

# **The NIH Roadmap Epigenomics Program: A Community Epigenetics Resource**

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**Program Director, NIH Roadmap Epigenomics Program  
National Institute of Environmental Health Sciences**

# Where is the data: sites with unique features

**Consortium homepage** <http://roadmapepigenomics.org>

- View data on genome
- protocols
- standards

**NCBI** <http://ncbi.nlm.nih.gov/epigenomics>

<http://ncbi.nlm.nih.gov/geo/roadmap/epigenomics>

- View data
- Download data
- Compare samples

**Human Epigenome Atlas** <http://epigenomeatlas.org>

- View data on genome or with Atlas gene browser
- Download data
- Tools at Genboree Workbench

**WashU VizHub** <http://vizhub.wustl.edu>

- Next-gen browser <http://epigenomegateway.wustl.edu>
- UCSC visualization hub at <http://genome.ucsc.edu>

OVERVIEW

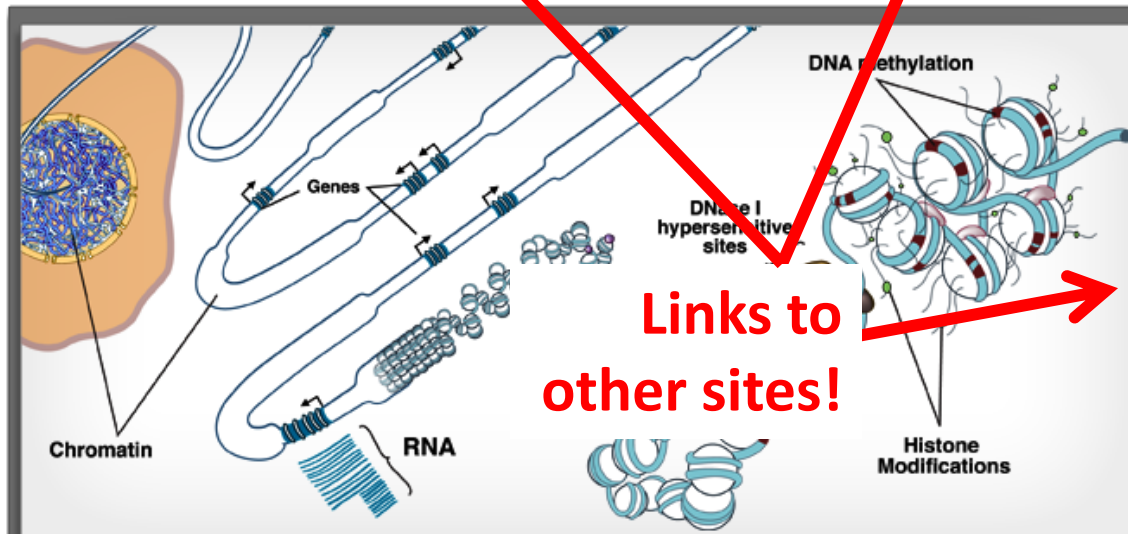
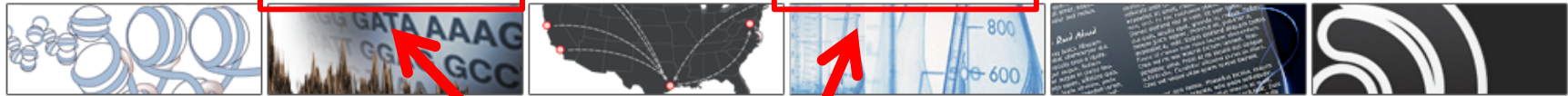
PROJECT DATA

MAPPING CENTERS

PROTOCOLS & STANDARDS

PUBLICATIONS

NEWS



**Links to  
other sites!**

VIEW/DOWNLOAD QUICK LINKS

Genome Browsers

- <http://www.epigenomebrowser.org>
- <http://genomebrowser.wustl.edu/>
- <http://epigenomegateway.wustl.edu/>

Data Repositories

- [NCBI Epigenomics Gateway](#)
- [Epigenome Atlas](#)

**NIH Roadmap Epigenomics Mapping Consortium**

The NIH Roadmap Epigenomics Mapping Consortium was launched with the goal of producing a public resource of human epigenomic data to catalyze basic biology and disease-oriented research. The Consortium leverages experimental pipelines built around next-generation sequencing technologies to map DNA methylation, histone modifications, chromatin accessibility and small RNA transcripts in stem cells and primary ex vivo tissues selected to represent the normal counterparts of tissues and organ systems frequently involved in human disease. The Consortium expects to deliver a collection of normal epigenomes that will provide a framework or reference for comparison and integration within a broad array of future studies. The Consortium also aims to close the gap between data generation and its public dissemination by rapid release of raw sequence data, profiles of epigenomics features and higher-level integrated maps to the scientific community. The Consortium is also committed to the development, standardization and dissemination of protocols, reagents and analytical tools to enable the research community to utilize, integrate and expand upon this body of data.

NEWS

**27** [Disease Risk Links to Gene Regulation](#)

MAY

**6** [Epigenome effort makes its mark](#)

OCT

[Archives](#)



# Two ways to browse: Visual Browser

**ROADMAP epigenomics PROJECT**

HOME PARTICIPANTS DATA PROTOCOLS QUALITY METRICS TOOLS PUBLICATION

Search:

**Data Types** **Download Data** **Data Quality**

**DATA TABLE** **VISUAL DATA BROWSER**

Data Tables Embryonic Stem Cells Fetal Tissues Adult Cells & Tissues

**Mouse over sites, click for table**

NCBI at their sites. metrics for all histone modification and chromatin accessibility data.

