Supporting information

Proteomic analysis reveals that sugar and fatty acid metabolisms play a central role in sterility of the male-sterile line 1355A of cotton

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Running Title*: proteomic analysis of male-sterile line 1355A of cotton*

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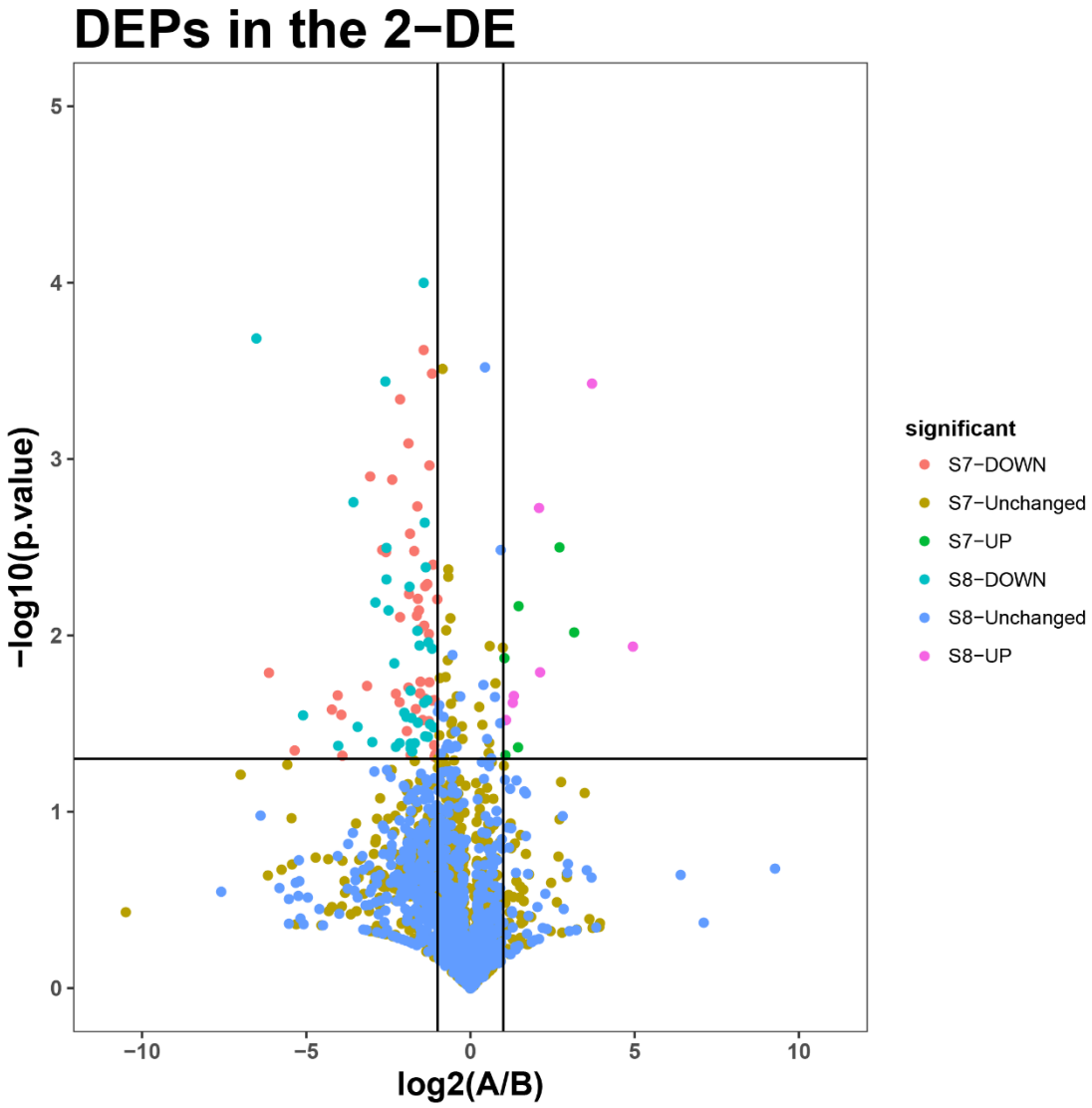
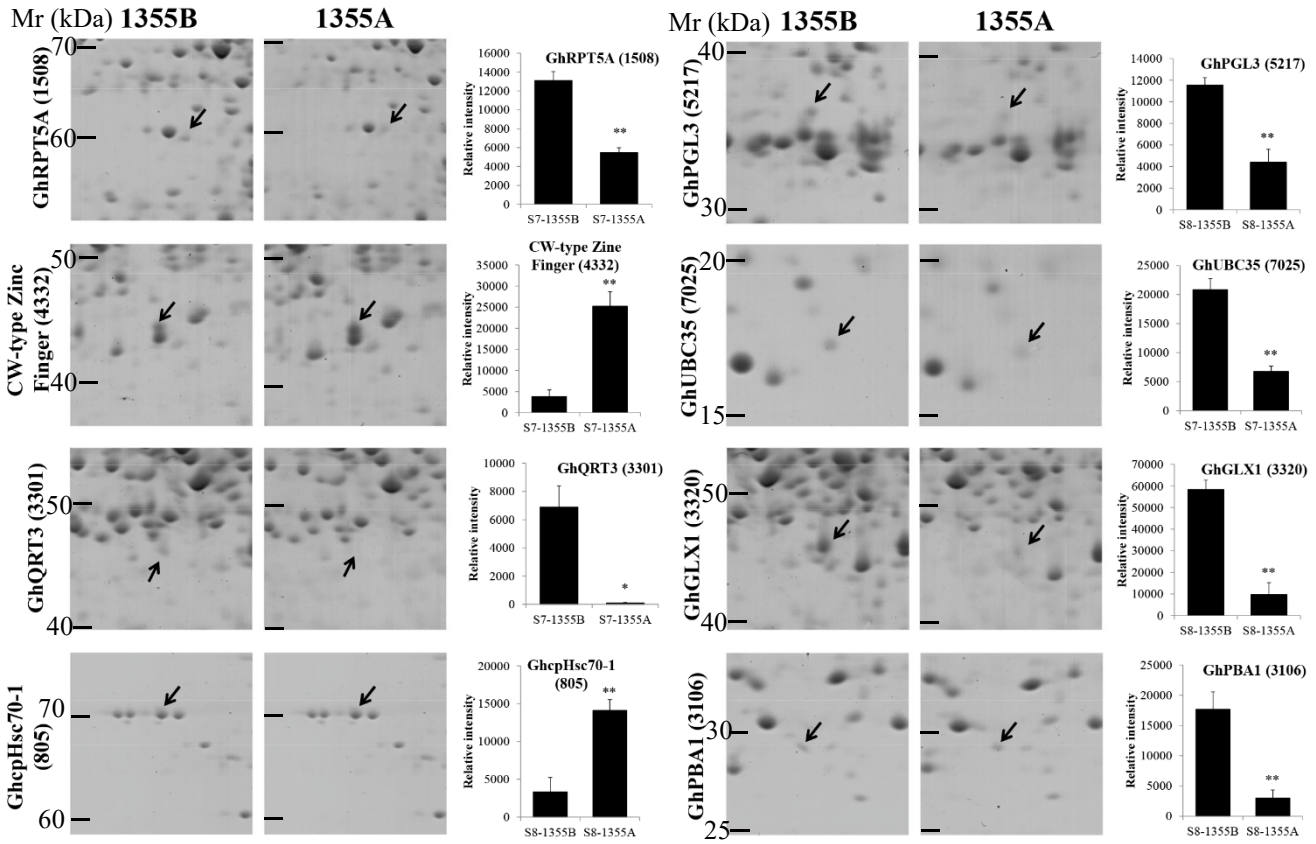
Supplementary Fig. S1



