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Supplementary Data

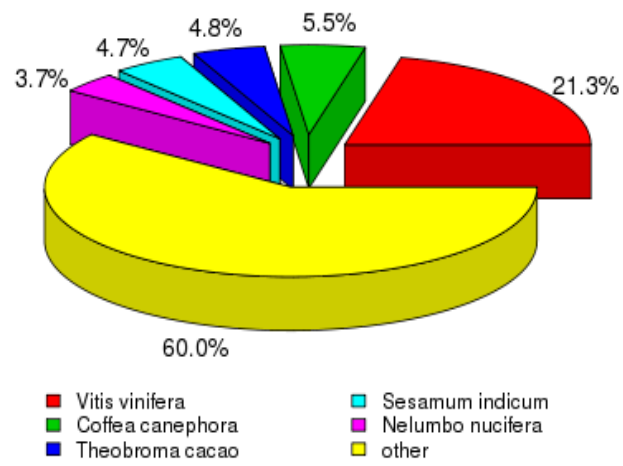


Fig. S1: Species distribution of the top BLAST hits

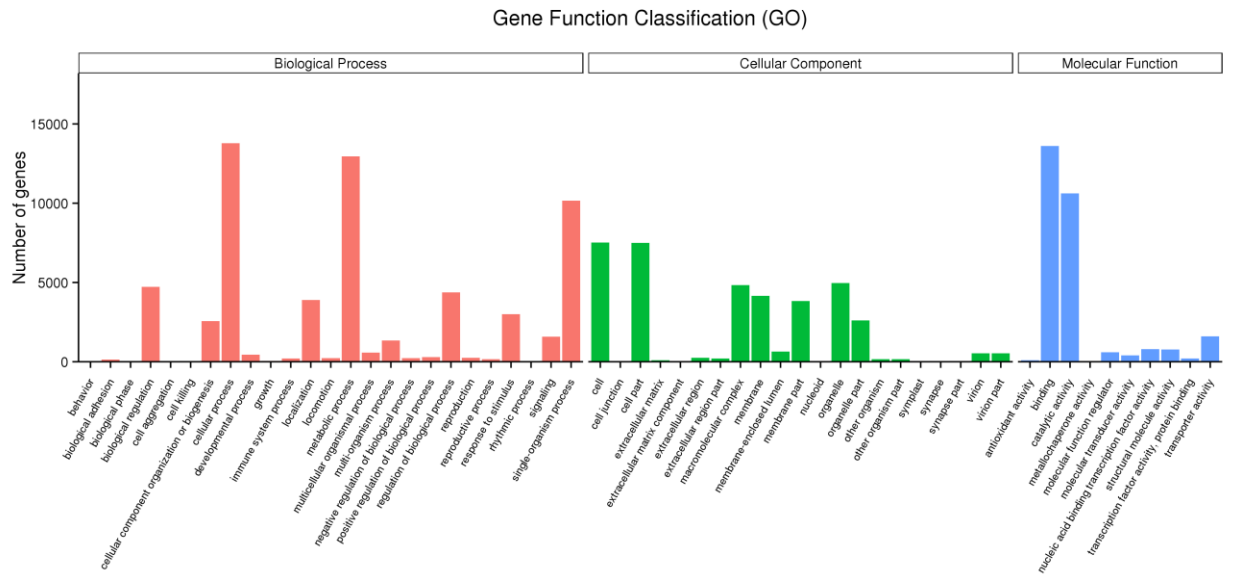


Fig. S2: GO function categories of all unigenes

