Combining mesocosms with models to unravel the effects of global warming and ocean acidification on temperate marine ecosystems

Running title: Mesocosm data improves biodiversity forecasts

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Abstract

1. Ocean warming and species exploitation have already caused large-scale reorganization of biological communities across the world. Accurate projections of future biodiversity change require a comprehensive understanding of how entire communities respond to global change.
2. We combined a time-dynamic integrated food web modelling approach (Ecosim) with a community-level mesocosm experiment to determine the independent and combined effects of ocean warming and acidification, and fisheries exploitation, on a temperate coastal ecosystem. The mesocosm enabled important physiological and behavioural responses to climate stressors to be projected for trophic levels ranging from primary producers to top predators, including sharks.
3. We show that under current-day rates of exploitation, warming and ocean acidification will benefit most species in higher trophic levels (e.g. mammals, birds, demersal finfish) in their current climate ranges, with the exception of small pelagic fish, but these benefits will be reduced or lost when these physical stressors co-occur.
4. We show that increases in exploitation will, in most instances, suppress any positive effects of human-driven climate change, causing individual species biomass to decrease at high-trophic levels. Species diversity at the trailing edges of species distributions is likely to decline in the face of ocean warming, acidification and exploitation.
5. Synthesis and applications. We showcase how multi-level mesocosm food web experiments can be used to directly inform dynamic food web models, enabling the ecological processes that drive the responses of marine ecosystems to scenarios of global change to be captured in model projections and their individual and combined effects to be teased apart. Our approach for blending theoretical and empirical results

from mesocosm experiments with computational models will provide resource managers and conservation biologists with improved tools for forecasting biodiversity change and altered ecosystem processes due to climate change.

Keywords: biodiversity change, fisheries exploitation, food web models, climate change, multiple stressors, species interactions, trophic modelling

INTRODUCTION

Marine ecosystems and resources are facing significant challenges due to the cumulative effects of multiple global and local stressors, including overfishing, eutrophication, pollution, habitat destruction, climate change, and ocean acidification (Cheung, 2018; Halpern et al., 2015). Hence, significant effort is needed to generate reliable projections of future changes in marine food webs and fisheries productivity.

Past attempts to forecast climate-driven changes in populations of fisheries species have incorporated the direct impact of temperature on species physiology using deterministic food web models (Blanchard et al., 2012; Brown et al., 2010), end-to-end climate models (Olsen et al., 2018), and species distribution models (Cheung et al., 2011; Peterson et al., 2002). Most of these projections, however, are based on species thermal niches or ecological proxies that do not consider real time observations from the natural system or experimental settings. Thus, they ignore the potentially large role of indirect (e.g. shifting predator-prey relationships) and interactive drivers of change (e.g., with ocean acidification) on model outcomes. Although thermal niches play an important role in governing species distributions and their population sizes, the occurrence and abundance of species is also heavily regulated by life-history traits, metapopulation processes and biotic interactions (Fordham et al., 2013; Mellin et al., 2016). While modelling architectures have been developed to improve our understanding of how multiple drivers of global change (including warming, acidification and exploitation) interact and affect marine communities (Fulton and Gorton, 2014; Kaplan et al., 2010; Koenigstein et al., 2018), accounting for complex biotic responses to multiple stressors at the level of the food web has proved difficult.

The role of indirect effects of climate change (e.g. shifting predator-prey relationships) on marine communities has received less attention than direct effects, even though they are likely to strongly shape future marine communities (Lord et al., 2017; Nagelkerken et al., 2017). Empirical data that enables biotic interactions to be quantified under near-future climate change scenarios is urgently needed to better project and understand the role of direct and indirect drivers of climate change on biological systems. A promising avenue is to use large-scale mesocosm experiments to quantify the potential effect of global warming on the strength of biotic interactions, rates of species turnover and composition, along with many other key ecological processes that drive population- and community-level responses to climate change (Fordham, 2015; Nagelkerken et al., 2020). Although scale, closed boundaries, simplified ecological communities, and replication can impose challenges for researchers using mesocosm experiments, they have the potential to quantify community-to-ecosystem level responses to scenarios of global warming (Sagarin et al., 2016), particularly if climate change mesocosm experiments align with regional climate projections for their study system (Korell et al., 2020).

Dynamic food web simulation models have shown that scenarios of increased temperature or acidification, modelled in isolation, could positively or negatively affect future fisheries through increased primary productivity (Brown et al., 2010) or higher mortality of invertebrates (Griffith et al., 2011; Marshall et al., 2017), respectively. However, the cumulative effects of ocean warming and acidification on complex natural food webs remain largely unknown, despite both stressors being a consequence of human-induced greenhouse gas emissions, affecting marine systems in unison (Brierley and Kingsford, 2009).

We combined empirical data from mesocosm experiments with dynamic food web models to test whether: (1) the combination of ocean warming and acidification is likely to exert synergistic, additive or antagonistic effects on food web structure and function for a temperate coastal ecosystem, and (2) whether increased exploitation will amplify these projected responses to increased greenhouse gas emissions. We use the mesocosm experiments to integrate physiological and behavioral responses of organisms to different scenarios of warming and/or acidification into the food web model, based on observations at trophic levels ranging from primary producers to top predators (including sharks). We show that integrating mesocosm experiments with dynamic food web models can provide ecologically robust frameworks for exploring the consequences of climate change on the structure and function of future food webs and their production capacity.

MATERIALS AND METHODS

We integrated empirical data from two food-web-level mesocosm studies (and other sources) into an existing food web model for the Port Philip Bay (PPB) temperate coastal marine ecosystem (Victoria, Australia) (Koopman, 2005) using Ecopath (Christensen et al., 2008). We validated the food web model retrospectively, using hindcast validation and then simulated likely future community-level changes for the PPB ecosystem (Fig 1).

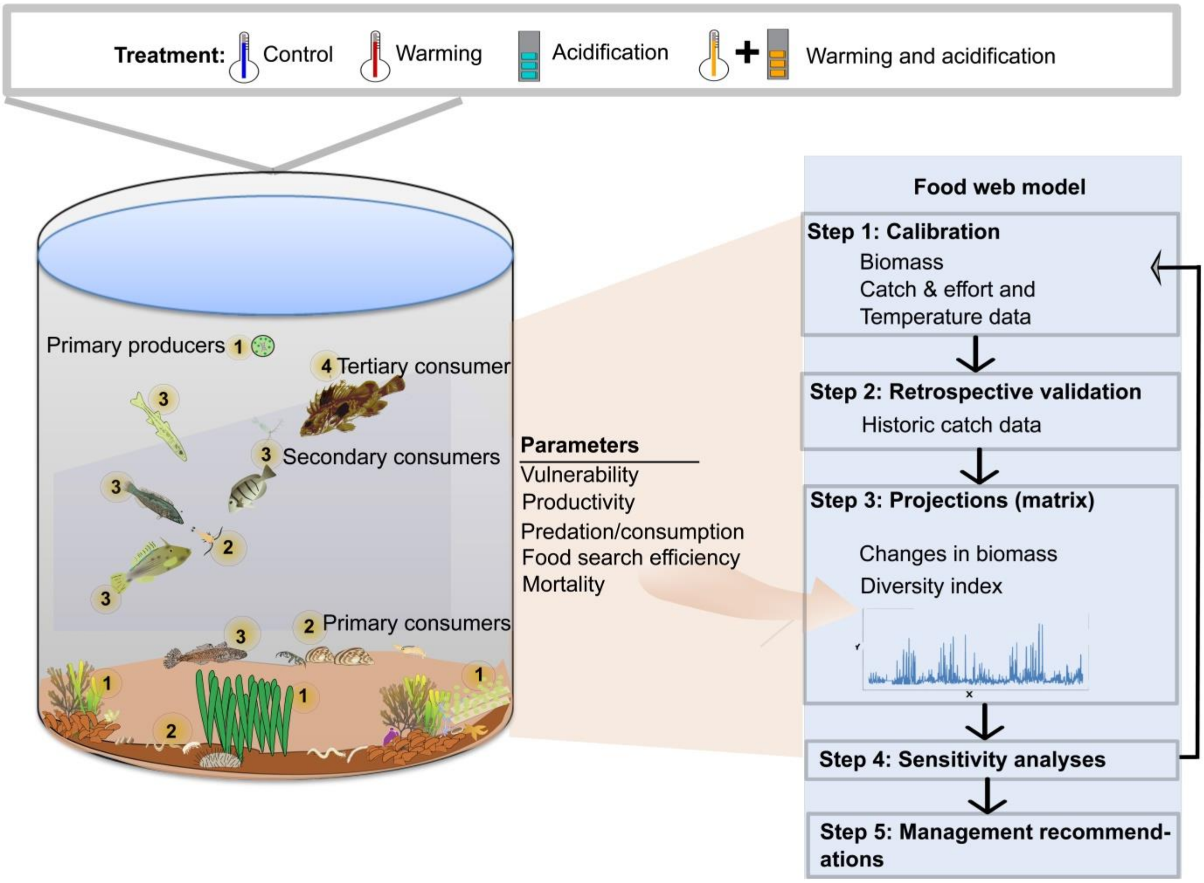

Figure 1: Conceptual representation of how different food web parameters from mesocosm experiments can be integrated with dynamic modelling approaches to project the state of future ecosystems. Several trophic level groups are illustrated e.g.: 1) primary producers: phytoplankton, macroalgae, seagrass, algal turf, microphytobenthos; 2) primary consumers: gastropods, shrimps, copepods, bivalves, polychaetes, sea urchins, sea stars, sponges, ascidians, tanaids; 3) secondary consumers: carnivorous (pelagic) fish, omnivorous fish, herbivorous fish, carnivorous (benthic) fish; 4) tertiary consumer: scorpionfish (behavioural experiment). Organism symbols were drawn by the authors or were courtesy of the Integration and Application Network, University of Maryland Center for Environmental Science (ian.umces.edu/symbols/).

Food web model and scenarios

Ecopath is a mass-balance food-web modelling approach used to create a baseline snapshot of the ecosystem and quantify the flow of energy between food web functional groups (Christensen et al., 2008). The model requires four primary input variables: biomass (B), production/biomass ratio (P/B), consumption/biomass ratio (Q/B), and diet composition. Experimental data from two large-scale mesocosms (Pistevos et al., 2015; Ullah et al., 2018), and field data published elsewhere, were used to calculate these input variables (see Supporting Information).

Differential equations were used to estimate biomass fluxes for each species and/or functional group within the food web using foraging arena theory (Ahrens et al., 2012). Vulnerability parameters were used to define predator consumption rates (Q_{ij}) (Equation 1) (see Supporting Information). For each predator-prey interaction, we calculated Q_{ij} at time t as,

$$Q_{ij}(t) = \frac{a_{ij} \times v_{ij} \times B_i(t) \times B_j\,(t) \times f(t)}{2 \times v_{ij} \times a_{ij} \times B_j(t)} \qquad \text{(Eq. 1)}$$

where a_{ij} is the effective search rate of predator j feeding on prey i, B_i is the biomass of the prey, B_j is the predator biomass, and v_{ij} is the vulnerability of prey i to predator j (Christensen et al., 2008). The forcing function $f\,(t)$ was used to account for external drivers changing through time affecting Q_{ij}.

Climate change was incorporated into model projections using forcing functions that temporally affect the consumption and production of functional groups (Ainsworth et al., 2011; Cornwall and Eddy, 2015) based on observations from the mesocosm experiments (see below). Specifically, we used the estimated effects of warming, acidification and their combination on prey vulnerability, search activity (higher trophic levels), mortality and productivity (primary producers) of trophic groups to alter modelled consumption (Q/B_i) and production (P/B_i) rate.

We developed four 85-year simulations (2015-2100): a no-climate-change scenario (baseline), ocean warming (T), ocean acidification (OA) and their combination (OAT). The climate change scenarios assumed a 2.8 °C increase in warming by 2100, representing a high representative concentration pathway scenario (RCP 8.5) for the Port Phillip Bay region (1.9

to 3.8 °C increase from a 20-year baseline focused on 1995 (Clarke et al., 2011)). We considered only RCP 8.5 because it was feasible to do the mesocosm experiment under only one RCP scenario. Uncertainty in parameter estimates for biomass (B), production (P/B) and consumption (Q/B) rates, and ecotrophic efficiency (EE) was simulated by varying these parameters randomly within bounds of ± 20% coefficient of variation.

The no-climate-change scenario (NC) assumes that model parameters do not change in the future, with model drivers, including fishing effort, set to the last year of the historical observation data (2015). For the three climate change scenarios (T, OA, and OAT), we incorporated direct and indirect climate-driven changes in species interactions and mortality of trophic functional groups in the food web. The effects of climate change were assessed by comparing biomasses and ecological indicators observed under the NC scenario with that of the climate change scenarios. Exploitation was initially held constant at 2015 levels for 21st Century climate change scenarios because fisheries management is generally done at decadal temporal resolutions, or finer (Fulton et al., 2018), meaning little is known about how exploitation rates are likely to change by the end of the century. However, we did run further scenarios to test the response of future food webs to increased exploitation. We did this by increasing exploitation by 1.5, 2 and 5-fold compared to present-day fishing pressure.

Mesocosm experiment

Empirical data from the mesocosm experiments were used to quantify the effects of climate change on food web structure and function, including trophic level biomass and diversity (Fig. 1; Supporting Information). Three response variables were derived and combined to estimate prey vulnerability to higher order trophic levels (trophic level ≥ 2) using behavioural experiments under the different mesocosm treatments (NC, T, OA, OAT). I) “prey attraction” was calculated as the percentage of time spent in the area close to a food cue relative to the time spent in the entire field of view (Goldenberg et al., 2018). II) ‘food search activity’ was given as the number of position changes in the area close to a food cue relative to the time spent in this area (Goldenberg et al., 2017). III) ‘boldness’ was measured as the percentage of time spent directly in front of a predator within the area close to a food cue relative to the time spent in the entire area close to the food cue. We averaged across the three response variables, weighting each variable equally, to obtain a composite vulnerability index of prey to its predator. For chondrichthyans, we calculated effective search activity as the total time taken by Port Jackson sharks (*Heterodontus portusjacksoni*) to successfully locate prey hidden in the sand using olfactory cues (see methods in (Pistevos et al., 2015) for details). Mortality as a direct function of biomass decline was quantified for functional groups not predated in the system. Primary productivity was measured from community metabolism as gross oxygen production (mg $O_2/m^3/min^1$) once per mesocosm at the end of the experiment. See Supporting Information for more details.

We calculated relative effect sizes for prey vulnerability, search activity, mortality and productivity by comparing the NC (control) scenarios with climate change treatments. These effect sizes were used to derive the model forcing functions for different climate change scenarios (OA, T, and OAT) (Table S1). The forcing function (input) and responses (biomass) were standardized to the base scenario by dividing the response value by the base values under a particular scenario. We used linear interpolation to construct a time series for all the forcing function parameters between 2015 and 2100. While it is common practice in climate change ecology to interpolate temporally between climate snapshots (Fordham et al., 2012), doing so can potentially mask important decadal variation (Fordham et al., 2018). We were limited to this approach because the mesocosm experiments were snapshots focussed on year 2100. The forcing functions were applied to appropriate functional groups in the model (Table

S1). We provide a more detailed explanation of the estimation of different forcing function parameters in the Supporting Information.

Analysis and model validation

We pooled food web functional groups into 10 community levels, including pelagic groups (mammals, birds, cephalopods, pelagic finfish), demersal groups (chondrichthians and demersal finfish) and their prey (benthic crustaceans, invertebrates, small pelagic crustaceans, primary producers) (Table S2). We calculated effect sizes for changes in biomass under different model scenarios using Hedges' *g* (Lakens, 2013). We calculated and compared key biodiversity indicators under different model scenarios, including the Shannon index (Shannon and Weaver, 1963) and Kempton's Q index (Ainsworth and Pitcher, 2006). The Shannon diversity index captures changes in evenness, whereas the Kempton's Q index captures changes in both evenness and richness at the level of functional groups (see Supporting Information for details).

We did an ecosystem model skill assessment (Olsen et al., 2016) and a global sensitivity analysis (Fordham et al., 2016) to determine the influence of input parameters on model results (see Supporting Information). To assess ecosystem model skill for our PBB model — and verify that parameters from our mesocosm were transferrable to the PPB coastal marine system — we validated hindcast simulations using independent catch-data (Table S3). Historical abundances (1993 and 2011) were simulated using the full-PBB model and sub-models with only functional groups in the mesocosm experiment. We assessed model-skill using a wide range of metrics (Olsen et al., 2016; Stow et al., 2009): root mean squared error (RMSE), average error (AE), average absolute error (AAE), modelling efficiency (MEF), and Pearson (*P*) and Spearman (*S*) correlation.

We determined the sensitivity of Ecopath input parameters — biomass (B), production (P/B) and consumption (Q/B) rates, and ecotrophic efficiency (EE) — on estimates of change in biomass under a scenario of projected ocean warming and acidification (OAT) and a scenario that included a moderate level of exploitation as well as OAT. To do this we used the built-in Monte Carlo routine within Ecosim module, which allows model input parameters to be varied (Coll and Steenbeek, 2017; Heymans et al., 2016). Specifically, we ran 100 Monte Carlo simulations with B, P/B and Q/B and EE varying randomly within bounds of ± 20% coefficient of variation. Initial and projected future biomass for 3 community groups (cephalopods, pelagic finfish and invertebrates) were recorded for the year 2100. We used generalized linear models (GLM) to explore the relative importance of different model input parameters on projected changes in future biomass (Fordham et al., 2016). We did this by calculating standardized regression coefficients (SRC) along with the coefficients and their confidence intervals. Furthermore, we assessed the quality of input data for the PPB model using food web diagnostics (Link, 2010) and explored the effects of parameter uncertainty on model outputs using sensitivity analysis. See Supplementary Information for more details.

RESULTS

Biomass changes under future climate change

Model simulations show that the total biomass of most higher-trophic-order community groups (mammals, cephalopods, chondrichthians, and demersal finfish) is likely to benefit from ocean warming (T) or acidification (OA), when modelled separately (Fig. 2, Fig S1). However, the combination of the two stressors has an antagonistic effect on biomass increase. At the level of individual species or functional group the positive effects on biomass are more disparate (Figs. S2, S3).

Our models project an average increase in marine mammal biomass of 85% by the end of the 21st Century under the combined effect of acidification and warming (OAT) compared to no-climate-change and current levels of fish exploitation (‘no change’ scenario) (Fig. 2A). Modelling acidification (OA) and warming (T) separately resulted in even higher average increases in marine mammal biomass: 254% and 213%, respectively. Cephalopod biomass is projected to increase by 144% under OAT, while warming and acidification in isolation likely boost biomass by 237% and 205%, respectively. Although chondrichthyans showed the largest increase in their biomass under warming, this increase in biomass was affected by parameter uncertainty. Demersal finfish and seabirds are projected to increase their biomass the most in response to OA (252% and 165%, respectively), with a smaller increase under T. Pelagic finfish showed a negative response to warming, irrespective of acidification, with small pelagics (mostly planktivores) showing severe depletions (>70%) under both under T and OAT (Fig. S2).

