

Supplementary material 1. MYB, WRKY and AP2/ERF transcription factor gene sequences from *Arabidopsis thaliana* used for phylogenetic analysis.

>NP_567626.1 MYB-like 102 [Arabidopsis thaliana]
MARSPCCEKNGLKKG PWTSEEDQKLVDYIQKHGYGNWRTL PKNAGLQRCGKSCRLRW TNYLRPDIKRG
RF
SFEETIIQLHSLGNKWSAIAARLPGR TDNEIKNFWNTHIRKLLRMGIDPVTHSPRLDLLDISSILA
SSLYNSSSHHMNMSRLMMDTNR RHHQHPLVNPEILKLATSLFSQNNQNLVVDHDSRTQEKQTVYS
QTG
VNQYQTNQYFENTITQELQSSMPPFPNEARQFNNMDHFFNGFG EQNLVSTSTTSVQDCYNPSFNDYSS
SN
FVLDPSSYDQSFNFAN SVLNT PSSSPSPTTLN SSIYINSSSCSTEDEIESYCSNLMKFDIPDFLDVNGFII
>AT3G27810.1 | Symbols: ATMYB21, ATMYB3, MYB21 | myb domain protein 21 |
chr3:10307596-10310093 FORWARD LENGTH=226
MEKRGGSSGSGSSAEAEVRKGPWTMEEDLILINIANHGDGVWNSLAKSAGLKRTGKSCRLRWLN Y
LRPDVRRGNITP
EEQLIIMELHAKWGNRWSKIAKHLPGR TDNEIKNFWRTRI QKYIKQSDVTTTSSVGS HHSSEINDQAAS T
SSHNVFCTQD
QAMETYSPTPTS YQHTNMEFN YGNYSAAAVTATVDYVPMTVDDQTGENYWGMDDIWSSMHLLNG
N
>AT5G40350.1 | Symbols: MYB24, AtMYB24 | myb domain protein 24 | chr5:16138703-
16140946 REVERSE LENGTH=214
MEKRESSGSGSGDAEVRKGPWTMEEDLILINIANHGEVWNSLAKSAGLKRTGKSCRLRWLN YLRP
DVRRGNITPEEQ
LTIMELHAKWGNRWSKIAKHLPGR TDNEIKNFWRTI QKYI KSGETTTVGSQSSEFINHHATTSHVMND
TQETMDMYSP
TTSYQHASNINQQLNYGNYPESGSIMMPLSVDQSEQNYWSVDDLWPMNIYNGN
>AT1G22640.1 | Symbols: ATMYB3, MYB3 | myb domain protein 3 | chr1:8006289-8007219
FORWARD LENGTH=257
MGRSPCCEKAHMNKGAWTK EEDQLLDYIRKHGEGCWRS LPRAAGLQRCGKSCRLRW MNYL RPD LKR
GNFTEEEDELIK
LHSLGNKWSLIAGRLPGR TDNEIKNYWNTHIKRKL LSRGIDPNSHRLINESV VSPSSLQNDV VETIHLDFS
GPVKPEPV
REEIGMVNNESSGTTSEKDYGNEEDWVLNLELSVGPSYRYESTRKVSVD SAESTRRWGSELF GAHESD
AVCLCCRIGL
FRNESCRCRVSDVRTH
>AT4G38620.1 | Symbols: ATMYB4, MYB4 | myb domain protein 4 | chr4:18053866-
18054876 FORWARD LENGTH=282
MGRSPCCEKAHTNKGAWTK EEDERLVAYIKAHGEGCWRS LPKAAGLLRCGKSCRLRW INYL RPD LKRG N
FTEEEDELIK
LHSLGNKWSLIAGRLPGR TDNEIKNYWNTHIRK LIRNGIDPTSHRPIQESSASQDSKPTQLEPVTSNTINI
SFTSAPK
VETFHESISFPGKSEKISMLTFKEEKDECPVQEKFPDLNLELRISLPDDVDRLQGHGKSTTPRCFKCSLGMIN
GMECRCG
RMRCDVVGGSSKGS DMSNGDFLGLAKKETTSLGFRSLEMK
>AT4G34990.1 | Symbols: AtMYB32, MYB32 | myb domain protein 32 | chr4:16661370-
16662289 REVERSE LENGTH=274

MGRSPCCEKDHTNKGAWTKEEDDKLISYIKAHGEGCWRSRSLRQRCGKSCRLRWINYLRPDLKRG
FTLEEDDLIK
LHSLGNKWSLIATRLPGRTDNEIKNYWNTHVKRKLLRKGIDPATHRPINETKTSQDSSDSSKTEDPLVKILS
FGPQLEK
IANFGDERIQKRVEYSVVEERCLDLNLELRISPPWQDKLHDERNLRFGRVKYRCSACRFGFGNGKECSCN
NVKQCQTEDSS
SSSYSSTDISSSIGYDFLGLNNTRVLDSTLEMK
>AT5G60890.1 | Symbols: ATMYB34, ATR1, MYB34 | myb domain protein 34 |
chr5:24495029-24496220 FORWARD LENGTH=295
MVRTPCCKEIGIKKGAWTPEEDQKLIAYLHLHGEGGWRTLPEKAGLKRCGKSCRLRWANYLRPDIKRG
SPEEDDTIHK
LHALKGNKWAAIATSLAGRTDNEIKNYWNTNLKRLKQKIDAITHKPINSTGQTGFEPKVNPKPVYSSGSA
RLLNRVASK
YAVELNRDLLTGIISGNSTVAEDSQNSGDVDSPTSTLLNKMAATSVLINTTTTYSGFSDNCSFTDEFNEFFN
NEEISDIY
TTVDNFGFMEELKSILSYGDASAGVIENSPEVNVADAMEFIDSWNEDDNMVGVFV
>AT1G34670.1 | Symbols: AtMYB93, MYB93 | myb domain protein 93 | chr1:12709128-
12710423 FORWARD LENGTH=365
MGRSPCCDENGLKKGAWTPEEDQKLIDYIHKHGHGSRALPKLADLNRCGKSCRLRWNYLRPDIKRG
KFSAEETILH
LHSILGNKWSAIATHLQGRTDNEIKNFWNTHLKKLIQMGIDPVTHQPRDLFASLPQIALANLKDIEQT
SQFSSMQG
EAAQLANLQYLQRMFNSSASLTNNNGNNSPSSILDIDQHMANLLNSMVSWNKDQNPADFPVLEEA
NDQNQDLFPLGF
IIDQPTQPLQQKYHLNNSPELPSQGDPLLDHVPFSLQTPLNSEDHFIDNLVKHPTDHEHEHDDNPSSW
VLPPLIDNNP
KTVTSSLPHNNPADASSSSSYGGCEAASFYWPDICFDESLMNVIS
>AT5G65230.1 | Symbols: AtMYB53, MYB53 | myb domain protein 53 | chr5:26068290-
26069408 FORWARD LENGTH=310
MGRSPSSDETGLKGPWLPEEDDKLINYIHKHGHSSWSALPKLAGLNRCGKSCRLRWNYLRPDIKRGKF
SAEETILN
LHAVLGNKWSMIASHLPGRTDNEIKNFWNTHLKKLIQMGFDPMTHQPRDDIFSSLSQLMSLSNLRGL
VDLQQQFPMED
QALLNLQTEMAKQLFQYLLQSPAPMSINNINPNILNLLIKENSVTSNIDLGFLSSHLQDFNNNNLPSLKT
LDDNHFSQ
NTSPIWLHEPPSLNQTMLPTHDPACQSVDFGSGNQASSSHDQEVAVTDSVDWPDHHLFDDSMFPDISY
QS
>AT3G02940.1 | Symbols: MYB107, AtMYB107 | myb domain protein 107 | chr3:662141-
663830 FORWARD LENGTH=321
MGRSPCCDESGLKGPWLPEEDQKLINHIRKHGHGSRALPKQAGLNRCGKSCRLRWNYLRPDIKRG
NFTAEEETIIN
LHSLGNKWSIAGHLPGRTDNEIKNYWNTHIRKLIQMGIDPVTHRPRDHLNVLALPQLLAAANFN
NLLNLNQNQL
DATSVAKAQLLHSMIQVLSNNNTSSSFDIHHHTNLFQSSFLNLPNIENPYDQTQGLSHIDDQPLDSFS
SPIRVVAYQ
HDQNFIPPLISTSPDESKETQMMVKNKEIMKYNDHTSNPSSTSTFTQDHQPWCIDIIDDEASDSYWKEIIE
QTCSEPWPF

E

>AT5G16770.1 | Symbols: AtMYB9, MYB9 | myb domain protein 9 | chr5:5515209-5516734
FORWARD LENGTH=336

MGRSPCCDENGLKKGWWTQEEDDKLIDHIQKHGHSWRALPKQAGLNRCGKSCRLRWTNYLRPDIKR
GNFTEEEEQTIIN
LHSLGKNSIAGNLPGRTDNEIKNYWNTHLRKLLQMGIDPVTHRPRTDHLNLAALPQLIAAANFN
SLLNLNQNVQL
DATLAKAQLLHTMIQVLSTNNNTNPSFSSSTMQNSNTNLFQGASYLENQNLFGQSQNFSHILEDENL
MVKTKIIDNPL
DSFSSPIQPGFQDDHNSLPLLPASPEESKETQRMINKDIVDYHHHDASNSSSNSTFTQDHHHPWCDT
IDDGASDSFW
KEIIEQTCSEPWPFPPE

>AT4G17785.1 | Symbols: MYB39 | myb domain protein 39 | chr4:9881867-9883368
REVERSE LENGTH=360

MGRSPCCDQDKGVKKGWLPPEEDDKLTAYINENGYGNWRSLPKLAGLNRCGKSCRLRWMNYLRPDIRR
GKFSDEESTIV
RLHALLGNKWSKIAGHLPGRTDNEIKNYWNTHMRKLLQMGIDPVTHEPRTNDLSPILDVSQMLAAAI
NNGQFGNNLLN
NNTALEDILKLQLIHKMLQIITPKAIPNISSFKTNLLNPKPEPVNSFNTNSVNPKPDPAGLFINQSGITPEA
ASDFIP
SYENVWDGFEDNQLPGLVTVSQESLNTAKPGTSTTTKVNDHIRTGMMPCYYGDQLLETPSTGSVSVSPE
TTSLNHPSTAQ
HSSGDFLEDWEKFLDDETSWSCWKSFLDLTSSPVPW

