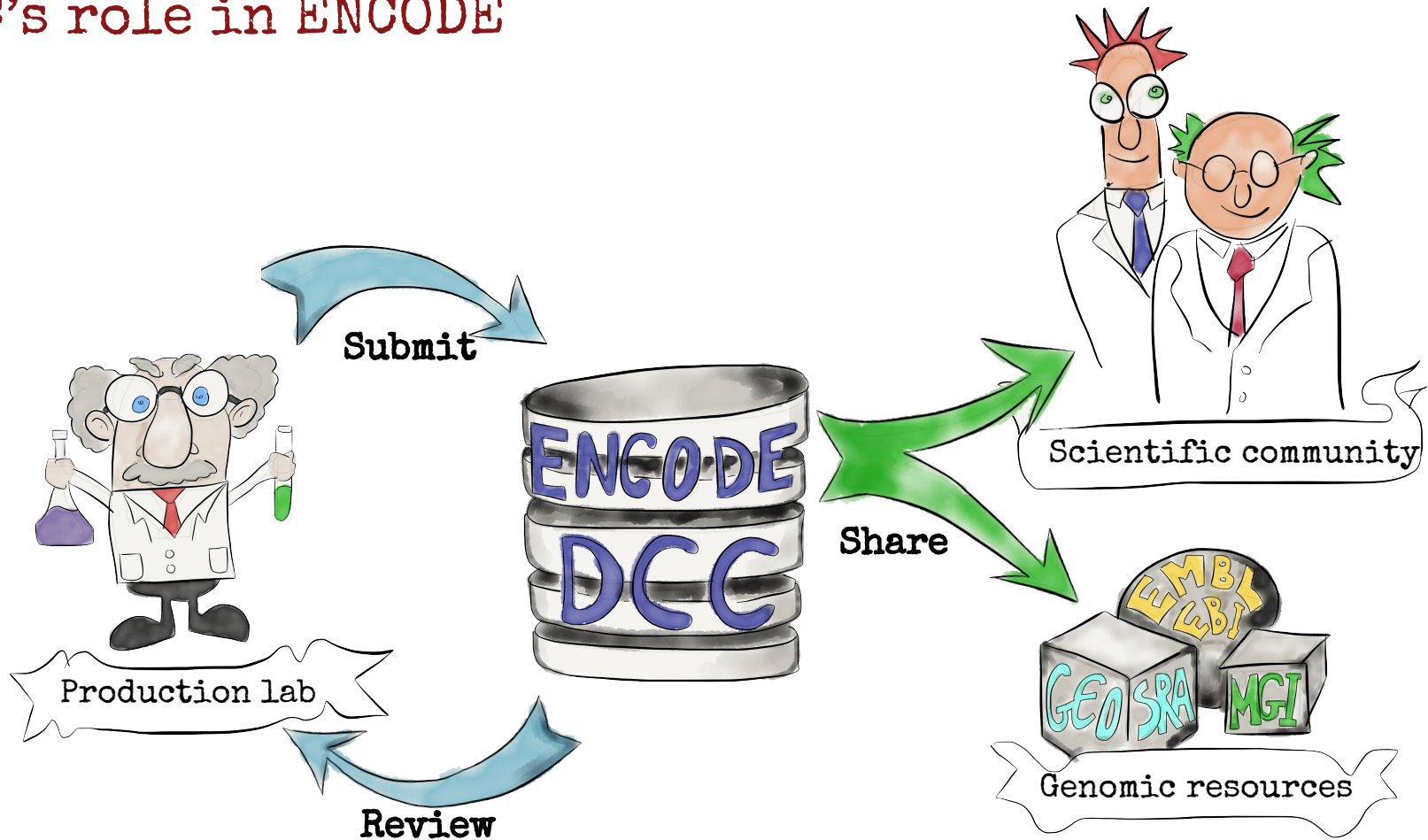


Intro to the ENCODE portal

Jason Hilton, PhD

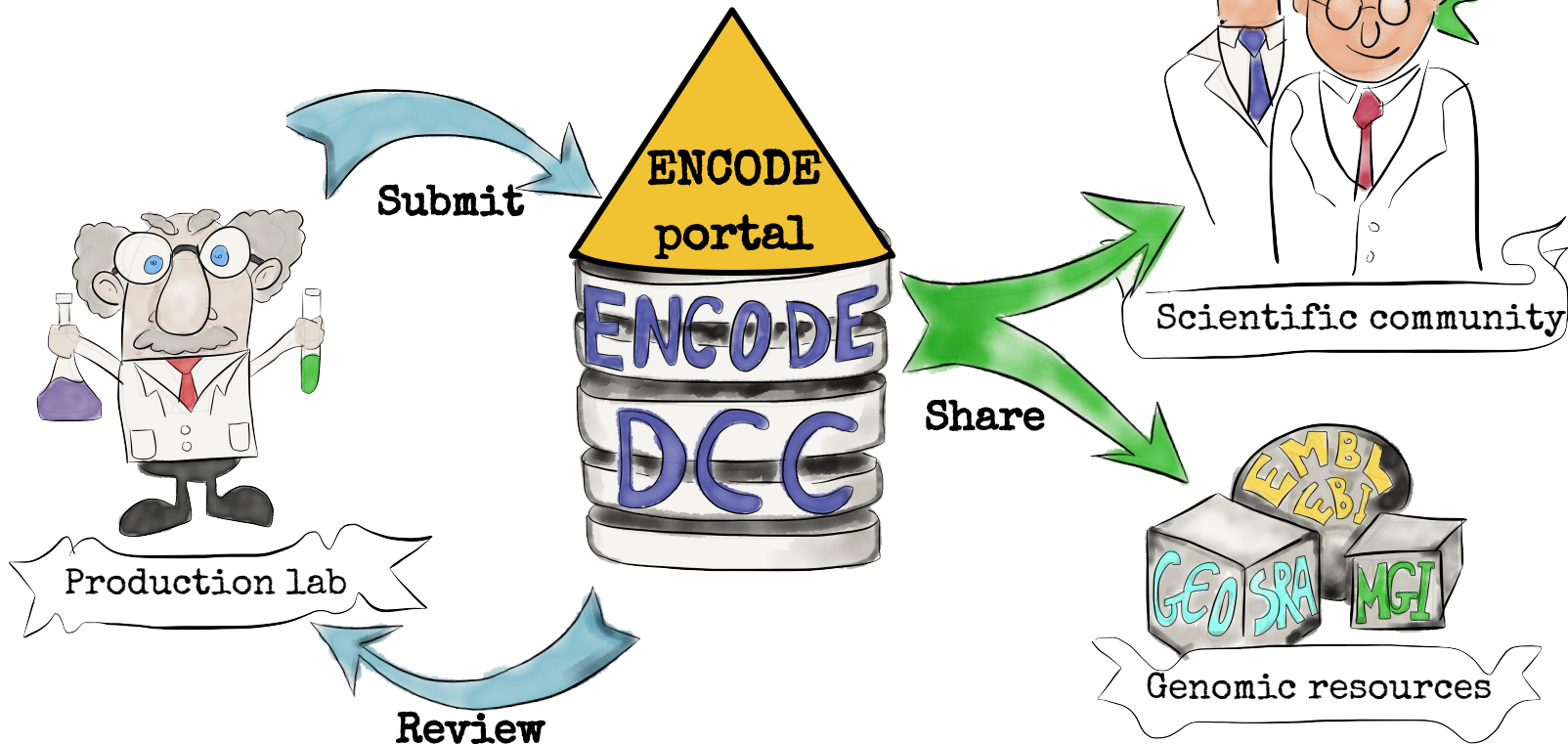
ENCODE Data Coordination Center

DCC's role in ENCODE



DCC's role in ENCODE

The ENCODE portal is a main tools for the DCC



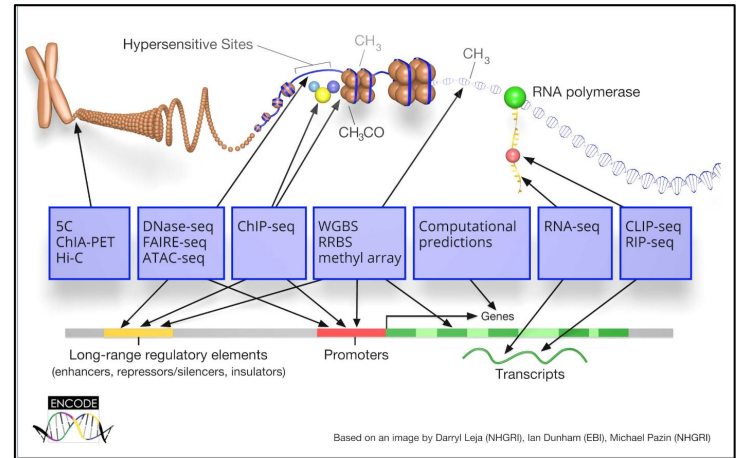
ENCODE portal

encodeproject.org

15K experiments

46 assay “flavors”

600TB data files



ENCODE portal

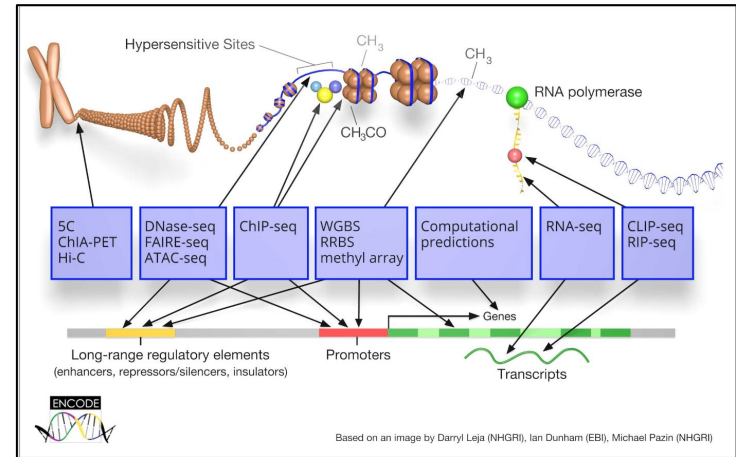
encodeproject.org

15K experiments

PRIMARY ORGANIZATIONAL
UNIT ON ENCODE PORTAL

46 assay “flavors”

600TB data files



Outline

An ENCODE experiment

Browse & Search experiments

Visualize & Download files from many experiments

Searching by a region of interest

Access the ENCODE portal programmatically

An ENCODE experiment
<https://www.encodeproject.org/ENCSR982QIF>

The experiment page

The screenshot shows the ENCODE website interface. At the top, there is a navigation bar with 'ENCODE', 'Data', 'Encyclopedia', 'Materials & Methods', and 'Help'. A search bar is on the right. Below the navigation bar, a breadcrumb trail reads 'EXPERIMENTS / CHIP-SEQ / HOMO SAPIENS / ASCENDING AORTA'. The main heading is 'Experiment summary for ENCSR982QIF'. There are two columns: 'Summary' and 'Attribution'. The 'Summary' column lists various experimental details, and the 'Attribution' column lists the lab, award, project, and related datasets. Below these columns is a 'Tags' section with a 'GTEx' tag. At the bottom, there is a section for 'Isogenic replicates' with a table showing one replicate.

Isogenic replicate	Technical replicate	Summary	Biosample	Antibody	Library
1	1	female adult (51 year) ascending aorta tissue	ENCBS273PSC	ENCAB000AQN	ENCLB626HJU

The image shows a screenshot of the ENCODE project website. The main heading is "Experiment summary for ENCSR982QIF". A red box highlights the "Summary" section on the left side of the page. To the right of the main page content, there is a larger, detailed view of the "Summary" section, also outlined in red. This detailed view lists various experimental parameters such as Status (released), Assay (ChIP-seq), Target (H3K27ac), Biosample summary (Homo sapiens ascending aorta female adult (51 year)), Biosample Type (tissue), Replication type (unreplicated), Nucleic acid type (DNA), Size range (200-600), Fragmentation method (sonication (generic)), Strand specificity (Non-strand-specific), Platform (Illumina HiSeq 2500), and Controls (ENCSR494YJW). Below the summary, there is a table for "Isogenic replicates" with one row showing a single replicate.

Isogenic replicate	Technical replicate	Summary	Biosamp
1	1	female adult (51 year) ascending aorta tissue	ENCBS27

Summary

Status: ● released

Assay: ChIP-seq

Target: [H3K27ac](#)

Biosample summary: *Homo sapiens* ascending aorta female adult (51 year)

Biosample Type: tissue

Replication type: unreplicated

Nucleic acid type: DNA

Size range: 200-600

Fragmentation method: sonication (generic)

Strand specificity: Non-strand-specific

Platform: [Illumina HiSeq 2500](#)

Controls: [ENCSR494YJW](#)

Attribution

Lab: Br
Award: US
Project: EN
External resources: GI
Aliases: br
Date submitted: No
Date released: Ju
Related datasets: EN
Tags:

An ENCODE experiment

<https://www.encodeproject.org/ENCSR982QIF>

Experiment grouping

The screenshot shows the ENCODE project website interface. At the top, there are navigation links for 'ENCODE', 'Data', 'Encyclopedia', 'Materials & Methods', and 'Help', along with a search bar. The main content area displays details for experiment ENCSR982QIF. Two callout boxes, outlined in red, provide a detailed view of the attribution information.

Callout Box 1 (Left):

- Attribution:** ENCODE PHASE 3
- Lab:** Bradley Bernstein, Broad
- Award:** U54HG006991 (Bradley Bernstein, Broad)
- Project:** ENCODE
- External resources:** [GEO:GSE101384](#)
- Aliases:** bradley-bernstein:Project Element 2547
- Date submitted:** November 13, 2016
- Date released:** June 8, 2017
- Related datasets:** [ENCSR818FUR](#)
- Tags:** GTEx

Callout Box 2 (Right):

- Attribution:** ENCODE PHASE 3
- Lab:** Bradley Bernstein, Broad
- Award:** U54HG006991 (Bradley Bernstein, Broad)
- Project:** ENCODE
- External resources:** [GEO:GSE101384](#)
- Aliases:** bradley-bernstein:Project Element 2547
- Date submitted:** November 13, 2016
- Date released:** June 8, 2017
- Related datasets:** [ENCSR818FUR](#)
- Tags:** GTEx

ENCODE Data Encyclopedia Materials & Methods Help Search...

