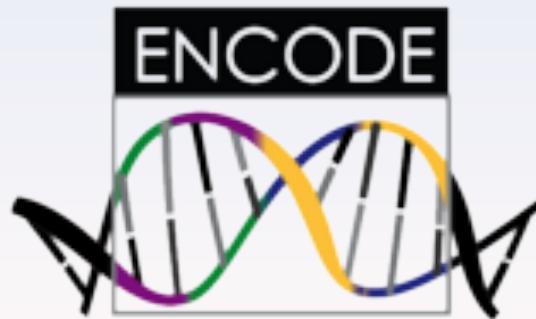


ENCODE Genome-Wide Data on the UCSC Genome Browser

Melissa Cline

ENCODE Data Coordination Center (DCC)

UC Santa Cruz



<http://encodeproject.org>

Slides at <http://genome-preview.ucsc.edu/>

UCSC Genome Browser

Genomes - **Blat** - **Table Browser**

ENCODE (highlighted with a red box)

Neandertal

Blat

Table Browser

Gene Sorter

In Silico PCR

Genome Graphs

Galaxy

VisiGene

Proteome Browser

Utilities

Downloads

Release Log

News (highlighted with a red box)

To receive announcements about ENCODE data releases and related news by email, subscribe to the [encode-announce mailing list](#). For more information about how to access this data, see the free online [OpenHelix ENCODE tutorial](#).

16 June 2011

We announce today the kind assistance records into three OMIM Allelic Variants in the OMIM Genes.

OMIM Allelic Variants in the OMIM Genes

Usage Resources (highlighted with a red box)

Release Log

Data Policy

Data Standards

Publications

Contributors

Pilot Project

Jobs

Contact Us

ENCODE

Human

Data Summary

Search

Downloads

Genome Browser (hg19)

Preview Browser (hg19)

Session Gallery

Cell Types

Mouse

Data Summary

Search

Downloads

Genome Browser (mm9)

Preview Browser (mm9)

Cell Types

General

Registered Variables

Antibodies

News

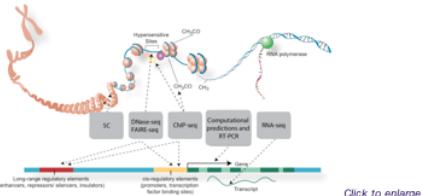
News Archives ▶

Encyclopedia of DNA Elements

About ENCODE Data

The [Encyclopedia of DNA Elements](#) (ENCODE) Consortium is an international collaboration of research groups funded by the National Human Genome Research Institute (NHGRI). The goal of ENCODE is to build a comprehensive parts list of functional elements in the human genome, including elements that act at the protein and RNA levels, and regulatory elements that control cells and circumstances in which a gene is active.

WARNING: This is a test site. Data and tools here are under construction, have not been quality reviewed, and are subject to change at any time. For high-quality reviewed annotations on our production server, visit <http://encodeproject.org>.

 ENCODE data are now available for the entire human genome. All ENCODE data are free and available for immediate use via :

- [Search](#) for displayable tracks and downloadable files
- [Download](#) of data files
- [Visualization](#) in the UCSC Genome Browser (ENCODE data marked with the NHGRI logo)
- [Data mining](#) with the UCSC Table Browser and other [UCSC Genome Bioinformatics tools](#)

[Click to enlarge](#)

To search for ENCODE data related to your area of interest and set up a browser view, use the UCSC [Track Search tool](#) (Advanced features). The [Data Summary](#) shows a comprehensive listing of ENCODE data that is released or in preparation. Early access to pre-release ENCODE data is provided at <http://genome-preview.ucsc.edu>. If you would like to receive notifications of ENCODE data releases and related news by email, subscribe to the [encode-announce mailing list](#). For more information about how to access this data, see the free online [OpenHelix ENCODE tutorial](#).

To complement the human ENCODE data, Mouse ENCODE experiments are currently underway. Early access to this data is available on the Mouse mm9/NCBI37 browser at the UCSC preview site. The [Mouse ENCODE Data Summary](#) lists experiments that are planned or in progress.

All ENCODE data is freely available for download and analysis. However, before publishing research that uses ENCODE data, please read the [ENCODE Data Release Policy](#), which places some restrictions on publication use of data for nine months following data release. [Read more](#) about ENCODE data at UCSC.

News

8 July 2011 - Mouse ENCODE data releases: DNasel hypersensitivity (UW DNasel HS) and histone modifications (LICR Histone)

Two tracks of ENCODE data were released on the mm9 genome browser, from the UCSD/Ludwig Institute for Cancer Research and the University of Washington Mouse ENCODE groups.

Histone Modifications by ChIP-seq from ENCODE/LICR: This track shows a comprehensive survey of cis-regulatory elements in the mouse genome by using ChIP-seq to identify transcription factor binding sites and chromatin modification profiles in many mouse tissues and primary cells, including bone marrow, cerebellum, cortex, heart, kidney, liver, lung, spleen, mouse embryonic fibroblast cells (MEFs) and embryonic stem (ES) cells.

DNasel Hypersensitivity by Digital DNasel from ENCODE/University of Washington: This track shows DNasel sensitivity measured genome-wide in mouse tissues and cell lines using the Digital DNasel methodology and DNasel hypersensitive sites.

1 July 2011 - ENCODE data releases: Broad ChromHMM, Open Chrom Synth, UChicago TFBS, Duke Affy Exon

Four tracks of ENCODE production data and analysis were released in June, from the Broad Institute (Kellis lab), OpenChromatin (Duke, UNC, UT-A) and University of Chicago (White lab) ENCODE groups. This is the first data release from the University of Chicago ENCODE group, which joined the Consortium as part of the NIH ARRA stimulus grants.

Chromatin State Segmentation by HMM from ENCODE/Broad: This track, and the companion hg18 track, display chromatin state segmentation of the human genome into fifteen states grouped to predict functional elements.

DNasel/FAIRE/ChIP Synthesis from ENCODE/OpenChrom(Duke/UNC/UTA): This track displays a synthesis of open chromatin regions and binding of selected regulatory factors, based on three complementary methodologies.

Transcription Factor Binding Sites by Epitope-Tag ChIP-seq from ENCODE/University of Chicago: This track maps human transcription factor binding sites genome-wide using expressed transcription factors as GFP tagged fusion proteins after BAC recombination.

What is ENCODE?

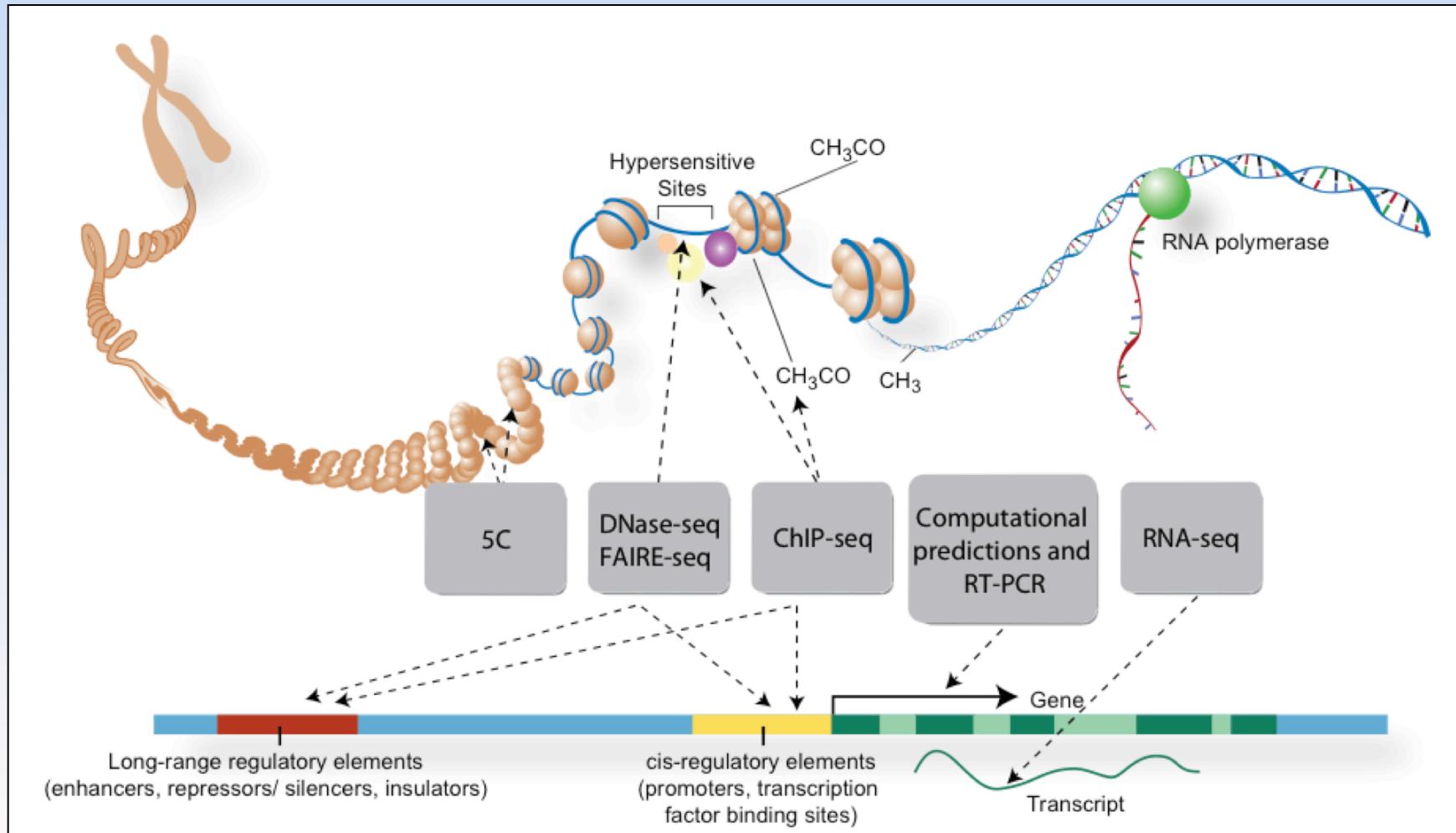
- International consortium project with the goal of cataloguing the functional regions of the human genome

```
GTTTGCATCTTG  
CTGCTCTAGGAAATC  
CAGCAGCTGTCACCA  
TGTAAACAAGCCAG  
GCTAGACCAGTTACC  
CTCATCATCTTAGCT  
GATAGCCAGCCAGCC  
ACACAGGCATGAGT
```

