How To: Run the ENCODE Transcription Factor (TF) ChIP-seq analysis pipeline on DNAnexus

Overview: In this exercise, we will run the ENCODE Uniform Processing ChIP-seq Pipeline on a small test dataset containing reads from only chromosome 21 from a human ZBED1 ChIP-seq experiment. The biosample was the K562 CML cell line.

The ENCODE Portal page for the experiment is here:
https://www.encodeproject.org/experiments/ENCSR286PCG/

The pipeline was specified by the ENCODE Analysis Working Group and implemented at the ENCODE Data Coordinating Center (DCC). Today we will run the pipeline on the DNAnexus cloud platform.

The ENCODE pipeline code is open-source and lives on github at: https://github.com/ENCODE-DCC/chip-seq-pipeline

Summary of Steps: Here is a high-level summary of what you will learn to do in this exercise.

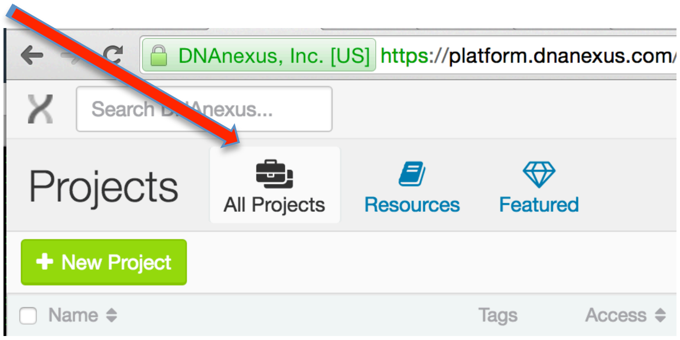
- **Find** the ENCODE Uniform Processing Pipeline project on DNAnexus.
- **Copy** the pipeline software and files from that project to a new project in your account.
- **Complete** the specification of inputs to the workflow.
- **Run** the pipeline workflow on the cloud.
- **Monitor** the run's progress.
- **Visualize** the output.

Skip ahead to step 9 if you have already copied the ChIP-seq pipeline files from the ENCODE Universal Pipelines project.

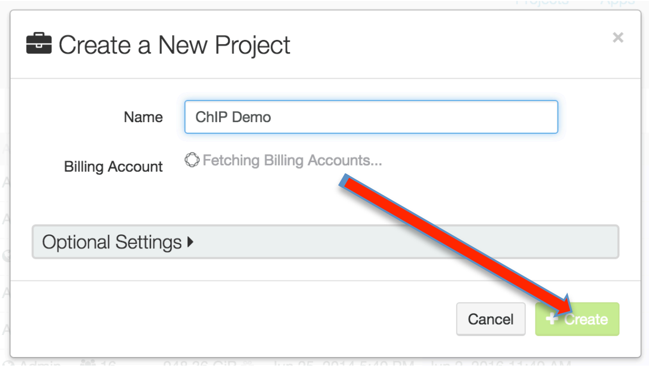
Step-by-step:

1) You will need to create an account on the DNAnexus website www.dnanexus.com. Log in to your DNAnexus account.

2) Once logged into your DNAnexus account, create a new project. Select "All Projects" and then click "New Project".



3) Give your project a new name and click "Create".

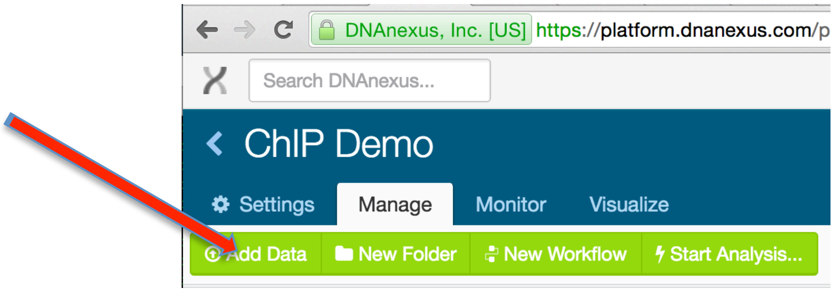


Create a New Project

Name: ChIP Demo

Billing Account: Fetching Billing Accounts...

4) Select “Add Data” …

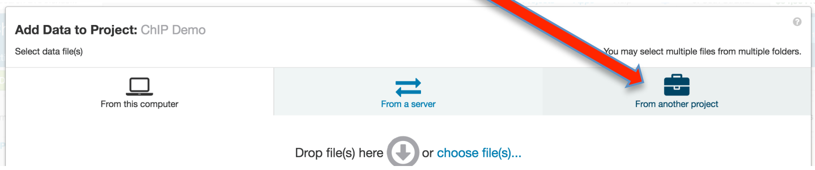


DNAnexus, Inc. [US] https://platform.dnanexus.com/p

Search DNAnexus...

ChIP Demo

5) … select “From another project” …



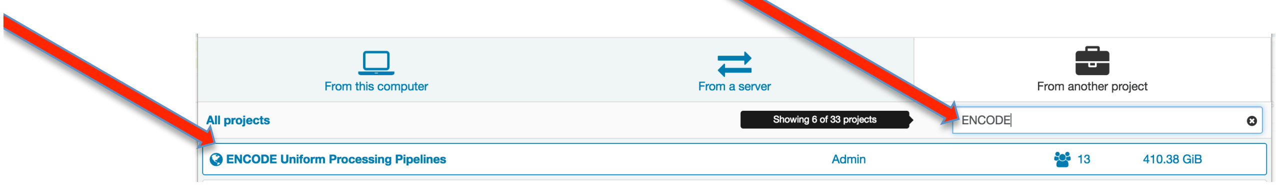
Add Data to Project: ChIP Demo

Select data file(s)

You may select multiple files from multiple folders.

Drop file(s) here or choose file(s)...

6) Type “ENCODE” in the search box and select “ENCODE Uniform Processing Pipelines”

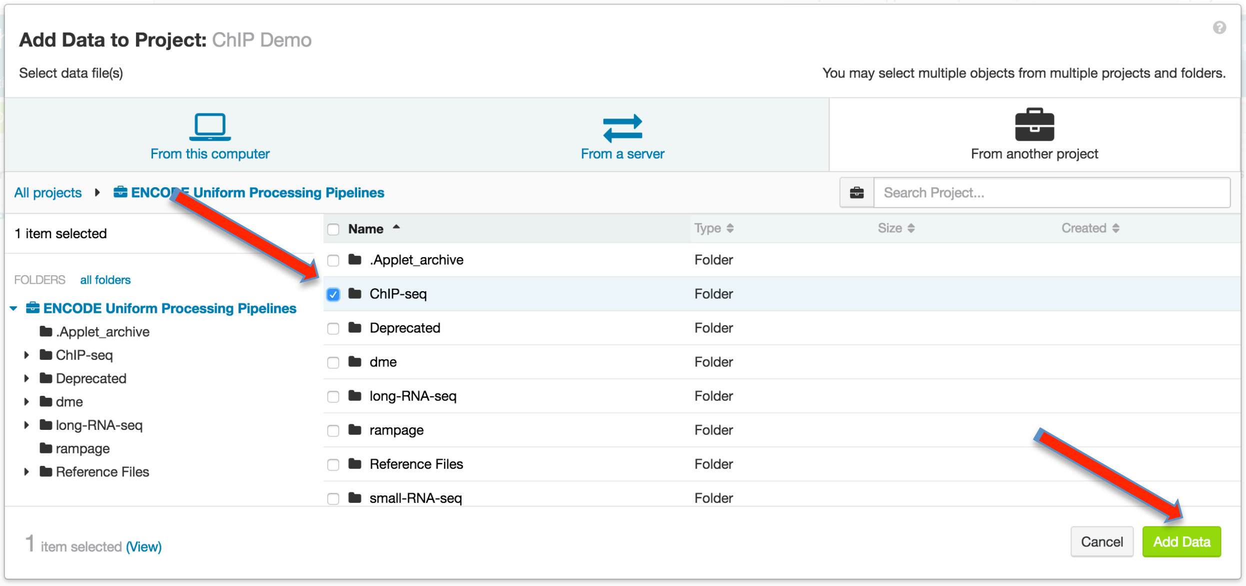


Showing 6 of 33 projects

ENCODE

ENCODE Uniform Processing Pipelines	Admin	13	410.38 GiB

7) Click the box next to “ChIP-seq” and select “Add Data”.



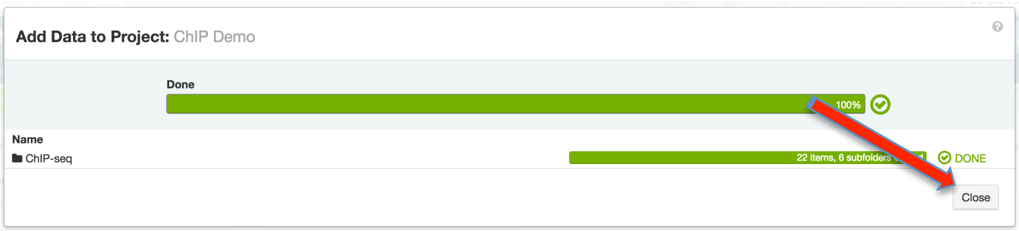
Add Data to Project: ChIP Demo

Select data file(s)

You may select multiple objects from multiple projects and folders.

