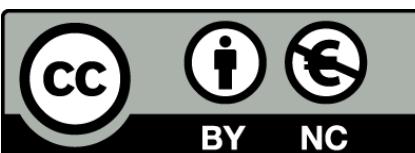


岡山大バイオインフォマティクス ワークショップ

#3-1 RNA-seqハンズオン・カウントデータの可視化

国立遺伝学研究所 大量遺伝情報研究室 坂本美佳



カウントデータの可視化

webツールでらくらく

- iDEP
- RNAseqChef

カウントデータ

2日目につくったカウントデータを使いましょう

まだできていない場合は、GitHubに置いてあるカウントデータを利用

カウントデータ

https://github.com/motthy/okayama_ws2024/

The screenshot shows a GitHub repository page for 'okayama_ws2024'. The repository is public and was last updated 4 days ago. A red circle highlights the 'data' folder in the commit history.

Commits:

- motthy ho1 bug fix (8a2c2e3 · 4 days ago) 13 Commits
 - data (add kallisto count · 2 weeks ago)
 - shellscript_basic (add results · 2 weeks ago)
 - .gitignore (delete large files · 2 weeks ago)
 - LICENSE (Initial commit · 2 weeks ago)
 - README.md (new file handout1 · last week)
 - handout1.md (ho1 bug fix · 4 days ago)
 - handout2.md (new file handout2 · last week)

About: RNA-seq analysis workshop, from 2024-02-06 to 2024-02-08

- Readme
- MIT license
- Activity
- 0 stars
- 1 watching
- 0 forks

Releases: No releases published [Create a new release](#)

Packages:

iDEP

<http://bioinformatics.sdsu.edu/idep96/>

<http://149.165.154.220/idep11/>

idep rnaseq でキーワード検索

iDEP

入力ファイル

- カウントデータ (raw count) ds1.genes.results.rename.tsv

- 実験条件 ds1_experiments.csv

	DRR357080	DRR357081	DRR357082	DRR357083	DRR357084
treatment	DMSO	DMSO	5H4PB	5H4PB	5H4PB

The screenshot shows a GitHub repository interface for 'okayama_ws2024'. The repository is public and has 1 branch and 0 tags. The main branch is 'main'. The commit history is as follows:

- motthy ho1 bug fix (4 days ago)
 - data (2 weeks ago)
 - add kallisto count (2 weeks ago)
- shellsript_basic (2 weeks ago)
- .gitignore (2 weeks ago)
- LICENSE (2 weeks ago)
- README.md (last week)
- handout1.md (4 days ago)
- handout2.md (last week)

At the bottom of the commit list, there are links for 'README' and 'MIT license'.

iDEP

- ・では、データ入力からやってみます

生物種

First time here? Just click [Load Demo](#) below to see some magic!

1. Choose a species or upload a pathway file

Select [Human](#) 

Or: Upload a custom pathway .GMT file [Browse...](#)

2. Choose data type

[Read counts data \(recommended\)](#) [Info](#)

3. Expression data (CSV, text, or xlsx)

[Browse...](#) [Load Demo:](#) 2 groups; Human

4. Optional: Experiment Design (CSV or text)

[Browse...](#)

Gene IDs Global Settings

[Public Data](#) [Cite iDEP](#) [Questions?](#)

iDEP: integrated Differential Expression & Pathway analysis 

Ready to load data files.

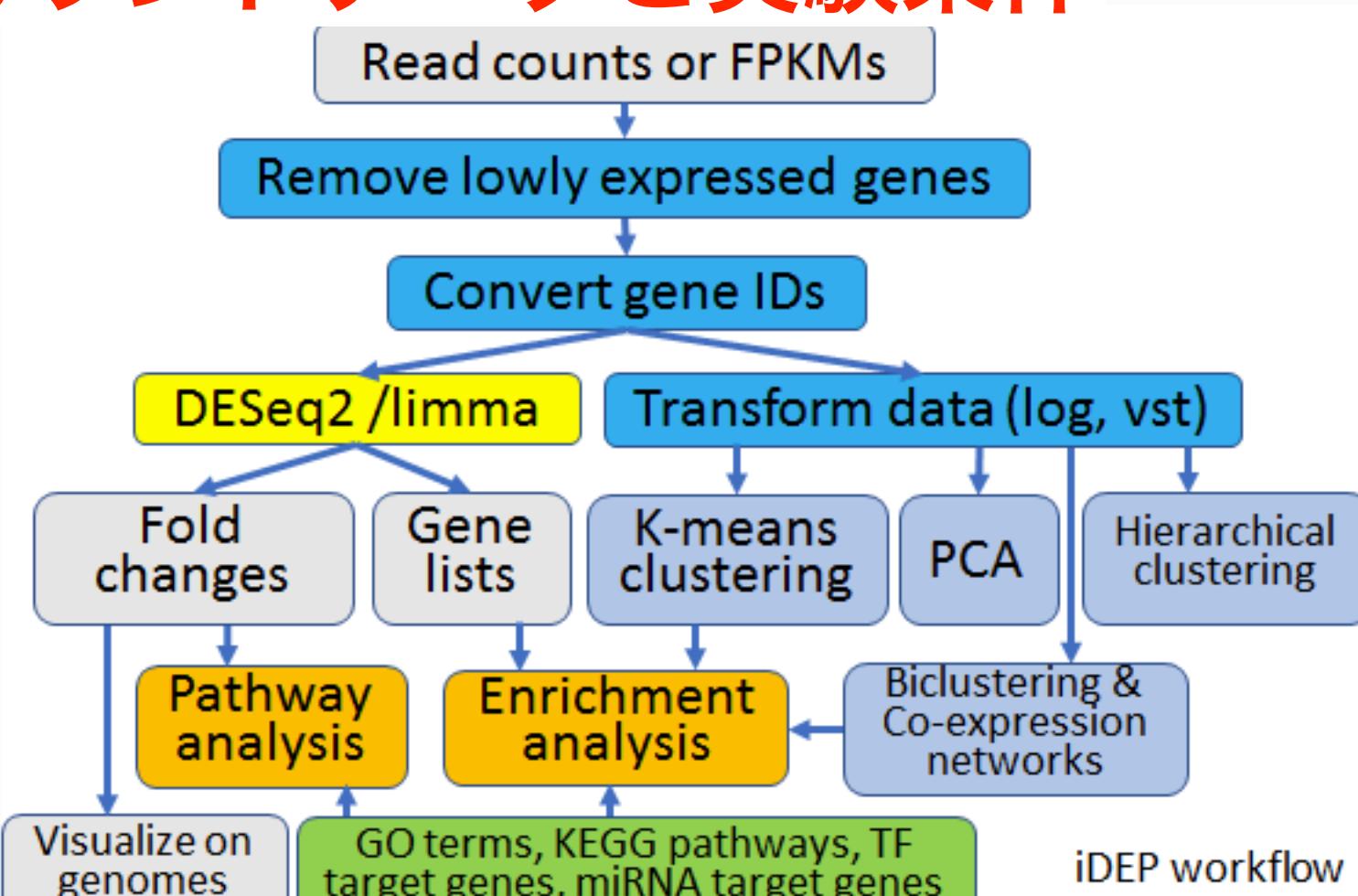
iDEP 1.13: interactive & reproducible

- Exploratory analysis, D.E.G., and pathway analyses on bulk RNA-seq data,
- Rich, interactive visualization: clustering, KEGG pathways, genome view, etc.
- Download HTML reports for some steps, documenting parameters and results,
- Download dozens of publication-ready figures in minutes,
- Download R code and data objects, which can be used in RStudio to reproduce results,
- Install locally as an R package or as a Docker container ([Windows](#), [MacOS](#))
- Completely rewritten using Shiny modules with the Golem framework.

Please [Email Jenny \(gelabinfo@gmail.com\)](#) or report issues on our [GitHub page](#). iDEP is still under active development and testing. We welcome any suggestions or questions.

ABSOLUTELY NO WARRANTY. Please double check your results using other tools.

カウントデータと実験条件



```

graph TD
    A[Read counts or FPKMs] --> B[Remove lowly expressed genes]
    B --> C[Convert gene IDs]
    C --> D[DESeq2 /limma]
    C --> E[Transform data (log, vst)]
    D --> F[Fold changes]
    D --> G[Gene lists]
    E --> H[K-means clustering]
    E --> I[PCA]
    E --> J[Hierarchical clustering]
    F --> K[Pathway analysis]
    G --> L[Enrichment analysis]
    H --> M[Biclustering & Co-expression networks]
    I --> M
    J --> M
    M --> N[Visualize on genomes]
    M --> O[GO terms, KEGG pathways, TF target genes, miRNA target genes]
  
```

iDEP workflow

iDEP 1.13 [Load Data](#) [Pre-Process](#) [Clustering](#) [PCA](#) [DEG1](#) [DEG2](#) [Pathway](#) [Genome](#) [Bicluster](#) [Network](#) [About](#)

1. Choose a species or upload a pathway file

Select
Human

Or: Upload a custom pathway .GMT file

Browse...

2. Choose data type

Read counts data (recommended)
Info

3. Expression data (CSV, text, or xlsx)

Browse...
ds1.genes.results.rename.tsv
Upload complete

Load Demo:
2 groups; Human

4. Optional: Experiment Design (CSV or text)

Browse...
ds1_experiment.csv
Upload complete

Gene IDs

Global Settings
[Public Data](#)
[Cite iDEP](#)
[Questions?](#)

Study_design	DRR357080	DRR357081	DRR357082	DRR357083	DRR357084
treatment	DMSO	DMSO	5H4PB	5H4PB	5H4PB

	DRR357080	DRR357081	DRR357082	DRR357083	DRR357084
ENSG000000000003	469	494	353	411	489.26
ENSG000000000005	0	0	0	0	0
ENSG00000000419	1294.01	1412.78	1182	1206	1508
ENSG00000000457	384.01	334	270	262	373
ENSG00000000460	489.92	526	404.4	464	467
ENSG000000000000	0	0	0	0	0
ENSG000000000001	26.19	26.19	26.19	26.19	26.19
ENSG000000000010	3	3	3	3	3
ENSG000000001084	1667	1919	13855.45	14752.31	18852
ENSG000000001167	529	495	407	473	537

データを読み込んだ状態

iDEP: integrated Differential Expression & Pathway analysis



Ready to load data files.

iDEP 1.13: interactive & reproducible

- Exploratory analysis, D.E.G., and pathway analyses on bulk RNA-seq data,
- Rich, interactive visualization: clustering, KEGG pathways, genome view, etc.
- Download HTML reports for some steps, documenting parameters and results,
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- Download R code and data objects, which can be used in RStudio to reproduce results,
- Install locally as an R package or as a Docker container ([Windows](#), [MacOS](#))
- Completely rewritten using Shiny modules with the Golem framework.

