

Supplementary Materials

TaLCYE-A1	ME-STGAAISAPFGCRALRWAGQRPLRAAD-----ARRRRVSGPGPGP-----EQWRS-	47
TaLCYE-B1	ME-STGAAISAPFGCRALRWAGQRPLRPAD-----ARRRRVSGPGPGP-----EQWRS-	47
TaLCYE-D1	ME-STGAAISAPFGCRALRWAGQRPLRPAD-----GRRRRVSGPGPGP-----EKWRS-	47
AetLCYE	ME-STGAAISAPFGCRALRWAGQRPLRPAD-----GRRRRVSGPGPGP-----EKWRS-	47
HvLCYE	ME-STGAAISAPFGCRALRWAGQRPLRAAD-----ARRRRVSGPGPGP-----EQWRS-	47
OsLCYE	MEFSGGATVSAPFGCCRAAWGAAAGAGAE-GRSRRVVP----RAVE-----PRRRGRW	49
PamLCYE	MG-LSGAAISAPLGCRLPRGAVGGGGKAR-RAEAERWR----WAGA-----GRRSGGA	48
BdLCYE	ME-FTGATVSAPFGCRALRGGGQRPLRAAGLAADGRRRRRAAGSKPGA-----QQWRNNR	53
ZmLCYE	MG-LSGATISAPLGCCVLRCAVG-GGKAL-KADAERWR----RAGW-----SRRVGGP	47
SobLCYE	MG-LSGATISAPLGCRLRRGAVG-GGKAR-KAEAERWR----RAGW-----SRRVGGP	47
PhLCYE	MG-LSGAAISAPLGCRLPRSAFGGGGKAR-GAEAERWR----RAGA-----GRRSGGA	48
AtLCYE	-----MECVGARNFAAMAV-----STFPSWSCRKFPVVKRYSYRNIRFGLC	42
NtLCYE	-----MDCIGARNFATMAV-----FTCPRFKSLGRRRIMPRKKQP-----IW	37

Plant β -Lcy conserved region

TaLCYE-A1	KASCVATEKP--DEKAAPGL--EFADDEDYVKGGGGELLYVQMQATKAMESQSKIASKLL	103
TaLCYE-B1	KASCVATEKP--DEKAAPGLGVDFADEEDYVKGGGGELLYVQMQATKAMESQSKIASKLL	105
TaLCYE-D1	KASCVATEKP--DEKAAPGLGVDFADEEDYVKGGGGELLYVQMQATKAMESQSKIASKLL	105
AetLCYE	KASCVATEKP--DEKAAPGLGVDFADEEDYVKGGGGELLYVQMQATKAMESQSKIASKLL	105
HvLCYE	KASCVATEKP--DEKAAPGLGVDFADEEDYVKGGGGELLYVQMQATKAMESQSKIASKLL	105
OsLCYE	MVRCVATEKHKDAAARRGGVEVEFADEEDYVKGGGGELLYVQMQASKMSDSQSKIASKLL	109
PamLCYE	KVRCVATEKHDEAA---AAVGVEFADEEDYVKGGGGELLYVQMQATKAMESQSKIASKLL	105
BdLCYE	KVRCVATEKHKDNKAAAAGLGVEFADEEDYVKGGGGELLYVQMQATKAMESQSKIASKLL	113
ZmLCYE	KVRCVATEKHDETAAVGAAVGVEFADEEDYVKGGGGELLYVQMQSTKPMESQSKIASKLL	107
SobLCYE	KVTCVATEKHDETA---VGVEFADEEDYVKGGGGELLYVQMQATKPMESQSRISKLL	103
PhLCYE	KVRCVATEKHDETA---AAVGVEFADEEDYVKGGGGELLYVQMQATKPMESQSKIASKLL	105
AtLCYE	SVRASG--GGSSGSESCVAVREDFADEEDYVKGAGGSEILFVQMQQNKMDQESKLVDKLP	100
NtLCYE	P-IHMQ--VKCSGNESCVVVKEDFADEEDYVKGAGGSELVFMQQNKMDLQSKLSDKLR	94

