

Supplementary Information

Regulation of ethylene-responsive *S/WRKYs* involved in color change during tomato fruit ripening

Ling Wang^{1, 2, 4†}, Xue-lian Zhang^{1, 3, †}, Lu Wang^{1, 2, 4}, Yanan Tian^{1, 3}, Ning Jia^{1, 2, 4}, Shuzhen Chen^{1, 3}, Ning-bo Shi^{1, 2, 4}, Xuemei Huang^{1, 2, 4}, Chu Zhou^{1, 3}, Yaowen Yu^{1, 2, 4}, Zhao-qi Zhang^{1, 2, 4*}, Xue-qun Pang^{1, 3, 4*}

¹ State Key Laboratory for Conservation and Utilization of Subtropical Agro-bioresources, South China Agricultural University, Guangzhou, 510642, China; ² College of Horticulture, South China Agricultural University, Guangzhou, 510642, China; ³ College of Life Sciences, South China Agricultural University, Guangzhou, 510642, China; ⁴ Guangdong Provincial Key Laboratory of Postharvest Science of Fruits and Vegetables, Guangzhou 510642, China

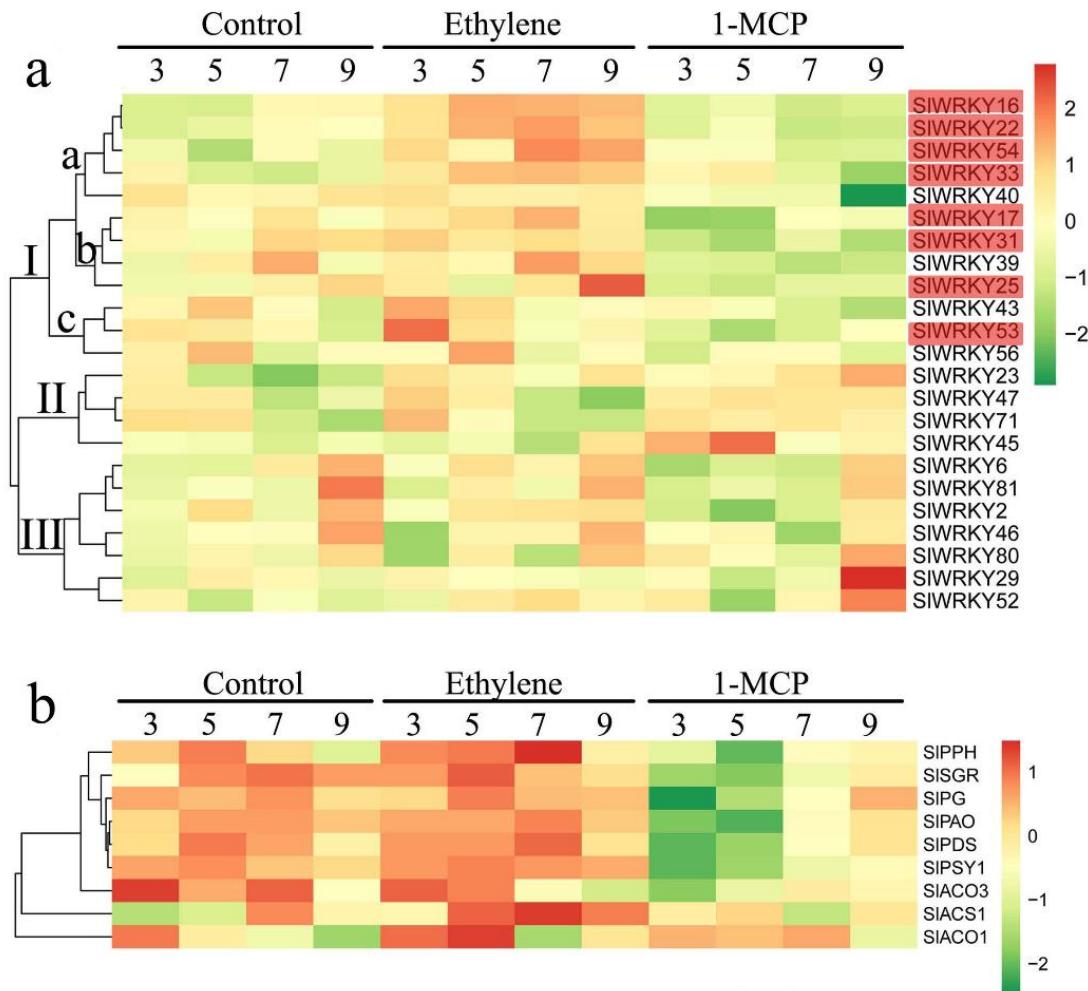
*Authors for Correspondence:

Xue-qun Pang, e-mail: xqpang@scau.edu.cn

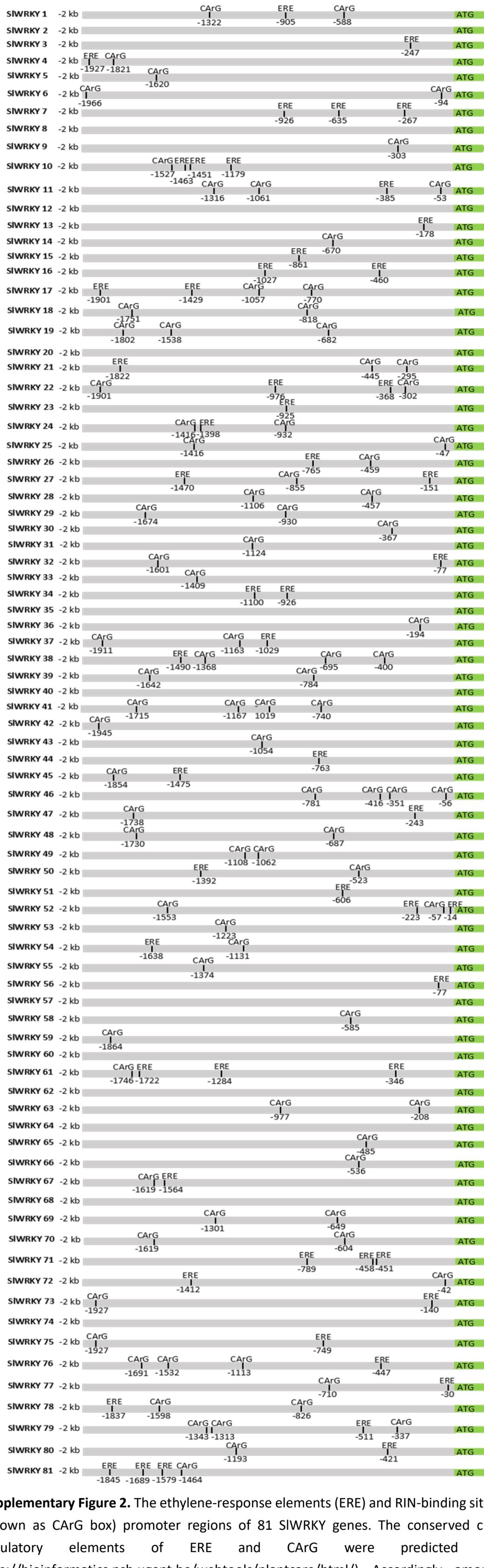
Zhao-qi Zhang, e-mail: zqzhang@scau.edu.cn

†These authors contributed equally to the paper.

