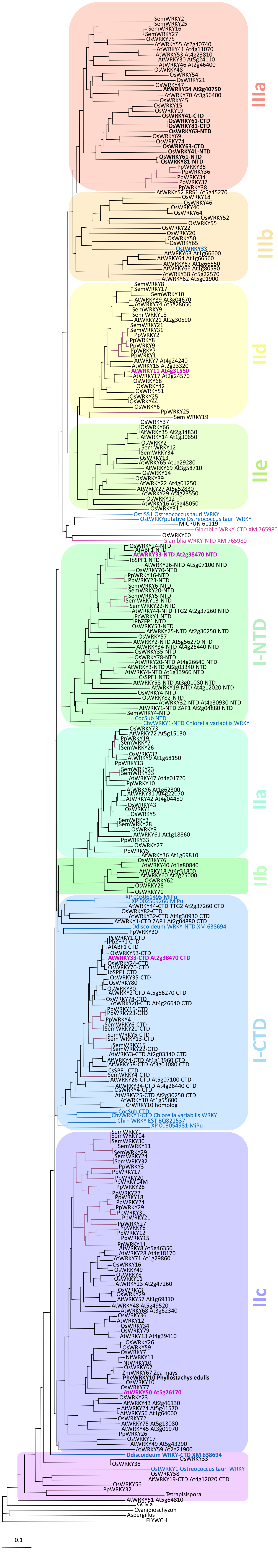


## Supplementary Files

Supplementary Figure 1	Phylogram of WRKY DNA binding domains	p. 2
Supplementary Table 1	WRKY protein sequences used for phylogenetic analyses	p. 4
Supplementary Table 2	AtWRKY protein sequences used for homology modeling	p. 17
Supplementary Figure 2	AtWRKY1 cDBD - DNA binding interface	p. 18
Supplementary Table 3	Sites of close proximity during MD studies	p. 19
Supplementary Table 4	DNA sequences of AtWRKY used for protein expression	p. 23
Supplementary Table 5	Raw absorbance values of DPI-ELISA screens	p. 24
Supplementary Figure 3	S-plot diagrams of all four DPI-ELISA screens	p. 28
Supplementary Table 6	Relative binding values of DPI-ELISA screens	p. 30
Supplementary Table 7	Alignment of positive DNA probes of DPI-ELISA screen	p. 36
Supplementary Table 8	Alignment of WRKY DBDs to identify conserved proximity sites	p. 42
Supplementary Figure 4	Comparison of models for WRKY DBD-DNA interaction sites	p. 48



**Supplementary Figure 1|** Phylogram of WRKY DNA binding domains.

Phylogenetic tree based on all WRKY\_GCM1-like domains contained in Supplementary Table 1. The Phylogram was rooted with their zinc finger-like domain of Homo sapiens FLYWCH (*HsFLYWCH*) as an out-group.

Tree topology has been confirmed by using three different programs. Groups and subgroups of WRKY I to III are color coded.

Supplementary Table 1| WRKY protein sequences used for phylogenetic analyses.

>OsWRKY1
SEAPIIADGCQWRKYGQKMAKGNPCPRAYYRCTMATGCPVRKQVQRCAEDRSILITTYEGTHNHPLP
>OsWRKY2
GGEVVPDDLWAWRKYGQKPIKGSPPYPRGYRCSSSKGC SARKQVERSRADPTMLVVVITYTSDHNHPWP
>OsWRKY3
SEIDHLEDGYRWRKYGQKAVKNSPFPRSYRCTNSKCTVKKRVERSDDPSVVIITTYEGQHCHHTAS
>OsWRKY4-NTD
AIEQPAKDGYNWRKYGQKQLKDAESPRSYKCTR DGCPVKKIVERSSDGCIKEITYKGRHSHPRP
>OsWRKY4-CTD
SEVDLDDGYRWRKYGQKVVGKGNRPRSYKCTADGCNVRKQIERASADPKCVLTTTYTGRHNHDP
>OsWRKY5
SEAPMISDGCQWRKYGQKMAKGNPCPRAYYRCTMASQCPVRKQVQRCAKDKSILITTYEGTHSHPLP
>OsWRKY6
KVADIPSDNYSWRKYGQKPIKGSPPHPRGYRCS SKKDCPARKHVERCRSDPAMLLVITYENEHNHAQP
>OsWRKY7
SEIEILDGKYKWRKYGKKS VKNSPNRNYRCS TE GCVKVRVERDKDDPSYVVTTYEGTHNHVSPS
>OsWRKY8
SEVDHLEDGYRWRKYGQKAVKNSSYPRSYRCTAPRCGVKVRVERSEQDPSMVIITTYEGQHTHPSP
>OsWRKY9
KPRVSI SDGCQWRKYGQKMAKGNPCPRAYYRCTMAIGCPVRKQVQRCAEDKTVLITTYEGNHNHQLP
>OsWRKY10
SEVEVLDDGFKWRKYGKKA VKSSPNRNYRCSAAGCGVKKRVERDGD DPRYVVTTYDGVHNHATP
>OsWRKY11
SEVDHLEDGYRWRKYGQKAVKNSPYPRSYRCTTPKCGVKKRVERSYQDPSTVIITTYEGQHTHHSP
>OsWRKY12
ADGGVSSDLWAWRKYGQKPIKGSPPYPRGYKCS SSMKGC MARKMVERSPAKPGMLVVITYMAEHCHPVP
>OsWRKY13
GEGPPSDSWAWRKYGQKPIKGSPPYPRGYRCS SSKGCPARKQVERSRADPTVLLVITYSFEHNHPWP
>OsWRKY14
GEGNTP TDSWAWRKYGQKPIKGSPPYPRAYYRCS SSKGCPARKQVERSRNDPDTVIIVITYSFEHNHSAT
>OsWRKY15
QDVGPLDDGFSWRKYGQKDILGAKYPRAYFRCTHRHTQGCHASKQVQRADGDP LLFDVVYHGDHTCAHG
>OsWRKY16
SEVDHLEDGYRWRKYGQKAVKNSPYPRSYRCTTQKCPVKKRVERSYQDPAVVIITTYEGKHTHP IP
>OsWRKY17
NNGGLADDGYKWRKYGQKSIKNSPNRPSYRCTNPRCNAKKQVERAVDEPDTLIVTYEGLHLHYTY
>OsWRKY18
LTPIPHTDGH LWRKYGEKKIKNSSFPRLYYRCSYRDDRNCMATKV VQQENDADPPLYRVITYIHPHTCNPS
>OsWRKY19
QDTASLDDGLSWRKYGQKDILGAKYPRAYFRCTHRHTQGCNATKQVQRADGDP LLFDVVYLGDHTCGQA
>OsWRKY20
ITPSPYKDG YQWRKYGQKNIQDSNYLRLYFKCTFSRERSCAAKKQVQRDAGEPPMFLVITYLNEHTCQQP
>OsWRKY21
VRSGTTTDGFIWRKYGQKEINGCKHPRLYRCAFRGQGLATRRVQQSQSQDDPAAAFVIAIYYGEHTCGGD
>OsWRKY22
YTYAPYHDGYQWRKYGQKMIRGNSFPRCYRCTYHQDHGCPASKHVEQHNS EDPPLFRVIYTNEHTCGTS



>OsWRKY23  
SDNDILDDGYRWRKYGQKAVKNSKHPRSYRCTHHTCNVKKQVQRLAKDTSIVVTTYEGVHNHPCEKL

>OsWRKY24-NTD  
SQRRSSDDGYNWRKYGQKQVKGSENPRSYKCTFPNCPTKKKVERS LDGQITEIVYKGTHNHAKP

>OsWRKY24-CTD  
SDIDILDDGYRWRKYGQKVVKGNPNPRSYKCTTAGCPVRKHVERASHDLRAVITTYEGKHNHDVP

>OsWRKY25  
RVADIPADEYSWRKYGQKPIKGSYPYRGGYRSTVKGCPARKHVERAADDPATLVVTTYEGDHRHSP

>OsWRKY26  
SDDEILDDGYKWRKYGKKS VKNSPNRNYRSTEGCNVKKRVERDKNDPRYVVTMYEGIHNVCP

>OsWRKY27  
CSAPTVDKGCQWRKYGQKTAKGNPWPRGYRCTGAPGCPVKKQVQRCNHDTSVLVTTYDGVHNHPIT

>OsWRKY28  
DLSLVVKDGYQWRKYGQKVTKDNPCPRAYFRCSFAPACPVKKKQVRSADDNTVLVATYEGEHNHAQP

>OsWRKY29  
SEIDHLEDGYRWRKYGQKAVKNSPFPRSYRCTNSKCTVKKRVERS SDDPSVITTYEGQSHHTV

>OsWRKY30  
SEVDILDDGYRWRKYGQKVVKGNPNPRSYKCTHPGCSVRKHVERS SHDLKSVITTYEGKHNHEVP

>OsWRKY31  
AASGPAPDLWAWRKYGQKPIKGSYPYRGGYRCSNKNCAARKQVERCRFDPSFLLLTYTGAHSGHDVP

>OsWRKY32  
CQGPTMNDGCQWRKYGQKVAKGNPCPRAYRCTVAPGCPVKKQVQRCLEDMSILVTTYEGTHNHPLP

>OsWRKY33  
VNIDILDAGFRWRKYGQKVVKGNPNPSRGTTSPRCSPIPPAFTAANGAGAAFQRTKDKPRDDL FVESLLC

>OsWRKY34  
SEVDVLDDGYKWRKYGQKVVKNSLHPRSYFRCTHSNCRVKKRVERLSTDCRMVITTYEGRHTHSPC

>OsWRKY35-NTD  
AAAVAEDGYSWRKYGQKQVKHSEYPRSYKCTHASCAVKKKVERSHEGHVTEI IYKGNHHPKP

>OsWRKY35-CTD  
SEVDILDDGYRWRKYGQKVVKGNPNPSSSSMDADRSLVVVVVIRSYYKCTHPGCLVRKHVERASHDLKSV  
ITTYEGKHNHEVP

>OsWRKY36  
SDVDVLDDGYKWRKYGQKVVKNSLHPRSYRCTHNNCRVKKRVERLSEDCRMVITTYEGRHTHTPC

>OsWRKY37  
SGEVVPSDLWAWRKYGQKPIKGSYPYRGGYRCS SSKGCSARKQVERSRTDPNMLVITYTSEHNHPWP

>OsWRKY38  
INIDILDAGFRWRKYGQKVVKGNPNPRSYKCTTVGCPVRKHVERALHDTRAVITTYAGAVVQRDPVGS  
ANGAGAAFQRTKDKPRDDL FVESLLC

>OsWRKY39  
PADGVSADVWAWRKYGQKPIKGSYPYRGGYRCS SSKGCPARKQVERS RSDPNTFILTYTGEHNHSAP

>OsWRKY40  
ETPVPHYDGHQWRKYGQKH IKNKSKHPRSYRCTYRQE EKCKATKTVQQREDLHHANSYNGDHPIMYTVVYY  
GQHTCCKGP

>OsWRKY41-NTD  
KVSSTVEDGF SWVKYQKDILGTMYPRSYFRCIHRHTKGCLATKQVQPTDDHQILDVIYYGEHTCDQS

>OsWRKY41-CTD  
QDVGPLDDGYSWRRYGLKDILGAKYPRSYFRCTHRNTQGCVATKQIQRRDGDPLLFVYVYHGDHTCSER

>OsWRKY42  
RNADIPADDYSWRKYGQKPIKGSYPYRGGYKCTV RGC PARKHVERDPGEPAMLIVTYDGDHRHGEP

>OsWRKY43
SDAPMISDGCQWRKYGQKMAKGNPCPRAYYRCTMAAGCPVRKQVQRCAEDRTLITTYEGNHNHPLP
>OsWRKY44
RVADIPADEYSWRKYGQKPIKGSPPYRGYYRCSTVKGCPARKHVERAADDPATLVVTTYEGDHRHSP
>OsWRKY45
VVVKNLDDGQAWRKYGQKEIQNSKHPKAYFRCTHKYDQMCTAQRQVQRCDDDPASVRYVTYIGEHTCRDP
>OsWRKY46
DTYAPYDDGHQWRKYGEKLLSNSNFPRCTYKNDMKCPATKQVQKDTNDPPLFSVTYFNHHTCNSS
>OsWRKY47
VTKLELEDGRQWRKYGQKHIQDSPNNPRSYRCTHRPDQGCMAKQVQTSSESNSSEFVLSYYGEHTCRDP
>OsWRKY48
EKARTSEDDGFLWRKYGQKEIKNSKHPRLYYRCSYKDDHGCTATKQVQQSEEDPSLYVITYFGDHTCSCQ
>OsWRKY49
SEVDHLEDGYRWRKYGQKAVKNSPFPRSYRCTTQKCPVKKRVERSYQDAAVVITTYEGKHTHP IP
>OsWRKY50
VTTVPDFDGYQWRKYGQKQIEGAMYPRSYRCTNSTNQGLAKKTVQRNGGGGAAGYTVAYISEHTCKSI
>OsWRKY51
KVADIPADDFSWRKYGQKPIKGSPPYRGYYKCTLRGCPARKHVERDPADPSMLIVTYEGEHRHTPS
>OsWRKY52
F'FPVPHEDGFQWRKYGEKKIQGTHFTSVNTQEDDGGVAMDS
>OsWRKY53-NTD
GGNNKLEDGYNWRKYGQKQVKGSENPRSYKCTYNGCSMKKKVERSLADGRITQIVYKGAHNHPKP
>OsWRKY53-CTD
SDIDILDDGFRWRKYGQKVVGKGNPNPRSYKCTTVGCPVRKHVERASHDTRAVITTYEGKHNHDVP
>OsWRKY54
ERKATMDDKFLWRKYGQKEIKNSKHPRFYRCSYKDDHGCTATKQVQQSETADDDTASPVYIITYFGEHTC RHG
>OsWRKY55
DTFAPHNDGHQWRKYGEKKINNCNFPRTNDQCQLTFFKRSTA
>OsWRKY56
CGGKMPADGYKWRKYGQKSIKNNPHPRCATRSIIDPI
>OsWRKY57
AKNSLSYDGYSWRKYGQKQVKGSEFPRSYKCTHTPTCPVKKRKMVEMTPDGRIAEIVYNGEHNHPKP
>OsWRKY58
SENDILDDGYRWRKYGQKAVKNSDFPSDELLEFSDVDNTQTATENLRFIPLGRVYITG
>OsWRKY59
SDDEILDDGYKWRKYGKKSVMKNSPNPRNYRCSYKCTVGCNVKKRVERDKNDPRYVVTYEGIHNVCP
>OsWRKY60
VQLVMPEDGYEWKKGQKFIKNIQKNRSYFRCDQRCCGAKKKVEWHPHDPGLNLRVVYDGAHHHGSP
>OsWRKY61-NTD
RMSYTEDDGFQWRKYGQKQVKGSEFPRSYKCTHTPTCPVKKRKMVEMTPDGRIAEIVYNGEHNHPKP GV
>OsWRKY61-CTD
KDVGPDDGYSWKRYGQKNIFGANYPYRCSYKCTHTPTCPVKKRKMVEMTPDGRIAEIVYNGEHNHPKP GV
>OsWRKY62
SMAETVKDGYQWRKYGQKVTRDNPYPYRCSYKCTHTPTCPVKKRKMVEMTPDGRIAEIVYNGEHNHPKP GV
>OsWRKY63-NTD
VRSNTEDDGLSWSKYEQKEILGAKFPYRCSYKCTHTPTCPVKKRKMVEMTPDGRIAEIVYNGEHNHPKP GV
>OsWRKY63-CTD
VTSVPADDGYSWRKYGQKNVLFVSYLRYRCSYKCTHTPTCPVKKRKMVEMTPDGRIAEIVYNGEHNHPKP GV

>OsWRKY64  
ETPVPHYDGHQWRKYGQKHINNSKHPRSYRCTYRQECKATKTVQQREDLHHANSYNGDHPVMYTVVYY  
GQHTCCKGP

>OsWRKY65  
VTVPDFDGYQWRKYGQKQIEGAMYPRSYRCTNSTNQGLAQKTVQRNGGGAAGYTVAYISEHTCKSI

>OsWRKY66  
SGEVVPSDLWAWRKYGQKPIKGSYPRGYRCSKSGCSARKQVERSRTDPNMLVITYTSEHNHPWP

>OsWRKY67  
SEVEILDDGFKWRKYGKAVKNSPNRNYRCSSTEGCNVKKRVERDREDHRYVITTYDGVHNHASP

>OsWRKY68  
KIADIPPDEYSWRKYGQKPIKGSYPRGYRCSSTVRCGCPARKHVERATDDPAMLVVTYEGEHRHTPG

>OsWRKY69  
GAEGPADDGHSWRKYGQKDILGAKHPRGYRCTRNTQGCATKQVQRTDDASLFDVVYHGEHTCRPG

>OsWRKY70-NTD  
QSRSSDDGYNWRKYGQKQMKGSENPRSYRCTFPGCPTKKKVEQSPDGQVTEIVYKGAHSHPKP

>OsWRKY70-CTD  
SDIDILDDGYRWRKYGQKVVKGPNRNYRCSSTAGCPVRKHVERASNDLRAVITYEGKHNHDVP

>OsWRKY71  
DLSLVVKDGYQWRKYGQKVTKDNPFRAYFRCSFAPACPVKKKQVQSAEDNTILVATYEGEHNHGQP

>OsWRKY72  
SQVDILDDGYRWRKYGQKAVKNNKFRSYRCTHQGCNVKKQVQLSRDETVVVVTTYEGTHTHPIE

>OsWRKY73  
CDAPTMDGCGWRKYGQKIAKGNPCPRAYRCTVAAGCPVRKQVQRCADDMSILITTYEGTHNHPL

>OsWRKY74  
VENPPVDDGHSWRKYGQKEILGAKHPRGYRCTRHSQGCMAKQVQRTDEDAMVFDVIYHGEHTCVHK

>OsWRKY75  
NTEQPDDGYTWRKYGQKDILGSRYPYRCSSTHKNYGCCEAKKQVQLDDDPFTYEVTYCGNHTCLTS

>OsWRKY76  
DTSLVVKDGQWRKYGQKVTRDNPSPRAYFRCAFAPSCPVKKKQVQSAEDSSLLVATYEGEHNHPHP

>OsWRKY77  
SEVDVLDDGYRWRKYGKMMVKNSPNRNYRCSSEGCVRKKRVERARDDARFVVVTTYDGVHNHPAP

>OsWRKY78-NTD  
VAEKSAEDGYNWRKYGQKHVKGSENPRSYRCTHPNCDVKKLLERSLDGQITEVVYKGRHNHPKP

>OsWRKY78-CTD  
SEVDILDDGYRWRKYGQKVVKGPNRNYRCSSTNTGCPVRKHVERASHDKSVITYEGKHNHEVP

>OsWRKY79  
SDVDVLDDGYKWRKYGQKVVKNQHPRSYRCTQDNCRVKKRVERLAEDPRMVIITYEGRHVHSPS

>OsWRKY80  
SEVDILDDGYRWRKYGQKVVKGPNRNYRCSSTHQGCSVRKHVERASHDLKSVITYEGKHNHEVP

>OsWRKY81-NTD  
RMSYTEDDGFVSWRKYGQKDVEGAMHPTTQSNYFRCAHKMTTGCKARKKQVQRTDGDPLMVDVVYKGVHSCAG  
V

>OsWRKY81-CTD  
KDVGPPDDGYSWKRYGQKNIFGANYPRCYRCHKTTTGCTATKNAQATDGDPLLFVYHGEHTCDLQ

>OsWRKY82-NTD  
VSVNMVGDGFNWRKYGQKQVKSSENSRSYRCTNSNCLAKKKVEHCPDGRVVEIIRGTHNHEPP

>OsWRKY82-CTD  
VQAGKTSYDGYRWRKYGQKIVKGNPNRNYRCSSTHDGCPVRKHVEKAPDDNNIVVYEGKHNHDQP

>AtWRKY1-NTD\_ZAP1\_At2g04880\_NTD  
IREKVMEDGYNWRKYGQKLVKGNFVRSYRCTHPNCKAKKQLERSAGQVVDTVYFGEHDHPKP

>AtWRKY1-CTD\_ZAP1\_At2g04880\_CTD  
TLFDIVNDGYRWRKYGQKSVKGSPPYPRSYRCSPPGCPVKKHVERS SHDTKLLITTYEGKHDHDM P

>AtWRKY2-NTD\_At5g56270\_NTD  
AGGAPAEDGYNWRKYGQKLVKGSEYPRSYKCTNPNCQVKKKVERSREGHITEI IYKGAHNHLKP

>AtWRKY2-CTD\_At5g56270\_CTD  
SDVDILDDGYRWRKYGQKVVKGNPNPRSYKCTAPGCTVRKHVERASHDLKSVITTYEGKHNHDVP

>AtWRKY3-NTD\_At2g03340\_NTD  
NADKPADDGYNWRKYGQKQVKGSDFPYPRSYKCTHPACPVKKKVERS LDGQVTEI IYKGQHNEHP

>AtWRKY3-CTD\_At2g03340\_CTD  
SEVDLLDDGYRWRKYGQKVVKGNPYPRSYKCTTPDCGVRKHVERAATDPKAVVTTYEGKHNHDVP

>AtWRKY4-NTD\_At1g13960\_NTD  
NVDKPADDGYNWRKYGQKQVKGSEFPYPRSYKCTNPVPCPVKKKVERS LDGQVTEI IYKGQHNEHP

>AtWRKY4-CTD\_At1g13960\_CTD  
SEVDLLDDGYRWRKYGQKVVKGNPYPRSYKCTTPGCGVRKHVERAATDPKAVVTTYEGKHNHDLP

>AtWRKY10\_At1g55600  
SDEDNPNDGYRWRKYGQKVVKGNPNPRSYFKCTNIECRVKKHVERGADNIKLVVTTYDGIHNHPSP

>AtWRKY19-NTD\_At4g12020\_NTD  
NVDKQVNDGYNWKYQKQVKGSKFPLSYKCTYLGCPSKRKVERS LDGQVAEIVYKDRHNHEPP

>AtWRKY19-CTD\_At4g12020\_CTD  
SEVDNLDDGYRWRKYGQKVVKGNPYPRFSSSKDYDVVIRYGRADISNEDFISHLRASLCRRGISVYEKFNE  
VDALPKCRVLIIVLTSTYVPSNLLNILEHQHTED

