

# BoxPlotter\_v2 tutorial

- 🏠 Home Directory
- 📁 /project/mzy
- 📁 /projectnb/mzy
- 📁 /restricted/projectnb/mzy
- 📁 /project/wax-arch
- 📁 /projectnb/wax-arch
- 📁 /project/wax-dk
- 📁 /projectnb/wax-dk
- 📁 /project/wax-es
- 📁 /projectnb/wax-es
- 📁 /restricted/project/waxmanlab
- 📁 /restricted/projectnb/waxmanlab

1

2

## New Directory

Directory name

your\_boxplotter\_directory

OK

Cancel

🔍 Open in Terminal ▾

🔄 Refresh

+ New File

📁 New Directory

📶 Upload

⬇ Download

Globus

📄 Copy/Move

🗑 Delete

⬆ / projectnb / wax-es / [Change directory](#)

📄 Copy path

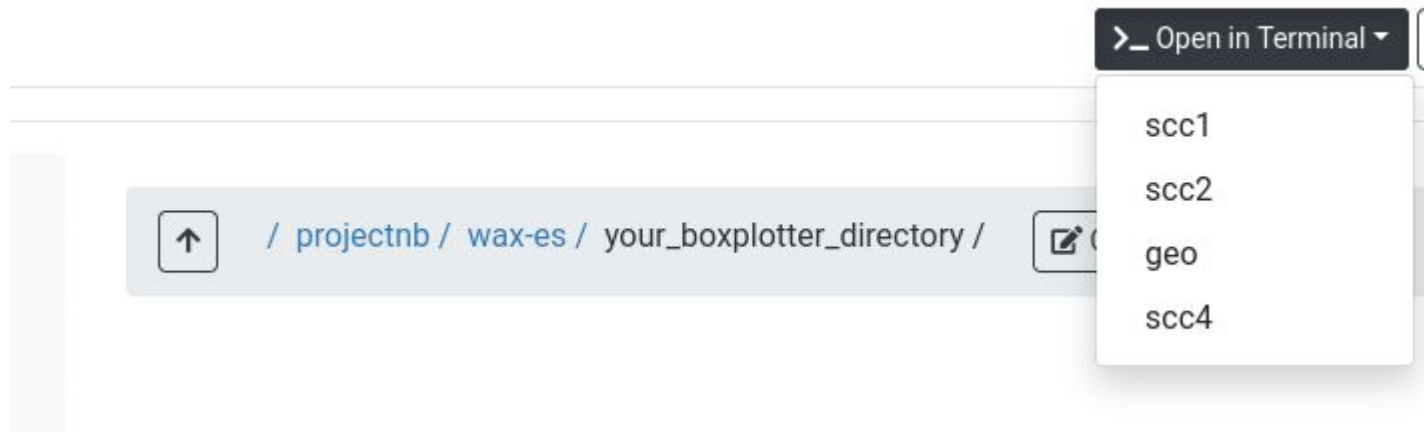
**Find your directory and click on it to open**

☐ Show Owner/Mode ☐ Show Dotfiles Filter:

Showing 44 rows - 0 rows selected

<input type="checkbox"/>	Type ▲	Name	Size	Modified at
<input type="checkbox"/>	📁	00_shinyapp	-	7/8/2025 11:37:37 AM

**Make sure you're in the correct directory and open the Terminal**



**To clone Boxplotter into the current directory, enter the following command and press Enter:**

```
git clone /projectnb/wax-es/WAXMANLAB_SOFT/BoxPlotter_v2 .
```

**After cloning the directory you can click to “My interactive sessions” on the top of the page**

SCC OnDemand Files ▾ Quotas ▾ Login Nodes ▾ Interactive Apps ▾  My Interactive Sessions 

## Interactive Apps

## Desktops

Desktop

MATLAB

Mathematica

QGIS

SAS

STATA

Spyder

VirtualGL Desktop

## Servers

Jupyter Notebook

MATLAB Server

RStudio Server

Shiny App Server

TensorBoard Server

VS Code Server

Webserver

## RStudio Server

This app will launch an RStudio server on a compute node.

Rstudio Version

2024.12.0+467

R Version

4.4.3

Additional modules to load (space separated, optional)

Select Modules

Pre-Launch Command (optional)

Number of hours

12

Number of cores

1

Number of gpus

0

Project

wax-dk

Extra qsub options

☐ I would like to receive an email when the session starts

Launch

## Interactive Apps

### Desktops

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MATLAB

Mathematica

QGIS

SAS

STATA

Spyder

VirtualGL Desktop

### Servers

Jupyter Notebook

MATLAB Server

RStudio Server

Shiny App Server

## RStudio Server (349871)

Host: >\_scc-wi4

Created at: 2025-06-11 09:16:54 EDT

Time Remaining: 11 hours and 59 minutes

Session ID: 4eed9c37-ecb2-4287-b0cc-914a422436c3

Rstudio Version: 2024.12.0+467

R Version: R/4.4.3 texlive/2023 pandoc/2.5

Additional modules to load (space separated, optional):

Pre-Launch Command (optional):

