

S1 Simulation Model 1

For the first type of simulations (model 1) we used the software package Genome, a coalescent-based whole-genome simulator (Liang et al. 2007). We simulated a population with effective size $N = 10,000$, and randomly extracted 10,000 haplotypes from this population. The simulated region consists of 10 independent subregions, and each subregion contains 10 fragments; the recombination rate between consecutive fragments was taken as the default value (0.0001).