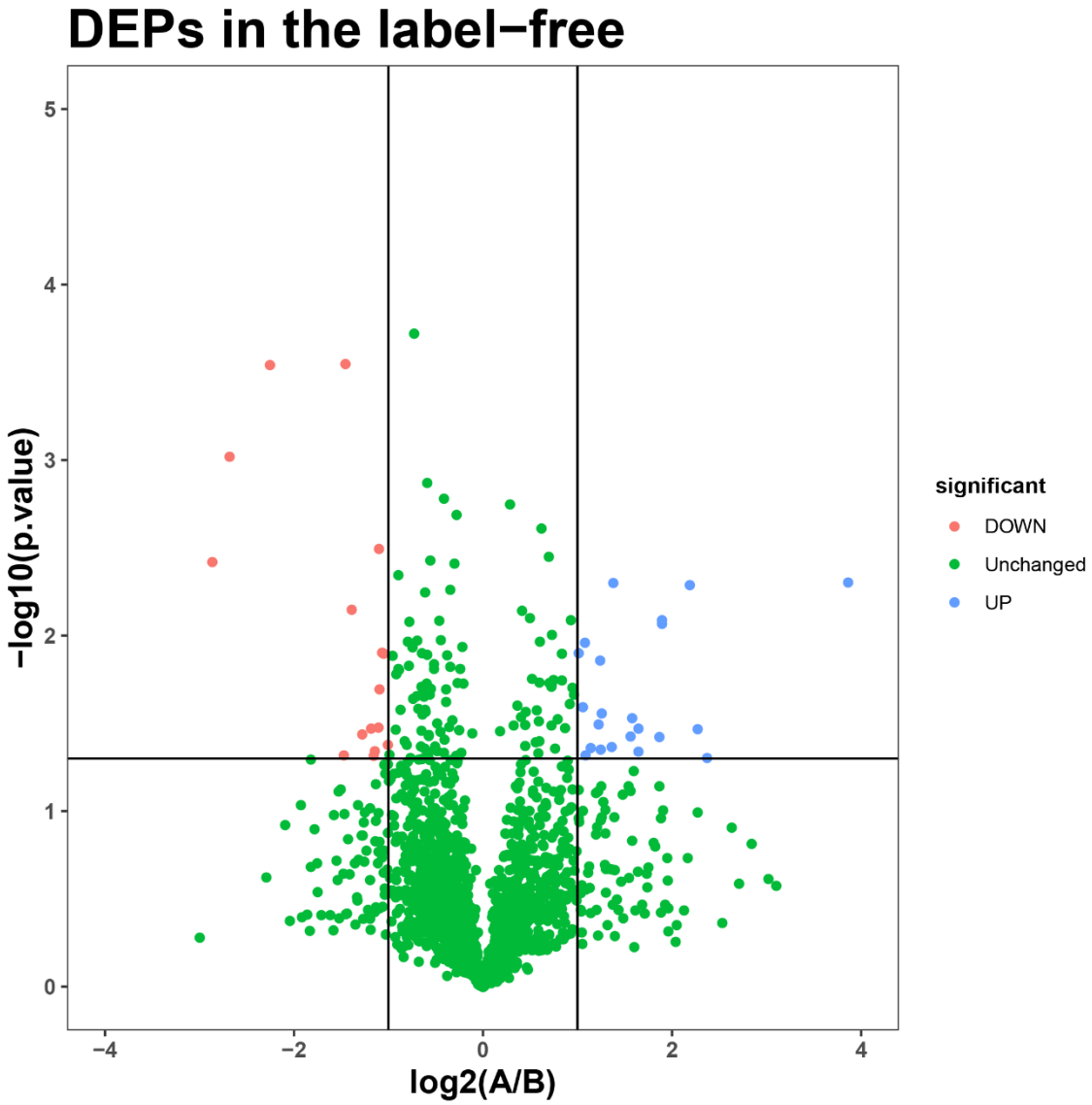
Supplementary Fig. S1 Volcano plots of the differentially expressed proteins (DEPs) in the comparisons of the male-sterile line 1355A and the male-fertile line 1355B by using 2-DE, S7-up and S7-down, Stage 7 up-regulated proteins and Stage 7 down-regulated proteins; S8-up and S8-down, Stage 8 up-regulated proteins and Stage 8 down-regulated proteins.

