

Introduction to Bioinformatics Summer Series



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BTEP Bioinformatics Introduction Bioinformatics software Bioinformatics education Unix Biowulf
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Course Overview

The BTEP Bioinformatics Summer Series is five classes that introduce novices and new NIH scientists the essentials for getting started with bioinformatics analysis of next generation sequencing (NGS) data. Topics include a broad survey of bioinformatics resources available to all scientists at NIH, an overview of the NIH High Performance Computing System (Biowulf), a discussion and comparison between programming languages R and Python, and tips for making data FAIR and data analyses reproducible. These classes are open to NIH audience only.

- August 7, 2025 (Thursday, 1 PM – 2 PM):
 - Introduction to Bioinformatics Resources will inform participants of software (commercial and open-source), self-learning tools, and resources for bioinformatics and data science.
- August 14, 2025 (Thursday, 1 PM – 2 PM):
 - Introduction to Unix and Biowulf will serve as a crash course for using the NIH Unix-based High Performance Computing system (Biowulf). Participants will learn to navigate through directories, work with files, and use bioinformatics applications that are installed on the system.
- August 21, 2025 (Thursday, 1 PM – 2 PM):
 - Overview of R and Python will discuss the benefits that these two popular programming languages can bring to a bioinformatics project. After this session, participants should be able to decide which language to use for a given data analysis.
- September 4, 2025 (Thursday, 1 PM – 2 PM):
 - Managing Data Analysis Projects using Jupyter Lab. This class will introduce participants to Jupyter Lab, a tool for maintaining data, code, output, and description of analyses all in one place, which facilitates transparency and reproducibility of data analysis.

Course Expectations / Learning Objectives

This course will make participants aware of available bioinformatics training resources and software at NIH. Participants will walk away from these classes with the knowledge and confidence needed to pursue bioinformatics and continual self learning. In sum, after this course series, participants will:

- Be able to describe available training resources and software available for bioinformatics at NIH.

- Know the rationale and basics of getting started with working on Unix-based high performance computing platforms.
- Be informed of when to use Python or R in a bioinformatics project.
- Understand best practices for managing and organizing data.
- Become familiar with rationale and tools used to make data analysis reproducible.

Required Course Materials

Participants will not need to have bioinformatics experience to attend and there are no required course material. However, the following may help with following along.

- **Biowulf account** (<https://hpc.nih.gov/docs/accounts.html>). This would be helpful for participants to follow along in the Unix and Biowulf class. Biowulf will also provide a limited number (40) of student/temporary accounts for those who would like to follow along. Student/temporary accounts are meant for use during teaching activities and must be approved and supplied by Biowulf.
- Have R, Python, and/or Jupyter Lab installed on participant's government furnished computer. Reach out to institutional computing help desk to request installation of software. NCI CCR affiliates can submit a ticket with service.cancer.gov for software installation.
- To install R, see <https://cran.r-project.org/> (<https://cran.r-project.org/>)
- To install Python, see <https://www.python.org/downloads/> (<https://www.python.org/downloads/>)
- To install Jupyter Lab, see <https://jupyter.org/install> (<https://jupyter.org/install>)

Bioinformatics Resources at NIH

Introduction to Bioinformatics Resources

Introduction to Unix and Biowulf

Unix for Bioinformatics Beginners Slides

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Unix for Bioinformatics Beginners

Joe Wu, PhD (BTEP)

August 14, 2025

- `ssh` (connect to remote computer such as a high performance computing cluster)
- `pwd` (print working directory)
- `cd` (change directory)
- `ls` (list directory content)
- `mkdir` (make a directory)
- `touch` (creates an empty file)
- `nano` (basic editor for editing text files)
- `cp` (make a copy of files or folders)
- `mv` (rename files/folder or move files or folders to different location)
- `rm` (to remove files or folders)
- `cat` (print file content to screen)
- `less` (page through file content)
- `column` (display tabular data nicely aligned on screen)
- `wc` (word count, line count and character count)
- `grep` (pattern search)
- `sinteractive` (request compute and time resources on Biowulf's compute node to perform interactive data analysis and file transfers)
- `sbatch` (used to submit analysis Biowulf rather than working interactively, step-by-step)
- `module` (find, load, and unload applications installed on high performance computing clusters)
- `man` (view manual for a command)

Tip

All Unix commands follow the syntax of `command option(s) input`. Think of the `command` as a verb in natural language. The `input` is what users would like the command to act on and `option(s)` changes the default way in which a command runs.

Connecting to Remote Computer

As bioinformatics often deal with dataset that are too large to be analyzed using compute resources on a personal computer, a motive for learning Unix command line is to enable scientists to perform bioinformatics analyses on high performance computing systems such as

Biowulf at NIH. To connect to a remote computer, the `ssh` command construct below can be used and the breakdown is as follows.

- `ssh`: The command for connecting to a remote computer.
- `username`: The user name that is used to sign onto a remote computer such as high performance computing system. For Biowulf, `username` will be replaced by the user's NIH user name. Username is followed by `@` (ie. the "at" symbol).
- `remote`: This is the name of the remote computer. For Biowulf this would be `biowulf.nih.gov`.

```
ssh username@remote.computer
```

The command above could be annunciated as `ssh username at remote.computer`.

To sign onto Biowulf, the NIH high performance computing system, use the following. Again, replace `username` with the user's NIH user name.

```
ssh username@biowulf.nih.gov
```

Next, enter the user specific password for the remote computer. Note that nothing shows up when the password is being type, but keep typing and hit enter when ready to sign on.

The Command Prompt

In Unix, the command prompt is where users issue commands to interact with the computer. For example, upon connecting to Biowulf, users will see the prompt shown below. Replace `username` with the user's NIH user name. The prompt below tells users that they are connected to Biowulf and are currently in the `home` directory (denoted by `~`).

```
[username@biowulf ~]$
```

Warning

The prompt will look different depending on the computer system. It can also be customized, so do not panic if a prompt does not look exactly like that above.

Knowledge Check 1

Enter passcode `woc1gu` to answer the multiple choice question in the Slido poll. ||

Print the Working Directory

Terminology

The working directory is the folder in a computer system in which a user is currently in.

It is a good idea to know which directory a user is currently in as data analysis progresses. To check, use the following.

```
pwd
```

For instance, upon signing on to Biowulf users will land in the home directory (also denoted by ~). The `pwd` command will give the directory path below (replace username with the user's specific user name).

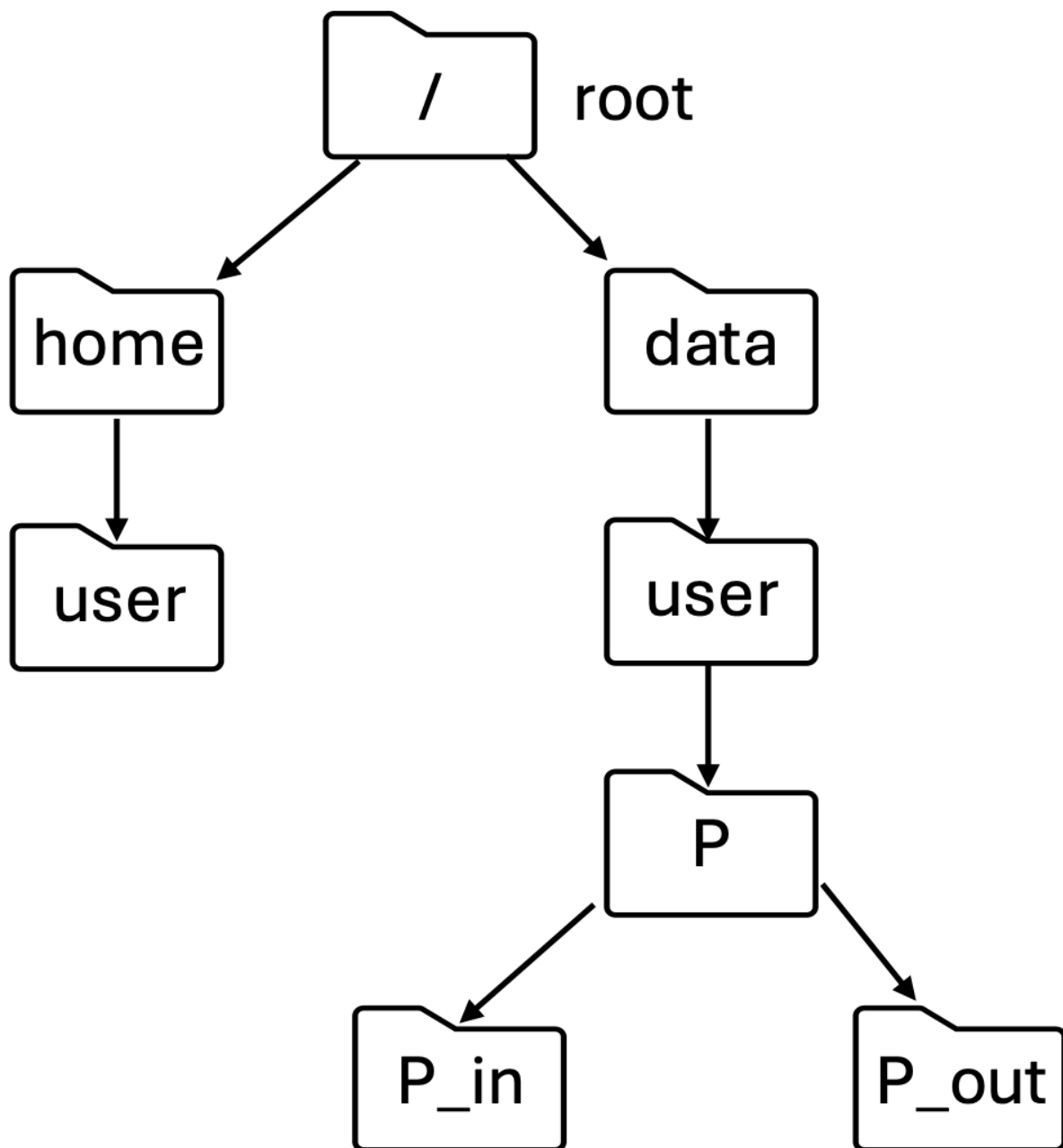
```
/home/username
```

Note

In Unix, a directory path indicates where in the file system hierarchy a user is. Directory paths that start with `/` are known as absolute. Each part of the directory path is separated by `/` and followed by the name of the folder in the file system hierarchy.

The figure below shows a basic and typical hierarchy of the Unix and Unix-based high performance computing systems. At the upper most level there is the root directory, which is denoted by `/`. Branching of from `/` there are a `home` and `data` folders. The `home` directory has limited space so users use the `data` folder for analysis. In the example below, the `data` folder contains hypothetical project directory `P`, which in turn has folders that store input (`P_in`) and output (`P_out`). Directory paths that do not start from `/` are known as relative (ie. `P/P_in`).

Example File Hierarchy



Change Directory

Note

The user's home directory on Biowulf is not the place to store analysis input and output as it only has 16gb of storage space and quota cannot be increased. The user's data directory can be used for this as storage quota can be increased at the request of the user.

To change directory use the `cd` command follow by the directory to change into. Upon signing onto Biowulf, users should change into their `data` directory to performing analyses. To do this use the following. Replace `username` with the user's specific user name.

```
cd /data/username
```

The prompt will contain the user's NIH user name rather than `~` if the directory change to `/data/username` is successful.

```
[username@biowulf username]$
```

Knowledge Check 2

Use the passcode `g1apic` to answer the following question on Slido.

I

The `pwd` command can be used to check whether the directory change is successful.

```
pwd
```

If the directory change is successful, the following path will be shown, again replace `username` with the user's NIH user name.

```
/data/username
```

To go back to the user's home directory use `cd`, `cd ~`, or `cd /home/username`. Use `cd ..` to go back one directory. To go back two directories, use `cd ../../`. To go back three directories use `cd ../../../` and so on.

Grab Some Examples Data

If the participants choose to follow along using either a personal Biowulf or one of the student accounts, please stay in the `/data/username` folder (remember to replace `username` with the participants own Biowulf log-in ID).

Spoiler

Copying of files and folders will be covered later in this tutorial but because the instructor wants the audience to copy over example data to their Biowulf `/data/username` directory, a glimpse of it will be shown here.

There is a folder called `unix_demonstration` in `/data/classes/BTEP`. Use the `cp` command construct below to copy into the user's Biowulf `/data` directory. In command construct below, `cp` is used copy content in Unix. The option `-r` tells it copy a folder and all of its contents. The arguments are the file or folder to be copied and the name of the copy or destination in which to place the copy. In the example below, a copy of the `unix_demonstration` in `/data/classes/BTEP` needs to be made, so the first argument would be `/data/classes/BTEP/unix_demonstration`. The second argument for the `cp` construct below is the destination to place the copy, which is here or `.` in the user's Biowulf `/data` directory.

```
cp -r /data/classes/BTEP/unix_demonstration .
```

After the `cp` command finishes, users will be automatically returned to the prompt. Make sure that the `unix_demonstration` is actually there by doing the following.

```
ls
```

Knowledge Check 3

Use the passcode `ulsgtd` to answer the question in the Slido poll.



Listing Directory Content

Stay in the `/data/username/unix_demonstration` folder for these exercises.

To view the files and subfolder within a directory, the `ls` command can be used. For instance, `ls` will retrieve the following items in the `unix_demonstration` directory when issued.

```
file.txt example_fastq.fq example_rna_sequencing_counts.csv
```

Unix commands come with options that alter its default behavior. The `-l` option of `ls` gives a detailed view of each item in a directory, line-by-line. For instance, on the left hand column of the table below, lines that start with `-` are files while those starting with `d` are folders. The fifth column list the file or folder size. Note `file.txt` has a file size of 0 bytes since it is empty. Also, `ls -l` by default displays the files size in bytes.

```
-rw-r-----. 1 owner group      0 Jun 15 16:20 file.txt
-rw-r-----. 1 owner group 29108029 Jul  3 13:35 example_fastq.fq
-rw-r-----. 1 owner group 29108029 Jul  3 13:35 example_rna_sequenci
```

Creating a New Directory

Stay in the `/data/username/unix_demonstration` folder for these exercises.

To make a new folder, use the `mkdir` command followed by the name of the folder.

```
mkdir folder
```

Recall

As mentioned previously, if the first column in the `ls -l` results starts with `d` then this indicates a directory, which is what folder should be.

```
ls -l
```

```
-rw-r-----. 1 owner group      0 Jun 16 10:09 file.txt
drwxr-x---. 2 owner group    4096 Jun 16 10:18 folder
-rw-r-----. 1 owner group 29108029 Jul  3 13:35 example_fastq.fq
-rw-r-----. 1 owner group 29108029 Jul  3 13:35 example_rna_sequenci
```

Knowledge Check 4

Use the passcode `myu18x` to answer the following question.

I

Editing Files

Stay in the `/data/username/unix_demonstration` folder for these exercises.

Nano is a basic file editor that is built into Unix and enables editing of plain text files including `txt`, `csv`, `fasta`, `genbank`, `gtf`, and `fastq`. To edit a file using Nano, just use `nano` followed by the file name.

Unix is an operating system, just like Windows or MacOS.
Linux is a variety of Unix, and sometimes the names are used interchangeably.

For instance, to add the text above to file.txt, use:

```
nano file.txt
```

Then copy and paste the text into the editor. Hit control-x and then save to go back to the command prompt.

Note

If a file does not exist, then the nano command will create it as well as open the editor to enable editing. To create a blank file without opening the Nano editor, use the touch command instead.

```
touch bioinformatics.txt
```

```
ls -l
```

```
-rw-r-----. 1 owner group      0 Jun 16 18:13 bioinformatics.txt
-rw-r-----. 1 owner group    135 Jun 16 18:13 file.txt
drwxr-x---. 2 owner group   4096 Jun 16 10:18 folder
-rw-r-----. 1 owner group 29108029 Jul  3 13:35 example_fastq.fq
-rw-r-----. 1 owner group 29108029 Jul  3 13:35 example_rna_sequencing.fq
```

Copying Files and Folders

Stay in the /data/username/unix_demonstration folder for these exercises.

To copy a file use cp followed by the file name and the name of the duplicate.

For instance, to make a copy of bioinformatics.txt called btep_bioinformatics.txt, do:

```
cp bioinformatics.txt btep_bioinformatics.txt
```

```
ls
```

```
bioinformatics.txt  btep_bioinformatics.txt  example_fastq.fq  example_
```

The `cp` command can be used to copy a file into a folder. Just provide the file and the path to the folder in which to copy it. If a new name is desired for the duplicate, then append it to the destination folder path separated by a `/`. For instance, the command below will make a duplicate of `bioinformatics.txt` in folder called `bioinformatics_for_beginners.txt`.

```
cp bioinformatics.txt folder/bioinformatics_for_beginners.txt
```

Tip

To see contents of a folder other than those in the working directory, supply the path to the folder to the `ls` command.

```
ls folder
```

```
bioinformatics_for_beginners.txt
```

To copy a folder include the `-r` option in `cp`. The `-r` option recursively copies everything in a folder. The arguments are the folder to copy and the name of the duplicate folder.

```
cp -r folder bioinformatics_folder
```

The `-1` option of `ls` prints directory content one item per line.

```
ls -1
```

```
bioinformatics_folder
bioinformatics.txt
btep_bioinformatics.txt
example_fastq.fq
example_rna_sequencing_counts.csv
file.txt
folder
```

```
ls bioinformatics_folder
```

```
bioinformatics_for_beginners.txt
```

Renaming Files and Folders

Stay in the `/data/username/unix_demonstration` folder for these exercises.

