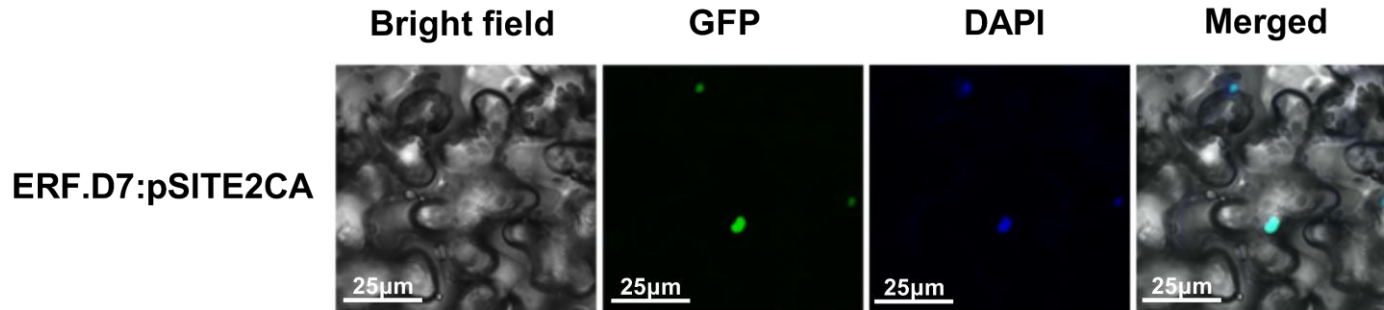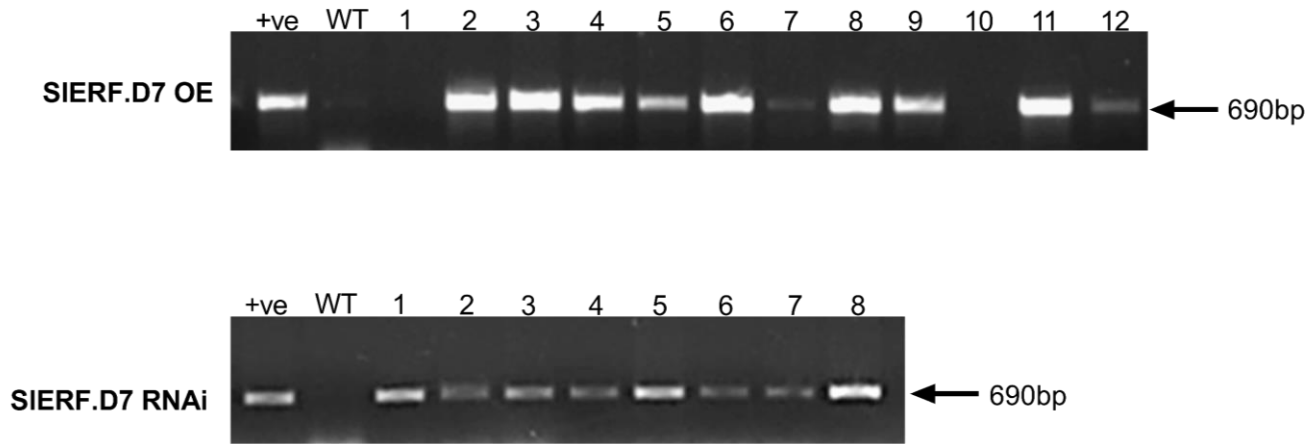**Figure S1**

