

Single-Cell RNA Sequencing (scRNA-seq) analysis of Congestive Heart Failure (CHF)

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Dataset used for the analysis

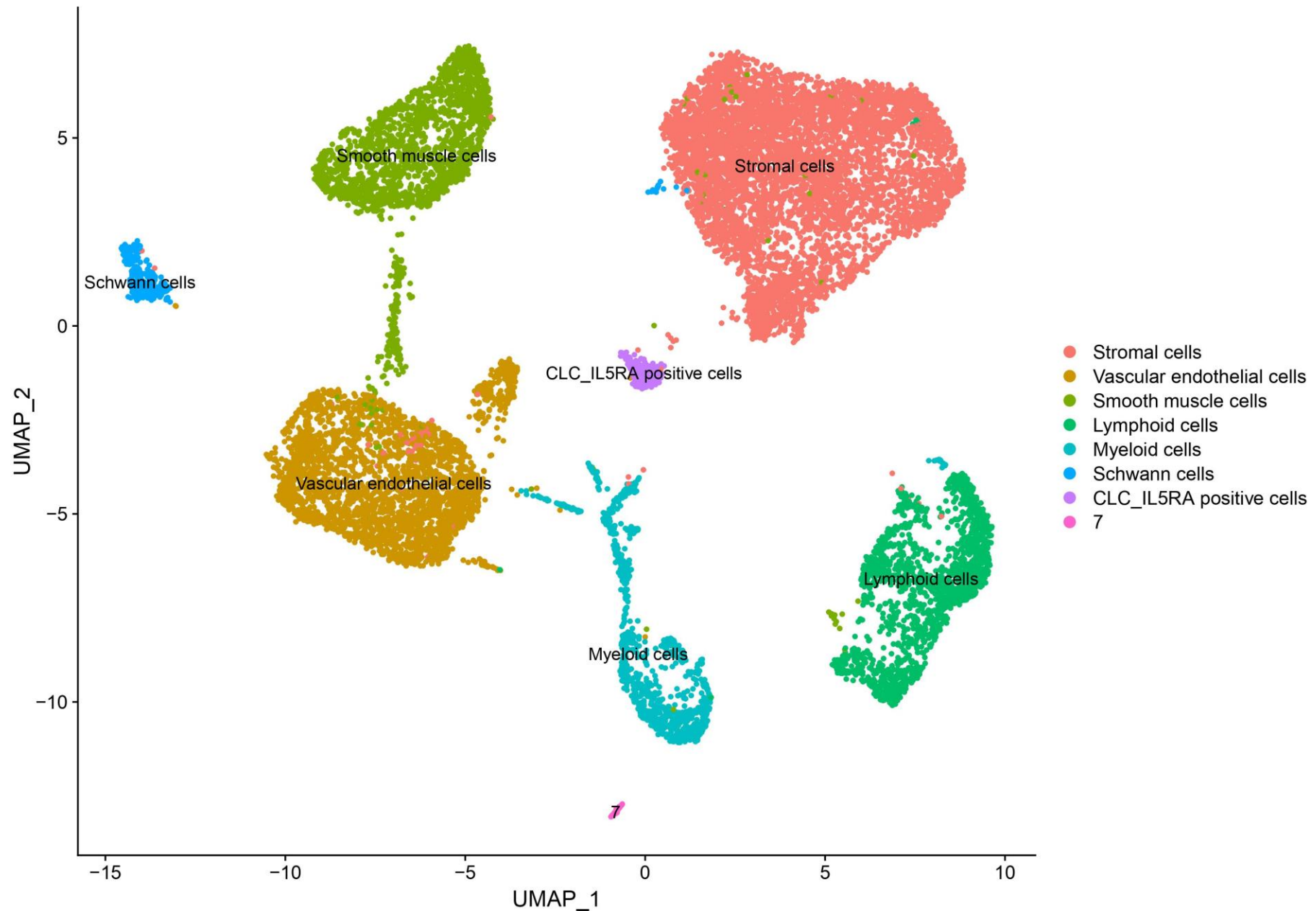
This analysis was done using, two types of human **left ventricular samples**:

1. one control sample (non-failing, non-transplantable heart) and
2. one heart failure sample (with a history of hypertension).