EXPERIMENTS / CHIP-SEQ / HOMO SAPIENS / ASCENDING AORTA

Experiment summary for ENCSR982QIF

Summary Attribution

Status: ● released Attribution: ENCODE PHASE 3

Lab: Bradley Bernstein, Broad

Isogenic replicates

Isogenic replicate ^	Technical replicate v	Summary	Biosample v	Antibody v	Library v
1	1	female adult (51 year) ascending aorta tissue	ENCBS273PSC	ENCAB000AQN	ENCLB626HJU

Platform: Illumina HiSeq 2500

Controls: ENCSR494YJW

Isogenic replicates

Isogenic replicate ^	Technical replicate v	Summary	Biosample v	Antibody v	Library v
1	1	female adult (51 year) ascending aorta tissue	ENCBS273PSC	ENCAB000AQN	ENCLB626HJU

Files Visualize

GRCh38 Include deprecated files

Association graph File details

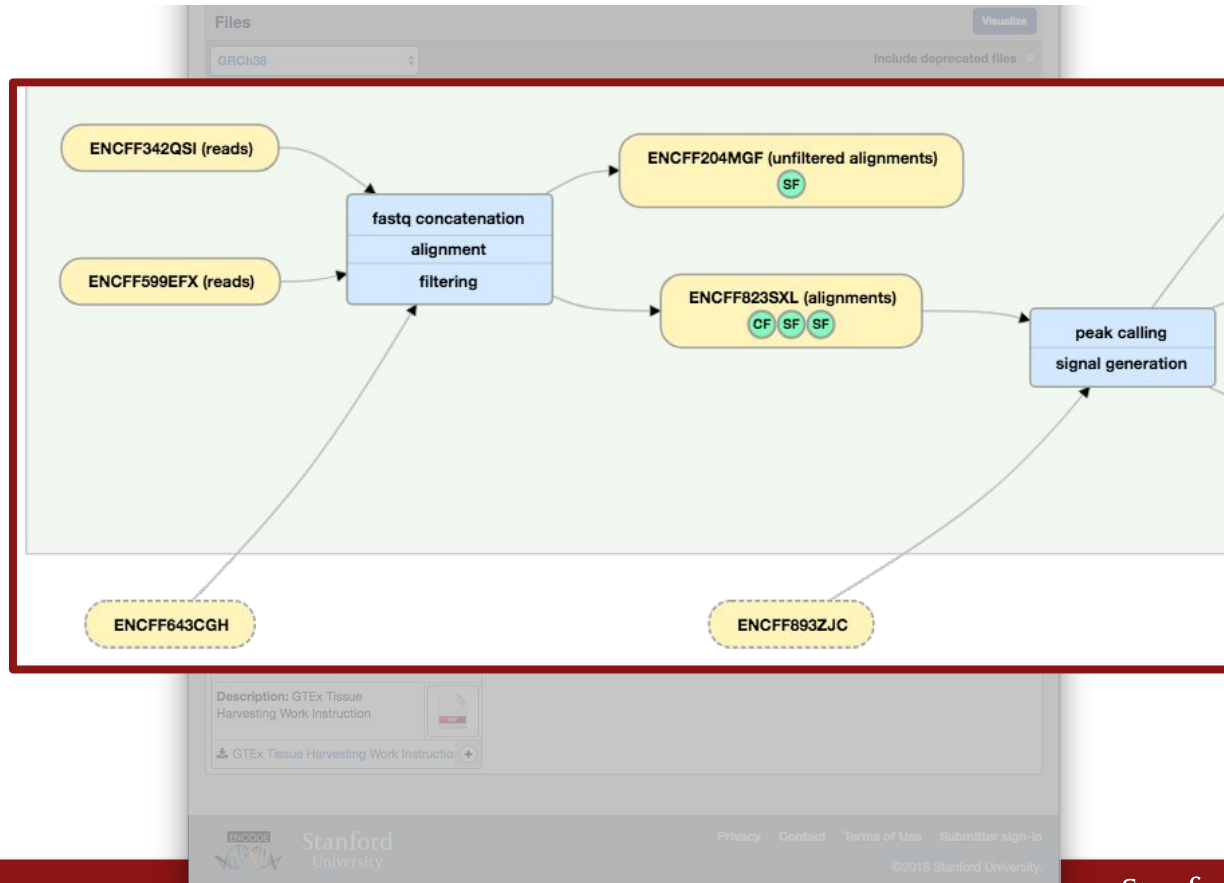
Download Graph

Documents

<p>High Resolution Pathology Slide Image</p> <p>Description excerpt: High-resolution whole slide digital images of pathological specimens (SVS...</p> <p>84258.svs</p>	<p>Pipeline Protocol</p> <p>Description: ChIP mapping pipeline. Includes overview and references for the pipeline</p> <p>ChIP-seq_Mapping_Pipeline_Overview.r</p>	<p>General Protocol</p> <p>Description: PRC Case Summary Report For Case 4</p> <p>ENC_Case-4_DEJ_PRCcsr_Redacted.p</p>
<p>General Protocol</p> <p>Description: GTEx ENCODE Tissue Recovery Form II, Case 4</p> <p>ENC_Case-4_DEJ_TRF_revised.pdf</p>	<p>Data Sheet</p> <p>Description: Mapping of high resolution images (SVS format) ids to tissues</p> <p>Encode Public IDs.pdf</p>	<p>General Protocol</p> <p>Description: Epigenomics Alternative Mag Bead ChIP Protocol v1.1 exp</p> <p>Epigenomics_Alternative_Mag_Bead_CI</p>
<p>Extraction Protocol</p> <p>Description: GTEx Tissue Harvesting Work Instruction</p> <p>GTEx Tissue Harvesting Work Instructio</p>		

Privacy [Contact](#) [Terms of Use](#) [Submitter sign-in](#)

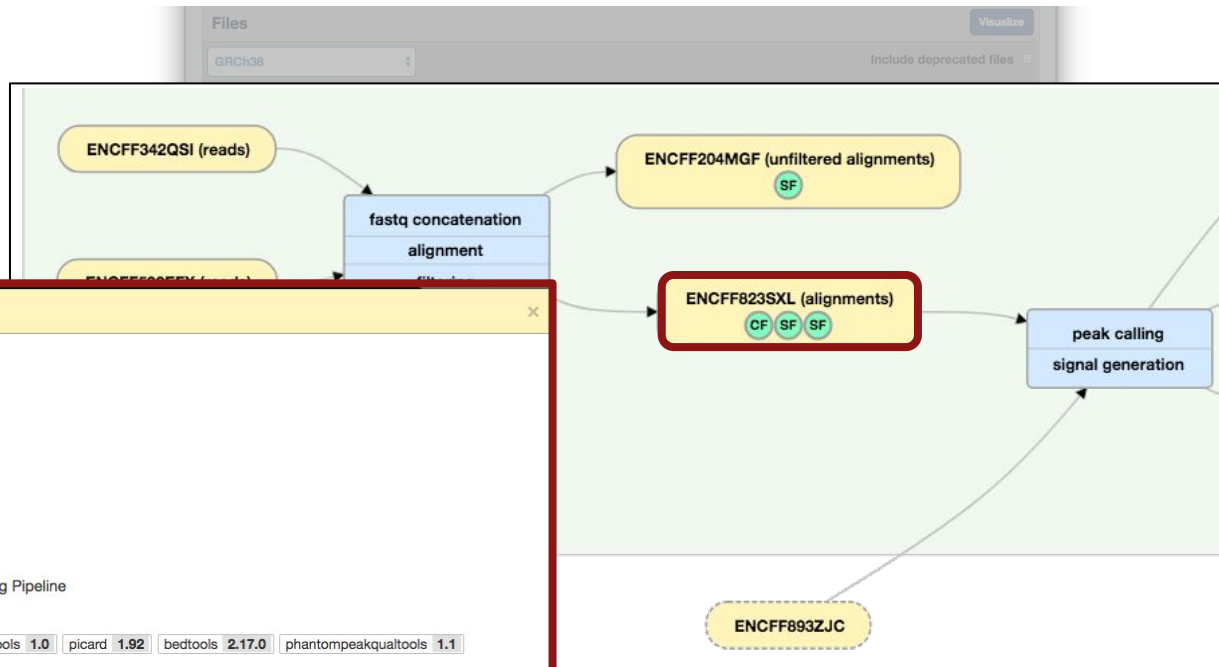
©2018 Stanford University.



An ENCODE experiment

<https://www.encodeproject.org/ENCSR982QIF>

File details



bam **ENCFF823SXL**

Status: ● released

Output: alignments

Biological replicate(s): [1]

Technical replicate(s): [1_1]

Mapped read length: 76

Mapping assembly: GRCh38

Lab: ENCODE Processing Pipeline

Date added: 2016-11-16

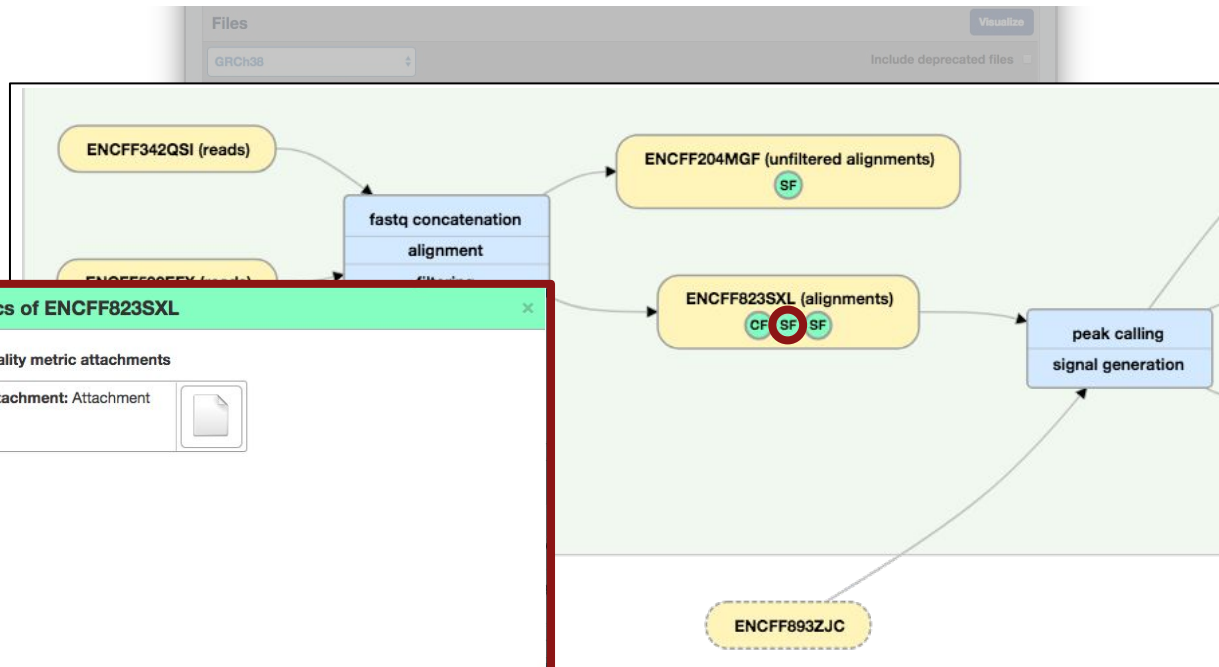
Software: bwa 0.7.10 samtools 1.0 picard 1.92 bedtools 2.17.0 phantompeakqualtools 1.1

File size: 1.96 GB

File download: [ENCFF823SXL](#)

File quality metrics: Chipseq filter quality metrics Samtools flagstats quality metrics Samtools flagstats quality metrics


Close



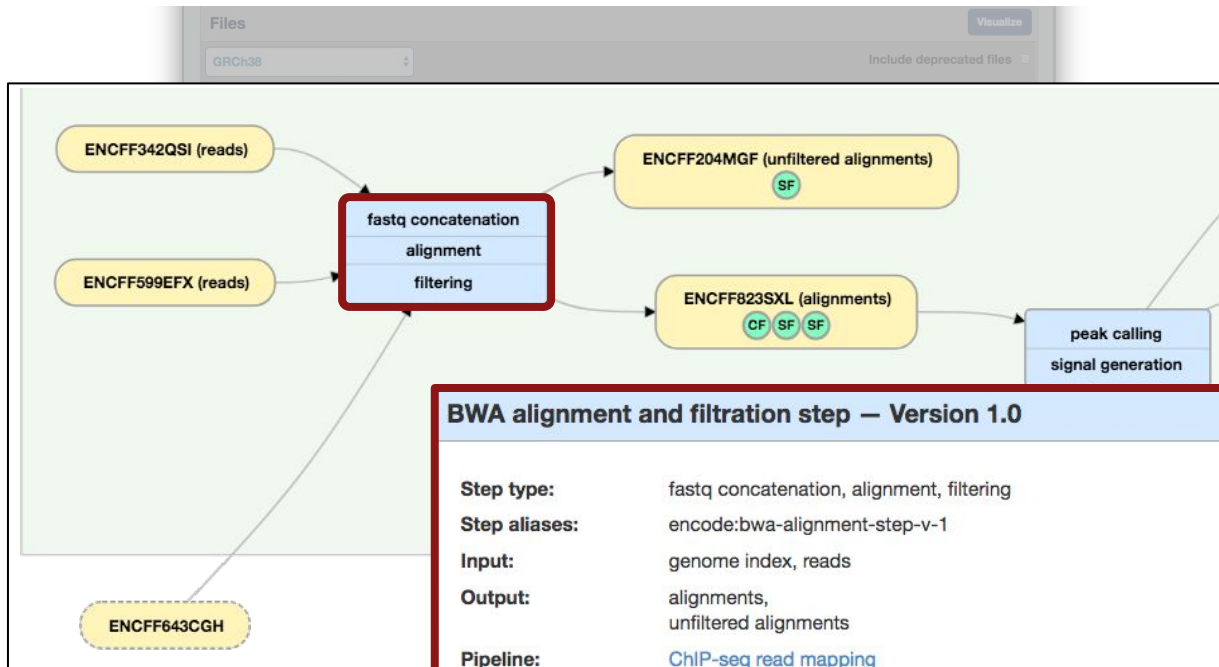
Samtools flagstats quality metrics of ENCF823SXL

# reads with duplicates passing QC:	0
# reads with duplicates failing QC:	0
# reads mapped passing QC:	42194897
% reads mapped passing QC:	100.00%
# reads mapped failing QC:	0
Processing stage:	filtered
# of total reads passing QC:	42194897
# of total reads failing QC:	0

Quality metric attachments

Attachment: Attachment 

Close



BWA alignment and filtration step – Version 1.0

Step type: fastq concatenation, alignment, filtering
Step aliases: encode:bwa-alignment-step-v-1
Input: genome index, reads
Output: alignments, unfiltered alignments
Pipeline: [ChIP-seq read mapping](#)
Software: `bwa 0.7.10` `samtools 1.0` `picard 1.92` `bedtools 2.17.0` `phantompeakqualtools 1.1`

Close


An ENCODE experiment

<https://www.encodeproject.org/ENCSR982QIF>

File graph <-> table









Files Visualize

GRCh38 Include deprecated files





























Association graph **File details** 

Displaying 10 of 10 files

Raw sequencing data

Isogenic replicate	Library	Accession	File type	Run type	Read	Lab	Date added	File size	Audit status	File status
1	ENCLB626HJU	ENCFF599EFX  	fastq	SE76nt		Bradley Bernstein, Broad	2016-11-13	1.34 GB		 released
1	ENCLB626HJU	ENCFF342QSI  	fastq	SE76nt		Bradley Bernstein, Broad	2016-11-13	1.33 GB		 released

Processed data

Accession	File type	Output type	Isogenic replicate	Mapped read length	Mapping assembly	Lab	Date added	File size	Audit status	File status
ENCFF109PKU  	bigWig	fold change over control	1		GRCh38	ENCODE Processing Pipeline	2017-06-07	953 MB		 released
ENCFF204MGF  	bam	unfiltered alignments	1	76	GRCh38	ENCODE Processing Pipeline	2016-11-16	2.33 GB		 released
ENCFF823SXL  	bam	alignments	1	76	GRCh38	ENCODE Processing Pipeline	2016-11-16	1.96 GB		 released
ENCFF291LEP  	bed narrowPeak	stable peaks	1		GRCh38	ENCODE Processing Pipeline	2017-06-07	1.8 MB		 released
ENCFF020COG  	bed narrowPeak	peaks	1		GRCh38	ENCODE Processing Pipeline	2017-06-07	2 MB		 released
ENCFF569JIQ  	bigBed narrowPeak	peaks	1		GRCh38	ENCODE Processing Pipeline	2017-06-07	5.19 MB		 released
ENCFF818NBU  	bigBed narrowPeak	stable peaks	1		GRCh38	ENCODE Processing Pipeline	2017-06-07	3.39 MB		 released

An ENCODE experiment
<https://www.encodeproject.org/ENCSR982QIF>

ENCODE IS ALL
OPEN ACCESS!!!!

