

## Cytological and molecular characterization of carotenoid accumulation in normal and high-lycopene mutant oranges

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### Supplementary data

**Figure S1.** Carotenoid biosynthetic pathway in higher plants with the sites inhibited by CPTA and NFZ indicated.

**Figure S2.** The mRNA sequences of *phytoene synthase 1* (*PSY1*) alleles, *PSY1-a* and *PSY1-b*, in Newhall and Cara Cara oranges.

**Figure S3.** The mRNA sequences of *lycopene  $\beta$ -cyclase* (*LCYB*) alleles, *LCYB-a* and *LCYB-b*, in Newhall and Cara Cara oranges.

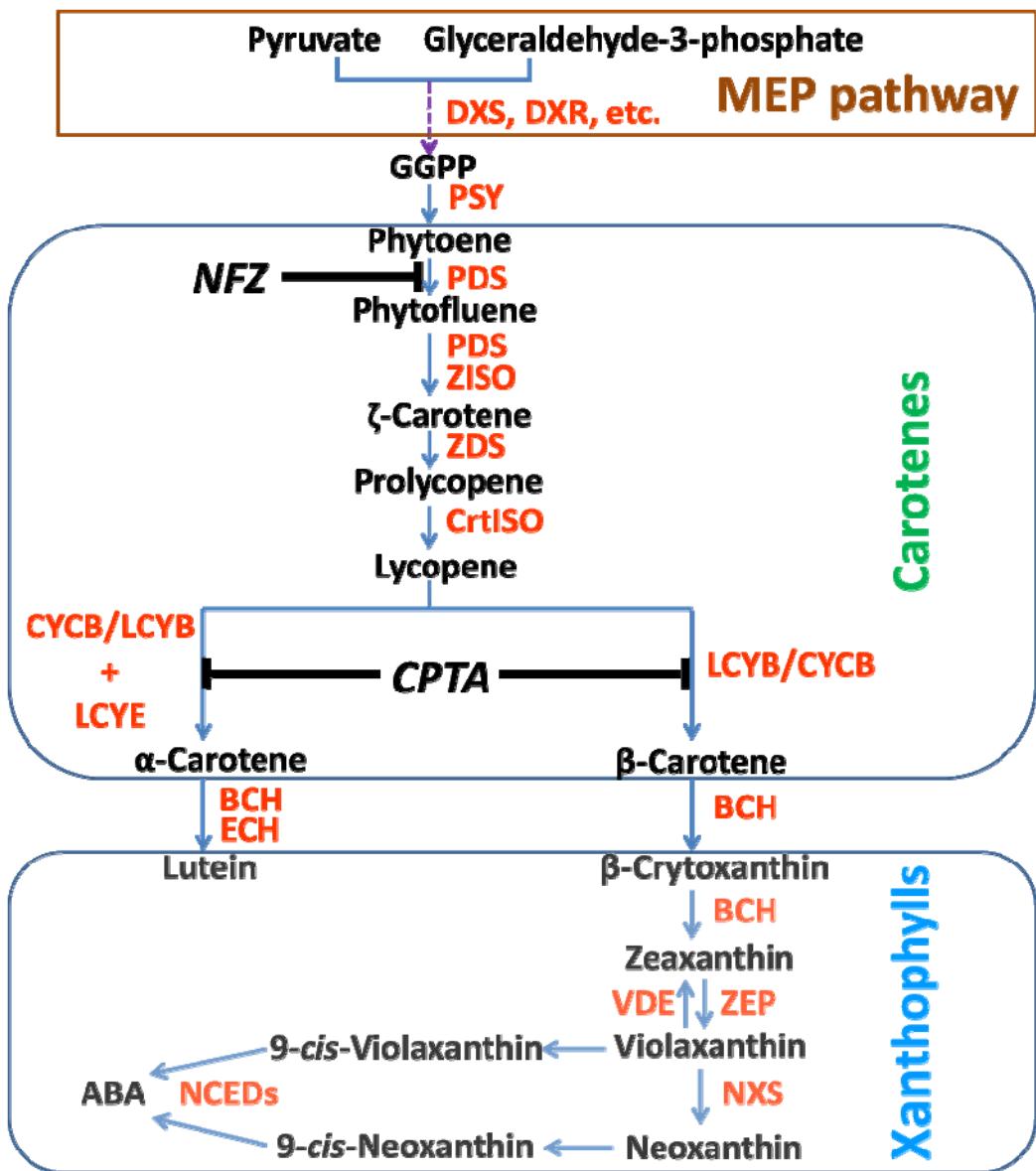
**Figure S4.** The mRNA sequences of *chromoplast-specific lycopene  $\beta$ -cyclase* (*CYCB*) alleles, *CYCB-a* and *CYCB-b*, in Newhall and Cara Cara oranges.

**Figure S5.** The observation of red crystalline chromoplast under the light microscope in 2-(4-chlorophenylthio)-triethylamine hydrochloride (CPTA) treated albedo layers of Newhall, control Newhall and control Cara Cara oranges.

**Table S1.** List of primers for real-time quantitative PCR.

**Table S2.** Effects of 2-(4-chlorophenylthio)-triethylamine hydrochloride (CPTA) and norflurazon treatments on accumulation of carotenoids in *in vitro* cultured flesh tissues of Newhall and Cara Cara.

