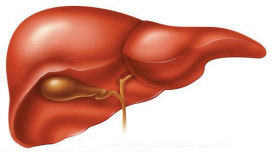
Find and Visualize ENCODE Data
www.encodeproject.org

J. Seth Strattan, PhD
ENCODE Data Coordinating Center (DCC)
Keystone Chromatin and Epigenetics
March, 2016

ENCODE DCC Delivers ENCODE Data



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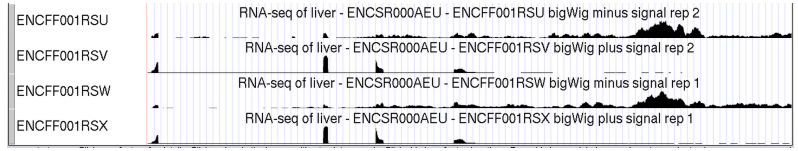
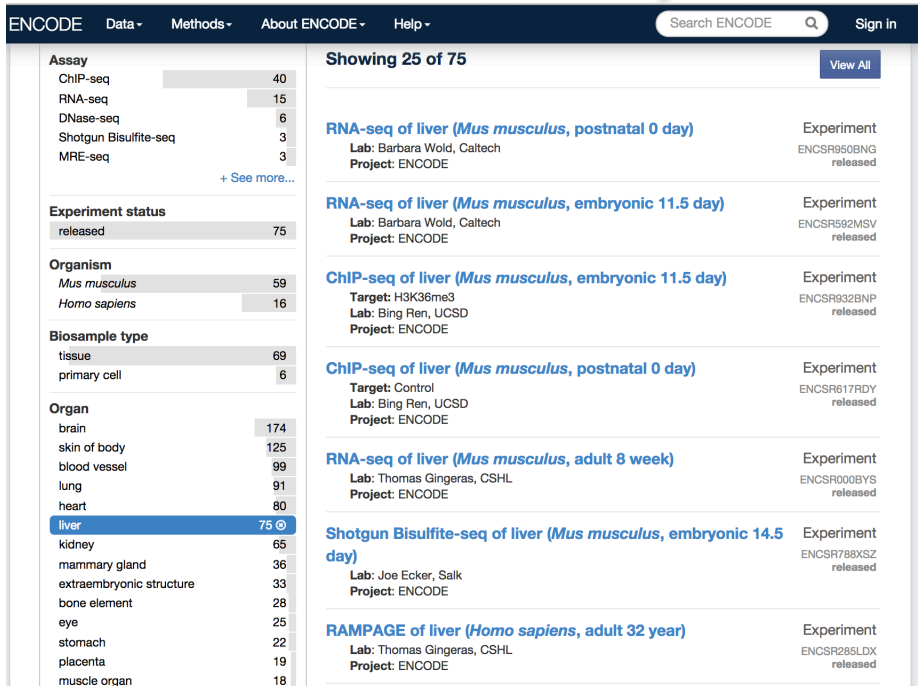


Sample → Library → Primary Data → Processed Data

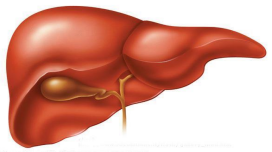


ENCFF001RTZ	fastq	reads	2	(1, 1)	Esther Chan	2013-08-15	Download	pending
ENCFF001RSV	bigWig	plus signal		(2, 1)	Esther Chan	2013-07-26	Download	pending
ENCFF001RSU	bigWig	minus signal		(2, 1)	Esther Chan	2013-07-26	Download	pending

AWS S3 Bucket
ENCODE Files

J. Seth Strattan, PhD ENCODE DCC

ENCODE DCC Delivers ENCODE Metadata



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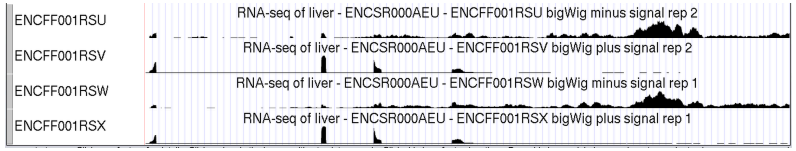

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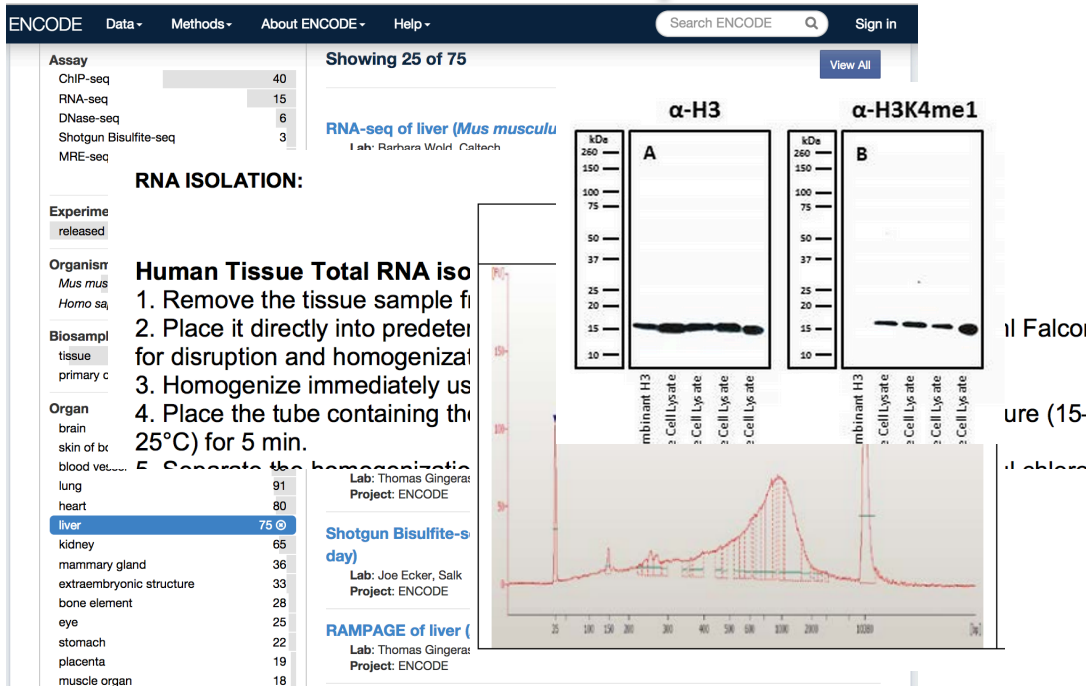
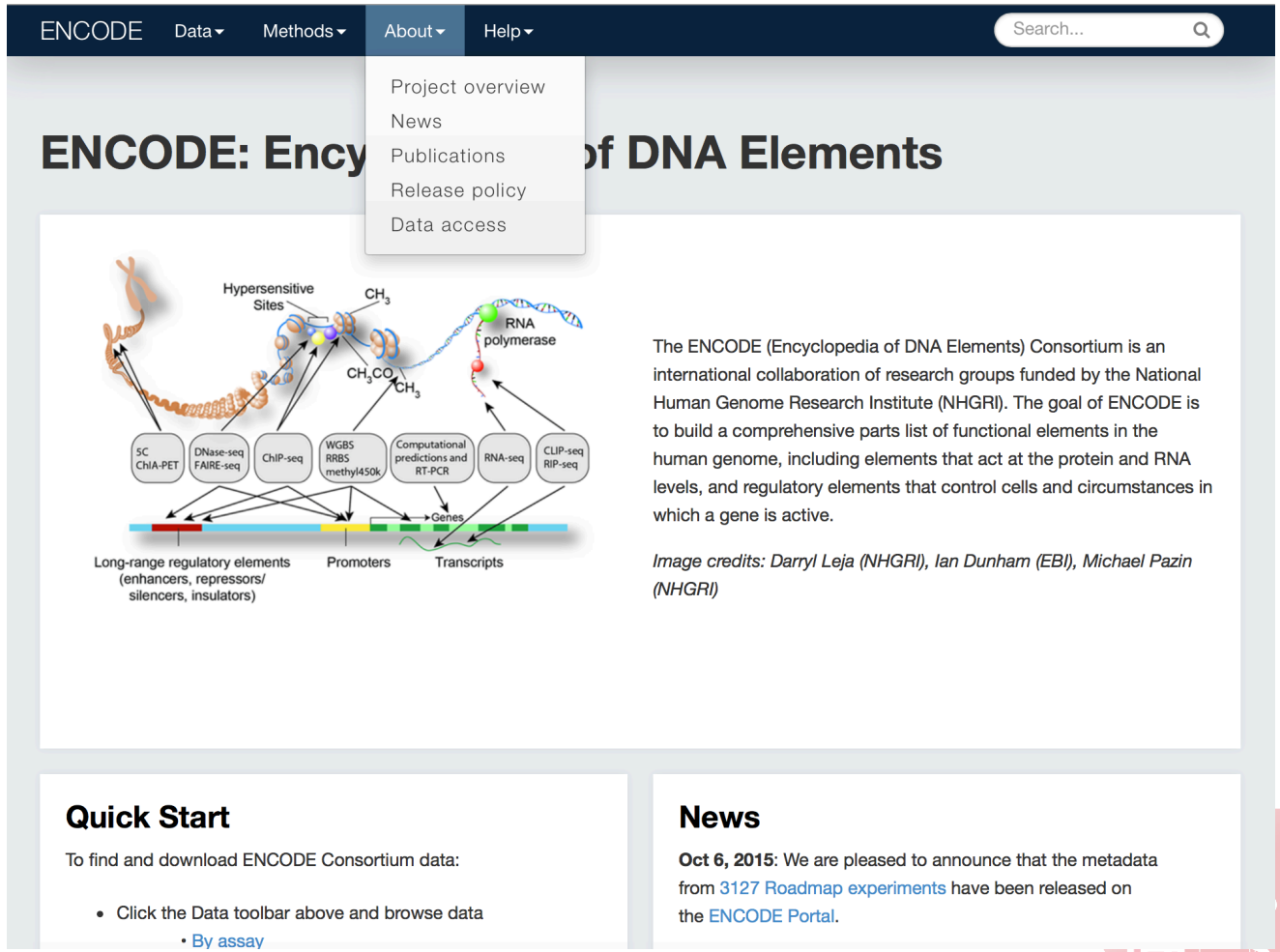


