

White fluorescent  
light (Control)



UV-B radiation



Fig S1. UV-B radiation on tea plant seedlings

UV-B conditions ( $300 \mu\text{W}\cdot\text{cm}^{-2}$ , photoperiod of 12 h per day, provided with a special lamp (PHILIPS NARROWBAND TL 20W, Poland) with characteristic peak at  $311\text{nm}$ .25/18°C (light/dark)



Fig S2. Shading treatment on tea plants in the tea garden.

The shading experiment was carried out in Anhui Agricultural University research tea plantation (31°. 55' North, 117°. 12' East; Hefei City, Anhui Province, China). 12 rows of *C. sinensis* cv. Shuchazao tea plants (50 m long and 1.4 m wide of each row, 2 m between and 0.6 m within row spacing) were selected for the treatments.

The tea plants were 10 years old from cuttage propagation (1.4 m wide and 1.5 m tall from the soil surface, 0.5 m between plants within the row).

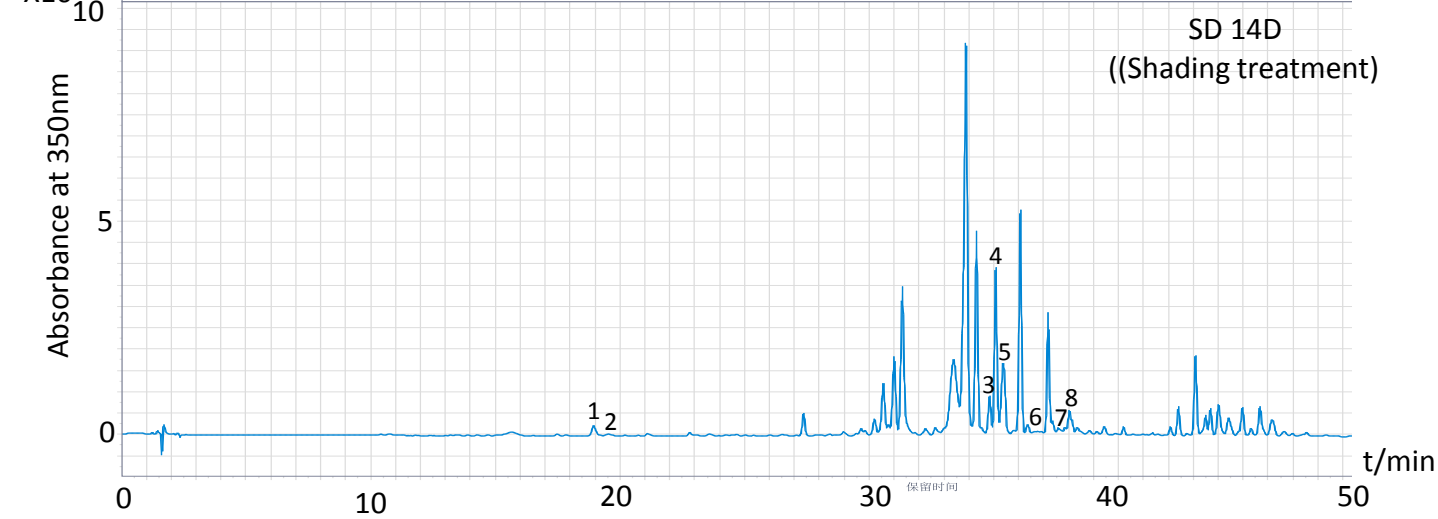
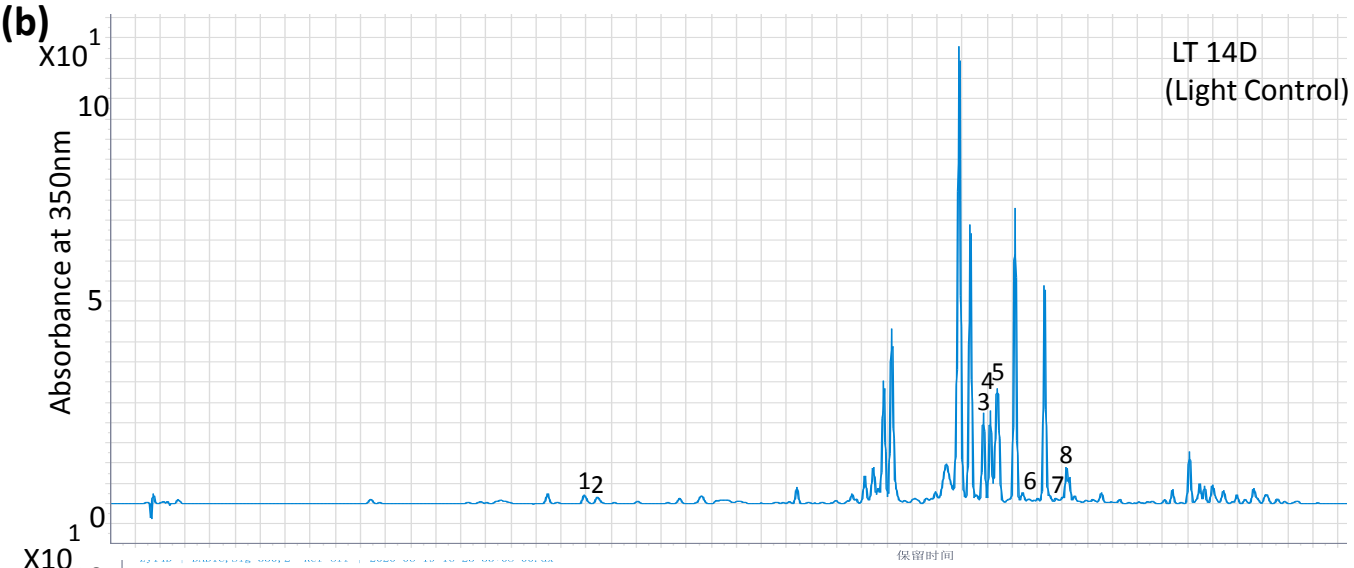
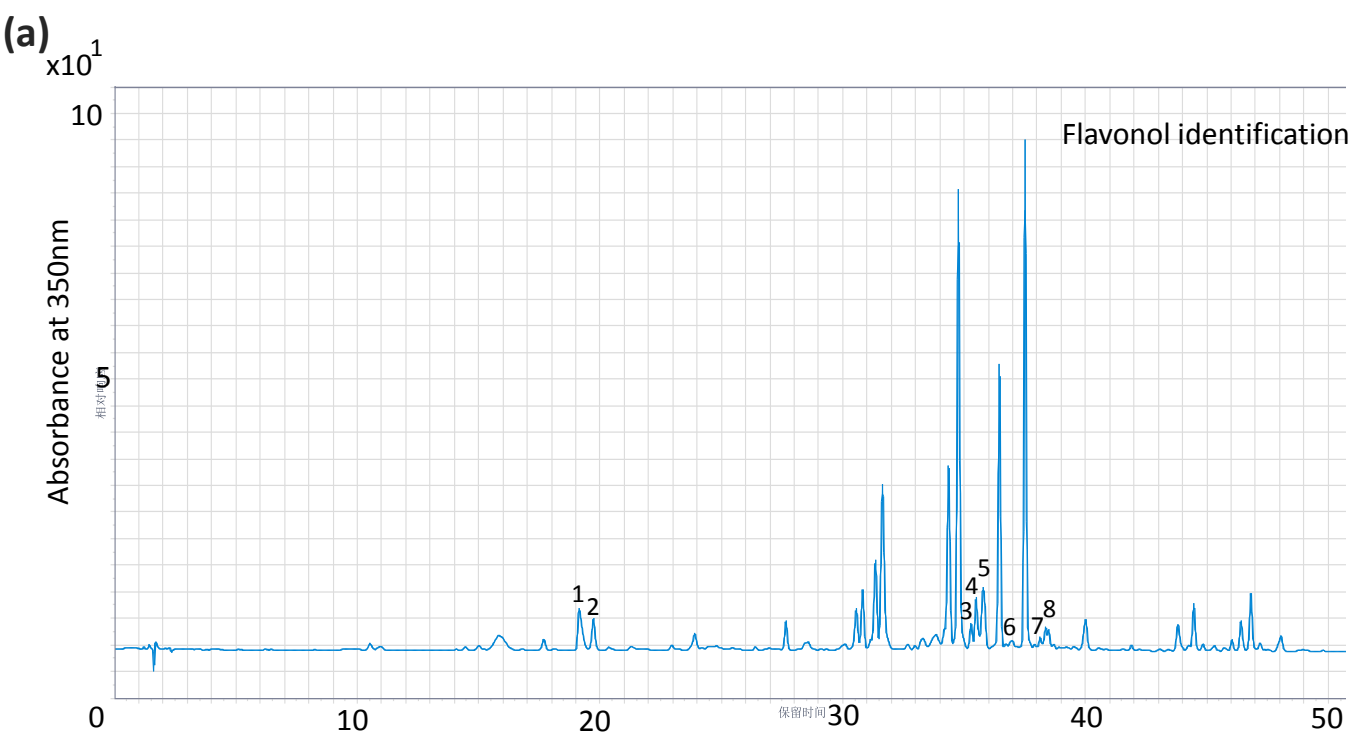


Fig S3. Chromatogram of UPLC for phenolic compounds in tea leaves: UPLC Chromatogram at 350nm.

