
Supplemental material

Table S1. RT-PCR of primers of *CmPEBP* genes.

Genes	Forward primer sequence (5'—3')	Reverse primer sequence (5'—3')
<i>CmFT1</i>	ATGTCTTGCAATAGGGAGGGT	TATCTTCTTCTGGCGGCATT
<i>CmFT2</i>	ATGCCGAGGGAAAGGGA	TCCGTCTTCCACCAAATCTA
<i>CmFT3</i>	ATGCCGAGGGAAAGGGA	TCCGTCTTCTACCAAATCCA
<i>CmTFL1</i>	ATGTCGCTTGCAATAGGG	TCTTCTTCGTGCGGCATT
<i>CmTFL2</i>	ATGTCTTGCAATAGGGAGGGT	TTATCTTCTTCTGGCGGCATT
<i>CmTFL3</i>	ATGGCAAGATTAACTTCGGG	TCGTCTTCTGGGAGCTGTTT
<i>CmTFL4</i>	ATGTCAAGAATGAATGAGCCA	ATCTTCTACGGGCTGCATTT
<i>CmMFT1</i>	ATGGCAAGATTAACTTCGGG	TCGTCTTCTGGGAGCTGT
<i>CmMFT2</i>	ATGGGTTCAACGGCATTTTA	AACCGAGATTCTTCCTCTTCCTAG

Table S2. qRT-PCR of primers of *CmPEBP* genes.

Genes	Forward primer sequence (5'—3')	Reverse primer sequence (5'—3')
<i>CmFT1</i>	CCAGCGACAACAGGAGCACAG	ACTGGAGATCCGAGGTTGTAGAGC
<i>CmFT2</i>	CCCAAGGCCAACAATAG	ATAAACTGCGGCTACTGG
<i>CmFT3</i>	GTGATATGAGAGCCCAAGGC	TCCGAGGTTGTAGAGCTCCG
<i>CmTFL1</i>	CTGATGCTACTTTTGGACGG	CGGTAACCCCAAGTCATTTT
<i>CmTFL2</i>	GGACGGGAGATTGTGAGCTA	TGGCCTCACTGATTGCCTTG
<i>CmTFL3</i>	GACATCCCAGGCACCACT	GTCATTCTCACGAGCAAAGC
<i>CmTFL4</i>	GAGGTGGTGGACACATTCGC	TGGAACGTCTGGATCGGTCA
<i>CmMFT1</i>	TGGTGAATGGTCAAGGTGC	ACCCTCTGGTAGACCTTTT
<i>CmMFT2</i>	CAACATTCCTGGTGGCTCCTTGAC	TGGACTCAGATTGTGCTTGCTTG
<i>CmEF</i>	ATTGAGCGATCCACCAACTTGAC	CCATACCAGGCTTGATGACACCAG

Table S3. Comparison of the 9 CmPEBP ORFs and putative amino acid sequences.

	Putative protein sequences identity (%)								
	<i>CmFT1</i>	<i>CmFT2</i>	<i>CmFT3</i>	<i>CmTFL1</i>	<i>CmTFL2</i>	<i>CmTFL3</i>	<i>CmTFL4</i>	<i>CmMFT1</i>	<i>CmMFT2</i>
<i>CmFT1</i>	100.0	90.8	91.4	56.3	50.6	56.4	58.7	19.5	36.9
<i>CmFT2</i>	92.2	100.0	93.7	54.5	49.4	55.8	57.6	18.2	38.7
<i>CmFT3</i>	92.6	96.4	100.0	55.1	49.4	55.2	56.4	18.2	36.9
<i>CmTFL1</i>	56.0	54.4	55.4	100.0	91.0	65.5	76.8	19.0	38.2
<i>CmTFL2</i>	56.5	54.9	55.9	99.0	100.0	61.7	71.9	17.8	36.0
<i>CmTFL3</i>	54.6	53.9	53.7	66.4	66.9	100.0	65.3	19.5	37.1
<i>CmTFL4</i>	57.2	55.7	56.6	79.0	79.7	64.1	100.0	17.1	38.7
<i>CmMFT1</i>	35.7	35.5	34.7	38.0	37.8	38.6	37.0	100.0	19.6
<i>CmMFT2</i>	47.2	47.6	47.6	48.9	49.2	47.2	47.7	39.1	100.0

The identity of ORF sequences (%)