Please [Email Jenny \(gelabinfo@gmail.com\)](#) or report issues on our [GitHub page](#). iDEP is still under active development and testing. We welcome any suggestions or questions.

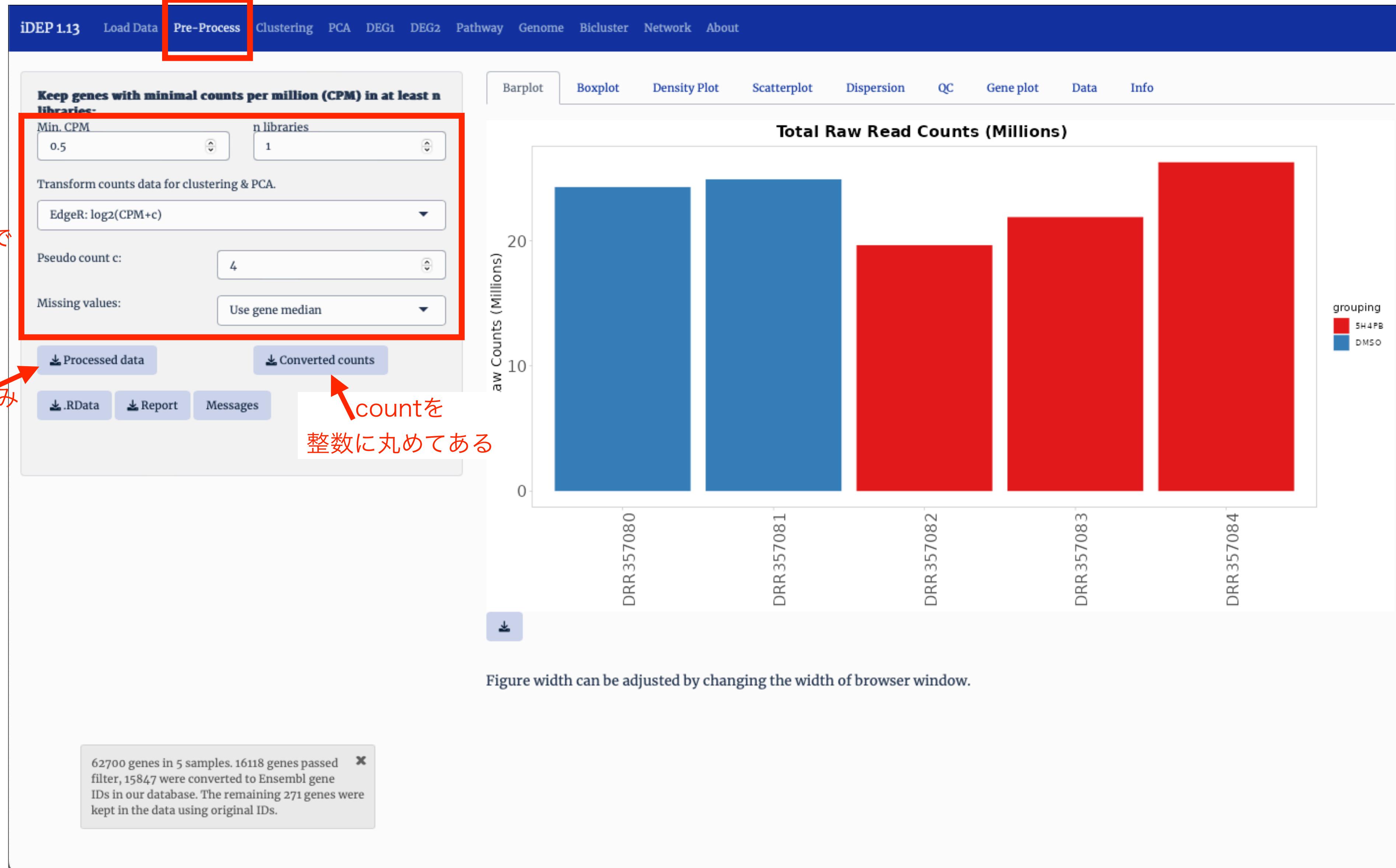
ABSOLUTELY NO WARRANTY. Please double check your results using other tools.

Pre-Processタブに移動

<http://149.165.154.220/idep11/>

デフォルト設定で

symbolに変換済み



iDEP 1.13 Load Data Pre-Process Clustering PCA DEG1 DEG2 Pathway Genome Bicluster Network About

Keep genes with minimal counts per million (CPM) in at least n libraries:

Min. CPM: 0.5 n libraries: 1

Transform counts data for clustering & PCA.

EdgeR: $\log_2(CPM+c)$

Pseudo count c: 4

Missing values: Use gene median

[Processed data](#) [Converted counts](#)

[.RData](#) [Report](#) [Messages](#)

[Questions?](#)

Boxplot **Barplot** **Boxplot** **Density Plot** **Scatterplot** **Dispersion** **QC** **Gene plot** **Data** **Info**

Distribution of Transformed Data

Transformed Expression

grouping: SH4PB (red), DMSO (blue)

DRR357080 DRR357081 DRR357082 DRR357083 DRR357084

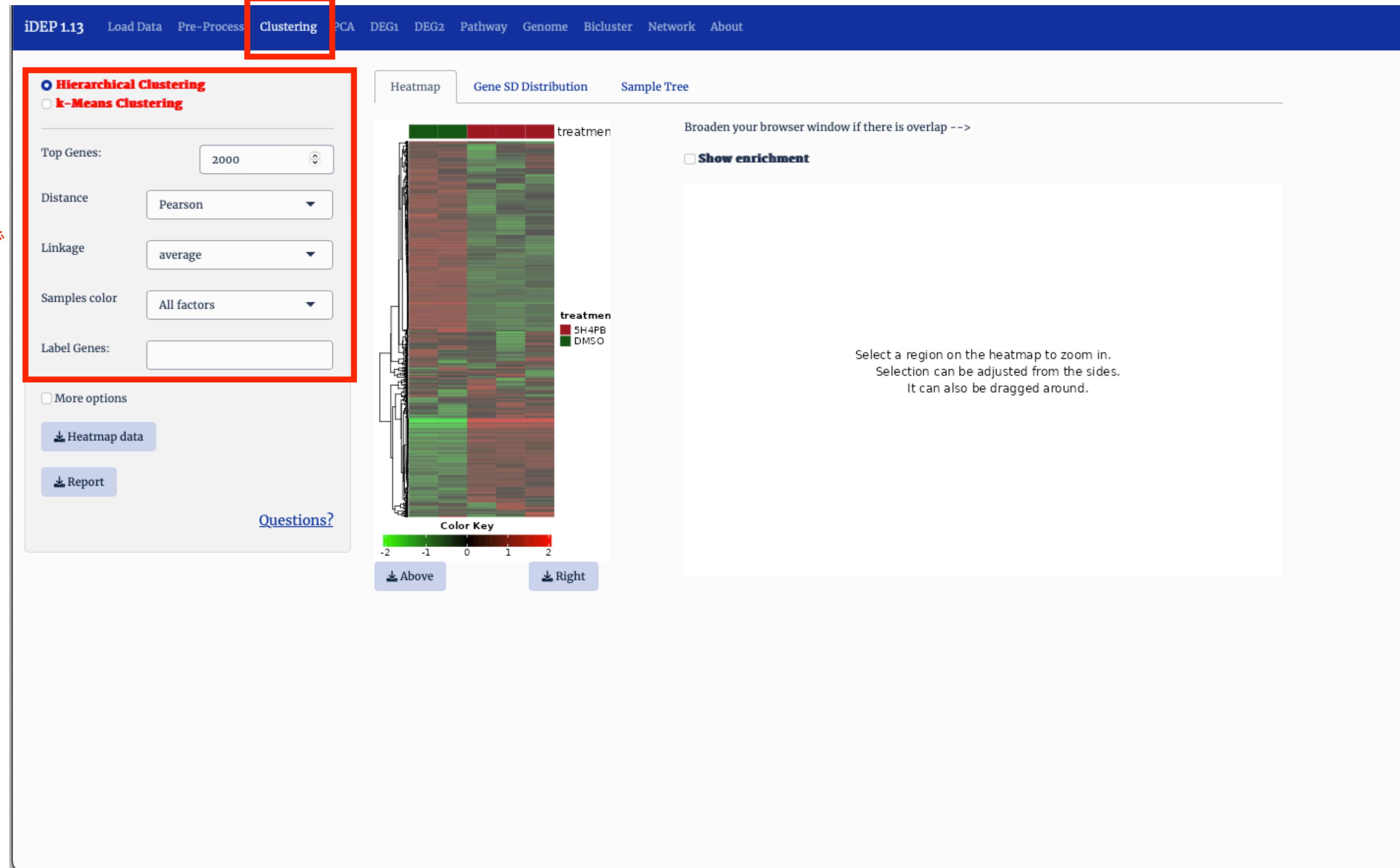
[Download](#)

