



UNIVERSITY OF CALIFORNIA

SANTA CRUZ

Genomics
Institute

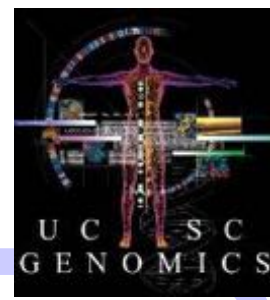


UCSC Genome Browser

Brian Lee
UC Santa Cruz

Genomics in Action Workshop
University of Oregon

@GenomeBrowser 



Acknowledgements

funding:

National Human Genome Research Institute (NHGRI)

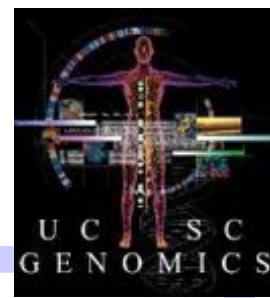
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Acknowledgements

UCSC Browser team

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UCSC = UC Santa Cruz

!= USC, USCS, UCSF, UCSD....



Browser Team



Overview Objectives

Site Overview

Site Architecture, Navigation and Configuration

Lesser Known Treasures

Multiple Highlights & Keyboard Shortcuts

BLAT across multiple Species

Gene Interactions Tool and Track

New Data Tracks, Formats and Tools

New CRISPR and GeneHancer Tracks

New Interact Data Format

New Short Links to Sessions & Public Sessions

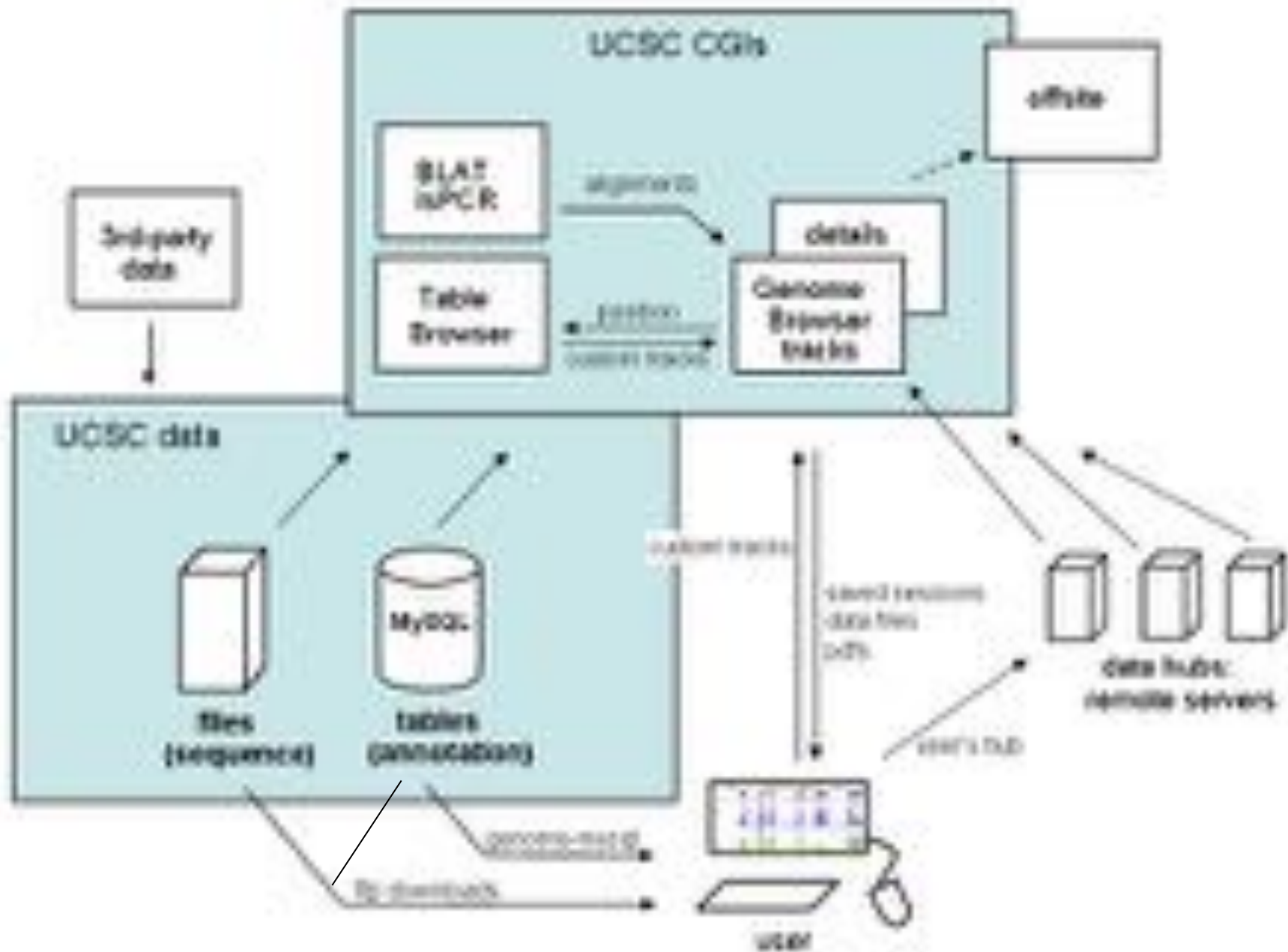
UCSC Genome Browser

**Display engine for genomic annotations.
Consistent interface across genomes.**

A tool for inquiry-driven discovery.