Files

GRCh38 Include deprecated files

Association graph **File details**

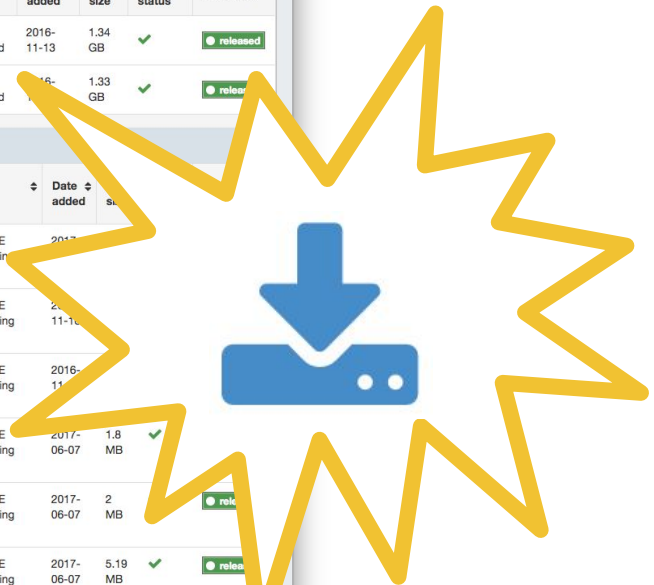
Displaying 10 of 18 files

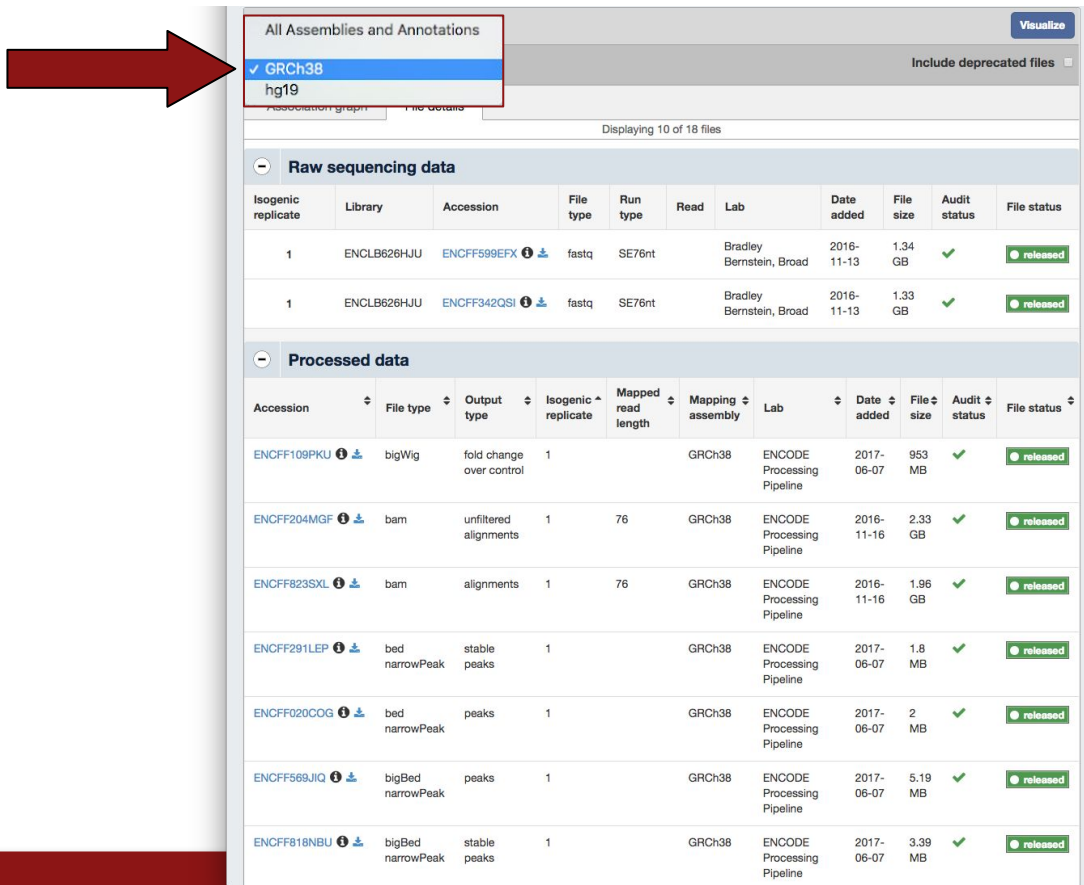
Raw sequencing data

Isogenic replicate	Library	Accession	File type	Run type	Read	Lab	Date added	File size	Audit status	File status
1	ENCLB626HJU	ENCFF599EFX	fastq	SE76nt		Bradley Bernstein, Broad	2016-11-13	1.34 GB	✓	released
1	ENCLB626HJU	ENCFF342QSI	fastq	SE76nt		Bradley Bernstein, Broad	2016-11-13	1.33 GB	✓	released

Processed data

Accession	File type	Output type	Isogenic replicate	Mapped read length	Mapping assembly	Lab	Date added	File size	Audit status	File status
ENCFF109PKU	bigWig	fold change over control	1		GRCh38	ENCODE Processing Pipeline	2017-06-07		✓	released
ENCFF204MGF	bam	unfiltered alignments	1	76	GRCh38	ENCODE Processing Pipeline	2016-11-13		✓	released
ENCFF823SXL	bam	alignments	1	76	GRCh38	ENCODE Processing Pipeline	2016-11-13		✓	released
ENCFF291LEP	bed narrowPeak	stable peaks	1		GRCh38	ENCODE Processing Pipeline	2017-06-07	1.8 MB	✓	released
ENCFF020COG	bed narrowPeak	peaks	1		GRCh38	ENCODE Processing Pipeline	2017-06-07	2 MB	✓	released
ENCFF569JIQ	bigBed narrowPeak	peaks	1		GRCh38	ENCODE Processing Pipeline	2017-06-07	5.19 MB	✓	released
ENCFF818NBU	bigBed narrowPeak	stable peaks	1		GRCh38	ENCODE Processing Pipeline	2017-06-07	3.39 MB	✓	released





All Assemblies and Annotations Visualize









Include deprecated files

▼ GRCh38
hg19





























Association graph File details

Displaying 10 of 18 files

Raw sequencing data

Isogenic replicate	Library	Accession	File type	Run type	Read	Lab	Date added	File size	Audit status	File status
1	ENCLB626HJU	ENCFF599EFX  	fastq	SE76nt		Bradley Bernstein, Broad	2016-11-13	1.34 GB		 released
1	ENCLB626HJU	ENCFF342QSI  	fastq	SE76nt		Bradley Bernstein, Broad	2016-11-13	1.33 GB		 released

Processed data

Accession	File type	Output type	Isogenic replicate	Mapped read length	Mapping assembly	Lab	Date added	File size	Audit status	File status
ENCFF109PKU  	bigWig	fold change over control	1		GRCh38	ENCODE Processing Pipeline	2017-06-07	953 MB		 released
ENCFF204MGF  	bam	unfiltered alignments	1	76	GRCh38	ENCODE Processing Pipeline	2016-11-16	2.33 GB		 released
ENCFF823SXL  	bam	alignments	1	76	GRCh38	ENCODE Processing Pipeline	2016-11-16	1.96 GB		 released
ENCFF291LEP  	bed narrowPeak	stable peaks	1		GRCh38	ENCODE Processing Pipeline	2017-06-07	1.8 MB		 released
ENCFF020COG  	bed narrowPeak	peaks	1		GRCh38	ENCODE Processing Pipeline	2017-06-07	2 MB		 released
ENCFF569JIQ  	bigBed narrowPeak	peaks	1		GRCh38	ENCODE Processing Pipeline	2017-06-07	5.19 MB		 released
ENCFF818NBU  	bigBed narrowPeak	stable peaks	1		GRCh38	ENCODE Processing Pipeline	2017-06-07	3.39 MB		 released

The screenshot shows the ENCODE data browser interface. A modal window titled "Open visualization browser" is open, displaying options for visualizing data. The modal contains the following content:

Assembly Visualize with browser...

GRCh38: Quick View **BETA** UCSC Ensembl

hg19: Quick View **BETA** UCSC

Close

The background interface shows a table of processed data with the following columns: Accession, File type, Output type, Isogenic replicate, Mapped read length, Mapping assembly, Lab, Date added, File size, Audit status, and File status.

Accession	File type	Output type	Isogenic replicate	Mapped read length	Mapping assembly	Lab	Date added	File size	Audit status	File status
ENCF109PKU	bigWig	fold change over control	1		GRCh38	ENCODE Processing Pipeline	2017-06-07	953 MB	✓	released
ENCF204MGF	bam	unfiltered alignments	1	76	GRCh38	ENCODE Processing Pipeline	2016-11-16	2.33 GB	✓	released
ENCF823SXL	bam	alignments	1	76	GRCh38	ENCODE Processing Pipeline	2016-11-16	1.96 GB	✓	released
ENCF291LEP	bed narrowPeak	stable peaks	1		GRCh38	ENCODE Processing Pipeline	2017-06-07	1.8 MB	✓	released
ENCF020COG	bed narrowPeak	peaks	1		GRCh38	ENCODE Processing Pipeline	2017-06-07	2 MB	✓	released
ENCF569JIQ	bigBed narrowPeak	peaks	1		GRCh38	ENCODE Processing Pipeline	2017-06-07	5.19 MB	✓	released
ENCF818NBU	bigBed narrowPeak	stable peaks	1		GRCh38	ENCODE Processing Pipeline	2017-06-07	3.39 MB	✓	released

An ENCODE experiment

<https://www.encodeproject.org/ENCSR982QIF>

Quick viz on ENCODE portal

The screenshot displays the ENCODE portal interface. On the left, a table lists processed data files. A modal window titled "Open visualization browser" is overlaid, showing options for "GRCh38" (Quick View BETA, UCSC, Ensembl) and "hg19" (Quick View). The main page shows a search bar and a navigation menu. A "Showing 4 of 4 results" section is visible, with a "Quick View BETA" button selected. Below this, a genomic track view is shown for the region 22:29,758,202..29,918,204. The track includes various annotations such as GENCODE, Repeats, and signal tracks for GRCh38 and hg19 assemblies.

Accession	File type	Output type	Isogenic replicate
ENCF109PKU	bigWig	fold change over control	1
ENCF204MGF	bam	unfiltered alignments	1
ENCF823SXL	bam	alignments	1
ENCF291LEP	bed narrowPeak	stable peaks	1
ENCF020COG	bed narrowPeak	peaks	1
ENCF589JIQ	bigBed narrowPeak	peaks	1
ENCF818NBU	bigBed narrowPeak	stable peaks	1

File status	Count
released	4
in progress	0

Content category	Count
annotation	2
signal	2

Content type	Count
fold change over control	1
peaks	1
signal p-value	1
stable peaks	1

File format	Count
bam	2
bed	2
bigBed	2
bigWig	2

Specific file format type	Count
narrowPeak	2

Project	Count
ENCODE	4

Mapping assembly	Count
GRCh38	4
hg19	4

Lab	Count
ENCODE Processing Pipeline	4

Showing 4 of 4 results

22:29,758,202..29,918,204

Genome 29,800,000 29,850,000 29,900,000

GENCODE

Y_RNA <ASCC2 >AC004819.1

UQCR10 >MTMR3

ZMAT5 <RNU6-331P

Repeats

rep1 stable peaks

rep1 foldchg

rep1 pval sig

rep1 peaks

An ENCODE experiment

<https://www.encodeproject.org/ENCSR982QIF>

Viz at UCSC/Ensembl

The image displays two overlapping screenshots of the UCSC Genome Browser. The background screenshot shows a list of processed data files with columns for Accession, File type, Output type, Isogenic replicate, and Mapped read length. The foreground screenshot is a detailed view of a genomic region on chromosome 11, specifically chr11:11,102,837-11,267,747 (164,911 bp). The interface includes a navigation bar with 'Genomes', 'Genome Browser', 'Tools', 'Mirrors', 'Downloads', 'My Data', 'View', 'Help', and 'About Us'. The main title is 'UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly'. Below the title, there are navigation controls for moving and zooming. The genomic track displays various data layers: hg38 coordinates, H3K27ac histone ChIP-seq, H3K27ac DNase-seq, ENCODE v4 Comprehensive Transcript Set, RefSeq gene predictions, RefSeq gene models, Gene Expression in 53 tissues, H3K27ac Mark, DNase Clusters, Conservation, Multiple Alignments, and Common SNPs. The 'UCSC' button in the 'Open visualization browser' dialog is highlighted with a red box.

Open visualization browser

Assembly Visualize with browser...

GRCh38: Quick View BETA **UCSC** Ensembl

hg19: Quick View BETA UCSC

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

chr11:11,102,837-11,267,747 164,911 bp

Scale chr11: 50 kb

hg38

11,100,000 11,200,000

H3K27ac histone ChIP-seq of Homo sapiens female adult (53 year) ascending aorta tissue - ENCSR982QIF

H3K27ac DNase-seq of ascending aorta. Fold change over control pool ENCSR982QIF - ENCF1109PKU

New haplotype sequences to GRCh38 Reference Sequence

ENCODE v4 Comprehensive Transcript Set (only basic displayed by default)

RefSeq gene predictions from NCBI

RefSeq gene models from NCBI

Gene Expression in 53 tissues from GTEx RNA-seq of 6555 samples (576 donors)

H3K27ac Mark (Often Found Near Regulatory Elements) on 7 cell lines from ENCODE

DNase Clusters

Conservation

Multiple Alignments of 166 Vertebrates

Common SNPs (15)

STRE

LINE

SL1

SNR

SINE

Low Complexity

Repeat Elements by RepeatMasker

Other

Unknown

Files Visualize

GRCh38 Include deprecated files

Association graph File details

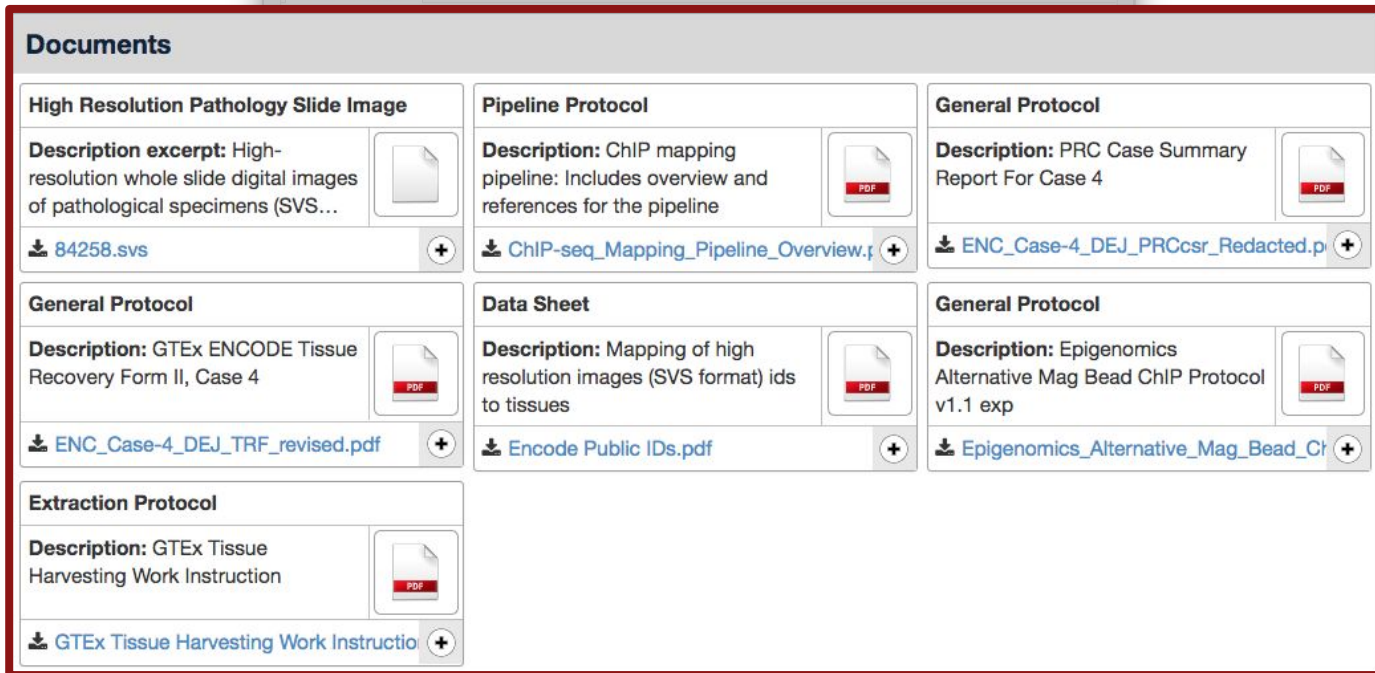
Documents

<p>High Resolution Pathology Slide Image</p> <p>Description excerpt: High-resolution whole slide digital images of pathological specimens (SVS...)</p> <p>84258.svs</p>	<p>Pipeline Protocol</p> <p>Description: ChIP mapping pipeline. Includes overview and references for the pipeline</p> <p>ChIP-seq_Mapping_Pipeline_Overview.r</p>	<p>General Protocol</p> <p>Description: PRC Case Summary Report For Case 4</p> <p>ENC_Case-4_DEJ_PRCcsr_Redacted.p</p>
<p>General Protocol</p> <p>Description: GTEx ENCODE Tissue Recovery Form II, Case 4</p> <p>ENC_Case-4_DEJ_TRF_revised.pdf</p>	<p>Data Sheet</p> <p>Description: Mapping of high resolution images (SVS format) ids to tissues</p> <p>Encode Public IDs.pdf</p>	<p>General Protocol</p> <p>Description: Epigenomics Alternative Mag Bead ChIP Protocol v1.1 exp</p> <p>Epigenomics_Alternative_Mag_Bead_Cl</p>
<p>Extraction Protocol</p> <p>Description: GTEx Tissue Harvesting Work Instruction</p> <p>GTEx Tissue Harvesting Work Instructio</p>		

ENCODI
Stanford University

Privacy Contact Terms of Use Submitter sign-in

©2018 Stanford University.



