

Supplementary Material

Table S1. Sample site of six red pear cultivars

No.	Cultivars	Species	Stages
a	'5 Hao'	Inter specific <i>Pyrus</i> hybrid	15/35/55/75/95/115 DAFB
b	'Red Bartlett'	<i>Pyrus communis</i>	15/35/55/75/95/115 DAFB
c	'Red Zaosu'	<i>Pyrus. bretschneideri</i>	15/35/55/75/95/115 DAFB
d	'Palacer'	<i>Pyrus communis</i>	15/35/55/75/95/115 DAFB
e	'Red Sichou'	<i>Pyrus communis</i>	15/35/55/75/95/115 DAFB
f	'Starkrimson'	<i>Pyrus communis</i>	15/35/55/75/95/115 DAFB

Table S2. Sequences of primers used for qRT-PCR analysis

Gene/Copy	Gene ID.	Encoded protein		sequence of forward (5'-3') and reverse @primers (5'-3')
PAL	GU390550.1	phenylalanine ammonia lyase	F	5'-TGTTC AAGCTATCTGCCAGGGAA-3'
			R	5'-TGGAATGGAATGCAGCACTCAAGC-3'
CHI	NW_008988454.1	chalcone isomerase	F	5'-ATCGAGGGCAAGTTGGTGAA-3'
			R	5'-CCTGTGACGACGTCCTTGAT-3'
CHS	KF387513.1	chalcone synthase	F	5'-ACTGTTCGAGGAAGTTCGAA-3'
			R	5'-CGGGATATGTGGCTTGATCC-3'
F3H	NW_008988143.1	flavanone 3-hydroxylase	F	5'-TGGGTCTGGAATGTGGCTATGGA-3'
			R	5'-TGGGAAGACATGGATCACCGTTCA-3'
DFR1	NW_008988041.1	Dihydroflavonol4-reductase	F	5'-GATTCATCACCATTATCCCACTC-3'
			R	5'-TGCCAACTTTGACATCAACGAG-3'
DFR2	NW_008988081.1	Dihydroflavonol4-reductase	F	5'-GCCCAAAGTTGTCCAATGTCT-3'
			R	5'-GCTTGTAAGTGAATCCCAAATCTG-3'
ANS1	MF489223.1	anthocyanidin synthase	F	5'-AGCTTCAACACCAAGTGCAAGCTC-3'
			R	5'-TTGGATGAAGGGAGGCTGGAGAAA-3'
ANS2	XM_009370901	leucoanthocyanidin dioxygenase	F	5'-AGCGACATACCAATTGAGCC-3'
			R	5'-CCTCGAGGGCCATTCAATCTT-3'
ANR	DQ251189.1	anthocyanidin reductase	F	5'-CATGTGGAGGATGTCTGCC-3'
			R	5'-GGGGTATCTTTTGTGAGG-3'
UFGT1	NW_008988899.1	anthocyanidin3-O-glucosyltransferase	F	5'-CTGGAACCTGAAGTTGTGAATCTG-3'
			R	5'-AGCCACTTAAGCAACCACTATC-3'
UFGT2	NW_008988121.1	anthocyanidin 3-O-glucosyltransferase	F	5'-GGACACTATCGGAACTCAAGG-3'
			R	5'-AGGTCGAGTCTTCGAAACAG-3'
MYB10	NW_008988216.1	R3R3 myb-type transcript factor	F	5'-TCATCGACAAAGAATGGAA-3'
			R	5'-CTAACTGAAGGCTGGGACA-3'
MYB10b	NW_008988130.1	R3R3 myb-type transcript factor	F	5'-AGATTTACAGAGGACGAA-3'
			R	5'-CCCCTAACCTAACTAGA-3'
bHLH3	XM_018647540.1	basic helix-loop-helix protein	F	5'-ACTTCGGCAGTGGCGTTC-3'
			R	5'-TCACATTCTCGGTTTCAGCAA-3'
bHLH33	XM_009341833.2	basic helix-loop-helix protein	F	5'-GTGATGCAAACACTTAGGGAGC-3'
			R	5'-TTGCCACTCACGTTATCCTTCA-3'
GST	XM_009372312.2	glutathione S-transferase	F	5'-AAGTATGCAGGCCGTGGTC-3'
			R	5'-CAGGTCTGTTGAAGTTGTGGC-3'
COP1	NW_008988230.1	E3 ubiquitin-protein ligase	F	5'-TTGCATGTTTCTCTCCGCCT-3'
			R	5'-GCCAGACATTGCAACAGGTG-3'
PIF3.1	XM_009367742.2	phytochrome interacting factor 3	F	5'-TGCAAGGAGCACATTCCCT-3'
			R	5'-GGGAGCTAAGGGCGCATATT-3'
PIF3.2	XM_018649444.1	phytochrome interacting factor 3	F	5'-ATCCCAAGCGTCGTTTCCAT-3'
			R	5'-GTTACTGGATCTGGCCTCGG-3'
ACTIN			F	5'-CCATCCAGGCTGTTCTCTC-3'
			R	5'-GCAAGGTCCAGACGAAGG-3'

