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Tini a Tangaroa

The 2020 stock assessment of red rock lobsters (*Jasus edwardsii*) in CRA 5

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EXECUTIVE SUMMARY

Webber, D.N.¹; Starr, P.J.²; Roberts, J.³; Rudd, M.B.⁴; Pons, M.⁵ (2021). The 2020 stock assessment of red rock lobsters (*Jasus edwardsii*) in CRA 5.

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This document describes the 2020 stock assessment of red rock lobsters (*Jasus edwardsii*) in CRA 5 (Canterbury/Marlborough). The stock assessment used the lobster stock dynamics (LSD) model. Data inputs and all technical decisions were discussed and agreed upon by the Rock Lobster Working Group, which oversaw this work.

The base case model was fitted to length frequency (LF) data, sex ratio data, tag-recapture data, and standardised catch-per-unit-effort (CPUE) indices. This base case model differed from previous CRA 5 stock assessments by splitting the catch, CPUE, and length frequency data into two regions based on observed differences in CPUE trends, LF patterns, and sex ratios between regions. This document describes the procedure used to find an acceptable base case model and shows the model fits. Three MCMC sensitivity trials were done to test assumptions in the base case model. These included: fitting to the puerulus settlement index with a forced lag of three years to recruitment to the model, dropping the vessel explanatory variable in the CPUE index series, and trailing an alternative regional catch split. The puerulus index was not included in the base case model, because it did not match model estimates of peak recruitment based on the sampling data from the fishery. A sensitivity using an alternative pre-1963 catch history differed the most from the base case model, indicating that the uncertainty in the historical catches is likely to be a major source of uncertainty in this stock assessment.

Model inference for this assessment was based on maximum *a posteriori* (MAP) fits and Markov chain Monte Carlo (MCMC) simulations. This document describes the diagnostics for each and presents the results of MAP and MCMC sensitivity trials.

This stock assessment describes a stock that was initially heavily fished and declined to its lowest levels during the 1990s. From this low level, the stock rapidly increased in size up until about 2010. Since then the stock has declined a little, but is well above the soft and the hard limits, and is projected to remain above these limits for the next five years at the specified catch levels.

A stock-specific vulnerable biomass reference level, based on simulated projections across constant catches and harvest rates and constrained by a probability of no more than 5% of falling below the soft limit, has been developed and accepted for CRA 5. The current median CRA 5 vulnerable biomass was estimated to be well above this reference level and was projected to decrease over the next five years under present catches and recent (10 year) average recruitment, but still remain at about twice the reference level on average.

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1. INTRODUCTION

This work addresses Objective 4 of the Fisheries New Zealand contract CRA2019-01. This one-year contract, which began in April 2020, was awarded to the New Zealand Rock Lobster Industry Council Ltd (NZ RLIC Ltd), who sub-contracted Objective 4 to the rock lobster stock assessment team.

Objective 4 - Stock assessment: To estimate biomass and sustainable yields for rock lobster stocks.

The National Rock Lobster Management Group (NRLMG) decided that CRA 4 and CRA 5 should be assessed in 2020. Data were compiled for both stocks by a team comprising Paul Starr (Starrfish), D'Arcy Webber (Quantifish Ltd), Merrill Rudd (Scaleability), Jim Roberts (independent consultant), and Maite Pons (independent consultant). All team members contributed to the assessments of CRA 4 and CRA 5 concurrently. This stock assessment was completed in a workshop during September and October 2020, based in Wellington but also held remotely due to the COVID-19 pandemic. Decisions on data and modelling choices were discussed and approved by the Rock Lobster Working Group (RLWG). The stock assessment was presented to and approved by the Fisheries New Zealand mid-year Plenary during November 2020 (Fisheries New Zealand 2020).

The CRA 5 Quota Management Area (QMA) includes all of Tasman Bay and Golden Bay as well as the Marlborough Sounds, then extends down the northern part of the east coast of the South Island, past Kaikōura and Banks Peninsula as far down as the Waitaki River (Figure 1).

Potting and hand-gathering are the preferred methods for recreational fishers in CRA 5. Most of the recreational catch is taken during the summer months, which is consistent with all New Zealand rock lobster recreational fisheries. The region also sustains a dive charter industry catering to recreational fishing during summer. The customary allowance allows lobsters to be taken under permit.

The CRA 5 Total Allowable Commercial Catch (TACC) was last changed in April 1999 and is currently 350 tonnes. Allowances set by the Minister of Fisheries in 1999 were 40 tonnes for customary catch, 40 tonnes for recreational catch, and 37 tonnes for illegal unreported removals, for a total TAC of 467 tonnes. After the 2015 stock assessment, the Minister raised the recreational allowance to 87 tonnes for the 2016–17 fishing year but left the TACC and the other allowances unchanged, increasing the Total Allowable Catch (TAC) from 467 tonnes to 514 tonnes. Each component of the fishery is meant to stay within its allowance. The TACC is set through the provisions of the Quota Management System (QMS) and the management of the recreational fishery is accomplished by setting a daily bag limit of a maximum of six rock lobster per day. In 2020, the Minister for Oceans and Fisheries introduced additional measures to manage recreational fishing of rock lobsters in CRA 5, including telson clipping, an accumulation limit of three daily bag limits (i.e., eighteen lobsters), and “bag and tag” conditions requiring a single day’s catch to be stored in a clearly labelled bag or container. Other management tools include a minimum legal size (MLS) of 54 mm tail width (TW) for males and 60 mm TW for females for both the commercial and recreational fisheries, and a general prohibition of the take of berried females and soft-shelled individuals.

In 2008, CRA 5 industry members adopted a voluntary procedure to shelve Annual Catch Entitlement (ACE) when CPUE fell below a threshold (Breen 2009). This was never triggered and a formal evaluated management procedure (MP) was adopted in 2010 (Haist et al. 2011). The updated 2015 CRA 5 stock assessment (Starr & Webber 2016) included management procedure evaluation (MPE) which led to a revised MP that operated up to 2019. Unlike other CRA QMAs, the operation of the CRA 5 MPs never resulted in a TACC change in any year from 2008 to 2019 (Fisheries New Zealand 2020).

The 2019–20 fishing year marked the transition of the collection of rock lobster catch and effort data from a paper-based Catch Effort Landing Return (CELR) system to an electronic reporting (ER) system dependent on a user interface operated from tablets or smart phones. In August 2020, a preliminary analysis of 2019–20 data revealed that data collected electronically are not comparable to

data collected on paper forms (see Starr 2021 appendix B for details). Consequently, the RLWG agreed to temporarily suspend updating CPUE indices beginning with the 2019–20 spring/summer season. MPs were also temporarily discontinued.

The previous stock assessment of CRA 5 was done in 2015 (Starr & Webber 2016). This document presents a new stock assessment for CRA 5 which includes updates to the catch-per-unit-effort (CPUE) standardisation procedure as well as length frequency and tagging data up to the end of the 2019–20 fishing year. All tables referred to in this document can be found in Section 6 and all figures are in Section 7. The data used in this stock assessment are documented by Starr et al. (2021).

2. STOCK ASSESSMENT

The previous stock assessment of CRA 5 in 2015 (Starr & Webber 2016) used the multi-stock length-based model (MSLM, Haist et al. 2009). The 2020 stock assessment used the lobster stock dynamics (LSD) model (Webber et al. 2018a). The LSD model is coded in Stan (Stan Development Team 2016, 2017) and has been used as the main assessment software for CRA 2 (2017), CRA 6 (2018), CRA 1 (2019), CRA 3 (2019), and CRA 4 (2020).

Unlike previous CRA 5 stock assessments, this assessment did not assume a single homogeneous stock across the six rock lobster statistical areas (916, 917, 918, 919, 932, and 933). Instead, two separate regions were defined: region 1 consisting of statistical areas 917, 918, and 919, and region 2 comprised statistical areas 916, 932, and 933. These two regions were separated because they showed differing CPUE abundance trends and catch histories. There were also differences between the two regions in the length frequency sampling data. Data analyses supporting this separation and the estimation of catch histories are presented by Starr et al. (2021). Growth was assumed to be the same in both regions, given a lack of contrast in the growth information from the available regional tag recovery data.

Maximum *a posteriori* (MAP) estimation and Markov chain Monte Carlo (MCMC) simulation were used to make inference about the CRA 5 stock. Initially, a MAP base case model was developed and then a series of MAP sensitivity trials were explored. Four models, including the base case and three sensitivity trials, were extended to a full Bayesian implementation using MCMC.

The suspension of CPUE indices from the 2019–20 spring/summer season as a result of the shift from paper to electronic monitoring prevented the development of a new MP based on the outcome of this stock assessment. Instead, projections explored vulnerable biomass in relation to proposed reference levels based on methods described by Rudd et al. (in press a). The reference levels presented in this document were reviewed and accepted by the RLWG at a meeting in February 2021.

2.1 Data

The data used in this stock assessment are documented by Starr et al. (2021) and the temporal extent of these data is illustrated in Figure 2. Following the procedure adopted by the five most recent stock assessments (CRA 2, Webber et al. 2018b; CRA 6, Rudd et al. 2019; CRA 1, Rudd et al. 2021; CRA 3, Webber et al. 2020; and CRA 4, Rudd et al. in press b), a vessel explanatory variable was included in the CPUE standardisation model (see Starr et al. 2021) and CPUE was split into five series:

- The catch rate (CR) series is an annual arithmetic daily catch rate from 1963 to 1973 and only applies to region 1. The catchability coefficient (q) was assumed constant over this period.
- The Fisheries Statistics Unit (FSU) series is a seasonal standardised index from spring-summer (SS) 1979 to autumn-winter (AW) 1989. The standardisation model included year, month, statistical area, and vessel explanatory variables. The FSU CPUE standardisation

included all vessels. There are separate series for region 1 and region 2. Catchability coefficients (q) for each region were assumed to be constant over this period.

- The Catch Effort Landing Return (CELR) series is a seasonal standardised series from SS 1989 to AW 2019 (i.e., with no SS 2019 observation). CPUE for SS 2019 would typically be included, but the RLWG agreed to temporarily suspend updating CPUE indices beginning with SS 2019 because data collected electronically is not comparable with data collected on paper forms (Starr 2021). The standardisation model included year, month, statistical area, and vessel explanatory variables, filtered for vessels that had fished CRA 5 for at least five years. There are separate series for region 1 and region 2. The catchability coefficients (q) for each region were assumed to improve over time at a constant rate. This series was fitted in the assessment model with a fixed q_{drift} parameter which represented an assumed rate of change associated with improved fishing efficiency, shared across the two regions.

This assessment used tag-recapture observations from tags released in CRA 5, including statistical areas 916, 917, 918, and 933, identified either by the statistical area of release or the project ID. As indicated above, no difference in growth was detected between the two CRA 5 regions. Consequently, growth in both regions was based on a single model fitted to all the CRA 5 tag recoveries.

From 1945 to 1949, there was no MLS for red rock lobster in New Zealand. MLS restrictions were initially implemented for New Zealand red rock lobster as measurements of tail length in inches. This measurement standard was subject to some abuse because tails could be stretched, but was accepted because a significant fraction of the catch came from Fiordland where it was permissible to tail lobsters at sea. The MLS was changed to a width measurement (in mm) across the spines of the second abdominal segment (called tail width or TW) in 1988 for all New Zealand red rock lobsters, requiring the conversion of the pre-1988 regulations into equivalent TW measurements for use in the stock assessment model (Breen et al. 1988). The TW values used for the MLS in the model are provided in Table 1.

Although the 2015 CRA 5 stock assessment used the puerulus settlement series in the base case assessment (Starr & Webber 2016), the puerulus series was only used in a sensitivity run for this assessment. This was because the puerulus series did not match model estimates of peak recruitment suggested by the fishery data (even though the growth parameter estimates were credible), leading to the conclusion that the CRA 5 puerulus series was not a consistent representation of the temporal recruitment pattern experienced by this fishery. Furthermore, the randomisation test previously used to test for puerulus significance failed to accept the three-year lag option which was determined from external juvenile growth modelling to be the most likely lag period between settlement and model recruitment. Puerulus data were applied to both region 1 and region 2 in the *lag3* sensitivity run, despite the collectors being located in Kaikōura (statistical area 917 within region 1).

2.2 Model

This stock assessment did not treat CRA 5 as a single homogeneous area. Instead, it split the QMA into two regions: region 1 which comprised statistical areas 917, 918, and 919; and region 2 which comprised 916, 932, and 933. The model assumed no movement of lobsters between regions because there is no evidence of substantial movements in the tag-recapture data.

The first model year was set to 1945, because this was the first year of available commercial fishery catch data and the available data indicate that there were significant removals from CRA 5 in the late 1940s and early 1950s (see figure 8 of Starr et al. 2021). The last model year was 2019–20 (designated by the first year of the pair, i.e., 2019), because this was the last complete fishing year with data. Fishing years extend from 1 April to 31 March and the first fishing year in the model is 1979–80. The years from 1945 to 1978 are January–December calendar years and January–March 1979 catches are added to 1978 to facilitate the transition from calendar year to fishing year. The model delineates two six-month seasons within a model year: AW (April to September) and SS (October to March).

Seasonal data begin with the 1979–80 fishing year but 1945 to 1978 are reported as complete calendar years. The model tracks the numbers of immature females, mature females, and males in 31 2-mm TW bins (i.e., {[30, 32), [32, 34), ..., [90, ∞)}). The specifications for the base case model are provided in Section 2.5.1 below. All model parameters are listed in Table 2 and fixed values for some parameters and model settings are provided in Table 3.

2.3 Parameters and priors

Estimated model parameters include productivity parameters (i.e., average recruitment, natural mortality, and growth), maturation parameters, and fishery parameters (i.e., catchability, selectivity, and vulnerability) (Table 2). Uninformative priors and wide parameter bounds were specified for most model parameters (Table 4).

Wide uniform priors were specified for q for each CPUE series and the recruitment deviates (Table 4). Beta distributions (with both shape parameters set to 1) were used for all priors bounded between 0 and 1, including $Gdiff$ and all vulnerability parameters (Table 4). An informative lognormal prior was specified for natural mortality (M) and an informative normal prior based on an unpublished meta-analysis was specified for the growth parameters $Gshape$ and GCV (Table 4). Uninformative normal prior distributions were specified for all other model parameters (Table 4). These uninformative normal priors are essentially flat across sensible ranges for each of these parameters and, therefore, do not influence the outcome of the stock assessment, although they help the model software (Stan) during the warm-up phase of the MCMC algorithm.

The vulnerability of immature females and mature females during the SS season was assumed to be the same in each region. The four vulnerability parameters (i.e., one for each sex and season) in each region were estimated relative to the vulnerability of males during the AW season (which was fixed to 1) (Table 5).

Handling mortality was assumed to be 10% for all lobsters returned to sea before 1990 and 5% from 1990 to 2019. This step reduction in handling mortality was agreed by the RLWG to coincide with the start of the live export market and the introduction of rock lobsters into the QMS, under the assumption that fishers would be taking more care in the handling of this valuable asset once they became quota owners. Handling mortality was applied to undersized lobsters of each sex taken in either season by the size-limited (SL) fishery as well as to mature females taken in the AW SL fishery. It was assumed that there were no discards in the non-size-limited (NSL) fishery. The value H_{2019} is the model estimate of the amount of handling mortality (in tonnes) in the final fishing year (2019).

2.4 Assessment indicators

No additional indicators were considered beyond those included in the 2019 CRA 1 and CRA 3 stock assessments (Table 6, Webber et al. 2020, Rudd et al. 2021). The main indicators were related to the relative estimates of vulnerable biomass, adjusted vulnerable biomass⁶, spawning stock biomass (SSB), and total biomass, including the probabilities of each of the biomass indicators falling below current levels after projecting the current catch forward for five years. Probabilities were calculated from all samples of the posterior distribution.

Vulnerable biomass was defined as start-of-season AW biomass, which does not include mature females. Vulnerable biomass takes the MLS, selectivity, and sex/seasonal vulnerability into account and is the estimated biomass available to be caught by the fishery at the beginning of the AW season. Adjusted vulnerable biomass was calculated by applying the MLS and selectivity from the final model year to all previous years, including those years where alternative regulations were applicable.

⁶ In past stock assessments, this quantity was called “vulnerable reference biomass” rather than “adjusted vulnerable biomass”. This change was made to distinguish clearly between rock lobster reference points and this biomass definition.

The probability of the *SSB* being below the soft and hard limits was also calculated. *SSB* was defined as the biomass of all mature females at the start of AW. *SSB*₀ was the *SSB* at unfished equilibrium with *R*₀. The soft and hard limits were set to the default values from the Harvest Strategy Standard (Ministry of Fisheries 2011) of 20% *SSB*₀ and 10% *SSB*₀, respectively.

The derived values used as assessment indicators are summarised in Table 6. Probabilities were calculated using samples from the posterior distribution.

2.5 Maximum *a posteriori* inference

Maximum *a posteriori* (MAP) inference was used for exploring alternative modelling choices without committing the computing time required for Bayesian inference. A base case was developed, and sensitivities, described in Section 2.5.2, were used to test the base case assumptions.

2.5.1 MAP base case

2.5.1.1 Matching the previous assessment model

The 2015 CRA 5 stock assessment model used the multi-stock length-based model (MLSM) (Haist et al. 2009) as the software platform. Although the LSD model was extensively tested against MLSM when it was developed and was found to produce the same results, there have been several updates to the LSD code over the past few years, so the first step in the 2020 assessment involved matching the results from the LSD model to the 2015 MLSM base case assessment. The first model included data up to and including the 2014 fishing year (model *1_base2015_noDD*, see Table 7). Following the initial emulation of the previous base case, key model assumption changes and new data sets that had become available for the 2020 assessment were iteratively added until the resulting model held the attributes of a new base case but was still based on data that were current up to the end of 2014. This iterative procedure was first used in the previous CRA 1 and CRA 3 2019 stock assessments and was recommended to be used as the first phase of applying the LSD model to all updated stock assessments (Webber et al. 2020, Rudd et al. 2021).

For CRA 5, this procedure used nine steps, sequentially described in Table 7, where each subsequent model included the cumulative modifications from the previous models. The data were re-weighted for each run, aiming for a standard deviation of the normalised residual (SDNR) of 1.0 for all CPUE series and the sex ratio (Breen et al. 2003, Francis 2011). Note that the tag data are self-weighting and the length frequency (LF) weight is derived using the Francis approach (Francis 2011).

The first model in Table 7 aimed to match the adjusted vulnerable biomass that was estimated by the 2015 assessment and does so reasonably well (Figure 3). This model included the catch, CPUE, LFs, and tag data used in the 2015 stock assessment (up to and including the 2014–15 fishing year). As was done in the 2015 assessment, the FSU and CELR CPUE series were combined into one series and a single catchability coefficient was estimated. The model also assumed no density dependence and the CPUE series did not include a vessel explanatory variable.

The nine sequential steps listed in Table 7 have been superimposed in Figure 4. The adjusted vulnerable biomass was estimated to be lower in recent years in the model that did not fit to the puerulus index (*2_base2015_noP*), and slightly lower again when the FSU and CELR CPUE series were fitted separately by estimating separate catchability coefficients for each series (*3_splitq*). The model run that updated the handling mortality from 0.1 to 0.05 in 1990 resulted in almost no change to the adjusted vulnerable biomass series. However, adding the new Bayesian CELR series (which included the vessel variable but was truncated at 2014) resulted in the largest relative change in biomass compared with the 2015 assessment, and the remaining models resulted in much smaller changes to the biomass trajectory. Including the vessel explanatory variable in the CPUE resulted in a substantial drop in the biomass trajectory. This is consistent with other recent rock lobster stock assessments (e.g., CRA 2, Webber et al. 2018b), where vessels with lower relative catch rates appear

to preferentially leave the fishery, resulting in a biased CPUE series if this progressive loss is not included in the standardisation procedure.

2.5.1.2 Searching for a 2020 base case

Once an adequate match to the previous single stock assessment model was achieved, the final model (*9_newLF*) needed to be updated to include all data (catch, CPUE, LF, and tagging) to the end of the 2019 fishing year. The team then began exploratory model runs to develop a new base case stock assessment model, with the most important change being the move to a two-region model. The two-region model was selected as the better model because this produced improved fits to the CPUE series compared with the single region model. There were also large differences in the regional catch histories as well as differences in the regional LF data and sex ratios (see appendix C of Starr et al. 2021).

The selection of a CRA 5 base case run involved many steps and several dead-ends. The following is abbreviated sequence of steps that led to a new CRA 5 base case.

1. Adding in all data up to the end of 2019–20 fishing year.
2. Creating a two-region model, with separate catch histories and CPUE series: six selectivities (four in region 1 to accommodate two epochs and two sexes, and only two in region 2 for the two sexes because no data were available before 1993 in region 2), eight vulnerabilities (four for each region), a single two-sex growth model, and a shared estimated M .
3. This model failed to estimate a credible $qdrift$ parameter. Consequently, the RLWG opted to fix $qdrift$ at 1% per year. This decision was carried forward for all sensitivity runs and subsequent MCMC simulations.
4. Abandoned estimation of separate selectivities for epoch 1 and epoch 2 in both regions. There were insufficient early data to estimate the shift associated with the change in escape gaps.
5. At this stage in the modelling, the estimate for the size at maximum selectivity for mature females was 90 mm, which is also the plus group and the upper bound set for this parameter. This estimate was unacceptable because it was not credible and led to poor MCMC diagnostics because the estimate was on the upper limit of the parameter bounds. Changing the estimation order in the vulnerability table (see Table 5) resulted in a more credible mature female selectivity ogive (maximum selectivity estimated at 69 mm for region 1 and 61 mm in region 2) even though two of the associated newly estimated vulnerabilities hit the maximum value of 1. The RLWG considered this result to be preferable over the previous unrealistic estimate for size at maximum selectivity for mature females.
6. Relegated the puerulus settlement series to a sensitivity run because the peak puerulus settlement indices did not match the interpretation of the LF data in the stock assessment model (see discussion below).
7. Attempted a three-region model to accommodate the large LFs in statistical area 918 and the corresponding high CPUE in that area. This failed because there were too few sampling data for the new region 3 (comprised of areas 918 and 919) as well as estimating an equivalently high CPUE in both areas 917 and 918. In addition, this approach showed no improvement in the CPUE fit when using this more complex model and was abandoned.

In summary, the base case model dimensions and structural choices included:

- Model years: 1945–2019 (assuming an unfished population in 1945, ending with the 2019–20 fishing year);
- Two-region model: region 1 comprised of statistical areas 917, 918, and 919; region 2 comprised of statistical areas 916, 932, and 933;

- Two six-month seasons: AW (April-September) and SS (October-March) during each fishing year, starting in 1979;
- Three sex categories: immature females, mature females, males;
- Tail width bins: 31 2-mm wide bins from 30 mm to 90 mm tail width (last bin is a “plus group”);
- Size at recruitment: mean 33.35 mm with standard deviation 4 mm based on recent studies of juvenile growth (Roberts & Webber in prep.);
- Likelihoods:
 - Lognormal for three CPUE series (CR, FSU, and CELR),
 - Robust normal for tags,
 - Multinomial for LFs, fitted to proportions for males, immature females, and mature females, with each sex category normalised separately,
 - Multinomial for sex ratios;
- Data weighting determined iteratively. No re-weighting of tag data because they are self-weighting through the estimation of an observation error parameter;
- Fishing mortality dynamics: instantaneous using the Newton-Raphson algorithm to iteratively solve the Baranov catch equation (three Newton-Raphson iterations);
- Growth: Schnute-Francis model, sex-specific, shared between the two regions;
- Recruitment deviations (*Rdevs*) estimated: 1945–2017 (final two model years are set to the 2017 estimate, given no real information in data for these recruitments and the lack of a consistent puerulus settlement index);
- Handling mortality: two periods 1945–1989 fixed at 0.1 and 1990–2019 fixed at 0.05;
- Stock-recruitment relationship: off;
- Catch from 1945 to 2019, with illegal catch from 1945–1989 set at 10% of the commercial catch in those years and from 1990 to present set at 5% of the commercial catch, based on the pattern of CPUE, 1979–2019;
- Five CPUE series (CR for region 1 only, FSU and CELR for region 1 and region 2). Separate q parameters for CR (1963–1978 [region 1 only]), FSU CPUE (1979–1989 AW, separate q for regions 1 and 2), and CELR CPUE (1989 SS–2019 AW, separate q for regions 1 and 2):
 - q was constant for the CR and FSU CPUE series (no *qdrift* parameter),
 - q was assumed to improve over time at a constant rate of 1% per year for the CELR CPUE,
 - FSU and CELR series were standardised by including a vessel explanatory variable. The FSU series used all data and the CELR series was based only on vessels with at least five years in the fishery;
- Selectivity: sex-specific double-normal selectivity, with only one epoch in both regions. The right-hand limb selectivity was fixed at 200 to prevent a descending limb;
- Single natural mortality shared between the regions and sexes;
- Female-only maturation ogive shared between the regions;
- Eight vulnerability parameters: one per sex per season for each region, with immature and mature females during the SS sharing a vulnerability parameter in each region (see Table 5);
- Excluded the puerulus index;
- No density-dependent growth (cannot be reliably estimated);
- No modelling of the discard of large lobsters (logbook data indicate that discarding large lobsters was not common in CRA 5).

All tags and recaptures were included in the model, regardless of time at liberty, to maximise the amount of growth information from the tagging data in this stock assessment. The RLWG did not identify a residual pattern in growth estimates with increasing recapture events for the same tagged lobster. Because of this, the stock assessment used all CRA 5 tag-recapture data for any lobster, instead of just the initial recapture event.

To account for technological shifts over time, a vessel explanatory variable was included in the CPUE standardisation analysis and the estimation of a *qdrift* “technology creep” parameter was explored. Early model estimates of the *qdrift* parameter were very high ($qdrift = 0.045$) even when the CPUE series included a vessel explanatory variable. The RLWG agreed that a *qdrift* parameter should be included in the base model, so this parameter was fixed at 1% per year in all subsequent 2020 CRA 5 model runs.

A separate study using juvenile growth data estimated a three-year lag between puerulus settlement and recruitment to the stock assessment model (Roberts & Webber *in prep.*). Puerulus randomisation trials failed to confirm the three-year lag option to be the most likely lag period between settlement and model recruitment but instead identified lags of zero, one, and two years as the significant lags (Figure 5; lags of less than two years are highly improbable given the juvenile growth information). More importantly, the puerulus series did not match model estimates of peak recruitment derived from the fishery sampling (even though the growth parameter estimates were credible), leading to the conclusion that the CRA 5 puerulus series was not a consistent representation of the recruitment pattern experienced by this fishery (Figure 6).

The new base case model fitted the CELR CPUE series acceptably in both regions (Figure 7), although there were clear patterns in the residuals, particularly in the AW for both regions (Figure 8). However, these fits were superior to the equivalent fits for a model which assumed that CRA 5 was a single homogeneous region. The fit to the FSU series was surprisingly good in both regions (Figure 9) although there was some evidence of residual patterns in the fits to the AW series in both regions (Figure 10). The fit to the unstandardised CR series was not particularly good, although the overall downward trend was captured by the model (Figure 11) without a strong residual pattern (Figure 12).

Model fits to the LF data were generally acceptable, although there were some examples of poor fits (see Appendix I). In general, the model had difficulty in fitting the proportions at size near the MLS for both males and females, where the data suggested a higher abundance of individuals than the model could accommodate. This problem is visible in the LF residuals, where there are large positive residuals in the [52, 54) bin for males and the [58, 60) bin for mature females (Figure 13, Figure 14). The model also does a very poor job of fitting to immature female LFs, because they are poorly represented in the data and, consequently, have very little weight compared with the males and mature females.

The model estimates of growth for the [32, 34) length bin for males (about 10 mm/year) and for females (about 16 mm/year) (Figure 15) seemed fast relative to the estimated growth in these size classes from the independent analysis of juvenile (pre-recruit) growth by Roberts & Webber (*in prep.*). However, the model had no observations for any length less than about 44 mm TW and the shape of the model fit is determined by the recoveries in the 50–80 mm size range and the model parameterisation. Consequently, the RLWG agreed that this growth model was likely to be a reasonable representation of the growth in CRA 5. Based on the lack of residual patterns in the fits to the tagging data by statistical area (Figure 16), there was little or no evidence of differential growth among the component statistical areas of CRA 5. This validated the decision to treat this QMA as a single growth morph. Similarly, there was little evidence of a pattern in tag residuals by re-release category (Figure 17), validating the decision to include all tag recovery data in the model.

The sex-ratio fits were problematic for both sexes in the SS for both regions (Figure 18). Starr & Webber (2016) were also unable to obtain satisfactory fits to the recent SS sex ratios for a single region model. Unsurprisingly, the standardised residuals for these fits also showed patterns, indicating poor fits to these data (Figure 19).

The initial (i.e., unfished) size structure showed a common pattern seen in all rock lobster stock assessments, with a strong spike of immature females less than 40 mm TW and considerable numbers of males and females in the [90, ∞) plus group (Figure 20; note that the MCMC model fits to the LF data are presented in full in Appendix I).

Selectivity for males was the same in both regions while the female selectivity in region 1 was shifted to the right of the region 2 selectivity (Figure 21). Fifty percent of female maturation was estimated to occur by the 47 mm TW bin in this model, resulting in almost all females being mature by the time they reach the 60 mm MLS (Figure 22).

The high annual catches in the late 1940s and early 1950s did not result in very high annual fishing mortality (F) in region 1 (maximum F near 0.1; Figure 23) but the F estimates for region 2 seemed very high (near $F = 0.5$ in the early period but rising to $F > 1.5$ by the late 1960s; see Figure 23). The seasonal estimates of F for both regions were also high in the late 1980s and early 1990s, rising to $F = 0.3$ for region 1 and $F > 0.5$ for region 2 in this period.

There was a spike in estimated recruitment around 1990 for region 1, followed by an even stronger recruitment event in the early 2000s, while region 2 only showed one strong recruitment event in the early 1990s (Figure 24).

Plots of the adjusted vulnerable biomass indicated that the region 1 biomass was much larger than that of region 2, although the region 1 adjusted vulnerable biomass had been declining since around 2010 while the equivalent biomass for region 2 had been increasing after around 2015 (Figure 25).

All parameter estimates, likelihoods for all data components, indicators, and other derived parameters are presented for the base case in the first column of Table 8.

2.5.2 MAP sensitivity trials

The RLWG decided on eleven sensitivity trials as single variants relative to the base case (Table 9). These included sensitivities testing assumptions relating to: the inclusion of a vessel explanatory variable in the CPUE standardisation (*novessel*); fitting to the puerulus index (*lag3*); testing alternative pre-1963 catch time series (*catch_alt*); comparing back to a single-region model (*single_area*); doubling the illegal catch time series (*illegalX2*); increasing the CELR CPUE likelihood weight (*upCPUE*); removing the additive CELR CPUE process error (*process_error*); truncating the effective sample size for the logbook LFs (*trunc_weights*); and downweighting the CPUE, sex-ratio, and LF data set weights (*downCPUE*, *downSR*, *downLF*).

Parameter estimates, likelihoods for all data components, indicators, and other derived parameters for the sensitivity trials are presented in Table 8. Figure 26 compares the estimated selectivities by region for the base case run and all eleven sensitivity runs. Figure 27 compares the recruitment trajectories for the base case run and all eleven sensitivity runs. Recruitments for region 1 and region 2 were combined in this plot to allow for direct comparison with the *single_area* model run. Figure 28 compares the adjusted vulnerable biomass trajectories for the base case run and all eleven sensitivity runs. As for Figure 27, the biomass trajectories for region 1 and region 2 were combined to allow for direct comparison with the *single_area* model run.

Most of the sensitivity runs did not appreciably change the overall understanding of the CRA 5 stock status. In all runs, the stock status for region 2 was approximately half that for region 1, with region 1 ranging from 40 to 50% B_0 while region 2 tended to be near 20% B_0 (or less). The most notable exception to this was the run which downweighted the LF data (*downLF*), with the region 1 stock status dropping to 26% of B_0 while region 2 remained at 20% B_0 . The *single_area* sensitivity run resulted in a very low estimate of current stock status (below 10% of B_0) which was not credible. This lack of credibility lies in the very low R_0 estimate for the *single_area* sensitivity run which was near 1 000 000. This estimate was less than the region 1 estimate for all of the sensitivity runs except the *downSR* and *catch_alt* sensitivities. However, all these sensitivity runs also include region 2 estimates at about half the size of region 1. Because each model has the same catch history, the small stock size for the *single_area* sensitivity run has to support the same high catches, resulting in a very reduced stock status and very high estimates of fishing mortality. The 2015 single region CRA 5 stock

assessment (Starr & Webber 2016) base case estimated R_0 at 1 720 000 individuals, an estimate which is very similar to the combined R_0 (1 810 000 individuals) for the base case in this stock assessment. It is not known why the *single_area* sensitivity run estimated such a low CRA 5 stock size compared with the two region model or with the 2015 stock assessment. Non-convergence was considered as a reason why CRA 5 stock size was estimated to be lower in the single-region compared with two-region model, but this was unlikely because the same result was found when starting with different initial values. It is possible that the CPUE has diverged between the two regions so much since the last assessment that the single region model was not able to cope with this change.

The *novessel* and *lag3* runs resulted in stock status estimates that were nearly the same as the *base* run, indicating that the assumptions which underpin these runs do not materially change the understanding of this stock. The other sensitivity run with some impact on stock status (apart from the runs which downweight important data components) was the run which increased the weight on the CPUE data (*upCPUE*). However, the shift was not large, indicating that the LF data (principally) are not in conflict with the CPUE series.

The *catch_alt* sensitivity run explored an alternative catch history for the two CRA 5 regions because the very high fishing mortality rates estimated for region 2 in the base case run (Figure 23) lack credibility. This run showed more reasonable estimates of early (pre-1963) fishing mortalities in each of the two regions (Figure 29), although they were still high for region 2. This run also estimated a smaller overall stock size (combined $R_0 = 1\,512\,000$ individuals) compared with the *base* run (combined $R_0 = 1\,810\,000$ individuals), a difference of -16%.

A summary of the sensitivity runs is provided below.

- *novessel*: remove vessel explanatory variable from the CPUE series (but retain 1% *qdrift*)
 - no change in B_{2020}/B_0 ratio for region 1 but drop in B_{2020}/B_0 ratio for region 2 (from 0.2 to 0.16). SSB_{2020}/SSB_0 high for both regions;
- *lag3*: fit to puerulus index with a lag of three years
 - very similar results to base run;
- *catch_alt*: fit to an alternative catch history for regions 1 and region 2 (to 80%/20% instead of 57%/43% for pre-1963 catches)
 - R_0 reduced by 16% in both region 1 and region 2; B_{2020}/B_0 stock status estimates were almost the same as the base case in region 1 but dropped by 13% in region 2; SSB_{2020}/SSB_0 dropped by 27% and 17% in region 1 and region 2, respectively, relative to the base case (but were still above 40%);
- *single_area*: demonstrated the effect of moving from a single region to a 2-region model (but may not be a credible run given the very low estimate for R_0 which differs substantially from Starr & Webber (2016) and the combined 2 region stock sizes in this assessment)
 - B_{2020}/B_0 stock status very low (0.092); SSB_{2020}/SSB_0 status estimate still > 40% (0.431);
- *illegalX2*: double the illegal/unreported catch to 20%/10% assumption
 - about 10% higher stock size estimate relative to the base case; estimates of B_{2020}/B_0 and SSB_{2020}/SSB_0 stock status similar to base run;
- *upCPUE*: upweight the CPUE series relative the LF, tagging, and sex ratio data
 - reduced estimate of B_{2020}/B_0 stock status but SSB_{2020}/SSB_0 stock status higher than base run;
- *process_error*: reduce the CPUE process error in the most recent 5 years
 - similar estimate of B_{2020}/B_0 stock status and SSB_{2020}/SSB_0 stock status higher than base run;

- *trunc_weights*: truncate the LF weights to 25 (reduce the increasing trend in LF weights in recent years)
 - similar estimate of B_{2020}/B_0 stock status and SSB_{2020}/SSB_0 stock status slightly higher than base run;
- *downCPUE*: reduce the relative weight of the CPUE series
 - reduced estimate of B_{2020}/B_0 stock status for region 1 but doubled for region 2; similar for SSB_{2020}/SSB_0 stock status: reduced for region 1 but doubled for region 2;
- *downSR*: reduce the relative weight of the sex ratio data
 - slightly reduced estimate of B_{2020}/B_0 stock status but SSB_{2020}/SSB_0 stock status the same as base run;
- *downLF*: reduce the relative weight of the LF data
 - reduced estimate of B_{2020}/B_0 stock status for region 1 but higher for region 2; SSB_{2020}/SSB_0 stock status about the same for region 1 but higher for region 2.

2.6 Bayesian inference using Markov chain Monte Carlo (MCMC)

Bayesian inference was used to characterise parameter uncertainty. LSD uses the Stan software to run MCMC simulations using the Hamiltonian Monte Carlo (HMC) algorithm. The MAP values were used as starting values (Table 8). For the base case and three selected sensitivity tests (*lag3*, *novessel*, and *catch_alt*), the posterior distributions were explored with a total of 1000 samples across four chains, each with a warm-up phase of 500 iterations and length of 500 samples, retaining every second sample.

2.6.1 MCMC base case

MCMC was used to obtain samples from the posterior distribution for the base case model described in Section 2.5.1. The trace plots indicate that MCMC chains were well-mixed (Figure 30, Figure 31, Figure 32, and Figure 33). The traces for the key estimated biological parameters, such as M and R_0 , showed an acceptable level of stability, with MCMC chains staying away from parameter bounds. The posterior distributions for most model parameters updated the prior (Figure 34, Figure 35, and Figure 36), the exception being the male *Gshape* parameter (Figure 34). The posterior distribution of the *Gobs* parameter was beyond the traction of the prior, but this is of little concern given that the *Gobs* prior was derived from an unpublished meta-analysis based on the available tag release-recovery data available in 2015.

Figures for the base case model only are presented. These are comparable with those provided for the base case MAP results. The fit to the CELR CPUE was very similar to that presented for the MAP from the same model (compare Figure 7 with Figure 37). Similarly, the fit to the FSU CPUE series matched the equivalent MAP fit (compare Figure 9 with Figure 38). Finally, the fit to CR CPUE matched the MAP fit (compare Figure 11 with Figure 39). The posterior distributions of the estimated catchability coefficients were broad and the CELR CPUE catchability showed an increasing trend associated with the *qdrift* parameter fixed at 1% per year (Figure 40). The relative increase in these latter plots is about 25% over the 30-year period.

The fits to the LF data (all MCMC LF fits are presented in Appendix I) and the associated residuals (Figure 41, Figure 42) showed the same properties as were described for the equivalent MAP fits. There was a lack of fit in the bins associated with the male ([52, 54)) and female ([58, 60)) MLS, and the fits to the immature female LFs were very poor due to the low sample weights associated with these data. The fits to the sex-ratio data mirrored the MAP fit, with very poor correspondence with the observed female SS sex ratios in both region 1 and region 2 (compare Figure 18 with Figure 43).

The selectivity posterior plot showed little uncertainty in these parameters, indicating that the MCMC did not deviate very much from the MAP estimates (compare Figure 21 with Figure 44). In contrast,

the posterior distribution of the maturation ogive is more uncertain, although the median was indistinguishable from the MAP (Figure 45). However, the median estimate for *mat50* (at 46 mm) was very close to the MAP estimate (47 mm).

The plot of growth increment at length was almost identical to the equivalent MAP plot (compare Figure 15 with Figure 46). Tag residual plots across statistical areas (Figure 47) and re-release category (Figure 48) confirmed the conclusions reached from the MAP fits: growth was reasonably consistent across the four main CRA 5 statistical areas and across re-release categories. Two further plots show tag residuals by year of release (Figure 49) and by the size at release for each statistical area (Figure 50). The year of release appeared to have little or no bias, with growth consistent across the more than 40 years spanning the tag release data. There appeared to be a negative bias in growth as the initial size at release became larger. However, this is likely an artefact of low sample size, with relatively little data representing the larger size categories.

Fishing mortality appeared to be very high for region 2 in the late 1960s, with the median sitting well above $F = 1$, but with some realisations extending up to $F = 6$ (Figure 51). A plot showing the base case catches indicated that there were realisations where there was insufficient vulnerable biomass available to account for the region 2 catch (Figure 52). These results suggested that the catch history underlying the base case run probably assigned too much catch to region 2.

Region 1 recruitment spikes estimated for the early 1990s and early 2000s, with the size of the latter spike of the order of 4–6 times larger than average (Figure 53). Recruitment in region 2 was more modest, with only one spike in the early 1990s estimated at about twice the long-term average.

The plot of adjusted vulnerable biomass showed a sharp drop in biomass from about 2010 for region 1, while the region 2 biomass was increasing slowly from a low level after about 2015 (Figure 54). There were similar *SSB* trends for each region, with *SSB* well above the soft limit of 20% *SSB*₀, largely due to the maturation ogive which estimated that nearly all females were mature at the 60 mm TW MLS (Figure 55). Summaries of posterior distributions of parameter estimates and derived quantities are presented in Table 10A and Table 10B.

2.6.2 MCMC sensitivity trials

The RLWG chose three of the MAP sensitivity trials to be explored using MCMC: *novessel*, *lag3*, and *catch_alt*. These runs represented plausible alternative hypotheses that differed in the parameter space investigated (i.e., biomass trajectories) relative to the base case. All three sensitivities had acceptable MCMC diagnostics (not presented).

Parameter estimates, likelihoods for all data components, indicators, and other derived parameters for these MCMC sensitivity trials are presented in Table 10A and Table 10B. Comparisons of these sensitivity trials to the base case are shown for recruitment (Figure 56) and adjusted vulnerable biomass (Figure 57).

Most of the MCMC sensitivity runs did not appreciably change when compared with the equivalent MAP sensitivities (compare Table 9 with Table 10A). In all runs, the stock status for region 2 was approximately half that for region 1, with region 1 ranging from 40 to 50% *B*₀ while region 2 tended to be near 20% *B*₀ (or less).

The *novessel* and *lag3* runs resulted in stock status estimates that were nearly the same as the *base* run, indicating that the assumptions which underpin these runs do not materially change the understanding of this stock. The *catch_alt* sensitivity run explored an alternative catch history for the two CRA 5 regions because the very high fishing mortality rates estimated for region 2 in the base case run (Figure 23) lack credibility. The *base* model run also struggled to take the catch for several years in the late 1960s and early 1970s (Figure 52); however, this did not occur for *catch_alt* sensitivity (Figure 58), suggesting that the catch history used for this model may be more plausible than the catch

history used in the other model runs. There is a great deal of uncertainty in the early catch history, which was determined from port of landing, not area of capture, with the capture distribution by area inferred from data collected over a decade later (see Starr et al. 2021).

A summary of the sensitivity runs is provided below:

- *novessel*: remove vessel explanatory variable from the CPUE series (but retain 1% *qdrift*)
 - a small change in B_{2020}/B_0 ratio for region 1 but drop in B_{2020}/B_0 ratio for region 2 (median dropped from 0.226 to 0.184). SSB_{2020}/SSB_0 high (median = 0.81 for region 1 and 0.54 for region 2);
- *lag3*: fit to puerulus index with a lag of three years
 - very similar results to base run;
- *catch_alt*: fit to an alternative catch history for regions 1 and region 2 (to 80%/20% instead of 57%/43% for pre-1963 catches)
 - median R_0 reduced by 15% and 16% in region 1 and region 2 respectively; B_{2020}/B_0 stock status estimates were similar to the base case in region 1 but median dropped by 12% in region 2; median SSB_{2020}/SSB_0 dropped by 26% and 16% in region 1 and region 2, respectively, relative to the base case (but were still above 40%).

2.7 Projections

Five-year projections for the fishing years 2020–21 to 2024–25 were done for each of the four models taken to MCMC. The recreational and NSL catches were assumed to be the same as the final model year and were set to be constant when projecting forward. Commercial catch in 2020–21 was assumed to be 363.8 tonnes which included carryover from 2019–20 to cover missing catches due to disruptions to the fishery caused by the COVID-19 pandemic (Table 11). Table 11 also shows how the projection catches were allocated to each region, based on the 2019–20 catch split. The commercial catch was assumed to be 350 tonnes (present TACC) for 2021–22 to 2024–25.

Projected recruitment deviates were simulated from a normal distribution with mean and standard deviation calculated from the mean recruitment deviates for the period 2008–2017 with the standard deviation set to σ_R (Table 3). Projection recruitment deviates were used for 2018 and 2019 because recruitment was not estimated in the reconstruction model for these years (Figure 56).

The projected adjusted vulnerable biomass and SSB were predicted to decline over the next five years in the *base* case model run and the three sensitivity model runs (Figure 59, Figure 60). In the *base* case model run, the median 2020 adjusted vulnerable biomass for combined CRA 5 was predicted to be 42% of B_0 ($B_{2020}/B_0 = 0.418$ [90% credible interval (CI) = 0.340–0.521]) and was projected to decrease to a median value of 27.3% of B_0 by 2024, at current catch ($B_{2024}/B_0 = 0.273$ [90% CI = 0.188–0.397]). In the *base* case model run, the median 2020 SSB was predicted to be 71% of SSB_0 ($SSB_{2020}/SSB_0 = 0.711$ [90% CI = 0.641–0.810]) and was projected to decline to a median value of 66.6% of SSB_0 ($SSB_{2024}/SSB_0 = 0.666$ [90% CI = 0.565–0.800]) by 2024 (Table 10A).

