Figure S1 Generation of new purple Chinese cabbage 18M-245. F1 hydrid 15NG28 was obtained by crossing pak choi with Chinese mustard. Then 15NG28 was crossed with green Chinese cabbage Jiao Erye. 18M-245 was obtained by self-crossed purple plants from BC1 twice.
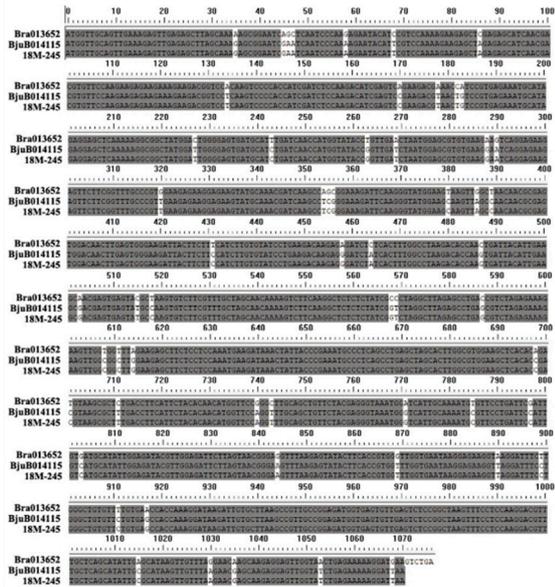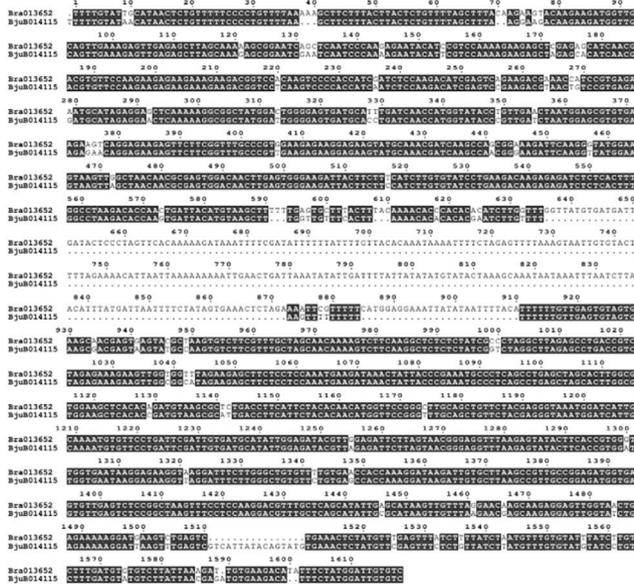
Figure S2 The nuclear acid sequence alignment of Bra013652 and BjuB014115. A. Coding sequences of Bra013652 and BjuB014115 share 94.06% similarity. B. Genomic sequence alignment of Bra013652 and BjuB014115. Bra013652 has a longer intron than BjuB014115.
