Table 1 Suppl. Primers used in the quantitative PCR validation of the *CsMYB* genes.

GeneID	Forward primer sequence 5′ - 3′	Reverse primer sequence 5′ - 3′
CsMYB11	CTCAGTCCAAAAGAGGTATTCT	GTAGAATGTGTGATGCCAGATC
CsMYB17	TCACAAGTCAAAAAGGGCT	GCTGCTGAAAGGGAAAATA
CsMYB29	TTGAAAAGGAATGGAAAGA	GCAGGTCGAGAATTATGGT
CsMYB38	GATTCTGAGTCGGCTTGTGA	ATTGATGCCCATTTGTTTCC
CsMYB39	GAAGAAAAAGAACCGCCCA	CAGTCCCACAGCAACCATG
CsMYB40	CTCACCCTATCCTTACCCG	TCTTCACCACTGCGTTCC
CsMYB41	TAACCAGCTCTCTCCTCA	ACAGTCGTCACCTTCATC
CsMYB42	TGGTGGTCAAGTAATAAGGC	CAGGTCTCGCTATGGGTC
CsMYB43	GTAATAAGGCGATTGGAAAG	CGAATAGAGAGAGAGTGAGC

Table 2 Suppl. List of the *CsMYB* genes sequences in the tea plant transcriptome.

Gene name	Gene ID	Gene length [bp]	CsMYB protein sequence
CsMYB1	Unigene27465_All	1324	MVRVPCCDENSGLIKKGPWTPEEDQKLLDYVQLHGRGSWRALPKHAGLNRCGKSCRLRWT NYLRPDIKRGKYSDEEEQIIINLHSVLGNKWSKIAFHLPGRTDNEIKNHWNTHLRKKLLQRGI DPQTHKPISDLNLFANLAHLLYASNLTNASNLTNLMNPWDNNNAFRQHSGATTQLAKIQLL QIMMQVINTTTPLPSIAQTQTSLSGHYNKNNTTIPQQAPLEFPNLDVNVNSQQQFNDFADIDK AIAWFGDGFQPQVVGANCNNKNSDCHTQSSESALPSINQGESKIDPTYPSTQSPTSNNFEAW EKLLDDEGHSWEDIL
CsMYB2	CL6459.Contig3_All	1260	MGRSPCCDERGLKKGPWTPEEDHKLVKYIHKHGHGSWRALPKLAGLNRCGKSCRLRWTN YLRPDIKRGKFSQEEEQTILNLHSILGNKWSAIATHLPGRTDNEIKNFWNTHLKKKLIQMGFD PMTHRPRTDIFSSLPHLIALANLKELVEHHSWEEQAVRLQTEAVQMASLQYLQYLLQPQPSM STFSNNSNSTVTDMETYNLLNSLSLMKDSSIQFGTPTPSSLGTTTTLQSIEDSFPFSHMPDLQV PSSFQAPMDNKDIVQASDYTVLSHGEHSPTSPWLASTTSPSPPMAAAPTSIANMGDACSTSSY EGGHSSFWPEVLLEDPLFHEIA
CsMYB3	Unigene577_All	420	MGRTPCCDKVGLKKGPWTPEEDQKLLAYIEEHGHGSWRALPSKAGLQRCGKSCRLRWTNY LRPDIKRGKFSLQEEQTIIQLHALLGNRWSAIATHLPKRTDNEIKNYX
CsMYB4	Unigene16855_All	763	MGRAPCCEKMGLKKGPWTPQEDQILTSYIQQHGHGNWRALPKQAGLLRCGKSCRLRWTN YLRPDIKRGNFSKEEEETIINWHEMLGNRWSAIAARLPGRTDNEIKNVWHTYLKKRPKNYHT TSNNKEQSITVPKFDSNASIESKSMKFHIPTHPRNESPGYAPSSPQQSSSELSSVTDLAGLPNN MVIKNESETFSQVDESFWSKKLSAEKSNMKSDFSSNGDELQFLVSSIPAATTTNSTMEHGNN KCSFNIDDDMDFWYNLLIRTGGHLPELPEF