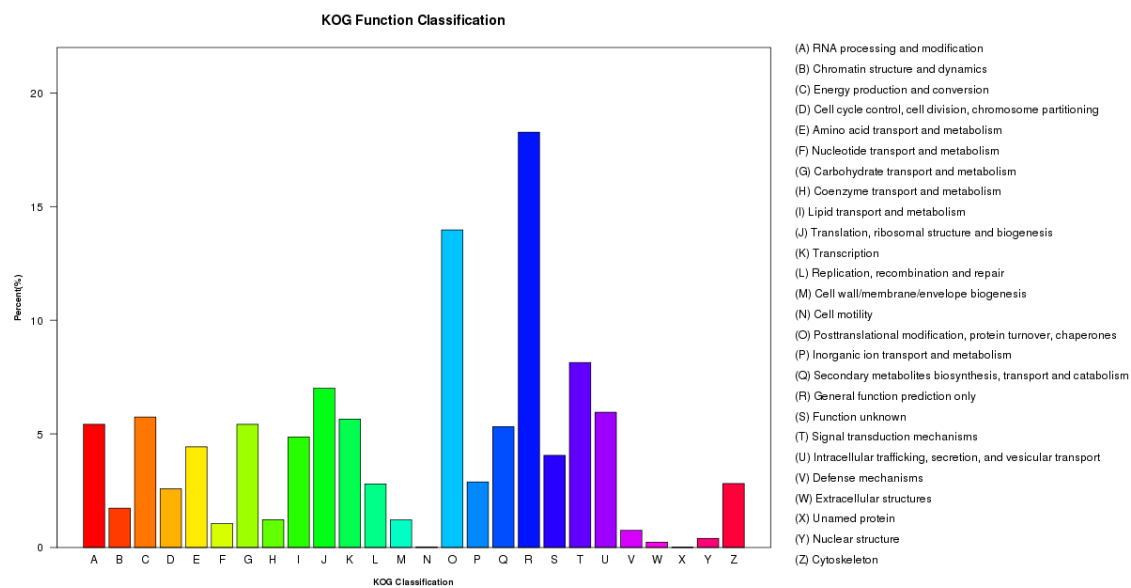


Fig. S3: KOG function classification of all unigenes

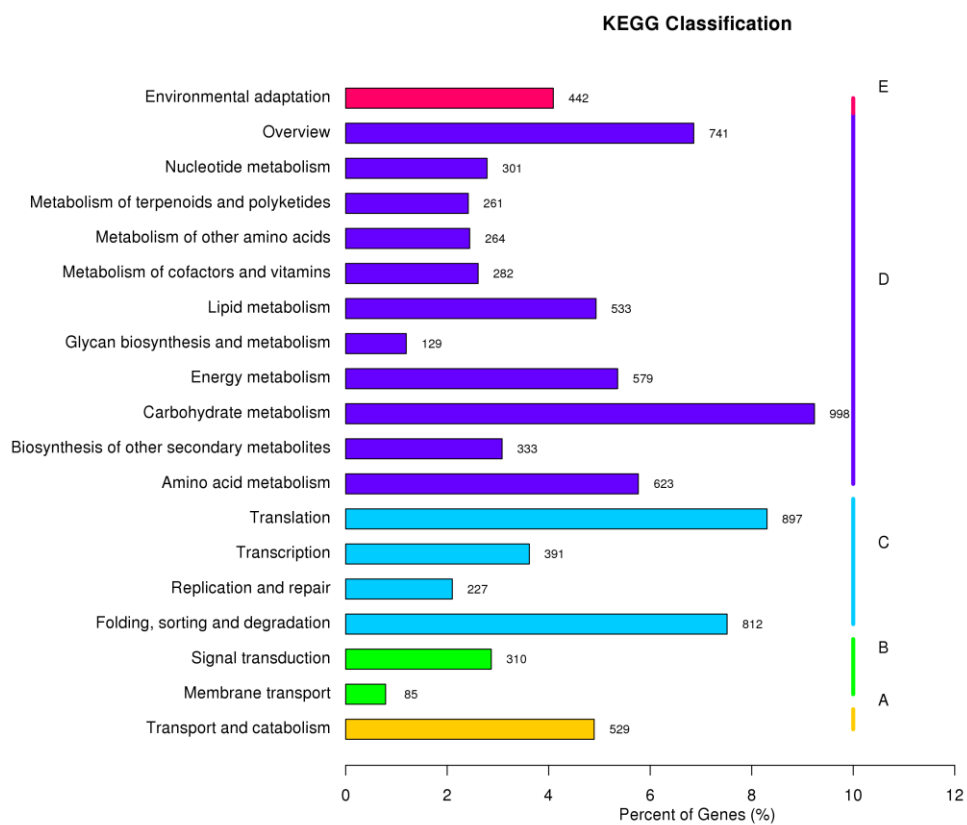


Fig. S4: KEGG classification of all unigenes

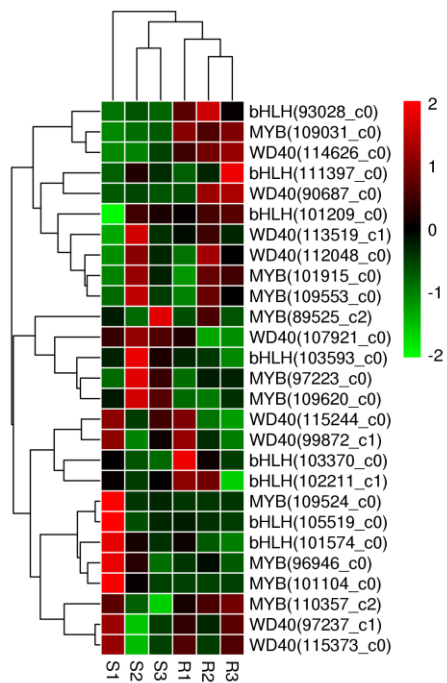


