

***New Phytologist* Supporting Information**

Article title: **Roles of RIN and ethylene in tomato fruit ripening and ripening-associated traits**

Authors: Shan Li, Benzhong Zhu, Julien Pirrello, Changjie Xu, Bo Zhang, Mondher Bouzayen, Kunsong Chen, Donald Grierson

Article acceptance date: 1 December 2019

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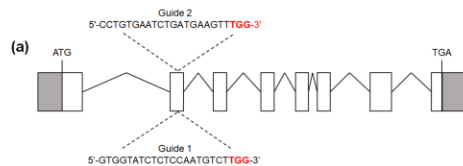
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Fig. S1. Construction of RIN-CRISPR tomato mutants. (a) Target sites designed for CRISPR/Cas9-mediated mutagenesis in the *RIN* gene. Boxes indicate exons and broken lines indicate introns. Three 20 bp target sequences and the protospacer-adjacent motif (PAM) are displayed in red color. (b) DNA editing and translation analysis in homozygous mutation alleles. DNA sequences in red color indicate the difference in *RIN* loci between WT and RIN-CRISPR mutant. The asterisks after amino acids indicate the predicted translation stop site.



(b) RIN-CRISPR-1

WT: AATTAAACGTTAATTATCTTATTCTTGTGTTCTAGTAGT
 Allele1: AATTAAACGTTAATTATCTTATTCTTGTGTTCTAGTAGT (432bp deletion)
 Allele2: AATTAAACGTTAATTATCTTATTCTTGTGTTCTAGTAGT (432bp deletion)

RIN-CRISPR-1 protein (68 AAs)

ATGGGTAGAGGGAAGTAGAATTGAAGAGAAATGAGAACAAATAATAGACAAGTTACCTTT
 MGRGKVELKRIENKINRQVTF
 GAAAGAGAGAAATGGACTCCTAAAGAAAGCTTATGAACCTTCTATCTTTGTGATGCTGAA
 AKRRNGLLKKAYELSLCDAEIA
 ATTGATTATTTCTCTAGTCTGGCAAGCTTATGAATTTGCGAACAATCGAAGATGTCGAAGAAC
 LLIIFSSRGKLYEFCSSNSSM
 ACTACAGAGATGATTGA
 TTKSII*

RIN-CRISPR-2

WT: TAGTATGTCCAAGACATTGGAGAGATACCACAGATCAATATGGTACAC
 Allele1: TAGTATGTCCAAGACATTGGAGAGATACCACAGATCAATATGGTACAC (11bp deletion)
 Allele2: TAGTATGTCCAAGACATTGGAGAGATACCACAGATCAATATGGTACAC (11bp deletion)

RIN-CRISPR-2 protein (74 AAs)

ATGGGTAGAGGGAAGTAGAATTGAAGAGAAATGAGAACAAATAATAGACAAGTTACCTTT
 MGRGKVELKRIENKINRQVTF
 GAAAGAGAGAAATGGACTCCTAAAGAAAGCTTATGAACCTTCTATCTTTGTGATGCTGAA
 AKRRNGLLKKAYELSLCDAEIA
 ATTGATTATTTCTCTAGTCTGGCAAGCTTATGAATTTGCGAACAATCGAAGATGTCGAAGAAC
 LLIIFSSRGKLYEFCSSNSSM
 TCGAAGATACACAGATCAATATGGTACACTGA
 SKIPIQILWYTT*

RIN-CRISPR-3

WT: TATGTCCAAGACATTGGAGAGATACCACAGATCAATATGGTAC
 Allele1: TATGTCCAAGACATTGGAGAGATACCACAGATCAATATGGTAC (1bp insertion)
 Allele2: TATGTCCAAGACATTGGAGAGATACCACAGATCAATATGGTAC (1bp insertion)

RIN-CRISPR-3 protein (78 AAs)

ATGGGTAGAGGGAAGTAGAATTGAAGAGAAATGAGAACAAATAATAGACAAGTTACCTTTGCA
 MGRGKVELKRIENKINRQVTF
 AAGAGAGAGAAATGGACTCCTAAAGAAAGCTTATGAACCTTCTATCTTTGTGATGCTGAAATGCT
 KRRNGLLKKAYELSLCDAEIA
 CTATATTTTCTCTAGTCTGGCAAGCTTATGAATTTGCGAACAATCGAAGATGTCGAAGAAC
 LLIIFSSRGKLYEFCSSNSSM
 TTGGAGAGATACACAGATCAATATGGTACACTGA
 LRLPIQILWYTT*

RIN-CRISPR-4

WT: GTGTTCTAGTATGTCCAAGACATTGGAGAGATACCACAGATCAATAT
 Allele1: GTGTTCTAGTATGTCCAAGACATTGGAGAGATACCACAGATCAATAT (1bp deletion)
 Allele2: GTGTTCTAGTATGTCCAAGACATTGGAGAGATACCACAGATCAATAT (1bp deletion)

RIN-CRISPR-4 protein (94 AAs)

ATGGGTAGAGGGAAGTAGAATTGAAGAGAAATGAGAACAAATAATAGACAAGTTACCTTTGCA
 MGRGKVELKRIENKINRQVTF
 AAGAGAGAGAAATGGACTCCTAAAGAAAGCTTATGAACCTTCTATCTTTGTGATGCTGAAATGCT
 KRRNGLLKKAYELSLCDAEIA
 CTATATTTTCTCTAGTCTGGCAAGCTTATGAATTTGCGAACAATCGAAGATGTCGAAGAAC
 LLIIFSSRGKLYEFCSSNSSM
 TTGGAGAGATACACAGATCAATATGGTACACTTGAAGAACCCAACTTCATCAGATTACAGAA
 W R D T T D T I M V H L K E P K L H Q I H R
 ACACTACCAAGATGATTGA
 TTTTKSII*

RIN-CRISPR-5

WT: GTGTTCTAGTATGTCCAAGACATTGGAGAGATACCACAGATCAATAT
 Allele1: GTGTTCTAGTATGTCCAAGACATTGGAGAGATACCACAGATCAATAT (2bp deletion)
 Allele2: GTGTTCTAGTATGTCCAAGACATTGGAGAGATACCACAGATCAATAT (2bp deletion)

RIN-CRISPR-5 protein (77 AAs)

