

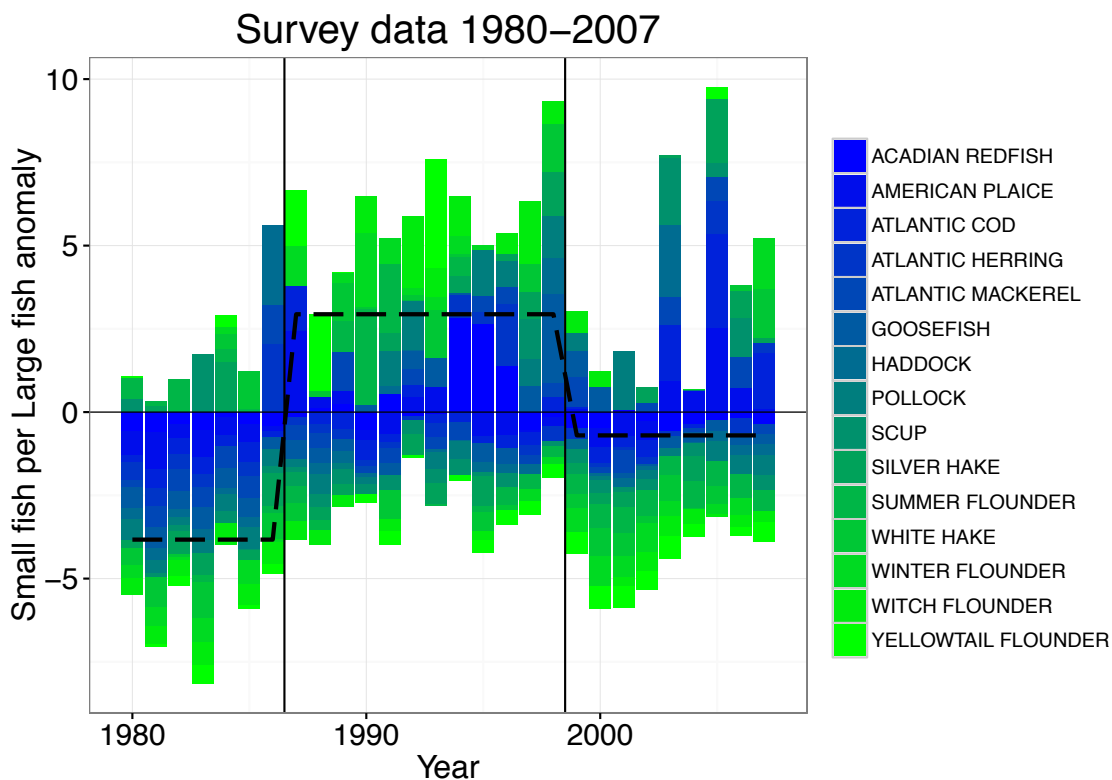
## Regime shifts in fish recruitment on the Northeast US continental shelf

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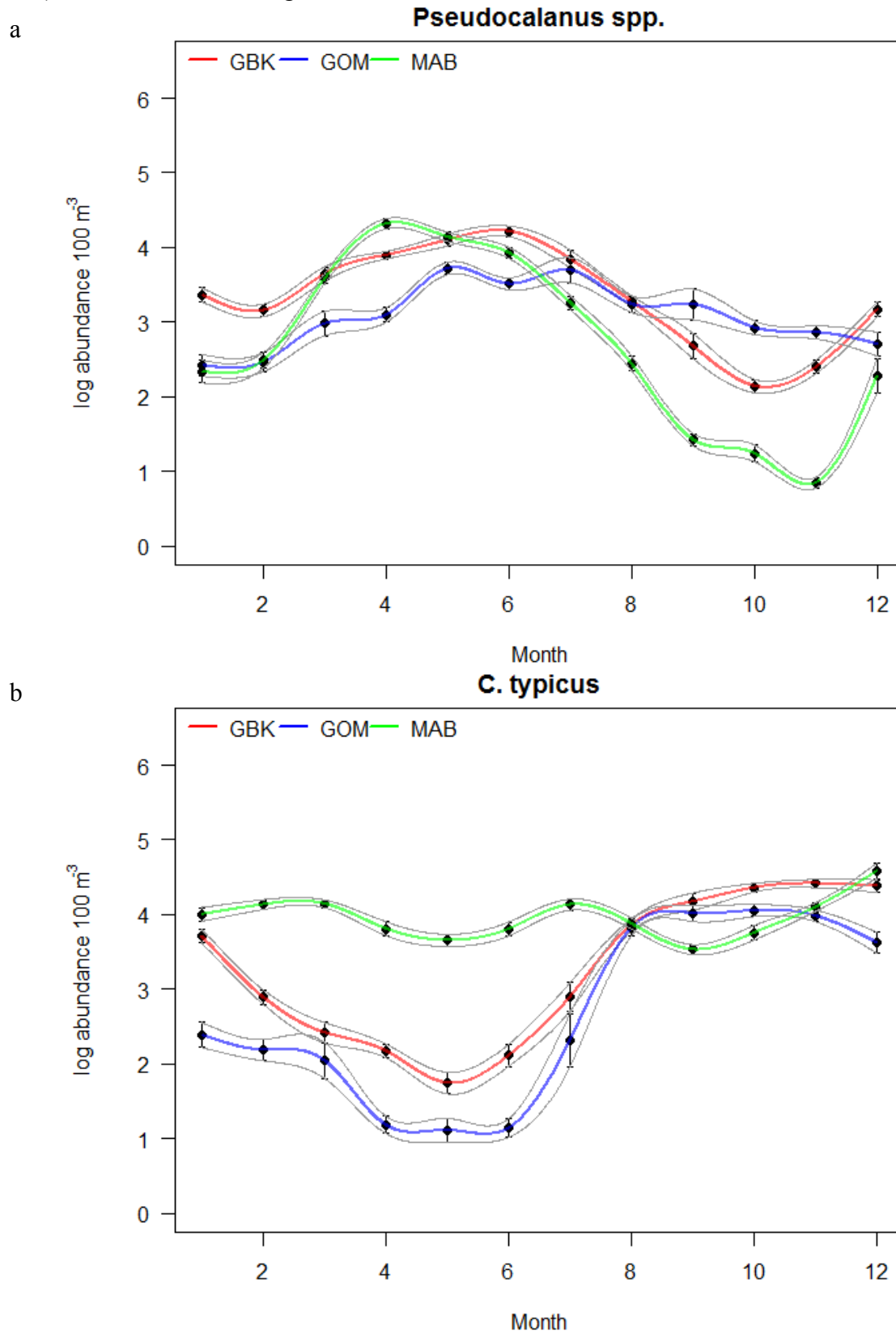
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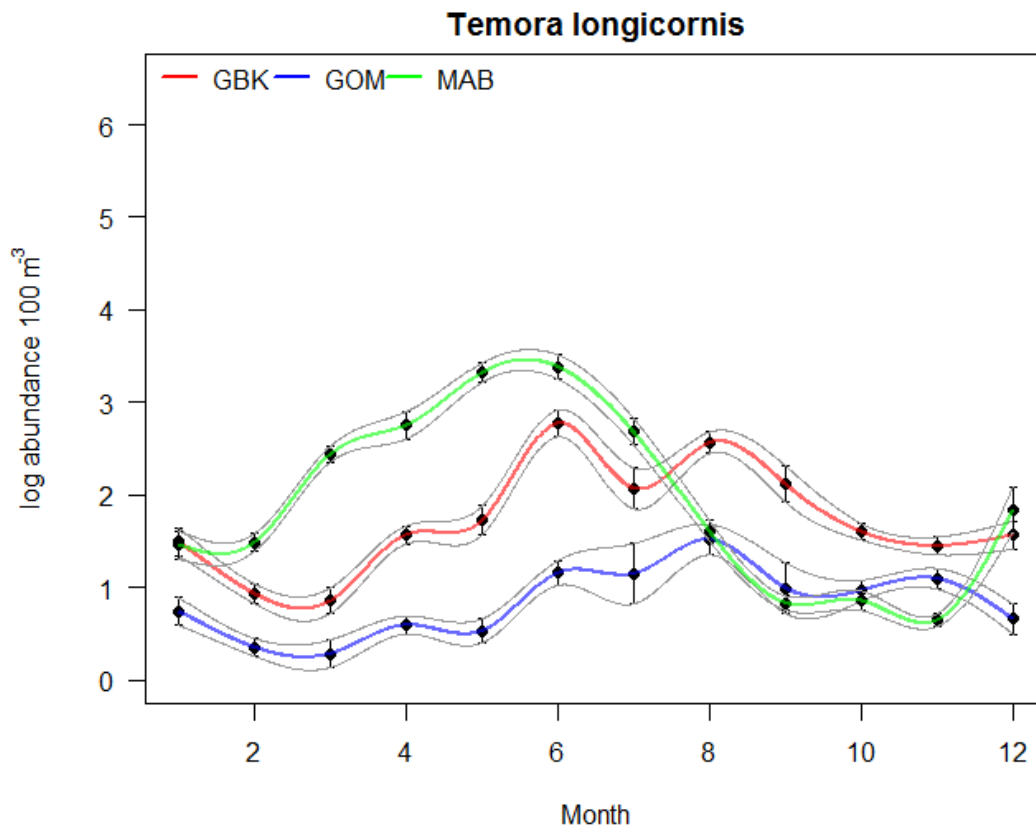