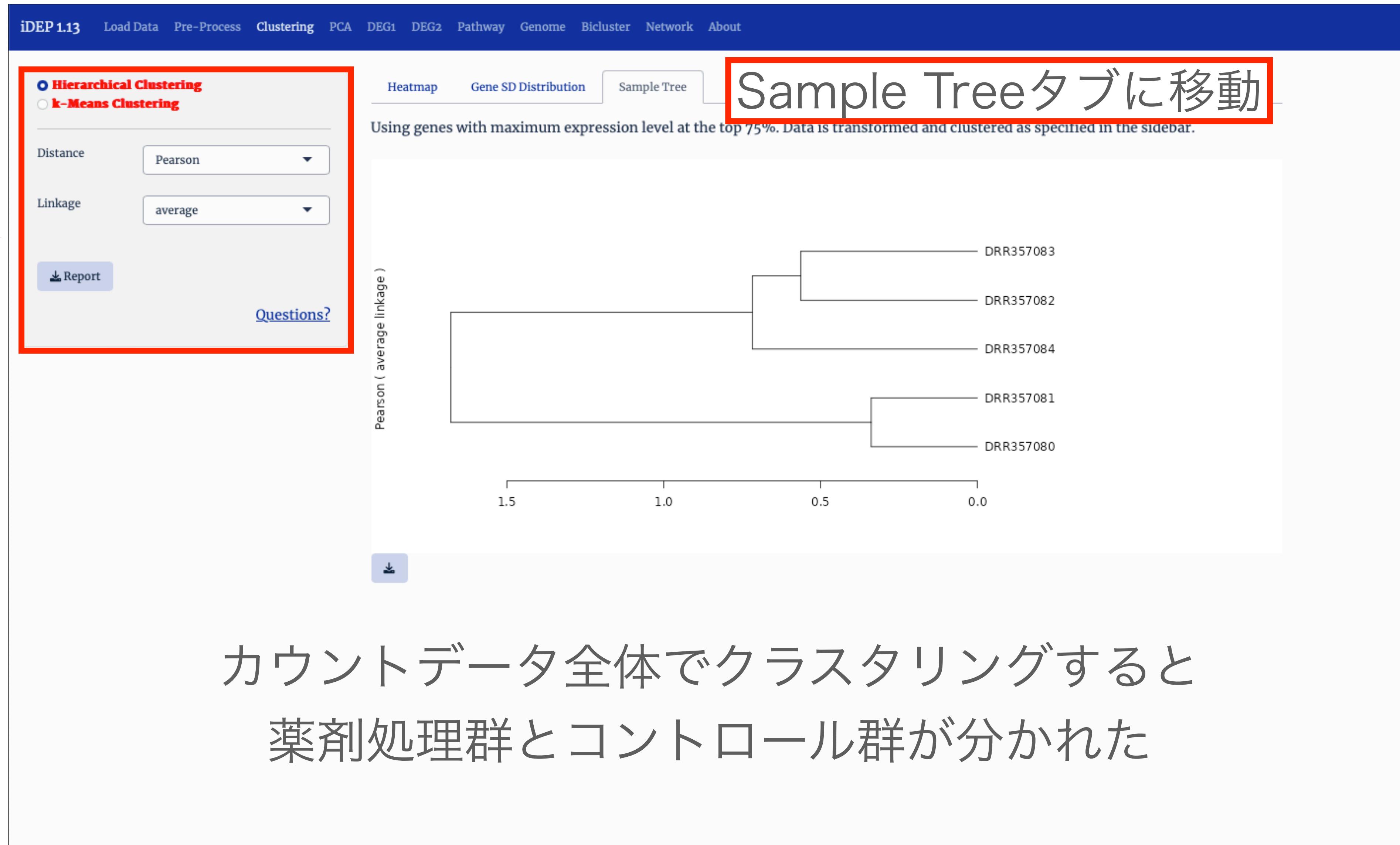
62700 genes in 5 samples. 16118 genes passed filter, 15847 were converted to Ensembl gene IDs in our database. The remaining 271 genes were kept in the data using original IDs. [X](#)

Clusteringタブに移動

<http://149.165.154.220/idep11/>

デフォルト設定で



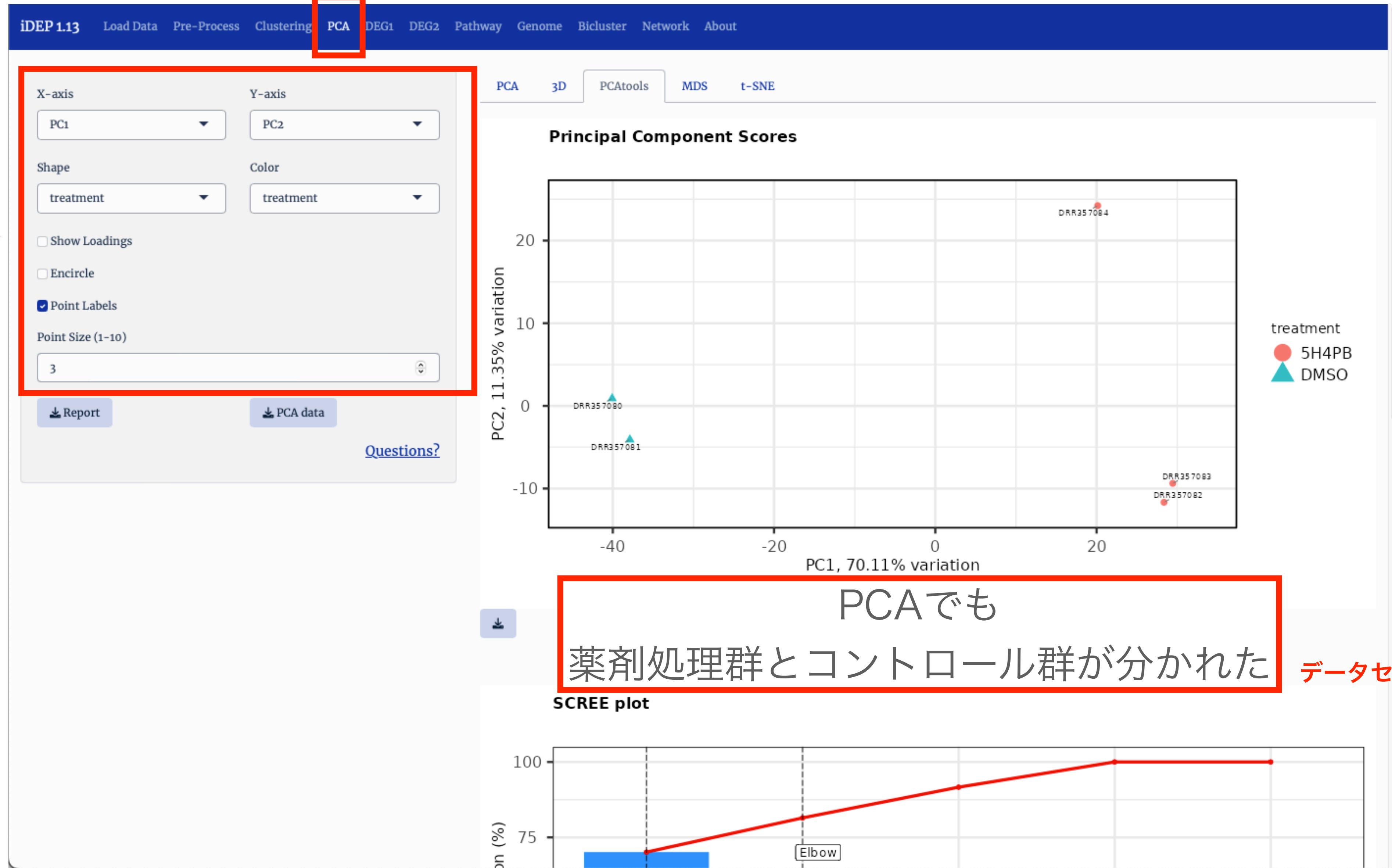


iDEP

PCAタブに移動

http://149.165.154.220/idep11/

デフォルト設定で



DEG1タブに移動

<http://149.165.154.220/idep11/>

デフォルト設定で

Method: DESeq2 Submit Run DEG analysis

FDR cutoff: 0.1 Min fold-change: 2

Threshold-based Wald Test Independent filtering of lower counts

Experiment Design Results Venn Diagram & UpSet plot R Code

1. Select 6 or less main factors. Or skip this step and just choose pairs of sample groups below.
 treatment

Reference/baseline level for treatment: DMSO ← コントロール (DMSO)

