

Figure S1. Fruit morphology of JNH and CY are shown. The bars of the sections are 1.0 cm.

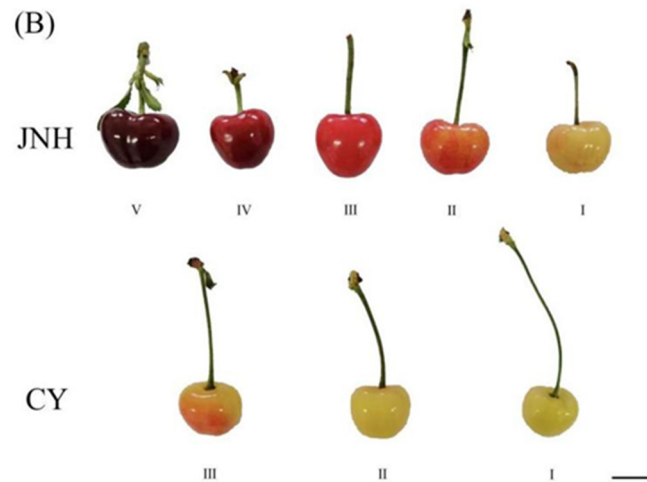


Figure S2. Different ripening stages (A) and maturity level (B) of JNH and CY were showed. The bars of the sections are both 1.0 cm.

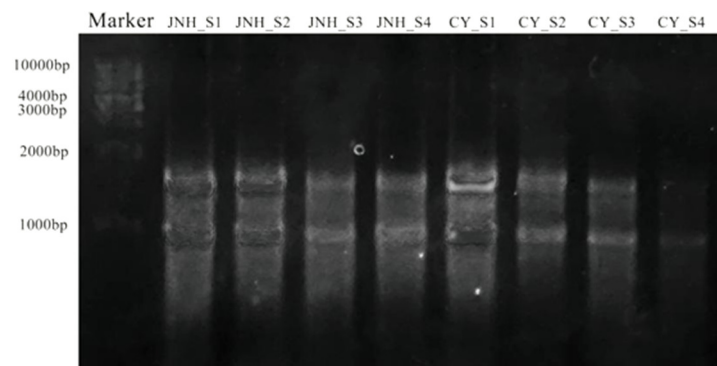
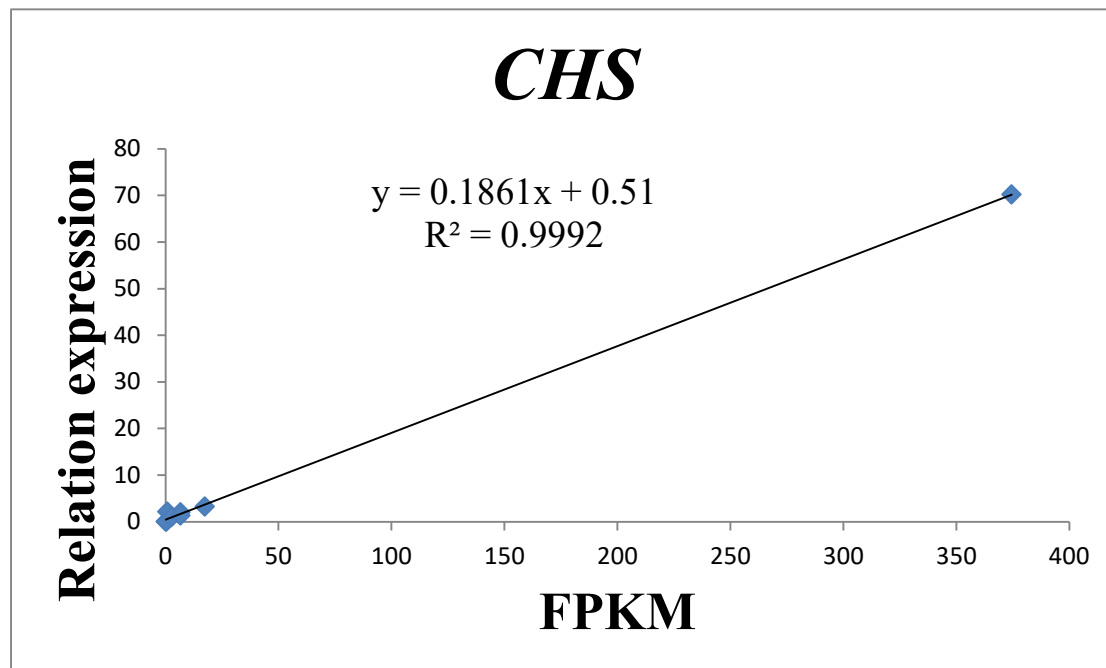
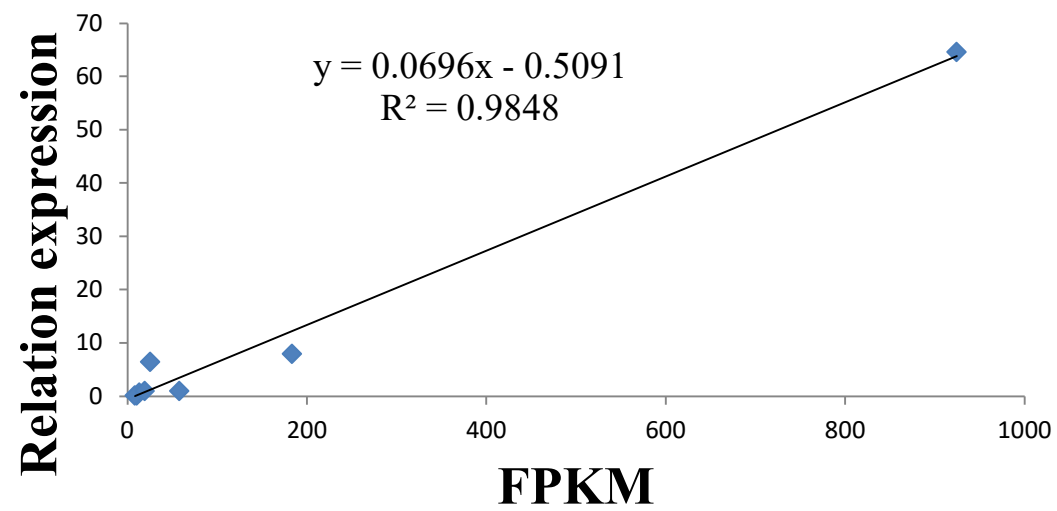


