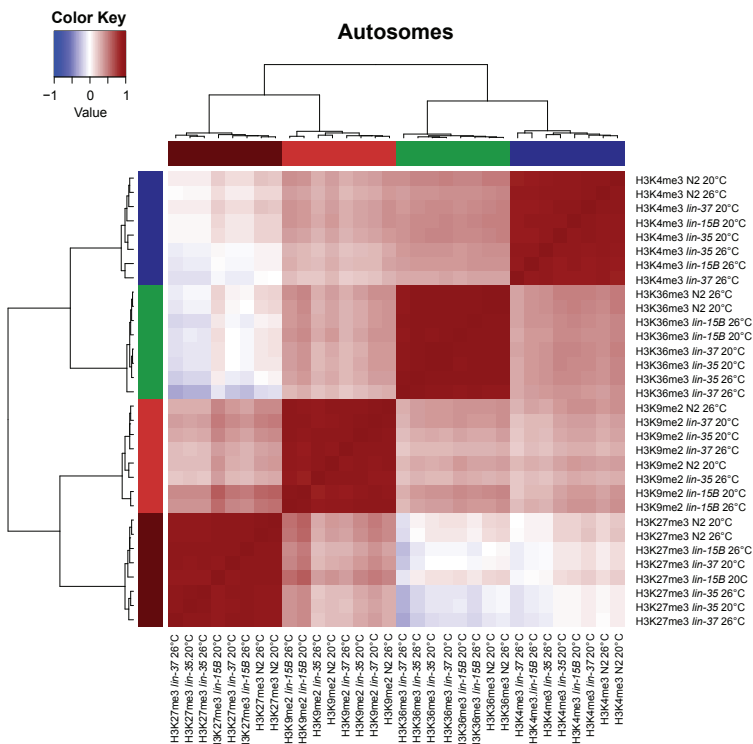


A



B

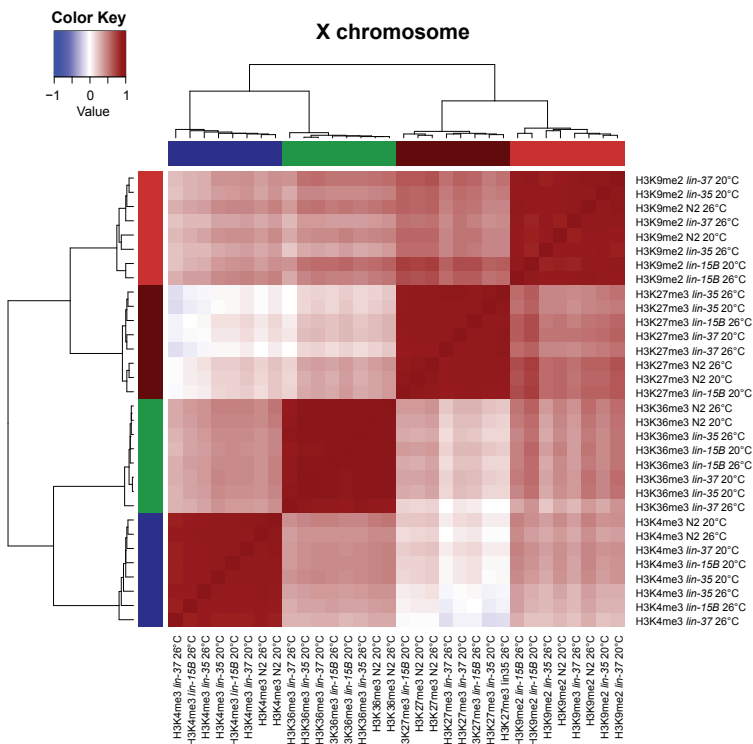


Figure S2: Heatmap and clustering of genome-wide ChIP-seq signals in genotypes and temperatures based on Pearson correlation. (A, B) Heatmap and hierarchical clustering of H3K9me2, H3K27me3, H3K36me3, and H3K4me3 ChIP-seq signals in 1kb windows in the different genotypes and temperatures based on Pearson correlation on the autosomes (A) and the X chromosome (B).