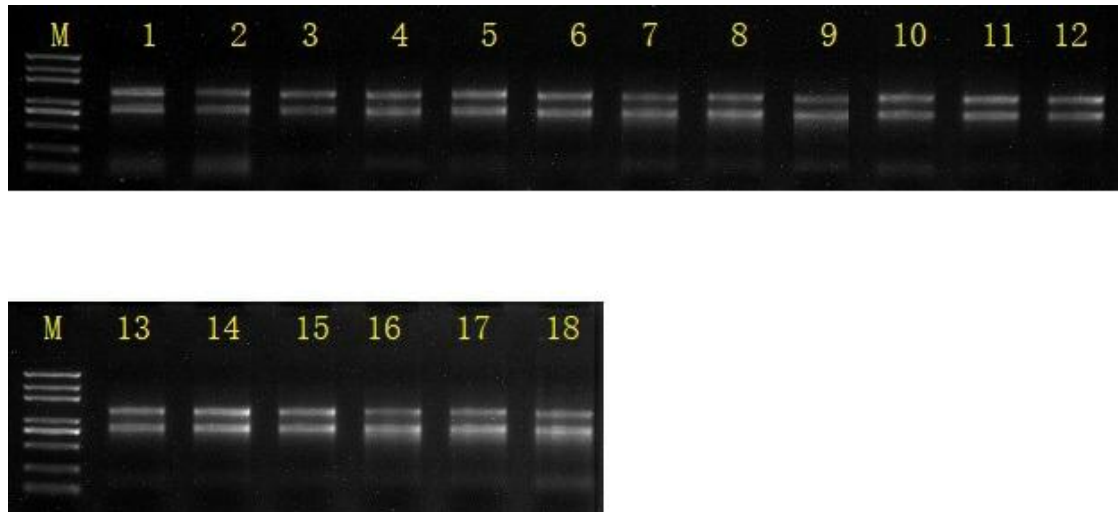
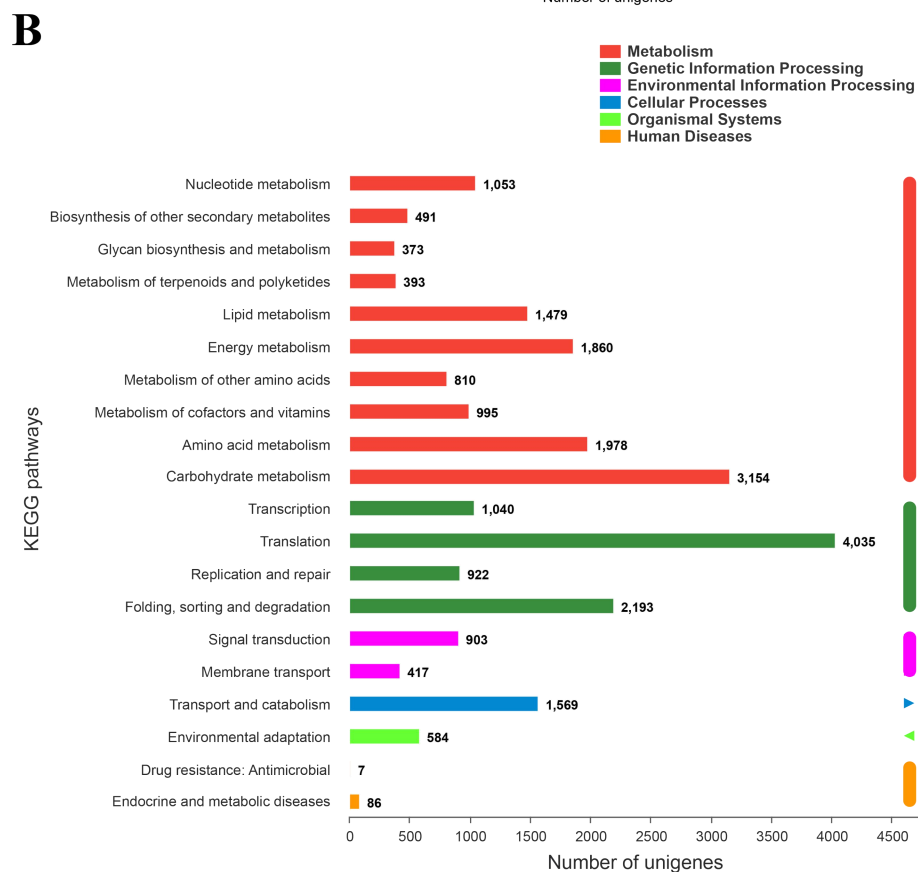