Dinucleotide binding signature

VIXGXGXGXGXXA

TaLCYE-A1	PIA-DETSVLDLVIIGCGPAGLSLAAESAKKGLTVGLIGP--DLPFTNNYGVWEDEFKDL	160
TaLCYE-B1	PIA-DETSVLDLVIIGCGPAGLSLAAESAKKGLTVGLIGP--DLPFTNNYGVWEDEFKDL	162
TaLCYE-D1	PIA-DETSVLDLVIIGCGPAGLSLAAESAKKGLTVGLIGP--DLPFTNNYGVWEDEFKDL	162
AetLCYE	PIA-DETSVLDLVIIGCGPAGLSLAAESAKKGLTVGLIGP--DLPFTNNYGVWEDEFKDL	162
HvLCYE	PIA-DETSVLDLVIIGCGPAGLSLAAESAKKGLTVGLIGP--DLPFTNNYGVWEDEFKDL	162
OsLCYE	PIP-DENSVLDLVIIGCGPAGLSLAAESAKKGLNVGLIGP--DLPFTNNYGVWEDEFKDL	166
PamLCYE	PIS-DENSVLDLVIIGCGPAGLSLASESAKKGLTVGLIGP--DLPFTNNYGVWEDEFKDL	162
BdLCYE	PIA-DETSVLDLVIIGCGPAGLSLAAESAKKGLTVGLIGP--DLPFTNNYGVWEDEFKDL	170
ZmLCYE	PIS-DENTVLDLVIIGCGPAGLSLASESAKKGLTVGLIGP--DLPFTNNYGVWEDEFKDL	164
SobLCYE	PIS-DENTVLDLVIIGCGPAGLSLASESAKKGLTVGLIGP--DLPFTNNYGVWEDEFKDL	160
PhLCYE	PIS-DETSVLDLVIIGCGPAGLSLASESAKKGLTVGLIGP--DLPFTNNYGVWEDEFKDL	162
AtLCYE	PIS-IGDGALDLVIGCGPAGLALAAESAKLGLKVGLIGP--DLPFTNNYGVWEDEFKDL	157
NtLCYE	QISSAGQTIIDLVIIGCGPAGLALAAESAKLGLNVGLVGP--DLPFTNNYGVWEDEFKDL	152

TaLCYE-A1	GLESCIEHVWKDTVVYLDLDR-NKPIMIGRAYGRVDRDLLHEELLRRCNDAAGVTYLNKSV	219
TaLCYE-B1	GLESCIEHVWKDTVVYLDLDR-NKPIMIGRAYGRVDRDLLHEELLRRCNDAAGVTYLNKSV	221
TaLCYE-D1	GLESCIEHVWKDTVVYLDLDR-NKPIMIGRAYGRVDRDLLHEELLRRCNDAAGVTYLNKSV	221
AetLCYE	GLESCIEHVWKDTVVYLDLDR-NKPIMIGRAYGRVDRDLLHEELLRRCNDAAGVTYLNKSV	221
HvLCYE	GLESCIEHVWKDTVVYLDLDR-NKPIMIGRAYGRVDRDLLHEELLRRCNDAAGVTYLNKSV	221
OsLCYE	GLESCIEHVWKDTIVYLDG-NKPIMIGRAYGRVDRDLLHEELLRRCNDAAGVTYLNKSV	225
PamLCYE	GLESCIEHVWKDTIVYLDN-NKPILIGRSYGRVDRDLLHEELLRRCNDAAGVTYLNKSV	221
BdLCYE	GLESCIEHVWKDTIVYLDH-NKPIMIGRAYGRVDRDLLHEELLRRCNDAAGVTYLNKSV	229
ZmLCYE	GLESCIEHVWKDTIVYLDN-NKPILIGRSYGRVDRDLLHEELLRRCNDAAGVTYLNKSV	223
SobLCYE	GLASCIEHVWKDTIVYLDN-NKPILIGRSYGRVDRDLLHEELLRRCNDAAGVTYLNKSV	219
PhLCYE	GLESCIEHVWKDTIVYLDN-NKPILIGRSYGRVDRDLLHEELLRRCNDAAGVTYLNKSV	221
AtLCYE	GLQKCIHVWRDTIVYLDLDR-DKPITIGRAYGRVDRDLLHEELLRRCNDAAGVTYLNKSV	216
NtLCYE	GLQACIEHVWRDTIVYLDLDR-ADPILIGRAYGRVDRDLLHEELLRRCNDAAGVTYLNKSV	211