Model: expression ~ treatment

2. Select one or more comparisons:
 treatment: 5H4PB vs. DMSO treatment: DMSO vs. 5H4PB

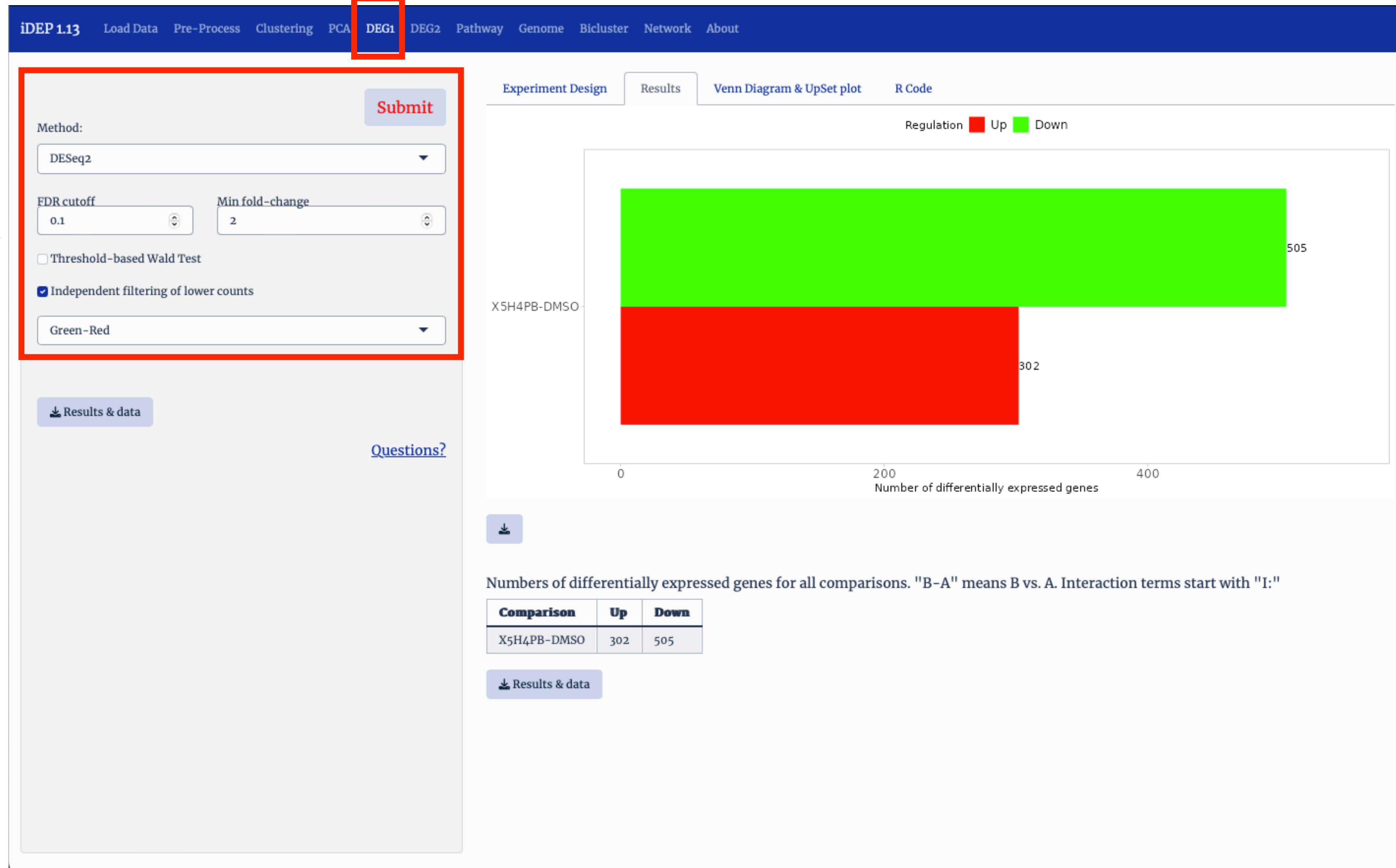
[More info on DESeq2 experiment design](#)

Results & data Questions?

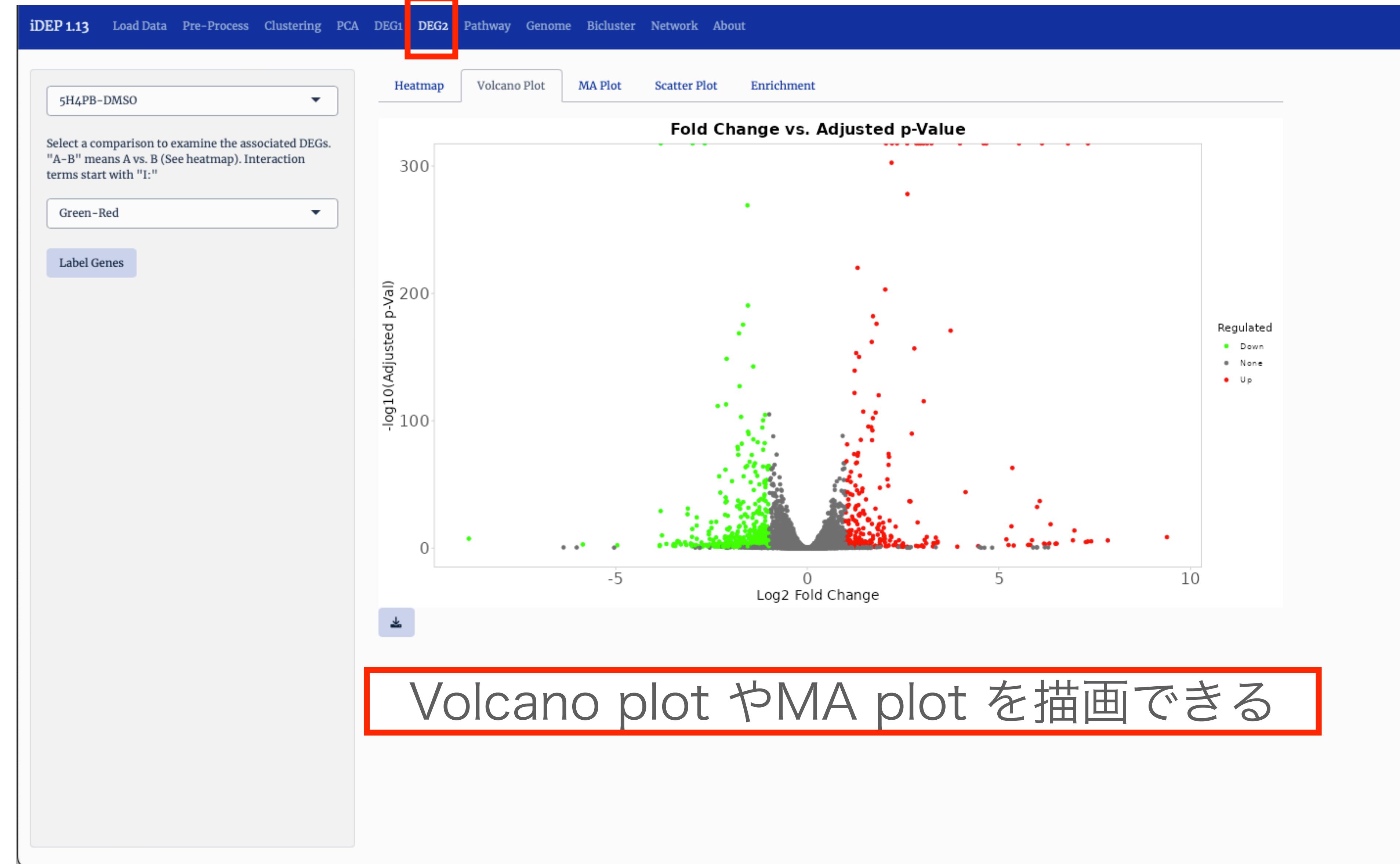
DEG1タブに移動

<http://149.165.154.220/idep11/>

デフォルト設定で



DEG2タブに移動

<http://149.165.154.220/idep11/>

Select a comparison:

Submit

Pathway analysis method:

Pathway database:

Pathway significance cutoff (FDR):

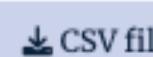
More options

 Report

Beware of P-hacking! If you try all the combinations, you can find evidence for anything.

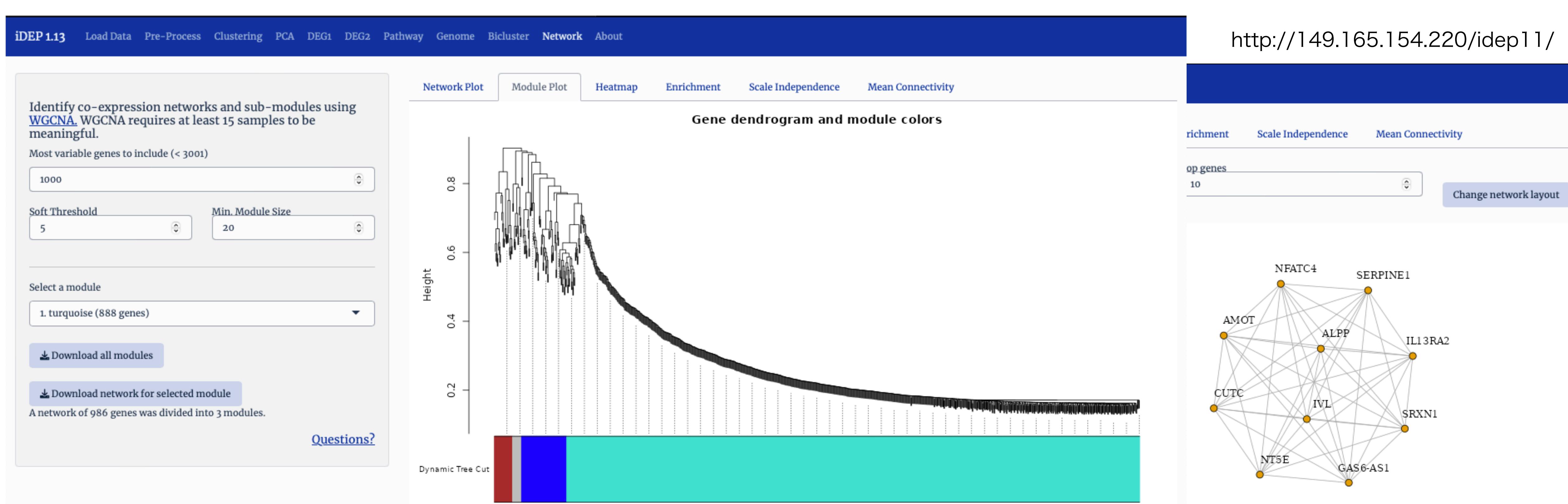
[Questions?](#)

Significant pathways		Tree	Network	Heatmap	KEGG	Info
Direction	GSEA analysis: 5H4PB vs DMSO	NES	Genes	adj.Pval		
Down	Staphylococcus aureus infection	-0.7273	20	1.9e-02		
	Viral protein interaction with cytokine and cytokine receptor	-0.6483	28	3.5e-02		
	Taurine and hypotaurine metabolism	-0.8326	7	8.1e-02		
	Autoimmune thyroid disease	-0.875	5	9.6e-02		
Up	Galactose metabolism	0.8218	21	1.8e-03		
	Porphyrin metabolism	0.7802	28	1.8e-03		
	Chemical carcinogenesis-DNA adducts	0.7668	31	1.8e-03		
	Ferroptosis	0.7564	32	1.8e-03		
	Glutathione metabolism	0.7156	39	1.8e-03		
	Metabolism of xenobiotics by cytochrome P450	0.6743	36	1.6e-02		
	Steroid hormone biosynthesis	0.7124	28	1.8e-02		
	Ascorbate and aldarate metabolism	0.8099	15	1.9e-02		
	Biosynthesis of nucleotide sugars	0.6859	30	1.9e-02		
	Proteasome	0.668	35	1.9e-02		
	Bile secretion	0.6425	36	2.5e-02		
	Glycerolipid metabolism	0.625	40	2.5e-02		
	Pentose and glucuronate interconversions	0.7361	20	3.3e-02		
	Fructose and mannose metabolism	0.698	26	3.3e-02		
	Ovarian steroidogenesis	0.6896	25	3.4e-02		
	DNA replication	0.6289	32	4.6e-02		

