

# A Genome-Wide Identification of the WRKY Family Genes and a Survey of Potential WRKY

## Target Genes in *Dendrobium officinale*

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## Supplementary method 1

### Completing the 3' of DoWRKY genes

Seedlings of *D. officinale* (about 8 months after germination) were used to extract total RNA with Column Plant RNAout2.0 (Tiandz Inc., Beijing, China) according to the manufacturer's protocol. The first cDNA strands were synthesized by reverse transcription PCR (RT-PCR) using an M-MLV Reverse Transcriptase Kit and used as templates for gene cloning (Promega, Madison, USA). The two specific primers were designed for completing 3' ends (see in the follows table). Then a SMARTer RACE cDNA Amplification Kit (Clontech Laboratories) was used to generate b 3' RACE-Ready cDNA according to the manufacturer's protocol. The 3' ends products were purified by using the Gel Extraction Kit (Dongsheng Biotech, Guangzhou, China). The purified fragments were cloned into pMD18-T vector (Takara Bio Inc.) and sequenced at the Beijing Genomics Institute (BGI, Shenzhen, China).

Primers used for completing the 3' of *DoWRKY* genes designing by Primer 5.0.

Primer names	Primer sequence
DoWRKY4F1	5'-ACCCTAAGATTAATAGGGTTG-3'
DoWRKY4F2	5'-GAAGAAGGTAAAGCACGAA-3'
DoWRKY24F1	5'-GGTGGGAATCTAAGCTGTGT-3'
DoWRKY24F2	5'-CAGATCGTGATGTTTTGG-3'
DoWRKY26F1	5'-GAAGAAGGAGAGCAGGCCGA-3'
DoWRKY26F2	5'-AGGAAGTATGGGCAGAAGAA-3'
DoWRKY28F1	5'-TCAGCGATGGACAATATTGACC-3'
DoWRKY28F2	5'-CATACAGGGATATAAGTTTC-3'
DoWRKY35F1	5'-GCCGTCGACTTTGTCTGCTC-3'
DoWRKY35F2	5'-GCGGCCGGTCTCCCAGACGA-3'
DoWRKY48F1	5'-AAGGGAACGTTATTAATGGCG-3'
DoWRKY48F2	5'-GTCGACCGAGATTTGCCTTTC-3'
DoWRKY54F1	5'-GCCGCGGTTCGGTGCAGAA-3'
DoWRKY54F2	5'-GTGGGCCTGGCGAAAGTATGGG-3'
DoWRKY68F1	5'-GAGAATGACGAAGTGAAGA-3'
DoWRKY68F2	5'-ATGATGGGTTCAAGTGGAG-3'
DoWRKY70F1	5'-CCGATGTTGGTGGTGGTGGGAG-3'
DoWRKY70F2	5'-GGCGGCCTGTCGGGTCAACG-3'

DoWRKY73F1	5'-ATGGAGTCAAGGCTCATGTT-3'
DoWRKY73F2	5'-ATATGCGTGCGAGCTGATCC-3'
DoWRKY75F1	5'-CCGCTCTCTCCGACCTCCAAC-3'
DoWRKY75F2	5'-GAGGGTGCAGTCGTGGACGA-3'

**Supplementary txt 1** AtWRKY protein sequences used for alignment are as follows:

AtWRKY4 (AT1G13960.1), AtWRKY61 (AT1G18860.1), AtWRKY71 (AT1G29860.1),  
 AtWRKY14 (AT1G30650.1), AtWRKY6 (AT1G62300.1), AtWRKY56 (AT1G64000.1),  
 AtWRKY64 (AT1G66560.1), AtWRKY9 (AT1G68150.1), AtWRKY57 (AT1G69310.1),  
 AtWRKY36 (AT1G69810.1), AtWRKY66 (AT1G80590.1), AtWRKY40 (AT1G80840.1),  
 AtWRKY3 (AT2G03340.1), AtWRKY59 (AT2G21900.1), AtWRKY15 (AT2G23320.1),  
 AtWRKY17 (AT2G24570.1), AtWRKY60 (AT2G25000.1), AtWRKY25 (AT2G30250.1),  
 AtWRKY21 (AT2G30590.1), AtWRKY35 (AT2G34830.1), AtWRKY33 (AT2G38470.1),  
 AtWRKY55 (AT2G40740.1), AtWRKY43 (AT2G46130.1), AtWRKY46 (AT2G46400.1),  
 AtWRKY23 (AT2G47260.1), AtWRKY58 (AT3G01080.1), AtWRKY70 (AT3G56400.1),  
 AtWRKY68 (AT3G62340.1), AtWRKY22 (AT4G01250.1), AtWRKY47 (AT4G01720.1),  
 AtWRKY42 (AT4G04450.1), AtWRKY41 (AT4G11070.1), AtWRKY28 (AT4G18170.1),  
 AtWRKY31 (AT4G22070.1), AtWRKY29 (AT4G23550.1), AtWRKY53 (AT4G23810.1),  
 AtWRKY7 (AT4G24240.1), AtWRKY34 (AT4G26440.1) AtWRKY20 (AT4G26640.1),  
 AtWRKY18 (AT4G31800.1), AtWRKY13 (AT4G39410.1), AtWRKY62 (AT5G01900.1),  
 AtWRKY26 (AT5G07100.1), AtWRKY75 (AT5G13080.1), AtWRKY72 (AT5G15130.1),  
 AtWRKY38 (AT5G22570.1), AtWRKY30 (AT5G24110.1), AtWRKY50 (AT5G26170.1),  
 AtWRKY74 (AT5G28650.1), AtWRKY24 (AT5G41570.1), AtWRKY8 (AT5G46350.1),  
 AtWRKY48 (AT5G49520.1), AtWRKY27 (AT5G52830.1), AtWRKY2 (AT5G56270.1),  
 AtWRKY51 (AT5G64810.1), AtWRKY67 (AT1G66550.1 ), AtWRKY63 (AT1G66600.1),  
 AtWRKY54 (AT2G40750.1).

## Supplementary txt 2

The amino acid sequences of 63 DoWRKY proteins as follows in FASTA format.

>DoWRKY1

MASSSGSVEASSASFSFASPYEASFSDLLAGEGSANDRLTGLTVRFGDRGGGGGGIPKFN  
SIPPPSLPISPPPISPPSYFAIPAGLSPAELLDSPVLLSSNNILFSPTTGTFFPSKTFNWRGINSGSN  
DNEGREENRAYYDFSFQNKQRSSFQQQRDAFKGSQQPWNYPQESNIKTEIPAANSSEMQ  
TLQLNTQVNSNNNVTTTEQRKSDDGYNWRKYGQKQVKGSENPRSYKCTFPNCPTKKKV  
ERNFEGQITEIVYKGTSHPKPQSTRNSSSSSQPVHPLAIVAVGSAASEHSHGGRLGASNL  
DSVATPDDSSVSFG EEDVDLSSHKSNLAGDEFDEEPPDAKRLRREGENDGASAAGNKTVR  
EPRVVVQTTSDIDILDDGYRWRKYGQKVVKGPNPRSYKCTTMGCPVRKHVERASHD  
LRSVITTYEGKHNHDVPAARGSRPPEDNSHGTTTAIRPSAISAAPRNSLFGQRLDANFQSY  
NGPFTLDMLSTQRNYGSNYMNQQQLKTKEEPKDDMFLESLLI

>DoWRKY2

MESHSLSLDLTIGIAKQSILQEPSPPPCLQEELKRVTEENMKLTSMLATMCESYDALRAQLI  
DMIGPTAAVASSEGARSSSPSAKRKSTESAGDAANSVSSANSCKKAKEEGSKPKIWKLYA  
RTDPSDSSLVVRDGYQWRKYGQKVTRDNPCTPRAYFRCSFAPTCPVKKKVQRSADDQCLL  
VATYEGEHNHYQSSAAEVENAVSRKTAGTADGVGASGAPETKDSRGEREEARQPELRERL  
VKDMASSLTKDSNFTAVIAAAISGRFLGISTAQEM

>DoWRKY3

MEKSHSEDLKMLIDVLREGNGHVMELEAHLYNYETFSSSETCLLLSSKLQSTFATAIAIMKL  
MEQRGLPSLPSSATDSPRSQSSERTFKEQERREMCKKRKSLPRWSEQVKACSGSAMEIPL  
DDGHSWRKYGQKDILGAKFPRCYRCTYRHSHGCVATKQIQRSNNSSSLFDITYRGAHT  
CNHGFQKPSPLTNEQIIHQNSFKVKTEALSSNEQKSESSPYFSFPLTPKSLKLESNVFSSS  
SNPENYEGLDLEIADIVCASNSTTENSEMLKIDFGVEQFVFDSEFSDFY

>DoWRKY4

MLPSTAEISLREGLVESHEVPMDQTSHIRFSFQSSSLPPLTCHPLGIIQNRLFASSTDVVAEAS  
SSSSPHLKETALLSSVPLRASEAASTLLRSTTNPCWSWSEETTRGPRATVDTHKNIGSMSD  
KSIHENLSNYTVNPKINRVGNL SVGAMRMKVKARRKVREPRFCFKTMSEVDVLDDG  
YKWRKYGQKVVKNQHPRSYYRCTQDNCRVKKRVERLAEDPRMVITTYEGRHAHSPSH  
DEDDQSQPSSMRSQQLSTSFFW