TaLCYE-A1	IIESPdGHRVVCGRDRKILCRLAIVASGAASGKLLLEYEVGGPRVCVQTAYGVEVEVE	279
TaLCYE-B1	IKESPdGHRVVCGRGRKILCRLAIVASGAASGKLLLEYEVGGPRVCVQTAYGVEVEVE	281
TaLCYE-D1	IKESPdGHRVVCGRGHKILCRLAIVASGAASGKLLLEYEVGGPRVCVQTAYGVEVEVE	281
AetLCYE	IIESPdGHRVVCGRGRKILCRLAIVASGAASGKLLLEYEVGGPRVCVQTAYGVEVEVE	281
HvLCYE	IIESPdGHRVVCGRDRKILCRLAIVASGAASGKLLLEYEVGGPRVCVQTAYGVEVEVE	281
OsLCYE	IMESPdGHRVVCCEGDREVLCLRAIVASGAASGRLLLEYEVGGPRVCVQTAYGVEVEVE	285
PamLCYE	ITESPDGHRVVCCEGRGKILCRLAIVASGAASGRLLLEYEVGGPRVCVQTAYGVEVEVE	281
BdLCYE	IIESPdGHRVVCCEGRGHKILCRLAIVASGAASGKLLLEYEVGGPRVCVQTAYGVEVEVE	289
ZmLCYE	IIESPdGHRVVCCEKGRGKILCRLAIVASGAASGRLLLEYEVGGPRVCVQTAYGVEVEVE	283
SobLCYE	IIESPdGHRVVCCEKGRGKILCRLAIVASGAASGRLLLEYEVGGPRVCVQTAYGVEVEVE	279
PhLCYE	IIESPdGHRVVCCEGRGKILCRLAIVASGAASGRLLLEYEVGGPRVCVQTAYGVEVEVE	281
AtLCYE	ITEASDGLRLVACDDNNVIFCRLAIVASGAASGKLLLEYEVGGPRVCVQTAYGVEVEVE	276