Number of hours: 12

Number of cores: 1

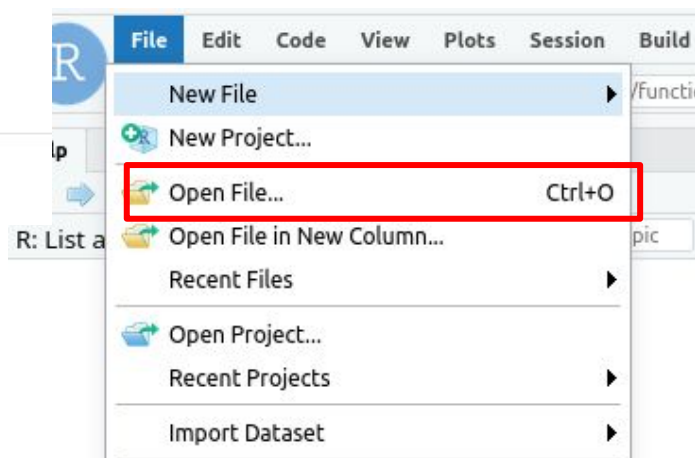
Number of gpus: 0

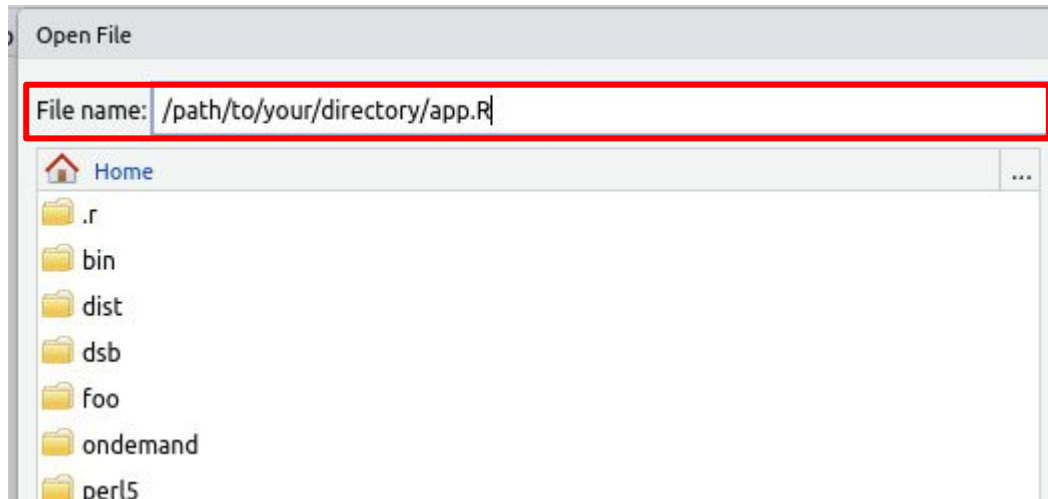
GPU compute capability: 3.5

Project: wax-dk

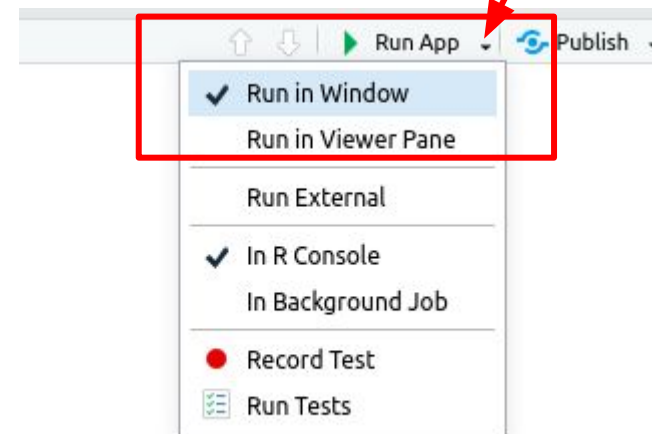
Extra qsub options:

 Connect to RStudio Server

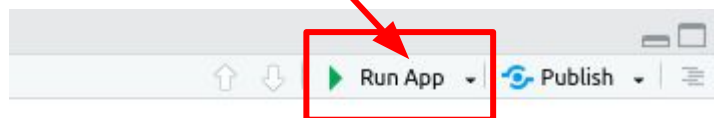




Click to small arrow to open dialog  
and select "Run in Window"



Click "Run App" to start shiny app



## BoxPlotter for ChIPseq Regions-of-Interest

### Upload Configuration File


Browse...

Choose XLSX file

Select an Excel file (.xlsx or .xls) to use as configuration for the boxplotter job.

Download the example file below to see the required format.

 Download Example File

 Download Instructions

# BoxPlotter for ChIPseq Regions-of-Interest

## Upload Configuration File

Browse...


example\_config.xlsx

Upload complete

Select an Excel file (.xlsx or .xls) to use as configuration for the boxplotter job.

Download the example file below to see the required format.

 Download Example Configuration File

 Download Instructions

### Uploaded File Information:

Filename: example\_config.xlsx

File size: 38.55 KB

File type: xlsx

**File name should not contain any spaces or special characters**

 Submit Boxplotter Job



✓ Job Submitted Successfully!

Job ID: 2578747

Configuration file: example\_config\_20260106\_133607.xlsx

Command executed: `qsub boxplotter.qsub /projectnb/wax-dk/max/src/rprojects/boxplotter_v2/uploaded_configs/example_config_20260106_133607.xlsx`

You can monitor the job status using:

`qstat -j 2578747`

Your results will be emailed to you as soon as the job finishes. Feel free to close this tab; your job will continue running in the background.