Hematopoietic cells: 70 available samples

Clear Section

Brain Multiple regions Brain sagittal Brain coronal

Breast Stem cells Luminal epithelial Myepithelial

Liver Duodenum Stomach GI Tract Small Intestine Rectum

Kidney Pancreatic islets Visceral fat

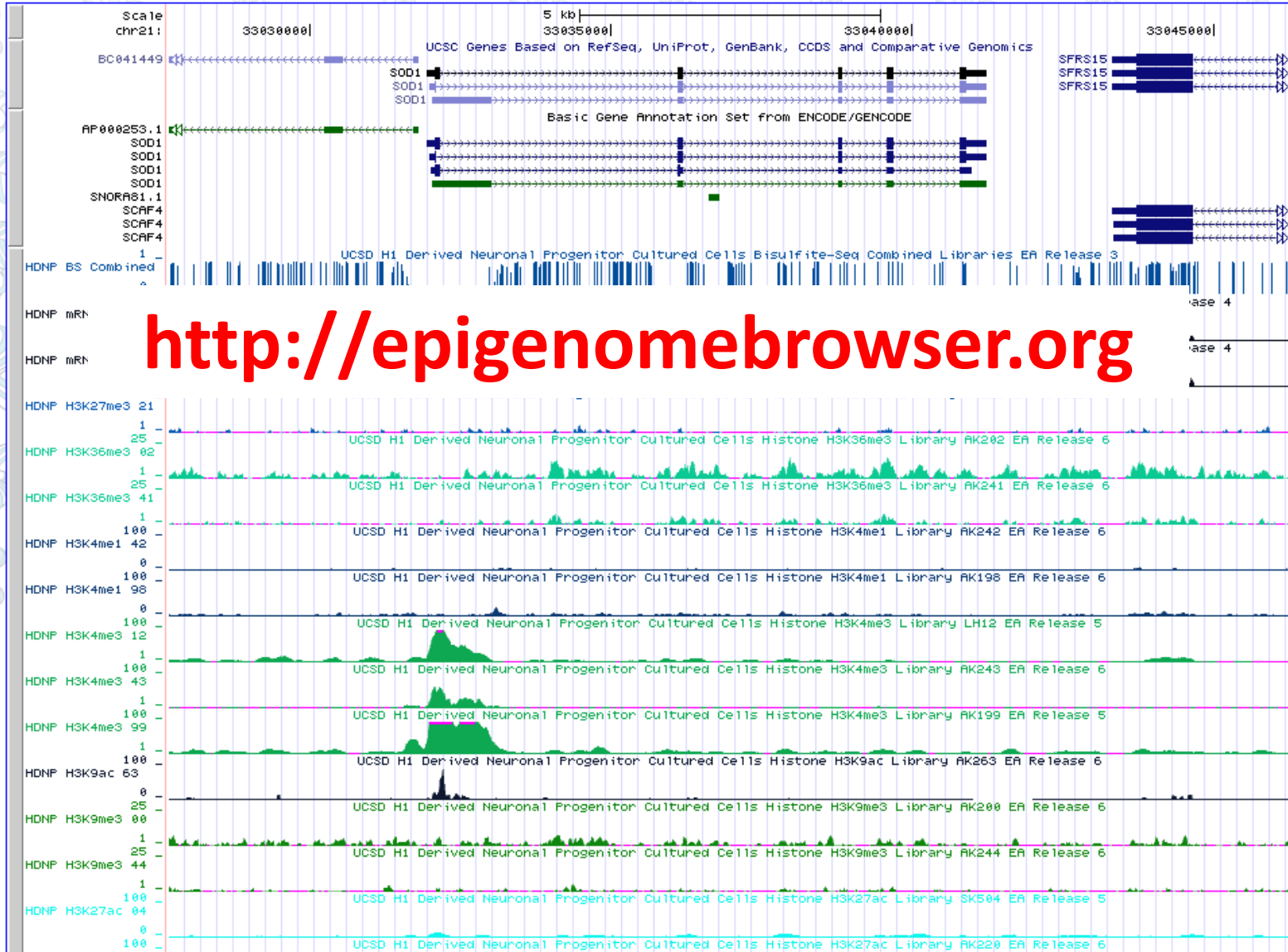
**Click Here for Data**

- Hematopoietic cells
- Stem cells (CD34+)
- B-Cells (CD19+)
- T-Cells (CD3+, CD4+, CD8+)
- Granulocytes (CD15+)
- PBMCs

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

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

position/search chr21:33,027,660-33,046,273    size 18,614 bp.



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# Hot off the presses : Roadmap data at GEO

## NIH Roadmap Epigenomics Project Data Listings

This page summarizes Roadmap Epigenomics project data that are available through the GEO repository. Additional data will be added as it becomes available.

**View tracks on genome viewer of your choice**

**Data download (.bed, .wig, some SRA, .bam)**

For data usage: Epig

Description of tab contents

Samples | Studies | **Matrix**

Search:

View tracks in:

Export:

GEO Accession	Sample	Experiment	View Track	Center	Download	Embargo end date
GSM605332	H1 cell line	H4K91ac	<input type="checkbox"/>	UCSD	<a href="#">sra</a> <a href="#">bed,wig</a>	2011-07-07
GSM667639	H9 cell line	H4K91ac	<input type="checkbox"/>	UCSD	<a href="#">sra</a> <a href="#">bed,wig</a>	2011-12-23
GSM667640	H9 cell line	H4K91ac	<input type="checkbox"/>	UCSD	<a href="#">sra</a> <a href="#">bed,wig</a>	2011-12-23
GSM521924	IMR90 cell line	H4K91ac	<input type="checkbox"/>	UCSD	<a href="#">sra</a> <a href="#">bed,wig</a>	2010-12-22
GSM521925	IMR90 cell line	H4K91ac	<input type="checkbox"/>	UCSD	<a href="#">sra</a> <a href="#">bed,wig</a>	2010-12-22
GSM667637	H9 cell line	H4K8ac	<input type="checkbox"/>	UCSD	<a href="#">sra</a> <a href="#">bed,wig</a>	2011-11-15
GSM667638	H9 cell line	H4K8ac	<input type="checkbox"/>	UCSD	<a href="#">sra</a> <a href="#">bed,wig</a>	2011-12-23
GSM521919	IMR90 cell line	H4K8ac	<input type="checkbox"/>	UCSD	<a href="#">sra</a> <a href="#">bed,wig</a>	2010-12-22
GSM521921	IMR90 cell line	H4K8ac	<input type="checkbox"/>	UCSD	<a href="#">sra</a> <a href="#">bed,wig</a>	2010-12-22
GSM521922	IMR90 cell line	H4K8ac	<input type="checkbox"/>	UCSD	<a href="#">sra</a> <a href="#">bed,wig</a>	2010-12-22
GSM521923	IMR90 cell line	H4K8ac	<input type="checkbox"/>	UCSD	<a href="#">sra</a> <a href="#">bed,wig</a>	2010-12-22
GSM605330	H1 cell line	H4K5ac	<input type="checkbox"/>	UCSD	<a href="#">sra</a> <a href="#">bed,wig</a>	2011-07-07
GSM667635	H9 cell line	H4K5ac	<input type="checkbox"/>	UCSD	<a href="#">sra</a> <a href="#">bed,wig</a>	2011-11-15
GSM667636	H9 cell line	H4K5ac	<input type="checkbox"/>	UCSD	<a href="#">sra</a> <a href="#">bed,wig</a>	2011-12-23
GSM667637	H9 cell line	H4K5ac	<input type="checkbox"/>	UCSD	<a href="#">sra</a> <a href="#">bed,wig</a>	2011-12-23

<http://www.ncbi.nlm.nih.gov/geo/roadmap/epigenomics>



## NIH Roadmap Epigenomics

This page summarizes Roadmap Epigenomics data. Additional data will be added as it becomes available.

For data on this page

Samples Studies

Center:

All

View tracks

Uncheck All

CD14 primary cells

CD15 primary cells

CD19 primary cells

CD20 primary cells

CD3 cord blood primary cells

CD3 mobilized primary cells

CD3 primary cells

CD34 cultured cells

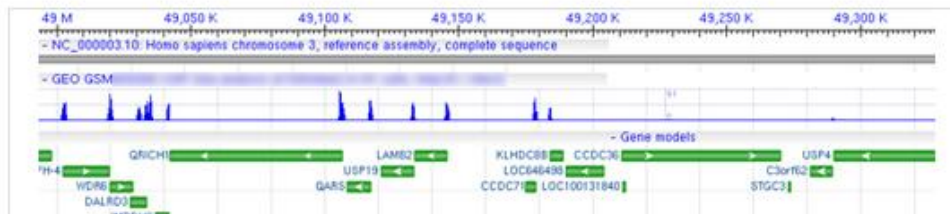
CD34 mobilized primary cells

### View tracks

**Warning:** Results can be slow if multiple tracks are selected.

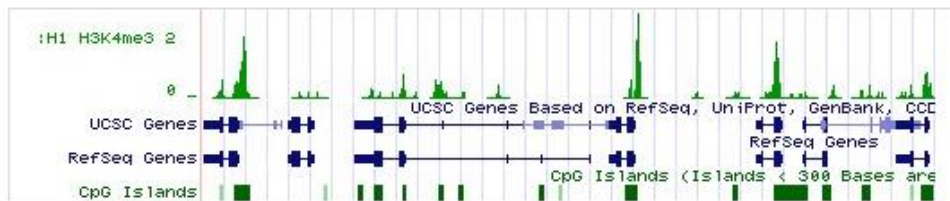
### Select chromosome to see data on NCBI Sequence Viewer:

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y M



### Select chromosome to see data on UCSC Genome Browser:

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y M



are available:  
page

H4K91ac  
H2BK20ac  
H2BK120ac  
H3K23me2  
H3K9me1  
H2A.Z  
H3T11ph  
H2AK9ac  
H4K12ac

7 1 4 15 1 12 6 8 7 8 7 3

# Genome-wide epigenetic data at NCBI: Epigenomics Gateway

NCBI Resources How To My NCBI Sign In

Epigenomics  
Beyond the Genome

Search: Epigenomics Limits Advanced search Help

Search Clear



Tutorials

Compare samples

Text search or browser search

**How to...**

- [How to Use the Sample Browser](#)
- [How to Manage Collections of Samples](#)
- [How to View Genome Tracks](#)
- [How to Download Genome Tracks](#)

**Epigenomics Tools**

- [Browse Experiments](#)
- [Browse Samples](#)
- [Compare Samples Beta](#)
- [Advanced Search](#)

**Scientific Background**


- [About Epigenetics](#)
- [About DNA Methylation](#)
- [About Histone Modifications](#)
- [About Chromatin Structure](#)

**Latest Studies**

- Genome-wide binding of the orphan nuclear receptor TR4 suggests its general role in fundamental biological processes [ESS000097]
- Paternally-induced transgenerational environmental reprogramming of metabolic gene expression in mam [ESS000110]
- Integrative model of genomic factors for determining binding site selection by estrogen receptor alpha in MCF-7 cancer [ESS000113]
- Reprogramming factor expression initiates widespread targeted chromatin remodeling [ESS000107]
- Genomic Profiling of HMG1 Reveals an Association with Chromatin at Regulatory Regions [ESS000103]

[See more...](#)

**NIH Roadmap Epigenomics**



About the Project  
Reference epigenome maps and their applications to human health.

- [Epigenomics Mapping Consortium](#)
- [Human Epigenome Atlas](#)
- [Roadmap Data in GEO](#)
- [Data Access Policies](#)

**Recent Review Articles**

- [Molecular-genetic markers in lung cancer diagnostics]. [Mol Biol (Mosk). 2011]
- [Pathology and pathobiology of the gastric carcinoma]. [Acta Chir Jugosl. 2011]
- Profiling epigenetic alterations in disease. [Adv Exp Med Biol. 2011]
- Prospects for epigenetic compounds in the treatment of autoimmune disease. [Adv Exp Med Biol. 2011]
- Epigenetic deregulation in rheumatoid arthritis. [Adv Exp Med Biol. 2011]

[See more...](#)

<http://www.ncbi.nlm.nih.gov/epigenomics>

# Epigenomics

Beyond the Genome

Search

Browse **Experiments** Samples

All experiments (1873)  
New experiments (567)  
Recently viewed (0)  
Clipboard (0)

**My Collections**  
Note: You haven't created any collections yet. Select some samples and use the "Send To" command to create and name your collection.

**Filters** ▾

Containing word(s):

**Species**

- All
- Caenorhabditis elegans
- Drosophila melanogaster
- Homo sapiens**
- Mus musculus

Select samples to add to clipboard or collection, or to view metadata (antibody, instrument, quality metrics, sample info)

Use filters to narrow selection

Filter

Or view on genome

**Feature Type**

- All
- DNA methylation
- gene expression
- H3K27me3
- H3K36me3
- H3K4me1
- H3K4me3

**Experiments (15)**

Select: All, None Selected: 5

	Experiment ID	Feature Type	Assay Type	Species	Cell Type	Tissue Type	Cell Line	Cell Population	Differentiation
<input type="checkbox"/>	ESX000001275	DNA methylation	DNA methylation	Homo sapiens	T lymphocyte	blood		CD8+ CD45RA+	naïve
<input type="checkbox"/>	ESX000001287	DNA methylation	DNA methylation	Homo sapiens	T lymphocyte	blood		CD8+ CD45RA+	naïve
<input checked="" type="checkbox"/>	ESX000001990	H3K4me3	histone modification	Homo sapiens	T lymphocyte	blood		CD8+ CD45RA+	naïve
<input checked="" type="checkbox"/>	ESX000001991	H3K9me3	histone modification	Homo sapiens	T lymphocyte	blood		CD8+ CD45RA+	naïve
<input checked="" type="checkbox"/>	ESX000001992	H3K9ac	histone modification	Homo sapiens	T lymphocyte	blood		CD8+ CD45RA+	naïve
<input checked="" type="checkbox"/>	ESX000001993	H3K4me1	histone modification	Homo sapiens	T lymphocyte	blood		CD8+ CD45RA+	naïve
<input checked="" type="checkbox"/>	ESX000001994	H3K27me3	histone modification	Homo sapiens	T lymphocyte	blood		CD8+ CD45RA+	naïve
<input type="checkbox"/>	ESX000001995	input control	input control	Homo sapiens	T lymphocyte	blood		CD8+ CD45RA+	naïve
<input type="checkbox"/>	ESX000002027	H3K4me3	histone modification	Homo sapiens	T lymphocyte	blood		CD8+ CD45RA+	naïve
<input type="checkbox"/>	ESX000002046	DNA methylation	DNA methylation	Homo sapiens	T lymphocyte	blood		CD8+ CD45RA+	naïve
<input type="checkbox"/>	ESX000002052	DNA methylation	DNA methylation	Homo sapiens	T lymphocyte	blood		CD8+ CD45RA+	naïve
<input type="checkbox"/>	ESX000002055	DNA methylation	DNA methylation	Homo sapiens	T lymphocyte	blood		CD8+ CD45RA+	naïve
<input type="checkbox"/>	ESX000002581	H3K36me3	histone modification	Homo sapiens	T lymphocyte	blood		CD8+ CD45RA+	naïve
<input type="checkbox"/>	ESX000002596	DNA methylation	DNA methylation	Homo sapiens	T lymphocyte	blood		CD8+ CD45RA+	naïve

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# The Human Epigenome Atlas



Home



Releases

Informatics

Publications

Forums

Contributors

## Human Epigenome Atlas

[The Current Release \(Release 8\) of the Human Epigenome Atlas](#)

The Human Epigenome Atlas is produced by the [NIH Epigenomics Roadmap Consortium](#).

The Human Epigenome Atlas includes human reference epigenomes and the results of their integrative and comparative analyses. Successive releases of the Atlas will provide progressively more detailed insights into locus-specific epigenomic states, including histone marks and DNA methylation marks across specific tissues and cell types, developmental stages, physiological conditions, genotypes, and disease states.

