

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*.

GbEXP31+Homologous_splice_sequence	TTGGAGAGGACACG	14
GbEXP31_cloning_1	CCCTCTATAAAGGAAGTTCATTTCA	TTGGAGAGGACACG	40
GbEXP31_cloning_2	CCCTCTATAAAGGAAGTTCATTTCA	TTGGAGAGGACACG	40
GbEXP31_cloning_3	CCCTCTATAAAGGAAGTTCATTTCA	TTGGAGAGGACACG	40
Consensus	ttggagaggacacg		
GbEXP31+Homologous_splice_sequence	CTCGAGATGCCAGTTCTCCAGACATGGGGCTGGACGA	54	
GbEXP31_cloning_1	CTCGAGATGCCAGTTCTCCAGACATGGGGCTGGACGA	80	
GbEXP31_cloning_2	CTCGAGATGCCAGTTCTCCAGACATGGGGCTGGACGA	80	
GbEXP31_cloning_3	CTCGAGATGCCAGTTCTCCAGACATGGGGCTGGACGA	80	
Consensus	ctcgatgtggccaggatcttcacatggggctggacga		
GbEXP31+Homologous_splice_sequence	ATGCCTCATGCAACTTTCTATGGAGGCGAGCACTGG	94	
GbEXP31_cloning_1	ATGCCTCATGCAACTTTCTATGGAGGCGAGCACTGG	120	
GbEXP31_cloning_2	ATGCCTCATGCAACTTTCTATGGAGGCGAGCACTGG	120	
GbEXP31_cloning_3	ATGCCTCATGCAACTTTCTATGGAGGCGAGCACTGG	120	
Consensus	atgcctcatgcaactttctatggagggcagcatggggctggacg		
GbEXP31+Homologous_splice_sequence	TACRATGCGCAGACACGGCGCTCTGACACTGCTG	134	
GbEXP31_cloning_1	TACRATGCGCAGACACGGCGCTCTGACACTGCTG	160	
GbEXP31_cloning_2	TACRATGCGCAGACACGGCGCTCTGACACTGCTG	160	
GbEXP31_cloning_3	TACRATGCGCAGACACGGCGCTCTGACACTGCTG	160	
Consensus	tacaatggcgccggcggtggatgtggaaatgttgacgc		
GbEXP31+Homologous_splice_sequence	CAGGGATATGGCACGACACGGCGCTCTGACACTGCTG	174	
GbEXP31_cloning_1	CAGGGATATGGCACGACACGGCGCTCTGACACTGCTG	200	
GbEXP31_cloning_2	CAGGGATATGGCACGACACGGCGCTCTGACACTGCTG	200	
GbEXP31_cloning_3	CAGGGATATGGCACGACACGGCGCTCTGACACTGCTG	200	
Consensus	caaggatatggcgacaaacggcgactctgagactgtctgc		
GbEXP31+Homologous_splice_sequence	TGTTCACAACTGCGGCTGAGCTTATGAAAT	214	
GbEXP31_cloning_1	TGTTCACAACTGCGGCTGAGCTTATGAAAT	240	
GbEXP31_cloning_2	TGTTCACAACTGCGGCTGAGCTTATGAAAT	240	
GbEXP31_cloning_3	TGTTCACAACTGCGGCTGAGCTTATGAAAT	240	
Consensus	tgttcaacaaatggggctggactgtggatgtatggaaat		
GbEXP31+Homologous_splice_sequence	CAAATGTAACGACGCCAACAGTGCTGCTGAAACAC	254	
GbEXP31_cloning_1	CAAATGTAACGACGCCAACAGTGCTGCTGAAACAC	280	
GbEXP31_cloning_2	CAAATGTAACGACGCCAACAGTGCTGCTGAAACAC	280	
GbEXP31_cloning_3	CAAATGTAACGACGCCAACAGTGCTGCTGAAACAC	280	
