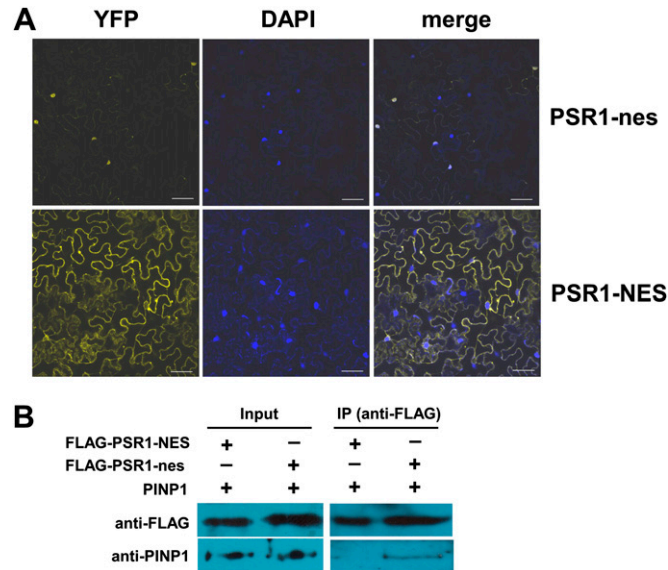


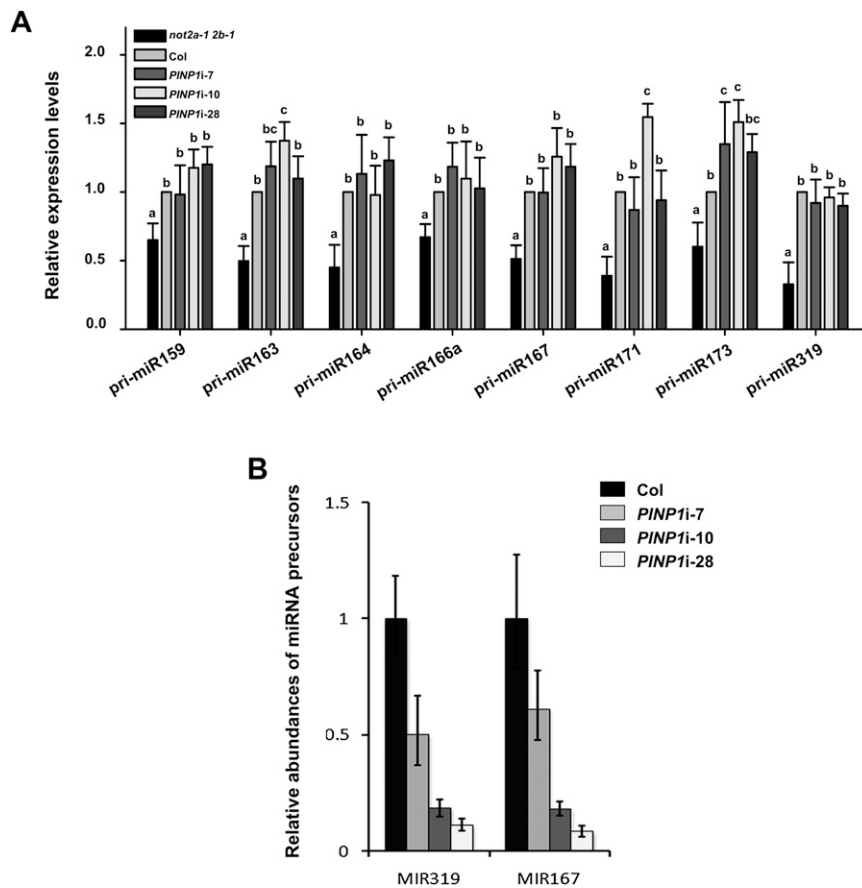
# Supporting Information

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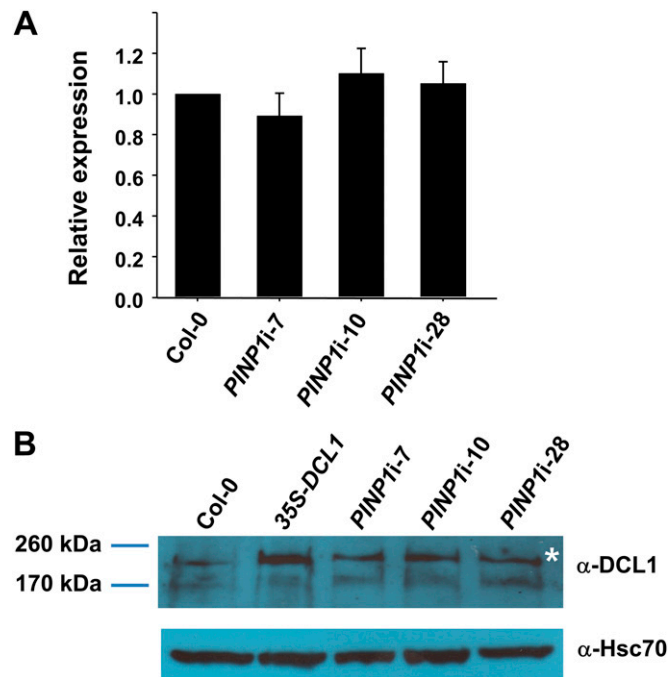


**Fig. S1.** Fusion to a NES impaired the interaction of PSR1 with PINP1 in plant cells. (A) Fusion to NES changed the localization of PSR1. Confocal microscopy of *N. benthamiana* epidermal cells showing the subcellular localization of PSR1-NES-YFP and PSR1-nes-YFP. DAPI staining was used to visualize the nuclei. Please note that the overall fluorescence was decreased to better visualize the predominant nuclear localization of PSR1-nes-YFP; the nuclear localization was completely lost by PSR1-NES-YFP. (Scale bars: 50  $\mu$ m.) (B) Coimmunoprecipitation of PSR1-NES or PSR1-nes with PINP1. The 3 $\times$ -FLAG-PSR1-NES/nes and PINP1 were coexpressed in *N. benthamiana*. The protein complex was pulled down by using anti-FLAG resins, and the enrichment of PINP1 was detected by an anti-PINP1 antiserum. This experiment was repeated twice with similar results.