<http://genome.ucsc.edu>

architecture



architecture: GTEx

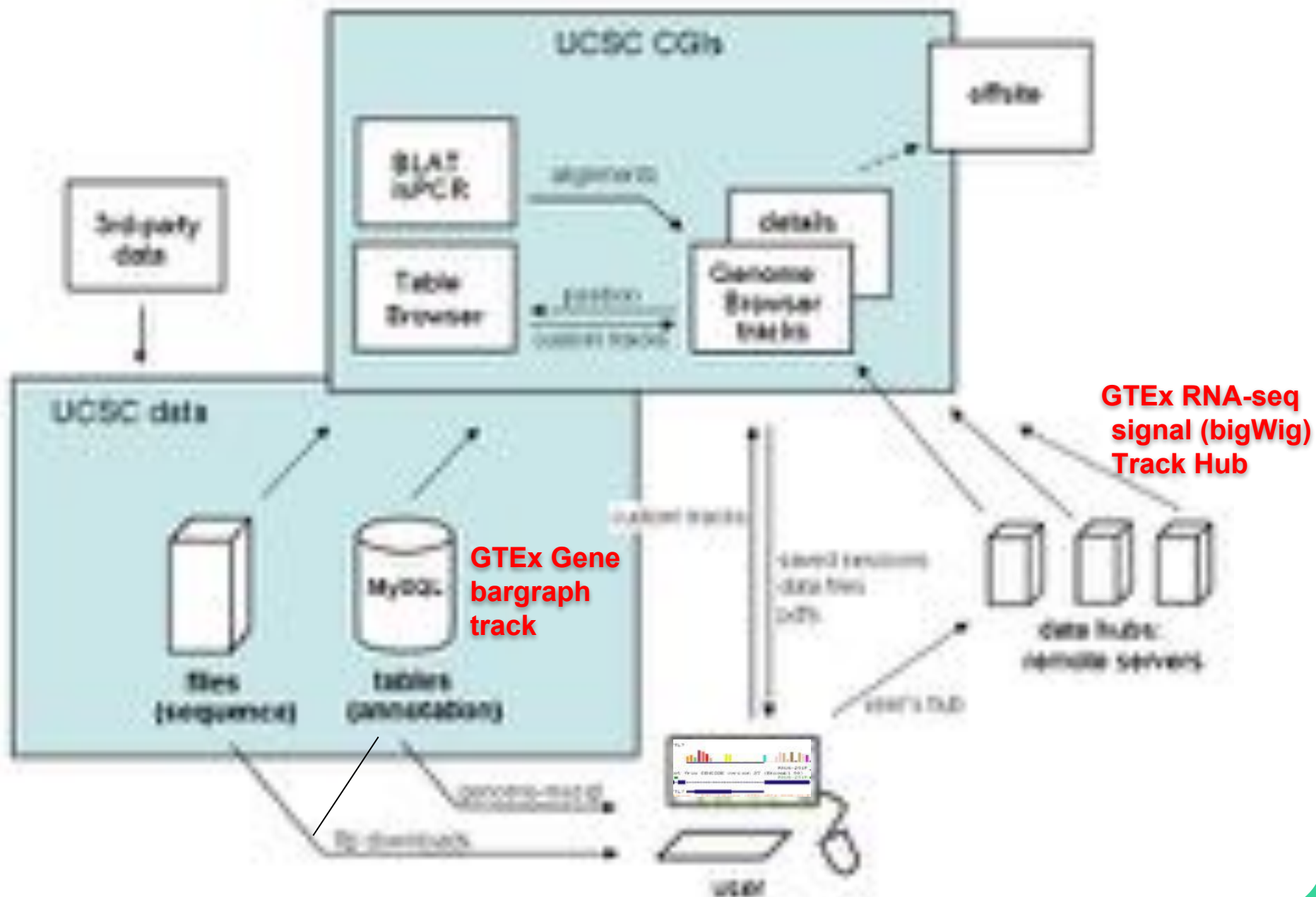
Top “GTEx Gene” track (available under Expression section) in bargraph display

- Summarizes Gene Expression in 53 tissues from GTEx RNA-seq of 8555 samples (570 donors) in one box

Lower individual signal tracks from “GTEx RNA-seq Signal Hub” (available from Public Hubs page)



architecture: GTEx



UCSC Genome Browser

Top Blue Bar Menu



The image shows the UCSC Genome Browser website. At the top, there is a navigation bar with the following items: Home, Genomes, Genome Browser, Tools, Videos, Downloads, My Data, Help, and About Us. A dropdown menu is open under the 'Genomes' link, showing the following options: Human (GRCh38.p12), Mouse (GRCm39), Mouse (GRCm38), Mouse (GRCm37), and Other. The main content area features a large blue DNA double helix graphic on the left and a 'Our tools' section on the right. The 'Our tools' section lists the following tools:

- Genome Browser: Interactive visualization genomic data
- BLAT: Rapidly align sequences to the genome
- Table Browser: Download data not in the Genome Browser database
- Variant Association Integrator: get functional effect predictions for variant calls
- Data Integrator: compare external data from the Genome Browser database
- Gene Sorter: Find genes that are similar by expression and other metrics
- Genome Browser's e-Query (EQE): Run the Genome Browser on other database servers
- Integrative PCR: Rapidly align PCR primer pairs to the genome
- LiftOver: Convert gene coordinates between assemblies

UCSC Genome Browser

Top Blue Bar Menu: Genomes a Gateway to Discover Multiple Assemblies

The screenshot displays the UCSC Genome Browser interface. At the top is a dark blue navigation bar with links for Home, Genome Browser, Tools, Mirrors, Downloads, My Data, Help, and About Us. Below this is a yellow header with two main sections: "Browse/Select Species" and "Find Position".

Browse/Select Species: This section features a row of six icons representing different species: Human, Mouse, Rat, Chicken, Zebrafish, and Fly. Below the icons is a search box labeled "Search" and a tree view of species. The tree view shows a hierarchy starting with "Mammals" and "Primates", with "Mus musculus" selected and highlighted in red.

Find Position: This section contains a "Mouse Genes Assembly" dropdown menu set to "May 2005 (Mus musculus (mMus2))". Below it is a "Position Search Term" input field with a "Go" button. A note below the search term says "Enter position, gene symbol or search term. Current position: chr1:100000000-100000000 (mMus2)".

Assembly Information: A blue header bar reads "Mus musculus - Genome Browser (mMus2) assembly". Below it, text provides details: "UCSC Genome Browser assembly ID: mMus2", "Sequencing/Assembly provider ID: Baylor College of Medicine and Broad Institute Mus2.0", "Assembly date: May 2005", "Accession ID: GCA_000004485.2", "NCBI Genome ID: XTT (Mus musculus)", "NCBI Assembly ID: 337822 (Mus2.0)", and "NCBI BioProject ID: 179617".

Search the assembly: A section with a bullet point: "By position or search term (Use the 'position or search term' box to find areas of the genome associated with many different attributes, such as a specific chromosome)".

Image: A photograph of a mouse is shown on the right side of the page, with the text "Mus musculus" and "Image courtesy: Science Photo Library" below it.

UCSC Genome Browser

Top Blue Bar Menu: Select Configure to see a list of all tracks for an assembly and alter display



The screenshot displays the UCSC Genome Browser interface. At the top, a dark blue navigation bar contains links for Home, Genome Browser, Tools, History, Downloads, My Data, Help, and About Us. Below this, a light blue header area includes a 'Browse/Select' dropdown menu, a 'Find Position' section with a search box for 'May 2005 Mouse (mm2) (NCBI)', and a 'Go' button. The 'Browse/Select' menu is open, showing options like 'Track Search' and 'Reset All View Settings'. Below the menu are several icons representing different track types. The main content area is divided into two columns. The left column shows a vertical track with a red bar and a mouse icon. The right column displays assembly information for 'Mouse (mm2) (NCBI)' and a small image of a mouse. A black arrow points from the text above to the 'Configure' option in the 'Browse/Select' menu.

