



# Manuscript pipeline

## Analysis Report

This report is generated by GranatumX

# Upload Files 1.0.0

Assay to upload: **TM\_droplet.csv.zip (107.64 MB)**

Sample metadata file to upload: **annotations\_droplet.csv (8.92 MB)**

File format: **"zip"**

Convert gene IDs: **false**

Species: **"mouse"**

Convert gene IDs into (HGNC symbol is recommended): **"symbol"**

Add extra info (from BioMart) into gene metadata: **true**

Enter your email address to get notified of any errors encountered in the pipeline: **false**

The assay has **23433** genes (with inferred ID type: Symbol) and **54865** samples.

The first few rows and columns:

```
0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0
3.0, 1.0, 3.0, 0.0, 1.0, 1.0, 1.0, 0.0, 0.0, 1.0
0.0, 1.0, 0.0, 0.0, 0.0, 1.0, 1.0, 1.0, 0.0, 1.0
0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0
2.0, 0.0, 0.0, 0.0, 0.0, 1.0, 0.0, 0.0, 0.0, 0.0
1.0, 0.0, 0.0, 0.0, 2.0, 1.0, 2.0, 0.0, 0.0, 0.0
0.0, 3.0, 0.0, 2.0, 0.0, 0.0, 0.0, 1.0, 0.0, 0.0
0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0
0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0
2.0, 0.0, 1.0, 2.0, 2.0, 0.0, 0.0, 3.0, 0.0, 2.0
```

# DeepImpute 2.0.0

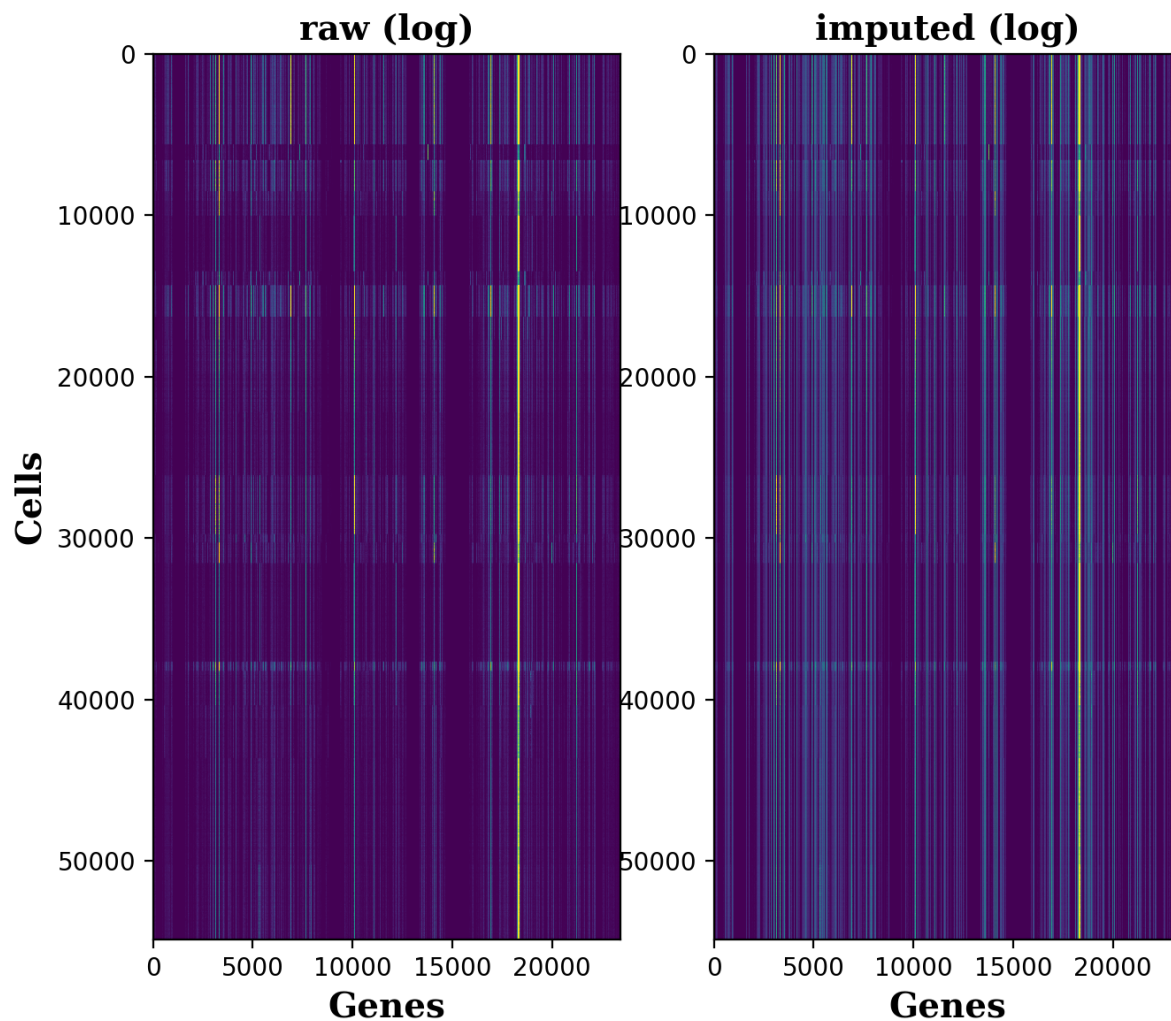
Random seed: **12345**

Use automatic gene imputation limit: **true**

Gene rank limit: **2000**

Cell subset: **1**

Assay: **[A]TM\_droplet.csv.zip** (from step 1: Upload Files 1.0.0)



Heatmaps

- Data frame number of rows: **54865**
- Data frame number of columns: **23433**
- Number of imputed genes: **3584**

- Percentage of dropout entries *before* imputation: **91.82%**
- Percentage of dropout entries *after* imputation: **81.17%**
- Accuracy (correlation) on masked data: **0.95**

