Text S1： Protein sequences for the MADS-box gene family in *D.oleifera*.

>evm.model.Chr3.1394 (DolMADS1)
MIRVMARKSKGRQKVEMTRMSKESNLLVTFSKRRSGLFKKASELCTLCGAEIAIIVFSPGK
KAFSFGHPCVDTIIDRFLSRSASTGSGATAQMVEAHRNASVRELNAQLTEVMNQLEGEKK
RGEELMGGKARKERCWWEAPIQELGMQQLEQLKAAMEDLKKNVAKQAEKAAAANNN
NNNVNVAPPSFFIGGSSSTAADVDVKLSAGHGLGLSMTPQGYTLGYGYGRGFF*

>evm.model.Chr14.2006 (DolMADS2)
MTKMEKESSRQVTFSKRCFGVFKKASELSILCGAQVAVIVFLSENKAFSFGNPSVNAVVDE
FLTRNRSPKTESNRNIEAQRNATMMDLSQRLNHVETCLRSRGSEARHWTG*

>evm.model.Chr14.2007 (DolMADS3)
MERKNKGRQRIAMTRIEKESSRQVTFSKRRFSLFKKASELSILCGAQVVVIVFSPGNKAFS
FGNPSVNAVVDQFLTQNRSLEMDCDRIIEGQQNTTMMELSQQLNHVENMLEVERQRGKA
LDQMRTTSRGEFLWKEPIDKMNMEQLEQMKTAMEDLKSKAIKQAEKLTQEQLASHFNAF
MAGLGFSGGGGVPPFHAGGASNIPPSLLARRGFSGAPFDVGASSSTPPMVPGFNRGSGRW
FK*

>evm.model.Chr14.1182 (DolMADS4)
MERKNRGRQRITMTKMEKESNQQVTFFKHHLSLFKKASELSILCGAQVAVIVFLPGNKAF
SFGNPSVNAVVNQFLTQNQSLEKENGLIIEAQQNATMMELSQRLNRVENMLEVERQRGQ
ALDQMRIASQGEFWWEQPIDKMNMEQLEQMKTTLEDLKNRAIKQVEKLTQEQAASHFN
TFVAGSSSLGNGGNVPSFLVSGASDDPPPLVIGRGFSGAPCDVKASTSAPSIVPGFDRGSSC
*

>evm.model.Chr12.1719 (DolMADS5)
MERKQKRTSMGRRKIEIKKIEKSSQLQVTFSKRRSGLFNKAGELSVLCGAQVAVIVTSLAG
KVFAFGHRLWTPSPIGFSLKETLTLPAVVQGTKN*

>evm.model.Chr15.726 (DolMADS6)
MATTNMKKKTTQGRQKIEIKKIESLSNRQVTFSKRRVGLFNKASELCVLTGAQVAVIVKSP
GKRIFAFGHPSVEYVLDRYLNGGAAAADGNLPSLSTTVFNRRYDEVVSELDQEKKRRGT
MEELKSREKNNNGGFWWDRPVGEIEWPELERYMAALEELKKKVTMRADEMMLMKDA
SSLPKLMFSMNPPTASPPPHDSFFNQEITHEAANYDSKLGFDDKLFCDYC*

>evm.model.Chr3.1391 (DolMADS7)
MATANTKKRTTQGRQKIEIKKIESLSNRQVTFSKRRVGLFNKASELCVLTGAQVAVIVKSP
GKRIFAFGHPSVDTVLDRYLNGGAAAAAVGNLPPLSTTVFNRRYDEVVSELDREKKRRGT
IEESNSREKNNGGFWWDRPVGEIEWPELEQYMSALEELKRKVTMRADEMMLIKGAASLP
KSMFAMKPPMASPPPAPPHDNFFNQAITHEAANHDSKLGFDDKLFCDYC*

>evm.model.Chr14.2012 (DolMADS8)
MAKKPRSLGRQKIKIAKIEIKNHLQVTFSKRRFGLFKKASELCTLCGVELAILVLSPAGRSS
LLVIRTSIPSSIGSSRKALRQTLVGATSLRLIRMLTYMSSIQLARVLDELEAEKRRGGTLDHL
RKAREYWWEGPIDGLGLHELEQLGDSLEELKKNVIAQANKLFVEGTTNPKPFFLVNGIEM
ANGFESKSTQISASSTIPHHVHSVGYINHGFF*

>evm.model.Chr9.2464 (DolMADS9)
MGTGKKKIEIKRVEKEQQRMVTFSKRRQGLFKKAGQLHSLAAASVAVVAFSPAGRPYTH
GDPSFGAVVDRYLANTTTGLEDSAAAMNMTKMSSWLHALQIDGSDDIQELVLMKKQLE
EIKEKVAEKIINAHDSSF*

>evm.model.Chr10.636 (DolMADS10)

MGTGKKKIEIKRVEKEQQRMVTFSKRRQGLFKKAGQLHSLAAASVAVVAASVAVVAFSPA
GRPYTHGDPSFGAIVDRYLANTTTGREDSAAAMNMTKMSSWLHALQIDGCDDIQELVLM
KKQLEQIKEKVAEKIINARDSSF*
>evm.model.Chr8.780 (DolMADS11)
MGRKRVDIKKIGDKARRQTTFTKRRDGLFKKMGDLCKMCEVEGAVITFTEVGNIFAFGNP
SVDHVIQQYVDKTSDSNGAQIDDSNEKGEEEEEKEAGGELGDEHVEILARLEAVKNTGE
MVDEALPMVESFLLQERVNGFTESS*
>evm.model.Chr6.296 (DolMADS12)
MNVKKVKRNKNPRIPFKVGKEGEERGNGEGKSGAEEDREQDKQAGDVRKEEEWLLKKA
YELSVLCDAELLSSSSPPWQAL*
>evm.model.Chr6.1753 (DolMADS13)
MTRKKVKLAFIINDSARKATFKKRKKGLMKKVSELSTLCGIDACAIIYSPYDAQPEVWPN
GLGVQRVLAQFKRMPEMEQSKKMVNQESFIRQRISKANEQLKKQLKDNREKEVAELMFH
CLTGRALQTVAMSDLHDLGWLLDQNLKDIYKRIESMRKAAAPPPPPPPPQPLPPLPPPPL
VPLAPPLLPRNTTTTTTSSTITTTAATSEMMMMRNRMQQVQEQKPIVDPIVAMEAMQRPH
WFTDWMNNPNEHLGFGGAGEEMMMLPFGDSHSVVWPAGPFFP*
>evm.model.Chr12.2056 (DolMADS14)
MVMMLQMGRAKLKMELIRDEKNRYRTFMKRNKGLTKKAYELKTLCSVDVCFIVYGPKL
DESPSDQEEIWPLNHDEIQALIDSYRKQSAEDRKRRTNDLTNFFEDRNKKAEETLTKLRKK
NDEAKYPTWNDRYNDFSVEELRQFGAVLENKLQEVKARVAAIRGSSAIAKNQANLLQDY
RFDDMTIYHHPMYNLQAAAGKGISLHQLHSNNYKSMVNPVMMMLMNENHNHFTSSSST
HHHDQLLLGGASGSSNFPVEWAPVCYDQAAAMGYYSFSMSAEAMVPYVQLPMIAGSSN
SQVHPLHHGIDDYYEVGEFHVKNQN*
>evm.model.Chr14.809 (DolMADS15)
MAGKKVNLSLIPNEDERRSAYQAWKNDLMKEAEKLTTSCGTEACAVILDPLSDEVDAVW
PSNMGAQQVITRFKAMIELEQAKSKQNQESLTSKMVDKVEEKLTEKVAENRAKEMHRTM
SQCMVSREQVKQLELEDLTEFISFLNTKIKEVEARRQAQGASLPQDMATTK*
>evm.model.Chr2.1001 (DolMADS16)
MELKKLCGTQEPASTLCGTKACVVCFGPNGELETWPENPSDVRAVLQMHDDYARNGRR
GSKINDSAELGSVEAGLTEKGFSGWEDRWLRGLSKEELANFLESVEDKLRGVEARIQFLE
KMTIEQQNWFAMNESYDEMAAAEMMIGSLWPQPLQAVNYESTLAEPAEFGYFGDDPMF
AIGTSTWALLNCYGDDGSSGCAWYW*
>evm.model.Chr4.494 (DolMADS17)
MVKRIENNKARNLTYKRRMAGIKKKAMELSTLCGIQASMVCFGPAGEIDTWPENPADVK
TVIDMYRRRIDEAKLDGRLEAEKIKEAEEEISRARIENLEKMMKLMRAILDVFTQRAELLK
EAEGGREKIPLRIEGLVEILDQIKVDPIDKLDSYFEEAIASMKKFCEAIGNYYNEMIPSSSSQ
SVD*
>evm.model.Chr5.1634 (DolMADS18)
MPRKKLELAWIVNDSARKAALKRRKEGFSKKAKELSSLCDAEVGFVLTSQDEAQRTVWP
SEETVKPMFDRLLMMMSPTQQTQKMENHESYLFDVAIKEVDTIIEKRKITRKKLKRC*
>evm.model.Chr5.1635 (DolMADS19)
MVMKKVKLAWIVNNSARKAALKRRKDGLSKKAKELSSLCDAEVGFVLTSQDHALRTVW
PSEEAVKLLLTGLRCCHPLNKPKKMEKQERYLFLIAIKEVDKINRGRKKNNGEEAQEMLN
RICEGTSNLDPFTAEGLDNLVLLMDEKLELVGYKEVDDASLQQAPTLLPQQFSLPPFPQSIK