>AtWRKY20-NTD\_At4g26640\_NTD  
TPSILADDGYNWRKYGQKHVKGSEFPYPRSYKCTHPNCEVKKLFFERSHDGQITDI IYKGTHDHPKP

>AtWRKY20-CTD\_At4g26640\_CTD  
SEVDILDDGYRWRKYGQKVVRGNPNPRSYKCTAHGCPVRKHVERASHDPKAVITTYEGKHDHDP

>AtWRKY25-NTD\_At2g30250\_NTD  
MVSRSNDGYGWRKYGQKQVKKSENPRSYFKCTYPDCVSKKIVETASDGQITEI IYKGGHNHPKP

>AtWRKY25-CTD\_At2g30250\_CTD  
SDIDVLIDGFRWRKYGQKVVKGNTPNPRSYKCTFQCGVKKQVERSAADERAVLTTYEGRHNHDIP

>AtWRKY26-NTD\_At5g07100\_NTD  
SSNKTSDGYNWRKYGQKQVKGSENPRSYFKCTYPNCLTKKKVETSLVKGQMI EIVYKGSNHNHPKPQSTKR  
S

>AtWRKY26-CTD\_At5g07100\_CTD  
SDIDILDDGYRWRKYGQKVVKGNPNPRSYKCTFTGCFVRKHVERAFQDPKSVITTYEGKHKHQIP

>AtWRKY32-NTD\_At4g30930\_NTD  
VPRTPARDGYNWRKYGQKQVKS PKGSRSYRCTYTECCA KIECSNDSGNVVEIVNKG LHTHEPP

>AtWRKY32-CTD\_At4g30930\_CTD  
GDVGICGDGYRWRKYGQKQVKG NPNHPRNYRCTSAGCPVRKH IETAVENTKAVI IYKGVHNHDM P

>AtWRKY33-NTD\_At2g38470\_NTD  
REQRKGEDGYNWRKYGQKQVKGSENPRSYKCTFPNCP TKKKVERSLEGQITEIVYKGSNHNHPKP

>AtWRKY33-CTD\_At2g38470\_CTD  
SDIDILDDGYRWRKYGQKVVKGNPNPRSYKCTTIGCPVRKHVERASHDMRAVITTYEGKHNHDVP

>AtWRKY34-NTD\_At4g26440\_NTD  
ACCAPADDGYNWRKYGQKLVKGSEYPRSYKCTHPNCEAKKKVERSREGHIEI IYTGDIHHSKP

>AtWRKY34-CTD\_At4g26440\_CTD  
SDIDILDDGYRWRKYGQKVVKGNPNPRSYKCTANGCTVTKHVERASDDFKSVLTTYIGKHTHVVP

>AtWRKY44-NTD\_TTG2\_At2g37260\_NTD  
TGDRSSVDGYNWRKYGQKQVKGSECPYPRSYKCTHPKCPVKKKVERSVEGQVSEIVYQGEHNHNSKP

>AtWRKY44-CTD\_TTG2\_At2g37260\_CTD  
VESDSLEDGFRWRKYGQKVVGGNAYPRSYRCTSANCRAKHVERASDDPRAFI TTYEGKHNHHL L

>AtWRKY45\_At3g01970  
SQVDILDDGYRWRKYGQKAVKNNPFPRSYKCTEEGCRVKKQVQRQWGDEGVVVTYQGVHTHAVD

>AtWRKY58-NTD\_At3g01080\_NTD  
NVDKPADDGYNWRKYGQKPIKGCEYPRSYKCTHVNCPVKKKVERS SDGQITQI IYKGQHDHERP

>AtWRKY58-CTD\_At3g01080\_CTD  
SEVDLLDDGYRWRKYGQKVVKGNPHPRSYKCTTPNCTVRKHVERASTDAKAVITTYEGKHNHDVP

>AtWRKY18\_At4g31800  
VTLQTVKDGFWQRKYGQKVTRDNPSPRAYFRCSFAPSCPVKKKVQRSAEDPSLLVATYEGTHNHLGP

>AtWRKY40\_At1g80840  
DTLTVVKDGYQWRKYGQKVTRDNPSPRAYFKCACAPSCSVKKKQVRSVEDQSVLVATYEGEHNHPMP

>AtWRKY60\_At2g25000  
DTSLTVKDGQWRKYGQKITRDNPSPRAYFRCSFSPSCLVKKKQVRSVSAEDPSFLVATYEGTHNHTGP

>AtWRKY6\_At1g62300  
SEAPMISDGCQWRKYGQKMAKGNPCPRAYRCTMATGCPVRKQVQRCAEDRSILITTYEGNHNHPLP

>AtWRKY9\_At1g68150  
CETATMNDGCQWRKYGQKTAKGNPCPRAYRCTVAPGCPVRKQVQRCELDMSILITTYEGTHNHP

>AtWRKY31\_At4g22070  
SEAAMISDGCQWRKYGQKMAKGNPCPRAYRCTMAGGCPVRKQVQRCAEDRSILITTYEGNHNHPLP

>AtWRKY36\_At1g69810  
CEDPSINDGCQWRKYGQKTAKTNPLPRAYRCSMSSNCPVRKQVQRCEGEEETSAFMTTYEGNHDHPLP

>AtWRKY42\_At4g04450  
SEAPMLSDGCQWRKYGQKMAKGNPCPRAYRCTMAVGCPVRKQVQRCAEDRTILITTYEGNHNHPLP

>AtWRKY47\_At4g01720  
SDATTVNDGCQWRKYGQKMAKGNPCPRAYRCTMAVGCPVRKQVQRCAEDTILITTYEGNHNHPLP

>AtWRKY61\_At1g18860  
KTRVSMNDGCQWRKYGQKIAKGNPCPRAYRCTIAASCPVRKQVQRCESEDMSILISTYEGTHNHP

>AtWRKY72\_At5g15130  
CDTPTMNDGCQWRKYGQKIAKGNPCPRAYRCTVAPGCPVRKQVQRCAEDMSILITTYEGTHSHSLP

>AtWRKY8\_At5g46350  
TEVDHLEDGYRWRKYGQKAVKNSPYPRSYRCTTQKCNVKKRVERSYQDPTVVITTYESQHNHP

>AtWRKY13\_At4g39410  
SEVDVLDDGYRWRKYGQKVVKNTQHPRSYRCTQDKCRVKKRVERLADDPVMVITTYEGRHLHSPS

>AtWRKY23\_At2g47260  
SEVDHLEDGYRWRKYGQKAVKNSPFPRSYRCTTASCNVKKRVERFRDPSTVVTTYEGQHTHISP

>AtWRKY24\_At5g41570  
SDDDLDDGYRWRKYGQKSVKHNAHPRSYRCTYHTCNVKKQVQRLAKDPNVVVTTYEGVHNHPCE

>AtWRKY28\_At4g18170  
SEVDHLEDGYRWRKYGQKAVKNSPYPRI IANGNENRSYRCTTQKCNVKKRVERSFQDPTVVITTYEGQHNH

>AtWRKY43\_At2g46130  
SDADILDDGYRWRKYGQKSVKNSLYPRSYRCTQHMCNVKKQVQRLSKETSIVETTYEGIHHPCE

>AtWRKY48\_At5g49520  
SDIDNLDDGYRWRKYGQKAVKNSPYPRSYRCTTVGCGVKKRVERSSDDPSIVMTTYEGQHTHPFP

>AtWRKY49\_At5g43290  
NSNGMCDDGYKWRKYGQKSIKNSPNRPSYKCTNPICNAKKQVERS IDESNTYI IITYEGFHFHYTY

>AtWRKY50\_At5g26170  
SEVEVLDDGFKWRKYGKKMVKNSPHPRNYKCSVDGCPVKKRVERDRDDPSFVITTYEGSHNHSSM

>AtWRKY51\_At5g64810  
SKIDVMDDGFKWRKYGKKSVKNNINKRLRLYREGNVKATCKKSLCDSVTCRQRDLFEEDEPEY



Supplementary Table 1|

>AtWRKY56\_At1g64000  
SDDVLDGGRWRKYGQKSVKNNNAHPRSYRCTYHTCNVKKQVQRLAKDPNVVVTTYEGVHNHPCE

>AtWRKY57\_At1g69310  
SDVDNLEDGYRWRKYGQKAVKNSPFPRSYRCTNSRCTVKKRVERSDDPSIVITTYEGQHCHQTI

>AtWRKY59\_At2g21900  
DEKVALDDGYKWRKYGKKPITGSPFPRHYHKSSPDCNVKKIERDTNNDYILTTYEGRHNHPSP

>AtWRKY68\_At3g62340  
SEVLHLDDGYKWRKYGQKPKVSDPFPRNYRCTTTWCDEVKKRVERSFSDDPSIVITTYEGQHTHPRP

>AtWRKY71\_At1g29860  
SEIDHLEDGYRWRKYGQKAVKNSPYPRSYRCTTQKCNVKKRVERSFDPSIVITTYEGKHNPPIP

>AtWRKY75\_At5g13080  
SQVDILDDGYRWRKYGQKAVKNNKFPRSYRCTYGGCNVKKQVQRLTVDQEVVVTTYEGVHSHPIE

>AtWRKY7\_At4g24240  
KMADIPSDEFSWRKYGQKPIKGSPPRGYKCSSVRGCPARKHVERALDDAMMLIVTYEGDHNHALV

>AtWRKY11\_At4g31550  
KIADIPPDEYSWRKYGQKPIKGSPPRGYKCSSTFRGCPARKHVERALDDPAMLIVTYEGEHRHNQS

>AtWRKY15\_At2g23320  
KMSDVPPDDYSWRKYGQKPIKGSPPRGYKCSSVRGCPARKHVERAADDSSMLIVTYEGDHNHSLV

>AtWRKY17\_At2g24570  
KIADIPPDEYSWRKYGQKPIKGSPPRGYKCSSTFRGCPARKHVERALDDSTMLIVTYEGEHRHHQS

>AtWRKY21\_At2g30590  
KVADIPPDDYSWRKYGQKPIKGSPPRGYKCSSMRGCPARKHVERCLEDPAMLIVTYEAEHNHPKL

>AtWRKY39\_At3g04670  
KIADIPPDEYSWRKYGQKPIKGSPPRGYKCSSVRGCPARKHVERCIDETSMLIVTYEGEHNHSRI

>AtWRKY74\_At5g28650  
KIADIPPDEYSWRKYGQKPIKGSPPRGYKCSSVRGCPARKHVERCVEETSMLIVTYEGEHNHSRI

>AtWRKY14\_At1g30650  
SGEVVPSDLWAWRKYGQKPIKGSPPRGYRCSSSKGCSARKQVERSRTPNMLVITYTSEHNHPWP

>AtWRKY16\_At5g45050  
DRGSRSSDLWVWRKYGQKPIKSSPYPRSYRCASSKGCFAKQVERSRTPNVSVITYISEHNHPFP

>AtWRKY22\_At4g01250  
AAEALNSDVWAWRKYGQKPIKGSPPRGYRCSSTKGCCLARKQVERNRSDPKMFIVTYTAENHPAP

>AtWRKY27\_At5g52830  
TQENLSSDLWAWRKYGQKPIKGSPPRYRCSSSKGCLARKQVERSNLDPNIFIVTYTGEHTHPRP

>AtWRKY29\_At4g23550  
KEENLLSDAWAWRKYGQKPIKGSPPRYRCSSSKGCLARKQVERNPNQPEKFTITYTNEHNHELP

>AtWRKY35\_At2g34830  
SGEVVPSDLWAWRKYGQKPIKGSPPRGYRCSSSKGCSARKQVERSRTPNMLVITYTSEHNHPWP

>AtWRKY65\_At1g29280  
GDTTPPSDSWAWRKYGQKPIKGSPPRGYRCSSTKGCPCARKQVERSRDDPTMLIVTYTSEHNHPWP

>AtWRKY69\_At3g58710  
GEVYPPSDSWAWRKYGQKPIKGSPPSGGLEMRKRRVALTVVGLTGYRCSSSKGCPCARKQVERSRVDPKSLMITYACDHNHPFP

>AtWRKY30\_At5g24110  
GVDRTLDDGFSWRKYGQKDILGAKFPRGYRCTYRKSQCEATKQVQRSDENQMLLEISYRGIHSCSQA

>AtWRKY38\_At5g22570  
SPDPIYDGYLWRKYGQKSIKSNHQRSYRCSYNKDHNCCEARKHEQKIKDNPPVYRTTYFGHHTCKTE

>AtWRKY41\_At4g11070  
GLEGPHDDIFSWRKYGQKDILGAKFPRSYRCTFRNTQYCWATKQVQRSDGDPTIFEVYRGTHTCSQG

>AtWRKY46\_At2g46400  
QENGSIDDGHCWRKYGQKEIHGSKNPRAYRCTHRFTQDCLAVKQVQKSDTDP SLFEVKYLGHNHTCNNI

>AtWRKY52\_RRS1\_At5g45270  
IPAIDEGDLWTRKYGQKDILGSRFPRGYRCAKFTHGCKATKQVQRSETSDNMLAITYLSEHNHPRP

>AtWRKY53\_At4g23810  
GLEGPQDDVFSWRKYGQKDILGAKFPRSYYRCTHRSTQNCWATKQVQRSDGDATVFEVYRGTHTCSQA

>AtWRKY54\_At2g40750  
VEAKSSEDRYAWRKYGQKEILNTTFPRSYYRCTHKPTQGCKATKQVQKQDQDSEMFQITYIGYHTCTAN

>AtWRKY55\_At2g40740  
NTDLPDDNHTWRKYGQKEILGSRFPRAYRCTHQKLYNCPAKKQVQRLNDDPFTFRVYRGSHTCYNS

>AtWRKY62\_At5g01900  
SSTPIYHDGFLWRKYGQKQIKESYQRSYYKCAKTKDQNCQAKKQVQKIQHNPPLYSTTYFGQHIQQLH

>AtWRKY63\_At1g66600  
SPNRLDDGFTWRKYGQKTIKTSLYQRCYYRCAKDKQNCYATKRVQMIQDSDPPVYRRTTYLGQHTCKAF

>AtWRKY64\_At1g66560  
SPTPRDDGFTWRKYGQKTIKTSPLYQRCYYRCTYAKDQNCNARKRVQMIQDNPPVYRRTTYLGKHVCKAV

>AtWRKY66\_At1g80590  
SPTPAHIDGFIWRKYGQKTIKTSPHQRWYYRCAKDKQNCDATKRVQKIQDNPPVYRNTYVYGQHACEAP

>AtWRKY67\_At1g66550  
SRTMCPNDGFTWRKYGQKTIKASAHKRCYYRCTYAKDQNCNATKRVQKIKDNPPVYRRTTYLGKHVCKAF

>AtWRKY70\_At3g56400  
IESTILEDAFSWRKYGQKEILNAKFPRSYYRCTHKYTGCKATKQVQKVELEPKMFSITYIGNHTCNTN

>AtWRKY12  
SDVDVLDDGYKWRKYGQKVVKNSLHPRSYYRCTHNNCRVKKRVERLSEDCRMVITTYEGRHNHIPS

>CrWRKY10\_homolog  
SDEDNPEDEGFRWRKYGQKVVKGNPNPRSYYFKCTNNDNCNVKHHVERGADNFKILVTSYDGIHNHPPP

>NtWRKY11  
SQIEILDDGYKWRKYGKKMKVSDPNPRNYYRCSI ESCPVKKRVERDKEDCRYVITTYEGVHNHQGP

>NtWRKY10  
SQIEILDDGYKWRKYGKKMKVSDPNPRNYYRCSVEGCPVKRVERDKEDCRYVITTYEGVHNHQGP

>PheWRKY10\_Phyllostachys\_edulis  
SEVEILDDGFKWRKYGKKAVKNSPNPRNYYRCSVEGCGVKRVERDGDPCYVITTYDGVHNHATP

>IbsPF1\_NTD  
REQRRSDDGYNWRKYGQKQVKGSENPRSYYKCTHPNCPTKKKVERALDQITEIVYKGAHNHPKP

>IbsPF1\_CTD  
SDIDILDDGYRWRKYGQKVVKGNPNPRSYYKCTSQGCPVRKHVERASHDIRSVITTYEGKHNHDVP

>AfABF1\_NTD  
SQRRSSDDGYNWRKYGQKQVKGSENPRSYYKCTFPNCPTKKKVEITSIEGQITEIVYKGTNHAKP

>AfABF1\_CTD  
SDIDILDDGYRWRKYGQKVVKGNPNPRSYYKCTTVGCPVRKHVERASHDLRAVITTYEGKHNHDVP

>CsSPF1\_NTD  
GSDKPADDGYNWRKYGQKLVKGSEFPRSYYKCTHLNCPKRRKIEGLPDGEITEIIVYKQHNHEPP

>CsSPF1\_CTD  
SEVDLLDDGYRWRKYGQKVVKGNPNPRSYYKCTSAGCNVRKHVERSSDTSKAVVITTYEGKHNHDVP

>PcWRKY1\_NTD  
RDQSKLDDGYNWRKYGQKQVKGSENPRSYYKCTYLNCPTKKKVEITFDGHITEIVYKGNHNHPKP

>PcWRKY1\_CTD  
SDIDILDDGYRWRKYGQKVVKGNPNPRSYYKCTQVGC PVRKHVERASHDLRAVITTYEGKHNHDVP

>PbZFP1\_NTD  
RDQSKLDDGYNRWKYGQKQVKGSENPRSYKCTYLNCPTKKKVVETTFDGHITEIVYKGNHNHPKP

>PbZFP1\_CTD  
SDIDILDDGYRWRWKYGQKVVGKGNPNPRSYKCTQVGCPCVRKHVERASHDLRAVITTYEGKHNHDVP

>Glamblia\_WRKY-NTD\_XM\_765980  
TIRELPADGYCWRKYGSKRLPNNSHPKSYFRCSVPGCQAKRYVTETDNRVLKTEYIGEHNHGKS

>Glamblia\_WRKY-CTD\_XM\_765980  
DQIESSIDFFRWKYGHKPQTDTRLDSKSYRCAFFNCPARRTITFFYSLSSDGTETVESVIVQYENQHT  
HPPD

>Ddiscoideum\_WRKY-NTD\_XM\_638694  
NISNIIVSDGYQWRWKYGQKNVKGSLHPRHYKCTFQGCNVRKQVERIGDTNQNSTVYKGEHCHGFP

>Ddiscoideum\_WRKY-CTD\_XM\_638694  
SSIDHLDDGFFWRWKYGQKSVKGSFPKSYFKCAELTCPVKKQVIQQDSKYINTYRKGHNHDPP

>CuWRKY50-Citrus\_unshiu  
SDVEILDDGFKWRWKYGKMKVKNPNPRNYKCSVDGCPVKKRVERDRDDPSYVITTYEGFHTHQS

>VvWRKY50-Vitis\_vinifera  
SEIEILDDGFKWRWKYGKMKVKNPNPRNYRCSVDGCNVKKRVERDREDPKYVITTYEGIHNHESP

>PtWRKY50-like-Populus-trichocarpa  
SEIEILDDGFKWRWKYGKMKVKNPNPRNYRCSVDGCNVKKRVERDREDPKYVITTYEGIHNHESP

>GmWRKY50-like\_Glycine\_max  
SEVEILDDGFKWRWKYGKMKVKNPNPRNYRCSVDGCVKKRVERDKDDPRYVITTYEGIHNHQSYI

>RcWRKY50-like Ricinus communis  
SEIEILDDGFKWRWKYGKMKVKNPNPRNYRCSVEGCPVKKRVERDKDDLRFVITTYEGIHNHPS

>MtWRKY50-like\_Medicago\_truncatula  
SEIEILDDGFKWRWKYGKMKVKNPNPRNYRCSVEGCPVKKRVERDKDDLRFVITTYEGIHNHPS

>ZmWRKY67\_Zea\_mays  
SEVEILDDGFKWRWKYGKMAVKNPNPRNYRCSSEGGCVKKRVERDRDDPRYVITTYDGVHNHASP

>VvWRKY51\_Vitis\_vinifera  
SDLEIMDDGFKWRWKYGKMSVKNPNPRNYKCSAGGCNVKKRVERDREDSSYVITTYEGVHNHESP

>PpWRKY1  
KLADIPSDEYSWRWKYGQKPIKGSPPHPRGYKCSSIRGCPARKHVERSMEDSSMLIVTYEGDHNHPQS

>PpWRKY2  
KLADIPDDYSWRWKYGQKPIKGSPPHPRGYKCSSIRGCPARKHVERSMEDPTMLIVTYEGNHLHRTQ

>PpWRKY3  
SEIDVMEDGYKWRWKYGQKAVKDSPPFRSYRCTNQTCPVRKRVERKAGDAGLVVTTYEGTHSHLSP

>PpWRKY4  
SDVDILDDGYRWRWKYGQKVVGKGNPHPRSYKCTNVGCPVRKHVERASNDPKAVITTYEGKHNHDVP

>PpWRKY5  
DGCQWRWKYGQKMAKGNPWPFRAYFRCTVSPGCPVRKQVQRCEEDTSLVTTYEGTHNHALS

>PpWRKY6  
SEVDVIDDGYKWRWKYGQKPVKSSPHPRNYRCTTANCPVRKRVERSIEDPGLIVTSYEGTHHPKI

>PpWRKY7  
KLADIPPEYSWRWKYGQKPIKGSPPHPRGYKCSSIRGCPARKHVERSMEDSTMLIVTYEGEHNHL

>PpWRKY8  
KLADIPDDYSWRWKYGQKPIKGSPPHPRGYKCSSIRGCPARKHVERSMEDPTMLIVTYEGEHNHPQS

>PpWRKY9  
KLADIPDDYSWRWKYGQKPIKGSPPHPRGYKCSSIRGCPARKHVERSMEDPTMLIVTYEGEHNHPQL

>PpWRKY10  
INDGQWRWKYGQKMAKGNPCPRAYRCTVMGCPVRKQVQRCAKDTSLVSTYEGTHNHPL

>PpWRKY11  
KTTDVMDDGYKWRKYGQKPVKSSPHPRNYYRCTTPNCPVRKRVERSTEDPDQVITTYEGRHTHQSP

>PpWRKY12  
TEVDVMEDGYKWRKYGQKPVKNSPHPRNYYRCTTAHCPVRKRVERSTEDPGLVITSYEGTHSH

>PpWRKY13  
QWRKYGQKMAKGNPCPRAYRCTVAPGCPVRKQVQRCADDISILVTTYEGTHNH

>PpWRKY14M  
SDVEIMEDGYKWRKYGQKAVKNSPHPRYRCTNPKCPVRKKVERSADDSSESVITTYEGTHTH

>PpWRKY15  
TEVDVIDDGYKWRKYGQKPVKNSVHPRNYYKCTTANCPVRKRVERCTDDPSHVLTTYDGTHTH

>PpWRKY16-NTD  
DRPSEDGYNWRKYGQKQVKGSEYPRSYKCTQANCPMKKKVERSHDGQVTEIVYKGDHNHPKP

>PpWRKY16-CTD  
SDVDILDDGYRWRKYGQKVVKGNPHPRSYKCTNVGCPVRKHVERASTDIKAVITTYEGKHNHDVP

>PpWRKY17  
SDVDIMEDGYKWRKYGQKAVKNSPYPRSYRCTNPDCPVRKRVERKADDHGLVTTYEGTHNH

>PpWRKY18  
TDVDIMDDGFKWRKYGQKAVKNSPHPRNYYRCTTPQCPVRKRVERSSEDAGLVITTYEGTHTH

>PpWRKY19  
MNDGCQWRKYGQKMAKGNPCPRAYRCTVAPGCPVRKQVQRCADDVSLITTYEGTHNHPL

>PpWRKY20  
SEVDVLEDGYKWRKYGQKAVKNSHPRSYRCTSHTCPVRKRIERKADDPGLVITTYEGTHNH

>PpWRKY21  
ADTDVLDDGYKWRKYGQKAVKNSPHPRNYYRCATPNCPVRKRVERCIEDPGLVATAYEGTHSHQFP

>PpWRKY22  
SDVEIMEDGYKWRKYGQKAVKNSPHPRSYRCTHMMCPVRKRVERSAEDTGLVITTYEGTHTH

>PpWRKY23-NTD  
DRPSEDGYNWRKYGQKQVKGSEYPRSYKCTQTNCPMKKKVERSHDGQVTEIVYKGDHNHPKP

>PpWRKY23-CTD  
SDVDILDDGYRWRKYGQKVVKGNPHPRSYKCTNVGCPVRKHVERASTDIKAVITTYEGKHNHDVP

>PpWRKY24  
TDVDIMDDGFKWRKYGQKAVKNSPYPRNYYRCTTPQCPVRKRVERSCEDSGLVITTYEGTHTH

>PpWRKY25  
IKGSPHPRGYKCSSMRGCLARKHVERSLEDSSMLIITYEGEHNHSRSTSVSAALLCT

>PpWRKY26  
SDVDIIDDGYRWRKYGQKPVKNSHPRNYYKCTTPNCLVKKQVERCTENPSNVMTTYGTHNH

>PpWRKY27  
TDTDVMDDGYKWRKYGQKAVKNSPHPRNYYRCTTLNCPVRKRVERCFDDPGVMVTTYEGTHTH

>PpWRKY28  
SILDIMEDGYKWRKYGQKAVKNSPHPRSYRCTNPKCPVRKKVERSADDSSELVITSYEGTHTH

>PpWRKY29  
TDVDVLDDGFKWRKYGQKAVKNSPHPRNYYRCTTPLCPVRKRVERSNEDAGLVITTYEGTHSH

>PpWRKY30  
TDLDMVEDGYKWRKYGQKTVLSSPYPRSYKCTTAGCRVRKQVSRVCDRGLVIASYEGEHHH

>PpWRKY31  
TDMVDLDDGFKWRKYGQKAVKNSPHPRNYYRCTTPLCPVRKRVERSKEDAGLVITTYEGTHSH

>PpWRKY32  
SDSTTMNDGCQWRKYGQNTAKGNLCPRGLLPLYCGALLSRPQAGFCDNVQRCVCAHDKSVLITTYEGTHNH  
IP

>PpWRKY33  
DGCHWRKYGQKMAKGNPCPRAYRCTLRLGCPVRKQVQRCADDLSILITTYEGTHNHP IPA

>PpWRKY34  
KRGIPDDGHRGWKKYGNKAIQNSNHCRGYYKCSLKECRAKCMVQLTDRDPTLFEVTVGKHSCSSS

>PpWRKY35  
KKGIPDDGHRGWKKYGNKSIQNSNHCRGYYKCSVKECRAKCMVQPTDKDPMVFEITYVGKHTCSST

>PpWRKY36  
KKGIPDDGHRGWKKYGNKSIQNSNHCRGYYKCSVKECRAKCMVQPTDTPVFEVTVGKHTCSST

>PpWRKY37  
KKGIPDDGHRGWKKYGNKAIQNSTFCRGYYKCSMKECRAKCMVQPTDTPNPSIFEVTVGKHTCSST

>PpWRKY38  
KKAIPDDDHRRGWKKYGNKTIQNSNFCRNLWEEETRTRTFVVAISGPTSECSDHVDMLDIRGYKCGMVDCRA  
KCMVQPTVQDPSIFEVTVGKHTCSGS

>SemWRKY1  
SDVDIMDDGFRWRKYGQKAVKNSPHRSYYRCTNSKCPVKKRVERSCEDPGIVITTYEGTHTH

>SemWRKY2  
APADDGFTWRKYGQKDILNSKFPRSYYRCTHQKELGCQATKYVQKCEDEPSMYQVTVYIGEHSQNA

>SemWRKY3  
WRKYGQKMAKGNPCPRAYRCTMASGCPVRKQVQRCADDTSVLVTTTYEGSHNHQLP

>SemWRKY4-NTD  
DGYNWRKYGQKQVKGCDNPRSYYRCTHPDCSAKLVERSVSGETTQIVYKGDHSHSKP

>SemWRKY4-CTD  
SEVDVLDDGYRWRKYGQKVVKGNPNPRSYYRCTNPGCPVRKHVERAADDPKAVITSYEGKHDHDP

>SemWRKY5-NTD  
FVERPSEDGFNWRKYGQKQVKGSEFPRSYYKCTSSGCPVKKKVERSQDQVTEIVYKGEHNHPRP

>SemWRKY5-CTD  
SEIDILDDGYRWRKYGQKIVKGNPYPRSYYKCTNVGCPVRKHVERASNDPKSVITTYEGKHNDVP

>SemWRKY6-NTD  
PAERSSDDGYNWRKYGQKLVKGSNPNPRSYYKCTYVNCMPKKKVERSPPDQVTEIVYEGEHNHPKP

>SemWRKY6-CTD  
SEVDILDDGYRWRKYGQKVVKGNPNPRSYYKCTNLGCPVRKHVERACDDPRAVITTYEGKHNDVP

>SemWRKY7  
MNDGCQWRKYGQKMAKGNPCPRAYRCTVAPGCPVRKQVQRCADDMSILITTYEGSHNHPLP

>SemWRKY8  
KIADIPQDEYSWRKYGQKPIKGSPPHPRGYYKCSLRGCPARKHVERCLDDPTMLRVTYEGEHSQVQ

>SemWRKY9  
KMAEIPDDYSWRKYGQKPIKGSPPHPRGYYKCSMRGCPARK

>SemWRKY10  
VSNKIADIPQDERKYGQKPIKGSPPHPRGYYKCSLRGCPARK

>SemWRKY11  
KKGQKRIREPRYAIQTRSEVDIMDDGYRWRKYGQKAVKNSPHRSYYRCTNTKCPVKKRVERSSDQGLV  
ITTYEGIHNH

>SemWRKY12  
MQQKRIVCVPVAGGGKPTGEVLPSPDMAWRKYGQKPIKGSPPHPRGYYRCSSSKGCARKQVERSRNDPTM  
LITTYTSEHNHPWPAHRNSLAGTTR

>SemWRKY13-NTD  
RPSEDGFNWRKYGQKQVKGSEFPRSYYKCTSSGCPVKKKVERSQDQVTEIVYKGEHNHPRP

>SemWRKY13-CTD  
SEIDILDDGYRWRKYGQKIVKGNPYPRSYYKCTNVGCPVRKHVERASNDPKSVITTYEGKHNDVP



>SemWRKY14  
SDVDIMDDGFRWRKYGQKAVKNSPHPRSYRCTNSKCPVKKRVERSCEDPGIVITTYEGTHTH

>SemWRKY15  
SEIDILDDGYRWRKYGQKVVGKGNPHPRYYYYKSSSGCAVRKHVERASNDPKSVITTYEGKHNDVP

>SemWRKY16  
DDGYTWRKYGQKDILGSRHPKSYRCTHKRESGCPAICYVQRSDSNPSSFQITRGEHTCNML

>SemWRKY17  
KIADIPQDEYSWRKYGQKPIKGSPPHPRGYYKCSSLRGCPARKHVERCLDDPTMLRVTYEGEHSBGVQ

>Sem\_WRKY18  
KMAEIPDDYSWRKYGQKPIKGSPPHPRGYYKCSSMRGCPARK

>Sem\_WRKY19  
MFLDGGTHQKASQAGIKGSPPHPRGYYKCSSLRGCPARKHVERCLDDPTTDAGERSHGVQPQ

>SemWRKY20-NTD  
PAERSSDDGYNWRKYGQKLVKGSNENPRSYRCTYVNCMPKKKVERSPPDGQVTEIVYEGEHNHPK

>SemWRKY20-CTD  
SEVDILDDGYRWRKYGQKVVGKGNPHPRSYRCTNLGCPVRKHVERACDDPRAVITTYEGKHNDVP

>SemWRKY21  
KLADIPDDYSWRKYGQKPIKGSPPHPRGYYKCSSMRGCPARK

>SemWRKY22-NTD  
ERPSEDGFNWRKYGQKQVKGSEFPRSYRCTHPSCPVKKKVERSYPDGQVTEIVYKGEHCHAKP

>SemWRKY22-CTD  
SEIDILDDGYRWRKYGQKVVGKGNPHPRYYYYKSSSGCAVRKHVERASNDPKSVITTYEGKHNDVP

>SemWRKY23  
MNDGCQWRKYGQKMAKGNPCPRAYRCTMSPGCPVRKQVQRCAEDTSLVITTYEGTHNHPLP

>SemWRKY24  
SDKEIMDDGYRWRKYGQKAVKNSPYPRSYRCTYTKCHVKKRVERSCKDSSLVITTYEGVHTH

>SemWRKY25  
APADDGFTWRKYGQKDILNSKFPRSYRCTHQKELGCQATKYVQKCEDEPSMYQVTYIGEHSQNA

>SemWRKY26  
MNDGCQWRKYGQKMAKGNPCPRAYRCTVAPGCPVRKQVQRCAEDMSILITTYEGSHNHPLP

>SemWRKY27  
DDGYTWRKYGQKDILGSRHPKSYRCTHKRESGCPAICYVQRSDSNPSSFQITRGEHTCNML

>SemWRKY28  
WRKYGQKMAKGNPCPRAYRCTMASGCPVRKQVQRCAEDTSLVITTYEGSHNHQLP

>SemWRKY29  
SEVDIMDDGYRWRKYGQKAVKNSPHPRSYRCTNTKCPVKKRVERSSEDQGLVITTYEGIHNH

>SemWRKY30  
SDVDIMDDGFRWRKYGQKAVKNSPHPRSYRCTNSKCPVKKRVERSCEDPGIVITTYEGTHTH

>SemWRKY31  
KLADIPDDYSWRKYGQKPIKGSPPHPRGYYKCSSMRGCPARK

>SemWRKY32  
SDKEIMDDGYRWRKYGQKAVKNSPYPRSYRCTYTKCHVKKRVERSCKDSSLVITTYEGVHTH

>SemWRKY33  
MNDGCQWRKYGQKMAKGNPCPRAYRCTMSPGCPVRKQVQRCAEDTSLVITTYEGTHNHPLP

>SemWRKY34  
TGEVLPSPDMAWRKYGQKPIKGSPPHPRGYYRCSKSSKGSARKQVERSRNDPTMLIITYTSEHNHPWP

>CocSub\_NTD  
NDDGYHWRKYGEKQVKGSPYPRSYRCSQNCQVKKIVERNPENGEVSKSASKGVHNHAKP

>CocSub\_CTD  
TDQDSMDDGYRWRKYGQKIVKGNPHPRSYKCTVAGCTVRKHVGRSATEAGVLVTSYEGQHNHPQP

>Tetrapisispora blattae CBS 6284  
SQSKLLDVEIEWEKYGVNLAEYILEDEELLALYHSGLL

>Cyanidioschyzon merolae  
RCILLEAFDCSWRKYEHSVGCLTAENLLPRVCQHVNFVPWNGHCENSRGCITNGETSTLVRYPVSIGDCD  
TGSSSIPGENDVVFSSIHSTEVW

>Chr\_h\_WRKY\_EST\_BQ821537  
VDITNMDDGYRWRKYGQKQVKGSPFPRAYYKCTHMGCSVRKHVERSAEDETFRFVVTYEGTHSHRLP

>XP\_003061495\_MiPu  
MPGVDDGYRWRKYGQKIIKGAFFPRSYRCTSANCPARKHVEGDPSSLSSLYEGEHNHEKP

>XP\_003054981\_MiPu  
TSDIRIDDGYRWRKYGQKLIKGSPPFRSYKCTSENSMQKHVEQSADNPPLYVVVYHSDRSQANVVYAK  
LKESAPTLKITMHGLDE

>XP\_002509266\_MiPu  
PAMPPESEDGYRWRKYGQKIIKGAFFPRSYRCTAPNCPARKHVEGDPKDPGSIAYEGTHNHEPP

>MICPUN\_61119  
RRSDIEEDGYVWHKYGAKNVRGRKVGYFKCAHRGCEARKKVWRQANGDEAVEREGTHTHAAG

>ChvWRKY1-NTD\_Chlorella\_variabilis\_WRKY  
MANDDGYNWRKYGEKQVKGSPFPRSYKCSHPGCPAKKMIEREPKTGRISQAEKNEHNHAKP

>ChvWRKY1-CTD\_Chlorella\_variabilis\_WRKY  
TDADGMDDGYRWRKYGQKIVKGNPHPRSYKCTHPGCNVRKQVERSGRNARMLVTTYEGTHTHDPP

>OstISS1\_Ostreococcus\_tauri\_WRKY  
HNAHAHEDGYRWRKYGQKNIKGSRHPRSYRCTERGCPARKKTELASDDESEDEGEDRMRVTYEGVHTHP  
KP

>OstWRKY1\_Ostreococcus\_tauri\_WRKY  
TSEEKLLDDGFRWRKYGNKMLSGQPHPRAYYKCTSGCGKGFLLQKHVERIASKGREKHLFLVTTYGRSPGCE  
QTEELLEELYENFRARARSGGENLVDSVQMTRKRC

>OstWRKY33\_Ostreococcus\_tauri\_WRKY  
DEGVDENDGFRWRKYGCKLIAGNMVPHPTERSYYRCKHFGCPARKRVEVEKVTGATRTVYEFEHTRDGR

>OstWRKYputative\_Ostreococcus\_tauri\_WRKY  
APSSAHADGYRWRKYGQKNIKGSSFPFRSYRCTERGCPARKKTELRRASEDGEMETVVCYEGEHTHAKP

>Aspergillus flavus  
DDDEVSTDGLKWRKKGKCRSDLDLGLYLCGSGRCILGCLADKDCRRGQTCLGGQCRTAGGANPPSCKPY  
KQLCGANECCSGVCRLGWRLTRECKHSHK

>FLYWCH\_1\_human  
WDSPDPLRPLEFLRTSLGGRFLVHESFLYRKEKAAGEKVYWMCRDQARLGCERSRAITQGHRIMVMRSHCH  
QPD

>GCMA\_human  
KTDWFQEWPDYAKHIYSSDKNAQRHLSSWAMRNTNNHNSRILKKSCLGVVVCGRDCLAEGRKIYLRP  
AICDKARQKQQRKRCPCNDGPLKLIPCRGHGGFPVTNFWRHDFRIFQSKGEHDHPKPKETKLEAEARRA  
M

**Supplementary Table 2|** *At*WRKY protein sequences used for homology modeling.

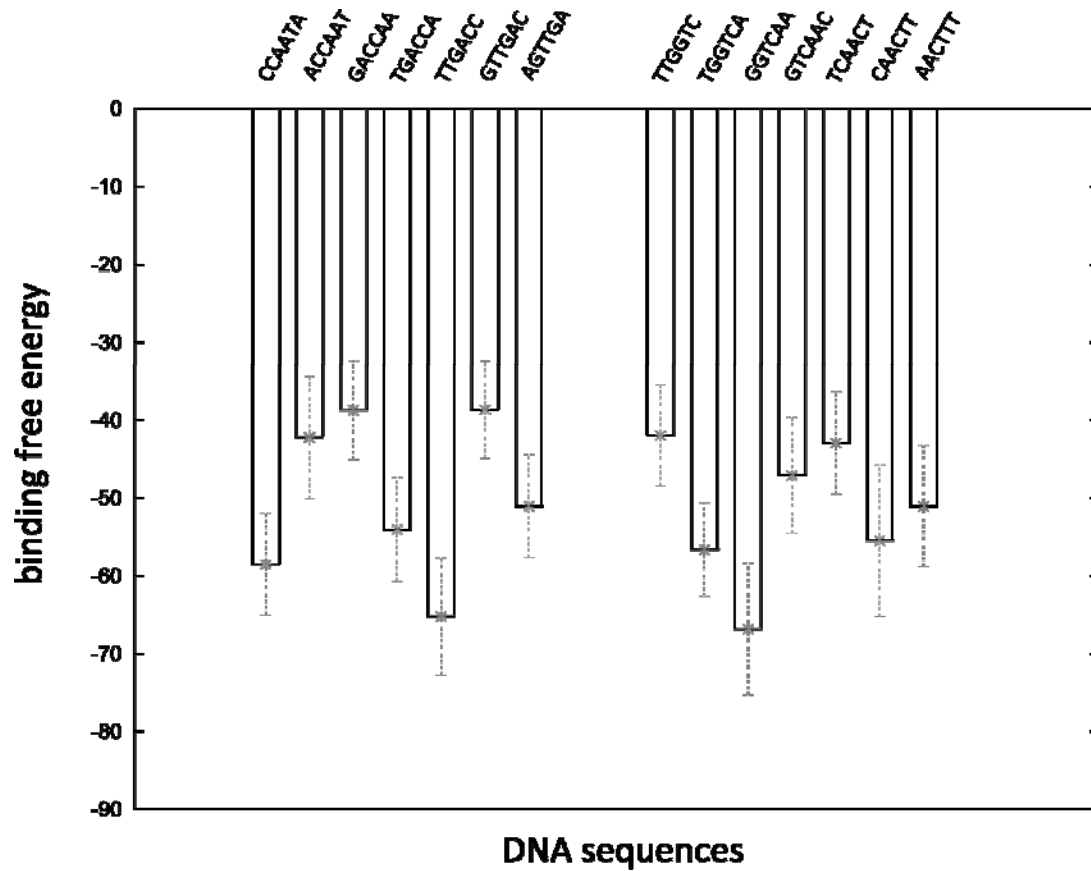
>AtWRKY1 cDBD  
SRIVVHTQTLFDIVNDGYRWRKYGQKSVKGSPPYRCSYRCSSPGCPVKKHVERSSHDTKLLITTYEGKHDHD  
MPPG

>AtWRKY11 DBD  
VRVPAISAKIADI PPDEYSWRKYGQKPIKGSPPRGYYKCSTFRGCPARKHVERALDDPAMLIVTYEGEHRH  
NQSA

>AtWRKY33 cDBD  
PRIVVQTSDIDILDDGYRWRKYGQKVVKGNPNRSYKCTTIGCPVRKHVERASHDMRAVITTYEGKHNHD  
VPAA

>AtWRKY33 nDBD  
NQAVSYNGREQRKGEDGYNWRKYGQKQVKGSNPNRSYKCTFPNCPTKKKVERSLEGQITEIVYKGSNHHPK  
PQS

>AtWRKY50 DBD  
GRVAFKTRSEVEVLDDGFKWRKYGKKMVKNSPHPRNYYKCSVDGCPVKKRVERDRDDPSFVITTYEGSHNHS  
SMN



**Supplementary Figure 2|** *At*WRKY1 cDBD - DNA binding interface. Binding free energies (in kcal/mol) are estimated between *At*WRKY1 cDBD and 14 different DNA sequences originating from the parsley PR1-1 Box W2 promoter sequence using MM-PBSA. The 12 base pair long DNA sequence containing the TTGACC motif at the position of the WRKY1 cDBD site has the second highest binding free energy, whereas only its reverse complement strand containing the GTTCAA sequence at the position of the WRKY1 cDBD site has a higher binding free energy.

