**Supplementary information** 

## A tomato MADS-box protein, SICMB1, regulates ethylene biosynthesis and carotenoid accumulation during fruit ripening

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Primer Name	Primer Sequence (5'–3')	Application
	CGG <u>GGTACCAAGCTT</u> ACTCTGTAGCACATTGGCATATCAC	To establish
SICMB1-i		SICMB1 RNAi
	CCG <u>CTCGAGTCTAGA</u> AGATTAGTATGAATATCACGCACAAGTC	lines; add KpnI+
		Hind III and XhoI
		+XbaI site
		underlined,
		respectively
SlCMB1-Full	TACATAGCCTTTTTTCTTTTCCT	Full-length
	TGAATATCACGCACAAGTCG	amplification of
NPT II	CTCAGAAGAACTCGTCAAGAAGG	Positive
	GACTGGGCACAACAGACAATC	transgenic plants
<i>SlCMB1</i> (Y2H)	CCG <u>GAATTC</u> ATGGGAAGAGGTAAGGTAGAATTGA	
	CGC <u>GGATCC</u> TCAGATTCTGAATTCGCCCCT	
<i>RIN</i> (Y2H)	CCG <u>GAATTC</u> ATGGGTAGAGGGAAAGTAGA	
	CGC <u>GGATCC</u> TCATAGATGTTTATTCAT	
	CGC <u>GGATCC</u> TTAAAGCATCCATCCATGAATA	Construction of
<i>SlMADS1</i> (Y2H)	CCG <u>GAATTC</u> ATGGGAAGAGGAAGAGTTG	yeast two -hybrid
	CGC <u>GGATCC</u> TTAAAGCATCCATCCATGAATA	vector
AP2a(Y2H)	CCG <u>GAATTC</u> ATGTGGAATTTAAATGATTCCCC	
	CGC <u>GGATCC</u> TCAAGGTCTCATAAAATAATGATGGA	
TAGL1(Y2H)	CCG <u>GAATTC</u> ATGGTTTTTCCTATTAATCAGG	
	CGC <u>GGATCC</u> TCAGACAAGCTGGAGAGGAG	

Supplementary Table S1. Specific primer sequences used for *SlCMB1* gene amplification and cloning procedures.

Primer Name	Primer Sequence (5'–3')	Product (bp)
SICAC	CCTCCGTTGTGATGTAACTGG	173 bp
	ATTGGTGGAAAGTAACATCATCG	
q-SlCMB1	TGAGCGTCAACTGGATTCATCTT	213 bp
	CCCTCTGACTGAGCAGGTTGTT	
ACO1	ACAAACAGACGGGACACGAA	181 bp
	CTCTTTGGCTTGAAACTTGA	
ACO3	CAAGCAAGTTTATCCGAAAT	113 bp
	CATTAGCTTCCATAGCCTTC	
4682	GAAAGAGTTGTTATGGCTGGTG	107 bp
AC52	GCTGGGTAGTATGGTGAAGGT	
ACS4	GCTCGGAGGTAGGATGGTTTC	151 bp
	GTTCCTCTTCCATTGTGCTTGT	
E4	AGGGTAACAACAGCAGTAGCA	167 bp
	CCCAACCTCCGTCTTCAC	
FS	GGCACCATTCAACATACCG	242 bp
20	CTTTCACCGAAGAAGCACG	
FRFI	TTTTAGTATCGGATGGACG	102 hn
	GGCGGAGAAACAGAAGTA	102 00
PSY1	AGAGGTGGTGGAAAGCAA	298 bp
1511	TCTCGGGAGTCATTAGCAT	
PDS	GCTTTACCCGCTCCTTTA	174 bp
105	ACCTTGCTTTCTCATCCA	
ICVR	TTGACTTAGAACCTCGTTATTGG	137 bp
LCID	AACAGTTCCCTTTGTCATTATCTC	
ICVE	GCCACAGGTTATTCAGTCGTCA	196 bp
LUIL	CCAGTCCAAATAGGAAAAACGAT	
СҮСВ	CGACGTGATCATTATCGGAGC	98 bp
	GTGGTGAAGGGTCAACACAACA	
RIN	CATCATGGCATTGTGGTGAGC	194 bp
	AATTCAAAGCATCCATCCAGGTAC	
TAGLI	CGCAATAACTCCCTGCCTGTA	143 bp
	GAAGATGAAGAGCCTTGACCC	
FI/I 1	AAAATCAGTGGGAAATCAACTCATC	139 bp
	CCTTGCTGCTGTGAAGAACTACC	
FUL2	CCGTGGGAGCAACAGAGTCAT	167 bp
	GGAGGCATCACAGAAGCACTG	
LoxC	TTTACTCCGCCCTACACGC	121 bp
	CCTGAAAGATCGACACCCA	
PE	GCTTGCGTCTTTGACAACTCAGG	137 bp
	GTGCCACCACTGCATTCGCTAT	

