Laser capture microdissection transcriptome (LCM RNA-seq) reveals *BcDFR* is a key gene in anthocyanin synthesis of Non-heading Chinese cabbage

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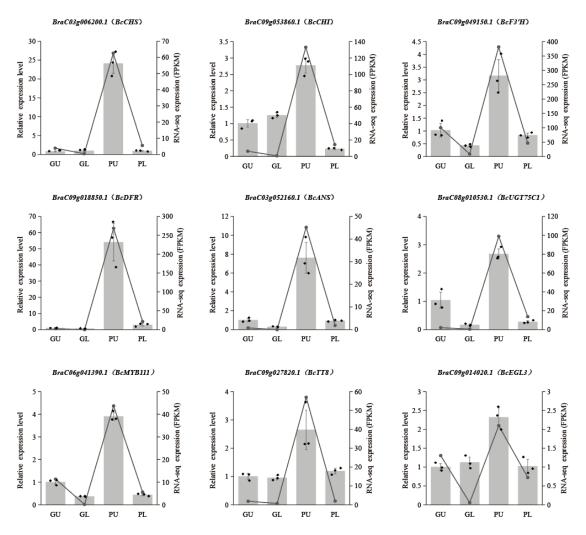


Fig. S1 Relative expression levels of genes involved in anthocyanin biosynthesis. Bar and line graphs represent the qRT-PCR and RNA-seq data, respectively. Scatter plots represent individual data values. Data are presented as mean \pm SD of three biological replicates.