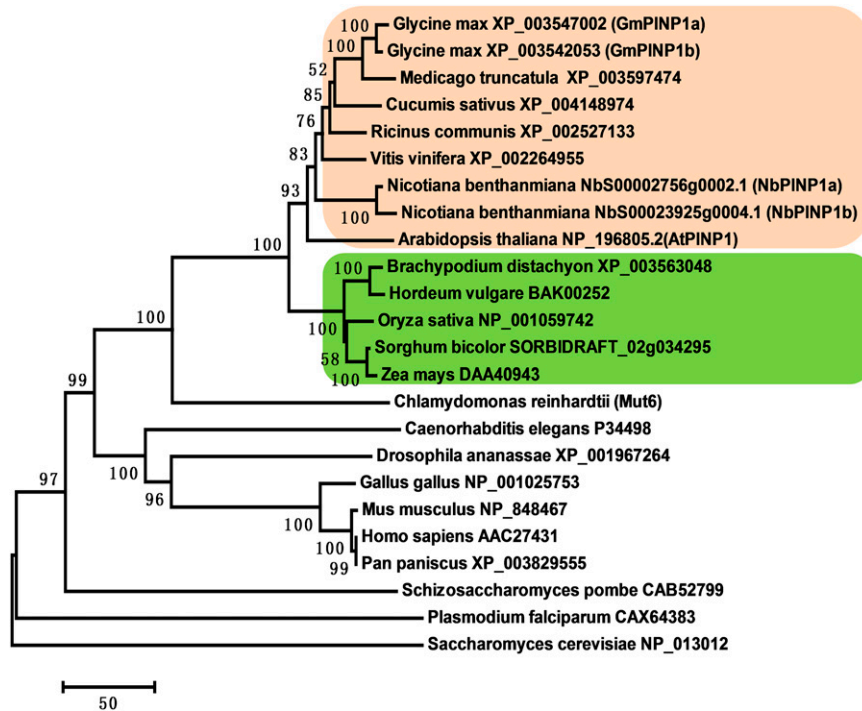




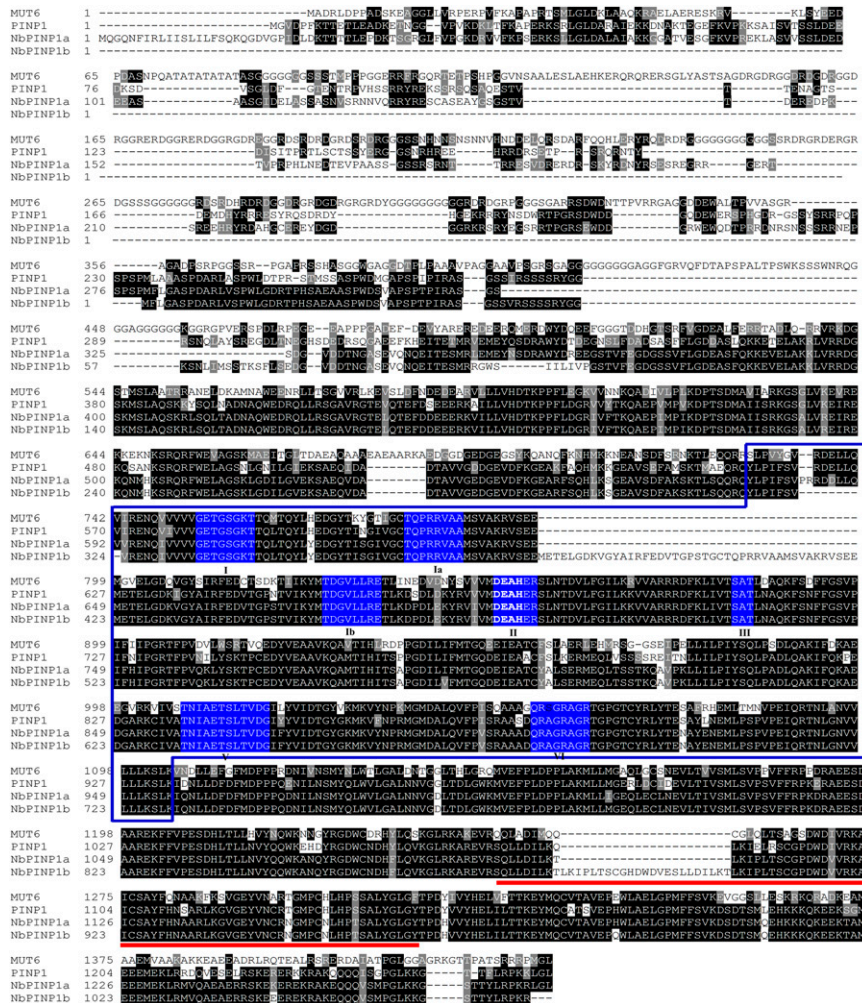
**Fig. S3.** PNP1 affects the pre-miRNA, but not pri-miRNA, levels. (A) Silencing of *PINP1* does not interfere with the transcription of *MIR* genes. Transcript abundances of pri-miRNAs in wild-type (Col-0), *PINP1*-silenced plants, and the *not2a-1 2b-1* mutant were determined by qRT-PCR. *AtUBQ10* was used as the internal standard. Values are means  $\pm$  SDs (as error bars) from three independent replicates. Letters represent differences with statistical significance ( $P < 0.05$ ) as determined by Duncan's multiple range test. (B) Levels of miR319 and miR167 precursors were determined by qRT-PCR in wild-type (Col-0) and *PINP1*-silenced plants. Primers were designed to anneal to the stem portion of the hairpins to amplify the reverse-transcribed products of both pri-miRNAs and pre-miRNAs. Because the abundances of pri-miR167 and pri-miR319 remain unchanged in *PINP1*-silenced plants (Fig. 2D), the decreased levels of miRNA precursors observed here were presumably due to lower levels of pre-miRNAs. This experiment was repeated twice with similar results.