CsMYB5	Unigene9066_All	1485	MVRTPCFDNNGRKKGAWSPEEDNKLRAYIQRYGHWNWRELPKFAGLSRCGKSCRLRWMN YLRPNVKRGNYTKEEEDIIIKLHEALGNKWSAIAAKLPGRTDNEIKNHWHTHLKKRSKQNKS AKIKNQSTGTDSDRSESKADHRERSTEMLKCEANHEVESDDQPCPILESSALFQEPSSSEISSL SSDYAMLSGGVNRALEDSLSSLDSFAEPIENFWTQPFLADTYCDDENNFSSNFVEGGFVSPFD SYYDDDSMDFLSQVLQELPKS
CsMYB6	Unigene29812_All	1331	MGRGRAPCCDKSKVKKGPWSPAEDFRLLTFIHNHGHTNWRSLPKLAGLLRCGKSCRLRWIN YLRPDLKRGNFTKEEEETIIKLHQSLGNKWSKIASYLPGRTDNEIKNVWNTHLKKRLIKKDA DDDHKNSRGSCSSPSSSSSYSSSSSSSNLRPHTHYESHQVCNMEKEVLLLAKNQDISSITTSSS ASDCAGPKEAISTSSSSNCSHQVDKAAVVVYDEVNKQKMSLNSDDHQQEVIEIPMEESDIDF WDMLDNLESNESQPQEFEFEASHNSQDSNLFGEDLDDHDHDPNRGIGIEWLRYLENELGLE DDDQCNNIIAAKYNDEVGQSGSSTTSIADHHQVMLMRPEIDQFFGI
CsMYB7	Unigene11586_All	818	MGRGRAPCCDKSKVKTGPWSPAEDLRLISFIHKNGYSNWRSLPIQAGLSRCGKSCRLRWINY LRPDVKRGNFTNEEEETIIKLHQTLGNKWSKIASYLPGRTDNEIKNVWNTHLKKRLAKKDEK NHKNQTNDFSRTSSFSTSSTSSFMSSYGNNEGTEELVLDEGQEGLANKSYEPKEDIPTTDHDH ELKESSSSSNSSISCDASDYSNSSARVDVSMPEPEPEPEVEEVDEKDDPAPPKKEX
CsMYB8	Unigene9876_All	1050	MGRAPCCEKVGLKRGRWTAEEDEILTKYIQANGEGSWRSMPKNAGLLRCGKSCRLRWINY LRSDLKRGNISSEEEEIITKLHSTLGNRWSLIAGHLPGRTDNEIKNYWNSHLSRKIQSFRRPCK NEAPPPMAVDLAKSTVATKRRGGRTSRSAMKKNKTQNPTKGPNPKPVKKTEPNASVPMPQ TPTLQTESLSSAISWQEESVVKINLDLEGNKEGVIVGSPHHDDHAGLALCGGEERKRKSEYN EGLDESGMLCFDDIMSDELVDPKGVTILGEERENDTAVFINEERESDAAAVVISEERERGGG AMNMSSNGESSSTNSYIDDWDWVWDWDAVVQGNEIWGDEEENMKFSWLWESDNGKGDS IVNNKLGEINCEKQEAVVAWLLS
CsMYB9	Unigene16553_All	1314	MGRAPCCSKVGLHRGPWTAREDALLTKYIQLHGEGNWRSLPKKAGLLRCGKSCRLRWMN YLRPDIKRGNISPDEDDLIIKMHALLGNRWSLIAGRLPGRTDNEIKNYWNTHLSKRLLSQGTD PNTHKKISDPHLKETKKRRSNNKKQKNKTKSNVVVIEKLKVHNPKPTRIKSLSSFSMSRNGSF GWTISGGSSSSHEGDHRGSLLVGTEVVHVPWSDFKDDVNHENRVGFLVGDDHQDRDLVNG SDLECHSQLLPMSDHTLEKLYEEYLQLLKAEDDVQVQLDSFAESLLI
