

Table S1. The GenBank accession numbers of 64 *SaWRKY* genes.

Gene name	GenBank accession number	Gene name	GenBank accession number
<i>SaWRKY1</i>	MG655189	<i>SaWRKY33</i>	MN335843
<i>SaWRKY2</i>	MN335812	<i>SaWRKY34</i>	MN335844
<i>SaWRKY3</i>	MN335813	<i>SaWRKY35</i>	MN335845
<i>SaWRKY4</i>	MN335814	<i>SaWRKY36</i>	MN335846
<i>SaWRKY5</i>	MN335815	<i>SaWRKY37</i>	MN335847
<i>SaWRKY6</i>	MN335816	<i>SaWRKY38</i>	MN335848
<i>SaWRKY7</i>	MN335817	<i>SaWRKY39</i>	MN335849
<i>SaWRKY8</i>	MN335818	<i>SaWRKY40</i>	MN335850
<i>SaWRKY9</i>	MN335819	<i>SaWRKY41</i>	MN335851
<i>SaWRKY10</i>	MN335820	<i>SaWRKY42</i>	MN335852
<i>SaWRKY11</i>	MN335821	<i>SaWRKY43</i>	MN335853
<i>SaWRKY12</i>	MN335822	<i>SaWRKY44</i>	MN335854
<i>SaWRKY13</i>	MN335823	<i>SaWRKY45</i>	MN335855
<i>SaWRKY14</i>	MN335824	<i>SaWRKY46</i>	MN335856
<i>SaWRKY15</i>	MN335825	<i>SaWRKY47</i>	MN335857
<i>SaWRKY16</i>	MN335826	<i>SaWRKY48</i>	MN335858
<i>SaWRKY17</i>	MN335827	<i>SaWRKY49</i>	MN335859
<i>SaWRKY18</i>	MN335828	<i>SaWRKY50</i>	MN335860
<i>SaWRKY19</i>	MN335829	<i>SaWRKY51</i>	MN335861
<i>SaWRKY20</i>	MN335830	<i>SaWRKY52</i>	MN335862
<i>SaWRKY21</i>	MN335831	<i>SaWRKY53</i>	MN335863
<i>SaWRKY22</i>	MN335832	<i>SaWRKY54</i>	MN335864
<i>SaWRKY23</i>	MN335833	<i>SaWRKY55</i>	MN335865
<i>SaWRKY24</i>	MN335834	<i>SaWRKY56</i>	MN335866
<i>SaWRKY25</i>	MN335835	<i>SaWRKY57</i>	MN335867
<i>SaWRKY26</i>	MN335836	<i>SaWRKY58</i>	MN335868
<i>SaWRKY27</i>	MN335837	<i>SaWRKY59</i>	MN335869
<i>SaWRKY28</i>	MN335838	<i>SaWRKY60</i>	MN335870
<i>SaWRKY29</i>	MN335839	<i>SaWRKY61</i>	MN335871
<i>SaWRKY30</i>	MN335840	<i>SaWRKY62</i>	MN335872
<i>SaWRKY31</i>	MN335841	<i>SaWRKY63</i>	MN335873
<i>SaWRKY32</i>	MN335842	<i>SaWRKY64</i>	MN335874

Table S2. The fold change of *SaWRKY* genes under SA stress in callus of *S. album* calculated from the $2^{-\Delta\Delta Cq}$ value.

