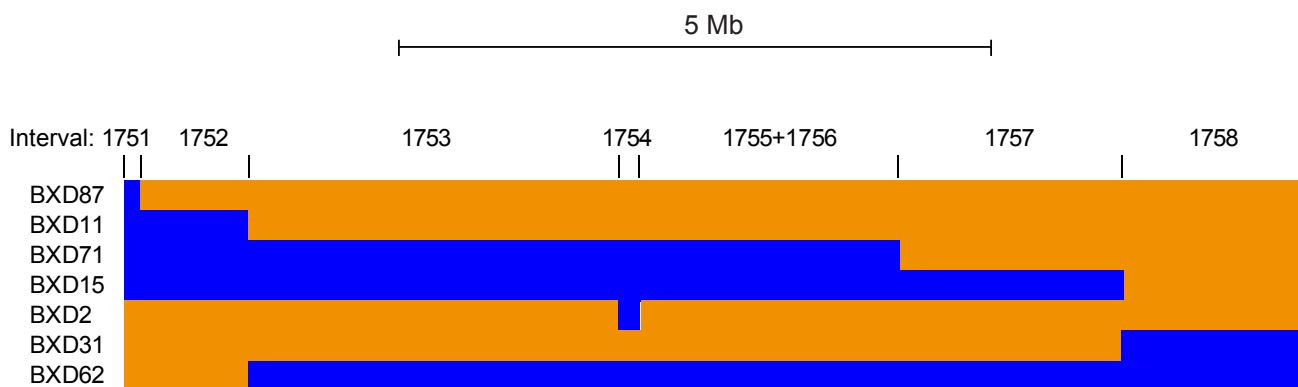
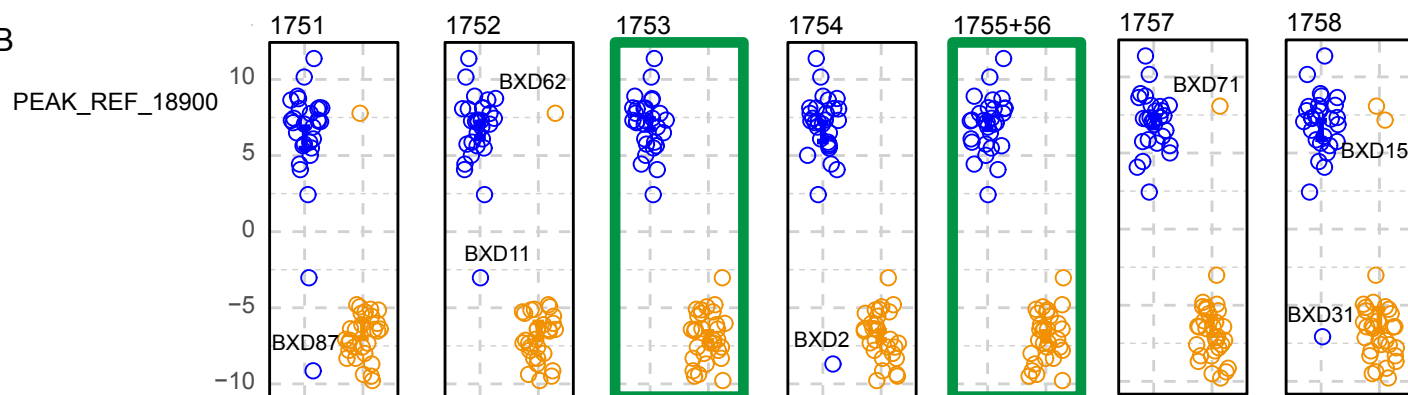


