

UCSC Genome Browser

WHAT IS IT?

Display engine for genomic annotations.

Consistent interface across genomes.

A tool for inquiry-driven discovery.

WHY USE IT?

To explore potential comparative genomics to gain insights in other species

UCSC Genome Browser

PAG 2020 Saturday Session Cattle/Sheep/Goat 1 George E. Liu Animal Genomics and Improvement Laboratory, USDA-ARS

Comparative Epigenomics and Genotype-Phenotype Association Analyses Revealed Conserved Genetic Architecture underlying Complex Traits between Cattle and Human



Dr. Liu's lab examined comparative genomics around the histone marks and found that they could transfer cell-type-specific information from the human data to infer similar issues about genes related to certain diseases. A specific example was PIK3CG, a gene high specifically expressed in mononuclear cells was significantly associated with both age-at-menopause in human and daughter-still-birth in cattle.

An example of viewing this region on the UCSC Browser:

http://genome.ucsc.edu/s/brianlee/Human_PIK3CG

UCSC Genome Browser

PAG 2020 Sunday Session Genomics of Non-Classical Model Animals Claudio V. Mello Oregon Health and Science University

What Comparative Studies of Parrot Genomes Can Teach Us about Longevity, Large Brains and Cognition



Dr. Mello identified genomic features under selection in parrots and other long-lived birds that included telomerase activity (TERT), DNA damage repair, control of cell proliferation, cancer, immunity, and anti-oxidative mechanisms. His group also identified many brain-expressed, parrot-specific paralogs with known functions in neural development or vocal-learning brain circuits seen in humans (AUS2). Slide from supplemental materials in his paper.

UCSC Genome Browser

PAG 2020 Sunday Session Genomics of Non-Classical Model Animals Claudio V. Mello Oregon Health and Science University

What Comparative Studies of Parrot Genomes Can Teach Us about Longevity, Large Brains and Cognition



An example of viewing this region on the UCSC Browser showing similar alignment information in the conservation track around human AUTS2 as in Dr. Mello's supplemental slides:

http://genome.ucsc.edu/s/brianlee/Human_AUTS2

UCSC Genome Browser

PAG 2020 Sunday Session Genomics of Non-Classical Model Animals Bridgett vonHoldt Princeton University

Everyone Is Your Friend! the Molecular Architecture of Hypersocial Canines



Dr. vonHoldt analyzed wolf and dog populations and discovered a 5-Mb genomic region on chromosome 6 in dogs previously found to be under positive selection in domestic dog breeding. They gathered data on friendliness between a captive wolf and pet dog populations and then examined variants. The region affected by structural variants associated with the exuberant sociability of domestic dogs related to a gene WBSOR17 on chr7 in humans linked to Williams-Beuren syndrome (WBS), a multisystem congenital disorder characterized by hypersocial behavior. Humans with this mutation have a lack of stranger danger and are overly cheerful. An example of viewing this region on the UCSC Browser:

http://genome.ucsc.edu/s/brianlee/Human_WBSOR17

UCSC Genome Browser

PAG 2020 Poster Session Hao Meng et al. Peking-Tsinghua Center for Life Sciences, Peking University

*Morphology and Genetics of Kinked Tails of Domestic Cats (*Felis catus*) in East and Southeast Asia*



Hao Meng and colleagues investigated the morphology and genetics of kinked tails in cats. Mutations in coding sequences (CDS) of T and HES7 were identified correlated to the short tails in Manx and Japanese bobtail breeds as well as some feral cats in Asia, However, about one third of short-tailed cats in China do not carry either variant. The poster described a new 1.6 Mb region with non-synonymous mutations were seen, suggesting changes in regulatory regions, the poster concluded.

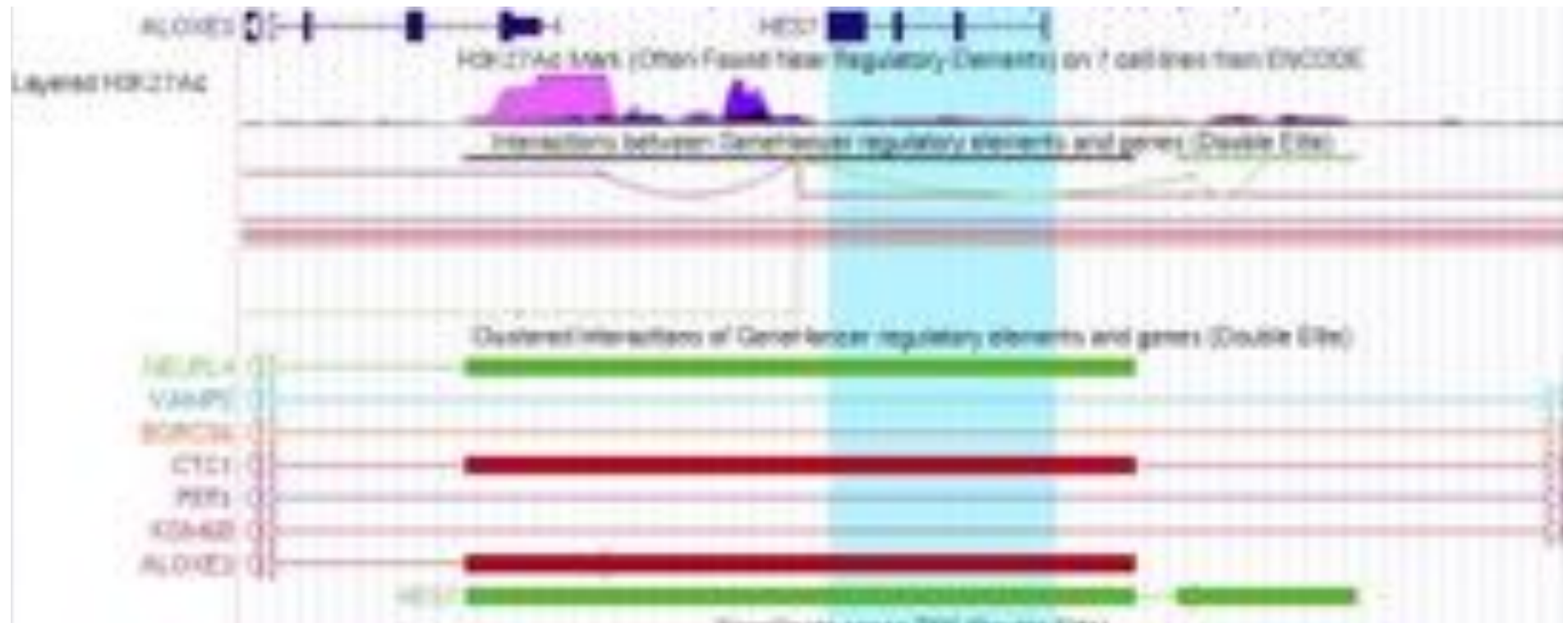
An example of viewing this region on the UCSC Browser with the regulatory Gene Interactions track turned on:

http://genome.ucsc.edu/s/brianlee/Human_HES7

UCSC Genome Browser

PAG 2020 Poster Session Hao Meng et al. Peking-Tsinghua Center for Life Sciences, Peking University

*Morphology and Genetics of Kinked Tails of Domestic Cats (*Felis catus*) in East and Southeast Asia*



In humans the interactions track seem to suggest this region around HES7 has many long distant interactions spanning across it from distant enhancers.