(a): Flavonols standards. 1 : M-3-O-Gal 2 : M-3-O-Glu 3 : Q-3-O-Gal 4 : kaempferol 3-O-galactosylrutinoside 5 : Q-3-O-Glu/R 6 : K-7-O-GLU 7 : K-3-Gal 8 : K-3-O-Glu

(b): Control and shading of flavonols were analyzed with UPLC.

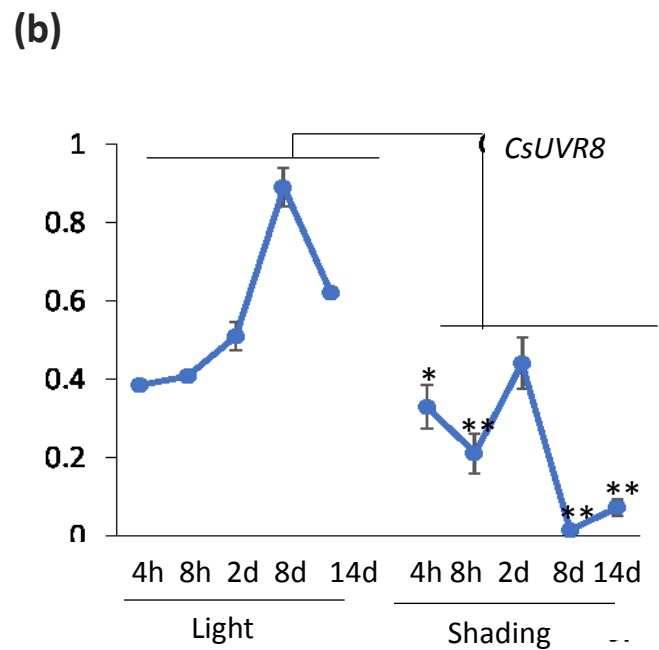
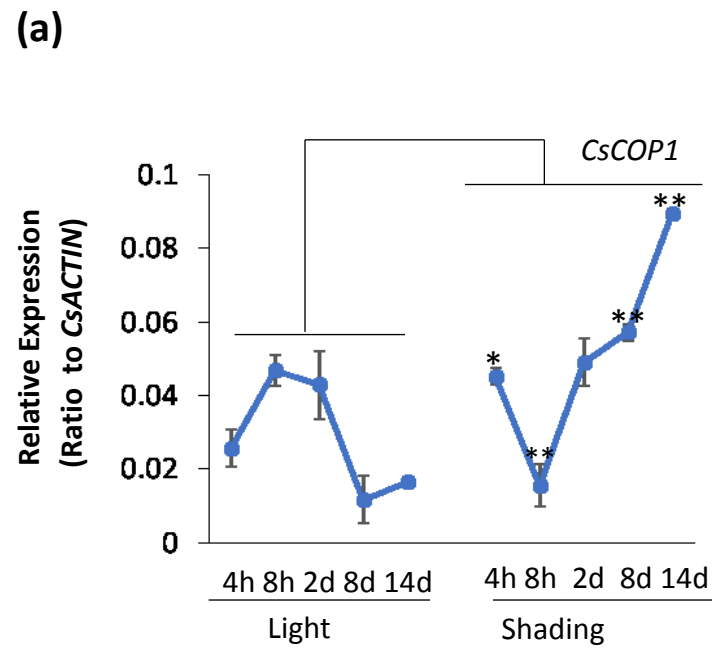
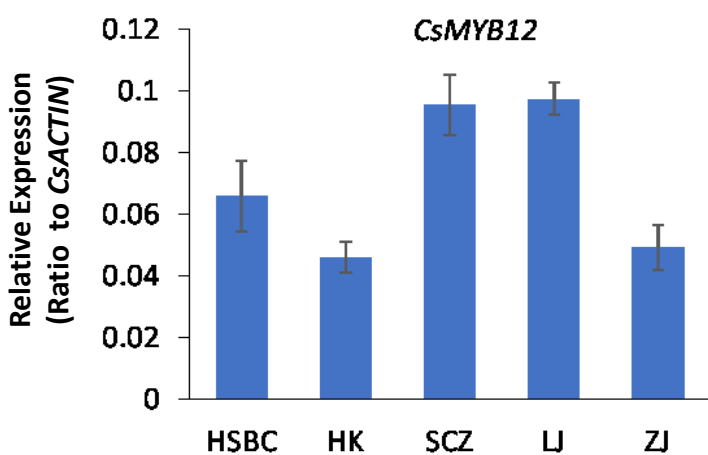


Fig S4. The shading effects *CsCOP1* and *CsUVR8* expression in tea leaves analyzed by qRT-PCR. Differences between SD and LT (control) were analyzed. Data were from three independent experiments and expressed as means  $\pm$  S.D. (n = 3). Differences were analyzed, \*p < 0.05; \*\*p < 0.01 in student's t-test.

(a)



(b)

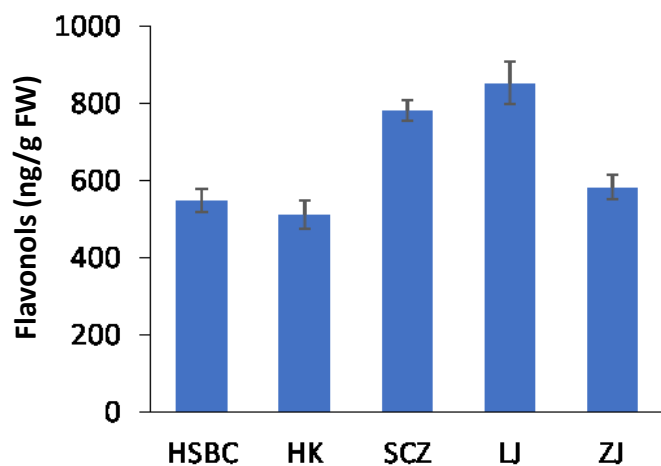


Fig S5. Relative expression level of CsMYB12 and contents of flavonoids metabolites in different tea plants

(a): Expression of CsMYB12 in different species of tea plant.

(b): Total Content of flavonols in different species of tea plants.

Long jing (LJ) ,Shu Cha Zao (SCZ) ,Huang Shan Bai Cha (HSBC), Huang Kui (HK) and Zi Juan (ZJ).

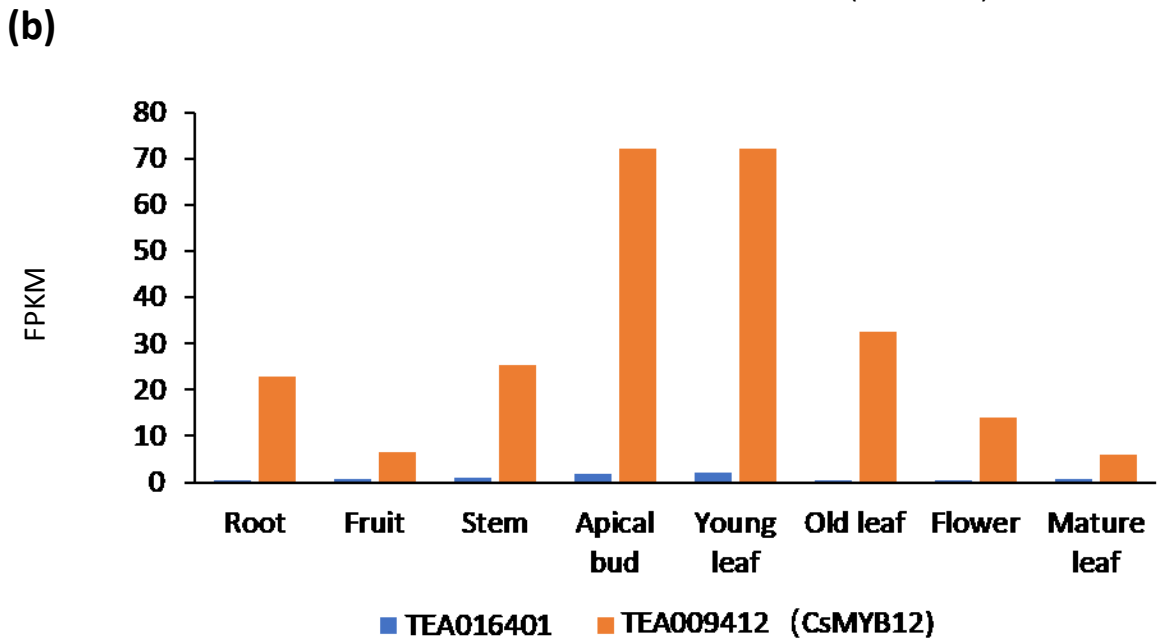
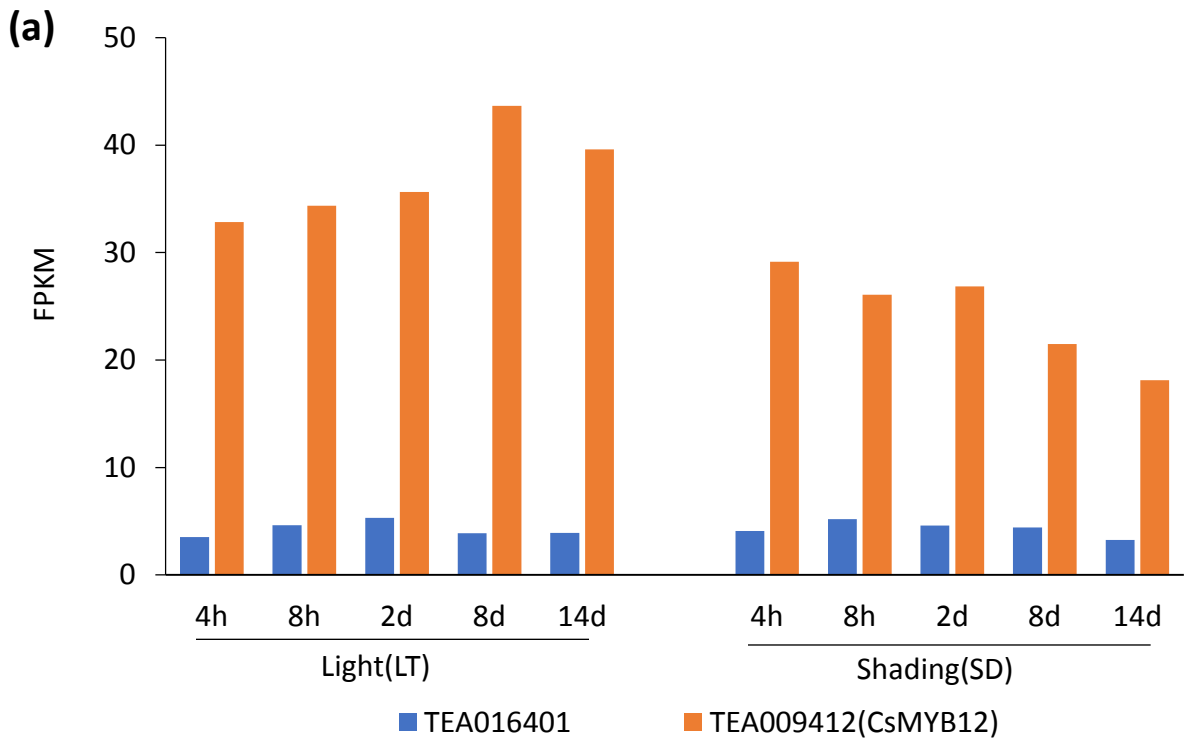


