

- Tutorial
- ML Overall Distribution Analysis
- Spatial Pattern Analysis
- Clustering Analysis and Cell Annotation
- Differential Analysis
 - Comparison Group Selection
 - Differential Screening and Visualization
 - Group-Specific Network
- Functional Association Analysis
- Data Visualization

Step4: Differential Analysis

Differential Feature Identification

Identify differentially expressed genes (DEGs) and differentially abundant metabolites (DAMs) using Seurat's FindMarkers function:

- Wilcoxon rank-sum test with Bonferroni correction
- Thresholds: $\log_2\text{FC} > 0.26$ & adjusted p-value < 0.05
- Post-hoc analysis treating each spatial spot as independent sample

Set thresholds below and click "Start differential screening":

Metabolomics $\log_2\text{FC}$ threshold:

Transcriptomics $\log_2\text{FC}$ threshold:

Metabolomics FDR threshold:

Transcriptomics FDR threshold:

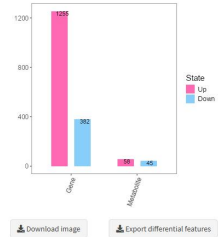
Note: Computation scales with feature count. Please avoid duplicate submissions.

Start differential screening

Differential Feature Summary

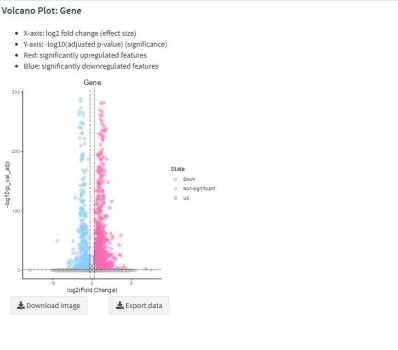
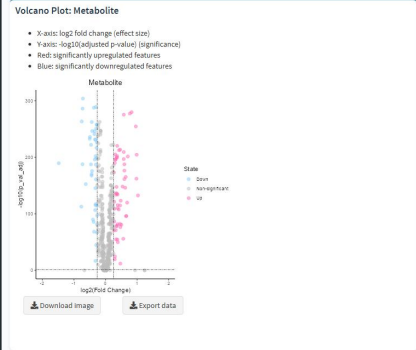
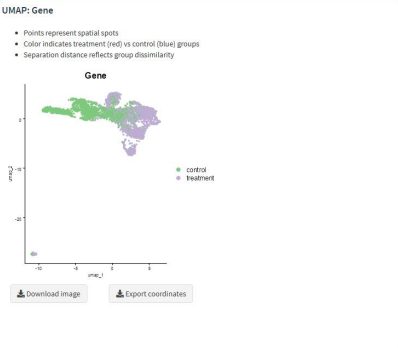
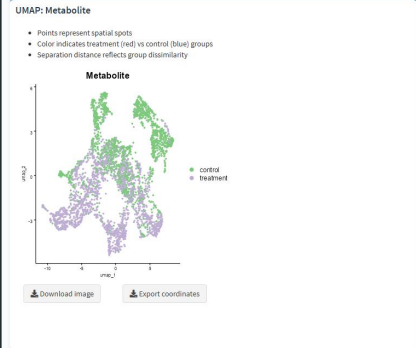
Barplot showing significantly upregulated (red) and downregulated (blue) features:

- Height indicates feature counts
- Annotations show total differential features per modality



Differential Feature Characterization

Multi-dimensional visualization of differential features:



Spatial Distribution of Differential Features

Examine spatial expression patterns of significant features:

