Subtitle: Supporting Information

Manuscript title： Metabolome and transcriptome analysis reveals the accumulation mechanism of carotenoids and the causes of color differences in persimmon (*Diospyros kaki* Thunb.) fruits

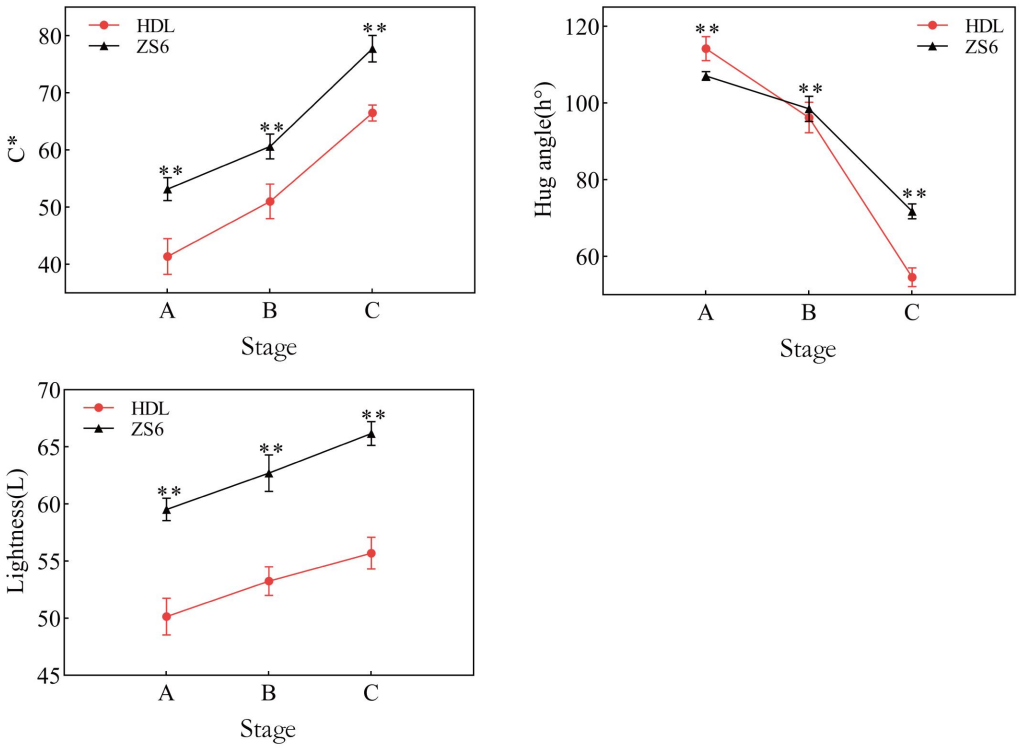
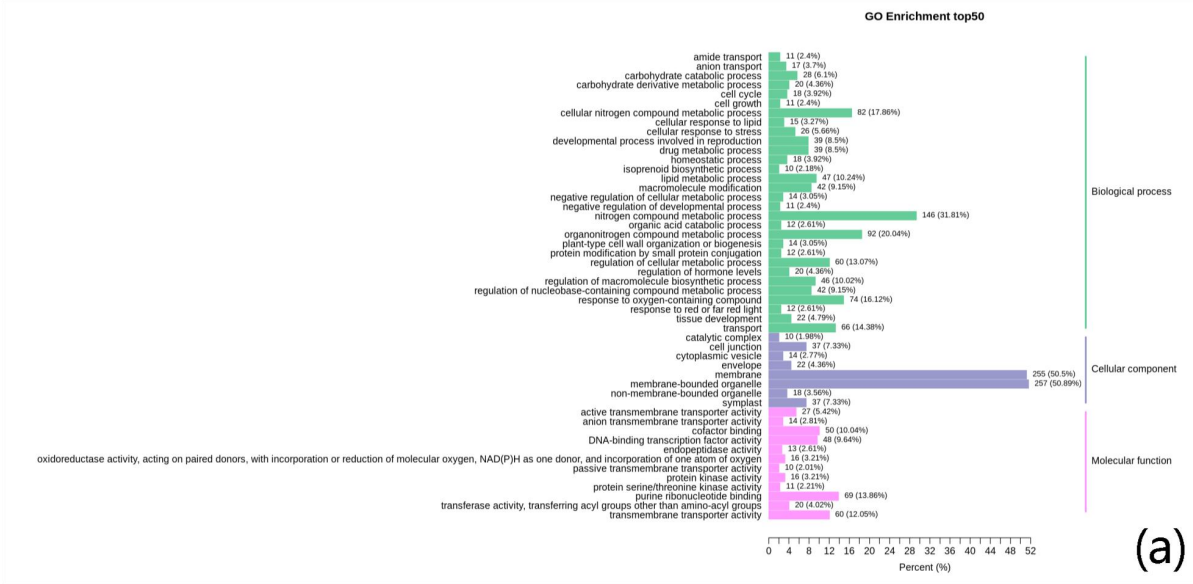
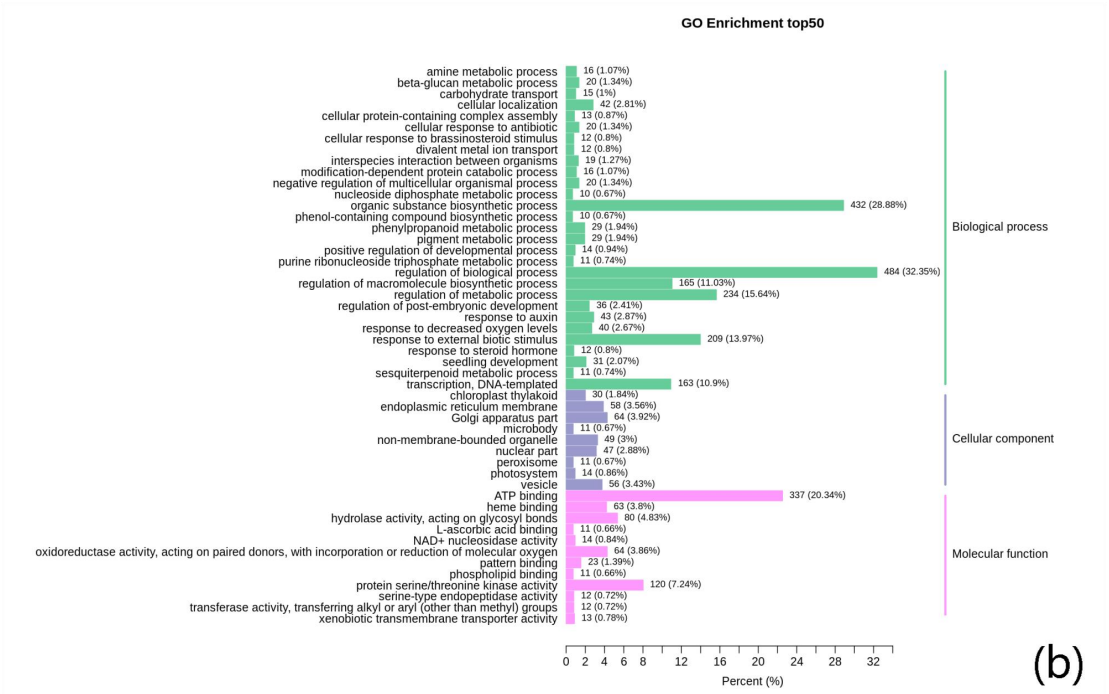