 CSV file

iDEP

ネットワーク解析も可能



RNAseqChef

- <https://imeg-ku.shinyapps.io/RNAseqChef/>
- 日本語マニュアル https://kan-e.github.io/RNAseqChef_manual_japanese/
- 統合TV <https://tgotv.dbcls.jp/20231213.html>

rnaseqchef でキーワード検索

RNAseqChef

動画による使い方説明（統合TV）

<https://togotv.dbcls.jp/20231213.html>

The screenshot shows a video player interface on the TOGO TV website. The video title is "RNAseqChef: 遺伝子発現変動を自動的に可視化するRNA-seq統合解析ツール @ 日本エピジェネティクス研究会リソースセミナー". The video is presented by 衛藤 貴 (Kei Ieda) from 熊本大学 発生医学研究所 細胞医学分野. The video duration is 34:16 and was recorded on 2023.12.13. The video content is a presentation about RNAseqChef, a tool for visualizing gene expression changes automatically using RNA-seq integrated analysis. The video includes a table of contents with 14 items, each with a timestamp and a link to the corresponding section. The video player also includes standard controls like play/pause, volume, and a search bar.

TOGO TV

RNAseqChef: 遺伝子発現変動を自動的に可視化するRNA-seq統合解析ツール @ 日本エピジェネティクス研究会リソースセミナー

2023/09/14

見どころダイジェスト

時間	内容
00:19	1. 目次
00:31	2. RNA-seq解析の概要
02:15	3. RNAseqChef の紹介
04:02	4. 解析例1: 二群間の比較解析(Pair-wise DEG)
07:24	5. Pair-wise DEG の補足
09:35	6. 解析例2: 複数のデータセットの統合解析(Pair-wise DEG + Venn diagram)
13:30	7. Venn diagramの補足
15:54	8. 解析例3: 時系列データの多重比較解析(Multi DEG)
21:37	9. 解析例4: 相関解析(Normalized count analysis)
25:41	10. 相関解析の補足
26:30	11. 解析例5: エンリッチメント解析(Enrichment viewer)
28:41	12. 解析例6: Public data の解析(GREINとの連携)
30:55	13. 補足: Public data の解析
32:42	14. まとめ: RNAseqChef を使用する利点

再生リストに保存

この動画のタグ

発現解析 遺伝子 ウェブツール NCBI

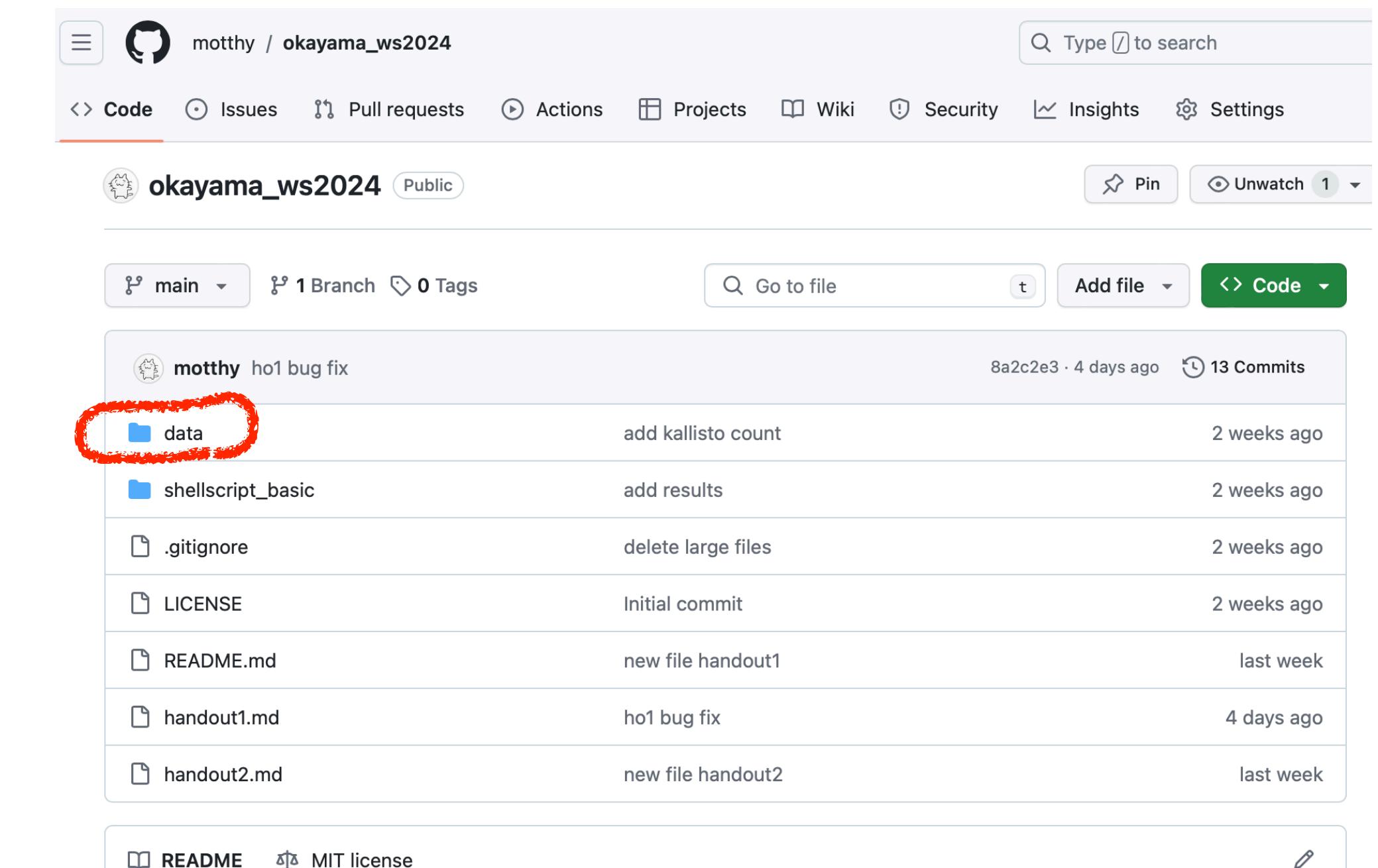
RNAseqChef

入力ファイル

- カウントデータ (raw count) ds1.genes.results.rename.tsv

- 実験条件 metadata.csv

	treatment
DRR357080	DMSO
DRR357081	DMSO
DRR357082	5H4PB
DRR357083	5H4PB
DRR357084	5H4PB



RNAseqChef

- ・では、こちらもデータ入力からやってみます

RNAseqChef

<https://imeg-ku.shinyapps.io/RNAseqChef/>

 RNAseqChef

Pair-wise DEG 3 conditions DEG Multi DEG Venn diagram Normalized count analysis Enrichment viewer More ▾

RNAseqChef

RNAseqChef, an RNA-seq data controller highlighting gene expression features, is a web-based application for automated, systematic, and integrated RNA-seq differential expression analysis.

Current version (v1.1.0, 2024/1/18)

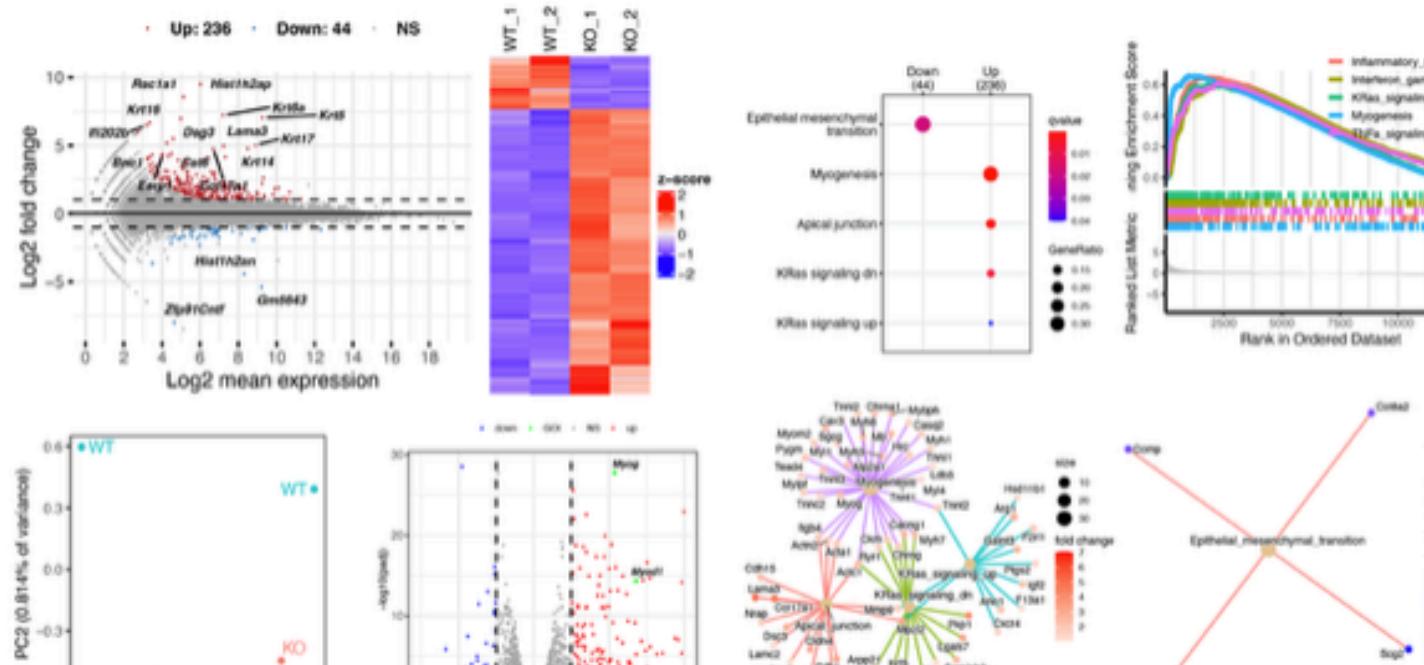
Enhance the visualization of the clustering analysis (PCA, MDS, and UMAP).
Implement a feature to enable the selection of a second pair for fold change cut-off in Multi DEG and Normalized count analysis.
Fix bug regarding the motif region of promoter motif analysis in Enrichment viewer.
See the details from 'More -> Change log'

