilot whales in northern regions was predicted to contract, particularly under the most extreme future scenario. For Māui dolphin, core habitat becomes increasingly more fragmented under more extreme future scenarios and core habitat in the South Taranaki Bight is absent in all future scenarios except mid-century under SSP2-4.5. Hector's and Dusky dolphin show the most notable range contraction of the delphinids, with core habitat of both species being predicted to contract to occur solely in the south and east of the South Island by 2090 under both SSP scenarios.

For whales, there was a similar diversity of responses of species distribution to future climate scenarios (Figure 3-31). Substantial changes in distribution for sperm whale were mostly notable for the most extreme (SSP3-7.0 at 2090) scenario only, with clear reduction in core habitat in the northern component of the EEZ and in offshore waters south of the Chatham Rise.

Core habitat for humpback whale is patchily distributed in coastal habitat that is utilised during the species migration including areas within the EEZ of Rangitahu/Kermadec Islands, with several areas of coastal habitat predicted to contract under future scenarios. Bryde's whale were predicted to undergo a contraction in core habitat in all future scenarios, with the Hauraki Guld remaining the only location with core habitat by 2090 under SSP3-7.0. Similarly, coastal habitat for southern right whales was predicted to decrease in the south of the South Island, with limited evidence for range expansion. There were relatively minor changes to distribution for blue whales, with new occurrence of core habitat on the Chatham Rise under all future scenarios.

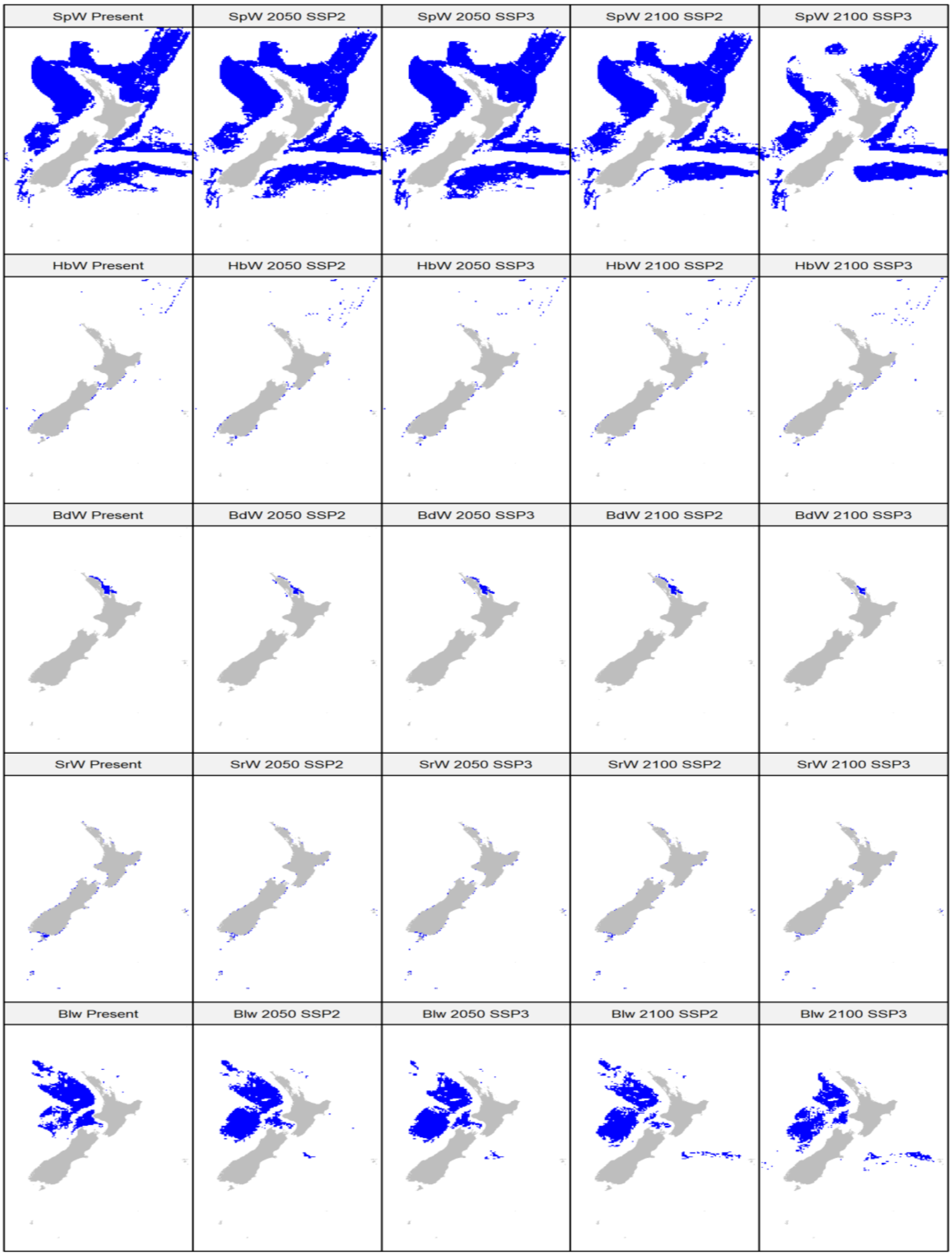

Figure 3-31: Core habitat distribution - whales. The predicted distribution of core habitat (HSI > 0.75) for whale species for the present day (left) and four future scenarios; mid-century (2050) and end-of century (2090) under SSP2-4.5 and SSP3-7.0 emissions scenarios. Species are sperm whale (SpW), humpback whale (HbW), Bryde's whale (BdW), southern right whale (SrW), blue whale (BlW).

Potential internal refugia for bottlenose dolphin under the most extreme future scenario are located in areas where core habitat is currently well-known: the north-east of the North Island, Fiordland, and some areas in the Marlborough Sounds (Figure 3-32). However, there is some range contraction in the inner Marlborough Sounds and broad areas of expansion (i.e., external refugia) in coastal habitat around both main Islands. Refugia for Orca exhibit minimal change to existing core areas in the North Island but show substantial external refugia around the South Island. Internal refugia for Māui dolphin is located within the currently recognised core area for the species on the west coast of the North Island, however there are contractions of the species offshore extent in this area and contractions predicted within the Kaipara Harbour and in the South Taranaki Bight. Māui dolphin show some expansion of core habitat suitability within the Manukau Harbour and in Hawkes Bay. Internal refugia for Hector’s dolphin were predicted in the south and east of the South Island only, in coastal waters of Otago and Southland, with no predicted areas for external refugia under the most extreme future scenario. Common dolphin showed internal refugia in more inshore habitat within their currently occupied core areas in the north of the North Island, with range contraction in more offshore waters in this area. External refugia for common dolphin were predicted in the north and west of the South Island and on the Chatham Rise. Long-finned pilot whale showed range contraction in the most northern of the species current core habitat, in the Hikurangi Margin and some areas in the Bounty Trough. Large internal refugia were predicted in the Bounty Trough, on the Challenger Plateau and north of the Chatham Rise, while the species exhibited minimal external refugia. Internal refugia for dusky dolphin occurred only in the south-east of the South Island with limited external refugia in the southernmost portion of this region.

Sperm whale exhibited range contraction in both the north and south of the EEZ, with limited prediction of range expansion but with broad internal refugia in offshore waters (Figure 3-33). Internal refugia for blue whale were predicted in the South Taranaki Bight and off the west coast of the North Island, while expansion of core habitat was predicted off the west coast of the South Island and on the Chatham Rise. Humpback whale internal refugia are widely distributed throughout South Island coastal waters, particularly Fiordland, Otago, Kaikoura and the Cook Strait with external refugia scattered around the east coast of the North Island and seamounts south of Rangitahu/Kermadec Islands. The Hauraki Gulf remains the only area of internal refugia for Bryde’s whales, with limited evidence of external refugia. For southern right whales, core areas are predicted to contract to more fragmented internal refugia around the North, South and Stewart Islands – with Foveaux Strait being the largest area of predicted range contraction.

