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 daugter-still-birth in cattle.

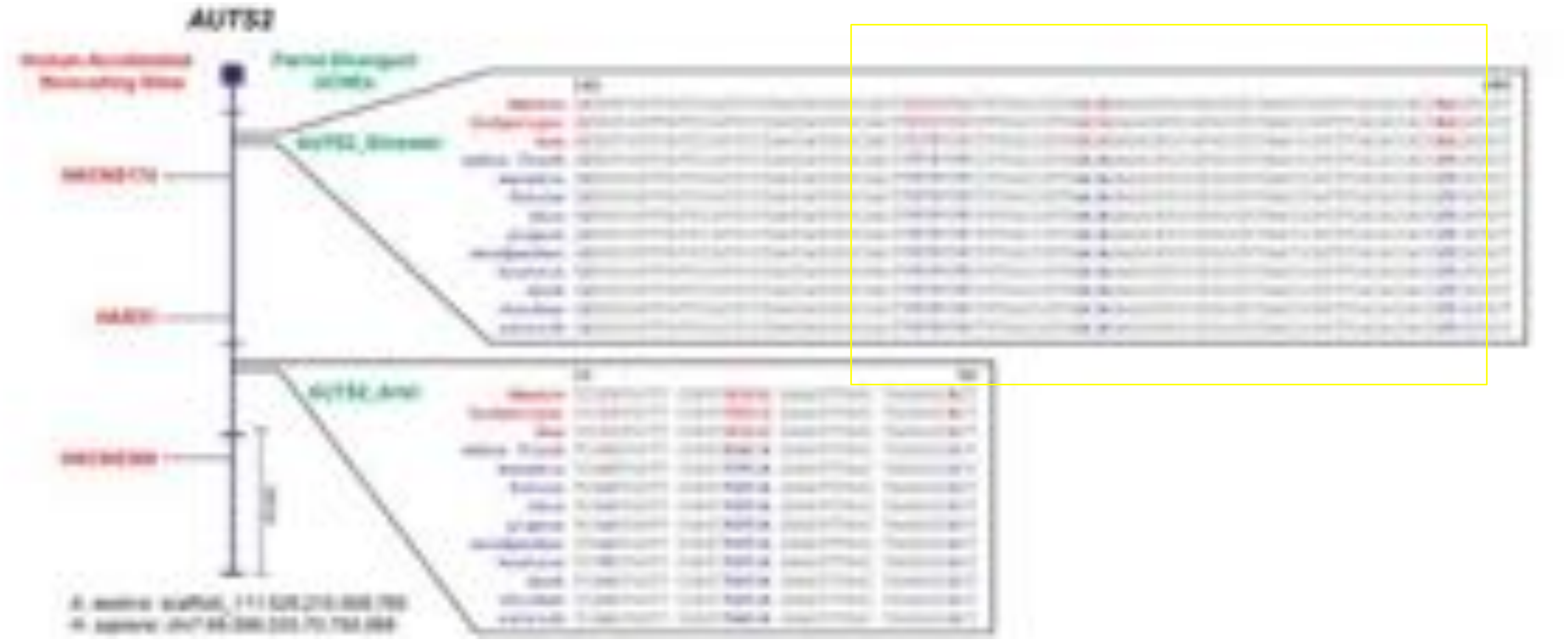
An example of viewing this region on the UCSC Browser:

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

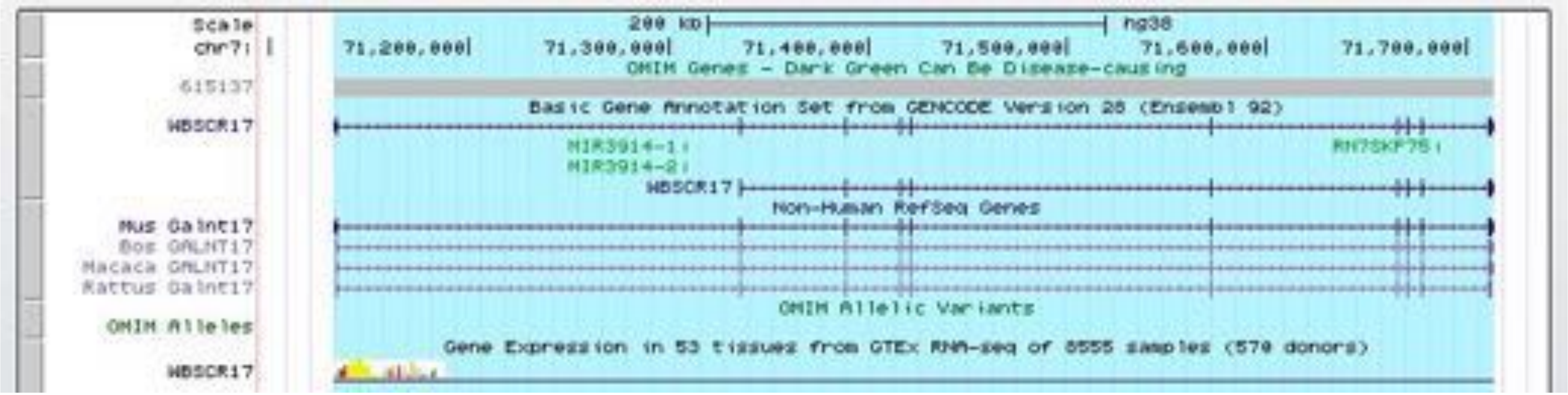
An example of viewing this region on the UCSC Browser showing similar alignment information in the conservation track around human AUTS2 as in Dr. Mello's supplemental slides:

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 WBSCR17 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_WBSCR17

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.