Publication

Etoh K. & Nakao M. A web-based integrative transcriptome analysis, RNAseqChef, uncovers cell/tissue type-dependent action of sulforaphane. JBC, 299(6), 104810 (2023)
<https://doi.org/10.1016/j.jbc.2023.104810>

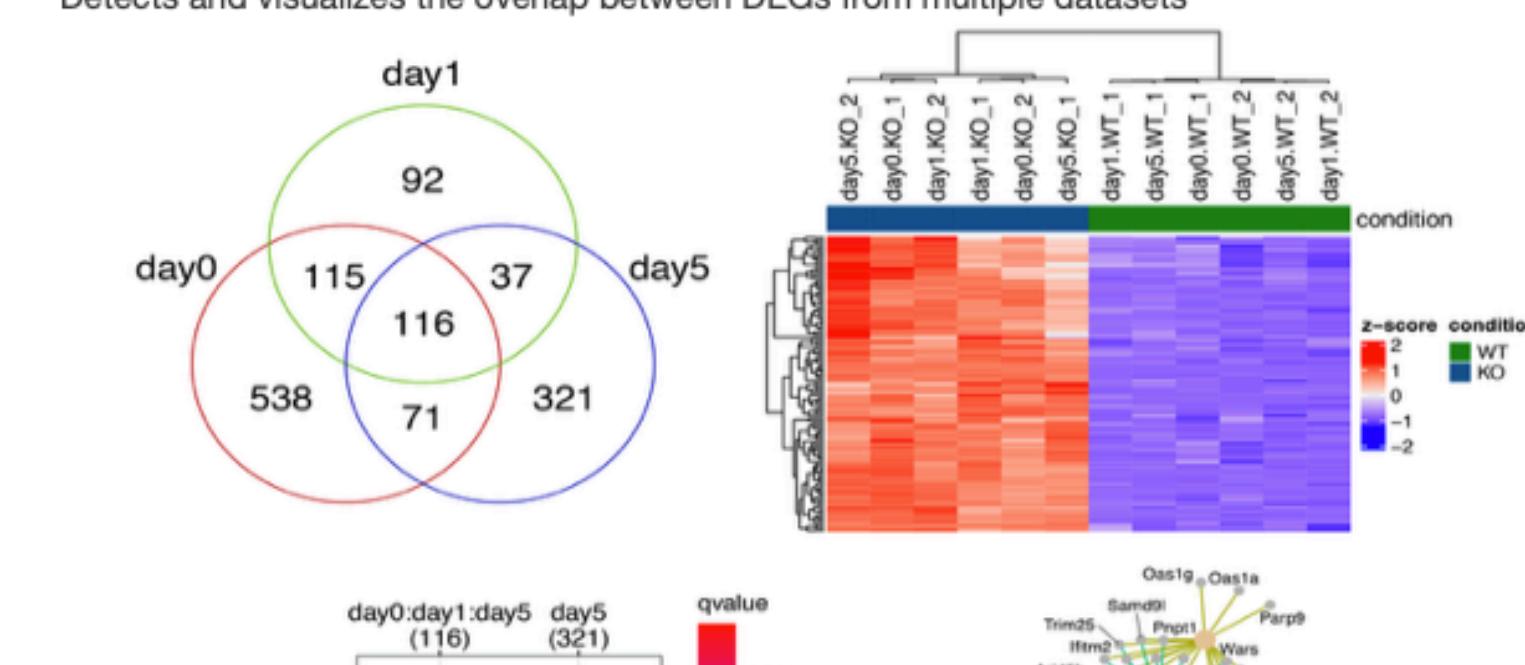
Pair-wise DEG

Detects and visualizes differentially expressed genes



Venn diagram

Detects and visualizes the overlap between DEGs from multiple datasets



RNAseqChef

<https://imeg-ku.shinyapps.io/RNAseqChef/>

DRAアクセスション=サンプル名なので
「Raw count + メタデータ」を選択

Input:

- Raw_count_matrix
- Option: Raw_count_matrix + Metadata
- Option: Batch mode (not displayed in the output panel)

Select a raw count matrix file i

Browse... ds1.genes.results.rename.tsv
Upload complete

Select a metadata file to define samples for the following analysis

Browse... metadata.csv
Upload complete

DEG analysis method:

- DESeq2
- EBSeq
- edgeR

FDR method

BH

Species **Homo sapiens を選択**

Cut-off conditions:

Fold Change	FDR	Basemean
2	0.05	0

Option: Select a normalized count file i

Browse... No file selected

Input Data Result overview GOI profiling Enrichment analysis

Raw_count_matrix:

Metadata:

Defined_raw_count_matrix:

Select samples:

5H4PB_1 5H4PB_2 5H4PB_3 DMSO_1
DMSO_2

この順番になってしまう...

Download defined raw count

Show 10 entries

左側がbaselineになる

	5H4PB_1	5H4PB_2	5H4PB_3	DMSO_1	DMSO_2
ENSG00000000003	353	411	489.26	469	494
ENSG00000000005	0	0	0	0	0
ENSG00000000419	1182	1206	1508	1294.01	1412.78
ENSG00000000457	270	262	373	384.01	334
ENSG00000000460	404.4	464	467	489.92	526
ENSG00000000938	0	0	0	0	0
ENSG00000000971	19.7	34.17	26.19	55.59	58.02
ENSG00000001036	3	0	3	2	0
ENSG00000001084	13855.45	14752.31	18852	1667	1919
ENSG00000001167	407	473	537	529	495