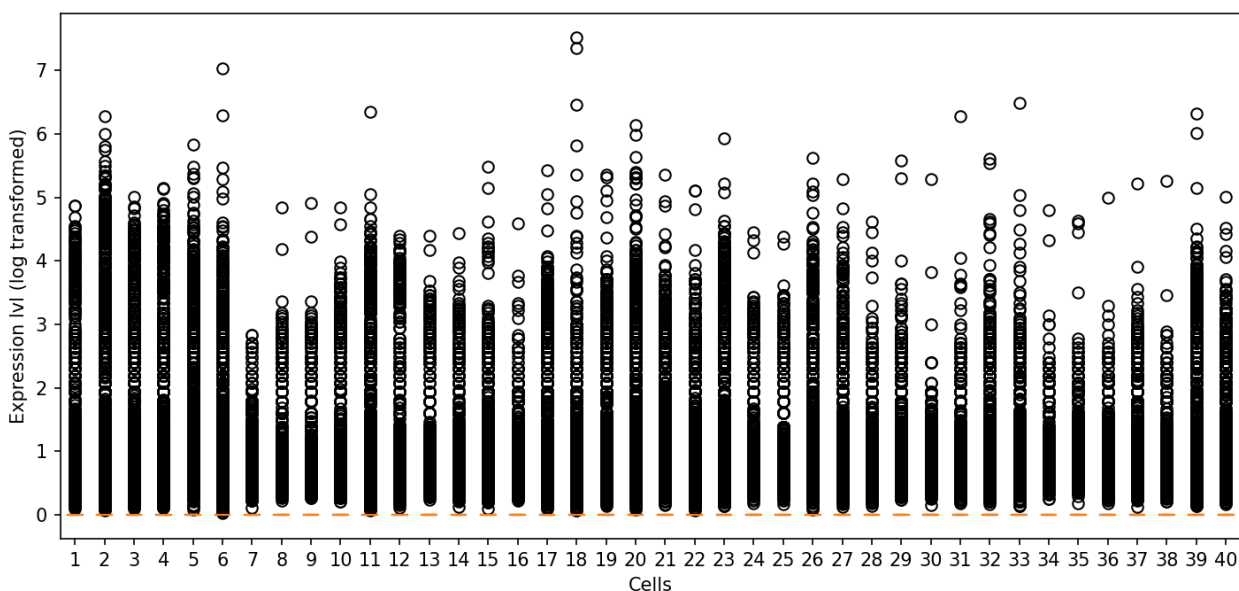
# Cell Normalization 1.0.0

Log transform in the boxplots: **true**

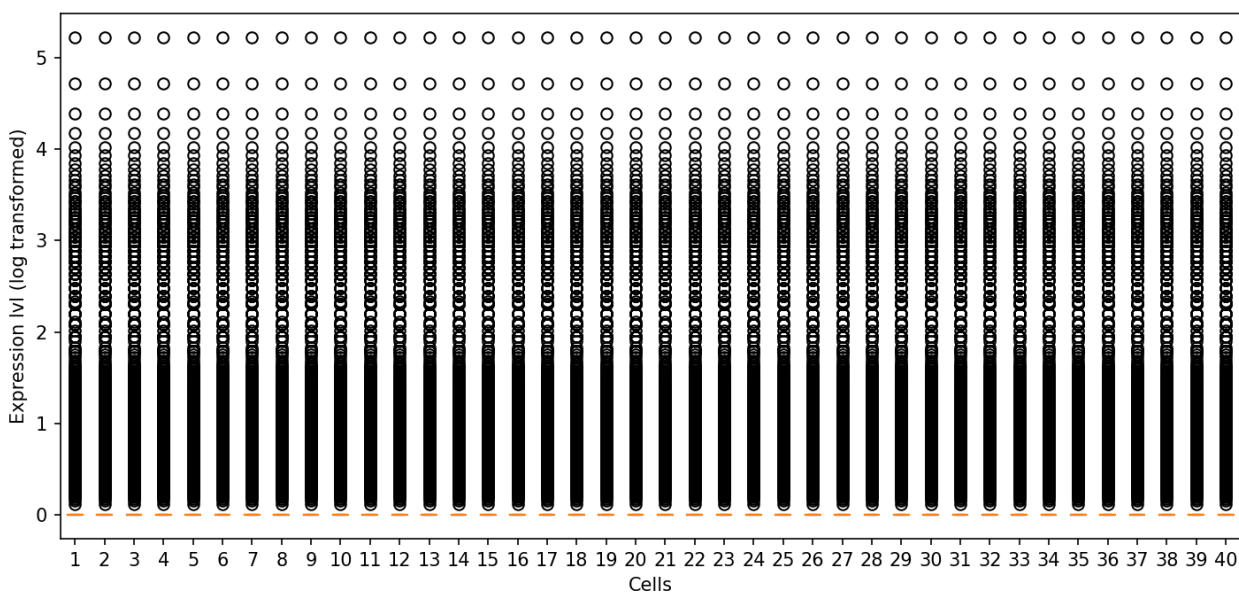
Normalization method: **"quantile"**

Number of cells to plot in the bar-plot: **40**

Assay: **Imputed assay** (from step 2: DeepImpute 2.0.0)



Before normalization: Each bar in the box plot represents one cell.



After normalization: Each bar in the box plot represents one cell.

