

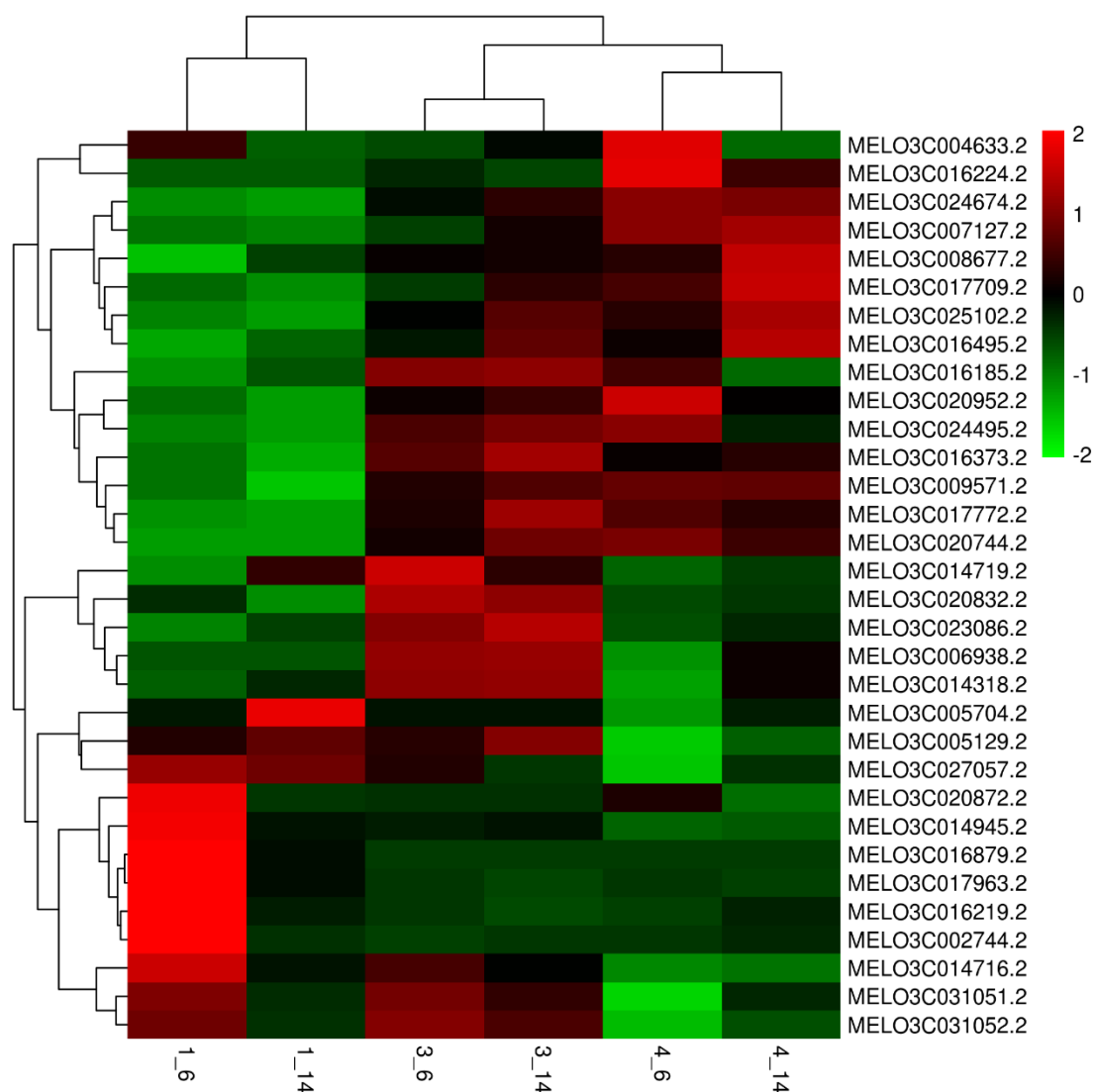


Fig. S1 Heat map representation and hierarchical clustering of structural genes involved in carotenoid biosynthesis in "B-14" and "B-6" melon cultivars at different growth stages.