Table S3. Rotated Component Matrix^a

	Component	
	1	2
<i>PAL</i>	0.885	-0.11
<i>CHI</i>	0.851	0.335
<i>F3H</i>	0.847	0.444
<i>ANS1</i>	0.837	-0.068
<i>CHS</i>	0.833	0.221
<i>DFR1</i>	0.812	-0.044
<i>UFGT2</i>	0.76	0.463
<i>bHLH3</i>	0.68	0.403
<i>bHLH33</i>	0.409	-0.042
<i>GST</i>	0.38	0.311
<i>MYB10b</i>	0.349	-0.062
<i>PIF3.1</i>	0.317	0.181
<i>DFR2</i>	-0.169	-0.047
<i>UFGT1</i>	-0.114	0.896
<i>MYB10</i>	0.16	0.867
<i>COP1</i>	0.19	0.849
<i>ANR</i>	0.245	0.561
<i>PIF3.2</i>	0.154	-0.272
<i>ANS2</i>	0.013	0.074

Extraction Method: Principal Component Analysis. Rotation Method: Varimax with Kaiser Normalization. ^a Rotation converged in 3 iterations.

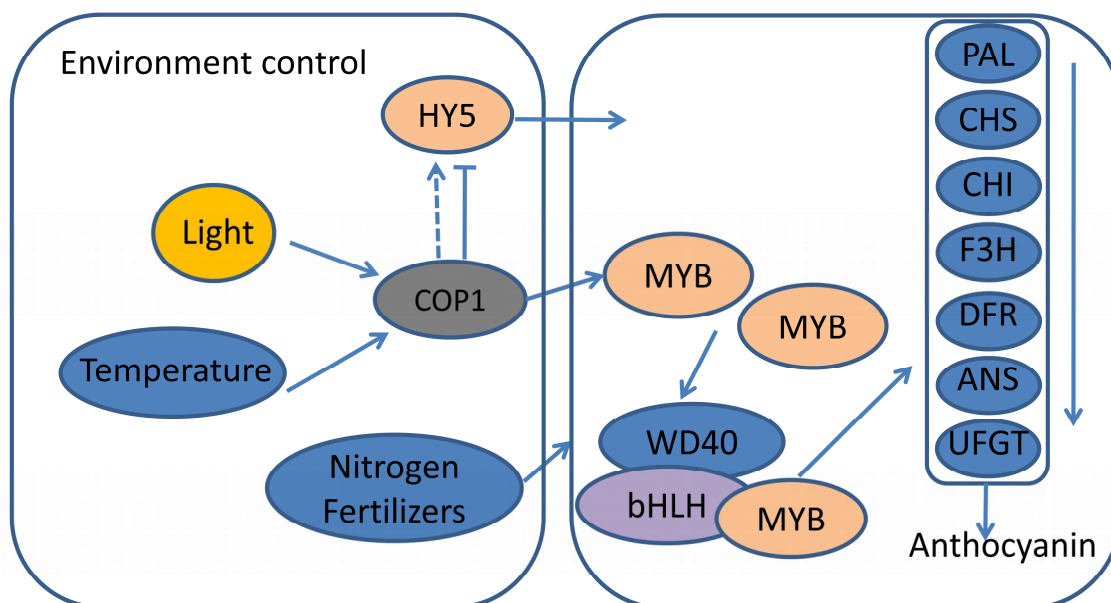


Figure S1. A schematic presentation of the flavonoid biosynthetic pathway leading to anthocyanins.