

Supplementary Materials

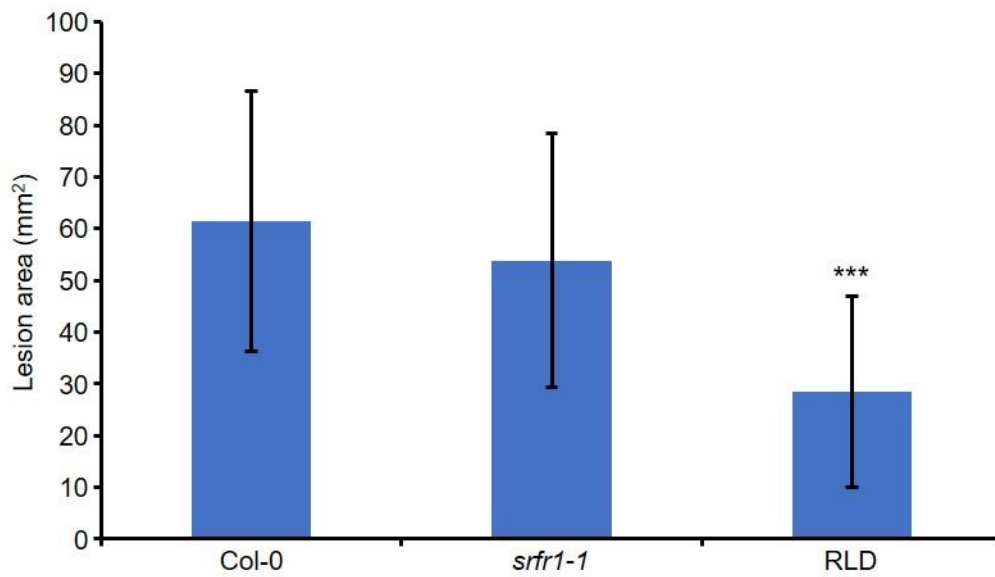
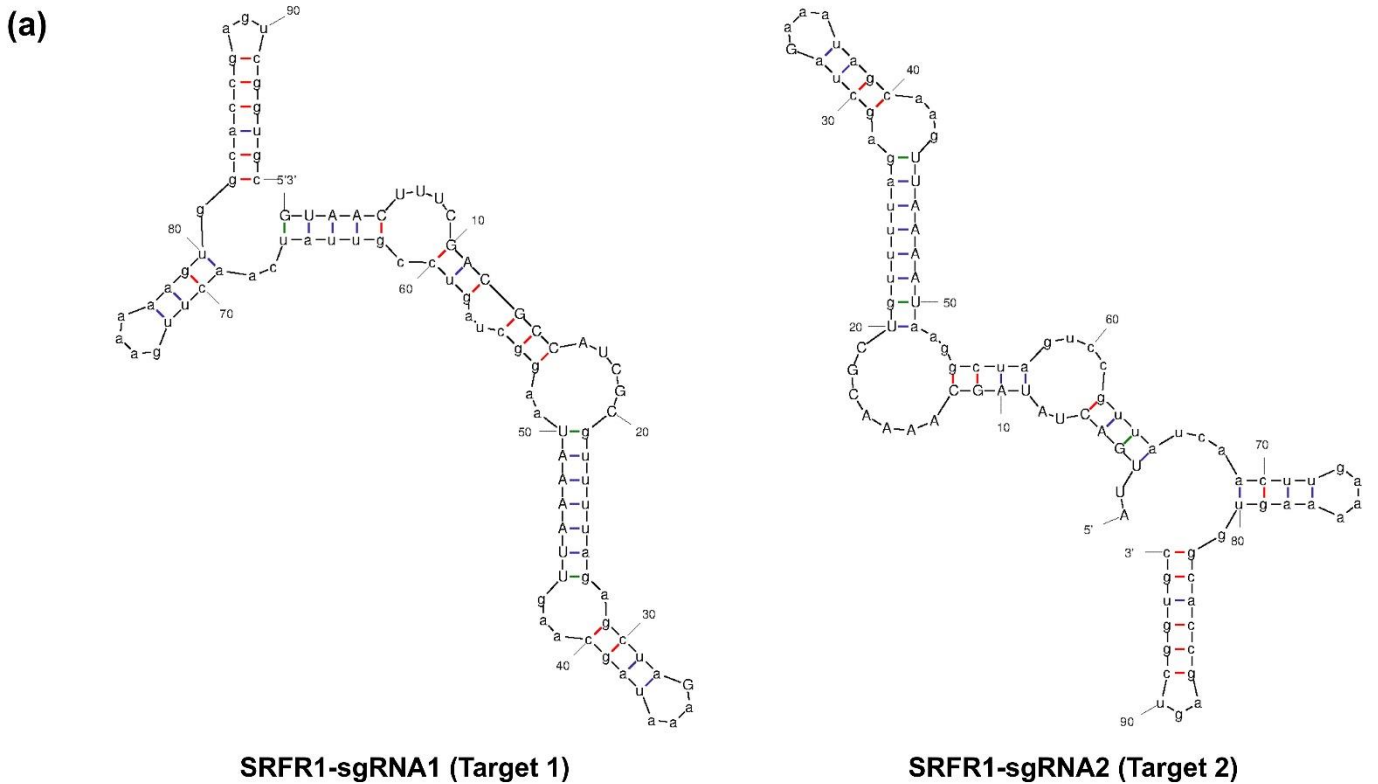


