

A

GROUP 1N

OsWRKY15 DTHPPEYDGYNWRICGGQKVVGCGCHQKFYYECSQANCGAEKSVTRSA-DGQIKKTVCKGSHNHPLS
OsWRKY16 YPNPTEYDGYNWRMCGQKLVGCGCHQKFYYECSQANCGAEKSVTRSA-DGQIKKTVCKGSHNHPRS
OsWRKY2N AIEQPAKDGYNWRKYGQKQLKDAESPRSYYKCTRDCPVKKIVERSS-DGCIKEITYKGRHSHPRP
OsWRKY47N LIITPAEDGYNWRKYGQKQVKNSEHPRSYYKCTFTNCAVKK-VERSQ-DGQITEIVYKGSNHPLP
OsWRKY51N VLDRPTDDGYNWRKYGQKAVKGGEYPKSYKCTHLNCLVRKNVEHSA-DGRIVQIIYRGQHTHERP
OsWRKY103N VLDRPTDDGYNWRKYGQKAVKGGEYPKSYKCTHLNCLVRKNVEHSA-DGRIVQIIYRGQHTHERP
AtWRKY58N NVDKPADDGYNWRKYGQKPIKGCEYPRSYYKCTHVNCVKKKVERSS-DGQITQIIYKGQHHERP
OsWRKY83N PVDKPADDGYNWRKYGQKVVGSDCPRSYYKCTHPNCVKKKVEHAE-DGQISEIIYKGKHNHQRP
AtWRKY3N NADKPADDGYNWRKYGQKQVKGSDFPSRYYKCTHPACPVKKKVERSL-DGQVTEIIYKGQHNHELP
AtWRKY4N NVDKPADDGYNWRKYGQKQVKGSEFPSRYYKCTNPGCPVKKKVERSL-DGQVTEIIYKGQHNHEPP
AtWRKY19N NVDKQVNDGYNWQKYGQKKVKGSKFPLSYKCTYLGCPSKRKVERSL-DGQVAEIVYKDRHNHEPP
OsWRKY22N SQRRSSDDGYNWRKYGQKQVKGSENPRSYYKCTFPNCPTKKKVERSL-DGQITEIVYKGTNHPAKP
OsWRKY69N QSRRSSDDGYNWRKYGQKQMKGSENPRSYYKCTFPGCPTKKKVEQSP-DGQVTEIVYKGAHSHPKP
AtWRKY33N REQRKGEDGYNWRKYGQKQVKGSENPRSYYKCTFPNCPTKKKVERSL-EGQITEIVYKGSNHPKP
AtWRKY26N SSNKTSDDGYNWRKYGQKQVKGSENPRSYYKCTYPNCLTKKKVETSLVKGQMI EIVYKGSNHPKP
AtWRKY25N MVSRSNDGYNWRKYGQKQVKKSENPRSYYKCTYPD CVSKKIVETAS-DGQITEIIYKGGHNHPKP
OsWRKY61N GGNNKLEDGYNWRKYGQKQVKGSENPRSYYKCTYNGCSMKKKVERSLADGRITQIVYKGAHNHPKP
OsWRKY73 AKNSLSYDGYSWRKYGQKQVKGSEFPSRYYKCTHPTCPVKKRVEMTP-DGRIAEIVYNGEHNHPKP
OsWRKY104 AKNSLSYDGYSWRKYGQKQVKGSEFPSRYYKCTHPTCPVKKRVEMTP-DGRIAEIVYNGEHNHPKP
AtWRKY44N TGDRSSVDGYNWRKYGQKQVKGSECPRSYYKCTHPKCPVKKKVERSV-EGQVSEIVYQGEHNHSPK
AtWRKY2N AGGAPAEEDGYNWRKYGQKLVKGSEYPRSYYKCTNPNQVKKKVERSR-EGHIT EIIYKGAHNHLKP
AtWRKY34N ACCAPADDGYNWRKYGQKLVKGSEYPRSYYKCTHPNCEAKKKVERSR-EGHIEIIYTGDIHHSKP
OsWRKY37N AAAVAEDGYSWRKYGQKQVKHSEYPRSYYKCTHASCAVKKKVERSH-EGHVTEIIYKGTNHPKP
OsWRKY59N VAEKSAEDGYNWRKYGQKHVKGSENPRSYYKCTHPNCDVKKLLERSL-DGQITEVVYKGRHNHPKP
AtWRKY20N TPSILADDGYNWRKYGQKHVKGSEFPSRYYKCTHPNCEVKKLFERSH-DGQITDIIYKGTHDHPKP
AtWRKY1N IREKVMEDGYNWRKYGQKLVKGNEFVRSYYRCTHPNCKAKKQLERSA-GGQVVDTVYFGEHDHPKP
OsWRKY48N VSVNMVGDGFNWRKYGQKQVKSSENSRSYYRCTNSNCLAKKKVEHCPD-GRVVEIIYRGTHNHEPP
AtWRKY32N VPRTPARDGYNWRKYGQKQVKSPKGSRSYYRCTYTECCAKK-IECSNDSGNVVEIVNKGHLTHEPP
DsWRKY1N NISNIVSDGYQWRKYGQKNVKGSLHPRHYKCTFQGCNVRKQVER-IGDTNQNSTVYKGEHCHGFP
ChrWRKY1N KQSVANS DGWQWRKYGKLVKGSPNPRSYYKCSHPGLAKKIVERSDSDGTVLST EYKGDHCHPAP
GlWRKY1N TIRELPADGYCWRKYGSKRLPNNSHPKSYFRCSVPGCQAKRYVTETD--NRVLKTEYIGEHNHGKS

