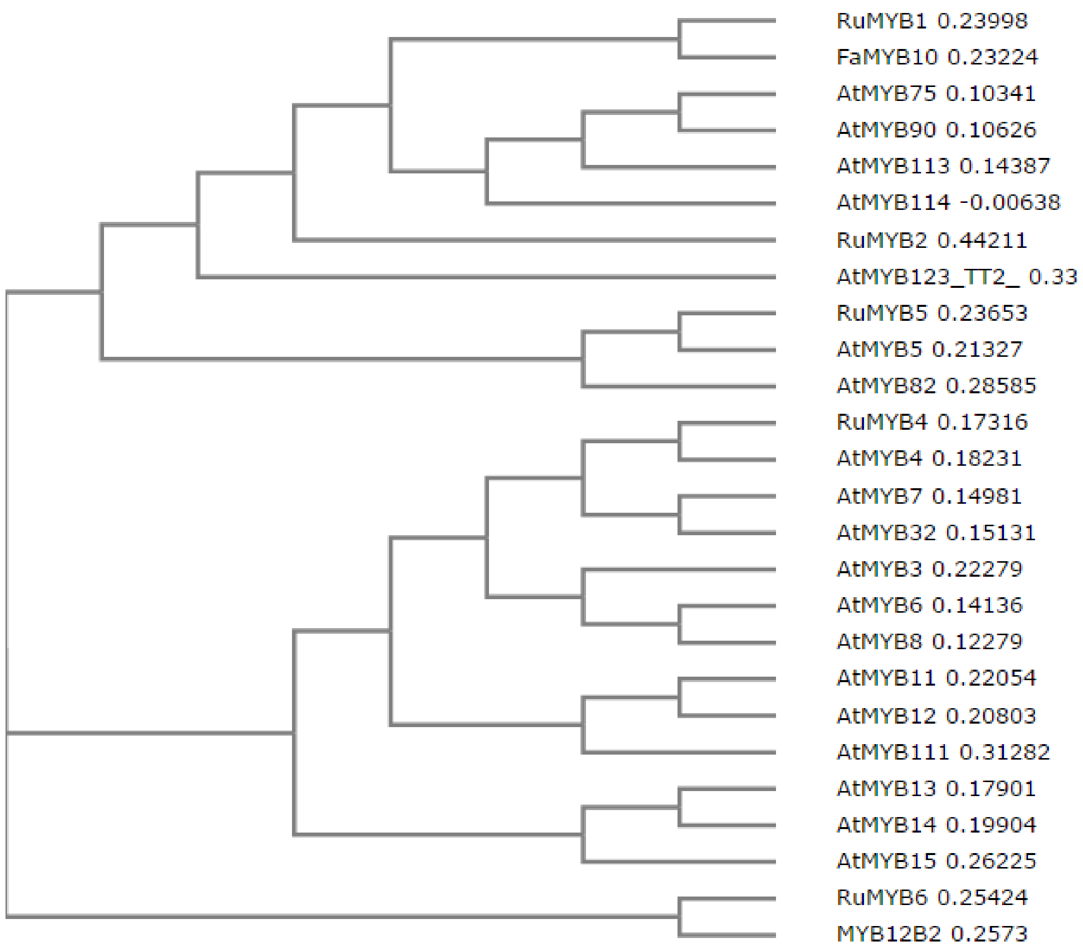
Supplemental material 3.

Phylogenetic relationship of RuMYB transcription factors with others MYB that plays a role in the regulation of flavonoid and phenylpropanoid metabolism in *Arabidopsis* and *Fragaria*. An unrooted phylogenetic tree was calculated using the CLUSTALW software using the implemented neighbor-joining method without the function for evolutionary distance correction. Evolutionary distances are proportional to the branch length. Twenty six protein sequences were selected as indicated in the figure**.**



>RuMYB1

MEVRKGAWTKEEDHLLRNYIEKHGEGRWHKVPLEAGLNRCRKSCRMRWLNYLKPNIKRGDFAEDEVDLMIRLRKLLGNRWSLIAGRLPGRTSNDVKNYWSARRRRKIDFGVPKDNEPPKITKTTIIRPRPRTFTKSLHHLSAEAATSMHSSEQNNSWPSSSPPIENGIDEWKTLMLEDVFTNFWVEDVASLTGTGVNSAEQGFETDLWHFLQEEAR