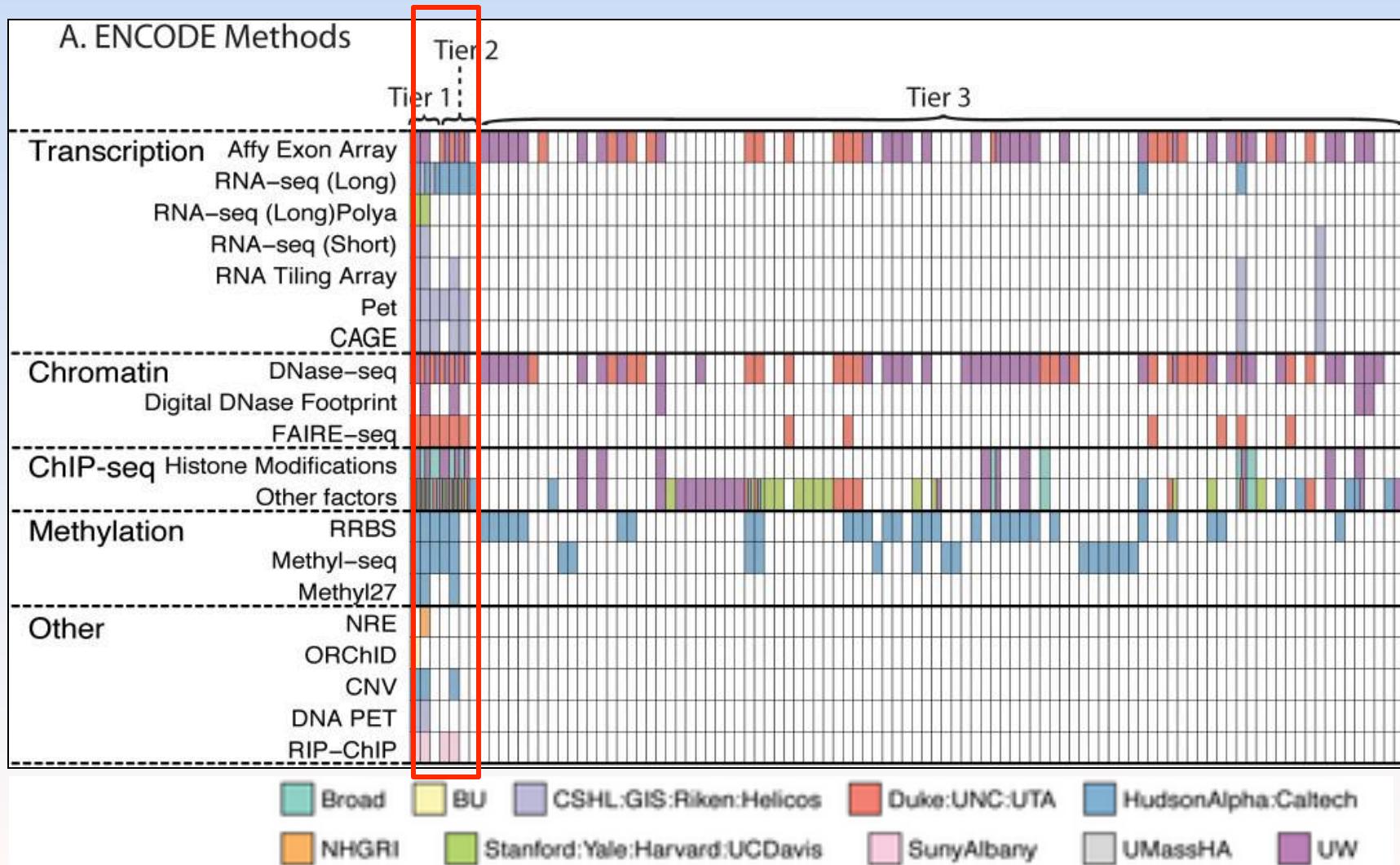


- A gold mine of experimental data for independent researchers with available disk space

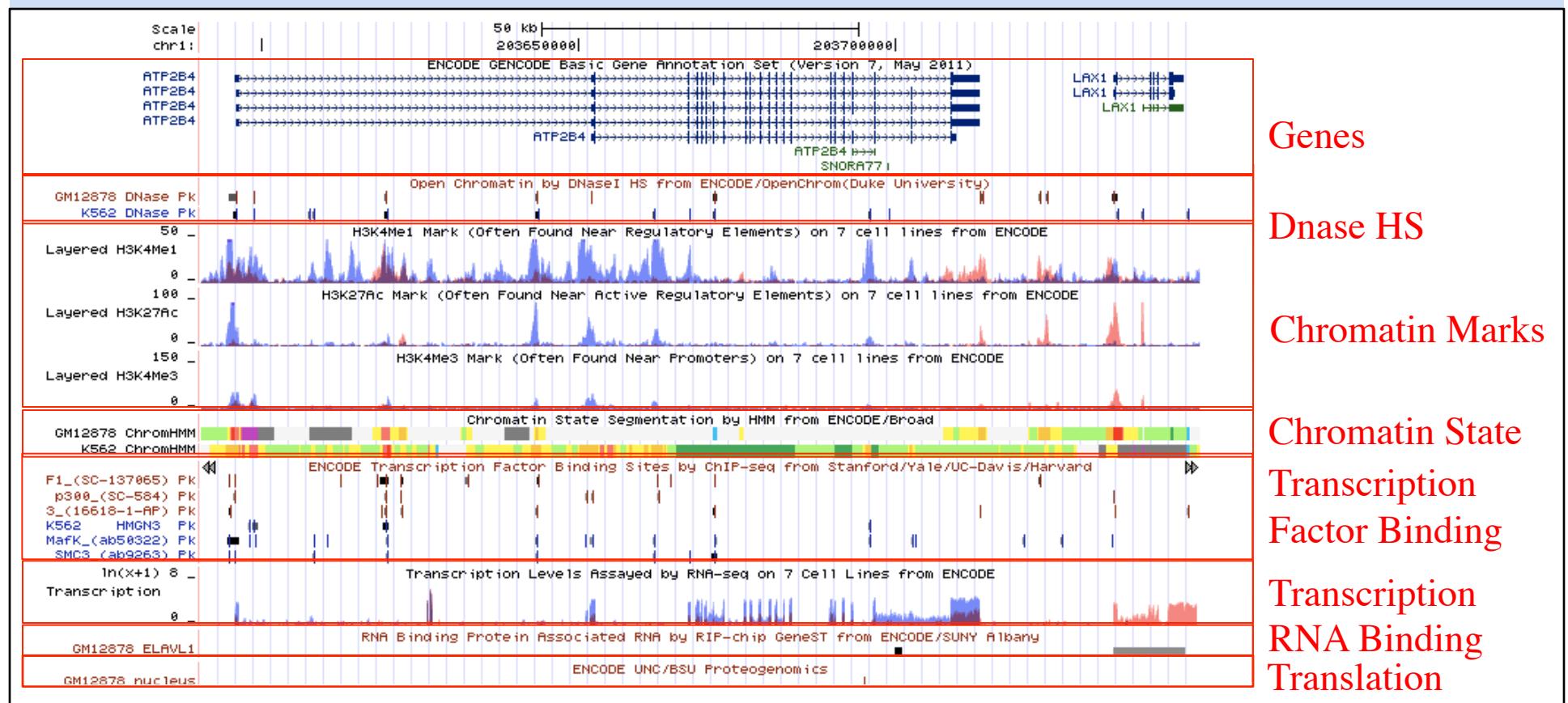
ENCODE covers diverse regulatory processes