**Table S3.** List of primers for full-length gene cloning.



**Supplementary Fig. S1.** Carotenoid biosynthetic pathway in higher plants with the sites inhibited by CPTA and NFZ indicated. BCH,  $\beta$ -carotene hydroxylase; CPTA, 2-(4-chlorophenylthio)-triethylamine hydrochloride; CRTISO, carotene isomerase; CYCB, chromoplast-specific lycopene  $\beta$ -cyclase; DDXS, 1-deoxy-D-xylulose 5-phosphate-synthase; DXR, 1-deoxy-D-xylulose 5-phosphate reductoisomerase; ECH,  $\epsilon$ -carotene hydroxylase; GGPP, geranylgeranyl diphosphate; LCYB, lycopene  $\beta$ -cyclase; LCYE, lycopene  $\epsilon$ -cyclase; MEP, 2-C-methyl-D-erythritol 4-phosphate; NCED, nine-*cis*-epoxycarotenoid dioxygenase; NFZ, norflurazon; NXS, neoxanthin synthase; PDS, phytoene desaturase; PSY, phytoene synthase; VDE, violaxanthin de-epoxidase; ZDS,  $\zeta$ -carotene desaturase; ZEP, zeaxanthin epoxidase; ZISO, 15-*cis*- $\zeta$ -carotene isomerase

	*            20            *            40            *            60            *            80	
PSY1-a	: CTACAGAGAGTTGAAGTTACAGGGGCTCAAATTTCTTTATCCAAAAAAATAATTTCACAGCATGTCGTGTTACATT	: 82
PSY1-b	: CTACAGAGAGTTGAAGTTACAGGGGCTCAAATTTCTTTATCCAAAAAAATAATTTCACAGCATGTCGTGTTACATT	: 82
	*            100            *            120            *            140            *            160	
PSY1-a	: GCTGGGGTTGATCACCTAACACTACAATTGCCAATTGCTTCGGGTCGCGATTCAAGTCAGGAGAGAAAACAGGCTGTT	: 164
PSY1-b	: GCTGGGGTTGATCACCTAACACTACAATTGCCAATTGCTTCGGGTCGCGATTCAAGTCAGGAGAGAAAACAGGCTGTT	: 164
	*            180            *            200            *            220            *            240	
PSY1-a	: TATTCACTAACAGATTCTTACCAACATCAAACCGGACTGCTGTTAATTCTAGACCTAACAGCTTAATAATAATAATAATA	: 246
PSY1-b	: TATTCACTAACAGATTCTTACCAACATCAAACCGGACTGCTGTTAATTCTAGACCTAACAGCTTAATAATAATAATAATA	: 246
	*            260            *            280            *            300            *            320	
PSY1-a	: A-----GCAGAGACGGAATTCTTATCCTTAGATAACAGATTGAGGCATCCTTGCTCATCTGGAAATCGACTTGCCGAAAT	: 322
PSY1-b	: ATAATAAGCAGAACGGAATTCTTATCCTTAGATAACAGATTGAGGCATCCTTGCTCATCTGGAAATCGACTTGCCGAAAT	: 328
	*            340            *            360            *            380            *            400            *	
PSY1-a	: ATCATGTATGGTTGCTAGCACTGCTGGAGAAGTGGCCATGCTTCAGAAGAAATGGTTACATGTTGCTCAAGCAGGCA	: 404
PSY1-b	: ATCATGTATGGTTGCTAGCACTGCTGGAGAAGTGGCCATGCTTCAGAAGAAATGGTTACATGTTGCTCAAGCAGGCA	: 410
	*            420            *            440            *            460            *            480            *	
PSY1-a	: GCCTTGGTTAATAAGCAACCAAGTGGGTTACTCGTGTATGTCGAAACCCAGATAATTGCTTACCCGGAACCTTAAAGTC	: 486
PSY1-b	: GCCTTGGTTAATAAGCAACCAAGTGGGTTACTCGTGTATGTCGAAACCCAGATAATTGCTTACCCGGAACCTTAAAGTC	: 492
	*            500            *            520            *            540            *            560            *	
PSY1-a	: TGCTCACTGAAGCTATGATCGTTGGAGAAGTTGCGCCGAGTATGCTAAAGACATTAACTTACTTGGGAACCTTGGCTGATGAC	: 568
PSY1-b	: TGCTCACTGAAGCTATGATCGTTGGAGAAGTTGCGCCGAGTATGCTAAAGACATTAACTTGGGAACCTTGGCTGATGAC	: 574
	*            580            *            600            *            620            *            640            *	
PSY1-a	: CCTGAAAGGCAGAGGGCTATATGGCTATATATGTTGTTGAGGACAGATGAGCTCGTTGATGGGCTAATGCTTC	: 650
PSY1-b	: CCTGAAAGGCAGAGGGCTATATGGCTATATATGTTGTTGAGGACAGATGAGCTCGTTGATGGGCTAATGCTTC	: 656
	*            660            *            680            *            700            *            720            *            7	
PSY1-a	: CACATAACTCCAACAGCTTAGACAGGTGGAGAAGCTTCCAGGGTGGAGAAGACCTTTCCGGGGTCGTCCATTGATATGCTTGATG	: 732
PSY1-b	: CACATAACTCCAACAGCTTAGACAGGTGGAGAAGCTTCCAGGGTGGAGAAGACCTTTCCGGGGTCGTCCATTGATATGCTTGATG	: 738
	*            40            *            760            *            780            *            800            *            820	
PSY1-a	: CTGCAATTATCAGATACAGTAACCAATTTCCTGTCGACATTAGCCATTCAGAGATATGATAGAAGGAATGAGGATGGACCT	: 814
PSY1-b	: CTGCAATTATCAGATACAGTAACCAATTTCCTGTCGACATTAGCCATTCAGAGATATGATAGAAGGAATGAGGATGGACCT	: 820
	*            840            *            860            *            880            *            900	
PSY1-a	: TAGGAAGTCAGATAACAAAACCTTGTGAATTATACTTGTATTGTTATTATGTTGCTGGGACCGTAGGGCTAATGAGTGT	: 896
PSY1-b	: TAGGAAGTCAGATAACAAAACCTTGTGAATTATACTTGTATTGTTATTATGTTGCTGGGACCGTAGGGCTAATGAGTGT	: 902
	*            920            *            940            *            960            *            980	
PSY1-a	: CCAGTTATGGGCATAGCACCTGACTCACAGGCAACAAACAGAGAGCGCTACAAATGCAAGCATTGGCACTAGGGATTGCTAATC	: 978
PSY1-b	: CCAGTTATGGGCATAGCACCTGACTCACAGGCAACAAACAGAGAGCGCTACAAATGCAAGCATTGGCACTAGGGATTGCTAATC	: 984
	*            1000            *            1020            *            1040            *            1060	
PSY1-a	: AGCTCACTAACATACTCAGAGATGTTGGAGAGGGATGCCAAGAGGAAGGGTTTATCTACCACAAAGATGAGTTGGCACAGGC	: 1060
PSY1-b	: AGCTCACTAACATACTCAGAGATGTTGGAGAGGGATGCCAAGAGGAAGGGTTTATCTACCACAAAGATGAGTTGGCACAGGC	: 1066
	*            1080            *            1100            *            1120            *            1140	
PSY1-a	: AGGGCTTCAGATGATGACATATTGCTGGAGAGGTGACCAATTGAGGAAACTCTATGAGAAGAACAAATTAAAGAGGGCA	: 1142
PSY1-b	: AGGGCTTCAGATGATGACATATTGCTGGAGAGGTGACCAATTGAGGAAACTCTATGAGAAGAACAAATTAAAGAGGGCA	: 1148
	*            1160            *            1180            *            1200            *            1220            *	
PSY1-a	: AGGATGTTCTTGTATGGCTGAGAACGGTGTGACCGAGCTGAGTGAAGCTAGTCAGATGGCCGGTATGGGCTTCATTGCTGT	: 1224
PSY1-b	: AGGATGTTCTTGTATGGCTGAGAACGGTGTGACCGAGCTGAGTGAAGCTAGTCAGATGGCCGGTATGGGCTTCATTGCTGT	: 1230
	*            1240            *            1260            *            1280            *            1300            *	
PSY1-a	: TGTACCGGCAAATACTGGATGAGATTGAGGCAATGATTACAACAACTTCACAAAGAGAGCTTATGAGTAAAGCCAAGAA	: 1306
PSY1-b	: TGTACCGGCAAATACTGGATGAGATTGAGGCAATGATTACAACAACTTCACAAAGAGAGCTTATGAGTAAAGCCAAGAA	: 1312
	*            1320            *            1340            *            1360            *            1380            *	
PSY1-a	: GATAGCTGCACTACCAATTGCAATGCRRAAATCCCTCTTACGCCGTCAGAATATACCAAGTAAGGCTTAAACTGAACAT	: 1388
PSY1-b	: GATAGCTGCACTACCAATTGCAATGCRRAAATCCCTCTTACGCCGTCAGAATATACCAAGTAAGGCTTAAACTGAACAT	: 1394
	*            1400            *            1420            *            1440            *            1460            *	
PSY1-a	: TTAACATCAAAGTTAGAACGATATAGTTGAAACGGGTTAAAGTGGAAATGATTGCTTGTATATTAG	: 1470
PSY1-b	: TTAACATCAAAGTTAGAACGATATAGTTGAAACGGGTTAAAGTGGAAATGATTGCTTGTATATTAG	: 1476
	*            1480            *            1500            *            1520            *            1540            *	
PSY1-a	: GAATTGTTGGTATGCAGCATGTTGATGGTAAAGTTAGAATAGTGTGAATCCAATTCCAAAGGCCGATGCCCTA	: 1549
PSY1-b	: GAATTGTTGGTATGCAGCATGTTGATGGTAAAGTTAGAATAGTGTGAATCCAATTCCAAAGGCCGATGCCCTA	: 1555
		GAATTGTTGGTATGCAGCATGTTGATGGTAAAGTTAGAATAGTGTGAATCCAATTCCAAAGGCCGATGCCCTA

