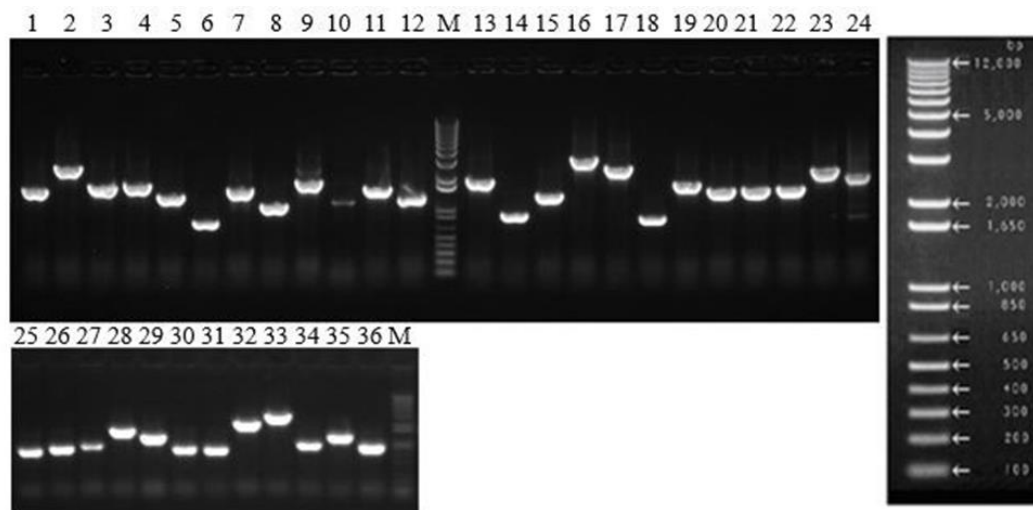
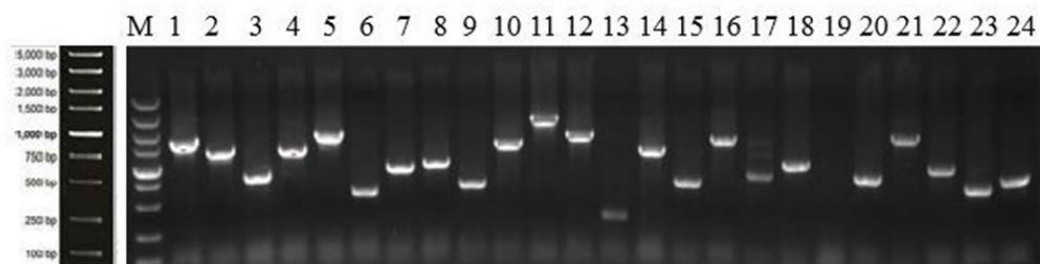


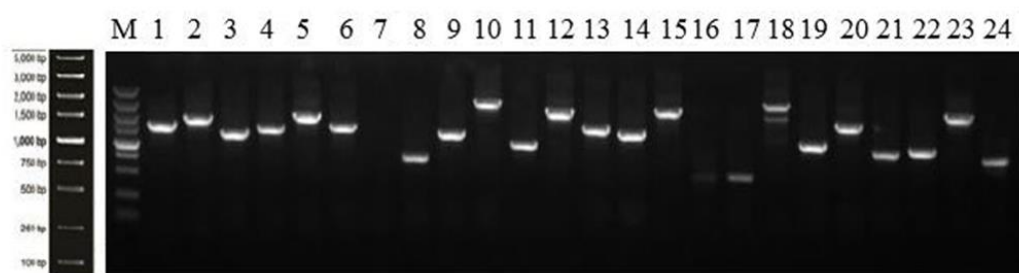


Supplemental Figure 1. The length of inserted fragments in the FL-cDNA entry clone library. 36 library colonies were randomly chosen to detect the length of inserted fragments by PCR.

