

Supplementary Information for

The novel gene *BrMYB2*, located on chromosome A07, with a short intron 1 controls the purple-head trait of Chinese cabbage (*Brassica rapa* L.)

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Figure S1 Electrophoresis results of *cBrMYB2* and different phenotypes of Chinese cabbage. **a** Electrophoresis results of *cBrMYB2* from purple head Chinese cabbage ‘11S91’, and its female parent ‘94S17’ and male parent ‘95T2-5’; **b-d** different white head Chinese cabbages; **e** orange head Chinese cabbage; **f-i** different purple head Chinese cabbages; **j** electrophoresis results of *cBrMYB2* from different phenotypes of Chinese cabbage. M1: DL2000 Marker.

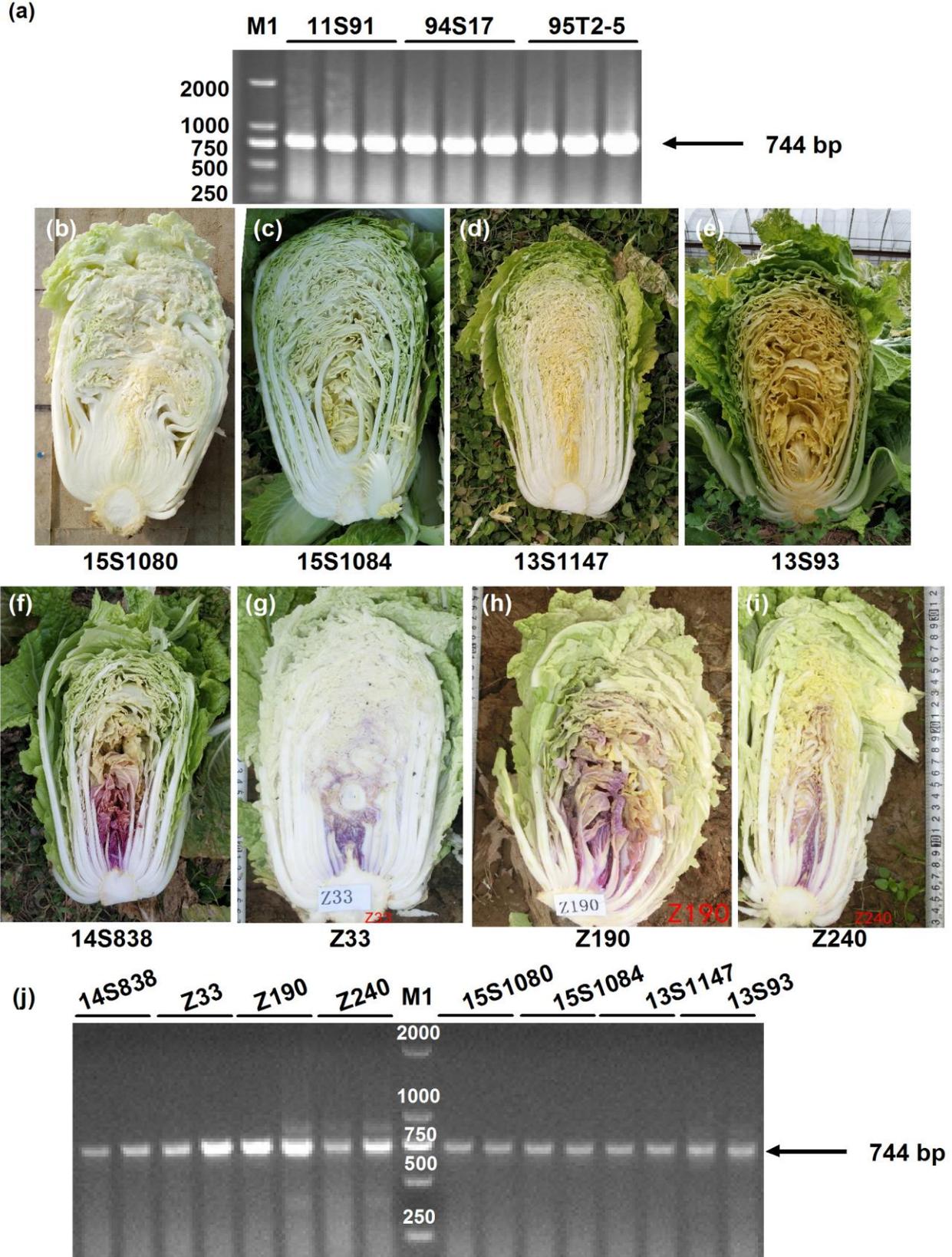


Figure S2 Multiple sequence alignment analysis of *BrMYBs* in *Brassica rapa*.

a Multiple sequence alignment analysis of *cBrMYB2* among purple head Chinese cabbage ‘11S91’ and its parents ‘94S17’ and ‘95T2-5’. ‘95T2-5’ and ‘11S91’ had consensus coding sequence (CDS). The *cBrMYB2* of ‘Chifu’ was downloaded from BRAD database.

CHIFU-cBrMYB2	ATGGAGGGTTCGTCCCAAGGGTTGAAAAAGGTGCATGGACTGCTGAAGAAGATAATCTCTTGAGGCAATGCATTGATAA	80
94S17-cBrmyb2	ATGGAGGGTTCGTCCCAAGGGTTGAAAAAGGTGCATGGACTGCTGAAGAAGATAATCTCTTGAGGCAATGCATTGATAA	80
11S91-cBrMYB2	ATGGAGGGTTCGTCCCAAGGGTTGAAAAAGGTGCATGGACTGCTGAAGAAGATAATCTCTTGAGGCAATGCATTGATAA	80
95T2-5-cBrMYB2	ATGGAGGGTTCGTCCCAAGGGTTGAAAAAGGTGCATGGACTGCTGAAGAAGATAATCTCTTGAGGCAATGCATTGATAA	80
Consensus	atggaggggttcgtcccaagggttgaaaaaggtgcatggactgctgaagaagataatctcttgaggcaatgcattgataa	
CHIFU-cBrMYB2	GTATGGAGAAGGGAATGGCACCAAGTTCCTTTAAGAGCTGGTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGT	160
94S17-cBrmyb2	GTATGGAGAAGGGAATGGCACCAAGTTCCTTTAAGAGCTGGTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGT	160
11S91-cBrMYB2	GTATGGAGAAGGGAATGGCACCAAGTTCCTTTAAGAGCTGGTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGT	160
95T2-5-cBrMYB2	GTATGGAGAAGGGAATGGCACCAAGTTCCTTTAAGAGCTGGTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGT	160
Consensus	gtatggagaagggaaatggcaccaagttcctttaagagctgggtctaaatcgggtgcaggaagagttgttagactaagatggt	
CHIFU-cBrMYB2	TGAACTATTTGAAGCCAAGTATCAAGAGAGGAAAACTCAACTCCGATGAAGTTGATCTTCTTATCGCCTTCATAAGCTT	240
94S17-cBrmyb2	TGAACTATTTGAAGCCAAGTATCAAGAGAGGAAAACTCAACTCCGATGAAGTTGATCTTCTTATCGCCTTCATAAGCTT	240
11S91-cBrMYB2	TGAACTATTTGAAGCCAAGTATCAAGAGAGGAAAACTCAACTCCGATGAAGTTGATCTTCTTATCGCCTTCATAAGCTT	240
95T2-5-cBrMYB2	TGAACTATTTGAAGCCAAGTATCAAGAGAGGAAAACTCAACTCCGATGAAGTTGATCTTCTTATCGCCTTCATAAGCTT	240
Consensus	tgaactatttgaagccaagtatcaagagagggaaaaactcaactccgatgaagttgatcttcttat cgccttcataagctt	
CHIFU-cBrMYB2	TTAGGAAACAGGTGGTCTTTAATTGCTGGTAGATTACCCGGTCGGACCGCCAATGACGTCAAAAATTACTGGAACACCCA	320
94S17-cBrmyb2	TTAGGAAACAGGTGGTCTTTAATTGCTGGTAGATTACCCGGTCGGACCGCCAATGACGTCAAAAATTACTGGAACACCCA	320
11S91-cBrMYB2	TTAGGAAACAGGTGGTCTTTAATTGCTGGTAGATTACCCGGTCGGACCGCCAATGACGTCAAAAATTACTGGAACACCCA	320
95T2-5-cBrMYB2	TTAGGAAACAGGTGGTCTTTAATTGCTGGTAGATTACCCGGTCGGACCGCCAATGACGTCAAAAATTACTGGAACACCCA	320
Consensus	ttaggaaacaggtggtctttaattgctggtagattacccggtcggaccgccaatgacgtcaaaaattactggaacaccca	
CHIFU-cBrMYB2	TTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
94S17-cBrmyb2	TTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
11S91-cBrMYB2	TTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
95T2-5-cBrMYB2	TTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
Consensus	tttgagtaagaaacatgaaccgggttgtaagaccagatgaaaagagaaacattccttgctcttataccacaccagccc	
CHIFU-cBrMYB2	AAAAAATCGACGTTTTCAAACCTCGACCTCGATCCTTACCCTTAAACAGCGGCTGCAGCCATAATAATGGCATGCCAGAA	480
94S17-cBrmyb2	AAAAAATCGACGTTTTCAAACCTCGACCTCGATCCTTACCCTTAAACAGCGGCTGCAGCCATAATAATGGCATGCCAGAA	480
11S91-cBrMYB2	AAAAAATCGACGTTTTCAAACCTCGACCTCGATCCTTACCCTTAAACAGCGGCTGCAGCCATAATAATGGCATGCCAGAA	480
95T2-5-cBrMYB2	AAAAAATCGACGTTTTCAAACCTCGACCTCGATCCTTACCCTTAAACAGCGGCTGCAGCCATAATAATGGCATGCCAGAA	480
Consensus	aaaaaatcgacgTTTTCAAACCTCGACCTCGATCCTTACCCTTAAACAGCGGCTGCAGCCATAATAATGGCATGCCAGAA	
CHIFU-cBrMYB2	GCTGCATTTGTTCCCTCTATGCCTTGGACACAACGATACTAATAATGTTTCTGAAAATATAATCACATGTAACAAAGATGA	560
94S17-cBrmyb2	GCTGCATTTGTTCCCTCTATGCCTTGGACACAACGATACTAATAATGTTTCTGAAAATATAATCACATGTAACAAAGATGA	560
11S91-cBrMYB2	GCTGCATTTGTTCCCTCTATGCCTTGGACACAACGATACTAATAATGTTTCTGAAAATATAATCACATGTAACAAAGATGA	560
95T2-5-cBrMYB2	GCTGCATTTGTTCCCTCTATGCCTTGGACACAACGATACTAATAATGTTTCTGAAAATATAATCACATGTAACAAAGATGA	560
Consensus	gctg cattgttcctctatgccttggacacaacgataactaataatgtttctgaaaatataatcacatgtaacaaagatga	
CHIFU-cBrMYB2	TGATAAATCTGAGCTTGTTAGTCATTTAATGGATGGTCAGAATAGGTGGTGGGAAAGTTTGCTAGATGAGAGCCAAGATC	640
94S17-cBrmyb2	TGATAAATCTGAGCTTGTTAGTCATTTAATGGATGGTCAGAATAGGTGGTGGGAAAGTTTGCTAGATGAGAGCCAAGATC	640
11S91-cBrMYB2	TGATAAATCTGAGCTTGTTAGTCATTTAATGGATGGTCAGAATAGGTGGTGGGAAAGTTTGCTAGATGAGAGCCAAGATC	640
95T2-5-cBrMYB2	TGATAAATCTGAGCTTGTTAGTCATTTAATGGATGGTCAGAATAGGTGGTGGGAAAGTTTGCTAGATGAGAGCCAAGATC	640
Consensus	tgataaatctgagcttgtagtcattttaatggatggtcagaataggtggggaaagtttgctagatgagagccaagatc	
CHIFU-cBrMYB2	CAGCTGCGCTCTTCCAGAAACTACAGCAATAAAAAAGGGCGCAACCTCCGCGTTTGACGTTGAGCAACTTTGGAGCCTG	720
94S17-cBrmyb2	CAGCTGCGCTCTTCCAGAAACTACAGCAATAAAAAAGGGCGCAACCTCCGCGTTTGACGTTGAGCAACTTTGGAGCCTG	720
11S91-cBrMYB2	CAGCTGCGCTCTTCCAGAAACTACAGCAATAAAAAAGGGCGCAACCTCCGCGTTTGACGTTGAGCAACTTTGGAGCCTG	720
95T2-5-cBrMYB2	CAGCTGCGCTCTTCCAGAAACTACAGCAATAAAAAAGGGCGCAACCTCCGCGTTTGACGTTGAGCAACTTTGGAGCCTG	720
Consensus	cagctgcgctcttccagaaactacagcaataaaaaagggcgcaacctccgcgtttgacgttgagcaactttggagcctg	
CHIFU-cBrMYB2	TTGGATGGAGAACTGGAACCTG	743
94S17-cBrmyb2	TTGGATGGAGAACTGGAACCTG	743
11S91-cBrMYB2	TTGGATGGAGAACTGGAACCTG	743
95T2-5-cBrMYB2	TTGGATGGAGAACTGGAACCTG	743
Consensus	ttggatggagaaactggaacttg	

b Multiple sequence alignment analysis of *cBrMYBs* in *B. rapa*.

CHIFU-cBrMYB2	ATGGAGGGTTCGTC	CCCAAGGGTTGAAAAAGGTGCATGGACT	GCTGAAGAAGA	TAATCTCTT	GAGGCAATGCATTGATAA	80
94S17-cBrMyb2	ATGGAGGGTTCGTC	CCCAAGGGTTGAAAAAGGTGCATGGACT	GCTGAAGAAGA	TAATCTCTT	GAGGCAATGCATTGATAA	80
11S91-cBrMYB2	ATGGAGGGTTCGTC	CCCAAGGGTTGAAAAAGGTGCATGGACT	GCTGAAGAAGA	TAATCTCTT	GAGGCAATGCATTGATAA	80
95T2-5-cBrMYB2	ATGGAGGGTTCGTC	CCCAAGGGTTGAAAAAGGTGCATGGACT	GCTGAAGAAGA	TAATCTCTT	GAGGCAATGCATTGATAA	80
CHIFU-cBrMYB1	ATGGAGGATTCGTC	CCCAAGGGTTGAAAAAGGTGCATGGACC	GCTGAAGAAGA	CAGTCTCTT	GAGGCAATGCATTGATAA	80
CHIFU-cBrPAP1	ATGGAGGGTTCGTC	CCCAAGGGTTGAAAAAGGTGCATGGACT	GCTGAAGAAGA	TAATCTCTT	GAGGCAATGCATTGATAA	80
Consensus	atggagg ttcg c	aagggttga	aaaaggtgcatggac	gctgaagaaga a	tctctt aggc atgcattgataa	
CHIFU-cBrMYB2	GTATGGAGAAGG	CAAAATGGCACCAAGTTCCTT	TAAAGAGCT	GGTCTAAAT	GGTGCAGGAAGAGT	160
94S17-cBrMyb2	GTATGGAGAAGG	CAAAATGGCACCAAGTTCCTT	TAAAGAGCT	GGTCTAAAT	GGTGCAGGAAGAGT	160
11S91-cBrMYB2	GTATGGAGAAGG	CAAAATGGCACCAAGTTCCTT	TAAAGAGCT	GGTCTAAAT	GGTGCAGGAAGAGT	160
95T2-5-cBrMYB2	GTATGGAGAAGG	CAAAATGGCACCAAGTTCCTT	TAAAGAGCT	GGTCTAAAT	GGTGCAGGAAGAGT	160
CHIFU-cBrMYB1	GTATGGAGAAGG	CAAAATGGCACCAAGTTCCTT	TAAAGAGCT	GGTCTAAAT	GGTGCAGGAAGAGT	160
CHIFU-cBrPAP1	GTATGGAGAAGG	CAAAATGGCACCAAGTTCCTT	TAAAGAGCT	GGTCTAAAT	GGTGCAGGAAGAGT	160
Consensus	gtatggagaagg	aaatggca caagttcct t	gagc gg ct	aat ggtg	aggaagag tgtagactaagatggt	
CHIFU-cBrMYB2	TGAACATTTGAAGCC	AAGTATCAAGA	GAGGAAAAC	TCAACTCC	GATGAAGTTGATCTTCTTAT	240
94S17-cBrMyb2	TGAACATTTGAAGCC	AAGTATCAAGA	GAGGAAAAC	TCAACTCC	GATGAAGTTGATCTTCTTAT	240
11S91-cBrMYB2	TGAACATTTGAAGCC	AAGTATCAAGA	GAGGAAAAC	TCAACTCC	GATGAAGTTGATCTTCTTAT	240
95T2-5-cBrMYB2	TGAACATTTGAAGCC	AAGTATCAAGA	GAGGAAAAC	TCAACTCC	GATGAAGTTGATCTTCTTAT	240
CHIFU-cBrMYB1	TGAACATTTGAAGCC	AAGTATCAAGA	GAGGAAAAC	TCAACTCC	GATGAAGTTGATCTTCTTAT	240
CHIFU-cBrPAP1	TGAACATTTGAAGCC	AAGTATCAAGA	GAGGAAAAC	TCAACTCC	GATGAAGTTGATCTTCTTAT	240
Consensus	tgaactat	tttgaagcc a	tatcaaga	aggaaaact a	ctc gatgaagttgatcttctt t	cg cttcata gctt
CHIFU-cBrMYB2	TTAGGAAACAGGTGGT	CTTTAATTGCTGGTAGAT	TACCCGGT	GGGACCGC	CAATGACCTCAAAAA	320
94S17-cBrMyb2	TTAGGAAACAGGTGGT	CTTTAATTGCTGGTAGAT	TACCCGGT	GGGACCGC	CAATGACCTCAAAAA	320
11S91-cBrMYB2	TTAGGAAACAGGTGGT	CTTTAATTGCTGGTAGAT	TACCCGGT	GGGACCGC	CAATGACCTCAAAAA	320
95T2-5-cBrMYB2	TTAGGAAACAGGTGGT	CTTTAATTGCTGGTAGAT	TACCCGGT	GGGACCGC	CAATGACCTCAAAAA	320
CHIFU-cBrMYB1	TTAGGAAACAGGTGGT	CTTTAATTGCTGGTAGAT	TACCCGGT	GGGACCGC	CAATGACCTCAAAAA	320
CHIFU-cBrPAP1	TTAGGAAACAGGTGGT	CTTTAATTGCTGGTAGAT	TACCCGGT	GGGACCGC	CAATGACCTCAAAAA	320
Consensus	taggaaacaggtggt	cttttaattgctggtaga	taccgggt	ggaccgc	aatga tcaa aa	tactggaacacca
CHIFU-cBrMYB2	TTTGAGTAAGAAACAT	GAACCGGGTTGTAAG	ACCAGATGAAA	AAGAGAAACAT	TCCCTTGCTCTTATACCAC	400
94S17-cBrMyb2	TTTGAGTAAGAAACAT	GAACCGGGTTGTAAG	ACCAGATGAAA	AAGAGAAACAT	TCCCTTGCTCTTATACCAC	400
11S91-cBrMYB2	TTTGAGTAAGAAACAT	GAACCGGGTTGTAAG	ACCAGATGAAA	AAGAGAAACAT	TCCCTTGCTCTTATACCAC	400
95T2-5-cBrMYB2	TTTGAGTAAGAAACAT	GAACCGGGTTGTAAG	ACCAGATGAAA	AAGAGAAACAT	TCCCTTGCTCTTATACCAC	400
CHIFU-cBrMYB1	TTTGAGTAAGAAACAT	GAACCGGGTTGTAAG	ACCAGATGAAA	AAGAGAAACAT	TCCCTTGCTCTTATACCAC	400
CHIFU-cBrPAP1	TTTGAGTAAGAAACAT	GAACCGGGTTGTAAG	ACCAGATGAAA	AAGAGAAACAT	TCCCTTGCTCTTATACCAC	400
Consensus	t t	tgag aagaaacatgaacc	g tgtaa	acc agatga	aagagaac tt c t	ctctt acc acc gccc
CHIFU-cBrMYB2	AAAAAATCGACGTTT	TCAAACCTCGACCTCGAT	CTTCAAC	CGTTAACAG	GGCTGCAGCCATAA	480
94S17-cBrMyb2	AAAAAATCGACGTTT	TCAAACCTCGACCTCGAT	CTTCAAC	CGTTAACAG	GGCTGCAGCCATAA	480
11S91-cBrMYB2	AAAAAATCGACGTTT	TCAAACCTCGACCTCGAT	CTTCAAC	CGTTAACAG	GGCTGCAGCCATAA	480
95T2-5-cBrMYB2	AAAAAATCGACGTTT	TCAAACCTCGACCTCGAT	CTTCAAC	CGTTAACAG	GGCTGCAGCCATAA	480
CHIFU-cBrMYB1	AAAAAATCGACGTTT	TCAAACCTCGACCTCGAT	CTTCAAC	CGTTAACAG	GGCTGCAGCCATAA	480
CHIFU-cBrPAP1	AAAAAATCGACGTTT	TCAAACCTCGACCTCGAT	CTTCAAC	CGTTAACAG	GGCTGCAGCCATAA	480
Consensus	aaaaaa	ga gtt	tcaaacctcgacctga	cttcac	gntaaaca	ggctgcagccat atggc gccaa aa
CHIFU-cBrMYB2	GCTGACATTTGCTCCT	CATGCTTGGACACAAC	GATTAATAA	TGTTCTGAAAATATA	ATC	560
94S17-cBrMyb2	GCTGACATTTGCTCCT	CATGCTTGGACACAAC	GATTAATAA	TGTTCTGAAAATATA	ATC	560
11S91-cBrMYB2	GCTGACATTTGCTCCT	CATGCTTGGACACAAC	GATTAATAA	TGTTCTGAAAATATA	ATC	560
95T2-5-cBrMYB2	GCTGACATTTGCTCCT	CATGCTTGGACACAAC	GATTAATAA	TGTTCTGAAAATATA	ATC	560
CHIFU-cBrMYB1	GCTGACATTTGCTCCT	CATGCTTGGACACAAC	GATTAATAA	TGTTCTGAAAATATA	ATC	560
CHIFU-cBrPAP1	GCTGACATTTGCTCCT	CATGCTTGGACACAAC	GATTAATAA	TGTTCTGAAAATATA	ATC	560
Consensus	g tg c tt	ttcctc at	ccttggga	aac a a	taataatgt t	tgaaaata at acat taa aaag tg
CHIFU-cBrMYB2	TGATAAATCTGACCT	TGTTAGTCAATTA	TGATGGATGGT	CAGAA	TAGTGGTGGGAAAG	640
94S17-cBrMyb2	TGATAAATCTGACCT	TGTTAGTCAATTA	TGATGGATGGT	CAGAA	TAGTGGTGGGAAAG	640
11S91-cBrMYB2	TGATAAATCTGACCT	TGTTAGTCAATTA	TGATGGATGGT	CAGAA	TAGTGGTGGGAAAG	640
95T2-5-cBrMYB2	TGATAAATCTGACCT	TGTTAGTCAATTA	TGATGGATGGT	CAGAA	TAGTGGTGGGAAAG	640
CHIFU-cBrMYB1	TGATAAATCTGACCT	TGTTAGTCAATTA	TGATGGATGGT	CAGAA	TAGTGGTGGGAAAG	640
CHIFU-cBrPAP1	TGATAAATCTGACCT	TGTTAGTCAATTA	TGATGGATGGT	CAGAA	TAGTGGTGGGAAAG	640
Consensus	ga aa t	tga ct	ta t	at	taataatggtg	agaa a gttggtg a agtttgcctaga gagagc aa a c
CHIFU-cBrMYB2	CAGCTGCGCTCTT	TCCAGAACTACAG	CAATAAAAAAG	GGCGCAACCT	CCGCGTTGACGTTGAGCA	720
94S17-cBrMyb2	CAGCTGCGCTCTT	TCCAGAACTACAG	CAATAAAAAAG	GGCGCAACCT	CCGCGTTGACGTTGAGCA	720
11S91-cBrMYB2	CAGCTGCGCTCTT	TCCAGAACTACAG	CAATAAAAAAG	GGCGCAACCT	CCGCGTTGACGTTGAGCA	720
95T2-5-cBrMYB2	CAGCTGCGCTCTT	TCCAGAACTACAG	CAATAAAAAAG	GGCGCAACCT	CCGCGTTGACGTTGAGCA	720
CHIFU-cBrMYB1	CAGCTGCGCTCTT	TCCAGAACTACAG	CAATAAAAAAG	GGCGCAACCT	CCGCGTTGACGTTGAGCA	720
CHIFU-cBrPAP1	CAGCTGCGCTCTT	TCCAGAACTACAG	CAATAAAAAAG	GGCGCAACCT	CCGCGTTGACGTTGAGCA	720
Consensus	c g g g t	ttcca aa	tac g a	aaaaag	gcaacct	gcgtttgacggtgagcaactttgga gctg
CHIFU-cBrMYB2	TTGGATGGAGAAAC	..TGGAACTTGA...				744
94S17-cBrMyb2	TTGGATGGAGAAAC	..TGGAACTTGA...				744
11S91-cBrMYB2	TTGGATGGAGAAAC	..TGGAACTTGA...				744
95T2-5-cBrMYB2	TTGGATGGAGAAAC	..TGGAACTTGA...				744
CHIFU-cBrMYB1	TTGGATGGAGAGACT	..TGGAACTTGA...				749
CHIFU-cBrPAP1	TTGGATGGAGAGACT	..TGGAACTTGA...				749
Consensus	tt gatgg ga ac	t gaacttga				