GROUP 1C

OsWRKY2C SEVDLLDDGYRWRKYGQK-VVKGNPFRPSYYKCTADGCNVRK-----QIERASADPKCVLTITGRHNDPP
 OsWRKY83C SEVDLLDDGYRWRKYGQK-VVKGNPHPRSYYKCTYAGCNVRK-----HIERASSDPKAVITTYEGKHNEPP
 OsWRKY51C SEIDLDDGYRWRKYGQK-VVKGNPYPRSYYKCTYLGCDVKK-----QVERSVEEPNAVITTYEGKHIHDVP
 OsWRKY103C SEIDLDDGYRWRKYGQK-VVKGNPYPRSYYKCTYLGCDVKK-----QVERSVEEPNAVITTYEGKHIHDVP
 AtWRKY3C SEVDLLDDGYRWRKYGQK-VVKGNPYPRSYYKCTTPDCGVRK-----HVERAATDPKAVVTTYEGKHNDVP
 AtWRKY4C SEVDLLDDGYRWRKYGQK-VVKGNPYPRSYYKCTTPGCGVRK-----HVERAATDPKAVVTTYEGKHNDLP
 AtWRKY58C SEVDLLDDGYRWRKYGQK-VVKGNPHPRSYYKCTTPNCTVRK-----HVERASTDAKAVITTYEGKHNDVP
 AtWRKY26C SDIDILDDGYRWRKYGQK-VVKGNPNPRSYYKCTFTGCFVRK-----HVERAFQDPKSVITTYEGKHQIP
 AtWRKY34C SDIDILDDGYRWRKYGQK-VVKGNPNPRSYYKCTANGCTVTK-----HVERASDDFKSVLTITYIGKHTVVP
 OsWRKY13 SEVDILDDGYRWRKYGQK-VVKGNPNPRSYYKCTHQGCSVRK-----HVERASHDLKSVITTYEGKHNEVP
 OsWRKY47C SEVDILDDGYRWRKYGQK-VVKGNPNPRSYYKCTHPGCSVRK-----HVERSSHDLSVITTYEGKHNEVP
 OsWRKY37C SEVDILDDGYRWRKYGQK-VVKGNPNPRSYYKCTHPGCLVRK-----HVERASHDLKSVITTYEGKHNEVP
 OsWRKY59C SEVDILDDGYRWRKYGQK-VVKGNPNPRSYYKCTNTGCPVRK-----HVERASHDPKSVITTYEGKHNEVP
 AtWRKY2C SDVDILDDGYRWRKYGQK-VVKGNPNPRSYYKCTAPGCTVRK-----HVERASHDLKSVITTYEGKHNDVP
 AtWRKY20C SEVDILDDGYRWRKYGQK-VVRGNPNPRSYYKCTAHGCPVRK-----HVERASHDPKAVITTYEGKHDHVP
 OsWRKY22C SDIDILDDGYRWRKYGQK-VVKGNPNPRSYYKCTTAGCPVRK-----HVERASHDLRAVITTYEGKHNDVP
 OsWRKY69C SDIDILDDGYRWRKYGQK-VVKGNPNPRSYYKCTTAGCPVRK-----HVERASNDLRAVITTYEGKHNDVP
 OsWRKY61C SDIDILDDGFRWRKYGQK-VVKGNPNPRSYYKCTTVGCPVRK-----HVERASHDTRAVITTYEGKHNDVP
 AtWRKY33C SDIDILDDGYRWRKYGQK-VVKGNPNPRSYYKCTTIGCPVRK-----HVERASHDMRAVITTYEGKHNDVP
 AtWRKY10C SDEDNPNDGYRWRKYGQK-VVKGNPNPRSYYKCTNIECRVKK-----HVERGADNIKLVVTTYDGIHNPSP
 AtWRKY25C SDIDVLIDGFRWRKYGQK-VVKGNTNPRSYYKCTFQCGVKK-----QVERSAADERAVLTITYEGRHNDIP
 AtWRKY45C SQVDILDDGYRWRKYGQK-AVKNNPFPRSYYKCTEEGCRVKK-----QVQRQWGDEGVVTTYQGVHTHAVD
 AtWRKY44C VESDSLEDGFRWRKYGQK-VVGGNAYPRSYYRCTSANCRAK-----HVERASDDPRAFITTYEGKHNHLL
 AtWRKY1C TLFDIVNDGYRWRKYGQK-SVKGSFYPRSYYRCSPPGCPVKK-----HVERSSHDTKLLITTYEGKHNDMP
 ChrWRKY1C DITN-MDDGYRWRKYGQK-QVKGSFPFRAYYKCTHMGCSVRK-----HVERSAEDETFRVVTYEGTHSHRLP
 DsWRKY1C NISNIVSDGYQWRKYGQK-NVKGSLHPRHYKCTFQGCNVRK-----QVER-IGDTNQNSTVYKGEHCHGFP
 AtWRKY32C GDVGICGDGYRWRKYGQK-MVKGNPHPRNYYRCTSAGCPVRK-----HIETAVENTKAVIITYKGVHNDMP
 OsWRKY48C VQAGKTSDDGYRWRKYGQK-IVKGNPNPRSYYRCTHDGCPVRK-----HVEKAPDDNNIVVTYEGKHNDQP
 GlWRKY1C DQIESSIDFFRWRKYGQK-PQTDTRLDSKSYRCAFFNCPARRTITFFYSLSSDGTETVESVIVQENQHTHPPD

GROUP 2_a + 2_b

Domains inside and above the box correspond to subfamily 2a and 2b in the classification by Eulgem et al. (2000), respectively.