**Supplementary Table 3|** Listed are the sites of close proximity (1-4 Å) during molecular dynamics simulation of *Arabidopsis thaliana* DNA binding domain WRKY1, WRKY11, WRKY11\_Q29K, WRKY33 c, WRKY33n, WRKY50 and WRKY50\_K26Q with DNA. Given is the occupancy in percent during 5 ns of simulation. Highlighted in red, blue and green are the proximity sites that exhibit more than 50 % occupancy and are present in seven, six or five simulations, respectively (n.s. – not shown in Figure 7). Highlighted in black are other proximity sites that exhibit > 50 % occupancy and presence in one to four of the MD simulations. The DNA sequence is as follows: 2-aagTTGACCaa-12; 23-ttCAACTGGtt-13. The amino acids of the respective proteins are numbered according to Supplementary Table 2.

DNA of consensus	W1 cDBD [%]		W11 DBD [%]		W11 DBD_Q29K [%]		W33 cDBD [%]		W33 nDBD [%]		W50 DBD [%]		W50 DBD_K26Q [%]		Fig. 7
Backbone T5	I37	71,2	I37	97,1	I37	95,8	I37	51,0	K37	99,8	V37	97,7	V37	96,8	n. s.
	K46	99,9	K46	99,9	K46	99,9	K46	99,9	K46	99,9	K46	99,9	K46	99,9	K 3
	Y62	99,9	Y62	99,9	Y62	99,9	Y62	99,9	Y62	99,9	Y62	99,9	Y62	99,9	Y 7
			Q49	52,7	K49	87,8	Q49	99,8	Q49	79,2	K49	95,2	Q49	99,6	Q/K 6
	D36	28,8	D36	59,1	D36	80,7	D36	42,9	R36	38,1	E36	58,5	E36	65,0	
							S60	67,1					N60	74,8	
Base T5	K46	99,6	K46	99,9	K46	99,8	K46	99,9	K46	99,9	K46	99,9	K46	99,9	K 3
	Y62	96,7	Y62	99,7	Y62	98,9	Y62	99,7	Y62	99,9	Y62	99,9	Y62	99,9	Y 7
			R45	95,0	R45	99,7	R45	60,4	R45	99,9	R45	59,9	R45	74,3	R 2
	I37	30,9	I37	94,4	I37	90,0	I37	20,8	K37	99,6	V37	89,0	V37	82,0	n. s.
									Y47	81,7					
				D36	20,9					E36	22,4				
								W44	23,0						
Backbone T6	Q49	99,3	Q49	99,4	K49	99,9	Q49	99,9	Q49	99,9	K49	99,8	Q49	99,9	Q/K 6
	K46	99,9	K46	99,8	K46	99,9	K46	99,9	K46	99,9	K46	99,9	K46	99,9	K 3
			G48	21,1			G48	59,4			N60	80,3	N60	95,9	
							S60	68,0			G48	33,1	G48	56,9	
	P58	33,7							P58	20,1			P58	25,7	
Base T6	K46	99,6	K46	99,9	K46	99,9	K46	99,9	K46	99,9	K46	99,9	K46	99,9	K 3
			Y47	84,6	Y47	64,2	Y47	61,2	Y47	99,5	Y47	57,8	Y47	75,5	Y 4
	Q49	83,9	Q49	90,2			Q49	99,9	Q49	97,0			Q49	99,9	Q/K 6
	G48	21,6	G48	71,7	G48	61,3			G48	77,1	G48	50,8	G48	25,9	
					R45	53,6			R45	56,9					
					K49	99,8					K49	99,4			
							S60	47,5					N60	87,2	



Supplementary Table 3|

DNA of consensus	W1 cDBD [%]		W11 DBD [%]		W11 DBD_Q29K [%]		W33 cDBD [%]		W33 nDBD [%]		W50 DBD [%]		W50 DBD_K26Q [%]		Fig. 7
Backbone G7			Q49	65,3	K49	98,2	Q49	52,8	Q49	92,8	K49	96,2	Q49	62,5	Q/K 6
									G48	32,3					
									Q51	20,5					
Base G7			Q49	47,4	K49	93,1	Q49	98,8	Q49	83,4	K49	88,5	Q49	99,6	Q/K 6
							G48	29,1	G48	37,8			G48	58,7	
							Y47	44,6	Y47	86,9			Y47	29,1	
									R45	25,3					
									K46	25,5					
Base A8			Y47	66,0	Y47	76,3	Y47	38,8	Y47	75,2					
					R45	41,3			R45	57,5					
Base A20			G48	38,6	G48	32,5	G48	31,2	G48	27,3			G48	62,1	
Base A19					R45	47,8			R45	48,1					
					R45	56,5									
Base C18			K46	21,1	K46	32,5							K46	26,7	
Backbone T17							R45	22,1			R45	56,8	R45	50,6	
Base T17	Y47	70,3	Y47	73,7	Y47	73,3	Y47	81,5	Y47	68,3	Y47	92,5	Y47	99,7	Y 4
					R45	46,0	R45	44,8	R45	69,0			R45	32,1	
	K46	22,7									K46	39,0	K46	66,3	
Backbone G16	R63	95,7	K63	73,1	K63	83,3	K63	99,8	K63	97,2	K63	91,2	K63	91,5	K/R 8
			F67	28,8			Y47	70,1			Y47	80,2	Y47	78,3	
							R45	99,9	R45	21,9	R45	99,9	R45	99,9	
			R68	36,0					K72	68,7			K72	42,1	
Base G16	R63	67,7	K63	46,3	K63	59,2	K63	95,9	K63	67,4	K63	50,4	K63	55,7	K/R 8
	Y47	77,4	Y47	32,9	Y47	41,8	Y47	64,4	Y47	41,5	Y47	94,0	Y47	97,8	
							R45	99,2	R45	26,3	R45	99,5	R45	93,1	
									K72	38,5			K72	27,9	
			R68	25,8											

DNA of consensus	W1 cDBD [%]		W11 DBD [%]		W11 DBD_Q29K [%]		W33 cDBD [%]		W33 nDBD [%]		W50 DBD [%]		W50 DBD_K26Q [%]		Fig. 7
Backbone G15	R63	99,9	K63	99,9	K63	99,8	K63	99,9	K63	69,5	K63	82,8	K63	80,8	K/R 8
	K72	99,9					R72	99,9	K72	99,9	K72	99,9	K72	99,9	K/R 9
	Y47	99,9	Y47	22,1	Y47	27,9	Y47	99,9	Y47	20,1	Y47	99,9	Y47	89,4	
							R45	96,9			R45	96,5	R45	97,2	
			R73	90,9	R73	85,6									
									K89	94,9					
	H74	21,8					V71	45,1							
						E90	35,3								
Base G15	K72	64,7					R72	99,9	K72	99,8	K72	99,4	K72	97,9	K/R 9
	Y47	99,1			Y47	28,5	Y47	99,9			Y47	99,1	Y47	78,8	
	R63	78,0	K63	94,2	K63	89,7	K63	99,2							
			R73	64,6	R73	53,0									
									K89	92,0					

DNA next to consensus	W1 cDBD [%]		W11 DBD [%]		W11 DBD_Q29K [%]		W33 cDBD [%]		W33 nDBD [%]		W50 DBD [%]		W50 DBD_K26Q [%]	
Backbone A2	R45	58,2	R45	83,7	R45	26,9								
											K43	84,3		
Backbone A3	R43	68,0	S43	58,5	S43	38,4	R43	86,8	N43	92,4	K43	99,8	K43	98,4
	R45	99,9	R45	93,9	R45	84,9			R45	52,9				
			W44	56,5	W44	27,1	W44	24,6	W44	47,9	W44	71,9	W44	22,6
						I37	22,5	K37	69,3					
Base A3	R45	94,8	R45	90,8	R45	74,2								
							R43	25,7			K43	96,6		
Backbone G4	W44	65,1	W44	92,2	W44	81,1	W44	95,2	W44	90,0	W44	97,6	W44	96,5
	I37	98,0	I37	99,9	I37	54,7	I37	99,1	K37	99,9	V37	99,9	V37	99,8
	Y62	23,8	Y62	89,4	Y62	47,5	Y62	97,8	Y62	72,6	Y62	93,3	Y62	89,4
			K46	97,7	K46	98,8	K46	97,7	K46	99,9	K46	99,7	K46	98,8
			S43	75,8	S43	65,0	R43	65,7	N43	63,0	K43	69,3	K43	76,3
	R45	75,4	R45	81,7	R45	77,1	R45	38,0	R45	61,8	R45	27,4	R45	25,2
								E39	20,8					

DNA next to consensus	W1 cDBD [%]		W11 DBD [%]		W11 DBD_Q <sup>29</sup> K [%]		W33 cDBD [%]		W33 nDBD [%]		W50 DBD [%]		W50 DBD_K <sup>26</sup> Q [%]	
Base G4	R45	33,5	R45	86,6	R45	76,9			R45	54,5	R45	29,5		
			W44	37,3	W44	44,3	W44	39,0	W44	41,8	W44	60,6	W44	62,4
									K37	99,5	V37	30,5	V37	40,2
			K46	24,3			K46	23,3			K46	24,9		
Backbone T13			K50	21,1	K50	56,8			K50	34,9	K50	82,0	K50	34,8
							R72	50,2						
					R73	60,2								
Base T13					LYS50	48,6			LYS50	31,3	LYS50	21,4		
Backbone T14	LYS72	72,3					ARG72	99,9	LYS72	95,4	LYS72	92,8	LYS72	71,0
	TYR47	42,9	TYR47	61,4	TYR47	92,0	TYR47	99,7	TYR47	33,9	TYR47	99,4	TYR47	77,4
	ARG63	21,7	LYS63	84,7	LYS63	72,0	LYS63	95,0						
			ARG73	53,6	ARG73	99,9								
					LYS50	46,3					LYS50	71,3	LYS50	25,9
			TYR61	37,3	TYR61	36,8	TYR61	53,8	TYR61	28,1	TYR61	30,8	TYR61	36,3
							HIS74	69,8						
									LYS89	97,6				
Base T14			TYR47	54,2	TYR47	64,7	TYR47	30,3	TYR47	32,7	TYR47	46,4	TYR47	34,8
	LYS50	25,3			LYS50	45,0	LYS50	30,1			LYS50	79,5	LYS50	42,7
							ARG72	99,9			LYS72	33,7		
					ARG73	96,5								

**Supplementary Table 4|** DNA sequences of *At*WRKY used for protein expression. In grey gene specific primers for PCR, in red primer regions for site directed mutagenesis.

AGI code	Gene name	Coding sequence
AT4G31550	WRKY11 DBD	ATGAAGAGAACCGTGAGAGTACCGGCGATAAGTGCAAAGATCGCCGATATTCACCGGACGAATATTCGTGGAGG AAGTACGGACAAAAACCGATCAAGGGCTCACCACACCCACGTGGTTACTACAAGTGCAGTACATTCAGAGGATGT CCAGCGAGGAAAACACGTGGAACGAGCATTAGATGATCCAGCGATGCTTATTTGTGACATACGAAGGAGAGCACCGT CATAACCAATCCGCGATGCAGGAGAATATTTCTTCTTCAGGCATTAATGATTTAGTGTTCCTCGCT
	WRKY11 DBD_Q <sup>29</sup> K	ATGAAGAGAACCGTGAGAGTACCGGCGATAAGTGCAAAGATCGCCGATATTCACCGGACGAATATTCGTGGAGG AAGTACGGAAAGAAACCGATCAAGGGCTCACCACACCCACGTGGTTACTACAAGTGCAGTACATTCAGAGGATGT CCAGCGAGGAAAACACGTGGAACGAGCATTAGATGATCCAGCGATGCTTATTTGTGACATACGAAGGAGAGCACCGT CATAACCAATCCGCGATGCAGGAGAATATTTCTTCTTCAGGCATTAATGATTTAGTGTTCCTCGCT
AT2G38470	WRKY33 nDBD	ATGAACAATCAAGCTGTATCTTACAATGGAAGAGAGCAAAGGAAAGGAGAGGATGGTTACAATTGGAGAAAGTAC GGACAAAAACAGGTGAAAGGAAGTGAATCCTCGGAGTTACTATAAGTGTACTTTCCCTAATTGTCCAACGAAG AAGAAAAGTGGAGAGATCTTTGGAAGGTCAGATCACAGAGATTGTGTATAAAGGAAGCCACAACCATCCTAAACCT CAGTCTACTAGAAGATCTTCTTCGTCTTCTTCGACTTTTCATTCAGCTGTGTACAATGCCAGTTTG
AT2G38470	WRKY33 cDBD	ATGAGAGAGCCGAGAATCGTAGTGCAGACAACGAGTGATATTGACATTCTTGACGACGGTTACAGATGGAGAAAA TACGGCCAGAAAGTCTGTTAAGGGAAACCCAAATCCAAGAAGCTACTACAAGTGCACAACCATCGGTTGTCCAGTG AGGAAACATGTGGAGAGAGCATCACACGACATGAGAGCAGTAATCACAACCTACGAAGGGAAACACAACCCAGT GTTCTTGCAGCTCGTGGTAGCGGTTACGCCACAAACAGAGCACCACAGGATTCGTCTTCAGTCCCGATTAGACCA GCTGCTATTGCTGGT
AT5G26170	WRKY50 DBD	ATGGGGAGAGTTGCGTTCAAGACACGGTCCGAGGTGGAAGTGCTTGACGACGGGTTCAAGTGGAGAAAGTATGGG AAGAAGATGGTGAAGAACAGCCACATCCAAGAACTACTACAAATGTTTCAGTTGATGGCTGTCCCGTGAAGAAA AGGGTTGAACGAGACAGAGATGATCCGAGCTTTGTGATAACAACCTTACGAGGGTTCCCAACACTCAAGCATG AAC
	WRKY50 DBD_K <sup>26</sup> Q	ATGGGGAGAGTTGCGTTCAAGACACGGTCCGAGGTGGAAGTGCTTGACGACGGGTTCAAGTGGAGAAAGTATGGG CAAAAGATGGTGAAGAACAGCCACATCCAAGAACTACTACAAATGTTTCAGTTGATGGCTGTCCCGTGAAGAAA AGGGTTGAACGAGACAGAGATGATCCGAGCTTTGTGATAACAACCTTACGAGGGTTCCCAACACTCAAGCATG AAC

**Supplementary Table 5|** Raw absorbance values of DPI-ELISA screens (cyane/white-probed with protein extract with respective WRKY DBD, orange-controls).

plate pos.	WRKY11	WRKY33c	WRKY50	WRKY33n	plate pos.	WRKY11	WRKY33c	WRKY50	WRKY33n
A1	0.65	2.1087	2.0019	0.7856	C5	0.55	1.4649	0.9164	0.5257
A2	0.31	1.2386	0.4032	0.4941	C6	0.48	1.7079	0.8717	0.3797
A3	0.34	0.715	0.3096	0.5655	C7	0.47	0.9457	0.3335	0.4013
A4	0.34	1.0465	0.5137	0.4797	C8	0.46	1.2998	0.8149	0.39
A5	0.42	1.5477	0.9649	0.687	C9	0.5	1.2396	0.3374	0.2982
A6	0.35	1.1817	0.8347	0.4907	C10	0.46	1.6042	0.7298	0.3533
A7	3.4	2.9214	2.2603	1.5161	C11	0.49	0.9917	0.4909	0.4795
A8	0.34	1.0255	1.0788	0.5008	C12	0.46	1.3099	0.7526	0.4179
A9	0.36	0.9935	0.3622	0.3528	C13	0.52	0.8373	0.6192	0.4314
A10	2.66	2.9373	1.452	0.521	C14	2.56	2.9322	1.8018	2.037
A11	0.75	1.443	0.5055	0.4389	C15	0.51	0.7818	0.2777	0.4304
A12	0.39	2.3229	0.9817	0.526	C16	0.48	1.1482	0.8958	0.4378
A13	0.37	0.8763	0.4218	0.4708	C17	0.48	0.9231	0.2064	0.3739
A14	0.37	1.0922	0.5316	0.5253	C18	0.52	1.1025	0.6195	0.4511
A15	0.37	0.8442	0.262	0.4714	C19	0.5	0.8603	0.3235	0.4946
A16	1.54	2.9287	2.216	0.573	C20	0.48	0.8328	0.5633	0.4355
A17	0.39	1.0181	0.4572	0.655	C21	0.48	0.8188	0.3446	0.3571
A18	0.43	1.407	0.876	0.5396	C22	0.47	1.1983	0.5032	0.4004
A19	0.37	0.6919	0.24	0.5131	C23	0.35	2.4587	0.1884	0.7164
A20	0.35	0.9461	0.4049	0.5406	C24	0.31	0.2648	0.2045	0.749
A21	0.36	1.6717	0.4284	0.4473	D1	0.44	1.4032	0.6974	0.5832
A22	0.38	1.6638	0.8718	0.522	D2	0.43	1.0473	0.2362	0.2978
A23	3.56	2.9385	0.1789	0.2315	D3	0.45	1.1416	0.4591	0.5333
A24	0.44	0.686	0.1852	0.2413	D4	0.46	1.2151	0.5369	0.417
B1	0.43	1.5361	0.4301	0.4656	D5	0.46	0.923	0.5627	0.4184
B2	0.75	1.6075	0.5034	0.3975	D6	0.46	1.3037	0.2373	0.3658
B3	0.42	1.7891	0.9969	0.5299	D7	0.47	1.2152	0.9535	0.3949
B4	0.5	2.4899	0.5656	0.4401	D8	0.48	0.9409	0.3902	0.4149
B5	0.43	1.1999	0.4247	0.4413	D9	0.47	1.2068	0.7252	0.3459
B6	0.44	1.261	0.385	0.463	D10	0.49	1.0273	0.2412	0.335
B7	0.46	1.7063	0.8911	0.3858	D11	0.48	1.2091	0.5932	0.4894
B8	0.45	1.1305	0.2684	0.3794	D12	0.48	1.1695	0.5171	0.4832
B9	0.47	1.5526	0.6388	0.3257	D13	0.49	1.0247	0.6451	0.422
B10	0.48	1.0746	0.2591	0.3141	D14	0.49	1.0856	0.2383	0.4043
B11	0.45	1.3997	0.5321	0.4081	D15	0.49	1.1206	0.2878	0.7166
B12	0.44	0.9907	0.301	0.4124	D16	0.48	1.1285	0.2378	0.4013
B13	0.47	1.293	0.7579	0.6162	D17	0.47	0.8908	0.3826	0.4444
B14	0.45	1.0717	0.2066	0.397	D18	0.47	0.9447	0.4083	0.3592
B15	0.45	0.9811	0.2691	0.5171	D19	0.48	0.8713	0.2664	0.4744
B16	0.44	1.2349	0.235	0.3391	D20	0.48	0.8604	0.1891	0.4072
B17	0.44	0.9865	0.402	0.4421	D21	0.49	1.2708	0.4105	0.3695
B18	0.45	1.1709	0.4778	0.5294	D22	0.5	2.6437	0.6652	0.4364
B19	0.44	0.927	0.2326	0.6537	D23	2.66	0.4464	0.2301	1.0625
B20	0.43	1.0974	0.2253	0.4322	D24	0.41	0.2371	0.2001	0.8589
B21	0.44	0.9318	0.5018	0.4396	E1	0.51	1.1687	0.398	0.5242
B22	0.61	1.5542	0.4053	0.4087	E2	0.51	1.6186	0.5811	0.4374
B23	2.92	2.9113	0.1892	0.2672	E3	0.64	0.8929	0.3216	0.6321
B24	0.46	1.6728	0.1784	0.2494	E4	0.66	2.6947	1.4331	0.476
C1	0.52	1.9277	0.5261	0.4913	E5	0.57	0.86	1.2056	0.4371
C2	0.42	1.3686	0.5229	0.4208	E6	0.53	1.7411	0.6932	0.4385
C3	0.47	0.866	0.996	0.5218	E7	0.55	0.8792	0.6745	0.4593
C4	0.49	1.8187	0.833	0.4697	E8	0.52	0.8993	1.1542	0.493



## Supplementary Table 5|

plate pos.	WRKY11	WRKY33c	WRKY50	WRKY33n	plate pos.	WRKY11	WRKY33c	WRKY50	WRKY33n
E9	0.54	0.7245	0.2831	0.3267	G16	0.49	0.785	0.9247	0.5127
E10	0.53	1.7528	1.0094	0.3546	G17	3.47	2.9249	1.2434	1.6722
E11	0.55	0.794	0.488	0.4556	G18	0.54	1.1164	1.2514	0.5987
E12	0.54	1.0115	0.5063	0.619	G19	0.57	0.7773	0.2456	0.6218
E13	2.66	2.9255	1.3679	1.2057	G20	0.51	0.8411	0.2512	0.4461
E14	0.56	0.8593	0.7039	0.4528	G21	0.45	0.9016	0.2841	0.4028
E15	0.57	0.9153	0.2512	0.386	G22	0.57	0.7956	0.3691	0.5002
E16	0.56	0.8434	0.6268	0.4286	G23	0.5	1.0569	0.2521	0.3457
E17	0.58	0.8598	0.2768	0.4234	G24	0.47	1.1035	0.3229	0.3917
E18	0.56	1.2155	1.0865	0.5233	H1	0.45	1.1006	0.4653	0.7377
E19	0.65	0.9577	0.2674	0.6585	H2	0.45	0.9116	0.2525	0.3261
E20	0.54	1.0039	0.321	0.6912	H3	0.46	1.302	0.4611	0.4337
E21	0.54	0.7379	0.6305	0.4713	H4	0.47	0.9088	0.3338	0.4827
E22	0.53	0.7899	0.266	0.4479	H5	0.48	2.3	0.7959	0.6786
E23	0.5	0.1916	0.1633	0.191	H6	1.65	2.9204	0.9447	0.4365
E24	0.5	0.2117	0.1719	0.2059	H7	0.49	1.676	0.6405	0.3903
F1	0.44	1.0159	0.3889	0.6392	H8	0.5	1.0477	0.3401	0.3605
F2	0.45	0.9799	0.2392	0.3166	H9	0.5	1.4036	0.7662	0.3224
F3	0.46	1.1559	0.3998	0.4448	H10	0.5	0.9646	0.3098	0.3416
F4	0.47	1.0629	0.2131	0.3879	H11	0.49	1.0989	0.3067	0.4094
F5	0.39	2.8839	0.5809	0.4214	H12	0.5	1.4416	0.4578	0.4109
F6	3.19	2.9229	0.9039	0.741	H13	0.51	0.9274	0.471	0.4438
F7	0.48	1.1258	0.3379	0.4421	H14	0.52	0.9374	0.2267	0.4132
F8	0.49	1.0552	0.4626	0.3923	H15	0.49	0.9707	0.4115	0.5869
F9	0.49	1.2476	0.4936	0.2758	H16	0.5	0.9424	0.3189	0.5123
F10	0.54	1.0073	0.2996	0.3141	H17	3.15	2.9299	1.127	1.3517
F11	0.5	1.2425	0.9335	0.4305	H18	0.49	0.9173	0.3166	0.4779
F12	0.5	1.7607	0.4489	0.399	H19	0.51	0.822	0.2544	0.6266
F13	0.5	0.9305	0.5875	0.4569	H20	0.51	0.8979	0.3502	0.4728
F14	0.52	0.8285	0.2052	0.3995	H21	0.51	0.9876	0.3872	0.441
F15	0.51	0.9638	0.3158	0.396	H22	0.51	2.6927	0.7402	0.4342
F16	0.53	0.9837	0.4073	0.4159	H23	0.5	2.0455	0.871	0.6013
F17	0.5	0.8635	0.2859	0.5327	H24	0.48	1.8957	0.6408	0.4682
F18	0.48	0.94	0.3025	0.433	I1	0.56	2.8628	1.4102	0.6238
F19	0.5	1.0312	0.6825	0.3772	I2	0.51	2.9216	1.5723	0.5471
F20	0.49	0.9836	0.2177	0.4538	I3	0.52	0.7957	0.3378	0.5069
F21	0.49	1.0824	0.4206	0.3612	I4	0.57	1.3715	0.8823	0.4173
F22	0.5	2.7127	0.735	0.424	I5	0.62	1.038	0.5385	0.5162
F23	0.46	0.301	0.1614	0.1854	I6	0.53	0.9627	0.5085	0.4429
F24	0.46	0.2577	0.1728	0.1913	I7	2.08	2.9273	1.8575	0.8778
G1	0.49	1.2954	0.4227	0.4555	I8	0.63	2.1893	1.052	0.4089
G2	0.44	1.0151	0.6031	0.4435	I9	0.56	0.8704	0.264	0.3241
G3	0.95	2.685	0.9866	0.9696	I10	0.54	1.2714	1.1087	0.3623
G4	0.5	1.4666	0.7857	0.4735	I11	0.56	0.8093	0.2398	0.5186
G5	0.55	0.8912	1.0407	0.6088	I12	3.19	2.9417	1.8507	1.5035
G6	0.46	1.8796	1.0263	0.4129	I13	0.97	1.3258	0.7646	0.5383
G7	0.53	1.1582	0.4919	0.3739	I14	0.58	1.7079	1.327	0.4747
G8	1.11	2.9349	1.0239	0.4635	I15	0.59	0.802	0.2556	0.4595
G9	0.53	1.1515	0.453	0.3361	I16	0.56	0.8983	0.8464	0.5043
G10	0.48	1.0463	0.668	0.3627	I17	1.14	1.7543	0.6781	0.7562
G11	0.66	1.3021	0.7923	1.2487	I18	0.56	1.5531	0.568	0.4645
G12	0.49	0.7998	1.0774	0.5601	I19	0.59	0.7926	0.2417	0.5658
G13	0.73	1.088	0.3783	0.4593	I20	0.56	0.9251	0.2499	0.5039
G14	0.51	1.187	0.789	0.4933	I21	0.59	0.9995	0.5605	0.4542
G15	0.5	0.7654	0.4095	0.5381	I22	0.56	0.9059	0.2563	0.6446