Supplemental Figure S1 DAPI staining of SIERF.D7 in *Nicotiana benthamiana*. Subcellular localization of SIERF.D7 in *Nicotiana benthamiana* leaves. The fusion construct (*SIERF.D7-pSITE-2CA*) were transiently expressed in 4-week-old *N. benthamiana* leaves by agroinfiltration and all images were collected under the Leica confocal microscope after agroinfiltration for 48 h. Additional DAPI and the Merged panel for Fig.1D indicates the nuclear staining.
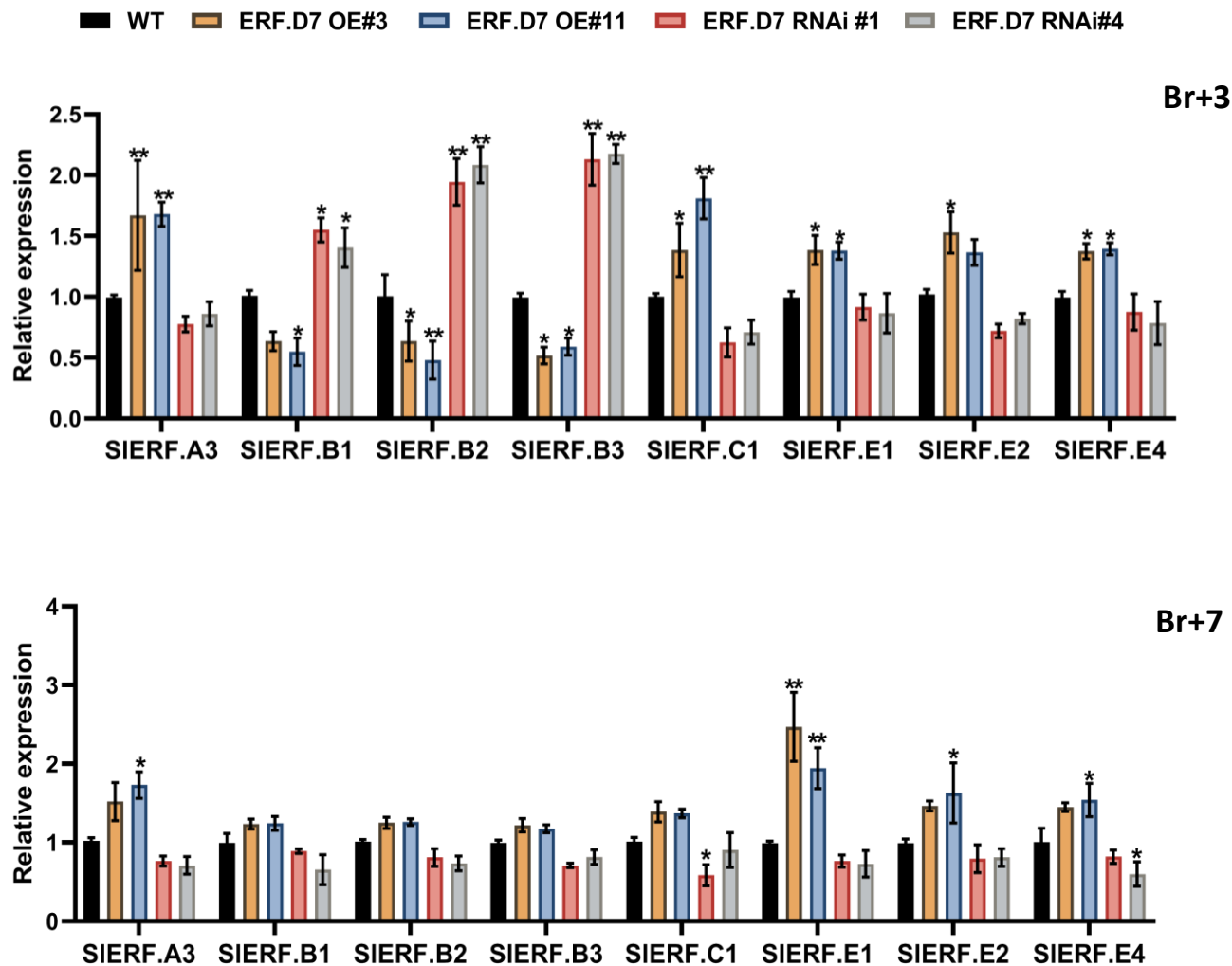
Figure S2

Figure S2. Kanamycin based PCR screening of *SlERF.D7* overexpression and silencing lines. The presence of transgene in the T2 transgenic lines was confirmed with PCR using *nptII* gene specific primers.

Figure S3

Figure S3 Phenotypic time-line of ethrel-treated and non-treated control fruits from mature green to red ripe stage. Mature green fruits from WT plants were injected a buffer solution containing 10 mM MES, pH 5.6, sorbitol (3% w/v) and 100 μM Ethrel (2-Chloroethylphosphonic Acid, 40% Solution, SRL Diagnostics). After the treatment, fruits were incubated in a culture room at 26°C, under a 16 h light/8 h dark cycle with a light intensity of 100 μmol m-2 s-1 and photographed for 7 days. The Br+7 panel for air and ethrel treated fruits are same as that of WT panel in Fig.6B.