Figure S1. The *Arabidopsis srfr1-1* mutant displays increased susceptibility to a South African pepper isolate of *Botrytis cinerea*. Detached leaves from 4-week-old plants grown under a 16 h light/8 h dark cycle at 22 °C were inoculated at dawn with 10 µL of half-strength grape juice containing 5×10^4 *B. cinerea* (pepper isolate) spores mL⁻¹ and lesion areas measured after 72 h using ImageJ. Data shown are mean lesion sizes \pm standard deviation from 48 (Col-0), 47 (*srfr1-1*) and 41 (RLD) detached leaves. Asterisks denote a significant difference of values for RLD compared to those for Col-0 and *srfr1-1* at *** $p < 0.0001$ as determined by Tukey's HSD test.

Rice	:	-----MGRRAELARWGGGRNMSKAIIRILDALHARSPTSIMHLCNRAFICYQLELHKHHVVKDCDRAILDLPAALQAYITKGRALSALGKKEEALINWQGYHVAVEHOSADLKQLELEEL	:	115
Arabidopsis	:	MATAITATSERRELAKHOSGRNMSKAIIRVLDLSLAK-ESSILDICNRAFICYQLELHKHHVVKDCDRAILDLPAALQAYITKGRALSALGKKEEALINWQGYHVAVEHOSADLKQLELEEL	:	119
Tomato	:	--MAKVTIDRELAKICSSKEWSKAIIRILDSLLAQ-TCVVIDICNRAFICYQLELHKHHVVKDCDRAILDLPAALQAYITKGRALSALGKKEEALINWQGYHVAVEHOSADLKQLELEEL	:	117
Potato	:	--MASTVTDRELAKICSSKEWSKAIIRILDSLLAQ-TCVVIDICNRAFICYQLELHKHHVVKDCDRAILDLPAALQAYITKGRALSALGKKEEALINWQGYHVAVEHOSADLKQLELEEL	:	117
Pepper	:	--MTKVTIDRELAKICSSKEWSKAIIRILDSLLAQ-TCVVIDICNRAFICYQLELHKHHVVKDCDRAILDLPAALQAYITKGRALSALGKKEEALINWQGYHVAVEHOSADLKQLELEEL	:	117
Rice	:	VSSVTCICETICEELRVLDASPCDK-----VVSIDRVVDTSCTATMAITATTVVTEENICNSGVISNCAVILLANDN-----KADN	:	191
Arabidopsis	:	IMDARRRIDGILKSATSPQETPA---YHSS--KSDP-----KSDKIDNHESSASSNGNSHESSEFGEOSKIVSPKSVASASKQSDGNSDLNCGSVYKPKENGKCGSITNGYYES	:	227
Tomato	:	LKIAKONTAVGSNNHVSQSSGPESNTGPIITST--KSGETODISKASDRFKTSSCGMLSESEKKNSSVVLONS-----SNNKSKHKKIHESSEK-----LEE-----RQANRTNN	:	217
Potato	:	LKIAKONTAVASNNHVSQSSGPESNTGPIITST--KSGETODISKASDRFKTSSCGMLSESEKKNSSVVLONS-----SNNKSKHKKIHESSEK-----LEE-----RQANRTNN	:	217
Pepper	:	LKIAKONTAPAVNDNLVSSSGPESNTGPIITSA--KSVETODISKASDRFKTSSCGMLSESEKKNSSVVLONS-----SKNAKHKKIKERKSDN-----FHE-----RQANRTNN	:	217
Rice	:	NKECSSPTKDTTGHHTPKKTTTPDK-----KSKAKGRKINSOTETVAL-SSSGETVAVDTTLFASKISKSKSISLDFRLSRGIAQVNEGKYNAVAISIFDQITREPTTYPEALIG	:	303
Arabidopsis	:	CPKCMG-----SDTHNLAE-----SDRFCEL--GINGNKISIKSSKSHAEACGCHSDPSRNNKYITARIS-CHSISVDFRLSRGIAQVNEGNYTPAISIFDQITREPTTYPEALIG	:	336
