



**Figure S2.** Patterns of histone modifications associated with maize genes. Genes were divided into 10 bins. ChIP-seq read counts of H3K36me3, H3K9ac, and H3K4me3 of each bin and 100-bp windows upstream and downstream were calculated and plotted for 29,289 maize genes (dashed lines) and 27 centromeric genes (solid lines).