Figure. S1 A comparison of two persimmon varieties' peel color difference index readings taken at various stages of fruit development.

** denotes significant variations between the two cultivars at the 0.01 significance level for the same time frame.





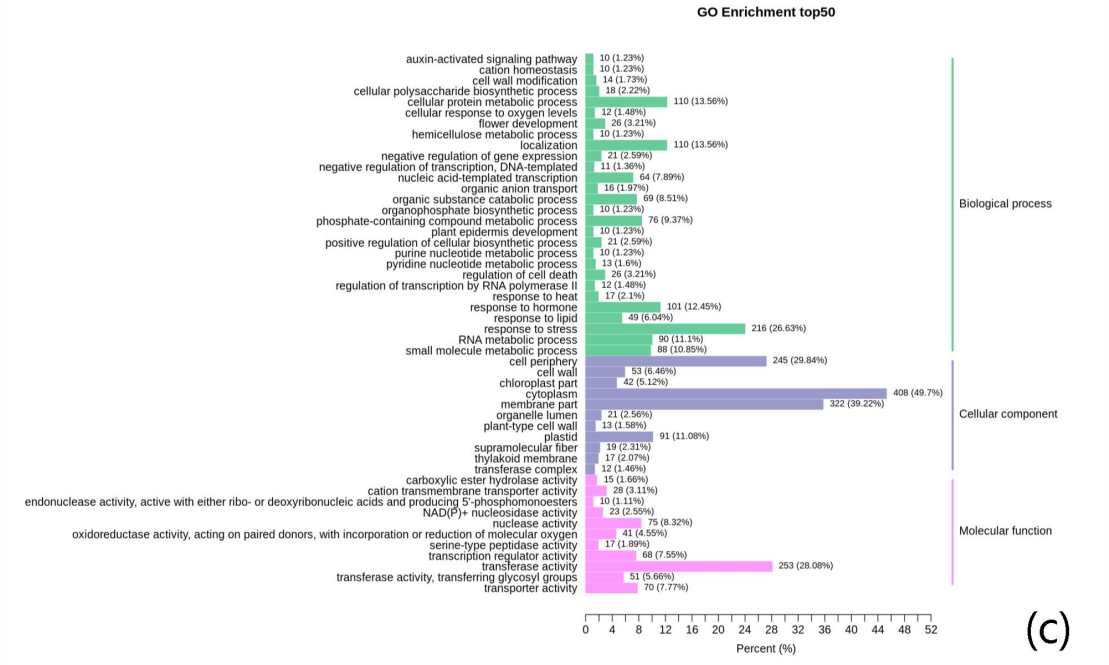


Figure. S2 GO terms that were enriched for those DEGs. (a) the shared DEGs during the development of "Zhongshi No.6" (ZS6PA vs. ZS6PB and ZS6PB vs. ZS6PC); (b) the shared DEGs during the development of "Hongdenglong" (HDLPA vs. ZHDLPB and HDLPB vs. HDLPC); (c) The share DEGs at the same stage of two cultivars (ZS6PA vs HDLPA, ZS6PB vs HDLPB, and ZS6PC vs HDLPC

