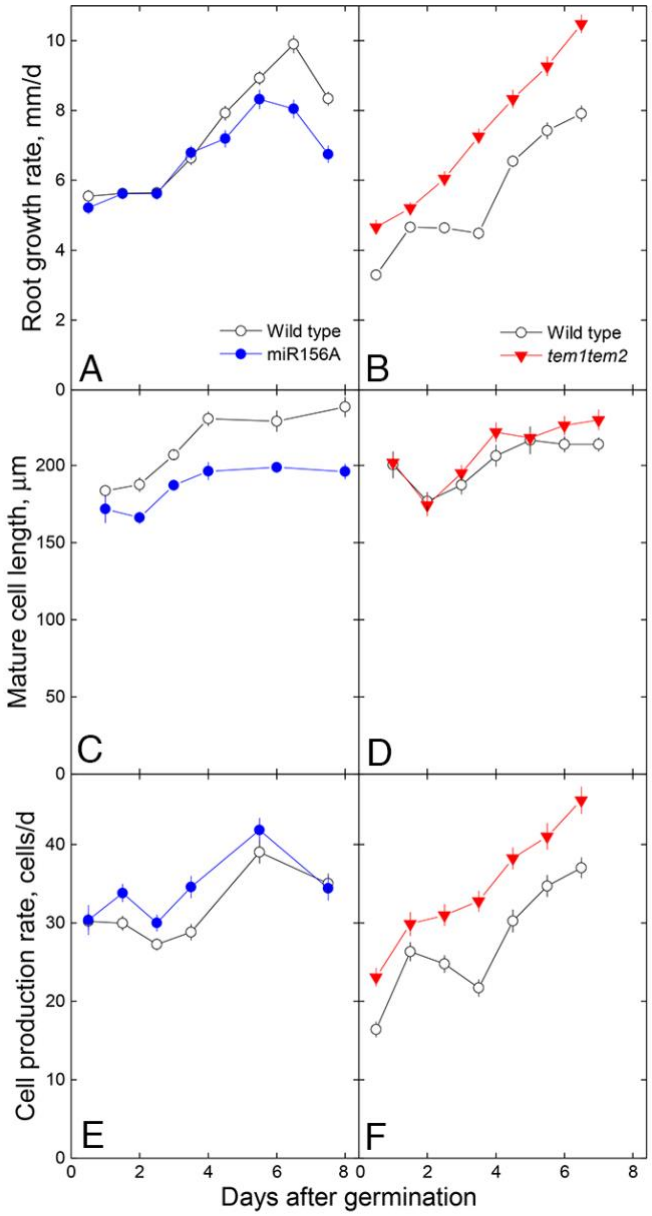

Fig. S1. Rates of growth and mature cell length vary as roots mature and are affected by known phase change regulators (A) Growth rate of wild type (n = 38) and *35S::miR156A* (n = 37) roots, and (B) wild type (n = 31) and *tem1tem2* double mutant (n = 28) roots. (C, D) Length of mature cortical cells in the indicated genotypes. Symbols represent means of 8 or 9 roots ± s.e.m.. (E, F) Number of cells produced per day, calculated from data in A – D.