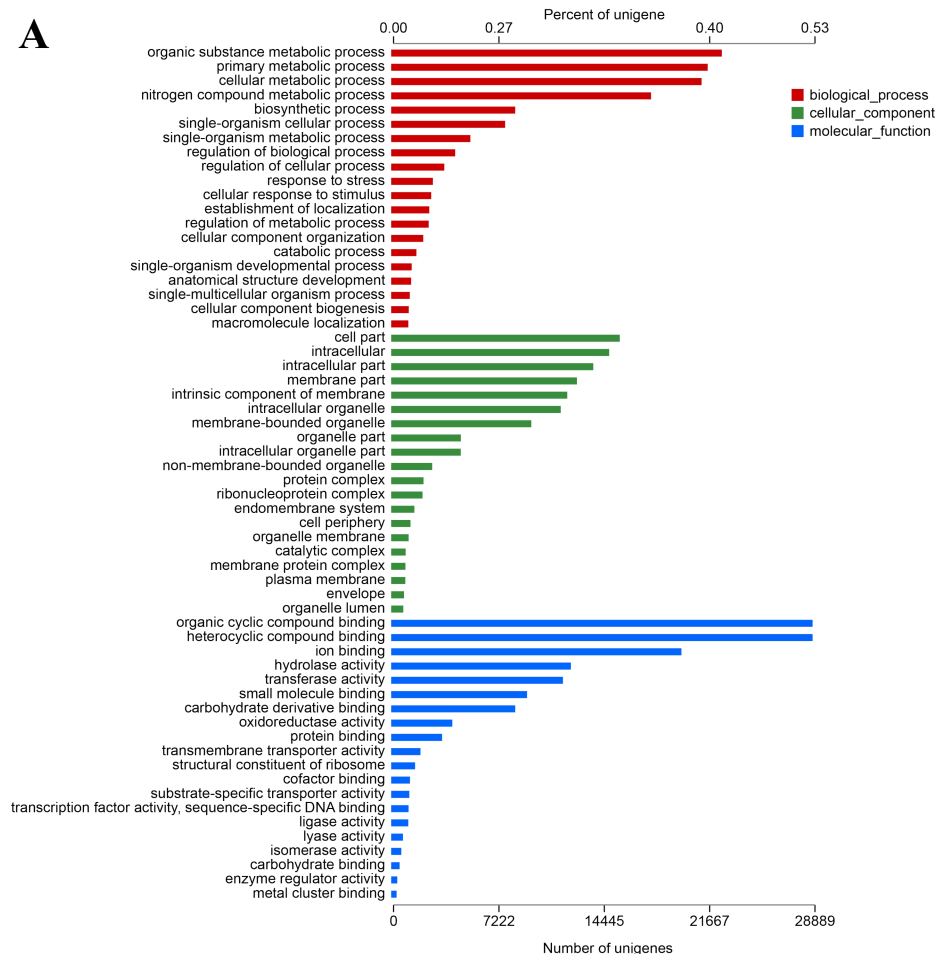


