

Supplementary figures

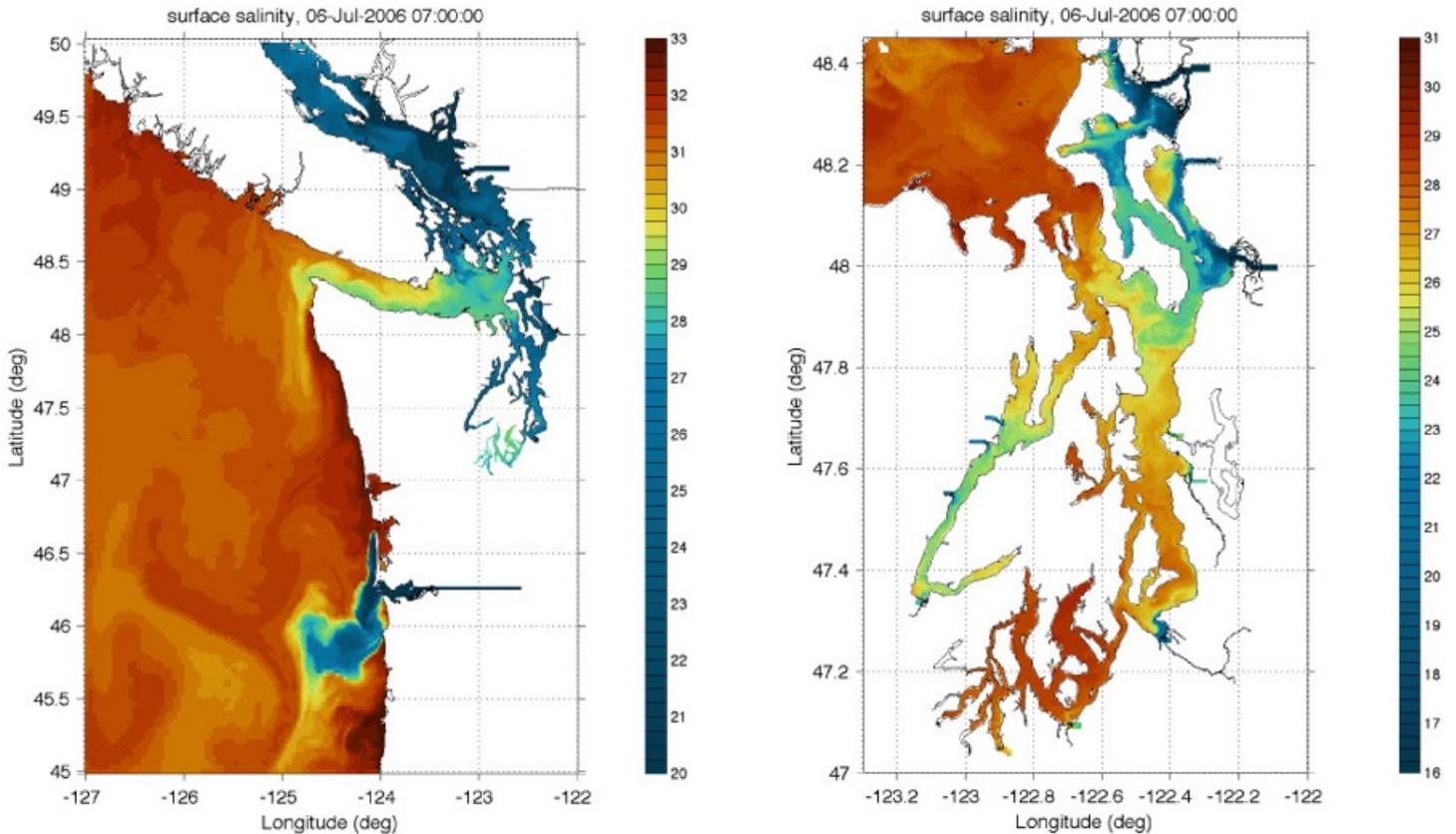


Figure S1 Example of hourly distribution of environmental variables calculated and tracked within the ‘Modeling the Salish Sea’ (MoSSea) model’s domain showing sea surface salinity from July 6, 2006 at 0700 h across (left) the full model domain and (right) a close-up of Puget Sound.