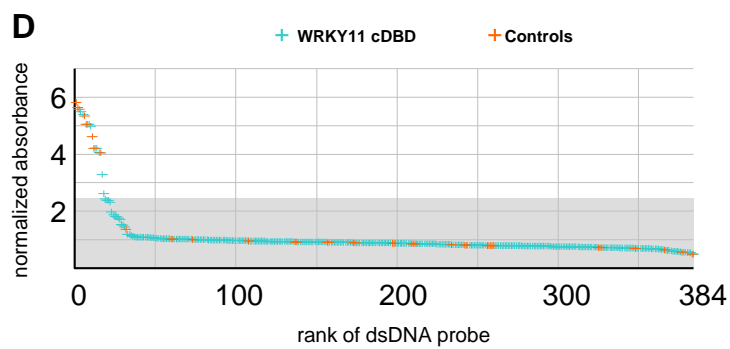
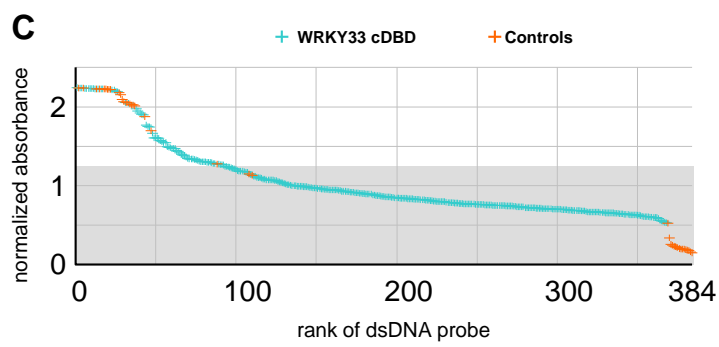
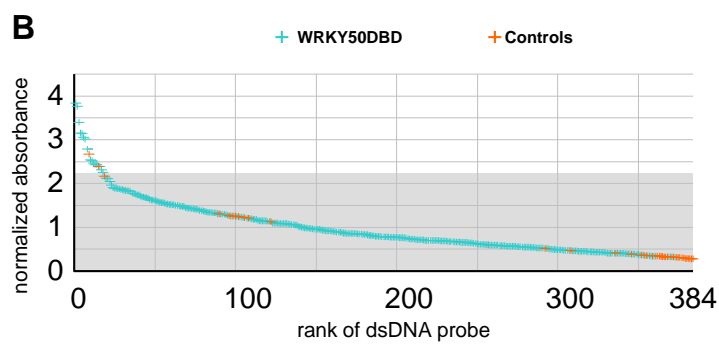
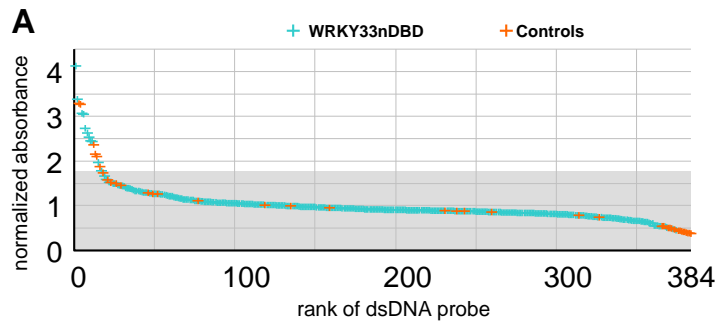
## Supplementary Table 5|

plate pos.	WRKY11	WRKY33c	WRKY50	WRKY33n	plate pos.	WRKY11	WRKY33c	WRKY50	WRKY33n
I23	0.55	1.192	0.4705	0.4208	L6	0.64	2.1113	0.4986	0.4695
I24	0.51	0.8554	0.357	0.4243	L7	0.6	1.4046	0.5579	0.4722
J1	0.55	2.9168	1.278	0.6358	L8	0.59	1.4256	0.3406	0.5041
J2	0.55	2.9158	0.7455	0.3691	L9	0.62	1.4366	0.567	0.3242
J3	0.51	1.3104	0.848	0.4379	L10	0.61	1.1905	0.28	0.3067
J4	0.54	0.994	0.6318	0.527	L11	0.91	1.7043	1.0802	0.823
J5	0.53	1.4498	0.5259	0.4059	L12	0.61	1.3163	0.3624	0.4497
J6	0.54	1.5388	0.3557	0.448	L13	0.64	1.0097	0.6754	0.4984
J7	0.61	2.4971	1.1101	0.4791	L14	1.08	2.9091	0.4161	0.4571
J8	0.56	1.1818	0.3204	0.4156	L15	1.15	2.5936	0.9205	0.7156
J9	0.55	1.7605	0.7812	0.3608	L16	0.63	1.1092	0.3619	0.4803
J10	0.54	1.2532	0.266	0.3194	L17	0.63	1.2468	0.5405	0.5576
J11	0.56	1.4015	0.3976	0.4369	L18	0.62	1.6265	0.3404	0.448
J12	0.58	1.7169	0.4682	0.4472	L19	0.64	1.2396	0.3445	0.6024
J13	0.58	0.9766	0.5531	0.6386	L20	0.64	1.0472	0.1889	0.5099
J14	0.57	0.9977	0.2276	0.4409	L21	0.62	1.2646	0.5437	0.4482
J15	0.56	0.9846	0.2741	0.5648	L22	0.64	2.7513	0.7692	0.4922
J16	0.56	1.2026	0.2799	0.4465	L23	0.63	1.0465	0.6408	0.4297
J17	0.58	1.0982	0.5109	0.6684	L24	0.61	0.9118	0.3368	0.3906
J18	0.56	0.9366	0.3254	0.5375	M1	0.86	0.2445	0.2073	1.1685
J19	0.56	1.1327	0.2381	0.6858	M2	0.5	0.2616	0.2394	1.0377
J20	0.69	0.9442	0.1858	0.422	M3	0.66	2.1099	0.8555	0.5084
J21	0.55	1.0037	0.3763	0.4481	M4	0.62	1.8181	0.7729	0.4646
J22	0.57	2.6537	0.7369	0.4716	M5	0.65	1.3564	0.5492	0.4531
J23	0.58	1.7667	1.4335	0.6249	M6	0.64	1.0258	0.626	0.4355
J24	0.54	0.8265	0.3849	0.502	M7	0.68	1.7127	0.6784	0.4442
K1	3.67	2.9238	0.1935	0.2672	M8	0.66	0.9809	0.782	0.4628
K2	0.64	1.5079	0.1857	0.246	M9	0.71	1.26	0.5927	0.2707
K3	0.53	0.8543	0.345	0.5607	M10	0.64	1.1259	0.9565	0.2743
K4	0.54	1.4081	0.9064	0.4664	M11	0.68	1.1702	0.5427	0.6418
K5	0.57	0.8258	0.3757	0.514	M12	0.68	1.9474	1.1019	0.6847
K6	0.54	1.2773	0.8994	0.4655	M13	0.69	0.8508	0.3869	0.566
K7	0.58	1.3272	0.4659	0.4544	M14	0.7	2.2907	0.9859	0.4889
K8	0.65	1.9523	0.8825	0.483	M15	0.68	0.873	0.3508	0.4206
K9	0.59	1.0097	0.4102	0.3294	M16	1.46	2.8737	1.4882	0.7079
K10	0.56	1.5825	0.8438	0.3643	M17	0.68	0.8328	0.2899	0.451
K11	0.59	1.0797	0.7156	0.6308	M18	1.25	2.9289	0.7882	0.5363
K12	0.56	1.0946	1.4962	0.5832	M19	0.69	0.9197	0.4221	0.3985
K13	1.51	1.0054	0.4533	0.4953	M20	0.67	0.9647	0.3111	0.4066
K14	0.58	1.7026	1.0976	0.5422	M21	0.67	1.5655	0.4766	0.4556
K15	0.6	0.8753	0.3752	0.4275	M22	0.67	1.9315	0.9516	0.4352
K16	0.58	0.9735	0.4636	0.4511	M23	0.65	1.2832	0.427	0.382
K17	0.59	0.7029	0.3627	0.4966	M24	0.65	1.1104	0.4545	0.424
K18	0.57	1.2657	0.8913	0.5234	N1	2.55	0.28	0.2763	1.6241
K19	0.6	0.8285	0.2719	0.5498	N2	0.58	0.2561	0.1898	0.6277
K20	0.56	0.8724	0.2715	0.427	N3	0.59	2.0283	0.8472	0.5788
K21	0.58	1.0593	0.64	0.4126	N4	0.57	1.2355	0.3339	0.4995
K22	0.58	0.9453	0.6696	0.5052	N5	0.57	1.6527	0.6734	0.4994
K23	0.56	1.2453	0.3448	0.372	N6	0.58	1.7377	0.3919	0.4817
K24	0.58	1.1095	0.4134	0.4412	N7	0.64	2.0584	0.8301	0.4466
L1	3.19	2.9198	0.2164	0.3885	N8	0.59	1.1211	0.2431	0.418
L2	0.57	2.8275	0.1674	0.2196	N9	0.59	1.4247	0.7397	0.2762
L3	1.18	2.9083	1.7748	1.2098	N10	0.58	1.0045	0.2287	0.2404
L4	0.58	1.6774	0.5041	0.425	N11	0.63	2.0348	0.6936	0.4968
L5	0.68	1.6927	1.4086	0.655	N12	0.6	1.5899	0.4381	0.4424

## Supplementary Table 5|

plate pos.	WRKY11	WRKY33c	WRKY50	WRKY33n
N13	0.61	1.0815	1.0899	1.2956
N14	0.61	1.0298	0.2332	0.4426
N15	0.59	0.9294	0.2885	0.5091
N16	0.61	0.9083	0.2833	0.4923
N17	0.61	1.0739	0.4459	0.447
N18	1.51	1.8586	0.3903	0.4342
N19	0.6	0.9253	0.2959	0.4567
N20	0.63	0.9979	0.2032	0.4778
N21	0.62	1.1446	0.5035	0.5469
N22	0.63	2.2244	0.7179	0.504
N23	0.62	1.2089	0.5766	0.4461
N24	0.63	1.5025	0.4488	0.4394
O1	0.54	0.2485	0.1724	0.2075
O2	0.54	0.2941	0.1877	0.1968
O3	0.59	0.8739	0.4129	0.5076
O4	0.55	1.3129	0.5002	0.722
O5	0.61	1.1988	0.5777	0.5987
O6	0.6	2.0991	0.736	0.4332
O7	0.6	0.9977	0.4812	0.5472
O8	0.59	0.9784	1.0338	0.4789
O9	0.61	1.6645	0.4552	0.2523
O10	0.59	1.7103	0.7999	0.2233
O11	0.63	1.0739	0.3808	0.4607
O12	0.62	0.9457	1.1145	0.5308
O13	3.52	2.9342	0.209	0.7375
O14	0.6	1.4815	0.2016	0.9249
O15	0.61	0.8961	0.2591	0.4328
O16	0.59	1.3445	0.8174	0.4574
O17	0.64	0.8747	0.348	0.4271
O18	0.62	0.8779	0.8391	0.4623
O19	0.61	0.8494	0.3308	0.4343
O20	0.62	0.8286	0.3077	0.4115
O21	0.64	0.992	0.6357	0.412
O22	0.62	1.9261	1.1066	0.4494
O23	0.62	1.6363	0.7071	0.4029
O24	0.6	0.924	0.4409	0.4212
P1	0.54	0.3206	0.1967	0.2157
P2	0.52	0.3362	0.1831	0.2126
P3	0.6	1.2877	0.6436	0.5217
P4	0.58	0.9659	0.357	0.4143
P5	0.64	2.5212	0.6444	0.6231
P6	0.58	1.8371	0.9255	0.3396
P7	0.57	1.9644	1.643	0.5132
P8	0.55	1.3517	0.408	0.4509
P9	0.55	1.2409	0.7415	0.263
P10	0.63	2.5555	0.4477	0.2697
P11	0.59	1.3061	0.7654	0.5713
P12	0.56	1.6335	0.4102	0.4685
P13	3.37	2.9188	0.3031	1.6134
P14	0.56	2.6579	0.1919	0.7826
P15	0.56	1.0876	0.8063	0.4843
P16	0.57	0.9869	0.4621	0.4814
P17	0.58	1.3841	0.7187	0.4616
P18	0.56	1.0022	0.4289	0.4488
P19	0.59	1.0319	0.326	0.5179

plate pos.	WRKY11	WRKY33c	WRKY50	WRKY33n
P20	0.6	0.9272	0.2038	0.4009
P21	0.59	0.9757	0.4006	0.4147
P22	0.58	2.6696	0.7154	0.4385
P23	0.57	1.2768	0.6425	0.4207
P24	0.57	1.0932	0.3312	0.3836



**Supplementary Figure 3|** S-plot diagrams of all four DPI-ELISA screens. The DPI-ELISA screen of WRKY33 nDBD (A), WRKY50 cDBD (B), WRKY33 cDBD (C) and WRKY11 cDBD (D) are shown. The photometric readout of the plates was normalized to the mean and ranked according to its relative normalized absorbance. Control probes: orange; library dsDNA probes: cyan; non-significant background signal is highlighted in grey, confidence level of positively revealed signals:  $p < 0.05$ .

**Supplementary Table 6|** Relative binding values of DPI-ELISA screens. Wells probed with WRKY protein extract are given with dsDNA probe sequences, plate position and binding in percent (raw absorbance values relative to highest - highest value equals 100%), mean, standard deviation and significance threshold are given below individual experiments.

sense probe 5' – 3'	antisense probe 5' – 3'	plate pos.	WRKY 11	WRKY 33c	WRKY 50	WRKY 33n
AAAAAAGTCTAGTCGTA AAAA	TTTTTACGACTAGACTTTTTTT	A1	18.73	71.68	88.57	38.57
AAAAAACGGTAAAGTCGACAAAA	TTTTGTGCGACTTACCGTTTTTT	C1	14.99	65.53	23.28	24.12
AAAAAATTACGTTTGTATTTGTA AAA	TTTTACAAATACAAACGTAATTTTT	E1	14.70	39.73	17.61	25.73
AAAAAACGATACGGTATCTAGAAAA	TTTTCTAGATACCGTATCGTTTTTT	G1	14.12	44.04	18.70	22.36
AAAAAATCCCACTTCAATCTAAAA	TTTTTAGAATGAAGTGGGATTTTTTT	I23	15.85	40.52	20.82	20.66
AAAAAATTACGCGGGATCGCCAAA	TTTTGGCGATCCCGCGTAATTTTTTT	K23	16.14	42.33	15.25	18.26
AAAAAAGCTTCGCGCCAGCGGAAAA	TTTTCCCGCTGCGCGCAAGCTTTTTTT	M23	18.73	43.62	18.89	18.75
AAAAATGACCAGGCTCGAGCAAAA	TTTTTGCTCGAGGCTGGTCATTTTTTT	O23	17.87	55.62	31.28	19.78
AAAAAAGTGCACGTTCAAGAAAA	TTTTTCTGAACGTTGGCACTTTTTTTT	A2	8.93	42.10	17.84	24.26
AAAAAACCGCGTCGCGCCCGGAAAA	TTTTCCCGGGCCGCGACGCGGTTTTTTT	C2	12.10	46.52	23.13	20.66
AAAAAAGGGCCACTATCGACGTCAAA	TTTTGACGTCGATAGTGGGCCCTTTTTTT	E2	14.70	55.02	25.71	21.47
AAAAAAGCTTCTATAGCTCCATGGAAA	TTTTCCATGGAGCTATAGAAGCTTTTTTTT	G2	12.68	34.51	26.68	21.77
AAAAAACCCGTGTTCGCGCGATAAAAA	TTTTTTATCGGCGCACACAGGGTTTTTTT	I24	14.70	29.08	15.79	20.83
AAAAAACTCAACTAGTGAACCACCAAAA	TTTTGGTGGTTCACTAGTTGAGTTTTTTT	K24	16.71	37.72	18.29	21.66
AAAAAATCCGATCGATGCATATATAAAA	TTTTATATATGCATCGATCGGATTTTTTTT	M24	18.73	37.75	20.11	20.81
AAAAAAGTGTAGATGTAGTTGATAAAA	TTTTATCAACTACAATCTAACACTTTTTTTT	O24	17.29	31.41	19.51	20.68
AAAAAAGGGCGAGCGCTGGATCCAAAA	TTTTGTGGATCCAGCGCTCGCCCTTTTTTT	B1	12.39	52.22	19.03	22.86
AAAAATCCTGTTTGGCTTTGATTTAAAA	TTTTAAAATCAAACGCAACAGGATTTTTTTT	D1	12.68	47.70	30.85	28.63
AAAAATGAATCAATTTTTGGGCTTAAAA	TTTTAAAGCCCAAAAATTGATTCATTTTTTT	F1	12.68	34.53	17.21	31.38
AAAAAAGTGTACTTATTACTTTAAAA	TTTTAAAGTATAATAAGTACAACCTTTTTTTT	H1	12.97	37.41	20.59	36.22
AAAAAAGGGAGTCATGCTTCTTGTAAAA	TTTTAAACAAGAGCATGACTCCCTTTTTTTT	J23	16.71	60.06	63.42	30.68
AAAAATCTTCACCTCACTTCGGTTAAAA	TTTTAAACCGAAGTGAAGTGAAGATTTTTTTT	L23	18.16	35.57	28.35	21.09
AAAAAAGTTCGTCGTTAACCCAGTTAAAA	TTTTAAACTGGGTAAAGCACGAACCTTTTTTT	N23	17.87	41.10	25.51	21.90
AAAAAATAAGTCTAGCGCTACGTA AAAA	TTTTTTACGTACGCGTAGCATTTTTTTTTT	P23	16.43	43.40	28.43	20.65
AAAAAATAAGTCTAGCGCTACGTA AAAA	TTTTCGGAAGTCCAAATTCGATTTTTTTTTT	B2	21.61	54.65	22.27	19.51
AAAAAATAATTCGAGCCTCGCGTAAAA	TTTTTACGCGAGGCTCGAAATTTTTTTTTT	D2	12.39	35.60	10.45	14.62
AAAAAAGTGTGCTAGCTCGAGTTCTAAAA	TTTTAAGAACTCGACGTACCAACCTTTTTTTT	F2	12.97	33.31	10.58	15.54
AAAAATATGTTTTTCGCTTTATTCTTAAAA	TTTTAAGAATAAAGCGAAAAACATTTTTTTT	H2	12.97	30.99	11.17	16.01
AAAAAATCTTTCGCTCGAGATTCTTAAAA	TTTTAAGAATCTCGACGCAAGATTTTTTTTTT	J24	15.56	28.10	17.03	24.64
AAAAAATAAGCCTGGGGTTCGCATAAAA	TTTTATGCGAACCCCGAGGCTTTTTTTTTT	L24	17.58	31.00	14.90	19.18
AAAAATCCACGACTCAGCAGCTCTTAAAA	TTTTAAGAGCTGCTGAGTCTGTGGATTTTTTTT	N24	18.16	51.08	19.86	21.57
AAAAACCTACGATGGTCTGATCTTAAAA	TTTTAAGATCAGAACCATCGTAGGTTTTTTT	P24	16.43	37.16	14.65	18.83
AAAAATTTTTGTTTTTTCGCTTTTAAAA	TTTTAAGGAAAAGCAAAAACAAAATTTTTTTT	A3	9.80	24.31	13.70	27.76
AAAAAAGGACATTTTTTCTTTTAAAA	TTTTCAAAAAGAAAAATGTCCTTTTTTTTTT	C3	13.54	29.44	44.06	25.62
AAAAACCTTCCCTCTTCTGCCTTAAAA	TTTTAAGCAGAAAGAGGGGAAAGTTTTTTT	E3	18.44	30.35	14.23	31.03
AAAAATTTGGTCTTCGCTCTCGTTAAAA	TTTTAAGCGAGGACGAAGACCAAAATTTTTTTT	G3	27.38	91.27	43.65	47.60
AAAAAAGCGTTACATCATATGGAAAA	TTTTTTCCATATGATGTAACGCTTTTTTTTTT	I3	14.99	27.05	14.94	24.88
AAAAATTTACTTTTACCTTTGTGTTAAAA	TTTTAAGCCAGGATCAAGTATAAAATTTTTTTT	K3	15.27	29.04	15.26	27.53
AAAAAAGCTTCGGAGCTTGAGAAAA	TTTTTCTCAAGACTCCGAAGCTTTTTTTTTT	M3	19.02	71.72	37.85	24.96
AAAAACTGTCTGTCTATATCACTTAAAA	TTTTAAGTGATAAGGACAGACAGTTTTTTTTT	O3	17.00	29.71	18.27	24.92
AAAAAACAACCTCCTAATAGCGAAAA	TTTTCGCTATTAGGAGGTTTTGTTTTTTTTT	A4	9.80	35.57	22.73	23.55
AAAAAAGTTCGACGATTGCGGGTAAAA	TTTTAACACAAAAGGTAAGGTAAGTAAAAATTTTTTTT	C4	14.12	61.82	36.85	23.06
AAAAAAGTTCATTGCTGCTGGTAAAA	TTTTAACACCAGCAGCAATGACCTTTTTTTTTT	E4	19.02	91.60	63.40	23.37
AAAAAAGTACATGCTAGATAATGTTAAAA	TTTTAACATTATCTACGCATGTACTTTTTTTT	G4	14.41	49.86	34.76	23.24
AAAAAAGTCTGGCGGGTTGAGAAAA	TTTTTCTCAACCCCGCCAGAGTTTTTTTTTT	I4	16.43	46.62	39.03	20.49
AAAAACCTTACTGTTGATCTGGTAAAA	TTTTAACCGAATCAACAGTAAGTTTTTTTTT	K4	15.56	47.87	40.10	22.90
AAAAAAGTTCGACGATTGCGGGTAAAA	TTTTAACCCGCAATCGTCGGCAACTTTTTTTT	M4	17.87	61.80	34.19	22.81
AAAAATTCACCTGATACTAGGGTAAAA	TTTTAACCTAGTATCAGGTGCAATTTTTTTT	O4	15.85	44.63	22.13	35.44
AAAAATTCGATTCACCTTAGGTTAAAA	TTTTAACCTAAGGGTGAAGTGAATTTTTTTT	B3	12.10	60.82	44.10	26.01
AAAAATGTCGATCCGCATGCAGTTAAAA	TTTTAAGTGCATGCGGATCGACCAATTTTTTTT	D3	12.97	38.81	20.31	26.18
AAAAAAGCTTCGCGCCCGGCTGGCAAAA	TTTTGCCAGCCGGGGCGACAGTTTTTTTTTT	F3	13.26	39.29	17.69	21.84
AAAAAAGCTCCCTACTACAACGAAAA	TTTTTCGGTTGTAGTATGGGAGTTTTTTTTT	H3	13.26	44.26	20.40	21.29
AAAAAATACTGCGCACTTGCCTCAAAA	TTTTGAGTGAAGTGCAGTATTTTTTTTTT	J3	14.70	44.55	37.52	21.50
AAAAAAGTCCGCCCTTAATTCATATAAAA	TTTTAATATGAATTAAGGGCGGACTTTTTTTT	L3	34.01	98.86	78.52	59.39
AAAAAATTCGTTTTCTGCTTTCAATAAAA	TTTTAATGAAAGACGAAAAACGAATTTTTTTT	N3	17.00	68.95	37.48	28.41

Supplementary Table 6|

sense probe 5' – 3'	antisense probe 5' – 3'	plate pos.	WRKY 11	WRKY 33c	WRKY 50	WRKY 33n
AAAAAAATCTTAGTCTCTATCTCATCAAAA	TTTTGATGAGATAGAGCTAAGATTTTTTTTT	P3	17.29	43.77	28.47	25.61
AAAAAAATTAGTCTCTTCGCTCCCAAAA	TTTTGGGAGACGAAGAGACTAATTTTTTTTT	B4	14.41	84.64	25.02	21.61
AAAAAACCCGGTTGGAGAAAATAATTA AAA	TTTTAATATATTTCTCCAACCGGGTTTTTTT	D4	13.26	41.31	23.75	20.47
AAAAAAATGGTGCCGCTGAGCAAATTA AAA	TTTTAATTTGCTCAGCGGCACCATTTTTTTTT	F4	13.54	36.13	9.43	19.04
AAAAAATCATTTTATTTGCCTTTCTAAAA	TTTTAGAAAGGCAAAAATAAAATGATTTTTTT	H4	13.54	30.89	14.77	23.70
AAAAAATCTTCTTGTCTTATTTCTAAAA	TTTTAGAAATAAGAAA CAAGAAGATTTTTTT	J4	15.56	33.79	27.95	25.87
AAAAAATCTATTCCATTTGCCTTTCTAAAA	TTTTAGAAGGCGAAATGGAATAGATTTTTTT	L4	16.71	57.02	22.30	20.86
AAAAAAGCCTTACCTTGTCTCTAAAA	TTTTAGAGGAACAAGGGTAAAGGCTTTTTTT	N4	16.43	42.00	14.77	24.52
AAAAAATCGGGCCCCGTTAGCACTCTAAAA	TTTTAGAGTGCTAACGGGGCCCCGATTTTTTT	P4	16.71	32.83	15.79	20.34
AAAAAAGTCATTTATAACCCAACTCTAAAA	TTTTAGAGTTTGGGTTATAATGACTTTTTTT	A5	12.10	52.61	42.69	33.73
AAAAAATATCGGGCACGCTTGTCTAAAA	TTTTAGACAAGACCGTGCCCGATATTTTTTT	C5	15.85	49.80	40.54	25.81
AAAAAAGGGTCTTTTCCAATGTCTAAAA	TTTTAGACATTTGAAAAGGACCCTTTTTTTT	E5	16.43	29.23	53.34	21.46
AAAAAATCTTTTTTCTTCAAGGTCTAAAA	TTTTAGACCTTGAAGAAAAAGAAATTTTTTT	G5	15.85	30.30	46.04	29.89
AAAAAAGTAGTTACTGCGAAAGTCTAAAA	TTTTAGACTTTCGCAGTAACACTTTTTTTTT	I5	17.87	35.29	23.82	25.34
AAAAAAGTGCCTTACGCTTGTATCTAAAA	TTTTAGATACAACGCTGAACGCACCTTTTTTT	K5	16.43	28.07	16.62	25.23
AAAAAAGCTCATGGCCCTGAGGATCTAAAA	TTTTAGATCCTCAGGGCCATGAGCTTTTTTT	M5	18.73	46.11	24.30	22.24
AAAAAATATATTTTCAGCTTTAATCTAAAA	TTTTAGATTAAAGCTGAAAATATATTTTTTT	O5	17.58	40.75	25.56	29.39
AAAAAATCCCTGCTCCCTGGTTCTCTAAAA	TTTTAGAACCCAGGGGAGCAGGGATTTTTTT	A6	10.09	40.17	36.93	24.09
AAAAAACCGTCTTATCTCTCGTCCCTAAAA	TTTTAGGACGAGAGATAAGACGGTTTTTTTT	C6	13.83	58.06	38.57	18.64
AAAAAAGGGTGTCTATTCGTCGACAAAA	TTTTGTGTCTGACGAATAAGCACCCCTTTTTTT	E6	15.27	59.19	30.67	21.53
AAAAAAGGGTCCGGTGCATACATGTA AAA	TTTTACATGTATGCACCGGACCCTTTTTTTTT	G6	13.26	63.90	45.41	20.27
AAAAAATGTGCTCTGCTCTGCTAAAA	TTTTAGGCGAGGGCAGAGGCACAATTTTTTT	I6	15.27	32.73	22.50	21.74
AAAAAATCCTATCTTGGCTTTGGCTAAAA	TTTTAGGCCAAAGCCCAAGATAGGATTTTTTT	K6	15.56	43.42	39.79	22.85
AAAAAAGGTTTGGGCTTACGTTATA AAA	TTTTATAACGTGAAGCCCAACCTTTTTTTTT	M6	18.44	34.87	27.70	21.38
AAAAAAGCTCGTCTCCGCTCCTGCTAAAA	TTTTAGCAGGAGGCGGAGACGAGCTTTTTTT	O6	17.29	71.36	32.56	21.27
AAAAAACCGACTGCACGCTGCTGCTAAAA	TTTTAGCAGCGAGCTGCAGGTCGGTTTTTTTT	B5	12.39	40.79	18.79	21.66
AAAAAATGCACGCTCCTTTCCCGCTAAAA	TTTTAGCGGAAAGGAGCGTTGCATTTTTTT	D5	13.26	31.38	24.89	20.54
AAAAAATATGTAGCTGCCGTTACGCTAAAA	TTTTAGCGTAACGGCAGCTACATATTTTTTT	F5	11.24	98.04	25.70	20.69
AAAAAATATTCGCCGTTAGCCACGCTAAAA	TTTTAGCGTGGTACC GGCGAATATTTTTTT	H5	13.83	78.19	35.21	33.31
AAAAAATCGCACTGCCGCGATGGCTAAAA	TTTTAGCCATCGGCGGAGTGCATTTTTTTTT	J5	15.27	49.28	23.27	19.93
AAAAAATCTTACTTTTGTCTTTACTAAAA	TTTTAGTAAAGACAAAAGTAAGAATTTTTTT	L5	19.60	57.54	62.32	32.16
AAAAAACATTCTAGTTCATGTTACTAAAA	TTTTAGTAAACATGAACTAGGAATGTTTTTT	N5	16.43	56.18	29.79	24.52
AAAAAATCAACCATTATGGTATTACTAAAA	TTTTAGTAATACCATAATGGTTGATTTTTTT	P5	18.44	85.71	28.51	30.59
AAAAAACCCAGCTCTGTTCTTACTAAAA	TTTTAGTAGAAACGAGCTGGGTGGTTTTTTTT	B6	12.68	42.87	17.03	22.73
AAAAAAGTATCAAAGCCTAGGGCTGAAAA	TTTTCAGCCCTAGGCTTTGATACTTTTTTTTT	D6	13.26	44.32	10.50	17.96
AAAAAAGTGGCCGCTAGTCAACTCAAAA	TTTTTGAGTTGACTAGCGGCCACTTTTTTTTT	F6	91.93	99.36	39.99	36.38
AAAAAAGTCTGCGCTGCAGGGCGGAAAA	TTTTCCGCCCTGCAGCCGACACTTTTTTTTT	H6	47.55	99.28	41.80	21.43
AAAAAAGTTACCAGTACGCGTCCGGAAAA	TTTTCCCGACCGCTACTGGTAACTTTTTTTTT	J6	15.56	52.31	15.74	21.99
AAAAAATCAGTCTGAGACTTACA ACTAAAA	TTTTAGTTGTAAGTCTCAGACTGATTTTTTT	L6	18.44	71.77	22.06	23.05
AAAAAAGTTCGCGGATTTCCGCCATAAAA	TTTTATGGCCGAAATCCGCGA ACTTTTTTTTT	N6	16.71	59.07	17.34	23.65
AAAAAAGTTCCAGGTCCGATGCTCAAAA	TTTTTGAGCATCGGACCTGGA ACTTTTTTTTT	P6	16.71	62.45	40.95	16.67
AAAAAAGTTTGACCTTGGCGTTCTGTA AAA	TTTTACGAACGCCAAGGTCAA ACTTTTTTTTT	A7	97.98	99.31	100	74.43
AAAAAACGGATTCGAACTTTTGTAAAA	TTTTACAAAAGTTTCAATCCC GTTTTTTTTT	C7	13.54	32.15	14.75	19.70
AAAAAACCTTCTGTTCTGTTCTGTA AAA	TTTTACAATCGAGAAATAAGAGGTTTTTTTT	E7	15.85	29.89	29.84	22.55
AAAAAAGTGTGTGCTTCTCTGTA AAA	TTTTACAGAGAGAAGCACAAACTTTTTTTTT	G7	15.27	39.37	21.76	18.36
AAAAAAGTCTAAGGACTTATAGCTGTA AAA	TTTTACAGCTATAAGTCTTAGACTTTTTTTTT	I7	59.94	99.51	82.18	43.09
AAAAAACAGCTCGGTGCCACTGTGAAAA	TTTTCCACAGTGGCACCAGGCTGTTTTTTTT	K7	16.71	45.12	20.61	22.31
AAAAAACACTGTATAGCATGGACGAAAA	TTTTCGTCCATGCTATACAGGTGTTTTTTTT	M7	19.60	58.22	30.01	21.81
AAAAATGCCCTTTTATCTTTATGTA AAA	TTTTACATAAAGATAAAAAGGCATTTTTTTTT	O7	17.29	33.92	21.29	26.86
AAAAAACGTTATGTATATCTATATGTA AAA	TTTTACATATAGATATACATACGGTTTTTTTT	A8	9.80	34.86	47.73	24.59
AAAAAACATCCACCCCGCGCGGAAAA	TTTTCGCGCCGCGGGTGTGGATGTTTTTTTT	C8	13.26	44.19	36.05	19.15
AAAAAAGTTCTGCTTTCCCTTTCTGTA AAA	TTTTACGAAAGGGAAGCAGAAACTTTTTTTTT	E8	14.99	30.57	51.06	24.20
AAAAAAGCGCTGACTGTAACTCGTA AAA	TTTTACGAGTTACAGTCAAGCCTTTTTTTTT	G8	31.99	99.77	45.30	22.75
AAAAAATACGCTACGTGGTTGTGTA AAA	TTTTACGACAACCAGTACGCTATTTTTTTTT	I8	18.16	74.42	46.54	20.07
AAAAAAGCTAAGCCTTGACAGTCTGTA AAA	TTTTACGACTGTCAAGGCTTACGCTTTTTTTTT	K8	18.73	66.37	39.04	23.71
AAAAAACCATCTCTTCTGTTCCATCGTA AAA	TTTTACGATGGAACGAAGGATGGGTTTTTTTT	M8	19.02	33.34	34.60	22.72
AAAAACTTCTAGTTTATGCTTCCGTAAAA	TTTTACGGAAGCATAACTAGAAGTTTTTTTT	O8	17.00	33.26	45.74	23.51
AAAAAACCTTCTGTTCCCTGTTCCGTA AAA	TTTTACGGGAACAGGGGACAGAAGTTTTTTTT	B7	13.26	58.00	39.42	18.94
AAAAAACCGGTTGTGAATGTGGAAGAAAA	TTTTCTTCCACATTCACAACCCGTTTTTTTT	D7	13.54	41.31	42.18	19.39
AAAAAATCGTAAATGCCATAGCCGTA AAA	TTTTACGGCTATGGGCATTTACGATTTTTTTTT	F7	13.83	38.27	14.95	21.70
AAAAAACCGTGTATAGTATTAGTGA AAA	TTTTCACTAATACTATGACACCGTTTTTTTT	H7	14.12	56.97	28.34	19.16
AAAAAATCAGCTGACTGTGGCGTAAAA	TTTTACGCCCAAGTACGGCTGATTTTTTTTT	J7	17.58	84.89	49.11	23.52
AAAAAACGCTATATATTGGTGTAGAAAA	TTTTCTAGCACCAATATATAGCGTTTTTTTT	L7	17.29	47.75	24.68	23.18
AAAAAACGCTCAAGTCTATCAGTAGAAAA	TTTTCTACTGATAGACTTGAGCGTTTTTTTT	N7	18.44	69.97	36.73	21.92