### Epigenome Atlas Release 8

- [Interactive Visualization and Download](#)
- [Data Download via http](#)
- [Data Download via ftp](#)

### More information and resources are available:

- [Roadmap Epigenomics Homepage](#)
- [NCBI Epigenomics Gateway](#)
- [UCSC browser mirror site at University of Washington](#)
- [UCSC browser mirror site at Washington University](#)

### Epigenome Atlas Release 8

Filter rows:

Selections

Choose Databases

AssayType

SampleType

Brain Sigmoid Colon

Brain Germinal Matrix

Brain Hippocampus Middle

Brain Inferior Temporal Lobe

Bisulfite-Seq

MeDIP-Seq

MRE-Seq

RRBS

DNase Hypersensitivity

Click for data

See the current release (Release 8) of the [Human Epigenome Atlas](#). (Best viewed over a high bandwidth connection)

Breast Luminal Epithelial Cells

Breast Myoepithelial Cells

Breast Stem Cells

Epigenome Atlas

Filter rows:

Epigenome Atlas

Genboree Workbench

Metadata & Data Flow

Analysis Pipelines

Data Quality



## Atlas Gene Browser for EA Release 4 (hg19)

- Start typing a gene name in the box below and select a gene from the pulldown list
- Use the scrollbar at the bottom of the table to see the genes on the right
- Choose specific gene elements if necessary (⚙️ next to gene name)
- Add genes one by one or via the pathway browser (🔴 next to gene name)
- Zoom into features of interest using the genome browser (🗺️ next to gene name)
- Click on the sample, assay or gene image to see related metadata



Click on this icon to generate a shareable link to this session

### Gene Features Legend



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### Epigenome Atlas Release 8

Filter rows:  Selections ▾ Choose Databases

SampleType	AssayType				
	Bisulfite-Seq	MeDIP-Seq	MRE-Seq	RRBS	DNase Hypersensitivity
Brain Oligodendrocytes					
Brain Germinal Matrix	1	2			
Brain Hippocampus Middle	1				
Brain Inferior Temporal Lobe				1	
Breast Luminal Epithelial Cells		6	10		
Breast Myoepithelial Cells		6	6		
Breast Stem Cells		8	8		

See the current release (Release 8) of the [Human Epigenome Atlas](#). (Best viewed over a high bandwidth connection)

Epigenome Atlas

Filter rows:

Epigenome Atlas

Genboree Workbench

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# Epigenomic (and other) analysis tools for your data, our data, or both

GENBOREE

BCM  
Baylor College of Medicine

System/Network Data QC and Pre-processing Genome Transcriptome Cistrome Epigenome Metagenome Visualization Help

Welcome to the Genboree Workbench! [Getting Started]

**Data Selector**

Refresh Data Filter: Select a filter...

- genboree.org
  - chadwickl\_group
  - EDACC
  - EDACC-Test
  - Epigenome Informatics Workshop (Mar 2012)
  - Epigenome ToolSet Demo Input Data
  - Epigenomics Roadmap Repository
  - Epigenomics Workshop - 9/09
  - JonathanMill\_Lab
  - paithank\_group
  - Public
  - ROI Repository
  - Targeted Atlases
  - vamin\_group

**Details**

Attribute	Value
-----------	-------

**Input Data**

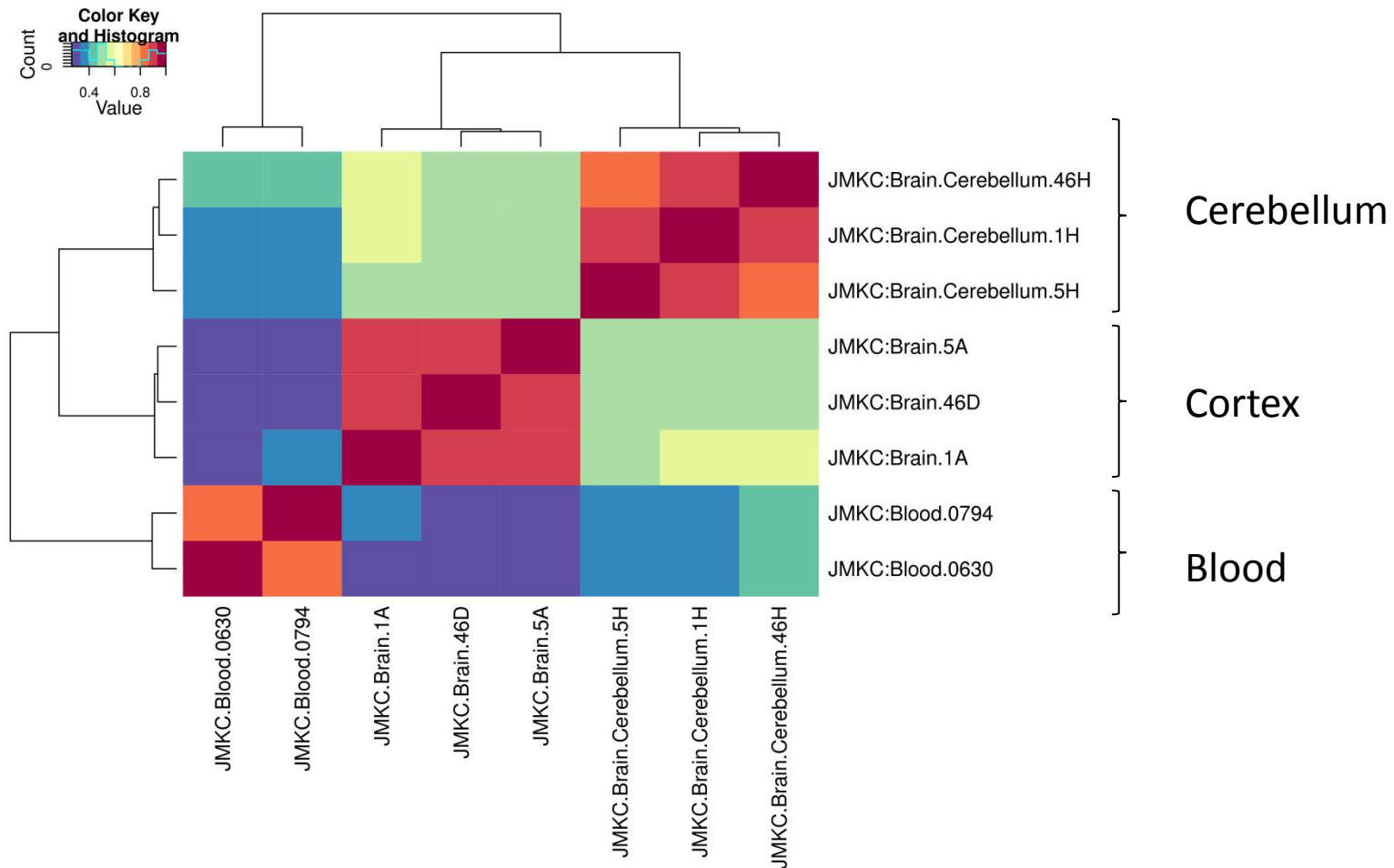
↑ ↓ ✕

**Output Targets**

↑ ↓ ✕

**Epigenomic analysis workshop a few times a year.**

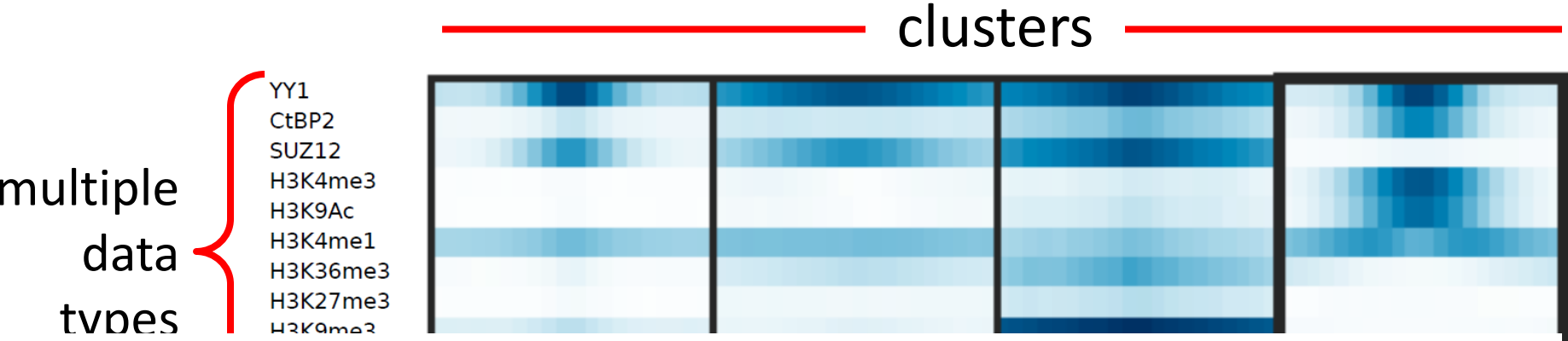
# Comparison of epigenetic profiles across specific ROIs (meDIP-seq, low CpG promoters)