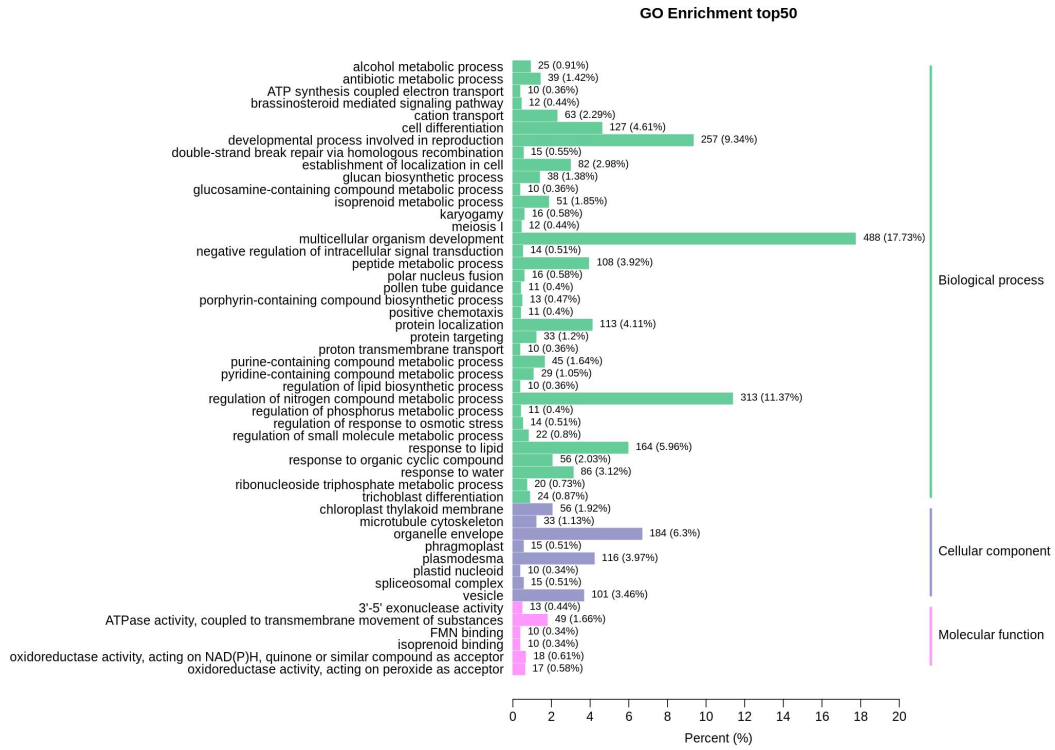
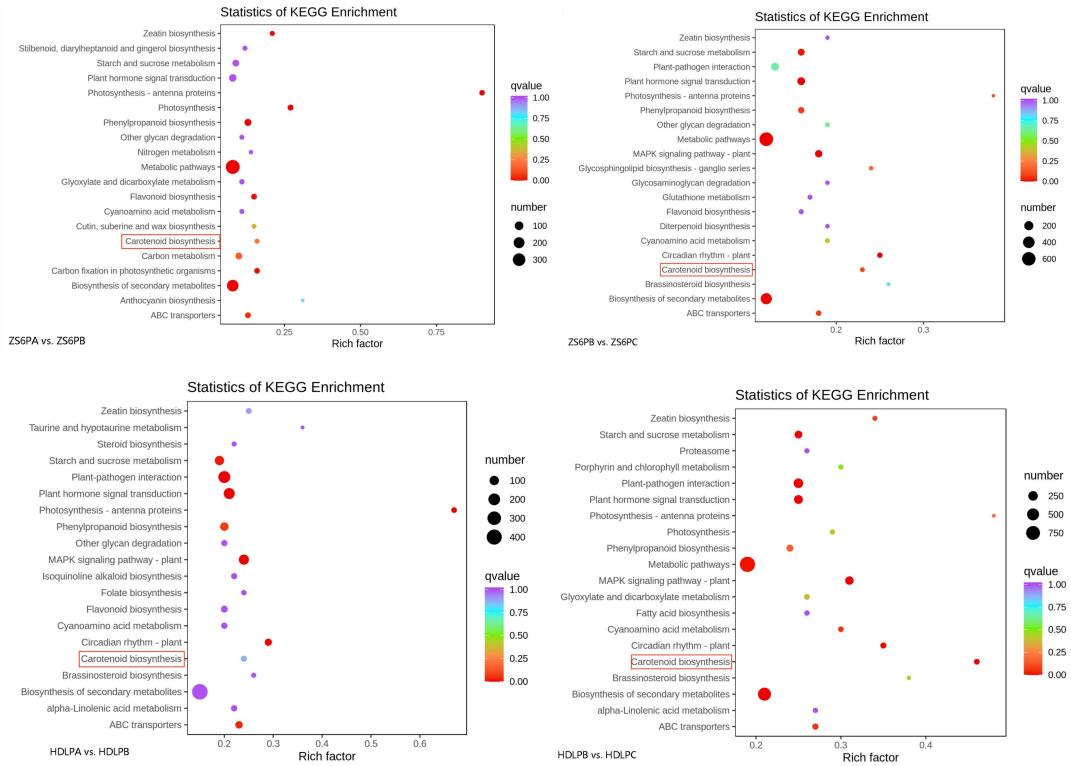