c Multiple sequence alignment analysis of *cBrMYB2* from different phenotypes of Chinese cabbage. The *cBrMYB2* of ‘Chifu’ was downloaded from BRAD database.

11S91-cBrMYB2	ATGGAGGGTTCGTCCCAAGGGTTGAAAAAAGGTGCATGGACIGCTGAAGAAGATAAATCTCTTGAGGCAATGCATTGATAA	80
14S838-cBrMYB2	ATGGAGGGTTCGTCCCAAGGGTTGAAAAAAGGTGCATGGACIGCTGAAGAAGATAAATCTCTTGAGGCAATGCATTGATAA	80
95T2-5-cBrMYB2	ATGGAGGGTTCGTCCCAAGGGTTGAAAAAAGGTGCATGGACIGCTGAAGAAGATAAATCTCTTGAGGCAATGCATTGATAA	80
Z33-cBrMYB2	ATGGAGGGTTCGTCCCAAGGGTTGAAAAAAGGTGCATGGACIGCTGAAGAAGATAAATCTCTTGAGGCAATGCATTGATAA	80
Z190-cBrMYB2	ATGGAGGGTTCGTCCCAAGGGTTGAAAAAAGGTGCATGGACIGCTGAAGAAGATAAATCTCTTGAGGCAATGCATTGATAA	80
Z240-cBrMYB2	ATGGAGGGTTCGTCCCAAGGGTTGAAAAAAGGTGCATGGACIGCTGAAGAAGATAAATCTCTTGAGGCAATGCATTGATAA	80
Chifu-cBrMYB2	ATGGAGGGTTCGTCCCAAGGGTTGAAAAAAGGTGCATGGACIGCTGAAGAAGATAAATCTCTTGAGGCAATGCATTGATAA	80
13S93-cBrmyb2	ATGGAGGGTTCGTCCCAAGGGTTGAAAAAAGGTGCATGGACIGCTGAAGAAGATAAATCTCTTGAGGCAATGCATTGATAA	80
13S1147-cBrmyb2	ATGGAGGGTTCGTCCCAAGGGTTGAAAAAAGGTGCATGGACIGCTGAAGAAGATAAATCTCTTGAGGCAATGCATTGATAA	80
15S1080-cBrmyb2	ATGGAGGGTTCGTCCCAAGGGTTGAAAAAAGGTGCATGGACIGCTGAAGAAGATAAATCTCTTGAGGCAATGCATTGATAA	80
15S1084-cBrmyb2	ATGGAGGGTTCGTCCCAAGGGTTGAAAAAAGGTGCATGGACIGCTGAAGAAGATAAATCTCTTGAGGCAATGCATTGATAA	80
94S17-cBrmyb2	ATGGAGGGTTCGTCCCAAGGGTTGAAAAAAGGTGCATGGACIGCTGAAGAAGATAAATCTCTTGAGGCAATGCATTGATAA	80
Consensus	atggaggggttcgtcccaagggttgaaaaaaggtgcatggactgctgaagaagataaattctcttgaggcaatgcattgataa	
11S91-cBrMYB2	GTATGGAGAAGGGAAATGGCACCAGTTCCTTTAAGAGCTGCTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGT	160
14S838-cBrMYB2	GTATGGAGAAGGGAAATGGCACCAGTTCCTTTAAGAGCTGCTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGT	160
95T2-5-cBrMYB2	GTATGGAGAAGGGAAATGGCACCAGTTCCTTTAAGAGCTGCTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGT	160
Z33-cBrMYB2	GTATGGAGAAGGGAAATGGCACCAGTTCCTTTAAGAGCTGCTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGT	160
Z190-cBrMYB2	GTATGGAGAAGGGAAATGGCACCAGTTCCTTTAAGAGCTGCTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGT	160
Z240-cBrMYB2	GTATGGAGAAGGGAAATGGCACCAGTTCCTTTAAGAGCTGCTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGT	160
Chifu-cBrMYB2	GTATGGAGAAGGGAAATGGCACCAGTTCCTTTAAGAGCTGCTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGT	160
13S93-cBrmyb2	GTATGGAGAAGGGAAATGGCACCAGTTCCTTTAAGAGCTGCTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGT	160
13S1147-cBrmyb2	GTATGGAGAAGGGAAATGGCACCAGTTCCTTTAAGAGCTGCTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGT	160
15S1080-cBrmyb2	GTATGGAGAAGGGAAATGGCACCAGTTCCTTTAAGAGCTGCTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGT	160
15S1084-cBrmyb2	GTATGGAGAAGGGAAATGGCACCAGTTCCTTTAAGAGCTGCTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGT	160
94S17-cBrmyb2	GTATGGAGAAGGGAAATGGCACCAGTTCCTTTAAGAGCTGCTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGT	160
Consensus	gtatggagaagggaaatggcaccagttcctttaagagctgctctaaatcgggtgcaggaagagttgtagactaagatggt	
11S91-cBrMYB2	TGAACACTATTTGAAGCCAAGTATCAAGAGAGGAAAACCTCAACICCGATGAAGTTGATCTTCTTATTCGCCTTCATAAGCTT	240
14S838-cBrMYB2	TGAACACTATTTGAAGCCAAGTATCAAGAGAGGAAAACCTCAACICCGATGAAGTTGATCTTCTTATTCGCCTTCATAAGCTT	240
95T2-5-cBrMYB2	TGAACACTATTTGAAGCCAAGTATCAAGAGAGGAAAACCTCAACICCGATGAAGTTGATCTTCTTATTCGCCTTCATAAGCTT	240
Z33-cBrMYB2	TGAACACTATTTGAAGCCAAGTATCAAGAGAGGAAAACCTCAACICCGATGAAGTTGATCTTCTTATTCGCCTTCATAAGCTT	240
Z190-cBrMYB2	TGAACACTATTTGAAGCCAAGTATCAAGAGAGGAAAACCTCAACICCGATGAAGTTGATCTTCTTATTCGCCTTCATAAGCTT	240
Z240-cBrMYB2	TGAACACTATTTGAAGCCAAGTATCAAGAGAGGAAAACCTCAACICCGATGAAGTTGATCTTCTTATTCGCCTTCATAAGCTT	240
Chifu-cBrMYB2	TGAACACTATTTGAAGCCAAGTATCAAGAGAGGAAAACCTCAACICCGATGAAGTTGATCTTCTTATTCGCCTTCATAAGCTT	240
13S93-cBrmyb2	TGAACACTATTTGAAGCCAAGTATCAAGAGAGGAAAACCTCAACICCGATGAAGTTGATCTTCTTATTCGCCTTCATAAGCTT	240
13S1147-cBrmyb2	TGAACACTATTTGAAGCCAAGTATCAAGAGAGGAAAACCTCAACICCGATGAAGTTGATCTTCTTATTCGCCTTCATAAGCTT	240
15S1080-cBrmyb2	TGAACACTATTTGAAGCCAAGTATCAAGAGAGGAAAACCTCAACICCGATGAAGTTGATCTTCTTATTCGCCTTCATAAGCTT	240
15S1084-cBrmyb2	TGAACACTATTTGAAGCCAAGTATCAAGAGAGGAAAACCTCAACICCGATGAAGTTGATCTTCTTATTCGCCTTCATAAGCTT	240
94S17-cBrmyb2	TGAACACTATTTGAAGCCAAGTATCAAGAGAGGAAAACCTCAACICCGATGAAGTTGATCTTCTTATTCGCCTTCATAAGCTT	240
Consensus	tgaactatTTGAAGCCAAGTATCAAGAGAGGAAAACCTCAACICCGATGAAGTTGATCTTCTTATTCGCCTTCATAAGCTT	
11S91-cBrMYB2	TTAGGAAACAGGTGGTCTTTAATTGCTGGTAGATTACCCGGICGGACCGCCAATGACGTCAAAAATTACTGGAACACCCA	320
14S838-cBrMYB2	TTAGGAAACAGGTGGTCTTTAATTGCTGGTAGATTACCCGGICGGACCGCCAATGACGTCAAAAATTACTGGAACACCCA	320
95T2-5-cBrMYB2	TTAGGAAACAGGTGGTCTTTAATTGCTGGTAGATTACCCGGICGGACCGCCAATGACGTCAAAAATTACTGGAACACCCA	320
Z33-cBrMYB2	TTAGGAAACAGGTGGTCTTTAATTGCTGGTAGATTACCCGGICGGACCGCCAATGACGTCAAAAATTACTGGAACACCCA	320
Z190-cBrMYB2	TTAGGAAACAGGTGGTCTTTAATTGCTGGTAGATTACCCGGICGGACCGCCAATGACGTCAAAAATTACTGGAACACCCA	320
Z240-cBrMYB2	TTAGGAAACAGGTGGTCTTTAATTGCTGGTAGATTACCCGGICGGACCGCCAATGACGTCAAAAATTACTGGAACACCCA	320
Chifu-cBrMYB2	TTAGGAAACAGGTGGTCTTTAATTGCTGGTAGATTACCCGGICGGACCGCCAATGACGTCAAAAATTACTGGAACACCCA	320
13S93-cBrmyb2	TTAGGAAACAGGTGGTCTTTAATTGCTGGTAGATTACCCGGICGGACCGCCAATGACGTCAAAAATTACTGGAACACCCA	320
13S1147-cBrmyb2	TTAGGAAACAGGTGGTCTTTAATTGCTGGTAGATTACCCGGICGGACCGCCAATGACGTCAAAAATTACTGGAACACCCA	320
15S1080-cBrmyb2	TTAGGAAACAGGTGGTCTTTAATTGCTGGTAGATTACCCGGICGGACCGCCAATGACGTCAAAAATTACTGGAACACCCA	320
15S1084-cBrmyb2	TTAGGAAACAGGTGGTCTTTAATTGCTGGTAGATTACCCGGICGGACCGCCAATGACGTCAAAAATTACTGGAACACCCA	320
94S17-cBrmyb2	TTAGGAAACAGGTGGTCTTTAATTGCTGGTAGATTACCCGGICGGACCGCCAATGACGTCAAAAATTACTGGAACACCCA	320
Consensus	ttaggaaacaggtggtctTTAATTGCTGGTAGATTACCCGGICGGACCGCCAATGACGTCAAAAATTACTGGAACACCCA	
11S91-cBrMYB2	TTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
14S838-cBrMYB2	TTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
95T2-5-cBrMYB2	TTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
Z33-cBrMYB2	TTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
Z190-cBrMYB2	TTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
Z240-cBrMYB2	TTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
Chifu-cBrMYB2	TTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
13S93-cBrmyb2	TTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
13S1147-cBrmyb2	TTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
15S1080-cBrmyb2	TTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
15S1084-cBrmyb2	TTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
94S17-cBrmyb2	TTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
Consensus	tttgagtaagaaacatgaaccgggttGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	

11S91-cBrMYB2	AAAAAATCGACGTTTTCAAACCTCGACCTCGATCCTTACCCETTAACAGCGGCTGCAGCCATAATAATGGCATGCCAGAA	480
14S838-cBrMYB2	AAAAAATCGACGTTTTCAAACCTCGACCTCGATCCTTACCCETTAACAGCGGCTGCAGCCATAATAATGGCATGCCAGAA	480
95T2-5-cBrMYB2	AAAAAATCGACGTTTTCAAACCTCGACCTCGATCCTTACCCETTAACAGCGGCTGCAGCCATAATAATGGCATGCCAGAA	480
233-cBrMYB2	AAAAAATCGACGTTTTCAAACCTCGACCTCGATCCTTACCCETTAACAGCGGCTGCAGCCATAATAATGGCATGCCAGAA	480
Z190-cBrMYB2	AAAAAATCGACGTTTTCAAACCTCGACCTCGATCCTTACCCETTAACAGCGGCTGCAGCCATAATAATGGCATGCCAGAA	480
Z240-cBrMYB2	AAAAAATCGACGTTTTCAAACCTCGACCTCGATCCTTACCCETTAACAGCGGCTGCAGCCATAATAATGGCATGCCAGAA	480
Chifu-cBrMYB2	AAAAAATCGACGTTTTCAAACCTCGACCTCGATCCTTACCCETTAACAGCGGCTGCAGCCATAATAATGGCATGCCAGAA	480
13S93-cBrmyb2	AAAAAATCGACGTTTTCAAACCTCGACCTCGATCCTTACCCETTAACAGCGGCTGCAGCCATAATAATGGCATGCCAGAA	480
13S1147-cBrmyb2	AAAAAATCGACGTTTTCAAACCTCGACCTCGATCCTTACCCETTAACAGCGGCTGCAGCCATAATAATGGCATGCCAGAA	480
15S1080-cBrmyb2	AAAAAATCGACGTTTTCAAACCTCGACCTCGATCCTTACCCETTAACAGCGGCTGCAGCCATAATAATGGCATGCCAGAA	480
15S1084-cBrmyb2	AAAAAATCGACGTTTTCAAACCTCGACCTCGATCCTTACCCETTAACAGCGGCTGCAGCCATAATAATGGCATGCCAGAA	480
94S17-cBrmyb2	AAAAAATCGACGTTTTCAAACCTCGACCTCGATCCTTACCCETTAACAGCGGCTGCAGCCATAATAATGGCATGCCAGAA	480
Consensus	aaaaaatcgacgTTTTCAAACCTCGACCTCGATCCTTACCCETTAACAGCGGCTGCAGCCATAATAATGGCATGCCAGAA	

11S91-cBrMYB2	GCTGGCATTGTTCCCTCTATGCCTTGGACACAACGATACTAAIAATGTTTCTGAAAAATAAATCACATGTAACAAAAGATGA	560
14S838-cBrMYB2	GCTGGCATTGTTCCCTCTATGCCTTGGACACAACGATACTAAIAATGTTTCTGAAAAATAAATCACATGTAACAAAAGATGA	560
95T2-5-cBrMYB2	GCTGGCATTGTTCCCTCTATGCCTTGGACACAACGATACTAAIAATGTTTCTGAAAAATAAATCACATGTAACAAAAGATGA	560
233-cBrMYB2	GCTGGCATTGTTCCCTCTATGCCTTGGACACAACGATACTAAIAATGTTTCTGAAAAATAAATCACATGTAACAAAAGATGA	560
Z190-cBrMYB2	GCTGGCATTGTTCCCTCTATGCCTTGGACACAACGATACTAAIAATGTTTCTGAAAAATAAATCACATGTAACAAAAGATGA	560
Z240-cBrMYB2	GCTGGCATTGTTCCCTCTATGCCTTGGACACAACGATACTAAIAATGTTTCTGAAAAATAAATCACATGTAACAAAAGATGA	560
Chifu-cBrMYB2	GCTGGCATTGTTCCCTCTATGCCTTGGACACAACGATACTAAIAATGTTTCTGAAAAATAAATCACATGTAACAAAAGATGA	560
13S93-cBrmyb2	GCTGGCATTGTTCCCTCTATGCCTTGGACACAACGATACTAAIAATGTTTCTGAAAAATAAATCACATGTAACAAAAGATGA	560
13S1147-cBrmyb2	GCTGGCATTGTTCCCTCTATGCCTTGGACACAACGATACTAAIAATGTTTCTGAAAAATAAATCACATGTAACAAAAGATGA	560
15S1080-cBrmyb2	GCTGGCATTGTTCCCTCTATGCCTTGGACACAACGATACTAAIAATGTTTCTGAAAAATAAATCACATGTAACAAAAGATGA	560
15S1084-cBrmyb2	GCTGGCATTGTTCCCTCTATGCCTTGGACACAACGATACTAAIAATGTTTCTGAAAAATAAATCACATGTAACAAAAGATGA	560
94S17-cBrmyb2	GCTGGCATTGTTCCCTCTATGCCTTGGACACAACGATACTAAIAATGTTTCTGAAAAATAAATCACATGTAACAAAAGATGA	560
Consensus	gctg c attgttccctctatgccttggacacaacgataactaaiaatgTTTTCTGAAAAATAAATCACATGTAACAAAAGATGA	

11S91-cBrMYB2	TGATAAATCTGAGCTTGTAGTCATTTAATGGATGGTCAGAATAGGTGGTGGGAAAAGTTTGCTAGATGAGAGCCAAGATC	640
14S838-cBrMYB2	TGATAAATCTGAGCTTGTAGTCATTTAATGGATGGTCAGAATAGGTGGTGGGAAAAGTTTGCTAGATGAGAGCCAAGATC	640
95T2-5-cBrMYB2	TGATAAATCTGAGCTTGTAGTCATTTAATGGATGGTCAGAATAGGTGGTGGGAAAAGTTTGCTAGATGAGAGCCAAGATC	640
233-cBrMYB2	TGATAAATCTGAGCTTGTAGTCATTTAATGGATGGTCAGAATAGGTGGTGGGAAAAGTTTGCTAGATGAGAGCCAAGATC	640
Z190-cBrMYB2	TGATAAATCTGAGCTTGTAGTCATTTAATGGATGGTCAGAATAGGTGGTGGGAAAAGTTTGCTAGATGAGAGCCAAGATC	640
Z240-cBrMYB2	TGATAAATCTGAGCTTGTAGTCATTTAATGGATGGTCAGAATAGGTGGTGGGAAAAGTTTGCTAGATGAGAGCCAAGATC	640
Chifu-cBrMYB2	TGATAAATCTGAGCTTGTAGTCATTTAATGGATGGTCAGAATAGGTGGTGGGAAAAGTTTGCTAGATGAGAGCCAAGATC	640
13S93-cBrmyb2	TGATAAATCTGAGCTTGTAGTCATTTAATGGATGGTCAGAATAGGTGGTGGGAAAAGTTTGCTAGATGAGAGCCAAGATC	640
13S1147-cBrmyb2	TGATAAATCTGAGCTTGTAGTCATTTAATGGATGGTCAGAATAGGTGGTGGGAAAAGTTTGCTAGATGAGAGCCAAGATC	640
15S1080-cBrmyb2	TGATAAATCTGAGCTTGTAGTCATTTAATGGATGGTCAGAATAGGTGGTGGGAAAAGTTTGCTAGATGAGAGCCAAGATC	640
15S1084-cBrmyb2	TGATAAATCTGAGCTTGTAGTCATTTAATGGATGGTCAGAATAGGTGGTGGGAAAAGTTTGCTAGATGAGAGCCAAGATC	640
94S17-cBrmyb2	TGATAAATCTGAGCTTGTAGTCATTTAATGGATGGTCAGAATAGGTGGTGGGAAAAGTTTGCTAGATGAGAGCCAAGATC	640
Consensus	tgataaactctgagcttgttagtcattttaatggatggtcagaataggtggTGGGAAAAGTTTGCTAGATGAGAGCCAAGATC	