Tomato	:	CKKLGYPSLVCSRLSISEDSRKSSAVTSSESSESEFNDQITISQNNKCDVRVELSDGCKRNNKKFCVARVN-KTMSINVDFRLSRGIAQVNEGKYNAVAISIFDQITREPTTYPEALIG	:	336
Potato	:	YKKLGYPSPVCSRLSISEDSRKSSAVTSSESSESEFNDQITISQNNKCDVRVELSDGCKRNNKKFCVARVN-KTMSINVDFRLSRGIAQVNEGKYNAVAISIFDQITREPTTYPEALIG	:	336
Pepper	:	CKKVGYPSLVCSRLSISEDSRKSSAVTSSESSESEFNDQITISQNNKCDVRVELSDGCKRNNKKFCVARINSKTMSINVDFRLSRGIAQVNEGKYNAVAISIFDQITREPTTYPEALIG	:	337
Rice	:	RGTAIAFORELDAISDFTKAIQSNPSAGEAWKRRGQARAALGESPVAIEDLTALKALEFPEDSDILHERGIVN--KTKDYNAAVEDLSICVKFKDNKNSAHTYGLGLSALGEYKRAED	:	421
Arabidopsis	:	RGTAIAFORELESATDFTKAIQSNPSAGEAWKRRGQARAALGESPVAIEDLTALKALEFPEDSDILHERGIVN--KSKDPTAAVKOLSLCLKQKKNKSAHTYGLGLSALGEYKKAEE	:	454
Tomato	:	RGTAIAFORELDAISDFTKAIQSNPSAGEAWKRRGQARAALGESPVAIEDLTALKALEFPEDSDILHERGIVN--KTKDEKCAVEDLSICVKFKDNKNSAHTYGLGLSALGEYKRAEE	:	454
Potato	:	RGTAIAFORELDAISDFTKAIQSNPSAGEAWKRRGQARAALGESPVAIEDLTALKALEFPEDSDILHERGIVN--KTKDEKCAVEDLSICVKFKDNKNSAHTYGLGLSALGEYKRAEE	:	454
Pepper	:	RGTAIAFORELDAISDFTKAIQSNPSAGEAWKRRGQARAALGESPVAIEDLTALKALEFPEDSDILHERGIVNFKTKDEKCAVEDLSICVKFKDNKNSAHTYGLGLSALGEYKRAEE	:	457
Rice	:	EHLLETKYDENFDISWAHLSGLYLDTCGPFERNMNEKVLQIDVSGKAYHLRGLVTHCMGRHRSNAIKDLSVAIKHESSTIECLYLRSCHYHAIGLYKBAVKDYSDLDLELDSMKKFVL	:	541
Arabidopsis	:	EHLLETKYDSDNYLEAWHILAQFYODLANSEKALCECHLOLQIDVSNVVKAYHLRGLVTHCMGRHRSNAIKDLSVAIKHESSTIECLYLRSCHYHAIGLYKBAVKDYSDLDLELDSMKKFVL	:	573
Tomato	:	EHKKAIOIERNFLEAWHILAQFYODLANSEKALCECHLOLQIDVSNVVKAYHLRGLLTHCMGHERNAIKDLSMGLSDSANIECLYLRSCHYHAIGLYKBAVKDYSDLDLELDSMKKFVL	:	574
Potato	:	EHKKAIOIERNFLEAWHILAQFYODLANSEKALCECHLOLQIDVSNVVKAYHLRGLLTHCMGHERNAIKDLSMGLSDSANIECLYLRSCHYHAIGLYKBAVKDYSDLDLELDSMKKFVL	:	574
Pepper	:	EHKKAIOIERNFLEAWHILAQFYODLANSEKALCECHLOLQIDVSNVVKAYHLRGLLTHCMGHERNAIKDLSMGLSDSANIECLYLRSCHYHAIGLYKBAVKDYSDLDLELDSMKKFVL	:	577
Rice	:	OCLAFYQKEALYTASKINLRFSCFNIDLDVDPLFKFYWCKRLHPKNVCEKVYROPPIRLSLRSGRLNKQEKETKHQITLILADSDIGKTOYNCRCGFIPNRCQRMAGLAATEIAQKV	:	661
Arabidopsis	:	OCLAFYQKEALYTASKYSEFELCFDIDDIDPMLFKFYWCKRLHPKNVCEKVYROPPIRLSLRSGRLNKQEKETKHQITLILADSDIGKTOYNCRCGFIPNRCQRMAGLAATEIAQKV	:	693
Tomato	:	OCLAFYQKEALYTASKYNSEFFSWFDIDIDIDPLFKFYWCKRLHPKNVCEKVYROPPIRLSLRSGRLNKQEKETKHQITLILADSDIGKTOYNCRCGFIPNRCQRMAGLAATEIAQKV	:	694
Potato	:	OCLAFYQKEALYTASKYNSEFFSWFDIDIDIDPLFKFYWCKRLHPKNVCEKVYROPPIRLSLRSGRLNKQEKETKHQITLILADSDIGKTOYNCRCGFIPNRCQRMAGLAATEIAQKV	:	694
