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An RNA-Seq analysis of the peach transcriptome with a focus on genes associated with skin colour

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Electronic Supplementary Material (ESM)

Table S1. Primers used for qPCR

ID in GDR database	Primer sequence (5'–3') F	Primer sequence (5'–3') R	Gene description
ppa004404m	cgctctagctaatttggctaaactc	gttatacagtgcctttatac	cytochrome P450,
ppa004433m	aggtccttagaatacgtaacgtg	catgcacaaagaattcctcc	F3‘H, VvF3‘h4
ppa004473m	gtgcatgcaggatatgattactgcgg	cgtcttcggtcatgtcccg	cytochrome P450,
ppa004544m	gtcaaagccaccttgttaggtg	tggcaggtcaatgtgataggg	cinnamate 4-hydroxylase,
ppa007636m	tccgagggcagagcgaagaac	ttgtggaggcttgtgaggattgg	*F3H, FHT*
ppa007738m	aagtgggtcactgccaagtgtgttc	gtggctcacagaaaactgcccat	*LDOX, ANS*
ppa007994m	gcagcgaatgttacaacgaag	ccacatgtcctatgatacgtg	*LAR1*
ppa008069m	ggtcgtccaggtgaacatactgcc	atttctcatgccatccatgccac	*DFR, dfr1*
ppa008295m	acttcaaggctaaggggctgctg	ccaagccagataaacgccaatcac	*ANR, ban*
ppa008402m	ggaccaggactgactgttgag	gcccacacgtttccaact	*CHS6*
ppa011276m	tgaagacctcaaggaacttctcaatgg	acacaggtgacaacgatactgccact	*CHI, CHI1, CHI2*
ppa018282m	caccggcaatggacaagacatgg	gcagacgcttcctaattactattcc	cinnamate 4-hydroxylase
ppa023080m	gtccatgatatctgtctgtgatg	cactgactgctgcagactgcagaga	*CHS6*
ppa1027182m	gagatgttggcaggtcatatttgg	gcgcctgaaaaaaccacgttgccg	Anthranilate N-benzoyltransferase protein
ppa005162m	ccgctgcctctcccaacactc	ccatcagccacatcaaacacctttat	*UFGT*
ppa009483m	ccaggagaatcggtgagcagaaaa	tcgagggtggaggacttgagaatg	*PpN1*

Table S2. Analysis of the fruit quality detection

Sample	Mean fruit mass (g)	Soluble solids (%)	TA (%)	TSS/TA	Firmness (kg/cm^2)	Vc (mg/100g)
QX	346.3^{a}	13.6^{a}	0.18^{a}	75.6^{b}	8.34^{a}	1.84^{a}
F	329.7^{a}	14.1^{a}	0.14^{a}	100.7^{a}	8.12^{a}	1.43^{a}

QX – cv. Qiuxue; F – cv. Feitao; TSS – inaccuracy; TA – titratable acidity; Vc – vitamin C; different letters indicate significance at 5% level

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Table S3. Summary statistics of the RNA-Seq output

Sample	Total reads	Base No.	GC content (%)	% ≥ Q30	Mapped reads	Mapped ratio (%)	Uniq mapped reads	Uniq mapped ratio (%)
QX	66 603 686	8 392 064 436	45.84	91.41	56 344 011	84.60	54 733 515	82.18
F	65 051 536	8 196 493 536	45.61	91.57	56 017 427	86.11	54 670 887	84.04

QX – cv. Qiuxue; F – cv. Feitao

Table S4. FPKM values calculated for genes differentially transcribed in the skins of fruit

Samples	0–1	1–5	5–10	10–100	> 100
QX	17167 (56.82%)	4160 (13.77%)	2136 (7.07%)	5447 (18.03%)	1301 (4.34%)
F	16995 (56.25%)	4305 (14.25%)	2217 (7.34%)	5410 (17.91%)	1284 (4.25%)

FPKM – fragments per kilobase of transcript per million fragments mapped; QX – cv. Qiuxue; F – cv. Feitao