ATGGGTAGAGGGAAGTAGAATTGAAGAGAAATGAGAACAAATAATAGACAAGTTACCTTTGCA
 MGRGKVELKRIENKINRQVTF
 AAGAGAGAGAAATGGACTCCTAAAGAAAGCTTATGAACCTTCTATCTTTGTGATGCTGAAATGCT
 KRRNGLLKKAYELSLCDAEIA
 CTATATTTTCTCTAGTCTGGCAAGCTTATGAATTTGCGAACAATCGAAGATGTCGAAGAAC
 LLIIFSSRGKLYEFCSSNSSM
 GGAGAGATACACAGATCAATATGGTACACTTGAAGAACCCAACTTCATCAGATTACAGAACTGCA
 G E I P Q I Q L W Y T T

RIN-CRISPR-6

WT: ACTTGAAGGAACCCAACTT-CATCAGATTACAGAAACAAC
 Allele1: ACTTGAAGGAACCCAACTT-CATCAGATTACAGAAACAAC (1bp insertion)
 Allele2: ACTTGAAGGAACCCAACTT-CATCAGATTACAGAAACAAC (1bp insertion)

RIN-CRISPR-6 protein (97 AAs)

ATGGGTAGAGGGAAGTAGAATTGAAGAGAAATGAGAACAAATAATAGACAAGTTACCTTTGCA
 MGRGKVELKRIENKINRQVTF
 AAGAGAGAGAAATGGACTCCTAAAGAAAGCTTATGAACCTTCTATCTTTGTGATGCTGAAATGCT
 KRRNGLLKKAYELSLCDAEIA
 CTATATTTTCTCTAGTCTGGCAAGCTTATGAATTTGCGAACAATCGAAGATGTCGAAGAAC
 LLIIFSSRGKLYEFCSSNSSM
 TTGGAGAGATACACAGATCAATATGGTACACTTGAAGAACCCAACTTCATCAGATTACAGAACTGCA
 L E R Y H R Y N Y G T L E G T Q T F I R F T
 GAACAACACAGAGATTGAAGCTTAA
 E Q L P R V F E A *

RIN-CRISPR-7

WT: GTGTTCTAGTATGTCCAAGACATTGGAGAGATACCACAGATCAATAT
 Allele1: GTGTTCTAGTATGTCCAAGACATTGGAGAGATACCACAGATCAATAT (1bp insertion)
 Allele2: GTGTTCTAGTATGTCCAAGACATTGGAGAGATACCACAGATCAATAT (1bp insertion)

RIN-CRISPR-7 protein (78 AAs)

ATGGGTAGAGGGAAGTAGAATTGAAGAGAAATGAGAACAAATAATAGACAAGTTACCTTTGCA
 MGRGKVELKRIENKINRQVTF
 AAGAGAGAGAAATGGACTCCTAAAGAAAGCTTATGAACCTTCTATCTTTGTGATGCTGAAATGCT
 KRRNGLLKKAYELSLCDAEIA
 CTATATTTTCTCTAGTCTGGCAAGCTTATGAATTTGCGAACAATCGAAGATGTCGAAGAAC
 LLIIFSSRGKLYEFCSSNSSM
 ATGGAGAGATACACAGATCAATATGGTACACTGA
 I G E I P Q I Q L W Y T T

RIN-CRISPR-8

WT: GTGTTCTAGTATGTCCAAGACATTGGAGAGATACCACAGATCAATAT
 Allele1: GTGTTCTAGTATGTCCAAGACATTGGAGAGATACCACAGATCAATAT (1bp insertion)
 Allele2: GTGTTCTAGTATGTCCAAGACATTGGAGAGATACCACAGATCAATAT (1bp insertion)

RIN-CRISPR-8 protein (78 AAs)

ATGGGTAGAGGGAAGTAGAATTGAAGAGAAATGAGAACAAATAATAGACAAGTTACCTTTGCA
 MGRGKVELKRIENKINRQVTF
 AAGAGAGAGAAATGGACTCCTAAAGAAAGCTTATGAACCTTCTATCTTTGTGATGCTGAAATGCT
 KRRNGLLKKAYELSLCDAEIA
 CTATATTTTCTCTAGTCTGGCAAGCTTATGAATTTGCGAACAATCGAAGATGTCGAAGAAC
 LLIIFSSRGKLYEFCSSNSSM
 ATGGAGAGATACACAGATCAATATGGTACACTGA
 I G E I P Q I Q L W Y T T

RIN-CRISPR-9

WT: AAGACATTGGAGAGATACCACAGATCAATATGGTACACTTGAAGGAACCCAACTTCA
 Allele1: AAGACATTGGAGAGATACCACAGATCAATATGGTACACTTGAAGGAACCCAACTTCA (2bp deletion)
 Allele2: AAGACATTGGAGAGATACCACAGATCAATATGGTACACTTGAAGGAACCCAACTTCA (2bp deletion)

RIN-CRISPR-9 protein (96 AAs)

ATGGGTAGAGGGAAGTAGAATTGAAGAGAAATGAGAACAAATAATAGACAAGTTACCTTTGCA
 MGRGKVELKRIENKINRQVTF
 AAGAGAGAGAAATGGACTCCTAAAGAAAGCTTATGAACCTTCTATCTTTGTGATGCTGAAATGCT
 KRRNGLLKKAYELSLCDAEIA
 CTATATTTTCTCTAGTCTGGCAAGCTTATGAATTTGCGAACAATCGAAGATGTCGAAGAAC
 LLIIFSSRGKLYEFCSSNSSM
 TTGGAGAGATACACAGATCAATATGGTACACTTGAAGGAACCCAACTTCATCAGATTACAGAA
 W R D T T D T I M V H L K E P K L I R F T E
 CACTACCAAGATGATTGAAGCTTAA
 Q L P R V F E A *

RIN-CRISPR-10

WT: GACATTGGAGAGATACCACAGATCAATATGGTACACTTGAAGGAACCCAACTT-CATCAGATT
 Allele1: GA-CATTGGAGAGATACCACAGATCAATATGGTACACTTGAAGGAACCCAACTT-CATCAGATT (4bp change)
 Allele2: GA-CATTGGAGAGATACCACAGATCAATATGGTACACTTGAAGGAACCCAACTT-CATCAGATT (4bp change)

RIN-CRISPR-10 protein (242 AAs including 21AAs changes)