An example of viewing this region on the UCSC Browser with the regulatory Gene Interactions track turned on.

http://genome.ucsc.edu/s/brianlee/Human_HES7

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, listing: Human (GRCh38.p11), Mouse (MGI 2019.01), Mouse (MGI 2019.02), Mouse (MGI 2019.03), 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 of genomic data
- BLAT: Rapidly aligns sequences to the genome
- Table Browser: Download data not in the Genome Browser database
- Variant Annotation 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 factors or genes
- 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 light blue 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, Zebrafish, Drosophila, and Yeast. Below the icons is a search box labeled "Search" and a list of species. The "Mouse" species is highlighted in red, and a mouse icon is visible in the left sidebar.

Find Position: This section contains a "Mouse Genes Assembly" dropdown menu set to "May 2015 (Mouse Genes (mMcMur2))". Below it is a "Position Search Term" input field with a "Go" button. A note indicates that the search term can be a gene symbol, a chromosome location, or a RefSeq ID.

Assembly Information: A blue header bar reads "Mouse Genes - Genome Browser (mMcMur2) assembly". Below it, the following details are listed:
UCSC Genome Browser assembly ID: mMcMur2
Sequencing/Assembly provider ID: Baylor College of Medicine and Broad Institute Mouse_2.0
Assembly date: May 2015
Accession ID: GCA_000004481.2
NCBI Genome ID: XXI (Mus musculus)
NCBI Assembly ID: 317527.2 (Mus_2.0)
NCBI BioProject ID: 179617

Search the assembly: A note explains that the search term can be a gene symbol, a chromosome location, or a RefSeq ID to find areas of the genome associated with specific attributes.

Image: A photograph of a mouse is shown on the right side of the page.

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 the following menu items: Home, Genome, Genome Browser, Tools, History, Downloads, My Data, Help, and About Us. The 'Genome Browser' menu is currently open, showing a 'Configure' option highlighted in blue. An arrow points from the text above to this 'Configure' option. Below the navigation bar, the main content area is divided into several sections. On the left, there is a 'Browse/Select Assembly' section with a 'Track Search' dropdown and a 'Reset All View Settings' button. Below this are several icons representing different tracks: 'Genes', 'Repeats', 'SNPs', 'Variants', 'Phylo-P', and 'Phylo-P'. A search box for 'Enter genomic coordinates here' is also present. The right side of the interface features a 'Find Position' section with a dropdown menu for 'Mouse (mm10) Assembly' set to 'May 2015 (Mouse Genomes Project)'. Below this is a 'Position Search Term' input field and a 'Go' button. The main content area shows a track for 'Mouse (mm10) Genome Browser - (mm10) assembly' with a 'View Settings' button. Below this, there is a section for 'UCSC Genome Browser assembly (mm10)' with details: 'Sequencing/Assembly provider ID: Baylor College of Medicine and Broad Institute (mm10)', 'Assembly date: May 2015', 'Accession ID: GCA_000145405.2', 'NCBI Genome ID: 777 (Mus musculus murinae)', 'NCBI Assembly ID: GCF_000001635.1 (mm10)', and 'NCBI BioProject ID: 11997'. A small image of a mouse is shown to the right of this text. At the bottom, there is a 'Search the assembly' 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'.

UCSC Genome Browser

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

The screenshot displays the UCSC Genome Browser interface. At the top, a blue navigation bar contains the following menu items: Home, Genome, Genome Browser, Tools, History, Downloads, My Data, Help, and About Us. Below the navigation bar, the page is divided into two main sections.

The first section is titled "Configure Image" and contains several configuration options:

- Image width: 1024 pixels
- total area width: 1024 characters
- font size: 12
- Display chromosome diagram above main graphic
- Show light blue vertical guidelines, or light red vertical window separators in multi-region view
- Display labels to the left of items in tracks
- Display description above each track
- Show track controls under main graphic
- Next/previous left navigation
- Next/previous zoom navigation
- Show exon numbers
- Enable highlight with drag-and-select (if unchecked, drag-and-select always zooms to selection)

The second section is titled "Configure Tracks on UCSC Genome Browser: Mouse lemur May 2018 (Mouse lemur/murMus1)" and includes a "Tracks" section with a "Group" dropdown menu. Below the tracks, there is a "Control track and group visibility more selectively below:" section. At the bottom of the page, a blue bar displays the "Mapping and Sequencing" track, which is currently expanded to show its sub-tracks.

Two black arrows point from the text above to specific elements in the screenshot: one points to the "font size" dropdown menu in the "Configure Image" section, and the other points to the "Group" dropdown menu in the "Configure Tracks" section.

