Supporting Information

Cheng et al. 10.1073/pnas.1105685108

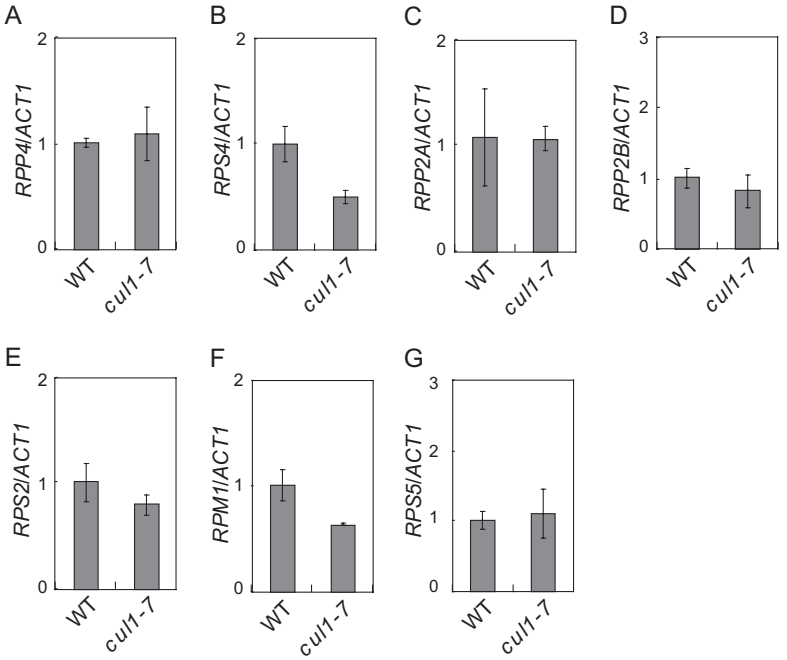

Fig. S1. qRT-PCR analysis of selected *R* gene transcript levels in WT and *cul1-7*. (*A*) *RPP4* levels in the indicated genotypes. (*B*) *RPS4* levels in the indicated genotypes. (*C*) *RPP2A* levels in the indicated genotypes. (*D*) *RPP2B* levels in the indicated genotypes. (*E*) *RPS2* levels in the indicated genotypes. (*F*) *RPM1* levels in the indicated genotypes. (*G*) *RPS5* levels in the indicated genotypes. Plants were grown on MS plates and RNA samples were prepared from 2-wk-old seedlings.

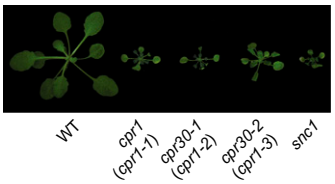

Fig. S2. Morphology of WT, *cpr1* (later renamed to *cpr1-1*), *cpr30-1* (renamed to *cpr1-2*), *cpr30-2* (renamed to *cpr1-3*), and *snc1*.

