

Figure.S1. Identification the positive cloning in vector construction by gel electrophoresis in subcellular localization of *GbEXPA31*. A. CDS full-length amplification of *GbEXPA31* B. Identification the positive cloning of *GbEXPA31* in transformed *Escherichia coli*. C. Identification the positive cloning of *GbEXPA31* in transformed *Agrobacterium tumefaciens*.

GbEXPA31+Homologous_splice_sequenceTTGGAGAGGACACG	14
GbEXPA31_cloning_1	CCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGACACG	40
GbEXPA31_cloning_2	CCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGACACG	40
GbEXPA31_cloning_3	CCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGACACG	40
Consensus	ttggagaggacacg	
GbEXPA31+Homologous_splice_sequence	CTCGAGATGGCCAGTTTCTCCAGACATGGGGCTGGACGA	54
GbEXPA31_cloning_1	CTCGAGATGGCCAGTTTCTCCAGACATGGGGCTGGACGA	80
GbEXPA31_cloning_2	CTCGAGATGGCCAGTTTCTCCAGACATGGGGCTGGACGA	80
GbEXPA31_cloning_3	CTCGAGATGGCCAGTTTCTCCAGACATGGGGCTGGACGA	80
Consensus	ctcgagatggccagtttctccagacatggggctggacga	
GbEXPA31+Homologous_splice_sequence	ATGCTCATGCAACTTTCTATGGAGGACGAGATGCCACTGG	94
GbEXPA31_cloning_1	ATGCTCATGCAACTTTCTATGGAGGACGAGATGCCACTGG	120
GbEXPA31_cloning_2	ATGCTCATGCAACTTTCTATGGAGGACGAGATGCCACTGG	120
GbEXPA31_cloning_3	ATGCTCATGCAACTTTCTATGGAGGACGAGATGCCACTGG	120
Consensus	atgctcatgcaactttctatggagggacgagatgccactgg	
GbEXPA31+Homologous_splice_sequence	TACAATGGGCGGCGCGTGTGGGTATGGAAATATGTACAGC	134
GbEXPA31_cloning_1	TACAATGGGCGGCGCGTGTGGGTATGGAAATATGTACAGC	160
GbEXPA31_cloning_2	TACAATGGGCGGCGCGTGTGGGTATGGAAATATGTACAGC	160
GbEXPA31_cloning_3	TACAATGGGCGGCGCGTGTGGGTATGGAAATATGTACAGC	160
Consensus	tacaatgggcgcgcggtgtgggtatggaaatatgtacagc	
GbEXPA31+Homologous_splice_sequence	CAAGGATATGGCACGAACACGCGAGCTCTGAGCATGTCTC	174
GbEXPA31_cloning_1	CAAGGATATGGCACGAACACGCGAGCTCTGAGCATGTCTC	200
GbEXPA31_cloning_2	CAAGGATATGGCACGAACACGCGAGCTCTGAGCATGTCTC	200
GbEXPA31_cloning_3	CAAGGATATGGCACGAACACGCGAGCTCTGAGCATGTCTC	200
Consensus	caaggatatggcacgaacacgcgagctctgagcatgtctc	
GbEXPA31+Homologous_splice_sequence	TGTTCAACAATGGGCTGAGCTGTGGAGCATGCTATGAAAT	214
GbEXPA31_cloning_1	TGTTCAACAATGGGCTGAGCTGTGGAGCATGCTATGAAAT	240
GbEXPA31_cloning_2	TGTTCAACAATGGGCTGAGCTGTGGAGCATGCTATGAAAT	240
GbEXPA31_cloning_3	TGTTCAACAATGGGCTGAGCTGTGGAGCATGCTATGAAAT	240