Fig S6. Expression patterns of TEA01640 and TEA009412

(a) Expression patterns of of TEA01640 and TEA009412 tea leaf under shading.

(b) Expression profiles of of TEA01640 and TEA009412 in different stages.



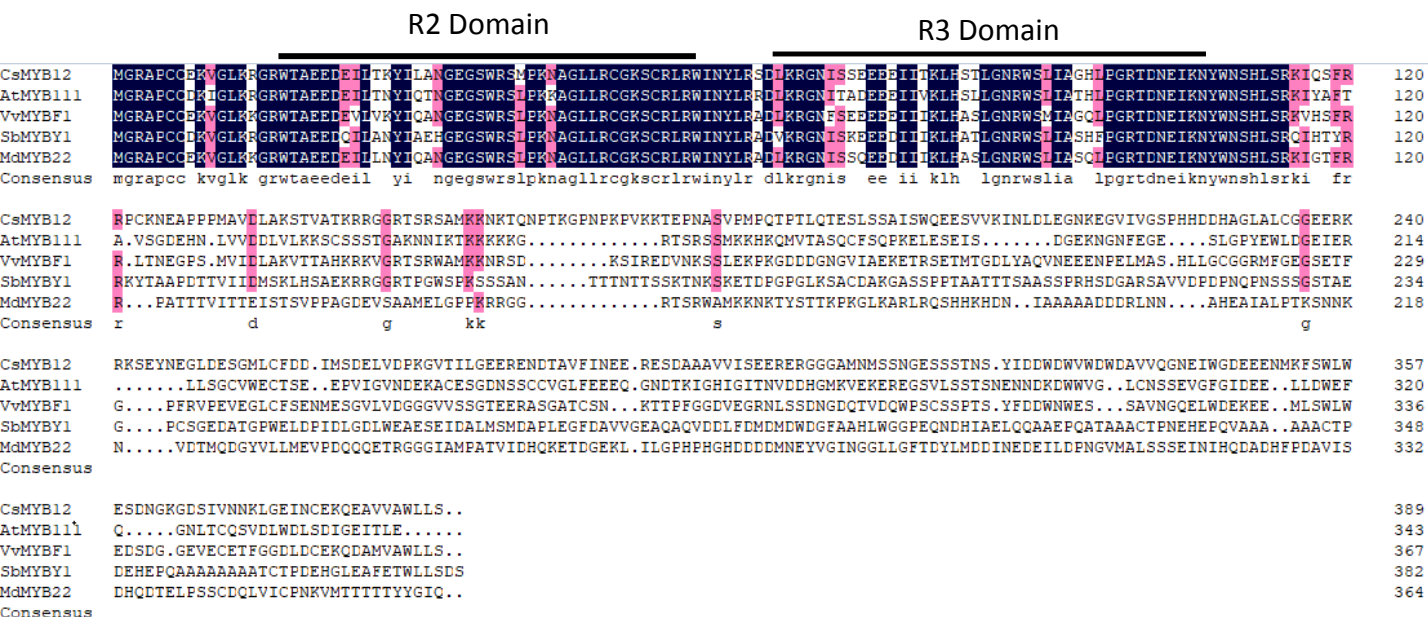
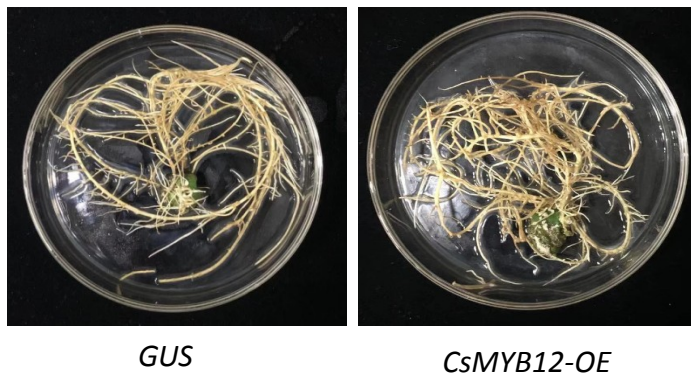


Fig S7. Amino acid sequence alignment of CsMYB12 and MYB homologues from other plants



**(a)**



**(b)**

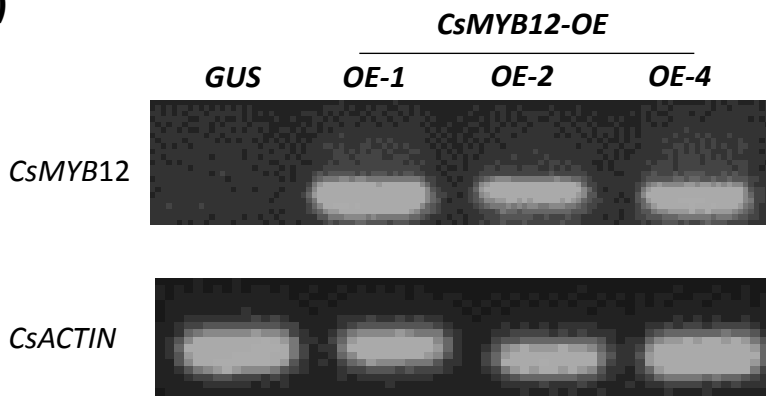


Fig S8. Generation of soybean hairy roots overexpressing *CsMYB12* or *GUS* genes.

(a) Photos of *CsMYB12-OE*- or *GUS*- overexpressing hairy roots

(b) Semi-quantitative RT-PCR examination of overexpression of *CsMYB12-OE* in representative transgenic hairy root lines.