	Name	Type	Size	Created
□	.Applet_archive	Folder		
☑	ChIP-seq	Folder		
□	Deprecated	Folder		
□	dme	Folder		
□	long-RNA-seq	Folder		
□	rampage	Folder		
□	Reference Files	Folder		
□	small-RNA-seq	Folder		

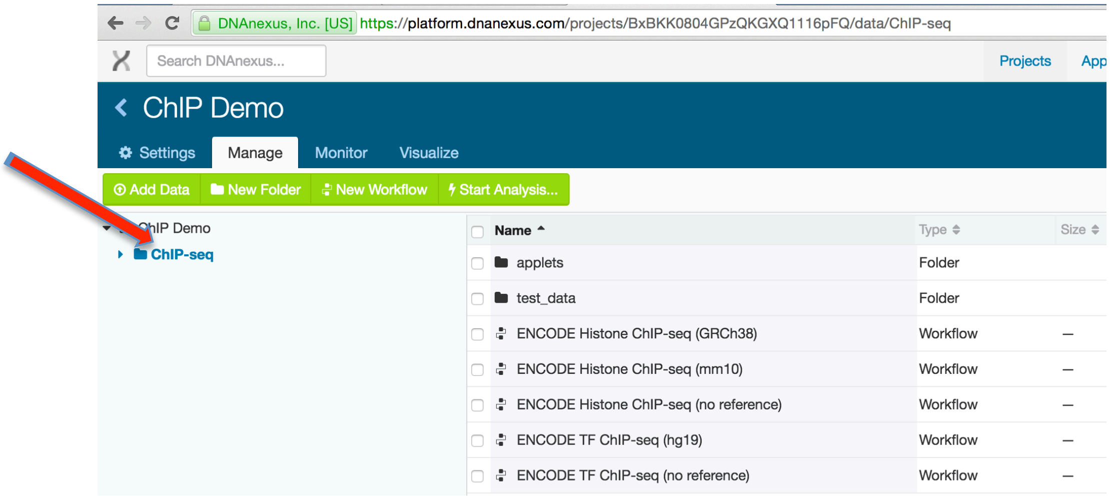
8) When finished, the following pop-up window should appear. Click “Close”.



Add Data to Project: ChIP Demo

Name		
ChIP-seq	22 items, 6 subfolders	DONE

9) To open the ChIP-seq folder, click the “ChIP-seq” text. You should see the files copied to your project.

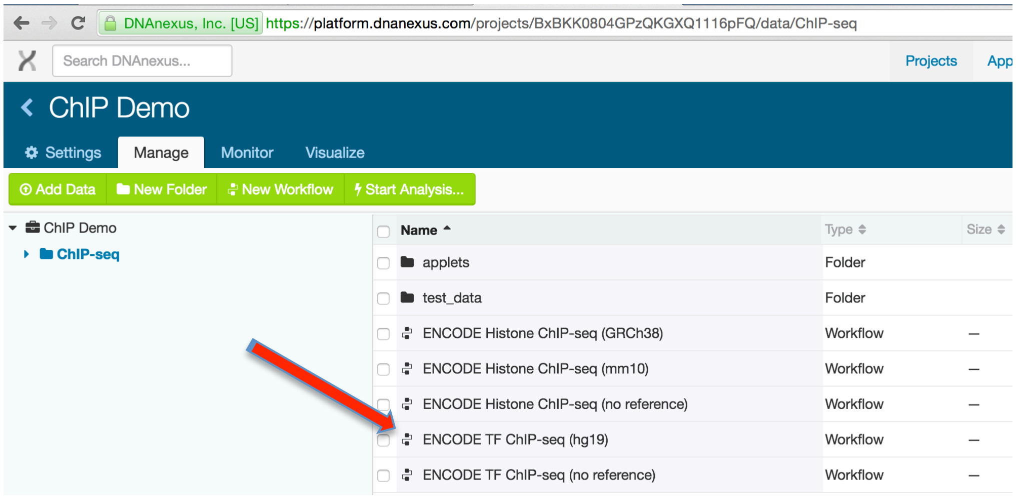


DNAnexus, Inc. [US] https://platform.dnanexus.com/projects/BxBKK0804GPzQKGXQ1116pFQ/data/ChIP-seq

	Name	Type	Size
□	applets	Folder	
□	test_data	Folder	
□	ENCODE Histone ChIP-seq (GRCh38)	Workflow	—
□	ENCODE Histone ChIP-seq (mm10)	Workflow	—
□	ENCODE Histone ChIP-seq (no reference)	Workflow	—
□	ENCODE TF ChIP-seq (hg19)	Workflow	—
□	ENCODE TF ChIP-seq (no reference)	Workflow	—

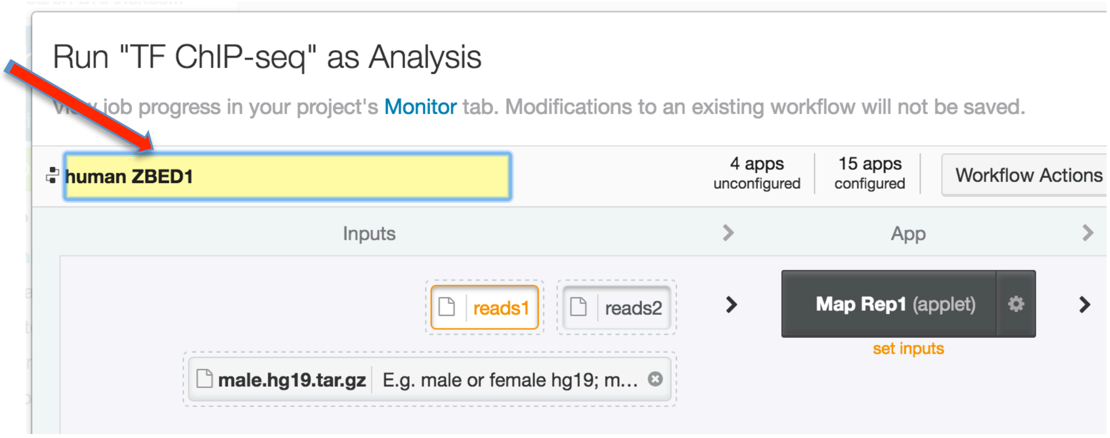
10) The example data in this exercise is from a human histone ChIP experiment, which we will map to the human hg19 assembly. Click on the “ENCODE TF ChIP-seq (hg19)” workflow to

open it.



Name	Type	Size
applets	Folder	
test_data	Folder	
ENCODE Histone ChIP-seq (GRCh38)	Workflow	—
ENCODE Histone ChIP-seq (mm10)	Workflow	—
ENCODE Histone ChIP-seq (no reference)	Workflow	—
ENCODE TF ChIP-seq (hg19)	Workflow	—
ENCODE TF ChIP-seq (no reference)	Workflow	—

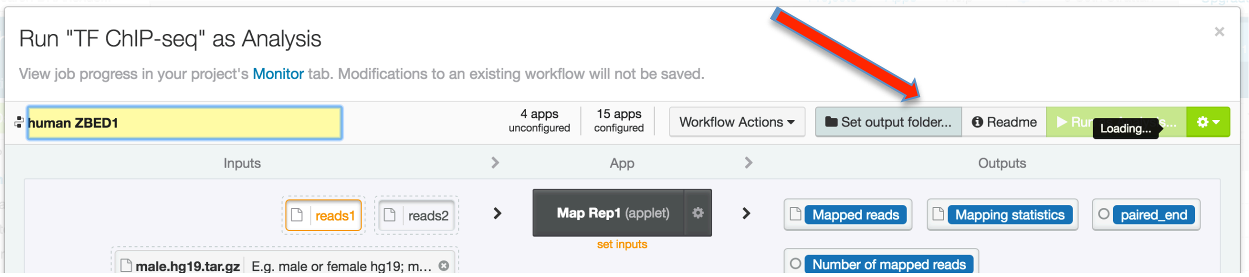
11) This window represents an “Analysis”, which is an instantiation of the TF ChIP-seq workflow. Give the analysis a name, like “human ZBED1”


Run "TF ChIP-seq" as Analysis

View job progress in your project's Monitor tab. Modifications to an existing workflow will not be saved.

human ZBED1

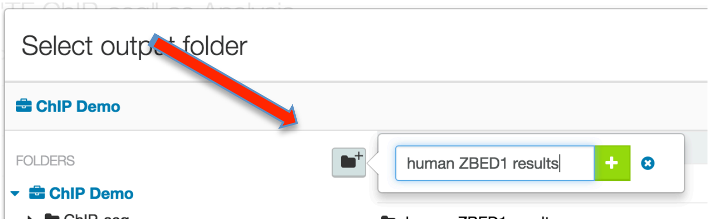
12) Click on “Set output folder …”


Run "TF ChIP-seq" as Analysis

View job progress in your project's Monitor tab. Modifications to an existing workflow will not be saved.

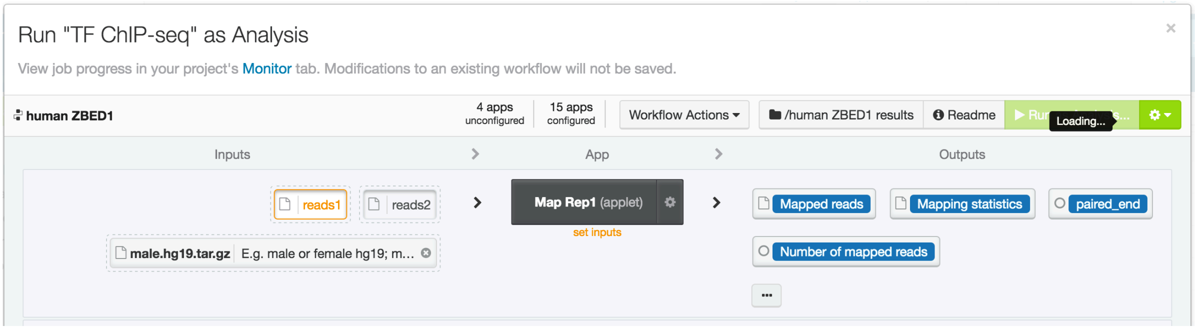
human ZBED1

13) Click on the new folder button to create a new folder and name it something like “human ZBED1 results”.



