

Tutorial 5 – Viewing the CHO & CH Genomes

The genome viewer is a tool to provide visualization of the Chinese hamster (CH) and Chinese hamster ovary (CHO) cell genomes. This tool currently provides visualization via JBrowse of the 2014 annotated CHO-K1 genome and the chromosome-sorted CH genome.

CHO-K1 Genome Viewer

The genome viewer for the CHO-K1 cell line can be reached by selecting the “Genome Viewer” resource from the Resources tab or by selecting the “CHO-K1 Genome Viewer” button from the homepage.

The screenshot displays the CHOgenome.org homepage. At the top, there is a navigation bar with tabs for 'General Info', 'Genomes', 'Resources', and 'Partners'. The 'Resources' tab is active, showing a dropdown menu with options: 'BLAST', 'Genome Viewer' (highlighted with a green box), 'Proteome', 'Data', and 'File Archive'. Below the navigation bar, the page is divided into several sections. On the left, there is a 'News' section with updates from October 9, 2014, and August 28, 2014. In the center, there is a 'Search RefSeq' section with a search box and a 'Search' button. Below this, there are several icons representing different tools: 'Gene Search', 'BLAST', 'CHO-K1 Genome Viewer' (highlighted with a green box), 'Proteome Browser', 'Downloads', and 'CH Genome Viewer'. On the right, there is an 'Events' section with a 'Previous Events' link and a list of events, including 'September 8 - September 10, 2014' and 'March 13 - March 14, 2014'. At the bottom, there is a footer with a link to 'Please report issues or provide feedback' and 'Use Legacy site', and the text 'CHOgenome.org version 2.0b'.

The address for the CHO-K1 genome viewer is:

http://www.chogenome.org/jbrowse/?loc=NW_003613580.1%3A3511734..5267690&tracks=DNA%2Cgene%2Cgc-content&highlight

CH Genome Viewer

The genome viewer for the chromosome-sorted Chinese hamster genome ([Brinkrolf et al](#)) can be reached by selecting the “CH Genome Viewer” button on the home page.

October 9, 2014

News

Update:

The CHO-K1 genome viewer has been updated from GBrowse to JBrowse, and contains the most up to date annotations (from 2014). The GBrowse instance for the 2012 annotated version of CHO-K1 is still available in the legacy version of the website (linked at the bottom of this page). The updated tutorial for viewing the genomes in JBrowse will be posted shortly.

We're getting a facelift in the near future!

August 28, 2014

The updates will provide a more organized approach to searching the data and going through results - especially important given the recent release of new genomes. Don't worry: all of the legacy genomes (CHO-K1 GenBank, and earlier CHO-K1 RefSeq) will be maintained on the website and will still be searchable. In fact, we will keep legacy pages operational for the foreseeable future in case you like the current look and feel.

As always, please let us know of any unusual or unexpected issues and to share your feedback on the new look and feel.

Update:

June 27, 2014

The BLAST server will periodically be unavailable for the next few days to permit updates to be made.

[see all](#)

Search RefSeq

Search the RefSeq CHO-K1 and Chinese hamster assemblies by gene name, symbol, or gene ID:

For detailed searches use [Advanced Search](#)

Welcome to the updated CHO Genome website! The updated website currently has all the information the previous CHO Genome website hosted, plus a few improved attributes. Tutorials for how to use this new website can be viewed here and we welcome any questions or suggestions you may have.

Events

Previous Events

Cell Line Development and Engineering Conference
Berkeley, CA, USA
September 8 - September 10, 2014
Leading experts, vendors, scientists, research scholars, and other interested parties related to the field of cell line development and engineering, from all parts of the globe, will be coming together to share their experience and recent advancements regarding various aspects of cell line development and engineering.
[read more](#)

CHOgenome Workshop 2014
Vienna, Austria
March 13 - March 14, 2014
The workshop was a great success. The latest developments in CHO-related sequence information, crosstalk between the genomic and bioprocess research, and genome scale science were well presented.
[read more](#)

2013 ESACT Meeting
Lille, France
June 23 - June 26, 2013
The CHOgenome.org workshop was titled "The www.CHOgenome.org Resource for the International CHO Biotechnology Community?". The workshop included presentations on current applications of genome scale information, where it is useful, and how has it helped in different research efforts, followed by discussion on the next steps for the cell culture community surrounding the CHO Genome effort.
[read more](#)

[see all](#)