The `mv` command can be used to rename files and folders.

To rename a file, use the `mv` command then provide the name of the file to rename and the new name of the file.

```
mv btep_bioinformatics.txt bioinformatics_for_noobies.txt
```

```
ls -l
```

```
bioinformatics_folder
bioinformatics_for_noobies.txt
bioinformatics.txt
example_fastq.fq
example_rna_sequencing_counts.csv
file.txt
folder
```

To rename a folder, use the `mv` command and then provide the name of the folder to rename and the new name of the folder.

```
mv folder project_folder
```

```
ls -l
```

```
bioinformatics_folder
bioinformatics_for_noobies.txt
bioinformatics.txt
example_fastq.fq
example_rna_sequencing_counts.csv
file.txt
project_folder
```

Moving Files and Folders

Stay in the `/data/username/unix_demonstration` folder for these exercises.

To move a file from one folder to another, the `mv` command can be used. The arguments in this application of the `mv` command is the file to be moved and the name of the folder in which the file will be moved to.

```
mv bioinformatics.txt bioinformatics_folder
```

```
ls bioinformatics_folder
```

```
bioinformatics_for_beginners.txt  bioinformatics.txt
```

Tip

`mv` can also move folders. Just supply the name of the folder to be moved as the first argument and the path of the destination folder.

Deleting Files and Folders

Stay in the `/data/username/unix_demonstration` folder for these exercises.

To delete a file use the `rm` command followed by the file name.

For instance, to delete `bioinformatics_for_noobies.txt` do:

```
rm bioinformatics_for_noobies.txt
```

Warning

There is no trash can or recycling bin in Unix. Once a file is deleted, it cannot be recovered. Use the `-i` option with `rm` to confirm deletion.

```
rm -i bioinformatics_for_noobies.txt
```

Type `n` for no and `y` for yes (to delete).

```
rm: remove regular empty file 'bioinformatics_for_noobies.txt'? n
```

Empty folders can be deleted using `rmdir`. On the other hand, folders with content can be removed using `rm -r`, where the `-r` option tells `rm` to delete the folder and recursively delete everything inside that folder.

```
rm -r -i project_folder
```

The command above will ask if the user wants to delete the `project_folder` and everything in it. Type `y` to confirm deletion. Users will be asked to confirm the deletion of each item in the folder.

```
rm: descend into directory 'project_folder'? y
rm: remove regular empty file 'project_folder/bioinformatics_for_beg'
rm: remove directory 'project_folder'? y
```

```
ls -l
```

```
bioinformatics_folder
bioinformatics_for_noobies.txt
example_fastq.fq
example_rna_sequencing_counts.csv
file.txt
```

Snapshots

If users were to delete something that was not meant to be removed, there is a chance that the item could be recovered from snapshots, which are just static backups of the user's `home` or `data` directories at a certain point in time. See [Biowulf's guide on snapshots \(https://hpc.nih.gov/storage/backups.html\)](https://hpc.nih.gov/storage/backups.html) to learn more.

The absolute path for the `home` directory snapshot is `/home/username/.snapshot` while that for the `data` directory is `/data/username/.snapshot`.

Knowledge Check 5

Use the passcode `tgrgvt` to answer the question in the Slido poll.

I

Viewing File Content

Stay in the `/data/username/unix_demonstration` folder for these exercises.

The `cat` command will print the entire content of a file to the terminal screen.

For instance, to view the content of `file.txt` in the terminal screen do:

```
cat file.txt
```

```
Unix is an operating system, just like Windows or MacOS.  
Linux is a variety of Unix, and sometimes the names are used interchangeably.
```

The `cat` command can also be used to view `fastq` or `fq` files, which contain sequences from high throughput sequencers. For long files that take a while to completely print, hit control-c to exit the `cat` command and return to the prompt.

```
cat example_fastq.fq
```

Tabular data in the form of `csv` files can be displayed by `cat` as well.

```
cat example_rna_sequencing_counts.csv
```

Paging through Files

Rather than printing file content in its entirety to the terminal, users can page through files using `less`.

```
less example_rna_sequencing_counts.csv
```

Users can use the up and down arrow on the keyboard to scroll up/down the file to view content. The up/down arrows enable scrolling line by line. Hit `q` to exit `less` and return to the command prompt.

Printing Tabular Data to Terminal Nicely Aligned

For tabular data in the form of `csv` files, which could contain multiple columns, the columns do not print to the terminal nicely aligned. The `column` command can fix this. Hit `q` to exit `less` and return to the command prompt.

The options and arguments in the column command include:

- Option -t: Creates a table.
- Option -s: Prompts users to provide the column separator (ie. comma for csv files)
- Argument: Name of the file which users would like to view (ie. example_rna_sequencing_counts.csv)
- | is the pipe operator, which sends output from one command as input for another (ie. less to enable paging through the data table)

```
column -t -s ',' example_rna_sequencing_counts.csv | less
```

{{Sdet}}{{Ssum}}column command output{{Esum}}

Geneid	HBR_1.bam	HBR_2.bam	HBR_3.bam	UHR_1.bam	UHR_2.bam
U2	0	0	0	0	0
CU459211.1	0	0	0	0	0
CU104787.1	0	0	0	0	0
BAGE5	0	0	0	0	0
ACTR3BP6	0	0	0	0	0
5_8S_rRNA	0	0	0	0	0
AC137488.1	0	0	0	0	0
AC137488.2	0	0	0	0	0
CU013544.1	0	0	0	0	0
CT867976.1	0	0	0	0	0
CT867977.1	0	0	0	0	0
CT978678.1	0	0	0	0	0
CU459202.1	0	0	0	0	0
AC116618.1	0	0	0	0	0
CU463998.1	0	0	0	0	0
CU463998.3	0	0	0	0	0
CU463998.2	0	0	0	0	0
U6	0	0	0	0	0
LA16c-60D12.1	0	0	0	3	2
LA16c-13E4.3	0	0	0	0	0
LA16c-60D12.2	0	0	0	0	4
ZNF72P	0	0	0	0	1
BNIP3P2	0	0	0	0	2
YME1L1P1	0	0	0	0	0
OR11H1	0	0	0	0	0
LA16c-60G3.6	0	0	0	0	3
ARHGAP42P3	0	0	0	0	2
LA16c-23H5.4	0	0	0	0	1
LA16c-60G3.8	0	0	0	0	2
LA16c-60G3.7	0	0	0	0	0
LA16c-60G3.5	0	0	0	0	0

LA16c-2F2.8	0	0	0	0	3
NEK2P2	0	0	0	0	1
LA16c-2F2.5	0	0	0	0	0
NF1P6	0	0	0	1	4
MED15P7	0	0	0	0	2
POTEH	0	0	1	7	7
POTEH-AS1	0	0	0	0	2
RNU6-816P	0	0	0	0	0
LA16c-3G11.7	0	0	0	2	1
LA16c-83F12.6	0	0	0	3	1
GRAMD4P2	0	0	0	0	1
DUXAP8	10	4	9	250	199
LL22NC03-N64E9.1	0	1	0	16	9
BMS1P22	0	1	3	25	24
LL22NC03-N14H11.1	4	2	0	98	38
NBEAP3	0	0	0	5	3
LA16c-60H5.7	0	0	0	11	6
LA16c-4G1.4	0	0	0	0	0
LA16c-4G1.3	0	0	0	0	3
AC092854.1	0	0	0	0	0
ABCD1P4	0	0	0	0	2
LA16c-17H1.3	0	0	0	0	0
PABPC1P9	0	0	0	0	1
SLC9B1P4	0	0	0	0	1
ACTR3BP2	0	0	0	0	0
CHEK2P4	0	0	0	0	0
KB-67B5.17	0	0	0	0	0
KB-67B5.12	0	0	0	0	0
KCNMB3P1	0	0	0	2	1
CCT8L2	0	0	0	1	2
FABP5P11	0	0	0	0	0
AP000547.1	0	0	0	0	1
TPTEP1	19	23	20	141	94
KB-7G2.9	0	0	1	3	4
SLC25A15P5	0	0	0	2	2
PARP4P3	0	0	0	1	1
ANKRD62P1-PARP4P3	0	1	0	3	3
ANKRD62P1	0	0	0	2	0
KB-7G2.8	0	0	0	0	0
VWFP1	2	2	4	1	2
AC005301.8	0	0	0	1	0
XKR3	0	0	0	3	4
HSFY1P1	0	0	0	0	0
GPM6BP3	0	0	0	0	0
AC007064.22	0	0	0	0	0
ZNF402P	0	0	0	1	1
AC007064.24	1	3	2	3	0

MTND1P17	0	0	0	0	0
AC007064.25	0	0	0	0	0
AC006548.19	0	0	0	0	0
IGKV10R22-5	0	0	0	0	0
IGKV20R22-4	0	0	0	0	0
IGKV20R22-3	0	0	0	0	0
IGKV30R22-2	0	0	0	0	1
IGKV10R22-1	0	0	0	0	0
AC006548.28	1	1	1	4	40
GAB4	0	0	0	0	0
AC006548.26	0	0	0	0	0
VN1R9P	0	0	0	0	0
CECR7	22	27	32	31	27
AC006946.16	7	6	4	3	3
AC006946.17	0	2	2	0	3
IL17RA	58	65	58	95	71
AC006946.12	0	1	1	1	1
CECR6	26	45	32	9	6
AC006946.15	3	3	1	0	2
CECR5	30	44	33	127	82
CECR5-AS1	0	2	2	1	2
CECR1	30	28	32	39	35
AC005300.5	0	0	0	1	0
FAM32B	0	1	0	0	0
CECR3	1	0	1	0	1
CECR9	0	0	0	0	0
RN7SL843P	0	0	0	0	0
CECR2	115	88	119	119	81
AC004019.10	1	5	1	0	1
CLCP1	1	2	0	0	0
DNAJA1P6	0	0	0	0	0
SLC25A18	100	111	74	6	8
AC004019.13	1	2	1	1	2
ATP6V1E1	392	454	391	244	181
BCL2L13	212	284	264	244	166
BID	70	85	84	112	76
MIR3198-1	0	0	0	0	0
LINC00528	1	0	0	1	2
MICAL3	339	429	425	211	145
XXbac-B461K10.4	6	6	9	1	2
MIR648	0	0	6	0	0
XXbac-B476C20.14	2	7	2	2	1
XXbac-B476C20.13	2	9	4	1	2
RHEBP3	1	2	3	0	0
FLJ41941	0	0	0	0	2
XXbac-B476C20.9	3	5	4	2	3
PEX26	135	174	137	205	135

XXbac-B476C20.11	0	0	1	3	0
XXbac-B476C20.10	0	0	0	0	0
ARL2BPP10	0	0	0	0	0
TUBA8	13	13	15	2	2
AC008079.10	55	68	53	14	14
USP18	3	6	2	28	14
AC008079.9	0	0	0	0	0
GGTLC5P	0	0	0	0	0
AC011718.2	1	0	0	0	0
AC011718.3	0	0	0	0	0
PPP1R26P3	0	0	0	0	0
XXbac-B33L19.6	0	0	0	0	0
FAM230A	0	0	0	2	4
XXbac-B33L19.12	0	0	0	0	0
GGTLC3	0	0	0	0	0
Metazoa_SRP	0	0	1	0	2
XXbac-B33L19.15	0	0	0	0	0
TMEM191B	6	1	3	0	2
PI4KAP1	18	11	36	65	33
SCARNA17	0	0	0	0	0
RN7SKP131	0	0	0	0	0
RIMBP3	1	2	0	2	3
XXbac-B33L19.10	0	0	0	0	0
CA15P2	0	0	0	0	0
PPP1R26P2	0	0	0	0	0
PPP1R26P4	0	0	0	0	0
AC008132.15	0	0	0	0	1
GGT3P	0	0	0	0	0
AC008132.14	0	0	0	0	0
E2F6P1	0	0	0	3	0
AC008132.13	0	0	1	1	3
BCRP7	0	0	0	0	0
AC008103.3	0	0	0	0	0
AC008103.4	0	0	0	0	0
DGCR6	73	91	76	24	13
PRODH	102	127	123	44	34
AC007326.1	0	0	0	3	1
AC007326.10	0	1	0	0	3
DGCR5	196	239	201	8	9
AC007326.9	11	9	12	1	0
DGCR9	30	30	27	5	2
AC000095.9	0	0	0	0	0
AC000095.11	9	5	9	0	0
CA15P1	4	3	5	1	2
DGCR2	304	354	314	308	178
Y_RNA	4	2	2	5	2
DGCR11	4	10	13	19	6

AC004461.4	1	1	0	0	2
DGCR12	2	1	7	2	2
AC004471.9	5	4	5	4	3
AC004471.10	1	1	0	0	2
TSSK1A	0	0	0	0	2
DGCR14	46	50	37	77	39
TSSK2	0	0	0	0	0
GSC2	0	0	0	0	0
LINC01311	3	1	3	11	8
SLC25A1	32	50	41	226	138
CLTCL1	33	40	36	102	71
AC000081.2	0	0	1	0	1
SNORA15	0	0	0	0	1
KRT18P62	1	1	0	1	0
HIRA	20	15	10	59	27
C22orf39	64	74	76	100	88
RN7SL168P	0	1	0	4	2
MRPL40	29	36	31	113	70
AC000068.5	5	4	1	6	8
UFD1L	38	58	53	228	148
AC000068.9	0	0	0	0	0
AC000068.10	0	0	0	0	2
CDC45	2	1	0	224	154
CLDN5	60	86	57	2	2
LINC00895	0	0	0	0	0
AC000077.2	0	0	0	0	1
AC000067.1	0	0	0	0	0
SEPT5	481	635	547	145	97
GP1BB	0	0	0	0	0
TBX1	1	0	2	7	9
GNB1L	14	17	8	39	36
AC000089.3	1	0	0	2	1
C22orf29	83	123	95	211	149
TXNRD2	55	52	41	84	68
AC000078.5	2	9	2	8	4
COMT	96	113	87	205	111
MIR4761	0	0	1	1	0
ARVCF	143	157	135	86	35
TANG02	36	47	38	68	48
MIR185	0	0	0	0	0
AC006547.13	7	17	15	13	9
AC006547.15	0	0	0	0	0
DGCR8	80	96	67	238	162
MIR3618	0	0	0	0	0
MIR1306	0	0	0	0	0
AC006547.8	0	0	0	0	0
TRMT2A	42	62	49	164	82

MIR6816	0	0	0	0	0
RANBP1	52	74	70	593	399
SNORA77	0	0	0	0	0
ZDHHC8	95	97	91	114	84
AC006547.14	6	5	4	3	3
XXbac-B444P24.8	0	1	3	0	0
LINC00896	0	3	0	7	4
RTN4R	74	93	84	19	11
MIR1286	1	3	0	0	0
XXbac-B444P24.10	1	1	0	1	4
DGCR6L	47	42	38	96	46
XXbac-B444P24.13	1	2	3	2	1
XXbac-B444P24.14	3	3	3	3	0
XXbac-B33L19.4	0	0	0	1	0
USP41	0	0	0	3	2
ZNF74	38	40	41	110	79
RNU6-225P	0	0	0	0	0
SCARF2	11	7	2	34	23
XXbac-B562F10.12	0	0	0	0	0
KLHL22	63	80	83	81	52
XXbac-B562F10.11	4	8	13	10	5
RNY1P9	0	0	0	0	0
RN7SL812P	0	0	3	1	0
KRT18P5	4	3	1	4	2
AC007731.1	0	0	0	0	0
MED15	94	110	87	258	156
AC007050.17	0	0	0	3	2
AC007050.18	0	0	1	0	0
SMPD4P1	2	4	2	1	3
IGLL4P	0	0	0	0	1
SLC9A3P2	0	0	0	0	0
AC007050.1	0	0	0	0	0
ABHD17AP4	0	1	3	0	2
POM121L4P	0	0	0	0	1
BCRP5	0	0	0	0	0
TMEM191A	5	7	5	0	4
PI4KA	1102	1211	1079	433	343
SERPIND1	13	11	8	158	109
SNAP29	33	48	44	114	82
AC007308.7	0	0	0	0	0
CRKL	343	423	367	758	482
XXbac-B135H6.15	5	3	4	1	6
AIFM3	85	82	100	7	13
LZTR1	140	179	126	297	188
XXbac-B135H6.18	4	5	1	1	2
THAP7	36	56	39	95	77
THAP7-AS1	4	7	6	9	2

