

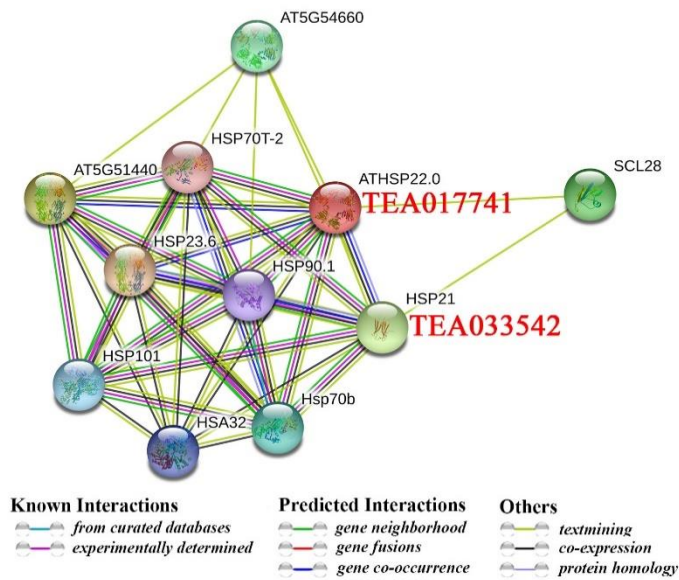


Figure S1. Putative interaction network of *AtHSP22.0*.

Homologous proteins in tea plant and Arabidopsis are shown in red and black, respectively. The genes in red suggest highly connected nodes or hub genes.

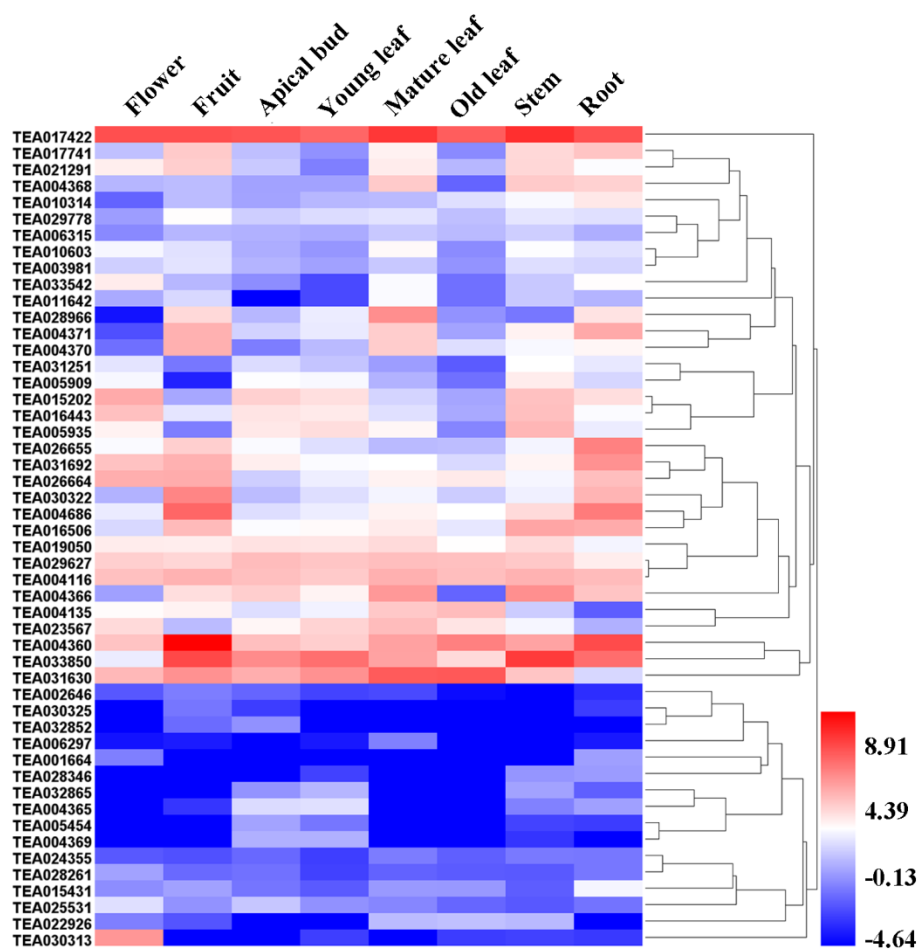


Figure S2 Expression profiles of *CssHSP* genes in different tissues.