>AT5G54230.1 | Symbols: MYB49, AtMYB49 | myb domain protein 49 | chr5:22016357-
22017845 REVERSE LENGTH=319

MGKSSSSESEVKKGPWTPEEDEKLVGYIQTHGPGKWRTLKPNAGLKRCGKSCRLRWTNYLRPDIKRGEF
SLQEEETIIQ
LHRLGNKWSAIAIHLPGRTDNEIKNYWNTHIKKLLRMGIDPVTHCPRINLLQLSSFLTSSLFKSMSQPM
NTPFDLTTS
NINPDILNHLTASLNNVQTESYQPNQQLQNDLNTDQTTFTGLLNSTPPVQWQNNGEYLGDYHSYTG
DPSNNKVPQAGN
YSSAAFVSDHINDGENFKAGWNFSSSMLAGTSSSSSTPLNSSSTFYVNGGSEDDRESFGSDMLMFHHHH
DHNNNALNLS

>AT4G05100.1 | Symbols: AtMYB74, MYB74 | myb domain protein 74 | chr4:2618557-
2619790 FORWARD LENGTH=324

MGRSPCCCKKNGLKKGPWTPEEDQKLIDYINIHGYGNWRTLKPNAGLQRCGKSCRLRWTNYLRPDIKRG
RFSFEEETII
QLHSIMGNKWSAIAARLPGRTDNEIKNYWNTHIRKLLKMGIDPVTHPRLLDLDISSILSSSIYNSSHHH
HHHHQQHMN
MSRLMMSDGNHQPLVNPEILKLATSLFSNQNHNNTHENNTVNQTEVNQYQTGYNMPGNEELQSWF
PIMDQFTNFQDLMP
MKTTVQNSLSYDDDCSKSNFVLEPYYSDFASVLTTPSSSPTPLNSSSSTYINSSTCSTEDEKESYSDNITNYS
FDVNGF
LQFQ

>AT1G69560.1 | Symbols: MYB105, LOF2, ATMYB105 | myb domain protein 105 |
chr1:26157755-26158906 FORWARD LENGTH=330

MEMVHADVASLITPCFPSSLSSSHSHHYNQQQHHCIMSEDQHHSMDQTTSSDYFSLNIDNAQHLSYYT
SHREEDMNPNL
SDSYNCNKKDTTVYRSCGHSSKASVSRGHWRAEDTKLKELVAVYGPQNWNLIAEKLQGRSGKSCRLRW
FNQLDPRINRR
AFTEEEEEERLMQAHRLYGKWKAMIARLFPGRDNSVKNHWHVIMARKFREQSSSYRRRKTMSVSLKPLI
NPNPHIFNDFDP
TRLALTHLASSDHKQLMLPVPFCPGYDHENESPLMVDMFETQMMVGDYIAWTQEATTFDFLNQTGKSE
IFERINEEKKPP
FFDFLGLGTV
>AT1G26780.2 | Symbols: MYB117, AtMYB117, LOF1 | myb domain protein 117 |
chr1:9271033-9272463 FORWARD LENGTH=359
MFITEKQVWMDEIVARRASSWDFPFNDINIHQHHRHCNTSHEFEILKSPLGDVAVHEEESNNNNPNF
SNSES GK KETT
DSGQSWSSSSSKPSVLGRGHWRPAEDVKLKELSIYGPQNWNLIAEKLQGRSGKSCRLRWFNQLDPRIN
RRAFTEEEEEER
LMQAHRLYGKWKAMIARLFPGRDNSVKNHWHVVMARKYREHSSAYRRRKLMSNNPLKPHLTNNHH
PNPNPNYHSFISTN
HYFAQPPEFNLTHHLVNNAPITSDHNQLVLPFHCFQGYENNEPPMVVSMFGNQMMVGDNVGATSD
ALCNIPHIDPSNQE
KPEPNDAMHWIGMDAVDEEVFEKAKQQPHFFDFLGLGTA
>AT4G37260.1 | Symbols: MYB73, ATMYB73 | myb domain protein 73 | chr4:17540602-
17541564 FORWARD LENGTH=320
MSNPTRKNMERIKGPWSPEEDDLLQRLVQKHGPRNWSLISKSIPGRSGKSCRLRWCNQLSPEVEHRAFS
QEEDETIIRAH
ARFGNKWATISRLNGRTDNAIKNHWNSTLKRKCSVEGQSCDFGGNGGYDGNLGEEQLKRTASGGGG
VSTGLYMSPGSP
SGSDVSEQSSGGAHVFKPTVRSEVTASSSGEDPPTYLSLSLPWTDETVRVNEPVQLNQNTVMDGGYTAE
LFPVRKEEQVE
VEEEEAKGISGGFGGGEFMTVVQEMIRTEVRSYMA DLQRGNVGGSSSGGGGGGSCMPQSVNSRRVGF
EFIVNQIGIGKME
>AT3G50060.1 | Symbols: MYB77 | myb domain protein 77 | chr3:18558146-18559051
REVERSE LENGTH=301
MADRVKGPWSQEEDEQLRRMVEKYGPRNWSAISK SIPGRSGKSCRLRWCNQLSPEVEHRPFSPEDETI
VTARAQFGNKW
ATIARLLNGRTDNAVKNHWNSTLKRKCSGGVAVTTVTETEEDQDRPKRRSVSFD SAFAPVDTGLYMSPE
SPNGIDVSDS
STIPSPSSPVAQLFKPMPISGGFTVVPQPLPVEMSSSSED PPTSLSLSLPGAENTSSSHNNNNNALMFP
ESQM KINVE
ERGEGRRGEFMTVVQEMIKAEVRSYMAEMQKTSGGFVVGGLYESGGNGGFRDCGVITPKVE
>AT4G33450.1 | Symbols: ATMYB69, MYB69 | myb domain protein 69 | chr4:16095746-
16096603 REVERSE LENGTH=250
MEMSRGSNSFDNKKPSCQRGHWRPVEDDNLRLQVLEQYGPKNWNFIAQHLYGRSGKSCRLRWYNQLD
PNITKKPFTEEEEE
RLKHAHQGNRWASARLFPGRDNSVKNHWHVIMARRKRENFSSSTATSTFNQTWHTVLSPSSSLTRLN
RSHFGLWRYR
KDKSCGLWPYSFVSPPTNGQFGSSSVSNVHHEIYLERRRKSKELVDPQNYTFHAATPDHKMTSNE
DGPMS
GDDGEKNDVTF

IDFLGVGLAS

>AT1G17950.1 | Symbols: ATMYB52, BW52, MYB52 | myb domain protein 52 |
chr1:6177764-6179063 FORWARD LENGTH=249

MMCSRGRHWRPAEDEKLRELVEQFGPHNWNIAIAQKLSGRSGKSCRLRWFNQLDPRINRNPFTEEEEERL
LASHRIHGNRWS
VIARFFPGRTDNAVKNHWHVIMARRGRERSKLRPRGLGHDGTVAAATGMIGNYKDCDKERRLATTAINF
PYQFSHINHFQ
VLKEFLTGKIGFRNSTTPIQEGAIQTKRPMEFYNFLQVNTDSKIHOLIDNSRKDEEEDVDQNNRIPNENC
VPPFDFLSV
GNSASQGLC

>AT1G73410.1 | Symbols: ATMYB54, MYB54 | myb domain protein 54 | chr1:27601852-
27603038 FORWARD LENGTH=243

MIMCSRGRHWRPAEDEKLKDLVEQYGPHNWNIAIALKLPGRSGKSCRLRWFNQLDPRINRNPFTEEEEERL
LAAHRIHGNRW
SIIARLFPGRTDNAVKNHWHVIMARRTRQTSKPRLLPSTTSSSSLMASEQIMMSSGGYNHNYSSDDRKKI
FPADFINFPY
KFSHINHLHLKFEFTGKIALNHKANQSKKPMEFYNFLQVNTDSNKSEIIDQDSGQSKRSDSDTKHESHVP
FFDFLSVGN
SAS

>AT2G38470.1 | Symbols: WRKY33, ATWRKY33 | WRKY DNA-binding protein 33 |
chr2:16108476-16110539 FORWARD LENGTH=519

MAASFLTMDNSRTRQNMNGSANWSQQSGRTSTSSLEDLEIPKFRSFAPSSISISPSLVSPSTCFSPSLFLDS
PAFVSSA
NVLASPTTGALITNVTNQGKINEGDKSNNNNFNLFDFSHTQSSGVSAPTTTTTTTTTTTTTTSSIFQSQE
QQKKNQSEQ
WSQTETRPNNQAVSYNGREQRKGEDGYNWRKYGQKQVKGSENPRSYKCTFPNCPTKKKVERSLEGQI
TEIVYKGSNHHP
KPQSTRSSSSSTFHSAVYNASLDHNRQASSDQPNNSNFHQSDSFGMQQEDNTTSDSVGDDEFEQGG
SSIVSRDEEDCG
SEPEAKRWKGDNETNGGNGGGSKTVREPRIVVQTTSDIDLDGGRWRKYGQKVVKGPNPRSYKCT
TIGCPVRKHVER
ASHDMRAVITTYEGKHNDVPAARGSGYATNRAPQDSSSVPIRPAAIAGHSNYTTSSQAPYTLQMLHNN
NTNTGPPGYAM
NNNNNSNLQTQQNFVGGGFSRAKEEPNEETSFFDSFMP

>AT4G31800.2 | Symbols: WRKY18 | WRKY DNA-binding protein 18 | chr4:15383296-
15384812 FORWARD LENGTH=309

MDGSSFLDISLDLNTNPFSAKLPKEVSVLASTHLKRKWLEQDESASELREELNRVNSENKKLTEMLARVCE
SYNELHNHL
EKLQSRQSPEIEQTDIPIKRRKQDPDEFLGFPGLSSGKTENSSSNEDHHHHHQHEQKNQLLSCKRPVTD
SFNKAKVST
VYVPTETSDTSLTVKDGFWWRKYGQKVTRDNPSPRAYFRCSFAPSCPVKKKVQRSAEDPSLLVATYEGTHN
HLGPNASEG