Select output folder

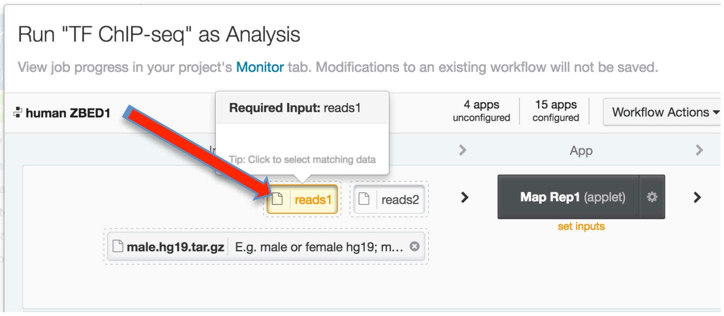
14) Now you should have named your analysis and specified an output folder for the results. Your workflow window should look like this:



Run "TF ChIP-seq" as Analysis

View job progress in your project's Monitor tab. Modifications to an existing workflow will not be saved.

15) Select the “reads1” input box for the “Map Rep1” stage (the first step in the workflow). Note that the data in this example are from single-end sequencing, so all the “reads2” inputs will be left blank. In a paired-end experiment the second fastq of the paired reads for each replicate would go in “reads2”.



Run "TF ChIP-seq" as Analysis

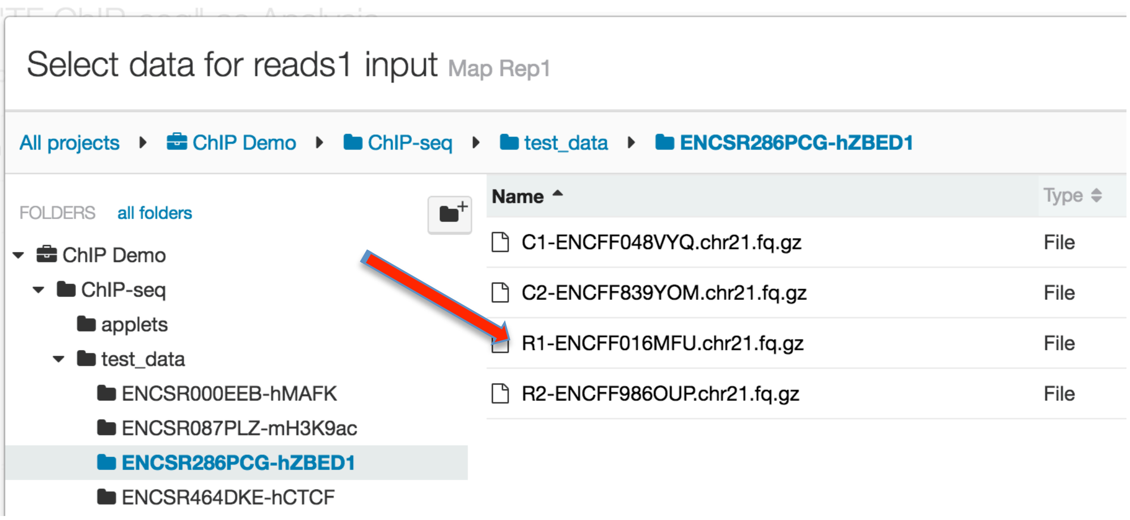
View job progress in your project's Monitor tab. Modifications to an existing workflow will not be saved.

Required Input: reads1

Tip: Click to select matching data

16) A new window opens where you will navigate to the input files. Expand the “Chip-seq” and then the “test_data” and then the “ENCSR286PCG-hZBED1” folders to see the list of data files. **Make sure to select the subfolder ENCSR286PCG-hZBED1 to limit the display to just the data for this experiment.**

The ENCSR286PCG-hZBED1 folder contains only reads for chromosome 21 from this experiment, for faster processing.



Select data for reads1 input Map Rep1

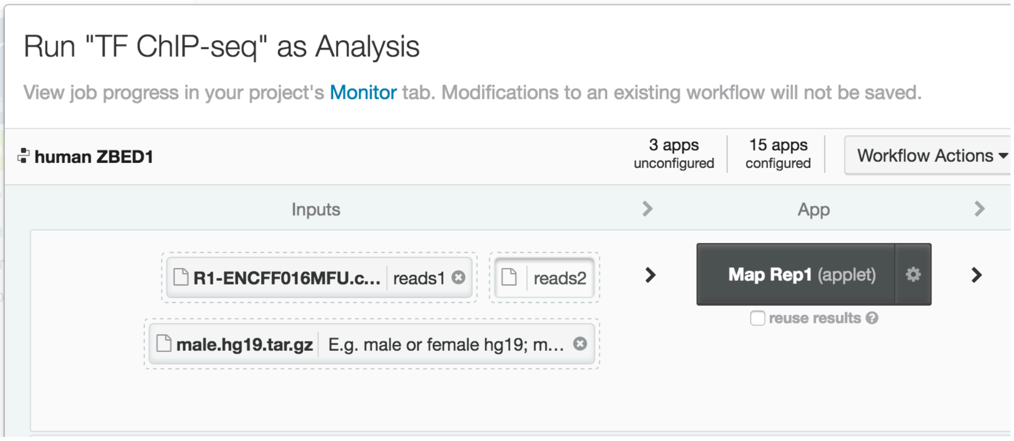
All projects ▸ ChIP Demo ▸ ChIP-seq ▸ test_data ▸ ENCSR286PCG-hZBED1

FOLDERS all folders

- ChIP Demo
  - ChIP-seq
    - applets
    - test_data
      - ENCSR000EEB-hMAFK
      - ENCSR087PLZ-mH3K9ac
      - ENCSR286PCG-hZBED1
      - ENCSR464DKE-hCTCF

Name ▴	Type
C1-ENCFF048VYQ.chr21.fq.gz	File
C2-ENCFF839YOM.chr21.fq.gz	File
R1-ENCFF016MFU.chr21.fq.gz	File
R2-ENCFF986OUP.chr21.fq.gz	File

17) Select "R1-ENCFF016MFU.chr21.fq.gz". You have now specified the input fastq for replicate 1 of this experiment.



Run "TF ChIP-seq" as Analysis

View job progress in your project's Monitor tab. Modifications to an existing workflow will not be saved.

human ZBED1 — 3 apps unconfigured — 15 apps configured — Workflow Actions

Inputs › App ›

R1-ENCFF016MFU.c... reads1 — reads2 › Map Rep1 (applet) ›

male.hg19.tar.gz E.g. male or female hg19; m...

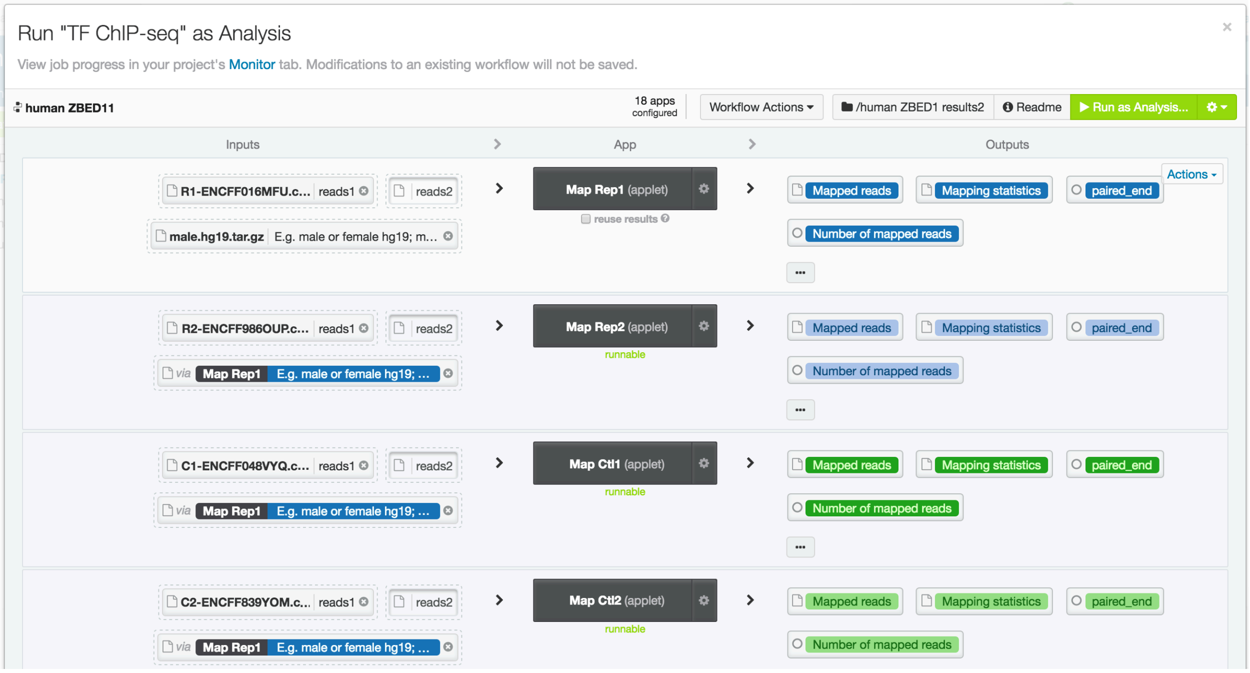
□ reuse results

18) Repeat the process to populate the reads1 inputs for the "Map Rep2" step, the "Map Ctl1" step, and the "Map Ctl2" step. The Rep2 input starts with "R2". The control inputs start with "C1" and "C2", respectively. Since the data for this experiment are produced by single-end sequencing, there are no inputs for "reads2". **Note: Make sure you choose the inputs that go with this experiment. They are all in the subfolder ENCSR286PCG-hZBED1**.