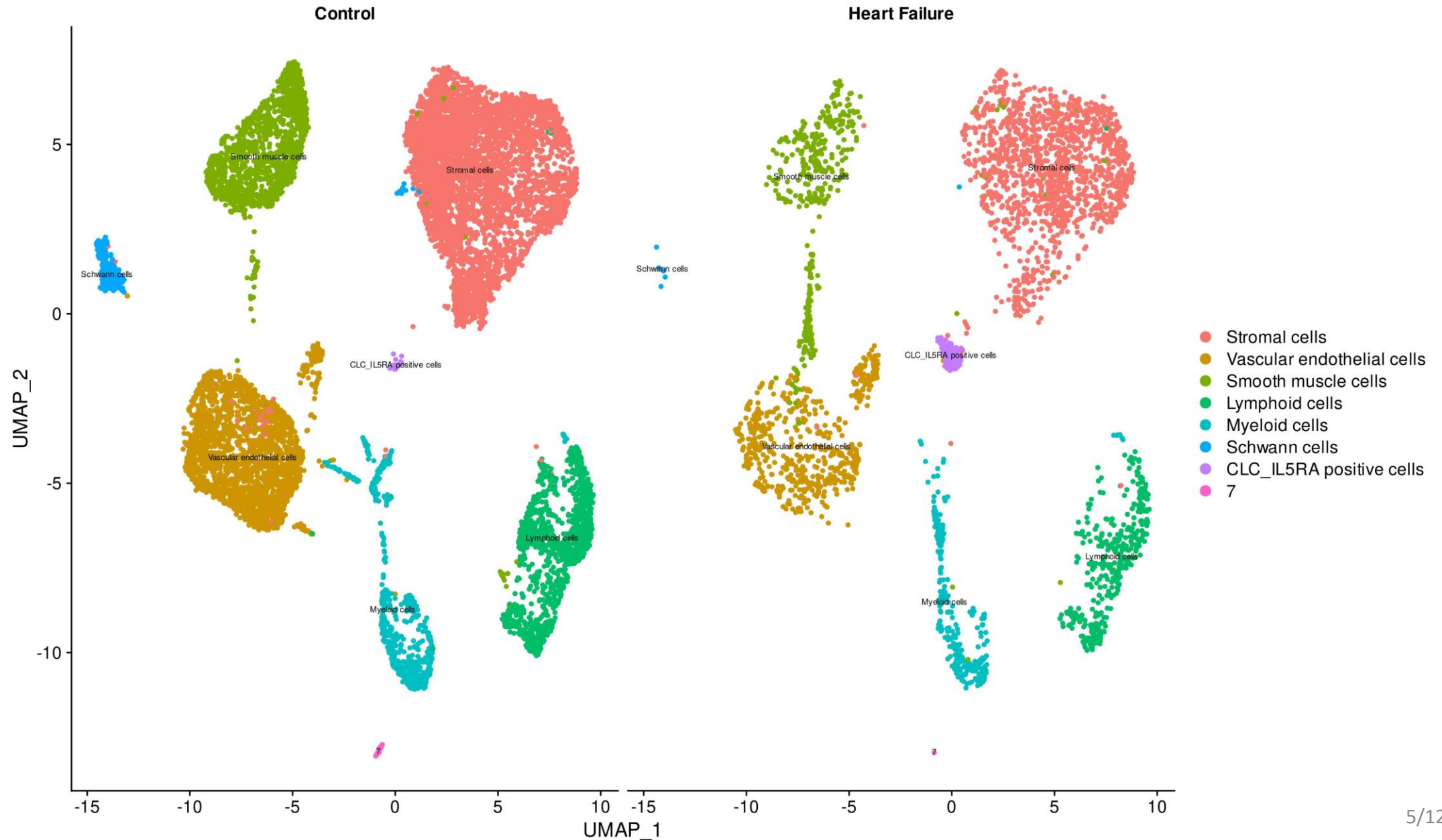
Aim

1. Explore the cellular landscape in Congestive Heart Failure
2. Identify the various cell markers and cell type
3. Identify the differentially expressed genes across the cell types

