

Figure S1. Validation of *HM143* by complementation. (A) Leaves of wild type(W), mutant(M), and different complemented plants (P1-P8), (B) Positive transformants were identified by detecting the presence of hygromycin marker gene. MK (Marker), P (Positive control), N (No template DNA), W (Wild type), M (Mutant), P1-P8 (different complemented plants). (C) Total chlorophyll content in IR64, *HM143* and C-HM143. Different letters indicate significant differences according to One-way ANOVA and Duncan's test ($P \leq 0.05$).

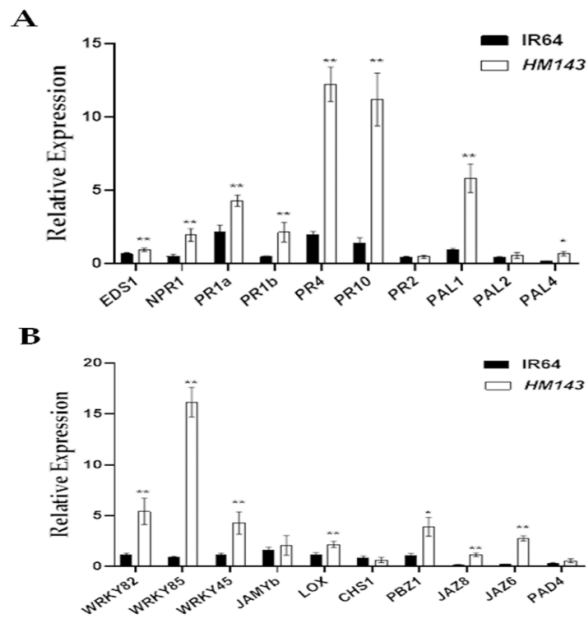


Figure S2. Expression of defense genes involved in SA and JA signaling pathway. (A) Expression analysis of SA signaling pathway genes. **(B)** Expression analysis of JA signaling pathway genes. Values are means \pm SD of three biological replicates; ** indicates significance at $P \leq 0.01$ and * indicates significance at $P \leq 0.05$ by Student's t test.

Table S1. List of primers used for this study

Primer	Primer sequence (5'-3')	Purpose
143gRNA	AGATCCAAGGCCATCCCTCC	CRISPR/Cas9
123-126-4-F	CACTGGACACGTCTGCAACA	Fine mapping
123-126-4-R	ACGCCTGCACCATCTTGGCCA	
127-130-1-F	GACGCTTAATTGTCAGCACA	
127-130-1-R	TTATGAACAGCTCCTGCCA	
123-126-8-F	GCATTATAGGATGTCCATG	
123-126-8-R	TAAACAGAGTATGCCAATCC	
126-1-F	ATGTTCTTAATATTTTCTTCC	
126-1-R	CCATGGGACTTGGGAGGTAT	
RM16686-F	GGCACTGCTTGCATATGGATCG	
RM16686-R	TGCCGCGAACTTATCCTCTCC	
RM16682-F	TGTATTTGCGTGGTGATTGG	PR genes
RM16682-R	TTAGGCAGGTACACAATGATGC	
<i>EDS1-F</i>	CATTCCAAGAACGAGGACACTG	
<i>EDS1-R</i>	CAAGACTCAAGGCTAGAACCGA	
<i>NPRI-F</i>	GGCAGGTGAGAGTCTACGAGGAA	
<i>NPRI-R</i>	GCTGTCATCCGAGCTAAGTGTT	
<i>PR1b-F</i>	AGAACTACGCCAGCCAGAGAAG	
<i>PR1b-R</i>	TTCTCGCCAAGGTTGTTCCG	
<i>PR10-F</i>	CACCATCTACACCATGAAGC	
<i>PR10-R</i>	AGCACATCCGACTTTAGGAC	
<i>PAL2-R</i>	GCATCAGCTTCCAACCTCG	
<i>PAL2-R</i>	GGTTTCGCACTCCATTACAGA	
<i>PR1a-F</i>	GGAAGTACGGCGAGAACATC	
<i>PR1a-R</i>	TGGTCGATCCACTGCTTCTC	
<i>PR4-F</i>	AGTATGGATGGACCGCCTTCTGT	
<i>PR4-R</i>	CTCGCAATTATTGTCGCACCTGTTT	
<i>PR2-F</i>	GGCAGGTGAGAGTCTACGAGGAA	
<i>PR2-R</i>	GCTGTCATCCGAGCTAAGTGTT	
<i>PAL4-F</i>	CTTCACAACAGCTAATCGAG	
<i>PAL4-R</i>	CGCACTCCATTTCAGTACCA	
<i>WRKY82-F</i>	AGTGAAAAGTAGTGAAAATTCCAG	
<i>WRKY82-R</i>	GTGCTAGTTTCAATTATTCTGCTTCGT	
<i>WRKY85-F</i>	CAGCAAGAAAAGGAATATACAAAT	
<i>WRKY85-R</i>	CTCAATGTGTTTCCTAACATTACA	
<i>WRKY45-F</i>	TTCCTTGTTGATGTGTCGTCTCA	
<i>WRKY45-R</i>	CCCCCAGCTCATAATCAAGAAC	
<i>JAMYb-F</i>	CCGAGCATGGTGACTAGCTCATCTT	
<i>JAMYb-R</i>	CCTTGCACCCAACCGTTAAGCTGTT	
<i>LOX-F</i>	GATGGCGGTGCTCGACGTGCT	
<i>LOX-R</i>	GCACCTGTTCTTGAGCTTTCTAT	
<i>PBZ1-F</i>	CCCTGCCGAATACGCCTAA	

