

Figure S1 Number and average expression of genes in each sample of transcriptome. YS, Huashuo; YR, Huarui.

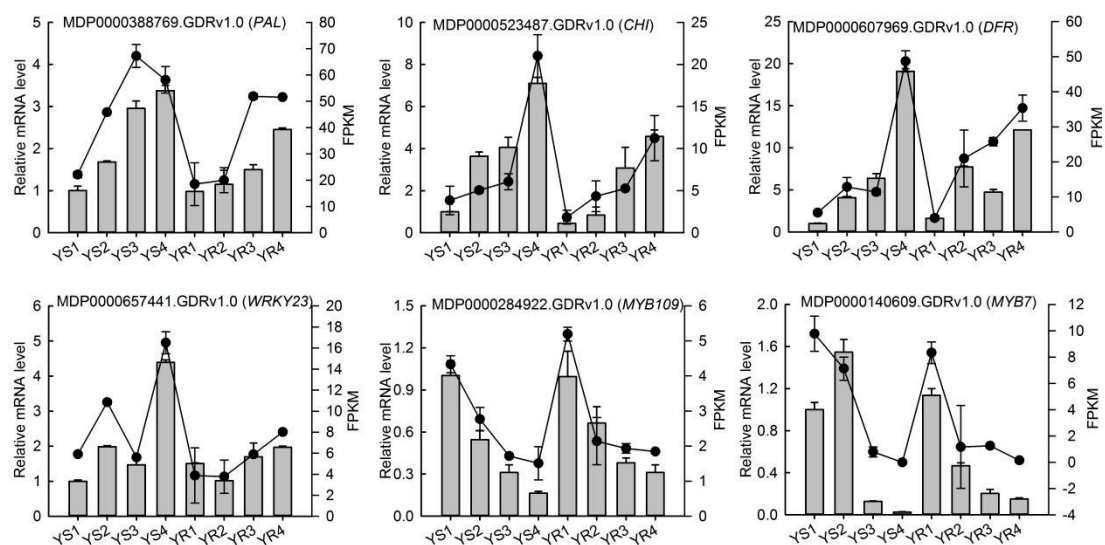


Figure S2 qRT-PCR validation of expression levels of 6 randomly selected genes identified by RNA sequencing. The histogram data represent qRT-PCR data (left y-axis) and the broken line represents RNA-seq data (right y-axis). The qRT-PCR assay had three biological replicates, each with three technical replicates ($n = 9$). The FPKM value of RNA-seq has three biological repetitions ($n = 3$). The error bars indicate the standard deviation. The x-axis represents the different samples. YS, Huashuo; YR, Huarui.

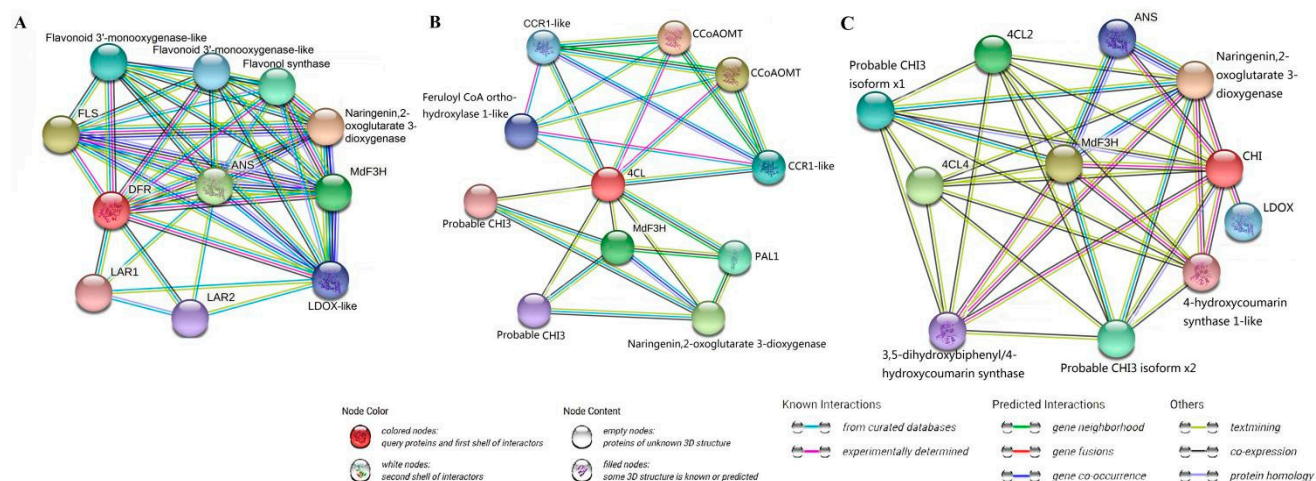


Figure S3 Interaction network analysis for MdDFR, Md4CL and MdCHI. Colored nodes represent different proteins, and the red one was the target protein I typed in. Node content, empty nodes represent proteins of unknown 3D structure, filled nodes represent proteins of 3D structure is known or predicted. Lines of different colors in the middle of nodes represent different relationships of proteins.

