Quillback rockfish abundance estimates within California's no-take MPAs

Tanya Rogers[1], Rebecca Miller[1,2], E.J. Dick[1]
[1]NOAA Fisheries, SWFSC, Fisheries Ecology Division
[2]University of California, Santa Cruz, Fisheries Collaborative Program
March 31, 2025

Key Findings

1. Model-based density estimates and habitat area estimates inside California no-take Marine Protected Areas (MPAs; north of Lopez Point, CA) were combined to estimate a mean abundance of 151,934 quillback rockfish (95% CI: 118,204-195,289) during the period 2014-2016.
2. Estimated mean abundance inside these no-take MPAs increased to 317,274 quillback rockfish (95% CI: 273,983-367,405) by the period 2019-2021.
3. Increases in quillback density between these two periods varied by region and protection status, with larger increases observed inside the MPAs, on average.
4. A large fraction of total quillback abundance inside California's no-take MPAs is found at the Farallon Islands.

Data

Counts of quillback rockfish from ROV survey transects were provided to NMFS SWFSC staff by the California Department of Fish and Wildlife (CDFW), along with auxiliary variables associated with each transect (e.g., transect area, year, location, depth). Data tables in Microsoft Access were merged and extracted following instructions in CDFW's "ROV Data User Manual." Years prior to 2014 were not included in the analysis, as they lacked statewide coverage. The southernmost observation of quillback rockfish in the data was 36° 16′ N. latitude, so all data south of 36° N. latitude (near Lopez Point, CA) were excluded (>1000 transects with no quillback observations). The data were further filtered (**Table 1**) to exclude average transect depths shallower than 10m, deeper than 120m, and transects that occurred over soft (non-rocky reef) habitat (see below for description of habitat data).

The ROV transects in the final data set (n=988) were conducted at 35 unique 'locations,' with 1-6 'sites' sampled per location, and several depths sampled per site. Sampling was done during 2 time periods ("super years"), and occurred either within an MPA or in a 'reference' area outside of MPAs. Super year 2015 combined data from 2014-2016, as survey sampling did not cover all locations in any single year. Similarly, super year 2020 combined data collected from 2019-2021. Not all locations had samples during both time periods and both inside and outside MPAs. Sampling coverage is summarized in **Figure 1**. The data are counts of quillback rockfish and area surveyed ('useable area' in the database) for each transect.

To obtain the total area of rocky habitat within MPAs at different depths, we used the high-resolution raster bathymetry (2 m) from the California Seafloor Mapping project (http://seafloor.otterlabs.org/csmp/csmp.html). These reef polygons are consistent with those used in other nearshore stock assessments (Dick et al 2016, Monk and He 2019). In ArcGIS Pro (ESRI 2024) we used the Contour Spatial analyst tool to build 10 m depth polygons for the rocky reef habitat within each MPA. For each of the 10 m depth polygons (n=272), the zonal stats tool was used to calculate reef area and average depth. This information (area of rocky habitat and average depth within 10m depth bins within each MPA) was used for model extrapolation.

MPAs were associated with one of the 35 location groups ("locations") within the ROV dataset. Only 25 of the 35 locations were used for extrapolation of abundance to no-take MPAs, as the remaining 10 were either associated with MPAs lacking rocky habitat or that allowed retention of groundfish. The total area of rocky habitat in each location is presented in **Figure 2** and **Table 2.** Due to sparse sampling of locations over time, locations were further grouped into 5 regions (clusters): North of Mendocino (North), Point Arena to Mendocino (North Central), SF Bay to Point Arena (Central), the Farallon Islands (Farallons), and south of SF Bay (South). See **Figure 3** for a map of the locations and their regions. Big Creek was the most southern location used. In the models, variable 'Cluster1' groups the North and North Central regions together, whereas variable 'Cluster2' keeps them separated.

One influential outlier was removed: a Mattole Canyon transect with an average depth of 117 m. This was deepest of all sampled transects, and deeper than any of the extrapolation areas. A relatively large number of quillback rockfish were observed there, in contrast with trends in the rest of the data, and it had a strong influence on the depth effect at deeper depths.

Models and rationale

The primary goal of the model is to extrapolate rockfish density to all rocky habitat within MPAs prohibiting groundfish catch, multiplying density by habitat area and summing across areas to get an estimate of total abundance within MPAs for each of the two time periods. The main axes of variation are spatial location, time period (super year 2015 or 2020), protection status (MPA, reference), and depth. Other covariates were measured in the ROV surveys (mostly related to bottom characteristics), but since these variables are not available in the extrapolation dataset, it is not possible to use these in the model.

The sampling 'sites' encompass only a small fraction of the total MPA area (**Figure 2**), and the area over which it is necessary to extrapolate cannot be easily assigned to a site (but it can be assigned to a location or cluster, and it can be assigned a depth within a location). Therefore, although incorporation of site as a random effect in the model may explain more variation in the observed data, extrapolation to areas outside of a known site would have the random effect set to 0. Thus, it made more sense to leave variation due to site in the overall error term. Depth, on the other hand, can potentially explain variation in density within and across sites, and is easily extended to the extrapolation area. Since the relationship between density and depth is expected to be smooth and roughly unimodal, but not necessarily symmetric, we chose to model depth effects with a Generalized Additive Model (GAM) smoother. Although predictions were only made for MPAs, we included all transects in the model, including those from the reference areas, to help to resolve depth effects. In doing so, we assumed depth effects to be the same across super years and protection statuses, but they were allowed to vary geographically.

To account for spatial effects, it made the most sense to use fixed spatial categories rather than continuous latitude effects or spatial random fields, since each MPA encompasses a relatively small area, and we are not attempting to interpolate large areas between them. While it is possible to estimate fixed effects for each location, each location does not have all years, protection statuses, and depths represented, and therefore interactions between location and each of these other terms cannot be evaluated. Some locations also have low sample sizes, and 13 of the 35 locations have had no quillback ever observed (noted by a red "X" in **Figure 1**).