Similarity matrix using Pearson correlation

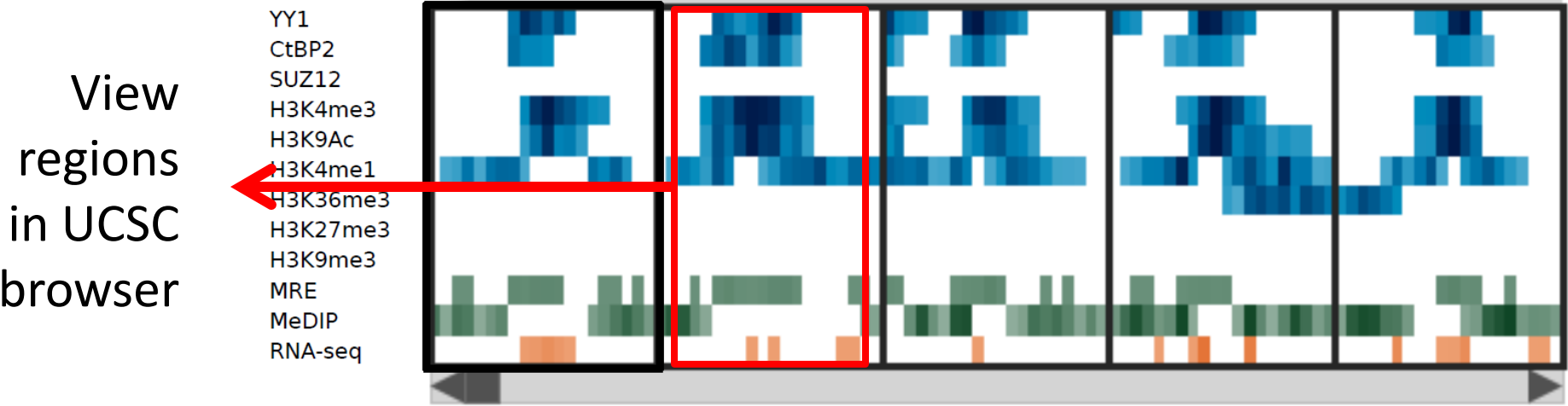
Davies et al., Genome Biol 2012

# Spark: cluster analysis of genomic regions of interest



<http://www.sparkinsight.org>

Download program, video tutorials



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# Roadmap Epigenomics VizHub at UCSC

[Genomes](#)[Genome Browser](#)[Tools](#)[Mirrors](#)[Downloads](#)[My Data](#)[About Us](#)[Help](#)

## Human (*Homo sapiens*) Genome Browser Gateway

The UCSC Genome Browser was created by the [Genome Bioinformatics Group of UC Santa Cruz](#).  
Software Copyright (c) The Regents of the University of California. All rights reserved.

clade	genome	assembly	position	search term	
Mammal	Human	Feb. 2009 (GRCh37/hg19)	chr6:152,355,873-152,487,408	<input type="text" value="enter position, gene symbol or search terms"/>	<input type="button" value="submit"/>

[Click here to reset](#) the browser user interface settings to their defaults.

## Human Genome Browser – hg19 assembly (sequences)

[Public Hubs](#)[My Hubs](#)

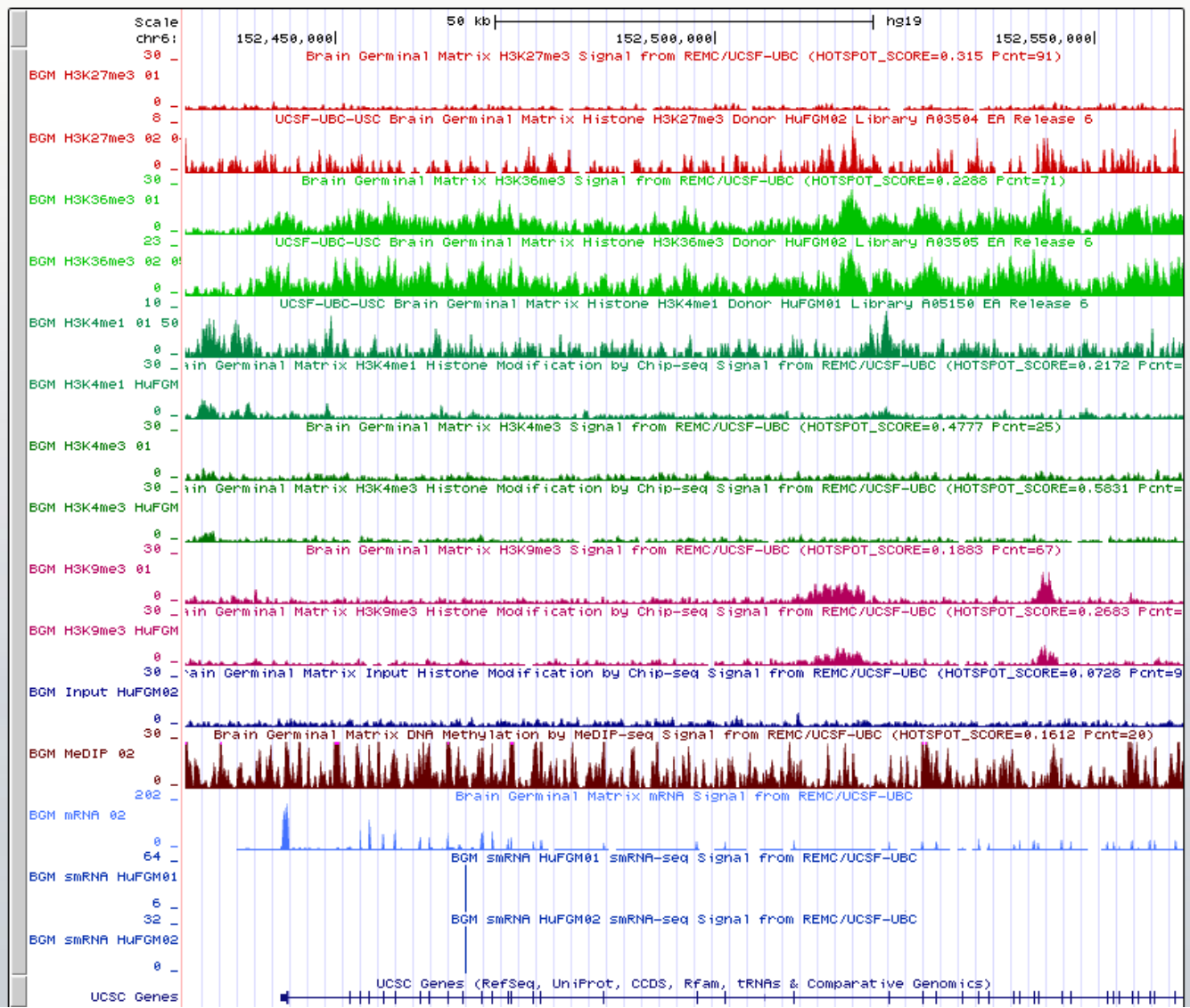
Display	Hub Name	Description	Assemblies	URL
<input type="checkbox"/>	ENCODE Analysis Hub	ENCODE Integrative Analysis Data Hub	hg19	<a href="http://ftp.ebi.ac.uk/pub/databases/ensembl/encode/integration_data_jan2011/hub.txt">http://ftp.ebi.ac.uk/pub/databases/ensembl/encode/integration_data_jan2011/hub.txt</a>
<input type="checkbox"/>	miRcode microRNA sites	Predicted microRNA target sites in GENCODE transcripts	hg19	<a href="http://www.mircode.org/ucscHub/hub.txt">http://www.mircode.org/ucscHub/hub.txt</a>
<input checked="" type="checkbox"/>	Roadmap Epigenomics Data Complete Collection at Wash U VizHub	Roadmap Epigenomics Data Complete Collection at Wash U VizHub	hg19	<a href="http://vizhub.wustl.edu/VizHub/RoadmapReleaseAll.txt">http://vizhub.wustl.edu/VizHub/RoadmapReleaseAll.txt</a>
<input type="checkbox"/>	UMassMed ZHub	UMassMed H3K4me3 ChIP-seq data for Autistic brains	hg19	<a href="http://zlab.umassmed.edu/zlab/publications/UMassMedZHub/hub.txt">http://zlab.umassmed.edu/zlab/publications/UMassMedZHub/hub.txt</a>
<input type="checkbox"/>	Cancer genome polyA site & usage	An in-depth map of polyadenylation sites in cancer (matched-pair tissues and cell lines)	hg19	<a href="http://johnlab.org/xpad/Hub/UCSC.txt">http://johnlab.org/xpad/Hub/UCSC.txt</a>