Gene Search
Search the RefSeq Chinese Hamster and CHO-K1 assemblies

BLAST
BLAST sequences against Chinese Hamster or CHO-K1 genomes

CHO-K1 Genome Viewer
View the 2014 annotated CHO-K1 genome

Proteome Browser
Search the 2-D gel and shotgun datasets

Downloads
Useful Chinese Hamster publications and files

CH Genome Viewer
View the chromosome-sorted Chinese Hamster genome

Please report issues or provide feedback [Use Legacy site](#)

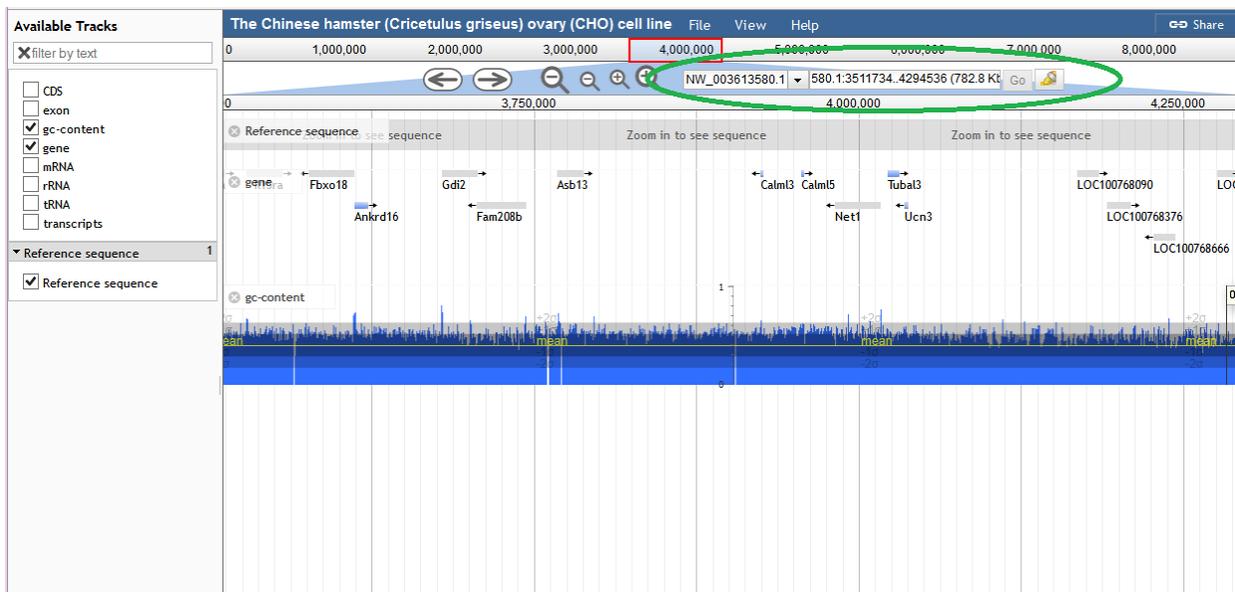
CHOgenome.org version 2.0b

The address for the CH genome viewer is:
<http://www.chogenome.org/JBrowse-1.11.0/>

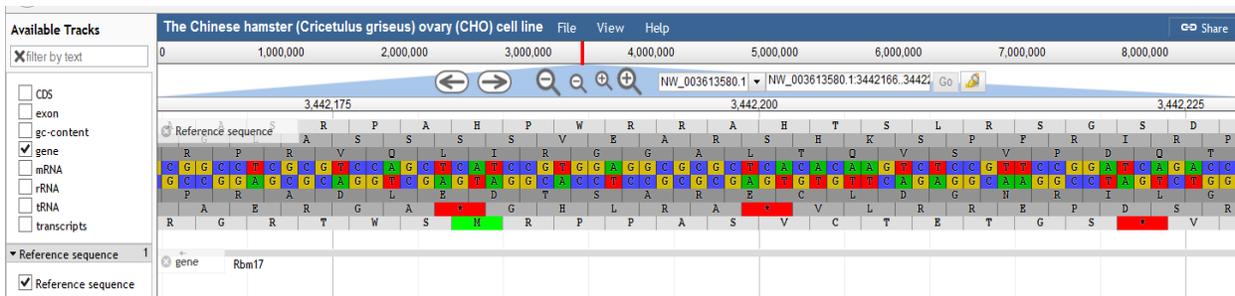
JBrowse

1) Loading Scaffolds

The 2014 CHO-K1 genome annotation is viewed using the JBrowse tool. The scaffold, not the chromosome, is the largest sequence assembly in this annotation. Scaffolds are labeled NW_0036#####.#, where # is equivalent to any digit from 0 to 9. If the desired scaffold ID number and range are known, they can be entered into the text boxes next to the zoom buttons (circled in green below). When the “Go” button is selected, the entered scaffold and range will be displayed. The scaffolds can also be selected from a drop down menu by clicking the down arrow next to the scaffold name. These scaffolds are sorted by size, with the longest scaffold at the top.