Fig. S5: Statistics of the numbers of transcription factors from all unigenes in blueberry fruit

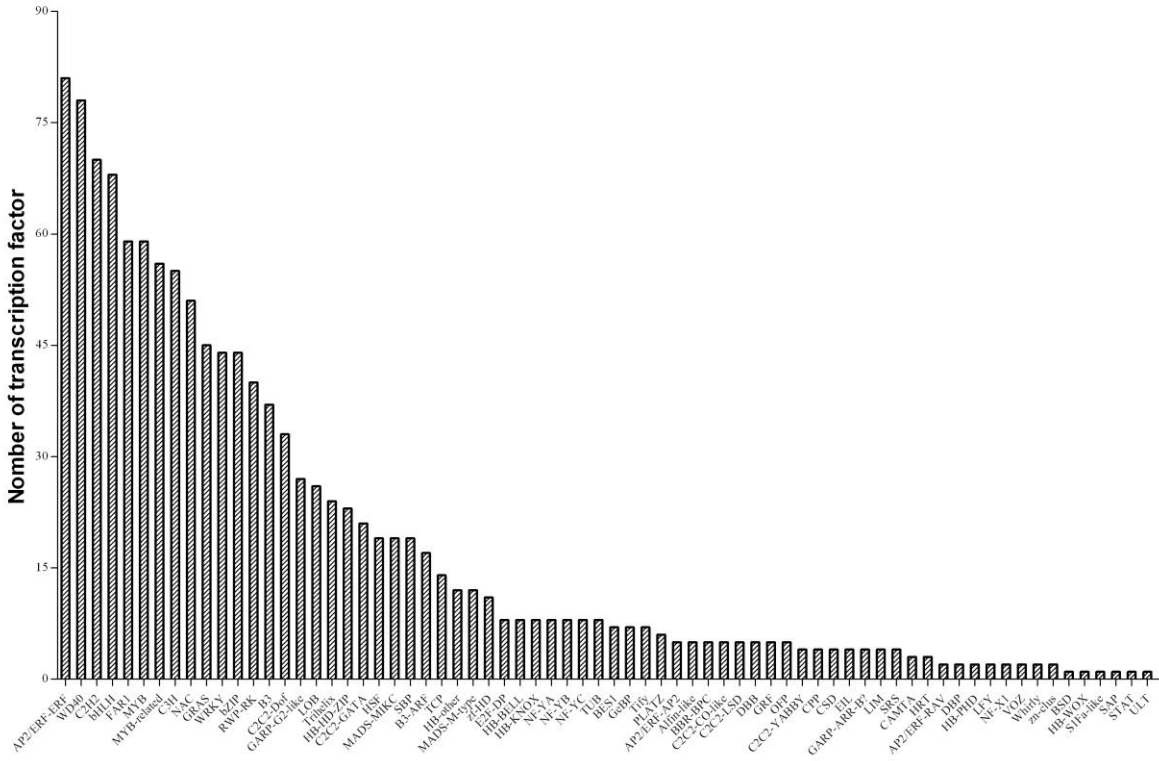


Fig. S6: Heat map illustrating the expression profiles of differentially expressed TFs