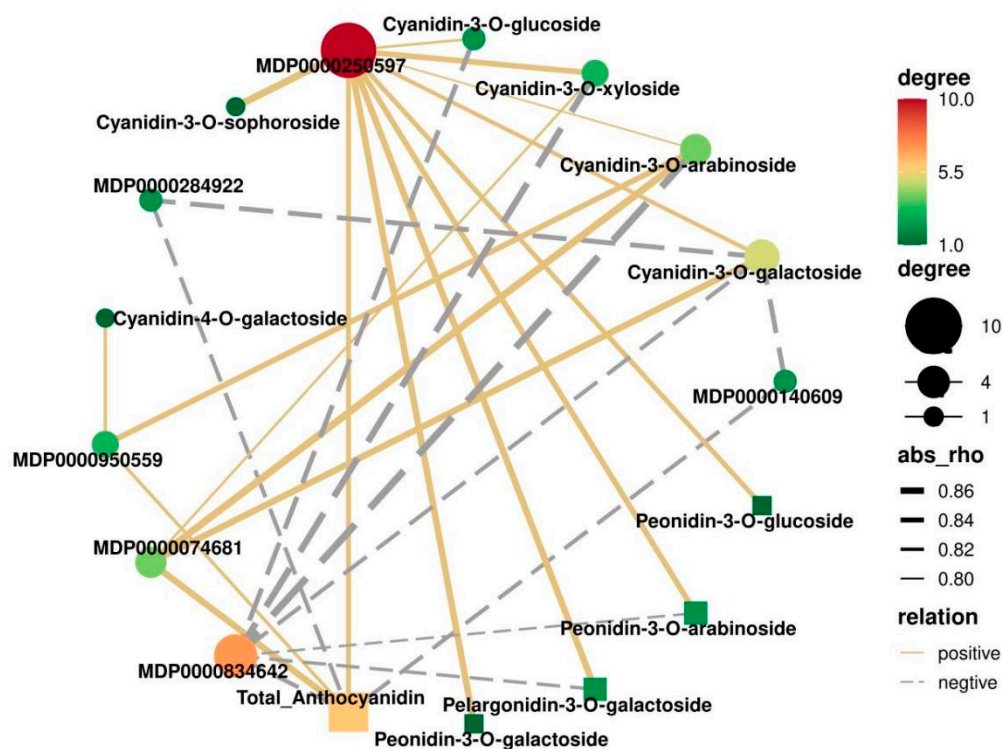


Figure S4 Correlation network of metabolites and genes (six key transcription factor) involved in

phenylpropanoid and flavonoid biosynthesis in YS and YR. Abs_rho represents the Pearson correlation coefficient (r). Degree represents the gene number. Relation represents the correlations with a coefficient (r) value > 0.8 (positive) or < -0.8 (negative). YS, Huashuo; YR, Huarui.

Table S1. Primers used for quantitative real-time PCR (qRT-PCR)

Gene	Forward primer (5'-3')	Reverse primer (5'-3')
Actin	TGACCGAATGAGCAAGGAAATTACT	TACTCAGCTTTGGCAATCCACATC
MDP0000523487 (CHI)	GCTACAAATGCGGTGATAG	CGCCTCCACTACAACCTCC
MDP0000607969 (DFR)	TTGAATCCAAGGACCCCGAG	CTTTTGGTGCTCCTCCACATTC
MDP0000388769 (PAL)	CGAGGAGTGTGACAAGGTGTTCCA	AGGAATGCAGCATGTAAACCGTGAC
MDP0000657441 (WRKY23)	GATGTGGTGAAGAGGGAGGA	ACAGGGAAGTGGGACAACAG
MDP0000284922 (MYB109)	TGATCCAGCAAATGCTTCAG	CCTCAACTCGATCAGAGCAA
MDP0000140609 (MYB7)	CATGACCACCAACAACAAGG	CATTAGTCCCCCTGCATTG

Table S2. Type and content of anthocyanins tested in this project

NO	Name	Class	RT	Equation	L	ULO	Q1	Q3	YS1	YS2	YS3	YS4	YR1	YR2	YR3	YR4	
					L		(Da)	(Da)									
					O												
					Q												
1	Cyanidin-3- <i>O</i> -galactoside	Cyanidin	6.89	y = 2550.97428 x + 743.84466		5	5000	449.1	287.1	2.4168040 3	1705.2421 7	3715.9838 53	5326.6619 67	36.703660 17	1331.7714 53	1934.0600 9	3478.4262 37
2	Cyanidin-3- <i>O</i> -arabinoside	Cyanidin	7.86	y = 1.05803e5 x + 9.08452e4	2	5000	419.1	287.1	0	63	83.983188	73	27	73	37	07	
3	Cyanidin-3- <i>O</i> -xyloside	Cyanidin	9.64	y = 6.97427e4 x + 6.06251e4	5	5000	419.1	287.1	0.0580077 78	35.963800 77	66.554791 37	180.72627 9	0.8644023 31	38.536028 47	56.384301 47	100.19230 95	
4	Cyanidin-3- <i>O</i> -glucoside	Cyanidin	7.43	y = 6.05479e4 x + 7.42416e4	5	5000	449.1	287.1	0	0	13.082111 33	51.438290 4		12.795841 5	9.6909638 53	33.307024 5	
5	Peonidin-3- <i>O</i> -galactoside	Peonidin	8.45	y = 17671.41022 x - 7094.46550	N A	N/A	463.3	301.1	0	27	37	5	33	83	97	83	
6	Pelargonidin-3- <i>O</i> -galactalactoside	Pelargonidin	7.75	y = 17671.41022 x - 7094.46550	N A	N/A	433.2	271.1	0	4	37	9	0	9	77	37	
7	Cyanidin-3- <i>O</i> -sophoroside	Cyanidin	6.87	y = 5.98279e4 x + 18688.60864	1	5000		287.1		0.0806582 72	0.2299011 49	1.0215119 21		0.1415314 2	0.1200133 13	0.3147726 73	
8	Peonidin-3- <i>O</i> -arabinoside	Peonidin	9.37	y = 1.18209e5 x + 8.00277e4	2	5000	433.2	301.1	0	18	0.0080107 07	0.0358364 69		0.0408584 66	0.0410912 85	0.2294221 27	

9	Pelargonidin-3-O-arabinoside	Pelargonidin	y = 17671.41022 x 8.7 - 7094.46550	N / A	N/A	271.0												
						403.1	6	0	0	0	25	0	29	46	44			
10	Peonidin-3-O-glucoside	Peonidin	y = 1.75134e5 8.97 x + 1.33017e5	2 /	5000					0.0191829	0.1477188		0.0059882	0.0065814	0.0232783			
						463.3	301.1	0	0	82	11	0	09	85	65			
11	Cyanidin-3-O-rutinoside	Cyanidin	y = 17671.41022 x 8.08 - 7094.46550	N / A	N/A	595.1												
									0.1233775	0.0902988	0.3686712		0.4953083	0.1251294	0.2213578			
						7	287.1	0	1	09	85	0	8	03	53			
12	Delphinidin-3-O-glucoside	Delphinidin	y = 6.68665e4 x + 6.43 13056.59708	5 /	5000												0.3113868	
						465.1	303.1	0	0	0	0	0	0	0	89			
13	Delphinidin-3-O-arabinoside	Delphinidin	y = 17671.41022 x 6.99 - 7094.46550	N / A	N/A													
								0.0495997	0.0310348	0.0286384		0.0458804		0.0322073				
						435.5	303.1	48	3	58	0	27	0	66	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 NO.	Total Reads Count	Total Bases	Average Read	Q20 Bases	Q30 Bases	GC Bases Ratio
		Count (bp)	Length (bp)	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%

Note: 1-8 sequential represent YS1-4, YR1-4. YS, Huashuo; YR, Huarui.