11S91-cBrMYB2	CAGCTGCGCTCTTTCCAGAAACTACAGCAATAAAAAAGGGCCCAACCTCCCGGTTTGACGTTGAGCAACTTTGGAGCCTG	720
14S838-cBrMYB2	CAGCTGCGCTCTTTCCAGAAACTACAGCAATAAAAAAGGGCCCAACCTCCCGGTTTGACGTTGAGCAACTTTGGAGCCTG	720
95T2-5-cBrMYB2	CAGCTGCGCTCTTTCCAGAAACTACAGCAATAAAAAAGGGCCCAACCTCCCGGTTTGACGTTGAGCAACTTTGGAGCCTG	720
233-cBrMYB2	CAGCTGCGCTCTTTCCAGAAACTACAGCAATAAAAAAGGGCCCAACCTCCCGGTTTGACGTTGAGCAACTTTGGAGCCTG	720
Z190-cBrMYB2	CAGCTGCGCTCTTTCCAGAAACTACAGCAATAAAAAAGGGCCCAACCTCCCGGTTTGACGTTGAGCAACTTTGGAGCCTG	720
Z240-cBrMYB2	CAGCTGCGCTCTTTCCAGAAACTACAGCAATAAAAAAGGGCCCAACCTCCCGGTTTGACGTTGAGCAACTTTGGAGCCTG	720
Chifu-cBrMYB2	CAGCTGCGCTCTTTCCAGAAACTACAGCAATAAAAAAGGGCCCAACCTCCCGGTTTGACGTTGAGCAACTTTGGAGCCTG	720
13S93-cBrmyb2	CAGCTGCGCTCTTTCCAGAAACTACAGCAATAAAAAAGGGCCCAACCTCCCGGTTTGACGTTGAGCAACTTTGGAGCCTG	720
13S1147-cBrmyb2	CAGCTGCGCTCTTTCCAGAAACTACAGCAATAAAAAAGGGCCCAACCTCCCGGTTTGACGTTGAGCAACTTTGGAGCCTG	720
15S1080-cBrmyb2	CAGCTGCGCTCTTTCCAGAAACTACAGCAATAAAAAAGGGCCCAACCTCCCGGTTTGACGTTGAGCAACTTTGGAGCCTG	720
15S1084-cBrmyb2	CAGCTGCGCTCTTTCCAGAAACTACAGCAATAAAAAAGGGCCCAACCTCCCGGTTTGACGTTGAGCAACTTTGGAGCCTG	720
94S17-cBrmyb2	CAGCTGCGCTCTTTCCAGAAACTACAGCAATAAAAAAGGGCCCAACCTCCCGGTTTGACGTTGAGCAACTTTGGAGCCTG	720
Consensus	cagctgCGCTCTTTCCAGAAACTACAGCAATAAAAAAGGGCCCAACCTCCCGGTTTGACGTTGAGCAACTTTGGAGCCTG	

11S91-cBrMYB2	TTGGATGGAGAAACTGGAACCTG	743
14S838-cBrMYB2	TTGGATGGAGAAACTGGAACCTG	743
95T2-5-cBrMYB2	TTGGATGGAGAAACTGGAACCTG	743
233-cBrMYB2	TTGGATGGAGAAACTGGAACCTG	743
Z190-cBrMYB2	TTGGATGGAGAAACTGGAACCTG	743
Z240-cBrMYB2	TTGGATGGAGAAACTGGAACCTG	743
Chifu-cBrMYB2	TTGGATGGAGAAACTGGAACCTG	743
13S93-cBrmyb2	TTGGATGGAGAAACTGGAACCTG	743
13S1147-cBrmyb2	TTGGATGGAGAAACTGGAACCTG	743
15S1080-cBrmyb2	TTGGATGGAGAAACTGGAACCTG	743
15S1084-cBrmyb2	TTGGATGGAGAAACTGGAACCTG	743
94S17-cBrmyb2	TTGGATGGAGAAACTGGAACCTG	743
Consensus	ttggatggagaaactggaacttg	

d Multiple sequence alignment analysis of *gBrMYB2* between purple head Chinese cabbage ‘11S91’ and its female parent ‘94S17’. ‘95T2-5’ and ‘11S91’ had consensus genomic DNA sequence (gDNA).

11S91-gBrMYB2	ATGGAGGGTTCGTCCCAAGGTTGAAAAAGGTGCATGGACTGCTGAAGAAGATAATCTCTTGAGGCAATGCATTGATAAGTATGGAGAAGGGAAATGGC	100
94S17-gBrmyb2	ATGGAGGGTTCGTCCCAAGGTTGAAAAAGGTGCATGGACTGCTGAAGAAGATAATCTCTTGAGGCAATGCATTGATAAGTATGGAGAAGGGAAATGGC	100
Consensus	atggaggggttcgtcccaagggttgaaaaagggtgcatggactgctgaagaagataatctcttgaggcaatgcattgataagatggagaagggaaatggc	
11S91-gBrMYB2	ACCAAGTTCCTTTAAGAGCTGGTATGTC.....TTTTTTTTGATAACATAAGAGCTGGTATGCTACTTTTATAATTTT.....CACACACACACACACACATA	197
94S17-gBrmyb2	ACCAAGTTCCTTTAAGAGCTGGTATGTC.....TTTTTTTTGATAACATAAGAGCTGGTATGCTACTTTTATAATTTT.....CACACACACACACACACATA	200
Consensus	accaagttcctttaagagctggtatgtc.....ttttttttgataacataagagctggtatgctactttttataatttt.....cacacacacacacacacata	
11S91-gBrMYB2	TAACATAAAGTACGTATATTCITTTTATTTTTCAGTACATTTATTCITCTCTCTGTCTAGTATTAGGAAATTAATTAACACCCGGGTACACAATCA	297
94S17-gBrmyb2	TAACATAAAGTACGTATATTCITTTTATTTTTCAGTACATTTATTCITCTCTCTGTCTAGTATTAGGAAATTAATTAACACCCGGGTACACAATCA	300
Consensus	taacataaagtacgtatattctttttattttttcagtacatttattctctctctgtctagattaggaaattaattaacacccgggtacacaatca	
11S91-gBrMYB2	TTGTTTTCTTTTCGTTTTAATGAAGGAATCATAGATTCATATGTTCTAATGTTTTTCATG.....AAAAAAAACATTTCGCTTCTTCATGTTTAAATTACAAA	397
94S17-gBrmyb2	TTGTTTTCTTTTCGTTTTAATGAAGGAATCATAGATTCATATGTTCTAATGTTTTTCATG.....AAAAAAAACATTTCGCTTCTTCATGTTTAAATTACAAA	398
Consensus	ttgttttcttttcgttttaatgaaggaatcatagattcatatgttctaatgtttttcatg.....aaaaaaaacatttcgcttcttcatgtttaattacaaa	
11S91-gBrMYB2	GCGAGAAAATGCAACTCTCTTTATTGATTCGTCGTTTTCTTTTTTTTTTTGAGAAAAGAGCTTTTTTGATTAGTGAACTTTTCTGCACGAACCCGTGTG	497
94S17-gBrmyb2	GCGAGAAAATGCAACTCTCTTTATTGATTCGTCGTTTTCTTTTTTTTTTTGAGAAAAGAGCTTTTTTGATTAGTGAACTTTTCTGCACGAACCCGTGTG	498
Consensus	gcgagaaaatgcaactctctttattgattcgtcgttttctttttttttgagaaaagagcttttttgattagtgaacttttctgcacgaacccgtgtg	
11S91-gBrMYB2	TTTGTGGAATATGTTGTTTATTTCGGTGTACTTTGATCCTTC.....TGATAAAAATTTACTTCCTTTGTT.....TTAAATATAAGATATTTTGGTAGAAGCA	597
94S17-gBrmyb2	TTTGTGGAATATGTTGTTTATTTCGGTGTACTTTGATCCTTC.....TGATAAAAATTTACTTCCTTTGTT.....TTAAATATAAGATATTTTGGTAGAAGCA	598
Consensus	tttgtggaatatgttgttttatttcgggtgtactttgatccttct.....tgataaaaatttacttccctttgtt.....ttaaataaagatattttggtagaagca	
11S91-gBrMYB2	CATATTAAGAAAACATTTTTTGTCTAGAAAATATCATTAAAACATAAAATTAATGGTGTTCACCAATTACAAAATAGACTATTAATAATGATTGGGT	697
94S17-gBrmyb2	CATATTAAGAAAACATTTTTTGTCTAGAAAATATCATTAAAACATAAAATTAATGGTGTTCACCAATTACAAAATAGACTATTAATAATGATTGGGT	698
Consensus	catattaagaaaactatfttttgttctagaaaatcattaaaactataaaatggtgttcaaccaattacaaaatagactatataaatgatgggt	
11S91-gBrMYB2	TCACAGTTTTTAATAAAGTAAAAGTTACCTAGAAAATGAAAACATTTTATA.....	749
94S17-gBrmyb2	TCACAGTTTTTAATAAAGTAAAAGTTACCTAGAAAATGAAAACATTTTATA.....TCTAATACTATAAAGAAGACTATTCTCTCTCTCAGCTTGCCACGTC	798
Consensus	tcacagtttttaataaagttaaagttacctagaaaattgaaaacatftttata.....	
11S91-gBrMYB2	749
94S17-gBrmyb2	ACTGAATCGAATTCCTAACATGCGACACGTGTTTCGTGCTCATGTTATACTCTGCGTTTCATTAAAGCTTGATGTGGGCTGGTGTTCGAATTACGGTTTT	898
Consensus	
11S91-gBrMYB2	749
94S17-gBrmyb2	GATACATATGGATCTCAATAATAATAGGCCATTTCAAATCATGAGAGATGCAAGCCGATTAGGGTTTCTGCTCTTCTTCTCATCGACCAAAAACA	998
Consensus	
11S91-gBrMYB2	749
94S17-gBrmyb2	GTTCCCAAAACAAAATGATGGGATTTTCGAGGTATCTCTTTGTTGATCTTCGATGGCCTCGTTCTGGTTACTCTCCTAATTAGATGAAACGCTCCAAGTT	1098
Consensus	
11S91-gBrMYB2	749
94S17-gBrmyb2	ACAGATCCATAGCCTTTATGACCTCTTAACCTCAAAGACCGAAATGAGGCACGATCTGACGTTGAATGCGAGTTTACTCTCTGTGAGGCGGTGTAATCT	1198
Consensus	
11S91-gBrMYB2	749
94S17-gBrmyb2	ACACAATATAAAGGTTAGCATCCTCCCTTGAACATCATCCTCGAAATCTAATAAAAACITCAAGGTAGTAGCTTTTGTGTTGATGTTTATCAAACCTCTA	1298
Consensus	
11S91-gBrMYB2	749
94S17-gBrmyb2	GGTTTTGTTGGTTCTTTGCTTTCTATTCTCTCCCAAGATCGTTAGATAAACATTTCCGGATCGCTTTTGATAATTTTTTTGTTCTTATCTACAGTT	1398
Consensus	
11S91-gBrMYB2	749
94S17-gBrmyb2	GGCTCAACACAAGCCACATGGTGTGGAAGATCTTTTACAACAGTCGTTCACTGTGAACCGGGGATTTTCGGAAGGCTATGGCAAAGATTCTGTGTGAGGA	1498
Consensus	
11S91-gBrMYB2	749
94S17-gBrmyb2	GATGAGTTGAGATGAGGATGAGAGTCTTACTTTTCTTTTGAAGAAATGATTGACGGTTCAAGACAATTAATCCATTAGCGCCCGCAACCTGTGGGAAG	1598
Consensus	
11S91-gBrMYB2	749
94S17-gBrmyb2	AGCTTTCGTAGTGTGTTTGTGTTTACTCGCCGGTGGCGTTGCGGAAGTTCAATTCATCGGCACCGTTTAAATGGCAACACCGACTCACTTCATCTCATCTCT	1698
Consensus	
11S91-gBrMYB2	749
94S17-gBrmyb2	TTGGGACGACACTCGCCCGTGGTAACATGCTTCTTATTGTCGGTGTGGTGACGTCAGCCTCTCCACACATTCAAACCGATGTTATTGACAATCAAAT	1798
Consensus	

11S91-gBrMYB2	749
94S17-gBrmyb2	ATTATGCAGCCTTTCTCAACATACAGAGCTTCCATAGTATTGTTAAATCTTAATCATGTCTGAGGATACCATCACCGTCCCTCTCAGCTGCTGGAAT	1898
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	GTACTCAGCTTGGTTGGATGGAGCGTCTGCTTGGCTGGAATTCAGAAAATCTGCTCCAAAGGAACCTGTCTGAACGTCATGATGCCTTTGGCCAAGAA	1998
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	TTATAACATGGTGGCTGATCCAAGAAATACCTGACATTCGAATCTTCTTAAGAGCACCAGATGTAAACATGTGACGAGGTGTCAAAGCTCTTCTAGATT	2098
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	GTAAGATTGGTCTCCATTGTTGTTTACTTAGGGTAAAGTTCTATTGCTTTGATCACTTCAACTTGCAAAATAGTGTAAACGGAACACATTCTATG	2198
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	CACIAATCTTATTCCATCATTCTTACTCCACTAATCAAGTTCAGTCCACGACTATTTATCATCCAGGAATCAAGTCTATTGTTAAATATAT	2298
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	TTGGAATCAGACAGCCAAAGCTATCCACAAATTTATGAACAATCTCTTCAAGACAAACTTATAATACACTGCCACTTTCAAAAATGTTTTGTGTA	2398
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	CACITCTTTGGACAGACGAAAATATGACCGTCTTATTAATGGTAAGTCTGGCTCAAACCAAGCATCAATGCCATCACGTTCTCTCTTATTATCTGA	2498
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	AAGGAGCAAGAGGAAAGCAGTTGTAGCACAGTCATGTTCCAGCTCCATATTTACAGAAAGCCATCATTGCCGAGTTGAGTTGCAGTATTGTGTAAGAT	2598
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	TTCTAACCCAGGAGTTTAGTGTGGAAAAATATAATTGGAGTGCAGTGTITATACCGAAAAGTCTCAGGCAGAGATATTGTGTAGTCTAAATGTCAT	2698
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	AAAAGGACAGAAAATATAGTAGTGAATCTGTTTTTTGTGCCAGTTATATCTCCGACTGTAGCTTGAAGAGCAAACTATCTAAGAGAGGTGAGATTG	2798
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	GTTTTAATCTGCCATTTCTGGAGAGTTGTGAAGATGTTGAAGAGAGCAAGGTGAAGAAATGTATTGCTCACGCTGGGTTGTAAGAGACAGTCTTAGCTA	2898
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	TTGGTTCTGATTCAGATTTTTCAGCTGCAAAATCTCAGACCGGTTTCTAAACCCAAAACAGCCITTTGGAAGACTTCTTTTTGTGTGTTCTCCTG	2998
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	GCGGTGATGGGCTACGGATCGCTGTGGTGACAGTGCAAAGGGGAGTGTGTGCGGGTGTATCAATCAATACTATAACAATCTTTGCTTACAAAGCTG	3098
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	TGTAAAGTATATTGTTATTATATAATGGTAAAAGAGTCGAAGTTGATGCTCAGTGGAGGAAATGAAGTAATGGAAAAAACTCCACTAGATGCAAGA	3198
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	AACAATAGTTTTCTAAGTAGCGTTGAAATATTATCAATAAAAATAAAAAGTATATAACAAACAATGTTTATTGATAAGATTCTAAACAATAAAGAGTGT	3298
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	TAAAGATTCGGCAAATAAATATTAGAAATGATCATGATACAAAATAITGCAAAGTTTTTTTTTTTTTTTGTCTAAAAGTAAATGTGTTGTGTTGATTTA	3398
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	AAATATTGCAAAGTTGTTATGAAAAATGTAATATCTGAAGATACCATCGAAAACAITTAAACAITTAAATTTTAAACACATTTCCAACAGTTAAAAATATCA	3498
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	ATTATCTTATATATAAATGAATATGCTACGCAAAAAATGTACAATAATCTTTTTATCAGCTACAGAAAACAGTTATGAAATTTTGTAAACAACATCAA	3598
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	ATGTATTATTAACCGAAAGTCAACATTTTATCTATTAATAAAGTATTATACATGCTTATCAACGTCCTACCACAAATTATAACTAATTAATCAAGTTGA	3698
Consensus		

11S91-gBrMYB2	749
94S17-gBrmyb2	AGCCAATATCTAATACTCAATATTTCTTTGTTCCAAAATCTTAATAATAAAAAATGAAAAATATTAGCAAAACATTGTTTACTTTTAATTTATTTTGA	3798
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	ATTATTTAGTATTAGTTAAGTTTATTAATAATTTAATTTGATATTGTAATTTGAATATATACAATCAAATACACATTTTTAAAAAATAGATGAAAGTA	3898
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	TTTTTAAACACGATATGTTACCTAATAAATATGCAAAAAATCATAATGATAAATTTTTAAAAATAAAAAAGCAATTAATGTTATGTAGATTTATTA	3998
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	TTTATTTATTTATGTCATTGAGATAAAAAATATAGCAAAAGGTGTAATAATTTTCATAATATATACTAGAAAAATTATATGCATCATTAAATATATATTA	4098
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	AAAACTAATTTAAATTTTATAAACAATAAAATATAAATTTGAAAGTAGTTTATATAAATGAATAAAATATACAAAATTATAGTTAATTTAAATTAATAATG	4198
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	ATATGAAAAATAAAATATGCTTTACATAATCGAACAAAGAAAAAATATAAAATAGTCTGACAACAAACAAAGATAGAAGAAATGAAATTAGTTGATTT	4298
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	ATACGAAACAAATAAGTTAAAAATATATATACTAACATAATAAAAAATATAATACAATATTTAAAAATCACAATAATTTGATTAGAAACCTACTAAATAG	4398
Consensus		
11S91-gBrMYB2	749
94S17-gBrmyb2	TAACAAAACCTGACTTGAAAGAAAAACAATTTAAAAAATAATGACCTGGATAAAAATAATCATTTTAAAAACAAAAATTTAAAAAATTTTAAATTTCCGCC	4498
Consensus		
11S91-gBrMYB2	823
94S17-gBrmyb2TATTGGATAATTAAACATCAAAA..TTCAATAAAACATCCTATTTTTAGGAACATATGGAGTAGGAGACGGCAAT	4598
Consensus	gccccgtaggcgggtttactctagttattggataattgaaacatcaaaaatttcacgtaaaaacatcctatTTTTAGGAACATATGGAGTAGGAGACGGCAAT	
11S91-gBrMYB2	923
94S17-gBrmyb2	GCAGTTTTGCTCGTCTTTAATAATATTAATGTCAATTTATTGGTTTTGTAGGCTAAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGTTGAAC	4698
Consensus	gcagttttgctcgtctcttttaataatattaaatgtcaattattggttttgttaggtctaaaatcggtgcaggaagagttgttagactaagatggttgaacta	
11S91-gBrMYB2	1023
94S17-gBrmyb2	TTTGAAGCCAAGTATCAAGAGAGGAAAACTCAACTCCGATGAAGTTGATCTTCTTATCGCCTTCATAAGCTTTTAGGAAACAGGTTTACATTCCAGACA	4798
Consensus	tttgaagccaagtattcaagagagggaaaaactcaactccgatgaagttgatctctctatcgcttcataagcttttaggaaacaggtttacattc agaca	
11S91-gBrMYB2	1122
94S17-gBrmyb2	CAAATTCAACTGTATTTTCGTATCCTCATTCCGCTAATCTAATCATTTGATTTGTTTTTTTTTTGATAAAAA..TACTTAAATTTATTTTCATATGTAAT	4898
Consensus	caaatccaactgtatcttctgatctcctcattccggtcctaatcctaatcatttgatttggTTTTTTTTTTGATAAAAA..tacttaaatTTATTTTCATATGTAAT	
11S91-gBrMYB2	1222
94S17-gBrmyb2	GATCCATTACTAAGTCAAATATATCCCTAATTTTTCAAATGCATGCTTAGGTGGTCTTAAATGCTGGTAGATTACCCGGTCGGACCGCCAATGACGTCA	4998
Consensus	gatccattactaagtcaaatatataccctaatttttcaaatgcatgcttaggtggctcttaattgctggtagattaccggctcggaccgccaatgacgtca	
11S91-gBrMYB2	1322
94S17-gBrmyb2	AAAATTACTGGAACACCCATTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCCA	5098
Consensus	aaaattactggaacacccatttgagtaagaaacatgaaccgggttgaagaccagatgaaaaagagaaacattccttgctcttataccacaccagccca	
11S91-gBrMYB2	1422
94S17-gBrmyb2	AAAAATCGACGTTTTCAAACCTCGACCTCGATCCTTCACCGTTAACAGCGGCTGCAGCCATAATAATGGCATGCCAGAAGCTGCATTGTTTCCTCTATGC	5198
Consensus	aaaaatcgacgTTTTCAAACCTCGACCTCGATCCTTCACCGTTAACAGCGGCTGCAGCCATAATAATGGCATGCCAGAAGCTGCATTGTTTCCTCTATGC	
11S91-gBrMYB2	1522
94S17-gBrmyb2	CTTGGACACAACGATACTAATAATGTTTCTGAAAAATAATCACATGTAACAAAGATGATGATAAATCTGAGCTTGTAGTCATTAAATGGATGGTCAGA	5298
Consensus	cttggacacaacgataactaataatgTTTCTGAAAAATAATCACATGTAACAAAGATGATGATAAATCTGAGCTTGTAGTCATTAAATGGATGGTCAGA	
11S91-gBrMYB2	1622
94S17-gBrmyb2	ATAGGTGGTGGGAAAGTTTGTAGTAGAGGCCAAGATCCAGCTGCGCTCTTTCCAGAACTACAGCAATAAAAAAGGGCGCAACCTCCCGGTTTGACGT	5398
Consensus	ataggtggtgggaaagtttGTAGTAGAGGCCAAGATCCAGCTGCGCTCTTTCCAGAACTACAGCAATAAAAAAGGGCGCAACCTCCCGGTTTGACGT	
11S91-gBrMYB2	1664
94S17-gBrmyb2	TGAGCAACTTTGGAGCCTGTGGATGGAGAAACTGGAACCTG	5440
Consensus	tgagcaactttggagcctgtggatggagaaactggaacttg	

chr1-fu-gbMY82 4196
13939-gbmy82 4197
1351147-gbmy82 4197
1551080-gbmy82 4197
1551084-gbmy82 4197
14938-gbMY82 749
15891-gbMY82 749
14938-gbMY82 749
9572-5-gbMY82 749
233-gbMY82 749
2190-gbMY82 749
2240-gbMY82 749
Consensus

chr1-fu-gbMY82 4397
13939-gbmy82 4397
1351147-gbmy82 4397
1551080-gbmy82 4397
1551084-gbmy82 4397
14938-gbMY82 749
15891-gbMY82 749
14938-gbMY82 749
9572-5-gbMY82 749
233-gbMY82 749
2190-gbMY82 749
2240-gbMY82 749
Consensus

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13939-gbmy82 4596
1351147-gbmy82 4596
1551080-gbmy82 4596
1551084-gbmy82 4596
14938-gbMY82 821
15891-gbMY82 821
14938-gbMY82 821
9572-5-gbMY82 821
233-gbMY82 821
2190-gbMY82 821
2240-gbMY82 821
Consensus

chr1-fu-gbMY82 4611
13939-gbmy82 4796
1351147-gbmy82 4796
1551080-gbmy82 4796
1551084-gbmy82 4796
14938-gbMY82 1021
15891-gbMY82 1021
14938-gbMY82 1021
9572-5-gbMY82 1021
233-gbMY82 1021
2190-gbMY82 1021
2240-gbMY82 1021
Consensus

chr1-fu-gbMY82 4810
13939-gbmy82 4995
1351147-gbmy82 4995
1551080-gbmy82 4995
1551084-gbmy82 4995
14938-gbMY82 1219
15891-gbMY82 1219
14938-gbMY82 1219
9572-5-gbMY82 1219
233-gbMY82 1219
2190-gbMY82 1219
2240-gbMY82 1219
Consensus

chr1-fu-gbMY82 5010
13939-gbmy82 5195
1351147-gbmy82 5195
1551080-gbmy82 5195
1551084-gbmy82 5195
14938-gbMY82 1419
15891-gbMY82 1419
14938-gbMY82 1419
9572-5-gbMY82 1419
233-gbMY82 1419
2190-gbMY82 1419
2240-gbMY82 1419
Consensus

chr1-fu-gbMY82 5210
13939-gbmy82 5395
1351147-gbmy82 5395
1551080-gbmy82 5395
1551084-gbmy82 5395
14938-gbMY82 1619
15891-gbMY82 1619
14938-gbMY82 1619
9572-5-gbMY82 1619
233-gbMY82 1619
2190-gbMY82 1619
2240-gbMY82 1619
Consensus

chr1-fu-gbMY82 5255
13939-gbmy82 5440
1351147-gbmy82 5440
1551080-gbmy82 5440
1551084-gbmy82 5440
14938-gbMY82 1664
15891-gbMY82 1664
14938-gbMY82 1664
9572-5-gbMY82 1664
233-gbMY82 1664
2190-gbMY82 1664
2240-gbMY82 1664
Consensus

Figure S3 Multiple sequence alignment analysis of BrMYB2 in different Chinese cabbages.