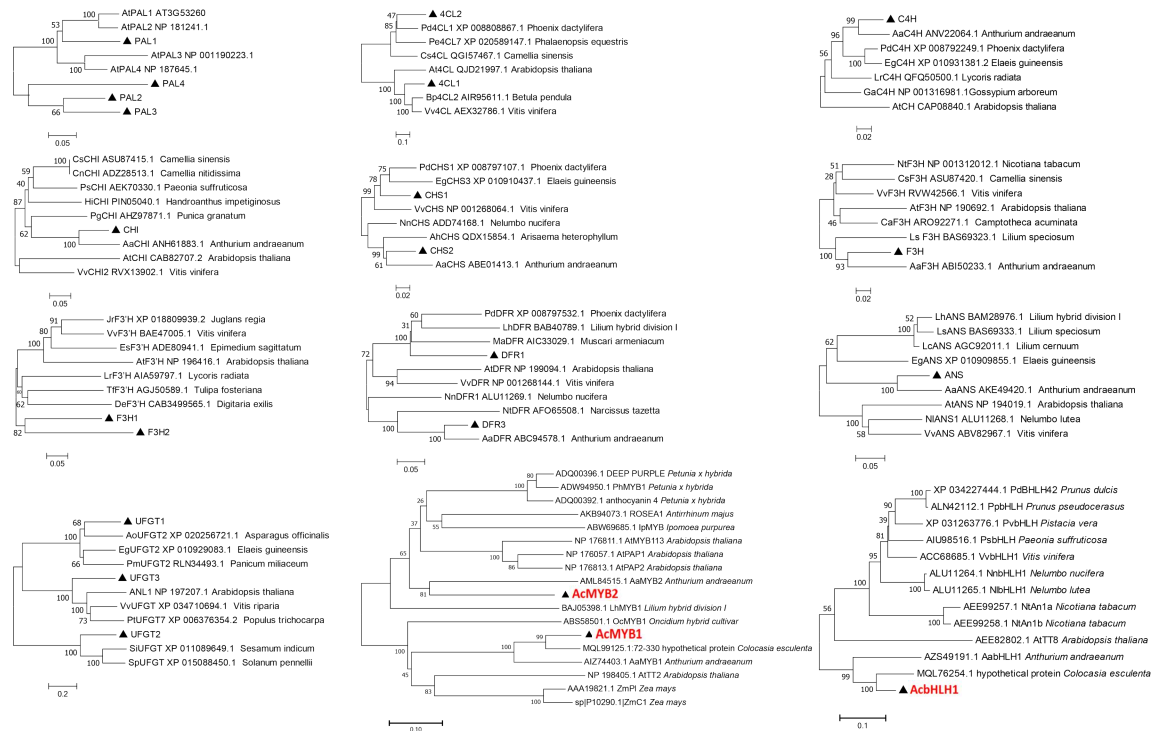
Supplementary Fig. S1. RNA quality of the samples used to generate the RNA-Seq libraries by a 2100 Bioanalyzer (Agilent Technologies, Inc., Santa Clara, CA, USA) system. Samples: 1-3(leaves of *A. commutatum* “Red Valentine” at satge 1); 4-6(leaves of *A. commutatum* “Red Valentine” at satge 2); 7-9(leaves of *A. commutatum* “Red Valentine” at satge 3); 10-12(leaves of the green mutant at satge 1); 13-15(leaves of the green mutant at satge 2); 16-18(leaves of the green mutant at satge 2), DNA marker distribution: 100bp, 250bp, 500bp, 750bp, 1000bp, 2000bp, 3000bp, 5000bp.