2.8 Reference levels

Work has been completed to develop model-based reference levels for red rock lobster stocks (Rudd et al. in press a). To calculate the reference level, a wide range of fixed catch and fixed F rules were projected forward 30 years, and the performance of each rule was assessed over the final 20 years of the projection period. Evaluated performance indicators included the average annual catch, the CV of catch over time, and the probability of falling below the soft limit. The rule that maximised catch while maintaining less than 5% chance of falling below the soft limit was identified for each rule type (fixed catch or fixed F). Fixed catch rules were further constrained by requiring 99% of the fixed catch amount to be taken for more than 95% of years and simulation replicates. The reference level (B_R ;

Table 6) was defined as the average adjusted vulnerable biomass between the maximum constrained fixed catch and fixed F rules.

The reference level projections done during the workshop assumed that projected recruitment deviates and the value for SSB_0 used in the risk constraint would be based on the final ten years of estimated recruitment deviates, in keeping with previous simulations used to evaluate MPs (e.g., Breen et al. 2017). The Fisheries New Zealand mid-year Plenary (November 2020) did not accept these reference levels, arguing that the final ten years may not be adequately representative of productivity over the next 30 years and asked for a longer period over which to estimate mean recruitment. It was agreed that the chosen recruitment reference period would span the full period with adequate length frequency data. Consequently, reference levels were recalculated using the estimated recruitment deviates starting in the first year with reasonable length data, either from the catch sampling or the logbook programmes. For CRA 5, this included 29 years from 1989 to 2017. The reference levels reported in this document and the methods used to estimate them are more thoroughly discussed by Rudd et al. (in press a).

Table 10A indicates that the median base case estimate of B_{2020} was well above B_R for both CRA 5 regions. Region 1 in CRA 5 was projected to decline, with the median estimate for B_{2024} dropping by about 50% compared with B_{2020} , and region 2 was expected to increase over the next five years under the projection assumptions for recruitment and catch. However, all projections predicted that both CRA 5 regions would remain well above B_R at the end of the projection period.

3. DISCUSSION

Overall, the LSD model fitted the CRA 5 input data reasonably well. Some exceptions included the region 1 CPUE in the 2017 and 2019 AW and the 2016–2018 SS, the region 2 CPUE in the 2002–2005 (both seasons), some of the early LFs, and the female SS sex-ratios from 2015 to 2019 (both regions). Despite these issues, the model was considered to do a reasonable job of representing the CRA 5 stock. It also represented an improvement over the 2015 stock assessment model, which had poorer fits to the CPUE data and also failed to fit the female SS sex ratios.

This assessment, like most rock lobster assessments, describes a stock that was initially heavily fished, resulting in a rapid decline in vulnerable biomass through to the mid-1950s, followed by a long period over which the vulnerable biomass stabilised from the mid-1950s to the mid-1960s. Stock size then declined, before stabilising again during the 1970s to early 1980s. The vulnerable biomass then rapidly declined in the face of heavy fishing pressure prior to the entry into the QMS, moving down to very low levels during the early 1990s. The overall stock size then increased strongly, to near unfished levels from the mid-1990s up to about 2010, and has since declined relatively rapidly (Figure 59). At the catch levels specified in the projections, the stock is expected to continue this downward trend for the next five years (Figure 59). A very similar pattern was observed for the SSB (Figure 60).

Under the *base case* model assumptions, the 2020 CRA 5 vulnerable biomass is estimated to be well above the estimated reference level (median $B_{2020}/B_R = 3.714$ [90% CI = 2.984–4.761]; Table 10A) and is predicted to decrease by 2024 under the specified catch levels and recent (10 year) average recruitment, but remain well above the reference level (median $B_{2024}/B_R = 2.433$ [90% CI = 1.620–3.611]; Table 10A). A similar pattern was observed in all three of the MCMC sensitivity runs.

3.1 Future research

This assessment updated the mean and standard deviation of the length at recruitment in the stock assessment model based on recent studies of juvenile growth (Roberts & Webber in prep.). This study was also used to inform the plausible time lag from puerulus settlement to recruitment to the stock assessment model and plausible growth rate around the size at recruitment for model runs fitting to the puerulus index. However, puerulus randomisation trials did not agree with the most plausible time lag

(three years from settlement to recruitment) and supported time lags that were biologically implausible (< 2 years). This discrepancy should be investigated further.

The degree of variability in inter-annual recruitment appears to be much greater from the puerulus settlement index than from the fishery information (Figure 6). A possible explanation for this could be that density-dependent mortality (e.g., Moyle et al. 2009) is impacting on the survival of stronger cohorts prior to recruitment to the fishery. The shape of this density-dependent mortality response could potentially be estimated by future assessments, informed by the stock assessment model fit to puerulus indices and previous analyses of this species (Breen & Booth 1989).

Another explanation for lack of fit to the puerulus index could be that sampling from just a small number of localised sites may not be representative of recruitment across the QMA, especially given that ocean current patterns likely will differ throughout a year and could lead to large scale variability given the fixed site design of the settlement collectors.

Alternative methods for estimating growth rate could be explored, such as developing technology for the direct ageing of lobsters from gastric ossicles (e.g., Gnanalingam et al. 2018, Huntsberger et al. 2020, Leland & Bucher 2017). Direct ageing studies could help to better inform growth at small and large sizes (i.e., < 45 mm and > 75 mm where tag-recapture data are lacking). Moreover, such information could be used to identify and correct potential biases in tag-based growth information due to size-based selectivity of fishery-based tag recaptures. Otherwise, estimating the growth rate of small and large lobsters would likely require surveys be done in the field (e.g., dive surveys or potting using different mesh sizes) and/or tank-based experiments (which may not be suitable for estimating the growth of lobsters in the wild).

The *ad hoc* procedure used to derive data set weights for LFs collected by the observer and logbook sampling programmes attempts to balance the two styles of data collection by weighting the samples in proportion to the sampled statistical area/month catch, the number of days sampled, and the number lobsters measured (Starr et al. 2021). The main difference between these two data sources is that the spatial and temporal coverage and number of vessels sampled by the logbook programme are far greater than for the observer sampling programme, which can only intensively sample a relatively small number of vessels during a few days each year. Although the current weighting procedure is not based on statistical theory, it has worked reasonably well in the past, placing reasonable relative weights within one or the other sampling programme. In most CRA QMAs, only one sampling programme predominates. However, the 2020 CRA 4 stock assessment demonstrated a weakness in the weighting procedure because it tended to favour the logbook samples over the observer samples when the two sampling programmes operated in the same area at similar levels of sampling intensity. Because of this, the CRA 4 stock assessment team arbitrarily down-weighted the logbook samples so that the observer samples could contribute to the stock assessment. Future work on LF standardisation methods and alternative relative data set weighting procedures is needed to avoid data set weighting issues experienced during the 2020 CRA 4 and CRA 5 assessments. Further work should investigate the use of a procedure similar to the one being used to weight the pāua LF data (P. Neubauer, Dragonfly Data Science, pers. comm.).

The LSD model is capable of estimating selectivity that is specific to region, sex, season, or year. However, the specifications for vulnerability are less flexible because they can only be specific to region, sex, or season. The option to include year-specific vulnerability should be added to the LSD model so that time-varying vulnerability can be explored in the future. This may help solve some of the issues identified when fitting sex-ratio data in this stock assessment. Furthermore, LF distributions can differ somewhat within regions (e.g., the LFs observed in different statistical areas that are assumed to be within the same region for modelling purposes) which can cause some issues during model fitting. However, the LSD model is not yet capable of estimating different selectivities for different “fisheries” within the same region. Adding this capability represents a large restructure of the code, but could be considered in the future.

The 2019–20 fishing year marks the transition of the collection of commercial catch and effort data from a paper-based system to electronic reporting. Previous experience with changes to the collection of catch and effort data in New Zealand has demonstrated that it is not possible to assume that data will be comparable across the two data collection systems. In addition, initial evidence showed poor compliance with data entry instructions by fishers switching to the new electronic system. The RLWG provisionally concluded that the new data collection system is not comparable to the previous system, and that there is consequently a break in the continuity of the CPUE time series (see appendix B of Starr 2021). As a result, it will not be possible to use the new electronic catch/effort data to generate a CPUE series that can be used to include in a stock assessment or drive an MP until sufficient data accumulate to create a new reliable series. A procedure for annual rapid updates of red rock lobster assessments has been developed, which involves running the base model from the last full assessment with additional years of catch, length frequency, and tagging data (Webber et al., 2021). CRA 5 will be the subject of a rapid assessment in 2021. Future work is proposed to develop MPs based on the results of the rapid updates and the updated reference levels for each QMA.

Estimates of non-commercial catch are infrequent and uncertain. These estimates should be improved with more frequent and better designed non-commercial catch surveys and reporting systems.

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6. TABLES

Table 1: Minimum legal size (MLS) limits for males and females over time. Note that MLS before 1987 were expressed in terms of tail length and have been converted to tail width using the procedure described by Breen et al. (1988).

Period	MLS (tail width, mm)	
	Males	Females
1945–1949	None	None
1950–1951	47	49
1952–1958	51	53
1959–1987	53	58
1988–1991	54	58
1992–2019	54	60

Table 2: Definitions of parameters and derived quantities discussed in the text.

Parameter	Definition
R_0	initial numbers recruiting
M	instantaneous rate of natural mortality
$Rdevs$	annual recruitment deviations
σR	standard deviation of $Rdevs$
qCR	catchability coefficient (relationship between the vulnerable biomass and CR series)
$qFSU$	catchability coefficient (relationship between the vulnerable biomass and FSU CPUE series)
$qCELR$	catchability coefficient (relationship between the vulnerable biomass and CELR CPUE series)
$Mat50$	size where 50% of immature females become mature
$Mat95add$	difference between $Mat50$ and the size at which 95% of immature females become mature
$Galpha$	annual growth increment at 50 mm TW
$Gbeta$	annual growth increment at 80 mm TW
$Gdiff$	the ratio of $Gbeta$ to $Galpha$
$Gshape$	parameter for shape of growth curve: 1 implies von Bertalanffy straight line; > 1 implies a concave upwards curve
GCV	standard deviation of growth-at-size divided by growth-at-size
$Gobs$	standard deviation of observation error for tag recaptures
$SellH$	shape of the left-hand limb of the selectivity curve (as if it were a standard deviation)
$SelM$	size at maximum selectivity
$vuln$	relative vulnerability by sex and season
$qdrift$	additive change in catchability coefficient each year
U_0	initial exploitation rate (the first model year is in equilibrium using this estimate)
Gdd	density-dependent growth parameter

Table 3: Fixed quantities used in the CRA 5 models. Region is denoted by either [1] for region 1 or [2] for region 2.

Quantity	Value	Quantity	Value
fixed parameters		recruitment	
σR	0.4	last year of estimated $Rdevs$	2017
male length-weight a	4.16e-6	years for estimating $Rdevs$ for	2008–2017
male length-weight b	2.935	years for estimating autocorrelation	1986–2017
female length-weight a	1.3e-5	recruitment size mean	33.35 mm
female length-weight b	2.545	recruitment size SD	4 mm
Gdd	0	other	
U_0	0	Newton-Raphson iterations	3
$qdrift$	0.01	Tail compression: male bins [1]	5 to 31
catch and handling		Tail compression: female immature	3 to 21
Handling mortality, 1945–1989	0.10	Tail compression: female mature bins	5 to 31
Handling mortality, 1990–2018	0.05	Tail compression: male bins [2]	5 to 31
growth		Tail compression: female immature	6 to 26
length at $Galpha$	50	Tail compression: female mature bins	6 to 31
length at $Gbeta$	80		
length at $Gmin$	0.0001		

Table 4: Specifications for estimated parameters in the CRA 5 models including the upper and lower bounds, prior type, and prior parameters (par 1 and par 2).

Region	Sex	Parameter	Lower bound	Upper bound	Prior type	par 1	par 2
		R_0	exp(1)	exp(25)	uniform		
		M	0.01	0.35	lognormal	0.12	0.4
		$Rdevs$	-2.3	2.3	normal		
		qCR	exp(-25)	1	uniform		
		$qFSU$	exp(-25)	1	uniform		
		$qCELR$	exp(-25)	1	uniform		
	female	$Mat50$	30	80	normal	50	30
	female	$Mat95add$	1	60	normal	5	5
	male	$Galpha$	1	20	normal	2	30
	male	$Gdiff$	0.001	0.99	beta	1	1
	male	$Gshape$	0.1	15	normal	4.81	0.38
	male	GCV	0.01	2	normal	0.59	0.0076
	female	$Galpha$	1	20	normal	2	30
	female	$Gdiff$	0.001	0.99	beta	1	1
	female	$Gshape$	0.1	15	normal	4.51	0.24
	female	GCV	0.01	2	normal	0.82	0.013
		$Gobs$	0.0001	10	normal	1.48	0.015
	male	$SelLH$	1	50	normal	10	10
	male	$SelM$	30	90	normal	50	30
	female	$SelLH$	1	50	normal	10	10
	female	$SelM$	30	90	normal	50	30
1		$vuln1$	0.01	1	beta	1	1
1		$vuln2$	0.01	1	beta	1	1
1		$vuln3$	0.01	1	beta	1	1
1		$vuln4$	0.01	1	beta	1	1
2		$vuln5$	0.01	1	beta	1	1
2		$vuln6$	0.01	1	beta	1	1
2		$vuln7$	0.01	1	beta	1	1
2		$vuln8$	0.01	1	beta	1	1
		$qdrift$	-0.08	0.08	normal	0	1

Table 5: Mapping of vulnerability (*vuln*) parameters. Vulnerability for males during the AW is fixed at 1 in both regions and all other *vuln* parameters are estimated relative to the vulnerability of males during the AW in each region.

Sex	Region 1		Region 2	
	AW	SS	AW	SS
male	1	<i>vuln1</i>	1	<i>vuln5</i>
immature female	<i>vuln2</i>	<i>vuln3</i>	<i>vuln6</i>	<i>vuln7</i>
mature female	<i>vuln4</i>	<i>vuln3</i>	<i>vuln8</i>	<i>vuln7</i>

Table 6: Reference points, performance indicators, and stock status probabilities for the CRA 5 stock assessment.

Type	Description
Reference Points	
B_0	beginning of season AW adjusted vulnerable biomass before fishing (1945)
SSB_0	female AW spawning stock biomass before fishing (1945)
B_{0TOT}	equilibrium total biomass
B_{0now}	equilibrium adjusted vulnerable biomass using mean 2008–2017 recruitment
SSB_{0now}	equilibrium female spawning biomass using mean 2008–2017 recruitment
$B_{0TOTNOW}$	equilibrium total biomass using mean 2008–2017 recruitment
B_{MIN}	the lowest beginning of season AW adjusted vulnerable biomass in the series
B_{2020}	beginning of season AW adjusted vulnerable biomass in 2020
B_{2024}	beginning of season AW adjusted vulnerable biomass in 2024
B_R	reference level in terms of AW adjusted vulnerable biomass (Rudd et al. in press a) is based on the mean recruitment from 1989 to 2017 for CRA 5.
SSB_{2020}	female spawning stock biomass at beginning of 2020 AW season
SSB_{2024}	female spawning stock biomass at beginning of 2024 AW season
$B_{2020TOT}$	beginning of season AW total biomass for 2020
$B_{2024TOT}$	beginning of season AW total biomass for 2024
$CPUE_{2019}$	AW CPUE at beginning of 2019 (in kg/potlift)
$CPUE_{2024}$	AW CPUE at beginning of 2024 (in kg/potlift)
H_{2019}	total handling mortality for 2019 (tonnes)
H_{2023}	total handling mortality for 2023 (tonnes)
Performance indicators	
B_{2020} / B_0	ratio of B_{2020} to B_0
B_{2024} / B_0	ratio of B_{2024} to B_0
B_{2020} / B_{0now}	ratio of B_{2020} to B_{0now}
B_{2024} / B_{0now}	ratio of B_{2024} to B_{0now}
B_{2024} / B_{2020}	ratio of B_{2024} to B_{2020}
SSB_{2020} / SSB_0	ratio of SSB_{2020} to SSB_0
SSB_{2024} / SSB_0	ratio of SSB_{2024} to SSB_0
SSB_{2020} / SSB_{0now}	ratio of SSB_{2020} to SSB_{0now}
SSB_{2024} / SSB_{0now}	ratio of SSB_{2024} to SSB_{0now}
SSB_{2024} / SSB_{2020}	ratio of SSB_{2024} to SSB_{2020}
$B_{2020TOT} / B_{0TOT}$	ratio of $B_{2020TOT}$ to B_{0TOT}
$B_{2020TOT} / B_{0TOTNOW}$	ratio of $B_{2020TOT}$ to $B_{0TOTNOW}$
$B_{2024TOT} / B_{0TOT}$	ratio of $B_{2024TOT}$ to B_{0TOT}
$B_{2024TOT} / B_{0TOTNOW}$	ratio of $B_{2024TOT}$ to $B_{0TOTNOW}$
$B_{2024TOT} / B_{2020TOT}$	ratio of $B_{2024TOT}$ to $B_{2020TOT}$
B_{male} / B_{female}	ratio of male total biomass to female total biomass in 2020 (MacDiarmid & Butler 1999, MacDiarmid et al. 2012)
Probabilities	
$P(B_{2020} > B_{MIN})$	probability B_{2020} is greater than B_{MIN}
$P(SSB_{2020} < 20\% SSB_0)$	probability SSB_{2020} is less than 20% SSB_0
$P(SSB_{2020} < 10\% SSB_0)$	probability SSB_{2020} is less than 10% SSB_0
$P(SSB_{2020} < 20\% SSB_{0now})$	probability SSB_{2020} is less than 20% SSB_{0now}
$P(SSB_{2020} < 10\% SSB_{0now})$	probability SSB_{2020} is less than 10% SSB_{0now}
$P(SSB_{2024} < 20\% SSB_0)$	probability SSB_{2024} is less than 20% SSB_0
$P(SSB_{2024} < 10\% SSB_0)$	probability SSB_{2024} is less than 10% SSB_0
$P(SSB_{2024} < 20\% SSB_{0now})$	probability SSB_{2024} is less than 20% SSB_{0now}
$P(SSB_{2024} < 10\% SSB_{0now})$	probability SSB_{2024} is less than 10% SSB_{0now}
$P(B_{2024} > B_{2020})$	probability B_{2024} is greater than B_{2020}
$P(SSB_{2024} > SSB_{2020})$	probability SSB_{2024} is greater than SSB_{2020}
$P(B_{2024TOT} > B_{2020TOT})$	probability $B_{2024TOT}$ is greater than $B_{2020TOT}$

Table 7: List of model runs used to iteratively update the base case used in the 2015 assessment of CRA 5 to a single region 2020 model run.

Model name	Model description
<i>1_base2015_noDD</i>	Mimics the 2015 assessment model (single homogeneous stock assumption): - Catch and CPUE used in 2015 assessment (up to and including the 2014 fishing year) - LF used in the 2015 assessment (up to and including the 2014 fishing year) - Tag data used in 2015 assessment - FSU and CELR CPUE series linked with single catchability parameter (q) and no vessel explanatory variable - No density dependence - Included puerulus index with lag of 2 years and truncated at 2014
<i>2_base2015_noP</i>	Same as <i>1_base2015_noDD</i> but does not fit to the puerulus index
<i>3_splitq</i>	Separate q parameters estimated for the FSU and CELR CPUE series
<i>4_handling</i>	Updated handling mortality to reflect the revision to 10%/5% assumption pre- and post-1990
<i>5_newCELR</i>	Included the updated CELR series using a Bayesian analysis with a vessel explanatory variable to be used in the 2020 assessment, but to 2015 only
<i>6_newFSU</i>	Included the FSU index run using a Bayesian analysis with a vessel effect to be used in the 2020 assessment, but to 2015 only
<i>7_newTagging</i>	Replaced old tag extract with new tag extract, to 2015 only
<i>8_newCatch</i>	Replaced old catch data with new catch data (includes updated illegal catch time series), to 2015 only
<i>9_newLF</i>	Replaced old length frequency data with updated length frequency data to 2015 only

Table 8: MAP outputs showing likelihoods, standard deviation of normalised residuals (SDNRs), median absolute residuals (MARs), likelihood weights, parameter estimates, and reference points. These values are by region where appropriate (regional values denoted by [1] and [2]) for the base case and all sensitivity runs. Growth increment values in mm TW, biomass values in tonnes, and R_0 in numbers. ‘–’: not applicable. Fixed values are indicated in grey. Text in red highlights the changed data set weights. SDNRs or MARs for tags and LF were not used because the tag likelihood is self-weighting and the LFs are iteratively reweighting using the Francis (2011) method. (Continued on next two pages)

	<i>base</i>	<i>novessel</i>	<i>lag3</i>	<i>catch_alt</i>	<i>single_area</i>	<i>illegalX2</i>	<i>upCPUE</i>	<i>process_error</i>	<i>trunc_weights</i>	<i>downCPUE</i>	<i>downSR</i>	<i>downLF</i>
Likelihoods												
Total	18 660	18 300	19 176	18 654	15 764	18 660	18 701	18 660	15 586	18 973	14 955	12 683
Prior	8 122	8 122	8 121	8 117	8 112	8 122	8 122	8 122	8 121	8 118	8 110	8 110
tag	79.6	81.8	86.2	73.1	92.1	80.1	95.7	79.9	73.5	58.0	67.0	61.6
sexr	4 097	4 048	4 100	4 105	2 022	4 098	4 102	4 098	2 939	4 095	420	4 091
LF	6 602	6 293	7 108	6 595	5 675	6 600	6 634	6 602	4 700	6 569	6 595	677
CR	-18.1	-18.2	-18.0	-18.1	-21.5	-18.2	-18.2	-18.1	-18.2	2.1	-18.1	-18.7
FSU [1]	-35.1	-39.2	-34.9	-35.3	-49.4	-35.0	-33.2	-35.1	-34.8	3.0	-33.8	-34.9
FSU [2]	-41.5	-41.6	-41.7	-40.0	–	-41.5	-40.0	-41.5	-41.5	-1.8	-41.8	-40.8
CELR [1]	-84.3	-79.2	-81.9	-84.6	-66.1	-84.1	-79.8	-84.4	-87.7	45.8	-83.7	-90.1
CELR [2]	-61.8	-67.7	-61.9	-57.9	–	-61.8	-80.3	-62.2	-64.3	84.5	-59.3	-71.4
puerulus	–	–	-1.0	–	–	–	–	–	–	–	–	–
Standard deviation of normalised residual (SDNR)												
sexr	1.035	1.037	1.045	1.065	0.977	1.037	1.055	1.036	0.943	1.026	0.434	1.001
CR	1.026	1.016	1.031	1.019	1.005	1.017	1.012	1.026	1.016	0.140	1.026	0.960
FSU [1]	1.032	0.992	1.043	1.025	1.001	1.037	1.123	1.035	1.047	0.213	1.092	1.042
FSU [2]	0.999	0.996	0.991	1.073	–	0.999	1.070	1.000	1.000	0.361	0.987	1.034
CELR [1]	1.051	1.020	1.096	1.048	1.058	1.055	1.633	1.051	0.994	0.812	1.062	0.965
CELR [2]	1.005	1.087	1.003	1.062	–	1.006	1.339	1.004	0.966	1.064	1.053	0.840
puerulus	–	–	1.191	–	–	–	–	–	–	–	–	–
Median of absolute residual (MAR)												
sexr	0.548	0.555	0.550	0.526	0.570	0.553	0.554	0.548	0.492	0.539	0.252	0.539
CR	0.304	0.308	0.291	0.356	0.461	0.305	0.342	0.304	0.315	0.090	0.313	0.537
FSU [1]	0.672	0.614	0.656	0.641	0.680	0.683	0.711	0.669	0.621	0.136	0.701	0.694
FSU [2]	0.710	0.901	0.689	0.854	–	0.700	0.873	0.717	0.733	0.236	0.802	0.824
CELR [1]	0.621	0.653	0.692	0.578	0.770	0.618	0.883	0.623	0.529	0.818	0.588	0.547
CELR [2]	0.765	0.837	0.748	0.836	–	0.759	0.776	0.764	0.749	0.918	0.785	0.636
puerulus	–	–	0.673	–	–	–	–	–	–	–	–	–
Likelihood weights												
sexr	6.480	6.400	6.480	6.480	5.250	6.480	6.480	6.480	6.480	6.480	0.648	6.480
LF [1]	1.110	1.056	1.220	1.110	1.465	1.110	1.110	1.110	1.110	1.110	1.110	0.111
LF [2]	0.904	0.860	0.943	0.904	–	0.904	0.904	0.904	0.904	0.904	0.904	0.090
CR	2.500	2.500	2.500	2.500	3.340	2.500	2.500	2.500	2.500	0.250	2.500	2.500
FSU [1]	5.300	6.200	5.300	5.300	4.900	5.300	5.300	5.300	5.300	0.530	5.300	5.300
FSU [2]	6.700	6.700	6.700	6.700	–	6.700	6.700	6.700	6.700	0.670	6.700	6.700
CELR [1]	5.650	2.500	5.700	5.650	2.300	5.650	11.300	5.650	5.650	0.565	5.650	5.650
CELR [2]	3.300	2.300	3.300	3.300	–	3.300	6.600	3.300	3.300	0.330	3.300	3.300
puerulus	–	–	0.400	–	–	–	–	–	–	–	–	–

<i>Parameters</i>	<i>base</i>	<i>novessel</i>	<i>lag3</i>	<i>catch_alt</i>	<i>single_area</i>	<i>illegalX2</i>	<i>upCPUE</i>	<i>process_error</i>	<i>trunc_weights</i>	<i>downCPUE</i>	<i>downSR</i>	<i>downLF</i>
<i>R₀</i> [1]	1 178 110	1 141 500	1 207 850	985 661	1 020 010	1 212 910	1 009 350	1 183 590	1 069 570	1 235 000	888 200	1 217 540
<i>R₀</i> [2]	631 618	608 475	616 768	525 642	—	656 052	575 477	631 114	602 965	713 302	505 892	729 833
<i>M</i>	0.180	0.179	0.183	0.163	0.125	0.179	0.173	0.181	0.174	0.185	0.148	0.207
<i>mat50</i>	46.75	46.87	46.14	47.69	50.95	46.79	47.21	46.79	47.22	47.12	54.61	48.70
<i>mat95add</i>	11.28	11.42	10.52	13.85	13.76	11.36	11.93	11.40	10.67	12.49	18.92	7.76
<i>Galpha</i> [male]	3.31	3.32	3.33	3.32	3.30	3.31	3.34	3.31	3.31	3.32	3.34	3.33
<i>Gbeta</i> [male]	2.60	2.63	2.59	2.55	2.66	2.60	2.66	2.60	2.60	2.46	2.56	2.53
<i>Gshape</i> [male]	4.93	4.95	5.17	5.07	5.23	4.92	4.89	4.93	4.98	5.08	5.14	5.21
<i>GCV</i> [male]	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.57
<i>Galpha</i> [female]	3.75	3.74	3.83	3.66	3.40	3.75	3.74	3.75	3.72	3.67	3.29	3.45
<i>Gbeta</i> [female]	1.47	1.49	1.47	1.46	1.42	1.47	1.49	1.47	1.47	1.46	1.50	1.43
<i>Gshape</i> [female]	5.54	5.52	5.68	5.24	4.62	5.54	5.53	5.54	5.41	5.36	4.49	4.70
<i>GCV</i> [female]	0.80	0.80	0.80	0.80	0.79	0.80	0.80	0.80	0.80	0.80	0.79	0.79
<i>Gobs</i>	1.24	1.24	1.24	1.24	1.24	1.24	1.24	1.24	1.24	1.24	1.24	1.24
<i>qdrift</i>	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
<i>qCR</i> [1]	0.0367	0.0399	0.0348	0.0499	0.0212	0.0363	0.0420	0.0366	0.0395	0.0758	0.0382	0.1322
<i>qFSU</i> [1]	0.0005	0.0006	0.0005	0.0006	0.0013	0.0005	0.0006	0.0005	0.0006	0.0010	0.0006	0.0021
<i>qFSU</i> [2]	0.0022	0.0030	0.0022	0.0024	0.0009	0.0022	0.0025	0.0022	0.0023	0.0030	0.0025	0.0025
<i>qCELR</i> [1]	0.0006	0.0006	0.0005	0.0006	—	0.0006	0.0007	0.0006	0.0007	0.0008	0.0007	0.0024
<i>qCELR</i> [2]	0.0030	0.0036	0.0030	0.0034	—	0.0030	0.0036	0.0030	0.0031	0.0066	0.0032	0.0034
<i>qPuerulus</i> [1]	—	—	1.23E-06	—	—	—	—	—	—	—	—	—
<i>qPuerulus</i> [2]	—	—	2.69E-06	—	—	—	—	—	—	—	—	—
<i>vuln1</i>	0.682	0.629	0.680	0.638	0.648	0.684	0.708	0.682	0.686	0.613	0.783	0.715
<i>vuln2</i>	0.582	0.594	0.559	0.585	0.188	0.563	0.517	0.570	0.537	0.613	0.366	0.457
<i>vuln3</i>	0.995	0.997	0.997	0.995	0.615	0.999	0.998	0.999	1.000	0.998	0.975	0.942
<i>vuln4</i>	0.999	0.999	0.993	0.999	0.554	0.997	0.985	0.997	0.999	0.999	0.986	0.766
<i>vuln5</i>	0.693	0.668	0.691	0.613	—	0.689	0.705	0.694	0.686	0.995	0.695	0.757
<i>vuln6</i>	0.108	0.107	0.110	0.128	—	0.108	0.095	0.107	0.129	0.128	0.098	0.108
<i>vuln7</i>	0.330	0.320	0.334	0.380	—	0.330	0.315	0.330	0.340	0.600	0.586	0.427
<i>vuln8</i>	0.287	0.286	0.290	0.324	—	0.290	0.269	0.287	0.298	0.337	0.485	0.358
<i>selL</i> male [1]	5.77	5.82	5.80	5.74	4.55	5.76	5.91	5.77	5.68	5.67	5.70	16.67
<i>selM</i> male [1]	56.70	56.87	56.57	56.40	55.18	56.67	57.14	56.71	56.41	56.25	56.09	82.16
<i>selL</i> female [1]	10.51	10.46	10.64	9.76	7.61	10.48	10.81	10.51	10.24	9.90	10.07	12.80
<i>selM</i> female [1]	68.60	68.90	68.41	67.19	63.69	68.49	69.33	68.61	67.79	67.42	67.92	78.18
<i>selL</i> male [2]	3.53	3.54	3.55	3.53	—	3.53	3.57	3.53	3.51	3.50	3.60	3.59
<i>selM</i> male [2]	54.62	54.63	54.61	54.46	—	54.64	54.72	54.63	54.51	54.52	54.69	54.95
<i>selL</i> female [2]	6.98	7.02	7.07	6.94	—	6.98	7.02	6.98	6.80	6.85	6.87	7.49
<i>selM</i> female [2]	61.60	61.60	61.53	62.22	—	61.65	61.45	61.60	61.54	62.27	62.26	62.55

	<i>base</i>	<i>novessel</i>	<i>lag3</i>	<i>catch_alt</i>	<i>single_area</i>	<i>illegalX2</i>	<i>upCPUE</i>	<i>process_error</i>	<i>trunc_weights</i>	<i>downCPUE</i>	<i>downSR</i>	<i>downLF</i>
Derived parameters: adjusted vulnerable biomass												
B_0 [1]	3 362	3 315	3 421	3 547	6 260	3 526	3 186	3 365	3 328	3 385	3 912	1 746
B_0 [2]	1 805	1 771	1 749	1 892	-	1 910	1 822	1 797	1 878	1 957	2 227	1 596
B_0 [total]	5 167	5 086	5 170	5 439	-	5 436	5 008	5 162	5 205	5 342	6 139	3 342
B_{0now} [1]	2 811	2 902	2 891	2 636	4 554	2 921	2 915	2 816	2 941	2 303	3 383	1 715
B_{0now} [2]	1 262	1 144	1 177	1 312	-	1 319	1 149	1 233	1 303	2 083	1 463	1 061
B_{0now} [total]	4 072	4 046	4 068	3 949	-	4 240	4 064	4 049	4 243	4 386	4 846	2 775
B_{MIN} [1]	567	507	612	519	395	586	430	569	494	655	484	140
B_{MIN} [2]	126	95	125	120	-	128	102	126	123	150	123	115
B_{MIN} [total]	693	602	738	639	-	714	533	695	616	805	607	256
B_{2020} [1]	1 608	1 681	1 730	1 636	576	1 667	1 402	1 619	1 482	1 277	1 559	454
B_{2020} [2]	362	286	344	328	-	368	249	346	352	949	319	316
B_{2020} [total]	1 970	1 967	2 074	1 965	-	2 035	1 651	1 965	1 834	2 225	1 878	770
B_{2020} / B_0 [1]	0.478	0.507	0.506	0.461	0.092	0.473	0.440	0.481	0.445	0.377	0.398	0.260
B_{2020} / B_0 [2]	0.200	0.162	0.197	0.174	-	0.193	0.137	0.192	0.187	0.485	0.143	0.198
B_{2020} / B_0 [total]	0.381	0.387	0.401	0.361	-	0.374	0.330	0.381	0.352	0.417	0.306	0.230
Derived parameters: spawning stock biomass (females only)												
SSB_0 [1]	2 739	2 679	2 807	2 614	3 811	2 861	2 512	2 743	2 616	2 686	2 347	1 975
SSB_0 [2]	1 469	1 428	1 434	1 394	-	1 548	1 432	1 463	1 475	1 552	1 337	1 184
SSB_0 [total]	4 208	4 107	4 241	4 008	-	4 409	3 944	4 205	4 090	4 238	3 684	3 159
SSB_{0now} [1]	2 219	2 273	2 301	1 887	2 704	2 297	2 230	2 224	2 241	1 769	1 971	1 852
SSB_{0now} [2]	996	895	936	940	-	1 037	877	973	992	1 600	853	753
SSB_{0now} [total]	3 215	3 168	3 238	2 826	-	3 334	3 107	3 198	3 233	3 369	2 824	2 605
SSB_{2020} [1]	2 001	2 030	2 053	1 361	1 642	2 041	1 877	2 005	1 920	1 607	1 719	1 352
SSB_{2020} [2]	824	735	753	645	-	844	703	807	798	1 278	521	612
SSB_{2020} [total]	2 825	2 765	2 806	2 006	-	2 885	2 580	2 811	2 718	2 885	2 239	1 964
SSB_{2020} / SSB_0 [1]	0.730	0.758	0.731	0.521	0.431	0.713	0.747	0.731	0.734	0.598	0.732	0.684
SSB_{2020} / SSB_0 [2]	0.561	0.515	0.525	0.463	-	0.545	0.491	0.551	0.541	0.823	0.389	0.517
SSB_{2020} / SSB_0 [total]	0.671	0.673	0.662	0.501	-	0.654	0.654	0.668	0.664	0.681	0.608	0.622
Derived parameters: total biomass												
B_{0tot} [1]	7 455	7 316	7 573	7 354	11 558	7 787	6 893	7 469	7 200	7 472	7 541	6 019
B_{0tot} [2]	3 997	3 900	3 867	3 922	-	4 212	3 930	3 983	4 059	4 316	4 295	3 608
B_{0tot} [total]	11 452	11 215	11 440	11 275	-	11 998	10 823	11 451	11 260	11 788	11 836	9 627
$B_{0totnow}$ [1]	6 208	6 379	6 380	5 447	8 384	6 425	6 282	6 226	6 339	5 065	6 499	5 876
$B_{0totnow}$ [2]	2 785	2 512	2 596	2 712	-	2 899	2 471	2 724	2 808	4 582	2 812	2 389
$B_{0totnow}$ [total]	8 993	8 891	8 976	8 159	-	9 324	8 753	8 950	9 147	9 648	9 311	8 266
$B_{2020tot}$ [1]	4 714	4 829	4 785	3 891	3 335	4 840	4 296	4 728	4 473	3 855	4 360	3 619
$B_{2020tot}$ [2]	1 852	1 642	1 614	1 549	-	1 902	1 536	1 811	1 798	3 077	1 465	1 705
$B_{2020tot}$ [total]	6 565	6 471	6 400	5 439	-	6 742	5 832	6 540	6 271	6 932	5 825	5 323
Other derived parameters												
$CPUE_{2019}$ [1]	6.754	8.369	7.236	7.884	0.670	6.915	6.952	6.802	6.307	11.867	6.922	1.960
$CPUE_{2019}$ [2]	1.186	1.095	1.159	1.210	-	1.187	0.953	1.133	1.178	7.235	1.093	1.099
H_{2019} [1]	12.514	12.062	12.210	4.787	21.666	12.340	13.135	12.444	13.518	12.921	11.790	13.209
H_{2019} [2]	2.791	3.153	2.658	2.244	-	2.819	3.235	2.848	2.894	1.803	3.101	3.071
H_{2019} [total]	15.305	15.215	14.869	7.031	-	15.159	16.370	15.292	16.412	14.724	14.892	16.281
B_{male} / B_{female} [1]	1.097	1.116	1.113	1.442	0.661	1.108	1.038	1.099	1.067	1.106	1.105	1.138
B_{male} / B_{female} [2]	0.837	0.807	0.818	0.907	-	0.839	0.763	0.831	0.833	1.038	0.943	0.977

Table 9: List of maximum *a posteriori* (MAP) sensitivity runs. Each model run below the base model run implements a single change to the base model run.

Model name	Model description
<i>base</i>	The base case model run as defined in Section 2.5.1. This is a 2-region model, the <i>qdrift</i> parameter is fixed at 1%, the CPUE series includes fishing vessel as an explanatory variable, and the model was not fitted to puerulus data
<i>novessel</i>	Fitted to a CPUE series that does not include fishing vessel as an explanatory variable
<i>lag3</i>	Fitted to the puerulus index with a 3-year lag
<i>catch_alt</i>	Catch split using 80/20% for pre-1963 catches (from 53/47%)
<i>single_area</i>	Single-region model
<i>illegalX2</i>	Doubled the illegal catch
<i>upCPUE</i>	Doubled the CELR CPUE likelihood weights
<i>process_error</i>	Reduced additive CELR process error from 0.25 to 0 for last 5 years
<i>trunc_weights</i>	Truncated relative LB LF weights to maximum of 25 (i.e., sum of weights across all three sexes cannot be greater than 25) in an attempt to reduce increasing trend in LF weights
<i>downCPUE</i>	Down-weighted all CPUE series, by multiplying the weights by 0.1
<i>downSR</i>	Down-weighted the sex ratio information by multiplying the weights by 0.1
<i>downLF</i>	Down-weighted length frequency data information by multiplying the weights by 0.1

Table 10A: MCMC outputs, reporting the 5%, 50% (median; highlighted in yellow), and 95% quantiles of the posterior distribution, showing likelihoods, standard deviation of normalised residuals (SDNRs), median absolute residuals (MARs), likelihood weights, parameter estimates, and reference points. These values are by region where appropriate (regional values denoted by [1] and [2]) for the base case and three sensitivity runs. Growth increment values in mm TW, biomass values in tonnes, and R_0 in numbers. ‘–’: not applicable. Values in grey for the $qdrift$ parameter were fixed in all model runs. Most of the projected values in this table differ slightly (i.e., 2–3 decimal places) from tables presented elsewhere (e.g., Fisheries New Zealand 2020) because the projections were repeated after the reference level (B_R) was finalised. The repeated projections were based on a new set of stochastic recruitment deviates which resulted in minor differences in projected values. (Continued on next two pages)

	base			lag3			novessel			catch_alt		
	5%	50%	95%	5%	50%	95%	5%	50%	95%	5%	50%	95%
Likelihoods												
Total	18 730	18 750	18 760	19 250	19 270	19 280	18 380	18 390	18 410	18 730	18 740	18 760
Prior	110	142	174	113	141	173	114	144	176	104	135	166
Tags	8 096	8 124	8 152	8 097	8 124	8 150	8 098	8 125	8 151	8 094	8 121	8 147
Sex ratio	4 095	4 101	4 109	4 098	4 104	4 111	4 047	4 053	4 060	4 102	4 108	4 117
LFs	6 599	6 609	6 620	7 105	7 115	7 126	6 290	6 300	6 312	6 591	6 602	6 614
CR	-18.710	-17.250	-14.160	-18.640	-17.210	-14.220	-18.770	-17.330	-14.320	-19.130	-17.400	-14.050
FSU [1]	-36.800	-33.750	-30.000	-36.450	-33.700	-29.690	-40.570	-37.800	-33.140	-37.050	-34.180	-30.230
FSU [2]	-41.970	-39.270	-35.190	-42.230	-39.420	-35.300	-42.170	-39.320	-34.510	-40.530	-37.790	-33.550
CELR [1]	-86.060	-80.270	-72.670	-84.280	-78.400	-71.790	-81.090	-75.480	-67.870	-84.900	-79.980	-73.750
CELR [2]	-65.200	-57.920	-48.990	-64.990	-58.360	-49.680	-70.370	-63.060	-54.390	-60.520	-53.420	-45.430
Puerulus	–	–	–	1.450	9.256	18.370	–	–	–	–	–	–
Standard deviation of normalised residuals (SDNR)												
Tag	1.220	1.240	1.250	1.220	1.233	1.248	1.220	1.233	1.249	1.221	1.237	1.253
Sex ratio	1.020	1.050	1.100	1.028	1.062	1.107	1.021	1.058	1.103	1.046	1.082	1.123
LFs	0.510	0.820	2.780	0.508	0.806	2.318	0.538	0.823	2.303	0.534	0.888	2.315
CR	0.940	1.060	1.290	0.950	1.066	1.270	0.930	1.054	1.261	0.891	1.044	1.308
FSU [1]	0.920	1.080	1.230	0.946	1.076	1.232	0.900	1.037	1.217	0.921	1.056	1.221
FSU [2]	0.960	1.090	1.240	0.946	1.076	1.252	0.956	1.087	1.274	1.032	1.151	1.314
CELR [1]	1.010	1.110	1.220	1.049	1.142	1.233	0.984	1.074	1.187	1.034	1.113	1.208
CELR [2]	0.930	1.060	1.210	0.937	1.052	1.183	1.030	1.148	1.273	1.008	1.121	1.240
Puerulus	–	–	–	1.210	1.304	1.404	–	–	–	–	–	–
Median of absolute residual (MAR)												
Tag	0.550	0.550	0.560	0.550	0.554	0.561	0.550	0.555	0.561	0.547	0.554	0.561
Sex ratio	0.510	0.540	0.580	0.513	0.546	0.581	0.516	0.548	0.585	0.505	0.544	0.593
LFs	0.070	0.070	0.070	0.070	0.072	0.073	0.065	0.067	0.069	0.065	0.067	0.069
CR	0.260	0.580	0.970	0.270	0.570	0.994	0.270	0.562	0.941	0.284	0.607	1.046
FSU [1]	0.550	0.770	1.020	0.575	0.783	1.022	0.453	0.657	0.903	0.513	0.727	0.994
FSU [2]	0.540	0.770	1.020	0.522	0.771	1.018	0.560	0.805	1.028	0.562	0.795	1.017
CELR [1]	0.510	0.670	0.850	0.565	0.733	0.897	0.555	0.703	0.902	0.592	0.705	0.851
CELR [2]	0.640	0.800	0.990	0.658	0.827	1.011	0.728	0.879	1.023	0.759	0.906	1.082
Puerulus	–	–	–	0.690	0.849	0.992	–	–	–	–	–	–
Parameters												
R_0 [1]	955 700	1 162 000	1 483 000	947 300	1 182 000	1 488 000	929 300	1 124 000	1 394 000	800 100	985 100	1 251 000
R_0 [2]	533 400	615 900	704 700	516 500	596 600	686 500	510 400	589 000	667 200	444 800	519 000	602 800
M	0.1700	0.1800	0.2000	0.1700	0.1849	0.2012	0.1700	0.1821	0.1983	0.150	0.167	0.184
q -drift	–	0.010	–	–	0.010	–	–	0.010	–	–	0.010	–
qCR [1]	3.000E-2	3.553E-2	5.062E-2	3.000E-2	3.373E-2	4.814E-2	3.000E-2	3.908E-2	5.464E-2	3.166E-2	4.763E-2	7.957E-2
$qFSU$ [1]	3.980E-4	5.010E-4	6.120E-4	3.840E-4	4.740E-4	5.870E-4	4.590E-4	5.710E-4	7.100E-4	4.270E-4	5.440E-4	6.740E-4
$qFSU$ [2]	1.669E-3	2.046E-3	2.501E-3	1.674E-3	2.017E-3	2.446E-3	2.266E-3	2.719E-3	3.327E-3	1.776E-3	2.137E-3	2.595E-3
$qCELR$ [1]	4.440E-4	5.670E-4	7.030E-4	4.250E-4	5.360E-4	6.630E-4	4.700E-4	5.850E-4	7.130E-4	4.890E-4	6.260E-4	7.750E-4
$qCELR$ [2]	2.438E-3	2.853E-3	3.302E-3	2.447E-3	2.839E-3	3.284E-3	2.941E-3	3.396E-3	3.911E-3	2.698E-3	3.145E-3	3.623E-3
$qPuerulus$ [1]	–	–	–	9.685E-7	1.256E-6	1.580E-6	–	–	–	–	–	–
$qPuerulus$ [2]	–	–	–	2.284E-6	2.764E-6	3.258E-6	–	–	–	–	–	–
$mat50$	43.330	46.020	48.360	41.980	45.260	47.510	43.170	46.180	48.370	44.140	47.060	49.520
$mat95add$	5.960	11.400	18.190	4.984	10.480	16.850	6.230	12.000	18.170	7.350	13.990	20.630
$Galpha$ [male]	3.230	3.300	3.360	3.250	3.321	3.393	3.230	3.301	3.368	3.235	3.306	3.377
$Gbeta$ [male]	2.380	2.600	2.800	2.390	2.607	2.787	2.430	2.628	2.828	0.777	0.796	0.817
$Gshape$ [male]	4.370	4.900	5.470	4.630	5.218	5.808	4.380	4.932	5.484	4.472	5.053	5.596
GCV [male]	0.560	0.570	0.580	0.560	0.569	0.581	0.560	0.569	0.580	0.557	0.569	0.580
$Galpha$ [female]	3.630	3.770	3.910	3.700	3.845	3.991	3.600	3.756	3.889	3.51	3.682	3.849
$Gbeta$ [female]	1.390	1.470	1.560	1.390	1.466	1.550	1.420	1.488	1.571	0.777	0.796	0.817
$Gshape$ [female]	5.200	5.580	5.930	5.400	5.721	6.044	5.170	5.556	5.921	4.777	5.32	5.698
GCV [female]	0.780	0.800	0.820	0.780	0.799	0.818	0.780	0.798	0.816	0.777	0.796	0.817
$Gobs$	1.210	1.240	1.260	1.210	1.237	1.261	1.210	1.237	1.260	0.777	0.796	0.817

