

Expanded View Figures

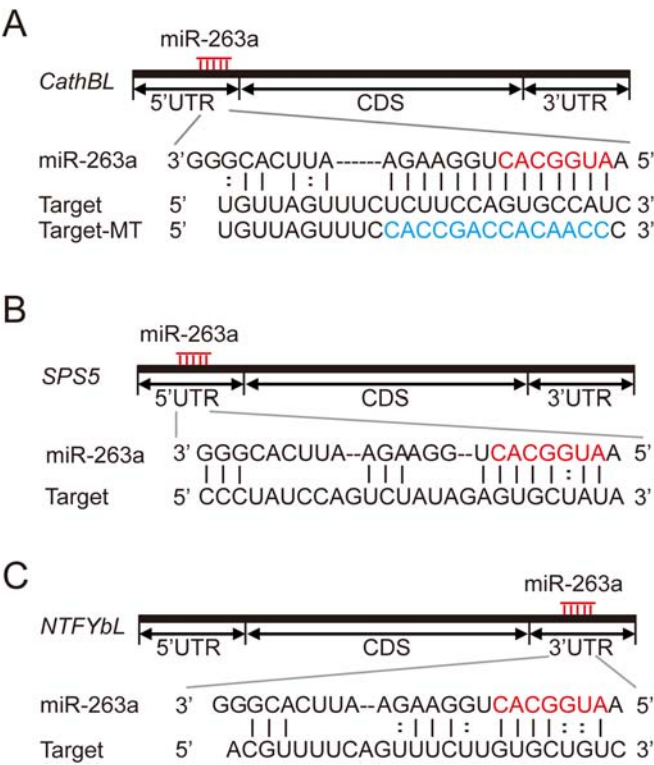


Figure EV1. Sequence alignments of miR-263a with the candidate target genes of SBPH.

(A) *Cathepsin B-like (CathBL)*. The mutated target (Target-MT) is also shown. (B) *Nuclear transcription factor Y subunit beta-like (NTFYbL)*. (C) *Serine protease snake-5 (SPS5)*. The miR-263a seed sequence is highlighted in red and the mutated sequences are indicated in blue.

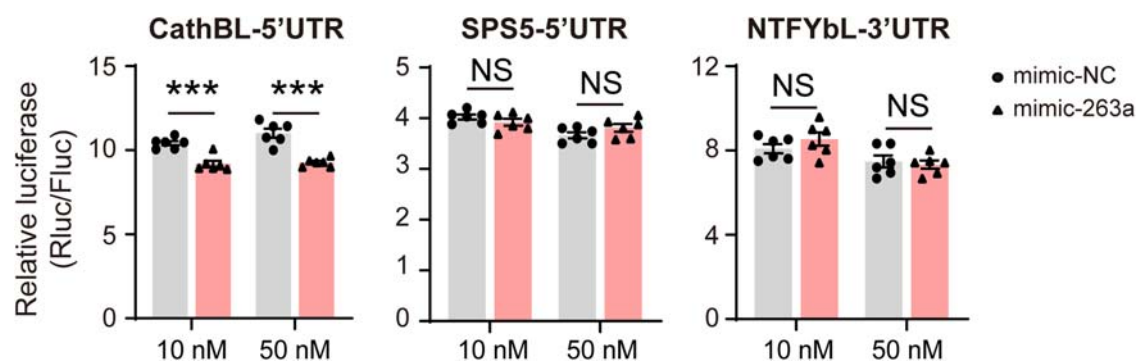


Figure EV2. Luciferase reporter assays in *Drosophila* S2 cells cotransfected with miR-263a/NC mimics and psiCHECK2 vectors containing *CathBL* 5'UTR, *SPSS* 5'UTR, and *NTFYbL* 3'UTR as the candidate targets of miR-263a.

P values from left to right, $P = 2.83 \times 10^{-4}$, $P = 1.27 \times 10^{-4}$. Six biological replicates were prepared. Values are shown as mean $\pm$ SE and were compared using Student's *t* test. NS, no significant difference. *** $P < 0.001$.