NtLCYE	IVES ^{TS} GHSLVE ^{EG} DIVIP ^{CR} FVTVASGAASGKFL ^Q YELGGPRVS ^{VQ} TAYGVEVEVD ^{NN}	271
	CM I	
TaLCYE-A1	PYNPSLMVFMDYRDCFKKEKFS---HPEEANTFLYAMAMSSTRVFFFEETCLASKDAMPFD	336
TaLCYE-B1	PYDPSLMVFMDYRDCFKKEKFT---HPEEANTFLYAMAMSSTRVFFFEETCLASKDAMPFD	338
TaLCYE-D1	PYDPSLMVFMDYRDCFKKEKFT---HPEEANTFLYAMAMSSTRVFFFEETCLASKDAMPFD	338
AetLCYE	PYDPSLMVFMDYRDCFKKEKFT---HPEEANTFLYAMAMSSTRVFFFEETCLASKDAMPFD	338
HvLCYE	PYDPSLMVFMDYSDCFKKEKFS---HPEEANTFLYAMAMSSTRVFFFEETCLASKDAMPFD	338
OsLCYE	PYDPSLMVFMDYRDCFKDKFS---HPEQNPFLYAMPMSSTRVFFFEETCLASKDAMPFD	342
PamLCYE	PYDPSLMVFMDYRDCFKKEKFS---HSEQNPFLYAMPMSSTRVFFFEETCLASKDALPFD	338
BdLCYE	PYDPSLMVFMDYRDCFKENFS---HPEEANTFLYAMPMSSTRVFFFEETCLASKDAMPFD	346
ZmLCYE	PYDPSLMVFMDYRDCFKKEFS---HTEQNPFLYAMPMSSTRVFFFEETCLASKDAMPFD	340
SobLCYE	PYDPSLMVFMDYRDCFKKEFS---HTEQNPFLYAMPMSSTRVFFFEETCLASKDAMPFD	336
PhLCYE	PYDPSLMVFMDYRDCFKKEFS---HSEQNPFLYAMPMSSTRVFFFEETCLASKDAMPFD	338
AtLCYE	PYDPSLMVFMDYRDTNEKVR---SLEAEPFLYAMPMTKSLFFFEETCLASKDAMPFD	333
NtLCYE	PYDPSLMVFMDYRDYVRHDAQ---SLEAKYPTFLYAMPMTKSTRVFFFEETCLASKDAMPFD	328
	CM II	
TaLCYE-A1	LLKKRLMSRLDAMGVRIKVEEWEWSYIPVGGSLPNTDQKNLAFGAAASMVHPATGYSVV	396
TaLCYE-B1	LLKKRLMSRLDAMGVRIKVEEWEWSYIPVGGSLPNTDQKNLAFGAAASMVHPATGYSVV	398
TaLCYE-D1	LLKKRLMSRLDAMGVRIKVEEWEWSYIPVGGSLPNTDQKNLAFGAAASMVHPATGYSVV	398
AetLCYE	LLKKRLMSRLDAMGVRIKVEEWEWSYIPVGGSLPNTDQKNLAFGAAASMVHPATGYSVV	398
HvLCYE	LLKKRLMSRLDAMGVRIKVEEWEWSYIPVGGSLPNTDQKNLAFGAAASMVHPATGYSVV	398
OsLCYE	LLKKRLMSRLDAMGVRIKVEEWEWSYIPVGGSLPNTDQKNLAFGAAASMVHPATGYSVV	402
PamLCYE	VLKKRLMYRLDAMGVRIKVEEWEWSYIPVGGSLPNTDQKNLAFGAAASMVHPATGYSVV	398
BdLCYE	LLKKRLMYRLDAMGVRIKVEEWEWSYIPVGGSLPNTDQKNLAFGAAASMVHPATGYSVV	406
ZmLCYE	LLKKRLMYRLNAMGIRILKVEEWEWSYIPVGGSLPNTDQKNLAFGAAASMVHPATGYSVV	400
SobLCYE	LLKKRLMYRLNAMGIRILKVEEWEWSYIPVGGSLPNTDQKNLAFGAAASMVHPATGYSVV	396
PhLCYE	VLKKRLMYRLDAMGVRIKVEEWEWSYIPVGGSLPNTDQKNLAFGAAASMVHPATGYSVV	398
AtLCYE	LLKTKMLRLDLTIGIRILKVEEWEWSYIPVGGSLPNTDQKNLAFGAAASMVHPATGYSVV	393
NtLCYE	LLKKKMLRLNLTIGVRIKQIYEEWEWSYIPVGGSLPNTDQKNLAFGAAASMVHPATGYSVV	388
	Charged Region	
TaLCYE-A1	RSLSEAPRYASVISDILNRNVYSGGYLPGSSSEMSSPSMLAWGTLWPQERKRQRSFFLFGL	456
TaLCYE-B1	RSLSEAPRYASVISDILNRNVYSGGYLPGSSSEMSSPSMLAWGTLWPQERKRQRSFFLFGL	458