UCSC Genome Browser

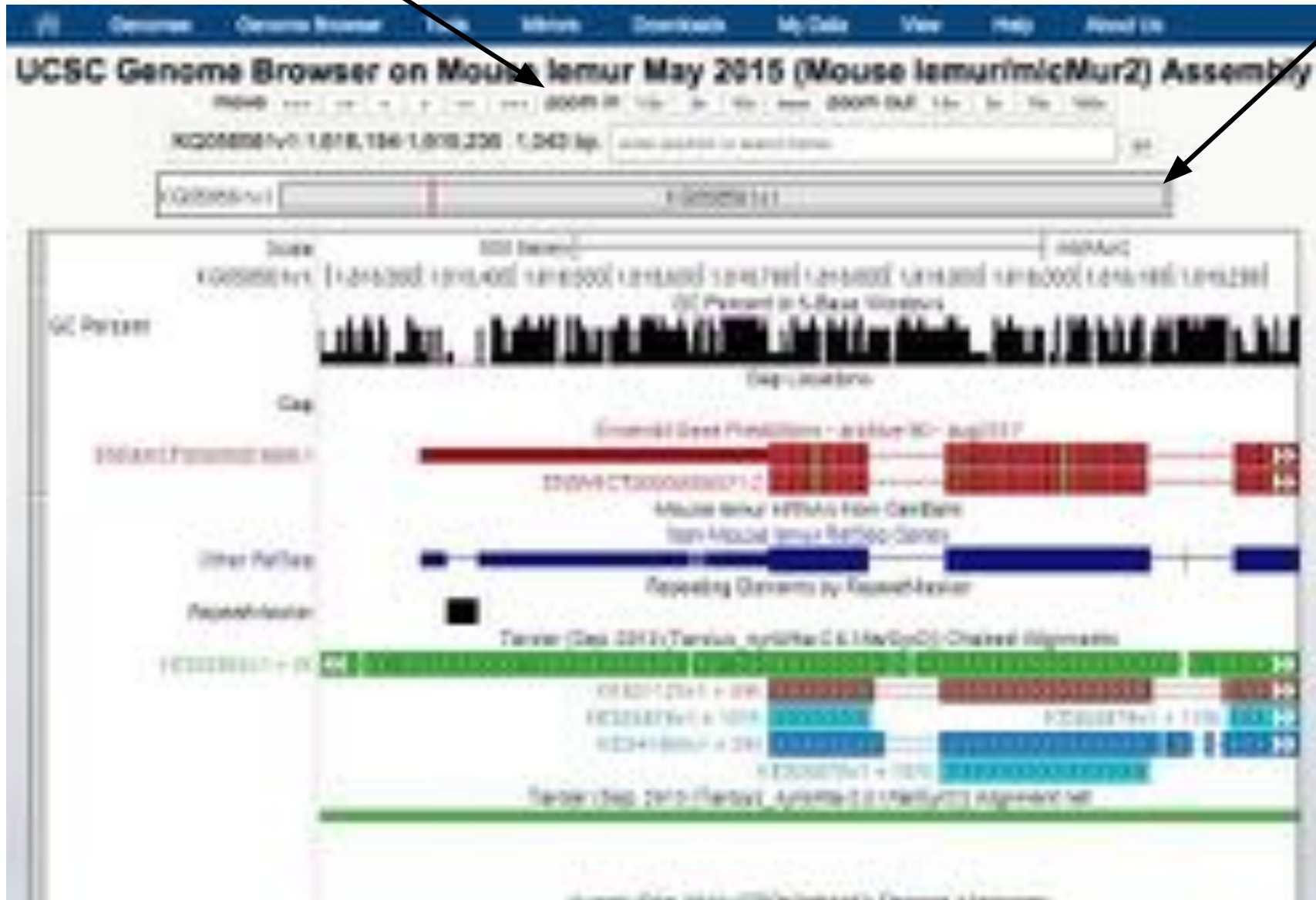
Bottom Blue Bars: Represent Groups Of Track Data (hide, dense, pack, full) Visibilities States

The image shows a screenshot of the UCSC Genome Browser interface. At the top, there are four blue bars representing track visibility states: 'hide', 'dense', 'pack', and 'full'. Below these are several track groups, each with a blue bar and four visibility state buttons. Two black arrows point to the blue bars for the 'Mapping and Sequencing' and 'Genes and Gene Predictions' 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	Repeat Masker (Repeat Masker)
	Repeat Masker	Repeat Masker (Repeat Masker)
Genes and Gene Predictions	Other RefSeq	Non-Mouse RefSeq Genes
	Ensembl RefSeq	Ensembl RefSeq gene predictions v4.1
	Ensembl Gene	Ensembl Genes
	Ensembl Gene	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
RNA 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 of the browser window. 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 color" section with a dropdown menu set to "Yellow" and a color palette. There is also a checkbox for "Don't show this again" and "Remember via View - Ctrl".

The background of the browser shows a genomic track with various colored bars representing different data tracks. Two black arrows point from the text above to the dialog box and the color palette in the screenshot.

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 lemurim(Mur2) Assemb. The 'Keyboard shortcuts' dialog box is open, displaying a list of shortcuts. The shortcuts are organized into two columns. The first column includes shortcuts for navigation (left/right 10%, 50%, 100% screen) and zooming (zoom in 50x, 100x, 200x, 300x, 400x, 500x, 1000x, 2000x, 3000x, 4000x, 5000x). The second column includes shortcuts for zooming to specific regions (jump to position bar, send to uncentered view) and other navigation functions (zoom out, zoom in, zoom to, zoom to ..., view GMA, view all track settings, tracks - BLAT, tracks - Table Browser, tracks - PCR, My Sessions, Public Sessions, Clear all Highlights).

Shortcut	Key	Shortcut	Key
left 10%	← [10]	zoom out	o (ctrl) ←
left 50% screen	← [50]	default tracks	d (ctrl) ←
left one screen	← [1]	default view	d (ctrl) ←
right 10%	→ [10]	hide all	h (ctrl) ←
right 50% screen	→ [50]	toggle tracks	t (ctrl) ←
right one screen	→ [1]	track collections	c (ctrl) ←
right one screen	→ [1]	track table	o (ctrl) ←
zoom in 50x	+= [50]	configure	o (ctrl) ←
zoom in 100x	+= [100]	refresh	r (ctrl) ←
zoom in 200x	+= [200]	jump to position bar	j (ctrl) ←
zoom in 300x	+= [300]	send to uncentered view	u (ctrl) ←
zoom in 400x	+= [400]	zoom view	z (ctrl) ←
zoom in five level	+= [5]	default view	d (ctrl) ←
zoom out 1.5x	-= [1.5]	view GMA	v (ctrl) ←
zoom out 2x	-= [2]	Reset all track Settings	r (ctrl) ←
zoom out 3x	-= [3]	Tracks - BLAT	t (ctrl) ←
zoom out 50x	-= [50]	Tracks - Table Browser	t (ctrl) ←
zoom out 100x	-= [100]	Tracks - PCR	t (ctrl) ←
zoom to ...	+= [t]	My Sessions	m (ctrl) ←
Zoom (1 screen)	1	Public Sessions	p (ctrl) ←
Zoom (2 screen)	2	Clear all Highlights	h (ctrl) ←
Zoom (3 screen)	3		
Zoom (4 screen)	4		
Zoom (5 screen)	5		
Zoom (6 screen)	6		
Zoom (7 screen)	7		
Zoom (8 screen)	8		
Zoom (9 screen)	9		
Zoom (10 screen)	0		
Highlight all (F6)	F6		

UCSC Genome Browser

Top Blue Bar Tools Menu: Select LiftOver to map coordinates 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, History, Downloads, My Data, Projects, Help, and About Us. Below this, a yellow header bar reads "Browse/Select Species". The main content area is divided into several sections: "RELEVANT SPECIES" with icons for Human, Mouse, Rat, Zebrafish, and Drosophila; "My Data Input" with a text field; "GENOMES FOR SPECIES" with a tree view of species; "Genome Browser" with a "Tools" dropdown menu; "Position" with input fields for "Genome Assembly" (set to hg19) and "Search Term"; and a "Genome Browser" section with a "Genome Browser assembly ID" field and a "View genome browser" button. The "Tools" dropdown menu is open, showing options like "LiftOver" (highlighted in blue), "Track Browser", "Variant Annotation", "Diagram", "Genome Graphs", "Gene Interactions", "Gene Sorter", "Gene Graphs", "Track Browser", "ViewGenes", and "Other Utilities". A black arrow points from the text above to the "LiftOver" option in the menu. On the right side, there is a small image of a dog and some text.

