

Expanded View Figures

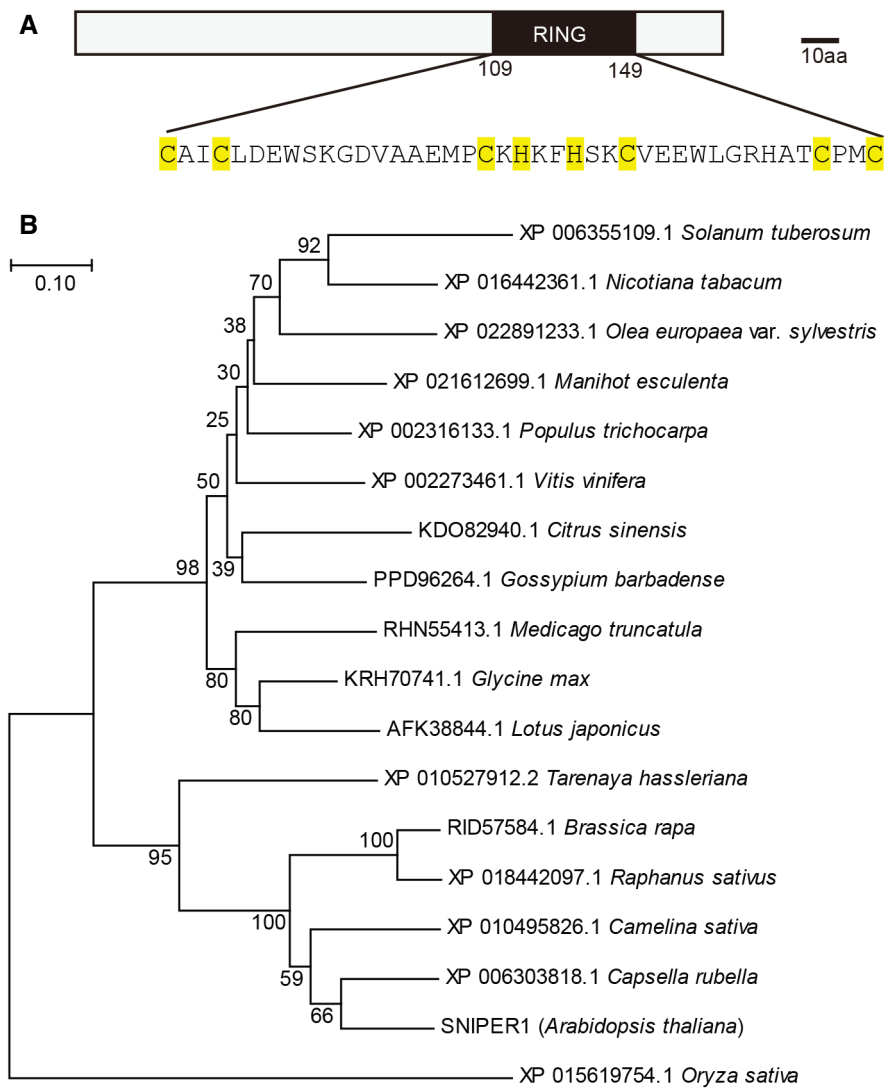


Figure EV1. Phylogenetic tree of SNIPER1 in dicots.

A Schematic structure of SNIPER1. The conserved residues of the RING domain are highlighted in yellow.

B Phylogenetic tree of putative SNIPER1 orthologs in dicots. Putative SNIPER1 orthologs were obtained from NCBI using SNIPER1 protein sequence as input. Closest orthology in *Oryza sativa* was used as an outgroup. Muscle was used for sequences alignment and a neighbor-joining tree was generated with JTT model and 5,000 bootstrap value in MEGA 7.0.