# Scanpy Gene Filtering 1.0.0

The gene has to be expressed in at least \_\_\_ cells: **3**

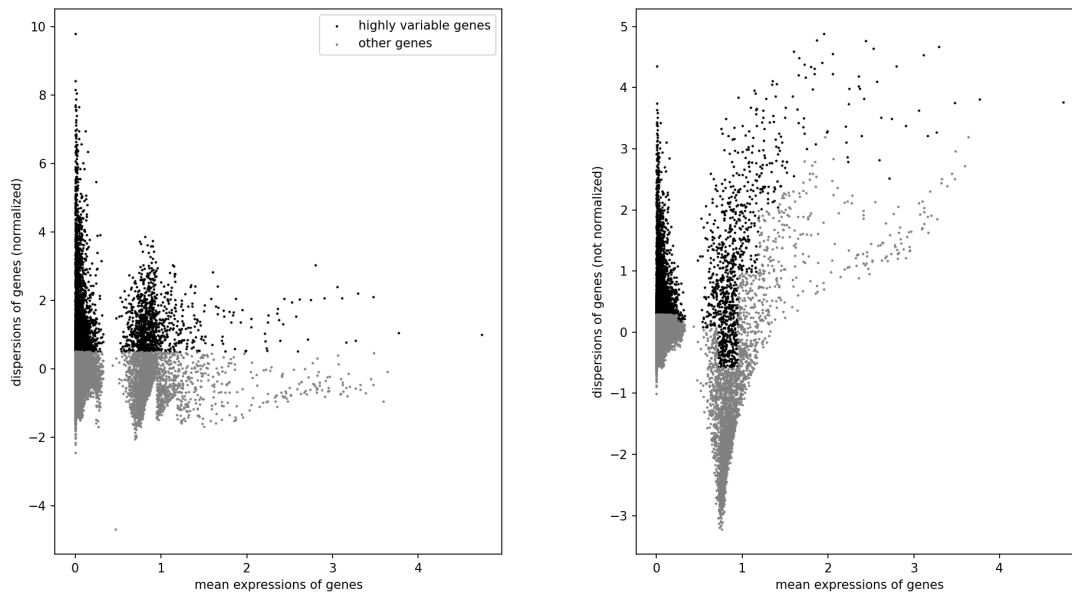
The average expression level of the gene has to be greater than: **1**

The average expression level of the gene has to be less than: **999999**

The dispersion of the gene has to be greater than: **0.5**

The dispersion of the gene has to be less than: **999999**

Assay: **Normalized assay** (from step 3: Cell Normalization 1.0.0)



Each dot represent a gene. The gray dots are the removed genes. The x-axis is log-transformed.

Number of genes before filtering: **23433**

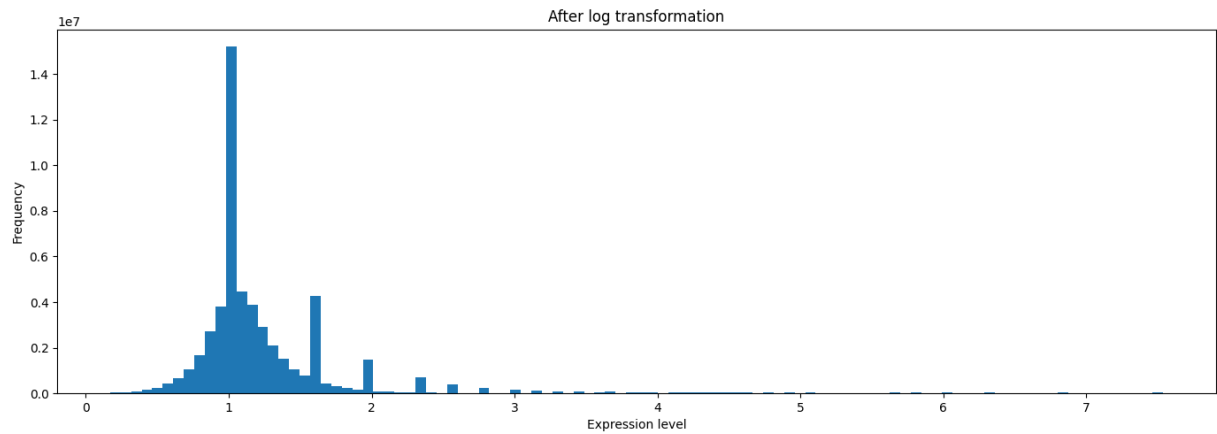
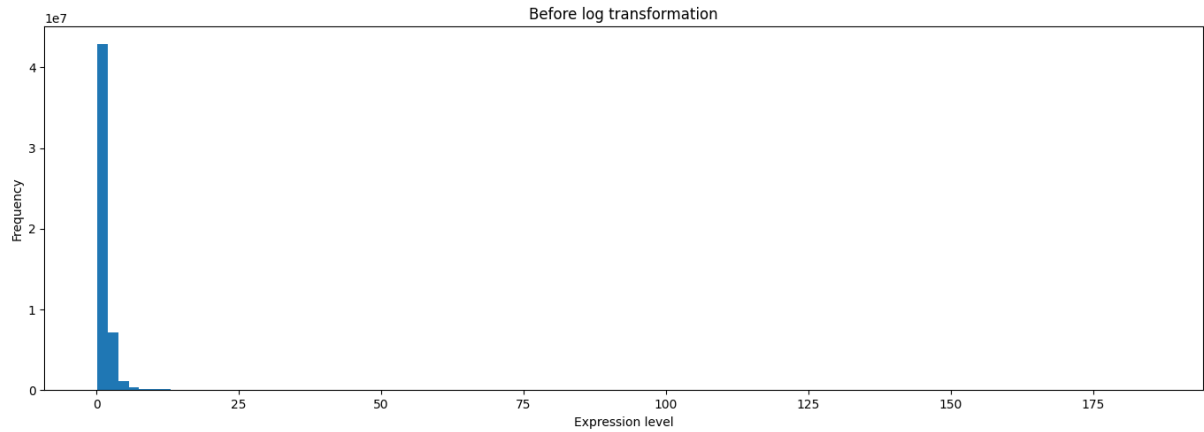
Number of genes after filtering: **3531**

# Log transformation 1.0.0

The base used for the log function: **2**

The pseudo counts added before log transformation (to avoid getting  $\log(0)$ ): **1**

Assay including matrix and genelds: **Filtered Assay** (from step 4: Scanpy Gene Filtering 1.0.0)

