Sample-Solution: Project 3

Single-cell Bioinformatics

CHAIR FOR
CLINICAL
BIOINFORMATICS
SAARLAND UNIVERSITY

Integrative Cellular Biology
& Bioinformatics

Spatial Transcriptomics

Task 0.1: Properties of the Slides

Give the spot size, the distance between spots and the number of spots for this technology.

- Spot-size 55 µm in diameter

- 100 µm center to center distance

- 4992 total spots per capture area

Spatial Transcriptomics

Task 0.2: Resolution of the spatial transcriptomics technology

Compare the resolution of the technology with the size of an average eucaryotic cell and explain what this means when dealing with the data

- Size of an eucaryotic cell: 10–100 μm

- A spot may capture the gene-expression of multiple cells so you have gene expression per spot and not per cell.

Spatial Transcriptomics

Task 0.3: Output of Space Ranger

Have a first look at the given data. Give the image taken of the sample, the coordinates of the spots and one gene-expression matrix

- Gene-expression matrix: .h5 file

- Images: .jpg images in spatial folder

- Coordinates: tissue_positions_list.csv

Filtering
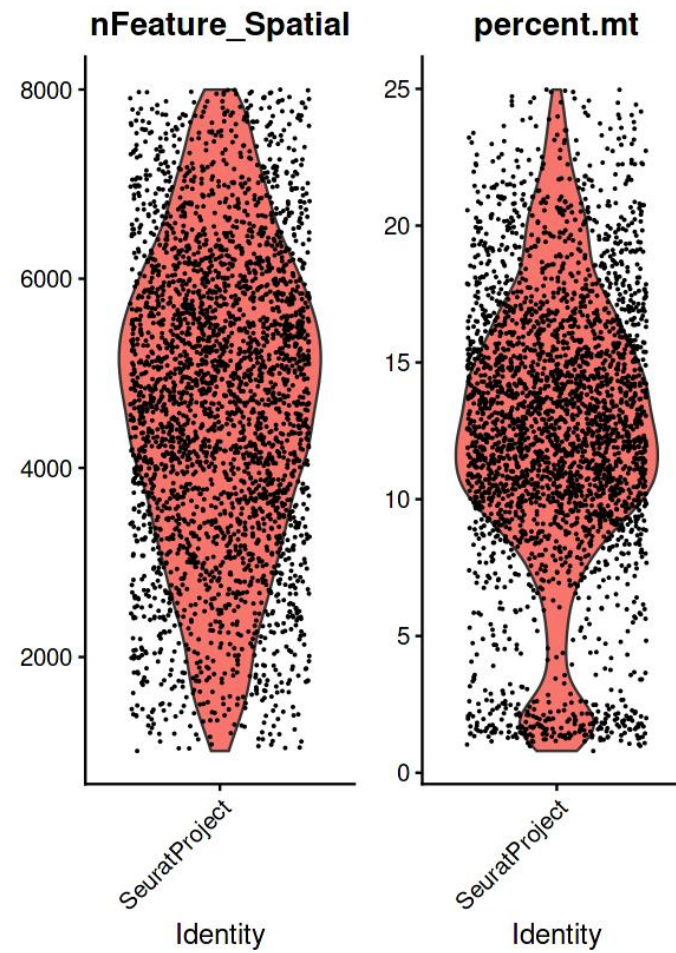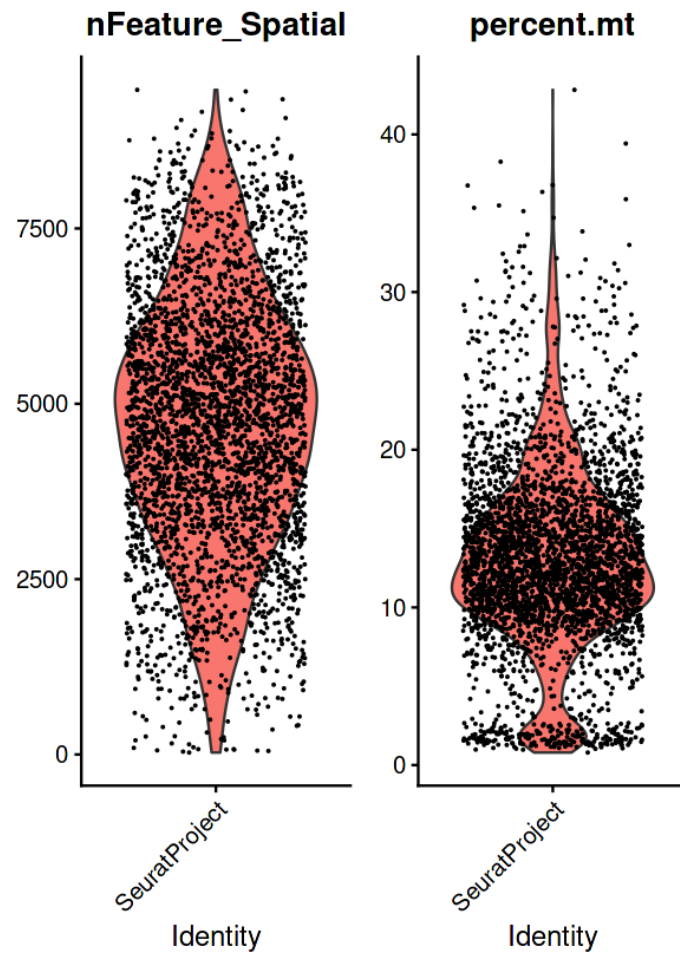
Filtering