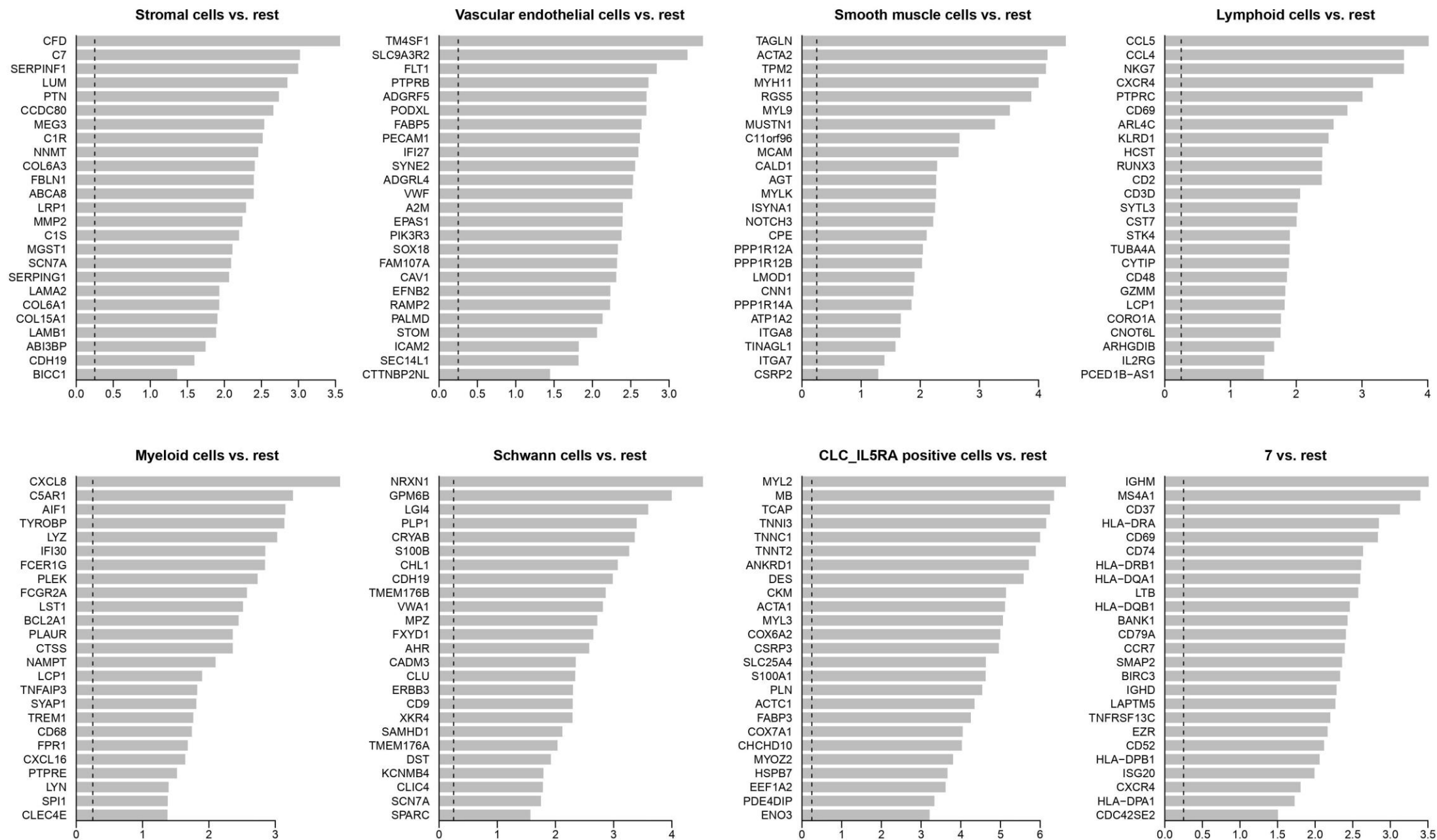
UMAPs of Heart single cell transcriptomes colored by cell type



