Supplementary information

Comparative transcriptome analysis of candidate genes involved in chlorogenic acid biosynthesis during fruit development in three pear varieties of Xinjiang Uygur Autonomous Region

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Table S1 Results of RNA sequencing and quality control

Sample	Clean reads (Mb)	Clean bases (Gb)	Error rate (%)	GC (%)	Q30 (%)
XL-1-1	51.95	7.78	0.0247	46.94	93.84
XL-1-2	53.85	8.08	0.0249	46.81	94.19
XL-1-3	62.71	9.40	0.0248	47.03	94.28
YH-1-1	49.29	7.37	0.0249	46.94	95.1
YH-1-2	60.13	8.97	0.0246	47.62	95.15
YH-1-3	54.84	8.20	0.0255	46.94	94.84
YL-1-1	63.06	9.44	0.0253	47.58	94.26
YL-1-2	48.45	7.26	0.0250	47.34	93.46
YL-1-3	51.85	7.77	0.0249	48.38	94.35
XL-2-1	48.39	7.19	0.0246	47.66	94.41
XL-2-2	44.15	6.58	0.0245	46.35	94.34
XL-2-3	46.13	6.87	0.0253	47.56	94.58
YH-2-1	48.05	7.16	0.0246	46.82	94.53
YH-2-2	50.40	7.52	0.0252	47.43	93.87
YH-2-3	48.49	7.23	0.0250	46.9	93.97
YL-2-1	49.11	7.31	0.0241	47.57	94.14
YL-2-2	46.57	6.95	0.0240	47.33	93.82
YL-2-3	43.05	6.41	0.0243	47.21	94.37
XL-3-1	43.67	6.51	0.0250	47.03	94.21
XL-3-2	42.89	6.40	0.0245	47.13	94.22
XL-3-3	49.98	7.44	0.0253	47.04	93.69
YH-3-1	45.88	6.84	0.0268	47.04	94.67
YH-3-2	54.18	8.09	0.0248	47.2	94.59
YH-3-3	51.46	7.69	0.0253	47.3	94.14
YL-3-1	51.05	7.61	0.0249	50.02	94.63
YL-3-2	40.41	6.03	0.0257	47.78	92.4
YL-3-3	43.72	6.52	0.0248	48.38	93.87

Table S2 De novo transcriptome assembly information of three pear varieties

Type	Number
Total unigene numbers	77130
Total base (bp)	71426493
Average length (bp)	926
N50 length (bp)	1496
GC percent (%)	41.23
Mean mapped percent (%)	73.42

Table S3 Primer sequences for real-time *qPCR*

Enzymes	Unigenes	Forward sequences (5'→3')	Reverse sequences (5'-3')
C3'H	*DN7379_c0_g1*	GAGGTGCTCAAGGAGAATG	AGGTTTGGTGCAGTGGTT
	DN16273_c0_g1	TCATCATTCTCATTTCCCTC	GGTGACCTCATCTTCCCTA
HCT	*DN18762_c0_g1*	CGAGACCCACCTCAGACA	CATTGCCAAAGAAACCAG
	DN12797_c0_g1	GCTGGAAGGGTCGTAGATG	CGAACGCAAGTTGATATTTT
	DN14529_c0_g1	CCTGGTGATTCCGAGCAT	CCGCCATAGGGTAGAACG
	DN38572_c0_g1	AAAGCCAACTCCAACATC	TTTCGGTTCCACCTGTAT
Tubulin alpha-3	*DN946_c0_g1*	ATGCCCAGTGACACCTCT	AGTGCCACCACCAACAGC

