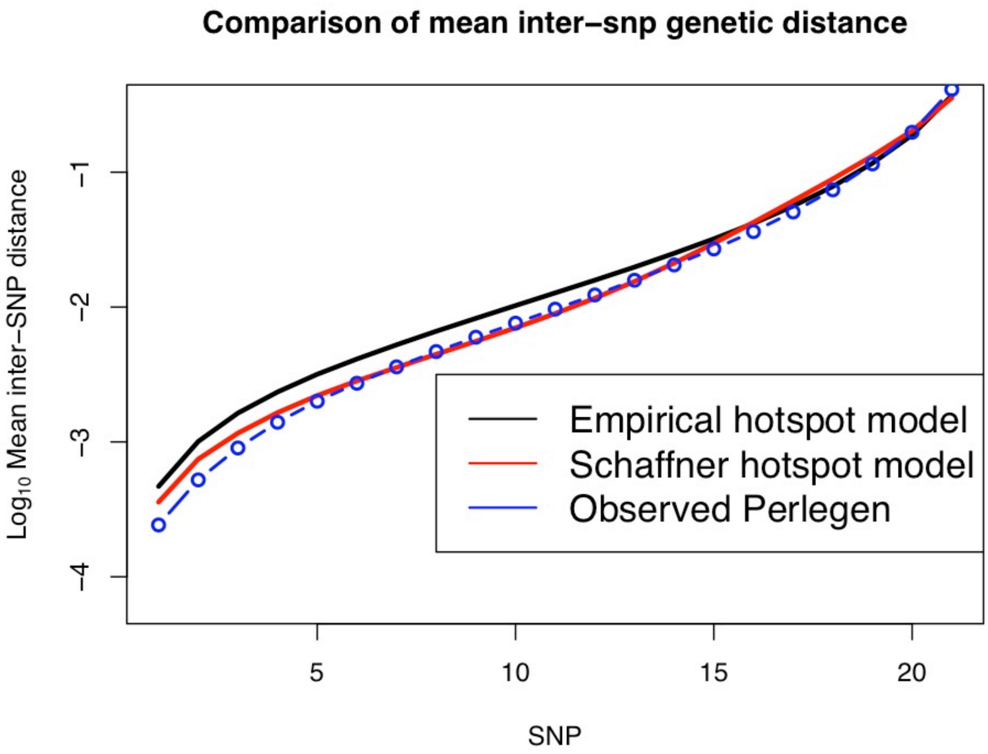

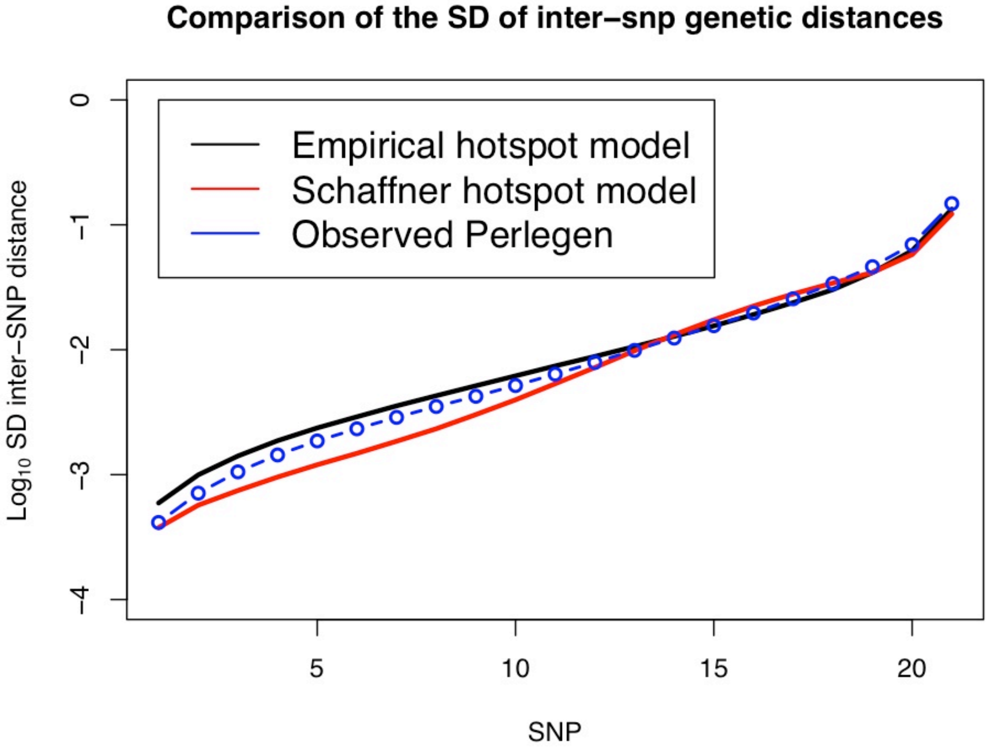

FIGURE S6.—Comparison between the mean and standard deviation (SD) across all 8833 windows of the observed inter-SNP genetic distances (as defined by the LDhat genetic map) and the mean genetic distances simulated using the modified Schaffner hotspot model and the empirical hotspot model (see Methods). The left-most point in the top figure represents the mean of the smallest inter-SNP distance, averaged over all windows, the second point, the second smallest inter-SNP distance, and so on. The actual *HCN* statistic used for inference was averaged over 10 different *HCN* statistics, each of which was generated from a different random sub-set of SNPs from each window (see Methods). 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.