ATGGGTAGAGGGAAGTAGAATTGAAGAGAAATGAGAACAAATAATAGACAAGTTACCTTTGCA
 MGRGKVELKRIENKINRQVTF
 AAGAGAGAGAAATGGACTCCTAAAGAAAGCTTATGAACCTTCTATCTTTGTGATGCTGAAATGCT
 KRRNGLLKKAYELSLCDAEIA
 CTATATTTTCTCTAGTCTGGCAAGCTTATGAATTTGCGAACAATCGAAGATGTCGAAGAAC
 LLIIFSSRGKLYEFCSSNSSM
 TTGGAGAGATACACAGATCAATATGGTACACTTGAAGGAACCCAACTTCATCAGATTCTCAG
 W R D T T D T I M V H L K E P K L S S I S Q
 ACACTACCAAGATGATTGAAGCTTAAACAAGAGTGGAGATTGACACAGCTTCAAAAGG
 NNYYQEYLKLTTRVEMLQSQSR
 CATTTCGTAGTGAGGATTGGGCAATTTGGGCAACAAAGACTTGGAAACAGCTTGAAGCTCAATTG
 HLLLEGLGQLGTLKDLLEQLLEQL
 GATTTCATGAGGCAATATGATGACAAAGACACACATCTTGATCAACTTGGCAAGCTT
 DSSLRQIRSTKTQHILDLQAL
 CAACAAAGGAACATCTCTACTGAAATGAACAAATCTTGAAGATAAGTTGGAAGAACTTGGT
 QKQEQSLTEMNKSLRLRIKLEELG
 GTTACCTTCAACATCATGGCATTTGGTGAGCAAGATGACATAATAGACATGAACAGCTTCT
 VTFQTSWHCGEQSVQYRHEQPS
 CATCATGAGGATTTTCAACATGTAATGCAATAATCATTTGCTTATAGTTACGGATACAGT
 HHLEGLFQKLVNHLPLPSGYD
 AATGTACAACCCGAAGATGAGCAACCATCAACACATGATGCTACTGGAGTTGTACCTGGATGG
 NVQPENAAAPSTHDTATGVVVPGW
 ATGCTTTGA
 M L *

Fig. S2. Phenotype of RIN-CRISPR tomato fruits.

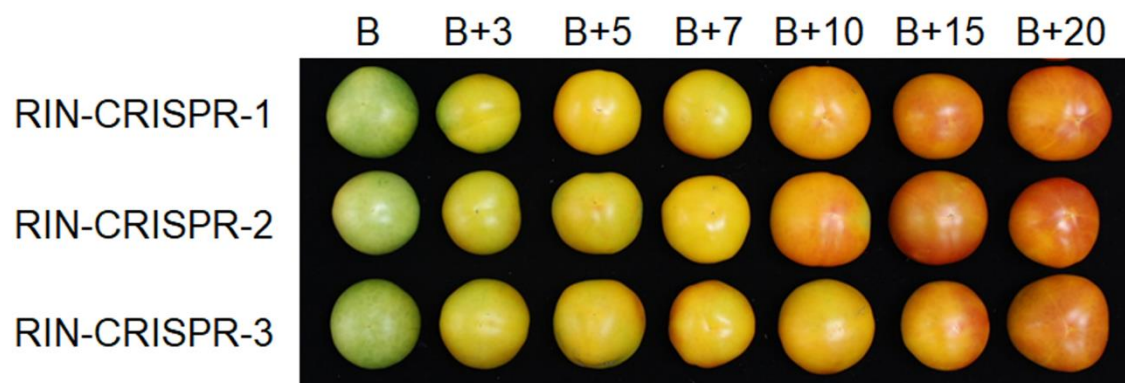


Fig. S3 qRT-PCR assay of genes involved in ethylene biosynthesis, perception and signaling. Analysis of qRT-PCR expression assay of genes involved in ethylene biosynthesis and perception (average of 3 biological replicates). Relative transcript levels were determined by qRT-PCR, relative to the expression of the tomato *ACTIN* gene internal control, expressed as $2^{-\Delta\Delta Ct}$ (Livak and Schmittgen, 2001). ACC synthesis (*ACS2*, *ACS4*); ACC oxidase (*ACO1*); Ethylene receptor (*ETR3/NR*, *ETR4*); Ethylene-response related (*E4*, *E8*); EIN3-like proteins (*EILs*); Ethylene response factors (*ERFs*). The error bars represent Mean $\pm$ SD, the lowercase letters indicate significant difference at $P=0.05$.