The screenshot displays a web interface for an ENCODE experiment. At the top, there are tabs for 'Files', 'Association graph', and 'File details'. The 'Files' tab is active, showing a search bar with 'GRCh38' and a button for 'include downloaded files'. Below this is a 'Documents' section with a grid of document cards. Each card includes a title, a description excerpt, a PDF icon, and a download link with a plus sign for more options.

Document Title	Description Excerpt	File Name
High Resolution Pathology Slide Image	Description excerpt: High-resolution whole slide digital images of pathological specimens (SVS...	84258.svs
Pipeline Protocol	Description: ChIP mapping pipeline: Includes overview and references for the pipeline	ChIP-seq_Mapping_Pipeline_Overview.pdf
General Protocol	Description: PRC Case Summary Report For Case 4	ENC_Case-4_DEJ_PRCcsr_Redacted.pdf
General Protocol	Description: GTEx ENCODE Tissue Recovery Form II, Case 4	ENC_Case-4_DEJ_TRF_revised.pdf
Data Sheet	Description: Mapping of high resolution images (SVS format) ids to tissues	Encode Public IDs.pdf
General Protocol	Description: Epigenomics Alternative Mag Bead ChIP Protocol v1.1 exp	Epigenomics_Alternative_Mag_Bead_ChIP_Protocol_v1.1_exp.pdf
Extraction Protocol	Description: GTEx Tissue Harvesting Work Instruction	GTEx Tissue Harvesting Work Instruction.pdf

An ENCODE experiment

<https://www.encodeproject.org/ENCSR982QIF>

ENCODE Data Encyclopedia Materials & Methods Help

EXPERIMENTS / CHIP-SEQ / HOMO SAPIENS / ASCENDING AORTA

Experiment summary for ENCSR982QIF

Summary	Attribution
Status: released	Lab: Bradley Bernstein, Broad
Assay: ChIP-seq	Award: U54HG006991 (Bradley Bernstein, Broad)
Target: H3K27ac	Project: ENCODE
Biosample summary: <i>Homo sapiens</i> ascending aorta female adult (51 year)	External resources: GEO:GSE101384
Biosample Type: tissue	Aliases: bradley-bernstein:Project Element 2547
Replication type: unreplicated	Date submitted: November 13, 2016
Nucleic acid type: DNA	Date released: June 8, 2017
Size range: 200-600	Related datasets: ENCSR618FUR
Fragmentation method: sonication (generic)	Tags:
Strand specificity: Non-strand-specific	
Platform: Illumina HiSeq 2500	
Controls: ENCSR494YJW	

Isogenic replicates

Isogenic replicate	Technical replicate	Summary	Biosample	Antibody	Library
1	1	female adult (51 year) ascending aorta tissue	ENGBS273PSC	ENCAB000AQN	ENCLB626HJU

Files Visualize

GRCh38 Include deprecated files

Association graph File details

Download Graph

Documents

High Resolution Pathology Slide Image Description excerpt: High-resolution whole slide digital images of pathological specimens (SVS... 84258.svs	Pipeline Protocol Description: ChIP mapping pipeline: Includes overview and references for the pipeline ChIP-seq_Mapping_Pipeline_Overview.r	General Protocol Description: PRC Case Summary Report For Case 4 ENC_Case-4_DEJ_PRCcsr_Redacted.p
General Protocol Description: GTEX ENCODE Tissue Recovery Form II, Case 4 ENC_Case-4_DEJ_TRF_revised.pdf	Data Sheet Description: Mapping of high resolution images (SVS format) ids to tissues Encode Public IDs.pdf	General Protocol Description: Epigenomics Alternative Mag Bead ChIP Protocol v1.1 exp Epigenomics_Alternative_Mag_Bead_CI
Extraction Protocol Description: GTEX Tissue Harvesting Work Instruction GTEX Tissue Harvesting Work Instructio		

Stanford University

Privacy Contact Terms of Use Submitter sign-in

©2018 Stanford University.

Browsing the ENCODE portal

ENCODE: Encyclopedia of DNA Elements

Navigation: [ENCODE](#) [Data](#) [Encyclopedia](#) [Materials & Methods](#) [Help](#)

Diagram: DNA Elements and Assays

The diagram illustrates the relationship between various assays and DNA elements. Assays include: 5C, ChIA-PET, Hi-C; DNase-seq, FAIRE-seq, ATAC-seq; CHIP-seq; WGBS, RRBS, methyl array; Computational predictions; RNA-seq; and CLIP-seq, RIP-seq. These assays identify features such as Hypersensitive Sites, CH₃, CH₃CO, RNA polymerase, Long-range regulatory elements (enhancers, repressors/silencers, insulators), Promoters, and Transcripts. The diagram is based on an image by Danyal Leji (NHGR), Ian Duxham (EBI), Michael Pazin (NHGR).

Search and Navigation:

- [About ENCODE Project](#) [Getting Started](#) [Experiments](#)
- Search ENCODE portal
- [ENCODE Q](#)
- [About ENCODE Encyclopedia](#) [Candidate Regulatory Elements](#)
- Search for Candidate Regulatory Elements
- Hosted by [SCREEN](#)
- [Human hg19 Q](#) [Mouse mm10 Q](#)

Species Selection: [HUMAN](#) [MOUSE](#) [WORM](#) [FLY](#)

Data Matrix

Project (Donut chart, total 14348)

- ENCODE
- Roadmap
- modERN
- modENCODE
- GGR
- community

Biosample Type (Donut chart, total 14348)

- cell line
- tissue
- whole organisms
- primary cell
- in vitro differentiated cells
- stem cell
- cell-free sample
- induced pluripotent stem cell line
- single cell

Assay Categories (Bar chart)

- DNA binding
- Transcription
- DNA accessibility
- RNA binding
- DNA methylation
- Reproducible binding
- Chromatin
- 3D chromatin structure
- Proteomics
- DNA sequencing
- RNA structure

Footer: [Twitter @EncodeDCC](#) [News More ENCODE news](#)

Browsing the ENCODE portal

Jumping in: matrix

The screenshot shows the ENCODE portal interface. A red arrow points to the 'Matrix' dropdown menu in the top navigation bar. The main content area features a diagram of DNA with various epigenetic marks (CH₃, CH₃CO) and RNA polymerase, with arrows pointing to boxes for different assays: 5C, ChIA-PET, Hi-C, DNase-seq, FAIRE-seq, ATAC-seq, ChIP-seq, WGBS, RRBS, methyl array, Computational predictions, RNA-seq, and CLIP-seq, RIP-seq. Below this are search bars for the ENCODE portal and candidate regulatory elements, and tabs for different species (Human, Mouse, Worm, Fly). The 'Data Matrix' section contains three charts: two donut charts for 'Project' and 'Biosample Type' (both totaling 14348) and a bar chart for 'Assay Categories'.

Project

Project	Count
ENCODE	~6000
Roadmap	~2000
modERN	~1000
modENCODE	~1000
GGR	~1000
community	~1000

Biosample Type

Biosample Type	Count
cell line	~6000
tissue	~2000
whole organisms	~1000
primary cell	~1000
in vitro differentiated cells	~1000
stem cell	~1000
cell-free sample	~1000
induced pluripotent stem cell line	~1000
single cell	~1000

Assay Categories

Assay Category	Count
DNA looping	~8000
Transcription	~3000
DNA accessibility	~2000
DNA binding	~1000
Regulation	~1000
Genomics	~1000
3D chromatin structure	~1000
DNA sequencing	~1000
RNA structure	~1000

Browsing the ENCODE portal

Jumping in: matrix

ENCODE: Encyclopedia of DNA Elements

Navigation: About ENCODE Project, Getting Started, Experiments

Search ENCODE portal

Assay Categories: 5C, ChIA-PET, Hi-C, DNase-seq, FAIRE-seq, ATAC-seq, CHIP-seq, WGBS, RRBS, methyl array, Computational predictions, RNA-seq, CLIP-seq, RIP-seq

Long-range regulatory elements (enhancers, repressors/silencers, insulators), Promoters, Transcripts, Genes

Species: HUMAN, MOUSE, WORM, FLY

Data Matrix

Project: 14348

Biosample Type: 14348

Assay Categories: DNA looping, Transcription, DNA accessibility, DNA binding, Replication timing, 3D chromatin structure, Gene expression, RNA structure

Legend for Project and Biosample Type:

- ENCODE
- Roadmap
- modERN
- modENCODE
- GGR
- community
- cell line
- tissue
- whole organisms
- primary cell
- in vitro differentiated cells
- stem cell
- cell-free sample
- induced pluripotent stem cell line
- single cell

Twitter @EncodeDCC | News More ENCODE news

Jump to
filtered
matrix

Browsing the ENCODE portal

Jumping in: matrix

Filter by
assay category
& organism

The screenshot shows the ENCODE portal interface. At the top, there's a navigation bar with 'ENCODE', 'Data', 'Encyclopedia', 'Materials & Methods', and 'Help'. A search bar is on the right. Below the navigation bar is the title 'ENCODE: Encyclopedia of DNA Elements'. A central diagram illustrates DNA elements including Hypersensitive Sites, CH₃, CH₃CO, RNA polymerase, and various assays: 5C, ChIA-PET, Hi-C, DNase-seq, FAIRE-seq, ATAC-seq, CHIP-seq, WGBS, RRBS, methyl array, Computational predictions, RNA-seq, and CLIP-seq, RIP-seq. Below the diagram are buttons for 'About ENCODE Project', 'Getting Started', and 'Experiments'. A search bar for the ENCODE portal is present. Further down, there are buttons for 'About ENCODE Encyclopedia' and 'Candidate Regulatory Elements', along with a search bar for candidate elements. At the bottom of the diagram area are buttons for 'Human hg19 Q.' and 'Mouse mm10 Q.'. Below the diagram is a 'Filtered Data Matrix' section with three charts: 'Project' (donut chart showing 10054 total), 'Biosample Type' (donut chart showing 10054 total), and 'Assay Categories' (bar chart showing the distribution of assays). The 'Project' chart includes categories: ENCODE, Roadmap, GGR, and community. The 'Biosample Type' chart includes: cell line, tissue, primary cell, in vitro differentiated cells, stem cell, and induced pluripotent stem cell line. The 'Assay Categories' chart lists: DNA binding, Transcription, DNA accessibility, RNA binding, DNA methylation, Replication, 3D chromatin structure, Genotyping, Proteomics, DNA sequencing, and RNA structure. At the bottom of the page, there are sections for 'Twitter @EncodeDCC' and 'News More ENCODE news', with a specific news item for 'June 2018 Data Release July 3, 2018'.

Browsing the ENCODE portal

Jumping in: matrix

Filter by
assay category
& organism

The screenshot shows the ENCODE portal interface. At the top, there's a navigation bar with 'ENCODE', 'Data', 'Encyclopedia', 'Materials & Methods', and 'Help'. A search bar is on the right. Below the navigation bar is the title 'ENCODE: Encyclopedia of DNA Elements'. A diagram illustrates DNA elements including Hypersensitive Sites, CH₃, CH₃CO, RNA polymerase, and various assays: 5C, ChIA-PET, Hi-C, DNase-seq, FAIRE-seq, ATAC-seq, CHIP-seq, WGBS, RRBS, methyl array, Computational predictions, RNA-seq, and CLIP-seq, RIP-seq. Below the diagram are search filters for 'About ENCODE Project', 'Getting Started', 'Experiments', 'About ENCODE Encyclopedia', and 'Candidate Regulatory Elements'. There are also search bars for 'Search ENCODE portal' and 'Search for Candidate Regulatory Elements'. At the bottom, there are tabs for 'HUMAN', 'MOUSE', 'WORM', and 'FLY'. A 'Filtered Data Matrix' button is highlighted with a red arrow. Below this are three charts: 'Project' (donut chart with 10054 total), 'Biosample Type' (donut chart with 10054 total), and 'Assay Categories' (bar chart showing the distribution of assays).

ENCODE: Encyclopedia of DNA Elements

Based on an image by Danyal Leja (NHGR), Ian Dunham (EBI), Michael Plazin (NHGR)

Filtered Data Matrix

Project: 10054

Biosample Type: 10054

Assay Categories: 6000

Twitter: @EncodeDCC

News: More ENCODE news

ENCODE DCC Retweeted

ENCODE Project

June 2018 Data Release

July 3, 2018

ENCODE
Search...