CsHSP24.6	MASTLLACPSPLVLNKSVPSPKPN...GPSSVFPSR...FSRVRACATGDNKDT.AIDVHFNNCT..	61
AthHSP21	MASTLSFAASALCSPLAPSPVSSKS...ATPFSVSFPRK...IPSRIRAC...DGREN.SIDVVCGGCK.	61
SlHSP26.2	MAYTSLTSSPLVSNVSVGGTSKINNKNVSPCSVFVPSNRRPTTRLVARATGDNKDT.SVDVHHSSAGGG	69
OsHSP26.7	MAAPFALVSRVSPAARLPIRAAVRRA...RPTVGLPSSGRARCLAVASAACENRDNTAVDVHVNQDGG.	65
CsHsp27.4	MSLYLS.NLTI.SLPI.SSQKTSTNSKLLCPKTPNFLNPG.....SFI.NRGCSNGI.KANAGDGRDSL.DH.L	63
GmHSP27.3	MAHTLSTNLALNLPTSRVVR.....P5RPTQVKPN.....KVMNGDAREKLEH.V	44
GmHSP25.3	MASALP.NVGFHARTSSSRNN.....KFSNVKLLPLT.....SKRNRFTCSNVKANAGGETS.....L	52
SlHSP25.7B	MAHCLS.RFPI.SQPI.LFSNN.....PKYSNSSLPIS.....SRKYCGNYKKLVNVVDERHNL.DH.L	55
Consensus	na t l s s s v n a n k na dv	
RegionIII-N		
CsHSP24.6	NCC..AVERRRPRLAVD.I.SPFGLLDPLSPNANRNLDRNRLFEDS.VTFP.....	111
AthHSP21	GNGGSVEKRPCCRLTND.VSPFGLLDPLSPNRTNRNLDTNRNLFEDT.NPVSG.....RNRGGS	120
SlHSP26.2	NNGGTAVERRPTR.NALD.VSPFGVLDPNSPNRTNRNLDTNRNLFEDT.NTFPG.....RNRA.S	126
OsHSP26.7	NCCGNAVCRPRRSALDGI.SPFGLVDPNSPNRTNRNLDTNRNLFEDT.VALGFPA.....TPRRSL	126
CsHsp27.4	CRANKSCQCSQPPKKRVAEAPPI.GLVDRFPTARTVCCNNTNERNMEDP.FVYTS.GVPSPTL.TETGG.	129
GmHSP27.3	HVPKHNKHHCLPKNKVAPTPPVGLVDRFPTARTVCCNNTNERNMEDP.FAFSTLEVPSPLPSEGVGG	113
GmHSP25.3	CKSKCCVC...PKNKVPCASPVLNCFPVARTVCCNNTNERNMEDP.LVYG...STSPLI.VVGDE	113
SlHSP25.7B	GRCKNTPC...PRKRTPCNAPVGLVDRFPTARTVCCNNTNERNMEDP.LAFN..GGPS...TDDI.G	113
Consensus	q vq r p p vd s p r g l l d p l p p a r t n q q n n d t n a r n f e d p f g	
RegionII-ACD		
CsHSP24.6	.AAEVRAPVDIKDDENEIKNRFDPGLSKEDVKVSVEDDLVIKGEHKREE.....GGDDSW	167
AthHSP21	GVSEIRAPVDIKKEEHEIKNRFDPGLSKEDVKISVEDNVLVIKGECKKE.....DSDDSW	176
SlHSP26.2	GTGEIRTPVDIKHDDENEIKNRFDPGLSKEDVKVSVENDMLVIKGEHKKEE.....DGRDKH	183
OsHSP26.7	ATGEVRIPVDINEDDKEVRNRFDPGLSREEVKVSVEDDALVIKGEHKKEEG.....EGAEGSGDGW	188
CsHsp27.4	YSR.GRTPVEIKEGEGEYKNRFDPGNTKDDVKVYVEEKNLVKAEKNPKDR.....NGCESEVENEE	191
GmHSP27.3	YRRRGRAPVEIKECESYKNRFDPGMNKEDVKVVEEKNLVKAEKAKKKKCEI.VELQCEKQCEEE	183
GmHSP25.3	YSK.GKIPVAIKEGCKDYKNRFNPGMNKNDVKVVEECNNLVKAEKALCEN.....HEGCAD.GNED	174
SlHSP25.7B	YRR.GRTPVEIKENEGEYKNRFDPGNTKEDVKVVLVEEKNLVKGEKNVKN.....NEKE....EE	169
Consensus	y egr p w d i k e e e y k n r f d n p g l s k e d v k v v e n l v i k g e k k e e d e	
RegionI-C		
CsHSP24.6	S.GRSYSSYDTRLRLPDNCEKDKIKAEKNKGVLLISIPKVKVERNVIDVEI	217
AthHSP21	S.GRSVSSYGTRLCLPDNCEKDKIKAEKKNGVLLITIPKTKVERKVIDVCI	226
SlHSP26.2	SVGRNYSYDTRLRLPDNVVKDKIKAEKKNGVLLISIPKTEVEKKVIDVCI	234
OsHSP26.7	VKERSVSSYDNRLALPDCEKSKVRAELKNGVLLVTIPKTEVERKVIDVQV	239
CsHsp27.4	VSAKSYGKYNRVALPENVEFEKIKAEVKDGVLYITIPKACGTSKVLDNV	242
GmHSP27.3	VSAKSYGRYSRIALPDNVCFENIKAEVKDGVLYITIPKATSYSNLDGV	234
GmHSP25.3	VPANSYGRYNHRIALPENIEFDKIKACVKDGLYVITIPKASTSSKVIQDV	225
SlHSP25.7B	VSAKSYGKYNTRIALPENIDFEKIKAEVKDGVLYITIPKASSNPKVFDNV	220
Consensus	w a r s y g s y t r l a l p d n e r d k i k a e v k d g v i y i t i p k a v e k v i d i q v	