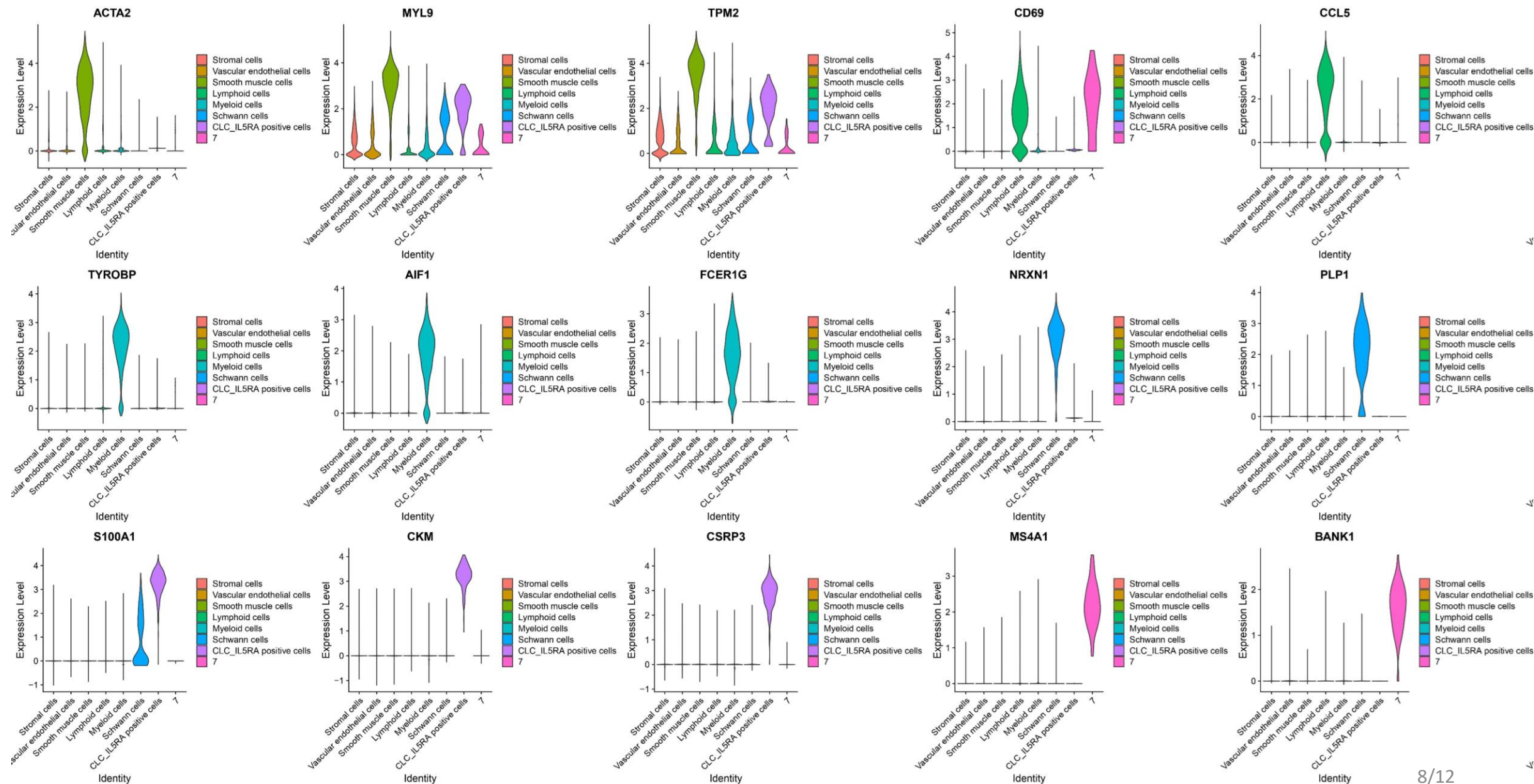
UMAPs of heart single cell transcriptomes colored by cell type