UCSC Genome Browser

Top Blue Bar Tools Menu: Select Blat to search DNA sequence 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 (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. The top navigation bar includes links for Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, and Help. The main title is "Mouse lemur BLAT Search". Below this, the "BLAT Search Genome" form is visible. The "Genome" dropdown menu is set to "Search ALL", which is highlighted by a black arrow pointing to it. Other options for the dropdown include "mouse", "Human", and "Mus musculus". The "Assembly" dropdown is set to "hg19", and the "Query type" is set to "any". The "Sort output" and "Output type" options are also visible. The search results area shows a list of nucleotide sequences, starting with "ATGCTTTTCCGCTCCAGTAADAGA...".

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

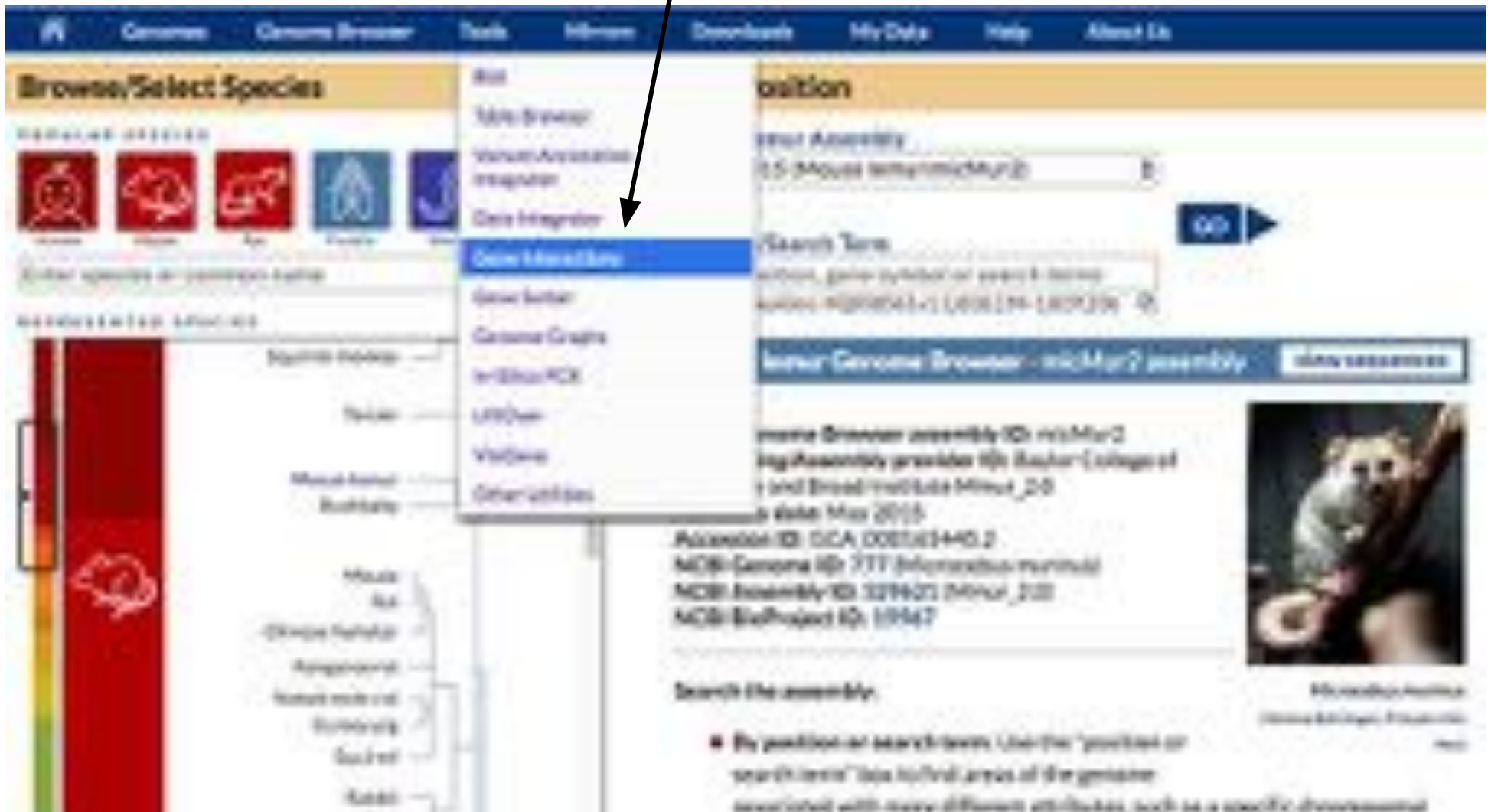
Click the IDs in the Assembly column to see the full BLAT output for that Database

Name	Genome	Assembly	Hits	Chrom
SearchingThisSequence	Mouse-embur	mmMus2	308	#100885604v1
SearchingThisSequence	Russulata	rsRus2	142	CLRT1881
SearchingThisSequence	Alpaca	alpAlp2	142	#2852881
SearchingThisSequence	Tree shrew	taTsh2	137	asaffac_143001.1-48178
SearchingThisSequence	Dogfish	scDog1	132	J-4079407
SearchingThisSequence	White whale	whWha1	128	#10207896
SearchingThisSequence	Bonobo	panPan2	127	chr1
SearchingThisSequence	Chimp	panPan1	126	chr1
SearchingThisSequence	Golden shrew-norway	scShre1	125	#10207811v1
SearchingThisSequence	Gibbon	gibGib2	123	J-884002
SearchingThisSequence	Cat	felFel1	122	chr1
SearchingThisSequence	Rabbit	oryOry2	122	chr1
SearchingThisSequence	Horse	equEqu2	121	chr15
SearchingThisSequence	Quail	galGal1	121	chr1

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 blue navigation bar contains the following links: Home, Genomes, Genome Browser, Tools, History, Downloads, My Data, Help, and About Us. Below this bar, the 'Browse/Select Species' section is visible, featuring a 'RECOMMENDED SPECIES' row with icons for Human, Mouse, Rat, Dog, and Pig, and a 'RECOMMENDED SPECIES' section with a tree view of species. A 'Tools' menu is open, listing various options: All, My Browser, View/Annotate Region, Data Integrator, **Gene Interactions** (highlighted in blue), Gene Index, Genome Graphs, In-Situ FISH, LocusZoom, VISTA, and Other Utilities. An arrow points from the text above to the 'Gene Interactions' option. The main content area shows a search for 'rs1042564' in the 'hg19 Mouse (mm9) assembly'. The search results display the gene 'LMO2' and its location on chromosome 10. A small image of a mouse is visible in the bottom right corner.

