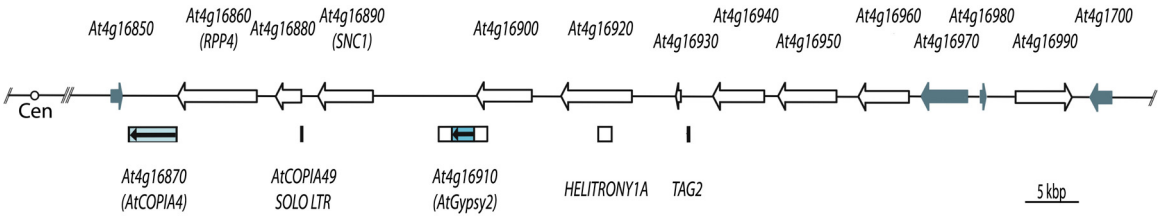
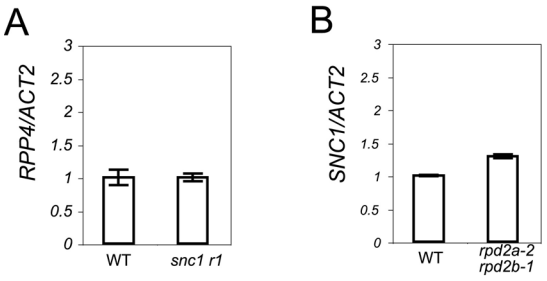
Supplemental Table 1. Nucleotide sequences for oligonucleotides or primers used.