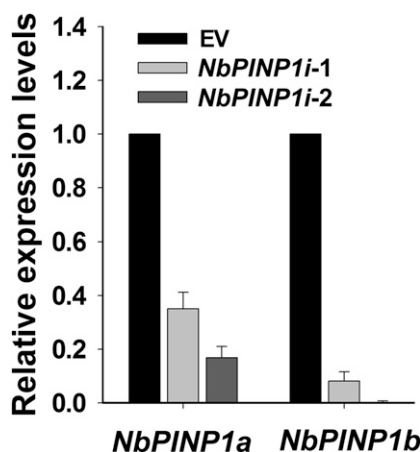
**Fig. 54.** Transcript and protein levels of DCL1 in *PINP1*-silenced plants. (A) *dcl1* transcript levels were determined by qRT-PCR in wild-type (Col-0) and *PINP1*-silenced lines. (B) DCL1 protein abundances were determined by Western blotting using an anti-DCL1 antibody (Agriser) in wild-type (Col-0), *p35S-DCL1*, and *PINP1*-silenced plants. \* labels the protein band corresponding to DCL1 with a predicted molecular mass of 210 kDa. Hsc70 was detected by using an anti-Hsc70 antibody as a loading control. Protein sample extracted from *Arabidopsis* plants overexpressing DCL1 was used as a control. This experiment was repeated twice with similar results.



**Fig. 55.** Phylogenetic analysis of PINP1 homologs in fungi, plants, and animals. Neighbor-joining tree of 24 PINP1 homologs, all containing the DEAH-box RNA helicase domain, was constructed by using full-length amino acid sequences. The clade containing PINP1 homologs in dicots is highlighted in yellow, and the clade with PINP1 homologs in monocots is highlighted in green. The soybean homologs GmPINP1a and GmPINP1b can also interact with PSR1 (Fig. 1A).



**Fig. S6.** Amino acid sequence alignment of MUT6 and P1NP1 homologs in *Arabidopsis* (PINP1) and in *N. benthamiana* (NbPINP1a and NbPINP1b). The blue box denotes the DEAH RNA helicase domain, and the conserved motifs are highlighted in blue. The red line labels the region of a conserved DUF1605 domain with unknown functions. Identical residues are shaded in black, and similar residues are shaded in gray.



**Fig. S7.** qRT-PCR analysis of the transcript abundances of *NbPINP1a* and *NbPINP1b* in *N. benthamiana* inoculated with *Agrobacterium* harboring either the empty VIGS vector TRV2-LIC (EV) or TRV2-LIC carrying the silencing constructs *NbPINP1i-1* or *NbPINP1i-2*. 18S rRNA was used as the internal standard. Error bars are SEs of three biological replicates. This experiment was repeated twice with similar results.

**Table S1. Characterization of T-DNA mutants of *PIN1* in *Arabidopsis* eco. Col-0**

T-DNA lines	Homozygous plants	Heterozygous plants	Wild-type	$\chi^2$ (2:1)	P value
CS24359	0	35	18	0.01	0.9203
SALK_062354	0	38	18	0.02	0.8875
SALK_019541	0	34	17	0.00	1.0000