<i>PBZ1-R</i>	CTCAAACGCCACGAGAAATTTG	
<i>CHS1-F</i>	GACTACCCGGACTACTACTTCA	
<i>CHS1-R</i>	CTTCCTGATCGCGACTTG	
<i>JAZ8-F</i>	CCAAACACGGCGGAAACAG	
<i>JAZ8-R</i>	GGTGGACGGGAAGTTCTCAAAG	
<i>JAZ6-F</i>	GGACATGCCGATCGCGAGGAA	
<i>JAZ6-R</i>	GCGCGAGTGCATGTGTCCA	
<i>PAD4-F</i>	CCAACATGTACCGCATCAAG	
<i>PAD4-R</i>	GGTTGTTTCGGTGGTAGTGGC	
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<i>OsMC1-F</i>	GCTTCATCAAGGCGGTGGAGT	
<i>OsMC1-R</i>	AAGTTGGCGACCTTGCGGATG	
<i>OsMC2-F</i>	CGACCCGTACAGGGTGCCGA	
<i>OsMC2-R</i>	GCACAGCGCCTCGTCGTAGC	
<i>OsMC3-F</i>	GGCTCCTTCGTCCGAAGAT	
<i>OsMC3-R</i>	CACAGGAGAAACGGTTTCCTGT	PCD-related
<i>OsMC4-F</i>	TCGACGTTTCGTGGAGATGCTC	genes
<i>OsMC4-R</i>	ATTCACGAGCCGCCTGATCTT	
<i>OsMC5-F</i>	GTGCCAGACCGACCAGACAT	
<i>OsMC5-R</i>	CCGCTCTTCTCCGACAGGAT	
<i>OsMC6-F</i>	CCACACCGCAGGGTTCTTCAT	
<i>OsMC6-R</i>	GTCCAGGCTGCTGAGTGATATCC	
<i>OsMC7-F</i>	ATACAGACCGTGCTGGCGTC	
<i>OsMC7-R</i>	AGGAATGGCGTCTCGGCGTT	
<i>OsMC8-F</i>	TCCGGCAAGTGCCTCGTAAC	
<i>OsMC8-R</i>	AGATAACAACGGAAGCATAAAGTC	
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<i>RbcL-F</i>	ATCGTGCTCGCGGTATCTTT	
<i>RbcL-R</i>	ACCAGGTGCATTACCCCAAG	
<i>CHLD-F</i>	GGAAAGAGAGGGCATTAG	
<i>CHLD-R</i>	CAATACGATCAAGTAAGTGTT	
<i>cab2R-F</i>	GTTCTCCATGTTTCGGCTTCT	
<i>cab2R-R</i>	GACGAAGTTGGTGGCGTAG	
<i>CHLH-F</i>	TGACTCAGACCCGACAAAGC	Photosynthesis-rela
<i>CHLH-R</i>	TCCCCTCGTACCACTTAGGG	ted genes
<i>CHLI-F</i>	CGGAGTAACCTTGGTGCTGT	
<i>CHLI-R</i>	CTTGGCAGCCCTGTTAGTCA	
<i>HEMA1-F</i>	ACACGCCATCTGTTTGAGGT	
<i>HEMA1-R</i>	CAAGCCTCCACTGTTTGGC	
<i>PsbA-F</i>	TGTAGCTGGTGATTTCGGCG	
<i>PsbA-R</i>	ATAACCATGAGCGGCCACAA	
<i>PorA-F</i>	ATCACCAAGGGCTACGTCTC	
<i>PorA-R</i>	GAGTTGTTGTTCCAGCTCCA	
<i>RbcS-F</i>	CCGTGAGAACCACAGATCCC	
<i>RbcS-R</i>	ACGTTGTCTGAAGCCGATGAT	
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134CDS-1	AGCGTGGGTCTCGGGCTCCATGGCGCGGTGCATCTCCTTCCT	CDS sequence