Gene name	3 h		6 h	
	fold change	regulation	fold change	regulation
<i>SaWRKY1</i>	2.206797275	up	1.14750389	
<i>SaWRKY2</i>	0.738134085		0.819406687	
<i>SaWRKY3</i>	14.90117762	up	9.509590983	up
<i>SaWRKY4</i>	1.472105145		0.39267108	down
<i>SaWRKY5</i>	0.929858303		0.548151006	
<i>SaWRKY6</i>	0.571152386		0.726327684	
<i>SaWRKY7</i>	1.813481997	up	0.691940304	
<i>SaWRKY8</i>	0.566519826		0.253004586	down
<i>SaWRKY9</i>	4.178668397	up	2.31997935	up
<i>SaWRKY10</i>	0.546480355		0.691907677	
<i>SaWRKY11</i>	1.420085027		5.212053281	up
<i>SaWRKY12</i>	0.442549493	down	0.744507345	
<i>SaWRKY13</i>	0.131955327	down	0.980030335	
<i>SaWRKY14</i>	0.521100051		0.553634974	
<i>SaWRKY15</i>	0.801186024		1.720169597	up
<i>SaWRKY16</i>	0.887492474		1.49123034	
<i>SaWRKY17</i>	0.635988087		1.198649418	
<i>SaWRKY18</i>	0.619998824		0.747507923	
<i>SaWRKY20</i>	1.110148034		0.91190098	
<i>SaWRKY21</i>	0.387679448	down	0.459665935	down
<i>SaWRKY22</i>	0.645768995		0.333305932	down
<i>SaWRKY23</i>	0.674368844		0.750873586	
<i>SaWRKY24</i>	0.51170785		1.551569184	up
<i>SaWRKY25</i>	3.867605091	up	4.482831502	up
<i>SaWRKY26</i>	0.440543513	down	0.400721111	down
<i>SaWRKY27</i>	0.274681837	down	0.165934562	down
<i>SaWRKY28</i>	4.173614691	up	0.608460515	
<i>SaWRKY29</i>	1.128701394		0.963280002	
<i>SaWRKY30</i>	0.47464644	down	0.481256398	down
<i>SaWRKY31</i>	0.863530447		0.909956815	
<i>SaWRKY32</i>	0.915718443		0.38254082	down
<i>SaWRKY33</i>	0.822791255		0.510075435	
<i>SaWRKY34</i>	0.446491486	down	0.371755134	down
<i>SaWRKY35</i>	1.174505475		23.57493436	up
<i>SaWRKY36</i>	0.468041766	down	0.251033015	down
<i>SaWRKY37</i>	2.686446144	up	10.67282853	up
<i>SaWRKY38</i>	2.26204041	up	1.362718363	
<i>SaWRKY39</i>	1.102451328		1.165597215	

<i>SaWRKY40</i>	2.48301904	up	2.642286316	up
<i>SaWRKY41</i>	1.113994177		0.694815365	
<i>SaWRKY42</i>	1.167922597		0.752770731	
<i>SaWRKY44</i>	0.764665187		1.148625057	

Table S3. The fold change of *SaWRKY* genes under MeJA stress in callus of *S. album* calculated from the $2^{-\Delta\Delta Cq}$ value.

Gene name	3 h		6 h	
	fold change	regulation	fold change	regulation
<i>SaWRKY1</i>	1.850499998	up	1.116481287	
<i>SaWRKY2</i>	1.234830365		0.944131409	
<i>SaWRKY3</i>	1.460169714		1.793155605	up
<i>SaWRKY4</i>	9.291316934	up	4.04942672	up
<i>SaWRKY5</i>	1.295365194		0.980524758	
<i>SaWRKY6</i>	1.554448956	up	1.221890726	
<i>SaWRKY7</i>	2.648604789	up	0.920299045	
<i>SaWRKY8</i>	1.863783813	up	0.948244669	
<i>SaWRKY9</i>	1.055996357		0.519400591	
<i>SaWRKY10</i>	0.598666561		0.558012883	
<i>SaWRKY11</i>	2.396926724	up	0.882103176	
<i>SaWRKY12</i>	1.366054073		1.153669389	
<i>SaWRKY13</i>	0.467230263	down	0.409969384	down
<i>SaWRKY14</i>	0.883029921		0.666614508	
<i>SaWRKY15</i>	1.587356106	up	1.319549139	
<i>SaWRKY16</i>	2.320418765	up	1.127707512	
<i>SaWRKY17</i>	1.769904088	up	1.303084813	
<i>SaWRKY18</i>	0.958319167		0.761902059	
<i>SaWRKY20</i>	1.675082345	up	0.973615387	
<i>SaWRKY21</i>	0.627552569		0.7860783	
<i>SaWRKY22</i>	1.481163575		1.203111244	
<i>SaWRKY23</i>	1.304516794		0.468479142	down
<i>SaWRKY24</i>	0.378559663	down	0.768066635	
<i>SaWRKY25</i>	0.530062154		0.412450775	down
<i>SaWRKY26</i>	2.804674798	up	1.615387795	up
<i>SaWRKY27</i>	1.294998757		0.448508441	down
<i>SaWRKY28</i>	1.38483034		0.398180941	down
<i>SaWRKY29</i>	2.486928841	up	1.061897949	
<i>SaWRKY30</i>	1.078970351		0.973538159	
<i>SaWRKY31</i>	1.258091073		0.787537378	
<i>SaWRKY32</i>	1.486242714		1.121918055	
<i>SaWRKY33</i>	0.630597355		0.58252386	
<i>SaWRKY34</i>	1.205765567		0.933522999	
<i>SaWRKY35</i>	1.215475927		0.783541428	
<i>SaWRKY36</i>	2.052148714	up	1.381840289	
<i>SaWRKY37</i>	0.587130922		1.220275288	
<i>SaWRKY38</i>	1.661171585	up	1.757088241	up
<i>SaWRKY39</i>	1.548007285	up	1.08405258	

