

# 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.

# Moudle1: Flow Cytometry Workflow

## Flow Cytometry

Overview

Upload Data

Normalization

Auto Gating

Statistic

Main Analysis

Download Results

### Load example data

You can load example data to test the app.

Run Example Data

### Load User data

Upload your meta data

Browse...

No file selected

Upload your penal data

Browse...

No file selected

Upload your fcs data

Browse...

No file selected

Load Meta Data

You can enter the raw data and metadata you are going to analyze in the Load Data screen, and of course you can explore with sample data.

## Moudle1: Flow Cytometry Workflow

```
class: SingleCellExperiment
dim: 50 1504420
metadata(2): experiment_info chs_by_fcs
assays(2): counts exprs
rownames(50): 75As 102Pd ... Live/Dead 208Pb
rowData names(3): channel_name marker_name marker_class
colnames: NULL
colData names(3): sample_id condition patient_id
reducedDimNames(0):
mainExpName: NULL
altExpNames(0):
```



Below, you can see the basic information about the data structure.

# Moudle1: Flow Cytometry Workflow

## Normalization

This section provides normalization and feature selection.

Normalization

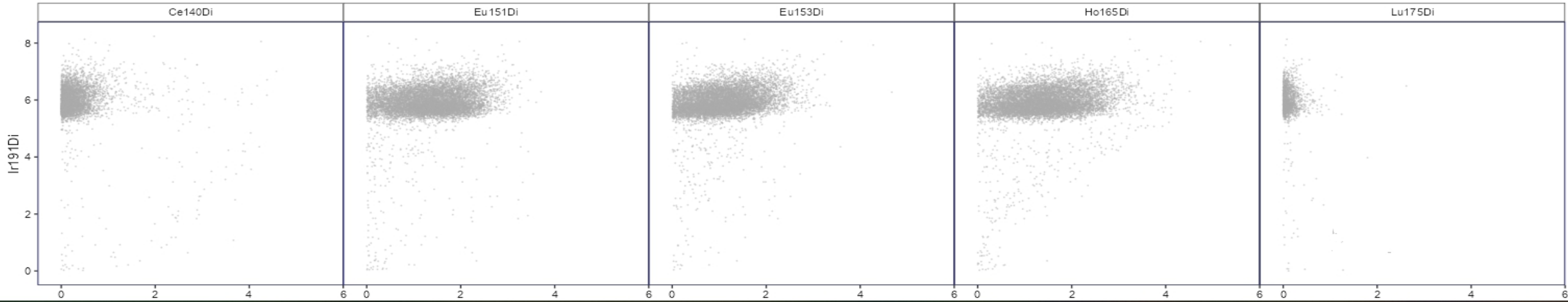
Event.Type	Count	Percentage....
Beads	10	0.00
Removed	2168	0.14

The table shows the standardized relevant data, and the graph shows the standardized scatter plot, which can help to understand the signal strength relationship between different elements in the data and whether they fit the expected distribution pattern.



