We performed the HMM analysis to identify the MADS-box genes in the recently published *Brassica* *rapa* genomes (Brara\_Chiffu\_V3.5) in the BRAD database ([BRAD (brassicadb.cn)](http://www.brassicadb.cn/#/Download/)). As a result, 26 candidate ABCED genes in the MADS-box family were isolated, and the protein sequences of most of them were the same as those in Brara\_Chiffu\_V1.5 (the version we used in the article) (Figure S1). The SMART and NCBI Conserved Domain Search Service were performed to ensure all the putative MADS-box protein sequences contained the typical MADS-box domain (PF00319). Surprisingly, 11 of the target genes in the Brara\_Chiffu\_V3.5 lacked MADS domain (*BraA01g045700.3.5C*, *BraA08g025540.3.5C*, *BraA09g025050.3.5C*, *BraA07g035150.3.5C*, *BraA05g003120.3.5C*, *BraA07g024420.3.5C*, *BraA09g050860.3.5C*, *BraA04g002810.3.5C*, *BraA01g010470.3.5C*, *BraA04g005910.3.5C* and *Bra09g047170.3.5C*) (Figure S2). In general, new versions of the genome may update and correct some genetic models due to advances in methods and technologies, but in the ABCDE model, it is doubtful that such a large number of genetic model corrections. We found that a large part of the N-terminus amino acid sequence was missing in 11 target proteins in Brara\_Chiffu\_V3.5 compared with those in Brara\_Chiffu\_V1.5 through sequence alignment (Figure S3). Therefore, the upstream 2,400-bp sequences of the CDS location which annotation in the GFF file of these genes were translated into the amino acid sequence, and NCBI Conserved Domain Search Service was performed to confirm whether these sequences contain MADS domain. A total of 4 genes were found MADS domain in the upstream 2400-bp sequence (Figure S4).

In conclusion, we think that there may be some errors in the gene annotation of Brara\_Chiffu\_V3.5, which will affect the accuracy of the experimental results. Therefore, we performed Brara\_Chiffu\_V1.5 as our reference genome.



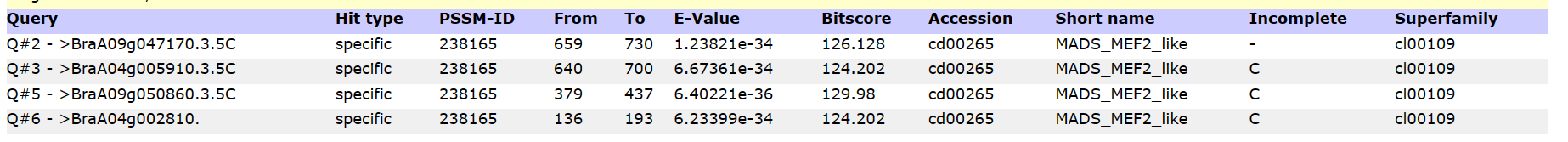
**Figure S1.** Phylogenetic relationships of ABCED genes in *Arabidopsis* *thaliana* and *Brassica* *rapa* (Brara\_Chiffu1.5 and V3.5). Black, blue and orange letters represent *A*. *thaliana*, *B*. *rapa* (Brara\_Chiffu1.5) and *B*. *rapa* (Brara\_Chiffu3.5) genes.



**Figure S2.** Phylogenetic relationships, conserved motif compositions and structural domains of *B. rapa* (Brara\_Chiffu\_V3.5) and *Arabidopsis* ABCDE class MADS proteins.



**Figure S3.** The result of sequence alignment of 11 target genes between Brara\_Chiffu\_V1.5 and Brara\_Chiffu\_V3.5. (**a**) *Bra004361* and *BraA07g035150.3.5C*; (**b**) *Bra003356* and *BraA07g024420.3.5C*; (**c**) *004716* and *BraA05g003120.3.5C*; (**d**) *Bra007067* and *BraA09g047170.3.5C*; (**e**) *Bra007419* and *BraA09g050860.3.5C*; (**f**) *Bra010955* and *BraA08g025540.3.5C*; (**g**) *Bra013364* and *BraA01g010470.3.5C*; (**h**) *Bra014552* and *BraA04g002810.3.5C*; (**i**) *Bra014822* and *BraA04g005910.3.5C*; (**j**) *Bra017376* and *BraA09g025050.3.5C*; (**k**) *Bra021470* and *BraA01g045700.3.5C*.



**Figure S4.** The MADS domain in the upstream amino acid sequences of the CDS location of the target genes.