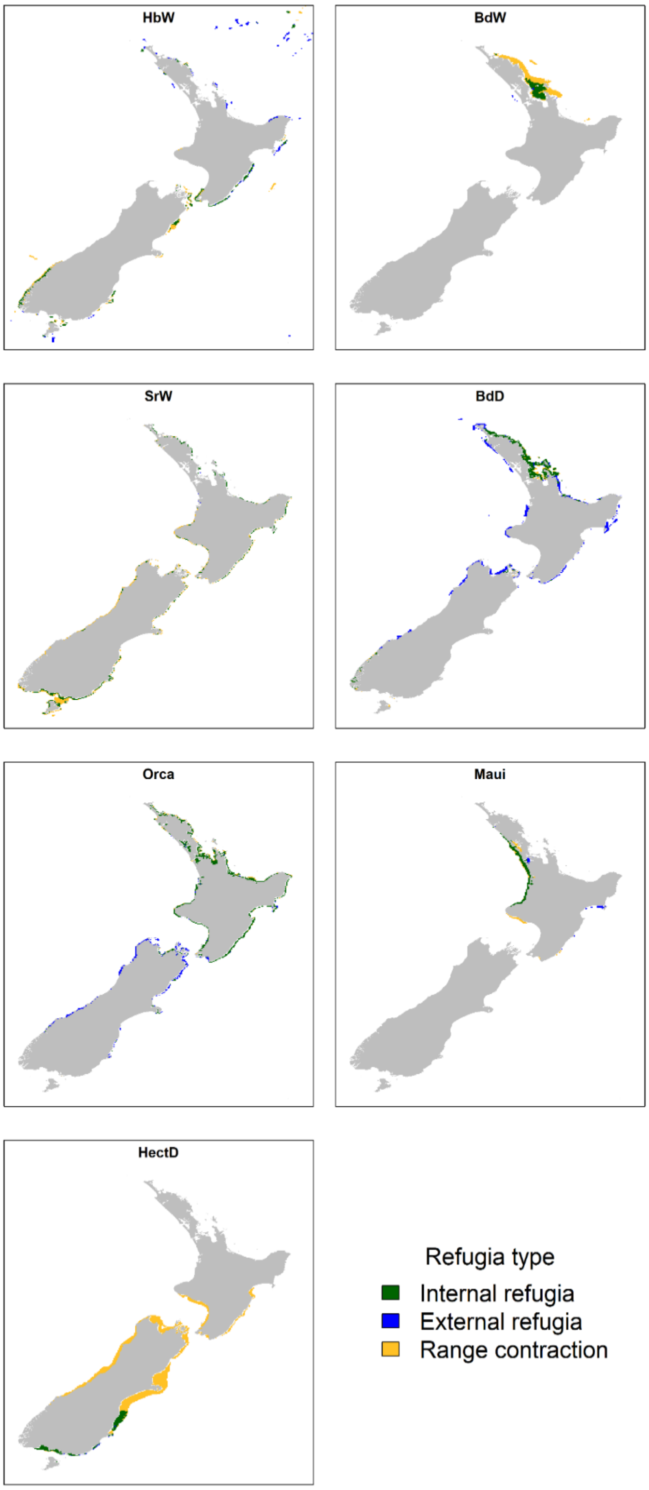

Figure 3-32: Potential refugia (SSP3) - coastal marine mammals. The distribution of two types of potential climate refugia for coastal marine mammals. Internal refugia are areas considered core habitat (HSI > 0.75) in both present day and the most extreme future scenario (2090, SSP3). External refugia are areas considered core habitat in the future but not for the present day. Area's showing range contraction (present day core habitat that is not considered core habitat in the future) are also shown. Species are humpback whale (HbW), Bryde's whale (BdW), southern right whale (SrW), bottlenose dolphin (BdD), Orca, Māui dolphin (Māui) and Hector's dolphin (HectD). Note species are grouped here by coastal habitat use to enable plotting of refugia under a common spatial extent to better aid visualisation.

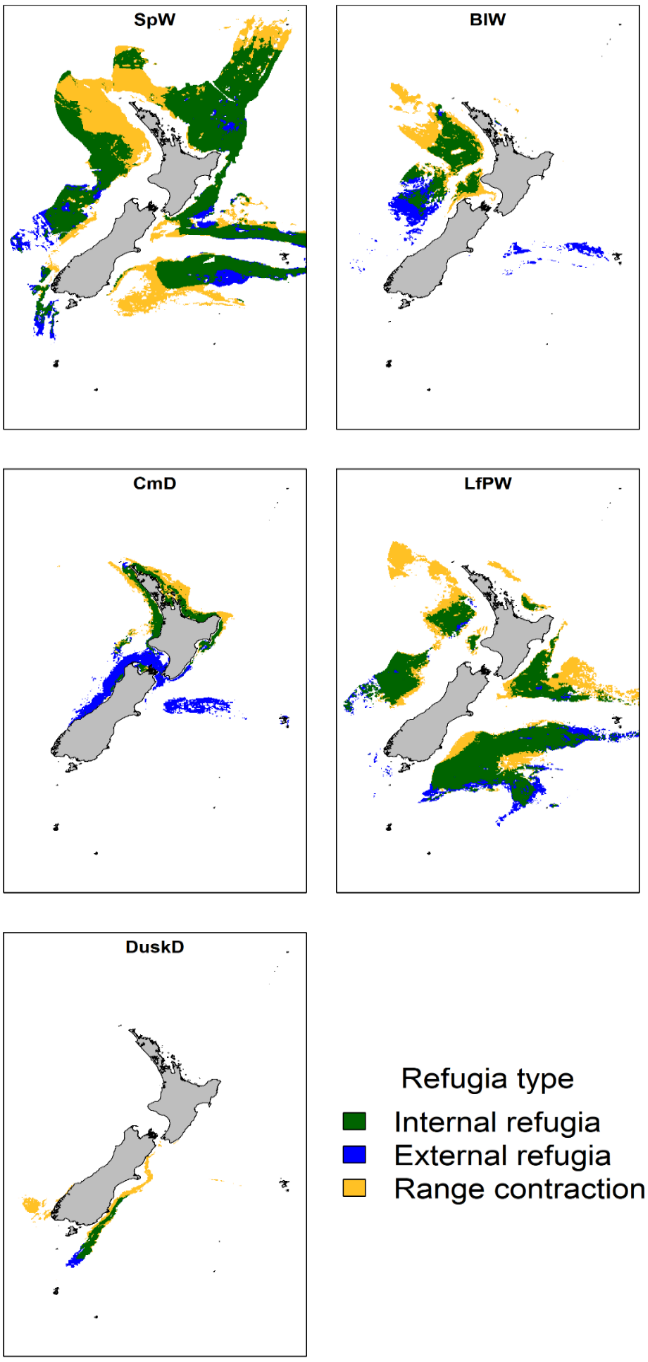

Figure 3-33: Potential refugia - offshore marine mammals. The distribution of two types of potential climate refugia for offshore marine mammals. Internal refugia are areas considered core habitat (HSI > 0.75) in both present day and the most extreme future scenario (2090, SSP3). External refugia are areas considered core habitat in the future but not for the present day (i.e., range expansion). Area's showing range contraction (present day core habitat that is not considered core habitat in the future) are also shown. Species are sperm whale (SpW), blue whale (BlW), common dolphin (CmD), long-finned pilot whale (LfPW), dusky dolphin (DuskD). Note species are grouped here by offshore habitat use to enable plotting of refugia under a common spatial extent to better aid visualisation.

3.2 Overlap with non-climate related threats

Analysis of the vulnerability of biogenic habitat-forming invertebrates to threats from bottom-contact fishing activities revealed high variability among taxa (Table 3-22). Generally, the spatial overlap between core habitat and areas of fishing stressors remained constant or decreased between predictions for the present day and for future scenarios. *Atrina* had the highest overlap between present day core habitat and fishing-related stressors (43.58%), followed by *Ostrea* (36.48%), *Crella incrustans* (36.04%), *Dactylia* (34.88%) and *Callyspongia* (30.36%). Under the most extreme future scenario (2090 under SSP3-7.0), this spatial overlap decreased to 27.19%, 28.59%, 30.19%, 30.30% and 28.78 for the five taxa respectively. However, at 2090 under SSP2-4.5, *Dactylia* and *Callyspongia* had slight increases in the overlap between core habitat and fishing-stressors. Due to the extreme contraction of core habitat for *Tucetona* under most future scenarios (Figure 3-11) there is limited overlap between this taxon and fishing related stressors in the future.

Table 3-22: Threat overlap -biogenic habitat-forming invertebrates. The percentage overlap between core habitat of biogenic habitat-forming benthic invertebrates and areas within the stressor-response footprint for bottom-impact fishing. Percent overlap is given for present day core habitat, the four future scenarios and for internal refugia for each taxon.

Taxa	Present day	2050 SSP2	2050 SSP3	2090 SSP2	2090 SSP3	Refugia (int)
Atrina	43.58	37.97	44.19	34.51	27.19	28.40
Callyspongia	30.36	29.82	27.99	32.22	28.78	30.80
Celleporina	21.17	15.91	15.09	18.03	9.13	5.44
Cinctipora.elegans	13.37	7.91	7.14	8.38	6.03	6.03
Crella.incrustans	36.04	34.43	33.97	34.69	30.19	31.32
Dactylia	34.88	35.28	32.56	35.22	30.30	33.32
Hornera	6.51	3.48	2.99	2.56	1.28	1.28
Iophon	24.76	23.15	24.88	23.73	20.03	19.84
Keratoisididae	0.61	0.33	0.44	0.38	0.47	16.68
Ostrea	36.48	38.54	35.21	33.81	28.59	0.46
Paragorgia	0.63	0.38	0.44	0.50	0.64	28.59
Tucetona	12.52	18.13	NA	NA	NA	0.56

The overlap of internal refugia with areas of high fishing-related stressors show that over 30% of areas that remain consistently part of core habitat coincide with locations where levels of bottom-contact fishing may comprise habitat suitability (Table 3-22). Taxa with the highest overlap of refugia and highly fished areas are *Dactylia*, *Crella incrustans, Callyspongia, Ostrea* and *Atrina* respectively. Areas of overlapping internal refugia for *Atrina* and areas with high bottom contact fishing are centred in a band of shelf-based habitat of the Otago coast (Figure 3-34). For *Callyspongia* and *Dactylia*, overlapping areas occur throughout the east and north coasts of the South Island with broad areas south of Banks Peninsula and scattered areas off East and North Capes. *Crella incrustans* has a similar distribution of overlapping areas with the addition of locations on the Taranaki coast. *Celloprina, Cinctopora elegans* and *Hornera* have highly reduced internal refugia under the most extreme climate change scenario, however all remaining refugia and areas of overlap with high bottom trawling intensity occur off the south coast of the South Island.

For *Iophon*, both refugia and areas of stressor overlap on the east coast of Northland, while overlapping areas for *Ostrea* occur around Banks Peninsula, in the Canterbury Bight and the south Otago coast.

