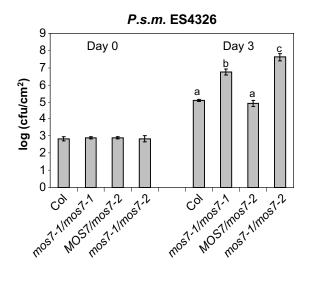
Supplemental Data, Cheng et al., (2009) Nuclear pore complex component MOS7/Nup88 is required for innate immunity and nuclear accumulation of defense regulators in Arabidopsis.

Cheng_Sup Fig1

MOS7 1 : MKFNFNETEDAPDSRRSPTPKEPVRWVELQSHPVFASLPSSQDEPAVSQIFERNEMAWDGDSRVYYWDSRRYL : 73 hNup88 1 :MAAABGPVGDGELWQTWIPNHVVELRIREGIKNQSPTEAEKPASSSLPSSEEBQIITRNVVFGLGG-ELFIWDGEDSS : 77 Mbo 1 :MSLTDVLEINKTELFAKIRNGIEVVQRTQNIIDCKDD-LLFAWHAKDSC : 48
MOS7 74 : IHRISIRICEPEPSSVLAAVPSKVMQEDLQVTESVSKISINKSGSAVIIAGSIGICVMYIFGRASVIEDNVICR : 147 hNup88 78 : FlvvRlR-CPSGGGEEPALSQYQRILCINPPIFEIYQVLISPTQHHVAIIGIKGIMVLELPKRWGKNSEFEGGKSTVNCS : 156 Mbo 49 : LlvRNWR-SSLAAKVNIQFQTLIESSLVSLEVDRVLASNEGSLVAISGPRGVVIMELPRRWGPDGYYKDGKPVITCR : 124
MOS7 148 : VVSIGSEIYTSSDSAITILQASWHEDSDTHIGILSSIAVERLEDISSDTELPEQEYYLQPGPPGRSRTASSIYPADES : 225 hNup88 157 : TTEVAEREETSS-TSLTIKHAAWYESEILLEHVVLLTSDNVIRIYSLREPQTPTNVIILSEAEEESLVLN : 225 Mbo 125 : TFGLDTQLELKN-PHLEVRQVRWHEHSVSDSTILVLLNNNTIRVYNHSKLRHVWQVGPEVLRSGANNSLCDFGELAVDED : 203
MOS7 226 : FGGDHLWDRFTVFILFTDGSIYILCPVVPFGSVYKWESVMEIYNDANMYGVKSSNSTAVSNSSLAIPWLEATFPDITEQG : 305 hNup88 226 : KGGKDEVVAYPLYILYENG : 274 Mbo 204 : IAPAKPRVTEFETAGNNETTLDKSNKTEVAAKSLEKQERIEWPMVVIRENG : 255
MOS7 306 : TRGENILVVKAQFYALLDASLALQGPIYKASSGDGJEDFAVREAECKGRAVSLIYNIVSKDSIIVTAWSAGQIQVDALVD : 385 hNup88 275 : ETFLTYISILHSPGNIWKAVGSIAHASAAFDNYGYDACAVLCLFCVFNILVIATESGMIYHCVVLF : 340 Mbo 256 : NIYILMTGVDSENTRLQGPVTITPQAHDNYGLESCALMIIPSIFPTIVIAESNGKIHHAILME : 318
MOS7 386 : EIQPVWISGNSSRIRMNSHNKIQGVANICESNISELPVAISNIPIDHTVWIGHPPELIRIAMVDLALPKMREGGSLVTUF : 465 hNup88 341 : GEEEDDHTSEKSWDSRIDLIP-SIYVEECVELEIALKIASGEDDEFDSDFSCPVKUH : 396 Mbo 319 : AEATEHSFNEVDDSVIIEPAEYVVHVLETVELEIGISAPATGKEGGNCPIYUK : 371
MOS7 466 : ALSILEERIYSIHDGGIDSTVIHSIPFTSQASGKDEALKTPSVHTVISTCQEESAVSPILGFVFISISF : 534 hNup88 397 : RIPKCESRYHCTHEAGVHSVGITWIHKIHKFIGSDEEDKDSLQEISTEQKCFVEHILCTRPLPCRQPAPIRGEWIVPIIL : 476 Mbo 372 : RIINEIRYFAYHNAGLHAVTVSFIAEIQRYLESESDEDRIELAVSASAEYILCTKFDSSETVNAVFGLALIQIPA : 447
MOS7 535 : GYSWIVAVLSSGECIVAEMKTWDILLPIHVSTDKTVSSSAIEKKPQENSCIISKELLAGPKIRIAPHALPNQRSTP : 610 hNup88 477 : GP-TMICITSTYECLIWPILSTVHPASPFILCTRELVEVAESSLRVLAETPDSFEKHIRSILQRSVANPAFLKASEKDIA : 555 Mbo 448 : GIVILLGSGQVISLKIVIDAQLIVTENENKPVDSEVSQQESGPPFVDTIKSLLQRSVNQFILADKLSS : 515
MOS7 611 : ANSV <mark>B</mark> GRSIILDYVKLFH <mark>EN</mark> YTEYAHKWHFELQH APNIKRIIDD <mark>Q</mark> HQRIAEANEKISKVEKNQSFIEKRIDKAIERHDS : 690 hNup88 556 : FPPE <mark>B</mark> CLQIISRATQVFREQYILKQDIAKEEIQRRVKLICDQKKKQLEDISYCREERKSIREMAERIADKYEEAKEKQED : 635 Mbo 516 : FSAQ <mark>B</mark> SFELINQAIEV <mark>IREQY</mark> IKRHDIVRAAFTRHINQIQLKKEQQLQEIQDLEQERELISERAHKIAERFEEISYNQEL : 595
MOS7 691 : IEQCIQRIRSIPGTHKKPITRAPIDEKSBIDQYAGVEVDAIQSSIETIRARVKKSTOKSHKGTVVAASQKKQYSKKNIIQ : 770 hNup88 636 : IMNRMKKIIHSFHSEIPVISDSERIMIKBIQIIP-DQIRHIGNAIKQVTMKKDYOQKMEKVIS-IPKPTIIIS : 707 Mbo 596 : IVRKCNAIMQRANASIENSVIAEREFSQEVIRIN-KVTQSIAAGIETAKKTENKORYHIAQSQEDIKKNAYEIP : 668
MOS7 771 : DTCMSCLOSTIAKISLMNSDNSKKVKIVESAIKSQESSFM : 810 hNup88 708 : AYCRKCIQSIIKEEGEHIREMVKQINDIRNHVNF : 741 Mbo 669 : EKCHRTITEIITQITGEIDRQITDVKRINKIVGI : 702

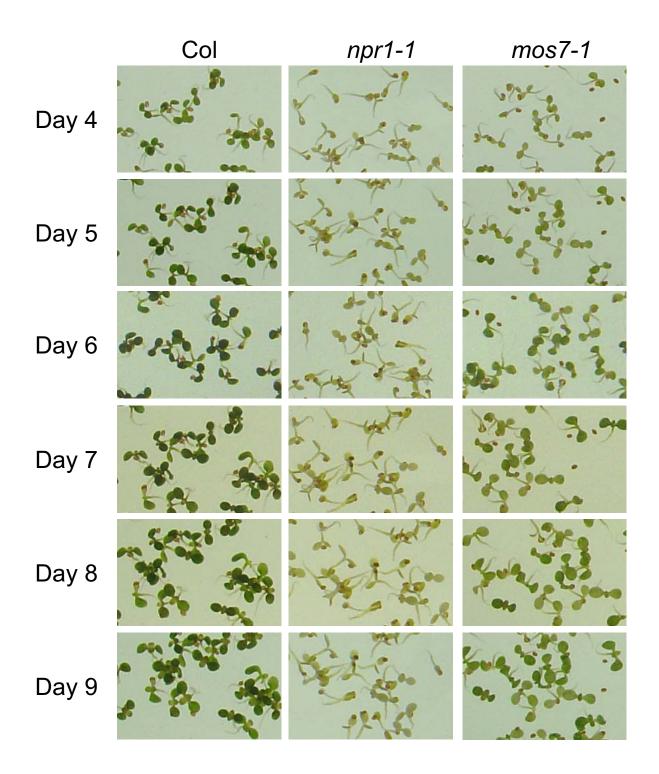
Supplementary Figure 1. Amino acid alignment of MOS7, human Nup88, and *Drosophila* Nup88.

Amino acid sequences from *Arabidopsis* MOS7 (accession number NP_196187), *Drosophila* DNup88 (Mbo; accession number NP_524330), and human hNup88 (accession number NP_002523) were aligned using ClustalW2 (Larkin et al. 2007). Sequence identities and similarities were shaded using Genedoc. Red bar indicates the 4 amino acids deleted in mos7-1. Identical amino acids are shaded in black, and amino acids with similar properties are shaded in grey.

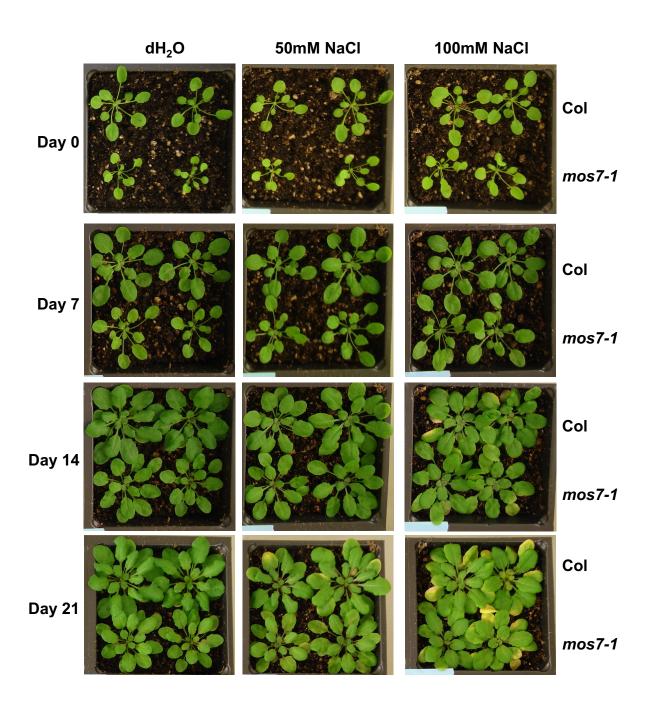


Supplementary Figure 2. Allelism test between *mos7-1* and *mos7-2* using *P.s.m.* ES4326.

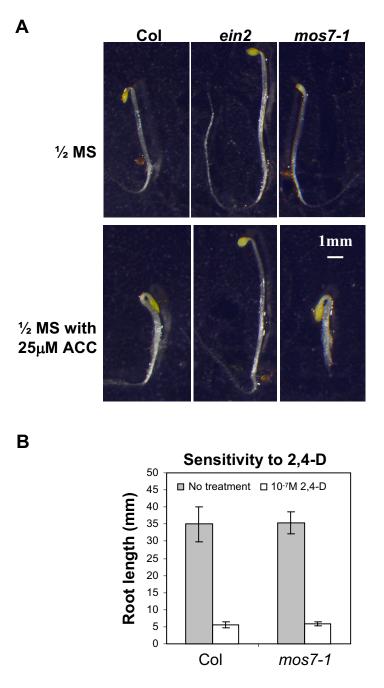
F1 plants from $mos7-1 \times mos7-2$ that carry one copy of each mutation were challenged with *P.s.m.* ES4326 at OD₆₀₀ = 0.0001. Leaf discs within the infiltrated area were taken at Day 0 and Day 3 to measure the bacterial growth in the leaves. Data were analyzed by one-way ANOVA. Different letters indicate statistically significant differences between genotypes. The bars represent averages of four replicates \pm SD.



Supplementary Figure 3. Tolerance of Col, *npr1-1*, and *mos7-1* plants to high concentrations of SA. Seeds were plated on MS medium containing 0.2 mM SA, and the pictures were taken from 4 to 9 days after germination.

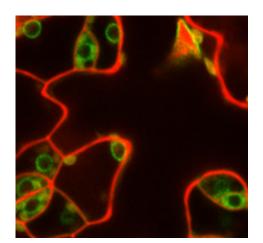


Supplementary Figure 4. Tolerance of Col and *mos7-1* **plants to high concentrations of sodium chloride.** Plants with 8 to 10 rosset leaves were flooded every 3 days with either distilled water (dH2O; control), 50mM or 100mM NaCl solution (Wu et al., 1996).



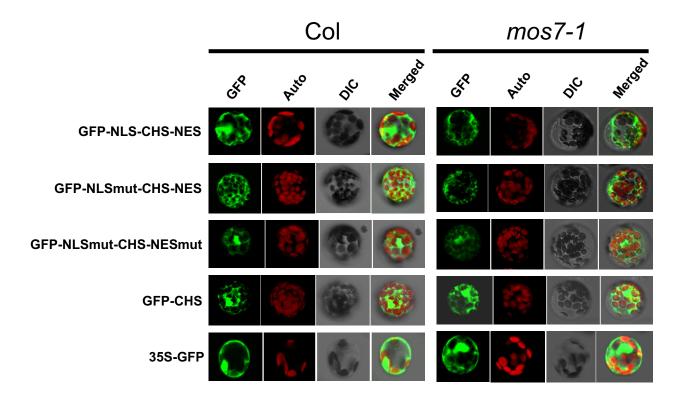
Supplementary Figure 5. Hormonal assays on mos7-1.

(A) Sensitivity of indicated genotypes to 25µM ACC (1-Aminocyclopropanecarboxylic acid). The experiment was carried out as described in Guzman and Ecker (1990) with minor modifications. In brief, seeds were sown on the specified plates and vernalized in the dark at 4°C for 72 h. The plates were placed in constant white light at 22°C for 6 hr and then placed in the dark at 22°C maintaining the same orientation and allowed to grow vertically for 3 more days. Representative plants are shown. (B) Sensitivity to the auxin analog, 2,4-D (2,4-Dichlorophenoxyacetic acid). Seedlings used for root length assay were grown as described in Lincoln et al. (1990) with modifications. In brief, seeds were first sown on ½MS plates and cold treated for 72h. Seeds were allowed to germinate for 3 days on ½MS plates and transferred to specified plates. Root lengths were measured 7 days after germination.



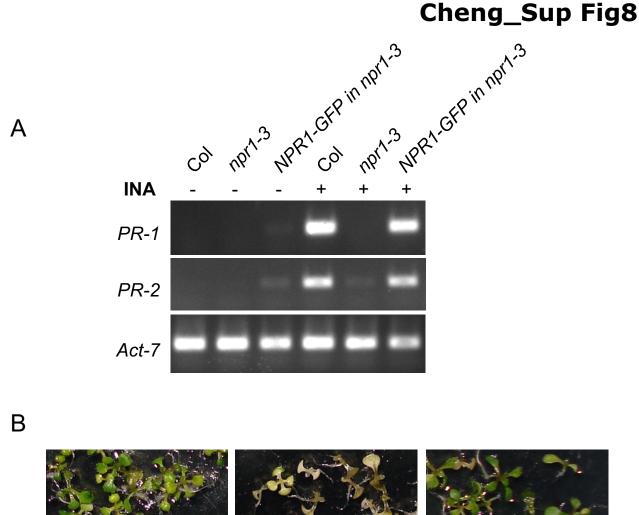
35S::mos7-1-GFP

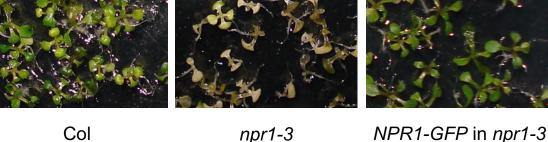
Supplementary Figure 6. Subcellular localization of mos7-1-GFP fusion proteins in leaf pavement cells. Plant cell walls were stained with 5mg/ml propidium iodine (red).



Supplementary Figure 7. *In vivo* nuclear transport assay of chalcone synthase (CHS) fused to GFP.

Arabidopsis protoplast were transiently transformed with CHS-GFP constructs (Haasen et al., 1999) and analyzed for GFP localization by confocal microscopy.



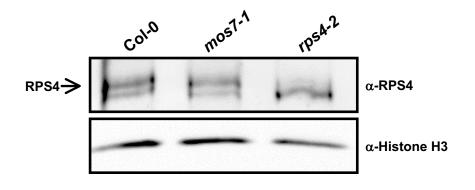


Supplementary Figure 8. Complementation of *npr1-3* by *NPR1-GFP* expressed under the control of its native promoter

(A) *PR* gene expression in the indicated genotypes. Total RNA was prepared from three week-old plants grown on MS medium in the presence (+) or absence (-) of $50 \,\mu$ M INA and reverse transcribed to obtain total cDNA. The cDNA samples were normalized by real-time PCR using *Actin7* (Act-7F: GGTGTCATGGTTGGTATGGGTC and Act-7R:

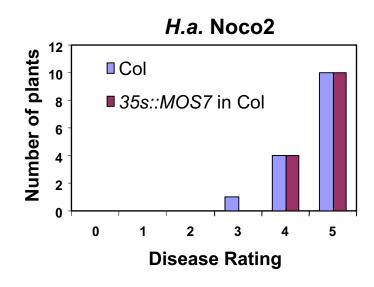
CCTCTGTGAGTAGAACTGGGTGC). *PR-1*, *PR-2*, and *Actin7* were amplified by 28, 30 and 30 cycles of PCR, respectively, using equal amounts of total cDNA and the products were analyzed by agarose gel electrophoresis with ethidium bromide staining.

(B) Tolerance of Col, *npr1-3*, and *npr1-3* transformed with *NPR1-GFP* to high concentrations of SA. Seeds were plated on MS medium containing 0.2 mM SA and the pictures were taken 10 days post germination.



Supplementary Figure 9. Nuclear RPS4 in mos7-1.

Immunoblot analysis of RPS4 in nuclear protein extracts of unchallenged leaf tissues. Equal loading was monitored by probing the membrane with anti-Histone H3.



Supplementary Figure 10. Over-expression of *MOS7* does not lead to enhanced disease resistance.

Resistance of Col and T1 plants from *35S::MOS7* in Col against *H.a.* Noco2. The infection was rated on plants 7 days after infection by counting the number of conidiophores per infected leaf: 0, no conidiophores on the plants; 1, no more than 5 conidiophores per infected leaf; 2, 6 to 20 conidiophores on a few of the infected leaves; 3, 6 to 20 conidiophores on most of the infected leaves; 4, 5 or more conidiophores on all infected leaves; 5, 20 or more conidiophores on all infected leaves. The experiment was repeated once with similar result.

Marker name	Primer Name	Primer Sequence $(5' \rightarrow 3')$	Polymorphism (Col-0/Ler)
K18I23	K18I23-F	AGATTCCAGCTCCGACGATG	172bp/205bp
	K18I23-R	ACGCGCCAAAAGTGCGTGTC	
MOP10	MOP10-F	CTACATGTCCATAGAACCTTC	118bp/129bp
	MOP10-R	CAGTTCTATCATGTATCCACC	
MJJ3	MJJ3-3F	TCTGACTCAATATGAGAGTCC	117bp/108bp
	MJJ3-3R	ATAACTTTATGGGCTGCAGTG	
K18J17	K18J17-F	CGCGATTAAAGATCCGGTA	119bp/107bp
	K18J17-R	TCGAGCAATAAGAGTGATTCC	
MHF15	MHF15-F	CAGAAAGGTCATGAAACCTAG	212bp/159bp
	MHF15-R	GAGCACCAATAAGGTTTCCTC	

Supplemental Table 1. Molecular markers used for map-based cloning of *mos7-1*.