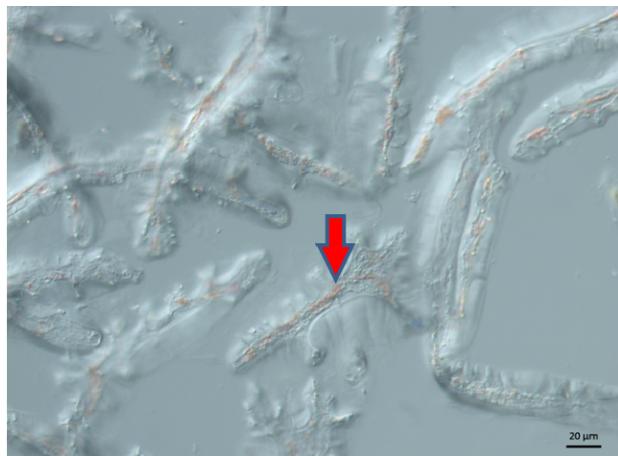
**Supplementary Fig. S2.** The mRNA sequences of *phytoene synthase 1* (*PSY1*) alleles, *PSY1-a* and *PSY1-b*, in Newhall and Cara Cara oranges. Note that, no difference in sequence was observed between the two oranges. Start codon and stop codon are underlined by red.

