Transition from TCSAM02 to GMACS: 1 function call

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1 Introduction

The Tanner crab assessment model is transitioning between the current modeling framework which has been used since 2017, TCSAM02, to GMACS, the modeling framework used in all other Bering Sea crab stock assessments. As part of this transition, the CPT and SSC requested that results from the two frameworks be compared under identical model scenarios, first for a single iteration of each model and then after optimizing the models. "Identical model scenarios" is understood here to mean model configurations that are "as close as reasonably possible" without altering the GMACS codebase such that continuity for assessments that already use GMACS would be interrupted. In this report, "exact equivalence" between a Tanner crab model in the two model frameworks is demonstrated by 1) creating a TCSAM02 model that replicates the 2025 assessment model as closely as possible to allow direct comparison with a GMACS model, 2) creating the equivalent model in GMACS, and 3) running both models for a single iteration to determine that the models return identical results (allowing for small margins of error due to the finite precision of the input files). Results after optimizing both models are presented in a separate report.

The TCSAM02 model used for this comparison replicates the 2025 assessment model in all features except that fishing mortality rates prior to available catch and/or effort data were set to zero whereas the assessment model included small, fishery-specific rates that were thought to possibly improve "spin-up" of the modeled population from 1948 (the model start year) to the year(s) at which data becomes available to inform the model. GMACS does not allow for this extension of fishing mortality rates to a model "spin-up" period and, while the effects of including these rates are minimal on data-informed model results, they were set to zero in the TCSAM02 model rather than trying to incorporate them into the GMACS framework to ensure direct comparability across the entire model time frame. In addition, the GMACS framework was modified to incorporate several features of the bespoke model that have more impact. Most significantly, these were 1) an alternative parameterization for a double normal selectivity curve used to describe male selectivity in the snow crab fishery and 2) a likelihood component for fits to male maturity ogives describing the size-specific fraction of new shell mature male crab relative to all new shell males as determined on the basis of survey data. The new likelihood component applies specifically to the *Chionoecetes* stocks. In the GMACS snow crab model (Szuwalski and Adams 2025), annual survey-derived male maturity ogives have been used directly (i.e., assuming no uncertainty) to determine the annual fraction of immature males that underwent the terminal molt to maturity prior to the NMFS survey (and were thus observed as new shell mature males) whereas in the bespoke model the process of terminal molt is parameterized as a smoothly-varying function of crab size that has been informed statistically by including a likelihood component for the fit to the observed ogives. The addition of the selectivity function as an option in GMACS was relatively straightforward and quick while the addition of the maturity ogive likelihood was much more tedious and involved developing new ADMB code to read in the maturity ogives as a data source, predict annual male maturity ogives as seen by the NMFS survey, and compute a likelihood associated with the differences between the predicted and observed ogives. Other minor changes involved adding additional results to the GMACS results files to facilitate direct comparisons with the TCSAM02 model results. The version of GMACS used here is 2.20.45a (compiled 2026-08-17), which is available from the "devel_202608-45" branch of the GMACS_tpl-cpp_code GitHub repository.

2 Tanner crab assessment model description

The 2025 Tanner crab assessment ((Stockhausen 2025)) was based on model configuration "22_03d5" and evaluated using the TCSAM02 modeling framework. The most relevant features of this model configuration include:

- time frame: 1948 - 2025
- biological/population dynamic processes
  - two sexes (males, females), two maturity states (immature, mature), two shell conditions (new shell, old shell)
  - 5 mm size bins from 25 mm CW to 185 mm CW (min and max cutpoint sizes), where the final size bin is an accumulator
  - recruitment
    - ln-scale means and annual deviations are estimated for two time periods
  - natural mortality
    - estimated by sex and maturity state for two time periods
  - molting and growth
    - molting occurs annually for immature crab
    - sex-specific post-molt size are modeled using two-parameter functions of pre-molt size
  - maturation (i.e., terminal molt)
    - sex-specific probability of terminal molt is estimated as a smooth function of size
- fishing mortality
  - based on four fleets: Tanner crab fleet (the directed fishery), snow crab fleet, Bristol Bay red king crab fleet, and groundfish fisheries
  - mortality is 100% for retained catch, 32.1% for discards in the directed fishery and the fisheries that capture Tanner crab as bycatch
  - ln-scale means and sex-specific annual deviations for capture rates are estimated by fleet for years when fleet-related fisheries are open
  - fishery selectivity for total catch is modeled as dome-shaped for males in the snow crab fishery; otherwise it is modeled using sex-specific ascending logistic functions

    * male-specific curves are estimated for three time periods for each of the bycatch fleets, annual deviations to the inflection point are estimated starting in 1991 for males in the directed fishery
  - retention in the directed fishery is modeled as an ascending logistic in two time periods

- survey catchability
  - two surveys are modeled: the annual NMFS EBS bottom trawl survey and the BSFRF side-by-side surveys (2013-2018)
  - fully-selected survey for the NMFS survey is sex-specific and estimated for two time periods; it is 1 for the BSFRF surveys
  - sex-specific survey selectivity is modeled as ascending normal curves of size; it is 1 at all sizes for both sexes for the BSFRF surveys

- data sources used to inform parameter estimation include:
  - annual estimated of fishery retained and total catch biomass and sex-specific size compositions from each of the four fishery fleets from at-sea and dockside observer sampling
  - annual survey biomass and size compositions from the two surveys (when conducted) for males, immature females, and mature females respectively
  - molt increment data from Tanner crab caught in the EBS
  - male maturity ogives estimated from individual chela height/carapace width measurements taken during the NMFS

3 Summary results for model comparisons at initialization using exactly equivalent parameter values

Summary results of the model comparison using exactly equivalent parameter values and a single model evaluation are presented in this section. More comprehensive comparisons are provided in sub-sections of Section 5 for the interested reader, but the comparisons presented here should suffice to demonstrate the almost exact agreement between the bespoke and GMACS model results under these criteria.

3.1 Management reference points

Comparison of management reference points included average recruitment, the OFL, F_{MSY}, F_{OFL}, B_{MSY}, and the biomass projected to the next year under the assumption that the OFL is taken (Table 1, Figure 1). The largest differences between the values calculated using the two modeling frameworks wre less than 0.5%, occurring for F_{MSY} and F_{OFL} which, in this model scenario, are identical. Differences in the remaining quantities were less than 0.1%.

3.2 Recruitment and MMB

Comparisons of the time series for recruitment are shown in Figure 2 and Table 2. Differences between the results from the two model frameworks are less than 10^{-7}%. Comparisons of the time series for mature male biomass are shown in Figure 3 and Table 3. Differences between the results for mature male biomass from the two model frameworks are less than 10^{-4}%.

3.3 Data-derived likelihoods

Aggregated data-derived likelihood components (from fits to catch biomass and abundnace, survey biomass, size compositions, growth data, and male maturity ogive data) are compared in Table 4. Differences are less than 0.06 likelihood units for size composition data and less than 10^{-5} units for the other data components.

3.4 Penalties and priors

Tables of likelihoods associated with penalties and prior probabilities for the "exactly equivalent" model scenario are given for GMACS in Table 5 and for the bespoke model in Table 6. These are the source of the biggest differences in implementation between the two models. All known penalties have been set to zero in both frameworks (by setting the associated multiplicative weights to zero), except for penalties on the "smoothness" of estimated maturity ogives in TCSAM02 (on sex- and size-specific parameters for the probability of terminal molt; basically penalties on the variance of second-differences with size and penalties on decreasing values with size) that have not been implemented in GMACS. While the priors on the survey catchability parameters are the same for the two frameworks, they differ for those on ln-scale recruitment deviations and mortality parameters. The priors differ quite substantially for recruitment deviations because GMACS calculates its prior relative to a single ln-scale mean for the entire model time frame while two time frames and two ln-scale means are defined in the TCSAM02 model. The priors differ for slightly for natural mortality (M) because GMACS parameterizes M's for immature crab, mature males, and mature females directly while TCSAM02 parameterizes M's for these population components as *multipliers* on a base value ($M = 0.23$). Consequently, it is not possible to define exactly equivalent priors for the two sets of parameters.

4 Summary

The results presented above provide enough information to conclude that, under identical-as-possible model configurations, the two modeling frameworks are equivalent in all respects except for the imposition of non-data likelihood priors and penalties. These latter cannot be truly matched without substantial revisions to one of the two frameworks and will be the primary source driving differences between model results achieved when estimation is turned "on".

5 Comprehensive model comparisons

More comprehensive comparisons between the GMACS and TCSAM02 models are presented in the following sections. Estimated model processes (e.g., growth, natural mortality, fishery selectivity, etc.) are compared in Section 5.1 using paired figures illustrating the estimates themselves and the differences between between the models. Fits to non-size composition data are compared in Section 5.4.1 while fits to survey size composition data are compared in Section 5.4.2 and fits to fishery size composition data are compared in Section 5.4.3. The likelihoods associated with the fits illustrated in the "Fits" sections are compared in Sections 5.5.1, 5.5.2, and 5.5.3. Finally, non-data-related likelihood penalties and priors are presented again in Section 3.4.

5.1 Model processes

5.1.1 Biological processes

Comparisons between results for biological processes incorporated in the models include allometry (sex-specific weight-at-size, Figure 4), size at recruitment (Figure 5), sex/life stage-specific natural mortality rates (Figures 6 and 7), sex-specific mean growth (Figure 8) and growth transition matrices (Figures 9-12), and sex/size-specific probabilities of terminal molt (Figure 13). In general, differences between the two model frameworks were less than 10^{-5}%.

5.1.2 Fishery characteristics

Comparison of fishery characteristics between the model frameworks included sex- and size-specific retention and capture/selectivity functions (Figures 14-18) and fully-selected capture rates (Figure 19). The retention, capture/selectivity functions, and capture rates all differed by less than 10^{-6} between the the two model frameworks.

5.1.3 Survey characteristics

Comparison of survey characteristics between the model frameworks included sex- and size-specific selectivity functions for the NMFS survey and availability functions for the BSFRF survey (Figures 20 and 21) and fully-selected survey catchability (Figure 22). The selectivity and availability functions differed by less than 10^{-6} between the the two model frameworks, as did fully-selected catchabilty.

5.1.4 Predicted population quantities

Comparison of population quantities between the model frameworks included recruitment, cohort progression, aggregated sex- and stage-specific population abundance, sex- and stage-specific population size compositions, aggregated sex- and stage-specific population biomass, and size-specific male maturity ogives (Figures 23-40). All quantities differed by less than 10^{-4}% between the the two model frameworks.

5.2 Predicted fisheries quantities

Comparison of fishery-related quantities between the model frameworks included fishery-specific capture abundance and biomass, total fishing mortality, and retained catch mortality (Figures 41 and 46). All quantities differed by less than $3x10^{-4}\%$ between the the two model frameworks.

5.3 Predicted survey quantities

Comparison of survey-related quantities between the model frameworks included sex-specific survey biomass (Figures 47 and 48). All quantities differed by less than $1x10^{-4}\%$ between the the two model frameworks.

5.4 Fits to data

Comparisons of fits to non-size composition data are presented in Section 5.4.1. Fits to survey size composition data are compared in Section 5.4.2. fits to fishery size composition data are compared in Section 5.4.3.

5.4.1 Fits to non-size composition data

5.4.1.1 Fits to growth (molt increment) data

The "fits" obtained for growth data using the two model frameworks are compared in Figure 49. They are essentially identical, with differences in simple (observed - predicted) residuals less than 10^{-9}.

5.4.1.2 Fits to male maturity ogive data

The "fits" obtained for male maturity ogive data using the two model frameworks are compared in Figure 50. They are essentially identical, with differences in simple (observed - predicted) residuals less than 10^{-8}.

5.4.1.3 Fits to survey biomass

The "fits" obtained to survey biomass data using the two model frameworks are compared in Figures 51-56. Both the data and predicted values are examined, and differences in results between the two model frameworks evaluated based on the differences between the Pearson's residuals, ρ, for each dataset. Because the likelihoods for survey biomass data assume lognormal error distributions, the Pearson's residuals for the model fits were calculated on the ln-scale as well:

$$\rho = \frac{(ln(O) - ln(P))}{\sqrt{ln(1 + cv^2)}} \tag{1}$$

where O is the observed value, P is the predicted value (i.e., from the lefthand plots in Figures 51-56), cv is the coefficient of variation for the observation (all on the arithmetic scale). The results from the two frameworks are essentially identical, with differences between the Pearson's residuals residuals less than 10^{-5}.

5.4.1.4 Fits to fishery catch biomass and abundance

The "fits" obtained to fishery catch biomass and abundance data using the two model frameworks are compared in Figure 57 for retained catch biomass, Figures 58-61 for total catch biomass, and Figure 62 for total catch abundance in the groundfish fisheries. Both the data and predicted values were examined, and differences in results between the two model frameworks were evaluated based on the differences between the Pearson's residuals, ρ, for each dataset. Because the likelihoods for fishery catch biomass and abundance data assume lognormal error distributions, the Pearson's residuals for the model fits were calculated in the same manner as those for survey biomass (Equation 1).

The results from the two frameworks are essentially identical, with differences between the Pearson's residuals residuals less than 10^{-3}.

5.4.2 Fits to survey size composition data

The equivalence between GMACS and TCSAM02 for fits to survey size composition data are evaluated in this section. For all survey size compositions, following standard practice, 5% tail compression was performed on both ends of each composition to stabilize model fitting. The resulting size compositions were fit directly by three sex/maturity categories: 1) males, 2) immature females, and 3) mature females. The survey size compositions were fit using these categories to reflect the similar categories used to fit survey biomass data.

Fits to survey size compositions from the NMFS and BSFRF surveys are compared between the model frameworks in Figures 63-74. The relevant observed and predicted size compositions from the two model frameworks are compared by year in the same figure followed by a figure showing the differences between the two frameworks for the associated Pearson's residuals, where Pearson's residuals, r were calculated for a given size composition by size bin in both frameworks using the formula

$$r = \frac{(O - P)}{\sqrt{\frac{(P+\delta)\cdot(1-(P+\delta))}{n}}}$$

where O and P are the observed and predicted values for a size bin, n is the effective sample size for the size composition, and δ is a small value (0.001 here) added to keep the denominator from becoming zero. Pearson's residuals reflect the degree of fit to the data by the predictions and thus the difference between the residuals from the two frameworks reflects on differences in contributions by size bin to differences in the overall likelihood. While it would have been more straightforward to show differences between the frameworks in the likelihoods by size bin, this was not available in the GMACS output.

The figures indicate almost exact agreement between the two frameworks for fits to the survey size composition data, with differences in the Pearson's residuals generally on the order of less than 0.00001.

5.4.3 Fits to fishery size composition data

The equivalence between GMACS and TCSAM02 for fits to fishery size composition data are evaluated in this section. For all fishery size compositions, following standard practice, 5% tail compression was performed on both ends of each composition to stabilize model fitting. The resulting retained catch size compositions were fit directly while the sex-specific total catch size compositions were fit by appending the female size compositions to the male size composition to form an "extended" size composition that allowed the sex-specific compositions to be fit simultaneously. It was necessary to fit the total catch size compositions in this fashion because the associated catch biomass data was fit in a sex-aggregated fashion.

Fits to fishery size compositions are compared between the model frameworks in Figures 75-92 for retained catch in the directed fishery (males only) and total catch in the directed, snow crab, BBRKC, and groundfish fisheries by sex. For each catch type (retained or total), fishery, and sex, the relevant observed and predicted size compositions from the two model frameworks are compared by year in the same figure followed by a figure showing the differences between the two frameworks for the associated Pearson's residuals, where Pearson's residuals, r were calculated for a given size composition by size bin in both frameworks using the formula

$$r = \frac{(O-P)}{\sqrt{\frac{(P+\delta)\cdot(1-(P+\delta))}{n}}}$$

where O and P are the observed and predicted values for a size bin, n is the effective sample size for the size composition, and δ is a small value (0.001 here) added to keep the denominator from becoming zero. Pearson's residuals reflect the degree of fit to the data by the predictions and thus the difference between the residuals from the two frameworks reflects on differences in contributions by size bin to differences in the overall likelihood. While it would have been more straightforward to show differences between the frameworks in the likelihoods by size bin, this was not available in the GMACS output.

Overall, the figures indicate almost exact agreement between the two frameworks for fits to the fishery size composition data, with differences in the Pearson's residuals generally on the order of less than 0.00001. Notable exceptions occur, however, for fits to female total catch size compositions in the snow crab fishery in 2024 (Figures 83 and 84) and in the BBRKC fishery in 1998 and 2018 (Figures 87 and 88). While notable in terms of the other fits, these differences are still quite small. The source of these differences are the slightly different criteria used in the two frameworks to determine the size bins included in the compression of size composition "tails"; generally, the results are obviously identical.

5.5 Data likelihoods

Comparisons of likelihoods for fits to non-size composition data are presented in Section 5.5.1. Likelihoods derived from survey size composition data are compared in Section 5.5.2. Likelihoods derived from fishery size composition data are compared in Section 5.5.3.

5.5.1 Non-size composition data likelihoods

5.5.1.1 growth and male maturity data

The likelihoods associated with growth (pre-molt, post-molt size data) and male terminal molt (male maturity ogives) data agreed between the two model frameworks to within 10^{-6} likelihood units (Figures 93 and 94).

5.5.1.2 fishery and survey time series data

Comparison of likelihood-related quantities for input data components between the model frameworks included summary likelihoods related to fishery catch biomass and abundance time series data (Figures 95-96) and to survey biomass time series data (Figure 97). Due to differences between the two frameworks in whether constant terms were included in the summary likelihoods, these were **not** directly comparable between the two models for fishery catch data and were not expected to agree (catch biomass: Figure 95; catch abundance: 96). In contrast, the constant terms were treated identically in the two frameworks when calculating summary likelihoods for the fits to survey biomass and thus these are directly comparable: these exhibited maximum differences on the order of 10^{-4} likelihood units (for male biomass from the NMFS survey, Figure 97).

To assess the fits to the fishery catch biomass and abundance time series data on a comparable basis, the individual likelihood values were recalculated from model output without the constant terms (Figures 98-100). The individual terms differed by less than $2x10^{-5}$ likelihood units between the the two model frameworks.

5.5.2 Survey size composition data likelihoods

The equivalence between GMACS and TCSAM02 for likelihood values arising from fits to survey size composition data from the NMFS and BSFRF surveys (Section 5.4.2) are evaluated in this section. In both frameworks, multinomial likelihoods were used to assess the degree of fit to the survey size composition data. The differences between the two frameworks for contributions to the overall model likelihood from fits to the survey size composition data were evaluated by comparing the associated negative log-likelihood values by survey (Figure 101) and by year for each survey (Figures 102 and 103).

For both surveys, the results are essentially identical–with most differences less than 0.00001 likelihood units.

5.5.3 Fishery size composition data likelihoods

The equivalence between GMACS and TCSAM02 for likelihood values arising from fits to fishery size composition data (Section 5.4.3) are evaluated in this section. In both frameworks, multinomial likelihoods were used to assess the degree of fit to the fishery size composition data. The differences between the two frameworks for contributions to the overall model likelihood from fits to the fishery size composition data were evaluated by comparing the associated negative log-likelihood values by fleet (Figure 104) and by year for each fleet for retained (directed fishery only, Figure 105) and total catch size compositions (Figures 106-109).

For the directed fishery and the groundfish fisheries, the results are essentially identical–with differences less than 0.00001 likelihood units. The differences are larger, but still less than 0.05 likelihood units, for the fits to the size compositions from the snow crab and BBRKC fisheries. These (small) differences arise from a single year (2024) for the snow crab data (Figure 107) and two years (1998, 2018) for the BBRKC data (Figure 108). As discussed in Section 5.4.3, these differences have been traced back to small differences in how the two frameworks compress the tails of the size distributions.

Tables

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Table 1. Management quantities. Units: biomass units in 1,000's t (OFL, prjB: projected biomass, Bmsy: MMB at MSY), fishing mortality units: year^{-1}, recruitment: millions.

type	tcsam	gmacs	%(tcsam-gmacs)
OFL	51.02	51.05	-0.0610
prjB	75.96	75.91	0.0579
Bmsy	43.22	43.22	0.0000
Fmsy	1.47	1.47	-0.3603
Fofl	1.47	1.47	-0.3603
avgRec	601.21	601.21	0.0000

Table 2. Comparison for total recruitment by year.

year	gmacs	tcsam	%(tcsam-gmacs)
1948	649.96	649.96	-2.89e-08
1949	650.53	650.53	-2.98e-08
1950	651.88	651.88	-3.32e-08
1951	654.28	654.28	-9.40e-09
1952	658.08	658.08	-3.68e-08
1953	663.78	663.78	-3.58e-08
1954	672.07	672.07	-3.93e-08
1955	683.88	683.88	-8.00e-09
1956	700.55	700.55	-3.21e-08
1957	723.88	723.88	-5.80e-09
1958	756.46	756.46	-6.14e-08
1959	802.21	802.21	-1.72e-08
1960	868.16	868.16	-7.88e-08
1961	967.83	967.83	-1.67e-08
1962	1,129.74	1,129.74	-5.29e-08
1963	1,420.67	1,420.67	-1.52e-08
1964	2,001.61	2,001.61	5.20e-09
1965	3,124.73	3,124.73	-1.70e-08
1966	4,788.51	4,788.51	6.30e-09
1967	5,346.37	5,346.37	-4.17e-08
1968	3,319.86	3,319.86	-3.88e-08
1969	2,048.26	2,048.26	-4.73e-08
1970	1,610.48	1,610.48	-4.96e-08
1971	969.13	969.13	-5.74e-08
1972	681.49	681.49	-2.97e-08
1973	1,031.26	1,031.26	-3.76e-08
1974	1,704.03	1,704.03	-1.00e-08
1975	3,205.15	3,205.15	3.23e-08
1976	2,092.32	2,092.32	-4.30e-08
1977	645.64	645.64	-6.00e-10
1978	402.48	402.48	-7.30e-09
1979	334.98	334.98	2.41e-08
1980	425.46	425.46	-3.86e-08
1981	376.89	376.89	3.25e-08
1982	1,243.19	1,243.19	-2.87e-08
1983	954.72	954.72	-3.98e-08
1984	1,049.53	1,049.53	-9.80e-09
1985	1,199.89	1,199.89	1.83e-08
1986	845.96	845.96	4.13e-08
1987	584.62	584.62	-8.50e-09
1988	263.89	263.89	1.30e-08

(continued)

year	gmacs	tcsam	%(tcsam-gmacs)
1989	143.70	143.70	-2.77e-08
1990	103.41	103.41	4.81e-08
1991	116.97	116.97	-4.60e-09
1992	122.15	122.15	-2.01e-08
1993	137.55	137.55	-2.09e-08
1994	230.34	230.34	-1.31e-08
1995	175.10	175.10	4.57e-08
1996	450.51	450.51	-1.47e-08
1997	169.02	169.02	-3.06e-08
1998	797.96	797.96	-8.00e-10
1999	254.96	254.96	4.90e-08
2000	1,134.80	1,134.80	0.00e+00
2001	373.51	373.51	1.47e-08
2002	1,237.85	1,237.85	-9.80e-09
2003	640.80	640.80	-4.72e-08
2004	233.94	233.94	4.32e-08
2005	136.69	136.69	2.64e-08
2006	247.75	247.75	3.90e-09
2007	515.00	515.00	3.86e-08
2008	1,607.52	1,607.52	4.05e-08
2009	573.31	573.31	-4.23e-08
2010	269.78	269.78	-4.84e-08
2011	85.52	85.52	-2.26e-08
2012	201.95	201.95	-2.23e-08
2013	97.67	97.67	2.33e-08
2014	118.82	118.82	-4.35e-08
2015	228.19	228.19	-2.60e-09
2016	972.23	972.23	-6.80e-09
2017	531.80	531.80	1.56e-08
2018	683.20	683.20	-1.91e-08
2019	217.71	217.71	1.79e-08
2020	1,745.74	1,745.74	-5.04e-08
2021	2,114.68	2,114.68	3.90e-08
2022	2,062.10	2,062.10	-2.00e-08
2023	933.18	933.18	-2.90e-08
2024	656.65	656.65	-4.90e-09

Table 3. Comparison for mature male biomass by year.

year	gmacs	tcsam	%(tcsam-gmacs)
1948	0.00	0.00	0.00000e+00
1949	0.00	0.00	0.00000e+00
1950	0.06	0.06	-1.48271e-05
1951	0.75	0.75	-1.16748e-05
1952	4.89	4.89	-1.33471e-05
1953	19.26	19.26	-1.55283e-05
1954	46.39	46.39	-1.82695e-05
1955	76.11	76.11	-2.12203e-05
1956	99.75	99.75	-2.34988e-05
1957	117.20	117.20	-2.52418e-05
1958	130.22	130.22	-2.66495e-05
1959	140.11	140.11	-2.77872e-05
1960	147.96	147.96	-2.86993e-05
1961	154.56	154.56	-2.94062e-05
1962	160.45	160.45	-2.99051e-05
1963	166.30	166.30	-3.02110e-05
1964	172.83	172.83	-3.03301e-05
1965	181.20	181.20	-3.02925e-05
1966	190.34	190.34	-2.97790e-05
1967	205.17	205.17	-2.90293e-05
1968	215.77	215.77	-2.67006e-05
1969	242.81	242.81	-2.44888e-05
1970	279.16	279.16	-2.27366e-05
1971	311.96	311.96	-2.12457e-05
1972	446.06	446.06	-2.17436e-05
1973	583.78	583.78	-2.33620e-05
1974	618.54	618.54	-2.57289e-05
1975	564.29	564.29	-2.79679e-05
1976	482.71	482.71	-2.99085e-05
1977	382.51	382.51	-3.11555e-05
1978	293.78	293.78	-3.13837e-05
1979	264.92	264.92	-3.00317e-05
1980	282.14	282.14	-2.75320e-05
1981	233.74	233.74	-2.39046e-05
1982	203.91	203.91	-2.36722e-05
1983	150.42	150.42	-2.47811e-05
1984	100.82	100.82	-2.54077e-05
1985	69.45	69.45	-2.43349e-05
1986	81.34	81.34	-2.51159e-05
1987	103.01	103.01	-2.46932e-05
1988	134.24	134.24	-2.42778e-05

(continued)

year	gmacs	tcsam	%(tcsam-gmacs)
1989	161.93	161.93	-2.47789e-05
1990	171.57	171.57	-2.46522e-05
1991	162.43	162.43	-2.48204e-05
1992	151.62	151.62	-2.64702e-05
1993	123.26	123.26	-2.87057e-05
1994	99.26	99.26	-3.11915e-05
1995	78.66	78.66	-3.37856e-05
1996	62.35	62.35	-3.60043e-05
1997	51.21	51.21	-3.73881e-05
1998	44.84	44.84	-3.75705e-05
1999	42.82	42.82	-3.62948e-05
2000	44.78	44.78	-3.41236e-05
2001	49.99	49.99	-3.17504e-05
2002	58.15	58.15	-2.97774e-05
2003	70.03	70.03	-2.83575e-05
2004	86.23	86.23	-2.73008e-05
2005	104.65	104.65	-2.70176e-05
2006	124.24	124.24	-2.67945e-05
2007	141.44	141.44	-2.71831e-05
2008	153.91	153.91	-2.78058e-05
2009	151.89	151.89	-2.98137e-05
2010	133.13	133.13	-3.25705e-05
2011	114.31	114.31	-3.45381e-05
2012	110.19	110.19	-3.36114e-05
2013	128.55	128.55	-3.04091e-05
2014	152.84	152.84	-2.88628e-05
2015	148.99	148.99	-2.97630e-05
2016	121.01	121.01	-3.13832e-05
2017	99.52	99.52	-3.44303e-05
2018	80.92	80.92	-3.65185e-05
2019	67.63	67.63	-3.76428e-05
2020	63.97	63.97	-3.63853e-05
2021	74.32	74.32	-3.16331e-05
2022	95.59	95.59	-2.85334e-05
2023	112.64	112.64	-2.82473e-05
2024	125.30	125.30	-2.81946e-05
2025	150.32	150.32	-2.63196e-05

Table 4. Negative log-likelihood contributions to the objective function by data type.

type	gmacs	tcsam	diff(tcsam-gmacs)
catch data	-171.05	-171.05	0.0001
index biomass data	273.91	273.91	0.0000
size comp. data	2,217.62	2,217.68	0.0594
growth data	511.05	511.05	0.0000
MMO data	428.91	428.91	0.0000

Table 5. GMACS negative log-likelihood values for general penalties and priors on parameters. All penalties were set to 0. Recruitment deviations: (normal) prior on ln-scale deviations from ln-scale mean, M: immature crab: (normal) prior on estimated M for immature crab, M: mature females: (normal) prior on estimated M for mature females, M: mature males: (normal) prior on estimated M for mature males, NMFS survey q: (normal) priors on estimated sex-specific catchability coefficients (i.e., q) for the NMFS survey. See text for details on comparison with TCSAM02 values.

parameter	NLL
Recruitment deviations	140.687093
M: immature crab	-1.863336
M: mature female	26.520441
M: mature males	25.396545
NMFS survey q, females 1982+	70.650964
NMFS survey q, males 1982+	24.253547

Table 6. TCSAM02 negative log-likelihood values for general penalties and priors on parameters. Smoothness: penalties on second differences and decreaing values in the size dependence of estimated male terminal molt parameters. Recruitment ('pDevsLnr'): sum of (normal) priors on individual recruitment deviation parameters. Natural mortality ('pDM1'): (normal) priors on estimated multipliers to base M for immature crab (level 1), mature males (level 2), and mature females (level 3). Surveys ('pQ'): (normal) priors on estimated survey catchability coefficients (i.e., q) for males (level 1) and females (level 2) in the NMFS survey. See text for details on comparison with GMACS values.

category	type	element	level	NLL
penalties	maturity	smoothness	1	1.2066368
penalties	maturity	smoothness	2	0.5823707
priors	recruitment	pDevsLnR	1	47.6309533
priors	recruitment	pDevsLnR	2	70.0317657
priors	natural mortality	pDM1	1	-0.3936517
priors	natural mortality	pDM1	2	26.8662580
priors	natural mortality	pDM1	3	27.9901408
priors	surveys	pQ	2	24.2535503
priors	surveys	pQ	4	70.6509606

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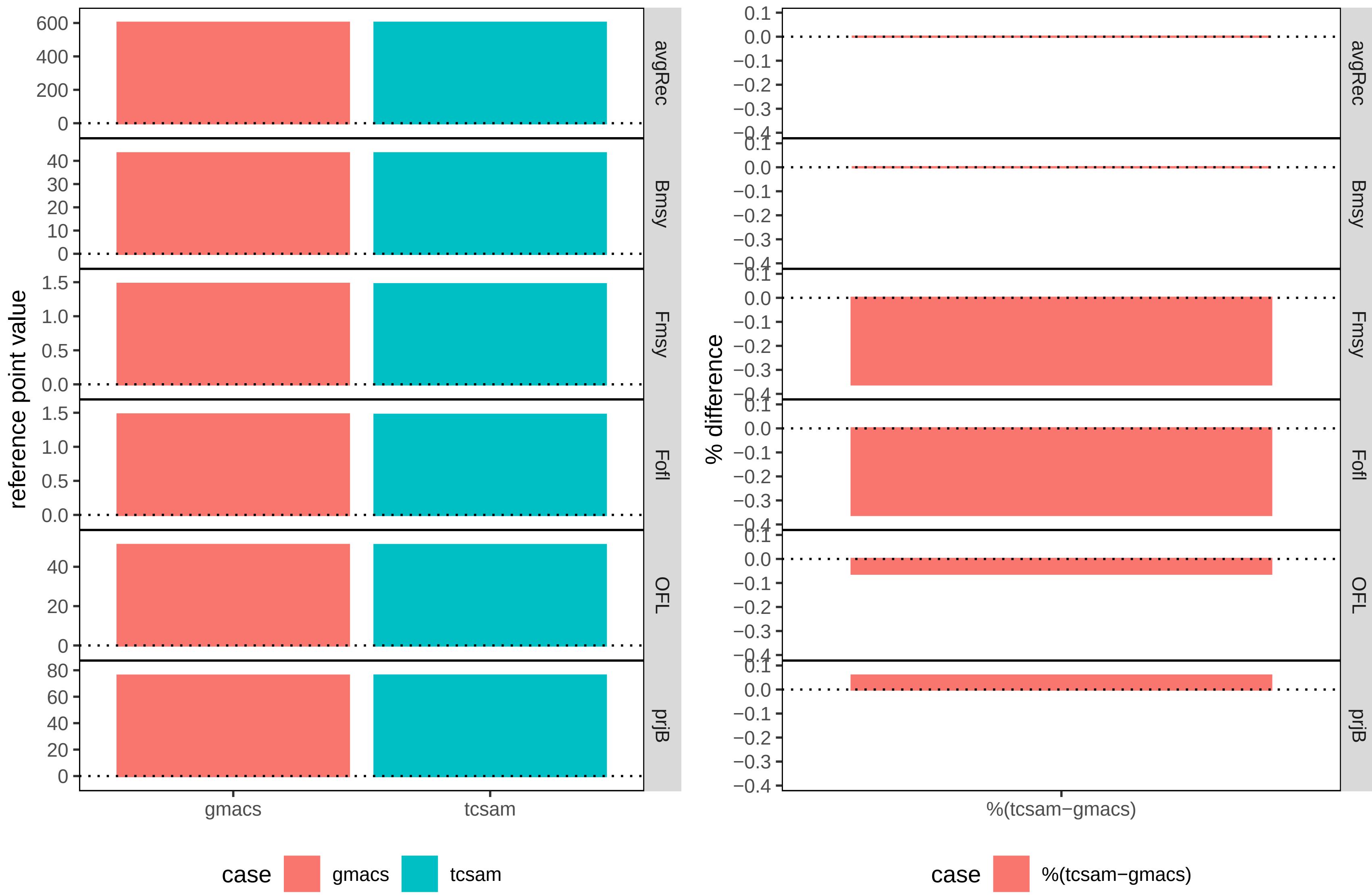


Figure 1. Comparison of management reference point values from the GMACS and TCSAM02 models. Left: values; right: % differences.

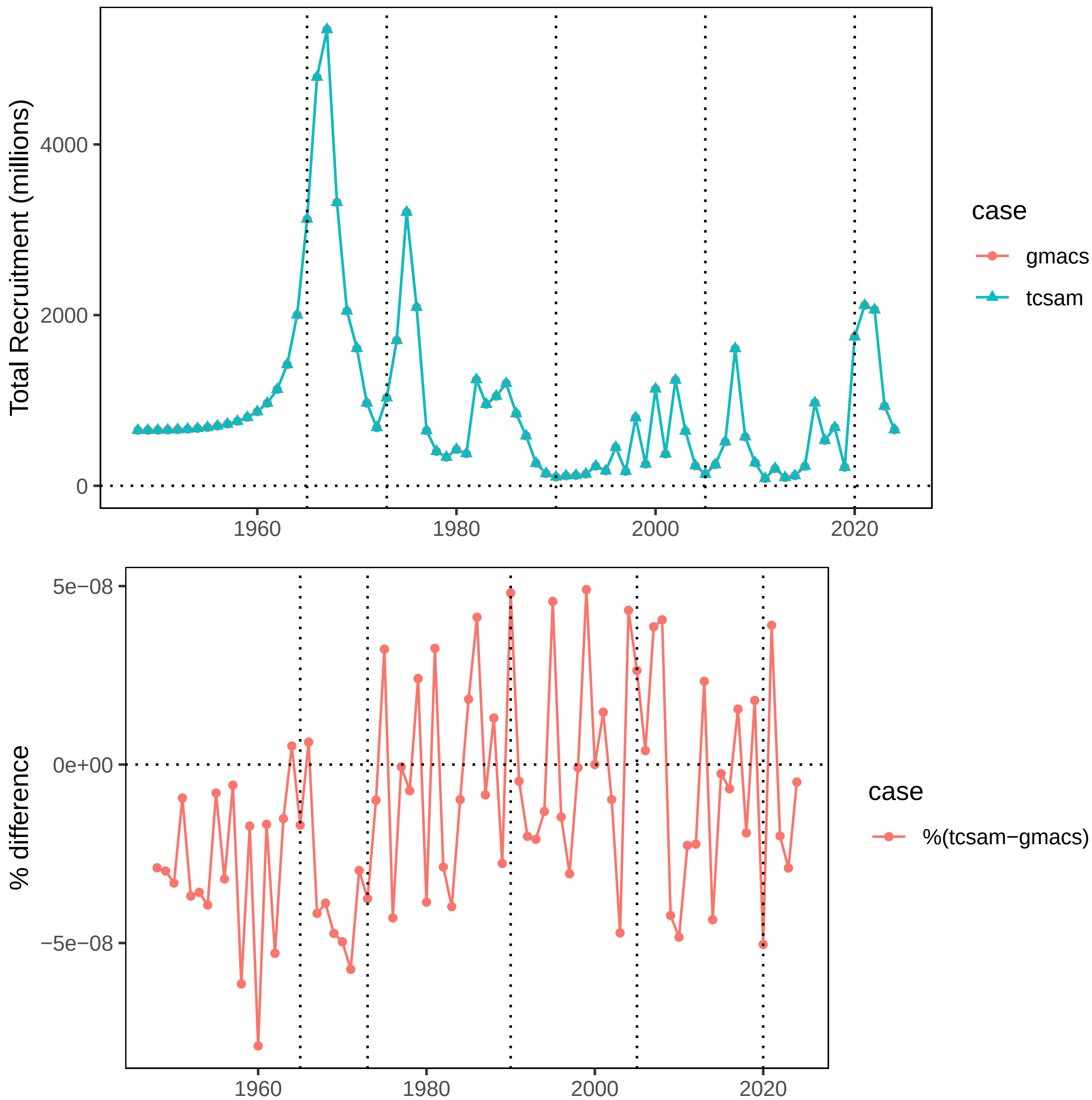


Figure 2. Comparison of recruitment by year from the GMACS and TCSAM02 models. Upper: values; lower: percent differences. The dotted vertical lines various temporal reference points: 1965-start of foreign fleet catch data; 1973-start of groundfish bycatch data; 1990-start of at sea observer estimates of total catch and size compositions in the crab fisheries; 2005-crab rationalization; 2020-no NMFS survey.

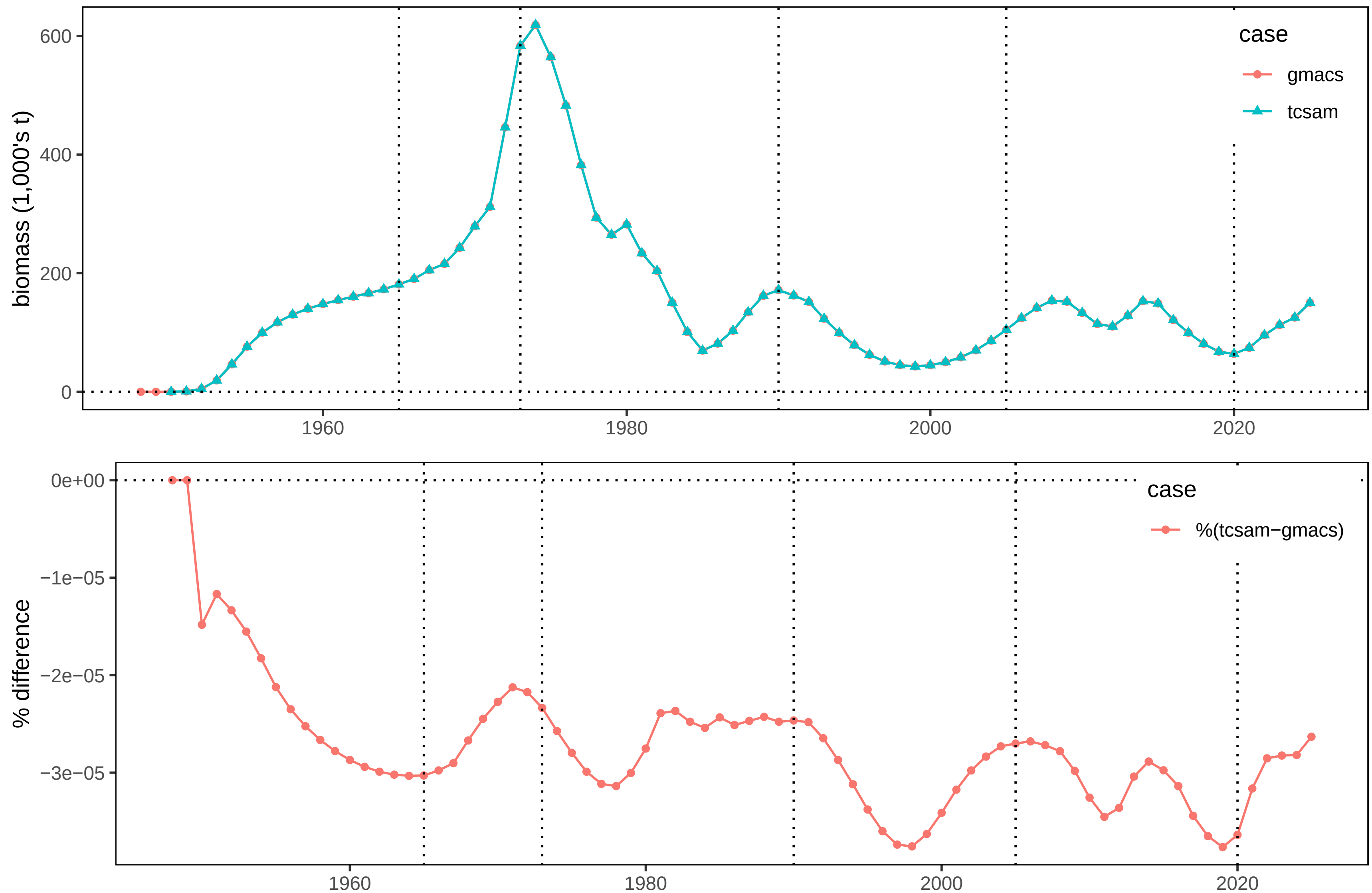
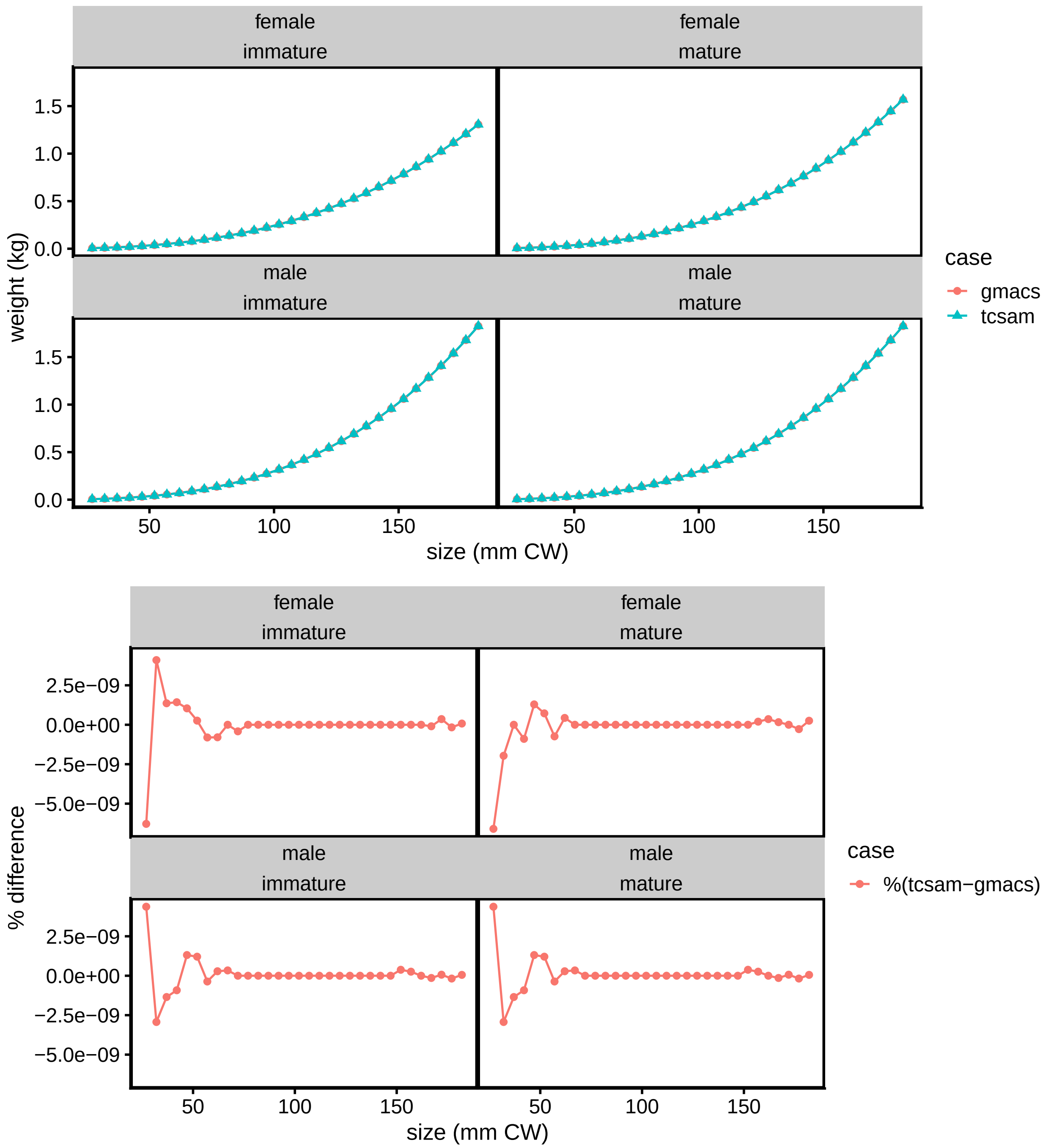


Figure 3. Comparison of the mature male biomass through time from the GMACS and TCSAM02 models. Left: values; right: percent differences. The dotted vertical lines indicate various temporal reference points: 1965-start of foreign fleet catch data; 1973-start of groundfish bycatch data; 1990-start of at sea observer estimates of total catch and size compositions in the crab fisheries; 2005-crab rationalization; 2020-no NMFS survey.



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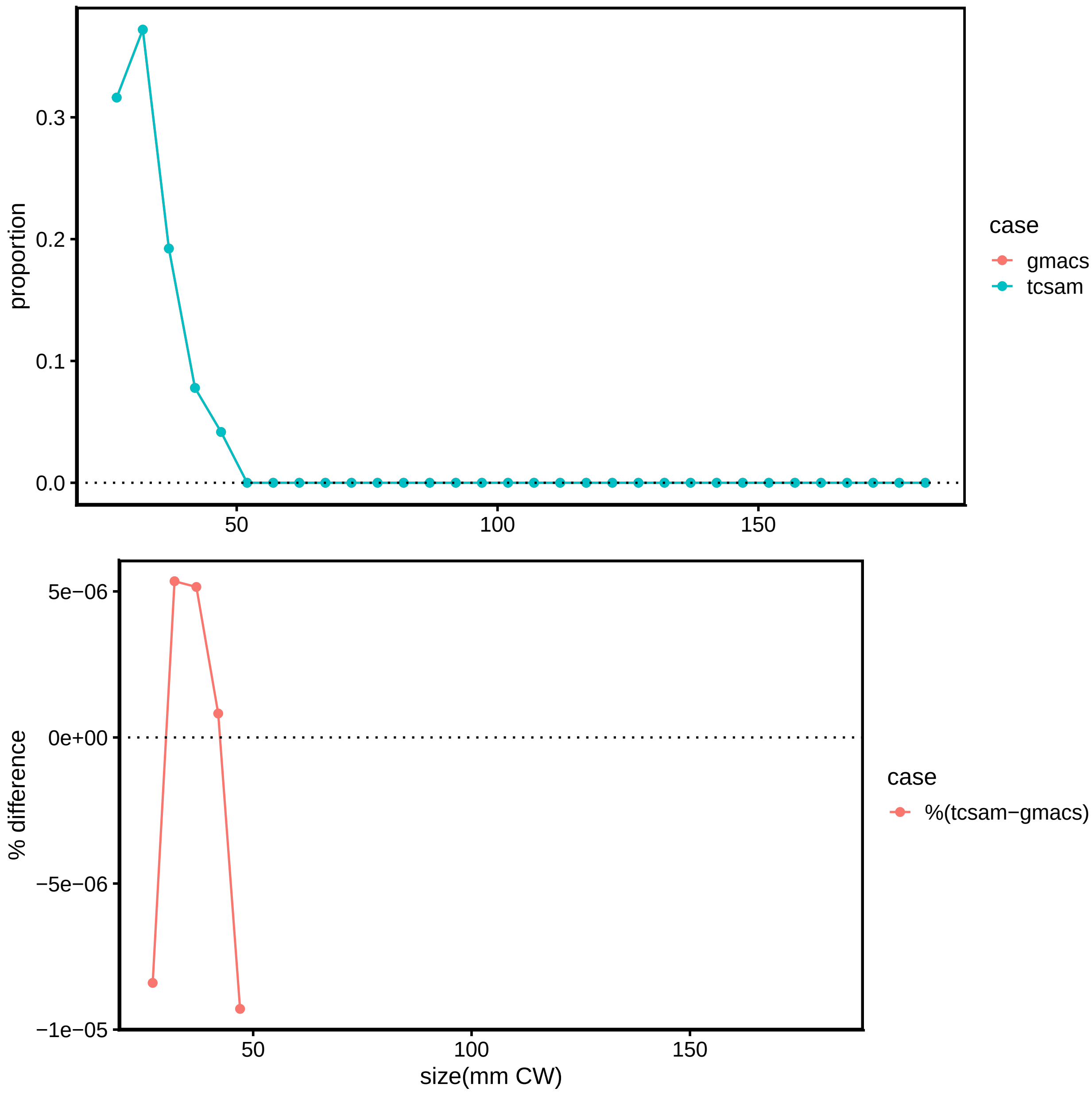


Figure 5. Comparison of size-at-recruitment from the GMACS and TCSAM02 models. Upper: values; lower: percent differences. The size distribution at recruitment is not sex-specific.

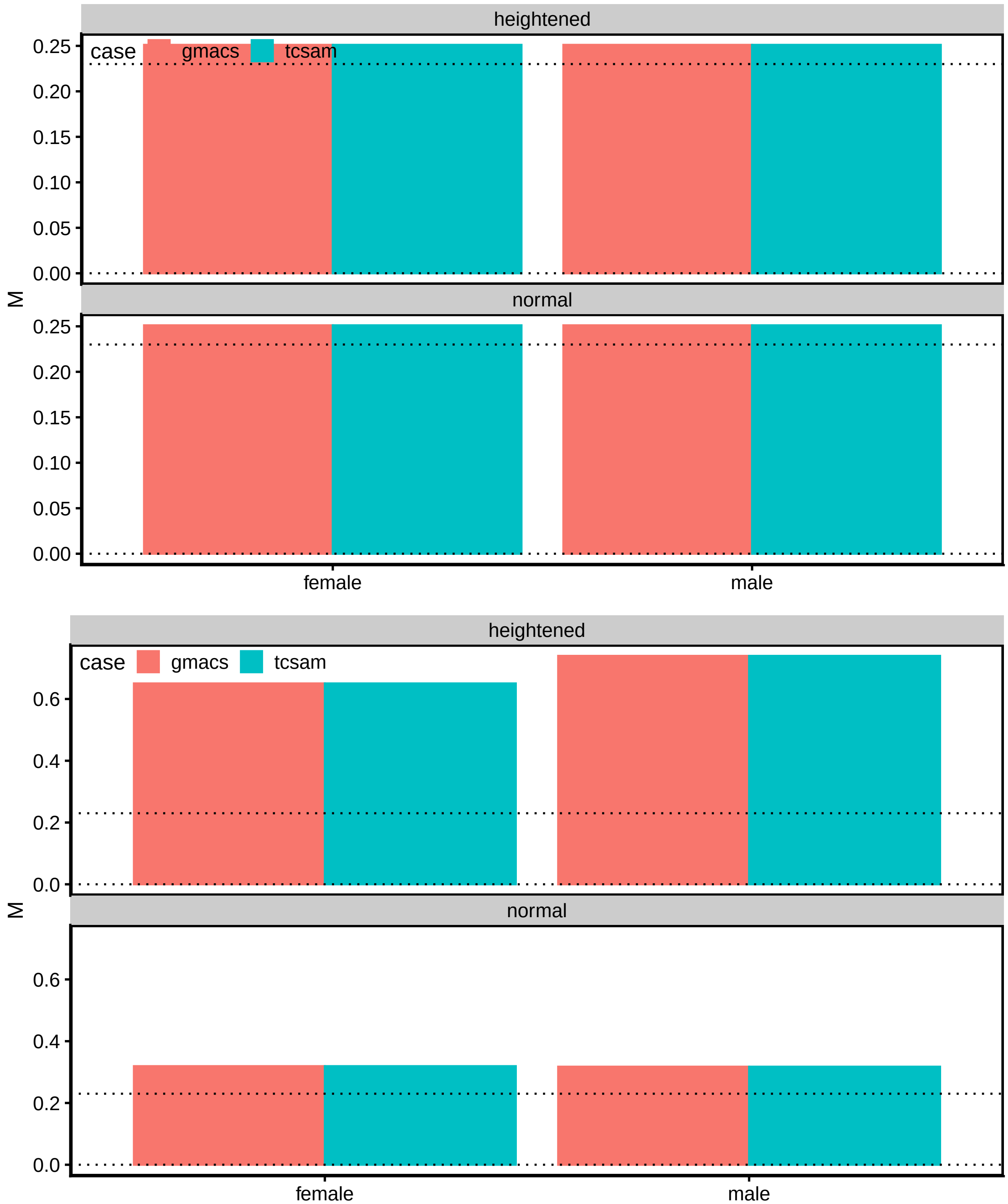


Figure 6. Natural mortality rates (M) used in the GMACS and TCSAM02 models, by biological category. Upper: immature crab; lower: mature crab. “heightened”: 1980-1984 time period; “normal”: remaining time period.

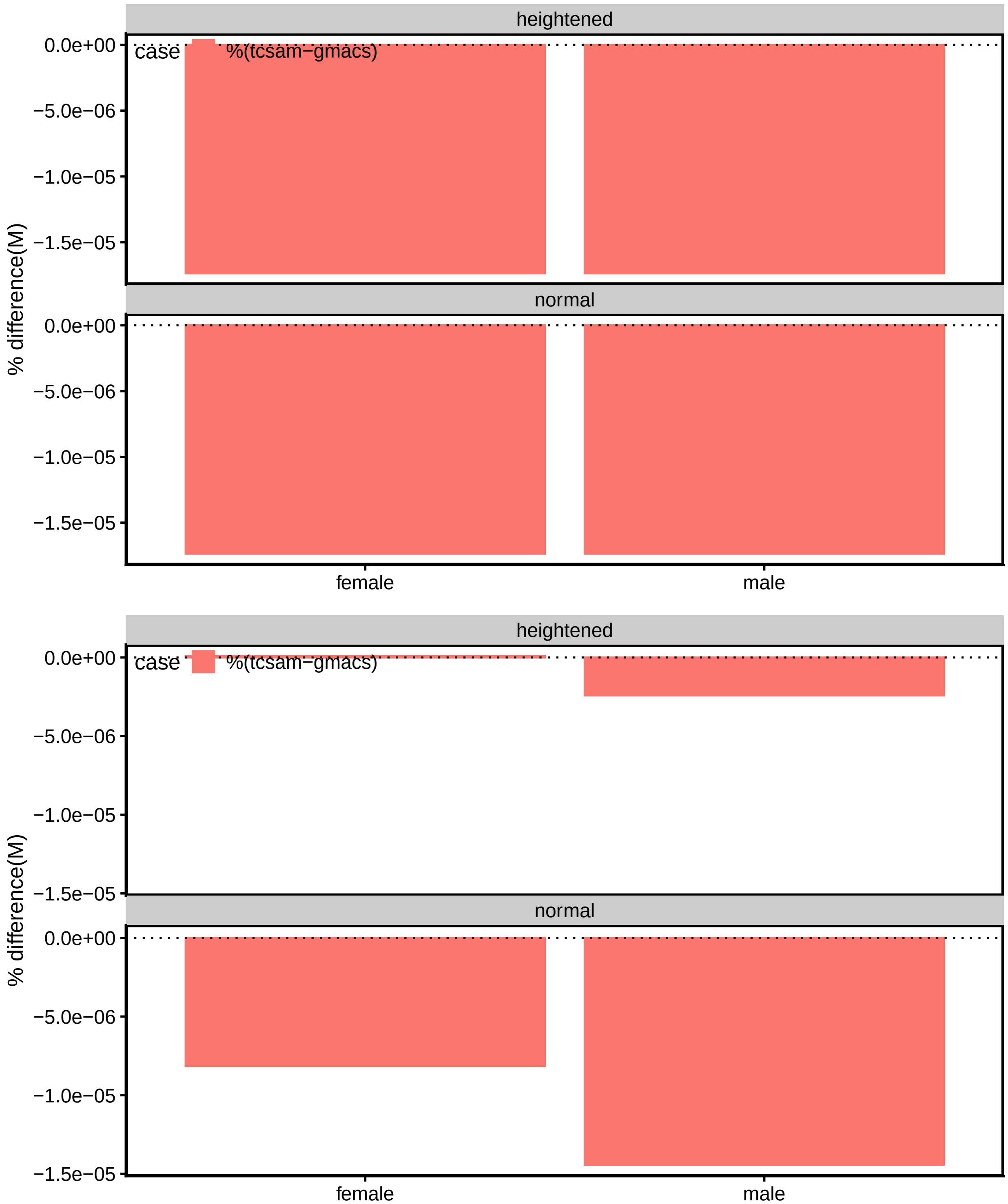


Figure 7. Percent difference in natural mortality rates (M) used in the GMACS and TCSAM02 models, by biological category. Upper: immature crab; lower: mature crab. “heightened”: 1980-1984 time period; “normal”: remaining time period.

