Supplementary Data

Supplementary Table S1. *Arabidopsis* mutant lines used in this study

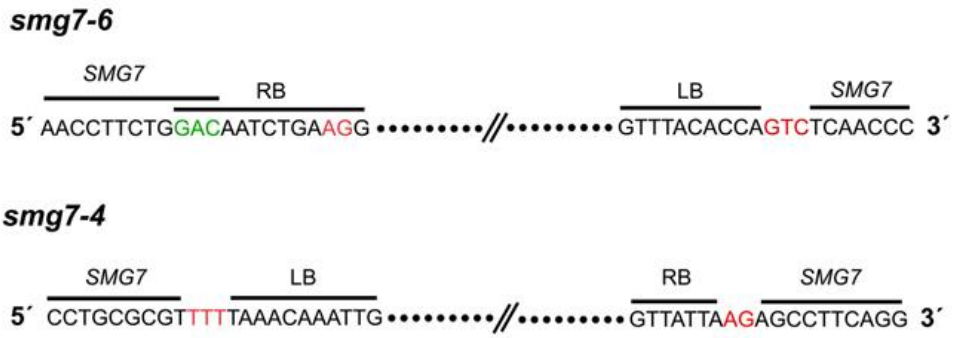
Mutation	T-DNA	References
smg7-1	SALK_073354	(29)
smg7-2	SALK_025699	this study
smg7-3	SALK_112476	(29)
smg7-4	SAIL_63F08	this study
smg7-5	SALK_144162	(29)
smg7-6	SALK_052532	this study
upf1-1/lba1	n.a.	(28)
upf1-2	SALK_004606	(27)
upf1-3	SALK_081178	(26) (27)
upf1-4	SALK_022721	(26) (27)
upf1-5	SALK_112922	(26)
upf3-1	SALK_025175	(25) (26)
upf3-2	SALK_097931	(26)
pad4-1	n.a.	(57)
snc1-11	SALK_047058	(40)
ndr1-1/PR1::GUS	n.a.	(58) (59)