Compare the found thresholds to the thresholds used for the scRNA-seq data in the first project. Explain the differences also with regard to how spatial transcriptomics data are produced.
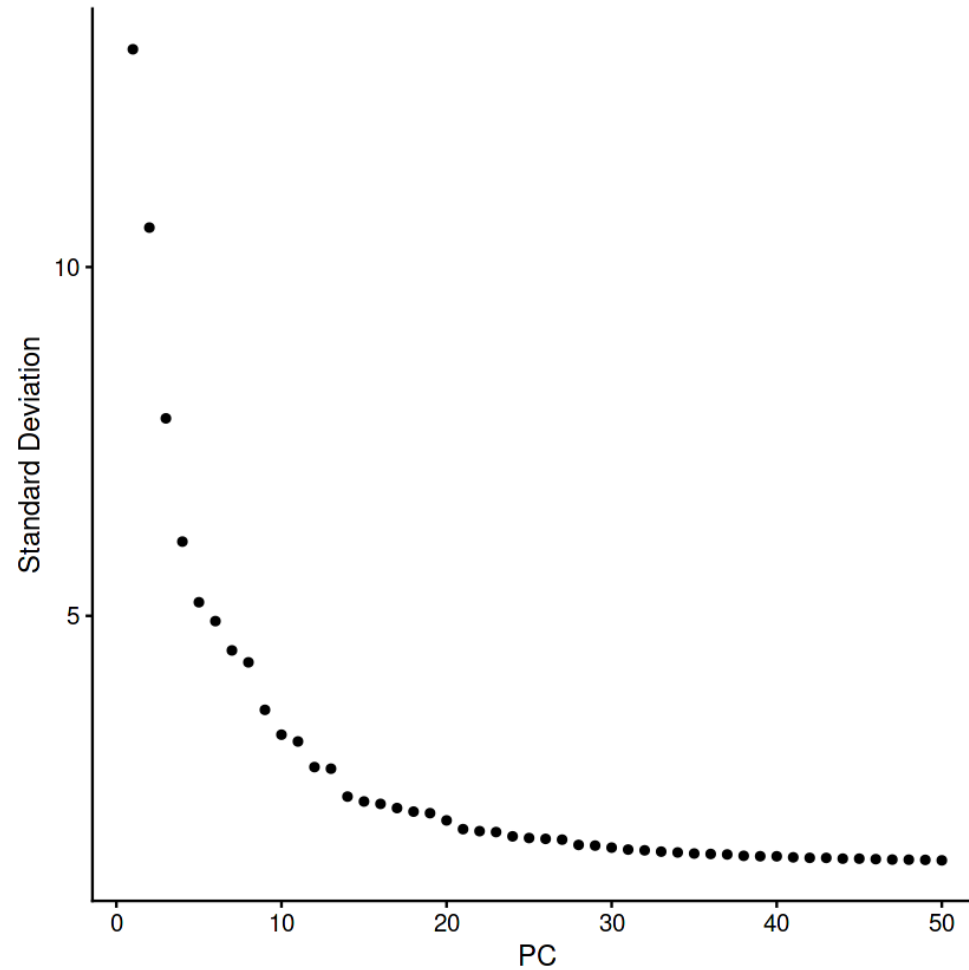
As we have gene-expression per spot and not per cell, the nCounts variable has higher values as we measure multiple cells at once.