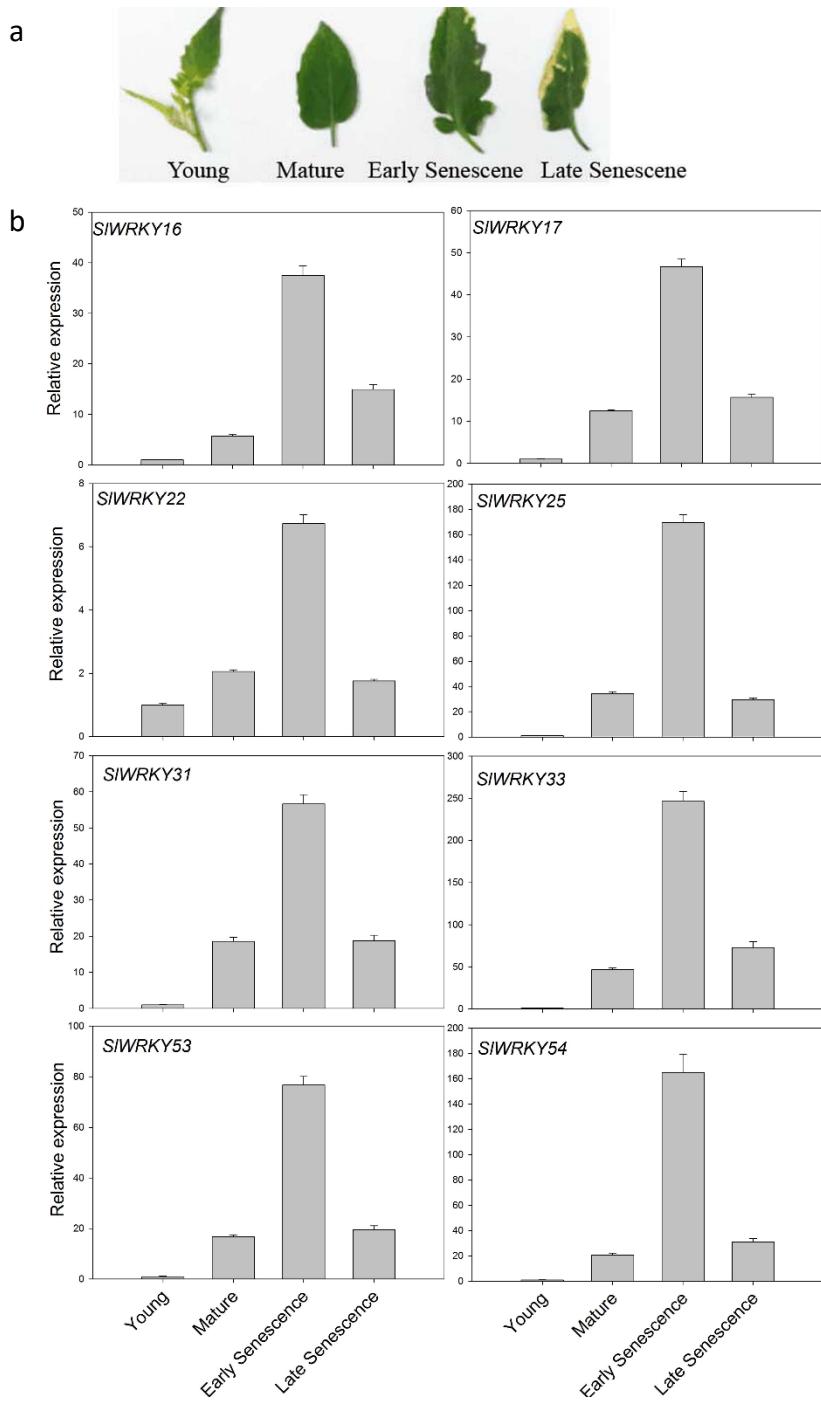
Running Title: Regulation of SIER-WRKYs during tomato color chang



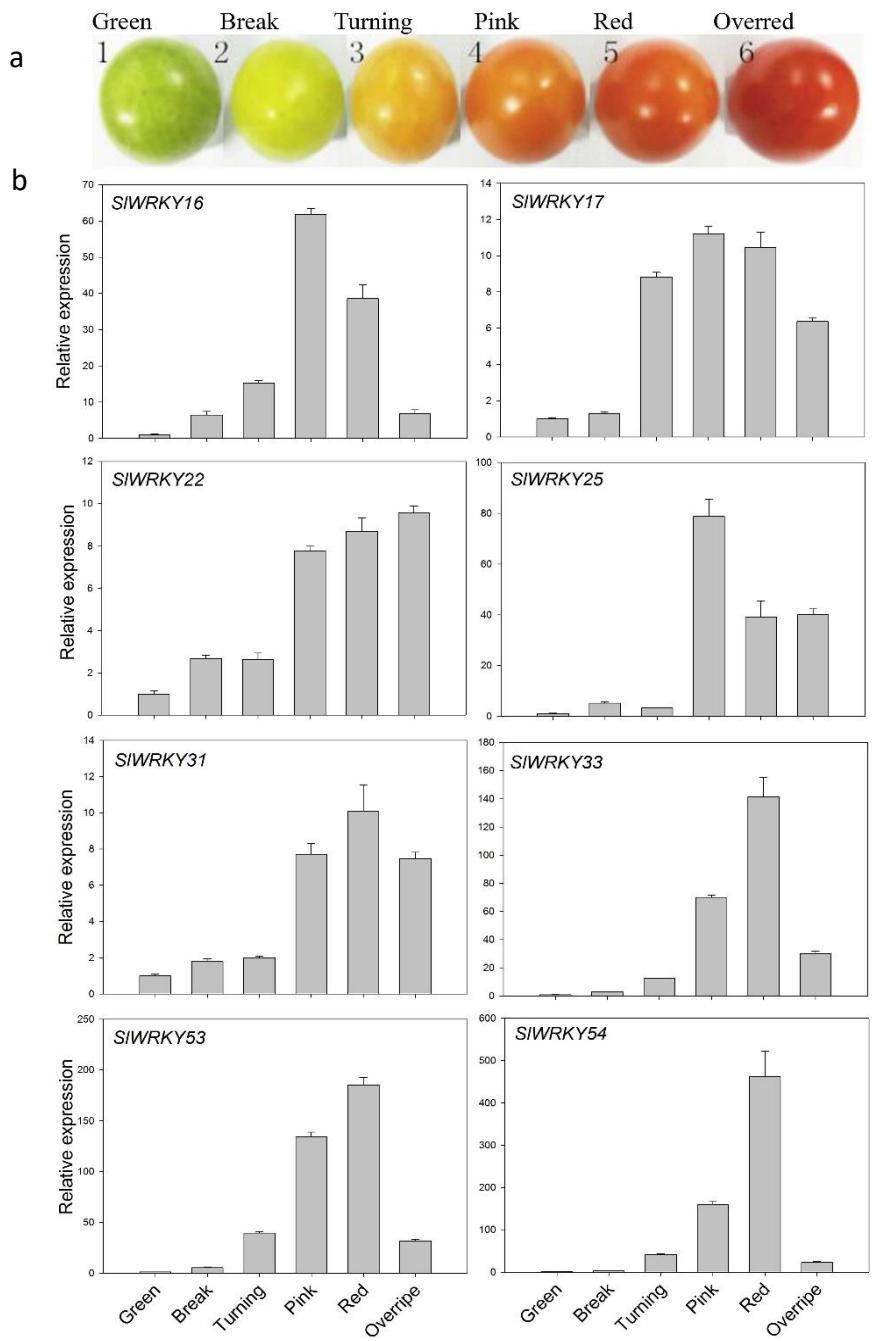
Supplementary Figure 1. Hierarchical cluster of transcript levels for color change related genes and the selected *SIWRKYs* during tomato fruit ripening in response to ethylene and 1-MCP. The complete linkage hierarchical clustering of these genes were performed by heatmap according to the ClustVis program available at <http://biit.cs.ut.ee/clustvis/>. The cluster was generated using the distance of the coefficient correlation of gene expression values by Pearson clustering algorithm method. (a) Hierarchical cluster of transcript levels for the 23 selected *SIWRKY* genes. (b) Hierarchical cluster of transcript levels for 5 color changerelated genes with the reference of 3 ethylene biosynthesis genes (*ACS1*, *ACO1* and *ACO3*) and a cell wall metabolism gene (*PG*). Red and green boxes respectively indicate higher and lower levels of expression compared to the levels before the treatments at day 0. The color density is directly proportional to the expression levels. The transcript levels were detected by Real-time RT-PCR in the samples collected from the control, ethylene or 1-MCP treated fruits at the indicated time points as described in Fig. 2. The labels for 8 ethylene responsive *SIWRKYs* in cluster I and selected for further analysis were highlighted in red.



