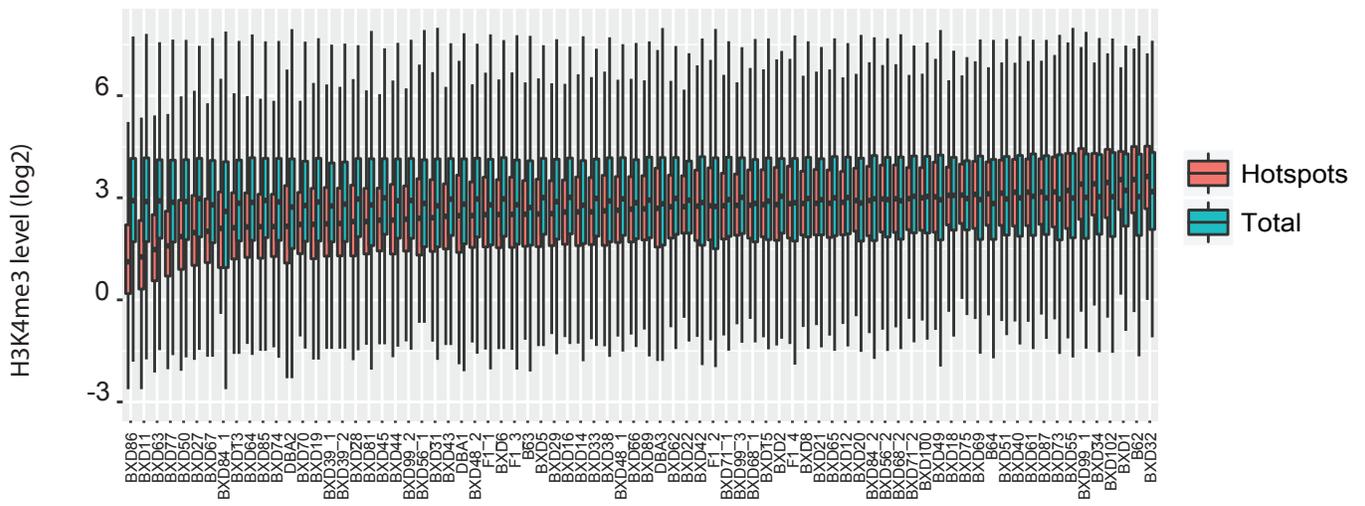
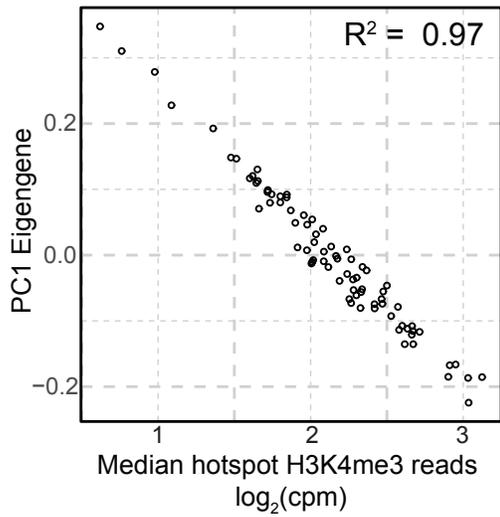