DANGQ*
>evm.model.Chr4.992 (DolMADS20)
MGRVKLQIKKIENTTNRQVTFSKRRNGLIKKAYELSVLCDVDVALIMFSPSGRVSIFSGNN
KRCCFKILESSRARTRKYVKRALAKLKVEAEADKRYQAARIFEGNASEITTLSEASTGHIL
EETLKCVRLRKQVLEEKYDYPGVQSTSQLHLPPEDGNLNSFVARHPDHILVGYRERSTKK
RVRVGIENILPAAAASSSFLPGGQNVVQLEDEDEPKQYYRHGGR*
>evm.model.Chr15.1924 (DolMADS21)
MGRVKLEIKRIENNTNRQVTFSKRRNGLIKKAYELSVLCDIEIALIMFSPSPSQRLNHFSGK
RRIEDVLSRYVNLSDHDRGGYVFSINTLKKIKDEDDMALEFTRMFEPDILGFTSIEELEACE
KNLLELMNRVAQRKKYLLSDHLSTFDPPSMQMYFEAQEGMPLSSASYQNDFVSWLPGTG
VNGDNNQNHIFGGGADHSCIALRHGDLYFP*
>evm.model.Chr7.1624 (DolMADS22)
MQMGRVKLKIKRLESSSSRLTTYSKRKNGLIKKASELSVLCDVDVILIMFSPSGKPVLWKG
KNSSIEGILERFAQLTPHERAKRKLESFDALKRSYSKSDHTVTVEDFFGPSYQTIGDLTVQA
NMLRTQVSVIQERLSDWNNLDKTDSLELLKQMEDYIRGLVGQIQTRKENIGKQKSLALGN
ICNQYQNGMHQSSSLGLEQQVQHFSWIQSDDSQHMISQIEPSVRETELSGGNSFGNSSGYI
GTVEREDISSRGLESGILCDLLRTDSSKNESIGSKTQTFRNEVKTESLRNEMTKTEFLINELI
RSECVKNELTRAESSRLQLYAQCTYPHPQNIFPDSKFQPAQDTNLPQSNHNYCTEGKSEPP
NFGYNSTSLCDWASSSGPSVTAFFDQRLYLQ*
>evm.model.Chr12.550 (DolMADS23)
MVGEACVCVEELNLGKESYGSIKCMRQLFISLLKRDFLFICSMGRVKLKIKKLESVSNRQV
TYSKRRNGILKKAKELSILCDIDIILLMFSPTGGATLFHGERSNIEDVIAKFAQLTPQERTKR
KVETLEALKKTFKKLDHDVNIQDFMGLSVQSVEEMSNQVRMLQAQLTELHRRLSCWSSP
EKIDNIDHLRQMEDSLKDSINRIQMQKENFVKHPLMSLECKNQFQSGMHLPLMMGGLQE
AQPLSWLPNNENQHMILTGEPNFLPQRCR*
>evm.model.Chr13.532 (DolMADS24)
MGRGRVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSNRGKLYEFCSSSS
MLKTLERYQKCNYGAPEPNVSAREALELSSQQEYLRLKARYEALQRTQRNLLGEDLGPL
NSKELESLERQLDMSLKQIRATRTQYMLDQLTELQRKEHALNEANKSLRQRLLEGNQIHSI
QWNPSAQDVGYGRQAAQPQDDAFFHPLDCEPTLQIGYQTDPITVAAAAAAAAGPSVNNY
MPGWLP*
>evm.model.Chr12.442 (DolMADS25)
MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSNRGKLFEFCSSSS
MPKTLERYRKCSYGSLDPSQPLNENQQNSYHEYLRLKTRVEILQRSQRNLLGDDLAPLST
KELEQLEHQLETSLKQIRSKKTQFMLDQLAELQRREQMLAEANKALRRKLEESAVAMPH
QPPWEAASGQHITYSHHLPPQSEGFFHHLPLGLNSTLQIGYNPAVGADEMNAMAPPQNAG
AFIPEWML*
>evm.model.Chr3.1740 (DolMADS26)
MGRGRVELKRIENKINRQVTFSKRRNGLLKKAYELSVLCDAEVALIIFSSRGKLYEFGSSGT
TKTLERYQRCCFNPQDNSIEHETQSWYQEVSKLRAKYESLQRTQRHLLGEDLGPLSVKEL
QNLEKQLEGALLQTRQRKTQIMIEQMEELRRKERQLGDINKQLKLKVSLELSSLQQAADQ
GQGLRPLPCSWTPNPSAGNSSFSLHPSHSNPMDCDTEPVLQIGYQYVSGEGPSVPRSMSGE
GNMVQGWVI*
>evm.model.Chr9.715 (DolMADS27)