OsWRKY86	SDAPMISDGCQWRKYGQKMAKGNPCPRAYYRCTMAAGCPVRKQVQRCAED-RTVLITTYEGNHNHPLP
AtWRKY42	SEAPMLSDGCQWRKYGQKMAKGNPCPRAYYRCTMAVGCPCVRKQVQRCAED-RTILITTYEGNHNHPLP
OsWRKY29	SEAPIIADGCQWRKYGQKMAKGNPCPRAYYRCTMATGCPVRKQVQRCAED-RSILITTYEGTHNHPLP
OsWRKY96	SEAPIIADGCQWRKYGQKMAKGNPCPRAYYRCTMATGCPVRKQVQRCAED-RSILITTYEGTHNHPLP
AtWRKY6	SEAPMISDGCQWRKYGQKMAKGNPCPRAYYRCTMATGCPVRKQVQRCAED-RSILITTYEGNHNHPLP
AtWRKY31	SEAAMISDGCQWRKYGQKMAKGNPCPRAYYRCTMAGGCPVRKQVQRCAED-RSILITTYEGNHNHPLP
OsWRKY43	SEAPMISDGCQWRKYGQKMAKGNPCPRAYYRCTMASQCPVRKQVQRCAKD-KSILITTYEGTSHHPLP
OsWRKY88	SEAPMISDGCQWRKYGQKMAKGNPCPRAYYRCTMAIGCPVRKQVT-----KLIYM-----HSHN-
AtWRKY47	SDATTVNDGCQWRKYGQKMAKGNPCPRAYYRCTMAVGCPCVRKQVQRCAED-TTILTTTYEGNHNHPLP
AtWRKY36	CEDPSINDGCQWRKYGQKTAKTNPLPRAYYRCSMSSNCPVRKQVQRCGEEETSAFMTTYEGNHDHPLP
OsWRKY26	CDTPTMNDGCQWRKYGQKISKGNPCPRAYYRCTVAPNCPVRKQVQRCADD-MSILITTYEGTSHHPLP
AtWRKY72	CDTPTMNDGCQWRKYGQKIAKGNPCPRAYYRCTVAPGCPVRKQVQRCADD-MSILITTYEGTSHHSLP
OsWRKY5	CDAPTMDGCQWRKYGQKIAKGNPCPRAYYRCTVAAGCPVRKQVQRCADD-MSILITTYEGTHNHPLS
OsWRKY17	CQGPTMNDGCQWRKYGQKVAKGNPCPRAYYRCTVAPGCPVRKQVQRCLED-MSILVTTYEGTHNHPLP
AtWRKY9	CETATMNDGCQWRKYGQKTAKGNPCPRAYYRCTVAPGCPVRKQVQRCLED-MSILITTYEGTHNHPLP
AtWRKY61	KTRVSMNDGCQWRKYGQKIAKGNPCPRAYYRCTIAASCPVRKQVQRCSED-MSILISTYEGTHNHPLP
OsWRKY32	CSAPTVDGCQWRKYGQKTAKGNPWPRGYRCTGAPGCPVKKQVQRCNHD-TSVLVTTYDGVHNHPIT
OsWRKY4	DLSLVVKDGYQWRKYGQKVTKDNPCPRAYFRCSFAPACPVKKKVQRSADD-NTVLVATYEGEHNAQP
OsWRKY18	DLSLVVKDGYQWRKYGQKVTKDNPCPRAYFRCSFAPACPVKKKVQRSAD-NTILVATYEGEHNGQP
OsWRKY58	DTSLVVKDGYQWRKYGQKVTRDNPSPRAYFRCAFAPSPVKKKVQRSAD-SLLVATYEGEHNPMP
AtWRKY40	DTTLVVKDGYQWRKYGQKVTRDNPSPRAYFKCACAPSCSVKKKVQRSVED-QSVLVATYEGEHNPMP
AtWRKY18	DTSLTVKDGFWWRKYGQKVTRDNPSPRAYFRCSFAPSPVKKKVQRSAD-PSLLVATYEGETHNLGP
AtWRKY60	DTSLTVKDGFWWRKYGQKITRDNPSPRAYFRCSFSPSCLVKKKVQRSAD-PSFLVATYEGETHNTGP
OsWRKY14	SMAETVKDGYQWRKYGQKVTRDNPSPRAYFRCAFAPSPVKKKLQRCAED-RSMLVATYEGEHNAHS

