Supporting Information

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Fig. S1. qRT-PCR analysis of selected *R* gene transcript levels in WT and *cul1-7*. (A) *RPP4* levels in the indicated genotypes. (B) *RP54* levels in the indicated genotypes. (C) *RPP2A* levels in the indicated genotypes. (D) *RPP2B* levels in the indicated genotypes. (E) *RP52* levels in the indicated genotypes. (F) *RPM1* levels in the indicated genotypes. (G) *RP55* 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.

А	WT tcagGGAT
100bp	cpr1-1 tcaaGGAT
_	<u> </u>
В	* 20 * 40 *
AT4G12560	: MATIPMDIVNDIFLRLPAKTLVRCRALSKPCYHLINDPDFIESHLHRVLQ : 50
Cpri	: MATIPHDIVNDIFLKLPAKILVKCKALSKPCIHLINDPDFIESHLHKVLQ : 50
	60 * 80 * 100
AT4G12560	: TGDHLMILLRGALRLYSVDLDSLDSVSDVEHPMKRGGPTEVFGSSNGLIG : 100
cprl	: TGDHLMILLRGALRLYSVDLDSLDSVSDVEHPMKRGGPTEVFGSSNGLIG : 100
	* 120 * 140 *
AT4G12560	: LSNSPTDLAVFNPSTRQIHRLPPSSIDLPDGSSTRGYVFYGLGYDSVSDD : 150 : LSNSPTDLAVFNPSTROIHRLPPSSIDLPDGSSTRGYVFYGLGYDSVSDD : 150
opri	
	160 * 180 * 200
AT4G12560	: YKVVRMVQFKIDSEDELGCSFPYEVKVFSLKKNSWKRIESVASSIQLLFY : 200
cprl	: YKVVRMVQFKIDSEDELGCSFPYEVKVFSLKKNSWKRIESVASSIQLLFY : 200
	* 220 * 240 *
AT4G12560 cpr1	: FYYHLLYRRGYGVLAGNSLHWVLPRRPGLIAFNLIVRFDLALEEFEIVRF : 250 : FYYHLLYRRGYGVLAGNSLHWVLPRRPGLIAFNLIVRFDLALEEFEIVRF : 250
op==	
	260 * 280 * 300
AT4G12560	: PEAVANGNVDIQMDIGVLDGCLCLMCNYDQSYVDVWMMKEYNVRDSWTKV : 300
cprl	: PEAVANGNVDIQMDIGVLDGCLCLMCNYDQSYVDVWMMKEYNVRDSWTKV : 300
3 7 4 7 1 0 5 6 0	* 320 * 340 *
cpr1	: FTVQKPKSVKSFSYMRPLVYSKDKKKVLLELNNTKLVWFDLESKKMSTLR : 350 : FTVOKPKSVKSFSYMRPLVYSKDKKKVLLELNNTKLVWFDLESKKMSTLR : 350
-	
	360 * 380 * 400
AT4G12560	: IKDCPSSYSAELVVSSLVLGCKGDLNNIKYRKEQQAKEAREAKIMQNTKR : 400
cpr1	: IKDCPSSYSAELVVSSLVLGCKGDLNNIKYRKEQQAKEAREAKIMQNTKR : 400
304012560	* 420 • PDDELSKCEKTUT * • 413
cpr1	: RMISCPKDSSWSYKPKTRDRS* : 421

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.

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Fig. S5. Molecular phylogenetic analysis 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)