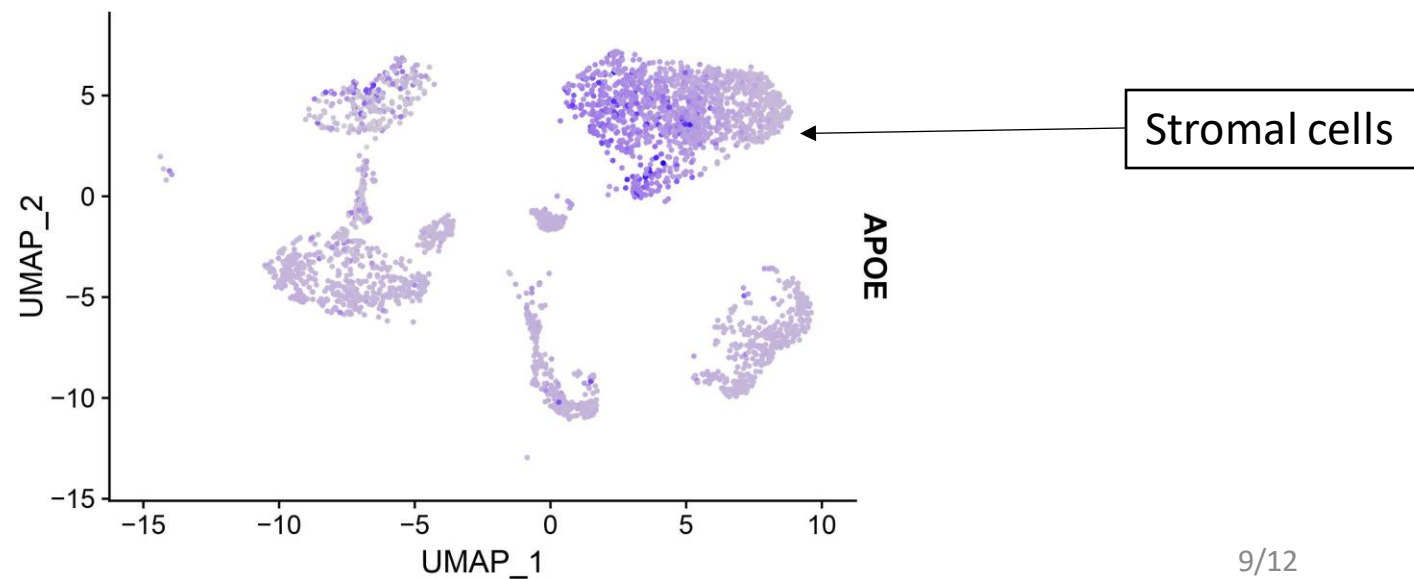
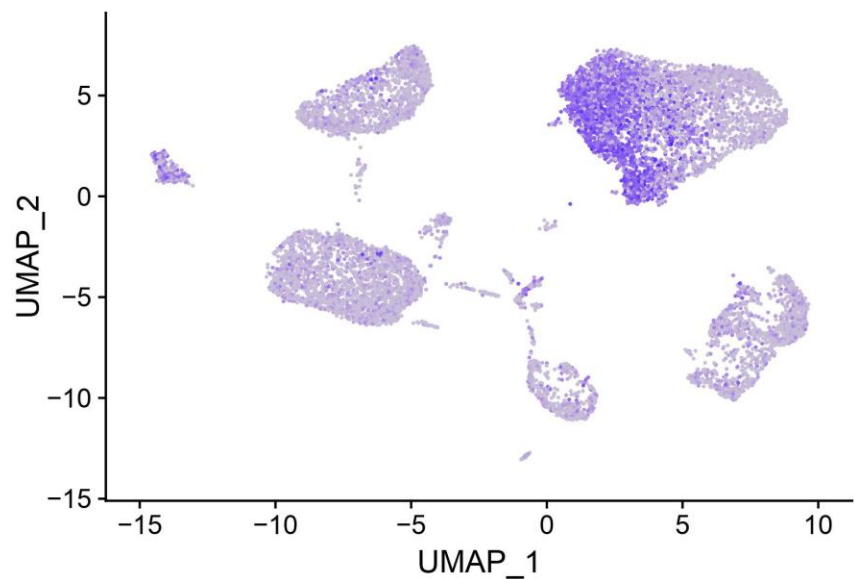
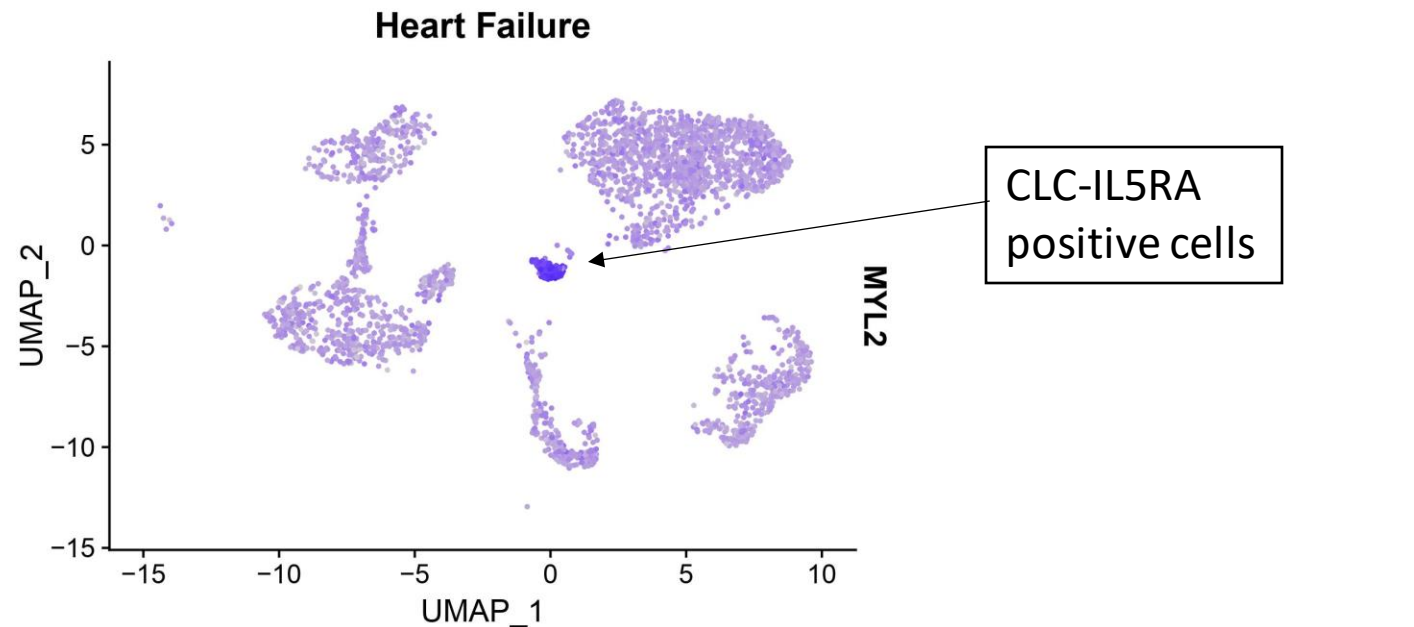
