

A box plot showing H3K4me3 levels (log2) for 1000 genes. The y-axis ranges from -3 to 6. The x-axis lists 1000 genes, with labels rotated vertically. The legend indicates two series: 'Hotspots' (red) and 'Total' (teal). For each gene, there are two box plots: a red one for 'Hotspots' and a teal one for 'Total'. The 'Total' values are generally higher than the 'Hotspots' values, with both series showing a similar distribution across the genes.

Scatter plot showing the relationship between Median hotspot H3K4me3 reads ($\log_2(\text{cpm})$) and PC1 Eigengene. The plot shows a strong negative correlation with $R^2 = 0.97$.

The dendrogram illustrates the hierarchical clustering of 48 samples based on their height. The y-axis represents the height, ranging from 0.00 to 0.30. The x-axis lists the samples, which are grouped into three main clusters: B (Bos taurus), F (Friesian), and X (Xenopus laevis). The dendrogram shows that samples within each group cluster together, and the three groups themselves cluster together at a height of approximately 0.30.

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