Given these constraints, we attempted two modeling approaches:

1. Include location effects, with a shared depth effect and time period*protection status interaction: Quillback_Rockfish~SuperYear*Protection+Location+s(Avg_Depth). This assumes that all locations with no quillback observed have zero fish, and that there is no spatial variation in the smoothed depth effect.
2. Pool data from several locations into clusters. This allowed all combinations of predictors to be present in each cluster. For the model, include a time period*protection status*cluster interaction, and a separate depth effect for each cluster: Quillback_Rockfish~SuperYear*Protection*Cluster+s(Avg_Depth, by = Cluster)

Survey area (usable fish area, converted to hectares) was used as an offset in all models. Tweedie and negative binomial error distributions with log link functions were tried. Based on QQ residual plots, the negative binomial was found to better represent the data, and was subsequently used.

For model selection, we evaluated the two models above as well as reduced versions of each model, and compared fits using AIC (and dAIC, defined as the AIC for each model minus the minimum AIC across all models). We did not evaluate every possible reduced model, but used an approach akin backward selection, in that we dropped terms and examined the effect on AIC, while also considering what would be biologically reasonable. For the second model in the list above, we tried both Cluster1 and Cluster2 as variables. We also tried adding location as an additional effect in this model. As a diagnostic check, predictions were made for all time periods, protection statuses, clusters, and the entire depth range, and plotted against the observed data.

Table 3 describes a representative collection of the best models and several models useful for comparison (more models were evaluated than are shown in the table, none of which had higher performance). We found that models using Cluster2 (and interactions with Cluster2) performed the best and were all within < 2 dAIC of each other. The model using both location and Cluster2 had higher AIC values. Of the best performing models, those that used a depth effect based on Cluster 2 had the lowest AIC; however, the depth effect in the North region was such that it did not extrapolate realistically (it continued to increase with depth, rather than declining). Therefore, we chose the most parsimonious model where the depth effect was based on Cluster1, which more realistically extrapolated. This final model had 2-way interactions between SuperYear:Protection and SuperYear:Cluster2, but not between Protection:Cluster2, and the depth effect was based on Cluster1. For a sensitivity test, we also report the results for two other models (one the same as the final model but with the full 3-way interaction between SuperYear, Protection, and Cluster2; the other the first model in the list above that uses additive location effects).

Diagnostic residual plots for the selected final model are presented in **Figure 4**. Observed and predicted values are presented in **Figure 5**. Marginal means are presented in **Figure 6**, which shows just the interaction between super year, protection, and cluster. In all clusters, there was little difference in quillback density between MPA and reference areas in super year 2015. Between super year 2015 and 2020, quillback density increased in the North, North Central, and Central clusters, more so in MPAs than in reference areas. In the Farallons, density increased inside MPAs, and decreased outside MPAs. In the South cluster, quillback density is very low in all areas. Within clusters, depth effects were unimodal. Peak densities occurred at the shallowest depths in Farallons, followed by the Central cluster, and then the North/North Central cluster. In the South cluster, peak densities occurred at relatively deep depths, but overall densities were quite low.

Predictions of density (fish/hectare) were made for the extrapolation dataset for each time period. Density was multiplied by the number of hectares, and then summed across all areas for each of the two time periods. Uncertainty was estimated using the delta method.

Models were initially fit with the gam function in the R package mgvc, which was used for model selection. The final model was refit (identically) with sdmTMB (all spatial effects turned off, family nbiom2) to take advantage of the index generating function within this package, which weights and sums up the extrapolated predictions and produces an appropriate estimate of uncertainty. To fit the 'location' model in sdmTMB, locations with no quillback rockfish observed had to be omitted.

Estimates of the total number of quillback rockfish in MPAs in both time periods are presented in **Table 4** and **Figure 7**. These numbers broken down by location are presented in **Figure 8**. The ROV data suggest that, for quillback abundance in the no-take MPAs, a large percentage was in the Farallons (52% in super year 2015, 31% in super year 2020), which has both a relatively large area of rocky habitat, and relatively high quillback densities.

As a back-of-the-envelope check, we also calculated a naïve abundance estimate using the arithmetic mean quillback density by location, protection status, and time period. Ignoring depth effects, we multiplied the extrapolation total area by the mean density (for the corresponding location, time period and protection status) and summed across areas. MPA locations with no sampling in a given year were treated as zeros rather than extrapolated. This produced an estimate that was not far off from the model estimates (**Table 4**). This suggests that while depth effects explain a lot of the within-site variation, the ROV sampling was representative 'enough' that averaging across depths produces approximately the same total. For the 4 locations that were sampled in 4 years (2 years during both time periods), we also present the raw average quillback density in each year (**Figure 9**) to illustrate interannual variability within super years.

References

Dick, E. J., Monk, M., Taylor, I., Haltuch, M., Tsou, T. S., & Mirick, P. (2016). Status of China rockfish off the US Pacific Coast in 2015. Pacific Fishery Management Council, 2016, 1-515.

ESRI. 2024. ArcGIS Pro 3.3.0 Environmental Systems Research Institute. Redlands, Calif

Monk, M. H. and X. He. 2019. The Combined Status of Gopher *Sebastes carnatus* and Black-and-Yellow Rockfishes *Sebastes chrysomelas* in U.S. Waters Off California in 2019. Pacific Fishery Management Council, Portland, OR.

Table 1. Description of data filtering steps and resulting sample sizes (number of ROV transects and total count of quillback rockfish) used to model quillback density inside no-take MPAs.

Description	Transects	Quillback
Merged and extracted data (years >2013 and north of Lopez Point)	1031	1541
Remove transects shallower than 10m and deeper than 120m	1020	1540
Remove transects that occurred over soft habitat based on location relative to GIS habitat classifications	988	1539

Table 2. Estimated rocky habitat area (hectares) by location group and MPA name, used for extrapolating density to absolute abundance inside no-take MPAs north of Lopez Point. Final extrapolation further divided each area into 10m depth bins to account for depth effects on density.