J. Seth Strattan, PhD ENCODE DCC

ENCODE Portal www.encodeproject.org

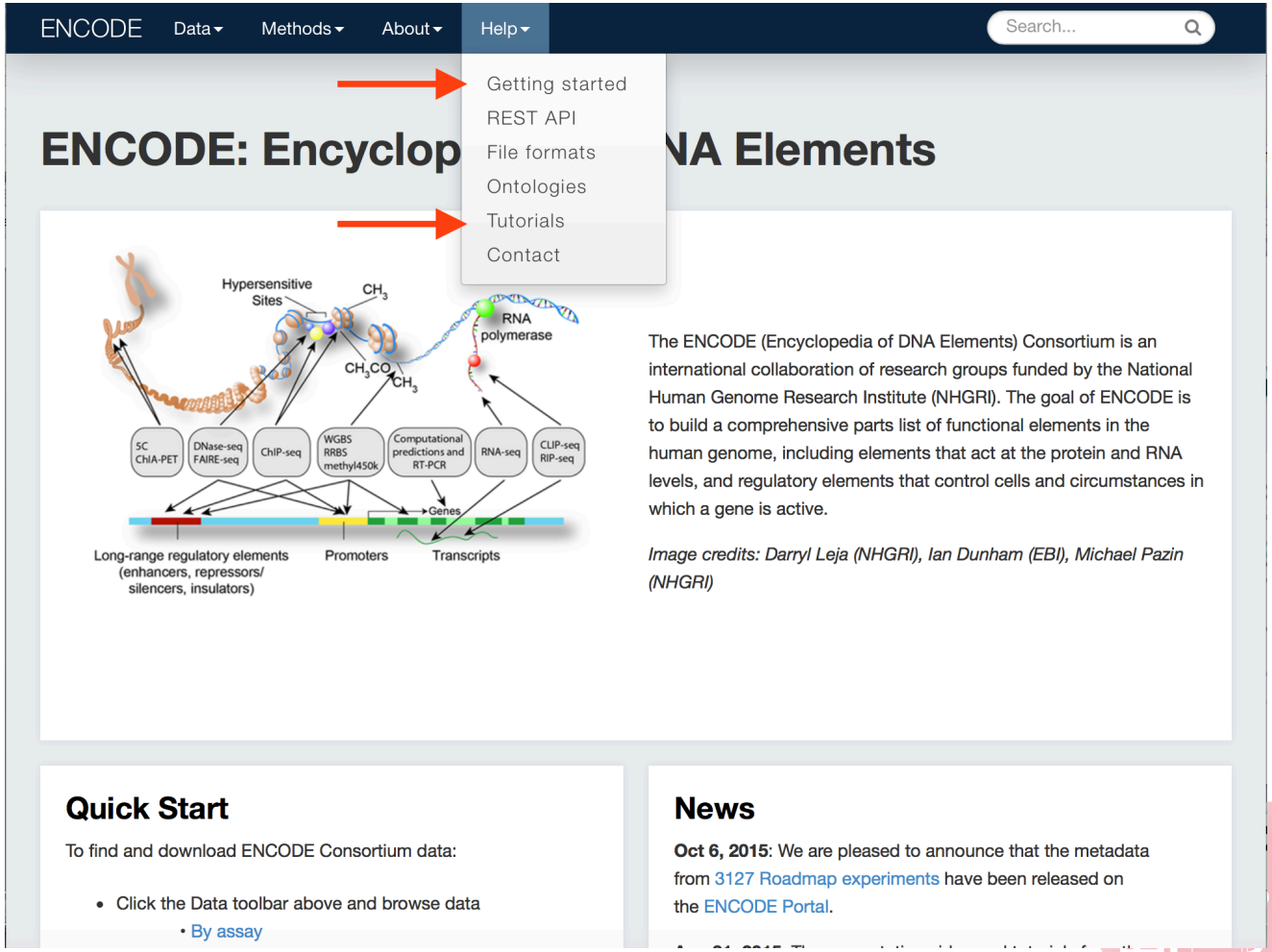
- The ENCODE Portal is the **canonical source** for ENCODE metadata and data.
- The Portal also documents **ENCODE standards** like antibody standards, data release.
- The Portal links to **documentation and tutorials**.
- Use the Portal to **browse, search, and visualize** what ENCODE has done.
- Understand ENCODE **data analyses**, and how you can replicate them.
- REST API for programmatic **search and download** of ENCODE metadata and data.



www.encodeproject.org … Getting Started

Help Menu Documents the Portal

- *Getting Started:* Portal organization
  - https://www.encodeproject.org/help/getting-started
- *Tutorials:*
  - https://www.encodeproject.org/tutorials
  - Links to slides from today's workshop
- *Contact*:
  - encode-help@lists.stanford.edu
  - @encodedcc



www.encodeproject.org … Getting Started

- https://www.encodeproject.org/help/getting-started
  - How to browse and facet.
  - How to access one file at a time.
  - Bulk download of files.
  - ENCODE data model and data organization.

ENCODE Data Methods About Help Search...

Getting Started

Introduction

Welcome to the ENCODE Portal! The ENCODE Portal serves as the primary source of data generated by the ENCODE Consortium and up-to-date information about the project, including data releases, publications, and upcoming tutorials. This site is developed and maintained by the Data Coordination Center (DCC). All data generated by the ENCODE consortium are submitted to the DCC and reviewed for quality prior to release to the scientific community. No account is needed to view released data.

This document describes what data are available at the ENCODE Portal, ways to get started searching and downloading data, and an overview to how the metadata describing the assays and reagents are organized. ENCODE data can be visualized and accessed from other resources, including the UCSC Genome Browser and ENSEMBL.

Please contact the ENCODE DCC via email (encode-help@lists.stanford.edu) or Twitter (@encodedcc) if you have any further questions.

Information available at the portal

The ENCODE Portal contains the following types of data generated by the ENCODE Consortium:

- Raw and processed data from a wide-range of assays
- Biological samples (also known as biosamples) that are used in the assays
- Antibody characterizations that are performed as part of the antibody characterization process defined by the consortium.

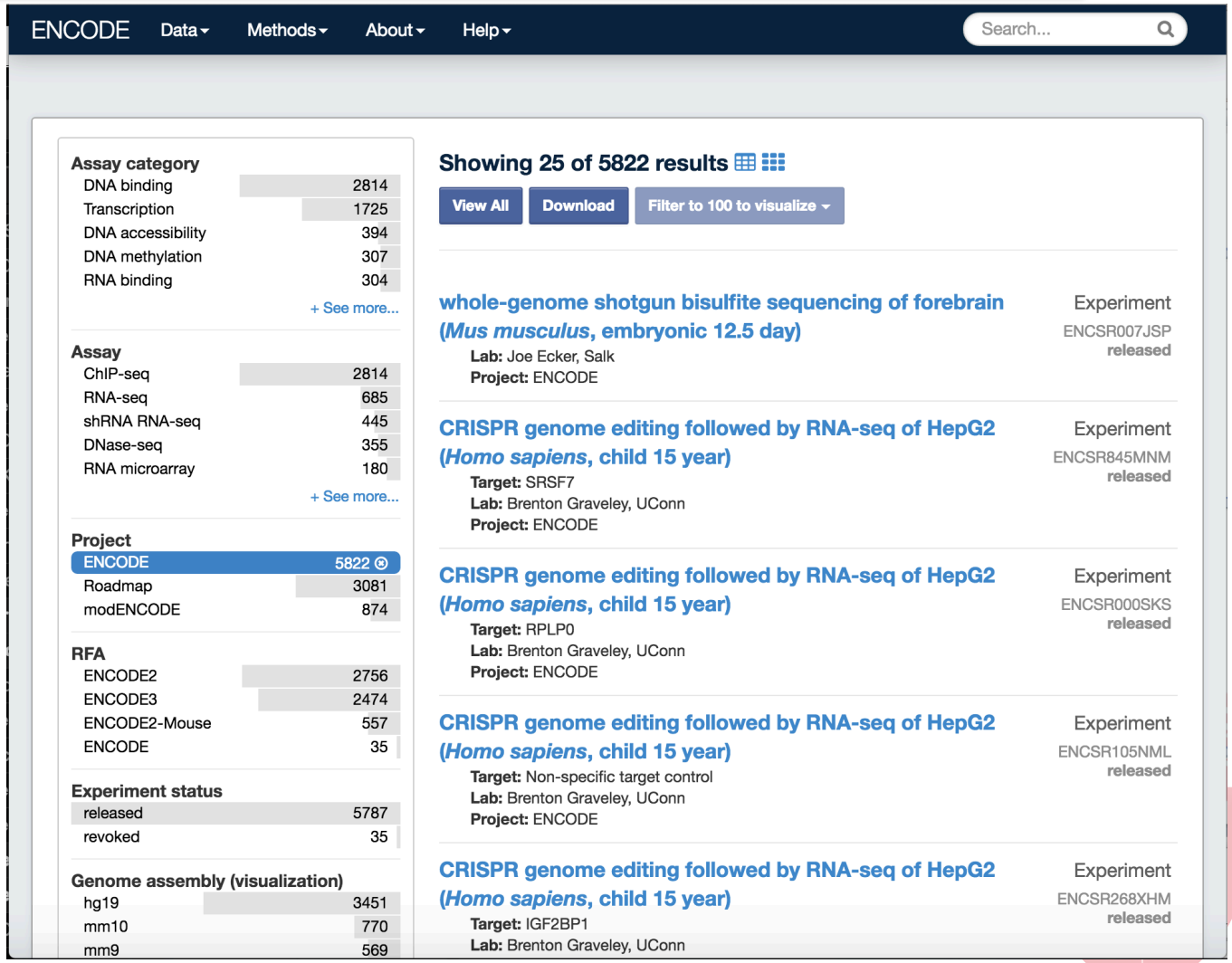
Additional information about the activities of the ENCODE Consortium are provided on the portal:

- Publications that have been written by consortium members

www.encodeproject.org … Faceted Browsing

Faceted Browsing of Assays

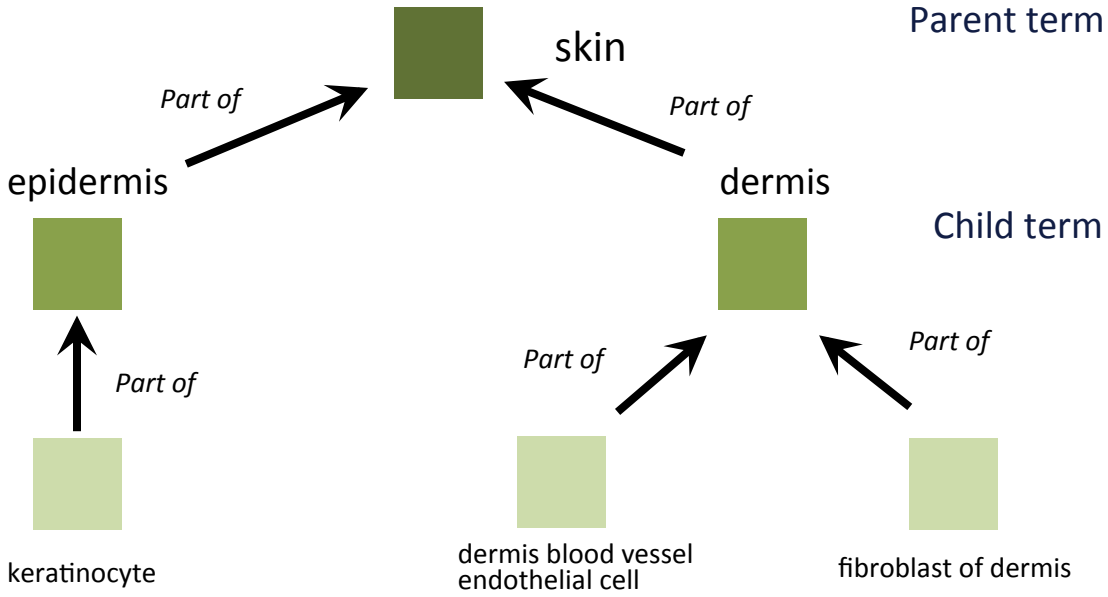
- Click on Data … Assays
- https://www.encodeproject.org/search/?type=Experiment
- In the center is a list of all ENCODE experiments.
- To the left are facets you can choose to filter the list.