Figure S4

Figure S4 The expression of ERF genes in wild type and *SIERF.D7 OE* and *SIERF.D7 RNAi* plants. RT-qPCR relative expression of *SIERF* genes in wild-type (WT) and *SIERF.D7* OE and RNAi tomato fruits at 3-day after Br (Br+3) and 7-day after Br (Br+7) with *Actin* gene as an internal control. Error bar means ±SD of three biological replicates. Asterisks indicate the statistical significance using Student's t-test: *, 0.01 < P-value < 0.05; **, 0.001 < P-value < 0.01..
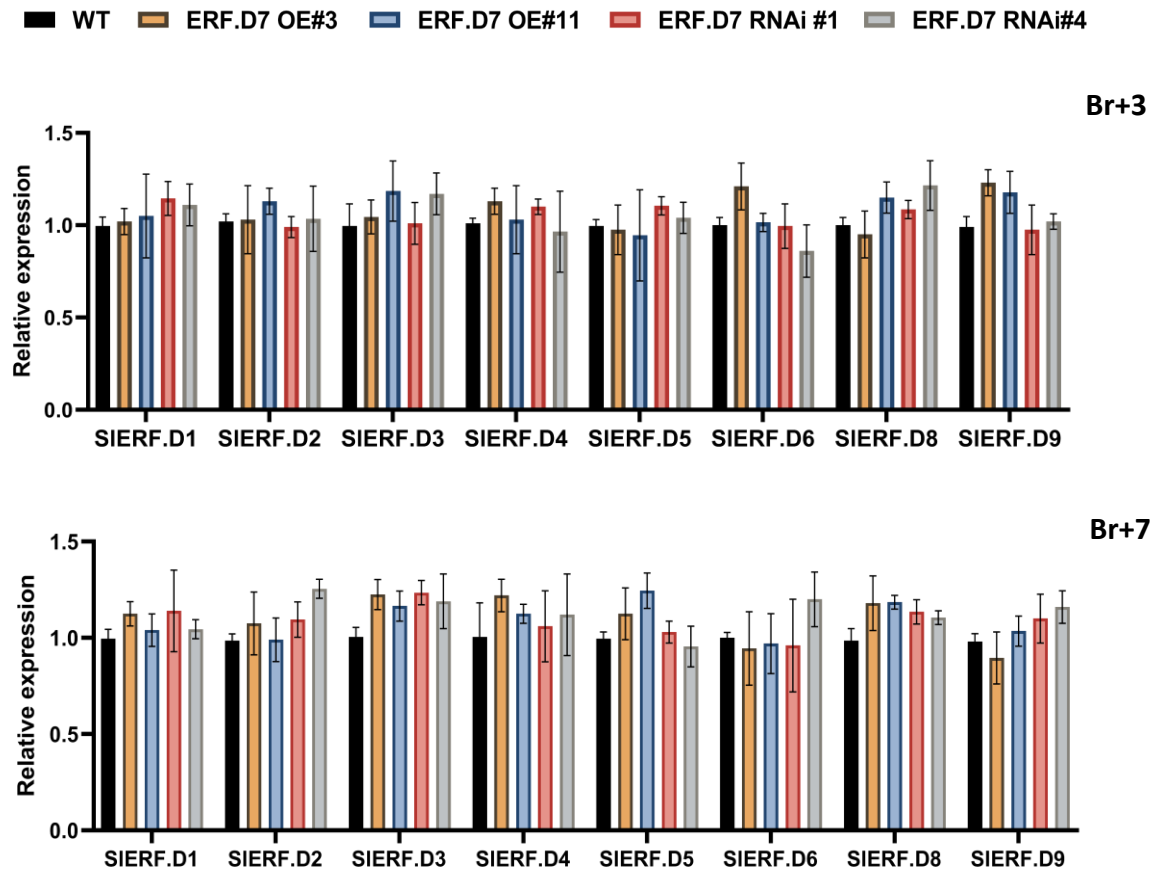
Figure S5 The expression of ERF.D clade genes in wild type and *SlERF.D7 OE* and *SlERF.D7 RNAi* plants.