Location Group	MPA Name	Habitat Area
Albion	Point Cabrillo State Marine Reserve	55.2
Año Nuevo	Año Nuevo State Marine Conservation Area	1098.1
Año Nuevo	Greyhound Rock State Marine Conservation Area	378.5
Asilomar	Asilomar State Marine Reserve	179.1
Asilomar	Lovers Point State Marine Reserve	19.9
Big Creek	Big Creek State Marine Conservation Area	3.6
Big Creek	Big Creek State Marine Reserve	128.7
Big Flat	Big Flat State Marine Conservation Area	91.9
Bodega Bay	Bodega Head State Marine Conservation Area	1438.1
Bodega Bay	Bodega Head State Marine Reserve	790.7
Carmel Bay	Carmel Pinnacles State Marine Reserve	123.0
Duxbury Point	Point Reyes State Marine Conservation Area	17.0
Duxbury Point	Point Reyes State Marine Reserve	162.6
MacKerricher	MacKerricher State Marine Conservation Area	223.0
Mattole Canyon	Mattole Canyon State Marine Reserve	249.7
Montara	Montara State Marine Reserve	793.8
N Farallon Islands	North Farallon Islands State Marine Reserve	230.5
Pillar Point	Pillar Point State Marine Conservation Area	302.1
Point Arena	Point Arena State Marine Conservation Area	58.1
Point Arena	Point Arena State Marine Reserve	487.6
Point Lobos	Point Lobos State Marine Conservation Area	130.7
Point Lobos	Point Lobos State Marine Reserve	589.7
Point St. George	Point St. George Reef Offshore State Marine Conservation Area	126.6
Point St. George	Pyramid Point State Marine Conservation Area	294.8
Point Sur	Point Sur State Marine Conservation Area	324.0
Point Sur	Point Sur State Marine Reserve	1103.2
Portuguese Ledge	Portuguese Ledge State Marine Conservation Area	20.5
Portuguese Ledge	Soquel Canyon State Marine Conservation Area	116.5
Reading Rock	Reading Rock State Marine Conservation Area	37.5
Reading Rock	Reading Rock State Marine Reserve	125.3
Saunders Reef	Saunders Reef State Marine Conservation Area	757.6
SE Farallon Islands	Southeast Farallon Island State Marine Conservation Area	794.3
SE Farallon Islands	Southeast Farallon Island State Marine Reserve	915.6
Sea Lion Gulch	Sea Lion Gulch State Marine Reserve	1049.5
South Cape Mendocino	South Cape Mendocino State Marine Reserve	1360.2
Stewarts Point	Del Mar Landing State Marine Reserve	27.5
Stewarts Point	Stewarts Point State Marine Conservation Area	113.8
Stewarts Point	Stewarts Point State Marine Reserve	397.2
Ten Mile	Double Cone Rock State Marine Conservation Area	335.1
Ten Mile	Ten Mile State Marine Reserve	328.6
Grand Total		15779.4

Table 3. AIC results for a representative collection of the best models for quillback rockfish density from the ROV survey, and several additional models for comparison. The model in bold (‘test_nb6.3’) is the final selected model. Those in italics are also presented for sensitivity purposes. Model name is the name in the code. The top 2 models were not used because they did not extrapolate realistically and their dAIC was relatively small.

Model	Description	Predictors	AIC	df	dAIC
test_nb6.1	all interactions; use cluster2; depth by cluster2	SuperYear * Protection * Cluster2 + s(Avg_Depth, by = Cluster2)	2432.88	40.20	0.00
test_nb6.5	drop 3-way interaction, protection:cluster; use cluster2; depth by cluster2	SuperYear + Protection + Cluster2 + SuperYear:Protection + SuperYear:Cluster2 + s(Avg_Depth, by = Cluster2)	2432.99	32.41	0.12
test_nb6.3	drop 3-way interaction, protection:cluster; use cluster2; depth by cluster1	**SuperYear + Protection + Cluster2 + SuperYear:Protection + SuperYear:Cluster2 + s(Avg_Depth, by = Cluster1)**	**2433.02**	**31.29**	**0.14**
test_nb6.4	drop 3-way interaction, use cluster2; depth by cluster1	SuperYear + Protection + Cluster2 + SuperYear:Protection + SuperYear:Cluster2 + Protection:Cluster2 + s(Avg_Depth, by = Cluster1)	2434.06	35.43	1.18
test_nb6	all interactions; use cluster2; depth by cluster1	*SuperYear * Protection * Cluster2 + s(Avg_Depth, by = Cluster1)*	*2434.29*	*39.27*	*1.41*
test_nb4	drop interactions with cluster; use cluster2; depth by cluster1	SuperYear * Protection + Cluster2 + s(Avg_Depth, by = Cluster1)	2445.84	27.43	12.97
test_nb7	all interactions; use cluster2; use location; depth by cluster1	SuperYear * Protection * Cluster2 + Location + s(Avg_Depth, by = Cluster1)	2454.00	63.65	21.12
test_nb5	all interactions; use cluster1; depth by cluster1	SuperYear * Protection * Cluster1 + s(Avg_Depth, by = Cluster1)	2454.18	35.02	21.30
test_nb8	all interactions; use cluster2; shared depth effect	SuperYear * Cluster2 * Protection + s(Avg_Depth)	2548.70	27.24	115.82
test_nb2	drop interactions with cluster; use location; shared depth effect	*SuperYear * Protection + Location + s(Avg_Depth)*	*2551.21*	*44.33*	*118.33*
test_nb3	drop interactions with cluster; use cluster2; shared depth effect	SuperYear * Protection + Cluster2 + s(Avg_Depth)	2555.30	14.61	122.42

Table 4. Extrapolated total number of quillback rockfish inside no-take MPAs north of Lopez Point. The naïve model is based on the raw average quillback density by location, protection status, and time period, ignoring depth effects, and treating MPA locations with no sampling in a given year as zeros.

Super Year	Total fish	Lower 95% CI	Upper 95% CI	Log Total fish	Log standard error	Model
2015	151934	118204	195289	11.931	0.128	Final model
2015	139712	106533	183225	11.847	0.138	Alternate model (cluster)
2015	134196	108643	165758	11.807	0.108	Alternate model (location)
2015	136795					Naïve model
2020	317274	273983	367405	12.668	0.075	Final model
2020	321549	276565	373850	12.681	0.077	Alternate model (cluster)
2020	290200	244104	345000	12.578	0.088	Alternate model (location)
2020	287432					Naïve model

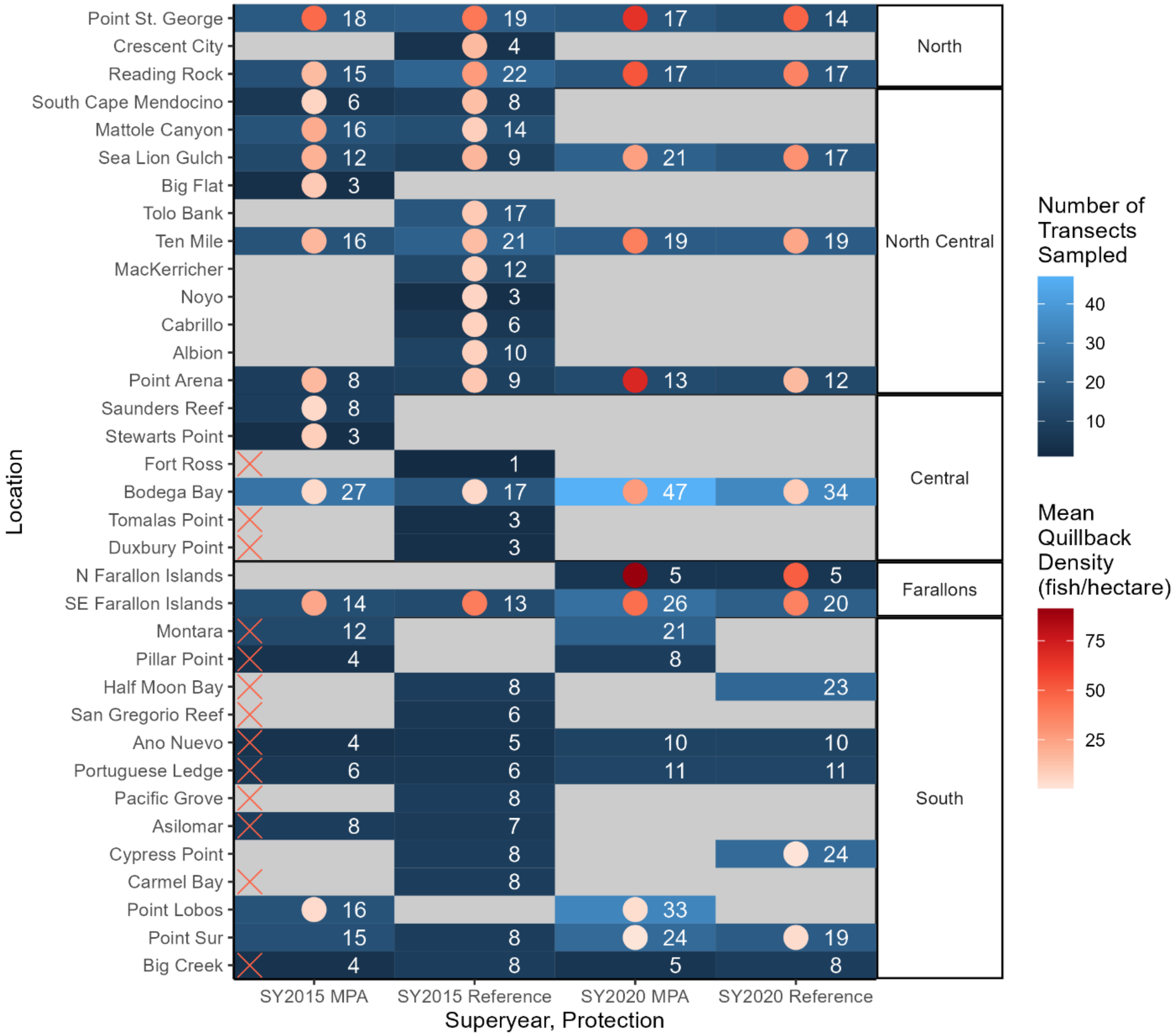

Fig. 1. Sampling coverage of the ROV survey data. Locations are arranged north to south, with labels on the right indicating the region (Cluster2) that they fall into. The blue color ramp and white numbers are the number of transects sampled in each super year/protection category, and red circles/color ramp are the average densities of quillback. Red x's are next to sites with no quillback observed.

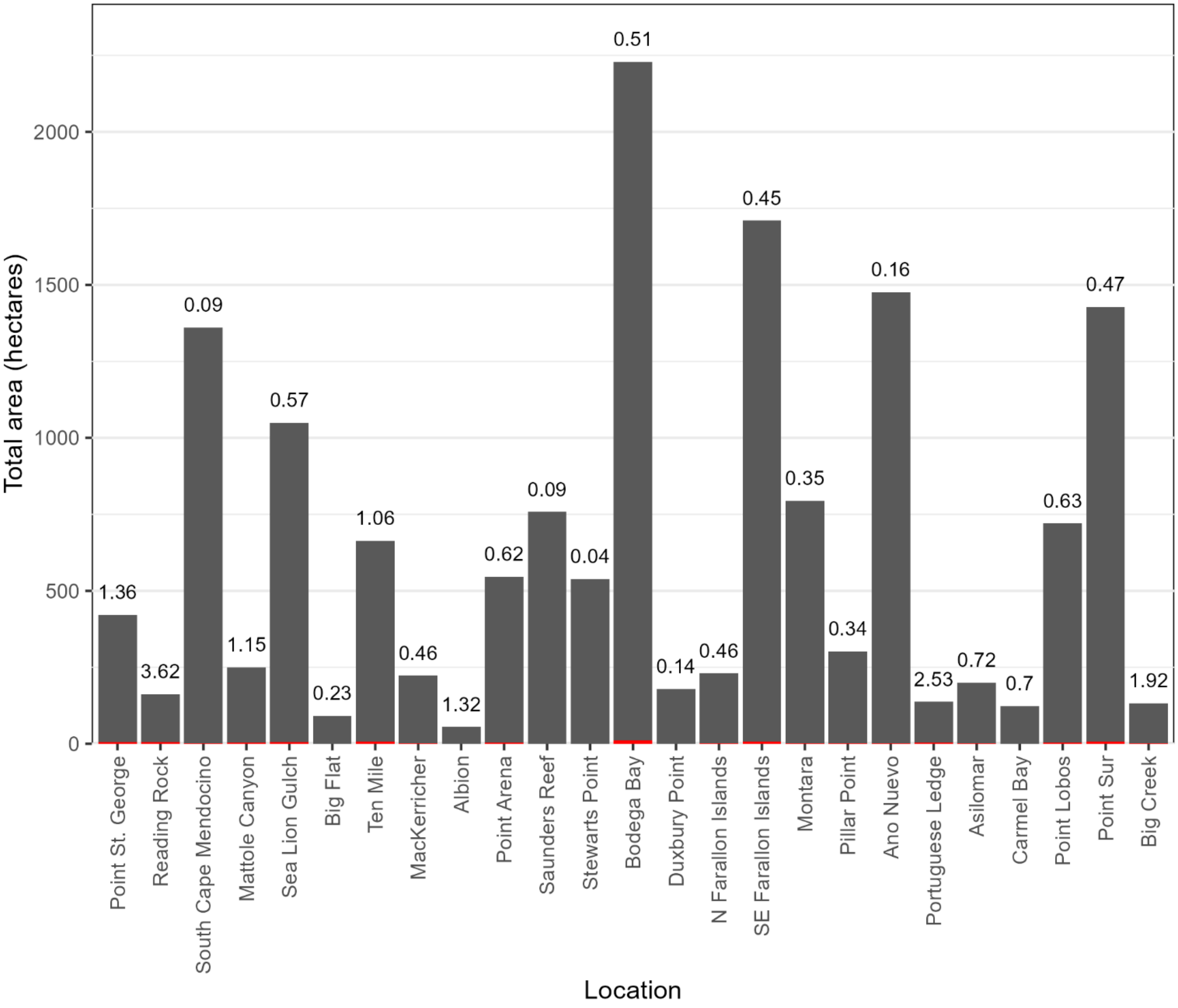

Fig. 2. Total area of rocky habitat within location groups (see Table 2 for MPA names). Locations are arranged north to south. Red area is the area sampled by the ROV survey at each location (both MPA and reference sites), summed for both time periods. In some cases, this area is too small to be visible in the plot. Number above each bar is the area sampled by the ROV as a percentage of the total area. The take home messages are that (1) the area of rocky habitat varies among locations, and (2) the extrapolation to all rocky habitat is based on a very small percentage of area that was sampled.

Fig. 3. Map of ROV sampling locations and their regional groupings.

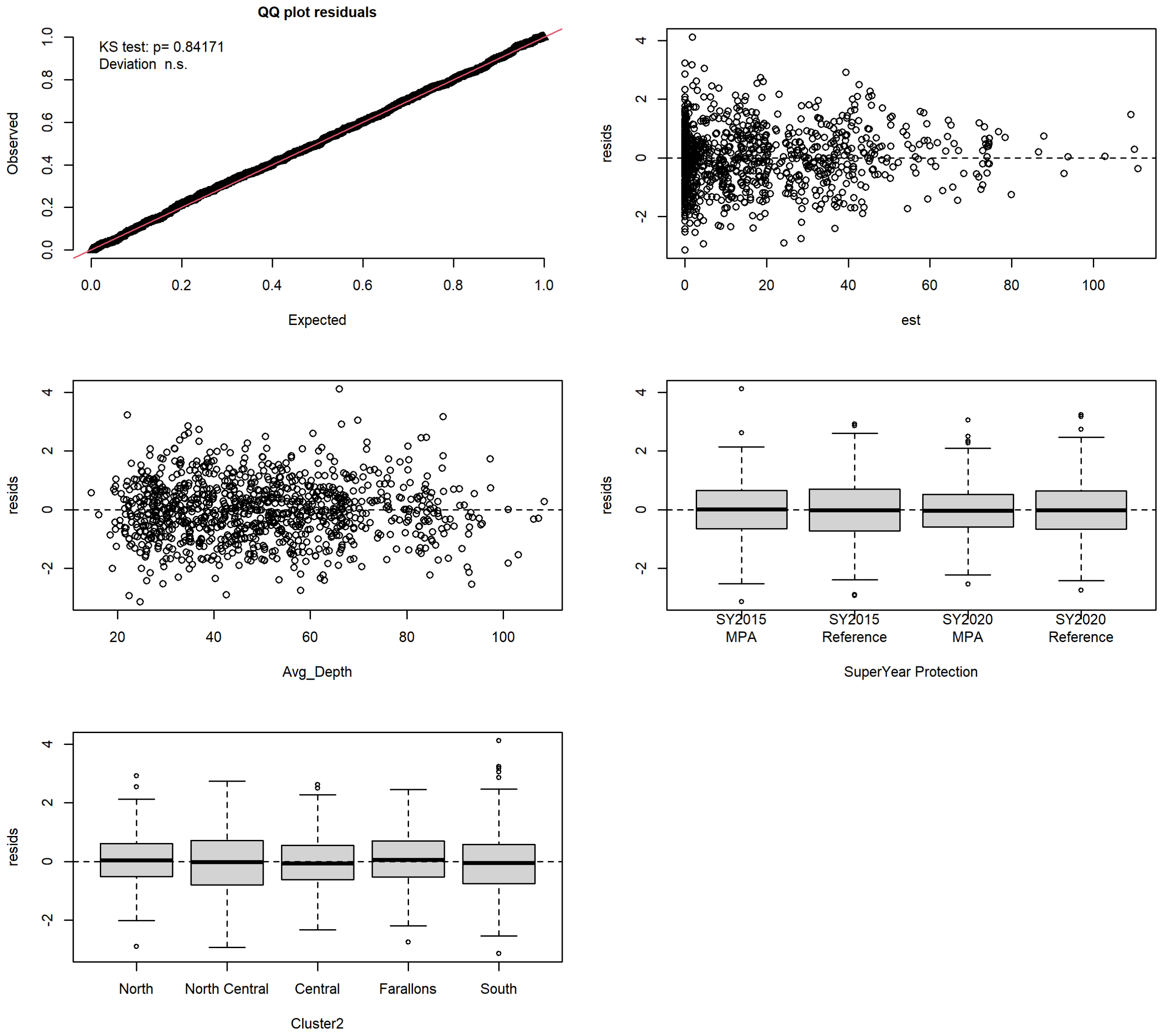

Fig. 4. Diagnostic residual plots for the final model for quillback rockfish density. Top left: Q-Q plot for Dharma residuals based on 500 simulations. Simulations also produce 55% zeros (observed: 56% zeros). Remaining plots: Residuals plotted against estimated values, depth, super year/protection, and cluster2.