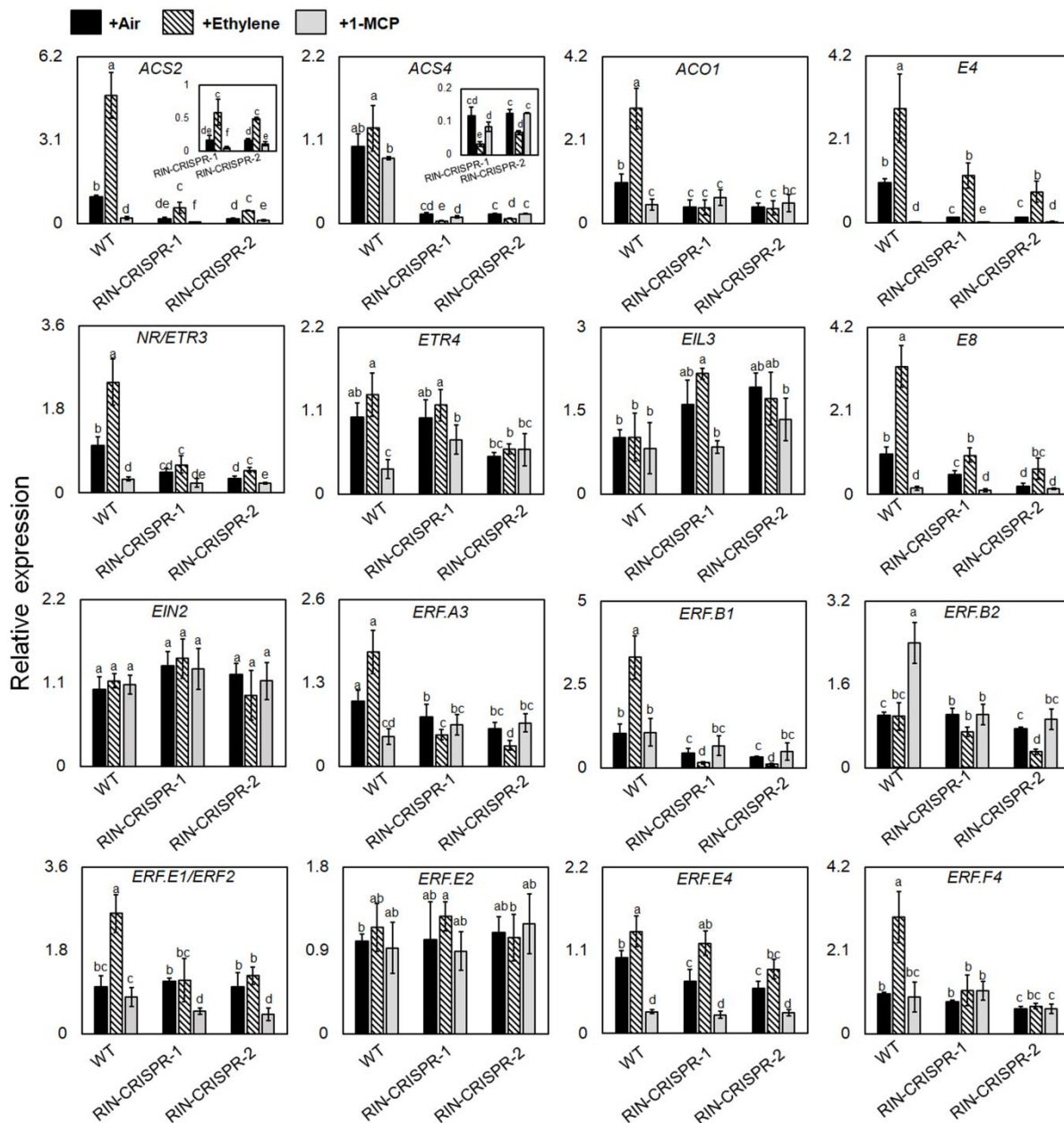


Fig. S4. Colour development in WT and RIN-CRISPR tomato fruits. Pericarp colour (a^* , L^* , b^*), measured by handheld colorimeter using the CIE $L^*a^*b^*$ colour system, a^* indicates red to green, L^* indicates lightness, b^* indicates yellow to blue (Komatsu *et al.*, 2016). The error bars represent Mean $\pm$ SD, the lowercase letters indicate significant difference.

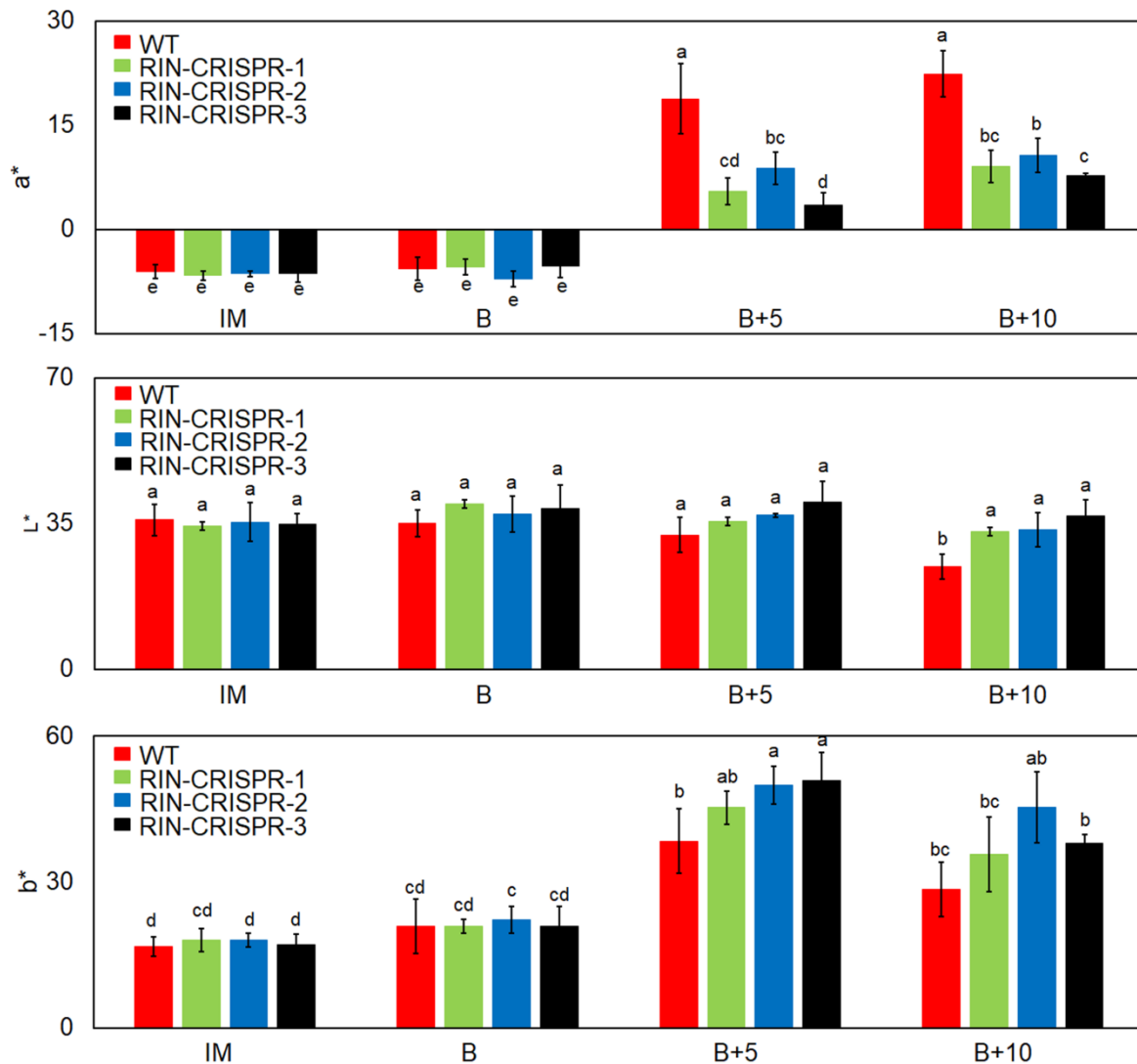
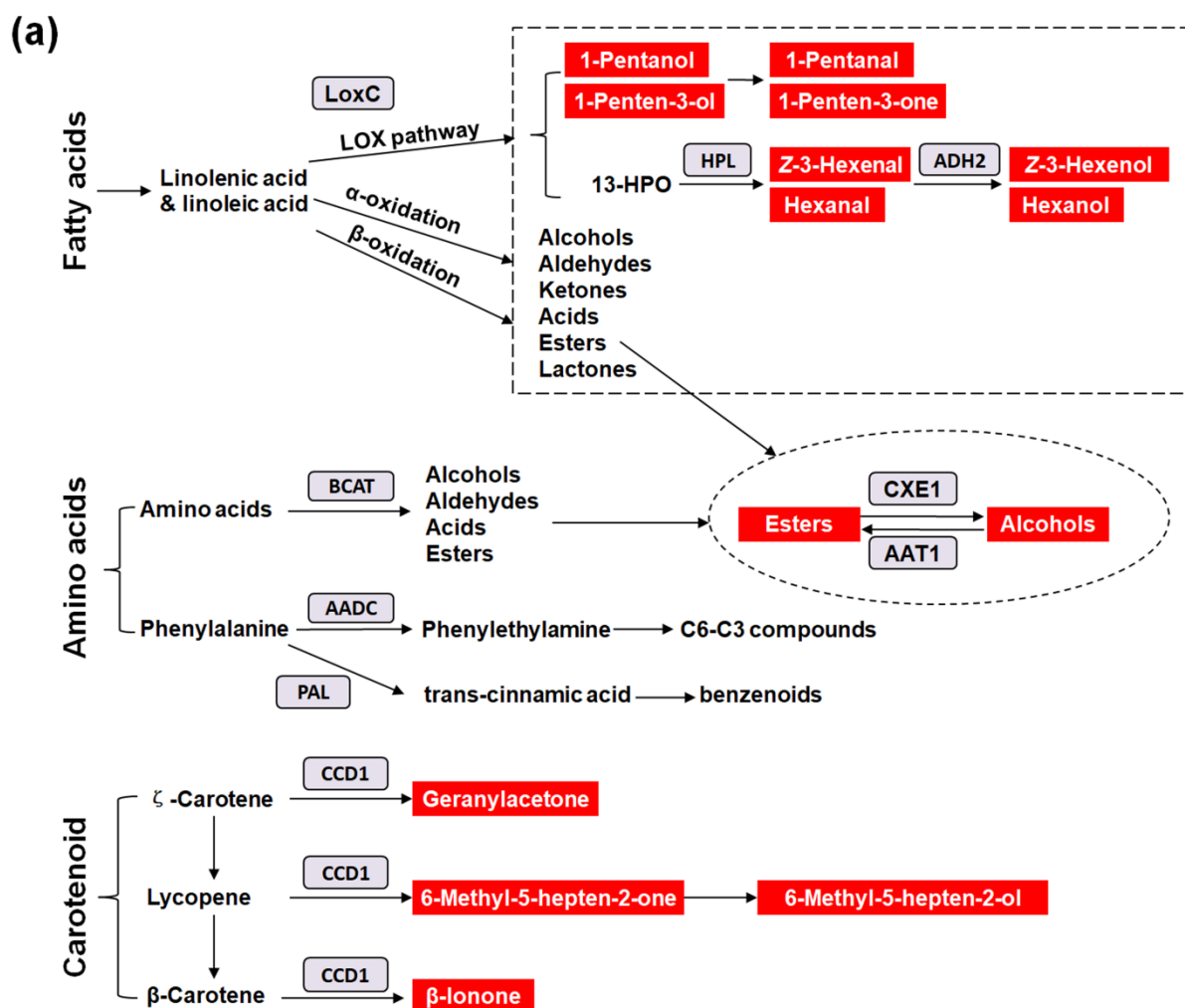