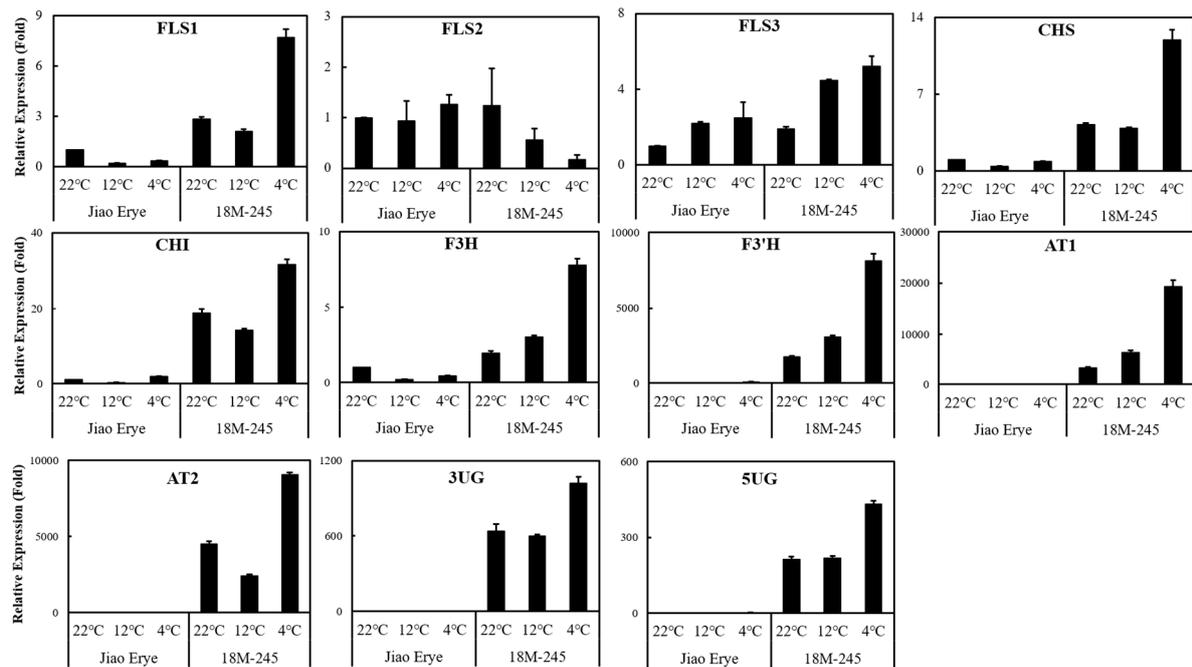
Figure S3 Expression pattern of structural genes under three different temperatures. Expression of anthocyanin-related structural genes under different temperatures was analyzed using RT-qPCR. GADPH was used as internal control.
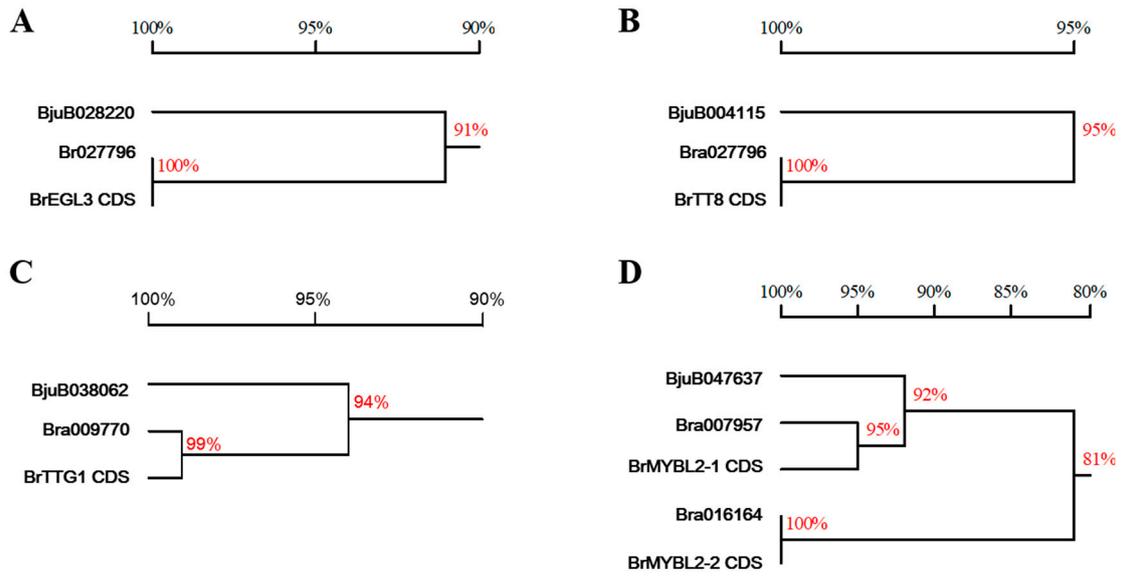
Figure S4 Homology tree showing the similarity of TFs CDS cloned from 18M-245 with the homologous genes from *Brassica* A and B genome. The tree was generated using DNAMAN software.

