**Supplementary Information**

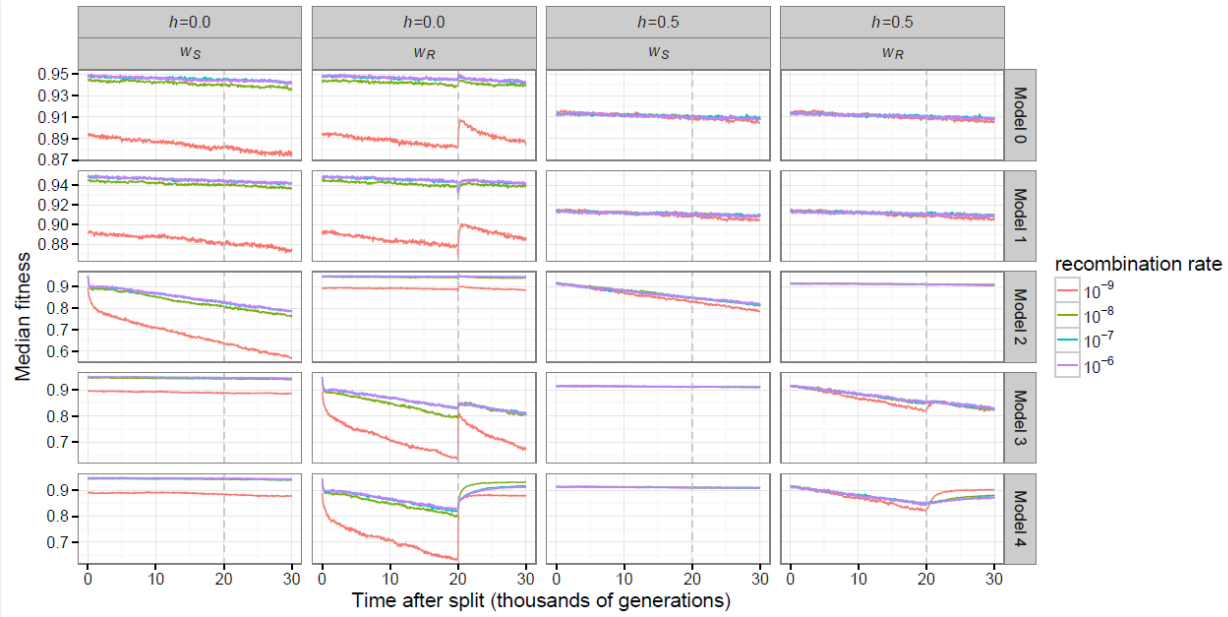


**Figure S1**. The change in the mean fitness of the source and recipient subpopulation in each model. The median (solid line) is shown for 200 simulation replicates. The vertical grey line depicts the time of gene flow. Different colors denote distinct recombination rates used in the simulations. The left two panels depict simulations with recessive mutations ($h$=0) while the right two panels show simulations with additive mutations ($h$=0.5). Variants that are fixed in both subpopulations are not considered in the calculation of fitness. The model numbers refer to the models shown in **Figure 1**.