Figure. S3 GO enrichment analysis that was enriched for those genes of sub Class 3, 4, 5, 8, 11, 15, and 19



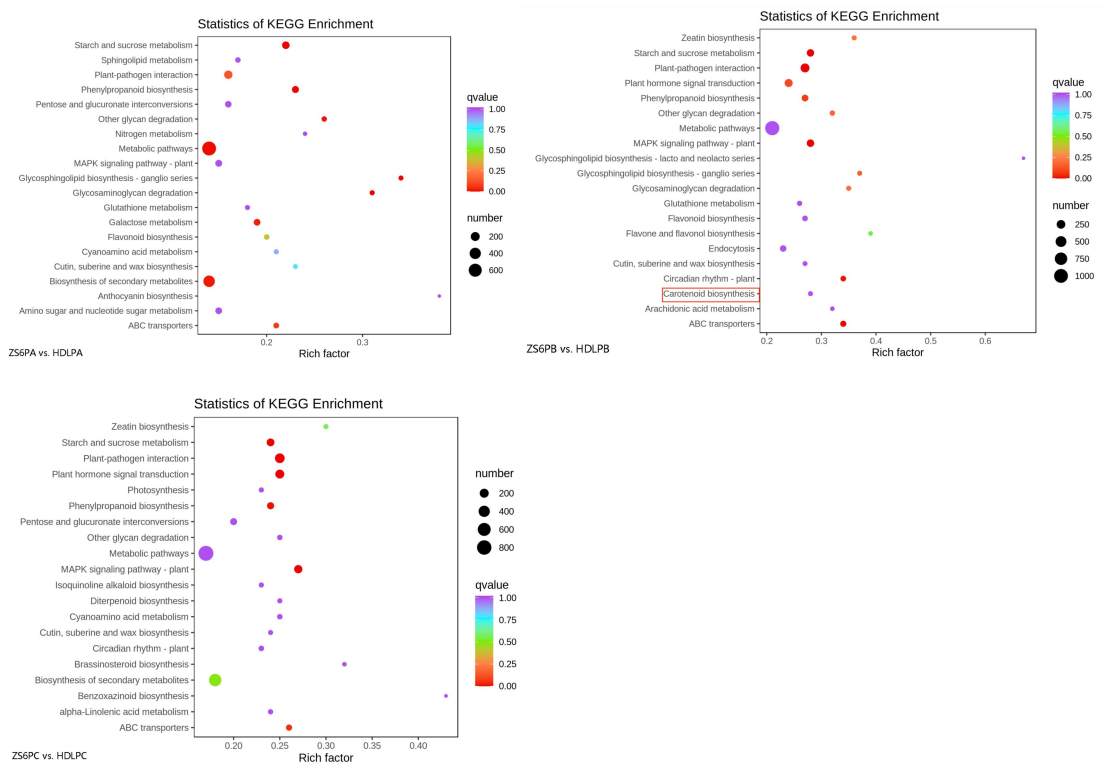


Figure. S4 Comparison of persimmon fruit development between two cultivars using a DEG KEGG enrichment distribution map; KEGG enrichment distribution map of DEGs in ZS6PA vs ZS6PB, ZS6PB vs. ZS6PC, HDLPA vs. HDLPB, HDLPB vs. HDLPC, ZS6PA vs. HDLPA, ZS6PB vs. HDLPB, and ZS6PC vs. HDLPC