Figure S3 Alignment of the Amino Acid Sequences of CsHSP24.6 and Its Homolog Proteins. Alignment is generated using DNAMAN with default parameters. Black indicates the location of conservative residues and gray indicate the location of similar residues. RegionI-C, RegionII-ACD and RegionIII-N are shown in red box. The following sequences used for the above sequence alignment: *Oryza sativa*(Os); *Arabidopsis thaliana*(At); *Glycine max* (Gm); *Selaginella moellendorffii*(Sm); *Solanum lycopersicum* (Sl); *Camellia sinensis* (Cs).

PG-binding domain

CspTAC5	.ELKRRATLRKSGEGEVVRVQCALQKLGYSCEEDMEYSSFSSTGERAVNTWQATLGTREDGIMTVELQEMLYREQQIGVSGLAINVDPKGNLTVVQK	273
PtpTAC5	..KKIRKTLRKSGEGEVKEMQDALQNLGYSCEEDMEYSSFSSTGERAVNTWQASLGASEDGMITTELLKRLYMEQHIDARMPISSETQKGSQATVPAE	270
RcpTAC5	..EKIRITLRKSGEGEVREMQDALLNLGYSCEEDMEYSSFSSTGERAVNTWQASLGAPEDGIMTAELLRLYVGGQNKVTGSTISIDQKESLTVSQK	261
VvpTAC5	..DQKIRKTLRVSGEGEVVRMQDALLNLGYSCEEDMEYSSFSSTGERAVNTWQASLGAPEDGIMTAELLRLYMEQHIEAAGLKRNDPKENDASPP.K	112
GmpTAC5	..VEIRISLRIGSGEGEVVRMQDALLNLGYSCEEDMEYSSFSSTGERAVNTWQASLGAPEDGIMTAELLRLYLEIRNKDTG...SATQDKQSTTVLPK	257
MtpTAC5	..VEIRIVLRIGSGEGEVVRMQDALLNLGYSCEEDMEYSSFSSTGERAVNTWQSSLGIPEDGIMTSHLLRLYLDIRTTDID...SVNETKKSASVLPK	268
AlpTAC5	KKKKRRTLRVSGEGDVQADQALLNLGYSCEEDMEYSSFSSTGERAVNTWQASLGVRDGMITAEELLRLFMDEDVETDK.....DEASTMKKE	268
AtpTAC5	KK..IRRTLRVSGEGDVQADQALLNLGYSCEEDMEYSSFSSTGERAVNTWQASLGVRDGMITAEELLRLFMDEDVETDK.....DEASTMKKE	261
BdpTAC5	SGSGRRRLRVSGEGEVVRMQDALLNLGYSCEEDMEYSSFSSTGERAVNTWQASIGTSEDCLMTSELLEMLFTGQTVDDLKT.....K	292
HvpTAC5	AGSGRRRLRVSGEGEVVRMQDALLNLGYSCEEDMEYSSFSSTGERAVNTWQASIGTSEDCLMTSELLEMLFTGRTKEDLR.....K	260
OspTAC5	GDGGRRTLRVGAEGEDVRMQDALLNLGYSCEEDMEYSSFSSTGERAVNTWQATVRVSECMITSDLLDMFTGQVGQDVKT.....K	240
SbpTAC5	DSSKRRTLRVGAEGEDVRMQDALLNLGYSCEEDMEYSSFSSTGERAVNTWQSTVGTSENGVMTSELLEMLFSGKTGEDAKT.....K	240
ZmpTAC5	GASESRRTLRVGAEGEDVRMQDALLNLGYSCEEDMEYSSFSSTGERAVNTWQATVGAENGVMSELLEMLFSGKTGEEVKT.....K	215