	base			lag3			novessel			catch_alt		
	5%	50%	95%	5%	50%	95%	5%	50%	95%	5%	50%	95%
<i>vuln1</i>	0.640	0.680	0.720	0.640	0.681	0.713	0.590	0.628	0.667	0.601	0.638	0.676
<i>vuln2</i>	0.370	0.590	0.860	0.378	0.595	0.872	0.385	0.599	0.875	0.392	0.613	0.895
<i>vuln3</i>	0.910	0.980	1.000	0.914	0.979	0.999	0.898	0.970	0.997	0.875	0.960	0.997
<i>vuln4</i>	0.900	0.960	1.000	0.895	0.966	0.997	0.912	0.973	0.998	0.947	0.987	0.999
<i>vuln5</i>	0.660	0.700	0.740	0.652	0.694	0.737	0.628	0.671	0.710	0.579	0.618	0.661
<i>vuln6</i>	0.070	0.120	0.210	0.074	0.128	0.211	0.068	0.120	0.204	0.082	0.145	0.234
<i>vuln7</i>	0.290	0.340	0.400	0.292	0.346	0.407	0.277	0.332	0.396	0.323	0.389	0.473
<i>vuln8</i>	0.260	0.300	0.340	0.257	0.300	0.345	0.253	0.296	0.346	0.284	0.332	0.389
<i>selL</i> male [1]	5.020	5.900	6.950	5.090	5.963	7.011	5.080	5.993	7.135	5.047	5.923	6.955
<i>selM</i> male [1]	55.500	56.940	58.600	55.470	56.830	58.460	55.670	57.190	59.050	55.390	56.690	58.290
<i>selL</i> female [1]	8.960	10.580	12.560	9.190	10.630	12.410	9.030	10.550	12.410	8.497	9.835	11.490
<i>selM</i> female [1]	66.080	68.560	71.520	66.030	68.260	70.890	66.440	68.910	71.700	65.190	67.160	69.490
<i>selL</i> male [2]	3.130	3.550	4.020	3.200	3.569	4.047	3.170	3.551	4.014	3.149	3.551	4.005
<i>selM</i> male [2]	53.940	54.570	55.330	53.900	54.540	55.270	53.930	54.560	55.290	53.820	54.440	55.110
<i>selL</i> female [2]	6.000	7.090	8.230	6.050	7.190	8.397	6.080	7.088	8.416	6.080	7.065	8.237
<i>selM</i> female [2]	60.210	61.740	63.280	60.180	61.620	63.160	60.330	61.720	63.320	60.940	62.330	63.980
Derived parameters: adjusted vulnerable biomass												
B_0 [1]	2 810	3 195	3 636	2 901	3 279	3 743	2 779	3 129	3 549	3 003	3 364	3 769
B_0 [2]	1 463	1 679	1 929	1 445	1 660	1 894	1 419	1 640	1 864	1 539	1 765	2 008
B_0 [total]	4 410	4 879	5 438	4 482	4 929	5 449	4 290	4 775	5 297	4 686	5 124	5 651
B_{0now} [1]	2 347	2 786	3 347	2 468	2 873	3 346	2 436	2 885	3 396	2 212	2 649	3 158
B_{0now} [2]	1 064	1 254	1 495	1 012	1 177	1 360	964	1 127	1 336	1 107	1 303	1 578
B_{0now} [total]	3 532	4 059	4 651	3 601	4 059	4 563	3512	4 016	4 588	3 462	3 973	4 548
B_{MIN} [1]	469.2	588	745.8	500.1	619.5	777.7	417.3	516.6	640.3	435.8	537.8	685.4
B_{MIN} [2]	61.46	127.9	153.3	62.56	125.8	155.3	54.69	90.64	112.3	109.8	127.4	148.1
B_{MIN} [total]	579.5	704.7	877.6	604	737.3	908.7	498.3	603.1	735.2	558.2	664.9	818.8
B_R [1]	–	475.759	–	–	475.759	–	–	475.759	–	–	475.759	–
B_R [2]	–	195.430	–	–	195.430	–	–	195.430	–	–	195.430	–
B_R [total]	–	671.189	–	–	671.189	–	–	671.189	–	–	671.189	–
B_{2020} [1]	1 260	1 650	2 222	1 327	1 732	2 262	1 319	1 713	2 242	1 255	1 686	2 205
B_{2020} [2]	305	382	477	287	360	442	240	302	369	277	351	436
B_{2020} [total]	1 632	2 031	2 604	1 687	2 092	2 658	1 623	2 011	2 546	1 615	2 038	2 579
B_{2024} [1]	413	825	1 403	486	889	1 445	466	860	1 441	583	1 078	1 620
B_{2024} [2]	332	496	724	277	427	597	240	390	574	309	470	690
B_{2024} [total]	869	1 340	1 965	880	1 321	1 885	817	1 262	1 862	1 069	1 557	2 156
B_{2020} / B_0 [1]	0.410	0.517	0.649	0.420	0.528	0.653	0.450	0.546	0.673	0.381	0.505	0.637
B_{2020} / B_0 [2]	0.176	0.226	0.289	0.170	0.217	0.269	0.145	0.184	0.232	0.156	0.198	0.257
B_{2020} / B_0 [total]	0.340	0.418	0.521	0.349	0.423	0.519	0.349	0.421	0.519	0.311	0.400	0.498
B_{2024} / B_0 [1]	0.137	0.257	0.424	0.156	0.272	0.423	0.155	0.274	0.445	0.179	0.325	0.475
B_{2024} / B_0 [2]	0.199	0.294	0.434	0.173	0.253	0.367	0.149	0.238	0.351	0.173	0.267	0.397
B_{2024} / B_0 [total]	0.182	0.274	0.392	0.184	0.268	0.374	0.178	0.265	0.379	0.204	0.307	0.418
B_{2020} / B_{0now} [1]	0.490	0.589	0.716	0.510	0.607	0.714	0.500	0.596	0.711	0.521	0.637	0.768
B_{2020} / B_{0now} [2]	0.254	0.303	0.361	0.257	0.308	0.354	0.219	0.268	0.313	0.223	0.268	0.318
B_{2020} / B_{0now} [total]	0.421	0.500	0.605	0.440	0.520	0.608	0.424	0.504	0.598	0.423	0.515	0.621
B_{2024} / B_{0now} [1]	0.167	0.293	0.446	0.189	0.310	0.453	0.183	0.299	0.454	0.256	0.407	0.545
B_{2024} / B_{0now} [2]	0.289	0.392	0.522	0.259	0.358	0.481	0.234	0.344	0.462	0.259	0.362	0.482
B_{2024} / B_{0now} [total]	0.235	0.327	0.443	0.233	0.325	0.434	0.221	0.315	0.424	0.286	0.393	0.507
B_{2024} / B_{2020} [1]	0.303	0.494	0.708	0.339	0.511	0.701	0.324	0.503	0.719	0.436	0.634	0.822
B_{2024} / B_{2020} [2]	0.964	1.288	1.762	0.877	1.169	1.565	0.877	1.287	1.754	0.972	1.339	1.809
B_{2024} / B_{2020} [total]	0.485	0.654	0.832	0.480	0.628	0.793	0.468	0.624	0.812	0.613	0.756	0.920
B_{2020} / B_R [1]	2.648	3.468	4.669	2.790	3.643	4.753	2.773	3.601	4.712	2.638	3.544	4.634
B_{2020} / B_R [2]	1.559	1.955	2.438	1.469	1.845	2.260	1.229	1.545	1.889	1.417	1.797	2.232
B_{2020} / B_R [total]	2.43	3.027	3.883	2.511	3.116	3.958	2.417	2.998	3.799	2.406	3.037	3.842
B_{2024} / B_R [1]	0.868	1.733	2.949	1.022	1.869	3.038	0.979	1.808	3.028	1.226	2.265	3.406
B_{2024} / B_R [2]	1.697	2.538	3.707	1.419	2.184	3.057	1.229	1.995	2.935	1.582	2.406	3.529
B_{2024} / B_R [total]	1.295	1.996	2.927	1.310	1.968	2.809	1.216	1.880	2.774	1.593	2.32	3.212
Derived parameters: spawning biomass (females only)												
SSB_0 [1]	2 337	2 671	3 123	2 393	2 737	3 167	2 293	2 597	2 968	2 258	2 551	2 914
SSB_0 [2]	1 261	1 408	1 557	1 242	1 384	1 516	1 224	1 357	1 493	1 208	1 341	1 474
SSB_0 [total]	3 721	4 079	4 554	3 745	4 121	4 563	3 601	3 949	4 357	3 565	3 893	4 271
SSB_{0now} [1]	1 905	2 264	2 797	1 985	2 326	2 748	1 960	2 319	2 792	1 594	1 948	2 387
SSB_{0now} [2]	877	1 017	1 202	835	953	1 082	787	905	1 053	835	964	1 132
SSB_{0now} [total]	2 875	3 298	3 832	2 911	3 283	3 726	2 848	3 231	3 735	2 538	2 923	3 389
SSB_{2020} [1]	1 708	2 057	2 587	1 749	2 092	2 550	1 765	2 093	2 586	1 107	1 454	1 892
SSB_{2020} [2]	710	833	997	650	764	894	625	732	875	553	669	821
SSB_{2020} [total]	2 500	2 900	3 459	2 496	2 869	3 352	2 470	2 832	3 344	1 742	2 125	2 584
SSB_{2024} [1]	1 368	1 848	2 457	1 453	1 900	2 501	1 434	1 890	2 493	693	1 072	1 538
SSB_{2024} [2]	686	868	1 119	629	788	981	583	753	950	559	729	955

	base			lag3			novessel			catch_alt		
	5%	50%	95%	5%	50%	95%	5%	50%	95%	5%	50%	95%
<i>SSB</i> ₂₀₂₄ [total]	2 209	2 731	3 403	2 190	2 688	3 334	2 153	2 646	3 300	1 377	1 808	2 347
<i>SSB</i> ₂₀₂₀ / <i>SSB</i> ₀ [1]	0.670	0.775	0.905	0.670	0.771	0.877	0.700	0.808	0.935	0.459	0.571	0.685
<i>SSB</i> ₂₀₂₀ / <i>SSB</i> ₀ [2]	0.508	0.595	0.701	0.479	0.552	0.642	0.464	0.541	0.649	0.413	0.501	0.614
<i>SSB</i> ₂₀₂₀ / <i>SSB</i> ₀ [total]	0.641	0.7 11	0.810	0.625	0.697	0.774	0.639	0.718	0.811	0.462	0.547	0.635
<i>SSB</i> ₂₀₂₄ / <i>SSB</i> ₀ [1]	0.538	0.690	0.890	0.546	0.694	0.865	0.578	0.727	0.928	0.288	0.425	0.573
<i>SSB</i> ₂₀₂₄ / <i>SSB</i> ₀ [2]	0.494	0.619	0.792	0.460	0.571	0.719	0.434	0.556	0.704	0.419	0.543	0.710
<i>SSB</i> ₂₀₂₄ / <i>SSB</i> ₀ [total]	0.554	0.668	0.803	0.549	0.655	0.770	0.561	0.670	0.806	0.366	0.467	0.582
<i>SSB</i> ₂₀₂₀ / <i>SSB</i> _{0now} [1]	0.830	0.911	1.000	0.840	0.906	0.974	0.830	0.905	0.985	0.656	0.740	0.836
<i>SSB</i> ₂₀₂₀ / <i>SSB</i> _{0now} [2]	0.772	0.817	0.879	0.751	0.800	0.860	0.757	0.809	0.866	0.628	0.693	0.759
<i>SSB</i> ₂₀₂₀ / <i>SSB</i> _{0now} [total]	0.828	0.882	0.949	0.823	0.875	0.929	0.823	0.877	0.940	0.660	0.725	0.799
<i>SSB</i> ₂₀₂₄ / <i>SSB</i> _{0now} [1]	0.683	0.811	0.968	0.691	0.816	0.971	0.692	0.815	0.978	0.413	0.546	0.692
<i>SSB</i> ₂₀₂₄ / <i>SSB</i> _{0now} [2]	0.738	0.851	1.005	0.715	0.826	0.979	0.709	0.828	0.969	0.640	0.754	0.895
<i>SSB</i> ₂₀₂₄ / <i>SSB</i> _{0now} [total]	0.732	0.829	0.946	0.719	0.820	0.939	0.721	0.820	0.940	0.520	0.615	0.733
<i>SSB</i> ₂₀₂₄ / <i>SSB</i> ₂₀₂₀ [1]	0.769	0.889	1.030	0.784	0.899	1.048	0.781	0.899	1.056	0.600	0.736	0.891
<i>SSB</i> ₂₀₂₄ / <i>SSB</i> ₂₀₂₀ [2]	0.912	1.036	1.199	0.904	1.029	1.183	0.894	1.023	1.181	0.953	1.086	1.262
<i>SSB</i> ₂₀₂₄ / <i>SSB</i> ₂₀₂₀ [total]	0.844	0.936	1.043	0.843	0.936	1.055	0.840	0.933	1.054	0.750	0.850	0.965
Derived parameters: total biomass												
<i>B</i> _{0tot} [1]	6 315	7 201	8 259	6 477	7 319	8 368	6 271	7 005	7 945	6 342	7 092	7 985
<i>B</i> _{0tot} [2]	3 375	3 790	4 182	3 323	3 699	4 065	3 281	3 671	4 044	3 326	3 730	4 106
<i>B</i> _{0tot} [total]	10 070	10 990	12 160	10 100	11 000	12 120	9 864	10 680	11 660	9 980	10 830	11 730
<i>B</i> _{0totnow} [1]	5 307	6 263	7 605	5 489	6 396	7 487	5 474	6 466	7 630	4 620	5 560	6 726
<i>B</i> _{0totnow} [2]	2 437	2 810	3 329	2 297	2 617	2 958	2 197	2 514	2 916	2 370	2 741	3 239
<i>B</i> _{0totnow} [total]	8 043	9 102	10 480	8 084	9 018	10 150	7 952	8 978	10 220	7 340	8 345	9 575
<i>B</i> _{2020tot} [1]	3 833	4 803	6 335	3 908	4 863	6 134	4 029	4 949	6 254	3 057	4 040	5 221
<i>B</i> _{2020tot} [2]	1 466	1 803	2 256	1 321	1 615	1 953	1 280	1 563	1 919	1 246	1 540	1 945
<i>B</i> _{2020tot} [total]	5 580	6 622	8 287	5 457	6 491	7 854	5 529	6 508	7 907	4 552	5 598	6 885
<i>B</i> _{2024tot} [1]	2781	3953	5493	2937	4046	5548	2 933	4 071	5 606	2 081	3 172	4 431
<i>B</i> _{2024tot} [2]	1417	1878	2492	1293	1673	2139	1188	1600	2066	1 227	1 653	2 199
<i>B</i> _{2024tot} [total]	4554	5843	7517	4500	5714	7274	4432	5680	7269	3 666	4 819	6 284
<i>B</i> _{2020tot} / <i>B</i> _{0tot} [1]	0.560	0.668	0.821	0.560	0.669	0.791	0.590	0.706	0.847	0.450	0.571	0.699
<i>B</i> _{2020tot} / <i>B</i> _{0tot} [2]	0.389	0.477	0.594	0.358	0.437	0.537	0.349	0.424	0.532	0.331	0.412	0.529
<i>B</i> _{2020tot} / <i>B</i> _{0tot} [total]	0.525	0.603	0.720	0.510	0.591	0.682	0.525	0.612	0.717	0.426	0.519	0.615
<i>B</i> _{2024tot} / <i>B</i> _{0tot} [1]	0.403	0.549	0.722	0.417	0.555	0.728	0.433	0.576	0.766	0.301	0.448	0.598
<i>B</i> _{2024tot} / <i>B</i> _{0tot} [2]	0.375	0.494	0.655	0.348	0.453	0.588	0.328	0.436	0.569	0.328	0.441	0.602
<i>B</i> _{2024tot} / <i>B</i> _{0tot} [total]	0.426	0.532	0.661	0.417	0.521	0.640	0.423	0.531	0.658	0.343	0.448	0.567
<i>B</i> _{2020tot} / <i>B</i> _{0totnow} [1]	0.680	0.770	0.878	0.680	0.767	0.864	0.680	0.768	0.865	0.628	0.722	0.832
<i>B</i> _{2020tot} / <i>B</i> _{0totnow} [2]	0.576	0.637	0.727	0.547	0.615	0.701	0.554	0.615	0.701	0.491	0.559	0.647
<i>B</i> _{2020tot} / <i>B</i> _{0totnow} [total]	0.666	0.729	0.816	0.654	0.723	0.798	0.660	0.728	0.804	0.591	0.670	0.757
<i>B</i> _{2024tot} / <i>B</i> _{0totnow} [1]	0.500	0.626	0.783	0.503	0.630	0.789	0.500	0.630	0.786	0.428	0.563	0.707
<i>B</i> _{2024tot} / <i>B</i> _{0totnow} [2]	0.548	0.664	0.816	0.529	0.639	0.786	0.517	0.634	0.764	0.489	0.599	0.736
<i>B</i> _{2024tot} / <i>B</i> _{0totnow} [total]	0.538	0.642	0.761	0.536	0.635	0.756	0.531	0.631	0.751	0.476	0.577	0.691
<i>B</i> _{2024tot} / <i>B</i> _{2020tot} [1]	0.687	0.811	0.968	0.694	0.820	0.981	0.691	0.818	0.971	0.651	0.778	0.916
<i>B</i> _{2024tot} / <i>B</i> _{2020tot} [2]	0.905	1.030	1.214	0.891	1.031	1.200	0.875	1.015	1.204	0.935	1.064	1.238
<i>B</i> _{2024tot} / <i>B</i> _{2020tot} [total]	0.786	0.877	0.988	0.774	0.875	1.005	0.768	0.869	0.992	0.761	0.862	0.972
Other derived parameters												
<i>CPUE</i> ₂₀₁₉ [1]	4.740	6.559	8.831	5.130	6.795	9.212	6.090	8.048	10.680	5.565	7.536	10.100
<i>CPUE</i> ₂₀₁₉ [2]	1.018	1.179	1.382	0.996	1.149	1.326	0.929	1.094	1.274	1.043	1.209	1.420
<i>CPUE</i> ₂₀₂₄ [1]	1.407	2.925	4.946	1.664	3.123	5.133	2.001	3.676	6.114	2.885	4.791	7.125
<i>CPUE</i> ₂₀₂₄ [2]	1.176	1.685	2.420	0.987	1.414	1.960	0.999	1.568	2.250	1.239	1.770	2.563
<i>H</i> ₂₀₁₉ [1]	11.000	12.110	13.530	10.890	11.980	13.280	10.750	11.840	12.940	4.337	4.803	5.421
<i>H</i> ₂₀₁₉ [2]	2.345	2.763	3.253	2.298	2.629	3.019	2.627	3.098	3.679	1.872	2.196	2.614
<i>H</i> ₂₀₁₉ [total]	13.660	14.890	16.310	13.450	14.640	15.900	13.730	14.920	16.240	6.422	7.024	7.746
<i>H</i> ₂₀₂₄ [1]	22.030	27.180	36.960	21.890	26.990	35.130	21.990	27.110	35.440	3.380	4.522	6.909
<i>H</i> ₂₀₂₄ [2]	1.649	2.253	2.894	1.722	2.386	3.079	1.764	2.412	3.179	1.408	1.999	2.672
<i>H</i> ₂₀₂₄ [total]	24.270	29.470	39.350	24.290	29.460	37.670	24.350	29.490	37.610	5.243	6.586	8.991
<i>B</i> _{male} / <i>B</i> _{female} [1]	1.030	1.097	1.163	1.040	1.108	1.176	1.040	1.112	1.177	1.346	1.420	1.478
<i>B</i> _{male} / <i>B</i> _{female} [2]	0.776	0.843	0.905	0.757	0.826	0.884	0.738	0.812	0.879	0.839	0.915	0.981

Table 10B: Probabilities calculated from the MCMC posteriors for the indicated derived parameters. These probabilities are by region where appropriate (regional values denoted by [1] and [2]) for the base case and three sensitivity runs. Some of the projected probabilities in this table differ from those published in Table 8 of the CRA 5 chapter of Fisheries New Zealand (2020) for the reason explained in the Table 10A caption.

Probabilities	base	lag3	novessel	catch_alt
$P(B_{2020} > B_{MIN})[1]$	1.000	1.000	1.000	1.000
$P(B_{2020} > B_{MIN})[2]$	1.000	1.000	1.000	1.000
$P(B_{2020} > B_{MIN})[total]$	1.000	1.000	1.000	1.000
$P(SSB_{2020} < 20\%SSB_{0now})[1]$	0.000	0.000	0.000	0.000
$P(SSB_{2020} < 20\%SSB_{0now})[2]$	0.000	0.000	0.000	0.000
$P(SSB_{2020} < 20\%SSB_{0now})[total]$	0.000	0.000	0.000	0.000
$P(SSB_{2020} < 10\%SSB_{0now})[1]$	0.000	0.000	0.000	0.000
$P(SSB_{2020} < 10\%SSB_{0now})[2]$	0.000	0.000	0.000	0.000
$P(SSB_{2020} < 10\%SSB_{0now})[total]$	0.000	0.000	0.000	0.000
$P(SSB_{2024} < 20\%SSB_0)[1]$	0.000	0.000	0.000	0.000
$P(SSB_{2024} < 20\%SSB_0)[2]$	0.000	0.000	0.000	0.000
$P(SSB_{2024} < 20\%SSB_0)[total]$	0.000	0.000	0.000	0.000
$P(SSB_{2024} < 10\%SSB_0)[1]$	0.000	0.000	0.000	0.000
$P(SSB_{2024} < 10\%SSB_0)[2]$	0.000	0.000	0.000	0.000
$P(SSB_{2024} < 10\%SSB_0)[total]$	0.000	0.000	0.000	0.000
$P(SSB_{2024} < 20\%SSB_{0now})[1]$	0.000	0.000	0.000	0.000
$P(SSB_{2024} < 20\%SSB_{0now})[2]$	0.000	0.000	0.000	0.000
$P(SSB_{2024} < 20\%SSB_{0now})[total]$	0.000	0.000	0.000	0.000
$P(SSB_{2024} < 10\%SSB_{0now})[1]$	0.000	0.000	0.000	0.000
$P(SSB_{2024} < 10\%SSB_{0now})[2]$	0.000	0.000	0.000	0.000
$P(SSB_{2024} < 10\%SSB_{0now})[total]$	0.000	0.000	0.000	0.000
$P(B_{2024} > B_{2020})[1]$	0.000	0.000	0.000	0.002
$P(B_{2024} > B_{2020})[2]$	0.914	0.792	0.876	0.941
$P(B_{2024} > B_{2020})[total]$	0.003	0.000	0.002	0.018
$P(SSB_{2024} > SSB_{2020})[1]$	0.101	0.116	0.110	0.005
$P(SSB_{2024} > SSB_{2020})[2]$	0.689	0.637	0.611	0.848
$P(SSB_{2024} > SSB_{2020})[total]$	0.150	0.163	0.145	0.020
$P(B_{2024tot} > B_{2020tot})[1]$	0.022	0.033	0.036	0.010
$P(B_{2024tot} > B_{2020tot})[2]$	0.652	0.646	0.568	0.765
$P(B_{2024tot} > B_{2020tot})[total]$	0.037	0.054	0.044	0.016
$P(B_{2020} > B_R)[1]$	1.000	1.000	1.000	1.000
$P(B_{2020} > B_R)[2]$	1.000	1.000	1.000	1.000
$P(B_{2020} > B_R)[total]$	1.000	1.000	1.000	1.000
$P(B_{2024} > B_R)[1]$	0.915	0.958	0.943	0.983
$P(B_{2024} > B_R)[2]$	0.999	0.998	0.988	1.000
$P(B_{2024} > B_R)[total]$	0.992	0.996	0.992	0.999

Table 11: Catch (tonnes) in the final model year and projected catch assumptions (highlighted in grey) by fishing year, region, and fishing sector.

Fishing year	Commercial	Recreational	Customary	Illegal
Region 1				
2019	272.16	60.24	8.07	18.92
2020	293.44	60.24	8.07	18.92
2021–2024	282.31	60.24	8.07	18.92
Region 2				
2019	65.02	14.44	1.93	4.54
2020	70.36	14.44	1.93	4.54
2021–2024	67.69	14.44	1.93	4.54
Total				
2019	337.18	74.68	10.00	23.46
2020	363.80	74.68	10.00	23.46
2021–2024	350.00	74.68	10.00	23.46

7. FIGURES

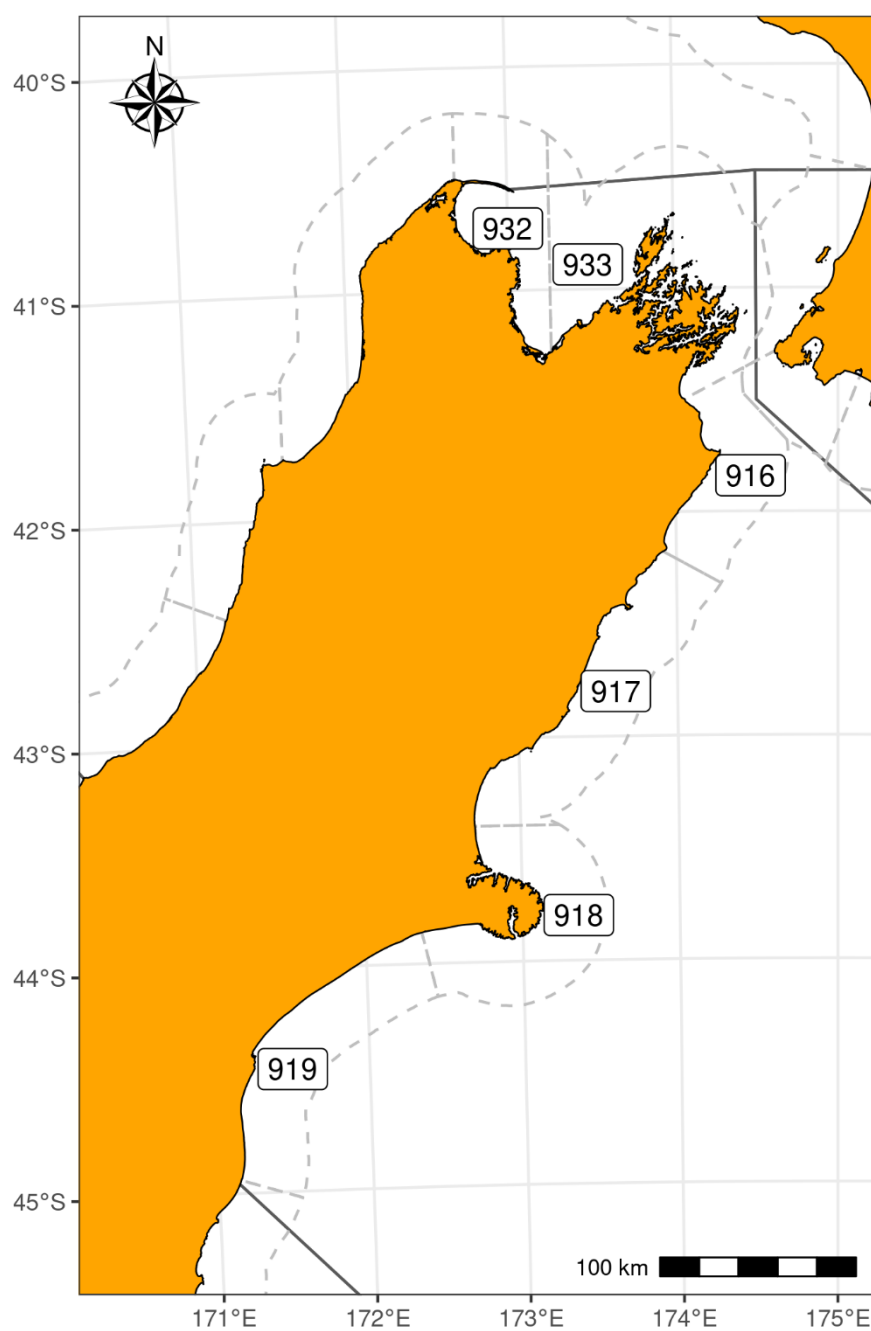


Figure 1: The CRA 5 QMA and its statistical areas off the east coast of the South Island. The QMA boundaries are defined by solid black lines and the statistical area boundaries by dashed grey lines.

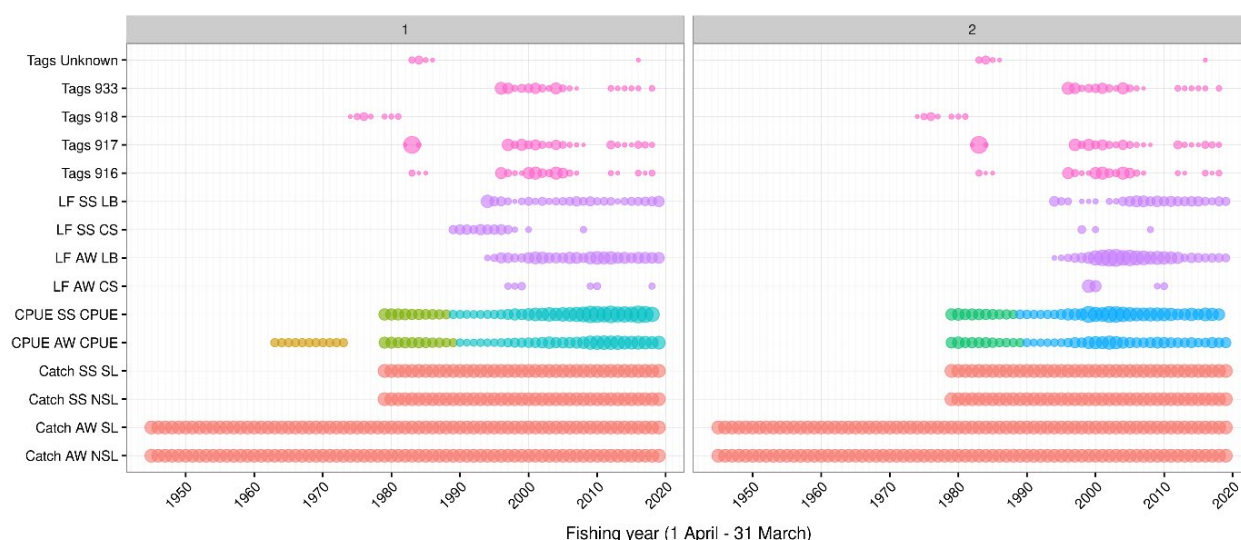


Figure 2: Data extent by fishing year used in the CRA 5 stock assessment for each region (1 = statistical areas 917+918+919, 2 = statistical areas 916+932+933). The size of the bubbles represents the relative number of recaptured tags, the effective sample size for length frequency distributions, the standard deviation for CPUE, or a fixed size for catch. Bubble colours vary for the different data sets (CPUE colours: CR = gold, FSU = green, and CELR = teal). See Starr *et al.* (2021) for a detailed description of these data.

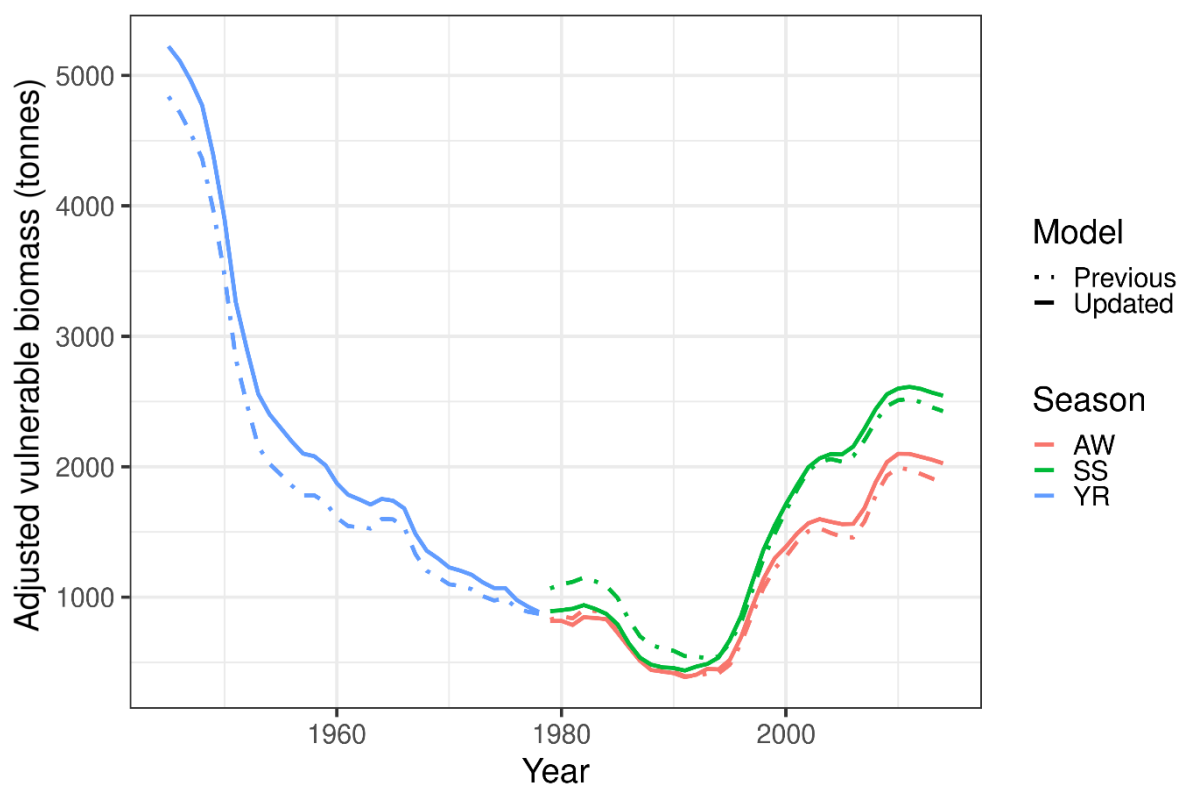


Figure 3: Comparison of the adjusted vulnerable biomass estimated using the LSD model in 2020 (i.e., model run 1_base2015_noDD, solid line) and the MLSM in the 2015 stock assessment (dashed line).

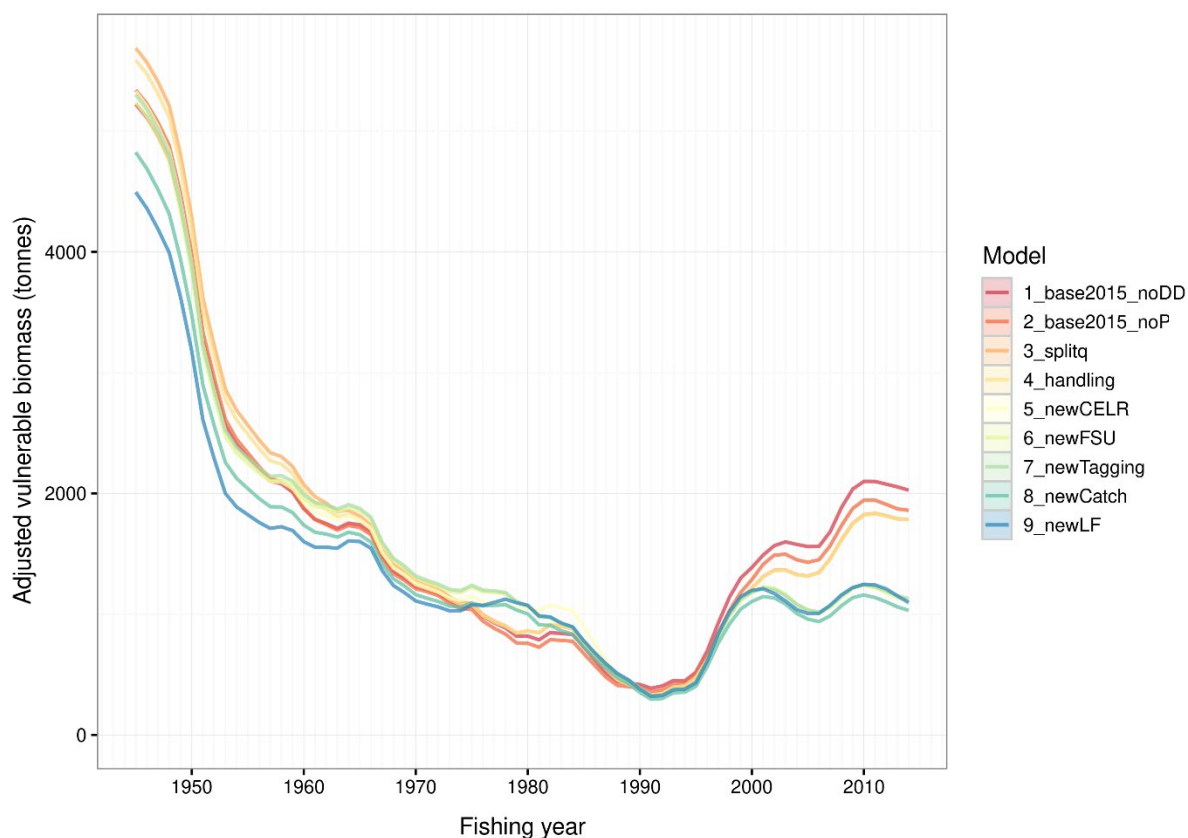


Figure 4: Comparison of MAP adjusted vulnerable biomass for all model runs leading up to the base case model run.

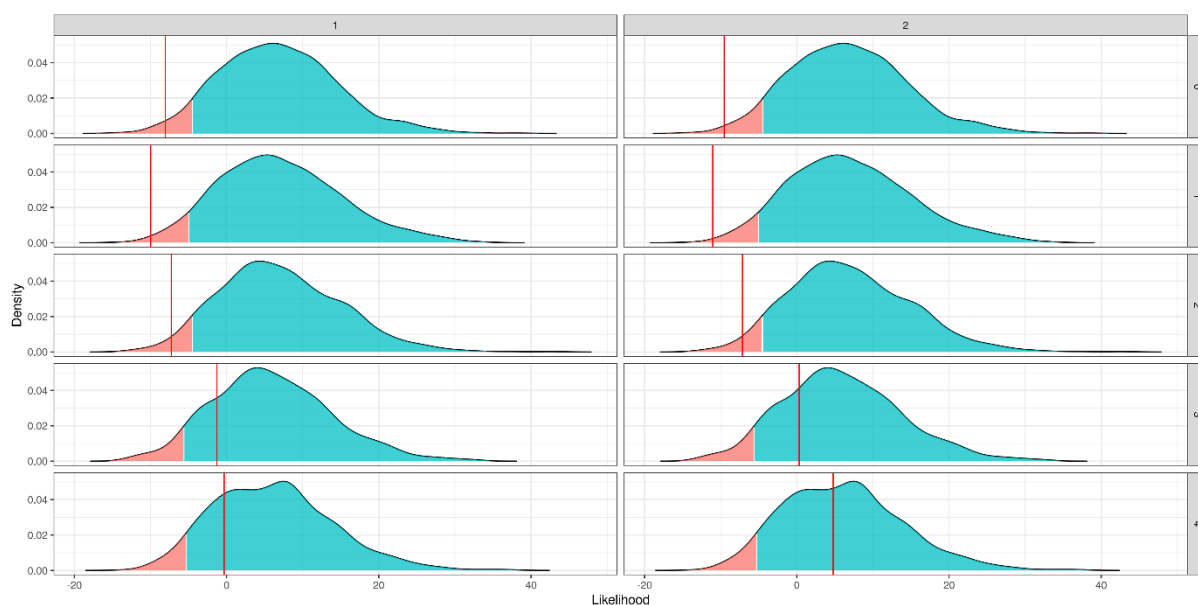


Figure 5: Puerulus randomisation trial results. The vertical red line in each panel represents the likelihood value for each lag when fitting to the puerulus data using the base case model for lags of zero (top) to four years (bottom) within region 1 (left) and region 2 (right). The density of the likelihood values for the randomised puerulus data are also shown where the red shaded region represents the lower 5% of the distribution. If the red line falls within the red shaded region then the lag is statistically significant. Note that lags of three and four years were not significant in either region.

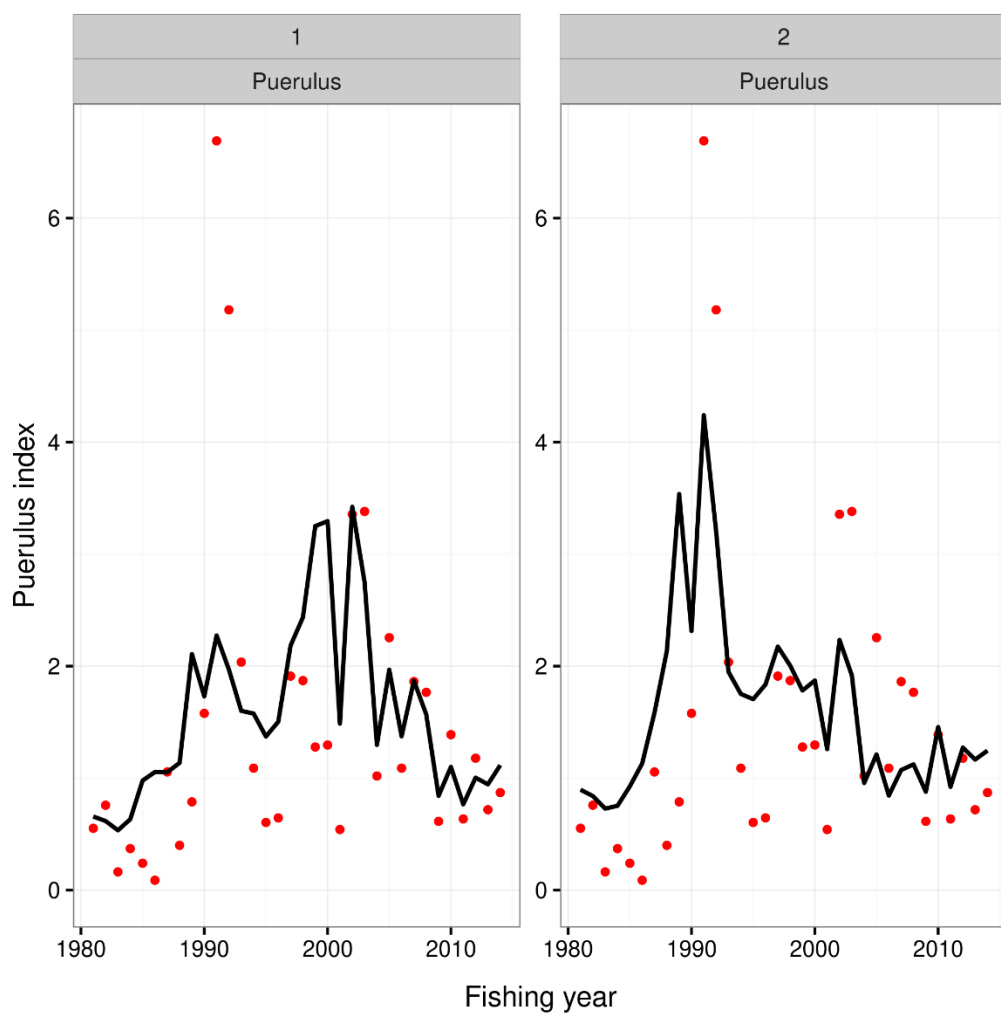


Figure 6: MAP model fit to the puerulus indices by fishing year and region in the lag3 model run. Note that the same puerulus indices are fitted to in region 1 and region 2, but region 1 and region 2 have separate recruitment series.

