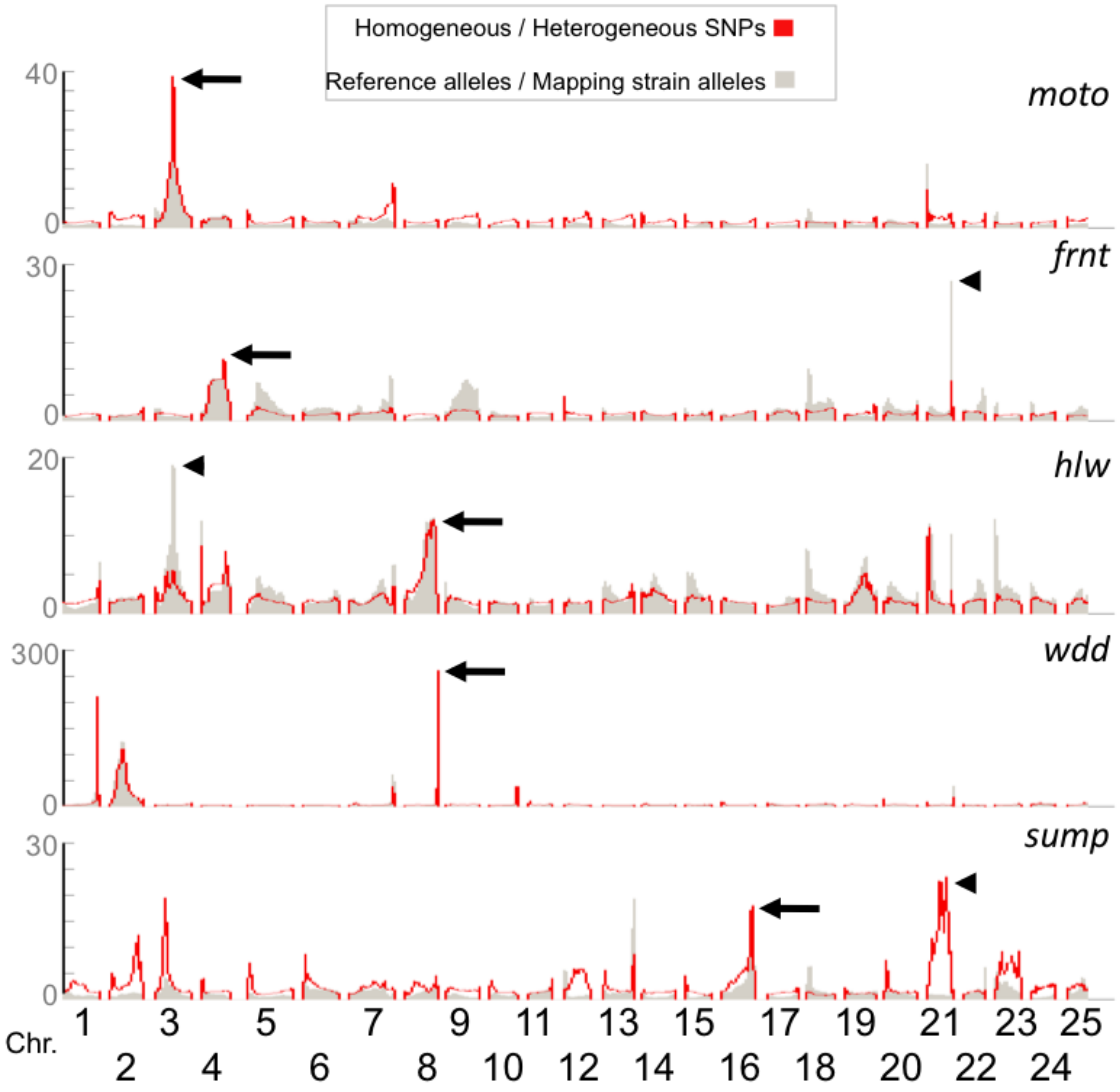

Figure S3 Mapping by combining both the frequency of heterogeneous SNPs and the frequency of mapping strain SNPs helps to eliminate false positives. Graphs show the comparison between the ratio of homogeneous to heterogeneous SNPs (red lines) to the ratio of reference genome alleles to mapping strain alleles (gray bars), for the five mutants analyzed (*moto, frnt, hlw, wdd, sump)*. Ratios were calculated for all 25 chromosomes using sliding windows of 20 cM in size, with an overlap of 19.75 cM between adjacent windows. Genetic distances were defined by the MGH meiotic map. The arrow indicates the linked region for each mutant. For three mutants (*moto, frnt, wdd*), both approaches independently predict the linked region as the region in the genome with the highest ratio. In the *hlw* and *frnt* mutants, other regions show the highest ratio of reference alleles to mapping strain alleles (arrowheads). These regions do not have a high ratio of homogeneous to heterogeneous SNPs. Similarly, for the *sump* mutant, region on Chr21 shows the highest ratio of homogeneous to heterogeneous SNPs, but this region does not have a high ratio of reference alleles to mapping strain alleles (arrowhead). Accordingly, these false positive regions would result in a lower mapping score in our combined analysis and thus would be ranked as less likely to be linked to the mutation.