Table S1 Primer sequences of genes selected for qRT-PCR

Num	Gene Symbol	Forward primer(5->3)	Reverse primer(5->3)
1	18S-RNA	GTGATGGTGTGAGTCACACTGTTC	ACGACCAGCAAGGTCCAAAC
2	MELO3C025102.2	TCTTCCCTCGTGCGATAC	TTAAACCGCCCAAGAAATTCCA
3	MELO3C006938.2	CGGTCTTTGGGATGGCCTA	GCAGCAACCTTTCTGAAGT
4	MELO3C004633.2	GGTTATTGGTTGTGGTCCTG	TGGACCAATGAGTCCAACTT
5	MELO3C014318.2	CAAAGCCAATCCTCTCTTTGA	GACAGTGGTGAATGCAGC
6	MELO3C016495.2	GGACCTTTGCTCCAGTATG	TACTGCTGGAGCTACGTG
7	MELO3C016224.2	GCTCCAGTCGATGAGCTAC	TTTGGGCCGTTACGAATGT

Table S2 Throughout and quality of Illumina sequencing

Sample	Raw Reads	Clean Reads	Q30(%)	GC(%)	Uniquely mapped	Multiple mapped
S1_14_1	7.49G	7.10G	94.92	45.44	47377429(96.33%)	647998(1.32%)
S1_14_2	7.33G	7.01G	94.77	45.00	46366449(96.07%)	684603(1.42%)
S1_14_3	7.45G	7.13G	94.68	44.87	47104966(96.19%)	642562(1.31%)
S1_6_1	7.09G	6.75G	94.61	45.04	44968412(96.42%)	582849(1.25%)
S1_6_2	7.37G	7.03G	94.50	45.01	46674228(96.34%)	605051(1.25%)
S1_6_3	7.59G	7.20G	94.56	45.05	47979822(96.40%)	649031(1.30%)
S3_14_1	7.51G	7.23G	94.65	44.48	47370941(96.06%)	763955(1.55%)
S3_14_2	7.65G	7.29G	94.72	44.46	48270911(96.14%)	763192(1.52%)
S3_14_3	7.37G	7.06G	94.68	44.26	46538134(96.23%)	692561(1.43%)
S3_6_1	7.16G	6.86G	94.83	44.62	45340498(96.24%)	711754(1.51%)
S3_6_2	7.10G	6.84G	94.89	44.47	44934361(96.13%)	706401(1.51%)
S3_6_3	7.59G	7.26G	94.97	44.52	48080335(96.25%)	755243(1.51%)
S4_14_1	7.71G	7.34G	94.58	44.83	48504505(95.88%)	777127(1.54%)
S4_14_2	7.74G	7.41G	94.98	44.52	48922828(96.04%)	801042(1.57%)
S4_14_3	7.23G	6.94G	94.82	44.77	45704575(96.00%)	692698(1.45%)
S4_6_1	7.41G	7.07G	94.88	45.00	46921764(96.27%)	722351(1.48%)
S4_6_2	7.44G	7.10G	94.85	45.00	47044095(96.17%)	692809(1.42%)
S4_6_3	7.71G	7.33G	94.77	45.02	48776651(96.37%)	734843(1.45%)

Table S3 Differentially expressed genes involved in carotenoid biosynthesis

Gene ID	Description	Gene expression					
		1_6	3_6	4_6	1_14	3_14	4_14
MELO3C020952.2	GGPS, Geranylgeranyl pyrophosphate synthase	28.1197	66.4066	125.1487	14.9408	78.8895	64.0898
MELO3C016185.2	PSY, Phytoene synthase	1.3330	3.8040	3.2031	1.8814	3.8853	1.7076
MELO3C025102.2	PSY, Phytoene synthase	17.9999	87.9917	110.0964	2.9864	137.6956	183.5960
MELO3C017772.2	PDS, 15-cis-phytoene desaturase	21.4223	67.8222	82.2063	17.5949	102.4350	71.3052
MELO3C020832.2	PDS, 15-cis-phytoene desaturase	4.0256	9.8523	3.2012	1.3748	9.0606	3.6977
MELO3C017709.2	Z-ISO,15-cis-zeta-carotene isomerase	5.4132	8.2812	16.0875	3.3590	14.4645	24.0221
MELO3C024674.2	ZDS, Zeta-carotene desaturase	15.5789	39.7716	67.6367	12.5453	50.4476	65.0881
MELO3C024674.2	Zeta-carotene desaturase	15.5789	39.7716	67.6367	12.5453	50.4476	65.0881
MELO3C009571.2	CRTISO, Prolycopene isomerase	12.9103	20.5435	23.8816	8.9538	22.8244	23.6788