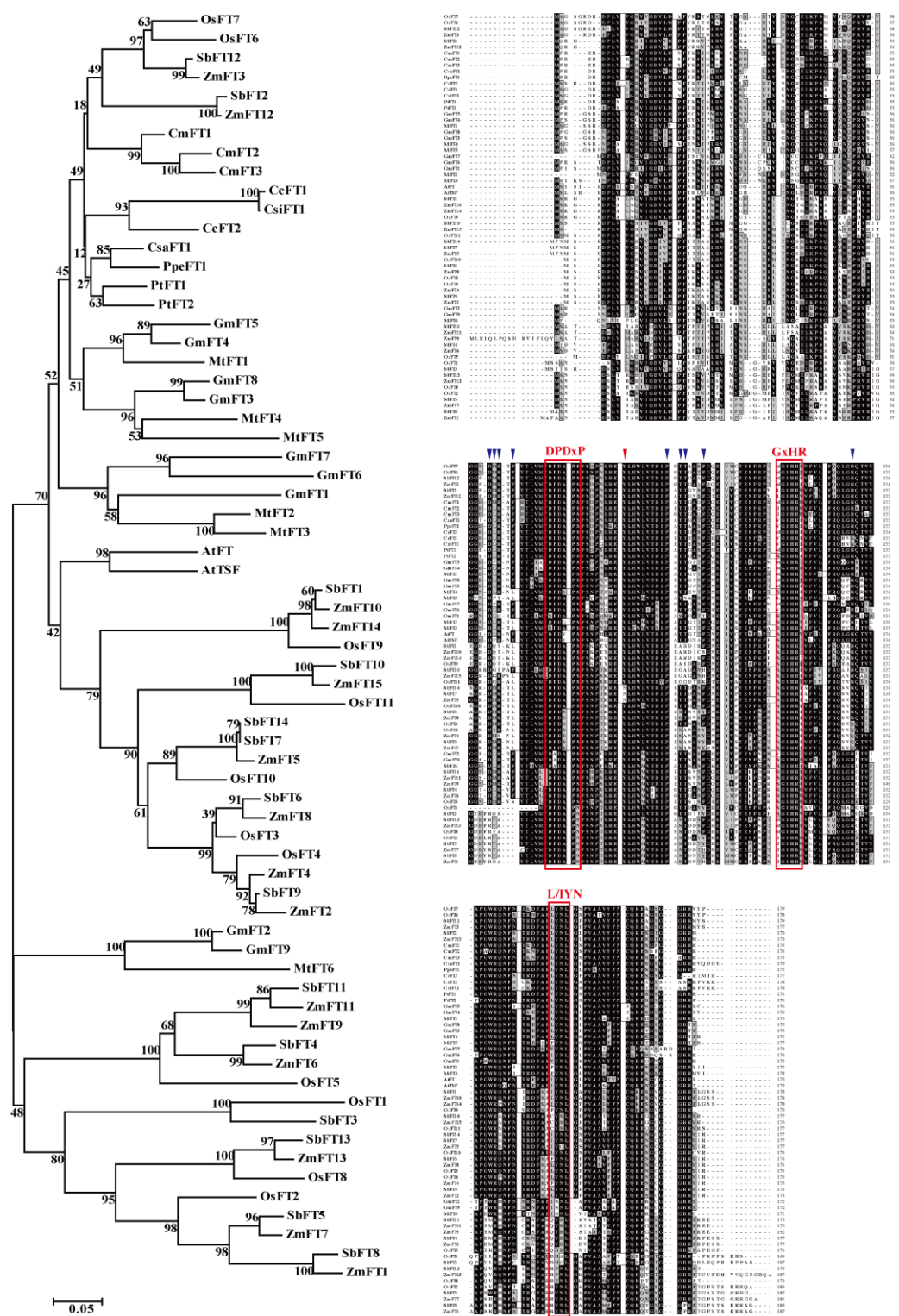


Figure S1. Predicted amino acid sequence alignment and phylogenetic tree of the *CmFTs* with the FT-like genes of other plant species.