‘11S91’ and ‘95T2-5’ had consensus BrMYB2 sequences, whereas ‘Chifu’ and ‘94S17’ had consensus BrMYB2 sequences.

BrMYB2-94S17.txt	MEGSSQGLKKGAWTAEEDNLLRQCIDKYGEGKWHQVPLRA	40
BrMYB2-11S91.txt	MEGSSQGLKKGAWTAEEDNLLRQCIDKYGEGKWHQVPLRA	40
Consensus	meggssqglkkgawtaeednllrqcidkygegkwhqvplra	
BrMYB2-94S17.txt	GLNRCRKSCRLRWLNLIKPSIKRGKLNSEVDLLIRLHKL	80
BrMYB2-11S91.txt	GLNRCRKSCRLRWLNLIKPSIKRGKLNSEVDLLIRLHKL	80
Consensus	glnrcrkscrlrwnlylkpsikrgklnsdevdllrlhkl	
BrMYB2-94S17.txt	LGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHEPGCKTQM	120
BrMYB2-11S91.txt	LGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHEPGCKTQM	120
Consensus	lgnrwsliagrlpgrtandvknywnthlskkhepgcktqm	
BrMYB2-94S17.txt	KKRNI PCSYTTPAQKIIVFKPRPRSFTVNSGC SHNNGMPE	160
BrMYB2-11S91.txt	KKRNI PCSYTTPAQKIIVFKPRPRSFTVNSGC SHNNGMPE	160
Consensus	kkrnipcsyttpaqkidvfkprprsftvnsgcshnngmpe	
BrMYB2-94S17.txt	ADIVPLCLGHNDTNNVSENIITCNKDDDKSELVSHLMDGQ	200
BrMYB2-11S91.txt	ADIVPLCLGHNDTNNVSENIITCNKDDDKSELVSHLMDGQ	200
Consensus	aivplclghndtnnvseniitcnkdddkselvshlmdgq	
BrMYB2-94S17.txt	NRWESLLDESQDPAALFPETTAIKKGATSAFDVEQLWSL	240
BrMYB2-11S91.txt	NRWESLLDESQDPAALFPETTAIKKGATSAFDVEQLWSL	240
Consensus	nrweslldesqdpaalfpettaikkgatsafdveqlwsl	
BrMYB2-94S17.txt	LDGETG	246
BrMYB2-11S91.txt	LDGETG	246
Consensus	ldgetg	

Figure S4 Electrophoresis results of *gBrMYB2* from different phenotypes of Chinese cabbage and co-segregation analysis using markers ‘BrP1’ and ‘BrP2’ in the F₂ population. **a** Electrophoresis results of *gBrMYB2* from purple head Chinese cabbage ‘11S91’, and its female parent ‘94S17’ and male parent ‘95T2-5’; **b** electrophoresis results of *gBrMYB2* from different phenotypes of Chinese cabbage; **c** co-segregation analysis using marker ‘BrP1’ in the F₂ population; **d** co-segregation analysis using marker ‘BrP2’ in the F₂ population. W: white head Chinese cabbage; P: purple head Chinese cabbage; H: hybrid Chinese cabbage. M1: DL2000 Marker; M2: DL10000 Marker; M3: DL5000 Marker.

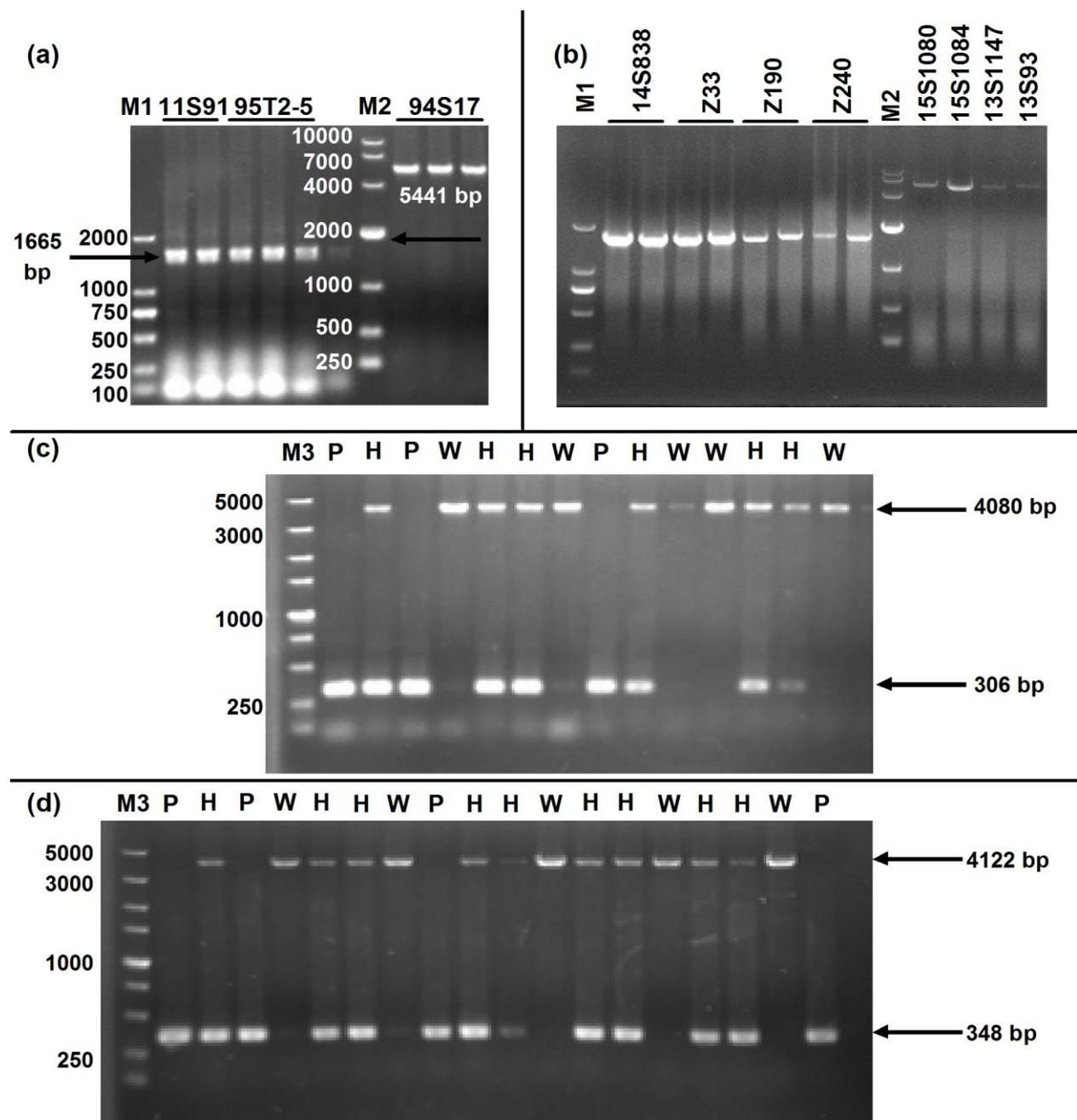


Figure S5 Multiple sequence alignment analysis of MYBs in different *Crucifer* species. At: *Arabidopsis*; Bo: *B. oleracea*; Br: *B. rapa*; Rs: *Raphanus sativus*. Arrowheads indicate differential proteins produced by SNPs between purple head Chinese cabbage ‘11S91’ and its female parent ‘94S17’.

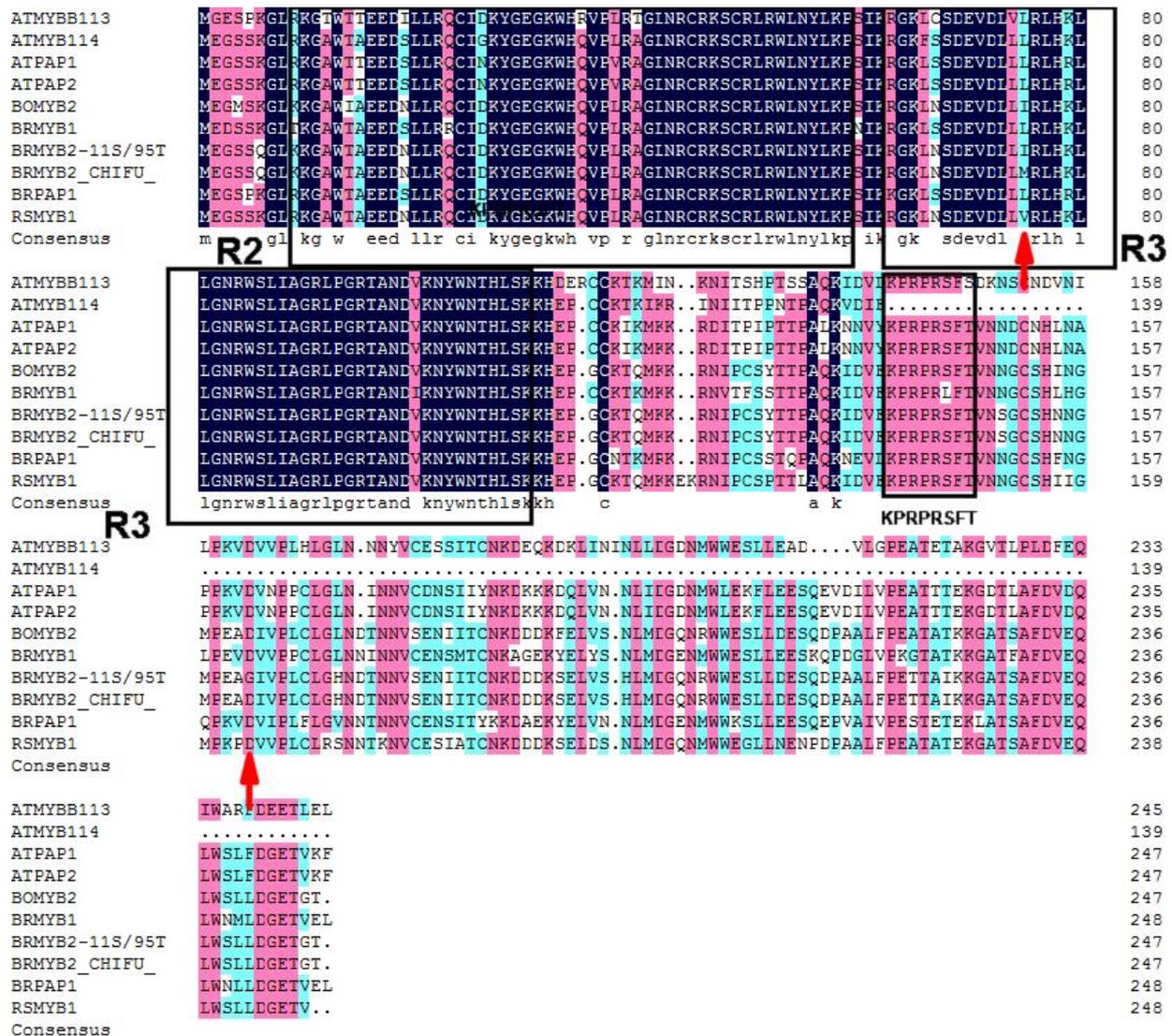


Figure S6 Multiple sequence alignment analysis of MYBs in different *Solanaceae* species.

CAA	MNTAIIAKSSGVRKGAWTEEEIFLLRKC IQNYGEGKWHIV	40
LEANT1	MNST.SMSSILGVRKGSWTDEEIFLLRKCIDKYGEGKWHIV	39
NTAN2	MNICTNKSSSGVKKGAWTEEEIVLLKKCIEKYGEGKWHQV	40
PHAN2	MSTS.NASTSGVRKGAWTEEEIILLRECIDKYGEGKWHIV	39
SMMYB	MNTA.TVAKSGVRKGAWTD.....RKCMKYG.GKWHVT	32
Consensuum	gv kg wt c yg gkwh	
CAA	PIRAGLNRCRKSCRIRWLNLYLRFHIKRGDFGWDEIDLILR	80
LEANT1	PIRAGLNRCRKSCRIRWLNLYLRFHIKRGDFEQDEVDLILR	79
NTAN2	PLRAGLNRCRKSCRIRWLNLYLRFHIKRGDFSFLVDLILR	80
PHAN2	PVRAGLNRCRKSCRIRWLNLYLRFHIKRGDFSLEVDLILR	79
SMMYB	..RSG.NRCRKSCR.RWN...YRHIKRGDADID.....	58
Consensus	r g nrcrkscr rw hikrgd d	
CAA	LHKLLGNRWSLIAGRLPGRTANDVKNYWNSHLQKKLIITAP	120
LEANT1	LHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKKINTTK	119
NTAN2	LHKLLGNRWSLIAGRLPGRTANDVKNYWNSHLRKKLIAPH	120
PHAN2	LHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLRKKLIAPH	119
SMMYB	.IRHKNRWSIAG....RRTANDVKNYWNTHIKKTNSRMR	93
Consensus	gnrws rtandvknywn	
CAA	HRQE.KKYNTALKITT.KNVIKPRPRPTFSSSAKNNISWCT	158
LEANT1	IVPREKINNKCGEISTKIEIKKQRRKYFSSSTMKN...VT	156
NTAN2	DQK..ESKQKAKKIT....IEPRPRPTFSKTNT....CV	149
PHAN2	DQKQ.ESKKNKAVKITE.NNIIKPRPRPTFSRPAMNMF.PCW	156
SMMYB	KHN....NAKIKNT.....IBRRITSSAKNVS...WCT	119
Consensus	r [K/R]PRPRPTFS	
CAA	NKSTVITNTLDKD.ERDKETGINICQKLTSETSSITDDGV	197
LEANT1	NN....NVILDEE.EHCKE...ISE..KQTPDASMDNVD	186
NTAN2	KS...NTNTVDKDIEGSSEI.IRFNDNLKPTTEELTDDGI	185
PHAN2	NGKSCNKNTIDKN.EGDTEI.IKFSD.EKQKPEESIDDL	193
SMMYB	NKN...MNITNTDKINRHKIGVNTCK.KGDATSSSIDDDG	155
Consensus	i d	
CAA	QWWTSLLENC.KEIEEDVAAVGIFEKKNKLVPSLLHDEIN	236
LEANT1	FWWINLLENCNDDIEEDEE...VVINYKTLTSLHHEEIS	223
NTAN2	QWADLLANN.YNNG.....IEEADNSSPTLLHEEMP	217
PHAN2	QWANLLANN.IEIEE.....LVSCN..SPTLLHEETA	223
SMMYB	VWWTSNCNIAAVSNK.....NHNNSMGNDGWLLSVD	187
Consensus	ww	
CAA	SLT.....MQQGQSDGW.....DDF	251
LEANT1	PFLNIGEGNSMQGQI SHENWGEFSLNLPQMGGVQNDDF	263
NTAN2	LLS.....	220
PHAN2	PSVNAE..SSLTQGGGSGL.....SDF	243
SMMYB	IDWNN.....	192
Consensus		
CAA	SADID.IWNLL	261
LEANT1	SAEID.IWNLL	273
NTAN2	220
PHAN2	SVDIDDIWDLV	254
SMMYB	192
Consensus		

Figure S7 Prediction of elements of *BrMYB2* promoter in 11S91. Sequence marked with different color was in accordance with element showing in figure statement, and figure mainly showed results at the upstream region of 1500 bp started from ATG translation start site.

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>userseq1980 1499nt
+ CTAAGTTTGA AAATCTGCAG ATGGATGAGA ATTAATCATT TGAGGAAGCTC AGTGAAAAAC TGAGTGCAAC
- GATTCAAACT TTTAGACGTC TACCTACTCT TAATTAGTAA ACTCCTTGAG TCACCTTTTG ACTCACGTTG

+ AGCAAATGAA GCACAAACAA TGGGAAAGAC ATACAAAGAC AAAAGGCTTG GAAGAAACTT CTCAGATGTT
- TCGTTTACTT CGTGTPTGTT ACCCTTTCTG TATGTTTCTG TTTTCCGAAC CTTCTTTGAA GAGTCTACAA

+ TACCCTCAAA GTTAAATCCA AGAAGACAGC TATGGACACT GCATTAGACA CTGACACAAT GGATTTTGGT
- ATGGGAGTTT CAATTTAGGT TCTTCTGTCG ATACCTGTGA CGTAATCTGT GACTGTGTTA CCTAAAACCA

+ GAATTCACGG GTCACTTACA AGCATATGAG ATGAATGAGA AACTCAAGGA AGAACTGTCT AAAAAAATCT
- CTTAAGTGCC CAGTGAATGT TCGTATACTC TACTTACTCT TTGAGTTCCT TCTTGACAGA TTTTTTTAGA

+ GAAACTAGAA AGCAGATTCA CATGCTGAAT AGTGGAAACCA AGGATCTGGA GAAGATTCTC TCTGTTAGAA
- CTTTGATCTT TCGTCTAAGT GTACGACTTA TCACCTTGGT TCCTAGA GCTTCTTAAGAG AGACAATCTT

+ GGGTAGGCAA GTCCAACCTT GTGTCTCGGT TACAGTGGAA AACTACAGTA AAACAGAGTT TGTTCGGCT
- CCCATCCGTT CAGGPTGAAA CACAGAGCCA ATGTCACCTT TTGATGTCAT TTTGTCTCAA ACAAGGCCGA

+ AAGACTTAAG AGATTGCGTC TGATACTACA GGAAGTAAGA TATCAACCAA GATCATCTAT TGTGAAACTG
- TTCTGAATTC TCTAACGCAG ACTATGATGT CCTTCATTCT ATAGTTGGTT CTAGTAGATA ACACTTTGAC

+ AAACCAGTGA GAACTATAAT GTAGGCTACT TCTGTGGTAA ATACATGCAC ATACCAAGAT AACTTTACAA
- TTTGGTCACT CTTGATATTA CATCCGATGA AGACACCATT TATGTACGTG TATGGTTCTA TATGAATGTT

+ ATTTCAAAAA AGAATCACTT CAAGTTGAC TTTGCTTTCC AATCTTTACA GGTTTAACGT TAAATATGAA
- TAAAGTTTTT TCTTAGTGAG GTCTCAACTG AAACGAAAGG TTAGAAATGT CCAAATGCA ATTTATACTT

+ ATTTGTAGTC AAACGATTAT GATGGATTTC ATCAAATCTT ATTGTTTTAA TATCAAATGA GGTTCAAGTT
- TAAACATCAG TTTGCTAATA CTACCTAAAG TAGTTTAGAA TAACAAAATT ATAGTTTACT CCAAGTTCAA

+ ACATATTTCT GAACTGCTA GCCAAAAGTA CATACTCACA ATGTGAGACA CTTTAAATAC GGAACAATTT
- TGTATAAAGA CTTGAGGGAT CGGTTTTTCAT GTATGAGTGT TACTACTCTGT GAAATTTATG CCTTGTAA

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+ GCAAAATAGT GATTTGTGTA CTCATAATTA TTGTAGCTGA TTTTGTGCTA CATACTTGTG TTGACAGAAA
- CGTTTATCA CTAAACACAT GAGTATTAAT AACATCGACT AAAAACAGAT GTATGTGAAC AACTGTCTTT