Supplementary Fig. S2



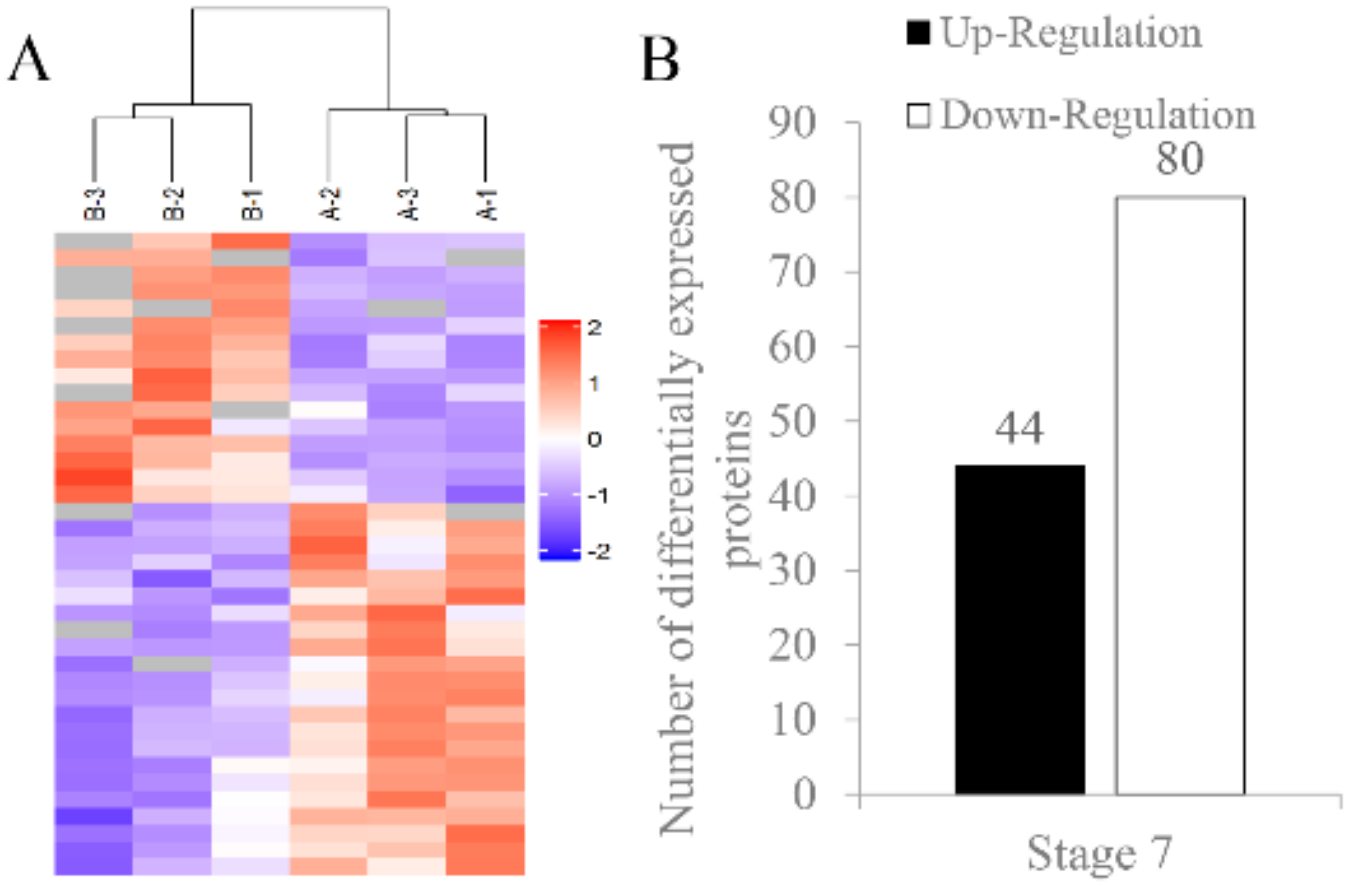
Supplementary Fig. S2 Representative differentially expressed protein spots shown on 2-DE maps and quantification of the signal intensities. GhRPT5A (regulatory particle triple-A ATPase 5A, ssp1508, A0A0B0MS04), CW-type Zinc Finger (ssp4332, A0A0D2Q9J7), GhUBC35 (ubiquitin-conjugating enzyme 35, ssp7025, A0A0B0PN86), GhPGL4 (6-phosphogluconolactonase 4, ssp5217, A0A0B0NNT9), GhQRT3 (pectin lyase-like superfamily protein, ssp3301, A0A0D2NIW7), GhGLX1 (glyoxalase I homolog, ssp3320, D2D330), GhcpHsc70-1 (chloroplast heat shock protein 70-1, ssp0805, A0A0B0MM52) and GhPBA1 (proteasome subunit beta, ssp3106, A0A0D2U4R1). Molecular weight (Mr, kDa) and isoelectric point calculated by using molecular weight standards and the PD-Quest software. The relative Mr is given on the left. The regions derived from the same 1355B and 1355A 2-DE gel, are given on the left and right respectively.