At the top of the graphic, the track called “Reference sequence” enables the user to view the region of choice. Once zoomed in far enough, this track displays the nucleotides on the scaffold. It shows the three possible translational frames for the nucleotide sequence and marks start (green) and stop (red) codons as well. The user is able to scroll the genome viewer tool using the arrows and zoom in using the (+/-) magnifying glasses above the “Reference Sequence” bar. The user can also zoom in to a specific area by double clicking on that area on the “Reference Sequence” track.

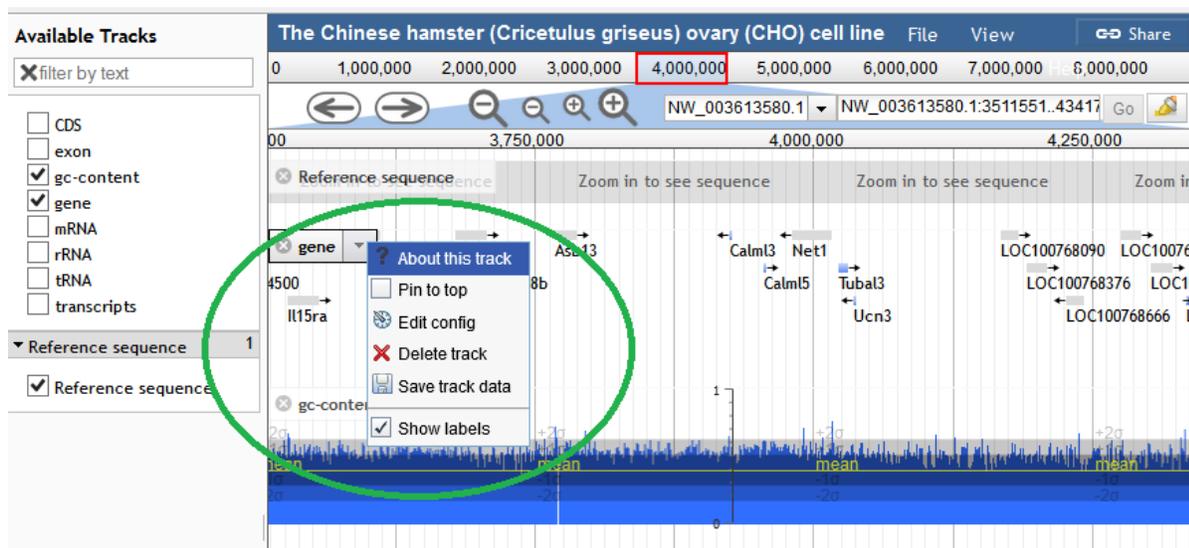


2) Feature Tracks

The tracks that are commonly filled on the gene viewer are GC Content, Gene, Exon, and mRNAs. The gc-content bar displays the percentage of bp's that are either a G or a C (calculated in a window of 100 bp), while the gene, exon, and mRNA tracks display the locations and descriptions of their respective genome features. By each track's label, there a (x) option which enables the user to turn off the track.

Hovering the mouse pointer over the track label, reveals a down arrow/menu with several options:

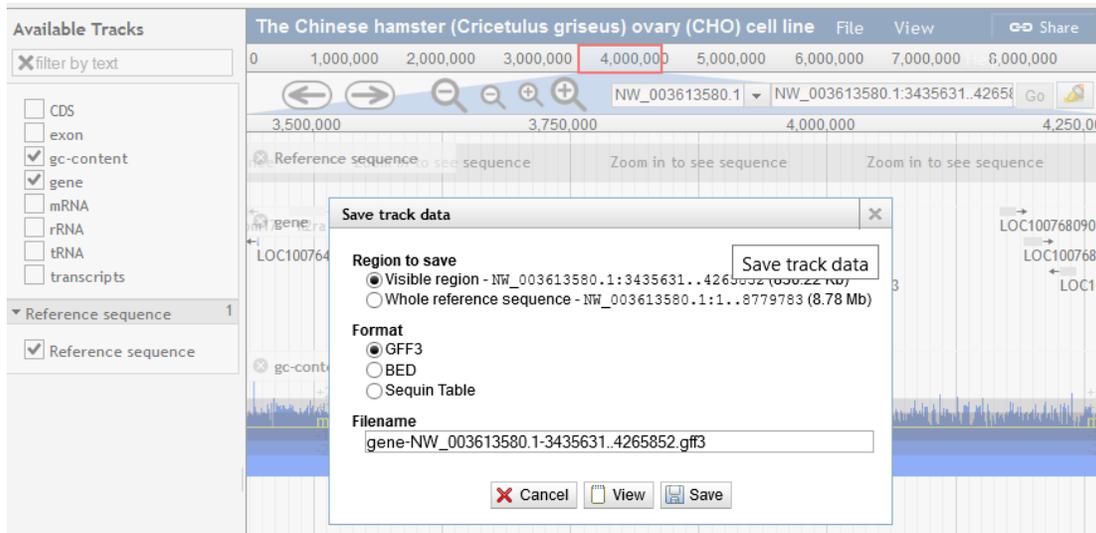
- “About this track” provides additional information about the specific track.
- “Pin to top” checkbox moves and keeps that track at the top of the track list when selected.
- “Edit config” enables the user to alter the settings of the track from the default values.
- “Delete track” permanently deletes the track for the current session.
- “Save track data” allows the user to download and save the track.
- “Show labels” checkbox makes the feature labels visible when checked. For instance, for the track gene, the gene names are visible when this box is checked.



