Supplemental Figures

A collage of different graphs

Description automatically generated with medium confidenceSupplemental Figure 1. Number of POP and HSP pairs found in 100 simulations for treatments that sampled 100 individuals annually, where each row depicts a treatment for the number of years at the end of the time series that the sampling was conducted.

A screenshot of a graph

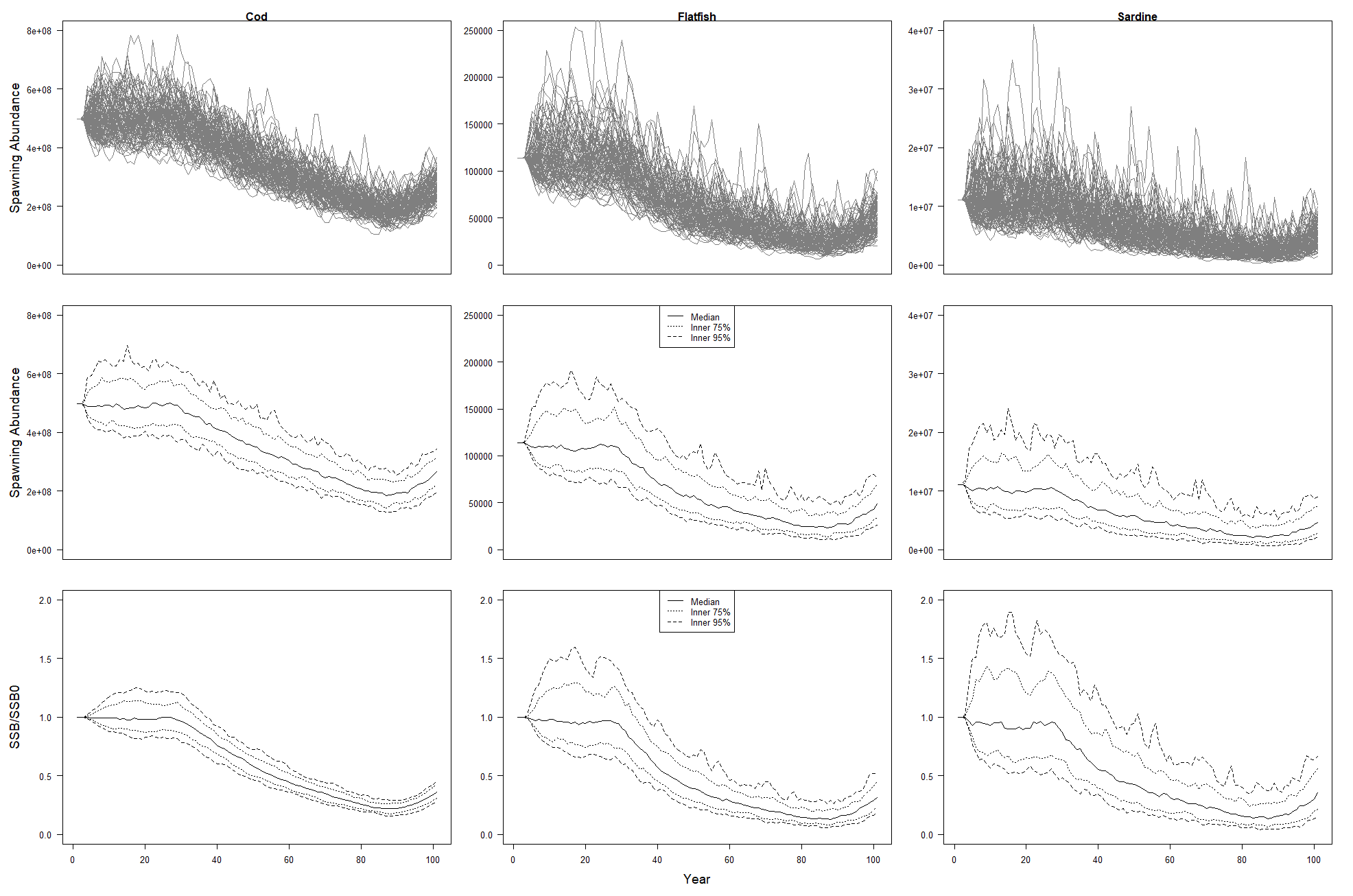
Description automatically generated

Supplemental Figure 2. Number of POP and HSP pairs found in 100 simulations for treatments that sampled 1,000 individuals annually, where each row depicts a treatment for the number of years at the end of the time series that the sampling was conducted.

