



Figure S2. *Genotyping by ChIP-seq allows for hotspot level resolution for genetic mapping.* (A)

H3K4me3 coverage track showing the indicated region of Chr 12 overlaid with the known genotypes for the RI line BXD1. The boundaries of the D2 and B6 genotypes are taken from publically available genetic maps delimited by the last informative SNPs on the genotype array.

A historical recombination crossover should exist between the D2 and B6 positions within the indicated ~ 40 kb interval. Three H3K4me3 peaks occur in this transition interval in male germ

cells. (B) Expanded region from A, showing coverage of H3K4me3 peaks from ChIP-seq.

Genotyping the DNA fragments isolated from the ChIP-seq experiment identified known SNPs within these peaks. The fraction of B6 SNPs identified are indicated under each peak. The value of the middle H3K4me3 peak suggested that the DNA sequence at this region is heterozygous, although this value is accounted for by multiple SNPs showing a transition from D2 to B6. (C)

Visualization of individual sequence fragments from ChIP-seq show a clear transition from homozygous D2 on the left side of the peak to homozygous B6 on the right side. D2 variants are indicated in orange, B6 variants are indicated in blue. A single 100 bp sequence fragment captures the transition from D2 to B6, suggesting that this is the location of historical crossover.

In addition, this peak was identified as a recombination hotspot by DMC1 ChIP-seq.