Table S5. Annotation of the set of differentially transcribed genes

DEG set	Annotated	COG	GO	KEGG	Swiss-Prot	nr
F vs QX	3060	1241	2407	528	2403	3059

QX – cv. Qiuxue; F – cv. Feitao

Table S6. KEGG classification of the set of differentially transcribed genes

Kegg_pathway	Ko_id	Genes No.	*P*-value
photosynthesis	Ko00195	16	3.99E-05
Flavonoid biosynthesis	Ko00941	14	0.000 6659 92
Phenylpropanoid biosynthesis	Ko00940	22	0.015 676 2
Plant-pathogen interaction	Ko04626	30	0.024 477 014
Beta-Alanine metabolism	Ko00410	12	0.032 795 153 6
Terpenoid backbone biosynthesis	Ko00900	12	0.043 333 829 8

Table S7. FPKM values of the subset of differentially transcribed genes related to flavonoid synthesis

Genes	QX	F	Annotation
ppa004404m	22.6581	5.926 15	cytochrome P450, putative
ppa004433m	1 239.63	222.734	F3‘H, VvF3‘h4
ppa004473m	13.9137	1.354 08	cytochrome P450, putative
ppa004544m	296.303	20.5072	cinnamate 4-hydroxylase, putative
ppa007636m	810.10	5.491 45	*F3H, FHT*
ppa007738m	5122.68	176.294	*LDOX, ANS*
ppa007994m	29.6519	2.560 05	*LAR1*
ppa008069m	1 075.985	3.701 856	*DFR, dfr1*
ppa008295m	90.7419	30.269 39	*ANR, ban*
ppa008402m	1741.94	2.652 29	*CHS6*
ppa011276m	331.882	16.043 5	*CHI, CHI1, CHI2*
ppa018282m	31.9109	4.294 73	cinnamate 4-hydroxylase, putative
ppa1027182m	8.0221	4.997 23	Anthranilate N-benzoyltransferase protein, putative
ppa023080m	460.331	0.677 769	*CHS6*

FPKM – fragments per kilobase of transcript per million fragments mapped; QX – cv. Qiuxue; F – cv. Feitao

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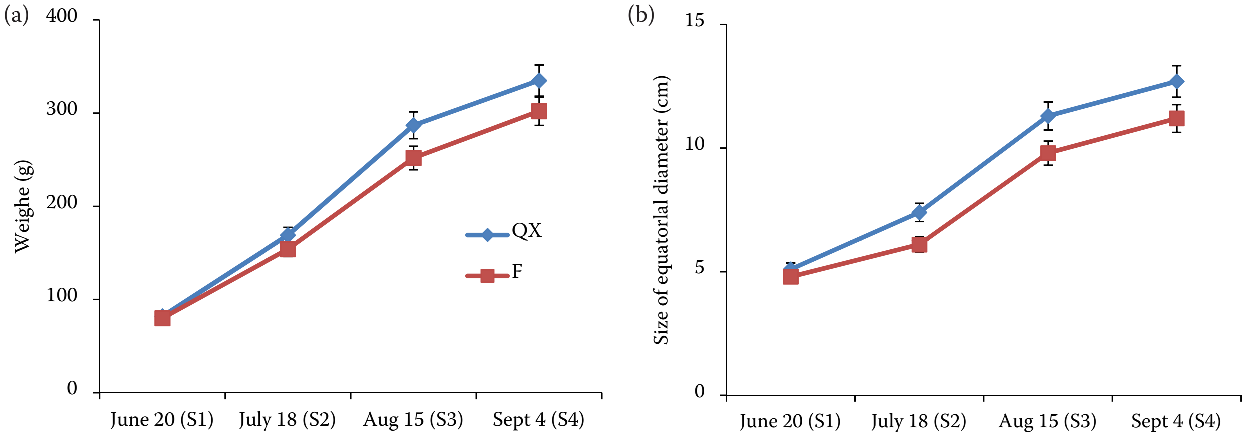

Figure S1. Growth of the fruit cv. Qiuxue (QX) and Feitao (F): fruit weight (a), fruit diameter (b), measured at stage 1 (June 20), stage 2 (July 18), stage 3 (August 15) and stage 4 (September 4)