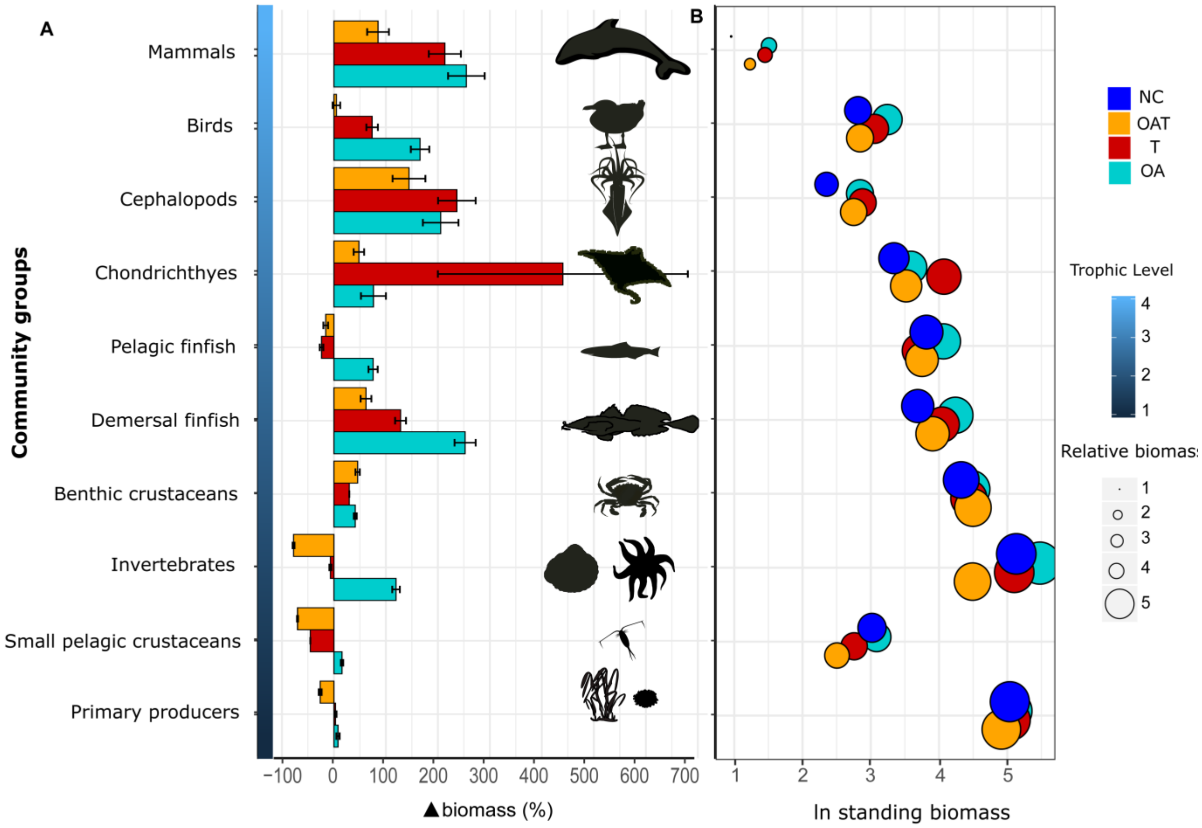

FIGURE 2:: A) Mean (± 95% confidence interval) relative change in biomass (Δ %) in year 2100 for different food web community groups under three climate change scenarios relative to a no-climate-change (NC) scenario. OA = ocean acidification, T = ocean warming, and OAT = combined ocean acidification and warming. Functional groups of food web models are aggregated to community groups (CGs) for better representation and clarity. The order of CGs is based on the mean trophic level (shown in blue). B) The future standing biomass (kg/km^2; ln- transformed) estimates for each CG. The bubble size is proportional to its biomass. Exploitation rates for all scenarios are modelled at present-day rates.

Conversely, ocean warming – either alone or in combination with ocean acidification – is projected to exert a negative effect on lower trophic-level faunal groups, with the exception of benthic crustaceans (Fig. 2A). Invertebrates (predominantly molluscs and invertebrates that do not possess a chitinous exoskeleton; Table S5), and small pelagic crustaceans (zooplankton) are projected to experience biomass declines of 7-78% and 45-70%, respectively, under T or OAT (Fig. 2).

The standing biomass of primary producers increased under OA and T, but decreased by ~ 26% under OAT (Fig. 1A), largely driven by a reduction of phytoplankton, micro-phytobenthos and macro-algal biomass (Fig. S3). Turf algae, in contrast, experienced a large increase in biomass (Fig. S3).

The combined effect of warming, acidification and exploitation

In the absence of ocean warming and acidification, exploitation reduced (by 1-32%) projected biomass in the year 2100 for most higher-order community groups under a 1.5- to 2-fold increase in exploitation rate (Fig. 3). Further increases in exploitation (up to 5-fold) exacerbated this declining trend (by 41-66%) for mammals, birds (due to reduced prey) and chondrichthians. Negative effects of up to a 2-fold increase in exploitation were suppressed at higher trophic levels (except for pelagic finfish) under modelled climate change (OA, T and OAT), due to greater top-down control of consumers on prey resources (Fig. 2). However, a 5-fold increase in exploitation caused the biomass of mammals and birds to collapse under warming scenarios, causing some functional groups for example cephalopods to increase in biomass (T: 178%; OAT: 144%) (Fig. S4). Whilst both T and OA scenarios positively affected higher trophic levels in the face of medium-to-high increases in exploitation, their largely negative effects on lower trophic levels (primary producers, small pelagic crustaceans and invertebrates) were not decreased by increased exploitation (Fig. 3; Fig. S5).

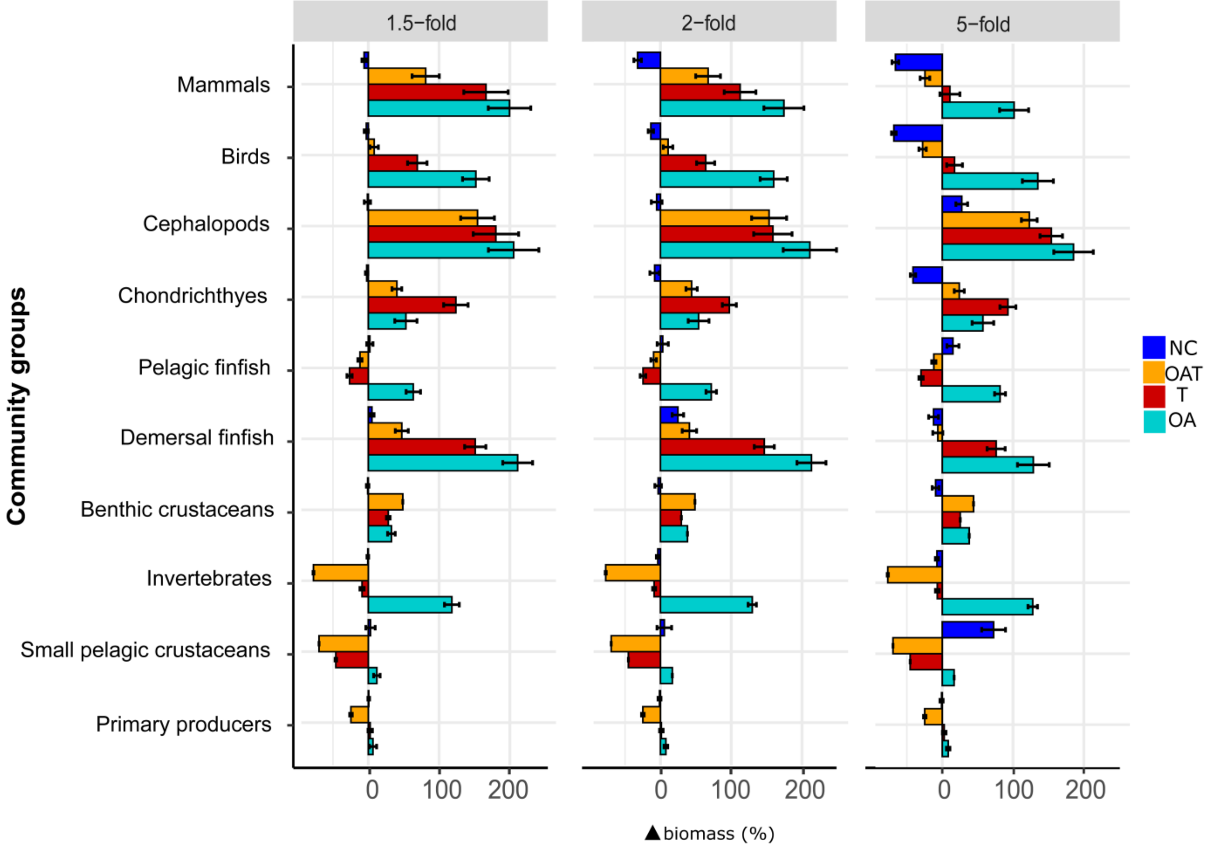

FIGURE 3: Mean (± 95% confidence interval) relative change in biomass (Δ %) in year 2100 compared to no change in climate and fishing from present-day levels (NC). OA = ocean acidification, T= ocean warming, and OAT = combined ocean acidification and warming. Functional groups are aggregated to community groups (CGs) for better representation and clarity. Number of ‘folds’ equals the magnitude of increase in fishing pressure starting in 2015.

Under the NC scenario, the Shannon diversity index remained relatively stable in the future under 1.5- and 2- fold increases in exploitation, whilst it decreased by ~ 4% under a 5-fold increase in exploitation (Fig. 4A). In contrast, the Shannon diversity index declined under all global change scenarios with the largest declines projected for OAT, under a 5-fold increase in exploitation (Fig. 4A). The Kempton Q metric for higher trophic levels showed a stronger decline (after year 2070) under OAT compared to the other climate change scenarios (Fig. 4B). A 5-fold increase in exploitation resulted in a steep and immediate decline in the Kempton Q index regardless of the climate change scenario.

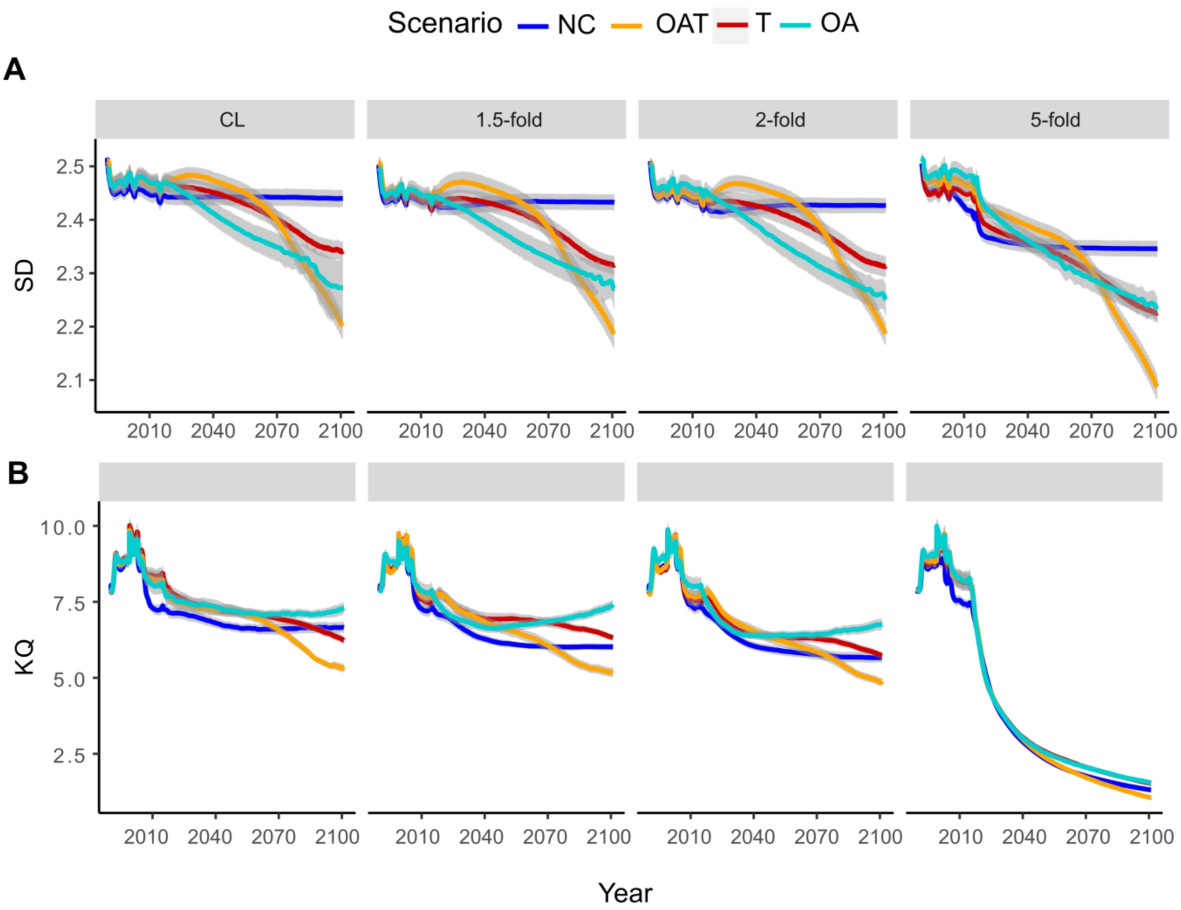

FIGURE 4: Ecological indicators of change in community composition, showing A) Shannon diversity index and B) Kempton Q index. The grey shadows represent the 95% percentile and 5% percentile. NC = no change in climate from present-day levels, OA = ocean acidification,

T = ocean warming, and OAT = combined ocean acidification and warming. CL= current level of fishing effort. Number of ‘folds’ equals the magnitude of increase in fishing pressure starting in 2015.

Model validation and sensitivity

Hindcasts of biomass from models parameterized using mesocosm data were correlated with empirical field data for carnivorous fish and omnivorous fish (correlation coefficient [r] = 0.54-0.82). The food web model skill assessment showed that models parametrized with mesocosm data are generally as skillful at projecting changes in biomass as models parameterized with field data (Fig. 5). Model projections for carnivorous and omnivorous fish biomass were relatively synchronous with independent biomass (survey) data, regardless of whether the models were parameterized using empirical data from the field ($r = 0.73$, RMSE ≤ 0.0001; $r = 0.82$, RMSE = 0.007, respectively) or mesocosm ($r = 0.69$, RMSE ≤ 0.0001; $r = 0.82$, RMSE = 0.007, respectively) data. Models parameterized with either field or mesocosm data did worse at projecting observed temporal variability in biomass for Port Jackson shark ($r = 0.12$, RSME = 0.011, $r = 0.29$, RSME = 0.011, respectively). Estimates of modelling efficiency (MEF) suggest that models for omnivorous fish and carnivorous fish do better than random (MEF > 0). This was not the case for Port Jackson sharks (Fig. S6). Importantly, bias (average error) in model projections remained low for all functional groups for models calibrated with field (carnivorous fish: + 0.24 g; omnivorous fish: - 0.02 g; Port Jackson shark: -0.12 g) or mesocosm data (carnivorous fish: + 0.18 g; omnivorous fish: -0.03 g; Port Jackson shark: -0.09 g).

The global sensitivity analysis (Table S6) showed that estimates of change in biomass (years 2015 to 2100) under an OAT scenario for pelagic finfish and invertebrates are most sensitive to changes in the Ecopath input parameter B followed by PB. For cephalopods, estimates of change in biomass were most sensitive to changes in QB, followed by PB. The most important parameter for each community remained the same regardless of whether exploitation was modelled or not.

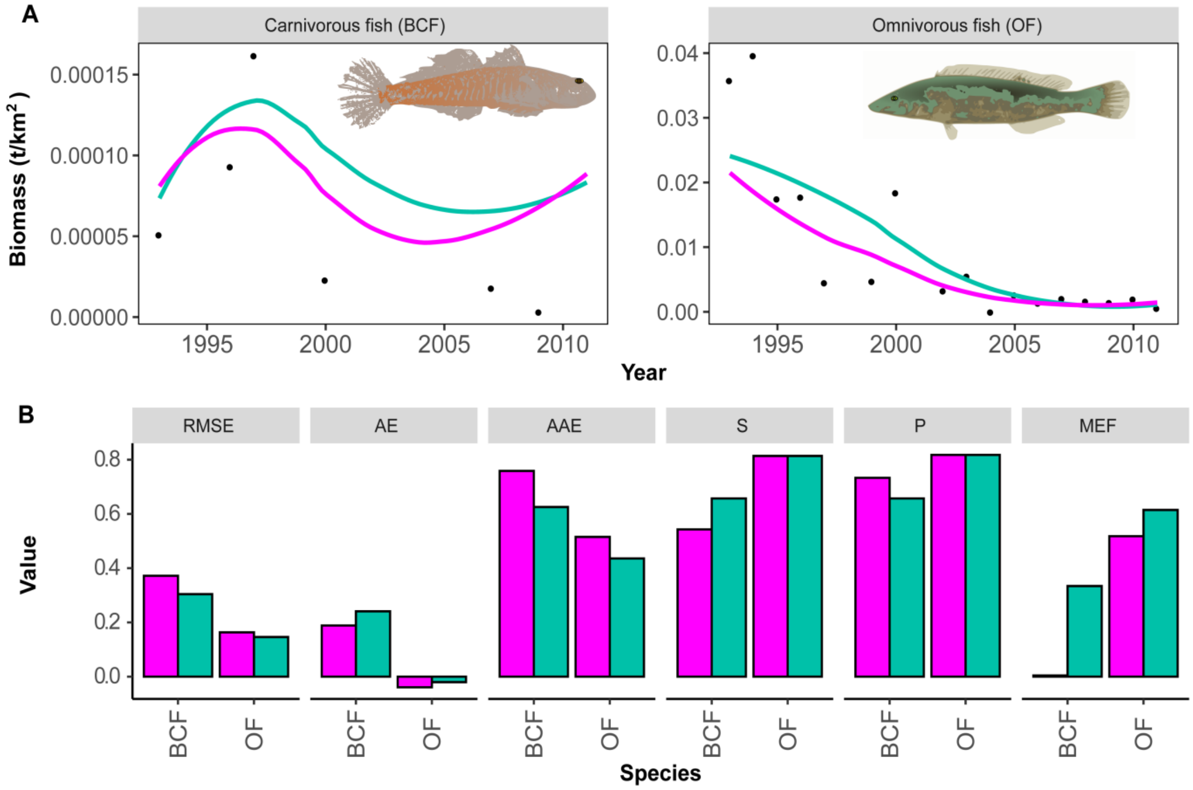

FIGURE 5: A) Mesocosm transferability. Comparison of the Port Phillip Bay (PPB) model built with the field (pink) and experimental data from the mesocosms (green) to standing catch biomass (tonnes per km^2; solid black dots) for two major functional groups between years 1993 and 2011. BCF = benthic carnivorous fish and OF = omnivorous fish.
B) Ecosystem model skill assessment for models built using empirical field (pink) and experimental mesocosm data (green) for Port Phillip Bay (between 1993 and 2011): root mean squared error (RMSE), average error (AE), average absolute error (AAE), Spearman rank (S) and Pearson (P) correlation, and modelling efficiency (MEF) for 2 species. Y-axis limited to show values between -0.05 and 1.00.