Consensus	tgttcaacaatgggctgagctgtggagcatgctatgaaat	
GbEXPA31+Homologous_splice_sequence	CAAAATGTACGACGACCCACAGTGGTGTCTGTCCACACACA	254
GbEXPA31_cloning_1	CAAAATGTACGACGACCCACAGTGGTGTCTGTCCACACACA	280
GbEXPA31_cloning_2	CAAAATGTACGACGACCCACAGTGGTGTCTGTCCACACACA	280
GbEXPA31_cloning_3	CAAAATGTACGACGACCCACAGTGGTGTCTGTCCACACACA	280
Consensus	caaatgtaacgacgacccacagtgggtgtctgtccaacaca	
GbEXPA31+Homologous_splice_sequence	ATAGTTGTGACTGCAACGAACCTTCTGCCCGCCCAATCTG	294
GbEXPA31_cloning_1	ATAGTTGTGACTGCAACGAACCTTCTGCCCGCCCAATCTG	320
GbEXPA31_cloning_2	ATAGTTGTGACTGCAACGAACCTTCTGCCCGCCCAATCTG	320
GbEXPA31_cloning_3	ATAGTTGTGACTGCAACGAACCTTCTGCCCGCCCAATCTG	320
Consensus	atagtttgtactgcaacgaacttctgcccgcccaatctg	
GbEXPA31+Homologous_splice_sequence	CTCTTCCCAACAATGCGGCGGATGGTCAATCTCCTCTCT	334
GbEXPA31_cloning_1	CTCTTCCCAACAATGCGGCGGATGGTCAATCTCCTCTCT	360
GbEXPA31_cloning_2	CTCTTCCCAACAATGCGGCGGATGGTCAATCTCCTCTCT	360
GbEXPA31_cloning_3	CTCTTCCCAACAATGCGGCGGATGGTCAATCTCCTCTCT	360
Consensus	ctcttcccaacaatgccggcggaatgggtcaatcctcctct	
GbEXPA31+Homologous_splice_sequence	CCTGCACCTTGTATCTCTCAGAGCCTGTTTTTCAGCATATT	374
GbEXPA31_cloning_1	CCTGCACCTTGTATCTCTCAGAGCCTGTTTTTCAGCATATT	400
GbEXPA31_cloning_2	CCTGCACCTTGTATCTCTCAGAGCCTGTTTTTCAGCATATT	400
GbEXPA31_cloning_3	CCTGCACCTTGTATCTCTCAGAGCCTGTTTTTCAGCATATT	400
Consensus	cctgcaccttgtatctctcagagcctgtttttcagcatatt	
GbEXPA31+Homologous_splice_sequence	GCCAGTTTCAGGGCAGGCAATTGTGCTGTAAATGTACCAA	414
GbEXPA31_cloning_1	GCCAGTTTCAGGGCAGGCAATTGTGCTGTAAATGTACCAA	440
GbEXPA31_cloning_2	GCCAGTTTCAGGGCAGGCAATTGTGCTGTAAATGTACCAA	440
GbEXPA31_cloning_3	GCCAGTTTCAGGGCAGGCAATTGTGCTGTAAATGTACCAA	440
Consensus	gccagtttcagggcaggcatgtgctgttaattgtaccaaa	
GbEXPA31+Homologous_splice_sequence	GGGTACCTTGCAGAGAGAGGGGGGATTCGGTTGCACAA	454
GbEXPA31_cloning_1	GGGTACCTTGCAGAGAGAGGGGGGATTCGGTTGCACAA	480
GbEXPA31_cloning_2	GGGTACCTTGCAGAGAGAGGGGGGATTCGGTTGCACAA	480
GbEXPA31_cloning_3	GGGTACCTTGCAGAGAGAGGGGGGATTCGGTTGCACAA	480
Consensus	gggtaccttgcagaagaagggggattcggttgcacaat	
GbEXPA31+Homologous_splice_sequence	CAATGGGCATTCACTTCAACCTCGTTCTGTAACCAAC	494
GbEXPA31_cloning_1	CAATGGGCATTCACTTCAACCTCGTTCTGTAACCAAC	520
GbEXPA31_cloning_2	CAATGGGCATTCACTTCAACCTCGTTCTGTAACCAAC	520