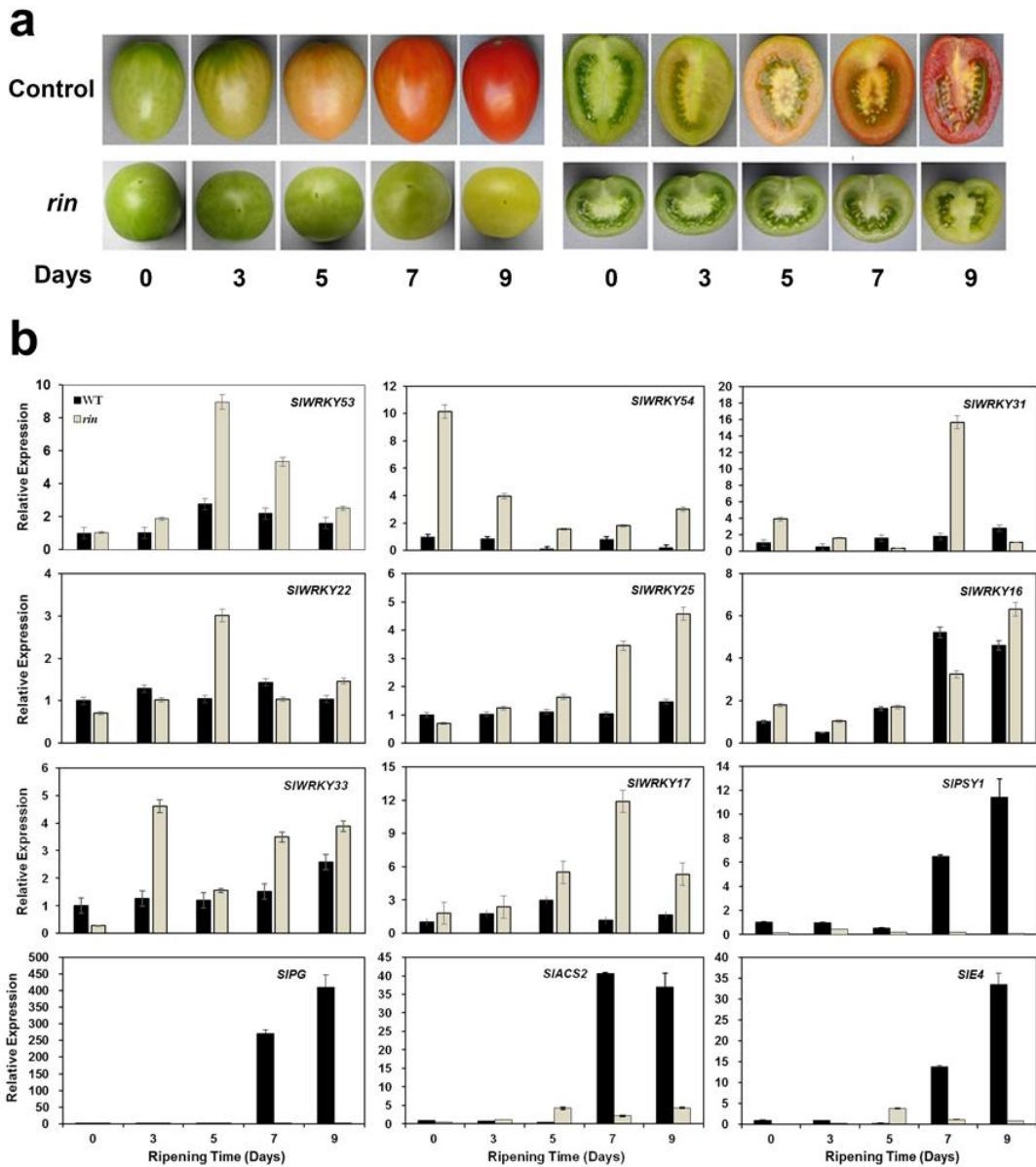
<http://bioinformatics.psb.ugent.be/webtools/plantcare/html/>). Accordingly, among selected 23 SIWRKY genes, *SIWRKY16, 17, 22, 23, 45, 47, 52, 54, 71, 80, and 81* existed ethylene-response elements, *SIWRKY6, 17, 22, 25, 29, 31, 33, 39, 45, 46, 47, 52, 53, 54, 80, and 81* existed CArG box.



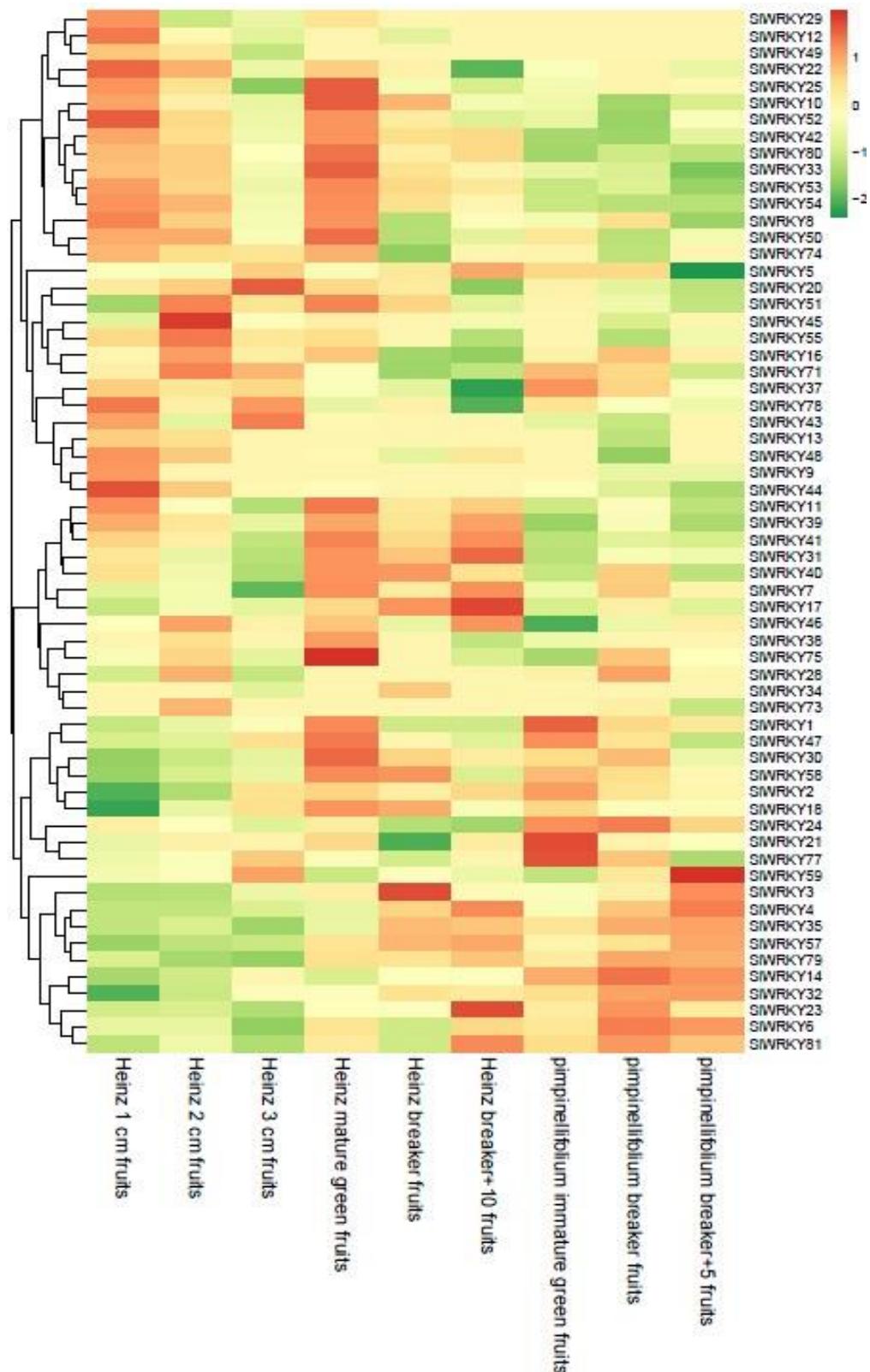
Supplementary Figure 3. Transcription profiling of the 8 *SIER-WRKY* genes during tomato leaf development. (a) Leaf samples were collected from young, mature, early senescent and late senescent leaves. (b) The transcription profiling of the 8 *SIER-WRKY* genes at these leaf developmental stages were as described in Supplementary Fig. S1a.