Supplementary Table 6|

sense probe 5' – 3'	antisense probe 5' – 3'	plate pos.	WRKY	WRKY	WRKY	WRKY
			11	33c	50	33n
AAAAAATTCGCGTGTATGTGTACGTAAAA	TTTTACGTACACATACACGCGGAATTTTT	P7	16.43	66.78	72.69	25.19
AAAAAAGCTAGTGTGCCACCAACGTAAAA	TTTTACGTTGGTGGCAGCACTAGCTTTTT	B8	12.97	38.43	11.87	18.63
AAAAAATACTCTTCCCTCGTTCCTGGTAAAA	TTTTACCAAGAACGAGGAAGAGTATTTTT	D8	13.83	31.98	17.26	20.37
AAAAAAGGAAAACGAGTTCATCTGGTAAAA	TTTTACCAGATGAACCTCGTTTTCTTTTT	F8	14.12	35.87	20.47	19.26
AAAAAACTCACGGCGTCACTATGGTAAAA	TTTTACCATAGTGACGCGGTGAGTTTTTT	H8	14.41	35.62	15.05	17.70
AAAAAACACAGCATTAGGCTATCGGTAAAA	TTTTACCGATAGCCTAATGCTGTGTTTT	J8	16.14	40.17	14.18	20.40
AAAAAACCGATTACCATTTTTACTGAAAA	TTTTCAGTAAAAATGGTAATCGTTTTTT	L8	17.00	48.46	15.07	24.75
AAAAAATAGACGCTACACTTACGGTAAAA	TTTTACCGTAAGTGTAGCGTCTAATTTTT	N8	17.00	38.11	10.76	20.52
AAAAAACCCGGCCGATGGTAGTAAAA	TTTTTACTACCATGGCGGCCGGTTTTTT	P8	15.85	45.95	18.05	22.14
AAAAAACCCGTGCCCTATTGCAAAAA	TTTTTGCAATAGGCAGGCACGGTTTTTT	A9	10.37	33.77	16.02	17.32
AAAAAACGCAACTCCGGATGTTGGGTAAAA	TTTTACCCACATCCGGAGTTGCGTTTTTT	C9	14.41	42.14	14.93	14.64
AAAAACGTTAACACTGATTTAGGGTAAAA	TTTTACCCTAAATCAGTGTAAACGTTTT	E9	15.56	24.63	12.52	16.04
AAAAAAGGTAGTCACATTACGAGGGTAAAA	TTTTACCCTCGTAATGTGACTACCTTTTT	G9	15.27	39.14	20.04	16.50
AAAAATAAACGTGTTTACTACTTAGTAAAA	TTTTACTAAGTATGAACACGTTTATTTTT	I9	16.14	29.59	11.68	15.91
AAAAAACTATAGTCTTTGTCATGATAAAAA	TTTTTATCATGACAAAGACTATAGTTTTTT	K9	17.00	34.32	18.15	16.17
AAAAATAGCGACTTCGACTCTCAGTAAAA	TTTTACTGAGAGTCAAGTTCGCTATTTTT	M9	20.46	42.83	26.22	13.29
AAAAATAGTGTGATGGTATCCAGTAAAA	TTTTACTGGATACCAATCACACTATTTTT	O9	17.58	56.58	20.14	12.39
AAAAAACTCTAGGTCATATTTATCAAAA	TTTTGAATAATATGACCTAGAGTTTTTT	A10	76.66	99.85	64.24	25.58
AAAAAACTCTCGGGTACAATTGCAAAAA	TTTTTGCAATTTGACCCGGAGAGTTTTTT	C10	13.26	54.53	32.29	17.34
AAAAAACTTTCTATTTCTGGATAAGTAAAA	TTTTACTTATCCAGAATAAGAAAGTTTTTT	E10	15.27	59.58	44.66	17.41
AAAAAATCGTTGTTATCGTATTTTAAAA	TTTTATAAATACGATAACAACGATTTTTTT	G10	13.83	35.57	29.55	17.81
AAAAAATCTTACCCCTCCGTTCTATAAAA	TTTTTATAGAAGCGGAGGGTAAAGTTTTTT	I10	15.56	43.22	49.05	17.79
AAAAAACCACTCTCTTTCGGACTATAAAA	TTTTTATAGTCCGAAAGAGAGTTGGTTTT	K10	16.14	53.80	37.33	17.88
AAAAAATGTCATCTGCGTCTGTATAAAA	TTTTATACAGACGCAAGATGGACATTTTT	M10	18.44	38.27	42.32	13.47
AAAAAAGTACGGATGCCCGCGCTATAAAA	TTTTTATACGCGGGGATCCGTACTTTTTTT	O10	17.00	58.14	35.39	10.96
AAAAAAGGTAATGCCGGTCCAGTATAAAA	TTTTTACTGGGACCGGCATTACCTTTTTTT	B9	13.54	52.78	28.26	15.99
AAAAAATATCCTATTCTAATTTATATAAAA	TTTTTATATAAATTAGAATAGGATATTTTT	D9	13.54	41.02	32.08	16.98
AAAAAATATTTGAGCTAGGTTATCAAAAA	TTTTTGATAACCTAGCTCAAATATTTTTTT	F9	14.12	42.41	21.84	13.54
AAAAAATCACAATACCTTCTCGTCATAAAA	TTTTATGACGAGAAGGATTTGTGATTTTT	H9	14.41	47.71	33.90	15.83
AAAAAAGAAATACCAGAACTATCATAAAA	TTTTATGATAGTTTCTGGTATTTCTTTTT	J9	15.85	59.85	34.56	17.71
AAAAAATGATGGCAATGCTCGCAAAAA	TTTTTTGCGAGCATTGGCAATCATTTTTTT	L9	17.87	48.84	25.09	15.92
AAAAAATGATTTGAGATCTCCGAGAAAA	TTTTCTCGGAGATCTGCAAATCATTTTTTT	N9	17.00	48.43	32.73	13.56
AAAAAATGCTTGCCCTGTCTCCATAAAA	TTTTATGGAGACAGGGCAAGCAGTTTTTT	P9	15.85	42.18	32.81	12.91
AAAAAATGTAATCGTGTCCACTCCATAAAA	TTTTATGGAGTGGACAGCAATACATTTTTTT	B10	13.83	36.53	11.46	15.42
AAAAAATCTCACTCTGGTCCCATATAAAA	TTTTATGGGACCAGGAGTGAGATTTTTTT	D10	14.12	34.92	10.67	16.45
AAAAAATGCGCCCTTCTGACATAAAAA	TTTTTTATGTGAGAAAGGGCGCATTTTTTT	F10	15.56	34.24	13.25	15.42
AAAAAATTTGTACTTTAAGTTTACATAAAA	TTTTTATGTAACCTTAAAGTACAAATTTTT	H10	14.41	32.79	13.71	16.77
AAAAAATGTTCAAGCTCGATCTACAAAA	TTTTGTAGATCGAGCTTGAACATTTTTTT	J10	15.56	42.60	11.77	15.68
AAAAAATCAGGTTTCGACTCCAGCAAAA	TTTTGCTGGAGTTCGAAACCGTATTTTTTT	L10	17.58	40.47	12.39	15.06
AAAAAATCATCCTATTGTTGCTGTCAAAA	TTTTGACAGCAACAATAGGATGATTTTTTT	N10	16.71	34.15	10.12	11.80
AAAAACGGTCCGATCGTTAATGATAAAA	TTTTTATCATTACGATCGCGACCGTTTTTT	P10	18.16	86.87	19.81	13.24
AAAAAATGCTAATCGGTGACCCGATAAAA	TTTTATCGGGTACCGATTAGCAGTTTTTT	A11	21.61	49.05	22.36	21.55
AAAAAAGTCCATAAATAAATGGATAAAA	TTTTATCCAATTTAGTTTATGGACTTTTTTT	C11	14.12	33.71	21.72	23.54
AAAAAATCAGATATTATTTACCCGAAAA	TTTTCGGGTCCAGAAATATAGGATTTTTTT	E11	15.85	26.99	21.59	22.37
AAAAAAGTCTCACCTTTAGTCTTAATAAAA	TTTTATTAAGACTAAAGGTGAGACTTTTTTT	G11	19.02	44.26	35.05	61.30
AAAAAATTTGATCATACTTCAAGTAAAA	TTTTCAACTGAAGTATGATACAATTTTTTT	I11	16.14	27.51	10.61	25.46
AAAAAATATTCGCTTTTGGCTGAATAAAA	TTTTATTCAGCCAAAAGCGGAATTTTTTT	K11	17.00	36.70	31.66	30.97
AAAAAATTCATGCTAATTTAACCTAAAA	TTTTTAAGGTTAAATAGCATGAATTTTTTT	M11	19.60	39.78	24.01	31.51
AAAAAATTCGCAACCTTACGTTTCAAAA	TTTTCGAACGTTGAGGTTGCGAATTTTTTT	O11	18.16	36.51	16.85	22.62
AAAAAAGACCGCAGCAAGAAATAAATAAAA	TTTTATTTAATTTCTGTGCTGGTCTTTTTTT	A12	11.24	78.96	43.43	25.82
AAAAAATGGAAGGAGGGATGAAATAAAA	TTTTATTTTATCCTCTCCTTCCATTTTTTT	C12	13.26	44.53	33.30	20.52
AAAAAATTTTGTGTTTAAATTTGGAAAA	TTTTCCAAAATTAATAAATAAATTTTTTT	E12	15.56	34.38	22.40	30.39
AAAAAATCCTTTTCTCTTTCTGTTTCAAAA	TTTTGAAAACAGAAAGAGAAAAGGATTTTTTT	G12	14.12	27.19	47.67	27.50
AAAAAATACATTTGACTTTGGGTTTCAAAA	TTTTGAAACCCAAAGTCAAATGATTTTTTT	I12	91.93	100	81.88	73.81
AAAAAATTTCTCCTTCTTTGTTCTTCAAAA	TTTTGAGAACAAGAAGGAGAAATTTTTTT	K12	16.14	37.21	66.19	28.63
AAAAAATAGTCTGATTCATCTTCAAAA	TTTTGAAGATTGAATCAGGACTAATTTTTTT	M12	19.60	66.20	48.75	33.61
AAAAAATCTGTTCTCGTTTCCCTTCAAAA	TTTTGAAGGGGAAACGAGAACAGATTTTTTT	O12	17.87	32.15	49.31	26.06
AAAAAATAAATCGCGGCTACTGTTTCAAAA	TTTTGAAGCAGTAGCCGCAATTTATTTTTTT	B11	12.97	47.58	23.54	20.03
AAAAAATGGTCTCATTCTACTTCAAAA	TTTTGAAGTAGAAATGAGAACCAATTTTTTT	D11	13.83	41.10	26.24	24.03
AAAAAACCCAGATTCCAGCAGTTCAAAA	TTTTGAAGTCTGGAATCTGGGGTTTTTTT	F11	14.41	42.24	41.30	21.13
AAAAACACTGCATATTGGGAGTTCAAAA	TTTTGAAGTCCCAATAGTGCAGTGTTTTTTT	H11	14.12	37.36	13.57	20.10
AAAAACCGGCAGTATTGGATATTCAAAA	TTTTGAATATCCAAATCGTCCGGTTTTTTT	J11	16.14	47.64	17.59	21.45
AAAAAAGTCTGCGTCTTACCCATCAAAA	TTTTGAATGGGATAGGACGAGACTTTTTTT	L11	26.22	57.94	47.79	40.40
AAAAAAGAAATGTCAGTGCCAAACAAA	TTTTGTTGGGACTGCAATTTCTTTTTTTT	N11	18.16	69.17	30.69	24.39



Supplementary Table 6|

sense probe 5' – 3'	antisense probe 5' – 3'	plate pos.	WRKY 11	WRKY 33c	WRKY 50	WRKY 33n
AAAAATCCATGTTTAAAGCTGGTCTCAAAA	TTTTGAGACCAGCTTAAACATGGATTTTT	P11	17.00	44.40	33.86	28.05
AAAAAAGTGTGCCCGTCCCATCTCAAAA	TTTTGAGATGGGACGGGACACAGTTTTTT	B12	12.68	33.68	13.32	20.25
AAAAAATCTTAGTTAGATTACCTCAAAA	TTTTGAGGTGAATCTAACTAAGAATTTTT	D12	13.83	39.76	22.88	23.72
AAAAACGCCGGACAATCAGGCGCTCAAAA	TTTTGAGCGCTGATTTGCCGCGTTTTTT	F12	14.41	59.85	19.86	19.59
AAAAACACTCACACCTATACGGCTCAAAA	TTTTGAGCCGTATAGGTGTGAGTGTTTTT	H12	14.41	49.01	20.25	20.17
AAAAAATCTGCTCCTCCGTTTACTCAAAA	TTTTGAGTAAAACGGAGGAGCAAGTTTTTT	J12	16.71	58.36	20.71	21.95
AAAAAAGAGTGGTTTATTAATGTATAAAA	TTTTTATACATTAATAAACACTCTTTTTT	L12	17.58	44.75	16.03	22.08
AAAAATCGGTACGCACCCCGGACTCAAAA	TTTTGAGTCCGCGGTGCGTACCGATTTTTT	N12	17.29	54.05	19.38	21.72
AAAAATAAGTAACCGAAGAACTCAAAA	TTTTGAGTTTCGTTCCGTTACTTATTTTTT	P12	16.14	55.53	18.15	23.00
AAAAAGACACTCTAATTCGCTAGGCAAAA	TTTTGCCCTACGGAATTAGAGTGTCTTTTTT	A13	10.66	29.79	18.66	23.11
AAAAATCCGTTCCATTTGTCGCTCAAAA	TTTTGACGGACAATGGGAACGGATTTTTT	C13	14.99	28.46	27.39	21.18
AAAAATGGTCGTCTACTCGTGGTCAAAA	TTTTGACCACGAGTACGACGACCATTTTTT	E13	76.66	99.45	60.52	59.19
AAAAACTACAACCTGCGCGGTGGTCAAAA	TTTTGACCACCGCGCAGGTTGTAGTTTTTT	G13	21.04	36.99	16.74	22.55
AAAAATGGAAGACCTATACCGGTCAAAA	TTTTGACCGGTATAGGTCTTTCCATTTTTT	I13	27.95	45.07	33.83	26.43
AAAAATATCTGATCCAATTTAGGTCAAAA	TTTTGACCTAAATGGATCAGATATTTTTT	K13	43.52	34.18	20.05	24.32
AAAAAGATGATTAGTAATTGCGGAAAAA	TTTTTTCCGCAATTAATAATCATCTTTTTT	M13	19.88	28.92	17.12	27.79
AAAAATATGGCACTCGCCGCACATCAAAA	TTTTGATGTGCGCGGAGTGCCATATTTTTT	L21	17.87	42.99	24.05	22.00
AAAAAGATCTAGGCCTTGGGACTCAAAA	TTTTTGAGTCCCAAGGCTAGATCTTTTTT	A14	10.66	37.13	23.52	25.79
AAAAAGATGACTCGTCTTACTCGAAAAA	TTTTTCGAGTAAGACGAGTCAATCTTTTTT	C14	73.78	99.68	79.72	100
AAAAACTCCCTCTCCTCTGCTTCCAAAA	TTTTGGAAGACAGAGGAGAGGGAGTTTTTT	E14	16.14	29.21	31.14	22.23
AAAAAGGAAGTACTGACGATCTGGAAAAA	TTTTTCCAGATCGTCACTTCTTTTTTT	G14	14.70	40.35	34.91	24.22
AAAAATTCCTGTCGCTCTCGCTCCAAAA	TTTTGGAGCGAGAGCGGACAGGAATTTTTT	I14	16.71	58.06	58.71	23.30
AAAAATCTAATCTAGCCTATGTCAAAAA	TTTTGGACATAGGCTAAGTTAGAATTTTTT	K14	16.71	57.88	48.56	26.62
AAAAAGGACGTCTTCGCTATGAGTAAAA	TTTTCACTCATAACCGAAGACGCTCTTTTTT	M14	20.17	77.87	43.62	24.00
AAAAAGCTGTCACGTAGTCCGCTCAAAA	TTTTGGACCGACTACAGTGACAGCTTTTTT	N21	17.87	38.91	22.28	26.85
AAAAATCCATTCTTCGCTTTATCCAAAA	TTTTGGATAAACCGGAAGAATGGATTTTTT	B13	13.54	43.95	33.53	30.25
AAAAAGTGTGTGGCTCAGGATTCAAAAA	TTTTGGGAATCCTGAGCCACACACTTTTTT	D13	14.12	34.83	28.54	20.72
AAAAACCTCTGTCTCTGCTCTCCAAAA	TTTTGGGAGAGCAGAGACAAGAGTTTTTT	F13	14.41	31.63	25.99	22.43
AAAAACCTTACCTATCCCTATCCAAAA	TTTTGGGATAGGGATAGGTAAGTTTTTT	H13	14.70	31.53	20.84	21.79
AAAAACTTCCCTCTGCTCTCCAAAA	TTTTGGGAGGACAAGGAGGGAAGTTTTTT	J13	16.71	33.20	24.47	31.35
AAAAATTTGCGCTTCACTCTGCCAAAA	TTTTGGGCGAGATGAAGCGCAATTTTTT	L13	18.44	34.32	29.88	24.47
AAAAATTTCTATTTTCACTTTGCCAAAA	TTTTGGGCAAGATGAATAGAAAATTTTTT	N13	17.58	36.76	48.22	63.60
AAAAATAATATCGATACTCATGCCAAAA	TTTTGGGCATGAGTATCGATATATTTTTT	P21	17.00	33.17	17.72	20.36
AAAAAGGGTATACCTCGCAGCCCTAAAA	TTTTTAGGGCTCGGATATACCTTTTTTT	B14	12.97	36.43	9.14	19.49
AAAAAGGGTCGCTGTGAGCTCATGAAAA	TTTTTCATGAGCTCACAGCGACCTTTTTT	D14	14.12	36.90	10.54	19.85
AAAAAGGGTTAGATGTCTTCAAAAAA	TTTTTTGAAGACATCTAAACCCTTTTTT	F14	14.99	28.16	9.08	19.61
AAAAAGGGTTGTGCGGAATTGCCAAAA	TTTTCGGCAATTCGCCACAAACCCTTTTTT	H14	14.99	31.87	10.03	20.28
AAAAAGCATATCTCAGAACTTGCCAAAA	TTTTGGCAAGTCTGAAGATATGCTTTTTT	J14	16.43	33.92	10.07	21.64
AAAAAGGCGCTGCTAGTTGCGGAGAAAA	TTTTCTCCCAACTACGACCGCCTTTTTT	L14	31.12	98.89	18.41	22.44
AAAAAGGCCACGGTAACCCCTTTGAAAA	TTTTCAAAGGGGTTACCGTGGCCTTTTTT	N14	17.58	35.01	10.32	21.73
AAAAAGGCCGTTGACCTCGGTCAAAAA	TTTTTAGACCGAGTCCAACCGCCTTTTTT	B22	17.58	52.83	17.93	20.06
AAAAAGGCCTTCGCTCGTGTTCGAAAA	TTTTCGTAAACACGAGCGAAGGCCTTTTTT	A15	10.66	28.70	11.59	23.14
AAAAAGGCTGTGGCAATGTTGTAAAAA	TTTTTACGAACATGGCCACAGCCTTTTTT	C15	14.70	26.58	12.29	21.13
AAAAAGGCTCCGGCCCAATCGCAAAAA	TTTTTGGCATTTGGGGCCGGAGCCTTTTTT	E15	16.43	31.11	11.11	18.95
AAAAAGGCTTCCACTTTGAGTTTGAAAA	TTTTGCAAACTCAAAGTGAAGCCTTTTTT	G15	14.41	26.02	18.12	26.42
AAAAAGCCCTTGCCTCTCTACAAAA	TTTTGGTAGAGAGGCGCAAGGGCCTTTTTT	I15	17.00	27.26	11.31	22.56
AAAAAGTGTGAGGAAGTTGGGTATGAAAA	TTTTCCATACCAACTTCTCACCTTTTTT	K15	17.29	29.75	16.60	20.99
AAAAATTTGTGGTGTTCGCAAAAAA	TTTTGGTGGCAGAAACCCACAAAATTTTTT	M15	19.60	29.68	15.52	20.65
AAAAATAGGCGTTATGCGTAAACCAAAA	TTTTGGTGTTAGCCATAACCGCTATTTTTT	O15	17.58	30.46	11.46	21.25
AAAAAGGTCAGTCCAGTCCATCAGAAAA	TTTTCTGATGACGTGGACTGGACCTTTTTT	A16	44.38	99.56	98.04	28.13
AAAAAGGTCGACGATCACCAGGAAAA	TTTTTCCGCGTATCGTCCAGACCTTTTTT	C16	13.83	39.03	39.63	21.49
AAAAAGGTTAGCCATGCCTGTGCAAAA	TTTTGCACAGGCATGGGCTAAACCCTTTTTT	E16	16.14	28.67	27.73	21.04
AAAAATTACTTCTCCTTCTCTTGCAAAA	TTTTGCAAAGGAAGGGAGAAAGTAATTTTTT	G16	14.12	26.69	40.91	25.17
AAAAATCCCCCGTTTCACTTTGCAAAA	TTTTGCAAGAGTGAACGGGGGATTTTTT	I16	16.14	30.54	37.45	24.76
AAAAATCGGGATCCGGCGGTGCAAAA	TTTTGCAACCGCCCGATCCCGATTTTTT	K16	16.71	33.09	20.51	22.15
AAAAAGTCTTACCGTATGCGTCAAAA	TTTTGCACGCATACGTGTAACGACTTTTTT	M16	42.07	97.69	65.84	34.75
AAAAATCTGATCTGTACCCTATGCAAAA	TTTTGCATAGGGTACAGATACGAATTTTTT	O16	17.00	45.70	36.16	22.45
AAAAAGTTATATATACCTGATCTCGAAAA	TTTTGCGAGATCAGGTATAAATAACTTTTTT	B15	12.97	33.35	11.91	25.39
AAAAACAGTTCGATGTACCCCGCAAAA	TTTTGCGGGGTGACATCGAACTGTTTTTT	D15	14.12	38.09	12.73	35.18
AAAAAGCGGTAGATGCGCAACTGTGAAAA	TTTTCACAGTTGCGCATCTACCGCTTTTTT	F15	14.70	32.76	13.97	19.44
AAAAAGCGGAATCTAGAACTATAAAAA	TTTTTATAGTTCTAGAATTCGCGCTTTTTT	H15	14.12	33.00	18.21	28.81
AAAAAGCGCCCGCACTGTTAATAAAAA	TTTTTATTAACAGTTCGGGCGCGCTTTTTT	J15	16.14	33.47	12.13	27.73
AAAAACTGACCGTACGCGCCACGCAAAA	TTTTGCGTGGGCGTGCAGGTCAGTTTTTT	L15	33.14	88.17	40.72	35.13
AAAAATCTAGGGTACCTATTGGCAAAA	TTTTGCCAAATAGGTACCCCTAGATTTTTT	N15	17.00	31.59	12.76	24.99