MARGKVQMKRIENPVHRQVTFCKRRAGLLKKAKELSVLCDAEIGVLIFSAHGKLYDLAT
KGTMQGLIERYMKSTGGTDQLPEQAGEQQLQESKEETCMLRSEIEFLQKGLRNMSGGGF
GTMTVDELHMLEKHLEIWIYQIRSAKMDIMCKEIQSLKNKEGILNAANKYLHDKIDEQHG
ITNFSPFAANPLTILNEIYQF*
>evm.model.Chr15.285 (DolMADS28)
MGRGKVELKRIENPSSRQVTFSKRRNGLMKKAFELSILCDAEIALLIFSPSGKAYQYSSHE
MDRTIARYKNEMGLPQSDNHGLRPVEVWRAEMEDLRRTLESLEAKQKHIAGEDLSVLG
MKELKQLERQMRTGVERIRSKKRRIISEHINDLKKKEHSSALRGQQMEAQQLIYAA*
>evm.model.Chr6.829 (DolMADS29)
MGRKKVEMKRIEDKSSRQVTFSKRRSGLIKKARELSVLCDVEIALFIFSNHGKLYEFCTGE
SSAKMLQRYQSHSEAEGKSEAETFSSTIPHELMQSALSHE*
>evm.model.Chr4.1980 (DolMADS30)
MGRGKLQLKRIEDKNSRQVTFSKRRSGLMKKARELSVLCDVDIGVFVFSGKGKLYEFCS
GDSLSKILQRYQVHSDAEVAGGSVQESEKLPVDLPRSSSLLEMVQRHLKEQNVEELKVAEI
VQLEHHLDAMLHKIRIRKSQKMKEAVTALYEKKIGPGKQLLAINIRKYKMAFGIA*
>evm.model.Chr9.685 (DolMADS31)
MGRGKIEIKRIENNTNRQVTFCKRRNGLLKKAYELSVLCDAEVALIVFSSRGRVYEFANNK
LVPCVTEEEQQFARYG*
>evm.model.Chr9.1843 (DolMADS32)
MNGEESLNLLATMAFPNQSAEVSPQRKMGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAY
ELSVLCDAEVALIVFSNRGRLYEYANNSVKETIQRYKKACSDSSNTGSVSELNAQYYQQE
AAKLRVQIGNLQNSNRHMRGESLSSLNLRELKNLETRLERGISRIRSKKNELLFAEIELMQ
KREIDLHNNNQYLRAKIAESERVQQQMTLMPAGGSDYELMPPQPFDARNYLQVNELQIN
HQYSRPDQTVLQLV*
>evm.model.Chr8.50 (DolMADS33)
MVFPSQESEASSQRKTGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALI
VFSSRGRLYEYANNSVRATIDRYKKACADVSNTGSVSEANTQFYQQEATKLRRQIKEIQNS
NRNISGEALSSLSFKELKNLEGRLERAISRIRSKKNELLFAEIEHMQKREIELQNANMYLRA
RIAEAERAQQQMNLMPGSDYQIMGSQPYDARSYIPVNFLETNNHYSRQDQTALQLV*
>evm.model.Chr4.1089 (DolMADS34)
MGRGKIVIRRIDNSTSRQVTFSKRRNGLLKKAKELAILCDAEVGVIIFSSTGKLYDFASTSM
KTIIERYHKSKEEHHQLANPISEVKFWQREAAMLRQQLQNLQEKHRQMMGEELNGMSV
KELQNLENQLEMSLRGVRMRKDQVLIDEIQELNRKGNIIHQENVELCKKVYGTSELSGAE
RNILPSNTSSLGEDSQVPVHLQLCQPHQENYDTPTRAKKL
>evm.model.Chr2.1616 (DolMADS35)
MGRGKIAIRRIDNATNRQVTFSKRRSGLLKKAKELSILCDAEVGVIVFSSTGKLYEFASTSM
KSVIERHNESKEEHHQLQDKVSEVKFWQREAGILRQQLHNLKEHHQQLMGEELYGLSVK
DLQNLENQLEMSLRGVRMKKDQILKDEIQELKRKGNFIHEENVELYKKVNLIRQENMQL
HKKAYSMRDVIPMNGNAQNPYTFSIGEELHVPISLQLSQPEQHRLEMQSRETRSRQSSLIT
LER*
>evm.model.Chr15.1537 (DolMADS36)
MGRGKIVVKPIENLTSRQVTFSKRRNGLLKKARELSILCDAEVGVIVFSSTGKLYEFSSS
SMGSIIEKYKREEEYHQLLSPTAEAKFWQREAESLKQQLNDLQESHRNKVLPMK*
>evm.model.Chr14.1022.1 (DolMADS37)

MVRGKTQMRRIENATSRQVTFSKRRNGLLKKAFELSVLCDAEVGLIIFSPRGKLYEFASSS
MQETMQRYQRHRKDVHADNRLVEENMQHLKLEAADMVKKIELLEVAKRNLLGEGLGS
CTVEELQQIEQQLERSVSTIRARKMQVFMEQIEQLKEKEKNLGAENSILHKKVIFEAASLIS
HFKLLVSTWQFSLFCSRFVDSHPLVFGKQMHNFCELIWHRWEMVLFILTVKSGLCVFPSM
AFFHSKNQTKTGRLYHAQRAMRVQMSRLNCSSVCLTGEPSALSISDYLGRYISSELRCNVC
N*
>evm.model.Chr3.1741 (DolMADS388)
MVRGKTQMRRIENDTSRQVTFSKRRNGLLKKACELSILCDAEVGVIIFSSRGKLYEFASSS
MKDTIQRYRKHAKAPPDDPETQQNMENLRLEAAKMTKKIELLEVAKRKLMGEGLGSCSV
EELKQMEQQLERSASIIRAKKMQVYMEQIDQLKEKYDQCLRQEPNEQREMVACRERGEN
LEVETDLFIGPPNGAGIRRALPPEN*
>evm.model.Chr13.2134 (DolMADS39)
MVRGKVQMKRIENATSRQVTFSKRRNGLLKKAYELSVLCDAEVALIIFSPKGRLNEFSSSN
MQRIIERYRERANDAQTNNLEMEQYTQQLKLEAANMAKSIELLEASQRKLLGQGLVSCS
VQELQETANQLERSLRNIRTRKEQVFKEQIDQLKERYSILLLEENARLSEKCGENGGKSAA
NQIEVGACSHSESSEVETQLFIGLPDHMRCSNSWQQTS*
>evm.model.Chr3.1025 (DolMADS40)
MVRGKIQMKRIENASSRQVTFSKRRSGLLKKAFELSVLCDAEVALIIFSPKGKLYEFSSSSV
NKTIERYQRNNKELGSGKAAPQEVLQHLKEEAISISDKIELLESSKRKLMGECLESCSIDEL
QQIEKQLEQSLSSIRRRKTMLFMEKIKQLKEEERSLTEENAKLREQCCGMQSQLLSITLSA
AGGREIYDVETELFIGPPAEGRTRRPL*
>evm.model.Chr9.124 (DolMADS41)
MARGKIQIKRIENSTNRQVTYSKRRNGLFKKANELTVLCDARVSIIMVSSTGKIHEYISPAA
TTKQLFDQYQKTLNTDLWSSHYERMQENLKKLKEVNRNLRRQIRQRMGESLNDLNFNE
MHGLEEDIESSLKVIRERKYKVIGNQIETFKKKMRNVEEINRNLMHEFGAREEDPHYGLID
NGVDYEHALGFLNAGPRMLALRLQPHHHTLHSGIGSHLTMGSHLTTESHLTTHALLE*
>evm.model.Chr2.1166 (DolMADS42)
MGNGKIEIKRIENPTNRQVTYSKRRNGLFKKAQELTVLCDAKISLLIFSSKGKYHEYISPNT
TTKKIYDQYQKTLGIDLWNTHYESMQEQWRKLKEINDKLRRETGQRKGGDLSYLSFDEL
RRLERNMAASLTTIRDRKYHVIKTQTETCKKKVRNLEERYGDLLLKYEAKCEDTWFGLT
ADHGDYNSAVGFANEACNLYASRLQAVGHHDLHHGGAF*
>evm.model.Chr4.1456 (DolMADS43)
MGRGKIEIKRIENSSNRQVTYSKRRNGIIKKAKEISVLCDAQVSLIIFASSGKMHEYCSPSTT
LTNILDKYHKQSDKRLWDAKHENLSNELDRIKKENDSMQIELRHLKGEDITSLHYKELMA
IEEALENGLARIRDKQANLSSKLYLSIDQSYLIREWSITT*
>evm.model.Chr14.625.2 (DolMADS44)
MGRGKIEIKRIENPNSRQVTFSKRRVGLLKKARELAILCDAEVAVIVFSNTGRLFEFSSAGM
DRTLSRYSNRMNSSEADLVEPKEEKQESLEVNILKDEVKELKLKQMQLLGKDLTHLDLKE
LQHLEEQLIEGLSSLKDRKEQLLMQQLEQSRVQEQRAVMENEILRKQVQELCRFLPSNER
LGSPYHVSHPMERDDYPVKQDALSLEVDNCEVDLRLGLSSGVCQEEMKALAQKETQSSN
SGSQMSLL*
>evm.model.Chr2.769_evm.model.Chr2.770 (DolMADS45)
MAREKIQIRKIDNATARQVTFSKRRRGLFKKAEELSVLCDADVALIIFSATGKLFEYSSSSM
KEILERHNLHSKNLGKLEQPSLELQLVENSNYSRLSKEVAEKIHQLRHMRGEQIQGLSIEEL