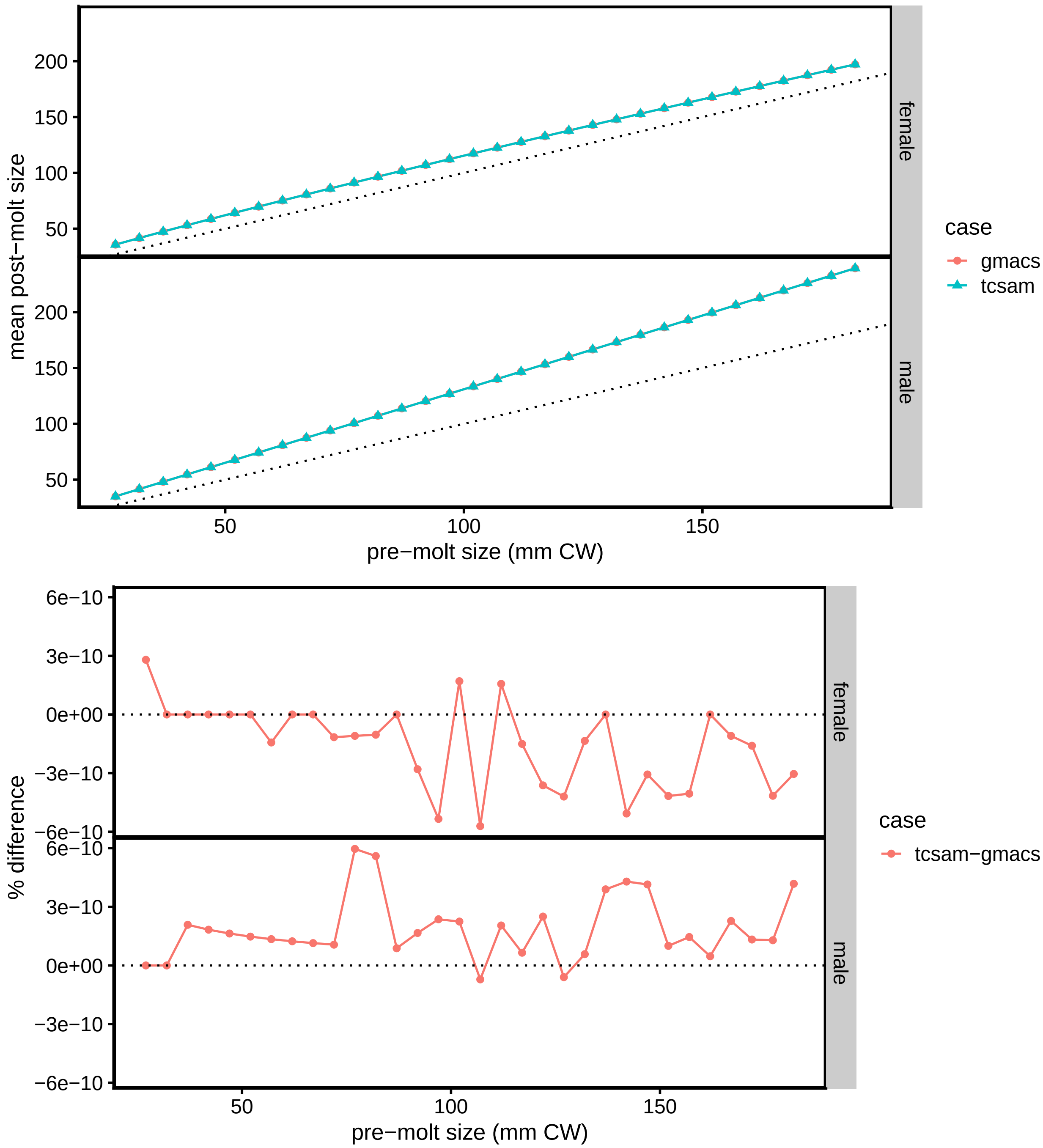


Figure 8. Mean postmolt size, as a function of premolt size, used in the GMACS and TCSAM02 models, by sex. Upper: values; lower: percent difference.

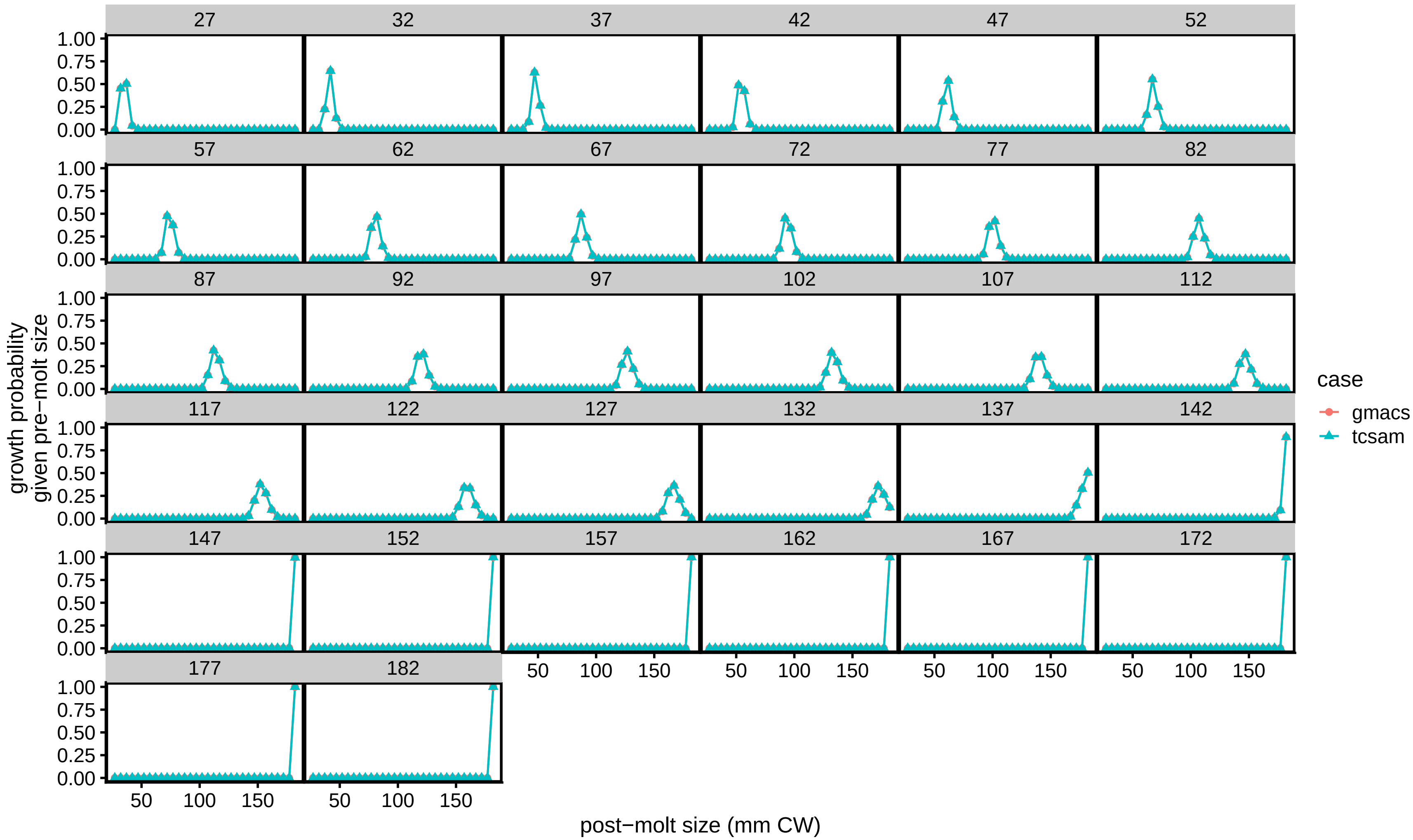


Figure 9. Distribution of postmolt sizes, as a function of premolt size, used in the GMACS and TCSAM02 models for males.

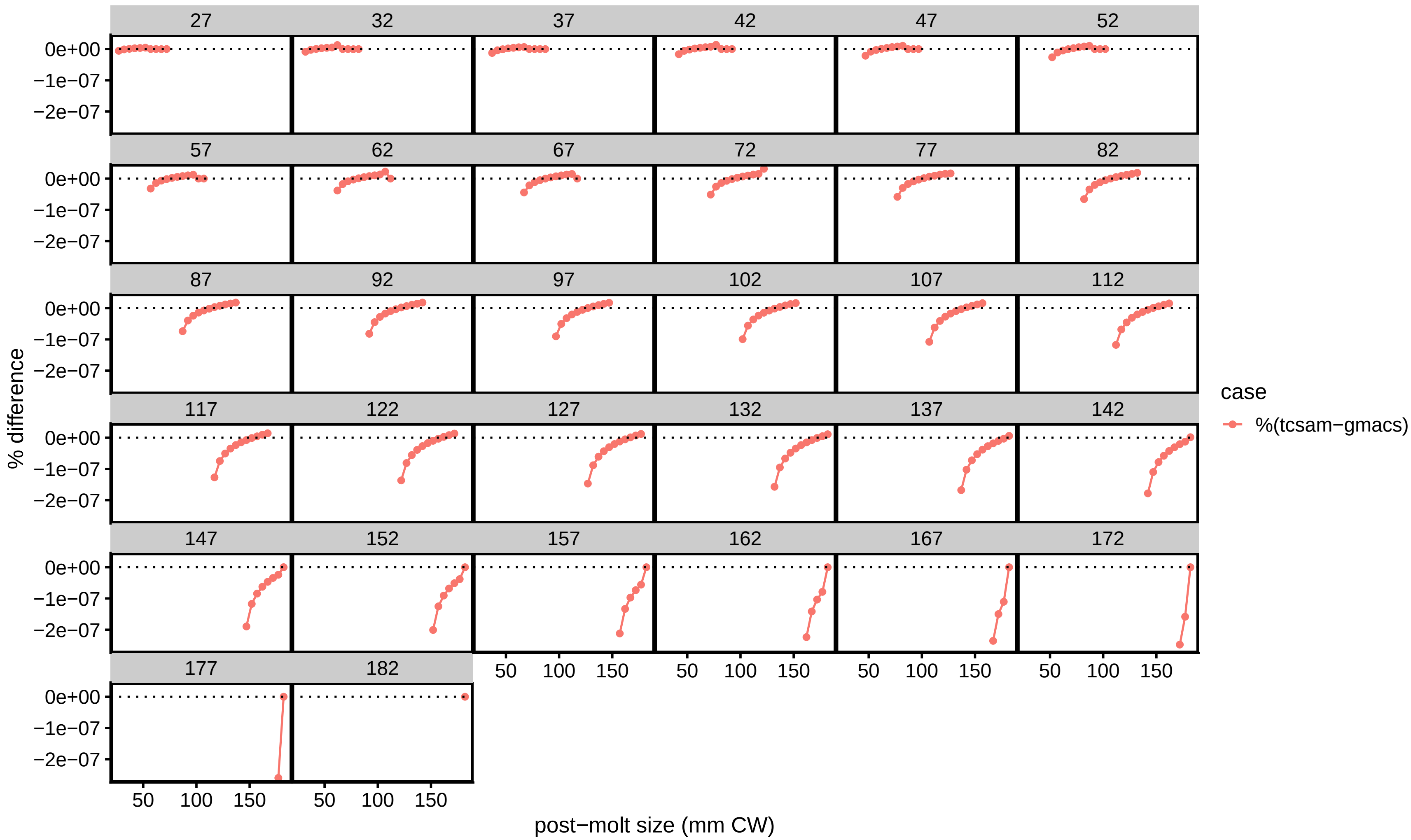
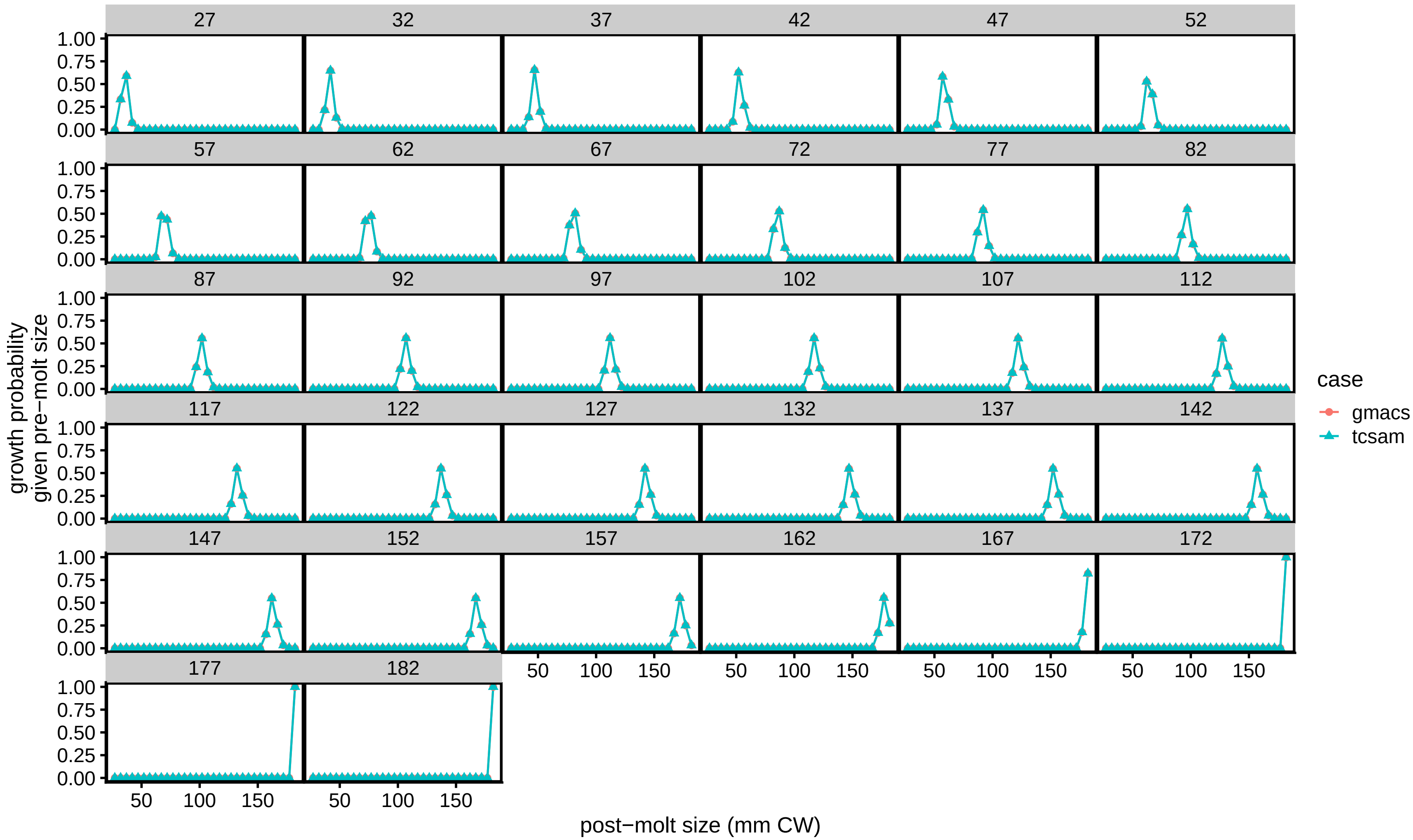


Figure 10. Percent difference in the distribution of postmolt sizes, as a function of premolt size, used in the GMACS and TCSAM02 models for males.



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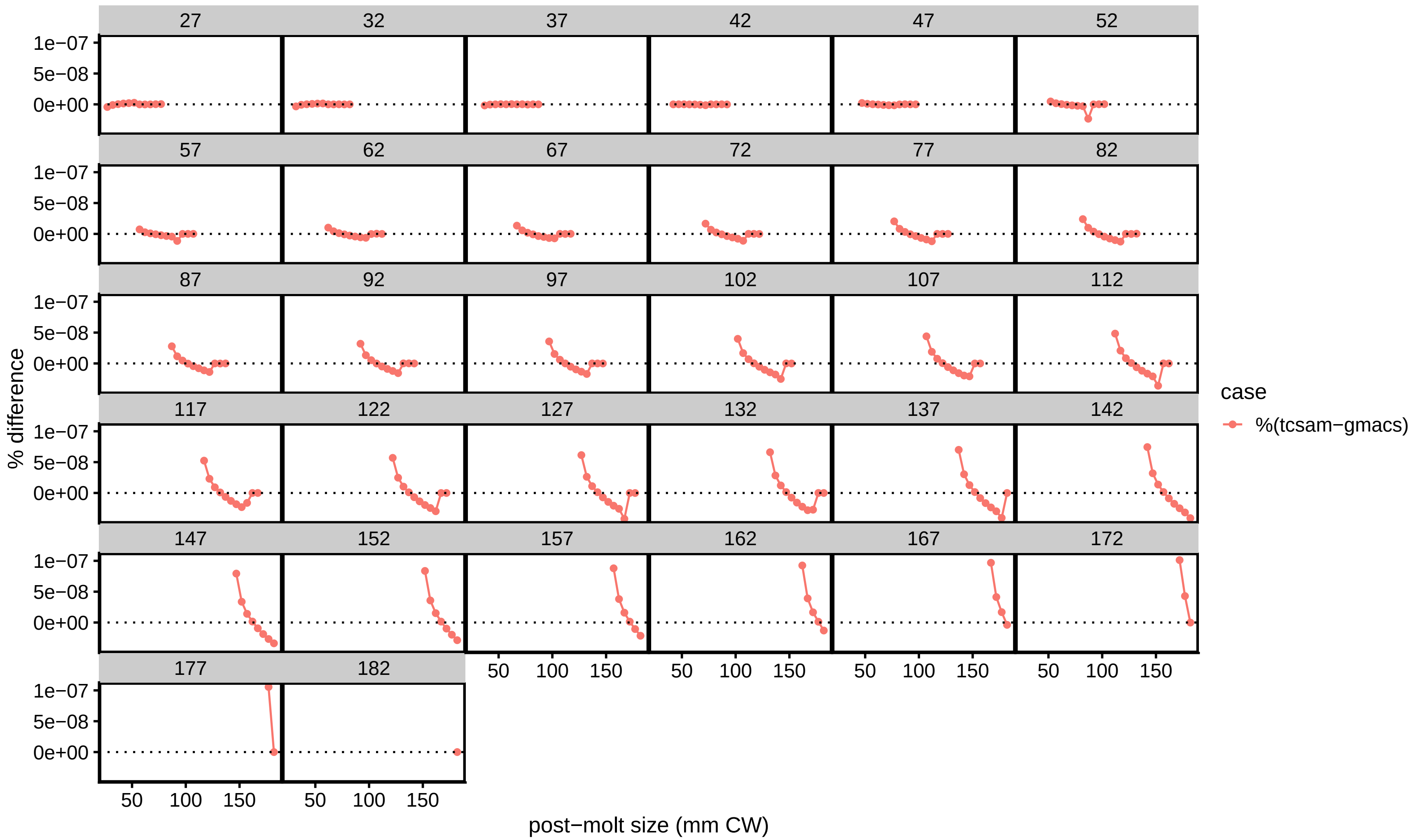
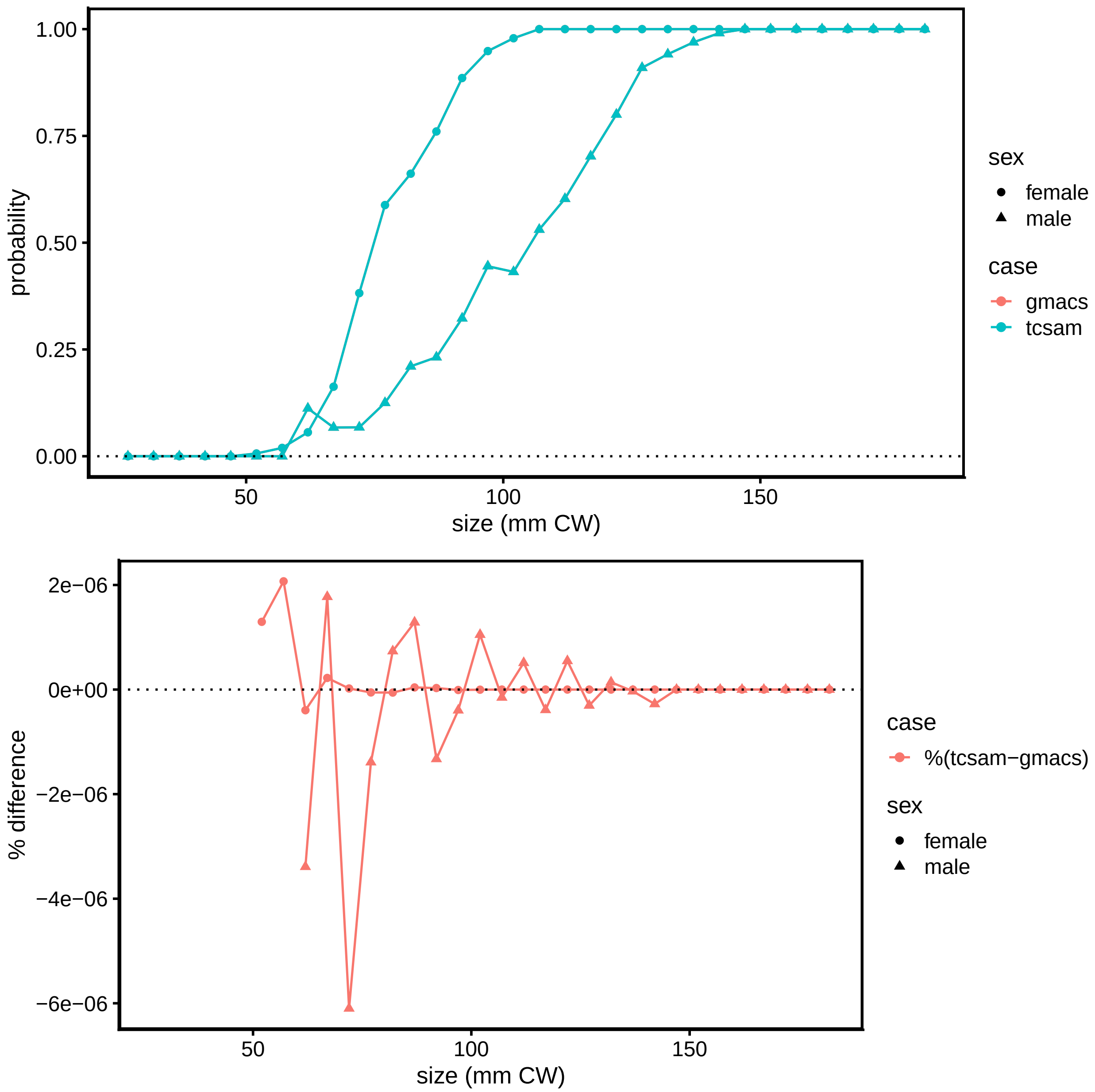


Figure 12. Percent difference in the distribution of postmolt sizes, as a function of premolt size, used in the GMACS and TCSAM02 models for females.



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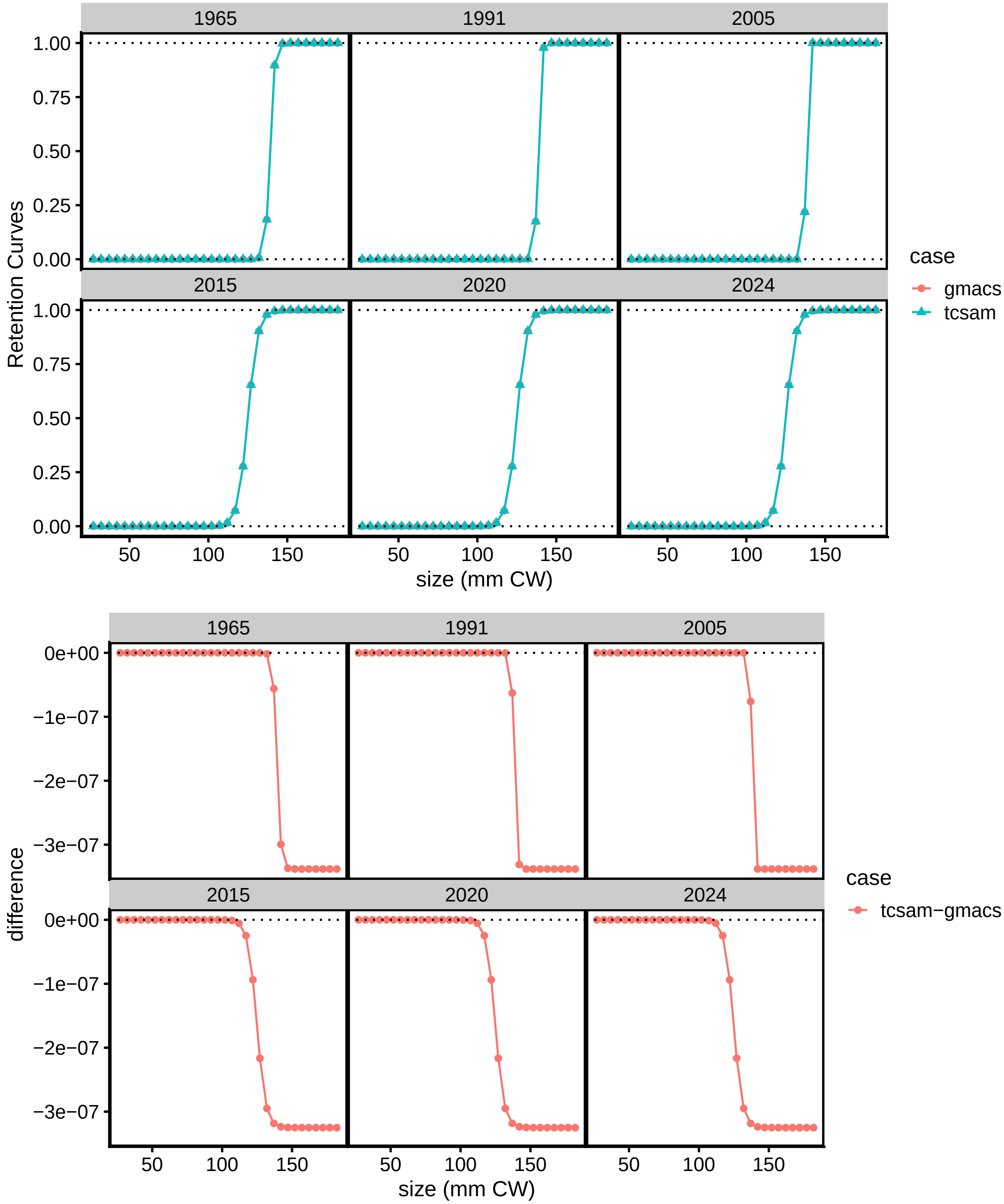
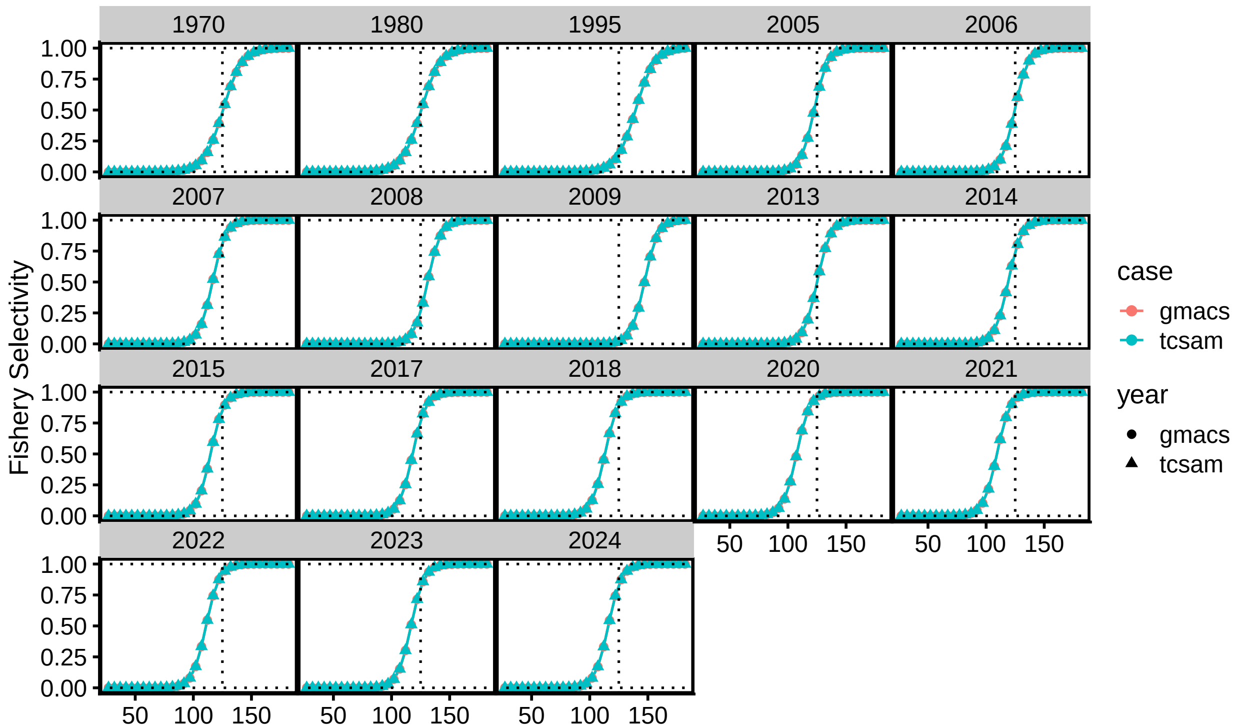
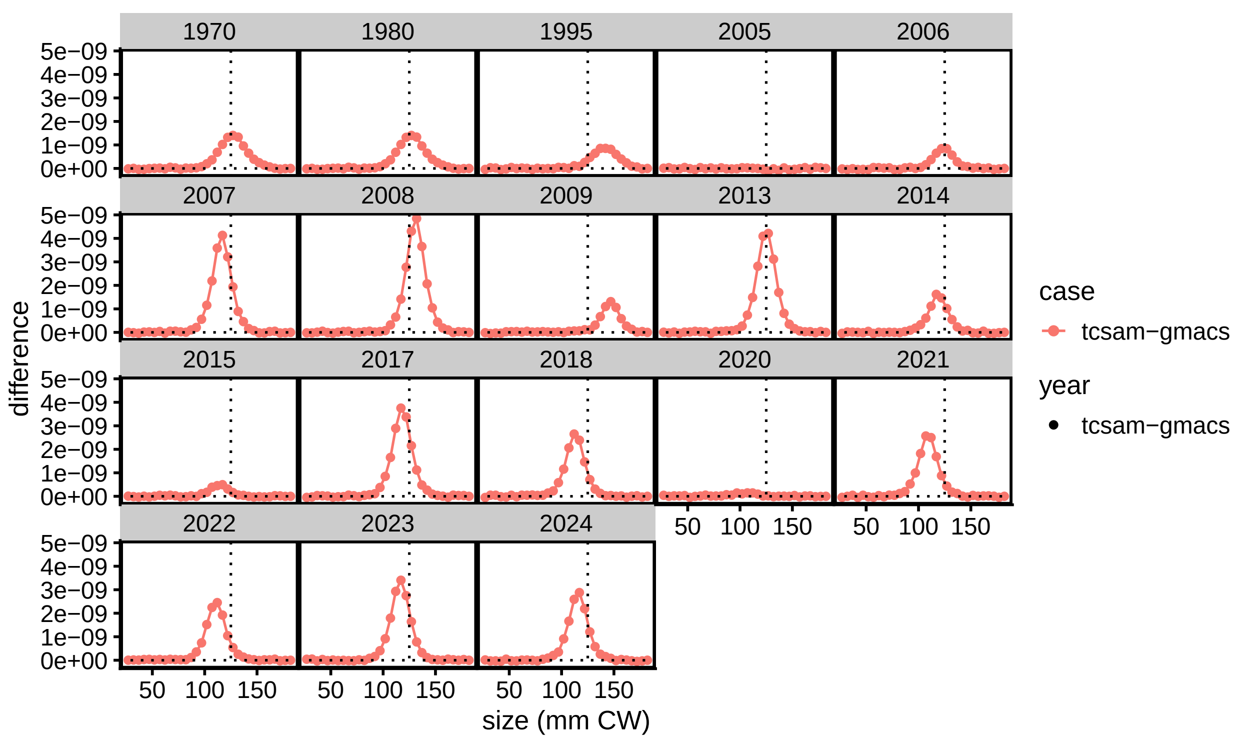


Figure 14. Comparison of the fishery retention curves used in the GMACS and TCSAM02 models. Upper: values for selected years; lower: differences.





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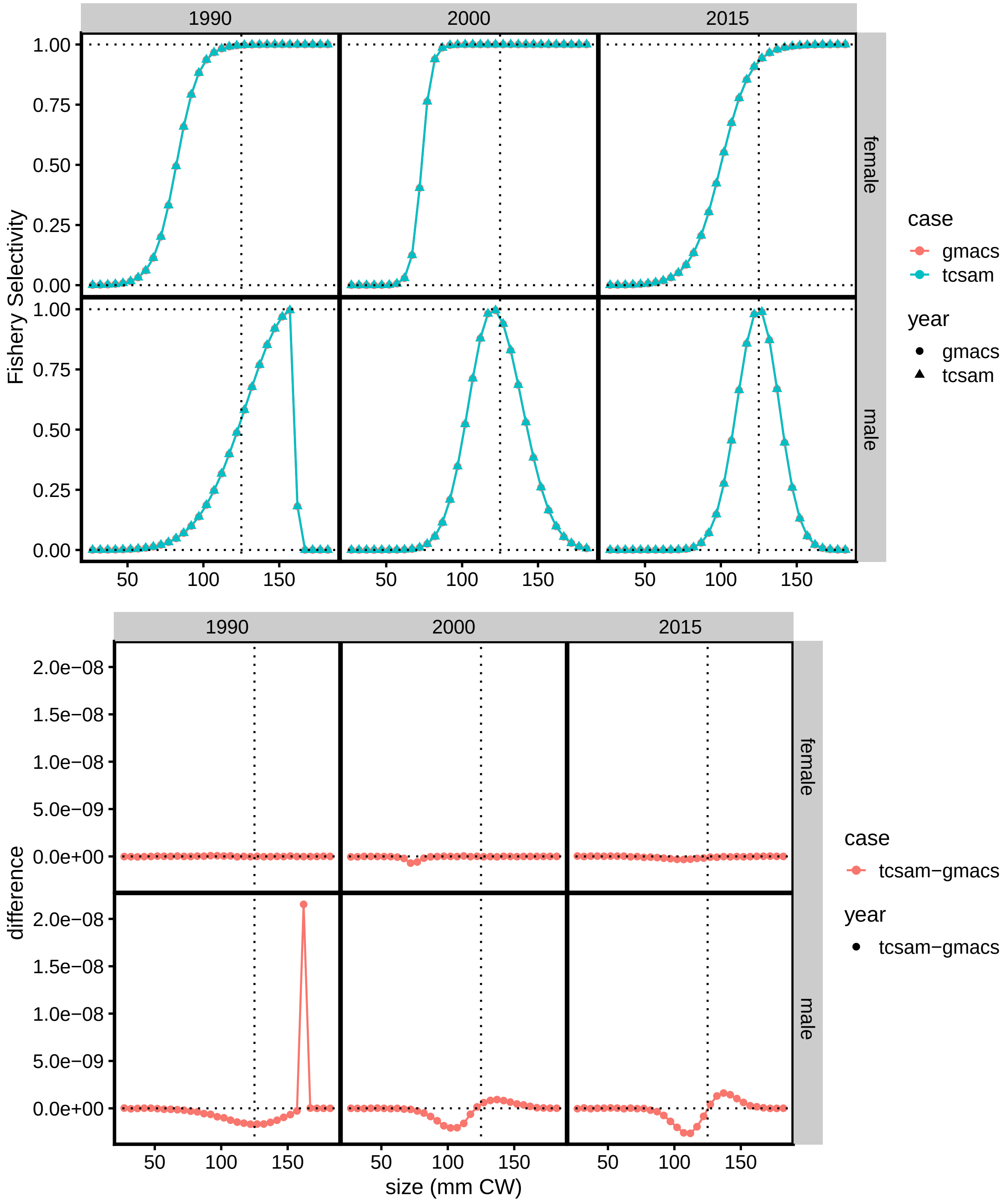

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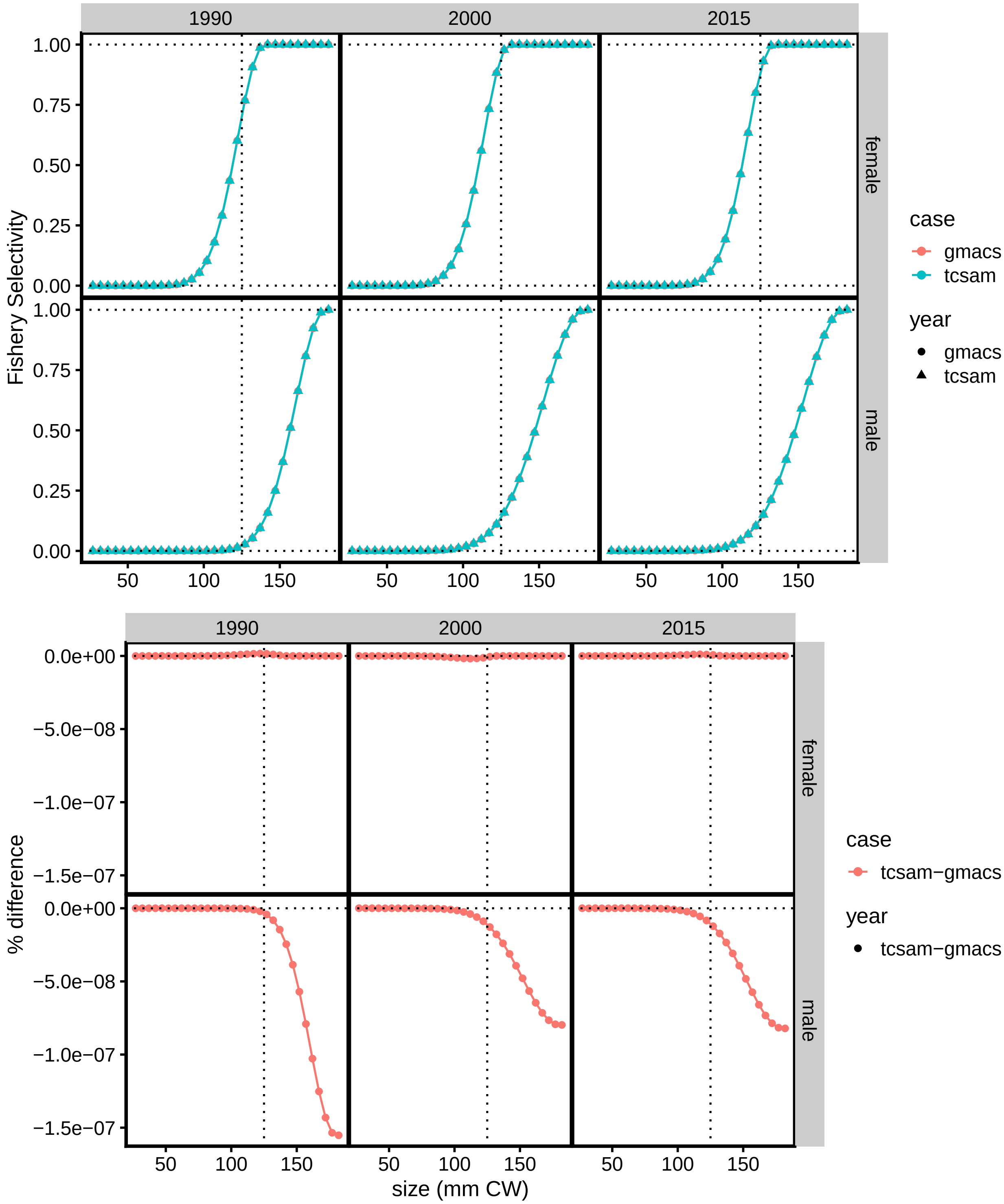

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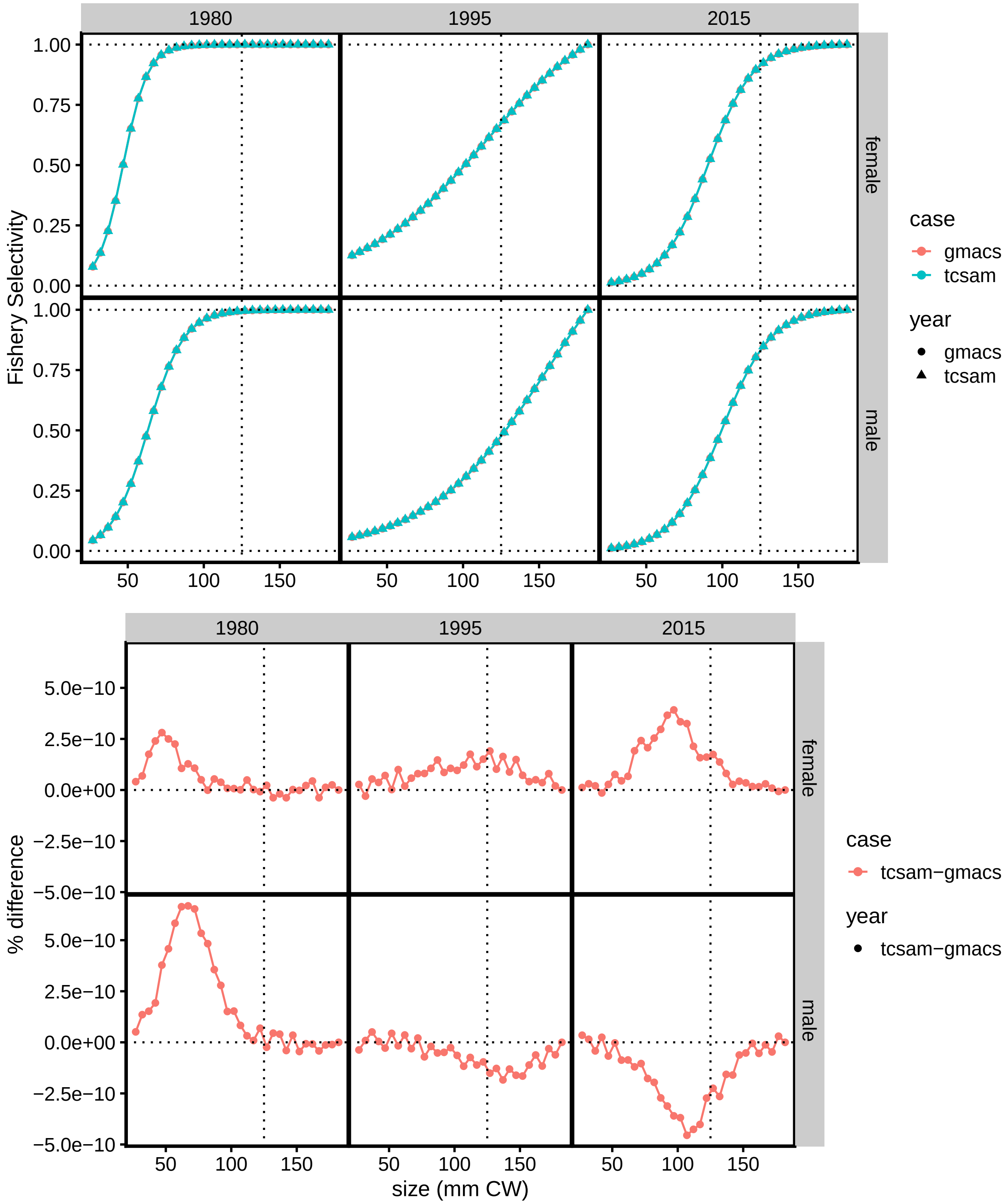

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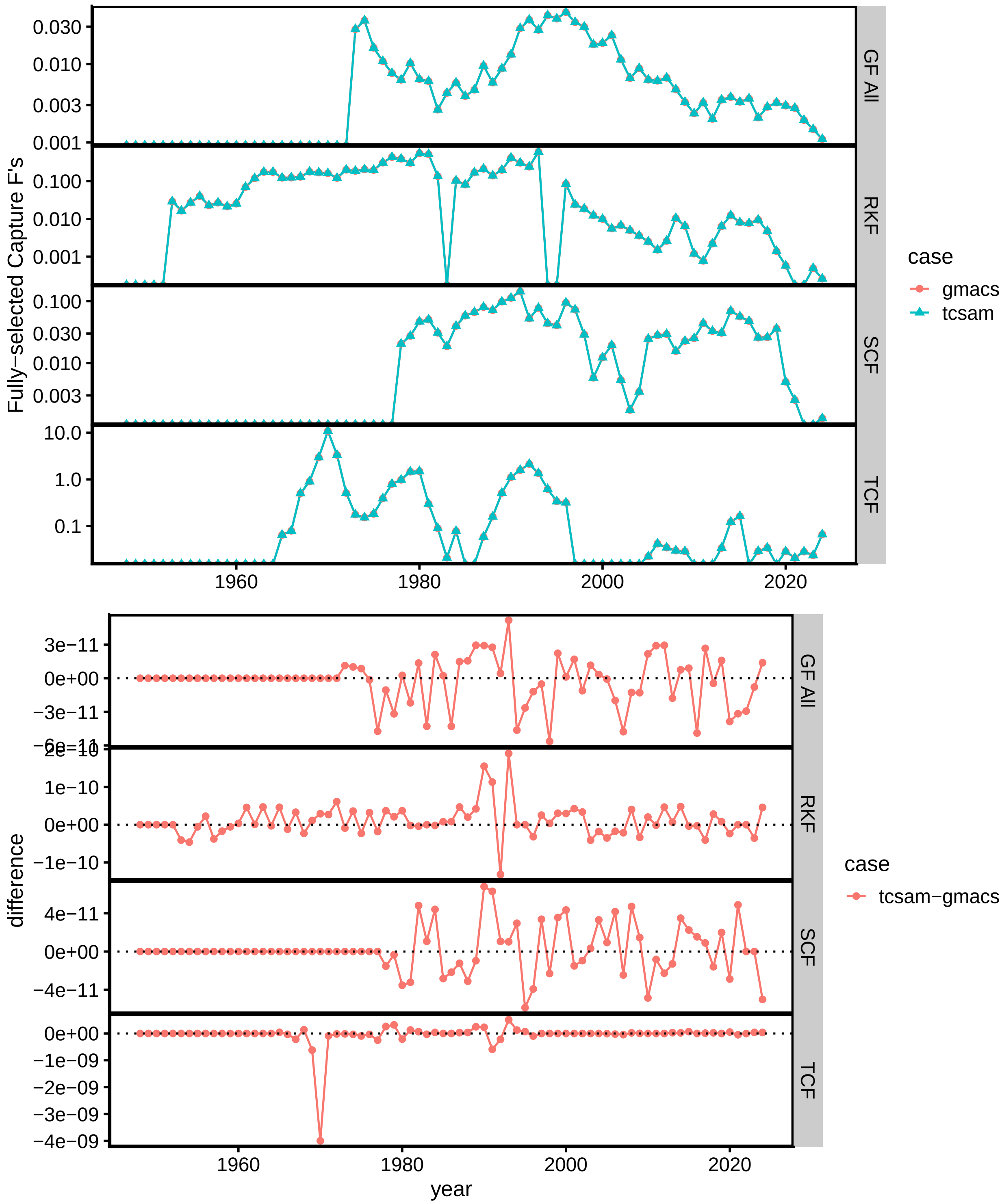

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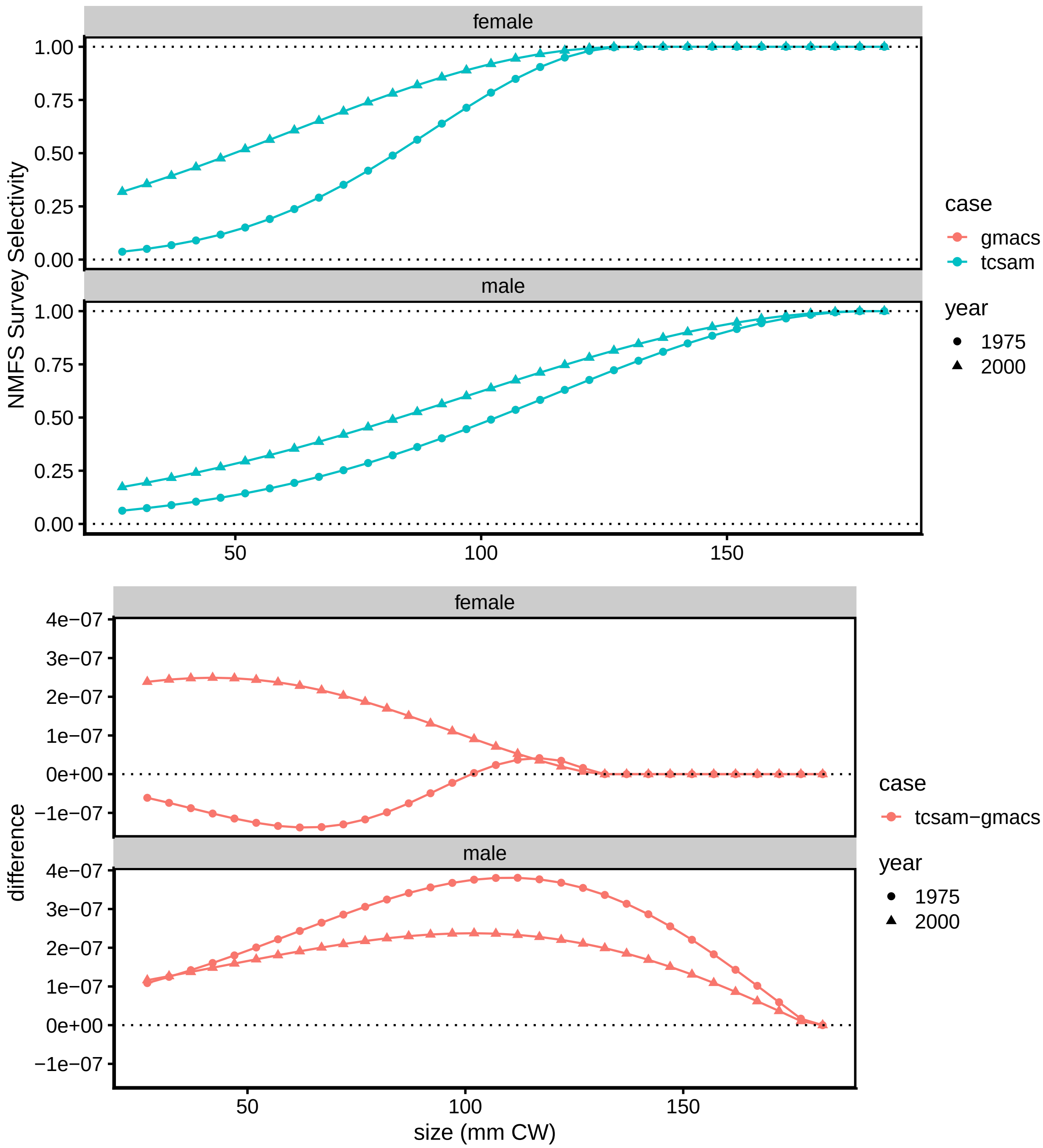

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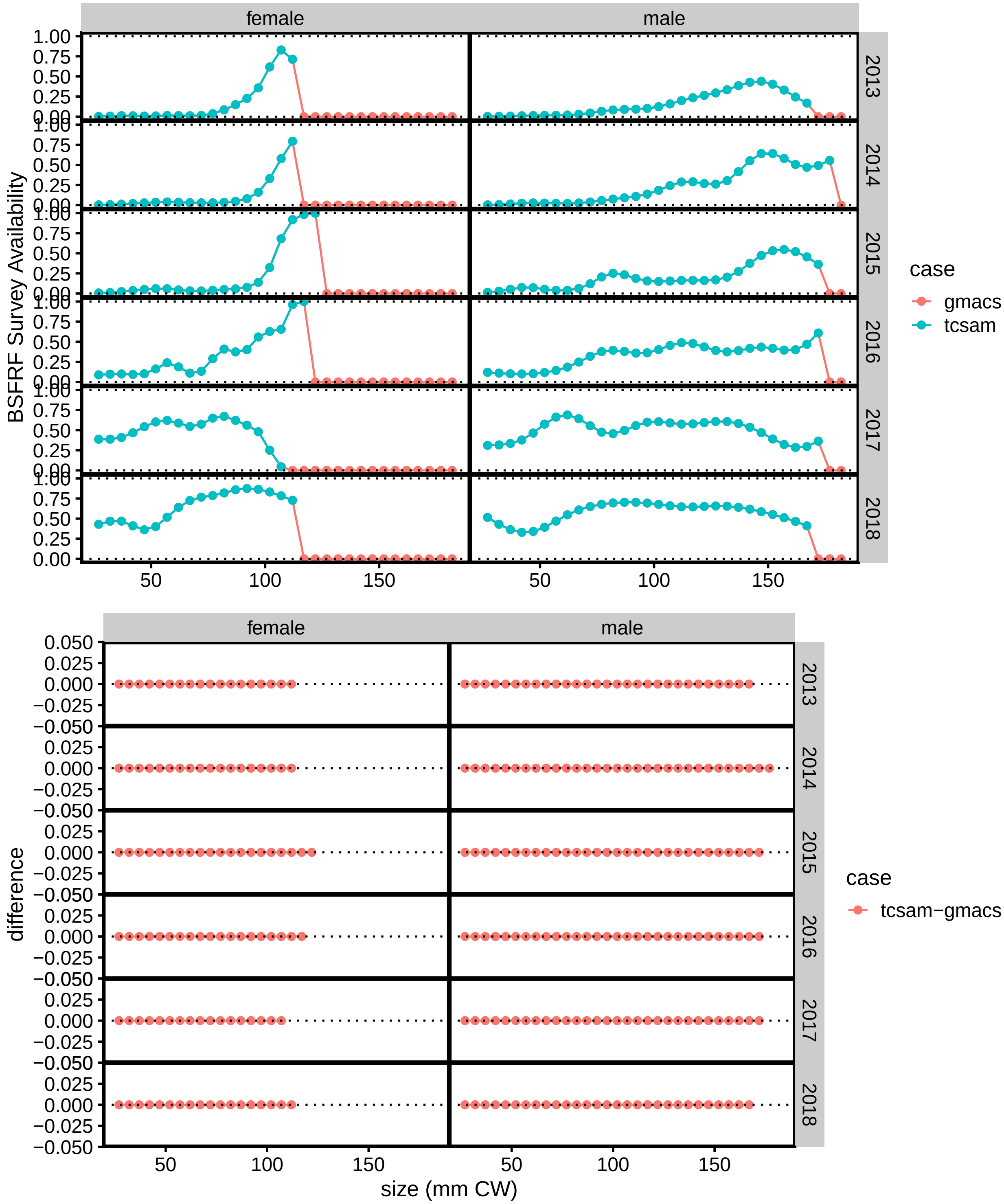

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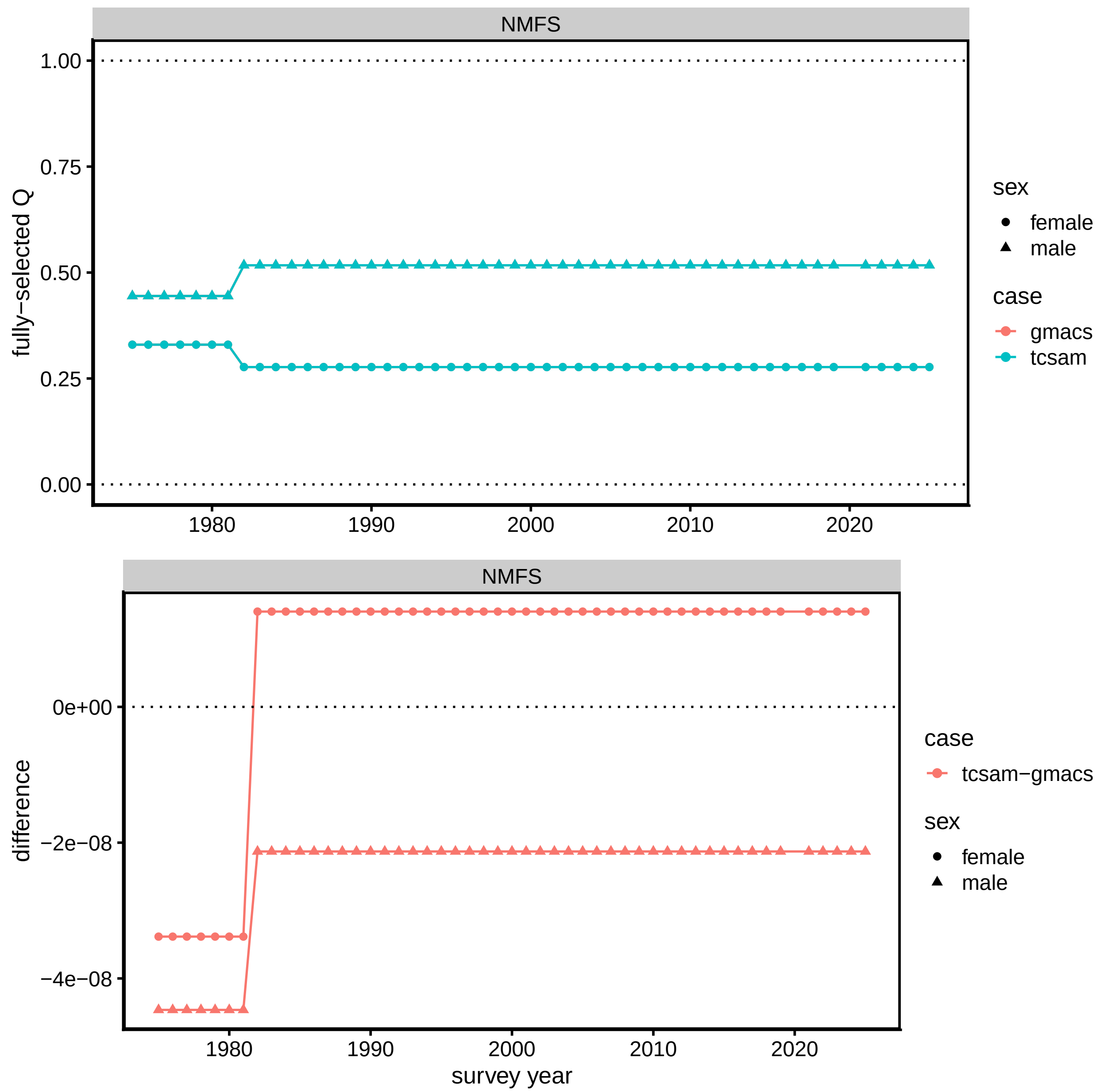
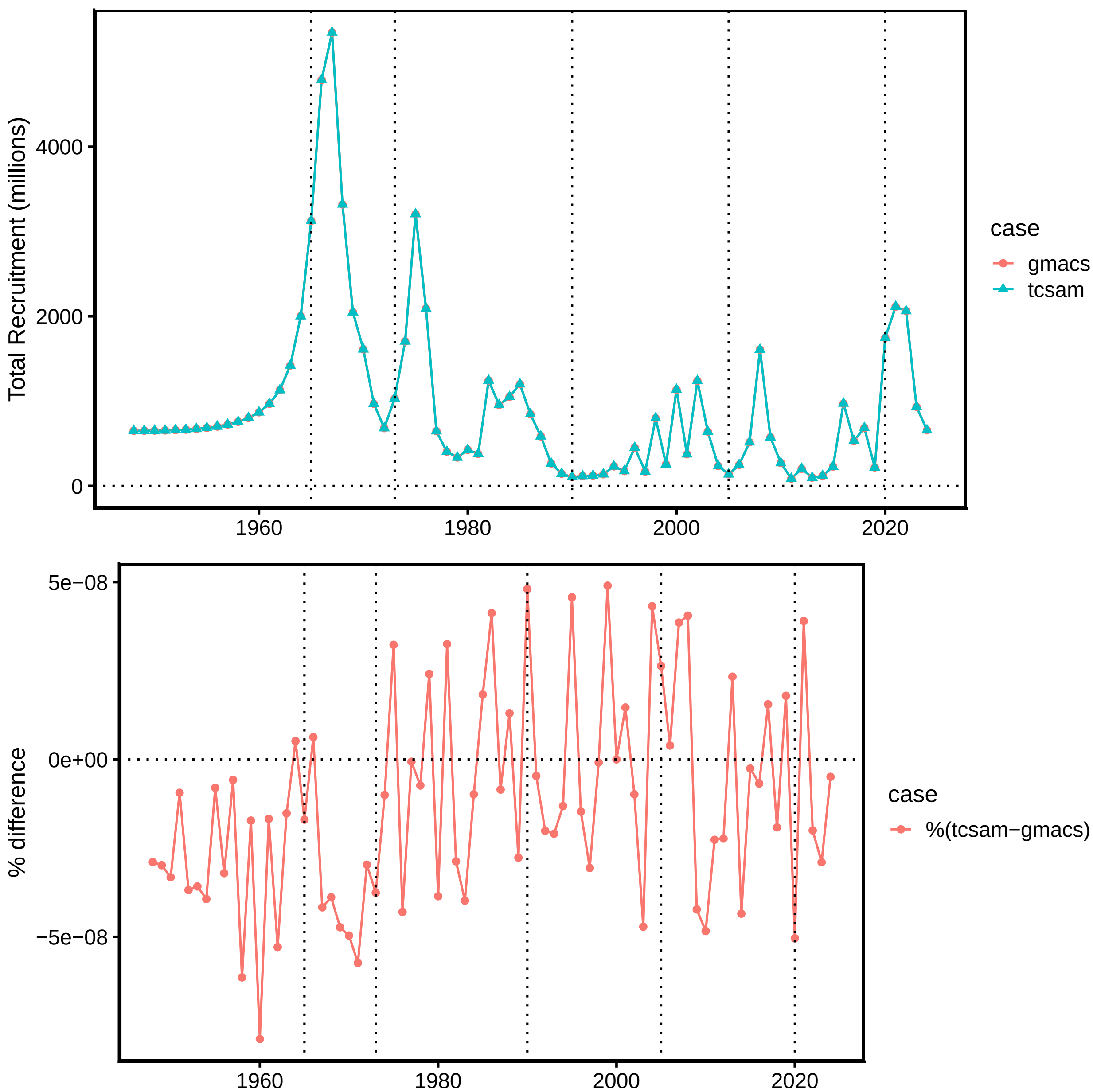


Figure 22. Comparison of fully-selected survey catchability ('q') for the NMFS survey by sex and year as used in the GMACS and TCSAM02 models. Upper: values; lower: differences. Fully-selected q's for the BSFRF surveys are 1 in both models and are not shown.