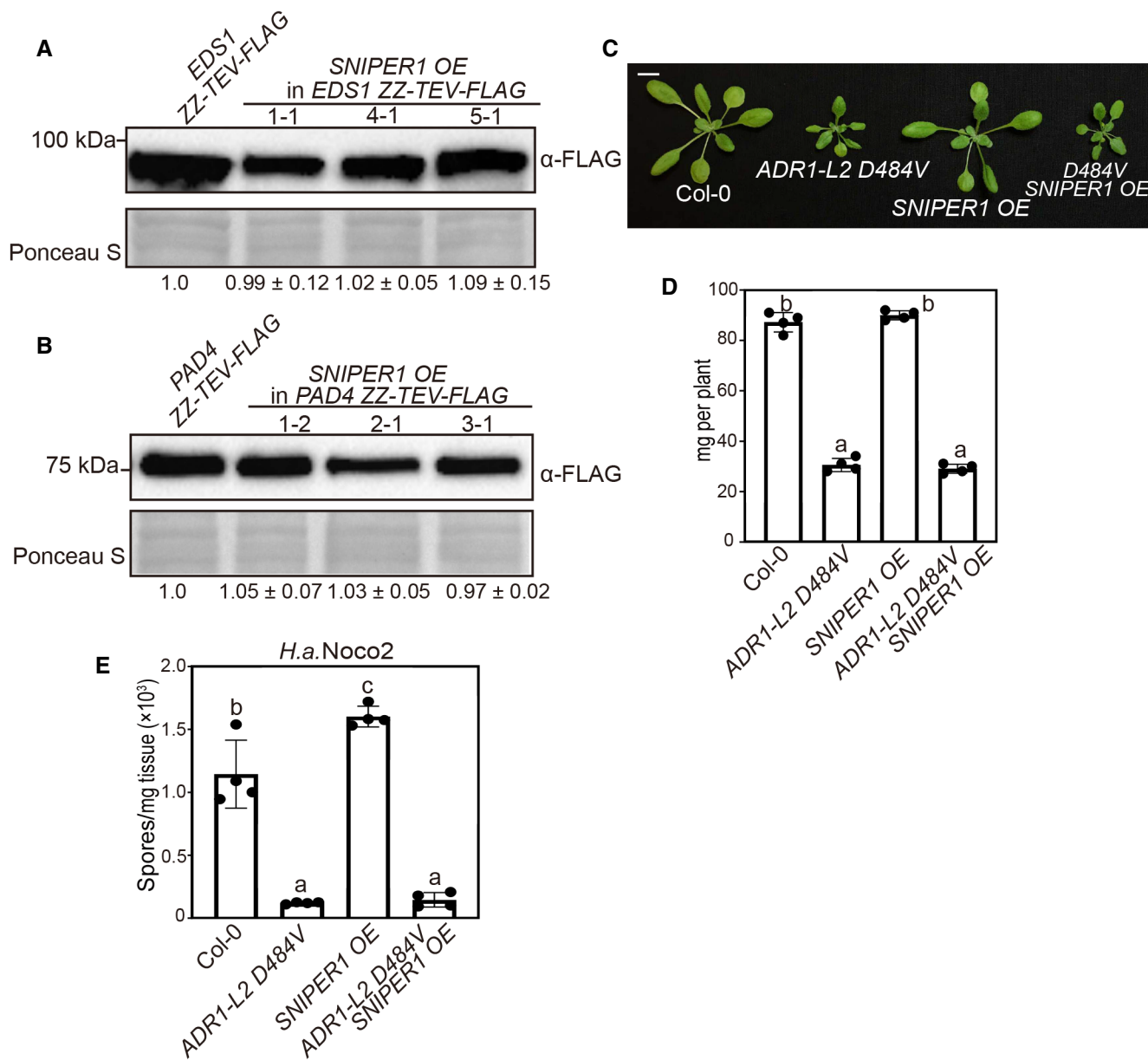


Figure EV2. SNIPER1 functions upstream of EDS1, PAD4, and ADR1 family helper NLRs.