	*      20      *      40      *      60      *      80	
LCYB-a	ACCAGGAGCTAGGTTGGCTCAAGAAGTCGTCAAAAGAGGAATA <u>GAGTTGTTCA</u> TTAAGGC <u>TAGTAGTAGTGCCTC</u>	: 82
LCYB-b	ACCAGGAGCTAGGTTGGCTCAAGAAGTCGTCAAAAGAGGAATA <u>GAGTTGTTCA</u> TTAAGGC <u>TAGTAGTAGTGCCTC</u>	: 82
	*      100      *      120      *      140      *      160	
LCYB-a	<u>TTTGGAC</u> CTAGTTCTGAAACCAAGAAGGAAATCTTGAG <u>TCTCCATGTATGACCCATCAAAGGGC</u> CTTGTTGTA	: 164
LCYB-b	<u>TTTGGAC</u> CTAGTTCTGAAACCAAGAAGGAAATCTTGAG <u>TCTCCATGTATGACCCATCAAAGGGC</u> CTTGTTGTA	: 164
	*      180      *      200      *      220      *      240	
LCYB-a	GACCTAGCAGTTGTCGGTGGCGCCCGCTGGGCTTGCTAGCAAG <u>TTCA</u> GAGGGCGGGCTTC <u>AGTTTGCTCGA</u>	: 246
LCYB-b	GACCTAGCAGTTGTCGGTGGCGCC <u>GCTGGGCTTGCTAGCAAG</u> TTCA <u>GAGGGCGGGCTTC</u> GGTTGCTCGA	: 246
	*      260      *      280      *      300      *      320	
LCYB-a	TTGATCCATCTCCC <u>AAATTGATTTGGCCAA</u> ATTA <u>TTATGGTGT</u> TTGGG <u>GATGA</u> TTTGAGGCC <u>CATGGATTGCTTGA</u> TTG	: 328
LCYB-b	TTGATCCATCTCCC <u>AAATTGATTTGGCCAA</u> ATTA <u>TTATGGTGT</u> TTGGG <u>GATGA</u> TTTGAGGCC <u>CATGGATTGCTTGA</u> TTG	: 328
	*      340      *      360      *      380      *      400      *	
LCYB-a	CCTTGATA <u>ACTACTGGTCTGGTCTGGTGTG</u> CACATTGATGATA <u>AATACA</u> AA <u>AGGATCTT</u> ATAGAC <u>CTTATGG</u> AGAGTT	: 410
LCYB-b	CCTTGATA <u>ACTACTGGTCTGGTCTGGTGTG</u> CACATTGATGATA <u>AATACA</u> AA <u>AGGATCTT</u> ATAGAC <u>CTTATGG</u> AGAGTT	: 410
	*      420      *      440      *      460      *      480      *	
LCYB-a	AATAGGAAGTTGCTGAAGTC <u>GAAGTC</u> AAAAATGCT <u>GCACAA</u> ATG <u>CATAACCA</u> ATGGTGT <u>TTAAGT</u> CC <u>ACCAAGCT</u> AA <u>AGGTT</u> ATTAAGG	: 492
LCYB-b	AATAGGAAGTTGCTGAAGTC <u>GAAGTC</u> AAAAATGCT <u>GCACAA</u> ATG <u>CATAACCA</u> ATGGTGT <u>TTAAGT</u> CC <u>ACCAAGCT</u> AA <u>AGGTT</u> ATTAAGG	: 492
	*      500      *      520      *      540      *      560      *	
LCYB-a	TTATTAC <u>TAAGAGTC</u> AA <u>AGGCTC</u> AA <u>ATCTTGTGATTTGCA</u> AT <u>GATGGT</u> GC <u>ACATT</u> CA <u>GGCTGCGCTT</u> CTTGAT <u>GTCACGGG</u>	: 574
LCYB-b	TTATTAC <u>TAAGAGTC</u> AA <u>AGGCTC</u> AA <u>ATCTTGTGATTTGCA</u> AT <u>GATGGT</u> GC <u>ACATT</u> CA <u>GGCTGCGCTT</u> CTTGAT <u>GTCACGGG</u>	: 574
	*      580      *      600      *      620      *      640      *	
LCYB-a	GTTCT <u>CTAGGTGTC</u> TT <u>GTCAGATGATA</u> AC <u>CCCTATA</u> AT <u>CCACGGT</u> TT <u>ACCAAGT</u> GG <u>CATATGG</u> AT <u>ACTAG</u> GT <u>GAGGTAGAA</u>	: 656
LCYB-b	GTTCT <u>CTAGGTGTC</u> TT <u>GTCAGATGATA</u> AC <u>CCCTATA</u> AT <u>CCACGGT</u> TT <u>ACCAAGT</u> GG <u>CATATGG</u> AT <u>ACTAG</u> GT <u>GAGGTAGAA</u>	: 656
	*      660      *      680      *      700      *      720      *      7	
LCYB-a	GAGCACCCGTT <u>GATTTAGACA</u> AG <u>ATGGTTTC</u> CAT <u>GGATGG</u> G <u>AGATTCG</u> C <u>ATCTGA</u> AC <u>AACAA</u> CC <u>ATCGGAGCT</u> CAA <u>AGGG</u>	: 738
LCYB-b	GAGCACCCGTT <u>GATTTAGACA</u> AG <u>ATGGTTTC</u> CAT <u>GGATGG</u> G <u>AGATTCG</u> C <u>ATCTGA</u> AC <u>AACAA</u> CC <u>ATCGGAGCT</u> CAA <u>AGGG</u>	: 738
	*      40      *      760      *      780      *      800      *      820	
LCYB-a	CAAATAG <u>CAAATTCT</u> ACT <u>TTTCTTTATG</u> CC <u>ATGCCCTT</u> CG <u>CAACACAGGAT</u> TT <u>CTGTA</u> AG <u>AGACTTCG</u> C <u>TAGTGGC</u>	: 820
LCYB-b	CAAATAG <u>CAAATTCT</u> ACT <u>TTTCTTTATG</u> CC <u>ATGCCCTT</u> CG <u>CAACACAGGAT</u> TT <u>CTGTA</u> AG <u>AGACTTCG</u> C <u>TAGTGGC</u>	: 820
	*      840      *      860      *      880      *      900	
LCYB-a	CGGGC <u>CTGGAGT</u> GC <u>CAATGAA</u> AG <u>ATATCCAGGAA</u> GA <u>ATGGCT</u> AG <u>ATTAAGC</u> ACT <u>TAGGC</u> AT <u>AAAAGTT</u> AA <u>AAGCATT</u>	: 902
LCYB-b	CGGGC <u>CTGGAGT</u> GC <u>CAATGAA</u> AG <u>ATATCCAGGAA</u> GA <u>ATGGCT</u> AG <u>ATTAAGC</u> ACT <u>TAGGC</u> AT <u>AAAAGTT</u> AA <u>AAGCATT</u>	: 902
	*      920      *      940      *      960      *      980	
LCYB-a	GAAGAG <u>GATG</u> A <u>CATTGTGTC</u> AT <u>CCGATGGG</u> G <u>GGGCC</u> CT <u>CCAGT</u> GT <u>CTCTCA</u> AA <u>AGAGTT</u> GT <u>GGGA</u> AT <u>AGGTGGTACCG</u>	: 984
LCYB-b	GAAGAG <u>GATG</u> A <u>CATTGTGTC</u> AT <u>CCGATGGG</u> G <u>GGGCC</u> CT <u>CCAGT</u> GT <u>CTCTCA</u> AA <u>AGAGTT</u> GT <u>GGGA</u> AT <u>AGGTGGTACCG</u>	: 984
	*      1000      *      1020      *      1040      *      1060	
LCYB-a	CTGGG <u>ATGGT</u> GC <u>ACCCCT</u> CA <u>ACTGG</u> CT <u>ATATGGT</u> GG <u>CAAGG</u> AC <u>TTAGCT</u> GC <u>GGCT</u> CC <u>CTTATGGT</u> GC <u>AAATG</u> CA <u>ATCGTTC</u>	: 1066
LCYB-b	CTGGG <u>ATGGT</u> GC <u>ACCCCT</u> CA <u>ACTGG</u> CT <u>ATATGGT</u> GG <u>CAAGG</u> AC <u>TTAGCT</u> GC <u>GGCT</u> CC <u>CTTATGGT</u> GC <u>AAATG</u> CA <u>ATCGTTC</u>	: 1066
	*      1080      *      1100      *      1120      *      1140	
LCYB-a	AAGC <u>CTCAGT</u> CT <u>GACAGA</u> AG <u>CAATTG</u> TC <u>AGGAC</u> AC <u>AAATTG</u> TC <u>GTCTGA</u> AG <u>TTTG</u> GG <u>CCCATAGAA</u> AG <u>GGGAGA</u>	: 1148
LCYB-b	AAGC <u>CTCAGT</u> CT <u>GACAGA</u> AG <u>CAATTG</u> TC <u>AGGAC</u> AC <u>AAATTG</u> TC <u>GTCTGA</u> AG <u>TTTG</u> GG <u>CCCATAGAA</u> AG <u>GGGAGA</u>	: 1148
	*      1160      *      1180      *      1200      *      1220      *	
LCYB-a	AGG <u>CAAAGGGAGT</u> CT <u>CTCTG</u> TT <u>GGTATGG</u> AT <u>ATCCTG</u> CT <u>CAAACTTG</u> ACT <u>TACCTGCC</u> ACT <u>AGAAGGTT</u> TT <u>CGATG</u> CTT	: 1230
LCYB-b	AGG <u>CAAAGGGAGT</u> CT <u>CTCTG</u> TT <u>GGTATGG</u> AT <u>ATCCTG</u> CT <u>CAAACTTG</u> ACT <u>TACCTGCC</u> ACT <u>AGAAGGTT</u> TT <u>CGATG</u> CTT	: 1230
	*      1240      *      1260      *      1280      *      1300      *	
LCYB-a	TTTTG <u>ATCTGGAGC</u> CT <u>GTTATTGG</u> AT <u>GGTTCTT</u> AT <u>CATCG</u> AG <u>ATGTTCT</u> CC <u>CCCAGCTT</u> AG <u>TTTTGG</u> CT <u>TT</u>	: 1312
LCYB-b	TTTTG <u>ATCTGGAGC</u> CT <u>GTTATTGG</u> AT <u>GGTTCTT</u> AT <u>CATCG</u> AG <u>ATGTTCT</u> CC <u>CCCAGCTT</u> AG <u>TTTTGG</u> CT <u>TT</u>	: 1312
	*      1320      *      1340      *      1360      *      1380      *	
LCYB-a	TCT <u>ATTCTC</u> AC <u>ATGCC</u> CT <u>TAATACT</u> CT <u>AGG</u> CT <u>AGAGAT</u> CA <u>GGCA</u> AA <u>GGGA</u> AC <u>CTTCC</u> TT <u>GGTAA</u> AT <u>GATCA</u> AA <u>ACAC</u>	: 1394
LCYB-b	TCT <u>ATTCTC</u> AC <u>ATGCC</u> CT <u>TAATACT</u> CT <u>AGG</u> CT <u>AGAGAT</u> CA <u>GGCA</u> AA <u>GGGA</u> AC <u>CTTCC</u> TT <u>GGTAA</u> AT <u>GATCA</u> AA <u>ACAC</u>	: 1394
	*      1400      *      1420      *	
LCYB-a	TTGGTACA <u>AGATACAGAT</u> TA <u>AGGTGACCA</u> <u>GATA</u> TT <u>ATAAT</u>	: 1436
LCYB-b	TTGGTACA <u>AGATACAGAT</u> TA <u>AGGTGACCA</u> <u>GATA</u> TT <u>ATAAT</u>	: 1436
	TTGGTACA <u>AGATACAGAT</u> TA <u>AGGTGACCA</u> <u>GATA</u> TT <u>ATAAT</u>	