Contact [genome@soe.ucsc.edu](mailto:genome@soe.ucsc.edu) to add a public hub.

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

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

chr6:152,430,210-152,561,745 131,536 bp. | go





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

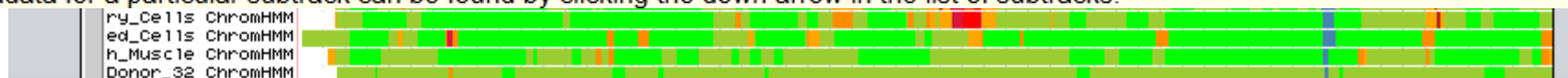
move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

## Display Conventions and Configuration

This track is a composite track that contains multiple subtracks. Each subtrack represents data for a different cell type and displays individually on the browser. The 18 states of the HMM, their associated segment color, and the candidate annotations are as follows:

- State 1 - DarkSalmon - TSS\_poised
- State 2 - Crimson - TSS\_flanking\_more\_upstream
- State 3 - Red - TSS\_active
- State 4 - OrangeRed - TSS\_weak\_lowH3k27ac
- State 5 - FireBrick - TSS\_flanking\_more\_downstream
- State 6 - Lime - Transcription
- State 7 - YellowGreen - Transcription\_weak
- State 8 - Dar - Enhancer-like\_genic
- State 9 - Orange - Enhancer\_weak
- State 10 - Orange - Enhancer\_active
- State 11 - Orange - Enhancer\_active\_with\_weakK4me1\_strong\_K27ac
- State 12 - Yellow - Enhancer\_poised
- State 13 - Silver - Repressed\_polycomb
- State 14 - Gainsboro - Repressed\_polycomb\_weakSignal
- State 15 - SteelBlue - Zinc\_finger\_genes\_H3K36me3\_K9me3
- State 16 - PaleTurquoise - Heterochromatin\_at\_repeats
- State 17 - LightCyan - Heterochromatin
- State 18 - White - Quiescent

Metadata for a particular subtrack can be found by clicking the down arrow in the list of subtracks.



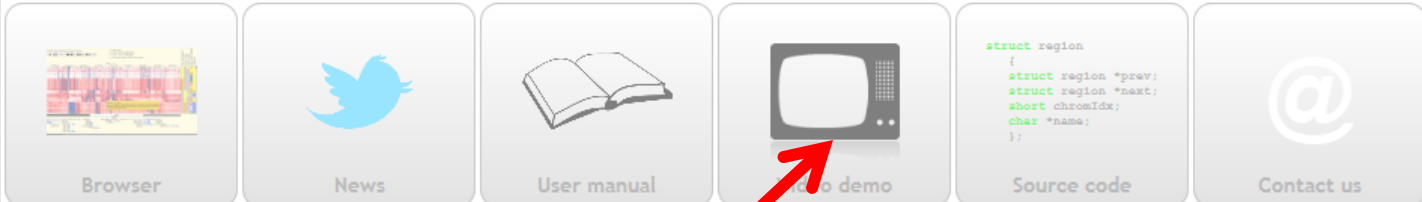


# A new epigenomics browser

[Washington University School of Medicine](#) > [Department of Genetics](#) > [Center for Genome Sciences & Systems Biology](#)

Washington University School of Medicine in St. Louis

## Human Epigenome Browser



**W**elcome to the gateway to the Human Epigenome Browser. This tool provides researchers with a cutting-edge resource for visualizing and interacting with whole-genome data. It hosts Human Epigenome Atlas data produced by the Roadmap Epigenomics project, but its use of advanced, multi-scale visualization and its user-friendly interface make it possible for investigators to upload and visualize their own data as custom tracks. **Tutorials!**

The Human Epigenome Browser is developed and maintained by the [Epigenome Informatics Group](#) at Washington University in St. Louis. If you have questions or comments related to the tools or data on this website, please feel free to contact us on our [public mailing list](#).

Best viewed on modern open-source web browsers -- [Google Chrome](#), [Chromium](#), [Firefox](#)  
Microsoft IE is not supported.

Collaboration Centers	Browser Mirrors	Cite us
<a href="#">Roadmap Epigenomics</a> <a href="#">ENCODE</a>	<a href="#">VizHub</a> <a href="#">UCSC Browser mirror</a>	<a href="#">See list of publications</a>
<a href="#">EDACC</a> <a href="#">NCBI GEO</a>		

[Giving](#) Center for Genome Sciences & Systems Biology, 4444 Forest Park Ave, CB8510, St. Louis, MO 63108  
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<http://epigenomegateway.wustl.edu>

Navigation controls: zoom in, zoom out, home, search, apps, message.

