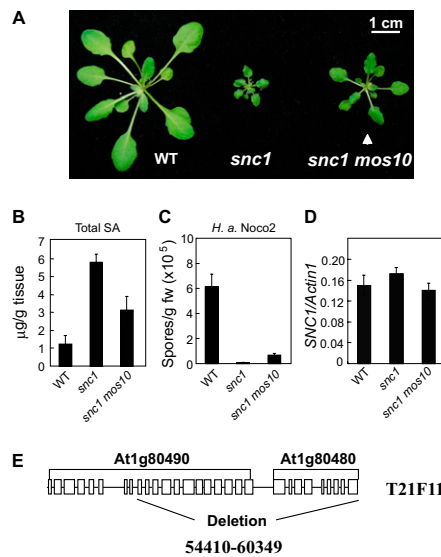


# Supporting Information

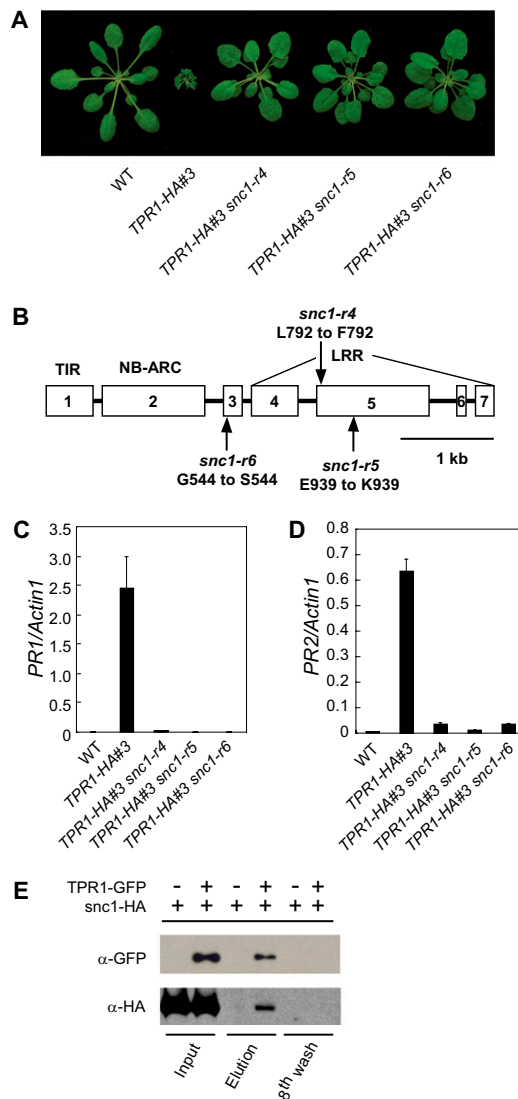
Zhu et al. 10.1073/pnas.1002828107



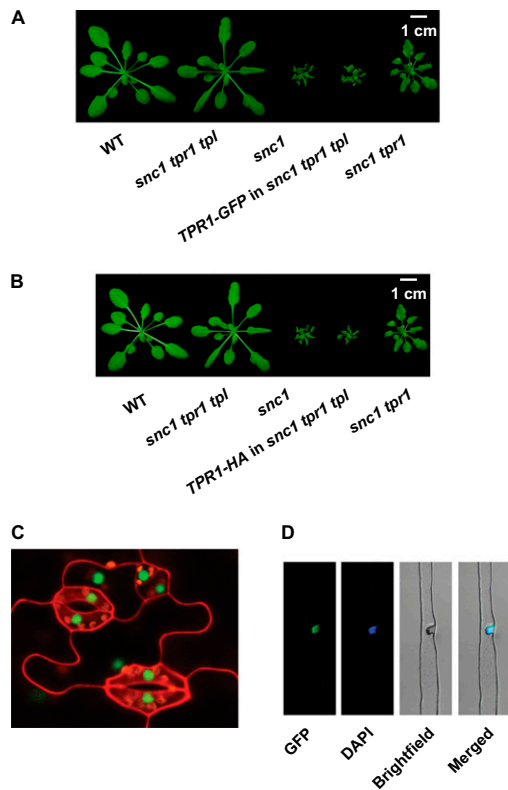
**Fig. S1.** Partial suppression of *suppressor of npr1-1*, *constitutive 1 (snc1)* mutant phenotypes by *modifier of snc1*, *10 (mos10)/topless-related 1 (tpr1)*. (A) Morphology of 4-wk-old Columbia (Col-0) wild-type, *snc1*, and *snc1-mos10* plants. (B) Total salicylic acid (SA) levels in wild-type, *snc1*, and *snc1-mos10* plants. Soil-grown 4-wk-old plants were collected for SA extraction. SA levels were measured with HPLC as previously described (1). Values are averages of four replicates  $\pm$  SD. (C) Growth of *Hyaloperonospora arabidopsidis (H. a.) Noco2* on wild-type, *snc1*, and *snc1-mos10*. Two-wk-old seedlings were sprayed with *H. a. Noco2* at a concentration of 50,000 spores/mL water. Infection was scored 7 d after inoculation by counting the number of spores per gram of leaf fresh weight (fw). Error bars represent SD from three measurements. (D) Real-time RT-PCR analysis of *SNC1* expression in wild-type, *snc1*, and *snc1-mos10* plants. (E) Sequences between nucleotides 54410 and 60349 on BAC clone T21F11 (AC018849.2) were deleted in *mos10*.