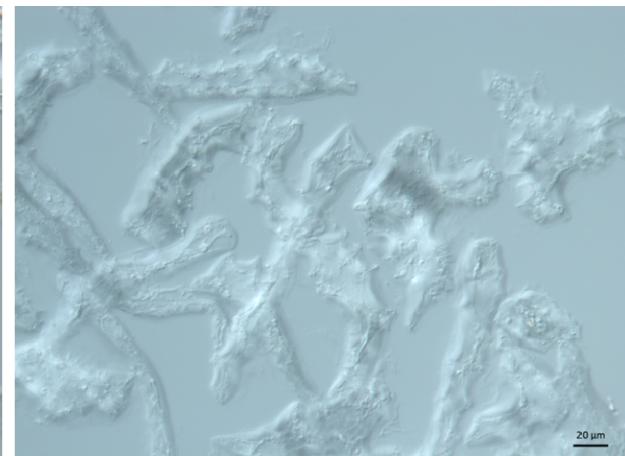
**Supplementary Fig. S3.** The mRNA sequences of lycopene  $\beta$ -cyclase (*LCYB*) alleles, *LCYB-a* and *LCYB-b*, in Newhall and Cara Cara oranges. Note that, no difference in sequence was observed between the two oranges. Start codon and stop codon are underlined by red.