GROUP 2_c

OsWRKY28 NNGGLADDGYKWRKYGQKSIKNSPNFRSYRRCCTNPRCNAKKQVERAVDEPDTLIVTYEGLHLHYTY
 AtWRKY49 NSNGMCDGDKYKWRKYGQKSIKNSPNFRSYRRCCTNPRCNAKKQVERSIDESNTYIITYEGFHFHYTY
 OsWRKY27 SEVEVLDDGFKWRKYGKKA VKSSPNFRNYYRCSAAGCGVKKRVERDGDPPRYVVTYDGVHNHATP
 OsWRKY63 SEVEILDDGFKWRKYGKKA VKNSPNFRNYYRCSSTEGCNVKKRVERDREDHRYVITTYDGVHNHASP
 OsWRKY36 SDDEILDDGYKWRKYGKKS VKNSPNFRNYYRCSSTEGCNVKKRVERDKNDPRYVVTMYEGIHNVCP
 OsWRKY46 SEIEILDDGYKWRKYGKKS VKNSPNFRNYYRCSSTEGCNVKKRVERDKDDPSYVVTYEGTHNVSP
 AtWRKY50 SEVEVLDDGFKWRKYGKKA VKNSPNFRNYYRCSVDGCPVKKRVERDRDDPSFVITTYEGSHNHSSM
 AtWRKY51 SKIDVMDGDKYKWRKYGKKS VKNNINRNNYYRCSSEGC SVKKRVERDGDAAAYVITTYEGVHNHESL
 OsWRKY20 SEVDVLDDGYRWRKYGKKA VKNSPNFRNYYRCSSEGC RVKKRVERARDDARFVVTYDGVHNHPAP
 OsWRKY12 SEVDVLDDGYKWRKYGQKVVKNSLHFRSYFRCTHSNCRVKKRVERLSTDCRMVITTYEGRHTHSPC
 OsWRKY98 SEVDVLDDGYKWRKYGQKVVKNSLHFRSYFRCTHSNCRVKKRVERLSTDCRMVITTYEGRHTHSPC
 OsWRKY99 SEVDVLDDGYKWRKYGQKVVKNSLHFRSYFRCTHSNCRVKKRVERLSTDCRMVITTYEGRHTHSPC
 AtWRKY12 SDVDVLDDGYKWRKYGQKVVKNSLHFRSYRRCCTHNNCRVKKRVERLSEDCRMVITTYEGRHNHIPS
 OsWRKY90 SDVDVLDDGYKWRKYGQKVVKNTQHFRSYRRCCTQDNC RVKKRVERLAEDPRMVITTYEGRHVHSPS
 AtWRKY13 SEVDVLDDGYRWRKYGQKVVKNTQHFRSYRRCCTQDKCRVKKRVERLADDPRMVITTYEGRHLHSPS
 AtWRKY24 SDDVLDDGYRWRKYGQKSVKNAHFRSYRRCCTYHTCNVKKQVQRLAKDPNVVTYEGVHNHPCE
 AtWRKY56 SDDVLDDGYRWRKYGQKSVKNAHFRSYRRCCTYHTCNVKKQVQRLAKDPNVVTYEGVHNHPCE
 OsWRKY31 SDNDILDDGYRWRKYGQKAVKNSKFRSYRRCCTHHTCNVKKQVQRLAKDTSIVVTYEGVHNHPCE
 AtWRKY43 SDADILDDGYRWRKYGQKSVKNSLYFRSYRRCCTQHMCNVKKQVQRLSKETSIVETTYEGIHHPCE
 OsWRKY78 SQVDILDDGYRWRKYGQKAVKNNKFRSYRRCCTHQGCNVKKQVQRLSRDETIVVTYEGTHHPPIE
 AtWRKY75 SQVDILDDGYRWRKYGQKAVKNNKFRSYRRCCTYGGCNVKKQVQRLTVDQEVVVTYEGVHSHPIE
 OsWRKY3 SEIDHLEDGYRWRKYGQKAVKNSPFRSYRRCCTNSKCTVKKRVERSSDDPSVITTYEGQHCHHTA
 OsWRKY49 SEIDHLEDGYRWRKYGQKAVKNSPFRSYRRCCTNSKCTVKKRVERSSDDPSVITTYEGQHSHTV
 AtWRKY57 SDVDNLEDGYRWRKYGQKAVKNSPFRSYRRCCTNSRC TVKKRVERSSDDPSIVITTYEGQHCHQTI
 AtWRKY48 SDIDNLDDGYRWRKYGQKAVKNSPYFRSYRRCCTTVGCGVKKRVERSSDDPSIVMTTYEGQHTHPFP
 OsWRKY24 SEVDHLEDGYRWRKYGQKAVKNSPYFRSYRRCCTTPKCGVKKRVERSYQDPSTVITTYEGQHTHHSP
 OsWRKY44 SEVDHLEDGYRWRKYGQKAVKNSPYFRSYRRCCTAPRCGVKKRVERSEQDPSMVITTYEGQHTHPSP
 OsWRKY35 SEVDHLEDGYRWRKYGQKAVKNSPYFRSYRRCCTTQKCPVKKRVERSYQDPAVVITTYEGKHTHPPI
 OsWRKY85 SEVDHLEDGYRWRKYGQKAVKNSPFRSYRRCCTTQKCPVKKRVERSYQDAAVVITTYEGKHTHPPI
 AtWRKY8 TEVDHLEDGYRWRKYGQKAVKNSPYFRSYRRCCTTQKCNVKKRVERSYQDPTVVITTYESQHNHPPI
 AtWRKY28 SEVDHLEDGYRWRKYGQKAVKNSPYFRSYRRCCTTQKCNVKKRVERSFQDPTVVITTYEGQHHPPI
 AtWRKY71 SEIDHLEDGYRWRKYGQKAVKNSPYFRSYRRCCTTQKCNVKKRVERSFQDPSIVITTYEGKHHPPI
 AtWRKY23 SEVDHLEDGYRWRKYGQKAVKNSPFRSYRRCCTTASCNVKKRVERSFQDPSIVITTYEGQHTHISP
 AtWRKY68 SEVLHLEDGYKWRKYGQKPVKDSPFERNYYRCTTTWC DVKKRVERSFSDPSSVITTYEGQHTHPRP
 AtWRKY59 DEKVALDDGYKWRKYGKKA PITGSPFRHYHKCSSPDCNVKKKIERDTNNPDYILTITYEGRHNHPSP

GROUP 2_d + 2_e

Domains inside and above the box correspond to subfamily 2d and 2e in the classification by Eulgem et al. (2000), respectively.