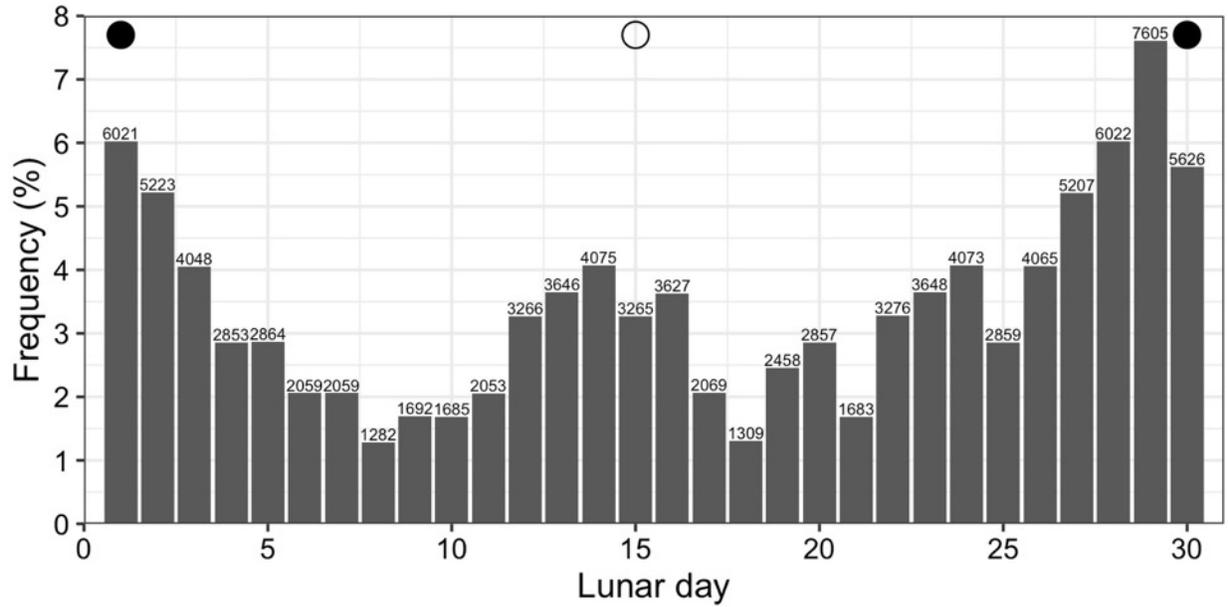


Figure S2 Release distribution of 100,000 simulated larvae for canary and yelloweye rockfish at each release site. Day 1 begins at first new moon in January for canary rockfish and the first new moon in May for yelloweye rockfish. Closed circle: new moon; open circle: full moon. Numbers above bars = number of larvae dispersal paths created for each release. Based on distribution of parturition for settlement groups of *Sebastes inermis* observed in Matsushima Bay, northern Japan. Figure re-created from Pasten et al. 2003 Figure 6.

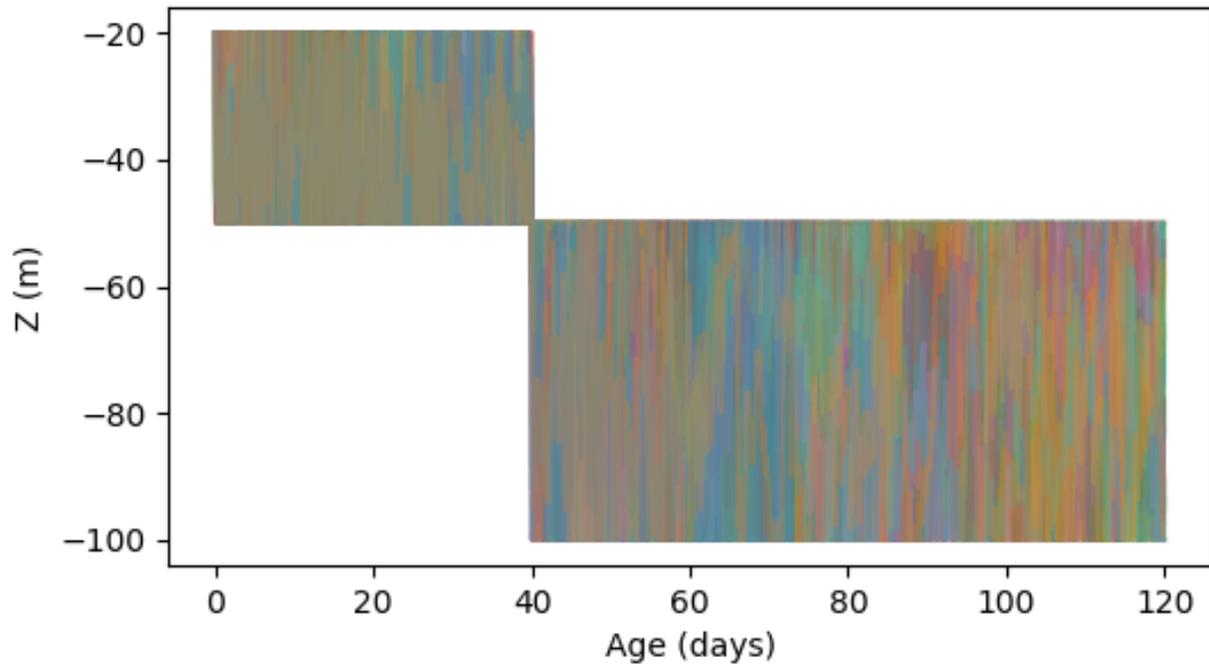


Figure S3 Example of depth (Z (m)) distribution of larvae for each release simulation as a function of pelagic larval duration (age in days). This specific example shows the vertical distribution of the pathways of 100 individual larvae (colored lines) shown in Figure 3b for canary rockfish released from Salt Spring Island in the Strait of Georgia basin.

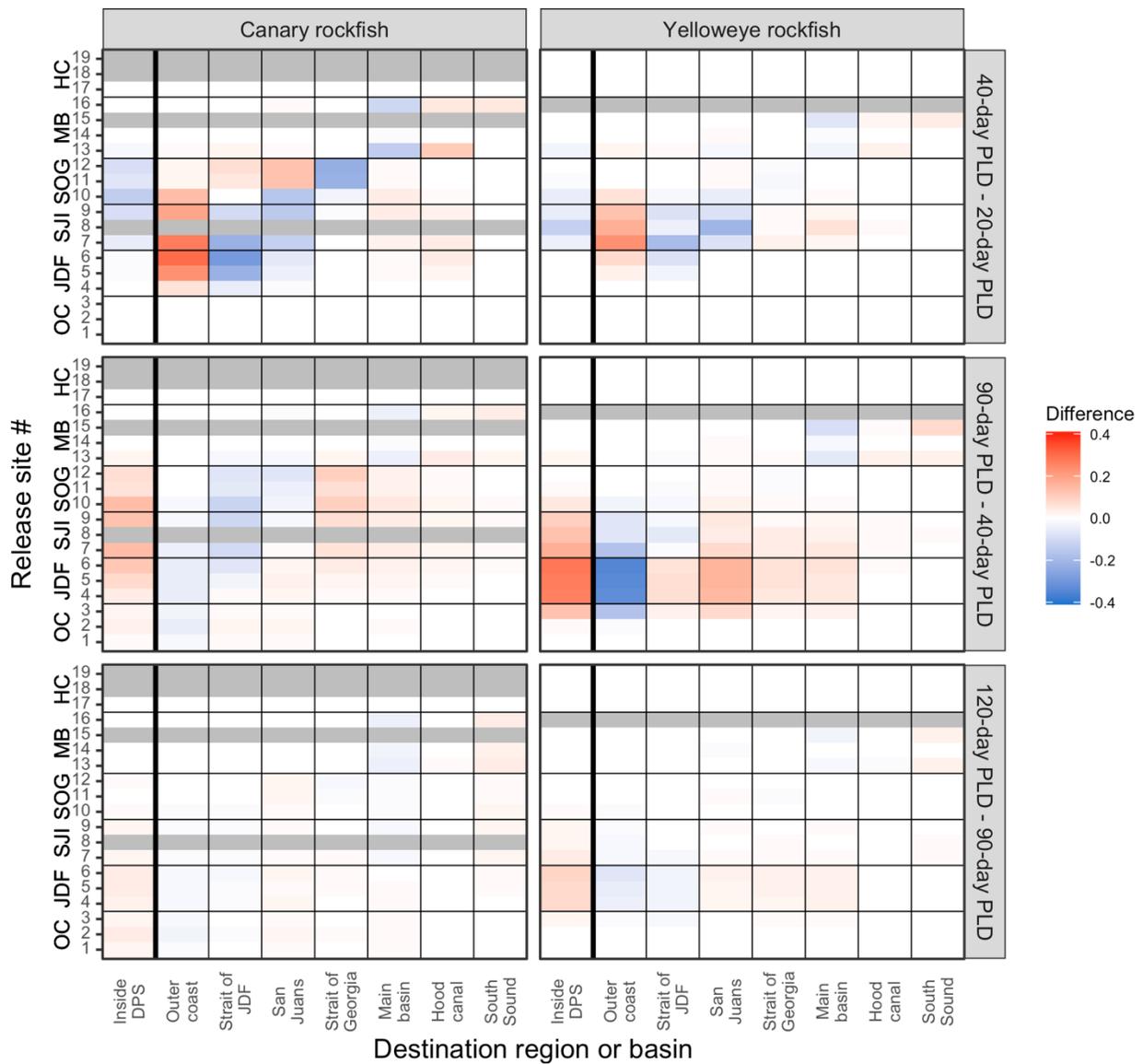


Figure S4 Differences in proportion of simulated (left) canary and (right) yelloweye rockfish larvae found within each destination region when released from each site between successive PLDs. Positive values (red) show that the proportion found for the longer PLD was greater than the proportion found from the shorter PLD. Negative values (blue) show that the shorter PLD had higher proportions. Release sites, organizing lines, and gray space are same as in Figure 4.