	*      20      *      40      *      60      *      80		
CYCB-a :	CTTTCTTGTCTTCTCATTTCTCGGCTGGCATGGCAACTCTCTAGGCCGTTTCTCCCTCTCTTAGCTAAAG	:	82
CYCB-b :	CTTTCTTGTCTTCTCATTTCTCGGCTGGCATGGCAACTCTCTAGGCCGTTTCTCCCTCTCTTAGCTAAAG	:	82
	*      100      *      120      *      140      *      160		
CYCB-a :	TTTCGCAAATAATTGATTCAACATCATCACGTTCATTTCTCTATTTCCATTAGGCCGAAAATGCATGTTCAAGAAAGGC	:	164
CYCB-b :	TTTCGCAAATAATTGATTCAACATCATCACGTTCATTTCTCTATTTCCATTAGGCCGAAAATGCATGTTCAAGAAAGGC	:	164
	*      180      *      200      *      220      *      240		
CYCB-a :	GGATCATCATCATCATCACAGGATCCGGACAAGGTTGGTAACCTCTAGAGTGACACCGGAGTCGGTACCTGAATT	:	246
CYCB-b :	GGATCATCATCATCATCACAGGATCCGGACAAGGTTGGTAACCTCTAGAGTGACACCGGAGTCGGTACCTGAATT	:	246
	*      260      *      280      *      300      *      320		
CYCB-a :	TTAGCTTTGATCCCCCTGGTTTATCCGCGATCGTATTGATATGACGTGATCATCATTGGCACTGGACAGCCGGCC	:	328
CYCB-b :	TTAGCTTTGATCCCCCTGGTTTATCCGCGATCGTATTGATATGACGTGATCATCATTGGCACTGGACAGCCGGCC	:	328
	*      340      *      360      *      380      *      400		
CYCB-a :	TCCGCTAGCTGAGCAAGTCTCATCGCGCATGGTCAAGGTATGTTGTTGATCCTCACCTCTTACGTGGCCTAA	:	410
CYCB-b :	TCCGCTAGCTGAGCAAGTCTCATCGCGCATGGTCAAGGTATGTTGTTGATCCTCACCTCTTACGTGGCCTAA	:	410
	*      420      *      440      *      460      *      480		
CYCB-a :	CAACTATGGAGTTGGGTTGATGAGTTGAGACATAGGACTTGTAGACTGTTGGACAAAACTTGCCGATGACTTGTGT	:	492
CYCB-b :	CAACTATGGAGTTGGGTTGATGAGTTGAGACATAGGACTTGTAGACTGTTGGACAAAACTTGCCGATGACTTGTGT	:	492
	*      500      *      520      *      540      *      560		
CYCB-a :	TTTATTAAATGATCACAAAGACCAAGTATCTAGACAGGCCCTACGGTCGTTAGTAGAAATATTTGAAGACAAAGTTATTAG	:	574
CYCB-b :	TTTATTAAATGATCACAAAGACCAAGTATCTAGACAGGCCCTACGGTCGTTAGTAGAAATATTTGAAGACAAAGTTATTAG	:	574
	*      580      *      600      *      620      *      640		
CYCB-a :	AGAATTGTGTTCAAAATGGAGTTAAGTTGATGAGTTGGCACTGTGAATCATCAGGAGTTCGAGTCCTCGATTG	:	656
CYCB-b :	AGAATTGTGTTCAAAATGGAGTTAAGTTGATGAGTTGGCACTGTGAATCATCAGGAGTTCGAGTCCTCGATTG	:	656
	*      660      *      680      *      700      *      720      *      7		
CYCB-a :	TTGTGATGGAAATGAGATTAAAGGCTAGCTTGATTGATGCTAGTGGCTTTGCTAGTAGTTGTTGAGTATGATAAG	:	738
CYCB-b :	TTGTGATGGAAATGAGATTAAAGGCTAGCTTGATTGATGCTAGTGGCTTTGCTAGTAGTTGTTGAGTATGATAAG	:	738
	*      40      *      760      *      780      *      800      *      820		
CYCB-a :	CCAAGAACCATGGATACCAATTGCTCATGGGATTTTAGCTGAGGTCACCCCTTTGATTGACAAAAATGGTT	:	820
CYCB-b :	CCAAGAACCATGGATACCAATTGCTCATGGGATTTTAGCTGAGGTCACCCCTTTGATTGACAAAAATGGTT	:	820
	*      840      *      860      *      880      *      900		
CYCB-a :	TCATGGATTGGAGAGATCCCATTAGGGAAATGAGCCTACTTGCAGGCTAGCAATTGAGCTCCAACTTTCTATGC	:	902
CYCB-b :	TCATGGATTGGAGAGATCCCATTAGGGAAATGAGCCTACTTGCAGGCTAGCAATTGAGCTCCAACTTTCTATGC	:	902
	*      920      *      940      *      960      *      980		
CYCB-a :	AATGCCATTGATTCAAATTGGTATTGGTATTTAGAAGAACATCTTGTAGTAGGCTAGGCTATTTGTTGATATAAGAGGTTAAC	:	984
CYCB-b :	AATGCCATTGATTCAAATTGGTATTGGTATTTAGAAGAACATCTTGTAGTAGGCTAGGCTATTTGTTGATATAAGAGGTTAAC	:	984
	*      1000      *      1020      *      1040      *      1060		
CYCB-a :	AGCAGAATGGCAGCGAGGTTAAGGCATATGGAAATTAGAGTTAAAGAGTATTGAGATGAAAATGTTGATTCCAATGG	:	1066
CYCB-b :	AGCAGAATGGCAGCGAGGTTAAGGCATATGGAAATTAGAGTTAAAGAGTATTGAGATGAAAATGTTGATTCCAATGG	:	1066
	*      1080      *      1100      *      1120      *      1140		
CYCB-a :	GAGGCTCTGCGCTGTGATCCCCTGGCTGGCTGATGCAATAGCTGATGCTTGGCTCAACCAGGATGATCAGAGGC	:	1148
CYCB-b :	GAGGCTCTGCGCTGTGATCCCCTGGCTGGCTGATGCAATAGCTGATGCTTGGCTCAACCAGGATGATCAGAGGC	:	1148
	*      1160      *      1180      *      1200      *      1220		
CYCB-a :	GGTGGCTCGGACCATGGCTCTGGCCCTGCTGGCTGATGCAATAGCTGATGCTTGGCTCAACCAGGATGATCAGAGGC	:	1230
CYCB-b :	GGTGGCTCGGACCATGGCTCTGGCCCTGCTGGCTGATGCAATAGCTGATGCTTGGCTCAACCAGGATGATCAGAGGC	:	1230
	*      1240      *      1260      *      1280      *      1300      *      1320		
CYCB-a :	AGGCCACITTCATCAGAAAGTGTGGAATGGGTGTGGCCAATTGACAGAAGATGCAATTAGGGAGTTTATTCTATGGTATGC	:	1312
CYCB-b :	AGGCCACITTCATCAGAAAGTGTGGAATGGGTGTGGCCAATTGACAGAAGATGCAATTAGGGAGTTTATTCTATGGTATGC	:	1312
	*      1340      *      1360      *      1380      *      1400		
CYCB-a :	AGACTTTGTTGAAGGCTGGATTGAGGGACTAGGGAGATCTTTGATGCTTCTTGTGATTGACAGAGATGCAATTAGGGAGTTTATTCTATGGTATGC	:	1394
CYCB-b :	AGACTTTGTTGAAGGCTGGATTGAGGGACTAGGGAGATCTTTGATGCTTCTTGTGATTGACAGAGATGCAATTAGGGAGTTTATTCTATGGTATGC	:	1394
	*      1420      *      1440      *      1460		
CYCB-a :	GTTTCTGCTCAAGGTTGTCTTGCAGAGCTTGTGGCTAAGGCTGTCTCTTGGACACGCCCTCGAATTCTCCAGG	:	1476
CYCB-b :	GTTTCTGCTCAAGGTTGTCTTGCAGAGCTTGTGGCTAAGGCTGTCTCTTGGACACGCCCTCGAATTCTCCAGG	:	1476
	*      1480      *      1500      *      1520      *      1540      *      15		
CYCB-a :	TTCTGATAATTGTTACCAAGTGGCTCTGGCTGGTAAAGATGGGAAATTGAGCTTGTGCCCCCTGAAACCATTTGAAAGATTAAATG	:	1558
CYCB-b :	TTCTGATAATTGTTACCAAGTGGCTCTGGCTGGTAAAGATGGGAAATTGAGCTTGTGCCCCCTGAAACCATTTGAAAGATTAAATG	:	1558
	*      60		
CYCB-a :	TTCTTGAAATAATTAGCGTCTC : 1579		
CYCB-b :	TTCTTGAAATAATTAGCGTCTC : 1579		