PppTAC5	QTEVALREMRKGAEGEDVRKELQALQBLGYSCEEDMEYSSFSSTGERAVNTWQASIGVRDGVLSPELLAMULSKTQTNAKSSK.EVPSRQSVSNQKA	394
SmpTAC5	SNKQIARSLKYGAECDVVKLQALAKLGYSCEEDMEYSSFSSTGERAVNTWQSSIGAAEDGIVTAQVLSQISEHQVITVN.....K	307
Consensus	klrrtlrvsgedvramqeallklgfyssgeedmeffssfsstgeravntwqaslgasedgimtaellerlf gq ed k tv k	
CspTAC5	EGANGAAVASITEISEIQTVVEESCVTVEVSEHVFLLGENRWEDPSRLTGRNSKQVGGAK.....SKDRITPCLSCGCEGRLLCCEGCGCEINBE	367
PtpTAC5	EGADGAAVTSVTEISEIHQKVVKE.EVTEVDVSHHVFLLGENRWEDPSRLNGRKQVSGSK.....TKDSTKCLTQCGEGRLLCCEGCGCEINBE	363
RcpTAC5	ESANGAAVASITEISETQKQIVKD.GVTEVKGSHHVFLLGENRWEDPSRLVSKDKQVGVSK.....PKDSMTPLSCGCEGRLLCCEGCGCEINBE	354
VvpTAC5	EGVNGALVASVTEISEIQKVLKEEGFTVEVSSQVVFLLGENRWEDPSRLVGRDKKGGGK.....PKDATTPCLTQCGEGRLLCCEGCGCEINBE	206
GmpTAC5	EVENGAAVASVAENSEGQKQDV.K.SDKTEVSHRGVFLGENRWEDPSRLFTRNG.VDRSK.....NKDVTTCLQCGCEGRLLCCEGCGCEINBE	348
MtpTAC5	EVENGAAVASVTEISEVQKVVGE.VDQTEASHHVFLLGENRWEDPSRLSTKVR.VDRGK.....NKDGTMLQCGCEGRLLCCEGCGCEINBE	360
AlpTAC5	EASNGSVFSSVTQVPEKKQSILKQDSNREDDVTQNRVFLGENRWEDPSRLIGRNKPVDSK.....STITKTCITQCGEGRLLCCEGCGCEINBE	362
AtpTAC5	AGNGAVFTSVTQVPEKKQSILKQDSNREDDVTQNRVFLGENRWEDPSRLIGRNKPVDRSE.....STNTKTCITQCGEGRLLCCEGCGCEINBE	355
BdpTAC5	AGLNGAVPVTGISEIQTAVREN...GISVSEHVFLLGENRWEDPSRLTKKPKISGA.....TAASTKCLTQCGEGRLLCCEGCGCEINBE	382
HvpTAC5	EGVNGALVPPVPAETAGVQPVVKK....IDYNKHVFLLGENRWEDPSRLTKKPKISGS.....TAASTKCLTQCGEGRLLCCEGCGCEINBE	348
OspTAC5	DGNGAALPSITEIABIQTIVVKGNGVSGVGLSENHVFLLGENRWEDPSRLTKKPKISSA.....TNASTKCLTQCGEGRLLCCEGCGCEINBE	333
SbpTAC5	DGTNGAAVPSVTGIAEVKTVITENGVAAGVSEHVFLLGENRWEDPSRLTKQKKPWSTG.....TAASTKCLTQCGEGRLLCCEGCGCEINBE	333
ZmpTAC5	DGTNGAAVPAVTGIAEVKTAVAENGVSQVSEHVFLLGENRWEDPSRLTKQKKTASTG.....TAASTKCLTQCGEGRLLCCEGCGCEINBE	308
PppTAC5	TGATSGSNTGCKRSFAEKKRIDENRDNIAENRNVFLGENRWEDPSRLRPKTNASSVSPRAGQKAVHTBEFSCGCGEGRLLCCEGCGCEINBE	494
SmpTAC5	TSAAIKPPSPPEVDRS.....STGRVFLGENRWEDPSRLHRRQANPAAS.....QNYTTCGCGEGRLLCCEGCGCEINBE	381
Consensus	eg ngaavasvteiseiqqkvkngv ev vsehrvflgenrwedpsrltgrnkpvs gsk tkdstkcltergegrllcledgtgpeniep	

