

Table S1 The primer sequences used in qRT-PCR

Gene	Forward primer (5'-3')	Reverse primer (5'-3')
Actin	TGACCGAATGAGCAAGGAAATTA	TACTCAGCTTTGGCAATCCACATC
	CT	
MDP0000523487 ( <i>CHI</i> )	GCTACAAATGCGGTGATAG	CGCCTCCACTACAACCTCC
MDP0000607969 ( <i>DFR</i> )	TTGAATCCAAGGACCCCGAG	CTTTTGGTGCTCCTCCACATTC
MDP0000388769 ( <i>PAL</i> )	CGAGGAGTGTGACAAGGTGTTC	AGGAATGCAGCATGTAAACCGTGA
	A	
MDP0000240643 ( <i>ANS</i> )	GTTCTGTCACTTGGCTTGGG	GGAGGATGAAGGTGAGTGCA
MDP0000657441 ( <i>WRKY23</i> )	GATGTGGTGAAGAGGGAGGA	ACAGGGAAGTGGGACAACAG
MDP0000686661 ( <i>CHS</i> )	TAGGCATCTCGGACTGGAAC	GACACACGCACTTGACATGT
MDP0000284922 ( <i>MYB-related 306-like</i> )	TGATCCAGCAAATGCTTCAG	CCTCAACTCGATCACAGCAA
MDP0000140609 ( <i>MYB7</i> )	CATGACCACCAACAACAAGG	CATTAGTCCCCCTGCATTTG
MDP0000127691 ( <i>MYB1</i> )	CGGCTGAGGTGGTGTAAATC	CTCTTGGCTCGGCAATAAG
MDP0000758053 ( <i>MYB1R1</i> )	GTCCGATCCCACTTCATCCT	CTAGACATGGCCTGAAACGC
MDP0000074681 ( <i>MYB1R1-like</i> )	CAATCCATTGCCTGCTCCTC	GTCATGGTGGGCTCAGTAGT

Table S2 Type and number of anthocyanins tested in this project

N O .	Name	Class	RT	Equa tion	LL O Q	U L O Q	Q 1 (D a)	Q 3 (D a)	YS1	YS2	YS3	YS4	YR1	YR2	YR3	YR4	HS1	HS2	HS3	HS4	HR1	HR2	HR3	HR4
1	Cyanidin-3-O-galactoside	Cyanidin	6.89	y = 2550.9742 8 x + 743.84466	5	5000	449.1	287.1	2.41680403	1705.24217	2715.983853	5326.661967	36.70366017	2298.43812	2010.726757	3478.426237	26.6289994	413.573935	609.3807043	2419.782317	6.339445693	121.8725117	935.4319287	1490.714583
2	Cyanidin-3-O-arabinoside	Cyanidin	7.86	y = 1.05803e5 x + 9.08452e4	2	5000	419.1	287.1	26.9395810	173.553.98005873	0.36370993188	63.84463673	40.88960837	130.8014707	0.927008345	9.11343001	16.74434223	65.40174173	0.096229065	4.491036143	20.3395484	34.406431		
3	Cyanidin-3-O-xyloside	Cyanidin	9.64	y = 6.97427e4 x + 6.06251e4	5	5000	419.1	287.1	0.05800778	35.96380077	66.55479137	180.726279	0.864402331	56.38430147	38.53602847	100.1923095	0.495484068	10.12807833	13.7644965	54.8474219	0.152599659	1.936452043	17.7630829	27.67031093
4	Cyanidin-3-	Cyanidin	7.4	y =	5	50	44	28	0	0	13.08	51.43	0	12.79	9.690	33.30	0	0	0	21.55	0	0	0	0

[illegible]