Here is a summary of the input files for this experiment:

Map Rep1: *R1-ENCFF016MFU.chr21.fq.gz*
Map Rep2: *R2-ENCFF986OUP.chr21.fq.gz*
Map Ctl1: *C1-ENCFF048VYQ.chr21.fq.gz*
Map Ctl2: *C2-ENCFF839YOM.chr21.fq.gz*

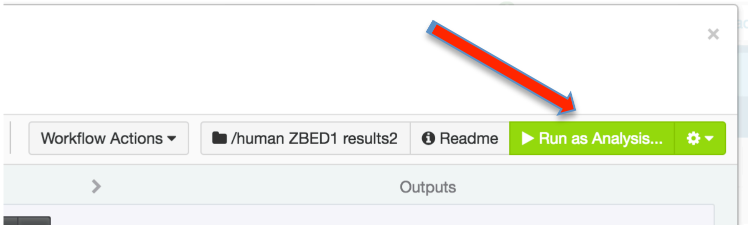
After you have populated all the "reads1" inputs, your workflow should look like this:



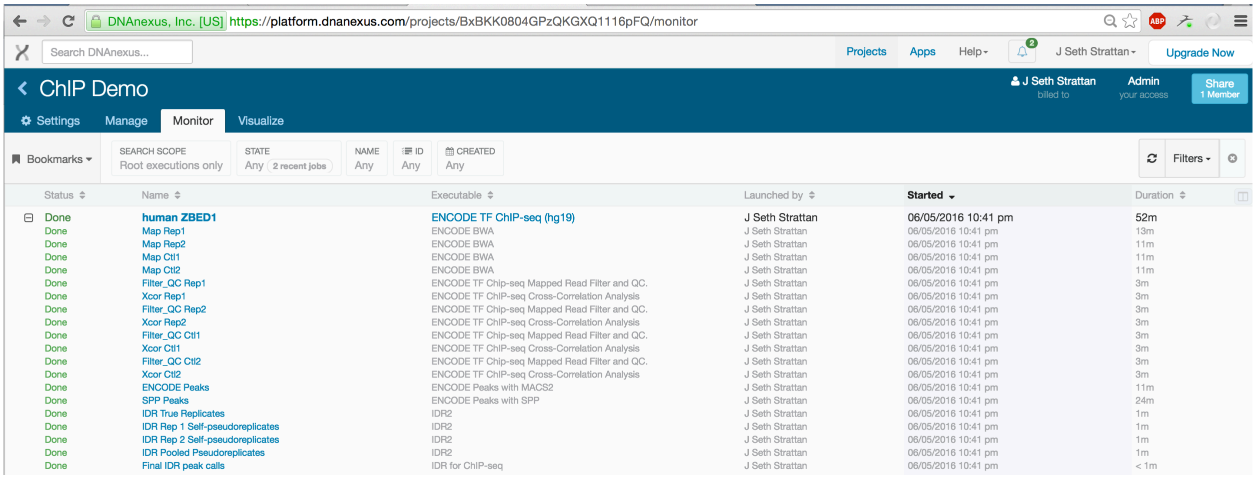
Run "TF ChIP-seq" as Analysis

View job progress in your project's Monitor tab. Modifications to an existing workflow will not be saved.

19) All of the other inputs, including the indexed hg19 genome reference, have been pre-filled in this workflow. All input requirements are satisfied, so click “Run as Analysis” to start the analysis.



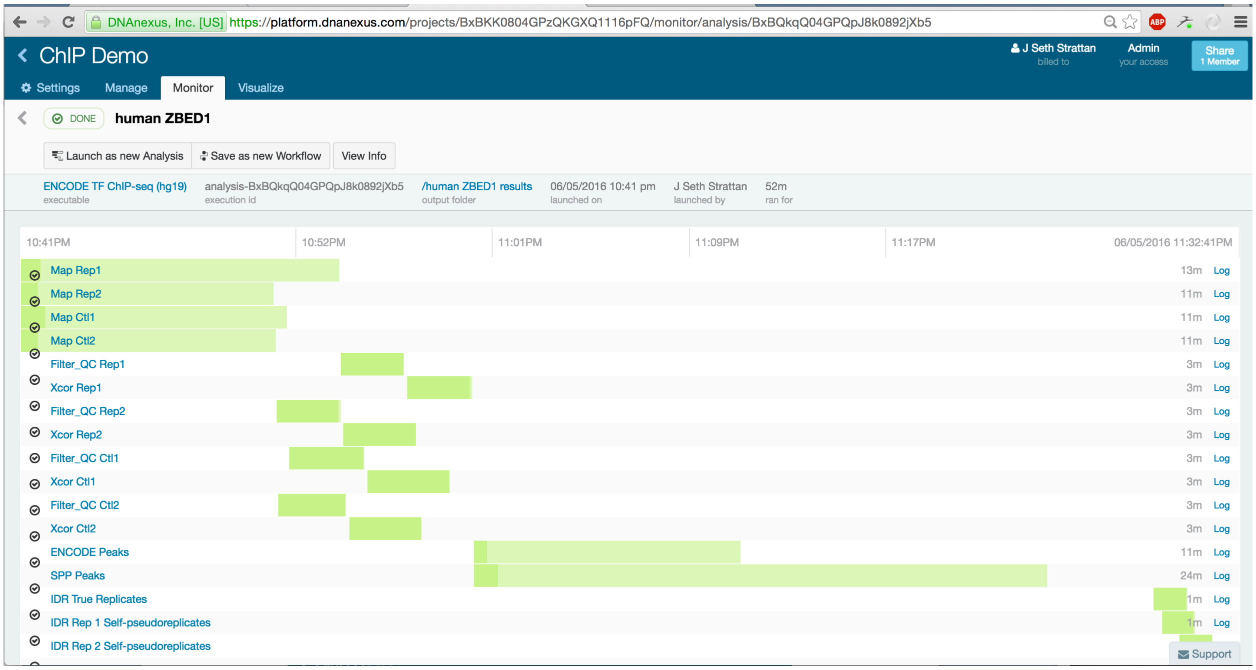
20) Starting the analysis will bring up the “Monitor” tab which will display the details of the pipeline steps as they run. Click on the “+” box to see all the analysis subjobs. If necessary, the “Terminate” button can be used to cancel the analysis.



SEARCH SCOPE: Root executions only
STATE: Any (2 recent jobs)
NAME: Any
ID: Any
CREATED: Any

	Status	Name	Executable	Launched by	Started	Duration
⊟	Done	human ZBED1	ENCODE TF ChIP-seq (hg19)	J Seth Strattan	06/05/2016 10:41 pm	52m
	Done	Map Rep1	ENCODE BWA	J Seth Strattan	06/05/2016 10:41 pm	13m
	Done	Map Rep2	ENCODE BWA	J Seth Strattan	06/05/2016 10:41 pm	11m
	Done	Map Ctl1	ENCODE BWA	J Seth Strattan	06/05/2016 10:41 pm	11m
	Done	Map Ctl2	ENCODE BWA	J Seth Strattan	06/05/2016 10:41 pm	11m
	Done	Filter_QC Rep1	ENCODE TF Chip-seq Mapped Read Filter and QC.	J Seth Strattan	06/05/2016 10:41 pm	3m
	Done	Xcor Rep1	ENCODE TF ChIP-seq Cross-Correlation Analysis	J Seth Strattan	06/05/2016 10:41 pm	3m
	Done	Filter_QC Rep2	ENCODE TF Chip-seq Mapped Read Filter and QC.	J Seth Strattan	06/05/2016 10:41 pm	3m
	Done	Xcor Rep2	ENCODE TF ChIP-seq Cross-Correlation Analysis	J Seth Strattan	06/05/2016 10:41 pm	3m
	Done	Filter_QC Ctl1	ENCODE TF Chip-seq Mapped Read Filter and QC.	J Seth Strattan	06/05/2016 10:41 pm	3m
	Done	Xcor Ctl1	ENCODE TF ChIP-seq Cross-Correlation Analysis	J Seth Strattan	06/05/2016 10:41 pm	3m
	Done	Filter_QC Ctl2	ENCODE TF Chip-seq Mapped Read Filter and QC.	J Seth Strattan	06/05/2016 10:41 pm	3m
	Done	Xcor Ctl2	ENCODE TF ChIP-seq Cross-Correlation Analysis	J Seth Strattan	06/05/2016 10:41 pm	3m
	Done	ENCODE Peaks	ENCODE Peaks with MACS2	J Seth Strattan	06/05/2016 10:41 pm	11m
	Done	SPP Peaks	ENCODE Peaks with SPP	J Seth Strattan	06/05/2016 10:41 pm	24m
	Done	IDR True Replicates	IDR2	J Seth Strattan	06/05/2016 10:41 pm	1m
	Done	IDR Rep 1 Self-pseudoreplicates	IDR2	J Seth Strattan	06/05/2016 10:41 pm	1m
	Done	IDR Rep 2 Self-pseudoreplicates	IDR2	J Seth Strattan	06/05/2016 10:41 pm	1m
	Done	IDR Pooled Pseudoreplicates	IDR2	J Seth Strattan	06/05/2016 10:41 pm	1m
	Done	Final IDR peak calls	IDR for ChIP-seq	J Seth Strattan	06/05/2016 10:41 pm	< 1m

21) Click on the analysis name (here we’ve named it “human ZBED1”) to watch the progress of each stage.