CspTAC5	QMEWVDEGANCPCYOCGLGYTIDOLCGEINTVV..	399
PtpTAC5	QLEWVGEANCPCYOCGLGYTIDCVCACTTLI..	395
RcpTAC5	QLEWVGEAMCPCYOCGLGYTIDCVCECTLLI..	386
VvpTAC5	QELIWDGAVNCPCYOCGLCHTIDCACECTTLI..	238
GmpTAC5	QLEWVDEGNCPCYOCGLGYTIDOLCGEINTMV..	380
MtpTAC5	QMEWVGEDTHPCYOCGLCHITDOLCGEINTMV..	392
AlpTAC5	QMEWVGEDTHPCYOCGLGYTIDCVCDCKNNL..	394
AtpTAC5	QMEWVGEDTHPCYOCGLGYTIDCVCDCKNNL..	387
BdpTAC5	QLEWVGEDTHPCYOCGLGYTIDCVCAKSKTYQS	416
HvpTAC5	QLEWVGEDTHPCYOCGLGYTIDCVCAKSKTYQS	382
OspTAC5	QLEWVGEDTHPCYOCGLGSIVDVCCEHTVATN	367
SbpTAC5	QLEWVGEDTHPCYOCGLGSILDVCDCCKVNAS	367
ZmpTAC5	QLEWVGEDTHPCYOCGLGSILDVCDCCKVNAS	342
PppTAC5	QELIWDGAVNCPCYOCGLCAIDCVCDCACTTRV	528
SmpTAC5	QASQFALPFGVTYTRNLNQLLITAGEGANCPCYOCGLGYTIDCVCDCKVAAAT	433
Consensus	qflewggedtkpcyocglgytvcgcdgkttv	