<i>SaWRKY40</i>	1.781933089	up	1.16922189	
<i>SaWRKY41</i>	1.215749675		1.193757678	
<i>SaWRKY42</i>	2.016003264	up	1.58294975	up
<i>SaWRKY44</i>	1.064059237		0.837382937	

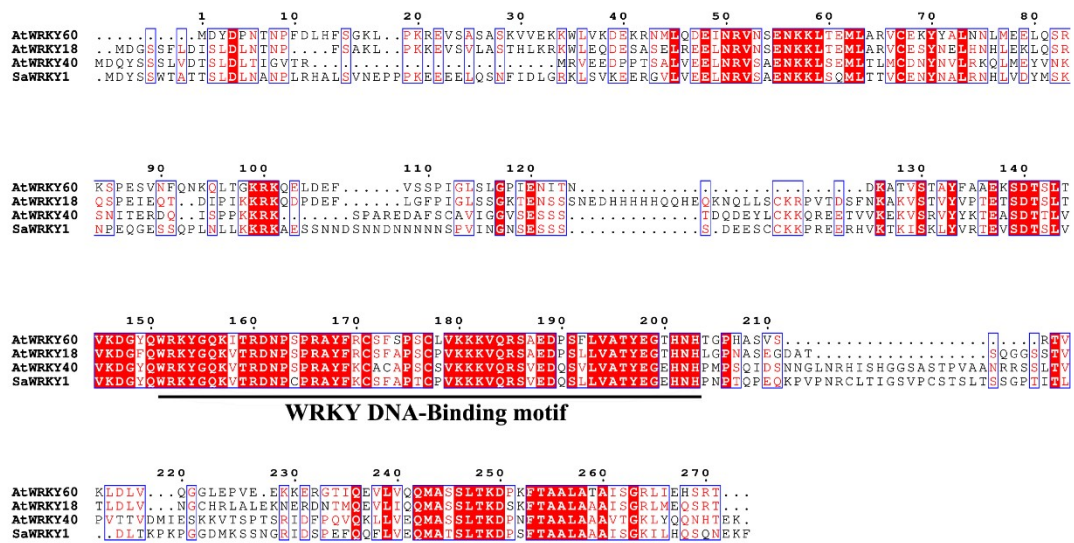


Figure S1. Multiple sequence alignment among SaWRKY1, AtWRKY40, AtWRKY18, and AtWRKY60.