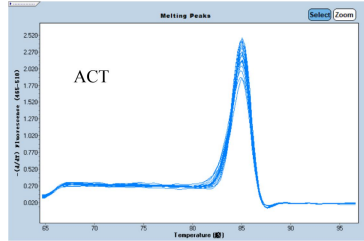
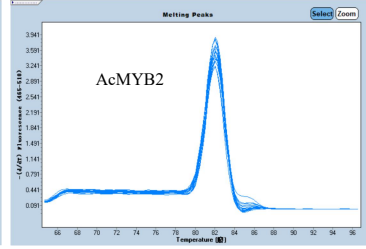
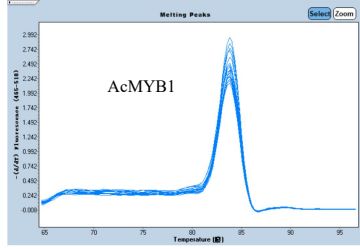
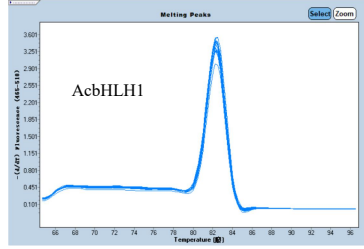
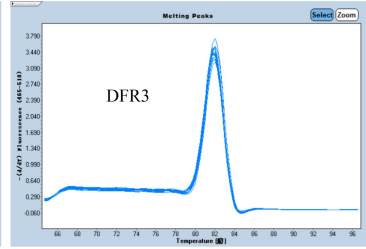
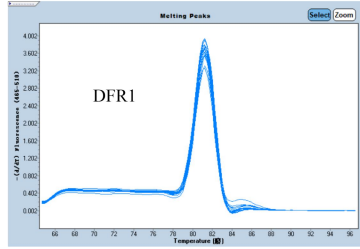
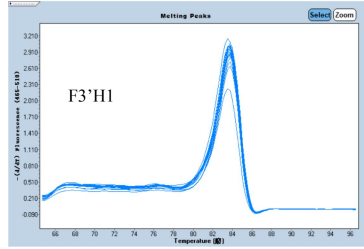
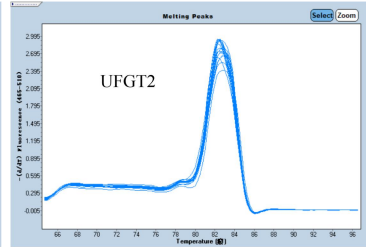
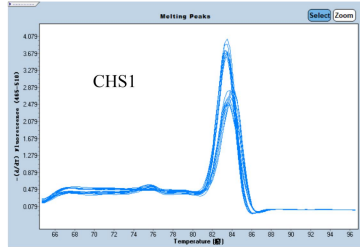
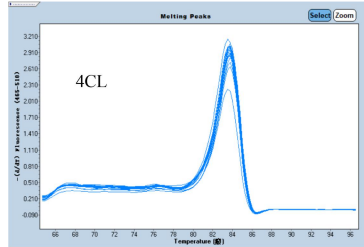
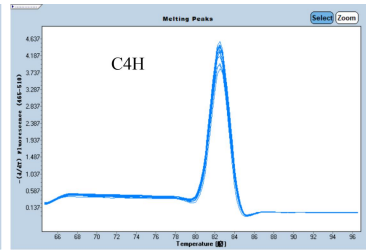
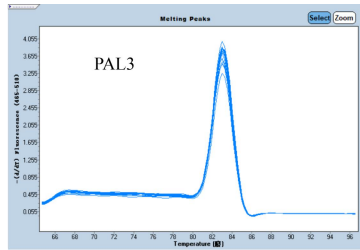
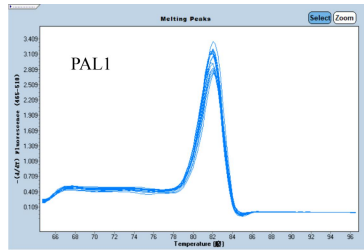
Supplementary Fig. S2. Functional categories of all unigenes in *A. commutatum* “Red Valentine” RNA-seq database. A. Gene Ontology (GO) classification of unigenes. All annotated unigenes were divided into three functional GO categories: biological process (BP), cellular component (CC) and molecular function (MF); B. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway classification.



