



Figure S9. RT-PCR and phenotyping of WT, septuple mutant and transformants with *ICK7*.

(A) *ICK7* transcript analysis. cDNAs synthesized from total RNAs were used to detect the *ICK7* transcripts in WT, septuple mutant and two transformants with *ICK7* genomic fragment. *Actin* (*ACT8*) was amplified as a control.

(B) Silique length of WT, septuple mutant and the two transformants. Ten siliques (6th-15th) from the bottom of the main inflorescence were measured for each plant. The averages and standard deviations are shown.

(C) Opened siliques of WT, septuple mutant and the two transformants showing the seed development. Scale bar = 1 mm.

(D) Number of seeds per silique (8 siliques (7th-14th) in the main inflorescence from each plant). The averages and standard deviations are shown.

(E) Number of aborted ovules per silique. Fully extended siliques (8 siliques for each plant) were opened and aborted ovules counted under a dissecting microscope. The averages and standard deviations are shown.

Data in (B, D, E) were analyzed using one-way ANOVA and post-hoc Tukey test, and significant differences are indicated by different letters (upper case) at $p < 0.01$ level.