

Table 1 Suppl. primers used in *CsWRKYs* studied under phytohormone applications and abiotic stresses.

<i>CsWRKY</i>	Forward primers (5'-3')	Reverse primers (5'-3')	Product size [bp]
<i>CsWRKY19</i>	GGAACGAAGCAGTGCAGATC	CAAGTGGTTTGTCTGGGCG	158
<i>CsWRKY22</i>	CTCTGGCTCCTCAAGTGCCG	CTGCTGCCTTCCAGGTACTC	145
<i>CsWRKY28</i>	GTTCCCTCGTCTAGCATCCCG	GCTTCTGGCTCGTCAGATGA	145
<i>CsWRKY31</i>	CAAGTGTTCTTTTCGCCCCAA	GATGACGCCGCAGAAACATG	195
<i>CsWRKY35</i>	GCCATATACAGCCGCAATGC	GTGGCTCGTCTTTGGCTCTA	134
<i>CsWRKY49</i>	GCTCTGCCGGATAATAGCAG	CGAGGGTATAGGGTGCTTGG	178
<i>CsWRKY2</i>	GCAGTTCAAAGGGGTGCTTG	CTTCCGGCGAGTGAGTTTCT	130
<i>CsWRKY11</i>	CAGAAGCATGTGAAGGGCAG	GCATCCTTGGCACGTTTATT	173
<i>CsWRKY13</i>	GCCTCTGACAACTTGGCTTC	CTCGGATGAGGAGATCCTTT	197
<i>CsWRKY18</i>	CTGCACTGTTGCACCTTCAT	GATGTTGAGCCGGACAATAG	177
<i>CsWRKY26</i>	CAATCAAGGGTTCTCCCAT	GTGGTTATGTTTCGCCTTCGT	137
<i>CsWRKY29</i>	CAAGAAGCTGCAACGCAAGG	GAGACGGTGAGATCGGTGAG	113
<i>CsWRKY30</i>	GCATCTGGTGAAAGCAATGA	GTGCTGTGACTCCTCCAATA	131
<i>CsWRKY33</i>	GCGGAGTCATGGACAGAACA	CTTACTTGCTTGGCAGCCTT	150
<i>CsWRKY41</i>	GGCAGCACCCGAAACAAATT	CTTCATCCACTGCGGGAGTT	154
<i>CsWRKY43</i>	CATTGCAGGCAAGAACAAGA	GATTAAGGCAGACGGGGAAC	164
<i>CsWRKY44</i>	CAACAGCAACACATGGGCAT	CTGCGGCACACCAATCAAAT	192

Table 2. List of the *CsWRKY* TFs family, classified according to the group and scaffold they belong (start and end refer to the location of the gene in the respective scaffold. Full length indicates genes length in base pairs.