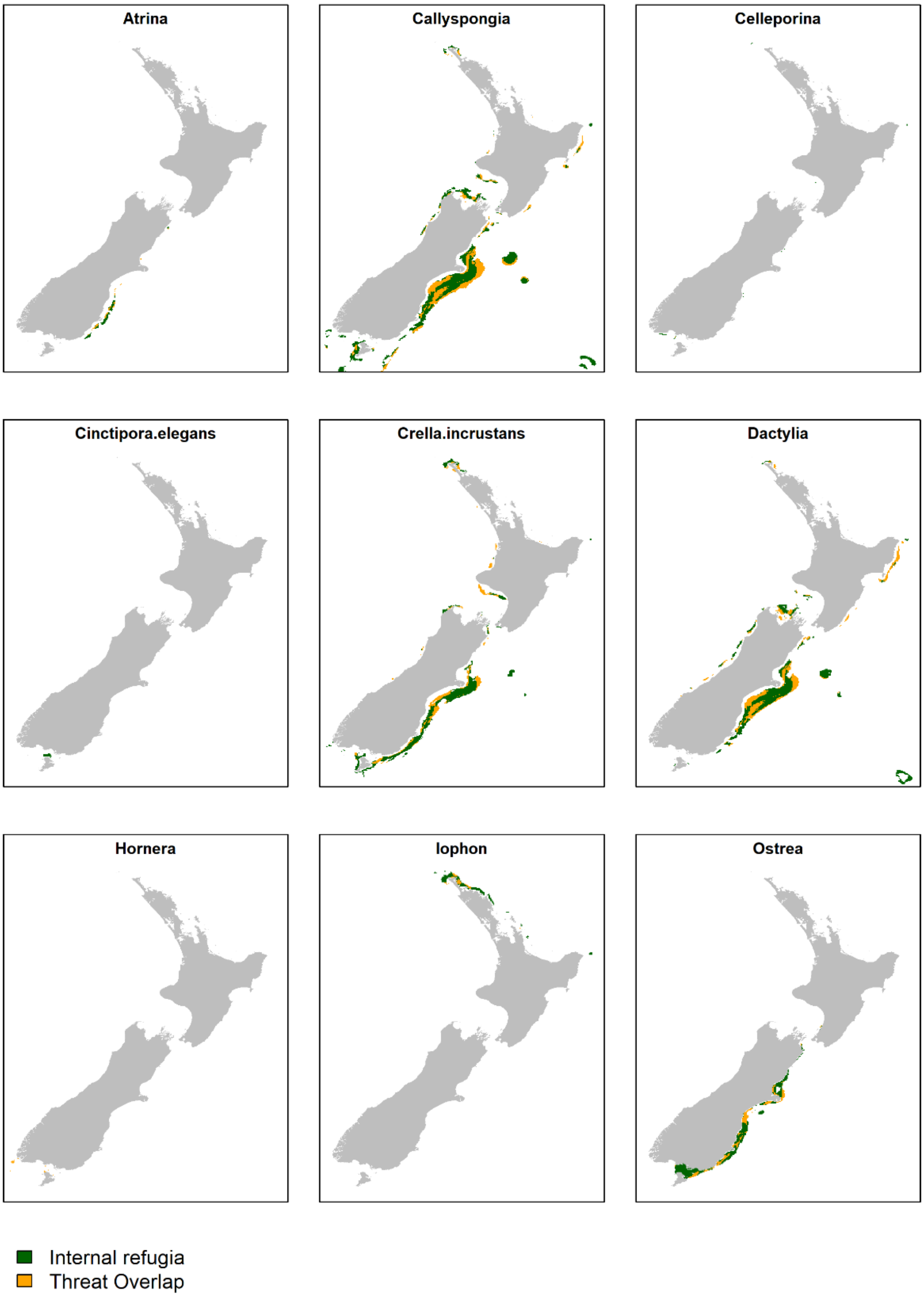

Figure 3-34: Refugia/Threat overlap - biogenic habitat-forming invertebrates. Area of overlap between internal refugia of core habitat and the stressor response footprint derived for bottom-contact fishing. Overlapping areas are shown in yellow for nine biogenic habitat-forming invertebrate taxa with extant refugia of core habitat under SSP3 at 2090. Green areas are refugia that are currently outside of the stressor-response footprint.

Threatened and at-risk macroalgae also had high variability in overlap between predicted core habitat and the stressor response footprint related to high light attenuation from suspended particulates (i.e., EBED) (Table 3-23). *P. dichotoma* had the highest overlap between present-day core habitat and high stressor intensity (71.36%), however this declined slightly under two future scenarios and overlap was 0 under the most extreme future scenario as core habitat was largely extirpated (Figure 3-26). *G. urvilleana* also had high overlap between present day core habitat which increased to 100% overlap in the single future scenario where core habitat remained. Present day core habitat for *P. lusoria* had 60.66% overlap with areas of high stressor intensity and this remained consistent in all future scenarios. For each species, internal refugia generally had much higher overlap with areas within the stressor response footprint than core habitat for any given scenario. There was 71.66% overlap between internal refugia and high stressor intensity *for P. ilusoria*, and these overlapping areas were spread throughout the species range in the north of the North Island (Figure 3-35). Overlap between refugia and high stressor intensity was between 42 and 45% for *A. nitidissima, G. macrocarpa*, and *P. binghamiae* with areas of overlap occurring in the north and west of Northland, off the Waikato coast, and for the latter species, in an isolated areas on the west coast of the South Island (Figure 3-35). *M. mutabile* had relatively low overlap of internal refugia and high stressor areas, with all overlap occurring in the inner Hauraki Gulf.

Table 3-23: Threat overlap - macroalgae. The percentage overlap between core habitat of threatened/at-risk macroalgae and areas within the stressor-response footprint for light attenuation at the seabed (EBED). Percent overlap is given for present day core habitat, the four future scenarios and for internal refugia for each taxon.

Taxa	Present day	2050 SSP2	2050 SSP3	2090 SSP2	2090 SSP3	Refugia (int)
Aeodes nitidissima	10.29	5.61	6.18	6.68	6.49	42.23
Gigartina macrocarpa	29.27	23.32	24.20	23.15	23.18	44.68
Grateloupia urvilleana	63.50	100.00	NA	NA	NA	NA
Microdictyon mutabile	18.21	11.44	10.44	16.47	10.00	8.87
Myriogloea intestinalis	6.23	0.00	10.42	9.26	13.70	NA
Pachymenia dichotoma	71.36	69.81	72.63	68.76	NA	NA
Pachymenia lusoria	60.66	62.28	62.69	62.49	60.04	71.66
Petalonia binghamiae	10.37	8.78	18.39	14.88	15.84	44.08

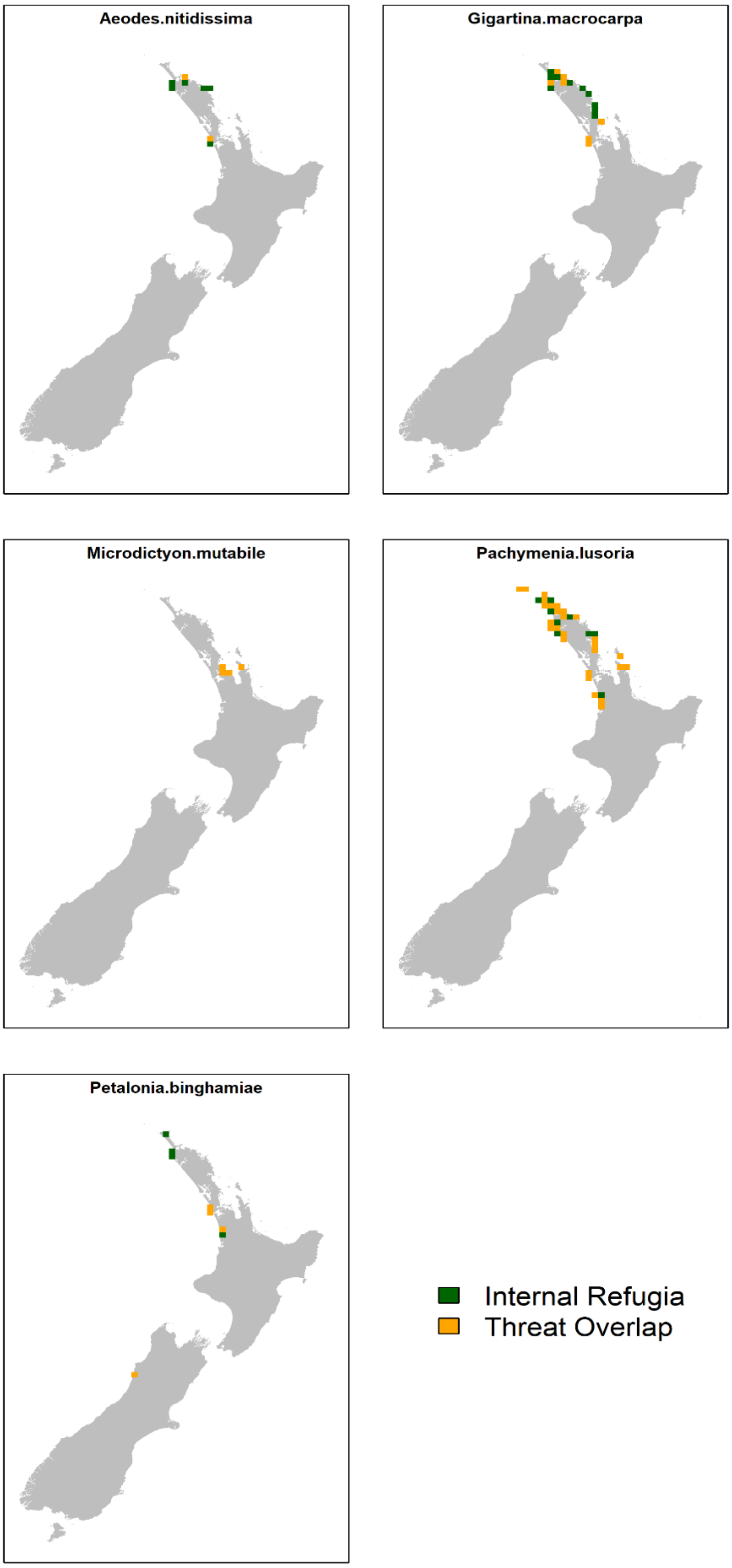

Figure 3-35: Refugia/Threat overlap - threatened macroalgae. Area of overlap between internal refugia of core habitat and the stressor response footprint derived for sedimentation impacts on light attenuation (EBED). Overlapping areas are shown in yellow for the five macroalgae species with internal refugia of core habitat under SSP3-7.0 at 2090. Green areas are refugia that are currently outside of the stressor-response footprint. Grid cell size aggregated to 10 km x 10 km for visualisation.

3.3 Comparison with ‘automated’ approach

Across the three taxonomic groups investigated, we observed substantial differences in the future distribution of core habitat between the models generated under this study and the ‘automated’ approach used by Anderson (2022). These differences were notable with respect to both the distribution of core habitat under the future scenario investigated (2090 under SSP3-7.0) and trends in the change in the extent of core habitat (Figure B-1 and Figure 3-36).