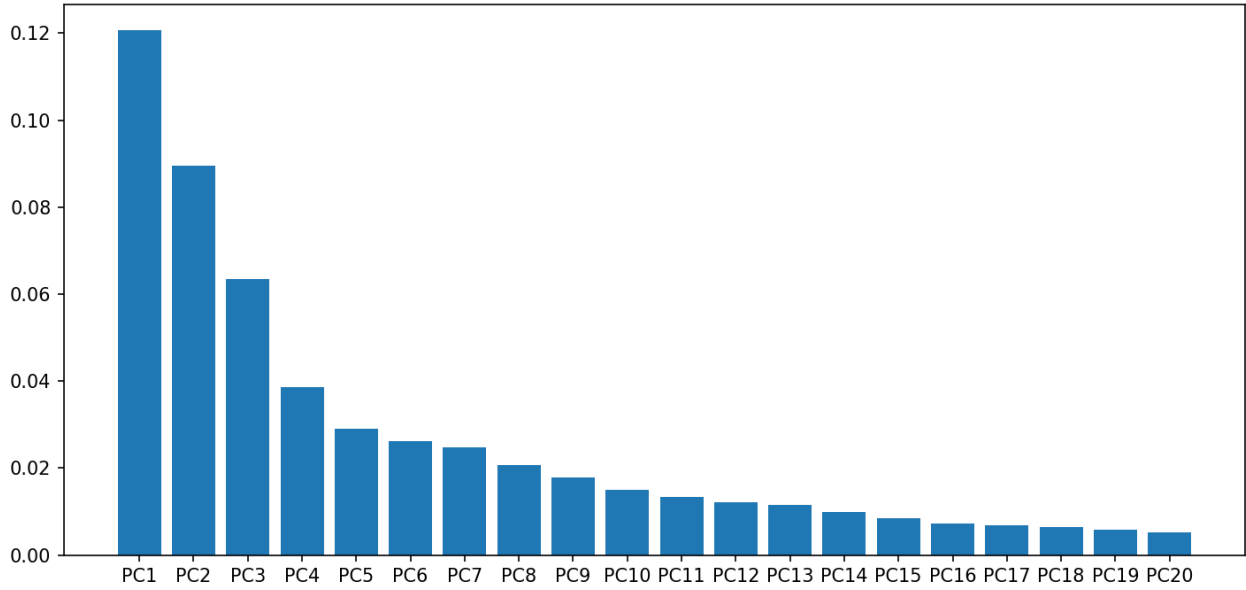


The distribution of expression level before and after log transformation. Only the values greater than the 5 percentile (usually zero in single-cell data) and lower than 95 percentile are considered.

# Principal Component Analysis 1.0.0

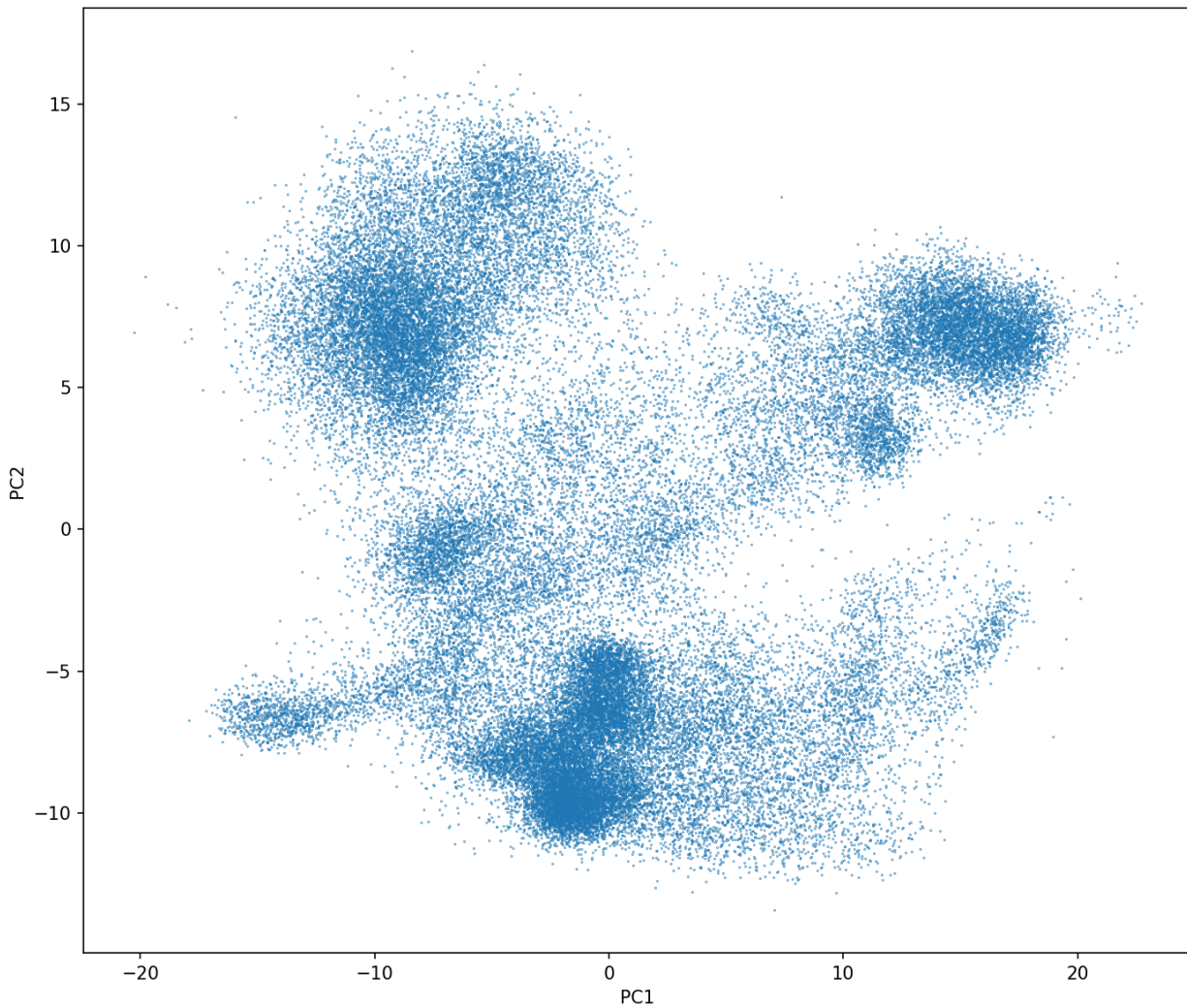
Number of top components to calculate: **2**

Assay: **Log transformed assay** (from step 5: Log transformation 1.0.0)



Explained variance (ratio) by each Principal Component (PC)