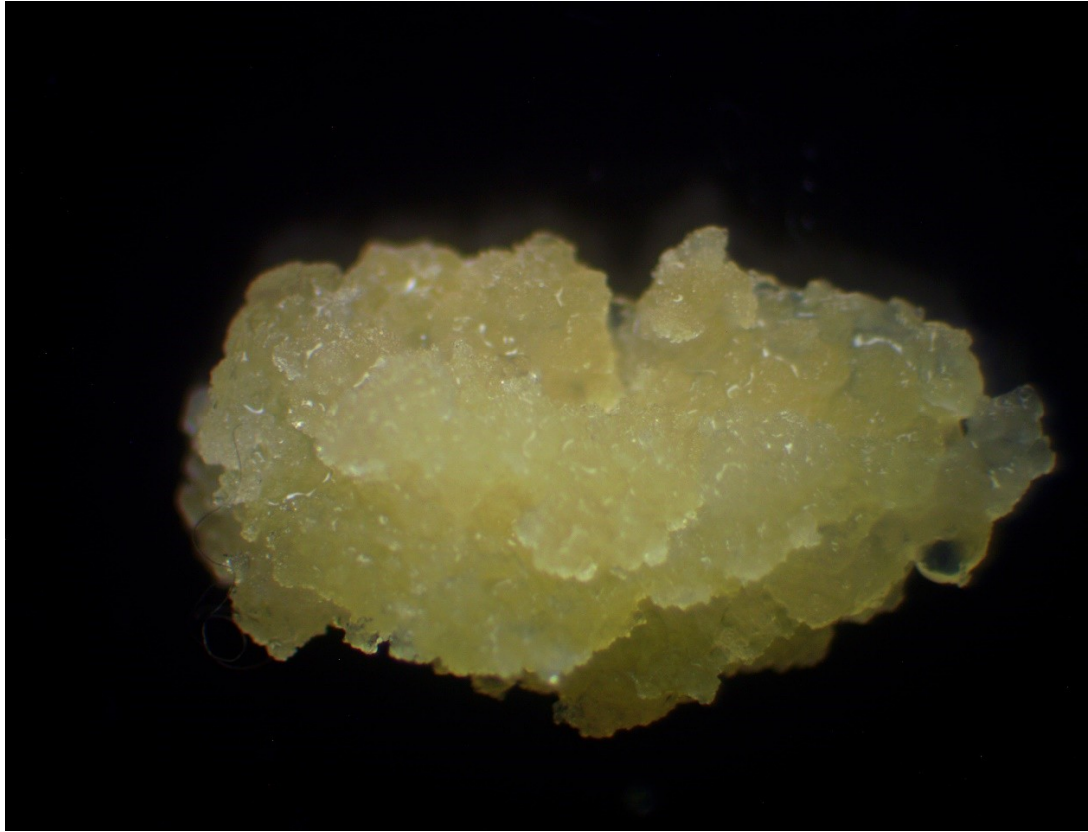


Figure S2. Callus used in this study.

Table S4. Primers used for RT-qPCR.