A, B EDS1 (A) and PAD4 (B) protein levels in 4-week-old soil-grown plants. Equal loading is shown by Ponceau S staining of a non-specific band. The numbers below represent the normalized ratio between the intensity of the protein band and the Ponceau S band \pm SD ($n = 3$). Molecular mass markers in kilo Daltons are indicated on the left. Three independent experiments were carried out with similar results.

C Morphology of 4-week-old soil-grown plants of Col-0, ADR1-L2 D484V, SNIPER1 OE, and ADR1-L2 D484V SNIPER1 OE. Scale bar = 1 cm.

D Fresh weights of plants in (C).

E Quantification of *H.a. Noco2* sporulation in the indicated plants at 7 dpi with 10^5 spores per ml water.

Data information: For (D, E) one-way ANOVA followed by Tukey's *post hoc* test were performed. Statistical significance is indicated by different letters ($P < 0.01$). Error bars represent mean \pm SD ($n = 4$). At least two independent experiments were carried out with similar results.

Source data are available online for this figure.

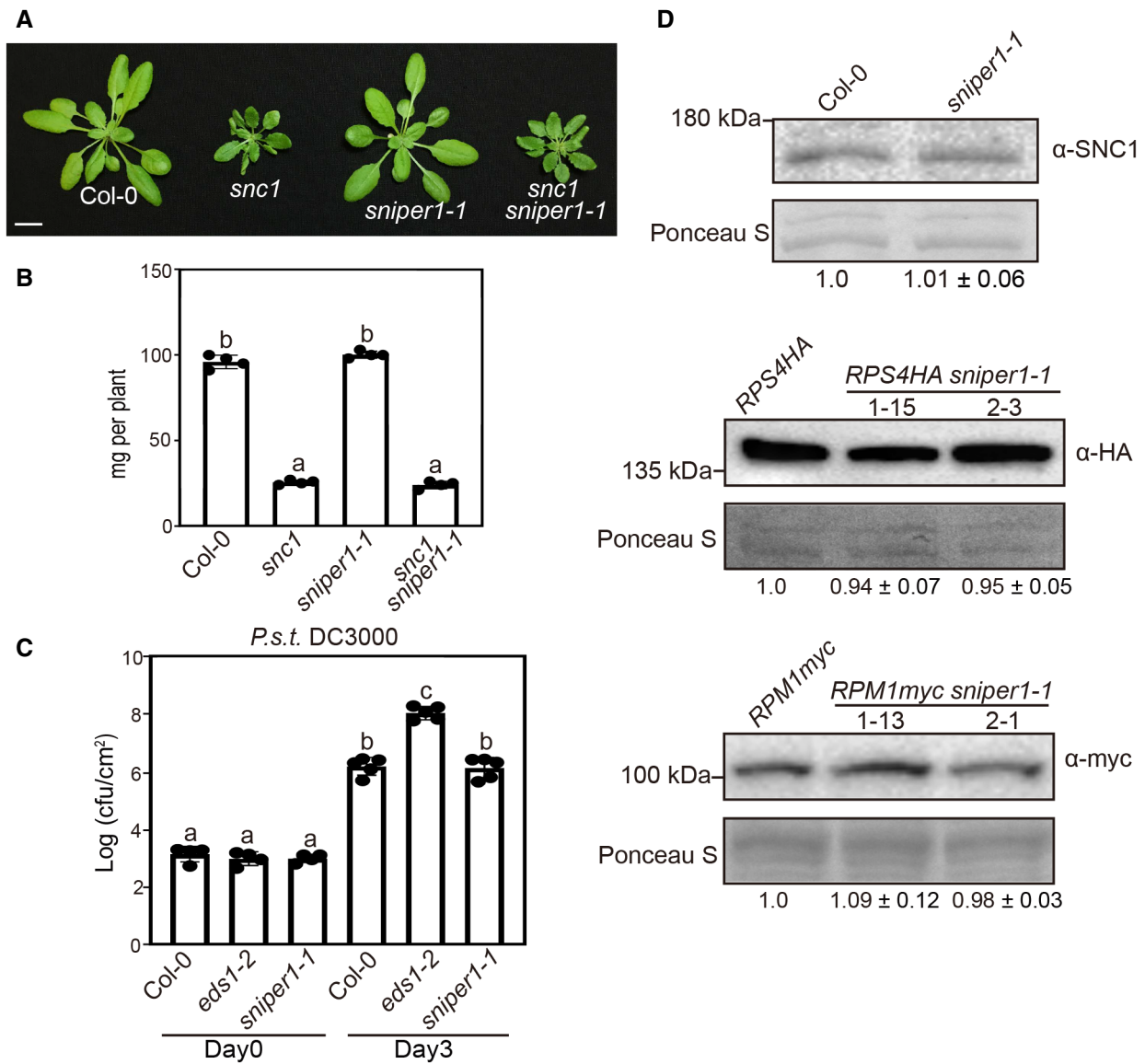


Figure EV3. Characterization of *sniper1-1* (SALKseq_054376) T-DNA insertion mutant.

A Morphology of 4-week-old Col-0, *snc1*, *sniper1-1*, and *snc1 sniper1-1*. Scale bar = 1 cm.

B Fresh weights of plants in (A). Error bars represent mean ± SD ($n = 4$).

C Bacterial growth of *P.s.t.* DC3000 on 4-week-old leaves of the indicated genotypes at 0 and 3 dpi with bacterial inoculum of $OD_{600} = 0.001$. Error bars represent mean ± SD ($n = 4$ for day 0; $n = 5$ for day 3).

D SNC1, RPS4-HA, and RPM1myc proteins levels in *sniper1-1* plants. Equal loading is shown by Ponceau S staining of a non-specific band. The numbers below represent the normalized ratio between the intensity of the protein band and the Ponceau S band ± SD ($n = 3$). Molecular mass markers in kilo Daltons are indicated on the left. Three independent experiments were carried out with similar results.

Data information: For (B, C) one-way ANOVA followed by Tukey's *post hoc* test were performed. Statistical significance is indicated by different letters ($P < 0.01$). Three independent experiments were carried out with similar results.

Source data are available online for this figure.