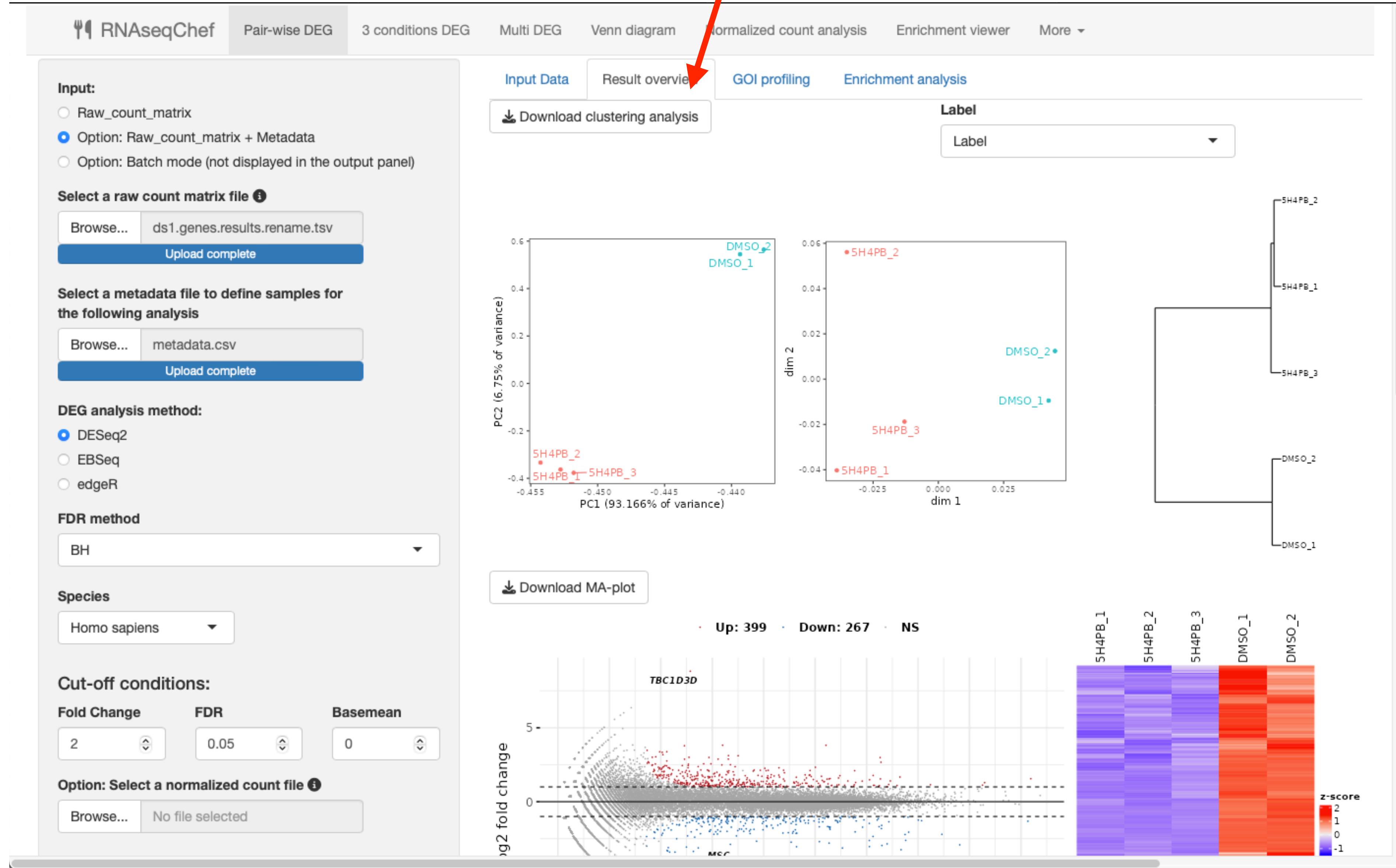
Showing 1 to 10 of 62,700 entries

Previous 1 2 3 4 5 ... 6,270 Next

RNAseqChef

Result overview タブに移動すると解析スタート

<https://imeg-ku.shinyapps.io/RNAseqChef/>



RNAseqChef

GOI profiling タブではVolcano plotを描画

<https://imeg-ku.shinyapps.io/RNAseqChef/>

The screenshot shows the RNAseqChef web interface. On the left, there are several input sections: 'Input' (radio buttons for Raw_count_matrix, Option: Raw_count_matrix + Metadata, Option: Batch mode), 'Select a raw count matrix file' (button to browse for 'ds1.genes.results.rename.tsv', status 'Upload complete'), 'Select a metadata file to define samples for the following analysis' (button to browse for 'metadata.csv', status 'Upload complete'), 'DEG analysis method' (radio buttons for DESeq2, EBSeq, edgeR, selected DESeq2), 'FDR method' (dropdown menu showing 'BH'), 'Species' (dropdown menu showing 'Homo sapiens'), 'Cut-off conditions' (input fields for Fold Change: 2, FDR: 0.05, Basemean: 0), and 'Option: Select a normalized count file' (button to browse, status 'No file selected'). On the right, the 'GOI profiling' tab is active, indicated by a red arrow. The tab has sub-options: Input Data, Result overview, GOI profiling (selected), and Enrichment analysis. Under GOI profiling, there are download buttons for 'volcano plot / MA plot' and 'heatmap'. Below these are 'Plot type' (dropdown set to 'Volcano plot'), 'X_axis range' (range from -10 to 9 with markers at -10 and 9), and 'Y_axis range' (range from 0 to 301 with markers at 0 and 301). A 'genes of interest (GOI)' input field and a 'GOI reset' button are also present. The main area displays a Volcano plot with the x-axis labeled 'log2 fold change' ranging from -10 to 5, and the y-axis labeled '-log10(padj)' ranging from 0 to 300. The plot shows two distinct clusters of points: blue points on the left (downregulated) and red points on the right (upregulated), separated by a vertical dashed line at log2 fold change = 0. A horizontal dashed line is at -log10(padj) = 0. A legend indicates that blue dots represent 'down', grey dots represent 'NS', and red dots represent 'up'.

RNAseqChef

Select a metadata file to define samples for the following analysis

Browse... metadata.csv
Upload complete

DEG analysis method:

- DESeq2
- EBSeq
- edgeR

FDR method

- BH

Species

- Homo sapiens

Cut-off conditions:

Fold Change	FDR	Basemean
2	0.05	0

Option: Select a normalized count file (必)

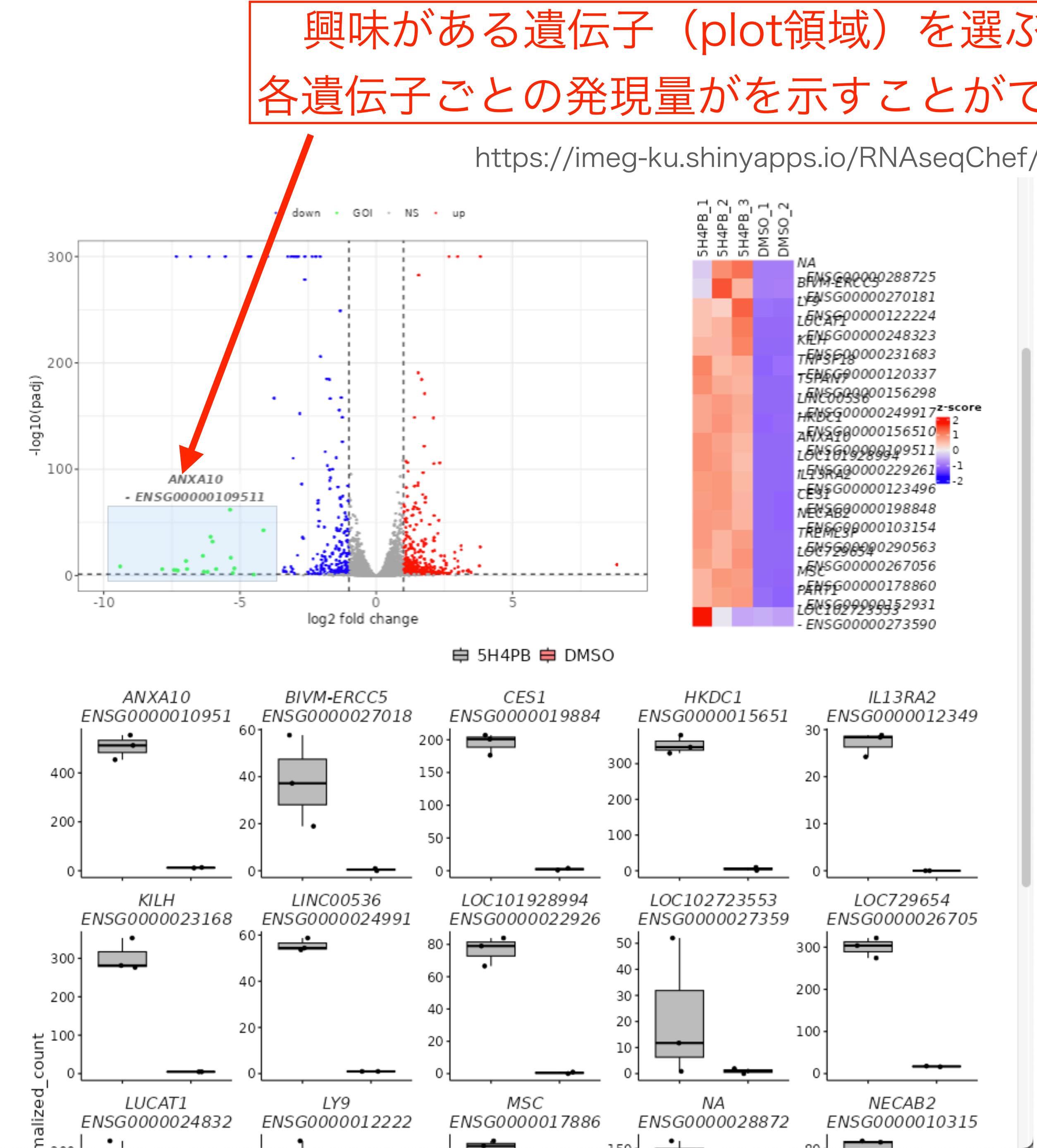
Browse... No file selected

Output plot size setting for pdf (0: default) (必)

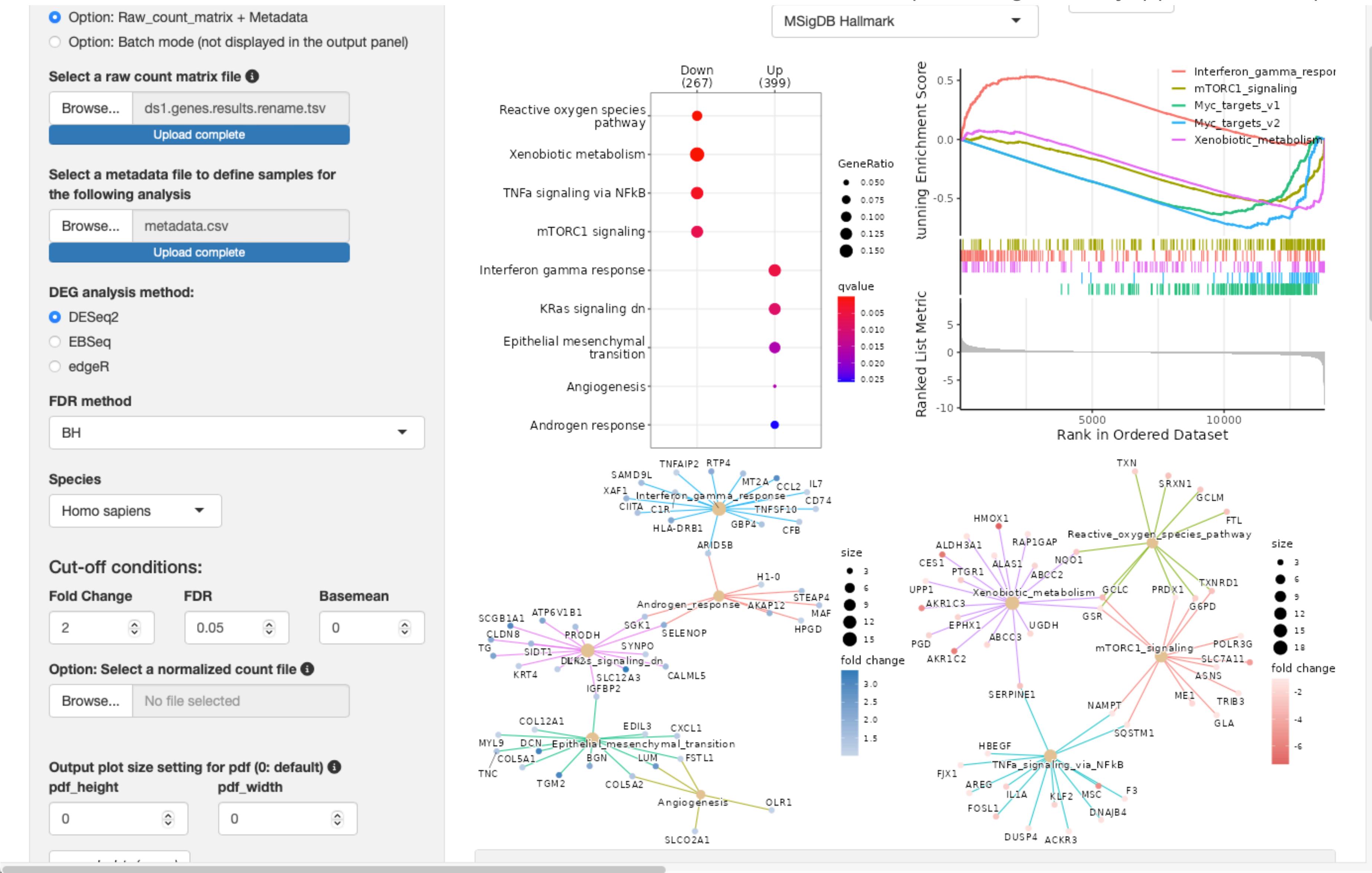
pdf_height	pdf_width
0	0

example data (mouse)

