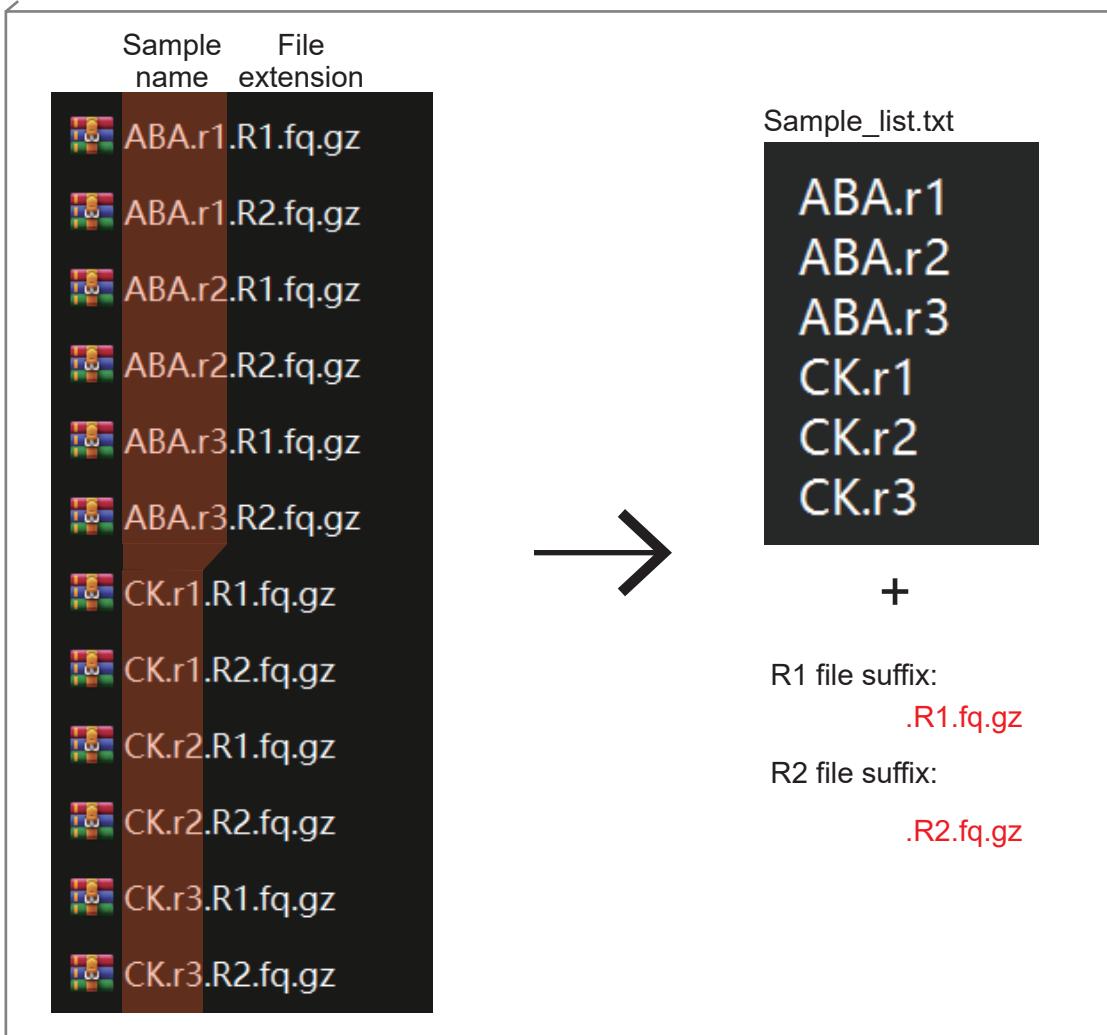
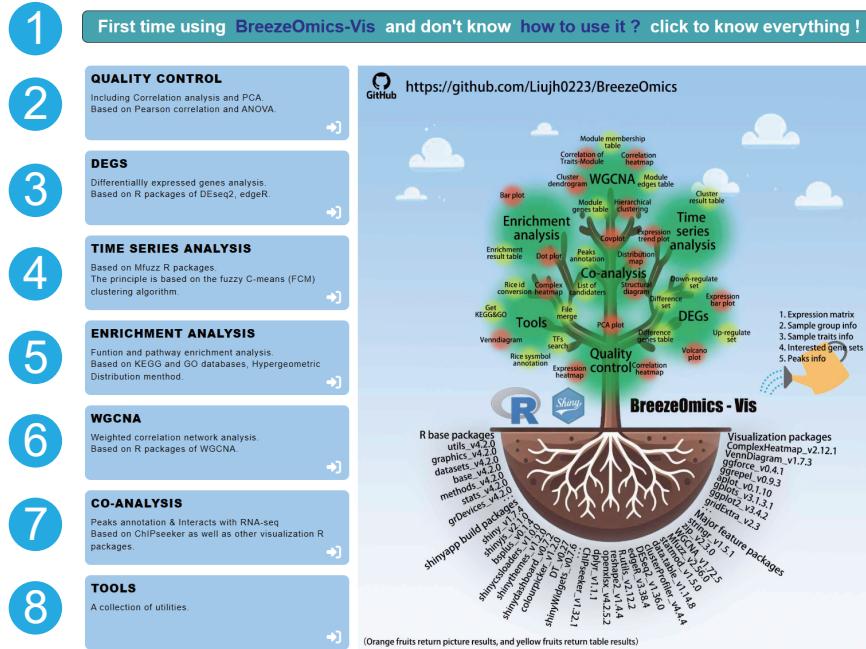


