



FIGURE S7.—Comparison of the distribution of inter-SNP genetic distances in the Perlegen data (from the LDhat genetic map) with the Schaffner and empirical hotspot models (see Methods). The distribution is tabulated over all 8833 windows across the genome. The increased proportion in the bin after 0.025 cM is due to the change in scale of the bins. As noted in Figure S6, here the observed and simulated inter-SNP genetic distances are based on selecting one random set of SNPs per window. The simulated inter-SNP genetic distances were determined assuming a constant population size, $N=10,000$, and re-scaling genetic distance for each window such that $\hat{c}_{window} = 0.25$ cM.