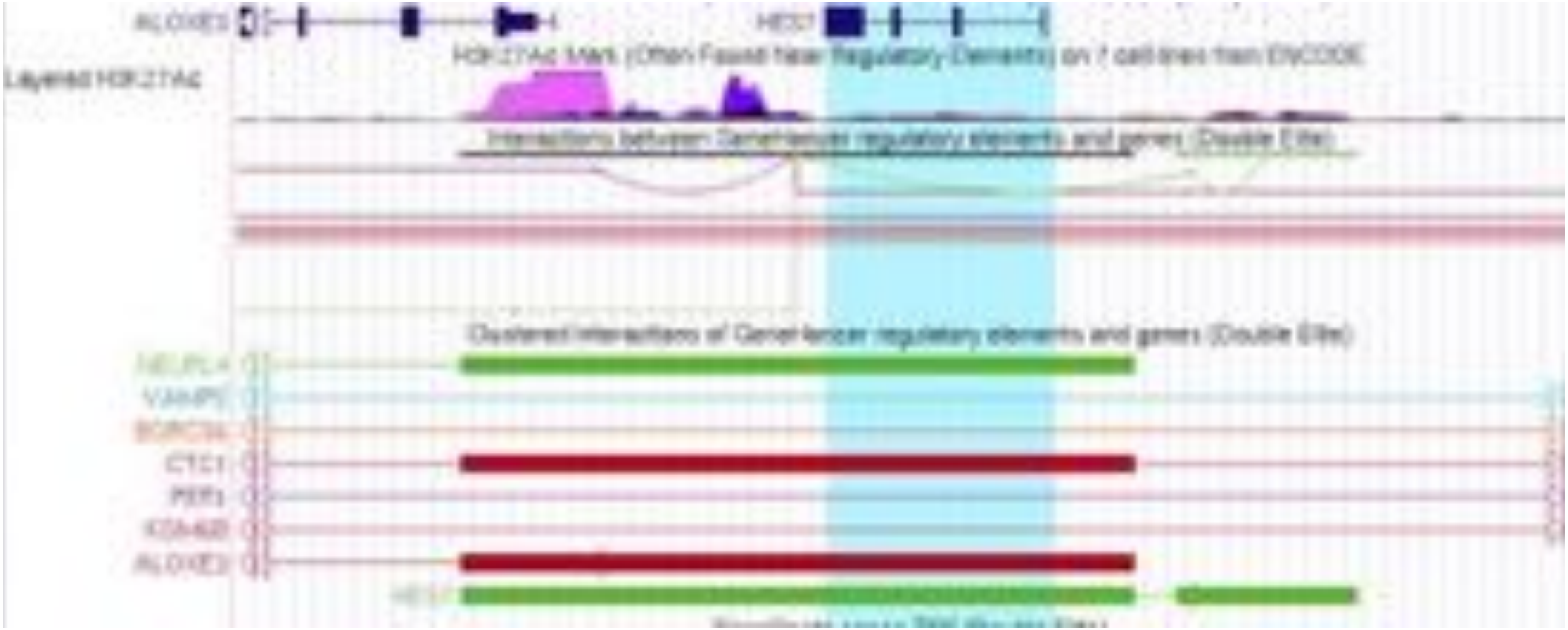
An example of viewing this region on the UCSC Browser with the regulatory Gene Interactions track turned on:

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

UCSC Genome Browser

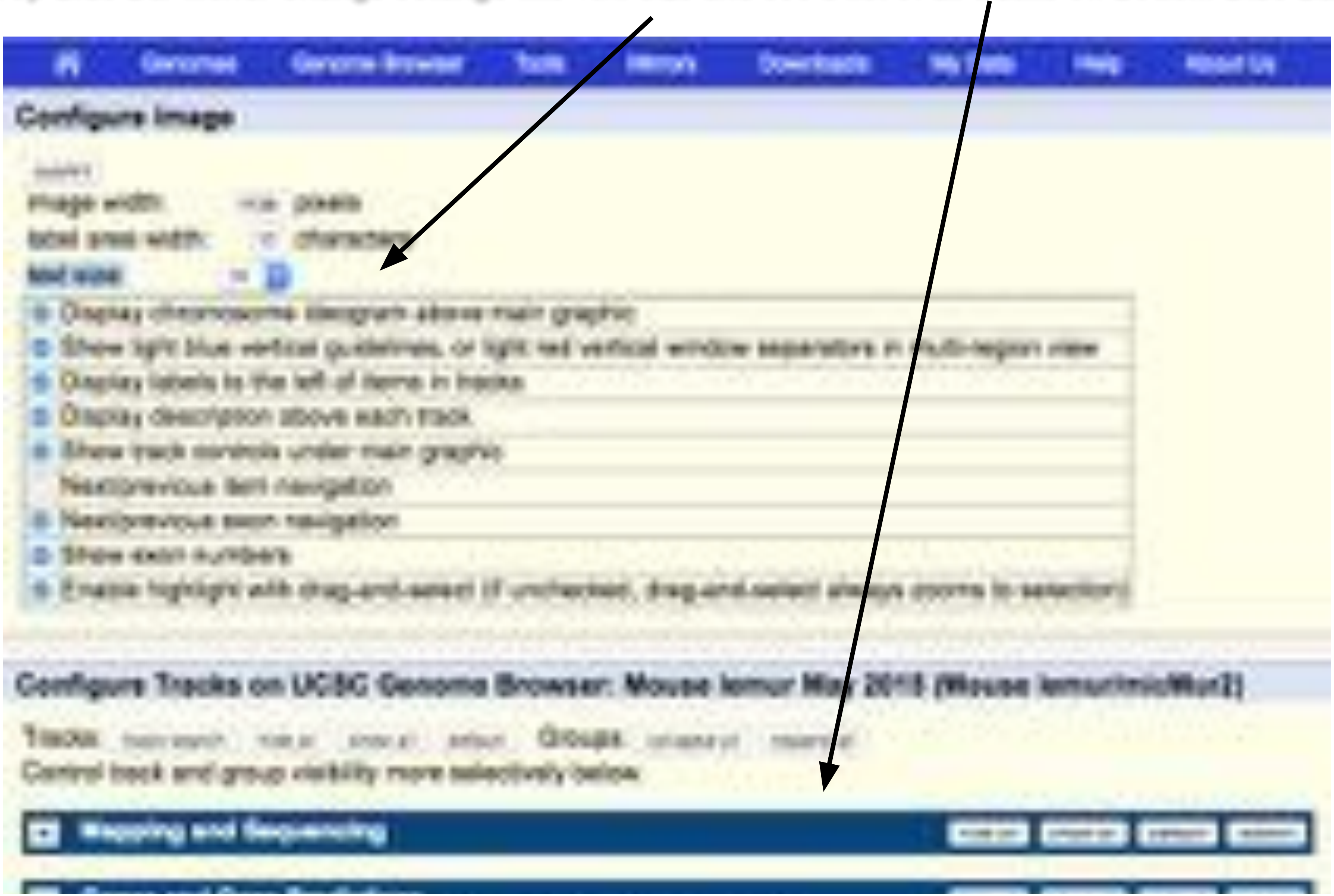
Top Blue Bar Menu: Genomes **a Gateway to Discover Multiple Assemblies**

UCSC Genome Browser

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

UCSC Genome Browser

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



Configure Image

image width: pixels

label area width: characters

text size:

Display chromosome ideogram 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 item navigation

Next/previous exon navigation

Show exon numbers

Enable highlight with drag-and-select (if unchecked, drag-and-select always zooms to selection)

Configure Tracks on UCSC Genome Browser: Mouse lemur May 2015 (Mouse lemur/micMur2)

Tracks: Groups:

Control track and group visibility more selectively below.