MELO3C016373.2	CRTISO, Prolycopene isomerase	11.3977	23.5368	23.8817	7.9813	28.4646	23.6788
MELO3C016495.2	CRTISO, Prolycopene isomerase	3.3758	8.5263	19.0451	5.8391	12.8245	20.8950
MELO3C020744.2	LCY1, Lycopene beta cyclase	11.7969	25.0206	33.2504	11.8186	32.3383	28.5331
MELO3C004633.2	LUT2, Lycopene epsilon cyclase	2.4084	0.8552	4.4704	0.5924	1.6634	0.4911
MELO3C016224.2	CCD4, Probable carotenoid cleavage dioxygenase 4	4.3795	19.4961	91.6328	4.6840	9.9135	45.6989
MELO3C014945.2	CYP97A3, Protein LUTEIN DEFICIENT 5	39.7734	14.0943	7.3139	15.0666	15.0252	8.0804
MELO3C016219.2	CYP707A2, Absciscic acid 8'-hydroxylase	187.1959	34.2675	27.5234	45.4248	24.2675	42.9371
MELO3C024495.2	CYP97C1, Carotene epsilon-monooxygenase	8.7436	27.4929	33.3063	6.6271	31.3088	17.6895
MELO3C016879.2	CYP711A1, Cytochrome P450 711A1	34.4051	0.3522	0.2124	5.6324	0.2300	0.2893
MELO3C008677.2	VDE1, Violaxanthin de-epoxidase	3.7712	6.0820	6.4335	5.2890	6.2433	8.2156
MELO3C017963.2	CCS, Capsanthin/capsorubin synthase	24.4558	2.7589	2.8586	5.6269	1.6547	1.9910
MELO3C006938.2	CHYB, CA2, Beta-carotene hydroxylase 2	27.3011	43.8954	22.9643	27.2795	44.1098	34.4184
MELO3C005704.2	CHYB, BETA-OHASE, Beta-carotene 3-hydroxylase 1	0.3720	0.3853	0.0909	0.9400	0.3791	0.3566
MELO3C014318.2	D27, Beta-carotene isomerase	2.7314	5.6998	1.8948	3.4803	5.7836	4.0800
MELO3C020872.2	ZEP, Zeaxanthin epoxidase	22.7244	18.7501	19.7932	18.6876	18.7486	17.9323
MELO3C031051.2	AAO3, Absciscic-aldehyde oxidase	15.9097	15.4990	6.0628	10.9970	13.6608	11.0286
MELO3C031052.2	AAO3, Absciscic-aldehyde oxidase	13.9270	14.4847	5.3971	9.4711	12.9335	8.5311
MELO3C014716.2	AAO3, Absciscic-aldehyde oxidase	10.9421	7.6331	2.3974	5.4482	5.7777	2.8915
MELO3C014719.2	AAO2, Indole-3-acetaldehyde oxidase	2.8028	13.2632	4.1498	8.6434	8.3696	5.3377
MELO3C005129.2	ABA2, Xanthoxin dehydrogenase	29.2888	29.8135	4.0886	35.7183	39.9972	15.6724
MELO3C027057.2	NCED1, 9-cis-epoxycarotenoid dioxygenase	36.7109	25.4836	4.3574	32.8760	17.7466	18.2397
MELO3C002744.2	NCED2,9-cis-epoxycarotenoid dioxygenase	1.6628	0.0160	0.0693	0.0779	0.0705	0.1315
MELO3C007127.2	NCED2, 9-cis-epoxycarotenoid dioxygenase	2.2099	10.1120	37.6042	0.3304	21.0035	41.5496
MELO3C023086.2	NCED6, 9-cis-epoxycarotenoid dioxygenase	7.9260	54.5373	16.9582	20.3301	64.0547	24.7464

Table S4 Screened list of differentially expressed genes related to chlorophyll metabolism