	genome	ACCGAAGCTA	CATAGTAAACTCI	TTCTCAAAGC	CATAATCCATC	CTTTCACACA	CAAAGATGGT	AGCTCACAAA	GAGACCGT	TGCGTAACC	90
LBC	900000	ACCGAAGCTAG	CATAGTAAACTCT	ITTCTCAAAGC CATGGCTCGTG	CATAATCCATC		CAAAGATGGT		GAGACCGT		90 180
LBC	genome	GGCGCATCAG	GATTCATTGGTTC	CATGGCTCGTG	ATGCGGCTAC	CTGGAACGTG	GTTATTTGT	CCGTGCCACI	GTTCGCCAI	CCTGGTACA	180
LBC			ACTCGTTAATTTC ACTCGTTAATTTC	CTCCTGAGAGT CTCCTGAGAGT	ATGTTAATAA ATGTTAATAA		GAGTGTTCTT			AAGAAAGTG AAGAAAGTG	270 270
ZBC			ITGATTTGCCAA# ITGATTTGCCAA#		CAACTCACTI CAACTCACTI	ITATGGAAAG ITATGGAAAG	CCGATTTATC CCGATTTATC	IGACGAAGG# IGACGAAGG#	AGCTACGA1 AGCTACGA1	GACGCCATA GACGCCATA	360 360
ZBO		AACGGATGCGA AACGGATGCGA	ACGGCGTTTTCC# ACGGCGTTTTCC#	ACATAGCAACT ACATAGCAACT							450 450
ZBO	genome genome		ATCCTACAAGATT ATCCTACAAGATT				GAAGTGATAA GAAGTGATAA				540 540
ZB(LB(igtgataaggca# Igtgataaggca#		AAGAATTGTG AAGAATTGTG	GTTTACTTCG GTTTACTTCG	TCTGCTGGAA TCTGCTGGAA	CGGTTAATGI CGGTTAATGI	TGAGGAACA TGAGGAACA	ICCAGAAAAA ICCAGAAAAA	630 630
ZBC LBC	genome genome	TGTCTATGATO TGTCTATGATO	GAAAACGATTGGA GAAAACGATTGGA	AGTGATCTTGA AGTGATCTTGA	CTTTATCATG	GTCCAAGAAG GTCCAAGAAG	ATGACAGGAT	GGTATATAT GGGTATATAT	ATTAAGGAT ATTAAGGAT	САТАТАТАА САТАТАТАА	720 720
	genome genome		IGAGGTTGATCT1 IGAGGTTGATCT1	ГСТТСАААБТА ГСТТСАААБТА		ITGATAAATT ITGATAAATT	GTTGGCAGAT GTTGGCAGAT	GTATTTCATO GTATTTCATO	TCGAAAACO	TTAGCCGAG TTAGCCGAG	810 810
ZBO	genome genome		GGGATTACGCGA# GGGATTACGCGA#			ATTAGTATTA ATTAGTATTA	TCCCGACATT	GGTGATCGGI GGTGATCGGI	CCATTTATA CCATTTATA	ACAACATCT ACAACATCT	900 900
ZBO			GCCTTATTACCGC GCCTTATTACCGC							AGAGGTTAA AGAGGTTAA	990 990
ZBO	genome genome	TTTAAACTGT# TTTAAACTGT#	AAATGTTTTAGG AAATGTTTTAGG	STAACGAGGCA STAACGAGGCA			AAGGACAGTA' AAGGACAGTA'	10100110110	GACGACTTA	TGCAATGCC	1080 1080
	genome	CATATATTCT	IGTACGAACAAGO	CTGCTGCCAAG	GGACGTTATC	GTTTGTTCCT	CTCACGATGC CTCACGATGC	AACGATTCTI	ACTATCTCC	GAGTTTCTC	1170 1170
	genome	AGGCAAAAAT	ATCCAGAATATAA ATCCAGAATATAA	ACGTGCCTTCA	ACGTAAGATT	ГТТТАТСААТ	ACCGGTTTAA	GCTTGTTTTG	CATATTCAG	TTAATTTTT TTAATTTTT	1260 1260
ZBO	genome	TTTTTCTGAAT	IATGAACTCTTTC	GGAACACGTTT	GAAGGAGTGC	GATGAGAATC	TAAAGAGCAT	TATGTTCAGI	TCCAAGAAG	CTGATTGAT	1350 1350
ZBC		ATGGGATTTA	ACTTCAAGTATAG	STCTCGAGGAT	ATGTTGGTGG	GAATCGATTG	AGACATGTCG	TCAAAAGGGI	TTTCTCCCT	GTCACTTTA	1440
LBC ZBC	c genome c genome		ACTTCAAGTATAG		GGCAGTGATG	GAATCGATTG	AGACATGTCG AGATTAAAAA	ICAAAAGGGI CGGATCTGC#		GTCACTTTA GATGGTATG	1440 1530
LBC	genome genome		IGAAATCTGAGGA				AGATTAAAAA ACATGTCGGC			GATGGTATG	1530 1620
LBC	genome	GTAGCTTGTA	AGAAGACCGAACC	CAGGGATGGCC	GGCGAGAAAA	GCCGATAGTC	ACATGTCGGC	ACAGCAGATO	TGTGCTTAG	AAATTGAAC	1620
ZBO	9		IATGGATCTATTO IATGGATCTATTO				GTTCTTTTA GTTCTTTTTA			TGGACTTAT TGGACTTAT	1710 1710
ZBO		TTATGGTATA? TTATGGTATA?	IGATATCATGTGI IGATATCATGTGI	IGAGTGTGTAA IGAGTGTGTAA	AATTATGAAI AATTATGAAI	ICAATATTAT ICAATATTAT	TAAATTAAAC TAAATTAAAC	CGTAAAATTG CGTAAAATTG	AACCCGTAI AACCCGTAI	CTAATATGG CTAATATGG	1800 1800
ZB(LB(genome genome		TATGAATGTGTG TATGAATGTGTG	GATTTGTTTTT GATTTGTTTTT	TTTTGTTCTT TTTTGTTCTT	ITTTAAGTTT ITTTAAGTTT	GTATGAAAGT GTATGAAAGT	GTTGTGGACI GTTGTGGACI	TATTTATGO TATTTATGO	TATATGATA TATATGATA	1890 1890
ZBO	genome genome		GTGTGTAAAATTA GTGTGTAAAATTA							GAATACATA GAATACATA	1980 1980
	genome genome		ATACAGTCTTACO ATACAGTCTTACO			GCTATATAA GCTATATAA	СGААААААТТ. СGААААААТТ.	ATACCTGAAC ATACCTGAAC	AAGAAAACA AAGAAAACA	AACATGAGG AACATGAGG	2070 2070
	genome genome		CAGACACGACCAT CAGACACGACCAT								