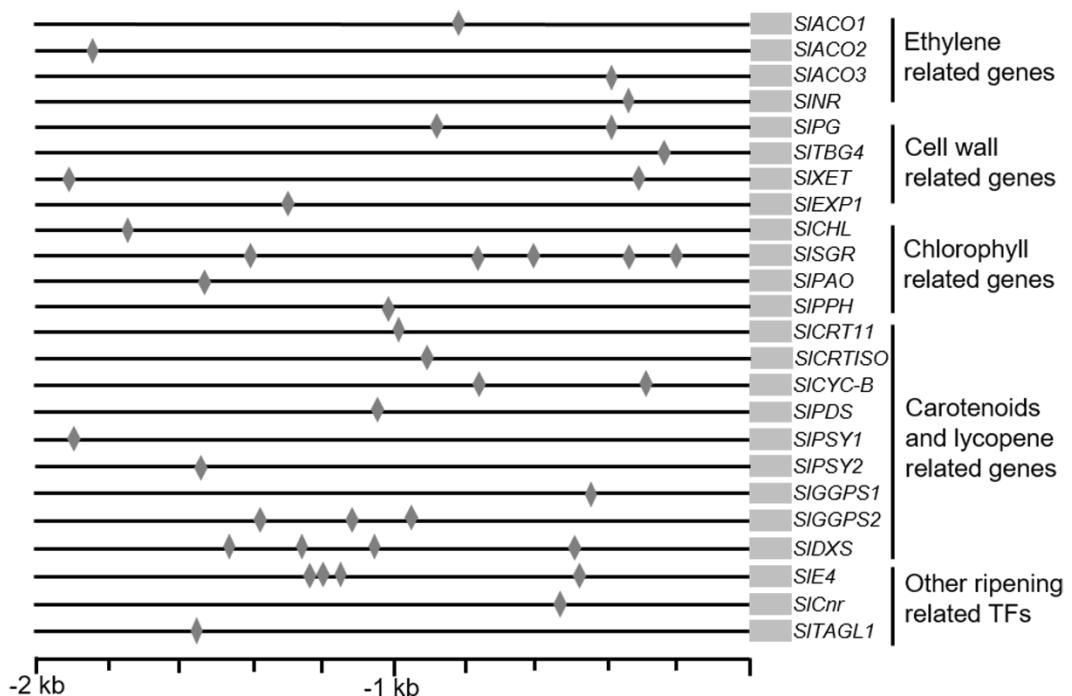
Supplementary Figure 4. Transcription profiling of the 8S_{IER}-WRKY genes in the tomato fruit ripening in plants. (a) Fruit pericarp samples were collected at green mature, breaking, turning, pink red and overripe stages during the fruit ripening in plants. (b) The transcription profiling of the 8 S_{IER}-WRKY genes at these stages were as described in Supplementary Fig. S1a.



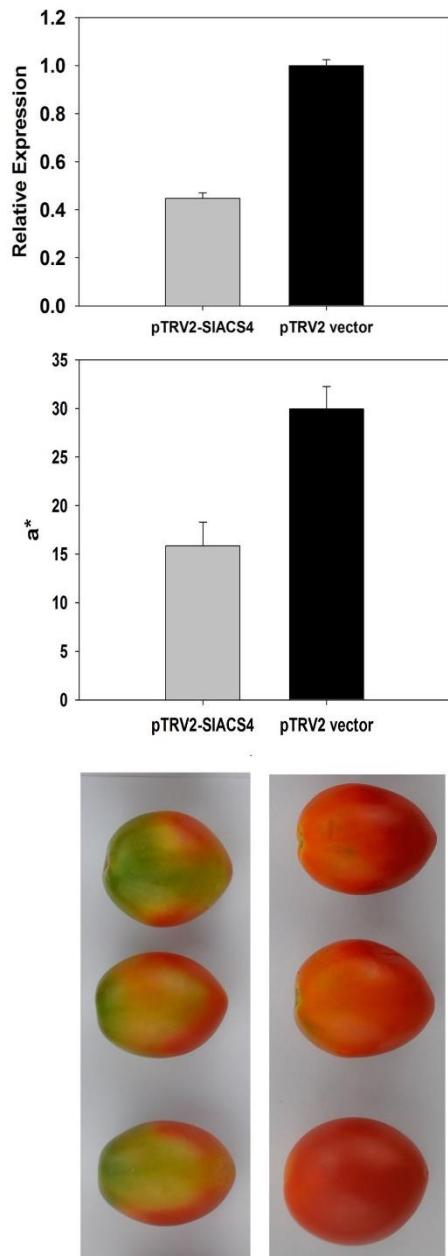
Supplementary Figure 5. Transcription profiling of the 8 *SIER-WRKY* genes and 4 fruit ripening related genes in wild type (WT) and *rin* mutant tomato fruit. The ripening inhibitor (*rin*) mutant (NIL LA3754) was a gift from Tomato Genetics Resource Center (USA). The *rin* mutant is a single gene mutation, fruit attain full size and produce viable seed; however, they are arrested in the fruit ripening ¹. The 8 ethylene-responsive *SIWRKY* (*SIER-WRKY*) genes were identified based on the gene transcription profiles in Fig. 4 and Supplementary Fig. S1a; the 4 typical fruit ripening related genes were selected according to Martel et al. (2011) ². (a) Fruit pericarp samples were collected at green mature, breaking, turning, pink red and overripe stages during the fruit ripening in plants. (b) The transcription profiling of the 8 *SIER-WRKY* genes and 4 fruit ripening related genes at these stages.



Supplementary Figure 6. Transcription profiling of the 81 *SIWRKY* genes of tomato fruit. The gene expression of fruit in different developmental process were obtained from the RNA-seq data at <http://ted.bti.cornell.edu/cgi-bin/TFGD/digital/home.cgi>.



Supplementary Figure 7. The WRKY-binding sites (known as W-box) promoter regions of tomato fruit ripening process related genes and TFs. In addition to the selected 9 ripening related genes, W-box binding sites in promoter region of other genes that involved in ethylene, cell wall, chlorophyll, carotenoids and lycopene metabolisms, as well as several ripening regulatory TFs were predicted. It suggests that SIWRKYS may be involved in regulation of fruit ripening. The conserved cis-regulatory elements were predicted at <http://bioinformatics.psb.ugent.be/webtools/plantcare/html/>.



Supplementary Figure 8. VIGS based transient gene silencing of an ethylene biosynthesis gene, *SIACS4* as a marker. Transcription profiling of the 8 *S/ER-WRKY* genes in the tomato fruit ripening in plants. The efficiency of the silencing was first confirmed by evaluation of silencing, using the same approach. The relative expression of the *SIACS4* gene, the red color a^* values and the appearance of the tomato fruits at 14 days after infiltration were shown in a same column.

Table S1. Correspondence between the unified nomenclature of the SIWRKY gene family and their Solyc identifiers. The relevance of other names as well as the function proposed in the literature are also listed.

New Names ^a	Solyc Identifier	Other Names	Reported function	References
SIWRKY4	Solyc05g012770.2.1	SpWRKY2	Pathogen resistance	³
SIWRKY31	Solyc06g066370	SIDW1	Disease resistance	⁴
SIWRKY40	Solyc06g068460.2	SIWRKY1	Disease resistance	⁵
SIWRKY73	Solyc03g113120.2	SIWRKY72a	Immune responses	⁶
SIWRKY74	Solyc06g070990.2	SIWRKY72b	Immune responses	⁶
SIWRKY80	Solyc03g095770.2	SIWRKY70	Insect infestation	⁷

^a The new names are issued according to Huang et al.⁸, and the Solyc chromosome identifier issued by ITAG 2.40 reference annotation ⁹.