CsMYB10	CL7.Contig4_All	1266	MGRAPCCSKVGLHRGPWTAREDALLTKYIQLHGEGNWRSLPKKAGLLRCGKSCRLRWMN YLRPDIKRGNISPDEDDLIIKMHALLGNRWSLIAGRLPGRTDNEIKNYWNTHLSKRLLSQGTD PNTHKKISDPHLKETKKRRSNNKKQKNKTKSNVVVIEKLKVHNPKPTRIKSLSSFSMSRNGSF GWTISGGSSSSHEGDHRGSLLVGTEVVHVPWSDFKDDVNHENRVGFLVGDDHQDRDLVNG SDLECHSQLLPMSDHTLEKLYEEYLQLLKAEDDVQVQLDSFAESLLI
CsMYB11	CL814.Contig1_All	501	MGRSPCCEKAHTNKGAWTKEEDQRLINYIRSHGEGCWRSLPKSAGLLRCGKSCRLRWINYL RPDLKRGNFTEQEDELIIKLHSMLGNKWSLIAGRLPGRTDNEIKNYWNTHIKRKLIVRGLDPQ THRPLNATASTTTANSKFDFRNASHSYSTLTDIDLTMNQNTFK

CsMYB12	CL4818.Contig2_All	953	MGRSPCCEKAHTNKGAWTKEEDDRLISYIRSHGEGCWRSLPKAAGLLRCGKSCRLRWINYL RPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIRRKLMNRGIDPA THRLINEPAPAATDATTTISFATAKEEEKVITTSGGFNCPDLNLELRISPPYQHELEPVKIGSGT VCFSCSLGIQNSKGCSCSNGGSSSSNSTGSAYDFLGLKSGVLDYRSLEMK
CsMYB13	Unigene13182_All	708	MGRSPCCEKEHTNKGAWTKEEDERLINYIKAHGEGCWRSLPKAAGLHRCGKSCRLRWINY LRPDLKRGNFTQEEDELIIHLHGLIGNKWSLIAARMPGRTDNEIKNYWNTHIKRKLLIRGIDP QTHRPLNHTPTTTTTTNYIINTTTITATATATATKSPHQPSLNSMPLTIPLLDNQNGSIDDASSS SSSSMINEQQQEVVHKELDLELSISLPNPPHHHHHHHH
CsMYB14	CL3408.Contig3_All	1160	MGRSPCCEKEHTNKGAWTKEEDERLINYIKAHGEGCWRSLPKAAGLHRCGKSCRLRWINY LRPDLKRGNFTQEEDELIIHLHGLIGNKWSLIAARMPGRTDNEIKNYWHSYLKKKKMAKIEQ TKPHTEPEYTNSNTGNTQSSLSSLKSTTRNLSFESFDNMEGTSMETNESISQLPKLLFAEWLSL DQFQGQDLTNSGRPAVSKDDPNYQYSFLNCLLMNEGAFGGKFHQELSNGSGTADEMSNPQ FKSEEGDQFVNFITEDDMCIHFNMDSDVFM
CsMYB15	CL8029.Contig1_All	1079	MGRSPCCEKEHTNKGAWTKEEDERLINYIKAHGEGCWRSLPKAAGLHRCGKSCRLRWINY LRPDLKRGNFTQEEDELIIHLHGLIGNKWSLIAARMPGRTDNEIKNYWNTHIKRKLIVRGLDP QTHRPLNATASTTTANSKFDFRNASHSYSTLTDIDLTMNQNTFKLVAMADDSSFDDGKCNS GTTEEAPPQLLQPPPLLAHHADQNCQSINLDLSIGLVPFQSLTRSESANSNSAEIELKKEQEEV VPYQFVVAARPSETPAPQAVCVCWQLGFQRGQLCSNCSTNGLYR
CsMYB16	CL5580.Contig3_All	630	MGCDKSTEKPKPKQKQKQKHKKGLWSPDEDQRLRNHILEHGHGCWSSVPINAGLQRNGKS CRLRWINYLRPGLKRGMFTASEEQTILTLHAMLGNKWSQIAQHLYGRTDNEIKNYWHSYLK KKVAKMEQTEPQNNTKLMSPNTESSLSSHKSTPRNPSFESFEHMEGSSTNTNQSIPQIFNFPRE PACFQNNLPKLLFAEWLS