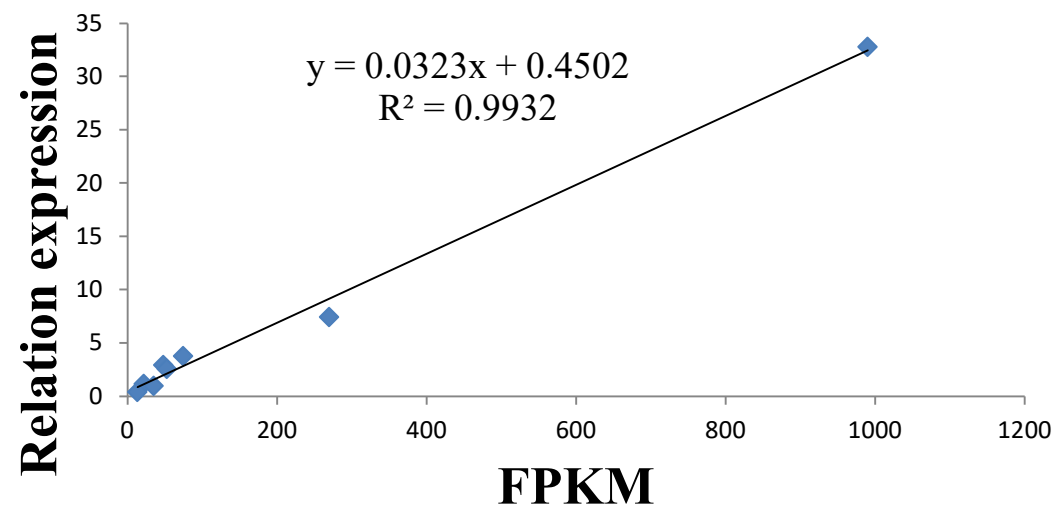
Figure S3. The agarose gel electrophoresis (1.5%) testing of the integrity of RNA.