GbEXPA31_cloning_3	CAATGGGCATTCACTTCAACCTCGTTCTGTAACCAAC	520
Consensus	caatgggcatttcaacttcaacctcggtctgtgaaccaac	
GbEXPA31+Homologous_splice_sequence	GTAGGAGGTGCAGGGGATGTCATGGGGTTTCCATCAAGG	534
GbEXPA31_cloning_1	GTAGGAGGTGCAGGGGATGTCATGGGGTTTCCATCAAGG	560
GbEXPA31_cloning_2	GTAGGAGGTGCAGGGGATGTCATGGGGTTTCCATCAAGG	560
GbEXPA31_cloning_3	GTAGGAGGTGCAGGGGATGTCATGGGGTTTCCATCAAGG	560
Consensus	gtaggaggtgcaggggatgtcaatggggtttccatcaagg	
GbEXPA31+Homologous_splice_sequence	GCTCAGGAACCGGGTGGCAGCCATGTCTCGCAACTGGGG	574
GbEXPA31_cloning_1	GCTCAGGAACCGGGTGGCAGCCATGTCTCGCAACTGGGG	600
GbEXPA31_cloning_2	GCTCAGGAACCGGGTGGCAGCCATGTCTCGCAACTGGGG	600
GbEXPA31_cloning_3	GCTCAGGAACCGGGTGGCAGCCATGTCTCGCAACTGGGG	600
Consensus	gctcaggaaccgggtggcagccaatgtctcgcaactgggg	
GbEXPA31+Homologous_splice_sequence	CCAAAATTGGCAGAGCAACTCCAACTCAACGGAACAAAGT	614
GbEXPA31_cloning_1	CCAAAATTGGCAGAGCAACTCCAACTCAACGGAACAAAGT	640
GbEXPA31_cloning_2	CCAAAATTGGCAGAGCAACTCCAACTCAACGGAACAAAGT	640
GbEXPA31_cloning_3	CCAAAATTGGCAGAGCAACTCCAACTCAACGGAACAAAGT	640
Consensus	ccaaaattggcagagcaactccaaactcaacgggacaaagt	
GbEXPA31+Homologous_splice_sequence	CTCTCCTTCAAGGTCAACCAAGCGATGGACAGACCGTCA	654
GbEXPA31_cloning_1	CTCTCCTTCAAGGTCAACCAAGCGATGGACAGACCGTCA	680
GbEXPA31_cloning_2	CTCTCCTTCAAGGTCAACCAAGCGATGGACAGACCGTCA	680
GbEXPA31_cloning_3	CTCTCCTTCAAGGTCAACCAAGCGATGGACAGACCGTCA	680
Consensus	ctctccttcaaggtcaccaccagcgatggacagacgctca	
GbEXPA31+Homologous_splice_sequence	CTTCATACAATGCTGCTCCAGCAACTGGCAATTGGCCA	694
GbEXPA31_cloning_1	CTTCATACAATGCTGCTCCAGCAACTGGCAATTGGCCA	720
GbEXPA31_cloning_2	CTTCATACAATGCTGCTCCAGCAACTGGCAATTGGCCA	720
GbEXPA31_cloning_3	CTTCATACAATGCTGCTCCAGCAACTGGCAATTGGCCA	720
Consensus	cttcataaatgctgctccagcaactggcaatttggcca	
GbEXPA31+Homologous_splice_sequence	GACTTTTAGCGAGCCCACTTGGCAATGAATCATGGTG	734
GbEXPA31_cloning_1	GACTTTTAGCGAGCCCACTTGGCAATGAATCATGGTG	760
GbEXPA31_cloning_2	GACTTTTAGCGAGCCCACTTGGCAATGAATCATGGTG	760
GbEXPA31_cloning_3	GACTTTTAGCGAGCCCACTTGGCAATGAATCATGGTG	760
Consensus	gacttttagcggagcccaacttggcaatgaattcatgttg	
GbEXPA31+Homologous_splice_sequence	AGCAAGG.....	742
GbEXPA31_cloning_1	AGCAAGGCGAGAGCTGTTCACCGGGTGGTG	793
GbEXPA31_cloning_2	AGCAAGGCGAGAGCTGTTCACCGGGTGGTG	793
GbEXPA31_cloning_3	AGCAAGGCGAGAGCTGTTCACCGGGTGGTG	793
Consensus	agcaagg	