DATSQGGSSVTLDLVNGCHRLALEKNERDNTMQEVLIIQQMASSLTKDSKFTAALAAAISGRLMEQSRT

>AT4G31800.1 | Symbols: WRKY18, ATWRKY18 | WRKY DNA-binding protein 18 |
chr4:15383296-15384812 FORWARD LENGTH=310

MDGSSFLDISLDLNTNPFSAKLPKEVSVLASTHLKRKWLEQDESASELREELNRVNSENKKLTEMLARVC
ESYNELHNH

LEKLSRQSPQIEQTDIPIKRRKQDPDEFGLGFIPLSSGKTENSSSNEDHHHHHQHEQKNQLLSCKRPVT
DSFNKAKVS
TVVYPTETS DTS LTVK DGFQWRKYGQKVTRDNPSPRAYFRCSFAPSCPVKKKVQRSAEDPSLLVATYEGTH
NHLGPNASE
GDATSQGGSSVTLDLVNGCHRLALEKNERDNTMQEVLIQQMASSLTKDSKFTAALAAAI SGRLMEQSR
T

>AT1G80840.1 | Symbols: WRKY40, ATWRKY40 | WRKY DNA-binding protein 40 |
chr1:30383834-30385356 FORWARD LENGTH=302
MDQYSSSLVDTSLDLTIGVTRMRVEEDPPTSALVEELNRVSAENKKLSEMLTLMCDNYNVLRKQLMEYVN
KSNITERDQI
SPPKRRKSPAREDAFSCAVIGGVSESSSTDQDEYLCKKQREETVVKEKVSRYVYKTEASDTTLVVKDGYQW
RKYGQKVTR
DNPSPRAYFKCACAPSCSVKKKVQRSVEDQSVLVATYEGEHNHPMPSQIDSNNGLNRHISHGGSASTPV
AANRRSSLTVP

VTTVDMIESKKVTSPTSRI DFPQVQKLLVEQMASSLTKDPNFTAALAAAVTGKLYQQNHTEK
>AT2G25000.1 | Symbols: WRKY60, ATWRKY60 | WRKY DNA-binding protein 60 |
chr2:10629812-10631095 FORWARD LENGTH=271
MDYDPNTNPFDLHFSGLPKREVSASASKVVEKKWLKDEKRNMLQDEINRVNSENKKLTEMLARVCEK
YYALNNLMEEL
QSRKSPESVNFQNKQLTGKRKQELDEFVSSPIGLSLGPIENITNDKATVSTAYFAAEKSDTSLTVK DGYQWR
KYGQKITR
DNPSPRAYFRCSFSPSCLVKKKVQRSAEDPSFLVATYEGTHNHTGPHASVSRTVKLDLVQGGLEPVEEKKE
RGTIQEVLV

QQMASSLTKDPKFTAALATAISGR LIEHSRT
>AT4G18170.1 | Symbols: WRKY28, ATWRKY28 | WRKY DNA-binding protein 28 |
chr4:10061508-10062691 FORWARD LENGTH=318
MSNETRDLYNYQYPSFSLHEMMNLPTS NPSSYGNLPSQNGFNPSTYSFTDCLQSSPAAYESLLQKTFGLS
PSSSEVFNS
SIDQEPNRDVTNDVINGGACNETETRVSPSNSSSEADHPGEDSGKSRKRELVG EEDQISKKVGKTKKTE
VKKQREPRV
SFMTKSEVDHLEDGYRWRKYGQKAVKNSPYPRSYRCTTQKCNVKKRVERSFQDPTVVITTYEGQHHP
IPTNLRGSSAA
AAMFSADLMTPRFAHDMFR TAA YTNNGGSVAAAALDYGYGQSGYGSVNSNPSSHQVYHQGGEYELLREI
FPSIFFKQEP

>AT4G24240.1 | Symbols: WRKY7, ATWRKY7 | WRKY DNA-binding protein 7 |
chr4:12571930-12573446 FORWARD LENGTH=353
MTVELMMSSYSGGGGGGDFPAIAAAKMEDTALREAASAGIHGVEEFLK LIGQSQQPTEKSQTEITAV
TDVAVNSFKKV
ISLLGRSRTGHARFRRAPASTQTPFKQTPVVEEEVEVEEKKPETSSVLTQKQTEQYHGGGSAFRVYCPTPIH
RRPPLSHN
NNNNQNQTKNGSSSSPMLANGAPSTINFAPSPV SATNSFMSSHRCDDSTHMSSGF EFTNPSQLS
GSRGKPLSSAS
LKRRCNSPSSRCHCSKKRKRVRVIRVPAVSSKMADIP SDEF SWRKYGQKPIKGS PPRGYKCSSVRG
CPARKHVER

ALDDAMMLIVTYEGDHNHALVLETTT MNHDKTL
>AT4G23810.1 | Symbols: WRKY53, ATWRKY53 | WRKY family transcription factor |
chr4:12392666-12393739 REVERSE LENGTH=324

MEGRDMLSWEQKTLLELINGFDAAKKLQARLREAPSPSSSFSSPATAVAETNEILVKQIVSSYERSLLLLL
WSSSPSVQ
LIPTPVTVPVANPGSVPEPASINGSRSEEFADGGGSSSHRQDYIFNSKKRKMPLKWSEKVRISPER
GLEGPQDDV
FSWRKYGQKDILGAKFPRSYYRCTHRSTQNCWATKQVQRSDGATVFEVYRGTHTCSQAITRTPPLASP
EKRQDTRVKP
AITQKPKDILESLSNLTVRTDGLDDGKDVFSFPDTPPFYNYGTINGEFGHVESPIFDVVDWVFNPTVEIDT
TFPAFLHE
SIYY

>AT5G22570.1 | Symbols: WRKY38, ATWRKY38 | WRKY DNA-binding protein 38 |
chr5:7495608-7496707 REVERSE LENGTH=289

MEMNSPHEKAVQAIRYGHSCAMRLKRRLNHPMADGGPLSSYDLAKSIVESFSNAISILSAKPETEDDQFS
DLSSRDSSPP
PQGSPSKKRKIDSTNSSENWRDDSPDIYYDGYLWRKYGQKSIKSNHQRSYYRCSYNKDHNCARKHE
QKIKDNPPVYR
TTYFGHHTCKTEHNLDIAIFIAGQDPLDDFKSTQMIRFGKDQDQEKESRSNGFSLSVKHEEDIIKEQAIDQY
REITSNDQD
CQDVIEEYLSSPSGSYPSSSSGSESADFNSDLLFDNPDSWDRYDQFYF

>AT5G01900.1 | Symbols: WRKY62, ATWRKY62 | WRKY DNA-binding protein 62 |
chr5:351136-352013 REVERSE LENGTH=263

MNSCQQKAMEKLLHGHGCANQLLIMDQTESDSSMEREDLAKSVLHCFSDALSILIDTNDHQDDQSNNS
SPQDSSPVLESS
RKPLHKRGRKTSMAESSDYHRHESSTPIYHDGFLWRKYGQKQIKESYQRSYYKAYTKDQNCBAKKQVQ
KIQHNPPLYS
TTYFGQHICQLHQAYATFPIDTDFEEHEGSHMIRFGHPNIFSSSTSNLRQHQNHQDRIKDEYMKPVIAE
DWSPSQWMS
SEVALAVEAFEFNPFWTSHDLSS

>AT2G40750.1 | Symbols: WRKY54, ATWRKY54 | WRKY DNA-binding protein 54 |
chr2:17000636-17002354 REVERSE LENGTH=346

MDSNSNNTKSIKRKVVVDQLVEGYEFATQLQLLLSHQHSNQHIDETRLVSGSGSVGGPDPVDELMSKIL
GSFHKTISVL
DSFDPVAVSVPIAVEGSWNASCDDSATPVSCNGGDSGESKKKRLGVGKGRGCYTRKTRSHTRIVEAKS
SEDRYAWRKY
GQKEILNTTFRSYFRCTHKPTQGCKATKQVQKQDQDSEMFQITYIGYHTCTANDQTHAKTEPFDQEIIM
DSEKTLAAS
AQNHNAMVQEQENNTSSVTAIDAGMVKEEQNNNGDQSKDYEGSSTGEDLSLVWQETMMFDDHQ
NHYYCGETSTTSHQF
GFIDNDDQSSFFDSYCADYERTSAM

>AT3G56400.1 | Symbols: WRKY70, ATWRKY70 | WRKY DNA-binding protein 70 |
chr3:20909082-20910409 REVERSE LENGTH=294

MDTNKAKKLVKMNQLVEGHDLTTQLQLLSQPGSGLEDLVAKILVCFNNTISVLDTFEPISSSSSLAAVEGS
QNASCND
GKFEDSGDSRKRKLPVKGKRGYKRRKRSETCTIESTILEDAFSWRKYGQKEILNAKFPRSFRCTHKYTGQ
CKATKQVQ
KVELEPKMFSITYIGNHTCNTNAETPKSKTCDHHDEIFMDESDHKSPSLSTSMKEEDNPHRHHGSSTEND
LSLVWPEMVF
EEDYHHQASYVNGKTSTSIDVLGSQDLMVFGGGGDFEFSENEHFSIFSSCSNLS

>AT2G30590.1 | Symbols: WRKY21 | WRKY DNA-binding protein 21 | chr2:13033891-13035303 FORWARD LENGTH=380
MEEIEGTNRAAVESCHRVLNLLHRSQQQDHVGFENLVSETREAVIRFKRVGSLSSSVGHARFRRAKKLQ
SHVSQSLLL
DPCQQRTEVPSSSSQKTPVLRSGFQELSLRQPSDSLTLGTRSFSLNSNAKAPLLQLNQQTMPSSNYPTLF
PVQQQQQQQ
QQQQQQEQQQQQQQQQQFHERLQAHHLHQQQQLQKHQAELMLRKCNGGISLSDNSSCTPTMS
STRSFVSSLSIDGSA
NIEGKNSFHFGVPSSTDQNSLHSCRKCPKLGDEHGLKCGSSSRCHCAKKRKHVRRSIRVPAISNKVADIP
PDDYSWRK
YGQKPIKGSYPYRGYYKCSSMRGCPARKHVERCLEDPAMLIVTYEAEHNHPKLPQAITT