Consensus	caaataatggcgaccacacggcgactgtgtccaaacaca		
GbEXP31+Homologous_splice_sequence	ATAGTTGTGACTCQACCGAACCTCTGCCCCAAATACTG	294	
GbEXP31_cloning_1	ATAGTTGTGACTCQACCGAACCTCTGCCCCAAATACTG	320	
GbEXP31_cloning_2	ATAGTTGTGACTCQACCGAACCTCTGCCCCAAATACTG	320	
GbEXP31_cloning_3	ATAGTTGTGACTCQACCGAACCTCTGCCCCAAATACTG	320	
Consensus	ataggttgtactcaacgaaacttcgtgccggcccaatactg		
GbEXP31+Homologous_splice_sequence	CTCTTCCCACAAATGCCCGCGGGATGGTCAATTCTCTCT	334	
GbEXP31_cloning_1	CTCTTCCCACAAATGCCCGCGGGATGGTCAATTCTCTCT	360	
GbEXP31_cloning_2	CTCTTCCCACAAATGCCCGCGGGATGGTCAATTCTCTCT	360	
GbEXP31_cloning_3	CTCTTCCCACAAATGCCCGCGGGATGGTCAATTCTCTCT	360	
Consensus	ctctttccaaacaaatggccggcggtatggcaatcttct		
GbEXP31+Homologous_splice_sequence	CCIGCACTTGTGACTCTCAGAGCCGTTTTAGCATATT	374	
GbEXP31_cloning_1	CCIGCACTTGTGACTCTCAGAGCCGTTTTAGCATATT	400	
GbEXP31_cloning_2	CCIGCACTTGTGACTCTCAGAGCCGTTTTAGCATATT	400	
GbEXP31_cloning_3	CCIGCACTTGTGACTCTCAGAGCCGTTTTAGCATATT	400	
Consensus	cctgcacttgtatcttcaagccgtttttccatgttttttt		
GbEXP31+Homologous_splice_sequence	GCCAAGTTCAGGGCAGGCATTGGCCGTTATGTTACAAA	414	
GbEXP31_cloning_1	GCCAAGTTCAGGGCAGGCATTGGCCGTTATGTTACAAA	440	
GbEXP31_cloning_2	GCCAAGTTCAGGGCAGGCATTGGCCGTTATGTTACAAA	440	
GbEXP31_cloning_3	GCCAAGTTCAGGGCAGGCATTGGCCGTTATGTTACAAA	440	
Consensus	gccaatgttccggccggccgtatggccgttatgttacaaa		
GbEXP31+Homologous_splice_sequence	GGGTAACCTTGCAGAGAAGGGGGGGGGGGGGGGGGGG	454	
GbEXP31_cloning_1	GGGTAACCTTGCAGAGAAGGGGGGGGGGGGGGGGGGG	480	
GbEXP31_cloning_2	GGGTAACCTTGCAGAGAAGGGGGGGGGGGGGGGGGGG	480	
GbEXP31_cloning_3	GGGTAACCTTGCAGAGAAGGGGGGGGGGGGGGGGGGG	480	
Consensus	gggttacccatggccgggggggggggggggggggggggg		
GbEXP31+Homologous_splice_sequence	CAATGCGCTCTCATACTTCAACCTCTGCTGCTAACCAAC	494	
GbEXP31_cloning_1	CAATGCGCTCTCATACTTCAACCTCTGCTGCTAACCAAC	520	
GbEXP31_cloning_2	CAATGCGCTCTCATACTTCAACCTCTGCTGCTAACCAAC	520	
GbEXP31_cloning_3	CAATGCGCTCTCATACTTCAACCTCTGCTGCTAACCAAC	520	
Consensus	caatggccatccatacttcaaccttcgttctgttacccacac		
GbEXP31+Homologous_splice_sequence	CTAGCGAGCTGCAAGGGGATGTCAATGGCGTTTCATCANG	534	