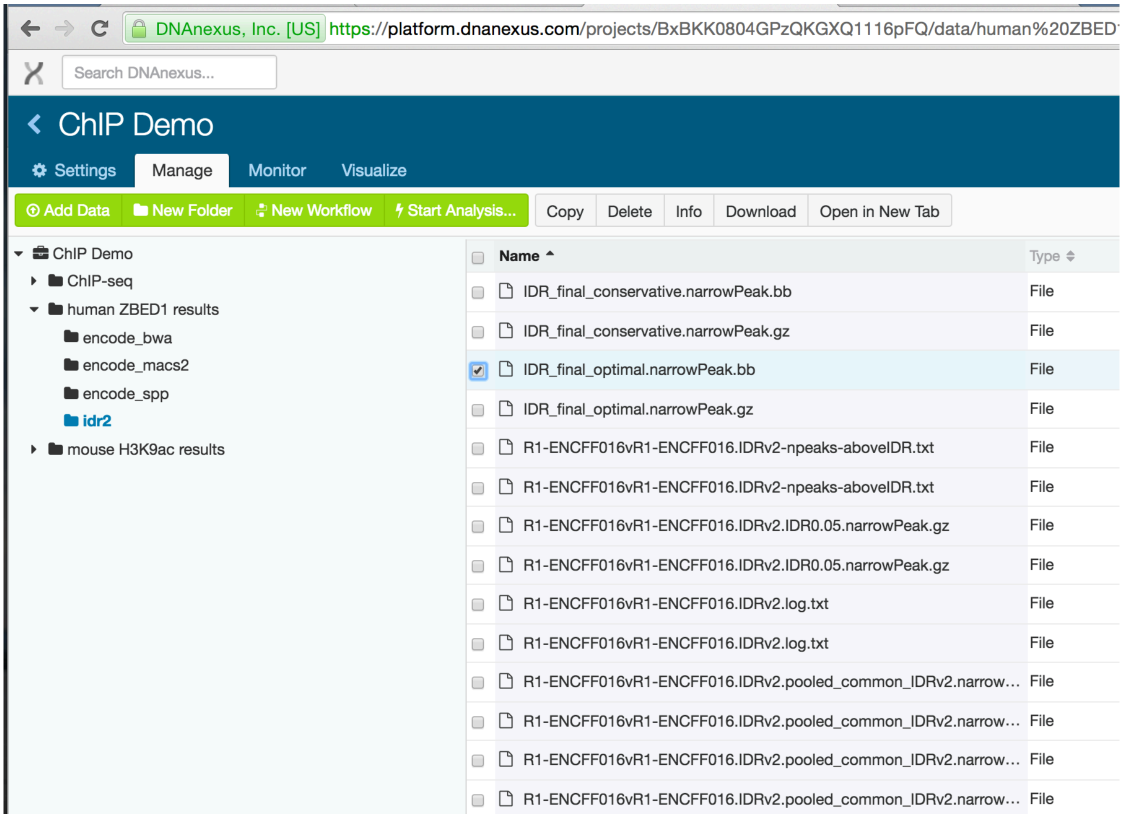
DNAnexus, Inc. [US] https://platform.dnanexus.com/projects/BxBKK0804GPzQKGXQ1116pFQ/monitor/analysis/BxBQkqQ04GPQpJ8k0892jXb5

human ZBED1

executable	execution id	output folder	launched on	launched by	ran for
ENCODE TF ChIP-seq (hg19)	analysis-BxBQkqQ04GPQpJ8k0892jXb5	/human ZBED1 results	06/05/2016 10:41 pm	J Seth Strattan	52m

Map Rep1	13m	Log
Map Rep2	11m	Log
Map Ctl1	11m	Log
Map Ctl2	11m	Log
Filter_QC Rep1	3m	Log
Xcor Rep1	3m	Log
Filter_QC Rep2	3m	Log
Xcor Rep2	3m	Log
Filter_QC Ctl1	3m	Log
Xcor Ctl1	3m	Log
Filter_QC Ctl2	3m	Log
Xcor Ctl2	3m	Log
ENCODE Peaks	11m	Log
SPP Peaks	24m	Log
IDR True Replicates	1m	Log
IDR Rep 1 Self-pseudoreplicates	1m	Log
IDR Rep 2 Self-pseudoreplicates		

22) Within the output folder you specified above, the results of the mapping stages can be found in the “encode_bwa” subfolder, the output of the signal-generation stage can be found in the “encode_macs2” subfolder, and the final peak calls are in the “idr2” subfolder.



DNAnexus, Inc. [US] https://platform.dnanexus.com/projects/BxBKK0804GPzQKGXQ1116pFQ/data/human%20ZBED

- ChIP Demo
  - ChIP-seq
  - human ZBED1 results
    - encode_bwa
    - encode_macs2
    - encode_spp
    - idr2
  - mouse H3K9ac results

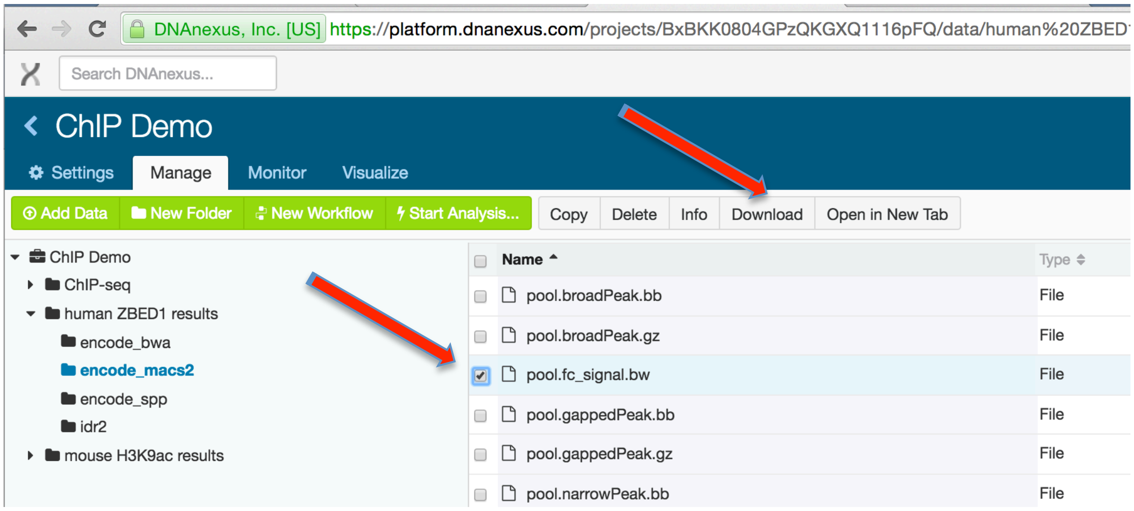
	Name	Type
□	IDR_final_conservative.narrowPeak.bb	File
□	IDR_final_conservative.narrowPeak.gz	File
☑	IDR_final_optimal.narrowPeak.bb	File
□	IDR_final_optimal.narrowPeak.gz	File
□	R1-ENCFF016vR1-ENCFF016.IDRv2-npeaks-aboveIDR.txt	File
□	R1-ENCFF016vR1-ENCFF016.IDRv2-npeaks-aboveIDR.txt	File
□	R1-ENCFF016vR1-ENCFF016.IDRv2.IDR0.05.narrowPeak.gz	File
□	R1-ENCFF016vR1-ENCFF016.IDRv2.IDR0.05.narrowPeak.gz	File
□	R1-ENCFF016vR1-ENCFF016.IDRv2.log.txt	File
□	R1-ENCFF016vR1-ENCFF016.IDRv2.log.txt	File
□	R1-ENCFF016vR1-ENCFF016.IDRv2.pooled_common_IDRv2.narrow…	File
□	R1-ENCFF016vR1-ENCFF016.IDRv2.pooled_common_IDRv2.narrow…	File
□	R1-ENCFF016vR1-ENCFF016.IDRv2.pooled_common_IDRv2.narrow…	File
□	R1-ENCFF016vR1-ENCFF016.IDRv2.pooled_common_IDRv2.narrow…	File

23) In a production environment, you will develop procedures or scripts to visualize and archive the results of multiple pipeline runs. But temporary URL’s can be generated for all outputs and used to quickly visualize some of the pipeline results. For this example, let’s look at the

pooled signal track and the final, replicated peak set. In the “encode_macs2” folder, select the following output file:

Pooled fold-over-control signal:
pool.fc_signal.bw

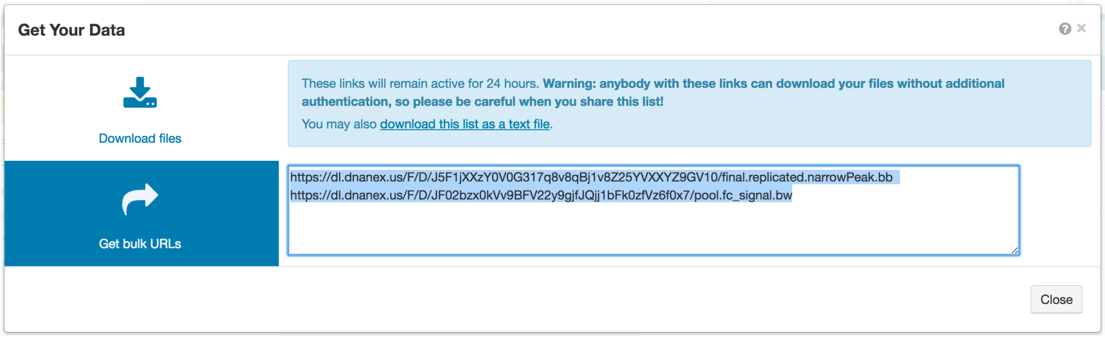
After selecting the file, click the “Download” button.



DNAnexus, Inc. [US] https://platform.dnanexus.com/projects/BxBKK0804GPzQKGXQ1116pFQ/data/human%20ZBED

	Name	Type
□	pool.broadPeak.bb	File
□	pool.broadPeak.gz	File
☑	pool.fc_signal.bw	File
□	pool.gappedPeak.bb	File
□	pool.gappedPeak.gz	File
□	pool.narrowPeak.bb	File

24) A new window will pop up. Select “Get bulk URLs” and copy the list of URLs. These URL’s will link to your output files and will remain active for 24 hours.