Table S4. Hormones related to anthocyanin accumulation

Cate gory	ID	Annotation	Accession	Anthocyanin species (>0.8)	Correlation coefficient
ABA	MDP00000 58337	HYR1, a UDP glycosyltransferase	at3g21760	1,2,3,4,5,6,8,9,total	0.82/0.94/0.86/0.93/0.8/0.88/0.85/0 .91/0.69/0.83
	MDP00002 42552	UDP-glucosyl transferase 71C4	at1g07250	1,2,3,4,5,6,7,8,9,10,total	0.86/0.89/0.91/0.93/0.91/0.92/0.92/ 0.93/0.88/0.88/0.87
	MDP00007 15898	HYR1, a UDP glycosyltransferase	at3g21760	1,2,3,4,5,6,8,9,total	0.82/0.94/0.86/0.93/0.82/0.89/0.87/ 0.92/0.72/0.83
	MDP00007 44887	NCED5(9-cis-epoxyc arotenoid dioxygenase5)	at4g19170	1,2,3,4,5,6,7,8,10,total	0.93/0.88/0.93/0.89/0.83/0.86/0.89/ 0.82/0.82/0.93
	MDP00002 31674	Protein phosphatase 2C family protein	at5g57050	2,3,4,5,6,8,9,total	0.9/0.82/0.89/0.81/0.87/0.83/0.92/0 .8
	MDP00001 62721	GRAM domain family protein	at5g13200	1,2,3,4,5,6,7,8,9,10,total	0.86/0.91/0.93/0.94/0.95/0.96/0.95/ 0.97/0.92/0.92/0.87
	MDP00001 69913	GRAM domain family protein	at5g13200	1,2,3,4,5,6,7,8,9,10,total	0.87/0.86/0.88/0.89/0.91/0.91/0.89/ 0.87/0.9/0.86/0.87
	MDP00002 50947	ABA-responsive element binding protein 3	at2g41070	1,2,3,4,6,8,9,total	-0.87/-0.89/-0.87/-0.9/-0.85/-0.8/-0 .83/-0.88
	MDP00004 63117	GRAM domain family protein	at5g13200	1,2,3,4,5,6,7,8,9,10,total	0.9/0.83/0.9/0.85/0.82/0.84/0.88/0. 81/0.83/0.9
	MDP00008 21241	GRAM domain family protein	at5g23370	1,2,3,4,5,6,7,8,total	0.88/0.86/0.89/0.86/0.8/0.84/0.84/0 .82/0.88
auxin	MDP00001 60094	a methyl IAA esterase	at3g10870	1,2,4,total	-0.85/-0.83/-0.81/-0.85
	MDP00002 81064	IAA-leucine resistant (ILR)-like 2	at3g02875	1,2,3,4,5,6,7,8,9,10,total	0.9/0.97/0.95/0.98/0.95/0.98/0.93/0 .97/0.97/0.89/0.91
	MDP00003 19659	IAA-leucine resistant (ILR)-like gene 5	at1g51760	1,2,3,4,5,6,7,8,9,10,total	0.88/0.88/0.92/0.88/0.9/0.91/0.92/0 .91/0.85/0.88/0.88

	MDP00000 26750	ARG1-like 1	at1g68370	1,2,total	0.81/0.81/0.81
	MDP00001 25975	GRR1-like protein 1	at3g62980	1,2,total	-0.83/-0.82/-0.83
	MDP00001 75425	like AUXIN RESISTANT 1	q9fel7 lax2_ medtr	1,2,total	-0.8/-0.8/-0.8
	MDP00002 34528	Auxin efflux carrier family protein	at1g70940	1,2,3,4,total	0.84/0.87/0.82/0.85/0.84
	MDP00003 85305	sorting nexin 2A	at5g58440	1,2,3,4,6,total	0.9/0.87/0.87/0.83/0.8/0.9
	MDP00001 29063	O-fucosyltransferase family protein	at5g65470	1,2,4,total	-0.81/-0.83/-0.83/-0.81
	MDP00001 48780	SAUR-like auxin-responsive protein family	p33083 ax6b _soybn	1,2,3,total	-0.86/-0.82/-0.82/-0.85
	MDP00001 48873	Aluminium induced protein with YGL and LRDR motifs	at4g27450	1,2,3,4,5,6,7,8,9,10,total	0.83/0.92/0.89/0.96/0.94/0.96/0.89/ 0.95/0.98/0.86/0.84
	MDP00002 31245	Auxin-responsive GH3 family protein	q60ey1 gh36 _orysa	1,2,3,4,5,6,8,9,total	0.85/0.95/0.87/0.93/0.8/0.88/0.84/0 .89/0.86
	MDP00002 34699	O-fucosyltransferase family protein	at5g65470	1,2,4,9,total	-0.8/-0.85/-0.86/-0.81/-0.81
	MDP00002 64686	SAUR-like auxin-responsive protein family	at4g12410	1,2,3,4,5,6,7,8,9,total	0.88/0.92/0.88/0.91/0.87/0.92/0.83/ 0.87/0.92/0.89
	MDP00002 82950	O-fucosyltransferase family protein	at3g30300	1,2,3,total	-0.86/-0.85/-0.82/-0.86
	MDP00003 07308	O-fucosyltransferase family protein	at1g22460	1,2,3,total	-0.86/-0.86/-0.8/-0.86
	MDP00006 12130	ATB2	at1g60710	1,2,3,4,5,6,7,8,9,total	0.92/0.94/0.92/0.93/0.82/0.89/0.83/ 0.85/0.84/0.92
	MDP00008 11081	Auxin-responsive GH3 family protein	at4g03400	1,2,3,4,6,9,total	-0.84/-0.9/-0.83/-0.89/-0.82/-0.84/- 0.85
	MDP00008 13577	Aluminium induced protein with YGL and LRDR motifs	gnl cdd 4848 3	2,3,4,5,6,8,9,total	0.92/0.84/0.92/0.81/0.88/0.87/0.9/0 .8
	MDP00008 76321	an auxin response factor	at1g19220	1,2,total	-0.86/-0.83/-0.85
BR	MDP00004 98540	Cytochrome P450 superfamily protein	at3g50660	1,2,3,6,9,total	-0.84/-0.81/-0.8/-0.83/-0.81/-0.84
	MDP00003 07964	brassinosteroid-6-oxid ase 1	q69f95 c85a _phavu	1,2,3,4,total	-0.89/-0.85/-0.83/-0.82/-0.89
	MDP00003 07964	brassinosteroid-6-oxid ase 1	q69f95 c85a _phavu	1,2,3,4,total	-0.89/-0.85/-0.83/-0.82/-0.89
	MDP00004 65581	Fatty acid hydroxylase superfamily protein	q9zt29 sc5d _tobac	1,2,3,4,5,6,7,8,9,total	-0.84/-0.87/-0.85/-0.89/-0.81/-0.85/ -0.81/-0.81/-0.83/-0.84
	MDP00001 91389	Squalene monooxygenase	o48651 erg1 _pangi	1,2,total	0.82/0.83/0.82
	MDP00002 78941	cyclopropyl isomerase (CPI1)	at5g50375	1,2,3,4,6,total	-0.88/-0.87/-0.85/-0.85/-0.8/-0.88
	MDP00002 97861	Squalene monooxygenase	o48651 erg1 _pangi	1,2,3,4,6,9,total	-0.91/-0.92/-0.87/-0.89/-0.85/-0.83/ -0.91
	MDP00004 13935	Squalene monooxygenase	o48651 erg1 _pangi	1,2,3,4,5,6,7,8,9,total	-0.9/-0.87/-0.89/-0.88/-0.84/-0.87/- 0.85/-0.84/-0.81/-0.9
	MDP00008 57446	Squalene monooxygenase	o48651 erg1 _pangi	1,2,3,4,5,6,7,8,9,10,total	0.84/0.9/0.89/0.92/0.93/0.95/0.89/0 .95/0.95/0.86/0.85