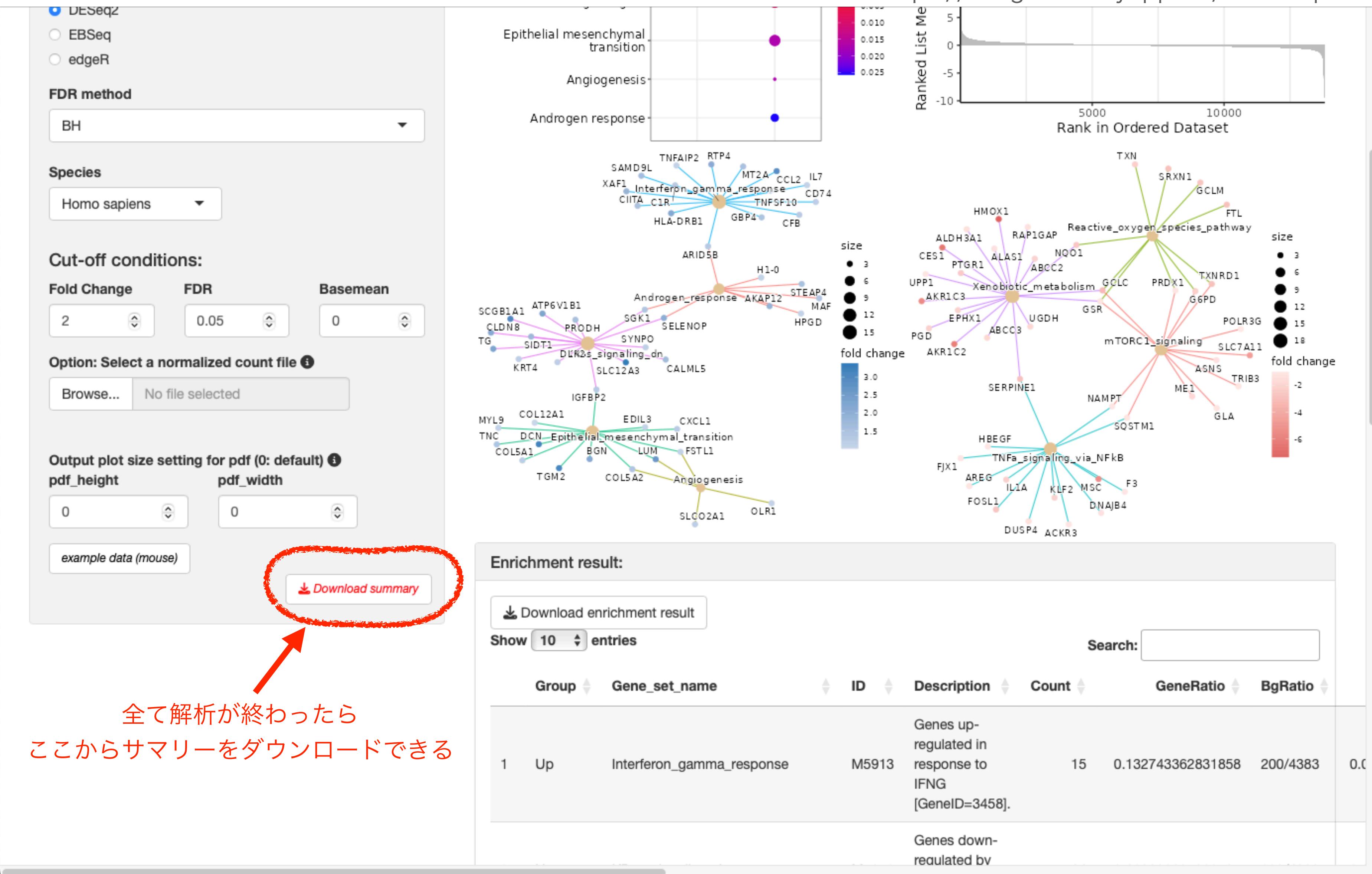
[Download summary](#)



RNAseqChef



RNAseqChef



RNAseqChef

<https://imeg-ku.shinyapps.io/RNAseqChef/>

RNAseqChef

Pair-wise DEG 3 conditions DEG Multi DEG Venn diagram Normalized count analysis Enrichment viewer More ▾

Input:

- Raw_count_matrix
- Option: Raw_count_matrix + Metadata
- Option: Batch mode (not displayed in the output panel)

Select a raw count matrix file i

Browse... ds1.genes.results.rename.tsv
Upload complete

Select a metadata file to define samples for the following analysis

Browse... metadata.csv
Upload complete

DEG analysis method:

- DESeq2
- EBSeq
- edgeR

FDR method

BH

Species

Homo sapiens

Cut-off conditions:

Fold Change FDR Basemean

2 0.05 0

Option: Select a normalized count file i

Browse... No file selected

Input Data Result overview GOI profiling Enrichment analysis

Raw_count_matrix:

Metadata:

Defined_raw_count_matrix:

Select samples:

5H4PB_1 5H4PB_2 5H4PB_3 DMSO_1
DMSO_2

Download defined raw count

Show 10 entries Search:

	5H4PB_1	5H4PB_2	5H4PB_3	DMSO_1	DMSO_2
ENSG00000000003	353	411	489.26	0	0
ENSG00000000005	0	0	0	0	0
ENSG00000000419	1182	1206	1508	1294.01	1412.78
ENSG00000000457	270	262	373	384.01	334
ENSG00000000460	404.4	464	467	489.92	526
ENSG00000000938	0	0	0	0	0
ENSG00000000971	19.7	34.17	26.19	55.59	58.02
ENSG00000001036	3	0	3	2	0
ENSG00000001084	13855.45	14752.31	18852	1667	1919
ENSG00000001167	407	473	537	529	495

Showing 1 to 10 of 62,700 entries Previous 1 2 3 4 5 ... 6,270 Next

こちらをbaselineにしたい

RNAseqChef

<https://imeg-ku.shinyapps.io/RNAseqChef/>

RNAseqChef

Pair-wise DEG 3 conditions DEG Multi DEG Venn diagram Normalized count analysis Enrichment viewer More ▾

Input:

- Raw_count_matrix
- Option: Raw_count_matrix + Metadata
- Option: Batch mode (not displayed in the output panel)

Select a raw count matrix file i

Browse... ds1.genes.results.rename.tsv
Upload complete

Select a metadata file to define samples for the following analysis

Browse... metadata.csv
Upload complete

DEG analysis method:

- DESeq2
- EBSeq
- edgeR

FDR method

BH

Species

Homo sapiens

Cut-off conditions:

Fold Change	FDR	Basemean
2	0.05	0

Option: Select a normalized count file i

Browse... No file selected

Input Data Result overview GOI profiling Enrichment analysis

Raw_count_matrix:

Metadata:

Defined_raw_count_matrix:

Select samples:

5H4PB_1 5H4PB_2 5H4PB_3 DMSO_1
DMSO_2

Download defined raw count

Show 10 entries

Search:

ここからカウントデータをダウンロードして、Excelなどで順番を入れ替える

	5H4PB_1	5H4PB_2	5H4PB_3	DMSO_1	DMSO_2
ENSG00000000003	353	411	489.26	469	494
ENSG00000000005	0	0	0	0	0
ENSG00000000419	1182	1206	1508	1294.01	1412.78
ENSG00000000457	270	262	373	384.01	334
ENSG00000000460	404.4	464	467	489.92	526
ENSG00000000938	0	0	0	0	0
ENSG00000000971	19.7	34.17	26.19	55.59	58.02
ENSG00000001036	3	0	3	2	0
ENSG00000001084	13855.45	14752.31	18852	1667	1919
ENSG00000001167	407	473	537	529	495

Showing 1 to 10 of 62,700 entries

Previous 1 2 3 4 5 ... 6,270 Next

RNAseqChef

RNAseqChef Pair-wise DEG 3 conditions DEG Multi DEG Venn diagram Normalized count analysis Enrichment viewer More ▾

Input:

- Raw_count_matrix
- Option: Raw_count_matrix + Metadata
- Option: Batch mode (not displayed in the output panel)

Select a raw count matrix file i

Browse... ds1_count_r.txt Upload complete

DEG analysis method:

- DESeq2
- EBSeq
- edgeR

FDR method

BH

Species

Homo sapiens

Cut-off conditions:

Fold Change	FDR	Basemean
2	0.05	0

Option: Select a normalized count file i

Browse... No file selected

Output plot size setting for pdf (0: default) i

Result overview GOI profiling Enrichment analysis

Raw_count_matrix:

Metadata:

Defined_raw_count_matrix:

Select samples:

DMSO_1 DMSO_2 X5H4PB_1
X5H4PB_2 X5H4PB_3

Download defined raw

Show 10 entries

順番を入れ替えたカウントテーブルを
読み込ませた

	DMSO_1	DMSO_2	X5H4PB_1	X5H4PB_2	X5H4PB_3
ENSG00000002079	6	9	8	22	21
ENSG00000002330	1202	1367	944	1125	1313
ENSG00000002549	574	559	458	555	693
ENSG00000002586	600.5	650.5	714	858	1005
ENSG00000002587	294	323	496	477	586
ENSG00000002726	841	873	143	171	235
ENSG00000002745	21	14	3	5	5
ENSG00000002746	1	0	0	1	0
ENSG00000002822	919.52	942.18	783.39	995.67	1177.94
ENSG00000002834	16245	16510	12378	14647	17536

Download MA-plot

Up: 267 Down: 399 NS

DEG_result: