

Figure S1

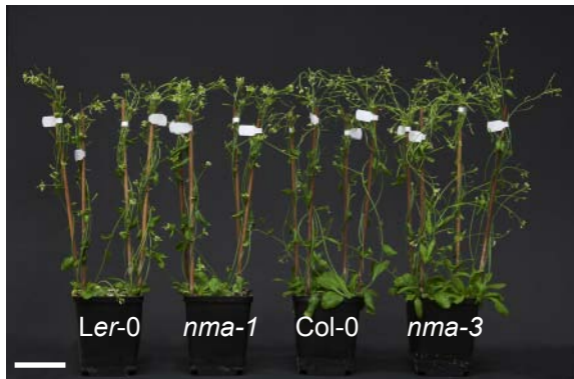


Figure S1: Adult phenotype of *nma-1* (*Ler-0* background) and *nma-3* (*Col-0* background) in comparison to corresponding wild-type plants. Scale bar = 5 cm

Figure S2

[number of cells]

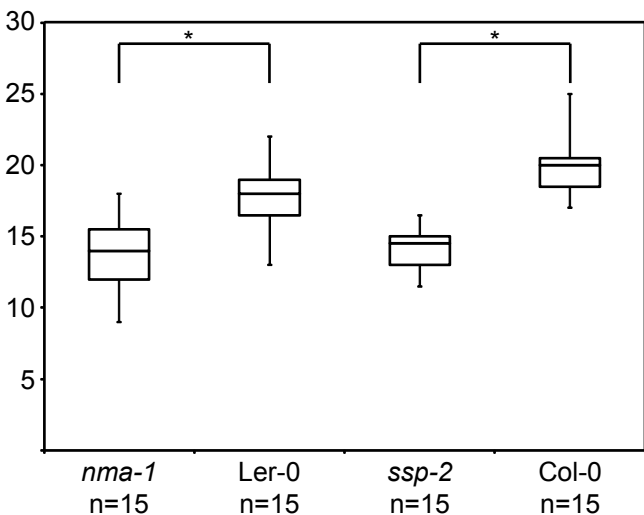


Figure S2: Number of cells in a central optical section of the proembryo 3 days after pollination.

Significant differences as indicated by Mann Whitney U-test ($p < 0.001$) are highlighted by an asterisk.

Boxes represent lower and upper quartiles around median, whiskers indicate maximum and minimum values. The number of examined embryos is given below each genotype.

Figure S3:

pollen tube length [μm]

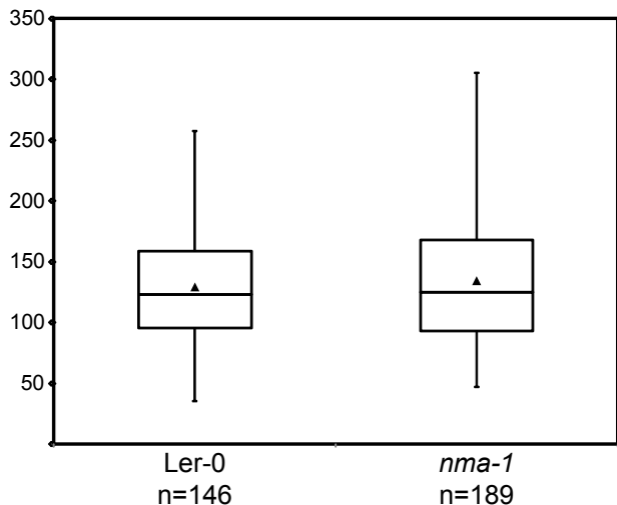


Figure S3: Pollen tube length of in vitro germinated pollen 6h after inoculation.

Boxes represent lower and upper quartiles around median, mean values are shown as triangles, whiskers indicate maximum and minimum values. The total number of analyzed pollen tubes is given below the genotype.

Figure S4:

suspensor length [μm]

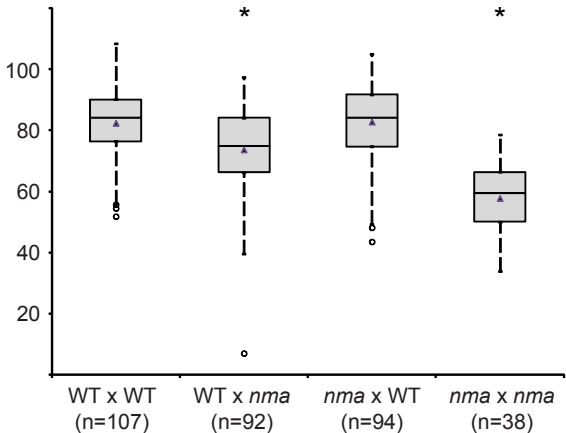


Figure S4: Measurements of suspensor length after reciprocal crosses of wild-type (Ler-0) and *nma-1* mutant plants.

Number of measured suspensors is given in brackets. Significant differences to wild-type cross (WT x WT) as indicated by Mann Whitney U-test ($p < 0.001$) are highlighted by an asterisk.

Boxes represent lower and upper quartiles around median. Mean values are shown as triangles.

Figure S5:

[recombinants]

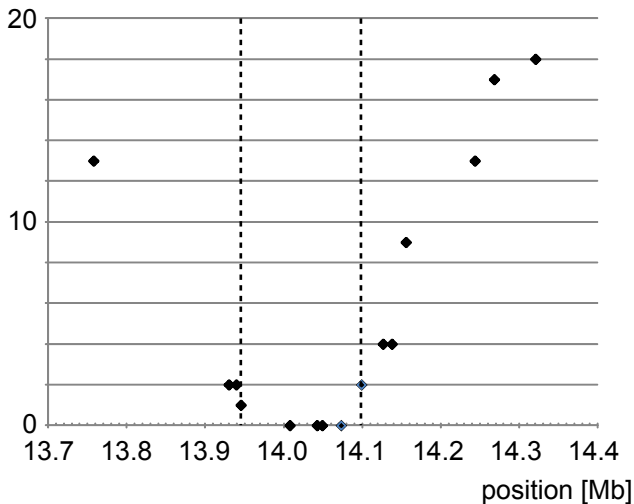


Figure S5: Fine mapping of *nma-1*.

Number of recombinants in a 563 kb genomic interval around *nma-1* on chromosome II are shown.

Dashed lines indicate an interval without further recombinations.

Figure S6:

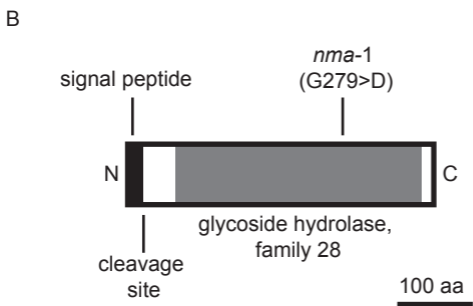
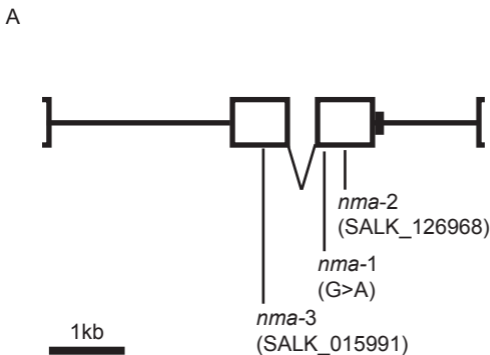


Figure S6: Graphic representation of the *NMA* gene and protein.

A, Gene model of the genomic *NMA* locus.

Exons are depicted as white boxes, 3'UTR as black box, intergenic regions as line. The position of *nma* alleles are shown below the model.

B, protein model of NMA. The predicted signal peptide is shown in black, the predicted polygalacturonase domain in grey. The position of the *nma-1* substitution is shown on top of the model.

Figure S7:

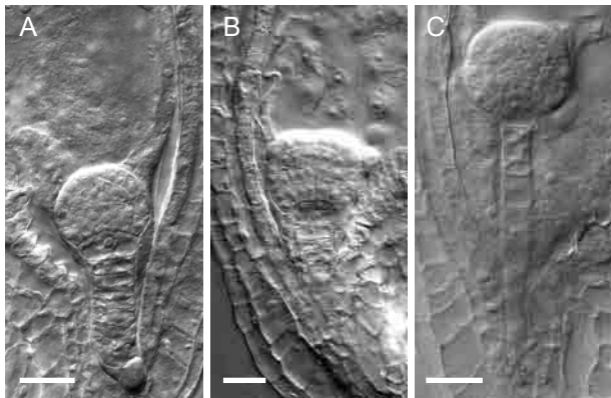


Figure S7: Embryonic phenotype of T-DNA insertion alleles of *nma*.

A, *nma-2*; B, *nma-3*; C, Col-0 wild-type.

Scale bar = 20 μ m

Figure S8:

suspensor length
[μm]

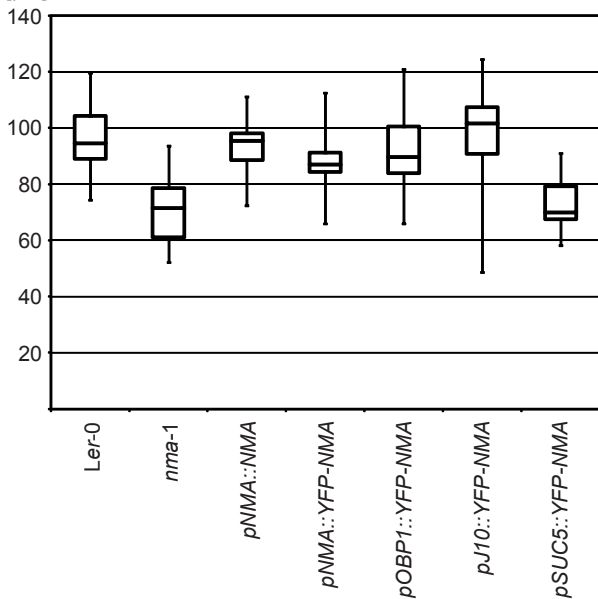


Figure S8: Complementation assay based on suspensor length.

The genotype of representative transgenic lines is given below chart. Boxes represent lower and upper quartiles around median. Whiskers depict maximum and minimum values.

Figure S9:

normalized expression level

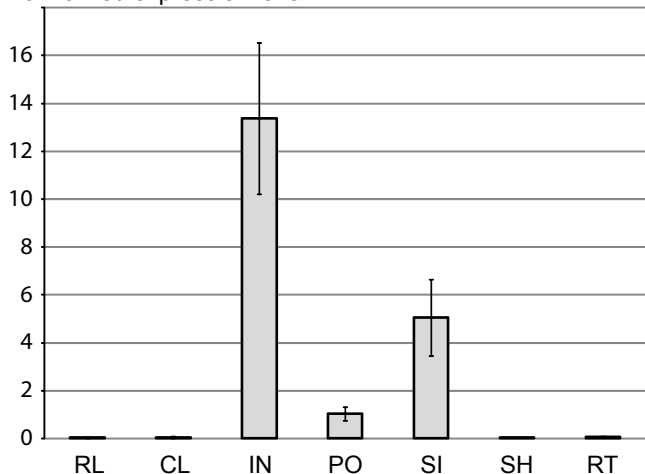


Figure S9: quantitative RT-PCR data of *NMA* expression in various tissue types.

RL, rosette leaves; CL, cauline leaves;

IN, inflorescences; PO, pollen; SI, siliques;

SH, seedling shoot including cotyledons and first leaves; RT, seedling root.

Values are normalized to average expression levels in pollen. Mean values of three biological replicates with standard deviations are shown.

Figure S10:

AZg33160 240137_#

Arabidopsis eFP Browser at bar.utoronto.ca
Winter et al., 2007. PLoS One 2(8): e718

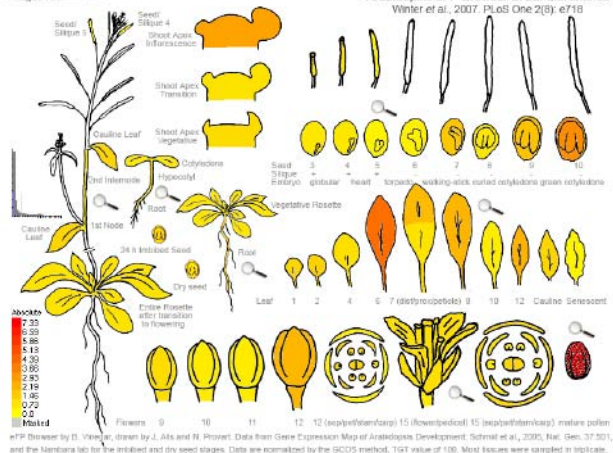


Figure S10: Graphic representation of *NMA* expression data in publicly available microarray data. Screen shot of the Arabidopsis eFP browser (Winter *et al.* 2007).

Figure S11:

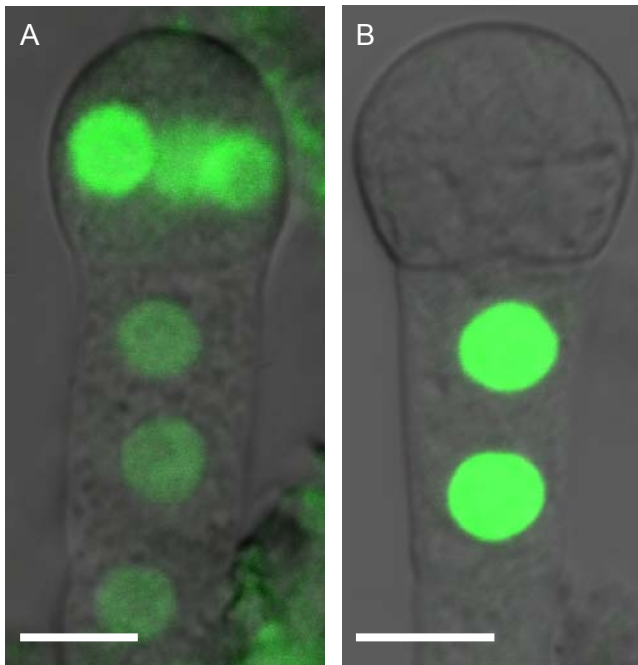


Figure S11: Expression of promoter::reporter gene fusions. A, *pOBP1::n3xGFP*; B, *pJ10::n3xGFP*. Scale bar = 10 μ m.

Figure S12:

Developmental stage

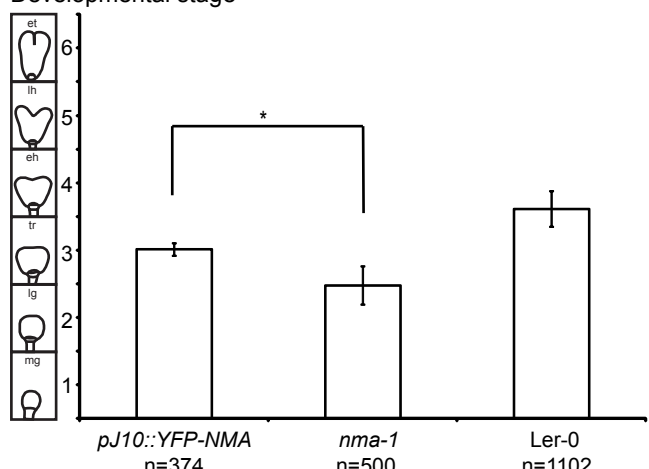


Figure S12: Average developmental stage of embryos 4 dap in *pJ10::YFP-NMA*, *nma-1*, and Ler-0.

Embryos were classified in 6 developmental stages. Numerical values were assigned to each stage.

Averages and standard deviations of at least three biological replicates are shown as bar graphs.

Asterisks indicate significant differences in pair-wise comparison (t-test; $p < 0.05$).

Table S1: Primer sequences

Primer name	Primer sequence
160-3, R	ctctcttcttctcctcgcc
At2g33160P-FC	cggatctgtgttttctcag
At2g33160P-RC	tctctcttcttggttgg
At2g33160-RC	aaggtagaggacgatgtgattc
LBb1.3	atfttgccgatttcggaac
NMA dC-F	aacaaacttgaatgagctgtaat
NMA dC-R	tgcgatacggacttagcccatgtctgatattaaa
NMAi1 AP-F	accaaaccaagaagagagagcgcgccaaaaattaattaagcgtctagggttctctgat
NMAi1 AP-R	atcagaagaaccctagacgcttaattaattttggcgcgccctctctcttggtttgg
NMAi1 ASP-F	ccacgaaggaatatcccgccgagcagcacttaattaaaatcttgacgtcagaaa
NMAi1 ASP-R	ttctgacgtcaaagatttaattaagtcgactggcgccgggatattcctcgtgg
NMAi1-F	ttggatactctgatgacagatgaggaccaggcatggta
NMAi1-R	taccatgccctggcgcacatcagacatcagagatatcaa
qRT-F	gcaaatctacaacgtcact
qRT-R	gacactaataccatgcct
NRT-F3	gtcgtacactagctatgaa
NRT-R4	aatgacgatagggtttccaa
p35Sas	aaaaaaggtaacccccgtgtctctccaaatg
p35Ss	tttttctcgagtcgacctgcaggcggccgca
pJ10as	aaaaaaggttaccctttacaccgtctcttgctctc
pJ10s	tttttctcgaggtgccatgtgtctatattct
pOBP1as	aaaaaaggttaccaatcggagaaagggtgaagctt
pOBP1s	tttttctcgagcatagatttgggtgtgatgtgg
pSUC5as	aaaaaaggttacctatgaaaagaaaacgagcag
pSUC5s	tttttctcgagtgagtaagaacaggtagtcc
RT 160.2 F	tttgtgtgagaacgttgggtg
RT 160.2 R	ggttttagtagcctcagta
RT-5F	tttgtgtgtccttctctc
RT-5R	aagtaatccaccgccagtaa
SSP1-I	ttagagaccacacgagaaggc
SSP1-R	taacatggcttggctctgatcc