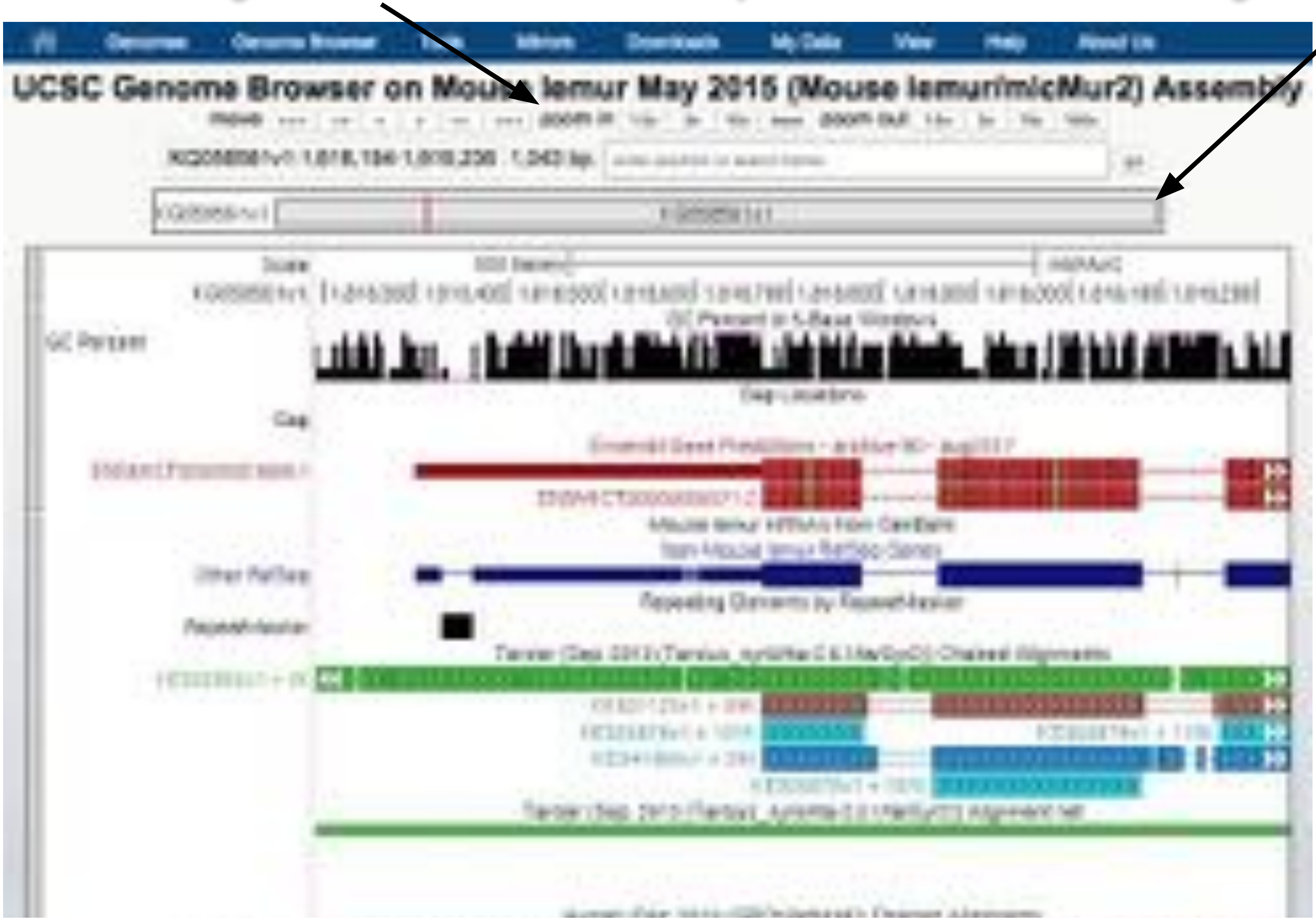
Mapping and Sequencing

UCSC Genome Browser

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

UCSC Genome Browser

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



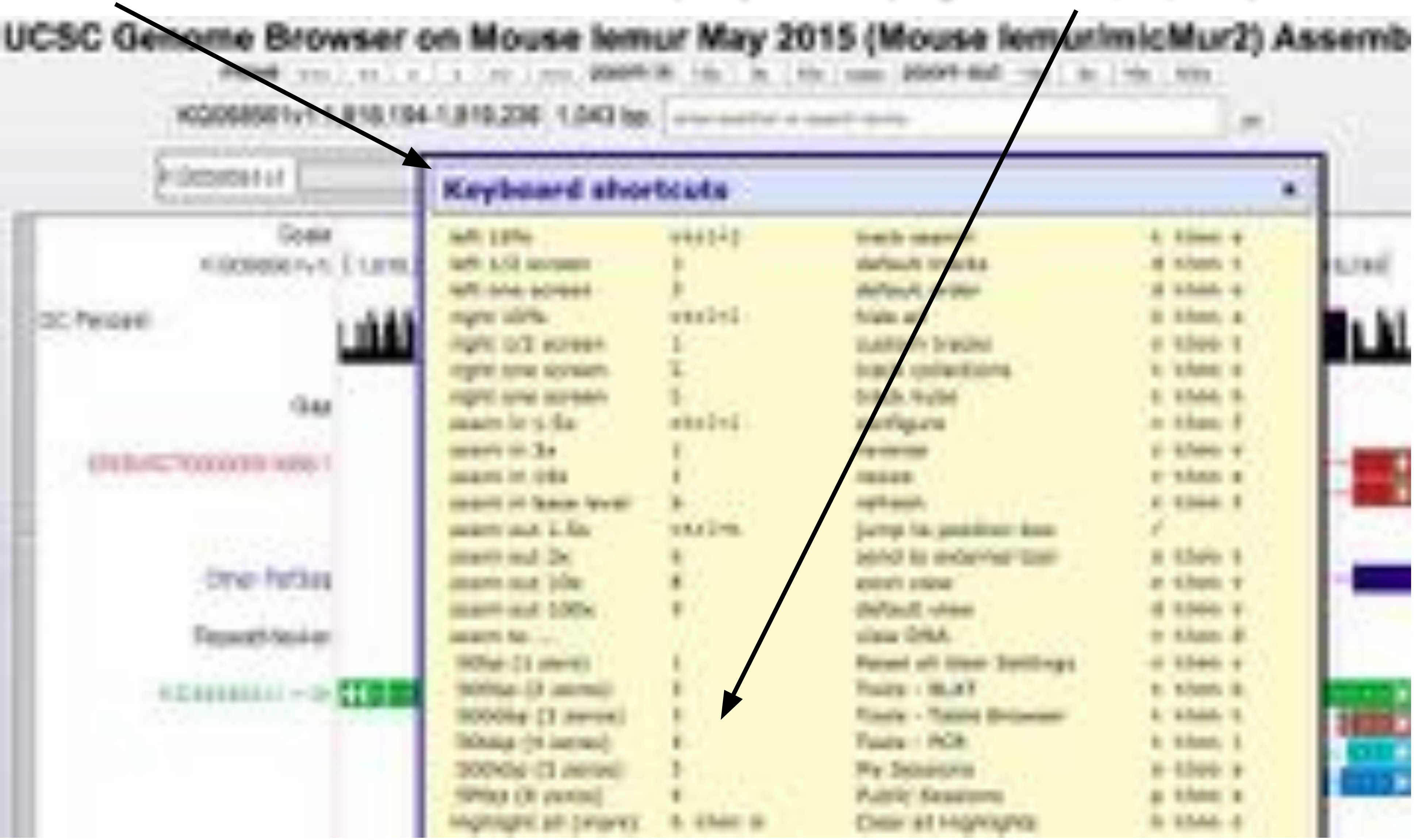
UCSC Genome Browser on Mouse lemur May 2015 (Mouse lemur/micMur2) Assembly