CsMYB17	CL8027.Contig1_All	1708	MGRHSCCFKQKLRKGLWSPEEDEKLINHITKYGHGCWSSVPKLAGLQRCGKSCRLRWINYL RPDLKRGTFSQQEENLIIELHAVLGNRWSQIAAQLPGRTDNEIKNLWNSSIKKKLKQKGIDPN THKPLSNAESEEKASGGSKSNELTNVEAENSDKGMAIHKSKRASVATENYFENNCNNNMTT PPSTTHEFFLDRFVSSHESSTAACKTSDFPAYFPFQQLNYGSDARLSVNTNTPNNLFLNPNTTT LFSSMSSPTIKPSISLPSSTPSMGSFDINGVHNWNTASFSNNGSSSSNGSTNSSSFFDNNGTFSW GPENCIKSEKEGEIHAIEGDPEEIKWSEYLQTPYLFGTTIQNQSAHQDIYSTETKTESHFNAQG SSTNWQQQSSQSADLYNKNFQRIAAAYGQFS
CsMYB18	Unigene3965_All	1048	MGRQPCCDKVGLKRGPWTIEEDHKLMNFILNNGIHCWRMVPKLAGLLRCGKSCRLRWINY LRPDLKRGEFSEAEENQIIQLHARLGNRWSKIASHFPGRTDNEIKNHWNTRIKKRLKMLGLD PVTHKPMEQNEKVDEEKTETITTDFDSSKEEEERLGVTVTMSEKHTKNHAEFVETREKQND KVDMAFDETTNDLLRSYELMLCRSLDDGGLLNTTTTTSTTSNSNYNPSFSLEDSLNPSCMGE SSSSIQEDSIQRWVDSVNSMLSWDSFNQLDEGLFFSENVQ
CsMYB19	CL1235.Contig2_All	1351	MGRQPCCDKVGLKKGPWTAEEDKKLINFILSNGQCCWRAVPKLSGLLRCGKSCRLRWTNY LRPDLKRGLLSDYEEKMVIDLHAQLGNRWSKIASHLPGRTDNEIKNHWNTHIKKKLRKMGI DPLTHKPLPTPPTDHDQPQQEQPQEDQQPPLPSLTCKISEVAVGQNSEIETSFESSITEEAKHKE KEEDINIEGPFDSLMDVNNGFCTDDIPLIEPHEINLLPPCTTAPSISSTTTTSSSSTSSSSASSSSSS YSSSNNNILEDLDLLPNFDSWQSDLSNSLVFWDDDVFISTFDLWINGGDIVTGI
CsMYB20	Unigene20256_All	1130	MGRQPCCDKLGVKKGPWTAEEDKKLINFILTNGQCCWRAVPKLAGLRRCGKSCRLRWTNY LRPDLKRGLLTESEEQLVIDLHARLGNRWSKIASRLPGRTDNEIKNHWNTHIKKKLLKMGID PVTHEPLANKESNPTEPSSNSELSRETNSNNQEQFQETSKVIIPSLEKKYSSDPSTENCYDDPLL GCLWGDESWEFPASGHSFSDISLPSLDESCAWLLDCQDFGVHDFGVDCFNDVNVMNTLNT
CsMYB21	Unigene7582_All	1488	MGRQPCCDKLGVKKGPWTAEEDKKLINFILTNGQCCWRAVPKLAGLRRCGKSCRLRWTNY LRPDLKRGLLNEAEEQLVIDLHARLGNRWSKIAARLPGRTDNEIKNHWNTHIKKKLLKMGI DPVTHEPLNEESKPTEASSTSSSSRADHSSESKNNHLQSQKTDNGIPNSEENSSCSPLTENCSG DDPLMSSFLWGNESIPLVDGSWEFPSDGLSFNDNNIGLPSWDEDCAWLLDCQDFGIHDFGID CFSDVEVIKTLNTLEMGNKQ
CsMYB22	Unigene15512_All	516	MVRPPCCDKLDVRRGHWTEEEDAKILAYVSKHGTGNWTDVPKKAGLRRCGKSCRLRWTN YLRPDLRQETFTPQEEELIIRLHAAIGSRWSIIAQQLAGRTDNDVKNYWNTKLRKKLSEMGID PVTHKPFSQILADYGNIDGLPKFGNRIGSLNRX