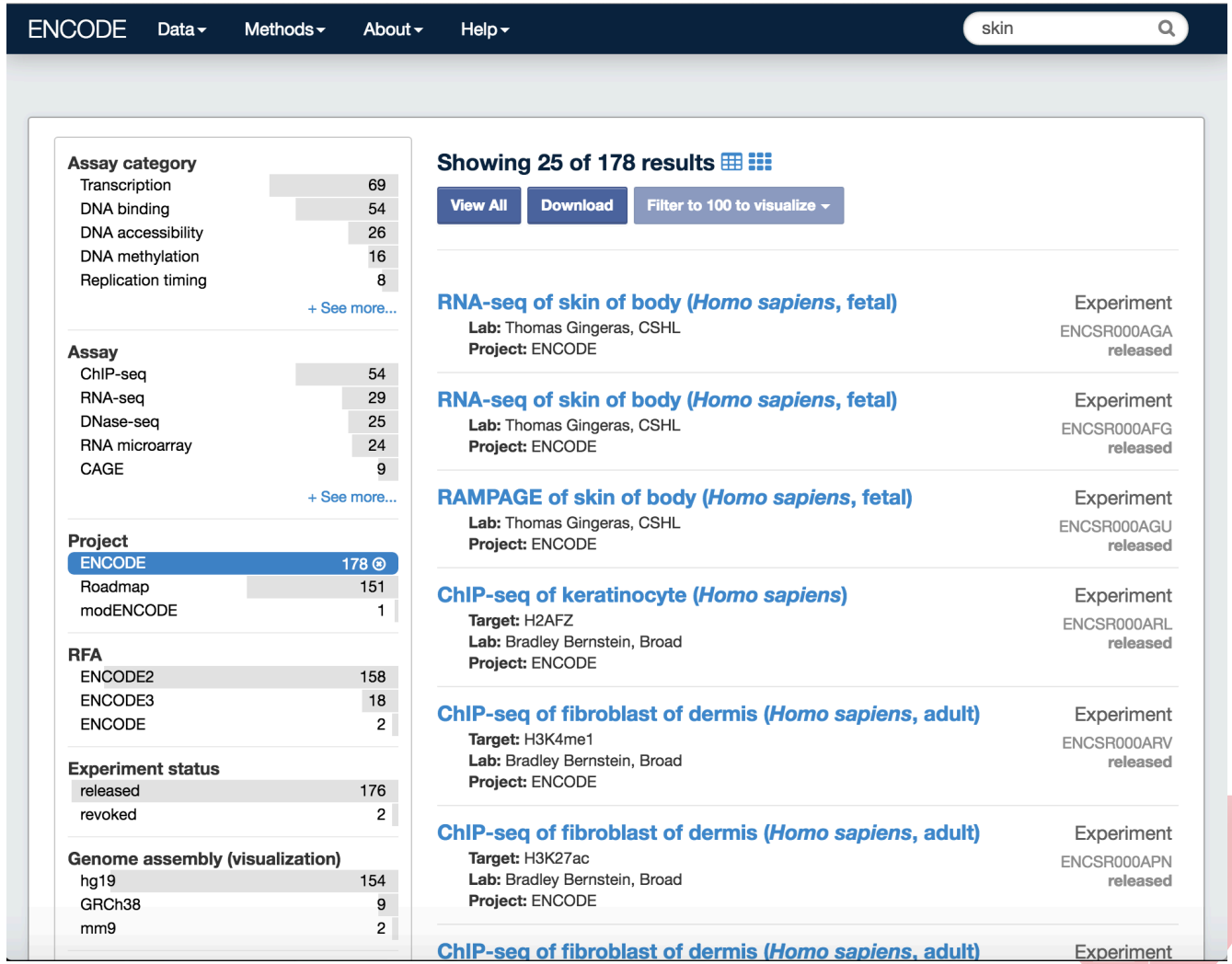


www.encodeproject.org … The Search Box

Keyword search powered by ontologies

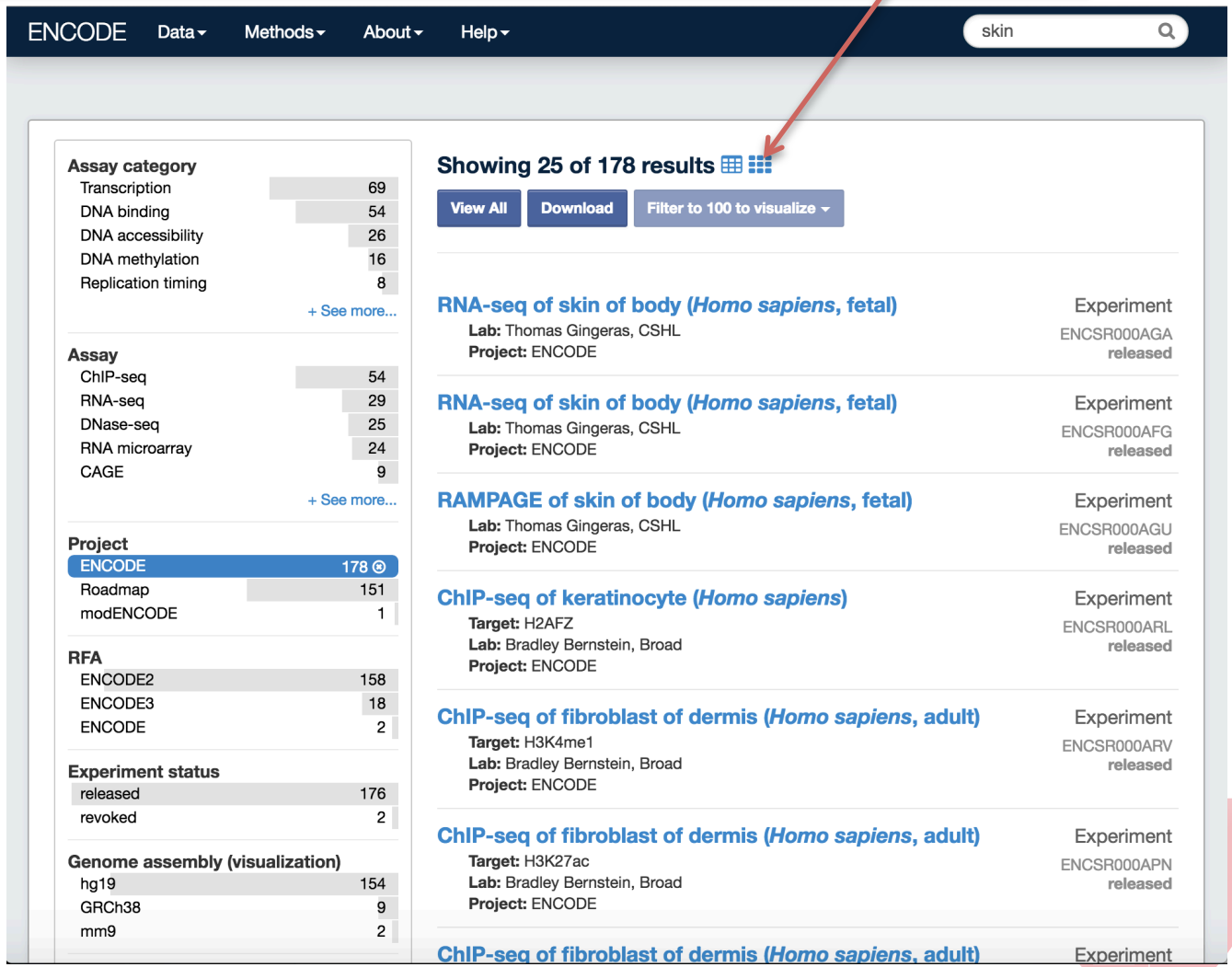
- Search for “skin” … select Experiments.
- Finds “skin of body” and “keratinocyte”





www.encodeproject.org … The Matrix

Click the matrix icon near “results”



www.encodeproject.org … The Matrix

The same list in matrix form

- See the search results as a matrix.
- Facts work here too.
- Select ChIP-seq … histone.

ENCODE Data Methods About Help skin

Experiment Matrix

Click or enter search terms to filter the experiments included in the matrix.

skin

Assay		Assay category		Target of assay		Date released		Available data	
ChIP-seq	54	Transcription	69	histone	31	February, 2011	29	fastq	134
RNA-seq	29	DNA binding	54	histone modification	31	April, 2011	14	bigWig	128
DNase-seq	25	DNA accessibility	26	narrow histone mark	16	March, 2011	14	bam	127
RNA microarray	24	DNA methylation	16	broad histone mark	15	March, 2012	14	bed broadPeak	73
CAGE	9	Replication timing	8	transcription factor	13	October, 2011	13	bigBed broadPeak	73
+ See more...		+ See more...		+ See more...		+ See more...		+ See more...	

Organism
- *Homo sapiens* 175
- *Mus musculus* 2

Biosample type
- primary cell 169
- tissue 7
- stem cell 2

Organ
- skin of body 178
- blood vessel 9
- lymphatic vessel 6

Project
- ENCODE 178
- Roadmap 151
- modENCODE 1

Genome assembly (visualization)
- hg19 154
- GRCh38 9
- mm9 2

178 results

Clear all filters

BIOSAMPLE \ ASSAY	ChIP-seq	RNA-seq	DNase-seq	RNA microarray	CAGE	DNAme array	RRBS	Repli-Seq	genotyping array	RAMPAGE	RNA-PET	Repli-chip	FAIRE-seq	WGBS	microRNA counts	microRNA-seq
primary cell																
keratinocyte	22	11	2	6	5			6			2		1			
fibroblast of dermis	14	2	1	1	1											
skin fibroblast	2		9	5			1									
foreskin fibroblast	6		2	2		1	1		1							
dermis blood vessel endothelial cell		1	4	4												
...and 10 more																
tissue																
skin of body		2								1						
lower leg skin		2														
zone of skin						1	1									
stem cell																
stem cell of epidermis											2					

Download Visualize

www.encodeproject.org … The Matrix

Skin ChIP-seq … histone

- Cells in the matrix are clickable.
- Produces a list of experiments that match the selected criteria.