Fig. S5. Biochemical origin of tomato fruit volatiles and the content in WT, RIN-CRISPR-1 and RIN-CRISPR-2 tomato fruits. (a) The information of major pathways is from Klee and Tieman (2018) and Aragüez and Valpuesta (2013). Compounds known to be important flavor volatiles are highlighted in red, and enzymes are shown in grey boxes. (b) Table of volatile content derived from different precursors, lipid, amino acid and carotenoid.



(b)

Content (μg·g ⁻¹ FW)	WT			RIN-CRISPR-1					RIN-CRISPR-2						
	B	B+5	B+10	B	Change	B+5	Change	B+10	Change	B	Change	B+5	Change	B+10	Change
Lipid derivatives	11.00 ^{cd}	27.45 ^{ab}	38.18 ^a	8.74 ^{de}	--	16.19 ^{bcd}	--	16.40 ^{bc}	-57%	8.41 ^e	--	18.09 ^{bc}	--	27.58 ^{ab}	--
Amino acid derivatives	0.51 ^d	1.20 ^b	1.79 ^a	0.71 ^{cd}	--	0.84 ^c	-30%	0.74 ^{cd}	-59%	0.85 ^{bc}	20%	0.81 ^c	-33%	1.06 ^{bc}	-41%
Carotenoid derivatives	1.70 ^c	15.12 ^a	4.23 ^b	0.96 ^d	-43%	0.89 ^{de}	-94%	2.41 ^c	-43%	0.31 ^f	-82%	0.64 ^e	-96%	2.27 ^c	-46%

The lowercase letters indicate significant difference between six groups in each row.

Fig. S6 Transcripts of cell wall modifying enzymes in RIN-deficient and WT fruits treated with ethylene and 1-MCP measured by qRT-PCR. Tomato fruits were picked at mature green (MG) stage, either treated with air, ethylene or 1-MCP for 48h as described in Materials and Methods. (a) Genes whose transcripts are increased to some extent by ethylene in both RIN-deficient and WT fruits. (b) Genes whose transcripts are repressed to some extent by ethylene in RIN-deficient fruits. (c) Genes whose transcripts displayed no obvious response to ethylene, but accumulated to a lower level than WT. (d) Genes whose transcripts displayed no obvious response to ethylene, but were present at an equivalent or higher level in RIN-deficient fruits compared to WT. Transcript levels were determined by qRT-PCR, relative to the expression of the tomato *ACT1N* gene internal control, expressed as $2^{-\Delta\Delta Ct}$ (Livak and Schmittgen, 2001). The error bars represent Mean $\pm$ SD, the lowercase letters indicate significant difference at $P=0.05$.