UCSC Genome Browser

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

UCSC Genome Browser

Press **?** to See **Shortcuts.** Use numbers ***1 to 6*** to quickly zoom to bp regions: 5*0* to 5,***000,000*** bp

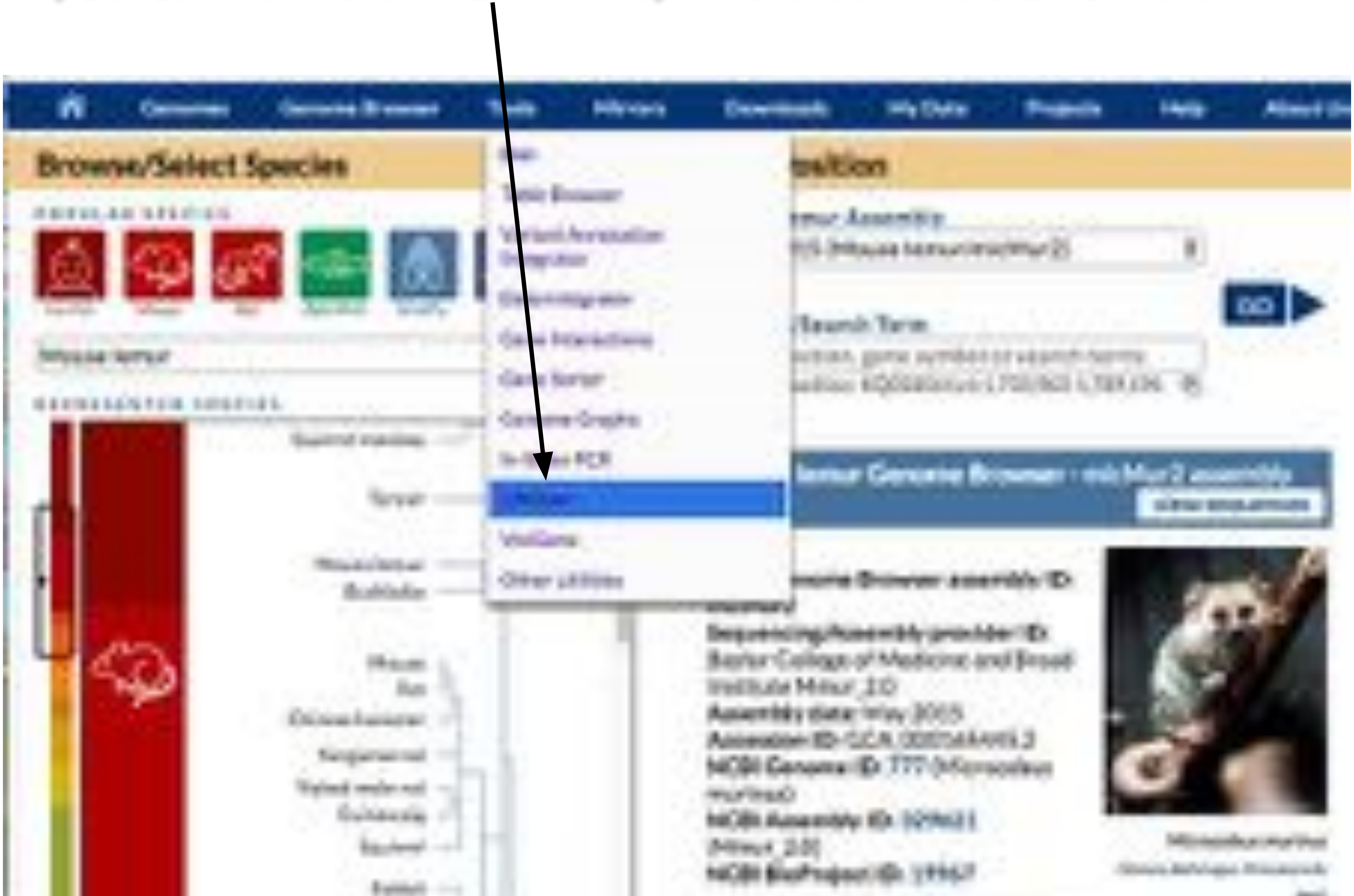


UCSC Genome Browser on Mouse lemur May 2015 (Mouse lemur/micMur2) Assemb

Keyboard shortcuts

UCSC Genome Browser

Top Blue Bar Tools **Menu: Select** LiftOver **to map coordinates across available Browsers**



UCSC Genome Browser

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

UCSC Genome Browser

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

Mouse lemur BLAT Search

BLAT Search Genome

Genome: Mouse lemur ☐ Search ALL

Query type: BLAT's guess

Sort output: query,score

Output type: hyperlink

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

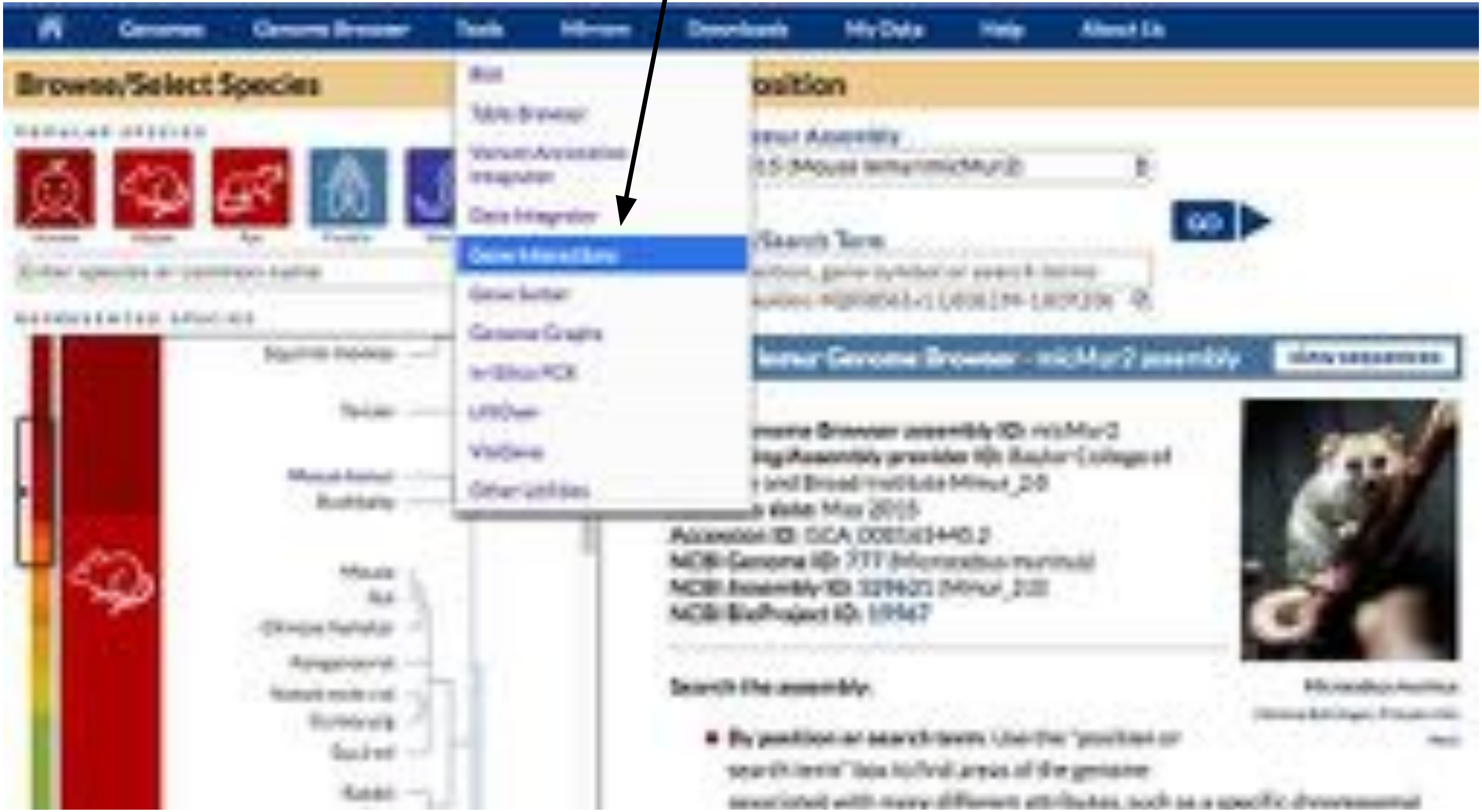
Click the link in the Assembly column to see the full BLAT output for that Genome