ENCODE experiments are planned for integrative analysis

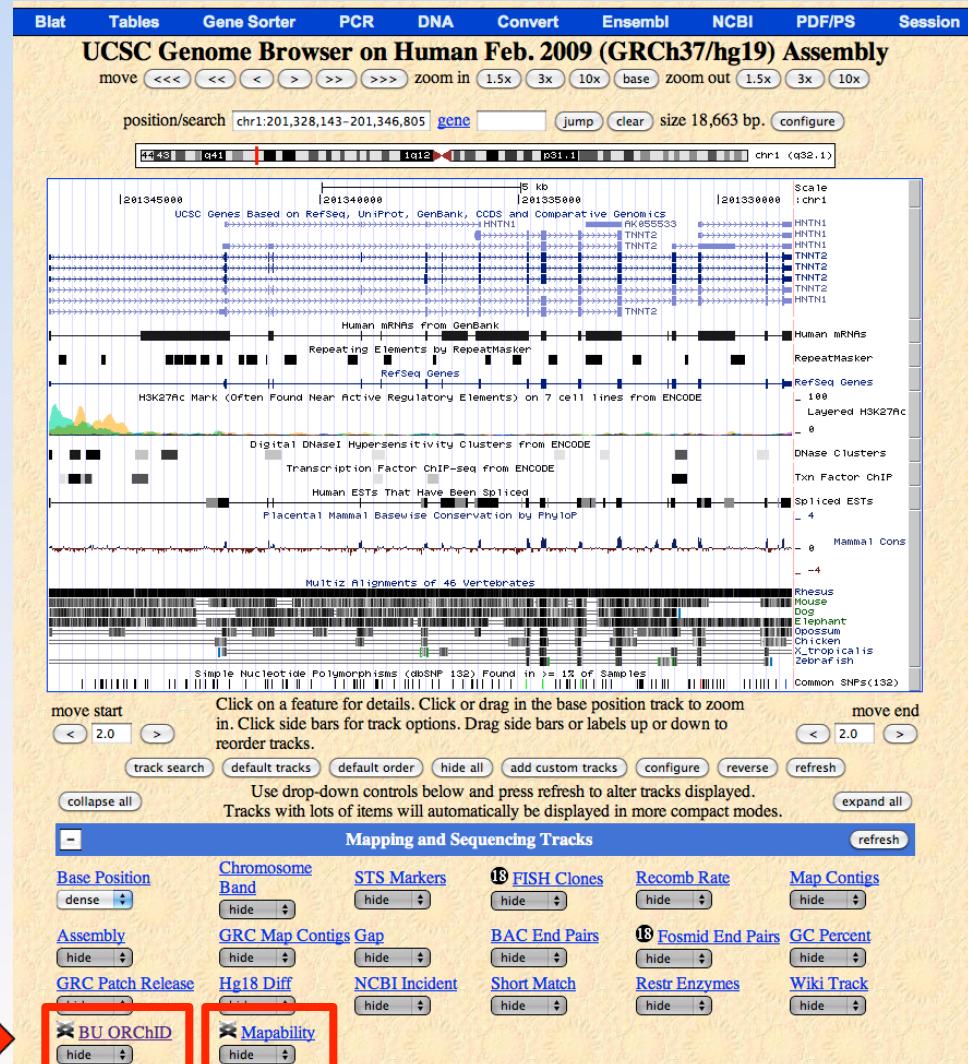
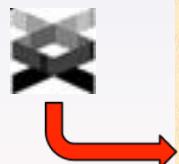


Example of ENCODE data



ENCODE tracks on the UCSC Genome Browser

*ENCODE tracks
marked with the
NHGRI helix*



There are currently 2061 ENCODE experiments at the ENCODE DCC

How to find the data you want



Finding ENCODE tracks the hard way

RIKEN CAGE Loc Track Settings

[Downloads](#) [Subtracks](#) [Description](#)

RNA CAGE Subcellular Localization from ENCODE/RIKEN ([ENC RNA-seq](#))

Maximum display mode:

Select views ([help](#)):

Plus Signal Minus Signal Alignments

Select subtracks by cell line and localization:

	All	GM12878	H1hESC	K562	HeLa-S3	HepG2	HUVEC	MCF7	NHEK	Prostate	All
Cell Line	(Tier 1)	(Tier 1)	(Tier 1)								Localization
Localization	[+/-]	[+/-]	[+/-]	[+/-]	[+/-]	[+/-]	[+/-]	[+/-]	[+/-]	[+/-]	[+/-]
Whole Cell	[+/-]		[+/-]	[+/-]							[+/-] Whole Cell
Cytosol	[+/-]		[+/-]								[+/-] Cytosol
Nucleus	[+/-]		[+/-]								[+/-] Nucleus
Polysome	[+/-]			[+/-]							[+/-] Polysome
Nucleoplasm	[+/-]			[+/-]							[+/-] Nucleoplasm
Chromatin	[+/-]			[+/-]							[+/-] Chromatin
Nucleolus	[+/-]		[+/-]								[+/-] Nucleolus

List subtracks: only selected/visible all (38 of 153 selected)

Views ^{†1}	Cell Line ^{†2}	Localization ^{†3}	RNA Extract ^{†4}	Rep ^{†5}	Track Name	Restr.
<input checked="" type="checkbox"/> Plus Signal	GM12878	Cytosol	PolyA-	1	GM12878 cytosol polyA- CAGE Plus strand start sites Generation 0 from ENCODE/RIKEN ...	schema 2009
<input checked="" type="checkbox"/> Plus Signal	GM12878	Nucleolus	Total RNA	1	GM12878 nucleolus total CAGE Plus strand start sites Generation 0 from ENCODE/RIKEN ...	schema 2010
<input checked="" type="checkbox"/> Plus Signal	GM12878	Nucleus	PolyA-	1	GM12878 nucleus polyA- CAGE Plus strand start sites Rep 1 from ENCODE/RIKEN ...	schema 2011
<input checked="" type="checkbox"/> Plus Signal	H1hESC	Whole Cell	PolyA-	1	H1-hESC whole cell polyA- CAGE Plus strand start sites Generation 0 from ENCODE/RIKEN ...	schema 2011
<input checked="" type="checkbox"/> Plus Signal	H1hESC	Whole Cell	PolyA+	1	H1-hESC whole cell polyA+ CAGE Plus strand start sites Rep 1 from ENCODE/RIKEN ...	schema 2011
<input checked="" type="checkbox"/> Plus Signal	H1hESC	Whole Cell	PolyA+	2	H1-hESC whole cell polyA+ CAGE Plus strand start sites Rep 2 from ENCODE/RIKEN ...	schema 2011
<input checked="" type="checkbox"/> Plus Signal	H1hESC	Cytosol	PolyA+	2	H1-hESC cytosol polyA+ CAGE Plus strand start sites Rep 2 from ENCODE/RIKEN ...	schema 2011
<input checked="" type="checkbox"/> Plus Signal	H1hESC	Nucleus	PolyA+	2	H1-hESC nucleus polyA+ CAGE Plus strand start sites Rep 2 from ENCODE/RIKEN ...	schema 2011
<input checked="" type="checkbox"/> Plus Signal	K562	Whole Cell	PolyA+	1	K562 whole cell polyA+ CAGE Plus strand start sites Rep 1 from ENCODE/RIKEN ...	schema 2011
<input checked="" type="checkbox"/> Plus Signal	K562	Whole Cell	PolyA+	2	K562 whole cell polyA+ CAGE Plus strand start sites Rep 2 from ENCODE/RIKEN ...	schema 2011
<input checked="" type="checkbox"/> Plus Signal	K562	Chromatin	Total RNA	1	K562 chromatin total CAGE Plus strand start sites Generation 0 from ENCODE/RIKEN ...	schema 2009
<input checked="" type="checkbox"/> Plus Signal	K562	Cytosol	PolyA-	1	K562 cytosol polyA- CAGE Plus strand start sites Generation 0 from ENCODE/RIKEN ...	schema 2009
<input checked="" type="checkbox"/> Plus Signal	K562	Cytosol	PolyA+	1	K562 cytosol polyA+ CAGE Plus strand start sites Rep 1 from ENCODE/RIKEN ...	schema 2011
<input checked="" type="checkbox"/> Plus Signal	K562	Cytosol	PolyA+	2	K562 cytosol polyA+ CAGE Plus strand start sites Rep 2 from ENCODE/RIKEN ...	schema 2011

Metzker ML. *Sequencing technologies - the next generation*. Nature Reviews: Genetics. 2010 Jan;11(1):31-46

Allen Brain Burge RNA-seq ENC Exon Array... ENC RNA-seq GNF Atlas 2 Illumina WG-6

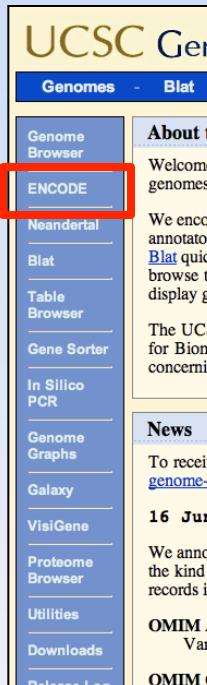
A better way to find ENCODE tracks

The image shows two side-by-side screenshots of the UCSC Genome Browser interface, demonstrating different search methods for ENCODE tracks.

