A Stroll Through the Developmental Landscape of Plants

Warre Dhondt[1], Michael Van de Voorde[2], and Prof. Dr. Ir. Steven Maere[3]

[1]Universiteit Gent

[2, 3]Evolutionary Systems Biology, VIB-Ugent Center for Plant Systems Biology

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1 Results

1.1 Single-cell transcriptomics of the *Arabidopsis* root

1. QC, removing protoplasting DE genes, why we did not filter cells, Normalization
2. Clustering: cell type annotation using markers from [**Brady2007**], enriched GO in meristematic clusters, expression of genes with known functionality in different cell types. (figure 1A-C)
3. Ploidy annotation, distribution in cell types (figure 1D)
4. Different dimensionality reductions, why we chose UMAP in this case (figure 1E/F)

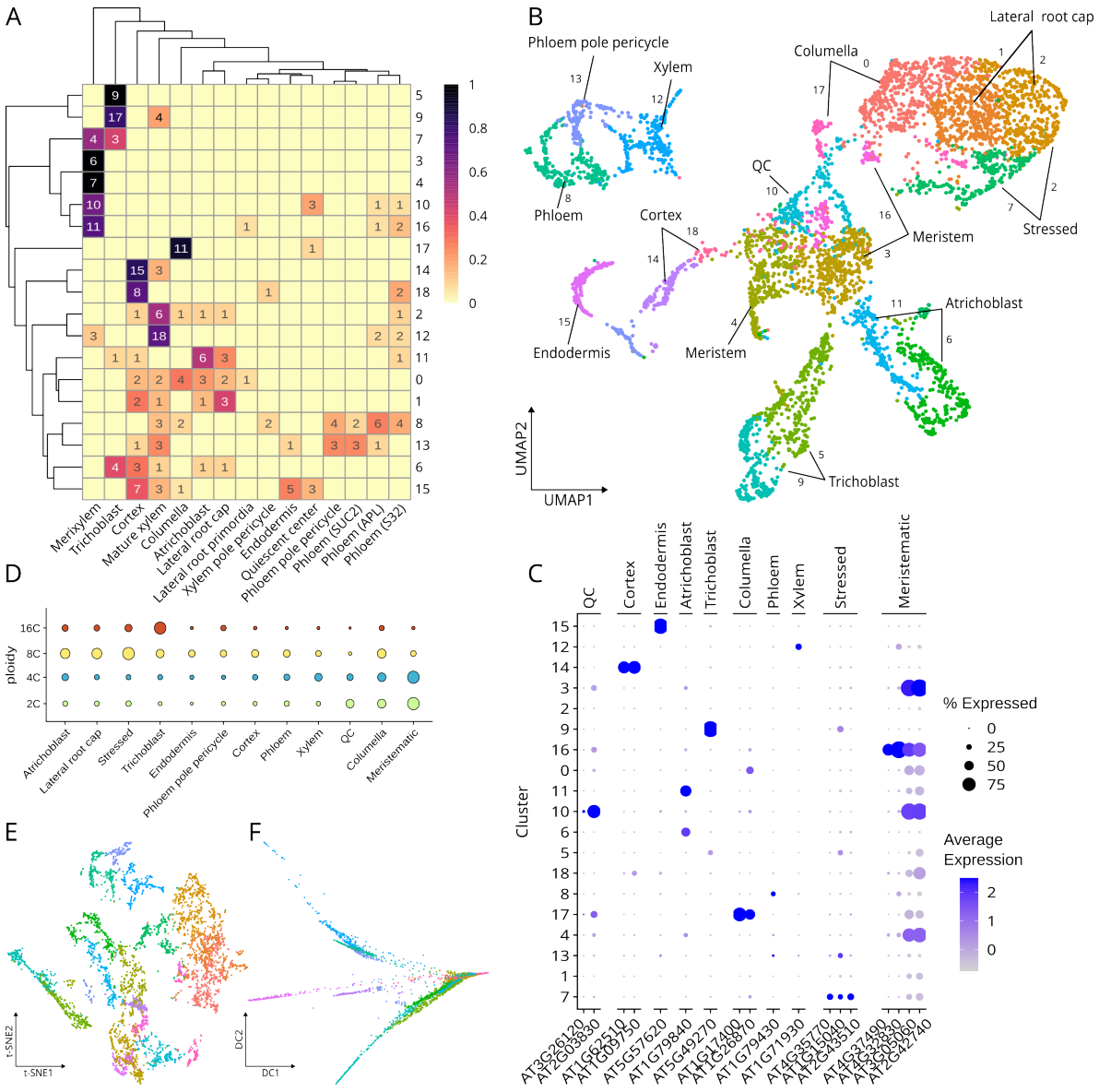

Figure 1: **Cell types of the *Arabidopsis* Root Identified by scRNA-Seq.**
(A) Heatmap showing the contribution of marker genes of different cell types to the cluster identity. The top 50 differentially expressed genes per cluster were mapped to marker genes of bulk RNA-Seq data of plant root tissue sections. The numbers in the matrix represent the number of DE genes of the top 50 of that cluster mapping to a certain tissue. The row colors are the normalized contribution of the cell types to the top DE genes of a given cluster. (B) UMAP of the 4727 *Arabidopsis* root cells. The (sub)clusters are colored and named according to their cell type annotation. Numbers besides the arrows indicate the cluster numbering as referred to in the text. (C) Dot plot showing expression of known cell type marker genes by the annotated cell types in the scRNA-Seq dataset. Dot sizes represent percentage expression in a cell type, color intensity reflects average normalized and scaled expression. (D) Dot plot showing the contribution of different ploidy levels to the cell types identified in the scRNA-Seq dataset. The ploidy level of each cell was identified by correlation with bulk RNA-seq reference expression profiles. (E) and (F): t-SNE and diffusion map, respectively, of the scRNA-Seq dataset. Cells are color-coded according to cell type annotation.