Close

After a successful submission, you can close this pop-up and the window behind it. All results will be delivered to your BU email.

▶ Submit Boxplotter Job

### Job Status

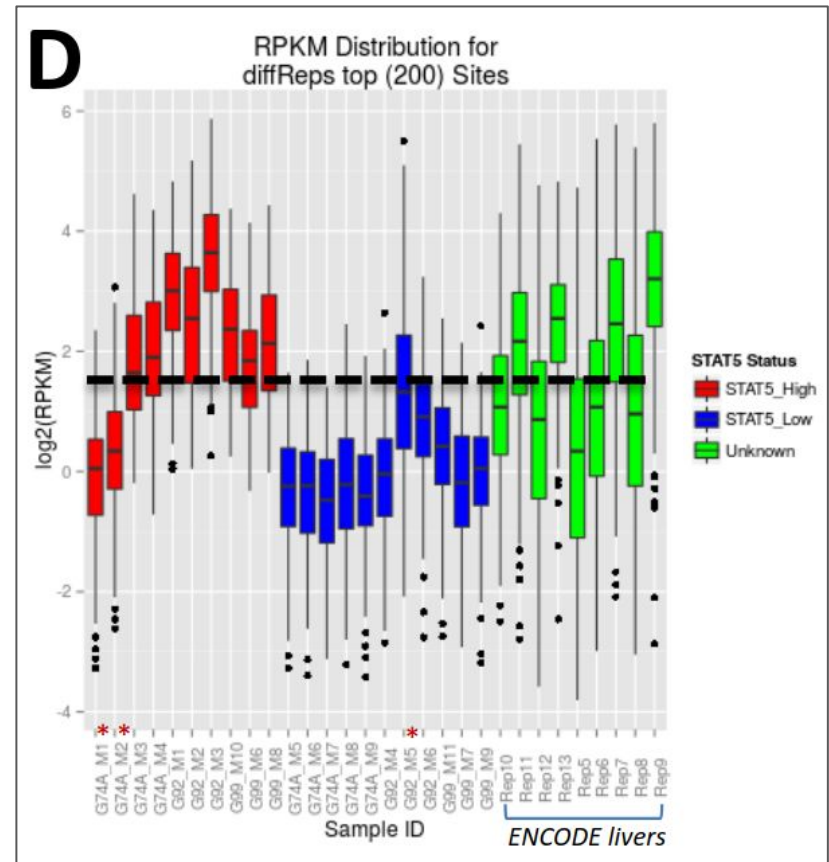
Job ID: 2578747  
Status: Submitted  
Configuration file: example\_config\_20260106\_133607.xlsx  
Submission time: 2026-01-06 13:36:09.416764

To check job status, run: `qstat -j 2578747`  
Feel free to close this tab; your job will continue running in the background.

Example of outputs and brief  
method explanation

## BoxPlotter for ChIPseq Regions-of-Interest

Based on the idea in the right picture, we decided to create a more general tool that would allow us to specify sets of regions and compare groups of different samples with each other.



DNase-seq data from 9 male livers (ENCODE) were compared to the STAT5-high/low profiles. **4 livers** showed chromatin accessibility patterns similar to **STAT5-high** livers, while **5 livers** resembled **STAT5-low** livers. These patterns were visualized using read count distributions across the top differential sites.

## Algorithm:

1. Calculate FRiP (Fraction of Reads in Peaks)
2. Extract fragment counts from BAM files over target regions for selected samples.
3. Normalize fragment counts using FRiP, generate aggregated and group-wise comparison plots, and compute statistics for group comparisons.

## FRiP Normalization:

1. Call MACS2 peaks per sample
2. Merge to union peak set
3. Count fragments per sample in union
4. Normalize to sample-average fragment count

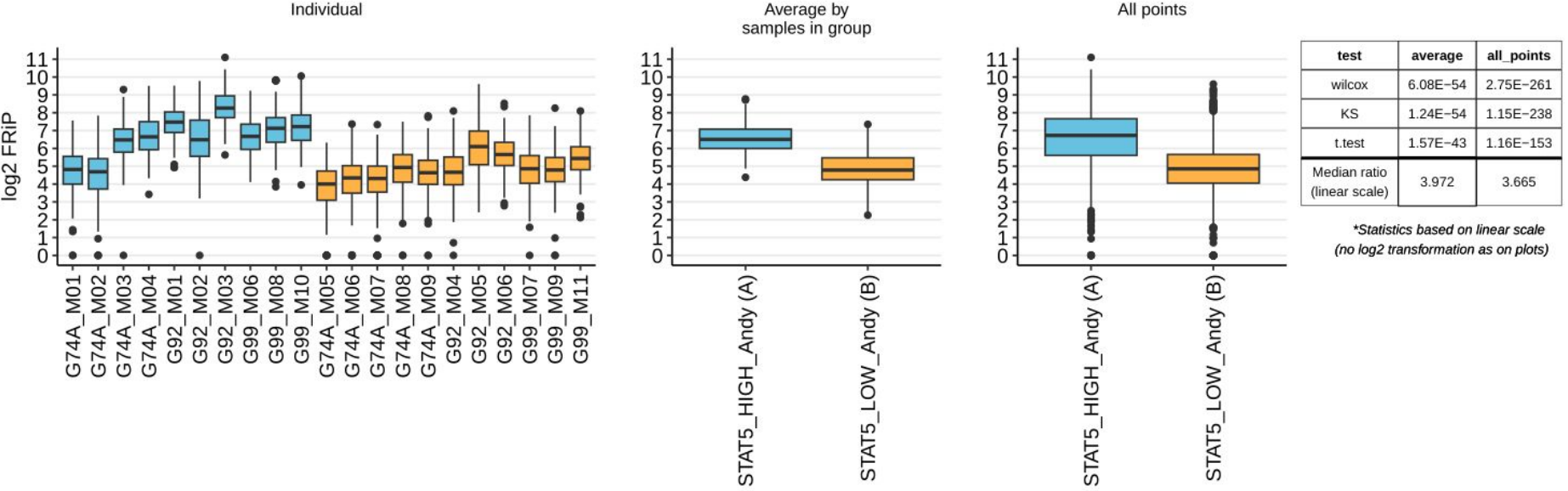
### Data transformation during normalization

