



Figure S3. Distribution of sequencing reads associated with histone modifications and CENH3 in the centromeric and pericentromeric regions of maize chromosome 2, 3, 4, 8, 9 and 10. Chromosomes were divided into 100-kb windows and read numbers of CENH3, H3K4me3, H3K27me2, H3K9ac, H3K27me3, H3K36me3 and randomly generated 150-bp reads were calculated in each window. The left y-axis represents the numbers of CENH3 ChIP-seq and random reads in each 100-kb window. The right y-axis represents the relative read density associated with different histone modifications.