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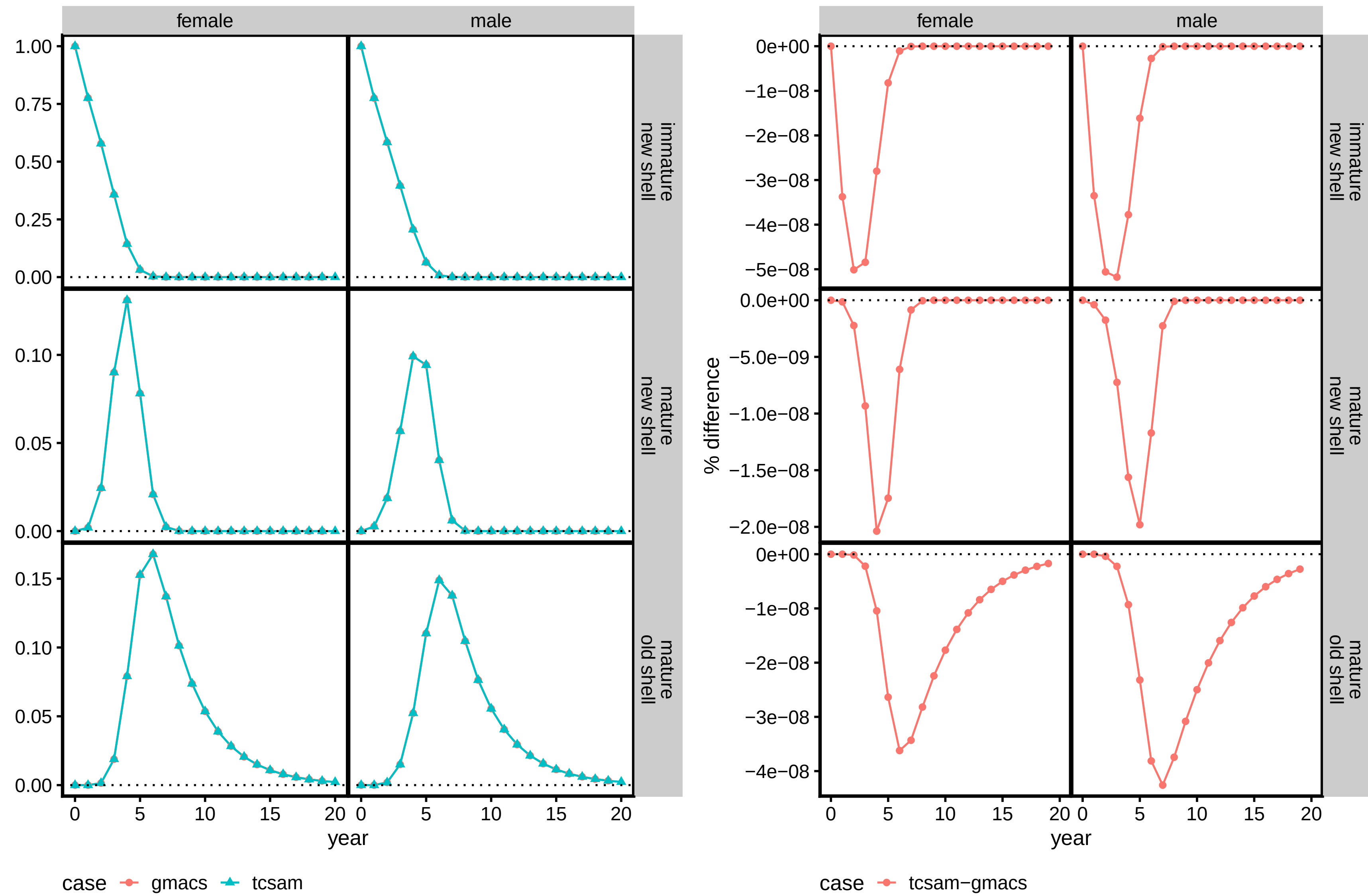

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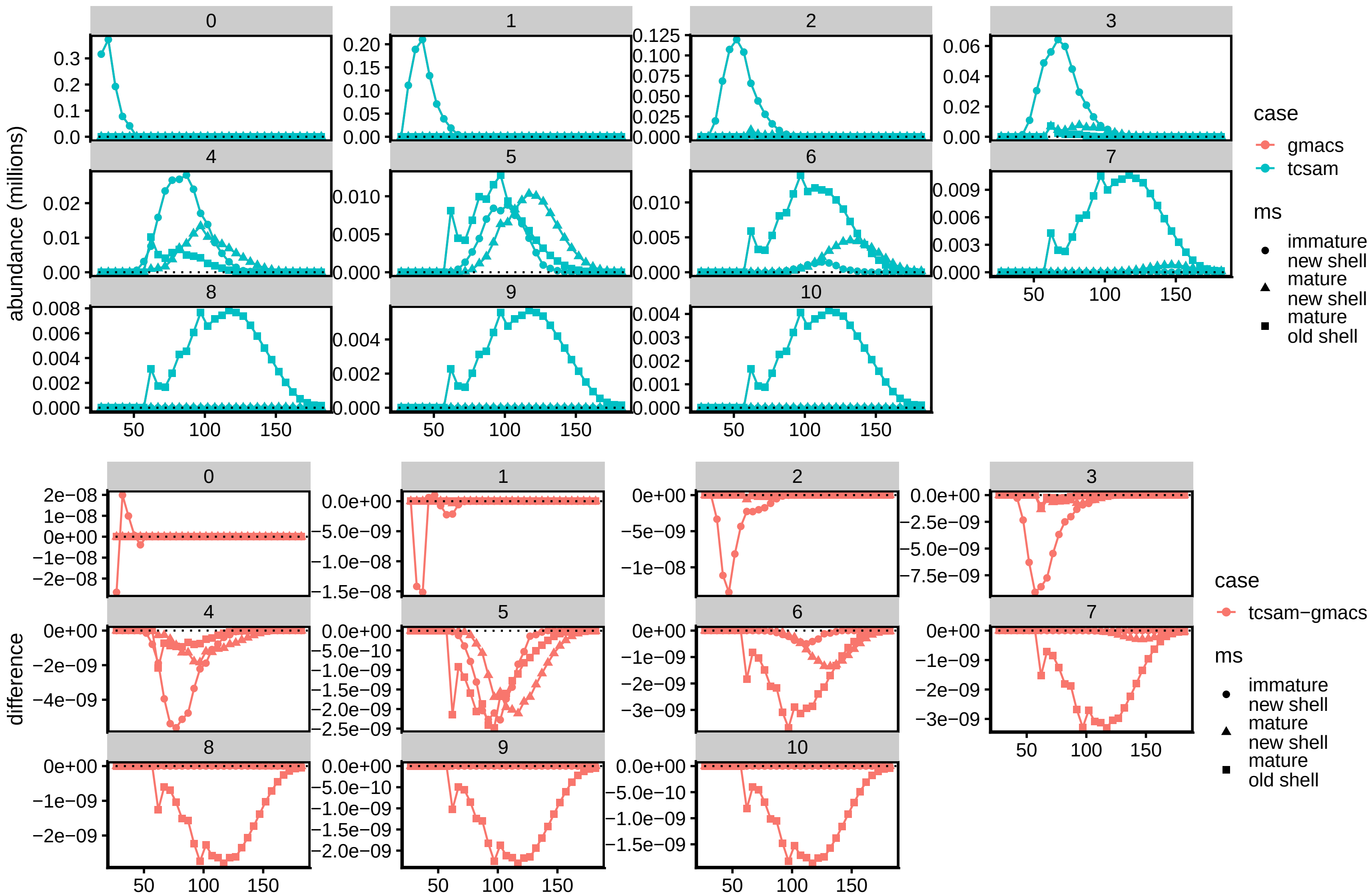

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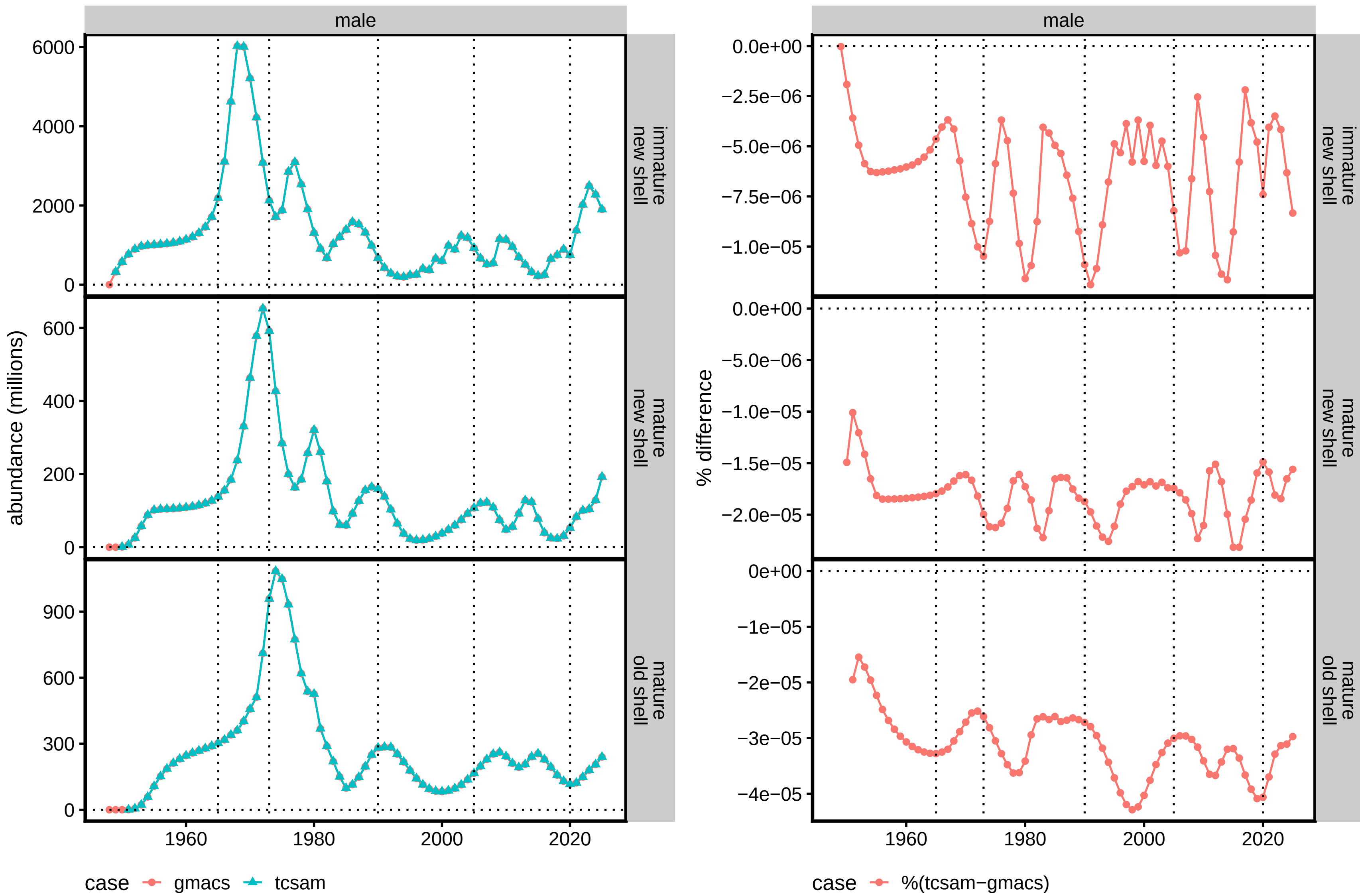

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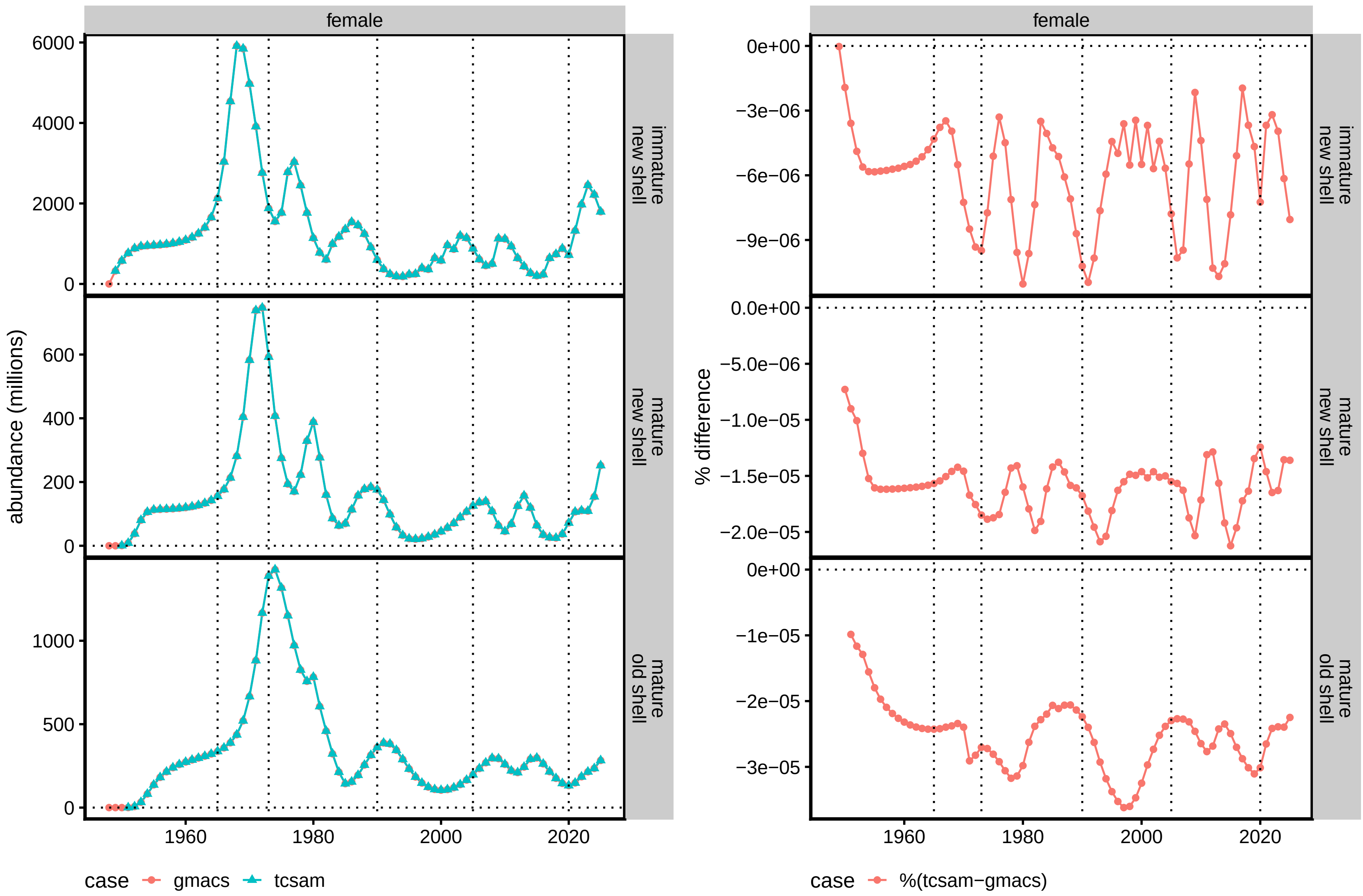

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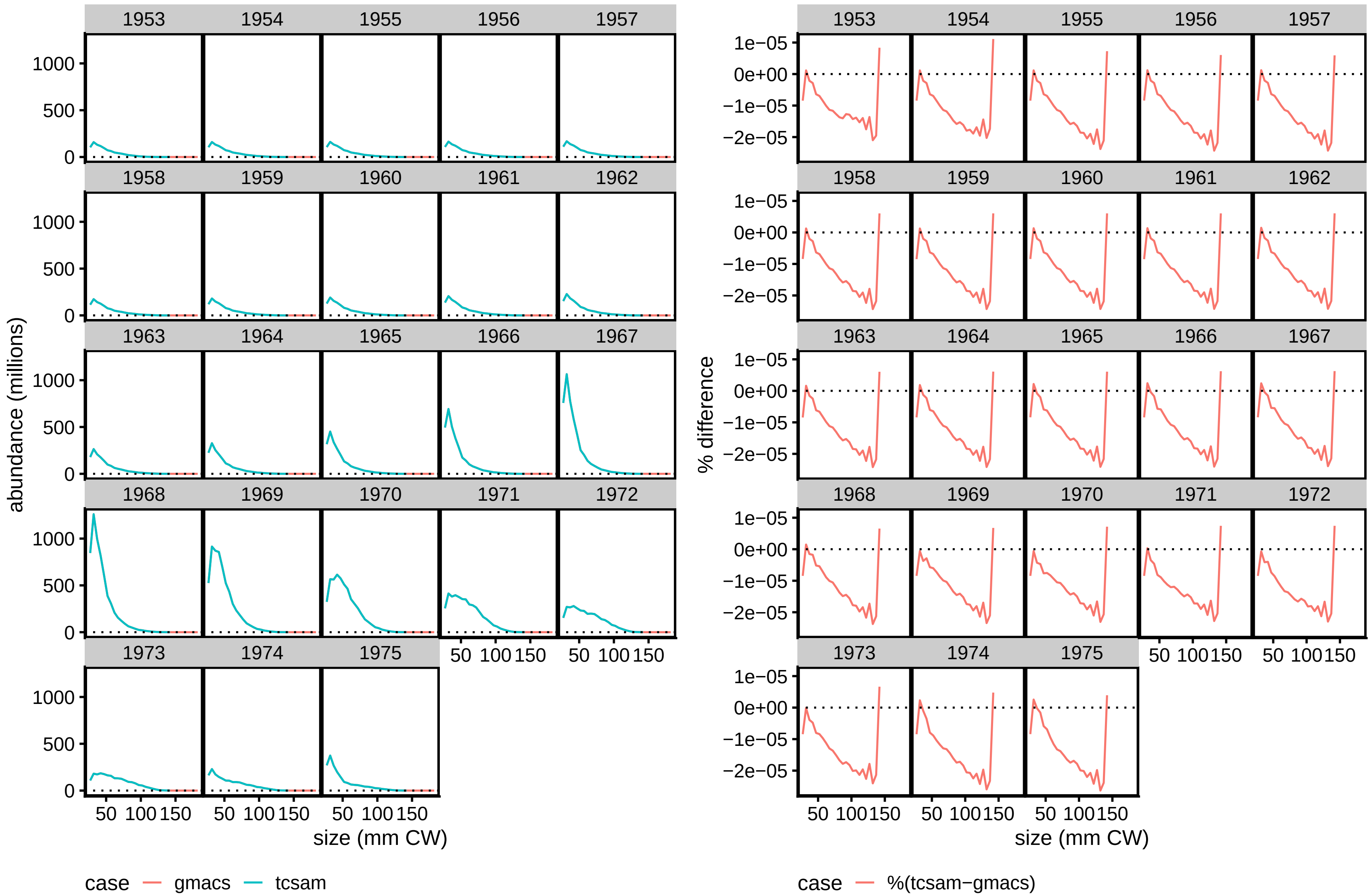

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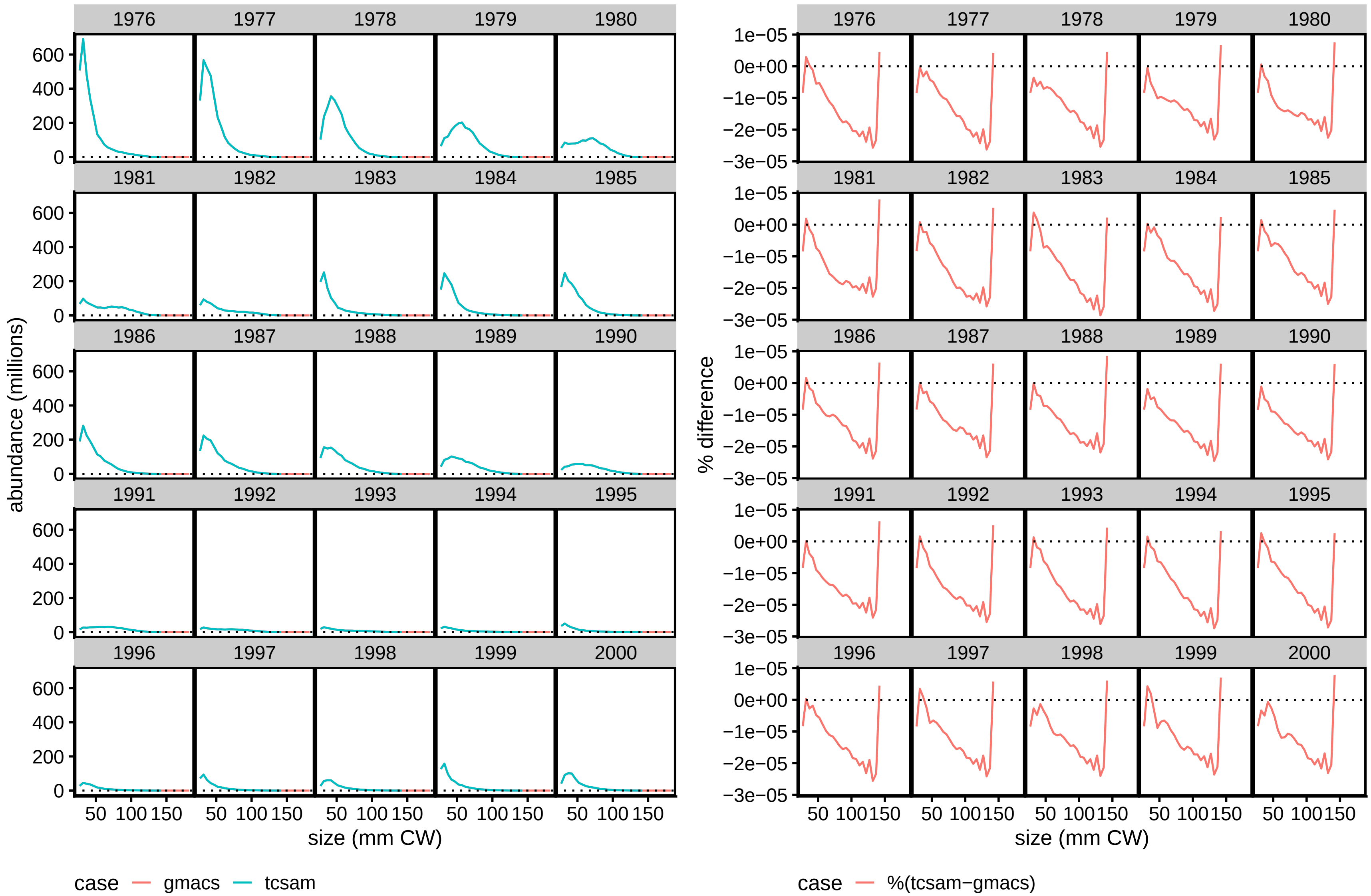

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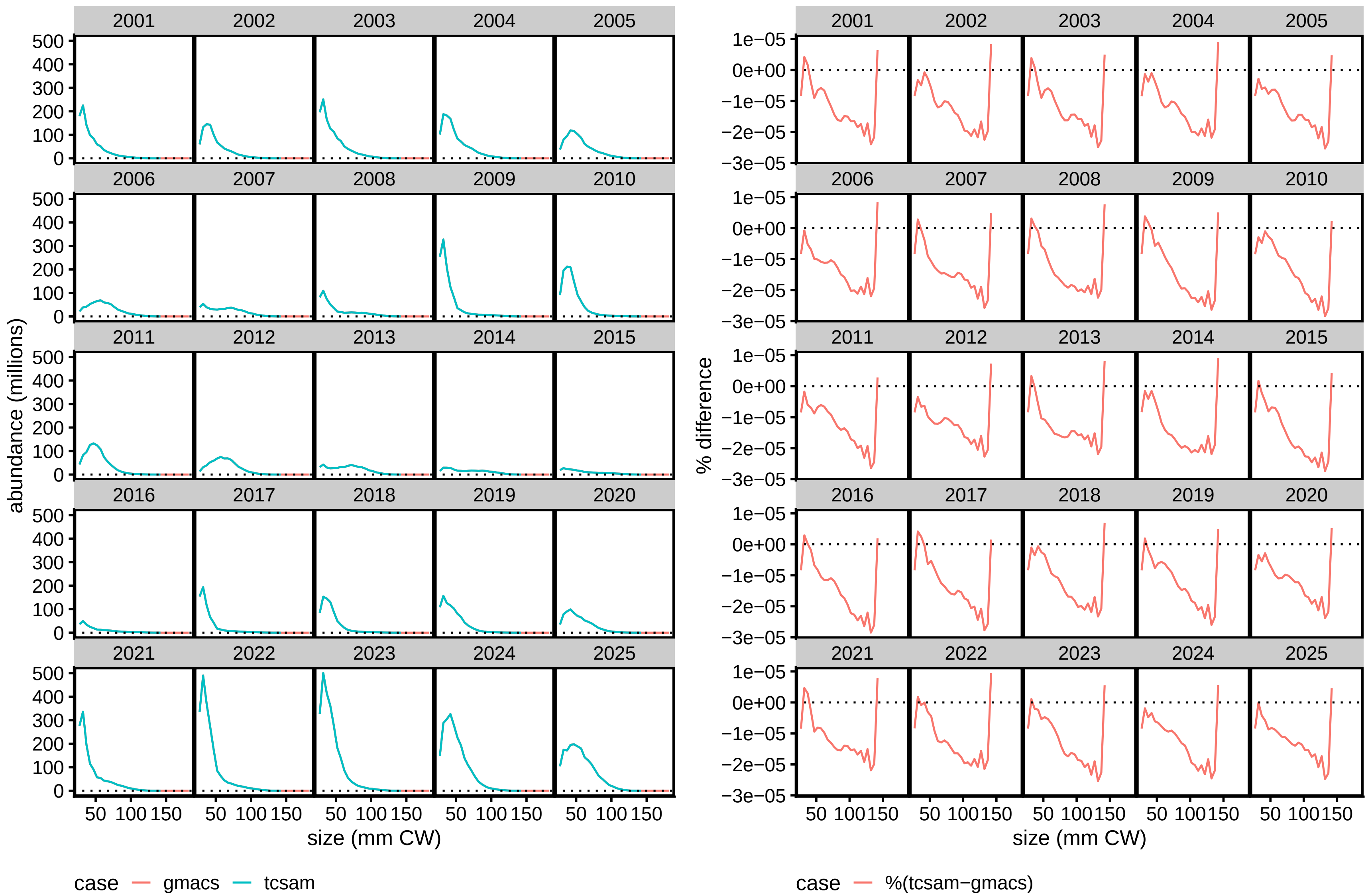

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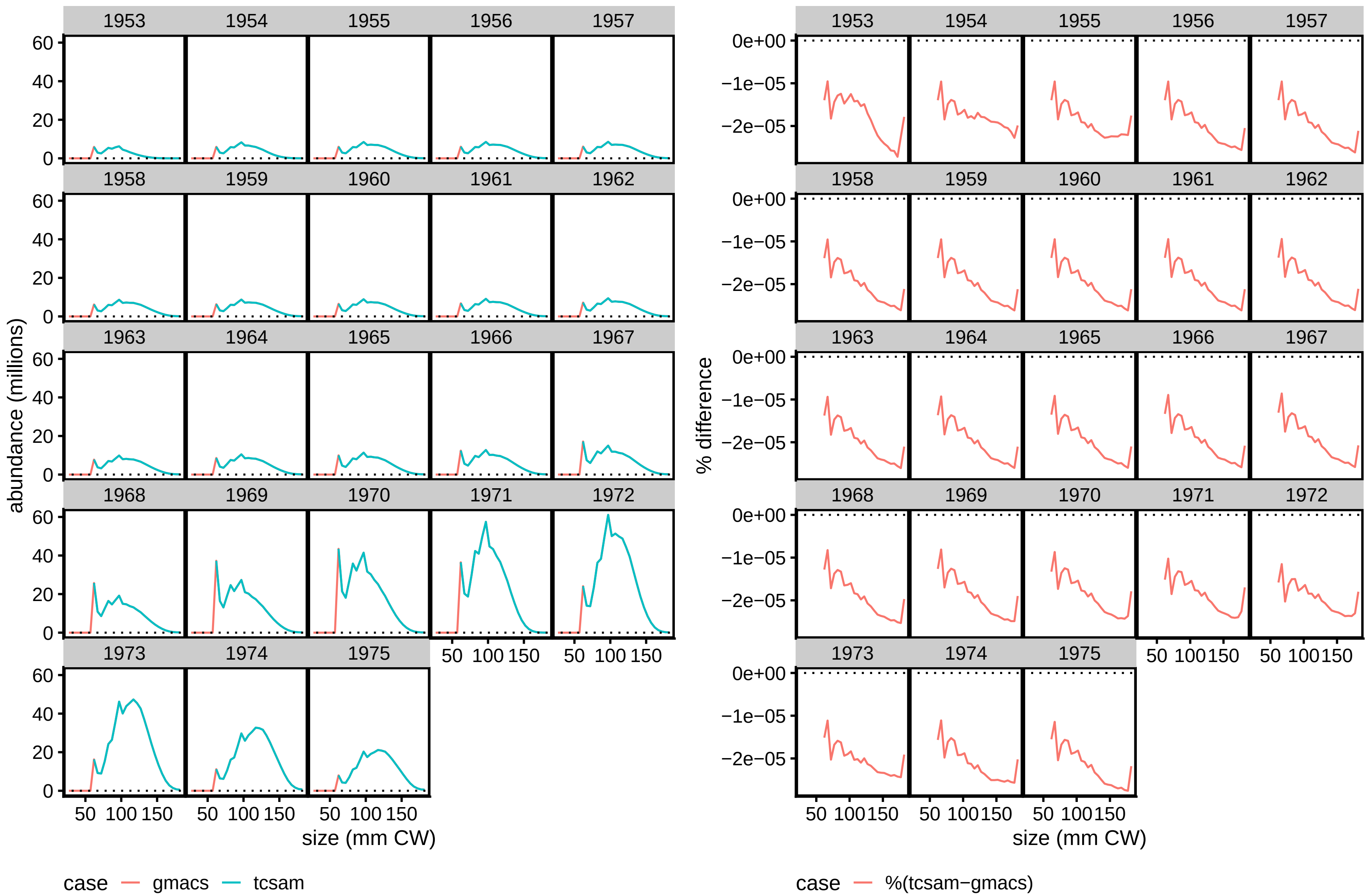

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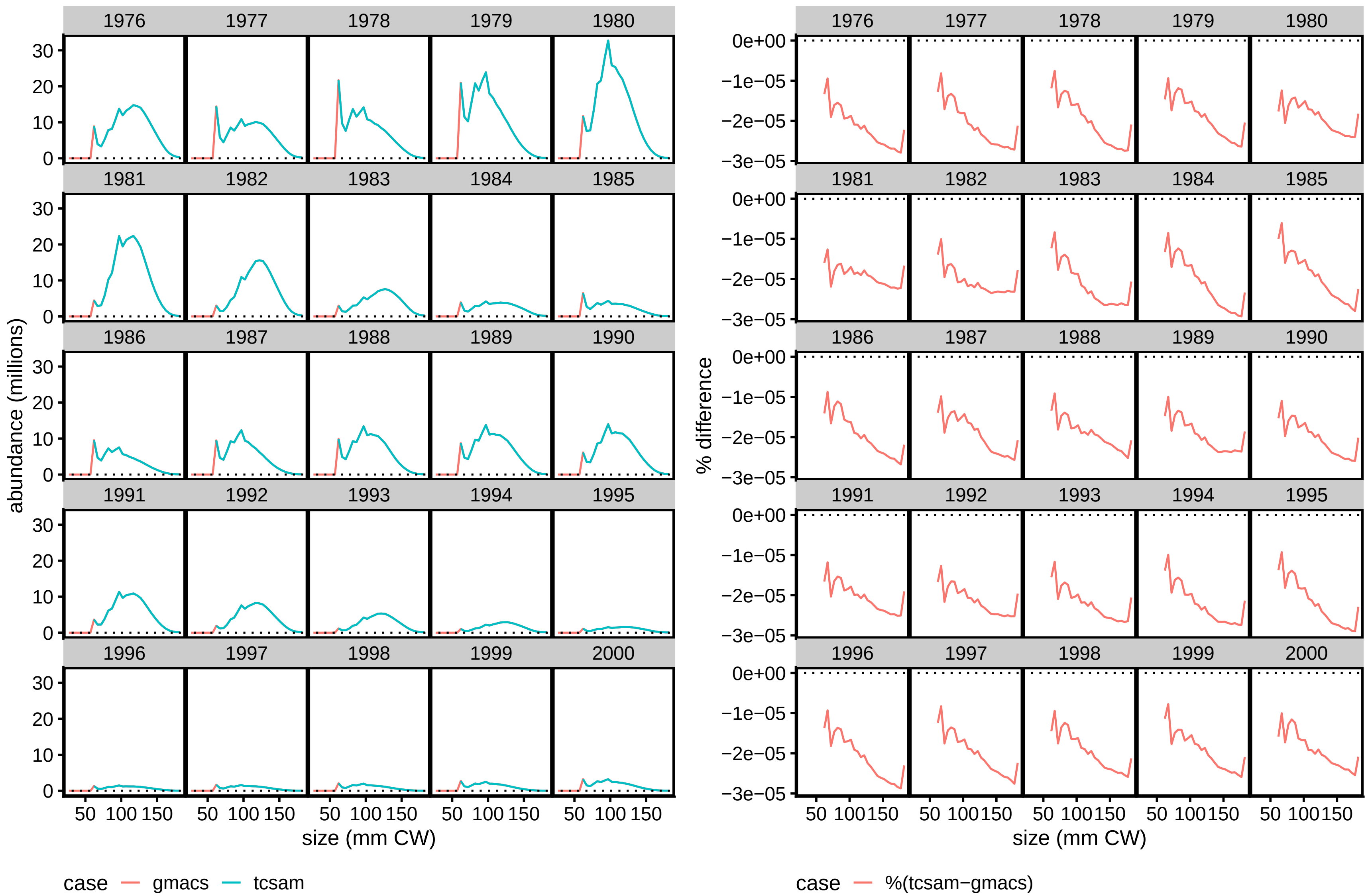

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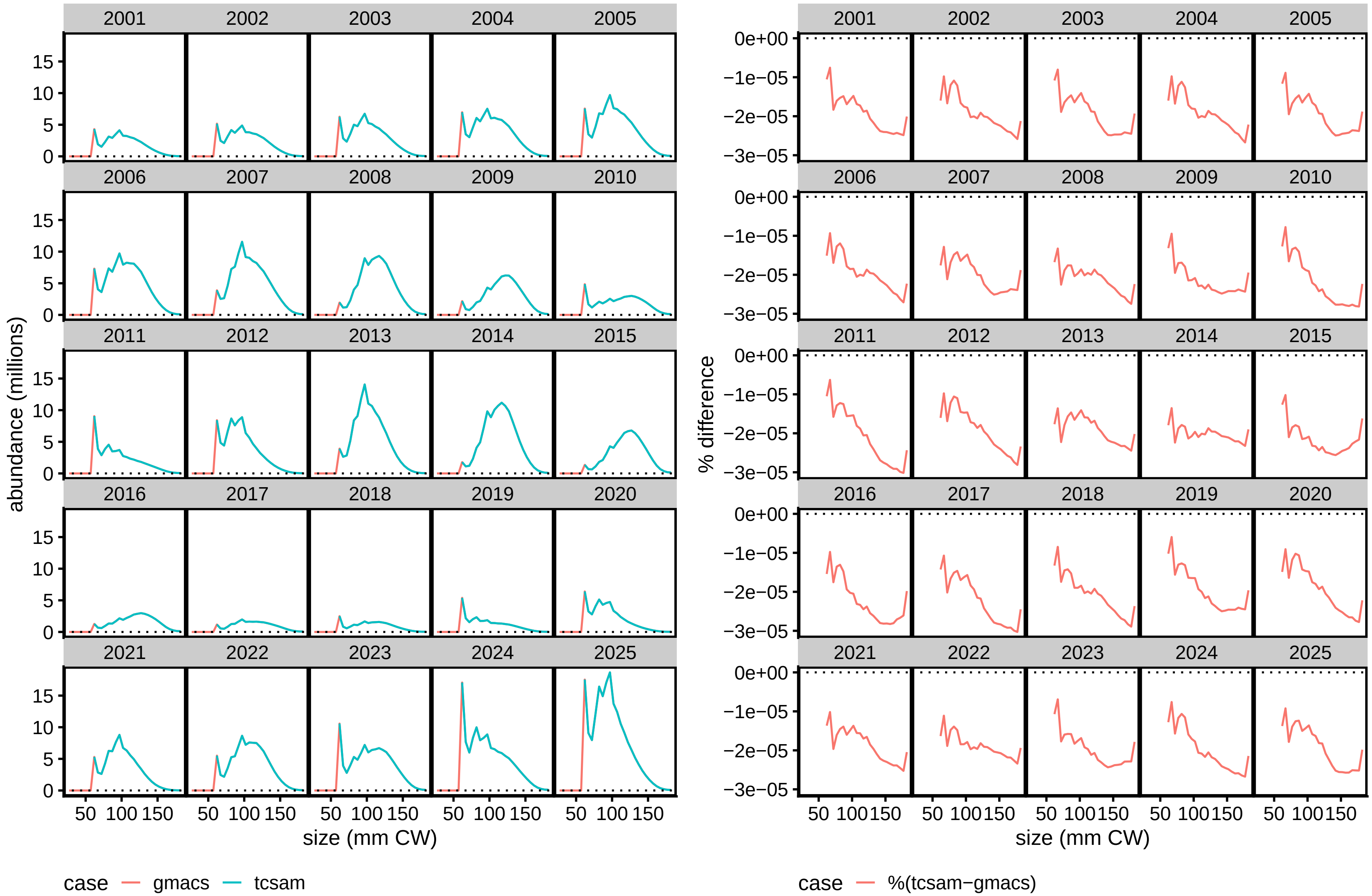

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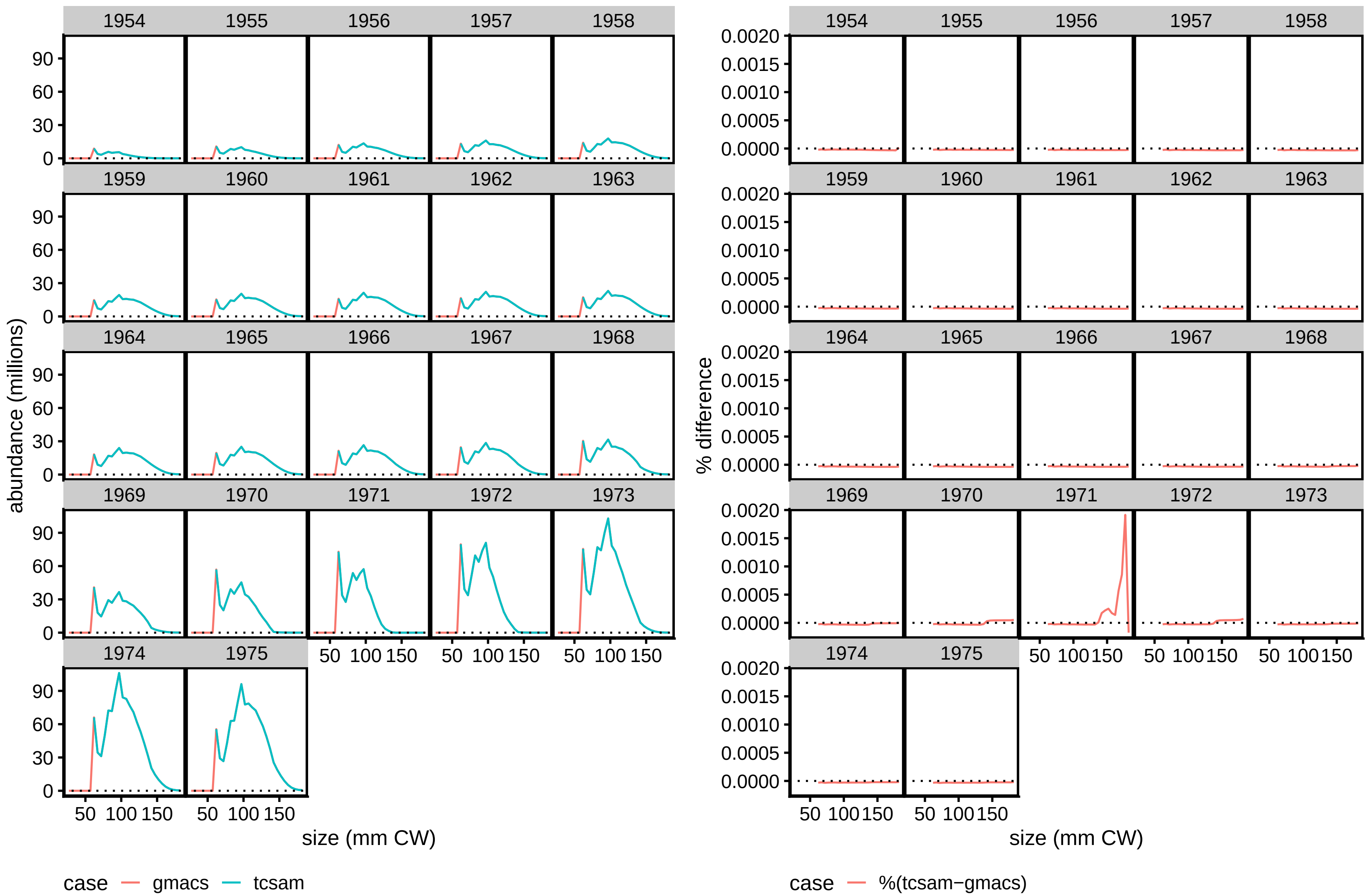

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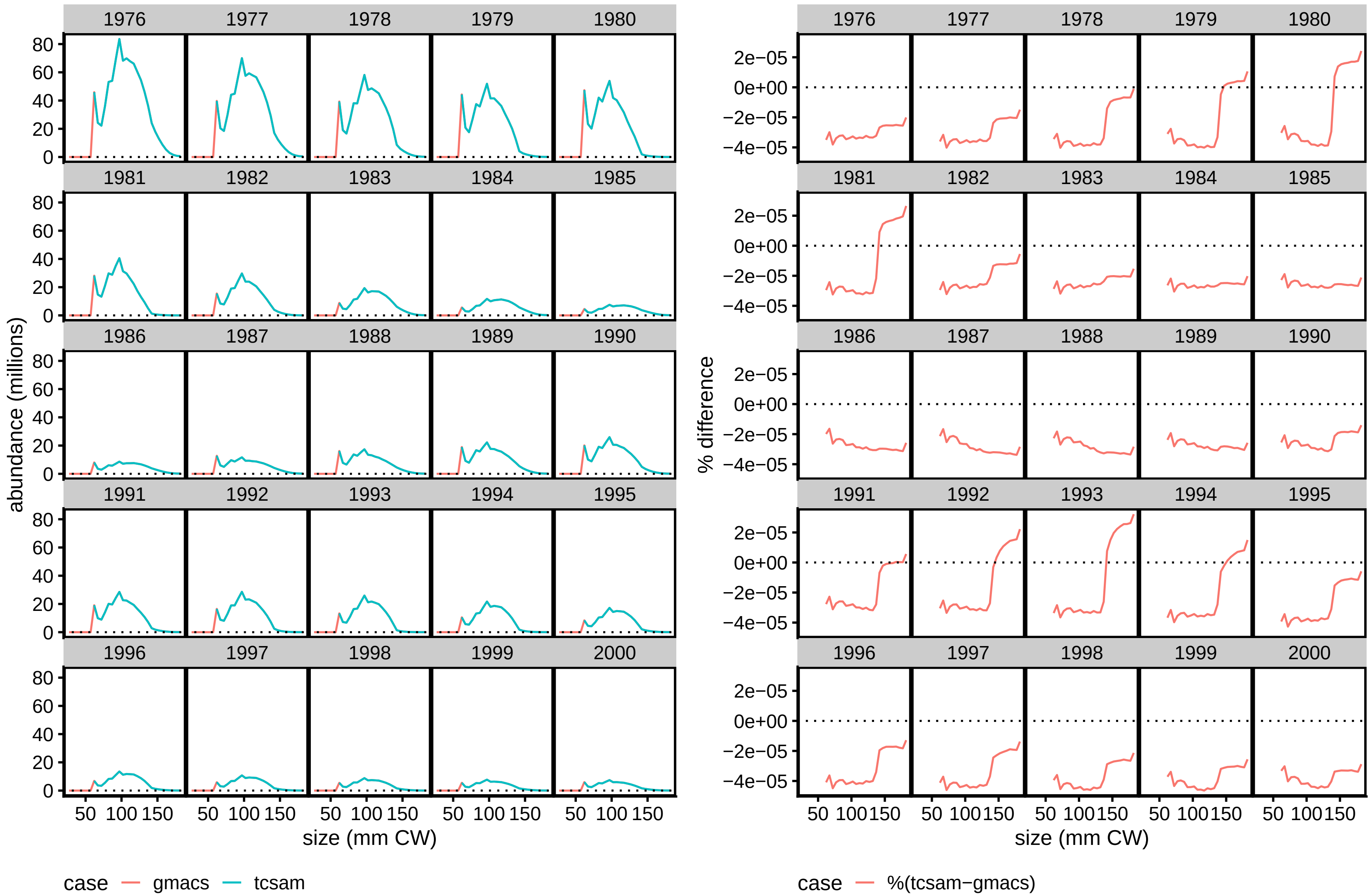
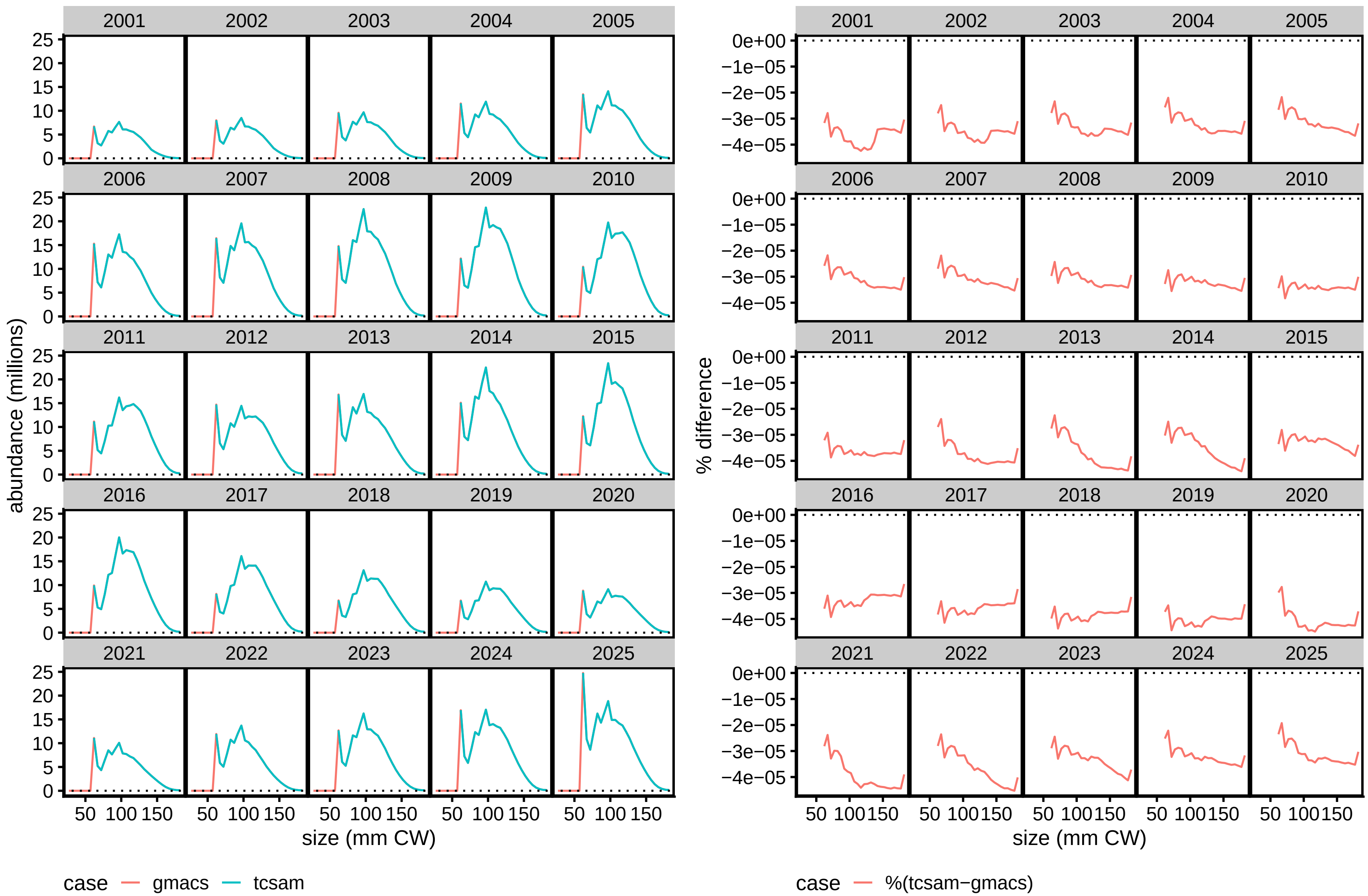


Figure 35. Comparison of the predicted population abundance-at-size through time (1976-2000) for mature, old shell males from the GMACS and TCSAM02 models. Left: values; right: percent differences.