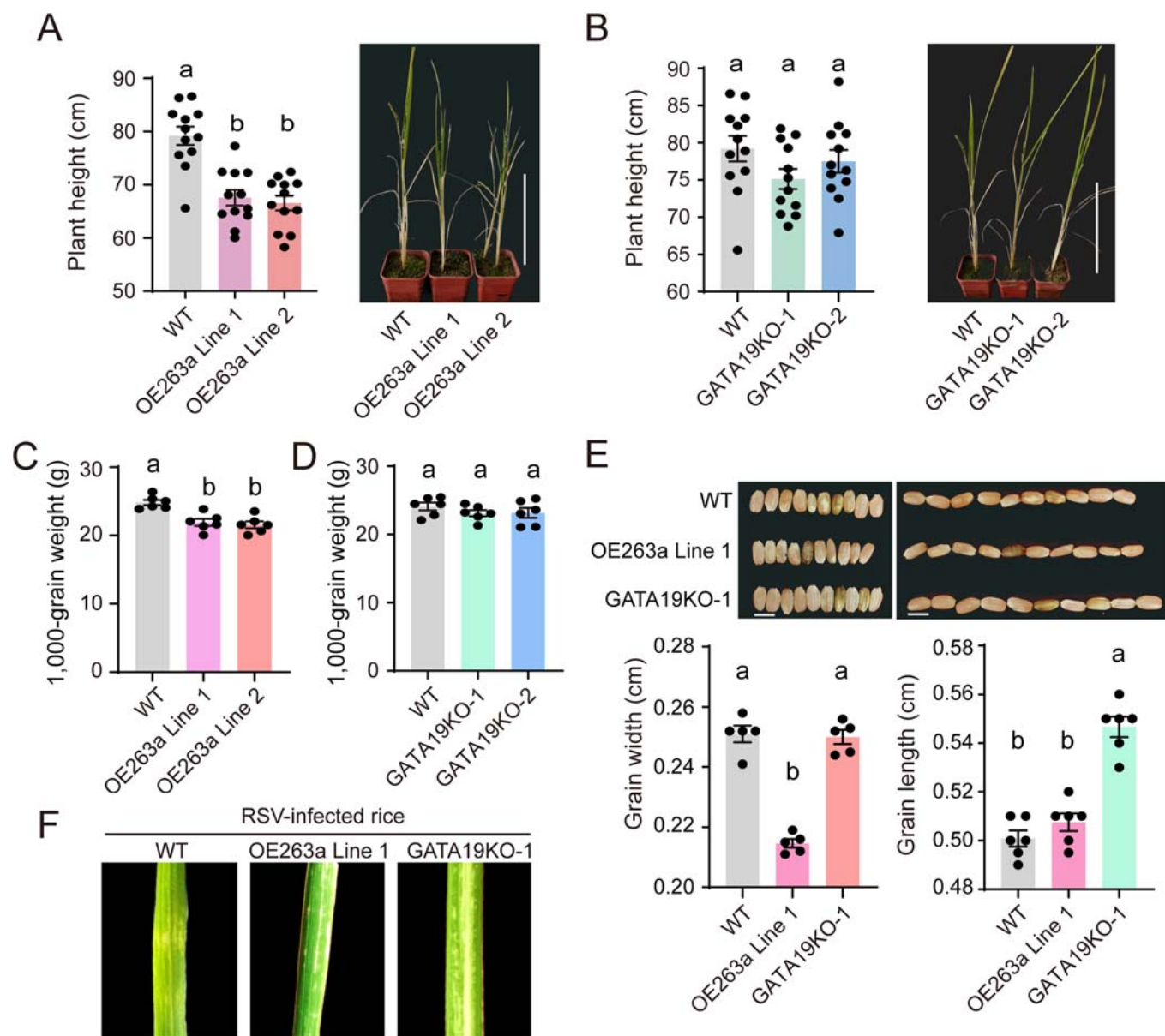


Figure EV3. Gross morphology of rice plants.

(A) Comparative plant height between WT and OE263a lines, with a scale bar representing 50 cm. Twelve biological replicates were prepared, with each replicate including one rice plant. (B) Plant height comparison between WT and GATA19KO lines, utilizing the same scale bar for reference. Twelve biological replicates were prepared, with each replicate including one rice plant. (C) The 1000-grain weight of WT and OE263a lines. Six biological replicates were prepared. (D) The 1000-grain weight of WT and GATA19KO lines. Six biological replicates were prepared. (E) Husked grain width and length of WT, OE263a, and GATA19KO lines. Scale bars: 5 mm. Five to six biological replicates were prepared, with each replicate including 10 grains. (F) Disease symptom of WT, OE263a, and GATA19KO lines after inoculation with RSV. For (A) to (E), the values are reported as mean $\pm$ SE. Data comparisons among multiple groups were performed using one-way analysis of variance (ANOVA) followed by Tukey's test. Different letters indicate significant differences.