Pepper	:	OCLAFYQKEALYTASKYNSEFFSWFDIDIDIDPLFKFYWCKRLHPKNVCEKVYROPPIRLSLRSGRLNKQEKETKHQITLILADSDIGKTOYNCRCGFIPNRCQRMAGLAATEIAQKV	:	697
Rice	:	SKAWRTRNP-----KNNAKVRRRRKDNAC-ONRGG-YCSTSLSGSPTS-SPNEDRISGSISLWHDVYNVAVKWRQISEPCDPVVWINKLSEEFNSFGFSHTPMLLGQAKIIRY	:	770
Arabidopsis	:	SKAWR--IEWRRSTKGTITNCKNNKRRRNINISLNRRGACGCTSSSSPTSTSYSLDDRSTGRSMMSWNHLYSLAVKWRQISEPCDPVVWINKLSEEFNTGFSHTPMLVGQAKVRY	:	810
Tomato	:	SKAWRAIQAEWRNSTKGITNCKSKRLRRRKKNISLNRRGACGCTSSSSPTSTSYSLDDRSTGRSMMSWNHLYSLAVKWRQISEPCDPVVWINKLSEEFNTGFSHTPMLVGQAKVRY	:	814
Potato	:	SKAWRAIQAEWRNSTKGITNCKSKRLRRRKKNISLNRRGACGCTSSSSPTSTSYSLDDRSTGRSMMSWNHLYSLAVKWRQISEPCDPVVWINKLSEEFNTGFSHTPMLVGQAKVRY	:	814
Pepper	:	SKAWRAIQAEWRNSTKGITNCKSKRLRRRKKNISLNRRGACGCTSSSSPTSTSYSLDDRSTGRSMMSWNHLYSLAVKWRQISEPCDPVVWINKLSEEFNTGFSHTPMLVGQAKVRY	:	817
Rice	:	YBYKSVLEAAKNILMDLRYNNABDRAIELIDIEKIKKTEVASSCELELHIVGTEYVVSFRCDSINFGRRLEGTRITQ-NMCKTSFDFAIRTPCTPSRWEEYDEEMSAWEAICAY	:	889
Arabidopsis	:	FPNFORILTIKAKITIDKLSVRSKOKVIDLSKDEKIKETNRAFTTDELENIVGETFWVATWCDSTSGSEGKRLGTRITQKBERGYDFAIRTPCTPSRWEEYDEEMSAWEALCAY	:	930
Tomato	:	FPNFORILTIKAKVIKENKSVCKNKEDRIIDLEPOOKIQETMAAESSDLIRVVGOFWLATWCNSALPEGKRLGTRITVW-KMGEGYDFAIRTPCTPSRWEEYDEEMSAWEALCAY	:	933
Potato	:	FPNFORILTIKAKVIKENKSVCKNKEDRIIDLEPOOKIQETMAAESSDLIRVVGOFWLATWCNSALPEGKRLGTRITVW-KMGEGYDFAIRTPCTPSRWEEYDEEMSAWEALCAY	:	933
Pepper	:	FPNFORILTIKAKVIKENKSVCKNKEDRIIDLEPOOKIQETMAAESSDLIRVVGOFWLATWCNSALPEGKRLGTRITVW-KMGEGYDFAIRTPCTPSRWEEYDEEMSAWEALCAY	:	936
Rice	:	CSDTNPRFEDMDIAVKAAILRMITYYWNFMPLRGTAVGFIVLLGLLAAANMEYTSIPKGLQVDWEAILEDPSFVDVSKWLYPSLKIGTSWKNKPDVTSFTTGSVVAALSTY	:	1009
Arabidopsis	:	CEENYGSFDDFVLETVRDAILRMITYYWNFMPLRGTAVGFIVLLGLLAAANMEYTSIPKGLQVDWEAILEDPSFVDVSKWLYPSLKIGTSWKNKPDVTSFTTGSVVAALSTY	:	1050
Tomato	:	CEENYGSFDDFVLETVRDAILRMITYYWNFMPLRGTAVGFIVLLGLLAAANMEYTSIPKGLQVDWEAILEDPSFVDVSKWLYPSLKIGTSWKNKPDVTSFTTGSVVAALSTY	:	1053
Potato	:	CEENYGSFDDFVLETVRDAILRMITYYWNFMPLRGTAVGFIVLLGLLAAANMEYTSIPKGLQVDWEAILEDPSFVDVSKWLYPSLKIGTSWKNKPDVTSFTTGSVVAALSTY	:	1053
Pepper	:	CEENYGSFDDFVLETVRDAILRMITYYWNFMPLRGTAVGFIVLLGLLAAANMEYTSIPKGLQVDWEAILEDPSFVDVSKWLYPSLKIGTSWKNKPDVTSFTTGSVVAALSTY	:	1056
Rice	:	DT : 1011	:	
Arabidopsis	:	ND : 1052	:	
Tomato	:	SD : 1055	:	
Potato	:	SD : 1055	:	
Pepper	:	SD : 1058	:	