ENCODE Data Methods About Help skin

Experiment Matrix

Click or enter search terms to filter the experiments included in the matrix.

skin

Assay		Assay category		Target of assay		Date released		Available data	
ChIP-seq	31	DNA binding	31	histone	31	February, 2011	22	bam	31
				histone modification	31	March, 2012	7	bed broadPeak	31
				narrow histone mark	16	August, 2012	1	bigBed broadPeak	31
				broad histone mark	15	November, 2011	1	bigWig	31
				transcription factor	13			fastq	31
				+ See more...				+ See more...	

Organism
Homo sapiens 31

Biosample type
primary cell 31

Organ
skin of body 31

Project
Roadmap 49
ENCODE 31

Genome assembly (visualization)
hg19 31

ASSAY

BIOSAMPLE

31 results

Clear all filters

ChIP-seq

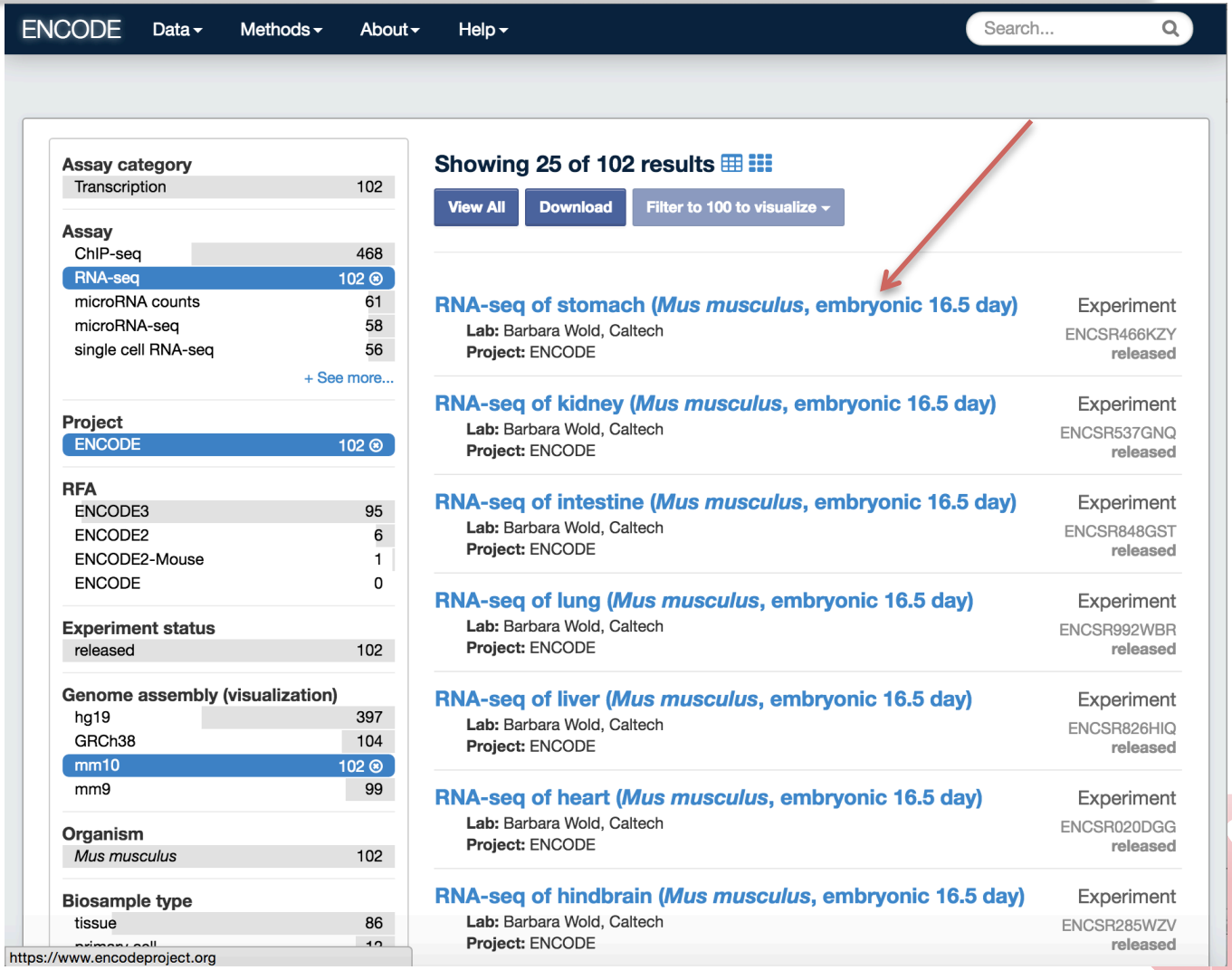
primary cell	
keratinocyte	15
fibroblast of dermis	11
foreskin fibroblast	2
fibroblast of pedal digit skin	1
fibroblast of skin of abdomen	1
fibroblast of upper leg skin	1

Download Visualize

www.encodeproject.org … Metadata to Data

Use metadata to find data

- Filter: RNAseq, ENCODE, mm10 assembly
- **Select an experiment:** https://www.encodeproject.org/experiments/ENCSR466KZY/
- **Note metadata on protocols, replicates, etc.**
- Graph: files are related by processing steps
- Download files from the graph or a list



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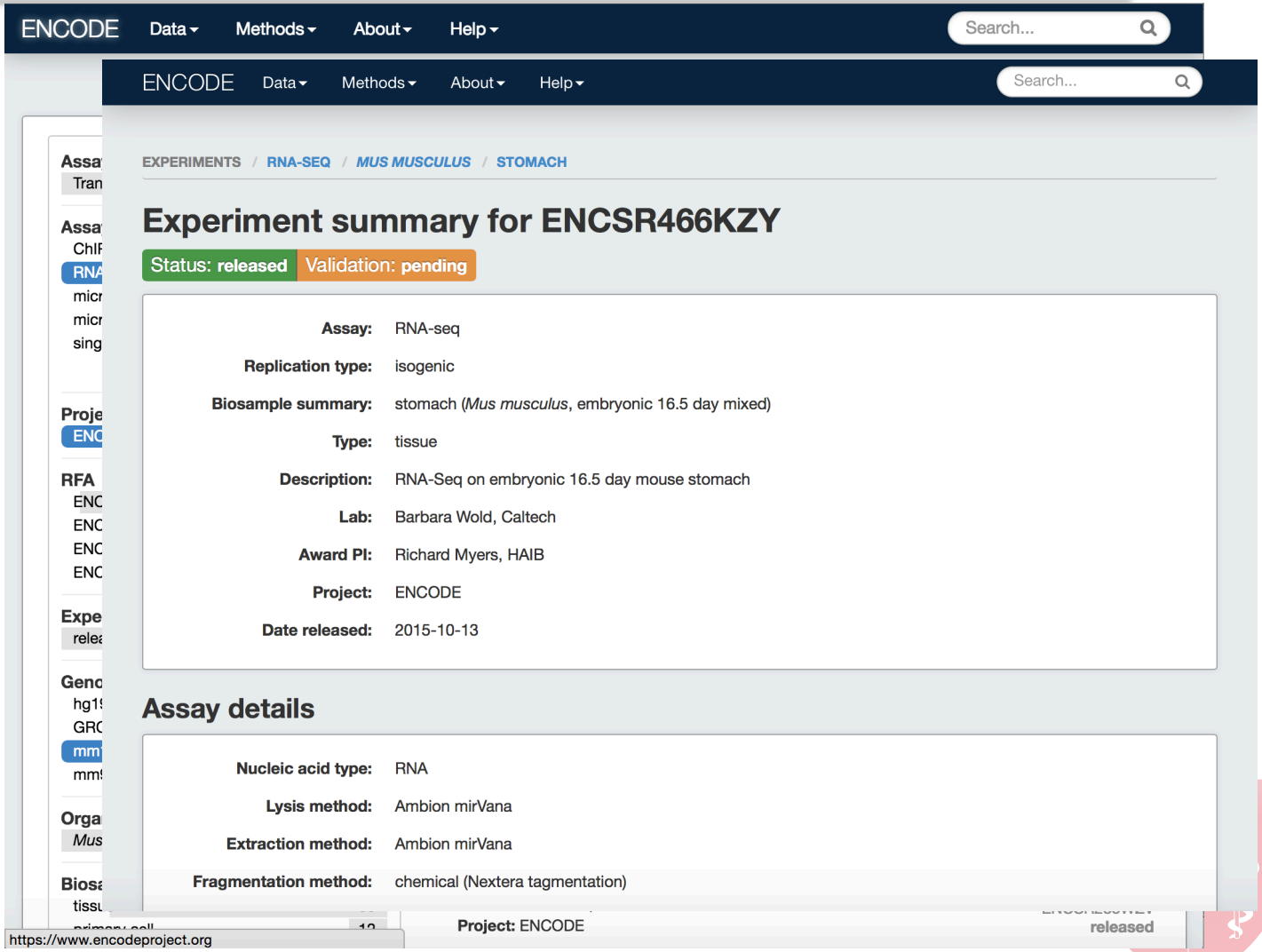