143CDS-2	AGCGTGGGTCTCGCTGACTGGAGCATCGACTCGATGCGTCCGTCCT	amplification
143-5	GATCACGGTCTCGACCTCCTTGTGTTTCGATAC	Promoter sequence
143-6	GCGATAGGTCTCGTGTTTGCACAGTGACCG	amplification
<i>UBI-F</i>	CCCTCCACCTCGTCCTCAG	Reference gene
<i>UBI-R</i>	AGATAACAACGGAAGCATAAAAGTC	
<i>RCCR1-F</i>	CGCATTCCTCATGGAATTT	
<i>RCCR1-R</i>	CTTCTCACGCTGTTGTCCA	
Osh36-F	AACGCATTTGTGGTTGGCTC	
Osh36-R	TCAACTTTGGCCGGTGTCTT	Senescence-
Osh57-F	ACCCTAAAGTAAATGAAGTC	Related genes
Osh57-R	CCTGCTCCTTGTCTTGTAC	
SGR-F	AGGGGTGGTACAACAAGCTG	
SGR-R	GCTCCTTGCGGAAGATGTAG	

Table S2.List of the 20 potential off-target sites

Sequence	Score	Locus	Gene	Region
ACATCCAAGGCCATCCCTCT AAG	8.6	Chr7:-15050489		Intergenic
AGCTCCA ACT CCATCCCTCC TGG	1.4	Chr5:-21075196		Intergenic
GAT TCCATGGCCATCCCTCC AGG	1.4	Chr7:+29470914	LOC_Os07g49210	CDS
AGCTCCAAG CCC TCCCTCC TAG	1.0	Chr7:-10977529		Intergenic
AGCTCCA GCT CCATCCCTCC TGG	0.8	Chr4:+35367918		Intergenic
AGCTCCA GCT CCATCCCTCC TGG	0.8	Chr11:-6133406		Intergenic
AGCTCCA GCT CCATCCCTCC TGG	0.8	Chr8:-17654804		Intergenic
AGCTCCA GCT CCATCCCTCC TGG	0.8	Chr11:+5529310		Intergenic
AGCTCCA GCT CCATCCCTCC TGG	0.8	Chr10:-3948507		Intergenic
AGCTCCA GCT CCATCCCTCC TAG	0.5	Chr9:-17888292		Intergenic
AGCTCCA CGT CCATCCA ATC GGG	0.5	Chr3:-10215007	LOC_Os03g18210	CDS
AGA AT CAAG A CCATCCT T CC TAG	0.3	Chr5:+14105545	LOC_Os05g24410	CDS
ACATCCA CC GCCATCCCT GC TGG	0.1	Chr8:+9008420		Intergenic
AGCTCCA ACT CCA CCC TCC TGG	0.1	Chr1:+6847610		Intergenic
AGCTCCA ACT CCA CCC TCC TGG	0.1	Chr8:+11059261	LOC_Os08g18044	Intron
AGCTCCA ACT CCA CCC TCC TGG	0.1	Chr5:+19551140		Intergenic
AGCTCCA ACT CCA CCC TCC TGG	0.1	Chr11:+3787600	LOC_Os11g07470	Intron
AGCTCCA ACT CCA CCC TCC TGG	0.1	Chr3:+26444886		Intergenic
AGCTCCA ACT CCA CCC TCC TGG	0.1	Chr4:+24196628		Intergenic
AGCTCCA ACT CCA CCC TCC TGG	0.1	Chr12:+6191726		Intergenic