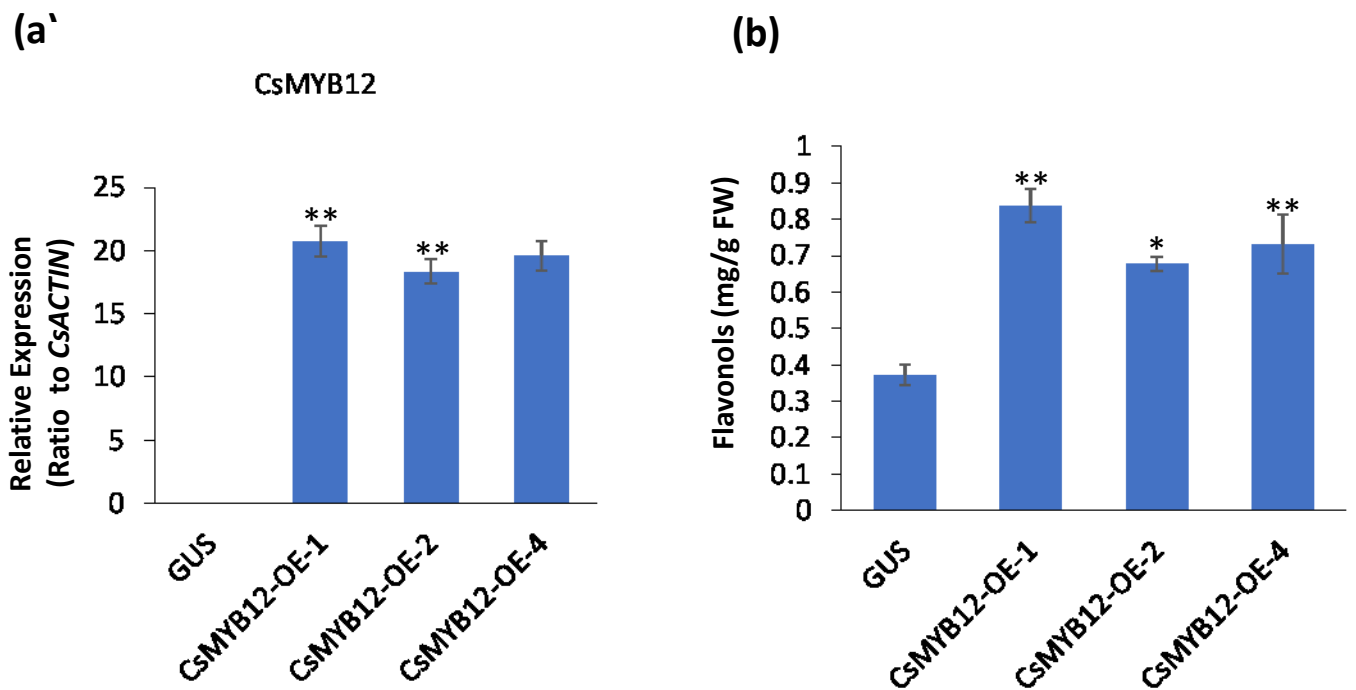


Fig S9. CsMYB12 overexpression affects flavonoids contents in hairy roots.

(a). qRT-PCR confirmation of *CsMYB12* expression in transgenic hairy root lines and GUS (control).  
 (b). UPLC chromatograms for flavonols profiles in *CsMYB12* overexpression hairy root lines and GUS (control).

Data were from three independent experiments and expressed as means  $\pm$  S.D. ( $n = 3$ ). Differences were analyzed, \* $p < 0.05$ ; \*\* $p < 0.01$  in student's t-test.

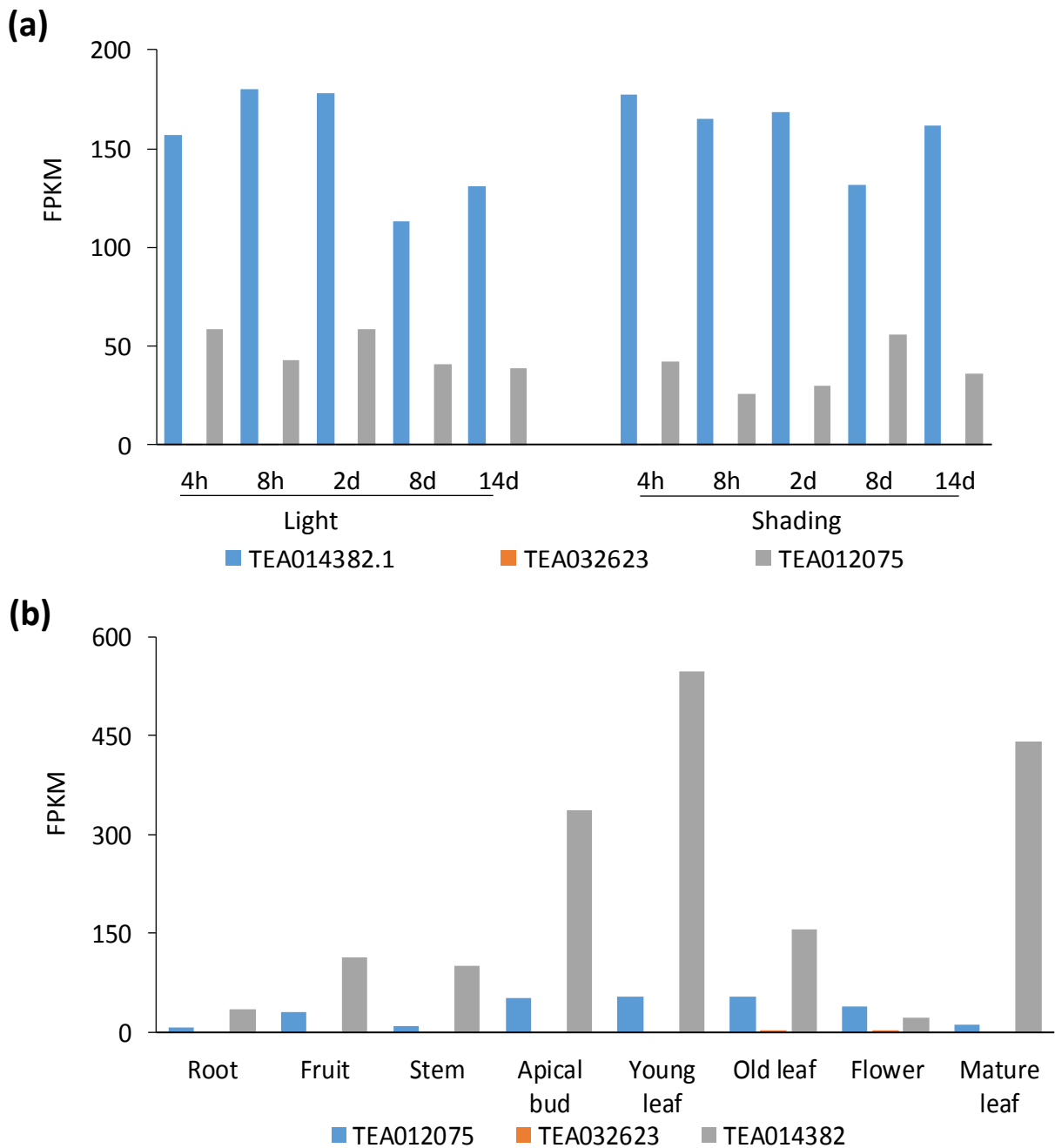


Fig S10. Expression patterns of HY5-like bZIP genes TEA012075, TEA032623 and TEA014382. (a) Expression patterns of TEA012075, TEA032623 and TEA014382 tea leaf under shading. (b) Expression profiles of TEA012075, TEA032623 and TEA014382 in different stages.

AtbZIP	<b>M</b> QEQATSS <b>L</b> AASSLPSSSERSSSS <b>A</b> PHLEI <b>K</b> EGIESDE <b>I</b> RRVPE <b>F</b> GG <b>E</b> AVG <b>K</b> ET <b>S</b> GR <b>E</b> S	60
CsbZIP1	<b>M</b> QEQATSS <b>I</b> AASSLPSSSERSSSS <b>A</b> LQ <b>L</b> EV <b>K</b> EG <b>M</b> ES <b>D</b> E <b>I</b> RRVPE <b>I</b> GG <b>E</b> A <b>A</b> RG <b>S</b> V <b>S</b> F <b>R</b> E <b>A</b>	60
Consensus	<b>m</b> qeqatss <b>i</b> aasslpssserssss <b>a</b> lhleikegiesd <b>e</b> irrvpe <b>f</b> g <b>e</b> aag <b>g</b> ets <b>f</b> rea	
AtbZIP	<b>G</b> SAT <b>G</b> Q <b>E</b> RT <b>Q</b> AT <b>V</b> G <b>S</b> CR <b>K</b> R <b>G</b> R <b>T</b> PA <b>E</b> K <b>E</b> N <b>K</b> R <b>L</b> K <b>R</b> L <b>L</b> R <b>N</b> R <b>V</b> SA <b>Q</b> Q <b>A</b> R <b>E</b> R <b>K</b> K <b>A</b> Y <b>L</b> S <b>E</b> L <b>E</b> N <b>R</b> V	120
CsbZIP1	<b>G</b> S <b>T</b> A <b>G</b> P <b>D</b> R <b>V</b> Q <b>A</b> S <b>S</b> . <b>E</b> G <b>M</b> R <b>K</b> R <b>G</b> R <b>S</b> P <b>A</b> D <b>K</b> E <b>N</b> K <b>R</b> L <b>K</b> R <b>L</b> L <b>R</b> N <b>R</b> V <b>S</b> A <b>Q</b> Q <b>A</b> R <b>E</b> R <b>K</b> K <b>A</b> Y <b>L</b> T <b>E</b> L <b>E</b> G <b>R</b> V	119
Consensus	<b>g</b> saagpdr <b>t</b> qass <b>g</b> eg <b>m</b> r <b>k</b> gr <b>s</b> pad <b>k</b> en <b>k</b> r <b>k</b> rl <b>l</b> rn <b>r</b> vs <b>a</b> qq <b>a</b> rer <b>k</b> k <b>a</b> yl <b>s</b> e <b>l</b> egr <b>v</b>	
AtbZIP	<b>K</b> D <b>L</b> E <b>N</b> K <b>N</b> S <b>E</b> L <b>E</b> R <b>I</b> S <b>T</b> L <b>Q</b> N <b>E</b> N <b>Q</b> M <b>L</b> R <b>H</b> I <b>L</b> K <b>N</b> T <b>T</b> G <b>N</b> K <b>R</b> G <b>G</b> G <b>G</b> S <b>N</b> A <b>D</b> A <b>S</b>	167
CsbZIP1	<b>K</b> D <b>L</b> E <b>K</b> K <b>N</b> S <b>E</b> L <b>D</b> E <b>R</b> V <b>S</b> T <b>L</b> Q <b>N</b> E <b>N</b> Q <b>M</b> L <b>R</b> H <b>I</b> L <b>K</b> N <b>T</b> T <b>A</b> G <b>M</b> Q <b>E</b> G <b>R</b> K.....	159
Consensus	<b>k</b> dlekkn <b>s</b> elder <b>l</b> st <b>l</b> q <b>n</b> en <b>q</b> ml <b>r</b> h <b>i</b> lk <b>n</b> tt <b>a</b> g <b>k</b> q <b>e</b> gg <b>g</b> gs <b>n</b> adas	

Fig S11. Amino acid sequence alignment of CsbZIP1 and AtbZIP .