Supplementary Table S2

List of oligos used in this study

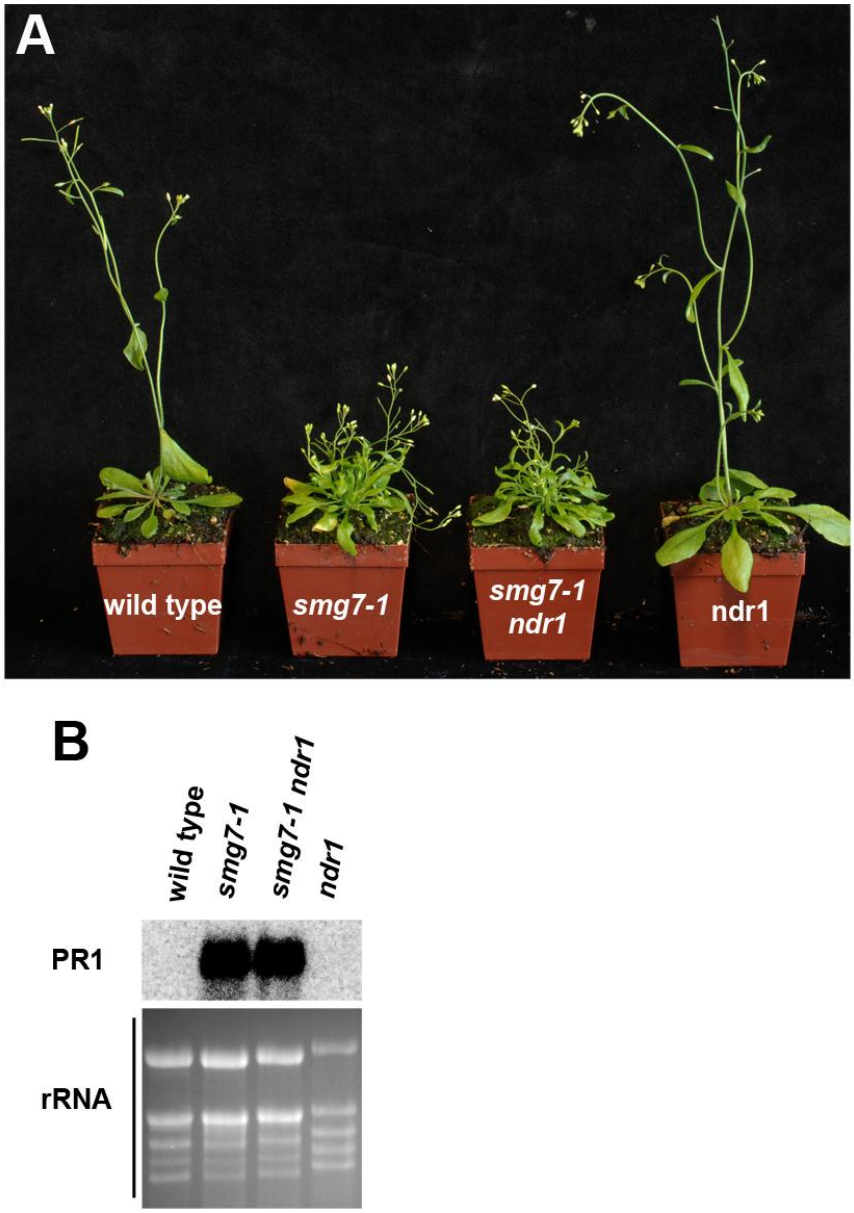
Name	Sequence	Note
PR1-F	ACAAGATTATCTAAGGGTTCACAA	Generation of PR1 Northern probe
PR1-R	TTAGTATGGCTTCTCGTTCACATA	Generation of PR1 Northern probe
PR5-F	ATGGCAAATATCTCCAGTATTCACA	Generation of PR5 Northern probe
PR5-R	ATGTCGGGGCAAGCCGCGTTGAGG	Generation of PR5 Northern probe
PDF1.2-F	ACACAACACATACATCTATACA	Generation of PDF1.2 Northern probe
PDF1.2-R	TTAACATGGGACGTAACAGATA	Generation of PDF1.2 Northern probe
NMD2-F2	ATGATTCACTTCCATTTGTTG	RT-PCR of AT2G45670
NMD2-R	AAAGCACCGAGTTGGAAGGAA	RT-PCR of AT2G45670
Pad4-1-PflMI-F	ATGAGTCGCATAAGACTAGCCAAG	Genotyping of pad4-1 mutants, PflMI digest
Pad4-1-PflMI-R	CCATTTCTTTCCTAAATGAAAATCA	Genotyping of pad4-1 mutants, PflMI digest
SNC1F	CTGGTGCCTGAATGAATTGGTGGA	Genotyping of snc1-11 mutants
SNC1R	GCGATGGTGGAACTGGATAGAGA	Genotyping of snc1-11 mutants
NDR-F	GACGAGATTGCTCATTGCCATTGG	Genotyping of ndr1-1 mutants
NDR-R2	CGAATAGCAAAGAATACGAGTAAA	Genotyping of ndr1-1 mutant allele
NDR-RW	AGACGACTCAGTAGGACACACA	Genotyping of ndr1 wild type allele
lba1-dCAPS-F	GTTGCCAGTGTTGATTCTTTTCTAG	Genotyping of lba1/upf1-1 mutants, XbaI digest
lba1-dCAPS-R	TCCAACATTGATTTTCAGGAGA	Genotyping of lba1/upf1-1 mutants, XbaI digest
UPF1-2F	AATATGAAGGGAGGCTTTGGTG	Genotyping of upf1-2 mutants
UPF1-2R	GCAGAACCACTTTCTACAAGAAGC	Genotyping of upf1-2 mutants
UPF1-3F	GATGAGTCTACTCAAGCAACAG	Genotyping of upf1-3 mutants
UPF1-3R	GAATCTCAAGACTCTCACCTG	Genotyping of upf1-3 mutants
upf1-4F	CGGGTGGATTTGCTGTTGAT	Genotyping of upf1-4 mutants
AtUPF1-1R	CCCATAAGCCAATGATACCAAA	Genotyping of upf1-4 mutants
AtUPF1-1F	ACAATCCAAATCTTCAGTCTCA	Genotyping of upf1-5 mutants
AtUPF1-2R	AGGGACAACAAAATCATGTCG	Genotyping of upf1-5 mutants
AtUPF3-4F	ACTTCTATTGTTGATCTCTGG	Genotyping of upf3-1 mutants
AtUPF3-6R	ATGCTGTTCCGGTTGTGGTGG	Genotyping of upf3-1/upf3-2 mutants
AtUPF3-1F	CCTGATTATCTTGAGTTTCTT	Genotyping of upf3-2 mutants
Est1b-1	GACCTTGGTAGCTGGTCCTGAG	Genotyping of smg7-1 mutants
Est1b-2	GGACAACAGGCCAACCATTCAAC	Genotyping of smg7-1 and smg7-5 mutants
Est1b-7	GCAAACCCAGATAGGCTACTAGCA	Genotyping of smg7-2, smg7-3 and smg7-6 mutants
Est1b-14	CGCTTGGACCTACGTTTATTGATG	Genotyping of smg7-2, smg7-3 and smg7-6 mutants
Est1b-15	GCTGCTTCTCTTGCTAGTAGCCTA	Genotyping of smg7-4
Est1b-16	TGAGTGCCTACGCATGTGTAAACA	Genotyping of smg7-4
Est1b-5	GCCCGTGACAACTTGATTGTTGCTT	Genotyping of smg7-5
LBb1.3	ATTTTGCCGATTTCGGAAC	SALK left border primer
LBc1	TGGACCGCTTGCTGCAACTCT	SALK left border primer
SAIL-LB3	TAGCATCTGAATTTCATAACCAATCTCGATACAC	SAIL left border primer
AT4G26410-F	GAGCTGAAGTGGCTTCCATGAC	qPCR analysis of At4g26410
AT4G26410-R	GGTCCGACATACCCATGATCC	qPCR analysis of At4g26410
PR1-qF2	GCTCTTGTAGGTGCTCTTGTTCTTCC	qPCR analysis of PR1
PR1-qF2	AGTCTGCAGTTGCCTCTTAGTTGTTC	qPCR analysis of PR1
NMD2-PTC-qF1	GTGCATGAAATAAAGAGAAAAGCTTC	qPCR analysis of At2g45670 -PTC
NMD2-uni-qR1	AGGGTAACCAGGGATGAAAGC	qPCR analysis of At2g45670 -PTC and +PTC
NMD2+PTC-qF1	AAGGGATGTAAATACAGAGAAAAGCTTC	qPCR analysis of At2g45670 +PTC