Supplementary Table 6|

sense probe 5' – 3'	antisense probe 5' – 3'	plate pos.	WRKY 11	WRKY 33c	WRKY 50	WRKY 33n
AAAAAAGCCATCATGGTTAGTGACAAAA	TTTTGTGACTACTAACATGATGGCTTTTT	P15	16.14	36.97	35.67	23.78
AAAAAATGCCGAGACCCCATGCCGCAAAA	TTTTGCCGGCATGGGGTCTCGGCATTTTT	B16	12.68	41.98	10.40	16.65
AAAAAAGCCGTGGGTGATGGTCACAGAAAA	TTTTCTGTGACCATCACCCACGGCTTTTT	D16	13.83	38.36	10.52	19.70
AAAAAACATTGATAAAATCTCCAGGCAAAA	TTTTGCCTGGAGATTTTATCAATGTTTT	F16	15.27	33.44	18.02	20.42
AAAAAATCTAGCTTTAACTTTAGCAAAA	TTTTGCTAAAGTAAAAAGCTAGAATTTTT	H16	14.41	32.04	14.11	25.15
AAAAAAGCTAGTCGATTCGGCTTAGAAAA	TTTTTCTAAGCCGAATCGACTAGCTTTTT	J16	16.14	40.88	12.38	21.92
AAAAACAACCTGGAGGATTTACAGCAAAA	TTTTGCTGTAATCCTCCAAGTTGTTTT	L16	18.16	37.71	16.01	23.58
AAAAAAGCTCCCGTCTCTTAGTTTAAAA	TTTTTAGAACTAAGAGACGGGAGCTTTTT	N16	17.58	30.88	12.53	24.17
AAAAAAGCTTCTCATGTTGTCTTAGGAAAA	TTTTCTAAGACAACATGAGAAGCTTTTT	P16	16.43	33.55	20.44	23.63
AAAAAAGCTTCAACATCTCGGTCCAAAA	TTTTTGAGCGCAGATGTTGAAAGCTTTTT	A17	11.24	34.61	20.23	32.16
AAAAACATAACCGCAAAATCCCTACAAAA	TTTTGTAGGGATTTTGGCGTTATGTTTT	C17	13.83	31.38	9.13	18.36
AAAAAAGTAGGTGCTGATGCTGGCCGAAAA	TTTTCGGCCAGCATCAGCACCTACTTTTT	E17	16.71	29.23	12.25	20.79
AAAAAAGTATAACGTGTTGTTGACCGAAAA	TTTTCGGTCAACAACACGTTTACTTTTT	G17	100	99.43	55.01	82.09
AAAAAAGTCGTCACGCACGTGAATACAAAA	TTTTGTATTACGTGCGTGACGACTTTTT	I17	32.85	59.64	30.00	37.12
AAAAAATTTGCTCTTTGGTTTTTCAAAAA	TTTTGTGAAAAACAAAAGAGCAAATTTTT	K17	17.00	23.89	16.05	24.38
AAAAAACCCGCGCTCGTGATTATCAGAAAA	TTTTGTGATAATCACGACGGCGGGTTTT	M17	19.60	28.31	12.83	22.14
AAAAATAATTACAAGTCGGCTCCACAAAA	TTTTGTGGAGCCGACTTGTAATTATTTTT	O17	18.44	29.73	15.40	20.97
AAAAAAGTGCACGCCCAATTATATAAAAA	TTTTTATATAAATGGTTCGTGCACTTTTT	A18	12.39	47.83	38.76	26.49
AAAAAATAGTACCGCTAATGGCTGACAAAA	TTTTGTGAGCCATTAGCGGTACTATTTTT	C18	14.99	37.48	27.41	22.15
AAAAAATCTTAAAGAAAGTTCCGACAAAA	TTTTGTGCGAACTTTCCTTAAGAGTTTT	E18	16.14	41.32	48.07	25.69
AAAAAAGTCCCGCGCTAAGCTTTAAAA	TTTTTTTAAAGCTTAGCGGGGACTTTTT	G18	15.56	37.95	55.36	29.39
AAAAAATGGTACTCAGAGTTATAGACAAAA	TTTTGTCTATAACTCTGAGTACCATTTTT	I18	16.14	52.80	25.13	22.80
AAAAACATGTCGCACCTGTACTAACAAAA	TTTTGTTAGTACAGGTGCGACATGTTTT	K18	16.43	43.03	39.43	25.69
AAAAACGTTGAACCTGGCCCTCAACAAAA	TTTTGTTGAGGCCAGGTTCAACGTTTT	M18	36.02	99.56	34.87	26.33
AAAAAAGTTCCGGGGCTTGGTTGGAAAA	TTTTTTCCAAACCAAGCCCGAACTTTT	O18	17.87	29.84	37.12	22.70
AAAAAATGATGTTGGCGCATTTAAACAAAA	TTTTGTTTAAATGCGCCAACATCATTTTT	B17	12.68	33.54	17.79	21.70
AAAAAAGTTTCTACTTGTGTCTGTGAAAA	TTTTACAGACACAAGTAGGAACTTTTT	D17	13.54	30.28	16.93	21.82
AAAAATCATCTCTATGTTATGTTGAAAA	TTTTCAACAATAACATAGAGATGATTTTT	F17	14.41	29.35	12.65	26.15
AAAAACATCGCTGTGCTTGACGTGAAAA	TTTTCAAGTCAACGACAGCGATGTTTT	H17	90.78	99.60	49.86	66.36
AAAAAATGGCTCGGGTCCAGGTTGAAAA	TTTTCAACCTTGAACCCGAGCCATTTTT	J17	16.71	37.33	22.60	32.81
AAAAATAGACCCGTGACCCACCATGAAAA	TTTTCAATGGTGGTTCAGGGTCTATTTTT	L17	18.16	42.38	23.91	27.37
AAAAACACTTAACTGAGTGGGATGAAAA	TTTTCAATCCCCTCAGTTAAGTGTTTTT	N17	17.58	36.51	19.73	21.94
AAAAAATTAATCCATGCTTATGCTGAAAA	TTTTCAGACATAAGCATGGATTAATTTTT	P17	16.71	47.05	31.80	22.66
AAAAAACCCGTTCTACCTTATTCCTGAAAA	TTTTCAGGAATAAGGTAGAACGGGTTTT	B18	12.97	39.80	21.14	25.99
AAAAACAGGCCGATTCGATCCCGAAAA	TTTTCCGGGATCGGAATCGGCCTGTTTT	D18	13.54	32.11	18.06	17.63
AAAAACCGATCATACATATCACTGAAAA	TTTTCAGTGATATGTGATGATCGGTTTT	F18	13.83	31.95	13.38	21.26
AAAAAATTTGTTCCGGCTCATAACTGAAAA	TTTTCAGTTATGAGCCCGAACAAATTTTT	H18	14.12	31.18	14.01	23.46
AAAAAATAGCTTATCCTTGCTTGTGAAAA	TTTTACAAGCAAGGATAAGCTAATTTTT	J18	16.14	31.84	14.40	26.39
AAAAAATTAACCGTTCGACGGCTGTGAAAA	TTTTCACACGCCTTCCGACGGTTAGTTTT	L18	17.87	55.29	15.06	21.99
AAAAAACACGCCATTGCACTGGTAAAA	TTTTTTACCAGTGTCAATGGCGTGTTTTT	N18	43.52	63.18	17.27	21.32
AAAAAATATGCTACTCCACCTTGATGAAAA	TTTTCATCAAGTGGAGTAGCATATTTTT	P18	16.14	34.07	18.98	22.03
AAAAAATGCCATTGTACCTGTGTTGAAAA	TTTTCGAACACAGGTACAATGGCATTTTT	A19	10.66	23.52	10.62	25.19
AAAAAATGCTAGACTCGGACATTCGAAAA	TTTTCGAATGTCGAGTCTAGACATTTTT	C19	14.41	29.24	14.31	24.28
AAAAACGCCTTATGCCTCCCGCTCGAAAA	TTTTCGAGCGGGAGGACAAAGCGTTTT	E19	18.73	32.56	11.83	32.33
AAAAAACCGCTTACATTGCGTTGTGAAAA	TTTTCGACAACGCAATGTAAGCGGTTTT	G19	16.43	26.42	10.87	30.53
AAAAAATGTCGGCTGTTAGGATATCGAAAA	TTTTCGATATCTAACAGCCGACATTTTT	I19	17.00	26.94	10.69	27.78
AAAAACGTGCGCGTGCATGTCATCGAAAA	TTTTCGATGACATGCACGGCAGCTTTTT	K19	17.29	28.16	12.03	26.99
AAAAACGGAAGATCGTACTGCTAGAAAA	TTTTCTAGCACTCAGCATCTTCCGTTTT	M19	19.88	31.26	18.67	19.56
AAAAAATTCAGAGCTTCGAGGTTCCGAAAA	TTTTCGGAACCTCGAAGCTCTGAATTTTT	O19	17.58	28.87	14.64	21.32
AAAAAATGGTTTCAATTTCCGTTCCGAAAA	TTTTCGGACGGAAAATTGAAACCATTTTT	A20	10.09	32.16	17.91	26.54
AAAAAATCCAGCGTATCCGACCCGAAAA	TTTTCGGGTCCGATACGCTGGGAATTTTT	C20	13.83	28.31	24.92	21.38
AAAAACTAGGTATCGGTAGGCGCCGAAAA	TTTTCGGCGCCTACCGATACCTAGTTTT	E20	15.56	34.13	14.20	33.93
AAAAACTCGCCTTGCATCTGTGCGAAAA	TTTTCGCACAGATGCAAGCGGAGTTTT	G20	14.70	28.59	11.11	21.90
AAAAACGCATCATAGTACGCCCAAAAA	TTTTTGGGGCGTAGCTATGATGCGTTTT	I20	16.14	31.45	11.06	24.74
AAAAACGCTCCGTTTTTGAATGCGAAAA	TTTTCGCATTGCAAAAACGGAGCGTTTT	K20	16.14	29.66	12.01	20.96
AAAAAATGTCGCCGTGTGTCTCGGAAAA	TTTTCGCGAGCACACACGGGCACATTTTT	M20	19.31	32.79	13.76	19.96
AAAAACTACTACCTTTGCTAAGCGAAAA	TTTTCGCTTAGGCAAAGGTAGTGTTTTT	O20	17.87	28.17	13.61	20.20
AAAAAATGCTTCAAGTTTTTGTATTAATA	TTTTTAAGATCAAAACTGAAAGCGTTTT	B19	12.68	31.51	10.29	32.09
AAAAAATCGTACATCTATCGTACGAAAA	TTTTCGTAGCGATAGATGTACGAGTTTT	D19	13.83	29.62	11.79	23.29
AAAAAATGCCATGTGCACCCGTACGAAAA	TTTTCGTACGGGTGCACATGGGCATTTTT	F19	14.41	35.05	30.20	18.52
AAAAACGTATTGATGCTATTTCAAAAA	TTTTTTGAAATAGACATCAATACGTTTT	H19	14.70	27.94	11.26	30.76
AAAAACCAGCTCAGTCTGAACAATA	TTTTTTGTTCCAGGACTGAGGCTGTTTT	J19	16.14	38.50	10.53	33.67
AAAAACAGTCTACACCGCTGTAGGAAAA	TTTTCTACAGCGGTGTAGACTGGTTTT	L19	18.44	42.14	15.24	29.57
AAAAACCCTAACGAATGCTTTCCGAAAA	TTTTCCGAAAAGCATTCGTTAGGGTTTT	N19	17.29	31.45	13.09	22.42

Supplementary Table 6

sense probe 5' – 3'	antisense probe 5' – 3'	plate pos.	WRKY 11	WRKY 33c	WRKY 50	WRKY 33n
AAAAAACCGAGTGTGGCCAGTTGCAGAAAA	TTTTCTGCAACTGGCAACACTCGGTTTTTT	P19	17.00	35.08	14.42	25.42
AAAAAATCGGGAACGTACGTCCGCGAAAA	TTTTCCGCGGACGTACGTTCCGCGATTTTTT	B20	12.39	37.30	9.97	21.22
AAAAAATGGCACACATGATCTCGGGAAAA	TTTTCCCAGATCATGTGTGCCAATTTTTT	D20	13.83	29.25	8.37	19.99
AAAAAATCAAAATGATCACTACGGGAAAA	TTTTCCCGTAGTGATCATTTTGAATTTTTT	F20	14.12	33.44	9.63	22.28
AAAAAATTAATACACACTTGGGGAAAA	TTTTCCCAAGTGTGTAATAGTAATTTTTT	H20	14.70	30.52	15.49	23.21
AAAAAACCTACATCGCATATAAGAGAAAA	TTTTCTCTTATATGCGATGTAGGGTTTTT	J20	19.88	32.10	8.22	20.72
AAAAAATTAGGACCACTCCCACTAGGAAAA	TTTTCTAGTGGGGATGGTCCTAATTTTTT	L20	18.44	35.60	8.36	25.03
AAAAAATGTCTTCTTACACCTCTAGAAAA	TTTTCTAGAGGGTGTAGAAGACATTTTTT	N20	18.16	33.92	8.99	23.46
AAAAAATACGTATATTCAGGCCCTAAAAA	TTTTTAGGGCCTGAATATACGTAGTTTTT	P20	17.29	31.52	9.02	19.68
AAAAAATGGCGACTGCCAGTGGTAGAAAA	TTTTTACCACCTGGCAGTCGCCAGTTTTT	A21	10.37	56.83	18.95	21.96
AAAAAATACCTCTACTCTAGCCTTAAAAA	TTTTTAAGGCTAGAGTAGAGGTAGTTTTT	C21	13.83	27.83	15.25	17.53
AAAAAATGAGAGAATTCGGGTTCAGAAAA	TTTTCTGAACCGGAAATCTCTCATTTTTT	E21	15.56	25.08	27.89	23.14
AAAAAATGGATGCGCTCACCAGTTAAAAA	TTTTTAAGTGGTGGAGCGCATCCAGTTTTT	G21	12.97	30.65	12.57	19.77
AAAAAATGGTGTATCTCCTCAATTAAAAA	TTTTTAATGAGGAGATACACCAGTTTTT	I21	17.00	33.98	24.80	22.30
AAAAAATCGACATAGAATCGGAAAAA	TTTTTTCCGCATCTATGTGCGAGTTTTT	L21	16.71	36.01	28.31	20.26
AAAAAATCAAAACAACGATGCCGTTAAAAA	TTTTTAACGGCATCGTTGTTTTGATTTTTT	M21	19.31	53.22	21.09	22.37
AAAAAATGTTGTTGCTGTTGGTCTAAAAA	TTTTTAGGACCAACAGCAACAACATTTTTT	O21	18.44	33.72	28.12	20.23
AAAAAATATCATTGTTACCGTTGCTAAAAA	TTTTTAGCAACGGTAACAATGATATTTTTT	A22	10.95	56.56	38.57	25.63
AAAAAATGGGCTCTGGCCACCCTAAAAA	TTTTTACGGTGGGCCAGAGCCCATTTTTT	C22	13.54	40.73	22.26	19.66
AAAAAATGGCGTCATAATGTGGTAAAAA	TTTTTACCACAATATGACGGCAATTTTTT	E22	15.27	26.85	11.77	21.99
AAAAAATGCAGACCTTCAGCTGGGTAAAAA	TTTTTACCAGCTGAAGGTCTGCATTTTTT	G22	16.43	27.05	16.33	24.56
AAAAAATAGTGGCTGCTCGTTCAAAAAA	TTTTTGTGAACGAGACAGCCAGTATTTTTT	I22	16.14	30.80	11.34	31.64
AAAAAATCCGGCTTGACGCTGCATAAAAAA	TTTTTATGCAGCGTCAAGCCGGAATTTTTT	K22	16.71	32.13	29.62	24.80
AAAAAATTAATCCTAGCCCTCATCAAAAAA	TTTTTGAATGAGGGCTAGGAGTAATTTTTT	M22	19.31	65.66	42.10	21.36
AAAAAATGGATCCTTACTTTAGGCCAAAAA	TTTTTGGCCTAAAGTAAAGATCCATTTTTT	O22	17.87	65.48	48.96	22.06
AAAAAATCGCGTCCGTGCTCAATCAAAAAA	TTTTTGGATTGAGCACGGACGCGATTTTTT	B21	12.68	31.68	22.20	21.58
AAAAAATGCTATCCGTGCTATGCCAAAAA	TTTTTGGCATAGACAGGATAGCATTTTTT	D21	14.12	43.20	18.16	18.14
AAAAAATGTGGTTACGGCCTCGATGAAAAA	TTTTTCAATCGAGGCCGTAACCAATTTTTT	F21	14.12	36.80	18.61	17.73
AAAAAATGTTTTTTAGAGGTGTGCAAAAAA	TTTTTGTGCACACCTCTAAAAACATTTTTT	H21	14.70	33.57	17.13	21.65
AAAAAATTCGGGACTAGTAGTGGTAAAAA	TTTTTACCACCTACTAGTCCCGAATTTTTT	J21	15.85	34.12	16.65	22.00
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	G23	14.41	35.93	11.15	16.97
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	G24	13.54	37.51	14.29	19.23
GGGGGGGGGGGGGGGGGGGGGGGGGGGG	CCCCCCCCCCCCCCCCCCCCCCCCCCCCC	H23	14.41	69.53	38.53	29.52
GGGGGGGGGGGGGGGGGGGGGGGGGGGG	CCCCCCCCCCCCCCCCCCCCCCCCCCCCC	H24	13.83	64.44	28.35	22.98
		<b>Mean</b>	<b>18.21</b>	<b>44.61</b>	<b>26.10</b>	<b>24.25</b>
		<b>SD</b>	<b>12.03</b>	<b>18.18</b>	<b>15.64</b>	<b>9.38</b>
		<b>Mean +2xSD</b>	<b>42.26</b>	<b>80.97</b>	<b>57.37</b>	<b>43.02</b>

**Supplementary Table 7|** Alignment of positive DNA probes of DPI-ELISA screen. Alignment of the DNA sequences of significantly bound dsDNA probes of the DPI-ELISA array experiments. The DNA core consensus was derived using MEME. The data corresponds to Figure 3C, 4A-D and 5A. The name of the dsDNA probe is given first, followed by the respective DNA sequence and the relative absorbance in percent (measured absorbance normalized to the background and relative to highest signal of the respective experiment). If the core consensus was not found in the DNA sequence the forward and the complement reverse strand are given. Black - GAC core used for DNA binding consensus in Figures; grey - other GAC or GTC cores; red - variance of the TTGACY core.

**WRKY33 cDBD vs. WRKY33 nDBD (Fig. 3C)**

Alignment of positives according to WRKY33 nDBD rel. absorbance:

202	AAAAAAGA	TTGACT	CGTCTTACTCGAAAAA	100%	
260	AAAAAAGTATAACGTGTTG	TTGACC	GAAAA	82.1%	
97	AAAAAAAGT	TTGACC	TTGGCGTTCGTAAAA	74.4%	
173	AAAAAATACAT	TTGACT	TTGGGTTTCAAAA	73.8%	
276	AAAAAACATCGCTGTCG	TTGACG	TTGAAAA	66.4%	
54	TTTTAATATGAATTAAGGG	CGGACT	TTTTT	59.4%	
195		TT	TTGACC	ACGAGTACGACGACCATTTTTT	59.2%
36	TTTTAAGCGAGGACG	AAAGACC	AAATTTTTT	47.6%	
101	TTTTACAGCTATAAGTCCT	TAGACT	TTTTT	43.1%	

Alignment of positives according to WRKY33 cDBD rel. absorbance:

173	AAAAAATACAT	TTGACT	TTGGGTTTCAAAA	100%	
202	AAAAAAGA	TTGACT	CGTCTTACTCGAAAAA	99.7%	
276	AAAAAACATCGCTGTCG	TTGACG	TTGAAAA	99.6%	
101	TTTTACAGCTATAAGTCCT	TAGACT	TTTTT	99.5%	
195		TT	TTGACC	ACGAGTACGACGACCATTTTTT	99.4%
260	AAAAAAGTATAACGTGTTG	TTGACC	GAAAA	99.4%	
97	AAAAAAAGT	TTGACC	TTGGCGTTCGTAAAA	99.3%	
54	TTTTAATATGAATTAAGGG	CGGACT	TTTTT	98.9%	
36	TTTTAAGCGAGGACG	AAAGACC	AAATTTTTT	91.3%	

Alignment of positives of only WRKY33 nDBD:

215	AAAAAATTTCTATTTTCATCTTTGCCCAAAA			63.6%
	TTTTGGGCAAAGATGAAATAGAAATTTTTT			
164	TTTTATT	AAGACT	AAAGGTGAGACTTTTTTT	61.3%

Alignment of positives of only WRKY33 cDBD:

137	TTTGAATAATA	TTGACC	TAGAGTTTTTTTT	99.9%
108	AAAAAAGGCCT	CTGACT	GTAACCTCGTAAAA	99.8%
271	AAAAACGTTGAACCTGGGCCTCAACAAAA			99.6%
	TTTGTGAGGCCCAGGTTCAACGTTTTTTT			
233	TTTTCTGATGACGTGGAC	TGGACC	TTTTTT	99.6%
91	TTTTTGAG	TTGACT	AGCGCCACTTTTTTTT	99.4%
92	TTTTCCGCCCTGCAGCCG	CAGACT	TTTTTT	99.3%
222	TTTTCTCCCAACT	ACGACC	GCCTTTTTT	98.9%
83	AAAAAATATGTAGCTGCCGTTACGCTAAAA			98.0%
	TTTTAGCGTAACGGCAGCTACATTTTTTT			
239	TTTTGCACGCATACGTGTA	ACGACT	TTTTT	97.7%
43	TTTTAACACCAGCAGCA	ATGACC	TTTTTTTT	91.6%
246	AAAAA	CTGACC	GTCAGCGCCCACGCAAAA	88.2%
160	TTTTATCATTAACGATC	GCGACC	GTTTTTT	86.9%
88	AAAAATCAACCATTATGGTATTACTAAAA			85.7%
	TTTTAGTAATACCATAATGGTTGATTTTTT			
117	AAAAAAATCAGC	CTGACT	CTGGCGTAAAA	84.9%
57	TTTTGGGAGACGAA	GAGACT	AATTTTTTTTT	84.7%

**WRKY11 DBD vs. WRKY33 nDBD (Fig. 4A)**Alignment of positives according to WRKY33 nDBD rel. absorbance:

202	AAAAAAGA	TTGACT	CGTCTTACTCGAAAAA	100%
260	AAAAAAGTATAACGTGTTG	TTGACC	GAAAA	82.1%
97	AAAAAAAGT	TTGACC	TTGGCGTTCGTAAAA	74.4%
173	AAAAAATACAT	TTGACT	TTGGGTTTCAAAA	73.8%
276	AAAAAACATCGCTGTCG	TTGACG	TTGAAAA	66.4%
195		TT	TTGACC ACGAGTACGACGACCATTTTTT	59.2%
101	TTTTACAGCTATAAGTCCT	TAGACT	TTTTT	43.1%

Alignment of positives according to WRKY11 DBD rel. absorbance:

260	AAAAAAGTATAACGTGTTG	TTGACC	GAAAA	100%
97	AAAAAAAGT	TTGACC	TTGGCGTTCGTAAAA	98.0%
173	AAAAAATACAT	TTGACT	TTGGGTTTCAAAA	91.9%
276	AAAAAACATCGCTGTCG	TTGACG	TTGAAAA	90.8%
195		TT	TTGACC ACGAGTACGACGACCATTTTTT	76.7%
202	AAAAAAGA	TTGACT	CGTCTTACTCGAAAAA	73.8%
101	TTTTACAGCTATAAGTCCT	TAGACT	TTTTT	59.9%

Alignment of positives of only WRKY33 nDBD:

215	AAAAAATTTCTATTTTCATCTTTGCCCAAAA			63.6%
	TTTTGGGCAAAGATGAAATAGAAATTTTTT			
164		TTTTATT	AAGACT AAAGTGAGACTTTTTT	61.3%
54	TTTTAATATGAATTAAGGG	CGGACT	TTTTT	59.4%
36	TTTTAAGCGAGGACG	AAGACT	AAATTTTTT	47.6%

Alignment of positives of only WRKY11 DBD:

91		TTTTTGAG	TTGACT AGCGGCCACTTTTTTT	91.9%
137		TTTTGAATAATA	TTGACC TAGAGTTTTTTT	76.7%
92		TTTTCCGCCCTGCAGCCG	CAGACT TTTTTT	47.6%
233		TTTTCTGATGACGTGGAC	TGGACC TTTTTT	44.4%
198		TT	TTGACC TAAATTGGATCAGATATTTTTT	43.5%
287	AAAAAACACGCCA	TTGACA	CTGGTAAAAAA	43.5%

**WRKY33 nDBD vs. WRKY50 nDBD** (Fig. 4B)

Alignment of positives according to WRKY50 DBD rel. absorbance:

97	AAAAAAAGT	TTGACC	TTGGCGTTCGTAAAA	100%
101	TTTTACAGCTATAA	GTCCT TAGACT	TTTTT	82.8%
173	AAAAAATACAT	TTGACT	TTGGGTTTCAAAA	81.9%
202	AAAAAAGA	TTGACT	CGTCTTACTCGAAAA	79.7%
54	TTTTAATATGAATTAAGGG	CGGACT	TTTTT	78.5%
195	TT	TTGACC	ACGAGTACGACGACCATTTTTT	60.5%

Alignment of positives according to WRKY33 nDBD rel. absorbance:

202	AAAAAAGA	TTGACT	CGTCTTACTCGAAAA	100%
97	AAAAAAAGT	TTGACC	TTGGCGTTCGTAAAA	74.4%
173	AAAAAATACAT	TTGACT	TTGGGTTTCAAAA	73.8%
54	TTTTAATATGAATTAAGGG	CGGACT	TTTTT	59.4%
195	TT	TTGACC	ACGAGTACGACGACCATTTTTT	59.2%
101	TTTTACAGCTATAA	GTCCT TAGACT	TTTTT	43.1%

Alignment of positives of only WRKY50 DBD:

233	TTTTCTGAT	GACGTGGAC TGGACC	TTTTTT	98.0%
1	TTTTTAC	GAC TAGACT	TTTTT	88.6%
120	AAAAAATTCGCGTGTATGTGTACGTAAAA			72.7%
	TTTTACGTACACATACACGCGGAATTTTTT			
174	AAAAAATTTCTCCTTCTTTGTTCTTCAAAA			66.2%
	TTTTGAAGAACAAGAAGGAGAAATTTTTT			
239	TTTTGCACGCATACGTGTA	ACGACT	TTTTT	65.8%
137	TTTTGAATAATA	TTGACC	TAGAGTTTTTTTT	64.2%
21	TTTTAAACAAGAAGC	ATGACT	CCCTTTTTT	63.4%
43	TTTTAACACCAGCAGCA	ATGACC	TTTTTTTT	63.4%
86	TTTTAGTA	AAGACA	AAAGTAAGAATTTTTT	62.3%
205	TTTTGGAGCGAGAG	CGGACA	GGAATTTTTT	58.7%

Alignment of positives of only WRKY33 nDBD:

260	AAAAAAGTATAACGTGTTG	TTGACC	GAAAA	82.1%
276	AAAAAACATCGCT	GTCG TTGACG	TTGAAAA	66.4%
215	AAAAAATTTCTATTTTCATCTTTGCCCAAAA			63.6
	TTTTGGGCAAAAGATGAAATAGAAATTTTTT			
164	TTTTATT	AAGACT	AAAGGTGAGACTTTTTTT	61.3%
36	TTTTAAGCGAG	GACG AAGACC	AAATTTTTT	47.6%

**WRKY11 DBD vs. WRKY33 cDBD** (Fig. 4C)

Alignment of positives according to WRKY33 cDBD rel. absorbance:

173	AAAAAATACAT	TTGACT	TTGGGTTTCAAAA	100%		
137	TTTGAATAATA	TTGACC	TAGAGTTTTTTT	99.9%		
202	AAAAAAGA	TTGACT	CGTCTTACTCGAAAAA	99.7%		
276	AAAAACATCGCT	TTGACG	TTGAAAA	99.6%		
233	TTTCTGAT	TGACGTGGAC	TGGACC	TTTTTT	99.6%	
101	TTTACAGCTATAA	GTCCCT	TAGACT	TTTTT	99.5%	
195		TT	TTGACC	ACGAGTACGACGACC	CATTTTTT	99.4%
260	AAAAAAGTATAACGTGTTG	TTGACC	GAA			99.4%
91		TTTTTGAG	TTGACT	AGCGGCCACTTTTTTT		99.4%
97		AAAAAAGT	TTGACC	TTGGCGTTCGTAAAA		99.3%
92		TTTCCGCCCTGCAGCCG	CAGACT	TTTTTT		99.3%

Alignment of positives according to WRKY11 DBD rel. absorbance:

260	AAAAAAGTATAACGTGTTG	TTGACC	GAA	100%		
97		AAAAAAGT	TTGACC	TTGGCGTTCGTAAAA	98.0%	
91		TTTTTGAG	TTGACT	AGCGGCCACTTTTTTT	91.9%	
173		AAAAAATACAT	TTGACT	TTGGGTTTCAAAA	91.9%	
276	AAAAACATCGCT	TTGACG	TTGAAAA	90.8%		
137	TTTGAATAATA	TTGACC	TAGAGTTTTTTT	76.7%		
195		TT	TTGACC	ACGAGTACGACGACC	CATTTTTT	76.7%
202		AAAAAAGA	TTGACT	CGTCTTACTCGAAAAA	73.8%	
101	TTTACAGCTATAA	GTCCCT	TAGACT	TTTTT	59.9%	
92		TTTCCGCCCTGCAGCCG	CAGACT	TTTTTT	47.6%	
233	TTTCTGAT	TGACGTGGAC	TGGACC	TTTTTT	44.4%	

Alignment of positives of only WRKY33 cDBD:

108	AAAAAAGGC	CTGACT	GTAACCTCGTAAAA	99.8%
271	AAAAACGTGAACCTGGGCCTCAACAAAA			99.6%
	TTTTGTTGAGGCCAGGTTCAACGTTTTTT			
222	TTTCTCCCAACT	ACGACC	GCCTTTTTT	98.9%
54	TTTAAATATGAATTAAGGG	CGGACT	TTTTT	98.9%
83	AAAAAATATGTAGCTGCCGTTACGCTAAAA			98.0%
	TTTGTAGCGTAACGGCAGCTACATTTTTTT			
239	TTTTGCACGCATACGTGTA	ACGACT	TTTTT	97.7%
43	TTTTAACACCAGCAGCA	ATGACC	TTTTTTT	91.6%
36	TTTAAAGCGAG	AAAGACC	AAATTTTTT	91.3%
246	AAAAAA	CTGACC	GTCAGCGCCCACGCAAAA	88.2%
	AAAAAA	CTGACC	GTCAGCGCCCACGCAAAA	
160	TTTTATCATTAACGATC	GCCACC	GTTTTTT	86.9%
88	AAAAAATCAACCATTATGGTATTACTAAAA			85.7%
	TTTTAGTAATACCATAATGGTTGATTTTTT			
117	AAAAAATCAGC	CTGACT	CTGGGCGTAAAA	84.9%
57	TTTTGGGAGACGAA	GAGACT	AATTTTTTTT	84.6%

Alignment of positives of only WRKY11 DBD:

198		TT	TTGACC	TAAATTGGATCAGATATTTTTT	43.5%
287	AAAAAACACGCCA	TTGACA	CTGGTAAAAA	43.5%	

**WRKY33 cDBD vs. WRKY50 DBD** (Fig. 4D)Alignment of positives according to WRKY50 DBD rel. absorbance:

97	AAAAAAAGT	TTGACC	TTGGCGTTCGTAAAA	100%
233	TTTTCTGATGACGTGGAC	TGGACC	TTTTTT	98.0%
101	TTTTACAGCTATAAGTCCT	TAGACT	TTTTTT	82.2%
173	AAAAAATACAT	TTGACT	TTGGGTTTCAAAA	81.9%
202	AAAAAAGA	TTGACT	CGTCTTACTCGAAAAA	79.7%
54	TTTTAATATGAATTAAGGG	CGGACT	TTTTTT	78.5%
239	TTTTGCACGCATACGTGTA	ACGACT	TTTTTT	65.8%
137	TTTTGAATAATA	TTGACC	TAGAGTTTTTTTT	64.2%
43	TTTTAACACCAGCAGCA	ATGACC	TTTTTTTT	63.4%
195	TT	TTGACC	ACGAGTACGACGACCATTTTTTT	60.5%

Alignment of positives according to WRKY33 cDBD rel. absorbance:

173	AAAAAATACAT	TTGACT	TTGGGTTTCAAAA	100%
137	TTTTGAATAATA	TTGACC	TAGAGTTTTTTTT	99.9%
202	AAAAAAGA	TTGACT	CGTCTTACTCGAAAAA	99.7%
233	TTTTCTGATGACGTGGAC	TGGACC	TTTTTT	99.6%
101	TTTTACAGCTATAAGTCCT	TAGACT	TTTTTT	99.5%
195	TT	TTGACC	ACGAGTACGACGACCATTTTTTT	99.4%
97	AAAAAAAGT	TTGACC	TTGGCGTTCGTAAAA	99.3%
54	TTTTAATATGAATTAAGGG	CGGACT	TTTTTT	98.9%
239	TTTTGCACGCATACGTGTA	ACGACT	TTTTTT	97.7%
43	TTTTAACACCAGCAGCA	ATGACC	TTTTTTTT	91.6%

Alignment of positives of only WRKY50 DBD:

1	TTTTTACGAC	TAGACT	TTTTTT	88.6%
120	AAAAAATTCGCGTGTATGTGTACGTAAAA			72.7%
	TTTTACGTACACATACACGCGGAATTTTTT			
174	AAAAAATTTCTCCTTCTTTGTTCTTCAAAA			66.2%
	TTTTGAAGAACAAGAAGGAGAAATTTTTT			
21	TTTTAAACAAGAAGC	ATGACT	CCCTTTTTT	63.4%
86	TTTTAGTA	AAAGACA	AAAGTAAGAATTTTTT	62.3%
205	TTTTGGAGCGAGAG	CGGACA	GGAATTTTTT	58.7%