8	Peonidin-3-O-arabinoside	Peonidin	9.37	y = 1.18209e5 x + 8.00277e4	2	5000	433.2	301.1	0	0.00810718	0.035836407	0.539397569	0	0.040858466	0.041091285	0.229422127	0	0	0.022817757	0.08899535	0	0.006724986	0.033778069	0.052526012
9	Pelargonidin-3-O-arabinoside	Pelargonidin	8.7	y = 17671.41022 x - 7094.46550	N/A	N/A	403.1	271.06	0	0	0	0.329387025	0	0.070632929	0.075310046	0.185404744	0	0	0	0	0	0	0	0
10	Cyanidin-3-O-rutinoside	Cyanidin	8.08	y = 17671.41022 x - 7094.46550	N/A	N/A	51.7	287.1	0	0.12337751	0.090298809	0.368671285	0	0.49530838	0.125129403	0.221357853	0	0	0	0.070857163	0	0	0	0
11	Delphinidin-3-O-glucoside	Delphinidin	6.43	y = 6.68665e4 x + 13056.597	5	5000	465.1	303.1	0	0	0	0	0	0	0	0.311386889	0	0	0	0	0	0	0	0

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1 2	Delphinidin-3-O-arabinoside	Delphinidin	6.99	y = 1767 1.410 22 x - 7094. 4655 0	N/A	N/A	43 5.5	30 3.1	0.049 5997 48	0.031 0348 3	0.028 6384 58	0 0	0.045 8804 27	0 0	0.032 2073 66	0 0	0.026 8285 04	0.034 2106 22	0 0	0.036 0527 904	0.039 0 4	0 0	0 0	
1 3	Delphinidin-3-O-rutinoside	Delphinidin	7.02	y = 3.677 95e4 x + 2284 8.445 83	5	50 00	77 3.2 1	30 3.1	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0.005 2760 85	0.015 0372 49	0 0	0.002 1456 35	0.013 2991 62			
1 4	Delphinidin-3-O-galactoside	Delphinidin	5.99	y = 6.065 81e4 x + 1.040 06e5	5	50 00	46 5.1	30 3.1	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0.091 9214 37	0 0			
1 5	Malvidin-3-O-sambubioside	Malvidin	9.46	y = 1767 1.410 22 x - 7094.	N/A	N/A	62 5.1 9	33 1.1	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0.036 4953 14	0 0	0 0	0 0	0 0	0 0	0 0	

				4655 0																				
1 6	Peonidin-3- O-glucoside	Peonidin	8.9 7	y = 1.751 34e5 x + 1.330 17e5	2 50 00	46 3.3	30 1.1	0 0	0 0	0.019 1829 82	0.147 7188 11	0 0	0.005 9882 09	0.006 5814 85	0.023 2783 65	0 0	0 0	0 0	0.073 0577 51	0 0	0 0	0.006 1351 78	0.026 2589 26	
1 7	Peonidin-3- O-(6-O-p-co umaroyl)-gl ucoside	Peonidin	12. 52	y = 1767 1.410 22 x - 7094. 4655 0	N/ A N/ A	60 9.1 6	30 1.1	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0 0	0.183 5969 89	0 0	0 0	0 0		

Note: LLOQ and ULOQ represent the lowest concentration and the highest concentration of the corresponding substance detected in the sample respectively. The substance with LLOQ and ULOQ value were quantified through the retention time (RT) and Q1, Q3 value of standard sample, and substances without values were semi quantitative. Semi quantitative analysis was mainly based on the fragmentation mode of mass spectrometry and the peak rule of liquid phase of substances with standards. Q1, Relative molecular mass of original ion. Q3, Relative molecular mass of the characteristic fragment after cleavage. The unit of anthocyanin content was µg/g. YS, Huashuo; YR, Huarui.

Table S3 Statistics of all sample quality control data

Sample	Total Reads	Total Bases	Average Read	Q20 Bases	Q30 Bases	GC Bases
NO.	Count	Count (bp)	Length (bp)	Ratio (%)	Ratio (%)	Ratio (%)
1	50939656.67	7145200980	140.32	97.48%	90.48%	47.11%
2	58922644.00	8273328673	140.41	97.94%	92.51%	46.91%
3	50589868.67	7127723224	141.1333333	97.88%	91.64%	47.29%
4	62619902.67	8786949099	140.3033333	98.28%	93.58%	46.86%
5	48690526.67	6875857480	141.2066667	97.33%	90.00%	47.39%
6	57012886.00	8029186252	140.81	98.17%	93.22%	47.02%
7	55532436.67	7754430281	139.5833333	97.94%	92.38%	47.09%
8	61891340.67	8466435258	137.0066667	98.31%	93.76%	47.68%
9	63498018.67	8887962070	139.99	98.01%	92.74%	47.23%
10	53440447.33	7431283743	139.02	98.25%	93.49%	46.64%
11	55905295.33	7819888806	139.9233333	98.13%	93.11%	47.11%
12	58483802.67	8241588138	140.92	98.24%	93.50%	46.87%
13	59403900.00	8330053551	140.2633333	98.11%	93.05%	47.29%
14	48662867.33	6880553146	141.3433333	98.23%	93.47%	47.28%
15	56215815.33	7915404767	140.7933333	98.17%	93.21%	46.61%
16	59272514.67	8332149512	140.5766667	98.21%	93.37%	46.85%