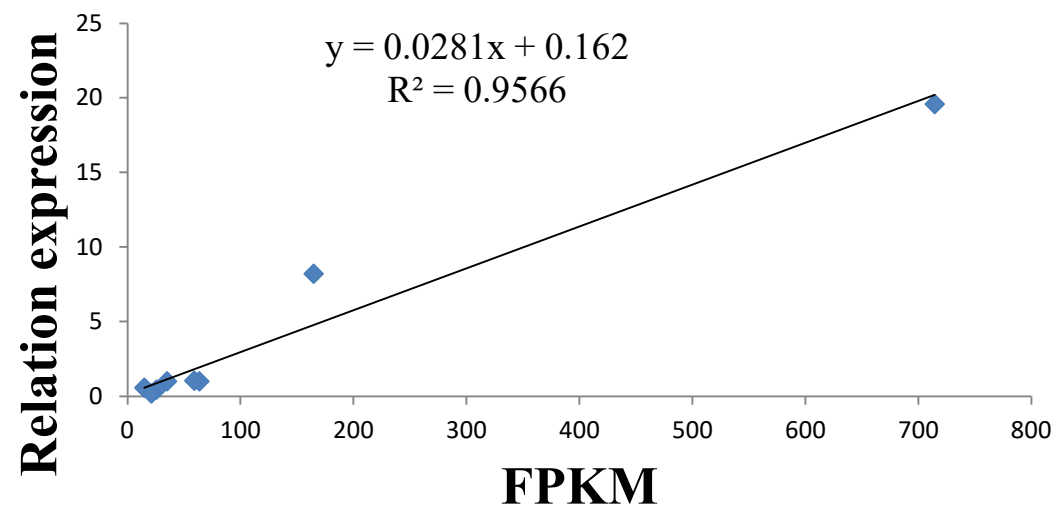
CHI



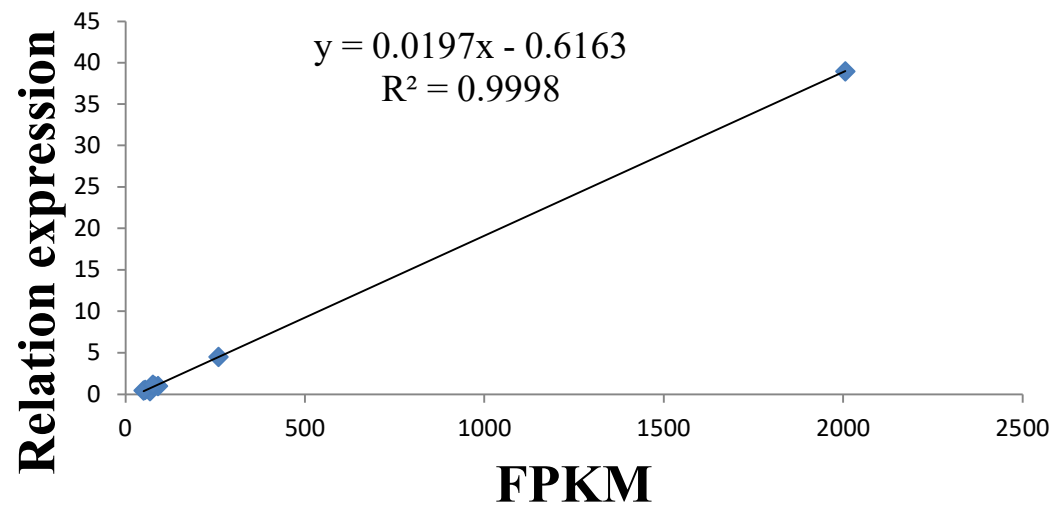
F3H



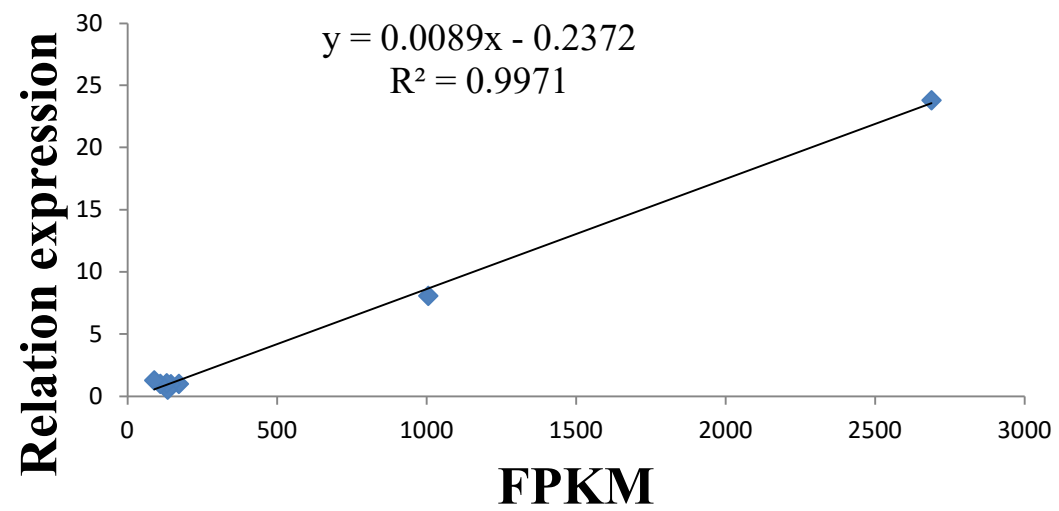
F3'H



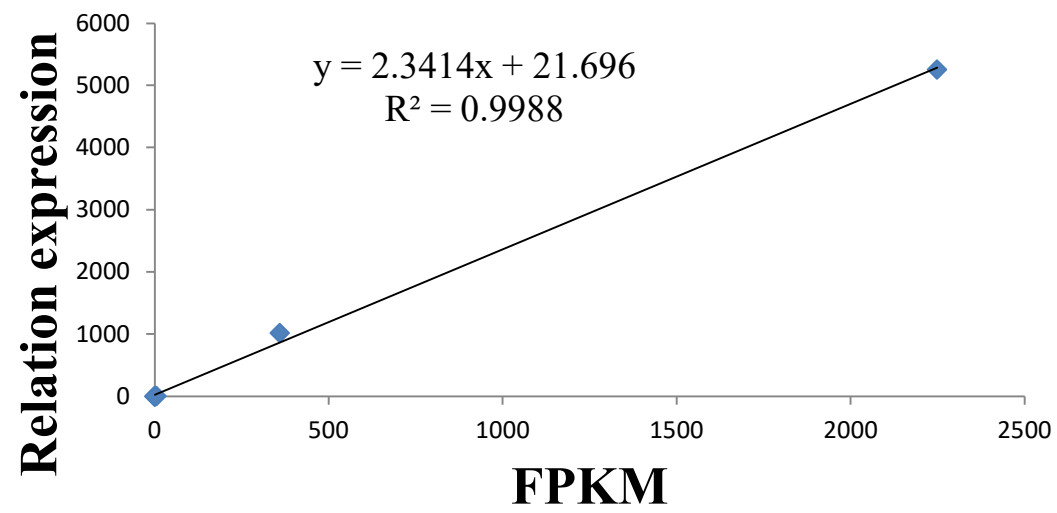
DFR



ANS



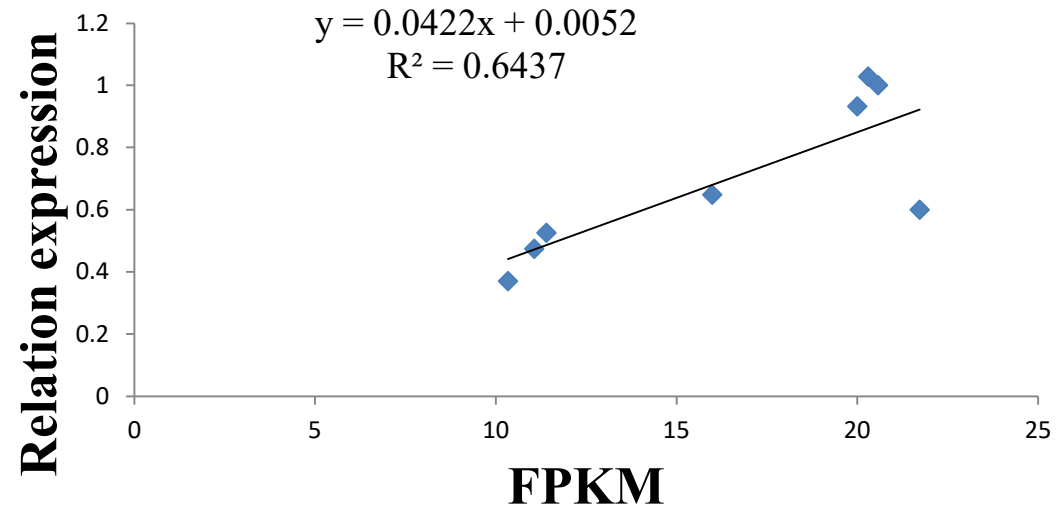
UFGT



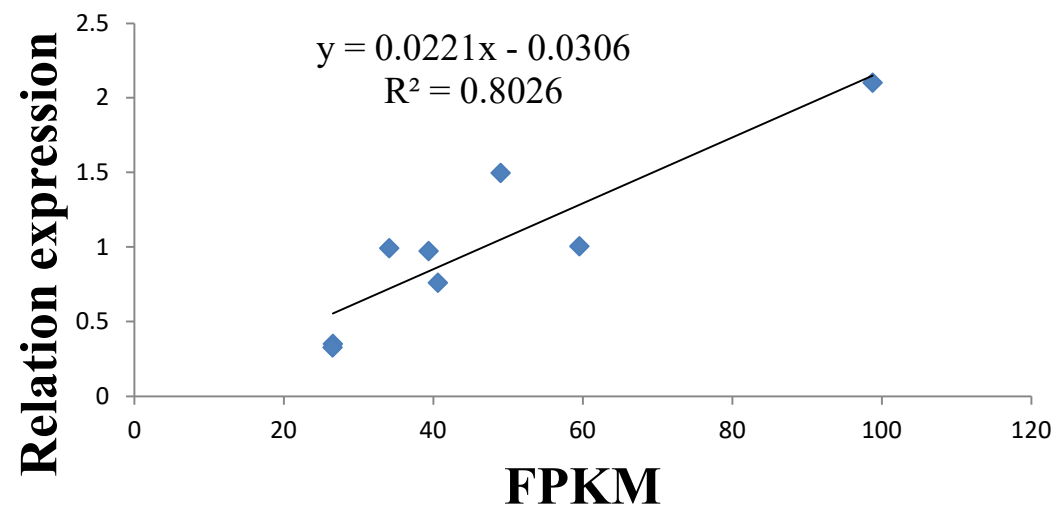
PDS

$$y = 0.0422x + 0.0052$$

