

Supplemental Table S1. List of the DNA primers used in this study.

Primer name	Sequence (5' to 3')
SlbHLH113-Q-F	TGCTGTTAGGAAAGCGGAGG
SlbHLH113-Q-R	TGGGGTTGGAGGAGCATAGA
SlbHLH133-Q-F	AATGGTGTACGCCCCGTATC
SlbHLH133-Q-R	AGTTGTTTGGTGGTGCCTGA
SlbHLH138-Q-F	AGTTGGAATCTGTTTCGGAC
SlbHLH138-Q-R	GGACTAGAAGGCTTATCGAA
PL5-Q-F	ATCGTGCGGATCAGGGAATC
PL5-Q-R	TTCCGGGTTTAGGGTTCACG
COBRA4-Q-F	CATCCGTCCCACTCGTTTCA
COBRA4-Q-R	TGCTACTTTTACGGCAGCCA
EXT10-Q-F	CCCCACCCGTAAAATCACCT
EXT10-Q-R	TGGTTGTGGAATAATGGCCAAG
EXT90-Q-F	CCTCCACCCTCACCAACAAA
EXT90-Q-R	GCAAGGGCAACTAGTCCCAA
CNR10-Q-F	TGTGGGGACTGTTTGCTTCA
CNR10-Q-R	CTCCTTGAACCTCCTGGAGCC
ACO-Q-F	AGGAAATCCCCGAGACATGC
ACO-Q-R	GCCTAGTCCCTCAGCACATC
ACO1-like-F	GTGCAAGGGGCCATTTTCATT
ACO1-like-R	AGCCCACCAATTTGATCTTGT
ACO1-Q-F	ACTGTGCAAAAGGCCAATTCAT
ACO1-Q-R	AGGTTGACAAGTAGAGCACCA
ERF.C7-Q-F	TCGAAAACGTCCATGGGGAA
ERF.C7-Q-R	AGGACCACGCATTGAGAGTG
ATP3-Q-F	GGGTGGGCAAGTATGGTCAA
ATP3-Q-R	CAAGCCTTATGTGGAGGGCA
SlbHLH113-AD-F	gtaccagattacgtcatatgATGGTTACTGGGAATATGTTGTGG
SlbHLH113-AD-R	atgccacccgggtggaattcTTATTGCCCTACCGGTGAAAGT
SIMAP70-1-BD-F	tcagaggaggacctgcatatgATGGCGGAGGATGGAAGTG
SIMAP70-1-BD-R	tcgacggatccccgggaattcTTATTGTGTGCGTGTTAACCCAC
SLIQD21a-BD-F	tcagaggaggacctgcatatgATGGGCAAGAAAGGAAGTGGT
SLIQD21a-BD-R	tcgacggatccccgggaattcTCAGTACTTTATTAACCAACCAAAATATATA TATATA
SIACTIN2-Q-F	TTGCTGACCGTATGAGCAAG
SIACTIN2-Q-R	GGACAATGGATGGACCAGAC

Supplemental Table S2. Intra-genotype statistical comparison of fruit shape index between values at different developmental stages and the initial level at 0 DPA.

	Time point	P-value	Significance
WT	5 DPA	0.0026	**
	10 DPA	0.0368	*
	15 DPA	0.0173	*
	Red ripe	0.1826	NS
SlbHLH113 OE	5 DPA	<0.0001	***
	10 DPA	<0.0001	***
	15 DPA	<0.0001	***
	Red ripe	<0.0001	***

Note: Statistical differences were assessed by independent samples *t*-test for pairwise comparisons between each developmental stage and the 0 DPA. NS indicates no significant difference ($P \geq 0.05$); * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

Supplemental Table S3. Promoter analysis of candidate genes for bHLH binding motifs within 3000 bp upstream of the start codon (ATG). Both sense and antisense strands were examined. Numbers in parentheses indicate the count of each motif type.

Gene ID	Gene name	E-box/G-box (CACGTG)	G-box-like motifs	Total bHLH binding sites
Solyc02g093580	PL5	No	2 (CACATG)	2
Solyc03g114890	COBRA4	Yes (1)	No	1
Solyc09g098510	EXT10	No	2 (CACATG)	2
Solyc01g006390	EXT90	No	2 (CACATG) 4 (CATGTG)	6
Solyc04g009860	ACO1	Yes (1)	1 (CAGGAG) 1 (CAGATG) 1 (CATGTG) 2 (CACGTT)	6
Solyc04g009850	ACO1-like	No	2 (CATGTG) 1 (CACGTT)	3
Solyc12g006380	ACO	No	2 (CATGTG) 1 (CAGGAG) 3 (CACATG)	6
Solyc11g011740	ERF.C7	No	1 (AACGTG)	1
Solyc11g013310	ATP3	Yes (1)	1 (CAGGAG) 1 (CATGTG)	3
Solyc07g041720	ABP19a	Yes (2)	2 (CACATG) 1 (CACGTT)	5
Solyc01g005470	CNR10	No	1 (CACGTT) 1 (CACATG)	2
Solyc04g048900		No	1 (CACGTT)	1
Solyc10g055760		Yes (1)	1 (CATGTG) 2 (CACGTT)	4
Solyc06g069790		No	3 (CACATG) 1 (CATGTG)	4
Solyc08g067340		Yes (1)	1 (CACGTG) 1 (CAGGAG)	3
Solyc03g095770		Yes (2)	3 (CACATG) 4 (CATGTG) 1 (CAGGTT)	10
Solyc09g015770		Yes (1)	1 (CAGGTT) 1 (CATGTG)	3
Solyc04g081000		No	1 (CAGGAG) 2 (CATGTG) 1 (CACATG)	4
Solyc10g055780		No	1 (CATGTG) 1 (CACGTG)	2
Solyc10g055810		No	1 (CACGTT)	1
Solyc05g050130		Yes (1)	2 (CATGTG)	3
Solyc10g055800		No	1 (CAGGAG) 1 (CATGTG) 1 (CACGTT)	3