(b)

sgRNA	TSL (3)	GSL (0)	CBP (>7)	TBP (>12)	IBP (>6)	GC (30-80%)
SRFR1-sgRNA1	3	0	5	11	0	55
SRFR1-sgRNA2	3	0	4	9	0	35

Figure S3. Secondary structures of sgRNAs predicted using Mfold online server. (a) Target sgRNA secondary structure; (b) Parameters calculated from the predicted secondary structures of sgRNAs. TSL: total stem-loop; GSL: Stem-loop in the guide sequence; CBP: consecutive base pair (guide sequence and the other sequence); TBP: total base pairs in guide sequence with other sequences; IBP: internal base pairs in sgRNA; GC content (%) of sgRNA. Further details about the criteria available on the webpage of the CRISPR-P 2.0 tool (<http://crispr.hzau.edu.cn/CRISPR2/>).

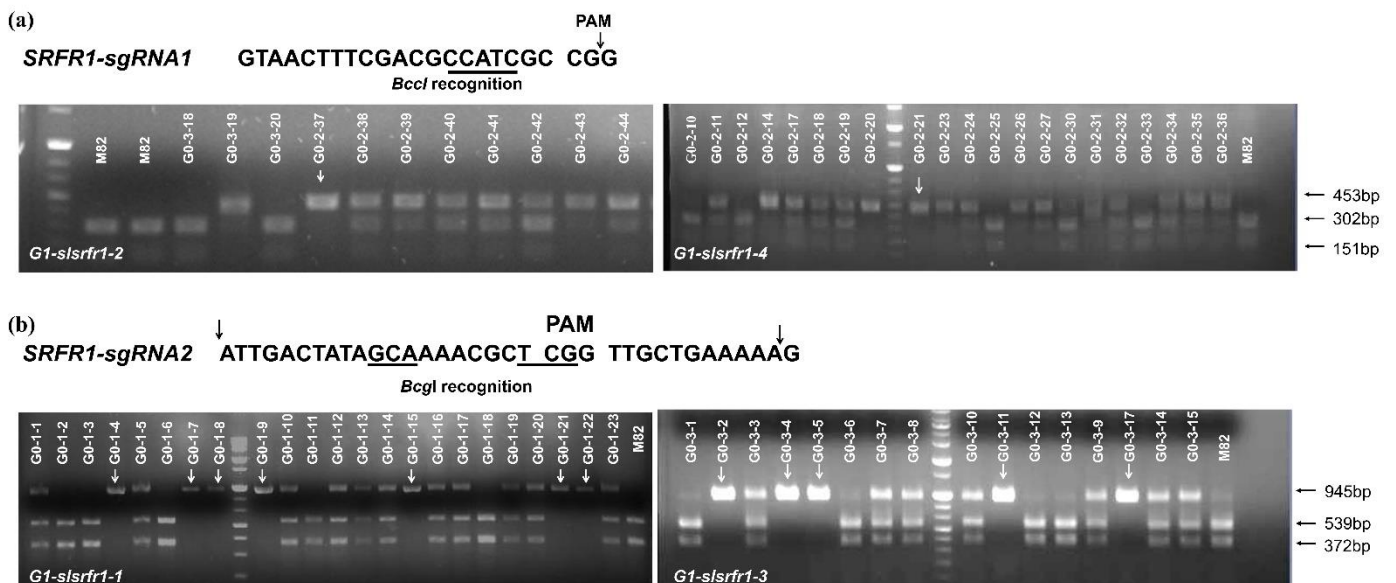




Figure S7. Plant response to *Fusarium oxysporum* f. sp. *lycopersici* in *SISRFR1* alleles. (a) Morphology of 6-week-old M82, *slsrfr1-3* and *slsrfr1-4* grown at 25 °C in 16 h light/8 h dark long-day photo-period; (b) Detached leaves from 6-week-old M82, *slsrfr1-3*, and *slsrfr1-4* were inoculated with 4 mm-diameter plugs of *F. oxysporum*. Photographs were taken at 8 DPI.