Note: 1-4 sequential represent YS1-4, 5-8 sequential represent YR1-4, 9-12 sequential represent HS1-4, 13-16 sequential represent HR1-4. YS, Huashuo; YR, Huarui.

Table S4 Hormones related to anthocyanin accumulation

	ID	Annotation	Accession	PCC
ABA	MDP0000058337	HYR1 (UDP glycosyltransferase)	at3g21760	0.717/0.798
	MDP0000715898	HYR1 (UDP glycosyltransferase)	at3g21761	0.714/0.798
	MDP0000307237	HYR1 (UDP glycosyltransferase)	at3g21762	0.763
	MDP0000929213	NCED5 (9-cis-epoxycarotenoid dioxygenase5)	at1g30100	0.722/0.725
	MDP0000774924	NCED4 (9-cis-epoxycarotenoid dioxygenase4)	at4g19170	-0.764
auxin	MDP0000281064	ILR1( IAA-LEUCINE RESISTANT 1)	at3g02875	0.79/0.743
	MDP0000125975	TIR1 (TRANSPORT INHIBITOR RESPONSE 1)	at3g62980	-0.714
	MDP0000175425	AUX1-like protein 2 (auxin influx	q9fel7 lax2_medtr	-0.706

		transporter)		
	MDP0000203334	auxin signaling F-box 3 (AFB3)	at1g12820	-0.753/-0.791/-0.72
	MDP0000469943	auxin signaling F-box 2 (AFB2)	at3g26810	-0.747
	MDP0000666539	GH3 auxin-responsive promoter	at2g14960	0.737
	MDP0000287459	NAD(P)-linked oxidoreductase superfamily protein	at1g60690	0.737
	MDP0000273979	O-fucosyltransferase family protein	at1g76270	0.71
	MDP0000612130	ATB2(NAD(P)-linked oxidoreductase superfamily protein)	at1g60710	0.83
	MDP0000873893	GH3 (Auxin-responsive GH3 family protein)	at2g14960	0.723
	MDP0000586656	auxin-responsive family protein	at4g17280	0.725
	MDP0000157110	outer arm dynein light chain 1 protein	at2g34680	-0.742
BR	MDP0000213283	the cytochrome p450 family	at2g26710	0.73
	MDP0000297861	equalene monooxygenase	o48651 erg1_pangi	-0.705/-0.707
	MDP0000260827	no description available	gnl cdd 36512	-0.726
	MDP0000746652	equalene monooxygenase	o48651 erg1_pangi: 715.0	0.7
	MDP0000161955	equalene monooxygenase	o48651 erg1_pangi: 760.0	0.736
	MDP0000202883	equalene monooxygenase	o48651 erg1_pangi: 734.0	0.738
	MDP0000191389	equalene monooxygenase	o48651 erg1_pangi: 758.0	0.708
CTK	MDP0000133146'	UDP-glucosyl transferase 85A2 (UGT85A2)	at1g22360	0.734/0.707/0.711/0.73
	MDP0000202898	UDP-glucosyl transferase 76E2 (UGT76E2)	at5g59590	0.792
	MDP0000780011	UDP-glucosyl transferase 85A2 (UGT85A2)	at1g22360	0.703
	MDP0000523619	UDP-Glycosyltransferase superfamily protein	at3g55700	0.713
	MDP0000145813	UDP-Glycosyltransferase superfamily protein	at3g55700	0.723
ETH	MDP0000195885	1-aminocyclopropane-1-carboxylate oxidase 1	q00985 acco1_maldo : 586.0	0.745
	MDP0000257135	ethylene receptor	at2g40940 : 827.0	0.709
	MDP0000226115	ethylene-responsive transcription factor 2	q40479 erf2_tobac : 175.0	0.769/0.706/0.707
	MDP0000689946	ethylene response factor	at5g47220	0.805/0.723
	MDP0000129942	multi-protein bridging factor 1	at3g24500	0.711
GA	MDP0000899351	2-oxoglutarate	at1g52800	0.715
	MDP0000185333	gibberellin 2-beta-dioxygenase 1	q9sq80 g2ox1_pea : 474.0	0.794
	MDP0000181482	DELLA protein GAI	q84tq7 gai_goshi : 786.0	-0.705
	MDP0000319522	GA receptor gene	at3g63010 : 530.0	0.78
JA	MDP0000450991	Lipoxygenase 1	p37831 lox1_soltu : 1206.0	0.719
SA	MDP0000455611	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	gnl cdd 86349 : 336.0	0.743/0.787
	MDP0000312765	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	gnl cdd 86349 : 321.0	0.768