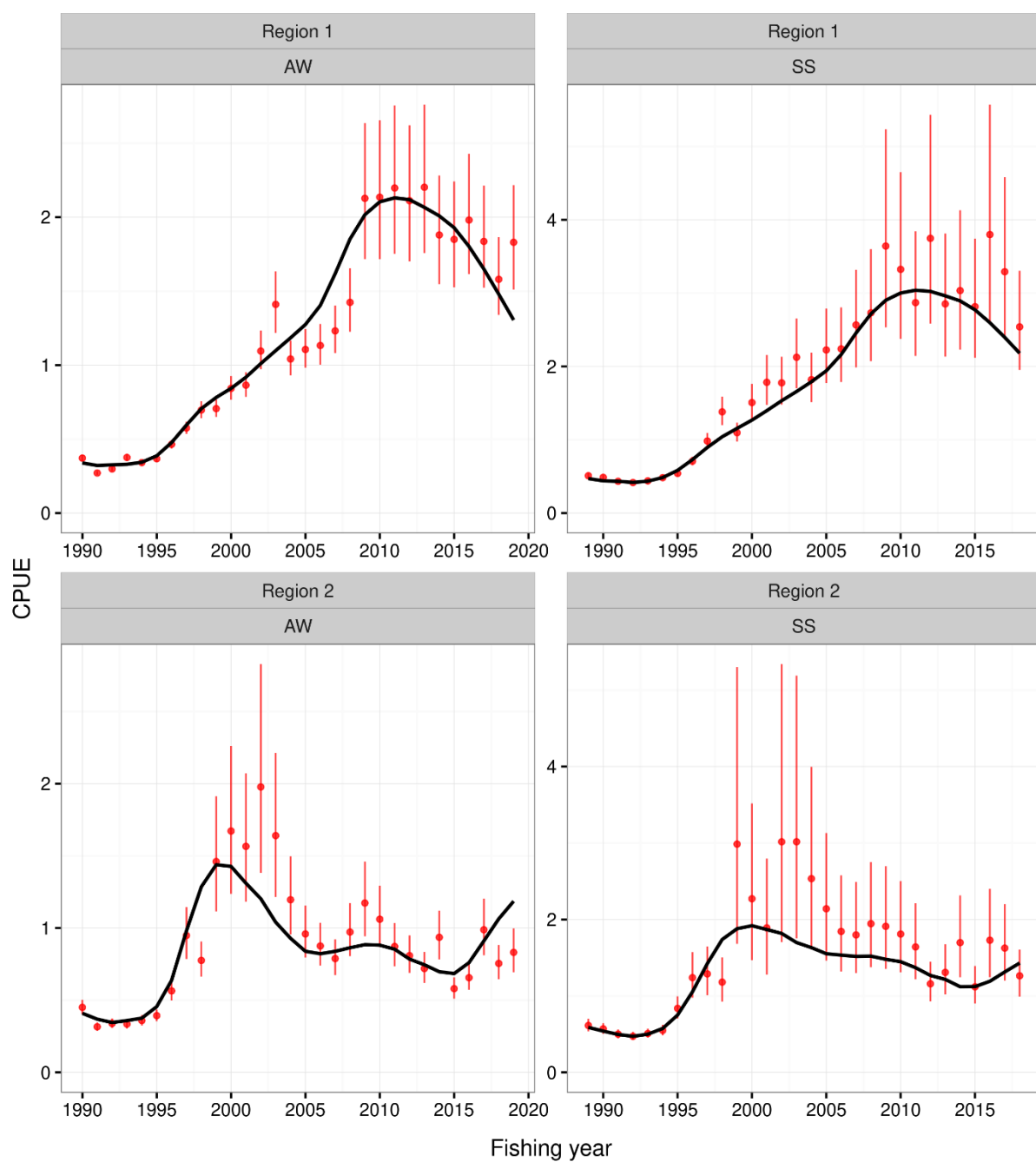


Figure 7: MAP model fit to the CELR CPUE indices by fishing year, season (AW = autumn-winter, SS = spring-summer), and region in the base case model run.

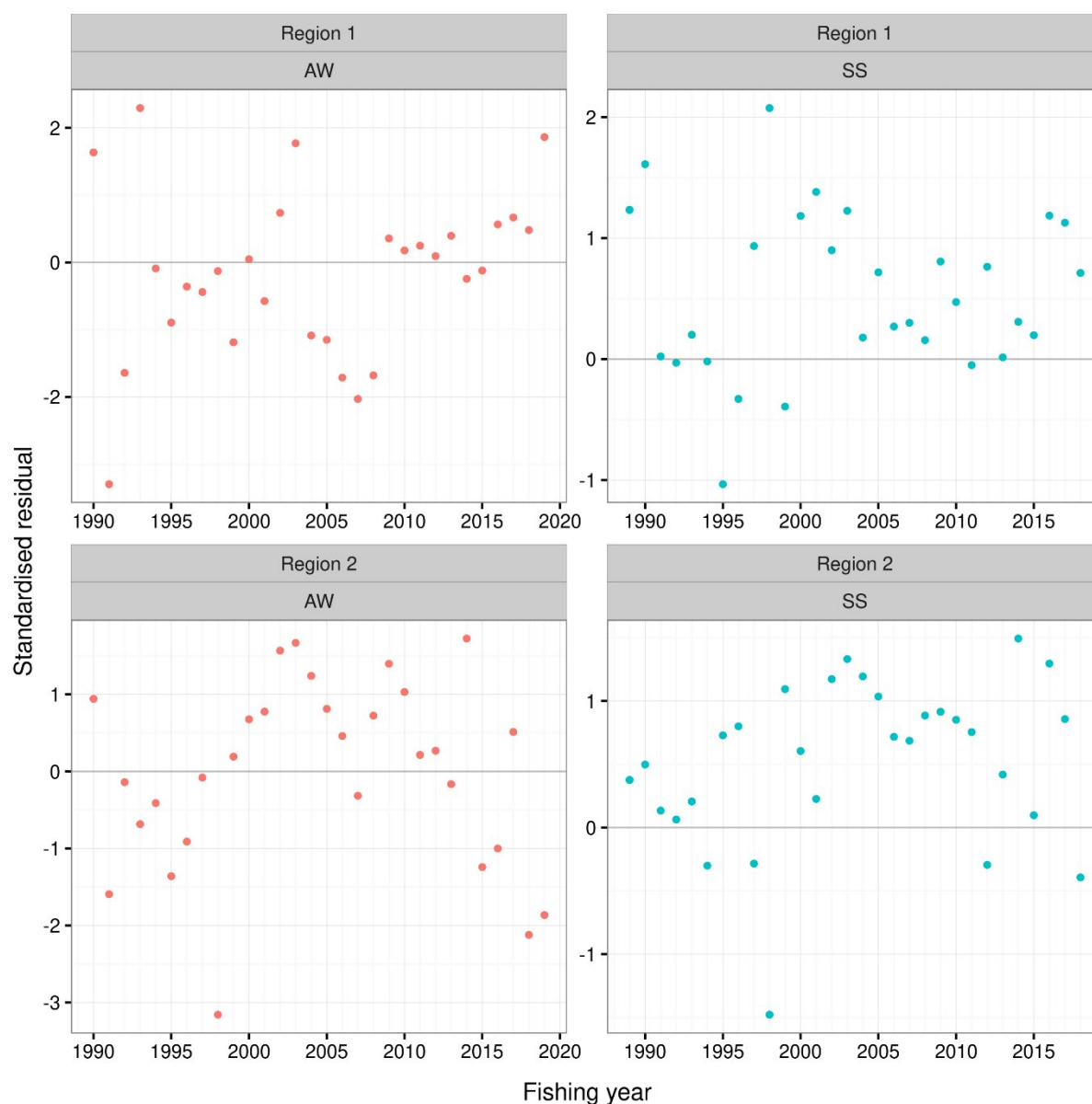


Figure 8: MAP standardised residuals from model fit to the CELR CPUE indices by fishing year, season (AW = autumn-winter, SS = spring-summer), and region in the base case model run.

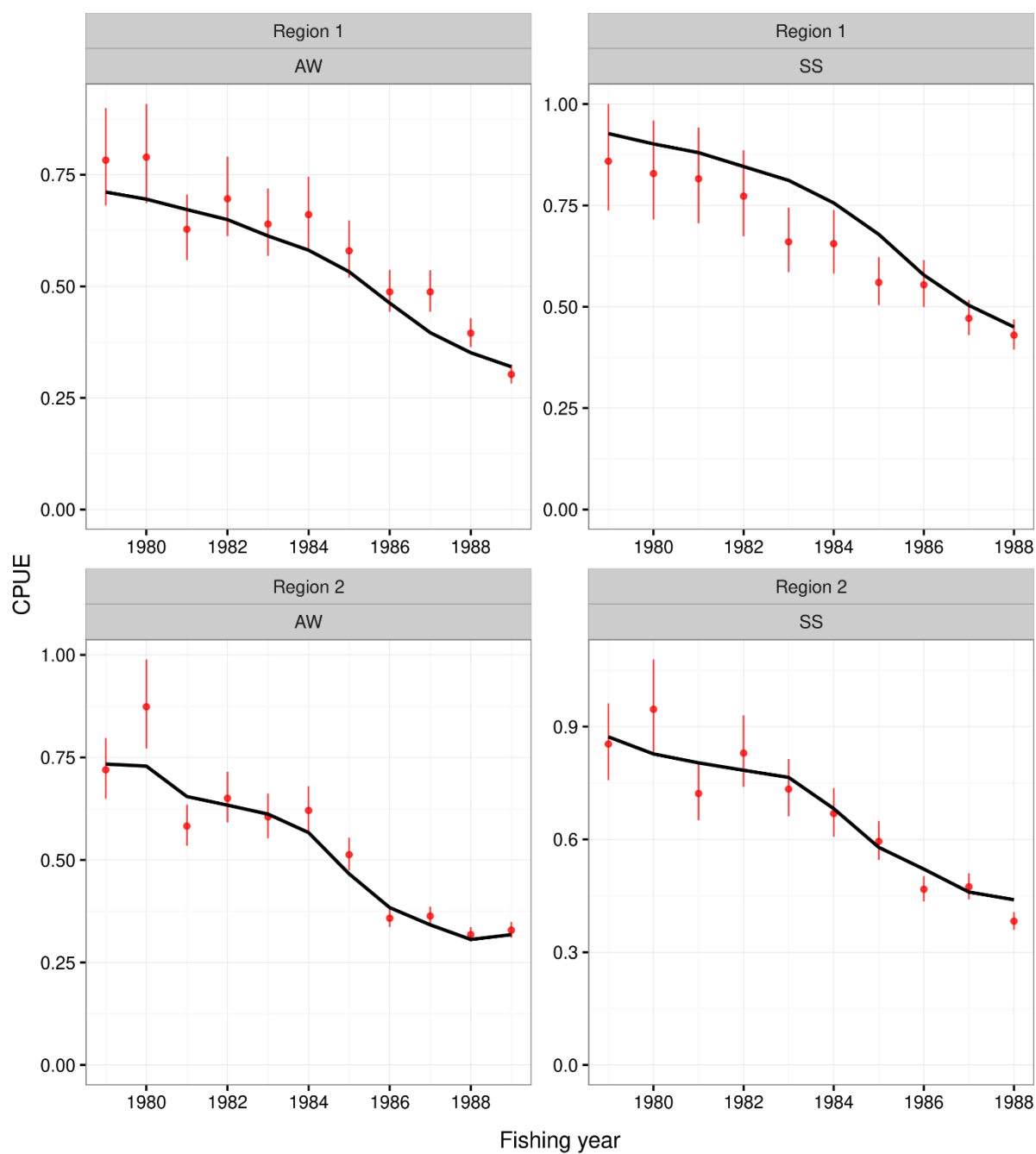


Figure 9: MAP model fit to the FSU CPUE indices by fishing year, season (AW = autumn-winter, SS = spring-summer), and region in the base case model run.

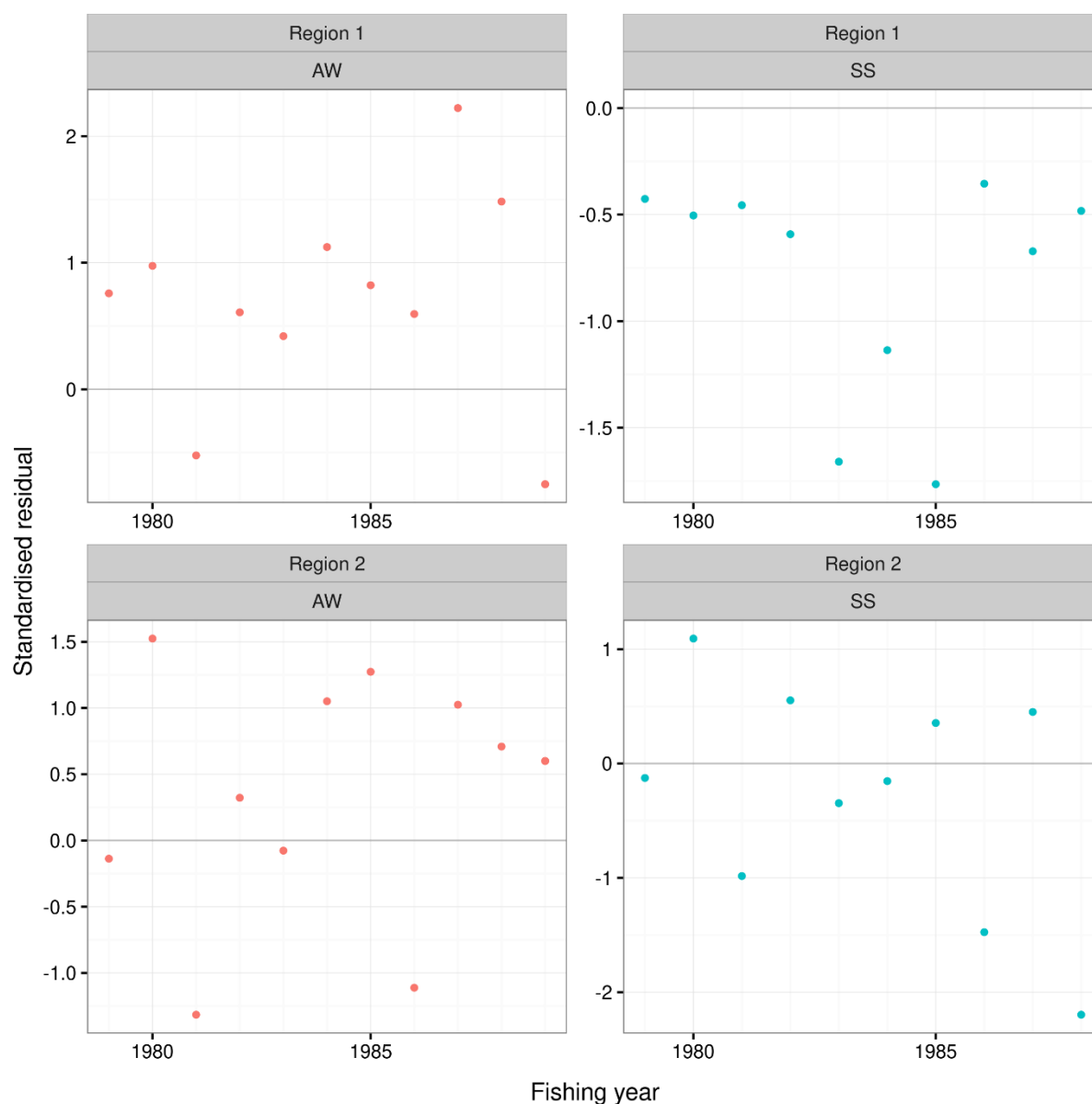


Figure 10: MAP standardised residuals from model fit to the FSU CPUE indices by fishing year, season (AW = autumn-winter, SS = spring-summer), and region in the base case model run.

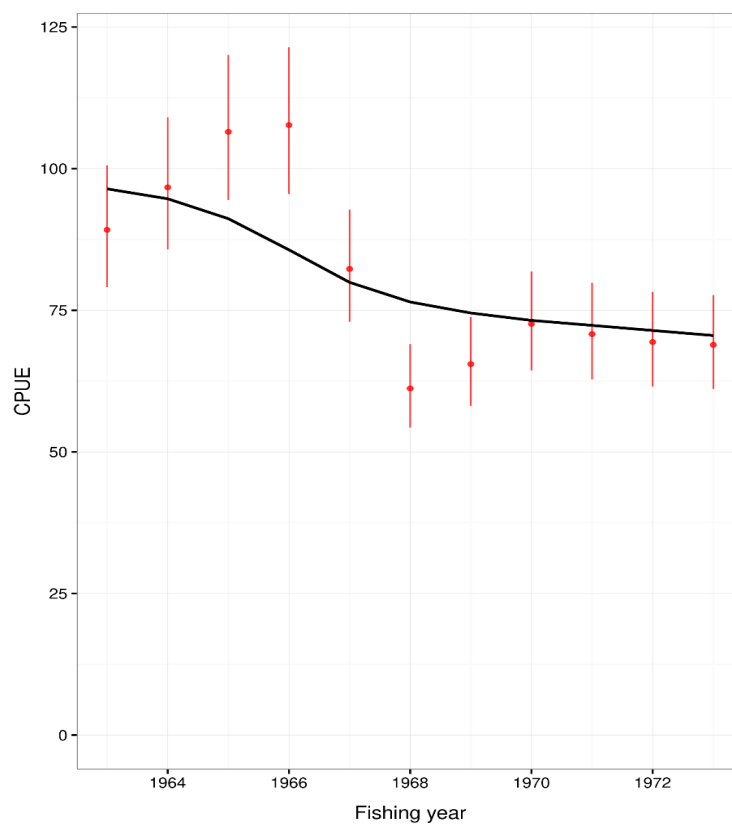


Figure 11: MAP model fit to the CR CPUE indices by fishing year in the base case model run.

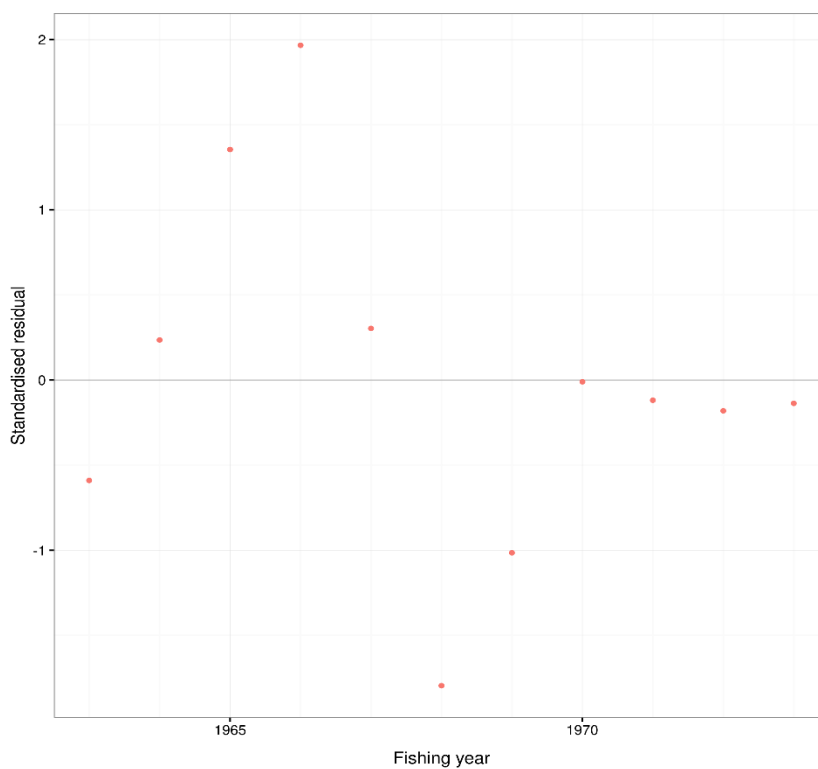


Figure 12: MAP standardised residuals from model fit to the CR CPUE indices by fishing year, season (AW = autumn-winter, SS = spring-summer), and region in the base case model run.

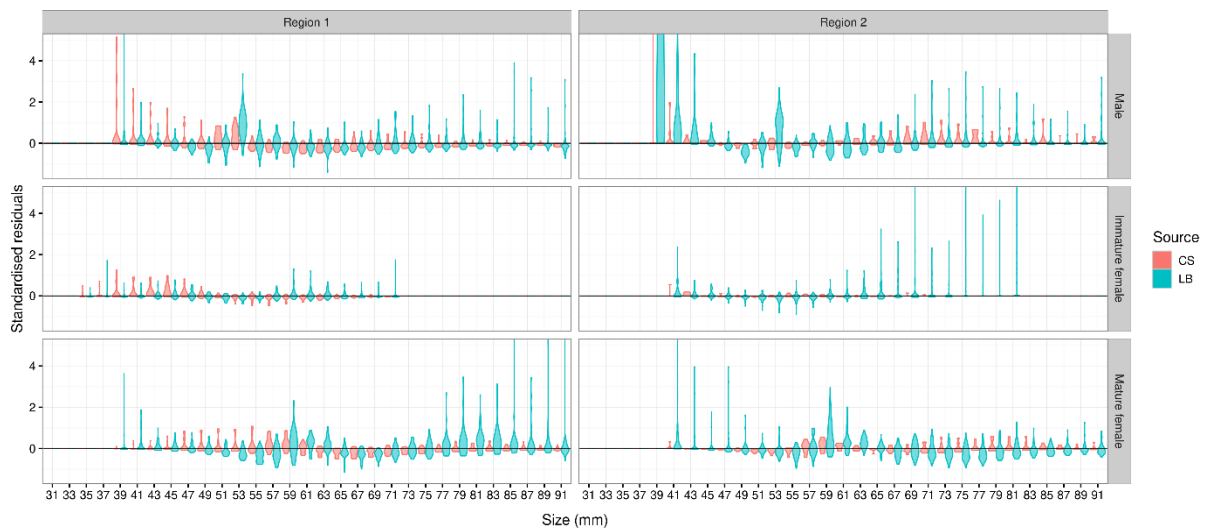


Figure 13: MAP standardised residuals from fits to the LF data by region, sex, 2 mm TW bin, and sampling source (CS = catch sampling, LB = logbook).

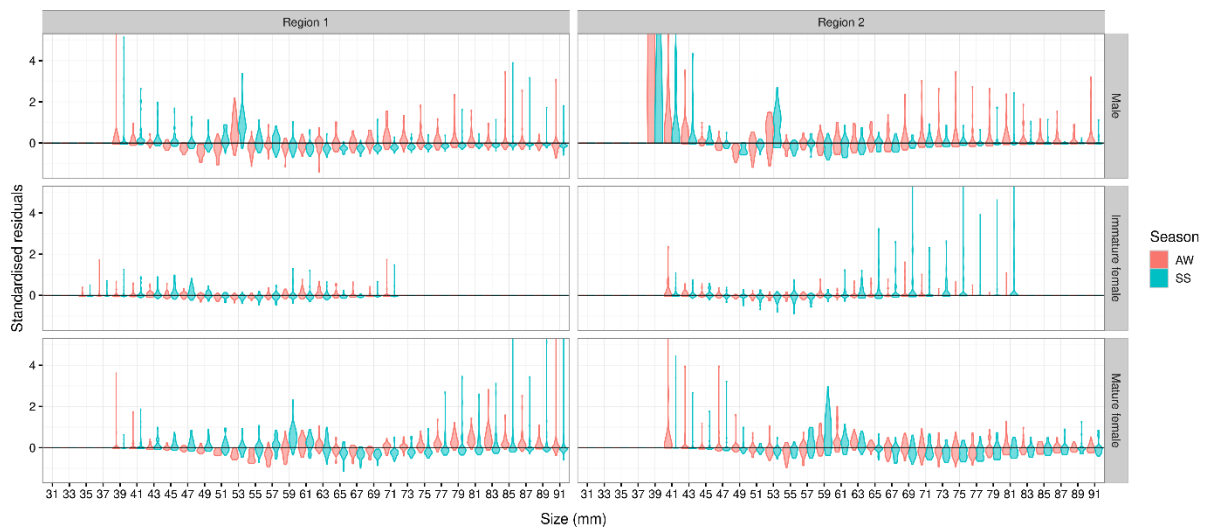


Figure 14: MAP standardised residuals from fits to the LF data by region, sex, year, 2 mm TW bin, and season (AW = autumn-winter, SS = spring-summer).

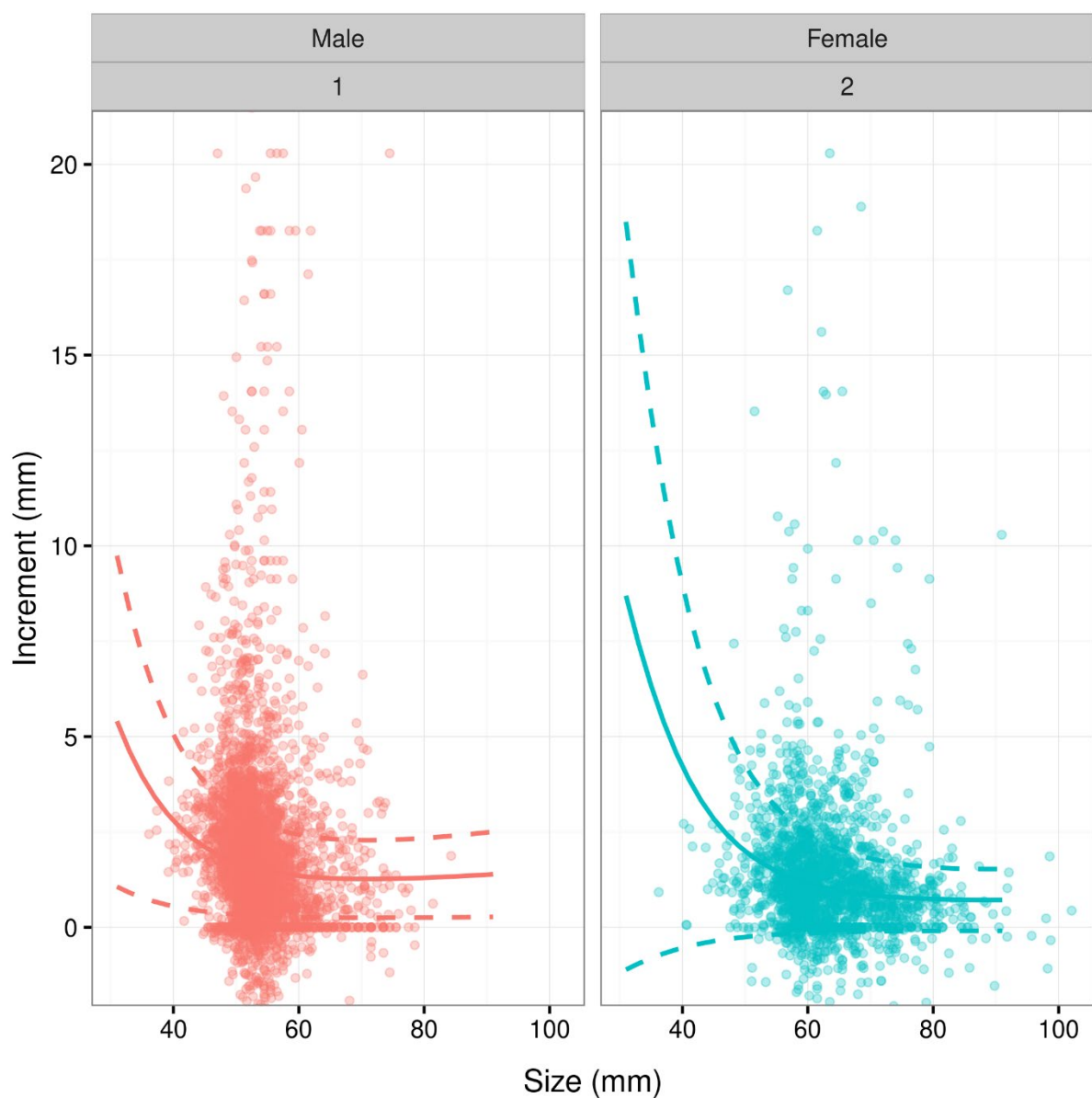


Figure 15: MAP predicted 6-monthly growth increment by size and sex in the base case model run showing the mean (solid line), ± 1 standard deviation (dashed line), and observed growth increments divided by time-at-liberty (points).

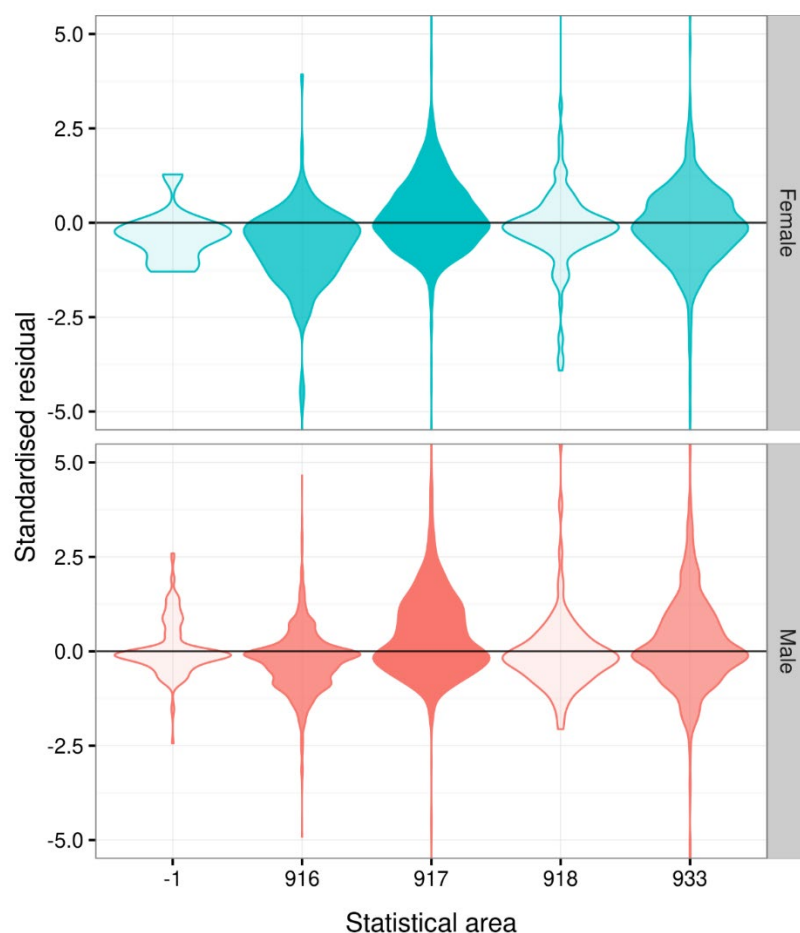


Figure 16: MAP standardised residuals of fits to tag-recapture data by statistical area of release and sex in the base case model run. Darker shading represents a higher number of tags. The group “-1” represents tags that could not be assigned to a statistical area but were tagged within CRA 5.

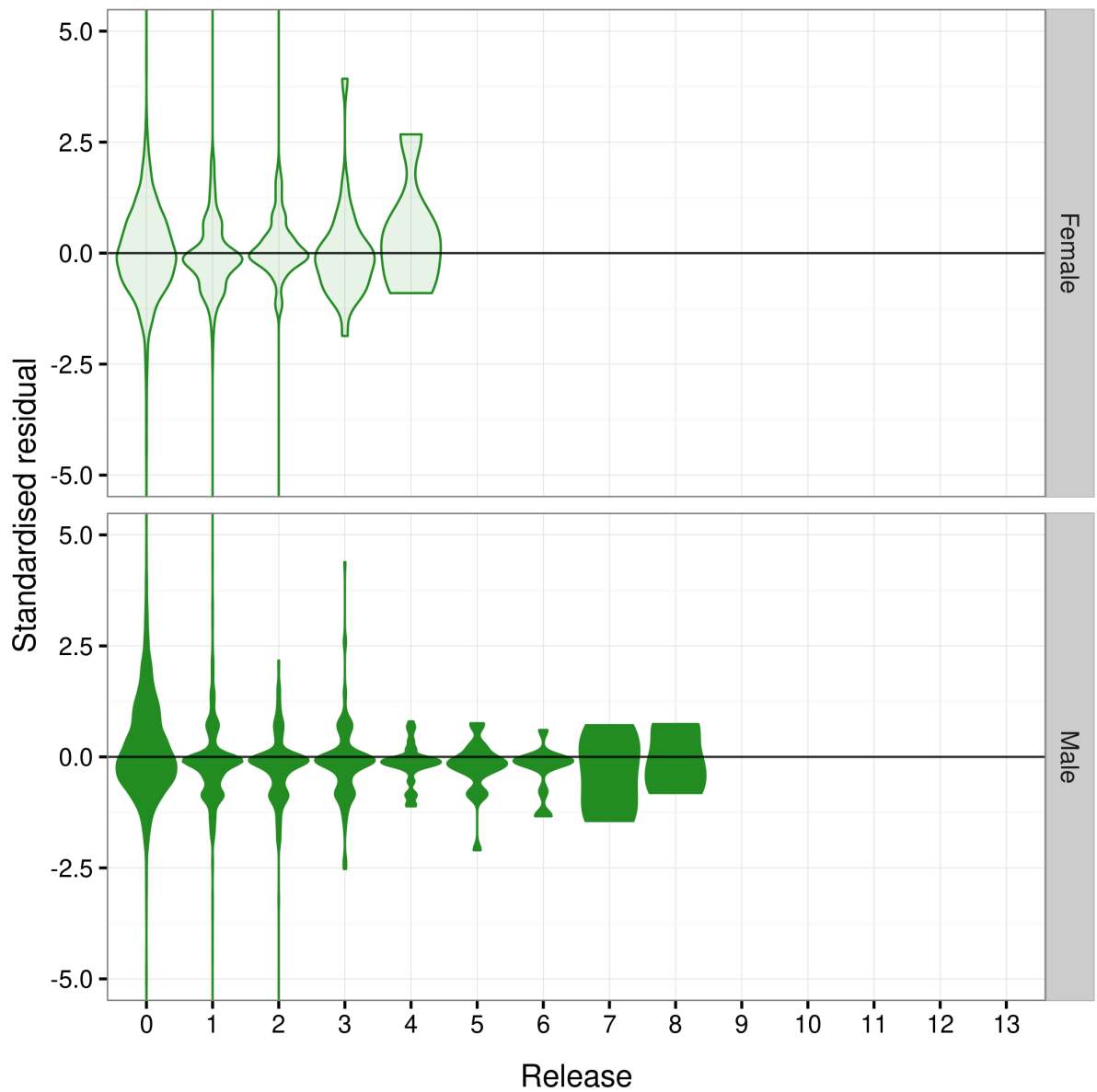


Figure 17: MAP standardised residuals of fits to tag-recapture data by re-release category and sex in the base case model run. Darker shading represents a higher number of tags.

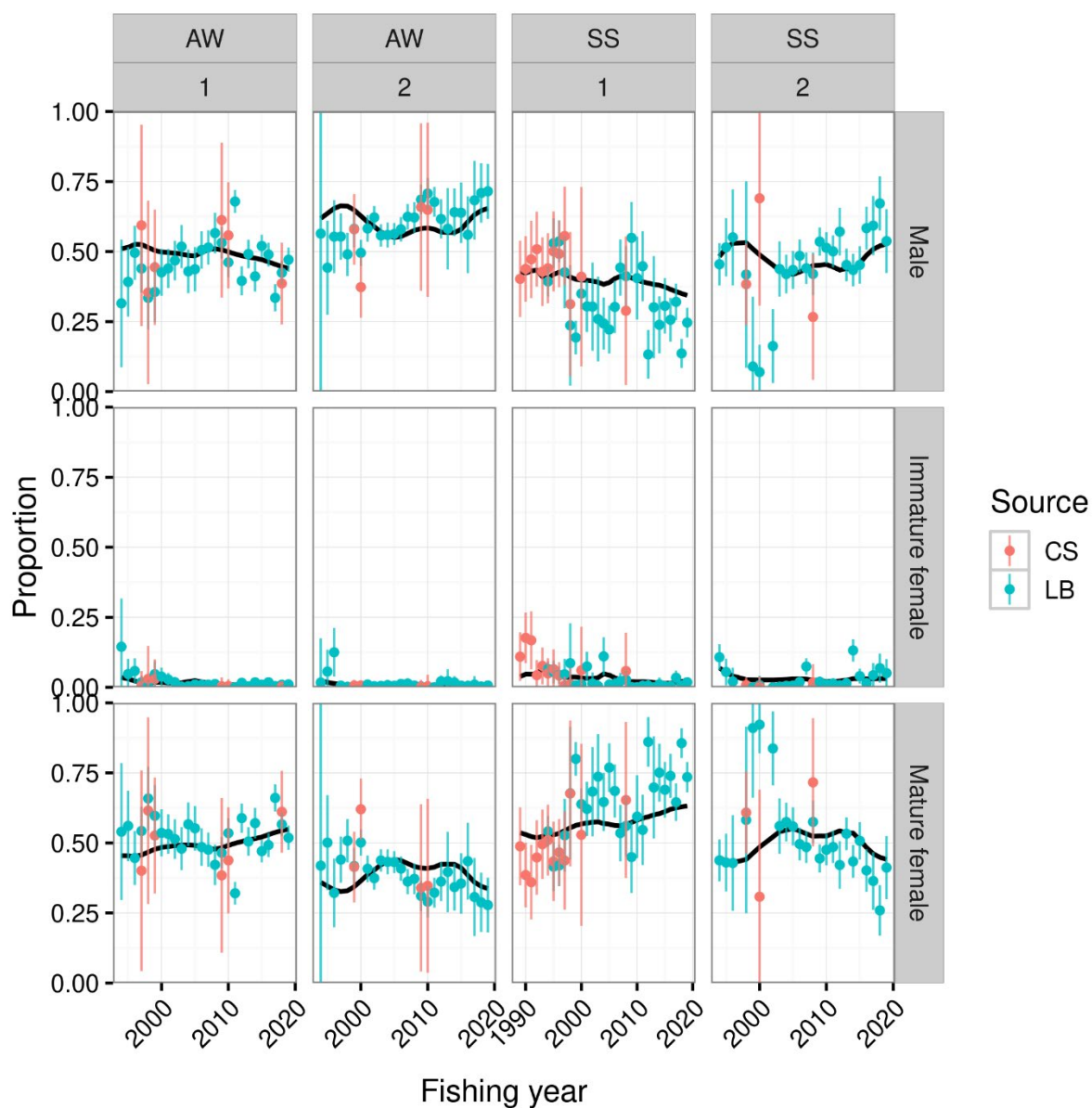


Figure 18: MAP model fit to the sex-ratios by fishing year, season (AW = autumn-winter, SS = spring-summer), region (1 = region 1, 2 = region 2), sex, and LF data source (CS = catch sampling, LB = logbook) in the base case model run.

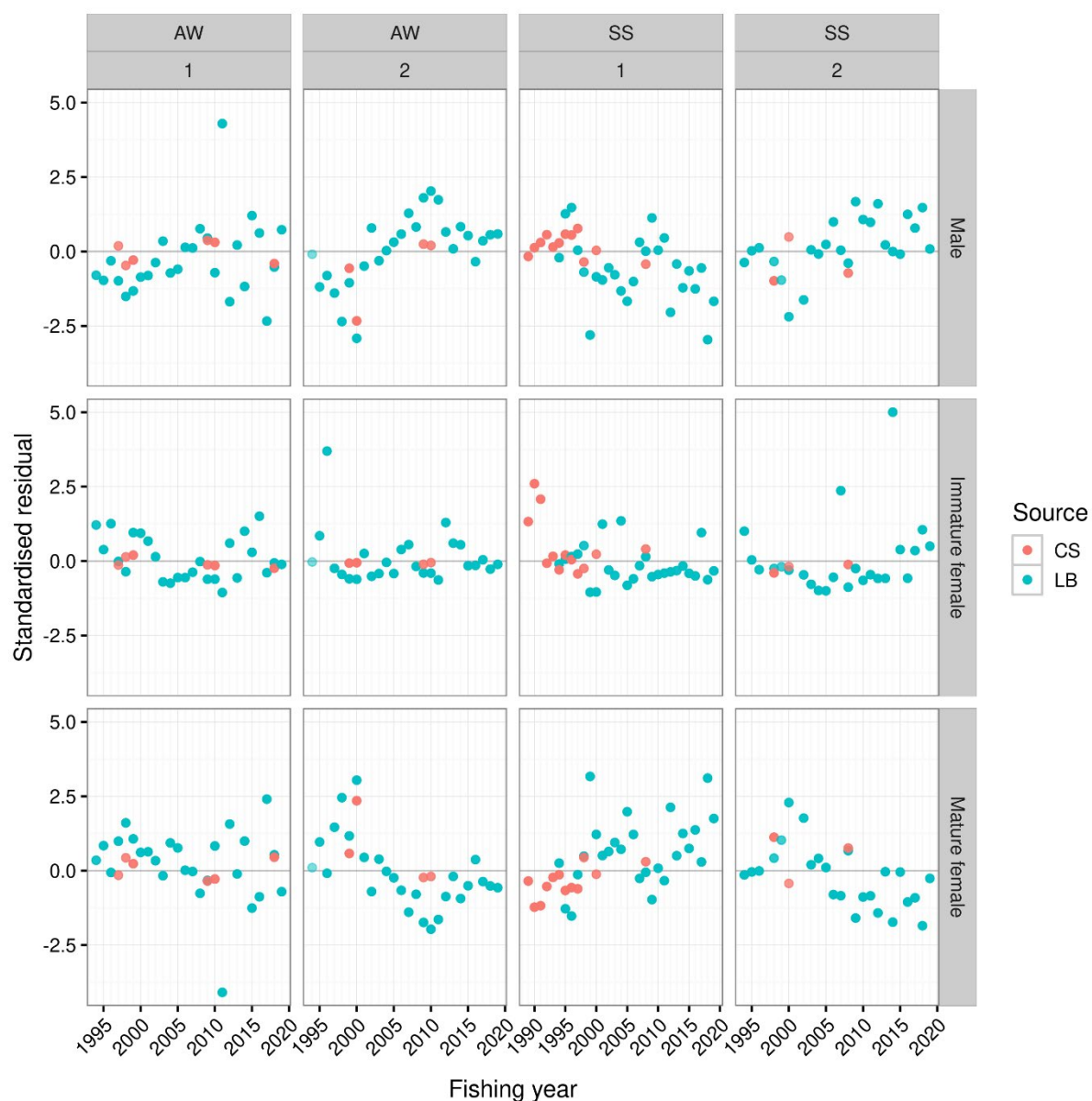


Figure 19: MAP standardised residuals for the model fit to the sex-ratios by fishing year, season (AW = autumn-winter, SS = spring-summer), region (1 = region 1, 2 = region 2), sex, and LF data source (CS = catch sampling, LB = logbook) in the base case model run.

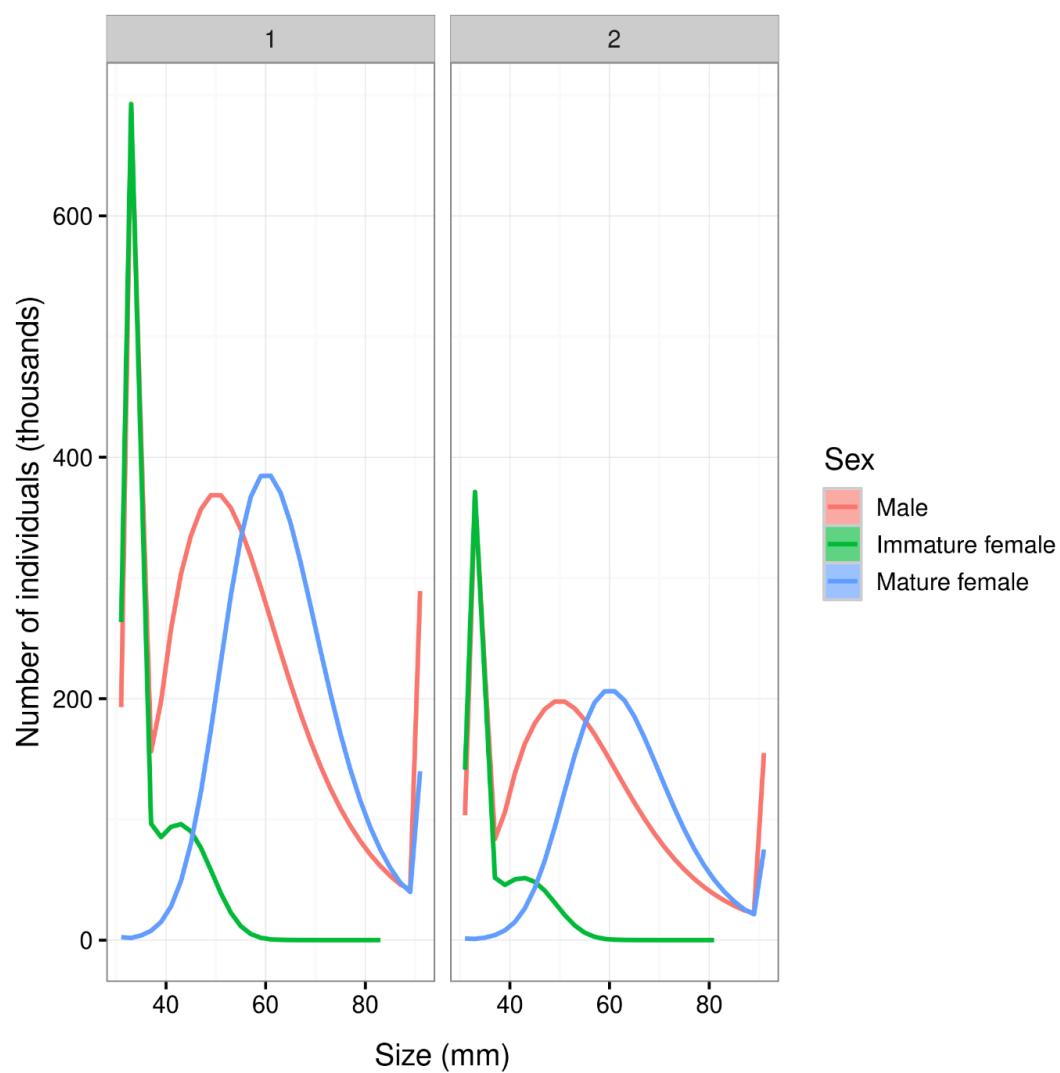


Figure 20: MAP initial number of individuals by size, sex category, and region in the base case model run.

