Figure S1. Mapping of CENH3-binding domains in maize chromosomes. The *y*-axis shows the fold (0-100) of enrichment of ChIP-seq reads using input sequences as a reference. Each chromosome was divided into 10-kb windows. Fold change between ChIPed reads and input reads of each window was calculated. Red and blue bars represent the fold change data from 0.2U and 5U ChIP-seq libraries, respectively.