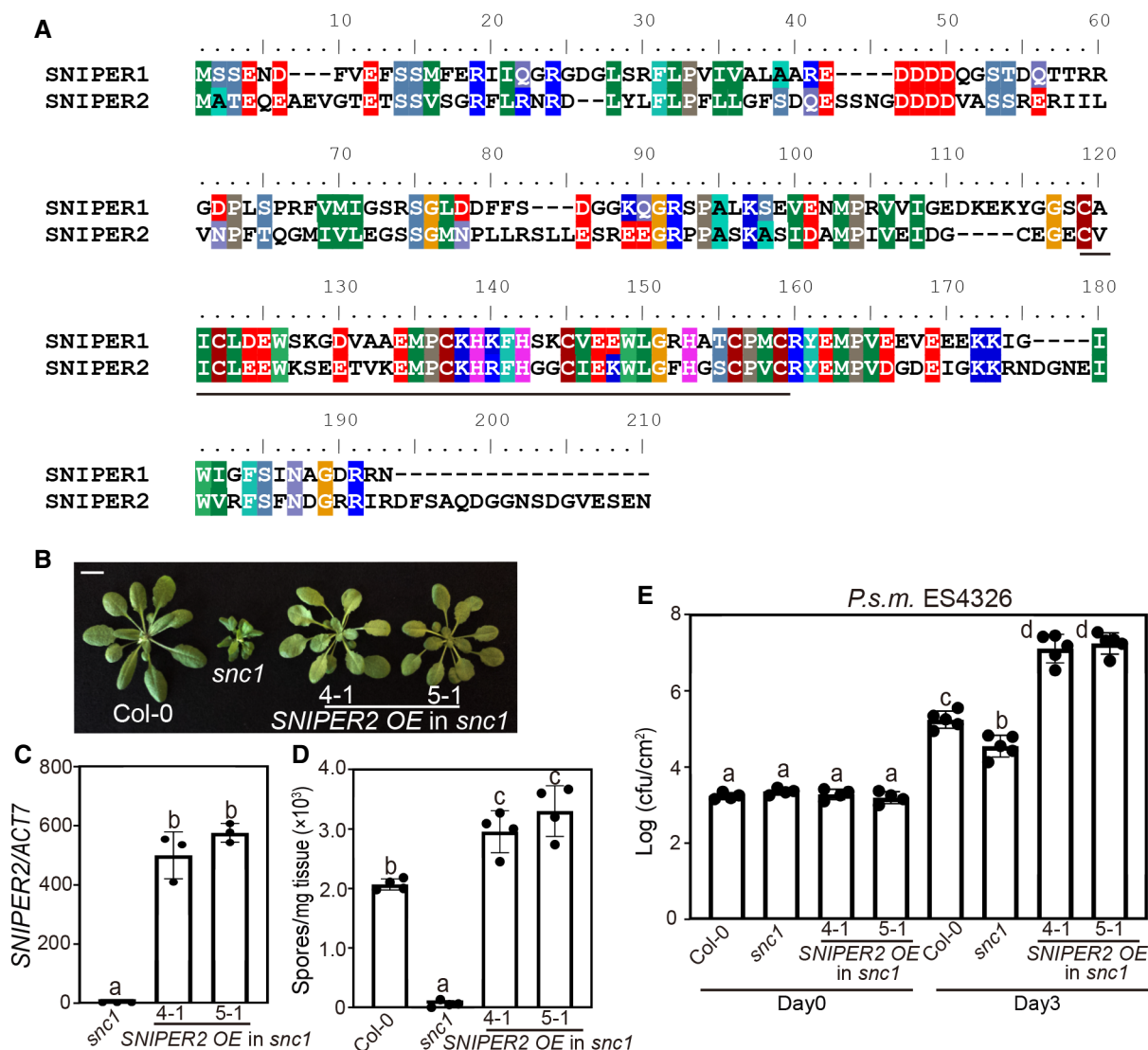


Figure EV4. Overexpression of SNIPER2 suppresses *snc1*-mediated autoimmunity.

A Full-length alignment of SNIPER1 and SNIPER2 by ClustalW. The RING domain is indicated by a black line.

B Morphology of 4-week-old soil-grown plants of Col-0, *snc1*, and two independent transgenic lines of SNIPER2 OE into *snc1* background. Scale bar = 1 cm.

C SNIPER2 gene expression in the indicated plants as determined by RT-PCR. Error bars represent mean \pm SD ($n = 3$). Two independent experiments were carried out with similar results.

D Quantification of *H.a. Noco2* sporulation in the indicated genotypes at 7 dpi with 10^5 spores per ml water. Error bars represent mean \pm SD ($n = 4$). Three independent experiments were carried out with similar results.

E Growth of *P.s.m.* ES4326 on 4-week-old leaves of the indicated genotypes at 0 and 3 dpi with bacterial inoculum of OD₆₀₀ = 0.001. Error bars represent mean \pm SD ($n = 4$ for day 0; $n = 5$ for day 3). Three independent experiments were carried out with similar results.

Data information: For (C–E) one-way ANOVA followed by Tukey's *post hoc* test were performed. Statistical significance is indicated by different letters ($P < 0.01$).