CsMYB23	CL1739.Contig1_All	1247	MGRAPCCDKSNVKRGPWSPEEDAKLKAYIDKLGTGGNWIALPQKIGLKRCGKSCRLRWLN YLRPNIKHGGFSEEEDNIICSLYISIGSRWSIIAAQLPGRTDNDIKNYWNTRLKKKFLGRRKQS NINRLSTSSQDPKDTNGQEDKSVLSNSALERIHLYMQLQSLQNPLSFYNNPELWPKLHTLQE KIIQSLQFLNENTTNPLMQHIDVPPPSSQPGQGQKVDFYEPPTVALNGSNVLESRLDGMEQFN AKIQPISTFQAELDALHLLNNETTGFPPQEDPISEFDCFKEMDGLKESVIWWSNDFNSKSASS NTRDATSVLQYQNYVSSYNLQ
CsMYB24	Unigene7763_All	1425	MGRAPCCDKANVKKGPWSPEEDAKLKSYIEQHGTGGNWIALPQKIGLKRCGKSCRLRWLN YLRPNIKHGGFSEEEDNLICSLYISIGSRWSIIAAQLPGRTDNDIKNYWNTRLKKKLLGKQRK EQQARRGNSCQKQRMRKGNENSSMVSSHNTNNQAPYWPELPAPMAIPYSNQEPRFNDHVSI RKVLIKLGGKFSDDHQYQHPIQDTATNHHHHHHQFLPVNLSYSHQAYAPSIEMVYSSSTDPL NTDTYQLANTQYGIDGTGMTMLPGQSGFQAEFEEMLYNNNNPQRLDGLEFFYGDMVVSNG TETTSGESMDWGEMSSMSYPPMISNYEGLLQQGTMLQESTFDELKSTTTV

CsMYB25	CL1485.Contig1_All	602	MGRAPCCDKSNVKRGPWSPEEDAKLKAYIDKLGTGGNWIALPQKAGLKRCGKSCRLRWLN YLRPNIKHGEFSEEEDRIICTLFASIGSRWSIIAAQLPGRTDNDIKNYWNTKLKKKLMGLLLPS NHHHHRKPPPYPPPPPPPPLQPPHSQLPSLSPPPPPLPLYNYNPIITGLHDQPNLMNNNNNNNN PPX
CsMYB26	Unigene11344_All	1194	MGRAPCCDKASVKRGPWSPEEDAKLKEYIEKNGTGGNWITLPQKAGLRRCGKSCRLRWLN YLRPNIKHGEFSDVEDRIICSLFASIGSRWSIIAAQLPGRTDNDIKNYWNTKLKKKLMKIGIGI VPSSPNQRRPHHHQPTTYPFISLLHHNSSSSPSPSPSSPLSSSSSYKYHNTQTSSFMGYDFEPFSI PSSSTNSTVLQTQEGYVSPNLLFGGEAASCSSSDGSFNSNNQISHGREMESDYGGHMGLQSY YHLYNGVGENLKYMVSSGVGGGNANNGLFYGGESETPIDYSSVEEIKQLINTNTNIYNNMN FYVDDNQREEKLMYY
CsMYB27	Unigene12921_All	1258	MGRAPCCDKASVKRGPWSPEEDAKLKEYIEKNGTGGNWITLPQKAGLRRCGKSCRLRWLN YLRPNIKHGEFSDVEDRIICSLFASIGSRWSIIAAQLPGRTDNDIKNYWNTKLKKKLVGMLSSS HTSSLASKCSNNNNNAYYTSTNQTNSFIGYELPNISTPSSNLLSTTTACSSAQEGYVGPMHTV LMFGGGGDQASCSNSSDGSYNNQISHGREMEHDYYGEHMGFHLQSYAYNGVDHENQNLM SSSSGGGDGNGFSVKPNGLLCGETPLIDYYSSLEEIKQLITTNNICSNNNNLNFFADENKTDEK VLYY
CsMYB28	Unigene26241_All	469	MEVEGRECNSAIQSEEEMMELRRGPWTVEEDMTLMNFIAKHGEGRWNSLARCAGLKRTGK SCRLRWLNYLRPDVRRGNITPEEQLLILELHCRWGNRWSKIAQHLPGRTDNEIKNYWRTRV QKHAKQLQCDVNSKQX