1. Li X, Zhang Y, Clarke JD, Li Y, Dong X (1999) Identification and cloning of a negative regulator of systemic acquired resistance, SN1, through a screen for suppressors of *npr1-1*. *Cell* 98: 329–339.

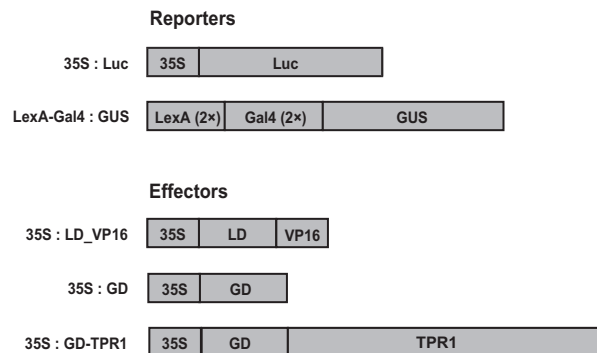




**Fig. S4.** Analysis of suppressor mutants of the *TPR1-HA* overexpression line #3 and association of *SNC1* and *TPR1* in nucleus. (A) Suppression of the stunted morphology of *TPR1-HA* overexpression line #3 by three suppressor mutants, *snc1-r4*, *snc1-r5*, and *snc1-r6*. (B) Mutations in *SNC1* identified from the three suppressor mutants. (C and D) Suppression of constitutive *PR1* (C) and *PR2* (D) expression in the *TPR1-HA* #3 overexpression line by the three suppressor mutants. (E) Association of *SNC1* and *TPR1* in nucleus. Coimmunoprecipitation of *snc1-HA* with *TPR1-GFP* in protein extracts of *TPR1-GFP* and *snc1-HA* double-tagged transgenic plants. Nuclear protein extracts were subjected to immunoprecipitation with anti-GFP magnetic beads. Crude lysates (input) and immunoprecipitated proteins (elution) were detected with anti-GFP or anti-HA antibodies.