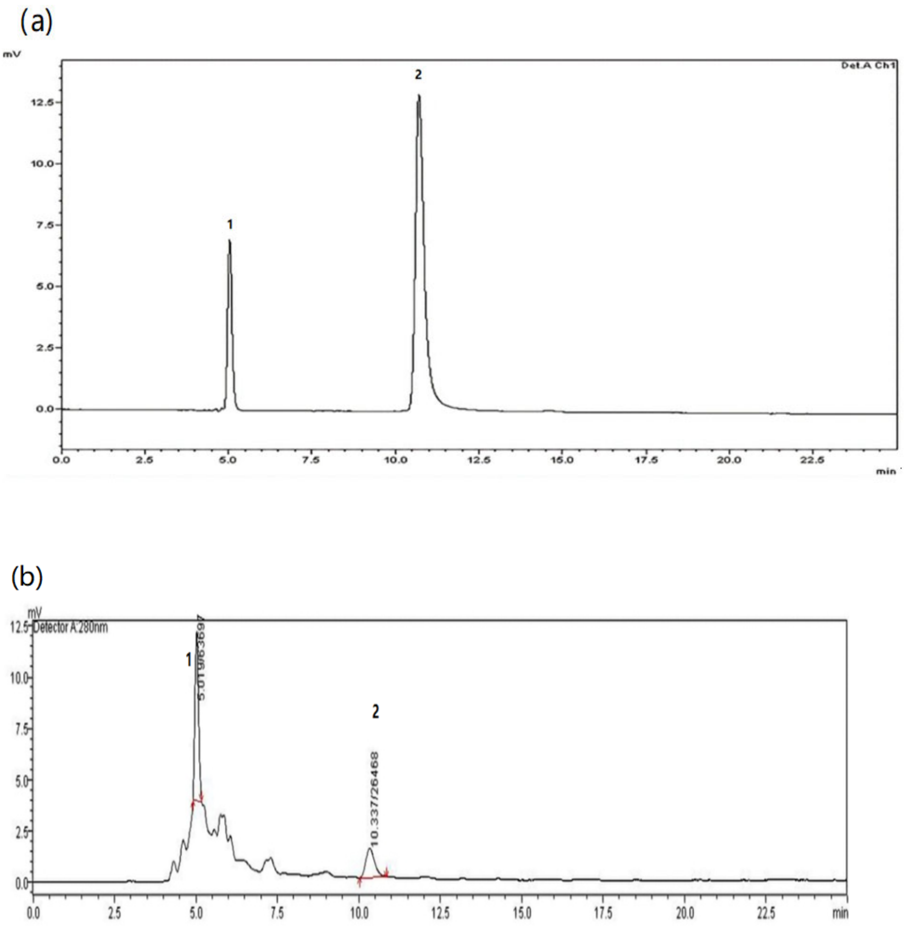

Fig. S1 **High-performance liquid chromatogram of the mixed standards and pear samples at 280 nm. (a) The chromatogram of standards (1. GGA; 2. arbutin); (b) The chromatogram of pear samples (1. GGA; 2. arbutin).**