SCTransform

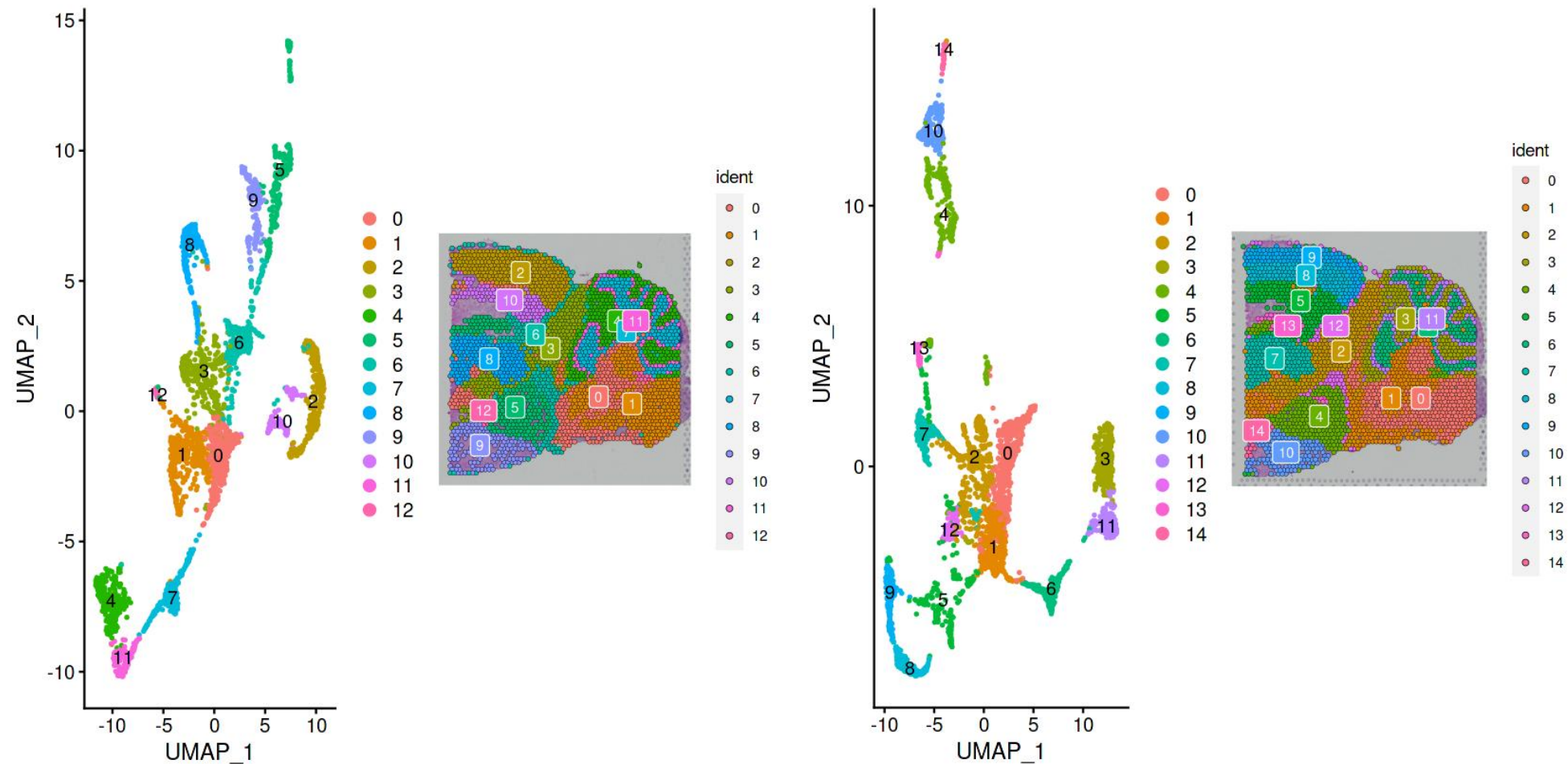**Which steps of the preprocessing from project 1 are replaced by this function?**

