SCPline

Make single-cell analysis available to every investigator

SCPline:An interactive shiny framework for the study of single-cell proteomics data preprocessing

SCPline is an integrated one-stop single-cell proteomics data preprocessing analysis tool developed by Guohua Wang Laboratory, aiming to provide efficient data preprocessing analysis for laboratory researchers.

Moudle2:scMultimics workflow

SCPline | Flow Cytometry | **Single Cell Multiomics** | MASS Workflow | Help

Multi-omics

- Overview
- Upload your data
- Normalization & Feature Selection
- PCA
- UMAP
- Clustering
- Download Results

Load example data

Load Example and run

Upload your input data

SingleCellExperiment Object (Accepted Format: .rds)

Browse... No file selected

You can try loading sample files or you can load your own data

Analysis method: Seurat

Min nFeature:

200

Min nFeature: Sets the minimum feature filtering standard

Min nCells:

3

Min nCells: Set the minimum number of cells for filtering

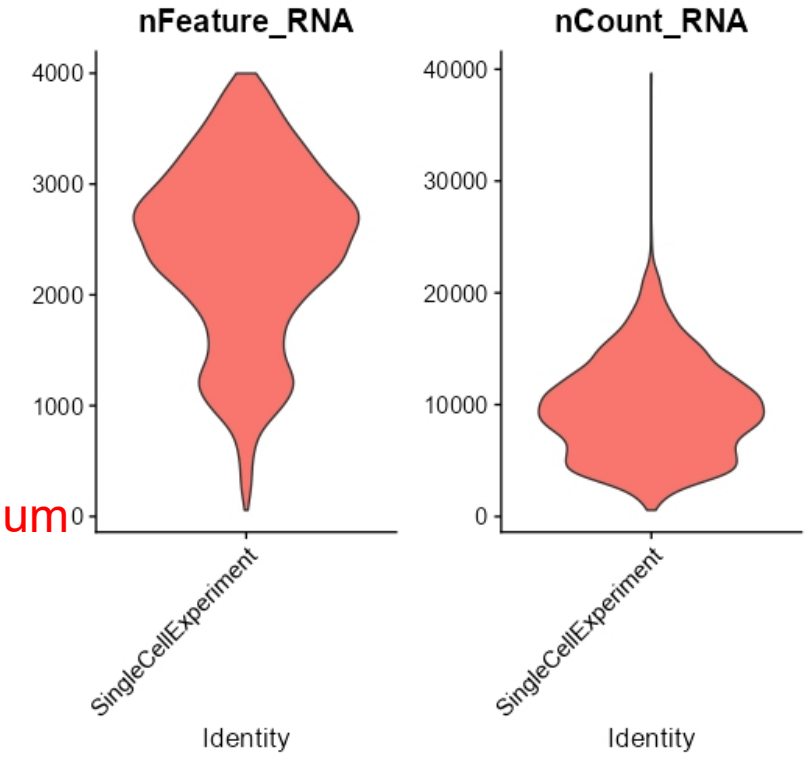
Project Name:

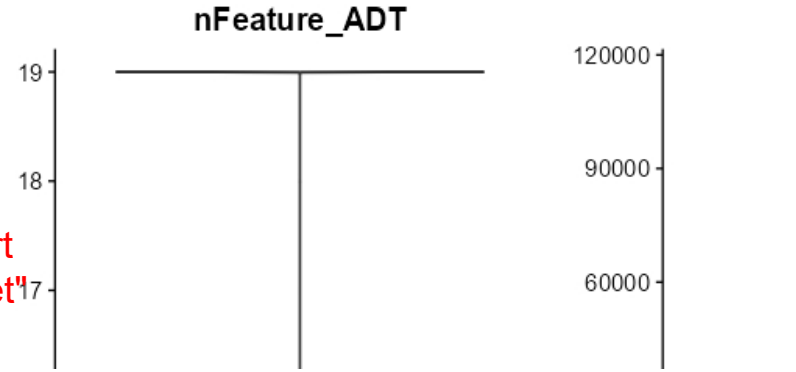
Project1

Project Name: Enter a project name for management and identification analysis.

Load Data and run | Reset

Click the "Load Data and run" button to start data loading and analysis, or use the "Reset" button to reset the input.