DISCUSSION

By integrating empirical data on species physiological and behavioural performance from two large-scale mesocosm experiments into dynamic food web models, accounting for historical exploitation rates, we show that climate change is likely to benefit the biomass of animals at higher trophic levels in some temperate marine ecosystems, albeit at a potential cost to biodiversity. Increased biomass under warming results from strengthened top-down control of consumers that occupy higher trophic levels, supported by a positive biomass response of some of their prey groups. Accordingly, the structure of future temperate marine food webs appears to be shaped by altered predator-prey dynamics, resulting from a reshuffling of predatory and prey species abundances in response to warming, and not a continuous fuelling of the food web from the bottom up as would be the case if ocean acidification was the dominant climate stressor (Nagelkerken et al., 2020; Sswat et al., 2018).

Organisms at higher trophic levels are likely to increase their top-down control on their prey, and therefore increase in biomass, in response to temperature-driven enhancements in their metabolic rates (Brown et al., 2010). Although an increase in top-down control by consumers has been previously suggested as a response to ocean warming for simplified (three-trophic- level) food webs (Goldenberg et al., 2017; Marino et al., 2018), a robust understanding of how higher-order consumers or apex predators will respond to global warming, and the subsequent effects for lower-order trophic levels, has until now been lacking. We show that under future scenarios of warming, the biomass of all higher-order consumers and apex predators (mammals, birds, cephalopods, chondrichthians, and demersal finfish) is likely to increase compared to a no-warming scenario due to amplified rates of prey consumption (pelagic finfish, invertebrates and small pelagic crustaceans), driven, in part, by increases in biomass of benthic crustaceans (major prey group in the system). Our new results, for a temperate marine ecosystem, suggest that the benefit of warming for higher trophic levels is likely to be universal, with associated negative effects for their prey at lower trophic levels.

Acidification alone is not expected to enhance top-down control by consumers because elevated CO_2 tends not to positively affect the metabolism of consumers (Carter et al., 2013; Kroeker et al., 2013). Recent food web studies showed that enhanced primary production can enlarge available prey resources, which can boost the growth of consumers under acidification (Nagelkerken et al., 2017; Sswat et al., 2018). This was true for all higher-order predators in our study, although for chondrichthians the biomass increase was weak. Elevated CO_2 is known to affect the foraging behaviour (e.g. reduced prey search efficiency and impaired odour tracking) of chondrichthians which might explain the reduced increase in biomass for this group (Pistevos et al., 2015). Because of their different physiology, highly active predators such as marine mammals, birds, and non-bony animals such as cephalopods tend to be more tolerant to increasingly acidic environmental conditions (Melzner et al., 2009). They benefit from amplified acidification only if increased resource availability at the bottom of the food web is transferred up the food web.

Although warming and acidification in isolation showed striking positive effects on the biomass of predators, their combined effect was antagonistic for many of the top consumers in the food web and caused a decline in the biomass of many lower-order consumers. Previous studies have shown that warming and acidification can antagonistically affect the growth of carnivores such as sharks by affecting prey search time (Pistevos et al., 2015), and of herbivores by increasing the degree of unpalatable or poor-quality food (Poore et al., 2013). Two of the major prey groups in our model (small pelagic crustaceans and invertebrates) experienced collapses in their biomass under the combined effect of warming and acidification, reducing the availability of resources for higher level consumers, resulting in reduced rates of change in consumer biomass under this scenario.

In contrast to other invertebrates, benthic crustaceans sustained a biomass increase under all modelled climate scenarios, enabling an increase in the biomass of their consumers (e.g. demersal finish, and consecutively some higher-order predators). Benthic crustaceans (e.g. lobsters, crabs, and shrimp) are generally considered to have a higher tolerance to acidification than other invertebrates (Kroeker et al., 2013) and show, in some cases, positive responses to warming (Faulkner et al., 2014). These observations could explain their successful propagation under scenarios of global warming.

Exploitation is a local stressor that negatively affected the biomass of all higher order community groups, except pelagic finfish. However, warming and acidification negated these negative effects, boosting the biomass of top predators at exploitation intensities equal to or smaller than a two-fold increase. Global-scale models, with static fishing rates, suggest that some commercial fisheries (ranging from crustaceans, small and large fish, to sharks) in high-latitude regions could experience an increase in future catches, owing to temperature-driven shifts in species distributional ranges (Cheung et al., 2010). However, we here limited our findings to changes in food webs based on current species distributions (i.e. at their climate trailing edges). Dynamic food web approaches also project a productivity increase in pelagic fisheries in response to forecast warming of oceans (Blanchard et al., 2012), and increased yields of commercially valuable fish stocks by 2050 under future warming (Merino et al., 2012). While the latter studies modelled food web responses, they used a simplified approach, with phytoplankton productivity as the only primary source of energy input, exploited species as the primary elements of the food web, and ocean warming as a single stressor. Here, using a more inclusive dynamic food web modelling approach, we show that opportunistic and less-targeted groups such as cephalopods are likely to flourish in their biomass at higher fisheries exploitation (≥ two-fold) rates due to a decrease in the biomass of major commercial species such as demersal finfish irrespective of climate change. Overall, we show that the greatest effects on future marine food webs are likely to arise at the top of the food web when overexploitation coincides with the combined effect of warming and acidification.

Ocean warming and acidification have a much greater negative effect on functional diversity in food webs than overexploitation. Future ocean warming and acidification can significantly reduce diversity (i.e., Shannon diversity) within temperate coastal food webs even under present-day exploitation levels, owing to declines in the biomass of primary producers (i.e. non-weedy species such as macrophytes and certain species of phytoplankton), small pelagic crustaceans, invertebrates, and pelagic fish species. Moreover, it can cause a reduction in evenness (Kempton Q index) for higher-order groups in the food web. These changes in diversity and evenness are likely to enable ecological opportunistic species to flourish (Woodruff, 2001), such as high-order cephalopods and lower-order “weedy” turf algae, leading to further simplification of community structure (Nagelkerken and Connell, 2015). Together, global warming and fishing will likely shift the distribution of biomass within the community and reduced diversity of future food webs.

By combining empirical data on species response to climate change from large mesocosms with historical population data (from scientific surveys and fisheries landings) in a dynamic food web model, we moved from experimental ecology to making projections and management recommendations aimed at safeguarding marine biodiversity under climate change. Blending mesocosm experiments with “real world” ecological models has been questioned on the grounds that they are unlikely to attain realistic projections (Carpenter, 1996). By independently validating our model projections against historical population data (trawl surveys), we not only show that our dynamic food web model does a fair to good job at reconstructing observed historical trends in biomass (particularly for selected functional groups), but that models based on mesocosm experiments provide a relatively close representation of 'real world' food webs. Therefore, mesocosms with realistic multifactorial experiments that capture food web complexity can indeed be used with confidence to parameterize ecosystem models and help to bridge the gap between simplified experimental conditions and the real world.

Our modelling approach, like other modelling techniques, has its own caveats. El Niño–Southern Oscillation (ENSO) is known to influence Australia's marine ecosystem through its year-to-year dynamics in climate variability (Lough and Hobday, 2011). These fine temporal scale climate dynamics could not be captured in the mesocosm experiment and therefore the food web model. This could, potentially, affect our modelled trajectories of biomass and community composition. To calculate the vulnerability of fish to their consumers, all fish species were considered into two major categories, namely carnivores and omnivores (feeding guilds). The somewhat poor fit of modelled projections to observed data for Port Jackson shark is likely to reflect an over-simplification of food web structure for the validation exercise (see Supplementary Information). Likewise, important and unaccounted uncertainties in the validation data (i.e., detection probability) could partly explain the difference between predicted and observed patterns of temporal variability in biomass (Guillera-Arroita, 2017). Despite these limitations, our study included the best available historical data and the most robust estimates of physiology and behaviour responses to global warming for a 4-trophic level temperate food web system.

CONCLUSIONS

Here we used a novel approach to simulate the effects of global warming, ocean acidification, and fishing on the biomass and diversity of species in a temperate coastal ecosystem, using experimental data on the effects of ocean warming and ocean acidification on species interactions and physiology, and historical fisheries (survey and catch) data. By simulating the potential magnitude and direction of biomass changes for different functional groups, we show that the structure and function of future temperate marine food webs under ocean warming is likely to be altered by predator-prey dynamics at the top of the food web rather than changes from the bottom up. Consumers at higher trophic levels are likely to benefit from ocean warming and acidification, but these benefits will be reduced or lost when these stressors co-occur. More generally, we show that mesocosm experiments can be integrated with food web models to better manage marine biodiversity in response to 21st century climate change.

DECLARATION OF INTEREST STATEMENT

The authors have no conflicts of interest to declare.

AUTHORS' CONTRIBUTIONS

HU, IN and DF conceived the research; HU and SG collected the data; HU developed the methods; HU analysed the data; HU, IN and DF wrote the manuscript; All authors contributed to revisions and approved the final submission.

DATA AVAILABILITY STATEMENT

Data will be available via the Dryad Digital Repository upon the acceptance of the article.

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Appendix A. Supporting Information

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Combining mesocosms with models to unravel the effects of global warming and ocean acidification on temperate marine ecosystems

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SUPPLEMENTARY INFORMATION

1. Modelling approach

We used Ecopath and Ecosim (EwE) (Christensen *et al.* 2008) to simulate the effect of future climate change and fishing effort on the biomass of different functional groups of a coastal marine food web. Ecopath is a food-web modelling approach used to create a baseline snapshot of the ecosystem and quantify the flow of energy between food web functional groups.

1) We developed a static food web (Ecopath) model using principals pertaining to trophic mass-balance, where removal from the system (e.g. predation, fishing, emigration, etc.) equal total production. To do this, we generated a static snapshot of the ecosystem focused on a baseline year of 1990. To parameterize the Ecopath model we used two 'master' equations: one for production (Equation 1) and the other for the energy balance (Equation 2). The first equation ensures energy-balance among groups by distributing total production of a group into the catch, predators' diet and other mortality (death caused by factors other than predation and catch).

The production of each group was calculated as (1):
Production = predation mortality + biomass accumulation + net migration + other mortality
and written as:

$$P_i = B_i \times M2_i + E_i + BA_i + P_i(1 - EE_i) \qquad \text{(Eq. 1)}$$

where P_i is the total production rate of the group (*i*), Bi is the biomass of a group (*i*), $M2_i$ is the instantaneous predation rate for the group (*i*), E_i is the net migration rate (emigration - immigration), BA_i is the biomass accumulation rate for (*i*), EE_i is the ecotrophic efficiency of (*i*) describing the proportion of the production utilized in the system, and $(1 - EE_i)$ represents mortality other than predation.

This formula incorporates all the production (or mortality) except gonadal products which are assumed to be ending up being eaten by other groups, hence here considered under other mortality. Therefore Equation 1 can be expressed as:

$$B_i\ (P/B)_i \times EE_i - \sum_{j=1}^{n} B_j \left(\frac{Q}{B}\right)_j \times DC_{ji} - E_i - BA_i = 0 \qquad \text{(Eq. 2)}$$

where P/B_i is the production/biomass ratio for (*i*), Q/B_j is the consumption/biomass ratio of the predator (*j*) and DC_{ji} is the fraction of prey (*i*) in the average diet of predator (*j*). All other variables are the same as those described for Equation 1.

The second equation computes the energy balance within a functional group such as:

$$Q_i = P_i + R_i + UA_i \qquad \text{(Eq. 3)}$$

where Q_i is the consumption by a group (*i*), P_i is the total production of the group (*i*), R_i is the respiration of the group (*i*) and UA_i is the unassimilated food of the group (*i*).

2) We used Ecosim to simulate the dynamics of each functional group over time using Ecopath inputs as starting information and incorporating different forcing functions associated with climate change. Ecosim keeps track of changes in the biomass of species (functional groups) as a function of temporal changes in their catch patterns, food-web complexity (predator-prey interaction), and environmental conditions (Walters, Christensen & Pauly 1997). We modeled changes in biomass for each trophic group (*i*) over time through using the differential equation (Equation 4) derived from Eq. 1 that is based on on the "foraging arena" theory and embedded within Ecosim (Walters, Christensen & Pauly 1997; Ahrens, Walters & Christensen 2012):

$$\frac{dB_i}{dt} = \left(\frac{P}{Q}\right)_i \sum_j Q_{ji}\,(t) - \sum_j Q_{ij}\,(t) + I_i - B_i \times (M_i + F_i + e_i) \qquad \text{(Eq. 4)}$$

where $\frac{dB_i}{dt}$is the biomass growth rate of group *i* in the time dt, $\frac{P}{Q_i}$ is its production/consumption ratio, *Qji* is the consumption of group *j* (predator) on prey group(s) *i*, Q_{ij} is the consumption for predation by all predators *j* on the group *i* (prey), I_i is the immigration rate, B_i is the starting biomass, M_i and F_i are the natural and fishing mortality rates of group *i*, respectively, and e_i is the density-dependent emigration rate. In our case, e_i and I_i were set as zero.

Following the "foraging arena" theory, consumption rates (Q_{ij}) are quantified using a nonlinear relationship between prey and predator, which assumes that only a portion of the biomass of the prey is available to a predator. This means that the biomass of prey *i* is divided between a vulnerable and a non-vulnerable state. The vulnerability concept incorporates density-dependency and expresses how far a group is from its carrying capacity (Christensen & Walters 2004; Christensen *et al.* 2008). The vulnerability rate can be modelled both as top-down and bottom-up controls of the predator-prey interactions. For example, vulnerabilities greater than 2 describe top-down control of the predator-prey relationship, where the predator biomass drives the prey mortalities, whilst vulnerabilities below 2 define bottom-up control, where the biomass of the predator has little effect on the predation mortality of that prey.

1.1. Food web model

We updated an existing food web Ecopath model for Port Philip Bay (PPB) (Koopman 2005), initially developed to model the benthic-demersal system of the Bay for the sand flathead (*Platycephalus bassensis*) fishery, with recent and more reliable data that include single species, groups of species and developmental phases of species (multi-stanza approach) focusing on both pelagic and demersal component of the ecosystem. PPB is a temperate coastal marine system which is designated as a sustainably managed ecosystem in terms of its fisheries exploitation (Flood *et al.* 2014). Fishing pressure decreased by approximately fivefold between 1990 and 2016 in PPB (Fig. S7). PPB is a temperate coastal marine system which is designated as a sustainably managed ecosystem in terms of its fisheries exploitation.

The model by (Koopman 2005) is composed of 30 different components or groups (that include single species, groups of species and developmental phases of one species) focused on 1990 (Table S4). Input data came from a wide variety of sources (Table S5). Biomass estimates for most species were based on trawl surveys conducted in 1990 (Hobday, Officer & Parry 1999). Site-based diet data (Table S7 and S8) were obtained from the literature, and when quantitative information was not available, proportions were estimated. A thorough technical description of the model, including all the data, basic input parameters, relevant assumptions, diagnostic features is provided by (Koopman 2005), located at http://dro.deakin.edu.au/view/DU:30026826.

The updated PPB model comprised 23 additional species or functional groups, including 3 multi-stanza functional groups (Table S4). These included species or groups at the top of the food web (e.g. large sharks, large pelagic fish, birds, mammals, southern calamari), demersal finfish (such as silver trevally, yellow-eye mullet, leatherjacket, rock flathead), pelagic finfish groups (e.g. Australian sardine, southern anchovy, Australian salmon, longfin pike, southern garfish), invertebrate trophic groups (such as filter-feeding molluscs, other grazing molluscs, predatory molluscs, abalone, southern rock lobster, sea urchins, exotic sea stars) and one primary producer group (algal turf). The inclusion

of these functional groups in our new food web model was done primarily to accommodate for apex predators and, invasive species, and to better simulate the likely appearance of opportunistic groups in the future.
The new comprehensive food web model included a total of 53 functional groups, with 17 groups of demersal finfish, 7 groups of pelagic finfish, 7 groups of chondrichthyans, 11 groups of invertebrates, 2 groups of cephalopods, 5 groups of primary producers, one bird and one mammal group, and a non-living group detritus (Table S4). Functional groups for the PPB model were designated based on different biological and ecological characteristics of the species such as feeding habits, growth rates, body size, consumption rates, diets, predators, and habitat distribution.

Apex predators such as mammals are ecologically important because they can constrain the parameters of other consumers and influence ecosystem structure and function through strong predation-driven consumptive effects or fear-driven non-consumptive effects with relatively few individuals (Roemer, Gompper & Van Valkenburgh 2009). We have therefore included marine mammals as a functional group in our PPB model. The inclusion of seabirds as a separate functional group in our model allowed us to appropriately account for a link between birds and vertebrate fish predators in the food web. Migratory patterns of seabirds were also taken into account by modeling temporarily-variant proportion of the diet composition of this group as imports to the system.

We included rock flathead in the updated PPB model since rock flathead showed an increasing contribution in the landings of major species caught at PPB in the recent decades compared to sand flathead and yank flathead that showed a decline. Because the southern calamari is by far the most important target species both in the recreational and commercial cephalopod fishery in PPB, we treated southern calamari as a separate functional group in our model.

We modeled complex trophic ontogeny and patterns in potential exploitation of juveniles (referred to as ‘stanzas’ here) for some key fish species (e.g. sand flathead). We modeled juvenile sand flathead as a stanza group for sand flathead because this makes their dynamics more ecologically realistic and provides insights on stock-recruitment relationships. To do this juvenile sand flathead were treated as a separate functional group in the model. In addition to sand flathead, we have added three more multi-stanza groups. This was done for the three species of highest commercial interest in PPB: King George whiting, red mullet, and snapper. To represent multi-stanza groups, we used baseline estimates of total mortality rate (Z) and diet composition for each stanza and biomass and QB (consumption over biomass) for the “leading” adult stanza. We also incorporated information on time (in months) between stanzas (e.g. adult and juvenile) (Bani & Moltschaniwskyj 2008; Smallwood, Hesp & Beckley 2013; Froese 2019). To do this we used the von Bertalanffy growth curve parameter (k) (Froese 2019), and the estimate of relative weight at maturity as a fraction of weight at infinity

(W_{mat}/W_{inf}) (Heymans *et al.* 2016; Froese 2019). Mortality rates and diet composition are assumed to be similar for individuals within each stanza.

We have added several trophic groups of small pelagic species to the model: Australian sardine, southern anchovy, southern garfish, Australian salmon and pike. Small pelagic species are ecologically and commercially important forage fishes (Pikitch *et al.* 2014) in ecosystems such as PPB (e.g. sardine, anchovy). The inclusion of higher taxonomic resolution for some foraging fishes enabled us to explore if particular predators had high diet dependencies on individual forage fish species (Koehn *et al.* 2016) making them more vulnerable to disturbance. We have also added few more individual small demersal fish (e.g. yelloweye mullet, silver trevally) as a separate functional group given the importance of the benthic compartment of the shallow coastal ecosystem of PPB. There were still several other small pelagic and demersal species which were modeled as an aggregated group due to their low individual biomass and importance in the model or due to their insufficient and unreliable taxonomic resolution.