QQLERSLEAGLSRVIEKKGGKIMQEINHLQHKGMQLMEEHERLRRQVMEGSNARKHGSA
DSDDMHYGEGHSSDSVTYNCNSTGPPQQDNDSSDTFLKLG*
>evm.model.Chr4.1127_evm.model.Chr4.1128 (DolMADS46)
MAREKIKIRKIDNITARQVTFSKRRRGIFKKAEELAVLCDANVALIIFSATGKLFEYASSSMK
DILGKYSLHSNKIESKDQPTLELQLENNNLVRLNKEVSEKTNQLRQMRGEDLQGLNLEEL
QRLEQALEAGLSRVLHTKGERIMNEIATLKRKGDQLIEENQQLKQKIIMLSKEKRPVANVA
IEWENNSIPEEGQSSESVTNVCSCSSAPPPEDYCSDTFLKLGLPYN*
>evm.model.Chr4.2220 (DolMADS47)
MYQNTRVEFESFNALMNTRLPLDLKPSFRWLAFLDGFFVPLNLARNRRFWFASAAHKLR
KQGIGGDGEREDSDQEDRQRDCQAGHLLKEEKRPFKKAEELSILCDADVALIIFSATGKLF
QYSSSSSMKEILEKYNLHSRNLEKLEQPSLELQLVENSNYHRLSKEVAEKSHQLRQMRGEE
LQGLNIDELQQLERSLEAGLSRVIQIKGEKIMKEIAHLQQKGAQLMEENEKLRQQIMEVSN
ARKHPGTEEGQSSESVTNICSNSARVLPDSESSDTSLKLG*
>evm.model.Chr14.2085 (DolMADS48)
MRSLSLSLNIVIPLWSNSLPIYYFKQKEDDLSFLSFKFFLVSFVFKCSACLDWWCRVILGEK
MVRQRIQIKKIDNVTARQVTFSKRRRGLFKKAHELSTLCDAEIAVIVFSTTGKLFEYSSSSM
KQVIERHNLQMANLVQHNQPSLELQLDNSAHAALSKEIEEKTRELSHLRGEELHGLSIEEL
QRLEKSLEAGLRRLLKTKGERLDKEITALNRKEAKLVEENACLKQQLLQMQMAIGGQTQ
EQGQSSESVINNGSPAAPQDYDSSDTSLKLGLPLRNCI*
>evm.model.Chr6.1988_evm.model.Chr6.1989 (DolMADS49)
MVRQRIQIKKIDNVSARQVTFSKRRRGLFKKAQELSTLCDAEVALLVFSSTDKLFKFSTSS
MEQVIERHSRENLGKLNDQPSLELQLESGPFAMLSKQLEDKSRKLSQLRGEELNGLNFEE
LKQLEKLVQGGLHRVLRAKGDKIEKEMIALKRKEARLMEENLCLKQQIE*
>evm.model.Chr6.294 (DolMADS50)
MGRESATEADREQDQQTSNLFQAQVRAVEEAHEISVLCDAEVALIVFSTKGKLFEYATDSS
MEKILERYERYSWAERQLVAPYHSQPPACWSMEYPKLAGRIEVLQLNIRRYVGEDLDPLSL
RELQYLEQQIETALKRIRTRKNQLMLESVSELQKKERALQDQNNLLVRKLKESEKTQGLG
QSRPSTFTMQPQLPLSQPLPTSLTIGFGGTFQARGGAVEDGTQAPLTSHSLPPWMLRQVHH
HQ*
>evm.model.Chr12.441 (DolMADS51)
MGRGRVQLRRIENKINRQVSFSKRRSGLLKKAHEISVLCDAEVGLIIFSTKGKLFEYATDSR
MDRILERYDRCSYAENQLTAANHESPGSWALQHAKLKARLEVLQRDQRHLMGEDIEHLS
LKELQTLENQLETALRHTRSRKNHLMNECITELQKKDKALREQIILLAKKIKEKEKEQAQ
QAPFEQPNPEPSSSSSGGQPLPFHSLNIGGAYQEAAGENGGDVEVAPVFQIQLPPWMLPHV
SG*
>evm.model.Chr13.921 (DolMADS52)
MGRGKVQLRRIENKINRQVTFSKRRAGLLKKAHEISVLCDAEVALIVFSHKGKLFEYSTDS
CMEKILERYERYSYAERQLIADPQTPGNWSLECTRLRSKIELLQRNHRHYMGHDLDSLTL
KELQNLEQQLDTALKHIRSRKNQLMYESISELQKKERAIQEQNNMLAKEIKEKEKTLAEH
SQWQQQNQAPNPSPFLLPQQLPCLNIGGSYQGEEPARRNELDLTLEPLFSCNPWMLCRMM
DNN*
>evm.model.Chr4.1452 (DolMADS53)
MGRGKIEVKRIESNTSRQVTFSKRRAGLLKKTHELSVLCDAQIGLIVFSNKGKLYEYCTHP
LSMGQIIERYLTVTGTRIPERDDREQIYNEFIRMKKETHNLQLSLHRYKGDDLSSAQYEDL

AALEQQLESSVIKVRARKEEMLEKENQEMYSWLMSNHIQKQQEQLDHHQQAMTELKLV
GGQQVLDQYTFFGEEQPSDILQHASVPPQLQPYRLQPTQPNLQEPSLQECSYGTDETLNLT
MMFAPNSCGLE*

Text S2： Protein sequences for the WRKY gene family in *D.oleifera*.

>evm.model.Chr11.469 (DolWRKY1)
ENGSIMQPKWSYYKCTHAGCTVRKHVERASHDLKSVITTYEGKHNHDVPAARNSSHVNS
SVPNTGPGQNACANASAATGPPHLHRPQPAQVHNGMVRFDRPPPLSSFGLPGRQQLGPPQ
GFSFGMNQHALAGLAMAGVGPPNQGKLPVLPVHHPYLGQQNPANEMGFMLPKGEPEAE
PPLSSSKDHLFTIKY*
>evm.model.Chr8.1140 (DolWRKY2)
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>evm.model.Chr15.1836 (DolWRKY10)
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>evm.model.Chr13.995 (DolWRKY12)
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>evm.model.Chr5.1550 (DolWRKY13)
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>evm.model.Chr15.515 (DolWRKY14)
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>evm.model.Chr10.865 (DolWRKY15)
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>evm.model.Chr12.585 (DolWRKY17)
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>evm.model.Chr14.111 (DolWRKY18)
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>evm.model.Chr5.1313 (DolWRKY24)
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>evm.model.Chr3.1110 (DolWRKY25)
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>evm.model.Chr5.1036 (DolWRKY26)
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>evm.model.Chr13.971 (DolWRKY27)
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>evm.model.Chr4.639 (DolWRKY29)
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>evm.model.Chr9.1792 (DolWRKY31)
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>evm.model.Chr2.515 (DolWRKY35)
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QLNNFLC*
>evm.model.Chr3.1635 (DolWRKY36)
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>evm.model.Chr6.833 (DolWRKY38)
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>evm.model.Chr14.1149_evm.model.Chr14.1150 (DolWRKY49)
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>evm.model.Chr10.1164 (DolWRKY50)
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>evm.model.Chr1.2020 (DolWRKY52)
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FDERILILPS*
>evm.model.Chr9.1589 (DolWRKY53)
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>evm.model.Chr10.1249 (DolWRKY55)
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>evm.model.Chr1.469 (DolWRKY57)
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>evm.model.Chr7.602 (DolWRKY58)
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>evm.model.Chr7.600 (DolWRKY60)
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>evm.model.Chr15.2073 (DolWRKY63)
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>evm.model.Chr1.470 (DolWRKY66)
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Text S3： Protein sequences for the NAC gene family in *D.oleifera*.
>evm.model.Chr3.762 (DolNAC1)
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>evm.model.Chr10.309 (DolNAC2)
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HIAP*