Group	Gene	Phytozome locus	scaffold	start	end	full length	<i>Citrus sinensis</i> anotation project locus	chromosome
I	<i>CsWRKY11</i>	orange1.1g009051m.g	3	3348929	3352620	3692	Cs1g03100	1
I	<i>CsWRKY22</i>	orange1.1g004963m.g	13	1838851	1843181	4331	Cs7g04260	7
I	<i>CsWRKY24</i>	orange1.1g010802m.g	15	1591146	1594814	3669	Cs7g03300	7
I	<i>CsWRKY35</i>	orange1.1g013222m.g	42	689265	692549	3285	Cs7g03080	7
I	<i>CsWRKY37</i>	orange1.1g008458m.g	49	532438	537337	4900	orange1.lt04068	-
I	<i>CsWRKY39</i>	orange1.1g036653m.g	68	482854	486663	3810	Cs2g04520	2
I	<i>CsWRKY40</i>	orange1.1g011340m.g	77	307046	310334	3289	Cs2g03840	2
I	<i>CsWRKY45</i>	orange1.1g014629m.g	172	174342	178393	4052	Cs2g02790	2
I	<i>CsWRKY49</i>	orange1.1g011483m.g	626	42514	46157	3644	Cs2g10310	2
IIa	<i>CsWRKY30</i>	orange1.1g025097m.g	25	996904	999151	2248	Cs5g04160	5
IIa	<i>CsWRKY31</i>	orange1.1g020831m.g	25	1006589	1008372	1784	Cs5g03010	5
IIb	<i>CsWRKY5</i>	orange1.1g040711m.g	1	3810277	3813167	2891	orange1.lt00419	-
IIb	<i>CsWRKY10</i>	orange1.1g010903m.g	3	2727603	2730035	2433	Cs5g02450	5
IIb	<i>CsWRKY16</i>	orange1.1g007099m.g	7	1958471	1961762	3292	Cs4g05760	4
IIb	<i>CsWRKY18</i>	orange1.1g009794m.g	9	279247	281128	1882	Cs4g07560	4
IIb	<i>CsWRKY23</i>	orange1.1g045987m.g	15	942103	943915	1813	Cs6g20850	6
IIb	<i>CsWRKY36</i>	orange1.1g008964m.g	49	126215	128926	2712	Cs6g21990	6
IIb	<i>CsWRKY43</i>	orange1.1g007546m.g	121	389458	391889	2432	Cs9g02040	9
IIb	<i>CsWRKY48</i>	orange1.1g036819m.g	568	96439	97905	1467	Cs5g30250	5
IIc	<i>CsWRKY1</i>	orange1.1g026216m.g	1	354623	357157	2535	Cs7g29580	7
IIc	<i>CsWRKY3</i>	orange1.1g046286m.g	1	2355401	2357338	1938	Cs7g29570	7
IIc	<i>CsWRKY6</i>	orange1.1g020713m.g	1	4236944	4238415	1472	Cs7g07140	7
IIc	<i>CsWRKY9</i>	orange1.1g043122m.g	3	164635	166589	1955	orange1.lt00425	-
IIc	<i>CsWRKY12</i>	orange1.1g045509m.g	3	3456550	3459372	2823	Cs7g06330	7
IIc	<i>CsWRKY15</i>	orange1.1g021142m.g	7	1347875	1349215	1341	Cs7g06320	7
IIc	<i>CsWRKY21</i>	orange1.1g031482m.g	13	646034	647324	1291	orange1.lt02600	-
IIc	<i>CsWRKY25</i>	orange1.1g017479m.g	16	1122184	1123697	1514	Cs6g10120	6
IIc	<i>CsWRKY32</i>	orange1.1g031298m.g	35	211943	212982	1040	Cs2g25560	2
IIc	<i>CsWRKY34</i>	orange1.1g030050m.g	38	626400	630108	3709	Cs6g09420	6
IIc	<i>CsWRKY38</i>	orange1.1g019375m.g	57	464133	466331	2199	Cs4g10020	4
IIc	<i>CsWRKY46</i>	orange1.1g038951m.g	189	257377	258688	1312	Cs4g09310	4
IIc	<i>CsWRKY47</i>	orange1.1g029257m.g	362	80427	84896	4470	Cs7g17180	7
IIc	<i>CsWRKY50</i>	orange1.1g026950m.g	1166	10456	13713	3258	Cs4g01710	4
IId	<i>CsWRKY8</i>	orange1.1g018215m.g	2	1863592	1865359	1768	orange1.lt00472	-
IId	<i>CsWRKY13</i>	orange1.1g017930m.g	6	1346375	1348315	1941	Cs2g19800	2
IId	<i>CsWRKY26</i>	orange1.1g018659m.g	22	289543	292094	2552	Cs9g19070	9
IId	<i>CsWRKY29</i>	orange1.1g019404m.g	25	483188	485204	2017	Cs9g18480	9
IId	<i>CsWRKY44</i>	orange1.1g018255m.g	124	381097	383496	2400	orange1.lt05133	-
IIe	<i>CsWRKY2</i>	orange1.1g019126m.g	1	2333743	2335147	1405	Cs8g13600	8
IIe	<i>CsWRKY7</i>	orange1.1g023982m.g	1	4402815	4404405	1591	Cs6g03950	6
IIe	<i>CsWRKY14</i>	orange1.1g022353m.g	7	901284	905441	4158	Cs6g06940	6
IIe	<i>CsWRKY17</i>	orange1.1g012605m.g	8	2345601	2348134	2534	Cs1g03870	1
IIe	<i>CsWRKY19</i>	orange1.1g021896m.g	9	1025605	1026760	1156	orange1.lt01175	-
IIe	<i>CsWRKY41</i>	orange1.1g015616m.g	97	230834	232265	1432	Cs2g09020	2
III	<i>CsWRKY4</i>	orange1.1g017895m.g	1	2647888	2651028	3141	orange1.lt01779	-
III	<i>CsWRKY20</i>	orange1.1g019737m.g	9	1409048	1410893	1846	Cs1g04180	1
III	<i>CsWRKY27</i>	orange1.1g018407m.g	24	82311	84401	2091	orange1.lt01713	-
III	<i>CsWRKY28</i>	orange1.1g021598m.g	24	87173	88697	1525	orange1.lt01686	-
III	<i>CsWRKY33</i>	orange1.1g020291m.g	36	115494	117084	1591	Cs3g23190	3
III	<i>CsWRKY42</i>	orange1.1g045032m.g	104	283550	285259	1710	Cs7g11020	7