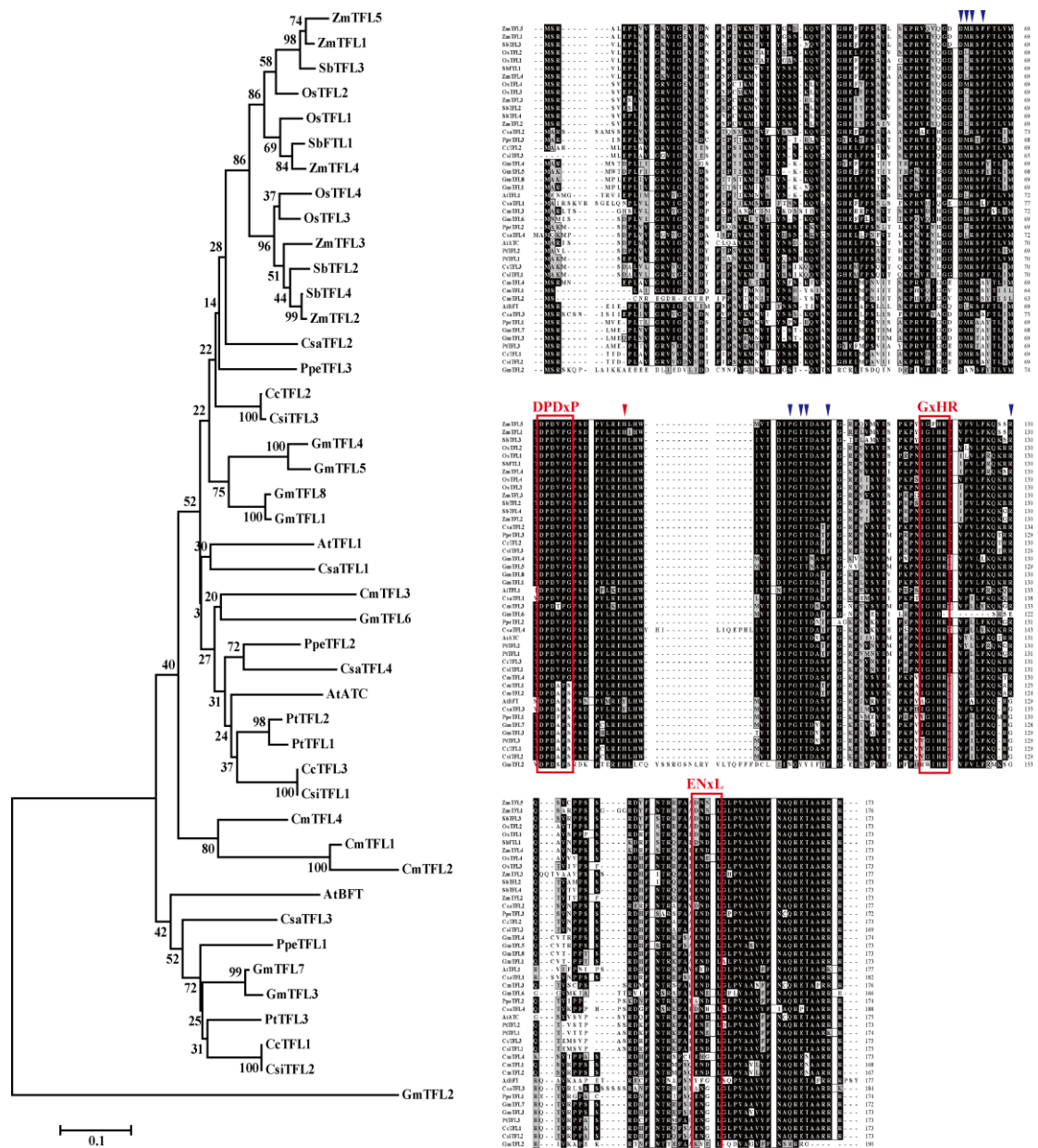


Figure S2. Predicted amino acid sequence alignment and phylogenetic tree of the *CmTFLs* with the TFL-like genes of other plant species.

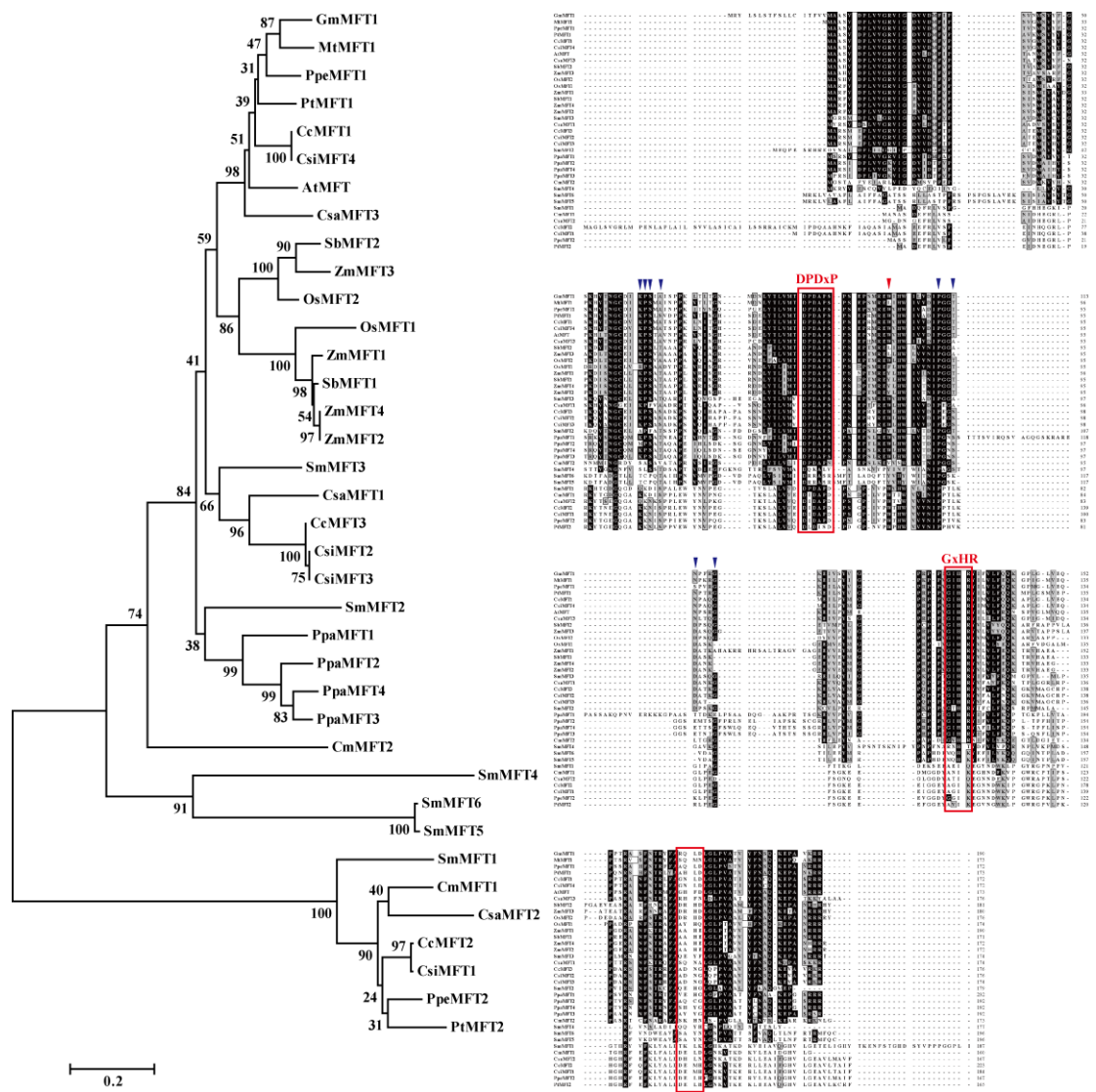


Figure S3. Predicted amino acid sequence alignment and phylogenetic tree of the *CmMFTs* with the MFT-like genes of other plant species.

