

Figure S1 A Venn diagram illustrating the number of SNPs meeting each of our three filtering criteria. Only those SNPs that met all three criteria (451) were included in our analysis.

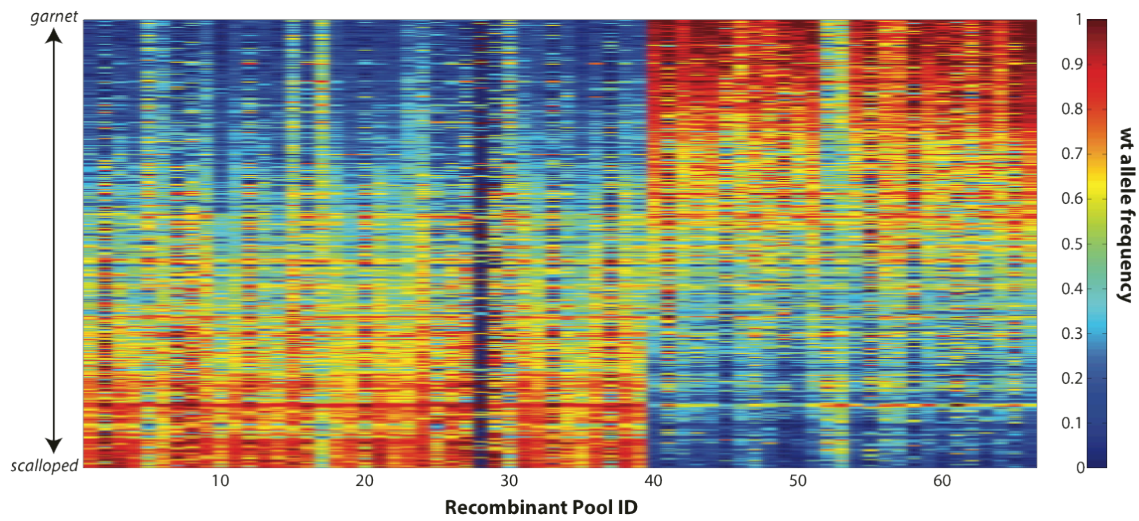


Figure S2 Heat map depicting the frequency of the wild-type (wt) parental allele at each of 451 SNPs for each of the 66 pools of 100 recombinant males. Each column represents a pool, with the top of the plot representing the 5' end of the *g-sd* region and the bottom representing the 3' end. Note that the expectation is that allele frequencies should start at 0 (blue) and increase to 1 (red) from top to bottom or vice versa, depending on the recombinant phenotype class comprising the pool. The pools are ordered such that all of the *g+* pools are presented first followed by the *+sd* pools. Note that in no pool do the empirical allele frequencies meet the theoretical expectation of varying monotonically across the *g-sd* region. For some pools, this expectation is weakly violated, as might be anticipated from sampling bias and variance. In others, the monotonic trend was weak or imperceptible, suggesting additional sources of variation. Only the former class of pools was used for subsequent analyses.

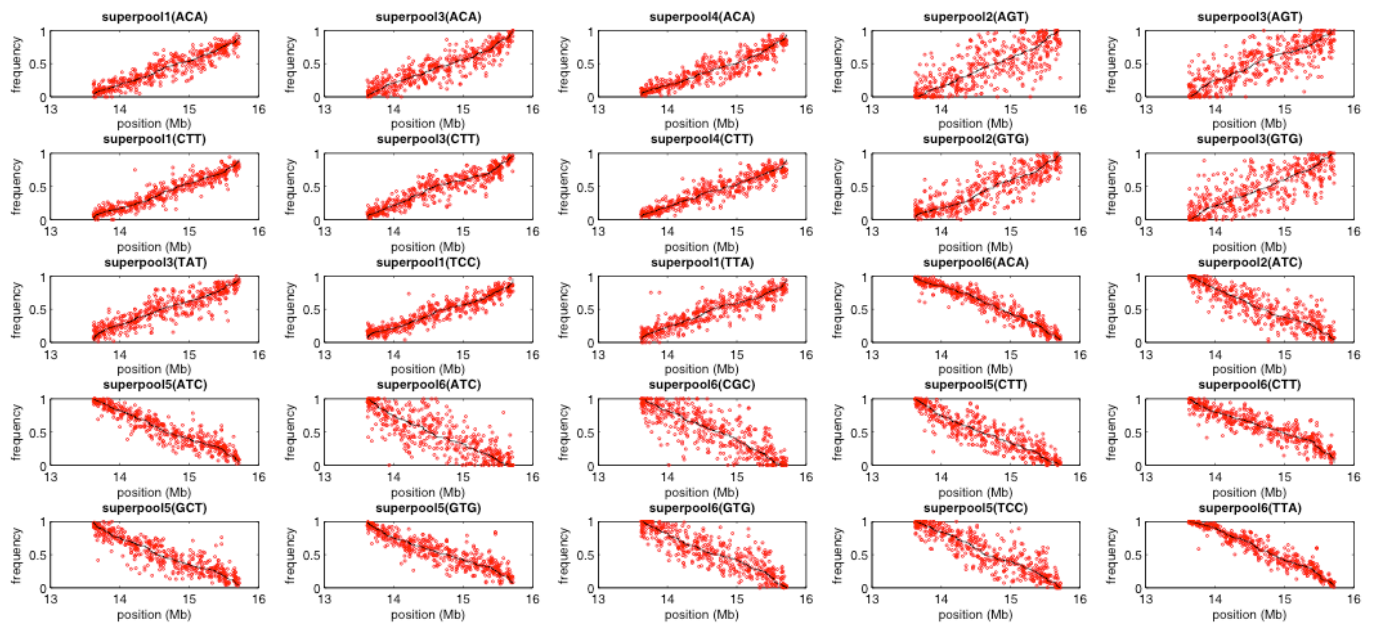


Figure S3 Raw data (open circles) and median-smoothed data (black line) for each of the 25 pools included in our analysis. Physical position (Mbp) is on the x-axis and frequency of the *g-sd* allele is plotted on the y-axis for each of the 451 SNPs included in our analysis.

File S1

Supporting data and k-values

Available for download as a compressed folder at <http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.112.146746/-/DC1>.