

## Supplementary Figures

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.

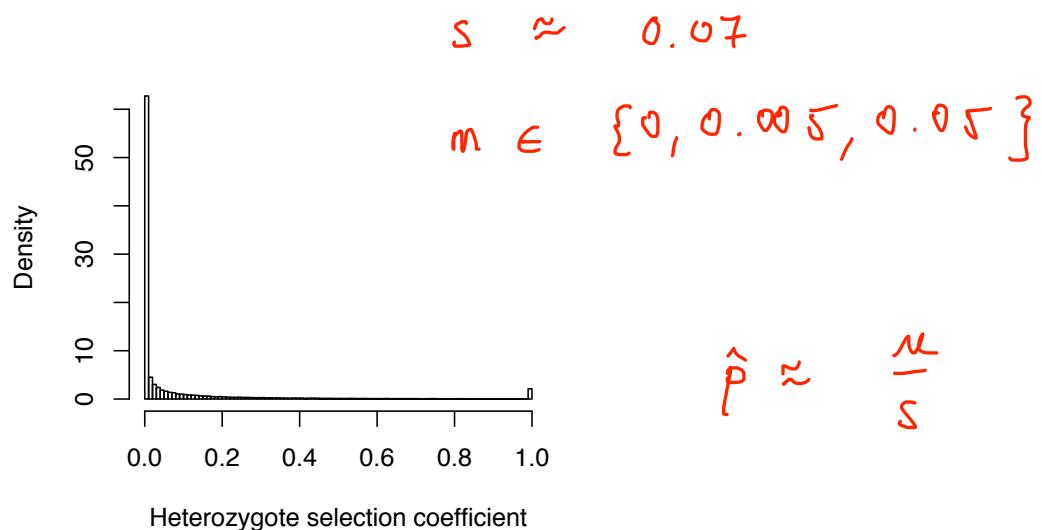


Figure S2: Relationship between  $B$  values computed for all simulations using the stickleback genome using the methods of Hudson and Kaplan (1996) and Nordborg et al. (1997).

| 1995?

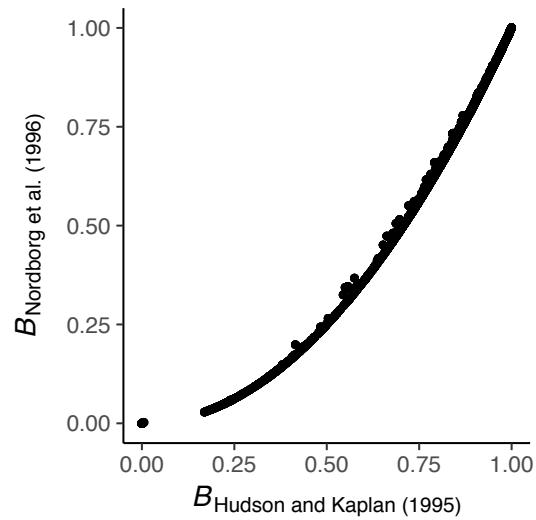


Figure S3: Comparisons of means  $F_{ST}$  (left column),  $d_{XY}$  (central column), and  $H_S$  (right column) between simulations with (black) and without (grey) BGS for all unrealistic treatments. Realistic treatments (*Default*, *No Migration*, *High Migration*, *Human* and *Large N*) are in Figure 1 in the main text. Error bars are 95% confidence intervals.