Name	Genome	Assembly	Hits	Chrom
SearchingThisSequence	Mouse lemur	micMur2	358	KQ058350v1
SearchingThisSequence	Bushbaby	otoGar3	163	GL873561
SearchingThisSequence	Alpaca	vicPac2	149	KB632887
SearchingThisSequence	Tree shrew	tupBel1	137	scaffold_142971:1-48176
SearchingThisSequence	Dolphin	turTru2	130	JH479407
SearchingThisSequence	Minke whale	balAcu1	128	KI537896
SearchingThisSequence	Bonobo	panPan2	127	chr7
SearchingThisSequence	Chimp	panTro5	126	chr7
SearchingThisSequence	Golden snub-nosed monkey	rhiRox1	125	KN297815v1
SearchingThisSequence	Baboon	papAnu2	123	JH684062
SearchingThisSequence	Cat	felCat8	122	chrE3
SearchingThisSequence	Rabbit	oryCun2	122	chr6
SearchingThisSequence	Horse	equCab2	121	chr15
SearchingThisSequence	Gorilla	gorGor5	121	chr7

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**



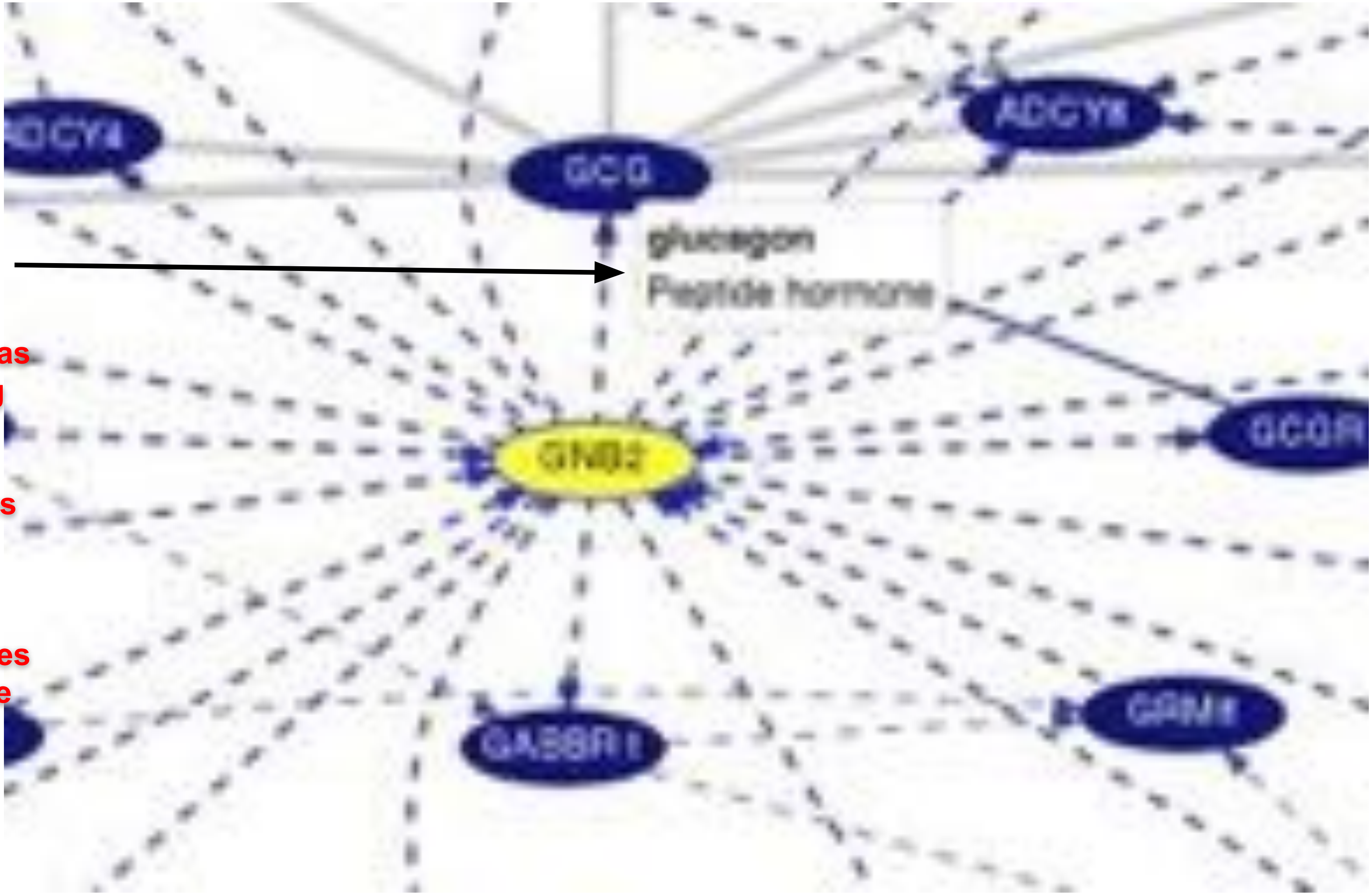
UCSC Genome Browser

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

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

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

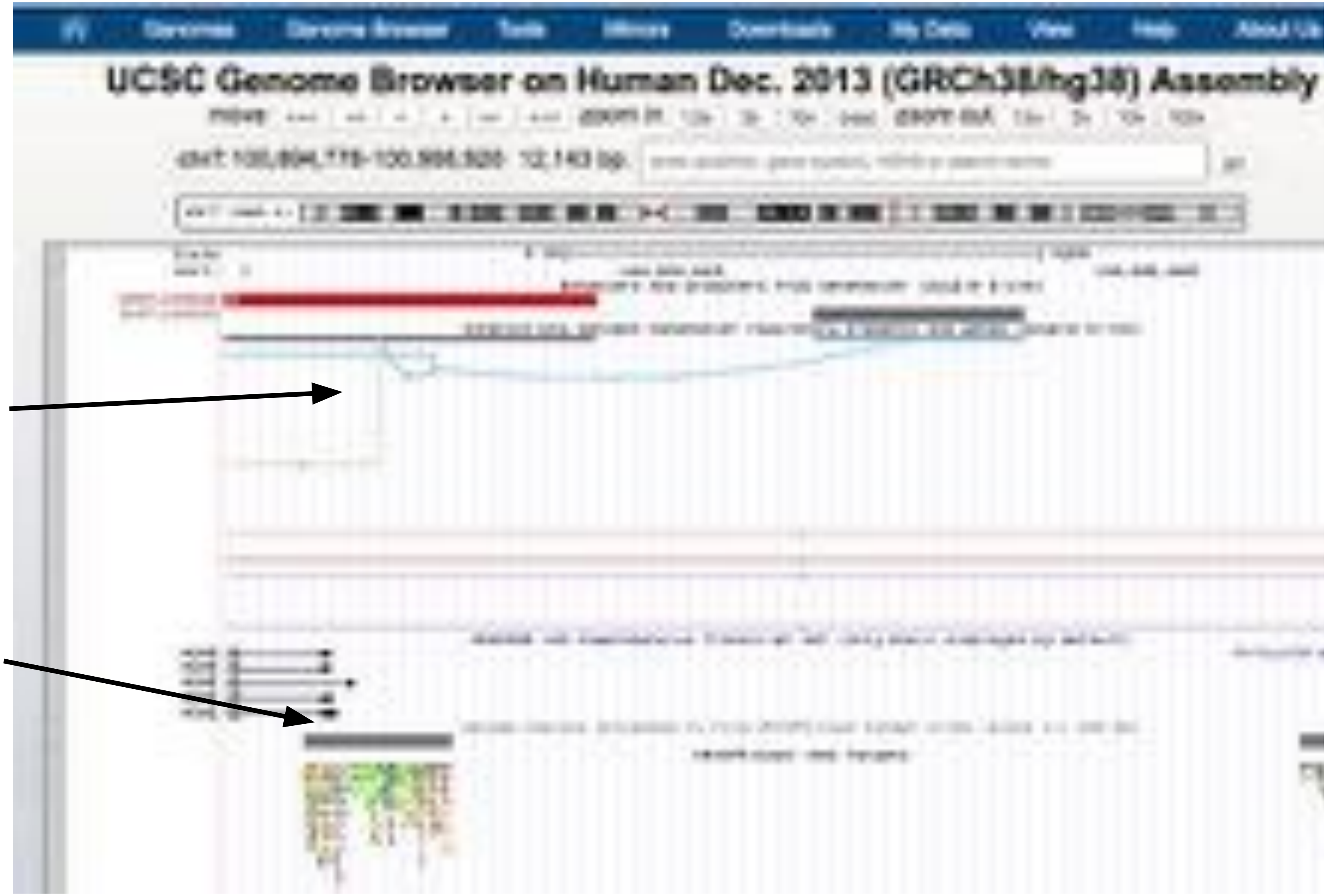
Under Regulation **section you can find the new** GeneHancer **tracks**

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.**

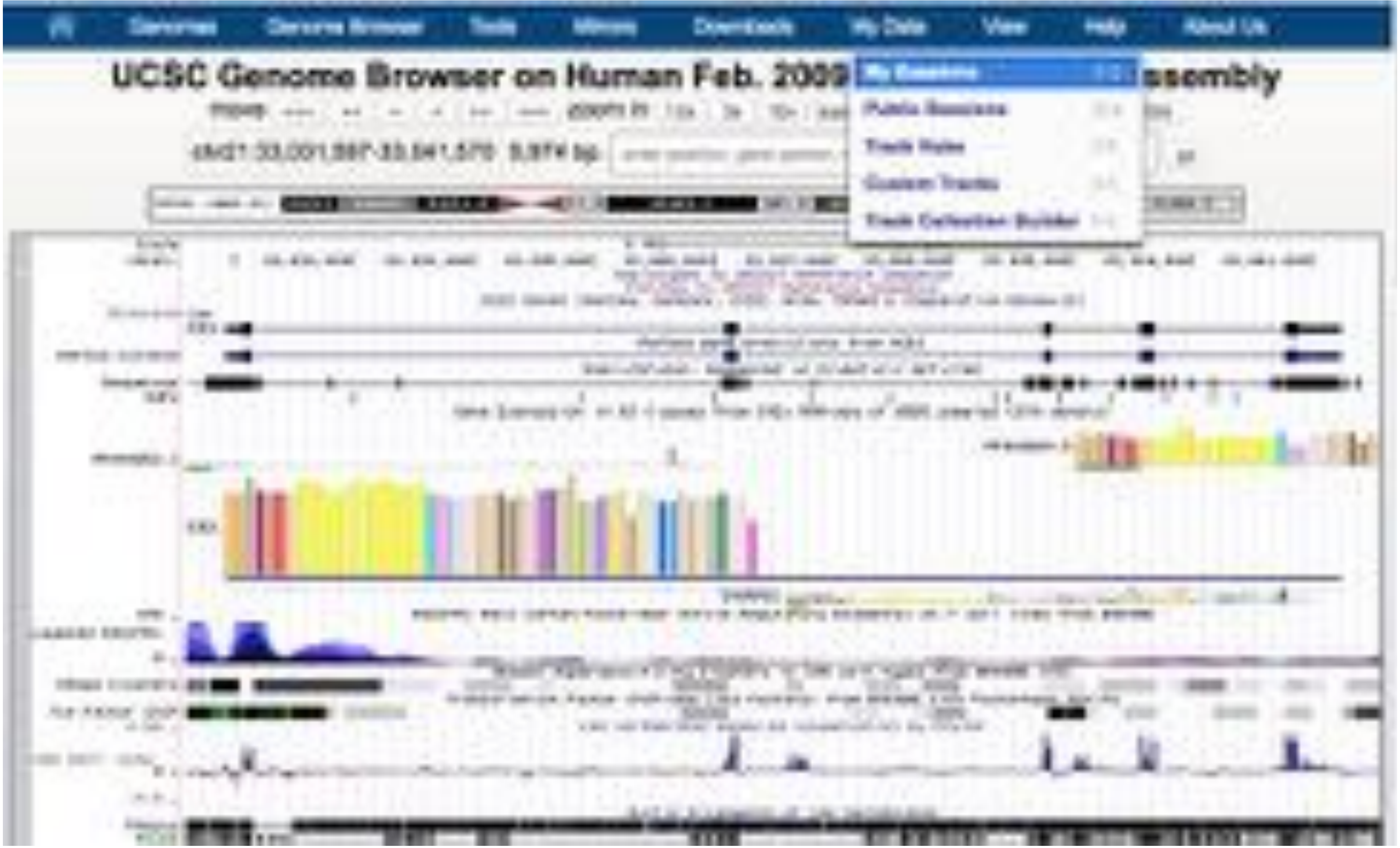
The CRISPR **track has colored targets** (green/yellow/red) **annotated for predicted cleavage around coding regions with details of potential off-targets listed.**