Supplementary Fig. S3. Phylogenetic trees of transcription factors and structural gene related to anthocyanin biosynthesis in *A. commutatum* “Red Valentine”. The phylogenetic trees were constructed using Neighbor-joining of MEGA software (Molecular Evolutionary Genetics Analysis version 7.0, Kumar et al., 2016) with 1000 bootstrap replicates. *CHI*: chalcone isomerase; *F3H*: flavanone 3-hydroxylase; *ANS*: anthocyanidin synthase.



Supplementary Fig. S4. Melting curves of the reference genes actin (ACT) and 12 qRT-PCR genes involved in anthocyanin biosynthesis and regulation. *PAL*: phenylalanine ammonia-lyase; *C4H*: trans-cinnamate 4-monooxygenase; *4CL*: 4-coumarate--CoA ligase 2; *CHS*: chalcone synthase; *UGFT*: UDP-flavonoid glucosyl transferase; *F3'H*: flavanone 3-hydroxylase; *DFR*: dihydroflavonol 4-reductase.



Supplementary Fig . S5. The phenotype of AcMYB2 transgenic tobacco with 35s promotor. A. Red leaf phenotype of transgenic plants overexpressing AcMYB2 against control plants. B. T-DNA region of the vector used in transgenic plants. LB: LB T-DNA repeat; NOST: NOS terminator; BpR: phosphinothricin acetyltransferase, NOSP:NOS promoter, 35S: CaMV 35S promoter; mGFP: green fluorescent protein; EcoR I, Xba I: restriction site; RB: RB T-DNA repeat.

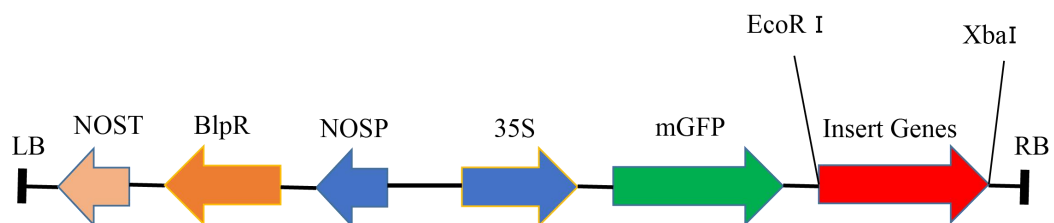
A



Control

35S: AcMYB1

B



Supplementary Table S1. Data used in transcription factor identification. 26 putative anthocyanin biosynthesis unigenes were identified in RNA-seq database, and then normalized the exact PKM value in two varieties at there stages to reduce the error caused by the exact means using the free online platform of Majorbio Cloud Platform (www.majorbio.com), the normalized data were list in the table.

Gene ID	R1	R2	R3	G1	G2	G3
TRINITY_DN103984_c0_g1	0.0635	1.4302	0.5109	0.2005	-0.3222	-1.8829
TRINITY_DN105397_c3_g1	-1.4951	0.5422	1.5370	-0.9361	-0.1157	0.4676
TRINITY_DN64962_c0_g1	-0.0395	1.1772	0.9478	-0.2078	0.0380	-1.9156
TRINITY_DN72679_c3_g2	-0.6362	1.2224	1.2901	-1.5314	-0.0465	-0.2985
TRINITY_DN75107_c2_g1	-0.1222	1.4176	0.9334	-1.3294	0.2331	-1.1325
TRINITY_DN78614_c3_g1	-0.2124	1.5022	0.6651	0.2392	-0.4679	-1.7263
TRINITY_DN78614_c3_g2	-0.6858	1.4068	1.2651	-1.1254	-0.0347	-0.8261
TRINITY_DN79161_c1_g2	-0.4868	1.6355	0.9138	-0.3524	-0.2776	-1.4324
TRINITY_DN81970_c0_g2	-0.2083	1.1365	1.0791	0.0330	-0.1782	-1.8622
TRINITY_DN84294_c0_g1	0.2258	1.4983	0.6467	-0.2457	-0.3671	-1.7580
TRINITY_DN89524_c3_g6	-0.2062	1.5062	0.9751	-1.1611	0.0633	-1.1773
TRINITY_DN90166_c0_g1	0.0432	1.4706	0.8455	-1.1114	0.1199	-1.3679
TRINITY_DN91923_c1_g1	-0.0708	1.4234	1.1266	-1.0461	-0.1786	-1.2544
TRINITY_DN93899_c0_g3	-0.1495	1.5601	0.8295	-0.3694	-0.2393	-1.6315
TRINITY_DN95047_c0_g3	-1.1106	0.0795	2.0114	-0.1339	-0.0119	-0.8344
TRINITY_DN95116_c0_g1	-0.2223	1.2928	1.0456	-0.3479	-0.0175	-1.7506
TRINITY_DN98590_c0_g2	-0.9606	1.7063	0.8840	-1.0277	-0.0296	-0.5723
TRINITY_DN98590_c0_g3	-0.3607	1.5693	0.8708	-0.3602	-0.1381	-1.5811
TRINITY_DN98590_c0_g4	-0.3412	1.5440	0.8765	-0.2267	-0.2322	-1.6205
TRINITY_DN99635_c0_g4	-0.2998	1.3339	1.1741	-1.1794	0.1305	-1.1593
TRINITY_DN106976_c3_g1	0.7398	1.4708	-0.7318	0.3369	-0.2036	-1.6121
TRINITY_DN74649_c0_g2	-0.1611	1.8531	-0.7847	-0.8083	0.7461	-0.8452
TRINITY_DN85368_c0_g3	-0.2086	1.6245	-1.6566	-0.0336	0.6541	-0.3798
TRINITY_DN93219_c1_g2	0.7917	0.0891	-0.5925	1.5896	-0.3374	-1.5406
TRINITY_DN95047_c0_g1	0.3902	1.2819	0.3401	0.3773	-0.4560	-1.9335
TRINITY_DN98854_c4_g1	0.5280	0.8612	0.1962	0.7199	-0.2130	-2.0922