**Fig. S1.** Recruit per spawner anomalies for the survey dataset using the 20% percentile cutoff for defining an age-1 fish (i.e., fish shorter than the 20<sup>th</sup> percentile of length are labeled age-1 fish). The vertical lines are the regime shift change points as determined by the chronological clustering algorithm. The dashed line is the average total annual anomaly within each regime.



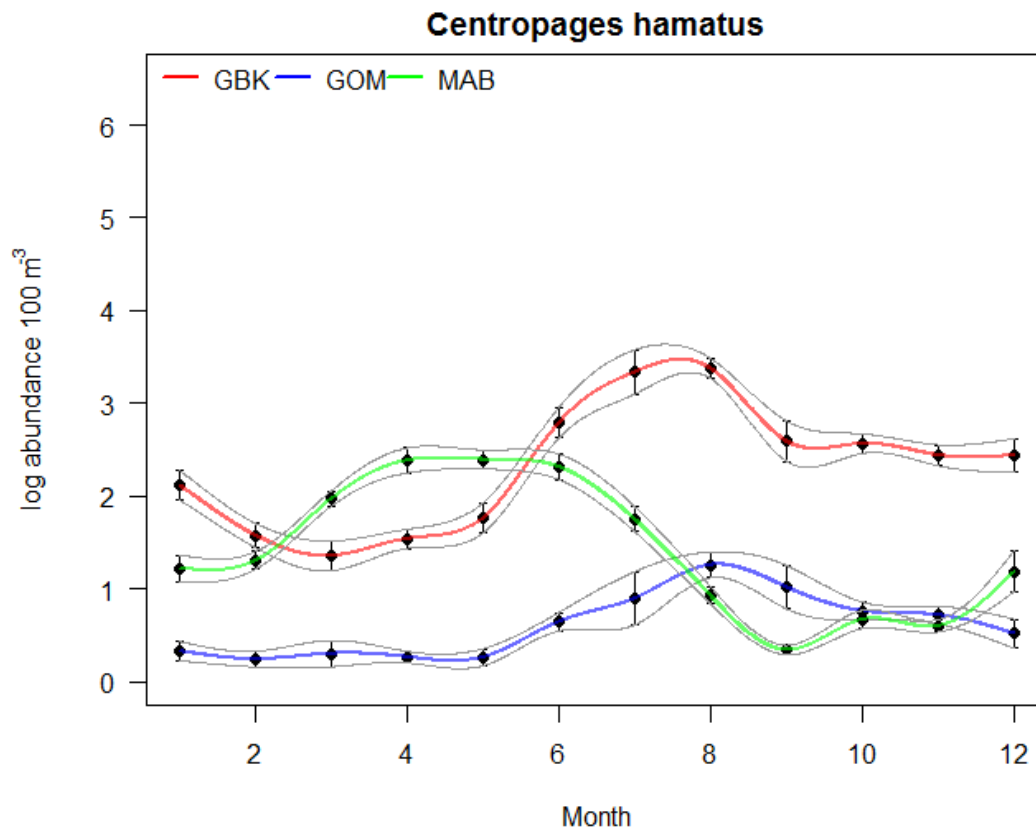
**Fig. S2.** Spline functions used to compute daily anomalies from monthly log abundance values for (a) *Pseudocalanus* spp., (b) *Centropages typicus*, (c) *Temora longicornis*, (d) *Centropages hammatius*. The mean anomaly (colored) and the 95% confidence intervals (error bars) are shown for each region.