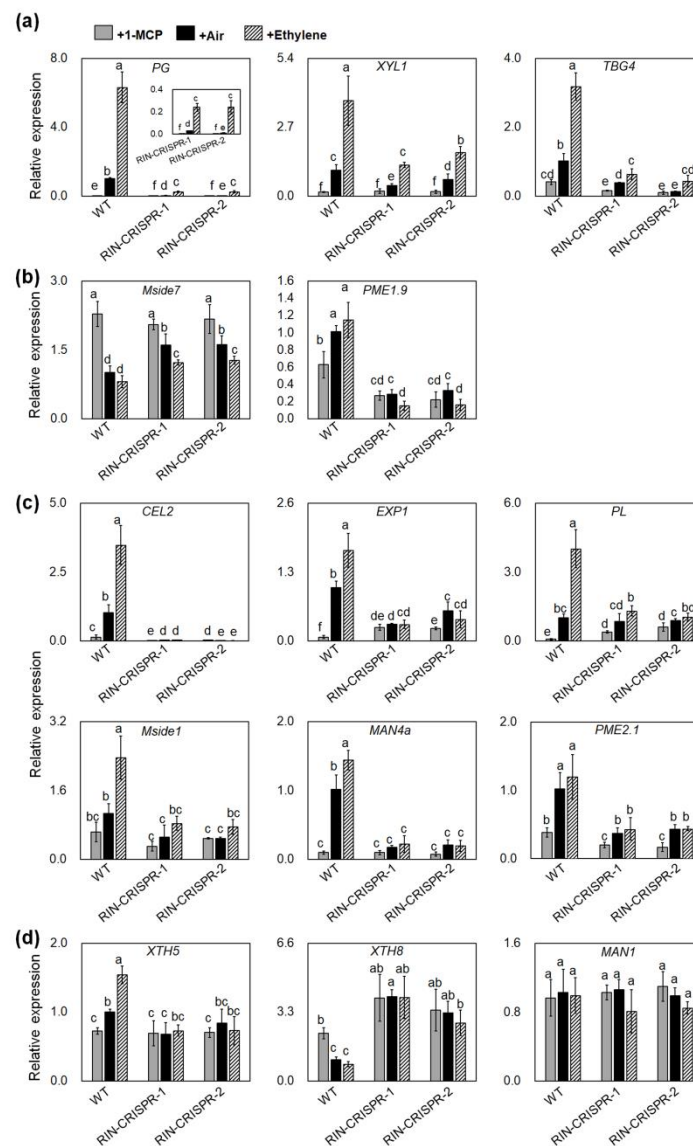


Fig. S7 RIN and ERF binding motifs in promoters of cell wall metabolising genes. Multiple CArG-box elements (MADS-box binding motifs, various CArG-box types (Fujisawa *et al.*, 2013) are present in the promoter regions (2.0 kb upstream of the ATG site) of cell wall genes, with the exception of *PL*, for which only 1.5kb promoter is available. The *PG* promoter has one GCC-box (GCCGCC, a putative AP2/ERF binding motif). A second AP2/ERF binding motif (ATCTA) described by Welsch *et al.* (2007) is also present in all cell wall genes examined in this study.

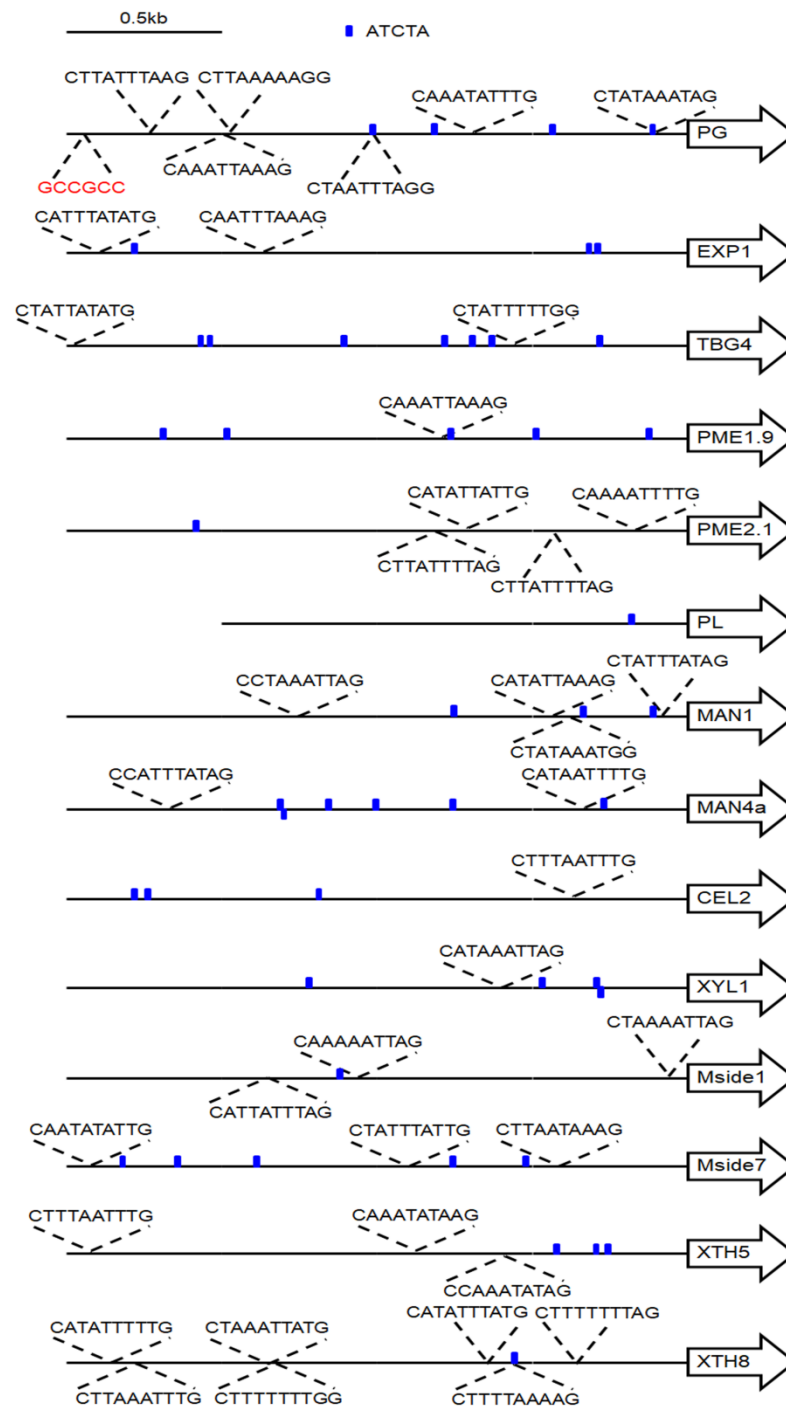


Table S1 Primer pairs for vector construction and target site mutation analysis.