We included an invasive species in our updated model. The exotic seastar (*Asterias amurensis*) is one of Australia's most serious invasive marine pests. It was introduced into Port Phillip Bay in 1995 and by 2000 its biomass peaked at 56% of the resident fish biomass in the deeper region of the Bay (Parry & Hirst 2016). This species was responsible for the decline in biomass of shovelnose stingaree, eagle ray, and globefish (Parry & Hirst 2016). Furthermore, it can lead to the local extinction of its prey, altering benthic community structure (Parry & Hirst 2016). Functional groups such as abalone, rock lobster, and sea urchin were also included in the updated model.

We split molluscs into three functional groups given their variable importance for trophic flows (Covich, Palmer & Crowl 1999) and to ensure that inter-specific competitions are considered. Algal turfs were incorporated as an additional functional group since they can dominate ecosystems, especially those prone to disturbances (Hatcher & Larkum 1983).

Basic model input parameters such as biomass (B), production per unit of biomass (P/B), consumption per unit of biomass (Q/B), and diet matrix were obtained directly for PPB taxa when available. These were primarily based on published surveys and sampling (Parry *et al.* 1995; Officer & Parry 1996). We also used various other sources (Tables S2, S4). If site-specific information was not available, we used the most appropriate estimates based on other ecosystems from the literature (Table S5).

1.2. Model balancing

We used the pre-balancing (PREBAL) approach to first ensure that the model parameter was in agreement with energetic laws for ecosystem structure (Link 2010). The initial diagnostics suggest that our model satisfies these underlying assumptions. For example, the slope of the biomass (on a log scale) declined by 5–10% across all taxa ordered by trophic level (Link 2010). We then balanced the model following key ecological rules and the laws of thermodynamics (Jørgensen & Fath 2004). We considered the model balanced when estimated ecotrophic efficiency (EE) values of all functional groups were <1 and where values were high (≥ 0.95) for exploited species and species with high naturally predation rates (such as small pelagic fish species), and low (< 0.5) for unexploited top predators (such as mammals and yank flathead).

We assumed an EE value of 0.95 for some heavily predated species in the ecosystems such as those with forage fish (Polovina 1984; Christensen & Pauly 1998; Christensen & Walters 2004). For groups with the little information on exploitation rates (e.g. cephalopods and calamari), biomass was estimated in Ecopath assuming an EE of 0.95 (Lassalle *et al.* 2011). We also made sure that the values of production/consumption (P/Q) for functional groups of the model were between 0.1 and 0.35, except for spinney gurnards (Christensen *et al.* 2008). This was achieved by incrementally changing the diet matrix of key functional groups in the model.

Updating the diet matrix with stomach content analysis based on local studies can improve Ecopath models (Ainsworth & Mumby 2015). In our case, most of the diet data came from the local ecosystem. It was, however, still necessary to adjust the diet of a few functional groups, including birds, banjo rays, small pelagics and small demersal fish. These adjustments were cross-checked with FishBase (Froese & Pauly 2018) to ensure confidence intervals of the estimation of trophic levels were reasonably close to the values published.

We assessed the quality of the model using the pedigree routine (Christensen *et al.* 2008), which assesses the precision of the input data, setting confidence intervals for uncertainty analysis (Christensen & Walters 2004; Morissette 2007). Pedigree values for input data range from 0 (when it is not based on local data) to 1 (fully rooted in local data). The pedigree index of our model computed as 0.52 (a measure of fit t = 4.32) which is in the upper part of the range (0.16–0.68) of 150 Ecopath models published (Morissette 2007), suggesting that the input data is reasonably robust and the model is of acceptable quality (Christensen *et al.* 2008).

Finally, we calculated Hedges' g as a measure of effect size for changes in biomasses for different functional groups using the following formula:

Hedges' $g = \frac{M1-M2}{SD*_{pooled}}$

where *M1–M2* = difference in means of two groups and SD^*_{pooled} = pooled and weighted standard deviation. To remove small positive bias within Hedges' *g* for small sample size (under 50), a correction factor was derived using the following equation:

$$\left(1 - \frac{3}{4(n_1 + n_2) - 9}\right)$$

1.3. Food web model calibration

The base Ecopath model was calibrated within the time dynamic Ecosim approach using historic time-series data from 1990 to 2015 to reconstruct the historical trends (Fig. S8). The hindcast approach was done using an automated stepwise fitting procedure (Scott *et al.* 2016). The fitting process identified highly influential interactions in the model and calibrates those to improve the statistical fit using the weighted sum of squared deviations (*SS*). The *SS* was calculated using the disparity between the logarithm of observed and predicted catches (Christensen *et al.* 2008). Then the Akaike Information Criterion (*AIC*) (Akaike 1974) and the *AIC* corrected for small sampling sizes (*AICc*) (Burnham & Anderson 2004) were calculated as follows:

$$AIC = nlog\left(\frac{minSS}{n}\right) + 2k$$

$$AICc = AIC + 2k(k-1)/(n-k-1)$$

where *n* is the number of observations, *minSS* is the minimum sum of squares resulting from the comparison between predicted and observed time series, and *k* is the number of parameters.

We used AIC to test for statistical support for an effect of changes in predator-prey dynamics (also called vulnerabilities: Vs): primary production (PP anomaly, considering the number of PP spline points (sPP) for smoothing the time series), and/or impact of fishing and possible combinations of all of the above-mentioned factors (Table S9). AIC penalizes for fitting too many parameters and comes up with a “best” model (the one yielding the lowest AIC) considering a good fit and the least number of estimated parameters. For our model selection, we used AICc since it accounts for small sample sizes (n of observations).

The updated Ecopath model was first calibrated with historical time series data to assess model performance before simulating the effect of future climate change on food web dynamics. The predictive skill was assessed using the sum of squares (SS) ratio between predicted and independent observation data (Christensen *et al.* 2008). The latter consisted of 52 time series of data covering a range of metrics, including observed biomass, landed catch, and fishing effort. The biomass time-series data were mostly for demersal and benthic groups (Gregory Parry, pers. com.). Among the groups, the estimated model biomass (future) for small demersal fish (miscellaneous groups) and rock flathead were not considered for the final model biomass calculation due to the poor model fit and spurious behavior.

The surveys of demersal fish assemblages were done annually using demersal trawl nets at 20 stations stratified by depth in Port Phillip Bay from 1990 to 2011. These surveys cover about 78% (1,506 km^2) of the whole PPB area (317 km^2-shallow, 155 km^2-west, 403 km^2-intermediate and 631 km^2-deep). The shallowest trawl of the bay was at 7 m while the deepest was at 20 m. There was no trawling in 1998 and 2001. We used average biomass across depth as our biomass time series input for the demersal fish functional group.

The time series for the commercial fisheries landings and fishing effort were obtained from the Department of Primary Industries (VFA 2016). The estimates of annual recreational catch in Port Phillip Bay for new functional groups were taken from (Fulton & Smith 2004). Recreational bycatch fisheries were supplied by Simon Conron (pers. com.). The chlorophyll *a* data on the PPB was taken from (EPA 2002), while the water temperature data were obtained from the Bureau of Meteorology of the Australian Government (BOM 2018). Chlorophyll *a* and water temperature data were used to calibrate the model using an environmental forcing function approach within EwE.

We first calibrated the model with chlorophyll as a sole environmental driver along with other parameters. This, however, did not show a good fit for some demersal groups in the model, particularly for chondrichthyans. We, therefore, added mean maximum annual temperature to account for their effect on zooplankton consumption indirectly via their intermediate predators. Temperature trends can affect the search rate and feeding area of a predator and at the same time change the vulnerability rate of a prey (Heymans *et al.* 2016). Adding the effects of temperature as an additional environmental driver improved the performance of our model fitting (Table S9). The best model from the fitting exercise was obtained when trophic interactions and fishing were included together in the model run (Step 6 in Table S9). The fitted vulnerability values of all the model functional groups are shown in Supplementary Table S10.

1.4. Representing global warming and ocean acidification

The estimation of predator-prey interactions in food web models is challenging due to their dynamic nature and often complex trophic structure. We addressed this challenge by using estimates of species interactions from two community-level mesocosm experiment, which includes both direct (Ullah *et al.* 2018) and indirect estimates of the vulnerability of prey to predators (Goldenberg *et al.* 2018), effective search rate of predators for their prey (Pistevos *et al.* 2015) and the mortality of some lower trophic prey groups accounted in the food web model (Ullah *et al.* 2018). In both experiments, the mesocosm had the same crossed design of elevated CO_2 and temperature with 3 replicate mesocosms per treatment combination. Both mesocosm systems I) assumed and simulated an increase in future temperature of approximately +2.8 ^{0}C, II) were multi-trophic from the producer (e.g. algae) through primary consumer (amphipod) to predator (e.g. either shark or carnivorous fish) capturing the complexity of a food web, III) include a total habitat volume of ~2,000 L, and IV) were supplied by a flow-through of seawater from the same source ensuring comparable nutrient levels. The similarity between the two systems is critical as geographical variation and experimental contexts can alter the effect of climate change on consumer-resource interactions and lead to additional sources of variability (Marino, Romero & Farjalla 2018).

We used predation pressure which is the consumption rate (mg/4hr/individual) of species relative to control condition (present day condition at 2100) to estimate the vulnerability (direct estimate) of lower trophic level (trophic level ≤ 2) species/functional groups to their predators. This was done using data from stomach content analysis and *in situ* feeding trials that incorporated different treatment effects (e.g. temperature, acidification or their combination) (Ullah *et al.* 2018). The estimation of prey vulnerability through *in situ* feeding trials is robust because feeding at the community level incorporates the complex interplay between morphology, physiology, behavior, population dynamics, and predator-prey interactions (Brodeur *et al.* 2017). For further details about the experimental design and stomach content analysis see (Goldenberg *et al.* 2018) and (Ullah *et al.* 2018), respectively.

We applied a combination of direct and indirect approaches to estimate the vulnerability of prey groups for higher order trophic groups (trophic level ≥ 2) under warming and acidification. The indirect approach was based on behavioral experiments related to foraging and predation of consumers. A detailed description of the experimental setup is given in (Goldenberg *et al.* 2018) and we provide here only a summary including the information most relevant to our study. After 2.5 months of exposure to the climate treatments, a total of 3 behavioral trials lasting 7 min. each were conducted in each mesocosm in the presence of a predator. The scorpionfish *Gymnapistes marmoratus* (a predator) was caged and presented with five prey species – little weed whiting (*Neoodax balteatus*), blue weedy whiting (*Haletta semifasciata*), longfin goby (*Favonigobius lateralis*), zebrafish (*Girella zebra*) and toothbrush leatherjacket (*Acanthaluteres vittiger*). This was done using a small container placed in front of the predator cage that emitted food cues to attract the prey species to the general area and encourage foraging related behaviours. Using video recordings, the position of each individual prey fish throughout the trial was assessed through manual tracking using the software Solomon Coder, and this was used to quantify foraging and risk-taking behaviours. The field of view of the camera was subdivided into an area distant to the food cue, which also provided shelter habitat and the area close to the food cue, which was unsheltered and faced the predator cage. The area close to the food cue was further subdivided into the side directly in front of the predator cage, where predation risk was highest, and the side further away.

Three response variables were derived and combined to estimate prey vulnerability. I) “prey attraction”, II) ‘food search activity’, and III) ‘boldness’. Prey fishes may approach a predator to inspect it – a characteristic behavior termed predator inspection (Pitcher, Green & Magurran 1986) – which likely reduces their vulnerability by decreasing the chance being predated by their predator. We excluded the data obtained during such predator inspection behavior for the calculation of the three response variables to obtain the vulnerable component of the prey isolated from its non-vulnerable components.

The direct mortality, vulnerability rate, and effective search rate were used as forcing functions in our Ecosim models. These functions were applied to appropriate species in the model (Table S1). We calculated the relative effect size of these rates under different climate scenarios compared to control conditions using the absolute values (Table S1). In all cases, the value for present-day baseline conditions was 1. Lastly, we used linear interpolation to generate an annual time series of values for forcing functions from 2015 to 2100. We used community-level groups because indicators at the community level are reliable for detecting effects of perturbations on marine ecosystems (Fulton, Smith & Punt 2005).

1.5. Calculation of diversity indexes

We examined indices of diversity and evenness at broad taxonomic scales (functional group). We expressed diversity within general functional pools by using a form of the Shannon diversity index (Shannon & Weaver 1963),

$$H' = \sum_{i=1}^{s} p_i \times \ln(p_i)$$

Where diversity (*H'*) is a function of the proportion (*p*) of each functional group *i* that makes up the total biomass of the *s* pools that make up a general functional pool which in our case either individual species or a functional group such as zooplankton. As *H'* increases, species diversity increases.

The diversity index Kempton’s *Q* (Kempton & Taylor 1976) describes the slope of the cumulative species logarithmic abundance curve. This is adapted in our modeling approach in a way where taxonomic species are also grouped into aggregate biomass pools of functionally similar organisms, species are replaced by the species groups of the model, and the biomasses of these groups serve as a proxy for the number of individuals in that species or groups (Ainsworth & Pitcher 2006). This modified Kempton's *Q* species diversity index was calculated considering organisms with trophic levels 3 or higher and defined as:

$$Q_i = \frac{0.8\,Fg}{\log(R_1/R_2)}$$

where *Fg* is the total number of functional groups in the model, and R_1 and R_2 are the representative biomass values of the 10th and 90th percentiles in the cumulative abundance distribution.

Within EwE a functional group cannot go extinct and is represented by a very low but non-zero biomass value. This means each simulation at its conclusion will contain the same number of functional groups as the base model. The Kempton's *Q* index is reasonably invariant to model structure since each functional group potentially can affect only one point on the log-abundance curve. Thus this may induce a change in the overall slope only marginally (Ainsworth & Pitcher 2006). In contrast, the Shannon index is considered more sensitive to the aggregation method used in the mass balanced model.

1.6. Approach used for the retrospective test

To independently evaluate our modelling approach and test the assumption that mesocosms provide a realistic representation of the real world, we built two simplified Ecopath models, one using mesocosm data and the other using published data for Port Philip Bay (see above). Both models comprised an equal number of functional nodes and similar food web functional groups, making their results directly comparable, allowing us to test whether the mesocosm parameters are relevant to the PPB system for the period 1990 and 2015. The rationale being that if the model based on mesocosm parameters can replicate the PPB model, we should have an increased level of confidence in using the forcing functions derived from the mesocosm to simulate future food web dynamics under global change. As well as testing for model congruence, we also tested the predictive skill of both models using independent validation data. We used the same P/B ratio, Q/B ratio and diet data for mesocosm and simplified Port Philip Bay model for all model groups. Biomass data (per unit area) for two fish functional groups (carnivorous and omnivorous fish) were used to calibrate and compare both the models. We did not include herbivores as an individual functional group in our model due to the absence of major herbivorous fish (in terms of biomass) in our modelled ecosystem. We also included chondrichthyans (Port Jackson sharks) in our model validation exercise. The presence of apex sharks and predators were required for a direct comparison of models parameterised using mesocosm and field-based observations since these top predators can exert significant cascade effects within the food web.

1.7. Model skill assessment and sensitivity analyses

To assess the skill of our model we used independent observation data for two model functional groups (Fig. 5A, Table S3) and calculated six model skill assessment metrics (Fig. 5B) as has been recommended for ecosystem model assessments (Stow *et al.* 2009; Olsen *et al.* 2016). These model skill assessment metrics were: root mean squared error (RMSE), average error (AE), average absolute error (AAE), correlation coefficient (Pearson and Spearman), and modeling efficiency (MEF). The global sensitivity analysis is described in the Methods in the main paper.

FIGURES

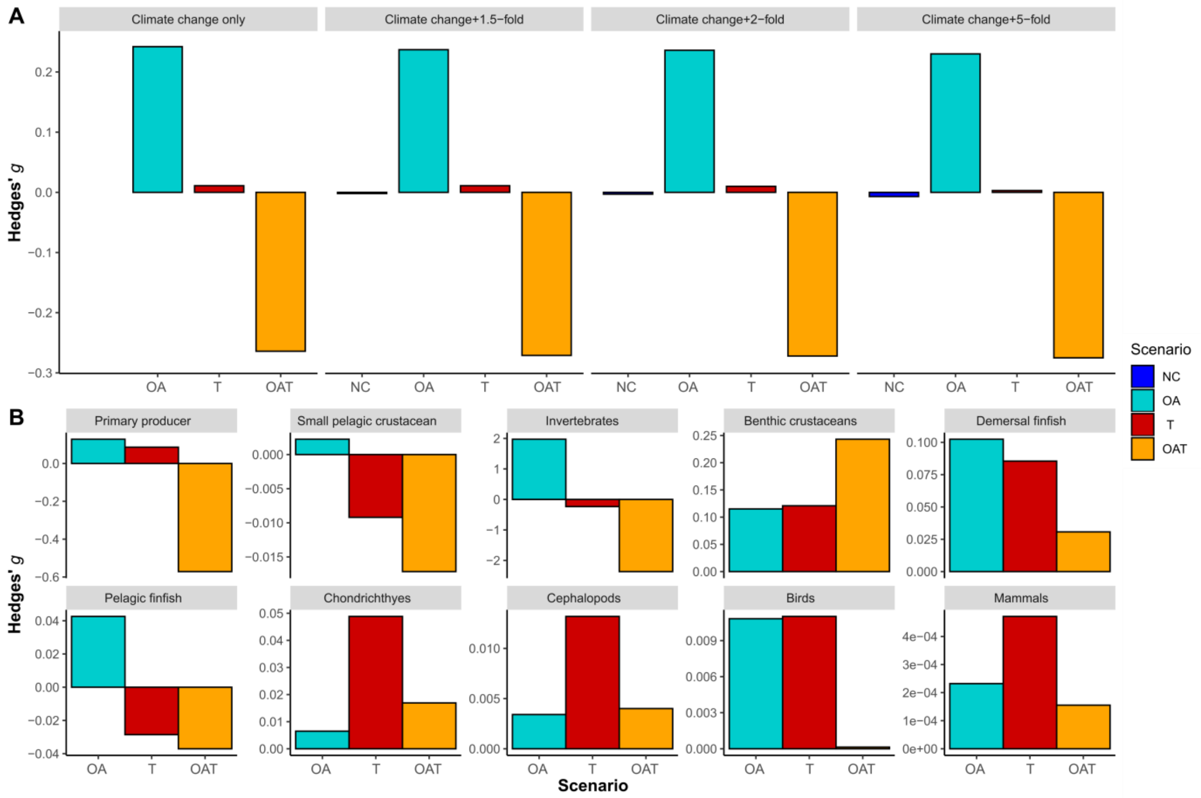

Figure S1: Mean effect size (in std. dev. unit) and the direction of impacts on the change in biomass (Δ) of (A) food web and (B) community groups under three climate change scenarios relative to a scenario of no change in climate and fishing from present-day levels (NC). Additionally, the mean effect size was also shown (A) under the combination of different climate and fishing effort scenarios relative to NC. Here the number with 'folds' refers to the magnitude of fishing increase that starts in the year 2015 and is held constant up to 2100 compared to the NC scenario.