Average	-0.1998	1.2937	0.6615	-0.3861	-0.0724	-1.2969
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Supplementary Table S2. Protein sequence of transcription factors and structural gene related to anthocyanin biosynthesis.

>PAL1

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PLFECLKGWNGAPIPIC

>PAL2

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>PAL3

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>C4H

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>4CL1

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>4CL2

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>CHS1

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V

>CHS2

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>CHI

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>F3H

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>F3'H1

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>F3'H2

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>DFR1

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NAHIFLFEHSEASGRYICSSHDATIFELAEMIKNRYPEYNVPTFEFEGIDNTIQHVRFSKKLEDLGF EYQYSMEEMFDMAI
QCCREKKLIQLKTEKLC DNEEICEAENKPMRC

>DFR3

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>ANS

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>UFGT1

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RSPPKHAHNLPDVTNLRVLEPGLERTAGRGLVWPSPWAPQVDVLAHPSIGGFVTHCGWNSCLESWFVGPMLAWP
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>UFGT2

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PGVSPSVEELRSFDRPCVDFDRDVSCMSASSAIAIKTCREMEAPYIDYVEAQYKGPVLLAGPVVPEALEGELEAKWASW
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>UFGT3

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V

>AcMYB1

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>AcMYB2

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>AcbHLH1

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MEDTSVQVSIIEADALLELQCPNRDGLLLKIMQAVHELGLETTAIQSSSADGIFVAEIRAKVRENIHGKRASIMEVKRVL
HLLFSQSLC

Supplementary Table S3. Primers used in reverse transcription quantitative polymerase chain reaction (RT-qPCR) analysis.