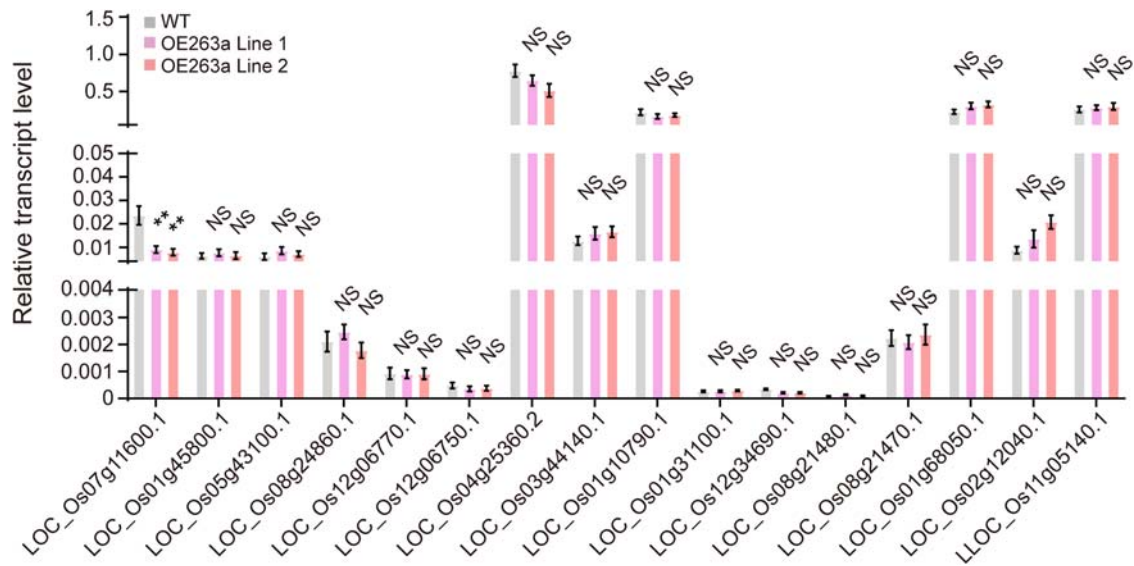


Figure EV4. Relative transcript levels of 16 candidate target genes of miR-263a in WT and OE263a rice lines. Eight biological replicates were prepared, with each replicate including two leaves. *P* values from left to right, *P* = 0.0041, *P* = 0.0062. Values are reported as mean ± SE and were compared by Student's *t* test. NS, no significant difference. ***P* < 0.01.