Primer name	Primer sequence	Primer name	Primer sequence
SaWRKY1F	5'-TGAGAGCAGCAACAACGATAG-3'	SaWRKY1R	5'-CGTTCTTCCCTTGGCTTCTT-3'
SaWRKY2F	5'-GCCTCATCCGCTCATCATAATA-3'	SaWRKY2R	5'-CTCCACCTATAGCCATCATCAAG-3'
SaWRKY3F	5'-CCGCCAAAGAGAGATCACAA-3'	SaWRKY3R	5'-CATTCTCCGTGCCGCTATTA-3'
SaWRKY4F	5'-GAAAGGGAACAAGCCGAAGA-3'	SaWRKY4R	5'-ACCTGTATCCATCCTCCAGAT-3'
SaWRKY5F	5'-TAGAGAGCAAAGGAGGTCAGA-3'	SaWRKY5R	5'-GGGAAGGTGCACTTGTAGTAA-3'
SaWRKY6F	5'-ACGAAGAGACGGACGTATGA-3'	SaWRKY6R	5'-CAACGCTCAACAGAGGAGAA-3'
SaWRKY7F	5'-TCATGAATCGGGTCCCTTTG-3'	SaWRKY7R	5'-TCCAGCGAGAAATCCAATCC-3'
SaWRKY8F	5'-GAGAAGGAACGGCTGATGTTAT-3'	SaWRKY8R	5'-GCTCAGGGCTCTTACTTTGTT-3'
SaWRKY9F	5'-CCCACCTTATCTTCAACGAAGT-3'	SaWRKY9R	5'-AGCTGAGGAGGATGGAGTTA-3'
SaWRKY10F	5'-GAGGAGGAAGAAGTGAATCAG-3'	SaWRKY10R	5'-GAGCTTGGAGAGATCGGTAATC-3'
SaWRKY11F	5'-GCTCAGTCATGTAACCGACAA-3'	SaWRKY11R	5'-CCAAGCGAAGATCCTCAA-3'
SaWRKY12F	5'-CTAGTGCTGGATGCTCTGTTAG-3'	SaWRKY12R	5'-ATTGTGCTTCCCTCGTATGT-3'
SaWRKY13F	5'-AGAAGTGCACCGTGAAGAAA-3'	SaWRKY13R	ATGGACAGTGGTGGTTGTG-3'
SaWRKY14F	5'-ACCTACGCCTTTGACCATAAC-3'	SaWRKY14R	5'-CGGCGATGGACGATGATAC-3'
SaWRKY15F	5'-GTCCGTGTTATCGTCTCTTC-3'	SaWRKY15R	5'-CTTGGCTTGCTCACTTTGTTAG-3'
SaWRKY16F	5'-ATTCATCGGGCCGTTTCTC-3'	SaWRKY16R	CTTCTTCTTCCGAGGGTTTC-3'
SaWRKY17F	5'-ACCCGAGACGATAAGAAGGA-3'	SaWRKY17R	5'-ATTGGTCGCTACTGGTATTGG-3'
SaWRKY18F	5'-GGTTATGATGGCGAAGGAGATG-3'	SaWRKY18R	5'-ACTACTCTGGGTTCTCGTATGG-3'
SaWRKY20F	5'-AGAGGAAGAGGAAGAGGAAGAG-3'	SaWRKY20R	5'-CCGCCGTTAGGGTTTGTAAAT-3'
SaWRKY21F	5'-GGTTCGGTTTACGATGAACT-3'	SaWRKY21R	5'-GGAGGAGGAAGGCATGTTATT-3'
SaWRKY22F	5'-TGGGCAGAAGCCAATCAA-3'	SaWRKY22R	5'-GGTCTTCCAAGCATCTCTCTAC-3'
SaWRKY23F	5'-ATCCACCACTTGCTCCAATC-3'	SaWRKY23R	5'-CGGGCACTTCTACTCTTGTAG-3'