Table S1: Statistics of output sequencing

Sample	Raw reads	Clean reads	Clean bases	N (%)	Q20 (%)	GC (%)	Total mapped	Mapped (%)
S1	32,719,179	31,931,865	3.19G	0.03	98	47	24783086	77.61
S2	31,521,567	30,809,881	3.08G	0.03	98	46	24954699	81
S3	36,212,105	35,312,504	3.53G	0.03	98	46	28017847	79.34
R1	36,354,583	35,470,177	3.55G	0.03	98	47	28404600	80.08
R2	35,303,040	34,459,743	3.45G	0.03	98	47	27817677	80.73
R3	35,508,183	34,696,928	3.47G	0.03	98	47	27844167	80.25

Table S2: Summary statistics of functional annotation for blueberry fruit unigenes in public databases

Database	109,480 Total Unigenes	
	Number of Unigenes	Percentage
Annotated in NR	31396	28.67
Annotated in NT	14053	12.83
Annotated in KO	8994	8.21
Annotated in SwissProt	21742	19.85
Annotated in PFAM	24959	22.79
Annotated in GO	25409	23.2
Annotated in KOG	11515	10.51
Annotated in all Databases	4022	3.67
Annotated in at least one Databases	37880	34.59

Table S3: Summary statistics of GO pathway in DEGs

GO accession ID	Description	p-value	DEGs	
			up	down
S2 vs S1	S2 vs S1	S2 vs S1		S2 vs S1
GO:0016491	oxidoreductase activity	2.20E-07	106	101
GO:0055114	oxidation-reduction process	2.20E-07	103	105
GO:0045735	nutrient reservoir activity	4.03E-07	4	12
GO:0005975	carbohydrate metabolic process	1.02E-06	75	64
GO:0003735	structural constituent of ribosome	1.02E-06	56	11
GO:0044710	single-organism metabolic process	7.37E-06	213	233
GO:0042254	ribosome biogenesis	2.88E-05	59	16
GO:0003824	catalytic activity	2.88E-05	365	409
GO:0005840	ribosome	3.33E-05	61	14
GO:1901564	organonitrogen compound metabolic process	3.33E-05	167	114
S3 vs S2	S3 vs S2	S3 vs S2		S3 vs S2
GO:0003735	structural constituent of ribosome	3.93E-23	5	53
GO:0005840	ribosome	2.59E-20	6	55
GO:0042254	ribosome biogenesis	2.01E-19	5	54
GO:0022613	ribonucleoprotein complex biogenesis	4.55E-19	5	54
GO:0030529	ribonucleoprotein complex	1.09E-18	8	58
GO:0006412	translation	4.69E-17	9	55
GO:0043043	peptide biosynthetic process	1.76E-16	9	55
GO:0005198	structural molecule activity	2.40E-16	9	55
GO:0043604	amide biosynthetic process	4.50E-16	9	59
GO:0006518	peptide metabolic process	8.58E-16	9	56
S3 vs S1	S3 vs S1	S3 vs S1		S3 vs S1
GO:0005975	carbohydrate metabolic process	6.45E-12	61	67
GO:0003824	catalytic activity	8.92E-09	339	271
GO:0044710	single-organism metabolic process	2.96E-06	201	145
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	3.10E-06	25	26
GO:0016798	hydrolase activity, acting on glycosyl bonds	5.06E-06	26	27
GO:0045735	nutrient reservoir activity	6.18E-06	11	2
GO:0044723	single-organism carbohydrate metabolic process	6.18E-06	38	39
GO:0055114	oxidation-reduction process	1.18E-05	97	58
GO:0016491	oxidoreductase activity	2.10E-05	91	62
GO:0008152	metabolic process	4.47E-05	388	285
R2 vs R1	R2 vs R1	R2 vs R1		R2 vs R1
GO:0016491	oxidoreductase activity	4.66E-06	60	18
GO:0055114	oxidation-reduction process	1.24E-05	59	19
R3 vs R1	R3 vs R1	R3 vs R1		R3 vs R1
GO:0003824	catalytic activity	0.00061383	199	163
GO:0044710	single-organism metabolic process	0.0049812	114	94
GO:0016491	oxidoreductase activity	0.0067239	45	49
GO:0008152	metabolic process	0.0092687	241	165
GO:0016762	xyloglucan:xyloglucosyl transferase activity	0.013587	5	1
GO:0048046	apoplast	0.013587	6	1
GO:0055114	oxidation-reduction process	0.013587	47	45
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	0.013587	14	15
GO:0009415	response to water	0.019254	0	5
GO:0016798	hydrolase activity, acting on glycosyl bonds	0.019254	14	16