>AT4G31550.1 | Symbols: WRKY11, ATWRKY11 | WRKY DNA-binding protein 11 | chr4:15290065-15291458 REVERSE LENGTH=325
MAVDLMRFPKIDDQTAIQEAASQGLQSMELIRVLSNRPEQQHNVDCEITDFTVSKFKTVISLLNRTGH
ARFRRGPVHS
TSSAASQKLQSQIVKNTQPEAPIVRTTTNHPQIVPPPSSVTLDFSKPSIFGTAKASAELEFSKENFSVSLNSSF
MSSAIT
GDGSVSNKIFLASAPLQPVNSSGKPLAGHPYRKRRCLEHEHSESFSGKVSGSAYGKCHCKSRKNRMKR
TVRVP AISAK
IADIPPDEYSWRKYGQKPIKGSPPHPRGYYKCSTFRGCPARKHVERALDDPAMLIVTYEGEHRHNQSAMQE
NISSSGINDL
VFASA

>AT3G01970.1 | Symbols: WRKY45, ATWRKY45 | WRKY DNA-binding protein 45 | chr3:326614-327159 REVERSE LENGTH=147
MEDRRCDVLFPCSSVDPRLTEFHGVDNSAQPTTSSEEKPRSKKKKKEREARYAFQTRSQVDILDDGYRW
RKYGQKAVKN
NPFPRSYYKCTEEGCRVKKQVQRQWGDEGVVVTTYQGVHTHAVDKPSDNFHHILTQMHIFPPFCLKE

>AT1G29280.1 | Symbols: WRKY65, ATWRKY65 | WRKY DNA-binding protein 65 | chr1:10236589-10237467 FORWARD LENGTH=259
MKRGLDMARSYNDHESSQETGPESPNSSTFNGMKALISSHSPKRSRRSVEKRVVNVPMKEMEGSRHKG
DTTPPSDSWAWR
KYGQKPIKGSYPYRGYYRCSSTKGC PARKQVERS RDDPTMILITYTSEHNHPWPLTSSTRNGPKPKPEPKPE
PEPEVEPE
AEEEDNKFMVLGRGIETTPSCVDEFWFTEMETTSSTILESPISSEKKTAVSGADDVAVFFPMGEEDESLF
ADLGELPE
CSVVFRHRSSVVG SQVEIF

>AT5G15130.1 | Symbols: WRKY72, ATWRKY72 | WRKY DNA-binding protein 72 | chr5:4904426-4906879 FORWARD LENGTH=548
MEVLLKLPSSSPLKDKFGSVQIHEANKGDGDHQELES AKAEMSEVKEENEKLGMLERIESDYKSLKLRF
FDIIQQEPS
NTATKNQNMVDHPKPTTDLSSFDQERELVLSLGRSSSPSDSVPKKEEKTDAISAEVNADEELTKAGLTL
GINNGNGG
EPKEGLSMENRANS GSEEAWAPGKVTGKRSSPAPASGGDADGEAGQQNHVKRARVCVRARCDTPTM
NDGCQWRKYGQKIA
KGNPCPRAYRCTVAPGCPVRKQVQRCADDMSILITTYEGTHSHSLPLSATTMASTTSA AASMLLSGSSSS
PAAEMIGNN

LYDNSRFNNNNKSFYSPTLHSPHPTVTLDLTAPQHSSSSSSLLSLNFNKFSNSFQRFSTSLNFSSTSTSS
NPSTLN
LPAIWGNNGYSSYTPYPYNNVQFGTSLNLGKTVQNSQSLTETLTALKALSDPSFHVSIAAAISTMVGSNGEQQI
VGPRHSISN
NIQQTNTTNNNKGCGGYFSSLLMSNIMASNQTGASLDQPSSQLPPFSMFKNSSSSSSTTNFVNKEEKS
>AT1G13960.1 | Symbols: WRKY4 | WRKY DNA-binding protein 4 | chr1:4776622-4779043
FORWARD LENGTH=514
MSEKEEAPSTSKSTGAPSRPTLSLPPRFSEMFFNGGVGFSPGPMTLVSNMFPDSDEFRSFSQLLAGAMS
SPATAAAAAA
AATASDYQRLGEGTNSSSGDVPDFKQNRPTGLMISQSQSPSMFTVPPGLSPAMLLDSPSFLGLFSPVQG
SYGMTHQQAL
AQVTAQAVQANANMQPQTEYPPPSQVQSFSSGQAQIPTSAPLPAQRETSDVTHIEHRSQQPLNVDPKPAD
DGYNWRKYGQK
QVKGSEFPSSYYKCTNPGCPVKKKVERS LDGQVTEIHYKQHNHEPPQNTKRGKNDNTANINGSSINNR
GSSELGASQF
QTNSSNKTREQHEAVSQATTTEHLSEASDGEEVGNGETDVREKDENEPDKRRSTEVRRISEPAASHR
TVTEPRIIVQ
TTSEVDLLDDGYRWRKYGQKVVKGNPYPRSYKCTTPGCGVRKHVERAATDPKAVVTTYEGKHNDLPA
AKSSSHAAAAA
QLRPDNRPGGLANLNQQQQQPVARLRLKEEQTT
>AT4G26440.1 | Symbols: WRKY34, ATWRKY34, MSP3 | WRKY DNA-binding protein 34 |
chr4:13357596-13359550 REVERSE LENGTH=568
MAGIDNKAAVMGEWFDCTTNRKRKAELGREFSLNYIKNEDSLQTTTFQESSRGALRERIAARSGFNA
PWLNTEDILQS
KSLTISSPGLSPATLLESPVFLSNPLSPTTGKLSVPSDKAKAELFDDITTSLAFQTISGSGLDPTNIALEPDDS
QDYE
ERQLGGLGDSMACCAPADDGYNWRKYGQKLVKGSEYPRSYKCTHPNCEAKKKVERSREGHIIIIYTG
HIHSKPPPNR
RSGIGSSGTGQDMQIDATEYEGFAGTNEINIEWTSPVSAELEYGSHSGSMQVQNGTHQFGYGDAADAL
YRDENEDDRTSH
MSVSLTYDGEVEESEKRRKLEAYATETSGSTRASREPRVVVQTTSDIDILDDGYRWRKYGQKVVKGNPNP
RSYYKCTAN
GCTVTKHVERASDDFKSVLTTYIGKHTHVPAARNSSHVAGSSGTLQGLATQTHNHNHYPMPHSRS
EGLATANSSLF
DFQSHLRHPTGFSVYIGQSELSL SMPGLTIGQEKLTSLQAPDIGDPTGLMLQLAAQPKVEPVSPQQGLDL
SASSLICRE
MLSRLRQI
>AT5G24110.1 | Symbols: WRKY30, ATWRKY30 | WRKY DNA-binding protein 30 |
chr5:8153416-8154633 REVERSE LENGTH=303
MEKNHSSGEWEKMKNEINELMIEGRDYAHQFGSASSQETREHLAKKILQSYHKS LTIMNYSGELDQVSQ
GGGSPKSDSD
QEPLVIKSSKSMRWSKVRIAPGAGVDRTLDDGFSWRKYGQKDILGAKFPRGYRCTYRKSQGCEATK
QVQRSDENQM
LLEISYRGIHSCSQAANVGTTMPIQNLEPNQTQE HGNLDMVKESVDNYNHQAHLHNLHYPLSSTPNLE
NNNAYMLQMRD
QNIIEYFGSTSFSSDLGTSINYNFPASGSASHSASNSPSTVPLESPFESYDPNHPYGGFGGFYS

>AT5G13080.1 | Symbols: WRKY75, ATWRKY75 | WRKY DNA-binding protein 75 |
chr5:4149928-4151019 REVERSE LENGTH=145
MEGYDNGSLYAPFLSLKSHSKPELHQGEEESSKVRSEGCSSVSSSKKGGKKQRYAFQTRSQVDILDDGYR
WRKYGQKAV
KNNKFPRSYRCTYGGCNVKKQVQRLTVDQEVVVTTYEGVHSHPIEKSTENFEHILTQMQUIYSSF

>AT5G49520.1 | Symbols: WRKY48, ATWRKY48 | WRKY DNA-binding protein 48 |
chr5:20090890-20092867 FORWARD LENGTH=399
MEKKKEEDHHHQQQQQQQKEIKNTETKIEQEQQEQKQEQISQASSSSNMANLVTSSDHHPLELAGNLS
SIFDTSSLPPFY
SYFEDHSSNNPNSFLDLLRQDHQFASSNSSSSFSFDAFLPNNNNNTSFFTDLPLQAESSEVVNTTPTSP
NSTSVSSSS
NEAANDNNSGKEVTVKQDEEGDQQQEQKGTQPKLAKKKKNQKKAREARFAFLTKSDIDNDDGYRWR
KYGQKAVKNSPYP
RSYYRCTTVGCGVKKRVERSSDDPSIVMTTYEGQHTHPFPMTPRGHIGMLTSPILDHGATTASSSSFSIPQ
PRYLLTQHH
QPYNMYNNNSLSMINRRSSDGT FVNPGPSSSFPFGYDMSQASTSTSSSIRDHGLLQDILPSQIRSDTINT
QTNEENKK

>AT3G04670.1 | Symbols: WRKY39, ATWRKY39 | WRKY DNA-binding protein 39 |
chr3:1266530-1267691 REVERSE LENGTH=330
MEEVEAANRSAIESCHGVLNLLSQRTSDPKSLTVETGEVVSKFKRVASLLTRGLGHGKFRSTNKFRSSFPQH
IFLESPIC
CGNDLSGDYTVLQVLAPEPLQMVPASAVYNEMEPKHQLGHPSLMLSHKMCVDKSFLELKPPPFRAPYQLIH
NHQQIAYSRSN
SGVNLKFDGSGSSCYTPSVSNGSRFSVSSLSMDASVTDYDRNSFHLLTGLSRGSDQQHTRKMCSSGSLKCGS
RSKCHCSKKR
KLRVKRSIKVPAISNKIADIPPDEYSWRKYGQKPIKGSPPHPRGYKCSSVRGCPARKHVERCIDETSMLIVTY
EGEHNHS
RILSSQSAHT