>evm.model.Chr12.50 (DolNAC4)
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>evm.model.Chr8.1206 (DolNAC5)
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>evm.model.Chr13.2400 (DolNAC6)
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>evm.model.Chr2.489 (DolNAC7)
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>evm.model.Chr5.873 (DolNAC9)
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>evm.model.Chr3.260 (DolNAC11)
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>evm.model.Chr13.591 (DolNAC22)
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>evm.model.Chr2.2254 (DolNAC24)
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>evm.model.Chr14.84.1 (DolNAC26)
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>evm.model.Chr11.1491.2 (DolNAC29)
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>evm.model.Chr9.2065 (DolNAC31)
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>evm.model.Chr8.1222 (DolNAC42)
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>evm.model.Chr2.1142_evm.model.Chr2.1143 (DolNAC46)
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ESSRSIGLKKTLVFYSGKAPRGIRTSWIMNEYRLPRHETERLQKAEISLCRVYKRSGIEDHS
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NLGLSKHSSYIGSLSSLSSSLPPASSMEDHERVFVDDLHGLMNFQQVSINHHHHQYNPSGQ
FATSQPQSESSAPVHMEPSSLQVAGFSDRLWEWNSITQGDKDYTSQFK*
>evm.model.Chr14.208 (DolNAC50)
MAIAATMSSSSQQDDPSLSKDDDVIDQHEHDMVMPGFRFHPTEEELIDFYLRRKVEGKRF
NVELITFLDLYRYDPWELPAMAAIGEKEWFFYVPRDRKYRNGDRPNRVTTSGYWKATGA
DRTIRGENSRSIGLKKTLVFYSGKAPKGIRTSWIMNEYRLPHHETERLQKAEISLCRVYKRP
GVEDHHHLSLPRSLLTRASSSKATQMDKMKNAATSQATMERSFQALGGPNNSQVADDRS
TEKMSETSGSSSTDVGLSKHNYNSYVAMAPMASMEQQSKQLLIPNCTTVFTGTNPNFNLV

PQNYNYNSVDELHRLVSYHQQQGNSIHHHHHQQQQHFYYNPSSQFSTLQPQPQPQPQPLP
QGALQAAFLDSRLWDWNAIDEGNKDYTSPFK*
>evm.model.Chr8.1171 (DolNAC51)
MDVEKNSWMEFASEQDDVPLPGFRFHPTDEELVGFYLRRKVEKRPISIELIKQVDIYKYDP
WDLPKASNVGDNEWYFFCKRGRKYRNSIRPNRVTGSGFWKATGIDKPIYSGNGESRQCIG
LKKSLVYYRGSAGKGTKTDWMMHEFRLPTDHDGKSTRHIDARNIAQEAEVWTICRILKR
NASNRKIMPDWREVSAKRISHANANSKACSTVESDSPTESYISFEAPANRPNEKNQFVNY
VPESYQMAAGRLNPVSQAPATVTYSNFFSPDMTEFIKYADWDELRAVVELSVDPFPA*
>evm.model.Chr11.525 (DolNAC52)
MEVEKLRTTMECSKDDRDRDGCGGGGGDDDVPLPGFRFHPTDEELVGFYLRRRVEKKPI
SIELIKHVDIYKYDPWDLPKGSNVGDNEWYFFCKRGRKYRNSIRPNRVTGSGFWKATGID
RPIYSSGGTCGCIGLKKSLVYYRGSAGKGTKTDWMMHEFRLPADHDTKSTKHIDVKNIM
TQEAEVWTLCRIFKRNVSSYRRCTSDWRSEATVRRGAVEASSKTCSVESDDQSNESYIDFR
TPAIRQNEKKHLVGHGYEANHMVAGQLNSISAAPSMASSYSSLNYGQEMNEFKYGDWDE
LRSVVEYAVDPLLT*
>evm.model.Chr2.1902 (DolNAC53)
MDEKIDNDKTDDIMLPGFRFHPTDEELVGFYLKRKIQRRPLPIELIKQVDIYKYDPWDLPK
LASTGEKEWYFYCPRDRKYRNSARPNRVTGAGFWKATGTDRPIYSSDGTKCIGLKKSLVF
YRGRAAKGIKTDWMMHEFRLPFVLDPASTKKILDKKLPTNDSWAICRIFKKTNSMAQRA
LSHSWVSPLSGIKAPSIFIQGATSTHFGSEIMSCTTETGPAIHLCCNNDLQQASTATFSHLDIP
SYNKHMNHIVCRTSPFSVPNGDIPTGFMFSPLEMSGPSNKNTIDVSSVLSALSPSPFGEVTE
ASESIDFEGPQQQFNGYSPQAIQERIGTREEDDMGLRKDPNTVPAYNQWGNIRAIGFPFSLP
SDLPDTWNPDLTWDSLPVPVRCQLIIPQIILYSITFIYRIHLTQDSRSRGLHQEYILFTVQFSYI
TSTTHIDVMFYLLSFLPSSSVFCTLSCFRLIILSVSANRNKVQVDWNRDFGGKNHKIVVEV
QC*
>evm.model.Chr4.1785 (DolNAC54)
MDEKFEMDDVMLPGFRFHPTDEELVGFYLKRKIQQRPLPIELIKQADIYKYDPWDLPKLA
CTGEKEWYFYCPRDRKYKNSARPNRVTGAGFWKATGTDRPIYSSDGSKCIGLKKSLVFYR
GRASRGIKTDWMMHEFRLPSIPETASTKKIIDKTLPPKWTITCATETGSTIQLCNNNDMHQ
GRTTSTAFPSVITTVYARKLRLWEDDMGMKKNPSAIHHNNQGGSIRSIGFPSSFPSNLTDA
WKPNLPWDSPPYPSEMSTTYSTKTCDA*
>evm.model.Chr13.262 (DolNAC55)
MDKRSDQTDKMDEIMLPGFRFHPTDEELVGFYLKRKVQQRPLSIELIKQLDIYKYDPWDL
PKLATTGEKEWYFYCPRDRKYRNSARPNRVTGAGFWKATGTDRPIYSSDGSKCIGLKKSL
VFYKGRAAKGIKTDWMMHEFRLPSLADSFPQKRLIDKAIPPNDAWAICRIFKKTSSNTAQR
AISHSCFSPLPDPTLDTFIQGSNSNQFTSENLPLMTNKSSSSAQFSSNSATDLQQSCITSFSPL
DIPISTMATKPPPSQVSISSVDLPSVYAFSCLDTSSSGPCRVDAPPMSMVLTMPQYSIMEDFC
KASHESIDQLSGLQDQHCHGGFSSANALSHEVQASAGHGEETSLMKHPNGAHLEDQWM
SIRSGAGNPYSLPLSMPAEYGLLWSSSPCPSEMSTSYSTNKCYT*
>evm.model.Chr13.2310 (DolNAC56)
MAASTLKFLAVGYRFCPTDYELINHFLRLKINGDEEAVSIIREVDIYKREPWDLAGMSLIPT
TDEEWFFFCAVDRKYQSGKRLNRATAAGYWKATGKDRTIKSVGRASVIGTKKTLVFHAG
RAPKGQRTPWKIHEYRAIGEELDGSKPGQPELEPEQMLRLQFSNAIHELPDGDDKVYTPFP
DVQTLLGSSCNLNYPISNDMGHVHMDQSGRNEQDDTFVDSILVTPDGYSCEDSGSRKNLA