>FaMYB10

MEGFGVRKGAWTKEEDELLKQFIEIHGEGKWHHVPLKSGLNRCRKSCRLRWLNYLKPNI
KRGEFAEDEVDLIIRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTYQRKKDQKTASYAKK
LKVKPRENTIAYTIVRPRPRTFIKRFNFTERYANIEHNHSEVSYTSSLPTEPPQTLQLENVT
DWWKDFSEDSTESIDRTMCSGLGLEDHDFFTNFWVEDMLLSASNDLVNISYV

>RuMYB2

MGRGPRCSKDGLNKGAWMATEDKLLLDYIKNHGEGKWSNVAKETGSHFLLNLINYFVNL
FLLVFFWKKGLIHYEHGVGLVHKLACWFFIFTTSRSIIVRWNMYVGLKRCGKSCRLRWMN
YLRPDIRRGSISDDEEELIVRLHKLLGNRYSHRSLINLPFFVNCNLSHVNLINLQMVSDSRE
TSWANRQNQELLELQFSENGTSSKFIPVMQCHCQNHSQYRHSTAAHSYSSWYCANCGS
SPKRRLLCGHKFRRLGQSCFSFTNVQTRLPMPINNYYWGWGSFRKFAHEFHDGFQHSG
FLQDTGLLCKLEQCHGPWRSWCSQRSHFSTTADDHGQECSSCFWVLGFISGVGLAWES
KCHAELISFLSVLSPIFIYIHVLQCLLLVLKKKKKVLVDAWP

>AtMYB123(TT2)

MGKRATTSVRREELNRGAWTDHEDKILRDYITTHGEGKWSTLPNQAGLKRCGKSCRLR
WKNYLRPGIKRGNISSDEEELIIRLHNLLGNRWSLIAGRLPGRTDNEIKNHWNSNLRKRLP
KTQTKQPKRIKHSTNNENNVCVIRTKAIRCSKTLLFSDLSLQKKSSTSPLPLKEQEMDQGG
SSLMGDLEFDFDRIHSEFHFPDLMDFDGLDCGNVTSLVSSNEILGELVPAQGNLDLNRPF
TSCHHRGDDEDWLRDFTC

>RuMYB4

MGRSPCCEKAHTNKGAWTKEEDDRLIAYIRAHGEGCWRSLPKAAGLLRCGKSCRLRWI
NYLRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIRRKLLTRG
IDPATHRPLNETAQDSATTTTISFAASSAIKEEDQKISTSIGIVGKESINPVQEKCPDLNLEL
RISPPSQTKPVESFKSGGRGVCFSCSLGLKDSKSCCSCGMDNIGPTSAGTSNIAYDFLGL
KNGVLDYRSLEMK

>AtMYB4

MGRSPCCEKAHTNKGAWTKEEDERLVAYIKAHGEGCWRSLPKAAGLLRCGKSCRLRWI
NYLRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIRRKLINRG
IDPTSHRPIQESSASQDSKPTQLEPVTSNTINISFTSAPKVETFHESISFPGKSEKISMLTFK
EEKDECPVQEKFPDLNLELRISLPDDVDRLQGHGKSTTPRCFKCSLGMINGMECRCGRM
RCDVVGGSSKGSDMSNGFDFLGLAKKETTSLLGFRSLEMK

>RuMYB5

MRNPSSSASASKGKSSAAAAAASASAPAVVSSSSSKTPCCVKVGLKRGPWTPEEDELLA
NYIKKEGEGRWRTLPKRAGLLRCGKSCRLRWMNYLRPSVKRGQIAPDEEDLILRLHRLLG
NRURPSUQHTYTYIHIYDSIPFGDSGUGLRLQCFYWIDDHDDDESVFIYRWSLIAGRIPGR
TDNEIKNYWNTHLSKKLISQGIDPRTHKPLNPDSSSGDHAAVNGASSSKTNQHRGMSSN
PNPKSPITSSSPVSTEEAAAPNARENGYLDQGNANDDLGVIVHGAGGYGNGMTSNDSD