Table S2. The sequences and main functions of WRKY-TFs that have been reported

Gene Name	Species	References	Gene Bank	Function
AtWRKY6	Arabidopsis	^{10,11}	NP_564792.1	Senescence
AtWRKY8	Arabidopsis	¹²	NP_199447.1	Induced by ACC
AtWRKY18	Arabidopsis	¹³	NP_567882.1	Senescence
AtWRKY22	Arabidopsis	¹⁴	NP_192034.1	Senescence
AtWRKY30	Arabidopsis	¹⁵	NP_568439.1	Senescence
AtWRKY33	Arabidopsis	¹⁶	NP_181381.2	Combine with promoter of ACS
AtWRKY53	Arabidopsis	¹⁷⁻¹⁹	NP_194112.1	Senescence
AtWRKY54	Arabidopsis	¹⁵	NP_181607.1	Senescence
AtWRKY57	Arabidopsis	²⁰	NP_177090.1	Senescence
AtWRKY70	Arabidopsis	^{15,21}	NP_191199.1	Senescence
AtWRKY75	Arabidopsis	²²	NP_196812.1	Senescence
OsWRKY23	<i>Oryza sativa</i>	²³	NP_001044163.1	Senescence
OsWRKY71	<i>Oryza sativa</i>	²⁴	NP_001046094.1	Induced by ACC
OsWRKY80	<i>Oryza sativa</i>	²⁵	NP_001063497.1	Senescence
GbWRKY1	<i>Gossypium barbadens</i>	²⁶	AFH35047.1	Induced by ACC
GhWRKY40	<i>Gossypium hirsutum</i>	²⁷	AGX24945.1	Response of

				ethylene signal
<i>BnWRKY1</i>	<i>Brassica napus</i> L	²⁸	ACI14383.1	Response of ethylene signal
<i>BnWRKY28</i>	<i>Brassica napus</i> L	²⁸	ACI14393.1	Response of ethylene signal
<i>BnWRKY32</i>	<i>Brassica napus</i> L	²⁸	ACI14396.1	Response of ethylene signal
<i>BnWRKY33</i>	<i>Brassica napus</i> L	²⁸	ACI14397.1	Response of ethylene signal
<i>BnWRKY40</i>	<i>Brassica napus</i> L	²⁸	ACI14400.1	Response of ethylene signal
<i>BnWRKY45</i>	<i>Brassica napus</i> L	²⁸	ACH99806.1	Response of ethylene signal
<i>BnWRKY69</i>	<i>Brassica napus</i> L	²⁸	ACI14405.1	Response of ethylene signal
<i>BnWRKY70</i>	<i>Brassica napus</i> L	²⁸	ACI14407.1	Response of ethylene signal
<i>BnWRKY75</i>	<i>Brassica napus</i> L	²⁸	ACI14409.1	Response of ethylene signal

Table S3. The primers of *S/WRKYs* and fruit ripening related genes for Real-time PCR

Gene Name	Gene ID	Primer (5' -3')	Length	Note
<i>S/WRKY2</i>	Solyc07g066220.2.1	ACCTACGAAGGGAAGCACA CGATTGACAGGCAACCTC	176bp	1
<i>S/WRKY6</i>	Solyc02g080890.2.1	TCAACCAAGCAAATCCTC TGATGGGTGGTGATGATG	179bp	
<i>S/WRKY15</i>	Solyc10g005680.1.1	GAAGAACAGCAGGCAGTAC AGTTGAATCCGGTCATAGA	117bp	
<i>S/WRKY16</i>	Solyc02g032950.2.1	TGG CAT CGA CTA CAT CAG TTA CAG TGG GAA ACG GAG	159bp	
<i>S/WRKY17</i>	Solyc07g051840.2.1	ACAACATCCTAGCAAATC C TTCACCGTGTCAAGCTACA	178bp	
<i>S/WRKY22</i>	Solyc01g095100.2.1	GAG AAG CAA GAA AGC AGC A TAT CGG AAA AGC AAT CTC C	169bp	
<i>S/WRKY23</i>	Solyc01g079260.2.1	TGGAGATGCTGATGGGAAG AAACGCAAATCTCGGCTCTT	118bp	1
<i>S/WRKY25</i>	Solyc10g011910.2.1	TAAAGGTTCCCCATACCCAAG GTTTTTGGCGGCTGATTG	183bp	1
<i>S/WRKY29</i>	Solyc08g081610.2.1	TTCTCCAGAAACACTTATGATCG AGACCAGCAAAGAAATCTCCA	144bp	
<i>S/WRKY31</i>	Solyc06g066370.2.1	ACAACCTATGAAGGGAAGCACA AGGGTGCTCCCATTCAGAC	175bp	1

		CGGTTAGGAAGCATGTGGAA		
<i>S/WRKY33</i>	Solyc09g014990.2.1	ATCTGGAGGGTGATTGGTGG	265bp	
		GCGGTAATGCCAAGACAAAC		
<i>S/WRKY39</i>	Solyc03g116890.2.1	TCAGTTCCCTGGTGATTACGC	134bp	
		AGGACCAACCATTACTCTCG		
<i>S/WRKY40</i>	Solyc06g068460.2.1	CTGCTGGACTTTGTTACC	298bp	
		GCCCAGTCAAGAAGAAGGTA		
<i>S/WRKY45</i>	Solyc08g067360.2.1	GAAAGTAGGGCTGCTGGTTA	233bp	
		CCAACCACCTCAAGCTGAA		
<i>S/WRKY46</i>	Solyc08g067340.2.1	AAGACGCCATTGTTCGACT	131bp	
		GGTGCTAACATCCGAGAG		
<i>S/WRKY52</i>	Solyc03g007380.1.1	CTGACACTAGCACCACCAC	158bp	
		CACATACCGAGGCTCCCATAA		
<i>S/WRKY53</i>	Solyc08g008280.2.1	CCTGTTGGATAAACGGCTTGG	105bp	
		CAACAAAGCAAGTGCAGAGG		
<i>S/WRKY54</i>	Solyc08g082110.2.1	TGGTTGTGTAGCAGCAGCA	110bp	
		ATTCATACAAGGAGCACAG		
<i>S/WRKY56</i>	Solyc08g081630.1.1	CATTAGCTCTCACAGGGT	220bp	
		GTAGCGTCGCAAGGATGTTG		
<i>S/WRKY71</i>	Solyc02g071130.2.1	TGCTCAAAGCCTCATGGTTCT	271bp	
		AAGAAGGAGAAGCAAGACCGTA		
<i>S/WRKY80</i>	Solyc03g095770.2.1	TCTTGATCGTACTTGTGGGTGC	179bp	1

<i>S/WRKY81</i>	Solyc09g015770.2.1	CTCAGATTGGTGGATGATGGT AAATCTTGTGGGTTGTCTTGG	163bp	1
<i>S/SGR</i>	Solyc08g080090.2.1	AAAATGGGACCATCCAACAA GCTGCTTCCACAAACCCCTAT	137bp	
<i>S/PPH</i>	Solyc01g088090.2.1	CCCATGATGAAGTCCCAGAG GGGAGAGGCTTCATGTTT	221bp	
<i>S/PAO</i>	Solyc11g066440.1.1	TGGATTAGCATACATTCTACACGAA TTGTGTTTGTGCTGTTCTGA	158bp	
<i>S/PSY1</i>	Solyc03g031860.2.1	CAAATGGGACAAGTTCATGGA TTCCTATGCCTCGATGAATCAA	70bp	3
<i>S/PDS</i>	Solyc03g123760.2.1	AAGGCGCTGTCTTATCAGGAAA TAAACTACGCTTGCTTCCGACA	106bp	3
<i>S/PG</i>	Solyc10g080210.1.1	TATTACTTGTGGTCCAGG ATCCTAACTCCATTTCG	126bp	
<i>S/ACO1</i>	Solyc07g049530.2.1	CACTAACGGGAAGTACAAGA ACCATACATAAGAAGAGCAA	269bp	2
<i>S/ACO2</i>	Solyc12g005940.1.1	GCATCCTCTACAATCCAGGA CATGTAGTAGGGACGCACA	332bp	2
<i>S/ACO3</i>	Solyc07g049550.2.1	GAGCGTGATGCACAGAGTGA CAATCACACACACATACACCA	349bp	2
<i>S/ACS1</i>	Solyc08g081540.2.1	CGGGCTAGTTCAACTCAGA CAACAACAACAAATCTAAGCCA	566bp	2

<i>SACS2</i>	Solyc01g095080.2.1	AAGCGCGATGAGGTTAGGTA AAAGTGGACGCAAATCCATC	119bp	4
<i>SIE4</i>	Solyc03g111720.2.1	GACCACTCTAAATGCCAGG TTCCTGAGCGGTATTGCTT	53bp	4
<i>EF-1α</i>	Solyc06g005060.2.1	AGATGGTCAGACCCGTGAAC TGGAGTACTGGGGGTGGTA	104bp	3

