

MLE, Schaffner hotspot model

10-14 15-48

35-48

30-34

27–29

25-26

23-24

20-22

15–19

10-14

1–9

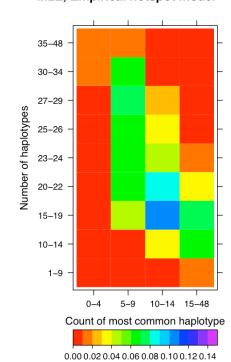
0-4

5–9

Count of most common haplotype

0.00 0.02 0.04 0.06 0.08 0.10 0.12 0.14

Number of haplotypes



MLE, Empirical hotspot model

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.