SaWRKY24F	5'-TCCACCCTCAGCACTTAAAC-3'	SaWRKY24R	5'-CTCTTCTCTTACCTCACCCATTT-3'
SaWRKY25F	5'-GCCGGGTCAATATCACTCAA-3'	SaWRKY25R	5'-TCACCACTTTCTGCCCATAC-3'
SaWRKY26F	5'-CCCTGATGATGACAGCCTAAT-3'	SaWRKY26R	5'-GCTCCATTTGCTCTTCCTTTC-3'
SaWRKY27F	5'-GGCTACCGATGGCGTAAATA-3'	SaWRKY27R	5'-ATGGATCTTCTGAGGACCTTTC-3'
SaWRKY28F	5'-CAAGTTCCCAAGAGGCTACTAC-3'	SaWRKY28R	5'-CCGATAAGTGACCTCGAAGATG-3'
SaWRKY29F	5'-ACGTGAAGAAGAGAGTGGAGAG-3'	SaWRKY29R	5'-ATGGCAACTGGTTGAGGTAAAG-3'
SaWRKY30F	5'-AAGCTGAGACAGTGAACGATG-3'	SaWRKY30R	5'-TCCCGCATTGAACACCTATAA-3'
SaWRKY31F	5'-AGAGGCGGAGAGAGTAGTTATAG-3'	SaWRKY31R	5'-GTTGGAGGGTGATGCAGTAA-3'
SaWRKY32F	5'-GAGGCGAGAGTAGCGTTTATG-3'	SaWRKY32R	5'-GCAGTGGTGCAACGATAGTA-3'
SaWRKY33F	5'-TTCTTCGCCCACTTGTCTAC-3'	SaWRKY33R	5'-GGAGCCCATAATCGCTCAA-3'
SaWRKY34F	5'-CCAAATCCAAATGCCTCCAATAG-3'	SaWRKY34R	5'-GGTAATCCTGAACCAGACTGAAA-3'
SaWRKY35F	5'-CCATGTCCACGAGCCTATTATC-3'	SaWRKY35R	5'-GGTGGTTATGTGTGCCTTCA-3'
SaWRKY36F	5'-GCGGAAGCAAGACTCTCATAA-3'	SaWRKY36R	5'-CAGCGGTATCCATCATTCACTAT-3'
SaWRKY37F	5'-CTTCGGAGGAGCTTTCTGATT-3'	SaWRKY37R	5'-CACGGTGGATAGAGCATTCTT-3'
SaWRKY38F	5'-AGTGAGGAAGTGGCTGATAATG-3'	SaWRKY38R	5'-GCTGGCTCTGAAACCCTATT-3'
SaWRKY39F	5'-AAGGTTGAGCGTCTCTTGAT-3'	SaWRKY39R	5'-CTACCATCTCTTGTTGGCTTACT-3'
SaWRKY40F	5'-GGTGCAGTTGGATGTGAATA-3'	SaWRKY40R	5'-CTCGTTTCCCTCGTTTCTCTTC-3'
SaWRKY41F	5'-GCTGTGCTCACGACTTATGA-3'	SaWRKY41R	5'-TGGCGGTCTGTTTAGTGTATG-3'
SaWRKY42F	5'-GTCATGGGAGAGTCAGAAAGATG-3'	SaWRKY42R	5'-GGAACCGCAAGGGATTAGTT-3'
SaWRKY44F	5'-GTGGAACGCTCTTATGATGGA-3'	SaWRKY44R	5'-GGCGTCTAGGTTGAGGTTTAG-3'
Fbp1F	5'-TGGCGTGCCTGTTTCTATC-3'	Fbp1R	5'-CGCACTCCATAGGTTTCTTCT-3'
Fbp3F	5'-CCTCGTGTACTGGGAAATGG-3'	Fbp3R	5'-GCAAGAACGCAATGCCTAAA-3'
ODDF	5'-TTTAGCATTGGGTGGGACTC-3'	ODDR	5'-CTTGGCGATTTGCATTGGTTA-3'
CSAF	5'-GCCAATATACCGAGGACAGAAG-3'	CSAR	5'-CAACCGCAAGATCACAAACAG-3'
FAB1AF	5'-AGCAGTTCTCAAAGGAGCTAAA-3'	FAB1AR	5'-ACCTTCGTGCGACAATAAAA-3'

PP2CF	5'-ACTGACCAGGCAATCCTTTC-3'	PP2CR	5'-ATCCATAACCTTCGGCCATTTA-3'
Atactin2F	5'- CAGAAGGATGCATATGTTGGTG-3'	Atactin2R	5'- TGTAGAAAGTGTGATGCCAGAT-3'

Method S1.

Total RNA was extracted from the leaves of 7-year-old *S. album* trees using Eastep[®] Super Total RNA Extraction kit (Promega, Shanghai, China) according to the manufacturer's instructions. One µg of total RNA was used to synthesize first strand cDNAs for 3' or 5' end amplification with the SMARTer RACE cDNA Amplification Kit (Clontech Laboratories Inc., CA, USA) in 20 µL volume. The two specific primers were designed for completing the *SaWRKY1* 3' end (F1: 5'-ACCCTACTCAGCCCGA GCAGAA-3'; F2: 5'-GGTGGAACAGATGGCTACC TCA-3') and 5' end (F1: 5'- GTTTCTTGTTTTTCGGCACTCAC-3'; F2: 5'-CGTGG CGGAGAGGGTTCG-3') with nested PCR. PCR products were purified using the Gel Extraction Kit (Dongsheng Biotech, Guangzhou, China). Purified fragments were then cloned into pMD-18-T vector (Takara, Dalian, China) and sequenced at the Beijing Genomics Institute (BGI, Shenzhen, China). After sequence comparison, the full open-reading frame of *SaWRKY1* was amplified using gene-specific primers (F: 5'-ATGGATTAC TCTTCTTGGACGGC-3'; R: 5'-TCAA AATTTTTCATTTTGACTTT-3') by RT-PCR.