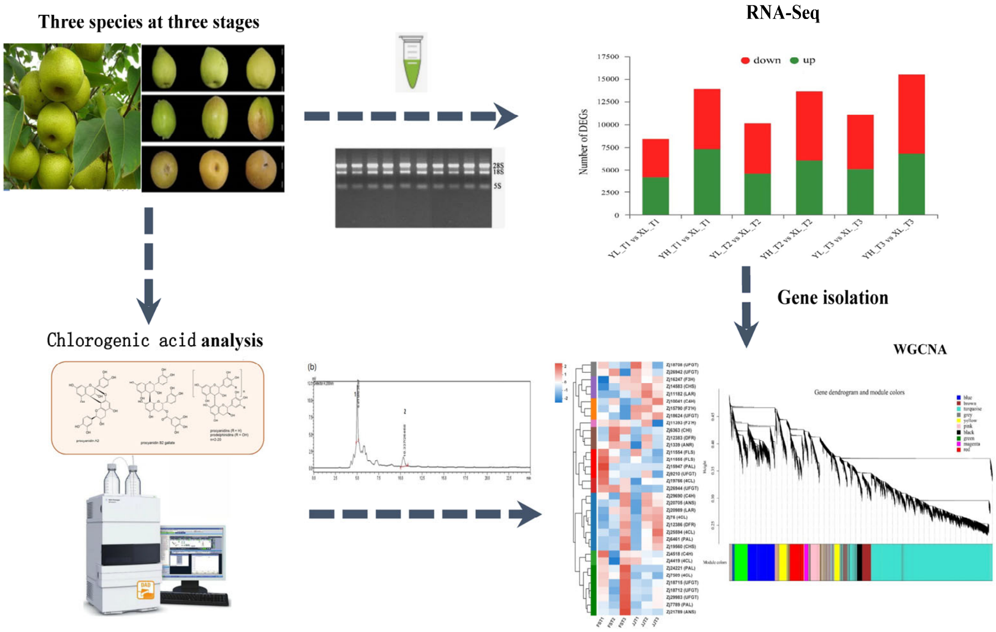

Fig. S2 Graphical scheme of study design

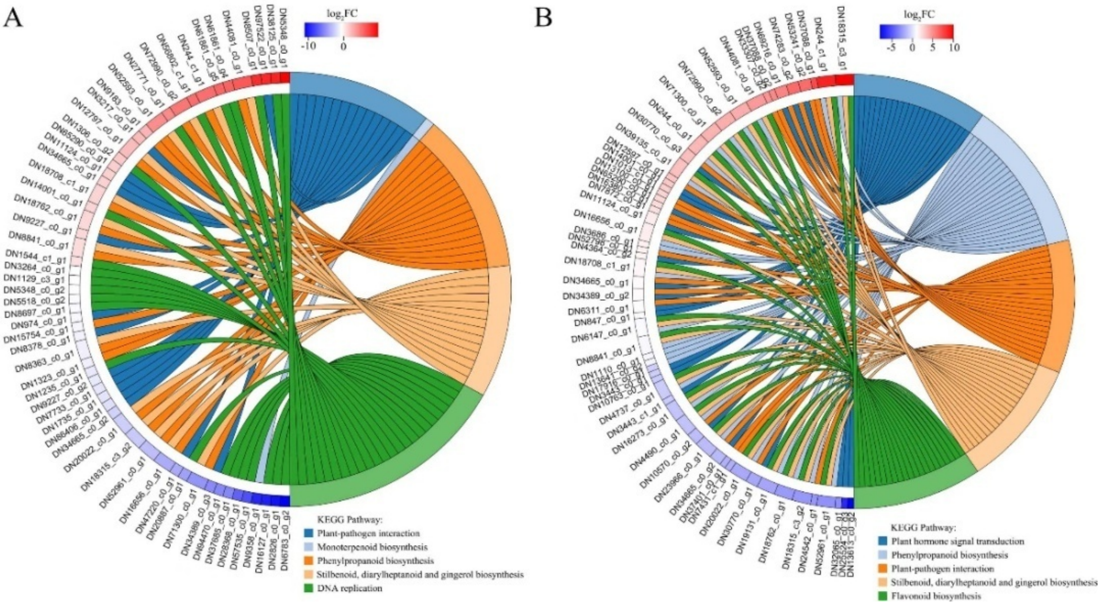

Fig. S3 Chord diagram of KEGG pathway enrichment analysis of two DEGs groups in T1.

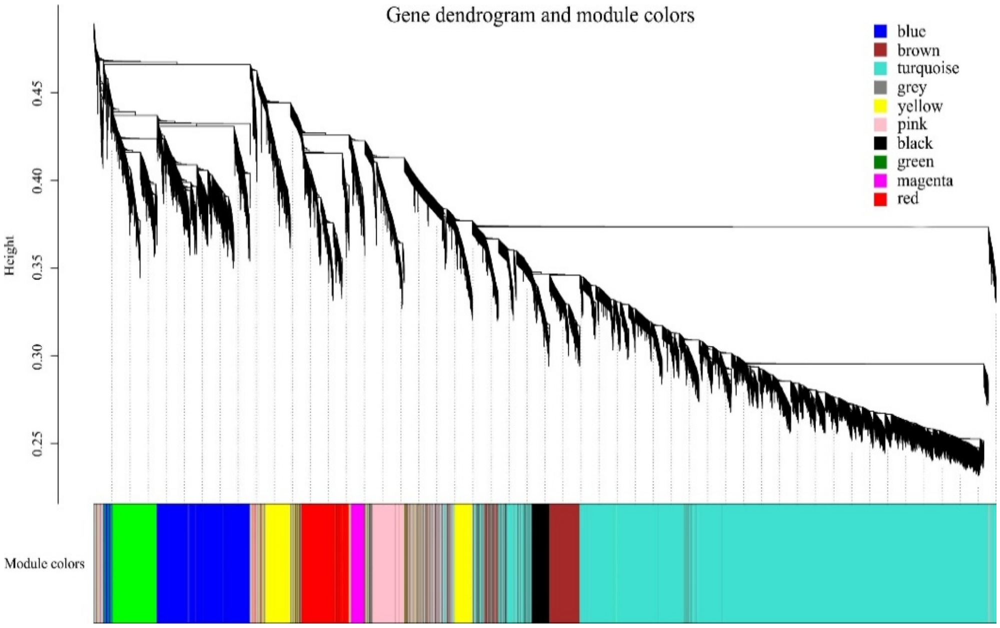

Fig. S4 Hierarchical cluster tree showing co-expression modules identified by WGCNA of DEGS

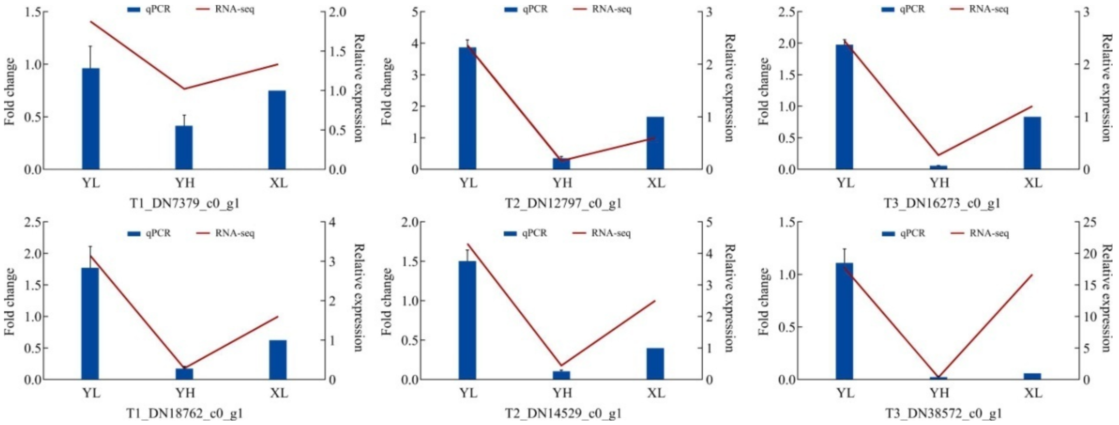

Fig. S5 Relative expression levels of six DEGs in 18 samples