GbEXP31_cloning_1	CTAGCGAGCTGCAAGGGGATGTCAATGGCGTTTCATCANG	560	
GbEXP31_cloning_2	CTAGCGAGCTGCAAGGGGATGTCAATGGCGTTTCATCANG	560	
GbEXP31_cloning_3	CTAGCGAGCTGCAAGGGGATGTCAATGGCGTTTCATCANG	560	
Consensus	gttagggatgttccatgttttttttttttttttttttttttt		
GbEXP31+Homologous_splice_sequence	GCTCAGGACACCGGGGCAAGCACTTCCAACTTCAACGACAAGT	574	
GbEXP31_cloning_1	GCTCAGGACACCGGGGCAAGCACTTCCAACTTCAACGACAAGT	600	
GbEXP31_cloning_2	GCTCAGGACACCGGGGCAAGCACTTCCAACTTCAACGACAAGT	600	
GbEXP31_cloning_3	GCTCAGGACACCGGGGCAAGCACTTCCAACTTCAACGACAAGT	600	
Consensus	gcttcaggaaaccgggttgcagccaaatgttcgcacactgggg		
GbEXP31+Homologous_splice_sequence	CCAAAATTGGCAGACCACTTCCAACTTCAACGACAAGT	614	
GbEXP31_cloning_1	CCAAAATTGGCAGACCACTTCCAACTTCAACGACAAGT	640	
GbEXP31_cloning_2	CCAAAATTGGCAGACCACTTCCAACTTCAACGACAAGT	640	
GbEXP31_cloning_3	CCAAAATTGGCAGACCACTTCCAACTTCAACGACAAGT	640	
Consensus	ccaaaaattggcagacaaacttccaaaccttcaacggcacaatgt		
GbEXP31+Homologous_splice_sequence	CTTCCTTCAAGGTCAACCAAGCGATGACAGACGGCTCA	654	
GbEXP31_cloning_1	CTTCCTTCAAGGTCAACCAAGCGATGACAGACGGCTCA	680	
GbEXP31_cloning_2	CTTCCTTCAAGGTCAACCAAGCGATGACAGACGGCTCA	680	
GbEXP31_cloning_3	CTTCCTTCAAGGTCAACCAAGCGATGACAGACGGCTCA	680	
Consensus	cttccttcgttccatgttttttttttttttttttttttttttt		
GbEXP31+Homologous_splice_sequence	CTTCATACATGCTGCTCCAGCACTGGCAATTGGCG	694	
GbEXP31_cloning_1	CTTCATACATGCTGCTCCAGCACTGGCAATTGGCG	720	
GbEXP31_cloning_2	CTTCATACATGCTGCTCCAGCACTGGCAATTGGCG	720	
GbEXP31_cloning_3	CTTCATACATGCTGCTCCAGCACTGGCAATTGGCG	720	
Consensus	cttcatatacatgttccatgttttttttttttttttttttttt		
GbEXP31+Homologous_splice_sequence	GACTTTAGCGAGGCCAACATGGCAATGAATTCAATGGT	734	
GbEXP31_cloning_1	GACTTTAGCGAGGCCAACATGGCAATGAATTCAATGGT	760	
GbEXP31_cloning_2	GACTTTAGCGAGGCCAACATGGCAATGAATTCAATGGT	760	
GbEXP31_cloning_3	GACTTTAGCGAGGCCAACATGGCAATGAATTCAATGGT	760	
Consensus	gacttttagcgccggccaaatgtggcaatgaattcatgggt		
GbEXP31+Homologous_splice_sequence	AGCAAGG.....	742	
GbEXP31_cloning_1	AGCAAGGCGAGGAGCTGTTTACCGGGGGTGTG	793	
GbEXP31_cloning_2	AGCAAGGCGAGGAGCTGTTTACCGGGGGTGTG	793	
GbEXP31_cloning_3	AGCAAGGCGAGGAGCTGTTTACCGGGGGTGTG	793	
Consensus	agcaagg		