TUBA3FP	2	1	2	6	6
P2RX6	35	33	31	23	19
SLC7A4	19	25	14	9	4
AC002472.11	0	0	1	0	0
MIR649	0	0	0	0	0
P2RX6P	5	2	2	0	1
LRRC74B	0	2	2	1	1
TUBA3GP	0	0	0	0	0
BCRP2	1	0	0	0	1
KB-1592A4.15	0	0	0	0	0
POM121L7	1	0	1	0	0
E2F6P2	0	1	0	0	0
FAM230B	0	0	0	0	1
KB-1592A4.14	0	0	0	0	0
GGT2	0	0	1	3	2
E2F6P3	0	0	0	0	0
POM121L8P	0	0	0	0	0
BCRP6	0	0	0	0	0
KB-1183D5.13	0	0	0	0	0
KB-1183D5.14	0	0	0	0	0
PPP1R26P5	0	0	0	0	1
KB-1183D5.18	0	0	0	0	0
KB-1183D5.16	0	0	0	0	0
RIMBP3B	0	1	0	0	2
RN7SKP63	0	0	0	0	0
HIC2	29	25	28	209	106
TMEM191C	1	1	6	1	5
PI4KAP2	28	26	20	96	60
RN7SKP221	0	0	0	0	0
RIMBP3C	0	0	0	0	1
UBE2L3	207	241	198	470	310
YDJC	18	28	24	155	83
CCDC116	2	0	1	5	3
KB-1440D3.14	0	0	0	2	1
SDF2L1	5	14	3	51	34
PPIL2	60	65	60	243	146
MIR301B	0	0	0	0	0
MIR130B	0	0	0	0	0
KB-1440D3.13	0	0	0	4	5
YPEL1	25	45	31	17	9
RN7SL280P	1	0	1	1	1
MAPK1	741	955	901	840	502
RNA5SP493	0	0	1	3	4
KB-1027C11.4	0	1	1	1	0
PPM1F	80	106	108	217	140
LL22NC03-86G7.1	26	50	28	69	74
TOP3B	2	0	1	12	10

PRAMENP	0	0	0	0	0
IGLVI-70	0	0	0	0	1
IGLV4-69	0	0	0	0	0
IGLVI-68	0	0	0	0	0
LL22NC03-23C6.13	0	0	0	0	1
LL22NC03-23C6.12	0	0	0	0	1
IGLV10-67	0	0	0	0	0
LL22NC03-23C6.15	0	0	0	0	0
IGLVIV-66-1	0	0	0	0	0
IGLVV-66	0	0	0	0	0
IGLVIV-65	0	0	0	0	0
IGLVIV-64	0	0	0	0	0
IGLVI-63	0	0	0	0	1
IGLV1-62	0	0	0	0	2
LL22NC03-88E1.18	0	0	0	0	0
IGLV8-61	0	0	0	0	0
LL22NC03-88E1.17	0	0	0	0	0
ABHD17AP5	0	0	0	0	0
LL22NC03-30E12.10	0	0	0	0	0
LL22NC03-30E12.11	0	0	0	0	0
IGLV4-60	0	0	0	0	0
LL22NC03-30E12.13	0	0	0	0	0
SOC52P2	0	0	0	0	1
IGLVIV-59	0	0	0	0	0
IGLVV-58	0	0	0	0	0
BMP6P1	0	0	0	0	0
IGLV6-57	0	0	0	1	0
IGLVI-56	0	0	0	0	0
IGLV11-55	0	0	0	0	0
IGLV10-54	0	0	0	0	0
IGLVIV-53	0	0	0	0	1
TOP3BP1	0	0	0	1	0
LL22NC03-123E1.5	0	0	0	0	1
VPREB1	0	0	0	1	0
CH17-264L24.1	12	12	18	16	15
LL22NC03-2H8.5	2	0	1	2	6
LL22NC03-2H8.4	0	0	0	0	0
LL22NC03-80A10.6	9	11	3	10	3
BMS1P20	3	1	7	6	1
IGLV5-52	1	2	3	0	0
IGLV1-51	1	4	1	0	1
IGLV1-50	1	3	0	0	0
LL22NC03-80A10.11	0	0	0	0	1
IGLV9-49	0	0	0	0	1
LL22NC03-75A1.9	0	0	0	0	0
IGLV5-48	0	0	0	0	0
IGLV1-47	0	0	0	0	0

LL22NC03-22A12.9	0	0	0	0	1
IGLV7-46	0	0	0	0	0
LL22NC03-22A12.12	0	0	0	0	0
IGLV5-45	0	0	0	0	0
IGLV1-44	0	0	0	0	0
IGLV7-43	0	0	0	0	0
IGLVI-42	0	0	0	0	0
IGLVVII-41-1	0	0	0	0	0
IGLV1-41	0	0	0	0	0
IGLV1-40	0	0	0	0	1
ASH2LP1	0	0	0	0	0
IGLVI-38	0	0	0	0	1
IGLV5-37	0	0	0	0	0
IGLV1-36	0	0	0	0	1
KB-288A10.17	0	1	0	0	1
IGLV7-35	0	0	0	0	0
KB-288A10.19	0	0	1	0	1
ZNF280B	28	37	39	65	55
ZNF280A	0	0	0	11	11
PRAME	0	0	0	822	472
LL22NC03-63E9.3	0	0	0	1	1
IGLV2-34	0	0	0	0	0
IGLV2-33	0	0	0	0	0
IGLV3-32	0	0	0	0	0
IGLV3-31	0	0	0	0	1
IGLV3-30	0	0	0	0	0
BCRP4	0	0	0	0	0
POM121L1P	0	0	0	0	1
GGTLC2	0	0	0	0	1
IGLV3-29	0	0	0	0	1
AC244250.2	0	0	0	0	0
IGLV2-28	0	0	0	0	0
IGLV3-27	0	0	0	2	0
IGLV3-26	0	0	0	0	0
IGLVVI-25-1	0	0	0	0	0
IGLV3-25	0	0	0	0	2
LL22NC03-102D1.16	0	0	0	0	0
LL22NC03-102D1.18	0	0	0	0	0
IGLV3-24	0	0	0	0	0
IGLV2-23	0	0	0	0	0
AC244250.1	0	0	0	0	0
IGLVVI-22-1	0	0	0	0	0
IGLV3-22	0	0	0	0	0
IGLV3-21	0	0	0	0	0
IGLVI-20	0	0	0	0	0
IGLV3-19	0	0	0	0	1
LL22NC03-48A11.14	0	0	0	0	0

AC244250.4	0	0	0	0	0
IGLV2-18	0	0	0	0	0
IGLL5	0	0	0	1	0
IGLV3-17	0	0	0	0	0
IGLV3-16	0	0	0	0	0
IGLV3-15	0	0	0	0	0
AC244250.3	0	0	0	0	0
IGLV2-14	0	0	0	26	12
IGLV3-13	0	0	0	0	0
IGLV3-12	0	0	0	0	0
LL22NC03-24A12.8	0	0	0	0	0
LL22NC03-24A12.9	0	0	0	0	0
AC244157.1	0	0	0	0	0
IGLV2-11	0	0	0	0	0
LL22NC03-84E4.13	0	0	0	0	0
IGLV3-10	0	0	0	0	0
LL22NC03-84E4.11	0	0	0	0	0
IGLV3-9	0	0	0	0	1
IGLV2-8	0	0	0	0	1
MIR650	0	0	0	0	0
LL22NC03-84E4.8	0	0	0	0	1
IGLV3-7	0	0	0	0	0
IGLV3-6	0	0	0	0	0
AC245028.1	0	0	0	0	0
IGLV2-5	0	0	0	0	0
IGLV3-4	0	0	0	0	0
IGLV4-3	0	0	0	0	0
IGLV3-2	0	0	0	0	0
IGLV3-1	0	0	0	0	0
MIR5571	0	0	0	0	0
IGLJ1	0	0	0	0	0
IGLC1	0	0	0	0	0
IGLJ2	0	0	0	0	0
IGLC2	0	0	0	706	503
IGLJ3	0	0	0	0	1
IGLC3	0	0	0	1170	317
IGLJ4	0	0	0	0	0
IGLC4	0	0	0	0	0
IGLJ5	0	0	0	0	1
IGLC5	0	0	0	0	0
IGLJ6	0	0	0	0	0
IGLC6	0	0	0	2	1
IGLJ7	0	0	0	0	0
IGLC7	0	0	0	8	5
AP000361.2	0	0	0	0	0
AP000362.1	0	0	0	1	0
RSPH14	4	8	5	1	0

GNAZ	223	247	214	32	17
AC000029.1	0	1	0	0	0
U7	0	0	0	0	0
RAB36	29	30	33	20	15
BCR	228	357	302	332	204
BCRP8	0	1	0	0	0
RN7SL263P	1	1	0	1	0
FBXW4P1	2	4	5	8	6
AP000343.1	0	2	0	0	0
AP000343.2	0	0	1	0	0
CES5AP1	2	2	0	0	1
ZDHC8P1	21	16	14	1	2
KB-1269D1.8	1	1	0	0	0
AP000344.3	0	0	0	0	1
AP000344.4	0	1	0	1	3
AP000345.1	0	0	1	0	1
AP000345.4	0	0	0	4	4
PCAT14	0	0	1	202	156
AP000345.2	0	0	0	0	2
IGLL1	0	0	0	0	0
KB-208E9.1	1	3	1	0	1
KB-1572G7.5	0	1	0	1	1
DRICH1	2	2	1	0	4
KB-1572G7.4	0	0	1	0	0
KB-1572G7.3	0	3	0	0	0
GUSBP11	1	0	1	1	0
AP000347.4	0	0	0	1	5
ASLP1	1	1	2	5	3
KB-1572G7.2	0	0	1	0	0
AP000347.2	4	4	8	12	8
RGL4	16	27	18	17	15
ZNF70	26	46	32	80	48
VPREB3	0	0	0	0	0
C22orf15	2	7	7	4	3
CHCHD10	44	53	39	46	36
MMP11	3	1	1	15	17
AP000349.2	0	0	0	0	0
SMARCB1	70	78	62	169	131
DERL3	4	8	7	81	43
KB-1125A3.11	0	3	0	1	0
SLC2A11	54	63	46	28	34
AP000350.10	0	0	0	0	0
KB-1125A3.12	4	4	1	8	5
RN7SL268P	1	1	1	4	1
MIF	3	3	3	3	1
MIF-AS1	5	1	5	8	11
AP000350.5	11	14	12	30	24

AP000350.1	0	0	0	0	0
AP000350.6	2	2	1	3	1
AP000350.7	0	0	0	0	0
AP000350.8	0	0	0	0	0
GSTT2B	3	4	3	10	4
KB-1125A3.10	0	0	0	0	0
DDTL	3	3	3	2	17
KB-226F1.2	1	2	1	1	4
DDT	4	5	4	18	8
AP000351.3	0	0	0	0	0
GSTT2	0	0	0	0	0
AP000351.4	0	0	0	1	0
GSTTP1	0	0	0	0	1
AP000351.13	0	0	0	0	1
CABIN1	280	320	309	509	296
KB-318B8.7	13	11	7	14	10
SUSD2	8	8	7	11	17
GGT5	22	31	23	10	4
AP000354.4	0	0	1	0	0
POM121L9P	1	1	2	0	1
BCRP1	0	0	0	0	0
AP000354.2	0	0	0	0	1
SPECC1L	64	80	70	156	82
SPECC1L-ADORA2A	0	1	0	0	1
ADORA2A	2	4	2	4	0
ADORA2A-AS1	2	5	5	6	12
UPB1	0	1	2	1	10
AP000355.2	0	0	0	0	1
GUCD1	62	62	62	384	214
SNRPD3	71	87	98	293	211
GGT1	9	14	13	86	42
LRRC75B	20	30	26	21	24
AP000356.2	0	0	0	0	0
BCRP3	2	1	2	5	5
POM121L10P	0	0	0	0	0
ARL5AP4	0	0	0	0	0
AP000357.4	0	0	0	0	1
LL22NC03-N95F10.1	0	0	0	0	0
AP000358.5	0	0	0	0	0
CRIP1P4	0	0	0	0	1
PIWIL3	0	0	0	1	3
SGSM1	151	187	161	5	8
SNORD56	0	0	1	0	0
TMEM211	0	0	1	0	1
KIAA1671	126	148	131	158	97
CTA-243E7.4	3	3	0	1	3
CTA-243E7.3	0	1	1	1	1

CTA-243E7.2	0	2	1	4	4
CTA-243E7.1	5	6	3	12	19
CTA-221G9.12	7	7	6	4	1
CTA-221G9.10	0	0	0	0	0
CRYBB3	0	1	1	1	0
CTA-221G9.7	0	1	0	0	0
CRYBB2	0	1	0	0	4
Z99916.1	0	0	0	0	0
CTA-221G9.11	0	0	0	0	0
RP3-462D8.2	0	0	0	0	1
IGLL3P	0	0	0	0	0
CTA-246H3.8	0	1	0	2	2
CTA-246H3.11	0	2	2	4	2
LRP5L	7	5	5	41	24
CTA-246H3.12	0	0	0	1	2
CTA-390C10.9	0	1	0	0	0
IGLVIVOR22-1	0	0	0	0	0
CRYBB2P1	24	27	23	54	37
MIR6817	0	0	0	0	0
CTA-390C10.10	10	18	11	12	8
AL008721.1	0	0	0	0	0
CTA-407F11.8	1	1	0	1	2
ADRBK2	206	283	260	170	134
CTA-407F11.7	0	0	1	2	3
YES1P1	3	5	4	9	4
RNA5SP494	0	0	0	0	0
MY018B	0	0	0	86	85
CTA-407F11.9	0	0	0	2	1
CTA-125H2.2	0	0	0	1	6
Z98949.1	0	0	0	1	1
CTA-125H2.1	0	0	0	0	0
RN7SKP169	0	0	0	0	1
CTA-125H2.3	0	0	0	0	0
CTA-796E4.3	0	0	0	0	1
CTA-796E4.4	1	0	0	0	1
SEZ6L	399	508	463	16	17
RP11-259P1.1	3	5	2	0	0
RNA5SP495	0	0	0	0	0
CTB-1048E9.7	0	0	0	0	1
ASPHD2	44	56	80	18	13
HPS4	114	176	183	318	202
SRRD	35	37	43	62	47
TFIP11	60	93	52	141	77
CTA-445C9.14	14	23	13	27	13
TPST2	38	39	38	85	46
MIR548J	0	0	0	2	0
HMGB1P10	2	3	2	9	10

CRYBB1	2	0	1	3	3
CRYBA4	1	0	0	0	1
ISCA2P1	0	0	0	0	1
MIAT	429	453	443	43	34
MIAT_exon1	0	0	0	0	0
CTA-373H7.7	0	4	0	0	0
MIAT_exon5_1	0	0	0	0	0
MIAT_exon5_2	0	0	0	0	0
MIATNB	4	6	8	11	14
MIAT_exon5_3	0	0	0	0	0
LINC01422	2	4	6	3	9
RP1-40G4P.1	0	0	0	0	0
CTA-992D9.11	0	0	0	0	8
RNU6-1066P	0	0	0	0	0
CTA-992D9.10	0	0	0	0	0
CTA-992D9.9	0	0	0	0	0
CTA-992D9.6	1	0	0	0	2
CTA-992D9.8	0	0	0	1	4
CTA-992D9.7	0	0	0	0	1
CTA-503F6.2	0	0	0	0	1
RP5-1172A22.1	1	0	0	2	1
CTA-929C8.5	0	0	0	0	0
CTA-929C8.7	0	0	0	0	0
CTA-929C8.6	0	0	0	0	3
CTA-929C8.8	1	3	1	0	0
RP1-205F14P.1	0	0	0	1	0
RP11-46E17.6	0	0	0	0	0
RP1-231P7P.1	0	0	0	0	2
RP1-213J1P__B.1	0	0	0	2	1
RP1-213J1P__B.2	0	0	0	0	0
RP11-375H17.1	0	0	0	0	1
MN1	44	34	31	123	93
PITPNB	80	92	64	111	87
TTC28-AS1	42	51	66	48	46
TTC28-AS1_1	0	0	0	0	0
MIR3199-2	1	0	0	1	0
TTC28-AS1_2	0	0	0	0	0
TTC28	87	123	79	191	108
TTC28-AS1_3	0	0	0	0	0
TTC28-AS1_4	0	0	0	0	0
RN7SL757P	1	0	0	0	0
SNORD42	0	0	0	0	0
MIR5739	0	0	1	3	2
RN7SL162P	0	0	0	0	0
CHEK2	1	5	3	98	82
HSCB	7	9	11	35	20
CCDC117	68	75	58	259	176