UCSC Genome Browser

Home Genome Browser Tools History Downloads My Data Help About Us

Browse/Select

Track Search
Reset All View Settings

Order: Genes, RefSeq, UCSC, RepeatMasker, RepeatMasker, RepeatMasker

Order: Genes, RefSeq, UCSC, RepeatMasker, RepeatMasker, RepeatMasker

Find Position

Mouse (mm2) Assembly
May 2005 Mouse (mm2) (NCBI)

Position Search Term
Enter position, gene symbol or search terms
Current position: chr2:100000-100000 (100000-100000)

Mouse (mm2) Genome Browser - (mm2) assembly [View Assembly](#)

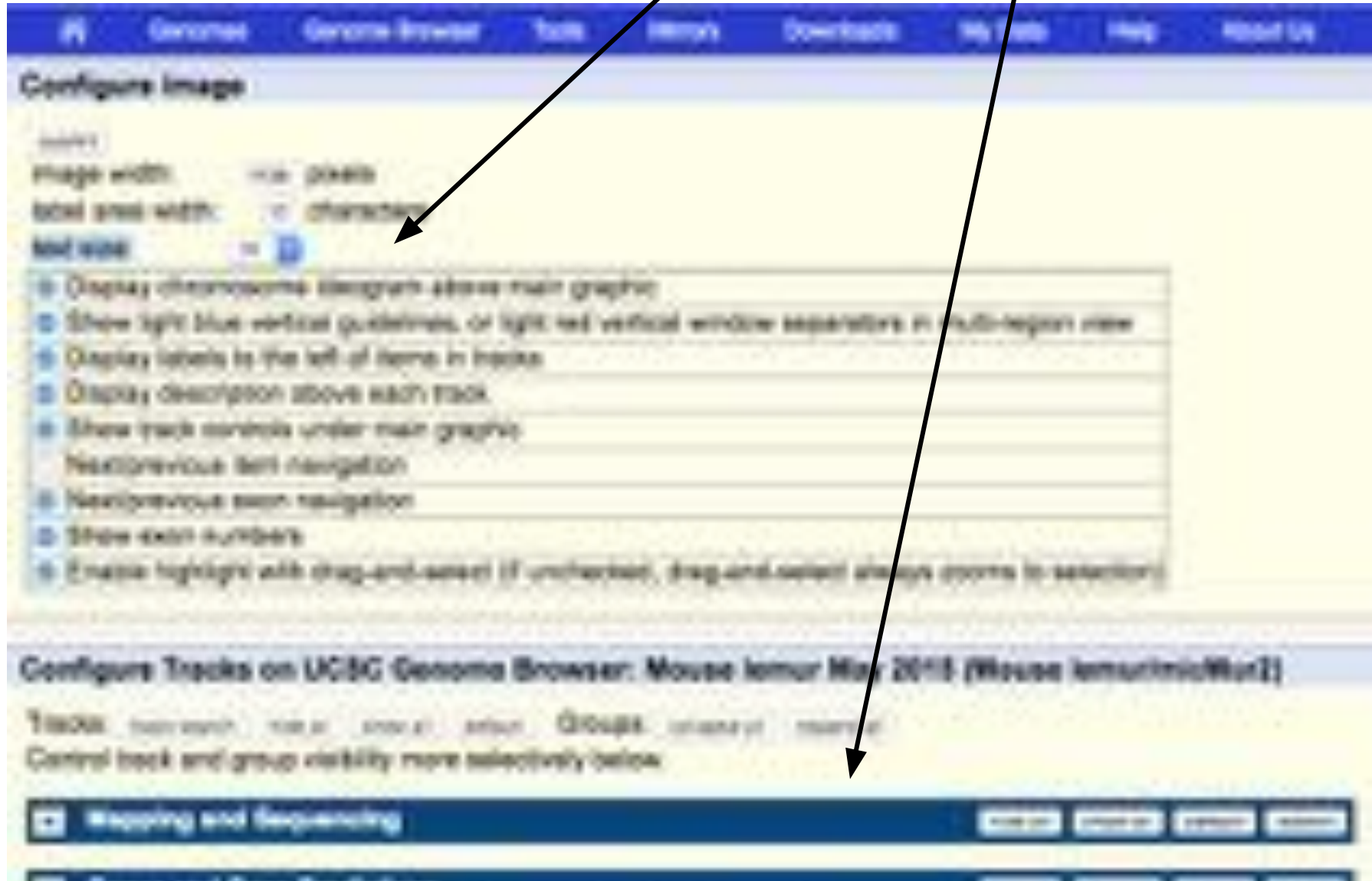
UCSC Genome Browser assembly (mm2)
Sequencing/Assembly provider ID: Baylor College of Medicine and Broad Institute (mm2_20)
Assembly date: May 2005
Accession ID: GCA_000145405.2
NCBI Genome ID: 777 (Mus musculus murinae)
NCBI Assembly ID: 127421 (mm2_20)
NCBI BioProject ID: 11967

Search the assembly

- By position or search term. Use the "position or search term" box to find areas of the genome associated with many different attributes, such as a specific chromosome

UCSC Genome Browser

Top Blue Bar Menu: Change settings like Text Size and see a list of all tracks on Bottom Blue Bars