Supplementary Table S2. Specific primer sequences used for qRT-PCR analysis

## **Supplementary Figures**

-3391 ACAAGGAAGAATTCTTGCCTATAATTAGTGTGGGTCTTACTTTGTATTGGGAGAAGACAAATAATGTAAGAAAAGATGAACAACTTTATATTGAGGTTAGCGTAGC  $-2857 \quad \text{AIGTCTAAGGATCTAAAGAAGTCCAACGATCTTATTATCACTCTATTTGGATGAGGAGGGGGGATAAGGACCACTAATTATTTGGATCTTCATGGATCTTACAAATTAGAATTAGAATTAGAATTAGAACTAAGAAGTCAACAATTAGAA$ -2323 ACAATGCAAAAAAAAGAACTTTATTCTAATATGTCATTTCTTATTTCAAGATGTAATTGTAGATTCTCGACCAAAAAGAGATAAGAGAATAAGAAATAAGAATAATCCAATATTA -2109 TATATAAAGACTATGAAAAATTAAAAATAGGCACTTATCTAATTTTATATTATATTATGAAATGAGGTGTACTAATTGATATTTATGAAATTGGAATTGTGATATTCAAC -1889 ATTITAGTITATGTGATTACAAAATCTTGATTITAAATATATTAAATATCAAAATATGGTGAAATATTGTTTGATATGGAGTAGACATGATGACACATTCTTAGGTATCTAAA -1676 AGGTTGTTATACATTTTATTAGCACCAAAAATTCTTGTAAAAACCCTTGATTGCTAAATACTTTTCGACTTGCAATTATATGTGTTGACAGTGTAAAAGATATTCACG -1350 AATACACGATTCATCCCATTCTTGGTTTTTGATGTTAGATCTTCATACTAACATATTATCCACGCACTATATGTCCAGTCATAGGTAGAAAAAATATGTGATCTCTTTAA -1242 TATAATTTAGATATTTTTTCGTCATGAATTAACTTTTGAATTTTATAGATATGAATATTCCAATATAAGGGGCTAATAATGTATCTCCAATAAAAGGTCTTTTCAAAA -1132 ACTCCCCAATCCCAGTAAGGGATACAAATACCTACAACCTTTAATATTATGTCTTACAATTTCCATTAAAATGGAAATGTGGGAAAAACTTTTATTTTTAGTAGTTT -1025 ATAAAATAATGAGAATTGGAAACTTTTTAATAAAATGTAATTACAAACGTTTCTGATACTTATTACGAATCGTGATTTACTCATTTAAAAAAATTGTATAAAAATGTATAAAAATT -698 TTTTGTAATTTGATACAAATTAAATACCACCCCAAAATAGGGGCAAAAACTTGATATTAAAAGGTTAGTTGGTGAGAAAACCAAAAATAATAATAGGTTAATAGGATAAT -592 -380 TTATTATTTTATTTTGCTATACATATGAGATAACATATTCCGTTATTAAAATATAAATGGGGTAGGAGAAATAATCTAAGAATAACTACCTAAGCTTTCAACTAAACAC -272 ACGATAA AATTTATCCTGAA ATTATTATACCTTATACGTCAGATATAAGAA AAATAGATACAATGTTGTAATATTAGGAA ACCCCATGGCCCAACAAAGCTATTTATT -164 TATTACCCTAAGAACAAAAGGACAGAAAAAAGGACCAAAAACCATAACCACAACATACCAATATCCTATTATACATAGCCTTTTTTCTTTTCCTTTTATCAAAACATGA CTAGATTTTGAGATTATAATAATAAGATTTTTGATACTATATTTTTATAATAATATTATAATGGGAAGAGGTAAGGGTAGAGATTGAAGAGAATAGAAAATAA

**Supplementary Fig. S1.** Promoter analysis of *SlCMB1* gene. Promoter sequence (3500 bp regions upstream the 5' end of the predicted ORF) of *SlCMB1* gene was extracted from SGN database and searched against the promoter database plant CARE (http://bioinformatics. Psb.ugent.be/webtools/plantcare/html/), ERE motif (ATTTCAAA) are the ethylene-responsive element in *SlCMB1* promoter region.



**Supplementary Fig. S2.** Hairpin construct of the *SlCMB1* gene for double-stranded RNAi vector. The *SlCMB1* gene-specific sequence in the antisense and sense orientations were linked with a PDK gene fragment and as a transcriptional unit for hairpin RNA expression which premoted by the CaMV 35S promoter and terminated by the OCS terminator. Among which, *Spe*I and *Xba*I are isocaudamers.



**Supplementary Fig. S3.** Multiple sequence alignment of *SlCMB1* and *RIN*. The 426 bp 3' specific fragment of *SlCMB1* used in this study is indicated by the red line.



**Supplementary Fig. S4.** Construct of SICMB1 and RIN gene for yeast two-hybrid vector. (A) The ORFs of *SIMADS-RIN*, *SIMADS1*, *SIAP2a*, *TAGL1* were cloned into pGBKT7 bait vector to obtain the vector pGBKT7-*SIMADS-RIN*, pGBKT7-*SIMADS1*, pGBKT7-*AP2a* and pGBKT7-*TAGL1*, respectively. (B) The ORF of *SICMB1* was cloned into pGADT7 prey vector to obtain the vector pGADT7-*SICMB1*.



**Supplementary Fig. S5.** Yeast two-hybrid assay for SICMB1 and SIMADS-RIN, SIMADS1, SIAP2a and TAGL1. TDO, SD medium without Trp, His, Ade (autoactivation assay); SDO, SD medium without Trp (autoactivation assay).