Normalization Scatter Plot

Normalization Line Plot



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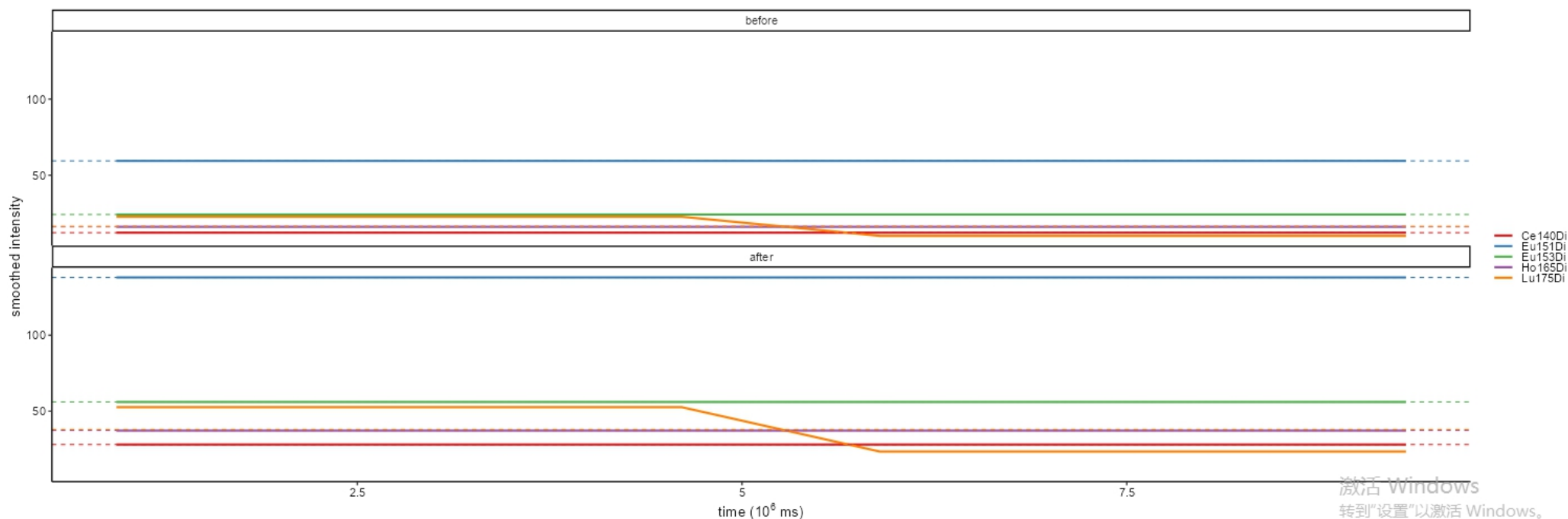
Download Results

### Normalization

Event.Type	Count	Percentage....
Beads	10	0.00
Removed	2168	0.14

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### Auto Gating

Note: If you selected the example data in previous steps, you can proceed with auto-gating analysis by clicking the button below—no additional configuration needed. If you are using your own data, please upload your custom gating strategy file here to ensure the analysis aligns with your specific experimental setup.

Upload your auto gating strategy file

Browse... No file selected

#### Auto Gating

sample	pop	percent
control-03	root	1.00
control-03	/Singlet1	0.97
control-03	/Singlet1/Singlet2	0.96
control-03	/Singlet1/Singlet2/Singlet3	1.00

Download Gating Results

In this section, please read the text instructions carefully, you can upload your own gating policy file. SCPLine provides real-time visualization of the results form on the line, and you can download the form locally.