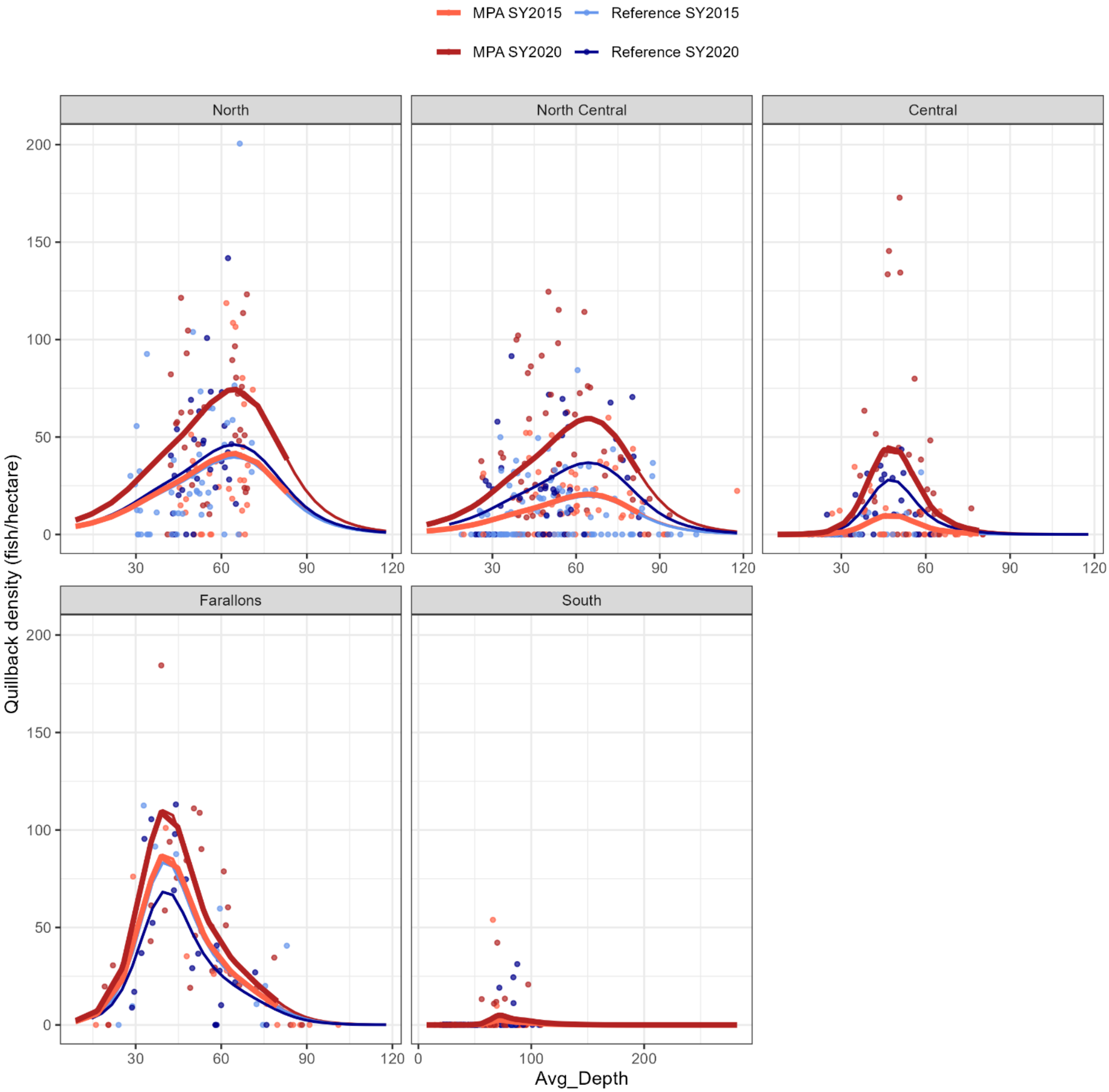

Fig. 5. Observed and predicted values of quillback density by depth, protection status, and time period, and cluster. Points are observed values. Lines are model predictions. Thicker lines are predictions for the range of depths in the extrapolation dataset. Note that the North and North Central regions share a depth effect. If a separate depth effect is used for the North, the extrapolated number fish continues to increase as depth increases (due to absence of data at deeper depths), which is unrealistic, so it is pooled with the North Central region for the purpose of estimating a depth effect. The omitted outlier is deepest point in the North Central region.

