



Figure S6: A histogram of the number of pairs sharing at each locus. We simulated 100 Wright-Fisher populations with $N = 10000$, $n = 100$, and one chromosome of length $L = 278\text{cM}$, and searched for IBD shared segments using $m = 1\text{cM}$. In the GENOME coalescent simulator, recombination is resolved only within blocks whose size we set to 0.01cM . For each such block (excluding the first and last $m(\text{cM})$ of the chromosome), we recorded the number of pairs sharing a segment containing it, and then plotted the histogram over all blocks. We also plot a Poisson PDF with the same mean as the observed distribution. The histogram is significantly broader than the Poisson (Index-of-Dispersion test P-value less than MATLAB's resolution), indicating that sharing tends to concentrate at specific loci.