Experiment Matrix

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

Assay	Assay category	Target of assay	Date released	Available data
ChIP-seq	DNA binding	transcription factor	July, 2013	2156
DNase-seq	Transcription	histone	October, 2011	445
siRNA RNA-seq	DNA	control	October, 2016	405
eCLIP	accessibility	RNA binding	November, 2016	384
polyA RNA-seq	RNA binding	protein	May, 2016	300
	DNA methylation	broad histone mark		900

Organism

- Human** 10054
- Mus musculus 1789
- Drosophila melanogaster 1384
- Caenorhabditis elegans 955
- Drosophila pseudoobscura 4

BIOSAMPLE

10054 results

ASSAY

Clear Filters 0

cell line	K562	HepG2	A549	GM12878	HEK293
	10	268	245	19	3
	11	7	10	1	2
	1	2	1	2	6
	1	2	6	1	9
	7	7	9	7	9
	50				

tissue	stomach	adrenal gland	liver	sigmoid colon	transverse colon
	51	20	10	3	5
	4	5	6	1	2
	45	11	4	8	6
	4	2	4	2	4
	5	2	1	1	1
	3	1	2	1	2
	51	2	4	4	4
	4		4	4	4

primary cell	foreskin keratinocyte	endothelial cell of umbilical vein	common myeloid progenitor, CD34+	keratinocyte	B cell
	37	2	5	3	13
	3	13	3	13	
	35	2	5	1	1
	2	1	2	1	6
	42	12	1		1
	23	2	5	3	6
	35	5	2	1	1

In vitro differentiated cell	dendritic cell	mesenchymal stem cell	neural stem progenitor cell	neural cell	trophoblast cell
	11				
	36	1	2	1	1
	32	1	2	1	2
	24	1	3	1	
	27	1	1	1	

stem cell	H1-hESC	H9	HT-hESC	HUES64	HUES40
	146	3	9	2	1
	37	7	1	4	1
	10	2	1	1	2
	9		1	1	1
	9				1

Induced pluripotent stem cell line	GM3338	IPS DF 18.11	IPS DF 6.9	IPS-20b	IPS-15b
	25	1			
	8	1	1	1	1
	8	1			1
	10				
	8				

...and 21 more

[See all biosamples](#)

Browsing the ENCODE portal

Experiment matrix

ENCODE Data Encyclopedias Materials & Methods Help

Experiment Matrix

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

Enter search term(s)

Assay: CHIP-seq 5601, DNase-seq 725, shRNA RNA-seq 523, eCLIP 459, polyA RNA-seq 392, DNA binding 5601, Transcription 2181, DNA accessibility 898, RNA binding 511, DNA methylation 473

Assay category: DNA binding 5601, Transcription 2181, DNA accessibility 898, RNA binding 511, DNA methylation 473

Target of assay: transcription start site, histone control, RNA binding protein, broad histone mark

Organism: **10054** results

- Maia musculus 1759
- Drosophila melanogaster 1384
- Caenorhabditis elegans 855
- Drosophila pseudoobscura 4

Biosample type

- cell line 5207
- tissue 2837
- primary cell 1277
- in vitro differentiated cells 509
- stem cell 327

Organ

- blood 2404
- body fluid 2404
- liver 1050
- lung 809
- epithelium 577

Project

- ENCODE 7477
- Roadmap 2156
- GGR 418
- community 3

Genome assembly (visualization)

- hg19 7320
- GRCh38 7415

Lab

- Bradley Bernstein, Broad 1670
- Michael Snyder, Stanford 1668
- John Stamatoyannopoulos, UW 1327
- Richard Myers, HAIB 1510
- Thomas Gingeras, CSHL 651

Audit category: **missing control alignments** 183, **extremely low read depth** 177, **missing analysis_step_run** 131, **missing antibody** 72, **extremely low spot score** 47

Audit category: **insufficient read depth** 1372, **control insufficient read depth** 720

10054 results

Clear Filters

Assay: CHIP-seq, DNase-seq, shRNA RNA-seq, eCLIP, polyA RNA-seq

Assay category: DNA binding, Transcription, DNA accessibility, RNA binding, DNA methylation

Target of assay: transcription start site, histone control, RNA binding protein, broad histone mark

Organism: Maia musculus, Drosophila melanogaster, Caenorhabditis elegans, Drosophila pseudoobscura

Biosample type: cell line, tissue, primary cell, in vitro differentiated cells, stem cell

Organ: blood, body fluid, liver, lung, epithelium

Project: ENCODE, Roadmap, GGR, community

Genome assembly (visualization): hg19, GRCh38

Lab: Bradley Bernstein, Broad; Michael Snyder, Stanford; John Stamatoyannopoulos, UW; Richard Myers, HAIB; Thomas Gingeras, CSHL

Audit category: missing control alignments, extremely low read depth, missing analysis_step_run, missing antibody, extremely low spot score, insufficient read depth, control insufficient read depth

10054 results

Clear Filters

cell line

K562 669 10 268 245 19 3 11 7 10 1 2 1 2 6

HepG2 355 3 255 210 11 3 5 3 6 2 2 6

A549 374 14 27 2 9 2 2 1 2

GM12878 227 2 13 3 3 6 7 1 2 1 2 6

HEK293 255 2 2

+ See 165 more...

tissue

stomach 51 20 10 3 5 4 5 6

adrenal gland 45 11 4 8 6 4 2 4 5 2

liver 73 2 3 1 2 1 2 1

sigmoid colon 51 2 4 4 4 4 4 2

transverse colon 39 4 4 4 4 4 4

+ See 128 more...

primary cell

foreskin keratinocyte 37 2 5 3 13 3

endothelial cell of umbilical vein 35 2 5 1 1 2 1 6

Assay: CHIP-seq, DNase-seq, shRNA RNA-seq, eCLIP, polyA RNA-seq

Assay category: DNA binding, Transcription, DNA accessibility, RNA binding, DNA methylation

Target of assay: transcription start site, histone control, RNA binding protein, broad histone mark

Organism: Maia musculus, Drosophila melanogaster, Caenorhabditis elegans, Drosophila pseudoobscura

Biosample type: cell line, tissue, primary cell, in vitro differentiated cells, stem cell

Organ: blood, body fluid, liver, lung, epithelium

Project: ENCODE, Roadmap, GGR, community

Genome assembly (visualization): hg19, GRCh38

Lab: Bradley Bernstein, Broad; Michael Snyder, Stanford; John Stamatoyannopoulos, UW; Richard Myers, HAIB; Thomas Gingeras, CSHL

Audit category: missing control alignments, extremely low read depth, missing analysis_step_run, missing antibody, extremely low spot score, insufficient read depth, control insufficient read depth

10054 results

Clear Filters

cell line

K562 669 10 268 245 19 3 11 7 10 1 2 1 2 6

HepG2 355 3 255 210 11 3 5 3 6 2 2 6

A549 374 14 27 2 9 2 2 1 2

GM12878 227 2 13 3 3 6 7 1 2 1 2 6

HEK293 255 2 2

+ See 165 more...

tissue

stomach 51 20 10 3 5 4 5 6

adrenal gland 45 11 4 8 6 4 2 4 5 2

liver 73 2 3 1 2 1 2 1

sigmoid colon 51 2 4 4 4 4 4 2

transverse colon 39 4 4 4 4 4 4

+ See 128 more...

primary cell

foreskin keratinocyte 37 2 5 3 13 3

endothelial cell of umbilical vein 35 2 5 1 1 2 1 6

ASSAYS

10054 results



Clear Filters

- CHIP-seq
- DNase-seq
- shRNA RNA-seq
- eCLIP
- polyA RNA-seq
- DNase-seq
- total RNA-seq
- small RNA-seq
- RNA microarray
- RAMPAGE
- genotyping array
- WGBS
- microarray

BIOSAMPLES

Browsing the ENCODE portal

Experiment matrix

ENCODE Data Encyclopedias Materials & Methods Help

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

Enter search term(s)

Assay: CHIP-seq (5601), DNase-seq (725), shRNA RNA-seq (523), eCLIP (459), polyA RNA-seq (392), DNA binding (5601), Transcription (2181), DNA accessibility (898), RNA binding (511), DNA methylation (473)

Target of: transcription factor, histone, control, RNA binding protein, broad histone mark

Organism: **1004** (Homo sapiens), 1759 (Mus musculus), 1384 (Drosophila melanogaster), 855 (Caenorhabditis elegans), 4 (Drosophila pseudoobscura)

Biosample type: cell line (5207), tissue (2837), primary cell (1277), in vitro differentiated cells (509), stem cell (327)

Organ: blood (2404), bodily fluid (2404), liver (1955), lung (809), epithelium (577), stomach (51), adrenal gland (45), liver (73), sigmoid colon (51), transverse colon (39)

10054 results

Clear Filters

BIOSAMPLES

ASSAYS

10054 results



Clear Filters

CHIP-seq
DNase-seq
shRNA RNA-seq
eCLIP
polyA RNA-seq
DNase array
total RNA-seq
small RNA-seq
RNA microarray
RAMPAGE
genotyping array
WGBS
microarray

cell line

K562	669	10	268	245	19	3	11	7	10	1	2	1	2	6
HepG2	355	3	255	210	11	3	5	3	6		2	2		6
A549	374	14			27	2		9	2		2	1		2
GM12878	227	2			13	3	3	6	7	1	2	1	2	6
HEK293	255						2		1		2			

+ See 165 more...

tissue

stomach	51	20			10	3	5	4		5		6		
adrenal gland	45	11		4	8	6	4	2		4		5	2	
liver	73	2			3	1	2	1		2		1		
sigmoid colon	51	2			4	4	4	4		4		2		
transverse colon	39	4				4	4	4		4	4			

+ See 128 more...

primary cell

foreskin keratinocyte	37	2			5		3			13			3	
endothelial cell of umbilical vein	35	2			5	1		1	2		1			6

Select:

- Assay
- Biosample
- Experiment count

-> narrowed Search results

Facets

Assay category

DNA binding	5601
Transcription	2161
DNA accessibility	898
RNA binding	511
DNA methylation	473

[+ See more...](#)

Target of assay

transcription factor	2641
histone	2216
control	1390
RNA binding protein	1276
broad histone mark	1253

[+ See more...](#)

Organism

<i>Homo sapiens</i>	10054
<i>Mus musculus</i>	1789
<i>Drosophila melanogaster</i>	1384
<i>Caenorhabditis elegans</i>	955
<i>Drosophila pseudoobscura</i>	4

[+ See more...](#)

Organ

blood	2404
bodily fluid	2404
liver	1050
lung	809
epithelium	577

[+ See more...](#)

The screenshot shows the ENCODE portal interface. At the top, there are navigation links for ENCODE, Data, Encyclopedias, Materials & Methods, and Help. A search bar is present. The main content area is titled 'Experiment Matrix' and displays a list of results with columns for Assay, Assay category, Target of assay, and Target of assay category. A '10054 results' summary is shown with icons for list, table, and chart views, and a 'Clear Filters' button. Below this, there are several facet panels: 'cell line', 'tissue', 'primary cell', and 'induced pluripotent stem cell line'. Each facet shows a list of categories with corresponding counts. The 'cell line' facet is highlighted in blue, showing results for K562, HepG2, A549, GM12878, and HEK293. The 'tissue' facet is highlighted in orange, showing results for stomach, adrenal gland, liver, sigmoid colon, and transverse colon. The 'primary cell' facet is highlighted in yellow, showing results for foreskin keratinocyte, endothelial cell of umbilical vein, and common myeloid progenitor. The 'induced pluripotent stem cell line' facet is highlighted in purple, showing results for GM3338, IPS DF 18-11, IPS DF 6.9, IPS-20b, and IPS-15b.

10054 results



- CHIP-seq
- DNase-seq
- shRNA RNA-seq
- eCLIP
- polyA RNA-seq
- DNase array
- total RNA-seq
- small RNA-seq
- RNA RNA-seq
- RAMPAGE
- genotyping array
- WGBS
- microarray

cell line																				
K562	669	10	268	245	19	3	11	7	10	1	2	1	2	6						
HepG2	355	3	255	210	11	3	5	3	6		2	2		6						
A549	374	14			27	2		9	2		2	1		2						
GM12878	227	2			13	3	3	6	7	1	2	1	2	6						
HEK293	255							2		1		2								

[+ See 165 more...](#)

tissue																				
stomach	51	20			10	3	5	4			5		6							
adrenal gland	45	11		4	8	6	4	2			4		5	2						
liver	73	2			3	1	2	1			2		1							
sigmoid colon	51	2			4	4	4	4			4		2							
transverse colon	39	4					4	4	4		4	4								

[+ See 128 more...](#)

primary cell																				
foreskin keratinocyte	37	2			5		3				13		3							
endothelial cell of umbilical vein	35	2			5	1		1	2		1		6							

Browsing the ENCODE portal

Experiment matrix

Facets

Assay category

DNA binding	545
Transcription	127
DNA accessibility	76
DNA methylation	32
Genotyping	11

[+ See more...](#)

Organism

Homo sapiens	10054
<i>Mus musculus</i>	1789
<i>Drosophila melanogaster</i>	1384
<i>Caenorhabditis elegans</i>	955
<i>Drosophila pseudoobscura</i>	4

[+ See more...](#)

Organ

blood	585
bodily fluid	585
liver	337
epithelium	181
skin of body	154
lung	127
connective tissue	121

The screenshot shows the ENCODE Experiment Matrix interface. At the top, there are navigation links for ENCODE, Data, Encyclopedias, Materials & Methods, and Help. A search bar is located on the right. Below the navigation, there are tabs for Assay, Assay category, Target of assay, Date released, and Available data. The main content area displays a heatmap titled "10054 results" with columns for various assays (e.g., ChIP-seq, DNase-seq, RNA-seq) and rows for different cell lines (e.g., K562, HepG2, GM12878, HEK293). The heatmap cells contain numerical values representing signal intensity. On the left side of the heatmap, there are several facet filters: Organism (Homo sapiens: 10054), Biosample type (cell line: 5207), Organ (blood: 2404), Project (ENCODE: 7477), and Genome assembly (hg19: 7520). Each facet filter shows a list of options with corresponding counts. The interface also includes a "Clear Filters" button and a "See more" link for each facet.

Browsing the ENCODE portal

Experiment matrix

Assay category

DNA binding	545
Transcription	127
DNA accessibility	76
DNA methylation	32
Genotyping	11

[+ See more...](#)

Organism

<i>Homo sapiens</i>	10054
<i>Mus musculus</i>	1789
<i>Drosophila melanogaster</i>	1384
<i>Caenorhabditis elegans</i>	955
<i>Drosophila pseudoobscura</i>	4

[+ See more...](#)

Organ

blood	585
bodily fluid	585
liver	337
epithelium	181
skin of body	154
lung	127
connective tissue	121

ENCODE Data Encyclopedia Materials & Methods Help

Search...

Experiment Matrix

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

Enter search term(s)

Assay category: Transcription 127

Assay: polyA RNA-seq 49, small RNA-seq 26, total RNA-seq 14, RNA microarray 11, RAMPAGE 10

Assay category: DNA binding 545, Transcription 127, DNA accessibility 76, DNA methylation 32, Genotyping 11

Organism: *Homo sapiens* 127, *Mus musculus* 16

Biosample type: cell line 81, tissue 29, primary cell 17

Organ: lung 127, connective tissue 121, musculature of body 112, brain 80, embryo 68, vasculature 65, intestine 63, limb 61, blood vessel 56, penis 55, mammary gland 50, extraembryonic component 47, kidney 45, uterus 45, large intestine 43, heart 41, stomach 36, esophagus 26, adipose tissue 24, gonad 23, adrenal gland 22, vein 22, pancreas 21, prostate gland 21, spleen 18, thyroid gland 16, placenta 15, testis 13, artery 11, lymphoid tissue 11, uterus 11, ovary 10, small intestine 10, nerve 8, bone element 7, breast 7, spinal cord 7, thymus 7, vagina 7, bronchus 6, eye 6, urinary bladder 6

127 results

Clear Filters

cell line	A549	IMR-90	NCI-H460	AG04450	WI38
A549	27	9	2	3	3
IMR-90	3	9	2	3	3
NCI-H460	2	2	1	3	1
AG04450	1	1	1	1	1
WI38				2	

tissue	upper lobe of left lung	left lung	lung	right lung
upper lobe of left lung	4	4	4	
left lung	6			
lung	3	1	1	1
right lung	5			

primary cell	fibroblast of lung	bronchial epithelial cell	lung microvascular endothelial cell	bronchus fibroblast of lung	epithelial cell of alveolus of lung
fibroblast of lung	2	1	2		1
bronchial epithelial cell		1	2		
lung microvascular endothelial cell			1	2	
bronchus fibroblast of lung				1	1
epithelial cell of alveolus of lung				1	1

[+ See 1 more...](#)

Download Visualize

Browsing the ENCODE portal

Use of ontology

Assay category

DNA binding	545
Transcription	127
DNA accessibility	76
DNA methylation	32
Genotyping	11

+ See more...