>DoWRKY5

MMESGTDMMVSELYQIHELARKLNENLELSHYEICRSLAKEIICAIEKTICTAKSSSTGETE  
LAFFNGREFHVDRLNKEFSTDNEPKKSKKRKIMATGTSQVRVSSDPGADMPPDDGHSWR  
KYGQKDILGAKHPRSYRCTHRKTQGCAAMKQVQKTDENSSIFDITYLGTHTCFISPQHI  
ASKTSYYNPQQSLDQQNSLVHLGFETNLKLTSSDLNKDPTSSFSFPSTPIEGMENSEN  
VLCSSQRTECCYGVNLSSALMSPTSYESNCFTWPSCEMSSEVDYALTEIISASNSVA  
DLPVMDVEFMRDYEEMDAEILFDTSIFFE

>DoWRKY6

MASSSTPPIIDKEEEANEKNIAEERNDRMMAIQEDAYNWRKYGRDWEHYIHNKMFRTYL  
RCKNKNCKARKKVDWPPNDPNNKIISYEGDHNHIINEEQNRVVIPEDDYKWKICGQQNIK  
RIQKKRSYFKCVNKNCKERKKVDWPPNEPNNIDISYEGDHNHRALATGHSENEEVGIEAN  
ENDLTTLRLGPART

>DoWRKY7

MAGMDDDVSADFDDWLPSSISPKTLFSDDSSQKTNDGSLSEPRKPGVVVNDNSNQDCATGIQ

VSEEYSTELENNTYNVPKSSTRGALSKRIAGRAGFGNLTLDTSQIRKTSFSDSPSTNDRSPLITIP  
PGLSPTMLLDSPNLVSNLSLIEPFRSTDKMDCMVCDNIGAAINGDNIDHATEDIDPPLPSFKL  
PLLPFSCAESTPALSHPQPNPQDGFSTLSKEKGSTDTLNSNHNSNHVPILDDPQEGDDGP  
KGEFTSAFLVAPTKDGYNWRKYGQKQVKGSEFPRSYYKCTYPNCEVKKKVELSQDGHAT  
EIIYKGTNHLKSSIPLSHSGNDLQIDELDPNQYASVPIEQCEQSSPYAETPDGADASSFLSN  
DDEDEQETHGSASPD RSDSDGETESKRRKLDACALEMNAASRAVREARVVVQTTSEIDIL  
DDGYRWRKYGQKVVKGPNPNRSYYKCTNPGCKVRKHVERAAYDVKSVITTYEGKHS  
VVPTARTSNQASSSTASIITTAASPSSCLLQKKA EAARMADCLGRFDTPAPLPGFGLPSRDQ  
QLGPAVNFYSYARALQGFNPNVAMAGLGNQTFKMSVLPPLPAYMSQNHPGTVGYVVQTI  
MAKEEPAVNSRPPVPGNLSVYHLSRRPMGP

>DoWRKY9

MSENGGAVSSAAEVNRPSISLPPRSTVESLFRGGPAEASPGPMTLASSFFEPSEYRSFSQIL  
AGAMVSPSVSTTAFDARGGGGRERASLNLEHSRPMNLMVAPSPLFTVPPGLSPGGLDSP  
AMFSSNLGHLGMSHQHALAQVTAQASDSHSQMSQAEPSSLSSASLIQPISAMNMTSSQ  
PMLFITSGKNIHNTESAFASHSDQRSQPA AIVADKPADDGYNWRKYGQKQVKGCEYPRSY  
YKCTHPKCPVKKKVERS LDGQVTEIIRGQHNHERPIPNKRSKEGAAEVNGNTYPDNS  
LQQDDHLNFRSSDGMVGLSKKEREVSEQLSGSSDDEELED EEAEDGEPEHKRRNLETR  
VIESSSHRTVTEPRIILQTTSEVDLLDDGYRWRKYGQKLVKGNPHPRIHFRKLSNLMLYSL  
RKMYS ELAYS

>DoWRKY10

MSGEKL GELFQHDSTIFDPYSLFSLRSGGPQGLESGLPQFSGFLDYLSSTDFGFTSSLSQE  
PFGLIGDRHKVCKAEPRATENVISSVFAGGGTRAMTANSSVSSSTEAA GEEESDKNEKNE  
EKEQEEED EENKDVKGVDGAD EDEKAKTVSKSRKKGEKRQRQPRFAFMTKSEVDHLE  
DGYRWRKYGQKAVKNSRYPRSYRCTTQKCLVKKRVERSHEDPSIVITTYEGQHTHHYPS  
NVRGSSHMLANPQSSMPPSFHDLFLQTLTPPLQQFNLPANYHELLLQNSIHP SFINSNP

>DoWRKY12

MSSSAGSFEASSAIFSFSTPHTTSFSDLLCGADDASTADETSKSVRGFSDKGGGGGIPKFKSI  
TPPSLPISPPPFPSSSYFAIPAGLSPAELLDSPVLLSSNNRLLPSPTTGT FPLKAFNWSGNSGN  
HYEDKKDVNRAFSDFSFQTQQLNVFKGSQQSWNYQEPNIKTELSAPNVQANNTIKEQK  
KSEDDGYNWRKYGQKQVKGSENP RSYYKCTFPNCPTKKKVEKNLEGQITEIVYKGTNHP  
KPQSTRN SSSSSSSQSFQPLVSSAAASEASEHSHGVRSGTAMESVATPDN SSVSFGED EVD R  
NIQRTNRASEEFEEEE PDAKRWKKEGENEGASVAGNKT VREPRVVVQTTSDIDILDDGYR  
WRKYGQKVVKGPNPNRSYYKCTTVGCPVRKHIERASYDLRAVITTYEGKHNDIPAARG  
SSNHSANRPPALENAQAITTTIRPSPA VAANSRFGQRFDTFQHSHPFALEMLPTDQGHYDD  
GFGSGFNPSNSYMNHHQQQQQQQQQQQKQTGNLFPVAKEEPRDDMFFESLLC

>DoWRKY14

MTEKIEEKLD FMTGAISPFLDAIEPSFGGGFFDLAADIDAGDRGSFGFVDLLGIHDL PQVL  
LDTESYGASAAPALESSETQNF PATPNSSSISSSSSESPDADPTMPASNPPEAEDESAEHDQ  
AKKMGSSDSKGRKKKGQKRQREPRFAFLTKSEVDHLEDGYRWRKYGQKAVKNSPFP RS  
YYRCTSALCGVKKRVERSSNDPSVVVTTYEGQHTHPSPIIPRGTHHFSAPPELVDLHRFQ  
LQSSYVLSSQPSNFHPVVTAA PPSFPPPAPRPIPVLGFGERTYCD SATGIGLRDHG  
LLQDLIPSDVMMKREQ

>DoWRKY15

MAEGGGGGGLAAPVEEGAKRPSISL PARFTVESLFRGGVSEASPGPMTLVSNFFAEDPES

ECRSFSQLLAGAMASPAAITAPRKFLVEGEDTAAARTSVETTIADERGRGVGGGGGGGERG  
GASLNLGHSRPMNLLVAQSPYFTVPAGLSPGGLLDSPAMFSNSAHFGMSHQALAQVTAQ  
AAHSHTQIHSQAIEYSSLSISLPQQVSTTNITTAQPMQSITSASYKFASALIPHCDQKAQPV  
ALVVDKPVDDGYNWRKYGQKQVKGSEFPRSYYKCTHPKCPVKKKVERSLDGHVTEIIV  
KGQHNHQKPVPNKRSKEGAAELNGNSDPNNADCRPQGDLSNLNKSSEGMTSLCKRARE  
SGHGASEQLTGSSDGEELGDAEAGIDEAEYSGESEQKKRNLETRVIESASHRMVTEPRIIV  
QTTSEVDVLDGGRWRKYGQKVVKGPNPHRSYYKCTNAGCNVRKHVERASTDPKAVIT  
TYEGKHNHDVPAARNSSHSTHALAGPANRNNSAPHVVESNNQIINGISDLRNNVHRPIAVL  
QLKGEHEMT

>DoWRKY18

MAVDLIGYAKMEDKMSIQDAAAAGFRGMENLIFHLNRHQKSSSHRNIDCREIAEHTVSK  
FKKMISILNRTGHARFRRGPAVFASSVVTTPPQPSVSLHPTPAMTAPVVQLQGLTLDFTKS  
SPVSGASKVDLNLAAATSAKYIKNSFSMSAPMSSTNSSFLSSITGDGSVSNGREGGSSSVLL  
APAPASAGGAVRSKPLSSACKKQCPHAHSEDIAGRFAGGRCHCSKRRKNRVKKTIRVP  
AISSKMADIPSDEYSWRKYGQKPIKGSYPRGYKCSSLRGCPARKHVERAPDDPSMLIVT  
YDGEHRHSQPSDPIVSDNTHCKI