RT-qPCR relative expression of SIERF.D clade gene members in wild-type (WT) and SIERF.D7 OE and RNAi tomato fruits at 3-day after Br (Br+3) and 7-day after Br (Br+7) with Actin gene as an internal control. Error bar means ±SD of three biological replicates.
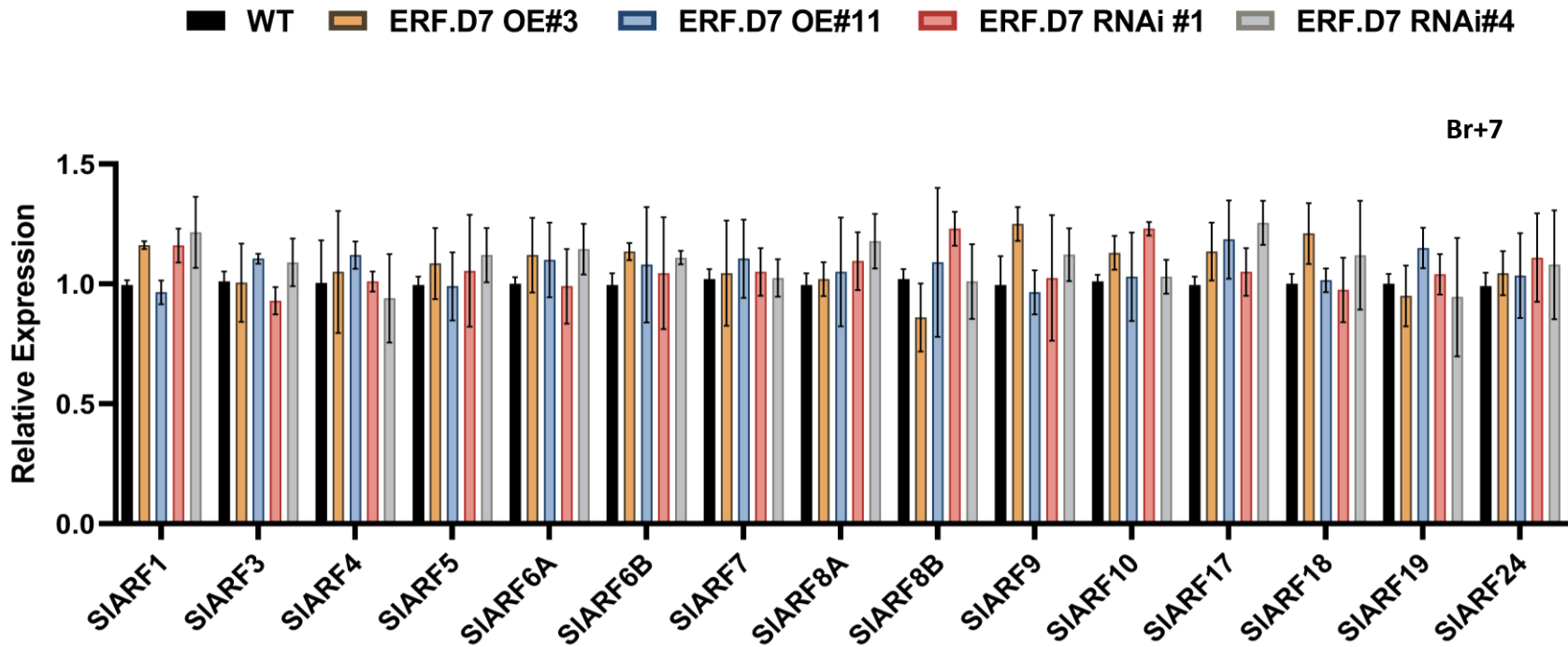
Figure S6

Figure S6 The expression of tomato *ARF* genes (Kumar et al., 2015) in wild-type and *SlERF.D7 OE* and *SlERF.D7 RNAi* plants. RT-qPCR relative expression of the selected *ARF* gene family members in wild-type (WT) and SlERF.D7 OE and RNAi tomato fruits at 7-day after Br (Br+7) with Actin gene as an internal control. Error bar means ±SD of three biological replicates.

.