UCSC Genome Browser

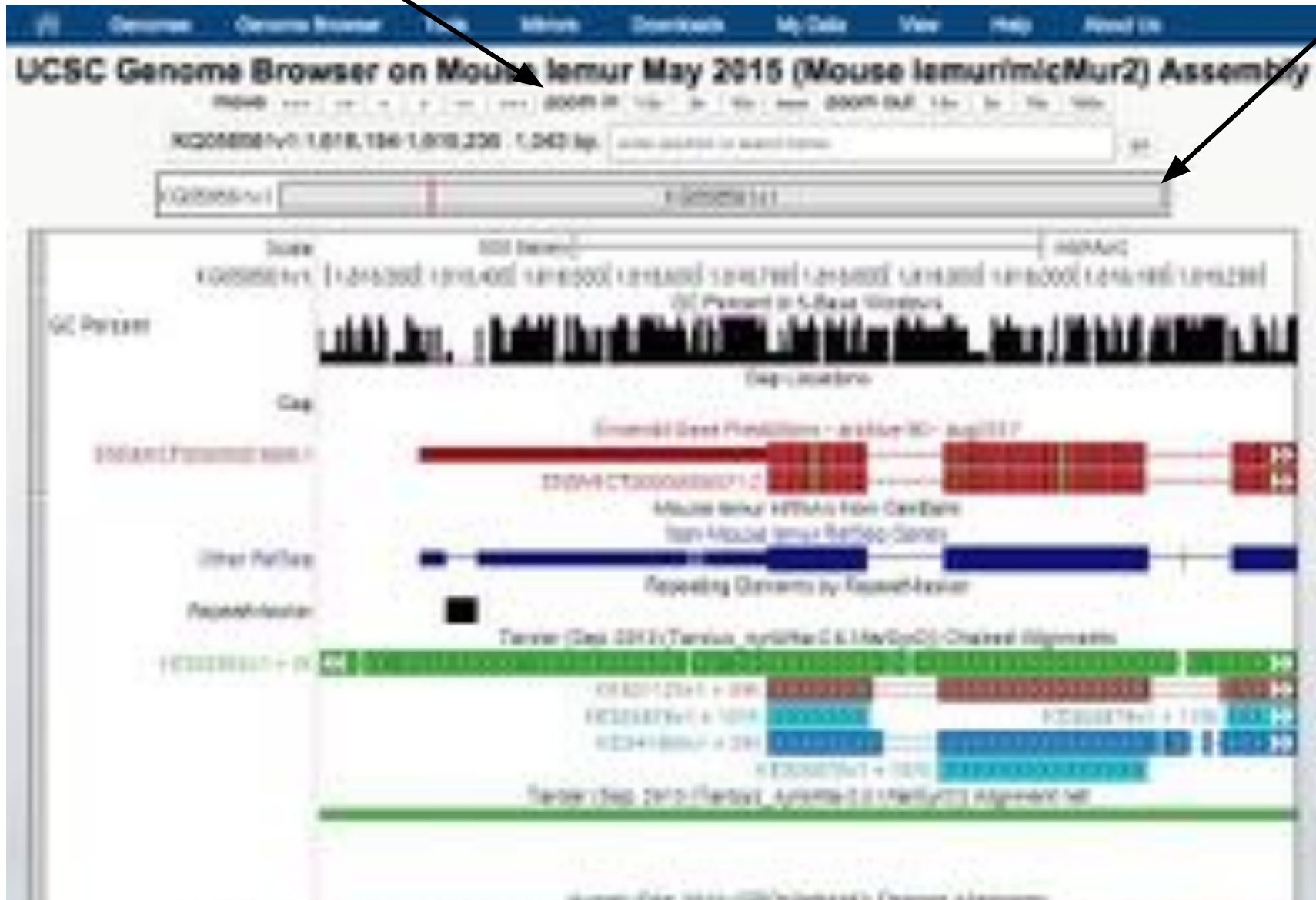
Bottom Blue Bars: Represent Groups Of Track Data (hide, dense, pack, full) Visibilities States

The image shows a screenshot of the UCSC Genome Browser interface. It features several track groups, each with a blue header bar and four visibility state buttons (hide, dense, pack, full). Two black arrows point to the 'hide' buttons of the 'Mapping and Sequencing' and 'Genes and Gene Predictions' track groups.

Track Group	Track Name	Track Description
Mapping and Sequencing	Gene Position	Chromosome position in bases. (Cross for zoom in 2x)
	Assembly	Assembly from Fragments
	Gap	Gap Locations
	CG Repeat	CG Repeat in 4-base Window
	BLAT	Alignment of BLAT (International Nucleotide Sequence Database Collaboration)
	RefSeq Acc	RefSeq Accession
	Repeat Masker	RepeatMasker Masked Regions (RepeatMasker)
	RepeatMasker	RepeatMasker Masked Regions (RepeatMasker)
Genes and Gene Predictions	Other RefSeq	Non-Mouse RefSeq Genes
	Ensembl RefSeq	Ensembl RefSeq gene predictions v4.1
	Ensembl Genes	Ensembl Genes
	Ensembl Genes	Ensembl Gene Predictions
	GeneMap	GeneMap Annotation Version 4
	Transcript Ensembl	GeneMap Ensembl Mappings Version 4
	Transcript RefSeq	GeneMap RefSeq Gene Mappings Version 4
	Transcript RefSeq	GeneMap RefSeq Gene Mappings Version 4
mRNA and EST		
Expression and Regulation		
Comparative Genomics		

UCSC Genome Browser

Browser: move region or zoom in or zoom out with top buttons or select chromosome region to jump



UCSC Genome Browser

Browser: Drag and Select to Zoom or to Create Highlights. Multiple highlights and colors are possible.

The image shows a screenshot of the UCSC Genome Browser interface. A dialog box titled "Drag and select" is overlaid on the left side. The dialog box contains the following instructions:

- Hold **Shift+drag** to show the details
- Hold **Alt+drag** to add a highlight
- Hold **Ctrl+drag (Windows)** or **Cmd+drag (Mac)** to zoom
- To cancel, press any key or drag mouse outside image
- Highlight the current position with a color in
- Clear all highlights with this - Clear highlights at a time in

Below the instructions, there is a "Highlight with:" section showing a yellow color swatch and a "Base" label. There is also a checkbox for "Don't show this again" and a "View" button. At the bottom of the dialog, there is a "Close" button.

The background of the image shows a genomic track with various colored highlights. A vertical color bar is visible on the left side of the track. The track itself contains several horizontal bars of different colors (red, purple, green, blue, yellow) representing genomic features. Two black arrows point from the text above to the dialog box and the color bar.

UCSC Genome Browser

Press ? to See **Shortcuts**. Use numbers **1 to 6** to quickly zoom to bp regions: **50 to 5,000,000 bp**

The screenshot shows the UCSC Genome Browser interface for Mouse lemur May 2015 (Mouse lemur(mMur2) Assemb. The 'Keyboard shortcuts' dialog box is open, displaying a list of shortcuts. The shortcuts are organized into two columns. The first column lists shortcuts for navigation and zooming, while the second column lists shortcuts for viewing and editing. The 'Zoom in 50x' shortcut is highlighted in green, and a black arrow points from the text above to it. Another black arrow points from the text above to the '?' icon in the top right corner of the dialog box.