XBP1	67	102	79	1082	636
Z93930.1	0	0	0	1	0
CTA-292E10.6	4	7	2	10	12
CTA-292E10.8	1	0	0	4	3
CTA-292E10.7	0	0	0	0	0
ZNRF3	97	103	102	99	89
ZNRF3-IT1	1	6	3	4	3
ZNRF3-AS1	6	3	3	8	2
C22orf31	0	2	0	0	1
KREMEN1	50	62	36	75	59
CTA-747E2.10	1	0	2	0	0
Z95116.1	0	0	0	0	0
RNU6-810P	1	0	0	0	0
RNU6-1219P	0	0	0	0	0
EMID1	11	19	29	12	6
RHBDD3	23	40	33	79	57
CTA-984G1.5	2	1	3	9	3
EWSR1	346	356	357	920	675
GAS2L1	73	77	66	32	23
RASL10A	9	27	17	0	2
AC002059.10	0	0	1	1	1
AP1B1	230	272	256	358	244
MIR3653	0	0	0	0	0
SNORD125	0	0	0	0	0
AC000041.8	0	0	0	0	0
RFPL4AP6	0	0	0	0	1
RFPL15	116	107	115	6	2
AC000041.10	0	0	0	0	0
RFPL1	0	0	0	0	0
AC000035.3	0	0	0	0	0
NEFH	194	265	253	27	24
THOC5	73	123	65	218	137
CTA-256D12.11	0	0	1	1	2
NIPSNAP1	105	131	119	291	188
NF2	206	270	235	445	307
RPEP4	2	4	1	2	0
RP1-76B20.11	0	1	0	0	1
RP1-76B20.12	0	0	0	0	0
CABP7	18	21	25	2	1
ZMAT5	16	12	6	20	20
UQCR10	83	94	104	185	98
ASCC2	35	42	39	144	91
MTMR3	36	46	35	29	15
AC004819.1	1	0	1	0	1
RNU6-331P	0	0	0	0	0
AC003681.1	0	0	1	0	0
RP3-394A18.1	81	94	75	86	63

MIR6818	0	0	0	0	0
HORMAD2-AS1	2	0	0	1	1
CNN2P1	0	1	0	0	1
HORMAD2	0	0	0	1	5
CTA-85E5.7	0	0	0	0	0
CTA-85E5.6	0	0	0	0	0
RP3-43804.4	0	0	0	0	2
RP1-102K2.6	0	0	0	2	0
LIF	2	3	3	154	97
RP1-102K2.8	0	0	0	3	1
OSM	0	0	1	0	0
RP1-102K2.9	2	3	0	0	1
GATSL3	5	6	3	2	0
RP1-130H16.18	0	0	0	0	0
TBC1D10A	13	15	14	39	30
SF3A1	184	232	179	388	259
CCDC157	3	15	9	9	8
RNF215	54	65	42	57	40
SEC14L2	53	81	68	42	33
RP4-539M6.19	0	0	0	0	0
AC004832.1	0	0	1	0	0
RP4-539M6.20	3	6	4	4	6
RNU6-564P	1	1	0	0	0
RP4-539M6.21	0	2	1	4	4
MTFP1	0	0	0	3	5
RP4-539M6.22	0	0	0	1	1
RP4-539M6.18	0	0	0	1	0
SEC14L3	1	0	0	0	2
RP4-539M6.14	0	0	0	0	0
SDC4P	0	0	0	0	0
SEC14L4	0	0	0	3	2
SEC14L6	4	12	3	3	7
SIRPAP1	0	0	0	0	0
GAL3ST1	19	18	21	4	6
PES1	65	80	70	271	202
RP1-56J10.8	0	0	0	0	1
TCN2	19	26	23	56	49
SLC35E4	18	32	26	21	12
DUSP18	8	13	9	12	10
CTA-963H5.5	1	2	0	3	0
OSBP2	119	137	98	113	57
AL022336.1	2	0	0	0	0
EIF4HP2	1	4	9	3	6
MORC2-AS1	1	2	3	5	2
MORC2	75	82	50	146	100
TUG1	188	227	207	545	349
TUG1_1	0	0	0	0	0

TUG1_2	0	0	0	0	0
TUG1_3	0	0	0	0	0
TUG1_4	0	0	0	0	0
RP3-430N8.11	0	0	0	0	0
RP3-430N8.10	0	0	0	0	0
RP3-412A9.17	0	0	0	2	5
RN7SL633P	0	0	0	0	0
SMTN	42	51	47	142	91
RP3-412A9.16	1	2	2	11	6
SELM	83	86	77	25	18
RP3-412A9.12	0	0	0	0	0
INPP5J	59	77	58	7	8
PLA2G3	1	5	2	13	12
RP3-412A9.15	0	0	0	0	0
MIR3928	0	0	0	0	0
RNF185	57	105	74	106	82
RNF185-AS1	0	0	0	0	0
LIMK2	96	119	103	113	70
RNU6-1128P	0	0	0	0	1
PIK3IP1	112	165	128	52	32
PIK3IP1-AS1	1	1	3	2	0
RNA5SP496	0	0	0	0	0
PATZ1	72	74	61	191	116
LINC01521	12	14	13	8	9
RNU6-338P	0	0	0	0	0
DRG1	83	105	96	191	143
EIF4ENIF1	95	107	96	94	77
RP11-247I13.11	0	0	2	1	1
RNU6-28P	1	0	0	0	1
SFI1	112	125	107	142	102
H2AFZP6	1	0	1	0	0
RP11-247I13.6	0	0	0	0	0
RP11-247I13.3	0	1	1	4	1
PISD	195	250	233	156	95
MIR7109	0	0	0	0	0
PRR14L	219	269	234	418	294
DEPDC5	51	79	76	77	50
RN7SL20P	0	0	0	1	2
CTA-440B3.1	0	0	1	1	2
RNU6-201P	0	0	0	0	0
RP1-180M12.1	0	1	2	0	0
C22orf24	0	6	6	4	2
YWHAH	1029	1363	1146	336	220
CTA-342B11.1	0	0	0	1	0
CTA-342B11.2	0	0	0	0	2
RN7SL305P	0	0	0	0	0
SC22CB-1E7.1	0	0	0	0	0

SLC5A1	0	0	0	0	6
AP1B1P1	0	0	0	0	1
RP1-127L4.10	0	0	0	0	0
AP1B1P2	0	0	0	0	0
RP1-127L4.7	0	0	0	1	0
C22orf42	0	2	0	0	1
RP1-90G24.8	0	0	0	0	0
RFPL3-AS1_1	0	0	0	0	0
RFPL2	5	3	10	1	1
AL008723.1	0	0	0	1	0
IGLCOR22-1	0	0	0	0	0
RP1-90G24.10	4	7	3	2	3
SLC5A4	7	12	5	13	9
CPSF1P1	41	43	42	6	12
RP1-90G24.6	1	1	3	0	0
RP1-90G24.11	0	3	0	1	0
RP1-149A16.12	0	1	1	1	0
RFPL3	0	0	0	0	0
IGLCOR22-2	0	0	0	0	0
RFPL3S	1	1	1	0	0
RFPL3-AS1_2	0	0	0	0	0
RP1-149A16.3	1	3	2	1	1
IGLVIVOR22-2	0	0	0	0	0
RP1-149A16.17	0	1	0	4	2
RP1-149A16.16	2	0	0	2	0
RTCB	109	150	124	339	182
BPIFC	0	0	0	0	2
FBX07	163	181	194	426	375
SYN3	74	110	78	11	12
LL22NC03-104C7.1	1	4	5	1	1
RNA5SP497	0	0	0	0	0
LL22NC01-116C6.1	0	0	1	0	1
TIMP3	214	271	243	805	491
CTA-415G2.2	0	0	0	0	0
RP1-302D9.1	0	0	0	0	0
RP1-302D9.2	0	0	0	0	0
RP1-302D9.5	0	0	0	0	1
LARGE	173	213	199	83	58
RP1-302D9.3	0	0	0	0	0
SC22CB-1D7.1	1	1	2	3	1
MIR4764	1	0	0	0	0
SNORA76	0	0	0	0	0
SNORA50	0	0	0	0	0
LARGE-IT1	0	0	0	0	0
LARGE-AS1	7	6	5	5	7
LL22NC03-32F9.1	0	0	0	1	0
LL22NC03-86D4.1	0	0	0	0	1

LL22NC03-13G6.2	0	1	2	0	0
RP1-101G11.2	0	0	0	0	0
RP1-101G11.3	0	0	0	3	4
RP1-288L1.5	2	3	0	0	1
RP1-288L1.4	0	0	1	0	0
ISX-AS1	1	0	0	2	1
ISX	0	0	0	6	4
LINC01399	0	0	0	1	0
CTA-714B7.7	0	0	0	0	0
RP3-323A16.1	0	0	1	75	77
CTA-714B7.4	0	0	0	0	0
COX7BP1	0	0	0	0	0
RNU7-167P	0	0	0	0	0
HMGXB4	32	45	49	124	103
RP3-510H16.3	2	0	1	0	0
TOM1	99	119	103	84	56
MIR3909	1	0	0	1	1
MIR6069	0	0	0	0	0
CTA-286B10.7	0	0	0	1	0
CTA-286B10.8	0	0	0	0	0
HMOX1	13	19	13	83	51
MCM5	29	32	34	544	294
RP4-569D19.5	0	0	0	4	1
RP4-569D19.8	0	0	0	0	0
RASD2	55	81	60	15	15
MB	0	1	0	9	8
CITF22-62D4.1	0	0	0	0	1
APOL6	64	54	56	331	197
RP1-41P2.7	0	0	0	0	0
MRPS16P3	0	0	0	0	0
APOL5	0	0	1	0	0
RBF0X2	621	738	711	515	367
NDUFA9P1	3	3	2	4	4
RP1-78B3.1	10	8	4	21	23
CTA-212A2.4	0	0	0	0	0
CTA-212A2.3	0	0	0	0	9
CTA-212A2.2	0	0	0	0	0
CTA-212A2.1	1	0	1	0	1
APOL3	8	6	12	39	33
Z95114.4	0	0	0	0	1
Z95114.3	0	0	0	0	0
Z95114.5	0	0	0	0	1
Z95114.6	0	0	0	0	1
Z95114.7	0	0	0	0	0
MTND1P10	0	0	0	0	1
APOL4	10	6	8	9	5
APOL2	113	151	135	148	112

APOL1	4	9	6	87	65
MYH9	449	512	485	2685	1608
MIR6819	0	0	0	1	1
RP4-633019__A.1	1	2	1	2	0
RPS15AP38	0	0	0	0	1
BX470187.1	0	0	0	0	0
RP5-1119A7.14	0	1	3	0	0
TXN2	27	41	39	82	49
FOXRED2	74	108	107	218	104
EIF3D	103	119	131	745	494
RP5-1119A7.11	0	0	0	0	0
RP5-1119A7.10	0	0	0	0	0
RP5-1119A7.17	41	56	44	0	0
CACNG2	33	34	48	0	1
RP1-293L6.1	3	2	4	0	0
IFT27	53	58	56	77	57
PVALB	100	129	102	25	17
CITF22-24E5.1	2	0	0	0	0
CTA-833B7.2	0	0	1	1	4
NCF4	3	7	1	24	17
CSF2RB	2	4	4	50	42
CSF2RBP1	0	0	0	0	1
LL22NC01-81G9.3	0	0	0	0	1
TEX33	0	0	0	0	0
TST	18	21	18	88	61
MPST	34	29	33	131	76
KCTD17	47	74	73	32	21
RN7SKP214	0	0	0	1	0
TMPRSS6	1	3	0	5	5
RP5-1170K4.7	0	0	0	0	1
IL2RB	1	0	0	6	6
AL022314.1	0	0	0	0	1
RP1-151B14.6	0	0	0	1	0
C1QTNF6	11	8	10	85	65
SSTR3	30	36	48	14	12
RP1-151B14.9	0	0	0	0	0
RAC2	8	8	5	111	79
CYTH4	13	18	16	22	19
ELFN2	106	137	114	19	17
RP1-63G5.7	1	2	1	1	3
RP1-63G5.8	0	0	0	0	0
MFNG	4	5	6	75	30
CARD10	2	5	5	97	76
RP5-1177I5.3	1	1	0	0	0
CDC42EP1	68	100	65	144	81
LGALS2	0	0	0	7	5
GGA1	119	155	128	307	193

SH3BP1	20	13	16	55	34
Z83844.1	1	3	1	7	2
PDXP	5	6	5	2	1
RN7SL385P	0	1	0	0	0
LGALS1	75	93	78	729	447
NOL12	9	10	15	28	17
RP1-37E16.12	0	0	0	0	0
TRIOBP	36	28	25	164	103
H1FO	106	146	112	252	167
GCAT	34	27	33	76	56
GALR3	1	0	2	1	1
ANKRD54	33	48	55	91	50
MIR658	0	0	0	0	0
MIR659	0	0	0	1	0
EIF3L	191	222	206	704	454
RP5-1014D13.2	12	23	15	48	32
RNU6-900P	0	0	0	0	0
MICALL1	52	64	62	149	96
RP5-1039K5.12	1	8	1	4	2
C22orf23	2	1	5	9	6
AL031587.1	0	2	0	0	0
RP5-1039K5.19	167	192	150	105	83
RP5-1039K5.17	0	0	0	0	0
POLR2F	15	28	17	12	8
MIR6820	0	0	0	0	0
SOX10	0	0	0	0	0
MIR4534	0	0	0	0	0
RP5-1039K5.16	6	3	10	4	7
RP5-1039K5.18	0	0	1	0	1
PICK1	79	81	85	46	33
RP5-1039K5.13	0	0	0	0	0
SLC16A8	9	13	11	11	5
BAIAP2L2	5	17	8	18	8
CTA-228A9.3	10	3	3	4	2
PLA2G6	61	57	62	86	48
CTA-228A9.4	2	3	4	13	7
MAFF	31	27	20	97	63
TMEM184B	207	235	215	191	140
RP1-506.5	0	0	0	1	0
RN7SL704P	0	0	0	0	1
AL020993.1	0	0	0	0	0
CSNK1E	232	229	222	592	338
RP3-449017.1	10	15	10	30	28
RP1-506.4	2	0	1	6	4
RP3-434P1.6	0	0	0	0	0
KCNJ4	49	70	50	2	1
KDELR3	6	7	7	106	92

DDX17	1532	1797	1637	2814	1818
DMC1	2	4	0	15	11
RP1-199H16.6	1	0	0	0	0
FAM227A	16	12	17	40	48
CBY1	17	19	13	25	22
RP3-508I15.10	3	1	0	0	4
RP3-508I15.9	12	7	15	7	9
TOMM22	52	67	51	178	112
JOSD1	149	161	133	261	204
GTPBP1	146	187	152	335	182
PRDX3P1	3	5	2	11	3
RP3-508I15.18	0	0	0	0	2
SUN2	289	369	314	266	151
RP3-508I15.19	0	2	0	4	1
RP3-508I15.20	1	1	1	2	3
RP3-508I15.14	1	0	2	3	0
RP3-508I15.21	1	5	2	4	9
RP3-508I15.22	0	1	1	4	0
DNAL4	19	42	34	46	18
NPTXR	390	446	394	69	59
CBX6	738	873	830	362	240
CTA-150C2.13	0	0	0	0	0
APOBEC3A	0	0	0	0	1
APOBEC3B	1	0	0	19	22
APOBEC3B-AS1	0	0	0	0	0
APOBEC3C	4	3	3	80	48
APOBEC3D	1	1	2	16	8
APOBEC3F	1	1	0	11	6
APOBEC3G	4	9	3	41	25
CTA-150C2.20	0	0	0	0	0
RP4-742C19.12	0	2	1	0	0
APOBEC3H	4	3	0	0	0
CBX7	185	257	208	25	21
COX5BP7	0	0	0	0	0
RP4-742C19.13	6	19	10	8	6
FUNDC2P4	0	0	0	0	0
PDGFB	34	45	32	40	28
RP3-333H23.8	0	0	0	0	0
RPL3	659	761	721	4027	2406
SNORD83B	0	0	0	0	0
SNORD83A	2	0	0	7	5
AL022326.1	0	0	0	1	1
SNORD43	0	0	0	0	0
SYNGR1	763	997	870	54	51
RP3-333H23.9	1	2	2	0	0
TAB1	99	91	70	82	75
MGAT3	257	328	274	35	15