>DoWRKY20

MAGIDDSVSIFADWAASNPSRPTFISKFFNEDTCRPFPLDGDNTHFGFAEPENHKSAMVN  
NEEVEKPALVHSSDIFLEPVQFNVSKESSKGALESERMAARAGFSTLTVNTSRNGTESVIYSP  
SNKRCSYVLLSPGVSPTTLESFVLSNAMAQPSPTTGKFPFARAEDSNMFSTLISEETDKT  
NVQLIEDVHADAFTPCLGSSFPFLSPENKFALSIEEERTLVNMGSSLQPDLPVCFTEA  
SETKEIAEDVKADSFLANESSPPDDNQNVEDPKGGEFSSMASSAAEEDGYNWRKYGQK  
HVKGSEFPRSYYKCTFVNCPVKKKVERSLEGHVTEIVYRGAHNHPKPPSNRRSSTSSSQSF  
SDTQMDNSDYHVINANFDGKPTLVNAQNGNGGSEWRGDGIEAVSSTIAEFATSNSMQTI  
SGSRYDGEALNLPAMSNDDEEDDGATHGSFSMGDAEAGEEMDSKRRKLDLCTIDMSA  
ASRAMREPRVVVQTTSEVDILDDGYRWRKYGQKVVKGPNPNRSYYKCTNPGCTVRKHV  
ERASHDLKSVITTYEGKHNHDVPTAKTNSHQSTGLSNSTATGIHPTHSLHRKAIEPIQIILMR  
FENHAPVDPFALPSRDPQFGTAAGFAFGFGHQGLTSLGIGSLGPMGLRMPAFAPVQSYLE  
HQRKVDDGGFIIPKGEKPEPIESDLPSIANAPKGYQFANRLSLGPYL

>DoWRKY23

MMNELEELNRVERSIGDQTGDEFTMQELLYSSDLPLLPWKFTEREPLSPSKLISKMLHGS  
PMKARMSMSCSNGEFDGLSNYRPAIALPEKGLTAKMENKYTLRIKTYGINGVADDGYKW  
RKYGQKSIKNSPNRSYYRCTNPRCNAKRQVERSTEDPDMLIITYEGLHLHYTYSHFLHS  
QAHDLSITKKPKTNSVDVQPRFLDQDQQLQTVLQEP LIIGRDGQQDNNLVEVEGFGKSA  
MGDEIMQEETLYNNNKNRHC SQGLLEDIVPLMVRKPSSPTTSSNEPSYPSQASSPSYSSS  
LCWTPETFHFAESVLSSIV

>DoWRKY24

MCRSCVQKNNHRLKSTRVSFKTKSDRDVLDGGRWRKYGKKMVKSSSNPSMFLGHLQP  
NGILWFACSSRDCTERQIERCFRVLNSATPKEKTQKAFLGVRVEMFGNWKHAIGKWCSI  
RLEMPHWHQKECISRAI

>DoWRKY25

MSEMSISGAGDHVASSIPPEISTTSAGARYKMMSPGRLPITRSPCLTIPPGFSPGALLESVLL  
TNMKAEPSPTTGTFAMPLILNNGLAALGSPKDSSKGCVSEDGSSPYFEFRPHIRLSSRPGL  
SSLAPLGSGLNSKQQEFVEKNQCLDNTGSSSSQVVKTECIAQSSPESTWSATASGSPVE

VFTLKANGFCEDASNELQLTKDLDCRIQASQSDQNGSNPLNAVEKSSSEDGYNWRKYGQK  
HVKGSEFPRSYYKCTHPNCQMKKQLERSHDGHITEIYKGRHDHPKPQASRRSAVGGVST  
GQEEEKEDGLSCFANFEEKFSNAHCHSSHVNPNCNSELSPVSVSDDEVEVGGGQSGLGGD  
DAADDDPESKRKMEVATIDANSIAKNNREPRVVVQTVSEVDILDDGYRWRKYGQKVVK  
GNPNPRSYYKCTNPGCSVRKHVERASHDPKAVITTYEGKHNHDVPAAKTTNNNNRESSPP  
LITDANIPRTYITHQYSQPEENAINLHLGVGVGSNHNLLNEKQHLSGLERIPSHHHHHH  
HHQYISSDCNNVMIQLNPVSKLYGSSNNVVFSGSRDNKGEGFSFSTQMNNSSSHYYPRADN  
LVMGP

>DoWRKY26

MEPQQNFPPILSQQPPFPILPEASGLHFCSSSILGGDEQNKGKGRGKESRPRFVFQTRS  
ESDILDDGFRWRKYGQKKVKNCSFPRSYYRCSQLTCNVKKQVQRLSSDAIVVTTYEGV  
HNHPCEKLMETLSPLLNQMQFLSQFQ

>DoWRKY27

MENKIDSTTGDPTWDFSSDGGGIAYLYGEGDGGGHGWAPPRIHEEDPDTWCSLPPDLS  
EASGSAAARSGGDAVSSSSSEGPPADPGDKPPADSPNNKTSKVKVQKRVRQPRFAFMKSEI  
DHLEDGYRWRKYGQKAVKNSPFPRSYYRCTNSKCTVKKRVERSSDDPSIVITTYEGQHCH  
HTVNFRAAAIGFHDHIRTSSLLENISPPPQQQQQQLYFPATTSLQSVPELPTVLPNDGGL  
GDIVSPGMRGRR

>DoWRKY28

MNCTEPCRRRVQRWTILTSVPHFDGYEWRKYGEKNIQGYKFPRSYYKCTHNKDQGCPA  
TKTIQQKEDNDCNPPKYEVIYSLHHICKTMGTNTHLDKKYSSAPINNTSSTTTTSSCQANS  
SQPLTLVADQLCPMESMLLSAEPQIEENGGIENSNTKSSPSTDLDLDFDSEWAKWLLSCTEK  
A

>DoWRKY30

MEEGSRIAFRTQTDEENLDDGFKWRKYGKKSVMKNSPNRNYYRCSTEGCLVKKRVERDN  
EDPSYVITTYEGIHNSHSSPGVVYYATQDSVSGRFHLSGEKWKEKNIALKVVDSDQSQL  
KNEDGIFLMIRQFRSFLKRKQRRHQQWIKGKFNKNVKASNDVIYYECKKLGRIKSECLNL  
KANPNKEKVDEKNSVKKGN

>DoWRKY31

MCDYFWQRMDQNNQGDLSDFRNSSSHTSNDSWHPLPEPAGAFAPPSNLFGDPFAEIGDP  
LLGEFATTNYFNSSETTIVKTNSTGRSDDCGAQKMLLEEGKSSIFSRMLQISPVIPSKMSA  
EIGPSPLVGTMAGDSSGCLQISSTRVQGIKRRKSQVKKVVCIPAPAAASGRPSGTGEVVPSD  
LWAWRKYGQKPIKGSYPYRGYYRCSKSKGCSARKQVERSRTDPNMLVITYTSEHNHPWPT  
QRNALAGSTRSHPSKSNNSASTSKNSPHNLNQLATNIKEEHKECSSSTINLVKEEAYEME  
KALVDPQDHDQVDFDESTFMMSDSNQPDFFADLAELESSDPMNLIFPKGFMGDHHA  
KLDEERERNKALDPFNMFDWEGGSSIEETKRGL

>DoWRKY32

MDFEKKKPPISFEEGGKMGDLCTSDDSSELIGFNVQKSCLKGVHNEKMAEMARLNMLK  
AFVSQSDQENIMFEINSSQNESKNLISSLPEESSYMLLSPGVNLSSMEYLDNFSVSLQALP  
DNNASLQENFELLEPFGRKEKTHDIAANQKASHFLDVNGSPPPPPDDHQNAEKGVNVEF  
SSFPESDPTKDGYNWRKYGQKQLKGCEFPKSYHKCTHPNCPVRKKIERSLQGHITEIYK  
SHNHPKPPNHRSSFSSSKQLHG PQSVSADHPGSVANFKGNPSLASSYDGFKPKWSDGF  
GGTSSASFTEFNDPSNVLKSSQLELESMESSSCVISIDKEDNEATHSSLSADYNIDQEMES  
KRRKQELCSIGRNTTSRAMRDRRIVVQIPSDLDIPYDGYRWRKYGQKVVKGNPNPRSYY

KCTNRGCSVRKHVERASDDLNSVICTYEGKHNHDVPSARNINLARYFPSSLAETAAMQLP  
GLYTRPELAQDSFMSLENCAPICTYGLLGRGKQLEPTTSFSFGFDQSNLASLCPGSDLMR  
RFKMPFFPIHQNMDRQVSSGNIIPMREPKNPEM

>DoWRKY33

MCDYFWKRENSQGDLDIFQSGGAALAGSAVAADIPTTITDHTWQPSPDPATALPLQN  
NCFLDNFANIKDPMLHELAGTGFFGSSEKTAPSNNLSSMAITVIRQPPPLVGLTDTMKVGG  
DVAISLPQTPAVKRRKNQARKVVCIPAPAVASNKPGGEVVPDLWAWRKYGQKPIKGSPPY  
RAEAIELGGTGTEVKEKKIDKCFVNQSRALLSFYTEQFLASPSLSISLCAFDLLHYGRRPD  
ICIKSRNLEGRANFKKKGYRCSSSKGCARKQVERSRTDPNMLVITYTSDHNHPWPTQR  
NALAGSTRSQSSKNNNNNASSKSSSINQKLPSSEITVREEEEEEEAKLISPISSFPFVKERK  
DMENSTVVEHLHDFNQVFFQKSLKELEPDDFFADLAVLDADSMMLDEEKNDKKTMDPF  
NMFGWDGGNSFGVTKRG