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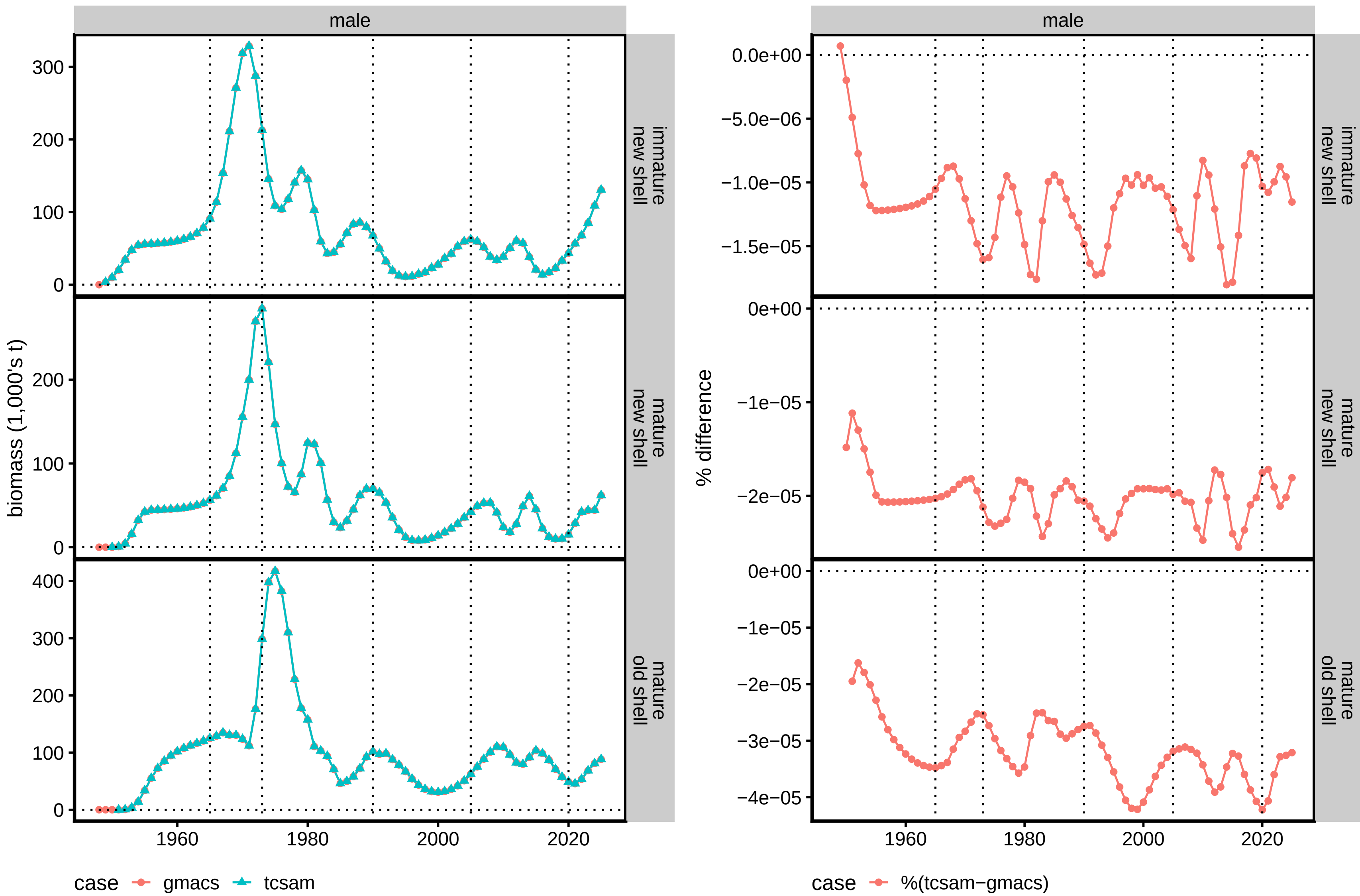

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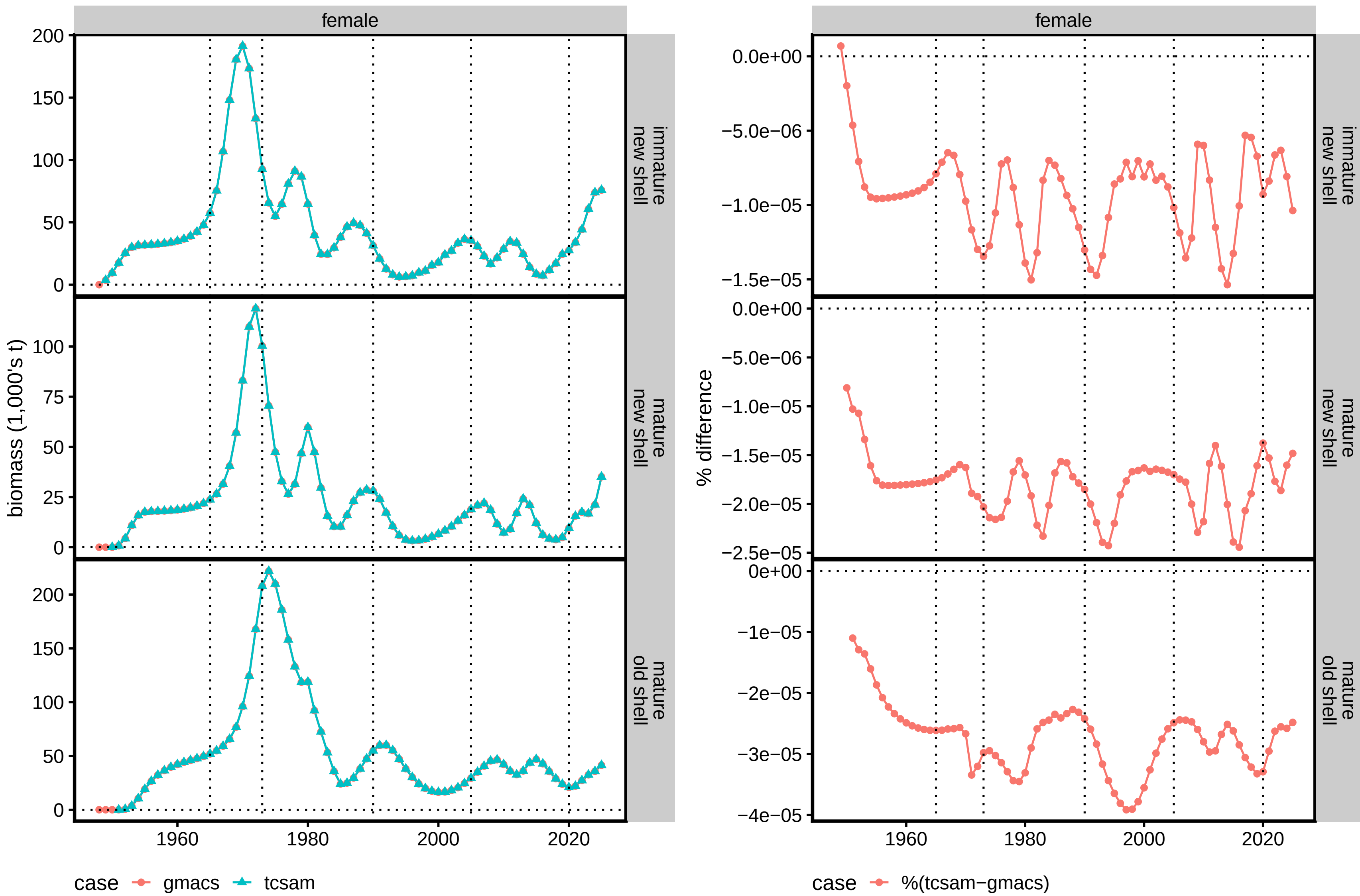

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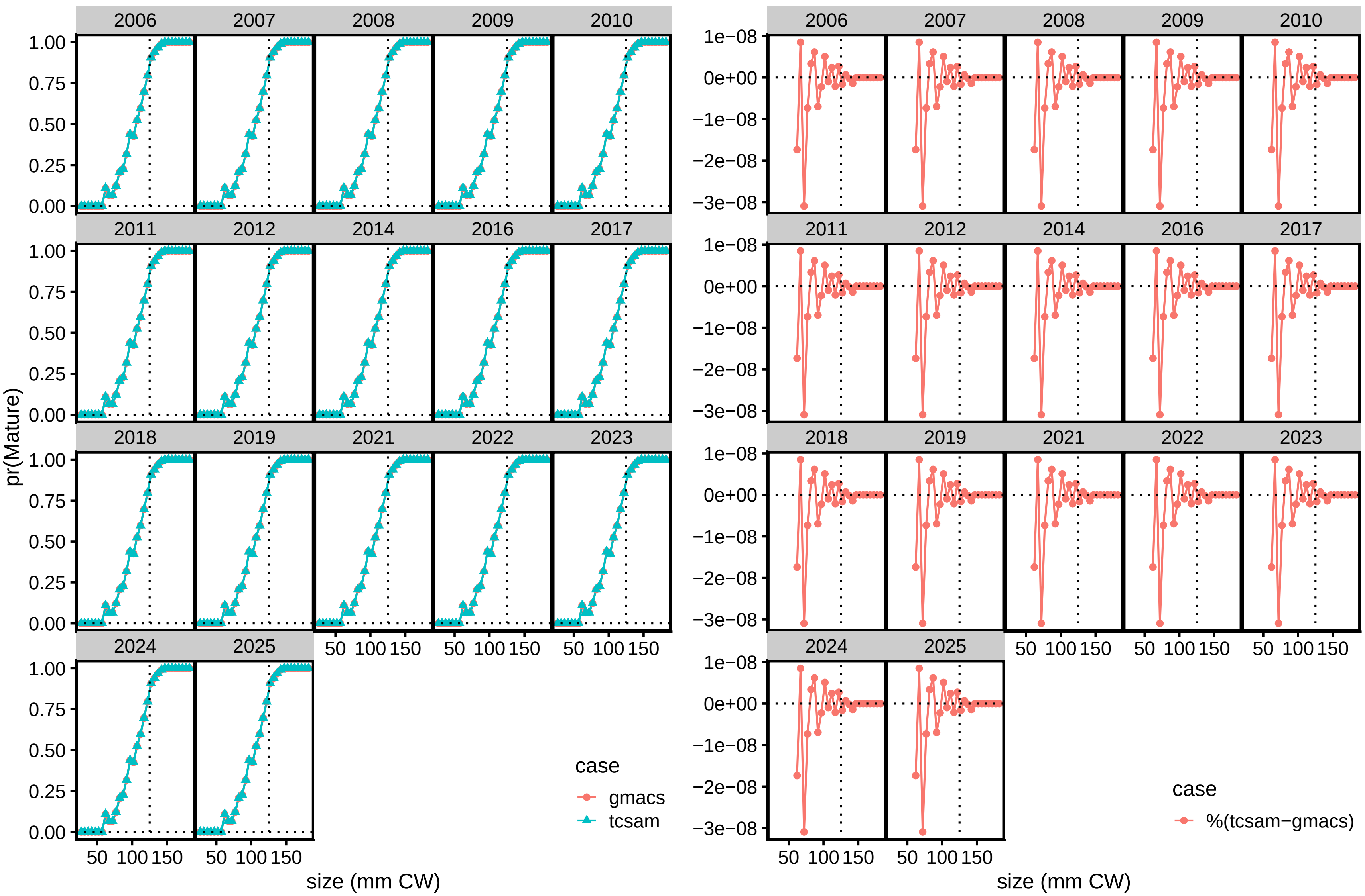

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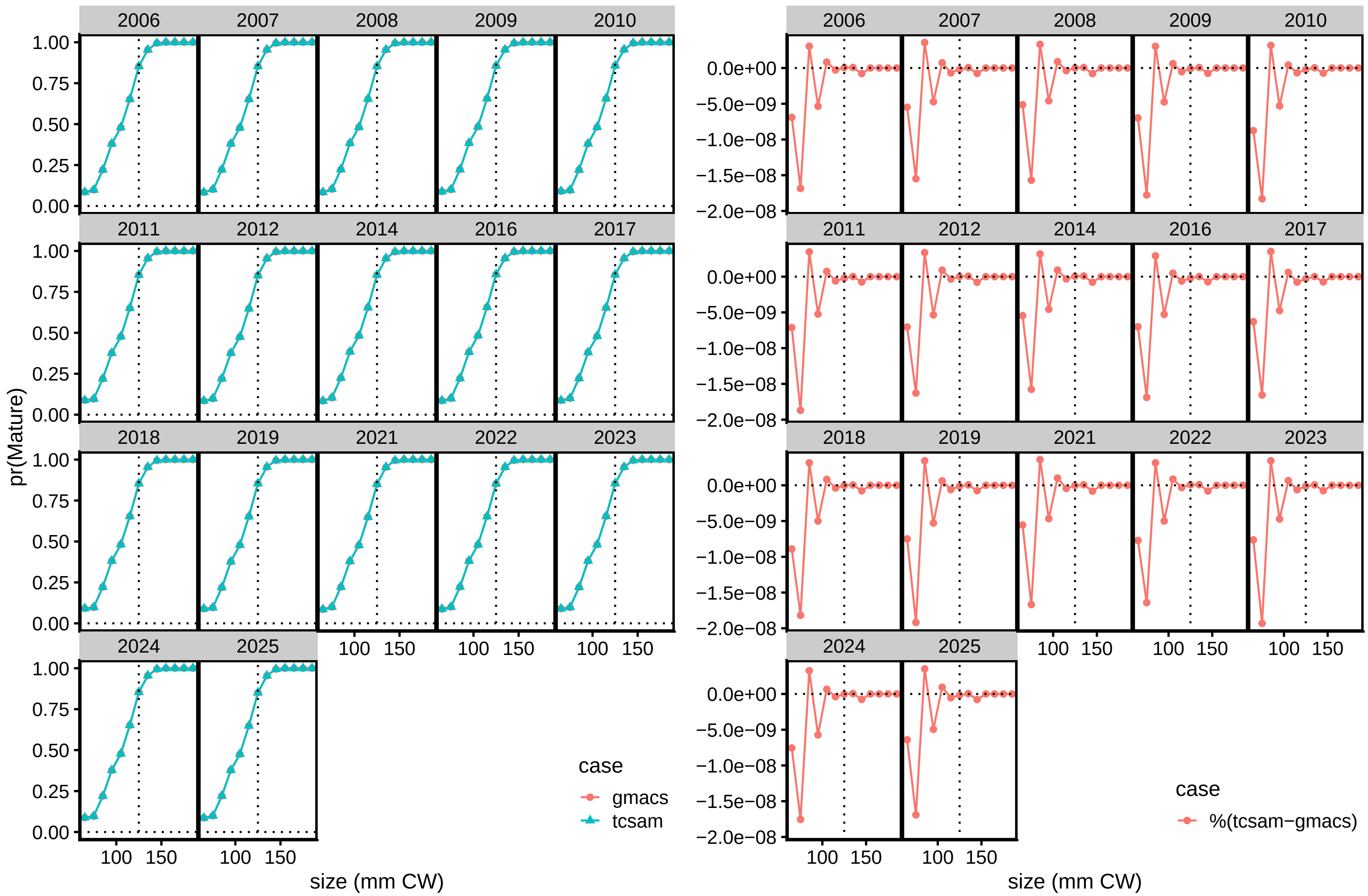

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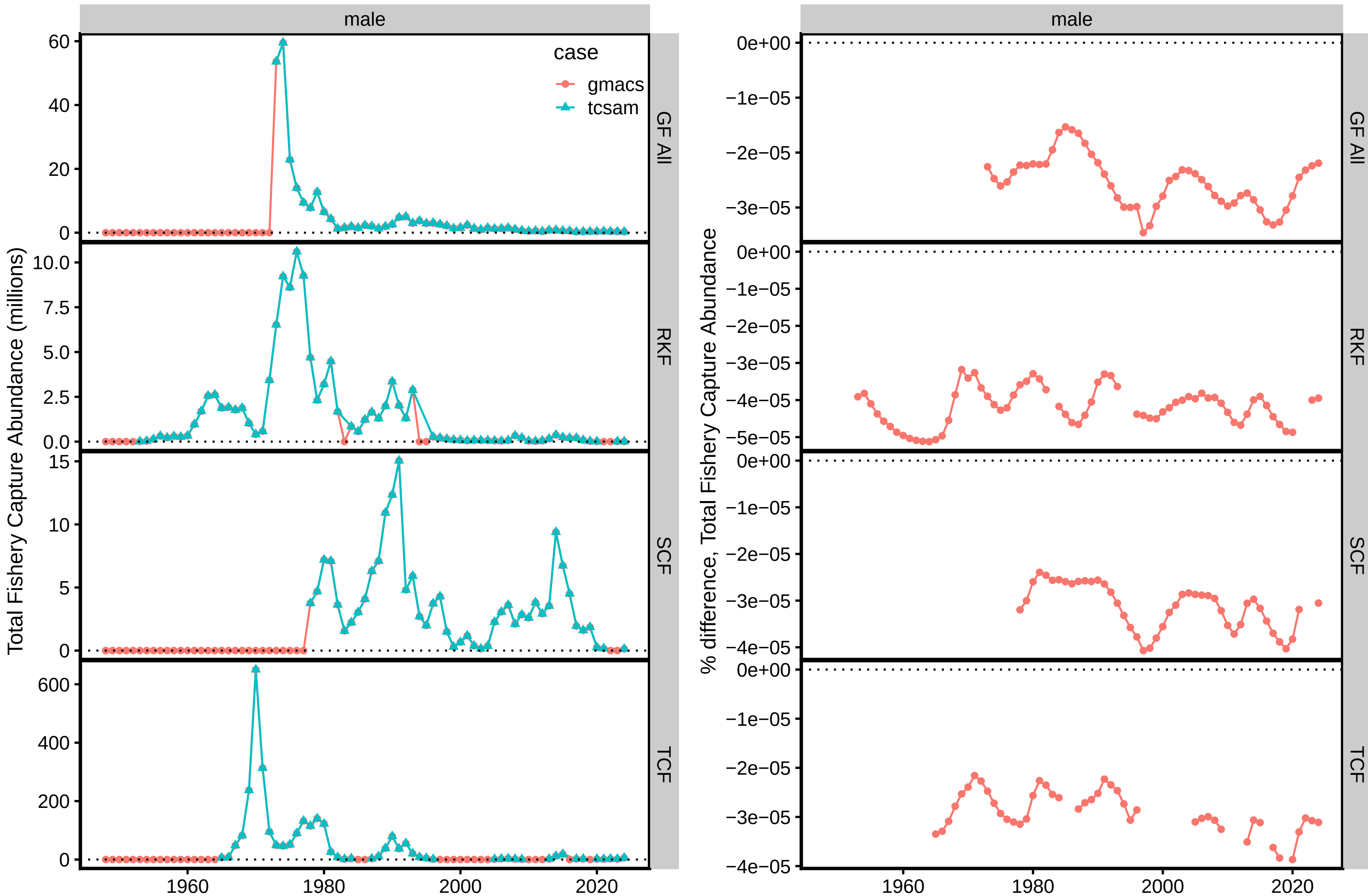

Figure 41. Comparison of the predicted capture abundance by fishery through time for males from the GMACS and TCSAM02 models. Left: values; right: percent differences.

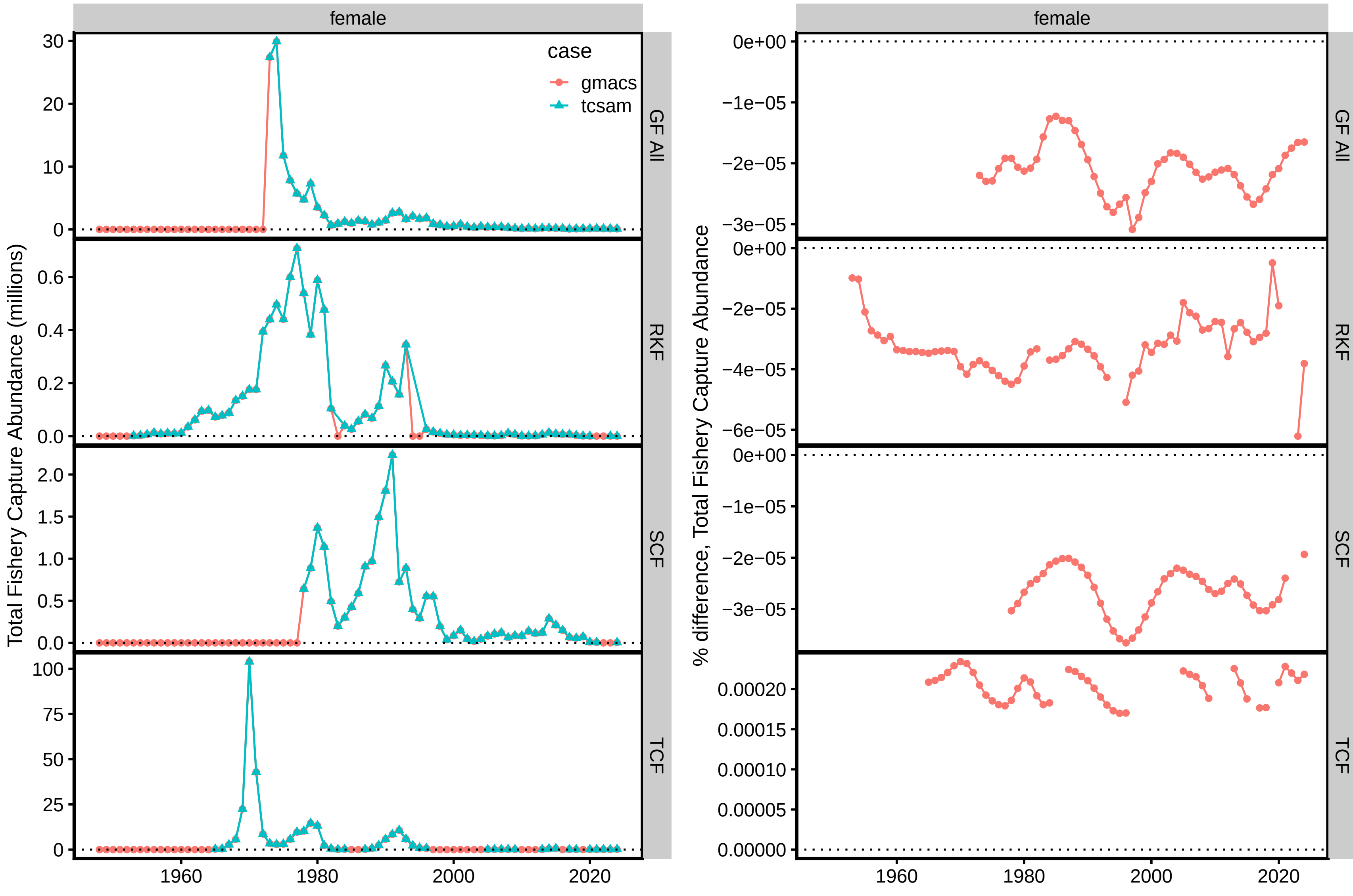

Figure 42. Comparison of the predicted capture abundance by fishery through time for females from the GMACS and TCSAM02 models. Left: values; right: percent differences.

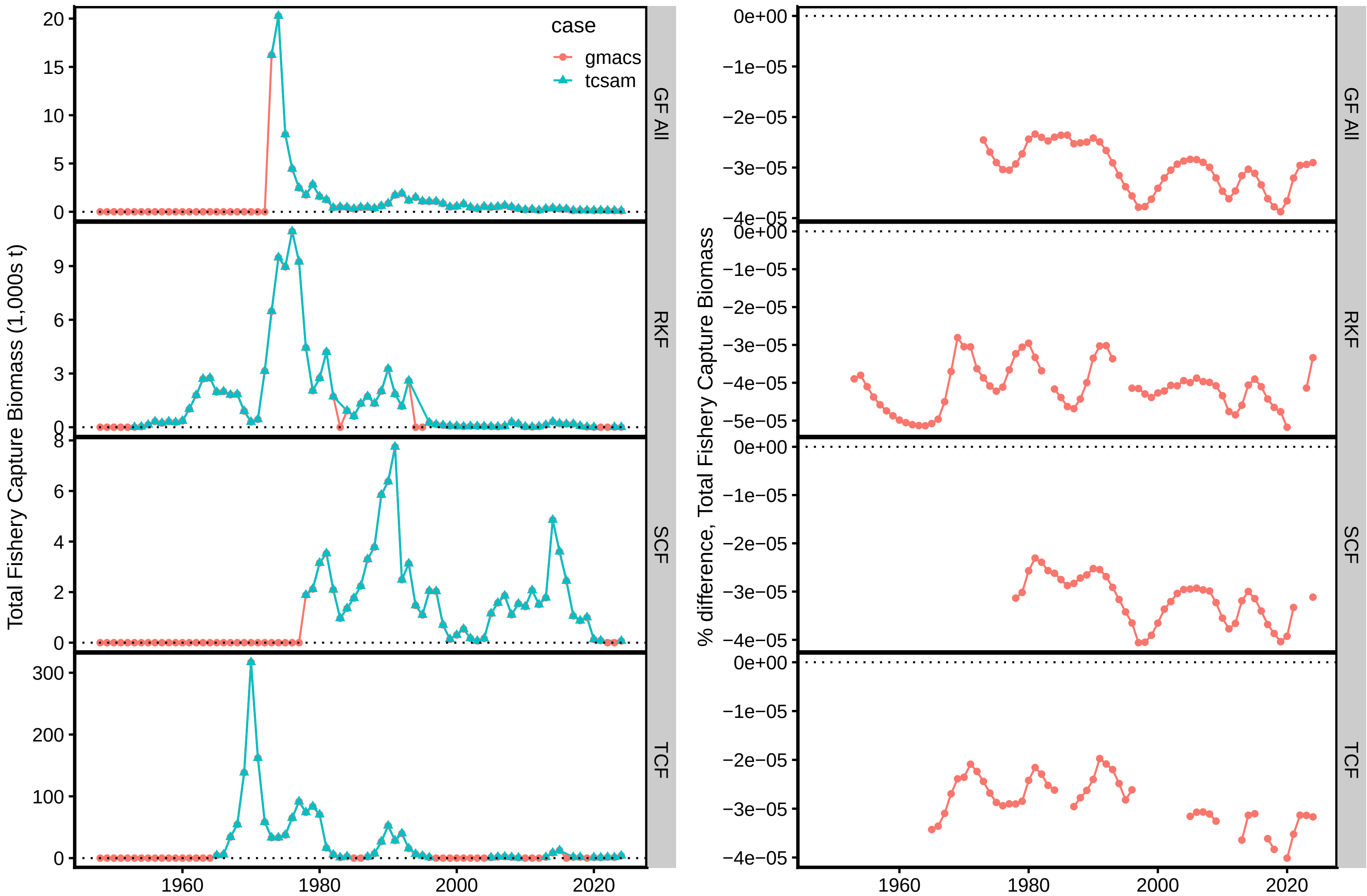

Figure 43. Comparison of the predicted capture biomass by fishery through time for males from the GMACS and TCSAM02 models. Left: values; right: percent differences.

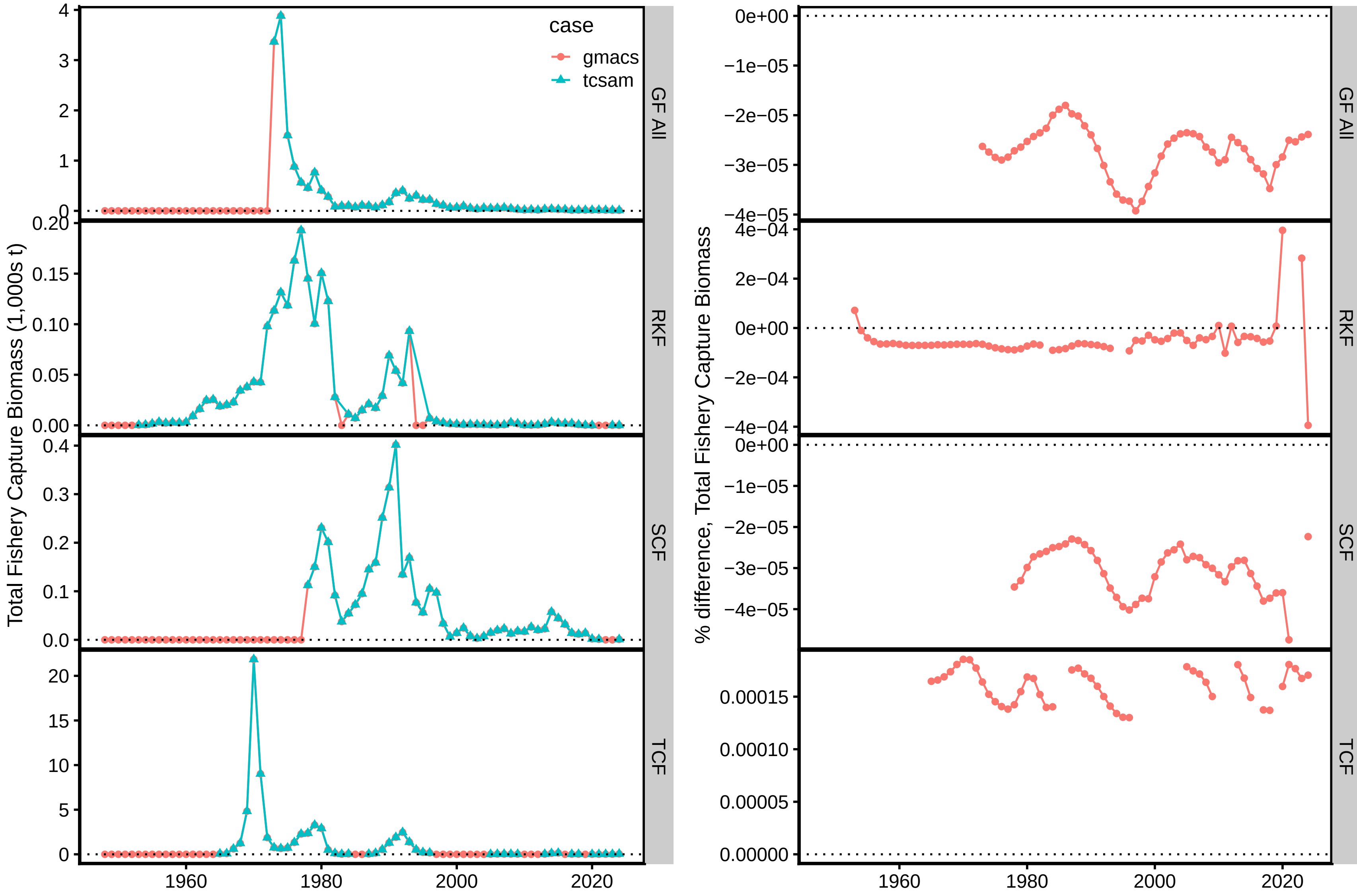

Figure 44. Comparison of the predicted capture biomass by fishery through time for females from the GMACS and TCSAM02 models. Left: values; right: percent differences.

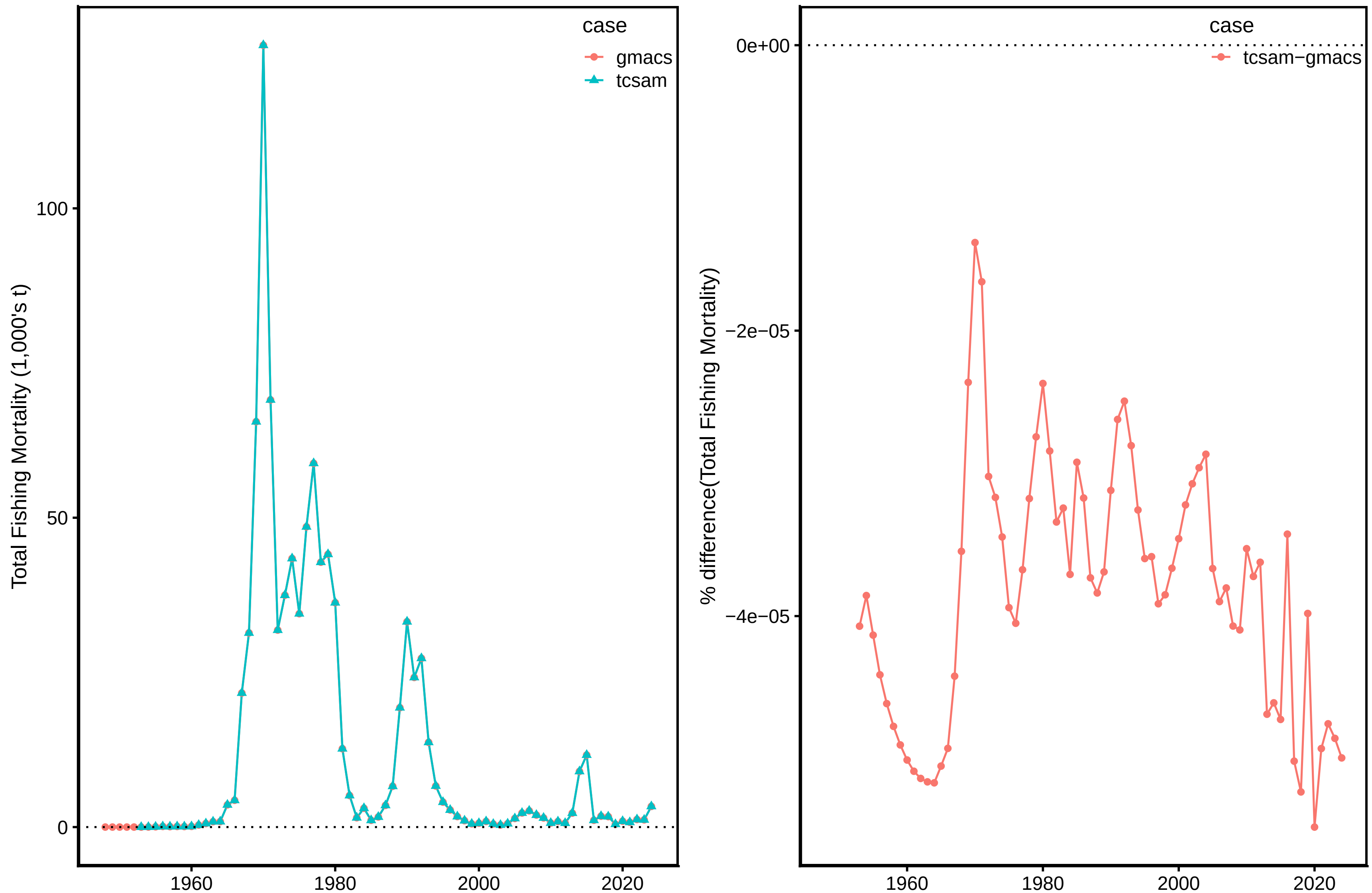

Figure 45. Comparison of the predicted total fishing mortality (biomass) through time from the GMACS and TCSAM02 models. Left: values; right: percent differences.

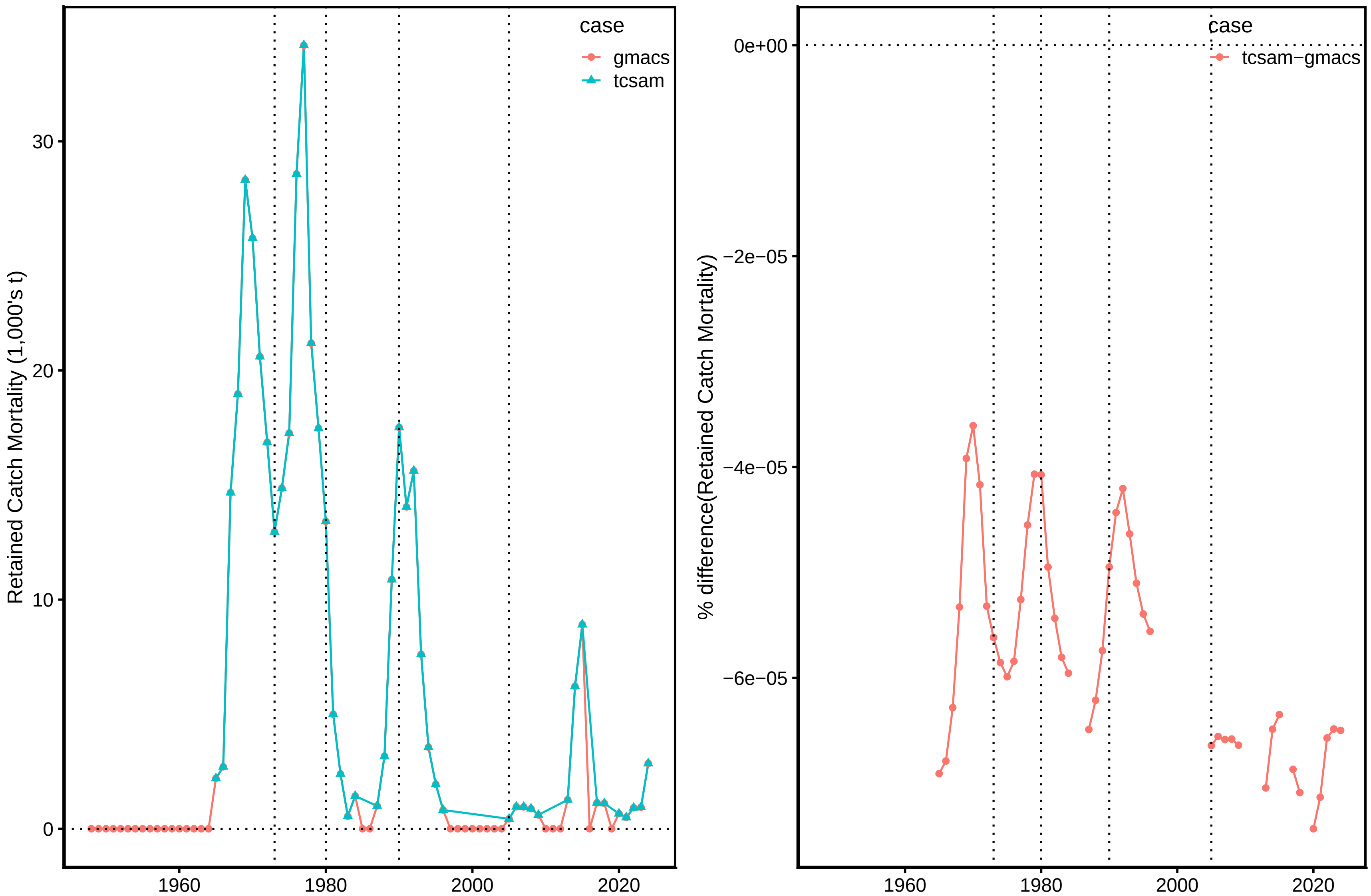

Figure 46. Comparison of the predicted retained catch mortality (biomass) through time from the GMACS and TCSAM02 models. Left: values; right: percent differences. Dotted vertical lines indicate 1973, 1980,1990, and 2005

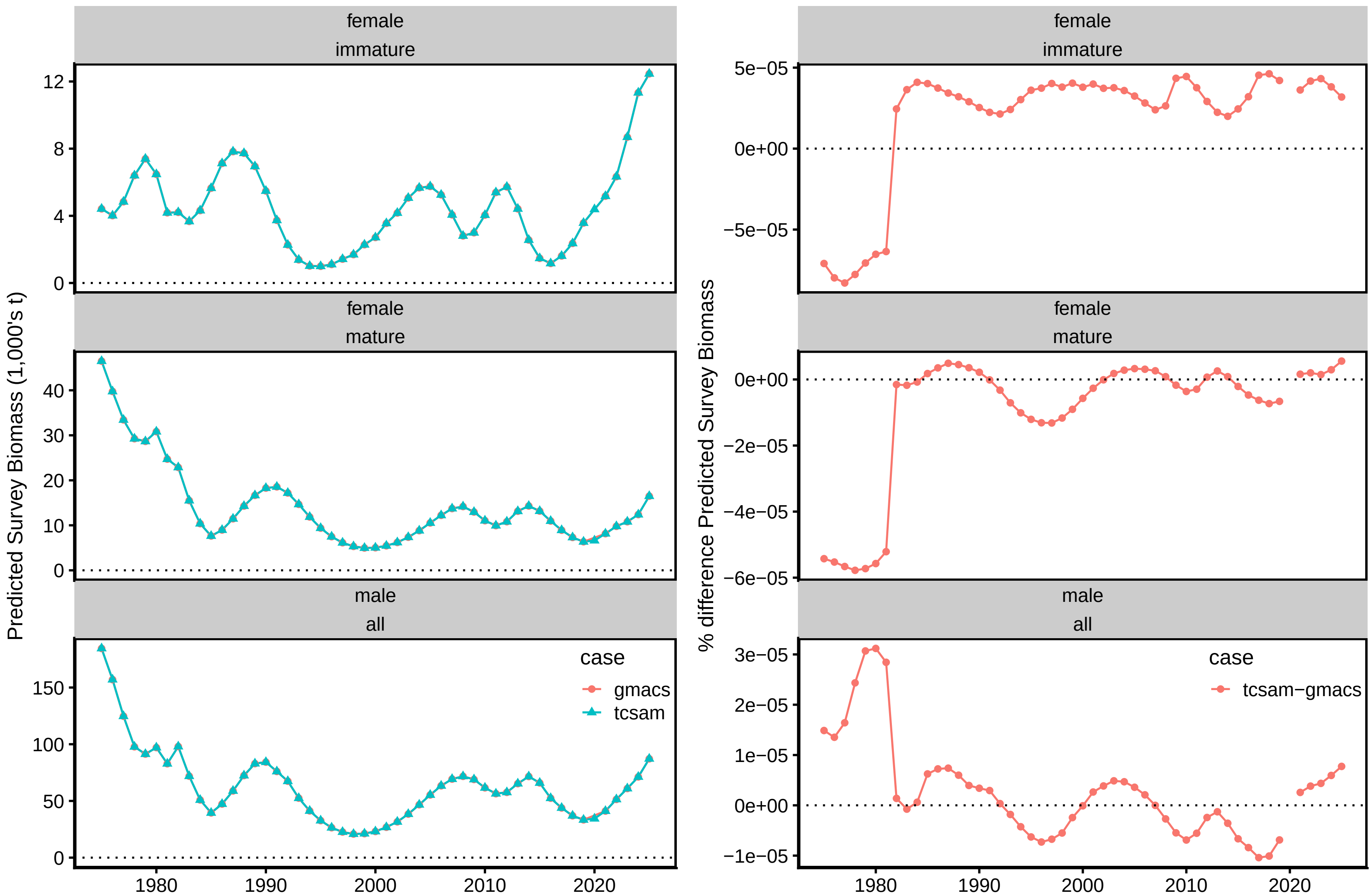

Figure 47. Comparison of the predicted NMFS survey biomass through time from the GMACS and TCSAM02 models. Left: values; right: percent differences.

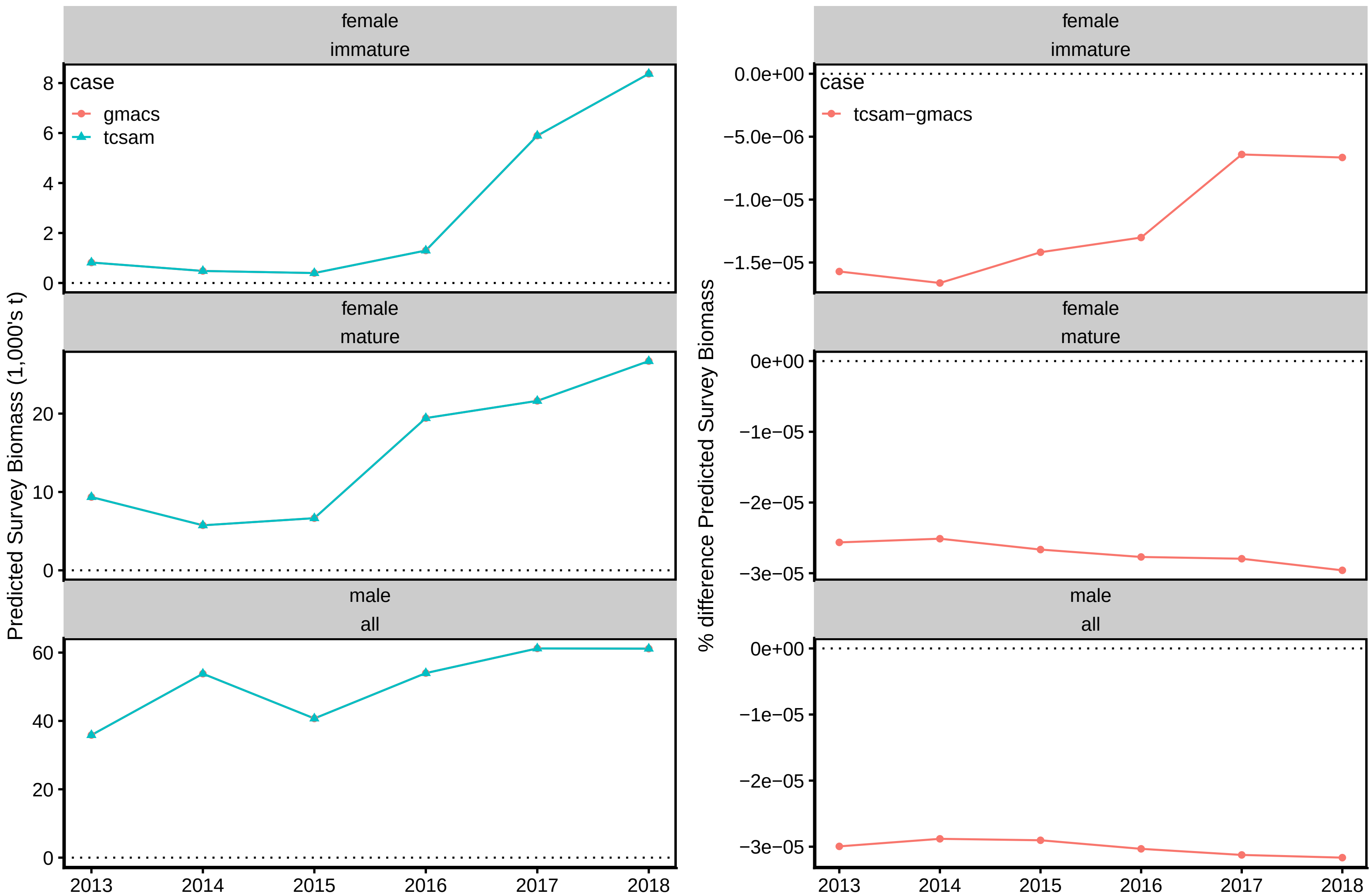

Figure 48. Comparison of the predicted BSFRF survey biomass through time from the GMACS and TCSAM02 models. Left: values; right: percent differences.

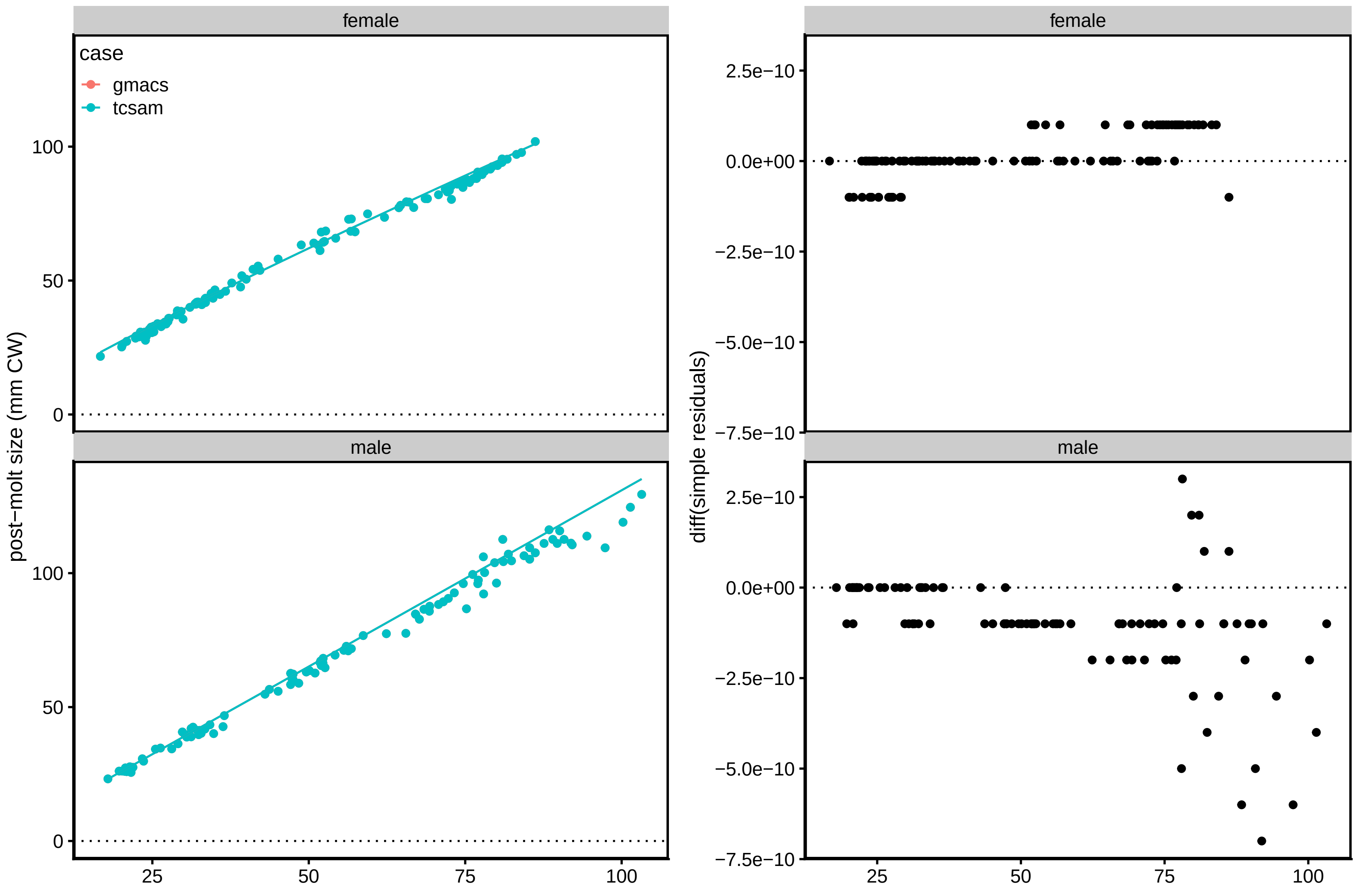

Figure 49. Comparison of fits to molt increment data by sex. Upper: observed–points, predicted–lines; Lower: differences in simple residuals between models.

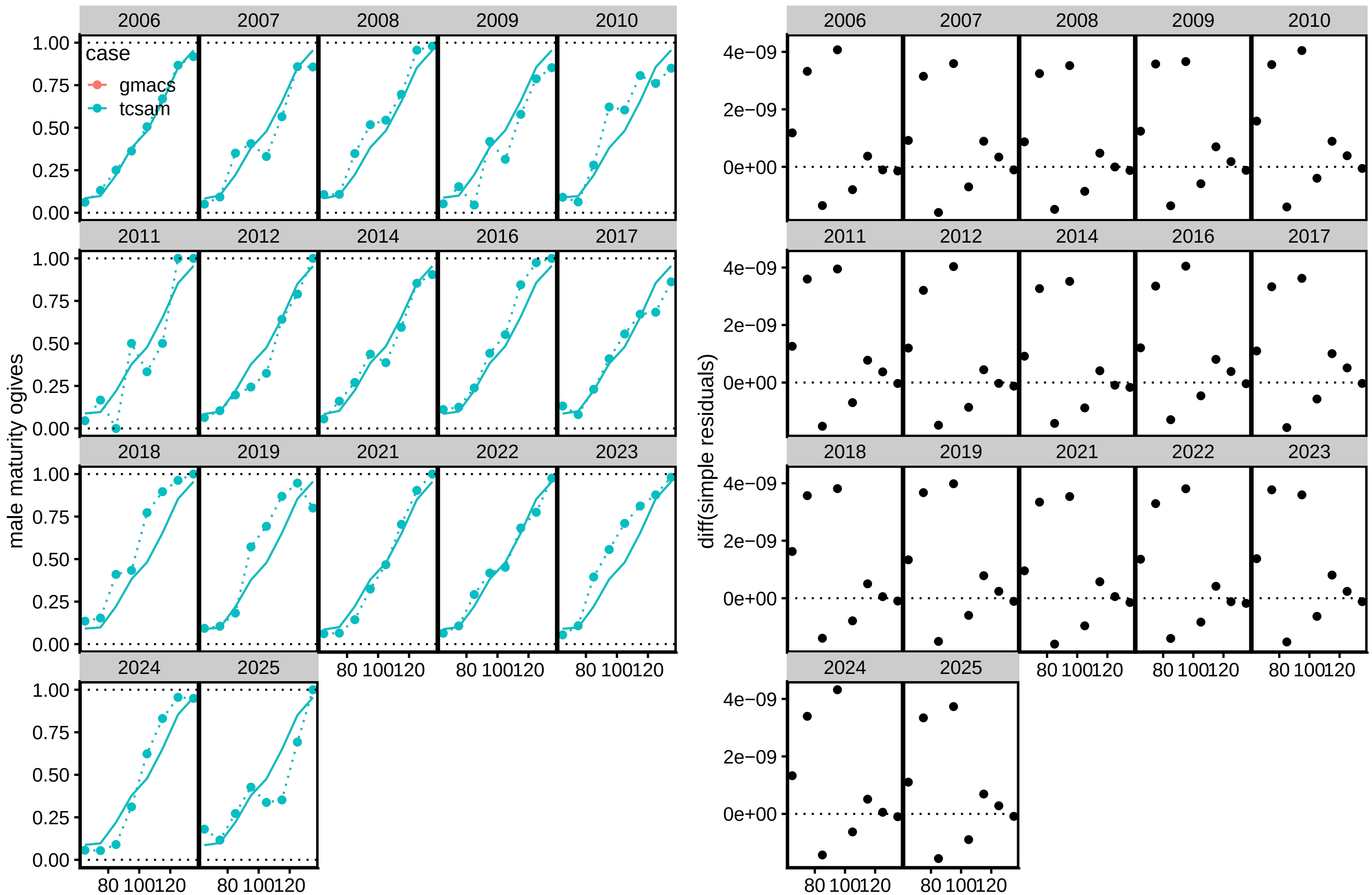

Figure 50. Comparison of fits to male maturity ogives based on chela height/carapace width measurements on males during the NMFS EBS bottom trawl surveys. Right: observed–points and dotted line, predicted–lines; Lower: differences in simple residuals between models.