**Table S2. Strains and plasmids used in this study**

Strains or plasmids	Description	Source
<i>E. coli</i> DH5 $\alpha$	F- $\Phi$ 80d <i>lacZ</i> $\Delta$ M15 $\Delta$ ( <i>lacZYA-argF</i> ) U169 <i>recA1 endA1, hsdR17</i> (rk-, mk+) <i>phoA supE44</i> $\lambda$ - <i>thi-1 gyrA96 relA1</i>	Invitrogen
<i>E. coli</i> BL21(DE3)	F- <i>ompT gal dcm lon hsdSB</i> (rB- mB -) $\lambda$ (DE3 [ <i>lacI lacUV5-T7 gene 1 ind1 sam7 nin5</i> ])	Invitrogen
<i>Agrobacterium tumefaciens</i> GV3101(pMP90)	Deletion of T-DNA of pTiC58, Rif <sup>R</sup> , Gent <sup>R</sup>	Holsters (1)
<i>A. tumefaciens</i> C58C1 (pCH32)	Rif <sup>R</sup> , Tet <sup>R</sup>	Mudgett et al. (2)
<i>P. infestans</i> isolate 1306	Tomato and potato pathogen, can infect <i>N. benthamiana</i>	Cvitanich and Judelson (3)
<i>Phytophthora capsici</i> strain LT263	Isolated from pumpkin, can infect <i>Arabidopsis</i>	Donahoo and Lamour (4)
pEG100	pEarleyGate100, a Gateway binary vector with cauliflower mosaic virus 35S promoter, Kan <sup>R</sup>	Earley et al. (5)
pEG100::PSR1A	pEG100 carrying <i>PSR1A</i> , Kan <sup>R</sup>	This study
pEG100::3 $\times$ FLAG-PSR1	pEG100 carrying <i>PSR1</i> tagged with 3 $\times$ FLAG at N terminus, Kan <sup>R</sup>	This study
pEG100::3 $\times$ FLAG-PSR1-NES	pEG100 carrying <i>PSR1-NES</i> (LALKLAGLDI) tagged with 3 $\times$ FLAG at N terminus, Kan <sup>R</sup>	This study
pEG100::3 $\times$ FLAG-PSR1-nes	pEG100 carrying <i>PSR1-nes</i> (LALKAAGADA) tagged with 3 $\times$ FLAG at N terminus, Kan <sup>R</sup>	This study
pEG100::3 $\times$ FLAG-PSR1A	pEG100 carrying <i>PSR1A</i> tagged with 3 $\times$ FLAG at N terminus, Kan <sup>R</sup>	This study
pEG100::3 $\times$ FLAG-PSR1M	pEG100 carrying <i>PSR1M</i> tagged with 3 $\times$ FLAG at N terminus, Kan <sup>R</sup>	This study
pEG100::amiRPINP1	pEG100 carrying amiRNA for <i>PINP1</i> silencing, Kan <sup>R</sup>	This study
pENTR1A	An entry vector for gateway system, Kan <sup>R</sup>	Invitrogen
pENTR1A::PSR1A	pENTR/b-TOPO carrying the <i>PSR1</i> gene, Kan <sup>R</sup>	This study
pENTR1A::3XFLAG-PSR1	pENTR/b-TOPO carrying the <i>PSR1</i> gene with 3 $\times$ FLAG tag at the N terminus, Kan <sup>R</sup>	This study
pENTR1A::3XFLAG-PSR1A	pENTR/b-TOPO carrying the <i>PSR1A</i> gene with 3 $\times$ FLAG tag at the N terminus, Kan <sup>R</sup>	This study
pENTR1A::3XFLAG-PSR1M	pENTR/b-TOPO carrying the <i>PSR1M</i> gene with 3 $\times$ FLAG tag at the N terminus, Kan <sup>R</sup>	Qiao et al. (6)
pENTR1A::PINP1	pENTR/b-TOPO carrying the <i>PINP1</i> gene, Kan <sup>R</sup>	This study
pEG101	pEarleyGate101, a Gateway binary vector carrying cauliflower mosaic virus (CaMV) 35S promoter and <i>YFP</i> , Kan <sup>R</sup>	Earley et al. (5)