>DoWRKY35

MFAMEKNDDGWDLFAVVRSCRAASQPPPPPLPTAKPAEAPSTSFYNEVEEFCKPFFSMVQ  
QPKPKPSTLSCSSSLAGAAARAAPRRPVSQTKYRSKKRSLRRILRWNQQRVVCEVPADG  
LAADMWAWRKYGQKPIKGSPPYPRGYRCSSSKGCARKQVERSRTDPAMFVITYTGDHN  
HSLPTHRNSLAGSTRQKFSSAASVGEESRTVCLPSTPLKREESGEEEEEEEEEDDDDEGIL  
LVEDMEVVAEDEVLFMGLEKLQDSPVAAAVTTGAVSEFFGGESCCFEDSFFLHSWSEESS  
SGATAAAGGCNT

>DoWRKY37

MQQFDGNGRMLQRVSTKLSVSTYGEDDLISLIQTLYIKQPPSSTMVSGYDSEPEWLEYKIK  
ETNMLTVDKYQQIGFFPTEKAFSLRYQTAGMLETVLRAGVLGEDDIGEESPRNLKLPSPFP  
SVCENCLYSLKEDMRIRAFHIMDPKGVVDMLLIFLEQRDDAPSSISSFSLQDVPDRIIFL  
GKWKGHSITKRSVYGATIAEADTVAFLELDENGQVVQMRMVRFLCSNSMAENIRTEAT  
GHTEAKRPSISLPPRPSDESLFRLEPAEASPNPMNLVSSFFSEDPESDCRSFSQLLAGAITLPE  
TRTTAEAATGEGRGRGGGLNLGQSQAMNLLAGQSPFFMAQSDLSPGGLLDFPAMFSSNL  
MQGQLGLAHQQAHSQMQMHLQSENPSLFSASLSRSFPTVKMPKVLHMPATTLDSNAY  
CSEVASASHSDQVPFPVPIVVDKPVDDGYNWRKYGQKQVKGSEYPRSYKCTQPNCVPK  
KKVERSDGQVTEIYKKGKHNHQPPSNKRKKEANMPNGSAELNGHIGFPTNSESHSQGN  
AITGLSKRDRESGNVAYDQLSGSSDGEEVDHEGMDERDYGESDQKKRNLETKLIESASH  
RTVTEARIIVQTTSEVDLLDDGYRWRKYGQKVVKGNPHRSYKCTNAGCSVRKHVERA  
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>DoWRKY39

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PAALLESHGITGQFSMSHQAVLATVTAQAQMQQLQAGYPSPSGLKNSVPHSMLPPMTPSP  
LQQRPLASTEAASSLETEQTPSYDQKSQSAFIVSKTSSDDGYNWRKYGQKQVKSTDRSR  
SYRCTNADCFAKKVERCPDGQVTEVIYRGQHSHEQPHKTKLSKERGHPSSGPFVTEG  
LDIPGIVTVESDPSTSKIDQNSSIDNPEQQLYCSSDCEGDGNSKAGEDPDDEPEPEPKRRLSL  
ITVTNPPPVFRTVKQPKVVMQTAVAGHVS DGYRWRKYGQKIVRGPNPNRSYRCTHDGC  
PVRKHVEKSSYDAKSMVITYEGKHNHDVPSLRYGLDPLPTALFIDSAPTAPAAETLNEHES  
KGDKIPSISNPPEIEKQLTGDKVLEFGDEKGLESAQALLSMSCDPSSGEEEGMKSQLFSEKS  
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>DoWRKY40

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KQVQRLSKDEGIVVTTYEGIHSHPTTEKNSDNFEQILSQMKIYTRS

>DoWRKY42

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TGLHLLSGDLSMGDGLVAAQETDEKKSEITAMKAKMGQMEEENQRLRNILAQMNO  
YSFLQMQFISMHKNKSTKGNTNLSNEELNKLEEGREGIVPKQFLEGRCEGTFNGDYC  
ALKSSFNGDQEEGKETVSILSSSSKSCEQAQEATMRKARVSVRVRSDAPMITDGCHWRK  
YGQKMAKGSTCPRAYRCTMAVGCPVRKQVQRCADDQITILITSYEGKHNHPLPPAAMS  
MASTTAAASMLLSGTIASSDSLMPNLLAQAVLPCPSGFATISASAPFPTVTLDLTQPPNP  
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>DoWRKY43

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VESMSSEDSYQRLRVDSKSSISKICVKTDPSDRITLVVKDGYQWRKYGQKVTRDNPSRA  
YFRCSFAPSPVKKKQSVDDLSILVATYEGEHNHRPPLQGETPSRASHGVSSTPNSAGQ  
TVTVDLTDWRWHVNSDKVSTETTSLEFQKVMIEQMAAALSKDPNFQTSANAIERILELP  
SSHN

>DoWRKY44

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AGEEDYGACEKDRKKNEEAGEEENGGEKDKNITKQKKKGEKRQREPRFAFMTKSEVDH  
LEDGYRWRKYGQKAVKNSNYPRSYRCTTQKCTVKKRVERSHQDPSIVITTYEGQHTHH  
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QISNYGALLQDIMPSFVKSSSTEKKYLVNHSQKRNRRATIRKVPQLTTVRKASGSAPDDKCI  
VKNLNSSDALISVNLNIFPDKSDIGFLENLDMVGSMPISPIKVVVDSENAGGIIVGGTVPS  
SVNSPLALSSKNREGGNLILDRSTSDHNSNDGGGQDAIMVCESISLRPDVVFPLGTFDLPV  
EVRVLCNDLALNDVAMEVMPQVDEPDGTLHECNVSHGVVAVDPSSNMFYVAQGNFGDK  
LMNVGDNELCGVNMGVVNIYSSELNPSIFFVTLPLYLVLVSSVGLRVNEQLVDVPIALLY  
ANALYTHMGVRSKGC

>DoWRKY45

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>DoWRKY47

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GSPVIGPPQLLAPGGGGPVEISSPRLIAGIKRRKSQAKKVVVICIPAPAAASGRPSGEVPSDL  
WAWRKYGQKPIKGSPPYRGYYRCSKSGSARKQVERSRDPNMLVITYTSEHNHPWPT  
QRNALAGSTRSHPSKTNNASSTSRSSLHNHKQFTDMKEEPKECSSNSSLHVKEEAHEE  
KEKALTDHGDHNDFDSVFEDESSFNEQMMSNLNQPDNFFADLAELDPDPMNIIFPKGFMG  
DKLEERDNNNNSKAMDPFIMFDWEGEKNIFGEAKRGL

>DoWRKY48

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LREEGEGNVNGVGERREKRKAVSGRGKKVSRPRFAFQTRSANDILDDGYRWRKYGQKA  
VKNSIHPRSYRCTHHTCNVKKQVQRLSKDTSIVVTTYEGVHNHPCEKLMEALSPLLKQI  
QFLTTRF

>DoWRKY49

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ESPLLASESPRESENSEKVFKKRKTCTRLNTQVLLCSPSSAVNDGYSWRKYGQKVILGSKFH  
RAYYRCSHRDTLGCATKQVQRSDDSSLFQISLHGDHTCGNHHCRRIPELPELHNTSPG  
AERLMIVSGDLQPGFSLTSPSICGPNDISAPNLRGSGSEMAEMLSGASWTMSESPHENWD  
FKDDFDLWSSTTIESTMVEFGAEFPDFFS

>DoWRKY50

KSTAKIANKIRKPRFAFQTRSKVDVLDDGYRWRKYGQKAVKNNNFPRSYRCTHDKDCSV  
KKQVQRLSMDEEIVVTTYEGVHTHPVVKCTDNFENILNQMIY

>DoWRKY51

MVCQVLADGLSGDLWAWRKYGQKPIKGSPPYRGYYRCSSSKGCCLARKQVERSRTDQGM  
FVITYTGEHNHPLPHRNSLAGSTRQKFPSSAGGEGGGGNLPEPSTSAGEGSRVLSPTPLTS  
GTEEDLFRPRKKKKQEGSTDEDEEEEEAEVGEEDELDMLLVEDMELVGEDEFLLMGFEE  
LQVSSSPAVDELKVSSSPAVHELSSWDGEPQQTGTPPWPPAMAD

>DoWRKY52

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KYGQKPIKGSPPYRGYYRCSSSKGCPCARKQVERSMDPTTFIVTYSSDHDHWPAMSKNQ  
RHQQNSPAAATGAATLPESICSKPVDVENNPVSSDNLATDQDEKLTDLMVEESAGLMPD  
AFGWFAQVSSPSSNSPAAASDAEFFCNPIFGDDCDKLSGTAVDEEEDALFAGLGELPECS  
VVFRRGFLERQWRGGEDAKPCGIEAEESTAAAASWCGSTS

>DoWRKY53

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DQIQSTKAEIGEVEKEENERLKNLLSQIVKDYQSLQMHHFFDIVKQEQPNLVTKPTDELTAIKT  
HEAEETELVSLRLGNSVTTDHKKQLEEKLINTSSKSKENGHIEGLTLGLDCKFEGYTNK  
NNSECKEVASNPSSDNSIDEMKEEEAVEPCPPNKMKNLRTGDDEVLQQTHVKKARVSVR  
VRCQTPTMNDGCQWRKYGQKIAKGNPCPRAYRCTVAPACPVRKQVQRCADDMSILITT  
YEGNHNHPLPMSATAMASTTSAASMLMTGSSTTHSSGIPDAFPSSASPIITGVNSGLHNL  
NFSLSNTRTTPFYLPNTTISPSYSITLTLTAPPSSTAQTSQFNRFSSSSSSSSSFSISMSS  
WSSRSGYMSCAAHDQSYKPNYPHDSFYQSYMQNPTSMASMNQNFFTDIAKAITSDF  
QSALQAAITTYVGASGSQSGQVLHHAQSYAGNEYSTASGLFTTSVPSSSSAQQGNLMAMS  
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>DoWRKY54

