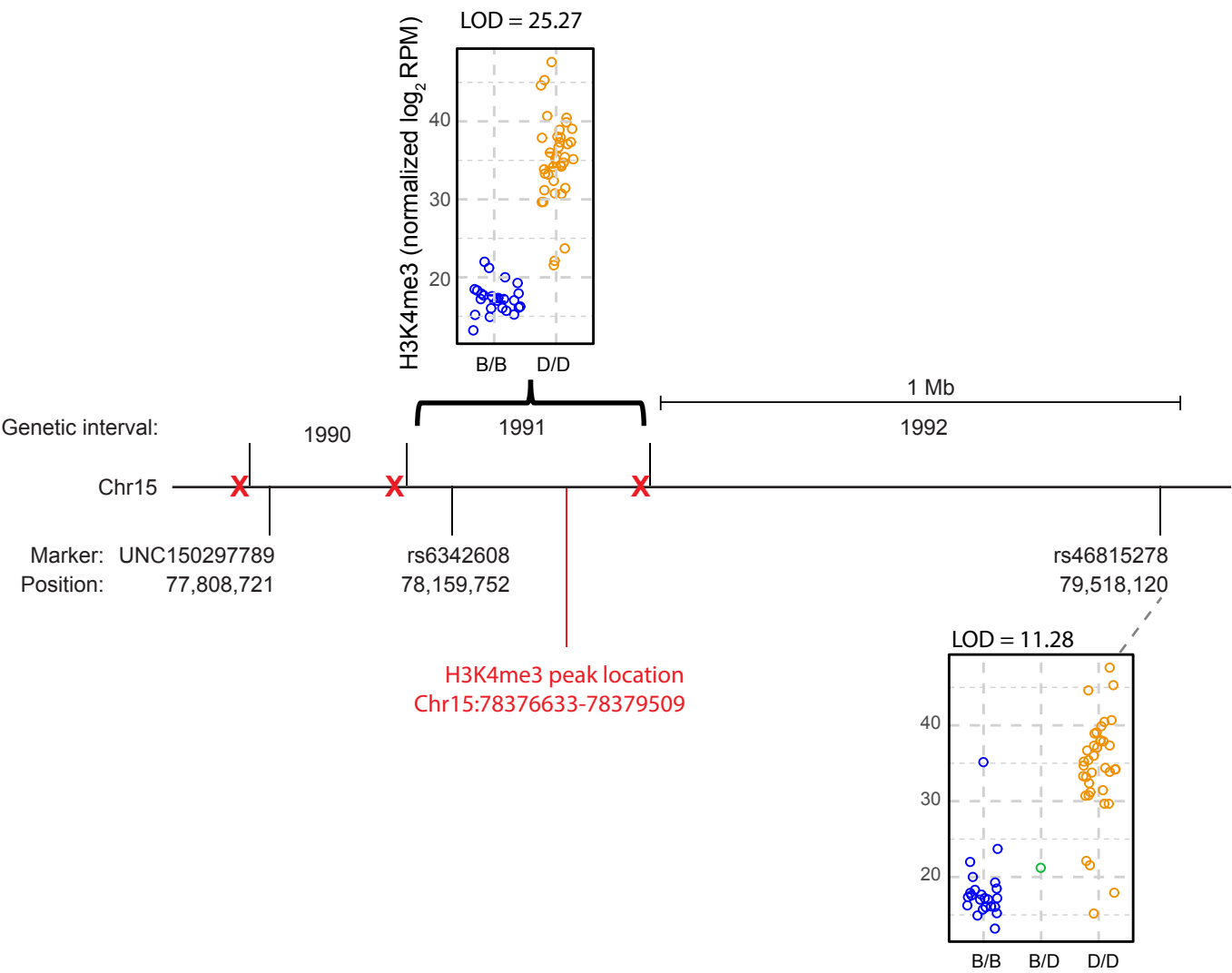
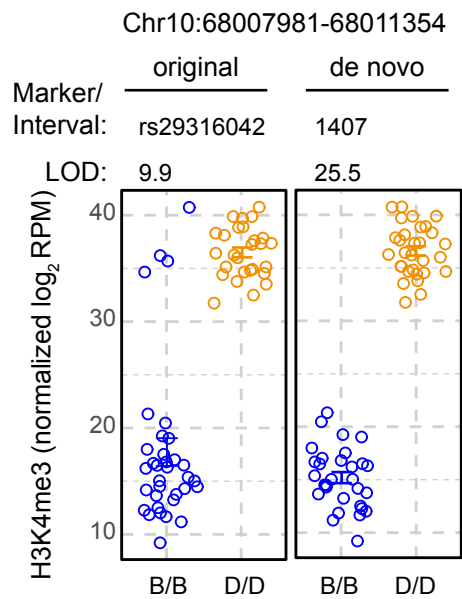