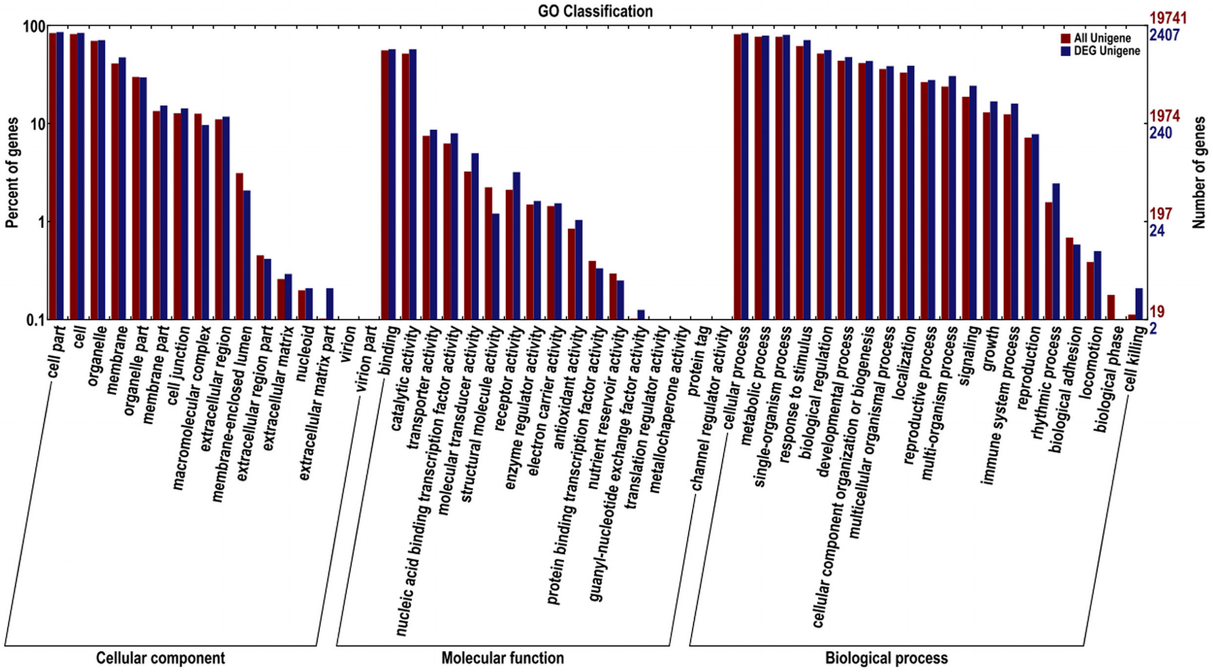

Figure S2. GO classification of differentially transcribed genes

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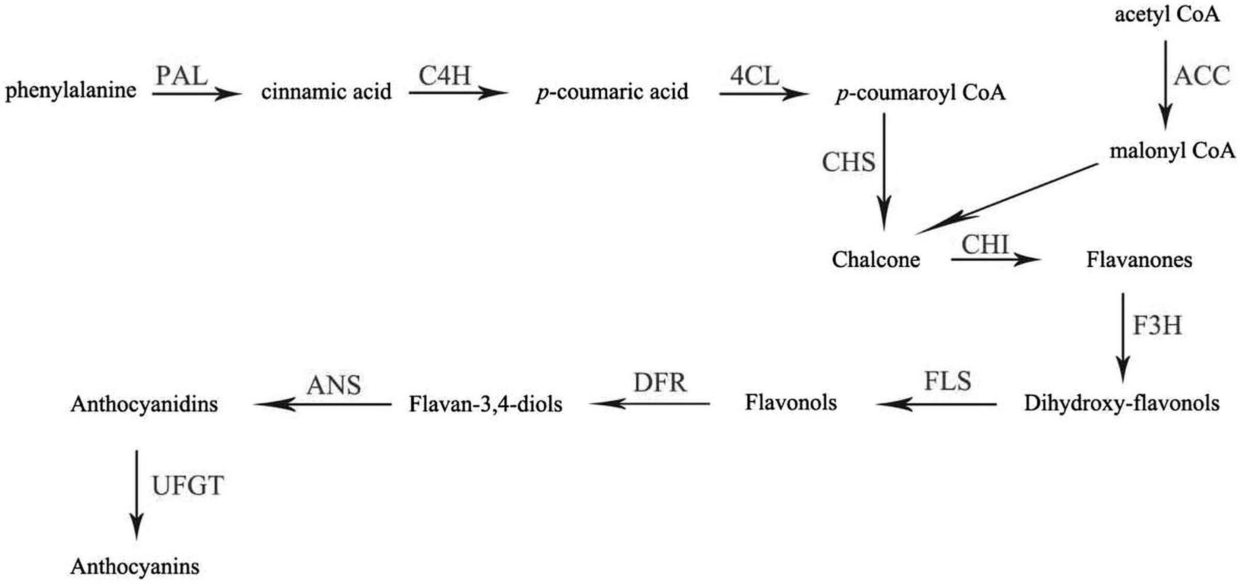