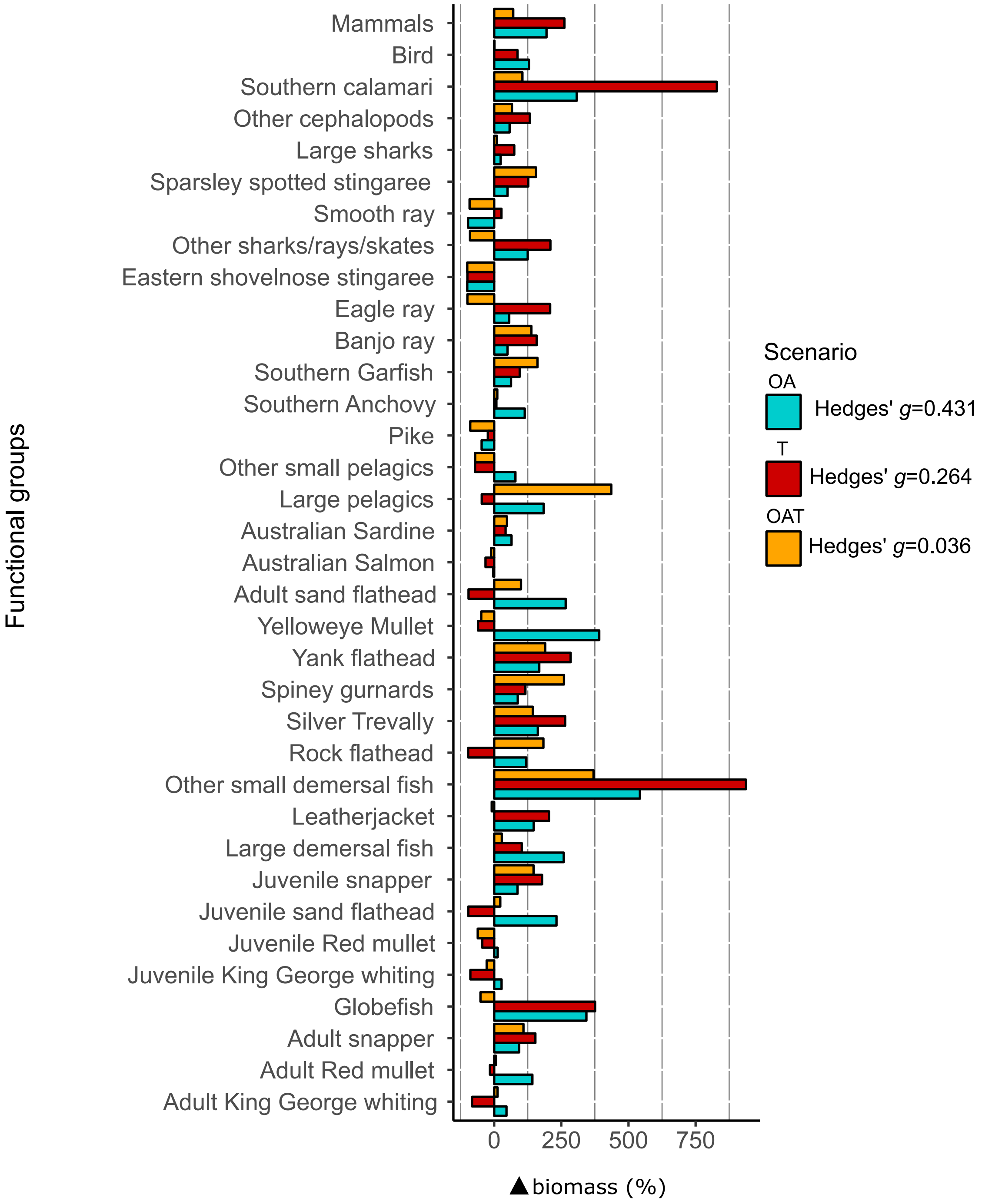

Figure S2: Change in biomass (Δ %) of different ecosystem functional groups (trophic levels ≥ 3) under three climate change scenarios relative to a no change in climate (NC) scenario. OA = ocean acidification, T = ocean warming, and OAT = combined ocean acidification and warming.

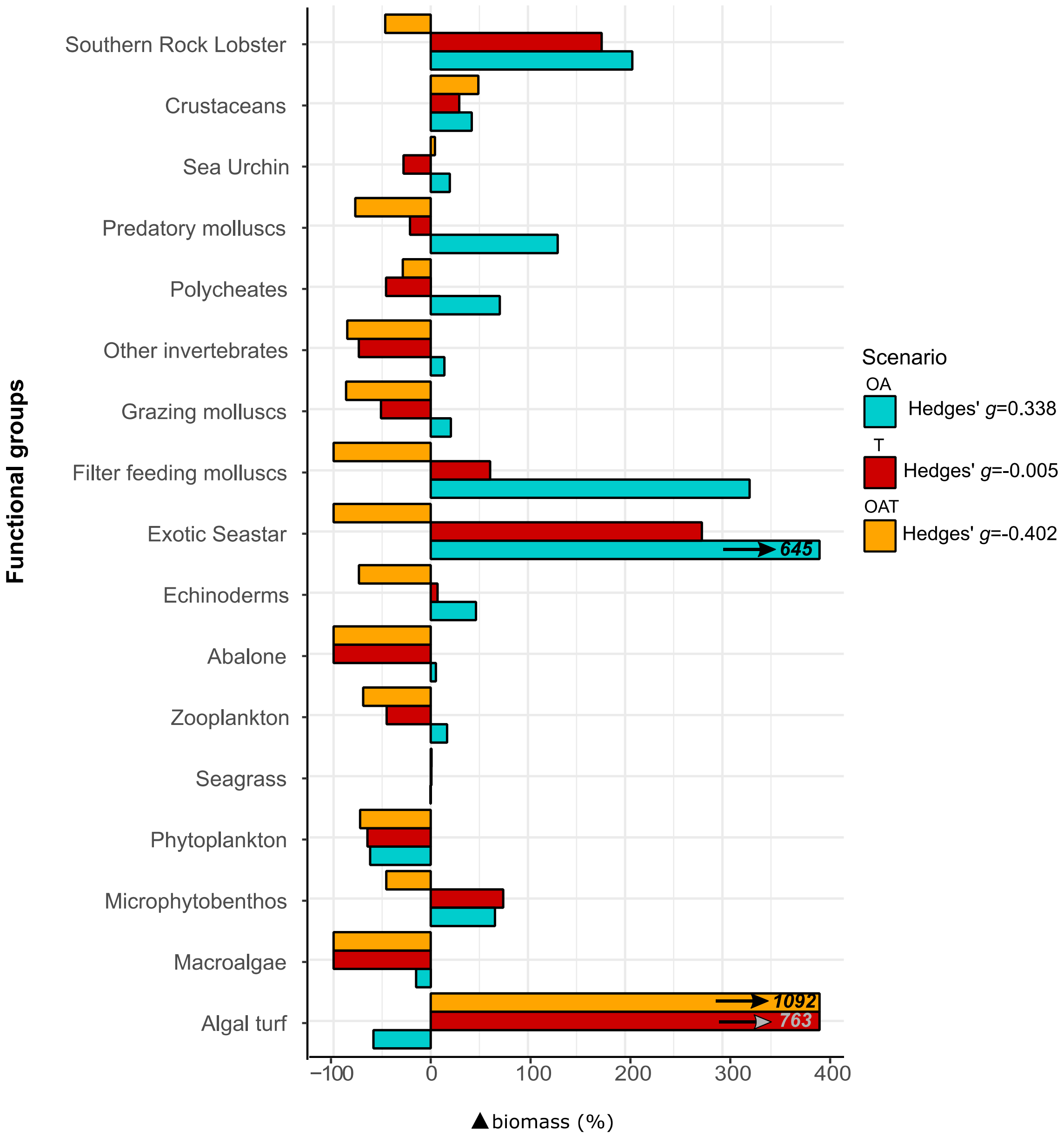

Figure S3: Change in biomass (Δ %) of different ecosystem functional groups (trophic levels < 3) under three climate change scenarios relative to a no change in climate (NC) scenario. OA = ocean acidification, T = ocean warming, and OAT = combined ocean acidification and warming. We limited the X axis between -100 and 400 for better visualization of the graph (algal turf and exotic seastar showed greater increases for certain scenarios).

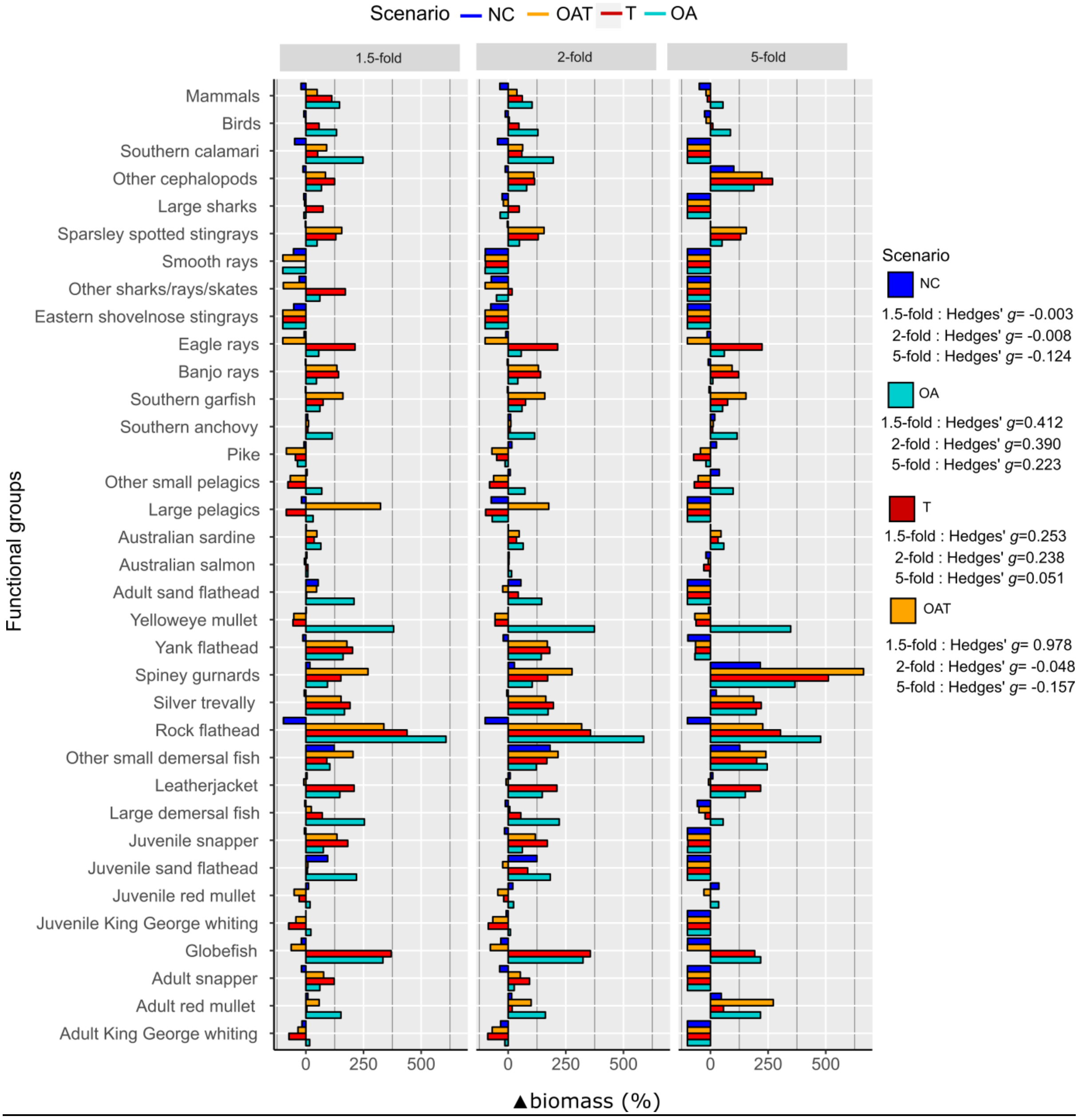

Figure S4: Change in biomass (Δ %) of different functional groups (trophic levels ≥ 3) under the combination of different climate and fishing effort scenarios relative to the biomass in 2100 under a scenario of no change in climate from present-day levels (NC). OA = ocean acidification, T = ocean warming, and OAT = combined ocean acidification and warming. Here the number with 'folds' refers to the magnitude of fishing increase that starts in the year 2015 and is held constant up to 2100 compared to the NC scenario.

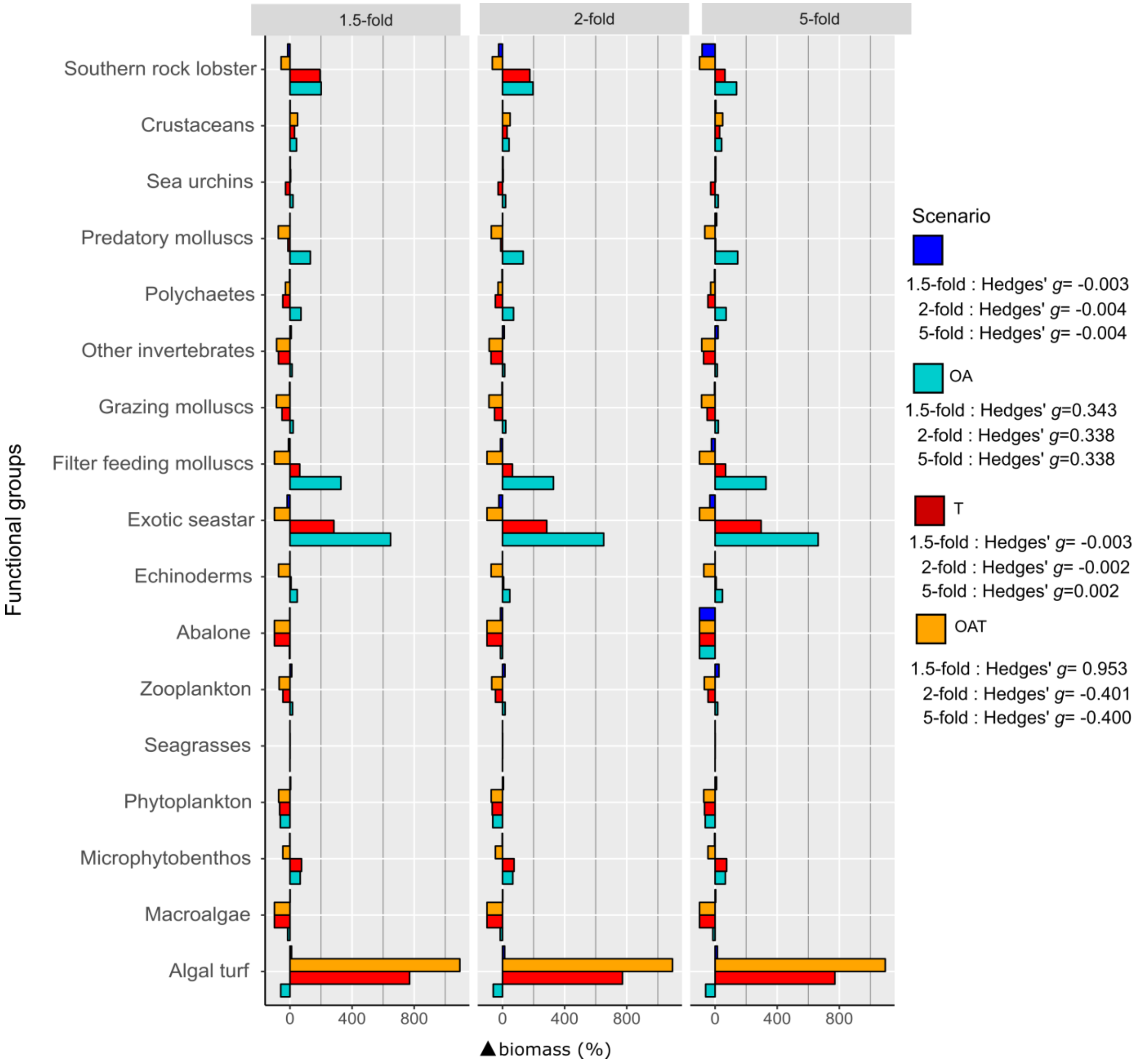

Figure S5: Change in biomass (Δ %) of different functional groups (trophic levels < 3) under the combination of different climate and fishing effort scenarios relative to the biomass in 2100 under a scenario of no change in climate from present-day levels (NC). OA = ocean acidification, T = ocean warming, and OAT = combined ocean acidification and warming. Here the number with ‘folds’ refers to the magnitude of fishing increase that starts in the year 2015 and is held constant up to 2100 compared to the NC scenario.

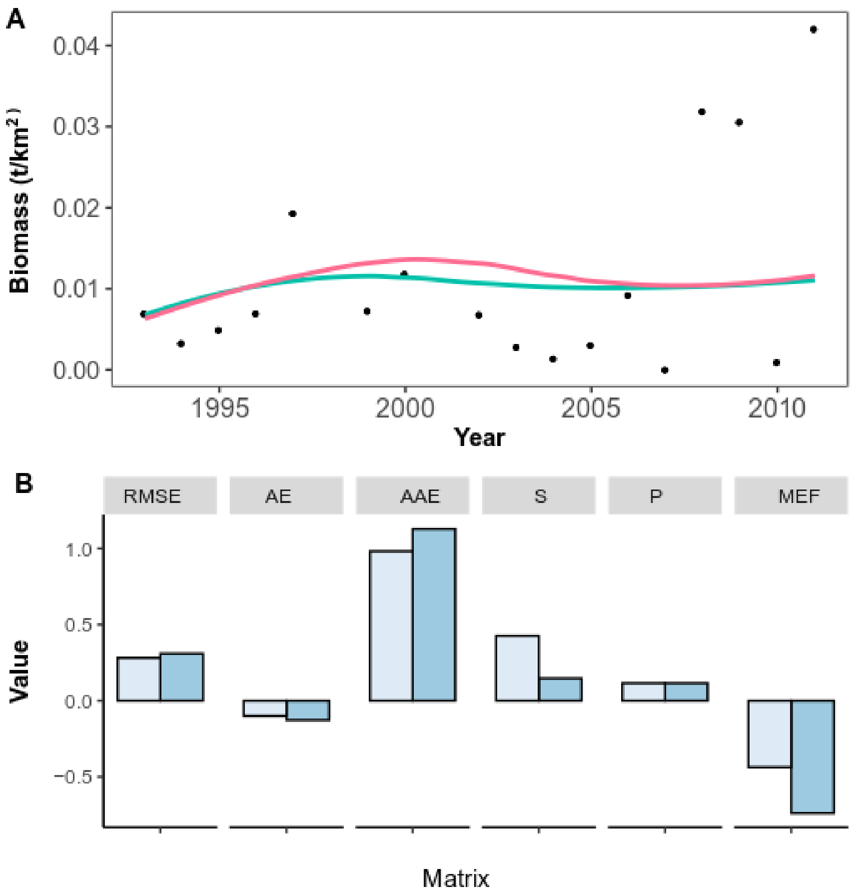

Figure S6: (A) Tests of mesocosm transferability. Comparison of the Port Phillip Bay (PPB) model (pink), calibrated using data from our mesocosm experiments (green) and observed standing biomass (tonnes per km^2) for Port Jackson shark between years 1993 and 2011. The PPB model was built using similar functional groups that comprise the mesocosm model. Black dots represent observed standing biomass in different years. Root-mean-square error (RMSE) indicates the differences (errors are measured in the same units as the response; here biomass (tonnes per km^2) between observed and predicted values by a model. (B) Hindcast model skill metrics for biomass data. Pairwise comparison of model skill for models built using empirical field (dark blue) and mesocosm data (light blue) for Port Phillip Bay (between 1993 and 2011): root mean squared error (RMSE), average error (AE), average absolute error (AAE), modelling efficiency (MEF), Spearman rank (S) and Pearson (P) correlation. Y-axis limited to show values between -0.8 and 1.2.