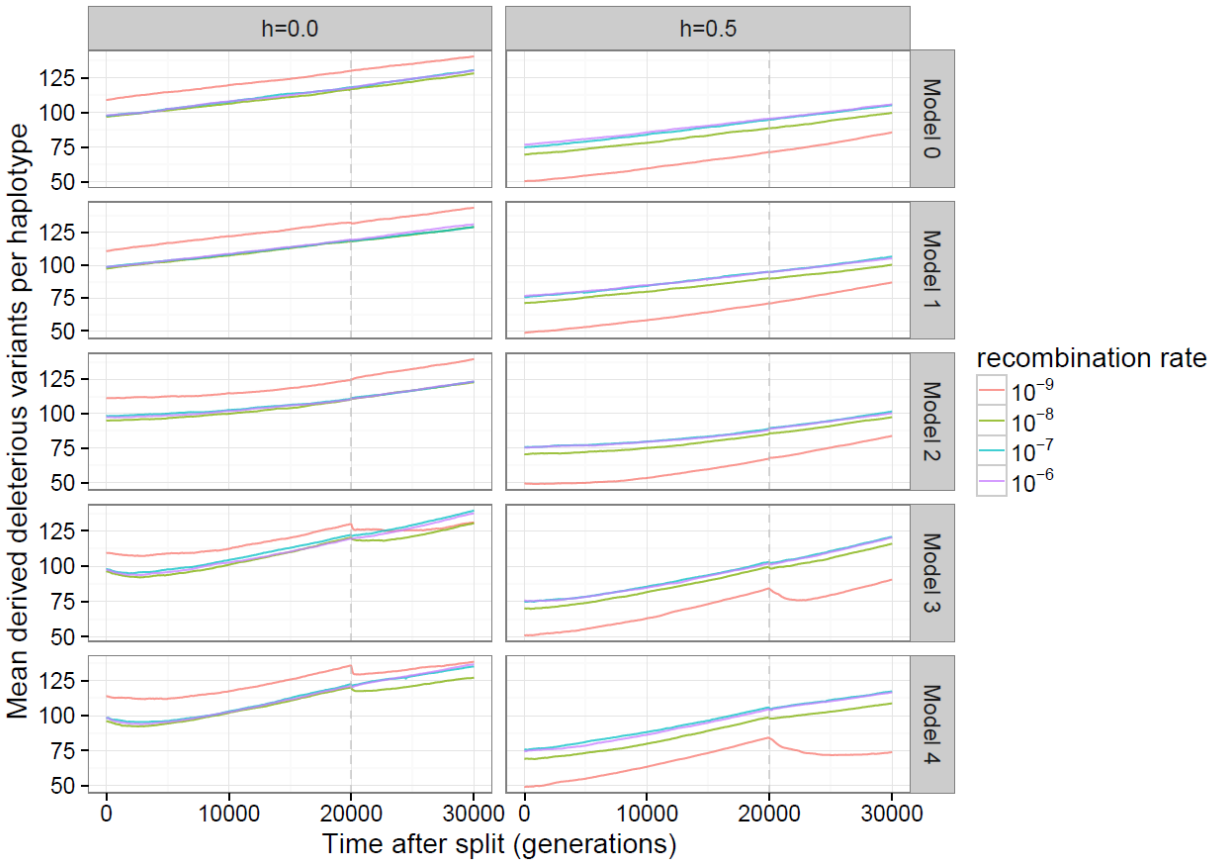


**Figure S2.** The change in the mean number of derived deleterious sites ($s$<0) per haplotype in each model in the recipient subpopulation. The mean (solid line) is shown for 200 simulation replicates. The vertical grey line depicts the time of gene flow. Different colors denote distinct recombination rates used in the simulations. The left panel shows simulations with recessive mutations ($h$=0) while the right panel shows simulations with additive mutations ($h$=0.5). Variants that are fixed in both subpopulations are not counted. The model numbers refer to the models shown in **Figure 1**.