Table S4 Summary statistics of KEGG pathway in DEGs

ID	Pathway	p-value	DEGs	Background genes
S2 vs S1	S2 vs S1	S2 vs S1	S2 vs S1	S2 vs S1
ko03010	Ribosome	2.20E-07	72	393
ko00360	Phenylalanine metabolism	9.13E-12	20	91
ko01200	Carbon metabolism	0.000714	51	423
ko00941	Flavonoid biosynthesis	0.00171	13	47
ko01230	Biosynthesis of amino acids	0.001932	43	348
ko00350	Tyrosine metabolism	0.002623	13	52
ko00400	Phenylalanine, tyrosine and tryptophan biosynthesis	0.002737	14	60
ko00940	Phenylpropanoid biosynthesis	0.002737	23	144
ko00196	Photosynthesis - antenna proteins	0.003316	9	29
ko00130	Ubiquinone and other terpenoid-quinone biosynthesis	0.006567	11	49
ko00052	Galactose metabolism	0.01279	14	75
ko00710	Carbon fixation in photosynthetic organisms	0.01279	20	138
ko00195	Photosynthesis	0.017612	15	89
ko04075	Plant hormone signal transduction	0.017876	24	190
ko00030	Pentose phosphate pathway	0.027934	14	87
ko00020	Citrate cycle (TCA cycle)	0.032136	17	118
ko00500	Starch and sucrose metabolism	0.034273	25	208
S3 vs S2	S3 vs S2	S3 vs S2	S3 vs S2	S3 vs S2
ko03010	Ribosome	5.91E-22	68	393
ko00941	Flavonoid biosynthesis	0.00254	10	47
ko00195	Photosynthesis	0.014217	12	89
S3 vs S1	S3 vs S1	S3 vs S1	S3 vs S1	S3 vs S1
ko00195	Photosynthesis	1.06E-06	23	89
ko00052	Galactose metabolism	0.0009684	16	75
ko00500	Starch and sucrose metabolism	0.0029895	27	208
ko00196	Photosynthesis - antenna proteins	0.004122	9	29
ko04075	Plant hormone signal transduction	0.0156975	23	190
ko00941	Flavonoid biosynthesis	0.0156975	10	47
R2 vs R1	R2 vs R1	R2 vs R1	R2 vs R1	R2 vs R1
ko00941	Flavonoid biosynthesis	1.66E-10	14	47
ko00940	Phenylpropanoid biosynthesis	3.27E-05	14	144
ko00360	Phenylalanine metabolism	5.38E-05	11	91
R3 vs R2	R3 vs R2	R3 vs R2	R3 vs R2	R3 vs R2
ko00062	Fatty acid elongation	0.0383897	3	32
ko00360	Phenylalanine metabolism	0.0383897	4	91
ko00040	Pentose and glucuronate interconversions	0.0383897	4	101
ko00982	Drug metabolism - cytochrome P450	0.0383897	3	56
ko04976	Bile secretion	0.0383897	3	56
ko00750	Vitamin B6 metabolism	0.0383897	2	16
ko00980	Metabolism of xenobiotics by cytochrome P450	0.0383897	3	58
R3 vs R1	R3 vs R1	R3 vs R1	R3 vs R1	R3 vs R1
ko00941	Flavonoid biosynthesis	2.23E-05	12	47
ko00940	Phenylpropanoid biosynthesis	0.0005334	17	144
ko00195	Photosynthesis	0.0005334	13	89
ko00360	Phenylalanine metabolism	0.0005334	13	91
ko04141	Protein processing in endoplasmic reticulum	0.0016149	25	322
ko04612	Antigen processing and presentation	0.0047062	10	73
R1 vs S1	R1 vs S1	R1 vs S1	R1 vs S1	R1 vs S1
ko00195	Photosynthesis	9.56E-08	23	89
ko00196	Photosynthesis - antenna proteins	0.0031841	9	29
ko00360	Phenylalanine metabolism	0.0040831	15	91
ko00940	Phenylpropanoid biosynthesis	0.005103	19	144
ko04918	Thyroid hormone synthesis	0.000930354	7	30
R2 vs S2	R2 vs S2	R2 vs S2	R2 vs S2	R2 vs S2
ko00195	Photosynthesis	0.00000956	13	89
R3 vs S3	R3 vs S3	R3 vs S3	R3 vs S3	R3 vs S3
ko00196	Photosynthesis - antenna proteins	0.0031841	6	29