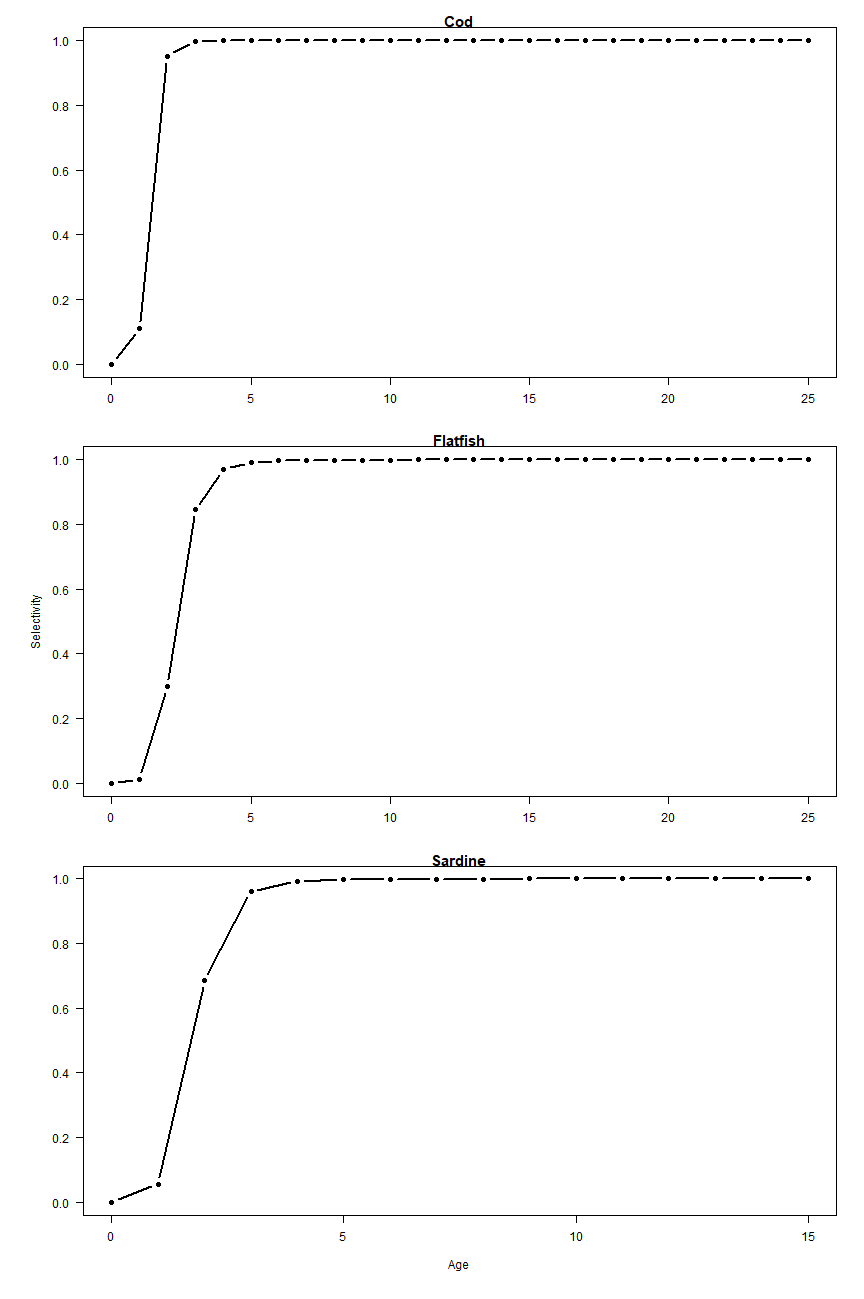
A collage of different graphs

Description automatically generated with medium confidence

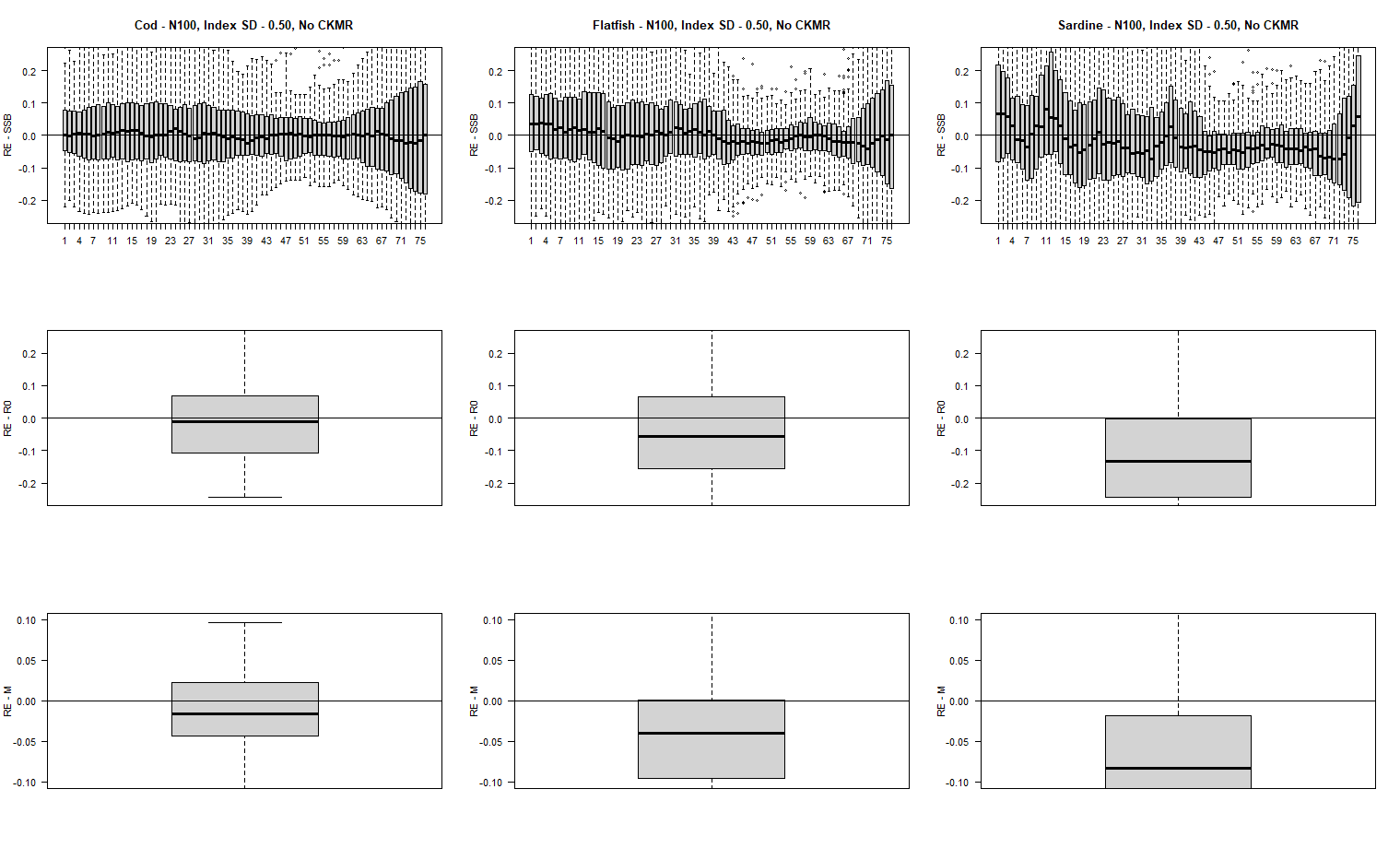
Supplemental Figure 3. Number of POP and HSP pairs found in 100 simulations for treatments that sampled 5,000 individuals annually, where each row depicts a treatment for the number of years at the end of the time series that the sampling was conducted.