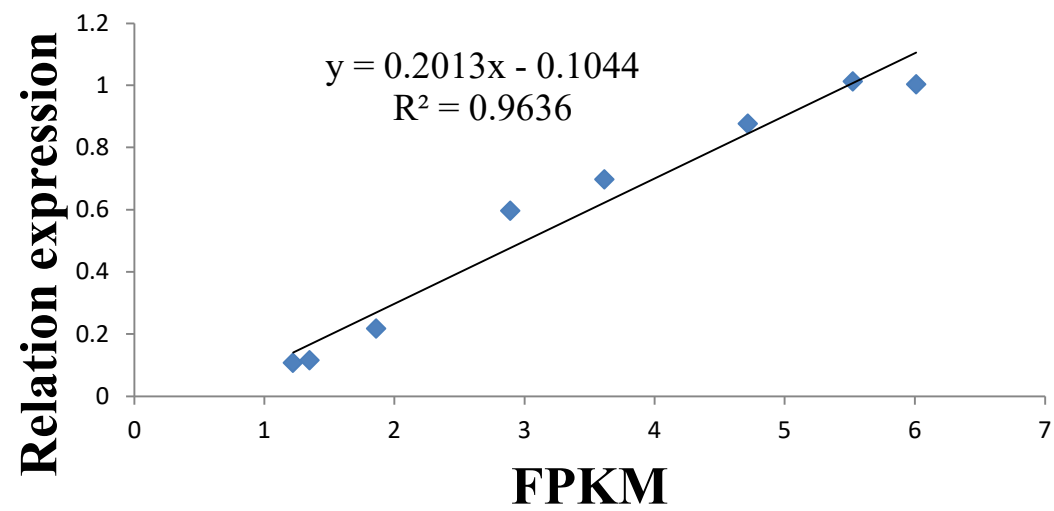
$$R^2 = 0.6437$$



HYB/BCH



LCY-B



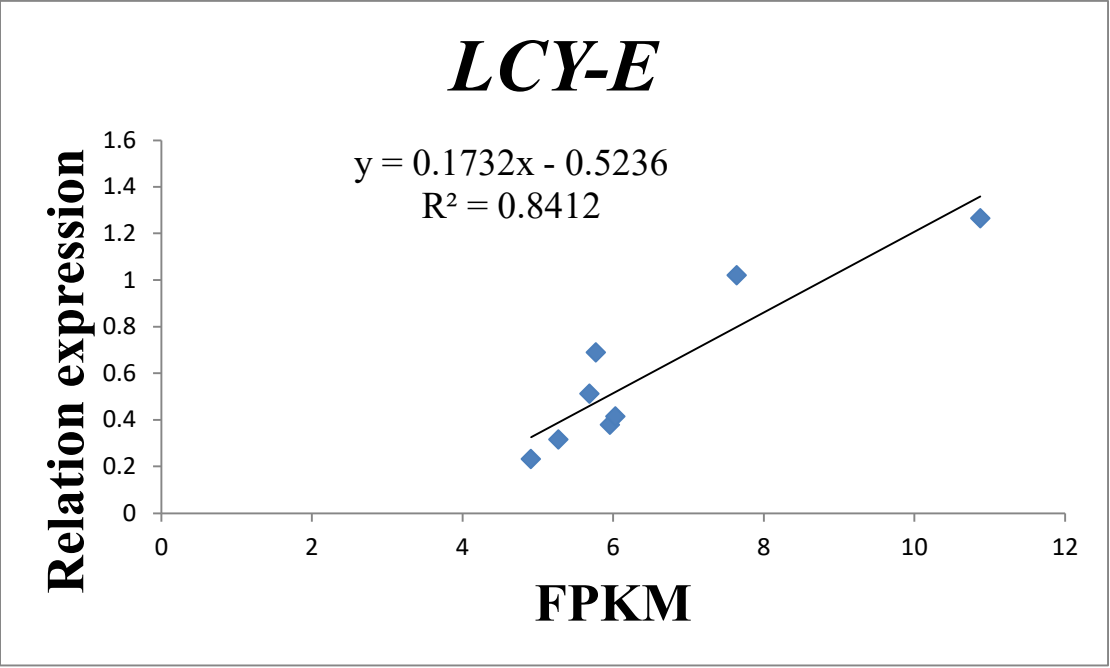


Figure S4. Correlation (R^2) of the expression levels of the 11 genes (*CHS*, *CHI*, *F3H*, *F3'H*, *DFR*, *ANS*, *UFGT*, *PDS*, *HYB*, *LCYB*, *LCYE*) measured by qRT-PCR and RNA-seq.

Table S1. Basic information of reference genome.

NCBI Reference Sequence	NW_018922178.1
Assembly Provider	Kazusa DNA Research Institute
Assembly Method	SOAPdenovo v. 2-rev240; GapCloser v. 1.10
Assembly Name	PAV_r1.0
Genome Coverage	327x
Sequencing Technology	Illumina HiSeq 2000

Table S2. The assembly statistic of the RNA-seq in this study.

	PAV_r1.0
Estimated genome size (bp)	352,883,670
Number of scaffolds	10,148
Size of scaffolds (bp)	272,361,615
Scaffold N50 (bp)	219,566
Longest scaffold (bp)	1,460,269
GC (%)	37.7
Mean size of genes (bp)	1,097
Repeat (%)	43.8

Table S3. The FPKM values underlying the heatmap from the transcriptome mapping data.