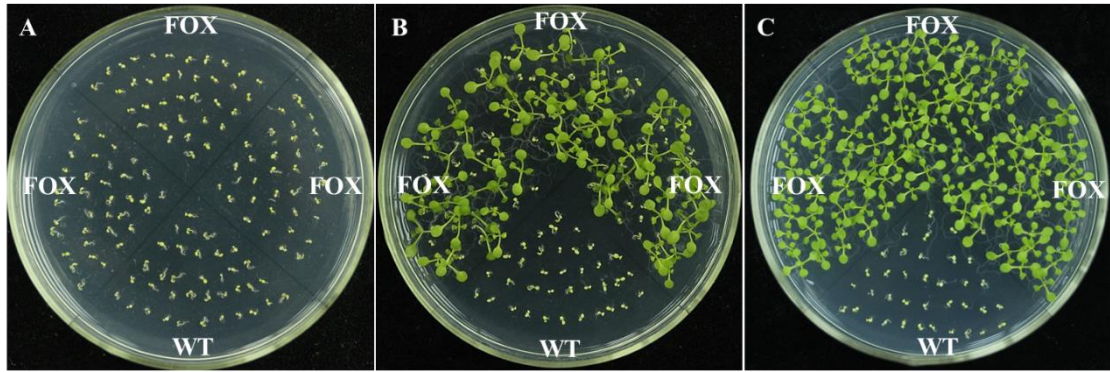


Supplemental Figure 2. The positive rate of cotton FL-cDNA expression library.

24 colonies were randomly selected for detection by PCR.



Supplemental Figure 3. The positive rate of cotton FL-cDNA Agrobacterium library. 24 colonies were randomly selected for detection by PCR.



Supplemental Figure 4. Screening of cotton FOX-Arabidopsis homozygous lines.

A, B and C, Seeds of FOX-Arabidopsis and WT were sown on the solid media of 1/2 MS containing PPT. The photograph was taken respectively when the seed grew for 5 days(A), 9 days(B) and 14 days(C).

GhCAS NAVQMAIRVSPARTL LPPSPSPSPSPVPSSII STKPSLKPCQPK PI SLS LPTSIAISLLALFS PPFEAK AI NLSNECI ISSLNEVEKTI DCVCEASSSALIVACQ 107
 GaCAS NAVQMAIRVSPARTL LPPSPSPSPSPVPSSAI STKPFLLKPCQPK PI SLS LPTSIAISLLALFS PPFEAK AI ILSNECI ISSLNEVEKTI DCVCEASSSALIVACQ 107
 GrCAS NAVQMAIRVSPARTL LPPSPSPSPSPVPSSII STKPSLKPCQPK PI SLS LPTSIAISLLALFS PPFEAK AI NLSNECI ISSLNEVEKTI DCVCEASSSALIVACQ 107
 AtCASMAMAENATKS SLS AKLTLPSSSTK KTL SLR QVSVALPTTISHLSLSEFASPPFEAKAAVSIPTCHVSSLTVEKTI NCVCETGSSVFATCR 93
 BnCASMAMAENATKS SVTTAKLTLPSSSS CKRRAR QVSVALPTTISHLSLSEFASPPFEAKAAVSIPTCHVSSLTVEKTI NCVCETGSSVFATCR 94
 GmCASNEI SALAS SATPPRPSLTPTSTSPHTVVTTTFSKPLRRSHVAVSLPTSITISLLALEA PPFEAKAAVSIPTCHVSSLTVEKTI DCVCEVCSGVLTACR 102
 Consensus s p s l p t i s i l f p p e a k a k q i s s i v e k t q v q e s d q

GhCAS IFDNGKVLKPAIDAGVPIACKACEEALNVPASP SEASKKACEAFGCTCLDTEPVLSAAKTAADAACCTHNVIEVAKPIASSTNETH TSAEPI TI VATCGALFNAYLLI 217
 GaCAS IFDNGKVLKPAIDAGVPIACKACEEALNVPASP SEASKKACEAFGCTCLDTEPVLSAAKTAADAACCTHNVIEVAKPIASSTNETH TSAEPI TI VATCGALFNAYLLI 217
 GrCAS IFDNGKVLKPAIDAGVPIACKACEEALNVPASP SEASKKACEAFGCTCLDTEPVLSAAKTAADAACCTHNVIEVAKPIASSTNETH TSAEPI TI VATCGALFNAYLLI 217
 AtCAS VFOVNCALKPALTLTALPIAKQACEEALNVPASP SEASKKACEANQSSGIDSEPVFNAAKTVIDMACCTSNALIEDAKPIASSTMDTH SSADPSVI VVAA GAATLAYLLL 203
 BnCAS VFOVNCALKPALTLTALPIAKQACEEALNVPASP SEASKKACEANQSSGIDSEPVFNAAKTVIDMACCTSNALIEDAKPIASSTMDTH SSADPSVI VVAA GAATLAYLLL 204
 GmCAS IAEVINCALKKGIETALPIVQCAEEALNVPASP SEASKKACEALQSSGVLTETPVLSAAKTVADAACTHNVIEVAKPIASSTVKTTH SSADPTVI AGTAGALFNAYLLI 212
 Consensus v g l k p p i a g e e a k a s p a s e a s k k a q e a q g d e p v a a k t d a q t k e a k p i a s s t i s p g a f a y l l

