

## **Supplementary data**

**Table S1.** Sequences of primers used in this study.

**Table S2.** *CaWRKY* groupIII genes.

**Table S3.** Analysis of the *C/S*-elements in the 2-kb promoter fragment of *CaWRKY* groupIII genes.

**Table S1.** Sequences of primers used in this study

Primer Name	Forward (5'-3')	Reverse (5'-3')
<b>For cloning*</b>		
<i>CaWRKY41</i> (CDS)	<u>GGGGACAAGTTTGTACAAAAAAGCAGG</u> <u>CTTCATGGAGAAAGTTAAAGGATTGG</u>	<u>GGGGACCACTTTGTACAAGAAAGCTG</u> <u>GGTCTTAACTAAAGAACTCTTCAATG</u>
<i>CaWRKY41</i> (promoter)	<u>GGGGACAAGTTTGTACAAAAAAGCAGG</u> <u>CTGAATAGAACCCTATCCGACG</u>	<u>GGGGACCACTTTGTACAAGAAAGCTG</u> <u>GGTTTTGTTGTAAAAACTCAAAT</u>
<i>CaWRKY41</i> (VIGS)	<u>GGGGACAAGTTTGTACAAAAAAGCAGG</u> <u>CTTCAAAAAACGCCAGAAACACA</u>	<u>GGGGACCACTTTGTACAAGAAAGCTG</u> <u>GGTCAATCCCAATCTCCGACAAATGA</u>
<b>For RT-qPCR</b>		
<i>CaWRKY41</i>	CACCAAACCATGACGCAGAA	TGAGCAGTGCAGAGTCATGT
<i>CaWRKY53a</i>	TGGAGAAAGTACGGCCAGAA	TCTCGTTTCTCTGGCGATGT
<i>CaWRKY52</i>	TCGTGGAAGCTTCAAAGTCA	ACACATGAAACACACTACCGA
<i>CaWRKY53</i>	CTCAACAGTCCACTCCTCGA	TCTCCGCACTGACTTTGACT
<i>CaWRKY54</i>	TGTCTCTCCTACAACCCCTG	TCTAGCTCCACACGTTCAAGT
<i>CaWRKY70</i>	TGGAGGAAATACGGGCAGAA	TGCTTCCGAATCTTTGCTGG
<i>CaWRKY30</i>	GGTCATCACTCGTGCACAAC	CATCGGATTGACTTTGGCCA
<i>CaWRKY41a</i>	TCCATACTTGTCGCGAAGT	GGCTGCCGAAACTGATAAG
<i>CaCAT1</i>	TGTTGCTGGTGTGGTGTGGT	GCCTCTCCTAGACGGCCTTTCA
<i>CaAPX1</i>	CAGGCAGAGGCAAGGGAGGTAA	CCCTACGAGCGAGCCTACGAAT
<i>CaAPX2</i>	TGATGCTCTGCCAATATCGGAT	CCAATTCCTCCCATGCCAAC
<i>CaCSD2</i>	TGTGGATGTGGCTTTGGTTCCC	TGAGGAAGGGAGTTTGCGACAC
<i>CaSOD1</i>	ACACAACCTCCACCATAGAGCCT	CCACCAACAATCGCACCAACAT
<i>CaPR1</i>	GCCGTGAAGATGTGGGTCAATGA	TGAGTTACGCCAGACTACCTGAGTA
<i>CaPR4</i>	CAACCCGCAGAACATCAACTGG	CCTCAAGCATCTACCGCAAGCA
<i>CaNPR1</i>	ACTTCTTCGCCGACGCCAAG	GCCAACACATTCACCAGAGCATC
<i>CaActin</i>	AGGGATGGGTCAAAGGATGC	GAGACAACACCGCCTGAATAGC
<i>AtRBOHC</i>	TCACCAGAGACTGGCACAATAAA	GATGCTCGACCTGAATGCTC
<i>AtRBOHD</i>	TATGCATCGGAGAGGCTGCT	TAGAGACAACACGTTCCCGGG
<i>AtRBOHE</i>	GTGATGCAAGATCAACCCTGA	GCCTTGCAAAATGTGTTCTCA
<i>AtRBOHF</i>	GGTGTCATGAACGAAGTTGCA	AATGAGAGCAGAACGAGCATCA
<i>AtCAT1</i>	AAGTGCTTCATCGGAAGGA	CTTCAACAAAACGCTTCACGA
<i>AtAPX1</i>	TGCCACAAGGATAGGTCTGG	CCTTCCTTCTCTCCGCTCAA