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Fig.S2 Gene and promoter sequence comparison results of *BcDFR* in **ZBC**, **LBC**. (a) Results of the 2146 bp full length genome sequence comparison. (b) Results of the 1296 bp promoter sequence comparison.

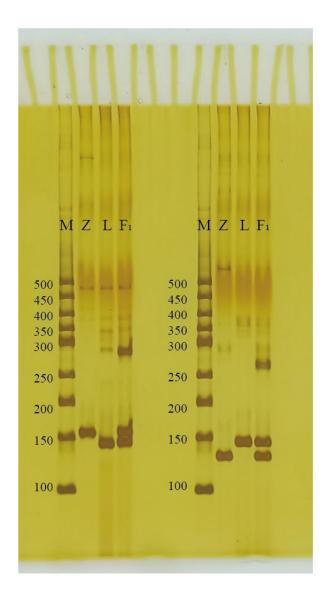


Fig.S3 Full-length polyacrylamide gel electrophoresis of amplification of insertion and deletion markers on ZBC, LBC and F₁.

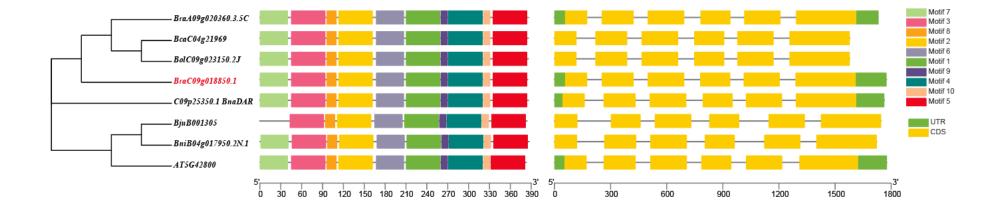


Fig.S4 Evolution, gene structure and conserved domain analysis of DFR homologs in Arabidopsis and six *Brassica species*.

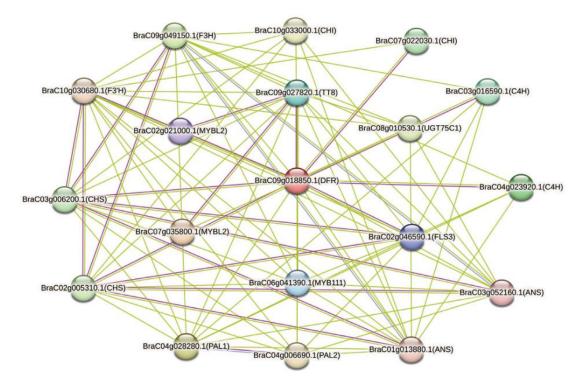


Fig.S5 Protein-protein interaction network between *BcDFR* and anthocyanin-related DEGs.

Heatmap

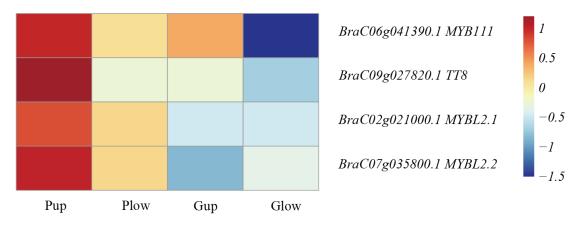


Fig.S6 Heat map of gene expression patterns of *BcMYB111*, *BcTT8* and *BcMYBL2*.