>AT1G62300.1 | Symbols: WRKY6, ATWRKY6 | WRKY family transcription factor |
chr1:23016887-23019155 REVERSE LENGTH=553
MDRGWSGLTLDSSSLDLLNPNRISHKNHRRFSNPLAMSRIDEEDDQKTRISTNGSEFRFPVSLSGIRDRED
EDFSSGVAG
DNDREVPGEVDFFSDKKSRCREDDEGFRVKKEEQDDRTDVNTGLNLRRTTGNTKSDSMIDDGESSEME
DKRAKNELVKL
QDELKMTMDNQKRELLTQVNSYTSLQMHLVSLMQQQQQQNNKVIEAAEKPEETIVPRQFIDLGPT
RAVGAEEDVSNS
SSEDRTRSGSSAAERRSNGKRLGREESPETESNKIQVNSTPTPTFDQTAETMRKARVSVRARSEAPMI
SDGCQWRKY
GQKMAKGNPCPRAYRCTMATGCPVRKQVQRCALDRSILITTYEGNHNHPLPPAAVAMASTTTAAANM
LLSGSMSSHGDM
MNPTNLLARAVLPCSTSMATISASAPFPTVTLDLTHSPPPPNGSNPSSSAATNNNHNSLMQRPQQQQQ
QMTNLPPGMLPH
VIGQALYNQSKFSGLQFSGGSPSTAAFSQSHAVADTITALTADPNFTAALAAVISSMINGTNHHDGEGNNK
NQ

>AT4G01250.1 | Symbols: WRKY22, AtWRKY22 | WRKY family transcription factor |
chr4:522839-524129 REVERSE LENGTH=298

MADDWDLHAVVRGCSAVSSSATTTVYSPGVSSHTNPIFTVGRQSNVAVSFGEIRDLYTPFTQESVVSFSCI
NYPEEPRKP
QNQKRPLSLSASSGSVTSKPSGNSRSKRRIQHKVCHVAAEALNSDVWAWRKYGQKPIKGSPPYPRGY
YRCSTSKGCL
ARKQVERNRSDPKMFIVTYAEHNHPAPTHRNSLAGSTRQKPSDQQTSSPTTTIATYSSSPVTSADDFVL
PVEDHLAVG
DLDGEEDLLSLSDTVVSDDFFDGLLEFAAGDSFSGNSAPASFDLSWVNSAATTTGGI
>AT5G46350.1 | Symbols: WRKY8, ATWRKY8 | WRKY DNA-binding protein 8 |
chr5:18801403-18803901 REVERSE LENGTH=326
MSHEIKDLNNYHYTSSYNHYNINNQNMINLPYVSGPSAYNANMISSQVGFDLPSKNLSPQGAFELGFEL
SPSSDDFFNP
SLDQENGLYNAYNYNSSQKSHEVVGDGCATIKSEVRVSASPSSSEADHHPGEDSGKIRKKREVRDGGEDD
QRSQKVVVTK
KKEEKKEPRVSFMTKTEVDHLEDGYRWRKYGQKAVKNSPYPRSYRCTTQKCNVKKRVERSYQDPTVVI
TTYEQHNHP
IPTNRRRTAMFSGTTASDYNPSSSPIFSDLIINTPRSFNSDDLFRVPYASVNVNPSYHQQHGFGHQESEFEL
LKEMFPSV
FFKQEP
>AT2G30250.1 | Symbols: WRKY25, ATWRKY25 | WRKY DNA-binding protein 25 |
chr2:12903553-12905089 REVERSE LENGTH=393
MSSTFTDLLGSSGVDCYEDDEDLRVSGSSFGGYPERTGSGLPKFKTAQPPPLISQSSHNFSTDYLDSP
LLLSSSHS
LISPTTGTFLQGFNGTTNNHSDFPWQLQSQPSNASSALQETYGVQDHEKKQEMIPNEIATQNNNQSF
TERQIKIPAYM
VSRNSNDGYGWRKYGQKQVKKSENPRSYFKCTYPDCVSKKIVETASDGQITEIYKGGHNHPKPEFTKRPS
QSSLPSSVN
GRRLFNPASVVSEPHDQSENSSISFDYSDLEQKSFKSEYGEIDEEEEEQPEMKRMKREGEDEGMSIEVSKGV
KEPRVVVQT
ISDIDVLIDGFRWRKYGQKVVKGNTNPRSYKCTFQCGVKKQVERSAADERAVLTTEYGRHNHDIPTAL
RRS
>AT4G18170.1 | Symbols: WRKY28, ATWRKY28 | WRKY DNA-binding protein 28 |
chr4:10061508-10062691 FORWARD LENGTH=318
MSNETRDLYNYQYPSSFSLHEMMNLPTSNPSSYGNLPSQNGFNPSTYSFTDCLQSSPAAYESLLQKTFGLS
PSSSEVFNS
SIDQEPNRDVTNDVINGGACNETETRVSPSNSSSEADHPGEDSGKSRRKRELVGEEDQISKKVGKTKKTE
VKKQREPRV
SFMTKSEVDHLEDGYRWRKYGQKAVKNSPYPRSYRCTTQKCNVKKRVERSFQDPTVVITTYEGQHNHP
IPTNLRGSSAA
AAMFSADLMTPRSFADMFRTAAYTNGGSVAAALDYGYGQSGYGSVNSNPSSHQVYHQGGEYELLREI
FPSIFFKQEP
>AT2G23320.1 | Symbols: WRKY15 | WRKY DNA-binding protein 15 | chr2:9924998-
9926154 FORWARD LENGTH=317
MAVELMTRNYISGVGADSFVQEAASGLKSIENFIGLMSRDSFNSDQPSSSSASASASAAADLESARNT
TADAAVSKFK
RVISLLDRTRTG HARFRRAPVHVISPVLLQEEPKTTPFQSPLPPPQMIRKGSFSSSMKTIDFSSLSVTTES
DNQKKIH

HHQRPSETAPFASQTQSLSTTVSSFSKSTKRKCENSELLTGKCASASSSGRCHCSKRRKIKQRRRIIRVPAISAK
 MSDVPP
 DDYSWRKYGQKPIKGSPPHPRGYKCSSVRGCPARKHVERAADDSSMLIVTYEGDHNHLSAADLAGAAV
 ADLILESS
 >AT5G26170.1 | Symbols: WRKY50, ATWRKY50 | WRKY DNA-binding protein 50 |
 chr5:9147176-9148128 REVERSE LENGTH=173
 MNDADTNLGSFSDDTHSVFEFPELDSLDEWMDDDLVSAVSGMNSYGYQTSVAGALFSGSSSCFSH
 PESPTKTYVAA
 TATASADNQNKKKKIKGRVAFKTRSEVEVLDDGFKWRKYGKKMVKNSPHPRNYYKCSVDGCPVKRVR
 ERDRDDPSFVI
 TTYEGSHNHSSMN
 >AT5G64810.1 | Symbols: WRKY51, ATWRKY51 | WRKY DNA-binding protein 51 |
 chr5:25908415-25909687 FORWARD LENGTH=194
 MNISQNPSPNFTYFSDENFINPFMDNDFSNLMFFDIDEGGNGLIEEEISSPTSIVSSETFTGESGGSGS
 ATTLKKES
 TNRGSKESDQTKETGHRVAFRTRSKIDVMDDGFKWRKYGKKSVMKNINIKRNYYKCSSEGCSVKRVERD
 GDDAAYVITTY
 EGVHNHESLSNVYYNEMVLSYDHDNWNQHSLRS
 >AT4G23550.1 | Symbols: WRKY29, ATWRKY29 | WRKY family transcription factor |
 chr4:12291831-12293088 FORWARD LENGTH=304
 MDEGDLEAIVRGYSGSDAFSGESSGTFSPSFLCPMETSSFYEPEMETSGLDELGELYKPFYFSTQTILTSS
 VSLPES
 KPFRRDDKKQRSHGCLLSNGSRADHIRISESKSKSKKNQKRVVEQVKEENLLSDAWAWRKYGQKPIKGS
 PYPRSYRCS
 SSKGCLARKQVERNPNPEKFTITYTNEHNHELPTRRNSLAGSTRAKTSQPKPTLTKSEKEVVSSPSNP
 MIPSADSS
 VAVQEMSVAETSTHQAAGAIEGRRLSNGLPSDLMSGSGTFPSFTGDFDELLNSQEFFSGYLWNY
 >AT1G55600.1 | Symbols: WRKY10, ATWRKY10, MINI3 | WRKY DNA-binding protein 10 |
 chr1:20774049-20776293 REVERSE LENGTH=485
 MSDFDENFIEMTSYWAPPSSPRTILAMLEQTDNGLNPSEIFPQESLPRDHTDQSGQRSGLRERLAAR
 VGFNLPTLNT
 EENMSPLDAFFRSSNPNPSPVVAISPGFSPSALLHTPNMVSDDSSQIIPPSSATNYGPLEMVETSGEDNAA
 MMMFNNDLPY
 QPYNVDLPSLEVFDIATEESFYIPSYEPHVDPIGTPLVTSFESELVDDAHTDIISIEDSESEDGNKDDDDDED
 QYEDED
 EDQYDQDQDVEDEEEKDEDNVALDDPQPPPKRRRYEVSNMIGATRTRSKTQRILQMESEDEDNPND
 GYRWRKYGQKVV
 KGPNPNSRYFKCTNIECRVKKHVERGADNIKLVVTTYDGIHNHPSPARRSNSSSRNRSAGATIPQNQND
 RTSRLGRAPP
 TPTPTPPSSYTPPEMRPFSSSLATEIDLTEVYMTGISMLPNIPVYENSGFMYQNDEPTMNAMPDGSVDY
 DGIMERLYFK
 FGVDM
 >AT2G37260.1 | Symbols: TTG2, ATWRKY44, WRKY44, DSL1 | WRKY family transcription
 factor family protein | chr2:15645277-15646792 FORWARD LENGTH=429
 MEVNDGERVVIKPVASRPSSSSGFRFTTELLTDSVTVSPQTTCEIVDAAIRPKTLRFNQPVAASVSCPRA
 EVKGIGNG