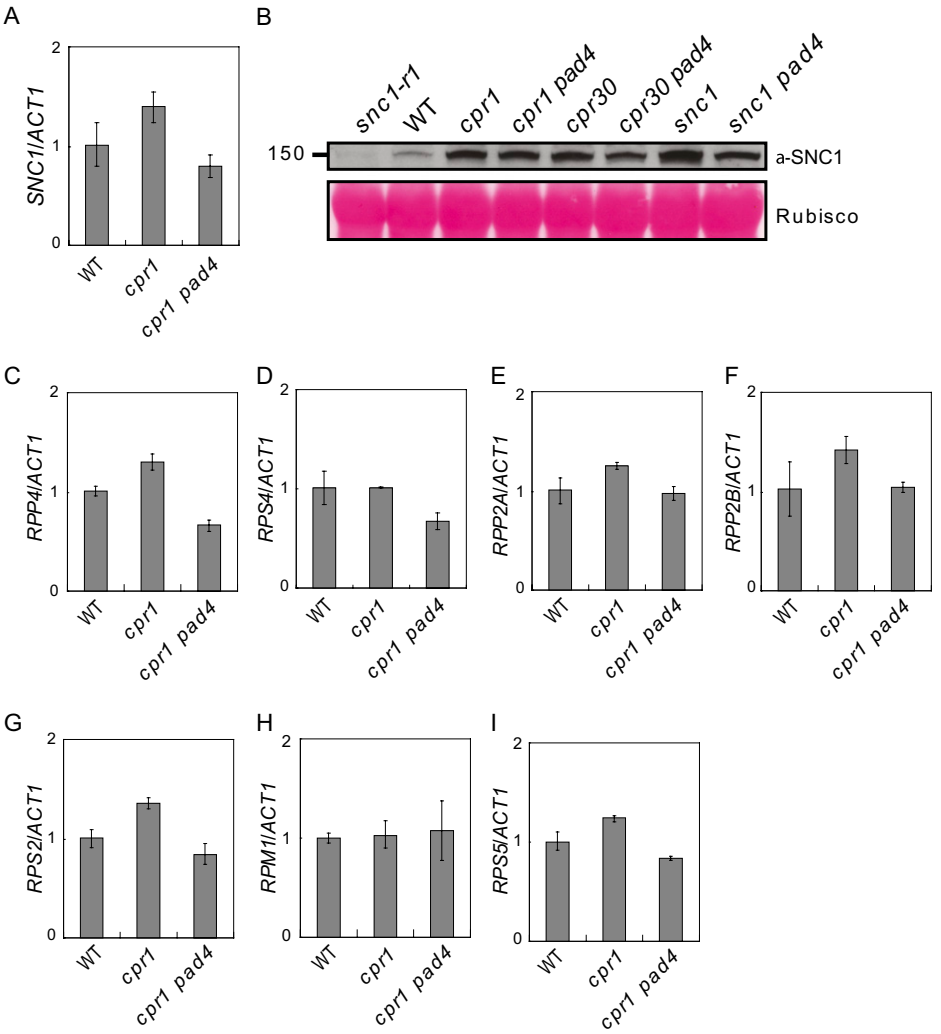

Fig. S3. Analysis of the transcript levels of *SNC1* and selected *R* genes and protein levels of SNC1 in WT, *cpr1*, and *cpr1 pad4* double mutant. (*A*) qRT-PCR analysis of *SNC1* in WT, *cpr1*, and *cpr1 pad4*. (*B*) Western blot analysis of SNC1 levels in *snc1-r1* (a loss-of-function deletion allele of *SNC1*), WT, *cpr1*, *cpr1 pad4*, *cpr30*, *cpr30 pad4*, *snc1*, and *snc1 pad4*. Rubisco levels were used as loading control. (*C*–*I*) qRT-PCR analysis of *RPP4* (*C*), *RPS4* (*D*), *RPP2A* (*E*), *RPP2B* (*F*), *RPS2* (*G*), *RPM1* (*H*), and *RPS5* (*I*) transcript levels in WT, *cpr1*, and *cpr1 pad4* double mutant.