Table S1 Primers used in this study.

Name	Sequence （5' to 3')
Primers for genotyping	
LDOX-F	TTTTTGTATAACATAACTCTGTTTTTCCCC
LDOX-R	GACACAATCCATAGAAATGTCTTCAC
Primers for Q-PCR	
BrLDOX RT-F	GAGTGGGAAGATTACTTCTTCCATC
BrLDOX RT-R	GCCTAGACCGATAGAGAGAGCCTTGAAGAC
BrDFR RT-F	GGAAAGCCGATTTATCTGACGAAGGAAG
BrDFR RT-R	CTTTCATTATCCCCAACACTCCATTCACTG
GADPH-F	GGTTCTCCTGATGACGATGACGTCTCC
GADPH-R	GTTGTGACATGAGAAGTGTTGATACTGTC
Primers for vector construction	
BjuB014115promoter-F	CTTAGTCCGTTGGTCATGTATGTTTCATCG
BjuB014115promoter-R	CTTCTTGTCTTCCTTAAAGCTAAAAC
EGL3 AD NdeI-F	TACGCTCATATGGCTACTGGAGAAAACAG
EGL3 AD EcoRII-R	ACCCGGGTGGAATTCACATATCCATGCAACTC
TT8 AD NdeI-F	TACGCTCATATGGATGAATTAAGTATTATACCG
TT8 AD EcoRI-R	ACCCGGGTGGAATTCGAGTTTATTATTATATATG
TTG1 AD NdeI-F	TACGCTCATATGATGGACAACTCAGCTCCGG
TTG1 AD EcoRI-R	ACCCGGGTGGAATTCAACTCTAAGGAGCTGC
MYBL2-1 AD NdeI-F	TACGCTCATATGAACATAGTCTGTGTCCGC
MYBL2-1 AD EcoRII-R	ACCCGGGTGGAATTCTTGACGCGTTGAACC
MYBL2-2 AD NdeI-F	TACGCTCATATGAACAAAATTAGCCACGGCG
MYBL2-2 AD EcoRII-R	ACCCGGGTGGAATTCCTGAAAAAGAAGAAG
F3'H RT-F	GCACACGGACATGCTTAGCACTTTAATC
F3'H RT-R	GCCCAGTCCACCGTACTTGCTGACG
CHI RT-F	CCCACCGTCACGAAACTTCAAGTTGATTC
CHI RT-R	GGTAAACTCCGATGACGGTGAAGATC
AT1 RT-F	GGCTCATCTTCAATCTCTTAACATCATCG
AT1 RT-R	GATAGTCTTTGAGGAAATGTTCGGTTGAG
AT2 RT-F	GTGCAGTCCAGCCCAACGGTTAACATAC
AT2 RT-R	GGACAGAGCGAGATAACTCGGGGGAC
CHS RT-F	CGTTGGATGAGATCAGAAAGGCAC
CHS RT-R	CTGTTGGTGATGCGGAAGTAGTAGTC
F3H RT-F	CGCTCGAGACTTCTTCGCCTTACCTC
F3H RT-R	GTCACTTTCACCCATCCTTCCGGCTTAG
3GT RT-F	ATGGGCGATTTTGGATCCGATGGATCGTC
3GT RT-R	GTAGAGGTTAAGAGGTTTGACCTGGTCTAG
5GT RT-F	ATGGCCAACTCGGTTAACGGTTGTAGTC
5GT RT-R	GAACCAAGCGTAGGACAAGCCTTCGG
FLS1 RT-F	GTCTCGCTCGAGACTTCTTCGCCTTAC
FLS1 RT-R	CATCCTTCCGGCTTAGTCGGCCACC
FLS2 RT-F	ATGGAAGTCAAGAAAGACCAGCACACATC

FLS2 RT-R	GAAGAACTGTGTACCAACCTCCTTCAACC
FLS3 RT-F	GAAAAACATGGGCTGATCATCTCTTTCACAG
FLS3 RT-R	GTAACCCTAGTCCTTCCGATAACCATC