Shortcut	Action	Shortcut	Action
left 10%	← [1]	track view	⌘ [v]
left 50% screen	← [5]	default tracks	⌘ [t]
left one screen	← [1]	default view	⌘ [v]
right 10%	→ [1]	hide all	⌘ [h]
right 50% screen	→ [5]	toggle tracks	⌘ [t]
right one screen	→ [1]	hide collections	⌘ [c]
right one screen	→ [1]	track help	⌘ [h]
zoom in 50x	⌘ [5]	configure	⌘ [c]
zoom in 3x	⌘ [3]	refresh	⌘ [r]
zoom in 10x	⌘ [1]	reset	⌘ [r]
zoom in five level	⌘ [5]	jump to position bar	⌘ [j]
zoom out 50x	⌘ [5]	send to end of track	⌘ [e]
zoom out 3x	⌘ [3]	zoom view	⌘ [v]
zoom out 10x	⌘ [1]	default view	⌘ [v]
zoom out 100x	⌘ [1]	view GMA	⌘ [g]
zoom to ...	⌘ [t]	reset all track settings	⌘ [r]
100x (1 level)	⌘ [1]	Tracks - BLAT	⌘ [b]
100x (3 levels)	⌘ [3]	Tracks - Table Browser	⌘ [t]
100x (6 levels)	⌘ [6]	Tracks - PCR	⌘ [p]
100x (13 levels)	⌘ [1]	My Sessions	⌘ [m]
100x (31 levels)	⌘ [3]	Public Sessions	⌘ [u]
Highlight all (FURY)	⌘ [a]	Clear all Highlights	⌘ [x]

UCSC Genome Browser

Top Blue Bar Tools Menu: Select Blat to search DNA queries across available Browsers



The screenshot displays the UCSC Genome Browser interface. At the top, a dark blue navigation bar contains links for Home, Genome Browser, Tools, Mirrors, Downloads, My Data, Help, and About Us. Below this, the 'Browse/Select Species' section is visible, featuring a 'FAVORITE SPECIES' row with icons for Human, Mouse, Rat, Zebrafish, and Drosophila, and an 'Enter species or assembly name' input field. A 'Tools' dropdown menu is open, listing various utilities such as 'Blat', 'Gene Browser', 'Genes & Annotations', 'Data Integrator', 'Gene Information', 'Gene Sorter', 'Genome Graphs', 'In Situ FISH', 'LiftOver', 'Variants', and 'Other Utilities'. The 'Blat' option is highlighted in blue. To the right of the menu, a search area is visible with a 'Position' input field containing 'chr1:100000000-100000000', a 'Search Term' input field, and a search button. Below the search area, there is a section for 'Genome Browser assembly (ID: hg19)' and a small image of a mouse.

UCSC Genome Browser

Top Blue Bar Tools Menu: Select Blat to search DNA queries across available Browsers

The screenshot shows the UCSC Genome Browser interface for a BLAT search. At the top, a blue navigation bar contains links for Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, and Help. Below this, the page title is "Mouse lemur BLAT Search". The main heading is "BLAT Search Genome". Underneath, there are several input fields and dropdown menus: "Genome:" with a dropdown menu showing "Search ALL" selected, "Assembly:" with a dropdown menu showing "mm10 (2011 mouse assembly)", "Query type:" with a dropdown menu showing "any", "Sort output:" with a dropdown menu showing "any", and "Output type:" with a dropdown menu showing "html". Below these fields is a large text area containing a DNA sequence. At the bottom of the page, there are navigation controls including "query" and "10/1000/1000" and "1/1000/1000".

Paste in a sequence (can rename) and select Search ALL to see hits across multiple species (otherwise searches just the current species)

UCSC Genome Browser

Top Blue Bar Tools Menu: Select Blat to search DNA queries across available Browsers



ALL Genomes BLAT Results

Click the IDs in the Assembly column to see the full BLAT output for that Database

Name	Genome	Assembly	Hits	Chrom
SearchingThisSequence	Mouse-embry	mmMus2	308	#100885604v1
SearchingThisSequence	BufoBufo	bfBufo2	143	GLBT1881
SearchingThisSequence	Alpaca	alpAlp2	142	#2853288T
SearchingThisSequence	Tree shrew	tsTree	137	alpAlp2_143001.1-48178
SearchingThisSequence	Dogfish	dfDogf	133	J-4079402
SearchingThisSequence	White whale	whWhal	128	#10307896
SearchingThisSequence	Bonobo	bonBon2	127	chrT
SearchingThisSequence	Chimp	chiChi2	126	chrT
SearchingThisSequence	Golden shrew-norway	gsNorw	125	#102697814v1
SearchingThisSequence	Gibbon	giGibo	123	J-8846002
SearchingThisSequence	Cat	caCat2	122	chrE3
SearchingThisSequence	Rabbit	rbRab2	122	chr6
SearchingThisSequence	Horse	hpHors	121	chr15
SearchingThisSequence	Quail	quQuai	121	chrT

BLAT ALL allows navigating across multiple species based on specific sequence similarity

UCSC Genome Browser

Top Blue Bar Tools Menu: Gene Interactions option brings you to text-mined protein interactions

The screenshot displays the UCSC Genome Browser interface. At the top, a dark blue navigation bar contains the following links: Home, Genomes, Genome Browser, Tools, History, Downloads, My Data, Help, and About Us. Below this bar, the main content area is divided into several sections. On the left, there is a 'Browse/Select Species' section with icons for various species and a search box. In the center, a 'Tools' menu is open, listing various utility tools. The 'Gene Interactions' option is highlighted in blue, and a black arrow points from the text above to this option. To the right of the menu, there is a 'Position' section with a search box containing '15-Mouse (mm9)Mus2' and a 'Go' button. Below the search box, there is a 'Search Term' section with a search box containing 'UCSC Genome Browser - mm9Mus2 assembly'. At the bottom right, there is a small image of a mouse and a 'My Recent Assemblies' section.

Tools Menu:

- Bit
- BigWig Browser
- Visualize Associated Intergenes
- Gene Integrator
- Gene Interactions**
- Gene Locator
- Genome Graphs
- hg18toMCE
- hg19to
- hg20to
- Other Utilities

Position:

Search Assembly: 15-Mouse (mm9)Mus2

Go

Search Term:

UCSC Genome Browser - mm9Mus2 assembly

UCSC Genome Browser - mm9Mus2 assembly

UCSC Genome Browser assembly ID: mm9Mus2
hg19Assembly greater than 1000 bp (College of
1 and Broad Institute Mouse_20
as of Mar 2015)

Accession ID: GCA_000161440.2
NCBI Genome ID: 277 (Mus musculus)
NCBI Assembly ID: 329401 (Mus_20)
NCBI BioProject ID: 11947

Search the assembly:

- By position or search terms. Use the "position or search terms" box to find areas of the genome associated with many different attributes, such as a specific developmental

UCSC Genome Browser

Top Blue Bar Tools Menu: Gene Interactions option brings you to text-mined protein interactions

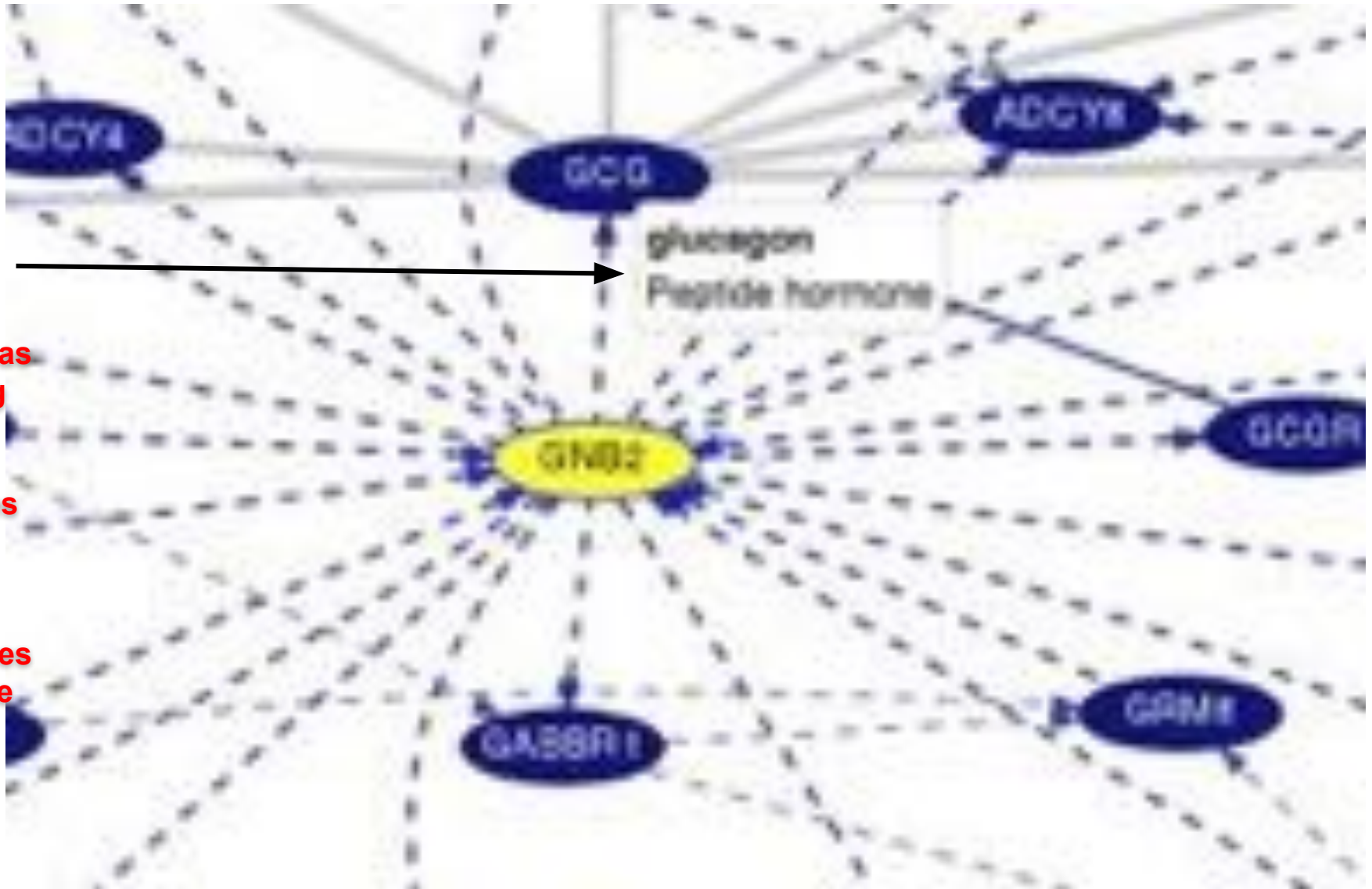


UCSC Genome Browser

Top Blue Bar Tools Menu: Gene Interactions option brings you to text-mined protein interactions

Putting the mouse over Genes will display information as will mousing over lines.

Clicking lines shows text-mining details or clicking genes recenters the graph.



UCSC Genome Browser

Lower Blue Bars: Different Track Groups including CRISPR and Gene Interactions and GeneHancer

The screenshot displays the UCSC Genome Browser interface with several track groups visible:

- Mapping and Sequencing**: Includes tracks like GENCODE v20, MGI Probed, Other Probes, etc.
- Genes and Gene Predictions**: Includes tracks like GENCODE v20, MGI Probed, Other Probes, etc.
- Phenotype and Literature**: Includes tracks like OMIM Alleles, Cancer Gene Expr..., ClinGen DNVs, ClinGen Variants, ClinGen CNVs, COSMIC Regions, etc.
- mRNA and EST**: Includes tracks like ENCODE RefSeq, etc.
- Expression**: Includes tracks like ENCODE RefSeq, etc.
- Regulation**: Includes tracks like ENCODE RefSeq, etc.
- Comparative Genomics**: Includes tracks like Conservation, etc.

Scrolling down for Human hg38 Tracks shows available tracks

Under Phenotype Literature section the Gene Interactions can be turned on by switching hide to full and clicking refresh.

UCSC Genome Browser

Lower Blue Bars: Different Track Groups including CRISPR and Gene Interactions and GeneHancer

The screenshot displays the UCSC Genome Browser interface with several track groups visible. The tracks are organized into sections: 'Mapping and Sequencing', 'Genes and Gene Predictions', 'Phenotype and Literature', 'miRNA and EDIT', 'Expression', 'Regulation', and 'Comparative Genomics'. The 'Genes and Gene Predictions' section includes tracks for GENCODE v20, MGI Probed, Other Probes, RefSeq, AUGUSTUS, and GCODE. The 'Phenotype and Literature' section includes tracks for OMIM Alleles, Cancer Gene Expr., ClinGen DNVs, ClinGen Variants, Coriell CNVs, and COSMIC Regions. The 'Regulation' section includes tracks for GENCODE Regulation, Genes and Gene Predictions, and Gene Interactions. The 'Comparative Genomics' section includes tracks for Conservation, Cons. 2, Cons. 20, Cons. 20 Promoter, Phylo-P, and Phylo-P Conserved.

Under Genes and Gene Predictions section you can find the CRISPR tracks.

Under Regulation section you can find the new GeneHancer tracks

UCSC Genome Browser

GeneHancer track uses new interact format to display human regulatory elements (enhancers and promoters) and their inferred target genes. CRISPR track shows color-coded predicted target sites.

GeneHancer has a track to denote enhancers and promoters and then an Interactions track to graphically show associations with nearby genes.