# Moudle1: Flow Cytometry Workflow

Auto Gating Singlet1

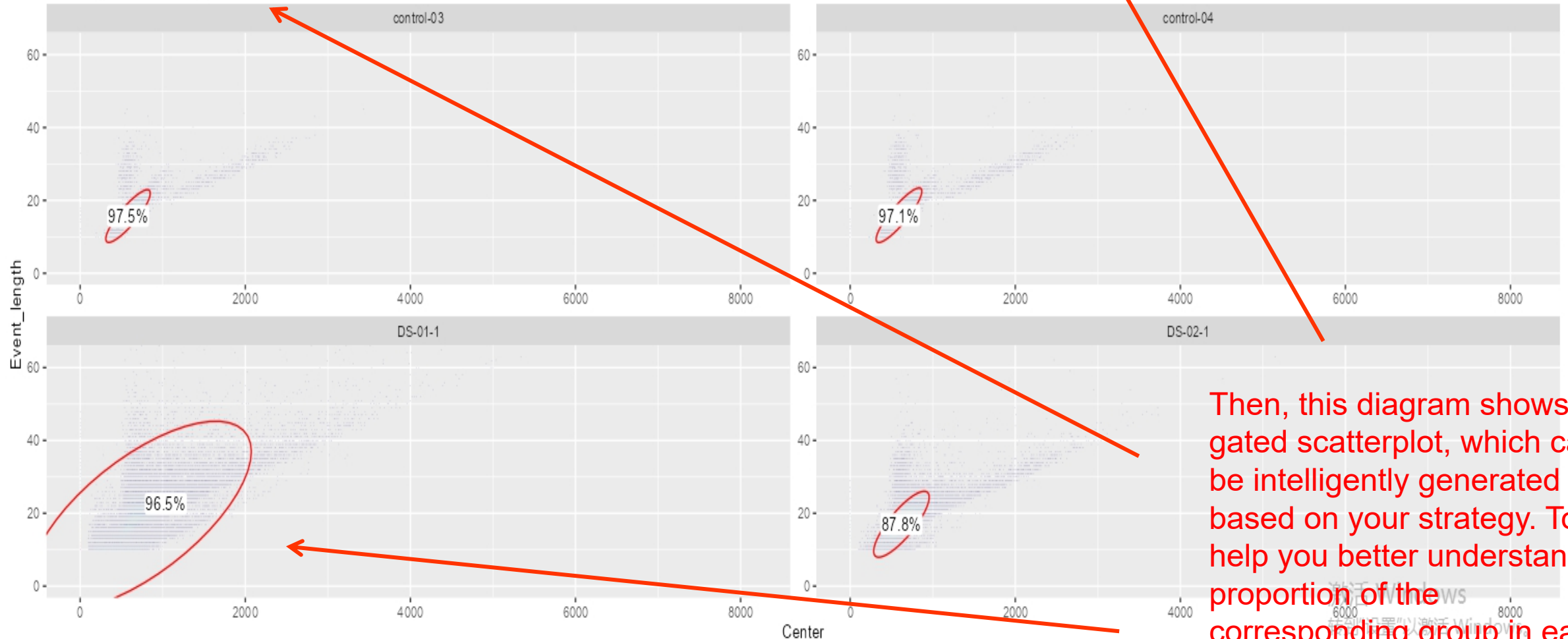
Auto Gating Singlet2

Auto Gating Singlet3

Auto Gating Cells

Auto Gating final

Gating Plot for: Singlet1



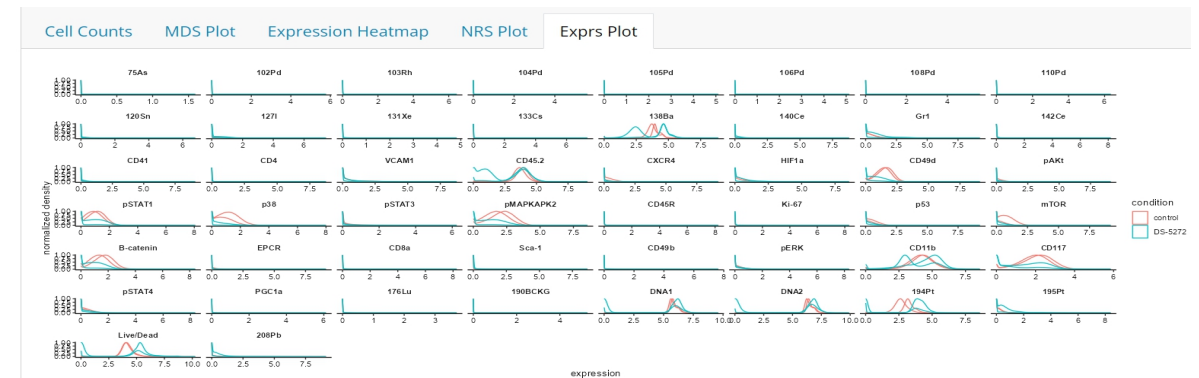
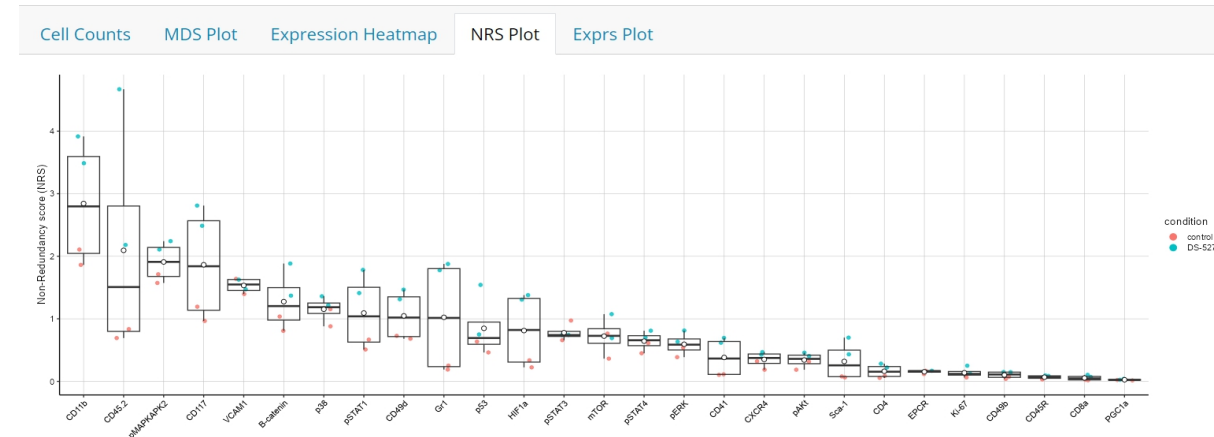