Supplementary Fig. S3



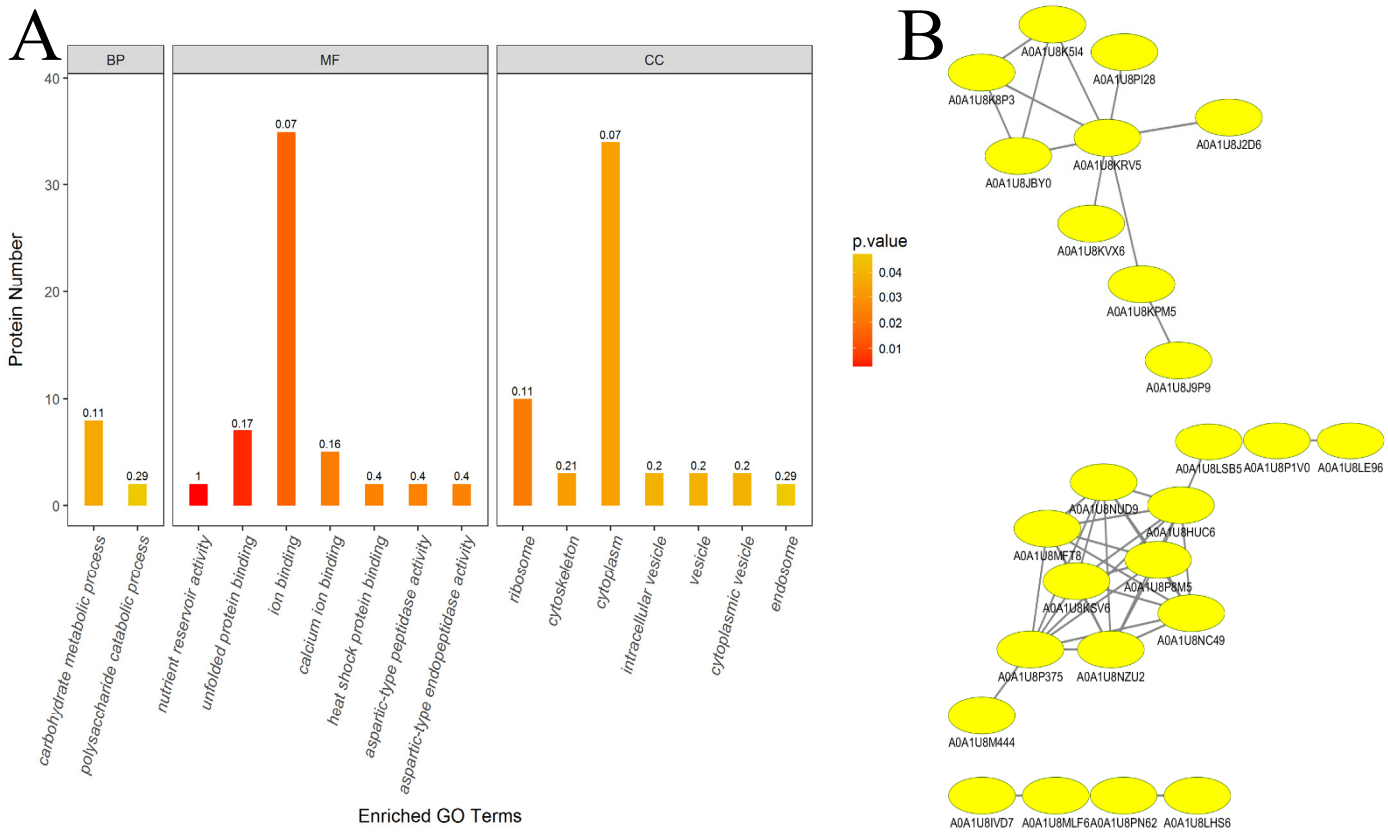
Supplementary Fig. S3 Volcano plots of the differentially expressed proteins (DEPs) in the comparisons of the male-sterile line 1355A and the male-fertile line 1355B at stage 7 by using label-free, and 38 significantly DEPs were detected at stage 7 between the 1355A and 1355B plants ($p \leq 0.05$ and fold-change ≥ 2 or ≤ 0.5).

Supplementary Fig. S4



Supplementary Fig. S4 The statistical analysis of differentially expressed proteins by label-free methods.
(A) Cluster analysis of the differentially expressed proteins.
(B) The number of differentially expressed proteins that were up- or down- regulated during analyzed stages.