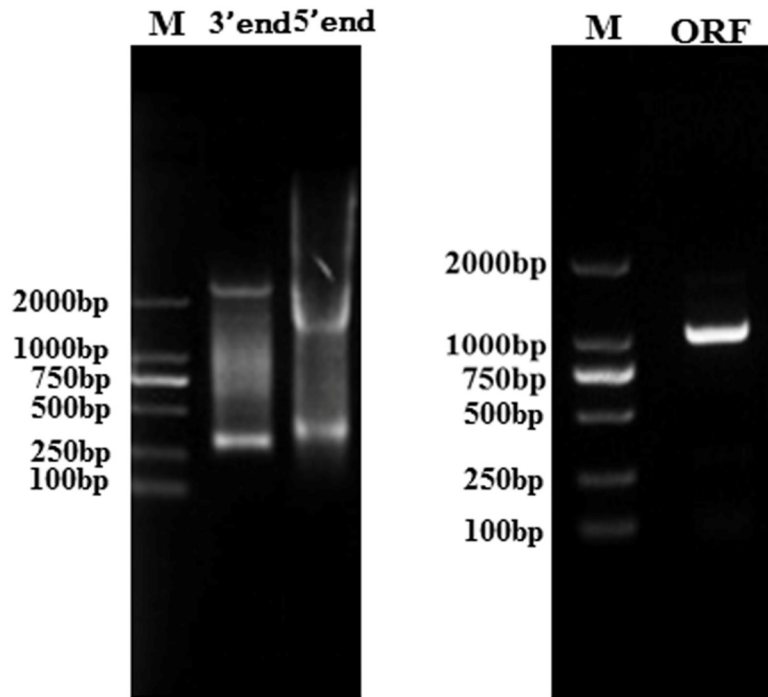


Figure S3. Amplification of 3' and 5' ends, as well as the ORF, of *SaWRKY1*.

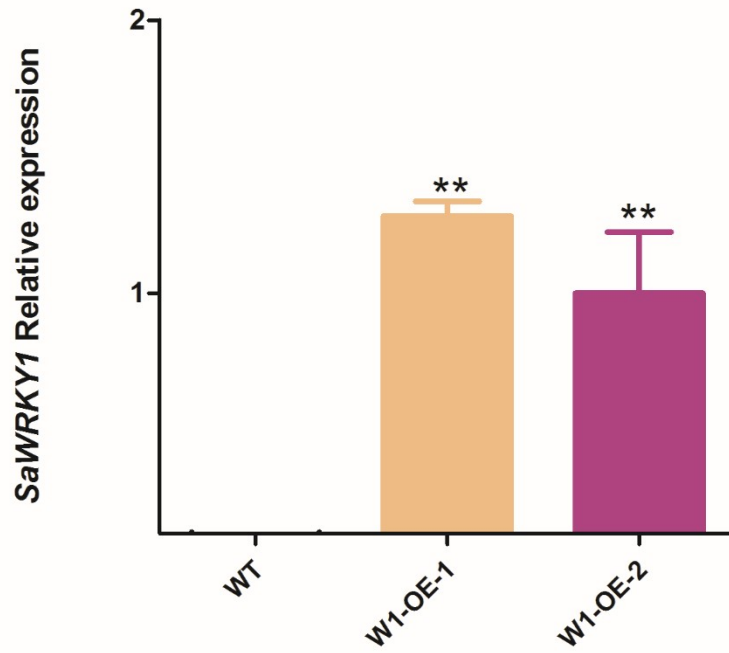


Figure S4. RT-qPCR analysis of *SaWRKY1* gene expression in wild type (WT) and transgenic *Arabidopsis*. Values shown are the means of three independent biological replicates \pm SE. Asterisk indicates significance at $P < 0.01$ between WT and transgenic lines using Duncan's multiple range test. *Atactin2* (AT3G18780) was used as the internal reference gene.