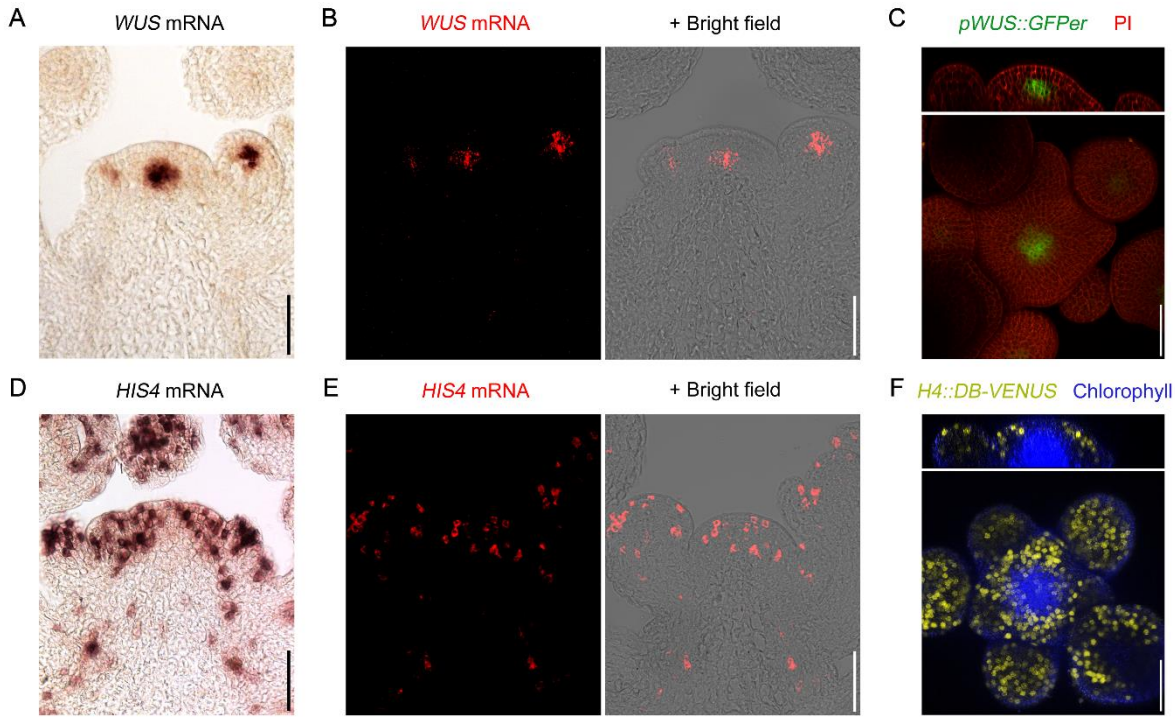


**Figure S1. Establishment of RNA FISH to investigate mRNA expression patterns in *Arabidopsis* shoot apices.**

**(A-B)** Spatial distribution of *WUS* mRNAs in the shoot apical meristem (SAM) revealed by chromogenic *in situ* hybridisation (**A**) and FISH (**B**).

**(C)** *WUS* promoter driving the expression of an endoplasmic reticulum (ER) localized-GFP. Top panel, SAM orthogonal view. Bottom panel, SAM top view.

**(D-E)** *HIS4* mRNA expression in the shoot apex revealed by chromogenic *in situ* hybridisation **(D)** and FISH **(E)**.

**(F)** Expression pattern of Venus YFP fluorescent protein under the control of the *HIS4* promoter. Venus YFP is fused with the destruction box (DB) domain of CYCB1;1 (Jones et al., 2017). Top panel, SAM orthogonal view. Bottom panel, SAM top view.

Scale bars, 50 µm.