Table S1

Gene name	Primer Sequence
SlERF.D7 (RT)	F 5'-CGATCTCAACATGACATGTC-3'
	R 5'-CTGAGGAGGAATCACCACTAGC-3'
SlERF.D7 TOPO	F 5'-CACCATGAAAAGATCAAGCTCTAAT-3'
	R 5'-CTATTTAGTTCCACCACTTGAAG-3'
SAUR68	F 5'-AGACAACACCACTGTTCTTTC-3'
	R 5'-GCCTTGAGAAACTTACTGTCC-3'
E8	F 5'-TGGCTCCGAATCCTCCCAGTCT-3'
	R 5'-GTCCGCCTCTGCCACTGAGC-3'
SlERF.D7pro	F 5'-TGCCTGAATTGTTGTTTGCCAGCT-3'
	R 5'CTTCTTTTGTTTTATTTCATATGG-3'
ACS2pro	F 5'-GGAAACTTCCTGTAACACAAAG-3'
	R 5'-TGTGAGGGATATATATAAGGGGA-3'
ACO1pro	F 5'-GATTTCAATATATACGACATAAATTTG-3'
	R 5'-AAAGGCATGAGATGTCAATATTTC-3'
SlERF.D7 OE	F 5'-ggatccATGAAAAGATCAAGCTCTAAT-3'
	R 5'-ggtaccCTATTTAGTTCCACCACTTGAAG-3'
SlERF.D7 RNAi	F 5'-ATGACATGTCTGCTATGGTTTCTGCTC
	R 5'-CGATATTATTGTCAGTACGAAGTAA
ACO1	F 5'-GCCAAAGAGCCAAGATTTGA-3'
	R 5'-TTTTTAATTGAATTGGGATCTAAGC-3
ACS2	F 5'-TGTTAGCGTATGTATTGACAACTGG-3'
	R 5'-TCATAACATAACTTCACTTTTGCATTC-3'
ACS4	F 5'-CTCCTCAAATGGGGAGTACG-3'
	R 5'-TTTTGTTTGCTCGCACTACG-3'
EIN2	F 5'-GTGTGCTGAATAAGTTTAGTGGAG-3'
	R 5'-TGCTGTACAATAGAAGAATGGAGG-3'
EIL2	F 5'-TGAAGATGATGGAAGTCTGTAAGG-3'
	R 5'-CCACTCCCTGAGATTATCCGA-3'
ETR2	F 5'-TTGGAGGAATCAATGAGGGC-3'
	R 5'-TCATTACGCGCACGAACAG-3'
ETR3	F 5'-TGCTGTTCGTGTACCGCTTT-3'
	R 5'-TCATCGGGAGAACCAGAACC-3'
ETR4	R 5'-TGGAGGAGTGAGTGTGGATGC-3'
	F 5'-ATGGCTGTCGTTCTTGGGC-3'
ETR5	F 5'-GTGCTCTGGGCCCTTCACTA-3'

	R 5'-GAACTTACGCACCCTCAATGC-3'
PSY1	F 5'-GGAAAGCAAACTAATAATGGACGG-3'
	R 5'-CCACATCATAGACCATCTGTTCC-3'
PDS	F 5'-GGTCACAAACCGATACTGCT-3'
	R 5'-AAACCAGTCTCGTACCAATCTC-3'
ZDS	F 5'-AGTGGTTTCTGTCTAAAGGTGG-3'
	R 5'-ACCGAGCACTCATGTTATCAC-3'
β-LCY1	F 5'-GTCCACTTCCAGTATTACCTCAG-3'
	R 5'-TGTCCTTGCCACCATATAACC-3'
β-LCY2	F 5'-CGGGTTATATGGTAGCAAGGA-3'
	R 5'-CAGATGCCGATAACTCATTACC-3'
CYC-β	F 5'-TGTTATTGAGGAAGAGAAATGTGTGAT-3'
	R 5'-TCCCACCAATAGCCATAACATTTT-3'
PG2a	F 5'-TCAAGGGCACAAGTGCAACAAAGG-3
	R 5'-TGCACGTAGCCTCTGATGGTTT-3'
RIN	F 5'-ATGCAGCACCATCAACACAT-3'
	R 5'-CTCCAAATTCAAAGCATCCA-3'
NOR	F 5'-AGAGAACGATGCATGGAGGTTTGT-3'
	R 5'-ACTGGCTCAGGAAATTGGCAATGG-3'
CNR	F 5'-GCCAAATCAAGCAATGATGA-3'
	R 5'-TCGCAACCATACAGACCATT-3'
AP2a	F 5'-AACGGACCACAATCTTGAC-3'
	R 5'-CTGCTCGGAGTCTGAACC-3'
TAGL1	F 5'-ACTTTCTGTTCTTTGTGATGCT-3'
	R 5'-TTGGATGCTTCTTGCTGGTAG-3'
FUL1	R 5'-GTTTTGCCACAACAACTGGACTC-3'
	R 5'-CTTGCTGCTGTGAAGAACTACC-3'
FUL2	F 5'-AATGGAGAAGTAGAAGGATCATCG-3'
	R 5'-GATAACATAATATTGTCCGCTTGC-3
ARF2A	F 5'-GCAAGGTCAAGAGTTATCGA-3'
	R 5'-CATTGGTTTCTGAGACAAGTC-3'
ARF2B	F 5'-TTTAACGAGTATCCAACCTTCC-3'
	R 5'-GGGTTTAGGCATAATTTCTCCA-3'
ARF2Apro	F 5'-ATATTCTTTATGTTCATTTTGGT-3'
	R 5'-TTGAGGGAAAGAGGGAGAGCC-3'
ARF2Bpro	F 5'-ATATTATGATAAAAATATTATGAAT-3'
	R 5'-TTCGTAAACACATACACTCAACGC-3'
ARF2A VIGS	F 5'-tctagaATGGCTGCTTCGGAGGTGTCGAT-3'
	R 5'-gaattcATTCACAACACGGCATAGAATC-3'