Figure S2. Sequence alignment of GbEXP31 fusing pART-CAM-EGFP.

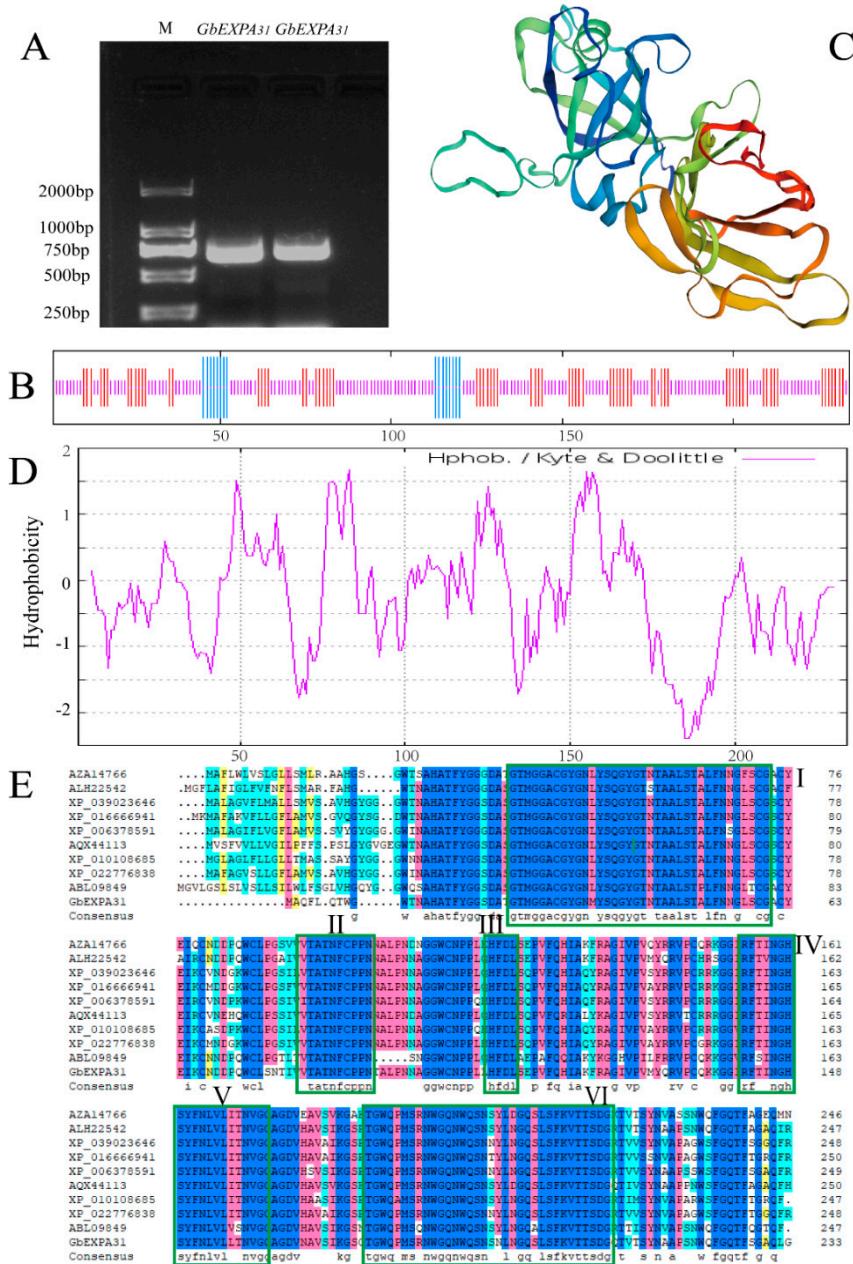


Figure S3. *GbEXPA31* cloning and characteristic analysis of *GbEXPA31*. (A) Gel electrophoresis image of *GbEXPA31*. (B) Tertiary structure of *GbEXPA31* (colors indicate the peptide chain order starting as dark blue from the N-terminus to red at the C-terminus). (C) Secondary structure prediction of *GbEXPA31* (long blue, short red, and short purple lines indicate alpha helices, extended strands, and random coils, respectively). (D) *GbEXPA31* hydrophobicity characteristic (purple waving line shows the hydrophobicity tendency of all amino acids; the positive and negative values indicate hydrophobicity and hydrophilicity, respectively). (E) Multiple sequence alignment of Ginkgo *GbEXPA31* with other species (AZA14766 from *Pinus taeda*; ALH22542 from *Pinus radiata*; XP_039023646 from *Hibiscus syriacus*; XP_016666941 from *Gossypium hirsutum*; XP_006378591 from *Populus trichocarpal*; AQX44113 from *Dendrobium officinale*; XP_010108685 from *Morus notabilis*; XP_022776838 from *Durio zibethinus*; ABL09849 from *Cunninghamia lanceolata*).

