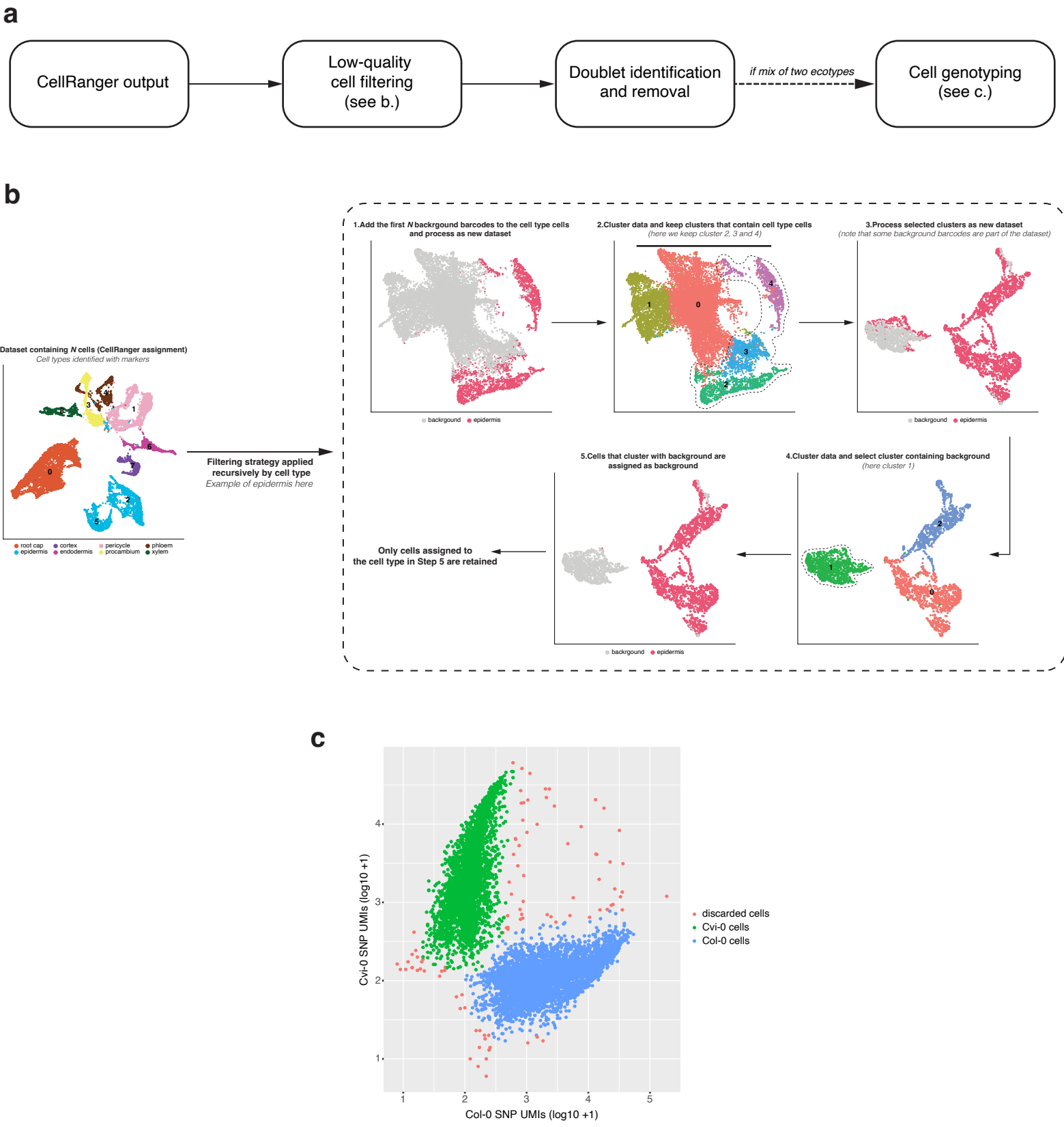
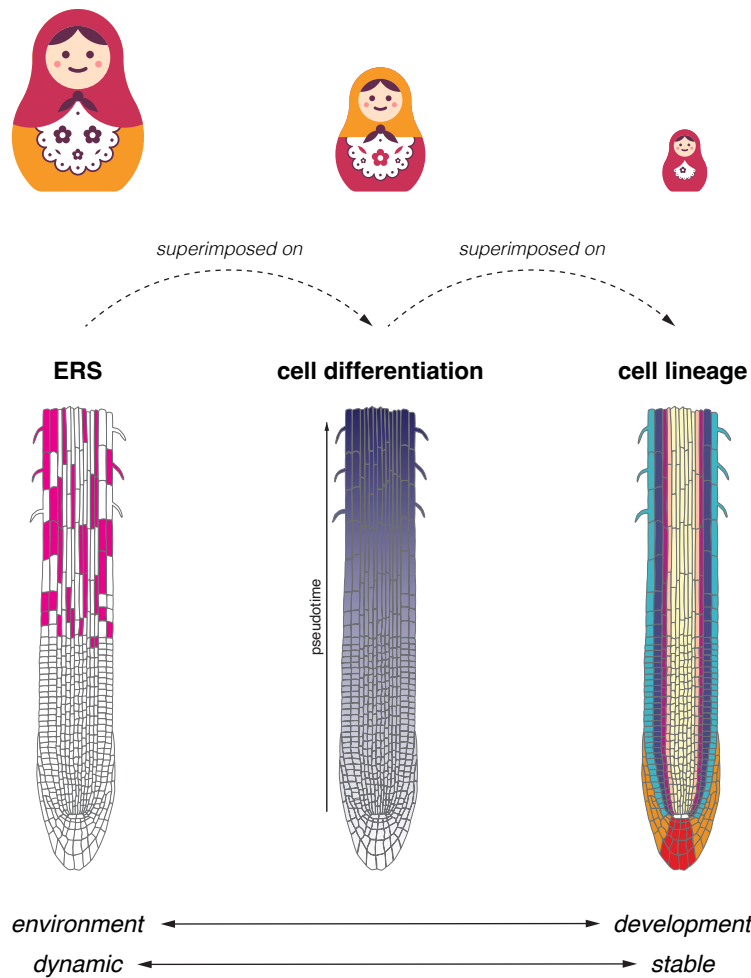

Supplementary information

An environmentally regulated dichotomy in cell lineages of the root

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Supplementary Fig. 1: Data pre-processing steps
a, Diagram showing the pre-processing workflow for each scRNA-seq library, from Cell Ranger output to the final set of retained cells. **b**, Diagram illustrating the steps used to filter low-quality cells (see Methods for further details). **c**, Single nucleotide polymorphism (SNP) unique molecular index (UMI) counts for Col-0 and Cvi-specific variants shown on a $\log_{10}$ scale. Colour indicates the genotype classification obtained by clustering.



Supplementary Fig. 2: Layers of cell identity in the root

Under unperturbed development, scRNA-seq data show that root cell identities at the tip can be defined by three parameters: (1) the cell type, (2) the differentiation stage, and (3) the presence or absence of the ERS. Much like nested dolls, these components of cell identity can be seen as layers superimposed on one another: the inner layers are stable, ontogenetically defined, and present in all cells, while outer layers such as the ERS are added only in some cells, shaped by external cues, and remain more dynamic. We anticipate that further perturbations may reveal additional layers of transcriptional identity, and that even the core layers may vary under contexts such as regeneration. Nested dolls illustration adapted from Good Studio/stock.adobe.com (Adobe Stock, asset ID 158585110).