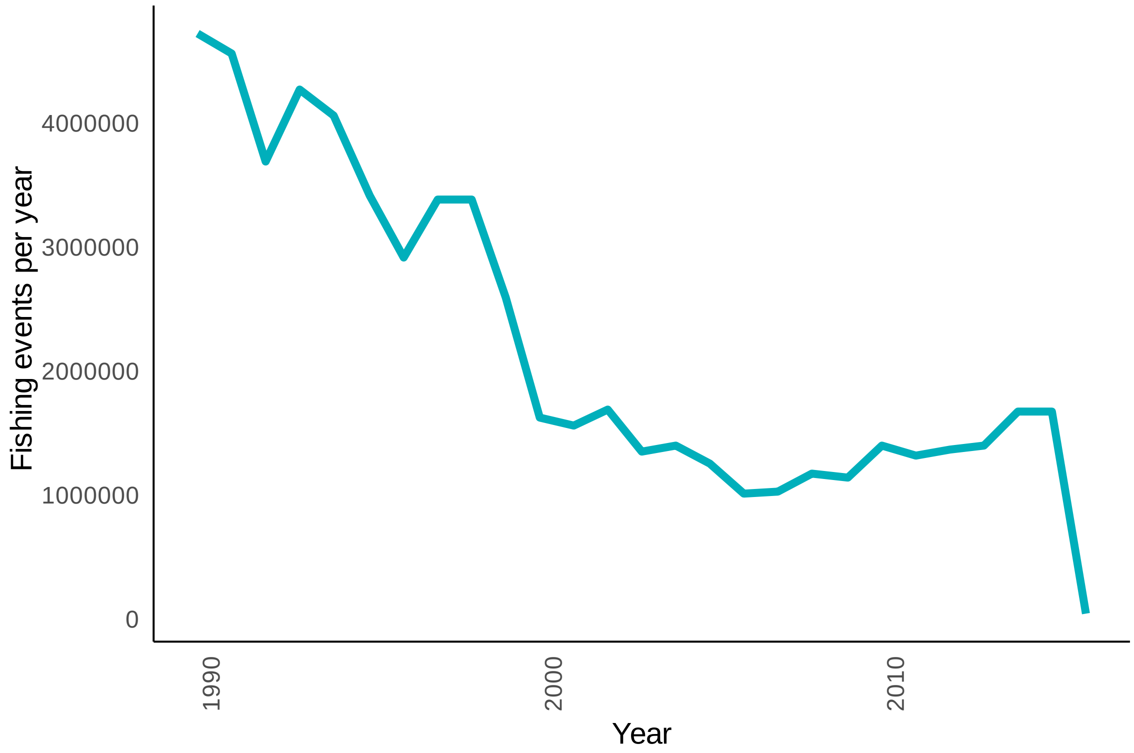

Figure S7: Historical trends of fishing efforts (fishing events) obtained for the commercial fishery in the Port Philip Bay ecosystem calculated by multiplying the number of fishing days and number of fishers.

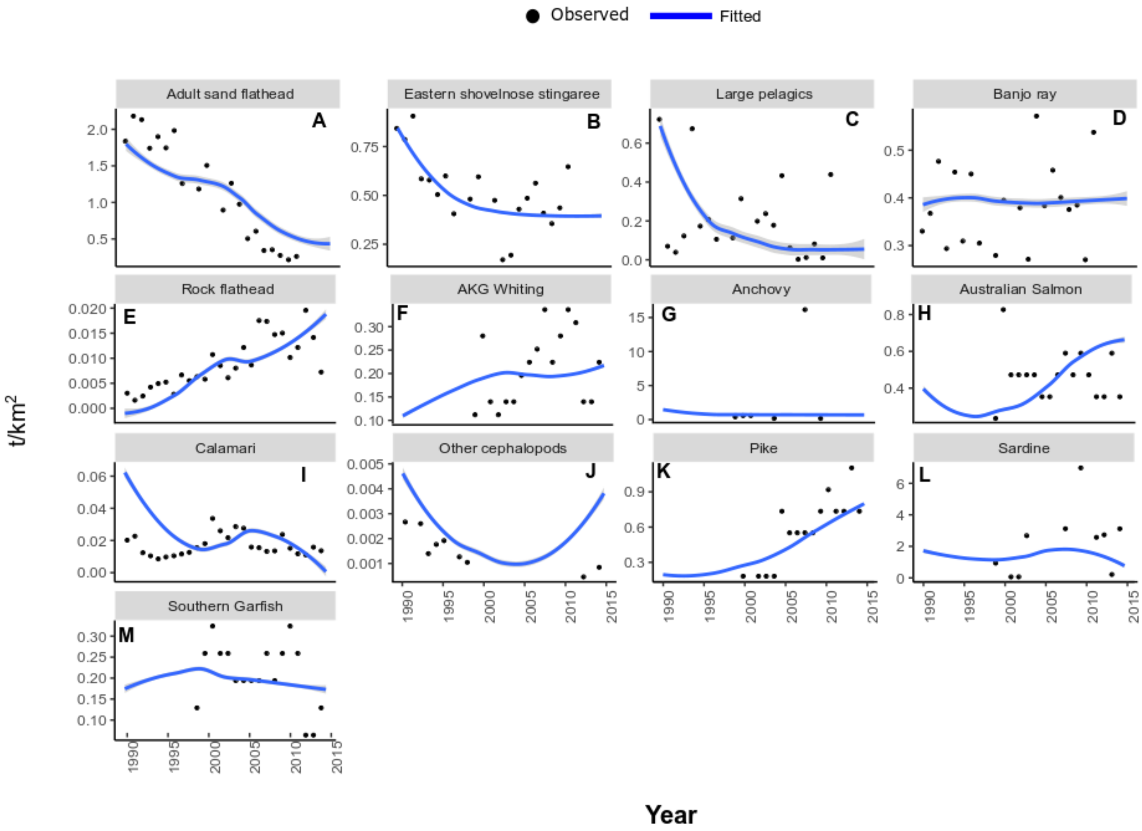

Figure S8: Predicted (solid lines) versus observed (dots) values (tonnes.km^{-2}) for some of the commercially and ecologically important groups within the Port Philip Bay ecosystem model fitted with available historical time series data (during the period 1990–2015). Groups (A-D) were fitted with biomass (tonnes.km^{-2}) survey (trawl) data while other groups (E-M) were fitted with CPUE (catch per unit effort) data.

TABLES

Table S1. Index (forcing function) used to drive the vulnerability parameters of future food web simulations (OA, T, and OAT). The effect size between the no-change-scenario (NC) and various climate scenarios is shown. OA = ocean acidification, T = ocean warming, and OAT = combined ocean acidification and warming. Source groups refer to consumers whose consumption depends on the vulnerability (parameters) of their prey groups. Forcing function as direct mortality for some of the model functional groups was also applied. For model functional groups or species number see Table S1.

Index used to drive vulnerability parameters	**Baseline value**	**Effect size**			**Applied on the following functional groups or species**	**Source group**
	NC	**OA**	**T**	**OAT**		
Vulnerability index of carnivorous fish	1	0.99	1.08	0.82	2 ,5, 6,10,11,14,15,17,18,22,23,24, 25,27,28,32,33,34,35	Relevant consumers/predators
Vulnerability index of omnivorous fish	1	1.07	1.16	0.85	16,26,29,30,31	Relevant consumer/predator
Vulnerability index of zooplankton	1	1.97	0.87	1.15	42	Carnivorous consumers
Vulnerability index of polychaetes	1	1.11	0.63	1.70	37	Carnivorous consumers
Vulnerability index of epifauna	1	0.99	1.24	1.79	36, 37	Carnivorous consumers
Vulnerability index of bivalves	1	0.78	1.43	2.15	38	Carnivorous consumers
Vulnerability index of gastropods	1	10.56	6.17	1.90	39	Carnivorous consumers
Vulnerability index of copepods	1	2.97	1.66	1.91	42	Omnivorous consumers
Vulnerability index of polychaetes	1	5.36	1.29	0.01	37	Omnivorous consumers
Vulnerability index of epifauna	1	3.10	2.88	0.88	36, 37	Omnivorous consumers
Vulnerability index of bivalves	1	1.65	3.18	0.91	38	Omnivorous consumers
Vulnerability index of gastropods	1	14.60	1.81	0.60	39	Omnivorous consumers
Search efficiency of chondrichthyans	1	0.21	1.07	0.32	2,5-8,10,11,14,16,17,21,22,24,27, 28, 30, 33,34,36-41,43,	Chondrichthyans
Algal turf productivity	1	1.07	1.82	1.58	49	Relevant consumers
Macrophytes productivity	1	1.28	0.24	0.46	48	Relevant consumers
Phytobenthos productivity	1	1.32	0.69	1.23	51	Relevant consumers
Phytoplankton productivity	1	1.66	0.44	0.99	50	Relevant consumers

Forcing function	**NC**	**OA**	**T**	**OAT**		Type
Biomass grazing molluscs	1	1.17	0.47	0.12	39	Mortality (as a function of biomass)
Biomass of filter feeders	1	1.24	0.28	0.15	38	Mortality (as a function of biomass)
Biomass of crustaceans	1	1.38	1.25	1.44	43	Mortality (as a function of biomass)
Biomass of polychaetes	1	1.74	0.50	0.68	37	Mortality (as a function of biomass)
Biomass of zooplankton	1	1.16	0.57	0.68	42	Mortality (as a function of biomass)

Table S2. Community groups considered for the representative model functional groups. Habitats and feeding guilds of the relevant groups are also shown. Feeding guild is only shown for the finfish group because model input data on species interaction was based on omnivorous and carnivorous finfish groups. Fg. no. = functional group number, NA = not applicable.

Fg. no.	Functional group name	Community group	Major species/common name	Habitat (water column)	Feeding guild
1	Large sharks	Chondrichthyans	*Notorynchus cepedianus*	Pelagic	NA
2	Large pelagics	Pelagic finfish	*Thyrsites atun, Pomatomus saltatrix, Seriolella brama, Seriolella punctata, Trachurus declivis*	Pelagic	Carnivorous
3	Bird	Bird	Australasian gannet *Morus serrator*	Bentho-pelagic	NA
4	Mammals	Mammals	Dolphins and seals	Bentho-pelagic	NA
5	Yank flathead	Demersal finfish	*Platycephalus speculator*	Demersal	Carnivorous
6	Rock flathead	Demersal finfish	*Platycephalus laevigatus*	Demersal	Carnivorous
7	Other cephalopods	Cephalopods	*Nototodarus gouldi*	Pelagic	NA
8	Southern calamari	Cephalopods	*Sepioteuthis australis*	Pelagic	NA
9	Smooth ray	Chondrichthyans	*Dasyatis brevicaudata*	Demersal	NA
10	Adult sand flathead	Demersal finfish	*Platycephalus bassensis*	Demersal	Carnivorous
11	Juvenile sand flathead	Demersal finfish	*Platycephalus bassensis*	Demersal	Carnivorous
12	Banjo ray	Chondrichthyans	*Trygonorrhina fasciata*	Demersal	NA
13	Eastern shovelnose stingaree	Chondrichthyans	*Trygonoptera imitata*	Demersal	NA
14	Adult King George whiting	Demersal finfish	*Sillaginodes punctata*	Demersal	Carnivorous
15	Juvenile King George whiting	Demersal finfish	*Sillaginodes punctata*	Demersal	Carnivorous
16	Large demersal fish	Demersal finfish	*Rhombosolea tapirina, Nemadactylus macropterus, Pentaceropsis recurvirostris, Eubalichthys mosaicus, Genypterus tigerinus, Gonorynchus greyi, Meuschenia freycineti, Platycephalus richardsoni*	Demersal	Omnivorous
17	Adult red mullet	Demersal finfish	*Upeneichthys vlamingii*	Demersal	Carnivorous
18	Juvenile red mullet	Demersal finfish	*Upeneichthys vlamingii*	Demersal	Carnivorous
19	Eagle ray	Chondrichthyes	*Myliobatis australis*	Demersal	NA

20	Other sharks/rays/skates	Chondrichthyans	*Squatina australis, Callorhynchus milii, Mustelus antarcticus, Dipturus whitleyi, Heterodontus portusjacksoni, Galeorhinus galeus, Urolophus gigas, Dentiraja lemprieri*	Demersal	NA
21	Sparsely spotted stingaree	Chondrichthyans	*Urolophus paucimaculatus*	Demersal	NA
22	Australian sardine	Pelagic finfish	*Sardinops sagax*	Pelagic	Carnivorous
23	Southern anchovy	Pelagic finfish	*Engraulis australis*	Pelagic	Carnivorous
24	Australian Salmon	Pelagic finfish	*Arripis trutta*	Pelagic	Carnivorous
25	Pike	Pelagic finfish	*Dinolestes lewini*	Pelagic	Carnivorous
26	Southern garfish	Pelagic finfish	*Hyporhamphus melanochir*	Pelagic	Omnivorous
27	Small pelagics	Pelagic finfish	*Hyperlophus vittatus, Cristiceps australis, Arripis georgianus*	Pelagic	Carnivorous
28	Silver trevally	Demersal finfish	*Pseudocaranx georgianus*	Demersal	Carnivorous
29	Yelloweye mullet	Demersal finfish	*Aldrichetta forsteri*	Demersal	Omnivorous
30	Leatherjacket	Demersal finfish	*Scobinichthys granulatus, Acanthaluteres vittiger, Acanthaluteres spilomelanurus, Thamnaconus degeni*	Demersal	Omnivorous
31	Small demersal fish	Demersal finfish	*Contusus brevicaudus, Ammotretis rostratus, Pseudophycis bachus, Neosebastes scorpaenoides, Neosebastes scorpaenoides, Neoodax balteatus,Contusus richei, Gymnapistes marmoratus, Kathetostoma laeve, Parequula melbournensis, Sillago flindersi, Vincentia conspersa, Lepidotrigla vanessa, Tetractenos glaber, Chelidonichthys kumu, Aracana ornate, Scorpaena papillosa, Aracana aurita, Favonigobius lateralis*	Demersal	Omnivorous
32	Globefish	Demersal finfish	*Diodon nicthemerus*	Demersal	Carnivorous
33	Spiney gurnards	Demersal finfish	*Lepidotrigla papilio*	Demersal	Carnivorous
34	Adult snapper	Demersal finfish	*Pagrus auratus*	Demersal	Carnivorous
35	Juvenile snapper	Demersal finfish	*Pagrus auratus*	Demersal	Carnivorous
36	Other invertebrates	Invertebrates	Acidian, tunicate, sponge, coral	NA	NA
37	Polychaetes	Invertebrates	*Phyllochaetopterus socialis* and other annelids	NA	NA
38	Filter feeding molluscs	Invertebrates	Mostly bivalves such as *Notospisula trigonella, Chioneryx cardiodes, Fulvia tenuicostata, Mytilus edulis*	NA	NA
39	Grazing molluscs	Invertebrates	Gastropods such as *Actinoleuca calamus, Micrastraea aurea, Rhyssoplax tricostalis, Phasianella australis, Bulla quoyii*, tunicate	NA	NA
40	Predatory molluscs	Invertebrates	*Ectosinum zonale, Austroginella johnstoni, E. zonale, Sigaretotrema umbilicata*	NA	NA

41	Echinoderms	Invertebrates	Mostly echinoids such as *Echinocardium cordatum* and other ophiuroids	NA	NA
42	Zooplankton	Small pelagic crustacean	Copepod, small copepods mostly *Paracalanus indicus* (Caldocera and larvaceans) and *Acartia tranteri*	NA	NA
43	Benthic crustaceans	Benthic crustacean	Small decapoda such as *Neocallichirus limosa*, *Dimorphostylis cottoni*, amphipods, crabs	NA	NA
44	Abalone	Invertebrates	Blacklip abalone and greenlip abalone	NA	NA
45	Southern rock lobster	Benthic crustacean	*Jasus edwardsii*	NA	NA
46	Sea Urchin	Invertebrates	Black urchin (*Centrostephanus rodgersii*) and white urchin (*Heliocidaris erythrogramma)*	NA	NA
47	Exotic seastar	Invertebrates	*Asterias amurensis*	NA	NA
48	Macroalgae	Primary producer		NA	NA
49	Algal turf	Primary producer		NA	NA
50	Phytoplankton	Primary producer		NA	NA
51	Microphytobenthos	Primary producer		NA	NA
52	Seagrass	Primary producer		NA	NA
53	Detritus	Detritus		NA	NA

Table S3. Basic input parameters for simplified Port Phillip Bay (PPB) and mesocosm models built for the retrospective test of mesocosm transferability. Values of trophic level (TL), biomass, production/biomass (P/B), consumption/biomass (Q/B), ecotrophic efficiency (EE), and production/consumption (P/C) ratios are shown. FGs = functional groups.