Target of assay

control 1

Organism

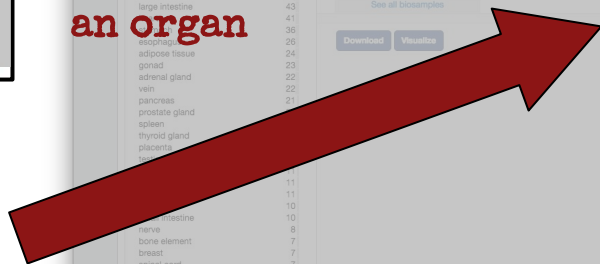
<i>Homo sapiens</i>	10054
<i>Mus musculus</i>	1789
<i>Drosophila melanogaster</i>	1384
<i>Caenorhabditis elegans</i>	955
<i>Drosophila pseudoobscura</i>	4

+ See more...

Organ

blood	585
bodily fluid	585
liver	337
epithelium	181
skin of body	154
lung	127
connective tissue	121

Sub-tissues & cell types
& cell lines derived from
an organ



127 results

Clear Filters

cell line

cell line	polyA RNA-seq	small RNA-seq	total RNA-seq	RNA microarray	RAMPAGE	CAGE	RNA-PET	polyA depleted RNA-seq
A549	27	9	2	3	3	1		
IMR-90	3	9	2		3	3		1
NCI-H460	2	2	1		3			
AG04450	1	1		1		1		1
WI38			2					

tissue

tissue	polyA RNA-seq	small RNA-seq	total RNA-seq	RNA microarray	RAMPAGE	CAGE	RNA-PET	polyA depleted RNA-seq
upper lobe of left lung	4	4	4					
left lung	6							
lung	3	1	1		1			
right lung	5							

primary cell

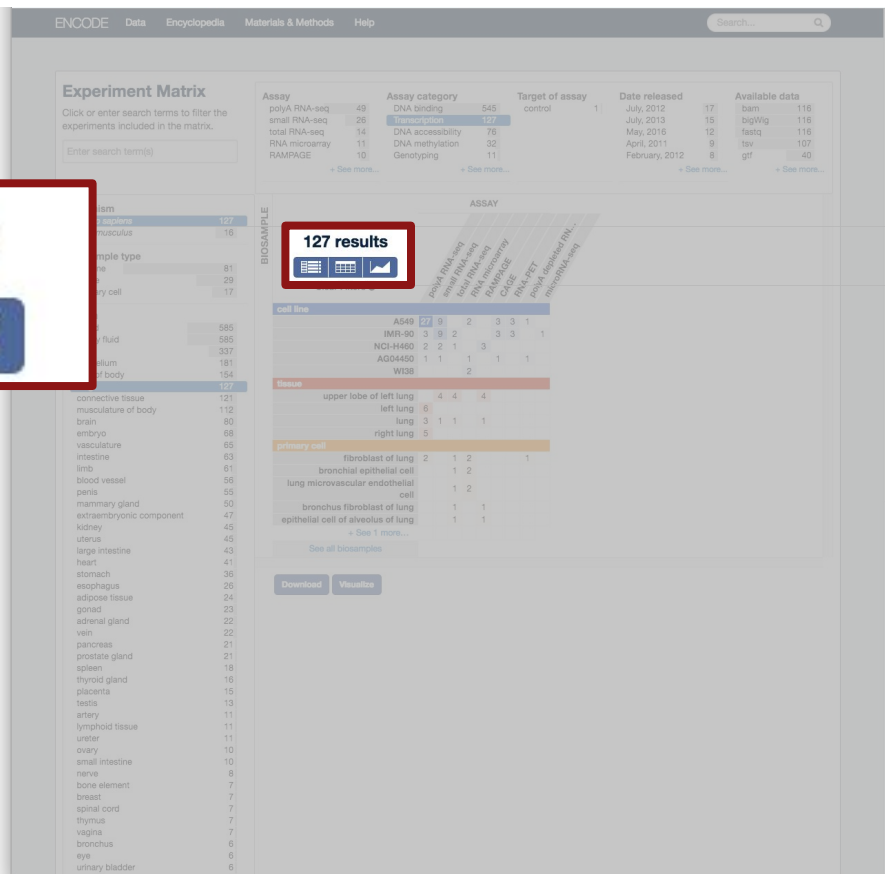
primary cell	polyA RNA-seq	small RNA-seq	total RNA-seq	RNA microarray	RAMPAGE	CAGE	RNA-PET	polyA depleted RNA-seq
fibroblast of lung	2	1	2					1
bronchial epithelial cell		1	2					
lung microvascular endothelial cell		1	2					
bronchus fibroblast of lung		1	1					
epithelial cell of alveolus of lung		1	1					

+ See 1 more...

Browsing the ENCODE portal

Different views

127 results



ENCODE Data Encyclopedias Materials & Methods Help

Search...

Experiment Matrix

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

Enter search term(s)

Assay	Assay category	Target of assay	Date released	Available data
polyA RNA-seq	DNA binding	control	July, 2012	bam 116
small RNA-seq	Chromatin state		July, 2015	bigWig 116
total RNA-seq	DNA accessibility		May, 2016	fastq 116
RNA microarray	DNA methylation		April, 2011	raw 107
RAMPAGE	Genotyping		February, 2012	gff 40

127 results

127 results

cell line

cell line	9	2	3	3	1
A549	9	2	3	3	1
JMR-90	3	9	2	3	3
NCI-H460	2	2	1	3	
AG04450	1	1	1	1	1
WISH		2			

tissue

tissue	4	4	4
upper lobe of left lung	4	4	4
left lung	6		
lung	3	1	1
right lung	5		

primary cell

primary cell	2	1	2	1
fibroblast of lung	2	1	2	1
bronchial epithelial cell		1	2	
lung microvascular endothelial cell		1	2	
bronchus fibroblast of lung	1	1		
epithelial cell of alveolus of lung	1	1		

Download Visualize

Browsing the ENCODE portal

Summary view



Browsing the ENCODE portal

Report view

The screenshot displays the ENCODE portal interface. At the top, there are navigation tabs for 'ENCODE', 'Data', 'Encyclopedia', 'Materials & Methods', and 'Help', along with a search bar. The main content is divided into a left sidebar and a main table area.

Assay category

DNA binding	545
Transcription	127
DNA accessibility	76
DNA methylation	32
Genotyping	11

+ See more...

Assay

polyA RNA-seq	49
small RNA-seq	26
total RNA-seq	14
RNA microarray	11
RAMPAGE	10

+ See more...

Experiment status

released	127
archived	20
revoked	1

Project

ENCODE	94
GGR	18
Roadmap	15

RFA

ENCODE2	82
ENCODE3	31
GGR	18
Roadmap	15
ENCODE2-Mouse	1

Genome assembly (visualization)

GRCh38	107
hg19	106

Organism

Homo sapiens	127
Mus musculus	16

Target of assay

control	1
---------	---

Biosample type

cell line	81
tissue	29
primary cell	17

Organ

blood	585
body fluid	585
liver	337
epithelium	181
skin of body	154
lung	127
connective tissue	121
musculature of body	112
brain	90
embryo	68
vasculature	65
intestine	63
limb	61
blood vessel	56
ovary	55

Showing results 1 to 25 of 127

Columns: [Table Icon] [List Icon] [Chart Icon] [Columns Icon] [Download TSV]

ID	Accession	Assay Type	Assay Nickname	Target label	Target gene	Biosample summary	Biosample	Description
ENCSR625HSH	ENCSR625HSH	RNA-seq	polyA RNA-seq			A549 treated with 100 nM dexamethasone for 25 minutes	A549	mRNA-seq of A549 cell line treated with 1 nM dexamethasone for 25 mins.
ENCSR831FZM	ENCSR831FZM	RNA-seq	polyA RNA-seq			A549 treated with 100 nM dexamethasone for 20 minutes	A549	mRNA-seq of A549 cell line treated with 1 nM dexamethasone for 20 mins.
ENCSR964GKZ	ENCSR964GKZ	RNA-seq	polyA RNA-seq			A549 treated with 100 nM dexamethasone for 15 minutes	A549	mRNA-seq of A549 cell line treated with 1 nM dexamethasone for 15 mins.
ENCSR742VGF	ENCSR742VGF	RNA-seq	polyA RNA-seq			A549 treated with 100 nM dexamethasone for 10 minutes	A549	mRNA-seq of A549 cell line treated with 1 nM dexamethasone for 10 mins.
ENCSR482TZY	ENCSR482TZY	RNA-seq	polyA RNA-seq			A549 treated with 100 nM dexamethasone for 5 minutes	A549	mRNA-seq of A549 cell line treated with 1 nM dexamethasone for 5 mins.
ENCSR937WIG	ENCSR937WIG	RNA-seq	polyA RNA-seq				A549	mRNA-seq of A549 cell line treated with 1 nM dexamethasone for 0 mins.

Browsing the ENCODE portal

Report view

The screenshot shows the ENCODE portal interface. At the top, there are navigation tabs for 'ENCODE', 'Data', 'Encyclopedia', 'Materials & Methods', and 'Help'. A search bar is located on the right. Below the navigation, there is a sidebar with 'Assay category' and a list of categories: 'DNA binding' (545), 'Transcription' (127), 'DNA accessibility' (76), 'DNA methylation' (32), and 'Genotyping' (11). The main content area displays 'Showing results 1 to 25 of 127' and a table of assay results. A 'Columns' button is highlighted in red. A dialog box titled 'Select columns to view' is open in the foreground, showing a list of columns with checkboxes. The dialog box has buttons for 'Select all', 'Select ID only', and 'Default sort'. The table below the dialog box shows columns: ID, Accession, Assay Type, Assay Nickname, Target label, Target gene, Biosample summary, Biosample, and Description. The table contains several rows of assay data.

ID	Accession	Assay Type	Assay Nickname	Target label	Target gene	Biosample summary	Biosample	Description
SH	ENCSTR629HSH	RNA-seq	polyA RNA-seq			A549 treated with 100 nM dexamethasone for 25 minutes	A549	mRNA-seq or A549 cell line treated with 1 nM dexamethasone for 25 mins.
BM	ENCRR831FZM	RNA-seq	polyA RNA-seq			A549 treated with 100 nM dexamethasone for 20 minutes	A549	mRNA-seq or A549 cell line treated with 1 nM dexamethasone for 20 mins.
KZ	ENCRR964GKZ	RNA-seq	polyA RNA-seq			A549 treated with 100 nM dexamethasone for 15 minutes	A549	mRNA-seq or A549 cell line treated with 1 nM dexamethasone for 15 mins.
BF	ENCRR742VGF	RNA-seq	polyA RNA-seq			A549 treated with 100 nM dexamethasone for 10 minutes	A549	mRNA-seq or A549 cell line treated with 1 nM dexamethasone for 10 mins.
ZY	ENCRR482TZY	RNA-seq	polyA RNA-seq			A549 treated with 100 nM dexamethasone for 5 minutes	A549	mRNA-seq or A549 cell line treated with 1 nM dexamethasone for 5 mins.
IG	ENCRR937WIG	RNA-seq	polyA RNA-seq				A549	mRNA-seq or A549 cell line treated with 1 nM dexamethasone for 0 mins.



Browsing the ENCODE portal

Report view

ENCODE Data Encyclopedia Materials & Methods Help

Showing results 1 to 25 of 127

Download TSV

ID	Accession	Assay Type	Assay Nickname	Target label	Target gene	Biosample summary	Biosample	Description
SH	ENCSTR629HSH	RNA-seq	polyA RNA-seq			A549 treated with 100 nM dexamethasone for 25 minutes	A549	
BM	ENCSTR831FZM	RNA-seq	polyA RNA-seq			A549 treated with 100 nM dexamethasone for 20 minutes	A549	nM dexamethasone for 20 mins.
KZ	ENCSTR964GKZ	RNA-seq	polyA RNA-seq			A549 treated with 100 nM dexamethasone for 15 minutes	A549	mRNA-seq or A549 cell line treated with 1 nM dexamethasone for 15 mins.
BF	ENCSTR742VGF	RNA-seq	polyA RNA-seq			A549 treated with 100 nM dexamethasone for 10 minutes	A549	mRNA-seq or A549 cell line treated with 1 nM dexamethasone for 10 mins.
ZY	ENCSTR482TZY	RNA-seq	polyA RNA-seq			A549 treated with 100 nM dexamethasone for 5 minutes	A549	mRNA-seq or A549 cell line treated with 1 nM dexamethasone for 5 mins.
IG	ENCSTR937WIG	RNA-seq	polyA RNA-seq				A549	mRNA-seq or A549 cell line treated with 1 nM dexamethasone for 0 mins.

Select columns to view

Select all Select ID only Default sort

- ID
- Assay Nickname
- Biosample summary
- Lab
- Biosample accession
- Linked Antibody
- Age
- Term ID
- Duration
- Post-synchronization time
- Submitter comment
- Documents
- External identifiers
- Schema Version
- Submitted by
- Lab aliases
- Experiment classification
- Additional data files
- Assay type
- Superseded by
- Developmental slims
- Revoked files
- Biosample synonyms
- Replication type
- System slims
- Accession
- Target label
- Biosample
- Project
- Biological replicate
- Species
- Age Units
- Concentration
- Duration units
- Post-synchronization time units
- Ontology ID
- References
- Date released
- Notes
- Lab
- Date submitted
- Controls
- Internal status
- Assay synonyms
- Assay category
- Assay ID
- Assay type
- Organ slims
- Assay objective
- Assembly
- Assay Type
- Target gene
- Description
- Status
- Technical replicate
- Life stage
- Treatment
- Concentration units
- Synchronization
- Replicates
- Biosample type
- Alternate accessions
- Internal tags
- Date created
- Grant
- Target
- Supersedes
- Pipeline error message
- Hub
- Month released
- Contributing files
- Original files
- Files
- Related series

Cancel View selected columns

Download TSV

Browsing the ENCODE portal

Search view

ENCODE Data Encyclopedia Materials & Methods Help

Showing 25 of 127 results

View All Download Filter to 100 to visualize

Assay category

- DNA binding 545
- transcription 127
- DNA accessibility 75
- DNA methylation 32
- Genotyping 11

Assay

- polyA RNA-seq 49
- small RNA-seq 26
- total RNA-seq 14
- RNA microarray 11
- RAMPAGE 10

Experiment status

- released 127
- archived 20
- revoked 1

Project

- ENCODE 94
- GGR 18
- Roadmap 15

RFA

- ENCODE2 82
- ENCODE3 31
- GGR 18
- Roadmap 15
- ENCODE2-Mouse 1

Genome assembly (visualization)

- GRCh38 107
- hg19 106

Organism

- Homo sapiens* 127
- Mus musculus* 16

Target of assay

- control 1

Biosample type

- cell line 81
- tissue 29
- primary cell 17

Organ

- blood 585
- body fluid 585
- liver 337
- epithelium 181
- skin of body 154
- Lung 127**
- connective tissue 121
- musculature of body 112
- brain 80
- embryo 68
- vasculature 65
- intestine 63
- limb 61

polyA RNA-seq of A549

Homo sapiens A549 treated with 100 nM dexamethasone for 25 minutes

Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549

Homo sapiens A549 treated with 100 nM dexamethasone for 20 minutes

Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549

Homo sapiens A549 treated with 100 nM dexamethasone for 15 minutes

Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549

Homo sapiens A549 treated with 100 nM dexamethasone for 10 minutes

Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549

Homo sapiens A549 treated with 100 nM dexamethasone for 5 minutes

Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549

Homo sapiens A549

Lab: Tim Reddy, Duke
Project: GGR

RAMPAGE of upper lobe of left lung

Homo sapiens upper lobe of left lung female adult (51 year)

Lab: Thomas Gingeras, CSHL
Project: ENCODE

RAMPAGE of upper lobe of left lung

Homo sapiens upper lobe of left lung female adult (53 years)

Lab: Thomas Gingeras, CSHL
Project: ENCODE

RAMPAGE of upper lobe of left lung

Homo sapiens upper lobe of left lung male adult (54 years)