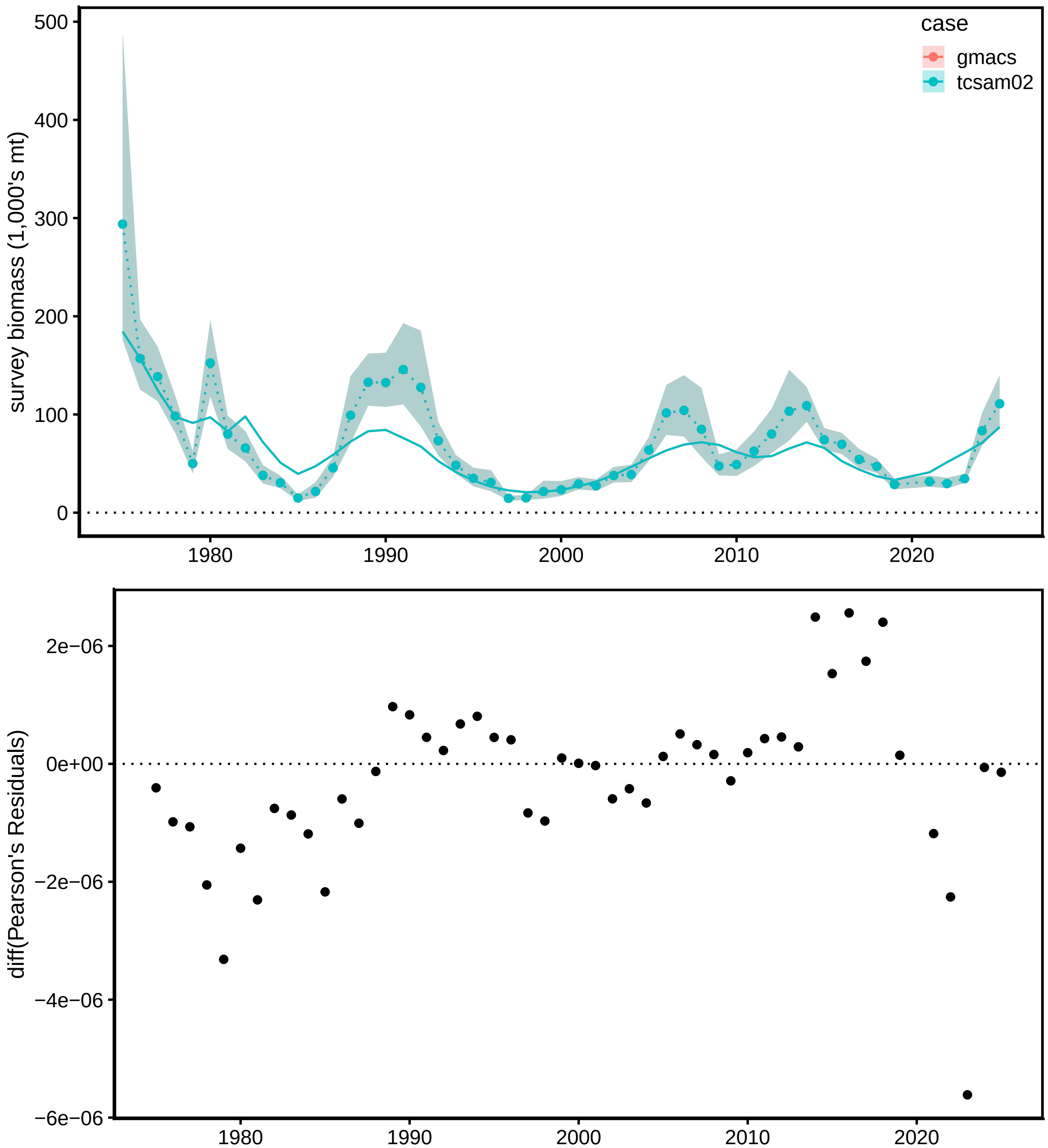

Figure 51. Comparison of fits to male survey biomass in the NMFS surveys. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

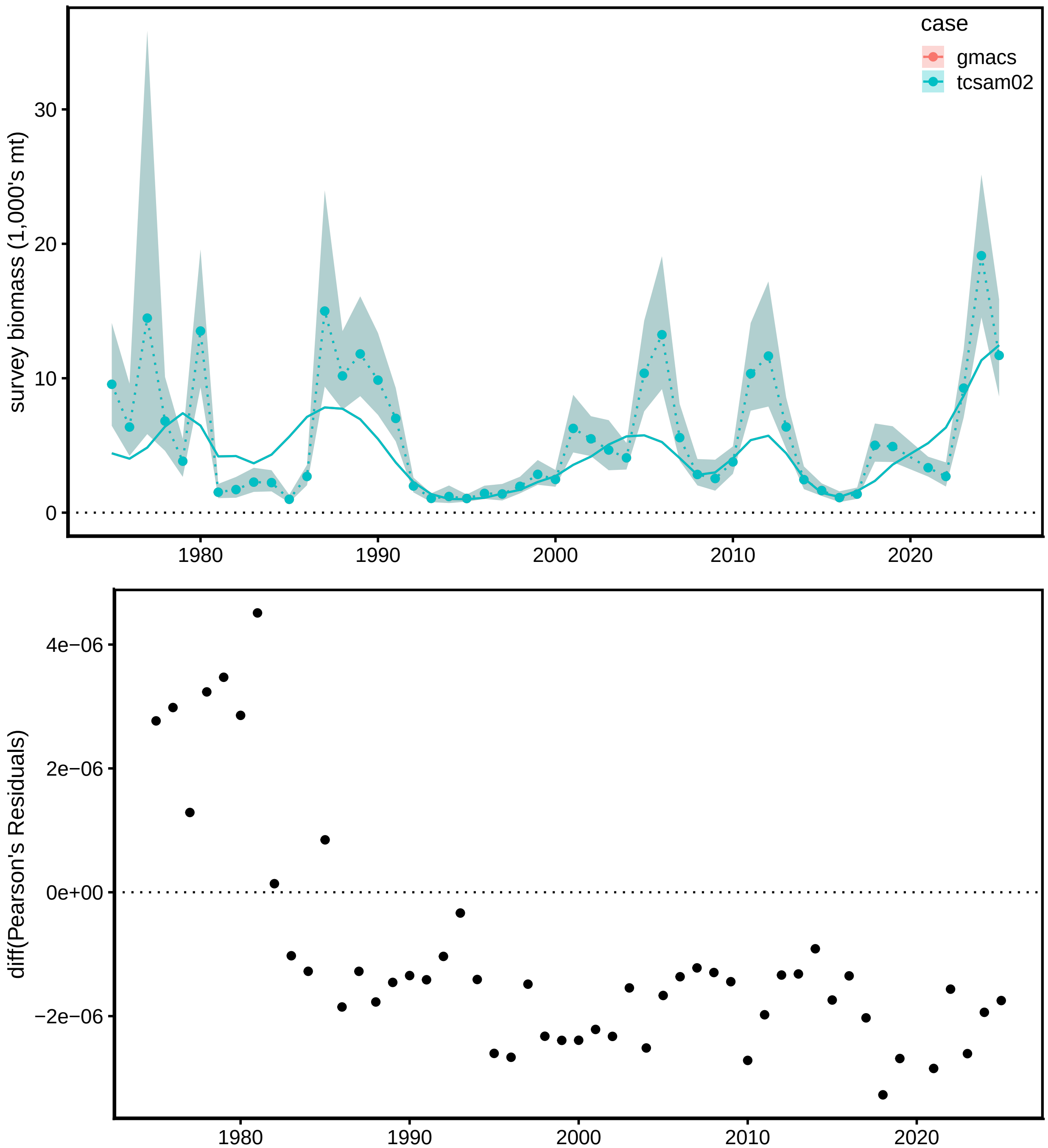

Figure 52. Comparison of fits to immature female survey biomass in the NMFS surveys. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

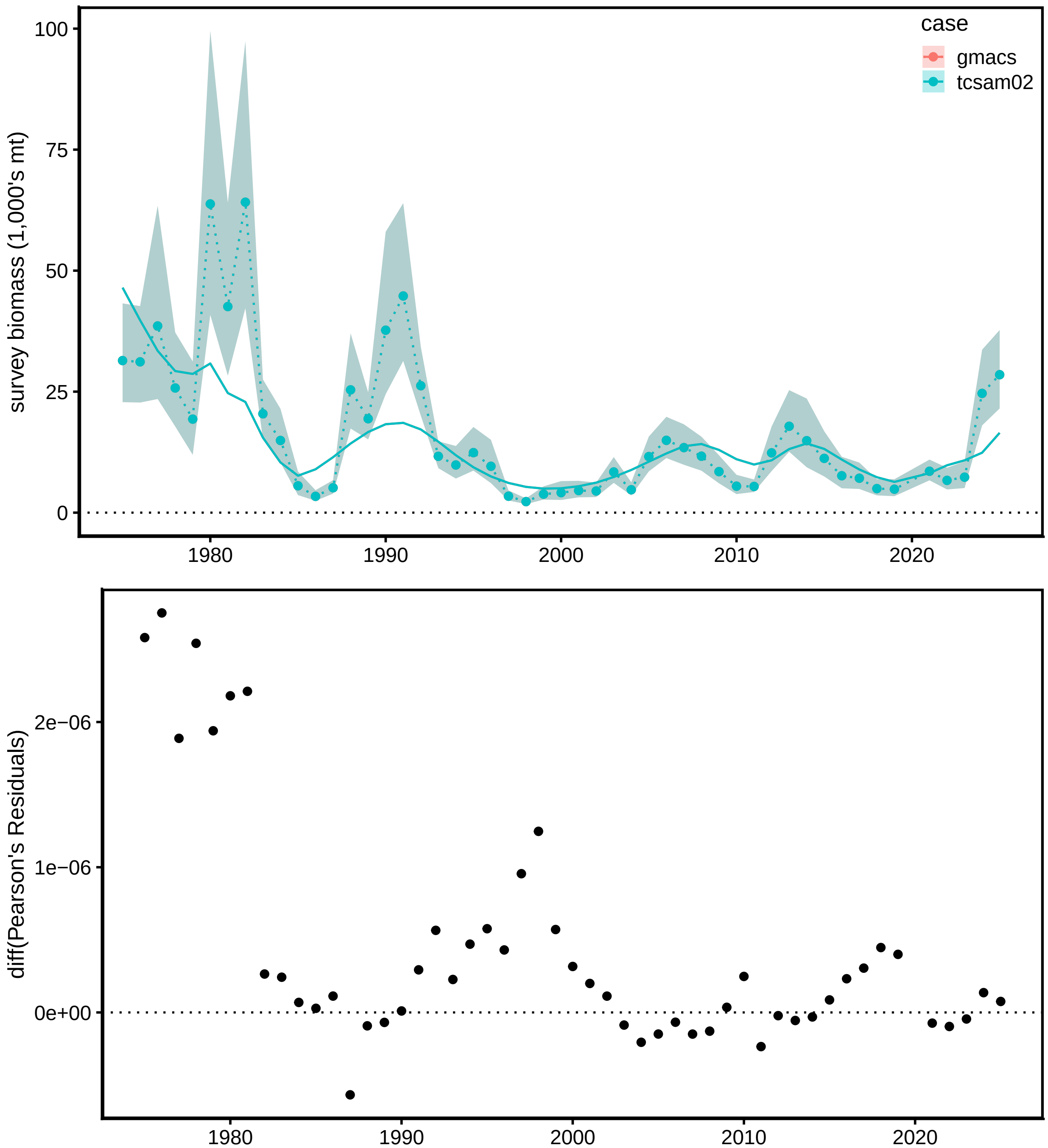

Figure 53. Comparison of fits to mature female survey biomass in the NMFS surveys. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

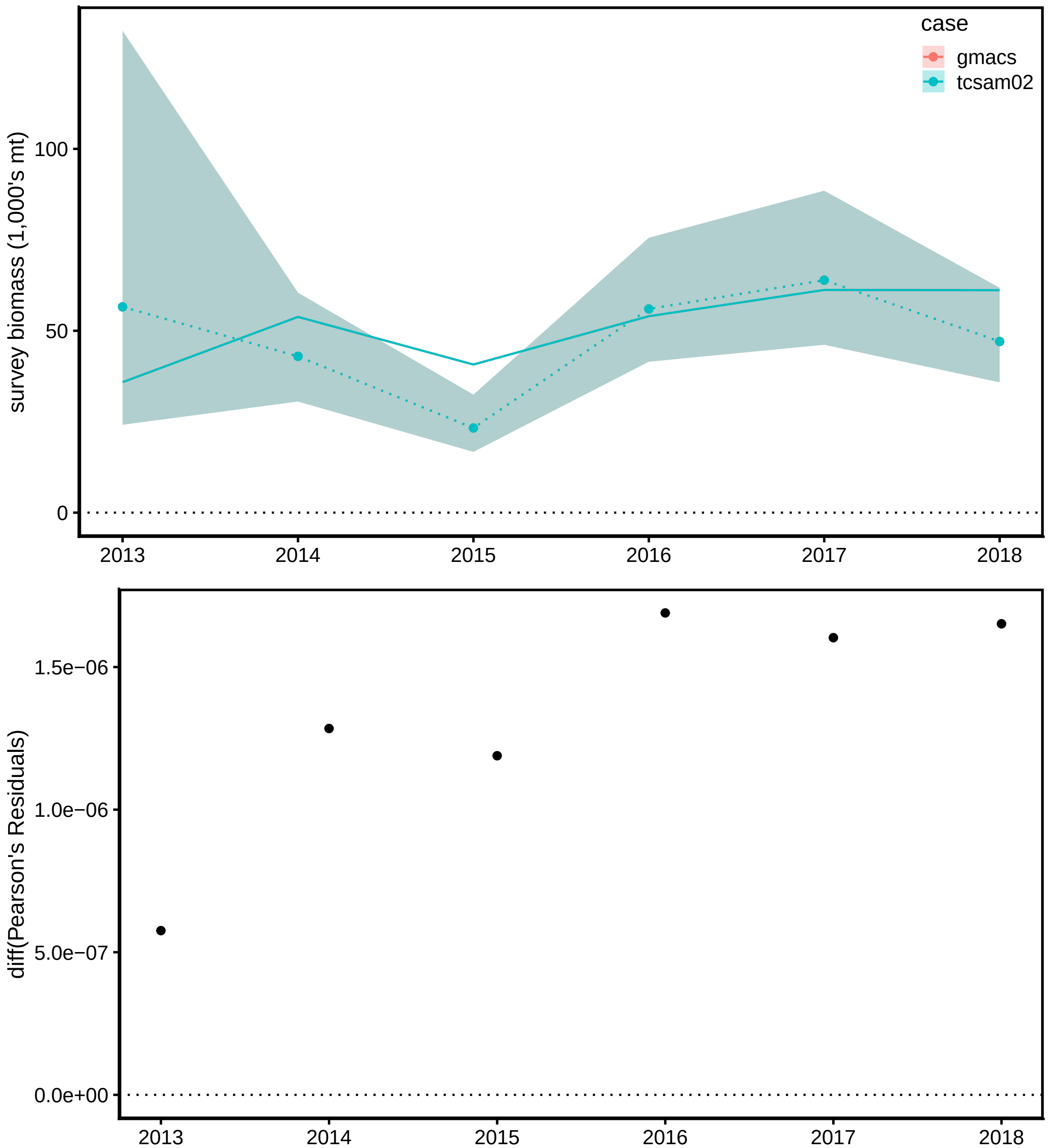

Figure 54. Comparison of fits to male survey biomass in the BSFRF surveys. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

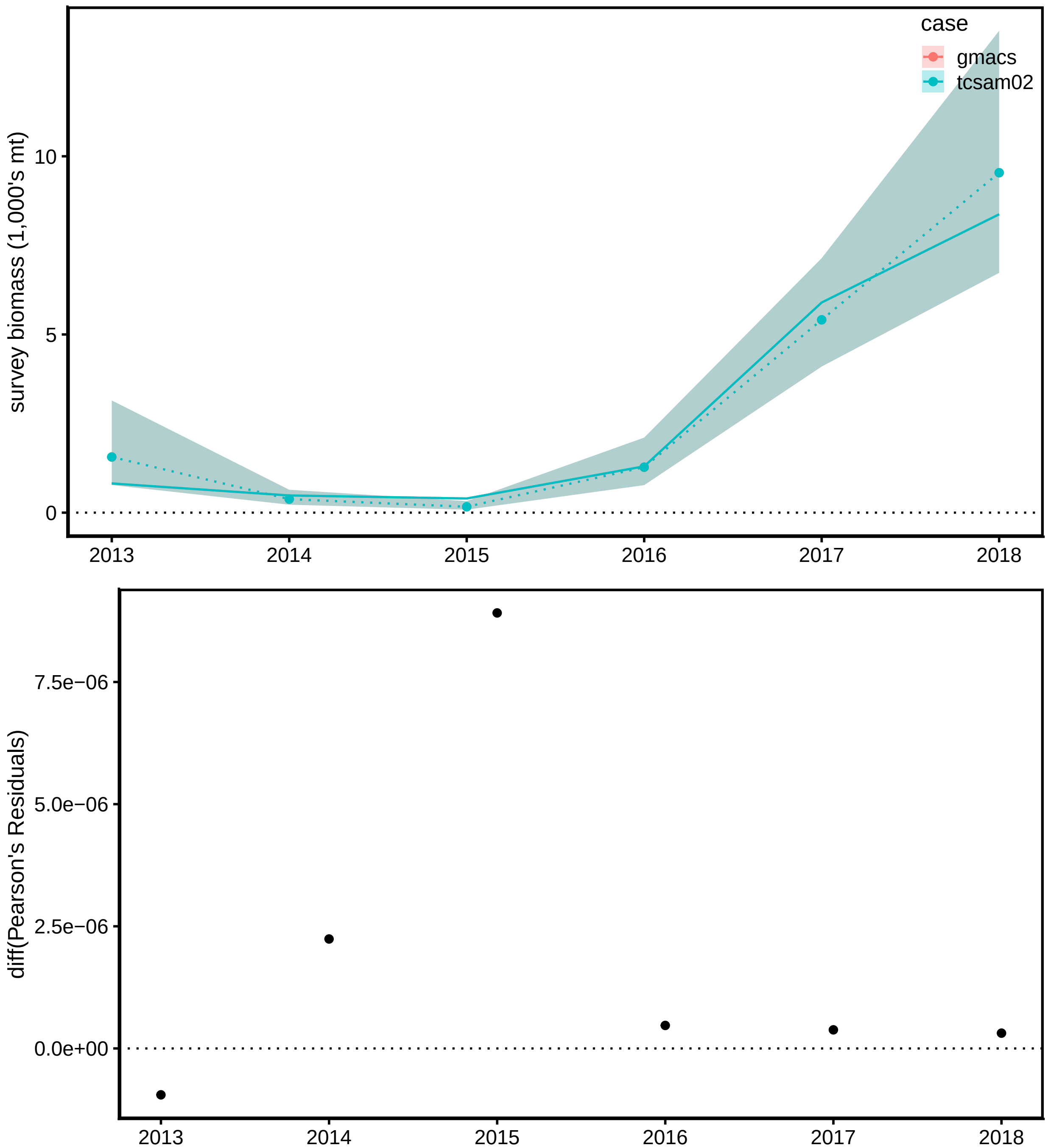

Figure 55. Comparison of fits to immature female survey biomass in the BSFRF surveys. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

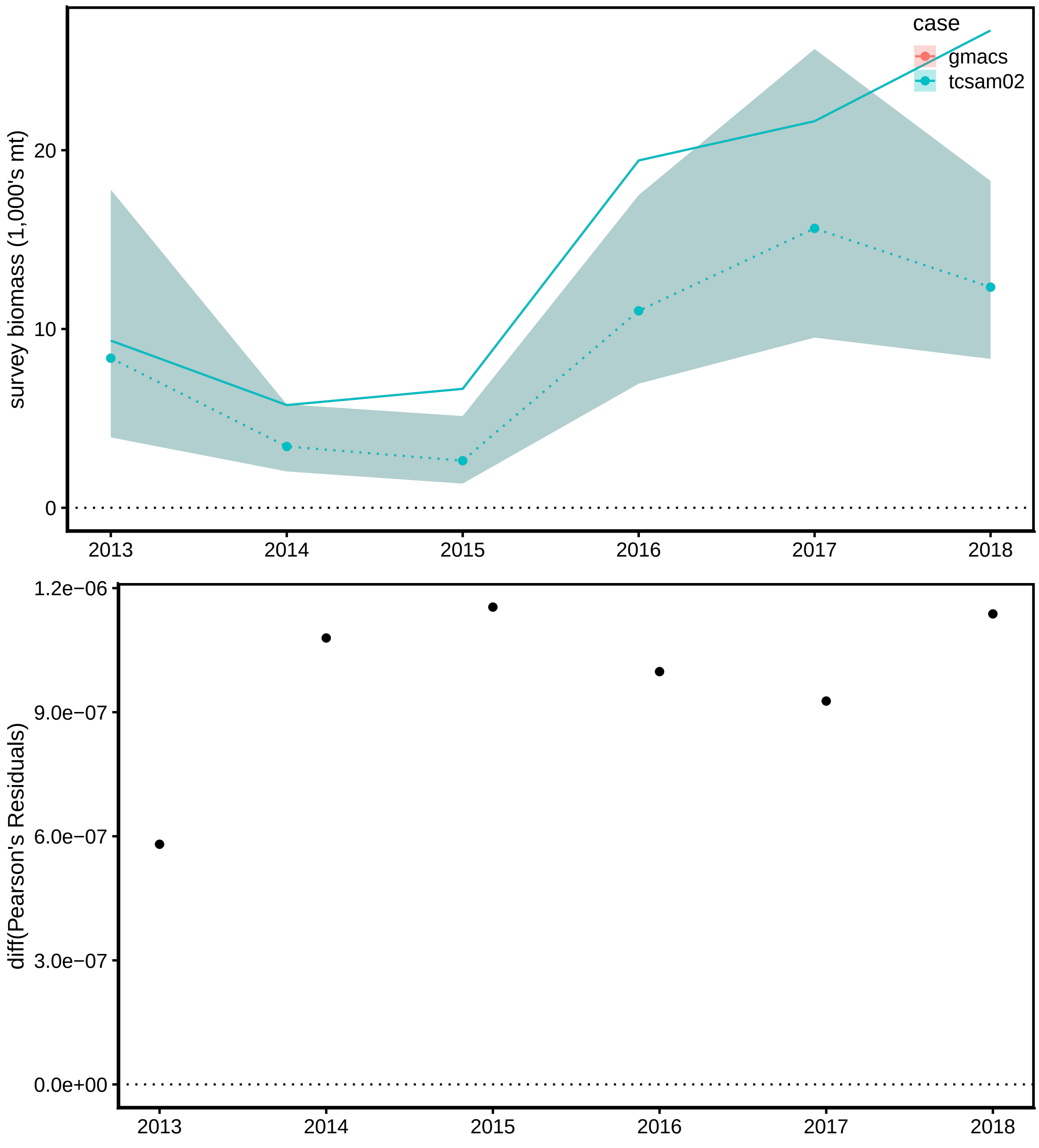

Figure 56. Comparison of fits to mature female survey biomass in the BSFRF surveys. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

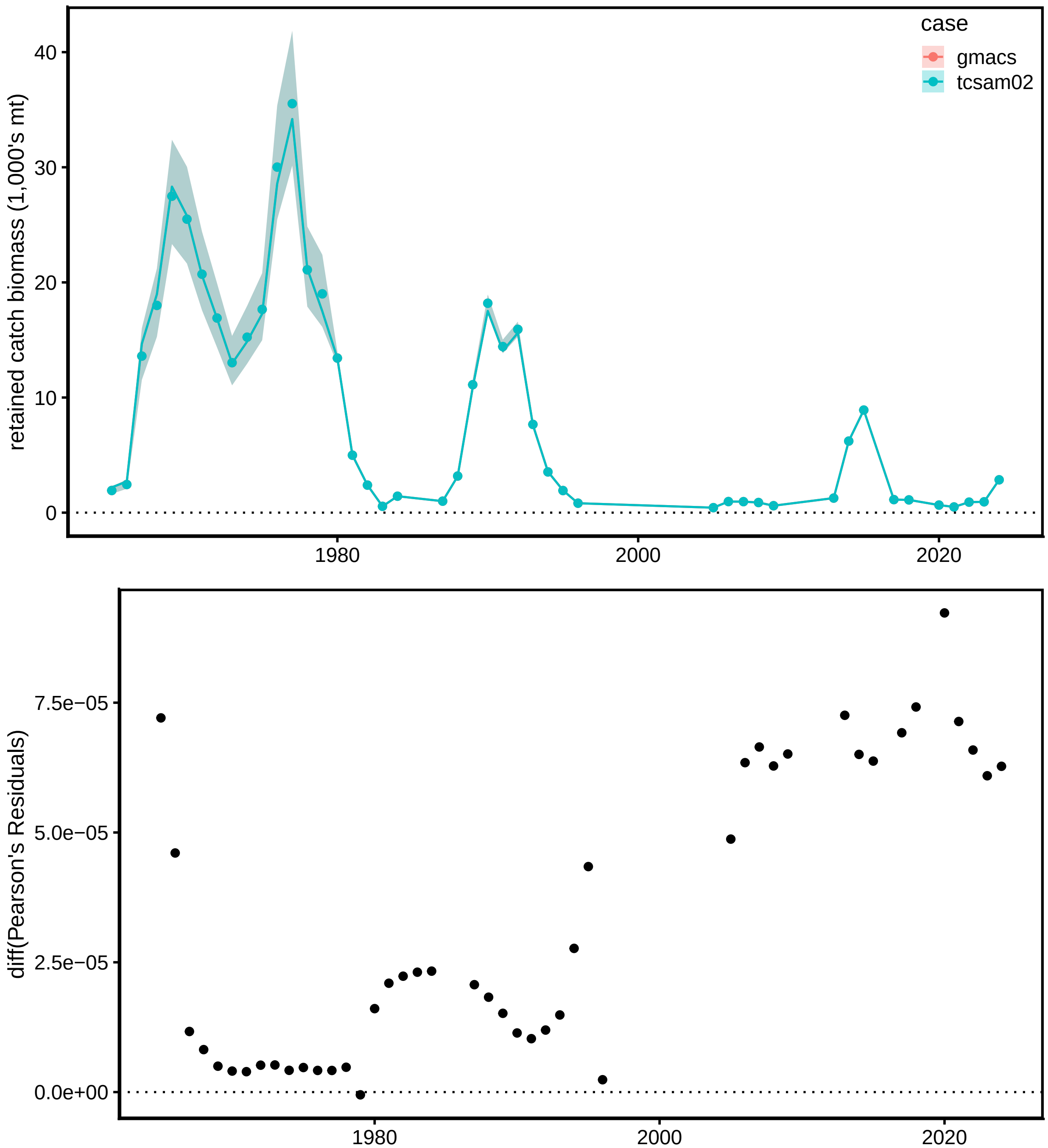

Figure 57. Comparison of fits to retained catch biomass in the directed fishery. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

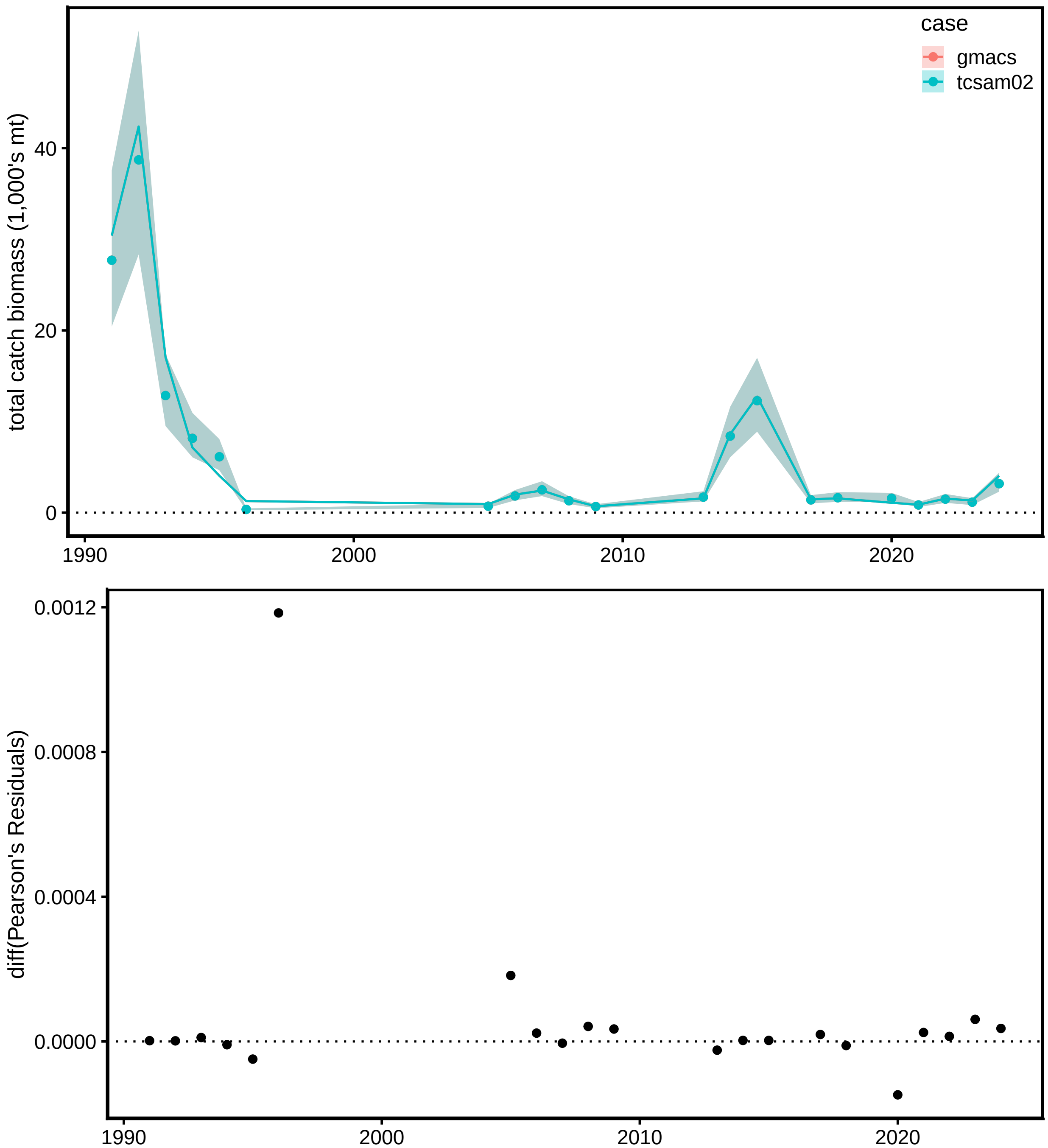

Figure 58. Comparison of fits to total catch biomass in the directed fishery. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

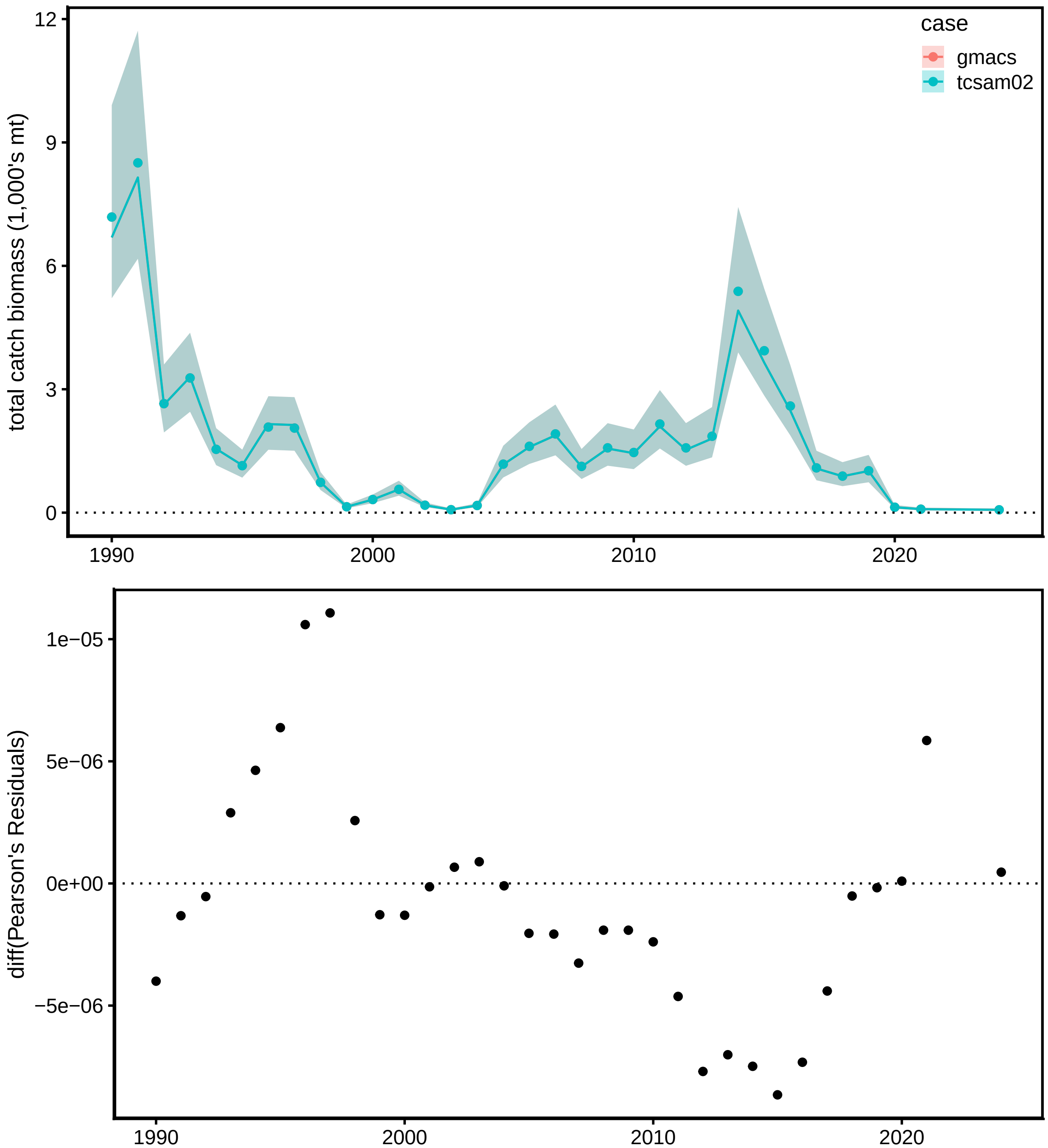

Figure 59. Comparison of fits to total catch biomass in the snow crab fishery. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

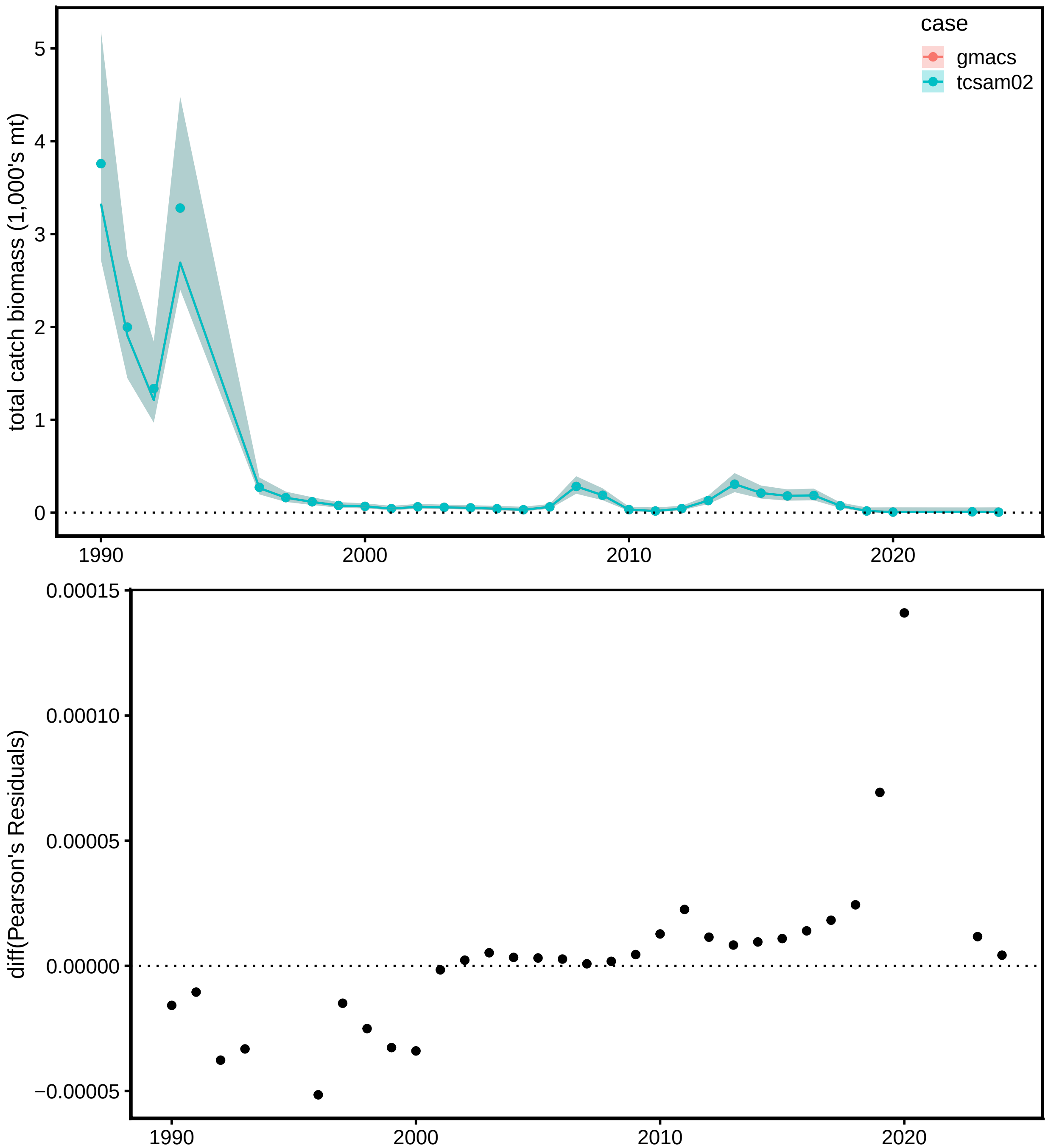

Figure 60. Comparison of fits to total catch biomass in the BBRKC fishery. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

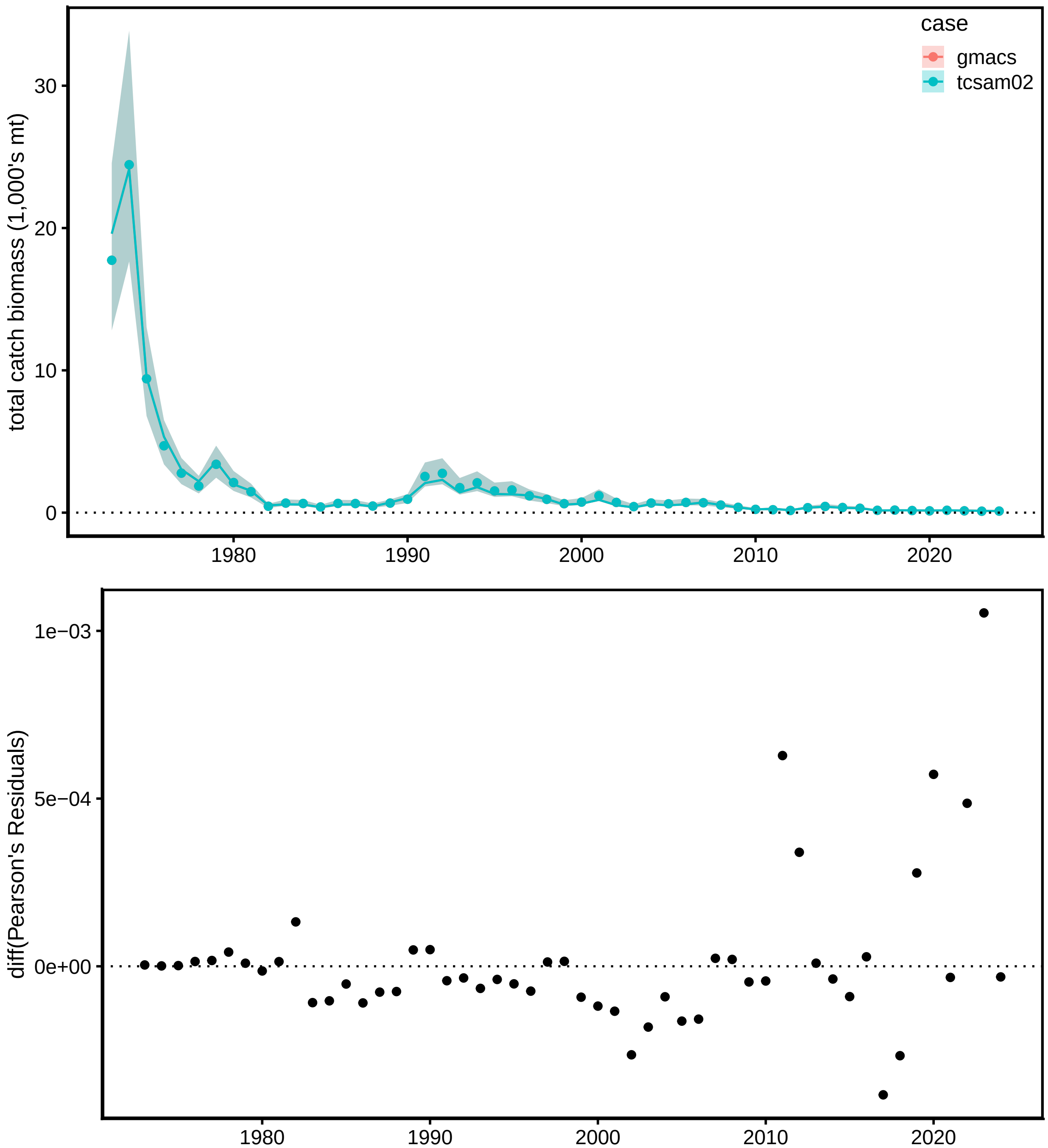

Figure 61. Comparison of fits to total catch biomass in the groundfish fisheries. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

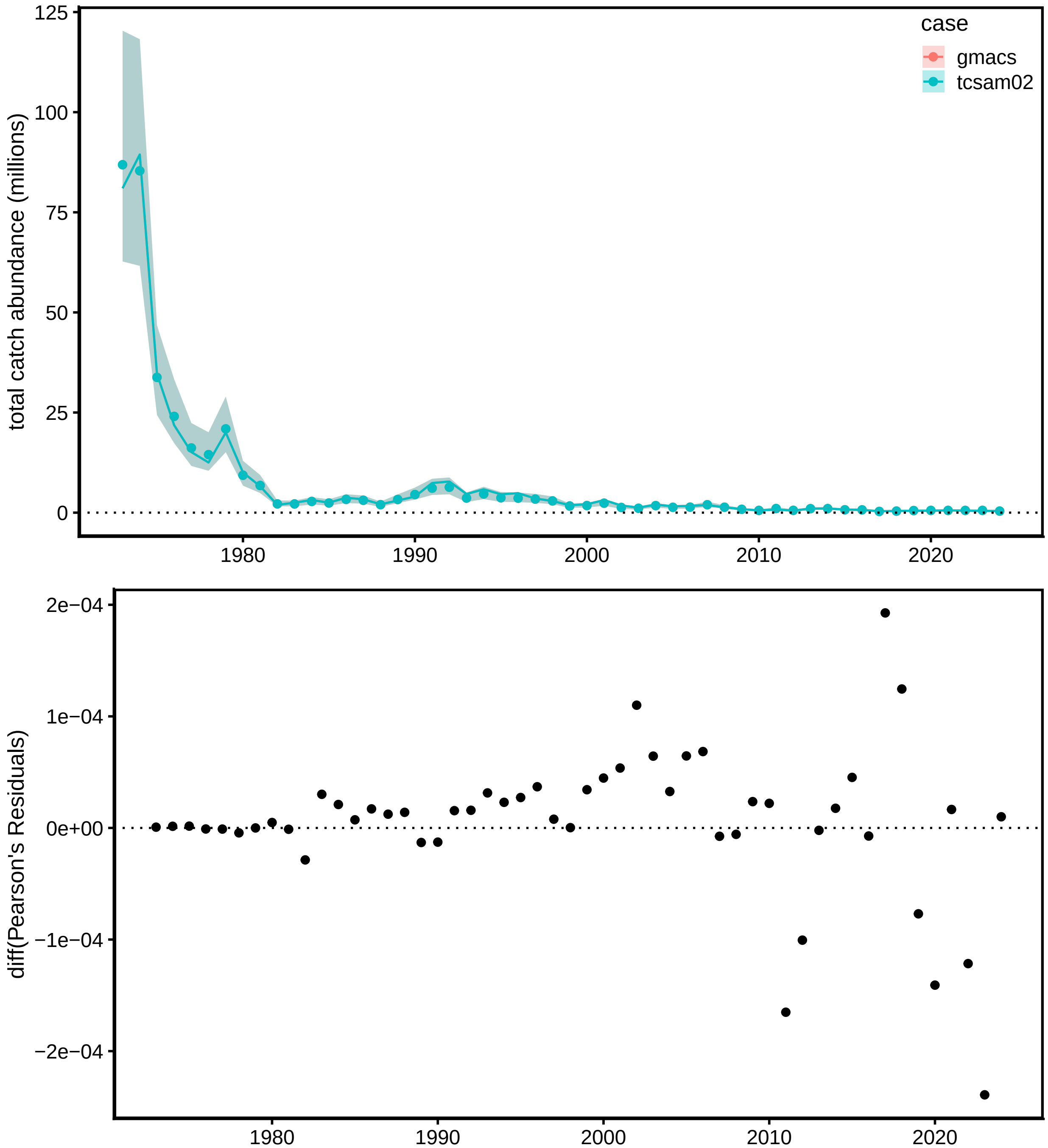

Figure 62. Comparison of fits to total catch abundance in the groundfish fisheries. Upper: observed–points, dotted line, and shading (90% lognormal CIs), predicted–lines; Lower: difference in Pearson's residuals between models.

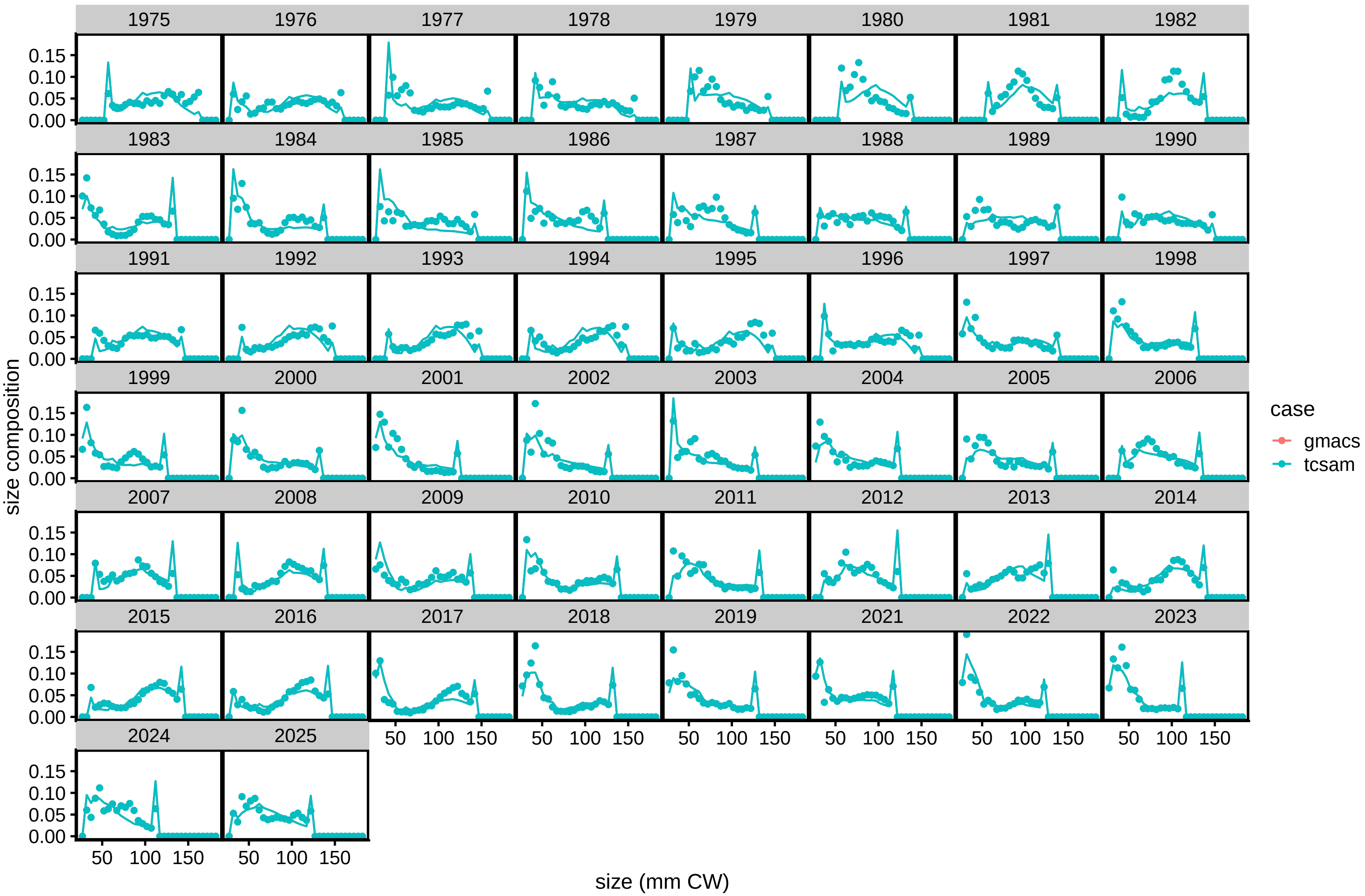

Figure 63. Fits to size composition data from the NMS surveys for males. Points: observed values; lines: predicted values.

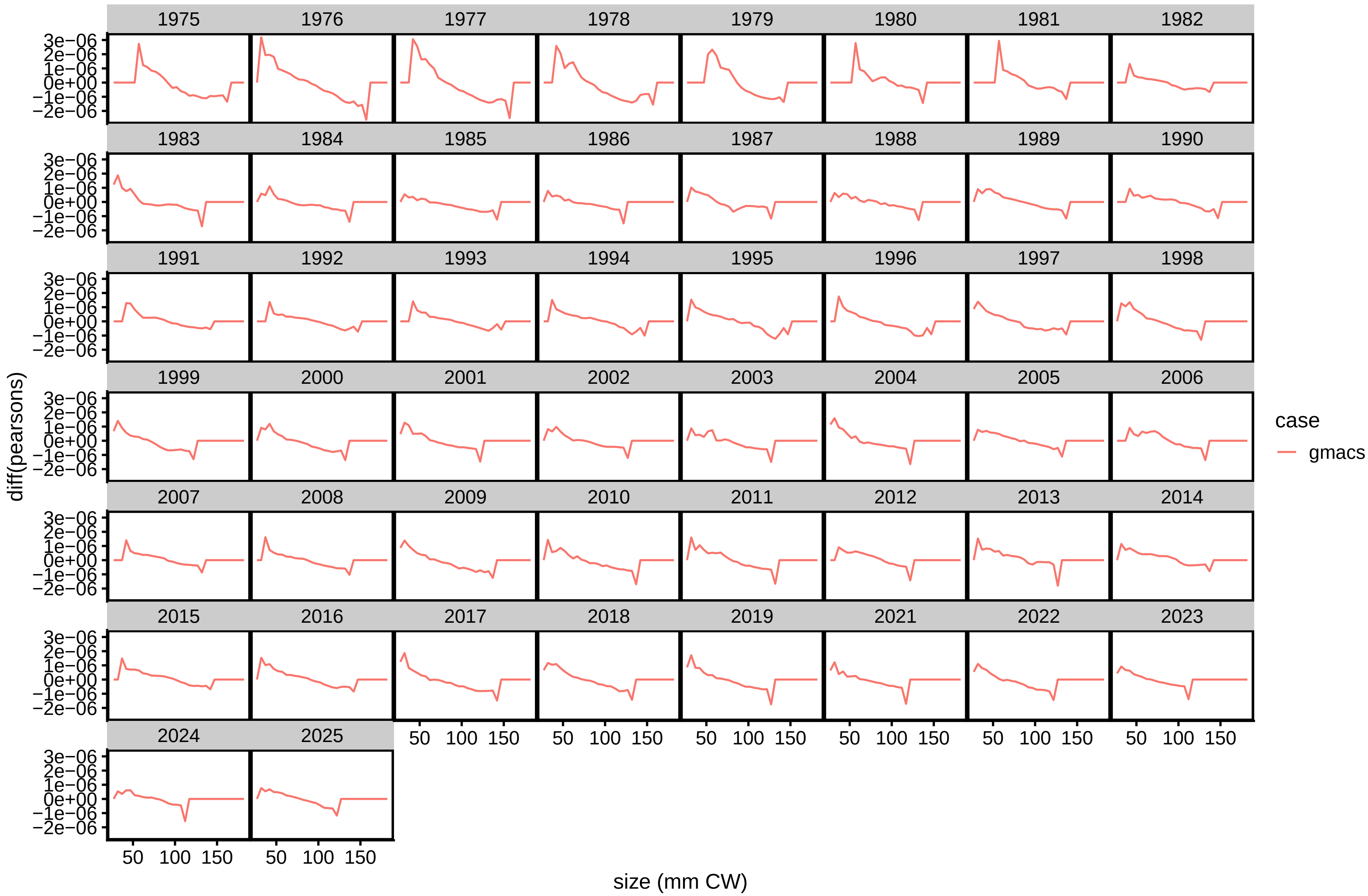

Figure 64. Differences from the TCSAM02 model in Pearson's residuals for fits to size composition data from the NMFS surveys for males.

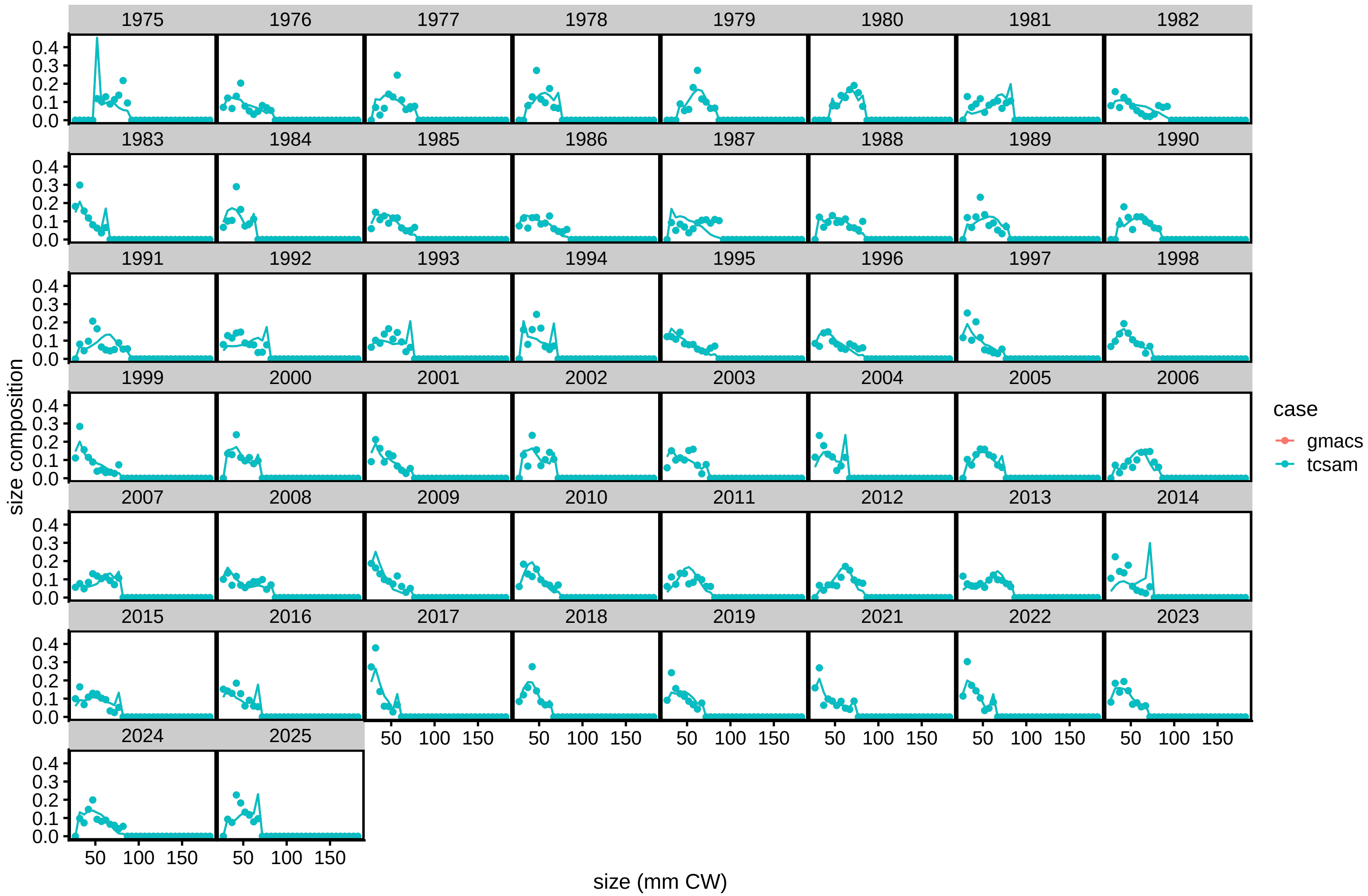

Figure 65. Fits to size composition data from the NMFS surveys for immature females. Points: observed values; lines: predicted values.

