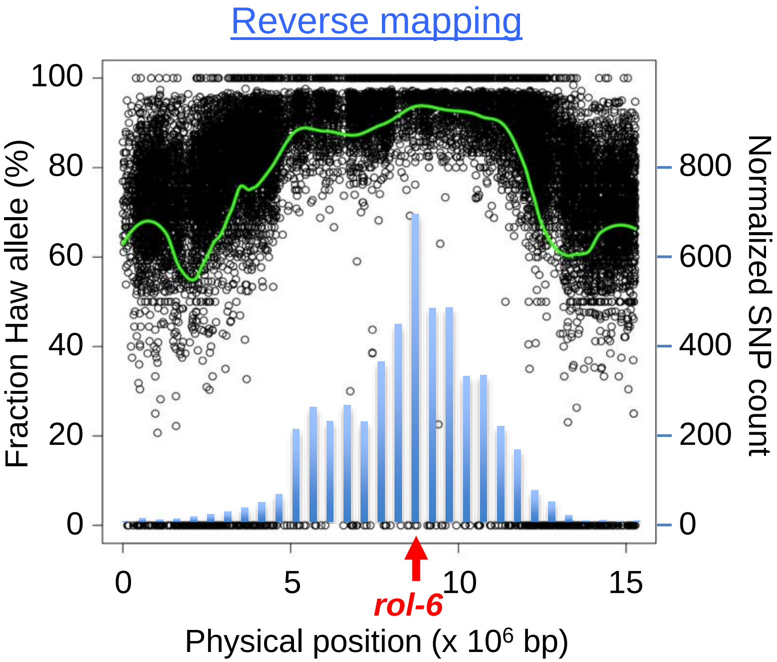

Figure S1. Reverse mapping of dominant mutations. Shown is the identical plot for Figure 2B, overlaid with a histogram (blue bars) of the normalized homozygous SNP count. The data were calculated in 0.5 Mb bins in the same manner as for CloudMap (Minevich *et al.,* 2012): [number of homozygous SNPs / (number of total SNPs – number of homozygous SNPs)] x average number of total SNPs per bin, per chromosome.