UCSC Genome Browser

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



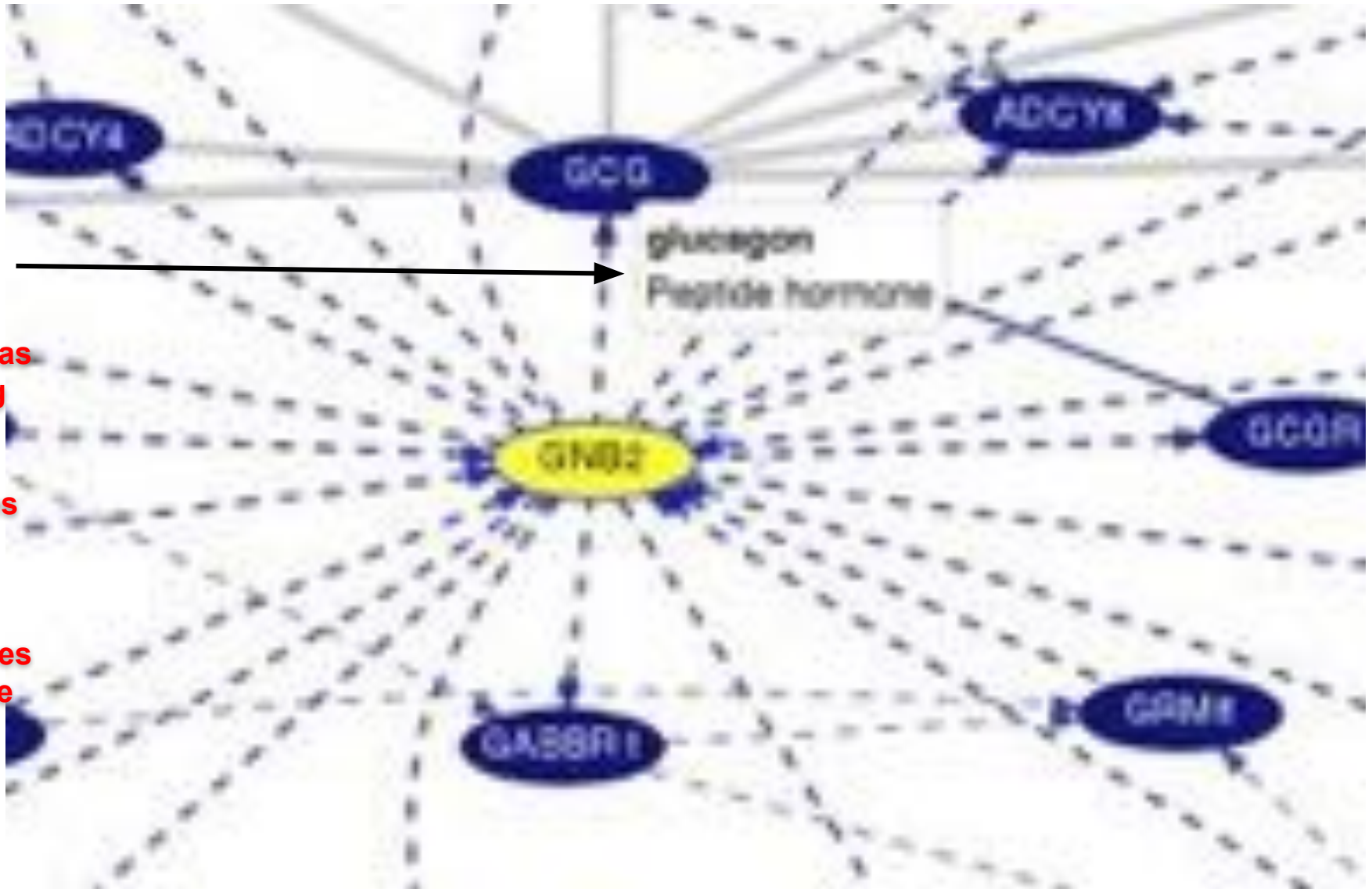
Graph shows genes related to the gene GNB2 where clicking other genes will recenter the graph.

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, etc.
- mRNA and EDT**: Includes tracks like ENCODER, RefSeq, etc.
- Expression**: Includes tracks like ENCODER, RefSeq, etc.
- Regulation**: Includes tracks like ENCODER, 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 is highlighted with a red arrow pointing to the 'CRISPR' track. The 'Regulation' section is highlighted with a red arrow pointing to the 'GeneHancer' track.

Track Group	Track Name
Mapping and Sequencing	GENCODE v20
	NCBI RefSeq
	Other RefSeq
	RefSeq GENCODE...
	AUGUSTUS
	GENCODE
	UCSC Transcripts
Genes and Gene Predictions	CRISPR
	CRISPRi, CRISPRa
	GenePred
	GeneMark-ES
	GeneMark-ES-Low
	GeneMark-ES-Low
	GeneMark-ES-Low
Phenotype and Literature	Cancer Gene Expr...
	Gene Interactions
	GenePhos
	GenePhos
	GenePhos
	GenePhos
miRNA and EDIT	miRNA
	miRNA
	miRNA
Expression	Expression
	Expression
	Expression
Regulation	Regulation
	Regulation
	Regulation
Comparative Genomics	Comparative Genomics
	Comparative Genomics
	Comparative Genomics
	Comparative Genomics
	Comparative Genomics
	Comparative Genomics