Group I N-terminal

CsWRKY22N AGGASSEDGYNWRKYGQKQVKGSEYP-RSYYKCTHPN---CQVKKKVERS-LEGHITEIYKGAHNHPKP
CsWRKY45N AGDRPSYDGYNWRKYGQKQVKGSEYP-RSYYKCTHPN---CPVKKKVERS-FDGGIAEIVYKGEHNHPKP
CsWRKY49N RESKKSDDGYNWRKYGQKQVKGSENP-RSYYKCTFPPS---CPTKKKVERS-LDGGITEIVYKGSNNHPKP
CsWRKY35N REQKRSEDGYNWRKYGQKQVKGSENP-RSYYKCTFPD---CPMKKKVERS-LDGGITEIVYKGSNNHPKP
CsWRKY11N VSDKPADDGYNWRKYGQKHVKGSEFP-RSYYKCTHPN---CPVKKKVERS-LDGGITEIVYKGSNNHPKP
CsWRKY24N AVDKPADDDGYNWRKYGQKPIKGNIEYP-RSYYKCTHPN---CPVKKKVERS-SNAQITQIYKNEHNHPKP
CsWRKY37N GPSMPSDDGYNWRKYGQKHVKGSEFP-RSYYKCTHPN---CEVKKLFERS-HDGGITEIVYKGTGHDHPKP
CsWRKY40N IREKVSDDGYNWRKYGQKLVKGNIEFP-RSYYKCTHPN---CLAKKQLDCT-HEGGIVDTIYSGDHCHPKV
CsWRKY39N IVKTPVSDGYNWRKYGQKQVKSPPKS-RSYYKCTYSD---CAKKEIECSD-HSGHVEIVNKGMSHDPKP

Group I C-terminal

CsWRKY22C SEVDILDDGYRWRKYGQKVVKGNNP-RSYYKCTSA-G---CTVRKHVERASHDLKSVITTYEGKNNHDPV
CsWRKY37C SEVDILDDGYRWRKYGQKVVKGNNP-RSYYKCTNA-G---CPVRKHVERASHDPKAVITTYEGKNNHDPV
CsWRKY11C SEVDLLDDGYRWRKYGQKVVKGNNP-RSYYKCTTT-G---CNVRKHVERASTDPKAVITTYEGKNNHDPV
CsWRKY24C SEVDLLDDGYRWRKYGQKVVKGNNP-RSYYKCTNP-G---CNVRKHVERAPDPKAVITTYEGKNNHDPV
CsWRKY49C SDIDILDDGYRWRKYGQKVVKGNNP-RSYYKCTHP-G---CPVRKHVERASHDLRAVITTYEGKNNHDPV
CsWRKY35C SDIDILDDGYRWRKYGQKVVKGNNP-RSYYKCTTT-G---CPVRKHVERASHDMRAVITTYEGKNNHDPV
CsWRKY40C SEVDVNDGYRWRKYGQKLVKGNP-RNYYRCSNS-G---CPAKKHVERASHDPKLVITTYEGRHHDMP
CsWRKY39C GDVGISDDGYRWRKYGQKVVKGNNP-RNYYRCSNS-G---CPVRKHVERASHDPKLVITTYEGRHHDMP
CsWRKY45C TDSEILSDGFRWRKYGQKVVKGNNP-----RLRLD---NNLTSNITS-----