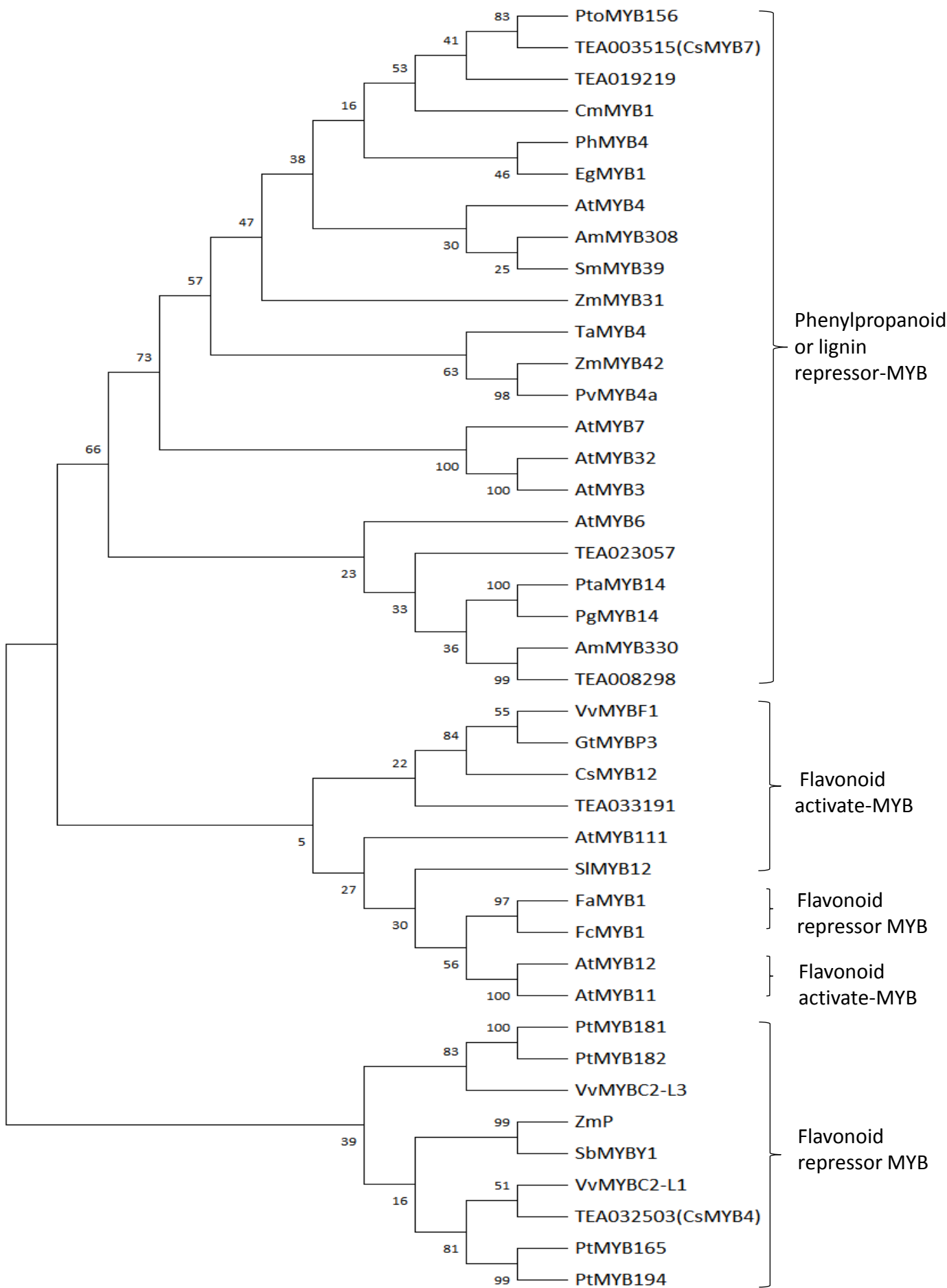


Fig S12. Phylogenetic analysis of CsMYB4, CsMYB7 and MYB homologues from other plants.

CsMYB4	.MRKPCCKQDINKGAWSECEIQRLIDYIQRNGICGWRITLFCAGLI....RCGKSCRLRWNYLRPDLKRGNFTEEDDELLIIRLHLLIGNWWSLIACRLPGRTDNEVKNYWNSHLFRK	114
CsMYB7	MGRSPCCCKAHTNKGAWTDEEDRILAYIRAHGEGCWRSLFKFAGLI....RCGKSCRLRWNYLRPDLKRGNFTEEDDELLIIRLHLLIGNWWSLIACRLPGRTDNEVKNYWNSHLFRK	115
AtMYB7	MGRSPCCCKEHNKGAWDEEEDERLVSYIRSHGEGCWRSLFRFAGLATMYBI...RCGKSCRLRWNYLRPDLKRGNFTEEDDELLIIRLHLLIGNWWSLIACRLPGRTDNEVKNYWNSHLFRK	120
AtMYB32	MGRSPCCCKDHTNKGAWTDEEDDKLISYIRAHGEGCWRSLFRSAGLQ....RCGKSCRLRWNYLRPDLKRGNFTEEDDELLIIRLHLLIGNWWSLIACRLPGRTDNEVKNYWNSHLFRK	115
AtMYB4	MGRSPCCCKAHTNKGAWTDEEEDERLVSYIRAHGEGCWRSLFKFAGLI....RCGKSCRLRWNYLRPDLKRGNFTEEDDELLIIRLHLLIGNWWSLIACRLPGRTDNEVKNYWNSHLFRK	115
VvMYB2-L1	.MRKPCCKQDINKGAWSECEIQRLIDYIRKNGEGCWRITLFCAGLI....RCGKSCRLRWNYLRPDLKRGNFTEEDDELLIIRLHLLIGNWWSLIACRLPGRTDNEVKNYWNSHLFRK	114
Consensus	mgrspccek htnkgawtkeed kli yikahgegwrslp aagll rcgkscrlrwinylrpdlkrgnftededdliiklhlhllgnkwsliagrllpgrtdneiknywnshlfrk	
CsMYB4*	LINMGIDETRRRLSQNLTHPC....IIGATGSAISSASRDHACQPLKTKGDH.....DQVS.....DAASCLDATWGLEPDLNLDLRLTAPQ.....	192
CsMYB7	LMNRGIDEATHRRPINEPAAAD.....VITISFATAATKEEEEEKI....SGFSIK.....EEKSPVRECC...PDLNLELRISPEYCNQ.....SDQPL	192
AtMYB7	LLSKGIDEATHRRGINEAKIS....DLKKTQDQIVKDVSVFKFEETDKSGDQ...KQNKYIRNGLVCKEERVVVEEKIG...PDLNLELRISPEYCNQ.....REISTCTASRF	219
AtMYB32	LLRKGIDEATHRRPINETKTSQDS.SDSSKTEDELVKILSFGPQLEKIANFGDE....RIQKRV.....EYSVVEERC...PDLNLELRISPEYCNQDKLHDERNLFRGVRKYRC	219
AtMYB4	LINRGIDETSHRPIQESSASQDSKPTQLEPVTSMNTINISFTSA PKVETFHESISFPGKSEKISMLTFKEERDECPVQEF...PDLNLELRISLHDDVDRLQGHG...KSTTPRCFKCSL	229
VvMYB2-L1	LINMGIDENRRLSHNFRPR....DFCIAAATISSGLNNHSPFPVKSVDGN.....DQTS.....DAGSCLDDNRRALPDLNLDVATIEQP.....	193
Consensus	lin gidpathrpine sq t t sf a gd k s e s vee p dlnlelrisspp q c	
CsMYB4	...SIAIVEEESKQNESTMSRKVES...TPP.....RTLVLER....	224
CsMYB7	KTISSVLGFSCSLGIQNSEECSCGDG...ISSNTGYDFLGLK...SGVLDYRSLEM	243
AtMYB7	YMENDECSSETVRCQTIENSSSISYSSIDISSNVGYDFLGLK...TRILDFRSLEM	273
AtMYB32	GFGNGKECSNNVRCQTEDSSSSSYSSDIDISSNIGYDFLGLNN...TRVLDFTILEM	273
AtMYB4	GMINGMECRGGRMRCDVVGGSSKGS...MSN...GFDFLGLAKKETTSLIGFRSLEM	281
VvMYB2-L1	...SLDTTEAKKHNESKVSRELEP...GPS.....STLLIFG...	225
Consensus	ns ec e kcq s ss s sss gydfllg t lldfrslem	