Lab: Thomas Gingeras, CSHL
Project: ENCODE

RAMPAGE of upper lobe of left lung

Homo sapiens upper lobe of left lung male adult (37 years)

Lab: Thomas Gingeras, CSHL
Project: ENCODE

small RNA-seq of upper lobe of left lung

Homo sapiens upper lobe of left lung female adult (51 year)

Lab: Thomas Gingeras, CSHL



Browsing the ENCODE portal

Search view

ENCODE Data Encyclopedia Materials & Methods Help

Showing 25 of 127 results

View All Download Filter to 100 to visualize

Assay category

- DNA binding 545
- Transcription 127**
- DNA accessibility 75
- DNA methylation 32
- Genotyping 11

Assay

- polyA RNA-seq 49
- small RNA-seq 26
- total RNA-seq 14
- RNA microarray 11
- RAMPAGE 10

Experiment status

- released 127**
- archived 20
- revoked 1

Project

- ENCODE 94
- GGR 18
- Roadmap 15

RFA

- ENCODE2 82
- ENCODE3 31
- GGR 18
- Roadmap 15
- ENCODE2-Mouse 1

Genome assembly (visualization)

- GRCh38 107
- hg19 106

Organism

- Homo sapiens 127**
- Mus musculus 16

Target of assay

- control 1

Biosample type

- cell line 81
- tissue 29
- primary cell 17

Organ

- blood 585
- body fluid 585
- liver 337
- epithelium 181
- skin of body 154
- Lung 127**
- connective tissue 121
- musculature of body 112
- brain 80
- embryo 68
- vasculature 65
- intestine 63
- limb 61

polyA RNA-seq of A549

Homo sapiens A549 treated with 100 nM dexamethasone for 5 minutes

Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549

Homo sapiens A549 treated with 100 nM dexamethasone for 5 minutes

Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549

Homo sapiens A549 treated with 100 nM dexamethasone for 5 minutes

Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549

Homo sapiens A549 treated with 100 nM dexamethasone for 5 minutes

Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549

Homo sapiens A549 treated with 100 nM dexamethasone for 5 minutes

Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549

Homo sapiens A549 treated with 100 nM dexamethasone for 5 minutes

Lab: Tim Reddy, Duke
Project: GGR

RAMPAGE of upper lobe of left lung

Homo sapiens upper lobe of left lung female adult (51 year)

Lab: Thomas Gingeras, CSHL
Project: ENCODE

RAMPAGE of upper lobe of left lung

Homo sapiens upper lobe of left lung female adult (53 years)

Lab: Thomas Gingeras, CSHL
Project: ENCODE

small RNA-seq of upper lobe of left lung

Homo sapiens upper lobe of left lung female adult (51 year)

ENCB728HKC released

Experiment ENCSR961FIG

Visualizing data

Search view

The screenshot shows the ENCODE search results page. The top navigation bar includes 'ENCODE', 'Data', 'Encyclopedia', 'Materials & Methods', and 'Help'. A search bar is located in the top right. The main content area is titled 'Showing 25 of 127 results' and features a 'Filter to 100 to visualize' button. The left sidebar contains various filters: Assay category (with 'Chromatin interaction' selected at 127), Assay (with 'polyA RNA-seq' selected at 49), Experiment status (with 'released' selected at 127), Project (with 'ENCODE' selected at 94), RFA (with 'ENCODE2' selected at 82), Genome assembly (visualization) (with 'GRCh38' selected at 107), Organism (with 'Homo sapiens' selected at 127), Target of assay (with 'control' selected at 1), Biosample type (with 'cell line' selected at 81), and Organ (with 'Lung' selected at 127). The main results list shows 25 experiments, each with a title, description, lab, and project. A red box highlights the 'Filter to 100 to visualize' button in the top right of the results area.

Assay category	Count
DNA binding	545
Chromatin interaction	127
DNA accessibility	76
DNA methylation	32
Genotyping	11

Assay	Count
polyA RNA-seq	49
small RNA-seq	26
total RNA-seq	14
RNA microarray	11
RAMPAGE	10

Experiment status	Count
released	127
archived	20
revoked	1

Project	Count
ENCODE	94
GGR	18
Roadmap	15

RFA	Count
ENCODE2	82
ENCODE3	31
GGR	18
Roadmap	15
ENCODE2-Mouse	1

Genome assembly (visualization)	Count
GRCh38	107
hg19	106

Organism	Count
Homo sapiens	127
Mus musculus	16

Target of assay	Count
control	1

Biosample type	Count
cell line	81
tissue	29
primary cell	17

Organ	Count
blood	585
body fluid	585
liver	337
epithelium	181
skin of body	154
Lung	127
connective tissue	121
musculature of body	112
brain	80
embryo	68
vasculature	65
intestine	63
limb	61

Experiment	Count
ENCSR925HSH	1
ENCSR664GKZ	1
ENCSR742VGF	1
ENCSR482TZY	1
ENCSR37FWIG	1
ENCSR089FOD	1
ENCSR780PEX	1
ENCSR004UBM	1
ENCSR738HKC	1
ENCSR961FIG	1

Filter to 100 to visualize

Visualizing data

Filter further to
≤100 experiments

Assay



ENCODE Data Encyclopedia Materials & Methods Help

Showing 25 of 49 results

Assay category: Transcription (49)

Assay:

- polyA RNA-seq: 49
- small RNA-seq: 26
- total RNA-seq: 14
- RNA microarray: 11
- RAMPAGE: 10

Experiment status:

- released: 49
- revoked: 1

Project:

- ENCODE: 18
- GGR: 18
- Roadmap: 13

RFA:

- GGR: 18
- ENCODE2: 15
- Roadmap: 13
- ENCODE3: 2
- ENCODE2-Mouse: 1

Genome assembly (visualization):

- GRCh38: 46
- hg19: 28

Organism:

- Homo sapiens: 49
- Mus musculus: 8

Target of assay:

- control: 1

Biosample type:

- cell line: 33
- tissue: 14
- primary cell: 2

Organ:

- lung: 49
- blood: 45
- body fluid: 45
- musculature of body: 44
- embryo: 29

Life stage:

- adult: 30
- embryonic: 15
- unknown: 3
- child: 1

Biosample treatment:

- dexamethasone: 21
- ethanol: 1

Available data:

- bam: 49

Visualize

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 25 minutes
Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 20 minutes
Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 15 minutes
Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 10 minutes
Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 5 minutes
Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549
Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 12 hours
Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 10 hours
Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 8 hours
Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 7 hours
Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 6 hours
Lab: Tim Reddy, Duke
Project: GGR

Visualizing data

Also available on
matrix view



BIOSAMPLE

ASSAY

49 results

Clear Filters

cell line

A549	27
IMR-90	3
NCI-H460	2
AG04450	1

tissue

left lung	6
right lung	5
lung	3

primary cell

fibroblast of lung	2
--------------------	---

Download Visualize

ENCODE Data Encyclopedia Materials & Methods Help

Showing 25 of 49 results

Assay category: Transcription (49)

Assay: polyA RNA-seq (49)

Experiment status: released (49)

Experiment: polyA RNA-seq of A549 (25 results shown)

Experiment	ENC9SR959BH	released
Experiment	ENC9SR831FZ	released
Experiment	ENC9SR664GKZ	released
Experiment	ENC9SR742VGF	released
Experiment	ENC9SR482TZY	released
Experiment	ENC9SR67WJG	released
Experiment	ENC9SR164TDP	released
Experiment	ENC9SR224PTG	released
Experiment	ENC9SR546PPG	released
Experiment	ENC9SR985TEN	released
Experiment	ENC9SR255V6V	released



Visualizing data

ENCODE Data Encyclopedia Materials & Methods Help

Showing 25 of 49 results

Assay category: Transcription (49)

View All Download Visualize

Assay	Experiment
seq of A549 A549 treated with 100 nM dexamethasone for 25 minutes	Experiment ENCGR859H4 released
seq of A549 A549 treated with 100 nM dexamethasone for 20 minutes	Experiment ENCGR831FZM released
seq of A549 A549 treated with 100 nM dexamethasone for 15 minutes	Experiment ENCGR64GKZ released
seq of A549 A549 treated with 100 nM dexamethasone for 10 minutes	Experiment ENCGR742VGF released
seq of A549 A549 treated with 100 nM dexamethasone for 5 minutes	Experiment ENCGR482TZY released
seq of A549 A549	Experiment ENCGR857WIC released
seq of A549 A549 treated with 100 nM dexamethasone for 12 hours	Experiment ENCGR154TDP released
seq of A549 A549 treated with 100 nM dexamethasone for 10 hours	Experiment ENCGR224PTG released
seq of A549 A549 treated with 100 nM dexamethasone for 8 hours	Experiment ENCGR546PPG released
polyA RNA-seq of A549 Homo sapiens A549 treated with 100 nM dexamethasone for 7 hours	Experiment ENCGR868TEN released
polyA RNA-seq of A549 Homo sapiens A549 treated with 100 nM dexamethasone for 6 hours	Experiment ENCGR255VEV

adult: 30, embryonic: 15, unknown: 3, child: 1

Biosample treatment: dexamethasone: 21, ethanol: 1

Available data: bam: 49

Lab: Tim Reddy, Duke
Project: GGR

Open visualization browser

Assembly Visualize with browser...

GRCh38:

UCSC

Ensembl

hg19:

UCSC

Close

Visualizing data

ENCODE Data Encyclopedias Materials & Methods Help

Showing 25 of 49 results

Assay category: Transcription 49

seq of A549
A549 treated with 100 nM dexamethasone for 25 minutes
by, Duke Experiment ENC0895894 released

seq of A549
A549 treated with 100 nM dexamethasone for 20 minutes
by, Duke Experiment ENC0895893 released

seq of A549
A549 treated with 100 nM dexamethasone for 15 minutes
by, Duke Experiment ENC0895892 released

seq of A549
A549 treated with 100 nM dexamethasone for 10 minutes
by, Duke Experiment ENC0895891 released

seq of A549
A549 treated with 100 nM dexamethasone for 5 minutes
by, Duke Experiment ENC0895890 released

seq of A549
A549
by, Duke Experiment ENC0895889 released

seq of A549
A549 treated with 100 nM dexamethasone for 12 hours
by, Duke Experiment ENC0895888 released

seq of A549
A549 treated with 100 nM dexamethasone for 10 hours
by, Duke Experiment ENC0895887 released

seq of A549
A549 treated with 100 nM dexamethasone for 8 hours
by, Duke Experiment ENC0895886 released

adult 30
embryonic 15
unknown 3
total 48

Biosample treatment
dexamethasone 21
ethanol 1

Available data
bam 49
bam-index 49

Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 7 hours
Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 6 hours
Lab: Tim Reddy, Duke
Project: GGR

Open visualization browser

Assembly Visualize with browser...

GRCh38:

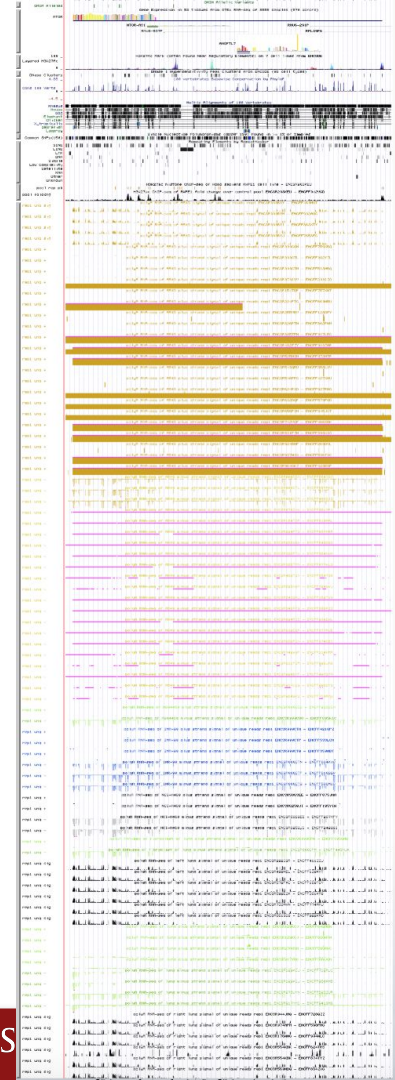
UCSC

Ensembl

hg19:

UCSC

Close



S

Batch file download

Also available on
matrix view

BIOSAMPLE

ASSAY

49 results

Clear Filters

cell line

A549	27
IMR-90	3
NCI-H460	2
AG04450	1

tissue

left lung	6
right lung	5
lung	3

primary cell

fibroblast of lung	2
--------------------	---

Download Visualize

ENCODE Data Encyclopedia Materials & Methods Help

Search...

Showing 25 of 49 results

Download Visualize

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 25 minutes
Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 20 minutes
Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 15 minutes
Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 10 minutes
Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 5 minutes
Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549
Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 12 hours
Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 10 hours
Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 8 hours
Lab: Tim Reddy, Duke
Project: GGR

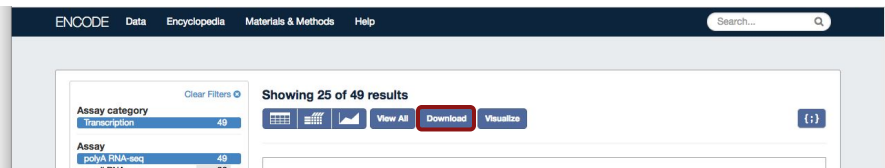
polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 7 hours
Lab: Tim Reddy, Duke
Project: GGR

polyA RNA-seq of A549
Homo sapiens A549 treated with 100 nM dexamethasone for 6 hours
Lab: Tim Reddy, Duke
Project: GGR

Download

No exp limit!

Batch file download



ENCODE Data Encyclopedia Materials & Methods Help

Search...

Showing 25 of 49 results

Assay category: Transcription (49)

Assay: polyA RNA-seq (49)

View All Download Visualize

Using batch download

Click the "Download" button below to download a "files.txt" file that contains a list of URLs to a file containing all the experimental metadata and links to download the file. The first line of the file will always be the URL to download the metadata file. Further description of the contents of the metadata file are described in the [Batch Download help doc](#).

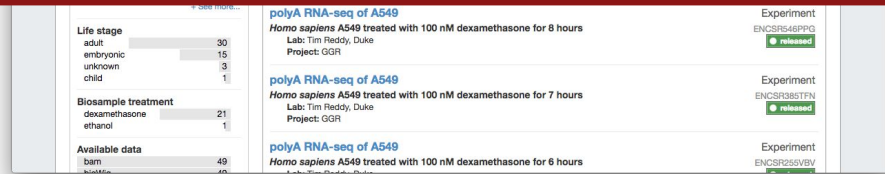
The "files.txt" file can be copied to any server.