+ AACAAATACGC TACTTATCAA GTTGTGTACT CATAATCAA CCCTCTGTCCT CTCTCTCTCT CTCTCTCTCT
- TTGTTATGCG ATGAATAGTT CAACACATGA GTATGTAGTT GGGAGACAGA GAGAGAGAGA GAGAGAGAGA

+ CTCCTCTCTCT CTCCTCTCTCT CTCTCTCTCT CTCCTCTCTCT CTCCTCTCTCT CTCTCTCTCT CTCCTCTCTCT
- GAGAGAGAGA GAGAGAGAGA GAGAGAGAGA GAGAGAGAGA GAGAGAGAGA GAGAGAGAGA GAGAGAGAGA

+ CTCCTCTCTCT CTCCTCTCTCT CTATTCTGTT TTTAACTCTG GTGCATGAAG CTGTTCTCTC TTTTAATCAT
- GAGAGAGAGA GAGAGAGAGA GATAAGACAA AAATFGAGAC CACGTACTTC GACAAGAGAG AAAATTAGTA

+ ATAAACCACC TTTCCACCAA TCATTAATCG TCCTTTCTGC TAACTTTGCT AAGAGGCATG TTTTTCCTTT
- TATTTGGTGG AAAGGTGGTT AGTAATTAGC AGGAAAGACG ATTGAAACGA TTCTCCGTAC AAAAAGGAAA

+ AAAGTACTGA AAAATATGAA GAGACTAAGT GATATGCTAT GCTATGACGA AAATGGACTA AGTGCTATGA
- TTTCATGACT TTTTATACTT CTCTGATTCA CTATACGATA CGATACTGCT TTTACCTGAT TCACGATACT

+ ACCTTTCTG TATTTAGTTT GAATCAGTAG CAGAACATAA ATAACATAAT TAGCAAATTA GACACGACAA
- TGGAAAAGAC ATAAATCAA CTTAGTCATC GTCTTGATT TATTGATTTA ATCGTTTAAAT CTGTGCTGTT

+ AATGTGCTAT GAACCTTTTT TGTTTCTGCA TCGTACCCTG GAAGTGTGTA AAAAAAAGA CACGACAAA
- TTACACGATA CTTGGAAAA ACAAGCGT AGCATGGGAC CTTCAACAAT TTTTTTTTCT GTGCTGTTTT

+ ATGFGGATGT TAGACATGCA CGTCACTTCT CTTTGCCCGT CACGTGTATA AATAAAGTCC TCGAAGGATT
- TAGACCTACA ATCTGTACGT GCAGTGAAGA GAAACGGGCA GTGCACATAT TTATTTCCAGG AGCTTCCTAA

+ TGTCAAGCCA CAATAGAAAC CCTTTTCCTC AAGCCTGCCT TTACGTATAA CTTTTTAAAA TAAAATTTGG
- ACAGTTCGGT GTTATCTTTG GGAAAAGGAG TTCGGACGGA AATGCATAT GAAAAATTTT ATTTTAAACC

+ TTAGATACTT CTAAAATTAT AGCTGGTCC
- AATCTATGAA GATTTTAATA TCGACCAGG

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+		5UTR Py-rich stretch
+		ABRE
+		AE-box
+		ARE
+		Box 4
+		Box I
+		CAAT-box
+		CGTCA-motif
+		CTAG-motif
+		ERE
+		G-Box
+		G-box
+		GA-motif

Figure S9 Results of PCR screening on T₁ and T₃ homozygous transgenic *Arabidopsis*. **a** T₁ CaMV35S:*cBrMYB2* lines detected by *BrMYB2* clone primer; **b** T₁ CaMV35S:*cBrmyb2* lines detected by *BrMYB2* clone primer; **c** T₃ transgenic lines detected by *BrMYB2* clone primer. M: DL2000 Marker.

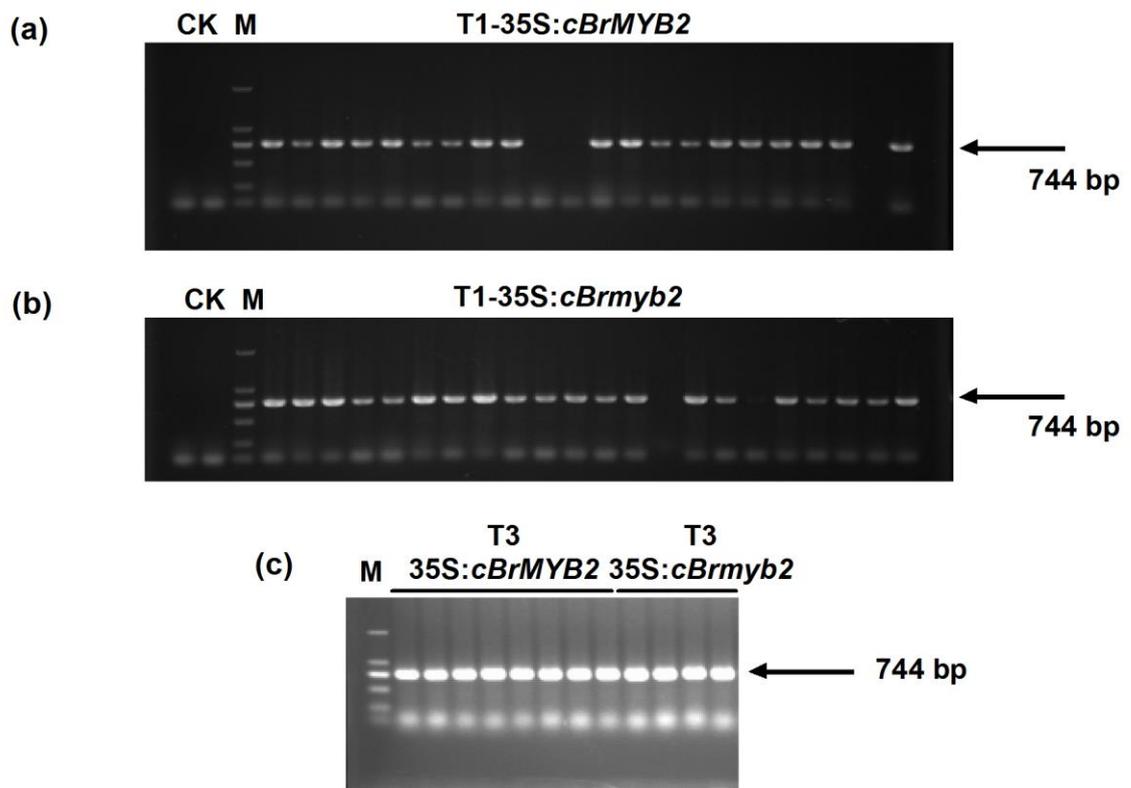


Figure S10 Identification of T₁ and T₃ homozygous transgenic *Arabidopsis* on MS solid medium containing 50mg·L⁻¹ kanamycin (Kan). **a** WT *Arabidopsis* without Kan; **b** WT *Arabidopsis* with Kan; **c** T₁ CaMV35S:*cBrMYB2* lines with Kan; **d** T₁ CaMV35S:*cBrmyb2* lines with Kan; **e-k** T₃ CaMV35S:*cBrMYB2* lines with Kan; **l-o** T₃ CaMV:*cBrmyb2* lines with Kan. Scale bar is 1.2 cm.

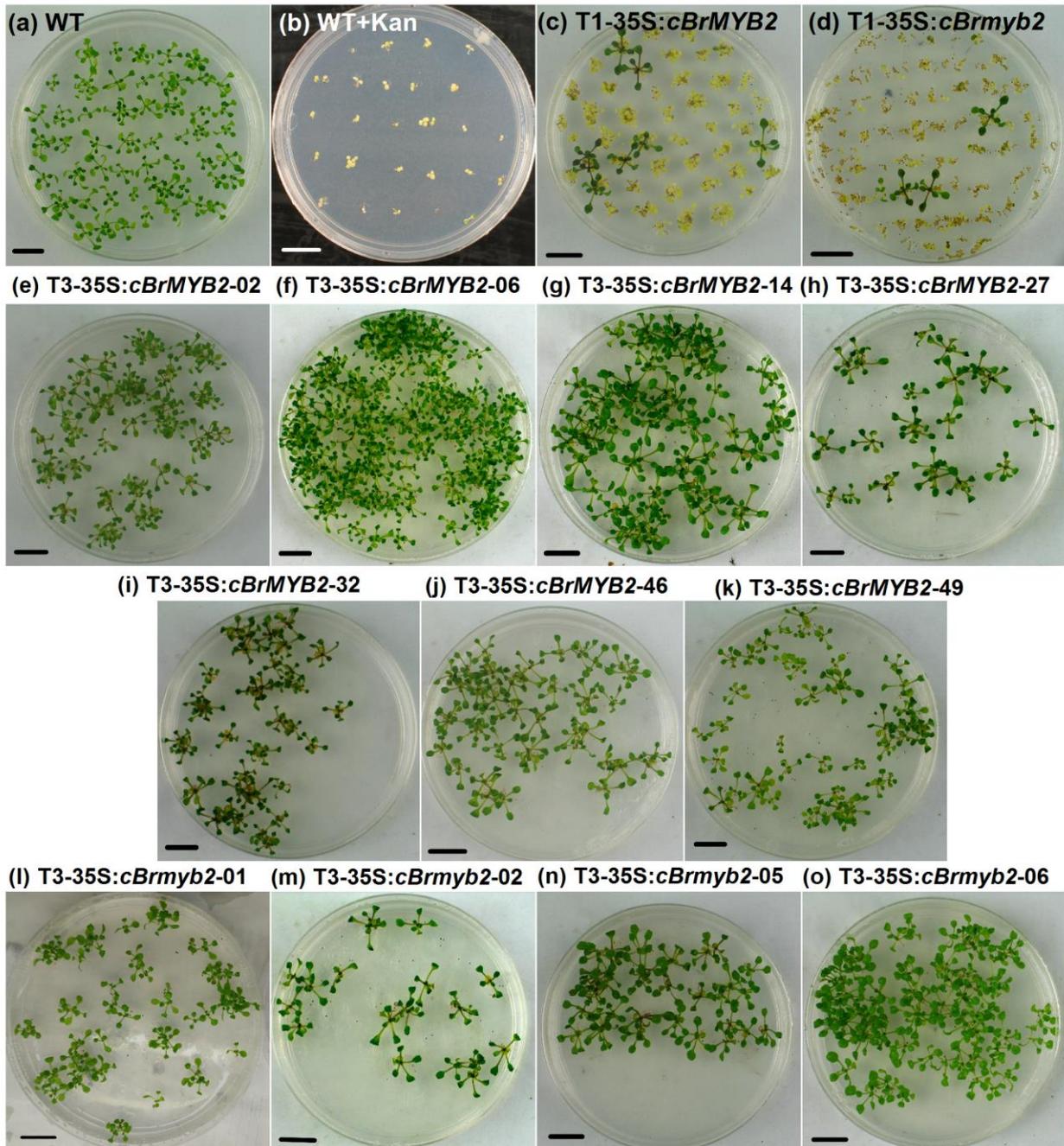


Figure S11 Gene expression patterns of anthocyanin biosynthesis in T₃ CaMV35S:*cBrMYB2* *Arabidopsis*. **a** WT *Arabidopsis*; **b-h** seven different CaMV35S:*cBrMYB2* lines; samples were 50-day *Arabidopsis* seedlings; **i** qRT-PCR and semi-qRT-PCR analysis of *BrMYB2*, and Line06 of T₃ *cBrMYB2* lines served as the control. **j-ab** Expression patterns of ABGs in *Arabidopsis*, and WT *Arabidopsis* served as the control in data analysis. Values are presented as means \pm SD (n = 3). The different letters above each column are significantly different at $p < 0.05$ by Duncan's test. The scale bar is 2 cm.

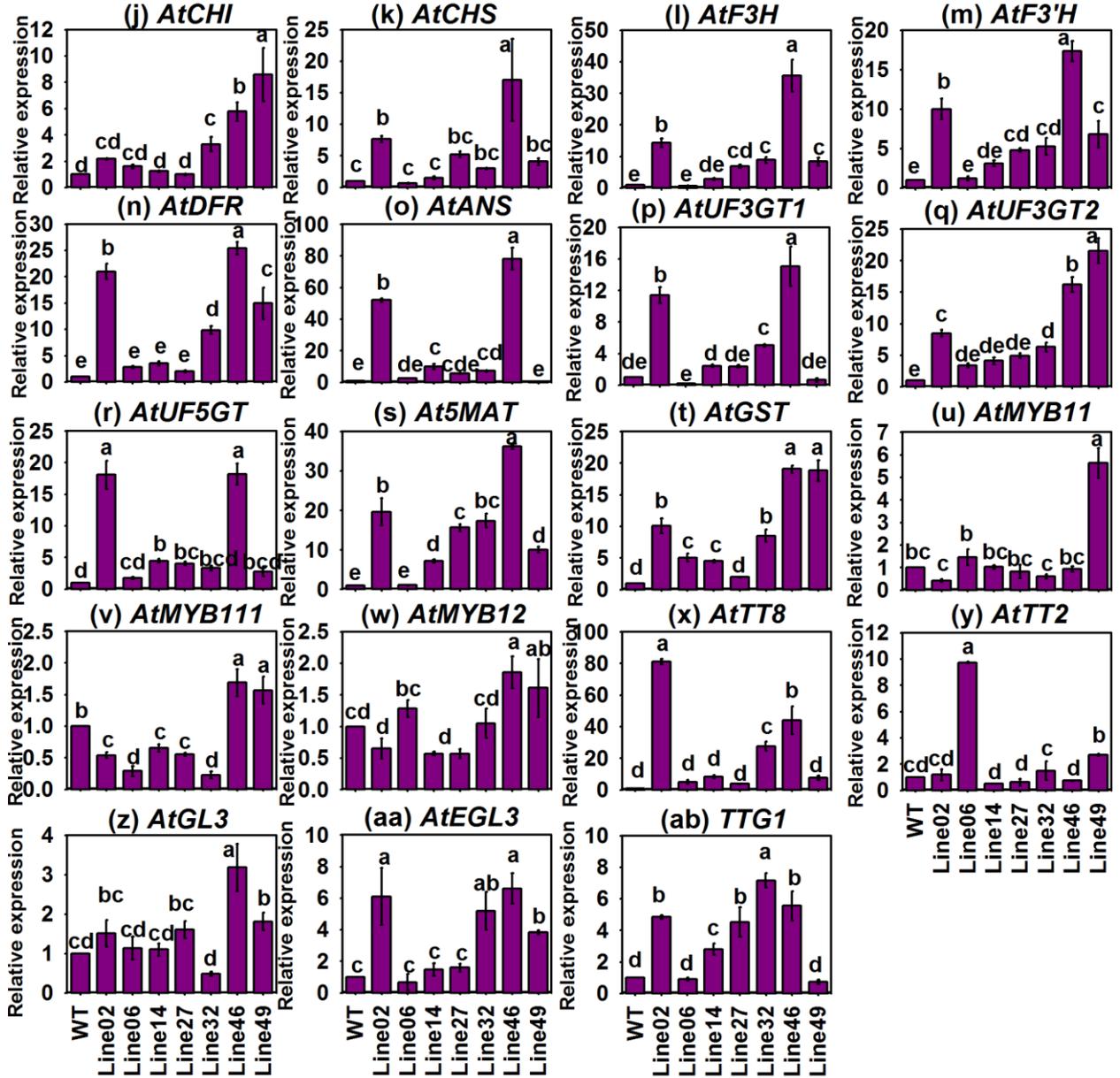
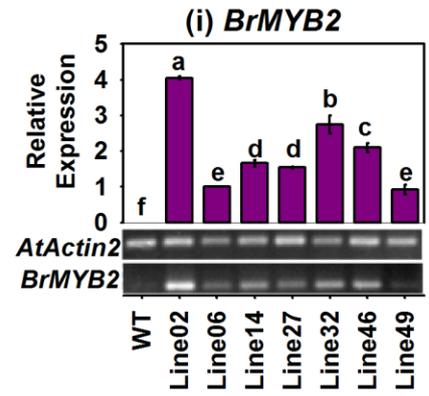
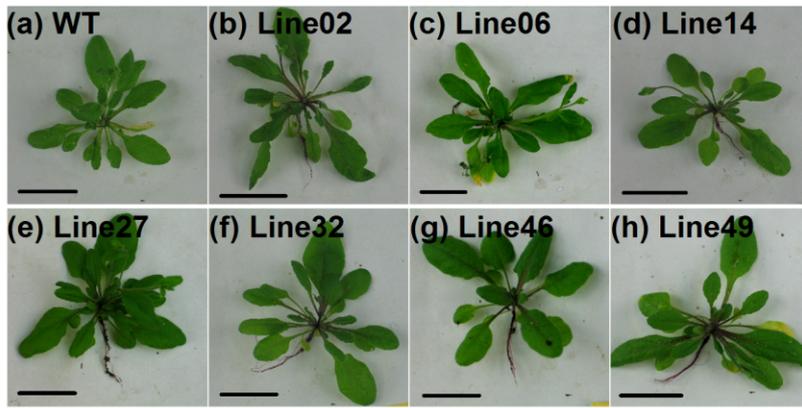


Figure S12 Results of PCR detecting on T₁ and T₃ homozygous transgenic *Arabidopsis* using *BrMYB2* clone primer. **a** T₁ CaMV35S:*gBrMYB2* lines; **b** T₁ CaMV35S:*gBrmyb2* lines; **c** T₃ of CaMV35S:*gBrMYB2* transgenic *Arabidopsis*; **d** T₃ of CaMV35S:*gBrmyb2* transgenic *Arabidopsis*, M1: DL2000 Marker; M2: DL10000 Marker.

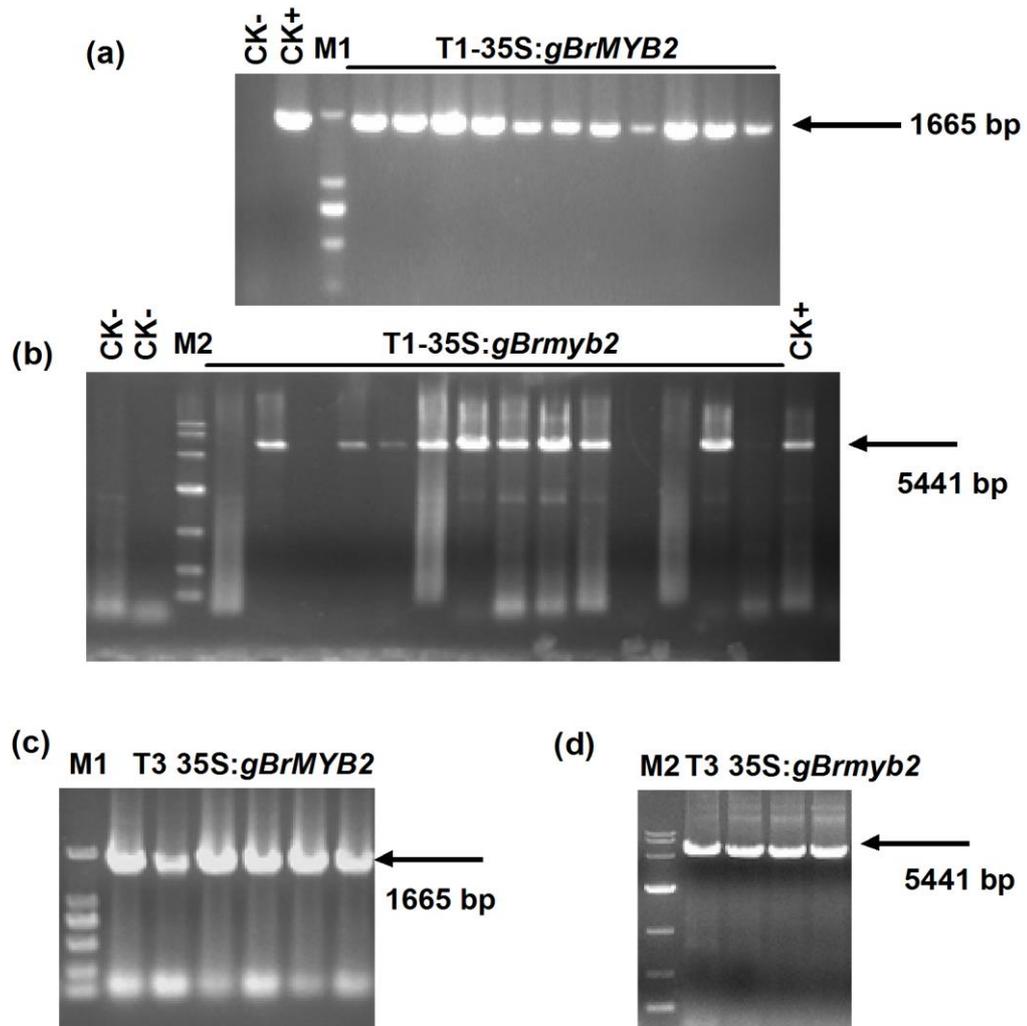


Figure S13 Identification of T₁ and T₃ homozygous transgenic *Arabidopsis* on MS solid medium containing 50mg·L⁻¹ Kan. **a** WT *Arabidopsis* without Kan; **b** WT *Arabidopsis* with Kan; **c** T₁ CaMV35S:*gBrMYB2* lines with Kan; **d** T₁ CaMV35S:*gBrmyb2* lines with Kan; **e** 50-day WT *Arabidopsis*; **f** 50-day T₁ CaMV35S:*cBrMYB2* lines; **g** 50-day T₁ CaMV35S:*gBrmyb2* lines; **h** 50-day T₁ CaMV35S:*gBrMYB2* lines. **i-k** T₃ CaMV35S:*gBrMYB2* lines with Kan; **l-n** T₃ CaMV35S:*gBrmyb2* lines with Kan. Scale bar is 1.2 cm.



Figure S14 Sequence alignment analysis of identified *BrMYB2* and *Brmyb2* using reverse transcription-PCR in transgenic *Arabidopsis* lines.