Note: 1 The primer quoted from the ⁸

2 The primer quoted from the ²⁹

3 The primer quoted from the ³⁰

4 The primer quoted from the ²

Table S4. The primers used for construction pH7WGY2-SIWRKYx vector

Name of Genes	Primers (5' -3')
<i>SIWRKY16</i> -pH7WGY2-For	TTACGAATTCGACCTGCAGatggataaaggatggggacttac
<i>SIWRKY16</i> -pH7WGY2-Rev	CAGTTGGAATTCTAGActactttccaggacc
<i>SIWRKY17</i> -pH7WGY2-For	TTACGAATTCGACCTGCAGatggccaaggaaagtggac
<i>SIWRKY17</i> -pH7WGY2-Rev	CAGTTGGAATTCTAGAgttgctggaaaactcga
<i>SIWRKY22</i> -pH7WGY2-For	TTACGAATTCGACCTGCAGatggaagaggattggatct
<i>SIWRKY22</i> -pH7WGY2-Rev	CAGTTGGAATTCTAGAaacgcccctgcgg
<i>SIWRKY25</i> -pH7WGY2-For	TTACGAATTCGACCTGCAGatggaaagctacaaagacatta
<i>SIWRKY25</i> -pH7WGY2-Rev	CAGTTGGAATTCTAGAacgaccgcctgccgc
<i>SIWRKY31</i> -pH7WGY2-For	TTACGAATTCGACCTGCAGatggctgctcaagttctc
<i>SIWRKY31</i> -pH7WGY2-Rev	CAGTTGGAATTCTAGAgcaaagcaatgactcc
<i>SIWRKY33</i> -pH7WGY2-For	TTACGAATTCGACCTGCAGatggcttcagggtggaaat
<i>SIWRKY33</i> -pH7WGY2-Rev	CAGTTGGAATTCTAGAgtaaggaaagagctgaag
<i>SIWRKY53</i> -pH7WGY2-For	TTACGAATTCGACCTGCAGatggattgtcatcaaactg
<i>SIWRKY53</i> -pH7WGY2-Rev	CAGTTGGAATTCTAGAtgaaaaatttgggtt
<i>SIWRKY54</i> -pH7WGY2-For	TTACGAATTCGACCTGCAGatggattggattcaattatga
<i>SIWRKY54</i> -pH7WGY2-Rev	CAGTTGGAATTCTAGAtctaaaaatcagagaaatt

Note : The letters of lowercases are linearized homologous sequences ends of pH7WGY2 vectors.

Table S5. The primers used for construction pAbAi-SIWRKYx vector for Y1H assay

Name of genes	Primers(5' -3')	Enzyme sites
<i>SISGR</i> -p-pAbAi-For	CGGggtaccGTTTCAACCTCTAATTTGGCAG	<i>Kpn</i> I
<i>SISGR</i> -p-pAbAi-Rev	ACGCgtcgacAAAACCTCCTGAATCTGGAGTTCC	<i>Sal</i> I
<i>SIPPH</i> -p-pAbAi-For	CGGggtaccATCATCCCAGAAAGCCCCTTTGAT	<i>Kpn</i> I
<i>SIPPH</i> -p-pAbAi-Rev	ACGCgtcgacCATCCCAGAGTCAGCTTCTAAAATCT	<i>Sal</i> I
<i>SIPAO</i> -p-pAbAi-For	CCCaagcttTGTGACCTTGAAC TGTTATGTAG	<i>Hind</i> III
<i>SIPAO</i> -p-pAbAi-Rev	CCctcgagTATTGAGTTAACATGTTTGTTGT	<i>Xho</i> I
<i>SIPSY1</i> -p-pAbAi-For	CGGggtaccGGCTAAATCGAAAATTGAATCGTT	<i>Kpn</i> I
<i>SIPSY1</i> -p-pAbAi-Rev	ACGCgtcgacTCTGAGCAAGAAAACCTGGTTGT	<i>Sal</i> I
<i>SIPDS</i> -p-pAbAi-For	CGGggtaccCGTCTAATATCTGGTGTCTCTC	<i>Kpn</i> I
<i>SIPDS</i> -p-pAbAi-Rev	ACGCgtcgacCAGTAAAACCTGCCATAAGGATAT	<i>Sal</i> I
<i>SIACO1</i> -p-pAbAi-For	CCCaagcttTTGGTTAGAGGGAGAATTGTG	<i>Hind</i> III
<i>SIACO1</i> -p-pAbAi-Rev	CCctcgagTGATGTACAATAATGAGGCTTGA	<i>Xho</i> I
<i>SIACO3</i> -p-pAbAi-For	CCCaagcttTCAAGTCAACGGATAGAAATTCA	<i>Hind</i> III
<i>SIACO1</i> -p-pAbAi-Rev	CCGctcgagGAAAAGAGTGATTCTTGAAAGG	<i>Xho</i> I

Table S6. The primers used for construction pGADT7-AD-WRKYx vector

Name of Genes	Primers (5' -3')	Enzyme sites
<i>S/WRKY16</i> -AD-For	CGCggatccATATGGATAAAGGATGGGACTT	<i>BamH I</i>
<i>S/WRKY16</i> -AD-Rev	CgagctcGCTACTGTTCTTCCAGGACCA	<i>Sac I</i>
<i>S/WRKY17</i> -AD-For	CGCggatccATGGCCAAGGAAGTGGACTCT	<i>BamH I</i>
<i>S/WRKY17</i> -AD-Rev	CgagctcTCAGTTGCTGGAAAACCTCGAAT	<i>Sac I</i>
<i>S/WRKY22</i> -AD- For	CGCggatccATATGGAAGAGGATTGGATCTAC	<i>BamH I</i>
<i>S/WRKY22</i> -AD-Rev	CCGCCGctcgagCTAAACGCCGCCTGCGG	<i>Xho I</i>
<i>S/WRKY25</i> -AD-For	GGGAATTCCatatgATGGAAGAAGATTGGGATCT	<i>Nde I</i>
<i>S/WRKY25</i> -AD-Rev	CCGCCGctcgagCACTACGGCGGCAGGCGGTGTTGA	<i>Xho I</i>
<i>S/WRKY31</i> -AD-For	CGCggatccATGGCTGCTTCAAGTTCTCT	<i>BamH I</i>
<i>S/WRKY31</i> -AD-Rev	CgagctcTCAGCAAAGCAATGACTCCATA	<i>Sac I</i>
<i>S/WRKY33</i> -AD-For	GGAATTCCatatgATGGCTTCTTCAGGTGGAAAT	<i>Nde I</i>
<i>S/WRKY33</i> -AD-Rev	CCGctcgagCTCAGTTAAGGAAAGAGCTGAAG	<i>Xho I</i>
<i>S/WRKY53</i> -AD-For	GGGAATTCCatatgATGGATTGTGCATCAAACCTGG	<i>Nde I</i>
<i>S/WRKY53</i> -AD-Rev	CCGctcgagGTCATGAGAAAAATTGGGGTT	<i>Xho I</i>
<i>S/WRKY54</i> -AD-For	GGAATTCCatatgATGGATTGTGGATTCAATTATG	<i>Nde I</i>
<i>S/WRKY54</i> -AD-Rev	CCGctcgagCTTATCTGAAAAAATCAGAGAAAT	<i>Xho I</i>

Table S7. The primers used for construction *pGreenII 0800-LUC* vector

Name of Genes	Primers (5' -3')
<i>SIACO1</i> -LUC-For	gtcgacggtatcgataagcttGTAGACTAATGCTGACGTTAAC
<i>SIACO1</i> -LUC-Rev	cgctctagaactagtggatccTGATGTACAAATAATGAGGCTTGA
<i>SIACO2</i> -LUC-For	gtcgacggtatcgataagcttCTTTCACACTGTTGAAGCCAT
<i>SIACO2</i> -LUC-Rev	cgctctagaactagtggatccAAGATTGAGGCTTGGTATTGGTATT
<i>SIACO3</i> -LUC-For	gtcgacggtatcgataagcttATGATACGTCGAAAATTCAAACG
<i>SIACO3</i> -LUC-Rev	cgctctagaactagtggatccGAAAAGAGTGATTCTTGAAAGG
<i>SIPAO</i> -LUC-For	gtcgacggtatcgataagcttTGTGACCTTGAACGTATGTTATGTAG
<i>SIPAO</i> -LUC-Rev	cgctctagaactagtggatccTATTGAGTTAACATGTTGTGT
<i>SIPDS</i> -LUC-For	gtcgacggtatcgataagcttCGTCTAATATCTGGTGTCTTCTC
<i>SIPDS</i> -LUC-Rev	cgctctagaactagtggatccGGTTCTGCACAATTAAAGCAAATA
<i>SIPG</i> -LUC-For	gtcgacggtatcgataagcttTAAGACAAAGGCCTAAAGGACA
<i>SIPG</i> -LUC-Rev	cgctctagaactagtggatccCATGAGCAAATTCTGTTCAAGAA
<i>SIPPH</i> -LUC-For	gtcgacggtatcgataagcttTCATCCAAGAAGCCCCTTTG
<i>SIPPH</i> -LUC-Rev	cgctctagaactagtggatccATCCCAGAGTCAGCTTCTAAAATCT
<i>SIPSY1</i> -LUC-For	gtcgacggtatcgataagcttGGCTAAATCGAAAATTGAATCGTT
<i>SIPSY1</i> -LUC-Rev	cgctctagaactagtggatccTCTGAGCAAGAAAACCTTGGTT
<i>SISGR</i> -LUC-For	gtcgacggtatcgataagcttGTTTCAACCTCTTAATTGGCAG
<i>SISGR</i> -LUC-Rev	cgctctagaactagtggatccACTCCTGAATCTGGAGTTCC

Note: The letters of lowercases are linearized homologous sequences ends of *pGreenII 0800-LUC* vectors.