Gene ID	Description	Gene expression					
		1_6	3_6	4_6	1_14	3_14	4_14
MELO3C004867.2	PAO, Pheophorbide a oxygenase	45.6706	20.7863	46.4835	19.5245	26.5158	34.0857
MELO3C035541.2	PAO, Pheophorbide a oxygenase	0.8315	0.1361	1.2249	1.5829	3.1732	3.7297
MELO3C005189.2	POX1, Protoporphyrinogen oxidase 1	9.1998	20.1105	24.5975	9.1281	18.9724	21.9347
MELO3C008208.2	POX2, Protoporphyrinogen oxidase 2	6.0428	5.7562	7.6904	16.3070	7.6519	8.7947
MELO3C006242.2	COX10, Protoheme IX farnesyltransferase	30.9642	19.7465	25.1298	33.9238	19.1044	22.8777
MELO3C016120.2	COX15, Cytochrome c oxidase assembly protein	4.5666	6.7467	9.6766	7.3530	8.1418	9.3589
MELO3C007233.2	CHLI, Magnesium-chelatase subunit ChII	32.7924	57.5428	127.1322	25.2638	93.1005	53.4685
MELO3C014571.2	CHLD, Magnesium-chelatase subunit ChID	10.1434	15.9460	12.8227	16.8399	14.4142	7.1206
MELO3C026000.2	CHLG, Chlorophyll synthase	34.9361	44.1191	33.9946	19.6196	41.1236	30.9775
MELO3C026160.2	CHLM, Magnesium protoporphyrin IX methyltransferase	63.2184	25.0710	41.0206	20.2988	31.7037	26.4776
MELO3C014712.2	CHLP, Geranylgeranyl diphosphate reductase	0.6132	0.4088	2.5394	0.8210	0.6142	2.1636
MELO3C017176.2	CHLP, Geranylgeranyl diphosphate reductase	23.2812	68.1179	127.8698	23.4735	96.3832	30.7724
MELO3C023131.2	CHLH, Magnesium-chelatase subunit ChIH	5.5349	68.0900	145.0748	1.2678	52.6180	58.8092
MELO3C014286.2	CLH2, Chlorophyllase-2	4.4229	8.2237	11.6441	6.1961	10.2281	12.2702
MELO3C011113.2	HEMA1, Glutamyl-tRNA reductase 1	33.9059	45.5292	51.8491	23.8664	51.2897	20.1317
MELO3C018565.2	HEMA2, Glutamyl-tRNA reductase 2	142.9519	22.7445	5.0638	53.4152	14.6574	12.1401

MELO3C008086.2	HEMB1, Delta-aminolevulinic acid dehydratase 1,	78.8422	64.7055	75.5363	54.2364	70.8675	63.0163
MELO3C024010.2	HEMC, Porphobilinogen deaminase	18.8412	25.2184	81.1137	22.5093	42.6499	31.8089
MELO3C016131.2	HEME1, Uroporphyrinogen decarboxylase 1	13.5793	17.1684	26.7788	22.4659	19.5783	18.5686
MELO3C010762.2	HEMH, Ferrochelatase-2	72.0768	24.2509	31.9115	36.2752	20.0622	37.5318
MELO3C013592.2	PORA, Protochlorophyllide reductase	3.2375	1.1783	8.4173	1.8176	3.4127	2.5397
MELO3C016714.2	PORA, Protochlorophyllide reductase	148.3747	339.2976	571.7425	105.1112	417.2457	214.6357
MELO3C006358.2	HCAR, 7-hydroxymethyl chlorophyll a reductase	4.8837	15.6582	25.3445	4.2049	21.5738	17.0589
MELO3C010350.2	HO1, Heme oxygenase 1	11.2102	21.6180	13.0663	13.1509	22.1563	16.8812
MELO3C016736.2	HO2, Probable inactive heme oxygenase 2	3.8183	6.2914	6.3906	4.3832	6.1334	5.9387
MELO3C029500.2	HY2, Phytochromobilin ferredoxin oxidoreductase	8.4997	8.0730	6.4240	4.5886	12.2069	9.7443
MELO3C010614.2	CAO, Chlorophyllide a oxygenase	16.7366	89.2360	99.4100	17.3610	88.0594	60.4608
MELO3C026802.2	CRD1, Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase	73.2959	253.0168	490.1623	34.7762	322.8260	164.4282
MELO3C006606.2	DVR, Divinyl chlorophyllide 8-vinyl-reductase	4.0426	5.4728	5.6100	6.5743	6.4370	2.3953
MELO3C010892.2	UROS, Uroporphyrinogen-III synthase	11.2061	8.2009	17.0411	9.8555	8.7166	11.3158
MELO3C015227.2	At5g26710, Glutamate--tRNA ligase	264.1536	28.5980	40.2471	295.1378	31.4403	39.5561
MELO3C015693.2	OVA3, Glutamate--tRNA ligase	17.0231	24.8484	32.3586	18.3372	26.8148	26.5627
MELO3C019619.2	Os05g0361200, Ferrochelatase-2	43.3270	50.3943	35.7526	32.1812	43.3126	28.7863
MELO3C016226.2	CPX, Oxygen-dependent coproporphyrinogen-III oxidase	187.4576	46.2469	70.3640	239.4888	48.0828	43.0569
MELO3C018572.2	GSA, Glutamate-1-semialdehyde 2,1-aminomutase	62.8088	53.8178	63.1913	70.8763	55.8806	59.8852
MELO3C025347.2	NYC1, Probable chlorophyll(ide) b reductase	13.7839	140.9867	131.0567	10.3011	211.3061	247.3177
MELO3C019918.2	NOL, Chlorophyll(ide) b reductase NOL	4.3169	8.5939	11.4912	6.6063	8.7110	12.7130
MELO3C020115.2	DCUP, Uroporphyrinogen decarboxylase	28.0328	33.1030	42.0972	27.9404	38.3389	22.7795
MELO3C020912.2	RCCR, Red chlorophyll catabolite reductase	61.4929	72.7201	85.3020	68.1077	84.1772	44.0519
MELO3C020913.2	RCCR, Red chlorophyll catabolite reductase	32.4496	35.8398	84.5843	84.4801	32.2111	40.4482
MELO3C013522.2	FH, Frataxin	15.8330	17.5373	22.7346	18.0707	20.8974	28.9511