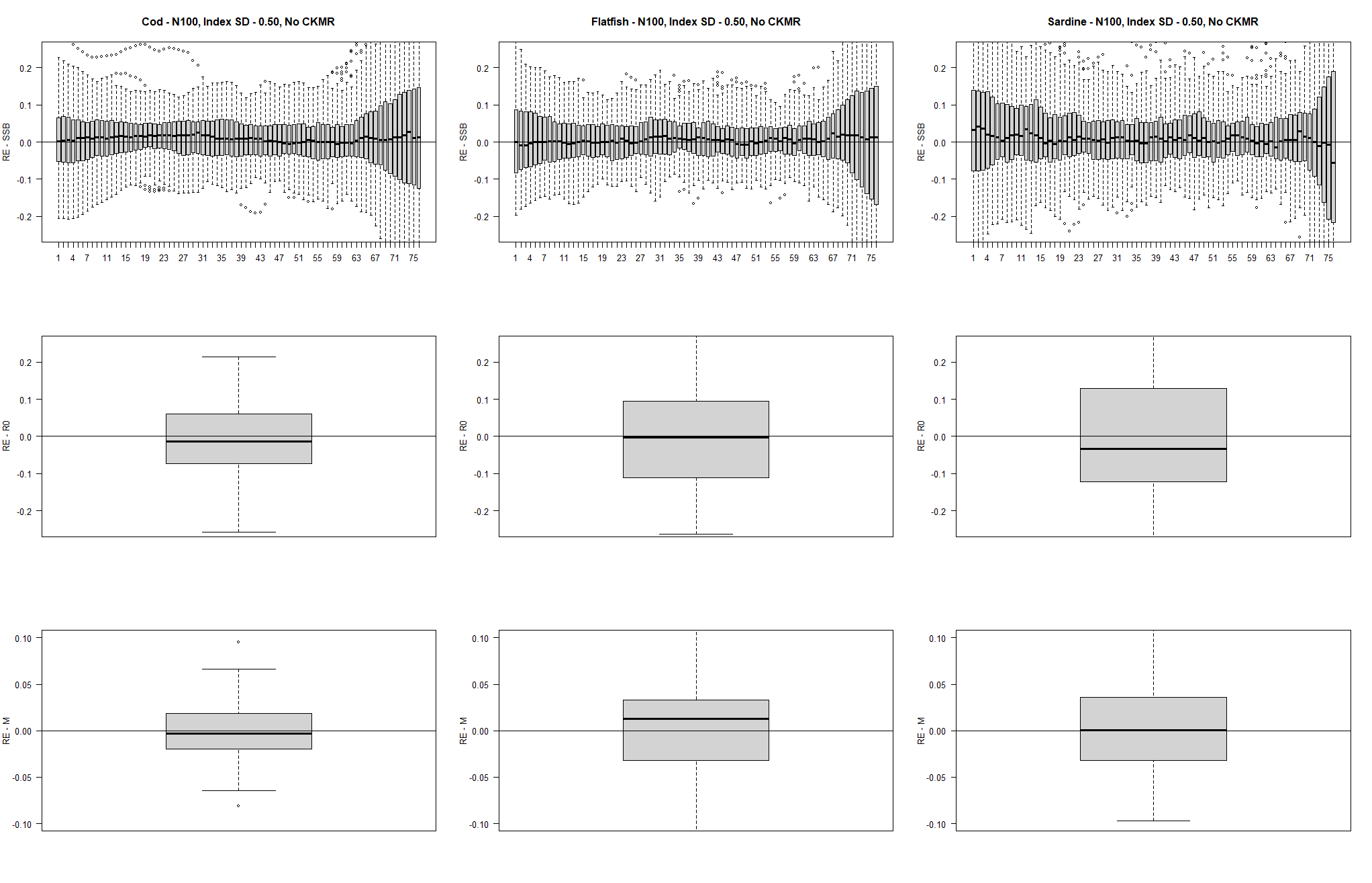
Supplemental Figure 4. Spawning abundance for individual simulation iterations (row 1), spawning abundance quantiles over simulations (row 2), and depletion quantiles over simulations (row 3) in the operating models for each life history type.



Supplemental Figure 5. Fishery selectivity of the three different life history types used in the operating model.



Supplemental Figure 6. Relative error in estimates of spawning stock biomass (top), unfished recruitment (middle), and natural mortality (bottom) for an estimation model fit to data from a sampling model with composition sample size=100 (see methods for which years have composition data) and the abundance index SD=0.5.



Supplemental Figure 7. Relative error in estimates of spawning stock biomass (top), unfished recruitment (middle), and natural mortality (bottom) for an estimation model fit to data from a sampling model with composition available in every year of the time series where the sample size=100 and the abundance index SD=0.5.