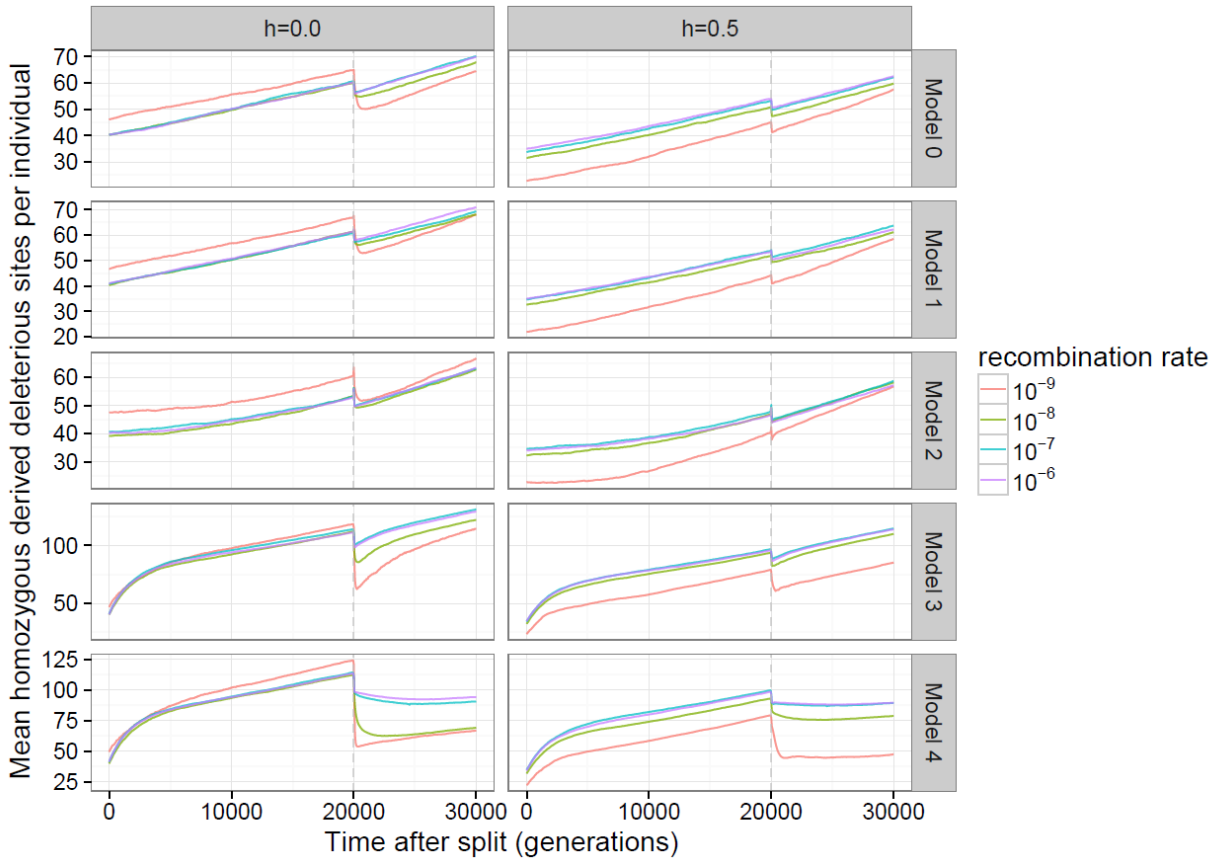


**Figure S3.** The change in the mean number of homozygous derived deleterious sites per individual in the recipient subpopulation. The mean (solid line) is shown for 200 simulation replicates. The vertical red line depicts the time of gene flow. Different colors denote distinct recombination rates used in the simulations. The left panel shows simulations with recessive mutations ($h$=0) while the right panel shows simulations with additive mutations ($h$=0.5). Variants that are fixed in both subpopulations are not counted. The model numbers refer to the models shown in **Figure 1**.

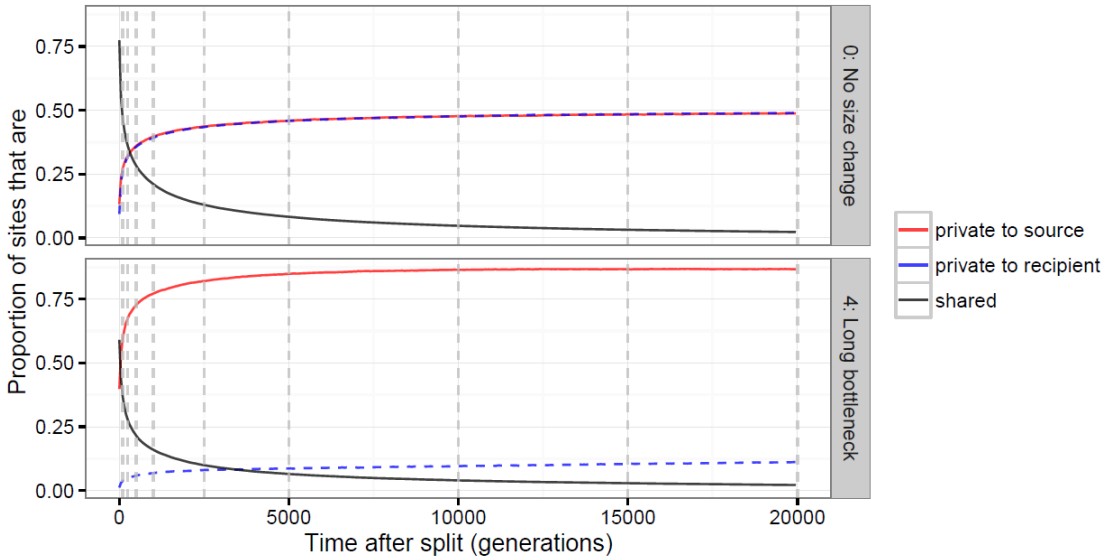


**Figure S4**. Population split time and population size impact the proportion of sites private to each subpopulation at the time of admixture. The proportions of sites that are private to the source and recipient subpopulations, or shared between subpopulations, are shown for 200 simulation replicates and two demographic models (Model 0 and Model 4, refer to **Figure 1**). The grey lines represent the time between population divergence and admixture (100, 250, 500, 1,000, 2,500, 5,000, 10,000, and 20,000 generations) in the demographic models as depicted in **Figure 4**.