Alignment of positives of only WRKY33 cDBD:

108	AAAAAAGGCCT	CTGACT	GTAACCTCGTAAAA	99.8%
276	AAAAAACATCGCTCTCG	TTGACG	TTGAAAA	99.6%
271	AAAAAACGTTGAACCTGGGCCTCAACAAA			99.6%
	TTTTGTTGAGGCCAGGTTCAACGTTTTTT			
260	AAAAAAGTATAACGTGTTG	TTGACC	GAAAA	99.4%
91	TTTTTTGAG	TTGACT	AGCGGCCACTTTTTTT	99.4%
92	TTTTCCGCCCTGCAGCCG	CAGACT	TTTTTT	99.3%
222	TTTTCTCCCACAAC	ACGACC	GCCTTTTTT	98.9%
83	AAAAAATATGTAGCTGCCGTTACGCTAAAA			98.0%
	TTTTAGCGTAACGGCAGCTACATATTTTTT			
36	TTTTAAGCGAGGACG	AAAGACC	AAATTTTTT	91.3%
246	AAAAA	CTGACC	GTCAGCGCCCACGCAAAA	88.2%
160	TTTTATCATTAACGATC	GCGACC	GTTTTTT	86.9%
88	AAAAAATCAACCATTATGGTATTACTAAAA			85.7%
	TTTTAGTAATACCATAATGGTTGATTTTTT			
117	AAAAAATCAGC	CTGACT	CTGGGCGTAAAA	84.9%
57	TTTTGGGAGACGAA	GAGACT	AATTTTTTTT	84.6%



**WRKY11 DBD vs. WRKY50 DBD** (Fig. 5A)Alignment of positives according to WRKY50 DBD rel. absorbance:

97	AAAAAAAGT	TTGACC	TTGGCGTTCGTAAAA	100%	
233	TTTTCTGAT	GACGTGGAC	TGGACC	TTTTTT	98.0%
101	TTTTACAGCTATAA	GTCCT	TAGACT	TTTTTT	82.2%
173	AAAAAATACAT	TTGACT	TTGGGTTTCAAAA	81.9%	
202	AAAAAAGA	TTGACT	CGTCTTACTCGAAAAA	79.7%	
137	TTTTGAATAATA	TTGACC	TAGAGTTTTTTTT	64.2%	
195	TT	TTGACC	ACGAGTACGACGACC	CATTTTTT	60.5%

Alignment of positives according to WRKY11 DBD rel. absorbance:

97	AAAAAAAGT	TTGACC	TTGGCGTTCGTAAAA	98.0%	
173	AAAAAATACAT	TTGACT	TTGGGTTTCAAAA	91.9%	
137	TTTTGAATAATA	TTGACC	TAGAGTTTTTTTT	76.7%	
195	TT	TTGACC	ACGAGTACGACGACC	CATTTTTT	76.7%
202	AAAAAAGA	TTGACT	CGTCTTACTCGAAAAA	73.8%	
101	TTTTACAGCTATAA	GTCCT	TAGACT	TTTTTT	59.9%
233	TTTTCTGAT	GACGTGGAC	TGGACC	TTTTTT	44.4%

Alignment of positives of only WRKY50 DBD:

1	TTTTTAC	GAC	TAGACT	TTTTT	88.6%
54	TTTTAATATGAATTAAGGG	CGGACT	TTTTT	78.5%	
120	AAAAAATTCGCGTGTATGTGTACGTAAAA			72.7%	
	TTTTACGTACACATACACGCGGAATTTTTT				
174	AAAAAATTTCTCCTTCTTTGTTCTTCAAAA			66.2%	
	TTTTGAAGAACAAGAAGGAGAAATTTTTT				
239	TTTTGCACGCATACGTGTA	ACGACT	TTTTT	65.8%	
21	TTTTAAACAAGAAGC	ATGACT	CCTTTTTTT	63.4%	
43	TTTTAACACCAGCAGCA	ATGACC	TTTTTTTT	63.4%	
86	TTTTAGTA	AAGACA	AAAGTAAGAATTTTTT	62.3%	
205	TTTTGGAGCGAGAG	CGGACA	GGAATTTTTT	58.7%	

Alignment of positives of only WRKY11 DBD:

260	AAAAAAGTATAACGTGTTG	TTGACC	GAAAA	100%	
91	TTTTTGAG	TTGACT	AGCGCCACTTTTTTTT	91.9%	
276	AAAAAACATCGCT	GTCG	TTGACG	TTGAAAA	90.8%
92	TTTTCCGCCCTGCAGCCG	CAGACT	TTTTTTT	47.6%	
198	TT	TTGACC	TAAATTGGATCAGATATTTTTT	43.5%	
287	AAAAAACACGCCA	TTGACA	CTGGTAAAAAA	43.5%	

**Supplementary Table 8|** Alignment of WRKY DBDs to identify conserved proximity sites. The alignment was performed using CLUSTAL 2.1 multiple sequence alignment. Highlighted are the sites important for WRKY-DNA interaction from which the consensus in Figure 7 was derived.

	<b><math>\beta_2</math></b>	<b><math>\beta_3</math></b>	<b><math>\beta_4</math></b>	
	123456	78		
OsWRKY33	WRKYGGKVVKGN-PNPSR	-GTFPSRCSPIPPAFTA	NGAGAAFQRTKDKPRD	----DLFVESLLC-----
OsWRKY58	WRKYGSKAVKNS-DPSPD	-DE---	LLFSDNDNTQTATENLRFIPLG	----RVYITG----
AtWRKY51_At5g64810	WRKYGSKSVKNN-INKRL	-RLYREG	----NVKKA	CKKSLCDSSVTCKRQR----DLFEEEDFPY-----
OsWRKY56	WRKYGSKSIKNN-PHPR	-----	-----	-----CATRSIIDPI-----
OsWRKY15	WRKYGSKDILGA-KYP	-----RAYFRCTHRHT	-QGCHAKQVQRADG	---DPLL---FDVVYHGDHTCAHG-----
OsWRKY19	WRKYGSKDILGA-KYP	-----RAYFRCTHRHT	-QGCHAKQVQRADG	---DPLL---FDVVYHGDHTCGQA-----
OsWRKY41-CTD	WRKYGSKDILGA-KYP	-----RSYFRCTHRNT	-QGCVAIKQIQRRDG	---DPLL---FDVVYHGDHTCSER-----
OsWRKY61-CTD	WRKYGSKNIFGA-NYP	-----RCYYRCIHKTT	-TGCTAKNAQATDG	---DPLL---FDVVYHGEHTCDLQ-----
OsWRKY81-CTD	WRKYGSKNIFGA-NYP	-----RCYYRCIHKTT	-TGCTAKNAQATDG	---DPLL---FDVVYHGEHTCDLQ-----
OsWRKY63-NTD	WSKYEKKEILGA-KFP	-----RAYFRCTHWNTKKGCM	AKVQRDDG	---DPLM---FDIVYHGEHTCQT-----
OsWRKY69	WRKYGSKDILGA-KHP	-----RGYYRCTHRNT	-QGCTAKQVQRTDD	---DASL---FDVVYHGEHTCRPG-----
OsWRKY74	WRKYGSKKEILGA-KHP	-----RGYYRCTHRHS	-QGCMAKQVQRTDE	---DAMV---FDVIYHGEHTCVHK-----
OsWRKY63-CTD	WRKYGSKNVLGF-SYL	-----RGYYRC	---AT-KGCQA	KQVQRHD---DGLL---FDVTFGEHTCADQ-----
OsWRKY41-NTD	WRKYGSKDILGT-MYP	-----RSYFRCTHRHT	-KGCLAKQVQPTDD	---DHQI---LDVIYGEHTCDQS-----
OsWRKY61-NTD	WRKYGSKDVEGA-MHPTTQ	-----SKSYFRCAHKMT	-TGCKAKKQVQRTDG	---DPLM---VDVVYKGVHSCAGV-----
OsWRKY81-NTD	WRKYGSKDVEGA-MHPTTQ	-----SN-YFRCAHKMT	-TGCKAKKQVQRTDG	---DPLM---VDVVYKGVHSCAGV-----
OsWRKY48	WRKYGSKKEIKNS-KHP	-----RLYYRCSYKDD	-HGCTAKQVQOSE	---EDPS---LYVITYFGDHTCSCQ-----
OsWRKY54	WRKYGSKKEIKNS-KHP	-----RFYYRCSYKDD	-HGCTAKQVQOSE	TADDDTASP---VYIITYFGEHTCRHG-----
OsWRKY21	WRKYGSKKEINGC-KHP	-----RLYYRCAFRG	-QGCLARRVQSQS	-QDDPAA---AFVIAYGEHTCGGD-----
OsWRKY47	WRKYGSKHIQDSPNNP	-----RSYYRCTHRPD	-QGCMAKQVQTSSES	---NSSE---FVISYGEHTCRDP-----
AtWRKY54_At2g40750	WRKYGSKKEILNT-TFP	-----RSYFRCTHKPT	-QGCKAKQVQKQDQ	---DSEM---FQITYIGYHTCOTAN-----
AtWRKY70_At3g56400	WRKYGSKKEILNA-KFP	-----RSYFRCTHKYT	-QGCKAKQVQKVEL	---EPKM---FSITYIGNHTCNTN-----
OsWRKY45	WRKYGSKKEIQNS-KHP	-----KAYFRCTHKYD	-QMCTARQVQRCDD	---DPAS---YRVTYIGEHTCRDP-----
OsWRKY75	WRKYGSKDILGS-RYP	-----RSYYRCTHKNY	-YGCFAKKVQRLDD	---DPFT---YEVTYCGNHTCCLTS-----
AtWRKY55_At2g40740	WRKYGSKKEILGS-RFP	-----RAYRCTHQKL	-YNCPAKQVQRLND	---DPFT---FRVTYRGSHTCYNS-----
SemWRKY2	WRKYGSKDILNS-KFP	-----RSYYRCTHQKE	-LGCQAKYVQKCED	---EPSM---YQVTYIGEHSQNA-----
SemWRKY25	WRKYGSKDILNS-KFP	-----RSYYRCTHQKE	-LGCQAKYVQKCED	---EPSM---YQVTYIGEHSQNA-----
SemWRKY16	WRKYGSKDILGS-RHP	-----KSYRCTHKRE	-SGCPAKYVQRSDS	---NPSS---FQITYRGEHTCNML-----
SemWRKY27	WRKYGSKDILGS-RHP	-----KSYRCTHKRE	-SGCPAKYVQRSDS	---NPSS---FQITYRGEHTCNML-----
AtWRKY41_At4g11070	WRKYGSKDILGA-KFP	-----RSYYRCTFRNT	-QYCWAKQVQRSDD	---DPTI---FEVTYRGTHTCOGL-----
AtWRKY53_At4g23810	WRKYGSKDILGA-KFP	-----RSYYRCTHRST	-QNCWAKQVQRSDD	---DATV---FEVTYRGTHTCOQA-----
AtWRKY30_At5g24110	WRKYGSKDILGA-KFP	-----RGYYRCTYRKS	-QGCEAKQVQRSDE	---NQML---LEISYRGIHSCSQA-----
AtWRKY46_At2g46400	WRKYGSKKEIHGS-KNP	-----RAYRCTHRFT	-QDCLAKQVQKSDT	---DPSL---FEVKYLGNHHTONNI-----
PpWRKY35	WKKYGNKSIQNS-NHC	-----RGYYKCSVKE	---CRAMKMVQPTDK	---DPMV---FEITYVGKHTCSST-----
PpWRKY36	WKKYGNKSIQNS-NHC	-----RGYYKCSVKE	---CRAMKMVQPTDT	---DPTV---FEVTVYVEKHTCSST-----
PpWRKY34	WKKYGNKAIQNS-NHC	-----RGYYKCSLKE	---CRAMKMVQLTDR	---DPTL---FEVTVYVGHKSGSS-----
PpWRKY37	WKKYGNKAIQNS-TFC	-----RGYYKCSMKE	---CRAMKMVQPTDT	---NPSI---FEVTVYLGKHTCSST-----
OsWRKY18	WRKYGSKKIKNNS-SFPR	-----LYYRCSYRDD	-RNCMAKVVQQEND	---ADPPL---YRVTYIHPHTCNPS-----
OsWRKY46	WRKYGSKKLSNS-NFP	-----RCTYKND	-MKCPAKQVQKDT	---NDPPL---FSVTVYFNHHTCNSS-----
OsWRKY22	WRKYGSKMIRGN-SFPR	-----CYRCTYHQD	-HGCPAKHVEQHNS	---EDPPL---FRVIYTNHHTCGTS-----
OsWRKY52	WRKYGSKKIQGT-HFT	-----SVNTQED	-DGGVADS	-----
OsWRKY55	WRKYGSKKINNC-NFP	-----RTNDQCQ	-LTFKSTA	-----
OsWRKY20	WRKYGSKNIQDS-NYLR	-----LYFKCTFSRE	-RSCAAKQVQQRDA	---GEPPM---FLVTVYLNHHTCGQP-----
OsWRKY50	WRKYGSKQIEGA-MYP	-----RSYYRCTNSTN	-QGCLAKTVQRNGG	---GGAAG---YTVAYISEHTCKSI-----

OsWRKY65	WRKYGKQIEGA-MYP-----RSYYRC	TNSTN-QGCLA	KTVQRNGG--GGAAG----	YTVAYISEHTCKSI-----	70
OstWRKY33_Ostreococcus_tauri_w	WRKYGKLIAGN-MVPHPT----	ERSYRCK--H-FGCPA	KRVEVEKV--TGAT-----	RTVYEFEHTRDGD-----	69
AtWRKY38_At5g22570	WRKYGKSIKKS-NHQ-----RSYYRC	SYNKD-HNCEA	KHEQKIKD--NPPV----	YRTTYFGHHTCKTE-----	69
AtWRKY62_At5g01900	WRKYGKQIKES-EYQ-----RSYKCA	YTKD-QNCEA	KQVQKIQH--NPPL----	YSTTYVGOHIQOLH-----	69
AtWRKY63_At1g66600	WRKYGKTIKTS-LYQ-----RCYYRC	AYAKD-QNCEA	KRVQMIQD--SPPV----	YRTTYLGOHTCKAF-----	69
AtWRKY64_At1g66560	WRKYGKTIKTS-PYQ-----RCYYRC	TYAKD-QNCEA	KRVQMIQD--NPPV----	YRTTYLKGKHKAV-----	69
AtWRKY67_At1g66550	WRKYGKTIKAS-AHK-----RCYYRC	TYAKD-QNCEA	KRVQKIKD--NPPV----	YRTTYLKGKHKAF-----	69
AtWRKY66_At1g80590	WRKYGKTIKTS-PHQ-----RWYYRC	AYAKD-QNCEA	KRVQKIQD--NPPV----	YRNTYVGOHACAP-----	69
OsWRKY37	WRKYGKPIKGS-PYP-----RGYYRC	SS--SK-GCSA	KQVERSRD--PNMLV----	ITYTSEHN-HPWP-----	67
OsWRKY66	WRKYGKPIKGS-PYP-----RGYYRC	SS--SK-GCSA	KQVERSRD--PNMLV----	ITYTSEHN-HPWP-----	67
AtWRKY35_At2g34830	WRKYGKPIKGS-PYP-----RGYYRC	SS--SK-GCSA	KQVERSRD--PNMLV----	ITYTSEHN-HPWP-----	67
AtWRKY14_At1g30650	WRKYGKPIKGS-PYP-----RGYYRC	SS--SK-GCSA	KQVERSRD--PNMLV----	ITYTSEHN-HPWP-----	67
OsWRKY2	WRKYGKPIKGS-PYP-----RGYYRC	SS--SK-GCSA	KQVERSRD--PTMLV----	VTYTSDHN-HPWP-----	67
Sem WRKY12	WRKYGKPIKGS-PYP-----RGYYRC	SS--SK-GCSA	KQVERSRD--PTMLI----	ITYTSEHN-HPWPAHRNSLAG	75
SemWRKY34	WRKYGKPIKGS-PYP-----RGYYRC	SS--SK-GCSA	KQVERSRD--PTMLI----	ITYTSEHN-HPWP-----	67
OsWRKY13	WRKYGKPIKGS-PYP-----RGYYRC	SS--SK-GCPA	KQVERSRD--PTVLL----	VTYSFEN-HPWP-----	67
AtWRKY65_At1g29280	WRKYGKPIKGS-PYP-----RGYYRC	SS--TK-GCPA	KQVERSRD--PTMLI----	ITYTSEHN-HPWP-----	67
OsWRKY14	WRKYGKPIKGS-PFP-----RAYYRC	SS--SK-GCPA	KQVERSRD--PDTVI----	VTYSFEN-HSAT-----	67
OsWRKY39	WRKYGKPIKGS-PYP-----RGYYRC	SS--SK-GCPA	KQVERSRD--PNTFI----	LTYTGEHN-HSAP-----	67
AtWRKY22_At4g01250	WRKYGKPIKGS-PYP-----RGYYRC	SS--SK-GCLA	KQVERNRS--PKMFI----	VTYTAEHN-HPAP-----	67
AtWRKY27_At5g52830	WRKYGKPIKGS-PYP-----RNYRCS	SS--SK-GCLA	KQVERSRD--PNIFI----	VTYTGEHN-HPRP-----	67
AtWRKY29_At4g23550	WRKYGKPIKGS-PYP-----RSYYRC	SS--SK-GCLA	KQVERNPN--PEKFT----	ITYTNEHN-HELP-----	67
OsWRKY12	WRKYGKPIKGS-PYP-----RGYYRC	SS--MK-GCMA	KMVERSPA--PGMLV----	VTYMAEHC-HPVP-----	67
AtWRKY16_At5g45050	WRKYGKPIKGS-PYP-----RSYYRC	SS--SK-GCPA	KQVERSRD--PNVSV----	ITYISEHN-HPFP-----	67
OsWRKY31	WRKYGKPIKGS-PYP-----RGYYRC	SS--NK-NCAA	KQVERCRF--PSFLL----	LTYTGAHSGHDVP-----	68
AtWRKY52_RRS1_At5g45270	WRKYGKDILGS-RFP-----RGYYRC	AYKFTG-GCKA	KQVQRSET--SNMLA----	ITYLSEHN-HPRP-----	69
OsWRKY25	WRKYGKPIKGS-PYP-----RGYYRC	SS--VK-GCPA	KHVERAAD--PATLV----	VTYEGDHR-HSPP-----	67
OsWRKY44	WRKYGKPIKGS-PYP-----RGYYRC	SS--VK-GCPA	KHVERAAD--PATLV----	VTYEGDHR-HSPP-----	67
OsWRKY42	WRKYGKPIKGS-PYP-----RGYYRC	SS--VK-GCPA	KHVERDPE--PAMLI----	VTYDGDHR-HGEP-----	67
OsWRKY51	WRKYGKPIKGS-PFP-----RGYYRC	SS--LR-GCPA	KHVERPAD--PSMLI----	VTYEGEHR-HTPS-----	67
AtWRKY11_At4g31550	WRKYGKPIKGS-PHP-----RGYYRC	SS--FR-GCPA	KHVERALD--PAMLI----	VTYEGEHR-HNQS-----	67
AtWRKY17_At2g24570	WRKYGKPIKGS-PHP-----RGYYRC	SS--FR-GCPA	KHVERALD--STMLI----	VTYEGEHR-HHQS-----	67
OsWRKY68	WRKYGKPIKGS-PYP-----RGYYRC	SS--VR-GCPA	KHVERATD--PAMLV----	VTYEGEHR-HTPG-----	67
AtWRKY39_At3g04670	WRKYGKPIKGS-PHP-----RGYYRC	SS--VR-GCPA	KHVERCID--TSMLI----	VTYEGEHN-HSRI-----	67
AtWRKY74_At5g28650	WRKYGKPIKGS-PHP-----RGYYRC	SS--VR-GCPA	KHVERCEE--TSMLI----	VTYEGEHN-HSRI-----	67
SemWRKY8	WRKYGKPIKGS-PHP-----RGYYRC	SS--LR-GCPA	KHVERCLD--PTMLR----	VTYEGEHS-HGVQ-----	67
SemWRKY17	WRKYGKPIKGS-PHP-----RGYYRC	SS--LR-GCPA	KHVERCLD--PTMLR----	VTYEGEHS-HGVQ-----	67
SemWRKY10	WRKYGKPIKGS-PHP-----RGYYRC	SS--LR-GCPA	K-----	-----	42
SemWRKY21	WRKYGKPIKGS-PHP-----RGYYRC	SS--MR-GCPA	K-----	-----	42
SemWRKY31	WRKYGKPIKGS-PHP-----RGYYRC	SS--MR-GCPA	K-----	-----	42
PpWRKY2	WRKYGKPIKGS-PHP-----RGYYRC	SS--IR-GCPA	KHVERSMED--PTMLI----	VTYEGNHL-HRTQ-----	67
SemWRKY9	WRKYGKPIKGS-PHP-----RGYYRC	SS--MR-GCPA	K-----	-----	42
Sem WRKY18	WRKYGKPIKGS-PHP-----RGYYRC	SS--MR-GCPA	K-----	-----	42
PpWRKY8	WRKYGKPIKGS-PHP-----RGYYRC	SS--IR-GCPA	KHVERSMED--PTMLI----	VTYEGEHN-HPQS-----	67
PpWRKY9	WRKYGKPIKGS-PHP-----RGYYRC	SS--IR-GCPA	KHVERSMED--PTMLI----	VTYEGEHN-HPQL-----	67
PpWRKY7	WRKYGKPIKGS-PHP-----RGYYRC	SS--IR-GCPA	KHVERSMED--STMLI----	VTYEGEHN-HL-----	65
PpWRKY1	WRKYGKPIKGS-PHP-----RGYYRC	SS--IR-GCPA	KHVERSMED--SSMLI----	VTYEGDHN-HPQS-----	67
AtWRKY21_At2g30590	WRKYGKPIKGS-PYP-----RGYYRC	SS--MR-GCPA	KHVERCLD--PAMLI----	VTYEAEHN-HPKL-----	67
AtWRKY7_At4g24240	WRKYGKPIKGS-PHP-----RGYYRC	SS--VR-GCPA	KHVERALD--AMMLI----	VTYEGDHN-HALV-----	67
AtWRKY15_At2g23320	WRKYGKPIKGS-PHP-----RGYYRC	SS--VR-GCPA	KHVERAAD--SSMLI----	VTYEGDHN-HSLS-----	67
OsWRKY6	WRKYGKPIKGS-PHP-----RGYYRC	SS--KK-DCPA	KHVERCRS--PAMLL----	VTYENEHN-HAQP-----	67
PpWRKY25	WRKYGKPIKGS-PHP-----IKGS-PHP-----RGYYRC	SS--MR-GCLA	KHVERLED--SSMLI----	ITYEGEHN-HSRSTSVSALL	56
Sem WRKY19	HOKASAGIKGS-PHP-----RGYYRC	SS--LR-GCPA	KHVERCLD--P-----	TTDAGERS-HG-----	VQPQ--61
AtWRKY6_At1g62300	WRKYGKMAKGN-PCP-----RAYYRC	SS--TGCPV	KQVQCAED--RSILI----	TTYEGNHN-HPPL-----	67

AtWRKY31_At4g22070	WRKYGQKMAKGN-PCP-----RAYYRCTMA---GGCPVKQVQRC AED--RSILI-----TTYEGNHN--HPLP-----67
AtWRKY42_At4g04450	WRKYGQKMAKGN-PCP-----RAYYRCTMA---VGCPVKQVQRC AED--RTILI-----TTYEGNHN--HPLP-----67
OsWRKY43	WRKYGQKMAKGN-PCP-----RAYYRCTMA---AGCPVKQVQRC AED--RTVLI-----TTYEGNHN--HPLP-----67
OsWRKY1	WRKYGQKMAKGN-PCP-----RAYYRCTMA---TGCPVKQVQRC AED--RSILI-----TTYEGTHN--HPLP-----67
OsWRKY5	WRKYGQKMAKGN-PCP-----RAYYRCTMA---SQCPVKQVQRC AKD--KSILI-----TTYEGTHS--HPLP-----67
OsWRKY32	WRKYGQKVAKGN-PCP-----RAYYRCTVA---PGCPVKQVQRC LED--MSILV-----TTYEGTHN--HPLP-----67
AtWRKY9_At1g68150	WRKYGQKTAKGN-PCP-----RAYYRCTVA---PGCPVKQVQRC LED--MSILI-----TTYEGTHN--HPLP-----67
OsWRKY73	WRKYGQKIAKGN-PCP-----RAYYRCTVA---AGCPVKQVQRC AED--MSILI-----TTYEGTHN--HPLP-----66
AtWRKY72_At5g15130	WRKYGQKIAKGN-PCP-----RAYYRCTVA---PGCPVKQVQRC AED--MSILI-----TTYEGTHS--HSLP-----67
PpWRKY19	WRKYGQKMAKGN-PCP-----RAYYRCTVA---PGCPVKQVQRC AED--VSILI-----TTYEGTHN--HPLP-----61
SemWRKY7	WRKYGQKMAKGN-PCP-----RAYYRCTVA---PGCPVKQVQRC AED--MSILI-----TTYEGSHN--HPLP-----62
SemWRKY26	WRKYGQKMAKGN-PCP-----RAYYRCTVA---PGCPVKQVQRC AED--MSILI-----TTYEGSHN--HPLP-----62
PpWRKY13	WRKYGQKMAKGN-PCP-----RAYYRCTVA---PGCPVKQVQRC AED--ISILV-----TTYEGTHN--HPLP-----54
SemWRKY23	WRKYGQKMAKGN-PCP-----RAYYRCTMS---PGCPVKQVQRC AED--TSILV-----TTYEGTHN--HPLP-----62
SemWRKY33	WRKYGQKMAKGN-PCP-----RAYYRCTMS---PGCPVKQVQRC AED--TSILV-----TTYEGTHN--HPLP-----62
AtWRKY47_At4g01720	WRKYGQKMAKGN-PCP-----RAYYRCTMA---VGCPVKQVQRC AED--TTILT-----TTYEGNHN--HPLP-----67
PpWRKY10	WRKYGQKMAKGN-PCP-----RAYYRCTVM---SGCPVKQVQRC AKD--TSILV-----STYEGTHN--HPLP-----61
SemWRKY3	WRKYGQKMAKGN-PCP-----RAYYRCTMA---SGCPVKQVQRC AED--TSVLV-----TTYEGSHN--HQLP-----56
SemWRKY28	WRKYGQKMAKGN-PCP-----RAYYRCTMA---SGCPVKQVQRC AED--TSVLV-----TTYEGSHN--HQLP-----56
OsWRKY9	WRKYGQKMAKGN-PCP-----RAYYRCTMA---IGCPVKQVQRC AED--KTVLI-----TTYEGNHN--HQLP-----67
AtWRKY61_At1g18860	WRKYGQKIAKGN-PCP-----RAYYRCTIA---ASCPVKQVQRC SED--MSILI-----STYEGTHN--HPLP-----67
PpWRKY33	WRKYGQKMAKGN-PCP-----RAYYRCTLL---RGCPVKQVQRC AED--LSILI-----TTYEGTHN--HPIPA-----61
OsWRKY27	WRKYGQKTAKGN-PWP-----RGYRCTGA---PGCPVKQVQRC NHD--TSVLV-----TTYDGVHN--HPIT-----67
PpWRKY5	WRKYGQKMAKGN-PWP-----RAYFRCTVS---PGCPVKQVQRC EED--TSILV-----TTYEGTHN--HALS-----60
AtWRKY36_At1g69810	WRKYGQKTAKTN-PLP-----RAYYRCSMS---SNCPVKQVQRC GEEE--TSAFM-----TTYEGNHD--HPLP-----68
OsWRKY28	WRKYGQKVTKDN-PCP-----RAYFRCSFA---PACPVKKQVQRC SADD--NTVLV-----ATYEGEHN--HAQP-----67
OsWRKY71	WRKYGQKVTKDN-PCP-----RAYFRCSFA---PACPVKKQVQRC SADD--NTILV-----ATYEGEHN--HGQP-----67
OsWRKY76	WRKYGQKVTRDN-PSP-----RAYFRCAFA---PSCPVKKQVQRC SADD--SLLLV-----ATYEGEHN--HPHP-----67
AtWRKY40_At1g80840	WRKYGQKVTRDN-PSP-----RAYFKACA---PSCPVKKQVQRC SADD--QSVLV-----ATYEGEHN--HPMP-----67
AtWRKY18_At4g31800	WRKYGQKVTRDN-PSP-----RAYFRCSFA---PSCPVKKQVQRC SADD--PSLLV-----ATYEGTHN--HLGP-----67
AtWRKY60_At2g25000	WRKYGQKITRDN-PSP-----RAYFRCSFA---PSCLVKKQVQRC SADD--PSFLV-----ATYEGTHN--HTGP-----67
OsWRKY62	WRKYGQKVTRDN-PYP-----RAYFRCAFA---PSCPVKKQVQRC AED--RSMVLV-----ATYEGEHN--HALS-----67
OsWRKY82-CTD	WRKYGQKIVKGN-PNP-----RSYRCTHD---GCPVKKHVEKAPDD--DNNIV-----VTYEGKHN--HDQP-----66
AtWRKY32-CTD_At4g30930_CTD	WRKYGQKMKVGN-PHP-----RNYRCTSA---GCPVKKHVETAVEN--TKAVI-----ITYKGVHN--HDMP-----66
XP_003061495_MiPu	WRKYGQKIIKGA-PFP-----RSYRCTSA---NCPVKKHVEGDPSSL--LSS-----LTYEGEHN--HEKP-----62
XP_002509266_MiPu	WRKYGQKIIKGA-AFP-----RSYRCTAP---NCPVKKHVEGDPK--PGS-----IAYEGTHN--HEPP-----64
AtWRKY44-CTD_TTG2_At2g37260_CT	WRKYGQKVVGGN-AYP-----RSYRCTSA---NCPVKKHVERASDD--PRAFI-----TTYEGKHN--HLLL-----67
AtWRKY1-CTD_ZAP1_At2g04880_CTD	WRKYGQKSVKGS-PYP-----RSYRCSSP---GCPVKKHVERSSHD--TKLLI-----TTYEGKHD--HDMP-----66
Ddiscoideum_WRKY-NTD_XM_638694	WRKYGQKNVKGSLHP-----RHYYKCTFQ---GCPVKQVQRC AED--IGD--TNQNS-----TVYKGEHC--HGFP-----65
PpWRKY30	WRKYGQKTVLSS-PYP-----RSYKCTTA---GCPVKQVQRC AED--RGLVI-----ASYEGEHN--HPLP-----63
CocSub_CTD	WRKYGQKIVKGN-PHP-----RSYKCTVA---GCTVKKHVGRSATE--AGVLV-----TSYEGQHN--HPQP-----66
ChvWRKY1-CTD_Chlorella_variabi	WRKYGQKIVKGN-PHP-----RSYKCTHP---GCPVKQVQRC AED--ARMLV-----TTYEGHTH--HDPP-----66
Chr WRKY_EST_BQ821537	WRKYGQKQVKGSLPP-----RAYKCTHM---GCPVKKHVERASDD--ETRFV-----VTYEGTHS--HRLP-----66
OsWRKY3	WRKYGQKAVKNS-PFP-----RSYRCTNS---KCTVKKVERSSDD--PSVVI-----TTYEGQHC--HHTAS-----67
OsWRKY29	WRKYGQKAVKNS-PFP-----RSYRCTNS---KCTVKKVERSSDD--PSVVI-----TTYEGQHS--HHTV-----66
AtWRKY57_At1g69310	WRKYGQKAVKNS-PFP-----RSYRCTNS---RCTVKKVERSSDD--PSIVI-----TTYEGQHC--HQTI-----66
AtWRKY48_At5g49520	WRKYGQKAVKNS-PYP-----RSYRCTTV---GCPVKKVERSSDD--PSIVM-----TTYEGQHT--HPPF-----66
OsWRKY8	WRKYGQKAVKNS-SYP-----RSYRCTAP---RCGVKRVKVERSEQD--PSMVI-----TTYEGQHT--HPSP-----66
OsWRKY11	WRKYGQKAVKNS-PYP-----RSYRCTTP---KCPVKKVERSEQD--PSTVI-----TTYEGQHT--HHSP-----66
AtWRKY23_At2g47260	WRKYGQKAVKNS-PFP-----RSYRCTTA---SCNVKRVKVERSPRD--PSTVV-----TTYEGQHT--HISP-----66
OsWRKY16	WRKYGQKAVKNS-PYP-----RSYRCTTQ---KCPVKKVERSEQD--PAVVI-----TTYEGKHT--HPIP-----66
OsWRKY49	WRKYGQKAVKNS-PFP-----RSYRCTTQ---KCPVKKVERSEQD--AAVVI-----TTYEGKHT--HPIP-----66
AtWRKY8_At5g46350	WRKYGQKAVKNS-PYP-----RSYRCTTQ---KCPVKKVERSEQD--PTVVI-----TTYEGQHN--HPIP-----66
AtWRKY28_At4g18170	WRKYGQKAVKNS-PYPRIIANGNENRSYRCTTQ---KCPVKKVERSEQD--PTVVI-----TTYEGQHN--HPIP-----72