TaLCYE-D1	RSLSEAPRYASVISDILNRNVYSGGYLPGSSSEMSSPSMLAWGTLWPQERKRQRSFFLFGL	458
AetLCYE	RSLSEAPRYASVISDILNRNVYSGGYLPGSSSEMSSPSMLAWGTLWPQERKRQRSFFLFGL	458
HvLCYE	RSLSEAPRYASVISDILNRNVYSGGYLPGSSSEMSSPSMLAWGTLWPQERKRQRSFFLFGL	458
OsLCYE	RSLSEAPRYASVISDILNRNVYFGEYLPGTSQSSSPSMLAWRTLWPQERKRQRSFFLFGL	462
PamLCYE	RSLSEAPRYASVISDILNRNVPAQYLPGNSQNYSPSMLGSDNHRSSQ--QDVARVLGL	455
BdLCYE	RSLSEAPRYASVISDILNRNVYSGGYLPGSSQDSSPSMLAWRTLWPQERKRQRSFFLFGL	466
ZmLCYE	RSLSEAPRYASVISDILNRNVPAEYMLGNSQNYSPSMLAWRTLWPQERKRQRSFFLFGL	459
SobLCYE	RSLSEAPRYASVISDILNRNVPAEYLLGNSQNYSPSMLAWRTLWPQERKRQRSFFLFGL	455
PhLCYE	RSLSEAPRYASVISDILNRNVPAQYLPGNSQNYSPSMLAWRTLWPQERKRQRSFFLFGL	457
AtLCYE	RSLSEAPRYASVIAEILREETTK--QI-----NSNISRQAWDTLWPPERKRQRAFFLFGL	446
NtLCYE	RSLSEAPKCAVLANILRQNHVK--NMLTSSSTTSISTQAWNTLWPQERKRQRSFFLFGL	446
	β -Ley motif	
TaLCYE-A1	ALIIQLDNKGIQTFFET--FFRLPKWMWQGLGSTLSSVDLMLFALYMFIAIPNTLRMNLV	515
TaLCYE-B1	ALIIQLDNKGIQTFFES--FFRLPKWMWQGLGSTLSSVDLMLFALYMFIAIPNTLRMNLV	517
TaLCYE-D1	ALIIQLDNKGIQTFFES--FFRLPKWMWQGLGSTLSSVDLMLFALYMFIAIPNTLRMNLV	517
AetLCYE	ALIIQLDNKGIQTFFES--FFRLPKWMWQGLGSTLSSVDLMLFALYMFIAIPNTLRMNLV	517
HvLCYE	ALIIQLDNKGIQTFFET--FFRLPKWMWQGLGSTLSSVDLMLFALYMFIAIPNTLRMNLV	517
OsLCYE	ALIIQLNNEGIQTFFET--FFRLPKWMWQGLGSTLSSVDLILFAYMFIAIPNTLRMNLV	521
PamLCYE	NPTICGSN---TVEILHVCHSSES-----IANGPRQT-----	484
BdLCYE	ALIIQLDNKGIQTFFET--FFRLPKWMWQGLGSTLSSVDLMLFALYMFIAIPNTLRMNLV	525
ZmLCYE	ALIIQLNNEGIQTFFEA--FFRVPRWMWQGLGSTLSSVDLILFAYMFIAIPNTLRMNLV	518
SobLCYE	ALIIQLNNEGIQTFFEA--FFRVPRWMWQGLGSTLSSVDLILFAYMFIAIPNTLRMNLV	514
PhLCYE	ALIIQLNNEGIQTFFEA--FFRVPRWMWQGLGSTLSSVDLILFAYMFIAIPNTLRMNLV	516
AtLCYE	ALIVQFDTEGIRSFRT--FFRLPKWMWQGLGSTLSSVDLILFAYMFIAIPNTLRMNLV	505
NtLCYE	ALIIQLDIEGIRSFRA--FELVPKWMWQGLGSTLSSVDLILFAYMFIAIPNTLRMNLV	505
TaLCYE-A1	RHLLSDPTGSAMIRTYLTL--- 534	
TaLCYE-B1	RHLLSDPTGSAMIRTYLTL--- 536	
TaLCYE-D1	RHLLSDPTGSAMIRTYLTL--- 536	
AetLCYE	RHLLSDPTGSAMIRTYLTL--- 536	
HvLCYE	RHLLSDPTGSAMIRTYLTL--- 536	
OsLCYE	RHLLSDPTGSTMIKTYLTL--- 540	
PamLCYE	-----SPL----- 487	
BdLCYE	RHLLSDPTGSAMIKTYLTL--- 544	
ZmLCYE	RHLLSDPTGSTMIKTYLTL--- 537	
SobLCYE	RHLLSDPTGSTMIKTYLTL--- 533	
PhLCYE	RHLLSDPTGSTMIKTYLTL--- 535	
AtLCYE	NHLLSDPTGATMIKTYLTKV--- 524	
NtLCYE	RHLLSDPTGATMIKTYLTF--- 524	