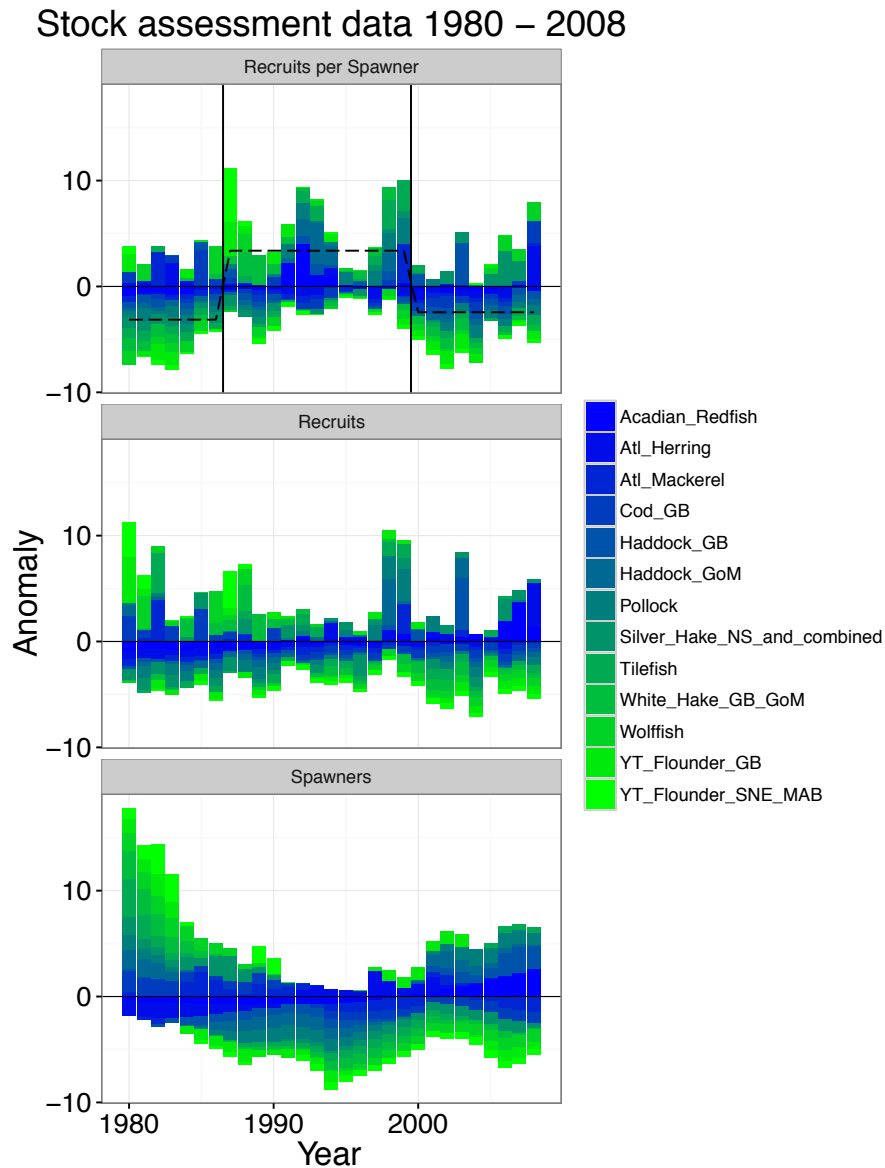
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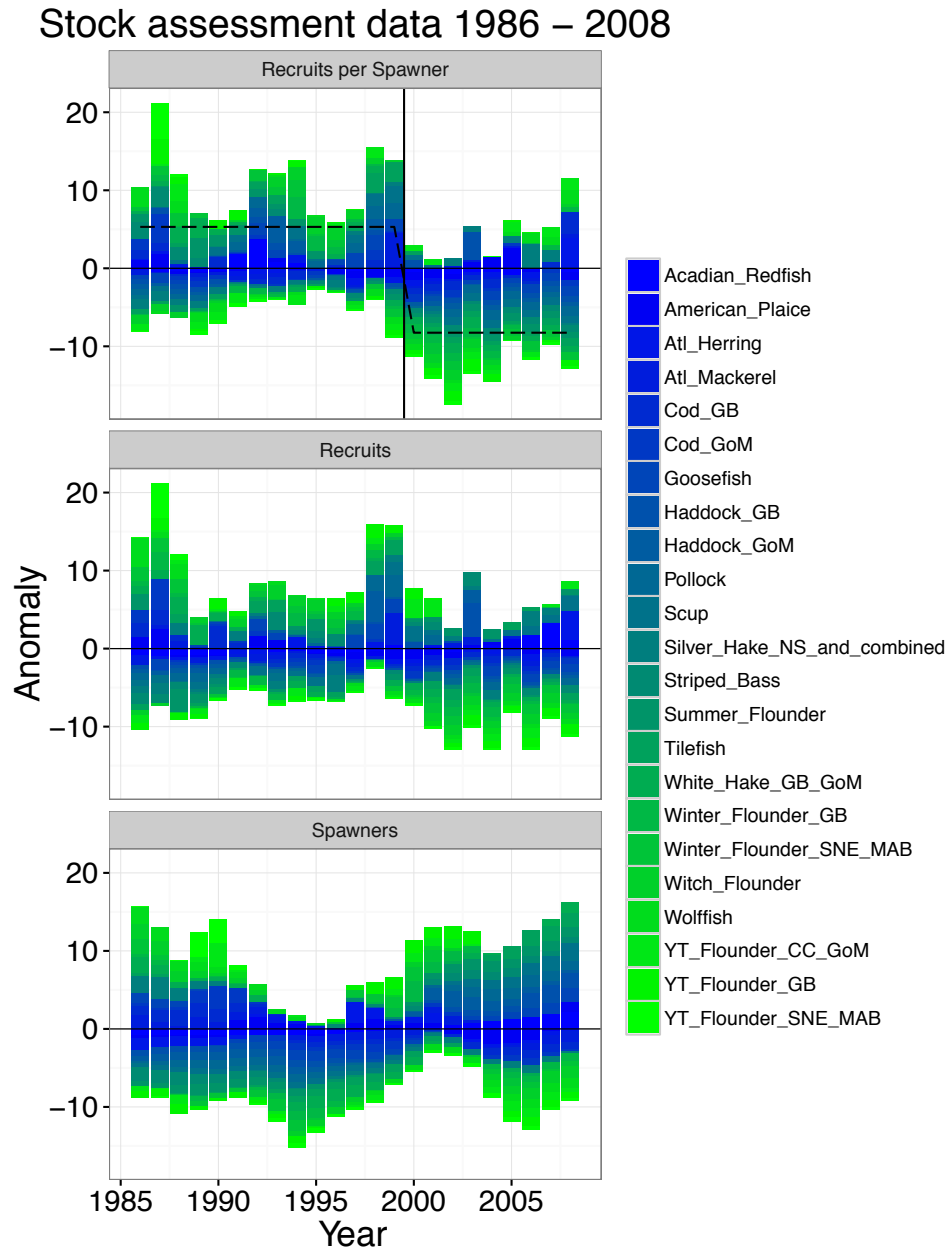
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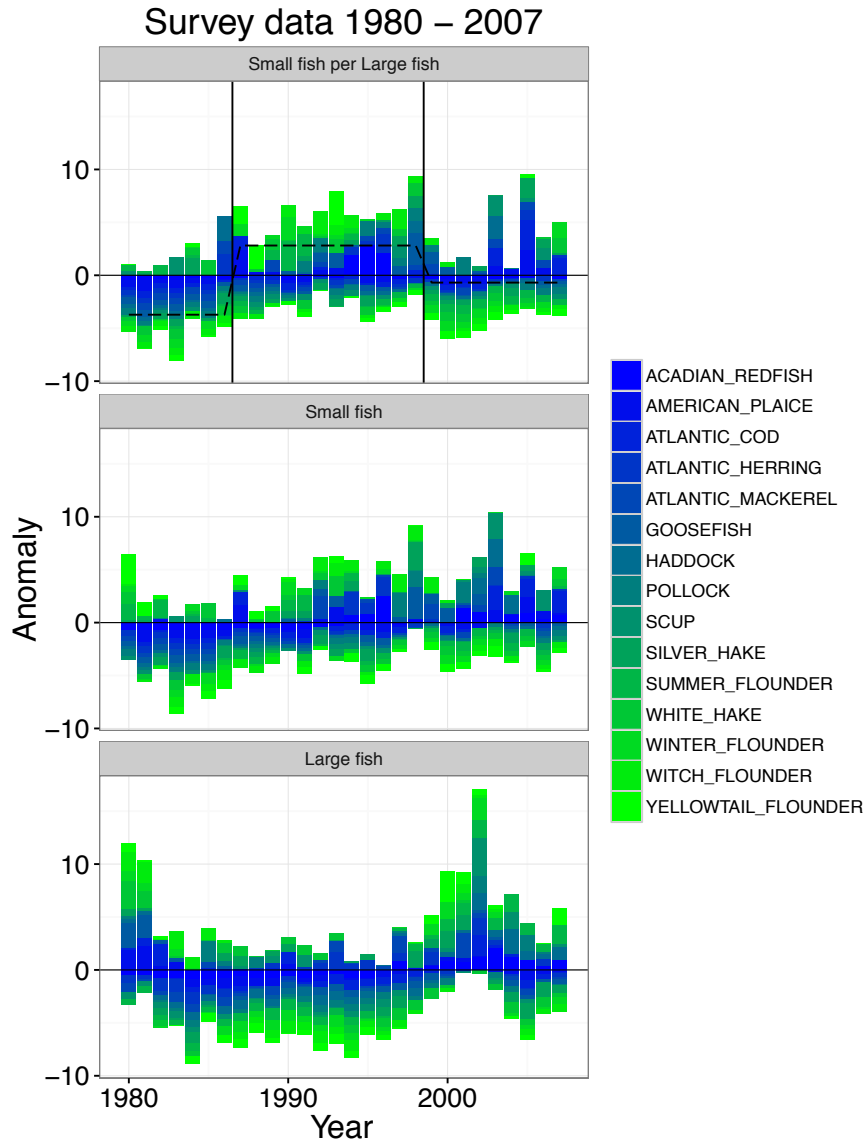
**Fig. S3.** Recruitment anomalies for stocks with stock assessments from 1980 to 2008. The top panel is recruits per spawner anomaly, the middle panel is recruits, and the bottom panel is spawners. Vertical lines are the regime shift change points as determined by the chronological clustering algorithm. The dashed line is the average total annual anomaly within each regime.