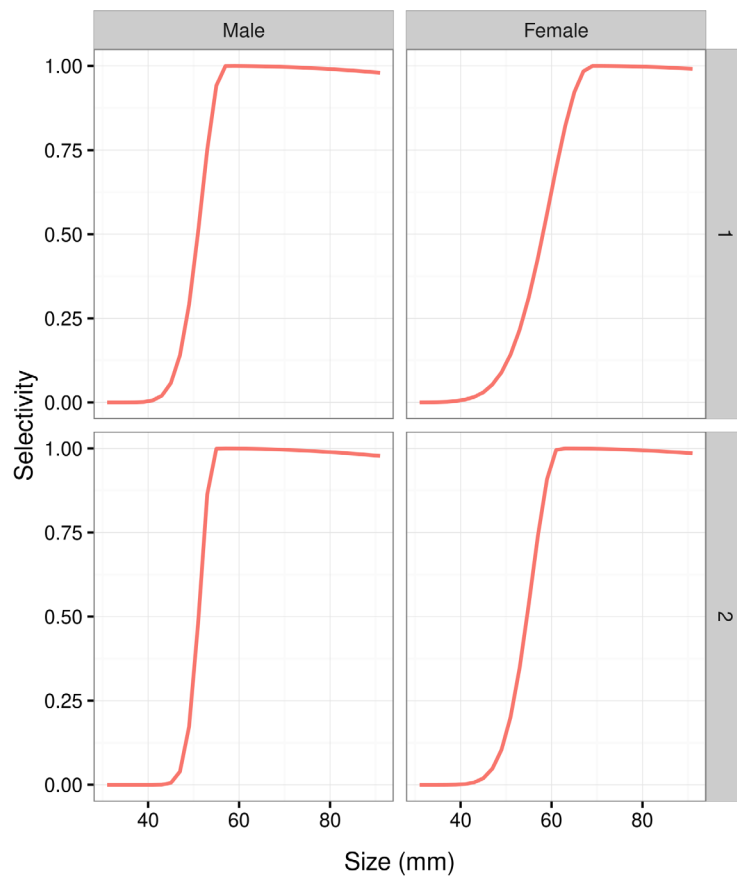


Figure 21: MAP of selectivity by sex and size for each CRA 5 region in the base case model run.

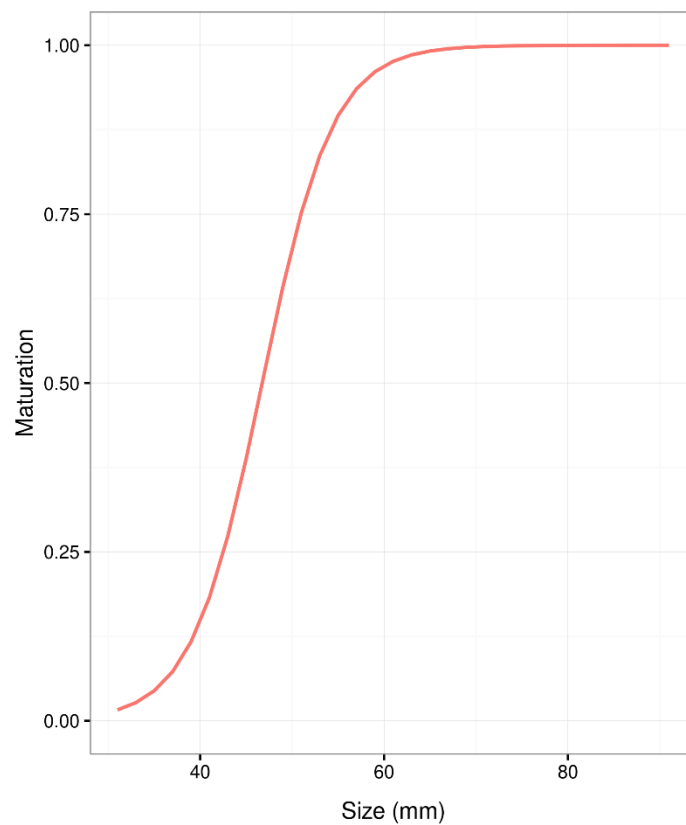


Figure 22: MAP of female maturation curve by size in the base case model run.

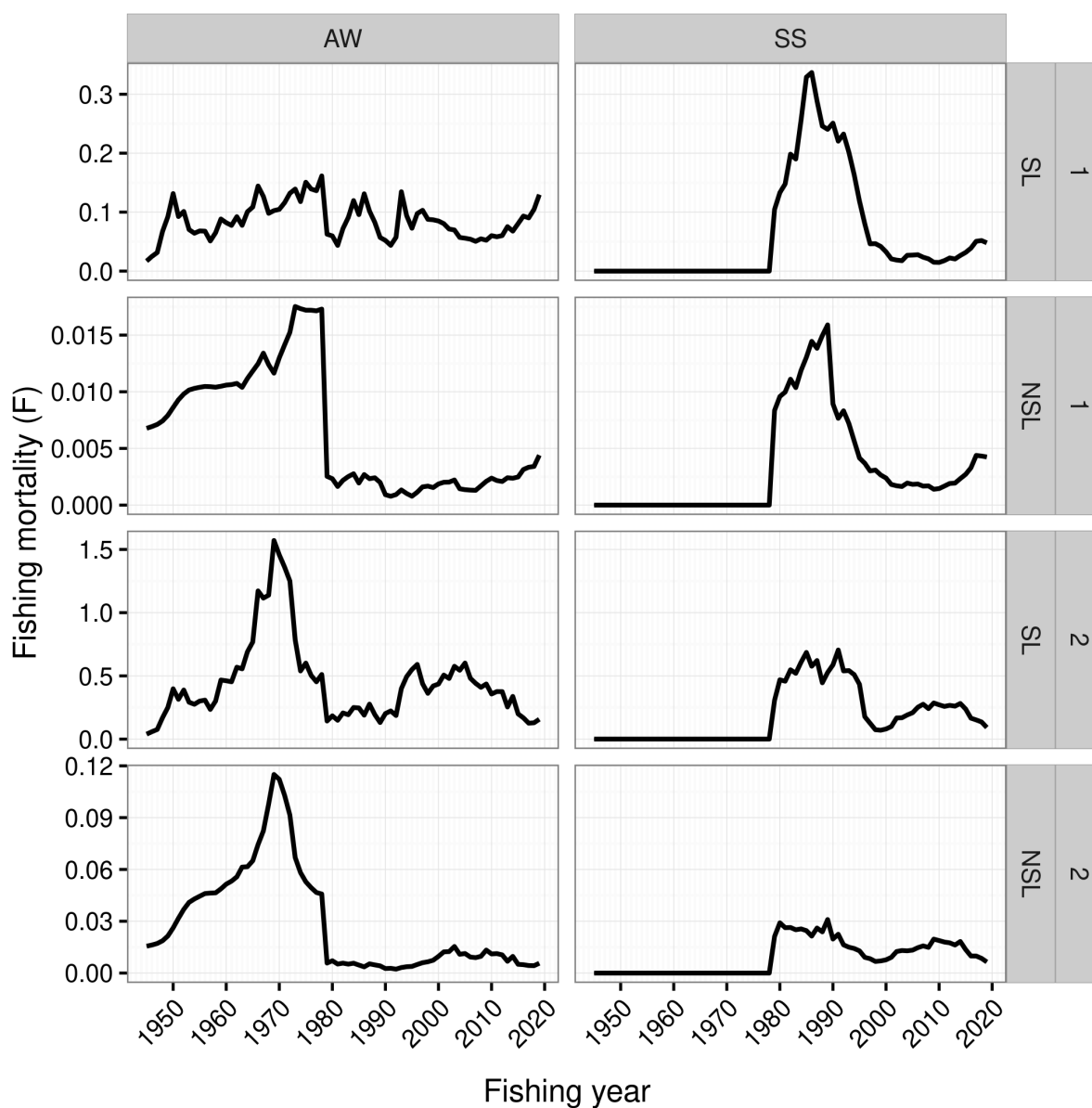


Figure 23: MAP of fishing mortality by year, season (AW = autumn-winter, SS = spring-summer), and region for the size limited (SL) and non-size limited (NSL) fisheries in the base case model run.

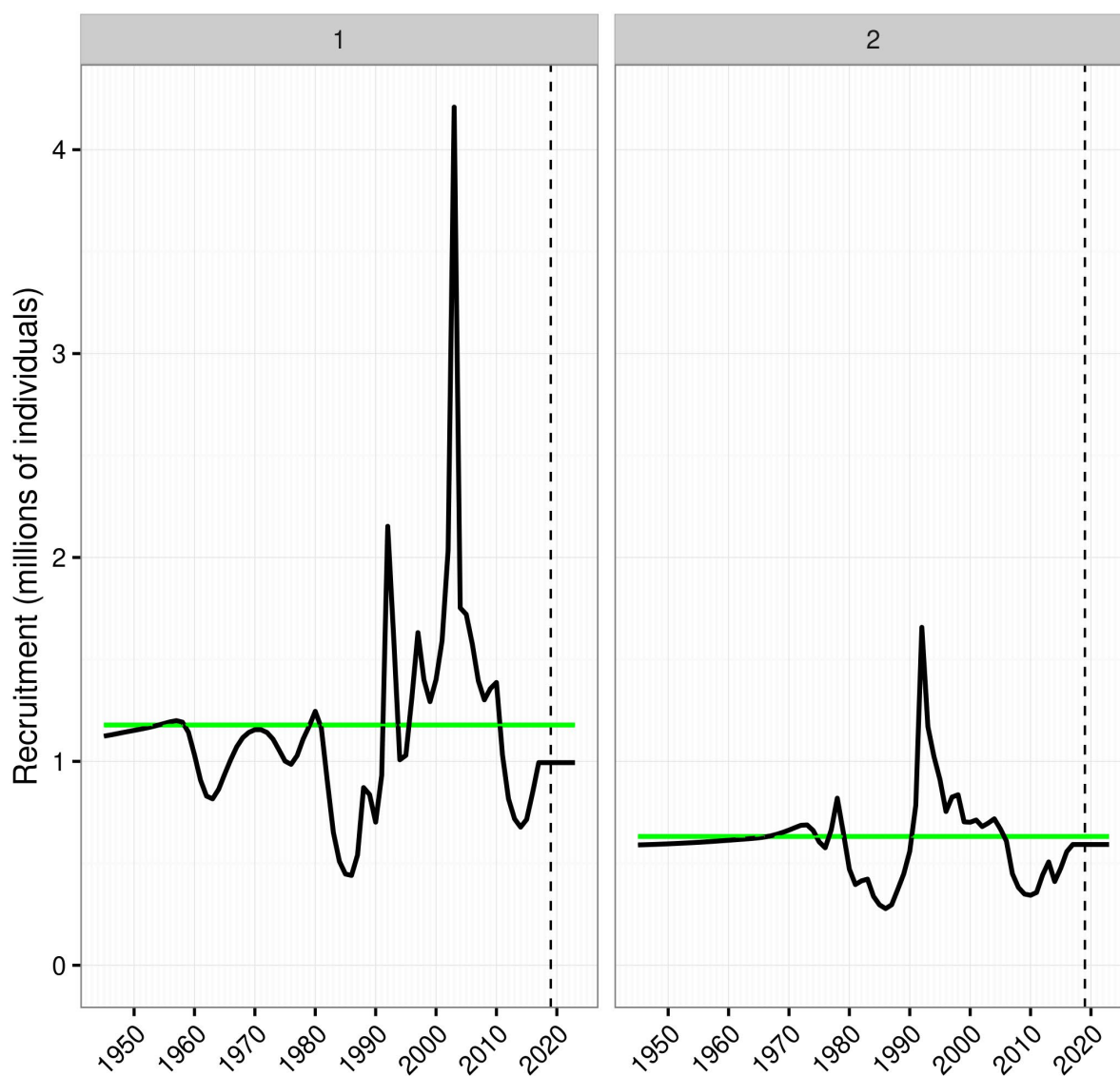


Figure 24: MAP of recruitment by region for the base case model run. Horizontal green line is R_0 and vertical dashed line is the final year of the reconstruction period.

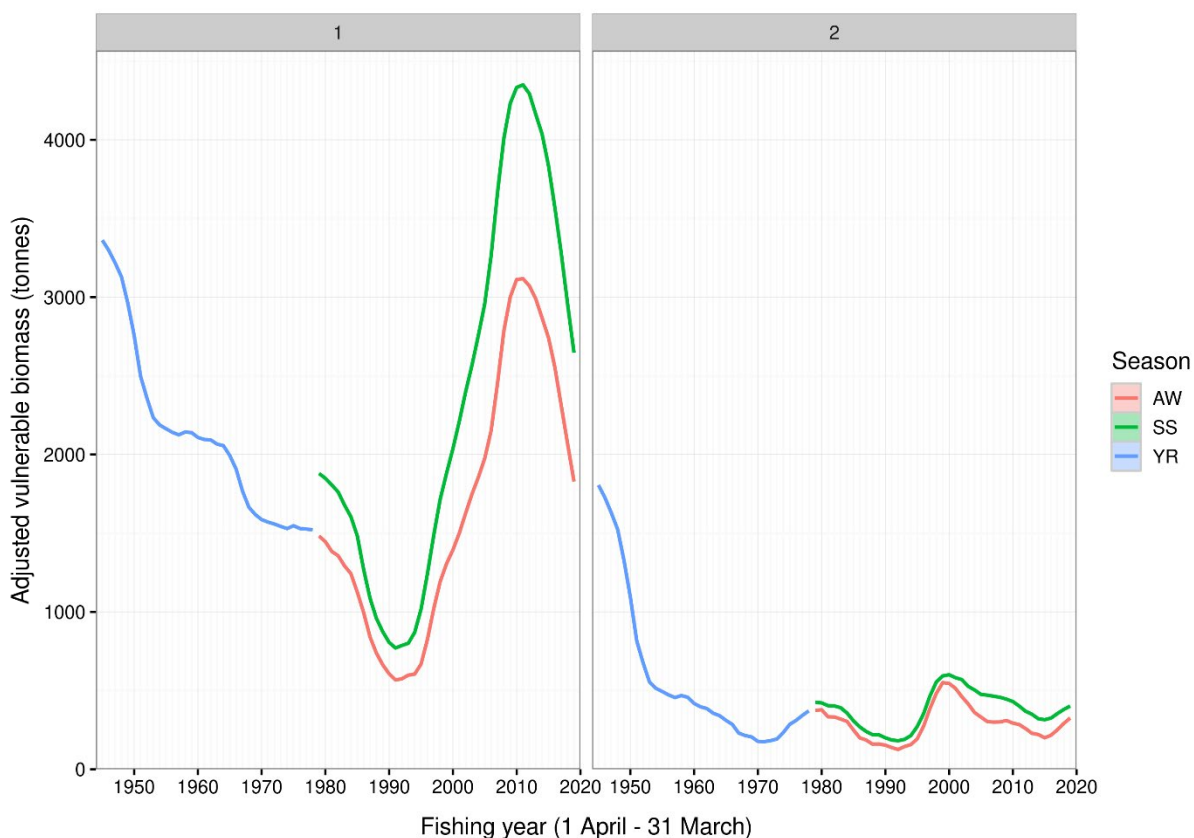


Figure 25: MAP of vulnerable biomass (tonnes) by region, season (AW = autumn-winter, SS = spring-summer, YR = single time step), and fishing year in the base case model run.

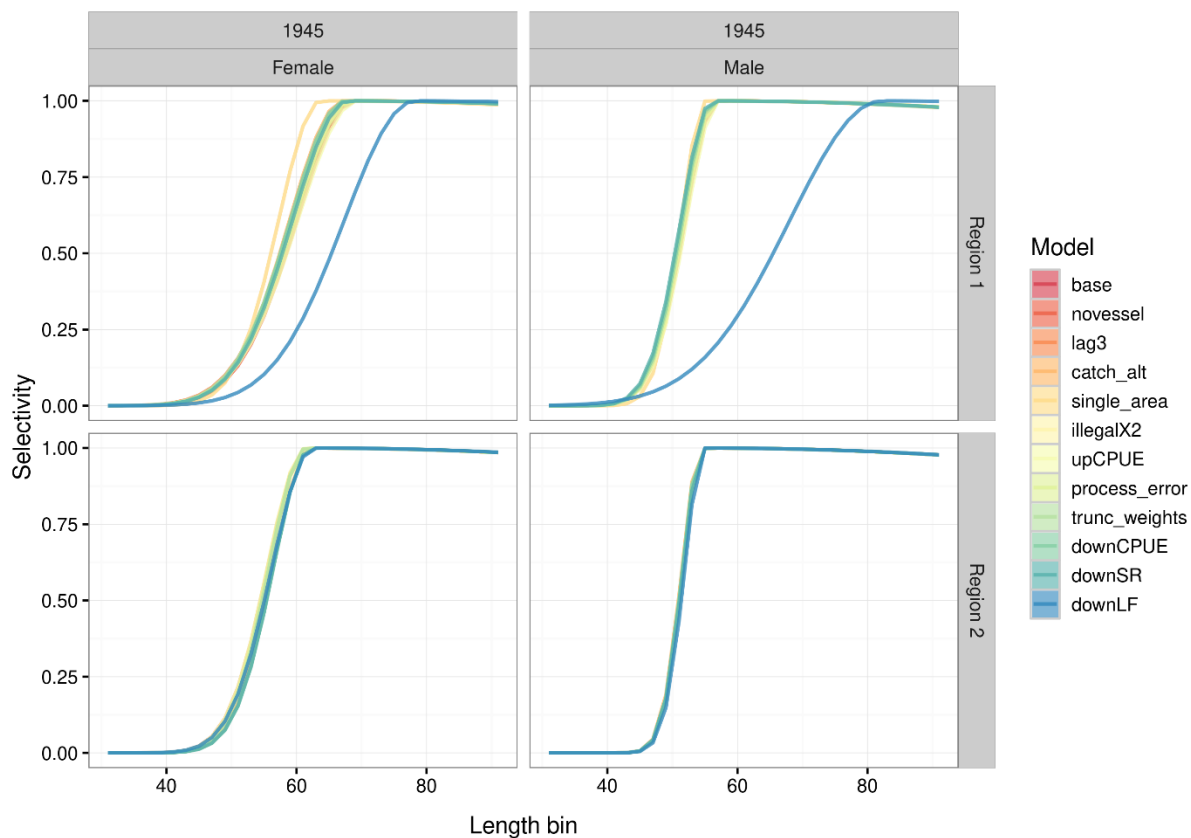


Figure 26: Comparisons of MAP selectivity curves by fishing year and region for each sensitivity run.

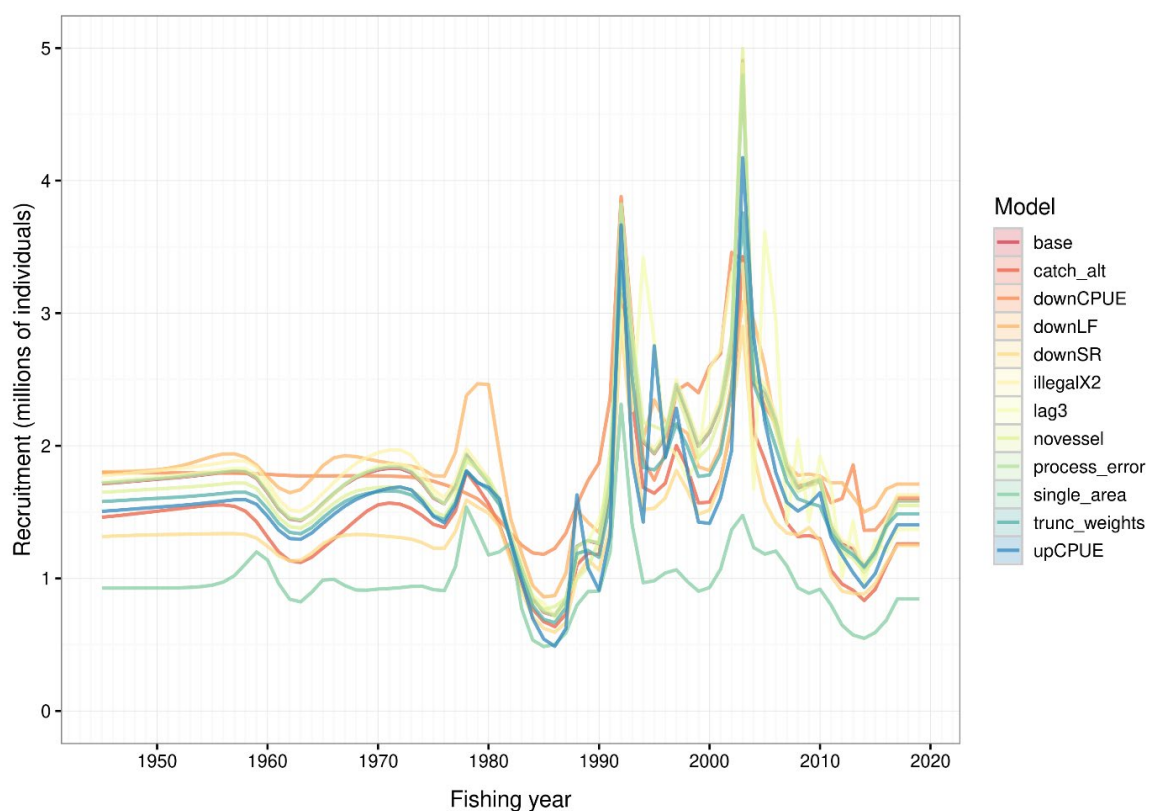


Figure 27: Comparisons of MAP recruitments by fishing year for each sensitivity run. Note that region 1 and region 2 recruitments have been combined into a single trajectory for this plot.

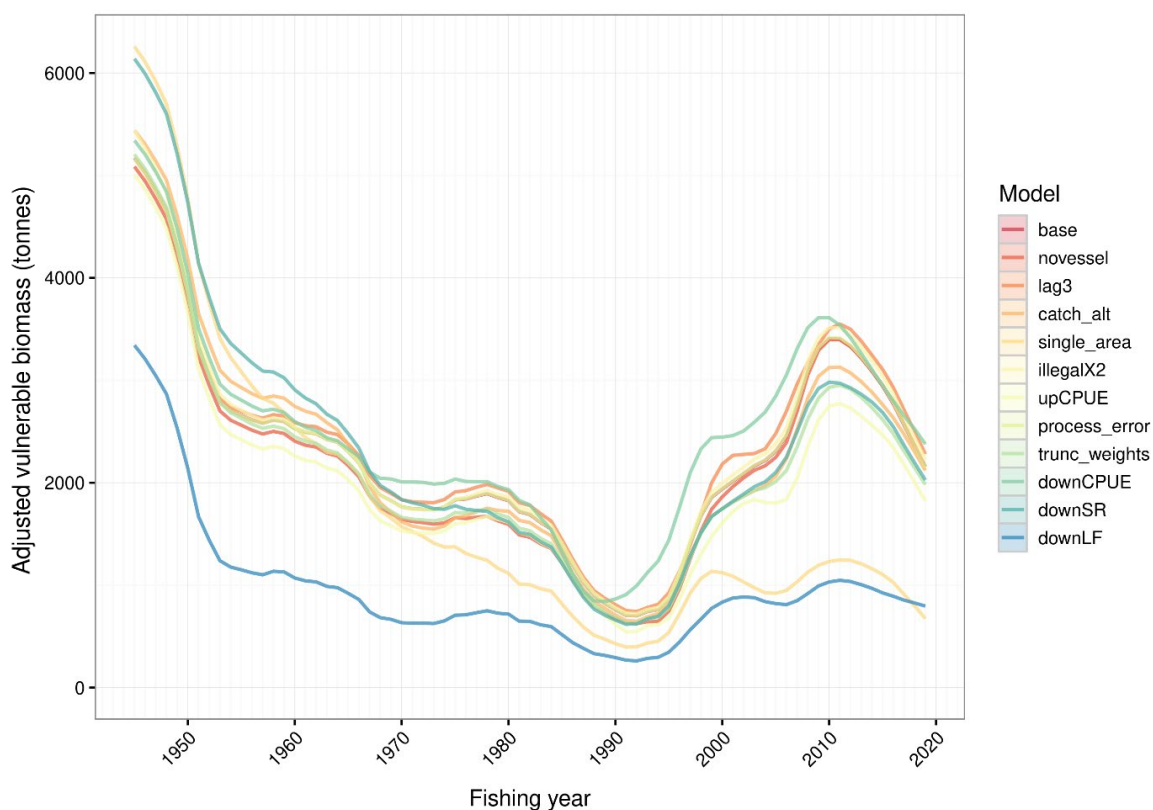


Figure 28: Comparisons of MAP adjusted vulnerable biomass by fishing year for each sensitivity run. Note that region 1 and region 2 adjusted vulnerable biomass estimates have been combined into a single trajectory for this plot.

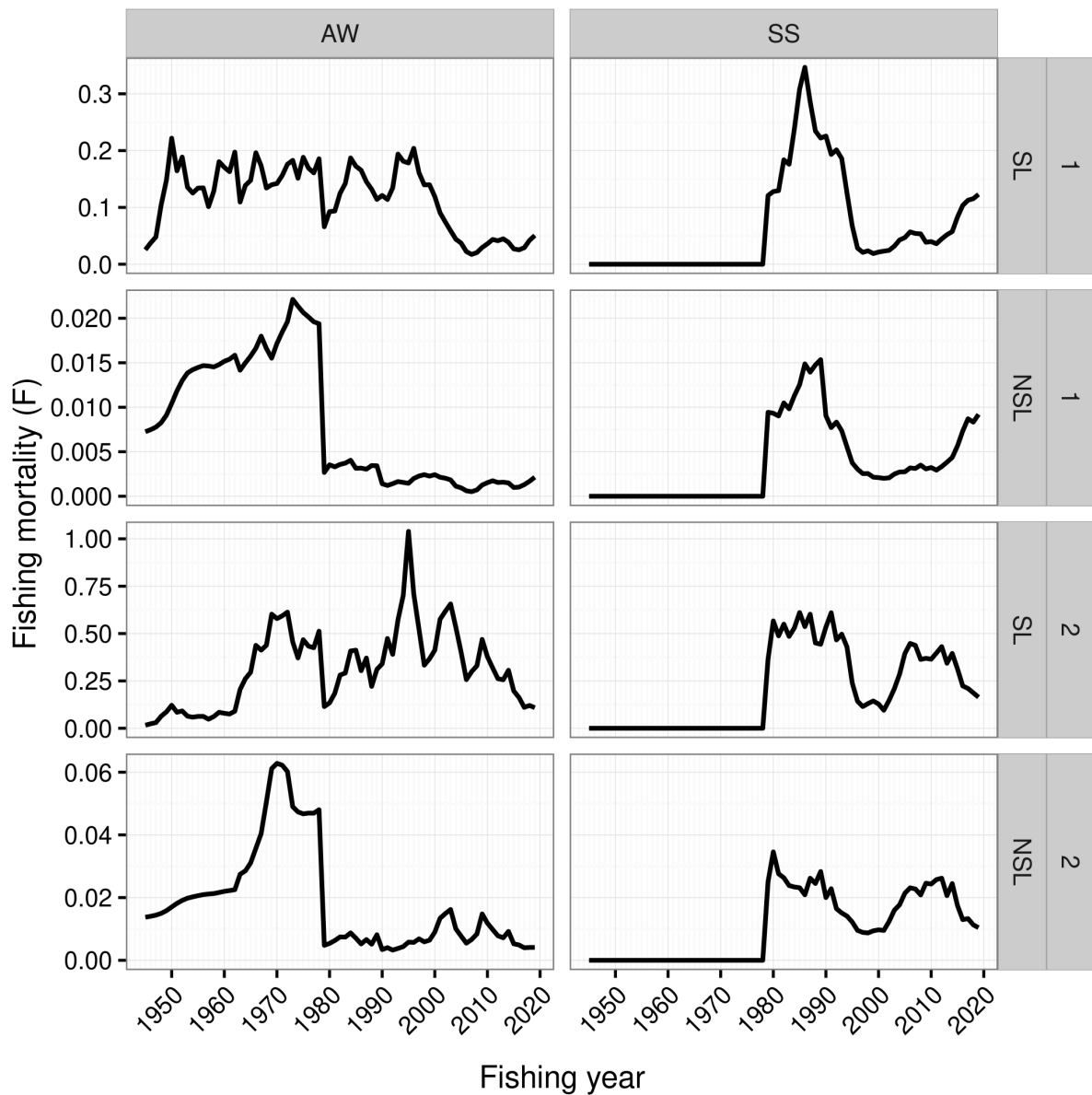


Figure 29: MAP of fishing mortality by year, season (AW = autumn-winter, SS = spring-summer), and region for the size limited (SL) and non-size limited (NSL) fisheries in the *catch_alt* sensitivity run.

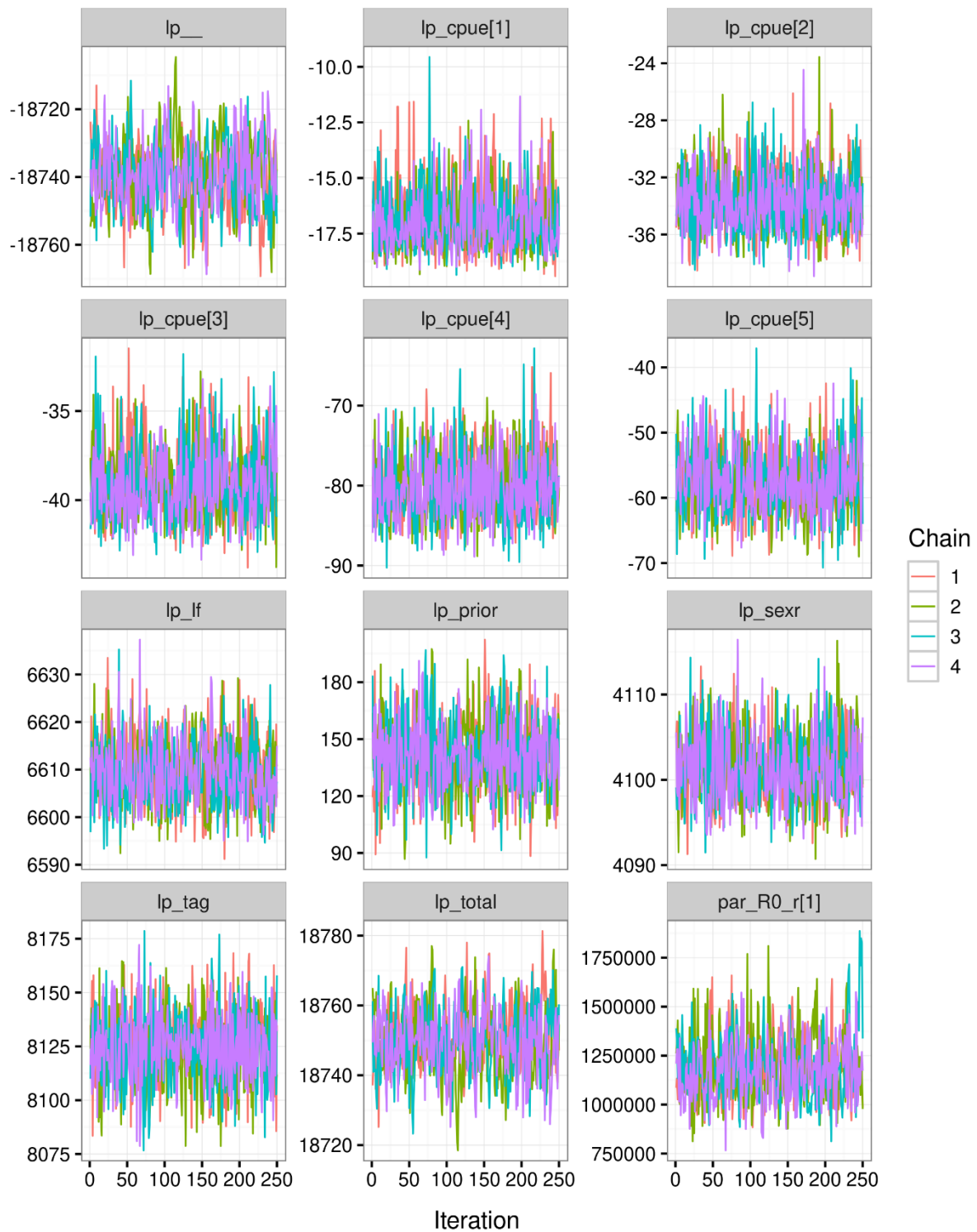


Figure 30: MCMC trace plots by independent chain for likelihood components and the R_0 parameter for region 1 for the base case model run.

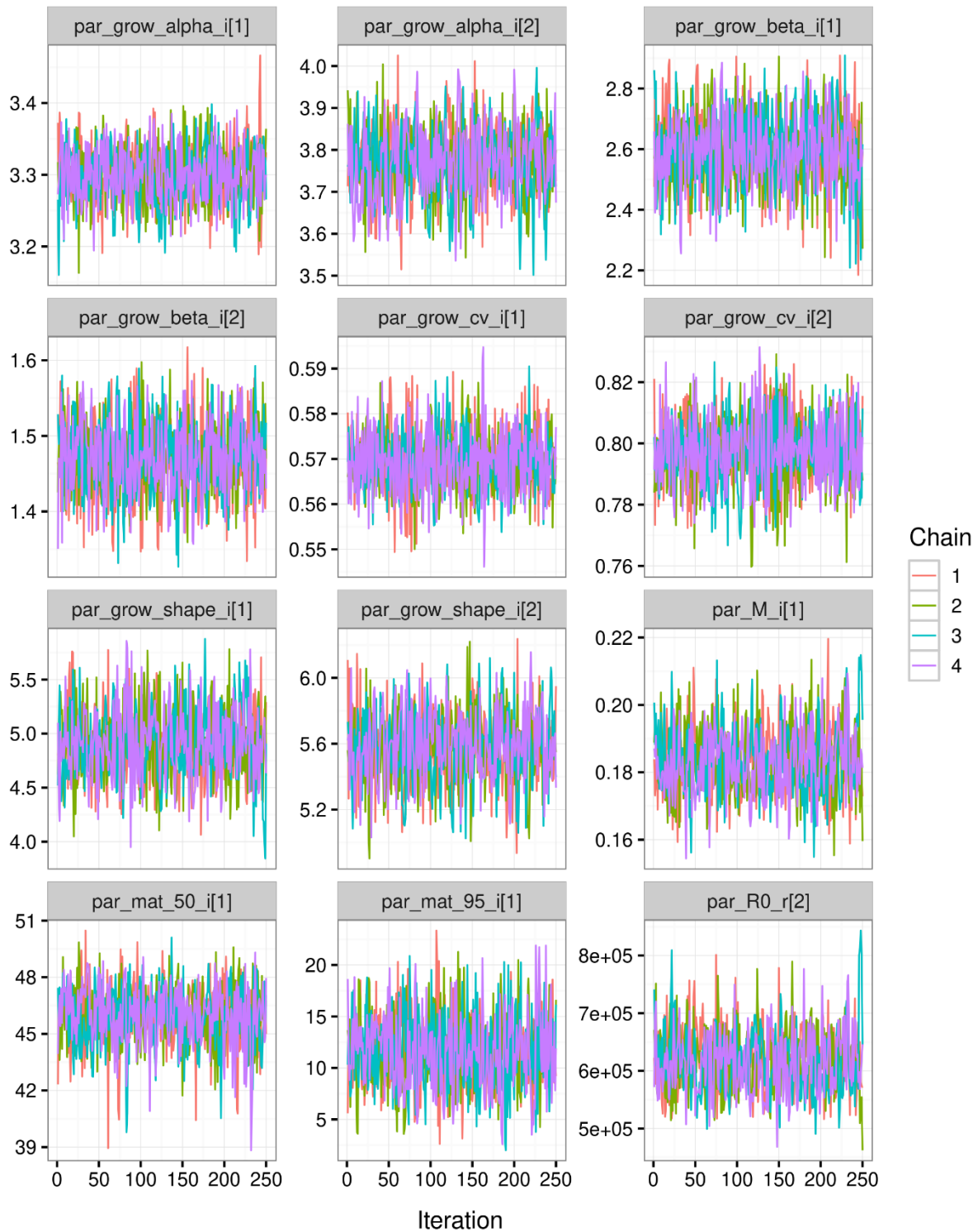


Figure 31: MCMC trace plots by independent chain for growth parameters, natural mortality (M), maturity parameters, and the region 2 R_0 parameter for the base case model run.

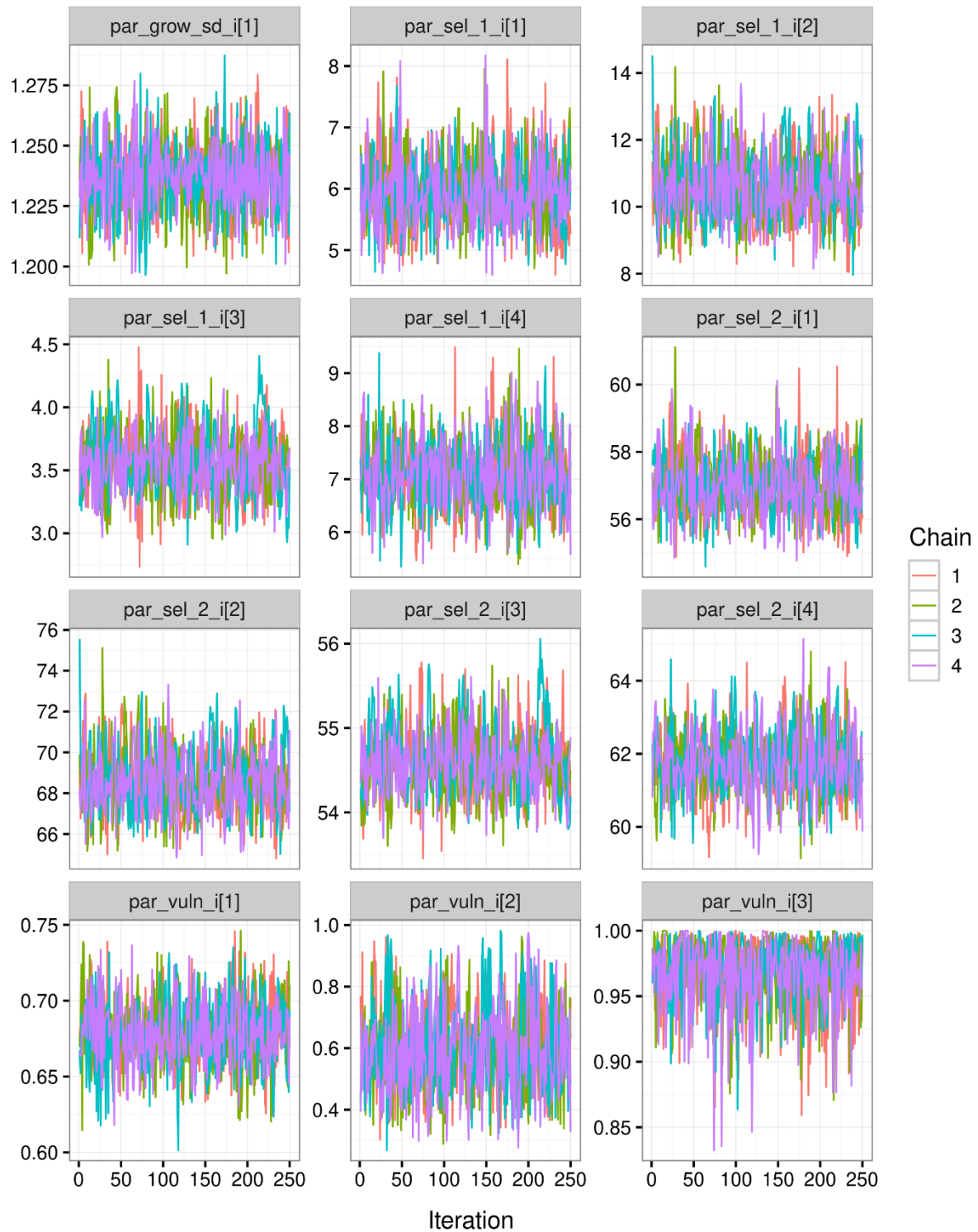


Figure 32: MCMC trace plots by independent chain for one of the growth parameters and selectivity and vulnerability parameters for the base case model run.

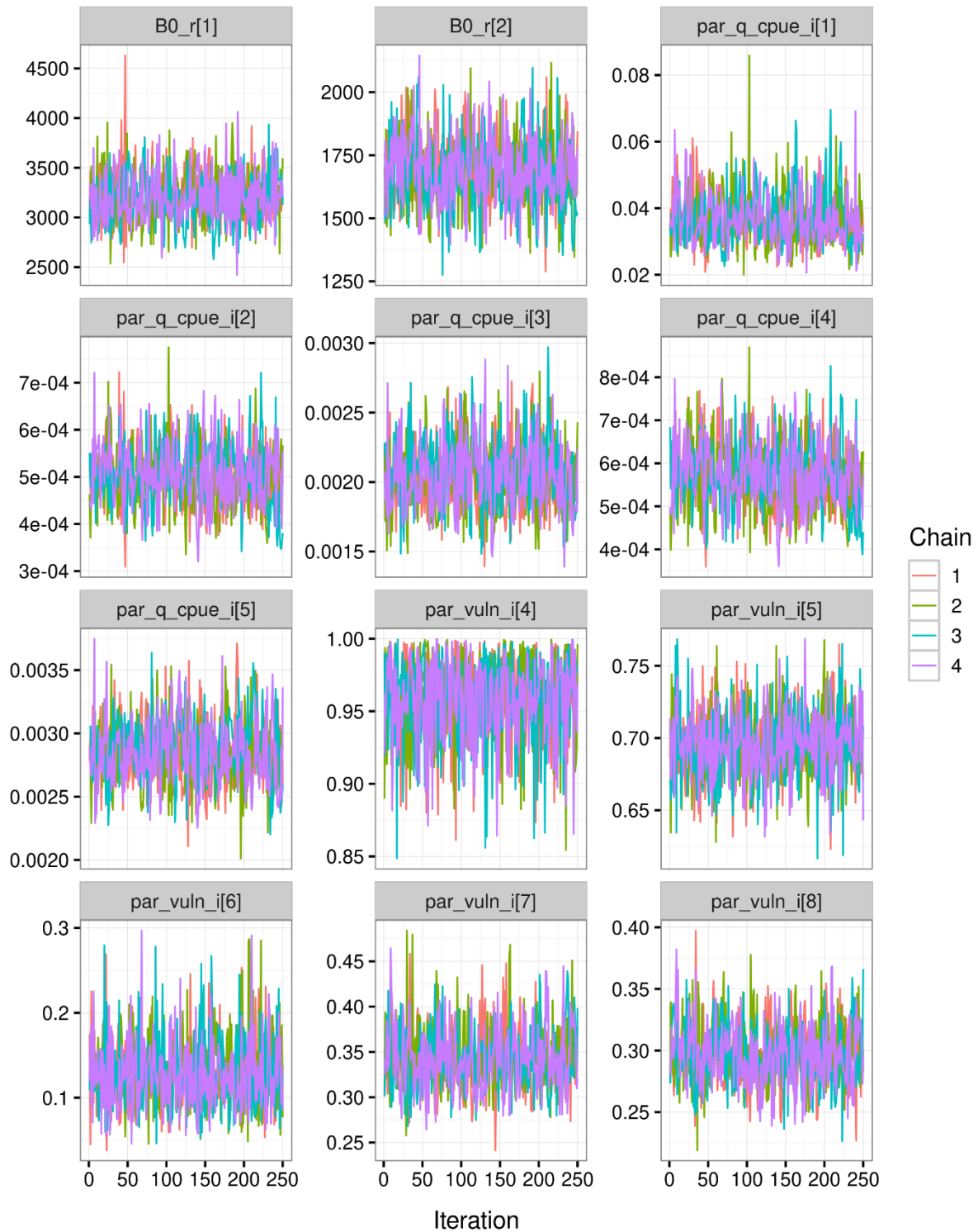


Figure 33: MCMC trace plots by independent chain for catchability coefficients (q) and remaining vulnerability parameters for the base case model run.