Figure S1. Polypeptide alignment of LCYE proteins encoded by a selection of plant species. Conserved residues are highlighted in yellow. The characteristic regions of plant LCYE protein are indicated above the sequence: Conserved β -LCY region, Di-nucleotide binding site, Cyclase motifs (CM) I and II, Charged region and β -LCY motif.

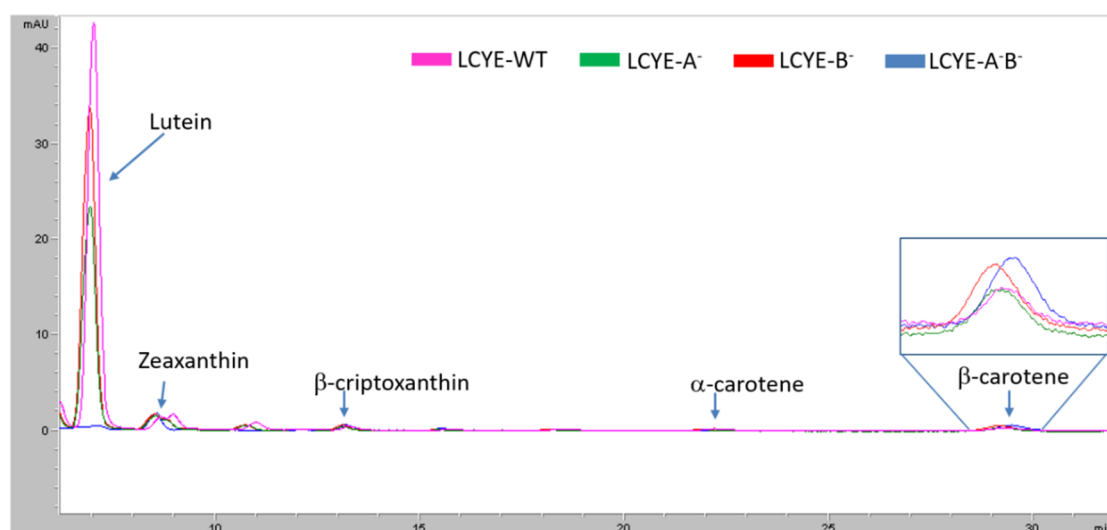


Figure S2. Representative HPLC-DAD chromatograms of grain carotenoids in LCYE-WT (wild type) and, LCYE-A⁻, LCYE-B⁻, LCYE-A-B⁻ mutants.

Table S1. Content ($\mu\text{g/g}$ d.w.) of each carotenoid detected in grain and leaf tissues on the biological replicates of WT and mutant accessions. The average values are reported in red. Variation % represent the increment/decrement of mean mutation in comparison to mean WT.

Type Mutation	Accession	Tissue	Lutein	Zeaxanthin	β -Cryptoxanthin	α -Carotene	β -Carotene
WT	LCYE-WT 104-1	grain	2.280	0.020	0.037	0.098	0.041
	LCYE-WT 104-1		2.346	0.020	0.028	0.096	0.033
	LCYE-WT 104-1		2.374	0.020	0.029	0.075	0.030
	LCYE-WT 108-2		1.690	0.025	0.021	0.045	0.044
	LCYE-WT 108-2		1.826	0.024	0.025	0.083	0.049
	average		2.103	0.022	0.028	0.079	0.040
A-	LCYE-A- E1-2	grain	1.807	0.040	0.020	0.044	0.042
	LCYE-A- E1-2		1.456	0.032	0.036	0.072	0.048
	LCYE-A- E1-2		1.770	0.038	0.022	0.043	0.041
	LCYE-A- C3-2		2.637	0.026	0.025	n.d.	0.058
	LCYE-A- C3-2		2.642	0.024	0.021	n.d.	0.057
	LCYE-A- C3-2		2.727	0.028	0.027	n.d.	0.057
	LCYE-A- MS28		1.430	0.029	0.021	0.039	0.038
	LCYE-A- MS28		1.253	0.030	0.021	0.038	0.036
	LCYE-A- MS28		1.352	0.027	0.025	0.056	0.036
	average		1.897	0.030	0.024	0.032	0.046
	variation %		-10%	+39%	-13%	-59%	+16%
B-	LCYE-B- G5-1	grain	1.922	0.028	0.020	0.040	0.049
	LCYE-B- G5-1		1.673	0.028	0.024	0.041	0.045
	LCYE-B- G5-2		1.181	0.026	0.024	0.076	0.030
	LCYE-B- G5-2		1.109	0.023	0.021	0.074	0.033
	LCYE-B- 104-4		1.556	0.028	0.029	0.057	0.056
	LCYE-B- 104-4		1.663	0.032	0.033	0.072	0.063
	LCYE-B- 104-4		1.606	0.029	0.040	0.065	0.061
	average		1.530	0.028	0.027	0.061	0.048
	variation %		-27%	+26%	-3%	-23%	+21%

