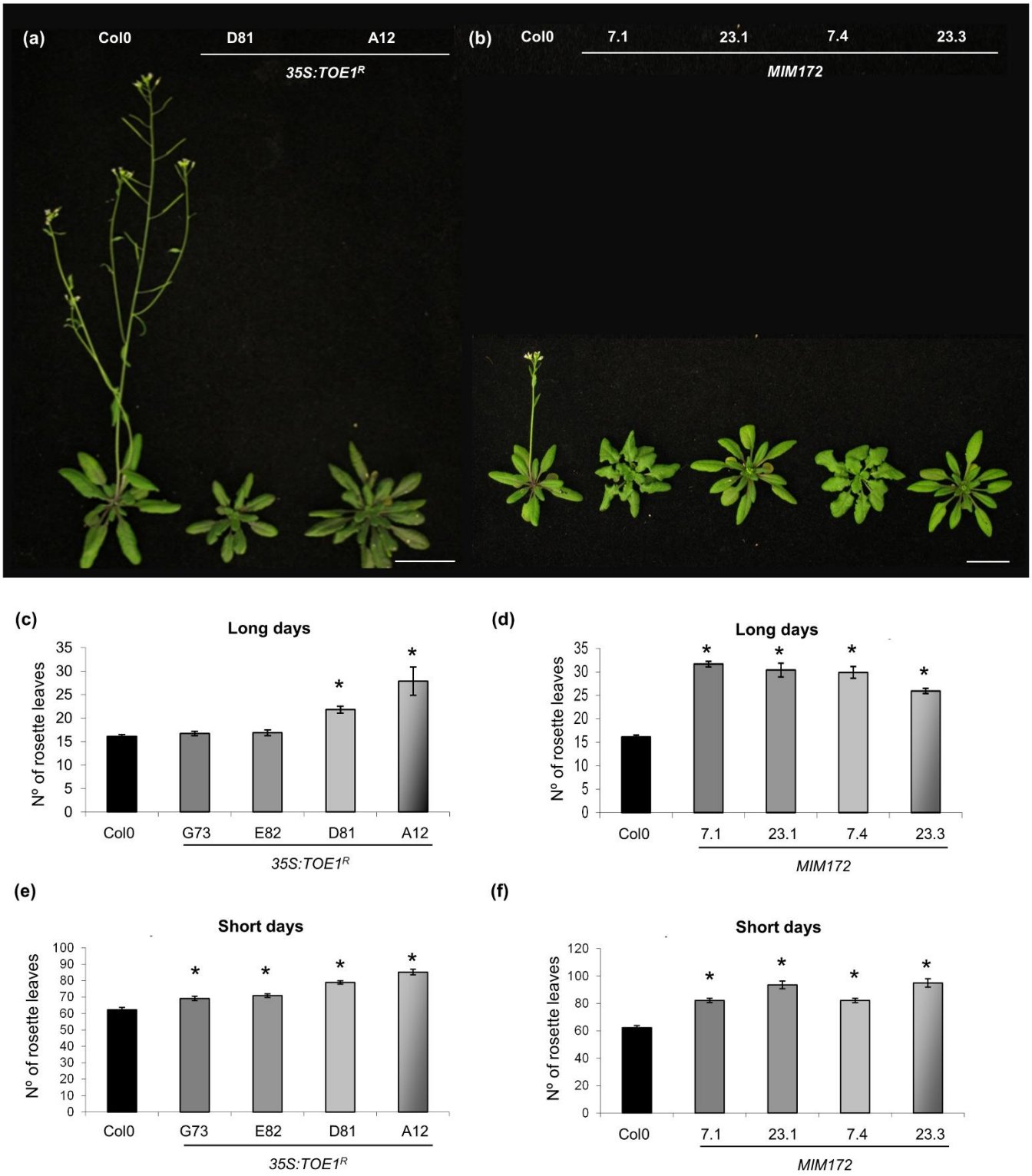

Figure S1. Delayed flowering time phenotype of *35S:TOE1^R* and mimicry lines as compared to Col-0 control. a-b. Flowering time phenotypes under long day conditions. Pictures from Col-0 ecotype, and *35S:TOE1^R-A12*, *35S:TOE1^R-D81* (a); *35S:MIMICRY172-7.1*, *35S:MIMICRY172-7.4*, *35S:MIMICRY172-23.1* and *35S:MIMICRY172-23.3* transgenic lines (b). Each line is detailed and scale bars, 2 cm. All Arabidopsis mutant lines studied showed late flowering phenotype compared to the control Col-0. **c-d.** Number of total leaves of each line under long day conditions. All lines analyzed, *35S:TOE1^R* (c) and mimicry (d) showed higher number of total leaves compared to Col-0 except *35S:TOE1^R-G73* and *35S:TOE1^R-E82,* with a weaker flowering phenotype (c). **e-f.** Number of total leaves of each line grown under short day conditions. All lines analyzed, *35S:TOE1^R* (c) and mimicry (d) showed higher number of total leaves compared to Col-0. Total leaves were counted from at least twenty independent plants per line and experiment. Error bars indicate standard error. Asterisks indicate statistically significant differences ($P < 0.05$) between transgenic lines and their corresponding control.