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Data Preprocessing

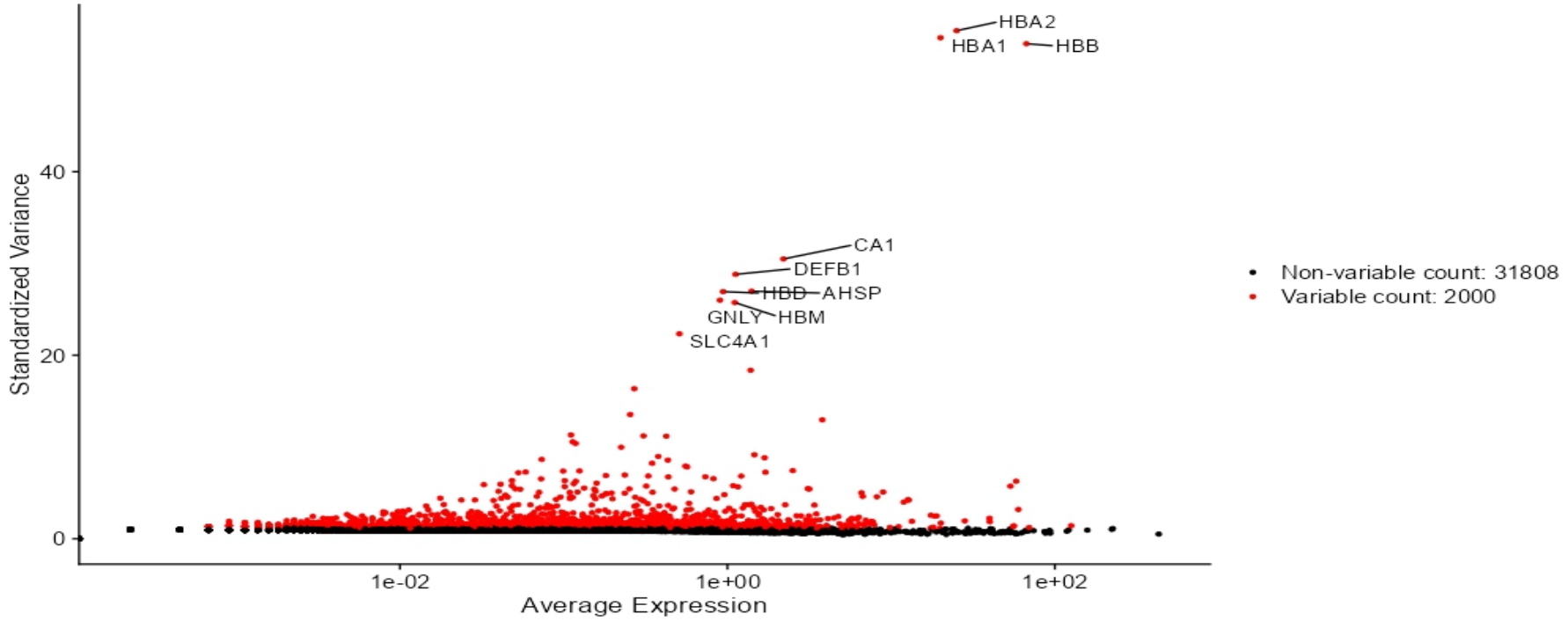
Number of variable features: 2000

Number of variable features: Sets the number of highly variable features to be selected, for example 2000.

Variable feature selection method: vst

Variable feature selection method: Selects a method for feature selection, for example, vst.