MGAT3-AS1	5	9	8	1	2
MIEF1	95	122	114	312	164
ATF4	291	358	307	1354	819
RPS19BP1	72	88	72	129	95
CACNA1I	106	139	136	2	7
ENTHD1	0	0	0	2	3
RP1-172B20.6	0	0	0	0	1
RN7SKP210	0	0	0	0	0
UQCRFS1P1	1	5	6	4	8
GRAP2	1	0	1	64	45
RP3-370M22.8	0	0	0	8	1
FAM83F	0	1	6	28	20
RP3-496C20.1	0	2	0	1	0
TNRC6B	582	686	592	528	327
RPL7P52	2	4	2	3	2
ADSL	40	41	48	302	176
RP5-1042K10.14	0	0	1	1	0
SGSM3	109	136	114	147	104
RP5-1042K10.10	1	2	1	4	4
MKL1	139	132	104	137	81
RP5-1042K10.13	0	0	1	1	1
RP5-1042K10.12	2	0	2	0	4
RP4-591N18.2	4	10	8	11	7
AL031594.1	1	1	1	2	2
COX6B1P3	1	0	0	1	0
RPL4P6	1	2	1	8	5
GAPDHP37	0	1	0	0	1
MCHR1	12	21	17	2	3
SLC25A17	39	39	40	119	96
RP3-408N23.4	1	1	3	5	1
JTBP1	1	1	0	6	1
MIR4766	0	0	0	2	0
ST13	389	470	463	880	640
XPNPEP3	31	43	39	149	105
DNAJB7	2	2	0	2	1
RNU6-379P	0	0	0	0	0
RBX1	50	68	60	122	77
AL080243.1	0	0	0	0	0
RP11-12M9.3	0	0	0	0	0
RP11-12M9.4	0	0	0	0	0
EP300	302	403	405	569	328
MIR1281	0	0	0	0	0
RNU6-375P	0	0	0	0	1
RP1-85F18.6	0	3	0	3	3
EP300-AS1	1	2	0	1	1
LRRC37A14P	0	1	0	0	0
L3MBTL2	91	96	83	108	82

RP4-756G23.5	6	8	9	2	5
CHADL	32	40	39	2	3
RANGAP1	256	316	267	464	296
MIR6889	0	0	0	0	0
ZC3H7B	417	531	475	453	288
TEF	335	384	341	43	34
RNU6-495P	0	2	0	0	0
CTA-223H9.9	0	0	2	4	1
TOB2	203	279	197	173	116
PHF5A	34	36	17	134	79
AC02	301	366	347	254	168
POLR3H	106	93	91	131	77
CSDC2	72	94	65	6	5
PMM1	34	40	55	51	31
DESI1	129	188	159	190	134
XRCC6	365	415	378	1431	973
NHP2L1	168	201	178	366	219
RNU6-476P	0	1	0	3	1
C22orf46	34	36	32	56	46
MEI1	1	5	1	8	6
HMG2P10	0	1	0	0	0
RNU6ATAC22P	0	0	0	0	0
CCDC134	9	24	19	39	24
RP5-821D11.7	12	14	13	34	18
SREBF2	497	669	575	627	384
MIR33A	0	1	2	0	0
SHISA8	33	31	18	0	0
TNFRSF13C	4	2	2	11	9
MIR378I	0	0	0	0	0
CENPM	0	3	1	65	35
LINC00634	28	16	21	0	1
SEPT3	721	907	863	54	38
CTA-250D10.19	4	3	4	0	1
WBP2NL	14	11	8	5	9
SLC25A5P1	0	0	1	0	1
NAGA	30	43	53	144	107
FAM109B	9	3	4	6	5
SNORD13P1	0	0	0	0	1
SMDT1	25	42	34	28	15
NDUFA6	67	101	81	167	109
RP1-257I20.14	2	1	2	8	4
NDUFA6-AS1	10	18	21	15	6
OLA1P1	1	0	3	3	0
CYP2D6	15	23	16	17	9
RP4-669P10.19	2	1	0	4	1
RP4-669P10.16	1	3	0	2	0
RP4-669P10.20	4	6	5	2	2

CYP2D7	6	9	8	2	3
CYP2D8P	2	3	4	6	7
TCF20	205	259	209	455	281
OGFRP1	0	3	1	13	6
Z83851.4	1	2	1	8	5
CTA-989H11.1	1	3	1	8	1
LINC01315	1	3	5	2	4
NFAM1	5	5	11	8	9
CTA-126B4.7	0	0	0	1	1
SERHL	4	3	5	2	2
RRP7A	59	89	80	157	86
Z93241.1	0	0	0	0	0
SERHL2	6	11	7	18	14
RRP7BP	20	30	18	52	42
RN7SKP80	284	319	228	250	413
RNU6-513P	0	0	0	0	0
POLDIP3	139	155	150	263	169
RNU12	6	10	7	17	4
CYB5R3	126	169	136	372	250
ATP5L2	0	3	1	2	0
A4GALT	8	5	2	36	23
RPL5P34	0	0	0	0	0
GOLGA2P4	0	1	0	0	1
RP1-47A17.1	0	0	1	1	2
ARFGAP3	53	65	44	187	145
PACSIN2	114	127	111	261	174
AL049758.2	0	1	0	1	0
AL022476.2	5	3	1	0	4
TTLL1	16	29	26	10	12
AL022237.3	0	1	0	0	0
BIK	1	3	6	4	5
MCAT	19	27	25	43	27
TSPO	12	10	13	136	88
TTLL12	57	94	59	278	212
SCUBE1	1	5	3	11	15
Z82214.3	0	0	0	0	0
Z82214.2	0	0	0	0	0
Z99756.1	0	0	0	1	0
RP4-754E20__A.5	1	0	0	1	3
MPPED1	122	154	138	1	3
EFCAB6-AS1	2	3	0	0	2
EFCAB6	36	43	35	6	4
RP3-388M5.8	1	0	1	0	0
HMGN2P9	0	0	0	0	0
RP3-388M5.9	3	3	6	2	4
SULT4A1	290	334	288	5	7
PNPLA5	3	2	2	0	3

Z97055.1	0	0	0	0	0
PNPLA3	6	5	5	45	37
SAMM50	45	46	50	132	118
RP4-796I17.5	0	1	0	0	0
PARVB	69	89	68	162	134
CTA-414D7.1	3	6	4	10	10
RP4-671014.6	3	7	5	18	15
PARVG	7	10	8	18	19
RP4-671014.5	0	0	1	3	1
RP4-671014.7	0	3	0	3	7
KIAA1644	149	205	176	162	111
RP1-32I10.10	0	0	0	0	0
RP1-32I10.11	0	0	0	0	0
CTA-397C4.2	0	0	0	0	0
MRPS18CP6	0	0	0	0	0
RP5-1033E15.3	0	0	0	0	0
LDOC1L	174	261	176	237	149
KRT18P23	0	0	0	0	2
LINC00207	0	0	0	0	4
LINC00229	0	0	0	0	0
ANP32BP2	0	0	0	0	0
PRR5	10	5	6	26	23
PRR5-ARHGAP8	0	1	0	1	1
ARHGAP8	2	1	2	6	6
PHF21B	15	14	9	16	16
RP1-127B20.4	1	1	0	1	1
RP4-753M9.1	1	5	0	5	4
NUP50-AS1	27	24	31	32	29
CTA-217C2.2	1	3	0	6	2
NUP50	131	172	154	413	289
CTA-268H5.12	0	0	0	0	1
KIAA0930	312	364	315	260	166
MIR1249	1	2	4	0	1
CTA-268H5.14	1	3	1	0	0
CTA-268H5.9	0	0	0	0	0
UPK3A	0	0	0	2	1
FAM118A	53	50	50	113	66
SMC1B	3	0	4	6	11
RIBC2	0	4	1	12	11
RP1-102D24.5	0	0	0	0	1
FBLN1	43	47	33	122	96
LINC01589	0	0	0	3	1
RNU6-1161P	0	0	0	1	0
CTA-941F9.10	16	22	15	31	17
ATXN10	193	253	246	199	154
MIR4762	1	0	0	0	1
RP1-37M3.8	0	3	2	5	1

WI2-85898F10.2	0	4	3	0	1
WI2-85898F10.1	1	0	0	0	0
WNT7B	7	11	6	9	9
CR536603.1	0	0	0	0	0
CITF22-92A6.2	3	2	2	4	5
CITF22-92A6.1	0	0	1	1	6
LINC00899	7	14	9	7	5
PRR34	7	12	15	7	2
RP6-109B7.5	4	8	3	0	0
PRR34-AS1	6	13	5	15	5
MIRLET7BHG	82	137	87	61	56
RP6-109B7.2	10	14	11	2	1
RP6-109B7.4	17	15	12	6	6
MIR3619	2	2	1	5	1
MIRLET7A3	0	0	0	0	0
MIR4763	0	0	0	0	0
MIRLET7B	0	0	0	0	0
PPARA	72	101	84	193	147
RP4-695020.1	0	1	1	3	5
CDPF1	15	13	11	28	11
PKDREJ	6	6	7	8	12
TTC38	29	28	20	90	71
GTSE1-AS1	2	2	3	2	2
GTSE1	2	2	1	145	111
TRMU	64	78	75	191	111
CELSR1	0	6	4	250	136
RP5-996D20.3	0	0	0	0	0
RP3-439F8.1	0	0	0	0	9
GRAMD4	97	106	75	156	96
CERK	209	249	268	298	188
CTA-29F11.1	2	6	12	14	13
TBC1D22A	39	52	47	78	50
U51561.1	1	1	2	1	4
FP325331.1	2	4	3	2	1
RP1-111J24.1	1	1	0	1	3
CITF22-49D8.1	0	1	0	0	2
LL22NC03-75H12.2	0	0	0	0	1
LINC00898	7	6	1	5	3
RP11-191L9.4	8	8	8	32	28
RP11-191L9.5	1	0	2	0	2
RP13-455A7.1	1	0	0	2	3
CTA-280A3.2	4	3	3	7	12
CTA-280A3__B.2	0	0	0	0	0
LL22NC03-27C5.1	0	0	0	0	2
LL22NC03-121E8.4	0	0	0	0	1
LL22NC03-121E8.3	0	0	0	0	0
MIR3201	0	0	0	0	0

RP11-536P6.3	0	0	0	0	0
FAM19A5	140	163	151	18	16
CTA-299D3.8	17	16	18	0	1
MIR4535	0	0	0	0	1
AL954742.1	0	0	0	0	0
LINC01310	8	7	6	0	9
RPL35P8	0	0	0	0	1
RP1-34P24.3	0	0	0	0	3
C22orf34	2	4	2	36	25
CTA-722E9.1	0	0	0	0	3
RP4-566L20.1	0	0	0	0	1
MIR3667	0	0	0	0	0
RP1-29C18.10	0	0	1	13	19
RP1-29C18.9	0	0	0	7	1
RP1-29C18.8	1	0	1	17	14
RP5-983L19.2	0	0	0	0	4
RN7SKP252	0	0	0	0	0
RPL5P35	0	0	0	0	1
BRD1	92	116	103	186	121
RP3-522J7.7	3	2	8	5	8
RP3-522J7.5	2	3	2	3	3
RP3-522J7.6	1	2	1	1	2
RP11-494016.3	0	1	0	0	0
RP11-494016.4	0	0	0	2	0
ZBED4	51	68	77	196	153
ALG12	21	30	40	53	27
CITF22-1A6.3	0	0	0	1	0
CRELD2	30	40	43	74	64
CITF22-49E9.3	0	0	0	1	4
PIM3	47	59	55	159	103
MIR6821	0	0	0	0	0
IL17REL	0	1	2	0	5
TTLL8	0	0	0	0	0
MLC1	297	324	307	13	12
MOV10L1	10	8	8	0	7
RP5-898I4.1	1	0	0	0	1
PANX2	59	71	74	9	7
TRABD	33	40	37	103	79
RP3-402G11.25	2	7	3	4	5
RP3-402G11.26	9	17	7	2	0
SELO	52	72	33	77	37
RP3-402G11.27	7	2	0	5	1
RP3-402G11.28	2	2	3	4	2
TUBGCP6	248	289	237	279	174
HDAC10	4	9	12	9	9
MAPK12	60	57	56	116	73
MAPK11	64	98	82	25	23

PLXNB2	241	301	248	475	285
DENND6B	61	101	67	36	20
XX-C283C717.1	0	1	0	0	0
XX-C00717C00720L.1	0	0	0	0	0
PPP6R2	170	249	259	227	150
RN7SL500P	0	0	1	0	0
SBF1	682	840	696	530	339
ADM2	0	2	1	27	21
MIOX	0	0	0	1	1
LMF2	57	73	69	174	113
NCAPH2	86	93	78	219	131
SC02	4	24	10	19	14
CTA-384D8.36	8	12	8	7	1
TYMP	23	24	30	58	22
ODF3B	9	11	9	11	12
CTA-384D8.35	0	1	0	0	1
CTA-384D8.34	0	0	0	0	0
CTA-384D8.31	0	0	0	6	2
KLHDC7B	0	0	1	3	8
SYCE3	0	0	1	0	0
CPT1B	5	3	5	9	8
CHKB-CPT1B	2	4	2	6	5
CHKB	6	8	4	11	8
CHKB-AS1	5	1	3	1	2
CTA-384D8.33	0	2	4	1	2
MAPK8IP2	410	545	482	13	17
ARSA	53	55	65	63	47
SHANK3	363	456	375	43	25
RNU6-409P	0	0	0	0	0
AC000036.4	0	2	1	0	1
ACR	0	0	0	0	2
AC002056.5	0	0	0	0	0
AC002056.3	0	0	0	0	0
RPL23AP82	41	59	54	32	23
RABL2B	74	62	54	68	50

{{Edet}}

Word, Character, and Line Count in a File

The `wc` command is used to obtain word, character, and line count in a file.

```
wc file.txt
```

The output (from left to right) for `wc` can be interpreted as follows.

- 2 indicates that the file has two lines.
- 23 indicates that the file has 23 words.
- 135 indicates that the file has 135 characters.
- The file in which statistics were generated (ie. `file.txt`).

```
2 23 135 file.txt
```

The `wc` results above can be obtained separately. For instance, to just get the number of lines in a file include the `-l` option.

```
wc -l file.txt
```

```
2 file.txt
```

Word count can be obtained using the `-w` option.

```
wc -w file.txt
```

```
23 file.txt
```

Character count can be obtained using the `-m` option.

```
wc -m file.txt
```

```
135 file.txt
```

Pattern Searching

Sometimes users may want to search for a keyword in a file. The `grep` command can be used to do this. The `grep` command prints every line in a file that contains the search pattern. The arguments in `grep` are as follows.

- Search pattern (ie. `Linux`)
- File to search (ie. `file.txt`)

```
grep Linux file.txt
```

```
Linux is a variety of Unix, and sometimes the names are used interchangeably
```

To search for lines that do not contain a pattern include the `-v` option.

```
grep -v Linux file.txt
```

```
Unix is an operating system, just like Windows or MacOS.
```

What would happen if "linux" with a lower case "l" is used as the search pattern instead of an upper case "L" as shown in the file.txt? Nothing is returned because `grep` is case sensitive. To ignore case, include the `-i` option.

```
grep linux file.txt
```

```
grep -i linux file.txt
```

```
Linux is a variety of Unix, and sometimes the names are used interchangeably
```

Working with Software Installed on Biowulf

The `module` command is important for anyone who wishes to work with software that are installed on Biowulf. This `avail` option enables users to browse the software that are available on the cluster.

```
module avail
```

Glimpse of `module avail` results. Users can scroll up/down using the arrow keys to learn what software are available. Hit `Q` to exit the `module avail` results and return to the prompt.

```
----- Global Aliases
bowtie1      -> bowtie/1.3.1          deeptrio/1.6.0 ->
bowtie2      -> bowtie/2-2.5.3       deeptrio/1.6.1 ->
deeptrio/1.5.0 -> deepvariant/1.5.0-deeptrio
```

```
----- /data/classes/BTEP/apps/
biostars/1.0

----- /usr/local/lmod/module
3DSlicer/4.8.1 hwloc/2.9
3DSlicer/5.2.2 (D) hwloc/2.9
```

To find if a particular software is available include the software name with the `avail` option.

```
module avail fastqc
```

```
----- Global Aliases

----- /usr/local/lmod/module
fastqc/0.11.8 fastqc/0.11.9 fastqc/0.12.1 (D)
```

Where:

D: Default Module

Module defaults are chosen based on Find First Rules due to Name/Version. See https://lmod.readthedocs.io/en/latest/060_locating.html for details.

If the `avail` list is too long consider trying:

"`module --default avail`" or "`ml -d av`" to just list the default modules.
 "`module overview`" or "`ml ov`" to display the number of modules for each category.

Use "`module spider`" to find all possible modules and extensions.

Use "`module keyword key1 key2 ...`" to search for all possible modules.

To get a description of a software use `module whatis`.

```
module whatis fastqc
```

```
fastqc/0.12.1 : fastqc: It provide quality control functions to
fastqc/0.12.1 : Version: 0.12.1
```

Warning

Upon signing onto Biowulf, users will land in the "log-in" node, which is not meant for analyzing data or transferring files. To perform these task, request time and resources on a compute node using the `sinteractive` command.