PC1 vs. PC2

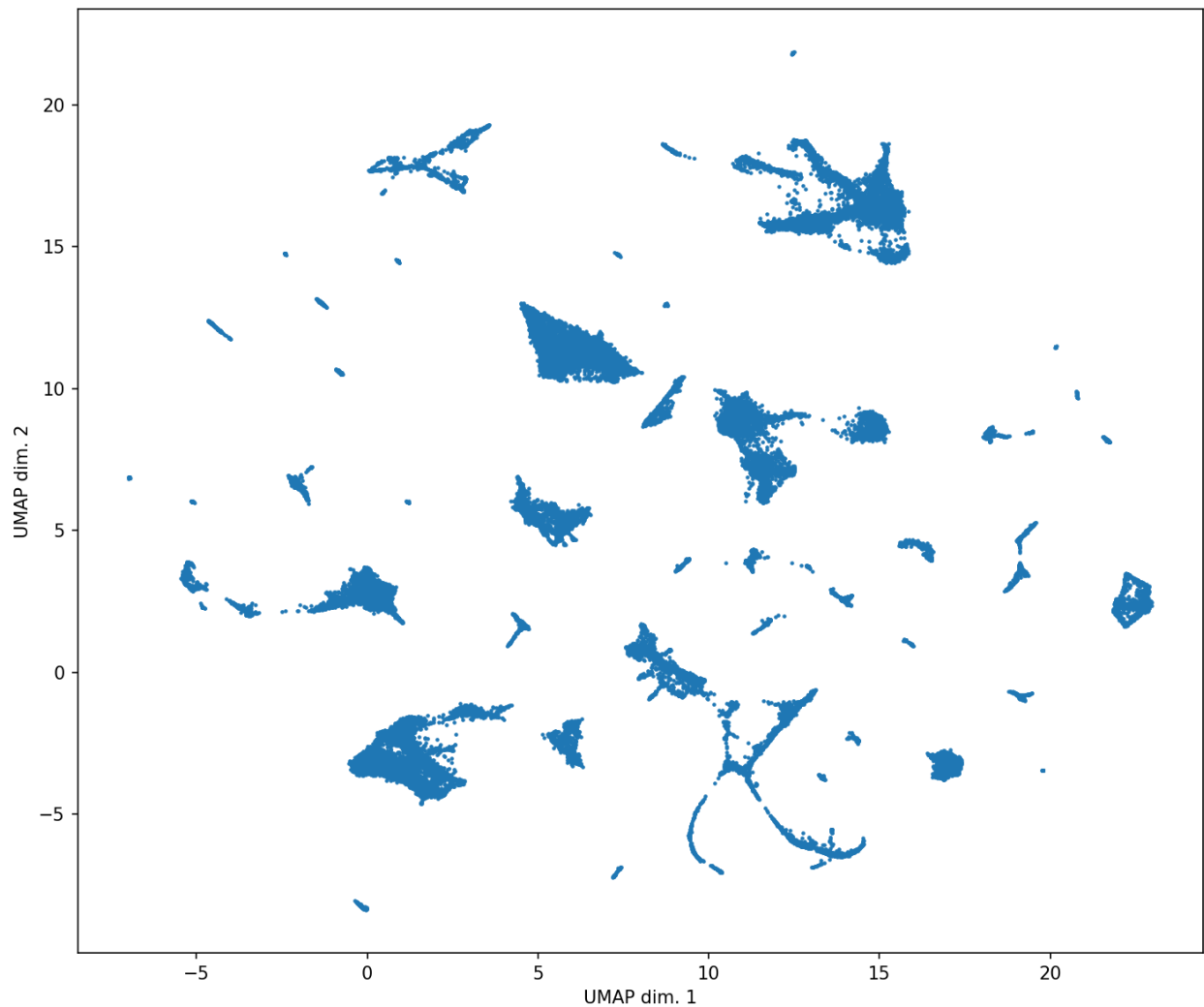
# UMAP 1.0.0

Number of neighbors (n\_neighbors, an integer): **15**

Minimum distance (min\_dist, a real number ranges from 0 to 1): **0.1**

Metric (metric): **"euclidean"**

Assay: **Log transformed assay** (from step 5: Log transformation 1.0.0)