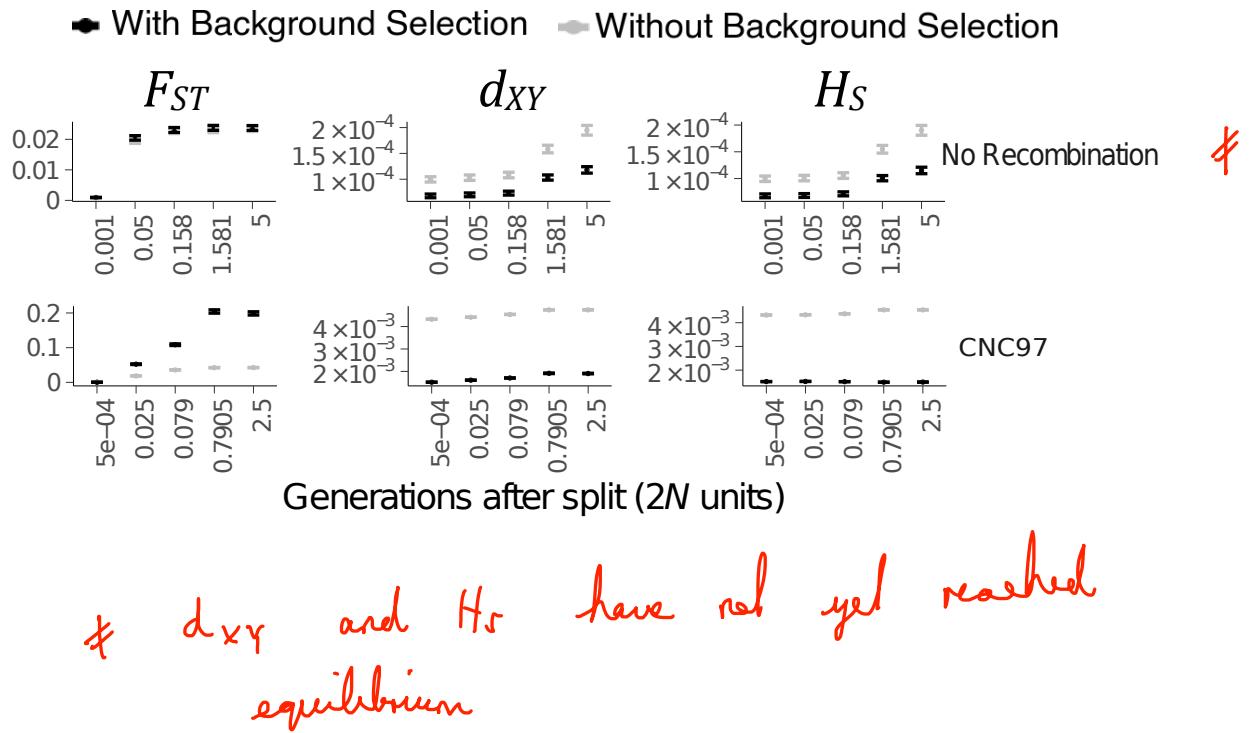
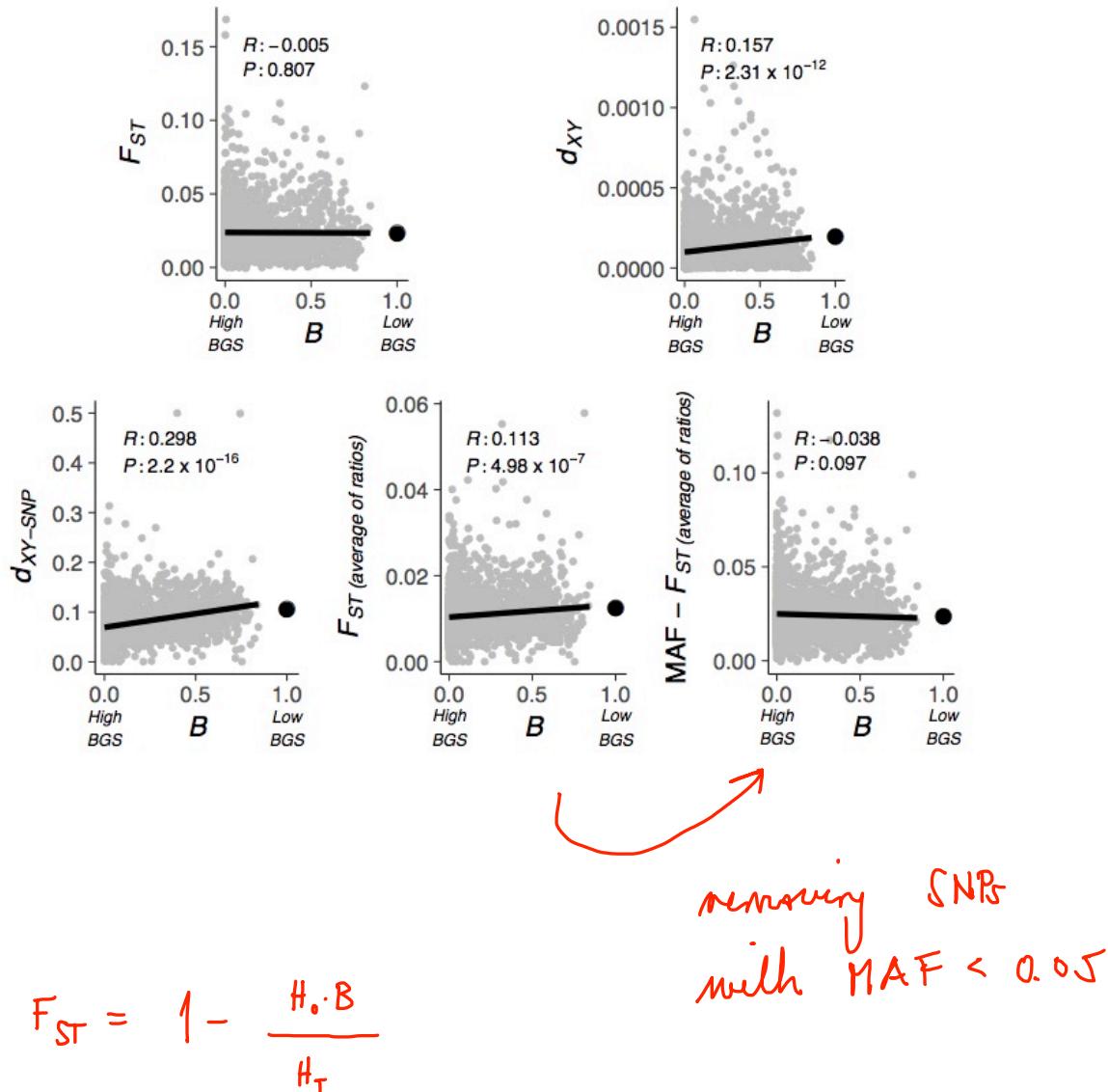


Figure S4: Correlations between  $B$  and  $F_{ST}$ ,  $d_{xy}$ ,  $F_{ST}$ (average of ratios),  $d_{xy-SNP}$ , and  $F_{ST}$ (average of ratios) after removing all loci that have minor allele frequency (MAF) lower than 0.05 (called MAF -  $F_{ST}$ (average of ratios)) for the treatment *No Recombination* 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 Pearson's correlation test.  $P$ -values and  $R$  are computed on the simulations with BGS (grey dots) only.



$$F_{ST} = \frac{G_p^2}{P(1-P)}$$

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.