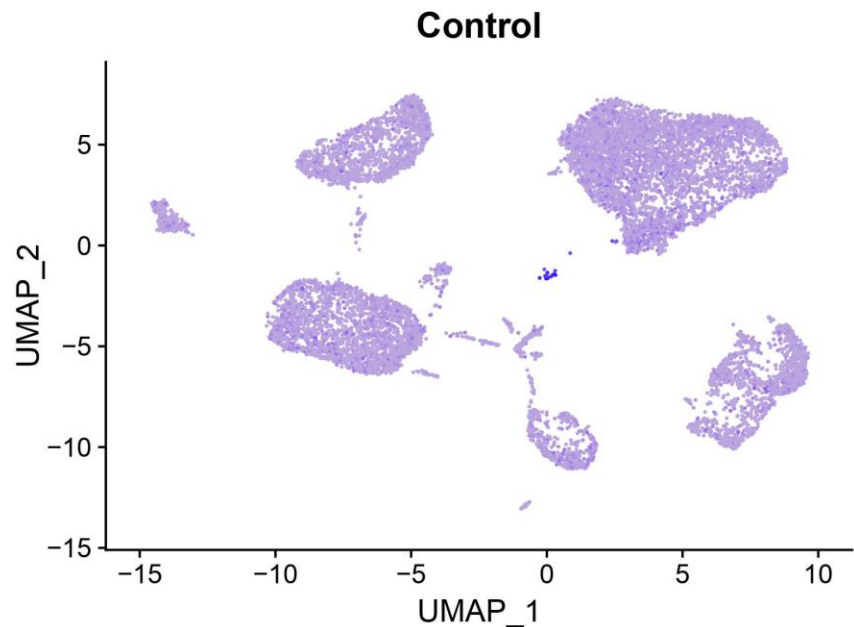
Bar graph representing the cell markers