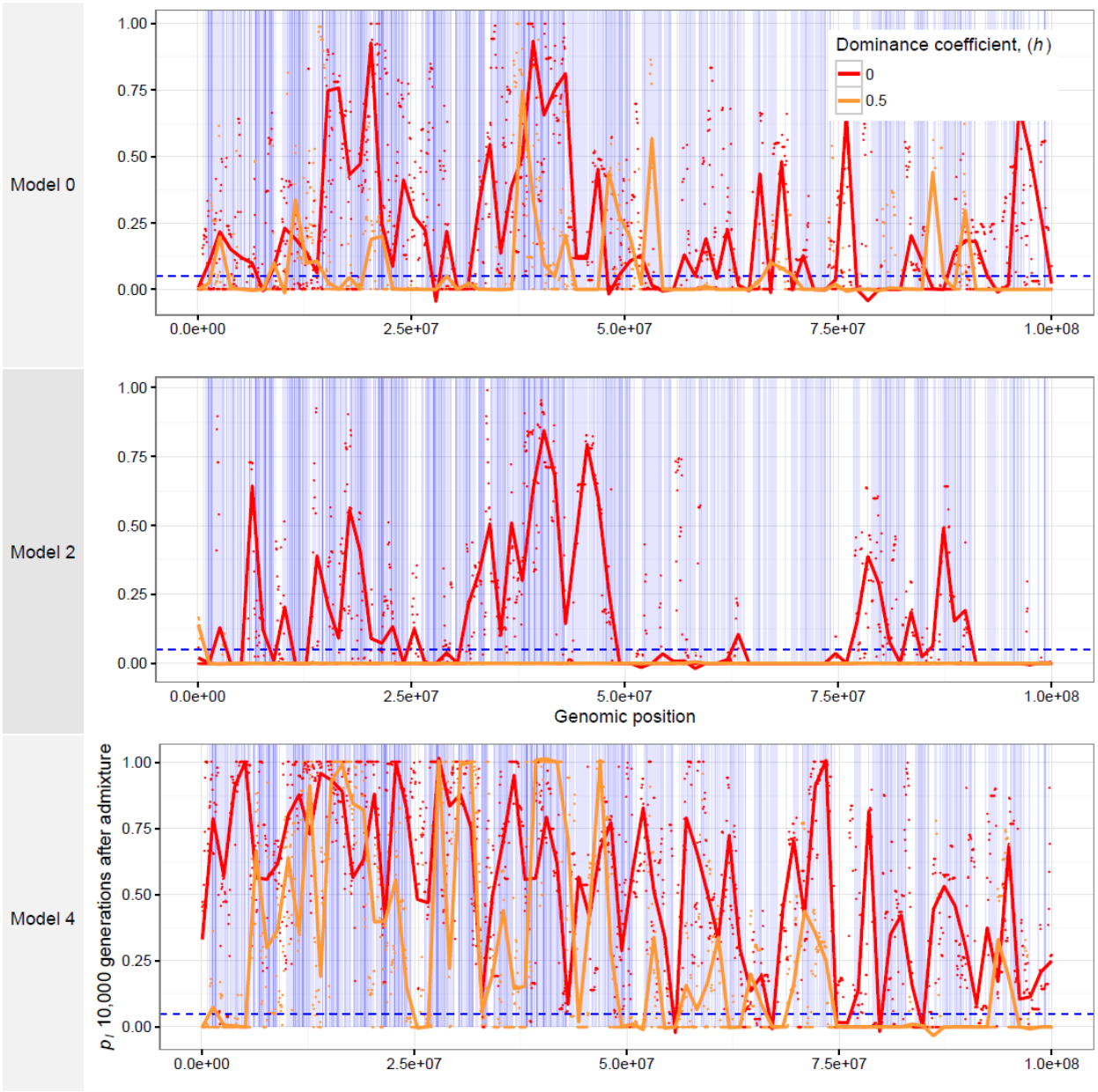


**Figure S5.** The genomic landscape of introgression of one simulation replicate for three demographic models. The frequency of ancestry that is introgression-derived is shown for non-overlapping 100kb windows in a simulated 100 Mb region of human chromosome 1 for the recipient subpopulation. The model numbers refer to the models shown in **Figure 1**. Points represent a single value for each 100kb window and lines are loess curves fitted to the data. The horizontal, blue dashed line represents the initial frequency of introgression-derived ancestry, $p_I$=0.05. Vertical blue bars represent genes in which deleterious mutations can occur. Red curves denote the results for recessive mutations ($h$=0) while orange curves show the results for additive mutations ($h$=0.5).