To learn more about the `sinteractive` command, see <https://bioinformatics.ccr.cancer.gov/docs/unix-on-biowulf-2024/Lesson4/#requesting-an-interactive-session> (<https://bioinformatics.ccr.cancer.gov/docs/unix-on-biowulf-2024/Lesson4/#requesting-an-interactive-session>)

To load a software use `module load` followed by the name of the package.

```
sinteractive
```

Users will see the following when the interactive session has been granted.

```
salloc: Pending job allocation 61831125
salloc: job 61831125 queued and waiting for resources
salloc: job 61831125 has been allocated resources
salloc: Granted job allocation 61831125
salloc: Waiting for resource configuration
salloc: Nodes cn0003 are ready for job
```

```
module load samtools
```

```
[+] Loading samtools 1.19 ...
```

Getting Help

To get help, use the `man` command which pulls up the manual for a command. Use the up and down arrow keys to scroll through the manual and learn about the different options. Hit `q` to return to exit `man` and return to the prompt.

For instance, to pull up the manual for `grep`, do the following.

```
man grep
```

Glimpse of `man` command output for `grep`.

```
GREP(1)                                General Commands Manual

NAME
    grep, egrep, fgrep - print lines matching a pattern

SYNOPSIS
    grep [OPTIONS] PATTERN [FILE...]
```

```
grep [OPTIONS] -e PATTERN ... [FILE...]
grep [OPTIONS] -f FILE ... [FILE...]
```

DESCRIPTION

grep searches for PATTERN in each FILE. A FILE of “-” stands for standard input. If no FILE is given, recursive searches examine the working directory and all subdirectories. If no PATTERN is given, recursive searches read standard input. By default, grep prints the matching lines.

In addition, the variant programs egrep and fgrep are the same as grep but use extended and fixed regular expressions, respectively. These variants are deprecated, but are provided for compatibility.

OPTIONS

Generic Program Information

--help Output a usage message and exit.

-V, --version

Output the version number of grep and exit.

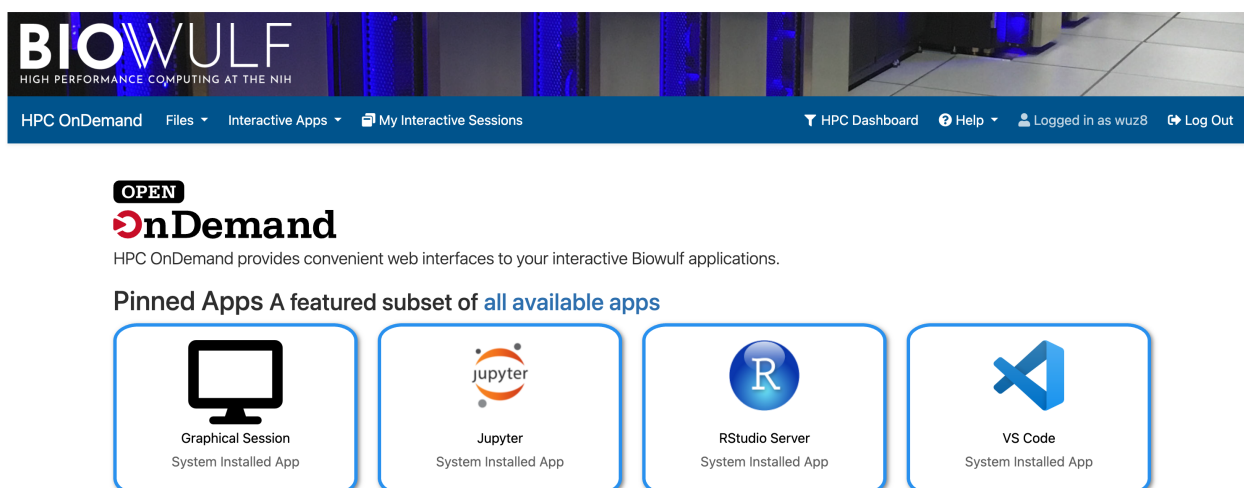
Want clear explanation of a command? Try <https://explainshell.com/#> (<https://explainshell.com/#>). It will explain each component in a command construct, just type it into the search box. For instance, below `ls -lhr folder` is used.

The screenshot shows the explainshell.com website with the command `ls -lhr folder` entered in the search box. The command is broken down into its components, each with a corresponding explanation:

- `ls(1)`: List directory contents
- `-l`: use a long listing format
- `-h, --human-readable`: with `-l`, print sizes in human readable format (e.g., 1K 234M 2G)
- `-r, --reverse`: reverse order while sorting
- `folder`: List information about the FILES (the current directory by default). Sort entries alphabetically if none of `-ctuvSUX` nor `--sort` is specified.

HPC OnDemand

HPC OnDemand enables researchers to access Biowulf resources such as graphical applications (R Studio, Jupyter Lab, IGV, Globus) and files from a web browser. To connect to Biowulf HPC OnDemand use <https://hpcondemand.nih.gov/> (<https://hpcondemand.nih.gov/>). See <https://bioinformatics.ccr.cancer.gov/btep/classes/getting-started-with-hpc-ondemand-a-new-interface-for-nih-hpc-users> (<https://bioinformatics.ccr.cancer.gov/btep/classes/getting-started-with-hpc-ondemand-a-new-interface-for-nih-hpc-users>) to access the training for HPC OnDemand.



Continual Learning

- See <https://bioinformatics.ccr.cancer.gov/docs/unix-on-biowulf-2024/> (<https://bioinformatics.ccr.cancer.gov/docs/unix-on-biowulf-2024/>) for a more detailed Unix and Biowulf class. Check the [BTEP Calendar](https://bioinformatics.ccr.cancer.gov/btep/) (<https://bioinformatics.ccr.cancer.gov/btep/>) for upcoming advanced Unix classes. Email ncibtep@nih.gov with questions.
- Coursera offers self learning classes for Unix and other data science related topics such as R and Python programming. See <https://bioinformatics.ccr.cancer.gov/btep/self-learning/> (<https://bioinformatics.ccr.cancer.gov/btep/self-learning/>) to learn how to request a Coursera license.
 - Example Coursera classes:
 - Hands-on Introduction to Linux Commands and Shell Scripting (<https://www.coursera.org/learn/hands-on-introduction-to-linux-commands-and-shell-scripting#modules>)
 - Command Line Tools for Genomic Data Science (<https://www.coursera.org/learn/genomic-tools#modules>)
 - Unix and Bash for Beginners Specialization (<https://www.coursera.org/specializations/unix-and-bash-for-beginners>)

R and Python

Overview of R and Python

Learning Objectives

In this presentation, we will:

- Learn about popular programming languages in bioinformatics
- Compare advantages and disadvantages of Python and R
- Discuss what you will need to learn to use these languages
- Discuss learning resources

Presentation Slides

Document Analysis using Jupyter Lab

Documenting Data Analysis with Jupyter Lab Slides

I

Documenting Data Analysis with Jupyter Lab

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September 4, 2025

Start Jupyter Lab

To start Jupyter Lab, type the following into the command prompt.

```
jupyter lab
```

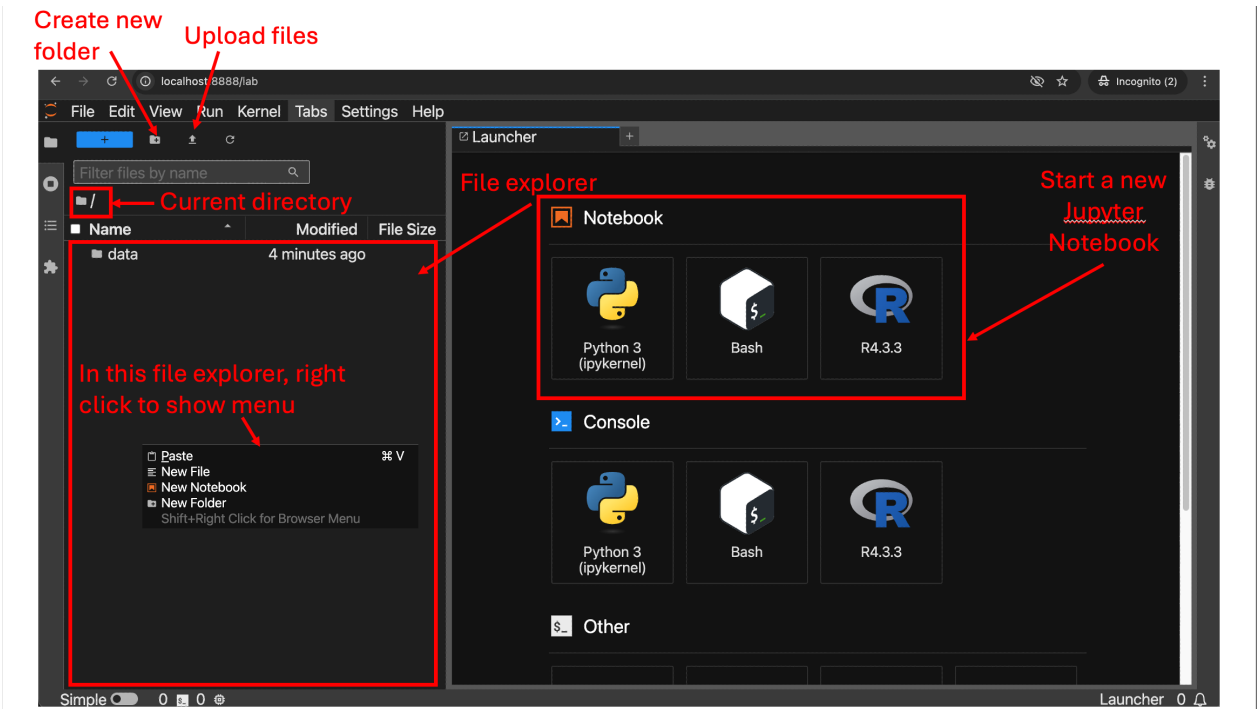
Jupyter Lab Interface

Upon starting Jupyter Lab, users will see an interface with the following.

- To the left, there is a file explorer where users can access files and subfolders available in the directory in which the Jupyter Lab session was started (also referred to as the project directory in these documents). In the example below, there is a subfolder called "data".
- A folder icon with a "+" enclosed can be used to create new folders within the project directory. These will be available in the file explorer.
- In case there are files or folders that are not in the project directory, users can use the upload button to transfer these so that they will appear in the file explorer. An alternative is to click and drag content into the file explorer.
- The Launcher contains options for starting a Jupyter Notebook in various languages. Users will have to install the specific language and add it into their Jupyter Lab environment to be able to use it. The link addressing Jupyter Lab language compatibility is included in the section titled "Jupyter Lab is Compatible with Many Languages". By default, the Python notebook option is available upon installing Jupyter Lab so no need to add it unless there is another version of Python that the user would like to utilize.
- Right clicking on the file explorer will bring up a menu where users can create new files, folders, and Jupyter Notebooks.

Warning

The file explorer will only display files and subfolders in the directory in which the Jupyter Lab session was created. To transfer files that reside in a different directory, either click and drag into the file explorer or use the upload button. Alternatively, users may create a symbolic link, which will appear in the file explorer to access content outside of the Jupyter Lab session directory.



Jupyter Lab is Compatible with Many Languages

- Bash, Python, and R
- See <https://docs.jupyter.org/en/latest/projects/kernels.html> (*https://docs.jupyter.org/en/latest/projects/kernels.html*) for a list of Jupyter compatible languages.

Start a New Jupyter Notebook

To start a new Jupyter Notebook, click on any of the available panels under the "Notebook" section in the Launcher. Each of the panels represent a notebook that will work with a specific language that was added to the Jupyter environment by the user.

This class will use a Python notebook as an example. Click on the "Python 3 (ipykernel)" panel to start a Python Jupyter Noteook. The instructor has Python 3.12.2 installed and this will be differ depeneding on what each user has installed. Remember to keep track of language and package versions to ensure analysis reproducibility.

The Jupyter Notebook is a part of Jupyter Lab.

The note book is where users

- Write code
- View and maintain output
- Document analysis steps using formatted text written in markdown

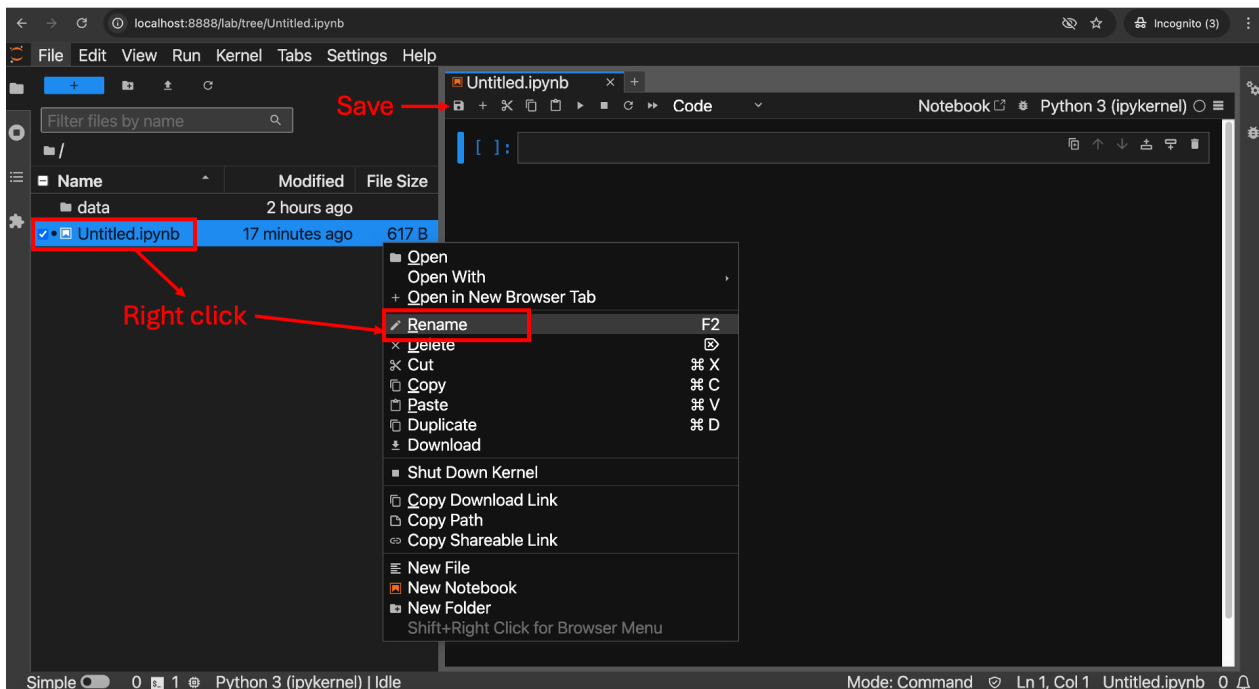
Note:

"Markdown is a lightweight markup language for creating formatted text using a plain-text editor." -- <https://en.wikipedia.org/wiki/Markdown> (<https://en.wikipedia.org/wiki/Markdown>)

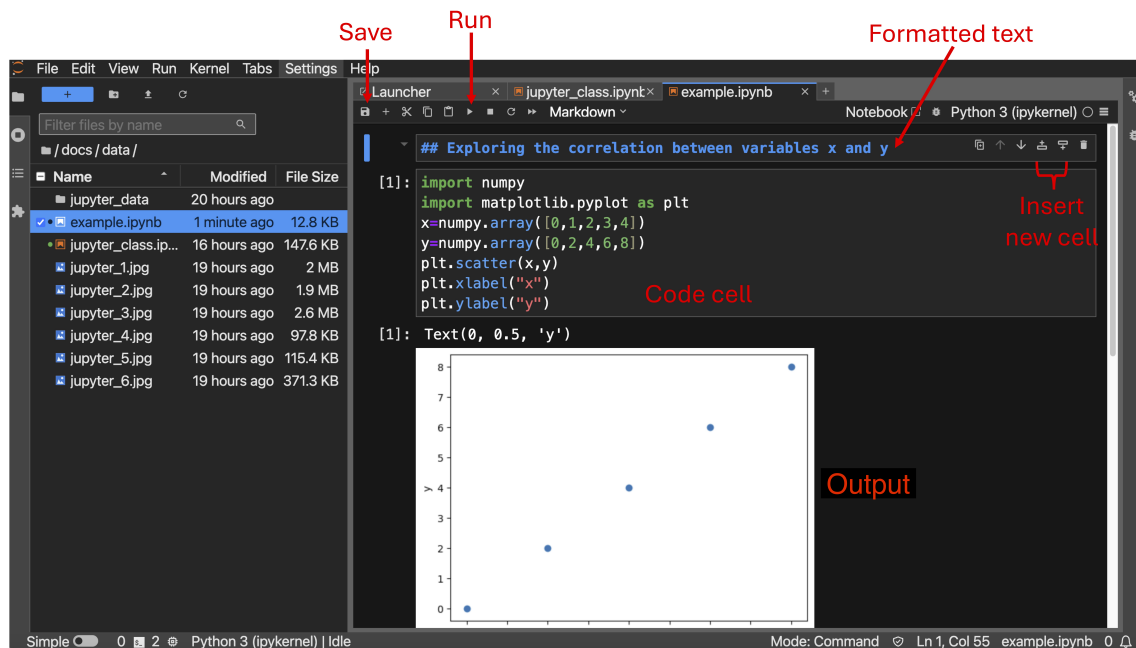
Rename Untitled Jupyter Notebook

A new Jupyter Notebook is given the name "Untitled". Change this to something meaningful either using the save icon on the notebook menu bar or right-clicking on the "Untitled.ipynb" notebook in the file explorer and choose "Rename".