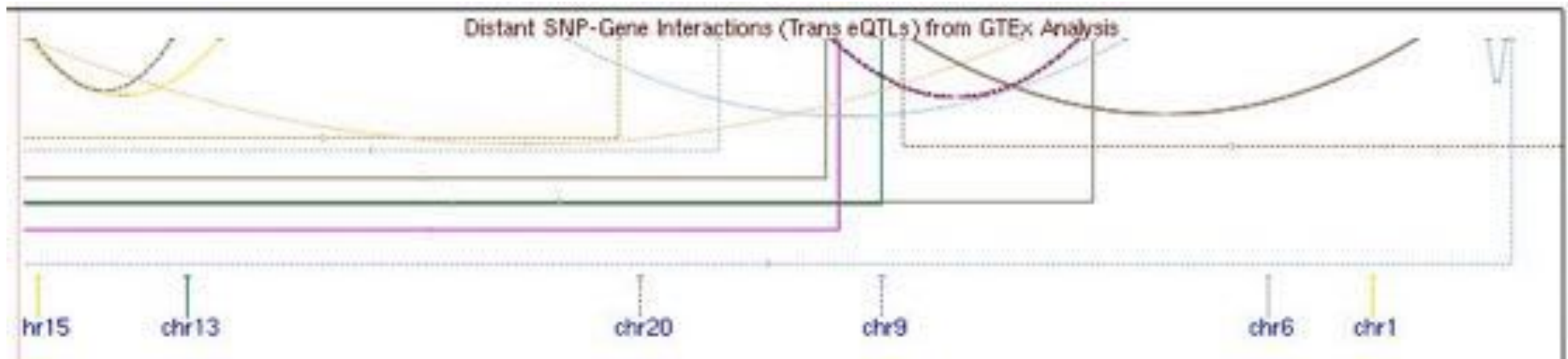
The CRISPR track has colored targets (green/yellow/red) annotated for predicted cleavage around coding regions with details of potential off-targets listed.



Interactions

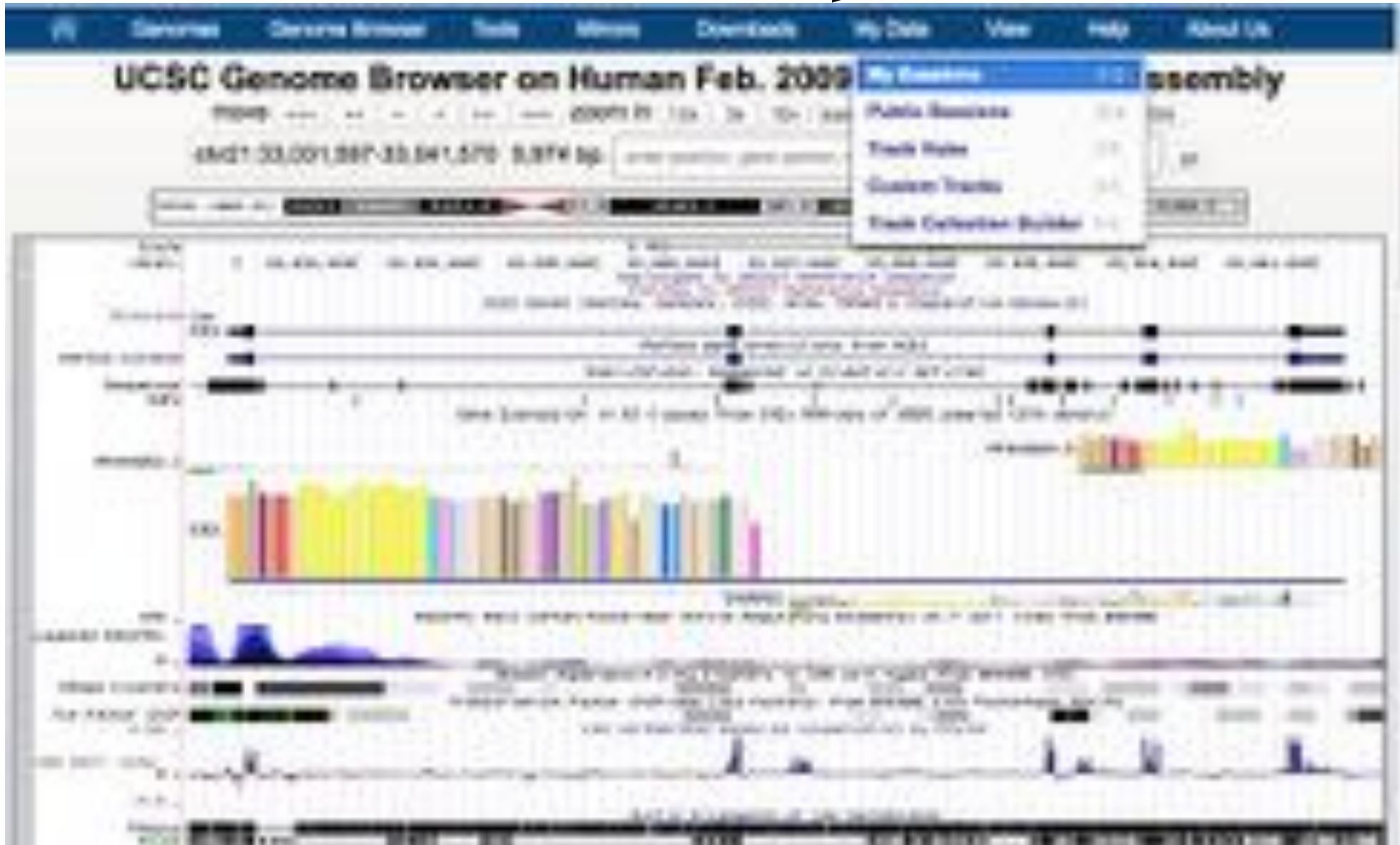
New data format

New data display



UCSC Genome Browser

My Data Top Blue Bar Menu



UCSC Genome Browser

My Data Top Blue Bar Menu: My Sessions Allows You to Create a Snapshot of Your Browsing