Supplementary Figure S1



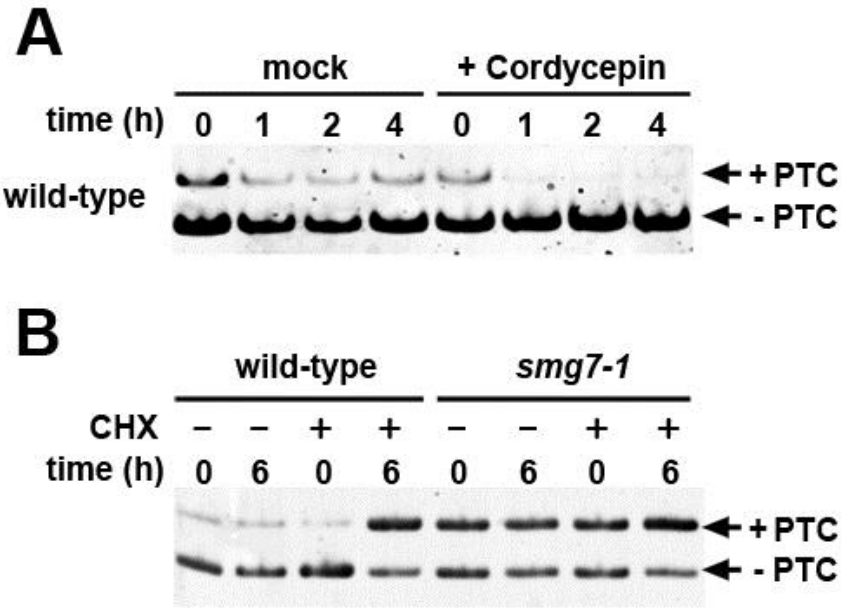
Supplementary Figure S1. Structure of T-DNA integration sites in *smg7-6* and *smg7-4* alleles. Sequences derived from the SMG7 gene and from T-DNA borders (LB, RB) are highlighted. Green letters indicate microhomology between SMG7 and T-DNA at the fusion junction; sequences formed *de novo* at the sites of insertions are in red.