Gene	Unigene ID	Forward primer (5'-3')	Reverse primer (5'-3')
<i>ACT</i>	TRINITY_DN92045_c1_g1	GCCGCCCCCATATTAAGTGA	GACGGCTCTATCCAAGCCAG
<i>PAL1</i>	TRINITY_DN98590_c0_g3	TCTCGCGTTCGATGGACTTG	AAGCCTAAGCAGGACCGCTA
<i>PAL3</i>	TRINITY_DN89524_c3_g6	GATGCTCGCGTTGAGGAAGT	CTACGGCGTGACTACCAACT
<i>C4H</i>	TRINITY_DN95047_c0_g1	CCTGCAGATAGGGGAGCTTG	GAGACGACGTTGTGGTCGAT
<i>4CL</i>	TRINITY_DN95116_c0_g1	CTACGGGATGACGGAGGC	ATGATCTGAGCTCCCCGGAT
<i>CHS1</i>	TRINITY_DN78614_c3_g1	CCGTACTCCTTGAGCACCTC	GGGCATCAACGACTGGAAC
<i>UFGT2</i>	TRINITY_DN90166_c0_g1	CTTCTTCTCCGTCTTCGCCG	AAGTCAGCGGCCTGGTAAAG
<i>F3'H1</i>	TRINITY_DN103984_c0_g1	GAGAGGCACCGACTTTGAGG	CTGCAAGGTGAGTCCGTAGG
<i>DFR1</i>	TRINITY_DN75107_c2_g1	GCTGAGCGTATTGAGCTCCT	CATCCAGCCGGTCATCTTGA
<i>DFR3</i>	TRINITY_DN99635_c0_g4	AGATGTACCTCCGCTGGCT	TCTAATTTGGATGGCCCCCTG
<i>AcbHLH</i>	TRINITY_DN107490_c2_g1	TGGCTTTCAGGGGCAAATGA	GTCCTCGTCCACCTTATCGG
<i>AcMYB1</i>	TRINITY_DN91028_c1_g1	GGCTCAACTACCTCAGACCG	AAGGACCACCTGTTGCCAAT
<i>AcMYB2</i>	TRINITY_DN62889_c2_g2	TGCTCCTACTGTGCAACCTT	TTGCTCGTCGTTTCCCTCAG

Supplementary Table S4. The PKM value of unigenes connected with chlorophyll biosynthesis and degradation.

HEMA: glutamyl-tRNA reductase;

HEMB: aaminolevulinic acid dehydratase;

HEMC: porphobilinogen deaminase;

HEMD: uroporphyrinogen-III synthase;

HEME: uroporphyrinogen decarboxylase;

HEMF: coproporphyrinogen III oxidase;

HEMG: oxygen-dependentprotoporphyrinogen oxidase;

CHLH/D/I: magnesium chelatase subunit H/D/I

CHLM: magnesium protoporphyrin DC methyltransferase

CRD(ACSF): magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase ;

PORA/B/C: protochlorophyllide reductase A/B/C;

DVR: divinyl chlorophyllide a 8-vinyl-reductase;

CAO: chlorophyllide a oxygenase;

NYCI/NOL: chlorophyll(ide)b reductase;

HCAR: 7- hydroxymethyl chlorophyll a reductase;

SGR: stay-green;

PPH: pheophytin pheophorbide hydrolase

PAO: pheophorbide a oxygenase;

RCCR: red chlorophyll catabolite reductase;

Gene		Unigene ID	G1	G2	G3	R1	R2	R3
Chlorophyll biosynthesis and cycle related genes	<i>HEMA</i>	TRINITY_DN63347_c1_g1	48.71	46.52	43.04	53.34	54.68	49.43
		TRINITY_DN95832_c0_g1	15.48	17.51	12.72	18.32	27.08	14.02
		TRINITY_DN63567_c0_g1	46.09	81.58	76.38	45.62	42.92	32.80
		TRINITY_DN95832_c0_g2	67.72	96.35	97.28	47.32	50.98	42.84
		TRINITY_DN74857_c0_g3	67.37	58.40	51.41	52.42	45.81	52.56
		TRINITY_DN83538_c2_g3	45.01	36.59	33.63	36.92	33.52	36.79