	MDP00001 57003	BRI1 like	at4g39400	1,total	-0.81/-0.8
	MDP00002 95859	GSK3-like protein kinase	at2g30980	1,2,3,4,6,7,8,total	-0.8/-0.85/-0.85/-0.83/-0.82/-0.81/- 0.81/-0.81
	MDP00001 30173	BES1/BZR1 homolog 4 (BEH4)	at1g78700	1,2,3,4,total	0.86/0.85/0.8/0.81/0.86
CTK	MDP00001 66723	cytokinin oxidase 4	gnl cdd 7268 1	1,2,3,4,5,6,7,8,9,10,total	0.9/0.96/0.95/0.97/0.93/0.97/0.92/0 .95/0.93 /0.86/0.91
	MDP00002 99496	UDP-glucosyl transferase 85A2 (UGT85A2)	at1g22360	1,2,3,4,6,9,total	-0.8/-0.89/-0.81/-0.84/-0.82/-0.86/- 0.81
	MDP00003 12902	cytokinin oxidase 2	at4g29740	1,2,3,4,5,6,7,8,9,10,total	0.83/0.92/0.91/0.95/0.94/0.96/0.92/ 0.98/0.95/0.89 /0.84
	MDP00008 13186	UDP-glucosyl transferase 85A7 (UGT85A7)	at1g22340	1,2,3,4,5,6,7,8,9,10,total	0.82/0.88/0.91/0.92/0.98/0.96/0.97/ 0.98/0.94/0.97/0.83
ETH	MDP00001 48169	ETO1-like 2	at3g51770	1,2,3,4,6,7,total	-0.9/-0.9/-0.9/-0.84 /-0.84 /-0.8/-0.91
	MDP00001 88827	similar to 2-oxoglutarate-depend ent dioxygenase	at1g06650	1,2,4,9,total	0.82/0.88/0.83/0.81 /0.82
	MDP00002 05515	2-oxoglutarate-depend ent dioxygenase	at1g06650	1,2,4,9,total	0.8/0.88/0.83/0.82/0.8
	MDP00002 65117	Pyridoxal-5'-phosphate -dependent enzyme family protein	at1g48420	1,2,3,4,6,9,total	0.92/0.92/0.88/0.9/0.87/0.86/0.92
	MDP00002 81562	similar to 2-oxoglutarate-depend ent dioxygenase	at1g06650	1,2,4,total	0.8/0.85/0.8/0.8
	MDP00006 44549	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	at1g49390	1,2,3,4,6,total	-0.9/-0.9/-0.85/-0.86/-0.8/0.9
	MDP00005 35274	ACC synthase 10	at5g51690	1,2,3,4,6,9,total	0.8/0.9/0.8/0.89/0.81/0.84/0.81
	MDP00001 27054	Integrase-type DNA-binding superfamily protein	at5g25190	2,3,4,5,6,7,8,9,total	0.91/0.85/0.91/0.84/0.9/0.8/0.88/0. 920.8
	MDP00001 61249	Integrase-type DNA-binding superfamily protein	at5g07580	1,2,3,total	-0.89/-0.84/-0.85/-0.89
	MDP00001 78263	Integrase-type DNA-binding superfamily protein	at5g11190	1,2,3,4,total	-0.81/-0.85/-0.8/-0.87/-0.82
	MDP00002 26115	ethylene responsive element binding factor 2	q40479 erf2 _tobac	1,2,3,4,5,6,7,8,9,total	0.85/0.96/0.9/0.96/0.89/0.94/0.85/0 .93/0.96/0.86
	MDP00002 57135	Signal transduction histidine kinase	at2g40940	1,2,3,4,6,9,,total	0.88/0.93/0.86/0.9/0.87/0.89/0.89
	MDP00002 87350	Integrase-type DNA-binding superfamily protein	at5g25390	1,2,3,4,5,6,8,9,total	-0.87/-0.93/-0.88/-0.92/-0.8/-0.88/- 0.83/-0.87/-0.87
	MDP00003 13063	Plant protein of unknown function	gnl cdd 6679 2	1,2,3,4,5,6,7,8,9,10,total	0.8/0.86/0.89/0.9/0.97/0.95/0.95/0. 98/0.93/0.95/0.81
	MDP00006 29527	ethylene responsive element binding factor 3	gnl cdd 4769 5	1,2,3,4,6,9,total	0.86/0.91/0.84/0.9/0.84/0.85/0.87

