

Figure S1: Overall distribution of selection coefficient in the heterozygotes. There are 2% lethal mutations, and the average selection coefficient of the non-lethal mutations is approximately 0.07.

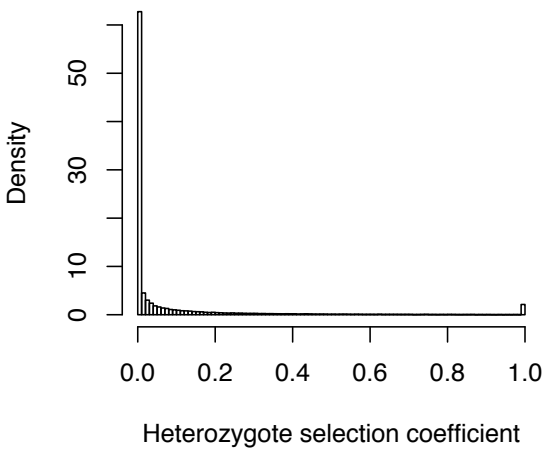


Figure S2: Comparisons of means  $F_{ST}$  (left column),  $d_{XY}$  (central column), and  $H_S$  (right column) between simulations with (black) and without (grey) BGS. Other treatments (*Default*, *No Migration*, *High Migration*, *Human* and *Large N*) are in Figure 1 in the main text. Error bars are 95% confidence intervals.

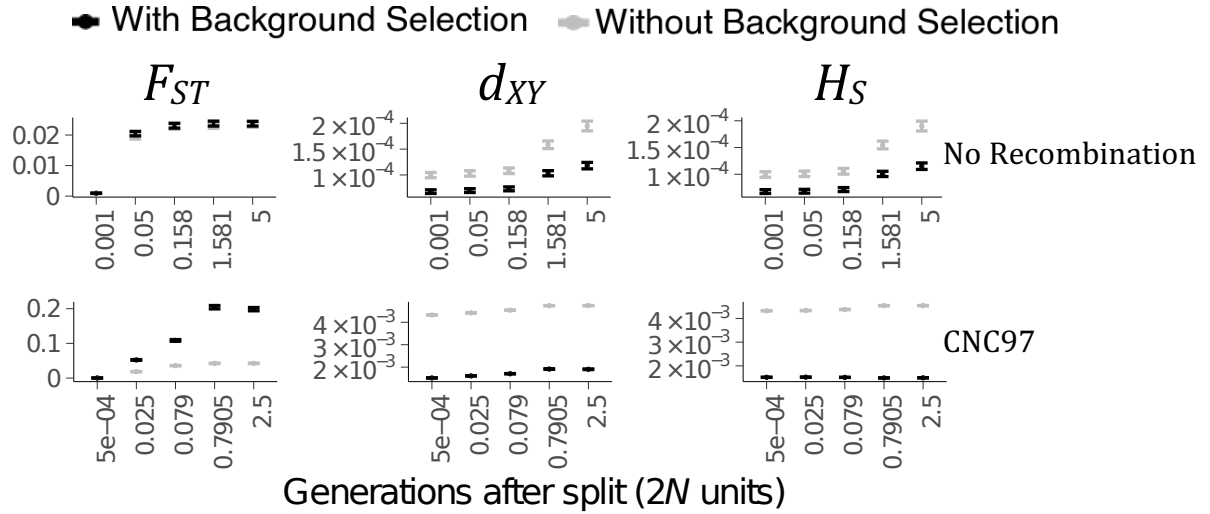


Figure S3: Correlations between  $B$  and  $F_{ST}$ ,  $d_{xy}$ ,  $F_{ST}$  (average of ratios),  $d_{xy-SNP}$ , and  $F_{ST}$  (average of ratios) after removing all loci that have minor allele frequency (MAF) lower than 0.05 (called MAF -  $F_{ST}$  (average of ratios)) for the treatment *No Recombination* only at the last generation ( $5 \times 2N$  generations after the split). Each grey dot is a single simulation with BGS. The large black dot is the mean of all simulations without BGS. The  $P$ -values are computed from a permutation test and  $r$  is the Pearson's correlation coefficient.  $P$ -values and  $r$  are computed on both simulations with and without BGS. Results are congruent when computing the correlation coefficients and  $P$ -value on the subset of simulations that have BGS.