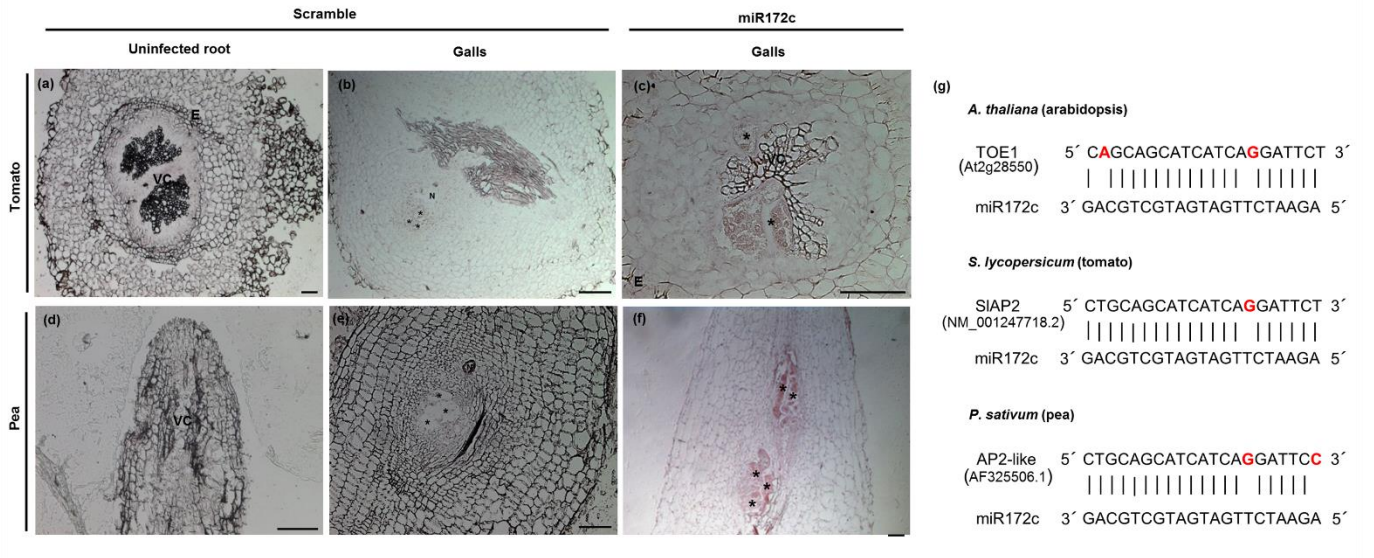

Figure S2. *In situ* detection of mature miRNA172c expression in crops. Tissues analysed alongside *Scramble* as a negative control and miRNA172c specific probe in tomato (**a-c**) and pea (**d-f**). **a.** Cross section of tomato uninfected root. **b.** Longitudinal section of *M. incognita* tomato gall at 7 dpi. **c.** Cross section of *M. incognita* tomato gall at 7 dpi. **d.** Longitudinal section of pea uninfected root apex. **e.** Longitudinal section of *M. incognita* pea gall at 7 dpi. **f.** Longitudinal section of *M. incognita* pea gall at 7 dpi. Asterisks indicate GCs; N, nematodes; VC, vascular cylinder; E, endodermis. Scale bars: 100 µm. **g.** Complementarity of the Arabidopsis miRNA172c probe used for hybridisation (*GACGTCGTAGTAGTTCTAAGA*) to that of TOE1 in Arabidopsis and homologues in different crop species studied (tomato and pea). In red bold, non-matching base pairs.

Table S1. List of primers used for qPCR analysis of *GAPC2*, *TOE1*, *TOE1R* and *FT*.

USED for	GENE ID	GEN name	Primer NAME	SEQUENCE (5'-3')
qPCR	At1g13440	GAPC2	Forward	GAGATTCGTAATGTTTTGATTTCG
qPCR	At1g13440	GAPC2	Reverse	CTTTCGGTGGAGGTCTTGTC
qPCR	At2g28550	TOE1	Forward	GCGTGGAGTTAGCTTGAGGA
qPCR	At2g28550	TOE1	Reverse	TCCAGTAAAGGCGATGATCC
qPCR	At2g28550	TOE1 resistant miR172	Forward	CTCAGTTGCAGCAGCATCGTCGGGCTTCTCACATTTCCGGCCA
qPCR	At2g28550	TOE1 resistant miR172	Reverse	TGGCCGGAAATGTGAGAAGCCCGACGATGCTGCTGCAACTGAG
qPCR	At1g65480	FT	Forward	CTGGAACAACCTTTGGCAAT
qPCR	At1g65480	FT	Reverse	AGCCACTCTCCCTCTGACAA

Table S3. Auxin responsive elements (*AuxRE*) present in the promoter regions of five genes that transcribe to miRNA172 and their sequence. a. miRNA172 mature sequences, in black, identical sequences among the five genes (a-b; c-d; and e), in red bold, non-matching base pairs between the five miRNA172 gene sequences. The number of auxin boxes in each of the gene regions are also indicated (Auxin Response Elements). Identification of the AuxRe motifs were performed with the online tool RSAT (van Helden, 2003). Name of each gene is detailed (Loci). **b.** miRNA172c sequence homology with tomato (*S.lycopersicum*) and pea (*P. sativum*) miRNA172.

a.- *Arabidopsis thaliana* (Arabidopsis)

miRNA ID	Loci	Sequence	Auxin Response Elements (1000pb)
ath-miRNA172	a	AGAAUCUUGAUGAUGCUGCA**U**	0
ath-miRNA172	b	AGAAUCUUGAUGAUGCUGCA**U**	2
ath-miRNA172	c	AGAAUCUUGAUGAUGCUGCA**G**	2
ath-miRNA172	d	AGAAUCUUGAUGAUGCUGCA**G**	1
ath-miRNA172	e	**G**GAAUCUUGAUGAUGCUGCA**U**	0

b.- *Solanum lycopersicum* (tomato)

```
ath-miR172c          1  agaaucuugaugaugcugcag  21
                        ||||||||||||||||||||
sly-miR172a,b        1  agaaucuugaugaugcugcau  21
```

- *Pisum sativum* (pea)

Not described yet.

References:

- Van Helden J. 2003. Regulatory sequence analysis tools. *Nucleic Acids Research* **31**(13): 3593-3596.