GSAPAMGALRSNLLLGNEDDEDINCCTDDVFSSFLNSLINEDPFAAAAAAAGQHQLQPLQ
LVQQPNGIAPSSDLSAPAFGGWESAVIMSSAFIQKDPHRVNVDQTQ

>AtMYB5

MMSCGGKKPVSKKTTPCCTKMGMKRGPWTVEEDEILVSFIKKEGEGRWRSLPKRAGLL
RCGKSCRLRWMNYLRPSVKRGGITSDEEDLILRLHRLLGNRWSLIAGRIPGRTDNEIKNY
WNTHLRKKLLRQGIDPQTHKPLDANNIHKPEEEVSGGQKYPLEPISSSHTDDTTVNGGDG
DSKNSINVFGGEHGYEDFGFCYDDKFSSFLNSLINDVGDPFGNIIPISQPLQMDDCKDGIV
GASSSSLGHD

>RuMYB6

MDVKPGRVSNTIRSSHEEEEDDVMMDLRRGPWTVEEDLALMNYIANHGEGRWNSLARC
AGLKRTGKSCRLRWLNYLRPDVRRGNITLEEQLLILELHSRWGNRWSKIAQHLPGRTDN
EIKNYWRTRVQKHAKQLKCDVNSKQFKDTMRYLWMPRLVERIQAAASSATASTAASSSIT
TTITTAPNPSYHFNNNFQSTGAGHVALQQATLIGSNNDLAASYTTPENSSTGASSDSFGN
QVSPVSELTDYYTTMSVNNNNPSPMEYFQAPNPHHQIGYRDSMTSPSGYVFNQGGLNS
HSFQAASAPEQNNNGQWGMDGGDFSDNLWNVEESDMWFLQQQLGNI

>MYB12B2

MERSLSGSSEEEMSITKGPWTEEEDSVLFNYITVHGEGHWNSVARYTGLKRTGKSCRLR
WLNYLRPNVRRGNITLEEQLLILDLHSRWGNRWSKIAEHLPGRTDNEIKNYWRTRVVKQA
EQLKCEVNSKQFRDTLRFVWMPRMLERIQAQASSSSSSSSGQAHQTTLISNAQAHSDPC
GVMTTNPSLLSEVSSSALDAHAPSLYDSSASYNLMGGGSSSSYSAEYCYYSDIAGNGFG
GSDLWTDENICFLQQLLADHDLS

>AtMYB3

MGRSPCCEKAHMNKGAWTKEEDQLLVDYIRKHGEGCWRSLPRAAGLQRCGKSCRLRW
MNYLRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIKRKLLS
RGIDPNSHRLINESVVSPSSLQNDVVETIHLDFSGPVKPEPVREEIGMVNNCESSGTTSEK
DYGNEEDWVLNLELSVGPSYRYESTRKVSVVDSAESTRRWGSELFGAHESDAVCLCCRI
GLFRNESCRNCRVSDVRTH

>AtMYB6

MGRSPCCEKAHTNKGAWTKEEDQRLVDYIRNHGEGCWRSLPKSAGLLRCGKSCRLRWI
NYLRPDLKRGNFTDDEDQIIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIKRKLLSHG
IDPQTHRQINESKTVSSQVVVPIQNDAVEYSFSNLAVKPKTENSSDNGASTSGTTTDEDL
RQNGECYYSDNSGHIKLNLDLTLGFGSWSGRIVGVGSSADSKPWCDPVMEARLSLL

>AtMYB7

MGRSPCCEKEHMNKGAWTKEEDERLVSYIKSHGEGCWRSLPRAAGLLRCGKSCRLRWI
NYLRPDLKRGNFTHDEDELIIKLHSLLGNKWSLIAARLPGRTDNEIKNYWNTHIKRKLLSKG
IDPATHRGINEAKISDLKKTKDQIVKDVSFVTKFEETDKSGDQKQNKYIRNGLVCKEERVV