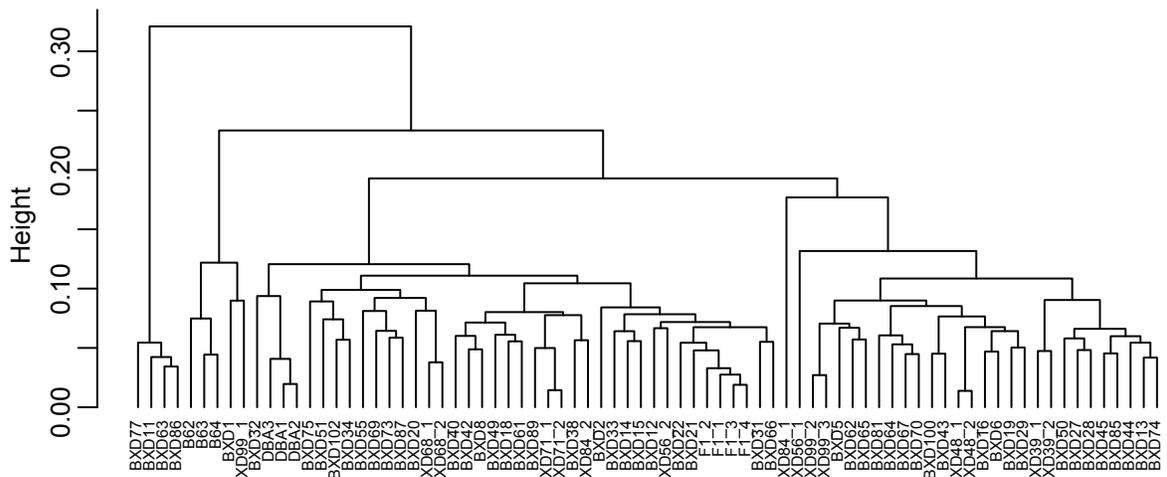
A



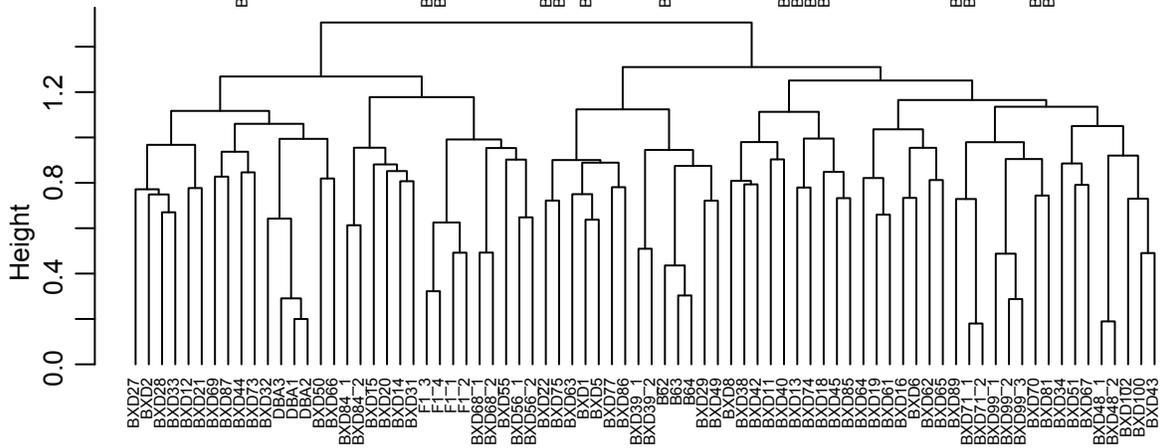
B



C



D



1 **Figure S6.** *PC1 accounts for variation in H3K4me3 level at hotspots.* (A) Box plot showing the  
2 distribution of H3K4me3 levels for all H3K4me3 peaks (green) and recombination hotspots only  
3 (red). Different strains, and sometimes replicates, show different levels of hotspot-specific  
4 H3K4me3, suggesting subtle differences in timing of meiotic entry or progression. While this  
5 could be due to genetic differences, the lack of similarity between biological replicates suggest  
6 other experimental noise, such as litter size or exact timing of birth. (B) Scatterplot of median  
7 H3K4me3 level at hotspots, defined by overlapping DMC1 SSSDs peaks, versus PC1 loadings  
8 for each BXD strain. The majority of the variance in PC1 can be explained by differences in  
9 H3K4me3 level at hotspots. (C) Hierarchical clustering using complete linkage and correlation-  
10 based distance for all H3K4me3 ChIP-seq samples using all 67,100 peaks after TMM  
11 normalization. A few biological replicates for BXD lines did not cluster together, namely BXD84,  
12 BXD56, and one replicate of BXD99. (D) Hierarchical clustering after subtraction of PC1 leads  
13 to complete clustering among replicates. To correct for these discrepancies PC1-subtracted  
14 data was used for QTL mapping and all further analyses in the manuscript.