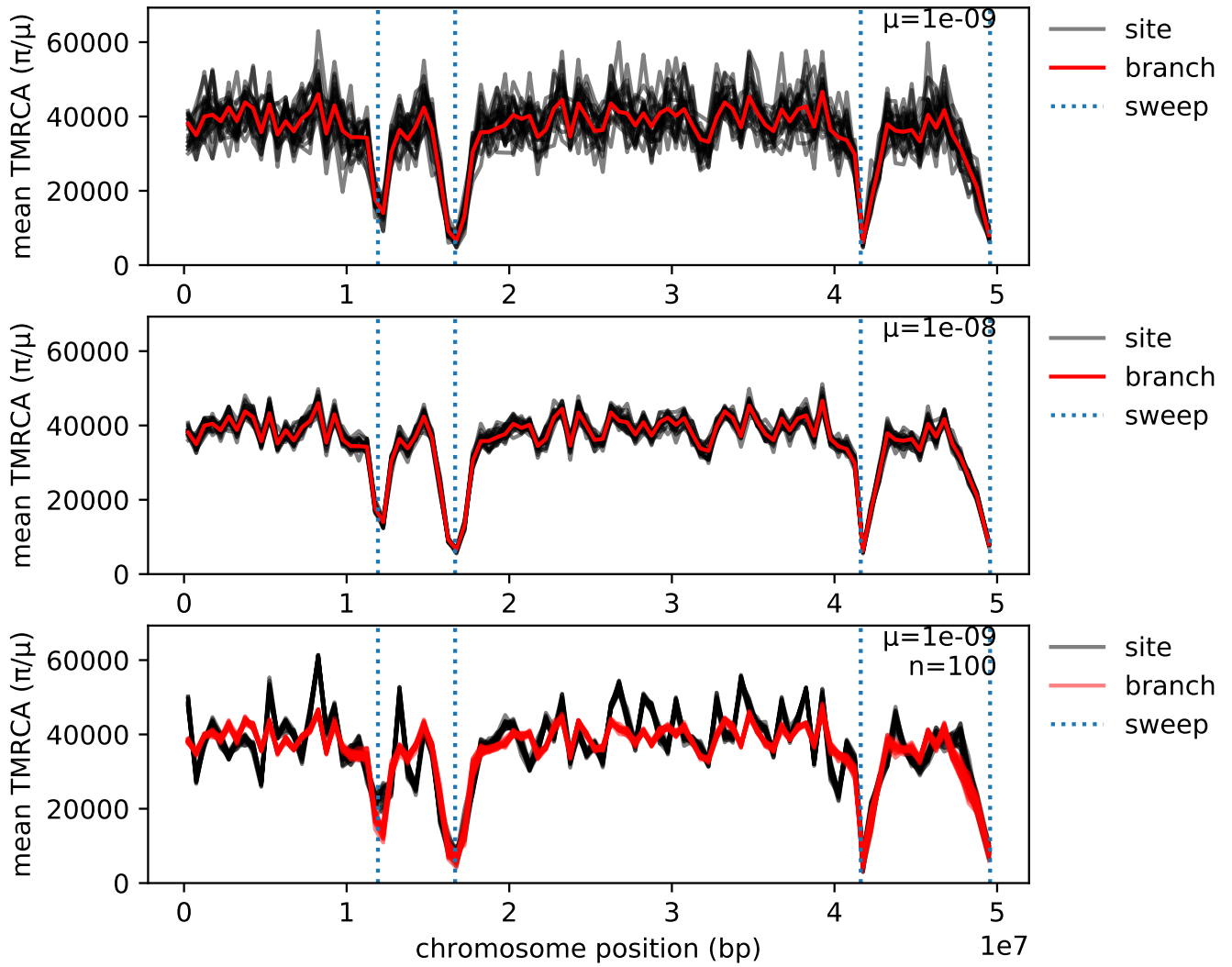
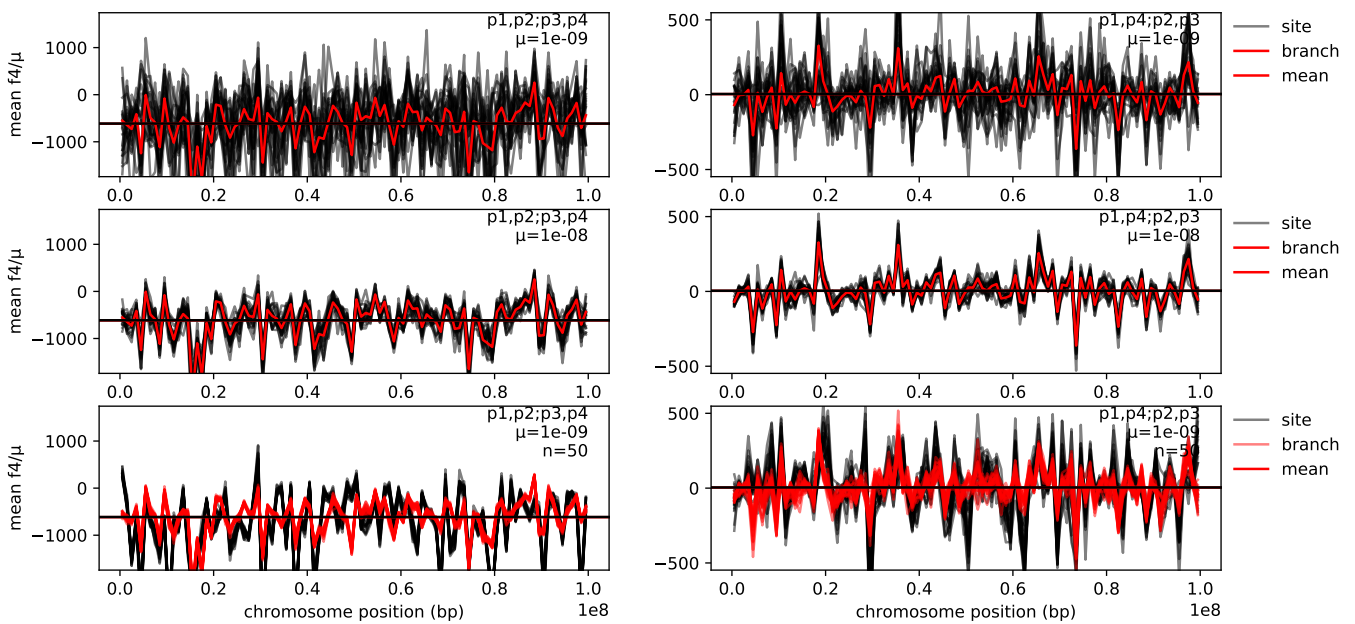


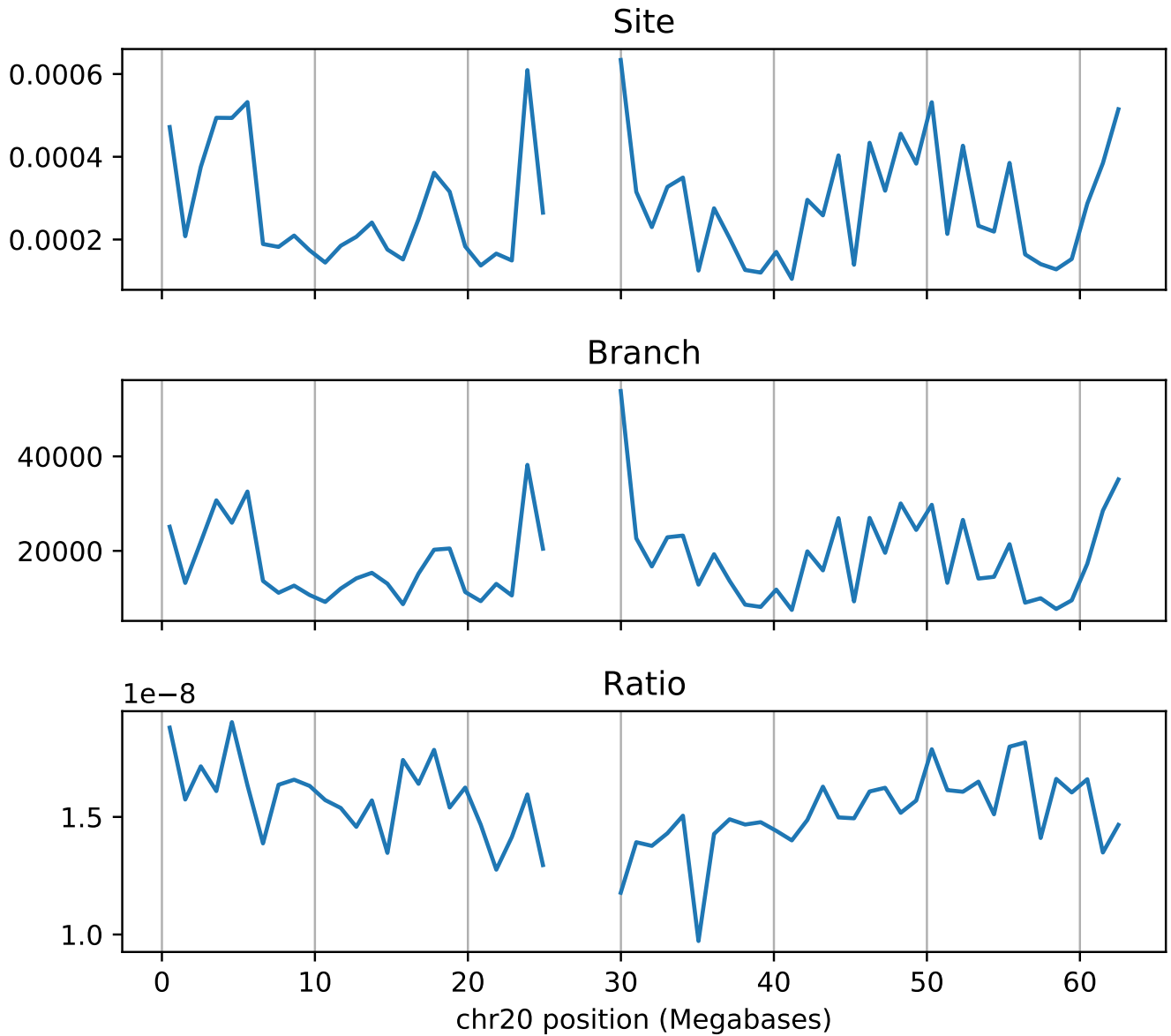
1 Supplementary figures



**Figure S1** As in Figure 5, but in a population of size 10,000.



**Figure S2** Values of the  $f_4$  statistic in megabase windows along the genome from the simulations of introgression described in the text. Statistics are shown in units of generations: Branch statistics are computed in units of time, which is in generations for these simulations; and Site statistics are reported in units of mutations per unit of sequence length, which we divide by mutation rate per unit of sequence length and per generation to obtain units of generations.



**Figure S3 (top)** Mean sequence diversity in 1Mb windows along human chromosome 20 of the GBR (Great Britain) sample of the 1000 Genomes Project, in units of mean number of pairwise differences per nucleotide. **(middle)** The dual Branch statistic as calculated from trees inferred by Relate (Speidel *et al.* 2019), in units of generations. **(bottom)** The ratio of the Site statistic to the Branch statistic. This figure differs from Figure 7 in that the trees were inferred using only GBR samples, and Relate was allowed to co-estimate population size and branch lengths, with mutation rate fixed at  $1.45 \times 10^{-8}$  mutations per generation; the trees shown in Figure 7 were inferred with a fixed effective population size of  $N_e = 15,000$ .