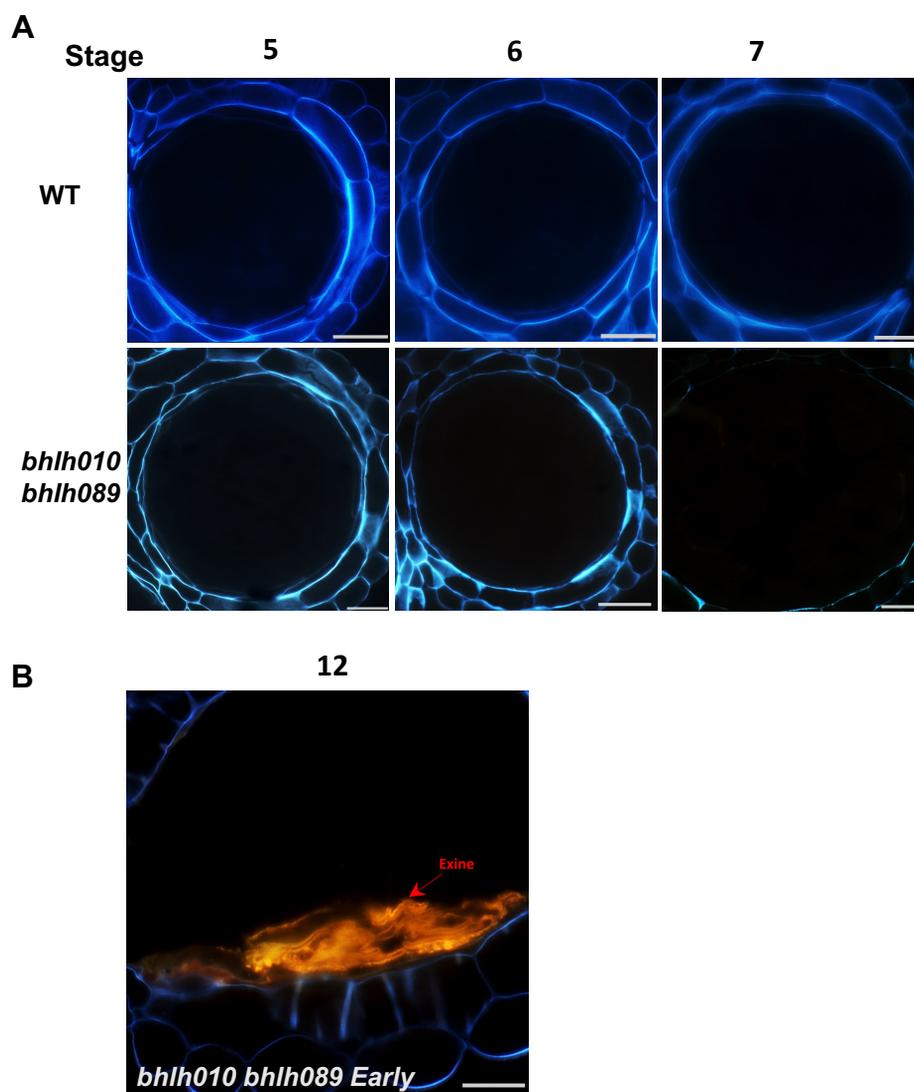


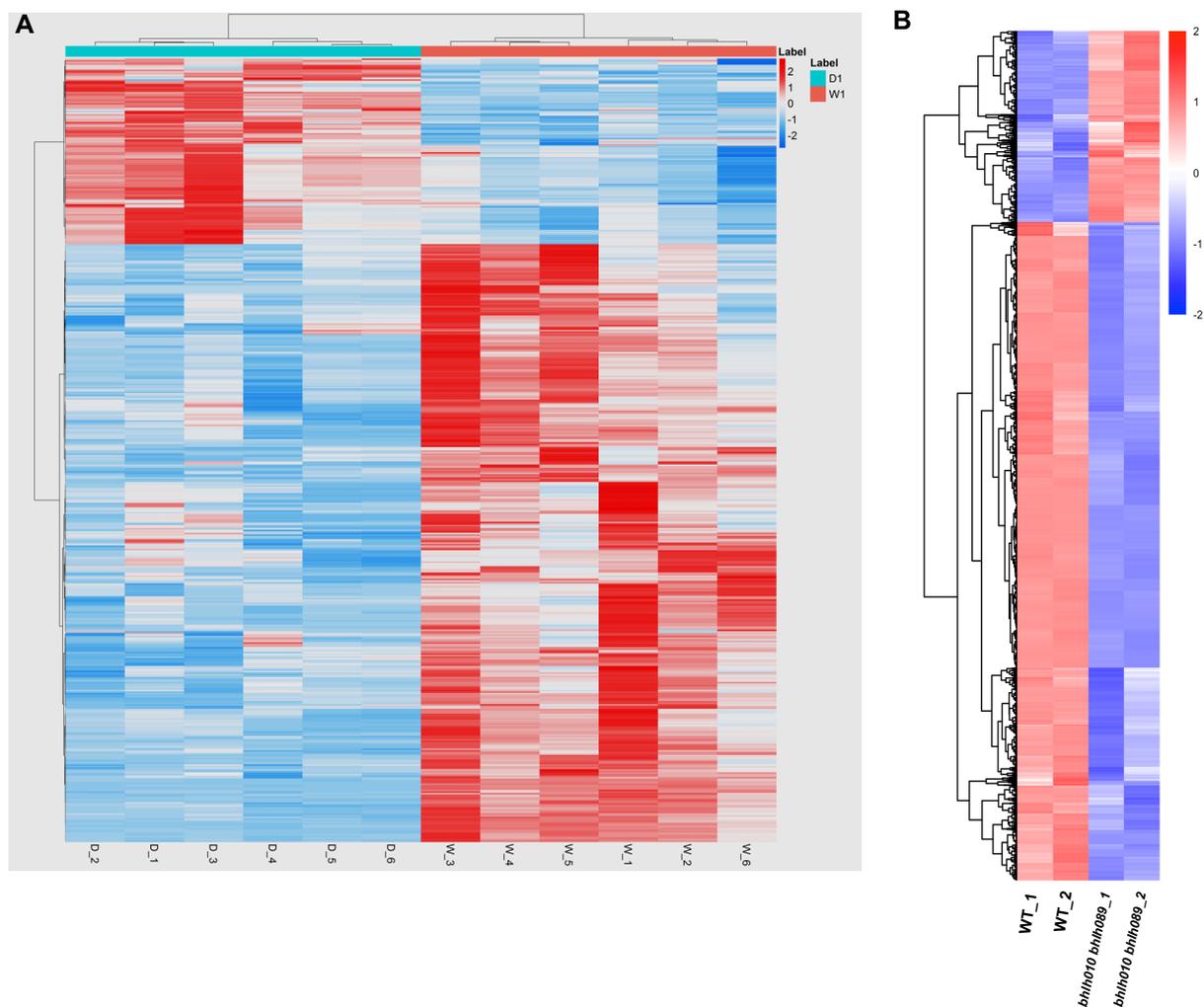
**Supplemental Figure S1.** The silique length of *bhlh010 bhlh089* mutant plants was obviously reduced. Student's *t*-test was used for difference comparison. \*\*\*\*,  $P < 0.0001$ . Data were means  $\pm$  SD ( $n = 3$ ).



**Supplemental Figure S2. Transverse sections of the pollen wall development were performed in WT and the *bhlh010 bhlh089* double mutant .**

(A) The development of pollen wall has not yet begun at stage 5-7. There was no significant difference between WT and *bhlh010 bhlh089* double mutant. Bars =10  $\mu$ m.