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

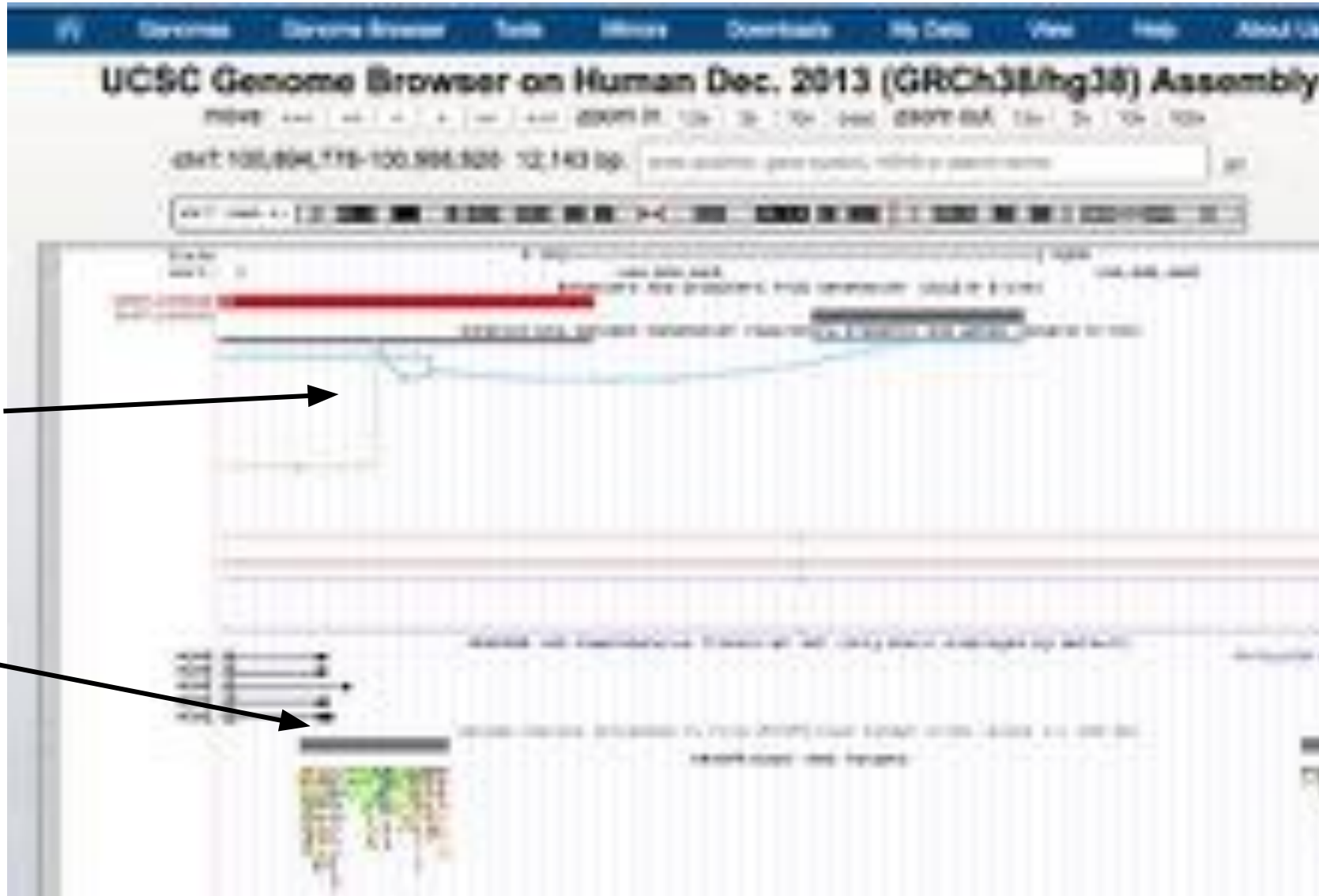
Under Regulation section you can find the new GeneHancer tracks

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.

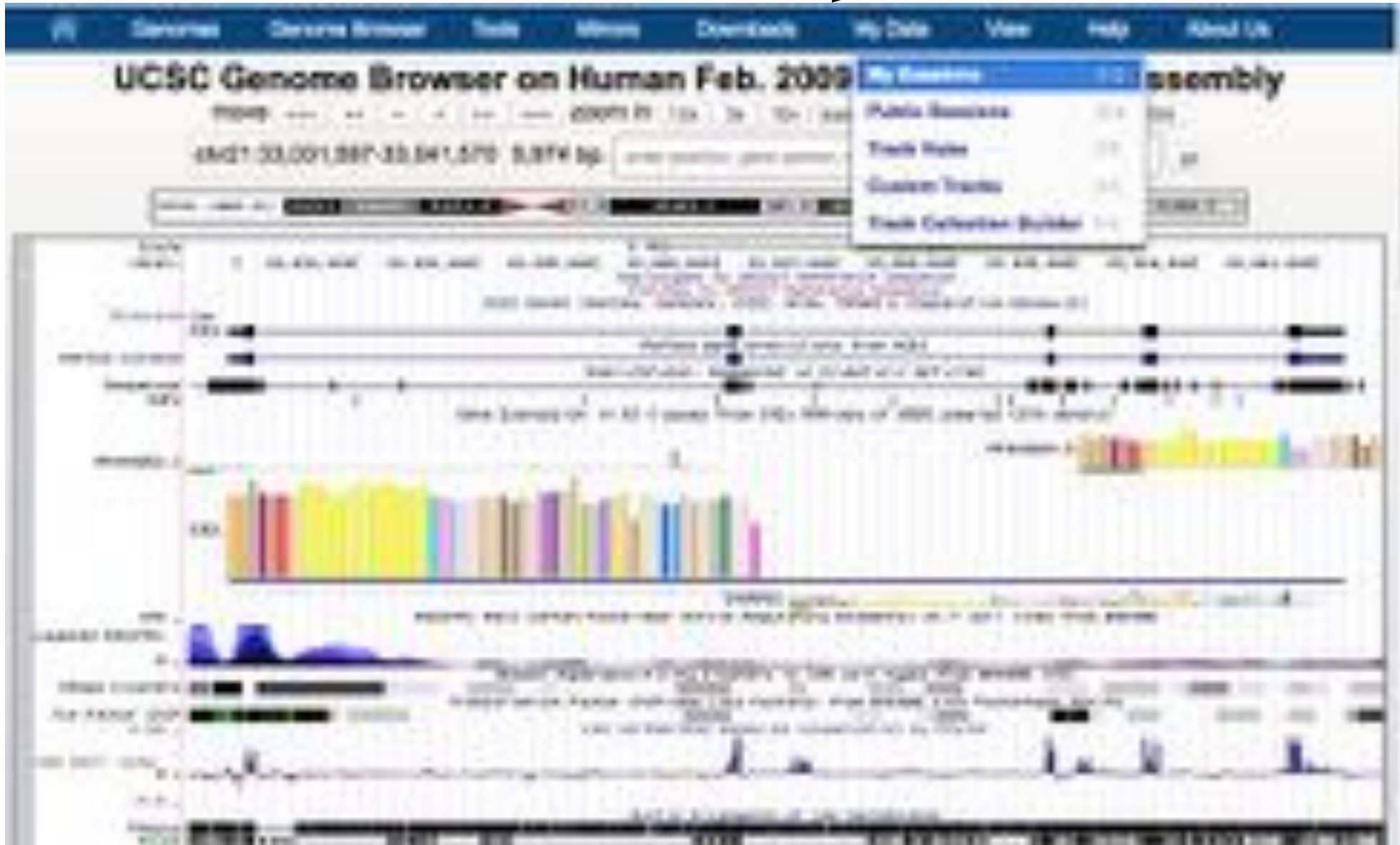
GeneHancer has a track to denote enhancers and promoters and then an Interactions track to graphically show associations with nearby genes.