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>DoWRKY55

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AMEGPLDDGYSWRKYGQKDILGAKFPRGYRCTYRHTHGCLATKQVQRSSSEDDFLFDV

TYRQVHTCNHCLQRTPTPSPKEENLIQNQASKPQAHPHQQQLLEQLKTGLRVKTEGFNFD  
EQLLESSPSFSFPSTPPNCIKPHNNLFSSASMPENQLMGNNSTTTSAESNYFSLSPCGVNNF  
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>DoWRKY57

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>DoWRKY59

MNIHILAE LRRLREQIGGNQIAHASAETKNNIYRAISGEVQGIDDEKVPVAVPKDEYQW  
NKY GQKLIK RIGNKHRCKKKDCGAKKKVEWAPSNPSTV RVLYEGNHNHQCARIDSDEVD  
EDAMIQANQYDLATQIFGRN

>DoWRKY60

MSEEQKGGDDDQIPTITIPQDEYEWTKY GQKLIK GIGNKYRSYFRCKKKDCGAKKKVEW  
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>DoWRKY62

MVERS LDGHTEI IYKGTHSHPKPQRIRKNSSSFEGFQGSTHHEGKDHSFNGQFGSITTENS  
SAYYGDAHDINMNSQRMRAVGPDYDDDEADAKKWKMEGEVEGISISSDRTVREP KVMV  
QTTSDIDVLDG YRWRKYGQKVVKGNPNPRSYYKCTTLGCSVRKHIERASTDLRAVITTY  
EGKHNHDVPAPRGSGLTNKTSFDDNNNIRTNNSSSSSYNMSNFTMAVRPSVASNSFFSP  
RTNGMDGIGFFRYENSMNSLFANELQKQNLQHLQKQGESVLSKAKKEPRDDLFTDSSL  
G

>DoWRKY63

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SSSFSPPPFLSLPGGLSPAVFLNSPIPLSSNAQILASEAIGSTFPTQTITWTGNNTNYLHELKE  
DRYHNKSYNSFSFETSTRPASLKSSSFHPSSIGFMASEEEAFEANQQSWSYQQPLITSND  
QIPNLQASSQSEYNYNYSNISAQSLREQRRLDDGYNWRKYGQKKVKG TENPRSYYKCTY  
PNCPTKKKVERS LDGHTEI IYKGTHSHPKSRIRKNSSSFEGFQGSTHHEGKDHSFNGQFG  
SITTENS SAYYGDAHDINMNSQRMRAVGPDYDDDEADA

KKW

>DoWRKY64

MAQKT VVIVRGEAKLGKHGGEAPPDDWSWRKYGQKPIKDS PYPRAYYRCSSSKGCSAK  
KQVERCKKDESLVIISY TSSHNHPGPVPSSLNKSINSSRIPFLNEDCRSSEKNRNVEDNYESS  
IVKCAQESTEKVQGE GDTISSSLIEPVNCSMEDDDIFDELDELPLPSSFNSLMKMVYCSLAI  
NEADLVVEKIVWHSVR

>DoWRKY65

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ECVNSQQDHTAVQLESPSSAVTSKGPVGKRKI QSTRKAASRKRGNPYSWKRVTSATIEDG  
HTWRKYGQKEIFSAKHPRSYFRCTYKYDQGCKATRQVQKSEEDPFLYVITYFGEHTCEAA  
KENNPRCREPCVVSFESNKINEIKQEIAFSSFP SHKQENEEEVVSNLTSVDSRSNCLEQPAM  
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>DoWRKY66

MAEHPFSQSSTVIDHL SRGYERLTQLLALISSSPANPSTTAPAMVLVDKAMCCIAAALSELQ  
TSSPRSVDSPTAAEDHRNGTDSKKRCKKNVQSWTIVTSVPHFDGHQWRKYGQKRIHSSEF  
PRSYYKCTH SKDKGCKATKIQQKEDKISNPPKYVVSYSVHHTCKAIETHEIPIVMDSLA  
ITNEHSTSSSQAASPD LSSPVL PKPVADIEQVSTIMDYTEPDHGEANWFEGSGLLSPFADSDI

DWERLMS

>DoWRKY67

MSYSSNLP LHAWPPPLVGLGDTMKVGGDVAVSLPQTPAVKRRKNQARKVVCIPAPAVASN  
KPGGEVVPSDLWAWRKYGQKPIKGSYPRAEAIELGGTGTEVKEKKIDKCFVNQSRALLS  
FYTEQFLASPSLSISLCAFDLLHYGRRPDICIKSRNLEGRANFKKKGYRCSSSKGC SARK  
QVERSRTDPNMLVITYTSDHNHPWPTQRNALAGSTRSQSSKNNNNNASSSSKSSSINQKLPS  
ESITVREEEEEEEAKLISPISSEFPFVKERKDMENSTVVEHLHDFNQVFFQKSLKELEPDD  
FFADLAVLDADSM SLDEEKNDKKTMDPFNMFGWDGGNSFGVTKRG

>DoWRKY68

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NSPNPRNLQSSANSRCFPKICKSSGVFRRQEELRRWSRRGRKVNFFLTMLELNIFNPWWIP  
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>DoWRKY69

MENKGGGGLTLEPNPFRAIKRRQSMDSAAGFEFPISLACREAAPSSHDDQKPAGEMDFSS  
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QSELGRMTEENQRLRGMLSQVTNNYNALHMHFMALMQQRNQNNKSNNITQSQEAVSD  
DQLRKQENVGVAIVPRQFIDLGLAAGDADEPSTHSSTDGGSQDPSSQS QANKEKSANSKE  
MMVFEREGNGFVREESPENSSHVWAPNNQPKVGGVGLKPAEQAEATMRKARVSVRAR  
SEAPMIADGCQWRKYGQKMAKGNPCPRAYRCTMATGCPVRKQVQRCAEDRSILITTYE  
GNHNHPLPPPAMAMASTTSAASMLLSGSMPSNDGLMNSNVLARTILPCSSSMATISASA  
PFPTVTLDLTQSPTPLQYQQRPPPPQFHLPTQPAQPSSLPHIFGQAIYNQSKFSGLQMSAE  
VARPPPHNLADTVSAATAAITADPNFTAALAAAITSIIGGTHQAGSSSNSGAVNN

>DoWRKY70

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AGGEQEHAVVVVSEAETGHGGRLGGPVGSTGQRPSRRRRDSGDTRTVRIPALRTGNLELP  
PDDGYTWRKYGQKAILGSKFPRSFRCTHRNFYGCKAKRKYVQLDADPNTYEITYCGNH  
TCQTSPTPLILPSMTPTTNE SMSGNVAIMTGASPPPAFPLSTSIELSSWFLKEHESEGKAPSR  
PFLSSHEVGESSRAHAGPSEQAAPPVRTGREGEGSVADLADAMFNSGSSSNSMDTIFTFKT  
D

>DoWRKY72

MALKAGSLLVPYAQSISLLIKLIRMEDMLDESVAKWLESLEEEFNMQDVLFHTEQVPLMA  
PQRATEPKSEVRS AELVNLLISKVYSGPTIGDIESALSLSCSDDGGRNYSALQEKGSSTK  
MDKYTLRLKTC DNGVADDGYKWRKYGQKLIKNSPNPRSYRCTNPRCNAKKQVERSTE  
DPETVIVTYEGLHLHFTYSHILLSQKNDQHAASLNALKKQKKQTELQPKESGQQHMQQI  
AQSIQNREQPQGNKHLRDGESYQEFLEDILLENPSMREKNIHGLLTDVQRQPQGMLEDVV  
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>DoWRKY73

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ESLPIEFDSCKRLRMDSKSSVSKICVRADPSETSLVVKDGYHWRKYGQKVTRDNPSPRAY  
FRCSFAPSCPVKKKVQRSANDLSILVATYEGEHNNHKAQLQSEGSGRLSHVGS SITPSLSINSS  
SPTIMVDLTNDKHLAEAKKACGEMASTEIQKFMIEQMAAAIAKDPTFRATLANVISGRIF

>DoWRKY74

MAVDLIGYAKMDDQITIQEAAAAGIRSMENLIFQLNRHHQKSTSSSATAATIDCREIADHT  
VSKFKKMISILNRTGHARFRRGPPSPILPAVKPTPQVAVLPSAPAMAVPVVPLQSLTLDFTK  
PSSVGGGSSDLAIVAASSGKYIKETFSISTPISSANSSFMSSITGDGSVSNRPGGTTSLLLPP  
APAISAGGVVSGKPPLAAYKKRCHSHAHSEDFAGKFAANGGRCHCSKRRKNRVKRTIRVP  
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>DoWRKY75