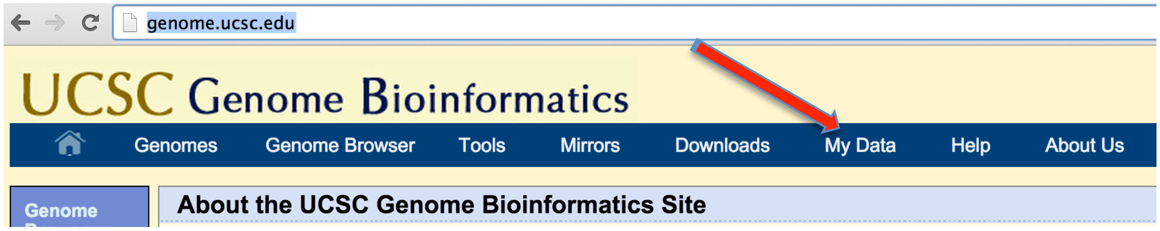


These links will remain active for 24 hours. **Warning: anybody with these links can download your files without additional authentication, so please be careful when you share this list!**

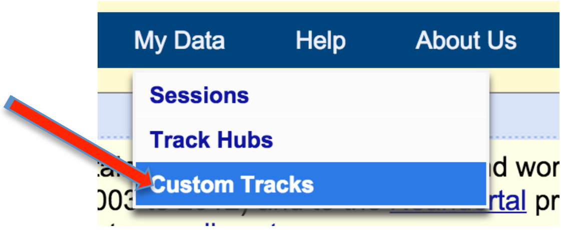
You may also download this list as a text file.

```
https://dl.dnanex.us/F/D/J5F1jXXzY0V0G317q8v8qBj1v8Z25YVXXYZ9GV10/final.replicated.narrowPeak.bb
https://dl.dnanex.us/F/D/JF02bzx0kVv9BFV22y9gjfJQjj1bFk0zfVz6f0x7/pool.fc_signal.bw
```

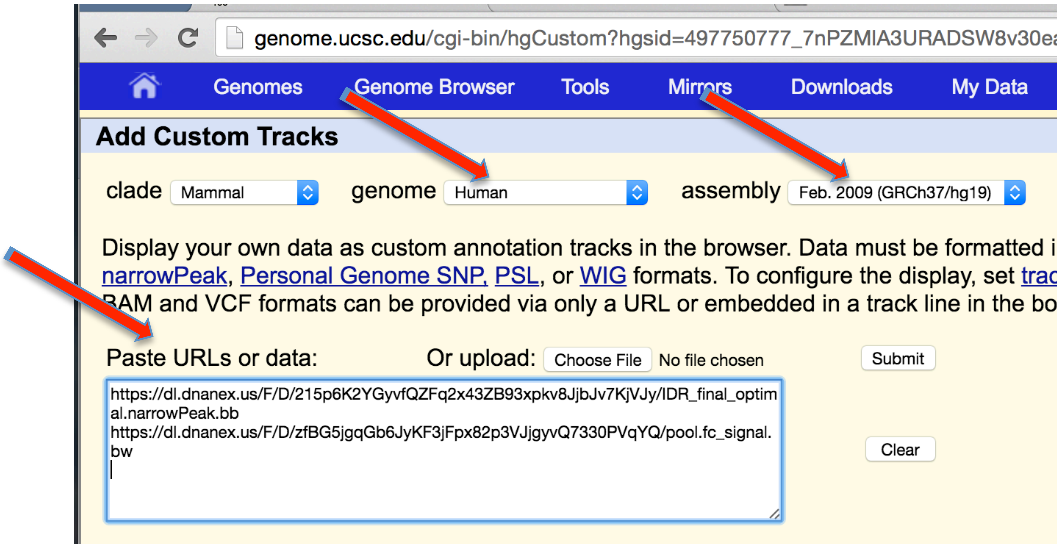
25) In this example you will use the UCSC Genome browser to visualize the results you just calculated as “custom tracks”. In a new web browser window or tab, go to http://genome.ucsc.edu/ and select “My Data” from the top options bar.



26) Select “Custom Tracks” from the options menu.



27) Paste the URLs you copied above into the text window. Be sure the reference genome is correct for this file (human hg19 for this demo). ***Tip: The UCSC Genome Browser is sensitive to white-space at the end of URL's. If there are spaces after the URL's you've pasted, delete them and make sure each URL is on its own line.***
Don't click "Submit", yet. We need one more track.



genome.ucsc.edu/cgi-bin/hgCustom?hgsid=497750777_7nPZMIA3URADSW8v30ea

Add Custom Tracks

clade Mammal genome Human assembly Feb. 2009 (GRCh37/hg19)

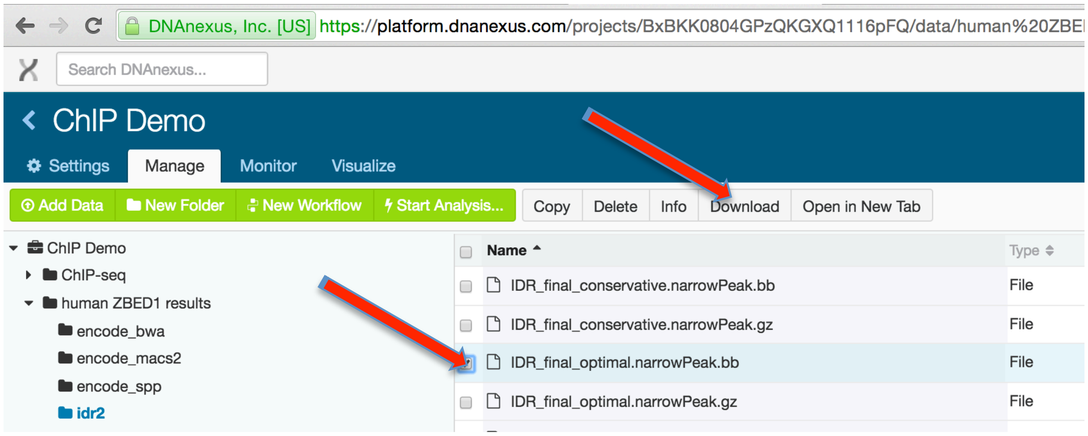
Display your own data as custom annotation tracks in the browser. Data must be formatted i
narrowPeak, Personal Genome SNP, PSL, or WIG formats. To configure the display, set trac
BAM and VCF formats can be provided via only a URL or embedded in a track line in the bo

Paste URLs or data: Or upload: No file chosen

```
https://dl.dnanex.us/F/D/215p6K2YGyvfQZFq2x43ZB93xpkv8JjbJv7KjVJy/IDR_final_optim
al.narrowPeak.bb
https://dl.dnanex.us/F/D/zfBG5jgqGb6JyKF3jFpx82p3VJjgyvQ7330PVqYQ/pool.fc_signal.
bw
```

28) In the same way that you generated a URL for the signal track, go back and generate a URL for the final replicated peak set. It is in the subfolder "idr2" and it is called:

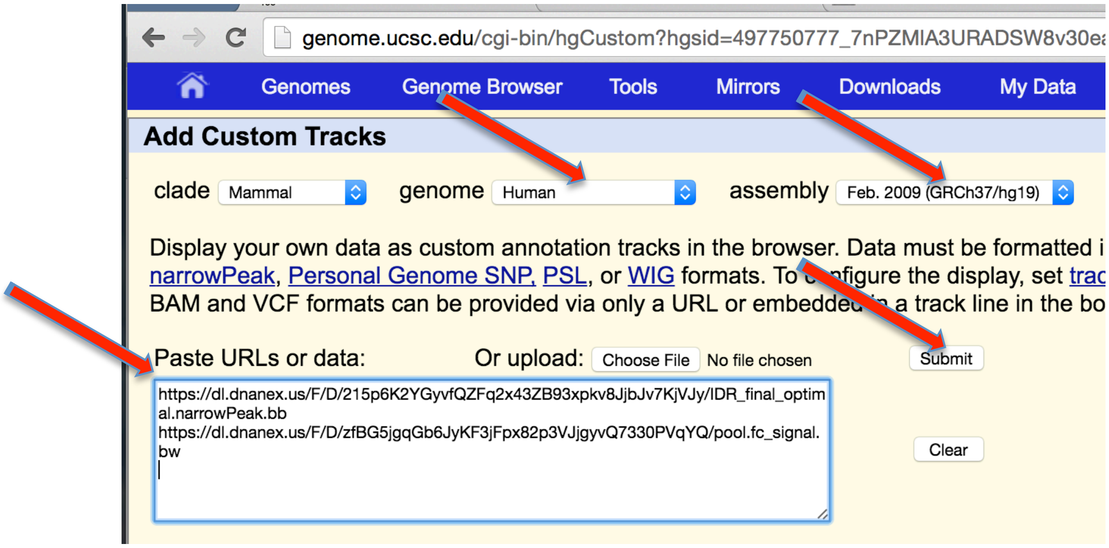
IDR_final_optimal_narrowPeak.bb



DNAnexus, Inc. [US] https://platform.dnanexus.com/projects/BxBKK0804GPzQKGXQ1116pFQ/data/human%20ZBE

Name	Type
IDR_final_conservative.narrowPeak.bb	File
IDR_final_conservative.narrowPeak.gz	File
IDR_final_optimal.narrowPeak.bb	File
IDR_final_optimal.narrowPeak.gz	File

Generate and copy the URL in the same way you did above and paste it into your "Add Custom Tracks" UCSC Genome Browser window. Click submit when you have both URL's pasted onto their own lines.