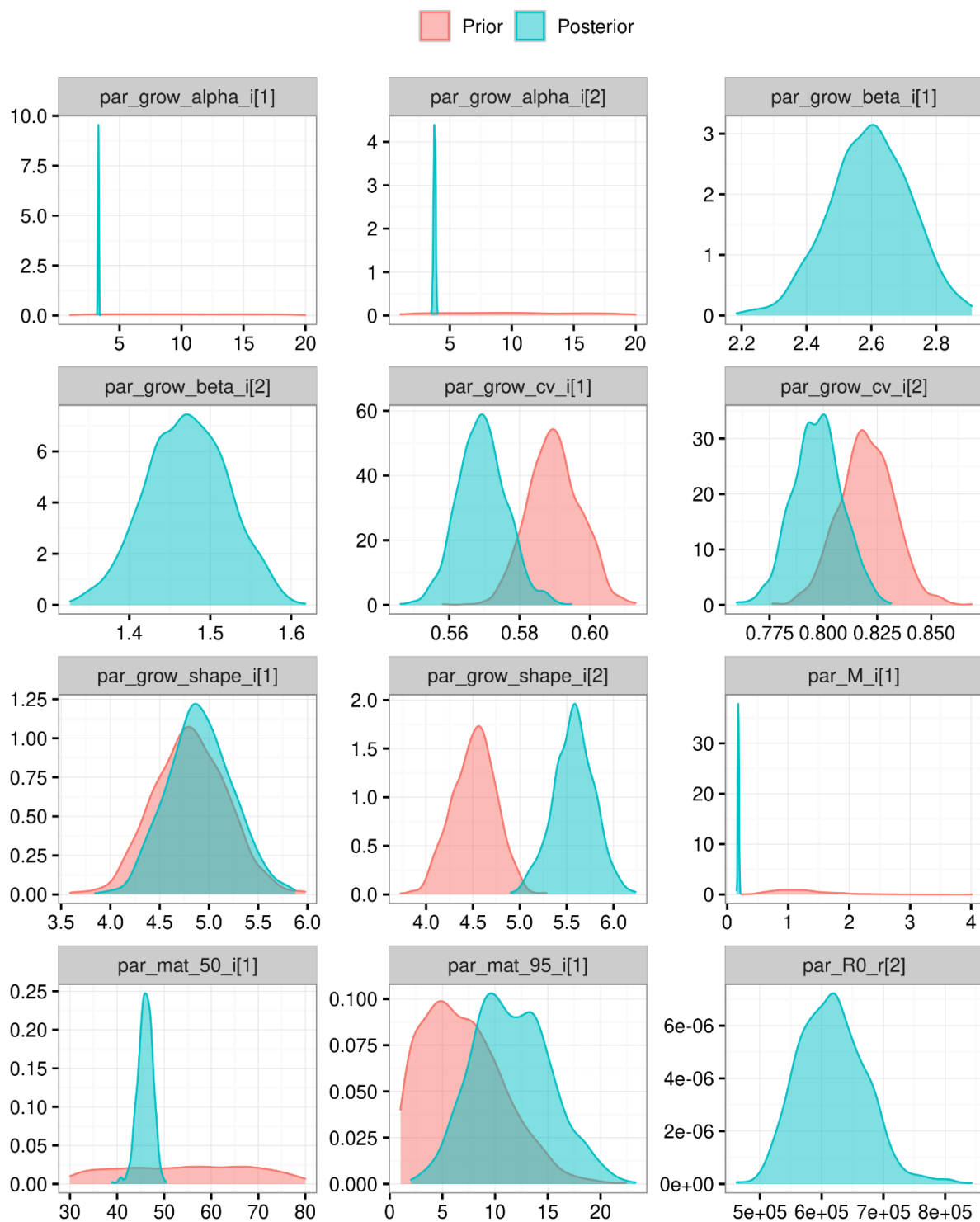


Figure 34: Density plots showing prior (red) and posterior distributions (blue) for growth, natural mortality (M), and maturity parameters for the base case model run.

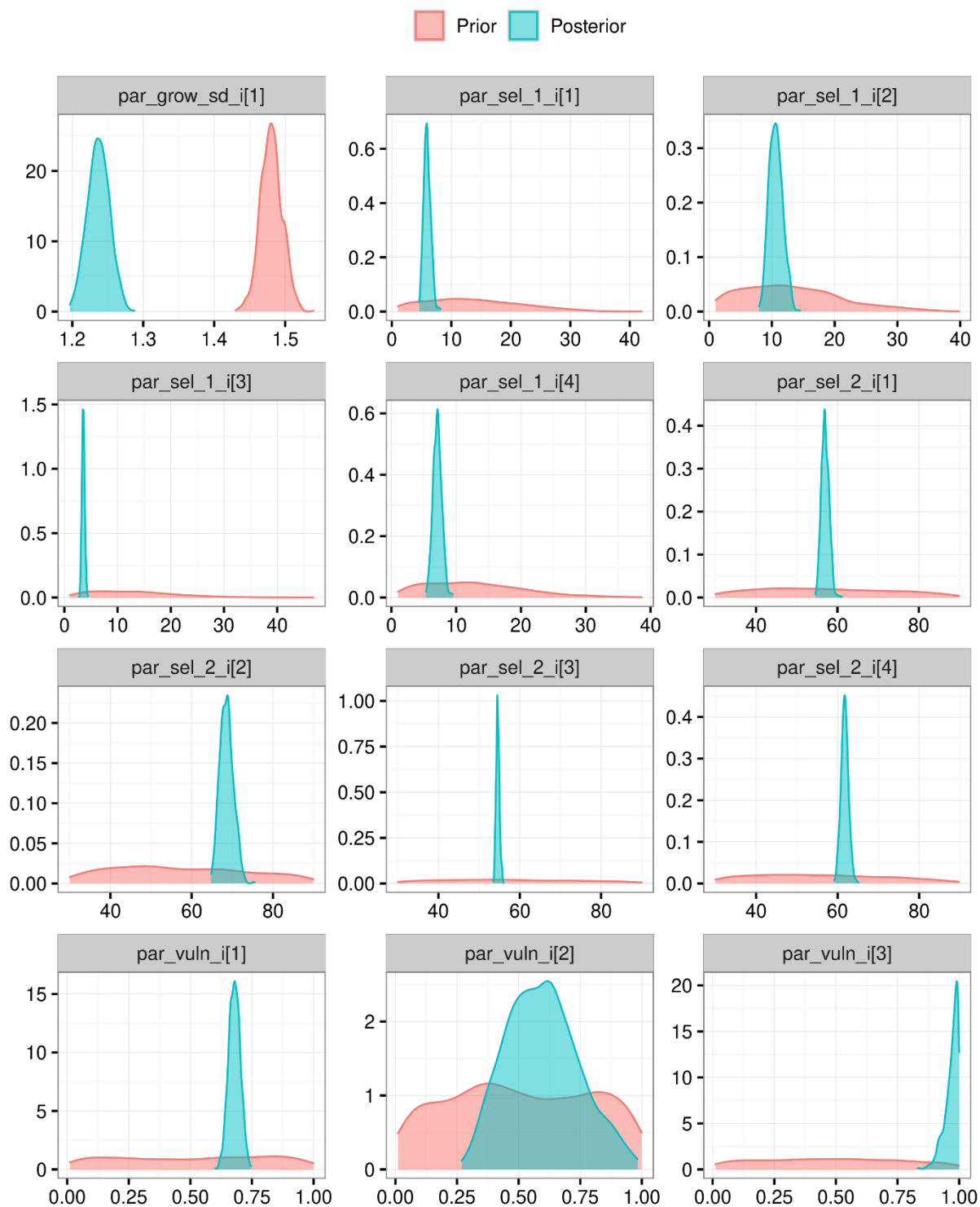


Figure 35: Density plots showing prior (red) and posterior distributions (blue) for growth, selectivity, and vulnerability parameters for the base case model run.

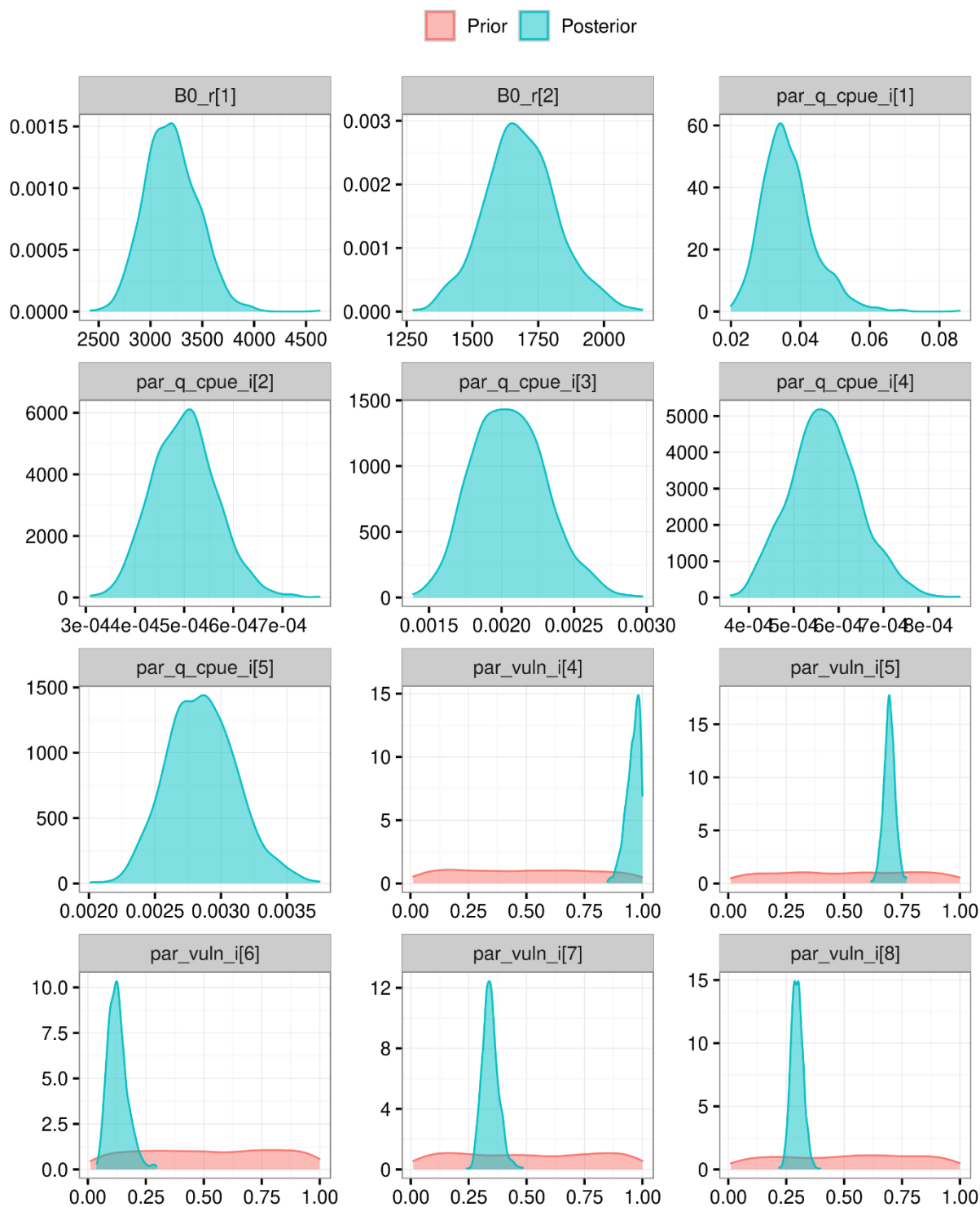


Figure 36: Density plots showing prior (red) and posterior distributions (blue) for B_0 , CPUE catchabilities, and the remaining vulnerability parameters for the base case model run.

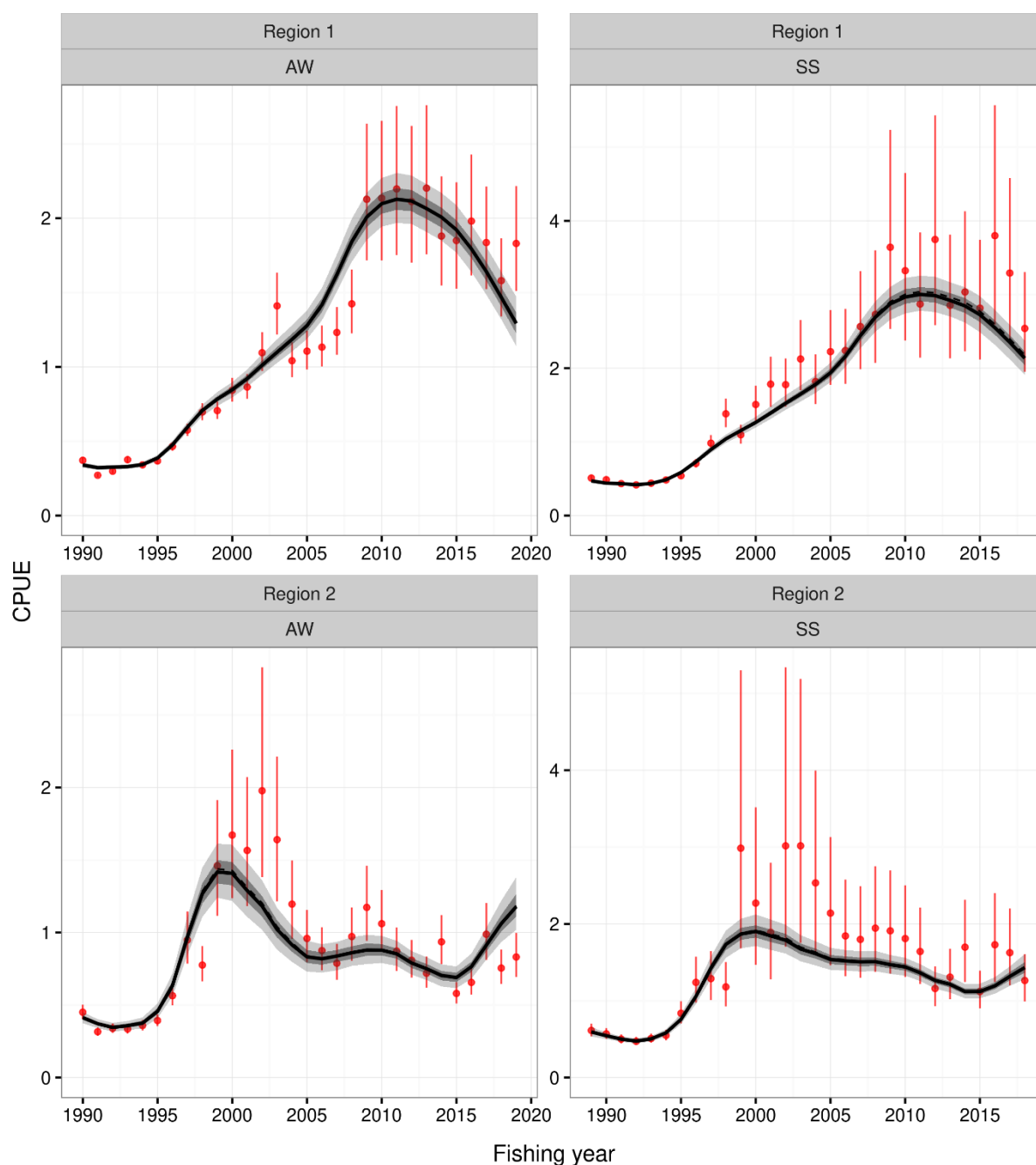


Figure 37: Posterior predicted CPUE compared with the CELR CPUE indices by fishing year, season (AW = autumn-winter, SS = spring-summer), and region in the base case model run. The solid line indicates the posterior median and grey shading with variable intensity indicates the 50% and 90% credible intervals. A dashed line (often not visible as it is covered by the median line) indicates the corresponding MAP estimates.

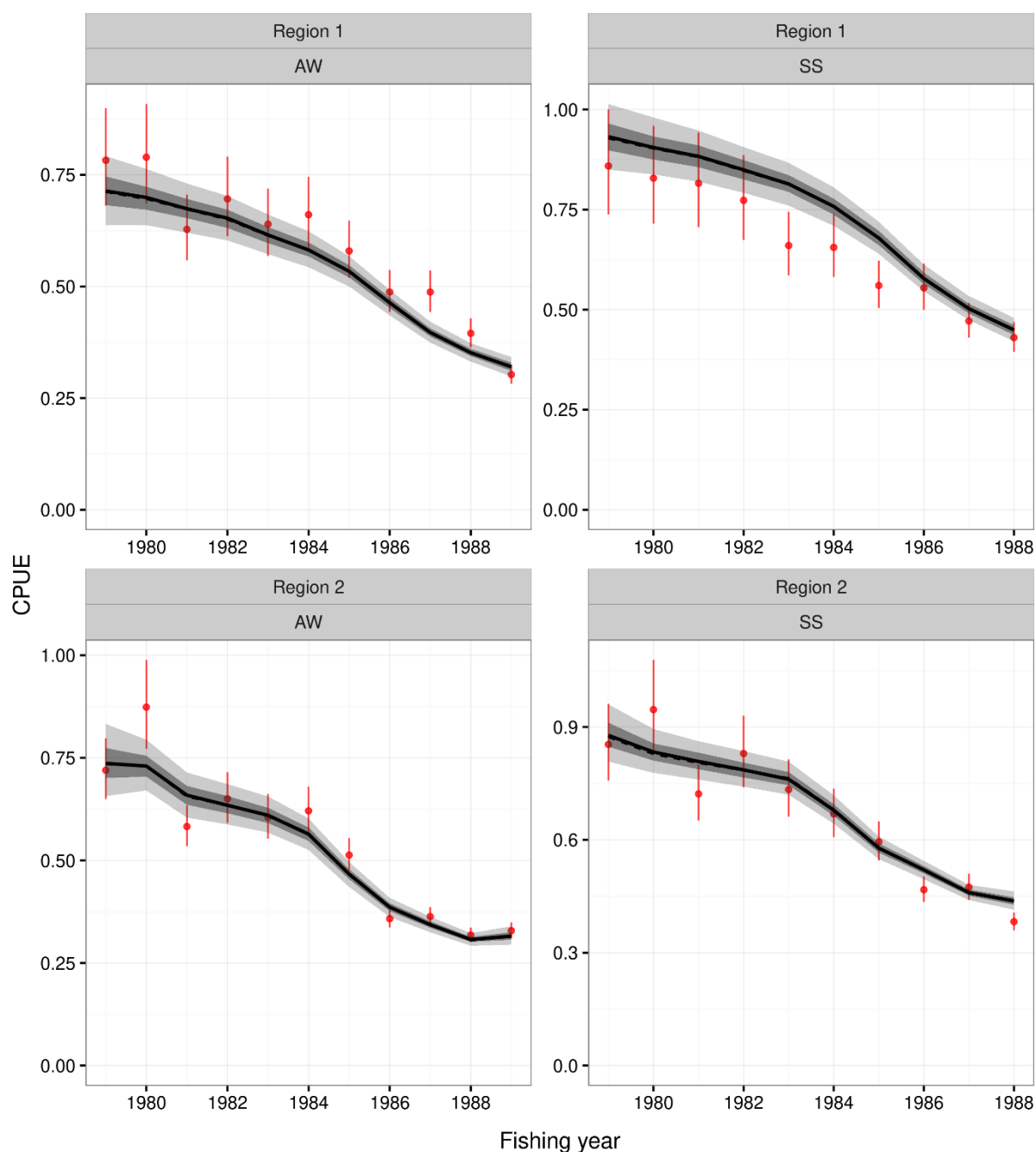


Figure 38: Posterior predicted CPUE compared with the FSU CPUE indices by fishing year, season (AW = autumn-winter, SS = spring-summer), and region in the base case model run. The solid line indicates the posterior median and grey shading with variable intensity indicates the 50% and 90% credible intervals. A dashed line (often not visible as it is covered by the median line) indicates the corresponding MAP estimates.

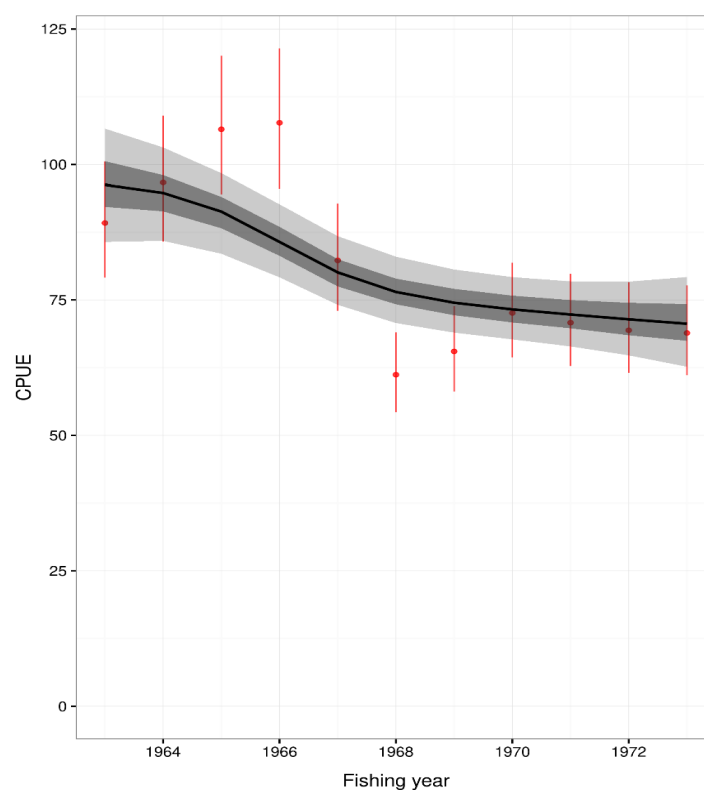


Figure 39: Posterior predicted CPUE compared with the CR CPUE indices by fishing year in the base case model run. The solid line indicates the posterior median and grey shading with variable intensity indicates the 50% and 90% credible intervals. A dashed line (often not visible as it is covered by the median line) indicates the corresponding MAP estimates.

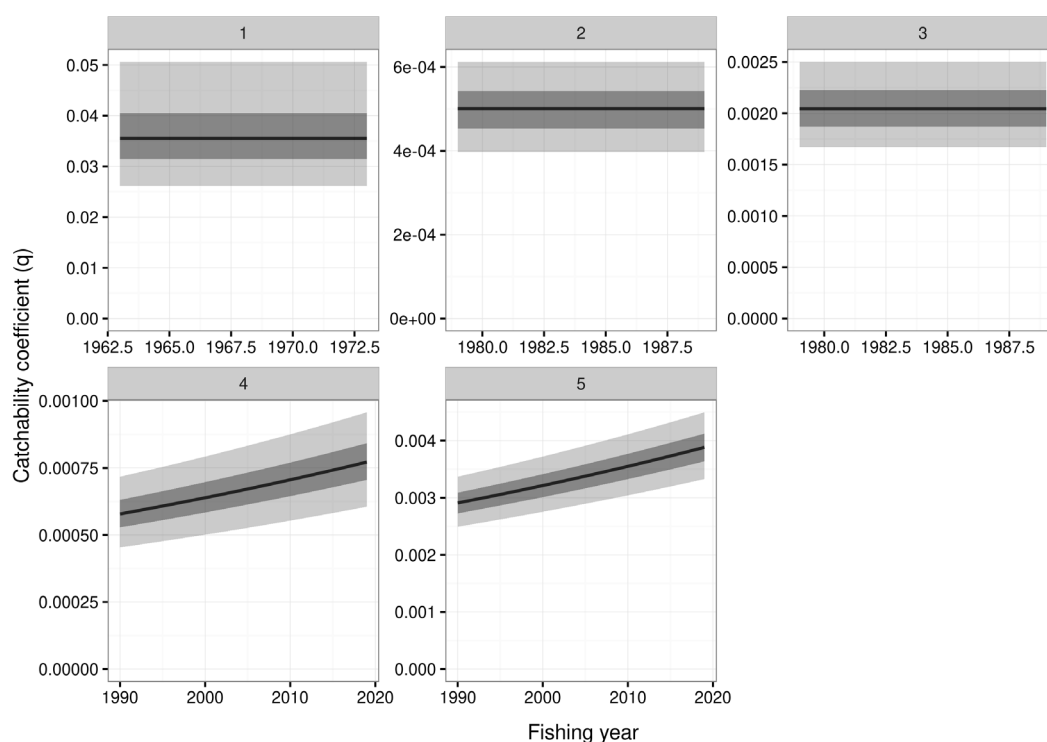


Figure 40: Posterior distribution of the catchability coefficient (q) by fishing year and CPUE series in the base case model run. The solid line indicates the posterior median and grey shading with variable intensity indicates the 50% and 90% credible intervals. The panels are: 1 = CR CPUE series in region 1; 2 = FSU CPUE series in region 1; 3 = FSU CPUE series in region 2; 4 = CELR CPUE series in region 1, 5 = CELR CPUE series in region 2.

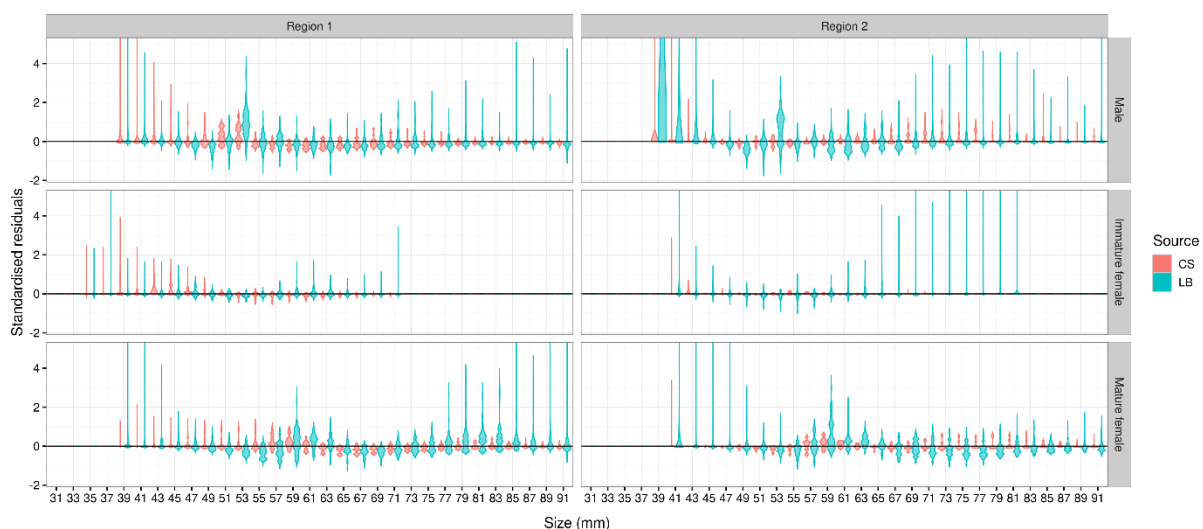


Figure 41: Posterior distribution of standardised residuals from fits to the LF data by region, sex, 2 mm TW bin, and sampling source (CS = catch sampling, LB = logbook).

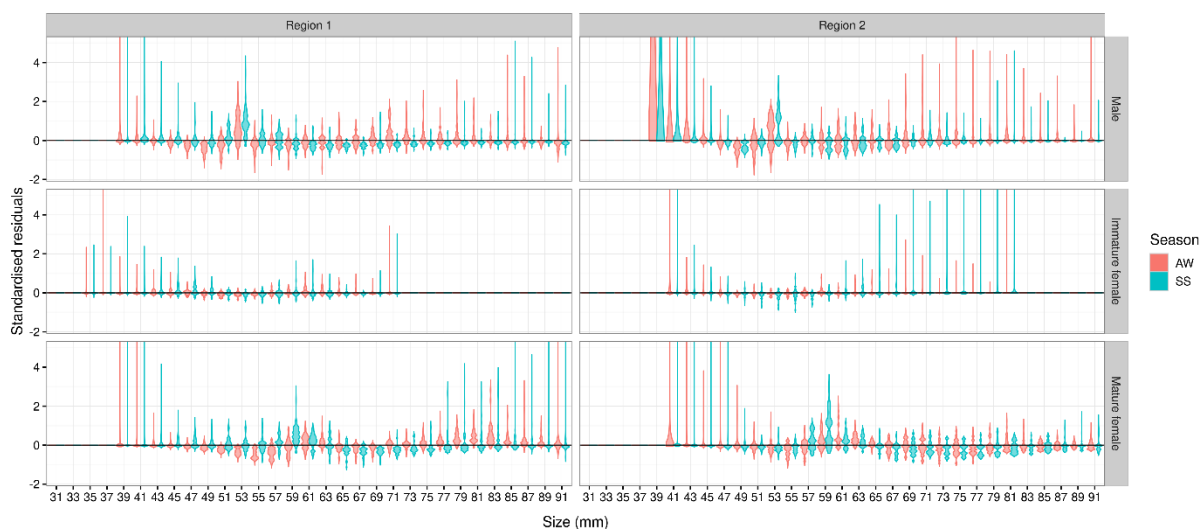


Figure 42: Posterior distribution of standardised residuals from fits to the LF data by region, sex, year, 2 mm TW bin, and season (AW = autumn-winter, SS = spring-summer).

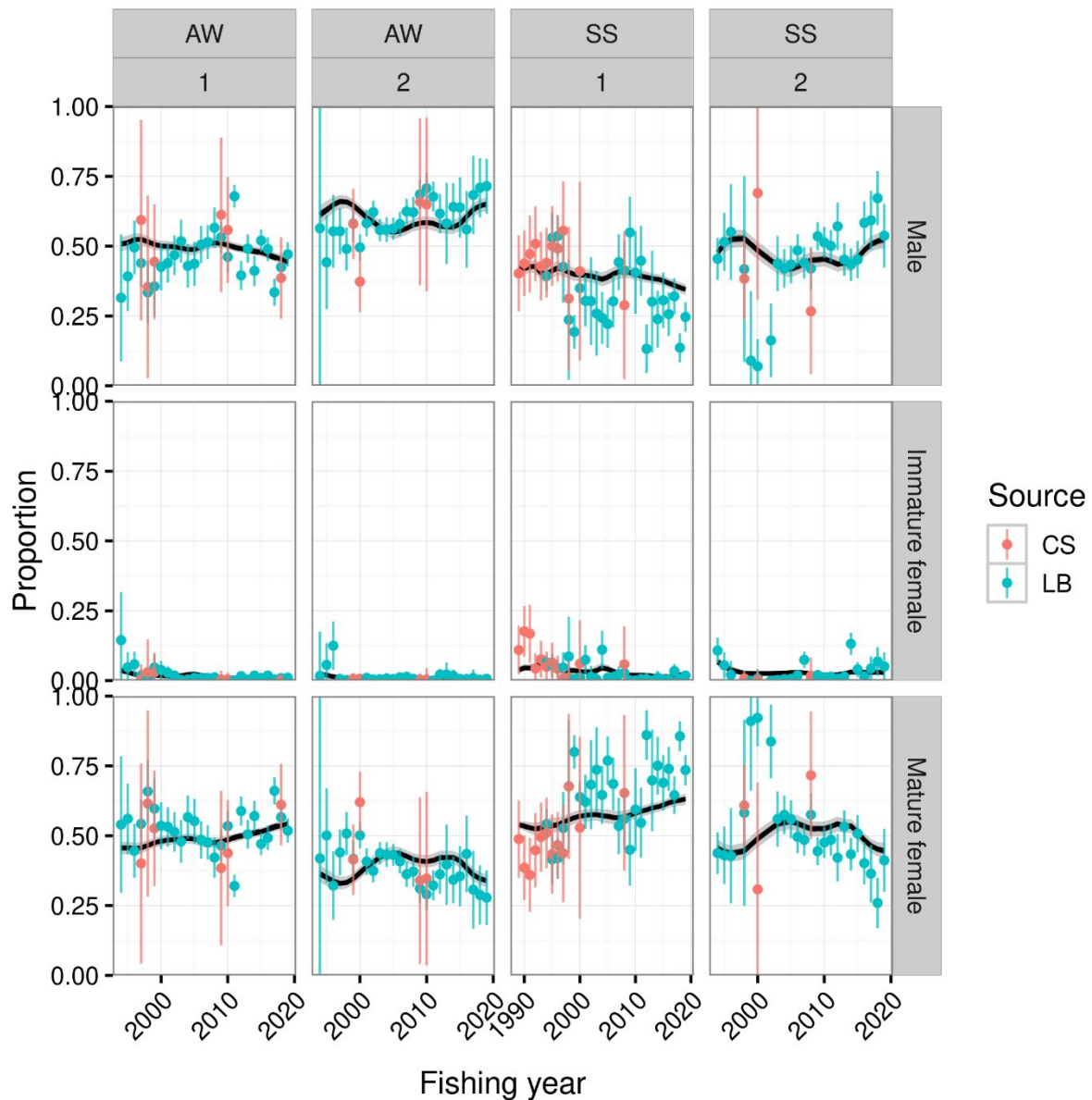


Figure 43: Posterior distribution of the sex-ratios compared to the observed sex-ratios by fishing year, season (AW = autumn-winter, SS = spring-summer), region (1 = region 1; 2 = region 2), sex, and LF data source (CS = catch sampling, LB = logbook) in the base case model run. The solid line indicates the posterior median and grey shading with variable intensity indicates the 90% credible intervals.

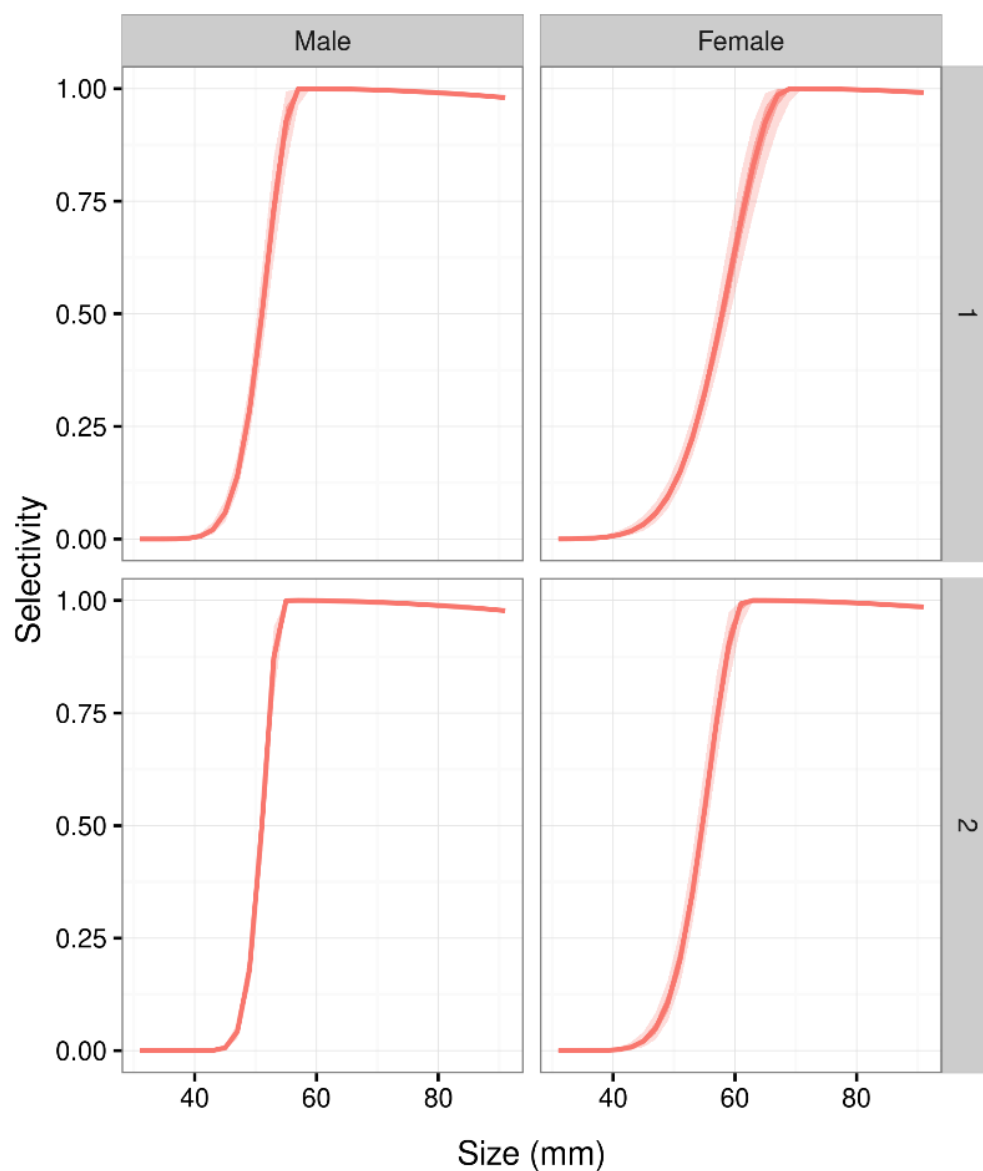


Figure 44: Posterior distribution of selectivity by sex, size, and region in the base case model run; the solid line indicates the posterior median and shading with variable intensity indicates the 50% and 90% credible intervals.

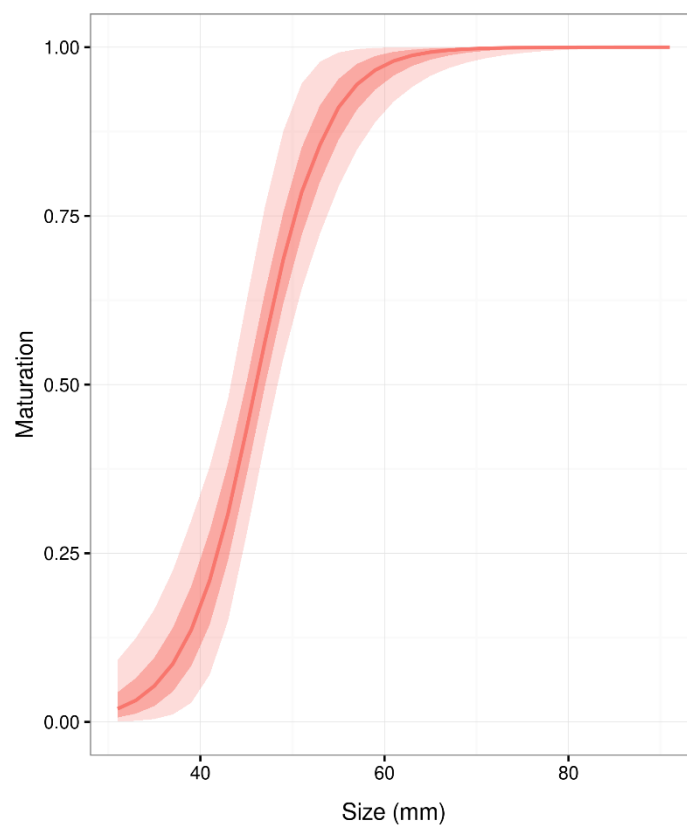


Figure 45: Posterior distribution of female maturation curve by size in the base case model run; the solid line indicates the posterior median and shading with variable intensity indicates the 50% and 90% credible intervals.

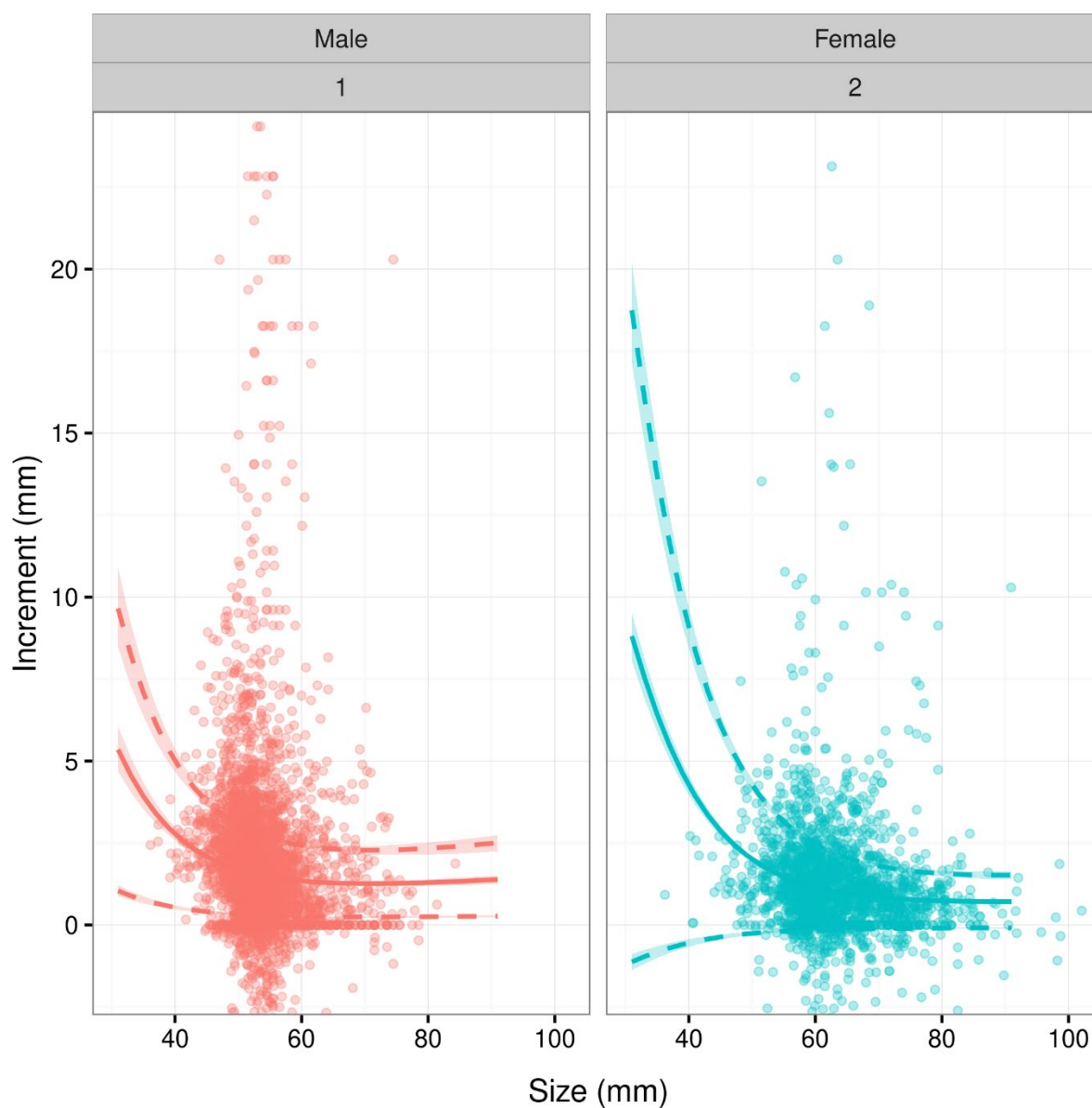


Figure 46: Posterior distribution of predicted 6-monthly growth increment by size and sex in the base case model run showing the mean (solid line), ± 1 standard deviation (dashed line), and observed growth increments divided by time-at-liberty (points).

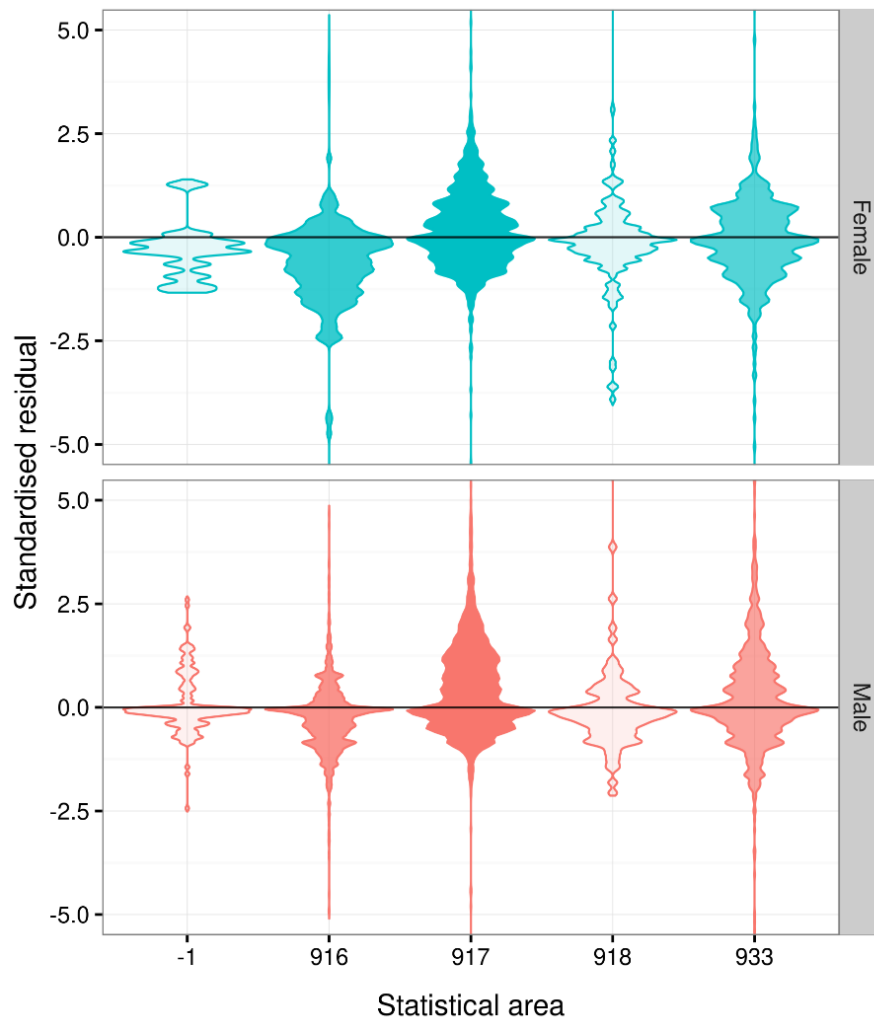


Figure 47: Posterior distribution of standardised residuals from model fit to the tag data by statistical area of release and sex in the base case model run. Darker shading indicates a higher number of observations.