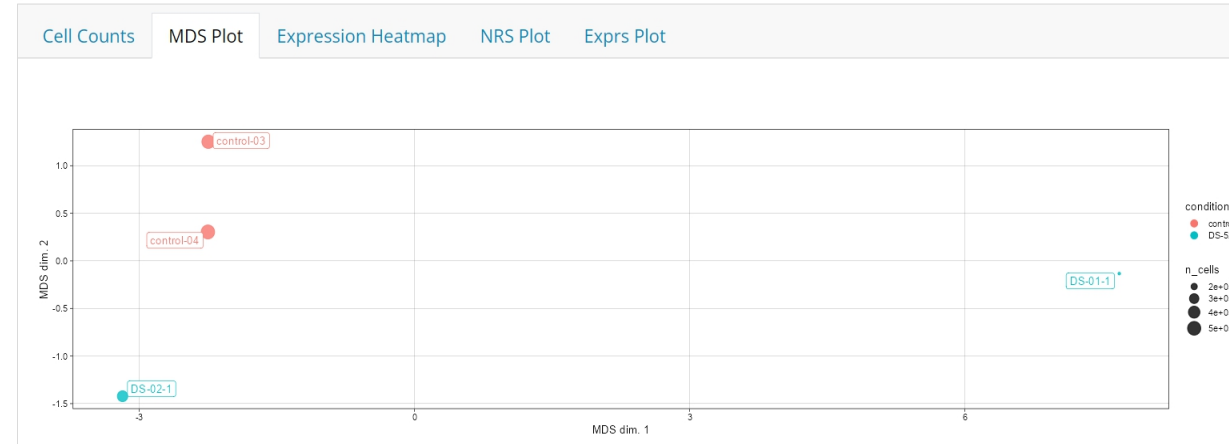
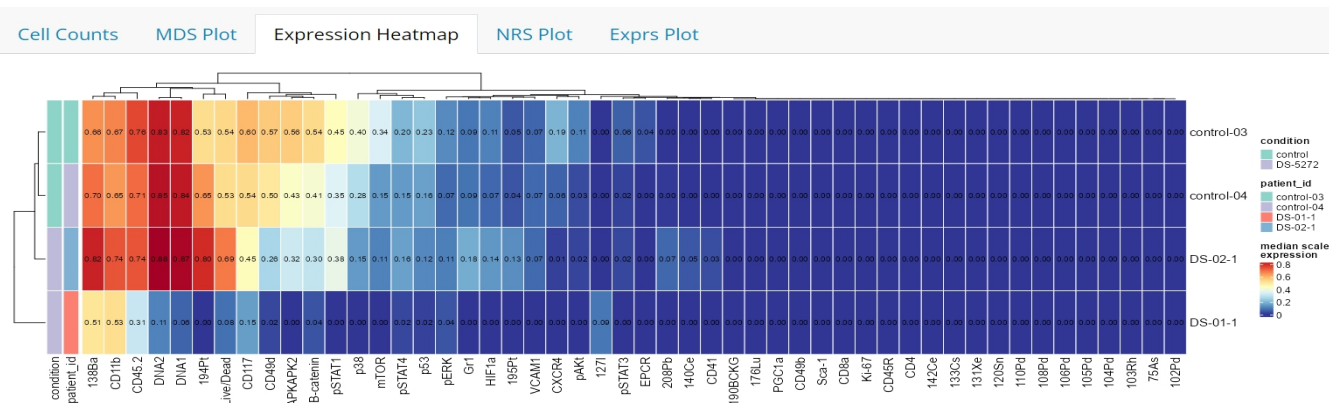
Then, this diagram shows the gated scatterplot, which can be intelligently generated based on your strategy. To help you better understand the proportion of the corresponding group in each sample.