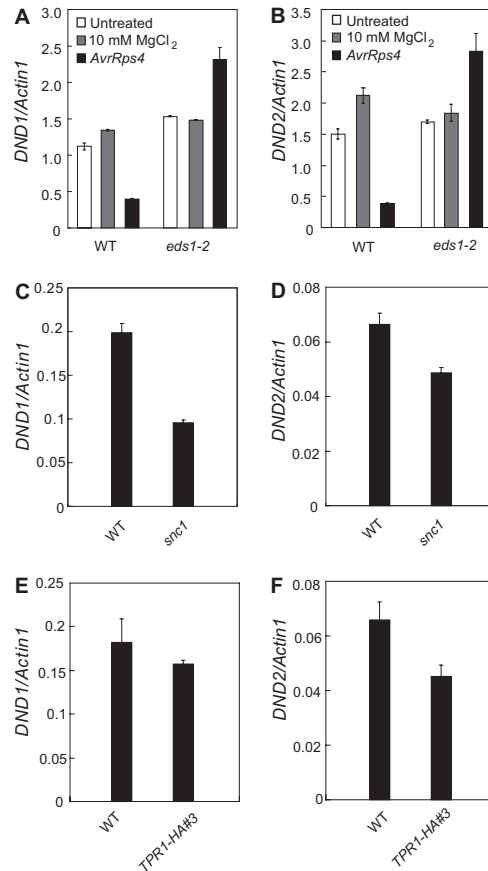
**Fig. S5.** Complementation of *snc1-tp1-tp1* mutant morphology by *TPR1-GFP* and *TPR1-HA* and localization of TPR1-GFP. (A) Complementation of *snc1-tp1-tp1* mutant morphology by *TPR1-GFP*. A construct expressing the TPR1-GFP fusion protein under the control of its native promoter was transformed into the *snc1-tp1-tp1* mutant. The picture was taken from 4-wk-old soil-grown plants. (B) Complementation of *snc1-tp1-tp1* mutant morphology by *TPR1-HA*. A construct expressing the TPR1-HA fusion protein under the control of its native promoter was transformed into the *snc1-tp1-tp1* mutant. The picture was taken from 4-wk-old soil-grown plants. (C) Localization of TPR1-GFP protein in leaf pavement and guard cells of *TPR1-GFP* transgenic plants. Plant cell walls were stained with 5 mg/mL propidium iodine (red). (D) Localization of TPR1-GFP protein in root hair cells of *TPR1-GFP* transgenic plants. The nuclei were stained with DAPI.



**Fig. S6.** Reporter and effector constructs used in the transfection assays. Luc, luciferase; GUS, GUS:  $\beta$ -glucuronidase.

Target	Fold enrichment	Annotation
At5g15410	8.5 ± 1.7	DND1 (Defense No Death 1)
At3g20820	11.5 ± 2.2	Leucine-rich repeat family protein
At1g51940	18.6 ± 2.2	Protein kinase family protein
At4g21960	3.1 ± 1.1	Peroxidase 42
At1g14720	7.2 ± 1.2	XRT2
At5g54250	5.4 ± 3.3	DND2 (Defense, No Death 2)
At5g56040	3.8 ± 1.6	Leucine-rich repeat protein kinase
At4g36540	7.6 ± 1.4	BR Enhanced Expression 2
At3g25500	3.9 ± 1.5	Formin Homolog 1
At5g07240	4.9 ± 1.4	IQ-domain 24; calmodulin binding
At5g61420	8.6 ± 3.1	AtMYB28
At3g19000	6.0 ± 1.7	2OG-Fe(II) oxygenase family protein

**Fig. S7.** List of target genes of TPR1 identified by ChIP followed by real-time PCR analysis. Transgenic plants expressing *TPR1-HA* were subjected to ChIP analysis using an anti-HA antibody. *TPR1-GFP* transgenic plants were used as negative controls. The fold of enrichment of a target promoter was calculated by dividing the amount of DNA immunoprecipitated from the *TPR1-HA* transgenic plants by that from the negative control plants.



**Fig. S8.** Real-time RT-PCR analysis of *Defense no Death 1 (DND1)* and *Defense no Death 2 (DND2)* expression. (A and B) Expression of *DND1* (A) and *DND2* (B) in wild-type and *eds1-2* plants in response to *Pseudomonas syringae* pv. *tomato (P.s.t.) DC3000 AvrRps4*. Plants were infiltrated with or without *P.s.t.* DC3000 *AvrRps4* (OD<sub>600</sub> = 0.001) in 10 mM MgCl<sub>2</sub>. Samples were taken 12 h after inoculation. (C and D) Expression of *DND1* (C) and *DND2* (D) in wild-type and *snc1* plants. (E and F) Expression of *DND1* (E) and *DND2* (F) in wild-type and *TPR1-HA* overexpression line #3.