For fish, some species (e.g., blue cod, hake, hapuku) had similar predicted changes in core habitat extent. Yet for most species, there was considerable differences in the change in extent, with several species (e.g., gurnard, hoki, kingfish, orange roughy, snapper, tarakihi) having different trends (i.e., increasing/decreasing extent) predicted by the two approaches. Generally, the automated approach had more extreme predictions for change in core habitat extent. While there were also some important differences in the predicted extent of present-day habitat between each approach (e.g., hapuku), these estimates were generally similar (Figure 3-36). This finding suggests the key differences between the approaches is related to forecasting future distributions. The predicted distribution of future core habitat was significantly different between the two approaches for most species, including those that had similar estimates of change in core habitat extent (Figure B-1).

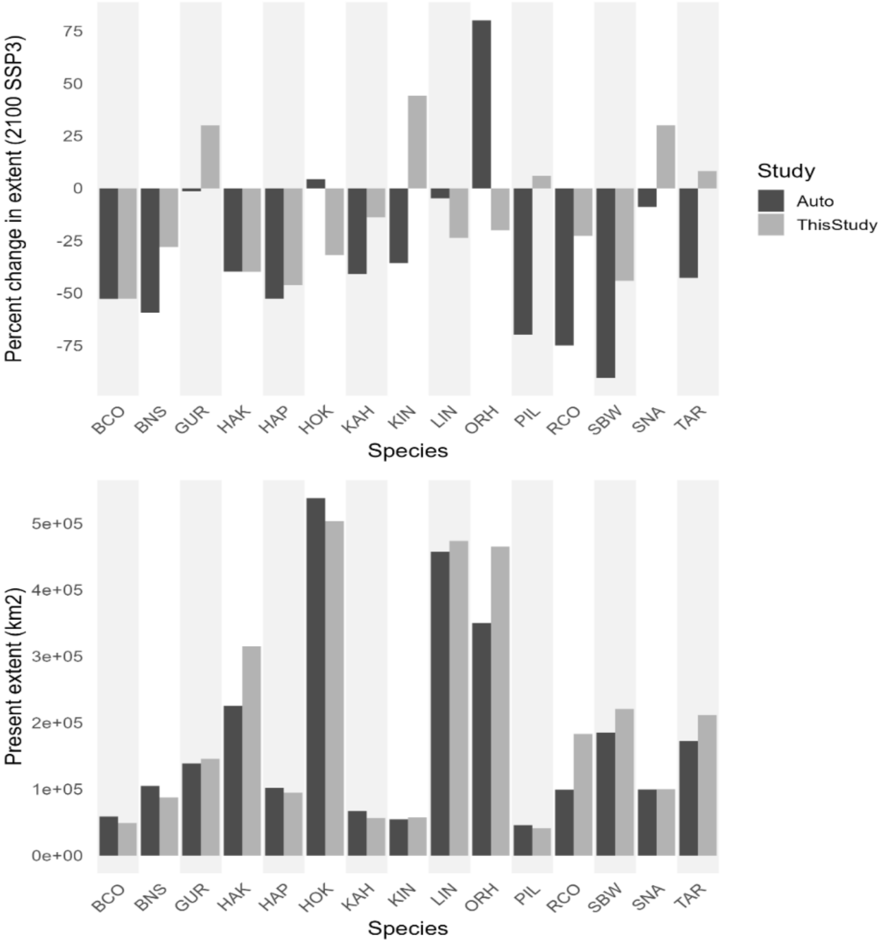

Figure 3-36: Approach comparison - fish. The predicted change in the extent of core habitat (i.e., HSI > 0.75) between the present day and future (2090 under SSP3-7.0) for fifteen species of fish. generated by this study and by Anderson 2022 (auto). The predicted total extent of core habitat for the present day is also shown to provide context on variability under present day conditions.

There were also large differences in the predicted change in extent of core habitat for the sponge taxa investigated by both Anderson (2022) and by this study (Figure 3-37). While the direction of the change in extent (i.e., increasing/decreasing) was different for only a single taxon, there were some large differences in the magnitude of predicted decreases in extent. Most taxa (e.g., *Dactylia, Lissodendoryx, Geodia, Hyalascus, Stelletta)* had at least ~25% difference in predicted decline in core habitat, while several (e.g., *Ecionemia, Haliclona*) had over 50% difference between the two approaches. Apart from two taxa (*Hyalascus, Suberites*), difference in the predicted extent of present-day core habitat were more moderate (Figure 3-37). However, the automated approach consistently predicted greater extent of present-day core habitat than models generated under this study. The predicted spatial distribution of future core habitat also differed significantly between the two approaches for most taxa, with there being relatively limited overlap of future core habitat between the approaches (Figure B-2).

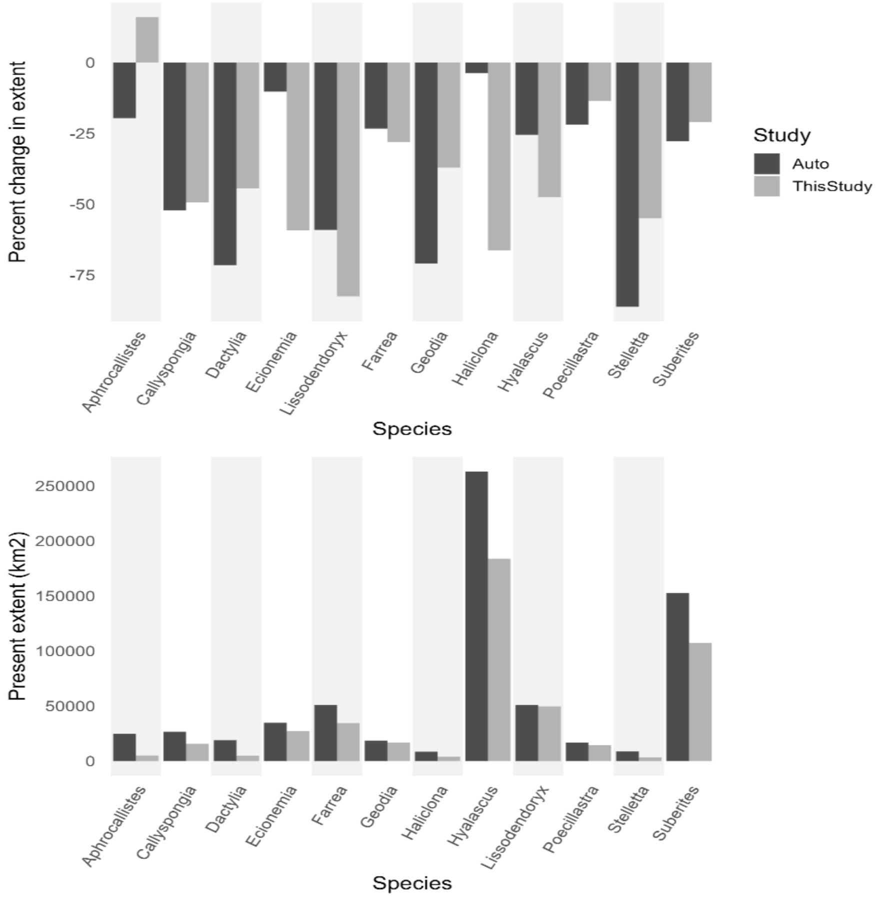

Figure 3-37: Approach comparison - sponges. The predicted change in the extent of core habitat (i.e., HSI > 0.75) between the present day and future (2090 under SSP3-7.0) for twelve sponge taxa, generated by this study and by Anderson 2022 (auto). The predicted total extent of core habitat for the present day is also shown to provide context on variability under present day conditions.

There was less variation in the predicted change in the extent of core habitat between the two approaches for kelp species, with both approaches predicting large declines in extent under the most extreme future scenario (Figure 3-38). Apart from two exceptions (*C. plumosum, E. radiata*) the difference in the predicted decline in extent was less than 15% between the studies. However, for the latter species the difference was substantial (~50%). In contrast to fish and sponges there were some large differences in the predicted extent of present-day core habitat, with the automated approach consistently predicting a greater extent (Figure). For some species (e.g., *X. gladiata, M. urvilliana*), the difference in the extent of present-day core habitat was substantial. The spatial distribution of future core habitat was similarly different between the two approaches, with the automated approach typically having broader and more widely distributed core habitat than predictions developed under this study (Figure B-3).

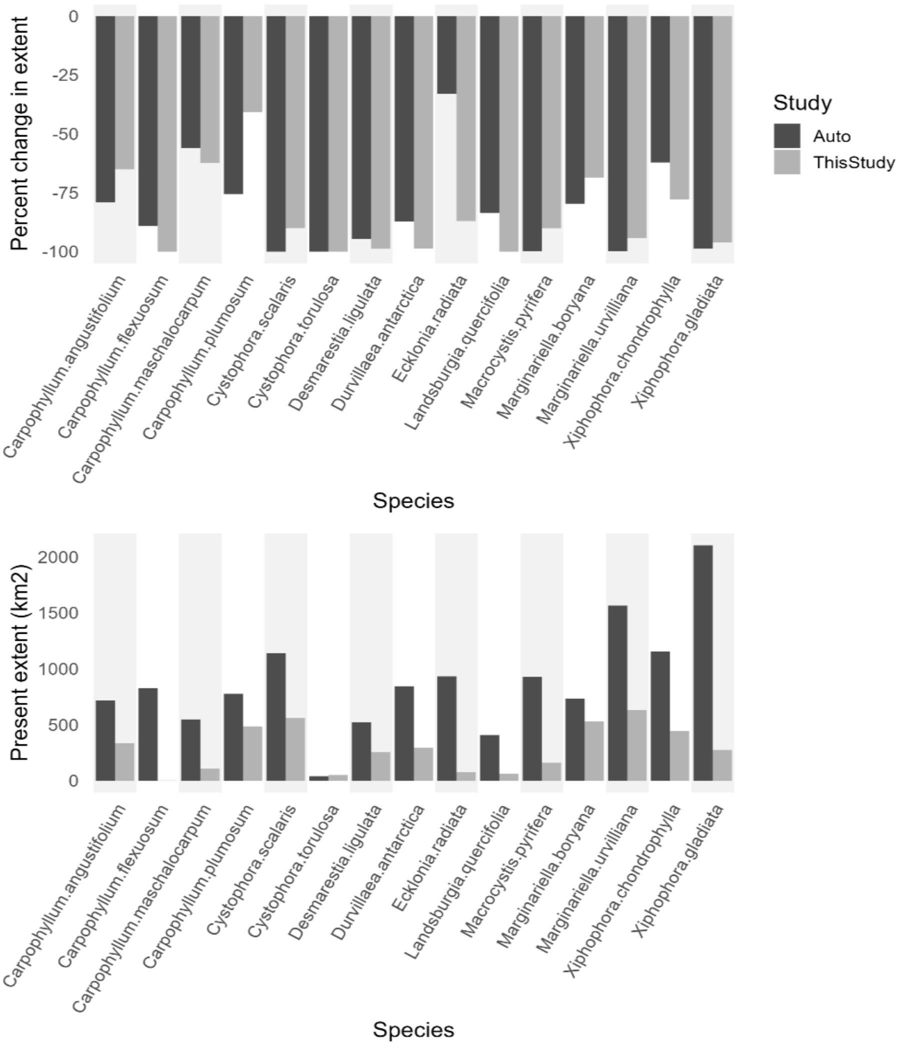

Figure 3-38: Approach comparison - kelp. The predicted change in the extent of core habitat (i.e., HSI > 0.75) between the present day and future (2090 under SSP3-7.0) for fifteen kelp taxa, comparing HSMs generated by this study and by Anderson 2022 (auto). The predicted total extent of core habitat for the present day is also shown to provide context on variability under present day conditions.

4 Discussion

By pooling resources across NIWA and DOC, this study has generated an important repository of spatial information on the future distribution of over 70 marine species under four future climate scenarios and for the present day. Spatial layers on these species' distribution are available via the DOC Marine Data Portal (https://doc-marine-data-deptconservation.hub.arcgis.com/). Alongside these data, we have undertaken analyses to characterise species vulnerability to climate change with respect to changes in habitat suitability and subsequent patterns in distribution and determined locations of potential refugia. We also illustrate simple spatial analyses that can be undertaken to integrate non-climate related stressors into decision-making around the prioritisation of species and areas for management. Together, the outputs generated by this study provide new opportunities for marine stakeholders to advance climate-smart MSP.

4.1 Summary of key findings

Under future climate scenarios, both declines and increases in core habitat extent were predicted for fish. The differences were consistent within species (i.e., consistent responses to all future scenarios within a species), but varied between species. For example, the biggest decrease in core habitat extent was found for blue cod under SSP3-7.0, while a large increase in core habitat extent was predicted for kingfish. Similarly, for marine mammals there was strong variation among species, with some showing positive responses under future scenarios (e.g., extended core habitat for bottlenose dolphins/common dolphins), while for Hector's dolphin, the extent of core habitat was predicted to decrease by >75% under future scenarios (SSP7.0 2090). Bryde's whale was similarly predicted to undergo a significant contraction in core habitat. These are both threatened species (Baker et al. 2010) and thus identifying their distinct vulnerability to climate change impacts on distribution is an important finding.

All biogenic habitat-forming taxa (which included *Jasus edwardsii* for reporting herein) were predicted to undergo a decline in core habitat extent under each future scenario. The same was true for all but one sponge taxa (*Aphrocallistes*), where the extent of core habitat decreased under both SSP2-4.5 and SSP3-7.0 scenarios. For macroalgae, decrease in core habitat (MaxTSS thresholded) was predicted for most kelp species, with strong declines for *Marginariella, Durvillaea* and *Cystophora spp.., Xiphophora gladiata* and *Macrocystis pyrifera*. The results for threatened/at risk macroalgae were not as consistent with some showing increased extent of occupied habitat under future climate scenarios, while others (*Grateloupia urvilleana, Pachymenia dichotoma*) showed decreased extent.

Based on the proportion of species that show declines in core habitat under future climate scenarios, the most vulnerable taxonomic groups are biogenic habitat-forming benthic invertebrates, sponges, and kelps. Most taxa modelled in these groups were predicted to undergo range contraction. For the threatened/at risk macroalgae, many species occupy relatively restricted extents of present-day core habitat, and thus those that are predicted to undergo decreases in habitat extent (*Grateloupia urvilleana*, *Myriogloea intestinalis)* are highly vulnerable to climate change impacts. The same is true for some other taxa groups, where species-specific vulnerabilities should be considered with reference to the predicted extent of present-day core habitat. Taxa which are particularly vulnerable based on having a small present-day extent and contracting range therefore include *Atrina*, *Celleporina*, *Hornera* and *Tucetona* (biogenic habitat-formers), *Haliclona* and *Stelletta* (sponges), and *Carpophyllum flexuosum* and *Xiphophora gladiata* (kelps), Bryde's whale and Hector's dolphins (marine mammals), blue cod and hapuku (fish).

The species and/or taxa groups that had greater predicted resilience to climate change impacts generally aligned with existing knowledge on traits that make species more vulnerable (e.g., narrow niche, restricted present-day distribution, specialist feeding modes) (Foden et al. 2013; Comte & Olden 2017; Chatzimentor et al. 2023). For instance, the sponges and biogenic habitat-formers (both invertebrates and kelps) exhibit broadly consistent decreases in core habitat extent.

Environmental variables and expected responses

From an ecological perspective, one would expect that sessile species would be less resilient than mobile ones, however, the models used here do not incorporate movement or connectivity. Instead, the predicted decreases in suitable habitat for many taxa is solely attributable to changes in the dynamic ESM variables available for the models (e.g., sea temperature, salinity, and productivity variables). For some species, vulnerability is likely related to their relatively narrow niche-width and/or their restricted present-day distribution (e.g., Hector's/Māui dolphin, blue cod). Globally, macroalgae have been found to be at risk of 'falling off the map' when 'stepping stones' (viable habitats) are unavailable as they shift polewards under climate change (Yesson et al. 2015; Krumhansl et al. 2016). This vulnerability is not restricted to macroalgae alone, other sessile or species of limited locomotive capability are at similar risk, while many other species (i.e., mobile species) are reportedly on the move (Hiddink et al. 2015; Hastings et al. 2020).

For species modelled in this study, broadly distributed species were found to be more resilient under future predictions (e.g., *Paragorgia*, *Suberites*, tarakihi, sperm whale), while those with limited distributions, particularly those further south, were found to be more vulnerable. This trend is evident across taxa groups with blue cod the most vulnerable of the fish taxa, *Cinctipora elegans* and *Lissodendoryx* the most vulnerable of the biogenic habitat-formers and sponges, respectively, *Marginariella boryana* the most vulnerable of the kelps, *Pachymenia dichotoma* the most vulnerable of the threatened macroalgae, and Hector's dolphin the most vulnerable of the marine mammals.

The HSMs developed in this study can be useful for exploring taxa-specific vulnerabilities to future climate scenarios and can be used within climate-smart MSP, e.g., for climate-smart marine protected area design (Patrizzi & Dobrovolski 2018; Gilmour et al. 2022). As for all predictive models, limitations and uncertainties should be carefully considered when using HSMs. Risks for using HSMs for management purposes are well recognised (e.g., Fourcade et al. 2018) but these are amplified for future climate HSMs where predictions cannot be independently verified (Thuiller & Münkemüller 2010). Considering this, the HSMs in this project were appraised by experts with knowledge of the ecology, habitat requirements, and distribution of modelled taxa. This additional model 'validation', which accompanies typical statistical model fit metrics, can be used to guide the use of each HSM.

Expert appraisal

This approach follows that used in previous projects involving the development of maps of species distributions in New Zealand waters (Stephenson et al. 2023a; Bennion et al. 2024a), with an additional assumption; if present-day distributions are environmental drivers are reasonably accurate, the predicted future distributions will be similarly accurate. Following previous work, it is recommended that HSMs with an expert appraisal of present-day distributions less than 'somewhat accurate (3)', should not be used for spatial management purposes. However, users of the outputs presented here may make their own choices around the degree of uncertainty they are comfortable including in spatial planning scenarios. Based on this threshold, 72 of a total of 73 models received an appraisal score of 'somewhat accurate (3)' or greater (26 received a score of 1, very accurate and 35 received a score of 2, accurate). Fish had consistently high expert appraisal scores (both coastal and deepwater), while 4 of the 5 whale species had expert appraisals of predictions as ‘somewhat accurate’. For these highly mobile species, it may be that their seasonal occurrence in NZ waters requires predictions with higher temporal resolution (i.e., seasonal/monthly) and their higher trophic position may mean that the biological processes that shape their distribution were poorly represented by the available environmental data.

Although some models received ‘passing’ scores for their present-day predictions, it is important to balance the appraisal with specific commentary from experts. For example, while the appraisal for *Cinctipora elegans* (bryozoan) was high (‘accurate’), the expert identified that: 1) environmental drivers for the HSM were not expected (‘somewhat accurate’), and 2) while most areas of present-day distributions were deemed accurate, some areas were not. This highlights the value of the expert appraisal, as statistical evaluation metrics (AUC/TSS) do not provide this level of detail (though the spatial cross validation can inform HSM usefulness at a bioregional level).

Where environmental drivers do not match those expected to be most important by experts, it is possible that the variables deemed highly important by the models are instead proxies of variables that are unavailable. For example, predatory species are typically driven by the distribution of prey and thus it is assumed the environmental signature of prey distribution is represented by the combination of environmental variables selected by the HSMs (Redfern et al. 2006; Torres et al. 2008). Given that prediction of distributions was based on environmental variables only, it is important to consider how use of proxies may contribute to uncertainties. When using future predictions, a conservative approach could therefore limit the use of HSMs to those which received adequate scores for both the present-day prediction criteria, as well as environmental variable criteria.