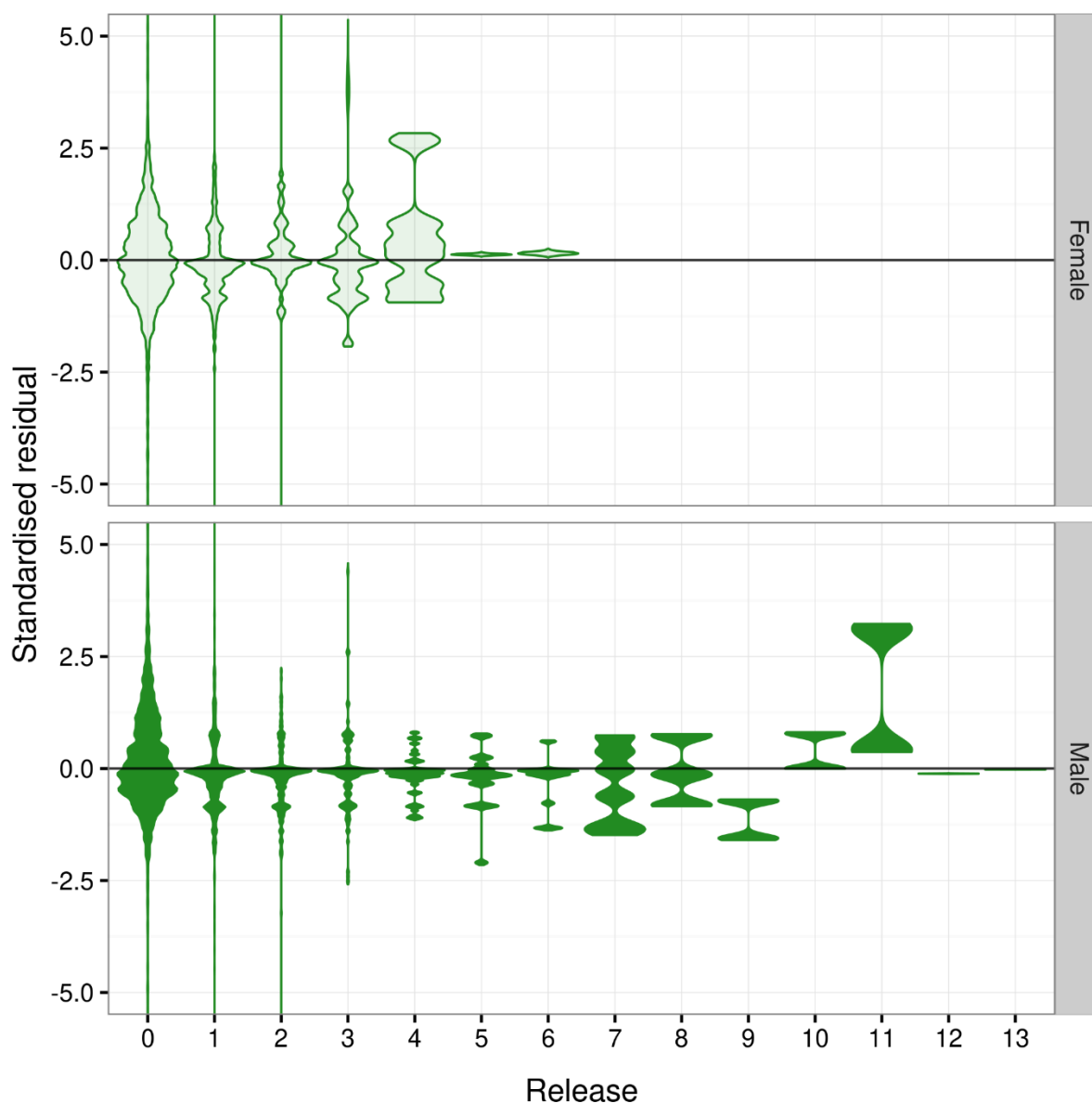


Figure 48: Posterior distribution of standardised residuals from model fit to the tag data by number of times released and sex in the base case model run. Darker shading indicates a higher number of observations.

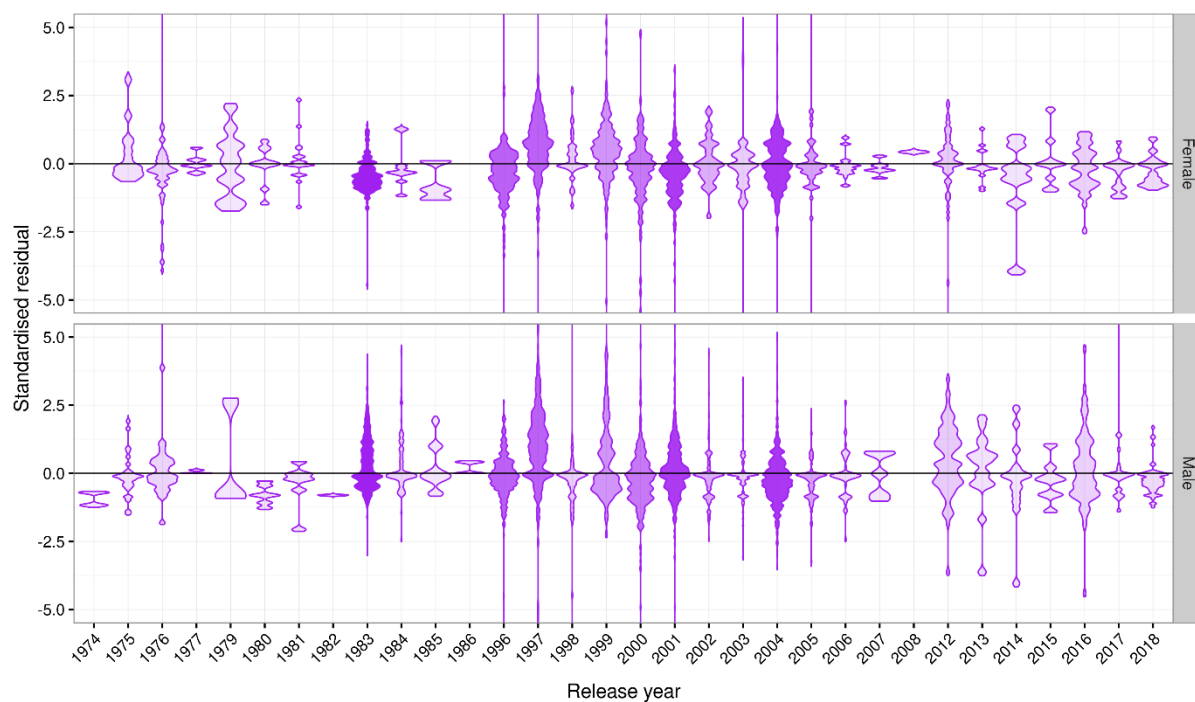


Figure 49: Posterior distribution of standardised residuals from model fit to the tag data by fishing year of release and sex in the base case model run. Darker shading indicates a higher number of observations.

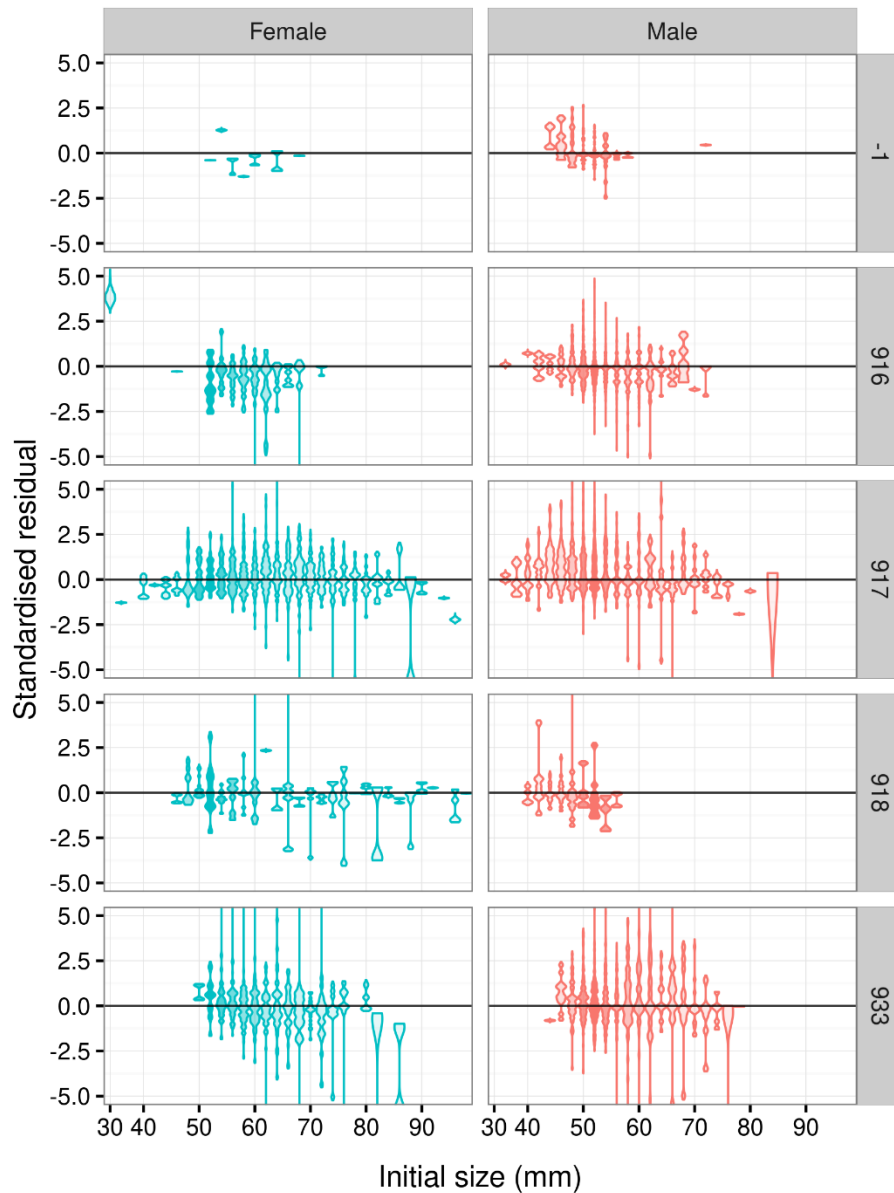


Figure 50: Posterior distribution of standardised residuals from model fit to the tag data by statistical area of release, initial size (tail width bin), and sex in the base case model run. Darker shading indicates a higher number of observations. “-1” indicates an unknown statistical area within CRA 5.

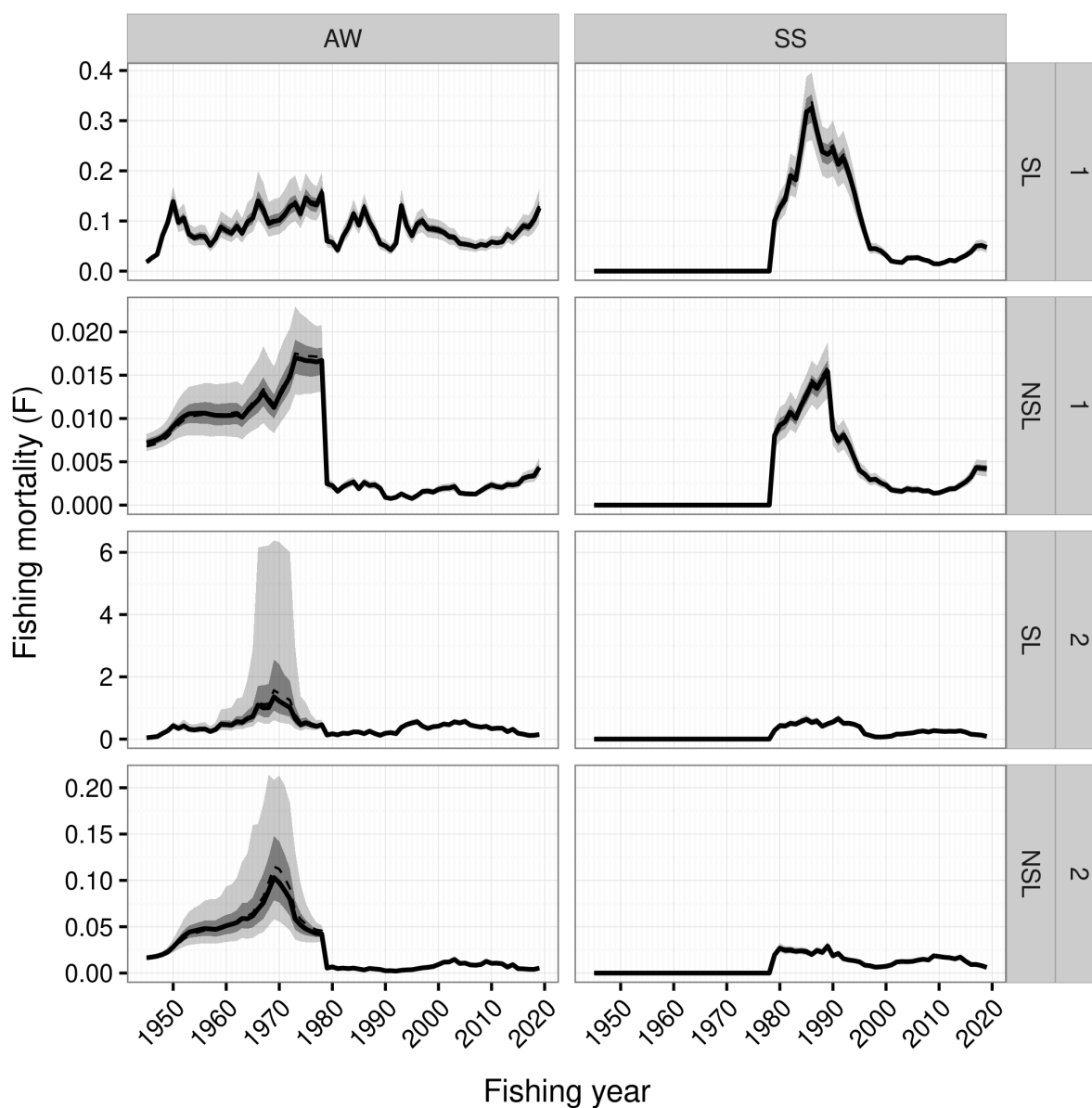


Figure 51: Posterior distribution of fishing mortality by year, season (AW = autumn-winter, SS = spring-summer), region, and fishery (SL = size limited; NSL = non size limited) for the base case model run. The dashed black line (not always visible) indicates the MAP, the solid black line indicates the median of the posterior and variable shading intensity indicating the 50% and 90% credible intervals.

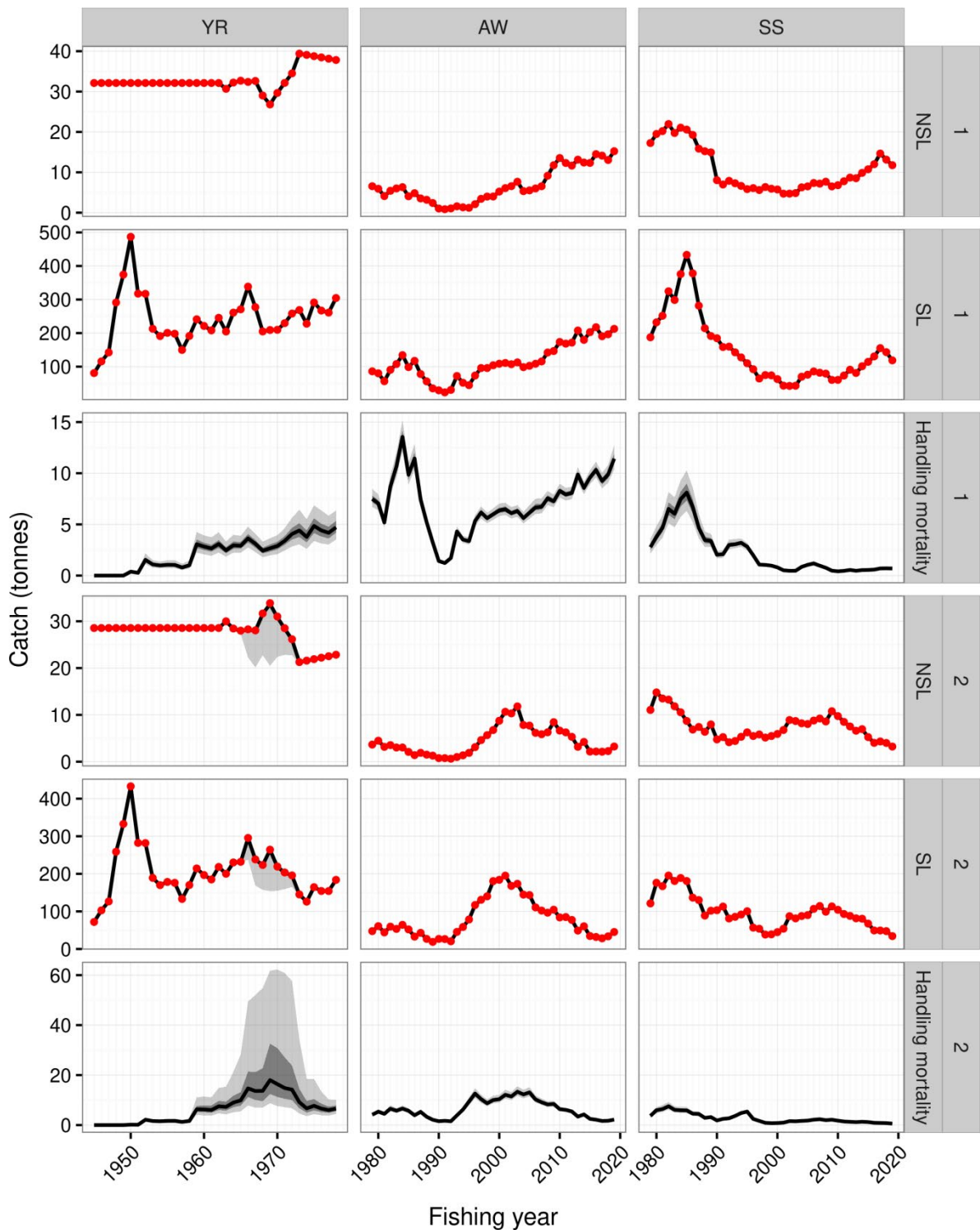


Figure 52: Posterior distribution of catch (tonnes) and handling mortality (tonnes) by fishing year, season (AW = autumn-winter, SS = spring-summer), region, and fishery (SL = size limited; NSL = non size limited) for the base case model run. The dashed black line (not always visible) indicates the MAP, the solid black line indicates the median of the posterior and variable shading intensity indicating the 50% and 90% credible intervals. Note that the columns separate the 1945–1978 annual catches (left column) from the 1979–2019 seasonal catches (right columns).

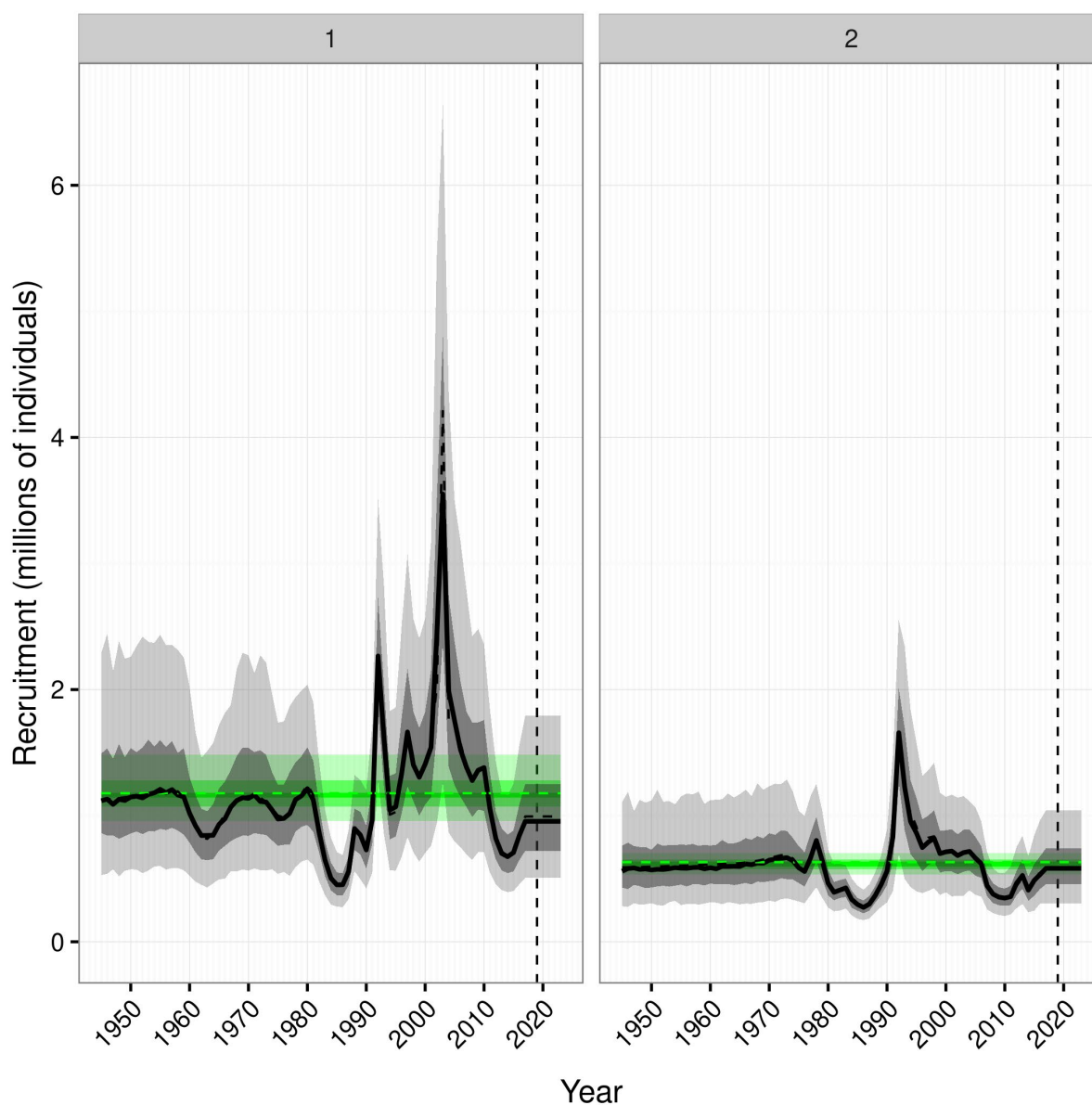


Figure 53: Posterior distribution of recruitment by region for the base case model run. Horizontal green line is R_0 and vertical dashed line is the final year of the reconstruction period. The solid black line indicates the median of the posterior and variable shading intensity indicates the 50% and 90% credible intervals.

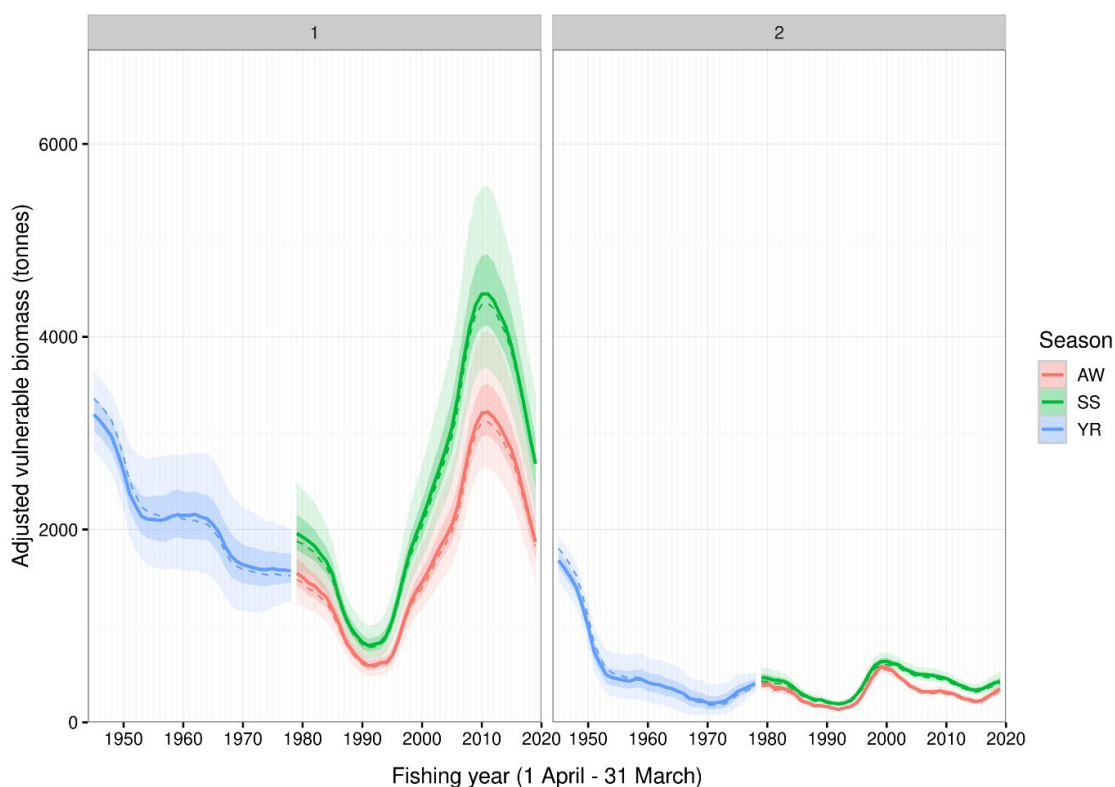


Figure 54: Posterior distribution of the adjusted vulnerable biomass by season (AW = autumn-winter, SS = spring-summer) and region for the base case model run. Dashed lines indicate the equivalent MAP estimates. Variable shading intensity indicates the 50% and 90% credible intervals.

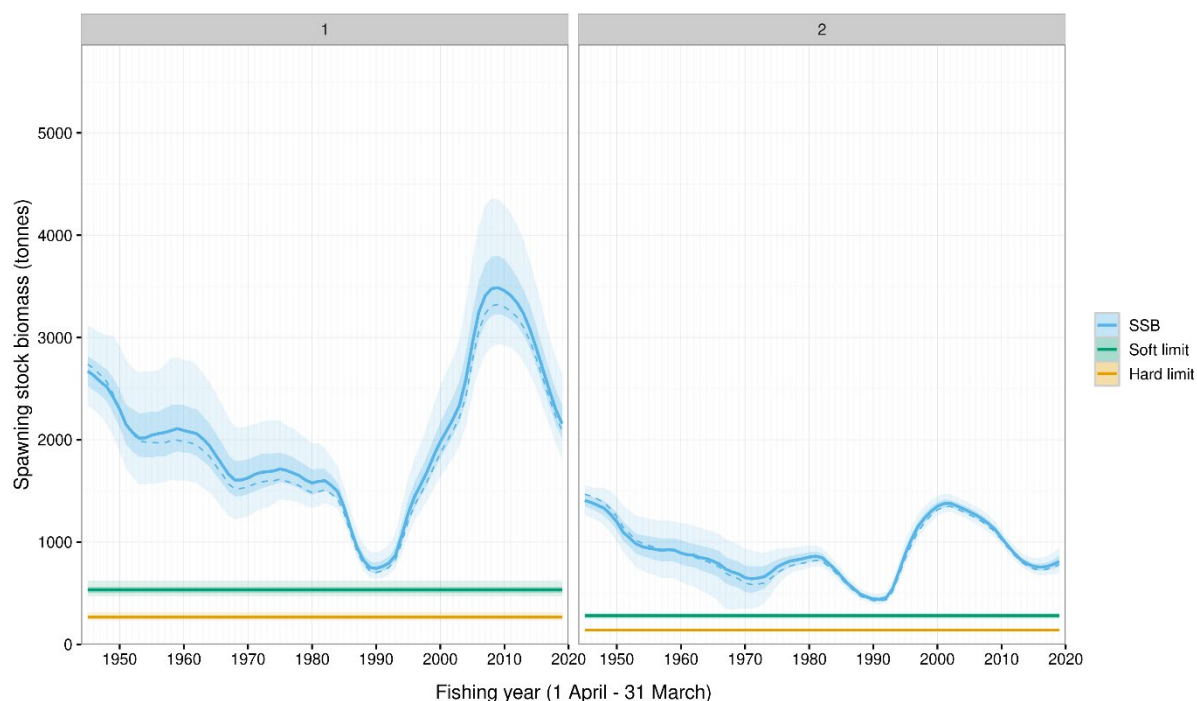


Figure 55: Posterior distribution of the spawning stock biomass (SSB) by region for the base case model run. Dashed lines indicating the equivalent MAP estimates. Variable shading intensity indicates the 50% and 90% credible intervals. Also plotted for each model run is the posterior distribution of the soft limit (20% SSB_0), and the hard limit (10% SSB_0).

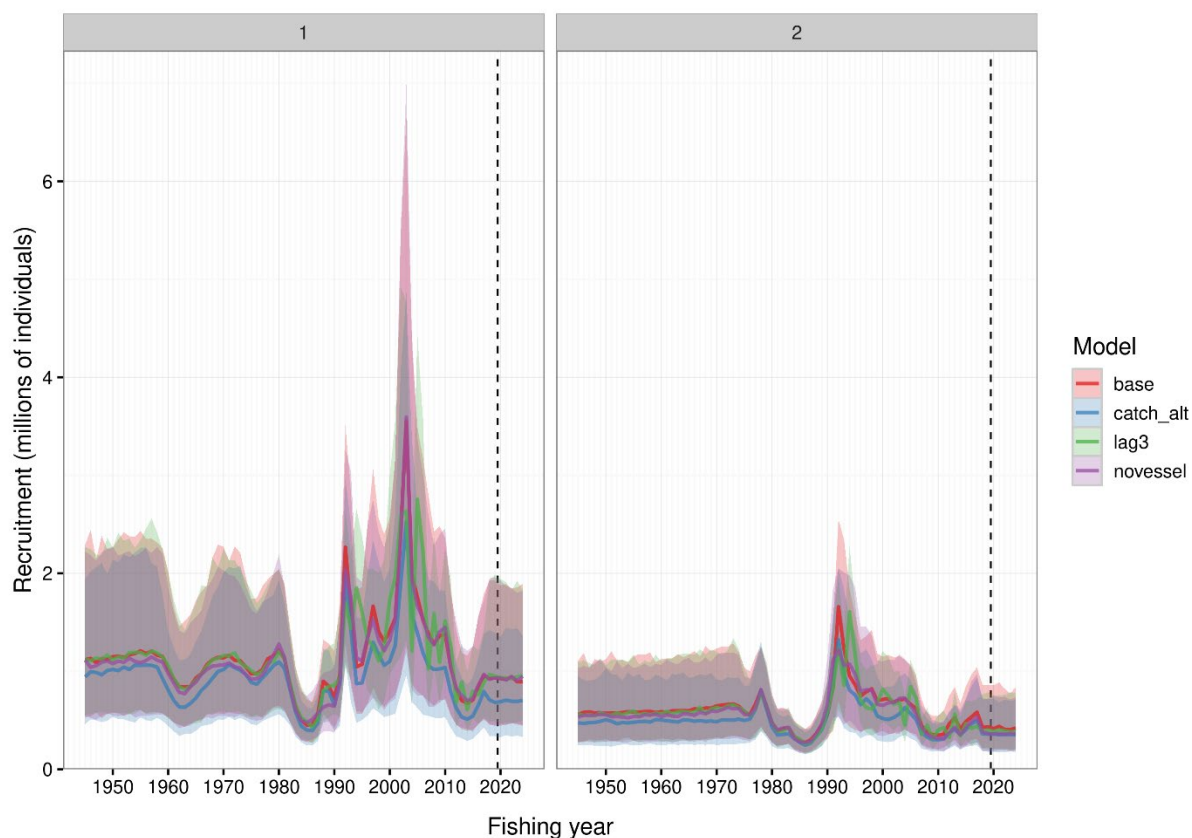


Figure 56: Posterior distribution of recruitment trajectories between the base run and the three sensitivity runs (*novessel*, *lag3*, and *catch_alt*), including projection years (beyond the dashed vertical line), for all MCMC model runs.

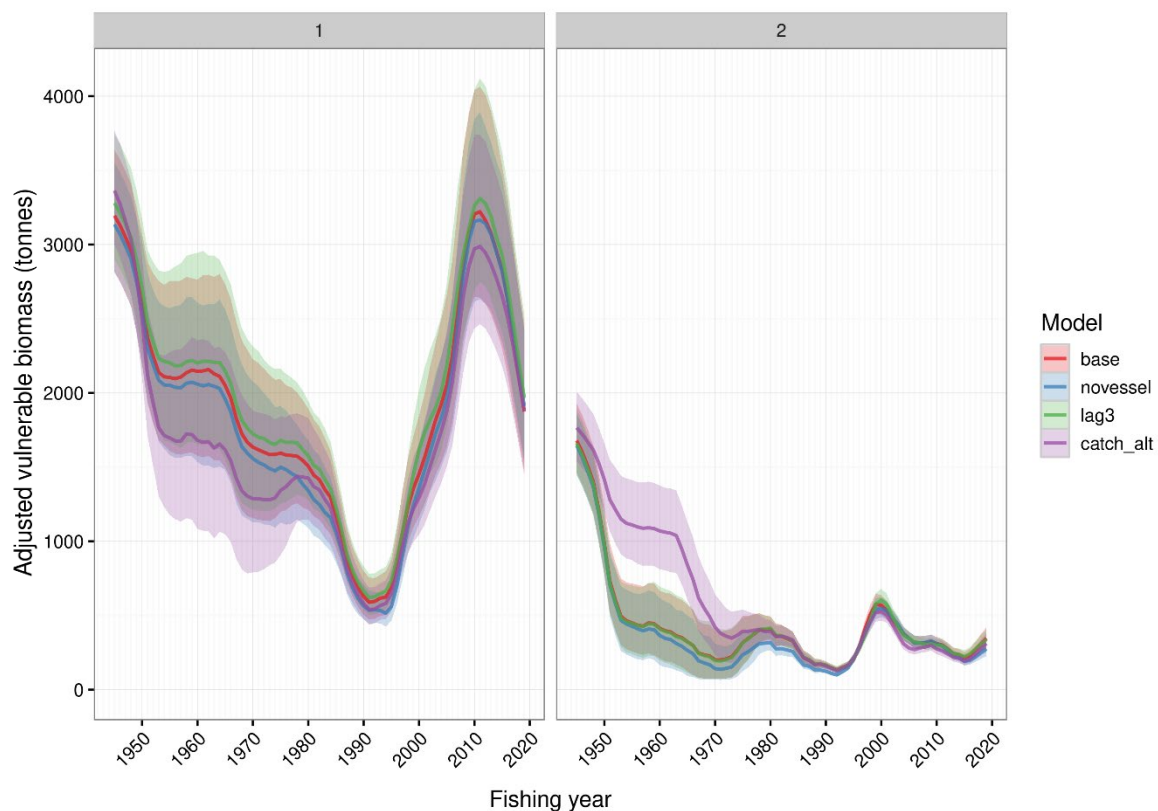


Figure 57: Posterior distribution of adjusted vulnerable biomass by region comparing the base case run and the three sensitivity runs (*novessel*, *lag3*, and *catch_alt*).

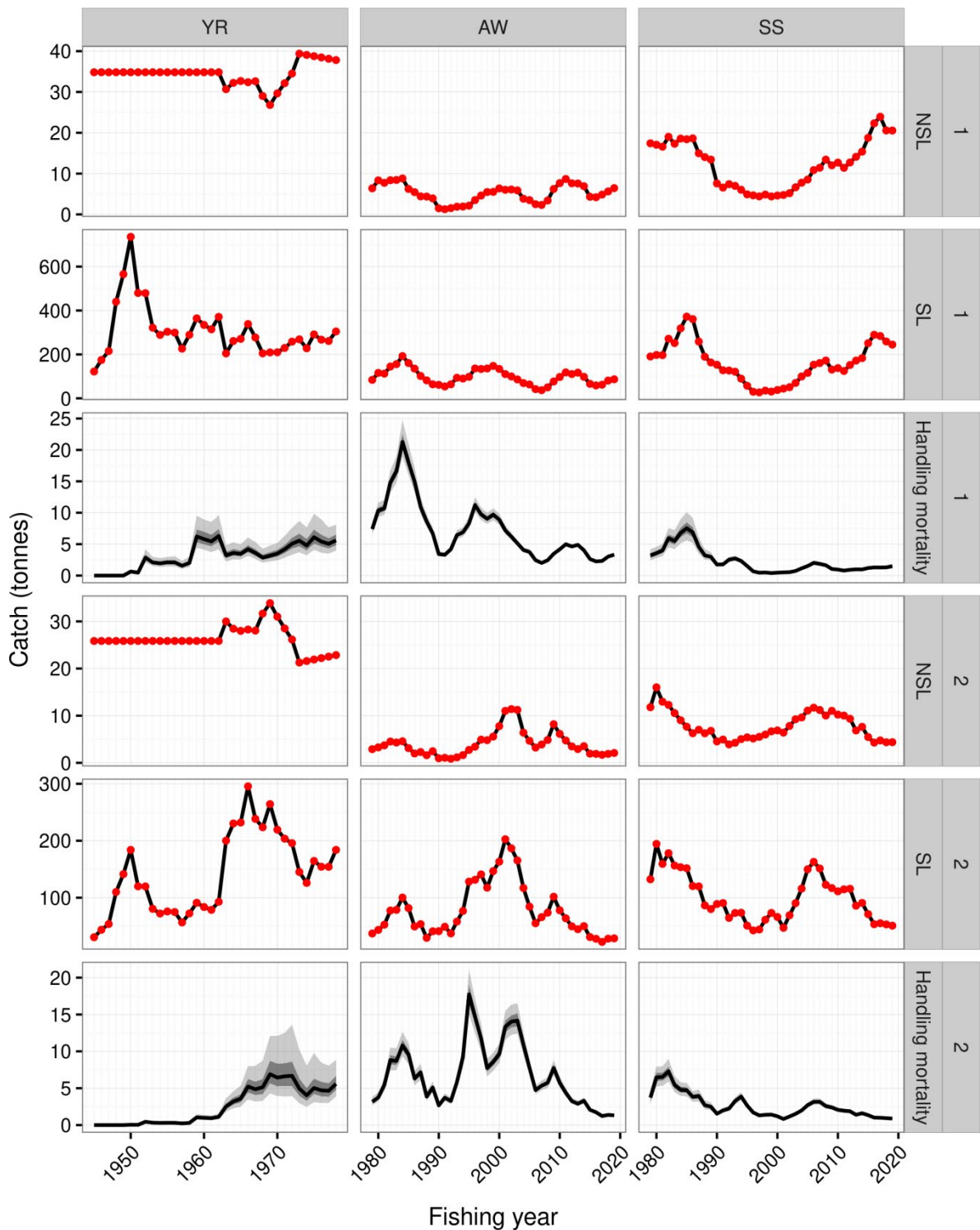


Figure 58: Posterior distribution of catch by year, season (AW = autumn-winter, SS = spring-summer), region, and fishery (SL = size limited; NSL = non size limited) for the *catch_alt* sensitivity run. The dashed black line (not always visible) indicates the MAP, the solid black line indicates the median of the posterior, and variable shading intensity indicates the 50% and 90% credible intervals. Note that the columns separate the 1945–1978 annual catches (left column) from the 1979–2019 seasonal catches (right columns).

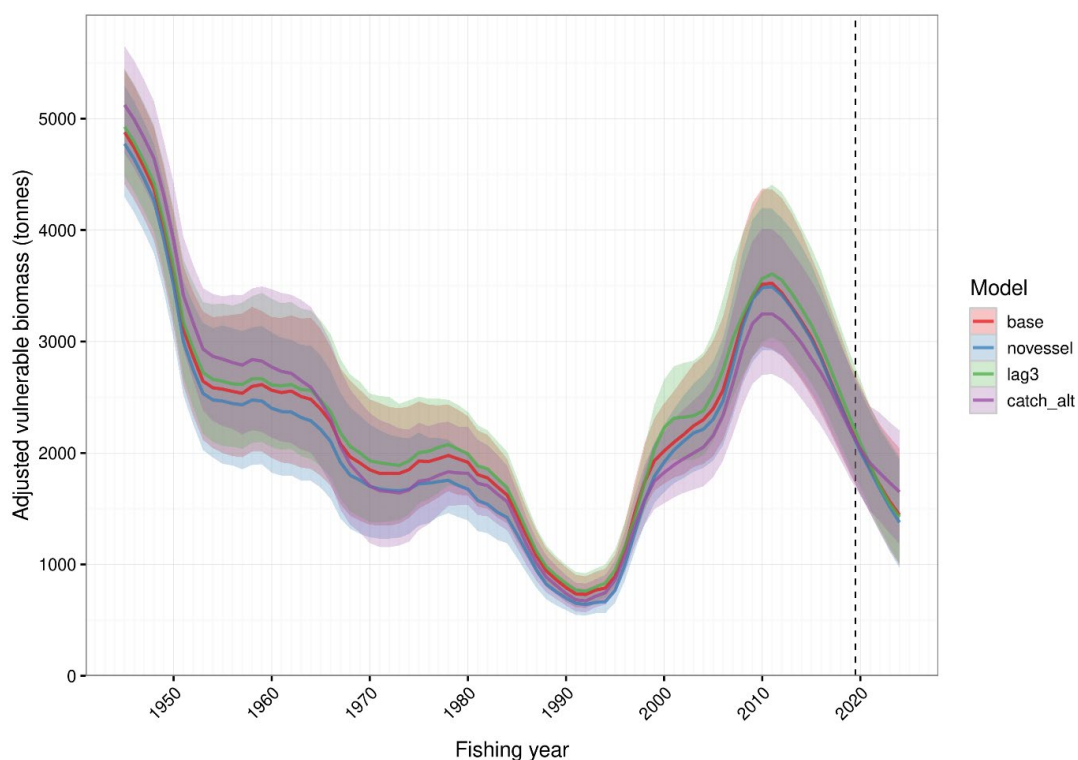


Figure 59: Posterior distribution of adjusted vulnerable biomass (tonnes) by fishing year, including the projections years (beyond the dashed vertical line), for all MCMC model runs. Note that the regional biomass trajectories have been combined into an overall CRA 5 trajectory.

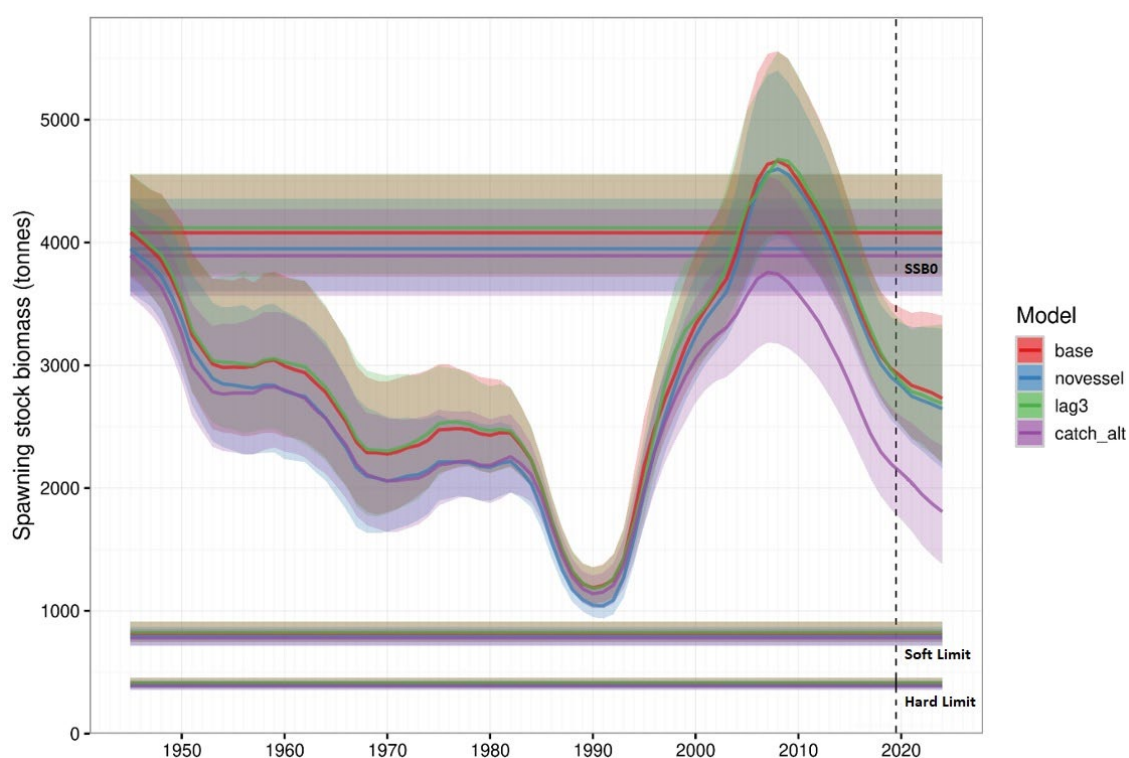


Figure 60: Posterior distribution of spawning stock biomass (tonnes) by fishing year, including the projections years (beyond the dashed vertical line), for all MCMC model runs. Unfished spawning stock biomass (top lines), the associated soft limits (20% SSB_0), and hard limits (10% SSB_0) are also shown. Note that the regional biomass trajectories have been combined into an overall CRA 5 trajectory.