Table S5 List of differentially expressed genes related to chlorophyll metabolism (ko00860).

Gene ID	Description	log2 Fold change		
		1_6 vs. 4_6	1_14 vs. 4_14	4_14 vs. 4_6
MELO3C005189.2	POX1, Protoporphyrinogen oxidase 1	1.2044	1.1582	/
MELO3C007233.2	CHLI, Magnesium-chelatase subunit ChII	1.7529	/	-1.3026
MELO3C014712.2	CHLP, Geranylgeranyl diphosphate reductase	1.8435	1.2911	/
MELO3C017176.2	CHLP, Geranylgeranyl diphosphate reductase	2.2565	/	-2.1035
MELO3C023131.2	CHLH, Magnesium-chelatase subunit ChIH	4.5112	5.4357	-1.3508
MELO3C002961.2	CHLH1, Magnesium-chelatase subunit ChIH1	/	-5.9663	/
MELO3C014286.2	CLH2, Chlorophyllase-2	1.1656	/	/
MELO3C014571.2	CHLD, Magnesium-chelatase subunit ChID	/	-1.3461	/
MELO3C018565.2	HEMA2, Glutamyl-tRNA reductase 2	-5.0718	-2.2313	/
MELO3C024010.2	HEMC, Porphobilinogen deaminase	1.8903	/	-1.3969
MELO3C010762.2	HEMH, Ferrochelatase-2	-1.4186	/	/
MELO3C013592.2	PORA, Protochlorophyllide reductase	1.1457	/	-1.7788
MELO3C016714.2	PORA, Protochlorophyllide reductase	1.7461	/	-1.4648
MELO3C006358.2	HCAR, 7-hydroxymethyl chlorophyll a reductase	2.1803	1.9189	/

MELO3C010614.2	CAO, Chlorophyllide a oxygenase	2.3498	1.6968	/
MELO3C026802.2	CRD1, Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase	2.5334	2.1383	-1.6295
MELO3C015227.2	At5g26710, Glutamate--tRNA ligase	-2.9624	-3.0034	/
MELO3C016226.2	CPX, Oxygen-dependent coproporphyrinogen-III oxidase	-1.6559	-2.5769	/
MELO3C025347.2	NYC1, Probable chlorophyll(ide) b reductase	3.0265	4.4819	/
MELO3C019918.2	NOL, Chlorophyll(ide) b reductase NOL	1.1909	/	/
MELO3C020912.2	RCCR, Red chlorophyll catabolite reductase	1.1555	/	-1.0058
MELO3C020913.2	RCCR, Red chlorophyll catabolite reductase	/	-1.1696	-1.1170
MELO3C006606.2	DVR, Divinyl chlorophyllide 8-vinyl-reductase	/	-1.5634	-1.2839
MELO3C011113.2	HEMA1, Glutamyl-tRNA reductase 1	/	/	-1.4143
MELO3C035541.2	PAO, Pheophorbide a oxygenase	/	/	1.5454
MELO3C035546.2	PAO, Pheophorbide a oxygenase	/	/	1.8917