AtWRKY71_At1g29860	WRKYGKAVKNS-PYP-----RSYRCTTQ---KCNVKKRVERSFQD--PSIVI----TTYEGKHN--HPIP-----66
AtWRKY68_At3g62340	WRKYGKQPVKDS-PFP-----RNYRCTTT---WCDVKKRVERSFSD--PSSVI----TTYEQOHT--HPRP-----66
SemWRKY1	WRKYGKAVKNS-PHP-----RSYRCTNS---KCPVKKRVERSCED--PGIVI----TTYEGTHT--H-----63
SemWRKY14	WRKYGKAVKNS-PHP-----RSYRCTNS---KCPVKKRVERSCED--PGIVI----TTYEGTHT--H-----63
SemWRKY30	WRKYGKAVKNS-PHP-----RSYRCTNS---KCPVKKRVERSCED--PGIVI----TTYEGTHT--H-----63
SemWRKY11	WRKYGKAVKNS-PHP-----RSYRCTNT---KCPVKKRVERSSSED--QGLVI----TTYEGIHN--H-----63
SemWRKY29	WRKYGKAVKNS-PHP-----RSYRCTNT---KCPVKKRVERSSSED--QGLVI----TTYEGIHN--H-----63
SemWRKY24	WRKYGKAVKNS-PYP-----RSYRCTYT---KCHVKKRVERSSKD--SSLVI----TTYEGVHT--H-----63
SemWRKY32	WRKYGKAVKNS-PYP-----RSYRCTYT---KCHVKKRVERSSKD--SSLVI----TTYEGVHT--H-----63
PpWRKY3	WRKYGKAVKDS-PFP-----RSYRCTNQ---TCPVKKRVERKAGD--AGLVV----TTYEGTHS--HLSP-----66
PpWRKY17	WRKYGKAVKNS-PYP-----RSYRCTNP---DCPVKKRVERKADD--HGLVV----TTYEGTHN--H-----63
PpWRKY20	WRKYGKAVKNS-THP-----RSYRCTSH---TCPVKKRIERKADD--PGLVI----TTYEGTHN--H-----63
PpWRKY14M	WRKYGKAVKNS-PHP-----RYYRCTNP---KCPVKKVERSAED--SELVI----TSYEGTHT--H-----63
PpWRKY28	WRKYGKAVKNS-PHP-----RSYRCTNP---KCPVKKVERSAED--SELVI----TSYEGTHT--H-----63
PpWRKY22	WRKYGKAVKNS-PHP-----RSYRCTHM---MCPVKKRVERSAED--TGLVI----TTYEGTHT--H-----63
PpWRKY6	WRKYGKQPVKSS-PHP-----RNYRCTTA---NCPVKKRVERSIED--PGLIV----TSYEGTHT--HPKI-----66
PpWRKY12	WRKYGKQPVKNS-PHP-----RNYRCTTA---HCPVKKRVERSTED--PGLVI----TSYEGTHS--H-----63
PpWRKY15	WRKYGKQPVKNS-VHP-----RNYKCTTA---NCPVKKRVERCTDD--PSHVL----TTYDGTHT--H-----63
PpWRKY11	WRKYGKQPVKSS-PHP-----RNYRCTTP---NCPVKKRVERSTED--PDQVI----TTYEGRHT--HQSP-----66
PpWRKY18	WRKYGKAVKNS-PHP-----RNYRCTTP---QCPVKKRVERSSSED--AGLVI----TTYEGTHT--H-----63
PpWRKY24	WRKYGKAVKNS-PYP-----RNYRCTTP---QCPVKKRVERSCED--SGLVI----TTYEGTHT--H-----63
PpWRKY29	WRKYGKAVKNS-PHP-----RNYRCTTP---LCPVKKRVERSNED--AGLVI----TTYEGTHS--H-----63
PpWRKY31	WRKYGKAVKNS-PHP-----RNYRCTTP---LCPVKKRVERSKED--AGLVI----TTYEGTHS--H-----63
PpWRKY21	WRKYGKAVKNS-PHP-----RNYRCATP---NCPVKKRVERCIED--PGLVA----TAYEGTHS--HQFP-----66
PpWRKY27	WRKYGKAVKNS-PHP-----RNYRCTTL---NCPVKKRVERCFDD--PGVMV----TTYEGTHT--H-----63
OsWRKY36	WRKYGKQVVKNS-LHP-----RSYRCTHN---NCRVKKRVERLSED--CRMVI----TTYEGRHT--HTPC-----66
AtWRKY12	WRKYGKQVVKNS-LHP-----RSYRCTHN---NCRVKKRVERLSED--CRMVI----TTYEGRHN--HIPS-----66
OsWRKY34	WRKYGKQVVKNS-LHP-----RSYFRCTHS---NCRVKKRVERLSTED--CRMVI----TTYEGRHT--HSPC-----66
OsWRKY79	WRKYGKQVVKNT-QHP-----RSYRCTQD---NCRVKKRVERLAED--PRMVI----TTYEGRHV--HSPS-----66
AtWRKY13_At4g39410	WRKYGKQVVKNT-QHP-----RSYRCTQD---KCRVKKRVERLADD--PRMVI----TTYEGRHL--HSPS-----66
OsWRKY26	WRKYGKQSVKNS-PNP-----RNYRCSTE---GONVKKRVERDKND--PRYVV---TMYEGIHN--HVCP-----66
OsWRKY59	WRKYGKQSVKNS-PNP-----RNYRCSTE---GONVKKRVERDKND--PRYVV---TTYEGIHN--HVCP-----66
OsWRKY7	WRKYGKQSVKNS-PNP-----RNYRCSTE---GONVKKRVERDKDD--PSYVV---TTYEGTHN--HVSPS-----67
NtWRKY11	WRKYGKQMVKDS-PNP-----RNYRCSIE---SCPVKKRVERDKED--CRYVI----TTYEGVHN--HQGP-----66
NtWRKY10	WRKYGKQMVKDS-PNP-----RNYRCSVE---GCPVKKRVERDKED--CRYVI----TTYEGVHN--HQGP-----66
OsWRKY67	WRKYGKAVKNS-PNP-----RNYRCSSTE---GONVKKRVERDRD--HRYVI----TTYDGVHN--HASP-----66
ZmWRKY67_Zea_mays	WRKYGKAVKNS-PNP-----RNYRCSSE---GCGVKKRVERDRDD--PRYVI----TTYDGVHN--HASP-----66
PheWRKY10_Phyllostachys_edulis	WRKYGKAVKNS-PNP-----RNYRCSSTE---GCGVKKRVERDRDD--PCYVI----TTYDGVHN--HATP-----66
OsWRKY10	WRKYGKAVKNS-PNP-----RNYRCSAA---GCGVKKRVERDRDD--PRYVV---TTYDGVHN--HATP-----66
OsWRKY77	WRKYGKQMVKNS-PNP-----RNYRCSSE---GCRVKKRVERARD--ARFVV---TTYDGVHN--HPAP-----66
AtWRKY50_At5g26170	WRKYGKQMVKNS-PHP-----RNYKCSVD---GCPVKKRVERDRDD--PSFVI----TTYEGSHN--HSSM-----66
OsWRKY23	WRKYGKAVKNS-KHP-----RSYRCTHH---TCNVKKQVQRLAKD--TSIVV----TTYEGVHN--HPCEKL-----68
AtWRKY43_At2g46130	WRKYGKQSVKNS-LYP-----RSYRCTQH---MCNVKKQVQRLSKE--TSIVE----TTYEGIHN--HPCE-----66
AtWRKY24_At5g41570	WRKYGKQSVKHN-AHP-----RSYRCTYH---TCNVKKQVQRLAKD--PNVVV---TTYEGVHN--HPCE-----66
AtWRKY56_At1g64000	WRKYGKQSVKNN-AHP-----RSYRCTYH---TCNVKKQVQRLAKD--PNVVV---TTYEGVHN--HPCE-----66
OsWRKY72	WRKYGKAVKNN-KFP-----RSYRCTHQ---GONVKKQVQRLSRD--ETVVV---TTYEGTHT--HPIE-----66
AtWRKY75_At5g13080	WRKYGKAVKNN-KFP-----RSYRCTYQ---GONVKKQVQRLTVD--QEVVV---TTYEGVHS--HPIE-----66
AtWRKY45_At3g01970	WRKYGKAVKNN-PFP-----RSYKCTEE---GCRVKKQVQVQWGD--EGVVV---TTYQGVHT--HAVD-----66
PpWRKY26	WRKYGKQPVKNS-HHP-----RNYKCTTP---NCLVKKQVERCTEN--PSNVM---TTYYGTHN--H-----63
OsWRKY24-CTD	WRKYGKQVVKGN-PNP-----RSYKCTTA---GCPVKKHVERASHD--LRAVI---TTYEGKHN--HDVP-----66
OsWRKY70-CTD	WRKYGKQVVKGN-PNP-----RSYKCTTA---GCPVKKHVERASHD--LRAVI---TTYEGKHN--HDVP-----66
PcWRKY1-CTD	WRKYGKQVVKGN-PNP-----RSYKCTQV---GCPVKKHVERASHD--LRAVI---TTYEGKHN--HDVP-----66
PbZFP1-CTD	WRKYGKQVVKGN-PNP-----RSYKCTQV---GCPVKKHVERASHD--LRAVI---TTYEGKHN--HDVP-----66
AfABF1-CTD	WRKYGKQVVKGN-PNP-----RSYKCTTV---GCPVKKHVERASHD--LRAVI---TTYEGKHN--HDVP-----66

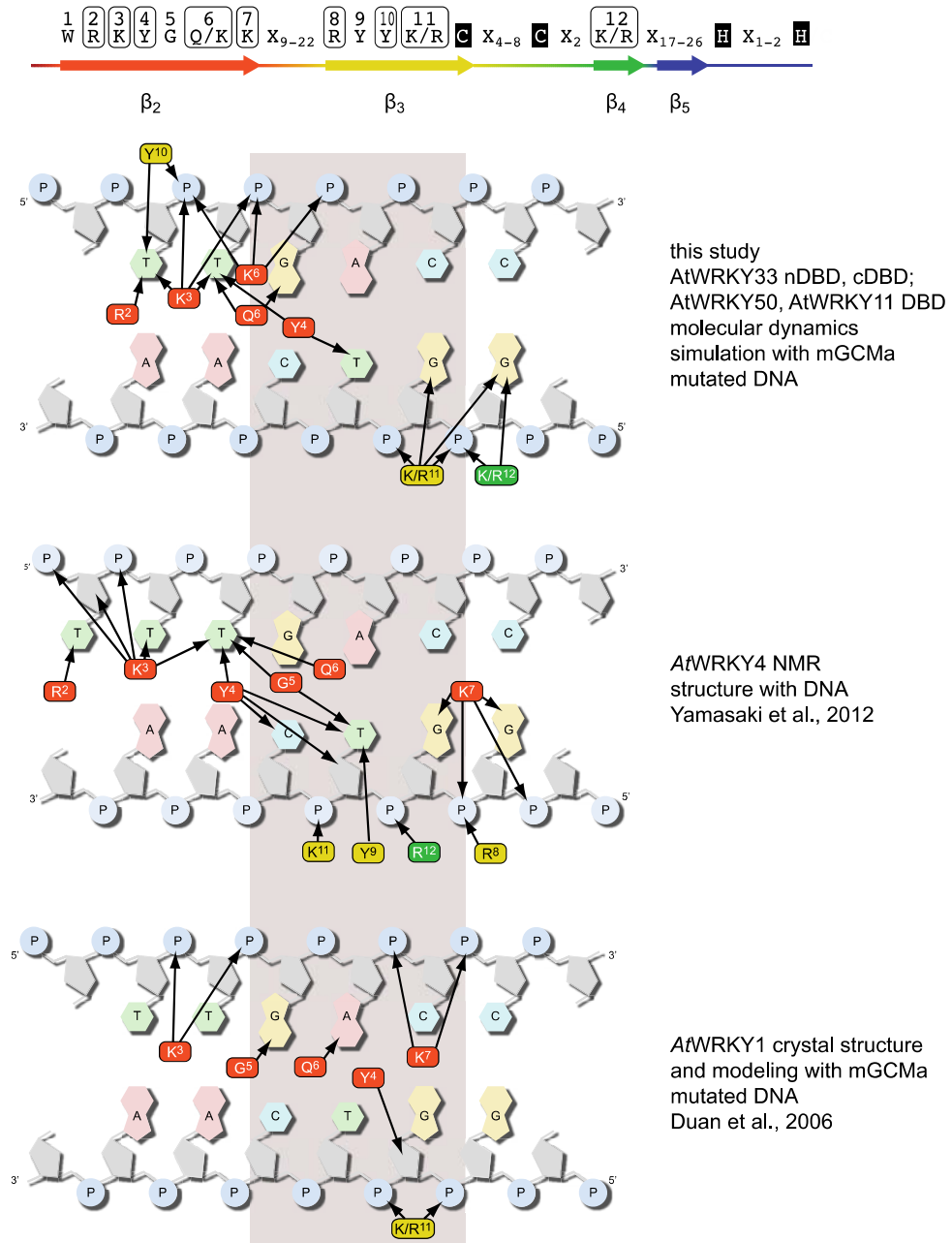


OsWRKY53-CTD	WRKYGQKVVKGN-PNP-----RSYKCTTV---GCPVKHVERASHD--TRAVI-----TTYEGKHN--HDVP-----	66
AtWRKY33-CTD_At2g38470_CTD	WRKYGQKVVKGN-PNP-----RSYKCTTI---GCPVKHVERASHD--MRAVI-----TTYEGKHN--HDVP-----	66
IbSPF1_CTD	WRKYGQKVVKGN-PNP-----RSYKCTSQ---GCPVKHVERASHD--IRSVI-----TTYEGKHN--HDVP-----	66
OsWRKY30	WRKYGQKVVKGN-PNP-----RSYKCTHP---GCSVKHVERASHD--LKSVI-----TTYEGKHN--HEVP-----	66
OsWRKY80	WRKYGQKVVKGN-PNP-----RSYKCTHQ---GCSVKHVERASHD--LKSVI-----TTYEGKHN--HEVP-----	66
AtWRKY2-CTD_At5g56270_CTD	WRKYGQKVVKGN-PNP-----RSYKCTAP---GCTVKHVERASHD--LKSVI-----TTYEGKHN--HDVP-----	66
OsWRKY78-CTD	WRKYGQKVVKGN-PNP-----RSYKCTNT---GCPVKHVERASHD--PKSVI-----TTYEGKHN--HEVP-----	66
AtWRKY20-CTD_At4g26640_CTD	WRKYGQKVVKGN-PNP-----RSYKCTAH---GCPVKHVERASHD--PKAVI-----TTYEGKHD--HDVP-----	66
PpWRKY16-CTD	WRKYGQKVVKGN-PHP-----RSYKCTNV---GCPVKHVERASTD--IKAVI-----TTYEGKHN--HDVP-----	66
PpWRKY23-CTD	WRKYGQKVVKGN-PHP-----RSYKCTNV---GCPVKHVERASTD--IKAVI-----TTYEGKHN--HDVP-----	66
PpWRKY4	WRKYGQKVVKGN-PHP-----RSYKCTNV---GCPVKHVERASND--PKAVI-----TTYEGKHN--HDVP-----	66
SemWRKY6-CTD	WRKYGQKVVKGN-PHP-----RSYKCTNL---GCPVKHVERACDD--PRAVI-----TTYEGKHN--HDVP-----	66
SemWRKY20-CTD	WRKYGQKVVKGN-PHP-----RSYKCTNL---GCPVKHVERACDD--PRAVI-----TTYEGKHN--HDVP-----	66
SemWRKY5-CTD	WRKYGQKIVKGN-PYP-----RSYKCTNV---GCPVKHVERASND--PKSVI-----TTYEGKHN--HDVP-----	66
Sem WRKY13-CTD	WRKYGQKIVKGN-PYP-----RSYKCTNV---GCPVKHVERASND--PKSVI-----TTYEGKHN--HDVP-----	66
SemWRKY15	WRKYGQKVVKGN-PHP-----RYKCSSS---GCAVKHVERASND--PKSVI-----TTYEGKHN--HDVP-----	66
SemWRKY22-CTD	WRKYGQKVVKGN-PHP-----RYKCSSS---GCAVKHVERASND--PKSVI-----TTYEGKHN--HDVP-----	66
AtWRKY3-CTD_At2g03340_CTD	WRKYGQKVVKGN-PYP-----RSYKCTTP---DCGVKHVERAATD--PKAVV-----TTYEGKHN--HDVP-----	66
AtWRKY4-CTD_At1g13960_CTD	WRKYGQKVVKGN-PYP-----RSYKCTTP---GCGVKHVERAATD--PKAVV-----TTYEGKHN--HDLP-----	66
AtWRKY58-CTD_At3g01080_CTD	WRKYGQKVVKGN-PHP-----RSYKCTTP---NCTVKHVERASTD--AKAVI-----TTYEGKHN--HDVP-----	66
CsSPF1_CTD	WRKYGQKVVKGN-PNP-----RSYKCTSA---GCVVKHVERASDD--SKAVV-----TTYEGKHN--HDVP-----	66
SemWRKY4-CTD	WRKYGQKVVKGN-PNP-----RSYKCTNP---GCPVKHVERAADD--PKAVI-----TSYEGKHD--HDTF-----	66
AtWRKY26-CTD_At5g07100_CTD	WRKYGQKVVKGN-PNP-----RSYKCTFT---GCFVKHVERAFQD--PKSVI-----TTYEGKHK--HQIP-----	66
AtWRKY34-CTD_At4g26440_CTD	WRKYGQKVVKGN-PNP-----RSYKCTAN---GCTVKHVERASDD--FKSVL-----TTYIGKHT--HVVP-----	66
OsWRKY4-CTD	WRKYGQKVVKGN-PRP-----RSYKCTAD---GCVVKQIRASAD--PKCVL-----TTYTGRHN--HDPP-----	66
AtWRKY25-CTD_At2g30250_CTD	WRKYGQKVVKGN-TNP-----RSYKCTFQ---GCGVKQVERAADD--BRAVL-----TTYEGRHN--HDIP-----	66
AtWRKY10_At1g55600	WRKYGQKVVKGN-PNP-----SYFKCTNI---ECRVKHVERGADN--IKLVV-----TTYDGIHN--HPSP-----	66
CrWRKY10_homolog	WRKYGQKVVKGN-PNP-----SYFKCTNN---DCNVKHVERGADN--FKILV-----TSYDGIHN--HPPP-----	66
Ddiscoidium WRKY-CTD_XM_638694	WRKYGQKSVKGS-PFP-----KSYFKCAEL---TCPVKQVIQ--QD--SK-YI-----NTYRGKHN--HDPP-----	63
OsWRKY24-NTD	WRKYGQKQVKGS-ENP-----RSYKCTFP---NCPVKKVERSL-D--GQITE-----IVYKGTNH--HAKP-----	65
AfABF1_NTD	WRKYGQKQVKGS-ENP-----RSYKCTFP---NCPVKKVERSL-E--GQITE-----IVYKGTNH--HAKP-----	65
OsWRKY70-NTD	WRKYGQKQVKGS-ENP-----RSYKCTFP---GCPVKKVEQSP-D--GQVTE-----IVYKGAHS--HPKP-----	65
AtWRKY33-NTD_At2g38470_NTD	WRKYGQKQVKGS-ENP-----RSYKCTFP---NCPVKKVERSL-E--GQITE-----IVYKGSNH--HPKP-----	65
IbSPF1_NTD	WRKYGQKQVKGS-ENP-----RSYKCTHP---NCPVKKVERAL-D--GQITE-----IVYKGAHN--HPKP-----	65
AtWRKY26-NTD_At5g07100_NTD	WRKYGQKQVKGS-ENP-----RSYFKCTYP---NCLVKKVERSLVK--GQIE-----IVYKGSNH--HPKPQSTKRS--	72
PcWRKY1_NTD	WRKYGQKQVKGS-ENP-----RSYKCTYL---NCPVKKVVETTF-D--GHITE-----IVYKGNHN--HPKP-----	65
PbZFP1_NTD	WRKYGQKQVKGS-ENP-----RSYKCTYL---NCPVKKVVETTF-D--GHITE-----IVYKGNHN--HPKP-----	65
AtWRKY25-NTD_At2g30250_NTD	WRKYGQKQVKGS-ENP-----RSYFKCTYP---DCVSKIVETAS-D--GQITE-----IIVYKGSNH--HPKP-----	65
PpWRKY16-NTD	WRKYGQKQVKGS-EYP-----RSYKCTQA---NCPMKKVERSH-D--GQVTE-----IVYKGDHN--HPKP-----	63
PpWRKY23-NTD	WRKYGQKQVKGS-EYP-----RSYKCTQT---NCPMKKVERSH-D--GQVTE-----IVYKGDHN--HPKP-----	63
SemWRKY6-NTD	WRKYGQKLVKGS-ENP-----RSYKCTYV---NCPMKKVERSP-D--GQVTE-----IVYEGEHN--HPKP-----	65
SemWRKY20-NTD	WRKYGQKLVKGS-ENP-----RSYKCTYV---NCPMKKVERSP-D--GQVTE-----IVYEGEHN--HPKP-----	65
SemWRKY5-NTD	WRKYGQKQVKGS-EFP-----RSYKCTSS---GCPVKKVERSQ-D--GQVTE-----IVYKGEHN--HPRP-----	65
SemWRKY13-NTD	WRKYGQKQVKGS-EFP-----RSYKCTSS---GCPVKKVERSQ-D--GQVTE-----IVYKGEHN--HPRP-----	62
SemWRKY22-NTD	WRKYGQKQVKGS-EFP-----RSYKCTHP---SCPVKKVERSY-D--GQVTE-----IVYKGEHC--HAKP-----	63
AtWRKY44-NTD_TTG2_At2g37260_NT	WRKYGQKQVKGS-ECP-----RSYKCTHP---KCPVKKVERSV-E--GQVSE-----IVYQGEHN--HSKP-----	65
OsWRKY57	WRKYGQKQVKGS-EFP-----RSYKCTHP---TCPVKKVEFTP-D--GRIAE-----IVYNGEHN--HPKP-----	65
AtWRKY2-NTD_At5g56270_NTD	WRKYGQKLVKGS-EYP-----RSYKCTNP---NCPVKKVERSR-E--GHITE-----IIVYKGAHN--HLKP-----	65
AtWRKY34-NTD_At4g26440_NTD	WRKYGQKLVKGS-EYP-----RSYKCTHP---NCEVKKVERSR-E--GHIE-----IIVYGDHI--HSKP-----	65
OsWRKY35-NTD	WRKYGQKQVKGS-EYP-----RSYKCTHA---SCAVKKVERSH-E--GHVTE-----IIVYKGTNH--HPKP-----	65
OsWRKY78-NTD	WRKYGQKHVKGS-ENP-----RSYKCTHP---NCDVKLLERSL-D--GQITE-----VVYKGRHN--HPKP-----	65
AtWRKY20-NTD_At4g26640_NTD	WRKYGQKHVKGS-EFP-----RSYKCTHP---NCEVKLFERSH-D--GQITD-----IIVYKGTND--HPKP-----	65
OsWRKY53-NTD	WRKYGQKQVKGS-ENP-----RSYKCTYN---GCSMKKVERSLAD--GRITQ-----IVYKGAHN--HPKP-----	66
SemWRKY4-NTD	WRKYGQKQVKGC-DNP-----RSYKCTHP---DCSAKLVERSVS--GETTQ-----IVYKGDHS--HSKP-----	58

AtWRKY3-NTD_At2g03340_NTD	WRKYGKQVKGS-DFP-----RSYKCTHP---ACPVKKVERSL-D--GQVTE-----IIYKGQHN-HELP----- 65
AtWRKY4-NTD_At1g13960_NTD	WRKYGKQVKGS-EFP-----RSYKCTNP---GCPVKKVERSL-D--GQVTE-----IIYKGQHN-HEPP----- 65
CsSPF1_NTD	WRKYGKLVKGS-EFP-----RSYKCTHL---NCPVKKIEGLP-D--GEITE-----IIYKGQHN-HEPP----- 65
AtWRKY58-NTD_At3g01080_NTD	WRKYGKPIKGC-EYP-----RSYKCTHV---NCPVKKVERSS-D--GQITQ-----IIYKGQHD-HERP----- 65
AtWRKY19-NTD_At4g12020_NTD	WRKYGKQVKGS-KFP-----LSYKCTYL---GCPVKKVERSL-D--GQVAE-----IVYKDRHN-HEPP----- 65
OsWRKY4-NTD	WRKYGKQVKGS-ESP-----RSYKCTRD---GCPVKKVERSS-D--GCIKE-----ITYKGRHS-HPRP----- 65
OsWRKY82-NTD	WRKYGKQVKSS-ENS-----RSYRCTNS---NCLAKKVEHCPD---GRVVE-----IIYRGTHN-HEPP----- 65
AtWRKY32-NTD_At4g30930_NTD	WRKYGKQVKSP-KGS-----RSYRCTYT---ECCAK-IECSNDS--GNVVE-----IVNKGLEHT-HEPP----- 65
AtWRKY1-NTD_ZAP1_At2g04880_NTD	WRKYGKLVKGN-EFV-----RSYRCTHP---NCKAKQLERSA-G--GQVVD-----TVYFGEHD-HPKP----- 65
CocSub_NTD	WRKYGKQVKGS-PYP-----RSYKCSQQ---NCQVKKIVERNPEN--GEVSK-----SASKGVHN-HAKP----- 61
ChvWRKY1-NTD_Chlorella_variabi	WRKYGKQVKGS-PFP-----RSYKCSHP---GCPAKMIEREPKT--GRISQ-----AELKNEHN-HAKP----- 63
OsWRKY17	WRKYGKSIKNS-PNP-----RSYRCTNP---RCNAKQVERAVDE--PDTLI-----VTYEGLEHL-HYTY----- 66
AtWRKY49_At5g43290	WRKYGKSIKNS-PNP-----RSYKCTNP---ICNAKQVERSIDE--SNTYI-----ITYEGFHF-HYTY----- 66
AtWRKY59_At2g21900	WRKYGKPKITGS-PFP-----RHYKCSPP---DCNVKKIERDTNN--PDYIL-----TTYEGRHN-HPSP----- 66
OstISS1_Ostreococcus_tauri_WRK	WRKYGKNIKGS-RHPR-----SYRCTER---GCPAKKTELASDESDEDEGDR-MRVTYEGVHT-HPKP----- 72
OstWRKYputative_Ostreococcus_t	WRKYGKNIKGS-SFPR-----SYRCTER---GCPAKKTELRRASEDGEMET---VVCYEGEHT-HAKP----- 69
MICPUN_61119	WRKYGKNVRGR-KVG-----YFKCAHR---GCEAKK-VWRQANGDEAVER-----EGTHT-HAAG----- 62
Glaublia_WRKY-CTD_XM_765980	WRKYGKPKQTD-RLDSK-----SYRCAFF---NCPARTITFFYSLSSDGTETVESVIQYENQHT-HPPD----- 74
OsWRKY60	WRKYGKFIKNI-QKN-----RSYFRCRDQ---RCGAKKVEWHPHDPGLNLR-----VVYDGAHH-HGSP----- 67
Glaublia_WRKY-NTD_XM_765980	WRKYGKRLPNN-SHP-----KSYFRCSVP---GCQAKRYVTETDNR---VLK-----TEYIGEHN-HGKS----- 64
PpWRKY32	WRKYGNLAKGN-LCP-----RGLLPLYCG---ALLSPQAGFCDNVQRCADHKS-VLITTYEGTHN-HPIP----- 72
Tetrapisispora	EKYGVLAEYI-LED-----EELLALYHS---GLL----- 38

Supplementary Figure 4|

AtWRKY1 cDBD SRIVVHTQTLFDIVNDGYRWRKYGOKSVKGSYPYRSYYRCS-PCPVKKhVERSSSHDTKLLITTYEGKHDDMPPG



**Supplementary Figure 4|** Comparison of models for WRKY DBD-DNA interaction sites.