Identify highly variable features



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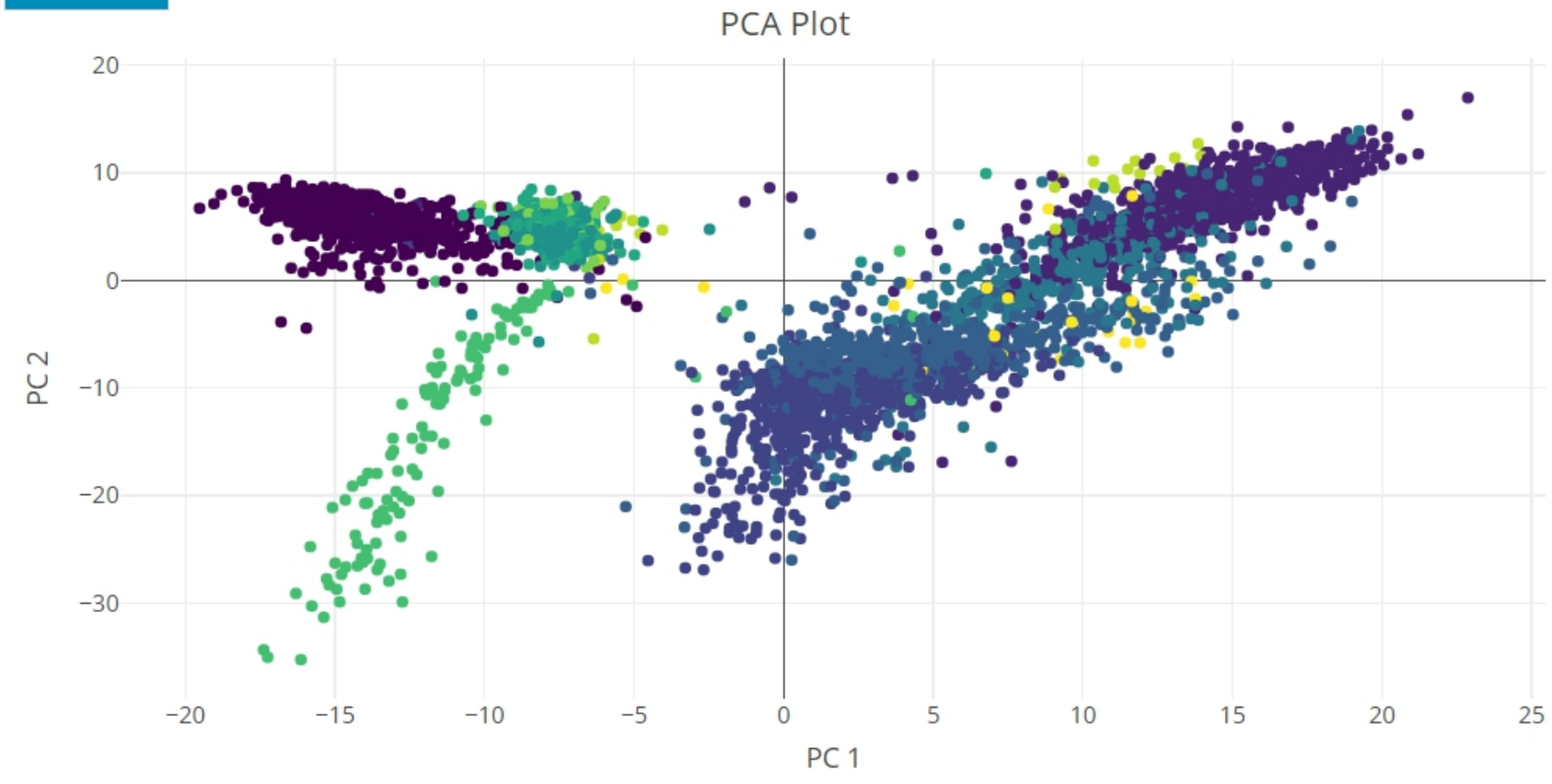
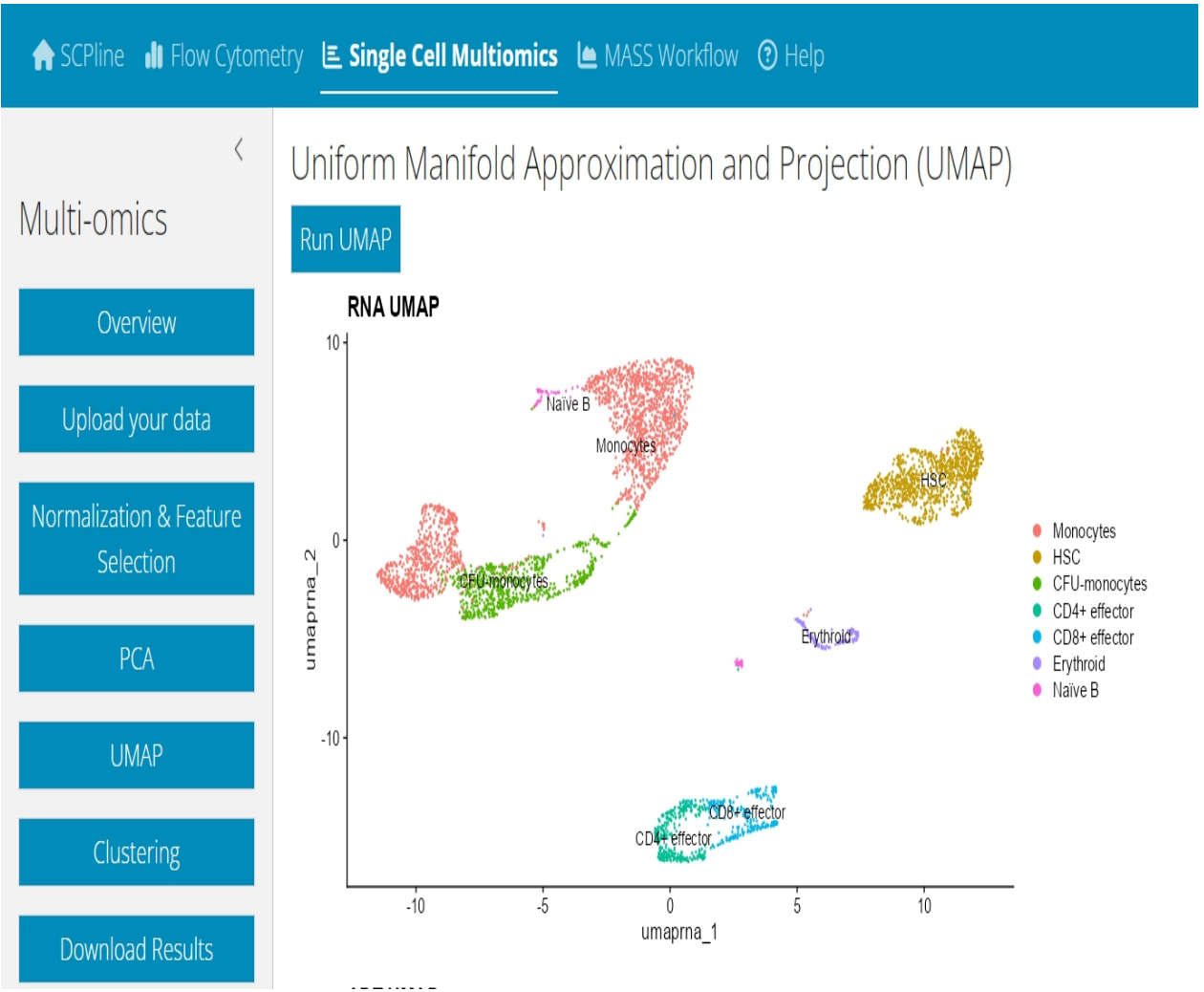
Principal Component Analysis (PCA)

