



2 **Figure S1.** Nucleotide diversity and Site Frequency Spectrum around neutral and selective  
3 sweeps. On panel (a), we plot the average nucleotide diversity calculated for 10 individuals with  
4 a sliding window of 10 Kb at 1 Kb intervals (in green the average over all replicates, and in red  
5 the expectation from eq. (5)) around a co-dominant allele going selectively to fixation with a  
6 selective strength  $s = 0.01$  in a diploid population of constant size  $N = 18,500$ , mutation rate  $\mu =$   
7  $1.63 \times 10^{-7}$  and recombination rate  $r = 3.5 \times 10^{-8}$  (average over 483 troughs obtained from >24,000  
8 simulations done with SLIM (Haller and Messer 2019)). On panel (b), we plot in green the  
9 average SFS in a 10 Kb window (over 61,471 SNPs) centered on the troughs, and in black the  
10 neutral expectation in a constant population corresponding to the background SFS. On panel (c),  
11 we plot the nucleotide diversity calculated for 10 individuals with a sliding window of 10 Kb at 1  
12 Kb intervals (in green the average over all replicates, and in red the expectation from eq. (5) for  
13 an allele fixing in 2200 generations) around a neutral valley of diversity (arbitrarily defined as  
14 regions of less than 7% of the background diversity). The population experienced a contraction  
15 2200 generations ago and the (diploid) population size was reduced from  $N_0 = 2.37 \times 10^6$  to  $N_c =$   
16 4400. We performed 10,000 simulations of 20 Mb genomes (one chromosome per genome) and  
17 obtained 432 troughs. The recombination rate was set to  $r = 3.5 \times 10^{-8}$  and the mutation rate was  
18  $\mu = 1.63 \times 10^{-9}$ . We plot on panel (d) the SFS in a 15 Kb window (32,090 SNPs) centered on the  
19 troughs in green, and in black the whole genome SFS.