pEG101::PSR1	pEG101 carrying <i>PSR1</i> in-frame fused to <i>YFP</i> , Kan <sup>R</sup>	Qiao et al. (6)
pEG101::PINP1	pEG101 carrying <i>PINP1</i> in-frame fused to <i>YFP</i> , Kan <sup>R</sup>	This study
pEG104	pEarleyGate104, a Gateway binary vector carrying <i>P35S-YFP</i> , Kan <sup>R</sup>	Earley et al. (5)
pEG301	pEarleyGate301, a Gateway binary vector without a promoter, Kan <sup>R</sup>	Earley et al. (5)
pEG301-pUBQ10::PSR1	pEG301 carrying <i>PSR1</i> with the UBQ10 promoter, Kan <sup>R</sup>	This study
pEG301-pUBQ10::amiRPINP1	pEG301 carrying an amiRNA for <i>PINP1</i> silencing with the UBQ10 promoter, Kan <sup>R</sup>	This study
pGEX4T-2	<i>E. coli</i> expression vector with a C-terminal GST tag, Amp <sup>R</sup>	Amersham
pGEX4T-2::PSR1	pGEX4T-2 carrying <i>PSR1</i> which expresses GST-PSR1, Amp <sup>R</sup>	This study
pET-mal	<i>malE</i> gene from pMAL-c2 is cloned into NdeI-XhoI site of pET28a, Kan <sup>R</sup>	Sweeney et al. (7)
pET-mal::PINP1	pET-mal carrying <i>PINP1</i> , Kan <sup>R</sup>	This study
pGBKT7	A yeast bait vector expressing proteins fused to the GAL4 DNA binding domain, Kan <sup>R</sup>	Clontech
pGBKT7::PSR1	pGBKT7 carrying <i>PSR1</i> , Kan <sup>R</sup>	This study
pGADT7	A yeast prey vector expressing proteins fused to the GAL4 activation domain, Amp <sup>R</sup>	Clontech
pGADT7::PINP1	pGADT7 carrying <i>PINP1</i> , Amp <sup>R</sup>	This study
pGADT7::GmPINP1a	pGADT7 carrying <i>GmPINP1a</i> , Amp <sup>R</sup>	This study
pGADT7::GmPINP1b	pGADT7 carrying <i>GmPINP1b</i> , Amp <sup>R</sup>	This study
pSPYNE	A binary vector carrying CaMV 35S promoter and the N-terminal (1-155 aa) domain of <i>YFP</i> for BiFC analysis, Kan <sup>R</sup>	Walter et al. (8)
pSPYCE	A binary vector carrying CaMV 35S promoter and the C-terminal (156-239 aa) domain of <i>YFP</i> for BiFC analysis, Kan <sup>R</sup>	Walter et al. (8)
pSPYNE::PSR1	pSPYNE carrying <i>PSR1</i> in frame fused with nYFP, Kan <sup>R</sup>	This study
pSPYNE::PSR1A	pSPYNE carrying <i>PSR1A</i> in frame fused with nYFP, Kan <sup>R</sup>	This study
pSPYNE::PSR1M	pSPYNE carrying <i>PSR1M</i> in frame fused with nYFP, Kan <sup>R</sup>	This study
pSPYCE::PINP1	pSPYCE carrying <i>PINP1</i> in frame fused with cYFP, Kan <sup>R</sup>	This study
TRV1	A VIGS vector with 2 $\times$ 35S promoter and the cDNA sequence of TRV strain Ppk20 RNA1, Kan <sup>R</sup>	Dong et al. (9)
TRV2-LIC	A VIGS vector with 2 $\times$ 35S promoter and the cDNA sequence of TRV strain Ppk20 RNA2, Kan <sup>R</sup>	Dong et al. (9)
TRV2::NbPINP1i-1	TRV2 carrying fragment 1 between <i>NbPINP1a/b</i> genes for gene silencing, Kan <sup>R</sup>	This study
TRV2::NbPINP1i-2	TRV2 carrying fragment 2 between <i>NbPINP1a/b</i> genes for gene silencing, Kan <sup>R</sup>	This study

