

**TABLE S2**

**Proportion of SNP segregating at different frequencies in simulated datasets as a function of the time the selected mutation arose ( $t_{sel}$ )<sup>a</sup>.**

Frequency <sup>b</sup>	$t_{sel} = 2400$ generations		$t_{sel} = 3200$ generations		$t_{sel} = 4000$ generations	
	Pop A	Pop AA	Pop A	Pop AA	Pop A	Pop AA
0-50%	0.029	0.037	0.012	0.012	0.015	0.014
>50-80%	0.029	0.206	0.007	0.193	0.008	0.189
>80-97.5%	0.219	0.745	0.014	0.785	0.006	0.784
Fixed	0.723	0.012	0.968	0.010	0.972	0.013

a. For these simulations,  $N_{AA} = 0.1N_A$  and  $\gamma = 100$  when  $t_{sel} = 3200$  and  $t_{sel} = 4000$ . When the selected mutations occur at the population expansion ( $t_{sel} = 2400$  generations),  $\gamma = 200$  to account for the larger population size while keeping  $s$  the same as before.

b. Frequency bins in a sample size of 40 chromosomes.