Chlorophyll degradation related genes	<i>HEMB</i>	TRINITY_DN98110_c0_g2	145.93	161.86	201.20	119.51	83.39	104.82
	<i>HEMC</i>	TRINITY_DN67480_c5_g1	323.86	253.02	150.97	268.48	145.90	117.76
	<i>HEMD</i>	TRINITY_DN78090_c2_g1	3.12	4.98	8.82	3.43	3.86	5.00
		TRINITY_DN93739_c1_g1	94.34	107.58	79.97	98.45	105.43	70.24
		TRINITY_DN101863_c2_g3	7.56	11.46	17.04	7.53	8.20	10.88
		TRINITY_DN103757_c0_g1	45.16	59.43	33.03	48.02	18.85	45.71
	<i>HEME</i>	TRINITY_DN66202_c2_g2	61.06	64.17	48.76	52.26	49.43	46.53
		TRINITY_DN76425_c1_g1	5.77	8.07	4.34	4.72	3.83	5.78
		TRINITY_DN101863_c2_g2	3.72	7.30	5.85	3.47	1.02	4.08
		TRINITY_DN63968_c0_g1	6.88	3.73	5.29	3.12	3.26	3.13
	<i>HEMF</i>	TRINITY_DN63968_c0_g4	191.91	167.99	120.25	132.88	97.91	107.24
		TRINITY_DN96909_c1_g1	172.35	166.96	115.40	139.25	102.38	90.52
	<i>HEMG</i>	TRINITY_DN105042_c2_g1	9.10	6.40	4.75	7.00	5.18	6.29
		TRINITY_DN95468_c3_g1	4.64	10.80	11.62	2.84	3.83	3.69
	<i>CHLH/D/I</i>	TRINITY_DN95468_c3_g6	6.33	5.85	7.61	5.35	5.64	4.53
		TRINITY_DN96966_c1_g3	12.45	28.24	35.59	6.76	9.46	9.04
	<i>CHLM</i>	TRINITY_DN78841_c1_g1	0.77	0.88	0.60	0.73	0.73	0.98
		TRINITY_DN88221_c0_g1	7.91	13.74	7.91	5.29	6.54	2.13
	<i>CRD(ACSF)</i>	TRINITY_DN78858_c3_g1	413.35	838.30	729.50	317.91	288.23	293.31
		TRINITY_DN93340_c1_g1	476.90	492.65	554.98	264.70	158.36	231.61
		TRINITY_DN90068_c2_g2	41.29	63.26	51.88	34.89	40.26	30.10
	<i>DVR</i>	TRINITY_DN101935_c0_g2	191.89	204.07	132.38	212.14	149.98	131.70
		TRINITY_DN58016_c0_g1	0.76	0.68	0.80	1.39	1.52	3.03
	<i>CAO</i>	TRINITY_DN86926_c2_g1	13.21	17.88	16.02	6.46	3.73	4.99
		TRINITY_DN87057_c1_g1	25.21	18.14	11.72	13.30	4.89	5.72
	<i>NYCI/NOL</i>	TRINITY_DN83767_c1_g1	29.04	26.03	30.12	24.91	14.61	18.93
		TRINITY_DN101603_c0_g1	59.47	104.45	121.06	72.11	93.30	95.77
		TRINITY_DN103561_c3_g1	3.98	3.74	4.86	2.38	3.51	5.51
	<i>HCAR</i>	TRINITY_DN89117_c0_g1	26.76	21.10	29.53	16.99	26.92	30.74
		TRINITY_DN89117_c0_g2	41.80	51.99	52.00	32.89	39.21	46.98
	<i>SGR</i>	TRINITY_DN83555_c0_g1	2.66	0.96	3.07	3.82	7.23	5.90
	<i>PPH</i>	TRINITY_DN81824_c0_g5	20.30	42.86	70.84	21.64	42.42	59.38
		TRINITY_DN89834_c0_g4	27.15	34.90	78.43	27.00	36.04	54.02

	TRINITY_DN96660_c0_g1	10.89	23.83	21.31	10.08	15.55	10.91
	TRINITY_DN79574_c1_g1	42.60	52.89	75.21	37.32	48.95	46.62
	TRINITY_DN96584_c1_g1	39.81	65.30	117.65	44.95	72.35	85.03
<i>PAO</i>	TRINITY_DN96961_c1_g1	36.50	58.61	77.46	32.06	48.45	64.67
	TRINITY_DN88053_c0_g6	44.54	112.65	219.90	45.54	96.62	151.59
	TRINITY_DN88961_c5_g8	6.75	13.17	17.33	9.40	13.69	15.65
<i>RCCR</i>	TRINITY_DN85771_c0_g1	69.81	119.19	136.00	85.47	107.34	115.52