Table S8. The primer used for construction *pCambia35tlegyfps* vector

Name of Genes	Primers (5' -3')
<i>SIWRKY16</i> -pCambia-For	ttacgaatttcgacctgcagATGGATAAAGGATGGGACTTA
<i>SIWRKY16</i> - pCambia-Rev	cagttggaaattctagaCTACTGTTCTTCCAGGACC
<i>SIWRKY17</i> - pCambia-For	ttacgaatttcgacctgcagATGCCAAAGGAAGTGGAC
<i>SIWRKY17</i> - pCambia-Rev	cagttggaaattctagaTCAGTTGCTGGAAAACTCGA
<i>SIWRKY22</i> - pCambia-For	ttacgaatttcgacctgcagATGGAAGAGGATTGGGATCT
<i>SIWRKY22</i> - pCambia-Rev	cagttggaaattctaga TCAAACGCCGCCTGCGG
<i>SIWRKY25</i> - pCambia-For	ttacgaatttcgacctgcagATGGAAGAAGATTGGGATCTAA
<i>SIWRKY25</i> - pCambia-Rev	cagttggaaattctagaTCAACGACCGCCTGCCGC
<i>SIWRKY31</i> - pCambia-For	ttacgaatttcgacctgcagATGGCTGCTCAAGTTCTC
<i>SIWRKY31</i> - pCambia-Rev	cagttggaaattctagaTCAGCAAAGCAATGACTCC
<i>SIWRKY33</i> - pCambia-For	ttacgaatttcgacctgcagATGGCTTCTCAGGTGGAAAT
<i>SIWRKY33</i> - pCambia-Rev	cagttggaaattctaga TCAGTTAAGGAAAGAGCTGAAG
<i>SIWRKY53</i> - pCambia-For	ttacgaatttcgacctgcagATGGATTGTGCATCAAACCTG
<i>SIWRKY53</i> - pCambia-Rev	cagttggaaattctagaTCATGAGAAAAATTGGGTT
<i>SIWRKY54</i> - pCambia-For	ttacgaatttcgacctgcag ATGGATTGTGGATTCAATTATGA
<i>SIWRKY54</i> - pCambia-Rev	cagttggaaattctaga TTATCTGAAAAAAATCAGAGAAATT

Note: The letters of lowercases are linearized homologous sequences ends of *pCambia35tlegyfps* vectors.

Table S9. The primers used for construction pGBK7-DBD-WRKYx vector

Name of Genes	Primers (5' -3')	Enzyme sites
<i>S/WRKY16</i> -DBD-For	CATGccatggAGATGGATAAAGGATGGGACTT	<i>Nco</i> I
<i>S/WRKY16</i> -DBD-Rev	ACGCgtcgacGCTACTGTTCTTCAGGACCA	<i>Sal</i> I
<i>S/WRKY17</i> -DBD-For	CGCggatccGTATGCCAAAGGAAGTGGACTCT	<i>BamH</i> I
<i>S/WRKY17</i> -DBD-Rev	ACGCgtcgacGTCAGTTGCTGGAAAATCGAAT	<i>Sal</i> I
<i>S/RIN</i> -DBD-For	tcagaggaggaccctgcatatgATGGTAGAGGGAAAGTAGAAT	Note
<i>S/RIN</i> -DBD-Rev	tcgacggatccccggaaattcAAGCATCCATCCAGGTACA	Note
<i>S/ERF7</i> -DBD-For	tcagaggaggaccctgcatatgATGGCTAGGGCACAAACAA	Note
<i>S/ERF7</i> -DBD-Rev	tcgacggatccccggaaattcTCACTGGATTGGTGAGAAGG	Note
<i>S/ERF2b</i> -DBD-For	tcagaggaggaccctgcatatgATGTGTGGTGGTGCAATT	Note
<i>S/ERF2b</i> -DBD-Rev	tcgacggatccccggaaattcTTAAACTACATTATAACTGGTTGT	Note

Note: The letters of lowercases are linearized homologous sequences ends of BD vector

Table S10. The primers used for construction BiFC vector

Name of Genes	Primers (5' -3')
<i>S/WRKY16-</i> - BiFC-For	tcagatctcgagctcaagcttATGGATAAAGGATGGGACT
<i>S/WRKY16</i> -BiFC-Rev	gactctagatcagggtggatccCTGTTCTTCAGGACC
<i>S/WRKY17</i> -BiFC-For	tcagatctcgagctcaagcttATGCCAAAGGAAGTGGA
<i>S/WRKY17</i> -BiFC-Rev	gactctagatcagggtggatccGTTGCTGGAAAACCTCGAA
<i>S/WRKY 33</i> -BiFC-For	tcagatctcgagctcaagcttATGGCTTCTCAGGTGGAAAT
<i>S/WRKY 33</i> -BiFC-Rev	gactctagatcagggtggatccGTTAAGGAAAGAGCTGAAGAAT
<i>S/WRKY 53</i> -BiFC-For	tcagatctcgagctcaagcttATGGATTGTGCATCAAATGG
<i>S/WRKY 53</i> -BiFC-Rev	gactctagatcagggtggatccTGAGAAAAATTGGGTTACCAA
<i>S/WRKY 54</i> -BiFC-For	tcagatctcgagctcaagcttATGGATTGTGGATTCAATTATGAAT
<i>S/WRKY 54</i> -BiFC-Rev	gactctagatcagggtggatccTCTGAAAAAATCAGAGAAATTGG
<i>S/ERF2b</i> -BiFC-For	tcagatctcgagctcaagcttATGTGTGGTGGTGCATTCT
<i>S/ERF2</i> -BiFC-Rev	gactctagatcagggtggatccAACTACATTATAACTGGTTGTAC
<i>S/ERF7</i> -BiFC-For	tcagatctcgagctcaagcttATGGCTAGGGCACACAA
<i>S/ERF7</i> -BiFC-Rev	gactctagatcagggtggatccCTGGATTGGTGAGAAGGAA
<i>S/RIN</i> -BiFC-For	tcagatctcgagctcaagcttATGGGTAGAGGGAAAGTAGAA
<i>S/RIN</i> -BiFC-Rev	gactctagatcagggtggatccAAGCATCCATCCAGGTACA

Table S11. The primers used for construction VIGS vector

Gene name	Primer (5'- 3')
LIC-S/WRKY16-For	<u>CGACGACAAGACCCTGGGTTAACATATGATGAACCG</u>
LIC-S/WRKY16-Rev	<u>GAGGAGAAGAGCCCTAATTGGAATTATGAGATAGATCGT</u>
LIC -S/WRKY17-For	<u>CGACGACAAGACCCTCATAACAAACCAATTATCCTAAGA</u>
LIC-S/WRKY17-Rev	<u>GAGGAGAAGAGCCCTAACATTGAATCTAGTTCCACAT</u>
LIC -S/WRKY22-For	<u>CGACGACAAGACCCTCATGCGGTGGTCAGAGGC</u>
LIC-S/WRKY22-Rev	<u>GAGGAGAAGAGCCCTGGTCTTGGGCTTGACATGTG</u>
LIC -S/WRKY23-For	<u>CGACGACAAGACCCTATTCAATTGACAACAAACGGTT</u>
LIC-S/WRKY25-Rev	<u>GAGGAGAAGAGCCCTTGATTGTTGACTTGAGCA</u>
LIC -S/WRKY31-For	<u>CGACGACAAGACCCTTGACGACTTCTTCACCGACCTT</u>
LIC-S/WRKY31-Rev	<u>GAGGAGAAGAGCCCTTGACGACTTCTTCACCGACCTT</u>
LIC -S/WRKY33-For	<u>CGACGACAAGACCCTAACTCATTCTTCTCTCAATT</u>
LIC-S/WRKY33-Rev	<u>GAGGAGAAGAGCCCTTCACTCCAGTTTGCTG</u>
LIC -S/WRKY53-For	<u>CGACGACAAGACCCTTATTCTGCACCACAACCAAC</u>
LIC-S/WRKY53-Rev	<u>GAGGAGAAGAGCCCTTGGATCCAGCTCCAAATG</u>
LIC -S/WRKY54-For	<u>CGACGACAAGACCCTGCTGCTGCTACACAACCA</u>
LIC-S/WRKY54-Rev	<u>GAGGAGAAGAGCCCTTACATGTTCAAGTGGAAACTC</u>
LIC -S/ACS4-For	<u>CGACGACAAGACCCTCTCCACTTCACTAACG</u>
LIC -S/ACS4-Rev	<u>GAGGAGAAGAGCCCTGCAAATCCATCCAACAAATA</u>

Note: The nucleotides underlined are LIC sequences.