The following command using cURL can be used to download all the files in the list:

```
xargs -n 1 curl -O -L < files.txt
```

Close

Download



polyA RNA-seq of A549

Homo sapiens A549 treated with 100 nM dexamethasone for 8 hours

Lab: Tim Reddy, Duke
Project: GGR

Experiment: ENCNSR546PPG (released)

polyA RNA-seq of A549

Homo sapiens A549 treated with 100 nM dexamethasone for 7 hours

Lab: Tim Reddy, Duke
Project: GGR

Experiment: ENCNSR386TFN (released)

polyA RNA-seq of A549

Homo sapiens A549 treated with 100 nM dexamethasone for 6 hours

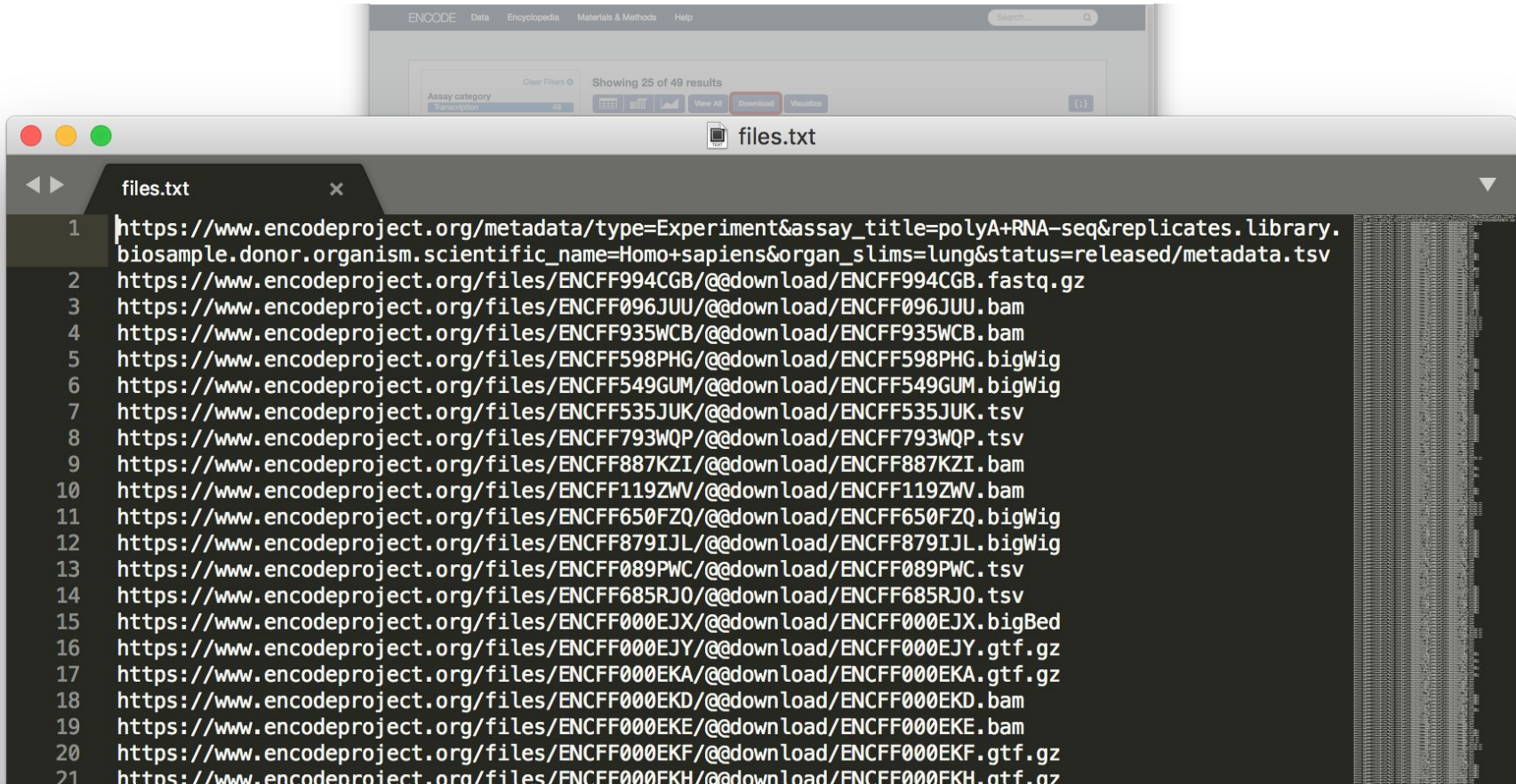
Experiment: ENCNSR256VEV

Life stage: adult (30), embryonic (15), unknown (3), child (1)

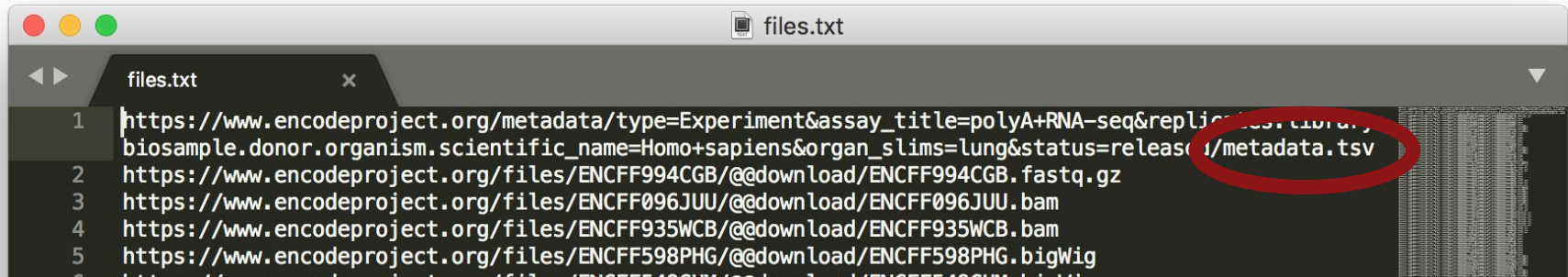
Biosample treatment: dexamethasone (21), ethanol (1)

Available data: bam (49)

Batch file download



Batch file download



```
files.txt
1 https://www.encodeproject.org/metadata/type=Experiment&assay_title=polyA+RNA-seq&replicate=1&library=ENCFF096JUU/metadata.tsv
2 https://www.encodeproject.org/files/ENCF096JUU/@download/ENCF096JUU.fastq.gz
3 https://www.encodeproject.org/files/ENCF096JUU/@download/ENCF096JUU.bam
4 https://www.encodeproject.org/files/ENCF096JUU/@download/ENCF096JUU.bigWig
5 https://www.encodeproject.org/files/ENCF096JUU/@download/ENCF096JUU.bigWig
```

metadata.tsv

one line for each data file in files.txt

file format, output type, read info, assembly

also assay, biosample, library specifics

Batch file download

To download all files, run command...

```
xargs -n 1 curl -O -L < files.txt
```

Batch file download

To download all files, run command...

```
xargs -n 1 curl -O -L < files.txt
```

Or copy/paste metadata.tsv link into browser
filter metadata.tsv,
collect download links (column AK in metadata.tsv),
put in new file to run command

```
xargs -n 1 curl -O -L < filtered_files.txt
```

Searching the ENCODE portal

Keyword Search

“liver”
“CTCF”
“gtex”
...

The screenshot shows the ENCODE portal homepage. At the top, there is a navigation bar with links for ENCODE, Data, Encyclopedia, Materials & Methods, and Help. A search bar is located in the top right corner, highlighted with a red circle. Below the navigation bar, the main heading is "ENCODE: Encyclopedia of DNA Elements". To the left, there is a diagram illustrating various genomic features and their associated assays. The diagram shows a DNA strand with various elements: Long-range regulatory elements (enhancers, repressors/silencers, insulators), Promoters, and Transcripts. Assays shown include 5C, ChIA-PET, Hi-C, DNase-seq, FAIRE-seq, ATAC-seq, ChIP-seq, WGBS, RRBS, methyl array, Computational predictions, RNA-seq, and CLIP-seq, RIP-seq. The diagram also shows Hypersensitive Sites, CH₃, CH₃CO, and RNA polymerase. To the right of the diagram, there are several search boxes. The first search box is labeled "Search ENCODE portal" and is highlighted with a red circle. Below it, there is another search box labeled "Search for Candidate Regulatory Elements" and a button "Hosted by SCREEN". At the bottom right, there are buttons for "Human hg19 Q" and "Mouse mm10 Q".

Searches the whole portal
(not just Experiments)

Searching the ENCODE portal

Region search

ENCODE Data Encyclopedia Materials & Methods Help Search...

- Matrix
- Search
- Summary
- Search by region**
- Reference epigenomes
- Publications

Encyclopedia of DNA Elements

About ENCODE Project Getting Started

Experiments

Search ENCODE portal 🔍

ENCODE Q

About ENCODE Encyclopedia

Candidate Regulatory Elements

Search for Candidate Regulatory Elements 🔍

Hosted by SCREEN

Human hg19 Q Mouse mm10 Q

5C ChIA-PET Hi-C DNase-seq FAIRE-seq ATAC-seq ChIP-seq WGBS RBS methyl array Computational predictions RNA-seq CLIP-seq RIP-seq

Long-range regulatory elements (enhancers, repressors/silencers, insulators) Promoters Gene Transcripts

Based on an image by Darryl Lujs (NIHGR), Ian Dunham (EBI), Michael Patin (NIHGR)

Browsing the ENCODE portal

Region search

ENCODE Data Encyclopedia Materials & Methods Help

Search...

- Matrix
- Search
- Summary
- Search by region**
- Reference epigenomes
- Publications

Encyclopedia of DNA Elements

5C
ChIA-PET
Hi-C

DNase-seq
FAIRE-seq
ATAC-seq

ChIP-seq

WGBS
RRBS
methyl array

Computational predictions

RNA-seq

Long-range regulatory elements
(enhancers, repressors/silencers, insulators)

Promoters

Gene

Transcripts

ENCODE

Based on an image by Darryl Leys (NIHRR), Ian Dunham (EBI, MA)

Human hg19 Q Mouse mm10 Q

ENCODE Data Encyclopedia Materials & Methods Help

Search...

Region search

Enter any one of human Gene name, Symbol, Synonyms, Gene ID, HGNC ID, coordinates, rsid, Ensemble ID

GRCh38

No annotations found

Search

Browsing the ENCODE portal

Region search

The image displays the ENCODE portal interface. The background shows the 'Encyclopedia of DNA Elements' page with a navigation menu (Matrix, Search, Summary, Search by region, Reference epigenomes, Publications) and a diagram of DNA elements including SC ChIA-PET Hi-C, DNase-seq FAIRE-seq ATAC-seq, ChIP-seq, WGBS 5mBS methyl array, Computational predictions, and RNA-seq. The foreground shows a 'Region search' form with the following components:

- ENCODE Data Encyclopedia Materials & Methods Help
- Search... Q
- Region search
- Enter any one of human Gene name, Symbol, Synonyms, Gene ID, HGNC ID, coordinates, rsid, Ensemble ID
- Search input field containing 'Sox'
- GRCh38 dropdown menu
- Search button
- Dropdown menu suggestions:
 - "SOXL (homo sapiens)
 - "SOXN (homo sapiens)
 - "Sox-13 (homo sapiens)
 - SOX1 (homo sapiens)
 - SOX10 (homo sapiens)
 - SOX11 (homo sapiens)
 - SOX12 (homo sapiens)
 - SOX14 (homo sapiens)
 - SOX17 (homo sapiens)
 - SOX18 (homo sapiens)

Browsing the ENCODE portal

Region search

ENCODÉ Data Encyclopedia Materials & Methods Help

Search...

Matrix
Search
Summary
Search by region
Reference epigenomes
Publications

Encyclopedia of DNA Elements

ENCODÉ Data Encyclopedia Materials & Methods

Region search

Enter any one of human Gene name, Symbol, Synonyms, Gene ID, HGNC ID, coordinates, rsid, Ensemble ID

Sox

- "SOXL (homo sapiens)
- "SOXN (homo sapiens)
- "Sox-13 (homo sapiens)
- SOX1 (homo sapiens)
- SOX10 (homo sapiens)
- SOX11 (homo sapiens)
- SOX12 (homo sapiens)
- SOX14 (homo sapiens)
- SOX17 (homo sapiens)
- SOX18 (homo sapiens)

ENCODÉ Data Encyclopedia Materials & Methods Help

Search...

Region search

Enter any one of human Gene name, Symbol, Synonyms, Gene ID, HGNC ID, coordinates, rsid, Ensemble ID

*Sox-13 (homo sapiens) GRCh38

Success

Searched coordinates: chr1:204073115-204127743

Assay

ChIP-seq	696
DNase-seq	668
eCLIP	104

Biosample term

HepG2	263
HEK293	105
MCF-7	84
K562	65
A549	41

+ See more...

Target

CTCF	117
POLR2AphosphoS5	11
RAD21	11
JUND	9
MAFK	9

+ See more...

Organism

Homo sapiens	1467
--------------	------

Organ

liver	300
kidney	196
blood	147
bodily fluid	147
mammary gland	109

+ See more...

Showing 25 of 1467

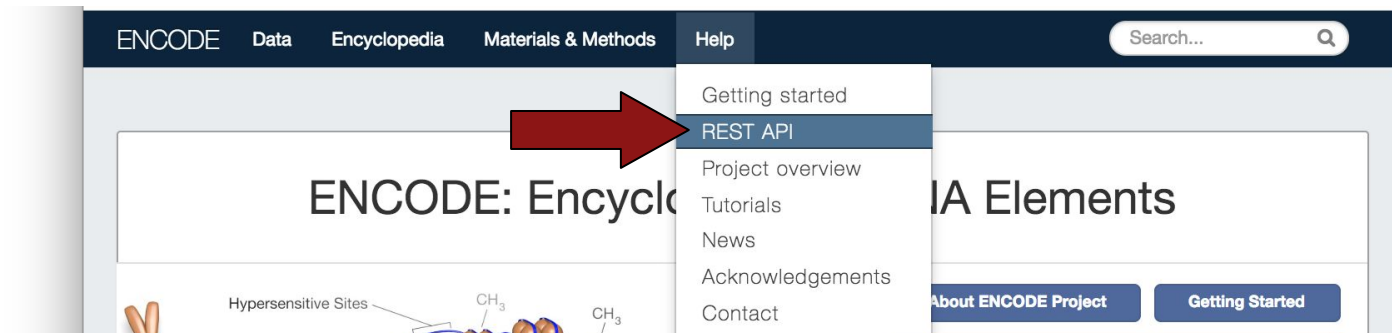
[View All](#) [Filter to 100 to visualize](#)

ChIP-seq of K562 Experiment
Homo sapiens K562 ENCSR13ZMCO
Target: REST released
Lab: Michael Snyder, Stanford
Project: ENCODE 2

eCLIP of HepG2 Experiment
Homo sapiens HepG2 ENCSR194HZU
Target: NOLC1 released
Lab: Gene Yeo, UCSD
Project: ENCODE

ChIP-seq of A549 Experiment
Homo sapiens A549 treated with 0.02% ethanol for 1 hour ENCSR000BOO
Target: FOSL2 released
Lab: Richard Myers, HAIB
Project: ENCODE 1 2

eCLIP of HepG2 Experiment
Homo sapiens HepG2 ENCSR861GYE
Target: LIN28B released
Lab: Gene Yeo, UCSD
Project: ENCODE



ENCODE DCC

encode-help@lists.stanford.edu
@EncodeDCC
<https://github.com/ENCODE-DCC>



Mike

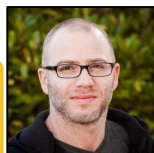
ASHG posters

414 RegulomeDB

1510 ENCODE portal

1598 ENCODE pipelines

1987 Roadmap/Reference Epigenomes



Idan



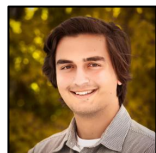
Ben



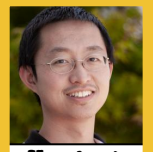
Seth



Jin



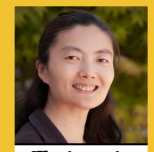
Paul



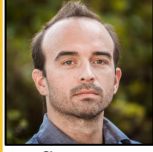
Yunhai



Zack



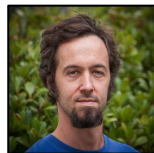
Weiwei



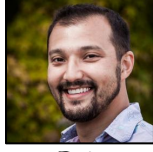
Casey



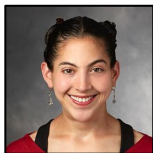
Forrest



Otto



Bek



Vanessa



Jennifer



Khine



Emma

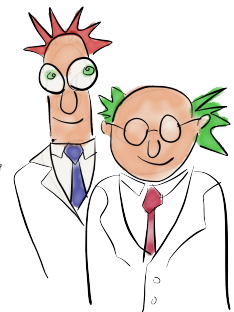


Phil



Keenan

Share 



Data

Pipelines

Software

NIH U24 HG009397

Stanford University