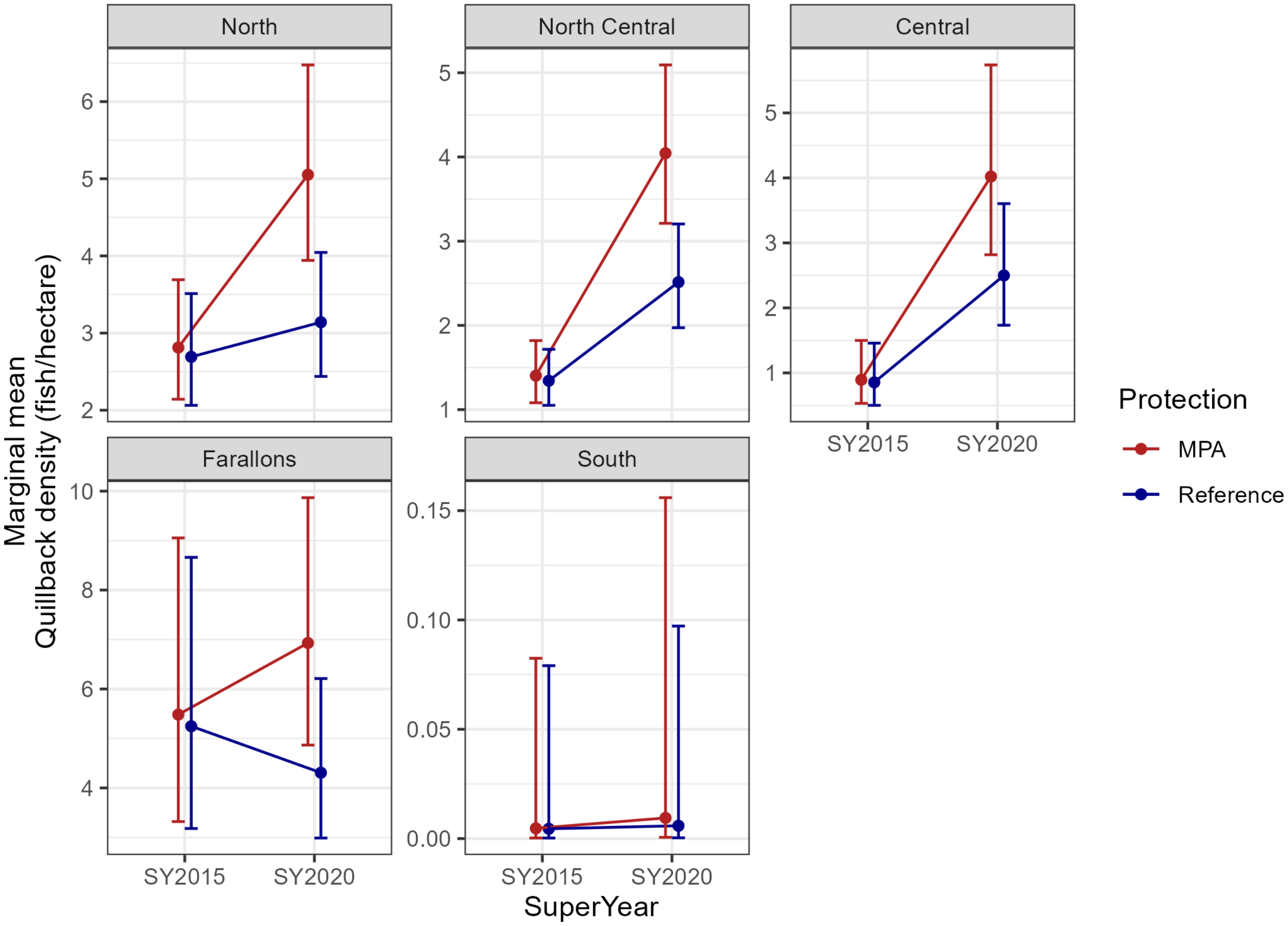

Fig. 6. Marginal means showing the interaction between cluster, time period, and protection status. The final model has an interaction between year:protection and year:cluster, but not between protection:cluster. Error bars are 95% CIs. Estimates were generated from the mgcv version of the model using the ggeffects package.

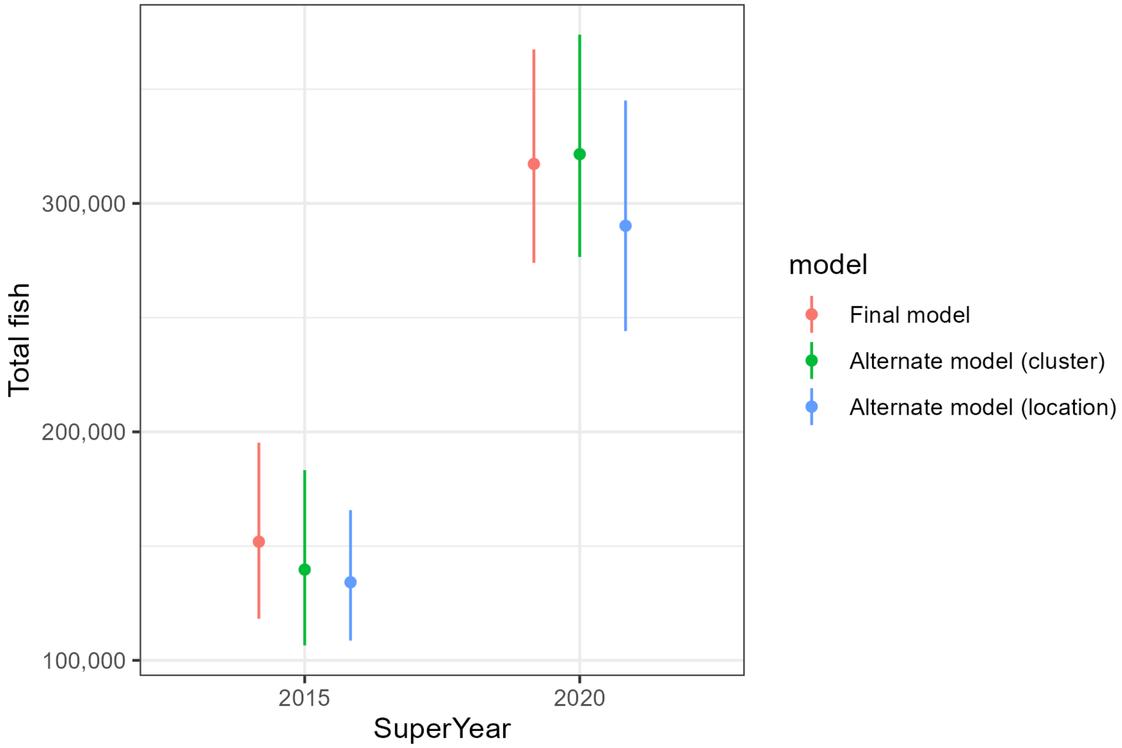

Fig. 7. Extrapolated total number of quillback rockfish in no-take MPAs by time period. Bars are 95% CIs.