References

1. Giovannoni, J. J. *et al.* Molecular genetic analysis of theripening-inhibitor andnon-ripening loci of tomato: A first step in genetic map-based cloning of fruit ripening genes. *Mol. Gen. Genet.* **248**, 195-206 (1995).
2. Martel, C., Vrebalov, J., Tafelmeyer, P. & Giovannoni, J. J. The tomato MADS-box transcription factor RIPENING INHIBITOR interacts with promoters involved in numerous ripening processes in a COLORLESS NONRIPENING-dependent manner. *Plant Physiol.* **157**, 1568-1579 (2011).
3. Li, J.-b. & Luan, Y.-s. Molecular cloning and characterization of a pathogen-induced WRKY transcription factor gene from late blight resistant tomato varieties Solanum pimpinellifolium L3708. *Physiol. Mol. Plant P.* **87**, 25-31 (2014).
4. Liu, B. *et al.* Tomato WRKY transcriptional factor SIDRW1 is required for disease resistance against Botrytis cinerea and tolerance to oxidative stress. *Plant Sci.* **227**, 145-156 (2014).
5. Molan, Y. & El-Komy, M. Expression of SI-WRKY1 transcription factor during B. cinerea tomato interaction in resistant and susceptible cultivars. *International Journal of Plant Breeding and Genetics* **4**, 1-12 (2010).
6. Bhattacharai, K. K., Atamian, H. S., Kaloshian, I. & Eulgem, T. WRKY72-type transcription factors contribute to basal immunity in tomato and Arabidopsis as well as gene-for-gene resistance mediated by the tomato R gene Mi-1. *Plant J* **63**, 229-240 (2010).
7. Atamian, H. S., Eulgem, T. & Kaloshian, I. SIWRKY70 is required for Mi-1-mediated resistance to aphids and nematodes in tomato. *Planta* **235**, 299-309 (2012).
8. Huang, S. *et al.* Genome-wide analysis of WRKY transcription factors in Solanum lycopersicum. *Mol. Genet. Genomics* **287**, 495-513 (2012).
9. Consortium, T. G. The tomato genome sequence provides insights into fleshy fruit evolution. *Nature* **485**, 635-641 (2012).
10. Robatzek, S. & Somssich, I. E. A new member of the Arabidopsis WRKY transcription factor family, AtWRKY6, is associated with both senescence - and defence - related processes. *Plant J* **28**, 123-133 (2001).
11. Robatzek, S. & Somssich, I. E. Targets of AtWRKY6 regulation during plant senescence and pathogen defense. *Genes Dev.* **16**, 1139-1149 (2002).
12. Chen, L., Zhang, L. & Yu, D. Wounding-induced WRKY8 is involved in basal defense in Arabidopsis. *Mol. Plant-Microbe In.* **23**, 558-565 (2010).
13. Potschin, M., Schlienger, S., Bieker, S. & Zentgraf, U. Senescence networking: WRKY18 is an upstream regulator, a downstream target gene, and a protein interaction partner of WRKY53. *J Plant Growth Regul.* **33**, 106-118 (2014).
14. Zhou, X., Jiang, Y. & Yu, D. WRKY22 transcription factor mediates dark-induced leaf senescence in Arabidopsis. *Mol. Cells* **31**, 303-313 (2011).
15. Besseau, S., Li, J. & Palva, E. T. WRKY54 and WRKY70 co-operate as negative regulators of leaf senescence in Arabidopsis thaliana. *J Exp Bot* **63**, 2667-2679, doi:10.1093/jxb/err450 (2012).
16. Li, G. *et al.* Dual-level regulation of ACC synthase activity by MPK3/MPK6 cascade and its downstream WRKY transcription factor during ethylene induction in Arabidopsis. *PLoS Genet.* **8** (2012).
17. Hinderhofer, K. & Zentgraf, U. Identification of a transcription factor specifically expressed at the onset of leaf senescence. *Planta* **213**, 469-473 (2001).

18. Miao, Y., Laun, T., Zimmermann, P. & Zentgraf, U. Targets of the WRKY53 transcription factor and its role during leaf senescence in Arabidopsis. *Plant Mol. Biol.* **55**, 853-867 (2004).
19. Miao, Y., Smykowski, A. & Zentgraf, U. A novel upstream regulator of WRKY53 transcription during leaf senescence in Arabidopsis thaliana. *Plant Biol.* **10**, 110-120 (2008).
20. Jiang, Y., Liang, G., Yang, S. & Yu, D. Arabidopsis WRKY57 functions as a node of convergence for jasmonic acid-and auxin-mediated signaling in jasmonic acid-induced leaf senescence. *Plant Cell* **26**, 230-245 (2014).
21. Ulker, B., Shahid Mukhtar, M. & Somssich, I. E. The WRKY70 transcription factor of Arabidopsis influences both the plant senescence and defense signaling pathways. *Planta* **226**, 125-137 (2007).
22. Li, Z., Peng, J., Wen, X. & Guo, H. Gene network analysis and functional studies of senescence-associated genes reveal novel regulators of Arabidopsis leaf senescence. *J Integr. Plant Biol.* **54**, 526-539 (2012).
23. Jing, S., Zhou, X., Song, Y. & Yu, D. Heterologous expression of OsWRKY23 gene enhances pathogen defense and dark-induced leaf senescence in Arabidopsis. *Plant Growth Regul.* **58**, 181-190 (2009).
24. Liu, X., Bai, X., Wang, X. & Chu, C. OsWRKY71, a rice transcription factor, is involved in rice defense response. *J Plant Physiol.* **164**, 969-979 (2007).
25. Ricachenevsky, F. K., Sperotto, R. A., Menguer, P. K. & Fett, J. P. Identification of Fe-excess-induced genes in rice shoots reveals a WRKY transcription factor responsive to Fe, drought and senescence. *Mol. Biol. Rep.* **37**, 3735-3745 (2010).
26. Zhang, S.-L. et al. GbWRKY1, a novel cotton (*Gossypium barbadense*) WRKY gene isolated from a bacteriophage full-length cDNA library, is induced by infection with *Verticillium dahliae*. (2012).
27. Wang, X. et al. GhWRKY40, a multiple stress-responsive cotton WRKY gene, plays an important role in the wounding response and enhances susceptibility to *Ralstonia solanacearum* infection in transgenic *Nicotiana benthamiana*. *PloS one* **9**, e93577 (2014).
28. Yang, B., Jiang, Y., Rahman, M. H., Deyholos, M. K. & Kav, N. N. Identification and expression analysis of WRKY transcription factor genes in canola (*Brassica napus* L.) in response to fungal pathogens and hormone treatments. *BMC Plant Biol.* **9**, 68 (2009).
29. Zhang, Z., Zhang, H., Quan, R., Wang, X.-C. & Huang, R. Transcriptional regulation of the ethylene response factor LeERF2 in the expression of ethylene biosynthesis genes controls ethylene production in tomato and tobacco. *Plant Physiol.* **150**, 365-377 (2009).
30. Guo, F., Zhou, W., Zhang, J., Xu, Q. & Deng, X. Effect of the citrus lycopene β -cyclase transgene on carotenoid metabolism in transgenic tomato fruits. *PloS one* **7**, e32221 (2012).