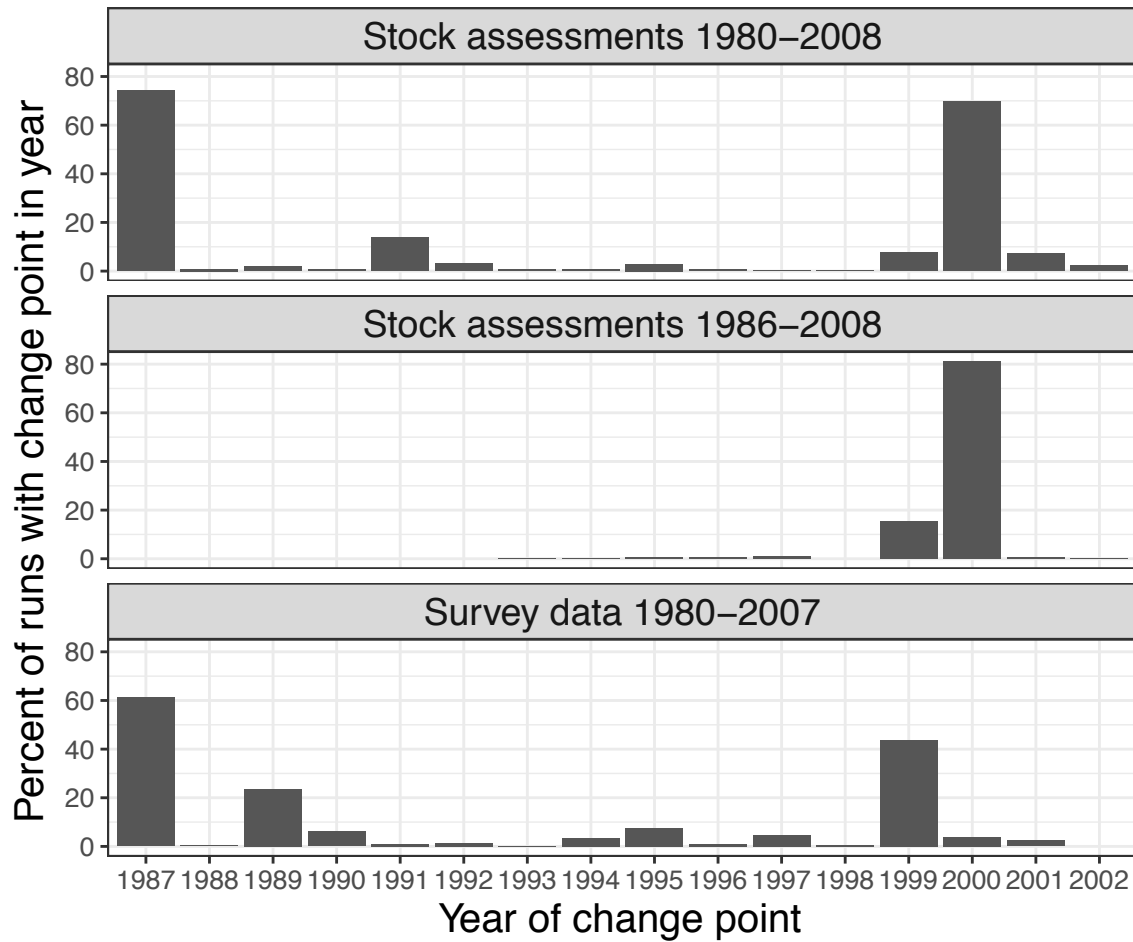
**Fig. S4.** Recruitmnet anomalies for stocks with stock assessments from 1986 to 2008. The top panel is recruits per spawner anomaly, the middle panel is recruits, and the bottom panel is spawners. Vertical lines are the regime shift change points as determined by the chronological clustering algorithm. The dashed line is the average total annual anomaly within each regime.



**Fig. S5.** Recruitment anomalies as estimated using data from the NEFSC bottom trawl survey. The top panel is small fish per large fish anomaly, the middle panel is recruits, and the bottom panel is spawners. Vertical lines are the regime shift change points as determined by the chronological clustering algorithm. The dashed line is the average total annual anomaly within each regime.



**Fig. S6.** Bootstrap analysis of change point years. One thousand bootstrap replicates were generated for each data set by randomly selecting species time series with replacement for inclusion in the bootstrap dataset. The chronological clustering algorithm was then applied to each bootstrapped dataset and the change point years were recorded. We find that the most common change point years of the bootstrap analysis (1987, 1999, and 2001) correspond to the same years in which the change points were found in the real data set, suggesting that the change point years are robust to the removal of any single species or stock.



**Fig. S7.** Copepod abundance (total abundance of top five taxa) anomaly time series. Vertical lines denote regime changepoints.