MSCDDSDSRNYVVYKPKAKLVSKATVSALANMLQGNRQQTWRQSEAVSYGKSVSQGTHRAGPNLVQ
 KVPSFTESETSTG
 DRSSVDGYNWRKYGQKQVKGSECPRSYKCTHPKCPVKKKVERSVEGQVSEIVYQGEHNHSPCLPR
 RASSISSGFQ
 KPPKSIASEGSMGQDPNNNLYSPLWNNQSNSTQNRTEKMSEGCVITPFEFAVPRSTNSNPGTSDSGCK
 SSQCDEGELDD
 PSRSKRRKNEKQSSEAGVSQGSVESDSLEDGFRWRKYGQKVVGGNAYPRSYRCTSANCRAKHVERAS
 DDPRAFITTYE
 GKHNHLLLLSPSSSTLPFNSQLSKQTI
 >AT3G23240.1 | Symbols: ERF1, ATERF1 | ethylene response factor 1 | chr3:8295705-
 8296361 FORWARD LENGTH=218 Activate Jasmonate stress
 MDPFLIQSPFSGFSPEYSIGSSPDSFSSSSNNYSLPFNENDSEEMFLYGLIEQSTQQTIDSDSQDLPIKSVS
 SRKSEK
 SYRGVRRRPWGKFAAEIRDSTRNGIRVWLGTFESAEEAALAYDQAAFSMRGSSAILNFAERVQESLSEIK
 YTYEDGCSP
 VVALKRKHSRMRMTNKKTKDSDFDHRSVKLDNvvVFEDLGEQYLEELLGSSSENSGTW
 >AT3G15210.1 | Symbols: ATERF-4, ERF4, RAP2.5, ATERF4 | ethylene responsive element
 binding factor 4 | chr3:5121472-5122140 FORWARD LENGTH=222
 MAKMGLKPDATTNQTTHNNAKEIRYRGVRKRPWGRYAAEIRDPGKKTRVWLGTFDTAEEAARAYDTAA
 RDFRGAKAKTNF
 PTFLESDQKVPTGFARSPSQSSTLDCASPPTLVVPSATAGNVPPQLELSLGGGGGGSCYQIPMSRPVYFL
 DLMGIGNVG
 RGQPPPVTSAFRSPVHVATKMACGAQSDSDSSVVDFEGGMEKRSQLLDLNLPPPEQA
 >AT1G50640.1 | Symbols: ERF3, ATERF3 | ethylene responsive element binding factor 3 |
 chr1:18757602-18758279 REVERSE LENGTH=225
 MRRGRGSSAVAGPTVVAAINGSVKEIRFRGVRKRPWGRFAAEIRDPWKKARVWLGTFDSAEAAARAYD
 SAARNLRGPKAK
 TNFPIDSSSPPPNLRFNQIRNQNQNQVDPFMDHRLFTDHDQQQFPIVNRPTSSSMSSTVESFSGPRPTT
 MKPATTKRYPR
 TPPVVPEDCHSDCDSSSVIDDDDDIASSRRRNPPFQFDLNFPLDCVDFNGADDLHCTDLRL
 >AT2G23340.1 | Symbols: DEAR3 | DREB and EAR motif protein 3 | chr2:9938186-9938716
 FORWARD LENGTH=176
 METEAAVTATVTAATMGIGTRKRDLPYKGYRMRKWKWVAEIREPNKRSRIWLGSYATPEAAARAYDT
 AVFYLRGPSAR
 LNFPELLAGLTVSNGGGRGGDLAAYIRRKAAEVAQVDALGATVVVNTGGENRGDYEKIENCRKSGNG
 SLERVDLNKLP
 DPENSDGDDDECVKRR
 >AT3G50260.1 | Symbols: CEJ1, ATERF#011, DEAR1 | cooperatively regulated by ethylene
 and jasmonate 1 | chr3:18634687-18635148 FORWARD LENGTH=153
 MDAGVAVKADVAVKMKRERPFKGYRMRKWKWVAEIREPNKRSRLWLGSYSTPEAAARAYDTAVFYLR
 GPTATLNFPELL
 PCTSAEDMSAATIRKKATEVGAQVDAIGATVVQNNKRRRVFSQKRDFGGGLLELVDLNKLPDENLDDD
 LVGK
 >AT1G78080.1 | Symbols: RAP2.4 | related to AP2 4 | chr1:29364790-29365794 FORWARD
 LENGTH=334
 MAAAMNLYTCRSFQDSGGELMDALVPFIKSVSDSPSSSSAASASAFSLPLPGYYPDSTFLTQPF
 SYGSDLQQ

TGS LIGLNNLSSSQIHQIQSQIHHPLPPTHHNNNSFSNLLSPKLLMKQSGVAGSCFAYGSGVPSKPTKLY
 RGVRRQHW
 GKWVAEIRLPRNTRLWLGTFTDAAEEAALAYDKAAYKLRGDFARLNFNLRHNGSHIGGDFGEYKPLHSS
 VDAKLEAICK
 SMAETQKQDKSTKSSKKREKKVSSPDLSEKVKAEENSVSIGGSPVTEFEESTAGSSPLSDLTFADPEEPPQ
 WNETFSLE
 KYPSEIDWDSILA
 >AT3G16770.1 | Symbols: RAP2.3, ATEBP, ERF72, EBP | ethylene-responsive element binding
 protein | chr3:5705784-5706768 FORWARD LENGTH=248
 MCGGAIISDYAPLVTKAKGRKLTAEELWSELDAASAADDFWGFYSTSKLHPTNQVNVKEEAVKKEQATEPG
 KRRKRKNVYR
 GIRKRPWGKWAAEIRDPRKGVVWLGTFNTAEAAAMAYDVAAKQIRGDKAKLNFDPDLHHPPPPNYTPP
 PSSPRSTDQPPA
 KKVCVVSQSESELSQPSFPVEICIGFGNGDEFQNL SYGFEPDYDLKQQISSLESFLELDGNTAEQPSQLDESV
 SEVDMWML
 DDVIASYE
 >AT3G14230.2 | Symbols: RAP2.2 | related to AP2 2 | chr3:4737616-4739000 REVERSE
 LENGTH=375
 MCGGAIISDFIPPPRSLRVTFNEFIWPDLNKVKASKKRSNKRSDFFDLDDDFEADFQGFKDDSAFDCEDD
 DDVFVNVKPF
 VFTATTKPVASAFVSTVGSAYAKKTVESAEQAEKSSKRKRKNQYRGIRQRPWGKWAAEIRDPRKGSREWL
 GTFTDAAEEAA
 RAYDAAARRIRGKAKVNFPEEKNPSVVSQKRPSAKTNNLQKSVAKPNKSVTLVQQPTHLSQQYCNSF
 DNSFGDMSFME
 EKPQMYNNQFGLTNSFDAGGNGYQYFSSDQGSNSFDCSEFGWSDHGPKTPEISSMLVNNNEASFVEE
 TNAACKLKPNSD
 ESSDLMAYLDNALWDTPLEVEAMLGADAGAVTQEEENPVELWSLDEINFMLEGDF
 >AT1G43160.1 | Symbols: RAP2.6 | related to AP2 6 | chr1:16263989-16264663 FORWARD
 LENGTH=192
 MVSMLTNVVSGETEPSASATWTMGHKREREEFSLPPQPLITGSAVTKECESSMSLERPKKYRGVRQRPW
 GKWAAEIRDPH
 KATRVWLGTFETAEEAARAYDAAALFRGSKAKLNFENVGTQTIQRNSHFLQNSMQPSLTIDQCPTLL
 SYSRCMEQQQ
 PLVGM LQPTEENHFFEKPWTEYDQYNYSSFG
 >AT1G13260.1 | Symbols: RAV1, EDF4 | related to ABI3/VP1 1 | chr1:4542386-4543420
 FORWARD LENGTH=344Repress
 MESSVDESTTSTGSICETPAITPAKKSSVGNLYRMGSGSSVVLDSENGVEAESRKLPSKYGVPQPNG
 RWGAQIYEK
 HQRVWLGTFNEEDEAARAYDVAVHRFRRRDAVTNFKDVKMDEDEVDLNSHSEIVDMLRKHTYNEE
 LEQSKRRRNGNG
 NMTRLLTSGLSNDGVSTTGFRSAEALFEKAVTPSDVGKLNRLVIPKHHAEKHFPLPSSNVSVKGVLLNFE
 DVNGKVWRF
 RYSYWNSSQSYVLTKGWSRFVKEKNLRAGDVVSFSRSNGDQQLYIGWKSRSGLDAGRVLRLFGVNI
 SPESSRNDVVG
 NKRVDTEMLSLVCSKKQRIFHAS
 >AT1G53170.1 | Symbols: ATERF-8, ATERF8, ERF8 | ethylene response factor 8 |
 chr1:19821539-19822096 REVERSE LENGTH=185

MPNITMGLKPDVPAPTNPHTHESNAAKEIRYRGVVRKRPWGRYAAEIRDPVKKTRVWLGTFTDAQQAAR
AYDAAARDFRGV
KAKTNFGVIVGSSPTQSSTVVDSPTAARFITPPHLELSLGGGGACRRKIPLVHPVYYNMMATYPKMTTCGV
QSESETSSV
VDFEGGAGKISPLDLNLAPP
>AT1G28370.1 | Symbols: ERF11, ATERF11 | ERF domain protein 11 | chr1:9956351-
9956851 REVERSE LENGTH=166
MAPTVKTAAVKTNEGNVRYRGVVRKRPWGRYAAEIRDPFKKSRVWLGTFTDPEEAARAYDKRAIEFRGA
KAKTNFPCYNI
NAHCLSLTQSLQSSTVESSFPNLNLGSDSVSSRFPPKIQVKAGMMVFDERSESDSSSVMDVVRYEGR
RVVLDLNLNF
PPPPEN
>AT3G20310.1 | Symbols: ATERF-7, ATERF7, ERF7 | ethylene response factor 7 |
chr3:7085957-7086691 REVERSE LENGTH=244
MRKGRGSSVVPALPVTAGGSVKEPRYRGVVRKRPWGRFAAEIRDPLKSRVWLGTFDSDAVDAARAYDTA
ARNLRGPKAKT
NFPIDCSPSSPLQPLTYLHNQNLCSPPVIQNIQIDPFMDHRLYGGGNFQEQQQQIISRASSMSSTVKSC
SGPRPMEAA
AASSVAKPLHAIKRYRTPPVAPEDCHSDCDSSSVIDDGDDIASSSSRRKTPFQFDLNFPLDGVDLFAG
GIDDLHCT
DLRL
>AT1G28360.1 | Symbols: ERF12, ATERF12 | ERF domain protein 12 | chr1:9951934-
9952503 FORWARD LENGTH=189
MASTTCAREVHYRGVVRKRPWGRYAAEIRDPWKKTRVWLGTFTDPEEAALAYDGAARFLRGIKAKTNFPS
PLSLDLNHLPS
APSAATAAANNQPHQHQLWFAAPPPVPPSSDHHHQHHRIFLRTGVLNDKTSDYSTEAPLYFTSSPNT
ATSSPGYQVVG
FPMMNSSPSPVTVRRGLAIDLNEPPPLWL
>AT1G03800.1 | Symbols: ERF10, ATERF10 | ERF domain protein 10 | chr1:957261-957998
REVERSE LENGTH=245
MTTEKENVTAVAVKDGGEKSKEVSDKGVKKRKNVTKALAVNDGGEKSKEVRYRGVRRRPWGRYAAEIR
DPVKKKRVWLG
SFNTGEEAARAYDSAAIRFRGSKATTNPLIGYYGISSATPVNNNLSETVSDGNANLPLVGDDGNALASPV
NNTLSETAR
DGTLPDCHDMLSPGVAEAVAGFFLDLPEVIALKEELDRVCPDQFESIDMGLTIGPQTAVEEPETSSAVDC
KLRMEPDLD
LNASP
>AT1G53910.1 | Symbols: RAP2.12 | related to AP2 12 | chr1:20135242-20136581
FORWARD LENGTH=358
MCGGAIISDFIPPPRRRVTSSEFIWPDLKKNLKGSKKSSKNRSNFFDFDAEFEADFQGFKDDSSIDCDDDF
DVGDFVADV
KPFVFTSTPKPAVSAAAEAGSVFGKKTGLDGAEKSANRKRKNQYRGIRQRPWGKWAAEIRDPREGARI
WLGTFKTAEEA
ARAYDAAARRIRGSKAKVNFPEENMKANSQKRSVKANLQKPVAKPNPNPSPALVQNSNISFENMCFME
EKHQVSNNNNNQ
FGMTNSVDAGCNGYQYFSSDQGSNSFDCSEFGWSDQAPITPDISSAVINNNNSALFFEEANPAKKLKSM
DFETPYNTEW