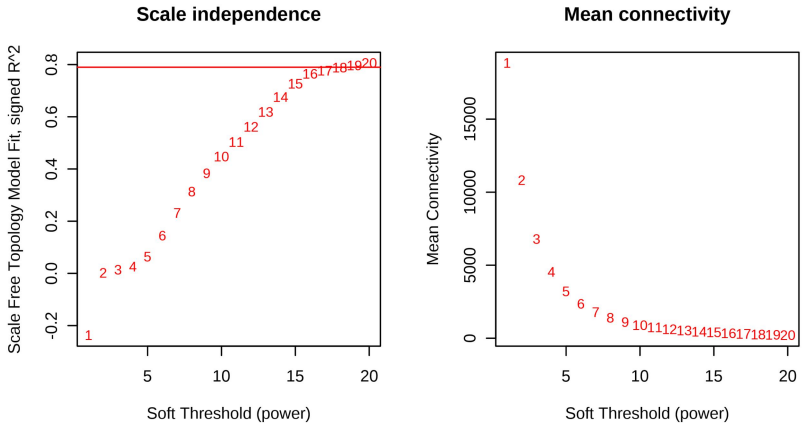


Figure. S5 Determination of soft-thresholding power (β)

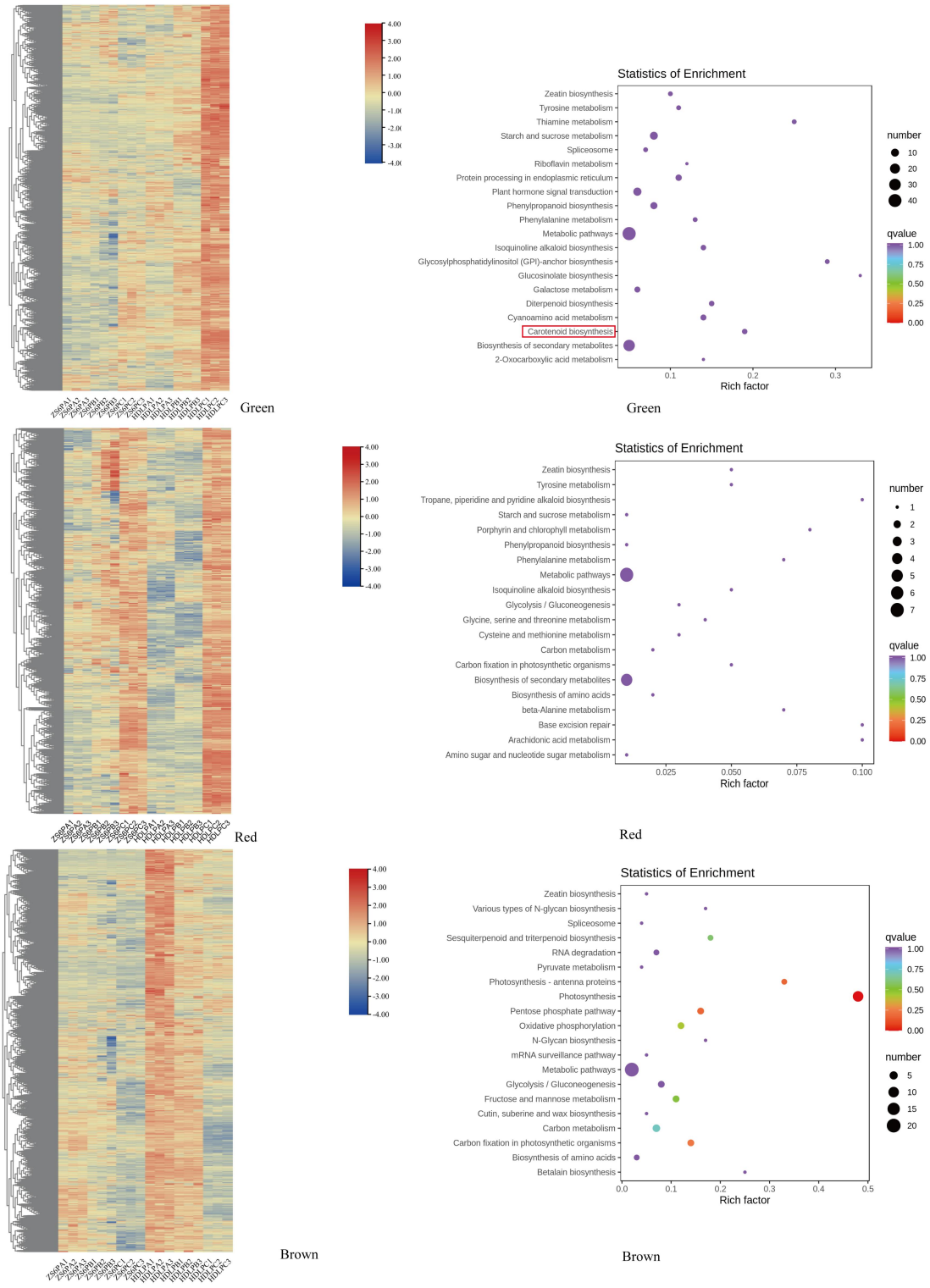


Figure. S6 Genes in three modules were put together using a heat map and KEGG analysis. (a)green; (b)red; (c)brown