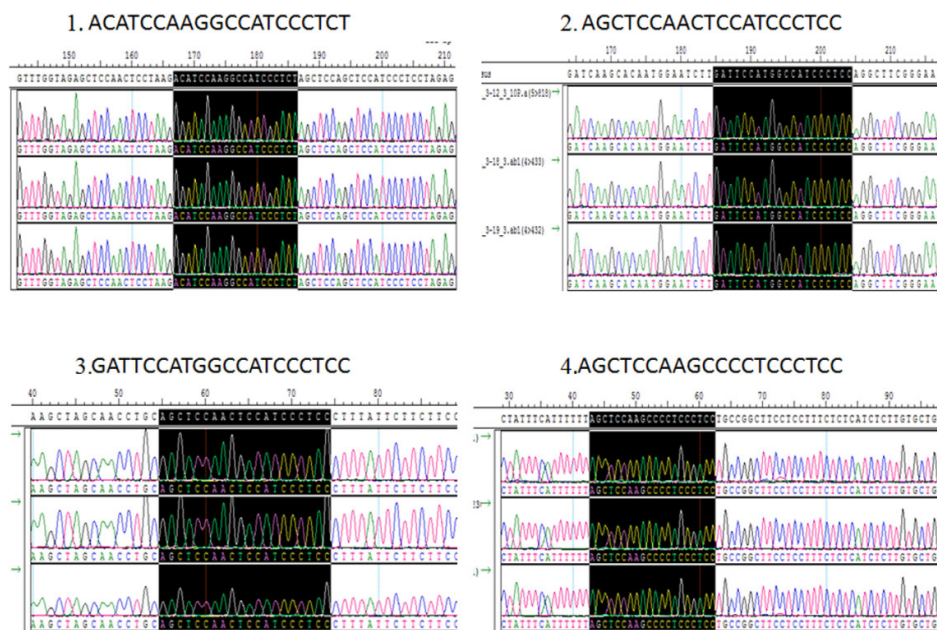


Figure S3. Sequence alignments of off-target sites 1, 2, 3, 4 in Cr-12, Cr-18 and Cr-19 respectively.

