

SUPPLEMENTAL DATA

(The tables are in one Excel file: Zheng Supplemental Tables)

Supplemental Table S1. Genes induced by ABA in wild-type (Ws)

Supplemental Table S2. Genes suppressed by ABA in wild-type (Ws)

Supplemental Table S3. Genes induced by ABA in *rop10-1*

Supplemental Table S4. Genes suppressed by ABA in *rop10-1*

Supplemental Table S5. Genes induced by ABA in wild-type (Ws) but not in *rop10-1*

Supplemental Table S6. Genes induced by ABA in *rop10-1* but not in wild-type (Ws)

Supplemental Table S7. Genes with higher expression in ABA-treated *rop10-1* than in ABA-

treated Ws

Supplemental Table S8. Genes commonly activated and repressed by ABA in Ws and *rop10-1*

Supplemental Table S9. Primers used in RT-PCR analysis

Supplemental Figure 1. Average fold changes in expression of ABA-affected genes in Ws and *rop10-1*. (A) The average fold change for 119 genes determined to be ABA-activated by the 2-fold cut-off in *rop10-1* but not in Ws. (B) The average fold change for 40 genes determined to be ABA-activated in Ws but not in *rop10-1*. “Ws: ABA/CK”, Ws - ABA vs. Ws - control (no ABA); “CK: *rop10*/Ws”, *rop10-1* - control vs. Ws - control; “*rop10*: ABA/CK”, ABA - *rop10-1* vs. control - *rop10-1*. The bar represents SD.