chr	start	end	width	G241_M01 (Male_2wk_ATAC)			
				RAW COUNTS	RAW_AFTER_WIDTH_NORM	AFTER_FRIP_NORM	FINAL_LOG2_AFTER_RIPPM_NORM
chr1	40293477	40294208	732	706	964.481	395.799	8.629
chr1	40299557	40299948	392	257	655.612	269.047	8.072
chr1	41608251	41608848	598	81	135.452	55.586	5.797
chr1	55136533	55136946	414	384	927.536	380.637	8.572
chr1	82154931	82155388	458	234	510.917	209.667	7.712
chr1	83896719	83897207	489	16	32.720	13.427	3.747
chr1	129796083	129796418	336	158	470.238	192.974	7.592
chr1	133837634	133838008	375	182	485.333	199.169	7.638
chr1	166251542	166251959	418	172	411.483	168.862	7.400
chr1	174860030	174860572	543	173	318.600	130.746	7.031
chr1	176420085	176420403	319	40	125.392	51.458	5.685
chr1	188149410	188149823	414	54	130.435	53.527	5.742
chr10	5728314	5728809	496	147	296.371	121.623	6.926

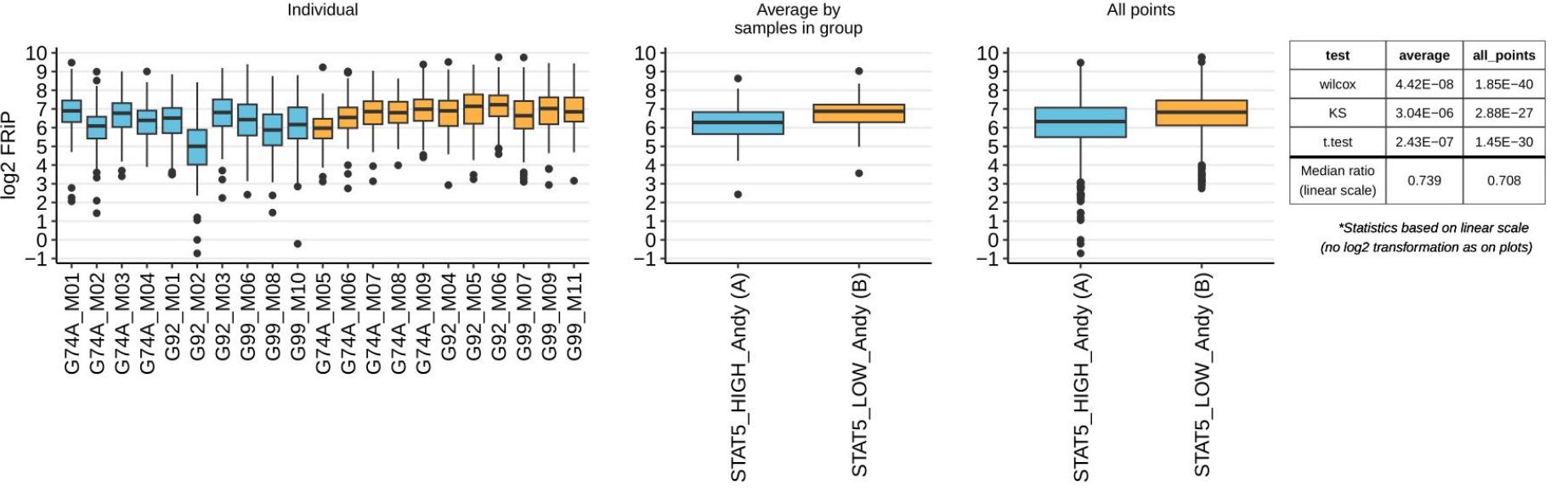
$1000 * \text{RAW\_COUNTS} / \text{WIDTH}$

