

Table S1 Median reduction in LDhat recombination rate estimates relative to the simulated rates.

Inversion frequency (%)	Median % reduction in LDhat rec. rates
10	7.8
20	26.4
30	46.3
40	60.4
50	67.4
60	66.9
70	68.9
80	74.5
90	70.8

The median percentage reduction in recombination rates estimated by LDhat compared to the simulated rates between adjacent pairs of SNPs within inversion loci (after adjustment for systematic over-estimation of median rates, which results from median recombination rates over short physical distance being low due to the non-uniform distribution of recombination in the genome) is shown across the range of inversion frequencies, for the simulation study described in the text and illustrated by Figure 1 and Table 1. We show the median reductions as Supporting Information only as we consider the mean reductions (see Table 1) a more appropriate guide in the comparison of the rates because, (i) over larger regions the median rates converge to the mean rates (the latter are not dependent on the distance over which they are measured), (ii) investigators are most likely to be interested in mean or total recombination rates over a region.

Supplementary literature cited

Hudson, R. R. (2001). "Two-locus sampling distributions and their application." Genetics **159**(4): 1805-1817.

Sabeti, P. C. et al. (2002). "Detecting recent positive selection in the human genome from haplotype structure." Nature **419**(6909): 832-837.

Voight, B. F., et al. (2006). "A map of recent positive selection in the human genome." PLoS Biology **4**(3): e72-e72.