GhCAS PPIVSEFISNDRGYKGLTPAQLDLI STQNYVMDIRSEKDRERAGVRLPSSAKNRVAI PLEELPSKLRSLVRNTRKVEAEIAALKI SYLNKI SRSSNI VINEISY 327
 GaCAS PPIVSEFISNDRGYKGLTPAQLDLI STQNYVMDIRSEKDRERAGVRLPSSAKNRVAI PLEELPSKLRSLVRNTRKVEAEIAALKI SYLNKI SRSSNI VINEISY 325
 GrCAS PPIVSEFISNDRGYKGLTPAQLDLI STQNYVMDIRSEKDRERAGVRLPSSAKNRVAI PLEELPSKLRSLVRNTRKVEAEIAALKI SYLNKI SRSSNI VINEISY 325
 AtCAS PPVFSALSFNDRGYKGLTPAQLDLI LCTNLYLVMDIRSEKDRERAGVRLPSSAKNRVAI PLEELPNKVGIVRNSRRVEAEIAALKI SYLNKI NGSNI ILLSY 311
 BnCAS PPVFSALSFNDRGYKGLTPAQLDLI LCTNLYLVMDIRSEKDRERAGVRLPSSAKNRVAI PLEELPNKVGIVRNSRRVEAEIAALKI SYLNKI NGSNI ILLSY 312
 GmCAS PPIVSEFISNDRGYKGLTPAQLDLI STQNYVMDIRSEKDRERAGVRLPSSAKNRVAI PLEELPSKLRGCVNVRKLEAEIAALKI SYLNKI NGSNI VINEISY 320
 Consensus p p s i s n r g y k g d l t p a q l d l n y d i r s e k k a g p r l p s a k n i p l e e l p k v n k e a e i a l k i s y l k i k n i s y

Rhodanese-like

GhCAS GDSAKIVARTILASLGFNCVWVADGFSGRNGVLC SRLGTC SYNFSLVEILSPSNVFPAAAKRFGTITS...TRFLPGA 401
 GaCAS GDSAKIVARTILASLGFNCVWVADGFSGRNGVLC SRLGTC SYNFSLVEILSPSNVFPAAAKRFGTITS...TRFLPGA 399
 GrCAS GDSAKIVARTILASLGFNCVWVADGFSGRNGVLC SRLGTC SYNFSLVEILSPSNVFPAAAKRFGTITS...TRFLPGA 399
 AtCAS TDSAKIVAKTIKVLGYNFYVADGFSGRNGVLC SRLGTC SYNFSAFVLSPSRIIPAAASRFGTIRSG...TRFLPSS 386
 BnCAS SDSAIVAKTIKVLGYNFYVADGFSGRNGVLC SRLGTC SYNFSAFVLSPSRIIPAAASRFGTIRSG...TRFLPSS 386
 GmCAS SDAIVAKTIKVLGYNFYVADGFSGRNGVLC SRLGTC SYNFSAFVLSPSRIIPAAASRFGTIRSG...TRFLPSS 397
 Consensus d a k v t l l g n v d g f s g g w l q s r l g d s y n f s l s p s p a a f g t s t k l p

Supplemental Figure 5. Protein structure analysis of GhCAS. The protein sequences of GhCAS (*Gossypium hirsutum*), GaCAS (*Gossypium arboreum*), GrCAS (*Gossypium raimondii*), AtCAS (*Arabidopsis thaliana*), BnCAS (*Brassica napus*) and GmCAS (*Glycine max*) were used to alignment by DNAMAN for conservation analysis of amino acid sequence.