A-B-	grain	LCYE-A-B- D2-2	0.027	0.028	0.029	n.d.	0.062
		LCYE-A-B- D2-2	0.028	0.028	0.030	n.d.	0.052
		LCYE-A-B- D2-2	0.031	0.029	0.028	n.d.	0.054
		LCYE-A-B- P2-8	0.050	0.012	0.040	n.d.	0.072
		LCYE-A-B- P2-8	0.072	0.030	0.073	n.d.	0.073
		LCYE-A-B- P2-8	0.089	0.019	0.083	n.d.	0.092
		LCYE-A-B- 103-1	0.099	0.036	0.033	n.d.	0.068
		LCYE-A-B- 103-1	0.060	0.036	0.030	n.d.	0.076
		LCYE-A-B- 103-1	0.064	0.038	0.037	n.d.	0.074
		average	0.058	0.028	0.043	n.d.	0.069
		variation %	-97%	+30%	+52%	-100%	+75%
WT	leaf	LCYE-WT 104-1	673.078	n.d.	28.052	18.340	250.678
		LCYE-WT 104-1	766.275	n.d.	33.473	21.322	287.327
		LCYE-WT 104-1	729.165	n.d.	32.440	20.460	275.953
		LCYE-WT 108-2	533.365	n.d.	25.190	16.089	224.013
		LCYE-WT 108-2	518.845	n.d.	23.767	15.170	210.745
		LCYE-WT 108-2	560.340	n.d.	27.720	17.105	229.898
		average	621.598	n.d.	28.518	18.029	245.587
A-	leaf	LCYE-A- E1-2	605.692	n.d.	31.942	3.608	1218.503
		LCYE-A- E1-2	484.955	n.d.	27.791	3.019	1024.446
		LCYE-A- E1-2	540.358	n.d.	28.926	3.251	1132.812
		LCYE-A- C3-2	450.577	n.d.	24.462	3.361	973.544
		LCYE-A- C3-2	515.624	n.d.	27.331	3.852	1079.698
		LCYE-A- MS28	663.182	n.d.	32.154	5.621	1234.423
		LCYE-A- MS28	356.633	n.d.	19.212	3.177	731.330
		LCYE-A- MS28	433.538	n.d.	24.991	4.356	958.272
		average	506.320	n.d.	27.101	3.781	1044.128
		variation %	-19%	n.d.	-5%	-79%	+325%
B-	leaf	LCYE-B- G5-1	445.745	n.d.	24.973	2.731	965.780
		LCYE-B- G5-1	330.002	n.d.	19.773	4.154	758.516
		LCYE-B- G5-1	546.358	n.d.	29.951	3.317	1123.132
		LCYE-B- G5-2	482.682	n.d.	28.223	3.169	1025.669
		LCYE-B- G5-2	472.760	n.d.	26.892	2.981	1005.342
		LCYE-B- 104-4	517.429	n.d.	29.384	4.199	1075.289
		LCYE-B- 104-4	494.082	n.d.	30.785	4.301	1125.585
		LCYE-B- 104-4	530.884	n.d.	29.159	3.974	1049.144
		average	477.493	n.d.	27.392	3.603	1016.057
		variation %	-23%	n.d.	-4%	-80%	+314%
A-B-	leaf	LCYE-A-B- D2-2	18.927	n.d.	23.176	17.006	235.177
		LCYE-A-B- D2-2	21.024	n.d.	23.355	12.525	230.319
		LCYE-A-B- D2-2	19.790	n.d.	26.247	11.875	264.986
		LCYE-A-B- P2-8	16.304	n.d.	37.719	10.282	358.305
		LCYE-A-B- P2-8	17.895	n.d.	34.201	8.016	328.246
		LCYE-A-B- P2-8	18.685	n.d.	31.363	6.252	301.383
		LCYE-A-B- 103-1	28.435	n.d.	26.632	6.186	263.228
		LCYE-A-B- 103-1	33.174	n.d.	30.954	6.815	303.999
		LCYE-A-B- 103-1	29.957	n.d.	27.978	4.625	276.341
		average	22.688	n.d.	29.069	9.287	284.665
		variation %	-96%	n.d.	+2%	-48%	+16%