	MDP00006 89946	ethylene responsive element binding factor 1	at5g47220	1,2,3,4,5,6,7,8,9,total	0.87/0.95/0.91/0.95/0.87/0.93/0.85/ 0.91/0.93/0.87
	MDP00007 69656	Plant protein of unknown function	gnl cdd 6679 2	1,2,3,4,5,6,7,8,9,10,total	0.81/0.84/0.9/0.88/0.97/0.94/0.97/0 .97/0.9/0.98/0.82
	MDP00008 39828	ethylene response factor 7	gnl cdd 4769 5	1,2,3,4,5,6,7,8,9,10,total	0.98/0.92/0.95/0.89/0.86/0.91/0.89 0.85/0.84/0.82/0.97
	MDP00008 42644	Integrase-type DNA-binding superfamily protein	at5g07580	1,total	-0.83/-0.82
GA	MDP00007 16315	GA3 oxidase	at1g15550	1,2,3,4,6,9,total	0.81/0.9/0.84/0.89/0.82/0.8/0.82
	MDP00001 37705	GA2 oxidase	q9sq80 g2ox 1_pea	1,2,3,4,5,6,7,8,9,10,total	0.93/0.91/0.96/0.93/0.95/0.95/0.97 0.94/0.89/0.94/0.93
	MDP00001 85333	GA2 oxidase	q9sq80 g2ox 1_pea	1,2,3,4,5,6,7,8,9,10,total	0.9/0.86/0.93/0.9/0.93/0.92/0.96/0. 91/0.84/0.94/0.9
	MDP00001 29445	ARM repeat superfamily protein	at5g37490	1,2,3,4,5,6,7,8,9,10,total	0.92/0.93/0.97/0.95/0.94/0.96/0.96/ 0.95/0.9/0.92/0.93
	MDP00002 42829	RGA-like 2	gnl cdd 6715 0	1,2,3,4,6,9,total	-0.9/-0.9/-0.86/-0.88/-0.83/-0.81/-0 .9
	MDP00003 19522	alpha/beta-Hydrolases superfamily protein	at3g63010	1,2,3,4,5,6,7,8,9,10,total	0.81/0.88/0.86/0.92/0.88/0.9/0.85/0 .91/0.89 /0.81/0.82
	MDP00006 69451	GRAS family transcription factor family protein	q84tq7 gai_ goshi	1,2,4,9,total	-0.83/-0.84/-0.8/-0.8/-0.83
	MDP00009 50387	DELLA protein GAI	q84tq7 gai_ goshi	1,2,4,9,total	-0.82/-0.84/-0.82/-0.81/-0.82
	MDP00006 69451	DELLA protein GAI	q84tq7 gai_ goshi	1,2,4,9,total	-0.83/-0.84/-0.8/-0.8/-0.83
JA	MDP00001 25303	lipoxygenase 1	gnl cdd 8468 0	1,2,3,4,5,6,7,8,9,10,total	0.83/0.93/0.91/0.95/0.94/0.96/0.92/ 0.97/0.95/0.88/0.84
	MDP00002 04470	LOX5	at3g22400	1,2,3,4,5,6,7,8,9,10,total	-0.89/-0.94/-0.92/-0.97/-0.91/-0.95/ -0.9/-0.92/-0.94/-0.85/-0.89
	MDP00002 15405	PLAT/LH2 domain-containing lipoxygenase family protein	at1g67560	1,2,3,4,5,6,7,8,9,10,total	-0.88/-0.87/-0.9/-0.89/-0.89/-0.9/-0 .89/-0.88/-0.86/-0.85/-0.88
	MDP00002 64666	Lipoxygenase 1	p37831 lox1 _soltu	1,2,3,4,5,6,7,8,9,10,total	0.82/0.87/0.9/0.89/0.96/0.95/0.94/0 .97/0.93/0.93/0.82
	MDP00004 23544	Lipoxygenase 1	p37831 lox1 _soltu	1,2,3,4,5,6,7,8,9,10,total	0.82/0.89/0.88/0.9/0.93/0.94/0.89/0 .95/0.94/0.86/0.82
	MDP00004 50991	Lipoxygenase 1	p37831 lox1 _soltu	1,2,3,4,6,8,9,total	0.85/0.95/0.86/0.92/0.88/0.83/0.9/0 .85
	MDP00005 20035	Lipoxygenase 1	p37831 lox1 _soltu	1,2,3,4,5,6,7,8,9,10,total	0.83/0.89/0.92/0.93/0.98/0.96/0.97/ 0.99/0.94/0.96/0.84
	MDP00005 48790	lipoxygenase	at1g55020	1,2,3,4,6,9,total	0.83/0.91/0.81/0.86/0.8/0.82/0.84
	MDP00009 23670	Lipoxygenase 1	p37831 lox1 _soltu	1,2,3,4,5,6,7,8,9,10,total	0.81/0.89/0.86/0.91/0.89/0.92/0.85/ 0.91/0.92/0.81/0.82
	MDP00002 73180	12-oxophytodienoate reductase 2	at2g06050	1,2,3,4,5,6,7,8,9,10,total	0.8/0.85/0.86/0.85/0.82/0.85/0.85/0 .84/0.81/0.81/0.81
	MDP00006 45422	12-oxophytodienoate reductase 2	at1g76680	1,7,total	0.81/0.8/0.81
SA	MDP00002 50047	UGT74E2	at1g05680	1,2,3,4,5,6,7,8,9,10,total	0.81/0.93/0.89/0.95/0.91/0.94/0.87/ 0.95/0.95/0.83/0.83
	MDP00003 05536	no description available	gnl cdd 8634 9	1,2,3,4,5,6,7,8,9,10,total	0.9/0.95/0.94/0.96/0.91/0.94/0.9/0. 93/0.91/0.85/0.91

	MDP00003 12765	no available	gnl cdd 8634 9	1,2,3,4,5,6,7,8,9,10,total	0.87/0.94/0.91/0.95/0.94/0.96/0.89/ 0.94/0.98/0.84/0.88
	MDP00002 50047	UGT74E2	at1g05680	1,2,3,4,5,6,7,8,9,10,total	0.81/0.93/0.89/0.95/0.91/0.94/0.87/ 0.95/0.95/0.83/0.83

Note: Anthocyanin category No. refer to table 2

Table S5. Main transcription factor information

Category	Gene ID	Anthocyanin species (>0.8)	Correlation coefficient
AP2/EREBP	MDP0000155743	2,3,4,5,6,7,8,9,10,total	0.84/0.9/0.89/0.98/0.94/0.98/0.97/0.91/0.99/0.8
	MDP0000178263	1,2,3,4,total	-0.81/-0.85/-0.8/-0.87/0.82
	MDP0000218344	1,2,3,4,5,6,7,8,9,total	0.87/0.96/0.9/0.93/0.82/0.9/0.81/0.87/0.89/0.88
	MDP0000242979	1,2,3,4,5,6,7,8,9,10,total	0.85/0.91/0.92/0.95/0.96/0.96/0.94/0.97/0.95/0.92/0.86
	MDP0000287350	1,2,3,4,5,6,7,8,9,total	-0.87/-0.93/-0.88/-0.92/-0.8/-0.88/-0.79/-0.83/-0.87/-0.87
	MDP0000316694	1,2,3,4,5,6,7,8,9,10,total	0.9/0.95/0.95/0.96/0.91/0.95/0.91/0.94/0.91/0.86/0.91
	MDP0000759299	1,2,3,4, 6, 8,9,total	-0.84/-0.92/-0.85/-0.89/-0.86/-0.81/-0.88/-0.85
	MDP0000854039	1,total	-0.82/-0.82
ARF	MDP0000173151	1,2,3,4,5,6,7,8,9,10,total	-0.95/-0.9/-0.95/-0.87/-0.85/-0.89/-0.89/-0.85/-0.81/-0.82/-0.95
	MDP0000179650	1,2,4,6,9,total	-0.82/-0.87/-0.84/-0.8/-0.83/-0.83
	MDP0000211459	1,2,3,4,6,8,9,total	0.83/0.94/0.85/0.93/0.88/0.84/0.9/0.84
	MDP0000310875	1,2,3,6,9,total	-0.84/-0.86/-0.81/-0.81/-0.82/-0.84
	MDP0000412781	1,2,3,4,6,9,total	-0.81/-0.85/-0.8/-0.8/-0.84/-0.86/-0.82
	MDP0000876321	1,2,total	-0.86/-0.83/-0.85
ARR	MDP0000224740	1,2,total	-0.82/-0.8/-0.82
	MDP0000290818	1,2,total	-0.81/-0.83/-0.81
	MDP0000585643	1,2,3,4,6,9,total	-0.8/-0.89/-0.8/-0.86/-0.84/-0.88/-0.81
bHLH	MDP0000154272	1,2,total	-0.82/-0.84/-0.82
	MDP0000214472	1,2,3,4,6,7,8,total	0.8/0.81/0.83/0.86/0.81/0.82/0.81/0.8
	MDP0000231650	1,2,3,4,6,9,total	-0.88/-0.88/-0.84/-0.82/-0.83/-0.83/-0.88
	MDP0000261874	1,2,3,total	-0.9/-0.84/-0.81/-0.89
	MDP0000312274	1,2,3,4,5,6,7,8,9,total	0.85/0.95/0.89/0.95/0.88/0.93/0.83/0.9/0.97/0.86
	MDP0000320691	1,total	-0.84/-0.83
	MDP0000439540	1,2,3,4,6,9,total	-0.86/-0.9/-0.86/-0.86/-0.84/-0.82/-0.87
	MDP0000779358	1,3,total	-0.86/-0.81/-0.86
	MDP0000799392	1,2,3,4,total	-0.83/-0.84/-0.8/-0.83/-0.83
	MDP0000829998	1,2,3,4,6,total	-0.81/-0.86/-0.83/-0.87/-0.8/-0.82
C2C2	MDP0000151848	1,total	-0.86/-0.86
	MDP0000194889	1,total	-0.8/-0.8
	MDP0000321180	1,2,9,total	-0.83/-0.82/-0.8/-0.83
	MDP0000551876	1,2,3,4,6,7,total	0.91/0.88/0.88/0.87/0.83/0.8/0.91

	MDP0000565292	1,2,3,4,6,9,total	-0.9/-0.9/-0.87/-0.88/-0.86/-0.84/-0.91
	MDP0000697407	1,3,5,6,7,9,total	0.81/0.8/0.82/0.82/0.8/0.81/0.81
	MDP0000713113	1,2,3,4,6,9,total	-0.89/-0.92/-0.86/-0.85/-0.85/-0.84/-0.89
	MDP0000901915	1,2,4,9,total	-0.8/-0.84/-0.8/-0.82/-0.8
	MDP0000201120	1,2,3,6,7,total	-0.87/-0.81/-0.87/-0.81/-0.84/-0.87
	MDP0000547254	1,total	-0.84/-0.84
C2H2	MDP0000122321	1,2,total	-0.85/-0.82/-0.85
	MDP0000128287	1,2,3,4,total	0.84/0.85/0.83/0.82/0.84
	MDP0000137826	1,2,3,4,5,6,7,8,9,10,total	0.8/0.85/0.9/0.9/0.99/0.95/0.97/0.98/0.93/0.98/0.81
	MDP0000190415	1,3,4,7,total	0.83/0.85/0.82/0.82/0.84
	MDP0000198015	1,3,4,7,total	0.83/0.82/0.8/0.81/0.83
	MDP0000200608	1,2,3,4,6,7,total	0.88/0.82/0.87/0.81/0.81/0.83/0.88
	MDP0000319225	1,3,total	0.83/0.8/0.82
	MDP0000453148	2,3,4,5,6,7,8,9,total	0.88/0.85/0.91/0.85/0.88/0.82/0.89/0.87/0.8
	MDP0000535412	1,2,3,4,6,9,total	-0.87/-0.91/-0.84/-0.87/-0.84/-0.85/-0.87
	MDP0000551046	1,2,total	-0.85/-0.8/-0.85
	MDP0000573176	1,2,3,4,5,6,7,8,total	0.87/0.87/0.89/0.88/0.8/0.84/0.84/0.82/0.88
	MDP0000610922	1,2,3,4,5,6,7,8,9,total	0.87/0.94/0.89/0.92/0.84/0.91/0.82/0.88/0.91/0.88
	MDP0000762756	1,2,3,4,5,6,7,8,9,10,total	0.9/0.91/0.91/0.93/0.89/0.92/0.88/0.89/0.89/0.82/0.91
	MDP0000807856	1,total	-0.82/-0.81
	MDP0000853499	1,2,3,4,5,6,7,8,9,10,total	0.84/0.91/0.9/0.92/0.93/0.94/0.9/0.93/0.95/0.86/0.85
C3H	MDP0000171955	1,2,3,total	-0.87/-0.8/-0.81/-0.87
	MDP0000673185	1,2,3,4,5,6,7,8,9,10,total	-0.8/-0.84/-0.85/-0.82/-0.86/-0.87/-0.86/-0.87/-0.84/-0.83/-0.8
E2F/DP	MDP0000232265	1,2,3,4,total	-0.85/-0.84/-0.8/-0.81/-0.85
	MDP0000316055	1,2,3,4,6,9,total	0.91/0.9/0.87/0.85/0.86/0.84/0.91
G2-like	MDP0000124687	1,2,total	-0.85/-0.83/-0.85
	MDP0000182154	1,2,3,total	-0.89/-0.8/-0.81/-0.88
	MDP0000202657	1,total	0.86/0.86
	MDP0000248927	1,2,3,4,6,9,total	0.8/0.88/0.8/0.85/0.8/0.81/0.8
	MDP0000320628	1,total	-0.8/-0.8
	MDP0000526864	1,2,3,total	-0.89/-0.83/-0.82/-0.89
GRAS	MDP0000669451	1,2,4,total	-0.83/-0.84/-0.8/-0.83
	MDP0000796348	1,2,total	-0.85/-0.87/-0.85
	MDP0000827722	1,2,3,total	-0.84/-0.81/-0.8/-0.83
	MDP0000950387	1,2,4,total	-0.82/-0.84/-0.82/-0.82
HB	MDP0000124827	1,2,3,4,5,6,7,8,9,10,total	-0.9/-0.89/-0.92/-0.91/-0.91/-0.93/-0.91/-0.91/-0.89/-0.87/-0.9
	MDP0000222305	2,4,total	0.87/0.83/0.8