ARF2B VIGS	F 5'-ctcgagCCTTGCTACAGCTTGGCATGC-3'
	R 5'-gagctcCGGTCTGGCCTAGGAATAGCAG-3,
SlERF.D1	F 5'-GGCAGCTGAAATAAGAGATCCATATAA-3'
	R 5'-CTAGCAGCCCCTTCAGCAGTAT-3'
SlERF.D2	F 5'-ACACAAGTAGCACCAGCACCACTA-3'
	R 5'-ACCCCAAAAAAAGCAAGAAAATT-3'
SlERF.D3	F 5'-ATTCATTTTCGGGTTGTGCAGTA-3'
	R 5'-CGACTATAATGATTTCTGCCGAACT-3'
SlERF.D4	F 5'-GTTGCTGCTTTAACCAATGTGATTAT-3'
	R 5'-CTTCCGGTACGCGAAACAAG-3'
SlERF.A3	F 5'-GCGAAATGGATCAACAGTTACCA-3'
	R 5'-ATTAGACGACTGAAGCTTGAATTCC-3'
SlERF.B1	F 5'-GAATGATGACGGAATTGTAATGAAGA-3'
	R 5'-TTCCACAATCCCAAATTGAAGA-3'
SlERF.B2	F 5'-AGTTTGCAGCGGAGATTCGT-3'
	R 5'-TGCCCTGTCATATGCCTTTG-3'
SlERF.B3	F 5'-CGGAGATAAGAGATCCAAGTCGAA-3'
	R 5'-CTTAAACGCTGCACAATCATAAGC-3'
SlERF.E1	F 5'-GTTCCTCTCAACCCCAAACG-3'
	R 5'-TTCATCTGCTCACCACCTGTAGA-3'
SlERF.E2	F 5'-ACTTCGTGAGGAAACCCTGAAC-3'
	R 5'-GTTACTAATATAAGTCATGTTGGGCTGAA-3'
SlERF.E4	F 5'-AGGCCAAGGAAGAACAAGTACAGA-3'
	R 5'-CCAAGCCAAACGCGTACAC-3'
SlActin	F 5'-TGTCCCTATTTACGAGGGTTATGC-3'
	R 5'-CAGTTAAATCACGACCAGCAAGAT-3'
SlGAPDH	F 5'- CTCCCACAACTTAACGGCAAA-3'
	R 5'-AAGATCGACAACGGAGACATCAG-3'
SlARF1	F 5'- TCTCCTTCATCATTCTCATACTG-3'
	R 5'- GAACCATTCTCACCATAACC-3'
SlARF3	F 5'- AATTGCACTATCAGACTTTGG-3'
	R 5'- TCTAGATATCCCAGAACTAGGA-3'
SlARF4	F 5'- CATTATTGTTGGTGACTTTGTG- 3'
	R 5'- GACCTTTGGAAACCTATTGG- 3'
SlARF5	F 5'- CCTTCAGAGTTTGTCATTCCT- 3'
	R 5'- AACATCATTCCAAATCTCATACC- 3'
SlARF6A	F 5'- CCAACATATCCCTAGTACTTCAG- 3'
	R 5'- GTGCCTGAGATATTAGTTGGT-3'
SlARF6B	F 5'- ACCCTCTAGTATCTTCATCCT- 3'