If the user clicks on a specific feature in a track, information about that feature will be provided. The image below shows information about the gene Rbm17. The pop-up window became visible when Rbm17 feature was clicked on in the gene track. Here, the gene's position, length, IDs, and nucleotide sequence are shown. Information about the gene's subfeatures, such as exons and mRNA, are also included. The FASTA sequence of the gene can be downloaded from this pop-up window by clicking on the “FASTA” save image at the top-right of the sequence.

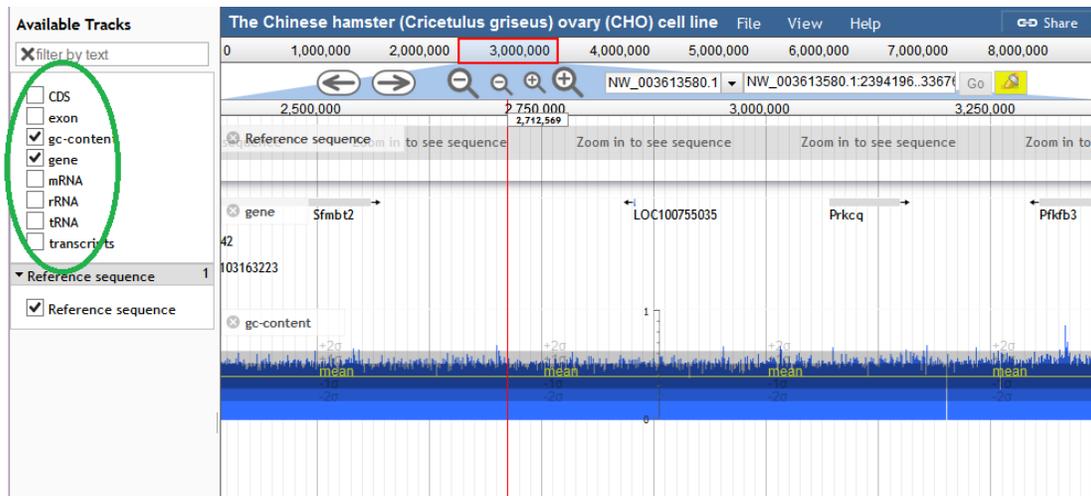
3) Downloading Sequences

The “Save track data” option can be used to download the annotations for the visible region or the entire scaffold. The type of file can be selected from the list of file options, including GFF3, BED, and Sequin Table. The user can then specify the filename and view it before downloading. The reference sequence can also be downloaded as a FASTA file by choosing the “Save track data” option for the track called “Reference sequence”.