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

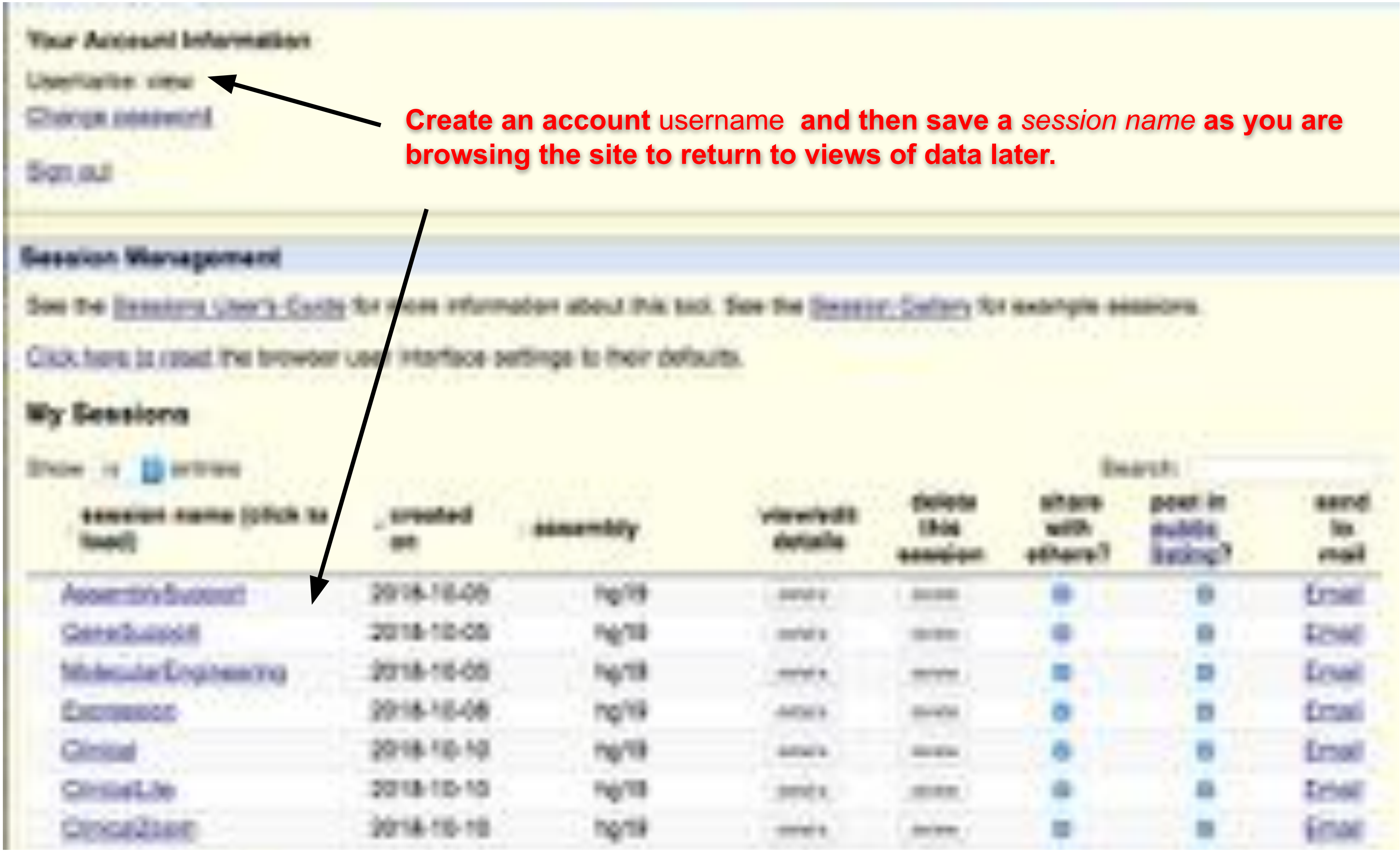
UCSC Genome Browser

My Data **Top Blue Bar Menu**



UCSC Genome Browser

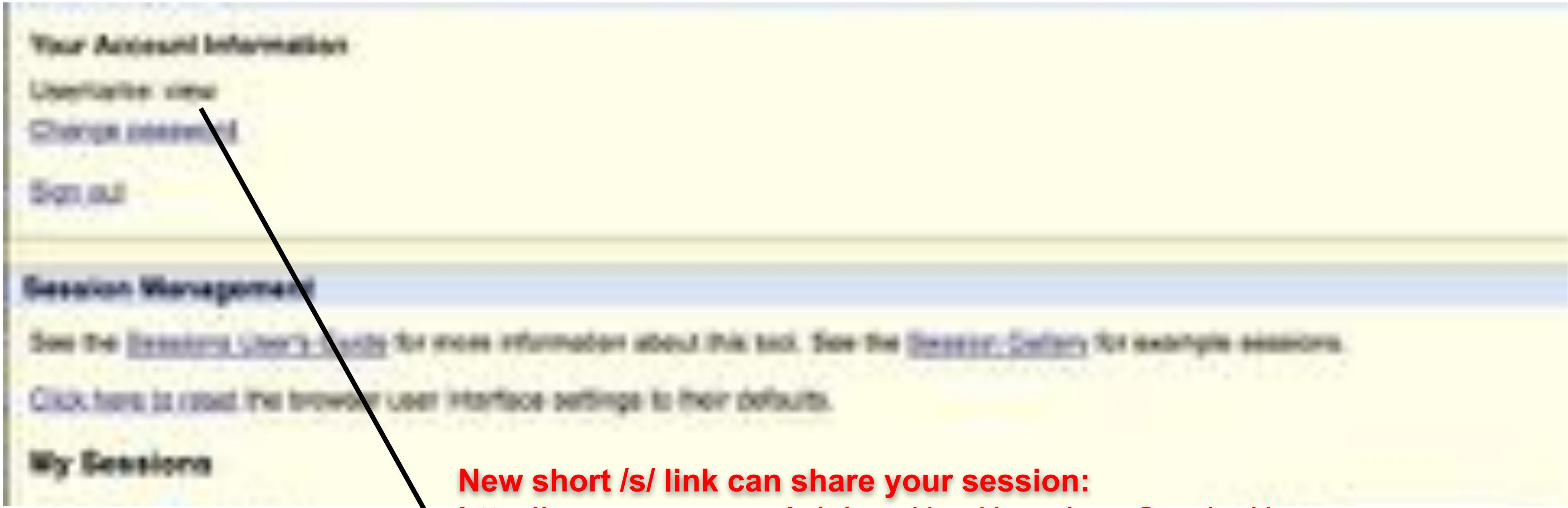
My Data **Top Blue Bar Menu:** My Sessions **Allows You to Create a Snapshot of Your Browsing**



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

UCSC Genome Browser

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



Your Account Information

Username:

Change password

Sign out

Session Management

See the Sessions User's Guide for more information about this tool. See the Session Gallery for example sessions.