VENQVSIYVNHNERNSVKYTQSFNESDGQVAPAQFDWSNRRKDPVPMAMCSRGYRTSIR
NEEYLRNNLVEFLGNCYVAPGGNQSIDMLSTSEESTSYGTGIKLRNRQVHNQPSGKNCWP
QGNAPRRIRLQRKLQVGSSCFSNKRVLSSKKQNHEMKPVEDKNEEARKKYPACVGPAIVI
DKFEQASFSNSNNVTEVAQQPGLDLKSGCGFPRGDDKEVPSTCLKASPLHSISSTMRKLRV
LAVLALFIVFGAYGFALGLKFIRDGTIFSLYK*
>evm.model.Chr1.149 (DolNAC57)
MEVLPLESLPVGFRFRPTDEELVNHYLRSKINSDNDAVSVIREVDVCKYEPWDLPDKSRIK
TTDDEWFFFCPKDRKYQNGQRLNRATVSGYWKATGKDRMVKSLKGRAVIGMKKTLVFY
TGRAPNGQRTNWVIHEYRATCKELDGTKPGQGSYVLCKLIKKHDEKLDGKSKKAAEEKV
DSPPTVESNTEDVKSEPVTPIPSAQGEKLPSSIDLVEHFDRRPQDARPEWPSSSSVSDDLAD
ETGDKKIMQPDPEIEELLKMFKVTYGDDKIFSPLHTHMLMDLEASCGLRYPDPNNDTGHR
HEGQYGSNEEEMDKFLDSVLISDEQSYENCDNYTNGAIENNTPRINLLQRVYVNETGSCS
ESEAEVAQAEFPGDFEGYGQIQQNIERESPVYMTMSTGTHQSSCISYGTDQRVLQSEFLGQ
NFLTTPSASAQLYENSPQESTNNNSISVESDVLETGIRIRTRQPPNRPIAEISKPQGSAPRRLR
LQKKLQVGSFCCTSFEGFSSNEKNDEAKLTVAKAGEDQEELVATVATASIVTQGISLSKSAT
DAEEVAEESSMNVKSGSCFPPGSDKGVSSAPRKISSSAYLLSVLVILGLAVALAGICYTFEF*
>evm.model.Chr3.1232 (DolNAC58)
MRGVSLQSLPLGFRFRPTDEELIRHYLRNKINGNDSAVQVIKEVDVCKCEPWDLPDMSVI
KGDDPEWFFFCPRDRKYPNGHRSNRATDAGYWKATGKDRMIKSRKTGTSKPGVIGMKK
TLVFHRGRAPKGERTNWIMHEYRATEEDLDGSSPGQGAFVLCRLFRKQDEKANHSKYDE
VEQTGLSSSTNKSSPDDNTSSDALQGTTTTYVQVRRQQEVTWRSDDITSNGHFCLGGCSS
DADNHSAEEAATEVHPQLAGDLVFEESTCEQVDCKVFSPLQMQMETEMGISIDALFCNDF
GIDHNGTQFQDGTGEQDVSFDLLELHQNNVEYPCEESTIFTTSAVCNDTKMFGHTPLLTH
GLPGNSYMEPSEIYHNMALEQNQTFLTYCQGQSSSDAPNHGMEDIGALYDNSVRQNVSS
ADSIIAPFYGSLTNLEASNGQSSVANCGCEVGETGIKIRTRQPVNRSHPKVVITQGHAPRRI
RLETKLSLVSASSCKLVDSSSCVDDEGHGAESTSEAREVGVVSDEADSNHPSVVDHNCKT
GSQVNRETSQVLNARHRVRTKQDGETGCCQIMSRAFSGIPPLLSRRNISMLHAVGICLIAIL
FIVSIGMWRCPSIELSQVK*
>evm.model.Chr15.1234 (DolNAC59)
MEIGASAVMDGEEDYIKHLPPGFRFHPTDEEIVIYYLVKKVNDSSFTAAAIGEVDFNHCEP
WDLQQKSKMGEKECYFFCRRHRKHPSATRANRITEAGYWRATGKDKEIYTTGKKSQLVG
LKKTLVFYKGKSSKGEKTDWIMNEYRLEPKFCHSNFPTKPKVYFHYIHVDLPSGFRFYPT
DEEIVCHYLNQKVINNNFTAAGIGEVDFNRCEPWDLHRTYVQTESIKQGCERTGRRKGTG
RDKQIYEKGKSSELVGMMKRLVFYKGRAPKGEKTNWVVHEYRLEGKFSYFNFFTKGQW
VVCRVFEKNSTTGIKKSSDGQVKGMNRG*
>evm.model.Chr1.2755 (DolNAC60)
MQYDGAKSLIQSENEWFFFSHCGRKYPNGSQSKRATVAGNWKATGKERNVKSGSDLIGT
KRTLVFHIGRAPKRERTEWLMHEFHMTGQSQDSLVVCRLRKNSEPRLNYMPREASSSQNL
LTAENNNNFSLSEACAEQSSLFKGAKLVECCSKDCSNSNNSRSDEQPIDAGSESDQKPKDE
FSQPGFTHQDCDDDECYAEILKDDIVDMGKSLLPRTPDLLPVVADKSEDERWSQQREQTC
RHMSFLSKAQQCEESD*
>evm.model.Chr13.1235 (DolNAC61)
MGEGSRREMELSIETSSMFPGFRFSPNDEELISFYLSKKLQGCDECVEVIAEVDLCKCDPW
DLPAKAVIQSDNEWFFFSPRGRKYPNGTQSKRATESGYWKATGKERNVRSGSNVIGTKRT

LVFHKGRAPKGERTEWIMHELCMNGMSQDSLVVCRLRKNLEFRSNDGQSSSSGRQLQTE
GDGNVNSLEADVIEQSGIPEGAKAVESCSKEGSSSYTSHSVQEQTDSGYESNQNFTRECSE
PGSSSHQVGDDEYCYDDFADIMEDDIVTLDGSLLAPTPNLLPAAADKKSEDQRPPQERVQ
EAGNFEGGSANRRIRFMRQTPETGNFELVEVDASNRHSIEELTRPSPERPPKCILSLVSDRG
VSRSSKRSLVFIFLGLLLVFVSLLELPWQRKGFKYPSFL*

>evm.model.Chr7.1563 (DolNAC62)

MDNRLGLAPGFRFYPTEEELLLFYLPKKIEGKRRDLELVIPVLYIYHFNPWDLPQQAGDLC
GKDTEPWFFFIPGLDHHQHRQDHHDHDHAEKESGRAPGRQNRLTASGYWKATGNVGYV
YSSSSSSSSSIMSNVVRIIGEKRTMVFYMGRAPCGIKTQWKMNEYRAIDEQALTTTSTTATP
KLRREFSLCRLYTKSKSSHAYERRPPGVAAARKVVPRQLPFYGPGATTSHYHRNVSEMDQ
RTALLQERENNYNEINRCLTTTAAGLVLSDHHHGHWNMASDNIDAVWDLKHLDCLLGED
*

>evm.model.Chr7.1561 (DolNAC63)

MDQDQPPGFRFYPTEEELISFYLQHKLEGGRQDLNRVIPVLYIYQFNPWDLPDFAGERCRG
DSEQWFFFIPRQEREASGGRPNRLTISGYWKATGSPGFVYSSGNRIIGVKRTMVFYKGRAP
AGRKTEWKMNEYRAIDGEASSSTNIAVPKLRQEFSLCRVYKKSKCLRTFDRRPAVAAPNL
APRADEASALSHPSHAACSREIGTNSPGESSSSGDHANNPCQTAGSAGSWDFASADIDEPM
WDWDQLNWF*

>evm.model.Chr15.1615 (DolNAC64)

MEILAYLVNESVYIYGTCKSRKLRAENKAEKIALQRQVQLMENISPTVPAGFRFYPTEEEL
VSFYLQNKLRGTRQDLDRVIPILYIYHFNPGDLPQFAGELCRKDPEQWFFFIPRLEKEARGG
RPNRLTTSGYWKATGSPSYVVYCSNNRVIGVKRTMVFYIGRAPTGRKTDWKMNEYRAIEG
EVSSSRNAIPKLRQDLSLCRVHRSSTSLRAFDRRPSSTFLHVFDRQPQAAVAGPDPAMAHQ
THYSGEAITSHDQTYLMMESASLPERFSLEHVGNDPSHQMLIRDNWDMFFEDQPLWDWE
QEQLN*