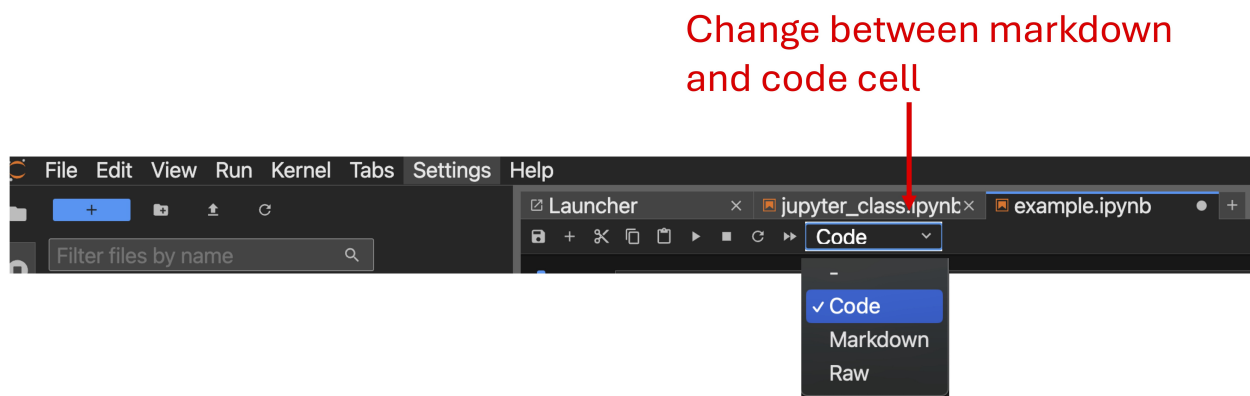
Jupyter Notebooks have extension ipynb, which stands for interactive Python notebook.



Keeping Code, Output, and Analysis Steps in One Place



Changing Between Markdown and Code



Ways to Access and Use Jupyter Lab

- Biowulf (<https://hpc.nih.gov/apps/jupyter.html> (<https://hpc.nih.gov/apps/jupyter.html>)). Biowulf is the NIH Unix-based high performance computing system.
- Requires getting a Biowulf account (<https://hpc.nih.gov/docs/accounts.html>)
- Jupyter is available through Biowulf's Open On Demand (<https://hpcondemand.nih.gov/>). Open On Demand enables users to run interactive applications such as Jupyter Lab through a web browser.
- NIH Anaconda Professional (<https://nih.sharepoint.com/sites/CIT-ApplicationRepository/SitePages/Anaconda.aspx>). This the way to go if users want to use Jupyter locally on

government issued computer. Click [here](https://forms.office.com/g/CArrnuE4cD) (<https://forms.office.com/g/CArrnuE4cD>) to request access.

Installing Jupyter Lab on Personal Computer

To run Jupyter Lab on a personal computer, users will need to have

1. Python
 - Comes with [Anaconda](https://nih.sharepoint.com/sites/CIT-ApplicationRepository/SitePages/Anaconda.aspx) (<https://nih.sharepoint.com/sites/CIT-ApplicationRepository/SitePages/Anaconda.aspx>) OR
 - Install as stand alone (<https://www.python.org/downloads/> (<https://www.python.org/downloads/>))
2. Jupyter Lab
 - Included full Anaconda.
 - Requires separate install if using Miniconda (<https://jupyter.org/install> (<https://jupyter.org/install>))
3. Install languages and language specific packages. For instance:
 - R
 - Julia
 - C++
4. Add the languages to Jupyter Environment (Python is automatically added)

Tip

Jupyter Lab is compatible with many languages. For more information about Jupyter compatible languages see <https://docs.jupyter.org/en/latest/projects/kernels.html> (<https://docs.jupyter.org/en/latest/projects/kernels.html>).

Code and Visualization

Jupyter Notebook enables organization of code, analysis steps, and output all in one place.

The example below will use Python code to demonstrate the utility of Jupyter Notebook for keeping code, output, and analysis steps all in one place.

- First, the `import` command of Python will be used to load packages `numpy` which is used for numeric computation and `matplotlib` which is a popular Python data visualization tool.
- Next, two numeric arrays (`x` and `y`) will be generated using `numpy` and its `array` sub-command. To call a Python sub-command just type the package name (ie. `numpy`), followed by a `.`, and then the sub-command. So to create an array, use `numpy.array`. The elements in the array are enclosed in `[]`.

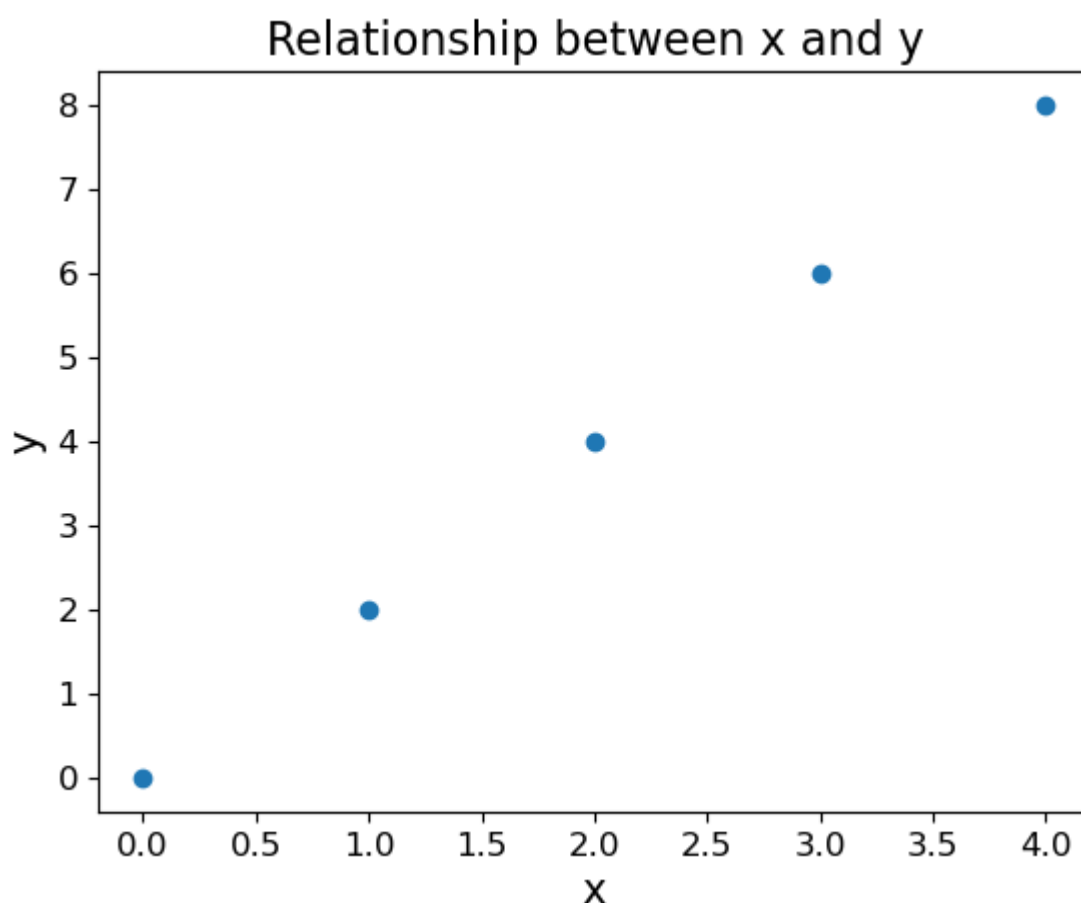
- Finally, a scatter plot will be generated using `matplotlib`'s `pyplot` module, which will be loaded under the alias `plt` for easy referencing in the code. The `scatter` sub-command will be used to generate the scatter plot showing the relationship between the values in array `x` versus those in array `y`. The arguments enclosed in `()` are name of the two arrays separated by a comma (ie. `(x,y)`).
- After scatter plot has been generated, the following sub-commands from `matplotlib`'s `pyplot` or `plt` will be used to customize the graph:
 - `xlabel`: assign label to the x axis, the option `size=` allows font size adjustment.
 - `ylabel`: assign label to the y axis, the option `size=` allows font size adjustment.
 - `plt.tick_params`: adjust axis tick mark label font size by setting the `labelsize` option.
 - `plt.title`: assigns a plot title and `size` is used to adjust the fontsize of the title.

```
# Import some Python packages
import numpy
import matplotlib.pyplot as plt
```

```
# Generate numeric arrays x and y using numpy
x=numpy.array([0,1,2,3,4])
y=numpy.array([0,2,4,6,8])
print("The array x contains: ", x)
print("The array y contains: ", y)
```

```
The array x contains:  [0 1 2 3 4]
The array y contains:  [0 2 4 6 8]
```

```
# Generate scatter plot using matplotlib
plt.scatter(x,y)
plt.xlabel("x", size=15)
plt.ylabel("y", size=15)
plt.tick_params(labelsize=12)
plt.title("Relationship between x and y", size=16)
plt.show()
```



Importing data tables into Jupyter Notebook

Users will be working with data tables during analyses. These can be imported into the a Jupyter Notebook although the approach for doing so will be language dependent.

The example below will use a Python package called *Pandas* (<https://pandas.pydata.org>) to import a data table. The data table contains the differential gene expression analysis results from the *HBR and UHR study* (https://rnabio.org/module-01-inputs/0001/05/01/RNAseq_Data/) and is in the comma separated value or CSV format where each column in the table is separated by a comma.

The file used is `hbr_uhr_deg_chr22_with_significance.csv`.

Step 1 in the process is to load `pandas` into the work environment using the `import` command of Python (ie. `import pandas`). The data will be stored in a data table called `hbr_uhr_deg_chr22`. Use `pandas.read_csv` to call the `read_csv` sub-command. Enclosed in parentheses is the path to the file `hbr_uhr_deg_chr22_with_significance.csv`. Once the data has been loaded, append the `.head()` attribute to the `hbr_uhr_deg_chr22` to preview the first five lines.

The `hbr_uhr_deg_chr22` data table contains five columns and these are:

- `name`: contains gene names

- log2FoldChange: gene expression change between two experimental conditions on the log2 scale
- PAdj: adjusted p-value indicating statistical confidence of the calculated gene expression change
- -log10PAj: negative of the values in the PAdj column on a log10 scale
- significance: whether the gene expression is up regulated, down regulated, or has no change

```
# Load the Pandas package
import pandas
```

```
# Import the data
```

```
hbr_uhr_deg_chr22=pandas.read_csv("./hbr_uhr_deg_chr22_with_significa
```

```
# View the first several lines of hbr_uhr_deg_chr22 using the head at
## of the imported data table (hbr_uhr_deg_chr22)
hbr_uhr_deg_chr22.head()
```

	name	log2FoldChange	PAdj	-log10PAdj	significance
0	SYNGR1	-4.6	5.200000e-217	216.283997	down
1	SEPT3	-4.6	4.500000e-204	203.346787	down
2	YWHAH	-2.5	4.700000e-191	190.327902	down
3	RPL3	1.7	5.400000e-134	133.267606	ns
4	PI4KA	-2.0	2.900000e-118	117.537602	down

Data visualization in Jupyter Notebook: scatter plot

The exercise below will use the Python package *Seaborn* (<https://seaborn.pydata.org>) to create a volcano plot for the HBR and UHR differential analysis results table that was previously imported. A volcano plot is essentially a scatter plot that shows magnitude of change on one axis and statistical confidence of the change on another axis. In the case of RNA sequencing differential expression, this will be log2 of fold change and -log10 of adjusted p-values.

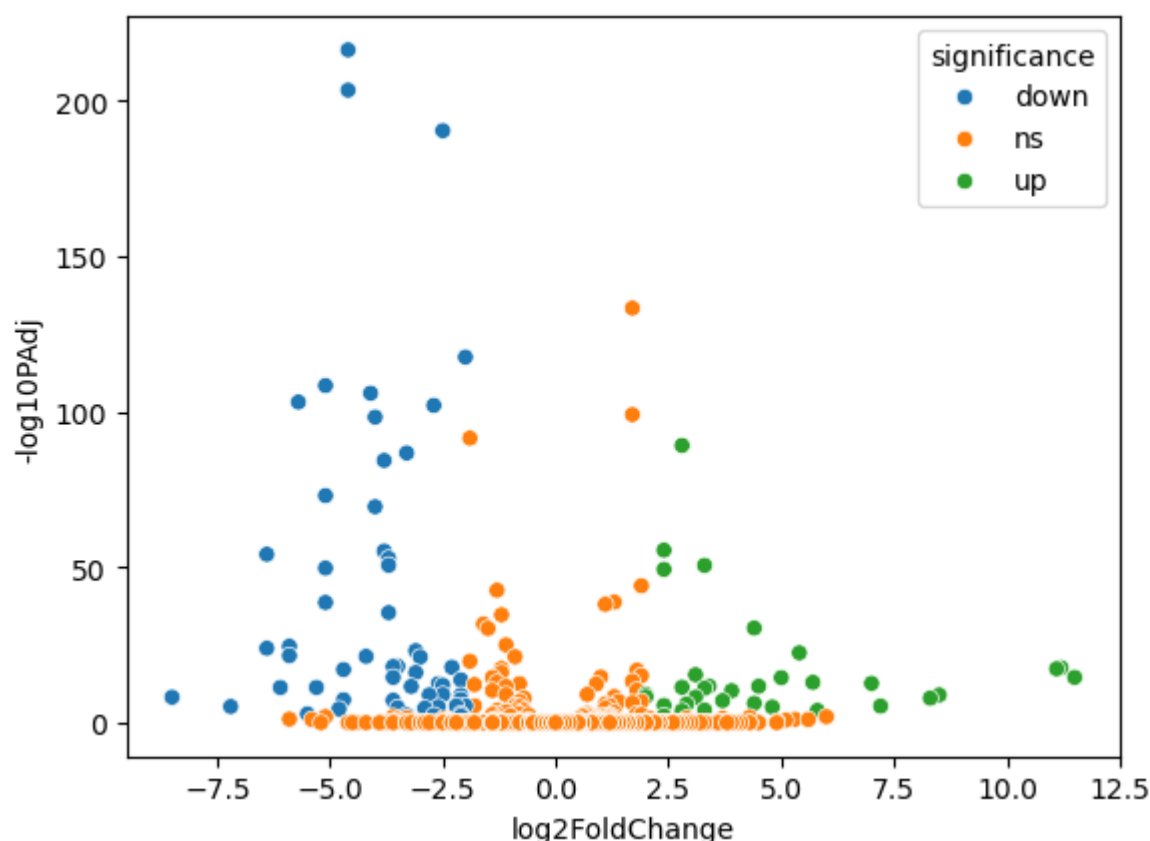
The `scatterplot` function in seaborn will be used to generate volcano plots. This function takes on arguments below:

- Data: hbr_uhr_deg_chr22 (differential gene expression analysis results table imported using `pandas.read_csv`)
- x: x-axis values (ie. gene expression log2FoldChange)
- y: y-axis values (ie. -log10 of adjusted p-value)

- hue: color dots by whether gene expression change is up, down, or has no change (see significance column of the data)

```
## Load the seaborn plotting package
import seaborn

seaborn.scatterplot(hbr_uhr_deg_chr22, x="log2FoldChange", y="-log10P/
plt.show()
```



Data visualization in Jupyter Notebook: heatmap

This exercise will use Seaborn's `clustermap` function to construct a gene expression heatmap of top differentially expressed genes in the HBR and UHR study. Heatmaps are another common visualization in RNA sequencing and allow scientists to identify clusters of samples with similar gene expression patterns.

First, import the dataset (`hbr_uhr_top_deg_normalized_counts.csv`) using `pandas.read_csv` and assign it to the variable `hbr_uhr_top_deg_normalized_counts`. The `clustermap` function of seaborn takes the following arguments and options.

