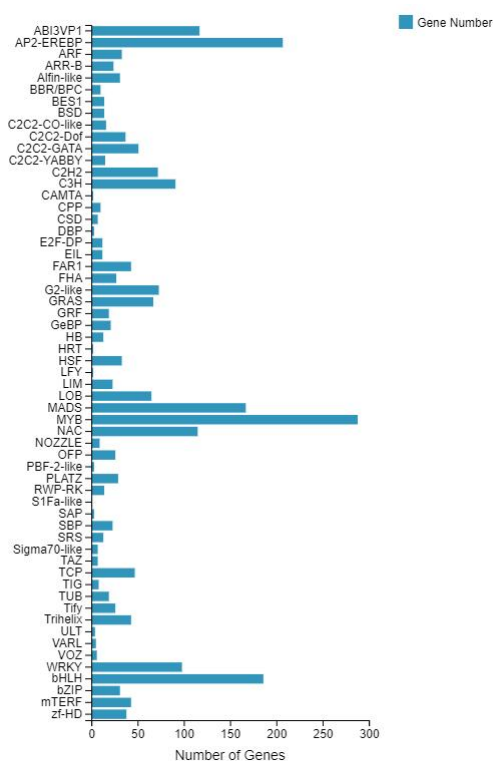


Table S1 Primers used for qRT-PCR

Gene ID	primer-F (5'-3')	primer-R (5'-3')
<i>Solyc04g081000</i>	GACAGAGGATGGGAGAAAGCC	CAGTTGGAAATCCAAGCACGG
<i>Solyc04g015530</i>	CCACCATTGCCACAGGTGAT	ATCCTCCCGGCCAAGTCTTA
<i>Solyc05g056620</i>	TCATGGCATTGTGGTGAGCA	TCAGGCCCTACTTGTGAGGT
<i>Solyc02g087860</i>	AGCAGAAGGTCGAGGCAATC	GATGCCGATGCCTTGCTAGA
<i>Solyc08g067230</i>	GAACTCAGGCACCTAAAGGG	TGTCTGCTCAAACACTTCCCC
<i>Solyc02g071730</i>	CTGCGCGCACAAATTGAAAA	ATGCTGATGCTGAGCTCTCT
<i>Solyc07g062710</i>	TTCTACGCCGTCGGATCAAG	TTCTCCGGGCTCATTCTTCG
<i>Solyc02g083950</i>	TGCAGGCAAAGTAGTAGCCG	AGCAGCAATGAGCCTCTTCTT
<i>SIEF-1α</i>	CCACCAATCTTGTACACATCC	AGACCACCAAGTACTACTGCAC

Table S2 qRT-PCR reaction system

Reactant of the system	The required volume
cDNA	2 μL
primer-F (10 μM)	0.5 μL
primer-R (10 μM)	0.5 μL
2×ChamQ SYBR qPCR Master Mix	10 μL
RNase-Free Water	7 μL
Total volume	20 μL

**Figure S1.**Classification of transcription factor families to which genes belong

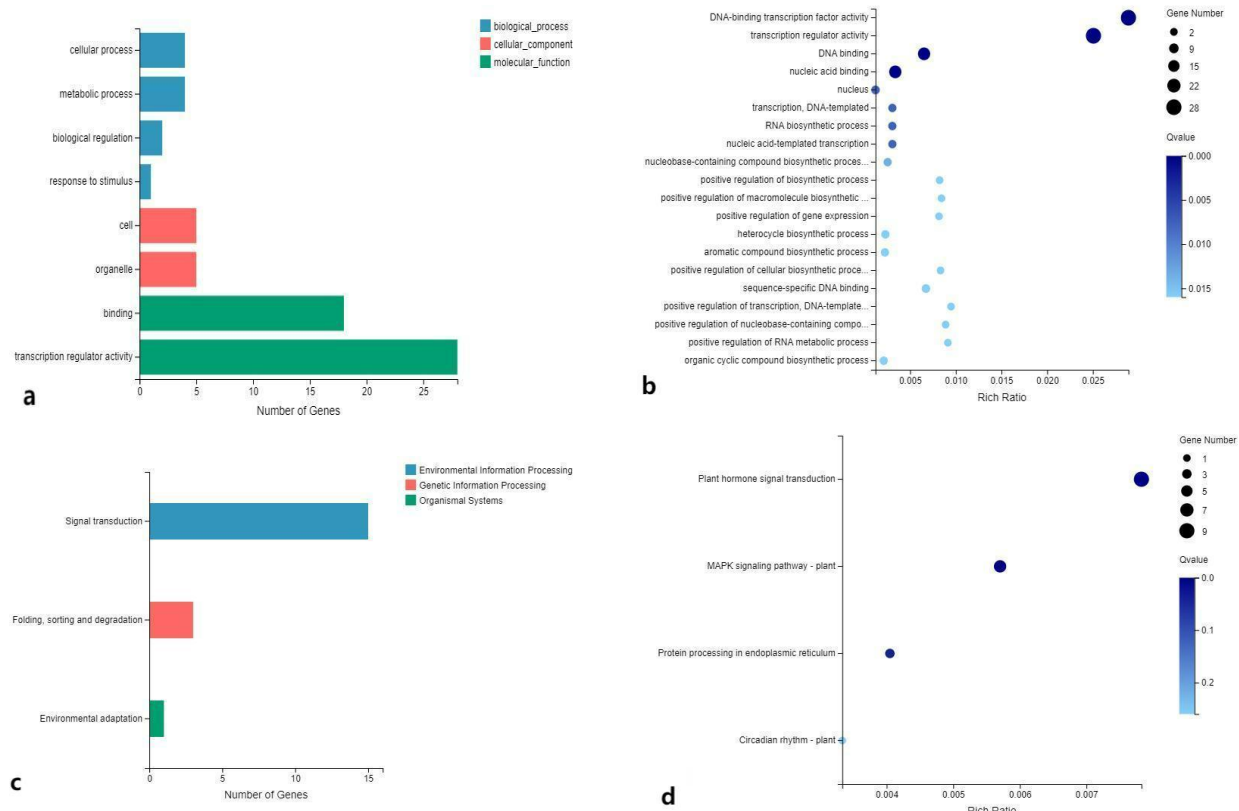


Figure S2.GO analysis and KEGG Pathway analysis of bZIP family.(a)GO classification of bZIP family(b)GO enrichment bubble map of the bZIP family(c)KEGG Pathway of bZIP family(d)KEGG Pathway enrichment bubble map of the bZIP family.

Note: Rich Ratio: enrichment ratio, the larger the bubble, the greater the number of genes