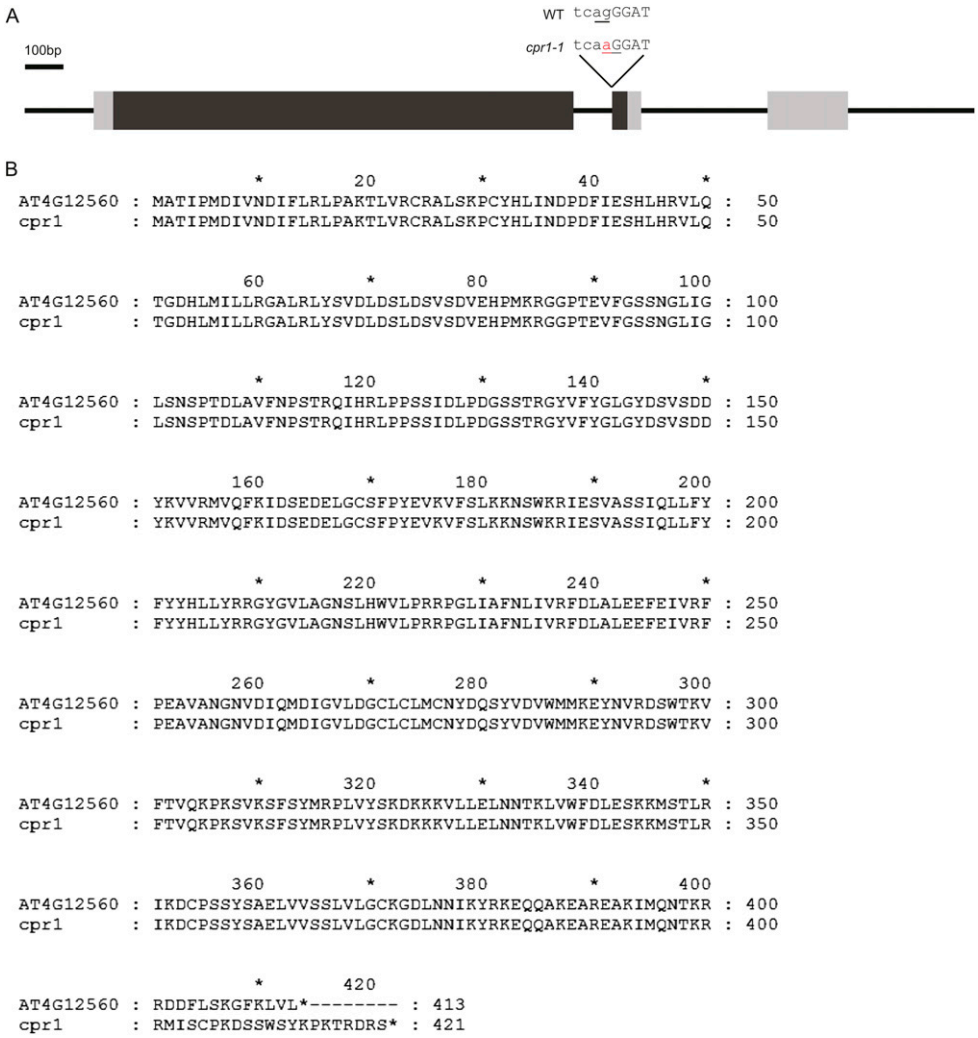

Fig. S4. Sequence analysis of *cpr1*. (*A*) Gene structure of *At4g12560*. Gray boxes indicate untranslated regions, black boxes are exons, and black lines are either intergenic region or introns. Uppercase letters are exons and lowercase letters are introns. Letters with underline are predicted splicing acceptor sites. (*B*) Protein alignment of wild-type CPR1 and cpr1-1. The asterisks at the end of the amino acid sequences indicate stop codons.

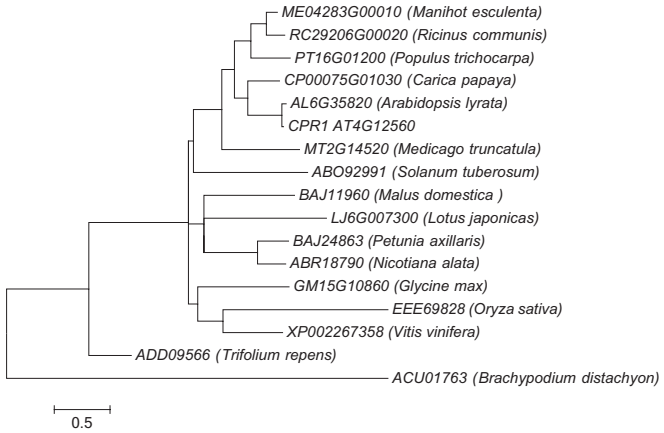

Fig. S5. Molecular phylogenetic anaylsis by Maximum-Likelihood method. A BLAST was performed on National Center for Biotechnology Information and PLAZA (http://bioinformatics.psb.ugent.be/plaza/blast/index) using CPR1 whole protein sequence as query. Homologs were found in 17 species and sequences were retrieved of the homologs with the highest similarity with CPR1 in each species. The evolutionary history was inferred by using the Maximum-Likelihood method based on the Jones et al. w/freq. model (1). The tree with the highest log likelihood (−7748.4484) is shown. A discrete γ-distribution was used to model evolutionary rate differences among sites [five categories (+G, parameter = 4.6404)]. The tree is drawn to scale with branch lengths measured in the number of substitutions per site. Evolutionary analyses were conducted in MEGA5 (2).

1. Jones DT, Taylor WR, Thornton JM (1992) The rapid generation of mutation data matrices from protein sequences. *Comput Appl Biosci* 8:275–282.
2. Tamura K, et al. (2011) MEGA5: Molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Mol Biol Evol*, in press.