Figure.S2. Sequence alignment of *GbEXPA31* fusing pART-CAM-EGFP.

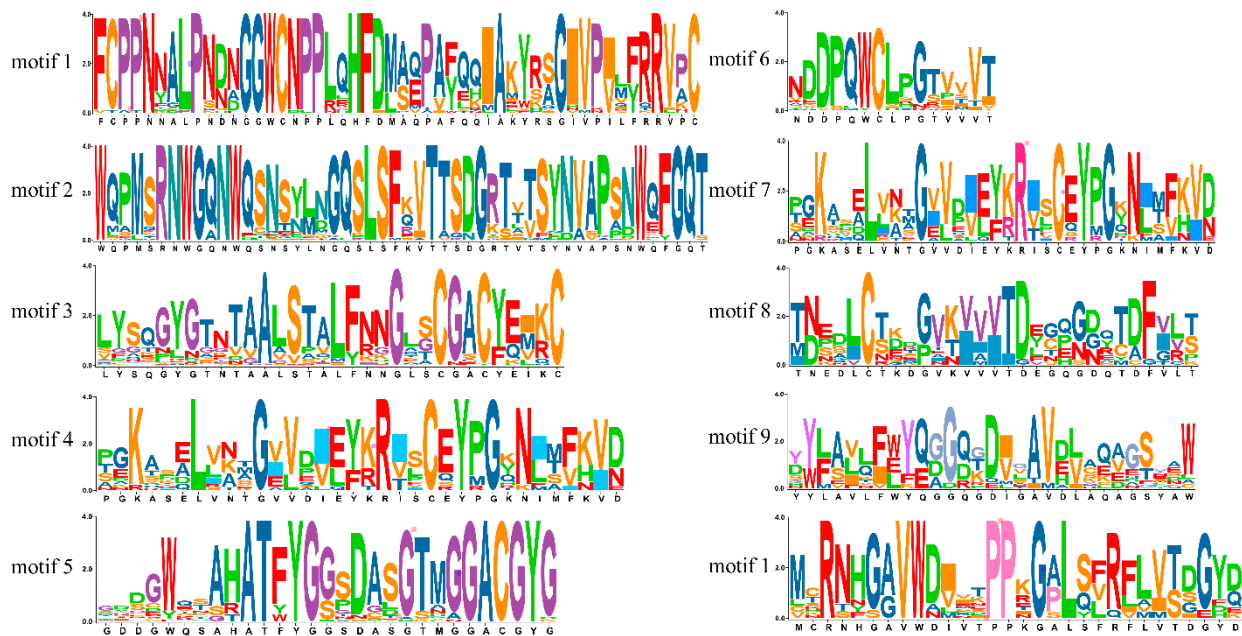


Figure S4. The motif logos in *GbEXP* family.