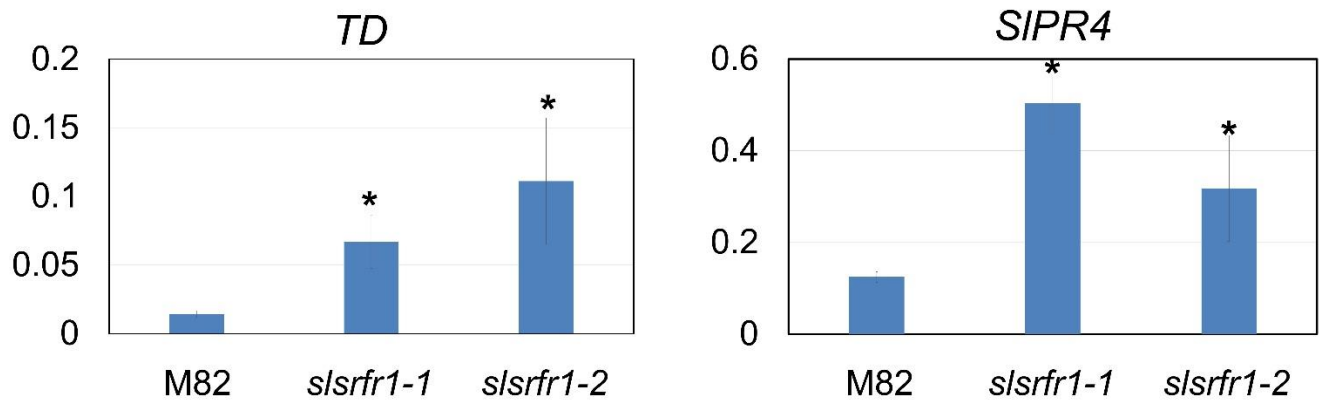


Figure S8. Expression of JA-responsive genes in CRISPR/Cas9-edited *slsrfr1* plants. The genes used for gene expression analysis refer to *TD* (*Solyc09g008670.2*) and *SIPR4* (*Solyc01g097240.2*). Gene expression levels of each gene were normalized with *SIACT* (*Solyc04g011500.3.1*) as an internal control. Error bars represent standard deviation. A statistically significant difference was determined by the Student's t-test (* $p < 0.05$).

Table S1. Genome editing contribution in *slsrfr1* G0 plants.

No.	G0 alleles	Indel frequency	Homozygote G1 plants identified from CAPS analysis	G1 alleles	Positon of editing	Type of event	Homozygote alleles/total analyzed lines
1	G0-1	60%	G0-1-4,7,8,9,15,21,22,40,41,44,54	<i>slsrfr1-1</i>	sgRNA2	-11 nt	11/57
2	G0-2	1%	G0-2-37	<i>slsrfr1-2</i>	sgRNA1	-1nt/-4nt	1/44
3	G0-3	44%	G0-3-2,4,5,11,17	<i>slsrfr1-3</i>	sgRNA2	+1 nt	5/20
4	G0-2	1%	G0-2-21	<i>slsrfr1-4</i>	sgRNA1	-32nt/-4nt	1/44

Table S2. Off-targeted data in all *SlSRFR1* alleles.