	R 5'-TCCGAGACCTTTGTATTGTG-3'	
SlARF7	F 5'- TCAACTCCTCAAACATACCT-3'	
	R 5'- TGAACTATCCAAATAATCCATCTG-3'	
SlARF8A	F 5'- TGACATCGAATGGAAATTCAG- 3'	
	R 5'- GTCTCTTAGCACTAACAAACAC-3'	
SlARF8B	F 5'- GTCAGTCCGTGATGATAGAG-3'	
	R 5'- GGAATCCAACCTACAATTTCC-3'	
SlARF9	F 5'- ATCATTCAATCTCAAATCAAAGGT-3'	
	R 5'- CCTCATCATTGTCTTCTTCAG-3'	
SlARF10	F 5'- ATTCTCTGTGCCTAGATACTG-3'	
	R 5'- CTATAAATGTGCCTAAACTTCCA-3'	
SlARF17	F 5'- TGAAGTTGATGAAGTTACTATGAG-3'	
	R 5'- TCCTCCATTATTCGCATCTG-3'	
SlARF18	F 5'- AATCTACACTCGGCATTGTC-3'	
	R 5'- AAGCTTCCTATCTTATCATTGGA-3'	
SlARF19	F 5'- TGGTGGATGAATCTGTTGTC-3'	
	R 5'- TACTTAGACAGCTCTGAACCT-3'	
SlARF24	F 5'- TCATTGTTGGATGTTTCAAAGG-3'	
	R 5'- GAAGTGTTGGAAAGTAGTATACTC-3'	

Table S1 List of primers used in this study.

Table S2

Plant Identity	Number of Seeds				Chi square values at Dof	P value
	Inoculated	Germinated	Resistance to Kanamycin	Susceptible to Kanamycin		
pCAMBIA2300Rip1::SlERF.D7 OE						
SlERF.D7 OE 1	33	33	30	3	0.4	0.80>p>0.50
SlERF.D7 OE 2	59	57	46	11	0.99	0.50>p>0.20
SlERF.D7 OE 3	64	64	54	10	3	0.20>p>0.05
SlERF.D7 OE 4	44	44	38	8	1.6	0.50>p>0.20

SlERF.D7 OE 5	42	42	30	12	0.29	0.80>p>0.50
SlERF.D7 OE 6	44	39	28	10	0.06	0.95>p>0.80
SlERF.D7 OE 7	64	64	54	10	3	0.20>p>0.05
SlERF.D7 OE 8	44	44	38	8	1.6	0.50>p>0.20
SlERF.D7 OE 9	49	46	39	7	2.3	0.20>p>0.05
SlERF.D7 OE 10	40	40	39	1	2.3	0.20>p>0.05
SlERF.D7 OE 11	39	36	29	7	0.59	0.50>p>0.20
SlERF.D7 OE 12	36	36	27	9	0	exact fit
pBI121Rip1::SlERF.D7 RNAi						
SlERF.D7 RNAi 1	44	43	35	8	0.94	0.50>p>0.20
SlERF.D7 RNAi 2	46	46	38	8	1.4	0.50>p>0.20
SlERF.D7 RNAi 3	40	40	28	12	0.53	0.50>p>0.20
SlERF.D7 RNAi 4	64	64	54	10	3	0.20>p>0.05
SlERF.D7 RNAi 5	40	40	39	1	2.3	0.20>p>0.05
SlERF.D7 RNAi 6	52	51	44	7	3.45	0.20>p>0.05
SlERF.D7 RNAi 7	49	46	39	7	2.3	0.20>p>0.05
SlERF.D7 RNAi 8	40	37	29	8	0.23	0.50>p>0.20

Table S2 Segregation analysis of kanamycin resistance in T_2 generation of *SlERF.D7 OE* and *SlERF.D7* RNAi transgenic tomato plants.Segregation analysis of the transgene was carried out by using all the fruiting transgenic lines. The inheritance and segregation of the transgene lines were analyzed by the expression and presence of the *nptII* gene in transgenic plants. Seven-day-old seedlings were grown on 1/2X MS medium containing 500mg/l kanamycin and were observed. Seedlings positive for transgene remained green, while segregated non-transformants seedlings underwent chlorosis and died. For each transgenic line, segregation ratios were calculated by calculating the number of kanamycin-resistant and kanamycin-sensitive seedlings.