LXLXL

Fig S13. Amino acid sequence alignment of CsMYB4, CsMYB7 and MYB homologues from other plants

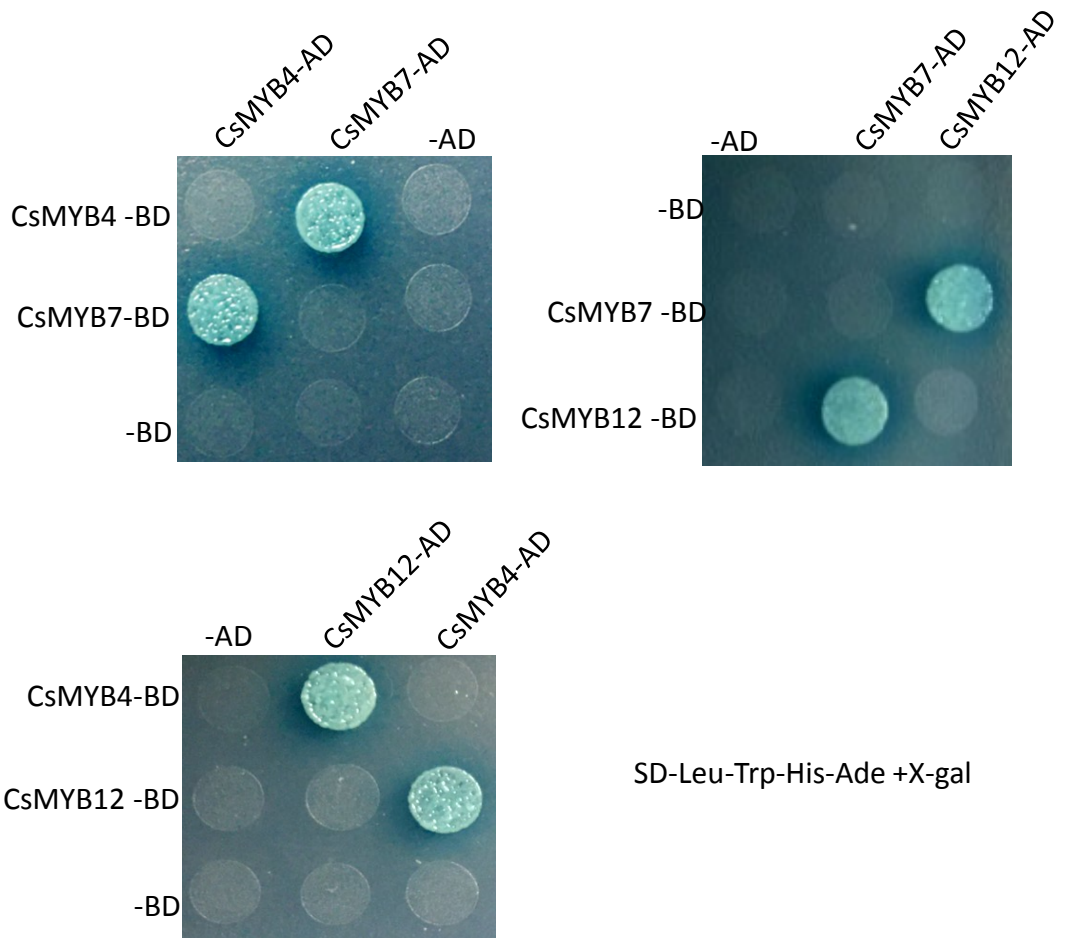
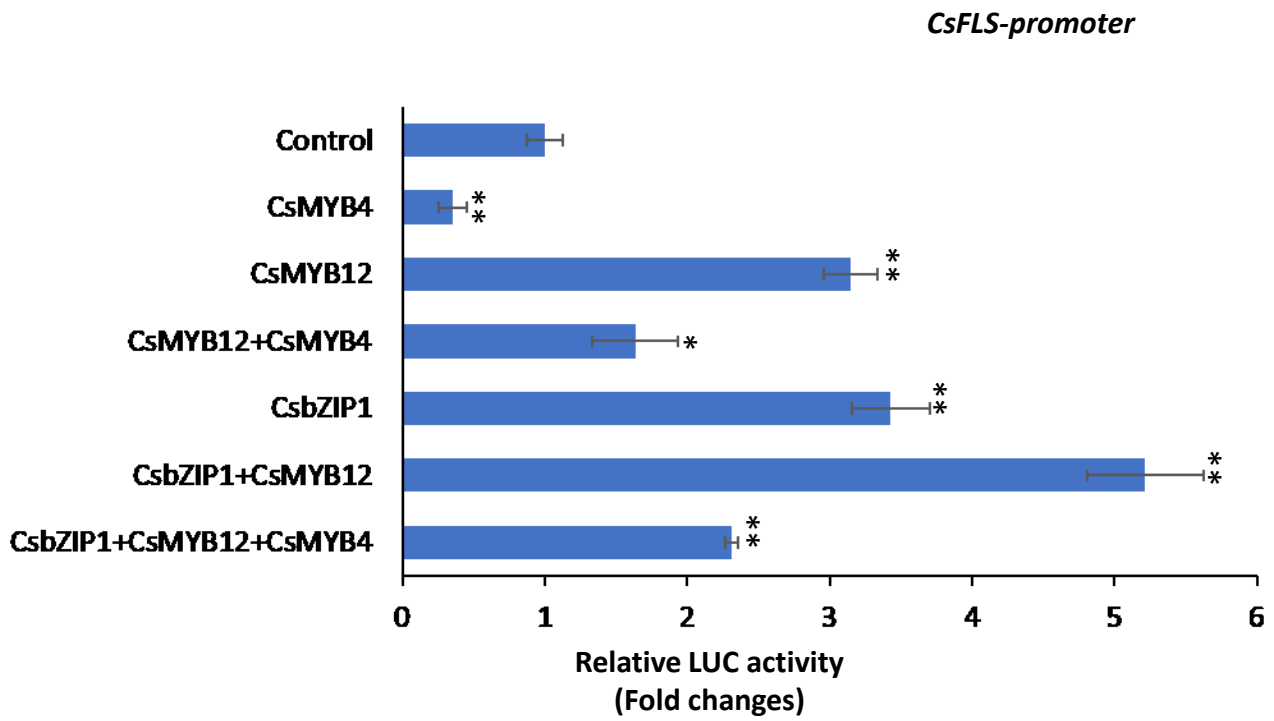


Fig S14. Interactions among CsMYB12, CsMYB4, and CsMYB7 in Y2H assays



(a)



(b)

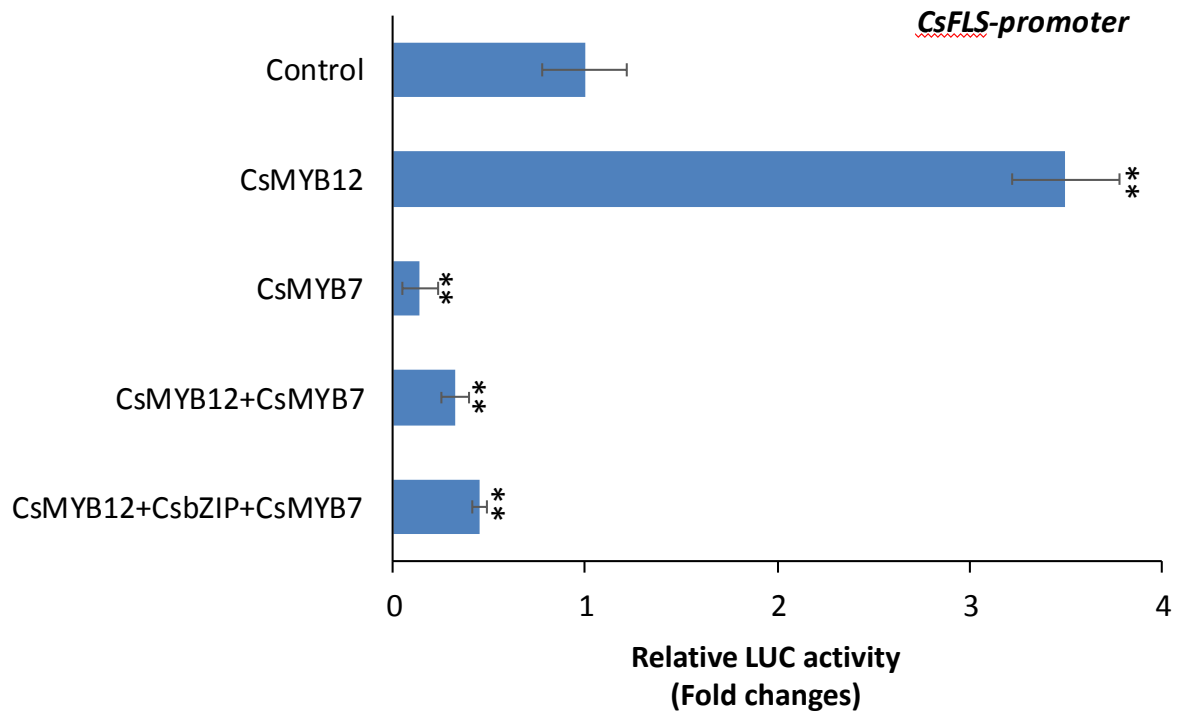


Fig S15. Transactivation assays of CsbZIP1, CsMYB12, CsMYB4 and CsMYB7 individually or in combination on the promoter activity of *CsFLS* in the luciferase reporter assay.