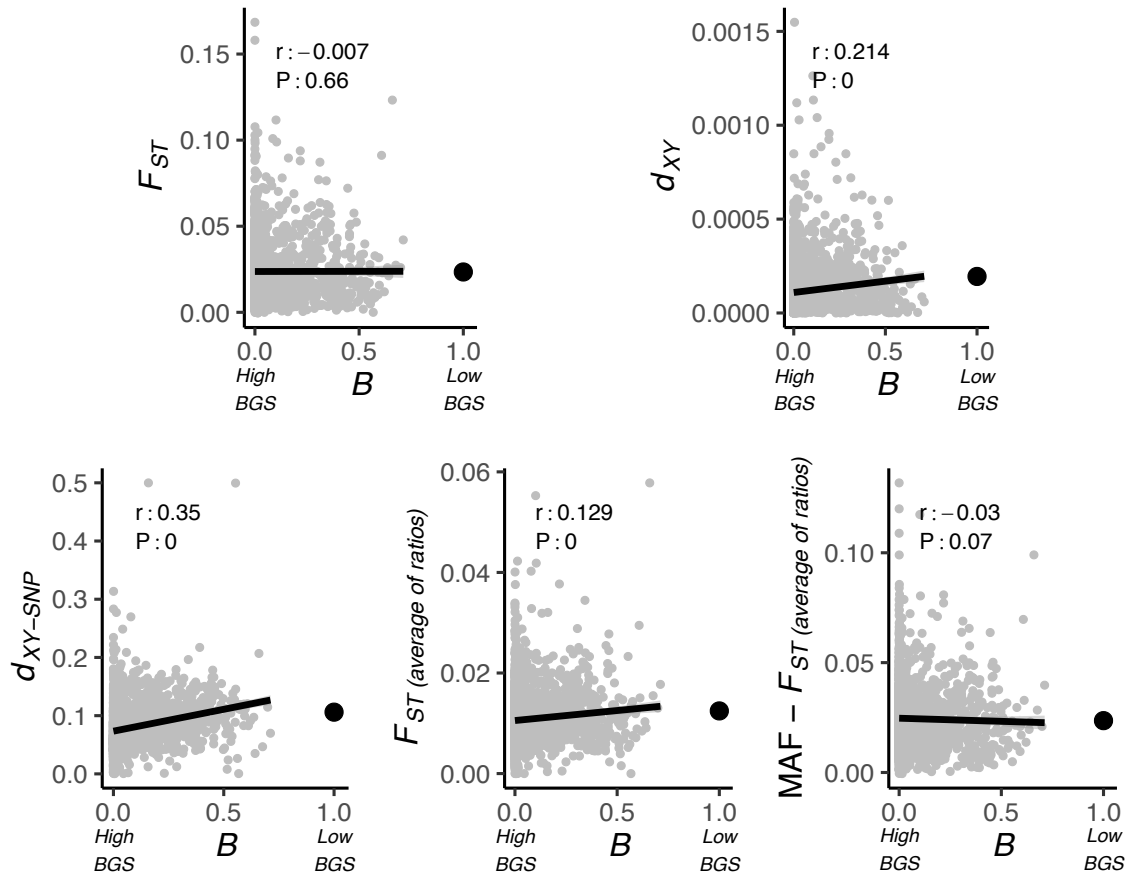


Figure S4: Comparison of false positive rate (FPR) returned by FDist2 between simulations with BGS (black) and without BGS (grey) for all treatments by generation. The significance level is 0.05 and is represented by the horizontal dashed line. Significance based on a Welch's  $t$ -test is indicated with stars (\*\* $P < 0.01$ ; \*  $P < 0.05$ ). Significance levels are the same with Wilcoxon tests except for *No Migration* where nothing comes out significant. Other treatments are presented in figure 4.

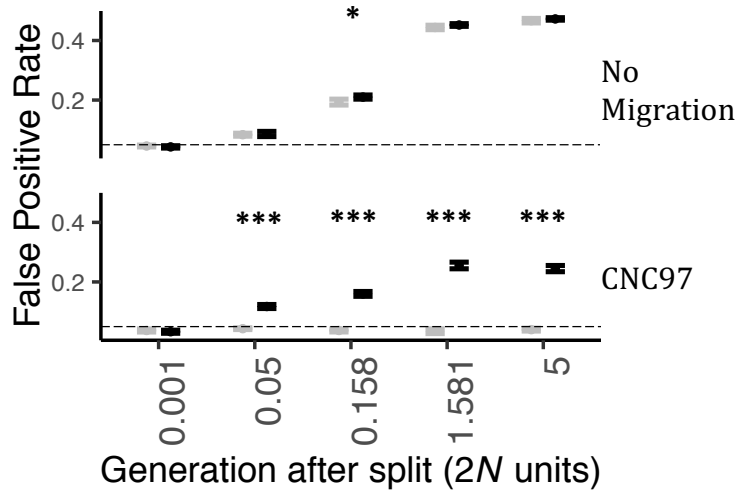


Figure S5: Relationship between total heterozygosity  $H_T$  and  $F_{ST}$  on a site per site basis. Each dot represents a single site. The black line is a Local Polynomial Regression (LOESS). Data is a random subset from the *Default* treatment at the last generation.

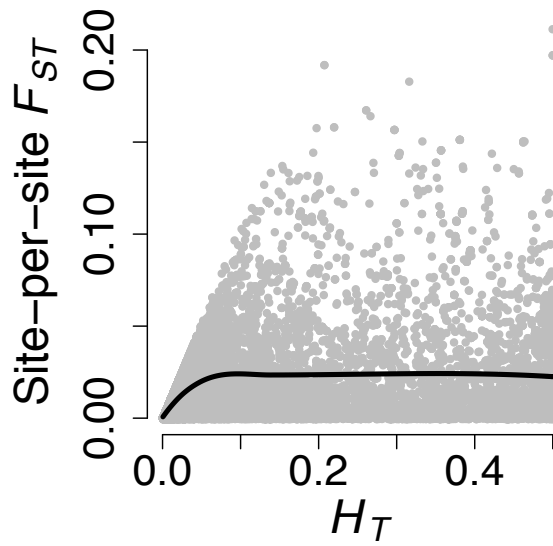


Figure S6: Regressions of total ( $H_T$ ; upper line) and within ( $H_S$ ; lower line) population expected heterozygosity on the coefficient of BGS ( $B$ ) for the last generation of the *Default* treatment. The two regression lines are not exactly parallel with  $H_S$  tending to  $H_T$  as  $B$  goes to low values (more intense BGS).