VEEKIGPDLNLELRISPPWQNQREISTCTASRFYMENDMECSSETVKCQTENSSSISYSSIDISSSNVGYDFLGLKTRILDFRSLEMK

>AtMYB8

MGRSPCCEKAHMNKGAWTKEEDQRLIDYIRNHGEGSWRSLPKSVGLLRCGKSCRLRWINYLRPDLKRGNFTDGEEQIIVKLHSLFGNKWSLIAGKLPGRTDNEIKNYWNTHIKRKLLNRGIDPKTHGSIIEPKTTSFHPRNEDLKSTFPGSVKLKMETSCENCASTSGTTTDEDLRLSVDCDYRYDHLDKELNLDLTLGYSPTRFVGVGSCY

>AtMYB11

MGRAPCCEKVGIKKGRWTAEEDRTLSDYIQSNGEGSWRSLPKNAGLKRCGKSCRLRWINYLRSDIKRGNITPEEEDVIVKLHSTLGTRWSTIASNLPGRTDNEIKNYWNSHLSRKLHGYFRKPTVANTVENAPPPPKRRPGRTSRSAMKPKFILNPKNHKTPNSFKANKSDIVLPTTTIENGEGDKEDALMVLSSSSLSGAEEPGLGPCGYGDDGDCNPSINGDDGALCLNDDIFDSCFLLDDSHAVHVSSCESNNVKNSEPYGGMSVGHKNIETMADDFVDWDFVWREGQTLWDEKEDLDSVLSRLLDGEEMESEIRQRDSNDFGEPLDIDEENKMAAWLLS

>AtMYB12

MGRAPCCEKVGIKRGRWTAEEDQILSNYIQSNGEGSWRSLPKNAGLKRCGKSCRLRWINYLRSDLKRGNITPEEEELVVKLHSTLGNRWSLIAGHLPGRTDNEIKNYWNSHLSRKLHNFIRKPSISQDVSAVIMTNASSAPPPPQAKRRLGRTSRSAMKPKIHRTKTRKTKKTSAPPEPNADVAGADKEALMVESSGAEAELGRPCDYYGDDCNKNLMSINGDNGVLTFDDDIIDLLLDESDPGHLYTNTTCGGDGELHNIRDSEGARGFSDTWNQGNLDCLLQSCPSVESFLNYDHQVNDASTDEFIDWDCVWQEGSDNNLWHEKENPDSMVSWLLDGDDEATIGNSNCENFGEPLDHDDESALVAWLLS

>AtMYB13

MGRRPCCEKIGLKKGPWSAEEDRILINYISLHGHPNWRALPKLAGLLRCGKSCRLRWINYLRPDIKRGNFTPHEEDTIISLHQLLGNRWSAIAAKLPGRTDNEIKNVWHTHLKKRLHHSQDQNNKEDFVSTTAAEMPTSPQQQSSSSADISAITTLGNNNDISNSNKDSATSSEDVLAIIDESFWSEVVLMDCDISGNEKNEKKIENWEGSLDRNDKGYNHDMEFWFDHLTSSSCIIGEMSDISEF

>AtMYB14

MGRAPCCEKMGVKRGPWTPEEDQILINYIHLYGHSNWRALPKHAGLLRCGKSCRLRWINYLRPDIKRGNFTPQEEQTIINLHESLGNRWSAIAAKLPGRTDNEIKNVWHTHLKKRLSKNLNNGGDTKDVNGINETTNEDKGSVIVDTASLQQFSNSITTFDISNDNKDDIMSYEDISALIDDSFWSDVISVDNSNKNEKKIEDWEGLIDRNSKKCSYSNSKLYNDDMEFWFDVFTSNRRIEEFSDIPEF

>AtMYB15

MGRAPCCEKMGLKRGPWTPEEDQILVSFILNHGHSNWRALPKQAGLLRCGKSCRLRWMNYLKPDIKRGNFTKEEEDAIISLHQILGNRWSAIAAKLPGRTDNEIKNVWHTHLKKRLEDYQPAKPKTSNKKKGTKPKSESVITSSNSTRSESELADSSNPSGESLFSTSPSTSEVSSMTLISHDGYSNEINMDNKPGDISTIDQECVSFETFGADIDESFWKETLYSQDEHNYVSNDLEVAGLVEIQQEFQNLGSANNEMIFDSEMDFWFDVLARTGGEQDLLAGL