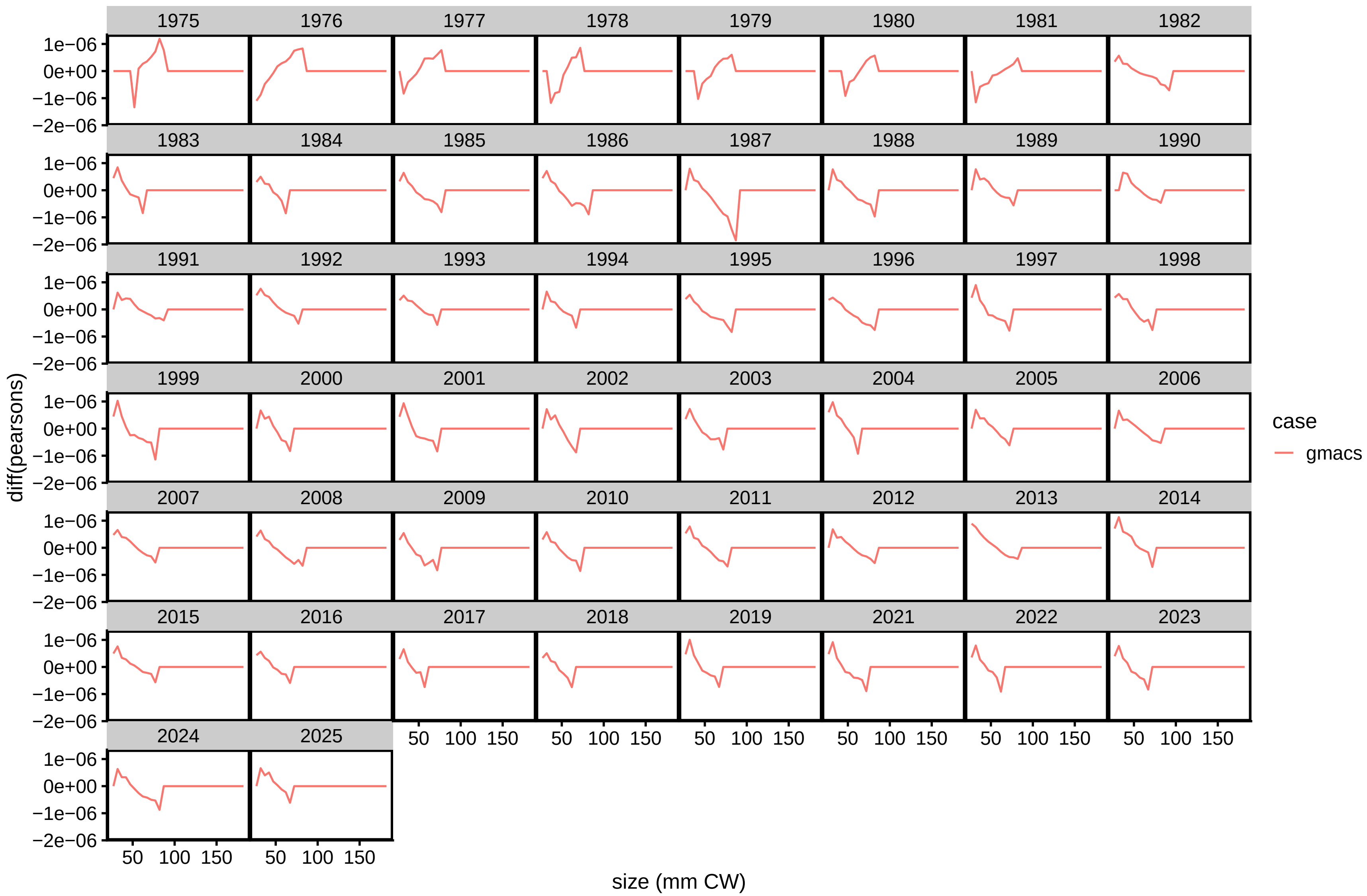

Figure 66. Differences from the TCSAM02 model in Pearson's residuals for fits to size composition data from the NMFS surveys for immature females.

Figure 67. Fits to total catch size composition data from the NMFS surveys for mature females. Points: observed values; lines: predicted values.

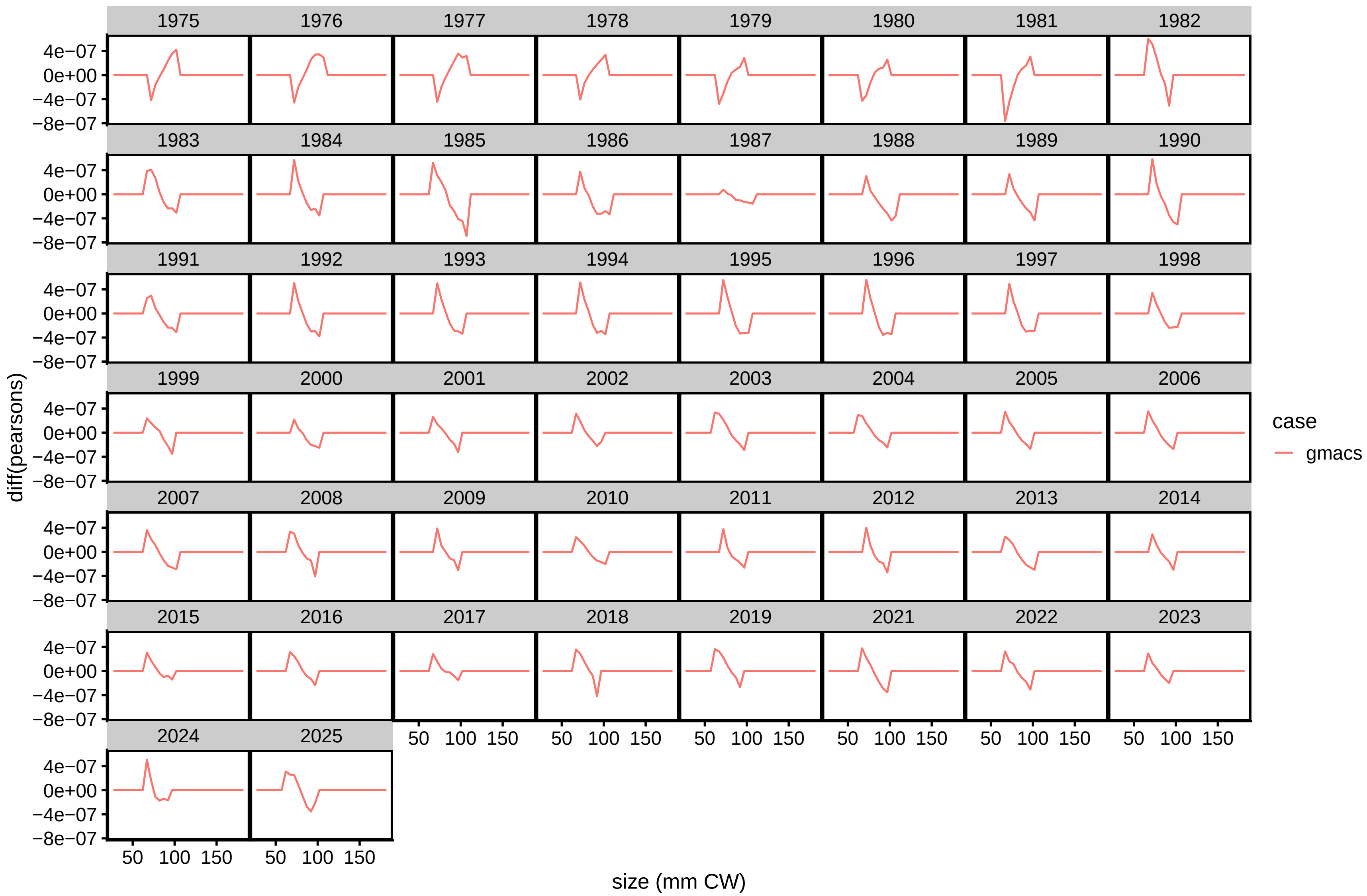

Figure 68. Differences from the TCSAM02 model in Pearson's residuals for fits to size composition data from the NMFS surveys for mature females.

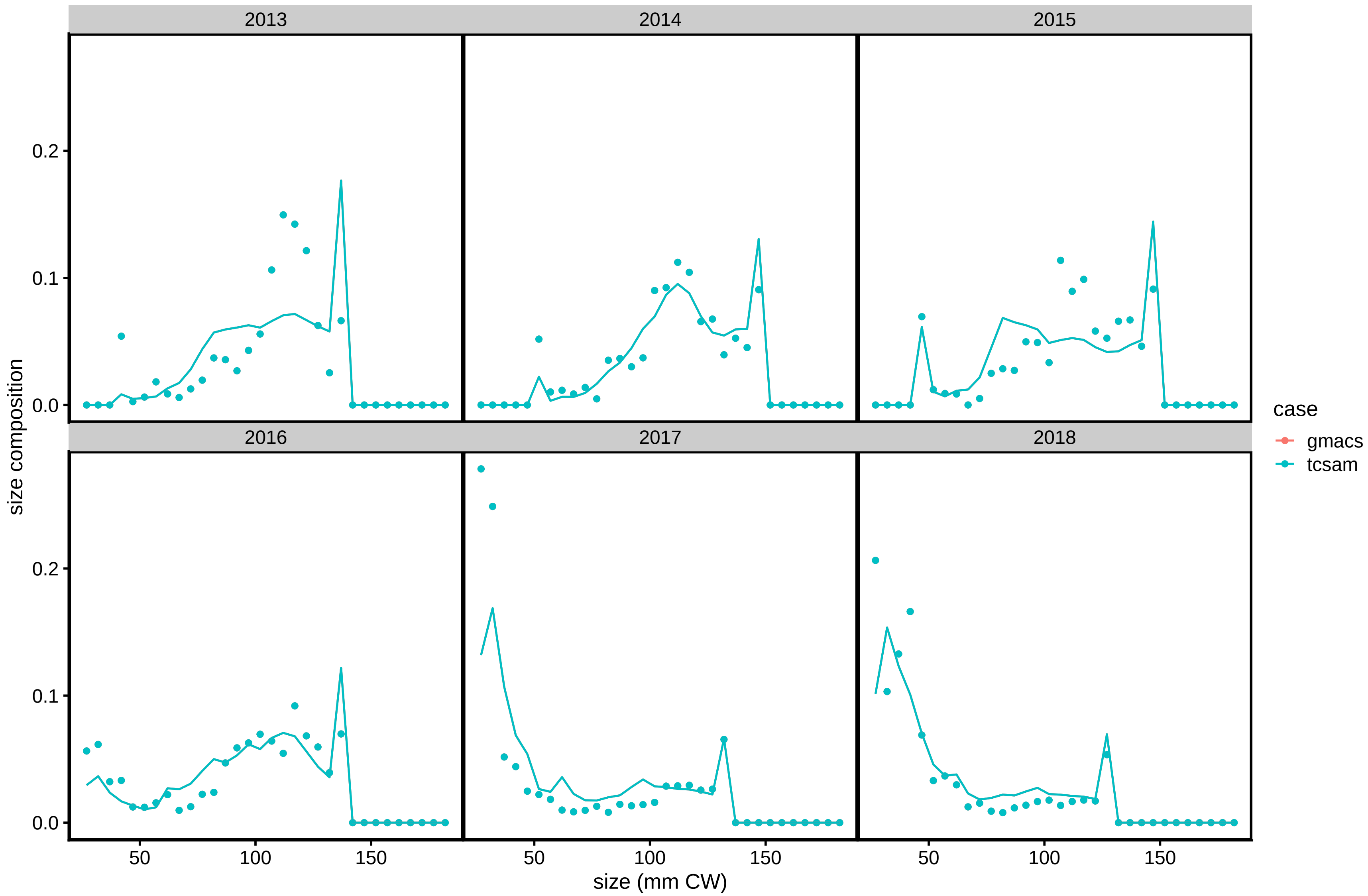

Figure 69. Fits to size composition data from the BSFRF surveys for males. Points: observed values; lines: predicted values.

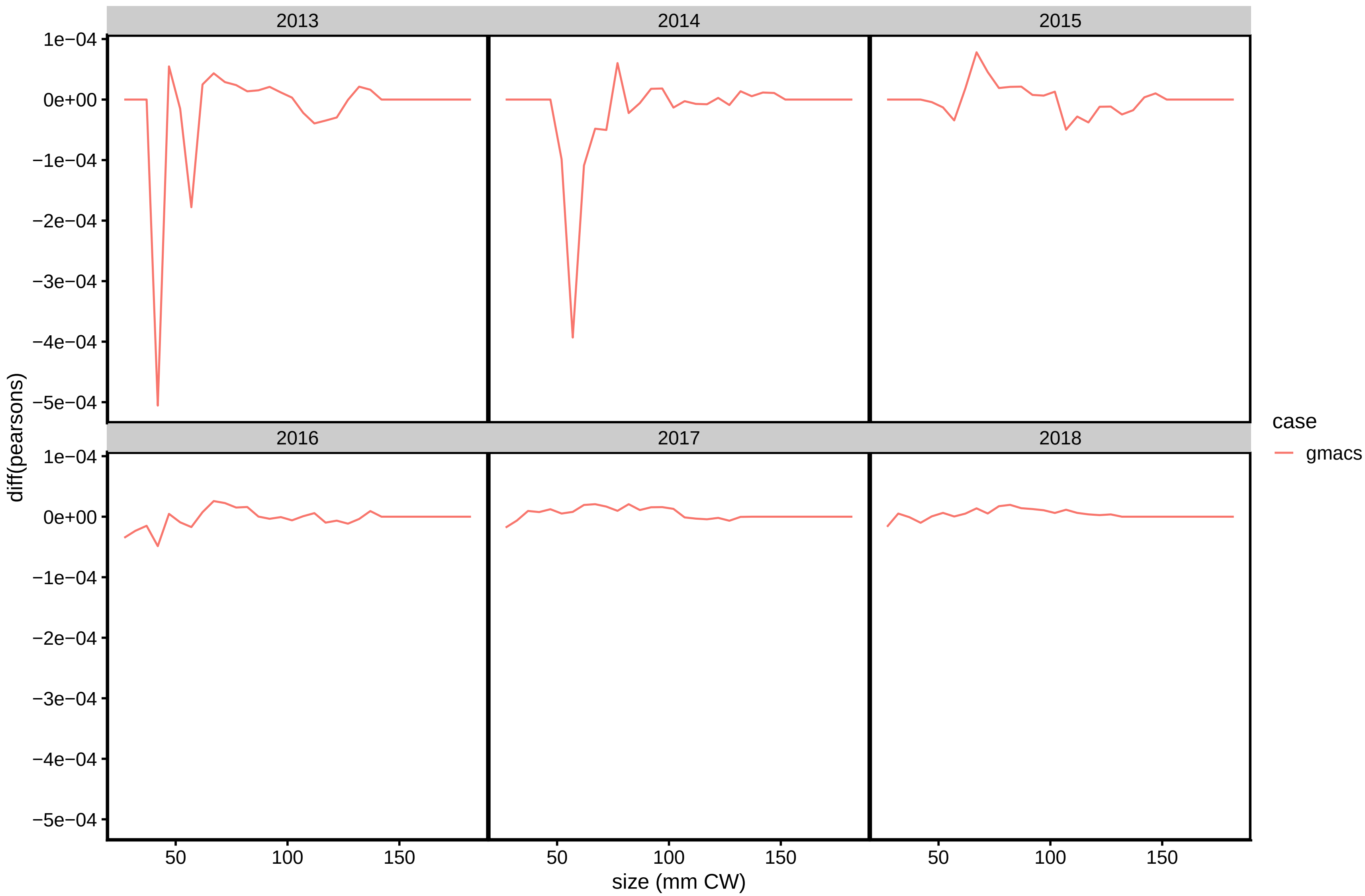

Figure 70. Differences from the TCSAM02 model in Pearson's residuals for fits to size composition data from the BSFRF survey for males.

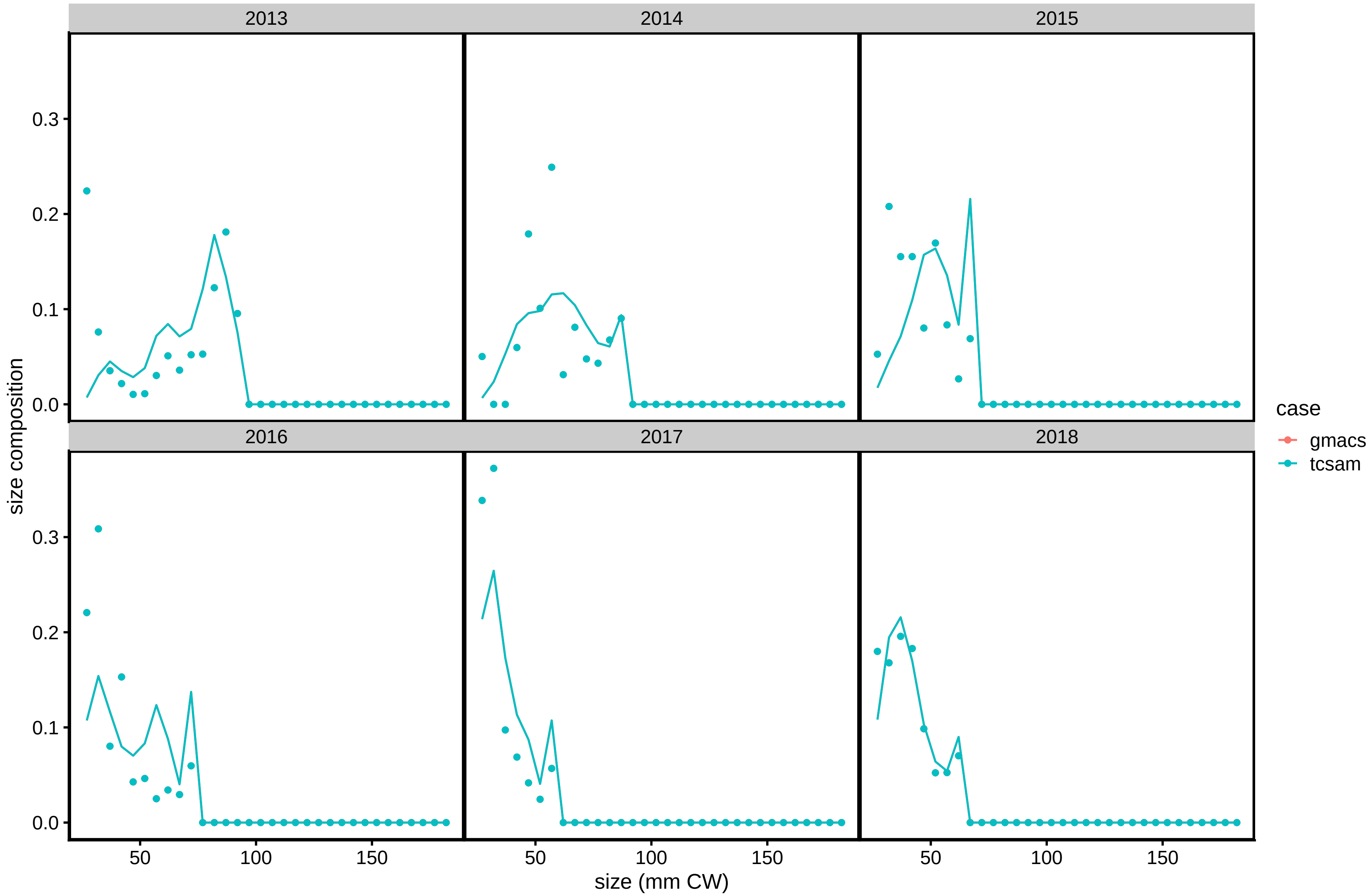

Figure 71. Fits to size composition data from the BSFRF survey for immature females. Points: observed values; lines: predicted values.

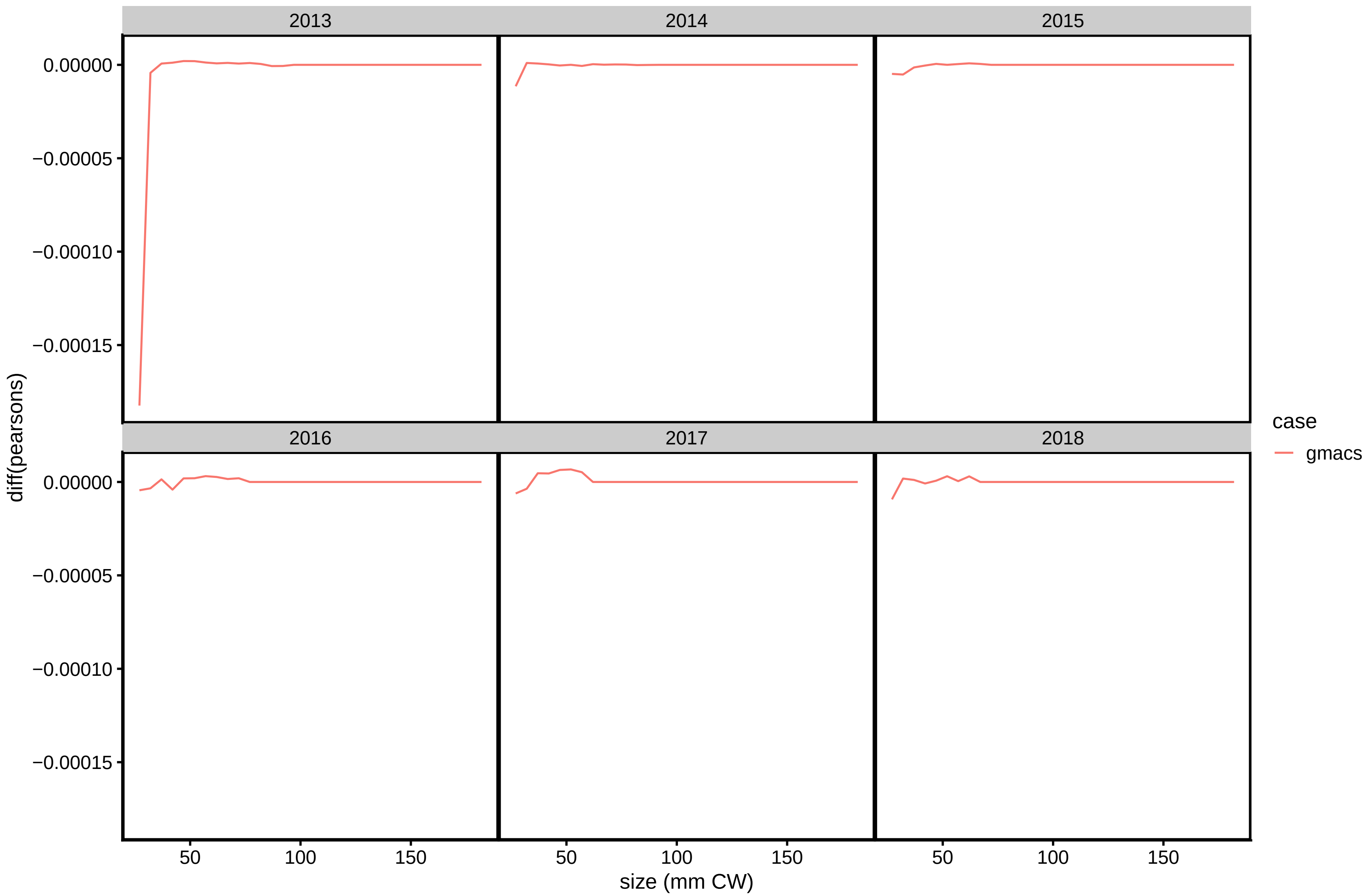

Figure 72. Differences from the TCSAM02 model in Pearson's residuals for fits to size composition data from the BSFRF surveys for immature females.

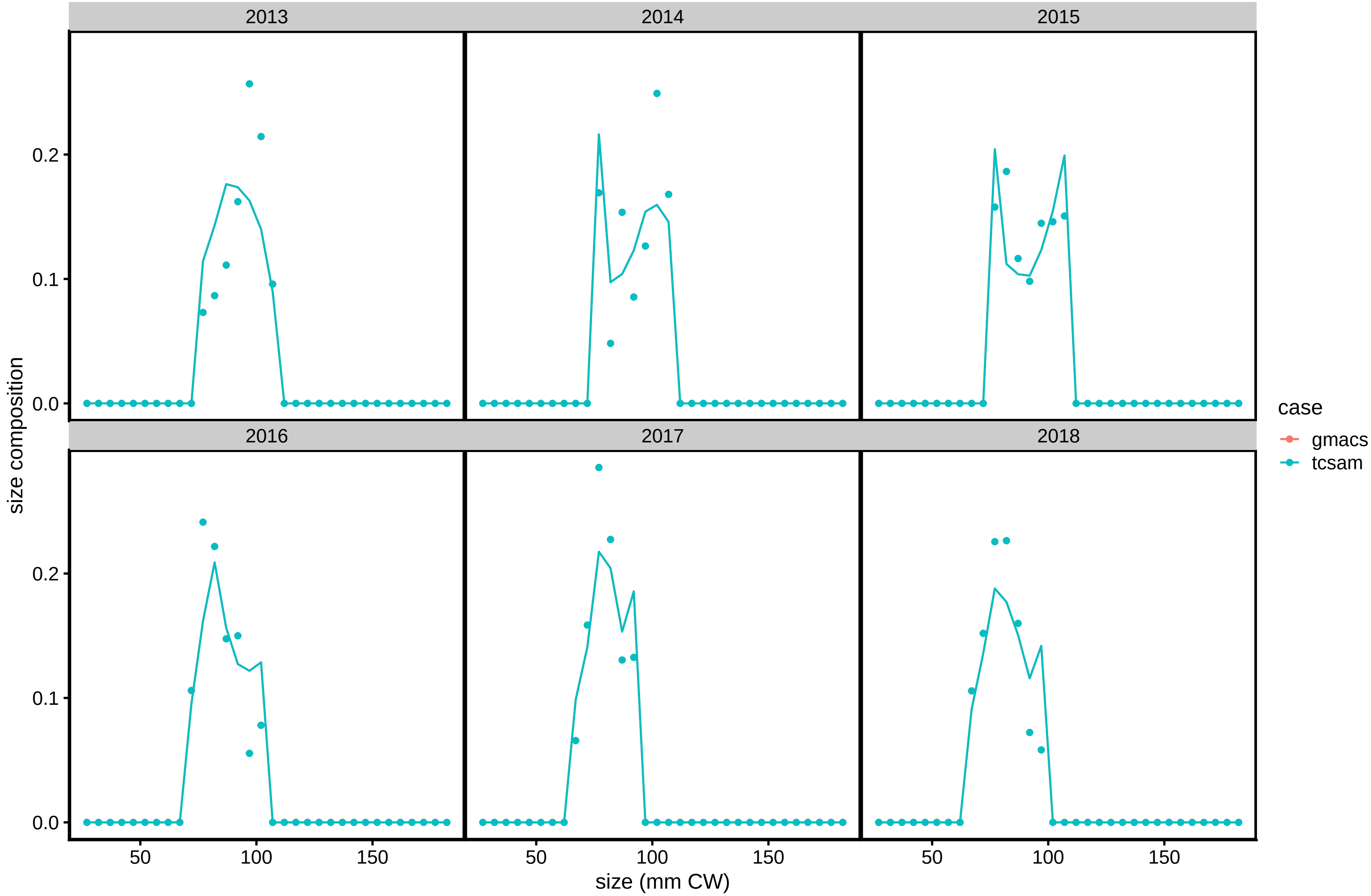

Figure 73. Fits to total catch size composition data from the BSFRF surveys for mature females. Points: observed values; lines: predicted values.

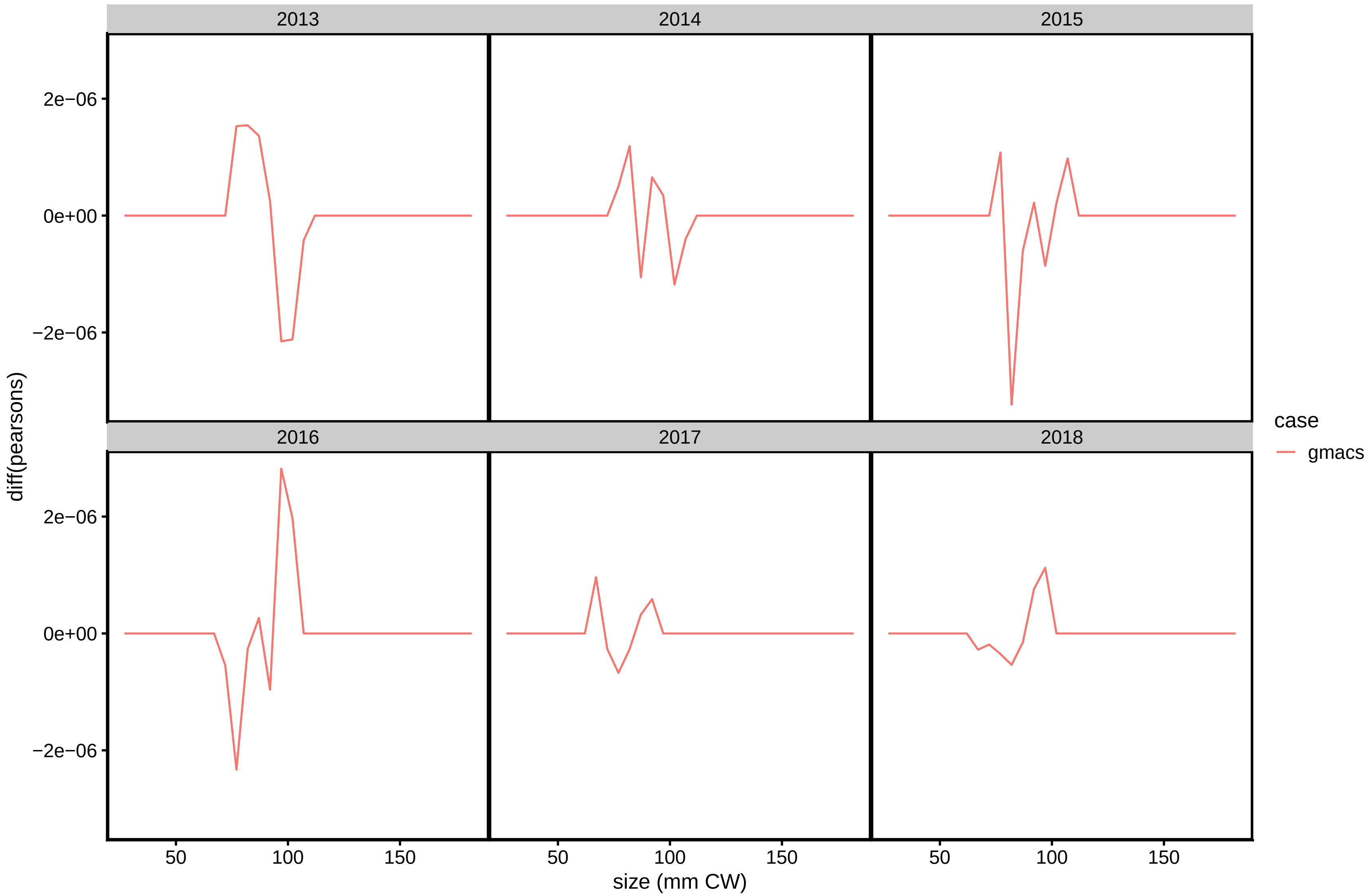

Figure 74. Differences from the TCSAM02 model in Pearson's residuals for fits to size composition data from the BSFRF surveys for mature females.

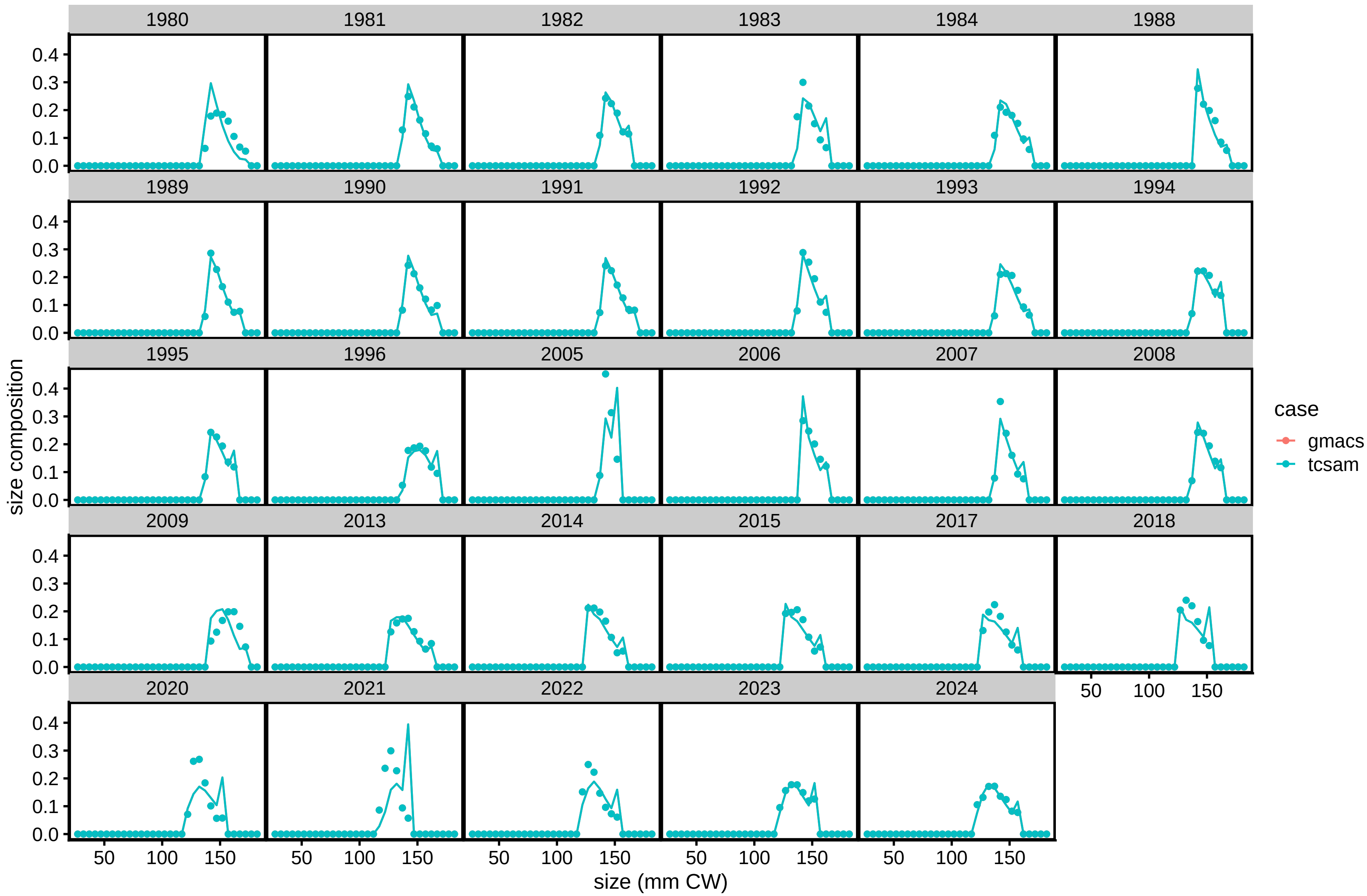

Figure 75. Fits to retained catch size composition data from the directed fishery. Points: observed values; lines: predicted values.

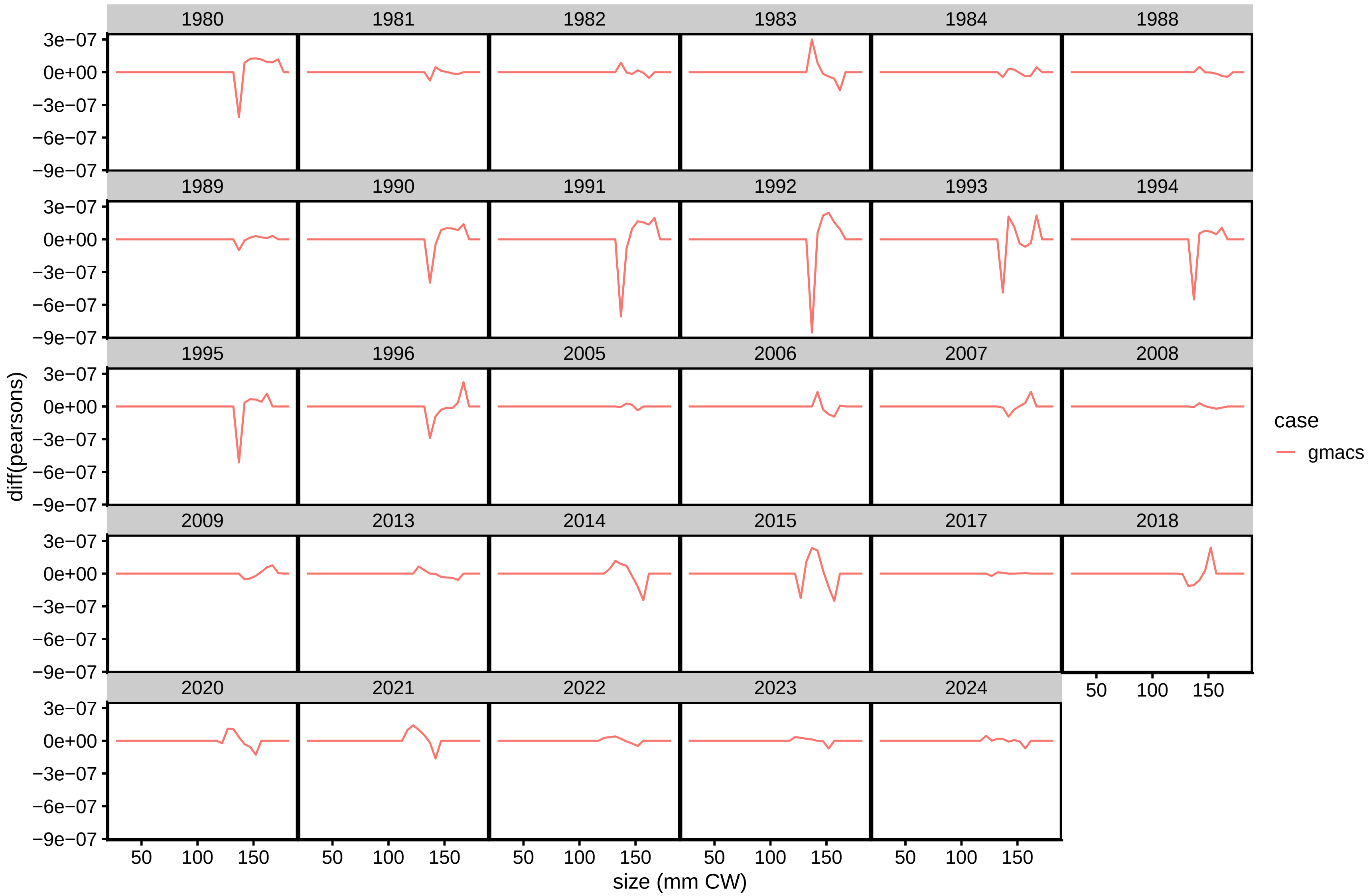

Figure 76. Differences from the TCSAM02 model in Pearson's residuals for fits to retained catch size composition data from the directed fishery.

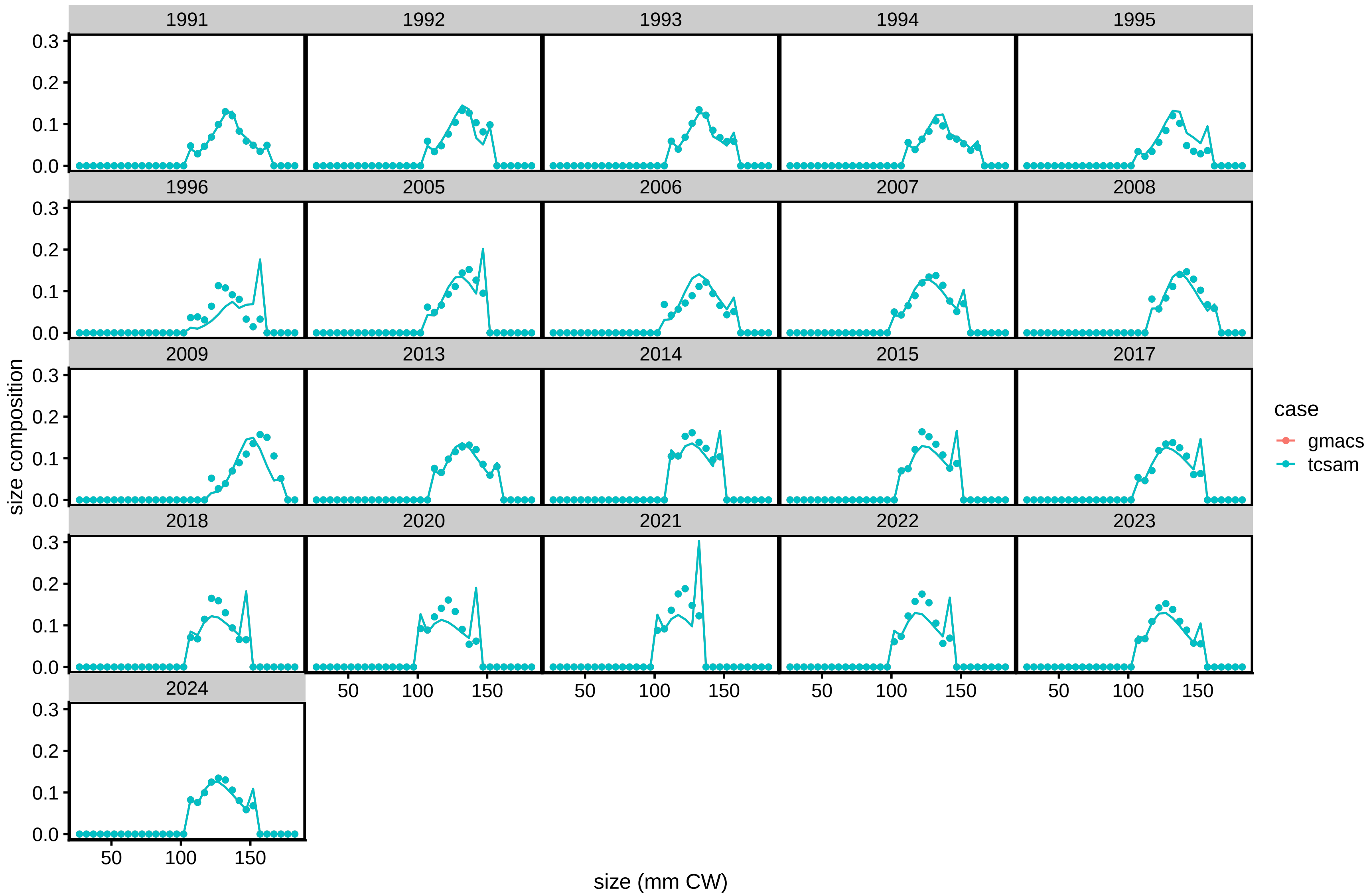

Figure 77. Fits to total catch size composition data from the directed fishery for males. Points: observed values; lines: predicted values.

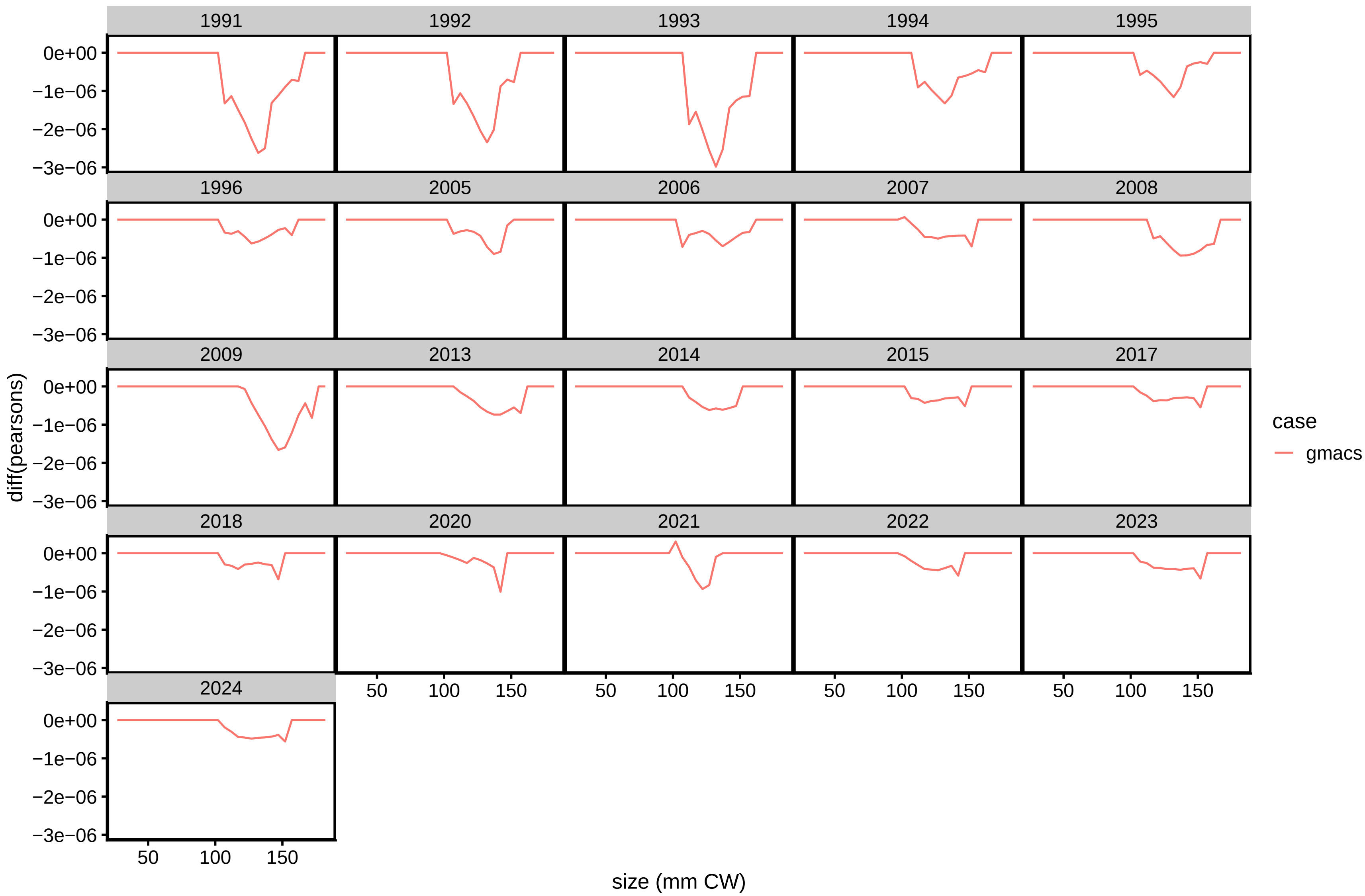

Figure 78. Differences from the TCSAM02 model in Pearson's residuals for fits to total catch size composition data from the directed fishery for males.

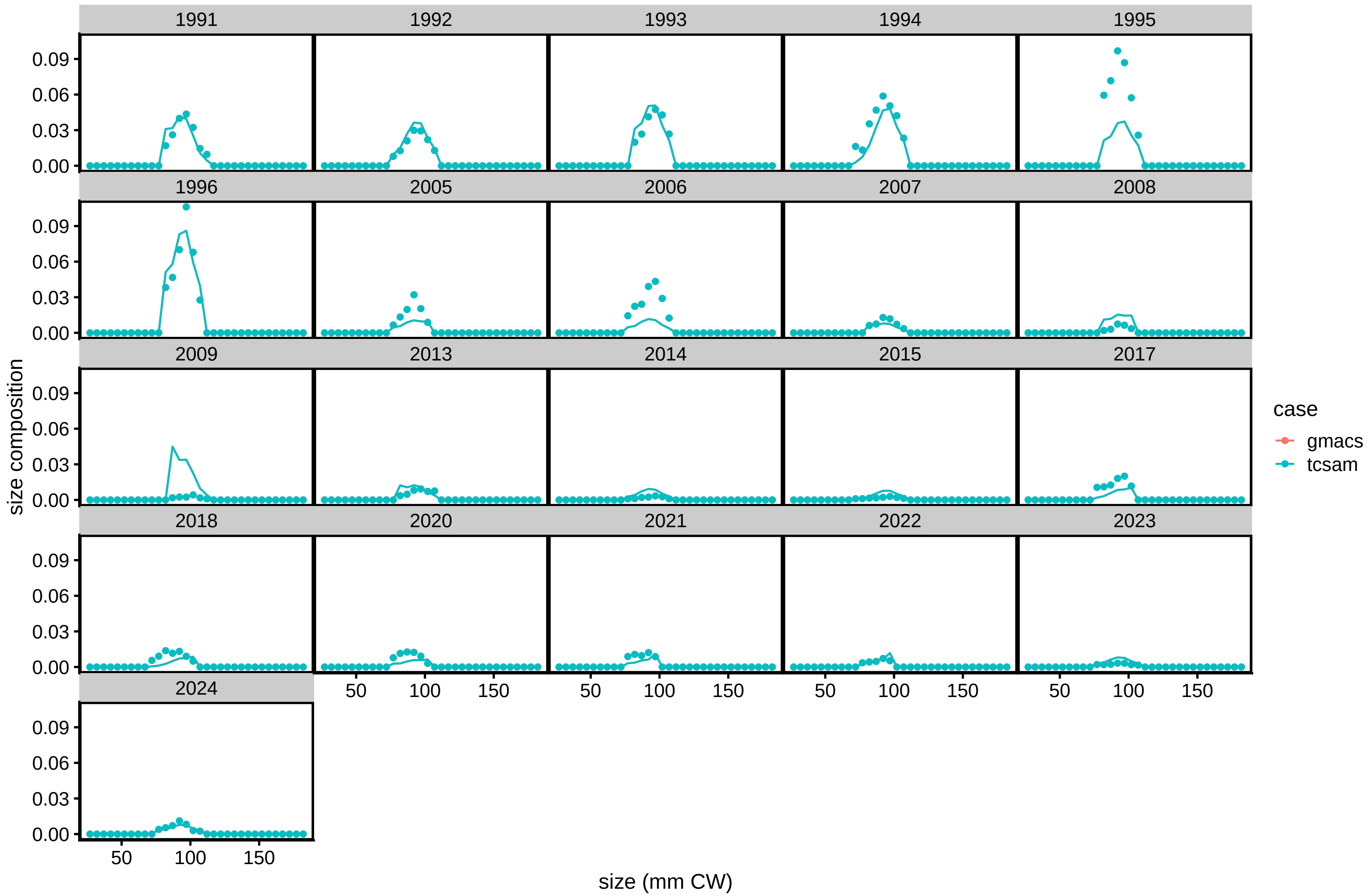

Figure 79. Fits to total catch size composition data from the directed fishery for females. Points: observed values; lines: predicted values.

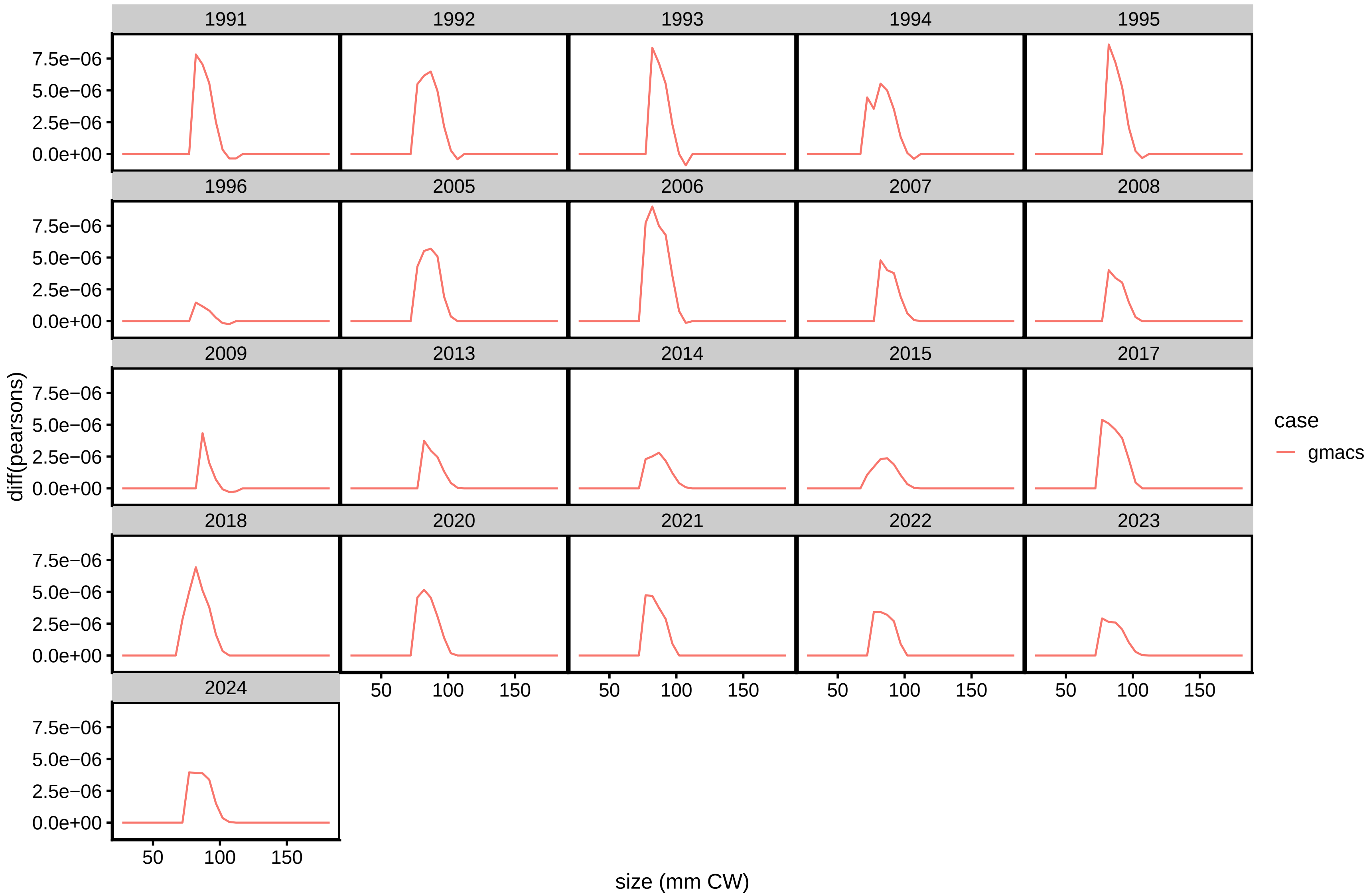

Figure 80. Differences from the TCSAM02 model in Pearson's residuals for fits to total catch size composition data from the directed fishery for females.