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KCTHNKDQGCQATKTIQKEDKVPNSPIYKVSYCMHHTCKPIETQENPFVMDSSAIMNST  
SSTTASSSYSSHELSSISFQAPSSDQPTVFPQLLEESTEQVFPMESMLLSSETRGDLAVLGLD  
WEWQDELITLGEFGDLIVRI

>DoWRKY76

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ARKKMDWPLNDPNNIDISCEGHSHRCMESMASSETTIIIEEQQEONIALAFNNALVVIP  
KDDYKWDKHGQKFIISIQKNRSYFRCANRNCKARKKVDWPRNESDNLYISYEGDHNHKV  
VAVGHSENEESGIAAN

>DoWRKY77

MGSNNGSSICLDLSIGTLQFSNSCMKQHNKINKLPLIHGSTKMEEQEIYSSQIEAEMLD  
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ASYKVNCAKEEVRETRPRISRMIRSDGLVVRDGYHWRKYGQKVIRDNPYPRAYFRCSF  
APVCPVKKKQVQRCTEDHSVLVVTYEGEHNHVQPLPGDSLNCRL

>DoWRKY78

MGSQDEEILSPPIWKSAAAMKELARGLDSVAKLASLLQVGSSKNGRPEAATAGLLAEIMC  
RISKAMAALES GGNISSCVTGNKEGVGGKSKMQSTRKAGYRRSRGSPYSWTRITSNTID  
DGHTWRKYGQKDIFSAKYPRSYFRCTHKFDQGCKASKQVQRSEDDPSLYVITYFGEHTC  
VDAKKATITPSRELCHIFESSNGENIKQETLTSFPLNQESEEVLNLTADSASDYFVSPK  
VDIKKSEEQTAAELGQEHNGPLALYTSMLNMGMEFMDYEEFLNFDHDLFQN

>DoWRKY79

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KKAUKNSPNRNYRCSSPGCEVKKRVERDRSDSSYVITIYEGTHNHISPDCKPYTTNPPQ  
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>DoWRKY80

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QSLTSSSNANNFLCSSNSSHESKTKVKSQQITKNGDRNSLDGYNWRKYGQKQVKGSEY  
PRGYRCTHPFCPVKMMVERS KDGEISEIVYRGDHNHPKSQKKEQISSRLREQTSVLDG  
NGGNFMDRAVTDLFLEENLFENKTENCDVEDFLDTGINRKALYSDSDTVLHALSLSFG  
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>DoWRKY81

MAAQALNDQKGVEDGYNWRKYGQKQVKGSENPRSYKCTYPNCPSKKKVEKTLEGQI  
TEIYKGGKSHAKPKPTRRNSYFGSDQTFNLNSQVLD SITNAENSSASYGDDDFDMNSMM

TKSQDGFDEDEPDWKKM

Supplementary Table 1 Primers used for qRT-PCR.

Primer name	Primer sequence	Primer name	Primer sequence
DoWRKY1F	5'-CCGTTTCGAGGATTTGGAGATAG-3'	DoWRKY45R	5'-CGTGGATTCGAGTGCAGATT-3'
DoWRKY1R	5'-GAGGAGGCGATATAGGAAGAGA-3'	DoWRKY47F	5'-CCAATCAAAGGGTCTCCTTACC-3'
DoWRKY2F	5'-TCCATGTCCGAGAGCTTATTTTC-3'	DoWRKY47R	5'-TAGGATCTGTCCGGCTTCTT-3'
DoWRKY2R	5'-CACTGATCATCGGCACTTCT-3'	DoWRKY48F	5'-TTCAGACGAGGAGTGCTAATG-3'
DoWRKY3F	5'-TCTCCTTACTTCTCTTTCCCTTTG-3'	DoWRKY48R	5'-GTGATGTGTGCAACGGTAATAG-3'
DoWRKY3R	5'-CCCTCGTAGTTCTCTGGATTTG-3'	DoWRKY49F	5'-CGACGACGATTCTTCTCTCTTC-3'
DoWRKY4F	5'-CAGACATCCACATACGATTCA-3'	DoWRKY49R	5'-CCCGGCGAAGTATTGTGTAA-3'
DoWRKY4R	5'-GTCGGTAGAGGAAGCAAACA-3'	DoWRKY50F	5'-TGGCTATCGTTGGCGTAAATA-3'
DoWRKY5F	5'-AGCACTGGTGAAACAGAGTTAG-3'	DoWRKY50R	5'-GCAATCCTTATGTGTGCATCTG-3'
DoWRKY5R	5'-TGGATTTCTTCGGCTCGTTATC-3'	DoWRKY51F	5'-GGAGAAGGAAGTGTTCGTCTTT-3'
DoWRKY6F	5'-GAACTGTAAGGCGAGGAAGAAG-3'	DoWRKY51R	5'-GCTACCTTCTGCTTCTTCTTC-3'
DoWRKY6R	5'-TTGCTAAGGCTCTGTGGTTATG-3'	DoWRKY52F	5'-GGACGTGGAGAATAATCCTGTATC-3'
DoWRKY7F	5'-TTACCATTCCTCCGGGTTTAAG-3'	DoWRKY52R	5'-CATAAGCCCTGCCGATTCTT-3'
DoWRKY7R	5'-ATGCAGTCCATCTTGTGAGTAG-3'	DoWRKY53F	5'-GAAGTTGATGGAGGAGGAGAAG-3'
DoWRKY9F	5'-GTGATGGTATGGTGGGTCTATC-3'	DoWRKY53R	5'-CCTGGATGAAGTGTGGTAGAT-3'
DoWRKY9R	5'-TGCTTCTTCATCCTCCAGTTC-3'	DoWRKY54F	5'-TGGGCAGAAGCCGATAAAG-3'
DoWRKY10F	5'-AGAGCCATGACTGCTAATTCC-3'	DoWRKY54R	5'-GGAGGAGTAGGTGACAATGAAC-3'
DoWRKY10R	5'-CTGCTCCTTCTCCTCATTCTTC-3'	DoWRKY55F	5'-GGCCACTTGATGACGGATATAG-3'
DoWRKY12F	5'-CGGTGAGGATGAAGTTGATAGG-3'	DoWRKY55R	5'-GCGGTATGTGCATCTGTAGTAG-3'
DoWRKY12R	5'-CCCTTCGTTCTCTCCTTCTTTC-3'	DoWRKY57F	5'-AGAACTGTAAGACGAGGAAGAAAG-3'
DoWRKY14F	5'-ATGACCAGGCGAAGAAGATG-3'	DoWRKY57R	5'-CCAACCTAAGGCTCGGTAGTTATG-3'
DoWRKY14R	5'-CTCTTCGTCAGAAACGCAAATC-3'	DoWRKY59F	5'-CCGTCAGGGTGTATATGAAGG-3'
DoWRKY15F	5'-ACAGAGCCGAGGATCATAGT-3'	DoWRKY59R	5'-TCATACTGGTTTGCTTGGATCA-3'
DoWRKY15R	5'-CCTTGGATGAGGGTTTCCTTTA-3'	DoWRKY60F	5'-AGGAACAGAAAGGTGGAGATG-3'
DoWRKY18F	5'-GCTACGCAAAGATGGAGGATAA-3'	DoWRKY60R	5'-CCGTAAGTATGACTCCTCGTATTC-3'
DoWRKY18R	5'-GTGGCGGTTGAGATGAAAGA-3'	DoWRKY62F	5'-GTGGAGAAAGTATGGGCAGAAG-3'
DoWRKY20F	5'-TGAAATGGAGGATCAGAATGG-3'	DoWRKY62R	5'-GTTGTAATCACCGCTCGTAAGT-3'
DoWRKY20R	5'-TCATATCGAGAGCCGCTTATTG-3'	DoWRKY63F	5'-GAGCTATCAGCAACCACCTTTA-3'
DoWRKY23F	5'-GAATAGGGTTGAGAGGAGCATAG-3'	DoWRKY63R	5'-CAGGCTTTGAGCCGAGATATT-3'
DoWRKY23R	5'-AATTTCCATGGCGGCAATAAG-3'	DoWRKY64F	5'-GCTCAGAAGACGGTGGTTATAG-3'
DoWRKY24F	5'-CTCGATCGAAGGCTGTAATGT-3'	DoWRKY64R	5'-GTACTTCTCCATGACCAGTAATC-3'
DoWRKY24R	5'-CTGGTTGAGAGGATGGTGATTAT-3'	DoWRKY65F	5'-GAAGCTGCGAAAGAGAACAATC-3'
DoWRKY25F	5'-TCACGAACATGAAGGCAGAG-3'	DoWRKY65R	5'-CTTGTGAGATGGGAAGGAAGAG-3'
DoWRKY25R	5'-GAATCCTTTGGAGAACCGAGAG-3'	DoWRKY66F	5'-GCACTCACAGCAAAGACAAAG-3'
DoWRKY26F	5'-GGGTTTAGATGGAGGAAGTATGG-3'	DoWRKY66R	5'-GACCACGTACTTTGGAGGATTAT-3'
DoWRKY26R	5'-GAGCTGAGAGCACCTGTAATAG-3'	DoWRKY67F	5'-TGGCTTCTCCTAGCTCTCTATC-3'
DoWRKY27F	5'-AGCTACTACCGTTGCACAAATA-3'	DoWRKY67R	5'-CCTTCTTCTAAGTTCCTGCTC-3'
DoWRKY27R	5'-GGCCTTCATAGGTTGTGATGA-3'	DoWRKY68F	5'-GGAAGGTAGAGGCTGAGTTTAAG-3'