Comparison with ‘automated’ approach

The comparison of outputs generated by the ‘automated’ approach undertaken by Anderson (2022) and those generated by this study revealed significant differences in predicted trends in core area extent and mapped distribution of core areas among most species. The differences between the two studies may be related to; 1) different combinations of environmental variables used to predict distribution and consideration of correlated variables – with expert opinion driving the variables selected in this study, 2) more nuanced ‘tuning’ of individual BRT and RF fits to achieve best performance and 3) updated occurrence data for some species. Of these, having expert advice to guide model inputs likely had the biggest influence on the deviation between the studies.

There were no clear insights as to circumstances where predictions agreed which may inform decision rules around when automated methods are suitable. However, future work could explore this more quantitatively – i.e., are there species characteristics that make them more suitable for an automated modelling approach. As it stands, it is recommended that would-be users of future predictions of marine species distribution utilise predictions that more closely adhere to best practice (e.g., Table 4-1), and in the case of the outputs generated by this study, those that can be guided by expert evaluation.

4.2 Decision points

This study has noted a broad range of decision points associated with the development of HSMs for predicting future species distribution and using the outputs of these models for MSP (Table 4-1). These decision points are typically associated with understanding the broad and significant uncertainties associated with this field of research and approaches to standardise the generation/use of these approaches. In Table 4-1, we have summarised the key decision points associated with forecasting future species distribution using HSMs and have provided guidance on the options associated with each decision point and recommended best practice where this is available. Key references for each decision point are also provided. It should be noted that the list of decision points is not exhaustive and simply refers to the points encountered during this study that may bear on the use of the outputs generated here. The few instances where the approach taken by this study differs from best practice are discussed below.

Table 4-1: Decision points. Decision points associated with the development of habitat suitability models for forecasting future species distribution and using the outputs of such models for marine spatial planning.

Decision point	Considerations	Solutions and best practice (where available)	References
Environmental variable selection	Spatiotemporal resolution and data coverage, ecological relevance, 'automated' selection, maximise or minimise model complexity, collinearity among variables and how to choose 'best' variables	Base selection on ecological relevance, known mechanistic relationships and ecological theory. Check correlation for present and future conditions, remove correlated variables and retain those of highest ecological relevance. Explore multiple resolutions of environmental data and test to avoid mismatches in scale Critical to include all variables that may change under climate change – not just thermal variability	(Elith & Leathwick 2009; Elith et al. 2010; Braunisch et al. 2013; Porfirio et al. 2014; Brun et al. 2020; Lauchlan & Nagelkerken 2020)
Modelling methods	Background data selection, model framework, model performance evaluation	Bias correction background data generation, ensemble model predictions, cross validation using withheld data and spatial cross-validation	(Araújo & New 2007; Phillips et al. 2009; Barbet-Massin et al. 2012)
Predictions	Number of future time periods and climate change scenarios (i.e., SSPs), source of dynamic variables, spatiotemporal resolution	Multiple time periods and SSP scenarios, ensemble ESMs and/or ESMs customised for region, statistically downscale ecologically relevant environmental data to match occurrence data, long-term (i.e., 20 yr averages) for long-term changes due to climatological variability	(Bradter et al. 2013; Porfirio et al. 2014; Goberville et al. 2015; Mannocci et al. 2017; Bryndum-Buchholz et al. 2023)
Thresholding habitat suitability index/probability of occurrence	When to apply a threshold, which to use?	Required when quantification of changes in areas occupied/unoccupied, but conservation planning may be impacted by the use of thresholds (i.e., continuous variables have more information). Use thresholds for specific objective and use multiple	(Liu et al. 2013; Guillera-Arroita et al. 2015; Muscatello et al. 2021; Santini et al. 2021; Hellegers et al. 2025a)

Decision point	Considerations	Solutions and best practice (where available)	References
		thresholds to determine consistency in trends.	
Uncertainty	Model uncertainty (e.g., variance around mean estimates), spatiotemporal coverage of occurrence/background data, other decision points	Uncertainty around all key model outputs (predictions, predictor importance, evaluation measures) should be quantified, spatial representation of coverage of spatiotemporal environmental envelope (i.e., environmental coverage), determine key contributors to forecast uncertainty (i.e., across all decision points)	(Elith & Leathwick 2009; Elith et al. 2010; Porfirio et al. 2014; Goberville et al. 2015)
Refugia	Internal (consistent) or external (including novel) refugia, SSP/time period and model type considerations, thresholding/continuous predictions, refugia 'quality'	Generate refugia based on ensemble predictions, characterise refugia considering multiple future scenarios and/or most extreme scenario (precautionary approach), MSP for refugia should consider a range of stressors linked to current 'condition' of habitat	(Araújo & New 2007; Ashcroft 2010b; Kavousi & Keppel 2018; Zelli et al. 2025a)
Non-climate-change related threats	Threats to consider, mapping 'stressor response footprint', 'future' stressor layers	Relevant all species/group threats with spatially explicit data on intensity that may compromise adaptation to climate change Calculate 'response footprint' where possible, proportional overlap with 'high intensity' areas may provide a proxy Forecasting future stressor layers is possible in some cases but carries considerable uncertainty and will not be available for all stressors	(Ramírez et al. 2018; Fragkopoulou et al. 2021; Low et al. 2023b; Cruz et al. 2024; Stephenson et al. 2024; Zelli et al. 2025a)

Climate change 'refugia' have been interpreted and calculated in a variety of ways (Araújo & New 2007; Loarie et al. 2009; Ashcroft 2010a; Kavousi & Keppel 2018; Zelli et al. 2025). One common approach for determining refugia is mapping 'climate velocity' - the rate of change in the environmental conditions that may affect species occurrence (e.g., temperature, pH, oxygen concentration) (Loarie et al. 2009). Climate velocity can provide useful information on areas where the biophysical environmental envelope remains stable (Van Hooidonk et al. 2013; Ban et al. 2016), however it does not include information about species/ecosystem response to change, and considering these responses is an essential component of determining refugia (Carroll et al. 2015). Mapping refugia based on intersecting present-day and future habitat (as per this study) includes information on species-levels responses to changing environmental conditions, however the biophysical changes upon which distribution is based are not typically mapped. Thus, mapping climate velocity and predicting changes in habitat suitability provide complementary information (Carroll et al. 2015). Future work should prioritise mapping climate velocity across a broad number of biophysical variables. Additionally, future work could incorporate life-history characteristics of species to determine the ability of source populations to colonize external refugia, which requires consideration of how far away external refugia are from areas where the current population exists, and the ability for species to traverse those distances in the timeframes that climate change impacts are expected to drive changes in species distributions. In the first instance, this could be examined by assessing the fragmentation and/or patchiness of external refugia identified. A more nuanced approach could involve the use of particle tracking models (based on underlying hydrodynamic models) and incorporating species-specific pelagic larval durations, where appropriate, to investigate whether external refugia could feasibly be colonized by source populations.

The NZ ESM was selected as the source of the dynamic (forecastable) environmental variables used to predict distribution in this study due to its demonstrated accuracy in NZ waters, statistically downscaled data and the availability of a broad range of biophysical variables that may affect species future distribution (i.e., not relying on thermal changes only).

While the NZ ESM is a 3-internal member ensemble model, it is largely based on its parent model the UK ESM (Sellar et al. 2019; Behrens et al. 2020). Thus, while many studies utilise a single GCM/ESM for future predictions of species distribution (Jensen et al. 2017; Kleisner et al. 2017; Martínez et al. 2018; Simon-Nutbrown et al. 2020; Fragkopoulou et al. 2021; Anderson et al. 2022; Zelli et al. 2025), future work should explore differences in predictions from broader multi-model ensembles (e.g., CMPI6) to determine prediction uncertainty due to the choice of GCM/ESM (Robinson et al. 2011; Porfirio et al. 2014).

Thresholding approaches to binarise HSM predictions into various categories can have a significant influence on the quantification of change in distribution and ranking of vulnerability (Liu et al. 2013, Santini et al. 2021, Hellegers et al. 2025). Best practise recommends the use of multiple thresholds, consideration of species characteristics (e.g., prevalence) and weighing options that may be most appropriate for a given objective (Hellegers et al. 2025). Typically, there is a trade-off between the risks of overprediction and underprediction with thresholds being better suited to minimise biases associated with one risk or another.

Based on a studies objective it may be important to ensure high accuracy of predicted presences, with predicting absence being of less relevance. In contrast for some studies (i.e., those that predict extinction/extirpation), predicting absences may be of critical importance. Alternatively, studies may map and quantify change using multiple thresholds to establish the uncertainty inherent in this decision point. In this study we have calculated multiple thresholds, each with strengths and weaknesses, that can be applied to the continuous HSI predictions developed here which may suit a range of applications. Our calculations of vulnerability, refugia and overlap with non-climate related threats used a single fixed threshold of HSI > 0.75 for high quality (i.e., core) habitat. Future work should determine the sensitivity of these analyses to threshold selection. Additionally, there are many situations where using a threshold is not advised (e.g., decision support analyses), due to the reduction in information available for undertaking spatial prioritisations (Guillera-Arroita et al. 2015; Santini et al. 2021).

4.3 Caveats and options for improvements

As noted, there are limitations associated with the models generated for this work and there are risks when using their predictions for spatial planning purposes. To produce accurate HSMs, ideally the full breadth of a species ecological niche is well represented in the training data. Furthermore, presence and absence information are preferred, but true-absence information is not always available at the scale required (Stephenson et al. 2021). Biases are therefore present in most datasets available for modelling, including biases towards species presence over absence, and spatial biases in both data types. For example, for some groups much of the occurrence information used here was generated from fisheries-dependent data which is biased towards fished areas (e.g., for benthic invertebrates), or generated from coastal/shore-based sampling which tend to be near safe harbours/accessible areas. Occurrence and background data for fish come from a comprehensive and standardized series of trawl surveys. However, several species modelled in this study occur outside of trawlable habitat (e.g., reef habitat) and thus distribution in these habitats may not be accurately represented. Moreover, catchability biases may exist for species not routinely sampled using trawl gear (e.g., pilchard). Combining data from a broader range of sources may reduce the uncertainties associated with relying on a single-method survey series and improve model transferability and thus predictive accuracy (Grüss et al. 2023).

