



FIGURE S8.—Observed *HCN* statistic for the Perlegen CEU sample and the *HCN* statistics for the best-fitting demographic models based on the Schaffner hotspot model and the empirical hotspot model. Windows based on genetic distance were defined using the LDHat genetic map (see Methods). See Table 2 for the parameter values generating the best-fitting *HCN* statistics. Note, the bins shown in the figure were the same ones used when inferring parameters.