>evm.model.Chr13.1250 (DolNAC65)

MEPQPPGFRFYPTEEELVSFYLRNKLEDNRPDFNLVIPTLNVYELDPWHLPKLSGELCRGD
TEQWFFFSPRQEREARGGRPSRTTASGYWKATGSPDYVVYSSVDNRVIGLKKTMVFYKGKA
PSSRKTKWKMHEYRAIEPQSTSPLGATDPRLRHEISLCRVYVVSGSFRAFDRRPFGAEASE
TSCSQQQVHCNNGAKTLLNSSQAAQTAEKTSSPESSKSEDDHLELPDANFGMVTEEEPLW
EWEQLNCLY*

>evm.model.Chr1.2743 (DolNAC66)

MASSFVEEPPTGDMPPGYRFYPTEEELVLFYLRNKLAGKRPEIDRVIPVVHGIYQLEPWQL
PKRSGELCRKDTEQWFFFTPRPEREVHGGRPCRTLASGYWKSSGSPDYVYSSSDGRVIGL
KKTMVFYMGKAGSGKKTKWKMNEYRAIETEEEAAIPRVRHELSLCRVYVVWGSFRGFE
RRPVGAEDVGAVRRRVHGYDGSATRASQESKRVEKAGSSESSYLGEEEFDVAETKPGLAA
ASNGGLVLDLEPLWEWEQLNVI*

>evm.model.Chr12.666 (DolNAC67)

MAGGMDKKKYPIGPEHYTQYEEVGIGVSASVHRLLCVPLNEIVAVKILDFERHNSDLIVLF
WFSREVFPWFQEQILFDCGGYKFDPTDYEALYYYLLPKVFGQHIKPWLVSDVDIYNYQPQ
NLPGFNAEASSFYFTPRELKFSKGSRPSRSTRDGKGFWKMTSKITKIKDLSGLPIGRKSTLV
YHLKGDDTKQKANKTDYIMQEYVLEKSLGSVGPTLGGGEKVCFQ*

>evm.model.Chr9.1962 (DolNAC68)

MQCIGVKKALVFYQGNPRKGMKTDWIMHEYRLLDDNHTHPRIKGSMRLDEWVLCRVRQ

KSNNPKQIGTCSEDISLNGIHQPIFPYSNDAQIYKHEQEEEEDLKMEHSLRNYLNSEEEDQP
SKLISKSTTDHRSNCINSPCNEEEMVAFKRTISVVSFGQAFPLSPSERLHSDAVPADNMEDS
SIFQICYLSNCV*
>evm.model.Chr1.1701 (DolNAC69)
MEENKTAMELPCGYKFSPGDKEIVKYFLKQKILNEPLEHDTIPCVDLECYDDPDHLPLRDF
KNKAENEWFFYTSRPKRKPFTKNGCWREHKEEGVLDGQELVGFVQKFDYYYNLVNPPEE
RKFEWYINEYRIEPSVMEACQLDETTKQKVLNLVVCKVFREEIETTMDEEVRNCQSSDEEI
EHE*
>evm.model.Chr4.961 (DolNAC70)
MLSLSSGSAFMGESRIYKSTSLSLPPGCRFYPSEEQLVTFYLTHKNNDDRRYPFDVITDLDL
YSYDPFGLPEAACFRFGRGGMRRHWYCYTAPVSRVSGGRGRKRRAGGGYWRSAGKIRE
VVAGGAEAGKFVVGTRKSFVFYLDESPGAAVRRTNLAMYEYALIGHHKASFVVCRVFLR
SCCRNRLVSESVASVRDVGIQREATVLSDILRKSSTMIGPPVFRPR*
>evm.model.Chr1.255 (DolNAC71)
MLLGYKFHPTNGELVSGYLLGKVTQNSLLTKSILIQERNFNDEIELSDIFATVKDDTKLYFF
THLKKKTEKSLRINQMVGKGTWRGVDKGMDIFDD*
>evm.model.Chr1.254 (DolNAC72)
MLLGYEFHPTDGELVSDYLLSKVTQNPLLAESILIHERNLYDEMELSEIFAIAEDNTKLYFF
THLKKKIEKGSRIDRTLKDYLLCMIKRKTSHLSPKWCRPMENEDFHDNHRDCLQNKDDEI
NAGKDELSVHDCMNCNGRIALPGSCFEDINNAAAATPQEKKRVLEPCMRIRSRFLSTMSH
C*
>evm.model.Chr6.788 (DolNAC73)
MACACPRAFGSAPTDEELLVQYLKPKAIPPGRRGTSSARRRPSTRLGTGPTGPPVLGTGRP
LEPTSKLWFQEQGVVGMKKTLVFYRGKPPTGTKTDWVMHEYRLGPAGPKAIATLALSLN
SSKPVENWVICRIFLKKRALNRNEEEIRKYKNFGPFRPVFYELLANGRTDLKLGLPAAASV
PAEASSSGSSGVTHISAHDEPNDHEEGTSSKSFP*
>evm.model.Chr4.1919.2 (DolNAC74)
MAGRSWIIDCKGIATKVKNAGISPGNQIKDCGAKRECPKCDYCIDNSDVSNEWPGLPAGV
KFDPSDTEILEHLAAKCSVGNSKPHMFIDEFIPTVDKAEGICYTHPEDLPGAKKDGSIIHFF
HRTTNAYSTGQRKRRKIHNQHSLIKEDVRWHKTGRTKPVIENGVQKGFKKIMVLYRISKK
GSKPEKSNWVMHQYHLGNEEDEPEGHYVVSKIFYQQHKESDDNDASQVIGDPDMGTIRT
SPRTPRSNTPNPPRPGKSVSCDDVADDYAPKLSPQEAEFSRETSHPCSATQFKDDLDNSTW
LAGESQPLHENCGDSLLCNEIFSPCSAPDASILNGGPGFSCQTNDIPGVDRNVTCGIADLEN
LELDTPPDFELAVSFFLWSIFLSKHSLIRLVRCAIPDPFAGSTVCLSGQYF*
>evm.model.Chr13.1056 (DolNAC75)
MAGPSWLVDSNRIATKIKSASSLCEPGKVNWKSNPSRPCPNCRYIIDNTDVTQEWPGLPRG
VKFDPSDQEIMWHLLAKVGVENMKLHPFIDEFIPTLNEDDGICYTHPQNLPGVKQDGSFS
HFFHRAIKAYNTGTRKRRKIHGDDFGDVRWHKTGKTKPVILDGVQKGCKKIMVLYVSPV
RGGKSEKTNWVMHQYHAGTGEDEKEGEYVISKVFYQQQVVKQTDKFENDLPEGADMM
ITKVDPVTPQSVTPDPPRTERRFSDFDPGQMSTTTCIDPSAQHATRHVEDEVLAEKPKHQA
PIMAENYADPVADNNDNQIGEDQKWWDSESQNLLDSQQLVEGLSLCDELLQSQSPSRDA
NENGELKVKACLSDYAQLGPEHLKKDLEECQDLVFDPANIELDTPPDFRLSQLEFGSQESY
LAWGGSKVVD*
>evm.model.Chr12.1103.7 (DolNAC76)