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**Table S3. Primers used in this study**

Experiment	Primer name	Primer sequence (5' to 3')
Y2H	AD-PINP1 EcoRI-F	CTACGAATTCATGGGGGTTGATCCATTCAAACCTA
	AD-PINP1 XhoI-R	CTACCTCGAGTCACAGTCCAAGCTTCTTAGGCCTG
	BD-PSR1-EcoRI-F	CTACGAATTCATGACTAAACCGTCGACGGAGGC
	BD-PSR1-BamHI-R	CTACGGATCCGTCAATTGTTCTAGCCACGCCT
	AD-GmPINP1a-EcoRI-F	CTACGAATTCATGGAGAAGGATGGAGCTGGAGCTG
	AD-GmPINP1a-ClaI-R	CTACATCGATTTTACAACCAAACTTCTTTGGTCTC
	AD-GmPINP1b-EcoRI-F	CTACGAATTCATGGAGAAGGATGGAAGTGGTGCTG
	AD-GmPINP1b-ClaI-R	CTACATCGATTTTACAACCAAACTTCTTTGGCCTC
Pull-down assay	GST-PSR1-BamHI-F	CTACGGATCCATGACTAAACCGTCGACGGAGGC
	GST-PSR1-EcoRI-R	CTACGAATTCGTCAATTGTTCTAGCCACGCCT
	MBP-PINP1-EcoRI-F	CTACGAATTCATGGGGGTTGATCCATTCAAACCTA
	MBP-PINP1-XhoI-R	CTACCTCGAGTCACAGTCCAAGCTTCTTAGGCCTG
BiFC assay	pSPYNE-PSR1-XbaI-F	CTACTCTAGAATGACTAAACCGTCGACGGA
	pSPYNE-PSR1-KpnI-R	CTACGGTACCTTGTCTTAGCCACGCCTTGT
	pSPYCE-PINP1-SalI-F	CTACGTCGACATGGGGGTTGATCCATTCAAACCTA
	pSPYCE-PINP1-KpnI-R	CTACGGTACCCAGTCCAAGCTTCTTAGGCCTGAGG
Co-IP assay	pENTR-PINP1-SalI-F	CTACGTCGACATGGGGGTTGATCCATTCAAACCTA
	pENTR-PINP1-XhoI-R	CTACCTCGAGTGCAGTCCAAGCTTCTTAGGCCTG
	TSK108-PSR1-EcoRI-F	CTACGAATTCATGACTAAACCGTCGACGGA
VIGS assay	TSK108-PSR1-XbaI-R	CTACTCTAGATCATTGTTCTAGCCACGCCT
	NbPINP1-VIGS1-F	CGACGACAAGACCCTGCTGCATCTTCTGGGAGTTC
	NbPINP1-VIGS1-R	GAGGAGAAGAGCCCTTGGAAACGATTATCACGACGA
	NbPINP1-VIGS2-F	CGACGACAAGACCCTCGTGTGGCAGCTATGAGTGT
qRT-PCR	NbPINP1-VIGS2-R	GAGGAGAAGAGCCCTTGGAGAATTTTTGGGCATT
	AGO1-F	TGGACCACCGCAGAGACAAT
	AGO1-R	CATCATACGCTGGAAGACGACT
	CUC2-F	TTTTCTCGTTTCGTTTCTA
	CUC2-R	TCCAATACAGTCAAGTCCA
	PHV-F	CAAGGCTACAGGAACCTC
	PHV-R	TGAGGATTTACAGCACCT
	SCL6-F	ACTCAAGACAACCTCAAGCA
	SCL6-R	GATAGATGCTTACAGAAACG
	SPL10-F	TGAGACAAAGCCTACACAGATGGA
	SPL10-R	GATGATGCAACCCGACTTTTTTATG
	At4G27990-F	CCGTCAAGTAATGAAACAC
	At4G27990-R	TGGGATACAGAAGTCAACAA
	At1G12775-F	GCTTTTTCTACTATGGGGAAG
	At1G12775-R	ATGAGAGTGGGTTTATGTCC
	ARF3-F	GGTGGCCTGGTTCAAATGGAG
	ARF3-R	CGGAAGAGGGTGATGATGATAC
	NbPINP1a/b-F	AGGGACTTGTACCCTGTTT
	NbPINP1a/b-R	TAGCCGCATCACTTCTCTCT
	NbPINP1a-F	CCTGGTATGACCGAGAAGAA
	NbPINP1a-R	CAAACCTCCGTCTGCAACTCA
	NbPINP1b-F	TTTTCTGTCCGAGGATGGAG
	NbPINP1b-R	CGATCTCCCATTTGAGCATT
	Nb18S-rRNA-F	TGACGGAGAATTAGGGTTTCG
	Nb18S-rRNA-R	CCTCCAATGGATCCTCGTTA
	PINP1-RT-F	ACATGACCGATGGAGTACTACTGA
	PINP1-RT-R	TCTACTGGAAGATGATACGAGCTG
	AtUBQ10-F	AAATCTCGTCTCTGTTATGCTTAAGAAG
	AtUBQ10-R	AAAGAGATAACAGGAACGGAAACATAGT
	DCL1-F	AATGGGCATCAGCCGTTTACGAGA
	DCL1-R	AAATCTTTGCATGAGCCGGTCC
	premiR319-F	TGAGTCCATTCACAGGTCTGT
	premiR319-R	TGGCGACTCGGTATTTGGAT
	premiR167-F	TGTTGTGTTTCATGACGATGGT
	premiR167-R	CAACGGGTGAACTGCGAA
	pri-miR159-F	GGAGCTCTACTTCCATCGTCA
pri-miR159-R	CCACGTTCTCATCAAACCTTT	
pri-miR163-F	GCATAGGTCTTGATTGGTGGA	
pri-miR163-R	CGTTGTCGTTGAAGAGGTTG	
pri-miR164-F	CCATTGACGATTGCATCCTCG	