OsWRKY33	GEGNTPTDSWA	WRKYGQKPIKGS	PHPRAYR	CSSSKG	CPARKQ	VERSRNDP	DTVIV	TYSF	HN-HSAT		
OsWRKY84	GEGPPPS	DSWA	WRKYGQKPIKGS	PHPRGYYR	CSSSKG	CPARKQ	VERSRADPT	VLLV	TYSF	HN-HPWP	
AtWRKY69	GEVYPPS	DSWA	WRKYGQKPIKGS	PHPRGYYR	CSSSKG	CPARKQ	VERSRVDPS	KLMT	TYACD	HN-HPFP	
AtWRKY65	GDTTPPS	DSWA	WRKYGQKPIKGS	PHPRGYYR	CSSSKG	CPARKQ	VERSRDDPT	MILIT	TYTSE	HN-HPWP	
OsWRKY34	SGEVVPS	DLWA	WRKYGQKPIKGS	PHPRGYYR	CSSSKG	CSARKQ	VERSR	TDPNML	VITYTSE	HN-HPWP	
OsWRKY57	SGEVVPS	DLWA	WRKYGQKPIKGS	PHPRGYYR	CSSSKG	CSARKQ	VERSR	TDPNML	VITYTSE	HN-HPWP	
AtWRKY35	SGEVVPS	DLWA	WRKYGQKPIKGS	PHPRGYYR	CSSSKG	CSARKQ	VERSR	TDPNML	VITYTSE	HN-HPWP	
AtWRKY14	SGEVVPS	DLWA	WRKYGQKPIKGS	PHPRGYYR	CSSSKG	CSARKQ	VERSR	TDPNML	VITYTSE	HN-HPWP	
OsWRKY1	GGEVVP	DLWA	WRKYGQKPIKGS	PHPRGYYR	CSSSKG	CSARKQ	VERSR	ADPTML	VITYTSD	HN-HPWP	
OsWRKY81	GGEVIP	DLWA	WRKYGQKPIKGS	PHPRGYYR	CSSSKG	CMARKQ	VERSR	SDPNML	VITYTSD	HN-HPWP	
OsWRKY23	ADGGVSS	DLWA	WRKYGQKPIKGS	PHPRGYYR	CSSSKG	CMARKQ	VERSP	AKPGML	VITYTSD	HN-HPWP	
OsWRKY60	ADGGVST	DLWA	WRKYGQKPIKGS	PHPRGYYR	CSSSKG	CMARKQ	VERSP	AKPGML	VITYTSD	HN-HPWP	
AtWRKY16	DRGSRSS	DLWV	WRKYGQKPIKGS	PHPRGYYR	CSSSKG	CFARKQ	VERSR	TDPNV	SIVITYTSD	HN-HPFP	
AtWRKY27	TQENLSS	DLWA	WRKYGQKPIKGS	PHPRGYYR	CSSSKG	CLARKQ	VERSN	LDPNIF	VITYTGE	HN-HPFP	
AtWRKY29	KEENLLS	DAWA	WRKYGQKPIKGS	PHPRGYYR	CSSSKG	CLARKQ	VERN	NPQNPE	KFTITYTNE	HN-HELP	
AtWRKY22	AAEALNS	DVWA	WRKYGQKPIKGS	PHPRGYYR	CSSSKG	CLARKQ	VERN	NRSDPK	MFI	TYTAE	HN-HPAP
OsWRKY54	PADGVS	ADVWA	WRKYGQKPIKGS	PHPRGYYR	CSSSKG	CPARKQ	VERSR	SDPNT	FILTYTGE	HN-HSAP	
OsWRKY6	AASGP	APDLWA	WRKYGQKPIKGS	PHPRGYYR	CSSSKG	CAARKQ	VERC	RFDP	SFLLLTYTGA	HN-HSAP	
OsWRKY52	VEQGPP	ADWS	WRKYGQKPIKGS	PHPRGYYR	CSSSKG	CPARKQ	VDK	CRND	ASLLI	TYTSD	HN-H