Supplemental Table1 Stress Treatment of Cotton Seedlings

Stress treatment	Concentration1	Concentration 2
PEG-6000	10%	20%
NaCl	100 mM	200 mM
ABA	10 μ M	100 μ M
H ₂ O ₂	1 mM	10 mM
MeJA	1 mM	10 mM
SA	1 mM	10 mM
BR	10 μ M	100 μ M
SNP	10 μ M	100 μ M

Supplemental Table 2 Cis-elements forecast of promoter in *GhCAS*

Cis-element	Sequence	Location	Function
ABRE	ACGTGGC	163、 546	cis-acting element involved in the abscisic acid responsiveness
ARE	TGGTTT	1338	cis-acting regulatory element essential for the anaerobic induction
ERE	ATTTCAAA	70	ethylene-responsive element
GARE-motif	AAACAGA	1103	gibberellin-responsive element
HSE	AAAAAATTT C	781、 826	cis-acting element involved in heat stress responsiveness
MBS	TAACTG	722	MYB binding site involved in drought-inducibility
BOX-W1	TTGACC	1413	fungal elicitor responsive element
TC-rich	ATTTTCTTC A	1162	cis-acting element involved in defense and stress responsiveness

Supplemental Table3 Experimental Primers

3' Biotin-DSN-attB2-	Biotin-GTTAAGCAGTGGATCAACGCAGAGTG
5' Adapter Sequences	TCGTCAAGCAGTGGATCAACGCAGAGTG GCCACAACCTTTGTACAAAAAAGTTGG
pDONR222-F	TCCCAGTCACGACGTTGTAAAACGACGGCCA GTCTT
pDONR222-R	AGAGCTGCCAGGAAACAGCTATGACCATGTA ATACGACTC
<i>GhPOD-F</i>	GGGGACAAGTTTGTACAAAAAAGCAGGCTAT GGGTGCCAAAGTTCTCT
<i>GhPOD-R</i>	GGGGACCACTTTGTACAAGAAAGCTGGGTTG TGAAGCTTGTTTGCAAG
<i>GhCAS-F</i>	GGGGACAAGTTTGTACAAAAAAGCAGGCTAT GGCAGTGCAGATGGCTATCCGAGT
<i>GhCAS-R</i>	GGGGACCACTTTGTACAAGAAAGCTGGGTTT TCCGCACCGGGAAGAACTT
<i>GhSDH-F</i>	GGGGACAAGTTTGTACAAAAAAGCAGGCTAT GGGTAAAGGAGGGAAA
<i>GhSDH-R</i>	GGGGACCACTTTGTACAAGAAAGCTGGGTTC ACAGGTTGAACATGACCT
<i>GhAPX-F</i>	GGGGACAAGTTTGTACAAAAAAGCAGGCTAT GACCAAGTGTTACCCAAC
<i>GhAPX-R</i>	GGGGACCACTTTGTACAAGAAAGCTGGGTTT ATGCATCAGCAAATCCTA
qPCR-UBQ7-F	AGAAGGCTGGTGGGGATTGAG
qPCR-UBQ7-R	ATGGGAGTAGAAGTACAGCGGCTAG
qPCR-histone 3-F	AAGGACATCCAGTTGGCTCGT
qPCR-histone 3-R	GGTTTGCTTGGTACGGGCCATCTTC
<i>GhAPX-qPCR-F</i>	GTTCTCCTGTCAGATCCTGTTT

<i>GhAPX</i> -qPCR-F	CCTAGCTCAGAGAGCTTCAGGT
<i>GhPOD</i> -qPCR-F	CGACACAAAAACACTGCTTTT
<i>GhPOD</i> -qPCR-F	TGTCTCCTTCTCAGACAAGCTC
<i>GhSDH</i> -qPCR-F	GAGATGACCGTCCCACCTTACAC
<i>GhSDH</i> -qPCR-F	TCAGTGGCTTCACATCGATCTT
<i>GhCAS</i> -qPCR-F	TGTCTCCTTCTCAGACAAGCTC
<i>GhCAS</i> -qPCR-R	TTATTCCGCACCGGGAAGAA