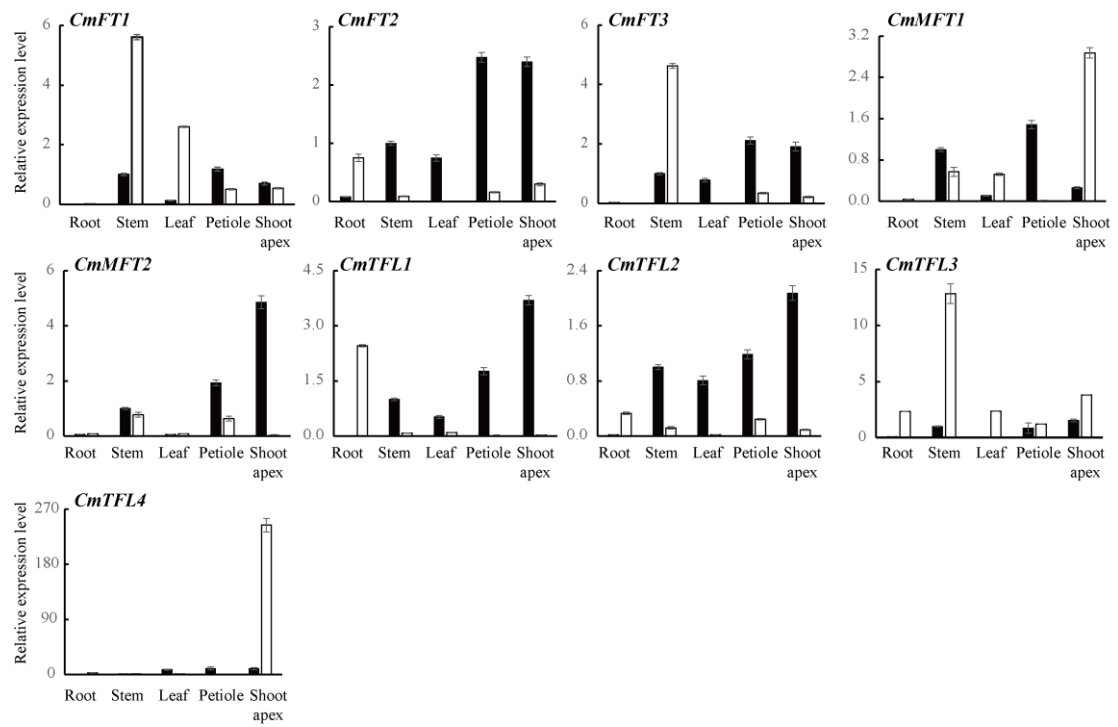


Figure S4. Tissue-specific expression profiles of *CmPEBPs*.

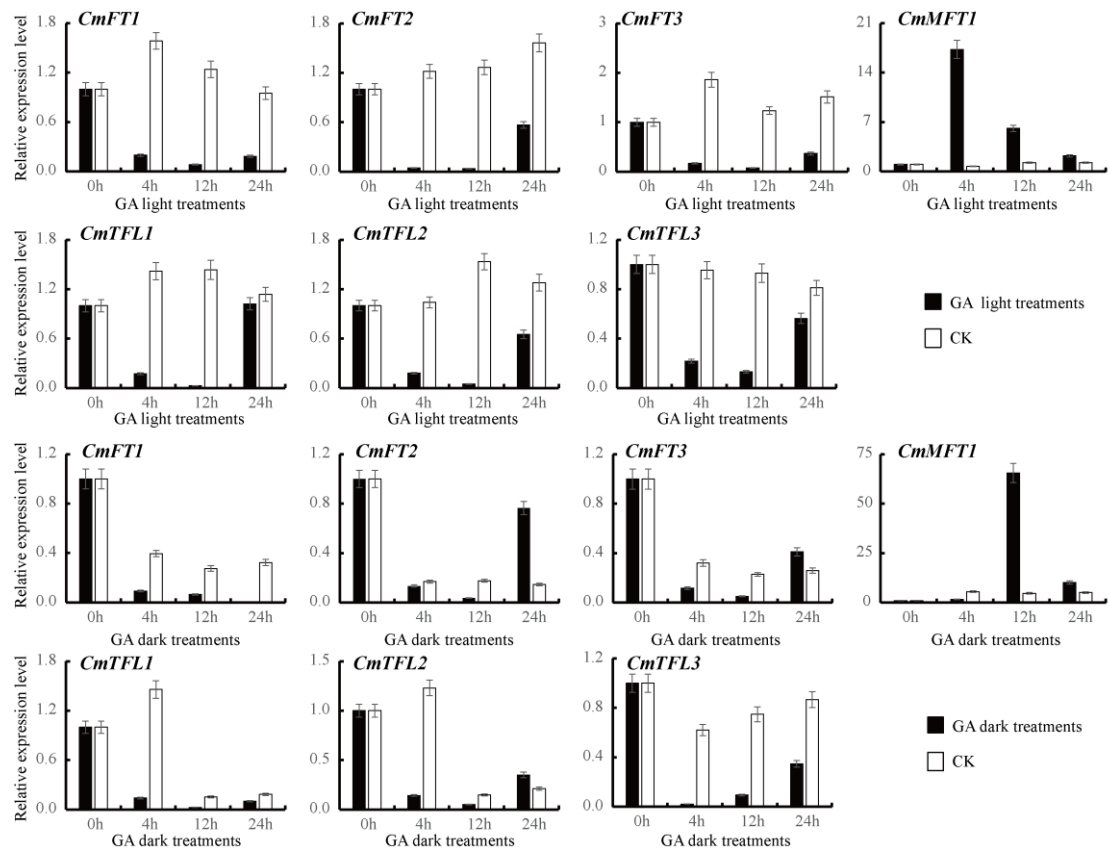


Figure S5. Expression profiles of *CmPEBP* genes in Chrysanthemum leaves under GA stresses.