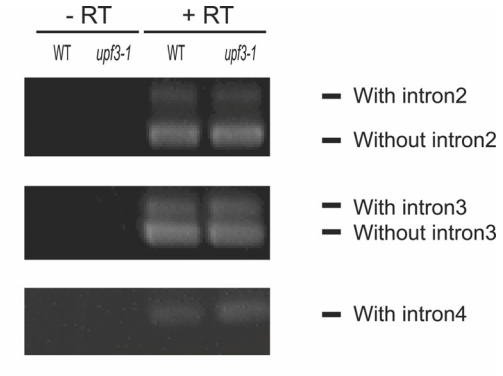
Oligo Name	Nucleotide Sequence (5'->3')	Purpose
KanF	CAA GATGGATTGCACGCAGGTTCTCC	To detect a trangene carrying kanamycin-resistace gene
KanR	CTCGTCAAGAAGGCGATAGAAGGCGA	To detect a trangene carrying kanamycin-resistace gene
At4g16890realtimeF	GCCGGATATGATCTTCGGAA	*SNC1* primer for realtime PCR
At4g16890realtimeR	CGGCAAGCTCTTCAATCATG	*SNC1* primer for realtime PCR
New890RealTime	6FAM-TGGCCTAGTGAAGCAG	*SCN1* Taqman probe for realtime PCR
act2realtimeF	TCGGTGGTTCCATTCTTGCT	*ACT2* primer for realtime PCR
act2RrealtimeR	GCTTTTTAAGCCTTTGATCTTGAGAG	*ACT2* primer for realtime PCR
act2Realtime	NED-AGCACATTCCAGCAGATGTGGATCTCCAA	*ACT2* Taqman probe for realtime PCR
860RealTimeF	GAAGGCACTCAAGGCCTCATT	*RPP4* primer for realtime PCR
860RealTimeR	GACAATAATCCCACCATAGCCTTT	*RPP4* primer for realtime PCR
860RealTime	6FAM-CTTGCCACGTAAACT	*RPP4* Taqman probe for realtime PCR
950RealtimeF	TGGGTGCAAGCTCTCACAGA	*At4g16950* primer for realtime PCR
950RealtimeR	TCATTAGGCCCGTTCAGAAGA	*At4g16950* primer for realtime PCR
950 TaqmanProbe	6FAM-TAG CAA ATA TAG CCG GAG AGG	*At4g16950* Taqman probe for realtime PCR
860GATE	CACCTGATTCCAGATCTTTCGAAGGCCA	Amplification of PCR product used for the construction of a probe detecting *RPP5* locus *R*-gene sense transcripts
860smRNA	GAGACAGGACTTCTTCAATGGCGGTGTT	Amplification of PCR product used for the construction of a probe detecting *RPP5* locus *R*-gene sense transcripts
GAPC F1	CTGTCAACGACCCCTTCATG	*GAPC* amplification in multiplex PCR
GAPC F1'	GCTCGTCGCTGTCAACGACCCCTTCATC-DIDEOX\	Poisoning of *GAPC* amplification
GAPC F2	CACTTGAAGGGTGGTGCCAAG	*GAPC* amplification in multiplex PCR
GAPC F2'	CTGCAGCTCACTTGAAGGGTGGTGCCAAG-DIDEO	Poisoning of *GAPC* amplification
GAPC R	CCTGTTGTCGCCAACGAAGTC	*GAPC* amplification in multiplex PCR and construction of antisense strand-specific cDNA libraries for *RPP5* locus *R*-gene
GAPC R'	AATGCTCGACCTGTTGTCGCCAACGAAGTC-DIEO)	Poisoning of *GAPC* amplification
balANTI	GACAGAAATTCCAGATC	Construction of antisense strand-specific cDNA libraries for *RPP5* locus *R*-genes
SALK005767U	TGGTTTGCCGAGAATAGCCAA	*RPP4* antisense transcript amplification in multiplex PCR
Salk_005767D2	CGTTTCTGGGATGAGTTGTATGAAA	*RPP4* antisense transcript amplification in multiplex PCR
890GATE3	AGAGCTCTGAGGTACAATGACAG	*SNC1* antisense transcript amplification in multiplex PCR
890GATE0	CACCTGACAAAAGGCTGGAGGTTCTTCCGAT	*SNC1* antisense transcript amplification in multiplex PCR
At4g16910LU3	TGAGGATCGCGGGCGTTACAGAT	*At4g1690* antisense transcript amplification in multiplex PCR
At4g16900U1.5	TCGTCTCATAGTGAGAGGCAACCAA	*At4g1690* antisense transcript amplification in multiplex PCR
Salk_123471D	GTGGAGCTGCCATCTCAAGGT	*RPP4* probe construction in RNA gel blot analysis
Salk_123471U	GGCAAATAAACGAGGCCCTGA	*RPP4* probe construction in RNA gel blot analysis
U6 snRNA	CACGCATAAATCGAGAAATGGTCCTGTCTC	Construction of U6 probe
anitLRRsmRNA5'	ACTTCTTCAATGGCGGTGTT	Amplification of PCR product used for the construction of a probe detecting *RPP5* locus *R*-gene antisense transcripts
anitLRRsmRNA3'	GAGACAGGTTCCAGATCTTTCGAAGGCCA	Amplification of PCR product used for the construction of a probe detecting *RPP5* locus *R*-gene antisense transcripts
siR1003	AGACCGTGAGGCCAAACTTGGCATCCTGTCTC	Construction of siR1003 probe
tasiR255	TTCTAAGTCCAACATAGCGTACCTGTCTC	Construction of tasiR255 probe
SNC1F	GTGGAGTTCCCATCTGAACATC	with SNC1exon3R primer covering intron2 of *SNC1*
SNC1exon3R	CCCCGTAATAACCAATTTCTAGATATTGC	with SNC1F primer covering intron2 of *SNC1*
SNC1exon3F	CGTTCAAAGGCATGCGTAATCTG	with SNC1R primer covering intron3 of *SNC1*
SNC1R	CCCATTTTGATTGCTGGAAAG	with SNC1exon3F primer covering intron3 of *SNC1*
SNC1exon4F	GGATGCCCGAATTTGAGAAACTTT	SNC1exon4F & SNC1intron4R covering intron4 of *SNC1*
SNC1intron4R	TCC AAG CGA CTG AAA AAA ACA TTG	SNC1exon4F & SNC1intron4R covering intron4 *of SNC1*