Supplementary Figure S2



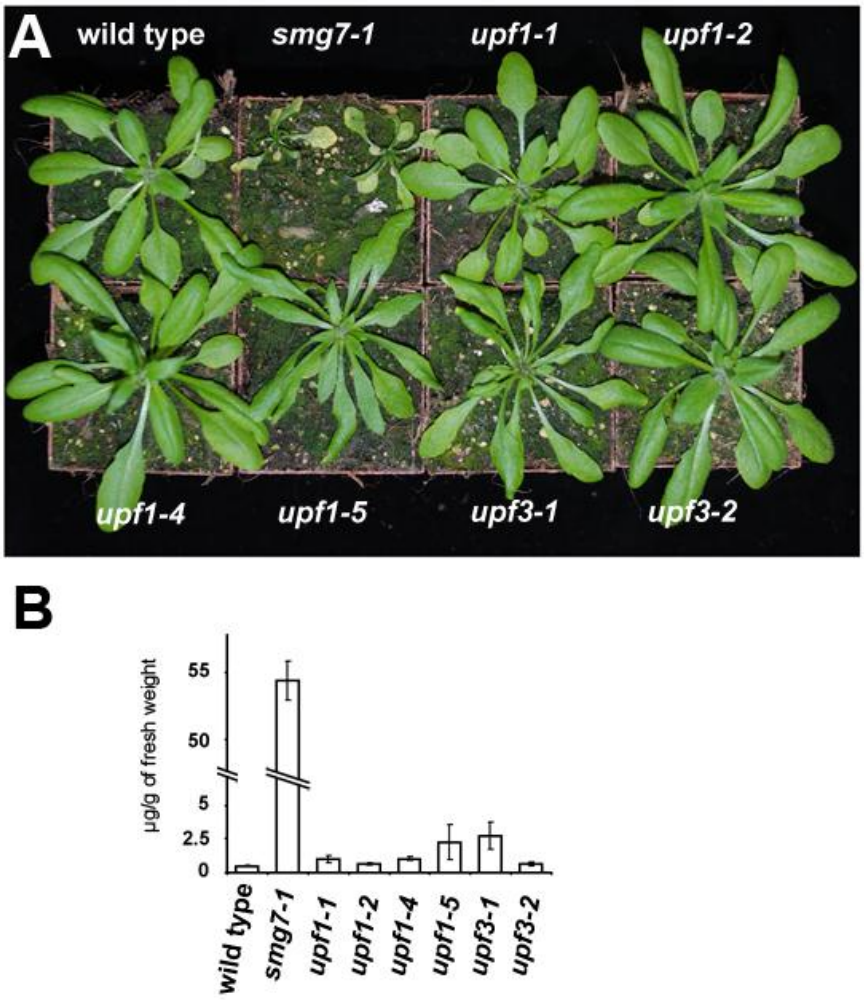
Supplementary Figure S2. Inactivation of NDR1 does not rescue growth defects of *smg7-1* mutants. **(A)** Six week old plants carrying different mutant combinations grown at 60% humidity. **(B)** Northern blot analysis of expression of *PR1* in leaves of *smg7-1 ndr1* mutants and control plants. Ethidium bromide stained gel with *rRNA* species is shown as a RNA loading control.

Supplementary Figure S3



Supplementary Figure 3. Alternatively spliced At2g45670 +PTC transcript is NMD target. **(A)** Stability of the +PTC transcript after inhibition of transcription with cordycepin in leaves of wild type plants. The +PTC transcript disappears within 1hr after cordycepin treatment **(B)** Effect of cycloheximide (CHX) on relative abundance of the +PTC transcript in wild type and *smg7-1* mutants. CHX treatment increases level of +PTC transcript in wild-type leaves.

Supplementary Figure S4



Supplementary Figure S4. *upf1-5* and *upf3-1* mutants exhibit subtler growth defects and a milder increase in SA than *smg7-1* plants. **(A)** Four week old NMD mutant plants cultivated at 19°C/16°C and 60-70% humidity. **(B)** Levels of free SA in leaves of NMD mutants. Note that the total level of SA in *smg7-1* mutants grown at 19°/16°C is higher than in the plants grown at 21°C (Figure 3D). This is consistent with improved growth performance of *smg7-1* mutants at higher temperature.

Supplemental References

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59. Shapiro, A.D. and Zhang, C. (2001) The role of NDR1 in avirulence gene-directed signaling and control of programmed cell death in Arabidopsis. *Plant Physiol*, **127**, 1089-1101.