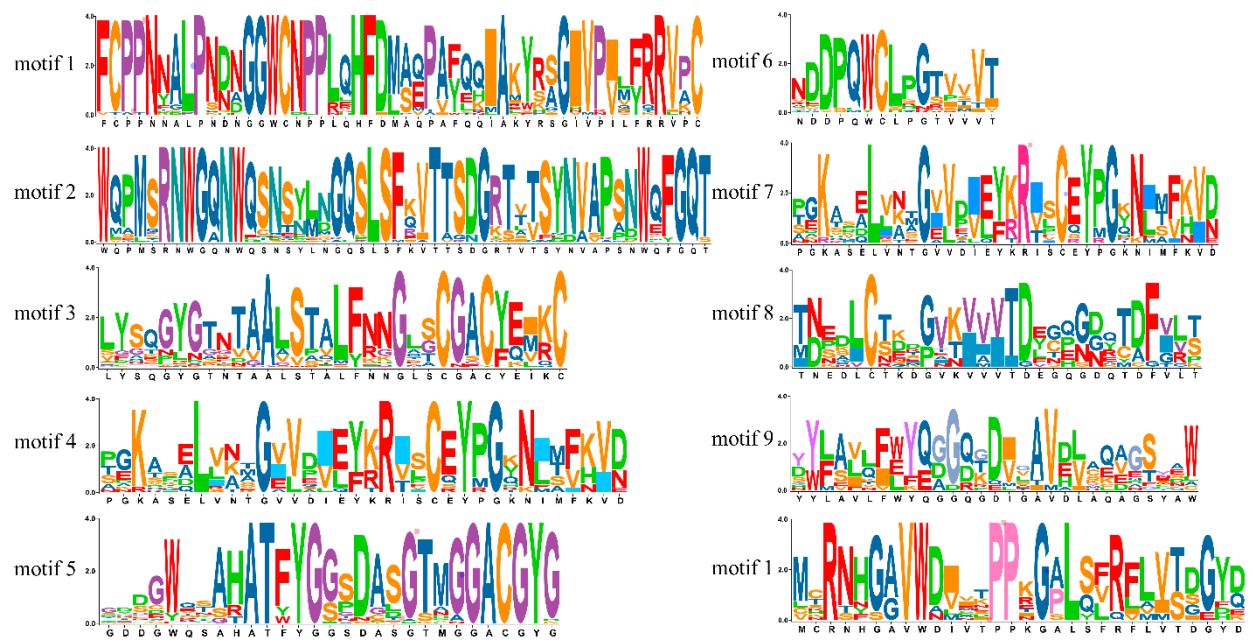


Figure S4. The motif logos in *GbEXP* family.