Several methods were used in this study to reduce impacts of biases in occurrence data on the HSMs. Firstly, a target-group approach was used to generate background data which ensures background data has the same biases as occurrences and with such data being more likely to represent absences than randomly generated ones (Phillips et al. 2009). Additionally, the expert appraisal step provided an avenue to explore the extent to which the occurrence information captured the ecological niche of modelled taxa (i.e., how well the biological records of species reflect expert view of taxa distribution). This information can help identify gaps/biases in the training data, which may contribute to erroneous spatial predictions. Most taxa scored ‘accurate’ or higher under the ‘distribution of occurrence records’ criteria, with some exceptions from benthic invertebrates (e.g., *Paragorgia* and *Haliclona*), and fish (e.g., orange roughy). Notably, several marine mammal species received scores of ‘somewhat accurate’ which is not surprising given the range of these species and therefore the breadth of the NZ EEZ that would need to be covered to accurately represent their distribution.

It is important to note that HSMs prediction of future distribution based on habitat suitability only and thus does not account for a range of factors (e.g., connectivity between habitats, dispersal ability, mechanistic processes, density dependence), that will influence whether areas are occupied or not. Taxa-specific environmental data was used to develop the HSMs, but the absence of accurate data on substrate type likely impacts the accuracy of HSMs for seafloor taxa (i.e., the benthic invertebrate and macroalgae) (Bowden et al. 2021). Further, the inclusion of data on biotic interactions (e.g., species interdependencies, predator-prey relationships) would likely improve the models for all taxa. The use of joint species distribution models (jSDMs) to incorporate species-species interactions (Stephenson et al. 2024) provides important avenues for future research given the available data. Similarly, the inclusion of mechanistic responses (e.g., based on mechanistic models) could have a significant impact on future predictions (Elith et al. 2010). For example, inclusion of behaviour and phenology to predict a species’ distribution limits (Briscoe et al. 2023) and/or incorporating species' thermal physiology to inform extrapolations under novel thermal conditions (Custer et al. 2024) may provide more ecologically meaningful predictions. Data on species abundance/density holds significantly more information than presence/absence. Thus, modelling species abundance/density is generally regarded as having greater ecological relevance, utility, discriminatory power and ability to account for biases than presence only or presence-absence models (Howard et al. 2014; Winship et al. 2020). Although broad-scale abundance-based datasets are rare, fisheries databases may provide an exception, and future work should continue to expand abundance-based SDMs for NZ fish species (e.g., Grüss et al. 2023).

Our analysis of non-climate related threats provides broad insight into the areas and species at heightened risk from climate change, based on the extent that projected refugia are intersected by stressor footprints. However, the analysis is limited by the use of static stressor footprints, which do not capture the future variability in stressors (both intensity and footprint). Methods are available to predict future variability in stressors, for example for bottom fishing the dynamic relative benthic status (dRBS) approach (e.g., Zelli et al. 2025) could be employed to provide predictions of future benthic status (Anderson et al. 2024). For the other stressor used here for macroalgae (light attenuation from suspended particulates) more nuanced approaches could incorporate outputs from hydrodynamic models to account for stressor footprint variability driven by currents under future scenarios.

Further, there is likely to be within-group variation for any set of species with respect to their response to stressors and thus the appropriateness of using a single threshold to determine a ‘stressor-response footprint’ for a given group should be determined.

While the assessment of vulnerabilities, threat overlap, and the HSMs themselves, should be considered alongside their limitations, they fill substantial gaps in the information available for climate-smart MSP and MPA planning. The preliminary assessments conducted here should be built upon, with introduction of real-world complexities (e.g., management aspirations and existing management boundaries) to inform specific objectives. Decision-support tools (like Zonation, Marxan, or prioritzr) could be used to test objectives for conservation targets, explore scenarios (e.g, effectiveness of proposed MPAs under future conditions), incorporate threats (e.g., commercial and recreational fishing, and large-scale energy infrastructure), conduct trade-off analysis (i.e., inclusion of ‘cost’ layers), and importantly, account for model uncertainty (see Stephenson et al. 2023b, for example). Running such scenarios will allow the outputs generated by this study to be critically tested and may identify opportunities for further refinement.

4.4 Closing remarks

The HSMs generated as part of this project provide an important resource that can be used to advance climate-smart spatial planning in New Zealand. Ways to improve the HSMs, further characterise uncertainty and the assessments of vulnerabilities/threats should be considered for future work, but they should not limit the use of the outputs generated here for investigations of conservation objectives under future scenarios. Meanwhile, research effort could be directed toward filing remaining species gaps (e.g., some taxa groups like seabirds and macroinvertebrates are not represented here) and/or improving the models for species that did not perform well. Building upon this work, assessing how components of ecosystem functioning (functional richness, resilience and redundancy) respond to future conditions would provide for a more holistic view of ecological vulnerabilities to climate change and other persistent, but variable, threats.

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Appendix A Expert appraisal scoring criteria

The following scoring criteria were used by experts to appraisal the key inputs and outputs of the habitat suitability models developed in this study. Noting that some species are poorly known, even by experts most knowledgeable for a particular group, experts also scored their own knowledge for each species they appraised.

1. Assessment of expert knowledge

Evaluation score	Description
1 – Very high	Expert confidently knows the **distribution** of the species (including relatively fine scale patterns)
2 – High	Expert confidently knows the **broadscale distribution** of the species
3 – Moderate	Expert has **some knowledge** of the likely distribution with some uncertainty
4 – Low	Expert has **little knowledge** of likely distribution and with large uncertainty

2. Occurrence records

Evaluation score	Description
1 – Very accurate	Records of species **reflect expert view of taxa distribution** (> 80% overlap)
2 – Accurate	Records of species reflect expert view of taxa distribution, but **some areas do not** (> 60% overlap)
3 – Somewhat accurate	Records of species **somewhat reflect** expert's view of the taxa distribution but there are **considerable inconsistencies** (i.e., large areas that do not reflect experts' views; > 40% agreement) – moderate spatial bias in records
4 – Inaccurate	Records of species **do not match** the expert's view of the taxa distribution (< 40% agreement) – high spatial bias in records

3. Environmental drivers	
Evaluation score	**Description**
1 – Very accurate	Of the environmental data available, the list and ranking of environmental drivers **closely matches** my understanding of the species' niche
2 – Accurate	Of the environmental data available, the list and ranking of environmental drivers **matches** my understanding of the species' niche
3 – Somewhat accurate	Of the environmental data available, the list and ranking of environmental drivers **somewhat matches** my understanding of the species' niche
4 – Inaccurate	Of the environmental data available, the list and ranking of environmental drivers **does not match** my understanding of the species' niche

4. Present day distribution. Spatial predictions reflect expert knowledge of species' distributions	
Evaluation score	**Description**
1 – Very accurate	Predicted distribution **reflects expert view** of taxa distribution (> 80% overlap)
2 – Accurate	Predicted distribution **reflects expert view** of taxa distribution, but **some areas may not** be correct (> 60% overlap)
3 – Somewhat accurate	Predicted distribution **somewhat reflects expert view** of the taxa distribution but there are **considerable inconsistencies** (i.e., regions of disagreement; > 40% agreement)
4 – Largely inaccurate	Predicted distribution contains **large inconsistencies with the expert's view** of the taxa distribution (i.e., large regions of disagreement; > 20% agreement)
5 – Inaccurate	Predicted distribution **does not match the expert's view** of the taxa distribution (i.e., < 20% agreement)

5. Future distributions. Any comments on predictions of future distribution

Evaluation score	Description
Comment	Any comments on the prediction of future distributions. For example, how feasible do these seem? Are there certain locations/species where you expect more/less change?