Normalization, feature-selection and scaling
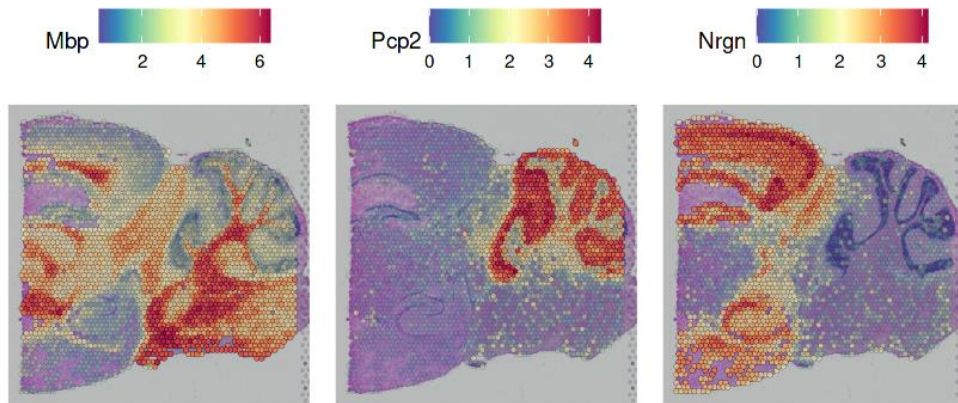
# Ellbow-plot for dimensionality reduction