FGs	Functional group name	TL		Biomass (t/km^2)	PB (/year)		QB (/year)		EE		P/C	
		PPB	Meso		PPB	Meso	PPB	Meso	PPB	Meso	PPB	Meso
1	Port Jackson shark	3.04	3.09	0.01	0.20	0.40	2.60	2.60	0.00	0.00	0.08	0.15
2	Herbivore fish	2.07	2.17	0.01	0.72	1.37	14.10	94.06	0.08	0.04	0.05	0.01
3	Omnivorous fish	2.99	2.99	0.04	1.09	1.17	12.55	111.75	0.00	0.00	0.09	0.01
4	Carnivorous fish (benthic)	2.82	2.91	0.00	1.27	1.00	17.30	28.99	0.14	0.00	0.07	0.03
5	Echinoderms	2.06	2.06	51.28	0.80	0.80	9.41	9.41	0.00	0.00	0.08	0.08
6	Herbivorous macroinvertebrates	2.00	2.00	4.02	2.09	0.50	10.49	8.46	0.00	0.00	0.20	0.06
7	Small epifaunal invertebrates	2.07	2.07	0.32	2.72	3.67	13.59	18.00	0.54	0.54	0.20	0.20
8	Filter Feeders	2.40	2.40	24.02	2.80	2.05	11.80	7.60	0.11	0.15	0.24	0.27
9	Macro-crustaceans	2.41	2.26	25.97	4.50	0.80	22.48	10.72	0.07	0.37	0.20	0.07
10	Tanaids	2.05	2.05	2.61	11.51	11.51	40.15	40.15	0.81	0.95	0.29	0.29
11	Copepod	2.00	2.00	1.38	23.80	108.71	38.61	336.98	0.67	0.63	0.62	0.32
12	Microzooplankton	2.00	2.00	0.90	36.80	23.11	59.78	63.49	0.08	0.67	0.62	0.36
13	Meiobenthos	2.00	2.00	9.12	8.88	8.88	58.40	58.40	0.80	0.80	0.15	0.15
14	Macrophytes	1.00	1.00	25.91	20.00	2.07		0	0.02	0.17		
15	Algal turf	1.00	1.00	0.71	30.85	28.87		0	0.39	0.40		
16	Phytobenthos	1.00	1.00	26.88	45.00	36.69		0	0.24	0.20		
17	Phytoplankton	1.00	1.00	6.41	259.30	299.29		0	0.53	0.29		
18	Detritus	1.00	1.00	12573					0.39	0.41		

Table S4. Biomass estimates (tonnes.km^{-2} total weight) and other functional group parameters of the updated Port Philip Bay (PPB) Ecopath model. Values of trophic level (TL), biomass, production/biomass (P/B) ratio, consumption/biomass (Q/B) ratio, ecotrophic efficiency (EE), and production/consumption (P/C) ratio were shown. FGs = functional groups.

FGs	Functional group name	TL	Biomass (t/km²)	PB (year-^{1})	QB (year^{1})	EE	P/C	FGs in PPB Model
1	Large sharks	4.33	0.01	0.18	1.75	0.60	0.10	Included
2	Large pelagics	4.02	0.72	0.40	3.92	0.62	0.10	Koopman, 2005
3	Bird	3.82	1.02	0.07	1.69	0.15	0.04	Included
4	Mammals	4.02	0.02	0.09	19.88	0.00	0.00	Included
5	Yank flathead	3.58	0.09	0.40	3.80	0.18	0.11	Koopman, 2005
6	Rock flathead	3.33	0.07	0.38	2.45	0.95	0.16	Included
7	Other cephalopods	3.48	0.18	1.70	6.00	0.95	0.28	Koopman, 2005
8	Southern calamari	3.47	0.25	1.83	8.00	0.95	0.23	Included
9	Smooth ray	3.33	0.14	0.32	2.72	0.47	0.12	Koopman, 2005
10	Adult sand flathead	3.46	1.84	0.40	2.31	0.43	0.17	Koopman, 2005
11	Juvenile sand flathead	2.40	0.42	0.40	4.20	0.95	0.10	Koopman, 2005
12	Banjo ray	3.45	0.33	0.23	2.37	0.22	0.10	Koopman, 2005
13	Eastern shovelnose stingaree	3.28	0.84	0.49	2.41	0.08	0.20	Koopman, 2005
14	Adult King George whiting	3.18	0.12	1.10	4.40	0.97	0.25	Koopman, 2005
15	Juvenile King George whiting	3.29	0.21	1.10	8.12	0.53	0.14	Included
16	Large demersal fish	3.40	0.05	0.92	4.33	0.79	0.21	Koopman, 2005
17	Adult Red mullet	3.13	0.05	0.92	5.19	0.92	0.18	Koopman, 2005
18	Juvenile Red mullet	2.02	0.01	1.84	13.04	0.69	0.14	Included
19	Eagle ray	3.14	0.41	0.20	3.37	0.02	0.06	Koopman, 2005
20	Other sharks/rays/skates	3.11	0.07	0.22	2.20	0.86	0.10	Koopman, 2005
21	Sparsley spotted stingaree	3.11	0.57	0.41	4.16	0.03	0.10	Koopman, 2005
22	Australian sardine	3.06	2.89	1.12	6.00	0.95	0.19	Included
23	Southern anchovy	3.04	2.54	0.70	5.04	0.95	0.14	Included
24	Australian salmon	3.96	0.41	0.44	4.20	0.95	0.10	Included
25	Pike	4.04	0.21	0.30	3.00	0.95	0.10	Included
26	Southern garfish	2.61	0.23	1.55	10.40	0.95	0.15	Included
27	Small pelagics	3.01	3.53	0.82	10.02	0.95	0.08	Koopman, 2005

28	Silver trevally	3.28	0.31	0.57	2.20	0.95	0.26	Included
29	Yelloweye mullet	3.02	0.15	1.32	10.60	0.95	0.12	Included
30	Leatherjacket	2.68	0.12	0.92	9.65	0.99	0.10	Included
31	Small demersal fish	3.10	0.72	1.42	12.31	0.95	0.12	Koopman, 2005
32	Globefish	3.11	1.17	0.68	3.04	0.14	0.22	Koopman, 2005
33	Spiny gurnards	3.05	0.04	0.87	2.40	0.95	0.36	Koopman, 2005
34	Adult snapper	3.31	0.26	0.49	2.20	0.98	0.22	Koopman, 2005
35	Juvenile snapper	3.05	0.20	0.55	3.71	0.77	0.15	Included
36	Other invertebrates	2.39	24.02	3.26	16.28	0.13	0.20	Koopman, 2005
37	Polychaetes	2.29	24.22	2.93	11.53	0.91	0.25	Koopman, 2005
38	Filter feeding molluscs	2.07	24.97	2.72	13.59	0.95	0.20	Included
39	Grazing molluscs	2.00	4.02	2.09	10.49	0.95	0.20	Included
40	Predatory molluscs	3.32	0.94	2.72	13.59	0.57	0.20	Included
41	Echinoderms	2.05	51.28	0.80	9.41	0.33	0.08	Koopman, 2005
42	Zooplankton	2.04	4.66	54.75	153.36	0.55	0.36	Koopman, 2005
43	Benthic crustaceans	2.05	25.97	4.50	22.48	0.95	0.20	Koopman, 2005
44	Abalone	2.00	0.26	0.73	12.41	0.70	0.06	Included
45	Southern rock lobster	3.23	0.03	0.73	12.41	0.53	0.06	Included
46	Sea urchin	2.00	4.72	0.88	11.68	0.71	0.08	Included
47	Exotic seastar	3.05	0.00	0.52	2.60	0.00	0.20	Included
48	Macroalgae	1	18.13	20.00	0.00	0.23		Koopman, 2005
49	Algal turf	1	0.71	30.85	0.00	0.97		Included
50	Phytoplankton	1	6.41	259.30	0.00	0.82		Koopman, 2005
51	Microphytobenthos	1	26.88	45.00	0.00	0.11		Koopman, 2005
52	Seagrass	1	58.21	11.13	0.00	0.07		Koopman, 2005
53	Detritus	1	12573			0.29		Koopman, 2005

Table S5 The source of basic input parameters for the Port Phillip Bay model. Juvenile fish groups represent those <3 years old. P/B = production/biomass, Q/B = consumption/biomass, M = natural mortality, Z = total mortality, F = fishing mortality, FGs = functional groups.

FGs	**Group name**	**Biomass (t/km²)**	**PB (/year)**	**QB (/year)**	**Ecotrophic efficiency (EE)**
1	Large sharks	Model estimation	Average of M for bronze whalers and 7-gilled sharks (Froese 2019)	Calculated empirically (Palomares & Pauly 1989)	Assumed *EE* = 0.60 (Blanchard, Pinnegar & Mackinson 2002)
2	Large pelagics	Trawl survey	(Annala 1994; Tilzey 1994) (Weighted by the relative abundance of component species)	Calculated empirically	
3	Bird	(Briggs *et al.* 1987)	(Briggs *et al.* 1987)	(Briggs *et al.* 1987)	
4	Mammals	(Fulton & Smith 2004)	(Fulton & Smith 2004)	(Fulton & Smith 2004)	
5	Yank flathead	Trawl survey	As for sand flathead	Calculated from (Officer & Parry 2000)	
6	Rock flathead	Model estimation	(Koopman 2005)	Averaged from sand and yank flathead	Assumed *EE* = 0.95(Polovina 1984)
7	Other cephalopods	Model estimation	(Manickchand-Heileman, Soto & Escobar 1998)	(O'Sullivan & Cullen 1983; Arreguín-Sánchez, Seijo & Valero-Pacheco 1993)	Assumed *EE* = 0.95 (Polovina 1984)
8	Southern calamari	Model estimation	(Fulton & Smith 2004)	(Watson *et al.* 2013)	Assumed *EE* = 0.95 (Polovina 1984)
9	Smooth ray	Trawl survey	Used *T*max from similar species (*Dasyatis chrysonota*)(Cowley 1997) to estimate M	Calculated from data in (Officer & Parry 1996; Officer & Parry 2000)	
10	Adult sand flathead	Trawl survey	Z (Calculated from catch curve)	Calculated from data in (Officer & Parry 1996)	
11	Juvenile sand flathead	Trawl survey	Z (Calculated from catch curve)	Model estimation	

12	Banjo ray	Trawl survey	M (Froese & Pauly 2018)	Calculated from (Officer & Parry 1996)	
13	Eastern S. stingaree	Trawl survey	M (Froese & Pauly 2018)	Calculated from (Officer & Parry 1996)	
14	Adult King George whiting	Trawl survey	M doubled to get Z (Fowler 2000)	Calculated empirically (Palomares & Pauly 1989)	
15	Juvenile King George whiting	Model estimation	M (Fowler 2000)	Model estimation	
16	Large demersal fish	Trawl survey	M (Froese & Pauly 2018), then added F. F from catch rate/biomass =0.1552/0.357=0.4347	Q/B, an average of related demersal fish (Froese & Pauly 2018)	
17	Adult red mullet	Trawl survey	M, an average of other species of goatfish (Froese & Pauly 2018)	Q/B, an average of other species of goatfish (Froese & Pauly 2018)	
18	Juvenile red mullet	Model estimation	As for adult red mullet (Froese & Pauly 2018)	Model derived	
19	Eagle ray	Trawl survey	Used *T*max from similar species (*Myliobatis californica*) (Martin & Cailliet 1988)to estimate M	Calculated from data in (Officer & Parry 1996)	
20	Other sharks /rays/skates	Trawls survey	(Froese & Pauly 2018)	Q/B, an average of similar species (Froese & Pauly 2018)	
21	Sparsely spotted stingaree	Trawl survey	(Froese & Pauly 2018)	Calculated from data in (Officer & Parry 1996)	
22	Australian sardine	Model estimation	Z value for similar species *Sardinella lemuru* (Gaughan & Mitchell 1999)	(Goldsworthy *et al.* 2013)	
23	Southern anchovy	Model estimation	(Goldsworthy *et al.* 2013)	(Goldsworthy *et al.* 2013)	Assumed *EE* = 0.95 (Polovina 1984)
24	Australian salmon	Model estimation	(Goldsworthy *et al.* 2013)	(Hughes *et al.* 2014)	Assumed *EE* = 0.95 (Polovina 1984)
25	Pike	Model estimation	(Froese & Pauly 2018)	(Froese & Pauly 2018)	Assumed *EE* = 0.95 (Polovina 1984)

26	Southern garfish	Model estimation	(Steer *et al.* 2012)	(Froese & Pauly 2018)	Assumed *EE* = 0.95 (Polovina 1984)
27	Small pelagics	Model estimation	M, an average of all species of small pelagic (Froese & Pauly 2018)	Calculated empirically (Palomares & Pauly 1989)	Assumed *EE* = 0.95 (Polovina 1984)
28	Silver trevally	Model estimation	(Farmer *et al.* 2005)	Calculated empirically (Palomares & Pauly 1989)	Assumed *EE* = 0.95 (Polovina 1984)
29	Yelloweye mullet	Model estimation	M doubled to get Z (Froese & Pauly 2018)	Calculated empirically (Palomares & Pauly 1989)	Assumed *EE* = 0.95 (Polovina 1984)
30	Leatherjacket	Trawl survey-2	M, an average of all species of the group (Froese & Pauly 2018)	Calculated empirically (Palomares & Pauly 1989)	
31	Small demersal fish	Model estimation	Average for unvegetated sites in(Edgar & Shaw 1995)	P/B divided by average P/Q for unvegetated sites in (Edgar & Shaw 1995)	Assumed *EE* =0.95 (Polovina 1984)
32	Globefish	Trawl survey-2	(Froese & Pauly 2018)	Calculated from data in (Officer & Parry 1996)	
33	Spiny gurnards	Trawls survey	Used M from similar species within family (Booth 1997)	Calculated from data in (Officer & Parry 1996)	
34	Adult snapper	Calculated empirically (Annala, Sullivan & O'Brien 2000)	(Fulton & Smith 2004)	Calculated empirically (Palomares & Pauly 1989)	
35	Juvenile snapper	Model estimation	(Fulton & Smith 2004)	Model estimation	
36	Other invertebrates	Calculated from (Wilson, Cohen & Poore 1993)	Average of values for all species from literature presented in (Edgar 1990; Wilson, Cohen & Poore 1993)	Calculated assuming P/Q ratio of 0.2 (Arreguín-Sánchez, Seijo & Valero-Pacheco 1993)	
37	Polychaetes	Calculated from (Wilson, Cohen & Poore 1993)	Average values for polychaetes from literature presented in (Edgar 1990; Wilson, Cohen & Poore 1993)	(Poore 1992; Wilson, Cohen & Poore 1993)	
38	Filter feeding molluscs	Calculated from (Wilson, Cohen & Poore 1993)	Average values for molluscs from literature presented in (Edgar 1990; Wilson, Cohen & Poore 1993)	Calculated assuming P/Q ratio of 0.2 (Arreguín-Sánchez, Seijo & Valero-Pacheco 1993)	

39	Grazing molluscs	Calculated from (Wilson, Cohen & Poore 1993)	Average values for molluscs from literature presented in(Edgar 1990; Wilson, Cohen & Poore 1993)	Calculated assuming P/Q ratio of 0.2 (Arreguín-Sánchez, Seijo & Valero-Pacheco 1993)	
40	Predatory molluscs	Calculated from (Wilson, Cohen & Poore 1993)	Average values for molluscs from the literature presented in (Edgar 1990; Wilson, Cohen & Poore 1993)	Calculated assuming P/Q ratio of 0.2 (Arreguín-Sánchez, Seijo & Valero-Pacheco 1993)	
41	Echinoderms	Calculated from (Wilson, Cohen & Poore 1993)	(Miller & Mann 1973)	(Miller & Mann 1973)	
42	Zooplankton	(Holloway & Jenkins 1993)	(Holloway & Jenkins 1993)	(Holloway & Jenkins 1993)	
43	Crustaceans	Model estimation	Average values for Crustaceans from the literature presented in (Edgar 1990; Wilson, Cohen & Poore 1993)	Calculated assuming P/Q ratio of 0.2 (Arreguín-Sánchez, Seijo & Valero-Pacheco 1993)	Assumed *EE* =0.95 (Polovina 1984)
44	Abalone	(Fulton & Smith 2004)	(Fulton & Smith 2004)	(Fulton & Smith 2004)	
45	Southern rock lobster	(Fulton & Smith 2004)	(Fulton & Smith 2004)	(Fulton & Smith 2004)	
46	Sea Urchin	(Worthington & Blount 2003)	(Fulton & Smith 2004)	(Fulton & Smith 2004)	
47	Exotic seastar	Calculated from (Parry, Werner & Heislers 2004)	(Palomares & Pauly 2019)	(Palomares & Pauly 2019)	
48	Macroalgae	(Murray & Parslow 1997)	(Murray & Parslow 1997)		
49	Algal turf	(Murray & Parslow 1997)	(Bozec, Gascuel & Kulbicki 2004)		
50	Phytoplankton	(Beardall, Roberts & Royle 1996)	(Beardall, Roberts & Royle 1996)		
51	Micro-phytobenthos	(Beardall & Light 1994)	(Beardall & Light 1994)		
52	Seagrass	(Bulthuis, Axelrad & Mickelson 1992)	(Bulthuis & Woelkerling 1983)		
53	Detritus	(Koopman 2005)			

Table S6. Results of global sensitivity analysis for the changes in biomass for three representative community groups under a combined ocean acidification and warming (OAT) scenario. Standardized regression coefficients (SRC) scaled between zero and 1 (based on unsigned values), actual model coefficients (Coeff) and their upper and lower confidence intervals (0.025 and 0.975 bootstrap percentiles, respectively) for changes in the mean biomass according to a generalized linear model, with the dependent variables: biomass (B), consumption/biomass (Q/B), production/biomass (P/B), and ecotrophic efficiency (EE), '2-fold' equals the magnitude of increase in fishing pressure starting in 2015.

Model	Community groups	Dependent variable	SRC	Coeff	Lower CI	Upper CI
Climate model only	Cephalopods	B	0.20	-0.38	-1.04	0.29
		QB	0.32	-0.03	-0.24	0.02
		PB	0.28	-0.11	-0.05	0.00
		EE	0.20	-0.46	-1.03	0.11
	Pelagic finfish	B	0.40	0.37	0.34	0.39
		QB	0.27	-0.12	-0.14	-0.11
		PB	0.30	0.91	0.81	1.02
		EE	0.03	0.31	0.06	0.56
	Invertebrates	B	0.51	0.17	0.15	0.19
		QB	0.16	-0.32	-0.45	-0.19
		PB	0.21	1.06	0.73	1.38
		EE	0.12	2.41	1.04	3.77
Climate model and 2-fold increase in fishing effort	Cephalopods	B	0.33	-0.70	-1.21	-0.19
		QB	0.54	-0.04	-0.06	-0.02
		PB	0.11	-0.04	-0.12	0.04
		EE	0.02	0.04	-0.39	0.48
	Pelagic finfish	B	0.41	0.38	0.36	0.41
		QB	0.25	-0.11	-0.13	-0.10
		PB	0.26	0.82	0.71	0.92
		EE	0.08	0.78	0.50	1.05
	Invertebrates	B	0.55	0.17	0.15	0.19
		QB	0.17	-0.31	-0.43	-0.20
		PB	0.23	1.07	0.80	1.34
		EE	0.04	0.81	-0.34	1.97

Table S7. Matrix of diet used as input. Raw data across functional groups of predators in columns and prey species in rows.