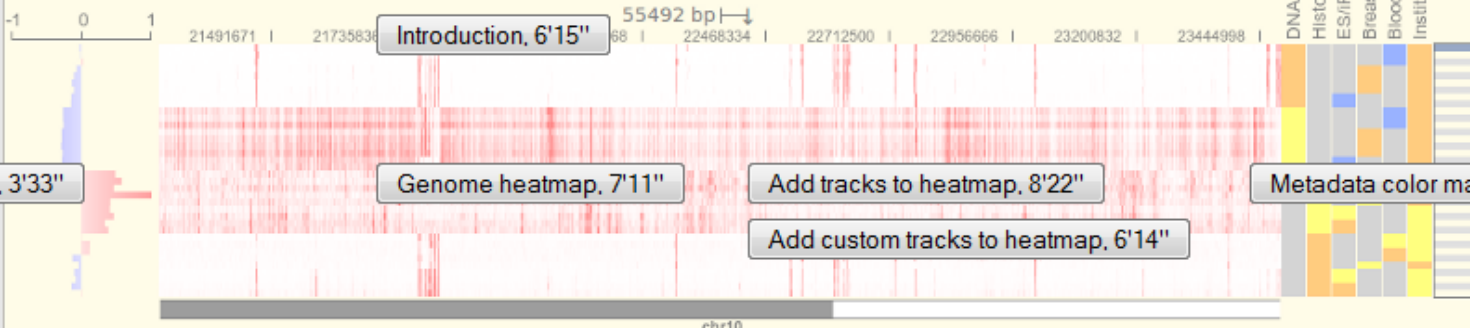
\*\* Displaying data for genome \*\*

In genome heatmap:

chr10 UCSC genome browser mirror



- 36 tracks
- start: chr10 21266927
- stop: chr10 23483842
- One pixel spans 2774 base pairs



Correlation, 3'33"

Introduction, 6'15"

Add tracks to heatmap, 8'22"

Metadata color map, 3'51"

Add custom tracks to heatmap, 6'14"



Hypothesis test, 8'48"

Pairwise comparison, 7'48"

Genomic feature tracks, 5'49"

Custom genomic feature tracks, 3'11"

Scaffold sequence

Viewing genome (gene set view is off)

Gene Set View

Custom gene set

KEGG pathways

Juxtaposition

Tracks

Statistics & analysis

Metadata

Session

Config & Misc

Cite us

Gene Set View, 8'39"

Genomic juxtaposition, 3'37"

Custom BAM track, 4'8"

Bird's Eye View, 4'5"

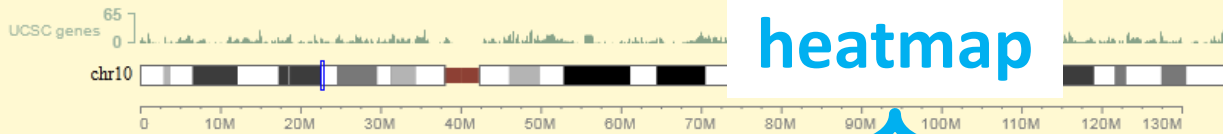
Gene Plot, 9'59"

bigBed file generator, 6'37"

Long-range genome interaction data visualization 7'6"

Gene list: CYP51A1, CYP2C19, CYP26B1, CYP11B2

Submit Clear

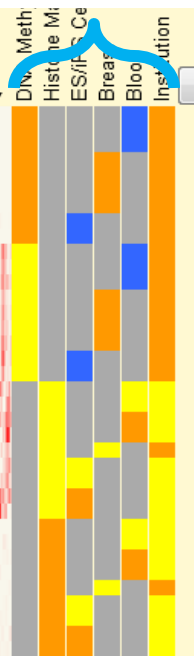
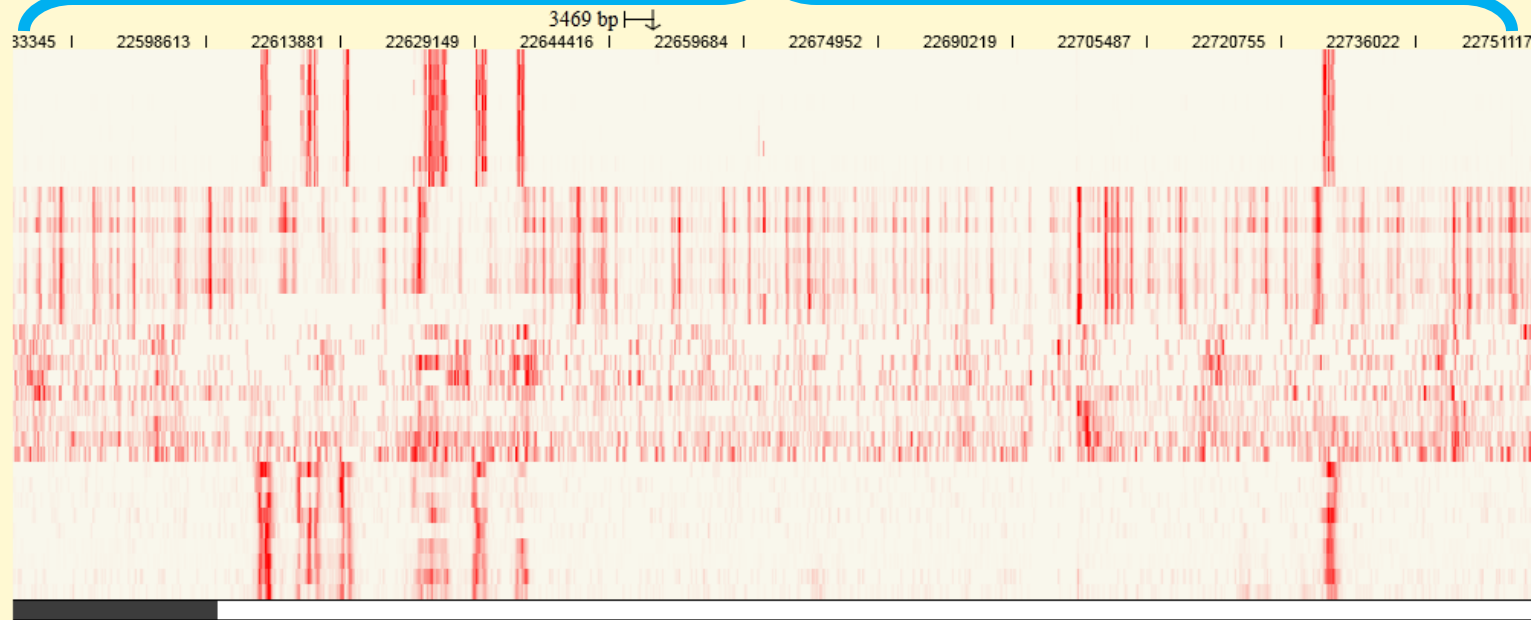


# heatmap

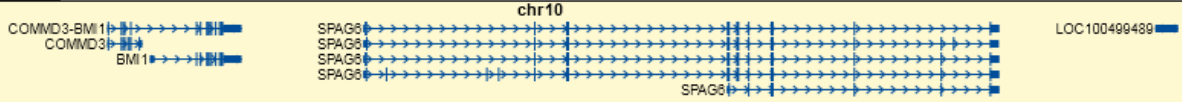
In genome heatmap:

- 36 tracks
- start: chr10 22576579
- stop: chr10 22750076
- One pixel spans 173 base pairs

# metadata



UCSC genes



↓ Genomic view

Genome heatmap

Genomic annotation

Custom track

↓ Statistics & analysis

Genome heatmap tracks

36 on display | 1868 available from current data set(s)

Track

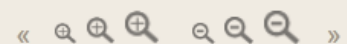
Data set

Configure

Find by GEO

?

Welcome!