$\text{RAW\_AFTER\_WIDTH\_NORM} / \text{FRiP}$

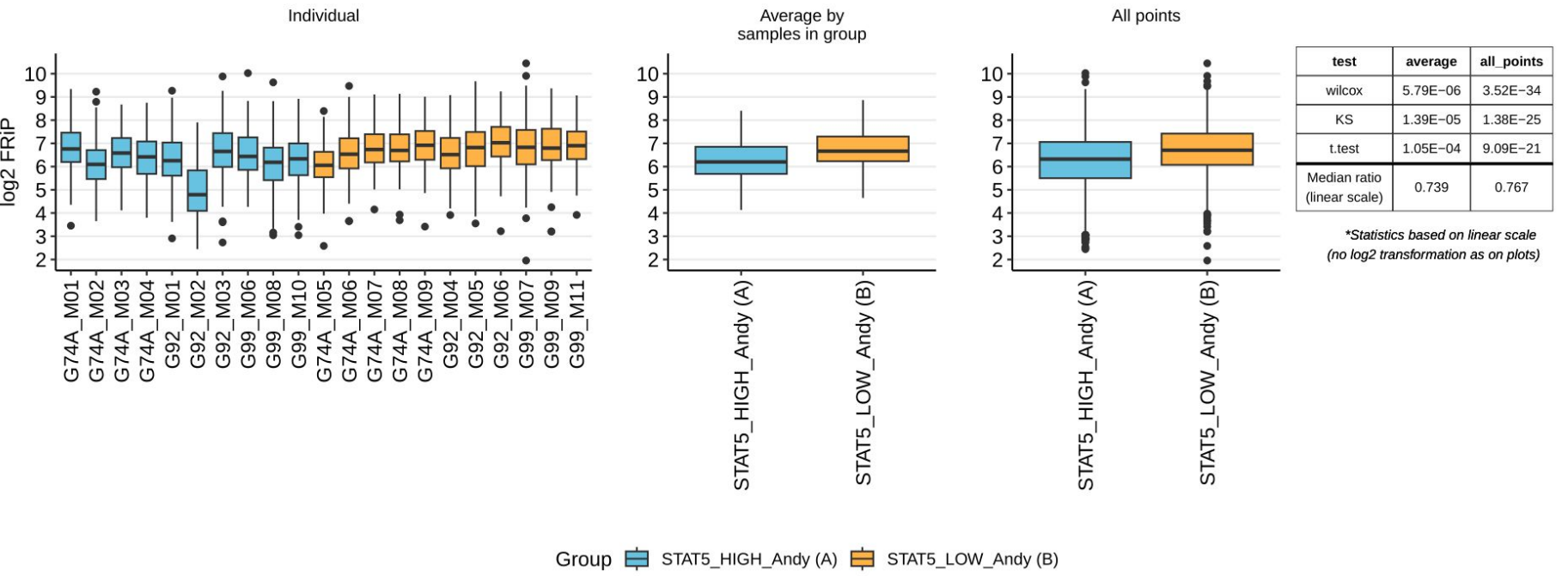
1. (A vs B) (A\_MB\_Dynamic\_1 (n=834)\_top200)



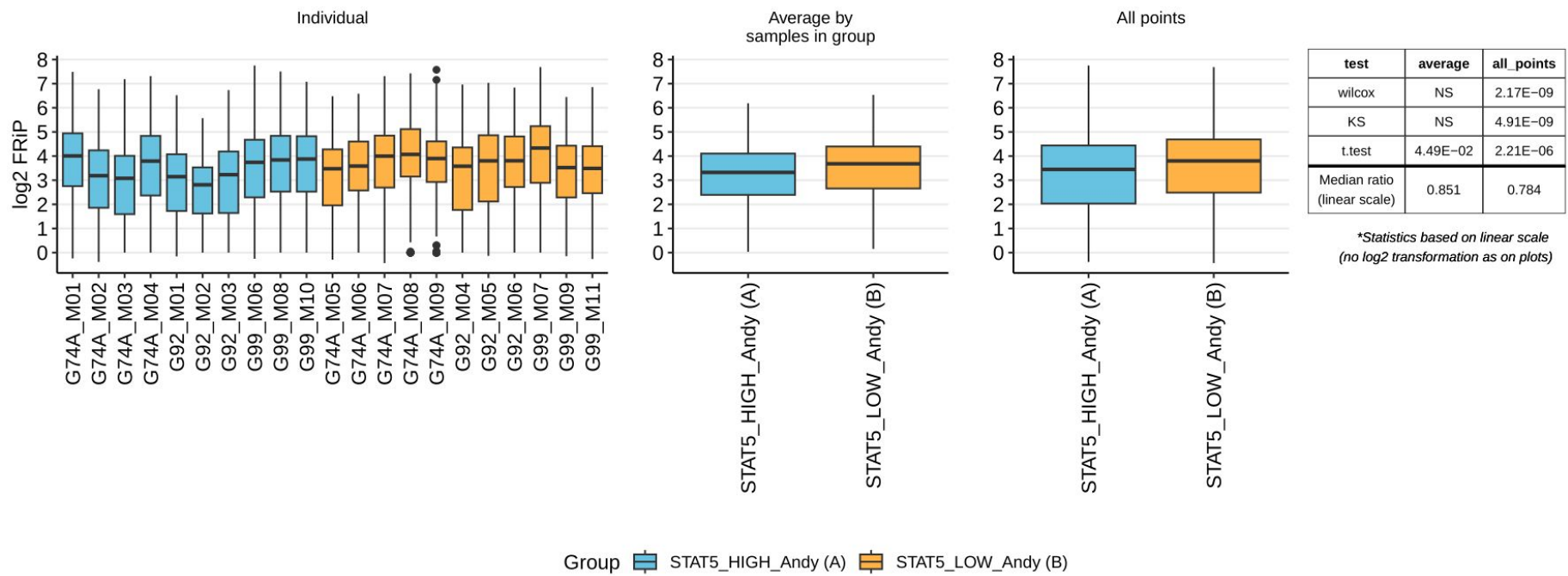
1. (A vs B) (B\_MB\_Static\_Group 1 (n=172))