	MDP0000305536	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	gnl cdd 86349 : 336.0	0.729/0.769
	MDP0000150382	UDP-glycosyltransferase	at2g43820	0.795

Table S5 Main transcription factors information

Category	Gene ID	Number of anthocyanin species (>0.7)	Correlation coefficient
bHLH	MDP0000261874	1, 2, 3, 6, 8	-0.710
	MDP0000312274	6, 8	0.740
	MDP0000212411	7	-0.730
	MDP0000644807	8, 16	0.710
	MDP0000137325	5	-0.720
MYB	<b>MDP0000127691</b>	4	0.760
	<b>MDP0000284922</b>	1, 4, 3, 5, 6, 8	-0.750
	<b>MDP0000758053</b>	5	0.700
MYB-Related	MDP0000074681	1, 2, 3, 5, 6, 8	0.780
	MDP0000191083	7	-0.740
	MDP0000257129	8	0.720
WRKY	<b>MDP0000792088</b>	8	0.730
	MDP0000794439	8	0.720
	MDP0000767097	2	0.770
	MDP0000759299	3, 7, 8	-0.713
	MDP0000242979	8	0.743
AP2/EREBP	MDP0000316694	8	0.755
	MDP0000189347	2	0.750
	MDP0000390121	8	0.708
ARF	MDP0000139073	7	-0.756
	MDP0000194603	7	-0.752
	MDP0000713113	8	-0.725
C2C2	MDP0000429215	7	-0.739
	MDP0000221444	5	0.721
	MDP0000331808	7	0.700
C2H2	MDP0000141403	7	-0.705
	MDP0000551046	4	-0.706
	MDP0000610922	7	0.754
C3H	MDP0000275117	6	-0.718
	MDP0000314593	8	-0.703
HAP	MDP0000818967	8	-0.748
	MDP0000190029	4	0.705
G2-like	MDP0000182154	8	-0.724
GRAS	MDP0000181482	7	-0.705
	MDP0000736852	6	-0.733
	MDP0000596661	4	-0.771
HB	MDP0000316497	8	0.714
	MDP0000222305	4	0.797
	MDP0000319456	2	0.753
HSF	MDP0000202716	6	0.704
	MDP0000692406	1	-0.725
TCP	MDP0000193947	8	0.773
	MDP0000156139	4	-0.712
	MDP0000881409	6	0.739
AS2	MDP0000136037	2	0.871
	MDP0000793302	7	-0.733
	MDP0000225062	2	-0.741

MDP0000127989	1	-0.704
MDP0000242236	7	-0.705
MDP0000131550	6	0.701
MDP0000143447	7	-0.712
MDP0000242107	7	-0.738
MDP0000792734	2	-0.715
MDP0000197091	8	-0.751
MDP0000220601	7	-0.719
MDP0000202290	7	-0.707
MDP0000473750	8	0.754
MDP0000526829	7	-0.807

Note: Anthocyanin category No. refer to table 2