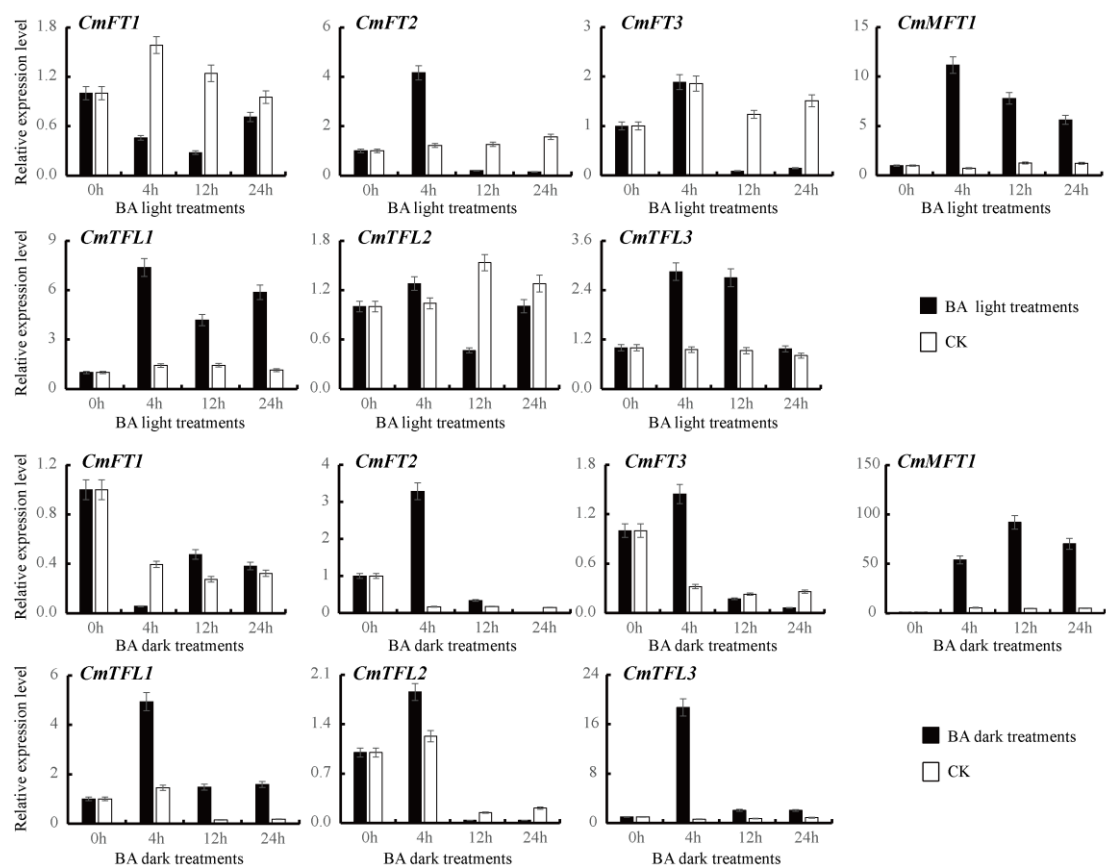


Figure S6. Expression profiles of *CmPEBP* genes in Chrysanthemum leaves under BA stresses.

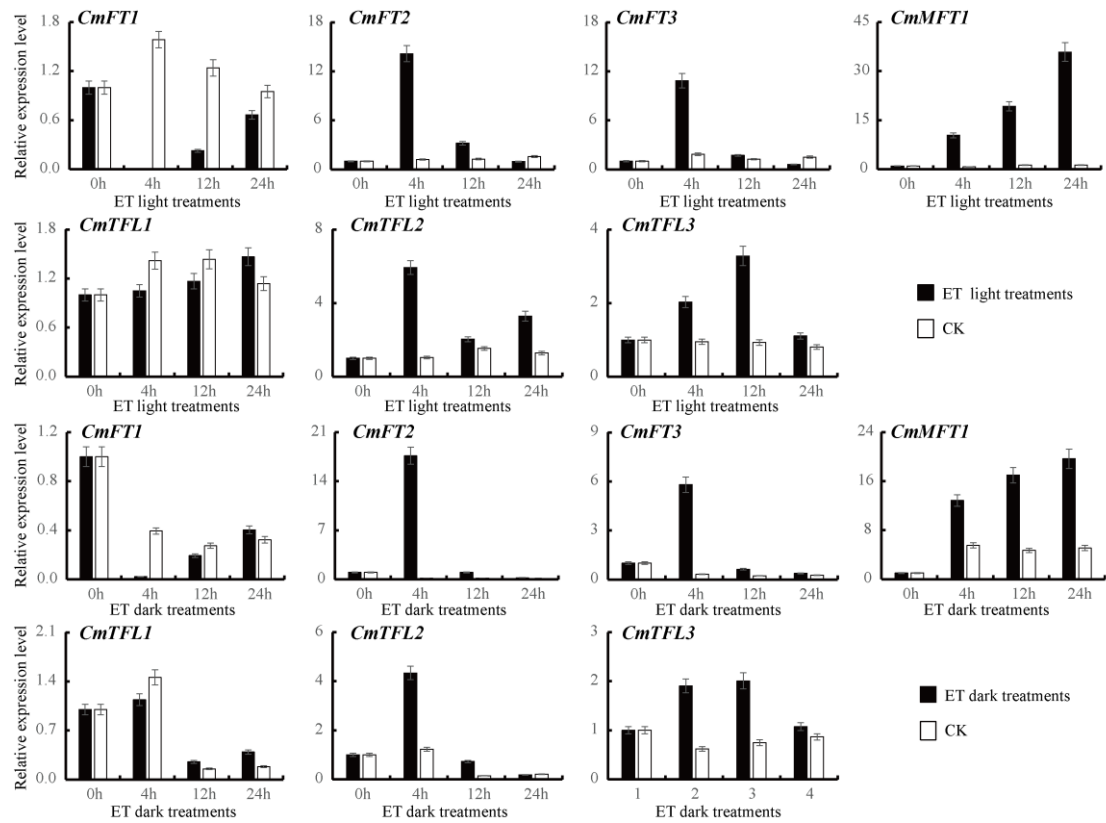


Figure S7. Expression profiles of *CmPEBP* genes in Chrysanthemum leaves under ET stresses.