Gene name	Gene ID	Gene length	FPKM ^a							
			Stage 1		Stage 2		Stage 3		Stage 4	
			JNH_S1	CY_S1	JNH_S2	CY_S2	JNH_S3	CY_S3	JNH_S4	CY_S4
<i>PAL</i>	110748671	1807	15.480	67.217	19.723	50.550	47.043	5.930	184.357	2.460
<i>C4H</i>	110750787	3544	266.053	680.623	304.750	267.917	375.540	208.727	1315.527	305.510
<i>4CL</i>	110758567	3818	7.583	7.287	6.703	4.293	21.180	3.270	169.313	2.047
<i>CHS</i>	110758924	2440	2.583	6.593	6.580	0.707	17.317	0.053	374.413	0.330
	BGI_novel_G000094	1897	3.310	6.577	4.577	1.220	20.067	0.130	397.700	0.573
<i>CHI</i>	110745765	1443	18.920	57.477	25.193	12.927	183.110	10.247	924.200	8.013
<i>F3H</i>	110758277	1994	34.690	74.277	52.360	47.783	269.347	21.393	989.887	13.070
<i>F3'H</i>	110753332	2528	63.473	35.080	58.933	25.510	164.737	14.793	714.377	21.210

<i>DFR</i>	110771557	2252	80.493	90.483	76.390	68.033	259.210	55.153	2006.030	50.067
<i>ANS</i>	110747768	1667	109.233	172.197	89.220	145.413	1005.627	134.663	2688.480	131.307
<i>UFGT</i>	110749579	1702	0.617	0.330	0.557	0.243	359.253	5.250	2248.373	1.953
<i>PSY</i>	110765927	2783	17.750	19.423	16.827	13.423	8.380	3.957	7.380	4.293
<i>PDS</i>	110747173	10762	20.300	20.573	19.997	21.723	15.983	11.063	11.397	10.333
<i>HYB/BCH</i>	110767732	2315	59.533	98.763	39.383	40.633	26.550	34.103	26.537	49.017
<i>LCY-B</i>	110770275	3176	6.010	5.523	4.717	3.613	2.890	1.860	1.347	1.220
<i>LCY-E</i>	110749277	4150	7.640	10.873	5.273	5.683	6.030	5.770	4.907	5.957
<i>ZEP</i>	110765909	6573	21.923	28.263	17.820	13.347	59.350	39.347	39.813	49.280

^a FPKM= total exon fragments / mapped reads (millions) * exon length (kb)

Table S4. Specific primers pairs for selected genes used in qRT-PCR.

Primers	Sequences (5'-3')	Base (bp)
<i>CHS-F</i>	CTTTGGGCATCTCGGATT	18
<i>CHS-R</i>	TCAACAGTGAGTCCTGGTCC	20
<i>CHI-F</i>	TCCACCGTCAGTCAAACCAC	20
<i>CHI-R</i>	CCTCCAAGTACACGCCAATC	20
<i>F3H-F</i>	TTGTGGAGGCTTGTGAGGAT	20
<i>F3H-R</i>	AAATGGCTGGAGACGATGAA	20
<i>F3'H-F</i>	TGTTGACTACTTTTGCTCTCGC	21
<i>F3'H-R</i>	GTTCTTGTTGGACTTGGGC	19
<i>DFR-F</i>	GAATCTGTTGTGTGACGGG	19
<i>DFR-R</i>	TCCATAGGAGTGGCGACAT	19
<i>ANS-F</i>	GCTACCGCCGAGTATGCTAA	20
<i>ANS-R</i>	TGGAACACACTTGGCAGAGA	20
<i>UFGT-F</i>	ATGTCGGACCTTTCAACCTA	20
<i>UFGT-R</i>	GGCACCACCATCCCATTACT	20
<i>PDS-F</i>	CCTCTGTCGTCACCTCGATCA	20
<i>PDS-R</i>	ATAATTGGCGGACAGGCATA	20
<i>LCYE-F</i>	CAACTGGATATTGAGGGCATCA	22
<i>LCYE-R</i>	CAAGGAAACCGTGCCACATC	20
<i>LCYB-F</i>	GGCTATATGGTGGCAAGGACTT	21
<i>LCYB-R</i>	CAGAATTGAGGCTTCGAACGA	22
<i>HYB-F</i>	TTTGGGATGGCCTACATGTTC	21
<i>HYB-R</i>	GGCACGTCGGCAATGG	16
<i>LCYB2-F</i>	CCCTATTTCCATTAGGCCGC	20
<i>LCYB2-R</i>	CACGTCATATCGAATACGATC	21
<i>β-ACTIN-F</i>	CCAGGGCTGTGTTTCCTTCTA	21
<i>β-ACTIN-R</i>	ATGATCTGCGTCATCTTTTCT	21