No.	off target candidates	Indel (%)					
	Alleles	sgRNA1-OFF_1	sgRNA1-OFF_2	sgRNA2-OFF_1	sgRNA2-OFF_2	sgRNA2-OFF_3	sgRNA2-OFF_4
1	<i>slsrfr1-1</i>	0	0	0	0	0	0
2	<i>slsrfr1-2</i>	0	0	0	0	0	0
3	<i>slsrfr1-3</i>	0	0	Failed	0	0	0
4	<i>slsrfr1-4</i>	0	0	0	0	0	0

Table S3. The *SRFR1* single guide RNA and target sequences used in the study.

No.	Name	gRNAs	Target position on genome	Number of off-targets (<4 MMs)
1	sgRNA1	GTAAC TTTCGACGCCATCGC	5'UTR and CDS	1
2	sgRNA2	ATTGACTATAGCAAAACGCT	CDS	3

Table S4. Potential off-targets of single guide RNAs used in this study.

Potential off-target sequence	Number of mismatch	Locus	Gene	Region
sgRNA1 : GTAAC TTTCG AAAA CATCGC				
GTAAC CTTCGAAGTC ATCGA	4	SL3.0ch08:-31939614		Intergenic
GTAAC TTTC AAGGCCATCGA	3	SL3.0ch05:+48464484		Intergenic
GAAACT TTTCG AAAA CATCGC	4	SL3.0ch08:+55060271		Intergenic
GTGA ATATCGACGCC ATCGA	4	SL3.0ch01:+65466561		Intergenic
GAAACT TTTCGACCTCATAGC	4	SL3.0ch07:+66595791		Intergenic
GTAAC TTTCGAAGGCTTTGC	4	SL3.0ch02:+35442157	gene:Solyc02g062950.3	CDS
sgRNA2 : ATTGACTATAGCAAAA ACGCT				
ATTGACTAA ACAAAAAACT	4	SL3.0ch05:+5657976		Intergenic
AATGA ATATAG AAAA AGCT	4	SL3.0ch01:-65718384		Intergenic
ATTGA ATATAG CAAAA TGTT	3	SL3.0ch03:+67920252		Intergenic
ATTGAT TATAGT AAAA ACACA	4	SL3.0ch12:+66227955	gene:Solyc12g096230.2	utr
ATT TACTA CAGCAAAA CACT	4	SL3.0ch04:-39705061	gene:Solyc04g049130.3	intron
T TAGACTATAGCA AT ACT	4	SL3.0ch09:-48437258		Intergenic
T TAGACTATAGCA AT ACT	4	SL3.0ch10:-22995255		Intergenic
ATTGACTATAGCA CAAAAAT	4	SL3.0ch10:+12194723		Intergenic
TTT GACTATAGAA ACAAGCT	4	SL3.0ch04:+62510472		Intergenic
AT GG ACTATAGCAAAA AAAT	4	SL3.0ch06:+3388631		Intergenic
ATTGA ATATACT AAAC CCCT	4	SL3.0ch11:+36073500		Intergenic
ATTGAC AATAACA AAA GGCT	3	SL3.0ch09:-46995239		Intergenic
ATTGACTATAGAA AAAGTTT	4	SL3.0ch11:+13491883		Intergenic
ATT TAGTA AAGCAAAA GGCT	4	SL3.0ch04:+7910625		Intergenic
GTT GACTATAGCAAAA ACGAC	3	SL3.0ch10:+17248976		Intergenic
ATTGACT CTAGCG AAA GGAT	4	SL3.0ch07:+13077343		Intergenic
ATTGACTAT TGCCAACCTCT	4	SL3.0ch12:-62098880		Intergenic
ATTGACTAT TCCCAATCGCT	4	SL3.0ch07:-36501993		Intergenic
A GT GACTATACCAAA TTGCT	4	SL3.0ch00:-19086437	gene:Solyc00g247300.3	CDS
A GT GACTATACCAAA TTGCT	4	SL3.0ch04:+52095679	gene:Solyc04g054257.1	CDS

The mismatched sequences are indicated by red

Table S5. Primers used in the off-target analysis.