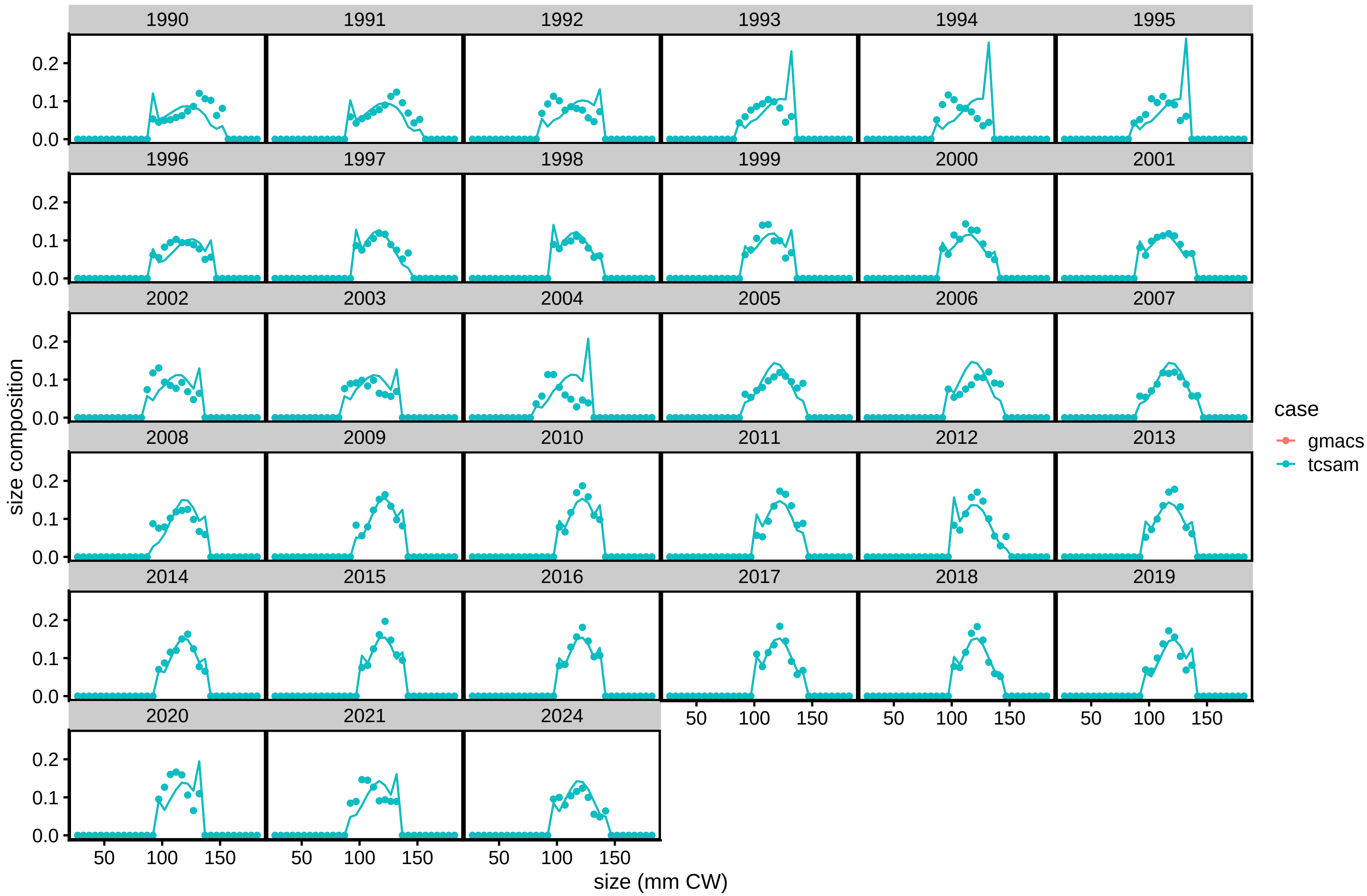

Figure 81. Fits to total catch size composition data from the snow crab fishery for males. Points: observed values; lines: predicted values.

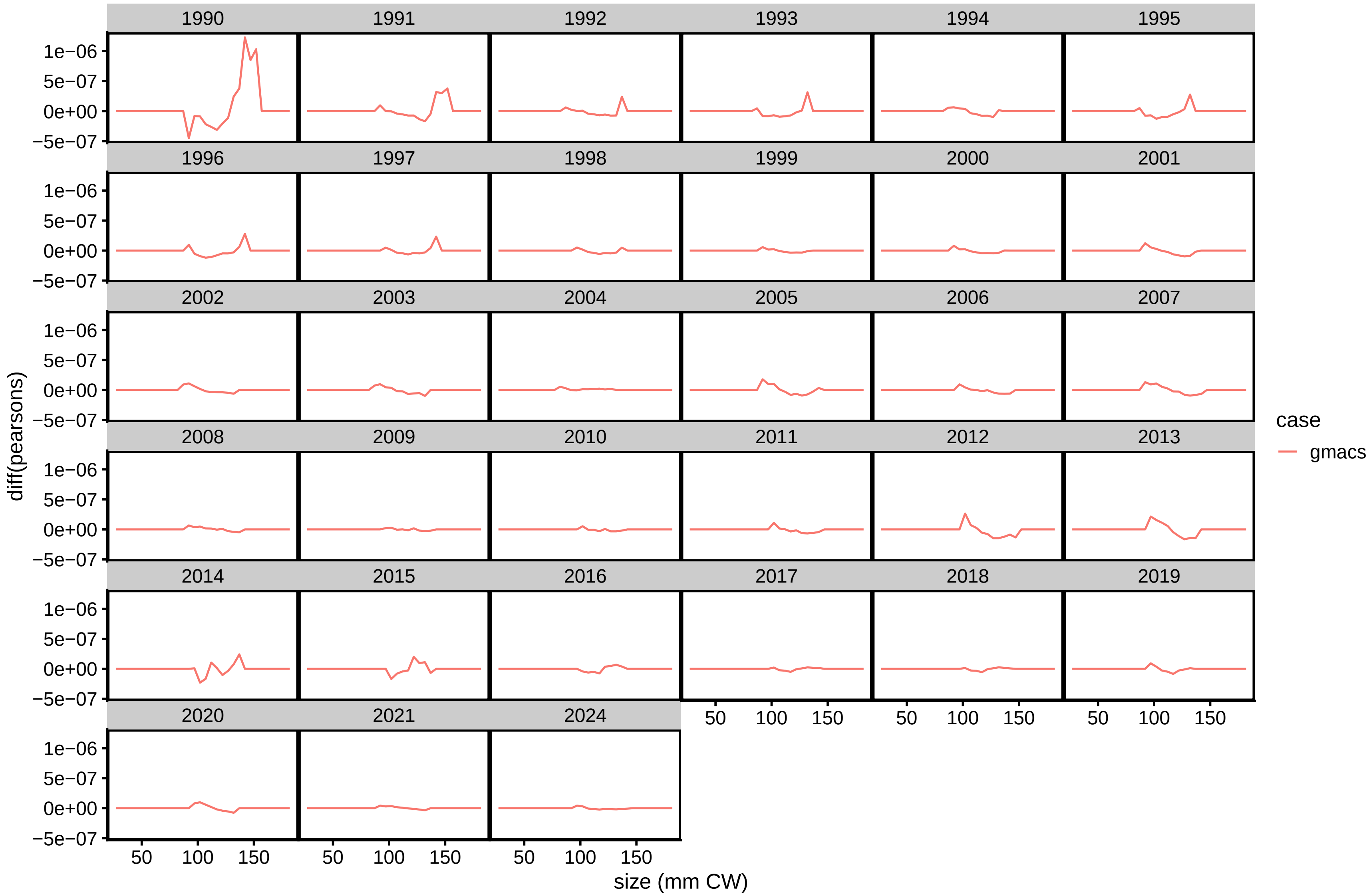

Figure 82. Differences from the TCSAM02 model in Pearson's residuals for fits to total catch size composition data from the snow crab fishery for males.

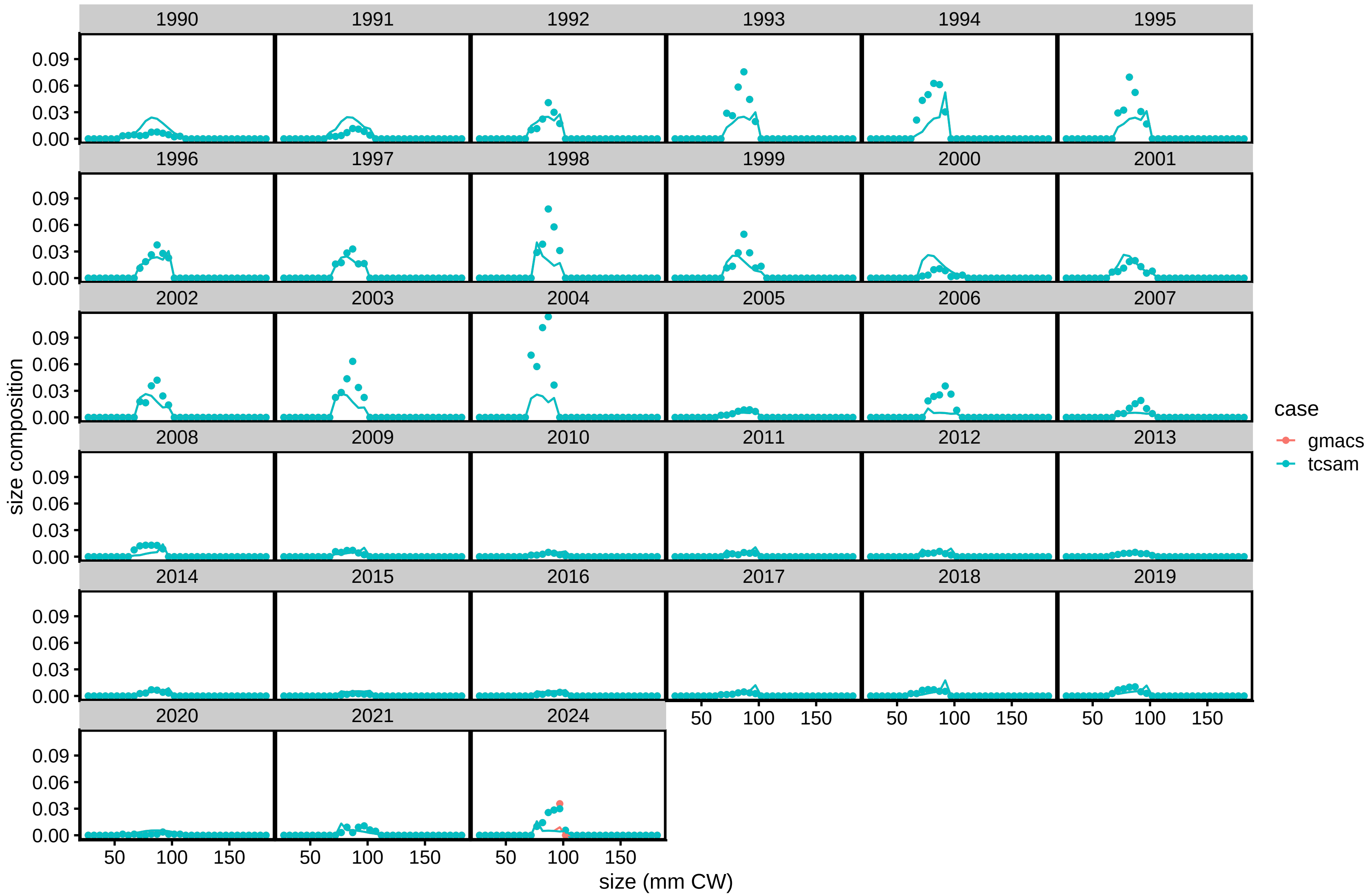

Figure 83. Fits to total catch size composition data from the snow crab fishery for females. Points: observed values; lines: predicted values.

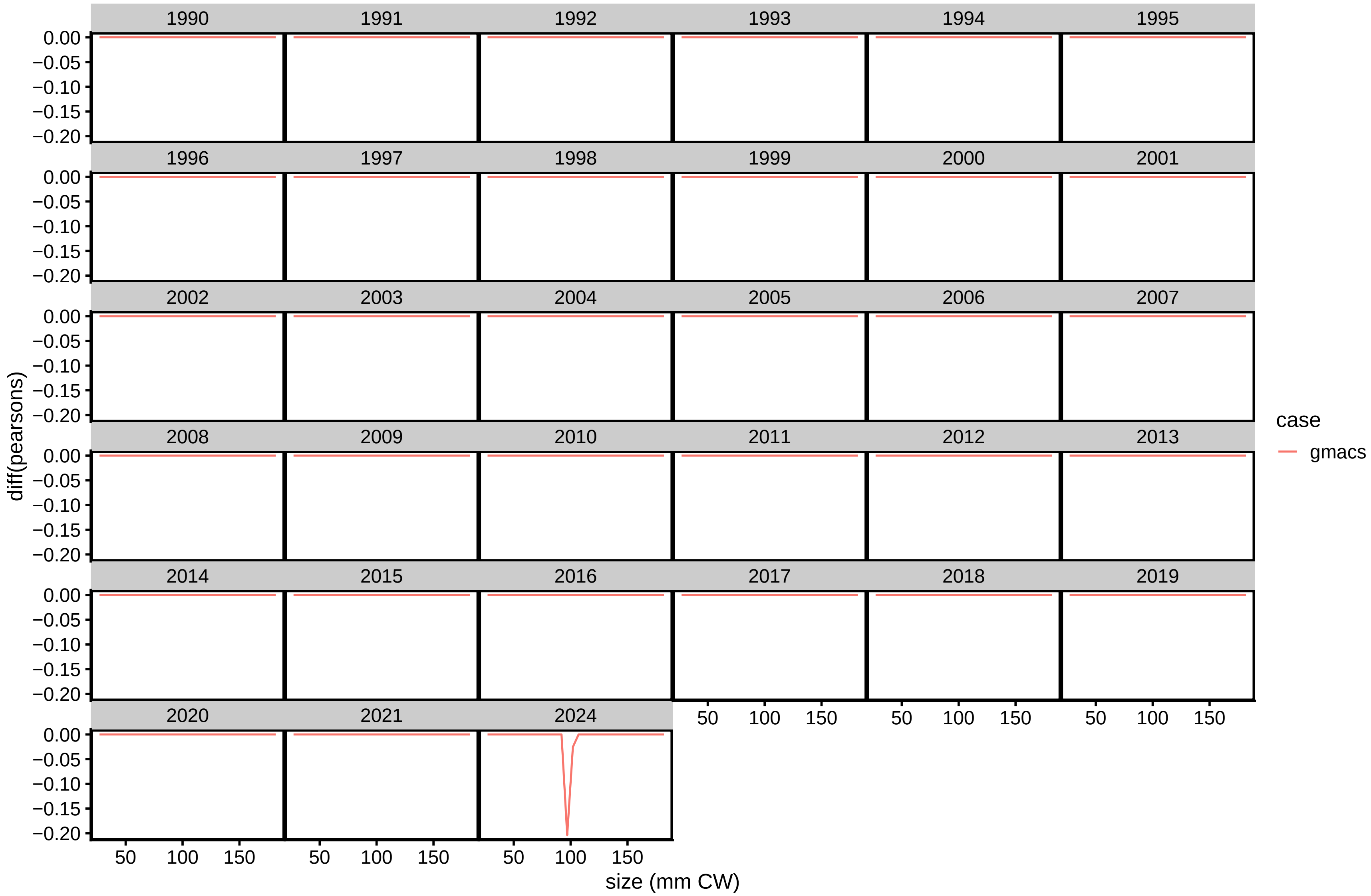

Figure 84. Differences from the TCSAM02 model in Pearson's residuals for fits to total catch size composition data from the snow crab fishery for females.

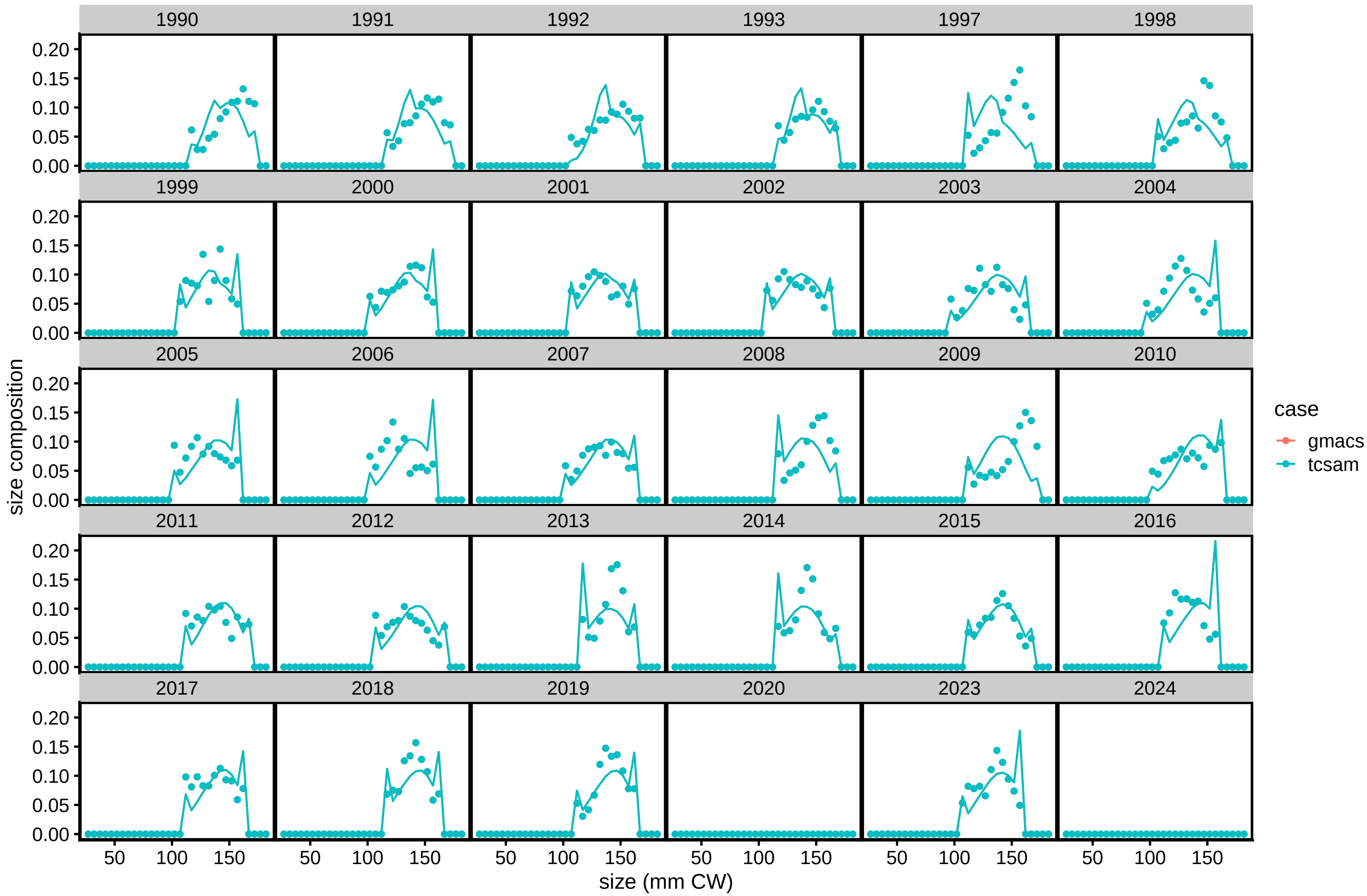

Figure 85. Fits to total catch size composition data from the BBRKC fishery for males. Points: observed values; lines: predicted values.

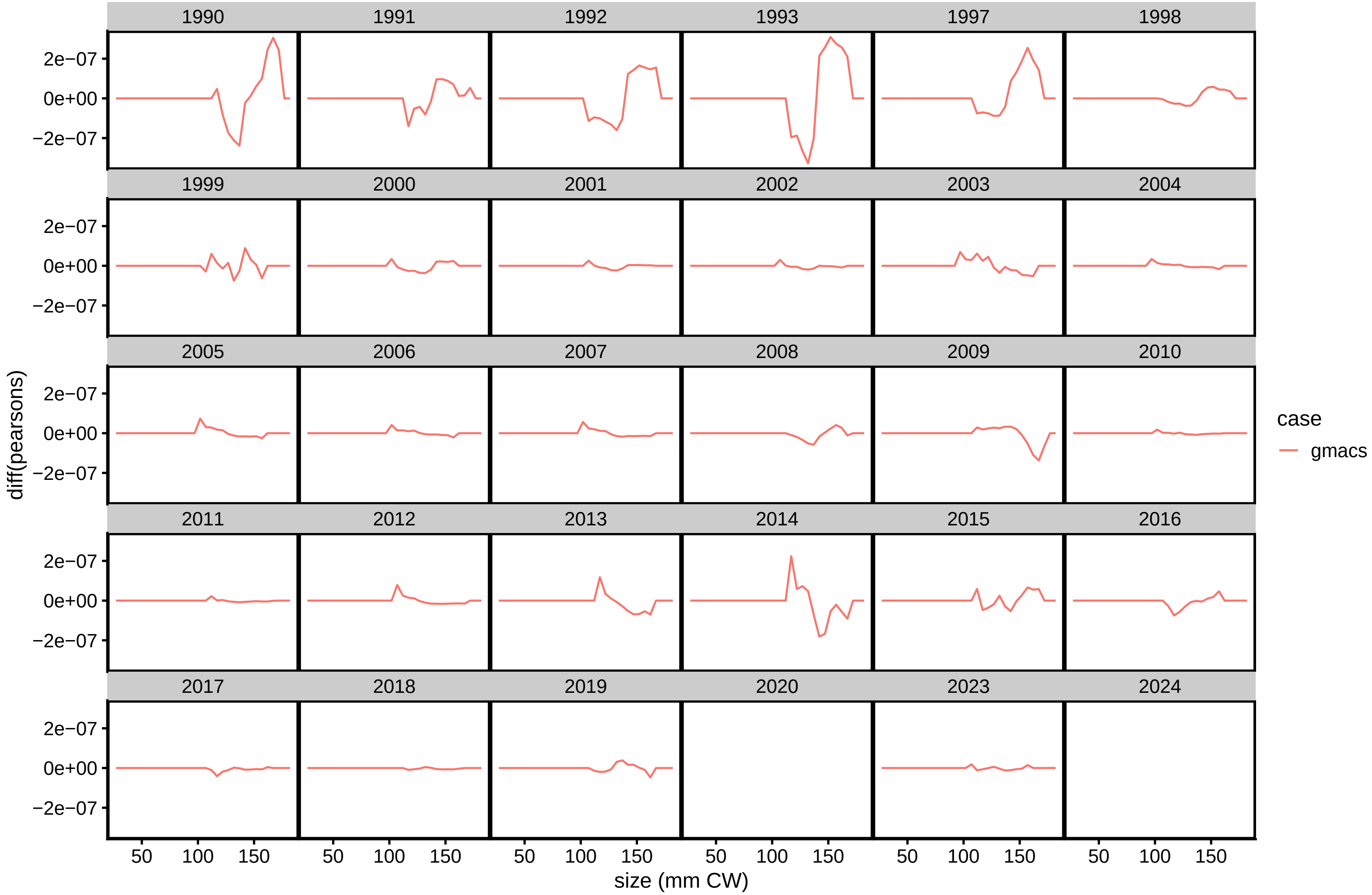

Figure 86. Differences from the TCSAM02 model in Pearson's residuals for fits to total catch size composition data from the BBRKC fishery for males.

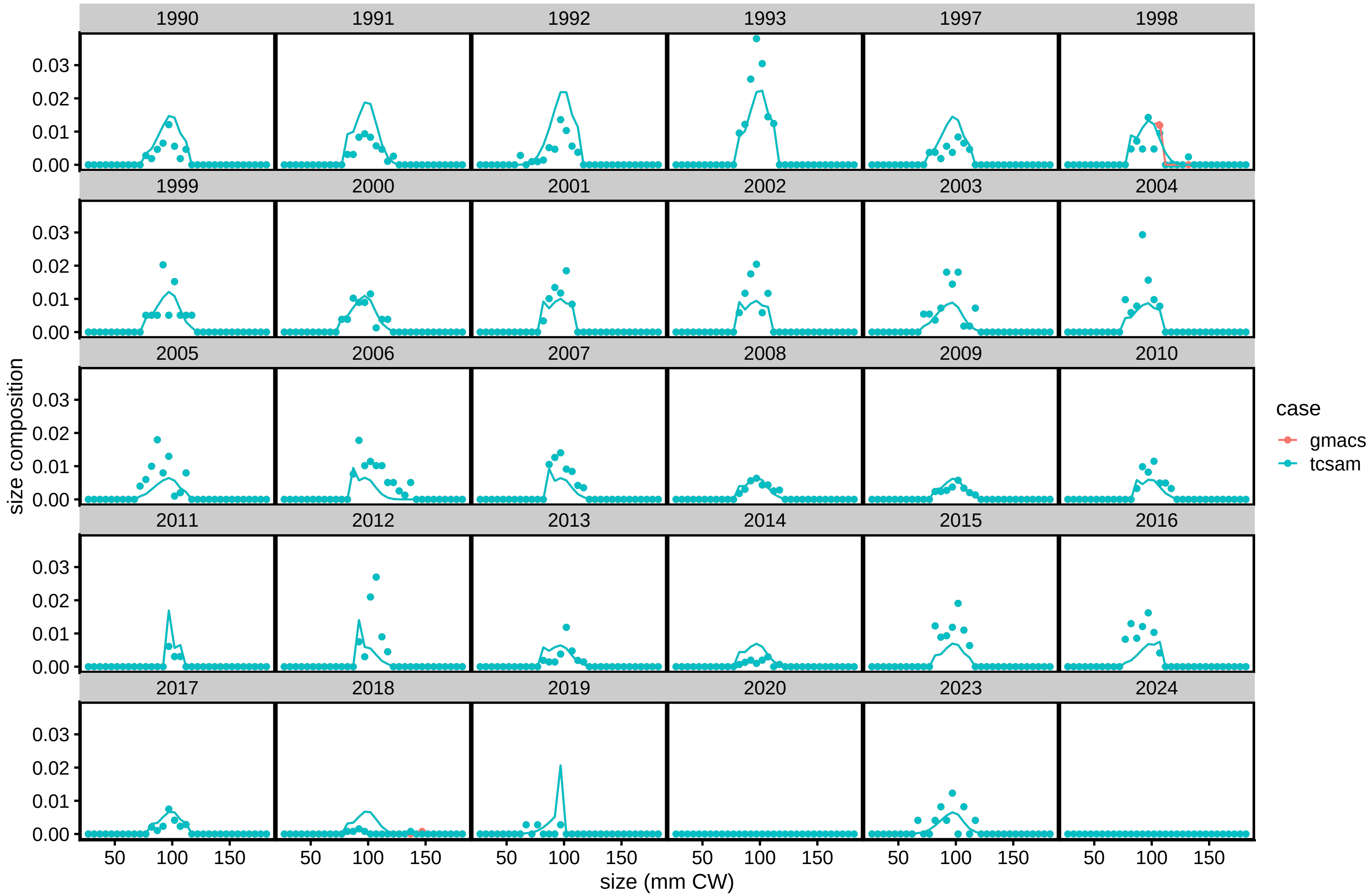

Figure 87. Fits to total catch size composition data from the BBRKC fishery for females. Points: observed values; lines: predicted values.

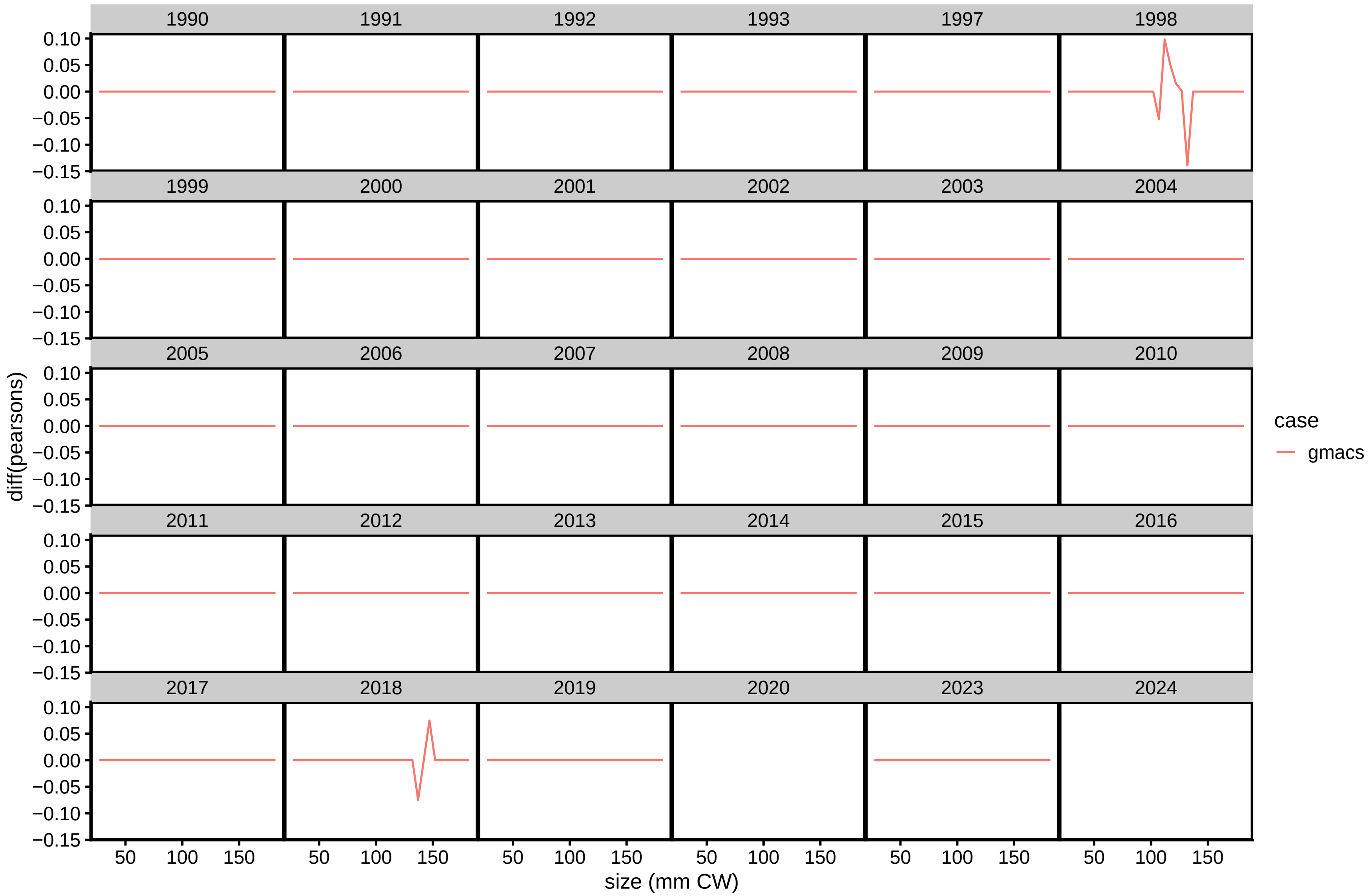

Figure 88. Differences from the TCSAM02 model in Pearson's residuals for fits to total catch size composition data from the BBRKC fishery for females.

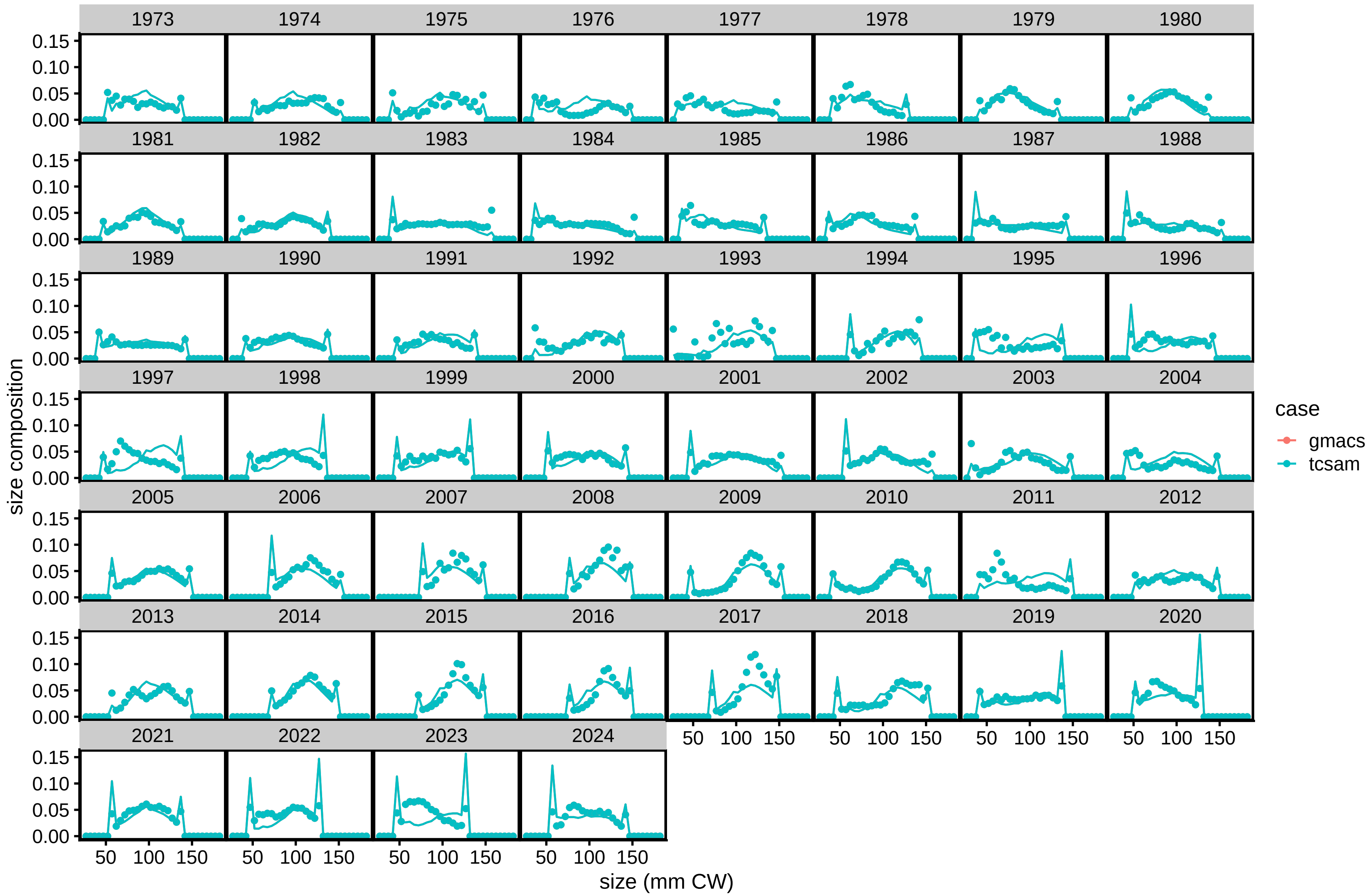

Figure 89. Fits to total catch size composition data from the groundfish fisheries for males. Points: observed values; lines: predicted values.

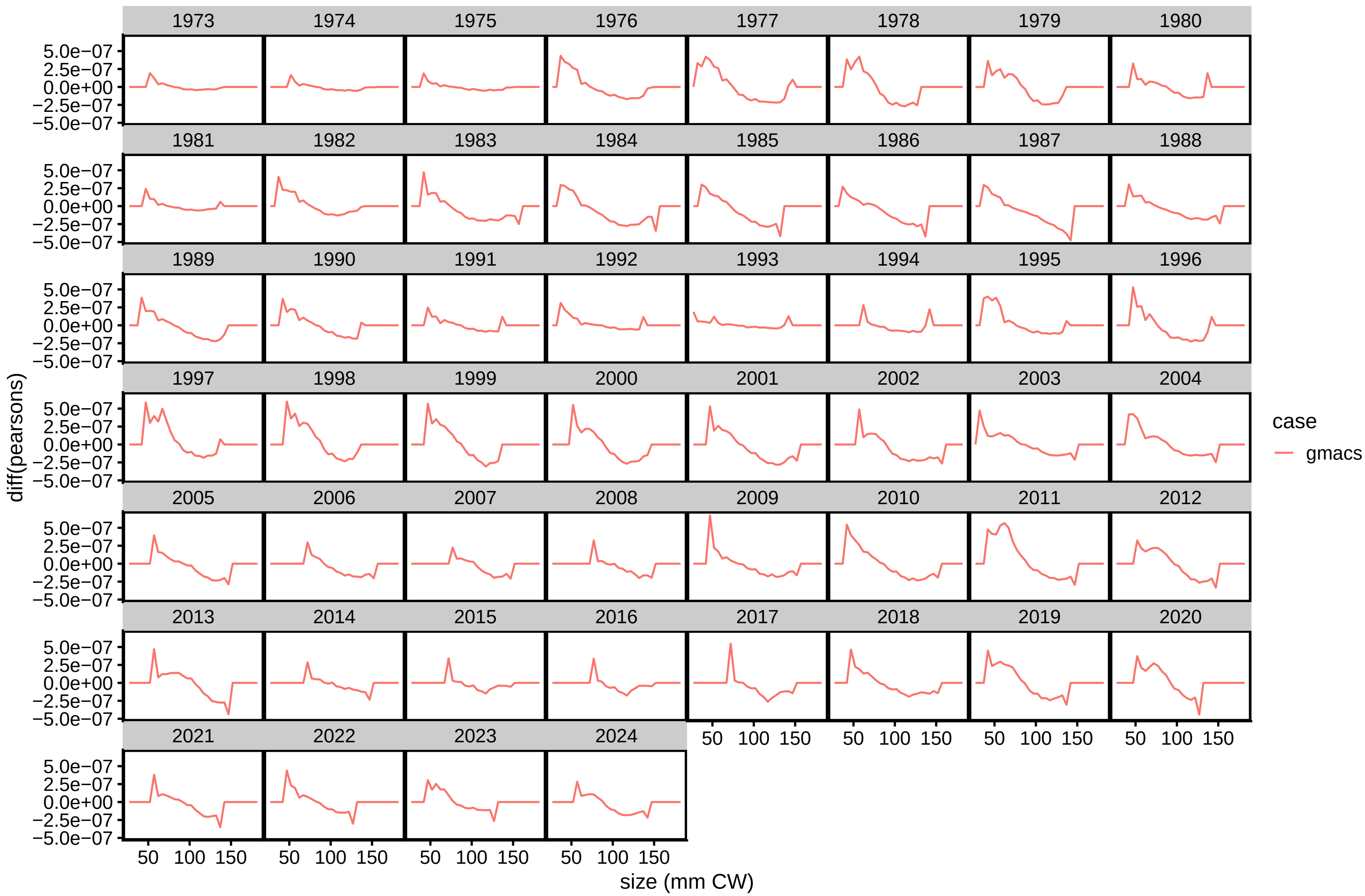

Figure 90. Differences from the TCSAM02 model in Pearson's residuals for fits to total catch size composition data from the groundfish fisheries for males.

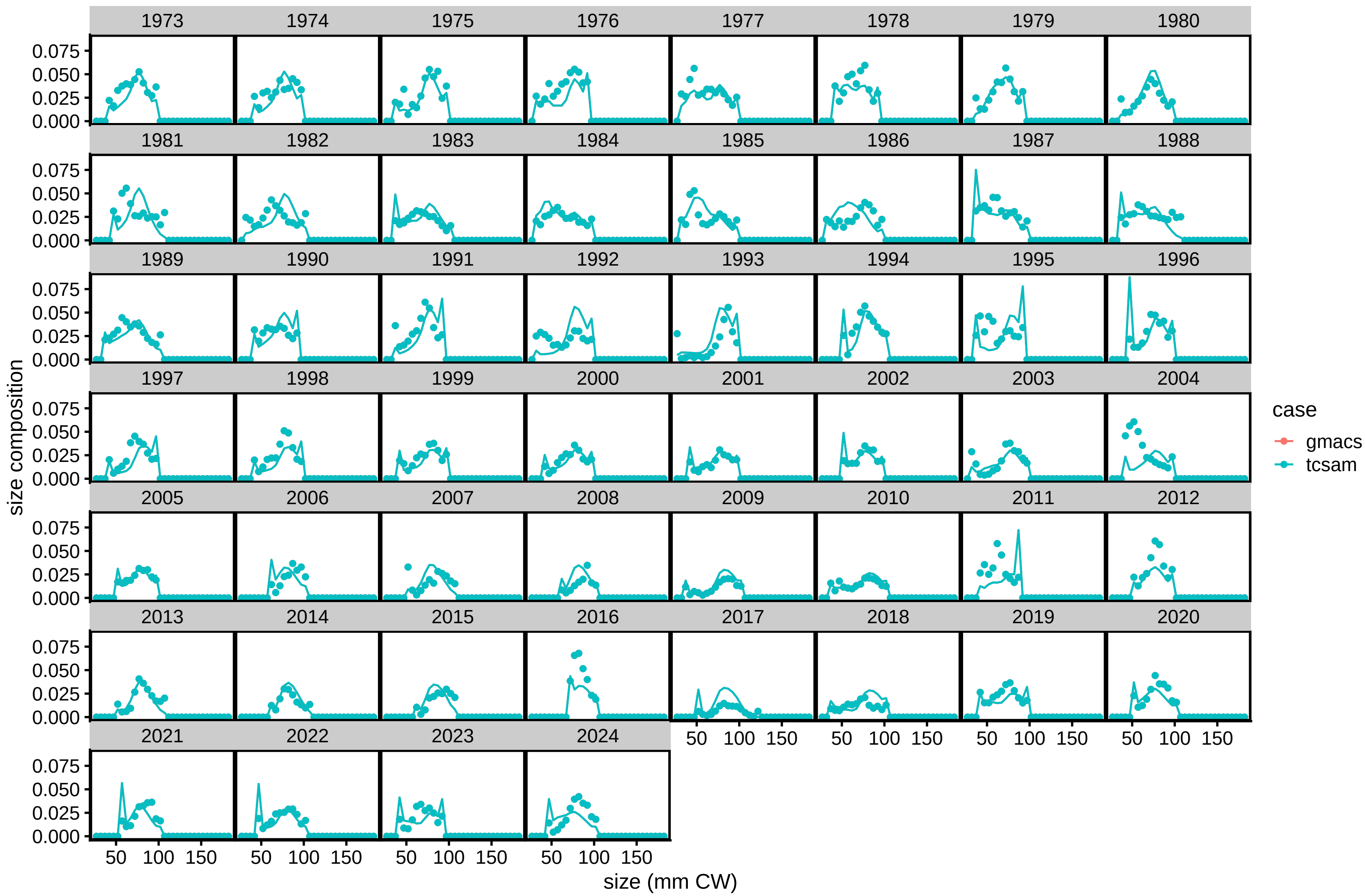

Figure 91. Fits to total catch size composition data from the groundfish fisheries for females. Points: observed values; lines: predicted values.

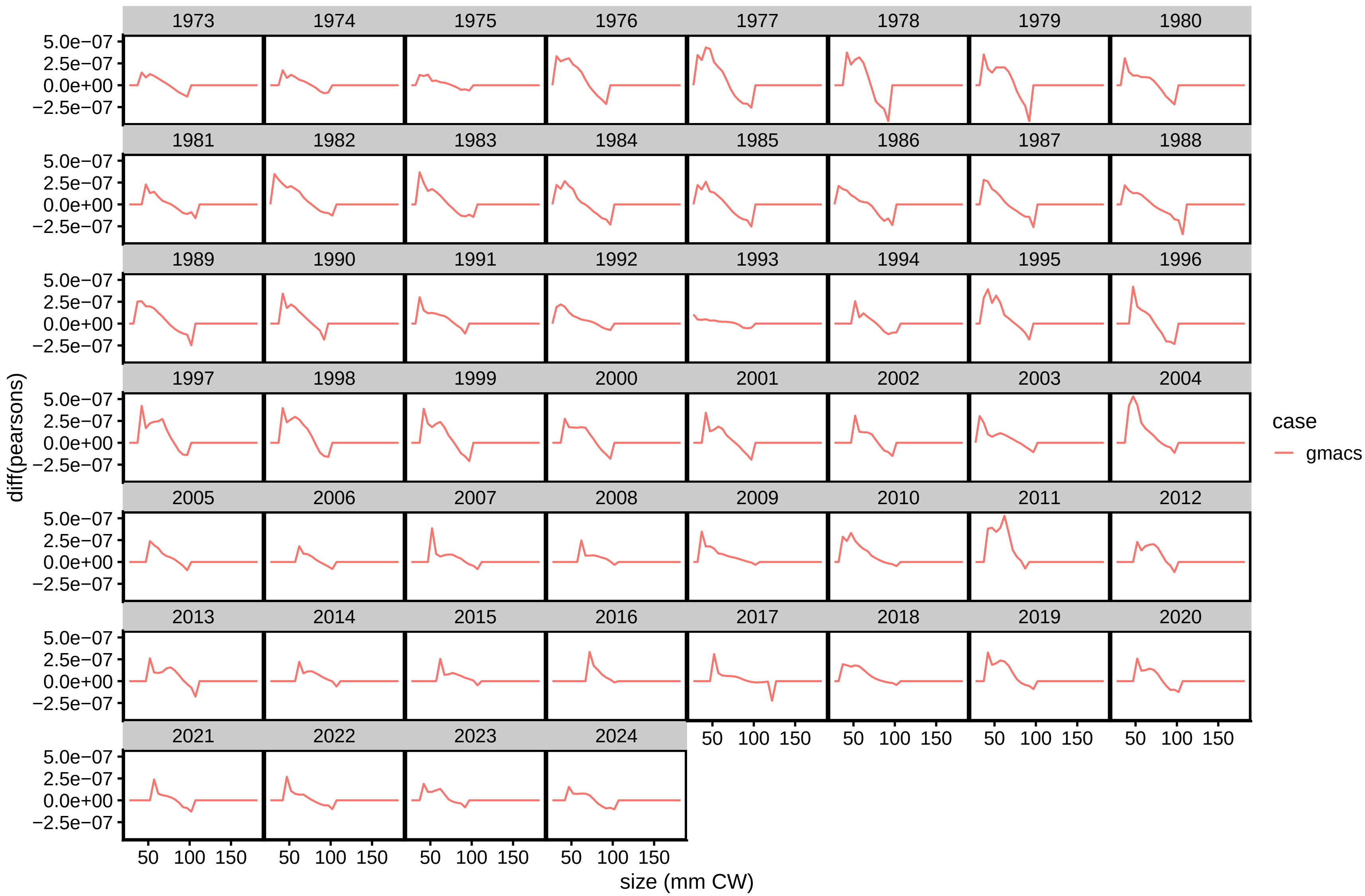

Figure 92. Differences from the TCSAM02 model in Pearson's residuals for fits to total catch size composition data from the groundfish fisheries for females.

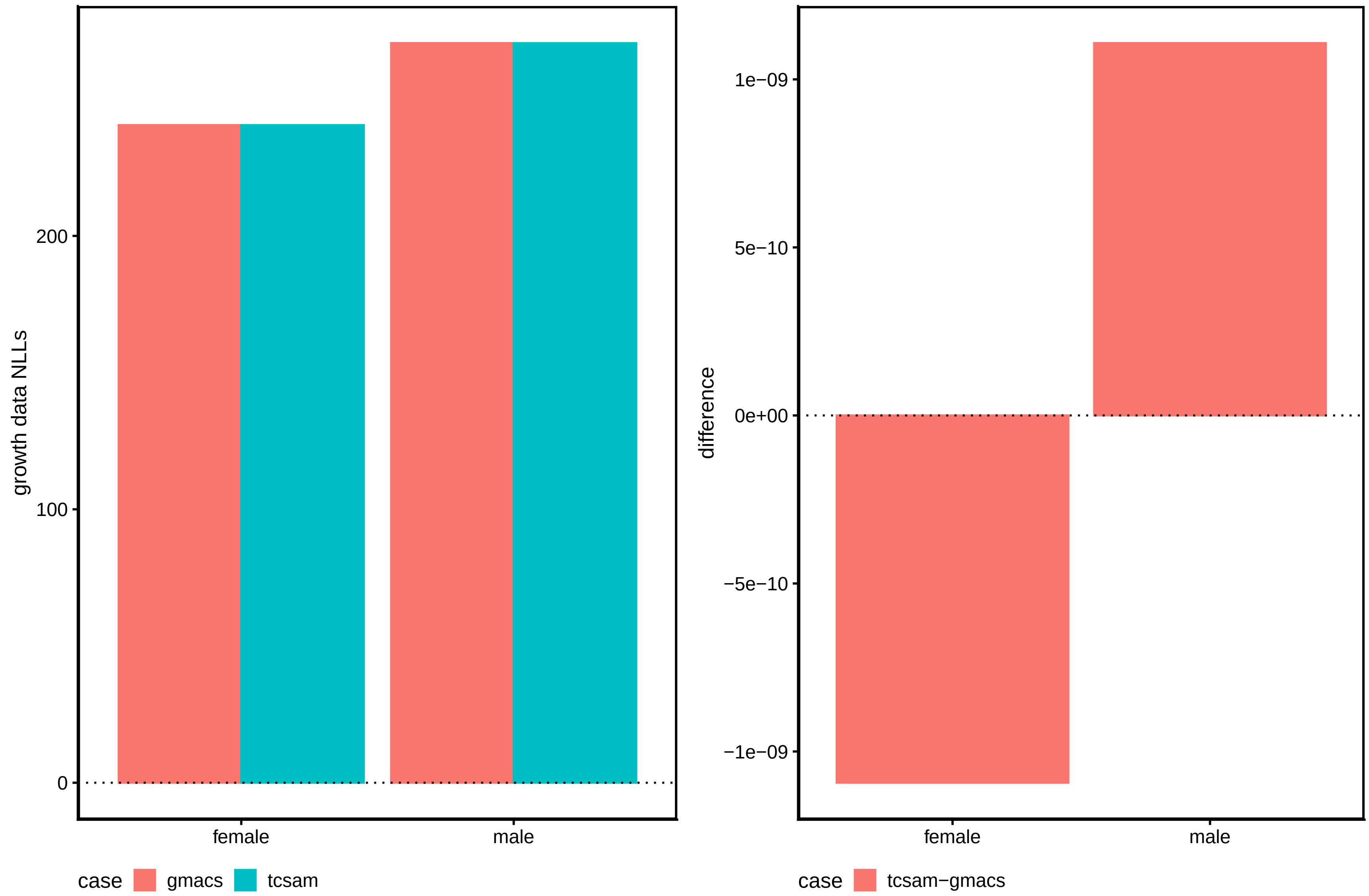

Figure 93. Comparison of summary negative log-likelihood (NLL) values for fits to sex-specific growth data from the GMACS and TCSAM02 models. Left: values; right: differences. These values are comparable between the model frameworks.

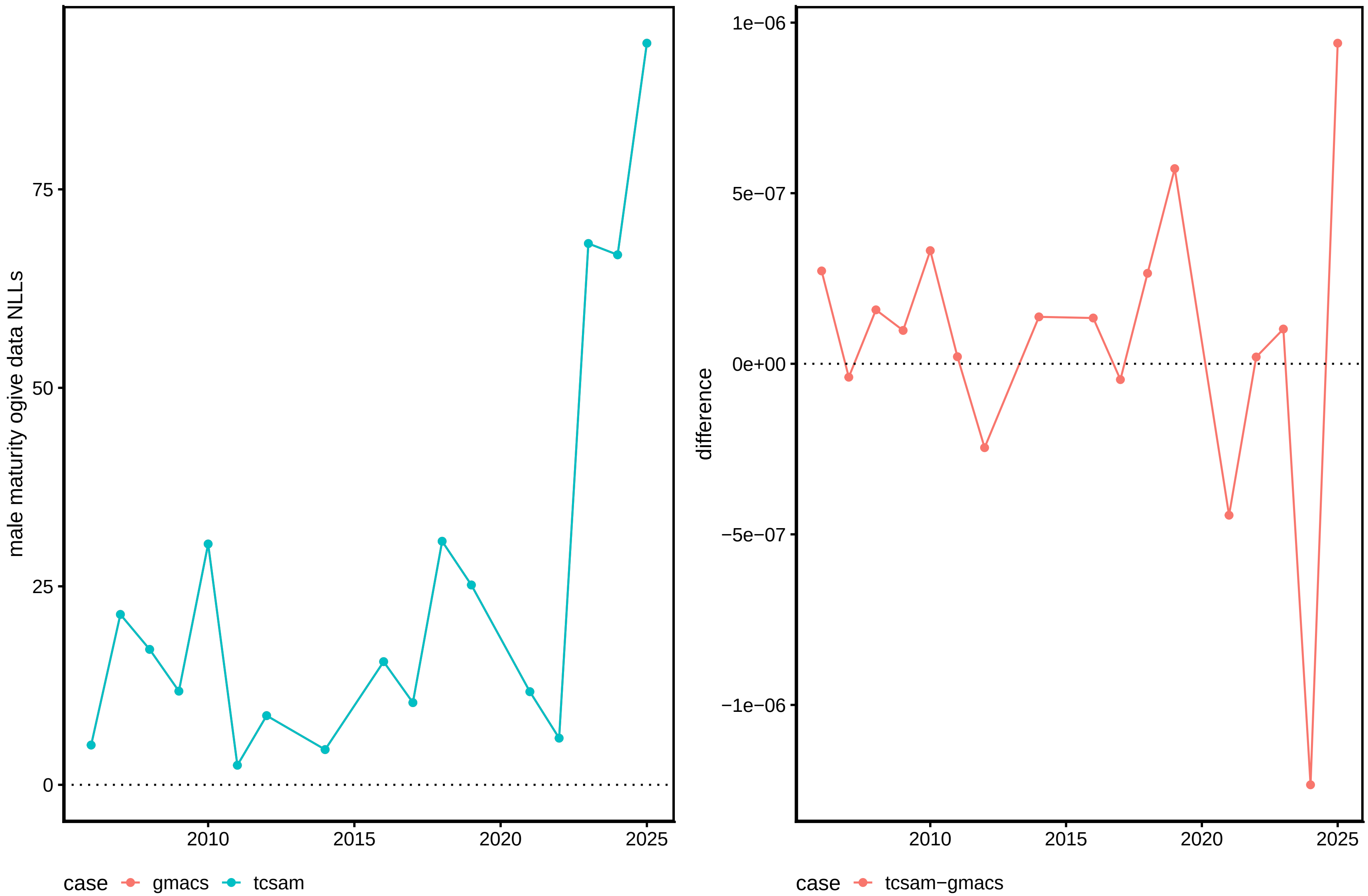

Figure 94. Comparison of summary negative log-likelihood (NLL) values for fits to male maturity ogive data from the GMACS and TCSAM02 models. Left: values; right: differences. These values are comparable between the model frameworks.

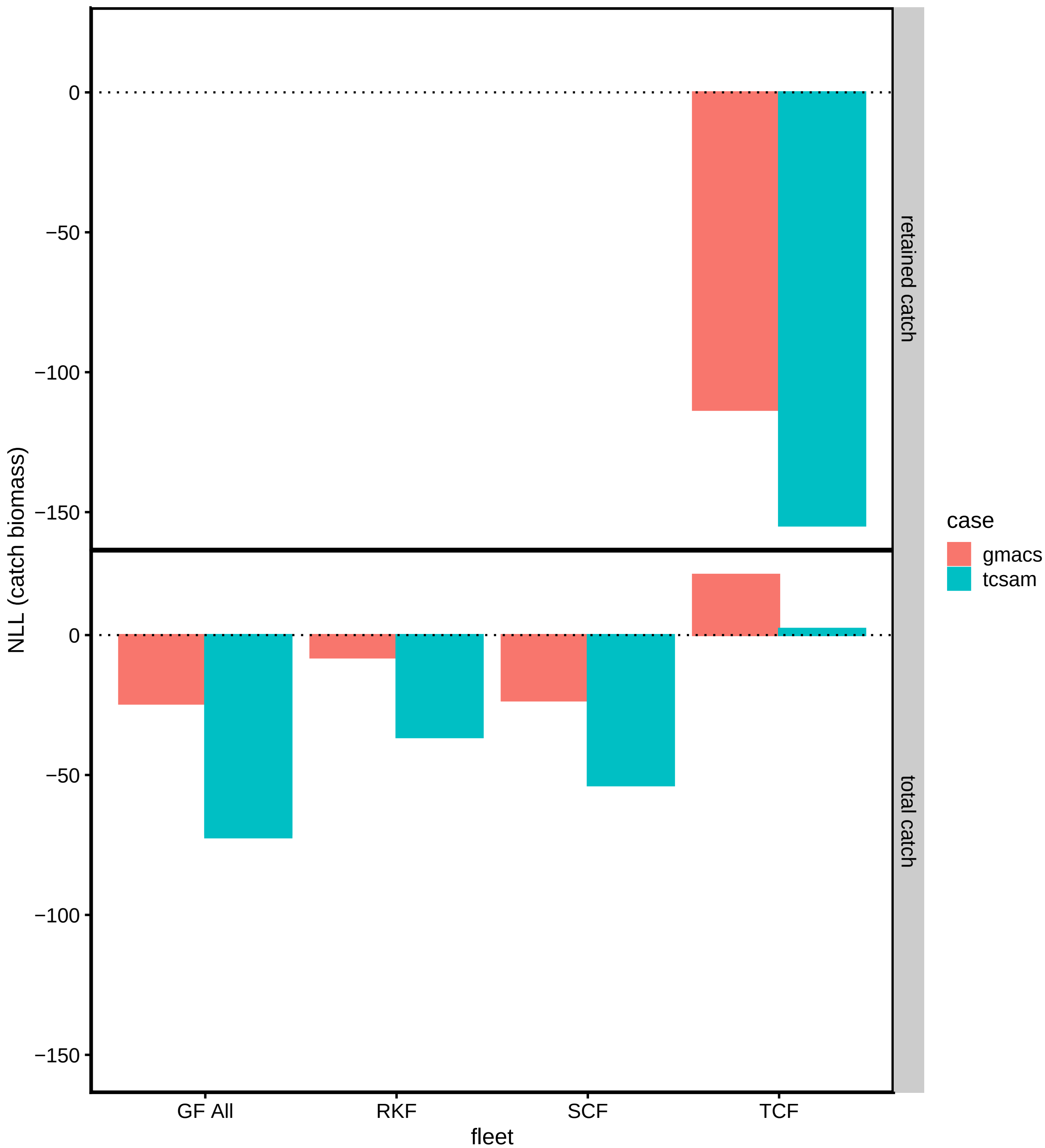

Figure 95. Comparison of summary negative log-likelihood (NLL) values for fishery catch biomass data from the GMACS and TCSAM02 models. Upper: retained catch; Lower: total catch. These values are **not** expected to agree between the models because constant terms in the NLL calculation are handled differently in the two model frameworks.