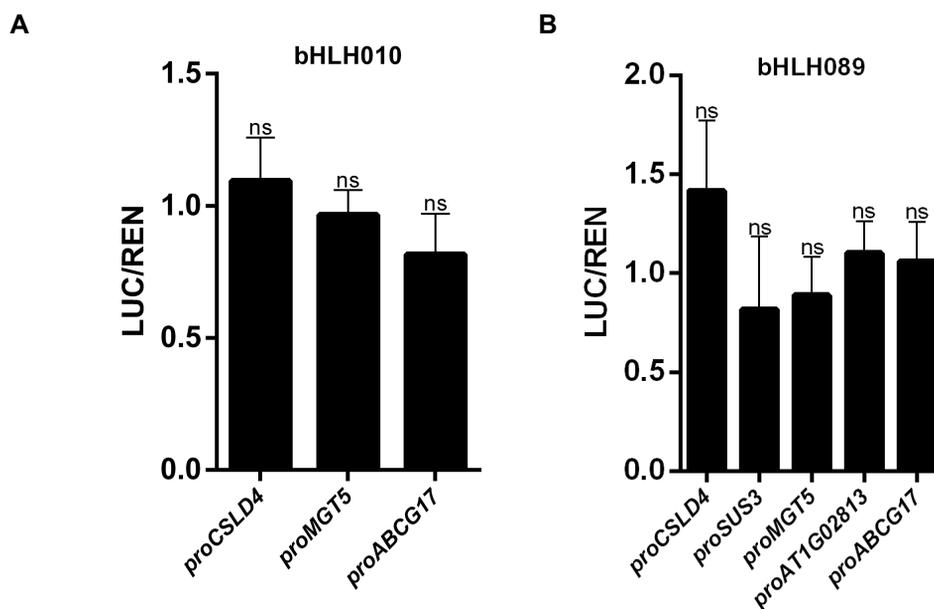
(B) The pollen of the first 12 flowers were completely aborted. It only forms the pollen exine, not intine. The red arrow indicates the exine. Bars =10  $\mu$ m.



**Supplemental Figure S3. Analysis of total differential genes and total differential metabolites of WT and *bhlh010 089* double mutants.**

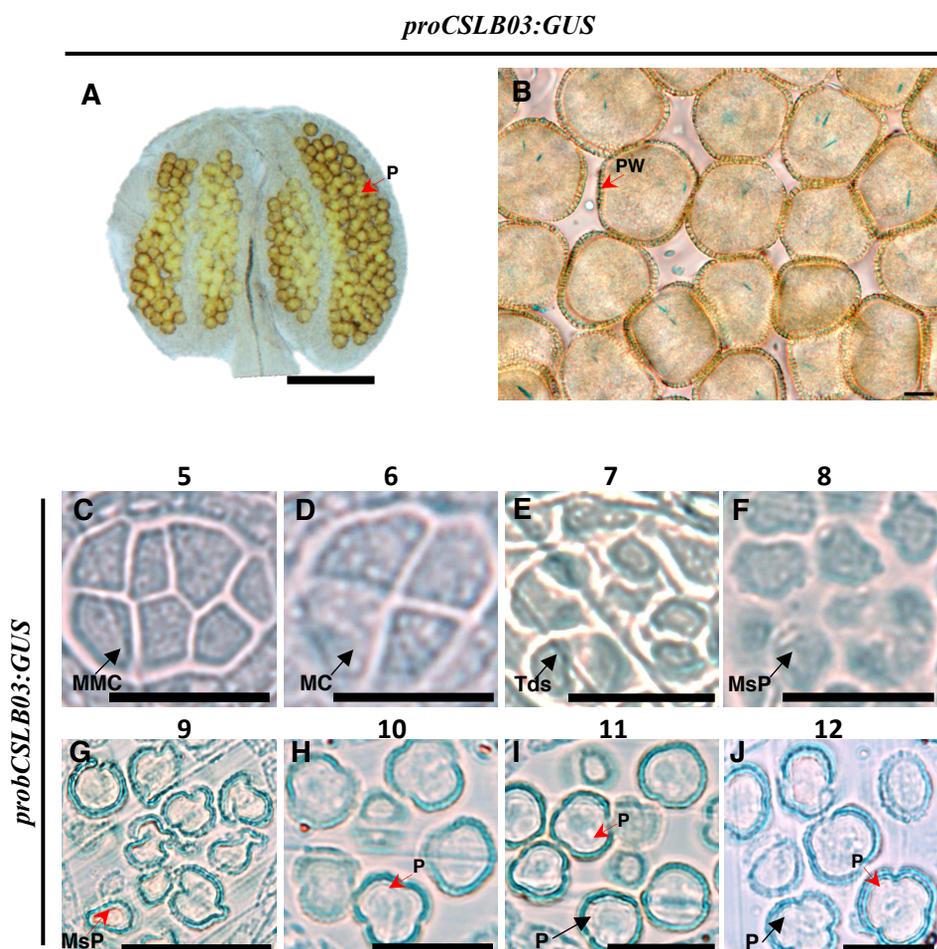
(A) The Heat maps represented total differential metabolites (DEMs) involved in WT (W1) and *bhlh010 bhlh089* (D1) double mutant inflorescence. Differential metabolites were screened out by VIP (Variable Importance in the Projection) value of OPLS-DA model ( $VIP \geq 1$ ) and independent sample *t*-test ( $p < 0.05$ ). Adduct manner:  $[M+H]^+$  and  $[M+Na]^+$  was selected in positive mode,  $[M-H]^-$  in negative mode. Mass error value: 30 PPM. red and blue color represents upregulated and downregulated DEMs.

