FIGURE S5.—Log_{10} of the χ^2 statistic for the goodness-of-fit test comparing the *HCN* statistic under different SNP ascertainment schemes (shown on the x-axis) to that with complete ascertainment for the complex demographic model. Here a sample size of 120 chromosomes from each population is used. Note that the SNP discovery sample sizes used here differ from those in Figures S1 and S3. The horizontal lines denote the 5% significance cutoff for population 1 (solid) and population 2 (dashed). The two curves for each population are from two entirely independent replicates of the entire process (see File S1) to assess stochastic variance.