Supplementary Fig. S5

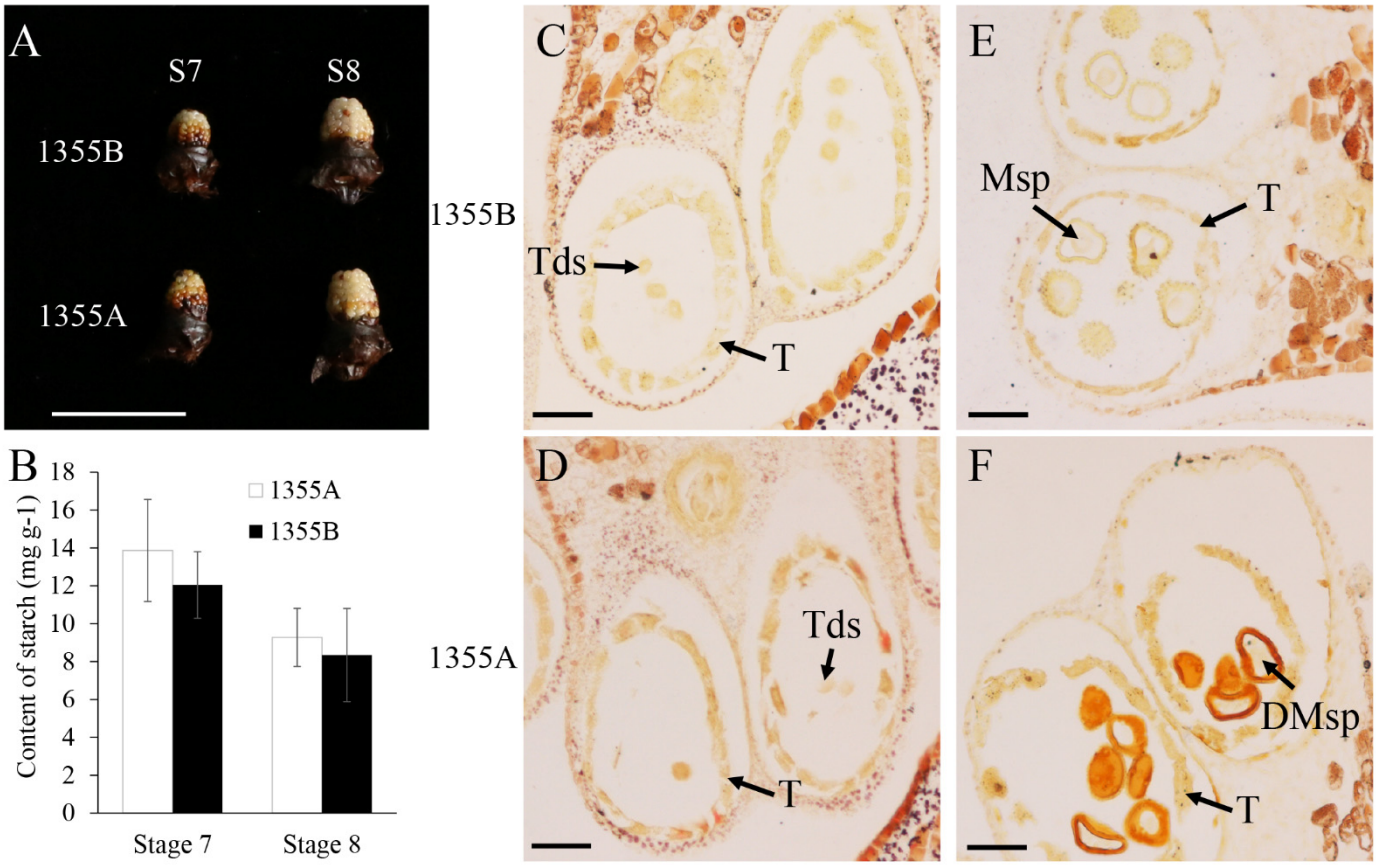


Supplementary Fig. S5 The bioinformatics analysis of the differentially expressed proteins by label-free methods.

(A) The GO enrichment analysis of the differentially expressed proteins.

(B) The Protein-Protein Interact Network (PPI) analysis of the differentially expressed proteins.

Supplementary Fig. S6



Supplementary Fig. S6 Starch detection of 1355A/B anther during analyzed stages.
(A) The buds of 1355A/B stained with I_2-KI.
(B) The contents of starch in 1355A/B anther.
(C-F) The anther wall in 1355A/B cross sections stained with Lugol solution. (C) and (D) were stage 7, (E) and (F) were stage 8; (C) and (E) were 1355B anther, (D) and (F) were 1355A anther. S7, stage 7; S8, stage 8; Tds, tetrads; T, tapetal layer; Msp, microspores and DMsp, degenerated microspores. Bars = 50 μm.