Appendix B Between approach differences of future core habitat

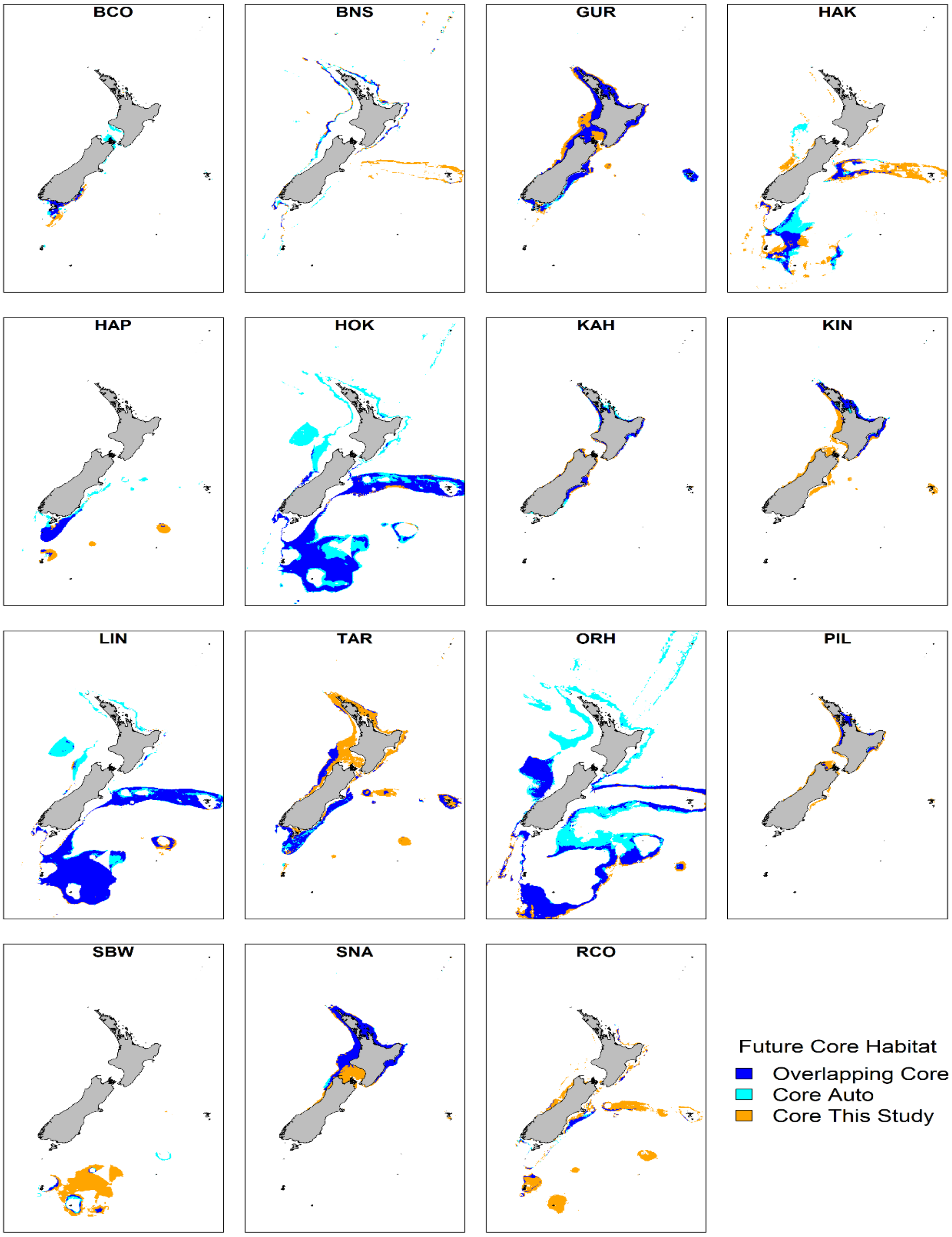

Figure B-1: Difference in core habitat - fish. The difference in the predicted distribution of future core habitat (HSI > 0.75) at 2090 under SSP3 generated using the 'automated' approach and by this study for 15 fish species. Overlapping core habitat is shown along with areas predicted as future core habitat by this study only, and by the automated approach only.

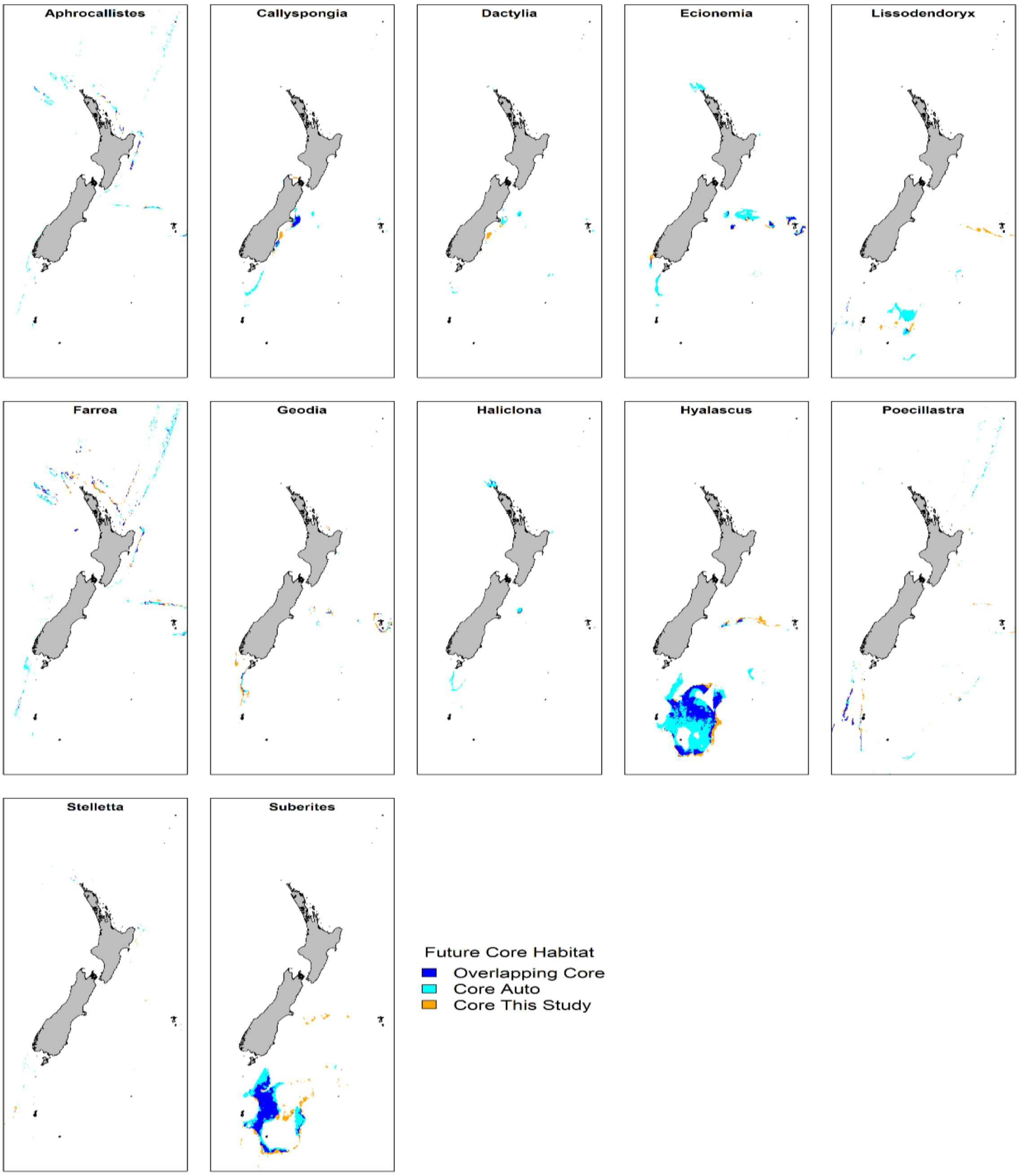

Figure B-2: Difference in core habitat - sponges. The difference in the predicted distribution of future core habitat (HSI > 0.75) in 2090 under SSP3 generated using the 'automated' approach and by this study for 12 sponge taxa. Overlapping core habitat is shown along with areas predicted as future core habitat by this study only, and by the automated approach only.

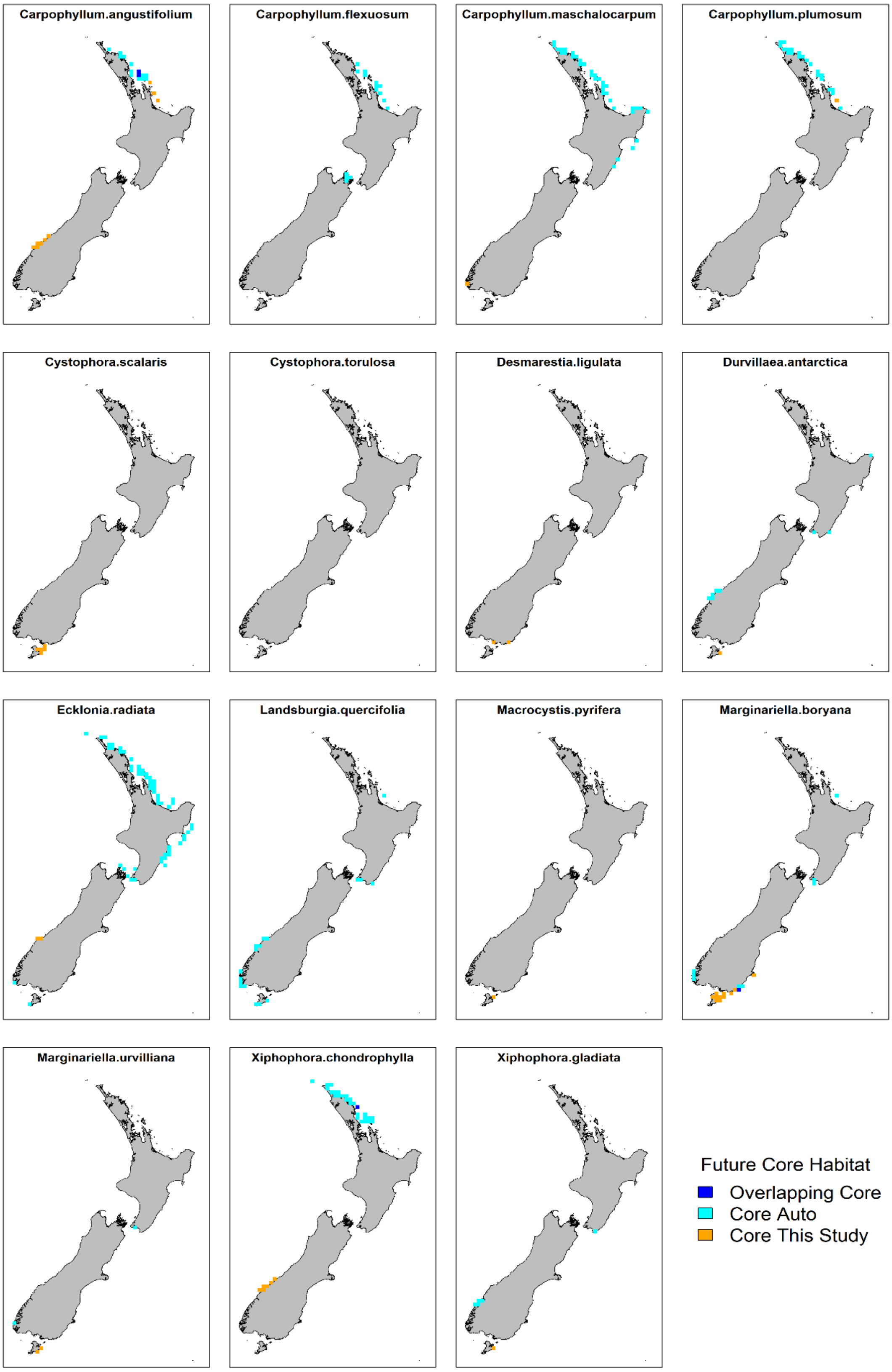

Figure B-3: Difference in core habitat - kelps. The difference in the predicted distribution of future core habitat (HSI > 0.75) in 2090 under SSP3 generated using the 'automated' approach and by this study for 15 kelp species. Overlapping core habitat is shown along with areas predicted as future core habitat by this study only, and by the automated approach only.