www.encodeproject.org … Metadata to Data

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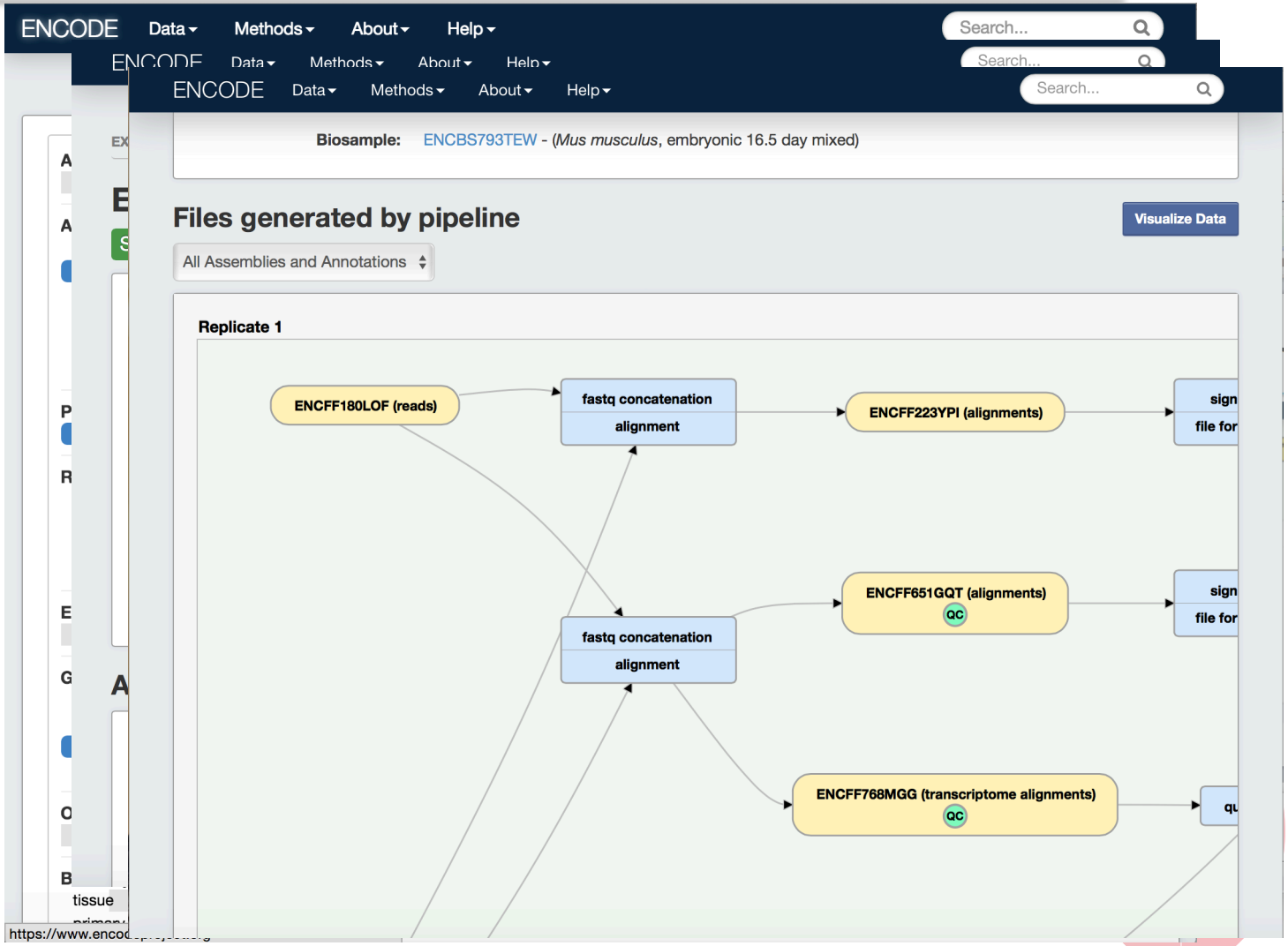

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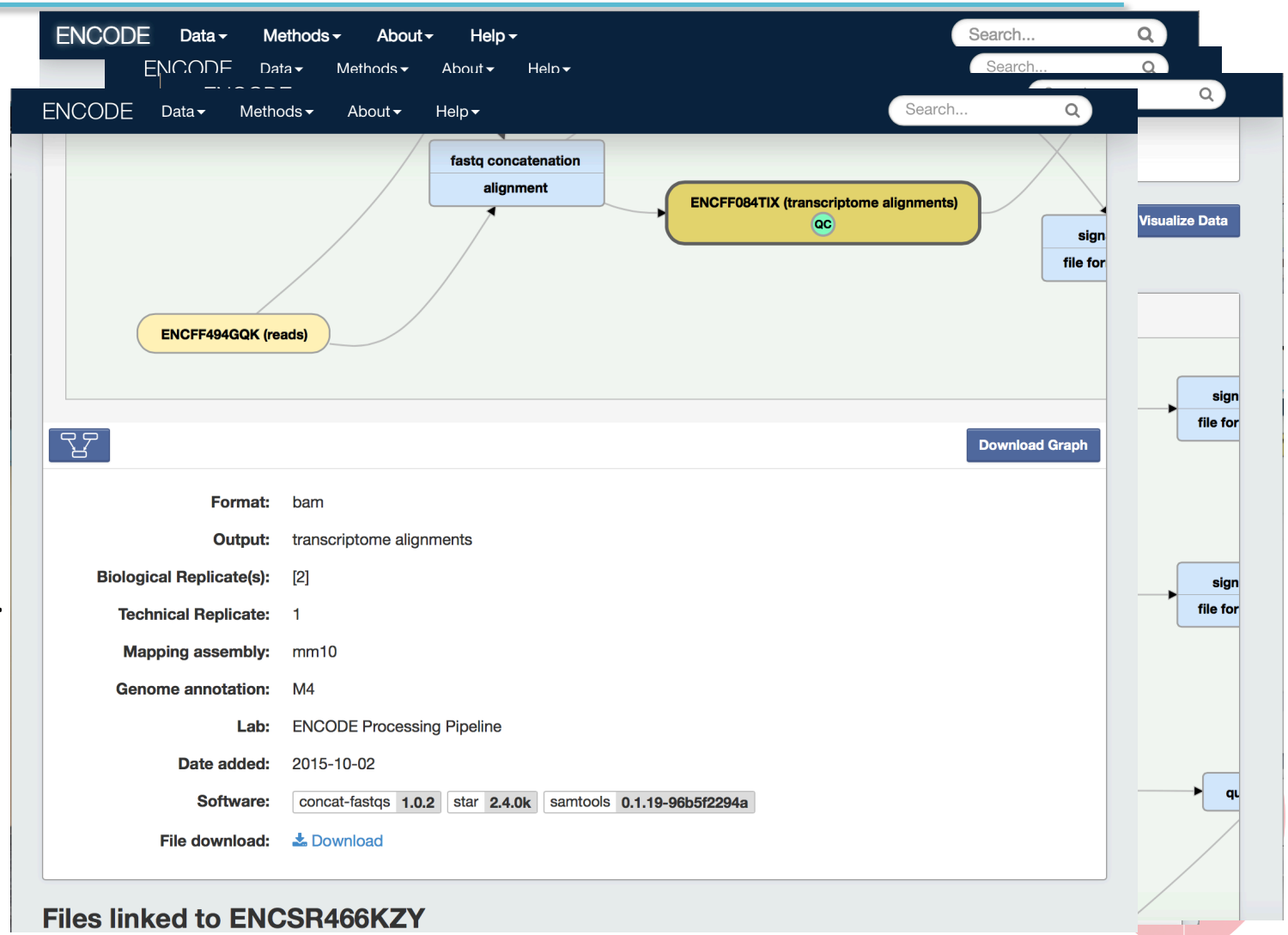

www.encodeproject.org … Metadata to Data

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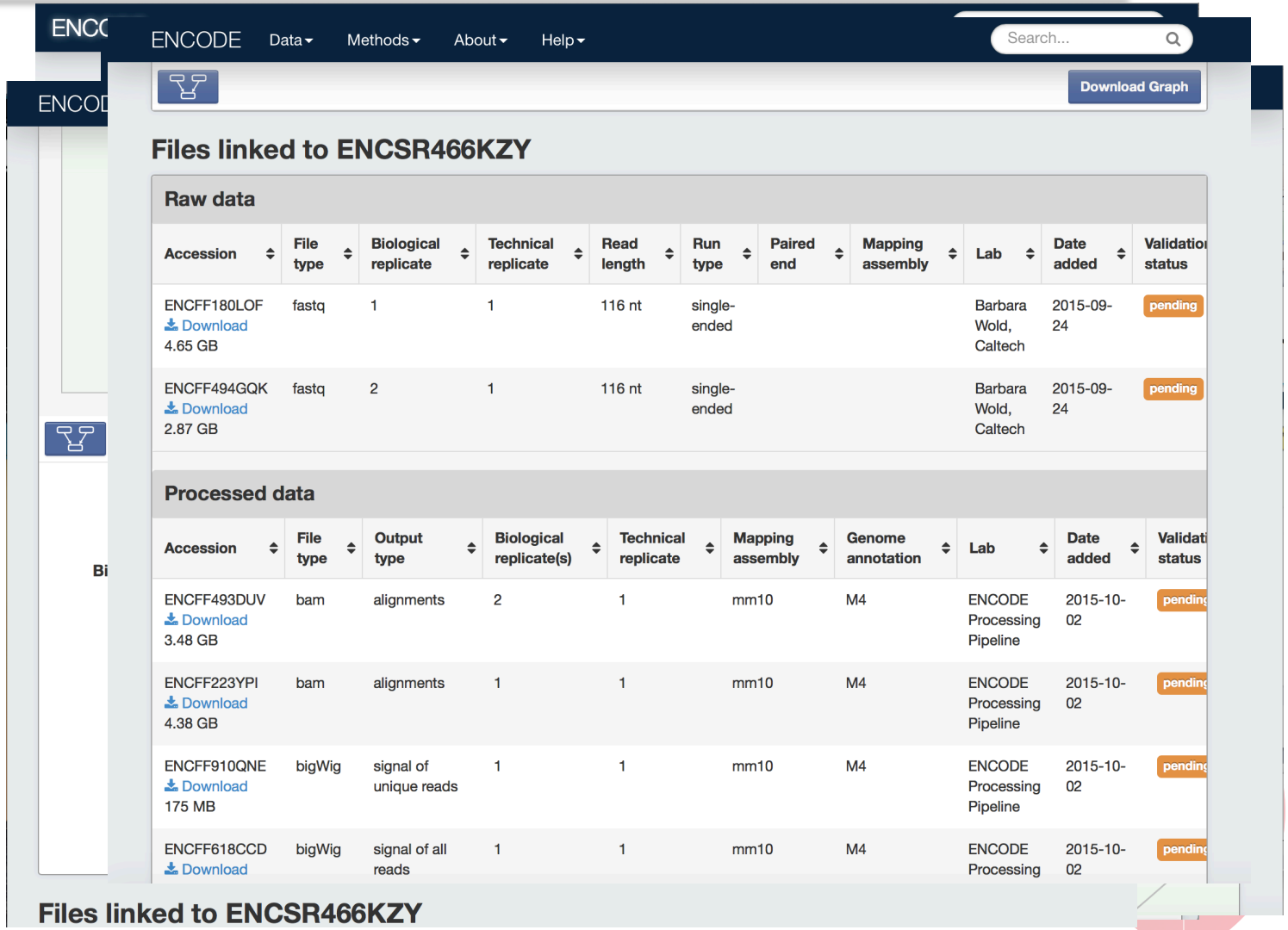
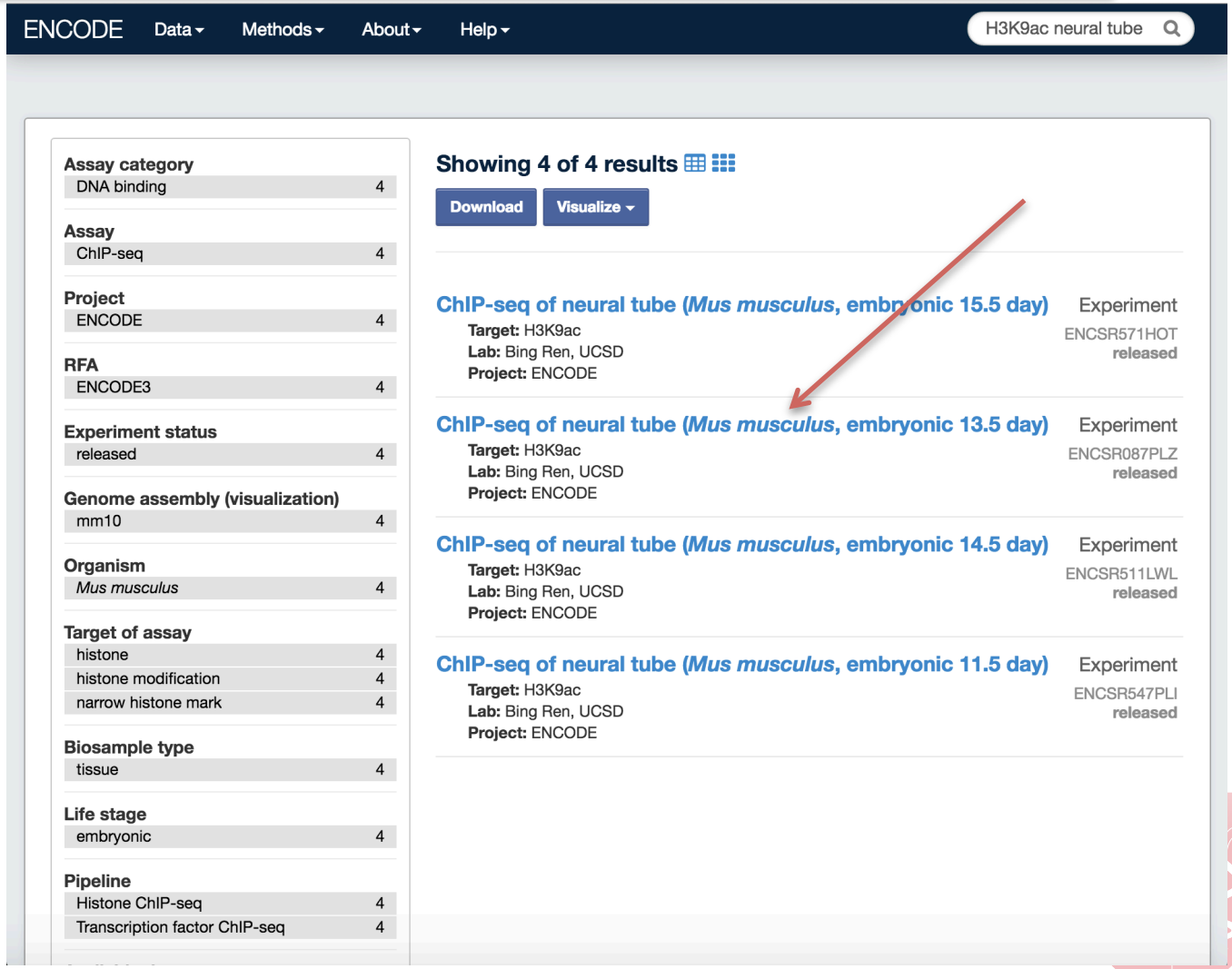