MQSLRSISSVDPSSALVVATSSKQSRYGFDFIDLTIIFLASRDWVGLPAGVKFDPTDQELIEH
LEAKVEAKDSKSHPLIDEFIPTIEGEDGICYTHPEKLPGVTRDGLSRHFFHRPSKAYTTGTR
KRRKIQTECDLQGGETRWHKTGKTRPVMVSGKQKGCKKILVLYTNFGKNRKPEKTNWV
MHQYHLGQHEEEKEGELVVSKIFYQTQPRQCNWSDRSGTGAGEGSVEPNSKRDSGGSGS
CSSKEVITQRDELSAAGVGGAMSSYSPMDIQQLKADHFGFAPFRKGFDEVGGVGEASTVR
EVQASGTCEERDMHEHQRPHHVSSHHHHHHLHHQISTATFNICRPSLPISTIIPPPNSLHQAS
IILDDDSFHVPRMMLQNESFQQQQQQQQQEQQLQQHHHKLVGRSASGLEELIMGCTSTD
HHIKEVSVYELFDPEIHNPLVNYVSPYQLSIYREKEK*
>evm.model.Chr5.68 (DolNAC77)
MNKGSSQLGSISSSDLIDAKLEEHHSVDPRAKHCPGCGHRLEAAKPNWVGLPAGVKFDPT
DQELIEHLEAKVEAAGDSKSHPLIDEFIPTIEGEDGICYTHPEKLPGVTRDGLSRHFFHRPS
KAYTTGTRKRRKIQTECDLQGGETRWHKTGKTRPVMVNGKQRGCKKILVLYTNFGKNR
KPEKTNWVMHQYHLGLHEEEKEGELVVSKIFYQTQPRQCNWSDRSTAAADGSSEPVVHD
NSRRDNSGGSGSCSSREVVITQSPSDELSAAAAAASISSFCGIDIQQLKADHFSFDPFRKSF
DEVGVVGEDPTTVMAVAAPGNCEQHHHHHHHHHHFEQLATAGFHISRPSQPISSVIAPPPL
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CTSSTDHHDHIKEESAIRSQQEAEWLKYSTFWPDPDHQDHHA*
>evm.model.Chr11.739 (DolNAC78)
MTWCISYCSDEPVIVRKTQSSCIETCPSCGHQIKCQEKAAGIHDLPGLPAGVKFDPNDQELI
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GTRKRRKVQTDMNGNETRWHKTGKTRPVFIPGGALKGYKKILVLYINFGKKKKPEKTNW
VMHQYHLGDNEDEKDGELVVSKVFYQRQPRQCGSVLREPSPGNTSQVKEHGHVVEFYK
SSISFDQRGNGVNRRQPEF*
>evm.model.Chr9.1963 (DolNAC79)
MRWCNDSDDQRAIQIISPSSGETRTLIDAKPDQTRFITCPSCGHNIELHDQGGIQDLPGLPA
GVKFDPSDQEILEHLEAKVSSDARRLHPLIDEFIPTLEGENGICYTHPEKLPGVSKDGLIRH
FFHRPSKAYTTGNRKRRKVNTEADGSETRWHKTGKTRPVFVGGAVKGFKKILVLYTNYG
RKRKPEKTNWVMHQYHLGHNEEEKDGELVVSKVFFQTQPRQCGSNIKDSVLIENSHEND
EDSVIKNTAYLEYYSPLISYHIGGQNGESPPQLIPNLVLEGDGSSFIHSSTQQCKQREGT*
>evm.model.Chr12.1857 (DolNAC80)
MRWCSSSATDSEDQRAVALISISSSSKDHRDGKSKQTRLITCPSCGHTIHLPVPDQAGIQDL
PGLPAGVKFDPSDQEIIEHLEAKVSSNAHNNKLHPLIDEFIPTLEGENGICCTHPEKLPGVSK
DGMIRHFFHRPSKAYTTGTRKRRKVLTEADGGETRWHKTGKTRPVVAGGAVRGFKKILVL
YTNYGRQRKPEKTNWVMHQYHLGDNEEEKDGELVVSKVFYQTQPRQCSSSGLKHTPIED
KKRSRNNNNNTNNFDQTAAGNTAYVEYYTNPPLNISYHDIGSQSRVSSAQLFPNLQVLQG
DGSSFIHLLSNGSKGKVLERK*
>evm.model.Chr9.21 (DolNAC81)
MYTPIPARHPRNIRSYWSDAELCMFLVSVAEGLAAIPENVKADVNPYQYLPSNLPENVTA
DVNPYQCLPSDLPDGIWYLMRSERKQNSEHGFWKATGEACEIFTNSSVIGWRTTLEFYKG
QAPHGRKTNWVMQEYKITEKSLHINSNSKESNLLCRVFPINETSPNQEGQNKLGVAEIAG
GNDSHPKSSSLVPNTSSTAVPGRMNESQVRRRDENTGPPTAAREILSEPLGNVPVNEYILG
GDFLELDDLADPESQSSCSDNTSCLSLTSDDYFDSQALLKDIGDEEHGRDDNCKFFIAKYA
KPNEVVICAPTSGSPIGSEGNKKPPAKDIGKQFLDGRVLENAIERQKADKGIEGLELEV*
>evm.model.Chr7.1603 (DolNAC82)

MALRGGVALVFTLLVFTTCSAQRIHRRSFPDGFVFGTASSAYQYEGAVKEGGRGLTVWDK
FAHSFGKVLDFSNADVADDQYHRYQEDIQLMKDMGMDAYRFSIAWSRIFPNGSGEINEAG
VNHYNKLINALLANGIEPYVTLYHWDLPQALEDRYKGWLHSNIIKDFTKYAETCFEKFGD
RVKHWITFNEPHTFTIQGYDVGLQAPGRCSILLHLFCRAGNSATEPYIVAHNVLLSHATVA
DIYAKKYKLKQRGSVGISFDVIWFESATNSTNDIEATQRAQDFQLGWFLDPLIFGDYPSSMI
KRVGSRLPRFTKAESALLKGSLDFVGINHYTTFYAQQNTSNIIGGLLNDSLADSGSTTLPFK
DGKPIADRANSIWLYIVPQGMRSLMNYIKHKYGNPPVIITENGMDDANNPFISIKDALKDQ
KRIQYHNDYLSNLLASIKEDGCNVKGYFVWSLLDNWEWAAGYTSRFGLYFVDYKDKLK
RFAVRDRFDVKLSPAASPPPSESKTRGLVMASSSRSSPLVHGEKRKIEEEKQEQKSQTTCKD
SGMDELEELVLPSGYRFSPTDPELVVHYLIKKIVGRGLPANIIKHIKDLYKYDPLELPISEFK
YGNENEAYFYTHIEQKDSHGSQQVLDTPSGYWREIDLGDFEVFYGWEIVGLKRSLAFYEG
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ERNSNLTSNSIDNEILSEIEDHSDADRR*
>evm.model.Chr2.499 (DolNAC83)
MELQAINRGGILFFPAQKWKNHNRFISNVKAVGHRLILKYTGSRRCSSKKFGTSICCSIGV
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QNFRTASVDDIASVHARAYVSGLEKAMDQAVEQGIIFIDGSGPTYATATTFKESLTAAGAGI
SLVDSVVAASKIRREPPSAFALIRPPGHHAVPKGPMGFCVFGNVAIAARYAQRVHGLKRVFI
IDFDVHHGNGTNDAFYDDPDIFFLSTHQDGSYPGTGKFDEVGHGNGEGTTLNLPLPGGSG
DIAMRTVFDEVIVPSAQRFKPDIILVSAGYDGHVLDPLANLQFTTGTYYMLASNIKQLARD
LCGGRCVFFLEGGYNLSSLSYSVVDSFRAFLGEPSLATKFDNPAILYEEPLAKGKKMKMM
KDDGGVQLPPGFLFEPTDEELILHFLYPKVGAASRPIAHPNIIPDLLHHLFPCDPWQLHGRA
FLTSHNRWYYFYGRKMDAAPEEPTETGYWKEVDSEEAVVVANSGNKAVIGLKRNFEFYV
NDGELAAGRGGGGGGGLKTDWLMQEYSLLCCTTTTTTAATIRRANHQHHHQLGTNSKL
VLYRAQERRGGISQDSDDELSSLDEDFFSSLDDNIGDDEIIS*

Text S4： Protein sequences for the SBP-box gene family in *D.oleifera*.
>evm.model.Chr13.521 (DolSBP1)
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Text S5： The sequences of miR156 and miR157 and their target genes of DolSBPs.

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>evm.model.Chr13.521 (DolSBP1)
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>evm.model.Chr14.920 (DolSBP3)

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>evm.model.Chr7.171 (DolSBP4)
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