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



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. It includes a 'Your Account Information' section with links for 'User name view', 'Change password', and 'Sign out'. 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' with columns for session name, creation date, assembly, and various actions. Two black arrows point from red text annotations to the 'User name view' link and the first row of the 'My Sessions' table.

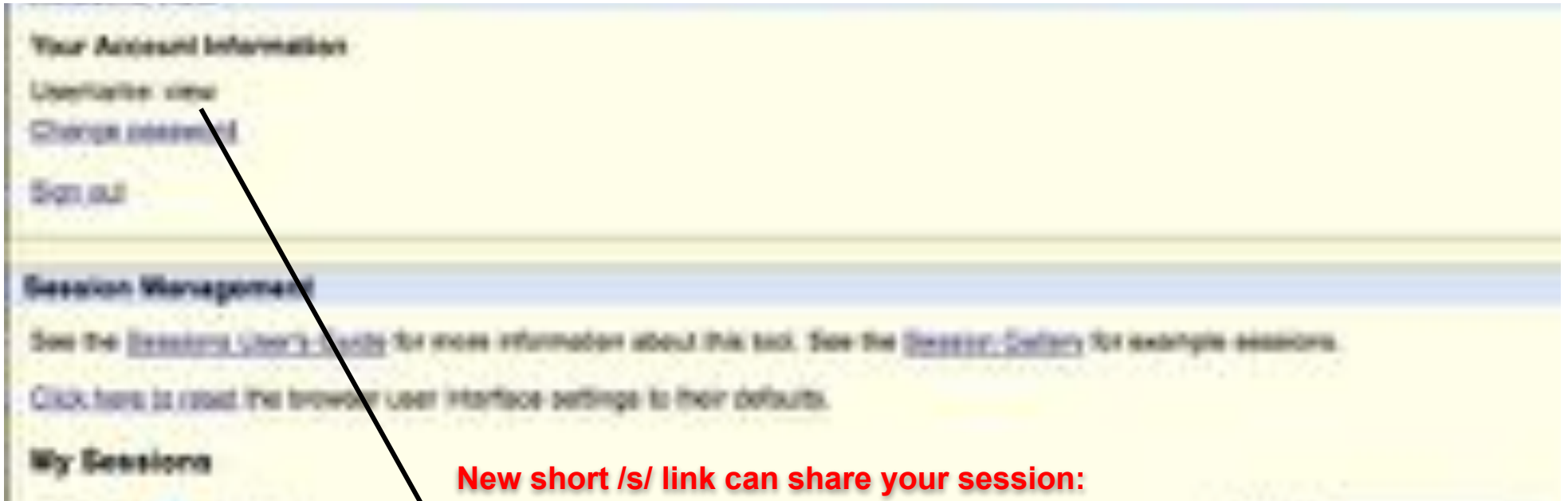
Create an account username and then save a session name as you are browsing the site to return to views of data later.

My Sessions

session name (click to load)	created on	assembly	view/del details	delete this session	share with others?	post in public listing?	send to mail
Assembly Browser	2018-10-08	hg19	view	delete	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
Gene Browser	2018-10-08	hg19	view	delete	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
Molecule Engineering	2018-10-08	hg19	view	delete	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Email
Expresso	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