<i>AtSOD1</i>	TCCATGCAGACCCTGATGAC	CCTGGAGACCAATGATGCC
<i>AtSOD2</i>	GAGCCTTTGTGGTTCACGAG	CACACCACATGCCAATCTCC
<i>AtGST2</i>	ATCACCAGTTCGACCCAGTG	CTCCTCTTCTGCAACAACGG
<i>AtZIP1</i>	GGACACACACATGGTTCGAC	GATAGTGCAGCCATGAGTGG
<i>AtZIP3</i>	CAGAAACATGTTTCTTCTCGTCAC	CGCAATAAATCCGGTGAACG
<i>AtZIP4</i>	GATCTTCGTCGATGTTCTTTGG	TGAGAGGTATGGCTACACCAGCAGC
<i>AtZIP5</i>	CGGGATTGTTGGCGTGGAAT	CCAAGACCCTCGAAGCATTG
<i>AtZIP9</i>	CAATAATCATAGGAATATCGCTTGG	AGAAAGCCATCATGGCAGAT
<i>AtUBQ10</i>	GGCCTTGATAATCCCTGATGAATA	AAAGAGATAACAGGAACGGAAACATA

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\*Sequences of the recombination sites of the Gateway system are underlined

**Table S2. *CaWRKY* groupIII genes**

Gene symbol	Gene locus	Domain in homologous gene in <i>Arabidopsis thaliana</i>	Identity	Protein encoded by homologous gene in <i>Arabidopsis thaliana</i>	Identity	Domain in homologous gene in <i>Solanum lycopersicum</i>	Identity	Protein encoded by homologous gene in <i>Solanum lycopersicum</i>	Identity	WRKY domain		Location	Group
										Conserved heptapeptide	Zinc-finger type		
<i>CaWRKY54</i>	CA01g01280	AtWRKY41&53	77.42%	AtWRKY53	27.38%	SIWRKY54	93.65%	SIWRKY54	76.33%	WRKYGQK	C <sub>2</sub> HC	2038036-2040409	III
<i>CaWRKY53a</i>	CA01g34460	AtWRKY53	77.42%	AtWRKY53	30.71%	SIWRKY53	85.71%	SIWRKY53	57.22%	WRKYGQK	C <sub>2</sub> HC	272190035-272192286	III
<i>CaWRKY53</i>	CA01g34470	AtWRKY53	80.33%	AtWRKY53	29.29%	SIWRKY53	90.48%	SIWRKY53	81.32%	WRKYGQK	C <sub>2</sub> HC	272193930-272196370	III
<i>CaWRKY41a</i>	CA01g34480	AtWRKY41	62.90%	AtWRKY41	21.92%	SIWRKY54	71.43%	SIWRKY53	45.73%	WRKYGQK	C <sub>2</sub> HC	272199809-272204804	III
<i>CaWRKY70</i>	CA03g12230	AtWRKY70	60.32%	AtWRKY70	18.53%	SIWRKY80	92.06%	SIWRKY80	64.04%	WRKYGQK	C <sub>2</sub> HC	92810679-92814562	III
<i>CaWRKY52</i>	CA03g19220	AtWRKY41	82.26%	AtWRKY41	25%	SIWRKY52	93.65%	SIWRKY52	75.20%	WRKYGQK	C <sub>2</sub> HC	211827372-211829150	III
<i>CaWRKY41</i>	CA08g08240	AtWRKY41&53	74.19%	AtWRKY41&53	21.43%	SIWRKY41	90.48%	SIWRKY41	75.66%	WRKYGQK	C <sub>2</sub> HC	125184240-125186984	III
<i>CaWRKY30</i>	CA10g06890	AtWRKY30&64	59.68%	AtWRKY70	13.55%	SIWRKY81	68.84%	SIWRKY81	30.17%	WRKYGQK	C <sub>2</sub> HC	74808336-74809350	III

**Table S3.** Analysis of the *C/S*-elements in the 2-kb promoter fragment of *CaWRKY* groupIII genes

Gene symbol	Gene locus	ABRE	ARE	AuxRR-core	CGTCA-motif	ERE	GARE-motif	HSE	LTR	MBS	TC-rich repeats	TCA-element	TGA-element	W-box	P-box	Total
<i>CaWRKY54</i>	<i>CA01g01280</i>	0	0	0	1	0	0	3	0	1	3	2	0	0	0	10
<i>CaWRKY53</i>	<i>CA01g34460</i>	0	2	0	2	1	1	0	0	3	1	0	0	1	0	11
<i>CaWRKY53a</i>	<i>CA01g34470</i>	0	1	0	0	0	0	2	0	0	2	0	0	0	0	5
<i>CaWRKY41a</i>	<i>CA01g34480</i>	1	0	1	4	0	0	0	1	1	0	1	0	1	2	12
<i>CaWRKY70</i>	<i>CA03g12230</i>	0	2	0	4	0	0	0	0	2	2	2	1	1	1	15
<i>CaWRKY52</i>	<i>CA03g19220</i>	0	0	0	0	2	0	2	0	2	2	1	1	1	0	11
<i>CaWRKY41</i>	<i>CA08g08240</i>	2	0	0	0	0	0	0	1	2	4	1	1	3	0	14
<i>CaWRKY30</i>	<i>CA10g06890</i>	0	0	0	0	0	0	3	0	4	0	1	1	1	0	10