CsMYB29	CL1884.Contig2_All	868	MSWGAMAKYLGWDVIEQEWRKGPWTAEEDRLLIEYVKLHGEGRWNTVASLAGLKRNGK SCRFRWVNYLRPDLKRGQITPHEETIILDLHARWGNRWSMIARTLPGRTDNEIKNYWRTHFK KKSKASPNNNEKAKARLLRKQQFQQQQRQHINQVDMKKMVSYLLDENENGVPSLAHQVG QEMATTMNPNTAEEQGLLYSMFIGYAYVPEPPKEDNISWEGLWNLDDNAHGNLGMACAPN KACLQSLSTPFY
CsMYB30	CL2334.Contig1_All	2497	MSHMTNESDDEMLSQDHTGSPLIDEGNCGGSMNGGVVLKKGPWTSAEDAILVDYVRKHGE GNWNAVQKHSGLFRCGKSCRLRWANHLRPNLKKGAFTPDEEKTIIELHAKMGNKWARMA AHLPGRTDNEIKNYWNTRIKRRQRAGLPLYPPEVCLQAFQENQQNQNASGDKGQHDLMQT DICEIPDVIFDSLKANHGVLPYVPELPDISTSSMLMKGLGSSQCYGSVPPMVHRQKRLRESPT SFSGHDGIVRNEPSPFDQTPDDNCDNMTSQFFGLSFPYDPDPITKNLLSFSGNQSSHFLINGNF SASKPTNGAVKLELPSLQYPETDFSSWGSSSPPALLESVDAFIQSPPSGTLQSDCLSPRNSGLL DALLHEAKTLSTKNQLSDKSSNSSTITPGDKANSSALDICETKWEEYGDSISPLGNSAASIFNE CTPVSVSGSSLDEITPENFPGSNVKSEADDQTWTMDGETKETATQLDFSRPDALLGSCWLGQ SVACAKDQGIGTDARAVALGDDLGNDYKHMAAGTALSPGWGFVSCSWNNMPAVCQMSE LP
CsMYB31	CL4933.Contig2_All	2345	MSHMTNESDDEMLSQDHTGSPLIDEGNCGGSMNGGVVLKKGPWTSAEDAILVDYVRKHGE GNWNAVQKHSGLFRCGKSCRLRWANHLRPNLKKGAFTPDEEKTIIELHAKMGNKWARMA AHLPGRTDNEIKNYWNTRIKRRQRAGLPLYPPEVCLQAFQENQQNQNASGDKGQHDLMQT DICEIPDVIFDSLKANHGVLPYVPELPDISTSSMLMKGLGSSQCYGSVPPMVHRQKRLRESPT SFSGHDGIVRNEPSPFDQTPDDNCDNMTSQFFGLSFPYDPDPITKNLLSFSGNQSSHFLINGNF SASKPTNGAVKLELPSLQYPETDFSSWGSSSPPALLESVDAFIQSPPSGTLQSDCLSPRNSGLL DALLHEAKTLSTKNQLSDKSSNSSTITPGDKANSSALDICETKWEEYGDSISPLGNSAASIFNE CTPVSVSGSSLDEITPENFPGSNVKSEADDQTWTMDGETKETATQLDFSRPDALLGSCWLGQ SVACAKDQGIGTDARAVALGDDLGNDYKHMAAGTALSPGWGFVSCSWNNMPAVCQMSE LP
CsMYB32	CL5361.Contig1_All	999	MGRRNRDGKEVSVMGVEEIRKGPWKEEEDEVLIKHVNKYGPRDWSSIRSKGLLNRTGKSCR LRWVNKLRPNLKNGVKFSAEEERTVLELQAQFGNKWAKIATYLPGRTDNDVKNFWSSRKK RLARILQSTSPPRQTKSHKSKDNALAVHEMPTLQAPEFTSPQMKEESYSKFQPCSSSSMEDPK MIHKMPQPNFMNPNMANIDSSQPSLNTTETDTKPSNEILLQLSFTHLPNSKLDLPILAESHAEP NFLDVFTSHQQQAFELGDVSQ
CsMYB33	CL6100.Contig2_All	1389	MGRRNRDGKEVSVMGVEEIRKGPWKEEEDEVLIKHVNKYGPRDWSSIRSKGLLNRTGKSCR LRWVNKLRPNLKNGVKFSAEEERTVLELQAQFGNKWAKIATYLPGRTDNDVKNFWSSRQK RLARLLQTPPPLSKSENSRRKVAVLHVVPTNTEAPKFSYSSMEEESSSKSRSCCSSLIDNSHTI NMVPLPDLLNPNLLNCEQNLLQLKFNLVDQKNRINESQPQVPFPIIPELQPDDPLGLGSRELM DPTFLDVFGNVDASDIGDMAQLPLVLPCGGRGENENPATPDSFFNDFPADIFDHMEPLPSPSE W