www.encodeproject.org … Visualization

Use metadata to find data:

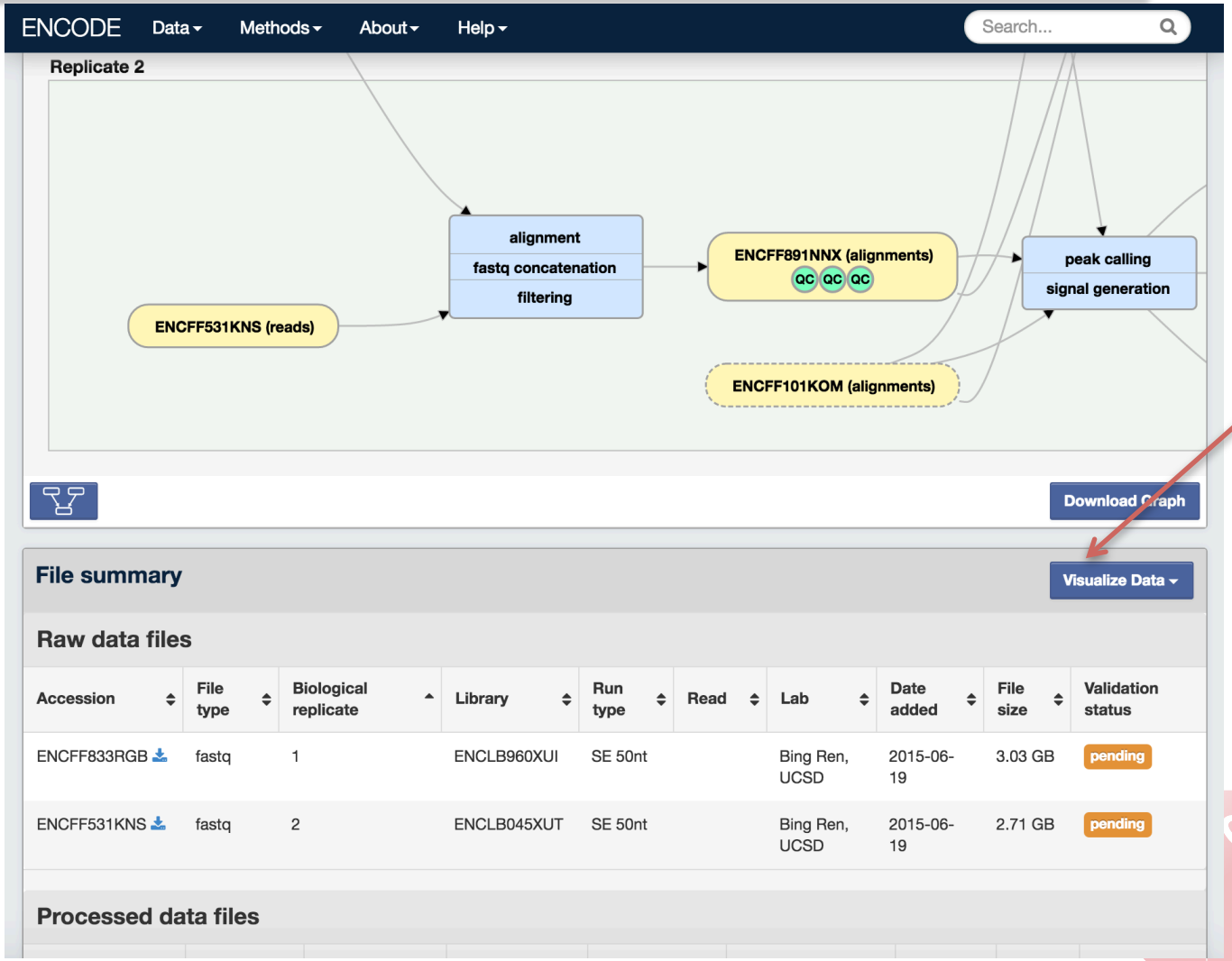
- Search for “H3K9ac neural tube”.
- Select an experiment, for example https://www.encodeproject.org/experiments/ENCSR087PLZ/
- Note metadata on protocols, replicates.
- Graph: files are related by processing steps.
- Download from the graph or a list.
- Click on “Visualize Data” to visualize the results of this experiment.



www.encodeproject.org … Visualization

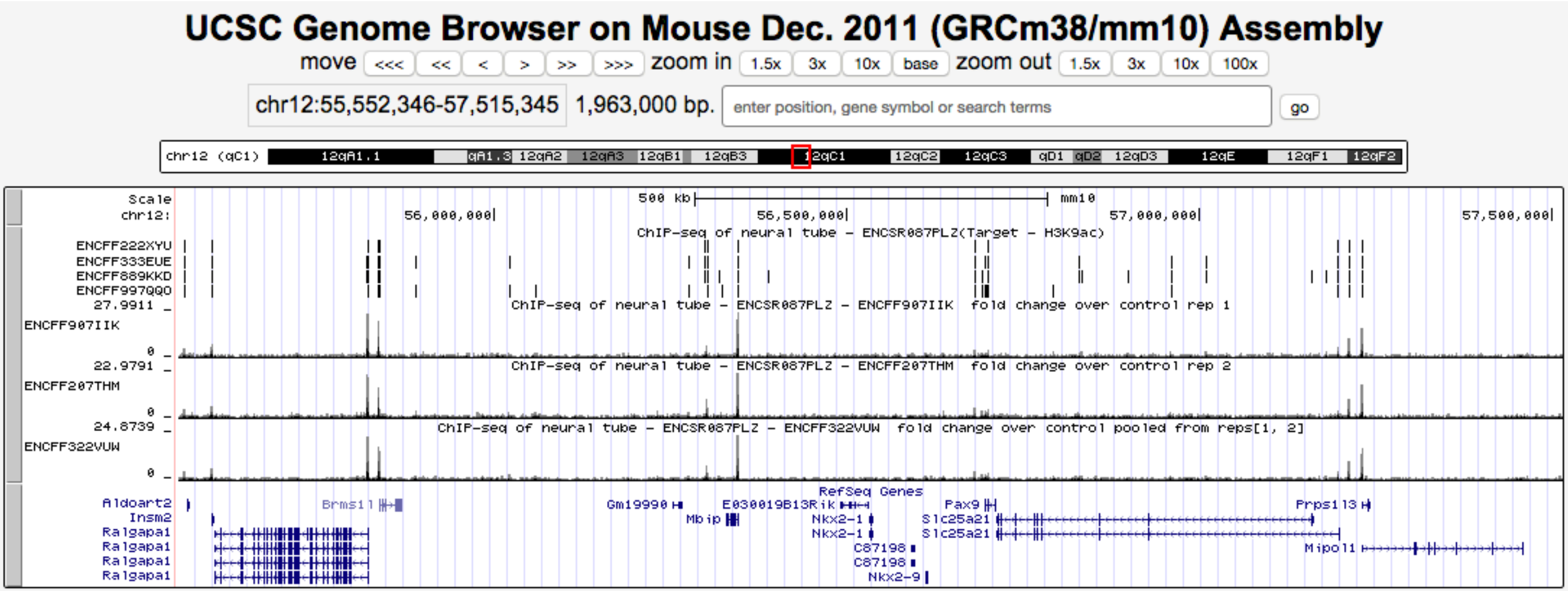
Use metadata to find data:

- Search for “H3K9ac neural tube”
- Facet on ChIP-seq; mouse; mm10 assembly
- Select an experiment, for example https://www.encodeproject.org/experiments/ENCSR087PLZ/
- Note metadata on protocols, replicates
- Graph: files are related by processing steps
- Download from the graph or a list
- Click on “Visualize Data”… mm10 to visualize the results of this experiment.