Table S5. Candidate genes involved in blueberry fruit sugar accumulation, organic acid metabolism and flavonoid biosynthesis

Function	Gene	Enzyme	KO	EC	No: All ^a	No: change ^b	
Genes related to sugar accumulation and organic acid metabolism							
Sucrose metabolism	SS	sucrose synthase	K00695	2.4.1.13	5	0	
	SPS	sucrose phosphate synthase	K00696	2.4.1.14	9	3	
	AI	acid invertase	K01193	3.2.1.26	3	3	
	NI	alkaline/neutral invertase	K01193	3.2.1.26	18	3	
	HK	hexokinase	K00844	2.7.1.1	7	1	
	FK	fructokinase	K00847	2.7.1.4	20	3	
	SUT	sucrose transporter			4	1	
	HXT	hexose transporter			1	0	
	Starch synthesis and hydrolysis	UGPase	UTP--glucose-1-phosphate uridylyltransferase	K00963	2.7.7.9	6	0
		pgm	phosphoglucomutase	K01835	5.4.2.2	5	2
glgC		glucose-1-phosphate adenylyltransferase	K00975	2.7.7.27	8	0	
glgA		starch synthase	K00703	2.4.1.21	2	0	
glgB		1,4-alpha-glucan branching enzyme	K00700	2.4.1.18	3	1	
PYG		starch phosphorylase	K00688	2.4.1.1	2	0	
amy		alpha-amylase	K01176	3.2.1.1	3	1	
		beta-amylase	K01177	3.2.1.2	8	1	
		alpha-glucosidase	K01187	3.2.1.20	7	1	
		6-phosphofructokinase	K00850	2.7.1.11	9	1	
Glycolysis/ Gluconeogenesis	FBP	fructose-1,6-bisphosphatase	K03841	3.1.3.11	7	1	
	pgi	glucose-6-phosphate isomerase	K01810	5.3.1.9	3	0	
	TPI	triosephosphate isomerase	K01803	5.3.1.1	9	0	
	ALDO	fructose-bisphosphate aldolase	K01623	4.1.2.13	6	2	
	GAPDH	glyceraldehyde 3-phosphate dehydrogenase	K00134	1.2.1.12	13	2	
		glyceraldehyde-3-phosphate dehydrogenase (NADP+)	K00131	1.2.1.9	3	0	
	PGK	phosphoglycerate kinase	K00927	2.7.2.3	13	1	
	gpm	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	K01834	5.4.2.1	3	0	
		2,3-bisphosphoglycerate-independent phosphoglycerate mutase	K15633	5.4.2.1	2	1	
	ENO	enolase	K01689	4.2.1.11	9	1	
rbcS	ribulose-bisphosphate carboxylase small chain	K01602	4.1.1.39	7	0		
ppdK	pyruvate, orthophosphate dikinase	K01006	2.7.9.1	3	0		
Citrate cycle	PK	pyruvate kinase	K00873	2.7.1.40	15	1	
	PEPCK	phosphoenolpyruvate carboxykinase (GTP)	K01596	4.1.1.32	6	0	
		phosphoenolpyruvate carboxykinase(ATP)	K01610	4.1.1.49	7	1	
	PEPC	phosphoenolpyruvate carboxylase	K01595	4.1.1.31	6	1	
	ASP	aspartate aminotransferase	K00813	2.6.1.1	3	0	
	PDC	pyruvate decarboxylase	K01568	4.1.1.1	9	1	
	PDH	pyruvate dehydrogenase E1 component subunit	K00162	1.2.4.1	15	0	