1. (A vs B) (C\_MB Static\_Group 2\_(n=186))

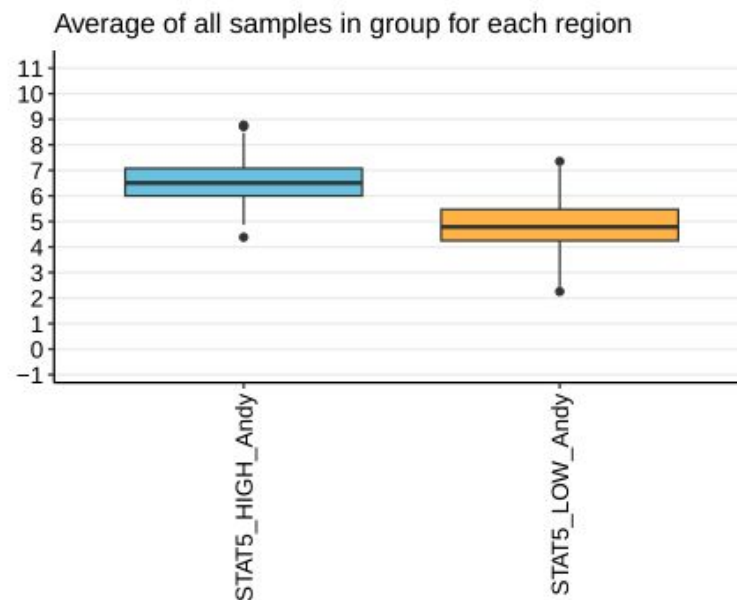
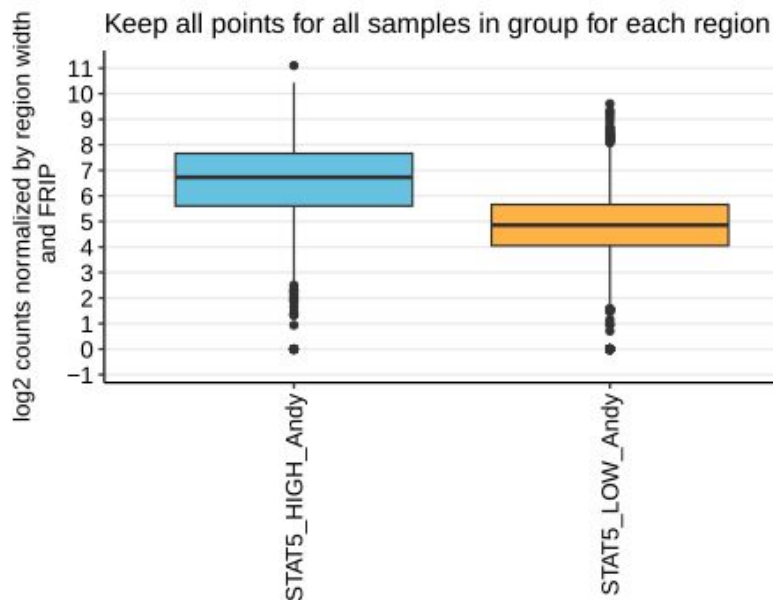


1. (A vs B) (D\_FB\_Static\_(top n=706)\_top200)





A\_MB\_Dynamic\_1 (n=834)\_top200

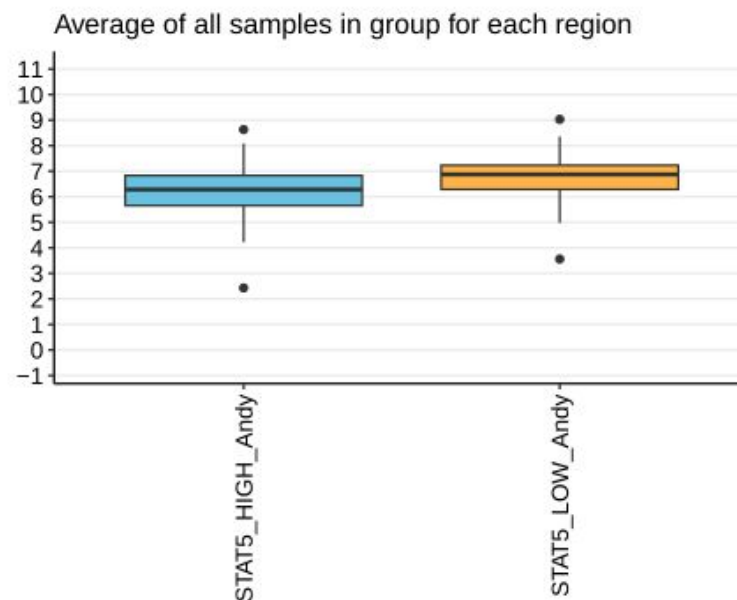
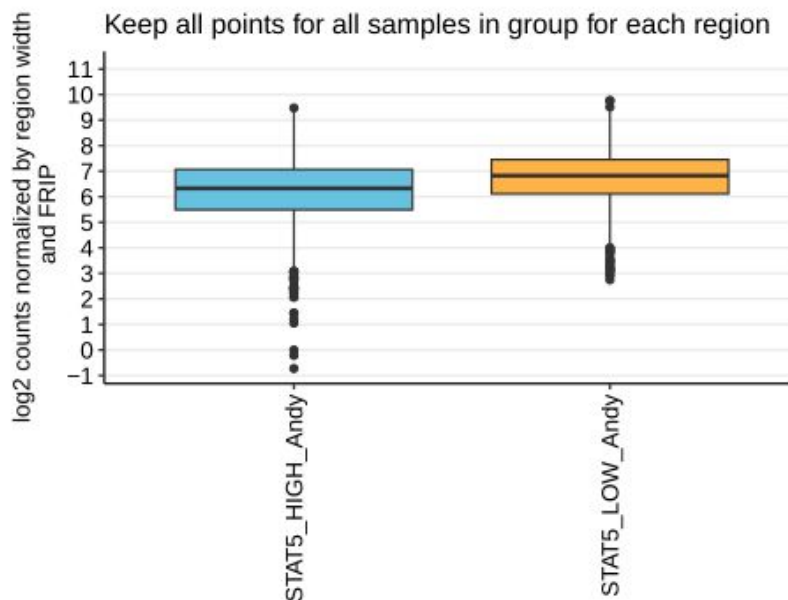