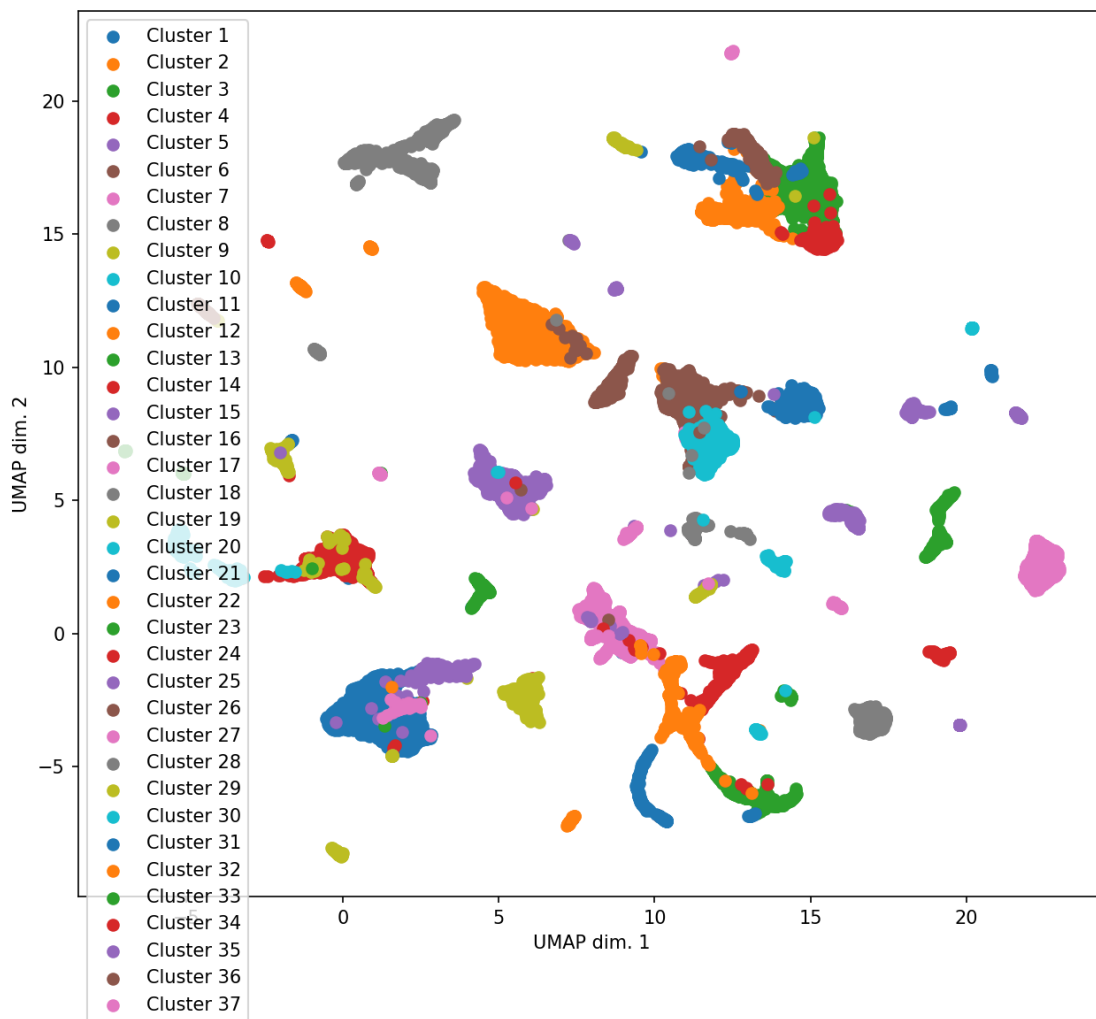
UMAP plot: each dot represents a cell

# ScanpyClustering 1.0.0

Random seed: **13513**

Assay including matrix and genelds: **Log transformed assay** (from step 5: Log transformation 1.0.0)

Cell coordinates for visualization: **UMAP coordinates** (from step 7: UMAP 1.0.0)



Scatter-plot using imported cell coordinates. Each dot represents a cell. The colors indicate the identified cell clusters.

# Sample Coloring 1.0.0

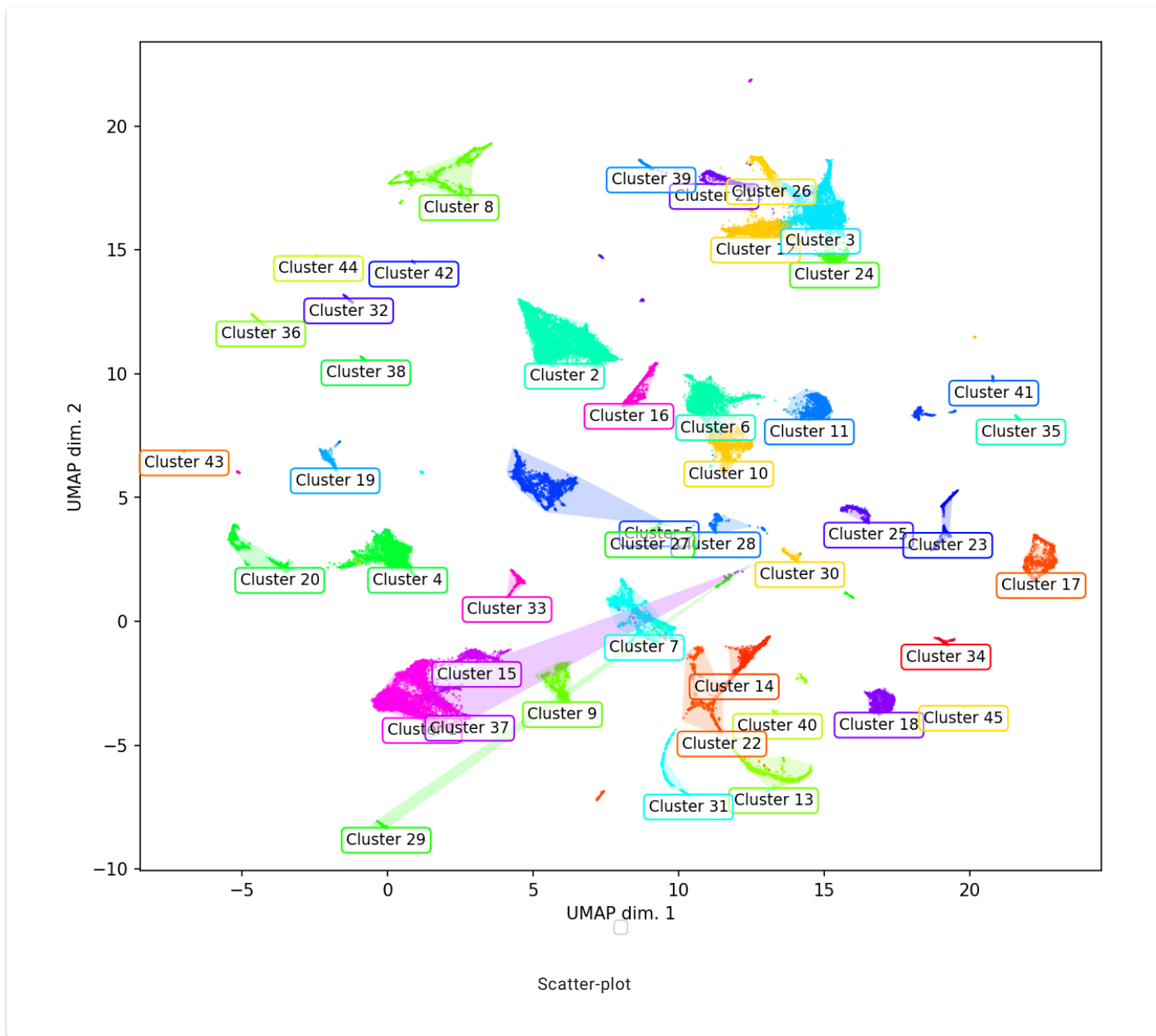
The type of the sample metadata: **"categorical"**

Bounding box factor times standard deviation (value should be > 0.0; 0.0 will be the convex hull): **0.1**

The fontsize of the labels: **9**

Values to use as colors: **Cluster assignment** (from step 8: ScanpyClustering 1.0.0)

Visualization data to plot: **UMAP coordinates** (from step 7: UMAP 1.0.0)