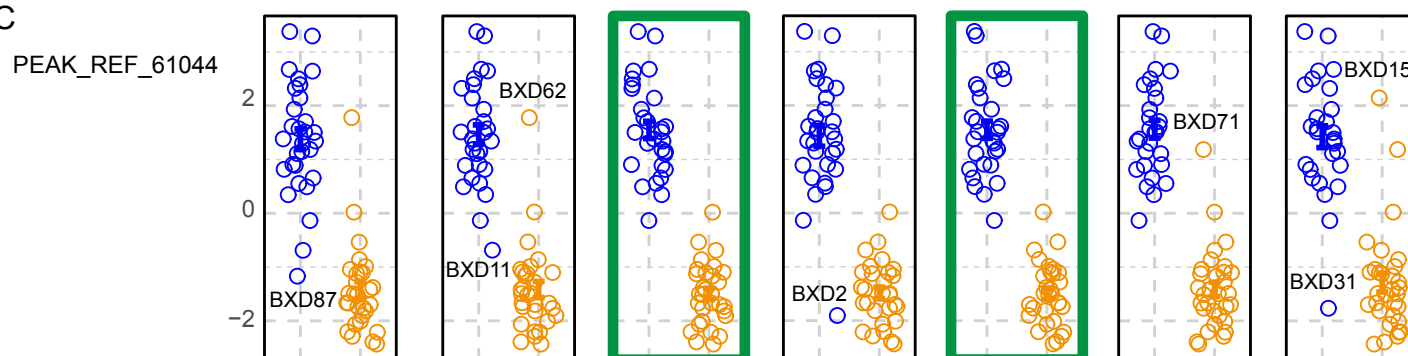
A



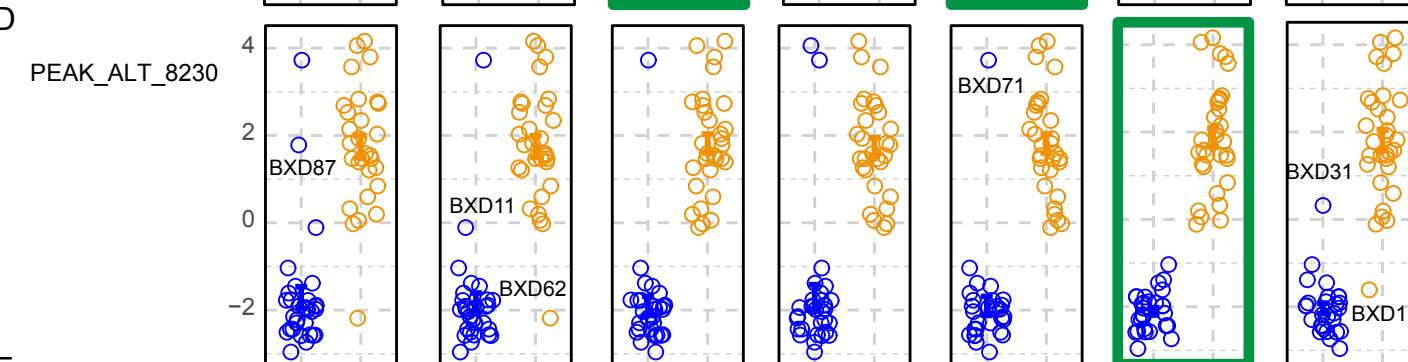
B



C



D



E

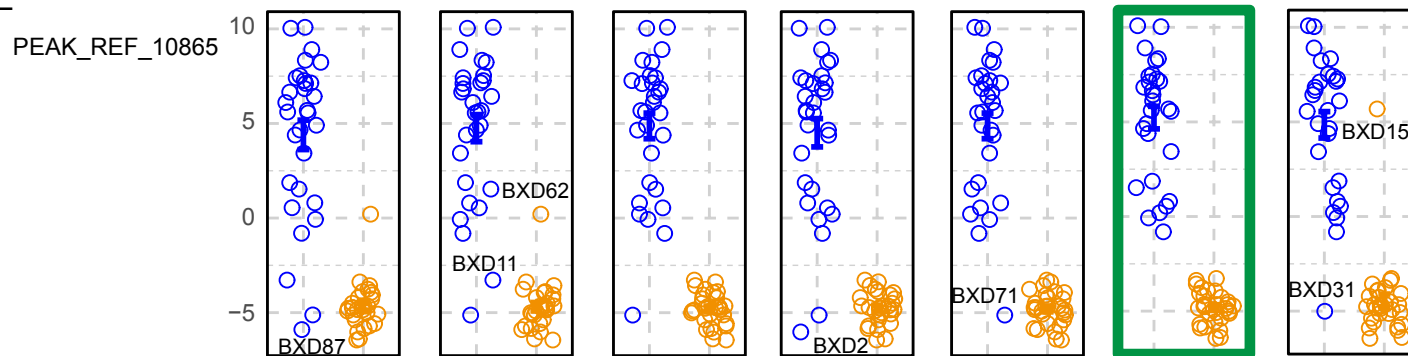


Figure S4. *The Chr 13 QTL is genetically compound.* (A) Schematic of strain distribution patterns, crossover positions, and genomic intervals at the Chr 13 locus for the seven BXD lines with crossovers that bifurcate this region. The B6 genotype is indicated in blue and D2 genotype in orange. Interval identifiers are indicated on top, see Supplemental Table S7 for mm10 base pair positions delineating these intervals. (B-E) Phenotype by genotype plots for each interval indicated in A along Chr 13. Strains for which the H3K4me3 phenotype does not agree with the average distributions by genotype are labeled. For example, in panel B at interval 1754 BXD2 is genetically B6 in this interval, however the phenotype of the peak has low H3K4me3 level, suggesting that the QTL is not located in this interval. (B) Example peak that maps to interval 1753, although the phenotype distribution is similar for intervals 1755+56. BXD strains 11 and 62 clearly show that the QTL is to the right of 1752 and BXD71 indicates that the QTL is to the left of interval 1757. (C) Similar to B, an example H3K4me3 peak that maps to intervals 1755+56. (D and E) Example H3K4me3 peaks that map to interval 1757. BXD71 shows that the QTL is located to the right of intervals 1755+56, while and BXD31 and BXD15 indicate that the QTL is located to the left of interval 1758.