>AtMYB32

MGRSPCCEKDHTNKGAWTKEEDDKLISYIKAHGEGCWRSLPRSAGLQRCGKSCRLRWINYLRPDLKRGNFTLEEDDLIIKLHSLLGNKWSLIATRLPGRTDNEIKNYWNTHVKRKLLRKGIDPATHRPINETKTSQDSSDSSKTEDPLVKILSFGPQLEKIANFGDERIQKRVEYSVVEERCLDLNLELRISPPWQDKLHDERNLRFGRVKYRCSACRFGFGNGKECSCNNVKCQTEDSSSSSYSSTDISSSIGYDFLGLNNTRVLDFSTLEMK

>AtMYB75

MEGSSKGLRKGAWTTEEDSLLRQCINKYGEGKWHQVPVRAGLNRCRKSCRLRWLNYLKPSIKRGKLSSDEVDLLLRLHRLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHEPCCKIKMKKRDITPIPTTPALKNNVYKPRPRSFTVNNDCNHLNAPPKVDVNPPCLGLNINNVCDNSIIYNKDKKKDQLVNNLIDGDNMWLEKFLEESQEVDILVPEATTTEKGDTLAFDVDQLWSLFDGETVKFD

>AtMYB82

MECKREEGKSYVKRGLWKPEEDMILKSYVETHGEGNWADISRRSGLKRGGKSCRLRWKNYLRPNIKRGSMSPQEQDLIIRMHKLLGNRWSLIAGRLPGRTDNEVKNYWNTHLNKKPNSRRQNAPESIVGATPFTDKPVMSTELRRSHGEGGEEESNTWMEETNHFGYDVHVGSPLPLISHYPDNTLVFDPCFSFTDFFPLL

>AtMYB90

MEGSSKGLRKGAWTAEEDSLLRLCIDKYGEGKWHQVPLRAGLNRCRKSCRLRWLNYLKPSIKRGRLSNDEVDLLLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHESSCCKSKMKKKNIISPPTTPVQKIGVFKPRPRSFSVNNGCSHLNGLPEVDLIPSCLGLKKNNVCENSITCNKDDEKDDFVNNLMNGDNMWLENLLGENQEADAIVPEATTAEHGATLAFDVEQLWSLFDGETVELD

>AtMYB111

MGRAPCCEKIGLKRGRWTAEEDEILTKYIQTNGEGSWRSLPKKAGLLRCGKSCRLRWINYLRRDLKRGNITSDEEEIIVKLHSLLGNRWSLIATHLPGRTDNEIKNYWNSHLSRKIYAFTAVSGDGHNLLVNDVVLKKSCSSSSGAKNNNKTKKKKGRTSRSSMKKHKQMVTASQCFSQPKELESDFSEGGQNGNFEGESLGPYEWLDGELERLLSSCVWECTSEEAVIGVNDEKVCESGDNSSCCVNLFEEEQGSETKIGHVGITEVDHDMTVEREREGSFLSSNSNENNDKDWWVGLCNSSEVGFGVDEELLDWEFQGNVTCQSDDLWDLSDIGEITLE

>AtMYB113

MGESPKGLRKGTWTTEEDILLRQCIDKYGEGKWHRVPLRTGLNRCRKSCRLRWLNYLKP
SIKRGKLCSDEVDLVLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHDERCCK
TKMINKNITSHPTSSAQKIDVLKPRPRSFSDKNSCNDVNILPKVDVVPLHLGLNNNYVCES
SITCNKDEQKDKLININLLDGDNMWWESLLEADVLGPEATETAKGVTLPLDFEQIWARFD
EETLELN

>AtMYB114

MEGSSKGLRKGAWTAEEDSLLRQCIGKYGEGKWHQVPLRAGLNRCRKSCRLRWLNYLK
PSIKRGKFSSDEVDLLLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHEPCCKT
KIKRINIITPPNTPAQKVDIF