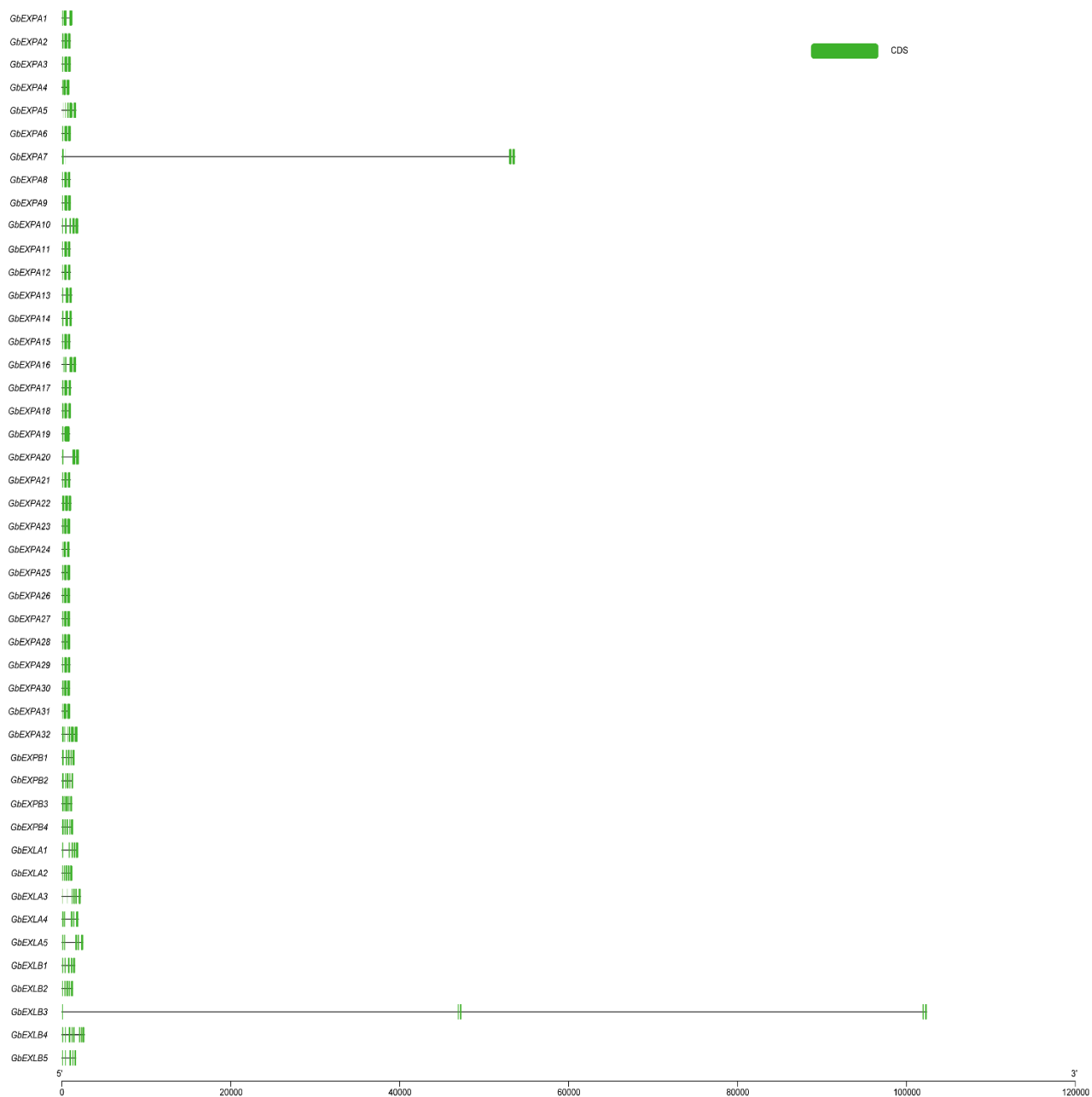


Figure S5. The exon-intron structures of *GbEXP* members.