Apps »

done

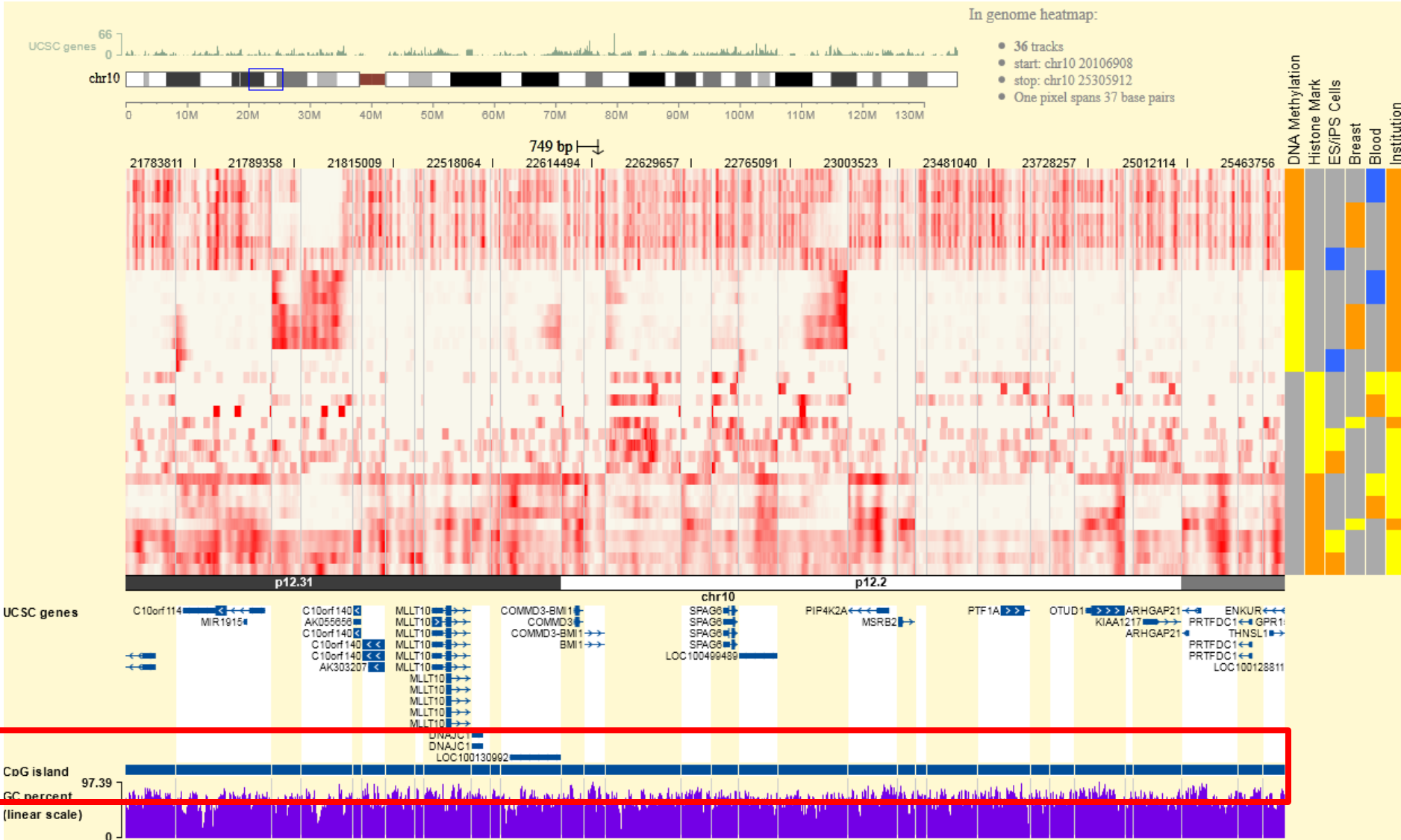
drawing genome heatmap...

done

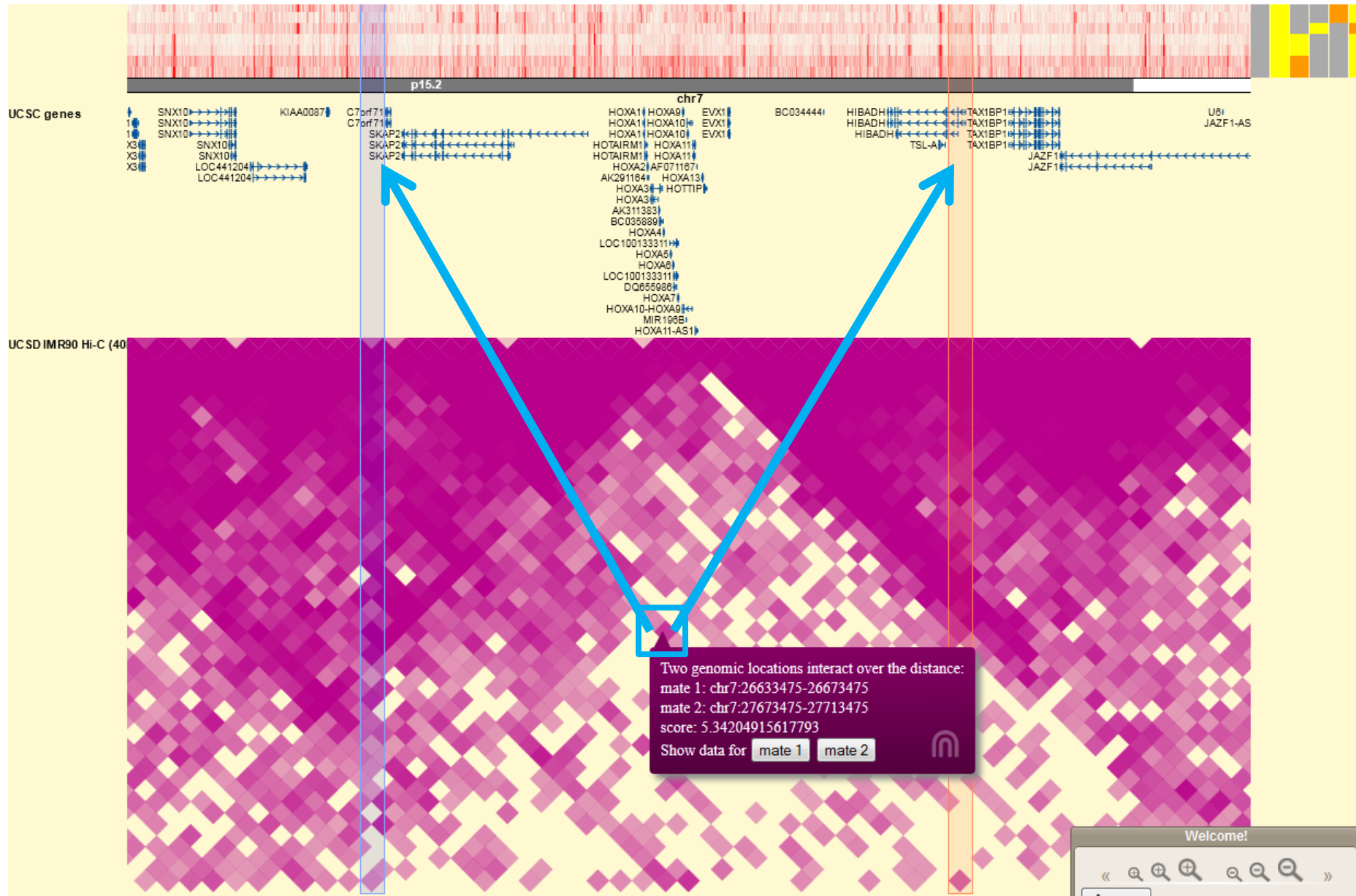
done



# Juxtaposition: Focus in on specific genomic features or genes



# Visualize genomic interactions



# Summary

- A *community resource of epigenomic maps* in a variety of primary human cells and tissues
- Data can be found at several sites, including NCBI, UCSC, and sites linked from <http://roadmapepigenomics.org>

## Thanks to...

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