nature plants

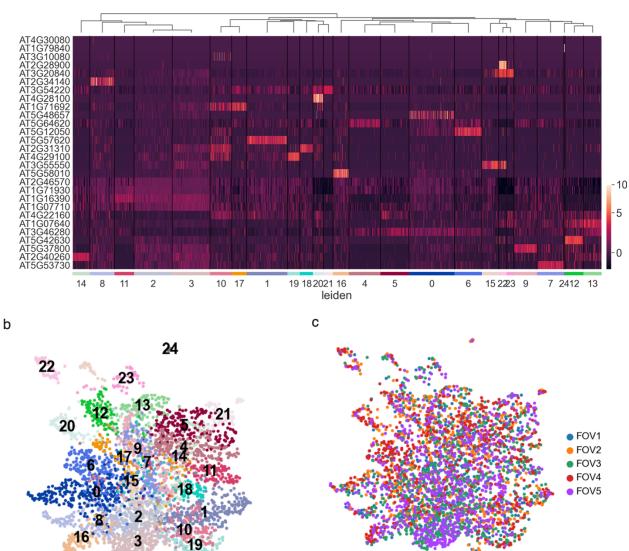


Brief Communication

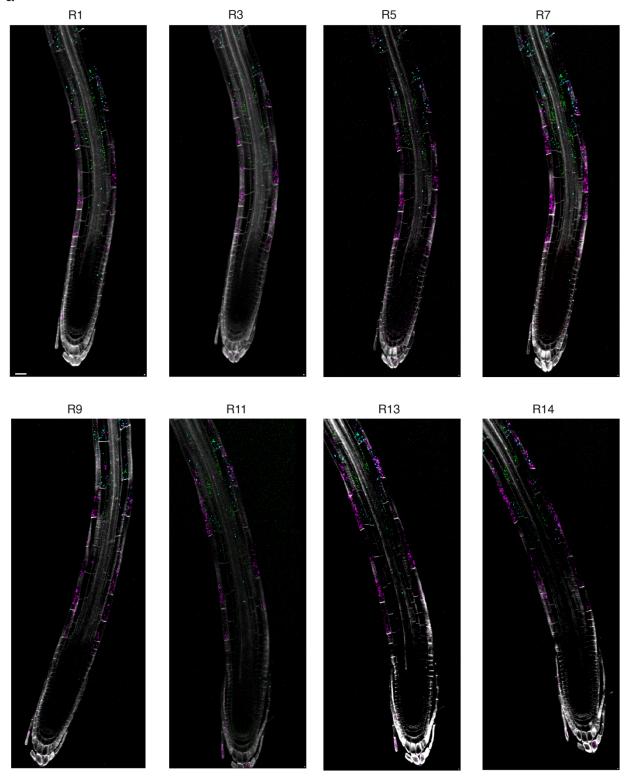
https://doi.org/10.1038/s41477-023-01439-4

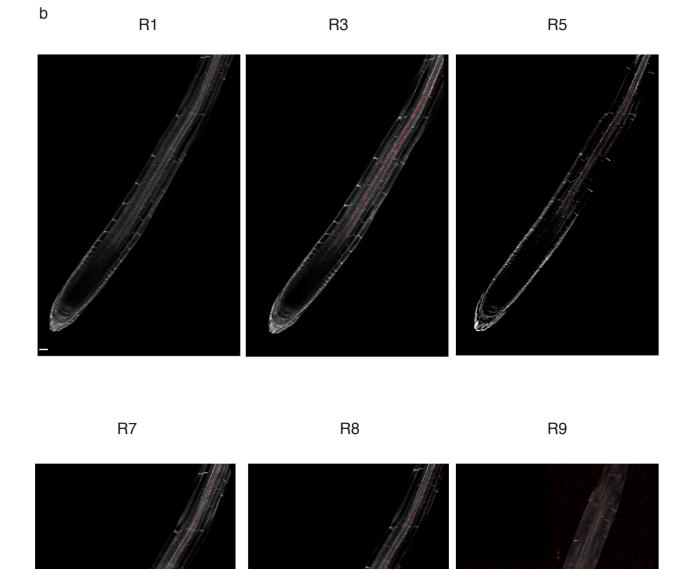
Multiplexed single-cell 3D spatial gene expression analysis in plant tissue using PHYTOMap

In the format provided by the authors and unedited



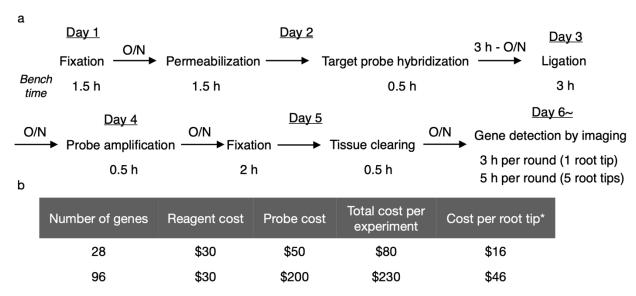
Supplementary Figure 1 | Spatial expression analysis of 28 genes with PHYTOMap a, Hierarchical clustering of 3608 cells from five root tips based on the relative expression (RE) of 28 genes. Leiden cluster IDs are indicated at the bottom. (b-c), UMAP visualization of the data shown in (a) colored by (b) Leiden clusters and (c) replicates.





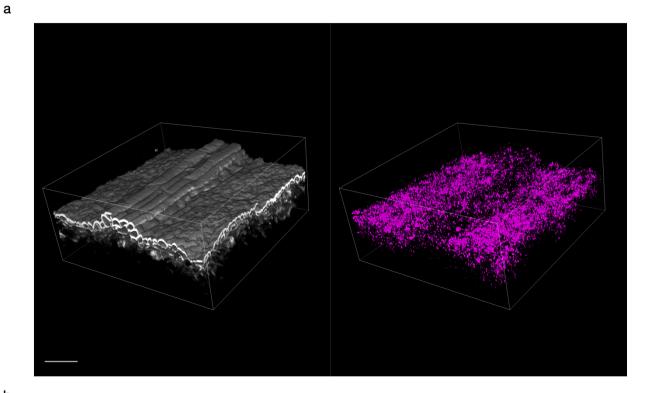
Supplementary Figure 2 | PHYTOMap across 14 rounds of imaging

a, Representative 2D optical sections from each imaging round. Magenta: AT3G46280 labeled with Alexa Fluor 555. Cyan: AT2G31310 labeled with Alexa Fluor 647. Green: AT5G57620 Alexa Fluor 488 b, Red: AT3G10080 labeled with Alexa Fluor 750. Signal was not detected after the 9th round. Scale bars = 25 μ m.

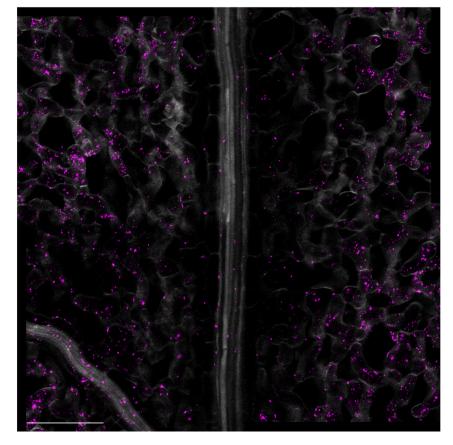


Supplementary Figure 3 | Timing and cost estimates of PHYTOMap

a, Diagram showing the key steps and timings of PHYTOMap. b, Cost estimates for PHYTOMap experiments at different scales. A sample that fits within a 14 mm diameter circle can be analyzed in one experiment using the protocols presented in this study. *Calculated for five root tips per experiment. It is possible to accommodate more root tips in one experiment.



b



Supplementary Figure 4 | PHYTOMap in Arabidopsis leaves

a, 3D rendering of cell wall staining (leaf) and UBQ10 (right) images in a whole-mount leaf of Arabidopsis. b, 2D PHYTOMap image of cell wall staining (white) and UBQ10 (magenta). Scale bars = $100 \mu m$.