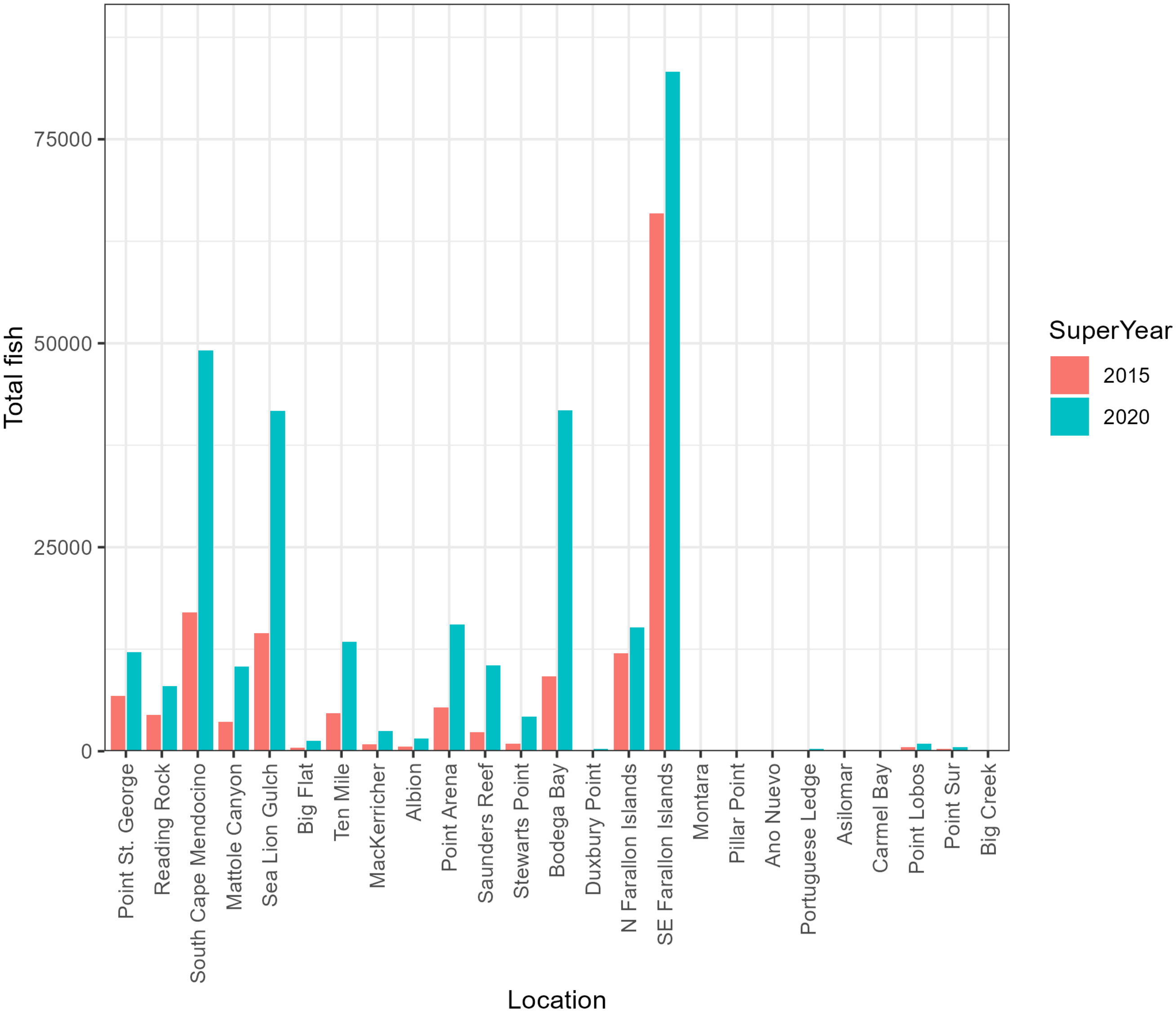

Fig. 8. Extrapolated total number of quillback rockfish in MPAs by location and time period. Locations are arranged north to south.

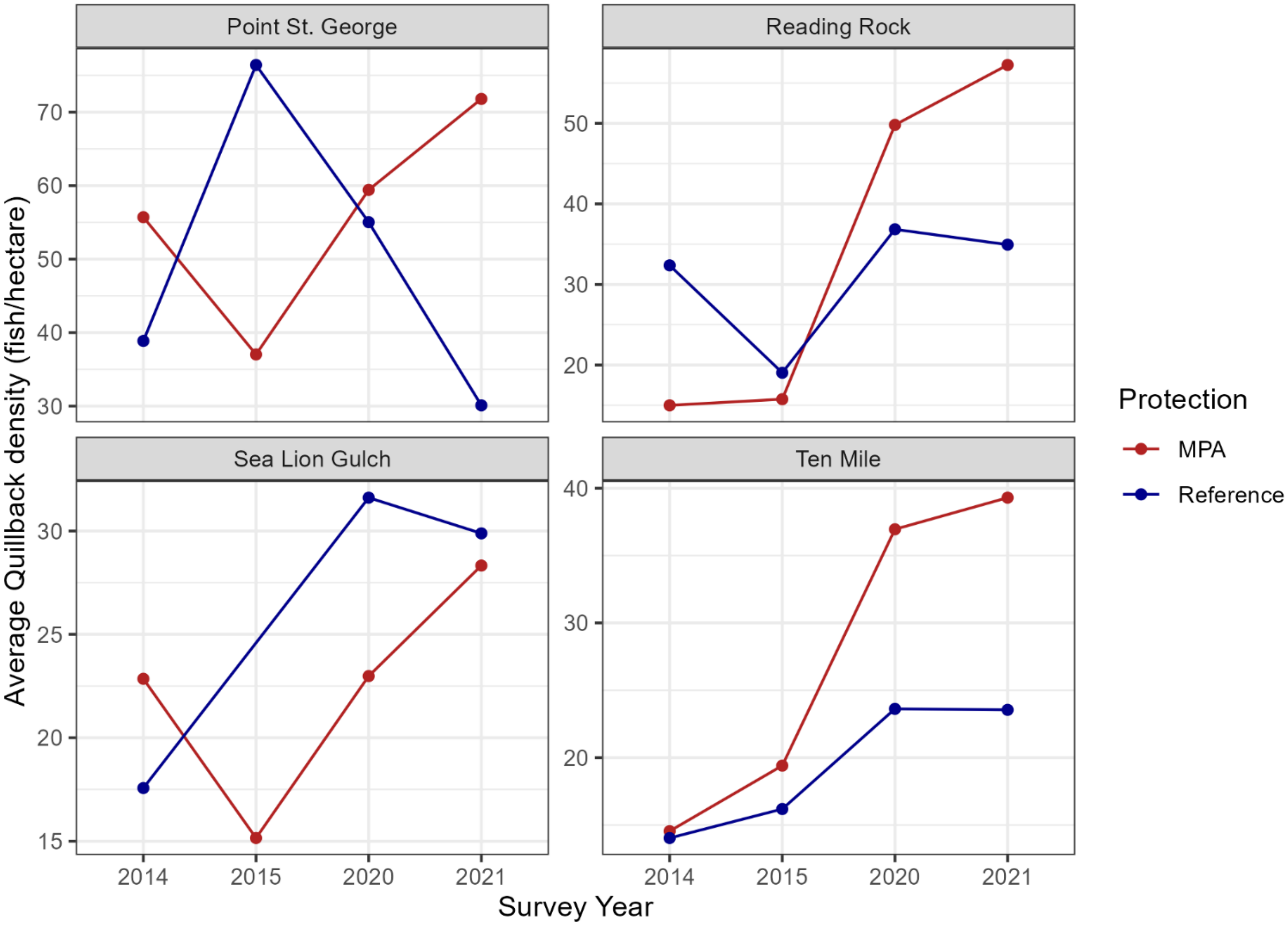

Fig. 9. Raw average quillback density by year for the 4 locations with 4 years of sampling (2 years during both super years).