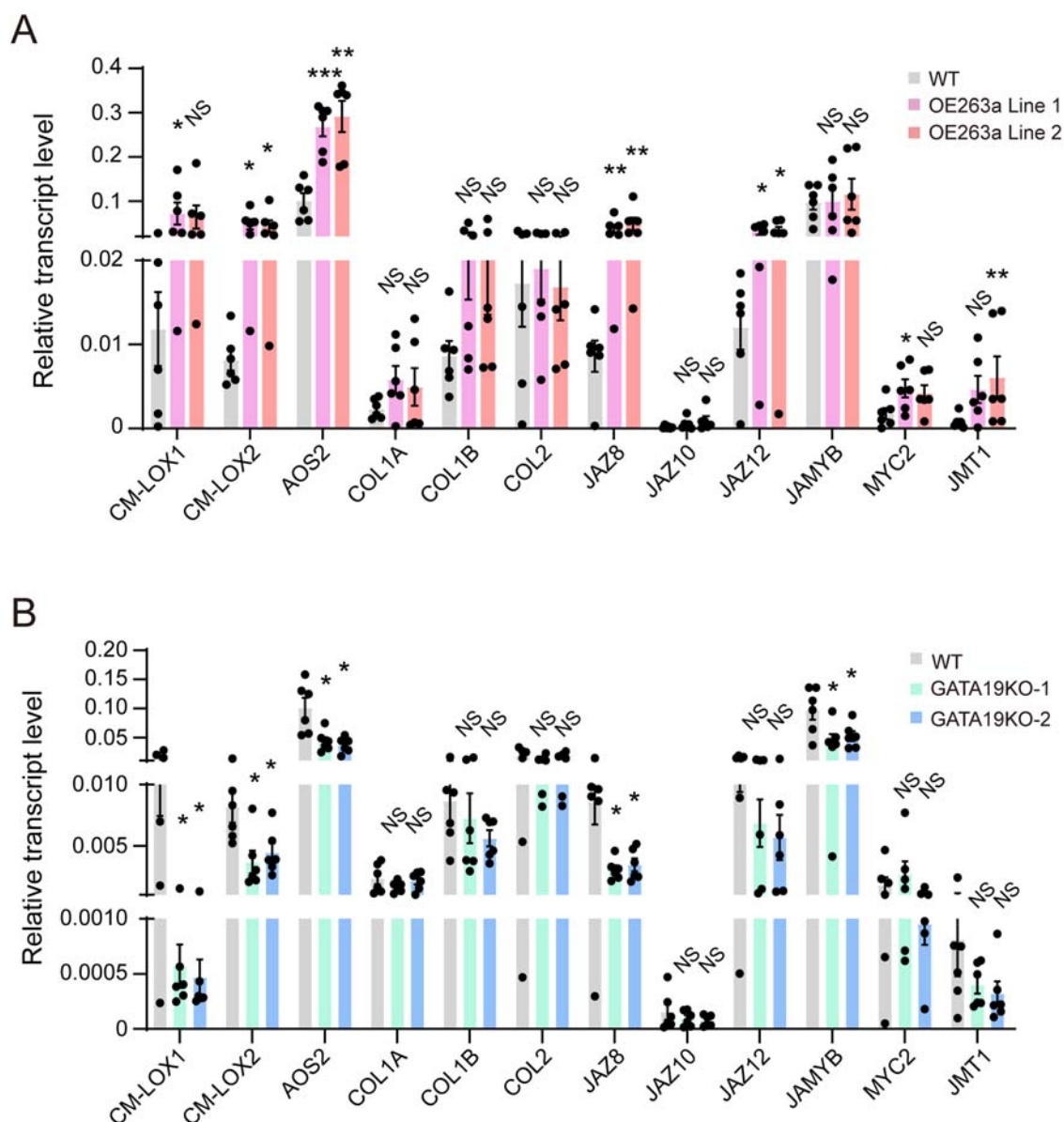


Figure EV5. Relative transcript levels of 12 genes relative to jasmonate signaling pathway in WT and OE263a lines (A), or in WT and GATA19KO lines (B).

Six biological replicates were prepared, with each replicate including two leaves. For (A), P values from left to right, $P = 0.0395$ (CM-LOX1), $P = 0.0171$ (CM-LOX2), $P = 0.0476$ (CM-LOX2), $P = 1.45E-04$ (AOS2), $P = 0.0022$ (AOS2), $P = 0.0043$ (JAZ8), $P = 0.0022$ (JAZ8), $P = 0.0299$ (JAZ12), $P = 0.0398$ (JAZ12), $P = 0.0400$ (MYC2), $P = 0.0087$ (JMT1). For (B), P values from left to right, $P = 0.0260$ (CM-LOX1), $P = 0.0260$ (CM-LOX1), $P = 0.0152$ (CM-LOX2), $P = 0.0296$ (CM-LOX2), $P = 0.0129$ (AOS2), $P = 0.0134$ (AOS2), $P = 0.0260$ (JAZ8), $P = 0.0260$ (JAZ8), $P = 0.0252$ (JAMYB), $P = 0.0354$ (JAMYB). Values are presented as mean $\pm$ SE and were compared by Student's t test. NS, no significant difference. * $P < 0.05$. ** $P < 0.01$. *** $P < 0.001$.

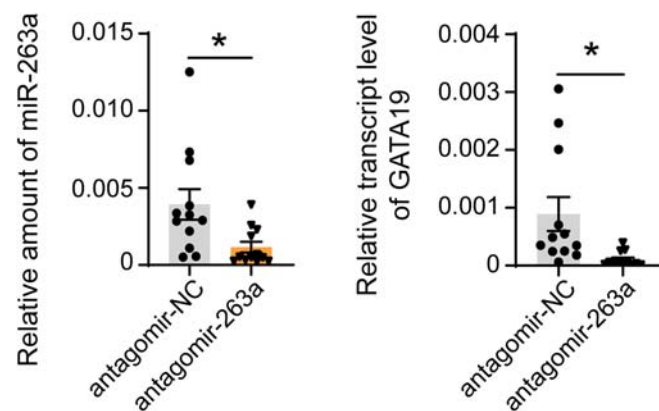


Figure EV6. Relative amount of miR-263a and relative transcript level of GATA19 in wild-type rice fed upon by nonviruliferous SBPHs with injection of antagomir-263a or NC.

OsU6 snRNA and *UBQ10* serve as internal references for miRNA and gene, respectively. Twelve biological replicates were prepared, with each replicate including two leaves. P values from left to right, $P = 0.0202$, $P = 0.0211$. Values are presented as mean $\pm$ SE and were compared by Student's t test. * $P < 0.05$.