Data were from three independent experiments and expressed as means  $\pm$  S.D. (n = 3). Differences were analyzed, \*p < 0.05; \*\*p < 0.01 in student's t-test.

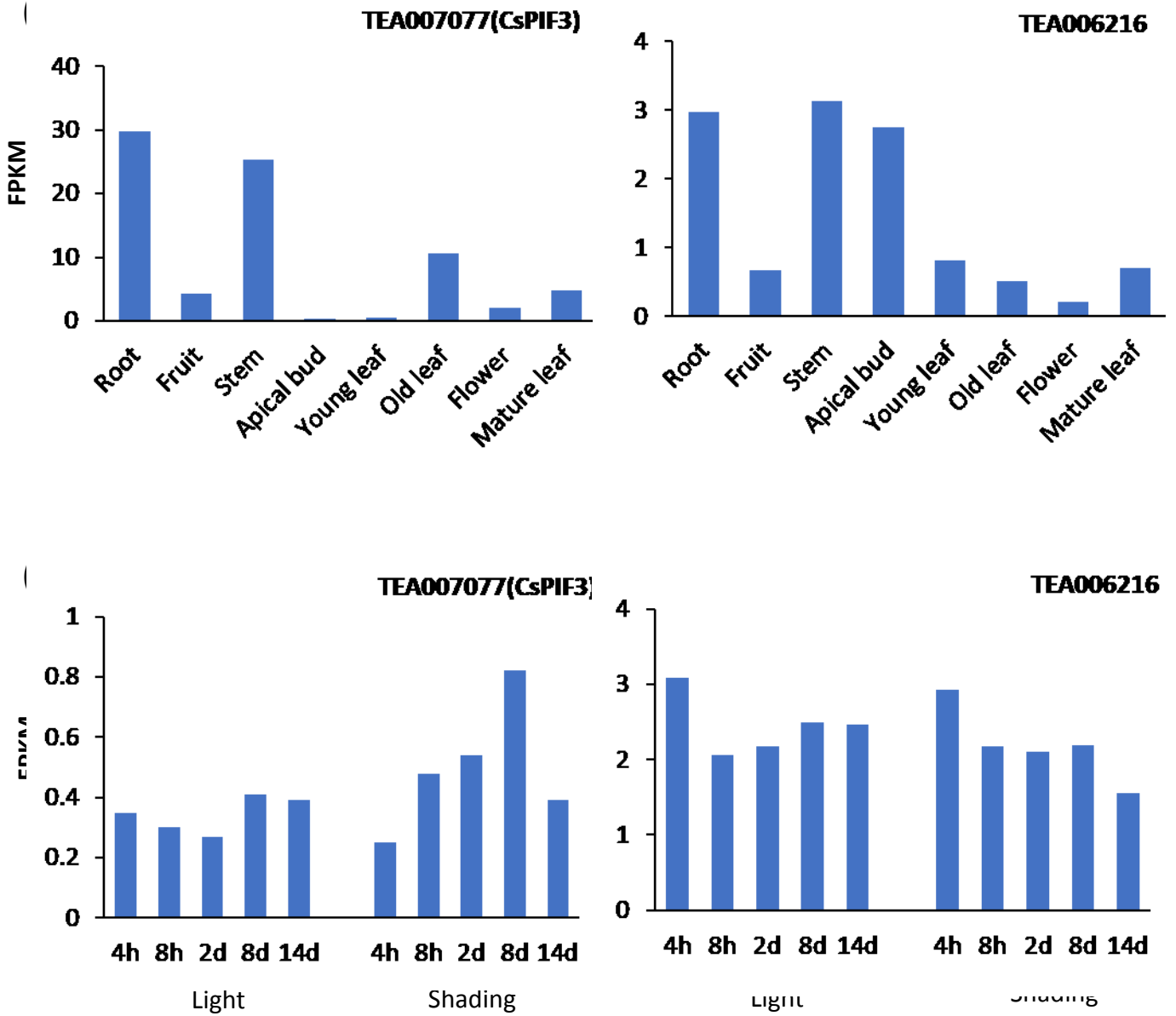


Fig S16. Expression patterns of TEA007077 and TEA006216.

(a) Expression profiles of TEA007077 and TEA006216 in different stages.

(b) Expression patterns of TEA007077 and TEA006216 tea leaf under shading.

AtPIF1	-----	-----STNESR	139
CsPIF3	ESSRARSGQFHDPWLFQEN-QTSIPSLRSKVSGIISNTSCNNKRDIIIVQPNLSRRPNTS		228
AtPIF3	AASSSQYNGFQSHSLYGSDRARDLPSQQT-----NPDR---FTQTQEPLITSNK		194
	<b>APA</b>	<b>..</b>	
AtPIF1	PPVRNFMNFSRLRGDF----NNGR-----GGESGPLLSKAVVRESTQVSPS		181
CsPIF3	SSFMNFPHF SRPSTLV RANLQ TIDAITS PGTSNVE PMGGK NKGND PC SGYFAQS-----		282
AtPIF3	PSLVNFSHF LRPATFAKTTNNNLHDTKEKS-----PQSPNVFQTR-----		235
	. ** :* *	:. .	
		<b>APB</b>	
AtPIF8	MSQCVPNCHIDDT PAAATTTVRSTT-----AADIPILDYEV AELTWENGQLGLHGLGP		53
AtPIF1	MHHFVPDFDTDDDYV---NNHNSLNHLPRKSITTMGEDDDLME LLWQNGQVVVQNQRL		56
CsPIF3	-MPFSEFYGMASGKLESAQ KTTTCLTDL-----SHVPHNEFVELVWENGQIMMQGSS		53
AtPIF3	-MPLFELFRLTKAKLESAQDRN-----PSPPVDEVVELVWENGQISTQSQS		46
	.	:. ** *:***: :.	

Fig S17. Amino acid sequence alignment of CsPIF3 and AtPIF1, AtPIF3 and AtPIF3.

(a)

CACCAAGATCGGCTGAACTCCAGTCTCTCTAACTAACATTCCCCATTTATTCCACCACACATGAGTGATTGTTTA  
TCTGCGCGAAGCGCCCACTACTTTTATTTTCAATACTGGCAGCGATCTCGAGGCCCAATCCCGAGGCGATTTC  
ACTAACTCTAAACTCCACGAGAAAAACGTCGGTTGACAGTCACCATGGCATAGTTGTCCAAACGACTTTTTGA  
AGAACGTGCACCGTCTGAAAATCTAGGCCCGAGCCGAGTTGAATTTGCCGTAGCTACCTTACCGACTGGCTT  
TTGGCTTCTCAAGTTACAATAGCCTCAATCAGGGATAAACGGCTATCACGTATGCGTCGACCCTACCGATCAAT  
GTTTATACATCCATTCAAACATATACATAAACGAAACGCGTACATACCAATACGAACTGCAACAAAATATTTAT  
CATAGAACGCTTTTTATTTGATAAAACAGGCAATATATTACATAGTTTTCAACGCGATCTACGTTTCAACCTTAC  
AACAAAGTACACTTATACGGCATCACCTCATCCTCACTCTTCTCGACCTCAAAGAAGAAAACGGAAAATGTTT  
ACTATGGTAGAATGGCGATGCCGAATCAATGCCCGACGCTCGAAGAGCTTCTGCGGCTTGAGATGCCATGATC  
CAACCGTGCCTAAATCCATGATTTTACATCGGCAAACCTTCTTCTACAAGTTTTTCTTTGTCTTTTGGATTCAA  
CTTTTTGGCCGTCATGAAAGCCTTTCTCATAGGCCCTCCGTTTCGCGTTTCCAGTGCGAACATACTCGCCGTCT  
CACGATCGGCAAGCGCGGAACTGATGAGCCGACTGGTAACCCTTTCTTCCACGATTGGGTTTCTGTGCCTGGC  
AGTTTGTGCCTGGGCCGCTTGGTCTTCTTAACTCGGTGATTGAATTATTATTATTATTATTATTATTATTAAATC  
AAAGTTGTTGAGAGTTACACAAAAGAAAGGCAAAAATAAATAAACACACCGTGTCTTGCTATACTTTAATATA  
CCTTACTTTACACCTACCTGAAGATTACCCATAGTTAATGTCCCTATAACTTATTATATGACATTTGATGATGCTAA  
TATCATAAAAGAGAGGCCACACCATCCACTCCCCTCAAACCTGTCTCACCAACTCACATCTAGAAGCAATTAG  
GGTCACTTCCCCCCTCTCTCTCTCTCTCTCTCTCTCCCTGTATATACATATATATATATATATATCTATAAAGA  
GTCAAAGGCTATAAAAACCATCTCAAGTACTCACAGGGGCCGCTTGGATTCCACCATATAACCACTGCA  
ACCCAAAGAAAAGAGAAAGAAGACAAAGAAAAGAAAAGAAAATTGCTAATCAG

(b)



Fig S18. Promoter analysis of CsMYB7.

(a). Promoter sequence of CsMYB7.

(b). The characteristics of cis-elements for binding of CsMYB7 in the flavonoid gene promoters.