Group IIa

CsWRKY30 DSSLIVKDGHWWRKYGQKVTNDNPP-RAYFRCSMASG-CPVKKKQVRCMEDKSFVATYEGEHNHDPVQ
CsWRKY31 NSTLIVKDGHWWRKYGQKVTNDNPP-RAYFKCSFAPS---CPVKKKQVRSAPDPSIVATYEGEHNHDPQ

Group IIb

CsWRKY10 CDTPTMNDGQWRKYGQKIAKGNPCP-RAYRRTISPT---CPVRKQVQRWHDMSILITTYEGTHNHPLP
CsWRKY13 CDTPTMNDGQWRKYGQKIAKGNPCP-RAYRRTIVAPS---CPVRKQVQRCAEDMSVLITTYEGTHNHPLP
CsWRKY5 SEAPLISDGQWRKYGQKMAKGNPCP-RAYRRTMAVG---CPVRKQVQRCAEDRTILITTYEGTHNHPLP
CsWRKY16 SEAPMITDGQWRKYGQKMAKGNPCP-RAYRRTMAVG---CPVRKQVQRCAEDRTILITTYEGTHNHPLP
CsWRKY36 SEASMSIDGQWRKYGQKMAKGNPCP-RAYRRTMASG---CPVRKQVQRCSQDRTILITTYEGTHNHPLP
CsWRKY43 SEAPMISDGQWRKYGQKMAKGNPCP-RAYRRTMAAG---CPVRKQVQRCAEDRTILITTYEGTHNHPLP
CsWRKY48 CQAATINDGQWRKYGQKIAKGNPCP-RAYRRTVAPG---CPVRKQVQRCLDMSILIT-----
CsWRKY23 CDAPTLNDGQWRKYGQKIRKRKP---MYTLFLFN-----YYKNVQRCAEDMSILITTYEGTHSHPLP

Group IIc

CsWRKY21 SDVEILDDGFKWRKYGKMKVKNP-RNYYKCSVDG---CPVKKRVERDRDDPSYVITTYEGFHTHQSN
CsWRKY47 SELEVMDGFKWRKYGKMKVKNP-RNYYKCSVDG---CPVKKRVERDRDDPSYVITTYEGFHTHQSN
CsWRKY1 SDVDVLDGFKWRKYGQKIVKNSLHP-RSYYRCTHNN---CRVKKRVERLSEDCRMVITTYEGRHNSPC
CsWRKY50 SDIDVLDGFKWRKYGQKIVKNTQHP-RSYYRCTQDN---CRVKKRVERLAEDPRMVITTYEGRHNSPS
CsWRKY12 SEVDHLEDGYRWRKYGQKAVKNSPFP-RSYYRCTNSK---CTVKKRVERSEDPTIVITTYEGQHCHHTV
CsWRKY38 SEIDHLEDGYRWRKYGQKAVKNSPFP-RSYYRCTNSK---CTVKKRVERSEDPTIVITTYEGQHCHHTV
CsWRKY15 SEVDHLEDGYRWRKYGQKAVKNSPFP-RSYYRCTNSK---CTVKKRVERSEDPTIVITTYEGQHCHHTV
CsWRKY6 SEVDHLEDGYRWRKYGQKAVKNSPFP-RSYYRCTNSK---CTVKKRVERSEDPTIVITTYEGQHCHHTV
CsWRKY25 SDIDHLDGFKWRKYGQKAVKNSPFP-RSYYRCTNSK---CTVKKRVERSEDPTIVITTYEGQHCHHTV
CsWRKY9 SQVDILDDGYRWRKYGQKAVKNSPFP-RSYYRCTNSK---CTVKKRVERSEDPTIVITTYEGQHCHHTV
CsWRKY34 SQVDILDDGYRWRKYGQKAVKNSPFP-RSYYRCTNSK---CTVKKRVERSEDPTIVITTYEGQHCHHTV
CsWRKY32 SQVDILDDGYRWRKYGQKAVKNSPFP-RSYYRCTNSK---CTVKKRVERSEDPTIVITTYEGQHCHHTV
CsWRKY3 SADDILDDGYRWRKYGQKAVKNSPFP-RSYYRCTNSK---CTVKKRVERSEDPTIVITTYEGQHCHHTV
CsWRKY46 WNGMADGFKWRKYGQKSIKNSP-RSYYKCTNPR---CSAKKQVERSCDDPDTLITTYEGHHLHFAY