Group name

STAT5\_HIGH\_Andy

STAT5\_LOW\_Andy

B\_MB\_Static\_Group 1 (n=172)



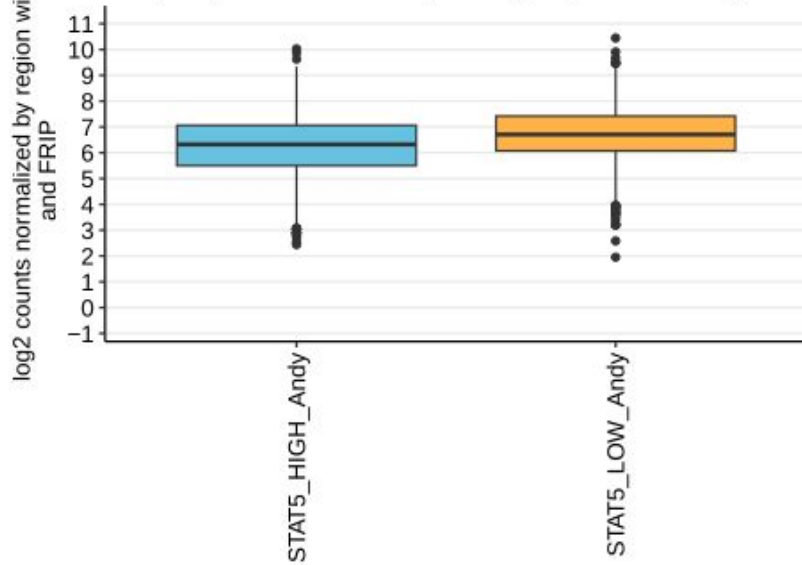
Group name

STAT5\_HIGH\_Andy

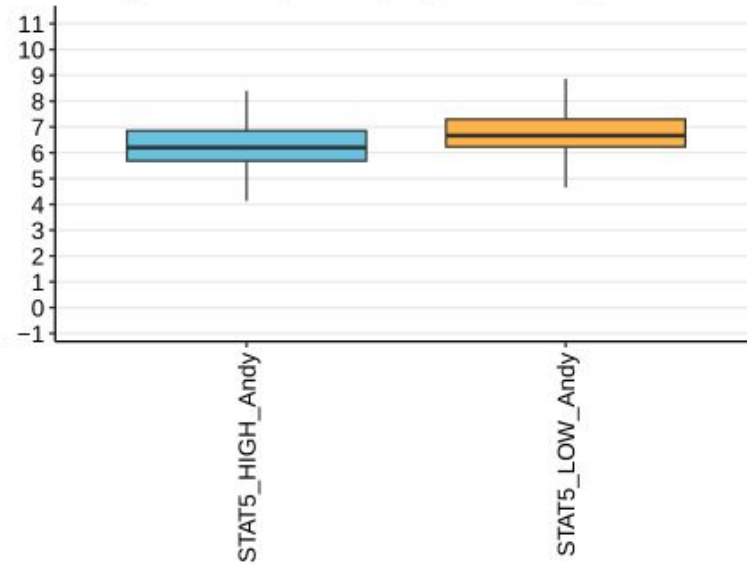
STAT5\_LOW\_Andy

C\_MB Static\_Group 2\_(n=186)