1. Name This Analysis Project
2. Select Previously Built Genome
3. Rawdata or Cleandata; if Raw Data, then Perform Fastp
4. Detection of unknown transcripts is not supported
5. Select the Folder Containing the FASTQ Files
6. Manually Create and Upload the Sample List File
7. Fill in the file extensions for FASTQ files R1 and R2.
8. Select the Number of Threads to Run
9. Click to Start Running
10. Monitor Task Progress and Status
11. Check the output files and click to export





BreezeOmics-Vis v1.0

This platform is committed to developing a simple, fast and understandable tool for visualizing omics analysis, and is free for all scientific researchers.
Developed based on the shiny framework of R language, it references ggplot2, clusterProfile, DESeq2, edgeR, limma and other related dependency packages.

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1. Guide Page: Introduction to the Features of BreezeOmics-Vis and Provision of Test Datasets for Testing.
2. Quality control model: PCA, Correlation Analysis, Hierarchical Clustering
3. DEGs model: Differential analysis based on DESeq2 and edgeR, supporting with/without biological replicates.
4. Time series analysis model: Based on the Fuzzy C-Means Clustering Algorithm.
5. Enrichment analysis model: Enrichment Analysis Based on Hypergeometric Distribution.
6. WGCNA: Weighted Gene Co-Expression Network Analysis Based on the WGCNA Package.
7. Co-analysis based on RNA-seq expression patterns and ChIP-seq peak information to explore candidate genes.
8. Tools, including multiple mini-tools such as Venn diagrams, heatmaps, scatter plots, and file merging statistics.

It is recommended to use the test data downloaded from "GUIDE/Sample Data for Testing" for testing.

"QUILTY CONTROL"

PRJNA779257_gene_count_matrix.csv

Step1: Upload you Matrix

Upload ↘

Browse... No file selected

Step2: Download you Group info

Download →

Download

Step3: Upload you Group info

Upload ↙

Browse... No file selected

✓ ENTER

Modify ↓

	group
wt_4_0h_rep1	wt_4_0h_rep1
wt_4_0h_rep2	wt_4_0h_rep2
wt_4_0h_rep3	wt_4_0h_rep3
wt_4_12h_rep1	wt_4_12h_rep1
wt_4_12h_rep2	wt_4_12h_rep2
wt_4_12h_rep3	wt_4_12h_rep3
zmice1_1_4_0h_rep1	zmice1_1_4_0h_rep1
zmice1_1_4_0h_rep2	zmice1_1_4_0h_rep2
zmice1_1_4_0h_rep3	zmice1_1_4_0h_rep3
zmice1_1_4_12h_rep1	zmice1_1_4_12h_rep1
zmice1_1_4_12h_rep2	zmice1_1_4_12h_rep2
zmice1_1_4_12h_rep3	zmice1_1_4_12h_rep3

	group
wt_4_0h_rep1	wt_4_0h
wt_4_0h_rep2	wt_4_0h
wt_4_0h_rep3	wt_4_0h
wt_4_12h_rep1	wt_4_12h
wt_4_12h_rep2	wt_4_12h
wt_4_12h_rep3	wt_4_12h
zmice1_1_4_0h_rep1	zmice1_1_4_0h
zmice1_1_4_0h_rep2	zmice1_1_4_0h
zmice1_1_4_0h_rep3	zmice1_1_4_0h
zmice1_1_4_12h_rep1	zmice1_1_4_12h
zmice1_1_4_12h_rep2	zmice1_1_4_12h
zmice1_1_4_12h_rep3	zmice1_1_4_12h

"DEGs"

Step1: Biological replicates

Multiple biological replicates ▾ Select whether there are biological replicates.

Step2: Upload you Matrix

Upload ↙ PRJNA779257_gene_count_matrix.csv

Browse... No file selected

Step3: Download you Group info

Download → groupinfo.csv

Download

Download

Step4: Upload you Group info

Upload ↙ groupinfo.csv

Browse... No file selected

Step5: Select the TR and the CO

Click →

Add the different gene grouping information

1.Naming 2.Select TR and CO 3.Add Group 4.Confirm

GroupName: OVS12 TR: wt_4_12h, wt_4_0h Add

Reset

TR: wt_4_0h, wt_4_12h, zmice1_1_4_0h, zmice1_1_4_12h

CO: wt_4_0h, wt_4_12h, zmice1_1_4_0h, zmice1_1_4_12h

Step6: Select the analysis software

DESeq2 Select Analysis Software. ▾

Filter low expression genes by edgeR
Selecting this option will remove 30% of lowly expressed genes.

✓ ENTER

RESET

“TIME SERIES ANALYSIS”

Step1: Upload you Matrix

?

Browse... No file selected

Upload ← PRJNA779257_gene_count_matrix.csv

Step2: Download you Group info

?

Download → groupinfo.csv

Step3: Upload you Group info

?

Browse... No file selected

Upload ← groupinfo.csv

↓ Modify

Step4: CPM normalization or not

?

YES NO

Should the expression matrix be normalized to CPM (Counts Per Million)?

 RESET

 ✓ ENTER