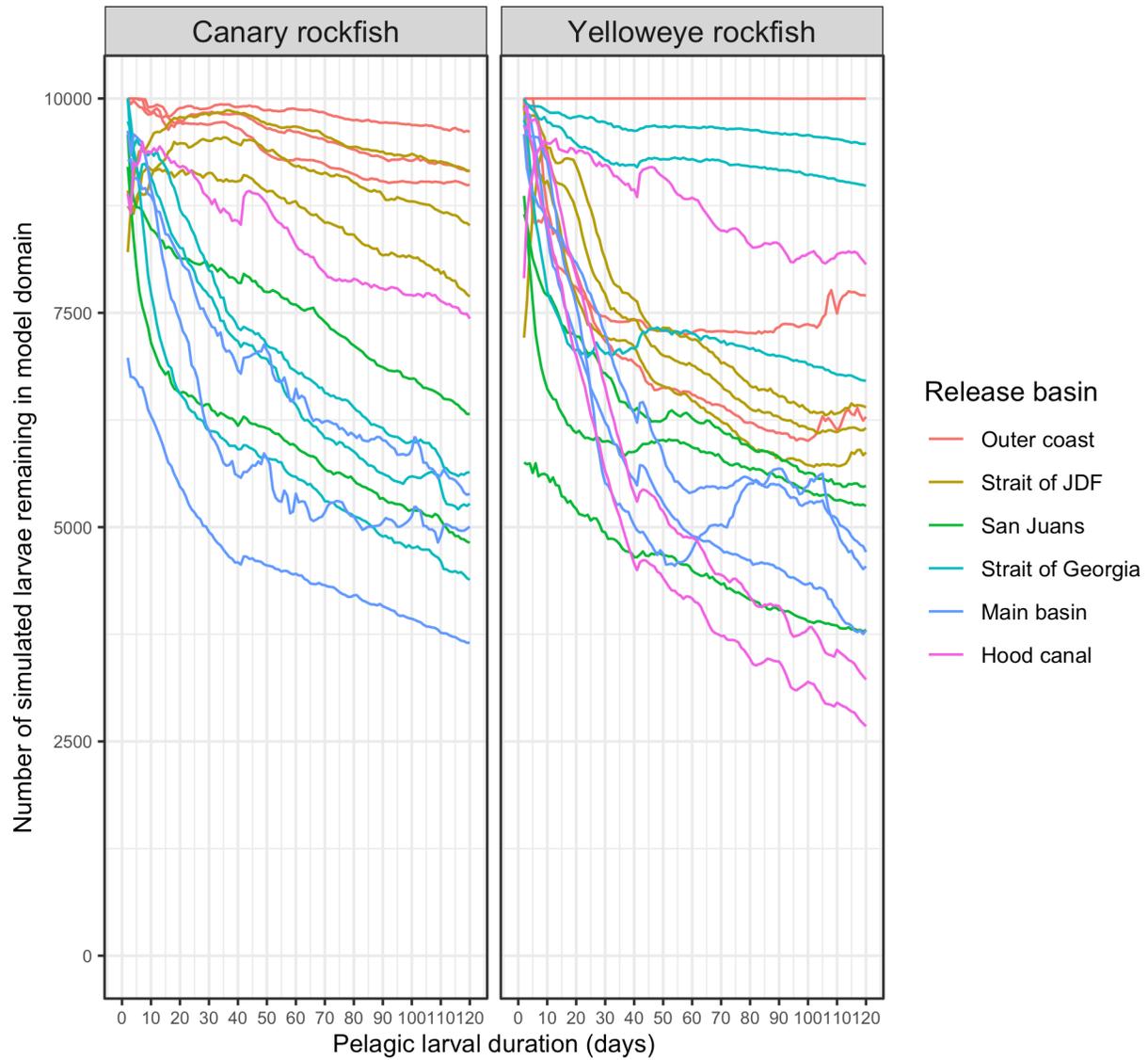


Figure S5 Number of simulated larvae remaining in model domain across dispersal period for canary (left) and yelloweye (right) rockfish. Increases in number of particles were due to particles being allowed to resolve their trajectories over time.