CsMYB34	CL2581.Contig1_All	1272	MERHRDEQVIKKGPWIAEEDEVLMNFVNKYGPKDWSTIRSMGLLPRTGKSCRLRWVNKLR PNLKIGCKFSAEEERVVIDLQARFGNKWATIASYLPGRTDNDVKNFWSTRQKRLARILHSPSS PLTSTLEKIKGKSHALVHEMPTPKAPEFNTPQMKEEASSSSKCQSCLSSSMGNSEILRIMSLPN FMMTPNSINLDSTTMPLLDTIETDHHNKSSTQTPLQHSFTHLPFLPESHDSVLGLSESNFLDVS ASTRQAVELENVSQINFGSPFLELDGTGRNDGRADSFFDELPADMFDYL
CsMYB35	Unigene4344_All	557	MHGGQNVGFLNYPSRILLEALNQGQTFQPKNYQAFGSTNVNLSDEVSCLTKEGGNRKKVES KRRRMHQKRTKKVHQTPIIVKGQWATEEDRLLVQLVKEYGEKKWSHIAQMLNGRMGKQC RERWHNHLRPDIKKDLWSEEEEMKLIEVHRQIGNKWATIAREMPGRTENTIKNHWNATKR

CsMYB36	CL5057.Contig1_All	1311	MDESTGGGGSSDDARTCPRGHWRPAEDEKLRQLVEQYGPQNWNSIADKLQGRSGKSCRLR WFNQLDPRINRRPFTEEEEDRLLAAHRIHGNKWALISRLFPGRTDNAVKNHWHVIMARKQR EQSKLCGKRIYQDTIESSSNASPSFGFRRRNSRTQEDYSLKCHFEGIKFFEFQTLNKDRIFPVSP SSSSPSWNFTRPTASATNNSSSVDLFGREGTDYINSSTYYCTTDSSNSSDQPLYRYGCRDFSPF GLPNYKRVVPSPFGYSKLGDGNRAHGVIKRDLVSFGDNLHPFAKIRRAIDEEENQNESVKQK DNIPAFIDFLGVGIS
CsMYB37	Unigene16536_All	1275	MENCAANTTTTSCESERGDHHHHHGSEEMKPNETDTSMEEEMDSKVCGRGHWRPAEDSKL RELVALYGPQNWNHIAENLEGRSGKSCRLRWFNQLDPKINRRAFSEEEEERLMAAHRVYGN RWAMIARLFPGRTDNAVKNHWHVLMARKFRDQSTAHRRRKLSQTESTTRQNSFRFCNGNFI INNHPPTQTQFQFGASSLGLGGLNNGVHNMITSGERDLLVDHASESCGGFADQTPFDFFTGV KRNGMTSFVRERRFWDMKRDDSTILTGLYPCHCHHHHPSQLMAMQHSPSCCNHMLISCVSE NMVSTTSDQVSVTEPSSTPSLIAADNTATSHFHEGETTATVSPSPPPFIDFLGVGTT
CsMYB38	Unigene5318_All	1551	MDDVTVVAGETTAADDGDTGGGVDVDAAAAVVGEGSGSGSSGGGQVGKKSSSWDRVKG PWSPEEDAILSRLVSDFGARNWSLIARGISGRSGKSCRLRWCNQLDPAVKRKPFTDEEDRIIV QAHTIHGNKWASIARLLQGRTDNAIKNHWNSTLRRRCMARGKFKLESSNMVEDISLDKSKA SSEDTLSCGDVNSFKSFEGKDISSGENMEEPWEDKAQPQGQSSIEEKEPPTLFHPVARVSAFN VYNPLDGQETVSSFPRLPIPMQRPLLQAVRPNAGMYKLLEGAYGERLIPHQCGHGCCGTESG GKSRSSLLGPEYVDFAEPPFIPTHELAAIATDISNIAWQKSGLDNSSVRAVENLNVRVTSGGPL VQMDHFEESRKNGHLRFEEGKNKLIGMMNDVLSTPTSRQPFSVSAKVGGRS