Visualize the Experiment

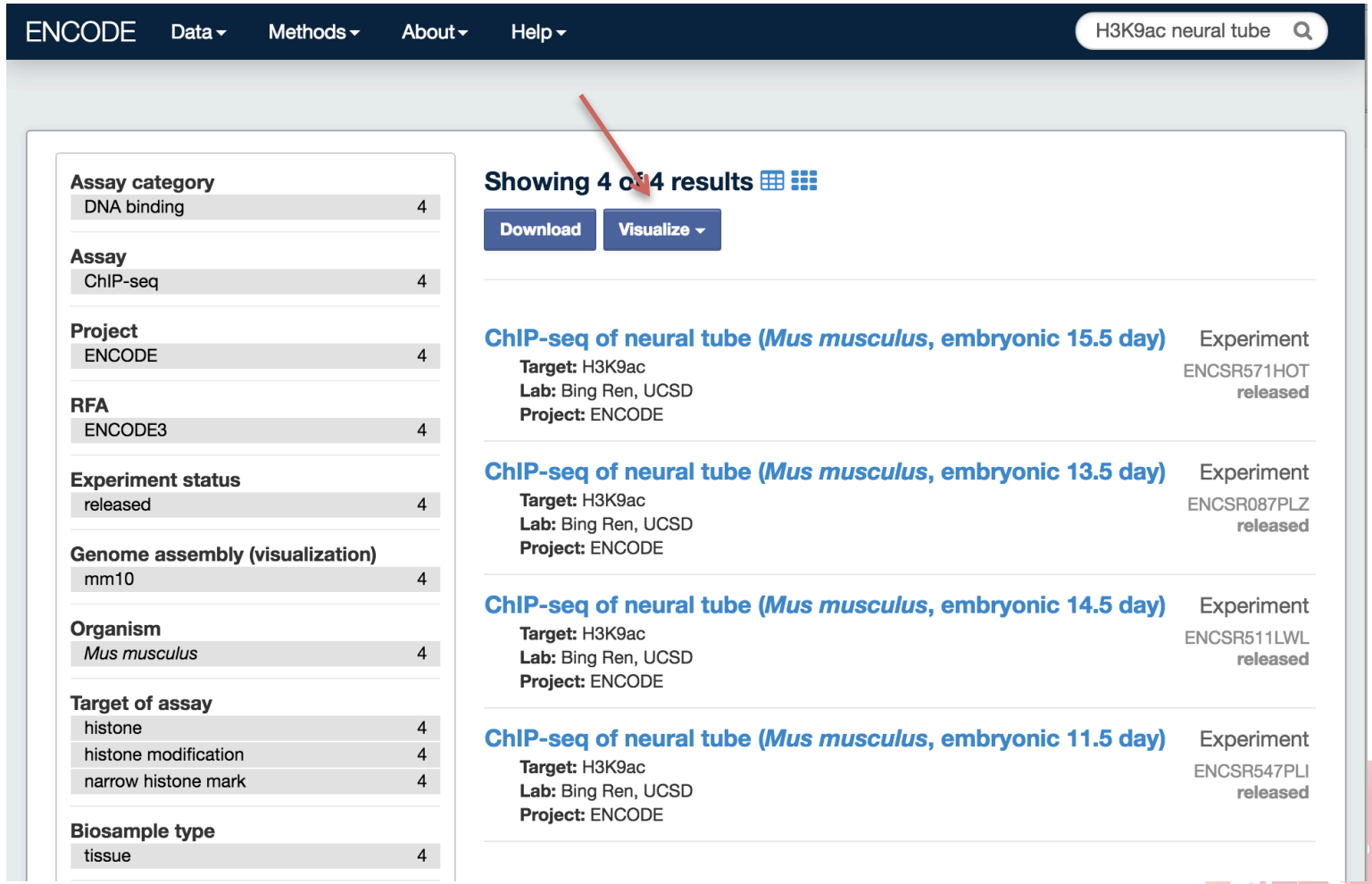
Adjust the browser settings to display fold-over-signal in ”full”



Find Several Experiments

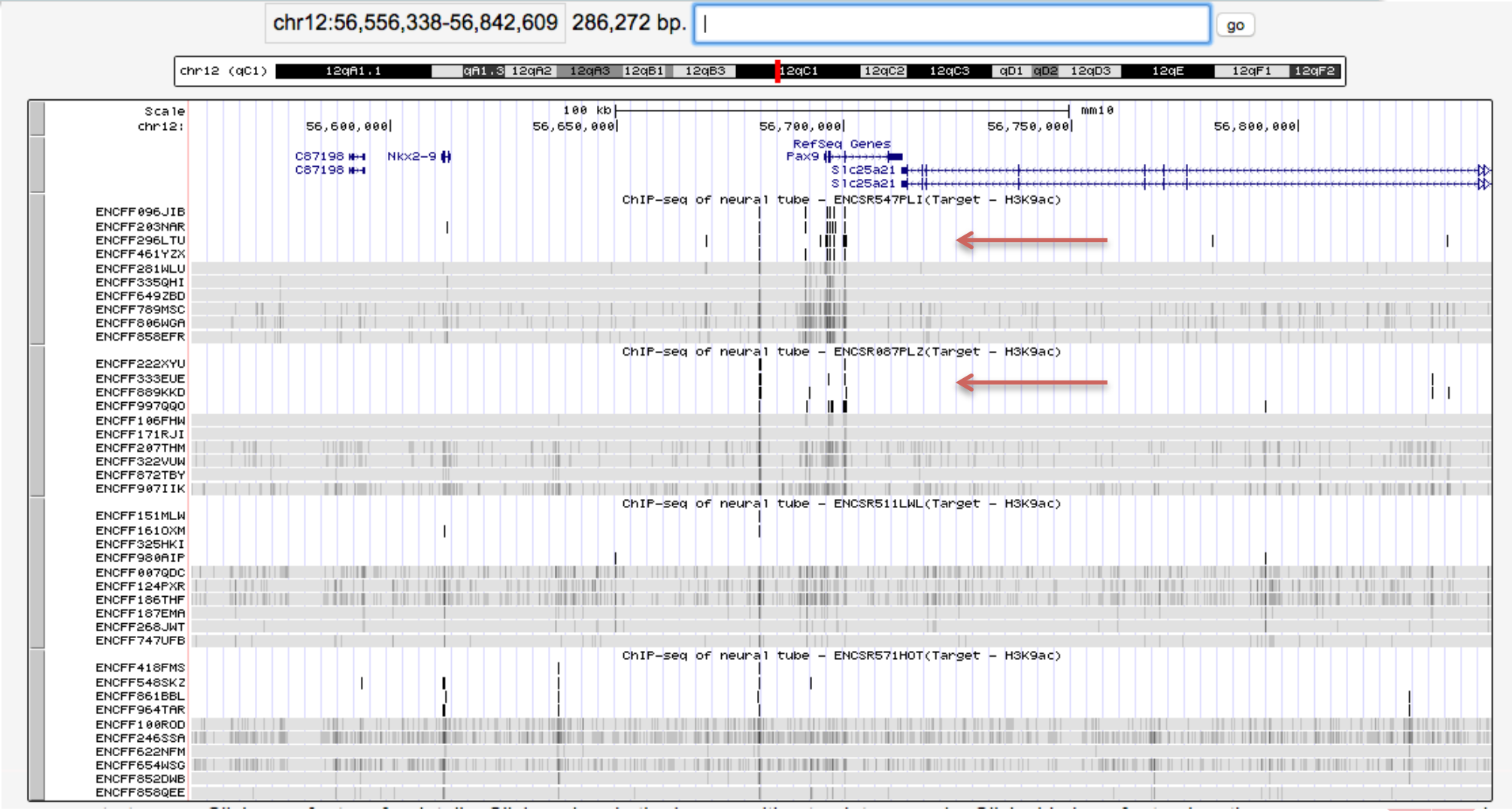
Use metadata to find data:

- Search for “H3K9ac neural tube”
- Get a list of several experiments
- Click on “Visualize Data” to visualize all the experiments matching this search.



Visualize Several Experiments

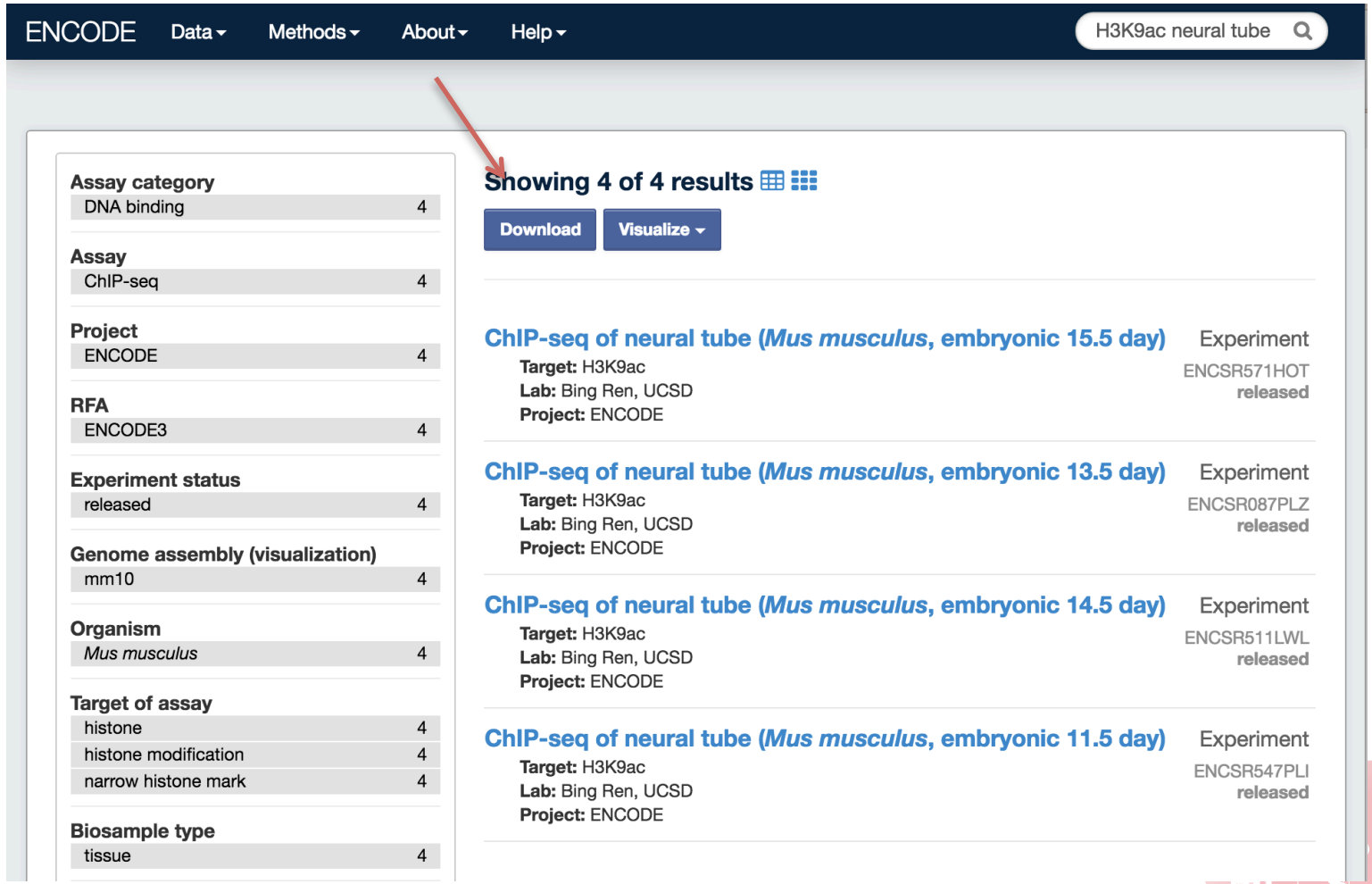
Stage-dependent H3K9ac signal present at Pax9 in neural tube at e11.5, e13.5.



