

## Figure or Table legends for supplementary materials

Figure S1 Enriched Gene Ontology (GO) terms among the common upregulated DEGs in response to drought stress.

Figure S2 Enriched Gene Ontology (GO) terms among the common downregulated DEGs in response to drought stress.

Figure S3 The Principal component analysis (PCA) and the heatmap of correlation analysis among replicates in the same group and between different groups. (a) PCA analysis; (b) heatmap of correlation analysis. The triangles represents the mean value of each group.

Figure S4 The enrichment of DEGs in GO terms related to drought stress. GO terms: (GO:0050896): response to stimulus; (GO:0006952): defense response; (GO:0006979): response to oxidative stress; (GO:0006950): response to stress; (GO:0055114): oxidation-reduction process; (GO:0009628): response to abiotic stimulus; (GO:0042744): hydrogen peroxide catabolic process; (GO:0045454): cell redox homeostasis; (GO:0006633): fatty acid biosynthetic process; (GO:0009408): response to heat; (GO:0009414): response to water deprivation; (GO:0042542): response to hydrogen peroxide; (GO:0009753): response to jasmonic acid; (GO:0000302): response to reactive oxygen species; (GO:0009867): jasmonic acid mediated signaling pathway; (GO:0009739): response to gibberellin; (GO:0009415): response to water; (GO:0031348): negative regulation of defense response; (GO:0009723): response to ethylene; (GO:0010286): heat acclimation; (GO:0009740): gibberellic acid mediated signaling pathway; (GO:0006635): fatty acid beta-oxidation; (GO:0009407): toxin catabolic process; (GO:0009686): gibberellin biosynthetic process; (GO:0080148): negative regulation of response to water deprivation.

Figure S5 Expression profiles of available *ZmbHLHs* in the present RNA-seq data. (a,b) Comparison between NT (drought) and NT (control) of upregulated *ZmbHLHs* (a) or downregulated *ZmbHLHs* (b); (c,d) Comparison between OE (control) and NT (control) of upregulated *ZmbHLHs* (c) or downregulated *ZmbHLHs* (d). Heatmaps were generated based on the FPKM value (Z-score method). The redder the color, the higher the gene expression level. FPKM, fragments per kilobase of transcript sequence per million fragments mapped. bHLHxxx represent putative *ZmbHLHs*.

Table S1 Primers used in the present study

Table S2 Summary of reads, mapped to B73 reference genome

Table S3 The top 20 of significantly enriched Gene Ontology (GO) terms among DEGs in response to drought stress

Table S4 DEGs differing in the highest and lowest expression level under drought conditions

Table S5 The nucleotide similarity of *ZmbHLHs* with *CgbHLH001*

Table S6 DEGs related to the photosynthesis