DASLDFLNEDAVTTQDNGANPMDLWSIDEIHSMIGGVF
>AED95489.1 ethylene responsive element binding factor 5 [Arabidopsis thaliana]Defence
MATPNEVSALWFIEKHLLDEASPVATDPWMKHESSATESSSDSSSIIFGSSSSSFAPIDFSEVCKPEI
IDLTPRSMFLSIPFEFDSEVSVSDFDFKPSNQNQNQFEPELKSQIRKPPLKISLPAKTEWIQFAAENT
KPEVTKPVSEEEKKHRYGVRQRPWGKFAAEIRDPNKGRSRVWLGTFTDAIEAARAYDEAAFRLRGSKAIL
NFPLEVGVKWKPRADEGEKKRKRDDDEKVTVVEKVLKTEQSVDVNGGETFPFVTSNLTELCDWDLTGFLN
F
PLLSPLSPHPPFGYSQLTVV
>AEE76737.1 Integrase-type DNA-binding superfamily protein [Arabidopsis
thaliana]Jasmonate stress
MESSNRSSNNQSQDDKQARFRGVRRRPWGKFAAEIRDPSRNGARLWLGTFTAEAAARAYDRAAFNL
GH
LAILNFPNEYPRMDDYSLRPPYASSSSSSSSGSTSTNVSQRNQREVFEEYLDKVLLELLDSEERKR
>NP_850162.1 ethylene-responsive element binding factor 15 [Arabidopsis
thaliana]Jasmonate stress
MEYSQSSMYSSPSSWSSSQESLLWNESCFLDQSSEPQAFFCPNYDYSDDFFSFESPEMMIKEEIQNGDVS
NSEEEEEKVGIDEERSYRGVRKRPWGKFAAEIRDSTRNGIRVWLGTFDKAEAAALAYDQAAFATKGSLATL
NFPVEVVRESLKKMENVNLHDGGSPVMALKRKHSLRNRPRGKKRSSSSSSSSSSSSSSSSSSSSSSTS
SSKQSVVKQESGTLVVFEDLGAEYLEQLLMSSC
>NP_199533.1 ethylene responsive element binding factor 2 [Arabidopsis
thaliana]Activation
MYGQCNIESDYALLESITRHLGGGGENELRLNESTPSSCFTESWGGPLKENDSEDMLVYGLLKDAFHF
DTSSDLSCFLDFPAVKVEPTENFTAMEEKPKKAIPVTETAVKAKHYRGVRQRPWGKFAAEIRDPKNGA
RVWLGTFTAEADAALAYDIAAFAFRMRGSRALLNFPLRVNSGEPDPVRITSKRSSSSSSSSSSSSSS
LKRRRKAENLTSEVVQVKCEVGDETRVDLLVS
>AEE75632.1 ethylene responsive element binding factor 4 [Arabidopsis thaliana]Activation
MAKMGLKPDATTNQTHNNAKEIRYRGVRKRPWGRYAAEIRDPGKTRVWLGTFTAEAAARAYDTAA
RD
FRGAKAKTNFPTFLELSDQKVPTGFARSPSQSSTLDCASPPTLVVPSATAGNVPPQLELSLGGGGGGSCY
QIPMSRPVYFLDLMGIGNVGRGQPPPVTSAFRSPVVHVATKMACGAQSDSDSSSVDFEGGMEKRSQ
LD
LDLNLPPPSEQA
>NP_001185352.1 uncharacterized protein AT1G68840 [Arabidopsis thaliana] repress
MDSSCIDEISSSTSESFSATTAKLSPPAAALRLYRMGSGSSVLDPENGLTESRKLPSKYGKVV
QPNGRWGAQIYEKHQRVWLGTFTNEQEEAARSYDIAACFRGRDAVVNFKNVLEDGDLAFLAHSKAEI
VD
MLRKHTYADELEQNNKRQLFLSVDANGKRNGSSTTQNDKVLKTREVLFEKAVTPSDVGKLNRLVIPKQHA
EKHFPLPSPSPAVTKGVLFEDVNGKVVFRYSYWNSSQSYVLTGWSRFVKEKNLRAGDVVTFERSTG
LERQLYIDWKVRSQPRENPVQVVVRLFGVDIFNVTTVKPNDVVAVCGGKRSRDVDDMFALRCSKKQAI
N
AL
>NP_001312182.1 ethylene-responsive transcription factor 4 [Nicotiana tabacum] increased
resistance to TMV
MAVKNKVSNGLKGGNVKTDGVKEVHYRGVRKRPWGRYAAEIRDPGKSRVWLGTFTAEAAKAYD
TAA
REFRGPKAKTNFSPSTENQSPSHSSTVESSSGENGVHAPPHAPLELDLTRLGSAADGGDNCRRS
GEVG

YPIFHQQPTVAVLPNGQPVLLFDSLWRAGVVNRQPYPHVTPMGFNGVNAGVGPVSDSSSAVEENQY
 DGK
 RGIDLNLAPPMEF
 >CAA0274193.1 unnamed protein product [Arabidopsis thaliana] induces activation of SA-responsive
 MVKTLQKTPKRMSSPSSSSSSSSSTSSSSIRMKKYKGVMRMSWGSWVSEIRAPNQKTRIWLGSYSTAEAA
 ARAYDAALLCLKGSSANNLNFPEISTSLYHIINNGDNNNDMSPKSIQRVAAAAAANTDPSSSSVSTSSP
 LLSSPEDLYDVVMSQYDQQVLSSESSSWYNCFDGDDQFMFINGVSAPYLTTSLSDDDFFEEGDIRLWNF
 C
 >AEC08512.1 ethylene-responsive element binding factor 15 [Arabidopsis thaliana] provided
 enhanced resistance to P. syringae, B. cinerea
 MEYSQSSMYSSPSSWSSSQESLLWNECFLDQSSEPQAFFCPNYDYSDDFFSFESPEMMIKEEIQNGDVS
 NSEEEKVGIDEERSYRGVVRKRPWGKFAAEIRDSTRNGIRVWLGTFDKAEAAALAYDQAAFATKGSLATL
 NFPVEVVRESLKKMENVNLHDGGSPVMALKRKHSLRNRPRGKKRSSSSSSSSSSSSSSSSSSSSSSSSTSRS
 SSKQSVVKQESGTLVVFEDLGAEYLEQLLMSSC
 >AEQ55265.1 ethylene-responsive transcription factor 5 [Glycine max] enhanced resistance
 to P. sojae
 MCGGAIISDFIGVGRGNLAAQELWSELDPFSDFLGFDTTNSKNQPPLQKIPDKKVSSCEKKKKSVVGA
 EKKKSDSGRARKNVYRGIRQRPWGKWAAEIRDPHKGVRVWLGTFTAEAAQAYDDAAIRIRGDKAKL
 NF
 PATTISAAAAPPSKKQRCLSPDIITESSSSSSHSTTGSTGESGGNDELCLKQIEWFLGLENELPVS
 NIGAEWDNMDDLWMLDDVVVPRHLIY
 >ABK96798.1 ethylene response factor 3 [Solanum tuberosum] negatively regulates
 resistance to phytophthora infestans
 MAPKEKIGAVTAAAVMAVGKLNIGISKEVHYRGVVRKRPWGRYAAEIRDPGKKSrvwLGTFTAEAAKAY
 D
 NAAREFRGAKAKTNFPQLKEEDLKFVKNEINRSPSQTSTVESSPVMVDSSSPLDLRLCGSIGGFNHN
 TVRFPISGGGFTGAVPAVNHMYLDALERAGVINLETNRKKTVDLFGGGSDTSTVIDFMRVDVKPTIAG
 LNLDLNFPPENM
 >AAC49740.1 Pti5 [Solanum lycopersicum] contributes to potato aphid resistance
 MVPTPQSDLPNENDSQEMVLYEVLNEANALNIPYLPQRNQLLPRNNILRPLQCIGKKYRGVRRRPWGK
 Y
 AAEIRDSARHGARVWLGTFTAEAAALAYDRAAFRMRGAKALLNFPSEIVNASVVDKLSLCSNSYTTNN
 NSDSSLNEVSSGTNDVFESRC
 >sp|Q9LVG2.1|TOE2_ARATH RecName: Full=AP2-like ethylene-responsive transcription
 factor TOE2; AltName: Full=Protein TARGET OF EAT 2 repression domain
 MLDLNLDVDSTESTQNERDSITVKGVSLNQMDSESVTSNSSVVNAEASSCIDGEDELCSRTVKFQFEILK
 GGGEEEEEDDERSAVMMTKEFFPVAKGMNFMDSQAQSSRSTVDISFQRGKQGGDFIGSGSGGGDAS
 RVM
 QPPSQPVKKSRRGPRSKSSQYRGVTFYRRTGRWESHWDGCGKQVYLGGFDTAHAARAYDRAAVKFRGL
 E
 ADINFIGDYEEDLKQMANLSKEEVVQVLRQSSGFSRNNSTRYQGVALQKIGGWGAQMEQLHGNMGC
 DKA
 AVQWKGREAASLIEPHASRMIPAAANVKLDLNLGISLSLGDGPKQKDRALRLHHVPNNSVCGRNTMME
 NH
 MAAAACDTPFNFLKRGSDHLNRRHALPSAFFSPMERTPEKGLMLRSHQSFARTWQGHQSSGGTAV
 AAT