# Sample Coloring 1.0.0

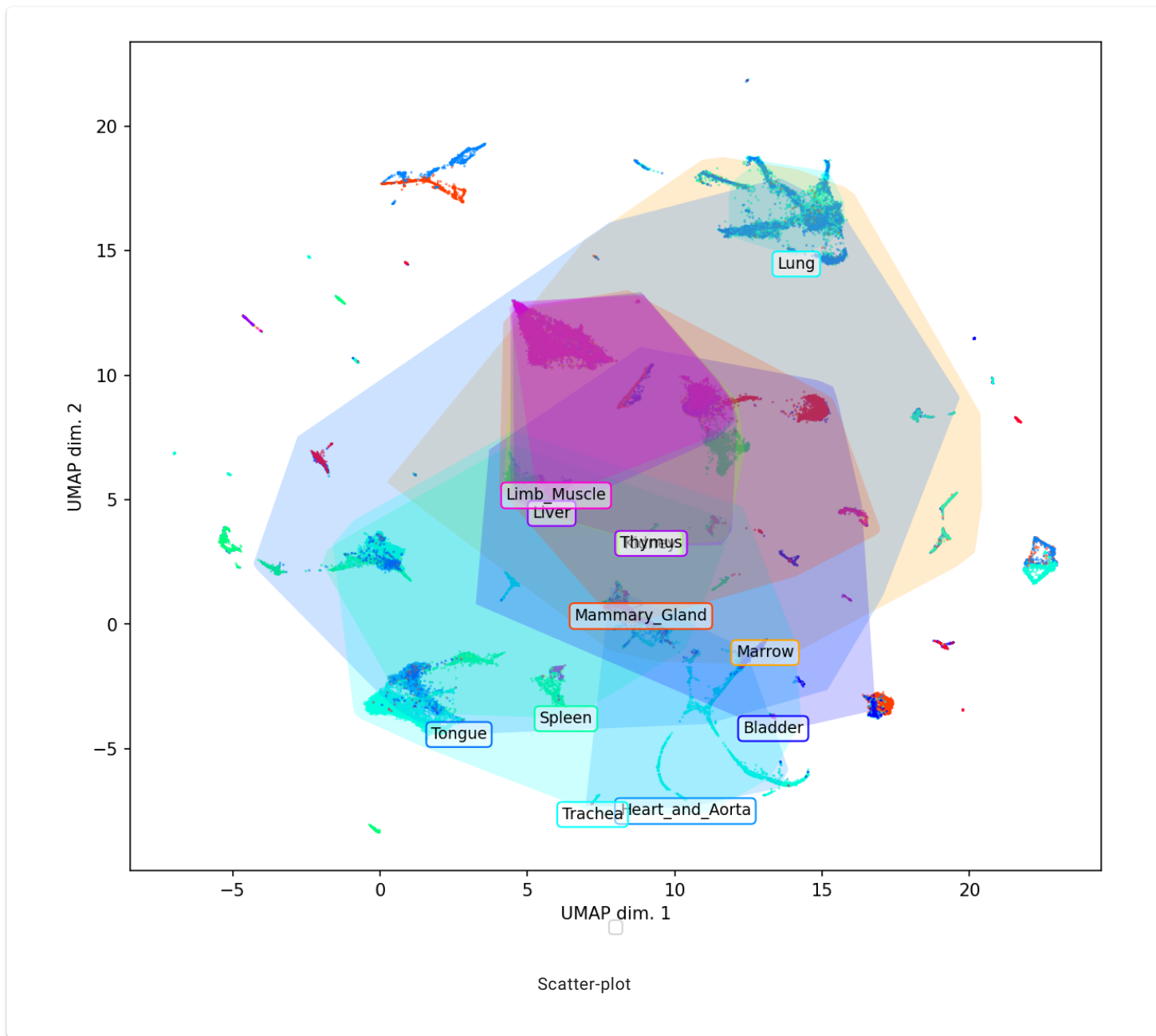
The type of the sample metadata: **"categorical"**

Bounding box factor times standard deviation (value should be > 0.0; 0.0 will be the convex hull): **0.1**

The fontsize of the labels: **9**

Values to use as colors: **[M]tissue** (from step 1: Upload Files 1.0.0)

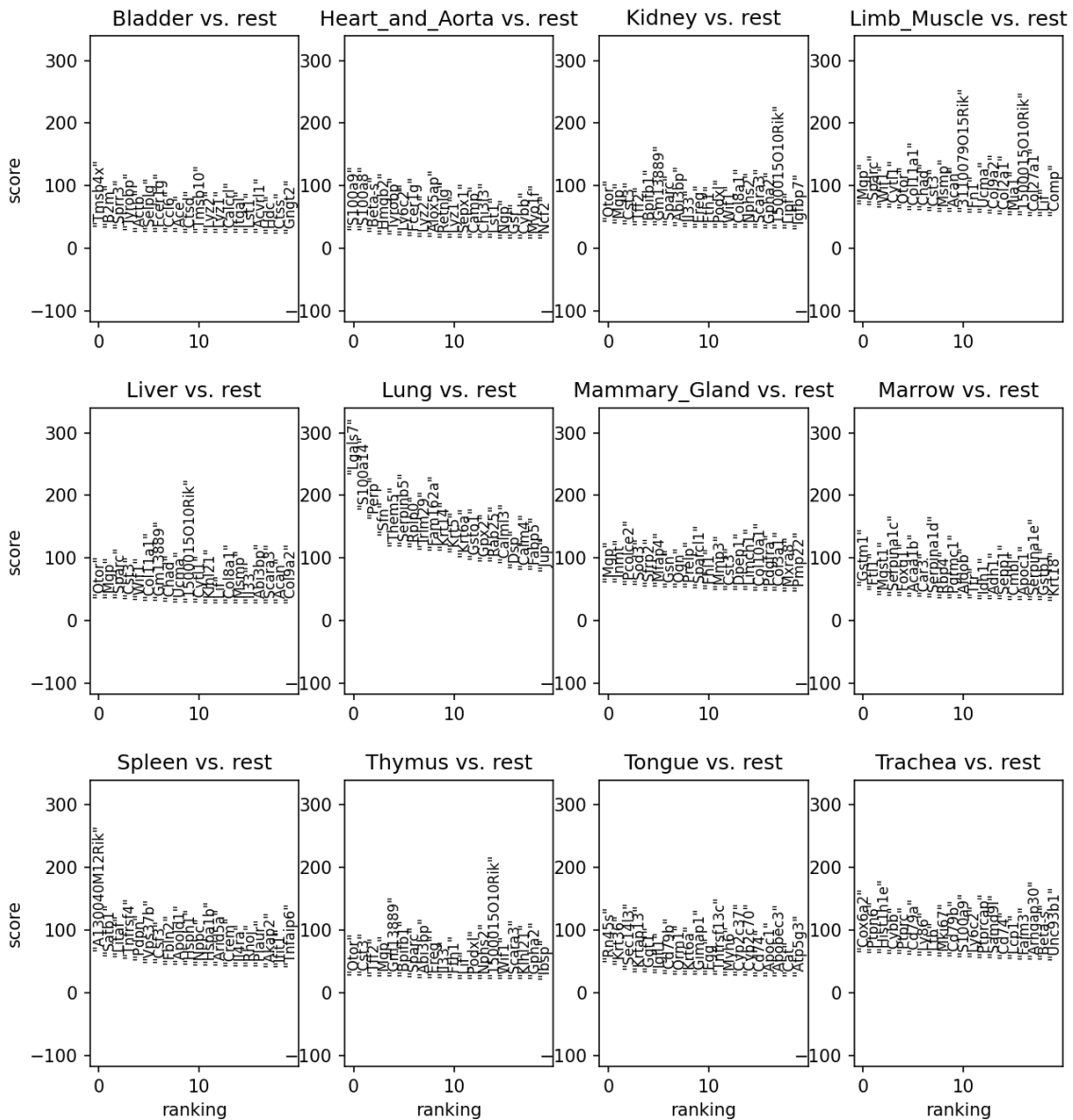
Visualization data to plot: **UMAP coordinates** (from step 7: UMAP 1.0.0)



