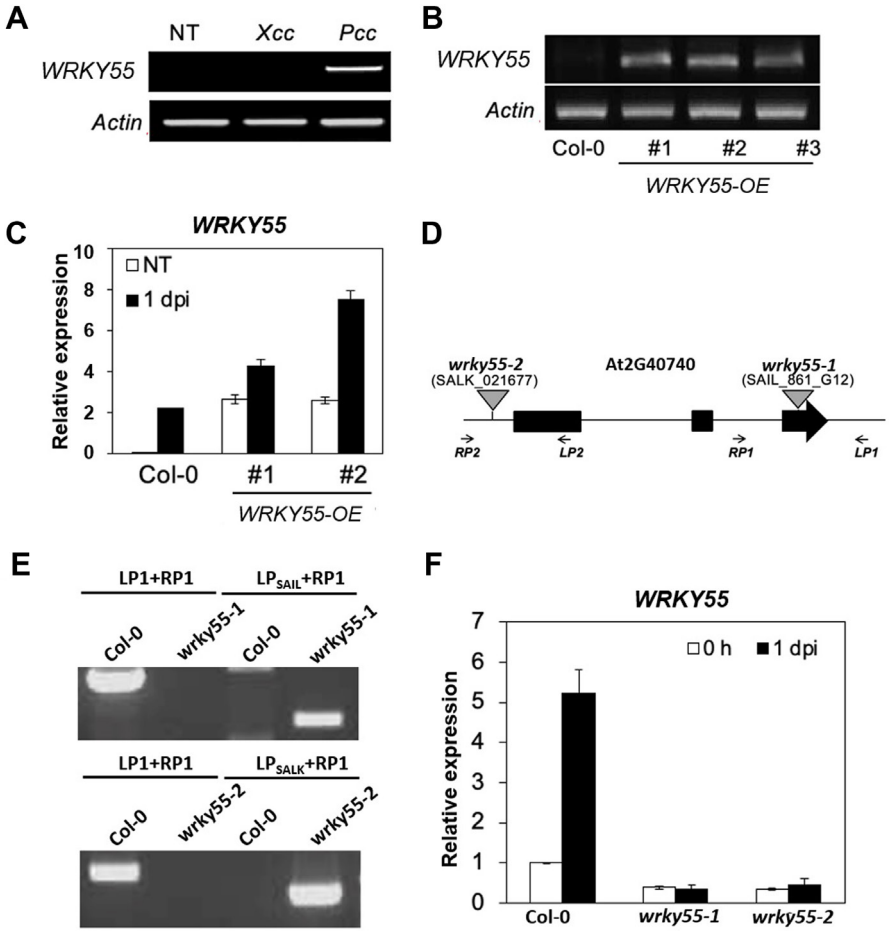

Supplementary Fig. 1. The expression of *WRKY55* in response to *Xanthomonas citri* subsp. *citri* (*Xcc*) and *Arabidopsis* overexpression or knock-out plants. (A) *WRKY55* expression by semi-quantitative RT-PCR. Induced *WRKY55* transcripts in Col-0 against *Pectobacterium carotovorum* ssp. *carotovorum* (*Pcc*) or *Xcc* were confirmed 24 h post-infection. Amplified *Actin* was used to demonstrate a loading control. (B) The transcript levels of *WRKY55* in three independent *WRKY55-OE* transgenic lines. RT-PCR with *WRKY55*-specific primers was employed to confirm the expression. *Actin* served as a loading control. (C) Monitoring the transcript levels of *WRKY55-OE* transgenic lines by quantitative RT-PCR (qRT-PCR) analysis with *WRKY55*-specific primers. qRT-PCR was fulfilled 24 h post-infection of *Pcc*. The relative expression of *WRKY55* was normalized to the expression of *Actin*. Scale bars represent standard deviation ($n = 3$). (D) The diagram of T-DNA insertion sites in two independent *wrky55* mutants: *wrky55-1* (SAIL_861_G12) and *wrky55-2* (SALK_021677). Primer pairs to confirm each mutant of *WRKY55* were shown at the bottom of the diagram. (E) Homozygous mutants of *wrky55*. PCR-based genotyping genomic DNA samples from Col-0, *wrky55-1*, or *wrky55-2* was performed with the primer pairs as shown in (D). (F) Expression of *WRKY55* in KO plants. qRT-PCR analysis to demonstrate the expression of *WRKY55* in Col-0 and *wrky55* mutant plants. The plant samples were inoculated with *Pcc* as described in (C).