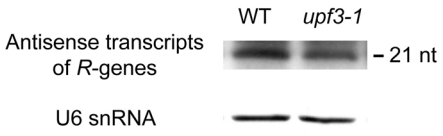
Supplemental Figure 1. Organization of *R-genes* located in the *RPP5* locus in the Columbia haplotype. Open and filled arrows indicate the *R-genes* and non-*R-genes* in the locus, respectively. Transposon originated sequences, which are demarcated by rectangles, are shown under the other genes in the locus. Arrows inside the filled rectangles indicate the polyprotein sequences of the *AtCopia4* and *AtGypsy2* retrotransposons. Start and end points of the arrows show the start and stop codons, respectively, and direction of arrows corresponds to the direction of transcription. Cen: centromere, LTR: long terminal repeat



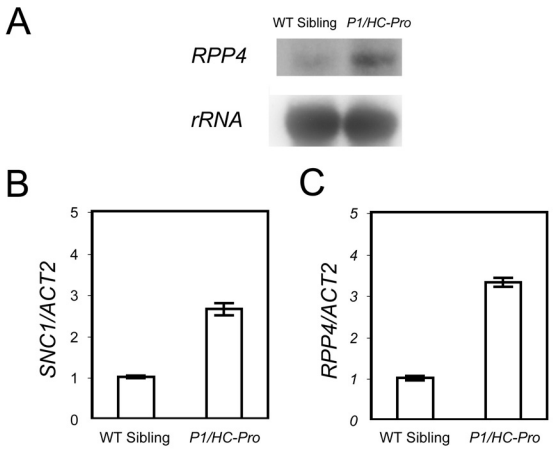
Supplemental Figure 2. The relative quantity of *RPP4* in the *snc1 r1* mutant and that of *SNC1* in the *rpd2a-2 rpd2b-1* double mutant are not changed compared to wild type plants. WT: wild type plants. (A) *RPP4* transcript level, relative to *ACT2*, determined by real-time RT-PCR. (B) Relative *SNC1* transcript level determined by real-time RT-PCR.



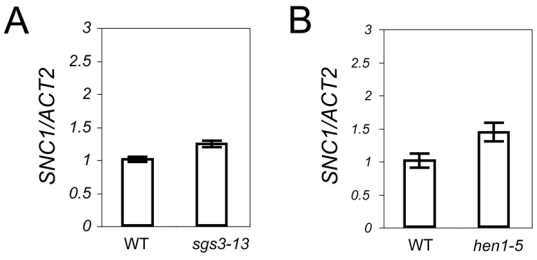
Supplemental Figure 3. *SNC1* transcripts are alternatively spliced to produce transcripts with or without introns. WT: wild type plants. The transcripts produced by intron-retention, in addition to the spliced intronless transcripts, were detected for *SNC1*.



Supplemental Figure 4. No significant difference in the accumulation of small RNA species originating from sense transcripts of *RPP5* locus *R*-genes was detected between wild type plants and *upf3-1* homozygotes. U6 snRNA, an ~100 nt small nuclear RNA, was used as a loading control.



Supplemental Figure 5. Expression levels of *SNC1* and *RPP4* were elevated in transgenic plants over-expressing a viral suppressor of RNA silencing, P1/HC-Pro. WT sibling: WT plants that do not carry a transgene for P1/HC-Pro. *P1/HC-Pro*: hemizygous transgenic plants over-expressing P1/HC-Pro under the control of 35S promoter. (A) The result of RNA gel blot analysis using an *RPP4* probe. (B) and (C) *SNC1* and *RPP4* transcript levels, relative to *ACT2*, determined by real-time RT-PCR.



Supplemental Figure 6. The relative amounts of *SNC1* were comparable in the *sgs3-13*, *hen1-5*, and wild type plants (WT). (A) and (B) *SNC1* transcript level, relative to *ACT2*, determined by real-time RT-PCR.