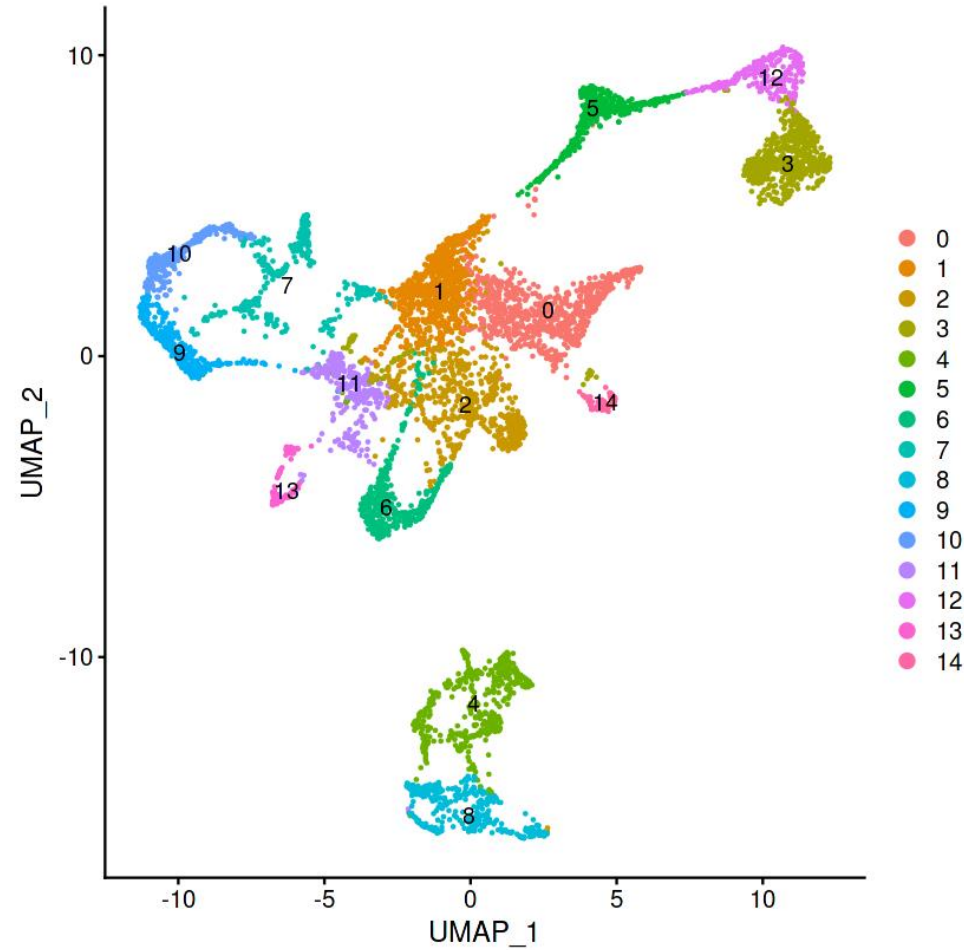# Dimensionality-reduction and clustering
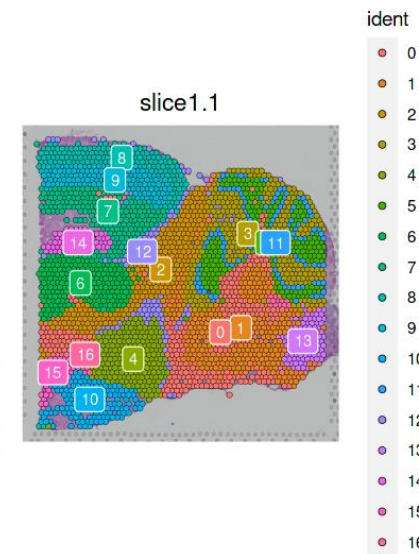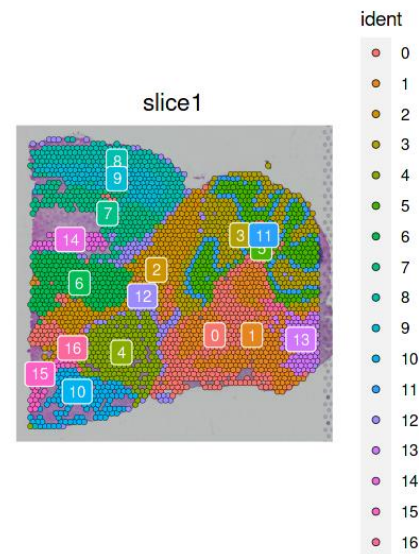
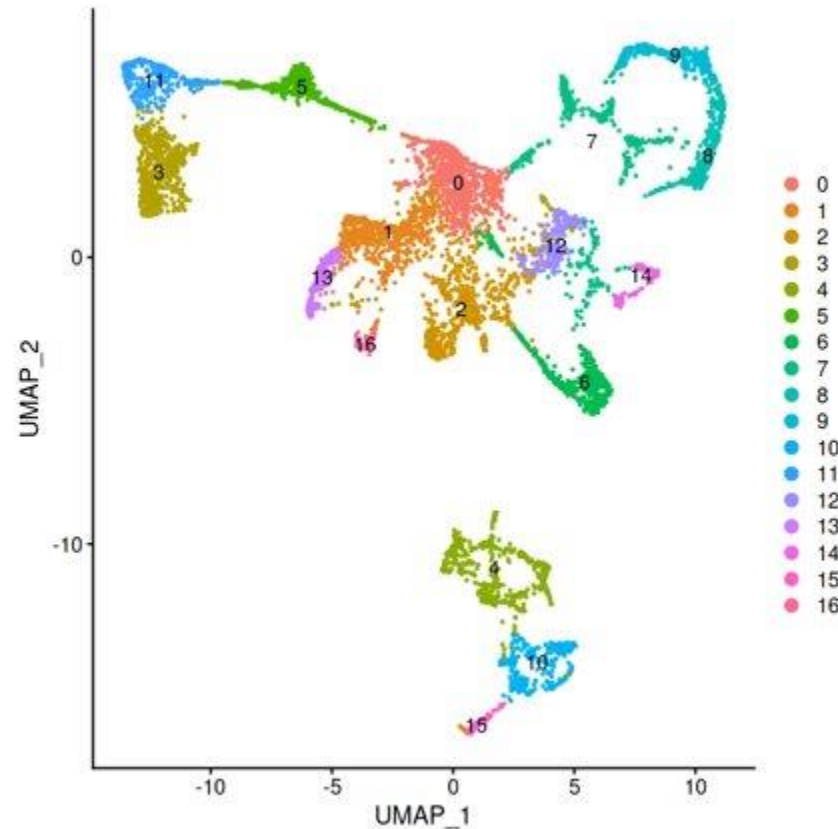# DEG analysis based on the spatial patterning

Compare the result to the result from Task 4.1. Are those genes also differentially expressed between clusters?