8. APPENDIX I: MCMC LENGTH-FREQUENCY FITS

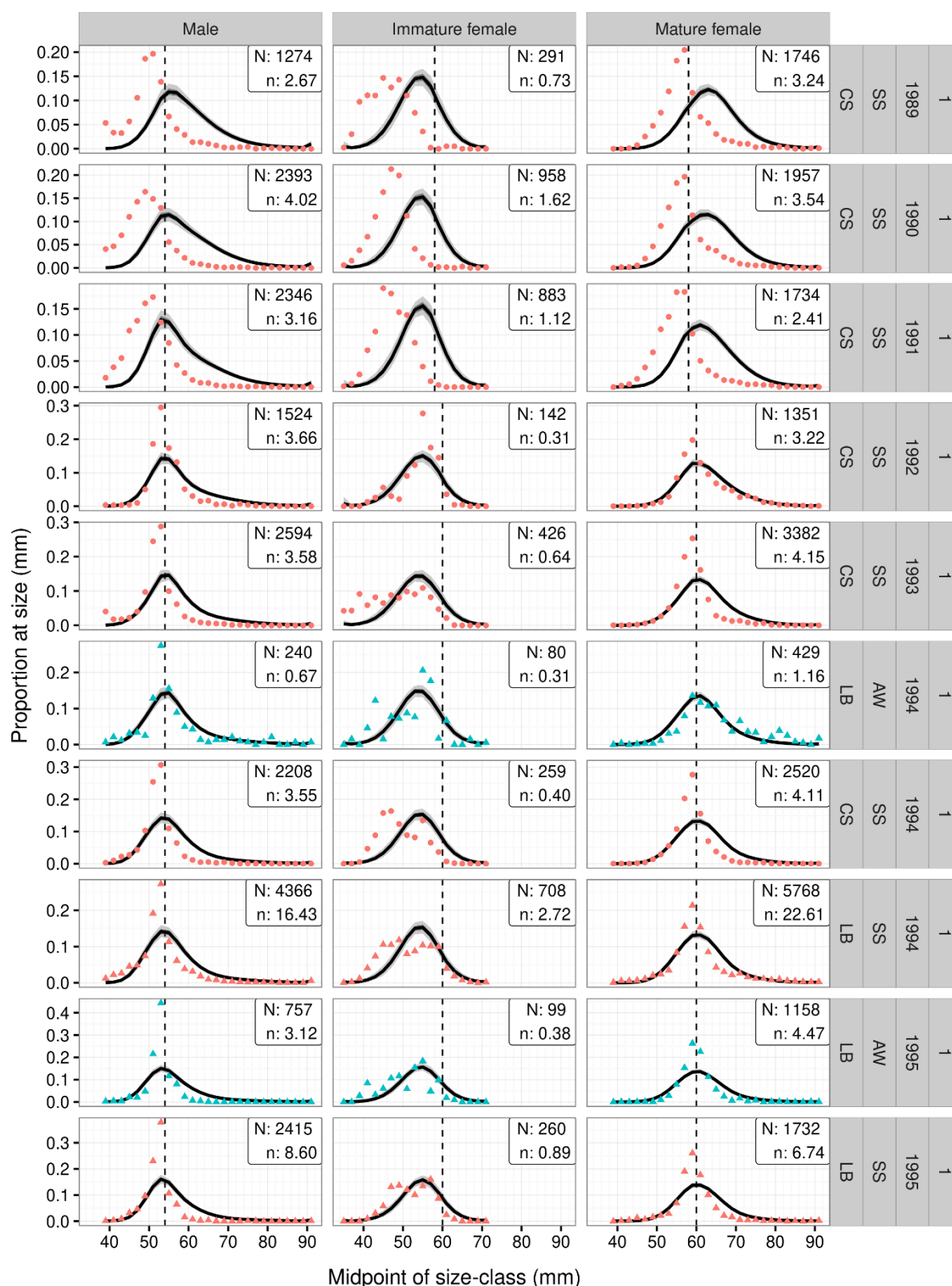


Figure 61: Posterior distribution of the LF fits compared with the observed LF distribution for region 1, fishing year, season (AW = autumn-winter, SS = spring-summer), data source (CS = catch sampling, LB = logbook), and sex in the base case model run. The solid line indicates the posterior median and grey shading with variable intensity indicates the 50% and 90% credible intervals. In each panel the value for “N” is the number of lobsters in the sample, and “n” is the effective sample size.

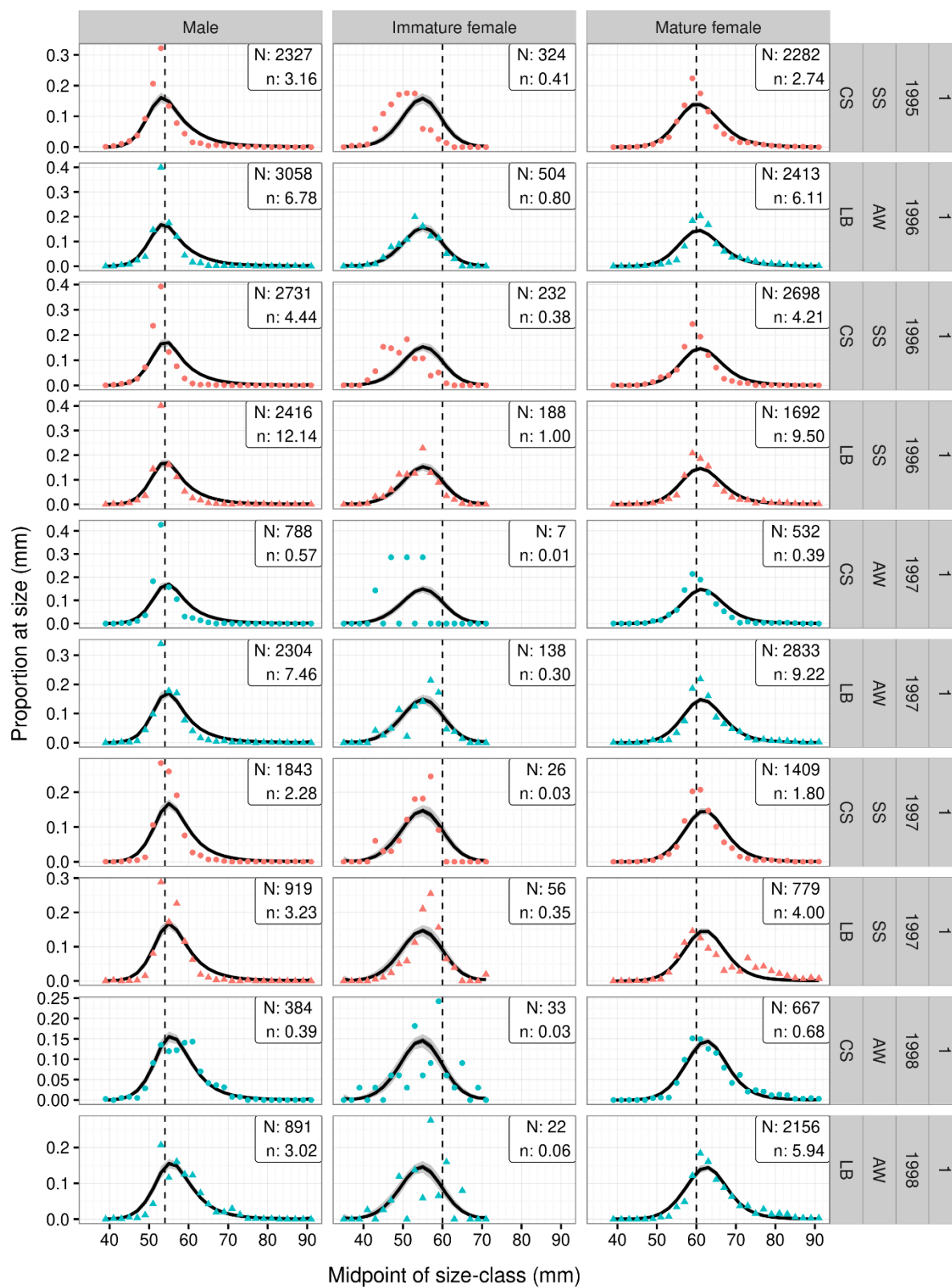


Figure 61 (cont.):

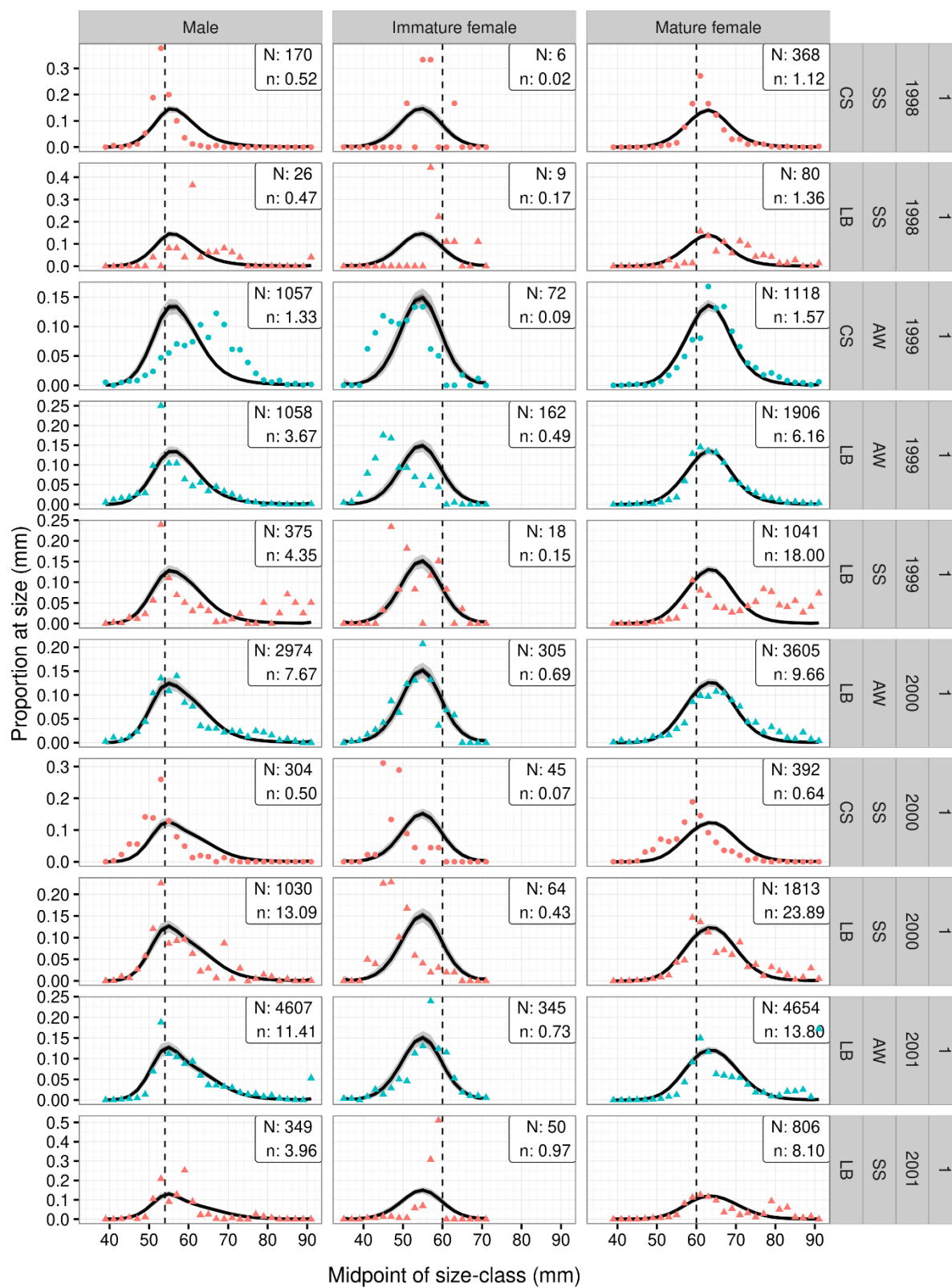


Figure 61 (cont.):

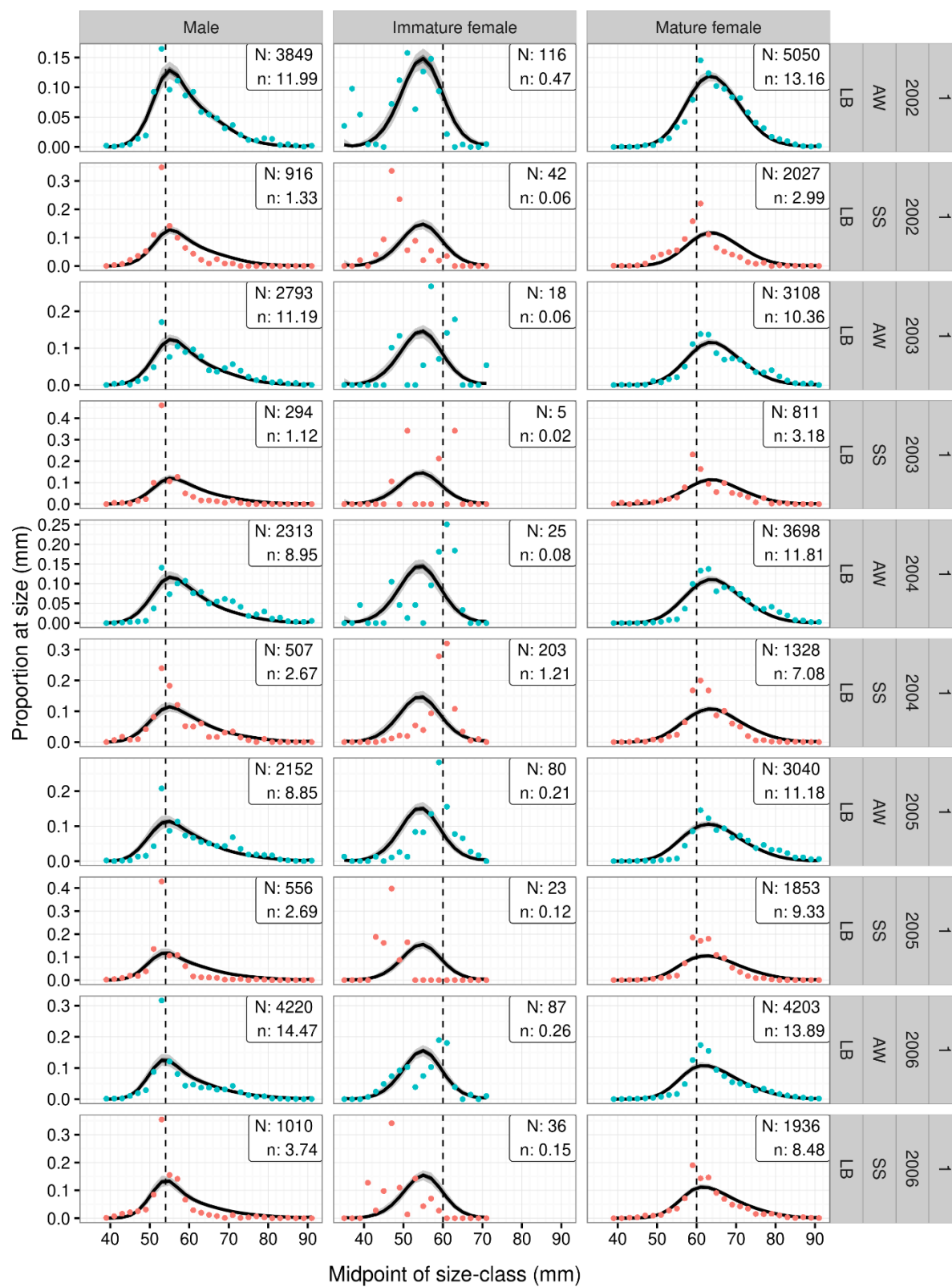


Figure 61 (cont.):

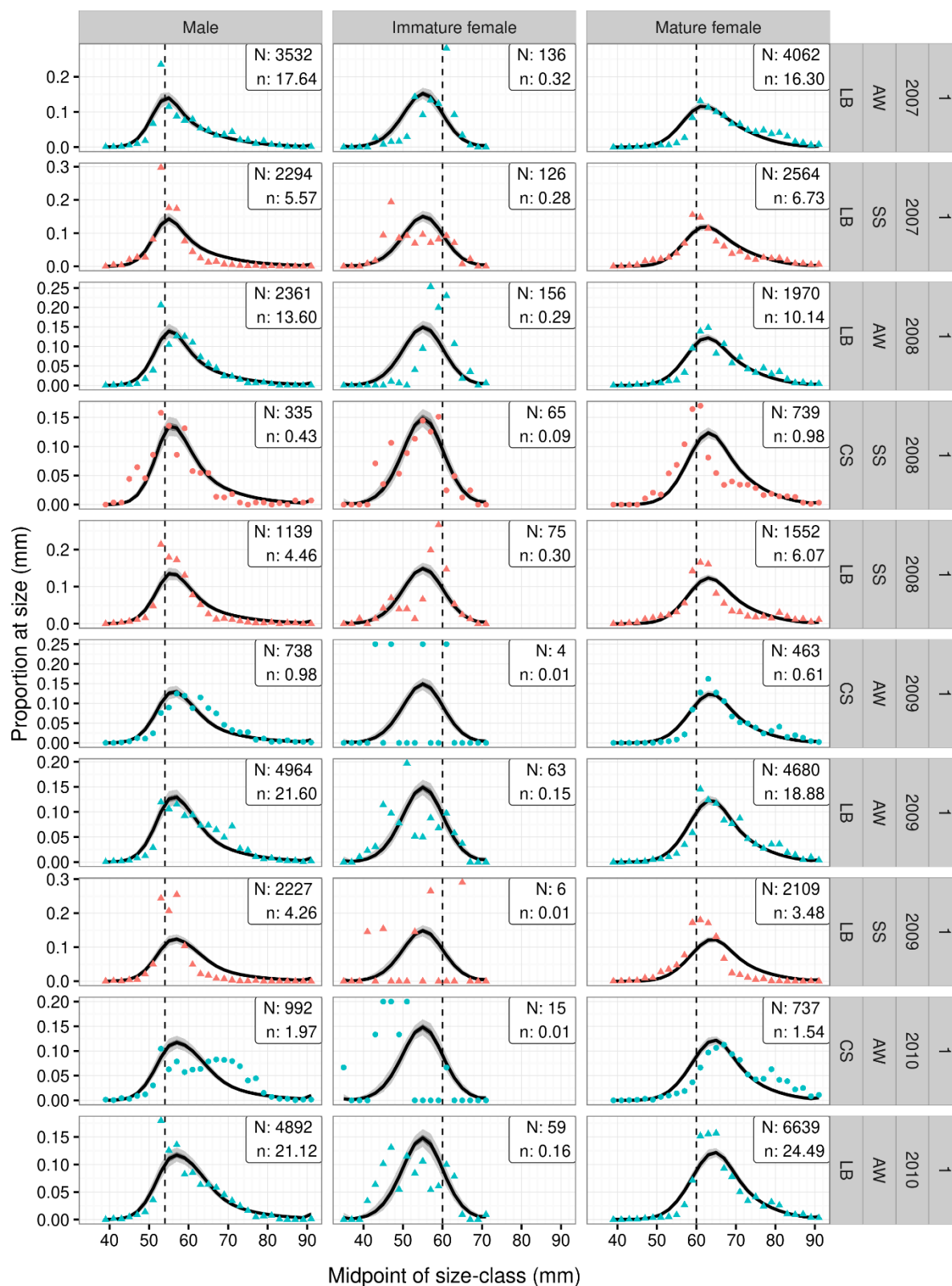


Figure 61 (cont.):

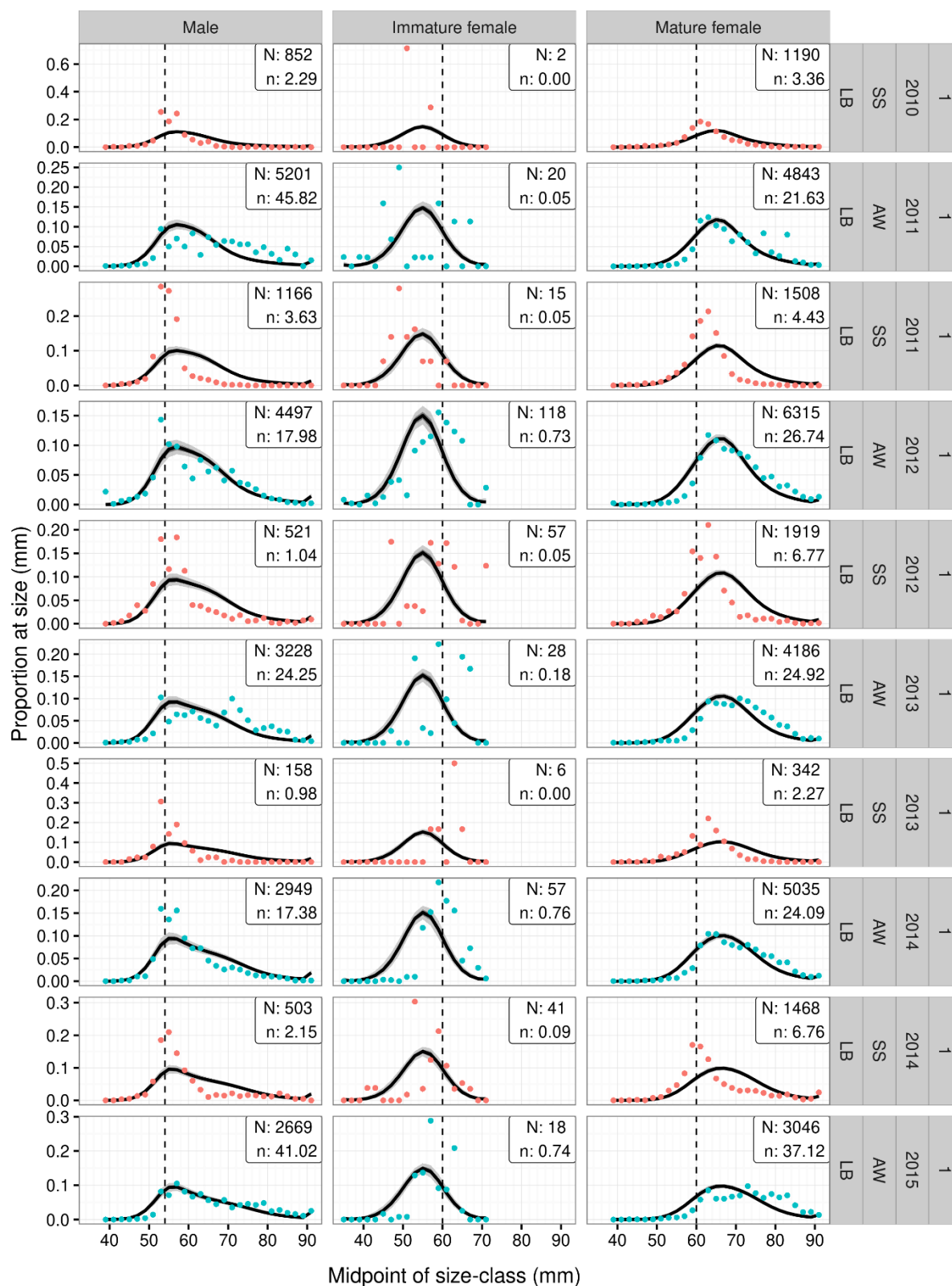


Figure 61 (cont.):

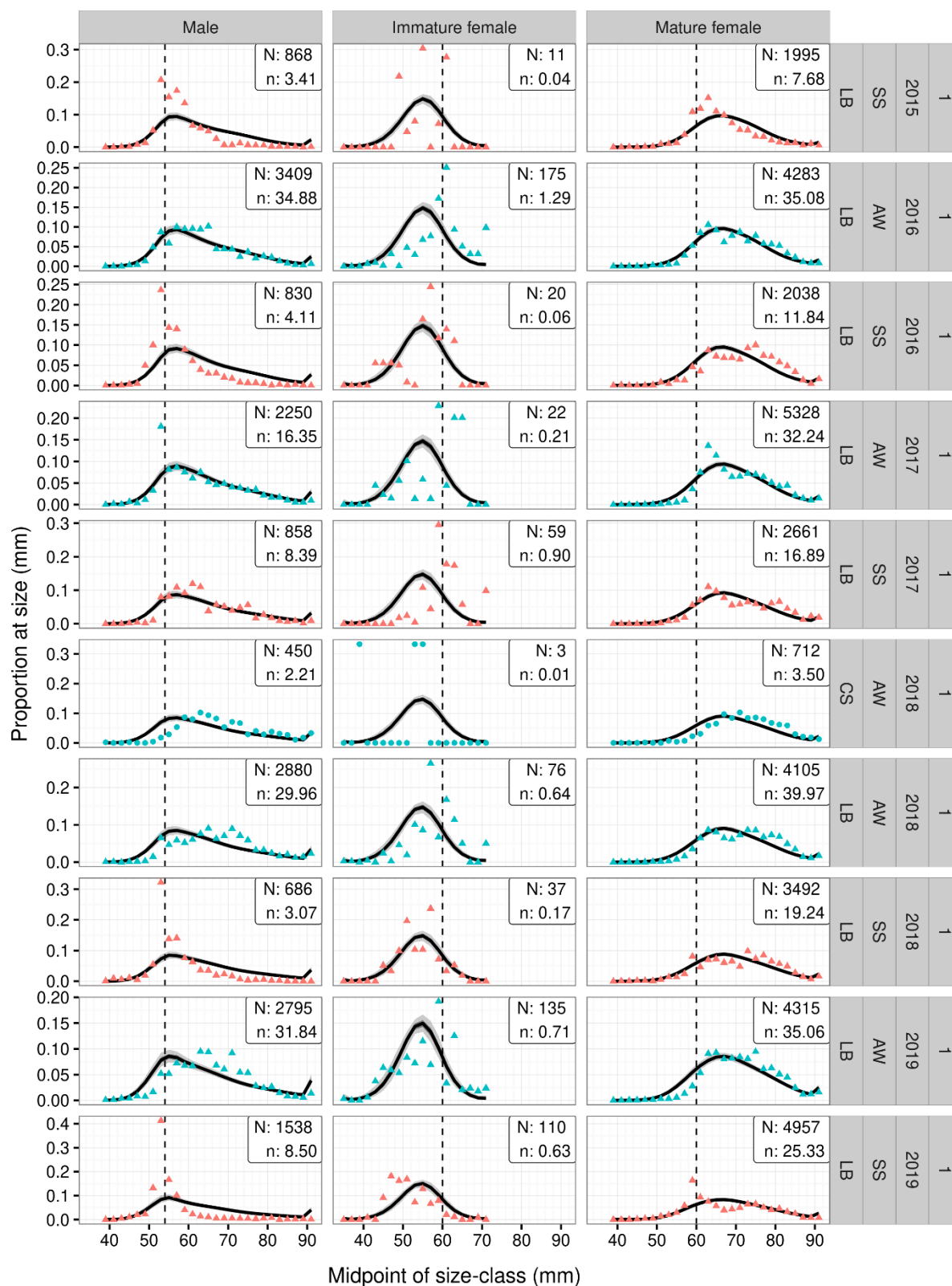


Figure 61 (cont.):

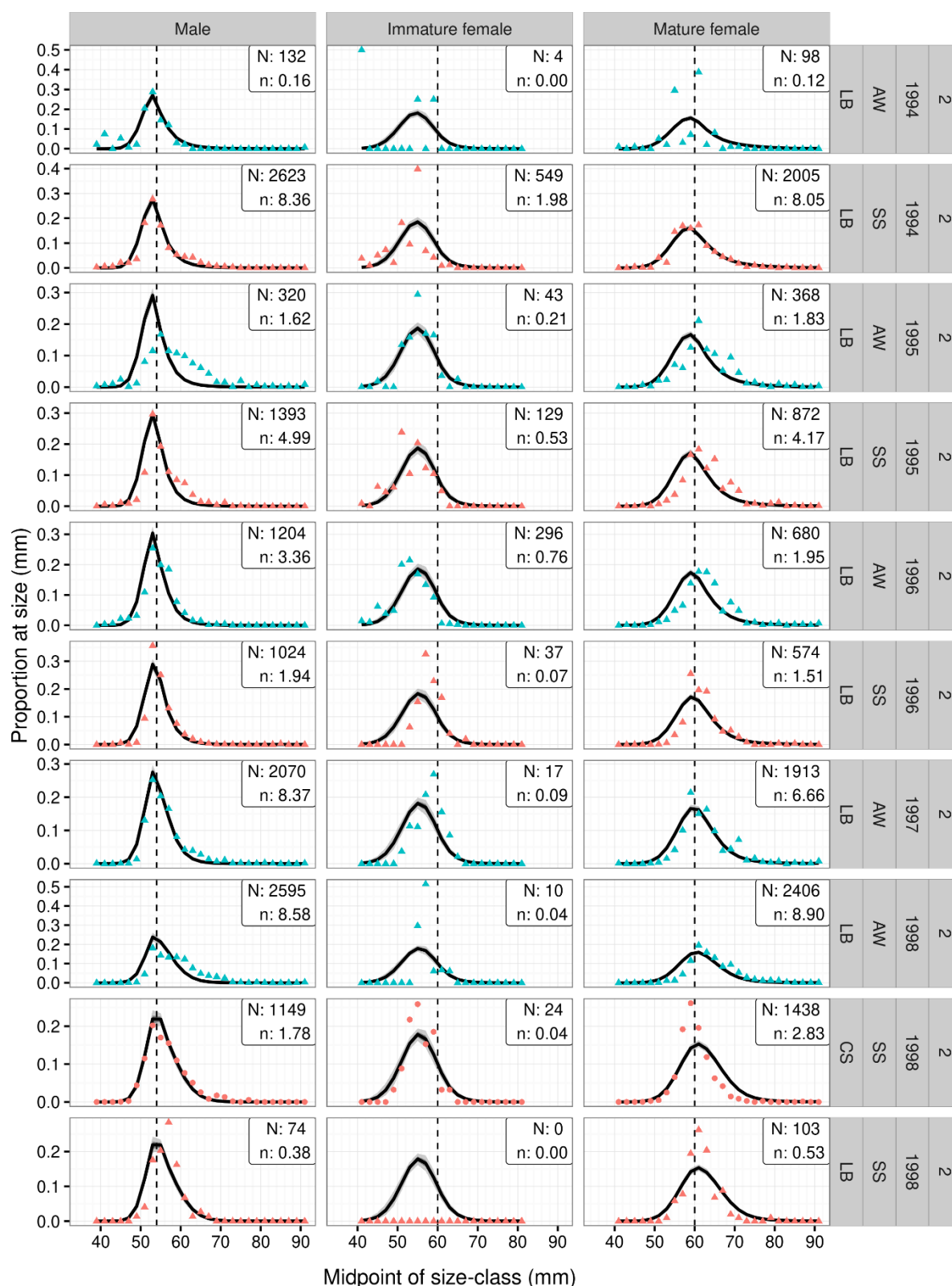


Figure 62: Posterior distribution of the LFs compared with the observed LF distribution for region 2, fishing year, season (AW = autumn-winter, SS = spring-summer), data source (CS = catch sampling, LB = logbook), and sex in the base case model run. The solid line indicates the posterior median and grey shading with variable intensity indicates the 50% and 90% credible intervals. In each panel the value for “N” is the number of lobsters in the sample, and “n” is the effective sample size.

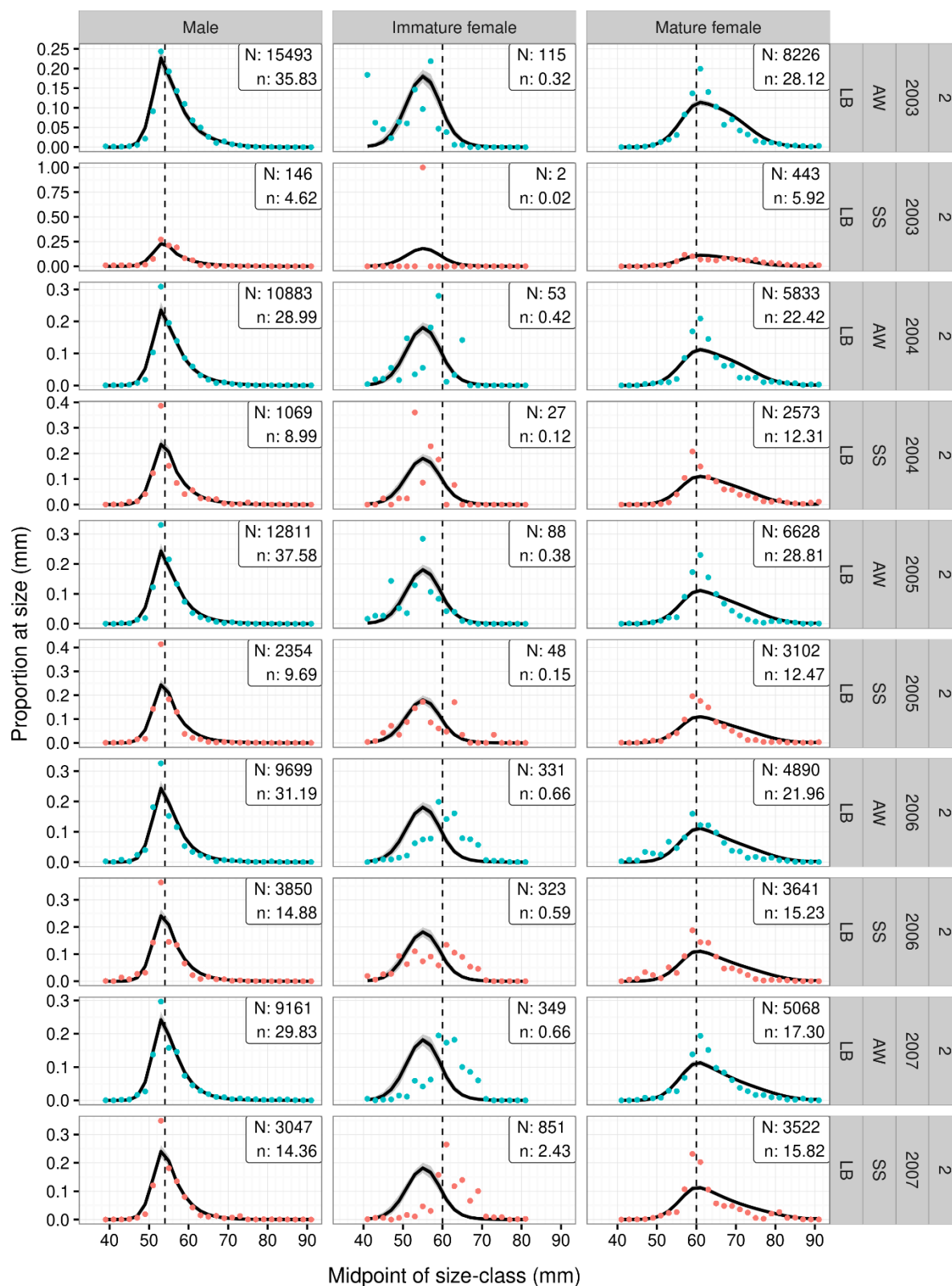


Figure 62 (cont.):

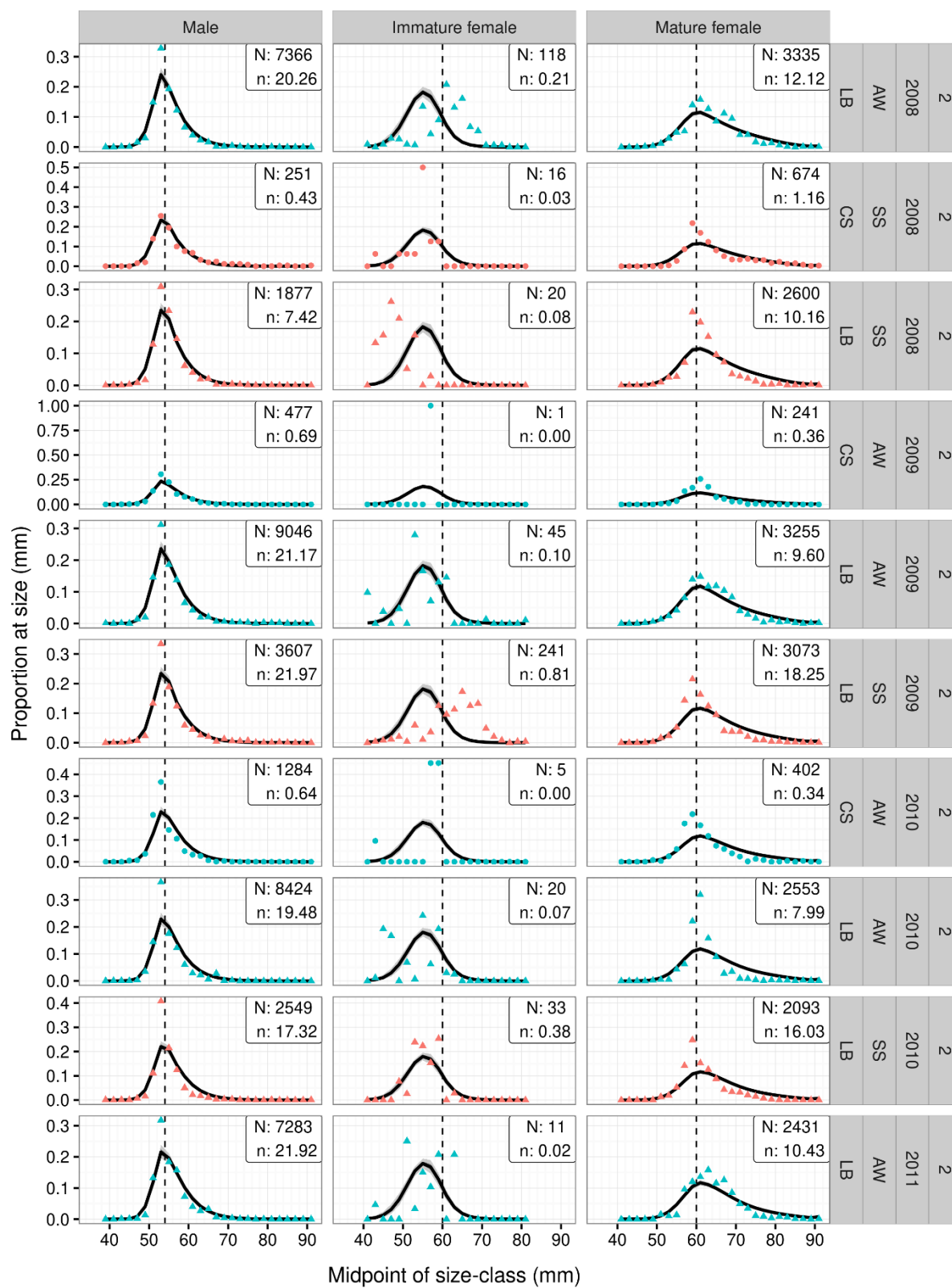


Figure 62 (cont.):

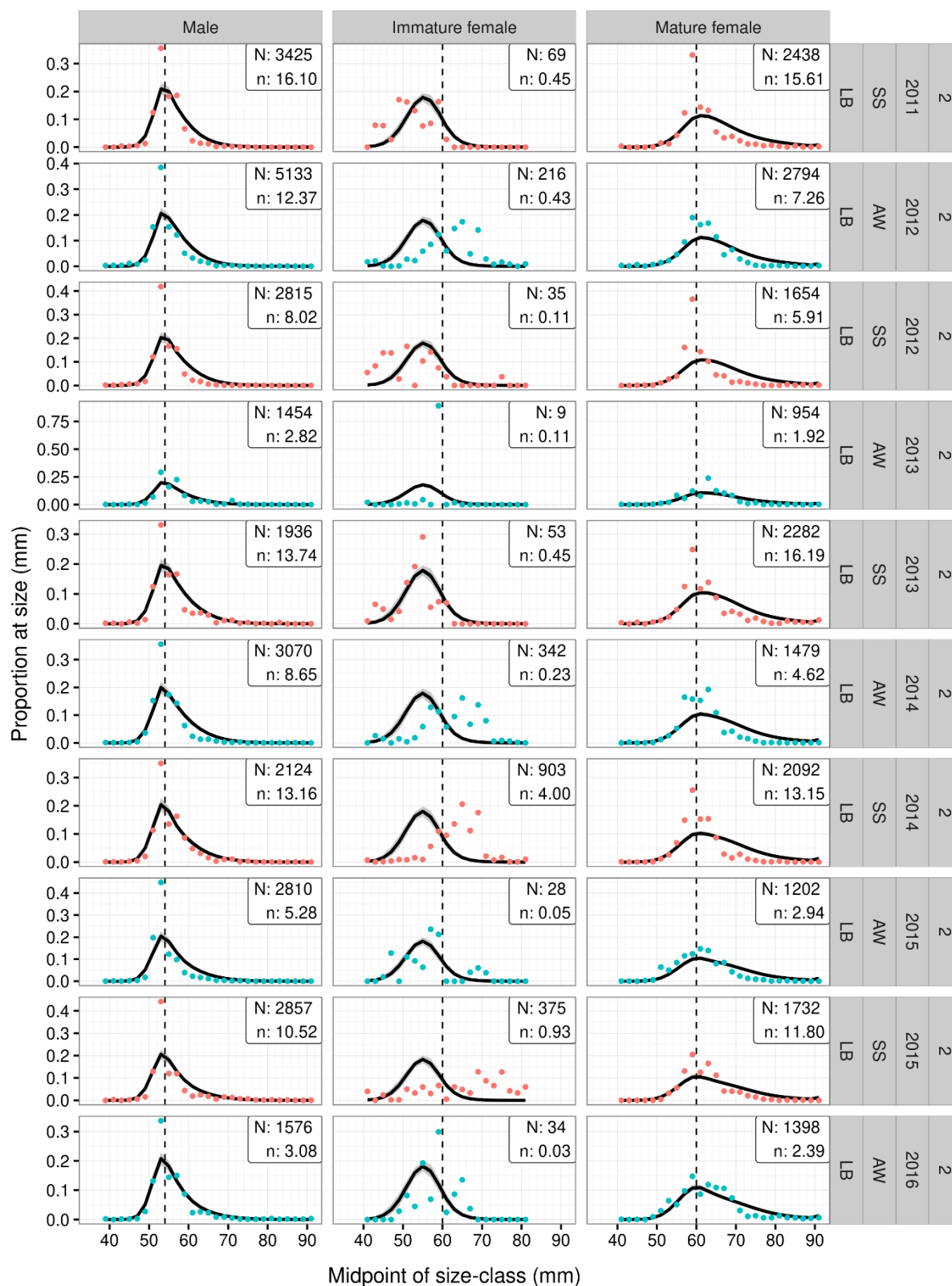


Figure 62 (cont.):

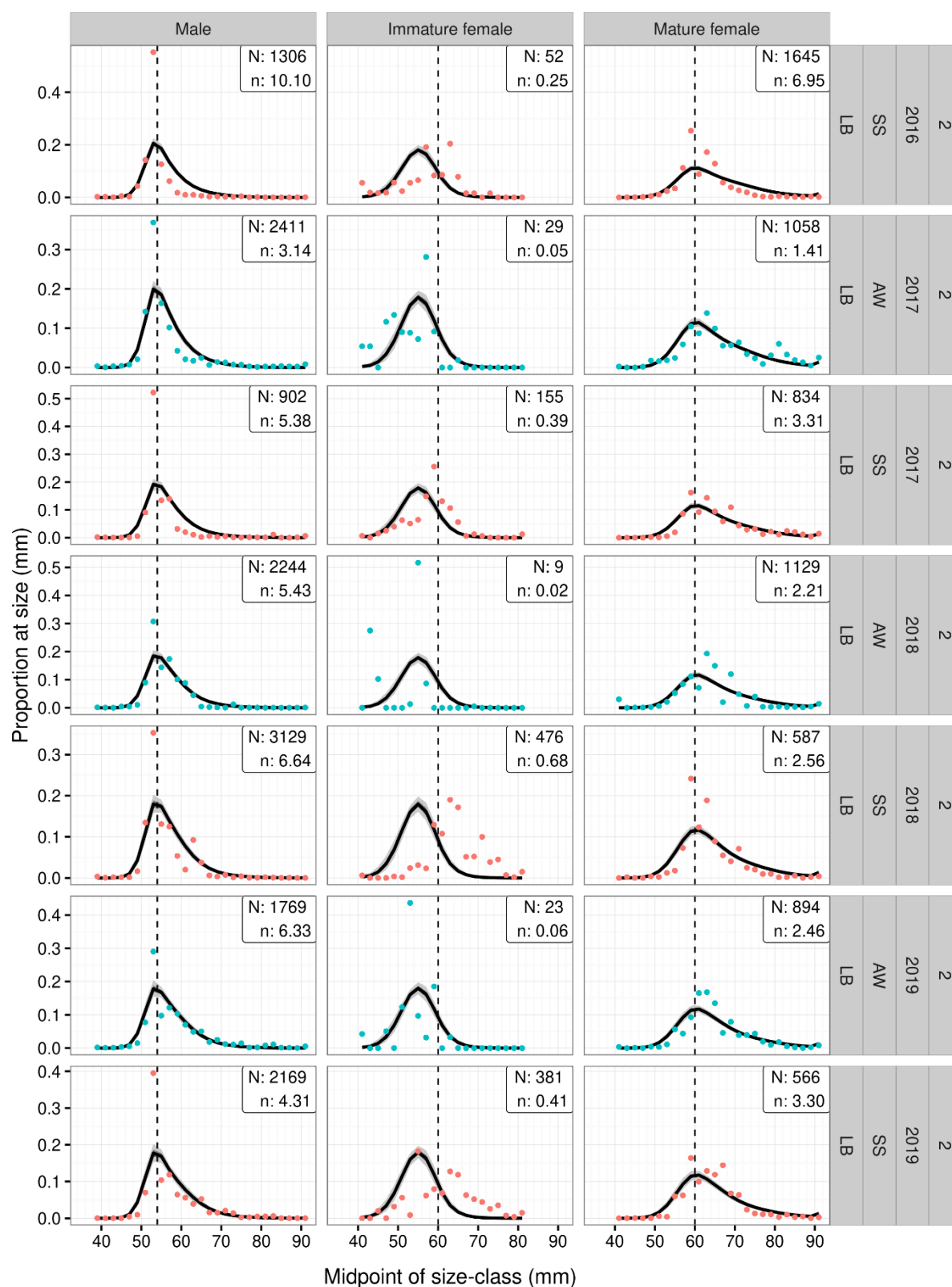


Figure 62 (cont.):