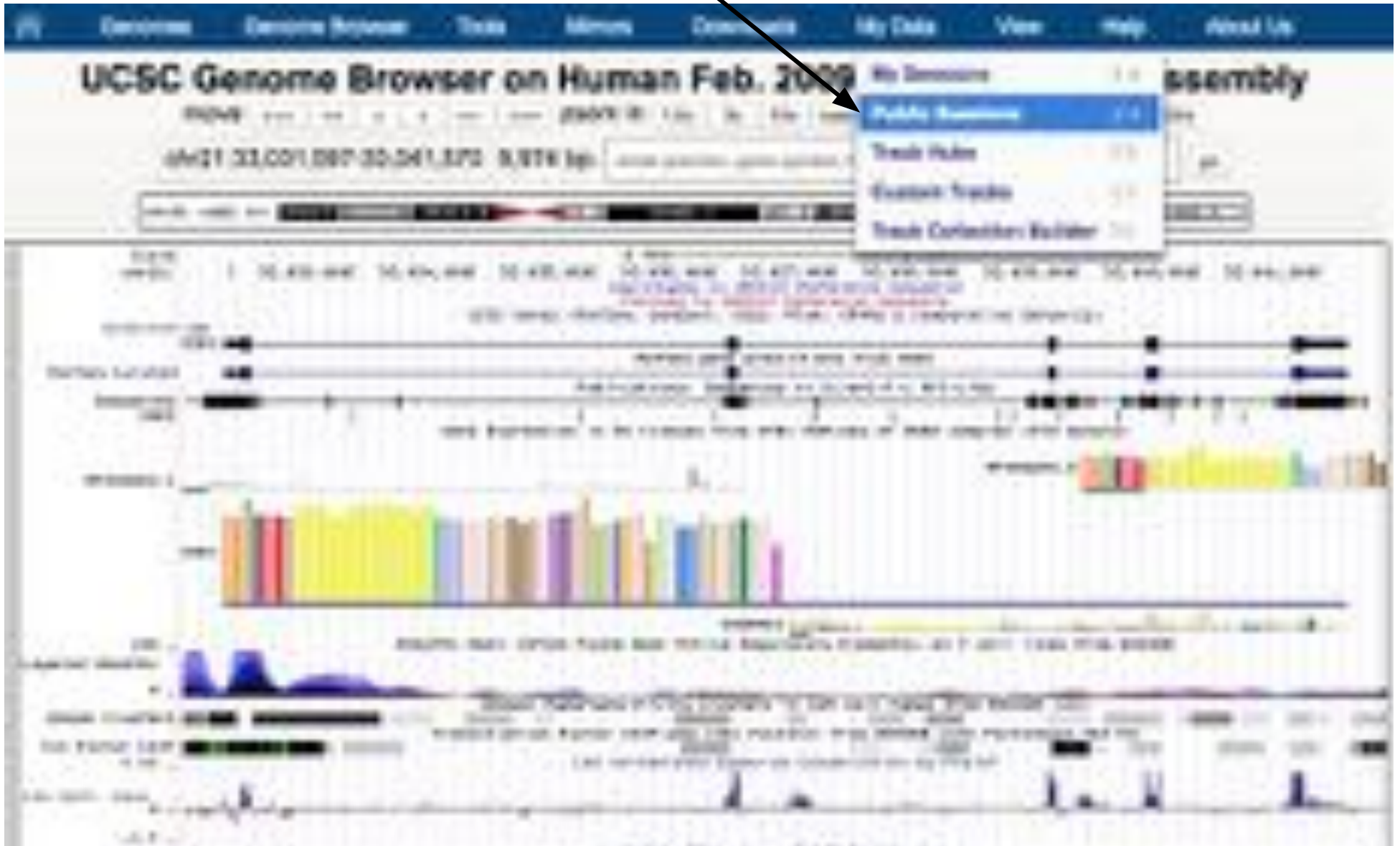


New short /s/ link can share your session:
<http://genome.ucsc.edu/s/yourUserName/yourSessionName>

<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, Mirrors, Downloads, My Data, View, Help, and About Us. The main header reads "UCSC Genome Browser on Human Feb. 2009". Below this, there is a search bar and a coordinate range: chr21:33,001,000-30,041,000 (8,978 bp). A dropdown menu is open under the "My Data" link, with "Public Sessions" highlighted. Other options in the menu include "Track Hubs", "Custom 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)

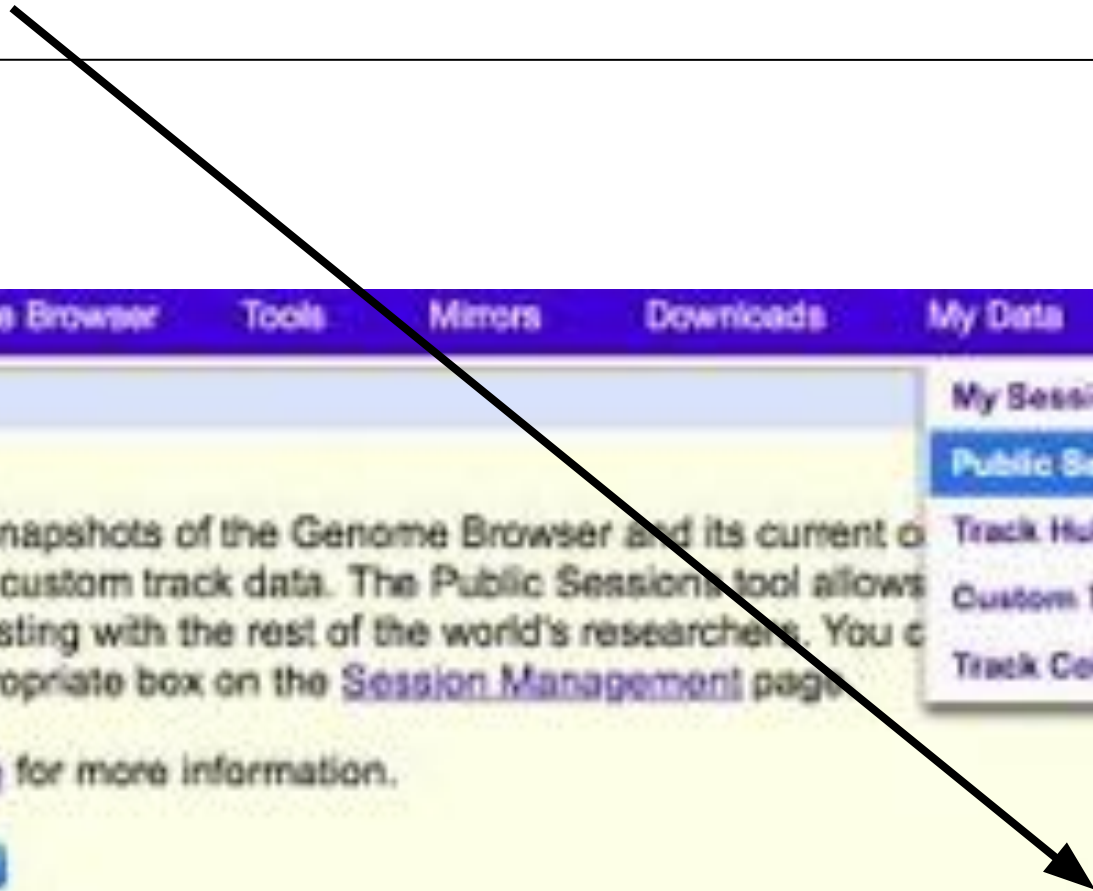
Sort by: 

Show:

Screenshot	Session Properties
	<p>Description: This sessionView is a collection of tracks centered around large genomic 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.</p> <p>Author: view</p> <p>Session Name: VariatorCNVs</p> <p>Genome Assembly: hg18</p> <p>Creation Date: 2010-12-18</p> <p>Views: (5)</p>
	<p>Description: This sessionView is a collection of tracks centered around clinical significance. Featured tracks include gene annotations, SNPs, CNVs, CIV (a cancer mutation database and our publications track built by mining sequences and SNPs in publications). The displayed region is focused around the HTT gene, responsible for Huntington's disease and Loss of Heterozygosity syndrome. Two other 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.</p> <p>Author: view</p> <p>Session Name: Clinical</p>

Search Public Sessions

Type in the Search box “**PAG 2020**”



Genomes Genome Browser Tools Mirrors Downloads My Data Projects Help

Public Sessions

Sessions allow users to save snapshots of the Genome Browser and its current displayed tracks, position, and custom track data. The Public Sessions tool allows sessions that they deem interesting with the rest of the world's researchers. You can add to this list by checking the appropriate box on the [Session Management](#) page.

See the [Sessions User's Guide](#) for more information.

Sort by:

Show entries

Search:

- My Sessions
- Public Sessions**
- Track Hubs
- Custom Tracks
- Track Collection Builder