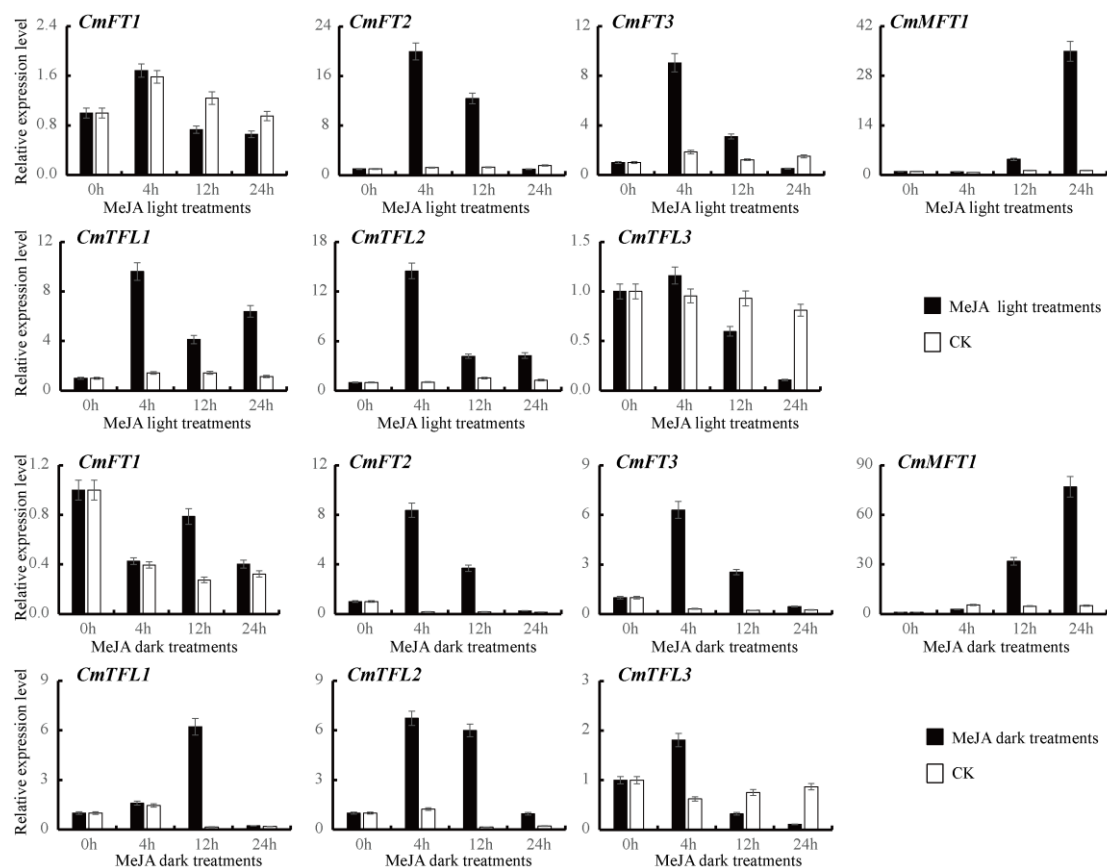


Figure S8. Expression profiles of *CmPEBP* genes in Chrysanthemum leaves under MeJA stresses .