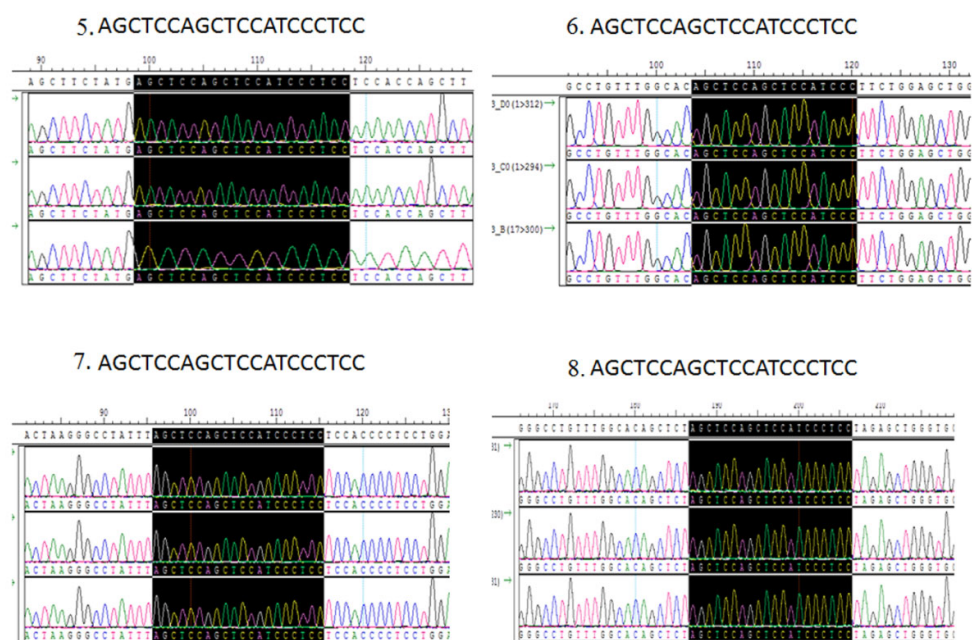


Figure S4. Sequence alignments of off -target sites 5, 6, 7, 8 in Cr-12, Cr-18 and Cr-19 respectively.

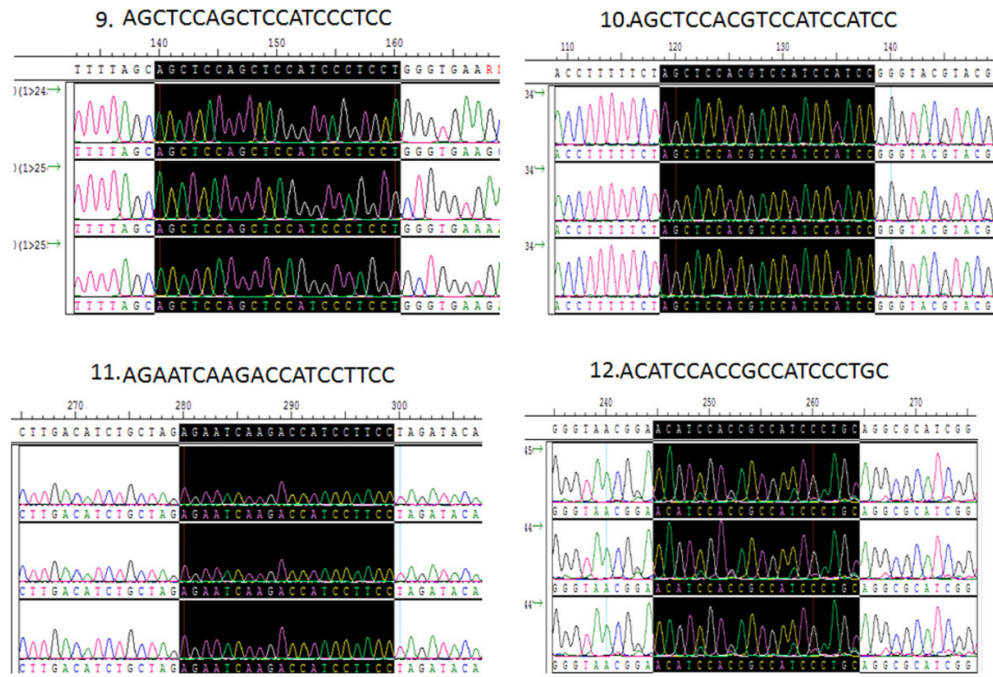


Figure S5. Sequence alignments of off -target sites 9, 10, 11, 12 in Cr-12, Cr-18 and Cr-19 respectively.