**Supplementary Fig. S4.** The mRNA sequences of *chromoplast-specific lycopene β-cyclase (CYCB)* alleles, CYCB-a and CYCB-b, in Newhall and Cara Cara oranges. Note that, no difference in sequence was observed between the two oranges. Start codon and stop codon are underlined by red.



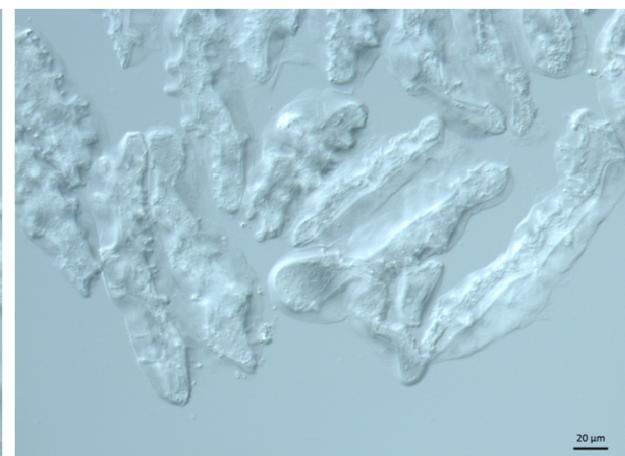
**CPTA treated Newhall  
albedo layers**



**Control Newhall  
albedo layers**



**Control Cara Cara  
albedo layers  
with red chromoplasts**



**Control Cara Cara  
albedo layers  
without red chromoplasts**

**Supplementary Fig. S5.** The observation of red crystalline chromoplast under the light microscope in 2-(4-chlorophenylthio)-triethylamine hydrochloride (CPTA) treated albedo layers of Newhall, control Newhall and control Cara Cara oranges. Bar, 20 $\mu$ m.

**Supplementary Table S1.** List of primers for real-time quantitative PCR

Gene	Primers (Forward; Reverse)	Genome accession
<i>Actin</i>	5'-CATCCCTCAGCACCTTCC-3'; 5'-CCAACCTTAGCACTTCTCC-3'	Cs1g05000
<i>BCH</i>	5'-GTTGCCATAATCAACGC-3'; 5'-CTCTCCGGAAATAAGGCA-3'	Cs9g19270
<i>CCD1</i>	5'-GCACGAAATGGAATAGTGGC-3'; 5'-CTTAGTAGGAGGAGTCTCG-3'	Cs7g01710
<i>CRTISO</i>	5'-ATTGATAACCCAAGCACTG-3'; 5'-TGAGGCAGATAATAGGCAAG-3'	Cs6g13340
<i>CYCB</i>	5'-CCCTATTCCATTAGGCCGC-3'; 5'-CACGTCATATCGAATACGATC-3'	Cs1g04120
<i>CYCB-a</i>	5'-GAGCAAGTCTCATCGCGTCATA-3' 5'-ACTTAGCCTTATGAAACTTAACCTCATTG-3'	
<i>CYCB-b</i>	5'-GCAAGTCTCATCGCGTCATGGTA-3' 5'-ACTTAGCCTTATGAAACCTAACGCCATT-3	
<i>DXR</i>	5'-GAAGTTAAAGTGGCTGATGC-3'; 5'-GAAGAATCCTGTGTTCGAC-3'	Cs5g05440
<i>DXS1</i>	5'-CCGCATTCTCATTCCCGACT-3'; 5'-TTGTGAGTGTAACTCTCCTCT-3'	Cs9g05150
<i>DXS2</i>	5'-TTCCGGGATTGCTATTGGAG-3'; 5'-AAATCAATTTCAGCCGCC-3'	Cs1g20530
<i>LCYB</i>	5'-GAACCAGGAGCTTAGGTCTG-3'; 5'-GCTAGGTCTACAACAAGGCC-3'	orange1.1t00772
<i>LCYE</i>	5'-AACCCATCTGATTGGTCGT-3'; 5'-AGAACACAGTAGCAAGCCT-3'	Cs4g14850
<i>NCED2</i>	5'-CCATGGCCTTGGACATGGCG-3'; 5'-TGATGCATTGGGGATGGAG-3'	Cs2g03270
<i>NCED3</i>	5'-CTTAGCCTTGGACGCAGTC-3'; 5'-GAATGCAGTCGGGACCTTT-3'	Cs5g14370
<i>PDS</i>	5'-TTCAGCCGATTGATTTC-3'; 5'-ACACCCTGCTTCTCATCCA-3'	orange1.1t02361
<i>PSYI</i>	5'-CTACAATGCAGCATTGGCAC-3'; 5'-CATGAAGTTCTCCATTAAATGG-3'	Cs6g15910
<i>PSYI-a</i>	5'-CAAGATGAGTTGGCACAGGCA-3' 5'-AGCCCATAACCGGCCATCG-3'	
<i>PSYI-b</i>	5'-CAAGATGAGTTGGCACAGGCG-3' 5'-GAAGCCCATAACCGGCCATCT-3'	
<i>PSY2</i>	5'-TTACAATGCAGCATTGGCCT-3'; 5'-CATGAAGTTCTCCATTAAAT-3'	orange1.1t00657
<i>VDE</i>	5'-ACCGAATGCCAGATCAAATGTGG-3'; 5'-CCACCATATCCATCCCATGC(A/G)TC-3'	Cs5g26080
<i>ZDS</i>	5'-TCATCCCAAGGTTAGAAG-3'; 5'-TACCAGACAAAGTTGCTCC-3'	orange1.1t06069
<i>ZEP</i>	5'-ACTTGTACACTGGAATTGCAGA-3'; 5'-CCCATATTGGCTGCATAGCATG-3'	orange1.1t04051
<i>ZISO</i>	5'-ACTCCGTCTCCTCCCTTCA-3'; 5'-TTACCTGCCAACCATCTGT-3'	Cs5g24730