Name	Primer	Sequence (5'-3')
1st PCR	U-F	CTCCGTTTTACCTGTGGAATCG
	gR-R	CGGAGGAAAATTCCATCCAC
	gRT-RIN-T1 For	GTGGTATCTCTCCAATGTCT GTTTTAGAGCTAGAAAT
	AtU3d-RIN-T1 Rev	AGACATTGGAGAGATACCAC TGACCAATGGTGCTTTG
	gRT-RIN-T2 For	CCTGTGAATCTGATGAAGTT GTTTTAGAGCTAGAAAT
	AtU3bT-T2 Rev	AACTTCATCAGATTCACAGG TGACCAATGTTGCTCC
2nd PCR	Pps-GGL	TTCAGAGGTCTCTCTCGACTAGTATGGAATCGGCAGCAAAGG
	Pgs-GG2	AGCGTGGGTCTCGTCAGGGTCCATCCACTCCAAGCTC
	Pps-GG2	TTCAGAGGTCTCTCTGACACTGGAATCGGCAGCAAAGG
	Pgs-GGR	AGCGTGGGTCTCGACCGACGCGTATCCATCCACTCCAAGCTC
Target site mutation analysis	Cas9-RIN-For	TATCAGTTGAGCACTTCGTTTT
	Cas9-RIN-Rev	GTCGTAATTCGTGAGTTTCAT
	Cas9-RIN-Seq	GAGTTGGAATACTTAGTTGTC

Table S2 Primer pairs for qRT-PCR assay.

ID	Gene	Name	Sequence(5'-3')	Reference
Solyc03g078400	<i>ACTIN</i>	ACTIN-F	CCTCAGCACATTCCAGCAG	Powell <i>et al.</i> , 2012
		ACTIN-R	CCACCAAACCTTCTCCATCCC	
Solyc01g095080	<i>ACS2</i>	ACS2-F	TGGATGATGGAACGGTTGATATTGC	Li <i>et al.</i> , 2018
		ACS2-R	CCATTGTTGCTTCTGTTCCATCGAAC	
Solyc05g050010	<i>ACS4</i>	ACS4-F	AAATCTCCACCTTCACTAACGAAC	Martel <i>et al.</i> , 2011
		ACS4-R	CCTAAGTCCTTGGAAAGACTAGACAC	
Solyc07g049530	<i>ACO1</i>	ACO1-F	CTTGAGGTGATCACTAACGGGAAGTACA	Li <i>et al.</i> , 2018
		ACO1-R	TGCTGGATATATTACTGCATCACTTCCTG	
Solyc09g075440	<i>NR</i>	ETR3/NR-F	ATCAGGTTGCTGTCGCTCTT	Li <i>et al.</i> , 2018
		ETR3/NR-R	GGCCATCTCTGCTTCTTGTC	
Solyc06g053710	<i>ETR4</i>	ETR4-F	AGCAATAATCATTCTCAGCCAG	Li <i>et al.</i> , 2018
		ETR4-R	TCTCCTTGCATCAACTGAACC	
Solyc03g111720	<i>E4</i>	E4-F	GACCACTCTAAATCGCCAGG	Liu <i>et al.</i> , 2018
		E4-R	TTCCTGAGCGGTATTGCTTT	
Solyc09g089580	<i>E8</i>	E8-F	TGGCTCCGAATCCTCCCAGTCT	Liu <i>et al.</i> , 2018
		E8-R	GTCCGCCTCTGCCACTGAGC	
Solyc09g007870	<i>EIN2</i>	EIN2-F	CTCAACCGTCTTCAGGGCATAG	Wang <i>et al.</i> , 2016
		EIN2-R	GTGGCGGCAAGTTTCCATTAG	
Solyc01g096810	<i>EIL3</i>	EIL3-F	CACGAGCCTCTCTTCTTCTTAC	Wang <i>et al.</i> , 2016
		EIL3-R	ACCGGCTTATGCTCAACTTC	
Solyc03g123760	<i>PDS</i>	PDS-F	CATTGATTATCCAAGACCAGAG	Wang <i>et al.</i> , 2016
		PDS-R	CCAGCAATAACAATCTCCAA	
Solyc03g031860	<i>PSY1</i>	PSY1-F	ATGTCTGTTGCCTTGTTATG	Li <i>et al.</i> , 2018
		PSY1-R	TTCCACCACCTCTATTGATT	
Solyc01g097810	<i>ZDS</i>	ZDS-F	TCTTGCTGGCTCATATACA	Li <i>et al.</i> , 2018
		ZDS-R	AGACTCAACTCATCAGATAGG	
Solyc10g081650	<i>CRTISO</i>	CRTISO-F	ATGAAGCGAAGAAAGAGGTTGT	Li <i>et al.</i> , 2018
		CRTISO-R	GCAAGGTATCGTCTGTGGGTCT	
Solyc04g079960	<i>GGPS2</i>	GGPPS2-F	TGAGGTTGATGTGGAGCGAATG	Li <i>et al.</i> , 2018
		GGPPS2-R	TAGGTCCTTACCCGCTGTCTTT	
Solyc03g007960	<i>SIBCH2/CHY</i>	CHY/SIBCH2-F	TCCGTCATAACCCGTTTCTCAG	Li <i>et al.</i> , 2018
		CHY/SIBCH2-R	CGCCAATCTCGGCTTTCTTCT	
Solyc01g067890	<i>DXS1</i>	SIDXS-F	AGCTTCCGGCTGGAAACAAA	Galpaz <i>et al.</i> , 2008
		SIDXS-R	CTAGCACAATAGCAGCATCC	
Solyc02g090890	<i>ZEP</i>	ZEP-F	CGGGTCCATCTCACATACAAAT	Moon <i>et al.</i> , 2011 (revised)