Click here to reset the browser user interface settings to their defaults.

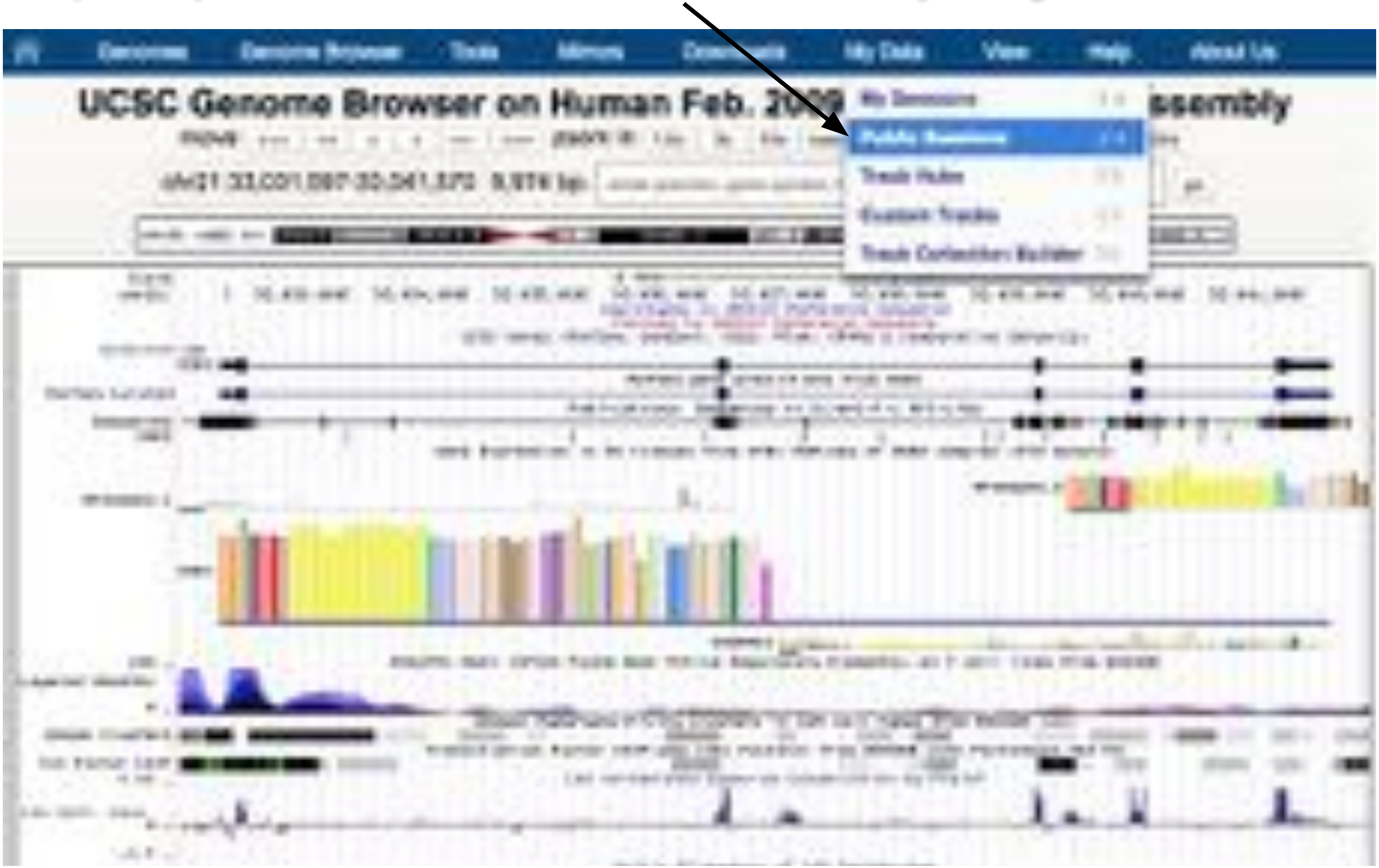
My Sessions

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**



Search Public Sessions

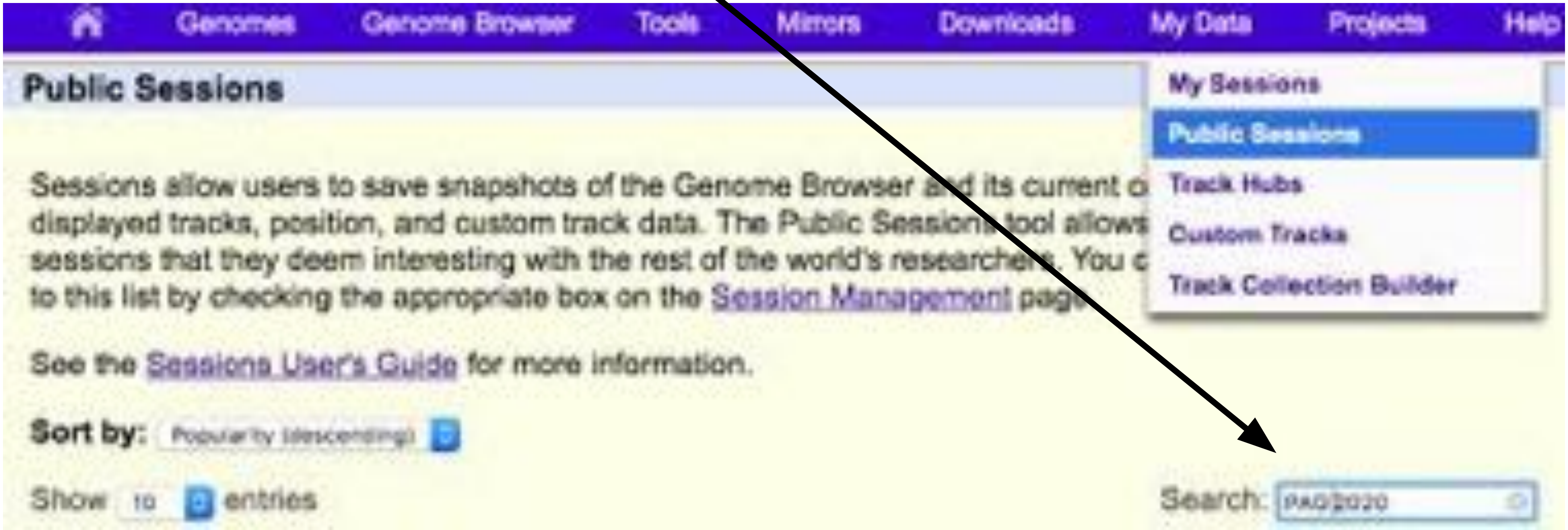
Search box “SessionView” (sorts to sessions with this unique tag)

- 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)

Search Public Sessions

Type in the Search box "PAG 2020"



Public Sessions

Sessions allow users to save snapshots of the Genome Browser and its current c
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 c
to this list by checking the appropriate box on the Session Management page.

See the Sessions User's Guide for more information.

Sort by: Popularity (descending)

Show 10 entries

Search: PAG 2020