(B) The Heat maps represented total differential genes (DEGs) involved in WT and *bhlh010 bhlh089* double mutant anthers. Relative expression was calculated by  $-\log_2$  (Fold change) and  $P < 0.01$ , red and blue color represents upregulated and downregulated DEGs.



**Supplemental Figure S4. The transcriptional activation capacity of bHLH010 and bHLH089 was detected.**

(A, B) Dual-Luciferase assay was used to detect transcriptional activation. (A) The transcription factor bHLH010 does not directly transcribes activated genes. (B) The transcription factor bHLH089 does not directly transcribes activated genes. Significant differences compared with the WT were determined using Student's *t*-test: ns indicates no significant difference. Data are shown as means $\pm$ SD (n =3).

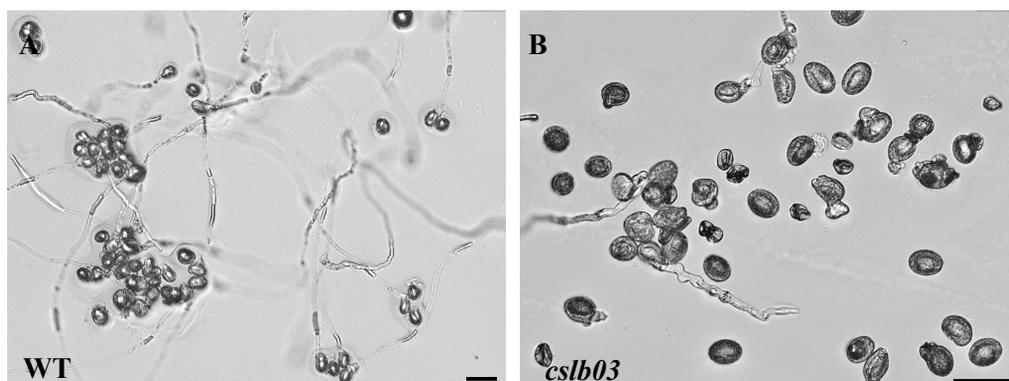


### Supplemental Figure S5. Tissue expression pattern of CSLB03.

(A) Tissue expression pattern of CSLB03 in *proCSLB03:GUS*, bar=50  $\mu$ m. CSLB03 is specifically expressed in the pollen of anthers. P, pollen.