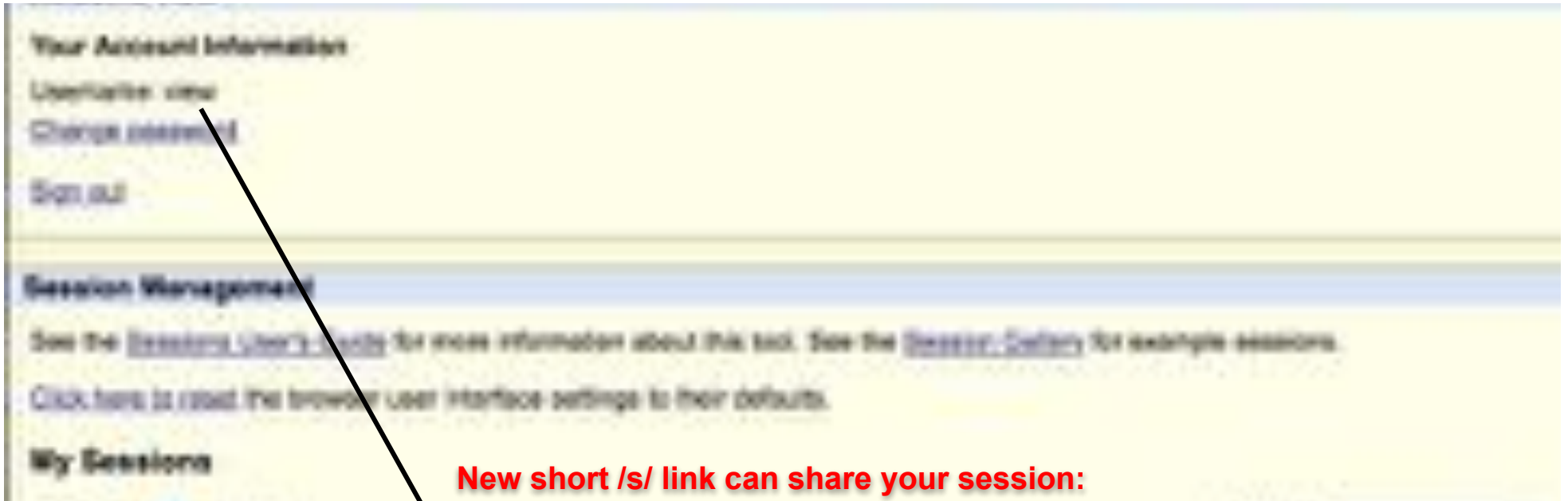
The screenshot shows the 'My Sessions' page in the UCSC Genome Browser. At the top, under 'Your Account Information', there are links for 'User name view', 'Change password', and 'Sign out'. A red arrow points from the text 'Create an account username and then save a session name as you are browsing the site to return to views of data later.' to the 'User name view' link. Below this is the 'Session Management' section with explanatory text and a link to reset browser settings. The main part of the page is a table titled 'My Sessions' showing a list of saved sessions. A red arrow points from the same text to the 'session name (click to load)' column of the table.

Create an account username and then save a session name as you are browsing the site to return to views of data later.

session name (click to load)	created on	assembly	view/ds details	delete this session	share with others?	post in public listing?	send to mail
AssemblySubset	2018-10-08	hg19	view	delete	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
GeneSubset	2018-10-08	hg19	view	delete	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
MoleculeEngineering	2018-10-08	hg19	view	delete	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
Expresscc	2018-10-08	hg19	view	delete	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
Clinical	2018-10-10	hg19	view	delete	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
Clinical3p	2018-10-10	hg19	view	delete	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
Clinical2set	2018-10-10	hg19	view	delete	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email

UCSC Genome Browser

My Data Top Blue Bar Menu: My Sessions Allows You to Create a Snapshot of Your Browsing



**New short /s/ link can share your session:
<http://genome.ucsc.edu/s/yourUserName/yourSessionName>**

<http://genome.ucsc.edu/s/view/AssemblySupport>
<http://genome.ucsc.edu/s/view/GeneSupport>
<http://genome.ucsc.edu/s/view/MolecularEngineering>
<http://genome.ucsc.edu/s/view/Expression>
<http://genome.ucsc.edu/s/view/Clinical>
<http://genome.ucsc.edu/s/view/ClinicalLite>
<http://genome.ucsc.edu/s/view/ClinicalZoom>

UCSC Genome Browser

My Data Top Blue Bar Menu: Public Sessions Access to Community Sharing

The image shows a screenshot of the UCSC Genome Browser interface. At the top, there is a navigation bar with links for 'Home', 'Genome Browser', 'Tools', 'Miscellaneous', 'Downloads', 'My Data', 'View', 'Help', and 'About Us'. Below this, the main title reads 'UCSC Genome Browser on Human Feb. 2009'. A search bar contains the coordinates 'chr21:33,001,000-30,041,000 9,978 bp'. A dropdown menu is open under the 'My Data' link, with 'Public Sessions' highlighted. Other options in the menu include 'Track Hubs', 'Event-based Tracks', and 'Track Collections Builder'. The main content area displays a genomic track with various annotations, including gene models, tracks, and a bar chart.

Search Public Sessions

Search box “**SessionView**” (sorts to sessions with this unique tag)

- Click on image to jump to session (sort by newest first)

Add your own Public Sessions via the “My Sessions” page (add descriptions to make them discoverable)



The screenshot displays a web interface for searching public sessions. At the top, there is a search bar and a 'Sort by' dropdown menu. An arrow points to the 'Sort by' dropdown menu. Below the search bar, there are two columns of session cards. Each card contains a thumbnail image, a description, and session details.

Sort by: [Dropdown menu]

Show: [Dropdown menu]

Session Properties

Description: This sessionView is a collection of tracks centered around large genetic variants (CNVs). The session is organized with gene annotations at the top, followed by the [CGI/Strat Var track](#), which displays variants observed in healthy individuals. The rest of the tracks include different databases that reveal large variants linked to disease phenotypes. The report displayed is a 2Mbp region on chr1 with many somatocopy variants present.

Author: view

Session Name: VariatorCNVs

Genome Assembly: hg18

Created Date: 2010-12-18

Views: (5)

Description: This sessionView is a collection of tracks centered around clinical significance. Featured tracks include gene annotations, SNPs, CNVs, [CIVIC](#) (a cancer mutation database and our publications track built by mining sequences and SNPs in publications), and the displayed region is focused around the HTT gene, responsible for Huntington's disease and Loss of Heterozygosity syndrome. Two similar sessions are also available: [ClinicalZoom](#) which shows the 10-resolution CAG repeat linked to Huntington's disease, as well as [ClinicalLite](#) which has a reduced number of tracks for increased clarity.

Author: view

Session Name: Clinical

Training and Mailing List

YouTube training channel:  bit.ly/ucscVideos

On-site workshops (training link on main page):

[http:// genome.ucsc.edu/training/](http://genome.ucsc.edu/training/)

Mailing list (training link on main page):

[http:// genome.ucsc.edu/contacts.html](http://genome.ucsc.edu/contacts.html)

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Ignite your career at the UC Santa Cruz Genomics Institute. Begin a new job as a software engineer, bioinformatician, computational biologist or data analyst. And when you live and work in Santa Cruz, you'll enjoy the best of California.