Supplementary File 4

Randomization test for effects of background selection on the abundance of ROH

We conducted a randomization test to determine if the increase in the abundance of ROH in regions of low recombination was greater on the simulated chromosome with purifying selection (the 'selection chromosome') than on the chromosome without purifying selection (the 'no selection chromosome'). We began by calculating the total Mb in ROH for each 200 kb window across the two chromosomes for each of the 20 simulation repetitions. Then, for each chromosome in each simulation replicate, we calculated the mean Mb in ROH for all windows within the low recombination region (positions 1.2 Mb – 1.8 Mb), and separately for all windows outside of the low recombination region. We then calculated the difference in the mean Mb in ROH between the low recombination region and the high recombination regions ($\Delta\overline{ROH}$) for each chromosome in each of the 20 simulation replicates. We wanted to test whether the average of $\Delta\overline{ROH}$ was statistically significantly different on the 'selection chromosome' than on the 'no selection chromosome'.

The randomization test proceeded according to the following steps:

1) Randomize the 'selection chromosome' versus 'no selection chromosome' label between the two estimates of $\Delta\overline{ROH}$ for each simulation repetition using the *sample* function in R.
2) Calculate the absolute value of the difference in $\Delta\overline{ROH}$ between the relabeled chromosomes for each simulation repetition ($|\Delta\overline{ROH}|$)
3) Repeat steps 1-2 10,000 times, each time saving the mean of the 20 randomized values of $|\Delta\overline{ROH}|$.
4) Calculate a *P*-value for the randomization test as proportion of the 10,000 values of the mean $|\Delta\overline{ROH}|$ that were larger than the observed value of the mean $|\Delta\overline{ROH}|$.