	MDP0000272542	1,2,total	-0.85/-0.83/-0.85
	MDP0000316497	1,2,3,4,5,6,7,8,9,10,total	0.88/0.92/0.93/0.93/0.96/0.96/0.93/0.95/0.96/0.91/0.88
	MDP0000405958	2,3,4,6,8,9,total	0.88/0.8/0.85/0.86/0.81/0.9/0.8
	MDP0000423596	1,2,3,total	-0.9/-0.87/-0.83/-0.9
	MDP0000596661	1,2,total	-0.85/-0.82/-0.85
	MDP0000840574	1,2,total	-0.81/-0.81/-0.81
	MDP0000899816	1,2,3,4,5,6,7,8,9,total	0.86/0.96/0.89/0.95/0.85/0.92/0.81/0.88/0.95/0.87
HSF	MDP0000155579	1,2,3,4,6,7,total	0.85/0.8/0.85/0.82/0.8/0.83/0.85
	MDP0000202716	1,2,3,4,5,6,7,8,9,10,total	0.87/0.94/0.94/0.96/0.97/0.98/0.96/0.99/0.96/0.93/0.88
	MDP0000319456	1,2,3,4,6,9,total	0.8/0.87/0.81/0.86/0.85/0.88/0.81
	MDP0000319910	1,2,3,4,5,6,7,8,9,total	0.91/0.93/0.91/0.9/0.87/0.92/0.85/0.86/0.92/0.91
MYB	MDP0000140609	1,total	-0.84/-0.83
	MDP0000164048	1,2,3,4,total	-0.89/-0.87/-0.88/-0.82/-0.89
	MDP0000194307	1,2,3,4,6,8,9,total	-0.91/-0.93/-0.88/-0.91/-0.88/-0.8/-0.87/-0.91
	MDP0000209974	1,2,3,4,6,8,total	0.82/0.87/0.86/0.84/0.83/0.82/0.83
	MDP0000250597	1,2,3,4,5,6,7,8,10,total	0.83/0.8/0.85/0.81/0.86/0.86/0.87/0.85/0.84/0.84
	MDP0000282792	1,2,3,4,6,9,total	-0.86/-0.87/-0.8/-0.82/-0.81/-0.84/-0.86
	MDP0000284922	1,total	-0.84/-0.83
	MDP0000478512	1,total	-0.83/-0.82
	MDP0000543585	1,total	-0.84/-0.83
	MDP0000659260	1,2,3,4,6,8,9,total	0.87/0.94/0.86/0.9/0.85/0.8/0.84/0.87
	MDP0000742771	1,2,3,4,6,9,total	-0.85/-0.9/-0.83/-0.88/-0.83/-0.85/-0.86
	MDP0000934638	1,2,3,4,5,6,7,8,9,10,total	0.93/0.91/0.93/0.92/0.87/0.91/0.89/0.85/0.87/0.83/0.93
	MDP0000950559	1,2,total	0.82/0.85/0.82
MYB-related	MDP0000074681	1,2,3,total	0.86/0.87/0.81/0.86
	MDP0000208448	1,2,3,4,6,total	0.81/0.83/0.81/0.8/0.8/0.82
	MDP0000209471	1,3,total	-0.89/-0.81-0.89
	MDP0000241185	1,2,3,4,6,8,9,total	-0.88/-0.93/-0.87/-0.87/-0.86/-0.8/-0.86/-0.88
	MDP0000255970	1,2,3,4,5,6,7,8,9,total	0.88/0.96/0.89/0.93/0.82/0.9/0.8/0.86/0.89/0.89
	MDP0000273563	1,2,3,4,total	-0.81/-0.85/-0.82/-0.84/-0.81
NAC	MDP0000158717	1,2,3,4,total	-0.88/-0.85/-0.81/-0.81/-0.87
	MDP0000228792	1,2,3,total	-0.84/-0.82/-0.81/-0.84
	MDP0000309382	1,2,3,4,5,6,7,8,9,10,total	0.93/0.97/0.95/0.96/0.92/0.97/0.89/0.93/0.95/0.82/0.94
	MDP0000404409	1,2,3,4,6,9,total	0.87/0.94/0.87/0.9/0.84/0.84/0.87
TCP	MDP0000523096	1,2,total	-0.83/-0.8/-0.82
	MDP0000763497	1,2,3,4,6,9,total	-0.86/-0.85/-0.84/-0.82/-0.85/-0.83/-0.86
	MDP0000920127	1,total	-0.83/-0.82