# Moudle1: Flow Cytometry Workflow

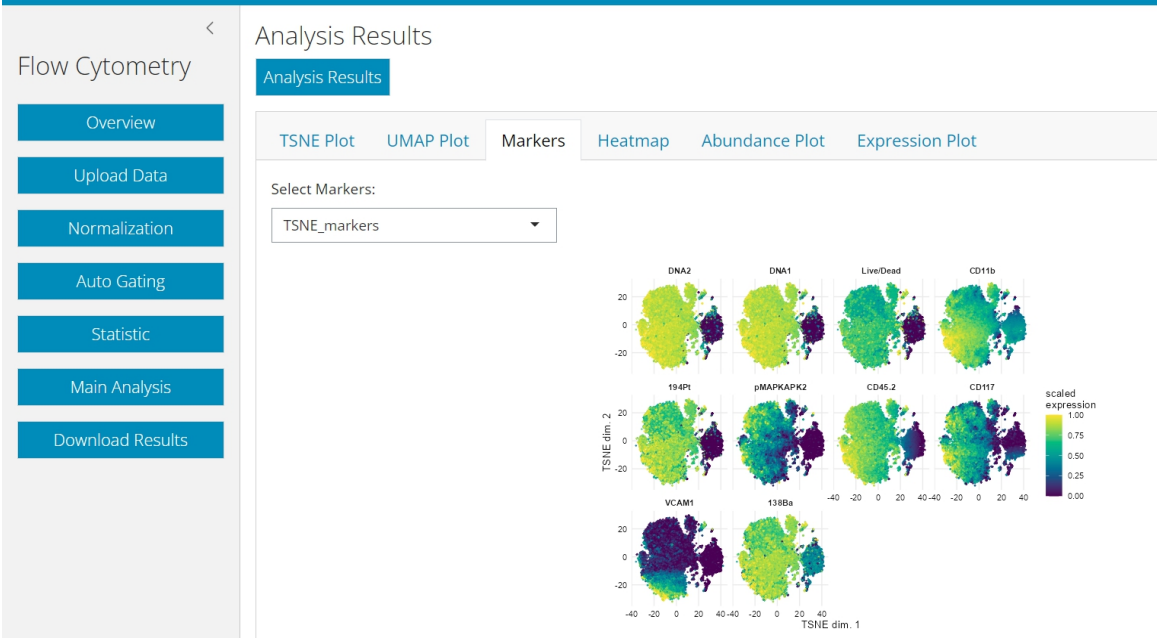
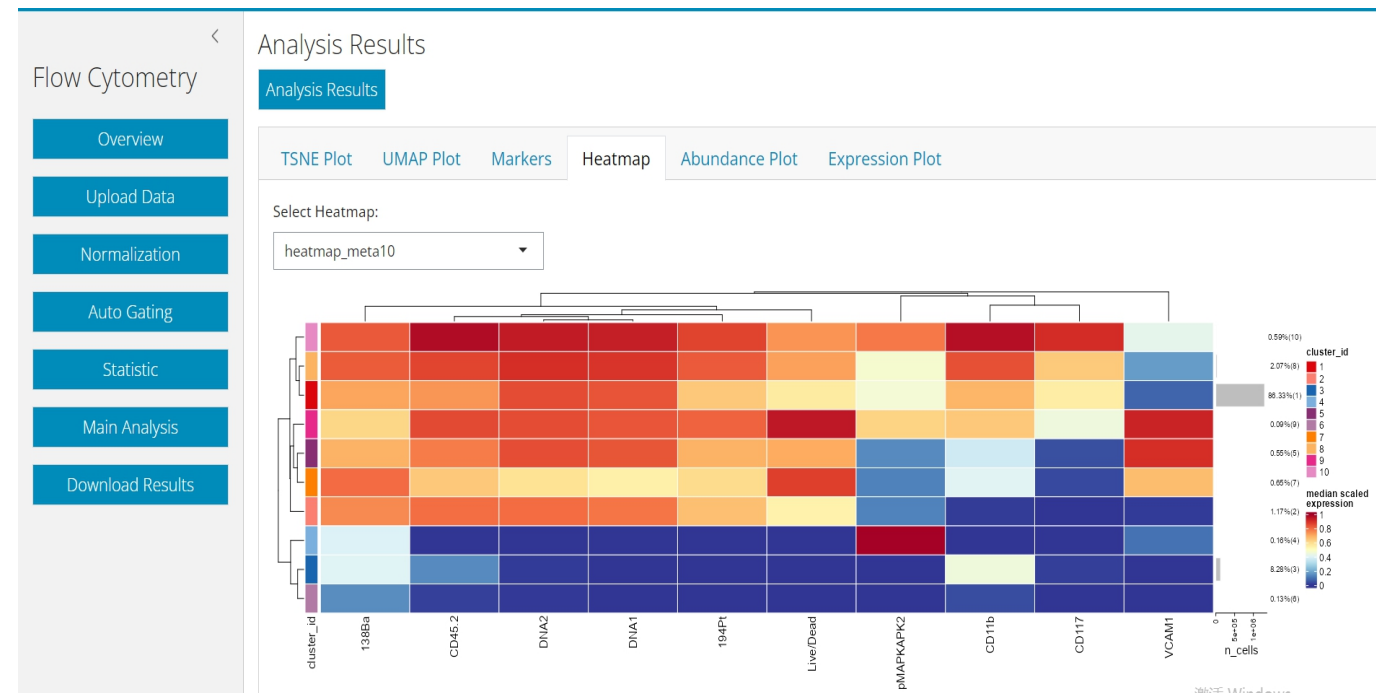
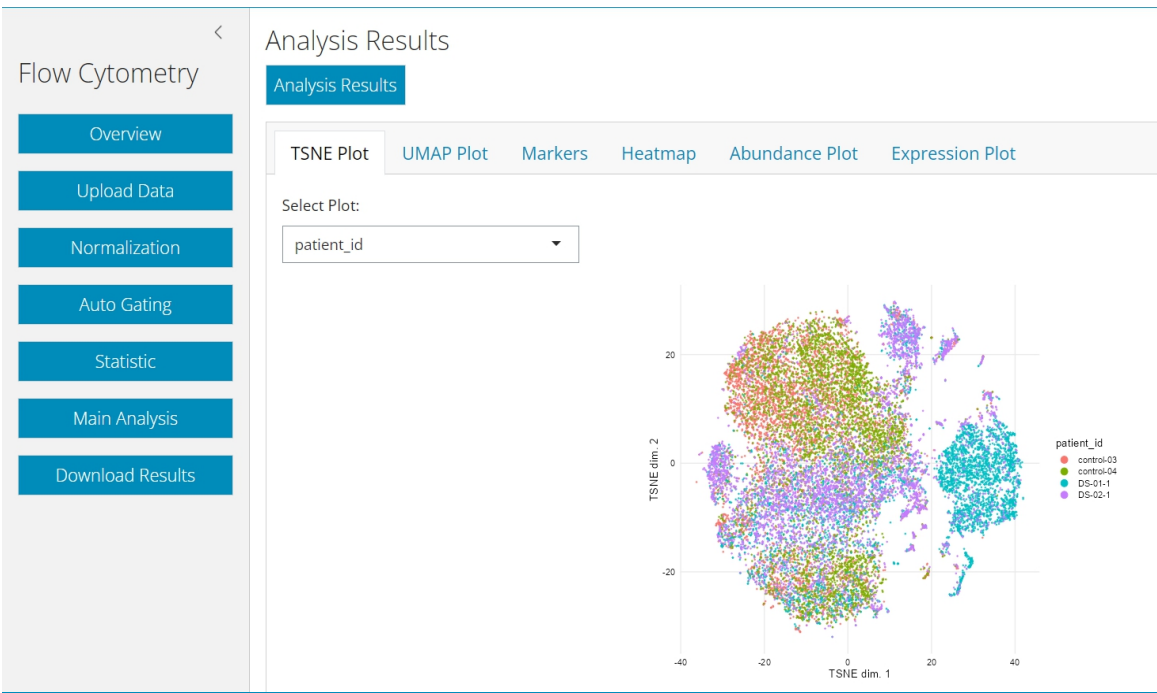


SCPline provided a variety of visualizations of the processed data to evaluate the differences between samples and the effects of the treatment, and analyzed the flow cytometry data from different angles.





# Moudle1: Flow Cytometry Workflow



SCPline provides two dimensionality reduction methods for cluster analysis, and continue to analyze and visualize the data after clustering, perhaps it can help you deeply analyze the characteristics of each group and the changes without experimental conditions.

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