DoWRKY28F	5'-AGCAAACATCATCTCAGCCTTTA-3'	DoWRKY68R	5'-TCTTTACAGCCTTCTTCCCATAC-3'
DoWRKY28R	5'-GCCGCCATTCTCCTCTATTT-3'	DoWRKY69F	5'-CCACATAACCTTGCCGATACA-3'
DoWRKY30F	5'-GTACGGGAAGAAGTCAGTCAAG-3'	DoWRKY69R	5'-GATGCGTTCCGCCGATAATA-3'
DoWRKY30R	5'-CGGGTCTTCGTTGTCTCTTT-3'	DoWRKY70F	5'-GGCGAGAGAATAATGGAGGATTG-3'
DoWRKY31F	5'-GGGAGATCACGATCATGCTAAG-3'	DoWRKY70R	5'-CAGCACCCGTTACCTGAATATC-3'
DoWRKY31R	5'-CCCTCCTTCCCAATCAAACA-3'	DoWRKY72F	5'-ACAAGGGATGCTGGAAGATG-3'
DoWRKY32F	5'-GGCTGTGAGTTTCTTGTAGT-3'	DoWRKY72R	5'-TGAGATGAAGAGGGAGGAGTAG-3'
DoWRKY32R	5'-GTGGTTGTGAGAGCCCTTATAG-3'	DoWRKY73F	5'-CACTCCCTCGCTATCCATAAAC-3'
DoWRKY33F	5'-TGGCTTCTCCTAGCTCTCTATC-3'	DoWRKY73R	5'-CGCCATCTGCTCAATCATAAAC-3'
DoWRKY33R	5'-CCTTCCTTCTAAGTTCCTGCTC-3'	DoWRKY74F	5'-GGACGATCAGATCACGATTGAG-3'
DoWRKY35F	5'-GGAGGAAGAAGAGGAGGAAGAA-3'	DoWRKY74R	5'-GCAGACGATGAGGTGGATTT-3'
DoWRKY35R	5'-GCAACTTCTCCAAGCCATAA-3'-3'	DoWRKY75F	5'-CATACTGCAAGCCATAGAG-3'
DoWRKY37F	5'-GTTGCTAGTGCCTCTCATTCT-3'	DoWRKY75R	5'-GCTGTAGGAAGAAGAAGCAGTAG-3'
DoWRKY37R	5'-CACTGTTTCTGCCCCGATTTTC-3'	DoWRKY76F	5'-GAACTGTAAGGCGAGGAAGAAG-3'
DoWRKY39F	5'-GACAAACCCACCTCCAGTTT-3'	DoWRKY76R	5'-GTGGTTTCTGAAGAGGCCATAG-3'
DoWRKY39R	5'-GCCACCTGTATCCATCACTTAC-3'	DoWRKY77F	5'-CTGATGGATTGGTTGTGAGAGA-3'
DoWRKY40F	5'-CGATAACGATGAACAAGCAAGAAG-3'	DoWRKY77R	5'-CTGGAGCAAAGGAGCATCTAA-3'
DoWRKY40R	5'-CTGAACCCTGGGAATCCATTAG-3'	DoWRKY78F	5'-CCAGAGAGCTCTGCATCATTAG-3'
DoWRKY42F	5'-ACTGGACTGCACCTTCTTTC-3'	DoWRKY78R	5'-TCTTCCTCGCTTTCTTGATTGA-3'
DoWRKY42R	5'-TTGCTGTTATCTCGCTCTTCTT-3'	DoWRKY79F	5'-AAGAGAGTGGAGAGAGATCGTAG-3'
DoWRKY43F	5'-TGGACCAACCAACTTCCTTATC-3'	DoWRKY79R	5'-CTTGGAGCTATGGCTAGTTGAG-3'
DoWRKY43R	5'-TGGACCAACCAACTTCCTTATC-3'	DoWRKY80F	5'-TTTCCACCAGGGATGGTTATG-3'
DoWRKY44F	5'-CCAGTTGAGGTTAGGGTTCTTT-3'	DoWRKY80R	5'-CAGCCACTACTTTAGGTGTTGA-3'
DoWRKY44R	5'-TTCATGCAGGGTTCCATCAG-3'	DoWRKY81F	5'-GGCAGCTCAAGCCCTAAAT-3'
DoWRKY45F	5'-GTGGGAGTGTTCAGGGTTAG-3'	DoWRKY81R	5'-CACTCCCTTTCCTTCTTCT-3'

Primer pairs for qRT-PCR were designed by online Primerquest software (<http://www.idtdna.com/Primerquest/Home/Index>).

Supplementary Table 2 The fold change of *DoWRKY* genes under cold stress in *D. officinale* root was calculated from the  $2^{-\Delta\Delta CT}$  value.

Gene name	2 h		6 h		12 h	
	fold-change	regulation	fold-change	regulation	fold-change	regulation
DoWRKY1	2.265331	up	2.233163	up	4.533601	up
DoWRKY2	1.990573	up	3.328046	up	1.935483	up
DoWRKY3	0.979795		0.239189	down	0.542564	down
DoWRKY4	1.970462	up	1.91479	up	1.024765	
DoWRKY5	0.481705	down	0.240917	down	0.249185	down
DoWRKY6	2.330698	up	0.58959	down	0.567205	down
DoWRKY7	1.417782		1.329188		1.882226	up
DoWRKY9	1.039162		1.007853		1.038145	
DoWRKY10	1.853142	up	0.970247		1.958816	up
DoWRKY12	0.978066		0.945284		1.90043	up
DoWRKY14	0.977318		0.971165		1.909692	up
DoWRKY15	0.959762		0.956212		0.997179	
DoWRKY19	1.831244	up	0.972421		1.045971	
DoWRKY20	0.955991		1.911853	up	3.150004	up
DoWRKY23	0.99987		1.750872	up	1.002972	
DoWRKY24	1.082131		1.197936		1.02526	
DoWRKY25	1.009331		0.980022		0.965477	
DoWRKY26	1.036478		1.018927		0.508697	down
DoWRKY27	0.988178		0.967737		1.02529	
DoWRKY28	4.333651	up	4.066062	up	4.132963	up
DoWRKY30	1.059679		1.000311		1.030325	
DoWRKY31	0.941963		0.968469		0.498762	down
DoWRKY32	0.946468		0.934729		1.810887	up
DoWRKY33	0.516479	down	1.044661		0.139306	down
DoWRKY35	0.990622		0.937629		0.935037	
DoWRKY37	0.964434		1.906962	up	1.957952	up
DoWRKY39	1.838454	up	1.644565	up	1.733134	up
DoWRKY40	0.482648	down	0.763109		0.925449	
DoWRKY42	0.922696		0.94964		0.428906	down
DoWRKY43	1.047766		1.042897		1.139457	
DoWRKY44	1.071638		1.041361		0.55732	down
DoWRKY45	0.985298		0.970262		1.985393	up
DoWRKY47	0.977998		1.012522		1.01356	
DoWRKY48	1.021827		0.978902		0.498674	down
DoWRKY49	0.971073		0.959472		0.923272	
DoWRKY50	0.797415		0.617126	down	0.138434	down
DoWRKY51	0.939788		0.99726		2.092202	up
DoWRKY52	0.490264	down	0.972072		1.004103	
DoWRKY53	0.724382		0.204241	down	0.190358	down

DoWRKY54	0.958466		0.983483		0.970596	
DoWRKY55	1.006814		0.480759	down	0.485327	down
DoWRKY57	0.685186		0.364109	down	0.350887	down
DoWRKY59	0.976442		1.276076		1.798678	up
DoWRKY60	1.029446		0.943787		1.034011	
DoWRKY62	0.423143	down	0.403636	down	0.558543	down
DoWRKY63	1.013416		0.995385		0.526386	down
DoWRKY64	0.21684	down	2.015148	up	7.034233	up
DoWRKY65	4.020655	up	3.912917	up	7.969208	up
DoWRKY66	6.132598	up	1.174955		9.37194	up
DoWRKY67	2.434081	up	1.717512	up	1.83204	up
DoWRKY68	2.371172	up	0.908109		0.936863	
DoWRKY69	1.269489		1.241931		2.114103	up
DoWRKY70	0.824168		1.066812		1.417243	
DoWRKY72	0.827595		1.222205		0.854065	
DoWRKY73	0.836346		0.717944		0.293085	down
DoWRKY74	1.352469		0.844445		1.30155	
DoWRKY75	0.876421		0.899544		1.036603	
DoWRKY76	0.802102		1.011095		0.949802	
DoWRKY77	0.981828		1.073242		0.455477	down
DoWRKY78	0.932631		0.901152		0.48763	down
DoWRKY79	0.856348		0.626862	down	0.862714	
DoWRKY80	0.821365		0.936888		1.063025	
DoWRKY81	1.257885		1.101006		1.026375	

Supplementary Table 3 The fold change of *DoWRKY* genes under cold stress in *D. officinale* stem was calculated from the  $2^{-\Delta\Delta CT}$  value.