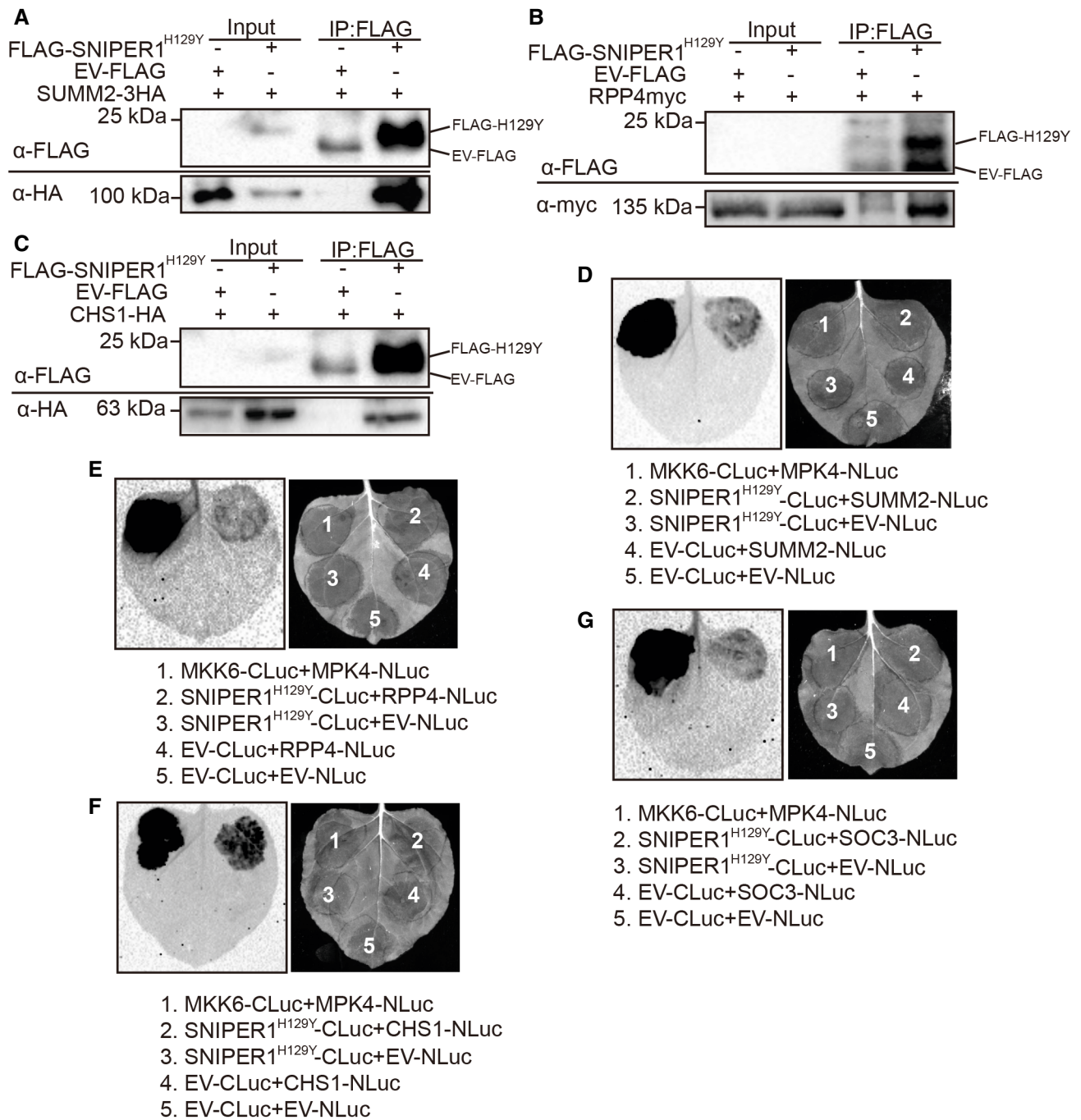


Figure EV5. DN SNIPER1 interacts with diverse sNLRs in planta.

A–C Immunoprecipitation of SUMM2-3HA (A), RPP4myc (B), and CHS1-HA (C) by FLAG-SNIPER1^{H129Y} in *N. benthamiana*. Two biological repeats were carried out with similar results.

D–G Interaction of SNIPER1^{H129Y}-CLuc with SUMM2-NLuc (D), RPP4-NLuc (E), CHS1-NLuc (F), or SOC3-NLuc (G) as tested by split-luciferase complementation assay in *N. benthamiana*. Three biological repeats were carried out with similar results.

Source data are available online for this figure.