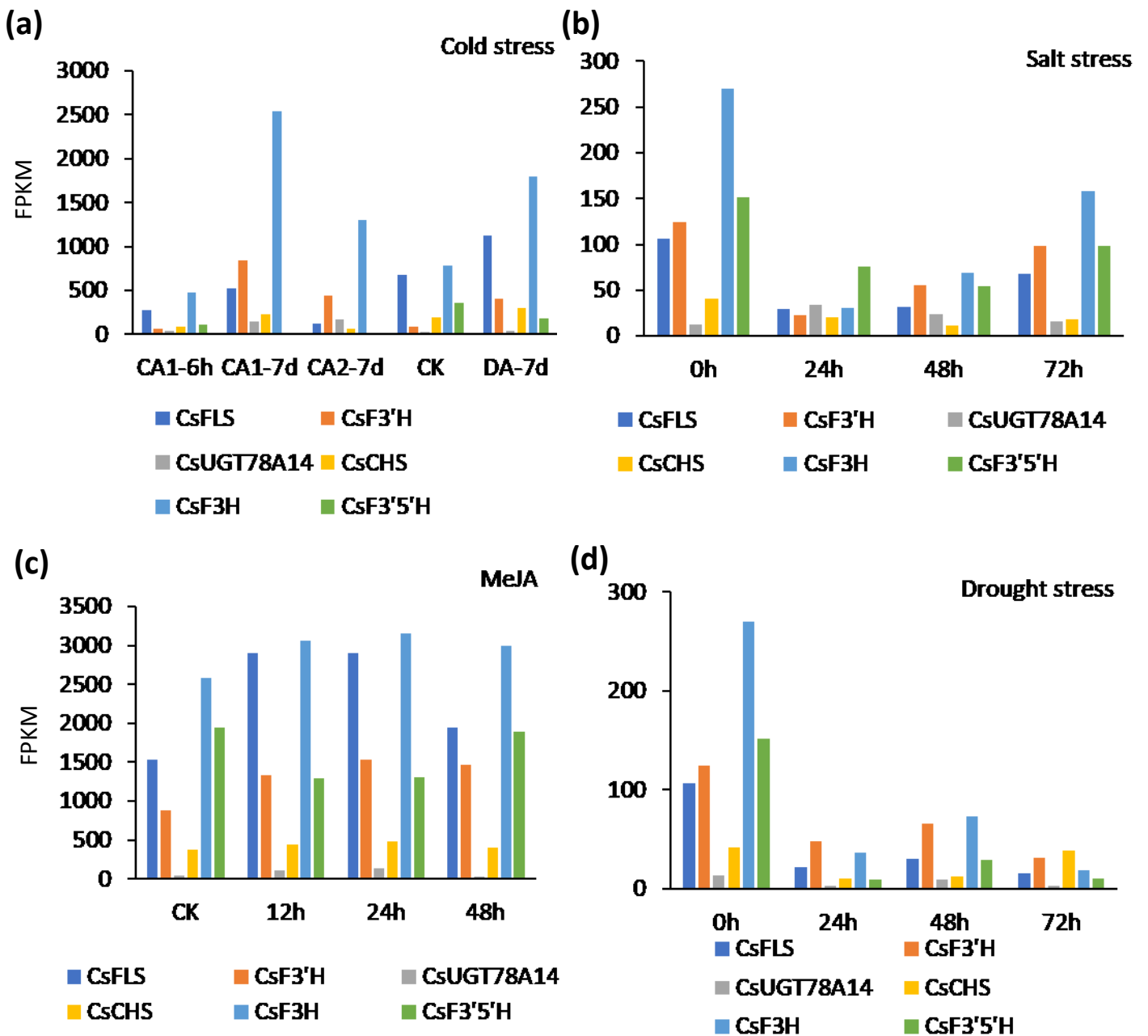


Fig S19. Expression of flavonol structural genes under various abiotic stresses

(a). Expression of *CsFLS*, *CsF3'H*, *CsCHS*, *CsF3H*, *CsF3'5'H*, and *CsUGT78A14* under cold stress.  
 (b). Expression of *CsFLS*, *CsF3'H*, *CsCHS*, *CsF3H*, *CsF3'5'H*, and *CsUGT78A14* under Salt stress.  
 (c). Expression of *CsFLS*, *CsF3'H*, *CsCHS*, *CsF3H*, *CsF3'5'H*, and *CsUGT78A14* under MeJA stress.  
 (d). Expression of *CsFLS*, *CsF3'H*, *CsCHS*, *CsF3H*, *CsF3'5'H*, and *CsUGT78A14* under PEG treatment.  
 Transcriptome data from experiments with tea cv. Shuchazao were retrieved from the tea plant information archive (<http://tpia.teaplant.org/index.html>).

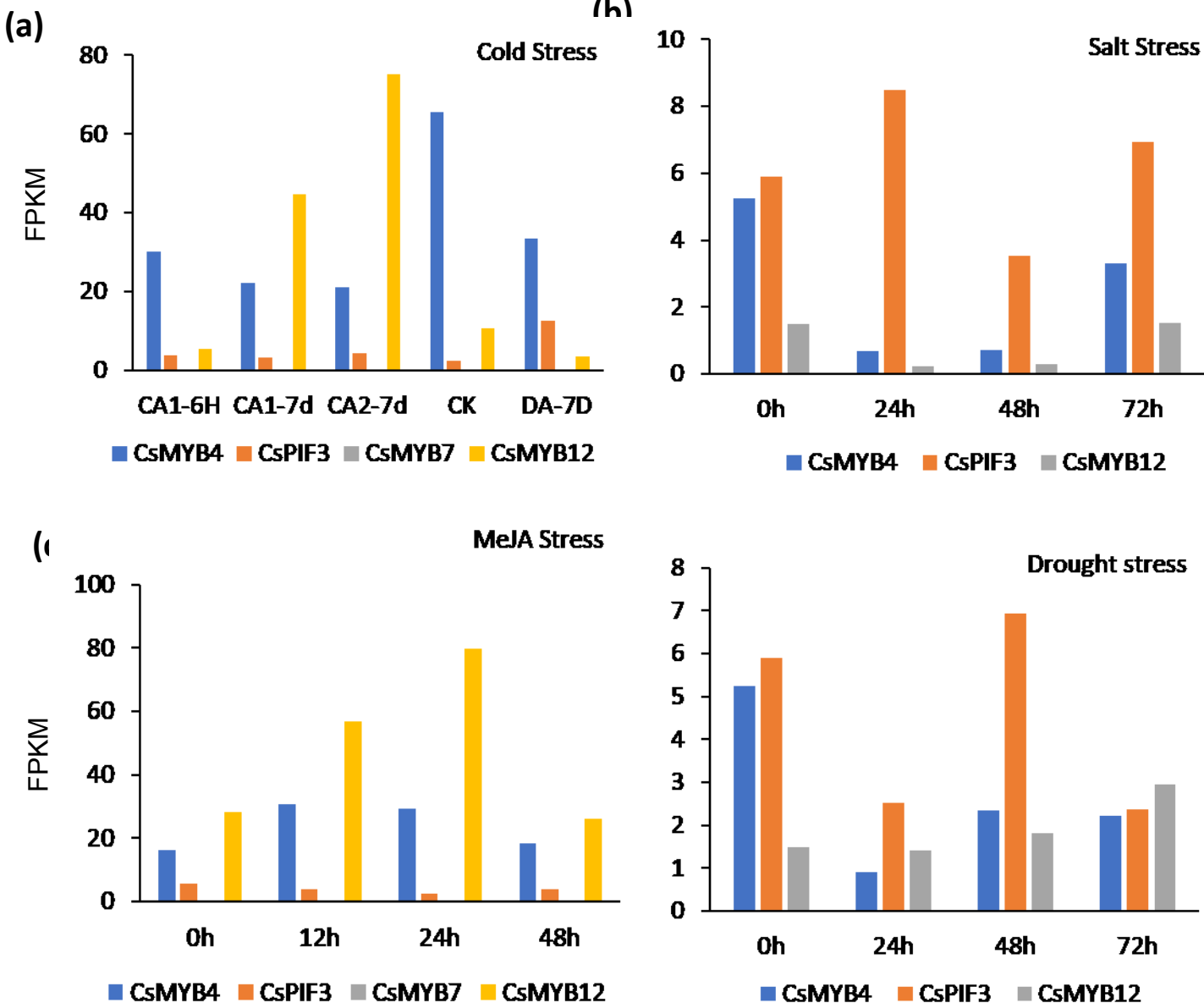


Fig S20. Expression of *CsMYB12*, *CSMYB4*, *CsMYB7* and *CsPIF3* in various abiotic stress

(a). Expression of *CsMYB12*, *CSMYB4*, *CsMYB7* and *CsPIF3* under cold stress.

(b). Expression of *CsMYB12*, *CsMYB4* and *CsPIF3* under Salt stress.

(c). Expression of *CsMYB12*, *CsMYB4*, *CsMYB7* and *CsPIF3* under MeJA stress.

(d). Expression of *CsMYB12*, *CsMYB4* and *CsPIF3* under drought stress.

Transcriptome data from experiments with tea cv. Shuchazao were retrieved from the tea plant information archive (<http://tpia.teaplant.org/index.html>).