Left Screenshot: This shows a basic search interface. At the top, there's a navigation bar with links to Home, Genomes, Genome Browser, Blat, Tables, Gene Sorter, PCR, Session, FAQ, and Help. Below this is a search bar with the placeholder "Search for Tracks in the Human Feb. 2009 (GRCh37/hg19) Assembly". Underneath the search bar is a "Visibility" panel where tracks can be hidden or shown by category like skeletal, RNA, etc. A red box highlights the "Advanced" tab in the search bar. At the bottom left, there's a "track search" button, which is also highlighted with a red box.

Right Screenshot: This shows an advanced search interface. It has a similar navigation bar and search bar. The "Advanced" tab is selected, indicated by a red box. The search field contains the term "skeletal". Below the search field is a dropdown menu titled "Experiment (Assay) type" with the option "Any" selected. A tooltip for "Experiment (Assay) type" says "Select multiple...". To the right of the search field, there's a section titled "ENCODE terms" with a list of checkboxes for various assays: AffyExonArray, Cage, ChipSeq, Cluster, Combined, DnaPet, DnaseDgf, DnaseSeq, FaireSeq, Gencode, Mapability, MethylRbbs, Orchid, RipGeneSt, RipTiling, RnaChip, and RnaSeq. The "Any" checkbox under "Experiment (Assay) type" is also checked.

Finding ENCODE metadata descriptions



The screenshot shows the UCSC Genome Browser homepage. On the left sidebar, under the "Genomes" section, there is a red box around the "ENCODE" link. Another red box highlights the "Cell Types" link under the "ENCODE" section.

UCSC Genomes - Blat

ENCODE

Cell Types

ENCODE Data Coordination Center at UCSC

Home - Data Policy - Help

ENCODE Common Cell Types

To facilitate integration of data between the contributing research groups, the ENCODE Consortium has identified common cell types for use by ENCODE contributors. These cell types are divided into two *Tiers*. **Tier1** cells are of higher priority, and should be used within experiments before **Tier2** cells. Rationale for the selection is described on the [NHGRI ENCODE Common Cell Types](#) page. Additional cell types beyond Tier1 and Tier2 may be used, but must be registered with the DCC before submitting data. These additional cell types are designated Tier3.

Click the link in the **Documents** column of the table below to access the cell culture protocol document.

Common Cell Types: Tier 1 and Tier 2

Cell, tissue or DNA sample: Cell line or tissue used as the source of experimental material.

cell	Tier	Description	Lineage	Karyotype	Sex	Documents	Vendor ID	Term ID	Label
GM12878	1	lymphoblastoid	International HapMap Project - CEPH/Utah - European Caucasian; Epstein-Barr Virus	relatively normal	F	protocol	Coriell GM12878	BTO:0002026 (non-specific)	GM12878
H1-hESC	1	Human Embryonic Stem Cells	embryonic stem cells	normal	M	protocol	Cellular Dynamics	CL:0000007	H1-hESC
K562	1	leukemia	"The continuous cell line K-562 was established by Lozzio and Lozzio from the pleural effusion of a 53-year-old female with chronic myelogenous leukemia in terminal blast crises." - ATCC	cancer	F	protocol	ATCC CCL-243	BTO:0000664	K562
K562b	1	leukemia (UCDavis)	"The continuous cell line K-562 was established by Lozzio and Lozzio from the pleural effusion of a 53-year-old female with chronic myelogenous leukemia."	cancer	F	Yale TFBS(Farnham)	ATCC CCL-243	BTO:0000664	K562b

Visualizing: Genome Browser tricks that every ENCODE user should know



Turning ENCODE subtracks and views on and off

SYDH Histone Track Settings

Histone Modifications by ChIP-seq from ENCODE/Stanford/Yale/Davis/Harvard

K562b H3K4me1
20
K562b H3K4me1 Histone Modifications by ChIP-seq Signal from ENCODE/SYDH
3

← Peaks ← Signal

Maximum display mode: dense [Reset to defaults](#)

Select views ([help](#)):

[Peaks](#) pack full ← View on/off

Select subtracks by factor and cell line:

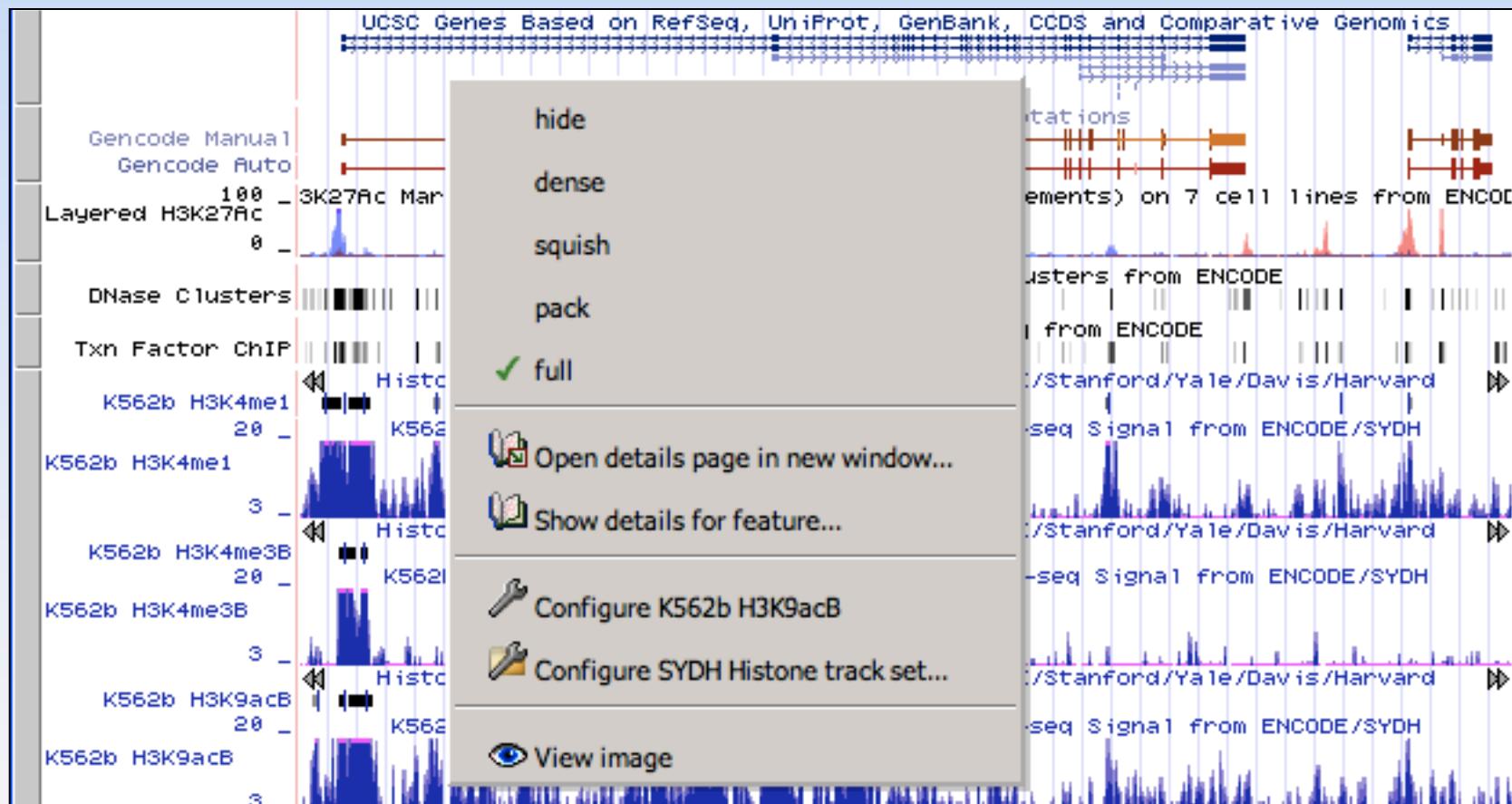
+ -	All	Factor	H3K4me3B	H3K4me1	H3K9acB	H3K9me3	H3K27me3B	H3K36me3B	Input
Cell Line	+ -	+ -	+ -	+ -	+ -	+ -	+ -	+ -	+ -
K562b (Tier 1)	+ -	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>		<input checked="" type="checkbox"/>			<input type="checkbox"/>
NT2-D1	+ -	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>		<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>		<input type="checkbox"/>
U2OS	+ -				<input checked="" type="checkbox"/>		<input checked="" type="checkbox"/>		<input type="checkbox"/>

