Description of Additional Supplementary Files

File name: Supplementary Data 1:
Description: The 104 maize leaf TFs selected for ChIP-seq

File name: Supplementary Data 2:
Description: Quality control information of the ChIP-seq libraries

File name: Supplementary Data 3:
Description: List of ChIP-seq and ATAC-seq libraries

File name: Supplementary Data 4:
Description: Pearson correlation of ChIP-seq library replicate bam files

File name: Supplementary Data 5:
Description: TF binding loci in the maize leaf

File name: Supplementary Data 6:
Description: TF classification based on their target gene GO-term and MAPMAN functional category enrichment

File name: Supplementary Data 7:
Description: The hub genes and the high TF occupancy regions

File name: Supplementary Data 8:
Description: eQTL enrichment in TF binding sites

File name: Supplementary Data 9:
Description: GWAS hit enrichment in TF binding sites

File name: Supplementary Data 10:
Description: The gene regulatory network

File name: Supplementary Data 11:
Description: Network modules

File name: Supplementary Data 12:
Description: Performance of bag-of-k-mers models

File name: Supplementary Data 13:
Description: Results of bag-of-k-mers models

File name: Supplementary Data 14:
Description: Performance of co-localization models