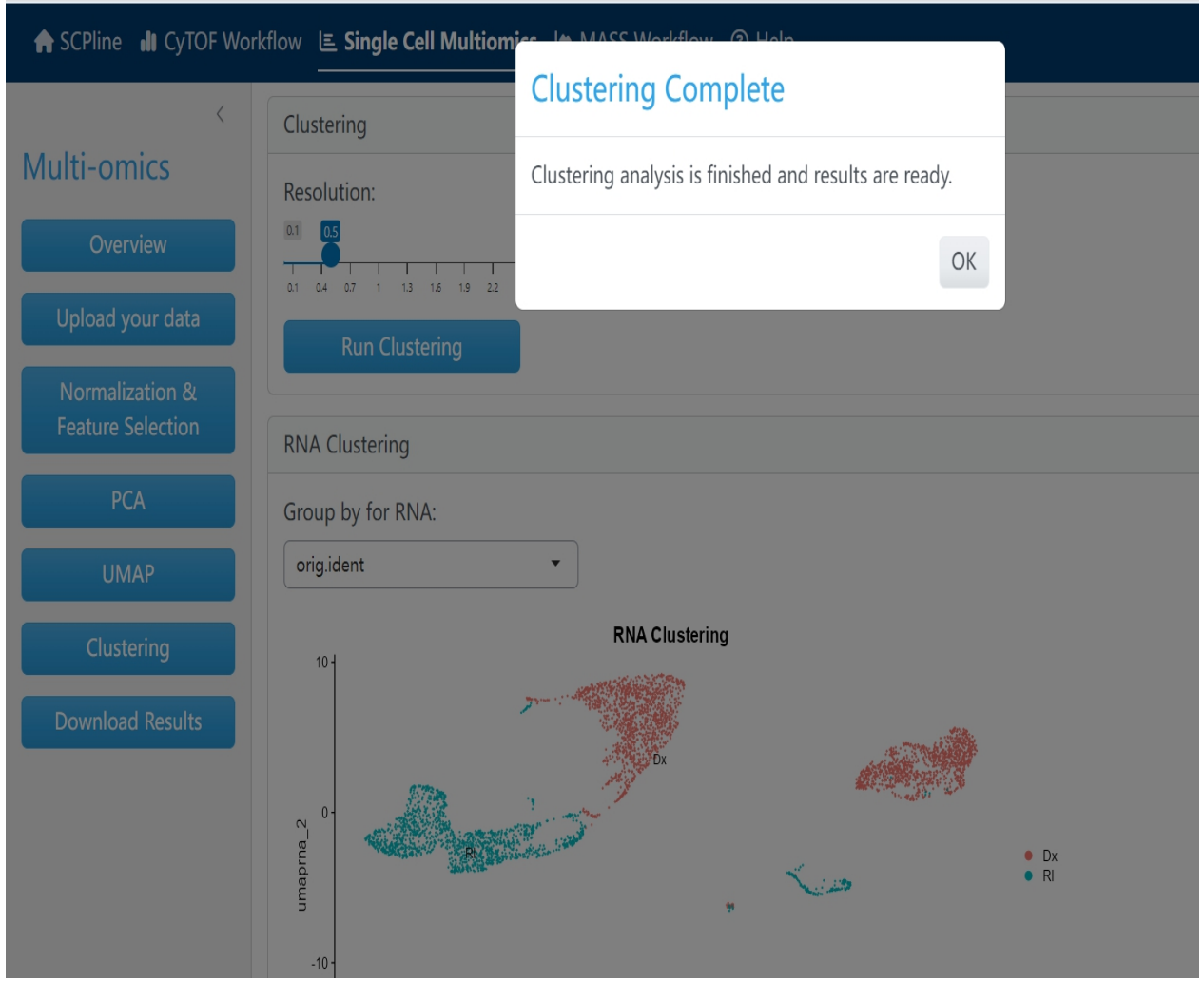
Run PCA

Click on ‘Run PCA’ under the ‘PCA’ tab to visualize PCA plot.



Moudle2:scMultimics workflow





Next comes UMAP and clustering, where the cluster analysis is complete

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Clustering

Resolution: 0.1 0.4 0.7 1 1.3 1.6 1.9 2.2 2.5 2.8 3

Run Clustering

Use the slider to adjust the clustering resolution to control the fineness of the clustering. Each time the parameter is selected, the corresponding clustering effect of the parameter is found in the drop-down box below

RNA Clustering

Group by for RNA: orig.ident

The drop-down box contains the metadata attributes of the uploaded data, and the attribute content of each data can be intelligently identified

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Visualization

Download RDS file (SingleCellExperiment Object)

Finally, click the download button to get the data after the pre-processing process

Metadata Information

orig.ident	nCount_ADT	nFeature_ADT	nCount_RNA	nFeature_RNA	sample	timepoint	UMAP_1	UMAP_2	percent.mito
Dx	4765.00	19	5002.00	1683	Pt-12-Dx	Dx	-2.64	-2.91	0.00
Dx	2031.00	19	7356.00	2353	Pt-12-Dx	Dx	3.13	-4.47	0.00
Dx	1799.00	19	5419.00	1754	Pt-12-Dx	Dx	2.97	-4.20	0.00
Dx	2715.00	19	6052.00	2068	Pt-12-Dx	Dx	4.47	-4.59	0.00
Dx	2734.00	19	8756.00	2799	Pt-12-Dx	Dx	1.50	-4.74	0.00
Dx	2278.00	19	6169.00	1909	Pt-12-Dx	Dx	-0.24	-4.55	0.00
Dx	4573.00	19	4068.00	1477	Pt-12-Dx	Dx	-2.38	-5.06	0.00
Dx	1585.00	19	9062.00	2507	Pt-12-Dx	Dx	3.23	-4.68	0.00
Dx	3683.00	19	10217.00	2322	Pt-12-Dx	Dx	-1.07	-3.54	0.00
Dx	900.00	19	8936.00	2275	Pt-12-Dx	Dx	-12.77	0.24	0.00