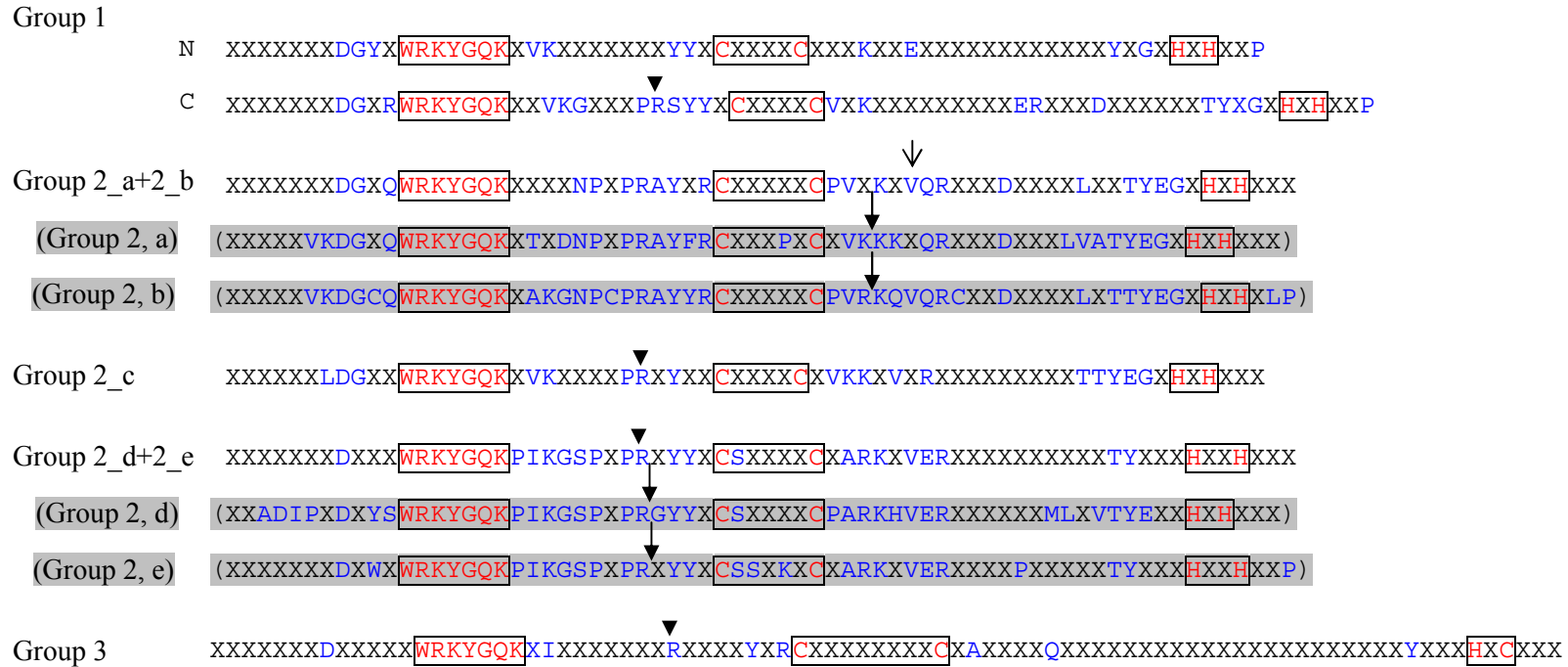
AtWRKY11	KIADIPP	DEYS	WRKYGQKPIKGS	PHPRGYYR	CSTFRG	CPARKQ	VERAL	DDPAM	LIVTYE	GEHR-HNQS	
AtWRKY17	KIADIPP	DEYS	WRKYGQKPIKGS	PHPRGYYR	CSTFRG	CPARKQ	VERAL	DDSTML	LIVTYE	GEHR-HHQS	
OsWRKY30	KIADIPP	DEYS	WRKYGQKPIKGS	PHPRGYYR	CSTFRG	CPARKQ	VERAT	DDPAM	LIVTYE	GEHR-HTPG	
AtWRKY39	KIADIPP	DEYS	WRKYGQKPIKGS	PHPRGYYR	CSSVRG	CPARKQ	VERC	IDETS	MLIVTYE	GEHR-HSRI	
AtWRKY74	KIADIPP	DEYS	WRKYGQKPIKGS	PHPRGYYR	CSSVRG	CPARKQ	VERC	VEETS	MLIVTYE	GEHR-HSRI	
OsWRKY89	KIADIPP	DEYS	WRKYGQKPIKGS	PHPRGYYR	CSSVRG	CPARKQ	VERC	VDDPAM	LIVTYE	GEHR-HTRG	
AtWRKY7	KMADIP	SDEF	WRKYGQKPIKGS	PHPRGYYR	CSSVRG	CPARKQ	VERAL	DDAM	LIVTYE	GEHR-HALV	
AtWRKY15	KMSDV	PPDDYS	WRKYGQKPIKGS	PHPRGYYR	CSSVRG	CPARKQ	VERA	ADDSS	MLIVTYE	GEHR-HSLS	
AtWRKY21	KVADIP	DDYS	WRKYGQKPIKGS	PHPRGYYR	CSSMRG	CPARKQ	VERC	LED	PAM	LIVTYE	GEHR-HPKL
OsWRKY42	KVADIP	ADDFS	WRKYGQKPIKGS	PHPRGYYR	CSTLRG	CPARKQ	VERD	PTD	PAM	LIVTYE	GEHR-HSPS
OsWRKY50	RNADIP	ADDFS	WRKYGQKPIKGS	PHPRGYYR	CSTVRG	CPARKQ	VERD	PGEPAM	LIVTYD	GHR-HGEP	
OsWRKY56	RVADIP	ADDFS	WRKYGQKPIKGS	PHPRGYYR	CSTVRG	CPARKQ	VERA	ADDPAT	LIVTYE	GEHR-HSPP	
OsWRKY80	KVADIP	SDNYS	WRKYGQKPIKGS	PHPRGYYR	CSSKGD	CPARKQ	VERC	RSDPAM	LIVTYE	NEHR-HAQP	
OsWRKY102	KVADIP	SDNYS	WRKYGQKPIKGS	PHPRGYYR	CSSKGD	CPARKQ	VERC	RSDPAM	LIVTYE	NEHR-HAQP	

