



Figure S2. Inferred mutation rates for a range of values of the genetic map error parameter α and starting heterozygosity range S . All estimates use our standard data set of eight non-African genomes. Data points represent the inferred rates (independent point estimates), and the lines are linear regression fits for each of the three choices of S as a function of α . We caution that the values for $S = 1-5$ and $10-20$ are less confident than those for our standard range of $5-10$. In particular, we believe that the genotype error correction is likely too strong for $S = 1-5$, and thus the $1-5$ values here are too low, but we do not have sufficient statistical power to generate a separate error estimate. We also note that the dependence of μ on α is stronger for larger S , because a higher heterozygosity at the starting points leads to a steeper relaxation of $H_S(d)$, so that the curve is more sensitive to the smoothing caused by map error.