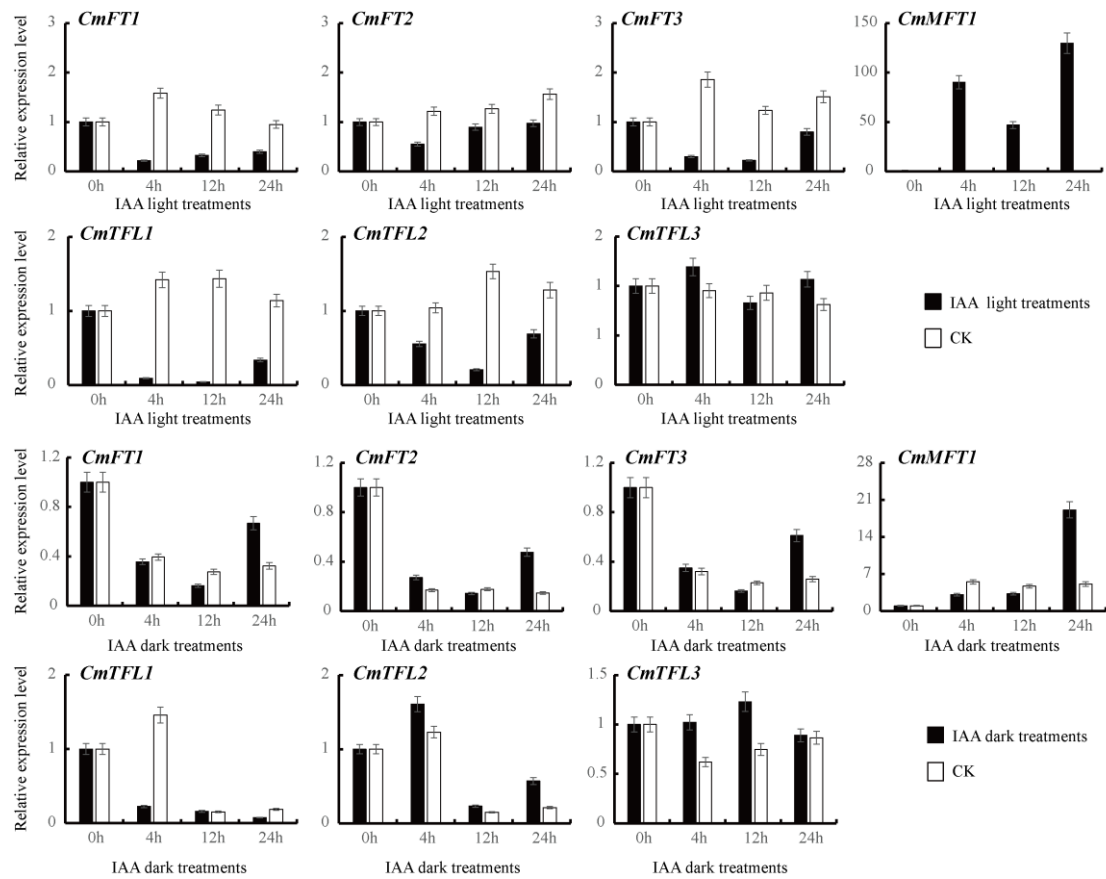


Figure S9. Expression profiles of *CmPEBP* genes in Chrysanthemum leaves under IAA stresses.

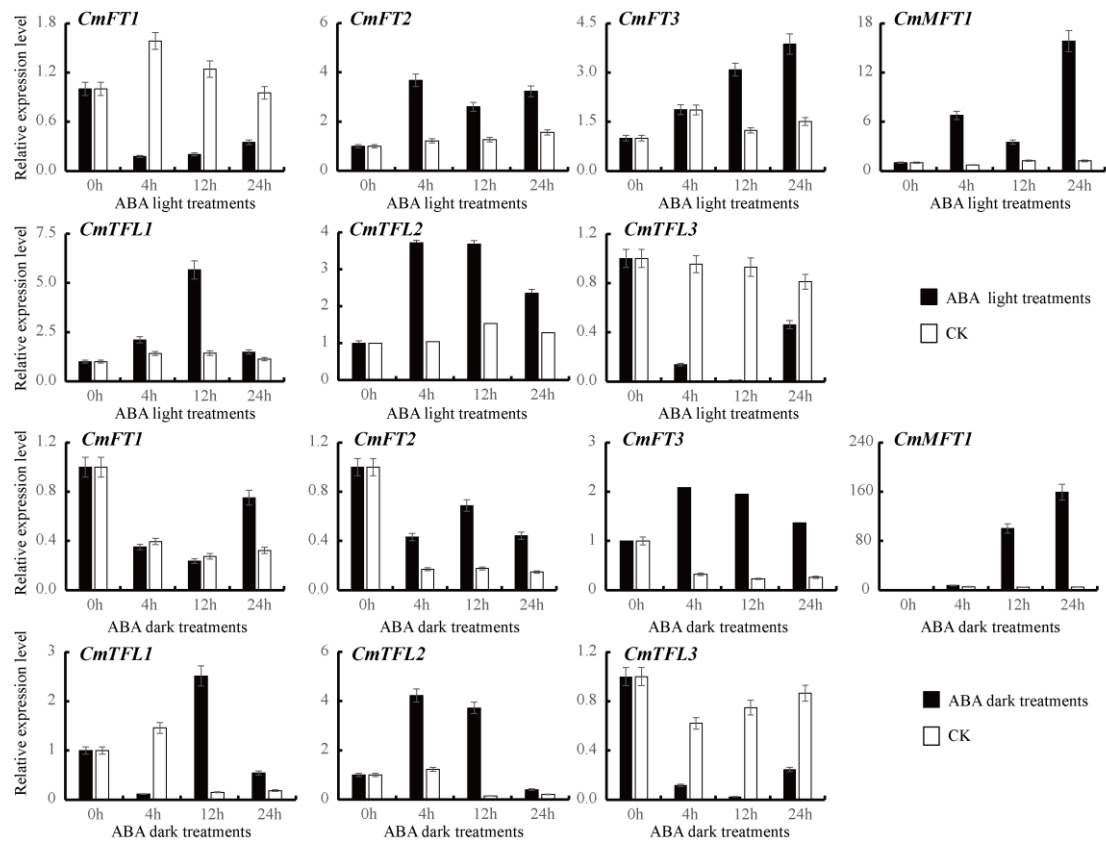


Figure S10. Expression profiles of *CmPEBP* genes in Chrysanthemum leaves under ABA stresses .