← Subtrack on/off

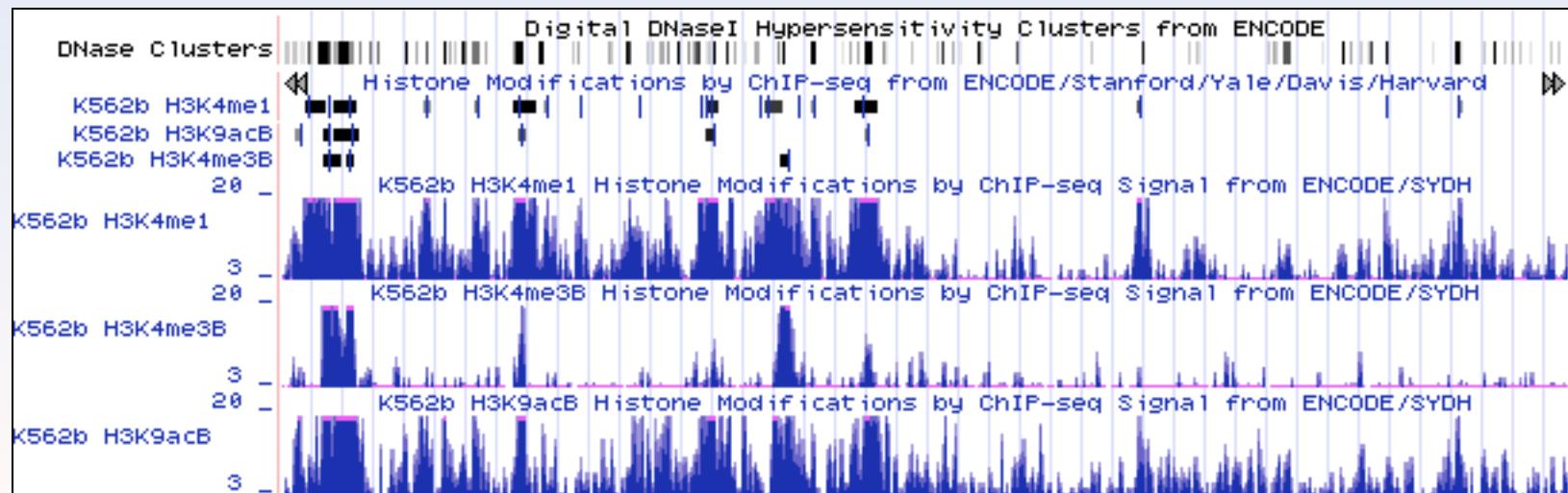
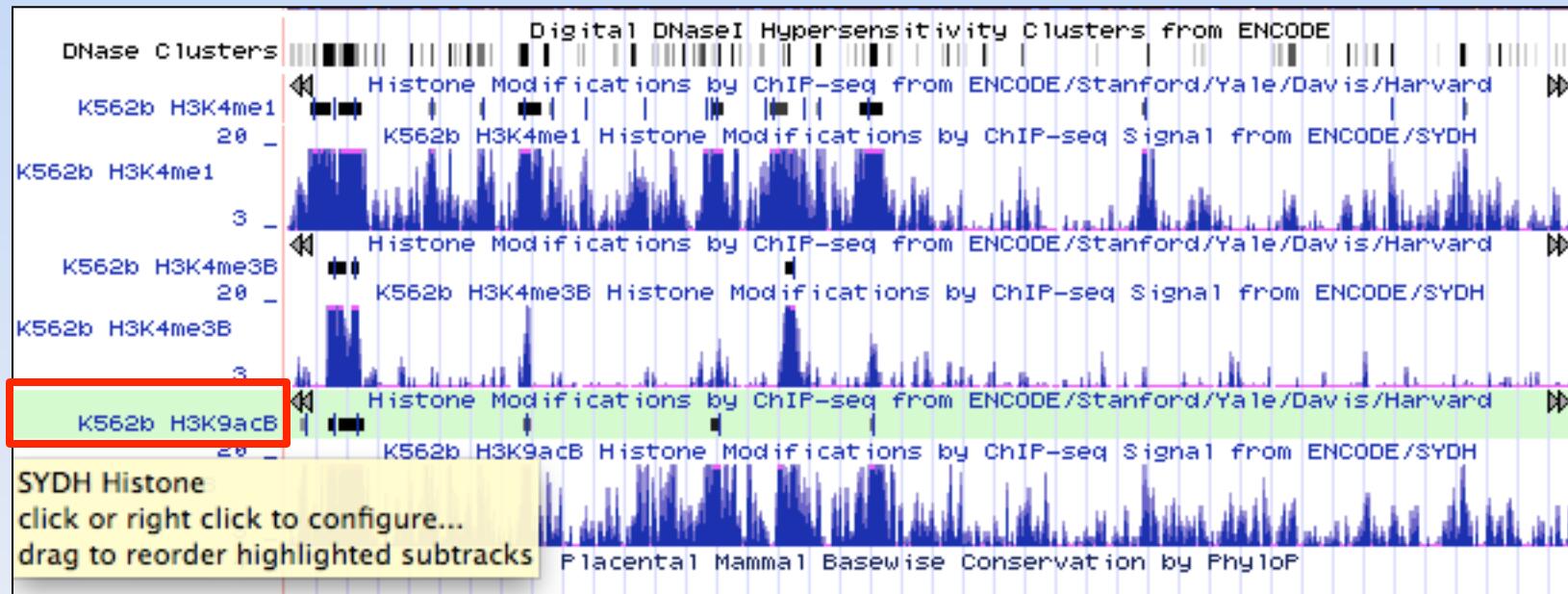
List subtracks: only selected/visible all (22 of 25 selected) [Top↑](#)

Cell Line ¹¹	Factor ¹²	Views ¹³	Track Name ¹⁴	Restricted Until ¹⁵
<input checked="" type="checkbox"/> K562b	H3K27me3B	Peaks	K562b H3K27me3B Histone Modifications by ChIP-seq Peaks from ENCODE/SYDH ...	schema 2011-03-11
<input checked="" type="checkbox"/> K562b	H3K27me3B	Signal	K562b H3K27me3B Histone Modifications by ChIP-seq Signal from ENCODE/SYDH ...	schema 2011-03-11
<input checked="" type="checkbox"/> K562b	H3K4me1	Peaks	K562b H3K4me1 Histone Modifications by ChIP-seq Peaks from ENCODE/SYDH ...	schema 2011-02-20
<input checked="" type="checkbox"/> K562b	H3K4me1	Signal	K562b H3K4me1 Histone Modifications by ChIP-seq Signal from ENCODE/SYDH ...	schema 2011-02-20
<input checked="" type="checkbox"/> K562b	H3K4me3B	Peaks	K562b H3K4me3B Histone Modifications by ChIP-seq Peaks from ENCODE/SYDH ...	schema 2011-03-11
<input checked="" type="checkbox"/> K562b	H3K4me3B	Signal	K562b H3K4me3B Histone Modifications by ChIP-seq Signal from ENCODE/SYDH ...	schema 2011-03-11
<input checked="" type="checkbox"/> K562b	H3K9acB	Peaks	K562b H3K9acB Histone Modifications by ChIP-seq Peaks from ENCODE/SYDH ...	schema 2011-03-11

Right-click to the subtrack display menu



Subtrack Drag and Drop



Sessions: the easy way to save and share your work

Screenshot of the UCSC Genome Browser Session sharing interface.

The top navigation bar includes: Home, Genomes, Blat, Tables, Gene Sorter, PCR, DNA, Convert, Ensembl, NCBI, PDF/PS, and Session (the latter is highlighted with a red box).

The main content area shows a session titled "hg19 Assembly".

Session controls: Send, Save Now, Discard.

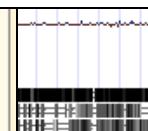
Email sharing fields:

- From: Melissa Cline <cline@soe.ucsc.edu>
- To: (empty input field)
- Add Cc | Add Bcc
- Subject: UCSC browser session hg19-demo
- Attach a file | Insert: Invitation

Session details:

- Rich formatting »
- Check Spelling ▾
- Session name: hg19-demo
- Created on: 2011-06-25
- Actions: use this session, delete this session, share with others?, link to session, send to mail
- Share with others? checkbox is checked.
- Send to mail button is highlighted with a red box.

Session preview:



Downloading data with less pain



1. Via the Downloads button on the track details page

Home Genomes Genome Browser Blat Tables Gene Sorter PCR Session FAQ Help

UTA TFBS Track Settings Downloads Subtracks Description

Open Binding Home Genomes Blat Tables Gene Sorter PCR Session FAQ Help

UTA TFBS Downloadable Files File Search Description

Open Chromatin TFBS by ChIP-seq from ENCODE/Open Chrom(UT Austin)

Data is RESTRICTED FROM USE in publication until the restriction date noted for the given data file.