genome.ucsc.edu/cgi-bin/hgCustom?hgsid=497750777_7nPZMIA3URADSW8v30e

Add Custom Tracks

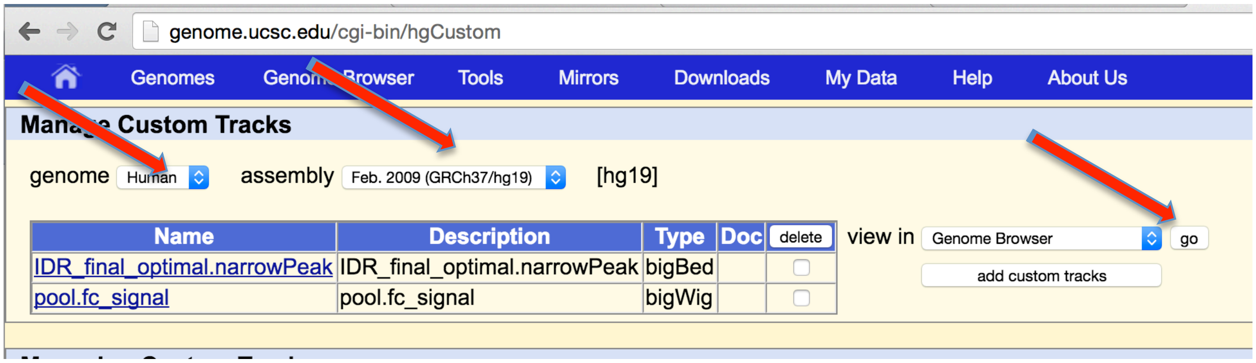
clade Mammal   genome Human   assembly Feb. 2009 (GRCh37/hg19)

Display your own data as custom annotation tracks in the browser. Data must be formatted i
narrowPeak, Personal Genome SNP, PSL, or WIG formats. To configure the display, set trac
BAM and VCF formats can be provided via only a URL or embedded in a track line in the bo

Paste URLs or data: Or upload: No file chosen

```
https://dl.dnanex.us/F/D/215p6K2YGyvfQZFq2x43ZB93xpkv8JjbJv7KjVJy/IDR_final_optimal.narrowPeak.bb
https://dl.dnanex.us/F/D/zfBG5jgqGb6JyKF3jFpx82p3VJjgyvQ7330PVqYQ/pool.fc_signal.bw
```

29) This will bring up the “Manage Custom Tracks” page. Double-check the assembly, and select “go” to visualize the tracks.



genome.ucsc.edu/cgi-bin/hgCustom

Manage Custom Tracks

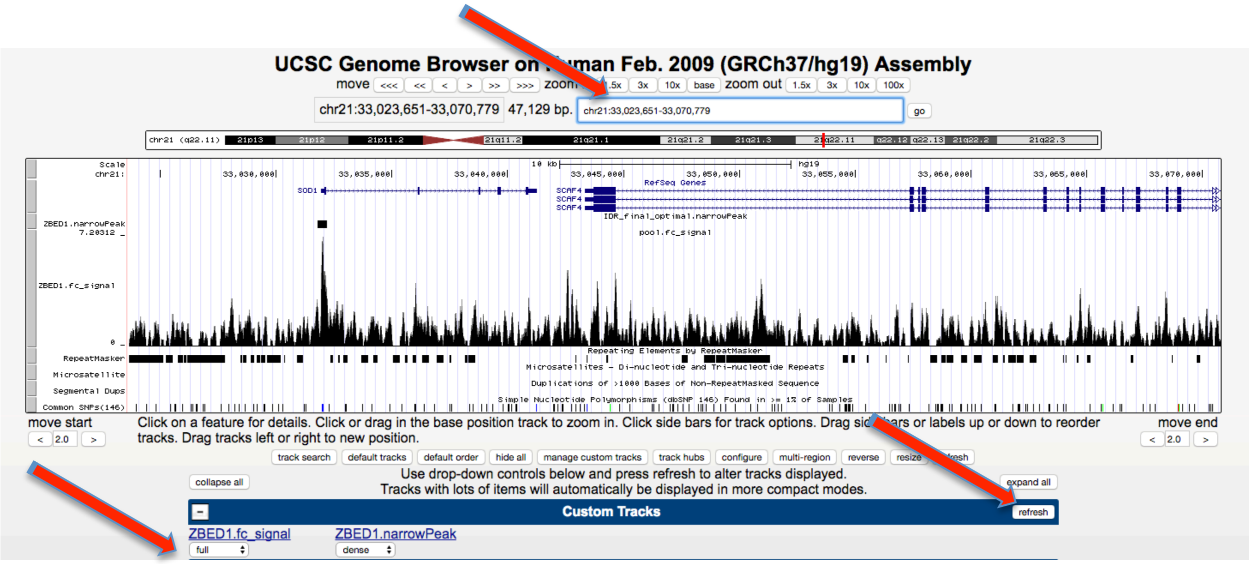
genome Human   assembly Feb. 2009 (GRCh37/hg19)   [hg19]

view in Genome Browser

Name	Description	Type	Doc	delete
IDR_final_optimal.narrowPeak	IDR_final_optimal.narrowPeak	bigBed		☐
pool.fc_signal	pool.fc_signal	bigWig		☐

30) Because the raw data were subsampled to only chromosome 21, enter a position on that chromosome. For example, chr21:33,023,651-33,070,779

Set the signal track to display in “full” mode. Do you see the strong signal for ZBED1 (the target for this experiment) at the SOD1 promoter? The black blocks in the replicated peaks track are the peaks that passed a stringent thresholding requiring the peaks to be observed in both replicates.



UCSC Genome Browser on uman Feb. 2009 (GRCh37/hg19) Assembly

chr21:33,023,651-33,070,779 47,129 bp. chr21:33,023,651-33,070,779

Click on a feature for details. Click or drag in the base position track to zoom in. Click side bars for track options. Drag sid ars or labels up or down to reorder tracks. Drag tracks left or right to new position.

Use drop-down controls below and press refresh to alter tracks displayed.
Tracks with lots of items will automatically be displayed in more compact modes.

Custom Tracks

ZBED1.fc_signal: full

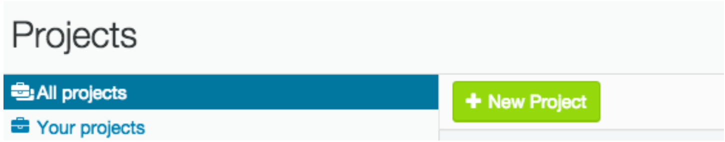
ZBED1.narrowPeak: dense

Congratulations! You have replicated an ENCODE analysis starting with primary data. You can repeat this process on your own data, and be assured that your results will be directly comparable to all the experiments the ENCODE DCC has analyzed.

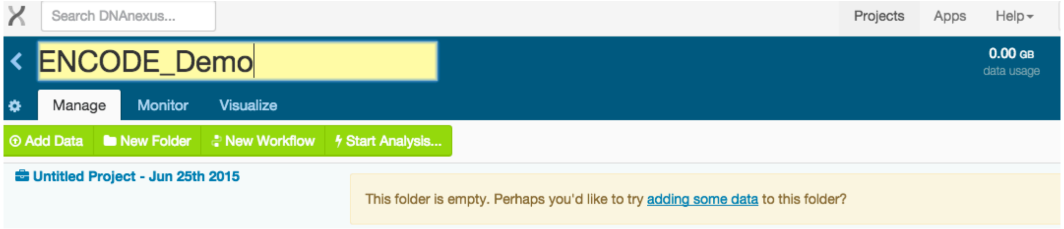
Other DNAnexus Tools:

To load data once you are in your own project

1) Start a “New Project” or find your own project in the DNAnexus homepage.



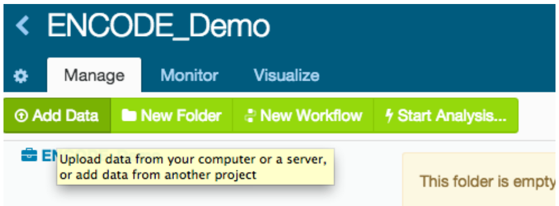
2) If new, name project in the upper left corner.



ENCODE_Demo

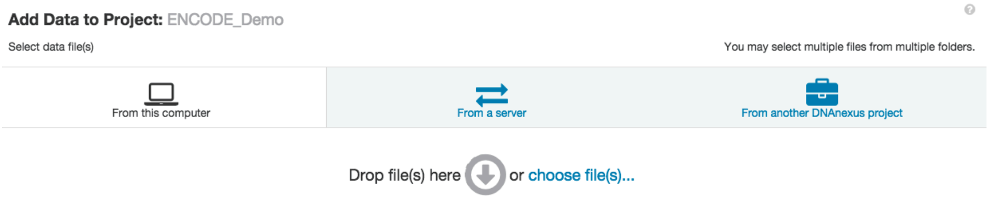
This folder is empty. Perhaps you'd like to try adding some data to this folder?

3) Select “Add Data” to select the files you want to use for analysis to your project.



Upload data from your computer or a server, or add data from another project

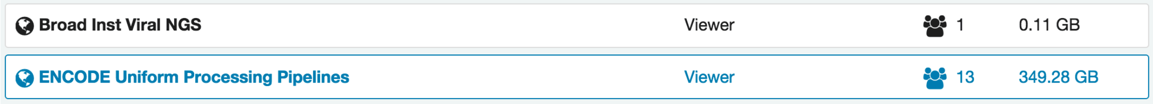
4) When the “Add Data to Project” window pops up, select “From another DNAnexus project.”



Add Data to Project: ENCODE_Demo

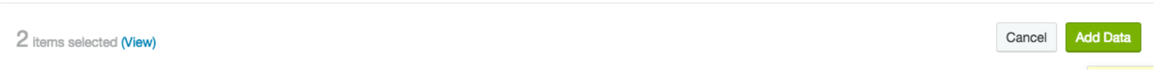
You may select multiple files from multiple folders.

5) Scroll down and select “ENCODE Universal Processing Pipeline” project to access the data.