		pyruvate dehydrogenase E2 component	K00627	2.3.1.12	5	1	
	CS	citrate synthase	K01647	2.3.3.1	7	1	
	ACO	aconitate hydratase	K01681	4.2.1.3	12	1	
NAD-IDH	isocitrate dehydrogenase (NAD ⁺)	K00030	1.1.1.41	9	2		
NADP-IDH	isocitrate dehydrogenase(NADP ⁺)	K00031	1.1.1.42	4	1		
OGDH	2-oxoglutarate dehydrogenase E1 component	K00164	1.2.4.2	10	1		
	2-oxoglutarate dehydrogenase E2 component	K00658	2.3.1.61	6	1		
LSC	succinyl-CoA synthetase alpha subunit	K01899	6.2.1.4/6.2.1.5	3	1		
SDH	succinate dehydrogenase (ubiquinone) flavoprotein subunit	K00234	1.3.5.1	4	1		
FH	fumarate hydratase, class II	K01679	4.2.1.2	1	0		
MDH	malate dehydrogenase	K00026	1.1.1.37	13	2		
ME	malic enzyme	K00029	1.1.1.40	9	1		
GABA shut	GAD	glutamate decarboxylase	K01580	4.1.1.15	7	1	
	GABA-AT	4-aminobutyrate—2-oxoglutarate transaminase	k07250	2.6.1.19	1	1	
	SSADH	succinate-semialdehyde dehydrogenase(NADP+)	K00135	1.2.1.16	2	0	
		succinate-semialdehyde dehydrogenase(NAD+)	K00139	1.2.1.24	1	0	
	GS	glutamine synthetase	K01915	6.3.1.2	7	1	
	glutamine synthase (NADPH/NADH)	K00264	1.4.1.13/1.4.1.14	12	1		
Genes related to flavonoid biosynthesis							
Phenylpropanoid biosynthesis	PAL	phenylalanine ammonia-lyase	k10775	4.3.1.24	10	2	
	C4H	trans-cinnamate 4-monooxygenase	k00487	1.14.13.11	5	1	
	4CL	4-coumarate--CoA ligase	k01904	6.2.1.12	13	2	
Flavonoid biosynthesis	CHS	chalcone synthase	K00660	2.3.1.74	4	2	
	CHI	chalcone isomerase	K01859	5.5.1.6	1	1	
	F3H	naringenin 3-dioxygenase	K00475	1.14.11.9	3	3	
	F3'H	flavonoid 3'-monooxygenase	K05280	1.14.13.21	4	1	
	F3'5'H	flavonoid 3',5'-hydroxylase	K13083	1.14.13.88	6	1	
	DFR	flavanone 4-reductase	K13082	1.1.1.219	3	1	
	ANS	leucoanthocyanidin dioxygenase	K05277	1.14.11.19	1	1	
	ANR	anthocyanidin reductase	K08695	1.3.1.77	1	0	
	LAR	leucoanthocyanidin reductase	K13081	1.17.1.3	4	0	
	FLS	flavonol synthase	K05278	1.14.11.23	1	1	
Flavone and flavonol biosynthesis	UF3GT	flavonol 3-O-glucosyltransferase	K10757	2.4.1.91	2	0	
	FOMT3	flavonol 3-O-methyltransferase	K05279	2.1.1.76	2	0	
Anthocyanin biosynthesis	UFGT	anthocyanidin 3-O-glucosyltransferase	K12930	2.4.1.115	4	2	
	UGT75C1	anthocyanin 5-O-glucosyltransferase	K12338	2.4.1.298	2	0	

^aNo. All indicates the total number of Unigenes. ^bNo. Change indicates the number of Unigenes with expression significantly changed during fruit ripening