Supporting documents:

- [files.txt](#) is a tab-separated file with the name and metadata for each download.
- [md5sum.txt](#) is a list of the md5sum output for each download.
- [Supplemental materials](#) contains additional files provided by the laboratory related to these downloads.

Filter files by: (select multiple categories and items - [help](#))

Antibody		
Cell Line:	Target:	View:
All	All	All

352 files	Cell Line ^{↓1}	Antibody Target ^{↓2}	View ^{↓3}	Size ^{↓4}	File Type ^{↓5}	Submitted	RESTRICTED Until	Additional Details
Download	Fibrobl	CTCF	Alignments	5.6 MB	bam.bai	2010-10-13	2011-07-13	replicate=1; origAssembly=hg19; dataVersion=ENCODE J
Download	Fibrobl	CTCF	Alignments	5.7 MB	bam.bai	2010-10-13	2011-07-13	replicate=2; origAssembly=hg19; dataVersion=ENCODE J
Download	Fibrobl	CTCF	Alignments	377 MB	bam	2010-10-13	2011-07-13	replicate=1; origAssembly=hg19; dataVersion=ENCODE J
Download	Fibrobl	CTCF	Alignments	382 MB	bam	2010-10-13	2011-07-13	replicate=2; origAssembly=hg19; dataVersion=ENCODE J
Download	Fibrobl	CTCF	Base_Overlap_Signal	172 MB	bigWig	2010-10-13	2011-07-13	origAssembly=hg19; dataVersion=ENCODE J
Download	Fibrobl	CTCF	Peaks	1.2 MB	narrowPeak	2010-10-13	2011-07-13	origAssembly=hg19; dataVersion=ENCODE J
Download	Fibrobl	CTCF	Signal	4.1 GB	bigWig	2010-10-13	2011-07-13	origAssembly=hg19; dataVersion=ENCODE J
Download	Fibrobl	Input	Alignments	6.1 MB	bam.bai	2010-10-14	2011-07-14	origAssembly=hg19; dataVersion=ENCODE J
Download	Fibrobl	Input	Alignments	745 MB	bam	2010-10-14	2011-07-14	origAssembly=hg19; dataVersion=ENCODE J

2. Via the File Selection tool

The screenshot shows the ENCODE Data Coordination Center at UCSC website. The left sidebar has a 'Downloads' link highlighted with a red box. The main content area is titled 'ENCODE Downloads'. It includes a search form for 'Search for Downloadable ENCODE Files in the Human Feb. 2009 (GRCh37/hg19) Assembly'. The search form has several dropdown menus and input fields. Two specific dropdowns are highlighted with red boxes: 'and Group:' set to 'Expression' and 'and Data Format:' set to 'Any'. Below these, there are two additional dropdowns with '+' buttons: 'Cell, tissue or DNA sample' (set to 'Urothelia') and 'Antibody or target protein' (set to 'Any'). A green header bar at the bottom of the search form contains the following columns: Treatment^{↓1}, UCSC Accession^{↓2}, Size^{↓3}, Type^{↓4}, and Additional Details^{↓5}. Under this header, there are two rows of file entries. The first row has a 'Download' button and a folder icon next to 'wgEncodeEH001076'. The second row has a 'Download' button and a folder icon next to 'UT189'. Both rows also include the file size (2.2 MB), grant (Crawford), lab (Duke), data type (AffyExonArray), view (SimpleSignal), cell type (Urothelia), and date.

Human
Data Summary
Search
Downloads

Genome Browser (hg19)
Preview Browser (hg19)
Session Gallery
Cell Types

Mouse
Data Summary
Search
Downloads

Genome Browser (mm9)
Preview Browser (mm9)
Cell Types

General
Registered Variables
Antibodies
Usage Resources
Release Log
Data Policy
Data Standards
Publications
Contributors
Pilot Project
Jobs
Contact Us

Encyclopedia of DNA Elements

About ENCODE Data

ENCODE Data Coordination Center at UCSC

Home - Help

ENCODE Downloads

This page contains links to directories containing raw and processed data for ENCODE data released as part of the ENCODE production phase (September 2007-present). For bulk download, retrieval by [FTP](#) is recommended. All files here are covered by the [ENCODE data release policy](#). Preview of unreleased data for

Home Genomes Blat Tables Gene Sorter PCR Session FAQ Help

Search for Downloadable ENCODE Files in the Human Feb. 2009 (GRCh37/hg19) Assembly

Track Name: contains

and Description: contains

and Group: is

and Data Format: is

+ and Cell, tissue or DNA sample is among Cell, tissue or DNA sample

+ and Antibody or target protein is among Antibody or target protein

ENCODE terms

search clear cancel

	Treatment ^{↓1}	UCSC Accession ^{↓2}	Size ^{↓3}	Type ^{↓4}	Additional Details ^{↓5}
<input type="button" value="Download"/> <input type="button" value=""/>	wgEncodeEH001076	2.2 MB	broadPeak	grant=Crawford; lab=Duke; dataType=AffyExonArray; view=SimpleSignal; cell=Urothelia; date	
<input type="button" value="Download"/> <input type="button" value=""/>	UT189	2.2 MB	broadPeak	grant=Crawford; lab=Duke; dataType=AffyExonArray; view=SimpleSignal; cell=Urothelia; date	

Publishing: the ENCODE data release policy



"IT STARTED WITH A SIMPLE CASE OF
PEER-REVIEW."

Every ENCODE subtrack has a “Restricted Until” date

Home Genomes Genome Browser Blat Tables Gene Sorter PCR Session FAQ Help

LICR Histone Track Settings Downloads Subtracks|| Description||

Histone Modifications by ChIP-seq from ENCODE/LICR ([All Expression and Regulation tracks](#))

Maximum display mode: [Reset to defaults](#)

Select views ([help](#)):

Data Release Policy

Data users may freely use ENCODE data, but may not, without prior consent, submit publications that use an unpublished ENCODE dataset until nine months following the release of the dataset. This date is listed in the *Restricted Until* column on the track configuration page and the download page. The full data release policy for ENCODE is available [here](#).

H3K4me3				H3K4me3									
Input		Input		Input		Input							
List subtracks: <input type="radio"/> only selected/visible <input checked="" type="radio"/> all (40 of 50 selected)													
Top↑													
Cell Line ^{↓1}	Factor ^{↓2}	Views ^{↓3}	Track Name ^{↓4}				Restricted Until ^{↓5}						
<input checked="" type="checkbox"/> Bone Marrow H3K4me1 Peaks			Bone Marrow H3K4me1 Histone Modifications by ChIP-seq Peaks from ENCODE/LICR ...	schema			2011-10-19						
<input checked="" type="checkbox"/> Bone Marrow H3K4me1	Signal		Bone Marrow H3K4me1 Histone Modifications by ChIP-seq Signal from ENCODE/LICR ...	schema			2011-10-19						
<input checked="" type="checkbox"/> Bone Marrow H3K4me3 Peaks			Bone Marrow H3K4me3 Histone Modifications by ChIP-seq Peaks from ENCODE/LICR ...	schema			2011-10-19						
<input checked="" type="checkbox"/> Bone Marrow H3K4me3	Signal		Bone Marrow H3K4me3 Histone Modifications by ChIP-seq Signal from ENCODE/LICR ...	schema			2011-10-19						
<input type="checkbox"/> Bone Marrow Input	Signal		Bone Marrow Input Histone Modifications by ChIP-seq Signal from ENCODE/LICR ...	schema			2012-01-26						
<input checked="" type="checkbox"/> Cerebellum	H3K4me1 Peaks		Cerebellum H3K4me1 Histone Modifications by ChIP-seq Peaks from ENCODE/LICR ...	schema			2011-12-07						
<input checked="" type="checkbox"/> Cerebellum	H3K4me1	Signal	Cerebellum H3K4me1 Histone Modifications by ChIP-seq Signal from ENCODE/LICR ...	schema			2011-12-07						

Key points of the ENCODE data release policy

- Anyone is free to download and analyze data.
- One cannot submit publications involving ENCODE data unless
 - the data has been at the ENCODE DCC for at least nine months, or
 - the data producers have published on the data, or
 - the data producers have granted permission to publish.
- Please acknowledge the ENCODE project and the data producers in all publications.