In this case all top 3 spatially variable features are also differentially expressed between the clusters.
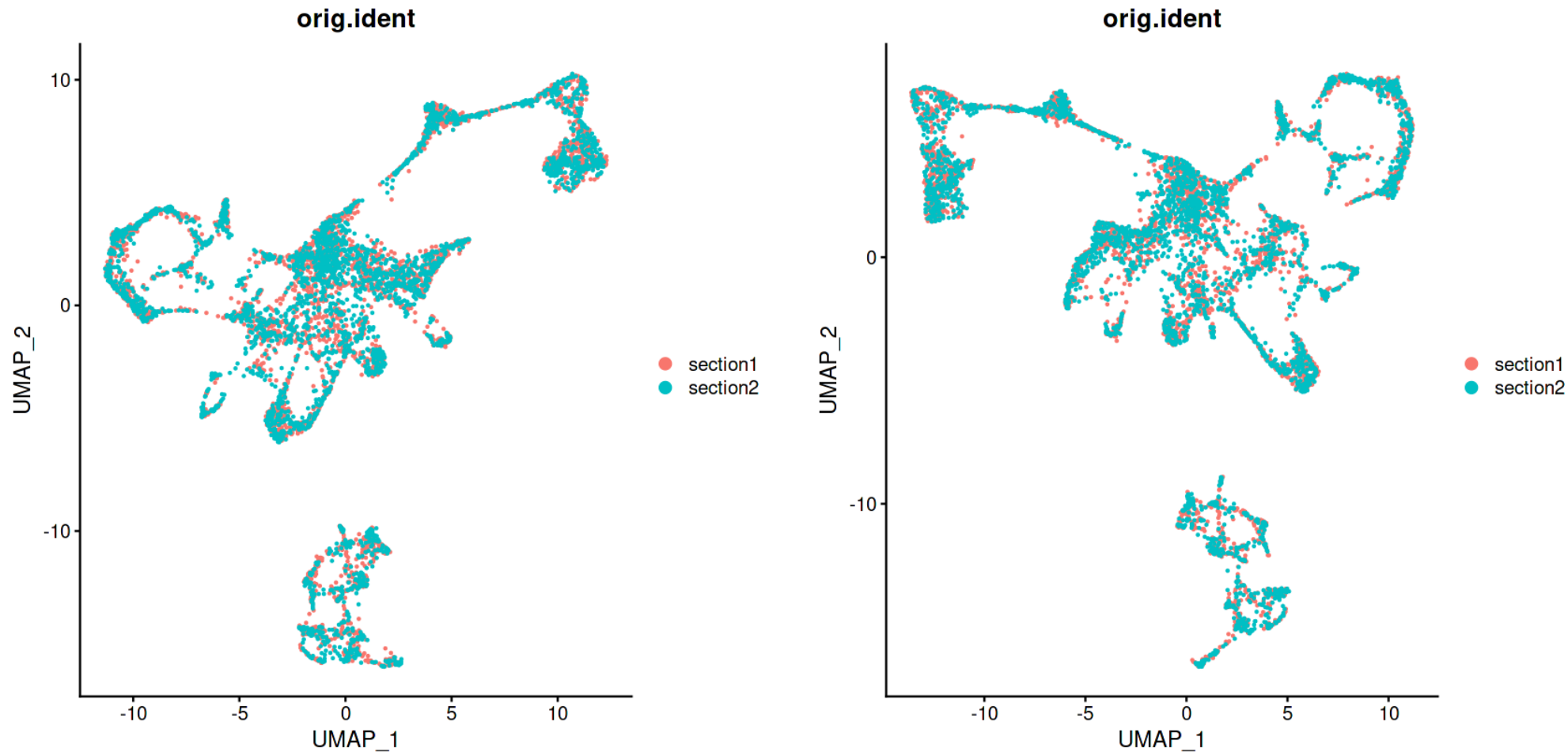
Merging without batch-detection
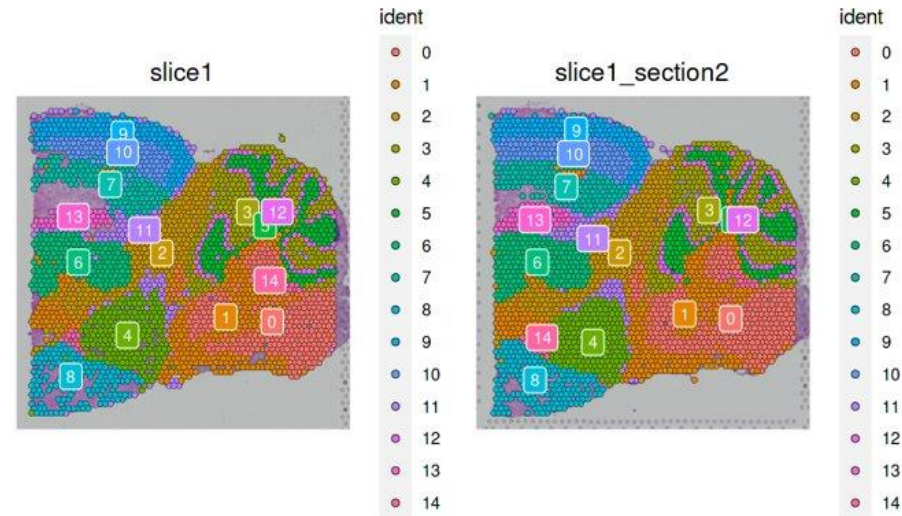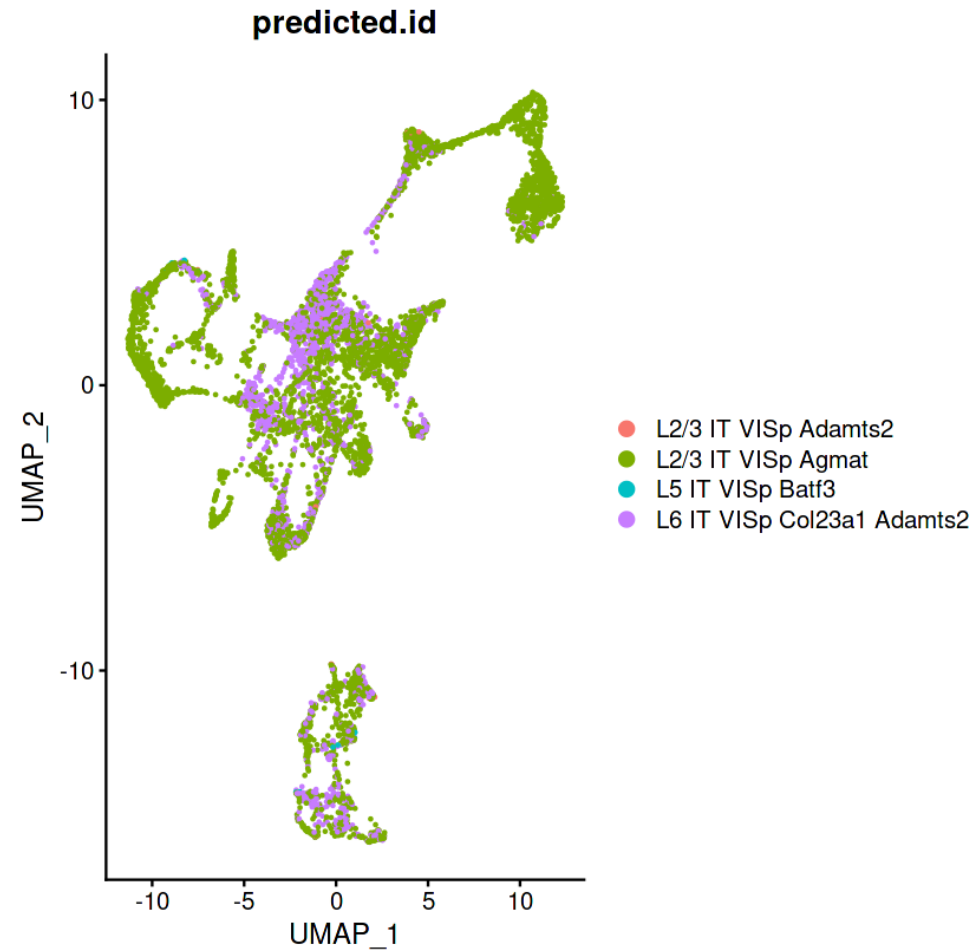
Merging without batch-detection

Detection of batch-effects

Decide and argue if Batch-correction is needed or not and use the according data for the further processing.
No batch-effects found, you can continue without batch-correction.

Cell-type identification

Marker-genes