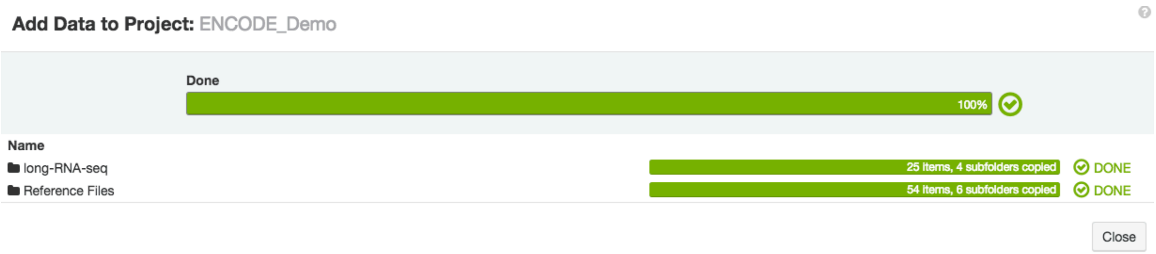


Broad Inst Viral NGS	Viewer	1	0.11 GB
ENCODE Uniform Processing Pipelines	Viewer	13	349.28 GB

6) Choose “Add Data” to select these files.



7) When these files are uploaded, the following window will pop up.

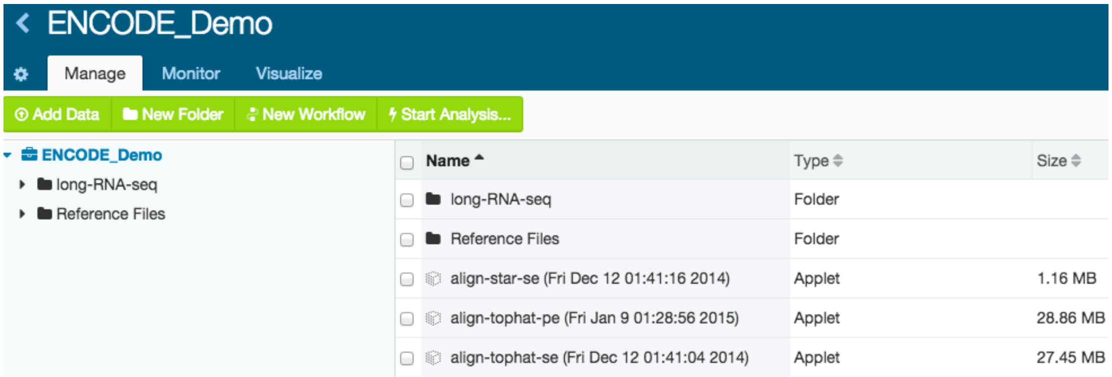


Add Data to Project: ENCODE_Demo

Done 100%

Name		
long-RNA-seq	25 items, 4 subfolders copied	DONE
Reference Files	54 items, 6 subfolders copied	DONE

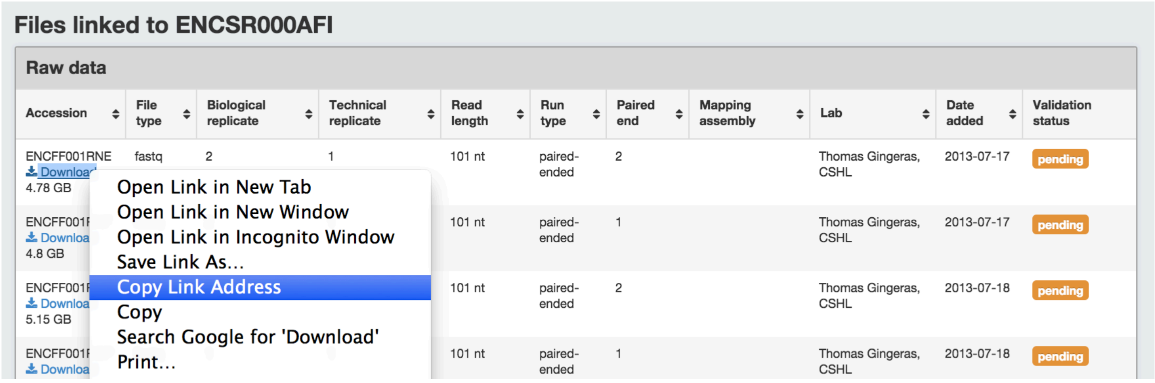
8) These files and associated applets will now appear in the Manage tab of your browser.



Name	Type	Size
long-RNA-seq	Folder	
Reference Files	Folder	
align-star-se (Fri Dec 12 01:41:16 2014)	Applet	1.16 MB
align-tophat-pe (Fri Jan 9 01:28:56 2015)	Applet	28.86 MB
align-tophat-se (Fri Dec 12 01:41:04 2014)	Applet	27.45 MB

To import a fastq file directly from the ENCODE portal to DNAnexus

1) Go to the ENCODE portal (encodeproject.org) and find the fastq file you are interested in using. Right click on this file and select "Copy Link Address."

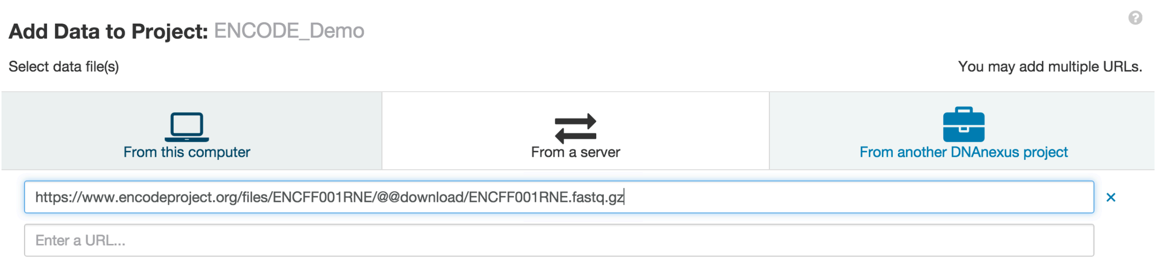


Files linked to ENCSR000AFI

Raw data

Accession	File type	Biological replicate	Technical replicate	Read length	Run type	Paired end	Mapping assembly	Lab	Date added	Validation status
ENCFF001RNE Downloa 4.78 GB	fastq	2	1	101 nt	paired-ended	2		Thomas Gingeras, CSHL	2013-07-17	pending
ENCFF001F Downloa 4.8 GB				101 nt	paired-ended	1		Thomas Gingeras, CSHL	2013-07-17	pending
ENCFF001F Downloa 5.15 GB				101 nt	paired-ended	2		Thomas Gingeras, CSHL	2013-07-18	pending
ENCFF001F Downloa				101 nt	paired-ended	1		Thomas Gingeras, CSHL	2013-07-18	pending

2) In the manage tab, under "Add Data" select the "From a Server" option and paste the URL into the box. Select "Add Data" and the file will upload.



Add Data to Project: ENCODE_Demo

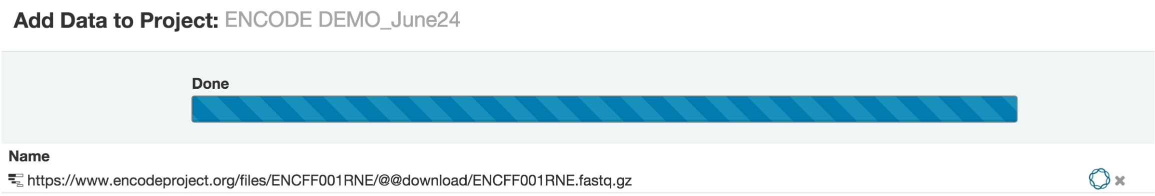
Select data file(s)

You may add multiple URLs.

From this computer | From a server | From another DNAnexus project

https://www.encodeproject.org/files/ENCFF001RNE/@@download/ENCFF001RNE.fastq.gz ×

Enter a URL...



Add Data to Project: ENCODE DEMO_June24

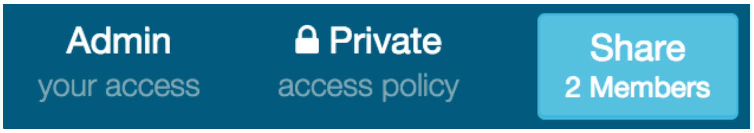
Done

Name

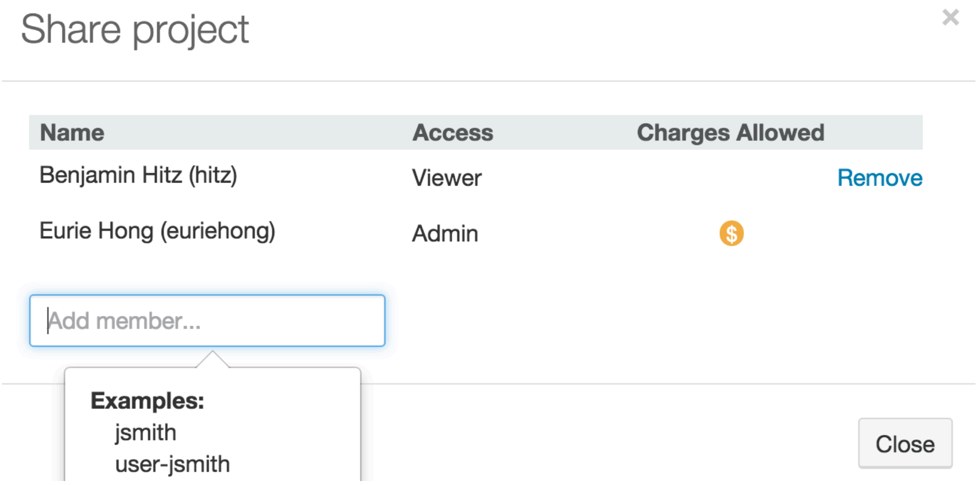
https://www.encodeproject.org/files/ENCFF001RNE/@@download/ENCFF001RNE.fastq.gz

To share project with another user

1) In order to share your project, select the blue “Share” button at the upper right corner of the browser page.



2) This will bring up a pop-up window where you can add user names and select permissions to allow collaborators access to view, edit, or contribute to your projects.



Share project

Name	Access	Charges Allowed	
Benjamin Hitz (hitz)	Viewer		Remove
Eurie Hong (euriehong)	Admin	$	

Add member...

Examples:
jsmith
user-jsmith

Close