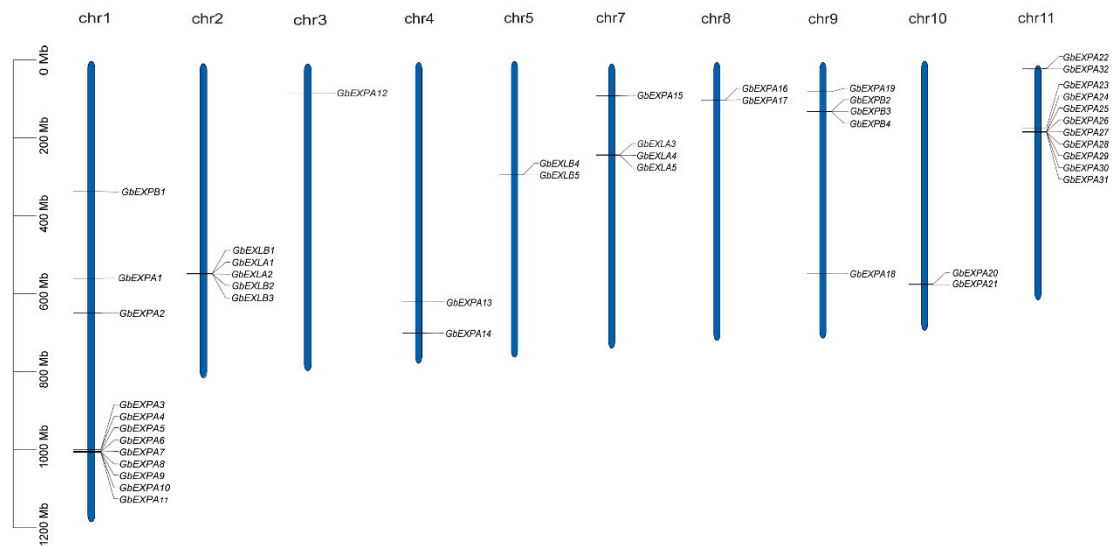


Figure.S6. Physical chromosomal locations of *GbEXPs*

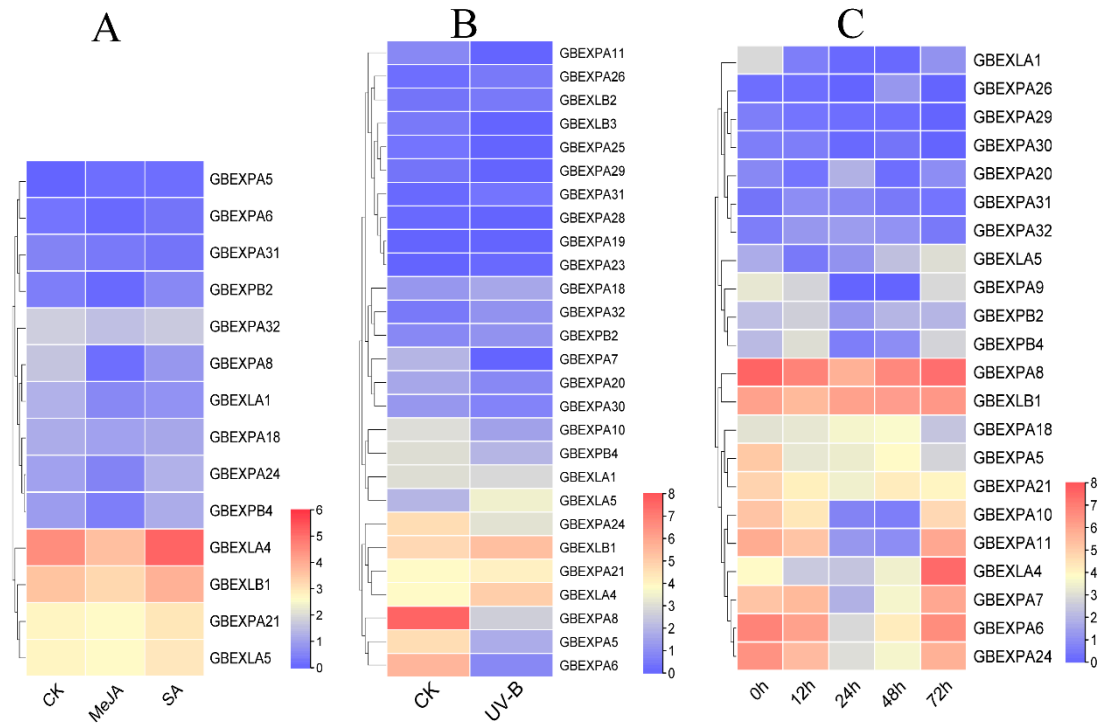


Figure.S7. Heatmap of *GbEXPs* expression in response to abiotic stress. (A) Expression profile of *GbEXPs* under methyl jasmonate (MeJA) and salicylic acid (SA) treatments. (B) Expression profile of *GbEXPs* under UV-B exposure. (C) Expression profile of *GbEXPs* under PEG-6000 stress.