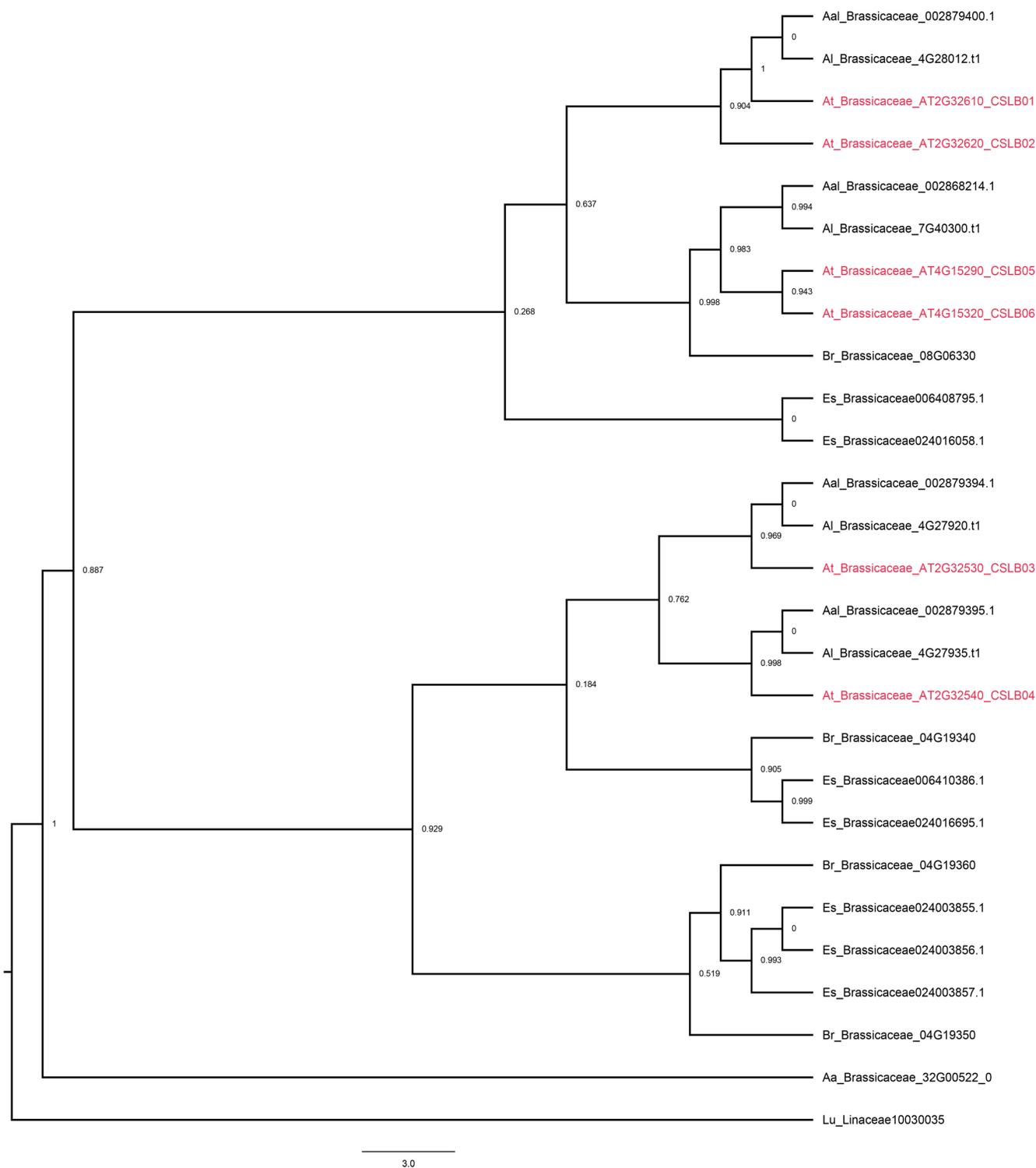
(B) CSLB03 is specifically expressed in the pollen. PW, pollen wall. bar=10  $\mu$ m.

(C-J) Transverse sections of the pollen development of CSLB03 in *proCSLB03:GUS* at stages 5–12. The CSLB03 was specially expressed in pollen. The CSLB03 expression level was highest in stage 9–12. MMC, Microspore mother cell; MC, Microspore cell; Tds, tetrad cells; MsP, microspore; P, pollen; PW, pollen wall. Bars =25  $\mu$ m.



**Supplemental Figure S6. The pollen germination of *cs/b03* mutant was severely abnormal.**

(A, B) Pollen germination experiment. Pollen germination of WT (A) was normal and that of *cs/b03* mutant (B) could not completely germinate or germination was slow. Bars =50  $\mu$ m.



### Supplemental Figure S7. Phylogenetic analysis of CSLB1/2/3/4/5/6 subfamily.

The bootstrap values are indicated near the nodes. Genes from Arabidopsis thaliana are highlighted in red.

Aa, *Aethionema arabicum*; Aal, *Arabis alpine*; At, *Arabidopsis thaliana*; Br, *Brassica rapa*; Es, *Eutrema salsugineum*; Lu, *Linum usitatissimum*.