Gene name	2 h		6 h		12 h	
	fold-change	regulation	fold-change	regulation	fold-change	regulation
DoWRKY1	1.978559	up	3.729832	up	3.727629	up
DoWRKY2	0.963284		0.958807		1.047581	
DoWRKY3	0.991002		0.840987		0.46765	down
DoWRKY4	0.515842	down	0.955601		0.961018	
DoWRKY5	0.989789		0.95229		0.489741	down
DoWRKY6	0.236484	down	0.311696	down	0.309769	down
DoWRKY7	0.499287	down	0.48959	down	0.497626	down
DoWRKY9	0.992045		0.942133		1.862031	up
DoWRKY10	0.505012	down	0.952971		0.980039	
DoWRKY12	1.029331		1.967985	up	1.963988	up
DoWRKY14	2.008905	up	1.978572	up	24.44417	up
DoWRKY15	0.982387		0.930468		0.919128	
DoWRKY19	1.020963		0.965149		0.978174	
DoWRKY20	0.996216		1.88666	up	1.768084	up
DoWRKY23	0.996287		1.119472		0.918883	
DoWRKY24	0.990862		0.957165		0.496485	down
DoWRKY25	1.015875		0.963873		0.975797	
DoWRKY26	1.933615	up	1.904293	up	0.902092	
DoWRKY27	0.498225	down	0.497844	down	0.479401	down
DoWRKY28	0.967644		1.928342	up	0.899999	
DoWRKY30	1.041043		0.965867		1.013071	
DoWRKY31	0.525282	down	0.764878		0.550235	down
DoWRKY32	1.064793		0.92683		0.932116	
DoWRKY33	0.736695		0.429154	down	0.293776	down
DoWRKY35	1.828691	up	1.840009	up	0.927246	
DoWRKY37	1.986425	up	1.968947	up	1.967264	up
DoWRKY39	1.017543		1.895791	up	1.894909	up
DoWRKY40	7.281612	up	11.0311	up	8.700599	up
DoWRKY42	3.995743	up	7.549858	up	7.064994	up
DoWRKY43	0.968988		1.158438		0.903429	
DoWRKY44	1.119839		1.139866		1.146968	
DoWRKY45	0.955679		0.926367		0.922151	
DoWRKY47	1.000923		0.977318		0.474632	down
DoWRKY48	0.987014		1.003871		0.463522	down
DoWRKY49	1.401035		1.645145	up	1.759266	up
DoWRKY50	0.577533	down	0.779937		0.757141	
DoWRKY51	1.068151		1.010333		1.010333	
DoWRKY52	0.511558	down	0.956512		0.974353	
DoWRKY53	0.31456	down	0.301076	down	0.174807	down

DoWRKY54	1.00862		0.482553	down	0.471822	down
DoWRKY55	1.97131	up	0.99776		0.953683	
DoWRKY57	0.902153		0.2787	down	0.222048	down
DoWRKY59	0.204969	down	0.159935	down	0.158516	down
DoWRKY60	3.093794	up	3.324029	up	1.270023	
DoWRKY62	3.219542	up	3.072899	up	1.33946	
DoWRKY63	1.051463		0.526551	down	0.51762	down
DoWRKY64	0.919817		0.787801		0.966855	
DoWRKY65	1.858142	up	3.24689	up	2.614288	up
DoWRKY66	1.198568		1.89081	up	4.722284	up
DoWRKY67	4.574224	up	4.080856	up	5.714229	up
DoWRKY68	1.078051		0.923888		1.139206	
DoWRKY69	2.219858	up	2.710736	up	3.966893	up
DoWRKY70	1.069007		1.098373		0.981706	
DoWRKY72	0.762916		0.719848		0.588838	down
DoWRKY73	0.877409		0.377186	down	0.560843	down
DoWRKY74	1.101376		0.983751		0.963808	
DoWRKY75	1.166543		2.184957	up	4.952336	up
DoWRKY76	0.830364		0.997346		0.92203	
DoWRKY77	0.877256		1.169656		0.958234	
DoWRKY78	0.97714		1.094654		1.158122	
DoWRKY79	0.912859		0.927852		0.996523	
DoWRKY80	0.8226		0.930583		1.017936	
DoWRKY81	0.917666		0.861284		0.936427	

Supplementary Table 4 The mean of FPKM value and fold change of *DoWRKY* genes under control and cold stress in *D. officinale* leaf.

gene name	control (FPKM mean)	cold treatment (FPKM mean)	fold change	regulation
DoWRKY1	37.58617	71.69538	1.907493634	up
DoWRKY2	15.4691833	32.09225	2.074592389	up
DoWRKY3	6.51223067	2.652049		
DoWRKY4	0.10295867	0.070751667		
DoWRKY5	13.352947	31.55624667	2.363242112	up
DoWRKY6	0	0		
DoWRKY7	27.5972333	13.59482	0.492615323	down
DoWRKY9	30.98927	27.15212667	0.876178325	
DoWRKY10	8.505595	5.690280333		
DoWRKY12	60.25857	18.59161	0.308530554	down
DoWRKY14	8.441295	29.08249667	3.445264816	up
DoWRKY15	34.8969567	47.93223667	1.373536298	
DoWRKY18	36.6834033	37.00455333	1.00875464	
DoWRKY20	15.8297733	17.197	1.086370578	
DoWRKY23	0.08892367	0.037388333		
DoWRKY24	2.29150933	0.4834		
DoWRKY25	57.2623067	77.15656333	1.34742325	
DoWRKY26	0.387865	0.227979333		
DoWRKY27	2.02340867	1.396272333		
DoWRKY28	0.12857933	0.018160333		
DoWRKY30	9.92869933	3.983945		
DoWRKY31	0.63641567	0.572590333		
DoWRKY32	2.098979	1.558955		
DoWRKY33	0.29632433	0.179211		
DoWRKY35	2.813717	3.708559		
DoWRKY37	9.139449	10.22312433	1.118571189	
DoWRKY39	16.0539933	16.12359	1.004335162	
DoWRKY40	4.783575	0		
DoWRKY42	38.2577567	48.31448333	1.262867652	
DoWRKY43	19.3435733	1.531395667	0.079168189	down
DoWRKY44	8.25805333	0.214149667		
DoWRKY45	56.3398633	25.22303333	0.447694258	down
DoWRKY47	0.77345367	0.312891		
DoWRKY48	0.12363667	0.127455667		
DoWRKY49	0.32230433	0		
DoWRKY50	0.35305167	0.094180333		
DoWRKY51	0.375303	0.124698667		
DoWRKY52	9.78057067	3.102335		
DoWRKY53	0.29487233	0.245218667		
DoWRKY54	10.8205053	6.922735333	0.639779301	down

DoWRKY55	13.2716433	1.382748	0.104188153	down
DoWRKY57	0.110151	0		
DoWRKY59	0.37069133	0.143092333		
DoWRKY60	0.37069133	0.143092333		
DoWRKY62	0.863337	0		
DoWRKY63	0.863337	0		
DoWRKY64	0	0.197575333		
DoWRKY65	28.56497	5.491928	0.192260941	down
DoWRKY66	1.62074967	0.191635		
DoWRKY67	0.29632433	0.179211		
DoWRKY68	0.03537267	0		
DoWRKY69	38.2577567	48.31448333	1.262867652	
DoWRKY70	0.16028533	0		
DoWRKY72	0.57739367	0.165394333		
DoWRKY73	5.22092933	1.015809667		
DoWRKY74	56.3398633	25.22303333	0.447694258	down
DoWRKY75	1.110346	0.895384		
DoWRKY76	0.01444067	0		
DoWRKY77	0	0.010516667		
DoWRKY78	62.96755	26.22064333	0.416415175	down
DoWRKY79	43.6600433	35.29937	0.808505153	
DoWRKY80	0.777636	0.453810333		
DoWRKY81	0	0		

Supplementary Table 5 The stress-related genes containing W-box elements in tier putative promoters.

Gene family	Annotation ID	W-box number	Position
Ethylene-responsive transcription factor	Dendrobium_GLEAN_10042967	3	-479, -431, -256
	Dendrobium_GLEAN_10049982	3	-698, -725, -892
	Dendrobium_GLEAN_10137828	3	-123, -194, -325
	Dendrobium_GLEAN_10056217	7	-253, -582, -505, -536, -511, -839, -11
	Dendrobium_GLEAN_10028885	3	-988, -140, -181
Disease resistance protein	Dendrobium_GLEAN_10110403	4	-551, -239, -589, -114
	Dendrobium_GLEAN_10136594	4	-438, -669, -399, -804
	Dendrobium_GLEAN_10028570	4	-675, -957, -591, -664
	Dendrobium_GLEAN_10064426	3	-390, -785, -117
Heavy metal transport / detoxification protein	Dendrobium_GLEAN_10020160	4	-963, -136, -98, -198
Peroxidase	Dendrobium_GLEAN_10006492	3	-730, -554, -169
	Dendrobium_GLEAN_10015395	3	-252, -150, -569
	Dendrobium_GLEAN_10021680	3	-153, -51, -437
	Dendrobium_GLEAN_10025405	6	-816, -628, -703, -9, -510, -124
	Dendrobium_GLEAN_10069749	4	-796, -96, -588, -913
NAC transcription factor	Dendrobium_GLEAN_10079456	3	-389, -558, -44
	Dendrobium_GLEAN_10034487	3	-344, -546, -34
	Dendrobium_GLEAN_10007482	3	-75, -65, -58
Dehydration-responsive element-binding protein	Dendrobium_GLEAN_10135906	3	-508, -25, -79