Additional Resources

- The OpenHelix ENCODE tutorial at
<http://www.openhelix.com/ENCODE/>
- [A User's Guide to the Encyclopedia of DNA Elements \(ENCODE\) in PLoS Biology](#)
- The ENCODE Project page at
<http://www.genome.gov/10005107>
- The UCSC Genome Browser User's Guide
at <http://genome.ucsc.edu/goldenPath/help/>

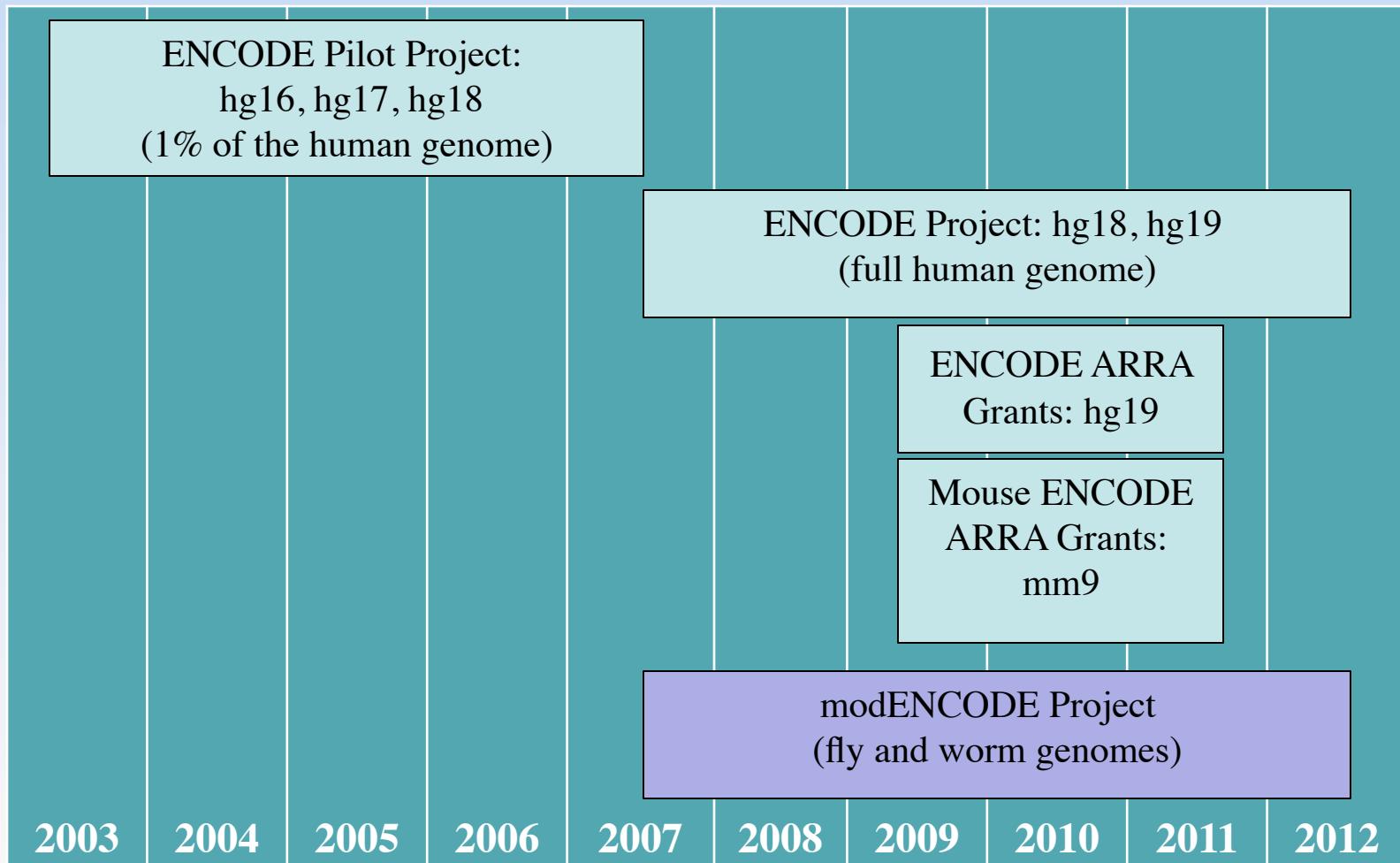
Acknowledgements

- **Cat Herding:** *Kate Rosenbloom and Jim Kent*
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- *The UCSC Genome Browser staff*
- *The ENCODE consortium*
- **Funding:** *NHGRI*

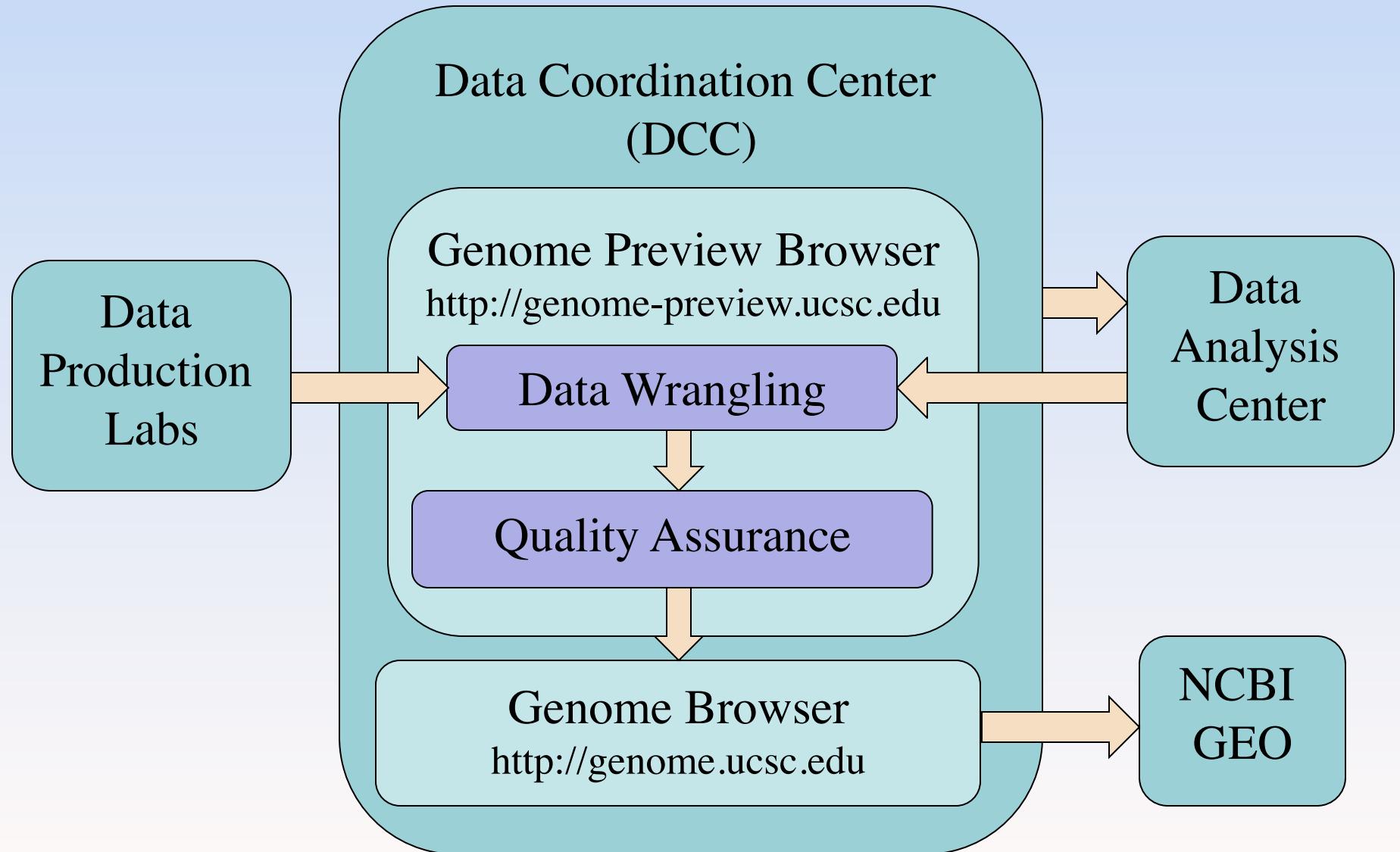
The End

Bonus Slides

ENCODE and related projects



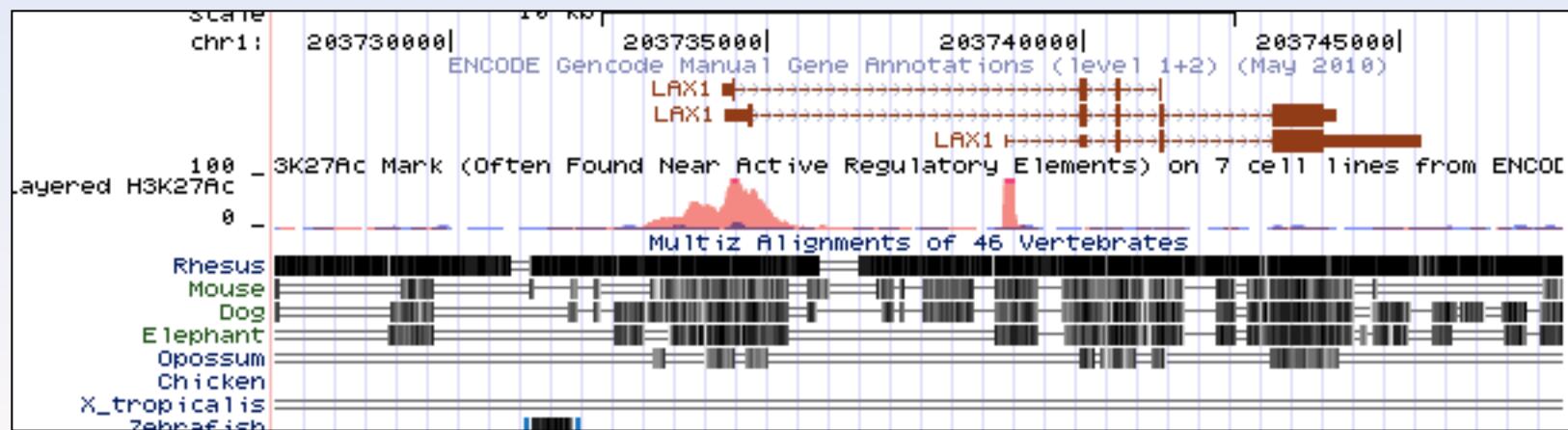
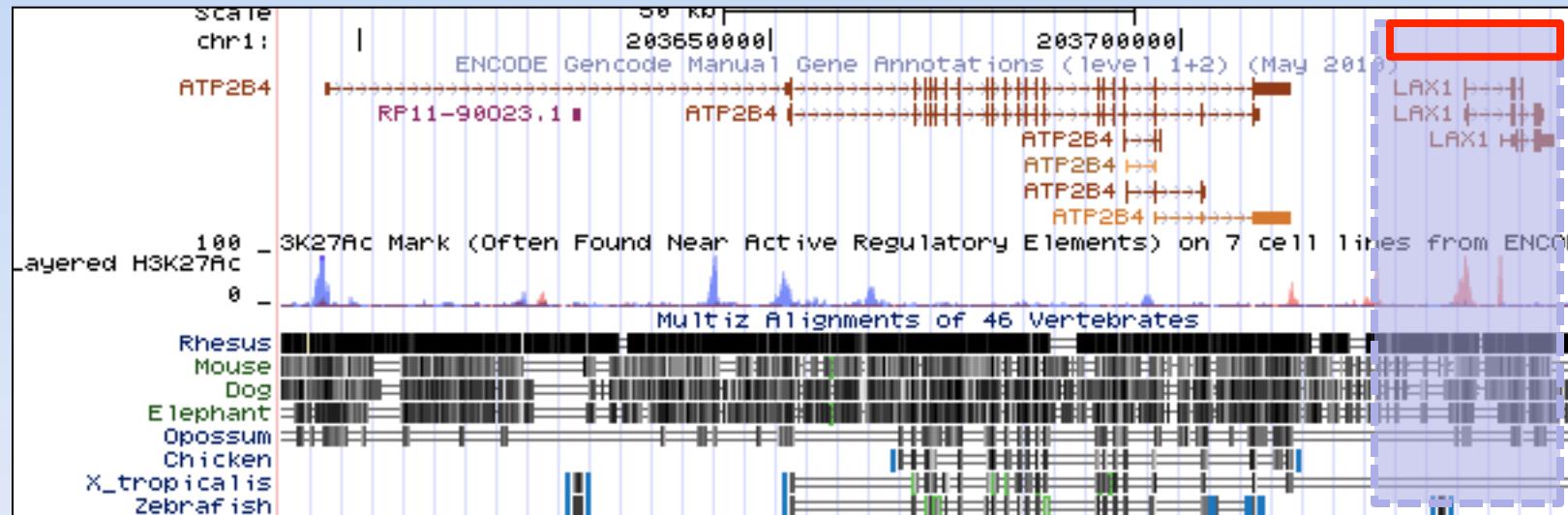
ENCODE Data Lifecycle



ENCODE Track Organization

<u>Supertracks</u> 8 in hg19	<u>Tracks</u> 45 in hg19	<u>Subtracks</u> 1584 in hg19
ENC RNA-Seq	Caltech RNA-seq	GM12878 - strand-specific, GM12878 - paired, H1hESC - strand-specific, ...
	CSHL Long RNA-seq	GM12878-Nucleus, K562-Nucleoplasm, HepG2-Cytosol, HSMM-WholeCell, ...
	Riken CAGE-Loc	GM12878-Nucleus, K562-Polysome, NHEK-Cytosol, BJ-WholeCell, ...
ENC Histone	Broad Histone	GM12878-CTCF, K562-H3K4me1, HepG2-H3K9ac, HSMM-H2A.Z, ...
	UW Histone	GM12878-H3K4me3, K562-H3K27me3, HUVEC-H3K36me3, BJ-H3K4me3, ...
...

Rectangular region-select



Display settings explained

Dense



Squish



Pack



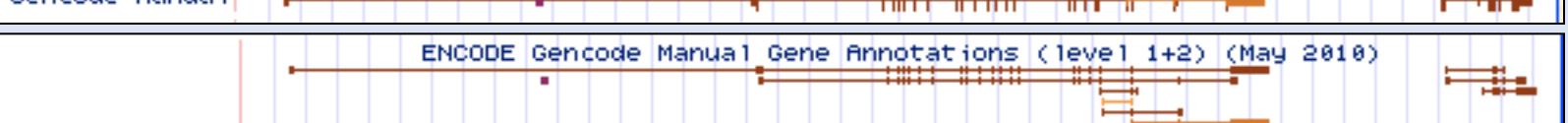
Full



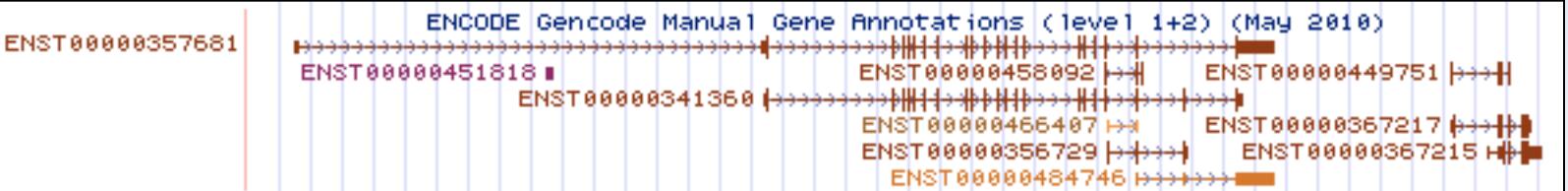
Dense



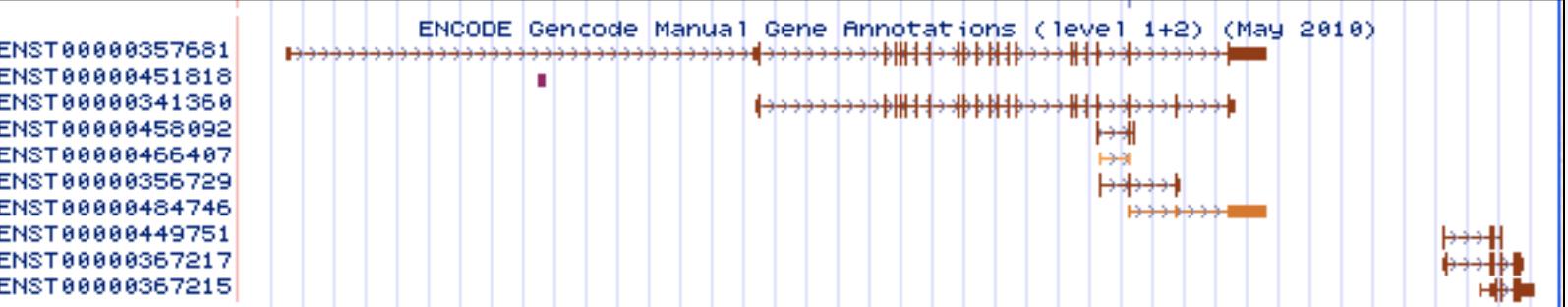
Squish



Pack



Full



3. Via NCBI GEO

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1: GSE29692 record: DNasel Hypersensitivity by Digital DNasel from ENCODE/University of Washington [*Homo sapiens*]

Summary: (Submitter supplied) This track is produced as part of the ENCODE Project. This track shows DNasel sensitivity measured genome-wide in different cell lines using the Digital DNasel methodology (see below), and DNasel hypersensitive sites. DNasel has long been used to map general chromatin accessibility and DNasel hypersensitivity is a universal feature of active cis-regulatory sequences. The use of this method has led to the discovery of functional regulatory elements that include enhancers, insulators, promoters, locus control regions and novel elements. For each experiment (cell type) this track shows DNasel sensitivity as a continuous function using sequencing tag density (Raw Signal), and discrete loci of DNasel sensitive zones (HotSpots) and hypersensitive sites (Peaks)." For data usage terms and conditions, please refer to <http://www.genome.gov/27528022> and <http://www.genome.gov/Pages/Research/ENCODE/ENCODEDataReleasePolicyFinal2008.pdf>

Project: ENCODE

[1 related Platform](#)

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