Figure S3. Genes involved in anthocyanin synthesis
ACC – acetyl CoA carboxylase; PAL – phenylalanine ammonia-lyase; C4H – cinnamate 4-hydroxylase; 4CL – 4-coumarate: CoA ligase; CHS – chalcone synthase; CHI – chalcone isomerase; F3H – flavanone 3-hydroxylase; FLS – flavonol synthase; DFR – dihydroflavonol 4-reducatase; ANS – anthocyanidin synthase; UFGT – UDP-flavonoid glucosyltransferase

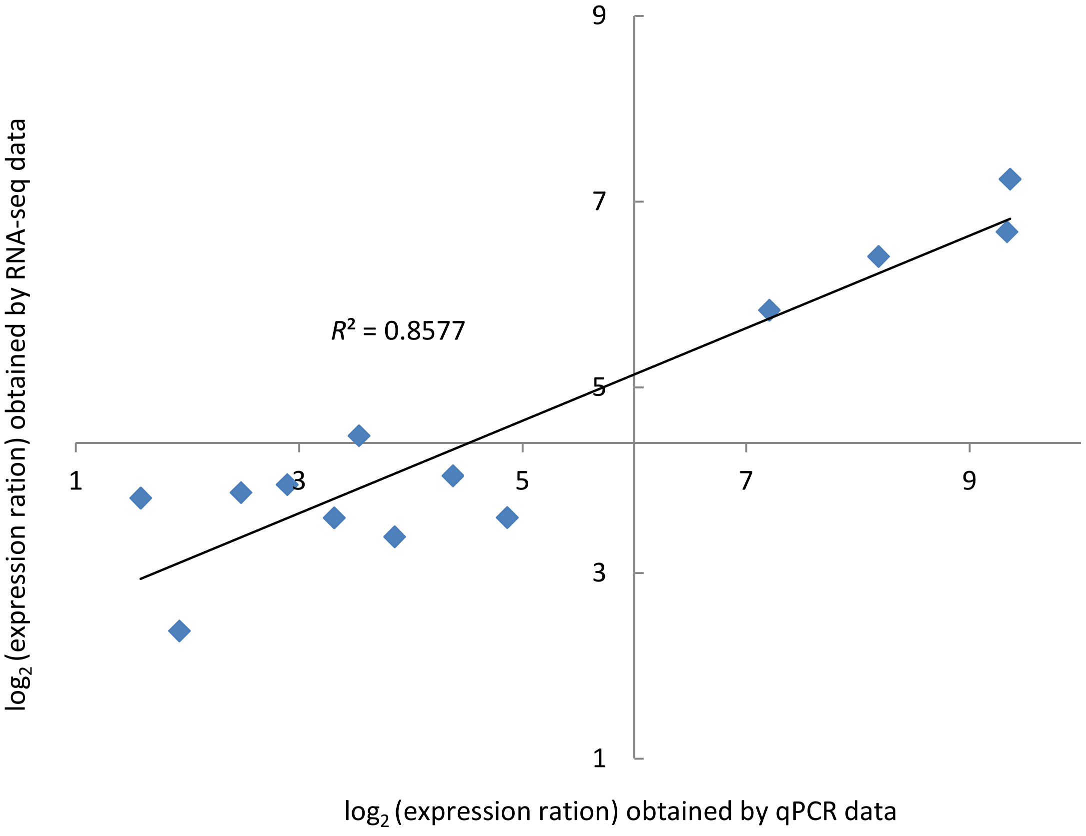

Figure S4. Transcript abundances of 14 genes derived from the RNA-Seq analysis and from qPCR