Table S1 Primer sequences for the genes studied in this research

Gene ID (Homologous gene)	Primer sequence (5′-3′)
GAPDH	F: AGCTCTTCCACCTCTCCAGT
	R: TGCTAGCTGCACAACCAACT
CRTISO	F: ATGGTGAGTACAGTCAATGC
	R: CGCTGCCTTGATCAACCAAG
CRTZ	F: TATCAGTACTCCGACTTGCC
	R: TCCTGGTCACCGGCTTCGAG
LCYE	F: TGTTGGACTTATTGGCCCAG
	R: CGACTAACTCGTCCATAAGC
PDS	F: TGTACAGAACCTGTTTGGAG
	R: GTGCTGGTAGAACTTCAGCG
PSY	F: TGAGCTTGATGACTGAAGCC
	R: CCATCTGTCTAATGCTGTAG
ZDS	F: CCTCGCCCTAAGTCCAGTAG
	R: AGCATAAGCAACAGGATCCC
Z-ISO	F: GCCTGGATTGATAACTCCAC
	R: AAGCCACTATGTACAATGGC
NCED	F: ATCCGGCTCAATTTGAGGAC
	R: CCGAGCTTGTTCCGGTTCAC
ABA2	F: CCGCCTCCAAGTTCGTTAAC
	R: ATACGGTGTAGTCCACTGCG

Table S2 Statistics on carotenoid lipid contents in two persimmon cultivars

lutein distearate	0.000E+00	0.000E+00	4.616E-02	0.000E+00	0.000E+00	0.000E+00
echinenone	0.000E+00	0.000E+00	4.203E-03	0.000E+00	0.000E+00	0.000E+00
8'-apo-beta-carotenal	0.000E+00	0.000E+00	1.681E-02	0.000E+00	0.000E+00	8.754E-03
rubixanthin laurate	0.000E+00	1.064E-01	2.876E-01	0.000E+00	0.000E+00	8.156E-02
β-cryptoxanthin palmitate	0.000E+00	6.858E-01	2.158E+00	0.000E+00	0.000E+00	5.947E-01
β-cryptoxanthin laurate	0.000E+00	2.132E-01	1.461E+00	0.000E+00	0.000E+00	3.789E-01
zeaxanthin-oleate-palmitate	0.000E+00	2.197E-02	5.736E-02	0.000E+00	1.201E-02	3.794E-02
β-cryptoxanthin oleate	0.000E+00	3.845E-02	4.871E-01	0.000E+00	0.000E+00	1.312E-01
lutein myristate	4.003E+00	3.078E+00	2.094E+00	2.030E+00	1.661E+00	1.296E+00
lutein dimyristate	7.741E+00	3.098E+01	3.787E+01	7.941E+00	1.339E+01	2.812E+01
violaxanthin dibutyrate	7.904E-02	1.184E-01	8.491E-02	8.245E-02	8.870E-02	6.597E-02
violaxanthin myristate	1.378E+00	2.887E+00	2.862E+00	1.705E+00	1.882E+00	2.292E+00
violaxanthin dimyristate	2.796E-01	2.463E+00	4.561E+00	2.914E-01	8.550E-01	3.072E+00
zeaxanthin dimyristate	1.250E-01	1.082E+00	1.665E+00	9.721E-02	3.750E-01	1.457E+00
lutein dilaurate	2.759E-01	1.243E+00	1.366E+00	2.751E-01	5.009E-01	8.399E-01
lutein dioleate	5.776E-02	2.218E-01	2.548E-01	1.467E-01	1.109E-01	2.145E-01
violaxanthin palmitate	2.885E-01	5.018E-01	4.196E-01	2.193E-01	1.975E-01	2.076E-01
violaxanthin-myristate-laurate	1.019E-01	8.763E-01	1.380E+00	1.212E-01	2.741E-01	9.862E-01
zeaxanthin-laurate-palmitate	3.395E-02	2.092E-01	3.173E-01	2.304E-02	5.885E-02	2.267E-01
lutein palmitate	1.041E+00	7.695E-01	5.388E-01	5.453E-01	2.716E-01	0.000E+00
violaxanthin-myristate-palmitate	0.000E+00	9.175E-01	1.830E+00	1.075E-01	2.996E-01	8.792E-01
zeaxanthin-laurate-myristate	1.758E-02	7.340E-02	1.163E-01	0.000E+00	2.561E-02	7.191E-02
antheraxanthin dipalmitate	2.554E-01	1.755E-01	0.000E+00	1.022E-01	1.031E-01	0.000E+00
lutein caprate	4.938E-02	2.510E-02	0.000E+00	3.223E-02	2.159E-02	0.000E+00
β-cryptoxanthin myristate	0.000E+00	7.421E+00	7.043E+01	0.000E+00	1.163E+00	1.910E+01
rubixanthin palmitate	0.000E+00	7.412E-01	2.481E+00	0.000E+00	9.538E-02	4.985E-01
violaxanthin dilaurate	0.000E+00	1.851E-01	2.859E-01	0.000E+00	8.625E-02	2.309E-01
violaxanthin-myristate-caprate	0.000E+00	4.125E-01	3.593E-01	0.000E+00	1.915E-01	3.731E-01
zeaxanthin dilaurate	0.000E+00	4.055E-02	4.992E-02	0.000E+00	1.207E-02	3.673E-02
zeaxanthin palmitate	1.230E-01	2.157E-01	2.215E-01	0.000E+00	0.000E+00	1.226E-01

Table S3 Statistics on the RNA-Seq libraries output and quality

Sample	Raw Reads	Clean Reads	Clean Base(G)	Error Rate (%)	Q20(%)	Q30(%)	GC Content (%)
ZS6PA1	63135212	61231892	9.18	0.03	98.08	94.17	46.93
ZS6PA2	46956128	45593756	6.84	0.03	97.68	93.48	45.88
ZS6PA3	67888518	65650680	9.85	0.02	98.1	94.25	46.78
ZS6PB1	46014034	44450428	6.67	0.03	97.69	93.6	47.03
ZS6PB2	47203072	44973940	6.75	0.03	97.55	93.2	45.38
ZS6PB3	45810292	43683900	6.55	0.03	97.54	93.16	44.43
ZS6PC1	44980124	41294250	6.19	0.03	97.4	92.94	47.4
ZS6PC2	45404650	43930532	6.59	0.03	97.39	92.92	46.88
ZS6PC3	45320340	43875436	6.58	0.03	97.44	93.02	47.16
HDLPA1	52148978	48754238	7.31	0.03	97.55	93.23	46.56
HDLPA2	48815312	47356226	7.1	0.03	97.56	93.22	46.22
HDLPA3	51265954	49901434	7.49	0.03	97.54	93.14	46.69
HDLPB1	46958840	45218462	6.78	0.03	97.54	93.24	46.27
HDLPB2	46390000	44813708	6.72	0.03	97.64	93.41	46.26
HDLPB3	44182296	42420258	6.36	0.03	97.98	94.17	46.26
HDLPC1	49566220	46670048	7	0.03	97.98	94.05	47.05
HDLPC2	46766544	44644114	6.7	0.03	97.53	93.23	46.75
HDLPC3	45713792	43546836	6.53	0.03	97.65	93.61	46.91

Table S4 Comparative statistical table with the reference genome

Sample	Total Reads	Reads mapped	Unique mapped	Multi mapped	Read1 mapped	Read2 mapped	+' mapped	-' mapped
ZS6PA1	61231892	49976378(81.62%)	47207215(77.10%)	3939468(4.52%)	23473287(38.34%)	23733928(38.76%)	23532866(38.43%)	23674349(38.66%)
ZS6PA2	45593756	37064500(81.29%)	35228383(77.27%)	2585065(4.03%)	17602113(38.61%)	17626270(38.66%)	17578473(38.55%)	17649910(38.71%)
ZS6PA3	65650680	53572434(81.60%)	50544372(76.99%)	4386621(4.61%)	25130956(38.28%)	25413416(38.71%)	25211825(38.40%)	25332547(38.59%)
ZS6PB1	44450428	36593026(82.32%)	34249905(77.05%)	3500356(5.27%)	17134403(38.55%)	17115502(38.50%)	17074279(38.41%)	17175626(38.64%)
ZS6PB2	44973940	36362474(80.85%)	34325628(76.32%)	2974297(4.53%)	17160270(38.16%)	17165358(38.17%)	17109354(38.04%)	17216274(38.28%)
ZS6PB3	43683900	35964265(82.33%)	33820625(77.42%)	3106453(4.91%)	16896552(38.68%)	16924073(38.74%)	16868333(38.61%)	16952292(38.81%)
ZS6PC1	41294250	33553623(81.25%)	31098321(75.31%)	3801822(5.95%)	15550195(37.66%)	15548126(37.65%)	15534036(37.62%)	15564285(37.69%)
ZS6PC2	43930532	35622575(81.09%)	33356204(75.93%)	3217848(5.16%)	16680271(37.97%)	16675933(37.96%)	16578677(37.74%)	16777527(38.19%)
ZS6PC3	43875436	35808636(81.61%)	33390805(76.10%)	3593869(5.51%)	16694105(38.05%)	16696700(38.05%)	16600455(37.84%)	16790350(38.27%)
HDLPA1	48754238	39665947(81.36%)	37501346(76.92%)	3116474(4.44%)	18720824(38.40%)	18780522(38.52%)	18721100(38.40%)	18780246(38.52%)
HDLPA2	47356226	38674121(81.67%)	36645678(77.38%)	2806112(4.28%)	18296132(38.64%)	18349546(38.75%)	18284571(38.61%)	18361107(38.77%)
HDLPA3	49901434	41035582(82.23%)	38801380(77.76%)	3166387(4.48%)	19399205(38.88%)	19402175(38.88%)	19351646(38.78%)	19449734(38.98%)
HDLPB1	45218462	36534201(80.79%)	34317907(75.89%)	3223970(4.90%)	17144174(37.91%)	17173733(37.98%)	17078230(37.77%)	17239677(38.13%)
HDLPB2	44813708	36247784(80.89%)	33964846(75.79%)	3464824(5.09%)	17000297(37.94%)	16964549(37.86%)	16906002(37.73%)	17058844(38.07%)
HDLPB3	42420258	34432804(81.17%)	32321179(76.19%)	3061458(4.98%)	16172175(38.12%)	16149004(38.07%)	16089999(37.93%)	16231180(38.26%)
HDLPC1	46670048	37748170(80.88%)	35417223(75.89%)	3658757(4.99%)	17598586(37.71%)	17818637(38.18%)	17621775(37.76%)	17795448(38.13%)
HDLPC2	44644114	36056795(80.76%)	33812578(75.74%)	3560654(5.03%)	16935407(37.93%)	16877171(37.80%)	16848380(37.74%)	16964198(38.00%)
HDLPC3	43546836	35280657(81.02%)	33115815(76.05%)	3376888(4.97%)	16569367(38.05%)	16546448(38.00%)	16513008(37.92%)	16602807(38.13%)

Note: '+' mapped: Compare the number of reads in the positive chain of the genome; '-' mapped: The number of reads in the negative chain of the genome.

Table S5 List of structural genes involved in carotenoid biosynthesis whose expression levels vary across cultivars

Gene	Gene name	Chr	start	end	strand
AAO3	evm.TU.fragScaff_scaffold_70.52	Chr1	24485386	24540473	-
AAO3	evm.TU.fragScaff_scaffold_70.73_evm.TU.fragScaff_scaffold_70.72	Chr1	23974823	24037234	+
ABA2	evm.TU.fragScaff_scaffold_16.986	Chr1	40537439	40538568	-
ABA2	evm.TU.fragScaff_scaffold_45.503	Chr10	35294144	35295246	-
ABA2	evm.TU.original_scaffold_1005.441	Chr6	789015	790197	-
ABA2	evm.TU.original_scaffold_1962.414	Chr7	36364626	36366521	-
ABA2	evm.TU.original_scaffold_1991.28	Chr5	14976657	14978939	+
ABA2	evm.TU.original_scaffold_463.70	Chr1	38820069	38821700	+
ABA2	evm.TU.original_scaffold_544.37	Chr15	39797302	39805125	+
ABA2	novel.7708	Chr6	43747260	43760041	+
CCD8	evm.TU.original_scaffold_2323.251	Chr8	4041124	4044434	+
CCS1	evm.TU.fragScaff_scaffold_113.261	Chr1	31289763	31291658	-
CRTISO	evm.TU.fragScaff_scaffold_27.297	Chr4	9737322	9765004	-
CRTISO	evm.TU.original_scaffold_1472.55	Chr10	1342700	1366246	-
CRTISO	evm.TU.original_scaffold_195.277	Chr12	3553427	3559317	+
CRTISO	evm.TU.original_scaffold_195.278	Chr12	3559433	3562404	+
CRTZ	evm.TU.fragScaff_scaffold_86.108	Chr1	53373742	53378212	-
DWARF27	evm.TU.fragScaff_scaffold_109.5	Chr7	15481891	15499379	+
LCYE	evm.TU.fragScaff_scaffold_56.238	Chr10	33489233	33498500	+
NCED	evm.TU.original_scaffold_1667.81	Chr11	22116865	22118025	-
NCED	evm.TU.original_scaffold_1667.82	Chr11	22116093	22116710	-
NCED	evm.TU.original_scaffold_1962.545	Chr7	34710677	34713163	+
NCED	evm.TU.original_scaffold_587.22	Chr13	31284885	31286903	-
PDS	evm.TU.fragScaff_scaffold_2.262	Chr6	15522999	15539793	-

PSY	evm.TU.original_scaffold_1207.62	Chr4	13986868	13991070	-
ZDS	evm.TU.original_scaffold_195.500	Chr12	5758989	5762489	-
ZDS	evm.TU.original_scaffold_2446.4	original_scaffold_2446	23483	26983	-
ZDS	evm.TU.original_scaffold_2571.16	original_scaffold_2571	140377	147988	+
ZDS	evm.TU.original_scaffold_868.31	Chr12	5991495	5999095	-
ZEP	evm.TU.fragScaff_scaffold_129.313_evm.TU.fragScaff_scaffold_129.314	Chr12	33735770	33740666	+
ZEP	evm.TU.fragScaff_scaffold_58.129	Chr8	12398377	12400984	+
ZEP	evm.TU.original_scaffold_171.100	Chr5	13179104	13180720	+
ZEP	evm.TU.original_scaffold_2323.333	Chr8	3084179	3086766	+
ZEP	novel.8387	Chr8	12404999	12407651	+
Z-ISO	evm.TU.fragScaff_scaffold_101.33	Chr15	6843828	6884278	-