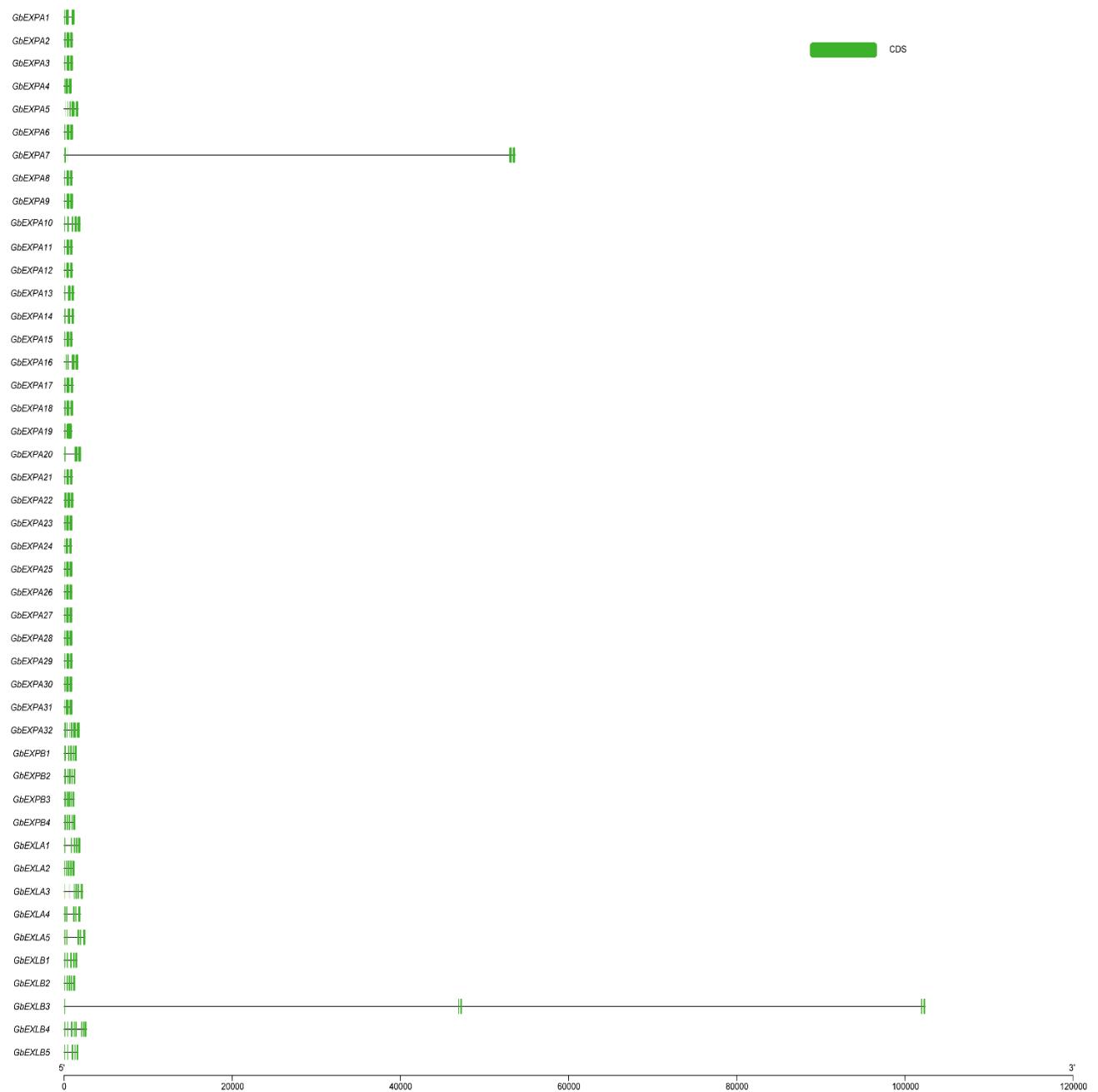


Figure S5. The exon-intron structures of *GbEXP* members.