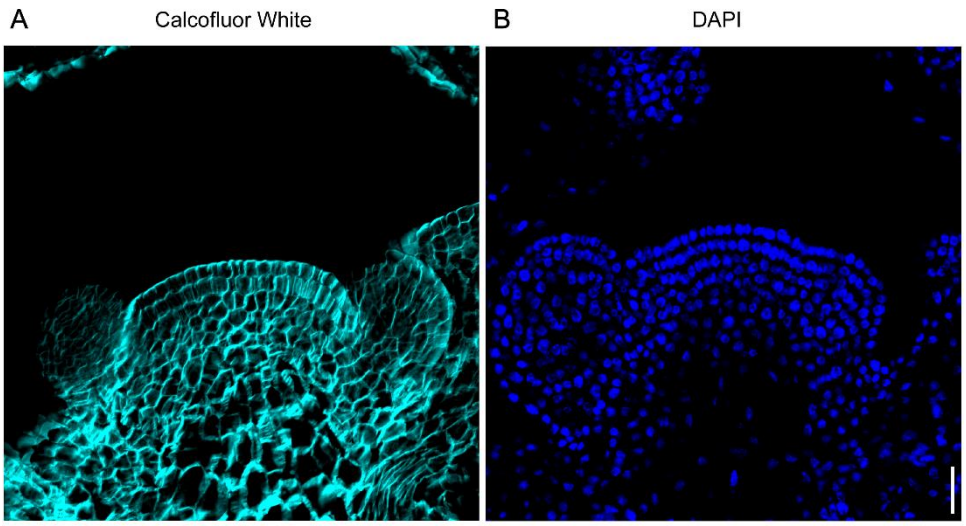


**Figure S2. Observation of cell wall and nucleus in meristem longitudinal sections by fluorescent dye staining.** Longitudinal sections of shoot apex were stained with Calcofluor White to label the cell wall and DAPI to show the nucleus. Scale bar, 20 μm.

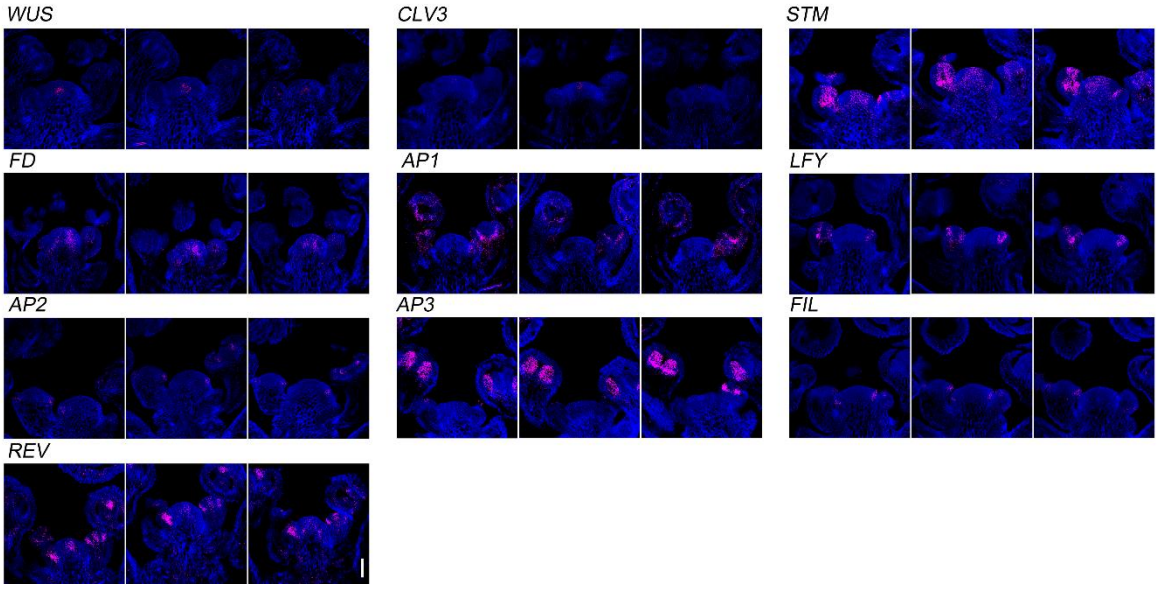


**Figure S3. mRNA spatial distribution of meristem and flower development RNAs.** Shown are serial sections of the shoot apex. Scale bar, 50 μm.

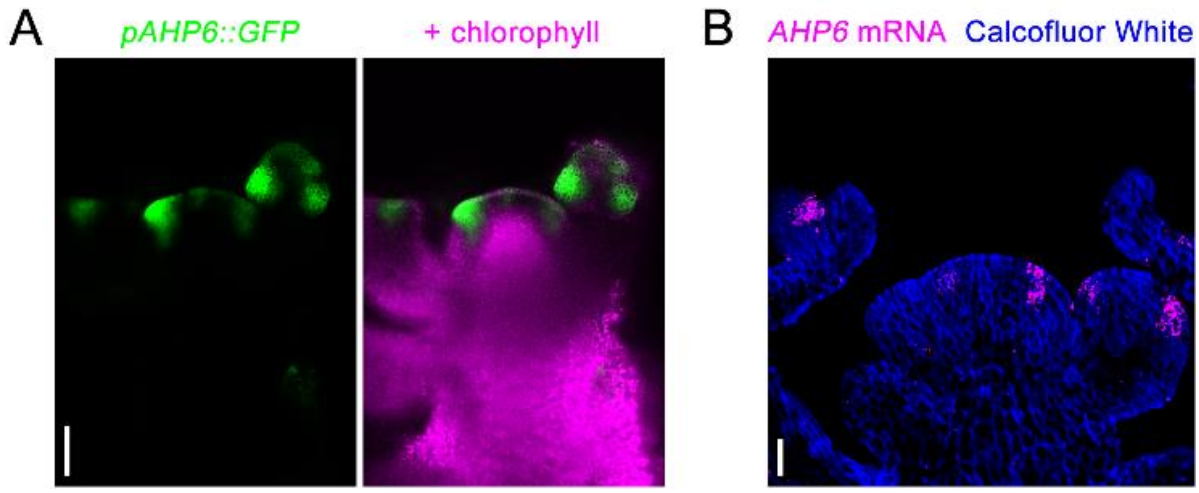


**Figure S4. Expression pattern of *AHP6* in the shoot apex and flower primordia.**

**(A)** *AHP6* promoter activity in *pAHP6::GFP* fluorescent reporter. Scale bar, 50 µm

**(B)** *AHP6* mRNA distribution by RNA FISH using an *AHP6* specific RNA probe. Scale bar, 20 µm

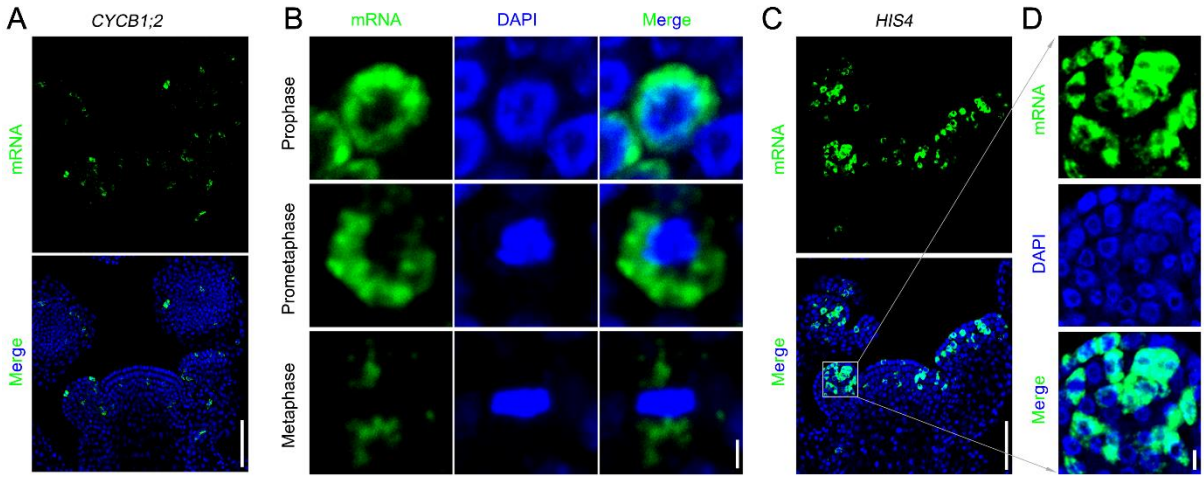


**Figure S5. Expression patterns of cell cycle gene mRNAs.**

**(A)** An overview of *CYCB1;2* gene expression at the SAM. Scale bar, 50 μm

**(B)** Localization of *CYCB1;2* mRNAs in dividing cells at different mitotic stages. Scale bar, 2 μm

**(C)** Distribution of *HIS4* mRNAs across the whole meristem. Scale bar, 50 μm

**(D)** An enlarged view of the regions from **(C)**. Scale bar, 5 μm

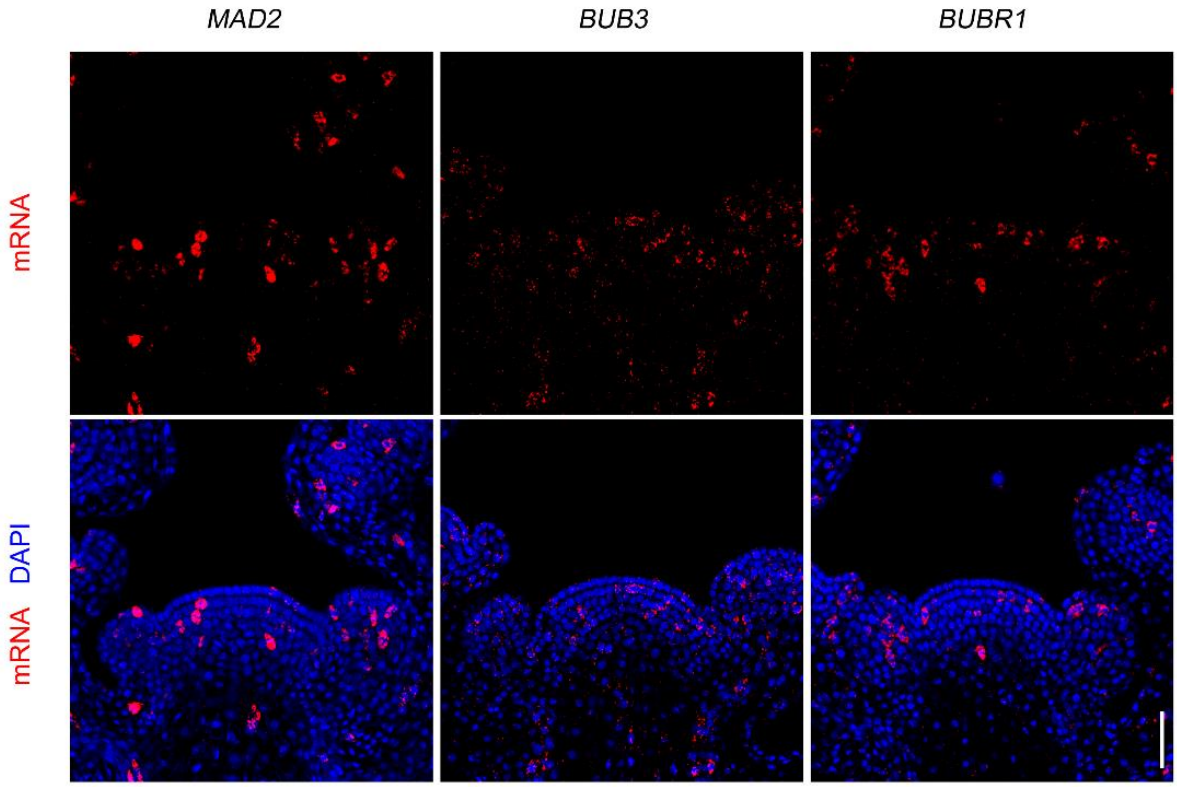


**Figure S6. Expression patterns of mitotic checkpoint complex (MCC) genes *MAD2*, *BUB3*, and *BUBR1*.** The mRNAs of all three genes were specifically expressed in mitotic cells. Scale bar, 50 μm

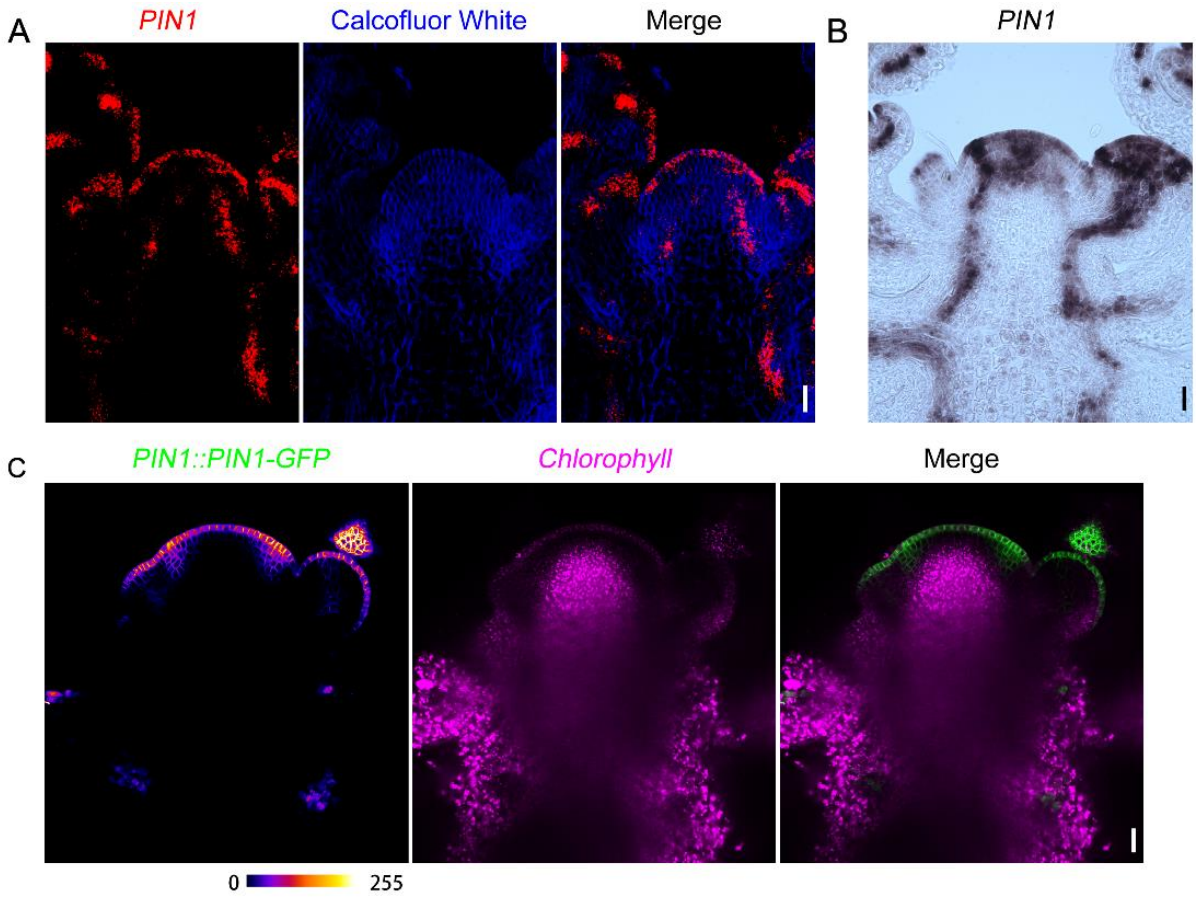


**Figure S7. PIN1 expression patterns in the shoot apex.**

**(A-B)** *PIN1* mRNA expression revealed by RNA FISH **(A)** and chromogenic *in situ* **(B)** using a *PIN1* specific antisense RNA probe.

**(C)** Expression pattern of PIN1-GFP fluorescent reporter. Scale bars, 20 µm

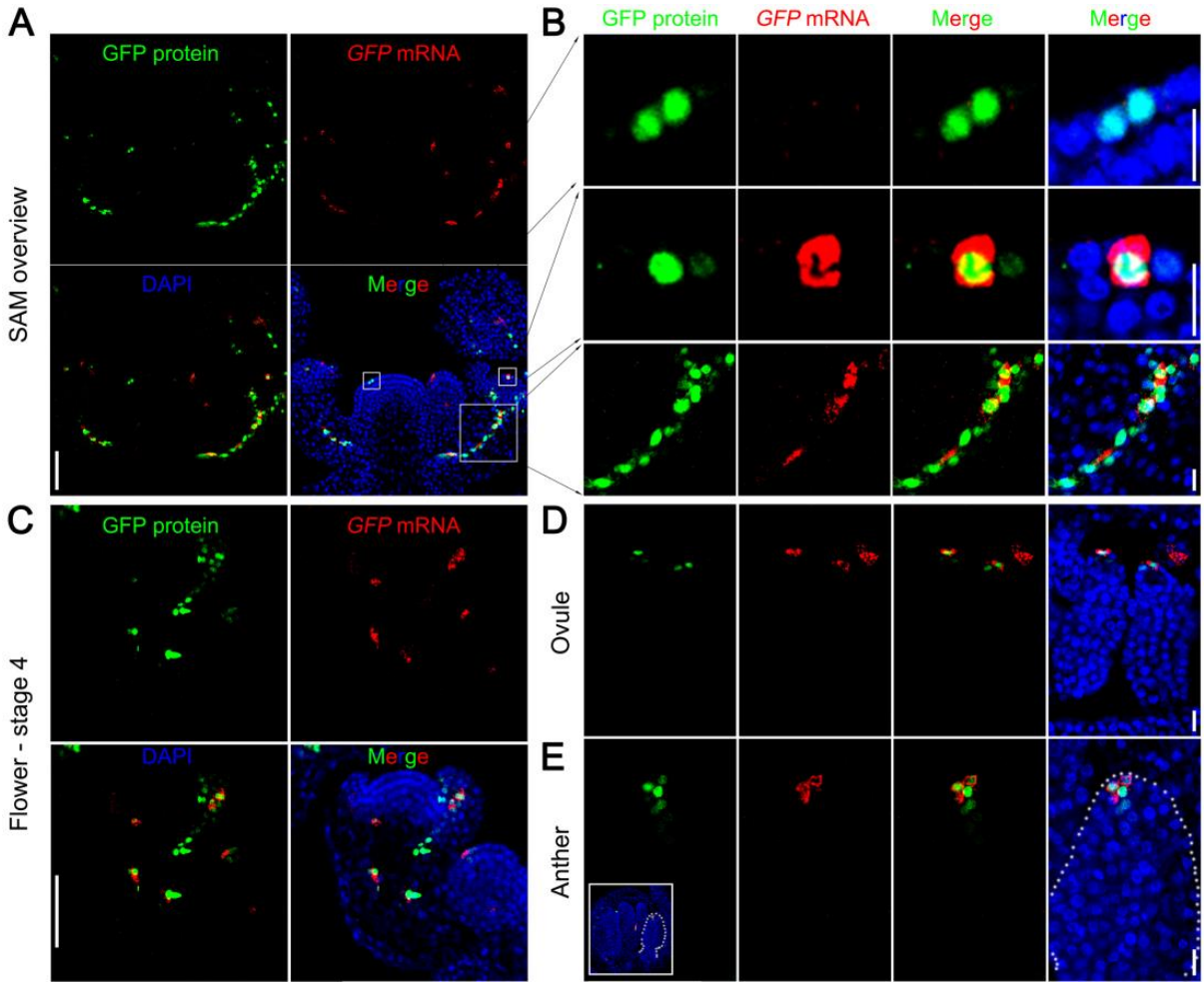


**Figure S8. Expression patterns of auxin reporter *DR5v2-n3GFP* in the shoot apex.**

**(A)** SAM overview showing the distribution of *GFP* mRNA and protein.

**(B)** Individual cells from the regions labelled in **(A)**.

**(C-E)** *GFP* mRNA and protein expression in flower primordia **(C)**, ovule **(D)**, and anther **(E)**.

Scale bars in **(A)** and **(C)**, 50 µm; **(B)**, **(D)** and **(E)**, 10 µm.