Table S2. PCR primer sequences.

Primer name	Sequence (5'-3')	Target	Genbank acc. N°	Application	Reference
LCY3A F2	AGGAGAAATGAGCACAAGTGTCTGC	ϵ -lycopene cyclase-A1	EU649785.1	Genotyping/1st PCR	In this paper
LCY3A R2	GGATGTCAAATGTTGCAAC				In this paper
LCY3A-ex9 F	GCTGCTAACCACTGTCTGATA	ϵ -lycopene cyclase-A1	EU649785.1	Genotyping/2nd PCR	In this paper
LCY3A-ex9 R	GCCAATCCAAAGAGGAAGAATG				In this paper
LCY3B F1	TACAAACGTCATTGTGTACA	ϵ -lycopene cyclase-B1	EU649786.1	Genotyping/1st PCR	In this paper
LCY3B R2	GGATGCCAAATGTTACAAGG				In this paper
LCY3B-ex7 F	GCTGAATTTCTGTTGAGTCTTGAT	ϵ -lycopene cyclase-B1	EU649786.1	Genotyping/2nd PCR	In this paper
LCY3B-ex7 R	CTTCTGGTCTGTGTTAGGTAAGG				In this paper
LCYE-B RT Fw	CAAAGAGAAGTTCACACAC	ϵ -lycopene cyclase	EU649786.1	RT-PCR	In this paper
LCYE 3B-ex7 Rev	CTTCTGGTCTGTGTTAGGTAAGG				In this paper
Actin Fw	CACTGGAATGGTCAAGGCTG	Reference gene	AK450528.1	qRT-PCR	Zhang et al. 2012
Actin Rev	CTCCATGTCATCCCAGTTG				Zhang et al. 2012
ZDS Fw	TTTAGACCTGACCAGAAGACACCA	ζ -carotene desaturase	FJ169496.1	qRT-PCR	Wang et al. 2014
ZDS Rev	AATAACTCCTCTCCAGCACCACA				Wang et al. 2014
PSY Fw	GTTTGGGCCTCTCTGTTGTTG	Phytoene synthase	EF600063.1	qRT-PCR	Wang et al. 2014
PSY Rev	GCCCTCTTGGTGAAGTTGTTG				Wang et al. 2014
PDS Fw	TGAACGCCCCAGTAAACCA	Phytoene desaturase	FJ517553.1	qRT-PCR	Wang et al. 2014
PDS Rev	TTCCGCCCCAACACATCTC				Wang et al. 2014
HDY Fw	ACCACATGGACAAGTTCGAGG	β -ring hydroxylase	JX171671.1	qRT-PCR	Wang et al. 2014
HDY Rev	TTGATCCTGGCGAGCTCCT				Wang et al. 2014
LCYE Fw	ACACACCCTGAGGAAGCCAA	ϵ -lycopene cyclase	EU649786.1	qRT-PCR	Wang et al. 2014
LCYE Rev	CGCATCCAACCGAGACATCAAC				Wang et al. 2014