Sl	Functional group name	1	2	3	4	5	6	7	8	9	10	11	12	13
1	Large sharks	0	0	0	0	0	0	0	0	0	0	0	0	0
2	Large pelagics	0.10	0	0.03	0.09	0	0	0.05	0	0	0	0	0	0
3	Birds	0	0	0.01	0	0	0	0	0	0	0	0	0	0
4	Mammals	0	0	0	0	0	0	0	0	0	0	0	0	0
5	Yank flathead	0.01	0	0	0	0	0	0	0	0	0	0	0	0
6	Rock flathead	0.01	0	0	0	0	0	0	0.01	0.01	0	0	0	0
7	Other cephalopods	0.06	0.00	0.03	0.06	0.089	0	0.02	0.02	0	0.02	0	0	0
8	Southern calamari	0.04	0	0.03	0.15	0.01	0.08	0.03	0.02	0	0.02	0	0.02	0
9	Smooth ray	0.07	0	0	0	0	0	0	0	0	0	0	0	0
10	Adult sand flathead	0.01	0	0	0.02	0	0	0	0.03	0.12	0	0	0.05	0
11	Juvenile sand flathead	0.02	0	0	0.02	0.04	0	0	0.03	0.20	0	0	0	0
12	Banjo ray	0.05	0	0	0	0	0	0	0	0	0	0	0	0
13	Eastern shovelnose stingaree	0.15	0	0	0	0	0	0	0	0	0	0	0	0
14	Adult King George whiting	0.01	0	0.00	0.00	0	0	0	0	0	0	0	0	0
15	Juvenile King George whiting	0	0	0.00	0.00	0	0	0	0.03	0	0	0	0	0
16	Large demersal fish	0.07	0	0	0	0	0	0	0	0	0	0	0	0
17	Adult red mullet	0	0	0	0.01	0	0	0	0	0	0	0	0.05	0
18	Juvenile red mullet	0	0	0	0.04	0	0	0	0	0	0	0	0	0
19	Eagle ray	0.09	0	0	0	0	0	0	0	0	0	0	0	0
20	Other sharks/rays/skates	0.02	0	0	0.01	0	0	0	0	0	0	0	0	0
21	Sparsely spotted stingaree	0.17	0	0	0	0	0	0	0	0	0	0	0	0
22	Australian sardine	0.03	0.59	0.28	0.05	0	0	0.05	0.02	0	0	0	0	0
23	Southern anchovy	0	0.26	0.08	0.05	0	0	0	0.04	0	0	0	0	0
24	Australian Salmon	0.03	0.02	0.02	0.02	0	0	0	0.02	0	0	0	0	0
25	Pike	0	0.02	0	0	0	0	0	0	0	0	0	0	0
26	Southern garfish	0	0.02	0.03	0.01	0	0	0	0.01	0	0	0	0	0
27	Small pelagics	0.01	0.00	0.07	0.05	0.05	0	0.08	0.05	0	0.304	0	0.16	0
28	Silver trevally	0.02	0.02	0.01	0.02	0	0	0	0	0	0	0	0	0
29	Yelloweye mullet	0	0	0.01	0.03	0	0	0.01	0.02	0	0	0	0	0
30	Leatherjacket	0.02	0	0	0	0.06	0	0.02	0	0	0	0	0.02	0
31	Small demersal fish	0	0	0.019	0.04	0.18	0.17	0.06	0.04	0	0.017	0	0.08	0
32	Globefish	0	0	0	0	0	0	0	0	0	0	0	0	0
33	Spiney gurnards	0.00	0	0	0	0.08	0	0.01	0	0	0	0	0	0
34	Adult snapper	0.02	0	0	0.06	0	0	0	0	0	0	0	0	0
35	Juvenile snapper	0	0	0.03	0.04	0	0	0	0	0	0	0	0	0
36	Other invertebrates	0	0	0.04	0	0.06	0.01	0.04	0.08	0	0.02	0	0.00	0
37	Polychaetes	0	0	0.06	0	0.00	0	0.01	0	0.13	0.05	0.10	0.00	0.94
38	Filter feeding molluscs	0	0	0.06	0	0	0	0.03	0	0	0.01	0.08	0.03	0.01
39	Grazing molluscs	0	0	0	0	0	0.01	0.01	0	0	0.09	0.02	0	0.01
40	Predatory molluscs	0	0	0	0.03	0	0	0.02	0.02	0	0.02	0	0	0.01
41	Echinoderms	0	0	0	0.10	0.01	0	0.03	0.10	0	0.00	0	0	0.04
42	Zooplankton	0	0	0	0.03	0	0.42	0	0.02	0	0	0.05	0	0
43	Benthic crustaceans	0	0.07	0.03	0.07	0.42	0.3	0.52	0.45	0.54	0.44	0.1	0.59	0.01
44	Abalone	0	0	0	0	0	0	0.01	0	0	0	0	0	0
45	Southern rock lobster	0	0	0	0.00	0	0	0.00	0.00	0	0	0	0.00	0

46	Sea Urchin	0	0	0.00	0	0	0	0	0	0	0.01	0	0	0
47	Exotic seastar	0	0	0	0	0	0	0	0	0	0	0	0	0
48	Macroalgae	0	0	0	0	0	0	0	0	0	0	0	0	0
49	Algal turf	0	0	0	0	0	0	0	0	0	0	0	0	0
50	Phytoplankton	0	0	0	0	0	0	0	0	0	0	0.63	0	0
51	Microphytobenthos	0	0	0	0	0	0	0	0	0	0	0	0	0
52	Seagrass	0	0	0	0	0	0.01	0	0	0	0.00	0	0	0
53	Detritus	0	0	0.05	0	0	0	0	0	0	0	0.02	0	0
54	Import	0	0	0.11	0	0	0	0	0	0	0	0	0	0
55	Total	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

Table S7 Continued

Sl	Functional group name	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
1	Large sharks	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	Large pelagics	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	Birds	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	Mammals	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	Yank flathead	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	Rock flathead	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7	Other cephalopods	0	0	0	0.00	0	0	0.01	0.00	0	0	0	0	0	0	0	0	0	0.00
8	Southern calamari	0	0	0.04	0	0	0	0.01	0	0	0	0	0.05	0	0	0.02	0	0	0
9	Smooth ray	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10	Adult sand flathead	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
11	Juvenile sand flathead	0	0	0	0.03	0	0	0	0	0	0	0	0	0	0	0	0	0	0
12	Banjo ray	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0	0
13	Eastern shovelnose stingaree	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
14	Adult King George whiting	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
15	Juvenile King George whiting	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
16	Large demersal fish	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
17	Adult red mullet	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
18	Juvenile red mullet	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
19	Eagle ray	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20	Other sharks/rays/skates	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21	Sparsely spotted stingaree	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	Australian sardine	0	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0	0	0	0	0
23	Southern anchovy	0	0	0	0	0	0	0	0	0	0	0.35	0.15	0	0	0	0	0	0
24	Australian Salmon	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	Pike	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	Southern garfish	0	0	0	0	0	0	0	0	0	0	0.1	0	0	0	0	0	0	0
27	Small pelagics	0	0	0	0	0	0	0	0	0	0	0.2	0.65	0	0	0.18	0	0	0
28	Silver trevally	0	0	0	0	0	0	0	0	0	0	0.05	0	0	0	0	0	0	0
29	Yelloweye mullet	0	0	0.05	0	0	0	0	0	0	0	0.05	0	0	0	0	0	0	0
30	Leatherjacket	0	0	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01
31	Small demersal fish	0	0	0.12	0.01	0	0	0	0	0	0	0.05	0	0	0	0	0.03	0	0.03
32	Globefish	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	Spiney gurnards	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	Adult snapper	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	Juvenile snapper	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	Other invertebrates	0.1	0.48	0.02	0.01	0	0.21	0.03	0.02	0.04	0	0	0	0.01	0.05	0.03	0.12	0.1	0.01
37	Polychaetes	0.5	0.34	0.15	0.20	0.00	0.06	0.03	0.22	0	0	0	0	0.08	0	0.05	0.21	0	0.04
38	Filter feeding molluscs	0	0.02	0	0	0	0.37	0.44	0.00	0	0	0	0	0	0	0.08	0	0.15	0.06
39	Grazing molluscs	0	0	0	0.00	0	0	0	0	0	0	0	0	0	0	0	0.05	0.01	0.03
40	Predatory molluscs	0	0	0.06	0.00	0	0	0	0.00	0	0	0	0	0	0	0	0.05	0	0.01
41	Echinoderms	0.07	0	0.24	0	0	0.03	0.07	0.00	0.00	0	0	0	0	0	0.02	0	0.10	0.02
42	Zooplankton	0	0.06	0	0	0.02	0	0	0	0.7	0.90	0	0	0.01	0.9	0	0.11	0.05	0
43	Benthic crustaceans	0.35	0.10	0.30	0.74	0.00	0.34	0.41	0.75	0.25	0.10	0.05	0	0.47	0	0.62	0.23	0.2	0.80
44	Abalone	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00
45	Southern rock lobster	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00
46	Sea Urchin	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

47	Exotic seastar	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	Macroalgae	0	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0.1	0.34	0
49	Algal turf	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0
50	Phytoplankton	0	0	0	0	0.26	0	0	0	0.00	0	0	0	0	0.05	0	0	0	0
51	Microphytobenthos	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
52	Seagrass	0.02	0	0	0	0	0	0	0	0	0	0	0	0.44	0	0	0.1	0.01	0
53	Detritus	0	0	0	0	0.71	0	0	0	0	0	0	0	0	0	0	0	0.02	0
54	Import	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	Total	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

Table S7 Continued

Sl	Functional group name	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47
1	Large sharks	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	Large pelagics	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	Birds	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	Mammals	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	Yank flathead	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	Rock flathead	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7	Other cephalopods	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8	Southern calamari	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
9	Smooth ray	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10	Adult sand flathead	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
11	Juvenile sand flathead	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
12	Banjo ray	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
13	Eastern shovelnose stingaree	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
14	Adult King George whiting	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
15	Juvenile King George whiting	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
16	Large demersal fish	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
17	Adult red mullet	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
18	Juvenile red mullet	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
19	Eagle ray	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20	Other sharks/rays/skates	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21	Sparsely spotted stingaree	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	Australian sardine	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	Southern anchovy	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	Australian Salmon	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	Pike	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	Southern garfish	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	Small pelagics	0	0	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0
28	Silver trevally	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	Yelloweye mullet	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	Leatherjacket	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	Small demersal fish	0	0	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0
32	Globefish	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	Spiney gurnards	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
34	Adult snapper	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	Juvenile snapper	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	Other invertebrates	0.00	0.00	0.04	0	0.01	0	0	0	0.3	0	0	0	0	0.08	0	0
37	Polychaetes	0.00	0.01	0.06	0	0.06	0.08	0	0	0.33	0.02	0	0.00	0	0.28	0	0.05
38	Filter feeding molluscs	0.30	0.01	0.09	0.026	0.09	0.08	0	0	0.16	0	0	0	0	0.31	0	0.35
39	Grazing molluscs	0.05	0.01	0.02	0	0.02	0	0	0	0.04	0	0.001	0	0	0	0	0.35
40	Predatory molluscs	0.05	0	0.02	0	0	0	0	0	0.07	0	0	0	0	0.08	0	0
41	Echinoderms	0.19	0	0.09	0	0.03	0	0	0	0	0	0	0	0	0	0	0.08
42	Zooplankton	0	0	0	0	0.04	0	0.07	0	0.06	0.01	0.04	0.02	0	0.01	0	0
43	Benthic crustaceans	0.4	0.97	0.48	0.97	0.11	0.08	0	0	0.03	0.02	0	0.02	0	0.23	0	0.12
44	Abalone	0	0	0	0	0	0	0	0	0.00	0	0	0.00	0	0.00	0	0
45	Southern rock lobster	0	0	0	0.00	0	0	0	0	0.00	0	0	0	0	0	0	0
46	Sea Urchin	0	0	0	0	0	0	0	0	0.01	0.00	0	0.00	0	0.01	0	0.05

47	Exotic seastar	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	Macroalgae	0	0	0	0	0	0	0.03	0.2	0	0.02	0.01	0.02	0.75	0	0.60	0
49	Algal turf	0	0	0	0	0	0	0	0.44	0	0	0	0	0	0	0.05	0
50	Phytoplankton	0	0	0	0	0.38	0.39	0.81	0	0	0.13	0.90	0.22	0	0	0	0
51	Microphytobenthos	0	0	0	0	0.25	0	0	0.35	0	0.01	0	0	0.1	0	0.20	0
52	Seagrass	0.00	0	0	0	0	0	0	0.02	0	0.01	0.05	0	0.15	0	0.10	0
53	Detritus	0	0	0	0	0.02	0.36	0.10	0	0	0.80	0	0.72	0	0.01	0.05	0
54	Import	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
55	Total	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

Table S8. The source of diet data for the Port Phillip Bay model. Juvenile fish groups represent those <3 years old.

Functional groups number	**Group name**	**Diet**
1	Large sharks	(Ebert 1991)
2	Large pelagics	(Officer & Parry 2000)
3	Bird	(Briggs *et al.* 1987)
4	Mammals	(Fulton & Smith 2004)
5	Yank flathead	(Officer & Parry 2000)
6	Rock flathead	(Froese & Pauly 2018)
7	Other cephalopods	(O'Sullivan & Cullen 1983; Arreguín-Sánchez, Seijo & Valero-Pacheco 1993)
8	Southern calamari	(Officer & Parry 2000)
9	Smooth ray	(Officer & Parry 2000)
10	Adult sand flathead	(Officer & Parry 2000)
11	Juvenile sand flathead	(Officer & Parry 2000)
12	Banjo ray	(Officer & Parry 2000)
13	Eastern shovelnose stingaree	(Officer & Parry 2000)
14	Adult King George whiting	(Officer & Parry 2000)
15	Juvenile King George whiting	(Officer & Parry 2000)
16	Large demersal fish	(Officer & Parry 2000)
17	Adult red mullet	(Officer & Parry 2000)
18	Juvenile red mullet	(Officer & Parry 2000)
19	Eagle ray	(Officer & Parry 2000)
20	Other sharks/rays/skates	(Officer & Parry 2000)
21	Sparsely spotted stingaree	(Officer & Parry 2000)
22	Australian sardine	(Froese & Pauly 2018)
23	Southern anchovy	(Froese & Pauly 2018)
24	Australian Salmon	(Hughes *et al.* 2014)
25	Pike	(Froese & Pauly 2018)
26	Southern garfish	(Robertson & Klumpp 1983)
27	Small pelagics	Assumed to be 100% zooplankton

28	Silver trevally	(French *et al.* 2013)
29	Yelloweye mullet	(Platell, Orr & Potter 2006)
30	Leatherjacket	(Hallett & Tweedley 2015)
31	Small demersal fish	(Officer & Parry 2000)
32	Globefish	(Officer & Parry 2000)
33	Spiney gurnards	(Officer & Parry 2000)
34	Adult snapper	(Officer & Parry 2000)
35	Juvenile snapper	(Officer & Parry 2000)
36	Other invertebrates	See crustaceans
37	Polychaetes	See crustaceans
38	Filter feeding molluscs	See crustaceans
39	Grazing molluscs	See crustaceans
40	Predatory molluscs	See crustaceans
41	Echinoderms	See crustaceans
42	Zooplankton	(Holloway & Jenkins 1993)
43	Crustaceans	Breakdown of feeding groups in (Wilson, Cohen & Poore 1993) Feeding groups allocated the following diet: deposit feeders eat detritus; predators eat inverts-distributed according to biomass; scavengers eat detritus; suspension feeders eat 7.5% zooplankton and 92.5% phytoplankton; grazers eat micro-phytobenthos and seagrass
44	Abalone	(Fulton & Smith 2004; Palomares & Pauly 2019)
45	Southern rock lobster	(Fulton & Smith 2004; Palomares & Pauly 2019)
46	Sea Urchin	(Fulton & Smith 2004; Palomares & Pauly 2019)
47	Exotic seastar	(Lockhart & Ritz 2001)

Table S9. Results of the temporally dynamic fitting procedure of the Port Phillip Bay Ecopath model from 1990s to 2015. T = temperature, SL = serial number, K = number of parameters included in the each model run, NVs = number of vulnerabilities included in each iteration, sPP = number of primary production spline points (for smoothing of the time series), SS = weighted sum of squared deviations. NVs and sPP are shown only for those models with the lowest Akaike Information Criterion (AIC). The "best" model (shown in bold) is the one yielding the lowest corrected Akaike Information Criterion (AICc) and used to fit the Port Philip Bay model.

T	SL	Steps	Description	K	NVs	sPP	SS	AIC	AICc
Yes	1	Baseline	Trophic interactions with default prey-predator Vulnerabilities (vij = 2; mixed effect). No environmental or fishery data are used to drive the model.	0	0	0	462.99	-39.53	-39.53
	2	Baseline and trophic interaction	Trophic interactions with different vulnerabilities. No environmental or fishery changes are used to drive the model.	24	24	0	262.95	-272.45	-270.13
	3	Baseline and environment	The "PP anomaly" is used to drive the model. No fishery data are used to drive the model.	3	0	3	439.10	-59.60	-59.60
	4	Baseline, trophic interactions and environment	No fishery data are used.	27	25	2	270.00	-253.00	-250.00
	5	Fishery	Fishing effort is included as model driver. Trophic interactions are set as default and no environmental data are used.	0	0	0	456.51	-46.59	-46.59
	6	Trophic interaction and fishery	No environmental data are used.	15	15	0	253.74	-309.83	-308.97
	7	Fishing and PP anomaly	Trophic interactions are set as default	8	0	8	425.16	-65.94	-65.71
	8	Trophic interactions, environment and fishery	All the components are jointly included in the model as drivers.	21	18	3	246.58	-311.00	-309.00
No	1	Baseline, trophic interactions and environment	No fishery data are used.	21	14	7	328.3	-167.9	-166.2

Table S10. Model estimated vulnerability parameters for different functional groups of the Port Phillip Bay Ecopath model.

Functional groups number	Functional groups	Vulnerability	S.	Functional groups	Vulnerability
1	Large sharks	2	27	Small pelagics	2
2	Large pelagics	2	28	Silver Trevally	>1000
3	Bird	2	29	Yelloweye Mullet	2
4	Mammals	2	30	Leatherjacket	1
5	Yank flathead	1	31	Small demersal fish	2
6	Rock flathead	52	32	Globefish	>1000
7	Other cephalopods	2	33	Spiny gurnards	2
8	Southern calamari	2	34	Adult snapper	2
9	Smooth ray	>1000	35	Juvenile snapper	2
10	Adult sand flathead	2	36	Other invertebrates	28
11	Juvenile sand flathead	2	37	Polychaetes	2
12	Banjo ray	2	38	Filter feeding molluscs	>1000
13	Eastern shovelnose stingaree	2	39	Grazing molluscs	2
14	Adult King George whiting	2	40	Predatory molluscs	2
15	Juvenile King George whiting	2	41	Echinoderms	2
16	Large demersal fish	1	42	Zooplankton	1
17	Adult Red mullet	2	43	Crustaceans	2
18	Juvenile Red mullet	2	44	Abalone	2
19	Eagle ray	2	45	Southern Rock Lobster	2
20	Other sharks/rays/skates	2	46	Sea urchin	2
21	Sparsely spotted stingaree	2	47	Exotic seastar	2
22	Australian Sardine	2			
23	Southern Anchovy	2			
24	Australian Salmon	2			
25	Pike	5			
26	Southern Garfish	2			

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