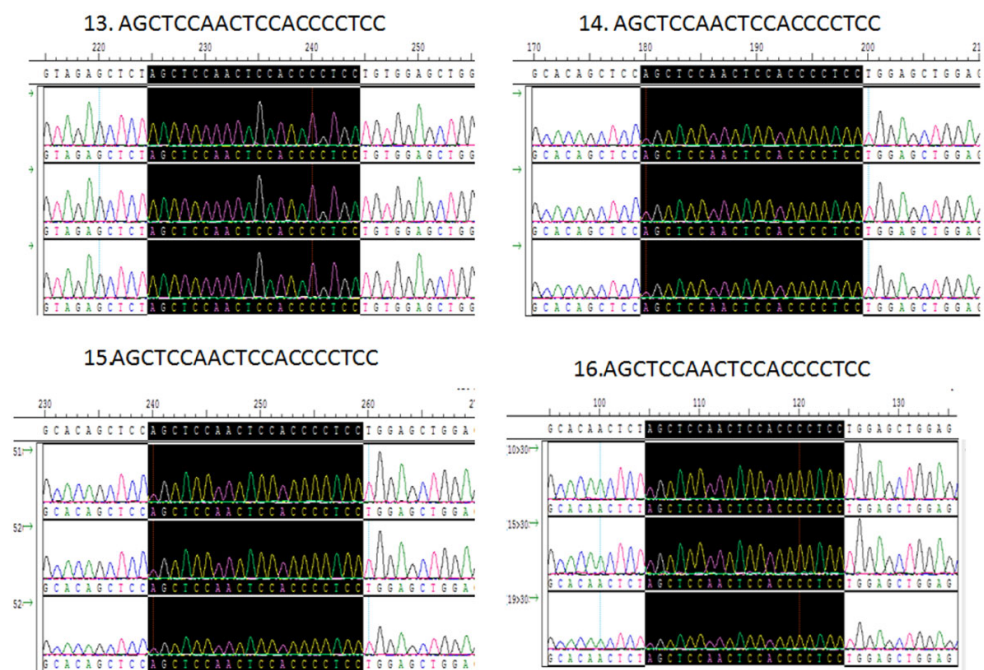


Figure S6. Sequence alignments of off -target sites 13, 14, 15, 16 in Cr-12, Cr-18 and Cr-19 respectively.

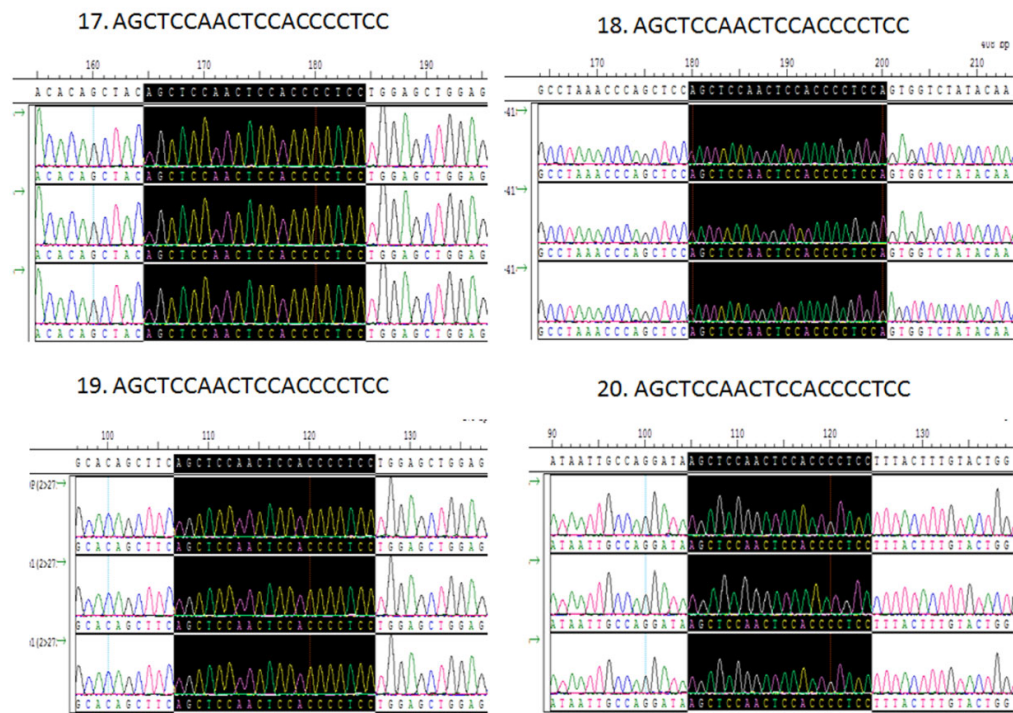


Figure S7. Sequence alignments of off-target sites 17, 18, 19, 20 in Cr-12, Cr-18 and Cr-19 respectively.