

File S1

LDhat is a package of programs written in the C language for the analysis of recombination from population genetic data. The key feature of the package is the estimation of population recombination rates using the composite likelihood method (HUDSON 2001).

The *interval* sub-method of LDhat was used to estimate recombination rates from the invertFREGENE simulated data, applying the largest available likelihood table available in the LDhat package suite, with n=192 sequences (96 individuals), and as suggested in the documentation, *interval* was run for 10000000 iterations to give more consistent results. The *stat* sub-method of LDhat was then run on the resulting estimates to return the mean recombination rate between adjacent SNPs. Finally, we used R to obtain the LDhat estimates in the same format as those given by the invertFREGENE recombination map and then performed a comparison between the true (simulated) and estimated recombination rates.