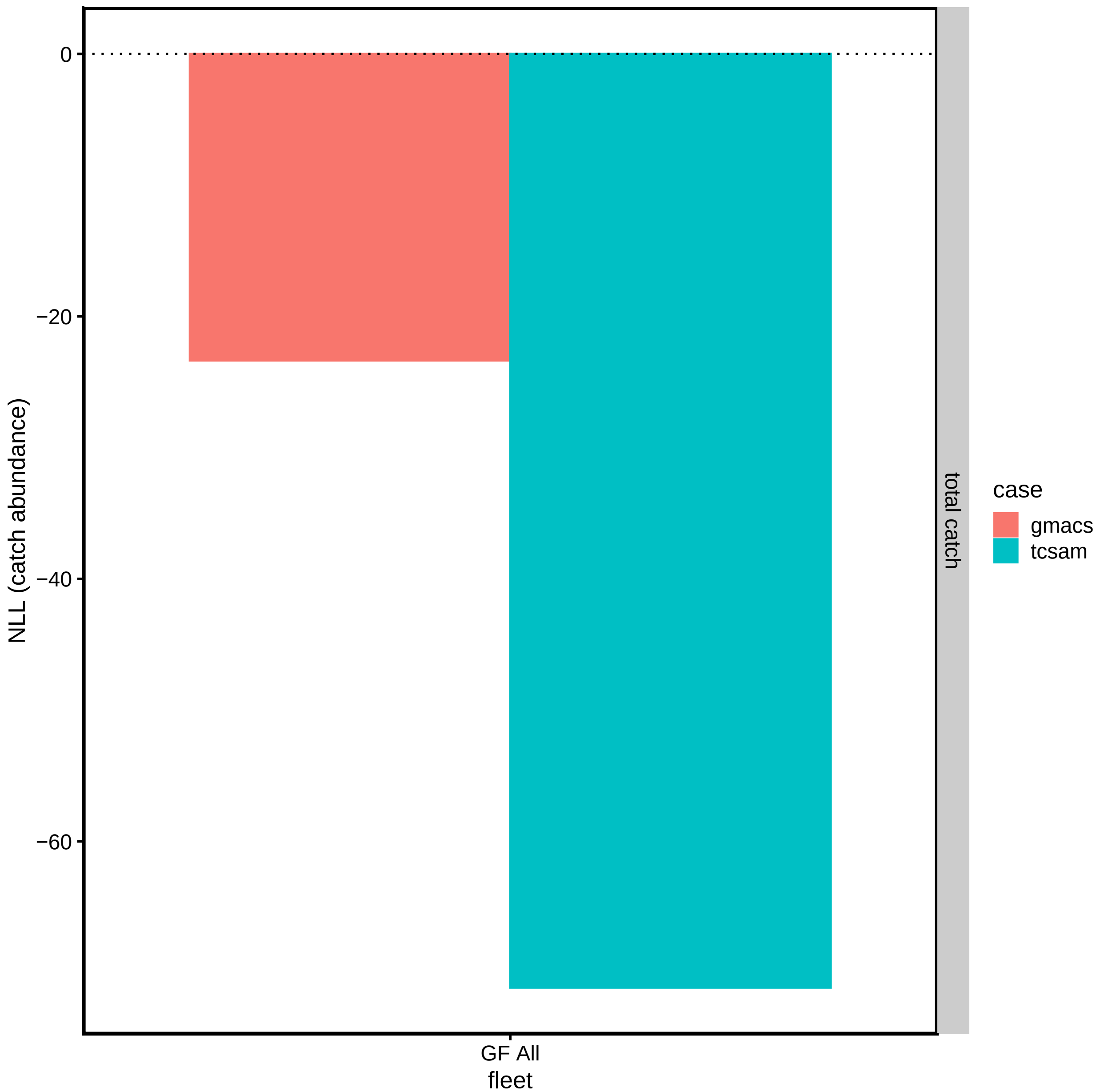

Figure 96. Comparison of summary negative log-likelihood (NLL) values for fishery catch abundance data from the GMACS and TCSAM02 models. Catch abundance is fit only from the groundfish fisheries. These values are **not** expected to agree between the models because constant terms in the NLL calculation are handled differently in the two model frameworks.

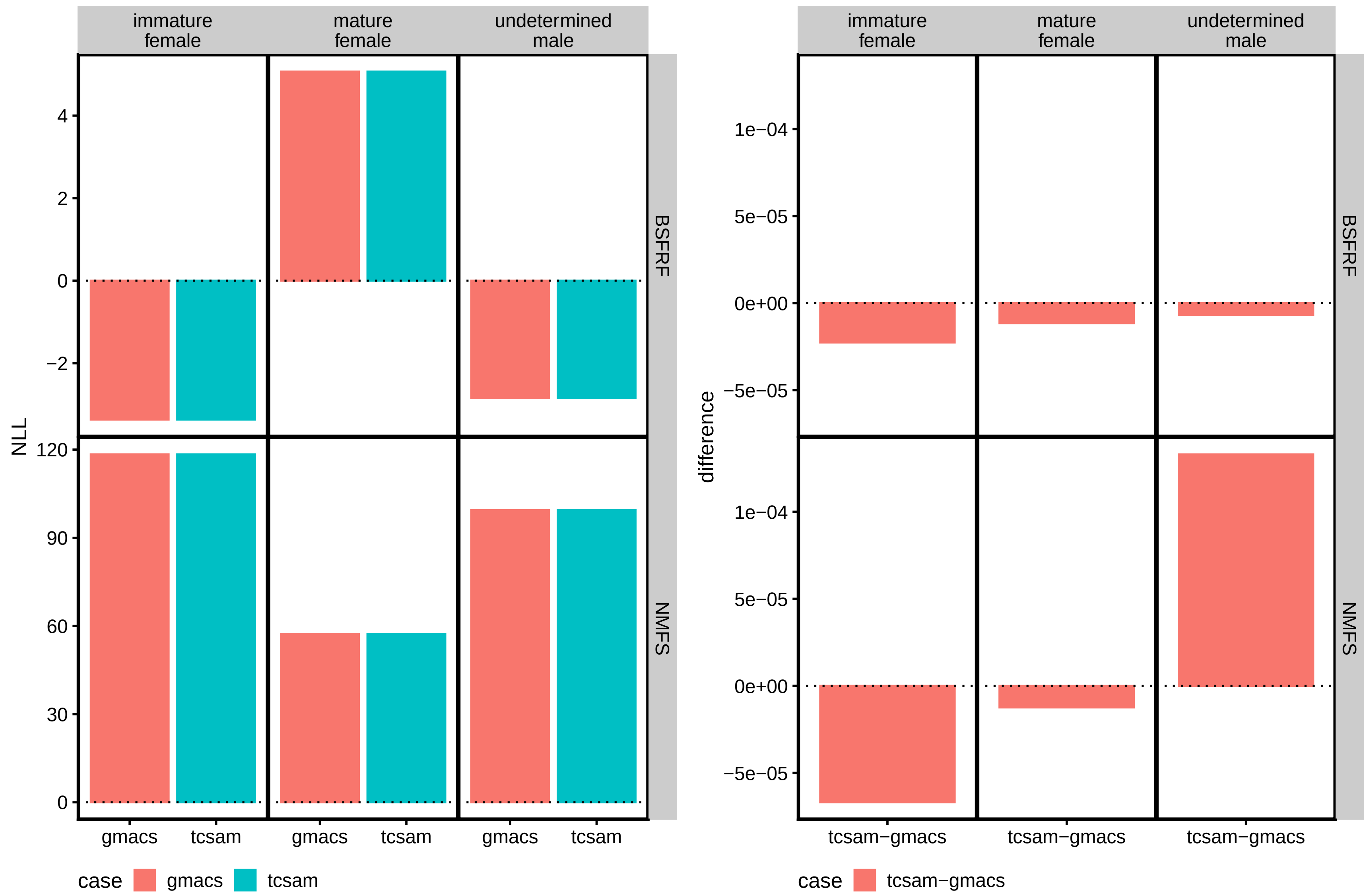

Figure 97. Comparison of summary negative log-likelihood (NLL) values for fits to survey biomass data from the GMACS and TCSAM02 models by fleet and biological category. Left: values; right: differences. These values are comparable.

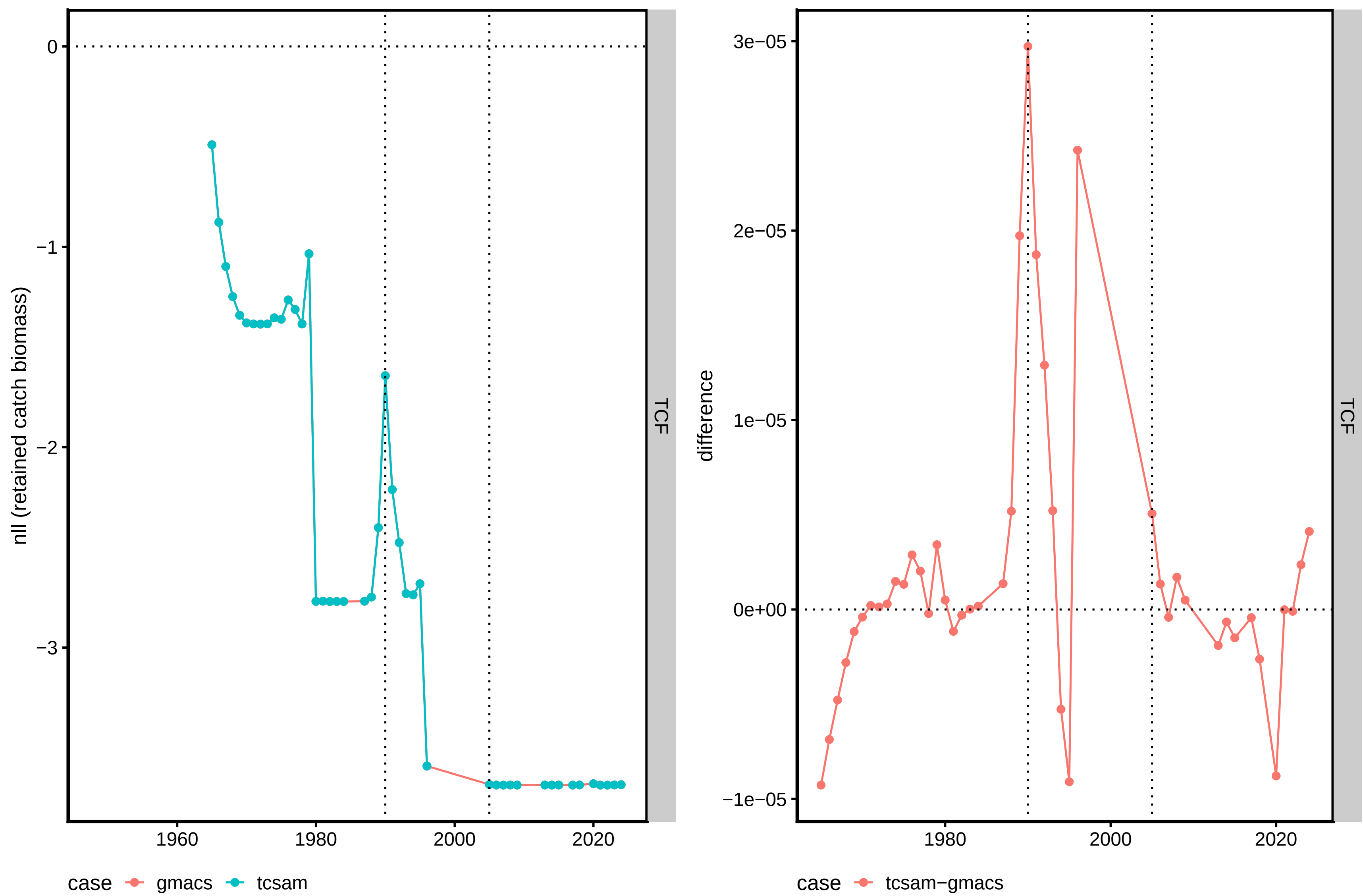

Figure 98. Comparison of summary negative log-likelihood (NLL) values for fits to fishery retained catch biomass data from the GMACS and TCSAM02 models. Left: values; right: differences. TCF: directed Tanner crab fishery. The vertical dotted lines indicate 1990 and 2005. These values are comparable.

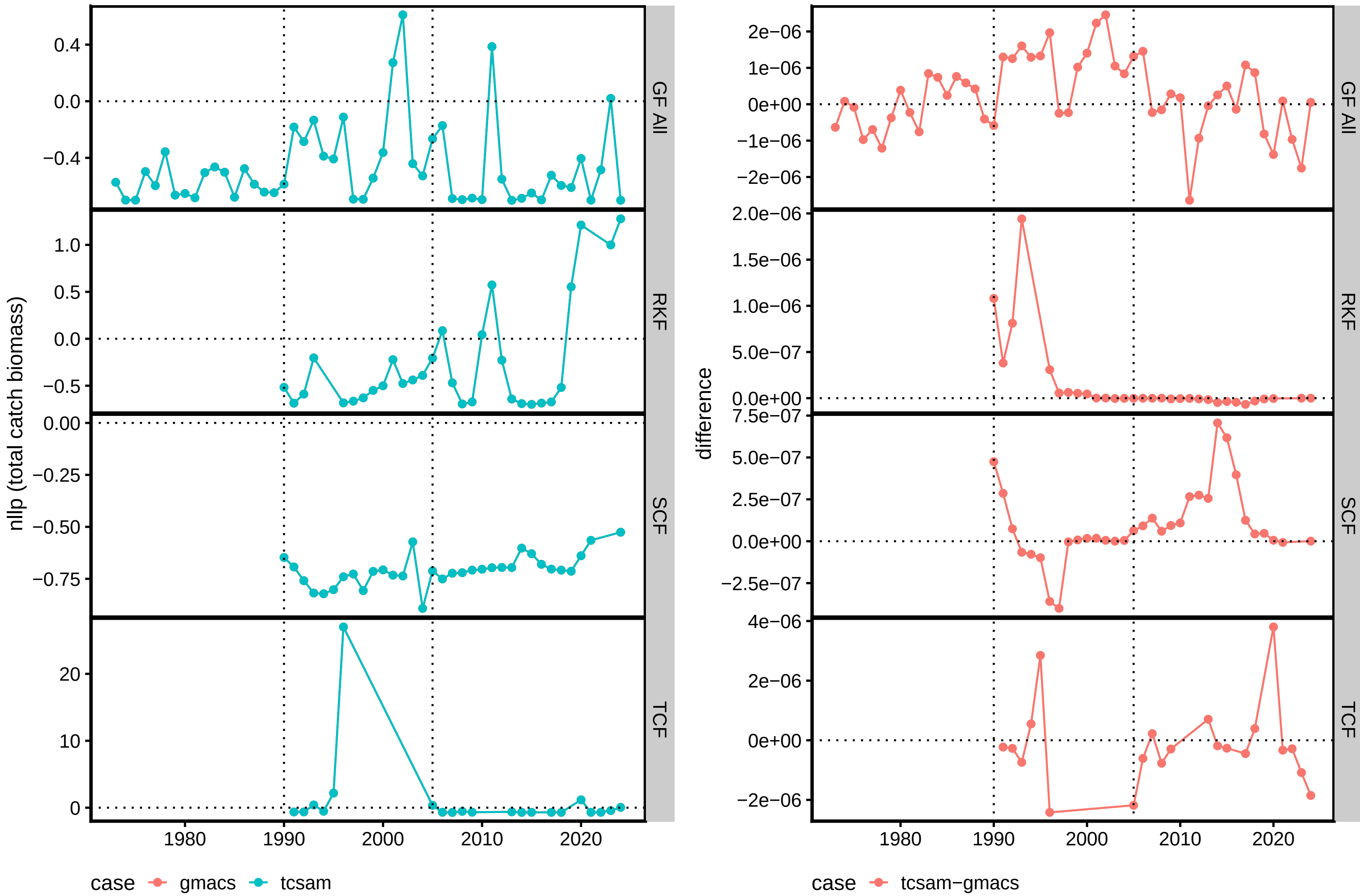

Figure 99. Comparison of summary negative log-likelihood (NLL) values for fits to fishery total catch biomass data from the GMACS and TCSAM02 models by fleet. Left: values; right: differences. TCF: directed Tanner crab fishery; SCF: snow crab fishery; RKF: BBRKC fishery; GF All: groundfish fisheries. The vertical dotted lines indicate 1990 and 2005. These values are comparable.

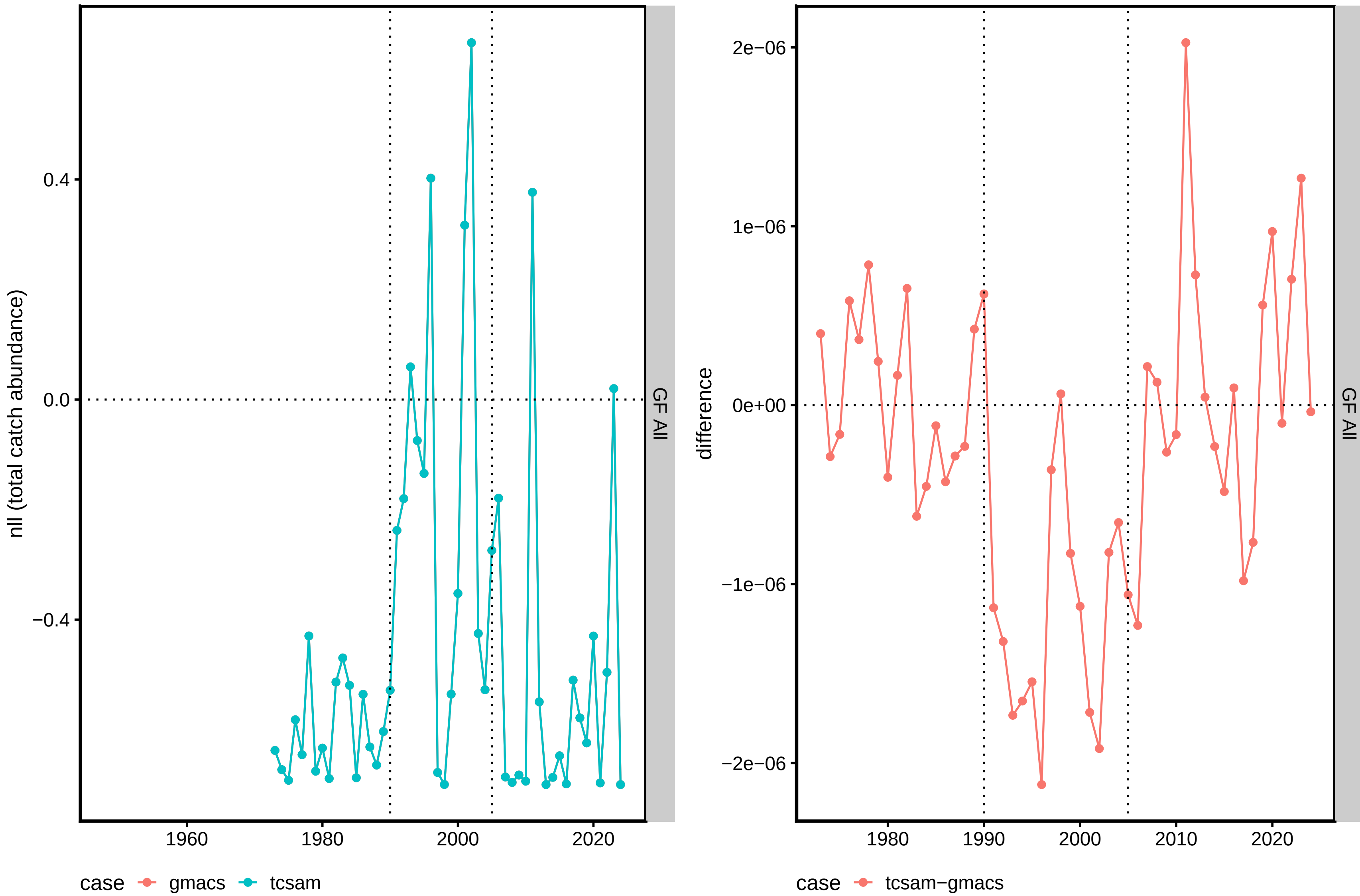

Figure 100. Comparison of summary negative log-likelihood (NLL) values for fits to fishery total catch abundance data from the GMACS and TCSAM02 models by fleet. Left: values; right: differences. Catch abundance data are fit only from the groundfish fisheries. The vertical dotted lines indicate 1990 and 2005. These values are comparable.

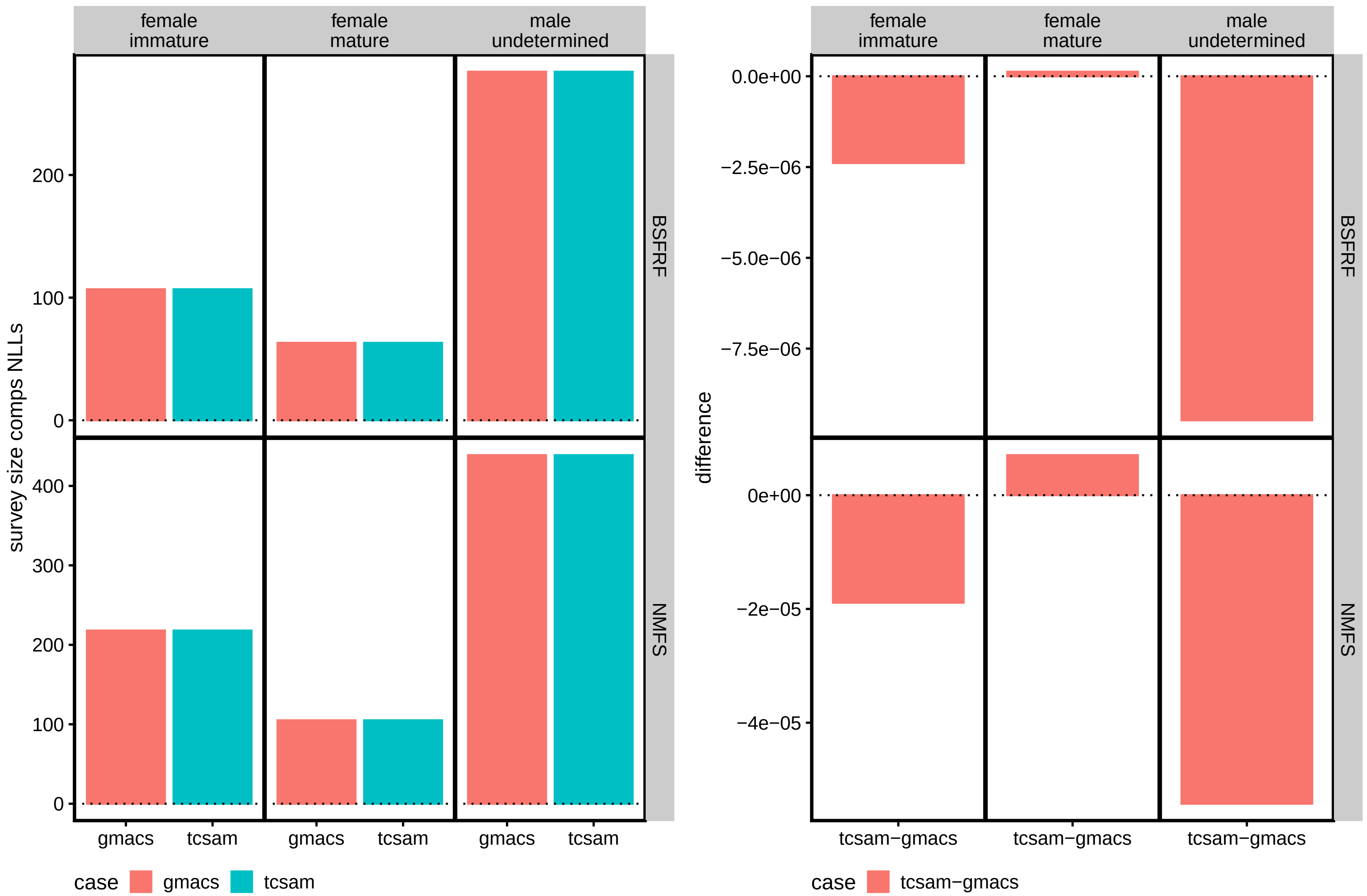

Figure 101. Comparison of negative log-likelihood (NLL) values for fits to survey size composition data from the GMACS and TCSAM02 models by fleet. Left: values; right: differences.

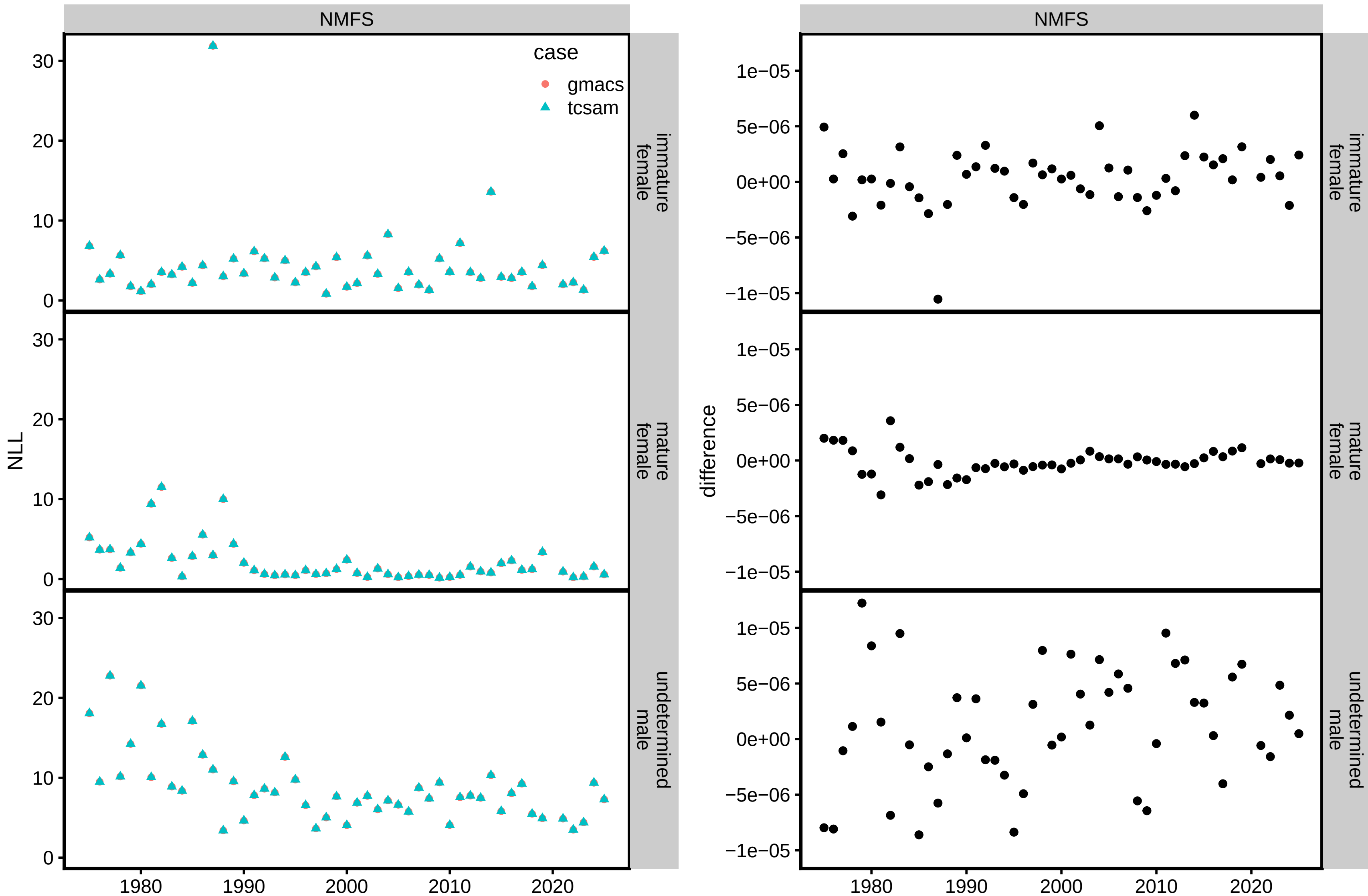

Figure 102. Comparison of negative log-likelihoods by year for Tanner crab size compositions from the NMFS surveys.Lefthand column: values; righthand column: differences from TCSAM02 model values.

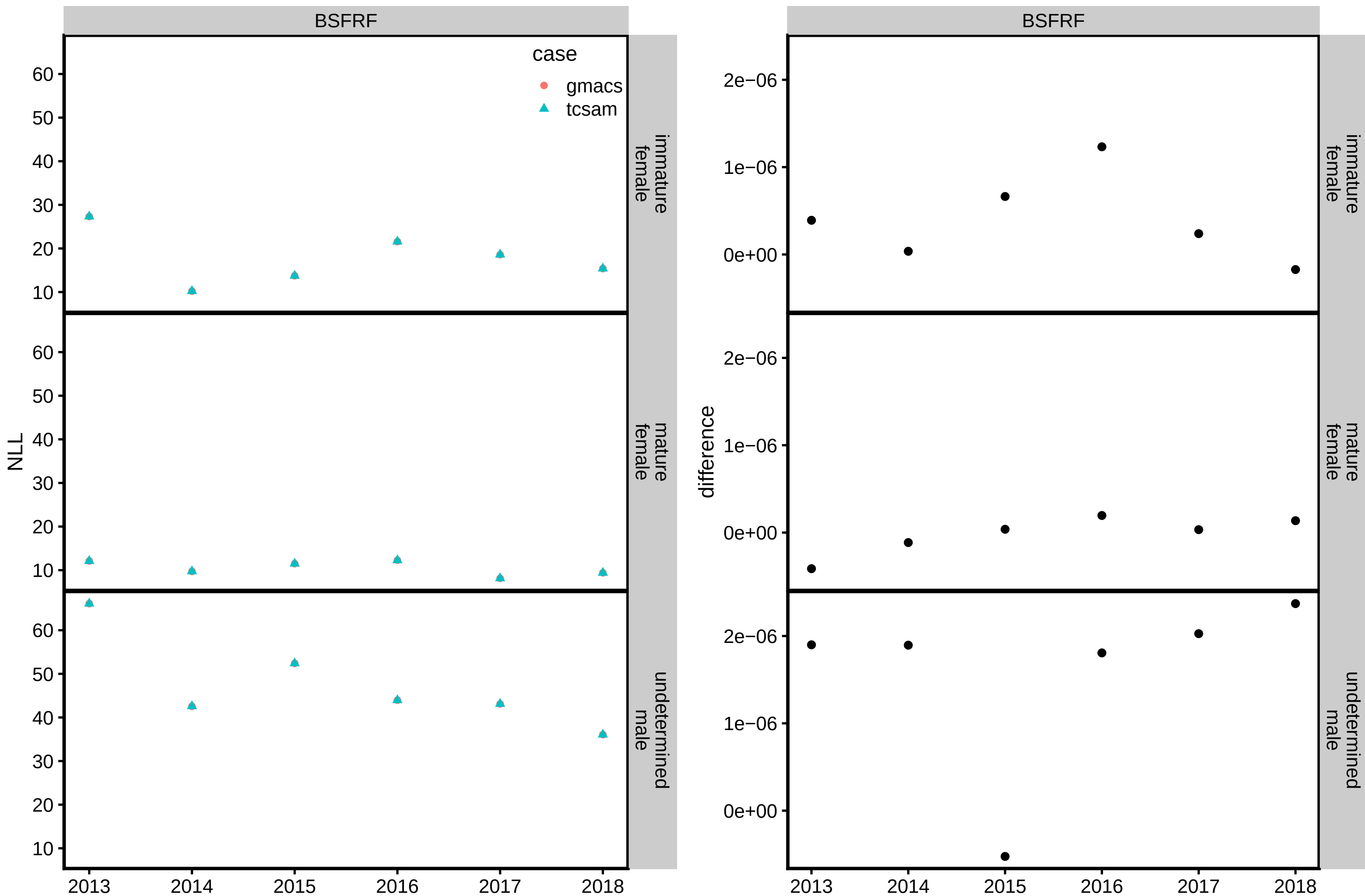

Figure 103. Comparison of negative log-likelihoods by year for Tanner crab size compositions from the BSFRF surveys.Lefthand column: values; righthand column: differences from TCSAM02 model values.

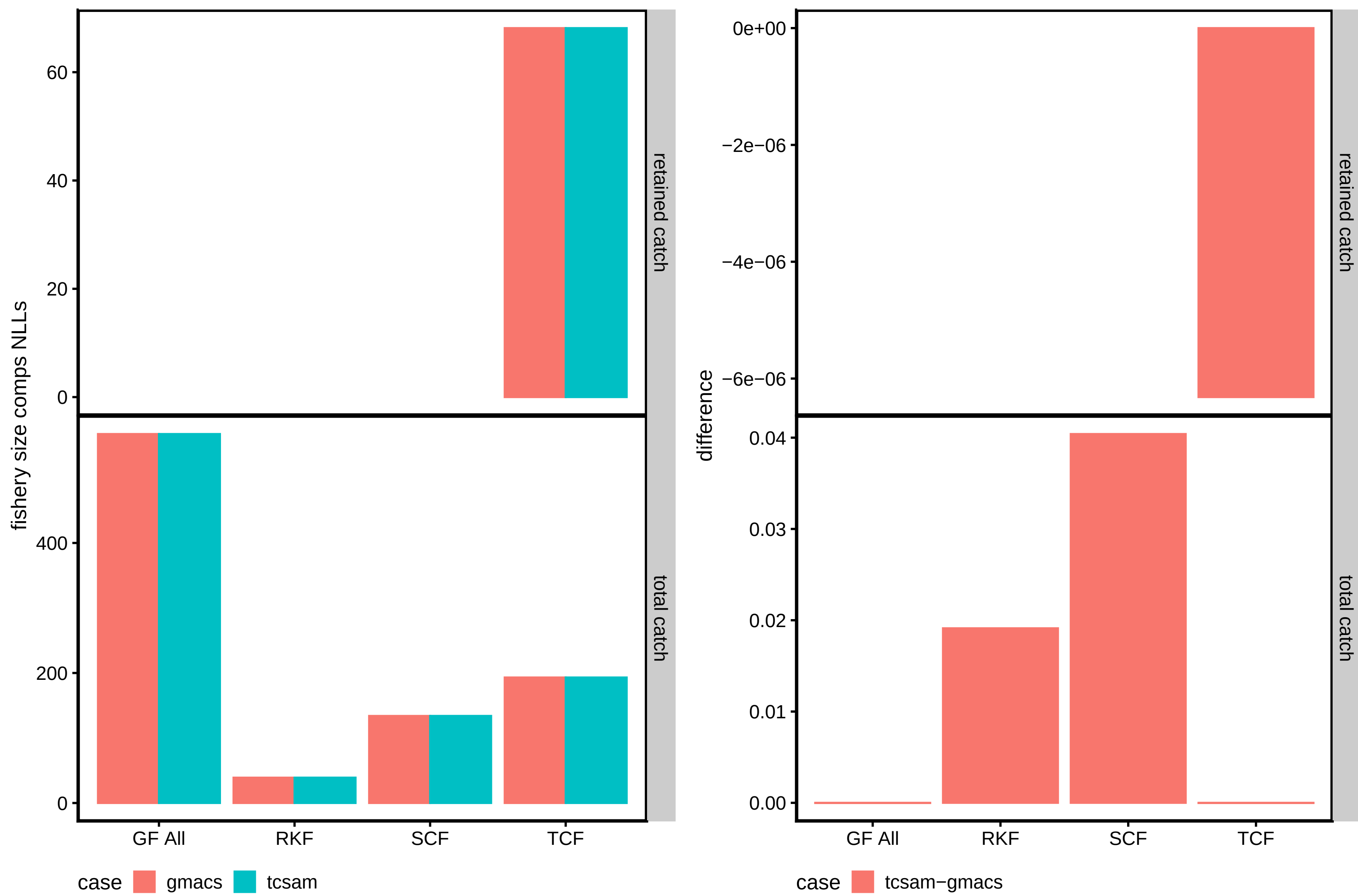

Figure 104. Comparison of negative log-likelihood (NLL) values for fits to fishery size composition data from the GMACS and TCSAM02 models by fleet. Left: values; right: differences.

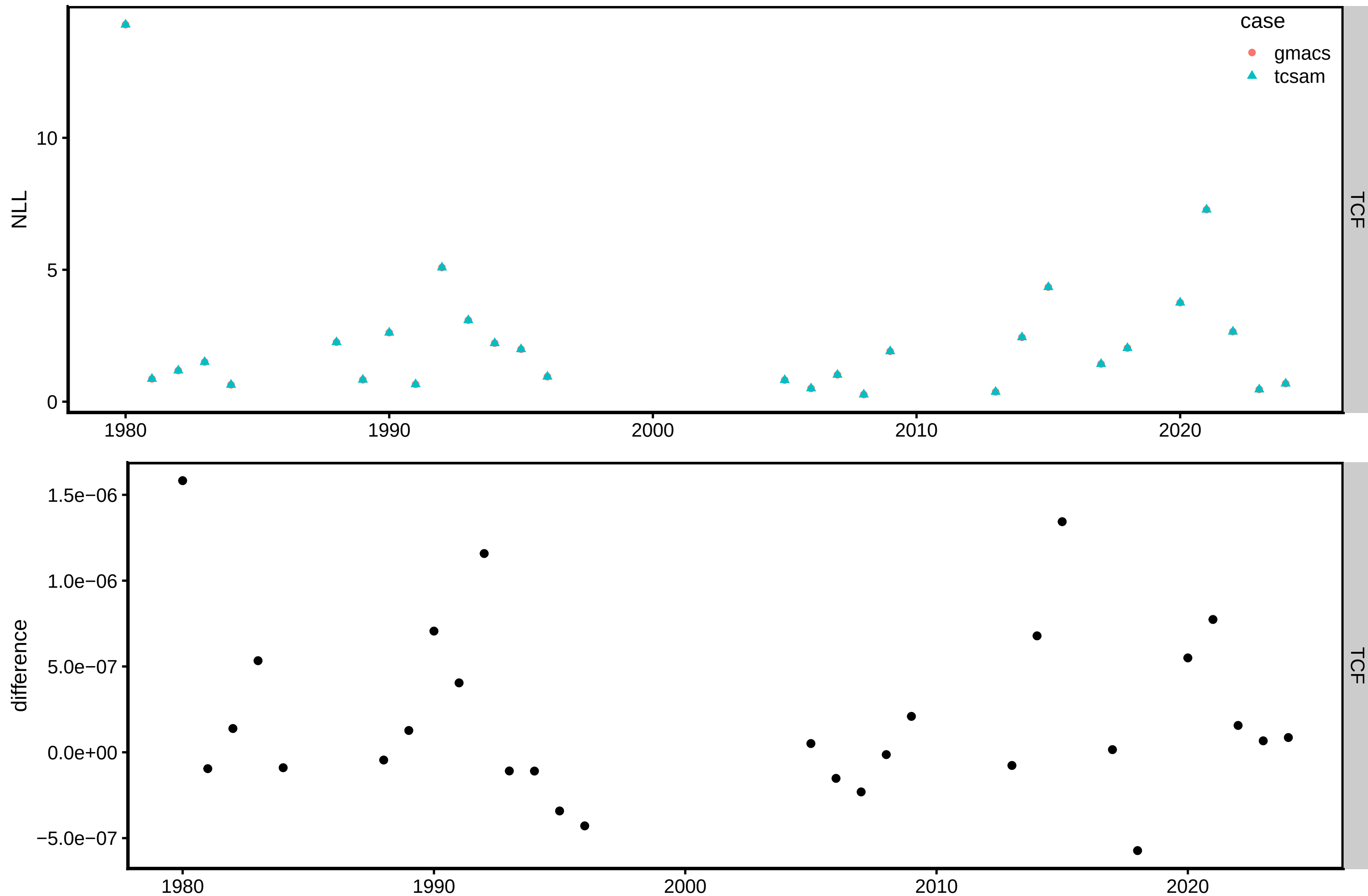

Figure 105. Comparison of negative log-likelihoods by year forTanner crab retained catch size comps in the directed fisheries.Upper plot: values; lower plot: differences from TCSAM02 model values.

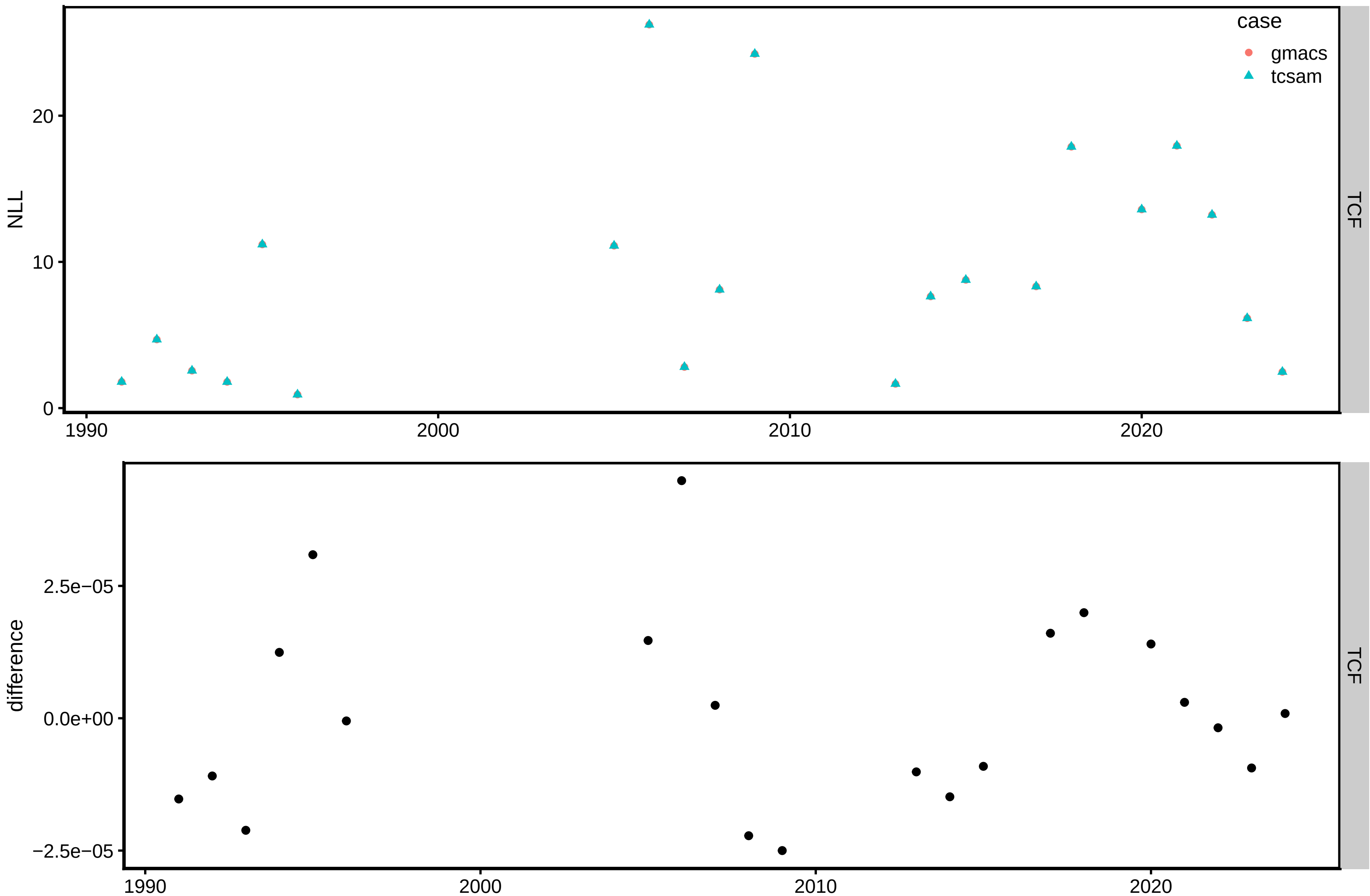

Figure 106. Comparison of negative log-likelihoods by year for Tanner crab total catch size comps in the directed fisheries.Upper plot: values; lower plot: differences from TCSAM02 model values.

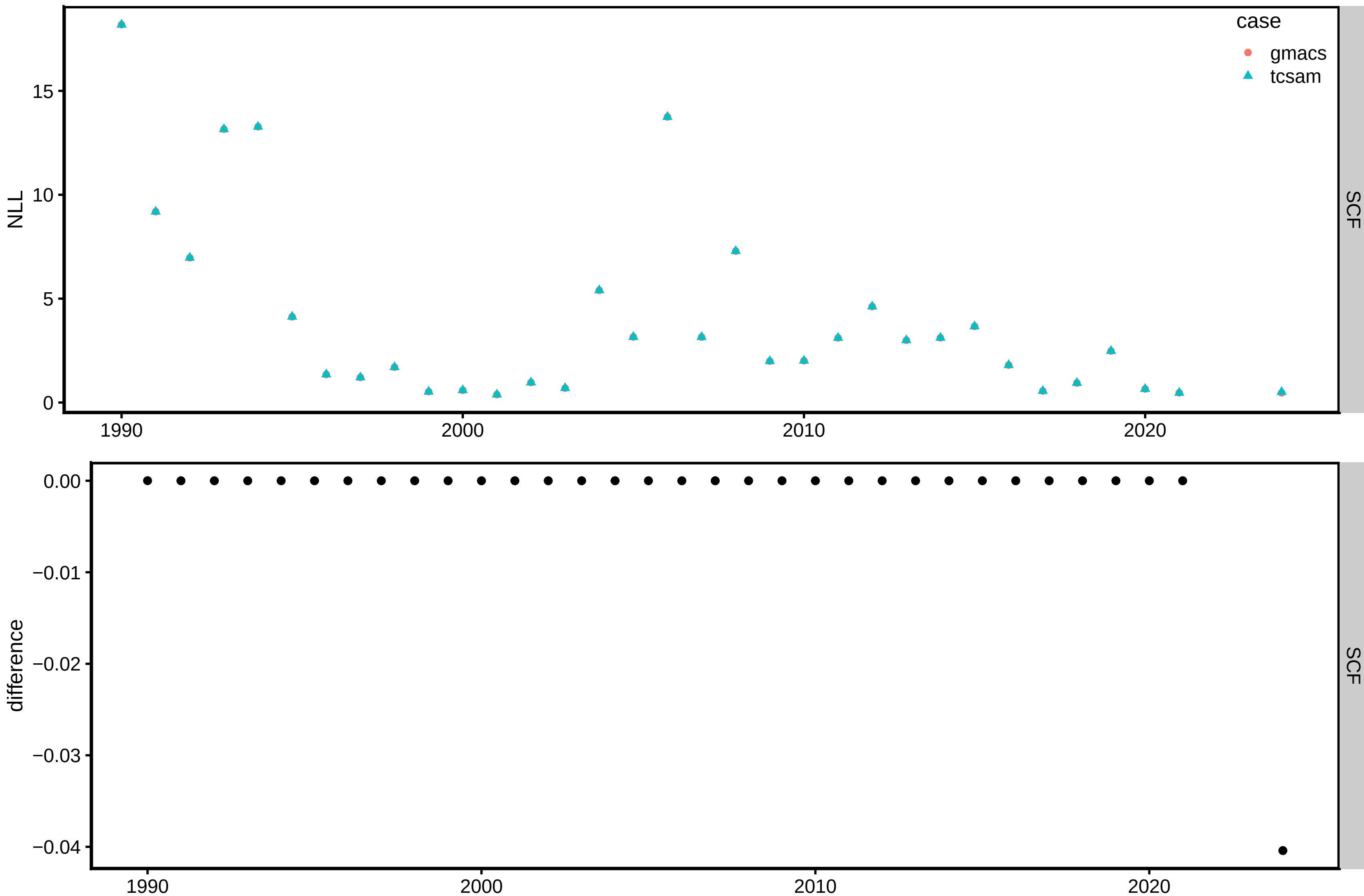

Figure 107. Comparison of negative log-likelihoods by year for Tanner crab total (by)catch size comps in the snow crab fishery.Upper plot: values; lower plot: differences from TCSAM02 model values.

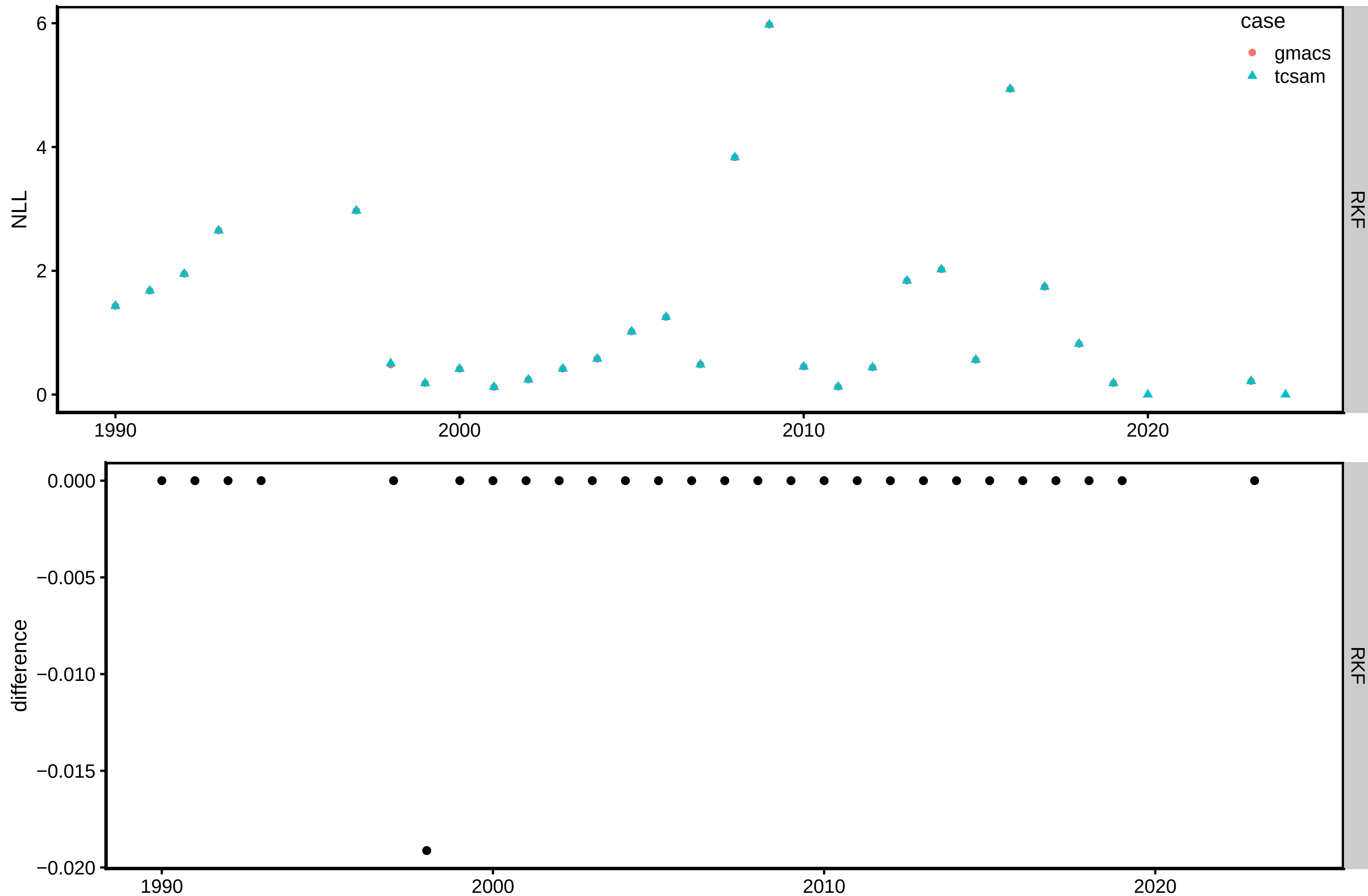

Figure 108. Comparison of negative log-likelihoods by year for Tanner crab total (by)catch size comps in the BBRKC fishery.Upper plot: values; lower plot: differences from TCSAM02 model values.

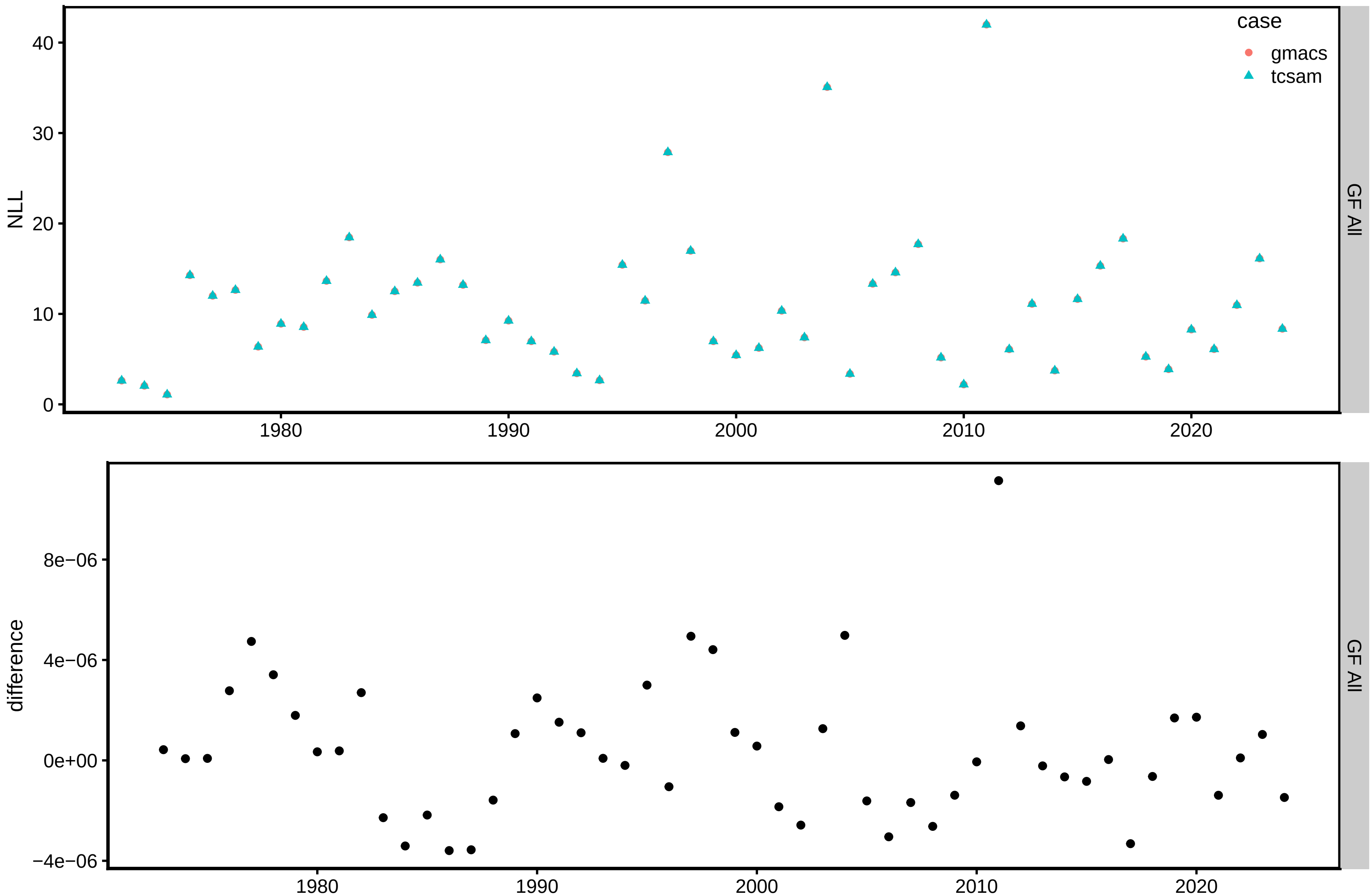

Figure 109. Comparison of negative log-likelihoods by year for Tanner crab total (by)catch size comps in the groundfish fisheries.Upper plot: values; lower plot: differences from TCSAM02 model values.

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