**Table S3. Cont.**

Experiment	Primer name	Primer sequence (5' to 3')
miRNA Northern blotting	pri-miR164-R	TTGATGGAGAAGCAGGGCAC
	pri-miR166a-F	CACCACTCACTTATCTTCTTC
	pri-miR166a-R	CAGTCGAAATTATAGAATCTAGGGT
	pri-miR167-F	GAAGCTGCCAGCATGATCTA
	pri-miR167-R	GGGTTTATAGAAGGGTGCGA
	pri-miR171-F	CCGCGCCAATATCTCAGTA
	pri-miR171-R	TGTCTCCATTTCAACACACACA
	pri-miR173-F	CTTCTTCTCACAATAAACCCA
	pri-miR173-R	AAGATCTCTAACATTAATCAT
	pri-miR319-F	AGAGGTTAGCATGTTGATGAC
	pri-miR319-R	CCTCAAGTTATCATATCGGAG
	miR159	TAGAGCTCCCTTCAATCCAAA
	miR167	TAGATCATGTTGGCAGTTTCA
	miR164	TGCACGTGCCCTGCTTCTCCA
	miR171	CGTGATATTGGCACGGCTCAA
	ASRP255	TACGCTATGTTGGACTTAGAA
	ASRP1151	AAGTATCATCATTCGCTTGGGA
	ASR5D8	AAAGGCCTTACAAGGTCAAGA
	miR173	GTGATTTCTCTCTGTAAGCGA
	miR393	GATCAATGCGATCCCTTGGGA
	miR166	GGGGAATGAACGCTGTTTCGCT
	miR390	GGCGCTATCCCTCCTGAGCTT
	miR168	TTCCCGACCTGCACCAAGCGA
	siR1003	ATGCCAAGTTTGGCCTCACCGTC
	AtSN1	ACCAACGTGTTGTTGGCCAGTGGTAAATCTCTCAGAT
	SimpleHAT2	TGGGTACCATTTTGACACCCCTA
Cluster4	AAGATCAAACATCAGCAGCGTCAGAGGCTT	
U6	AGGGGCCATGCTAATCTTCTC	
Silencing of <i>PINP1</i>	amiRPINP1	TCAGTATTCCAAAAGGACGT
NES	NES	CTGGCTTTGAAGTTAGCTGGTTGGATATC
	nes	CTTGCTTTAAGGCGGCTGGAGCTGATGCT

For PSR1, PSR1A, and PSR1M, the same primer sets were used in each experiment.