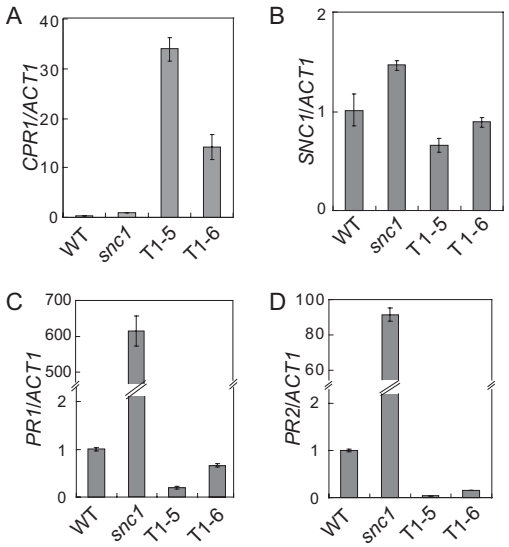

Fig. S6. qRT-PCR analysis of transcript levels of *CPR1* (*A*), *SNC1* (*B*), *PR1* (*C*), and *PR2* (*D*) in WT, *snc1*, and two independent *CPR1* overexpression lines in *snc1* mutant background (T1-5 and T1-6).

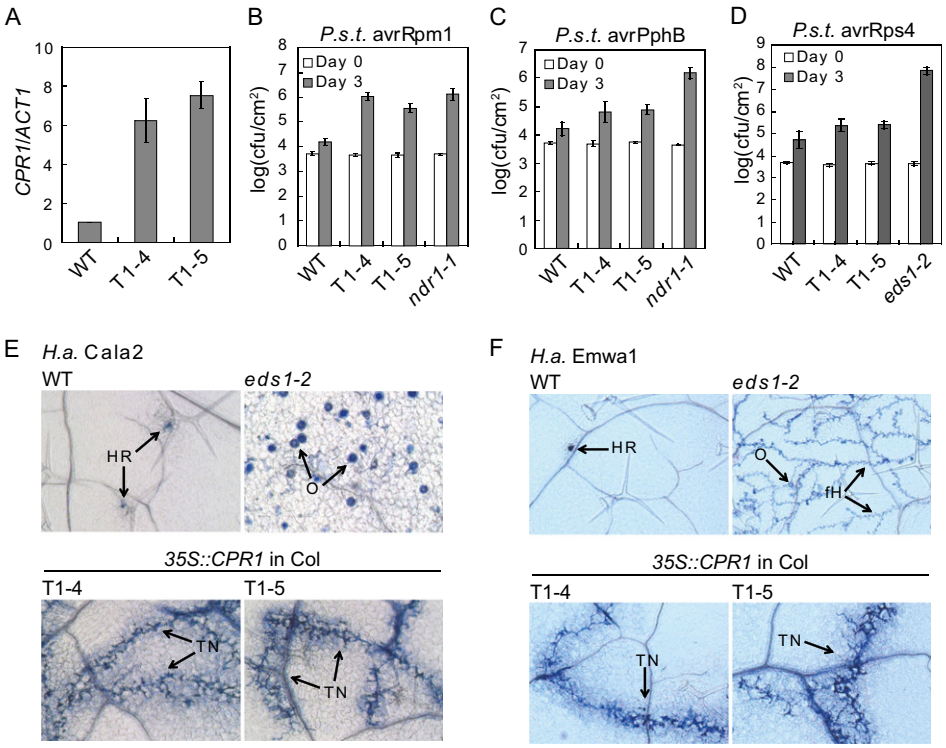

Fig. S7. Analysis of resistance mediated by RPM1, RPS5, RPS4, RPP2, and RPP4 in two independent transgenic lines (T1-4 and T1-5) overexpressing *CPR1* in wild-type Col background. (*A*) qRT-PCR analysis of the transcript levels of *CPR1* in WT, T1-4 and T1-5. (*B–D*) Growth of *Pseudomonas syringae* pv. *tomato* DC3000 carrying *avrRpm1* (*B*), *avrPphB* (*C*), and *avrRps4* (*D*) in T1-4 and T1-5. WT, *eds1-2*, and *ndr1-1* plants were used as controls. (*E* and *F*) Growth of *Hyaloperonospora arabidopsidis* Cala2 (*E*) and *H. arabidopsidis* Emwa1 (*F*) on T1-4 and T1-5 plants. WT and *eds1-2* plants were used as controls. fH, free hyphae; HR, hypersensitive response; O, oospores; and TN, trailing necrosis.