Keep all points for all samples in group for each region



Average of all samples in group for each region

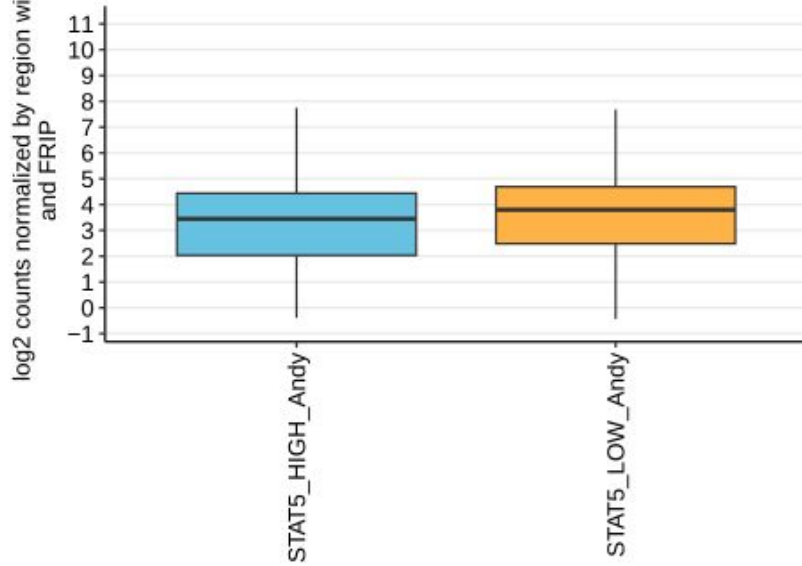


Group name

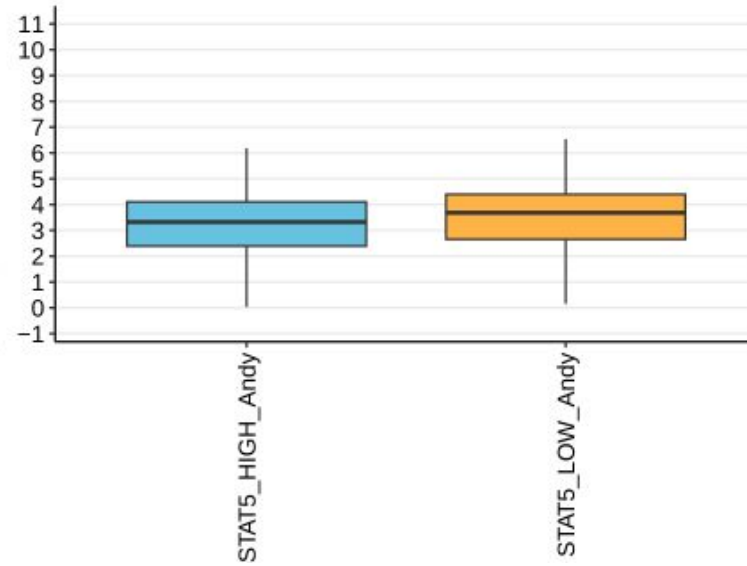
STAT5\_HIGH\_Andy  
STAT5\_LOW\_Andy

D\_FB Static\_(top n=706)\_top200

Keep all points for all samples in group for each region



Average of all samples in group for each region

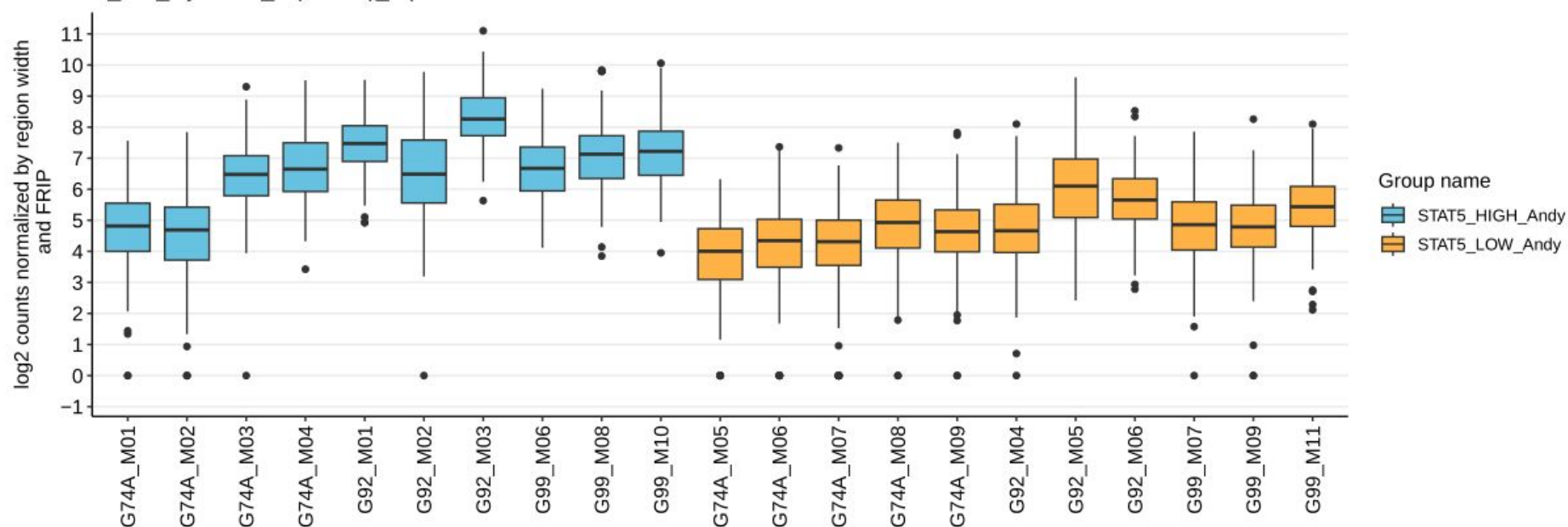


Group name

STAT5\_HIGH\_Andy  
STAT5\_LOW\_Andy



A\_MB\_Dynamic\_1 (n=834)\_top200



B\_MB\_Static\_Group 1 (n=172)