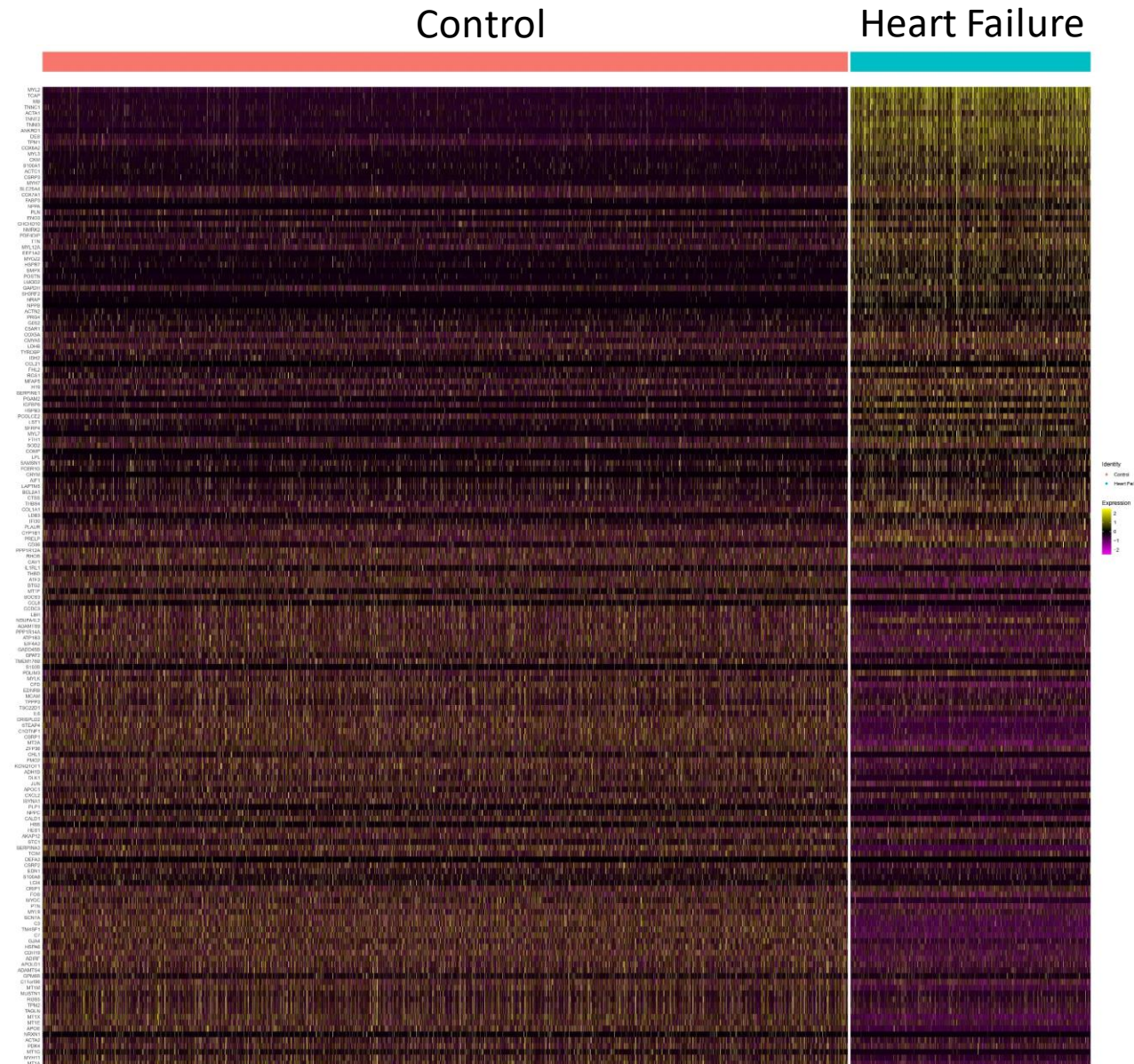
Violin plot representing the cell markers