# Marker Genes Identification 1.0.0

Assay including matrix and geneIds: **Log transformed assay** (from step 5: Log transformation 1.0.0)

Group vector: **[M]tissue** (from step 1: Upload Files 1.0.0)

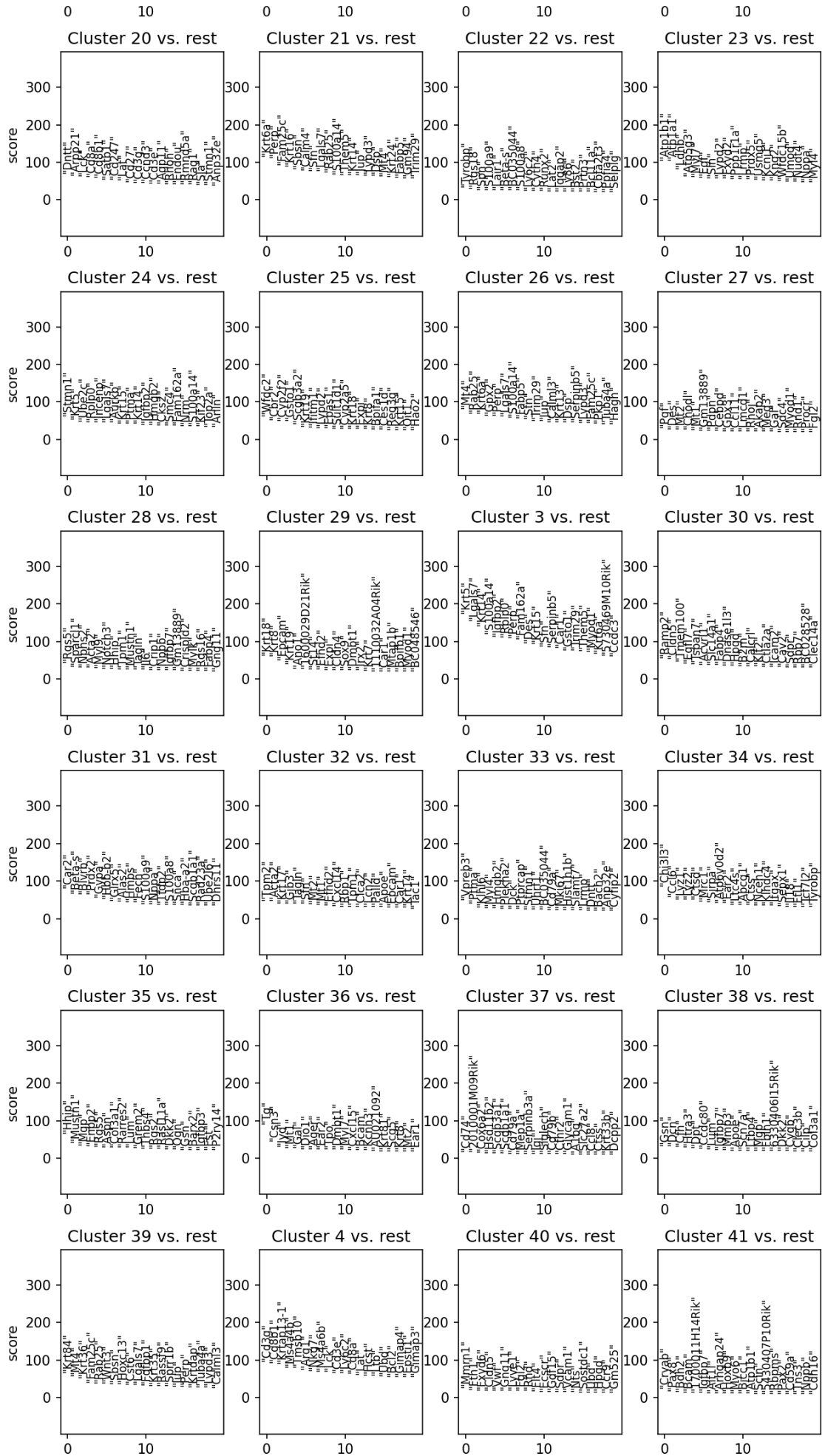


One-vs-rest marker genes











Use the browser back button to return to the project steps.