		ZEP-R	CCATGTTCACTTCGTAAATCAG	
Solyc05g052050	<i>ERF.A3</i>	ERF.A3-F	GCGAAATGGATCAACAGTTACCA	Liu <i>et al.</i> , 2014
		ERF.A3-R	ATTAGACGACTGAAGCTTGAATTCC	
Solyc05g052040	<i>ERF.B1</i>	ERF.B1-F	GAATGATGACGGAATTGTAATGAAGA	Liu <i>et al.</i> , 2014
		ERF.B1-R	TTCCACAATCCCAAATTGAAGA	
Solyc03g093560	<i>ERF.B2</i>	ERF.B2-F	AGTTTGACGCGGAGATTCTGT	Liu <i>et al.</i> , 2014
		ERF.B2-R	TGCCCTGTCATATGCCTTTG	
Solyc09g075420	<i>ERF.E1/ERF2</i>	ERF.E1-F	GTTCTCTCAACCCCAAACG	Liu <i>et al.</i> , 2014, 2016
		ERF.E1-R	TTCATCTGCTCACCACTGTAGA	
Solyc06g063070	<i>ERF.E2</i>	ERF.E2-F	ACTTCGTGAGGAAACCCTGAAC	Liu <i>et al.</i> , 2014
		ERF.E2-R	GTTACTAATATAAGTCATGTTGGGCTGAA	
Solyc01g065980	<i>ERF.E4</i>	ERF.E4-F	AGGCCAAGGAAGAACAAGTACAGA	Liu <i>et al.</i> , 2014
		ERF.E4-R	CCAAGCCAAACGCGTACAC	
Solyc07g053740	<i>ERF.F4</i>	ERF.F4-F	GAGCTAATGGCTGATTTTTGTATATAAGTTC	Liu <i>et al.</i> , 2014
		ERF.F4-R	AAATGGTAGAAACAGCACGAGAAAG	
Solyc06g059740	<i>ADH2</i>	ADH2-F	ATGTGTCCATGATGGCTGGG	Wang <i>et al.</i> , 2016
		ADH2-R	GGTGATGATGCAACGAAGGC	
Solyc08g014000	<i>LoxA</i>	LoxA-F	GAGGCGTGGGATAGGA	Hu <i>et al.</i> , 2014
		LoxA-R	GGATACGGGTAGTCAGCA	
Solyc01g099190	<i>LoxB</i>	LoxB-F	TGCTACAATGACTTGGGTGAA	Zhu <i>et al.</i> , 2014
		LoxB-R	CCTGTCCTGCCTCTACG	
Solyc01g006540	<i>LoxC</i>	LoxC-F	GTGCAAATACCATTAAAGGCTGTG	Li <i>et al.</i> , 2018
		LoxC-R	AGTCCAGTCTTATGATCAAGCTC	
Solyc01g087260	<i>CCD1B</i>	LeCCD1B-F	AGTTCTTCCACGCTACGCAAA	Simkin <i>et al.</i> , 2004 (revised)
		LeCCD1B-R	TCTCCCTCCTCCCAAGCAT	
Solyc07g049690	<i>HPL</i>	HPL-F	AGTGAGAGACAAAGTCGGCG	Wu <i>et al.</i> , 2018
		HPL-R	ACCACAAAGAAGCTCCCTT	
Solyc08g005770	<i>AAT1</i>	AAT1-F	CAATAAATTACCACAAGCCAAAAC	Goulet <i>et al.</i> , 2015
		AAT1-R	AACATTAGTATGGGGATTGGAG	
Solyc12g088220	<i>BCAT1</i>	SIBCAT1-F	GTGTTGCTCCTGTAGGGAGT	Wu <i>et al.</i> , 2018
		SIBCAT1-R	AATCCAACCCCTCTGTCTCTC	
Solyc08g068680	<i>AADC1A</i>	AADCA1-F	AGCGCGACGACGATTGTT	Tieman <i>et al.</i> , 2006
		AADCA1-R	GGTCTGCACCTGGTTGTG	
Solyc09g007900	<i>PAL3</i>	PAL3-F	CAATACTCTGCTTCAAGGCTAC	designed
		PAL3-R	CCAGCAATGTATGACAACGGG	
Solyc10g080210	<i>PG2a</i>	PG2a-F	TCAGCAAAGAGCCCAAATACTG	Li <i>et al.</i> , 2018
		PG2a-R	GCTTCCAATACTTATACCATGACCT	

Solyc06g051800	<i>EXP1</i>	EXP1-F	TGGTTCCTTCTCATTGGCAATTGG	Martel <i>et al.</i> , 2011
		EXP1-R	TTCAGTGAGGACTCGATTTCTTTCC	
Solyc07g064170	<i>PE1/PME 1.9</i>	PME1.9/PE1-F	GCTTGCGTCTTTGACAACTCAGG	Zhang <i>et al.</i> , 2018
		PME1.9/PE1-R	GTGCCACCACTGCATTGCTAT	
Solyc07g064180	<i>PME2.1</i>	PME2.1-F	TCCATTACAGCACAAGGAAGACA	Jeong <i>et al.</i> , 2018
		PME2.1-R	TGTTGCAACTCTTGTTGGCT	
Solyc10g047030	<i>XYL1</i>	XYL1-F	TGATCGGCAATTATGAAGGTATTC	Zhang <i>et al.</i> , 2018
		XYL1-R	CAGCACATCCTGGCTTGAAAT	
Solyc01g081060	<i>XTH5</i>	XTH5-F	CCACCACCAGAGTGCGAGAT	Zhang <i>et al.</i> , 2018
		XTH5-R	TTTTCTTAGGATGACGATGTCCG	
Solyc04g008210	<i>XTH8</i>	XTH8-F	TCCCAAGTGTGATATAGTCCTGGATTCTG	Muñoz-Bertomeu <i>et al.</i> , 2013
		XTH8-R	CCTCGGAGGCGATTAGCTTCCTTA	
Solyc09g010210	<i>CEL2</i>	CEL2-F	ACACATTGCCAAACGTCAGGT	Zhang <i>et al.</i> , 2018
		CEL2-R	CCCCTATGGTGAATCCTTTGTG	
Solyc03g111690	<i>PL</i>	PL-F	GCGATCAGGAGTTAGAACTGG	Zhang <i>et al.</i> , 2018
		PL-R	AATCCCCTTTTGCTTTGGTT	
Solyc12g008840	<i>TBG4</i>	TBG4-F	AAATGGTGAAGGCGTAGGTCG	Zhang <i>et al.</i> , 2018
		TBG4-R	AGGTTGTCCGAGTTAGTCTGG	
Solyc06g068860	<i>MAN1</i>	MAN1-F	ACACCGTCCTCCTGAGATTGG	Zhang <i>et al.</i> , 2018
		MAN1-R	GAGCCTCTGCTTCCACTTTAATC	
Solyc01g008710	<i>MAN4a</i>	MAN4a-F	TGGAGATTGGACTTGAAGGAT	designed
		MAN4a-R	CTTGAACCTGATTGTTGGAGAT	
Solyc03g119080	<i>Mside1</i>	Mside1-F	TGGAGATTGGACTTGAAGGAT	designed
		Mside1-R	CTTGAACCTGATTGTTGGAGAT	
Solyc02g084990	<i>Mside7</i>	MAN7-F	GAACTGATTTTCATCGCCAAC	designed
		MAN7-R	TTGAGCATCTTGAATGTGGG	

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