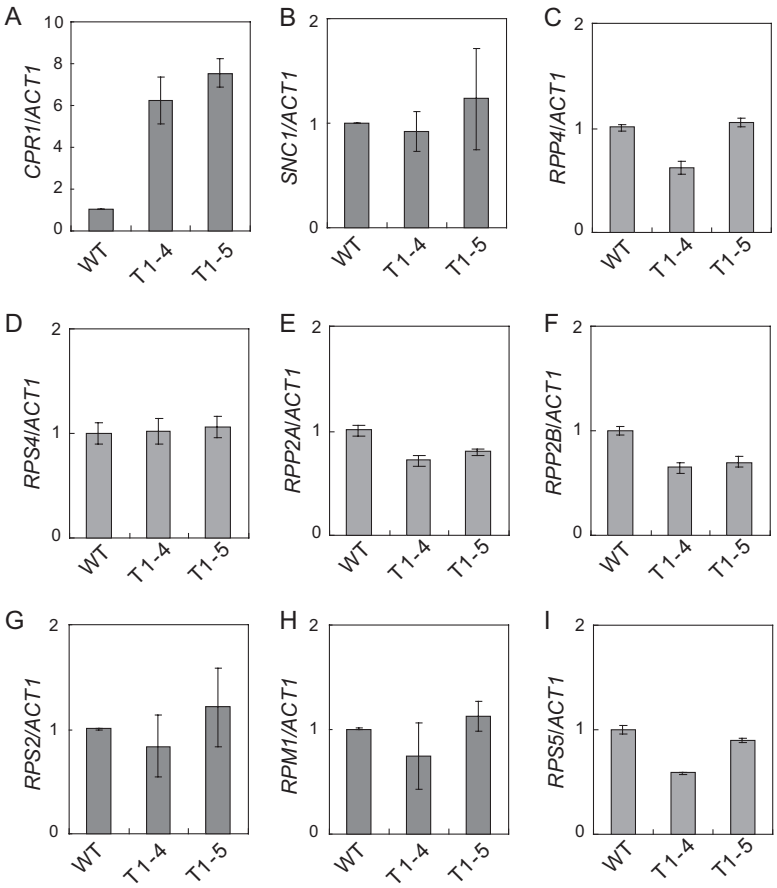

Fig. S8. qRT-PCR analysis of transcript levels of *CPR1* (*A*), *SNC1* (*B*), *RPP4* (*C*), *RPS4* (*D*), *RPP2A* (*E*), *RPP2B* (*F*), *RPS2* (*G*), *RPM1* (*H*), and *RPS5* (*I*) in WT and two independent *CPR1* overexpression lines in wild-type Col background (T1-4 and T1-5).

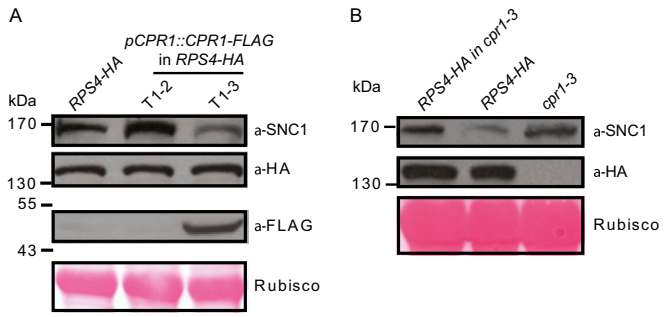

Fig. S9. RPS4-HA and SNC1 levels in two independent *RPS4-HA* lines (T1-2 and T1-3) transformed with *CPR1-FLAG* (*A*) and in cpr1-3 with RPS4-HA transgene (1) crossed into it (*B*). Total proteins were extracted from the indicated genotypes and probed with the specific antibodies to detect levels of CPR1-FLAG, RPS4-HA, and SNC1. Rubisco bands were used as loading controls.

1. Wirthmueller L, Zhang Y, Jones JDG, Parker JE (2007) Nuclear accumulation of the *Arabidopsis* immune receptor RPS4 is necessary for triggering EDS1-dependent defense. *Curr Biol* 17: 2023–2029.

Other Supporting Information Files

Table S1 (XLS)