**Supplementary Table S2.** Effects of 2-(4-chlorophenylthio)-triethylamine hydrochloride (CPTA) and norflurazon treatments on accumulation of carotenoids in *in vitro* cultured flesh tissues of Newhall and Cara Cara. The 0 week tissues were separated from fruit at S5 stage.

Treatment	Contents ( $\mu\text{g g}^{-1}$ FW)								
	Phytoene	Phytofluene	$\beta$ -Carotene	Lycopene	Violaxanthin	Luteoxanthin	<i>cis</i> -Violaxanthin	Others	Total carotenoids
Control (2 weeks) Newhall					0.20 $\pm 0.05$	0.20 $\pm 0.02$	0.56 $\pm 0.11$	0.12 $\pm 0.02$	1.08 $\pm 0.13$
Control (2 weeks) Cara Cara	24.07 $\pm 0.20$	3.87 $\pm 0.17$	0.14 $\pm 0.08$	5.85 $\pm 0.30$	0.12 $\pm 0.03$	0.11 $\pm 0.02$	0.36 $\pm 0.05$	0.57 $\pm 0.05$	35.08 $\pm 0.70$
CPTA (2 weeks) Newhall	1.60 $\pm 0.07$	0.39 $\pm 0.03$		13.91 $\pm 0.89$			0.14 $\pm 0.01$	1.41 $\pm 0.11$	17.44 $\pm 1.02$
CPTA (2 weeks) Cara Cara	10.64 $\pm 0.49$	1.91 $\pm 0.11$	0.24 $\pm 0.03$	7.39 $\pm 0.45$			0.03 $\pm 0.02$	0.82 $\pm 0.01$	21.04 $\pm 0.98$
Norflurazon (2 weeks) Newhall	32.22 $\pm 0.53$	1.77 $\pm 0.03$		0.01 $\pm 0.00$	0.03 $\pm 0.00$	0.04 $\pm 0.00$			34.07 $\pm 0.55$
Norflurazon (2 weeks) Cara Cara	46.60 $\pm 1.34$	3.04 $\pm 0.08$		2.62 $\pm 0.17$			0.02 $\pm 0.01$	0.53 $\pm 0.03$	52.81 $\pm 1.48$
Control (4 weeks) Newhall	0.03 $\pm 0.03$			0.17 $\pm 0.01$	0.27 $\pm 0.02$	0.60 $\pm 0.05$	0.41 $\pm 0.03$	1.48 $\pm 0.04$	
Control (4 weeks) Cara Cara	33.44 $\pm 1.44$	5.33 $\pm 0.24$		5.37 $\pm 0.46$	0.10 $\pm 0.02$	0.19 $\pm 0.05$	0.37 $\pm 0.04$	0.85 $\pm 0.09$	45.64 $\pm 2.24$
CPTA (4 weeks) Newhall	2.52 $\pm 0.03$	0.83 $\pm 0.02$		18.13 $\pm 0.69$	0.05 $\pm 0.00$	0.03 $\pm 0.00$	0.24 $\pm 0.00$	1.40 $\pm 0.06$	23.20 $\pm 0.80$
CPTA (4 weeks) Cara Cara	31.48 $\pm 1.28$	6.25 $\pm 0.23$		16.64 $\pm 0.74$	0.02 $\pm 0.00$		0.08 $\pm 0.02$	1.47 $\pm 0.05$	55.95 $\pm 2.29$
Norflurazon (4 weeks) Newhall	60.09 $\pm 3.37$	4.13 $\pm 0.20$		0.04 $\pm 0.01$	0.07 $\pm 0.00$	0.13 $\pm 0.02$	0.08 $\pm 0.01$	64.54 $\pm 3.59$	
Norflurazon (4 weeks) Cara Cara	82.76 $\pm 2.15$	5.10 $\pm 0.17$		0.64 $\pm 0.00$	0.03 $\pm 0.00$	0.05 $\pm 0.02$	0.24 $\pm 0.04$	88.82 $\pm 2.31$	

**Supplementary Table S3.** List of primers for full-length gene cloning

Gene	Primers (Forward; Reverse)
<i>CYCB</i>	5'- CTTCTTTGTCTTCTCATTTC-3' 5'- GAGACGCTAATTATTCAAGAAC-3'
<i>LCYB</i>	5'-TGAAGATTAGAACCAGGAG-3' 5'- GCATGAGTTATTAAGCACATTA-3'
<i>PSY1</i>	5'-CTACAGAGAGTTGAAGTTACAGGG-3' 5'-TAGGGCATCGGCCTTGGATTGTG-3'