T3-cBrmyb2-1	ATGGAGGGTTCGTCCTCCCAAGGGTTGAAAAAGGTCATGGACTGCTGAAGAAGATAATCTCTTGAGGCAATGCATTGATAAGTATGGAGAAGGGAAATGGC	100
T3-cBrmyb2-2	ATGGAGGGTTCGTCCTCCCAAGGGTTGAAAAAGGTCATGGACTGCTGAAGAAGATAATCTCTTGAGGCAATGCATTGATAAGTATGGAGAAGGGAAATGGC	100
T3-cBrmyb2-3	ATGGAGGGTTCGTCCTCCCAAGGGTTGAAAAAGGTCATGGACTGCTGAAGAAGATAATCTCTTGAGGCAATGCATTGATAAGTATGGAGAAGGGAAATGGC	100
T3-cBrMYB2-1	ATGGAGGGTTCGTCCTCCCAAGGGTTGAAAAAGGTCATGGACTGCTGAAGAAGATAATCTCTTGAGGCAATGCATTGATAAGTATGGAGAAGGGAAATGGC	100
T3-cBrMYB2-2	ATGGAGGGTTCGTCCTCCCAAGGGTTGAAAAAGGTCATGGACTGCTGAAGAAGATAATCTCTTGAGGCAATGCATTGATAAGTATGGAGAAGGGAAATGGC	100
T3-cBrMYB2-3	ATGGAGGGTTCGTCCTCCCAAGGGTTGAAAAAGGTCATGGACTGCTGAAGAAGATAATCTCTTGAGGCAATGCATTGATAAGTATGGAGAAGGGAAATGGC	100
T3-TgBrMYB2-1	ATGGAGGGTTCGTCCTCCCAAGGGTTGAAAAAGGTCATGGACTGCTGAAGAAGATAATCTCTTGAGGCAATGCATTGATAAGTATGGAGAAGGGAAATGGC	100
T3-TgBrMYB2-2	ATGGAGGGTTCGTCCTCCCAAGGGTTGAAAAAGGTCATGGACTGCTGAAGAAGATAATCTCTTGAGGCAATGCATTGATAAGTATGGAGAAGGGAAATGGC	100
T3-TgBrMYB2-3	ATGGAGGGTTCGTCCTCCCAAGGGTTGAAAAAGGTCATGGACTGCTGAAGAAGATAATCTCTTGAGGCAATGCATTGATAAGTATGGAGAAGGGAAATGGC	100
Consensus	atggaggggttcgctcccaagggttgaaaaaggctcatggactgctgaagaagataatctcttgaggcaatgcattgataagtatggagaagggaaatggc	
T3-cBrmyb2-1	ACCAAGTTCCTTTAAGAGCTGGTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGTTGAACATTTTGAAGCCAAAGTATCAAGAGAGGAAAACCTCAA	200
T3-cBrmyb2-2	ACCAAGTTCCTTTAAGAGCTGGTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGTTGAACATTTTGAAGCCAAAGTATCAAGAGAGGAAAACCTCAA	200
T3-cBrmyb2-3	ACCAAGTTCCTTTAAGAGCTGGTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGTTGAACATTTTGAAGCCAAAGTATCAAGAGAGGAAAACCTCAA	200
T3-cBrMYB2-1	ACCAAGTTCCTTTAAGAGCTGGTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGTTGAACATTTTGAAGCCAAAGTATCAAGAGAGGAAAACCTCAA	200
T3-cBrMYB2-2	ACCAAGTTCCTTTAAGAGCTGGTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGTTGAACATTTTGAAGCCAAAGTATCAAGAGAGGAAAACCTCAA	200
T3-cBrMYB2-3	ACCAAGTTCCTTTAAGAGCTGGTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGTTGAACATTTTGAAGCCAAAGTATCAAGAGAGGAAAACCTCAA	200
T3-TgBrMYB2-1	ACCAAGTTCCTTTAAGAGCTGGTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGTTGAACATTTTGAAGCCAAAGTATCAAGAGAGGAAAACCTCAA	200
T3-TgBrMYB2-2	ACCAAGTTCCTTTAAGAGCTGGTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGTTGAACATTTTGAAGCCAAAGTATCAAGAGAGGAAAACCTCAA	200
T3-TgBrMYB2-3	ACCAAGTTCCTTTAAGAGCTGGTCTAAATCGGTGCAGGAAGAGTTGTAGACTAAGATGGTTGAACATTTTGAAGCCAAAGTATCAAGAGAGGAAAACCTCAA	200
Consensus	accaagtctctttaagagctggctctaaatcgggtgcaggaagagttgtagactaagatggttgaacttttgaagccaaagtatcaagagagggaaaactcaa	
T3-cBrmyb2-1	CTCCGATGAAGTTGATCTCTTATCGCCCTTCATAAGCTTTTAGGAAACAGGTGGTCTTTAATTCGTGGTAGATTACCCGGTCCGACCGCCAATGACGTC	300
T3-cBrmyb2-2	CTCCGATGAAGTTGATCTCTTATCGCCCTTCATAAGCTTTTAGGAAACAGGTGGTCTTTAATTCGTGGTAGATTACCCGGTCCGACCGCCAATGACGTC	300
T3-cBrmyb2-3	CTCCGATGAAGTTGATCTCTTATCGCCCTTCATAAGCTTTTAGGAAACAGGTGGTCTTTAATTCGTGGTAGATTACCCGGTCCGACCGCCAATGACGTC	300
T3-cBrMYB2-1	CTCCGATGAAGTTGATCTCTTATCGCCCTTCATAAGCTTTTAGGAAACAGGTGGTCTTTAATTCGTGGTAGATTACCCGGTCCGACCGCCAATGACGTC	300
T3-cBrMYB2-2	CTCCGATGAAGTTGATCTCTTATCGCCCTTCATAAGCTTTTAGGAAACAGGTGGTCTTTAATTCGTGGTAGATTACCCGGTCCGACCGCCAATGACGTC	300
T3-cBrMYB2-3	CTCCGATGAAGTTGATCTCTTATCGCCCTTCATAAGCTTTTAGGAAACAGGTGGTCTTTAATTCGTGGTAGATTACCCGGTCCGACCGCCAATGACGTC	300
T3-TgBrMYB2-1	CTCCGATGAAGTTGATCTCTTATCGCCCTTCATAAGCTTTTAGGAAACAGGTGGTCTTTAATTCGTGGTAGATTACCCGGTCCGACCGCCAATGACGTC	300
T3-TgBrMYB2-2	CTCCGATGAAGTTGATCTCTTATCGCCCTTCATAAGCTTTTAGGAAACAGGTGGTCTTTAATTCGTGGTAGATTACCCGGTCCGACCGCCAATGACGTC	300
T3-TgBrMYB2-3	CTCCGATGAAGTTGATCTCTTATCGCCCTTCATAAGCTTTTAGGAAACAGGTGGTCTTTAATTCGTGGTAGATTACCCGGTCCGACCGCCAATGACGTC	300
Consensus	ctccgatgaagttgatctcttattcggccttcataagcttttaggaaacaggtggctctttaattcgtggtagattaccgggtccgacccccaatgacgtc	
T3-cBrmyb2-1	AAAAATACCTGGAACACCCATTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
T3-cBrmyb2-2	AAAAATACCTGGAACACCCATTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
T3-cBrmyb2-3	AAAAATACCTGGAACACCCATTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
T3-cBrMYB2-1	AAAAATACCTGGAACACCCATTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
T3-cBrMYB2-2	AAAAATACCTGGAACACCCATTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
T3-cBrMYB2-3	AAAAATACCTGGAACACCCATTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
T3-TgBrMYB2-1	AAAAATACCTGGAACACCCATTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
T3-TgBrMYB2-2	AAAAATACCTGGAACACCCATTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
T3-TgBrMYB2-3	AAAAATACCTGGAACACCCATTTGAGTAAGAAACATGAACCGGGTTGTAAGACCCAGATGAAAAAGAGAAACATTCCTTGCTCTTATACCACACCAGCCC	400
Consensus	aaaaatctggaacacccatttgagtaagaaacatgaaccgggttgtaagaccagatgaaaaagagaaacattccttgctcttataccacaccagccc	
T3-cBrmyb2-1	AAAAATACGACGTTTTCAAACCTCGACCTCGATCCTTCACCGTTAACAGCGGCTGCAGCCATAAATGGCATGCCAGAAGCTGCATTGTTCTCTATG	500
T3-cBrmyb2-2	AAAAATACGACGTTTTCAAACCTCGACCTCGATCCTTCACCGTTAACAGCGGCTGCAGCCATAAATGGCATGCCAGAAGCTGCATTGTTCTCTATG	500
T3-cBrmyb2-3	AAAAATACGACGTTTTCAAACCTCGACCTCGATCCTTCACCGTTAACAGCGGCTGCAGCCATAAATGGCATGCCAGAAGCTGCATTGTTCTCTATG	500
T3-cBrMYB2-1	AAAAATACGACGTTTTCAAACCTCGACCTCGATCCTTCACCGTTAACAGCGGCTGCAGCCATAAATGGCATGCCAGAAGCTGCATTGTTCTCTATG	500
T3-cBrMYB2-2	AAAAATACGACGTTTTCAAACCTCGACCTCGATCCTTCACCGTTAACAGCGGCTGCAGCCATAAATGGCATGCCAGAAGCTGCATTGTTCTCTATG	500
T3-cBrMYB2-3	AAAAATACGACGTTTTCAAACCTCGACCTCGATCCTTCACCGTTAACAGCGGCTGCAGCCATAAATGGCATGCCAGAAGCTGCATTGTTCTCTATG	500
T3-TgBrMYB2-1	AAAAATACGACGTTTTCAAACCTCGACCTCGATCCTTCACCGTTAACAGCGGCTGCAGCCATAAATGGCATGCCAGAAGCTGCATTGTTCTCTATG	500
T3-TgBrMYB2-2	AAAAATACGACGTTTTCAAACCTCGACCTCGATCCTTCACCGTTAACAGCGGCTGCAGCCATAAATGGCATGCCAGAAGCTGCATTGTTCTCTATG	500
T3-TgBrMYB2-3	AAAAATACGACGTTTTCAAACCTCGACCTCGATCCTTCACCGTTAACAGCGGCTGCAGCCATAAATGGCATGCCAGAAGCTGCATTGTTCTCTATG	500
Consensus	aaaaatcgcagcttttcaaacctcgacctcgatccttcaccggttaacagcggtgcagccataaattggcatgccagaagctgcattgttctctatg	
T3-cBrmyb2-1	CCTTGGACACAACGATACTAATAATGTTCTGAAAAATAAATCACATGTAACAAGATGATGATAAATCTGAGCTTGTAGTCAATTTAATGGATGGTCAG	600
T3-cBrmyb2-2	CCTTGGACACAACGATACTAATAATGTTCTGAAAAATAAATCACATGTAACAAGATGATGATAAATCTGAGCTTGTAGTCAATTTAATGGATGGTCAG	600
T3-cBrmyb2-3	CCTTGGACACAACGATACTAATAATGTTCTGAAAAATAAATCACATGTAACAAGATGATGATAAATCTGAGCTTGTAGTCAATTTAATGGATGGTCAG	600
T3-cBrMYB2-1	CCTTGGACACAACGATACTAATAATGTTCTGAAAAATAAATCACATGTAACAAGATGATGATAAATCTGAGCTTGTAGTCAATTTAATGGATGGTCAG	600
T3-cBrMYB2-2	CCTTGGACACAACGATACTAATAATGTTCTGAAAAATAAATCACATGTAACAAGATGATGATAAATCTGAGCTTGTAGTCAATTTAATGGATGGTCAG	600
T3-cBrMYB2-3	CCTTGGACACAACGATACTAATAATGTTCTGAAAAATAAATCACATGTAACAAGATGATGATAAATCTGAGCTTGTAGTCAATTTAATGGATGGTCAG	600
T3-TgBrMYB2-1	CCTTGGACACAACGATACTAATAATGTTCTGAAAAATAAATCACATGTAACAAGATGATGATAAATCTGAGCTTGTAGTCAATTTAATGGATGGTCAG	600
T3-TgBrMYB2-2	CCTTGGACACAACGATACTAATAATGTTCTGAAAAATAAATCACATGTAACAAGATGATGATAAATCTGAGCTTGTAGTCAATTTAATGGATGGTCAG	600
T3-TgBrMYB2-3	CCTTGGACACAACGATACTAATAATGTTCTGAAAAATAAATCACATGTAACAAGATGATGATAAATCTGAGCTTGTAGTCAATTTAATGGATGGTCAG	600
Consensus	ccttggacacaacgataactaataatgtttctgaaaaataaatacacatgtaacaagatgatgataaattctgagcttgttagtcattttaattggatggtcag	
T3-cBrmyb2-1	AATAGTGGTGGGAAAGTTGCTAGATGAGAGCCAAGATCCAGCTCGCCTCTTCCAGAAACTACAGCAATAAAAAAGGGCGCAACCTCCGCGTTTGACG	700
T3-cBrmyb2-2	AATAGTGGTGGGAAAGTTGCTAGATGAGAGCCAAGATCCAGCTCGCCTCTTCCAGAAACTACAGCAATAAAAAAGGGCGCAACCTCCGCGTTTGACG	700
T3-cBrmyb2-3	AATAGTGGTGGGAAAGTTGCTAGATGAGAGCCAAGATCCAGCTCGCCTCTTCCAGAAACTACAGCAATAAAAAAGGGCGCAACCTCCGCGTTTGACG	700
T3-cBrMYB2-1	AATAGTGGTGGGAAAGTTGCTAGATGAGAGCCAAGATCCAGCTCGCCTCTTCCAGAAACTACAGCAATAAAAAAGGGCGCAACCTCCGCGTTTGACG	700
T3-cBrMYB2-2	AATAGTGGTGGGAAAGTTGCTAGATGAGAGCCAAGATCCAGCTCGCCTCTTCCAGAAACTACAGCAATAAAAAAGGGCGCAACCTCCGCGTTTGACG	700
T3-cBrMYB2-3	AATAGTGGTGGGAAAGTTGCTAGATGAGAGCCAAGATCCAGCTCGCCTCTTCCAGAAACTACAGCAATAAAAAAGGGCGCAACCTCCGCGTTTGACG	700
T3-TgBrMYB2-1	AATAGTGGTGGGAAAGTTGCTAGATGAGAGCCAAGATCCAGCTCGCCTCTTCCAGAAACTACAGCAATAAAAAAGGGCGCAACCTCCGCGTTTGACG	700
T3-TgBrMYB2-2	AATAGTGGTGGGAAAGTTGCTAGATGAGAGCCAAGATCCAGCTCGCCTCTTCCAGAAACTACAGCAATAAAAAAGGGCGCAACCTCCGCGTTTGACG	700
T3-TgBrMYB2-3	AATAGTGGTGGGAAAGTTGCTAGATGAGAGCCAAGATCCAGCTCGCCTCTTCCAGAAACTACAGCAATAAAAAAGGGCGCAACCTCCGCGTTTGACG	700
Consensus	aatagtggtgggaaagtctgtagatgagagccaagatccagctcgctcttccagaaactacagcaataaaaaagggcgcaacctccgcttggacg	
T3-cBrmyb2-1	TTGAGCAACTTTGGAGCCTGTTGGATGGAGAACTGGAACCTG	743
T3-cBrmyb2-2	TTGAGCAACTTTGGAGCCTGTTGGATGGAGAACTGGAACCTG	743
T3-cBrmyb2-3	TTGAGCAACTTTGGAGCCTGTTGGATGGAGAACTGGAACCTG	743
T3-cBrMYB2-1	TTGAGCAACTTTGGAGCCTGTTGGATGGAGAACTGGAACCTG	743
T3-cBrMYB2-2	TTGAGCAACTTTGGAGCCTGTTGGATGGAGAACTGGAACCTG	743
T3-cBrMYB2-3	TTGAGCAACTTTGGAGCCTGTTGGATGGAGAACTGGAACCTG	743
T3-TgBrMYB2-1	TTGAGCAACTTTGGAGCCTGTTGGATGGAGAACTGGAACCTG	743
T3-TgBrMYB2-2	TTGAGCAACTTTGGAGCCTGTTGGATGGAGAACTGGAACCTG	743
T3-TgBrMYB2-3	TTGAGCAACTTTGGAGCCTGTTGGATGGAGAACTGGAACCTG	743
Consensus	ttgagcaactttggagcctgttggatggagaaactggaacttg	

Table S1 Primers used in this work.

Gene /Primer name	Forward Primer (5' to 3')	Reverse Primer (5' to 3')	Product (bp)	Gene		Utilization Description
				Arabido Num ber in BRA D	psis BlastN in NCBI	
QJ-46	TGCTATCTGACTT	ATACCTCATAACAC	178	—	—	Mapping
	GTGGTGTATCC	TGCATCCATAG				
LY-2	TTTATTATTGTGGA	CTTATACAAACTTC	123	—	—	Mapping
	CACCAACCATC	TAATGGCAAAGG				
LY-3	TAAACCTAAAAATA	TTAACGTGAGAGC	128	—	—	Mapping
	CATCTGCTTCC	TTGAATGC				
SSR14-36	TGTAATCATCCATA	GGGGGTTGTTGGCA	162	—	—	Mapping
	ACCATATAAGCG	TTTTAC				
<i>BrMYB2</i>	ATGGAGGGTTCGTC	TCAAGTTCAGTTT	1665/54	Bra00	6390	Gene cloning
	CCAAG	CTCCATCC	41	4162	(<i>AtPAP</i> 2)	
<i>BrMYB2</i>	GCTCTAGAATGGAG	GGGGTACCTCAAGT	1681	Bra00	6390	Vector
	GGTTCGTCCCAAG	TCCAGTTTCTCCAT				4162
		CC				

					2)	KpnI)
					AT1G6	Vector
		<u>GGGGTACCTCAAGT</u>				
<i>BrMYB2</i>	<u>CGGGATCC</u> ATGGAG	TCCAGTTTCTCCAT	5457	Bra00	6390	constuction
	GGTTCGTCCCAAG	CC		4162	(<i>AtPAP</i>	(BamHI and
					2)	KpnI)
<i>BrP1</i>	TGGTGTACTTTGAT	ACTGCATTCGCGTC	4080/30	—	—	Co-separation
	CCTTCGTG	TCCTAC	6			analysis
<i>BrP2</i>	CTTTTCTGCACGAA	ATTCGCGTCTCCTA	4122/34	—	—	Co-separation
	CCCG	CTCCATAT	8			analysis
					AT5G6	
<i>BrEF-1-α</i>	ATACCAGGCTTGAG	GCCAAAGAGGCCA	116	Bra03	0390	qRT-PCR
	CATACCG	TCAGACAA		1605	(<i>AtEF-1</i>	
					-α)	
					AT5G0	
<i>BrF3'H</i>	CCATCCACCAACAC	AGCTTCTCCGGCGT	347	Bra00	7990	qRT-PCR
	CACTCT	AACTCCTCC		9312	(<i>AtF3'H</i>	
)	
					AT5G4	
<i>BrDFR</i>	GACGGCGTTTTCCA	TCCCCAACACTCCA	94	Bra02	2800	qRT-PCR
	CATAG	TTCAC		7457	(<i>AtDFR</i>	
)	
<i>BrANS</i>	GAAGACGAAACCA	TTAGCCAACCTACT	220	Bra01	AT4G2	qRT-PCR
	TCCCGTGAGA	TCCATACC		3652	2880	

						(<i>AtANS</i>)	
						AT1G6	
<i>BrMYB2</i>	AGGTGGTCTTTAAT	TCCAAGGCATAGA	257	Bra00	6390	qRT-PCR	
	TGCT	GGAACAA		4162	(<i>AtPAP</i>		
						2)	
						AT4G0	
<i>BrTT8</i>	TAGATACACACATG	TCTTTGACATTCTC	168	Bra03	9820	qRT-PCR	
	GACATG	AACTCTCCACGA		7887	(<i>AtTT8</i>)		
<i>BrMYB2-Pro</i>	TGGAACAATGGAA	GGACCAGCTATAAT	2368	—	—	Promoter	
moter	AGATTGTCCAG	TTTAGAAGTATCT				cloning	
						Promoter	
<i>BrMYB2-Pro</i>	<u>CCAAGCTT</u> GGTCTT	<u>CGGGATCC</u> GGACC	2272	—	—	cloning and	
	CTGAGTATAAATGA	AGCTATAATTTTAG					vector
	GCATG	AAGTATCT					construction
						Promoter	
<i>BrMYB2-Pro</i>	<u>CCAAGCTT</u> GCATAA	<u>CGGGATCC</u> GGACC	2010	—	—	cloning and	
	GATGAGATGGAGA	AGCTATAATTTTAG					vector
	AACTG	AAGTATCT					construction
						Promoter	
<i>BrMYB2-Pro</i>	<u>CCAAGCTT</u> TCTGAAC	<u>CGGGATCC</u> GGACC	793	—	—	cloning and	
	TCCCTAGCCAAAAG	AGCTATAATTTTAG					vector
	TAC	AAGTATCT					construction
						Promoter	
<i>BrMYB2-Pro</i>	<u>CCAAGCTT</u> AGTTGT	<u>CGGGATCC</u> GGACC	642	—	—	Promoter	

4	GTACTCATA CATCA	AGCTATAA TTTTAG				cloning and
	ACCCT	AAGTATCT				vector
						construction
						Promoter
<i>BrMYB2-Pro</i>	<u>CCAAGCTTT</u> TATTCT	<u>CGGGATCC</u> GGACC				cloning and
5	GTTTTTAACTCTGG	AGCTATAA TTTTAG	498	—	—	vector
	TGCATG	AAGTATCT				construction
<i>AtACT2</i>	CACTTGCACCAAGC	GATTCCTGGACCTG	158	—	AT3G1	qRT-PCR
	AGCATG	CCTCATC			8780	
<i>AtCHS</i>	CGCATCACCAACAG	TCCTCCGTCAGATG	101	—	AT5G1	qRT-PCR
	TGAACAC	CATGTG			3930	
<i>AtCHI</i>	CCGGTTCATCGATC	ATCCCGGTTTCAGG	88	—	AT3G5	qRT-PCR
	CTCTTC	GATACTATC			5120	
<i>AtF3H</i>	CAGATCGTTGAGGC	ACGAGTCATATCCG	87	—	AT3G5	qRT-PCR
	TTGTGAGA	CCACTAAGT			1240	
<i>AtF3'H</i>	GCTCTCGCCGGAGT	CCAGCGACGCCTTG	74	—	AT5G0	qRT-PCR
	ATTCAA	TAAATC			7990	
<i>AtDFR</i>	AACGGATGTGACGG	TCCATTCACTGTCTG	93	—	AT5G4	qRT-PCR
	TGTTTT	GCTTTA			2800	
<i>AtANS</i>	CGATGAAAAGATCC	GCCAATTTACTTCC	215	—	AT4G2	qRT-PCR
	GTGAGA	ATAGCCT			2880	
<i>AtUGT79B1</i>	CAACTGGTTTTCCG	GCTTCCTCGACGGT	64	—	AT5G5	qRT-PCR
(<i>UF3GT2</i>)	TTTCTGGTT	TGATACAC			4060	

<i>AtUGT75C1</i>	CGAAGGCATTACCG	GCATCGTGTTCCAA	112	—	AT4G1	qRT-PCR
(5GT)	TCAGC	AGCAG			4090	
<i>AtUGT78D2</i>	CACCGCACAATCCA	GCATTTATCTCCGT	273	—	AT5G1	qRT-PCR
(UF3GT1)	ACTCT	CGCCAT			7050	
<i>At5MAT</i>	AGCCACGCTCCTCC	ACGGCATCTTTGTC	102	—	AT3G2	qRT-PCR
	ACTATC	GTCAGG			9590	
<i>AtGST</i>	TGGTCGAGGATCTC	TGAATTCTTCACCA	93	—	AT5G1	qRT-PCR
	AAAGTG	GCCAAA			7220	
<i>AtMYB11</i>	AAGTGGAGCAGAG	TTGTGCCCAACTGA	219	—	AT3G6	qRT-PCR
	GAACCCG	CATCCC			2610	
<i>AtMYB12</i>	TGATGGGGAGTTGC	AACGACTCCACCGA	114	—	AT2G4	qRT-PCR
	ATAACATA	TGGAC			7460	
<i>AtMYB111</i>	AATAACAAGACCA	AGAAACATTGTGA	92	—	AT5G4	qRT-PCR
	AGAAGAAGAAGAA	GGCCGTC			9330	
<i>AtTT8</i>	TGAATCAACCCATA	GGGGTGTGACATG	102	—	AT4G0	qRT-PCR
	CGTTAGACA	AGAAGTGT			9820	
<i>AtGL3</i>	AGTGTTTAGCCGTT	TGTCTTCCGTAATA	113	—	AT5G4	qRT-PCR
	CTCTTCTAGC	TGTTCTGTGG			1315	
<i>AtEGL3</i>	TTGGCACGACCGAA	TTGATAGTCTGATC	100	—	AT1G6	qRT-PCR
	CATA	TTGTCGATATTGT			3650	
<i>AtTTG1</i>	TCCTCGAAGATTAC	CGGGAGAGGCTTA	72	—	AT5G2	qRT-PCR
	AACAACCG	ACGGTCAT			4520	

<i>AtTT2</i>	GCGAAGGCAAATG	CCAAGAAGATTATG	160	—	AT5G3	qRT-PCR
	GAGCACT	GAGACGGA			5550	

Br: B. rapa; At: Arabidopsis.