CsMYB39	CL978.Contig1_All	1687	MDDVTVVAGETTAADDGDTGGGVDVDAAATVVGEGSGSGSSGGGQVGKKSSSWDRVKG PWSPEEDAILSRLVSDFGARNWSLIARGISGRSGKSCRLRWCNQLDPAVKRKPFTDEEDRIIV QAHTIHGNKWASIARLLQGRTDNAIKNHWNSTLRRRCMARGKFKLESSNMVEDISLDKSKA SSEDTLSCGDVNSFKSFEGKDISSGENMEEPWEDKAQPQGQSSIEEKEPPTLFHPVARVSAFN VYNPLDGQETVSSFPRLPIPMQRPLLQAVRPNAGMYKLLEGAYGERLIPHQCGHGCCGTESG GKSRSSLLGPEYVDFAEPPFIPTHELAAIATDISNIAWQKSGLDNSSVRAVENLNVRVTSGGPL VQMDHFEESRKNGHLRFEEGKNKLIGMMNDVLSTPTSRQPFSVSAKVGGRS
CsMYB40	Unigene11395_All	1398	MASLSRKDVDRIKGPWSPEEDELLQTLVQRHGPRNWSLISKSIPGRSGKSCRLRWCNQLSPQ VEHRAFTAEEDETIMKAHAKFGNKWATIARLLSGRTDNAIKNHWNSTLKRKCSSMSDDFNF PDGSHSHQPLKRSASVGPGTNVSGLYLNPSSPSGSDLSDSSFSGFPSAQVFRPVPLTGGVPPPV HQIETASTTVSDPPTSLTLSLPGSDSSDPSNQIATPPAPPQGGQNVDFGAAIGEKQFFSQEFLA VMQEMIKEEVRSYMSGIEQNGRCLQAEAIRNAVVKRIGISKIE
CsMYB41	CL6421.Contig1_All	3242	MASTKKDVDRIKGPWSPEEDDMLQKLVQKHGARNWSLISKSIPGRSGKSCRLRWCNQLSPQ VEHRAFTPEEDETIMRAHARFGNKWATIARLLSGRTDNAIKNHWNSTLKRKCSSMSTDEGD DCSNHQPLKRSVSAGSAVPVSGLYLNPSSPSGSDVSDSSLPVMSSSHVYRPVARTGGVLPPQ VETTSLKNDPTTSLSLSLPGVDSSDSSNRVNEATQLRPPPPAAALVSMNIEFASPSMAAAPAIV VPVQPVNQRNSEFGGVSSPAPETAFPQFSAELLGVMQEMIRKEVWNYMAGIEQIPTQQQGG YCMPQATADGFMNAVVKRIGISKIE
CsMYB42	Unigene8921_All	1384	MENRSWVMEATQKDVDRIKGPWSTEEDESLQKLVQRHGARNWSLISRFIPGRSGKSCRLRW CNQLSPEVEHRAFSPEEDDLILRAHARFGNKWATISRLLNGRTDNAVKNHWNSTLKRKFPA AMLEGDAGGGGDERGGGQVIRRLESGDVTVGINSESPSASASDASDSSLQVISQMNVNSNLF RPIARPVESTPISEMVIPPPPTALTLSLFGDSHPYEIHDKNYSPSPSAVTQPSHSRSQSTESGPST AAAVEKPMFSTEFLNVMQEMIKKEVRSYLSRGLDQSGMEGSVRNAGVKRIGISRID
CsMYB43	Unigene20100_All	1416	MENRSWVMEATQKDVDRIKGPWSTEEDESLQKLVQRHGARNWSLISRFIPGRSGKSCRLRW CNQLSPEVEHRAFSPEEDDLILRAHARFGNKWATISRLLNGRTDNAVKNHWNSTLKRKFPA AMLEGDAGGGGDERGGGQVIRRLESGDVTVGINSESPSASASDASDSSVQVISQMNVNSNLF RPIARPVESTPISEMVIPPPPTALTLSLFGDSHPYEIHDKNYSPSPSAVTQPSHSRSQSTESGPST AAAVEKPMFSTEFLNVMQEMIKKEVRSYLSRGLDQSGMEGSVRNAGVKRIGISRID