DNAJ domain

Frigure S4 Alignment of the Amino Acid Sequences of pTAC5 and Its Homolog Proteins. Alignment is generated using DNAMAN with default parameters. Black indicates the location of conservative residues and gray indicate the location of similar residues. PG-binding domain and DnaJ domin are shown in red box. Asterisk indicates the conserved cysteine residues. The following sequences used for the above sequence alignment: *Brachypodium distachyon* (Bd), XP_003580127; *Hordeum vulgare* (Hv), BAJ86305; *Sorghum bicolor*(Sb), XP_002446784; *Zea mays*(Zm), NP_001147545; *Oryza sativa*(Os), EEE61332; *Arabidopsis lyrata*(Al), XP_002870363; *Arabidopsis thaliana*(At), NP_193103; *Glycine max* (Gm), XP_003555492; *Medicago truncatula* (Mt), XP_003590698; *Populus trichocarpa*(Pt), XP_002297812; *Ricinus communis*(Rc), XP_002518117; *Vitis vinifera* (Vv),CBI33363; *Physcomitrella patens*(Pp), XP_001778192; *Selaginella moellendorffii*(Sm), XP_002963552.

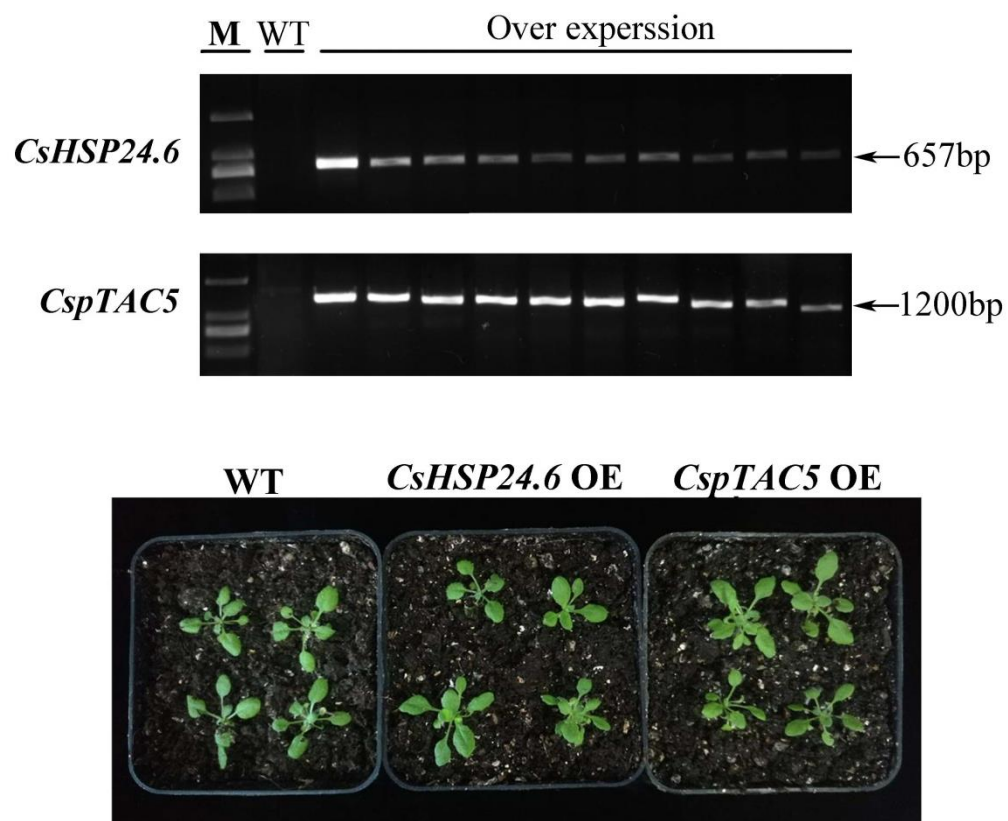


Figure S5. PCR identification and phenotypic observation of positive plants overexpression of *CsHSP24.6* and *CspTAC5*.