Table S2 MYBs involved in anthocyanin biosynthesis in different species.

Species	Gene name	GenBank/Tair/BRAD ID
Arabidopsis	<i>ATMYB113</i>	AT1G66370
Arabidopsis	<i>ATMYB114</i>	AT1G66380
Arabidopsis	<i>AtMYB75 (PAP1)</i>	AT1G56650
Arabidopsis	<i>AtMYB90 (PAP2)</i>	AT1G66390
Arabidopsis	<i>AtTT2</i>	AT5G35550
Arabidopsis	<i>AtMYBL2</i>	AT1G71030
Arabidopsis	<i>AtMYB11</i>	AT3G62610
Arabidopsis	<i>AtMYB12</i>	AT2G47460
Arabidopsis	<i>AtMYB111</i>	AT5G49330
Brassica rapa ‘Chifu’ (heading Chinese cabbage‘Chifu’)	<i>BrMYB2</i>	Bra004162
Brassica rapa ‘Chifu’ (heading Chinese cabbage‘Chifu’)	<i>BrPAP1</i>	Bra039763
Brassica rapa ‘Chifu’ (heading Chinese cabbage‘Chifu’)	<i>BrMYB1</i>	Bra001917
Head Chinese cabbage Line 94S17	<i>BrMYB2</i>	Bra004162
purple Chinese cabbage Line 11S/95T	<i>BrMYB2</i>	Bra004162
Cauliflower	<i>BoMYB1</i>	GU219985
Cauliflower	<i>BoMYB2</i>	GU219987
Cauliflower	<i>BoMYB3</i>	GU219988
Cauliflower	<i>BoMYB4</i>	GU219989
Snapdragon	<i>AmROSEA1</i>	ABB83826
Snapdragon	<i>AmROSEA2</i>	ABB83827
Snapdragon	<i>AmVENOSA</i>	ABB83828
Sweet potato	<i>IbMYB1</i>	BAG68211
Sweet potato	<i>IbMYB2-1</i>	BAF45116
Sweet potato	<i>IbMYB2-2</i>	BAF45117
Sweet potato	<i>IbMYB2-3</i>	BAF45118
Sweet potato	<i>IbMYB2-4</i>	BAF45119
Tomato	<i>LeANT1</i>	AAQ55181
Morning glory	<i>InMYB1</i>	BAE94389

Morning glory	<i>InMYB2</i>	BAE94709
Morning glory	<i>InMYB3</i>	BAE94710
Pepper	<i>CaA</i>	CAE75745
Petunia	<i>PhAN2</i>	AAF66727
Grape	<i>VvMYBA1</i>	BAD18977
Grape	<i>VvMYBA2</i>	BAD18978
Grape	<i>VvMYBA3</i>	BAD18979
Grape	<i>VIMYBA1-1</i>	BAC07537
Grape	<i>VIMYBA2</i>	BAC07540
Gerbera	<i>GMYB10</i>	CAD87010
Apple	<i>MdMYB1-1</i>	ABK58136
Apple	<i>MdMYB10</i>	ACQ45201
Apple	<i>MdMYBA</i>	BAF80582
Maize	<i>ZmP1</i>	AAA19819
Maize	<i>ZmC1</i>	AAA33482
Rice	<i>OsC1</i>	BAD04024
Black Spruce	<i>PmMYBF1</i>	AAA82943
Strawberry	<i>FaMYB1</i>	AAK84064
Oncidium Gower Ramsey	<i>OgMYB1</i>	ABS58501
Phalaenopsis hybrid cultivar	<i>PhMyb9</i>	ACH95795
Diplacus aurantiacus	<i>MaMYB</i>	ACA04006
Solanum melongena	<i>SmMYB</i>	AGK37072.1
Prunus cerasifera	<i>PcMYB10</i>	ABX71495
Prunus cerasifera	<i>PcMYBA</i>	ABX71495
Prunus persica	<i>PpMYB10</i>	EU155160
Nicotiana tabacum	<i>NtAN2</i>	ACO52470
Raphanus sativus	<i>RsMYB1</i>	AKM95888

Table S3 Expression patterns of ABGs in Chinese cabbage at head formation period. Seedlings of ‘94S17’ stayed at about 10 DAS were treated as the control in qRT-PCR data analysis. The means are values \pm SD. The different letters in each line are significantly different at $p < 0.05$ by Duncan’s test.

<i>Gene</i>	BR AD Ge ne ID	94S	94S	94S	94S	11S	11S	11S	11S	95T	95T	95T	95T	
		17- S1	17-S 2	17- S3	17- S4	91-S 1	91- S2	91-S 3	91-S 4	2-5- S1	2-5- S2	2-5- S3	2-5- S4	
Structural genes														
Biosynthetic genes in phenylpropanoid pathway														
<i>BrPAL1</i> .1	Bra 005 221	0.0 15 \pm 0.0	0.22 2 \pm 0. 092	0.3 04 \pm 0.0 70a b	0.26 4 \pm 0 .061	0.11 8 \pm 0. 006d	0.30 0 \pm 0. 019	0.13 8 \pm 0. 032	0.15 8 \pm 0. 027	0.06 4 \pm 0. 017	0.04 2 \pm 0 .001	0.03 9 \pm 0 .009	0.35 0 \pm 0 .000	
	<i>BrPAL1</i> .2	Bra 017 210	0.0 30 \pm 0.0	0.20 3 \pm 0. 035	0.0 98 \pm 0.0 24c de	0.23 1 \pm 0 .039	0.11 2 \pm 0. 018c	0.25 7 \pm 0. 035	0.14 9 \pm 0. 021	0.20 9 \pm 0. 077	0.09 0 \pm 0. 027	0.09 4 \pm 0 .005	0.06 4 \pm 0 .011	0.22 1 \pm 0 .049
		<i>BrPAL2</i> .1	Bra 006 985	0.0 69 \pm 0.0	0.38 8 \pm 0. 082	0.3 09 \pm 0.0 93e	0.37 0 \pm 0 .072	57.9 23 \pm 5.75 4cd	200. 563 \pm 56. 764 a	120. 524 \pm 36. 399 b	100. 073 \pm 36. 074 bc	56.1 85 \pm 10.9 26c d	125. 179 \pm 0. 000 b	14.8 58 \pm 0.64 7de
<i>BrPAL2</i> .2			Bra 039 777	0.0 17 \pm 0.0	0.04 4 \pm 0. 010	0.1 16 \pm 0.0 25c d	0.29 3 \pm 0 .022	0.06 1 \pm 0. 002e	0.03 4 \pm 0. 003	0.09 8 \pm 0. 015	0.05 8 \pm 0. 022	0.21 9 \pm 0. 002	0.02 8 \pm 0 .009	0.02 9 \pm 0 .006
	<i>BrPAL2</i> .3		Bra 003 126	0.0 21 \pm 0.0	0.01 3 \pm 0. 002f	0.0 20 \pm 0.0 06f	0.31 0 \pm 0 .070	1.09 7 \pm 0. 131c	0.31 8 \pm 0. 050	0.63 1 \pm 0. 145	0.38 6 \pm 0. 066	7.06 1 \pm 0. 505	1.18 8 \pm 0 .168	0.83 2 \pm 0 .208
		<i>BrPAL3</i> .1	Bra 028 793	2.2 94 \pm 0.6	0.12 5 \pm 0. 087	0.2 59 \pm 0.0	0.06 7 \pm 0 .005	5.23 1 \pm 0. 686b	1.72 8 \pm 0. 223	0.38 8 \pm 0. 005	0.09 3 \pm 0. 030	19.3 60 \pm 9.35	2.19 2 \pm 0 .342	0.76 2 \pm 0 .106

		59b	b	48b	b		b	b	b	9a	b	b	b
<i>BrPAL3</i> .2	Bra	0.0	0.01	0.0	0.02	0.01	0.01	0.04	0.07	0.00	0.01	0.00	0.00
	030	38±	4±0.	00±	2±0	7±0.	1±0.	1±0.	5±0.	0±0.	4±0	3±0	0±0
	322	0.0	001	0.0	.011	003c	002	000	000	000f	.002	.000	.000
		00b	d	00f	c	d	d	b	a		d	f	f
<i>BrPAL4</i> .0	Bra	0.2	0.07	0.1	0.07		0.23	0.20	0.66	0.18	0.14	0.05	0.09
	029	67±	9±0.	47±	1±0	1.62	5±0.	5±0.	9±0.	3±0.	4±0	1±0	7±0
	831	0.0	000	0.0	.009	3±0.	021	066	015	002	.044	.004	.005
		14c	c	00c	c	493a	c	c	b	c	c	c	c
<i>BrC4H</i> 1	Bra	0.3	0.10	0.2	0.26		1.25	0.54	0.51	0.01	0.12	0.01	0.03
	018	66±	9±0.	98±	8±0	0.11	5±0.	4±0.	3±0.	9±0.	3±0	3±0	7±0
	311	0.0	001	0.0	.061	9±0.	215	036	000	007	.006	.002	.004
		22c	d	23c	c	029d	a	b	b	d	d	d	d
<i>BrC4H</i> 2	Bra	0.0	0.11	0.8	2.51	0.15	0.39	0.58	0.95	0.09	0.05	0.06	0.46
	021	16±	9±0.	02±	0±0	4±0.	9±0.	2±0.	8±0.	3±0.	8±0	6±0	0±0
	636	0.0	022	0.0	.692	045d	087	161	036	000	.012	.014	.142
		03e	de	60b	a	e	cde	bcd	b	de	e	e	cde
<i>BrC4H</i> 3	Bra	0.0	0.02	0.0	0.08		0.02	0.08	0.04	0.06	0.00	0.02	0.02
	021	32±	3±0.	24±	7±0	0.10	6±0.	5±0.	7±0.	0±0.	7±0	6±0	6±0
	637	0.0	004	0.0	.007	7±0.	001	017	013	006	.002	.004	.009
		01d	ef	01e	b	023a	def	b	cd	c	f	def	def
<i>BrC4H</i> 4	Bra	0.8	0.17	1.2	1.18		2.26	3.11	0.99	0.38	0.03	0.20	0.24
	022	67±	4±0.	05±	3±0	1.12	8±0.	8±0.	5±0.	2±0.	9±0	2±0	2±0
	802	0.0	012	0.0	.237	5±0.	005	000	203	153	.000	.011	.128
		42d	ef	00c	c	125c	b	a	cd	e	f	ef	ef
<i>BrC4H</i> 5	Bra	0.0	0.04	0.0	0.06	0.07	0.02	0.02	0.08	0.02	0.00	0.00	0.01
	022	19±	1±0.	31±	1±0	2±0.	5±0.	9±0.	9±0.	7±0.	7±0	9±0	4±0
	803	0.0	008	0.0	.011	018a	008	011	083	003	.001	.005	.006
		03b	abc	08b	abc	b	bc	bc	a	bc	c	c	bc
<i>Br4CL1</i>	Bra	0.0	1.03	0.3	0.31		0.29	0.95	0.45	0.22	0.15	0.11	0.41
	030	55±	2±0.	72±	9±0	0.17	7±0.	8±0.	1±0.	4±0.	3±0	9±0	9±0
	429	0.0	590	0.0	.077	5±0.	029	006	237	048	.051	.075	.025
		02b	a	95b	b	037b	b	a	b	b	b	b	b
<i>Br4CL2</i> .1	Bra	0.3	0.00	0.1	0.00	3.17	6.24	74.4	31.8	4.15	0.69	0.00	0.00
	031	26±	0±0.	11±	0±0	7±1.	6±0.	68±	87±	2±0.	3±0	0±0	0±0
	262	0.0	000	0.0	.000	252d	360	4.43	0.73	733	.113	.000	.000
		08e	e	63e	e	e	c	0a	9b	cd	e	e	e
<i>Br4CL2</i> .2	Bra	0.2	0.42	2.2	1.05		0.71	0.99	1.20	0.22	0.03	0.05	0.23
	031	46±	8±0.	28±	3±0	0.13	1±0.	7±0.	1±0.	7±0.	5±0	3±0	4±0
	263	0.0	076	0.5	.219	9±0.	186	061	475	066	.008	.002	.024
		03c	cd	69a	b	012d	bc	b	b	cd	d	d	cd
<i>Br4CL2</i>	Bra	0.0	0.00	0.0	0.01	0.09	0.01	0.00	0.01	0.03	0.00	0.00	0.00

.3	031	44±	2±0.	09±	0±0	1±0.	6±0.	3±0.	6±0.	2±0.	6±0	5±0	6±0
	265	0.0	000	0.0	.003	035a	004	001	004	005	.002	.000	.002
		05b	d	01c	cd		cd	d	cd	bc	d	d	d
				d									
<i>Br4CL2</i>	Bra	0.3	0.36	0.3	0.43	0.12	0.36	0.83	0.73	0.21	0.14	0.30	0.23
.4	031	48±	6±0.	08±	6±0	3±0.	6±0.	0±0.	4±0.	0±0.	3±0	3±0	2±0
	266	0.0	303	0.1	.062	026b	106	258	083	052	.010	.003	.059
		14b	b	60b	b		b	a	a	b	b	b	b
<i>Br4CL3</i>	Bra	0.5	0.03	0.1	0.06	4.19	0.06	0.06	0.06	0.29	0.12	0.00	0.03
	004	42±	5±0.	33±	9±0	4±1.	4±0.	8±0.	1±0.	5±0.	1±0	5±0	1±0
	109	0.1	002	0.0	.013	065a	003	013	008	052	.046	.000	.006
		70b	b	21b	b		b	b	b	b	b	b	b
<i>Br4CL4</i>	Bra	0.0	0.07	0.0	0.10	0.09	0.09	0.21	0.02	0.03	0.02	0.00	0.10
.1	001	17±	0±0.	07±	1±0	6±0.	0±0.	7±0.	8±0.	6±0.	0±0	8±0	1±0
	819	0.0	016	0.0	.005	038b	022	083	001	010	.001	.006	.045
		05e	bcde	01e	b	c	bcd	a	cde	bcde	de	e	b
<i>Br4CL4</i>	Bra	0.0	0.02	0.0	0.03	0.10	0.13	0.04	0.01	0.26	0.09	0.06	0.01
.2	001	95±	5±0.	04±	6±0	7±0.	1±0.	7±0.	7±0.	3±0.	1±0	4±0	2±0
	820	0.0	000	0.0	.005	000b	014	009	004	154	.006	.041	.000
		20b	bc	01c	bc	c	b	bc	c	a	bc	bc	c
		c											

Early biosynthetic genes (EBGs)

<i>BrCHS</i>	Bra	3.6	0.99	1.3	0.32	39.0	0.17	0.03	0.99	17.7	1.28	0.20	0.13
1	008	54±	7±0.	06±	0±0	25±	0±0.	1±0.	4±0.	35±	3±0	9±0	3±0
	792	0.5	781	0.2	.041	16.0	015	007	022	6.50	.012	.041	.000
		19c	c	85c	c	85a	c	c	c	4b	c	c	c
<i>BrCHS</i>	Bra	4.0	1.16	4.5	0.45	93.3	0.58	0.18	6.47	122.	14.8	5.83	2.09
2	006	46±	6±0.	15±	2±0	22±	2±0.	4±0.	6±1.	949	90±	9±2	4±0
	224	0.5	299	0.0	.138	26.3	060	093	354	±27.	4.81	.141	.000
		65c	c	97c	c	01b	c	c	c	149	a	3c	c
<i>BrCHS</i>	Bra	3.5	0.17	0.3	0.25	29.9	1.61	0.41	1.56	8.17	4.26	2.32	0.33
3	023	98±	7±0.	71±	3±0	45±	9±0.	4±0.	1±0.	9±1.	7±1	8±0	8±0
	441	0.3	044	0.0	.042	0.00	014	018	765	301	.136	.531	.010
		13c	g	46e	fg	0a	de	efg	def	b	c	d	efg
<i>BrCHS</i>	Bra	0.6	0.22	0.2	0.05	35.2	0.98	0.07	0.23	14.5	4.68	0.74	0.27
4	036	99±	3±0.	37±	1±0	08±	1±0.	2±0.	5±0.	27±	4±0	1±0	3±0
	307	0.0	055	0.0	.019	14.2	332	008	038	3.26	.784	.049	.205
		12c	c	15c	c	13a	c	c	c	7b	c	c	c
<i>BrCHS</i>	Bra	0.1	0.00	0.0	0.00	0.12	0.24	4.65	0.74	0.10	0.00	0.00	0.00
5	020	75±	0±0.	00±	0±0	7±0.	0±0.	3±0.	6±0.	6±0.	0±0	0±0	0±0
	688	0.0	000	0.0	.000	000c	031	568	000	013	.000	.000	.000
		00c	c	00c	c		c	a	b	c	c	c	c

