**Figure S1.** — Log10 P-value of the goodness-of-fit test comparing the $H_{par}$ 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 40 chromosomes from each population is used. The solid horizontal line denotes the 5% significance cutoff. P-values <10^{-200} are set to 10^{-200}. 

- Pop 1: $n_{\text{window}} = 7,000$
- Pop 2: $n_{\text{window}} = 7,000$
- Pop 1: $n_{\text{window}} = 1,000$
- Pop 2: $n_{\text{window}} = 1,000$