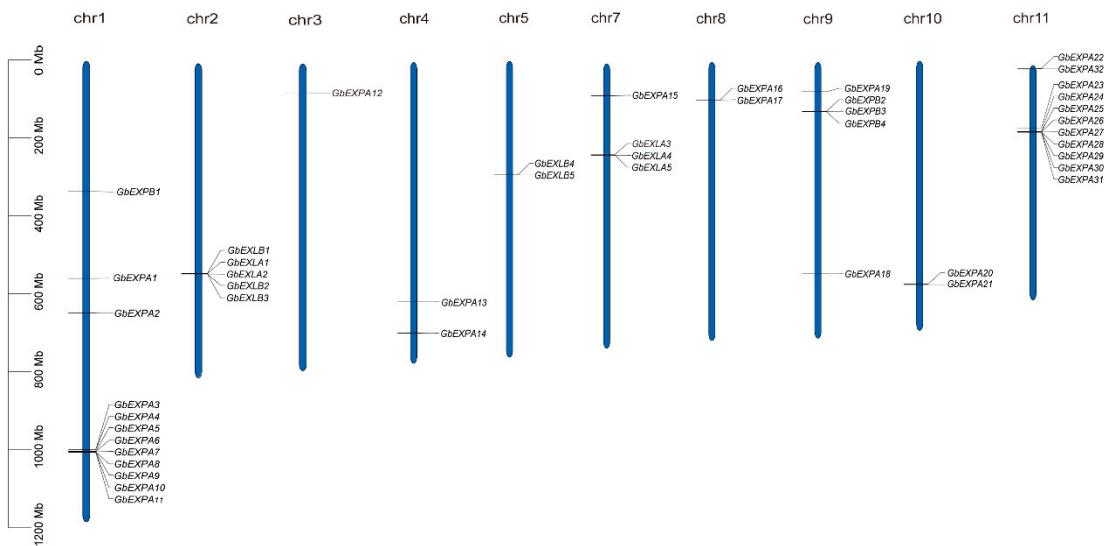


Figure.S6. Physical chromosomal locations of *GbEXPs*

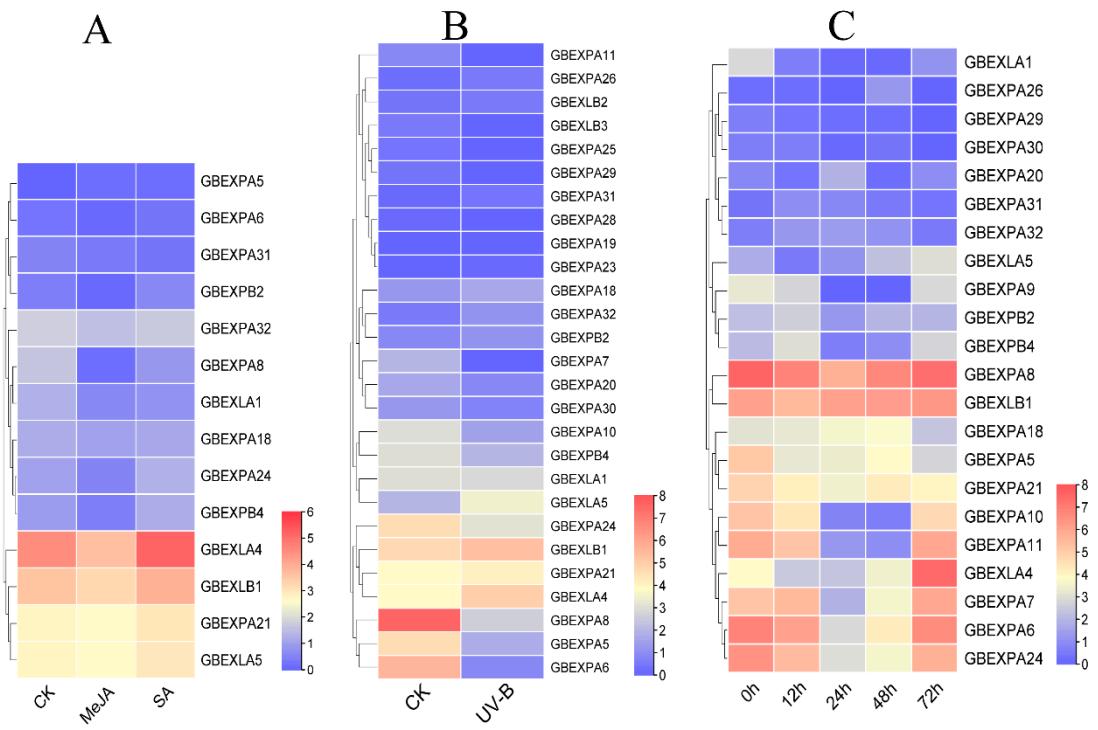


Figure S7. Heatmap of *GbEXPs* expression in response to abiotic stress. (A) Expression profile of *GbEXPs* under methyl jasmonate (MeJA) and salicylic acid (SA) treatments. (B) Expression profile of *GbEXPs* under UV-B exposure. (C) Expression profile of *GbEXPs* under PEG-6000 stress.