Triple-Helix	MDP0000156139	1,2,3,4,6,9,total	-0.83/-0.86/-0.8/-0.83/-0.81/-0.83/-0.83
	MDP0000158598	1,2,total	-0.84/-0.84/-0.84
	MDP0000209313	1,2,3,4,5,6,7,8,9,total	-0.93/-0.93/-0.93/-0.91/-0.85/-0.9/-0.86/-0.85/-0.87/-0.93
	MDP0000271048	1,2,3,4,6,total	-0.95/-0.88/-0.89/-0.82/-0.83/-0.95
WRKY	MDP0000119590	1,2,3,4,5,6,7,8,9,10,total	0.84/0.87/0.91/0.88/0.91/0.91/0.93/0.94/0.86/0.9/0.84
	MDP0000129882	1,2,3,4,6,total	0.87/0.82/0.84/0.83/0.82/0.86
	MDP0000144730	1,2,3,4,6,8,9,total	0.83/0.91/0.86/0.91/0.86/0.84
	MDP0000146390	1,2,3,4,5,6,7,8,9,10,total	0.9/0.91/0.92/0.88/0.89/0.93/0.88/0.89/0.9/0.82/0.91
	MDP0000177906	1,2,3,4,5,6,7,8,9,total	0.92/0.97/0.93/0.96/0.89/0.95/0.86/0.91/0.94/0.93
	MDP0000231668	1,2,3,4,5,6,7,8,9,10,total	0.85/0.95/0.92/0.97/0.93/0.96/0.9/0.96/0.95/0.86/0.86
	MDP0000257129	1,2,3,4,5,6,7,8,9,10,total	0.83/0.9/0.92/0.92/0.96/0.96/0.94/0.98/0.94/0.93/0.84
	MDP0000301666	1,2,3,4,5,6,7,8,9,10,total	0.91/0.9/0.96/0.92/0.98/0.97/0.99/0.96/0.92/0.97/0.91
	MDP0000304113	1,2,3,4,6,8,9,total	0.8/0.89/0.85/0.88/0.83/0.83/0.8/0.81
	MDP0000505247	1,2,3,4,5,6,7,8,9,10,total	0.8/0.91/0.87/0.92/0.88/0.92/0.84/0.93/0.92/0.8/0.81
	MDP0000507805	1,3,4,6,7,total	0.8/0.81/0.83/0.8/0.8/0.8
	MDP0000514115	1,2,3,4,5,6,7,8,9,total	0.81/0.86/0.85/0.89/0.81/0.84/0.81/0.83/0.83/0.82
	MDP0000767097	1,total	0.8/0.8
	MDP0000794439	1,2,3,4,5,6,8,9,total	0.87/0.92/0.86/0.9/0.82/0.89/0.84/0.9/0.88
	MDP0000935652	1,2,3,4,5,6,7,8,9,10,total	0.9/0.96/0.95/0.97/0.94/0.97/0.93/0.96/0.95/0.89/0.91
	MDP0000935996	1,2,3,4,5,6,7,8,9,10,total	0.95/0.97/0.95/0.96/0.89/0.95/0.87/0.89/0.93/0.8/0.95
bZIP	MDP0000250947	1,2,3,4,6,8,9,total	-0.87/-0.89/-0.87/-0.9/-0.85/-0.8/-0.83/-0.88
	MDP0000279891	1,2,3,4,6,9,total	-0.82/-0.86/-0.81/-0.84/-0.82/-0.83/-0.82
	MDP0000280559	1,2,3,4,total	0.9/0.86/0.83/0.81/0.9
	MDP0000310001	1,2,3,4,5,6,7,8,10,total	0.86/0.86/0.89/0.87/0.81/0.84/0.86/0.84/0.8/0.86
	MDP0000680042	1,2,4,total	-0.84/-0.81/-0.8/-0.84
	MDP0000738631	1,2,total	-0.83/-0.82/-0.83
	MDP0000834642	1,2,3,4,6,8,total	-0.83/-0.87/-0.86/-0.84/-0.82/-0.81/-0.83
Aux/IAA	MDP0000174664	1,total	-0.85/-0.84
	MDP0000176753	1,2,3,4,6,8,9,total	-0.86/-0.91/-0.88/-0.87/-0.85/-0.82/-0.81/-0.87
	MDP0000223496	1,2,3,4,5,6,7,8,9,10,total	0.81/0.82/0.89/0.86/0.96/0.92/0.96/0.94/0.89/0.97/0.81
	MDP0000296324	1,total	-0.8/-0.8
	MDP0000580010	1,2,total	-0.83/-0.81/-0.83
B3	MDP0000125949	1,2,3,total	-0.86/-0.84/-0.8/-0.86
	MDP0000192438	1,total	-0.84/-0.83
Global	MDP0000225062	1,2,total	-0.87/-0.82/-0.87
	MDP0000913105	1,2,3,total	-0.89/-0.85/-0.82/-0.89
Histone	MDP0000127989	1,2,3,total	-0.9/-0.85/-0.83/-0.89

	MDP0000322510	1,2,3,4,total	0.82/0.83/0.83/0.85/0.82
JUMONJI	MDP0000162827	1,3,total	-0.86/-0.82/-0.85
	MDP0000201290	1,2,4,total	-0.81/-0.83/-0.81/-0.82
	MDP0000298212	1,2,3,4,6,9,total	-0.85/-0.89/-0.83/-0.85/-0.86/-0.87/-0.85
PHOR1	MDP0000129445	1,2,3,4,5,6,7,8,9,10,total	0.92/0.93/0.97/0.95/0.94/0.96/0.96/0.95/0.9/0.92/0.93
	MDP0000199588	1,2,3,4,5,6,7,8,9,10,total	0.81/0.85/0.9/0.89/0.98/0.94/0.97/0.97/0.92/0.98/0.81
	MDP0000391355	1,2,3,4,5,6,7,8,10,total	0.9/0.83/0.9/0.85/0.85/0.86 0.88/0.83/0.82/0.9
	MDP0000928620	1,2,3,4,5,6,7,8,9,10,total	0.95/0.96/0.97/0.96/0.9/0.95/0.92/0.92/0.89/0.85/0.95
Psudo ARR	MDP0000150823	1,total	-0.81/-0.81
	MDP0000917419	1,2,3,4,6,7,total	0.9/0.82/0.88/0.81/0.8/0.83/0.9
SET-domain	MDP0000170814	1,total	-0.85/-0.85
	MDP0000248927	1,2,3,4,6,9,total	0.8/0.88/0.8/0.85/0.8/0.81/0.8
SNF7	MDP0000292973	1,2,3,6,9,total	0.8/0.81/0.8/0.83/0.84/0.81
	MDP0000304929	1,2,3,4,5,6,7,8,total	0.82/0.82/0.84/0.81/0.8/0.83/0.81/0.81/0.82
	MDP0000716576	1,2,3,4,5,6,7,8,9,10,total	0.81/0.87/0.85/0.88/0.9/0.92/0.85/0.9/0.94/0.82/0.82
OFP	MDP0000119191	1,2,total	-0.81/-0.84/-0.82
	MDP0000156202	1,2,total	-0.85/-0.84/-0.85

Note: Anthocyanin category No. refer to table 2