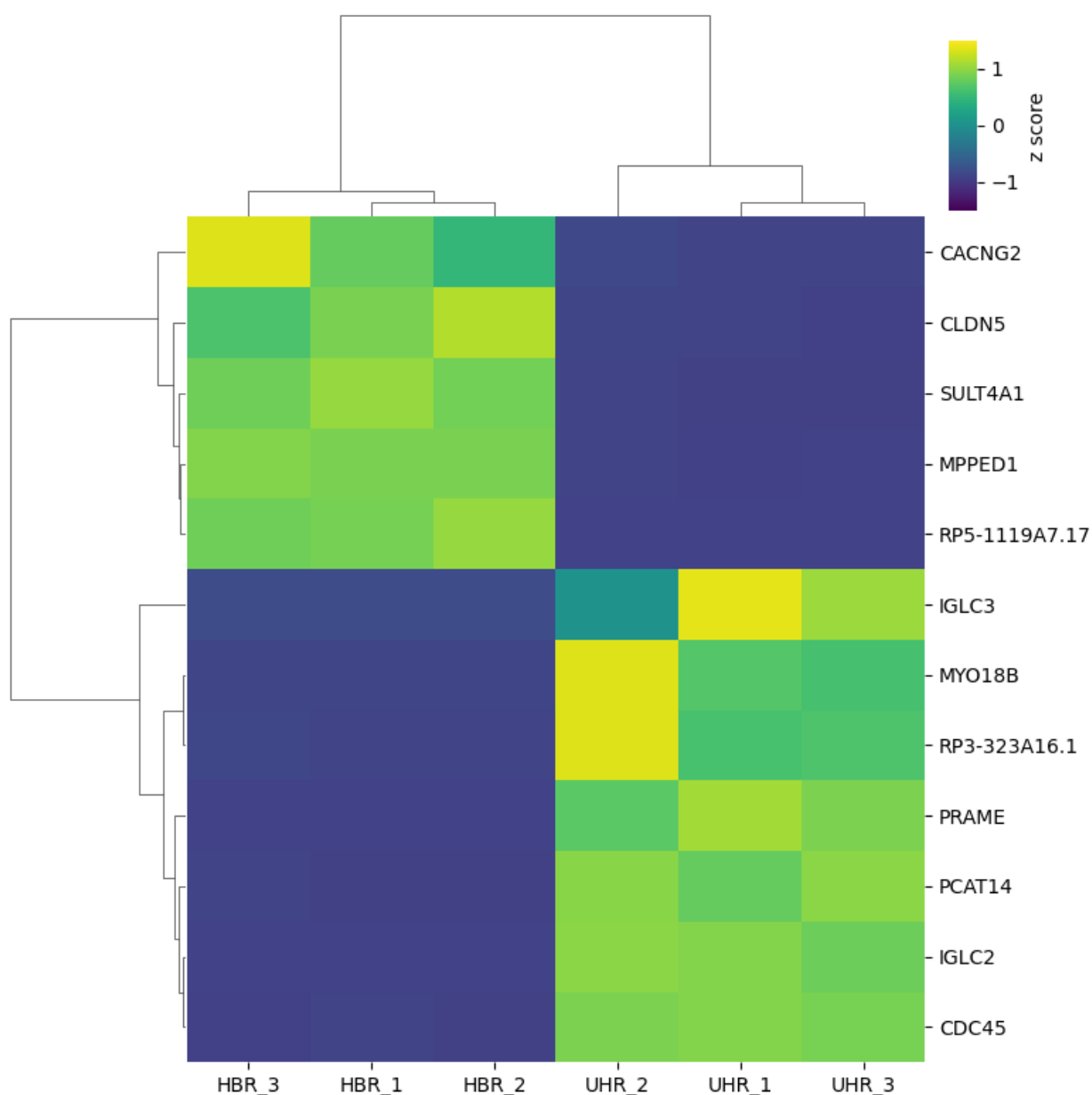
- Data: `hbr_uhr_top_deg_normalized_counts` (the expression counts table imported using `pandas.read_csv`).
- `z_score`: set this to 0 to scale the expression counts for each gene by the `z_score`.

- `cmap`: specify a coloring scheme (ie. `viridis`)
- `figsize`: specify figure size
- `cbar_kws`: specify title for the heatmap color bar using a key-value pair
- `cbar_pos`: specify coordinate to place the heatmap color bar

```
# Import the data
```

```
hbr_uhr_top_deg_normalized_counts=pandas.read_csv("./hbr_uhr_top_deg_
```

```
seaborn.clustermap(hbr_uhr_top_deg_normalized_counts,z_score=0,cmap='  
                    figsize=(8,8),vmin=-1.5, vmax=1.5,cbar_kws={"label":  
                    cbar_pos=(0.855,0.8,0.025,0.15))  
plt.show()
```



R Code in a Python Jupyter Notebook

Using the [rpy2.ipython](<https://rpy2.github.io>) package, users can run R code inside a Python Jupyter Notebook. This package requires user installation (see <https://pypi.org/project/rpy2/> (<https://pypi.org/project/rpy2/>)). To load rpy2.ipython, use %load_ext

```
# Load rpy2.ipython
%load_ext rpy2.ipython
```

Using R to generate a volcano plot

Here, R will be used to generate a volcano plot for the HBR and UHR study differential expression analysis results as was done using Python. To run R code in a Python Jupyter Notebook, place at the top of the code cell `%%R` then proceed to write the R code.

R's `read.csv` function takes on a file path enclosed in `"()` as an argument. There are many options for this command that could alter the default ways in which it imports data. Here, the file `hbr_uhr_deg_chr22_with_significance.csv` will be imported using `read.csv` with default settings and stored as `hbr_uhr_chr22_deg`. The `head` command will be used to preview the first six lines of the data table. Because the `"-` sign in the column name `-log10PAdj` violates R's column heading naming convention, `read.csv` by default changes the `"-` with `"X."`. This column will be renamed `neg.log10PAdj`.

```
%%R
# Import gene expression data using read.csv and store it as variable
hbr_uhr_chr22_deg <- read.csv("../hbr_uhr_deg_chr22_with_significance.csv")
```

```
%%R
# Look at the first few lines of counts using the head command
head(hbr_uhr_chr22_deg)
```

	name	log2FoldChange	PAdj	X.log10PAdj	significance
1	SYNGR1	-4.6	5.2e-217	216.2840	down
2	SEPT3	-4.6	4.5e-204	203.3468	down
3	YWHAH	-2.5	4.7e-191	190.3279	down
4	RPL3	1.7	5.4e-134	133.2676	ns
5	PI4KA	-2.0	2.9e-118	117.5376	down
6	SEZ6L	-5.1	4.2e-109	108.3768	down

```
%%R

# Rename the X.log10PAdj column header to neg.log10PAdj
colnames(hbr_uhr_chr22_deg)[4] <- "neg.log10PAdj"
```

```
%%R
# Load the ggplot2 package using R's library command
library(ggplot2)
```

Using ggplot2 to construct a volcano plot

To create the volcano plot initiate it with the `ggplot` command, which creates a blank plotting canvas. Enclosed in the `ggplot` command are the arguments and these are as follows.

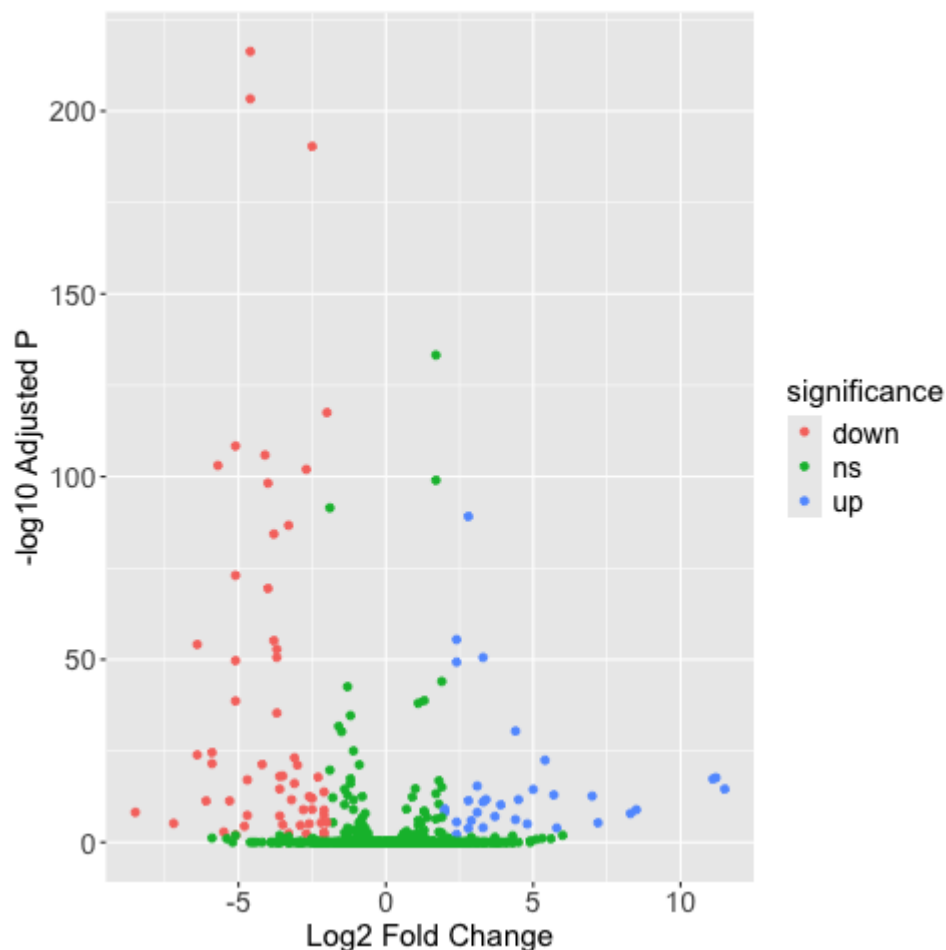
- Data table to generate a plot from: `hbr_uhr_chr22_deg`
- `aes`: specifies aesthetics of the plot include:
 - Values to plot on the x axis (ie. `log2FoldChange`)
 - Values to plot on the y axis (ie. `neg.log10PAdj`)
- What to color the points by (set by `color` and in this example values in the significance column in the data table showing whether gene expression change was statistically significant)

Next, specify the plot type. For a volcano plot (or scatter plot), `geom_point` will be used. The labels for the x and y axes are set by `xlab` and `ylab`, respectively. Finally, inside axis label, tick mark, and legend text font sizes are specified in `theme`.

```
%%R
```

```
# Construct volcano plot.
```

```
ggplot(hbr_uhr_chr22_deg, aes(x=log2FoldChange, y=neg.log10PAdj, color=
geom_point()+xlab("Log2 Fold Change")+ylab("-log10 Adjusted P")+
theme(axis.title.x=element_text(size=15),axis.title.y=element_text(size=15),
axis.text.x=element_text(size=14),axis.text.y=element_text(size=14),
legend.title=element_text(size=15),legend.text=element_text(size=14))
```



Running Unix commands

Users can run Unix commands within a Python Jupyter Notebook. To do this start a code block with "!" followed by the unix command. For instance, using the `pwd` command in the code block below to list the present working directory.

```
!pwd
```

```
/Users/wuz8/Library/CloudStorage/OneDrive-NationalInstitutesofHealth/tutorials/  
document_analysis_with_jupyter/docs/data
```

Writing Formatted Text

See <https://www.markdownguide.org/basic-syntax/> (<https://www.markdownguide.org/basic-syntax/>) for a markdown guide.

Custom heading sizes

Use # to specify heading levels

```
# Heading level 1 (largest)
## Heading level 2 (second largest)
### Heading level 3 (third largest)
...
```

Lists

Un-ordered lists: use * or -

```
- DNA
- RNA
- protein
- metabolite
```

Ordered list: use numbers

```
1. Obtain sequencing data
2. Perform pre-alignment QC
3. Adapter and/or quality trim
3. Align sequencing data to reference genome
4. Obtain gene expression count matrix
5. Run differential expression analysis
6. Pathway analysis
```

Insert images

- Via HTML: ``
- Via markdown: ``

Insert links

`[Description of website](insert url)`

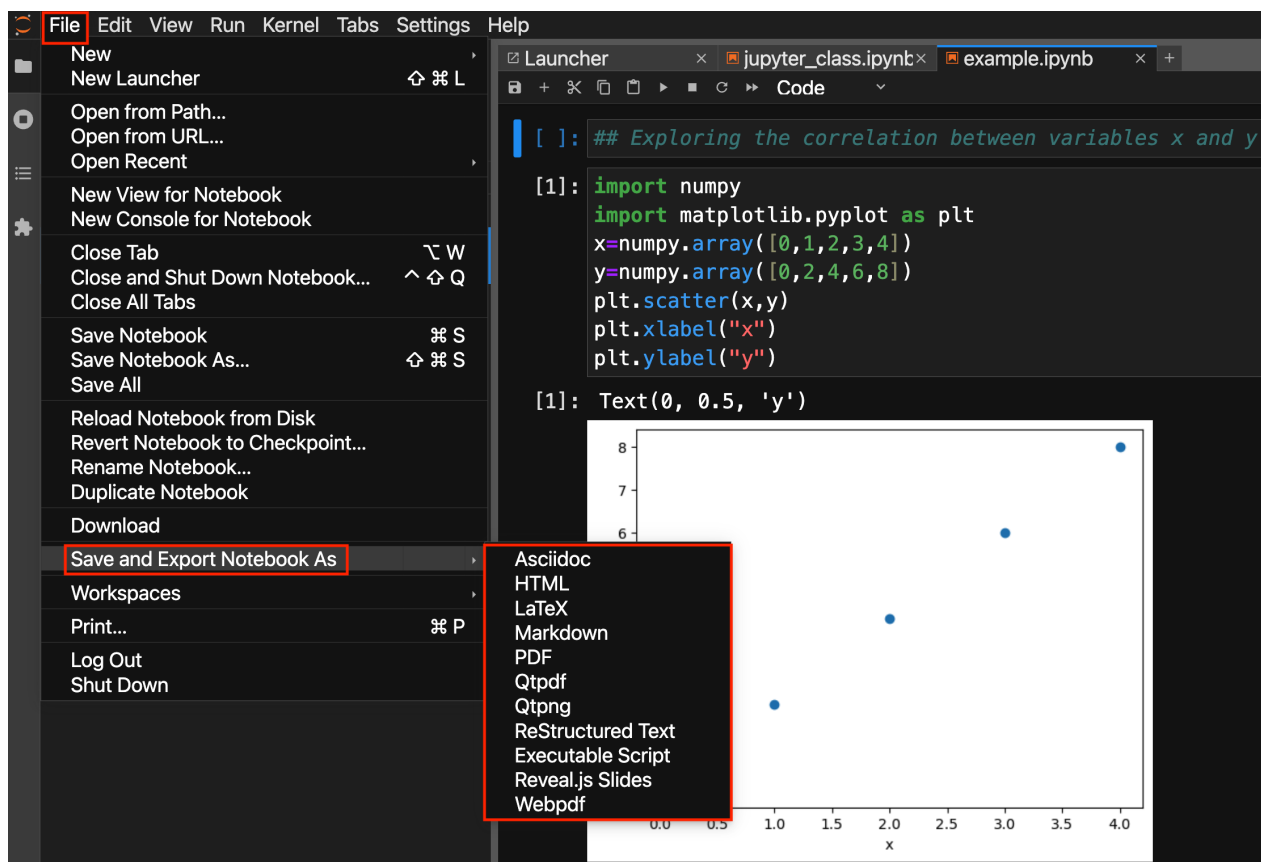
Build a Table of Contents

To build a table of contents that links from one section of a Jupyter notebook to another do the following, where

```
[Display name](#Section-header)
```

- Enclosed in [] is the display name for the link. The display name cannot have punctuations such as commas.
- Enclosed in () is the Markdown header for that section (ie. section header)
 - This is prepended by #
 - Each part the header is connected by -.

Exporting Jupyter Notebook using GUI



Exporting Jupyter Notebook using Command Line

Use the `jupyter nbconvert` command at the command prompt to convert Jupyter Notebook to various available format, including html, pdf, and slides. The format is specified after the `--to` option.

```
jupyter nbconvert --to format
```

Obtain Example Data and Jupyter Notebook

Option 1 for obtaining the class data and example Jupyter Notebook is to download the [jupyter_class_data.zip](#). Users may need to uncompress the zip file if local computer does not automatically do this.

Option 2 is to visit https://github.com/JWrows2014/document_analysis_with_jupyter (https://github.com/JWrows2014/document_analysis_with_jupyter), click on the green button labeled "<> Code" and select "Download as ZIP". The example Jupyter Notebook, data, and images will download as a zip file and unzipping, change into the project folder and start Jupyter Lab to try out the example notebook.

Sharing Jupyter Notebook

- [Github \(https://github.com\)](https://github.com)
 - Static notebook (ie. users will not be able to run)
- [Binder \(https://mybinder.org\)](https://mybinder.org)
 - Provide data
 - Provide list of packages
 - Users can run the notebook
 - [Example \(https://mybinder.org/v2/gh/ncbi/workshop-ncbi-data-with-python/main?filepath=notebooks%2Fworkshop.py\)](https://mybinder.org/v2/gh/ncbi/workshop-ncbi-data-with-python/main?filepath=notebooks%2Fworkshop.py)