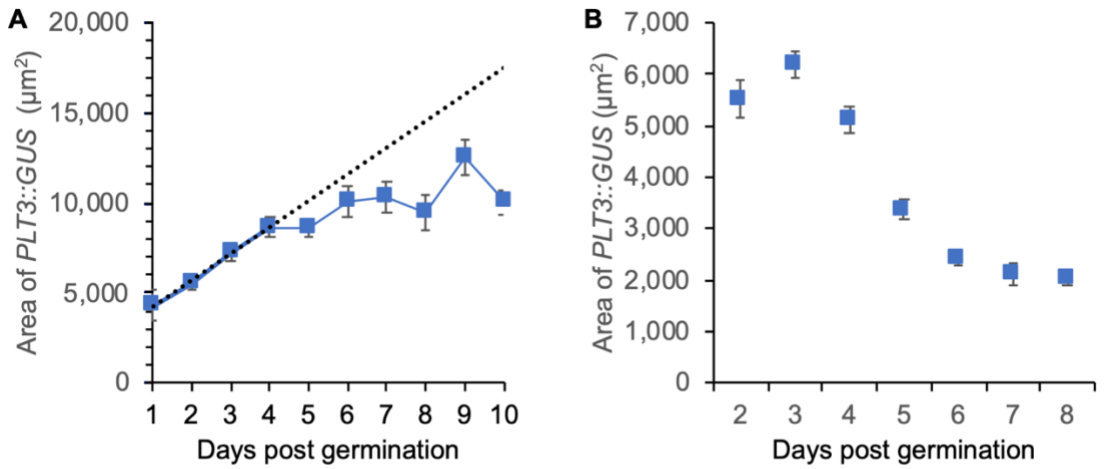

Fig. S2. The area of *PLT3::GUS* expression at the site of a lateral root primordium increases more slowly, or declines, after day 4. Each data point reflects the average area in which *PLT3::GUS* stain is visible around the presumptive site of a lateral root primordium. Data are (A) from the region of root that grew in the most recent 24 h. (On day 1, this is segment 1 as defined in Figure 5; on day 2 it is segment 2, and so on). (B) Data from the region that grew in the 24 h before that (No such region exists on day 1; on day 2, it is segment 1; on day 3 it is segment 2 and so on). Each point reflects the average of all the GUS-stained spots in the segments from 8 -10 roots ± s.e.m.. The decline in area was driven by decreased width of individual spots, where width runs parallel to the long axis of the root. Data from plants in this trial are also included in Table 1.

A B

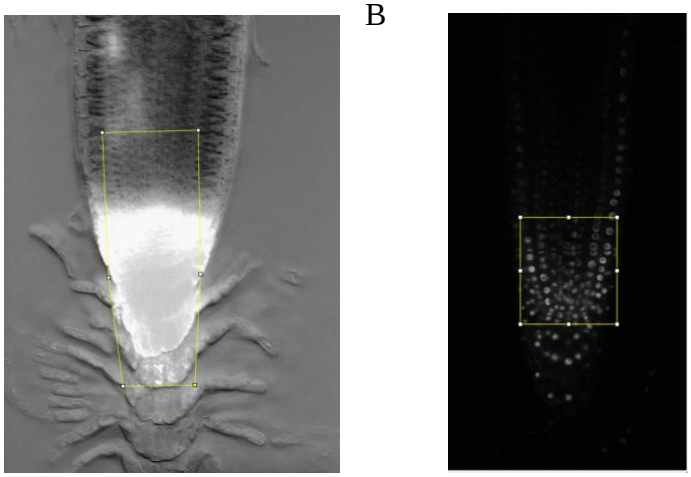

Fig. S3. Quantification of GUS staining and Venus fluorescence in Figure 3. Representative image showing the region of interest (ROI) used for quantification of (A) *PLT3::GUS* staining and (B) PLT2- VenusYFP fluorescence. (A) To quantify the blue signal in GUS stained roots, color images were opened in Image J, split into separate channels, and the red channel was inverted. The ROI was positioned as shown over the root tip and stem cell niche, and its mean gray level recorded. (B) For YFP fluorescence, single channel gray scale images were exported from Zen Black software and opened in Image J. The ROI was positioned such that the second narrow row of cells below the QC was included at the rootward end of the region, and the mean gray level of the region was recorded.

Table S1. Primer sequences.

Primer name	**Sequence**
Primer sequences for qPCR	
PLT2-F	CTTTGCCGCCTCACATTCAC
PLT2-R	TTTGGAACCTCTCCACCTTCG
PLT3-F	TCAGGAGGAAGAGTAGC
PLT3-R	TCTTTGTTCCCAGCAACTCG
TUB2-F	AGCAATACCAAGATGCAACTGCG
TUB2-R	TAACTAAATTATTCTCAGTACTCTTCC
Primer sequences for *plt2-3* genotyping	
plt2-3 F	CCAAACTTGCGTTTCTCAAA
plt2-3 R	AGAGGCACAAGTGACGACTG

PLT3 primers are from Du (2017).