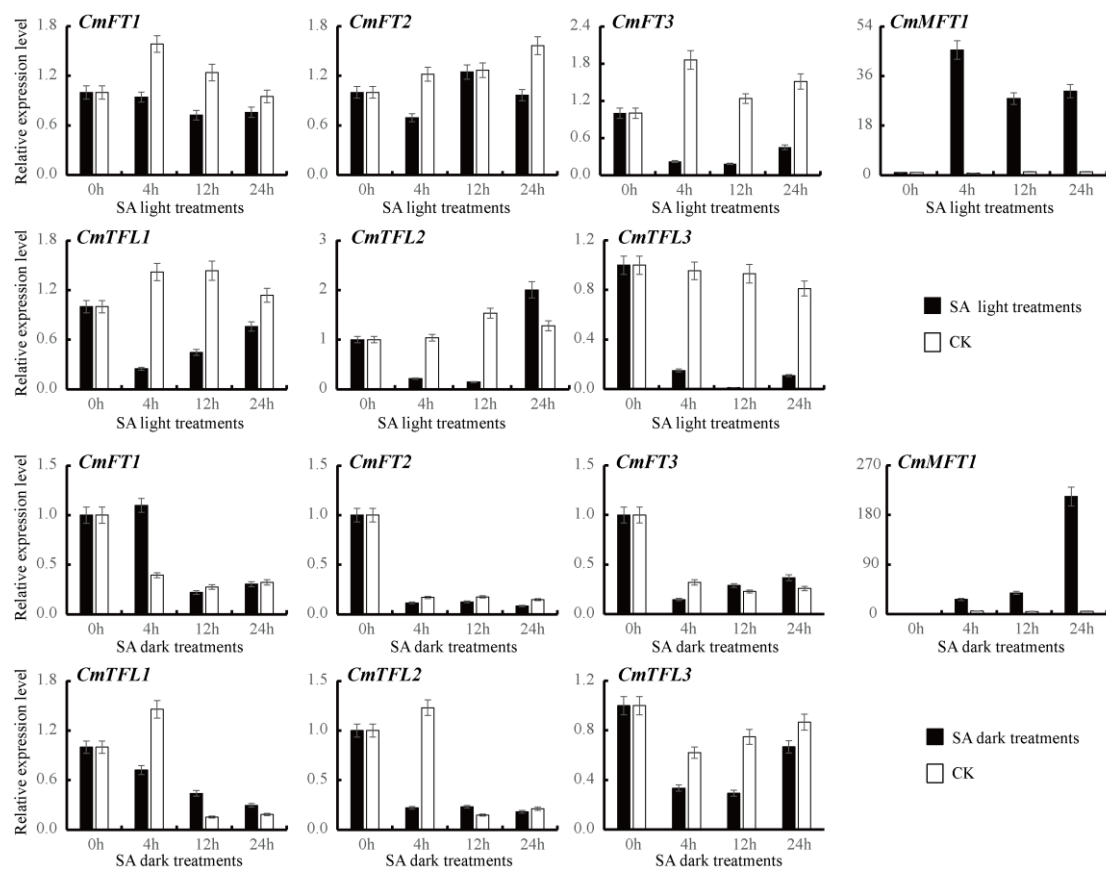


Figure S11. Expression profiles of *CmPEBP* genes in Chrysanthemum leaves under SA stresses.

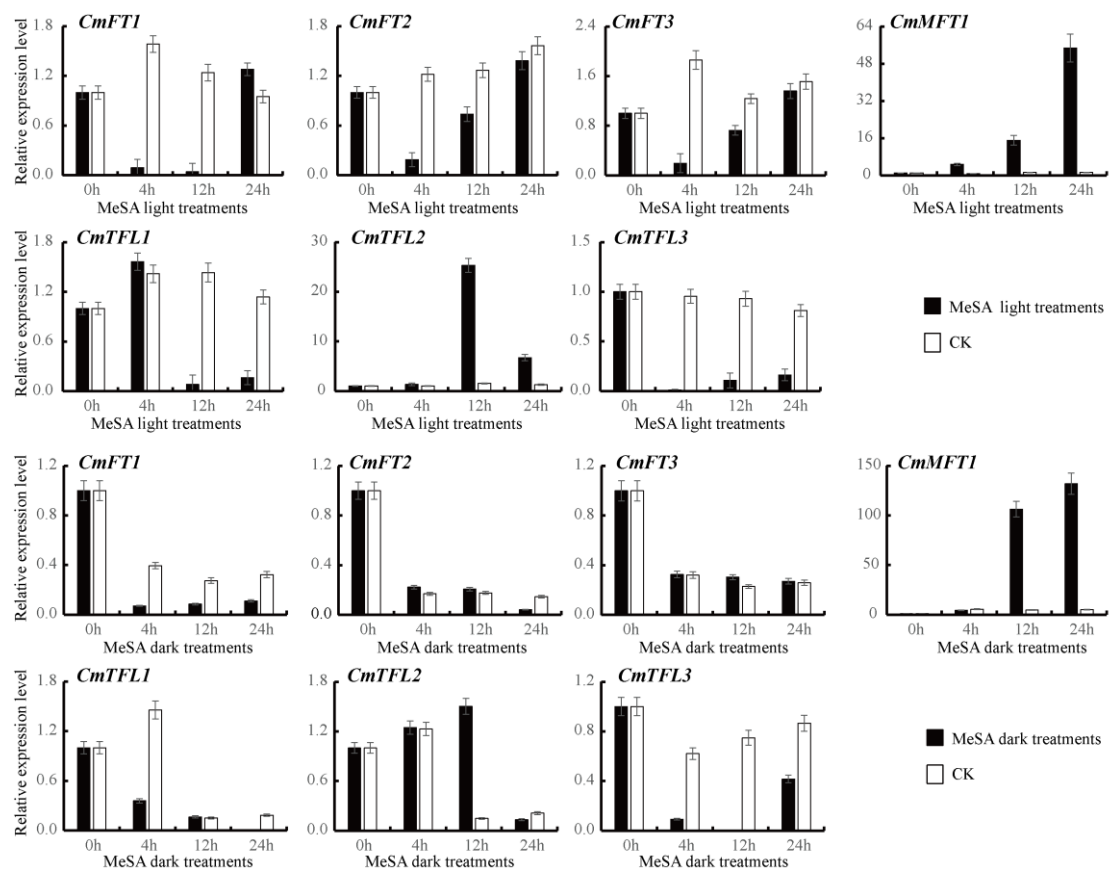


Figure S12. Expression profiles of *CmPEBP* genes in Chrysanthemum leaves under MeSA stresses .