Name	Sequences (5'→3')	Guide RNA	Potential off-target sequences
sgRNA1-OFF-1-F	GTCGTCGAATGCCTCCATCAGTC	sgRNA1 : GTAAC TTTCG AAAA CATCGC	GTAAC CTTCGAAGTC ATCGA
sgRNA1-OFF-1-R	GTTATTCACGAGTGGCGAGCAC		
sgRNA1-OFF-2-F	GTAGCTCCAGCACCATAATAAGCC		GTAAC TTTCGAAGGCTTTGC
sgRNA1-OFF-2-R	CAAGAAAAAGTCCTCGCCGC		
sgRNA2-OFF_1-F	ATCGTATTCAACATTAGCCTTACTGAGAAG	sgRNA2 : ATTGACTATAGCAAAA ACGCT	ATTGA ATATAG CAAAA TGTT
sgRNA2-OFF_1-R	AATTGCACAGGGAGGGGAAAC		
sgRNA2-OFF_2-F	TGGTAAAGAGCCTCACATGATGACC		GTT GACTATAGCAAAA ACGAC
sgRNA2-OFF_2-R	GTCTATGGGCTTGTAAGACCATTG		
sgRNA2-OFF_3-F	CGGATGCCCTAGTTCAAGGTG		ATT TACTA CAGCAAAA CACT
sgRNA2-OFF_3-R	GGAGAGATTCAATGACACTAAGAAGCTG		
sgRNA2-OFF_4-F	TTTCCAAAATCAGTTGTGTTGTAGCC		A GT GACTATACCAAA TTGCT
sgRNA2-OFF_4-R	GACGCCGATAAGTTTATGCCAGAG		

Table S6. Primers used in this study.

No.	Name	Sequence (5'-3')	Purpose
1	SISRFR1-F1	CGGTCAATAAAACACGTGTC	Genotyping
2	SISRFR1-R2	GAGCTTCATCCTACTCCTCG	Genotyping
3	SISRFR1BccI-R	GGAACAGTGAAAAACGTAAC	Genotyping
4	SISRFR1-MiSeq-1-F2	ACACTCTTTCCCTACACGACGCTCTTCCGATCTAATCGCATCAATTGAGCTGC	MiSeq
5	SISRFR1-MiSeq-1-R2	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTATGACGCAAGTTTGAGCAAG	MiSeq
6	SISRFR1-MiSeq-2-F2	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTTGGACATTTATGAATGA	MiSeq
7	SISRFR1-MiSeq-2-R2	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTAGGATCGAGCTGAAGTGCC	MiSeq
8	crU6C9-F1	CAGTCGGTCTCAGGAGTGATCAAAAGTCCCACATCGATCAGGTGATATATAGCAGCTTAGTTTA	SgRNA construction
9	crU6C9-R1	CAGTCGGTCTCACAATCGCTATGTCGACTCTATCATTATATAAACTAAGCTGCTATATATCACC	SgRNA construction
10	9gR-SISRFR1-g5-F1	CAGTCGGTCTCAATTGGTAACTTTTCGACGCCATCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAAC	SgRNA construction
11	9gR-R1	CAGTCGGTCTCAAGCGAAAAAAGCACCAGCTCGGTGCCACTTTTTCAAGTTGATAACGGACTAGCCTTATTTT	SgRNA construction
12	9gR-SISRFR1-g10-F1	CAGTCGGTCTCAATTGGATTGACTATAGCAAAACGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAAC	SgRNA construction
13	SIPR1-qRT-F	GCCATATTTCACTCTTGTGAG	qRT-PCR
14	SIPR1-qRT-R	TAGTCTGGCCTCTCGGACA	qRT-PCR
15	SIPR2-qRT-F	TCCAGGTAGAGACAGTGGTAAA	qRT-PCR
16	SIPR2-qRT-R	CTGGTTTCTTTGGTGTTCTGC	qRT-PCR
17	SIPR5-qRT-F	GCAACAACGTGCCATACACC	qRT-PCR
18	SIPR5-qRT-R	AGACTCCACCACAATCACC	qRT-PCR
19	TomloxD-qRT-F	GACAAGCAATAGCAGGAGTG	qRT-PCR
20	TomloxD-qRT-R	TAAGTGTGCCAACATCAGAC	qRT-PCR
21	SIACT-qRT-F	GAAATAGCATAAGATGGCAGACG	qRT-PCR
22	SIACT-qRT-R	ATACCCACCATCACACCAGTAT	qRT-PCR
23	SIGAPDH-qRT-F	CTGCTCTCTCAGTAGCCAACAC	qRT-PCR
24	SIGAPDH-qRT-R	CTTCCTCCAATAGCAGAGGTTT	qRT-PCR
25	TD-qRT-F	AGCTCAAACACACGCGCTGGA	qRT-PCR
26	TD-qRT-R	AACCCCCACCACCAACAGGT	qRT-PCR
27	SIPR4-qRT-F	CGATCTAAATTGATTTCATAGTACG	qRT-PCR
28	SIPR4-qRT-R	TCGTGAAGGATATACAAAATACA	qRT-PCR