

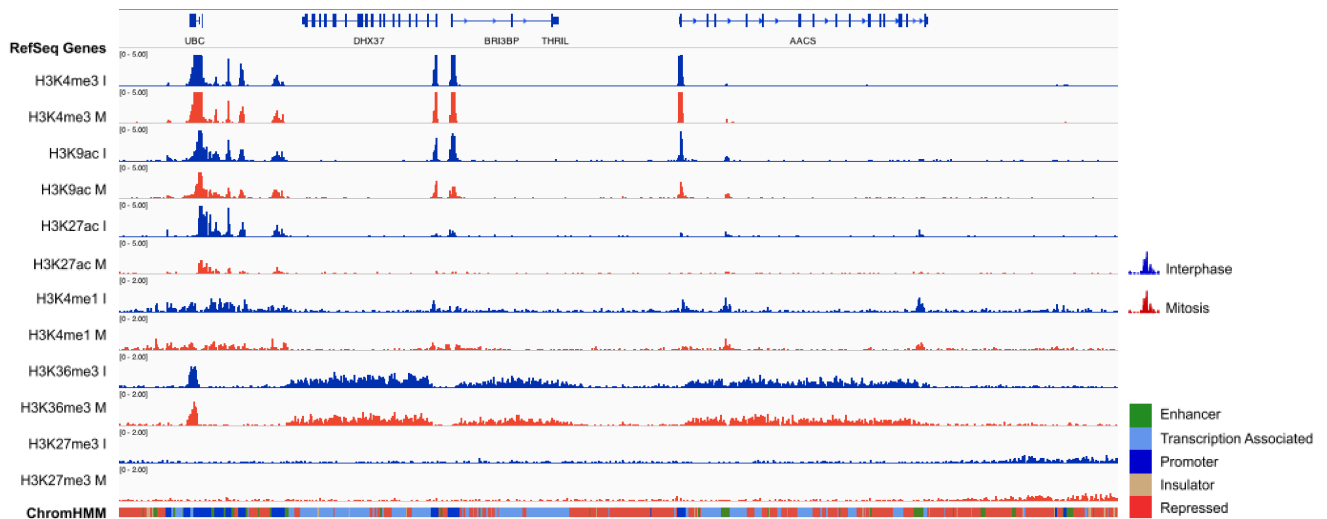
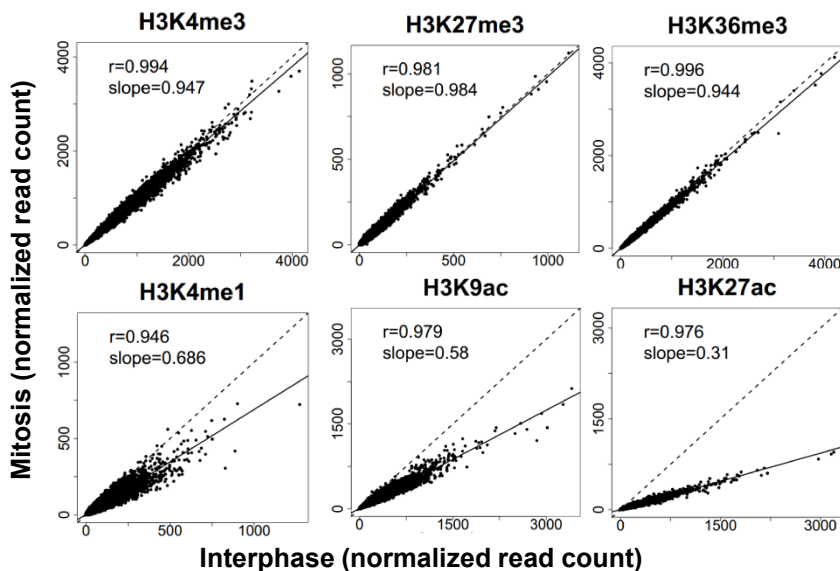
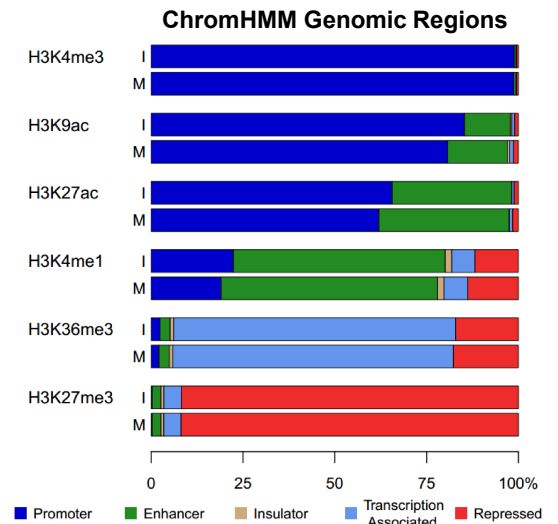
A**B****C**

Figure S4. High concordance between mitotic and interphase histone modification patterns (biological replicate). (A) Integrative genomic viewer (IGV) tracks showing the alignment for the indicated histone modification ChIP-seq results for interphase (blue) and mitosis (red) samples on an approximately 315kb region on Chromosome 1. The scale of each track was adjusted to the total number of reads using the Normalize Coverage Data option in IGV (see methods). The ChromHMM annotation for each genomic region is shown below the plot using the same color code as in C. (B) Scatter plots showing the normalized read counts for all the regions enriched in each modification (see methods for the peak calling details) in mitosis versus interphase. (C) Bar plots showing the percentage of reads in peak regions per ChromHMM category.