<i>BrCHI1</i>	Bra	0.3	0.13	0.1	0.14	1.43 9±0. 194a	0.26	0.54	0.18	1.15	0.31	0.08	0.11
	007	45±	5±0.	05±	1±0		6±0.	0±0.	8±0.	4±0.	8±0	9±0	8±0
	142	0.0	024	0.0	.020		036	138	008	181	.021	.014	.019
		60d	ef	19f	def		def	c	def	b	de	f	ef
<i>BrCHI2</i>	Bra	0.4	0.33	0.7	0.38	1.11 1±0. 066b	0.32	1.06	0.89	1.91	0.62	0.72	0.81
	003	07±	7±0.	52±	9±0		7±0.	1±0.	4±0.	0±0.	2±0	9±0	1±0
	209	0.0	050	0.1	.047		018	762	105	160	.087	.260	.133
		59c	c	c	c		c	b	bc	a	bc	bc	bc
<i>BrCHI3</i>	Bra	0.2	0.09	0.1	0.34	16.4	0.21	0.29	0.90	3.05	0.16	0.03	0.07
	017	79±	9±0.	22±	1±0	34±	9±0.	2±0.	7±0.	0±0.	6±0	5±0	7±0
	728	0.0	005	0.0	.101	7.08	067	003	191	953	.082	.011	.012
		79b	b	11b	b	5a	b	b	b	b	b	b	b
<i>BrF3H1</i>	Bra	0.3	0.60	1.2	1.06	4.73	3.25	20.9	0.71	5.93	2.92	1.65	0.49
	036	74±	9±0.	85±	2±0	9±1.	1±0.	98±	4±0.	3±2.	2±0	3±0	1±0
	828	0.0	054	0.0	.345	952b	117	1.78	025	174	.062	.329	.155
		29f	ef	80d	def	c	cd	6a	ef	b	cde	def	f
<i>BrF3H2</i>	Bra	0.0	0.03	0.0	0.00	0.01	0.02	0.00	0.03	0.00	0.10	0.00	0.00
	029	02±	9±0.	00±	0±0	9±0.	3±0.	0±0.	2±0.	0±0.	6±0	0±0	0±0
	996	0.0	000	0.0	.000	001d	003	000	007	000	.000	.000	.000
		00e	b	00e	e		d	e	c	e	a	e	e
<i>BrF3H3</i>	Bra	5.6	2.32	3.5	1.19	51.0	7.30	2.56	7.67	190.	14.2	4.17	2.74
	012	53±	6±0.	70±	6±0	27±	7±2.	3±0.	2±1.	193	45±	9±0	2±0
	862	0.1	149	0.2	.057	4.69	137	845	193	±80.	3.24	.649	.536
		35b	b	37b	b	0b	b	b	b	306	6b	b	b
<i>BrF3'H</i>	Bra	8.2	0.97	3.3	0.45	108.	2.86	0.42	3.25	273.	36.1	36.3	61.4
	009	41±	2±0.	74±	5±0	815	5±1.	4±0.	2±1.	828	95±	35±	97±
	312	0.0	253	0.4	.175	±48.	266	016	618	±63.	4.70	21.9	57.9
		00c	c	68c	c	826b	c	c	c	758	1c	72c	56b
<i>BrFLS1</i>	Bra	0.7	0.65	2.9	2.45	0.50	0.31	0.10	6.19	0.69	0.98	0.09	0.26
	009	93±	8±0.	66±	1±0	1±0.	4±0.	9±0.	9±1.	8±0.	9±0	5±0	6±0
	358	0.0	165	0.2	.338	123c	003	011	146	101	.200	.017	.004
		18c	cd	74b	b	d	cd	d	a	cd	c	d	cd
<i>BrFLS2</i>	Bra	0.0	0.20	0.1	0.53	0.02	0.05	0.00	0.13	0.00	0.01	0.00	0.19
	038	24±	6±0.	93±	5±0	3±0.	4±0.	3±0.	6±0.	7±0.	7±0	0±0	9±0
	647	0.0	050	0.0	.036	002d	001	001	006	001	.005	.000	.007
		08d	b	53b	a		d	d	c	d	d	d	b
<i>BrFLS3</i> .1	Bra	0.0	0.03	0.0	0.09	0.01	0.00	0.00	0.03	0.00	0.00	0.00	0.00
	038	15±	2±0.	37±	1±0	4±0.	4±0.	6±0.	1±0.	5±0.	9±0	1±0	9±0
	648	0.0	003	0.0	.019	000c	001	001	004	001	.002	.000	.002
		01c	b	00b	a	d	cd	cd	b	cd	cd	d	cd
<i>BrFLS3</i>	Bra	0.0	0.10	0.0	0.03	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.01

.2	029	12±	9±0.	06±	1±0	4±0.	1±0.	1±0.	1±0.	2±0.	1±0	2±0	4±0
	211	0.0	032	0.0	.004	000c	000	000	000	003	.000	.000	.000
		06b	a	00c	b		c	c	c	bc	c	c	bc
		c											
		0.0	0.17	0.0	0.05	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.07
<i>BrFLS3</i>	Bra	12±	9±0.	07±	9±0	4±0.	2±0.	0±0.	3±0.	4±0.	3±0	6±0	3±0
.3	029	0.0	031	0.0	.006	000c	001	000	003	003	.002	.004	.007
	212	03c	a	01c	b		c	c	c	c	c	c	b
		0.0	0.01	0.0	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.04	0.32
<i>BrFLS4</i>	Bra	00±	6±0.	00±	0±0	3±0.	0±0.	5±0.	0±0.	1±0.	8±0	8±0	7±0
	037	0.0	005	0.0	.009	000f	000f	000	000f	000f	.003	.004	.000
	747	00f	cd	00f	de			ef			c	b	a

Late biosynthetic genes (LBGs)

						2021				944.	106.	124.	
<i>BrDFR1</i>	Bra	3.9	13.0	9.5	2.17	.244	21.7	6.59	39.8	330	889	764	67.9
	027	61±	35±	30±	2±0	±26	16±	8±0.	30±	±97.	±12	±19	12±
	457	0.0	2.14	1.1	.075	6.15	0.00	807	1.20	640	.138	.294	15.9
		00c	3c	99c	c	2a	0c	c	9c	b	c	c	47c
		0.0	0.03	0.0	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00
<i>BrDFR2</i>	Bra	11±	4±0.	00±	0±0	0±0.	0±0.	0±0.	0±0.	9±0.	0±0	0±0	0±0
	019	0.0	000	0.0	.000	000d	000	000	000	009	.000	.000	.000
	062	00c	b	00d	d		d	d	d	a	d	d	d
		0.5	0.00	0.1	0.71	41.0	1.71	1.31	0.77	257.	0.01	0.00	6.36
<i>BrDFR3</i>	Bra	10±	0±0.	43±	6±0	15±	4±0.	1±0.	5±0.	521	6±0	0±0	8±0
	010	0.0	000	0.0	.000	8.07	000	000	000	±26.	.000	.000	.000
	535	00c	c	20c	c	7b	c	c	c	682	c	c	c
										a			
		1.2	1.28	0.8	3.11	1085	369.	478.	111.	155	571.	107.	85.5
<i>BrANS1</i>	Bra	93±	5±0.	18±	4±0	.657	451	581	382	4.46	825	177	84±
	013	0.0	049	0.0	.357	±33	±36.	±7.7	±52.	6±4	±23	±15	8.24
	652	43d	d	01d	d	2.50	281	52c	942	3.86	.648	.729	8d
						4b	c		d	1a	c	d	
		0.1	0.02	0.2	1.02	2.47	0.06	0.01	0.08	7.66	0.68	0.01	0.40
<i>BrANS2</i>	Bra	69±	5±0.	40±	6±0	7±0.	2±0.	6±0.	4±0.	4±0.	6±0	0±0	4±0
	019	0.0	009	0.0	.063	098b	023	002	004	685	.174	.000	.000
	350	33e	e	29d	c		e	e	e	a	cd	e	de
		0.0	0.00	0.0	0.00	0.41	0.00	3.80	0.08	0.02	0.00	0.00	0.00
<i>BrANS3</i>	Bra	00±	0±0.	00±	0±0	0±0.	0±0.	9±0.	8±0.	7±0.	0±0	0±0	0±0
	017	0.0	000	0.0	.000	483b	000	000	006	000	.000	.000	.000
	132	00c	c	00c	c		c	a	c	c	c	c	c
<i>BrANS4</i>	Bra	0.0	0.00	0.4	4.65	0.06	0.00	0.00	1.75	1.13	0.08	3.37	0.00

	000	00±	0±0.	55±	4±0	5±0.	0±0.	0±0.	3±0.	2±0.	9±0	3±0	0±0
	045	0.0	000f	0.0	.000	000f	000f	000f	000	009	.000	.174	.000
		00f		09e	a				c	d	f	b	f
		0.7		0.3	0.49		1.26	2.60	0.82	2.47	0.31	0.26	0.27
<i>BrUF3</i>	Bra	68±	0.37	73±	6±0	1.07	4±0.	3±0.	9±0.	7±0.	5±0	7±0	8±0
<i>GT1(Br</i>	023	0.0	1±0.	0.0	.123	8±0.	359	507	073	372	.043	.086	.026
<i>UGT78</i>	594	83b	021	14c	cd	182b	b	a	bc	a	cd	d	d
<i>D2()</i>		cd	cd	d	cd								
<i>BrUF3</i>	Bra	0.1	0.09	0.1	0.61	51.4	1.29	0.90	9.14	324.	92.9	9.26	12.6
<i>GT2(Br</i>	003	70±	6±0.	86±	3±0	96±	5±0.	0±0.	1±0.	920	31±	9±0	67±
<i>UGT79</i>	021	0.0	005	0.0	.209	4.89	103	145	714	±1.3	15.1	.559	1.27
<i>B1)</i>		41e	e	73e	e	3c	e	e	de	23a	94b	de	3d
<i>BrUF5</i>	Bra	0.2	0.01	0.0	0.13		0.28	0.43	0.29	5.40	2.81	1.73	0.03
<i>GT(BrU</i>	038	58±	6±0.	34±	4±0	5.34	6±0.	2±0.	1±0.	5±0.	9±0	6±0	3±0
<i>GT75C</i>	445	0.1	005	0.0	.038	6±0.	012	066	070	896	.815	.074	.004
<i>I()</i>		33d	d	10d	d	529a	d	d	d	a	b	c	d
		0.1	1.18	0.2	0.26	143.	5.32	4.78	1.22	364.	31.2	8.20	2.59
<i>Br5MA</i>	Bra	23±	7±0.	02±	3±0	840	4±0.	1±1.	9±0.	403	50±	0±1	9±0
<i>T</i>	036	0.0	280	0.0	.082	±36.	210	061	227	±12	5.64	.045	.536
	208	52c	c	10c	c	711b	0.00	c	c	2.97	7c	c	c
							0			219.			
<i>Brp-Co</i>	Bra	0.1	5.05	0.7	0.52	162.	4.37	1.53	0.87	722	89.7	7.88	1.94
<i>uT</i>	030	94±	1±0.	14±	3±0	091	3±0.	3±0.	3±0.	±16.	86±	6±1	4±0
	550	0.0	819	0.0	.123	±13.	555	492	042	682	38.0	.751	.252
		09d	d	44d	d	643b	d	d	d	a	38c	d	d
<i>BrSAT</i>	Bra	33.	56.6	5.3	1.66	24.5	38.0	74.7	4.16	5.95	4.18	0.65	0.31
	012	±2.	54±	67±	9±0	07±	01±	21±	4±0.	5±0.	5±0	1±0	7±0
	153	764	2.32	0.3	.439	2.52	10.2	8.57	994	380	.051	.318	.021
		c	3b	51e	e	9d	68c	0a	e	e	e	e	e
<i>BrUGT</i>	Bra	0.0	0.16	0.0	0.01	0.08	0.04	0.30	0.00	0.74	0.36	0.00	0.00
<i>84A1.1</i>	039	23±	5±0.	73±	5±0	4±0.	6±0.	0±0.	0±0.	6±0.	3±0	0±0	0±0
	547	0.0	036	0.0	.001	034c	004	047	000	110	.081	.000	.000
		04d	c	06c	d	d	d	b	d	a	b	d	d
<i>BrUGT</i>	Bra	0.1	0.07	21.	9.48	0.19	0.17	0.82	4.52	3.33	11.5	4.82	1.49
<i>84A1.2</i>	012	78±	0±0.	587	7±0	2±0.	2±0.	8±0.	5±0.	2±0.	11±	1±0	8±0
	784	0.0	005	±1.	.338	061g	000	347f	085	859	1.05	.189	.078
		21g	g	288	c		g	g	d	e	4b	d	f
				a									
<i>BrUGT</i>	Bra	0.4	0.20	0.9	0.15	1.04	0.24	2.45	1.22	0.25	0.26	0.00	0.00
<i>84A2.1</i>	031	88±	3±0.	19±	6±0	8±0.	0±0.	8±0.	7±0.	7±0.	6±0	0±0	0±0
	290	0.0	022	0.0	.003	380b	075	000	130	038	.007	.000	.000
		49d	e	51c	e	c	de	a	b	de	de	e	e
<i>BrUGT</i>	Bra	0.3	0.42	8.4	1.12	8.82	0.72	1.58	13.6	2.05	2.08	0.46	0.35

<i>BrMYB2</i>	Bra	0.6	2.88	0.5	0.31	24.1	1.90	1.20	1.59	37.7	0.88	0.92	1.84
	004	93±	5±1.	15±	4±0	64±	8±0.	5±0.	9±0.	49±	6±0	0±0	1±0
	162	0.4	102	0.1	.057	1.46	182	103	326	4.35	.220	.414	.619
		58c	c	28c	c	9b	c	c	c	6a	c	c	c
<i>BrPAP1</i>	Bra	1.7	1.06	0.7	1.06	0.67	1.90	4.35	2.20	0.02	0.60	0.53	1.26
	039	58±	4±0.	07±	2±0	5±0.	4±0.	0±1.	5±0.	6±0.	7±0	1±0	0±0
	763	0.3	000	0.2	.633	000c	542	604	494	006	.090	.337	.006
		11b	bcde	15c	bcd	de	bc	a	b	e	cde	de	bcd
<i>BrTT2</i>	Bra	0.0	1.74	0.2	0.33	0.07	0.20	0.00	0.33	0.07	0.06	0.00	0.00
	035	54±	4±0.	12±	6±0	9±0.	3±0.	0±0.	7±0.	8±0.	0±0	0±0	0±0
	532	0.0	000	0.0	.005	008d	058	000	142	010	.000	.000	.000
		13d	a	77c	b		c	d	b	d	d	d	d

**bHLH
regulatory
genes**

<i>BrTT8</i>	Bra	1.7	2.58	0.5	0.22	14.1	1.87	1.40	1.44	10.5	2.33	0.34	0.69
	037	17±	4±0.	11±	1±0	22±	7±1.	6±0.	2±0.	80±	1±0	5±0	7±0
	887	0.4	745	0.0	.086	1.83	028	632	112	3.20	.472	.086	.009
<i>BrEGL3-1</i>	Bra	1.3	0.03	0.0	0.00	0.30	0.02	0.00	0.00	0.86	0.10	0.00	0.00
	027	21±	7±0.	03±	0±0	0±0.	9±0.	0±0.	0±0.	3±0.	1±0	0±0	0±0
	653	0.1	004	0.0	.000	085c	002	000	000	228	.020	.000	.000
<i>BrEGL3-2</i>	Bra	0.9	0.71	0.9	1.20	0.40	0.84	0.71	5.41	0.62	1.22	0.33	2.35
	027	75±	0±0.	42±	6±0	9±0.	9±0.	2±0.	8±1.	2±0.	6±0	3±0	5±0
	796	0.4	222	0.0	.275	035c	105	067	096	059	.178	.267	.009
<i>BrGL3</i>	Bra	1.5	0.10	0.3	0.20	0.09	0.07	0.24	0.12	0.73	0.37	0.03	0.45
	025	75±	3±0.	49±	5±0	1±0.	4±0.	4±0.	4±0.	7±0.	4±0	9±0	8±0
	508	0.3	016	0.0	.003	015c	019	000	044	174	.015	.005	.377
	66a	cd	06c	cd	d	d	cd	cd	b	cd	d	bc	

**WD40
regulatory
genes**

<i>BrTTG1</i>	Bra	0.4	0.44	0.3	0.95	0.10	0.40	2.82	0.54	0.11	0.34	0.11	1.31
	009	19±	2±0.	86±	1±0	5±0.	3±0.	5±2.	2±0.	6±0.	0±0	4±0	3±0
	770	0.0	101	0.0	.195	014b	066	582	000	034	.021	.012	.000
	38b	b	56b	b			b	a	b	b	b	b	ab

**Negative
regulators
Single-Repeat
R3 MYB**

**regulatory
genes**

<i>BrCPC</i> <i>1</i>	Bra 004 539	0.4 13± 0.0	0.49 1±0. 155	0.2 76± 0.0	0.35 7±0 .024	0.20 5±0. 026d	0.17 2±0. 029	0.11 4±0. 024	0.85 8±0. 367	0.18 4±0. 032	0.09 8±0 .033	0.08 7±0 .041	0.04 4±0 .009
		15b c	b	00c def	cde	ef	def	ef	a	def	ef	ef	ef
		1.1 46± 0.0	1.67 0±0. 000	0.4 58± 0.0	1.41 7±0 .252	0.54 2±0. 147d	0.47 5±0. 076	0.35 8±0. 130	2.08 1±0. 536	0.38 7±0. 087	0.16 0±0 .106	0.13 5±0 .023	0.20 6±0 .011
<i>BrMYB</i> <i>L2.1</i>	Bra 016 164	0.0 23± 0.0	0.37 6±0. 040	0.1 86± 0.0	0.32 7±0 .032	0.01 9±0. 003c	0.01 6±0. 003	0.03 3±0. 000	0.30 0±0. 112	0.04 2±0. 020	0.01 0±0 .002	0.00 1±0 .000	0.00 8±0 .000
		01c	a	11b	a	c	c	a	c	c	c	c	c
		0.3 20± 0.1	5.67 8±0. 375	25. 476 ±4. 231	10.9 60± 2.65	0.00 8±0. 000e	1.25 9±0. 193	3.73 1±1. 113	12.9 94± 0.18	0.08 0±0. 016	0.67 9±0 .000	1.53 2±0 .410	31.8 75± 3.73
<i>BrMYB</i> <i>L2.2</i>	Bra 007 957	0.3 20± 0.1	5.67 8±0. 375	25. 476 ±4. 231	10.9 60± 2.65	0.00 8±0. 000e	1.25 9±0. 193	3.73 1±1. 113	12.9 94± 0.18	0.08 0±0. 016	0.67 9±0 .000	1.53 2±0 .410	31.8 75± 3.73
		28e	d	b	4c	e	de	4c	e	e	e	e	4a

**LATERAL
ORGAN
BOUNDARY
DOMAIN (LBD)
genes**

<i>BrLBD</i> <i>37.1</i>	Bra 012 164	0.4 55± 0.0	4.12 9±1. 448	1.4 24± 0.2	4.42 2±0 .824	0.52 1±0. 144c	1.04 6±0. 000	1.64 4±0. 075	5.11 8±1. 133	0.03 5±0. 003	0.12 4±0 .029	0.20 0±0 .075	2.00 3±0 .124
		90c de	a	57b cd	a	de	bcd e	bc	a	e	de	de	b
		0.6 70± 0.1	0.74 6±0. 154	4.5 43± 2.8	4.97 6±0 .355	0.06 5±0. 023c	0.20 8±0. 093	0.13 6±0. 021	2.28 0±0. 671	0.02 5±0. 005	0.82 0±0 .202	0.14 2±0 .023	0.92 4±0 .180
<i>BrLBD</i> <i>37.2</i>	Bra 031 833	0.6 70± 0.1	0.74 6±0. 154	4.5 43± 2.8	4.97 6±0 .355	0.06 5±0. 023c	0.20 8±0. 093	0.13 6±0. 021	2.28 0±0. 671	0.02 5±0. 005	0.82 0±0 .202	0.14 2±0 .023	0.92 4±0 .180
		44b c	bc	77a	a	c	c	b	c	bc	c	bc	
		2.0 49± 0.4	7.29 7±2. 113	5.1 08± 1.3	6.91 1±0 .140	0.06 2±0. 003d	0.24 8±0. 012	0.66 0±0. 005	6.13 5±1. 087	0.06 8±0. 012	0.34 0±0 .129	0.26 4±0 .109	0.82 9±0 .080
<i>BrLBD</i> <i>37.3</i>	Bra 037 847	2.0 49± 0.4	7.29 7±2. 113	5.1 08± 1.3	6.91 1±0 .140	0.06 2±0. 003d	0.24 8±0. 012	0.66 0±0. 005	6.13 5±1. 087	0.06 8±0. 012	0.34 0±0 .129	0.26 4±0 .109	0.82 9±0 .080
		19c	a	07b	a	cd	cd	ab	d	cd	cd	cd	
		0.3 11± 0.1	3.07 7±0. 388	0.5 03± 0.0	0.91 4±0 .159	0.45 2±0. 075d	0.38 9±0. 068	0.35 6±0. 096	1.17 4±0. 081	0.14 3±0. 028	0.25 0±0 .078	0.32 4±0 .045	1.92 6±0 .452
<i>BrLBD</i> <i>38.1</i>	Bra 036 040	0.3 11± 0.1	3.07 7±0. 388	0.5 03± 0.0	0.91 4±0 .159	0.45 2±0. 075d	0.38 9±0. 068	0.35 6±0. 096	1.17 4±0. 081	0.14 3±0. 028	0.25 0±0 .078	0.32 4±0 .045	1.92 6±0 .452
		15d	a	32d	c	d	d	c	d	d	d	d	b
		2.2 75± 1.2	2.69 4±0. 010	0.1 84± 0.0	0.29 3±0 .017	0.40 6±0. 019b	0.81 0±0. 264	0.74 5±0. 103	0.29 9±0. 074	0.37 2±0. 021	0.25 3±0 .023	0.11 6±0 .002	0.05 0±0 .013
<i>BrLBD</i> <i>38.2</i>	Bra 012 913	2.2 75± 1.2	2.69 4±0. 010	0.1 84± 0.0	0.29 3±0 .017	0.40 6±0. 019b	0.81 0±0. 264	0.74 5±0. 103	0.29 9±0. 074	0.37 2±0. 021	0.25 3±0 .023	0.11 6±0 .002	0.05 0±0 .013
		19c	a	32d	c	d	d	c	d	d	d	d	b

		59a	a	05b	b		b	b	b	b	b	b	b
<i>BrLBD</i> 39.1	Bra 011 772	5.1	112.	50.	94.5	21.1	8.50	132.	147.	1.35	11.5	4.93	50.5
		21±	654	916	72±	09±	1±2.	983	287	4±0.	42±	5±0	00±
		1.2	±14.	±2.	12.9	0.68	475	±37.	±47.	193	3.12	.271	17.3
		51d	678	621	49b	3cd	cd	ab	a	d	5cd	d	71c
<i>BrLBD</i> 39.2	Bra 017 831	0.4	4.62	1.4	0.24	1.16	0.24	2.00	0.24	0.10	0.17	0.06	0.04
		32±	2±0.	33±	4±0	5±0.	1±0.	0±0.	6±0.	6±0.	9±0	3±0	7±0
		0.0	420	0.0	.059	5±0.	107	037	054	030	.022	.013	.009
		65d	a	87c	de	086c	de	b	de	e	de	e	e
Transport genes													
<i>BrGST1</i>	Bra 008 570	0.4	1.64	0.8	1.51	193.	3.73	11.5	4.58	659.	68.9	78.8	35.5
		83±	5±0.	74±	7±0	324	9±0.	78±	3±1.	127	72±	09±	28±
		0.0	020	0.7	.458	±59.	671	0.13	806	±11	16.4	5.63	3.70
		58c	c	75c	c	890b	c	3c	c	1.83	87c	2c	8c
<i>BrGST2</i>	Bra 023 602	0.1	0.15	0.0	0.05	12.7	0.08	0.04	0.12	17.0	1.29	1.02	0.31
		16±	5±0.	14±	2±0	80±	2±0.	1±0.	4±0.	36±	1±0	1±0	4±0
		0.0	035	0.0	.016	2.32	020	006	028	1.58	.404	.169	.069
		02c	c	07c	c	3b	c	c	c	6a	c	c	c