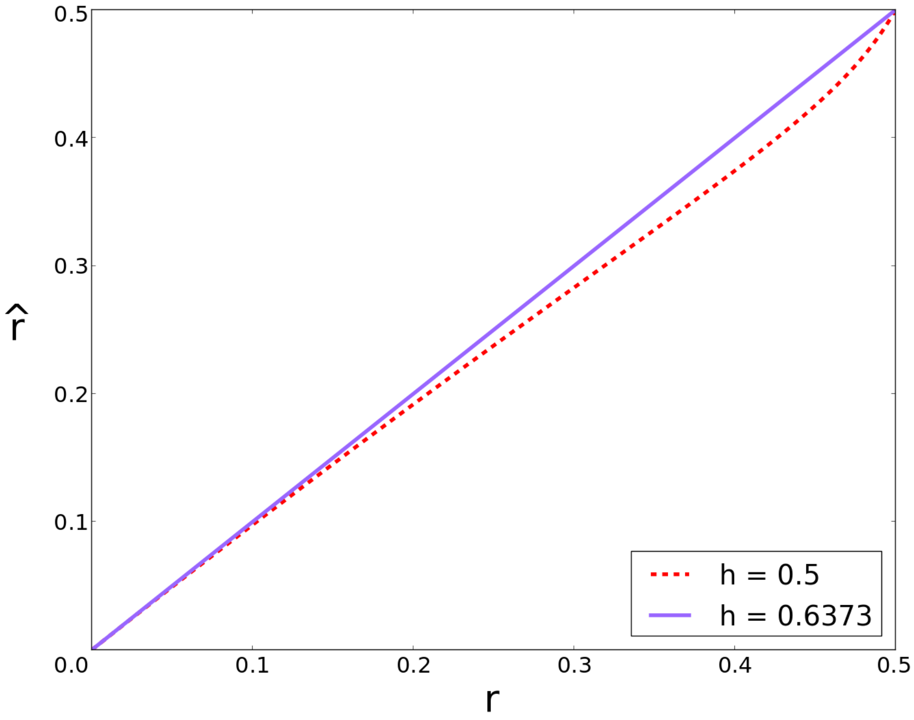

Figure S1: **Estimated recombination fractions, $\hat{r}$, of excess heterozygosity versus Mendelian expectations for $t = 3$.** Recombination fractions estimated from genotype frequencies under Mendelian expectations (h=0.5) versus under modeling a global heterozygosity advantage (h=0.6373) at generation $t = 3$ of a selfing population. This shows that if the population was retaining excess heterozygosity (at a rate of 63.73% each generation as opposed to the Mendelian 50%), then estimating recombination fractions under Mendelian expectations would shrink the map if observed at generation $t = 3$.