Find & Download Several Experiments

Use metadata to find data:

- Search for “H3K9ac neural tube”
- Get a list of several experiments
- Click on “Download” to download selected metadata and complete links to data.



Download Several Experiments

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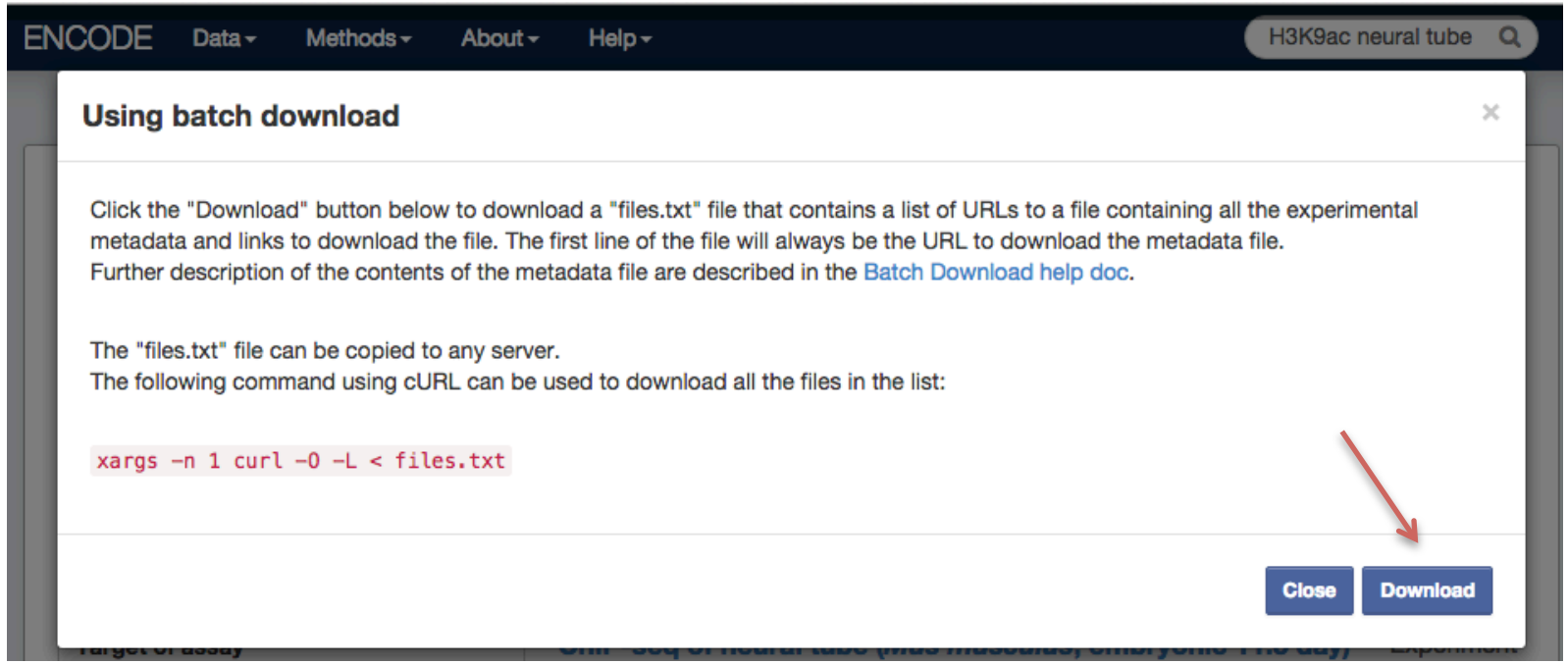

Download Several Experiments

- "Download" produces a file with a list of links to all the files for all the experiments in your search.
- You can iterate through the list in your own script.
- Or:

  `xargs -n 1 curl -O -L < files.txt`
- The first link is to a file called metadata.tsv that contains metadata you need to interpret what each file is.

files.txt

```
https://www.encodeproject.org/metadata/searchTerm=H3K9ac+neural+tube&type=Experiment&assay_term_name=ChIP-seq&assembly=mm10&replicates.library.biosample.donor.organism.scientific_name=Mus+musculus/metadata.tsv
https://www.encodeproject.org/files/ENCFF001ZTD/@@download/ENCFF001ZTD.fastq.gz
https://www.encodeproject.org/files/ENCFF001ZTG/@@download/ENCFF001ZTG.fastq.gz
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https://www.encodeproject.org/files/ENCFF419ANT/@@download/ENCFF419ANT.fastq.gz
https://www.encodeproject.org/files/ENCFF610QKS/@@download/ENCFF610QKS.fastq.gz
https://www.encodeproject.org/files/ENCFF061BZL/@@download/ENCFF061BZL.bam
https://www.encodeproject.org/files/ENCFF012NAU/@@download/ENCFF012NAU.bam
https://www.encodeproject.org/files/ENCFF276NPZ/@@download/ENCFF276NPZ.bed.gz
```

Download Several Experiments

- metadata.tsv: Each line contains metadata on a file from the download package.

A1 | File accession

	A	B	C	D	E	F	G	H	I	J	K
1	File accession	File format	Output type	Experiment accession	Assay	Biosample term id	Biosample term name	Biosample type	Biosample life stage	Biosample sex	Biosample organism
2	ENCFF001ZTD	fastq	reads	ENCSR547PLI	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
3	ENCFF001ZTG	fastq	reads	ENCSR547PLI	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
4	ENCFF396EQC	bam	alignments	ENCSR547PLI	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
5	ENCFF054OIO	bam	alignments	ENCSR547PLI	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
6	ENCFF461YZX	bigBed narrowPeak	peaks	ENCSR547PLI	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
7	ENCFF407KIQ	bed narrowPeak	peaks	ENCSR547PLI	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
8	ENCFF559AVR	bed narrowPeak	peaks	ENCSR547PLI	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
9	ENCFF603TPC	bed narrowPeak	peaks	ENCSR547PLI	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
10	ENCFF296LTU	bigBed narrowPeak	peaks	ENCSR547PLI	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
11	ENCFF203NAR	bigBed narrowPeak	peaks	ENCSR547PLI	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
12	ENCFF335QHI	bigWig	signal p-value	ENCSR547PLI	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
13	ENCFF281WLU	bigWig	signal p-value	ENCSR547PLI	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
14	ENCFF649ZBD	bigWig	signal p-value	ENCSR547PLI	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
15	ENCFF858EFR	bigWig	fold change over control	ENCSR547PLI	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
16	ENCFF789MSC	bigWig	fold change over control	ENCSR547PLI	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
17	ENCFF806WGA	bigWig	fold change over control	ENCSR547PLI	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
18	ENCFF089YRA	bed narrowPeak	replicated peaks	ENCSR547PLI	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
19	ENCFF096JIB	bigBed narrowPeak	replicated peaks	ENCSR547PLI	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
20	ENCFF002AOI	fastq	reads	ENCSR511LWL	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
21	ENCFF002AOO	fastq	reads	ENCSR511LWL	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
22	ENCFF683EHP	bam	alignments	ENCSR511LWL	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
23	ENCFF632XMI	bam	alignments	ENCSR511LWL	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
24	ENCFF980AIP	bigBed narrowPeak	peaks	ENCSR511LWL	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
25	ENCFF994QFR	bed narrowPeak	peaks	ENCSR511LWL	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
26	ENCFF161OXM	bigBed narrowPeak	peaks	ENCSR511LWL	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus
27	ENCFF151MLW	bigBed narrowPeak	peaks	ENCSR511LWL	ChIP-seq	UBERON:0001049	neural tube	tissue	embryonic	mixed	Mus musculus

Programmatic access via the ENCODE REST API

- All Portal content is accessible via URL's; just add `?format=json`
- The database record is returned in JSON format
- JSON can be parsed in your language of choice

GET_object.py

```python
#!/usr/bin/env python

import requests

URL = 'https://www.encodeproject.org/experiments/ENCSR236EGS/?format=json'

response = requests.get(URL)

experiment = response.json()

print experiment['accession']
print experiment['description']
```

Programmatic access via the ENCODE REST API

GET_object.py

```python
#!/usr/bin/env python

import requests

URL = 'https://www.encodeproject.org/experiments/ENCSR236EGS/?format=json'

response = requests.get(URL)

experiment = response.json()

print experiment['accession']
print experiment['description']
```

```
jseth:Keystone Epigenomics 2015 jseth$ ./GET_object.py
ENCSR236EGS
RNA-seq on a dissected area of layer V from an 8 month old male wild type C57Bl6 mouse
jseth:Keystone Epigenomics 2015 jseth$
```

Programmatic access via the ENCODE REST API

GET_search.py

```python
#!/usr/bin/env python

import requests

URL = ('https://www.encodeproject.org/search/?'
       'type=experiment&'
       'assay_term_name=ChIP-seq&'
       'replicates.library.biosample.donor.organism.scientific_name=Homo sapiens&'
       'target.investigated_as=transcription factor&'
       'replicates.library.biosample.biosample_type=in vitro differentiated cells&'
       'format=json')

response = requests.get(URL)

search_result = response.json()['@graph']

#extract and print the target for each experiment
print '\n'.join([experiment['target']['label'] for experiment in search_result])
```

Programmatic access via the ENCODE REST API

GET_search.py

```
#!/usr/bin/e

import reque

URL = ('http
        'type=
        'assay
        'repli                                                  omo sapiens&'
        'targe
        'repli                                                  tiated cells&'
        'forma

response = r

search_result = response.json()['@graph']

#extract and print the target for each experiment
print '\n'.join([experiment['target']['label'] for experiment in search_result])
```

```
jseth:Keystone Epigenomics 2015 jseth$ ./GET_search.py
SMC3
RAD21
MXI1
EP300
CTCF
EZH2
EZH2
CTCF
POLR2AphosphoS5
REST
TAF1
jseth:Keystone Epigenomics 2015 jseth$
```

The ENCODE Portal: Recap

- Interactive access to ENCODE metadata via faceted browsing and search
- Interactive retrieval of ENCODE data one file at a time
- Batch download of ENCODE metadata and data files
- Programmatic access using the ENCODE REST API

<u>Next: ENCODE's Integrative Results and More Visualization</u>

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