APPLFSNAASSGFSLSATRPPSSTAIHHP SQPFVNLNQGLYVIHPSDYISQHQHNL MNR PQPPP
>sp|Q6PV67.1|SNZ_ARATH RecName: Full=AP2-like ethylene-responsive transcription factor
SNZ; AltName: Full=Protein SCHNARCHZAPFEN repression domain
MLDLNLGILSTHNEDEDCKVPTSIFIQEEDSINPSNDNL SLITFGILKRNVEILPPPPPPPPPPPPSENE
LSGPGNEWL DLSSMQRNKQETLVMKKKSRRGPRSRSSHYRGVTFYRRTGRWESHIWDCGKQVYLG GFD
TA
YTAARAYDRAAIRFRGLQADINFIVDDYKQDIEKMKNLSKEEFVQSLRRASASLARGGSKYKNTHMRNDH
IHLFQNRGLNAAAACNEIRKMEGDIKGAHSGKNEHNDLELSLGISSSSKVRILEPADYYMGLNRSVTS
LHGKPLPGYLPITEIKPLKTVVASSGFPFITMINPSSLSLSCFDP
>sp|Q6PV68.1|SMZ_ARATH RecName: Full=AP2-like ethylene-responsive transcription
factor SMZ; AltName: Full=Protein SCHLAFMUTZE repression domain
MLDLNLKIFSSYNEDQDRKVPLMISTTGEEESNSSSSSTTDSAARDAFIAFGILKRDDDLVPPPPPPPHK
ETGDLFPVADARRNIEFSVEDSHWLNLSLQ RNTQKMVKSRRGPRSRSSQYRGVTFYRRTGRWESHI
W
DCGKQVYLG GFDYAAAARAYDRAAIKFRGLDADINFVDDYRHDIDKMKNLNKVEFVQTLRRESASFGR
GSSKYKGLALQKCTQFKTHDQIHLFQNRGWDAAAIKYNELGKGEGAMKFGAHIKGNHNDLELSLGISS
SESIKLTGDYKGINRSTMGLYGKQSSIFLPMATMKPLKTVAASSGFPFISMTSSSSSMSNCFDP
>sp|Q9SK03.2|RAP27_ARATH RecName: Full=Ethylene-responsive transcription factor RAP2-
7; AltName: Full=Protein RELATED TO APETALA2 7; AltName: Full=Protein TARGET OF EAT 1
repression domain
MLDLNLNADSP ESTQYGGDSYLD RQTS DNSAGNRVEESGTSTSSVINADGDEDCSTRAFTLSFDILKVG
SSSGGDESPAASASVTKEFFPVSGDCGHLRDVEGSSSRNWIDLSFDRIGDGETKLVTPVPTPAPVPAQV
KKSRRGPRSRSSQYRGVTFYRRTGRWESHIWDCGKQVYLG GFDTAHAAARAYDRAAIKFRGVDADINFT
L
GDYEEDMKQVQNL SKEEFVHILRRQSTGFSRGSSKYRGVTLHKCGRWEARMGQFLGKKAYDKAAINTN
GR
EAVTNFEMSSYQNEINSESNSEIDLNLGISLSTGNAPKQNGRLFHFP SNTYETQRGVSLRIDNEYMGKP
VNTPLPYGSSDHRLYWNGACPSYNNPAEGRATEKRSEAEGMMSNWGWQRPGQTS AVRPPQPPGQPP
PLFS
VAAASSGF SHFRPQPPNDNATRGYFYPHP
>sp|Q6J9N8.2|AIL7_ARATH RecName: Full=AP2-like ethylene-responsive transcription factor
AIL7; AltName: Full=Protein AINTEGUMENTA-LIKE 7; AltName: Full=Protein PLETHORA 7
repression domain
MAPPMTNCLTFSLSPMEML KSTDQSHFSSSYDDSSTPYLIDNFYAFKEEAEIEAAAAS MADSTTLSTFFD
HSQTQIPKLEDFL GDSFVRYSDNQ TETQDSSSLTPFYDPRHRTVAEGVTGFFSDHHQPDFKTINS GP EIF
DDSTTSNIGGTHLSSHVVESS TAKLGFNGDCTTTGGVLSLGVNNTSDQPLSCNNGERGGNSNKKKTVSK
KETSDDSKKKIVETLGRQTSIYRGVTRHRWTGRYEAHLWDNSCRREGQARKGRQVYLG GYDKEDRAARA
Y
DLAALKYWGSTATTNFPVSSYSKELEEMNHMTKQEFIASLRRKSSGFSRGASIYRGVTRHHQQGRWQAR
I
GRVAGNKDLYLGT FATEEEAAEAYDIAAIKFRGINAVTNFEMNRYDIEAVMNSSLPVGGAAAKRHKLKLA
LESPPSSSDHNLQQQLLPSSSPSDQNPNSIPCGIFEP SVLYYHQNFQHYPLVSDSTIQAPMNQAEF
FLWPNQSY
>OAO99396.1 DREB1A [Arabidopsis thaliana]ectopic expression dwarf phenotype
MNSFSAFSEMFGSDYESSVSSGGDYIPTLASSCPKKPAGRKKFRETRHP IYRGVRRRNSGKWWCEVREPN
KKTRIWLGTFTAEMAARAHDVAALALRGRSACLNFADSAWRLRIP ESTCAKDIQKAAAEALAFQDEM
C

DATTDHGFDMEETLVEAIYTAEQSENAFYMHDEAMFEMPSLLANMAEGMLLPLPSVQWNHNHEVDG
DDDD

VSLWSY

>sp|O82132.1|DRE2A_ARATH RecName: Full=Dehydration-responsive element-binding
protein 2A; Short=Protein DREB2A retards growth

MAVYDQSGDRNRTQIDTSRKRKRSRSGDGTVAERLKRWKEYNETVEEVSTKKRKVPAKGSKKGCMKG
KG

GPENSRCFRGVRQRIWGKWVAEIREPNRGSRLWLGTFTAQEAASAYDEAAKAMYGPLARLNFRSDA
S

EVTSTSSQSEVCTVETPGCVHVKTEDPDCEKPFSGGVEPMYCLENGAEEMKRGVKADKHWLSEFEHNY
W

SDILKEKEKQKEQGIVETCQQQQQDLSVADYGWPNVDVQSHLDSSDMFDVDELLRDLNGDDVFAGLN
QD

RYPGNSVANGSYRPESQQSGFDPLQSLNYGIPPFQLEGKDGNGFFDLSYLDLEN

>sp|Q8HOT5.2|ERF73_ARATH RecName: Full=Ethylene-responsive transcription factor
ERF073; Short=AtERF73; AltName: Full=Protein HYPOXIA RESPONSIVE ERF 1 activation of the
fermentative pathway under oxygen limitations

MCGGAVISDYIAPEKIARSSGKSSWRSNGVFDCSIYDFDGNFDELESDEPFVFSSTHKHHASGSASDGKK
KQSSRYKIRRRPWGRWAAEIRDPIKGVVWLGTFTAEAAARAYDLEAKRIRGAKAKLNFPNESSGKRK

AKAKTVQQVEENHEADLDVAVSSAPSSSCLDFLWEENNPDTLLIDTQWLEDIIMGDANKKHEPNDS
E

NNVDASLLSEELLAFENQTEYFSQMPFTEGNCDSSTLSSSLFDGGNDMGLWS

>OAP10407.1 HRE2 [Arabidopsis thaliana]activation of the fermentative pathway under
oxygen limitations

MCGGAIISDFIWSKSECQLGVSRRKRKPVSVSEERDGKRERKNLYRGIRQRPWGKWAAEIRDPSKGVR
VWLGTFTADEAARAYDVAAIKIRGRKAKLNFPNTQVEEADTKPGGNQNELISENQVESLSEDLMALED
YMRFYQIPVADDQSATDIGNLWSYQDSN

>OAP14595.1 ORA59 [Arabidopsis thaliana] ORA59 played a positive role in ethylene-
regulated responses

MEYQTNFLSGEFSPENSSSSSWSSQESFLWEESFLHQSFQSFLLSSPTDNYCDDFFAFESSIIKEEGKE
ATVAAEEEEKSYRGVRKRPWGKFAAEIRDSTRKIRVWLGTFTAEAAAALAYDQAAFALKGSLAVLNFP
DVVEESLRKMENVNLNDGESPVIALKRKHSMRNRPRGKKKSSSSSTLTSSPSSSSSYSSSSSSSLSSRS
RKQSVVMTQESNTTLVVLEDLGAEYLEELMRSCS

>NP_172758.1 Integrase-type DNA-binding superfamily protein [Arabidopsis thaliana]
controlling embryogenesis

MEKALRNFTETHSPDPNPLTKFFTEPTASPVSRRNLSSKDTTVTIAGAGSSTTRYRGVRRRPWGRYAA
EIRDPMSKERRWLGTFTAEQAACAYDSAARAARGAKARTNFTYPTAVIMPEPRFSFSNKSSPSARCPL
PSLPLDSSTQNFYGAPAAQRIYNTQSIFLRDASCSSRKTTPYNNNSFNGSSSSYSASKTACVSYSENNEN
SFFPEESDGTLLQEVVQEFLKKNRGVPPSPPTPPPVTSHHDNSGYFSNLTISENMVQETKETLSSKLD
RYGNFQANDDGVRAVADGGLSLGNSNEWGYQEMLMYGTQLGCTCRRSWG