GROUP 3

OsWRKY7 TPVP-HEDG--FQ**WRKYGE**KKIQGTH-FTR---SYFR**CT**YRDD-RG**CQ**ATKQIQ--KDKND-----PPMFQVTYSNE**HTCT**TT
OsWRKY77 TVVP-HEDG--YQ**WRKYGE**KKIQGTH-FTR---SYFR**CT**YRDD-RG**CQ**ATKQIQ--EDKND-----PPMFQVTYSNE**HTCT**TT
OsWRKY8 TYAP-YDDG--HQ**WRKYGE**KKLSNSN-FPR---FYR**CT**YKND-MK**CP**ATKQVQQ---KDTND-----PPLFSVTYFN**HTCN**SS
OsWRKY76 TYAP-YDDG--HQ**WRKYGE**KKLSNSN-FPR---FYR**CT**YKND-MK**CP**ATKQVQQ---KDTND-----PPLFSVTYFN**HTCN**SS
OsWRKY72 TFAP-HNDG--HQ**WRKYGE**KKINNCN-FPR---YYR**CT**YKDN-MN**CP**ATKQIQ--KDYS-----PPLYSVTYYNE**HTCN**SA
OsWRKY39 TFTP-HFDG--HL**WRKYGQ**KNIKDSA-FPR---LYR**CS**YRED-RQ**CL**ASKLVQQ---ENDD-----PPLYRVTYTYE**HTCN**TT
OsWRKY105 TFTP-HFDG--HL**WRKYGQ**KNIKDSA-FPR---LYR**CS**YRED-RQ**CL**ASKLVQQ---ENDD-----PPLYRVTYTYE**HTCN**TT
OsWRKY65 TPIP-HTDG--HL**WRKYGE**KKIKNSS-FPR---LYR**CS**YRDD-RN**CM**ATKVQQ---ENDAD-----PPLYRVTYI**HPHTCN**P-
OsWRKY94 TFTP-ENDG--FH**WRKYGE**KNILNSE-FRK---LYR**CG**YSDE-RK**CQ**AKKYVQQ---ENNKH-----PPEFRVTLTNE**HTCN**TV
OsWRKY38 TYAP-YHDG--YQ**WRKYGQ**KMIRGNS-FPR---CYR**CT**YHQD-HG**CP**ASKHVEQ---HNSED-----PPLFRVIYTNE**HTCG**TS
OsWRKY41 TASP-YDDG--YQ**WRKYGQ**KKINNTN-FPR---SYR**CS**YHRE-RR**CP**AQKHVQQ---RDGDDV---PALHVVVYTHE**HTCL**QG
OsWRKY40 TPSP-YKDG--YQ**WRKYGQ**KNIQDSN-YLR---LYF**CT**FSSRE-RS**CA**AKKVQQ---RDAGE-----PPMFLVTYLN**HTCQ**QP
OsWRKY9 AQAP-HNDG--HQ**WRKYGQ**KWISRAK-HSR---SYR**CA**NSKV-QG**CP**ATKTVQQMDS--SGNG---TSKLFNVDYYG**QHTCR**GD
OsWRKY101 AQAP-HNDG--HQ**WRKYGQ**KWISRAK-HSR---SYR**CA**NSKV-QG**CP**ATKTVQQMDS--SGNG---TSKLFNVDYYG**QHTCR**GD
OsWRKY62 TATP-DYDG--YE**WRKYGQ**KSISKTK-HSR---SYR**CT**NQKG-QG**CM**ATKTQQIENDNSSNS---VVKLYNVDFG**KHTCK**FG
OsWRKY10 TPVP-HYDG--HQ**WRKYGQ**KHINNSK-HPR---SYR**CT**YRQE-EK**CK**ATKTQQREDLHHANSYNGDHPIMYTVVY**YGQHTCK**KG
OsWRKY75 TPVP-HYDG--HQ**WRKYGQ**KHINNSK-HPR---SYR**CT**YRQE-EK**CK**ATKTQQREDLHHANSYNGDHPVMYTVVY**YGQHTCK**KG
OsWRKY45 TAVP-HYDG--HQ**WRKYGQ**KNINNSN-HQR---SYR**CS**YKHE-QN**CK**ATKTQQ---LDSAG-----ETIMYTVVY**YGQHTCK**TN
OsWRKY11 TTVP-DFDG--YQ**WRKYGQ**KQIEGAL-YPR---SYR**CT**NSTN-QG**CL**AKKTQVR---NGGG---GAAGYTVAYISE**HTCK**SI
OsWRKY74 TTVP-DFDG--YQ**WRKYGQ**KQIEGAM-YPR---SYR**CT**NSTN-QG**CL**AKKTQVR---NGGG---GAAGYTVAYISE**HTCK**SI
AtWRKY38 SPDPIYYDG--YL**WRKYGQ**KSIKSN-HQR---SYR**CS**YNKD-HN**CE**ARKHEQK---IKDN-----PPVYRTTYFG**HTCK**TE
AtWRKY62 SSTPIYHDG--FL**WRKYGQ**KQIKESE-YQR---SYR**CA**YTKD-QN**CE**AKKVQK---IQHN-----PPLYSTTYFG**HTCK**QLH
AtWRKY63 SPNRLDDG--FT**WRKYGQ**KTIKTSL-YQR---CYR**CA**YAKD-QN**CA**YATKRVQM---IQDS-----PPVYRTTYLG**HTCK**AF
AtWRKY64 SPTPRDDG--FT**WRKYGQ**KTIKTSP-YQR---CYR**CT**YAKD-QN**CN**ARKRVQM---IQDN-----PPVYRTTYLG**HTCK**AV
AtWRKY66 SPTPAHIDG--FI**WRKYGQ**KTIKTSP-HQR---WYR**CA**YAKD-QN**CD**ATKRVQK---IQDN-----PPVYRNTYVG**HTCK**ACAP
AtWRKY67 SRTMCPNDG--FT**WRKYGQ**KTIKASA-HKR---CYR**CT**YAKD-QN**CN**ATKRVQK---IKDN-----PPVYRTTYLG**HTCK**AV
OsWRKY19 RVAATLEDG--HV**WRKYGQ**KDIQNSP-YPR---SYR**CT**HKLD-QG**CG**ARRQTQRC--EADPSN-----YDITYYGE**HTCR**DP
OsWRKY71 VVVKNLDDG--QA**WRKYGQ**KEIQNSK-HPK---AYR**CT**HKYD-QL**CT**AQRQVQRC--DDDPAS-----YRVTYIGE**HTCR**DP
OsWRKY79 VTTKELEDG--RQ**WRKYGQ**KHIQDSPNNPR---SYR**CT**HRPD-QG**CM**ATKVQTS---ESNSSE-----FVISYYGE**HTCS**DP
AtWRKY54 VEAKSSEDR--YA**WRKYGQ**KEILNTT-FPR---SYR**CT**HKPT-QG**CK**ATKVQVQKQ--DQDSEM-----FQITYIGY**HTCT**AN
AtWRKY70 IESTILEDG--FS**WRKYGQ**KEILNAK-FPR---SYR**CT**HKYT-QG**CK**ATKVQVQKQ--ELEPKM-----FSITYIGN**HTCN**TN
OsWRKY68 VRSGTTTDG--FI**WRKYGQ**KEINGCK-HPR---LYR**CA**FRG--QG**CL**ATRRVQSQSQDDPAAA-----FVIAYYGE**HTCG**GD
OsWRKY93 RKATMDDK--FL**WRKYGQ**KEIKNSK-HPR---FYR**CS**YKDD-HG**CT**ATKVQVQVQSETADDDTASP-----VYIITYYFGE**HTCR**HG
OsWRKY21 QDVGPLDDG--FS**WRKYGQ**KDILGAK-YPR---AYR**CT**HRHT-QG**CH**ASKVQVR---ADGDP-----LLFDVVYHGD**HTCA**HG
OsWRKY97 QDVGPLDDG--FS**WRKYGQ**KDILGAK-YPR---AYR**CT**HRHT-QG**CH**ASKVQVR---ADGDP-----LLFDVVYHGD**HTCA**HG