Group IId

CsWRKY26 KLADIPDDYSWRKYGQKPIKGSPPH-RGYKCSMRG---CPARKHVERCLEPTMLIVTYEGEHNHPLP
CsWRKY44 KVADIPDEYTWWRKYGQKPIKGSPPH-RGYKCSMRG---CPARKHVERCLEPTMLIVTYEGEHNHPLP
CsWRKY29 KIADIPDEYTWWRKYGQKPIKGSPPH-RGYKCSMRG---CPARKHVERCLEPTMLIVTYEGEHNHPLP
CsWRKY8 KMADIPDDYSWRKYGQKPIKGSPPH-RGYKCSMRG---CPARKHVERCLEPTMLIVTYEGEHNHPLP
CsWRKY13 RLSDIPDDYSWRKYGQKPIKGSPPH-RGYKCSMRG---CPARKHVERCLEPTMLIVTYEGEHNHPLP

Group IIe

CsWRKY2 PAEGLSDVWAWRKYGQKPIKGSPPH-RGYKCSMRG---CLARKQVERNSRDPGMFIVTYTAENHHPAP
CsWRKY19 TADCLACDKWAWRKYGQKPIKGSPPH-RGYKCSMRG---CLARKQVERNSRDPGMFIVTYTAENHHPAP
CsWRKY7 KNEGPPSDFWWRKYGQKPIKGSPPH-RGYKCSMRG---CSAKKQVERCRTLASMLIITYTSSHNHPCP
CsWRKY17 SGEVVPSDLWAWRKYGQKPIKGSPPH-RGYKCSMRG---CSARKQVERNSRDPGMFIVTYTAENHHPAP
CsWRKY14 GESAPPSDSWAWRKYGQKPIKGSPPH-RGYKCSMRG---CPARKQVERNSRDPGMFIVTYTAENHHPAP
CsWRKY41 TEEKLSADLWAWRKYGQKPIKGSPPH-RGYKCSMRG---CAARKQVERNSRDPGMFIVTYTAENHHPAP

Group III

CsWRKY20 EGPFE--DGYSWRKYGQKIDILGAKYP-RSYYRCTYRNTQNCWATKQVQSRDEDPTFEVYTRGHTCTFNG
CsWRKY42 KDPQEDVSKSWRKYGQKIDILGAKYP-RGYRCTYRNGQGLATKQVQSRDEDPTIFEITYRGNHTCAQA
CsWRKY4 EGTLD--DGYCWRKYGQKIDILGRNFP-RGYRCTYRNGQGLATKQVQSRDEDPTIFEITYRGNHTCAQA
CsWRKY27 EIPPE--DGYTWWRKYGQKEILNSKYP-RSYYRCTYRNGQGLATKQVQSRDEDPTIFEVAYYGDHTCHMS
CsWRKY28 SSTSN--DGHAWRKYGQKEILNTHKP-RSYYRCTYRNGQGLATKQVQSRDEDPTIFEITYRGNHTCAQA
CsWRKY33 STLTD--DGHAWRKYGQKEILNTHKP-RSYYRCTYRNGQGLATKQVQSRDEDPTIFEITYRGNHTCAQA

Fig. 1 Suppl. CsWRKYs alignments by families. Common regions between the different families are marked in green, while common regions inside families are marked in red. Yellow highlighted zones refer to potential zinc ligands. Gaps have been inserted for an optimal alignment.