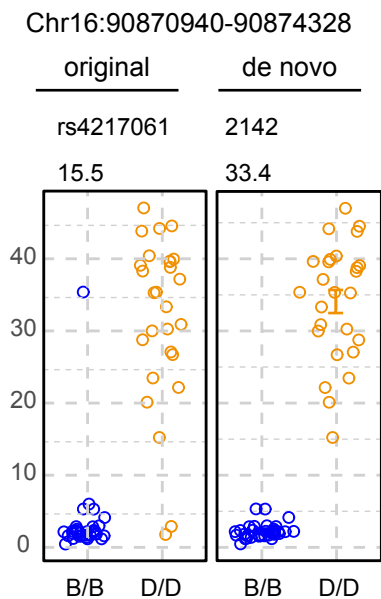
A



B



C



D

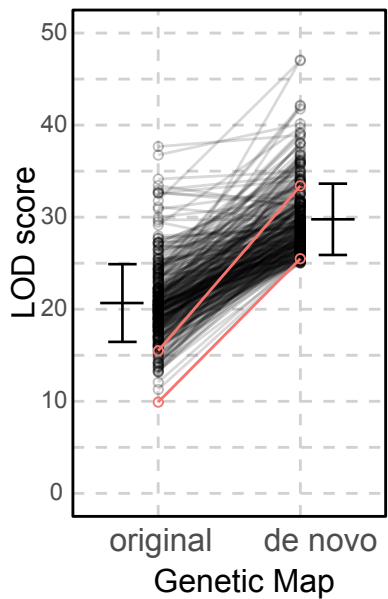


Figure S1. *De novo* genotypes from ChIP-seq data correct inconsistency between genotype and H3K4me3 phenotypes. (A) Schematic of example locus showing the position genetic intervals delineated by *de novo* genotypes (upper) and position of markers from publicly available SNP arrays (lower); red X indicates identified crossovers that separate genetic intervals. The position of the H3K4me3 peak used for QTL mapping is indicated with a red line. Above – Phenotype-by-genotype (PXG) plot showing H3K4me3 level for individual BXD strains binned by the genotype at the mapped QTL using *de novo* genotypes and interval mapping. Using the *de novo* map places the local QTL within the interval that actually contains the H3K4me3 peak. Below - PXG plot at the indicated marker (grey dashed line) with the highest LOD score mapped using publicly available genotypes. (B&C) Similar to B showing PXG plots for H3K4me3 peaks with *cis*-QTL. For each H3K4me3 peak the genomic location of the peak is indicated at the top. Markers for previous genotypes or intervals from *de novo* genotypes are indicated along with and LOD scores derived using both genotypes for QTL mapping. In both cases, the *de novo* genotype resulted in higher LOD scores and better agreement between genotype and H3K4me3 level. Genetic intervals and base pair positions for *de novo* genotypes are found in Supplemental Table S7. (D) Scatterplot showing LOD scores for 310 H3K4me3 mapped as *cis*QTL using both original and *de novo* genetic maps. Lines connect the same H3K4me3 peak between genetic maps to show changes in individual LOD scores. For 98% (n = 304/310) of H3K4me3 peaks, LOD scores improved with new genetic maps with a mean increase in LOD score of 9.1. Error bars indicated mean and standard error. Red circles and lines are the two examples from B and C.