OsWRKY67N VRSNTEDDG--LS**WSKYEQ**KEILGAK-FPR---AYFR**CT**HWNTKKG**CM**ATKEVQR----DDGDP-----LMFDIVYHGE**HTCT**QT
OsWRKY66N RMSYTEDDG--FS**WRKYGQ**KDVEGAM-HPTTQSNYFR**CA**HKMT-TG**CK**ARKKVQR----TDGDP-----LMVDVVYKGV**HS**CAGV
OsWRKY66C KDVGPDDG--YS**WKRYGQ**KNIFGAN-YPR---CYR**CI**HKTT-TG**CT**ATKNAQA----TDGDP-----LLFDVYHGE**HTCD**LQ
OsWRKY67C VTSVPADDG--YS**WRKYGQ**KNVLGFS-YLR---GYR**CA**---T-KG**CQ**ASKQVQR----HD-DG-----LLFDVTYFGE**HTCAD**Q
OsWRKY82 VENPPVDDG--HS**WRKYGQ**KEILGAK-HPR---GYR**CT**HRHS-QG**CM**ATKQVQR----TDEDA-----TVFDVIYHGE**HTCV**HK
OsWRKY100 VENPPVDDG--HS**WRKYGQ**KEILGAK-HPR---GYR**CT**HRHS-QG**CM**ATKQVQR----TDEDA-----TVFDVIYHGE**HTCV**HK
OsWRKY53 AEG-PADDG--HS**WRKYGQ**KDILGAK-HPR---GYR**CT**HRNT-QG**CT**ATKQVQR----TDDDA-----SLFDVVYHGE**HTCR**PG
AtWRKY41 LEG-PHDDI--FS**WRKYGQ**KDILGAK-FPR---SYR**CT**FRNT-QY**CW**ATKQVQR----SDGDP-----TIFEVYRG**HTCS**QG
AtWRKY53 LEG-PQDDV--FS**WRKYGQ**KDILGAK-FPR---SYR**CT**HRST-QN**CW**ATKQVQR----SDGDA-----TVFEVYRG**HTCS**QA
OsWRKY64 LEA-TPDDG--FS**WRKYGQ**KDILGAK-FPR---GYR**CT**YRNA-QG**CP**ATKQVQR----SDADL-----AVFDVTYQGA**HTCH**QK
AtWRKY30 VDR-TLDDG--FS**WRKYGQ**KDILGAK-FPR---GYR**CT**YRKS-QG**CE**ATKQVQR----SDENQ-----MLLEISYRG**IHSC**SQA
AtWRKY46 QENGSI DDG--HC**WRKYGQ**KEIHGSK-NPR---AYR**CT**HRFT-QD**CL**AVKQVQK----SDTDP-----SLFEVKYLG**NHTC**NNI
OsWRKY70 NTEQPPDDG--YT**WRKYGQ**KDILGSR-YPR---SYR**CT**HKNY-YG**CE**AKKKVQR----LDDDP-----FTYEVYCG**NHTCL**TS
AtWRKY55 NTDLPDDN--HT**WRKYGQ**KEILGSR-FPR---AYR**CT**HQKL-YN**CP**AKKQVQR----LNDDP-----FTFRVTYRG**SHTC**YNS
OsWRKY55 MKDDG--WN**WIKYGQ**KDIIGSK-YQR---SYL**RC**NQMHS-TG**CK**ARKIVEP----SNDDL-----NIWLVTYIY**EHNH**QQR
AtWRKY52 I PAIDEGDLWT**WRKYGQ**KDILGSR-FPR---GYR**CAY**KFT-HG**CK**ATKQVQR----SETDS-----NMLAITYLSE**HNH**PRP
OsWRKY87 LELGDRDDS--YP**WRKYGQ**KDILGAR-FAR---SYR**CAQ**ML--G**CT**ARKVQQ----SDDDP-----SRLEITYIG**LHTC**GGD

B



Additional File 2. Multiple alignments, domain classification and sequence conservation patterns of WRKY domains from rice (OsWRKY), Arabidopsis (AtWRKY), the green alga (ChrWRKY), the slime mold (DsWRKY) and *Giardia lamblia* (GIWRKY).

A. Multiple alignments of WRKY domains, which are classified into five groups (Group 1, 2_a+2_b, 2_c, 2_d+2_e, and 3) modified from Eulgem et al. (2000) (see text for details). Sequences in each group are aligned separately. The

heptapeptide WRKYGQK and the zinc-finger motif are in colors (pink for conserved amino acids and blue for substituted amino acids). Other amino acids conserved in all member domains in a group are highlighted in dark yellow.

B. The conservation patterns of WRKY domains. Since subgroups in Group 2, a and b, and d and e from Eulgem et al. (2000) are merged to form two new Groups 2_a+2_b and 2_d+2_e, respectively, the patterns are compared (old classifications highlighted in gray and in parentheses). WRKYGQK and zinc finger motif are highlighted in boxes, and other amino acids conserved in $\geq 90\%$ member domains are in blue. All other amino acids and indels are represented by "X". The conserved intron position is indicated by the arrow ($\downarrow$, phase 0) or arrowhead ($\blacktriangledown$, phase 2) in the new classification, while for the old classification the intron position is indicated as by Eulgem et al. (2000). Notice the intron position for Group 2_a+2_b from the present work is different from the previous result by Eulgem et al. (2000).