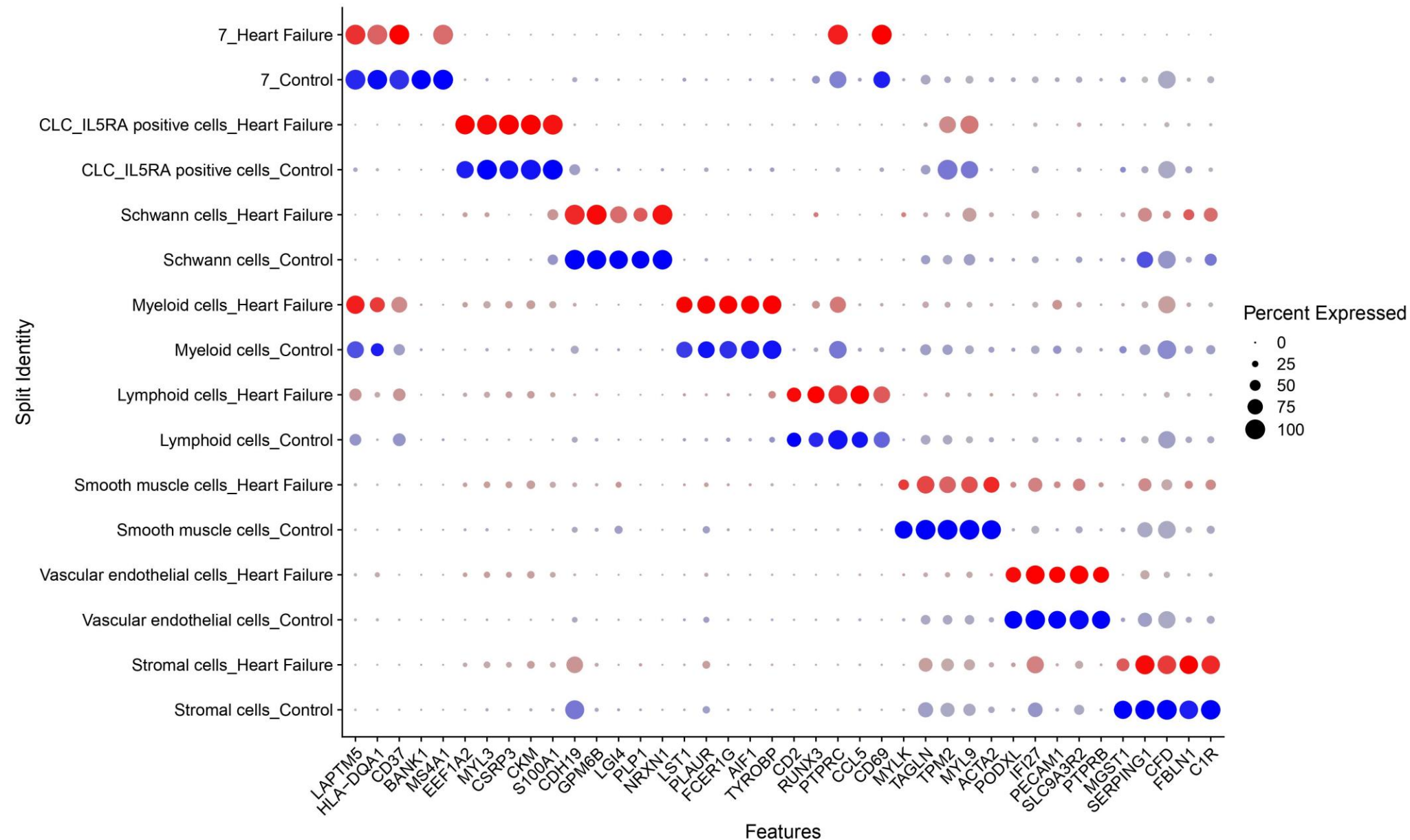
UMAPs of cells color coded with Differentially expressed genes



Heat map of Differentially expressed genes



Dot plot differentially expressed genes



THANK YOU

Don't wait for the right
opportunity: create it.

George Bernard Shaw

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