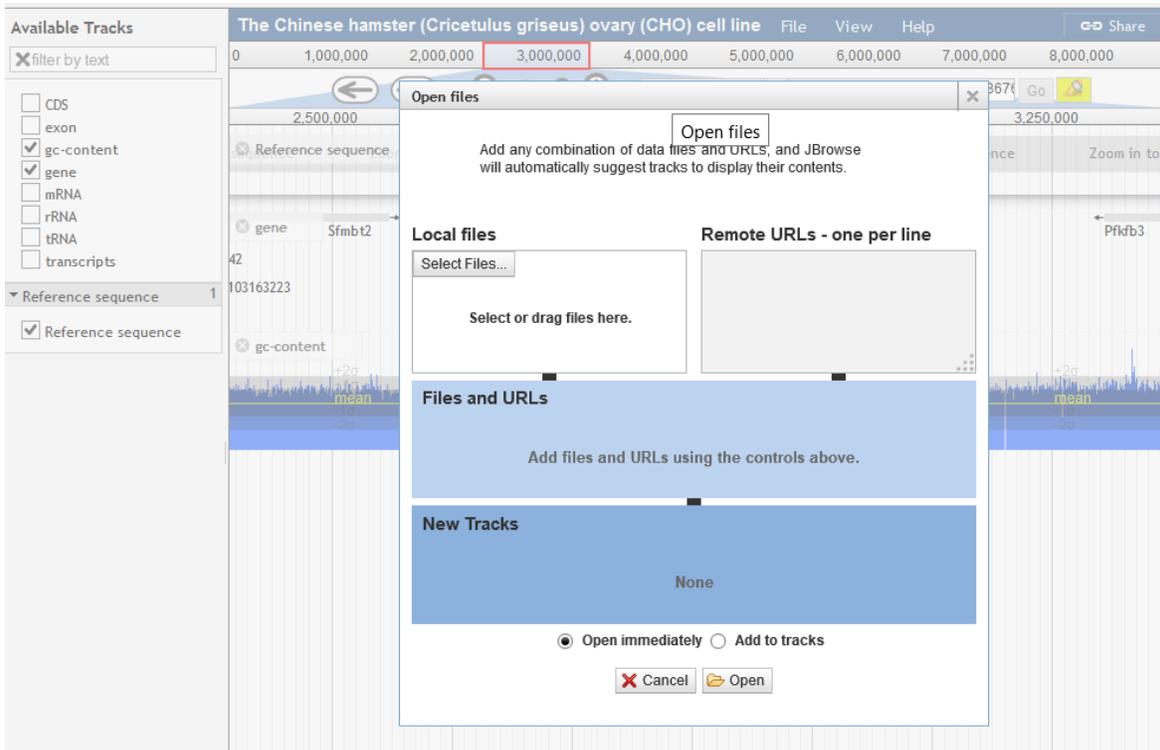


4) Browser Configuration

Add/Remove Tracks - To the left of the browser screen, there is a panel with a list of tracks. A track can be shown on the browser by checking the box next to the track name. Within the basic features, GC Content, Exon, Gene, and CDS are all preloaded tracks. Additional general tracks that are preloaded include mRNA, transcripts, rRNAs, and tRNAs. Any combination of these tracks may be enabled or disabled by the user.

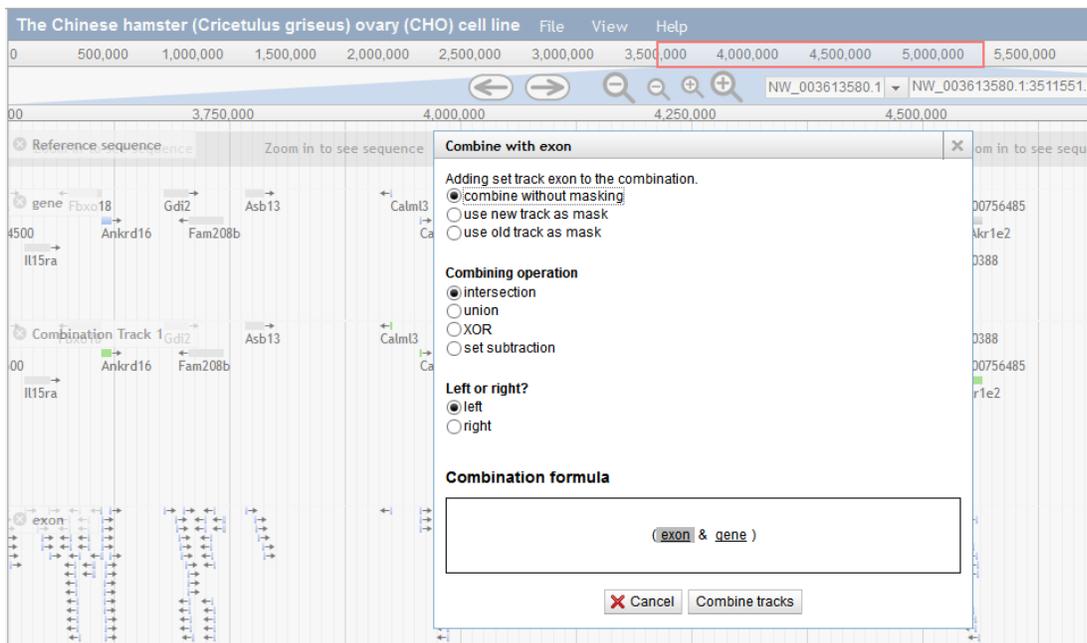


Upload Custom Tracks – To upload a custom track, click on File>Open (file is located right to the title of the browser). The following box will appear:



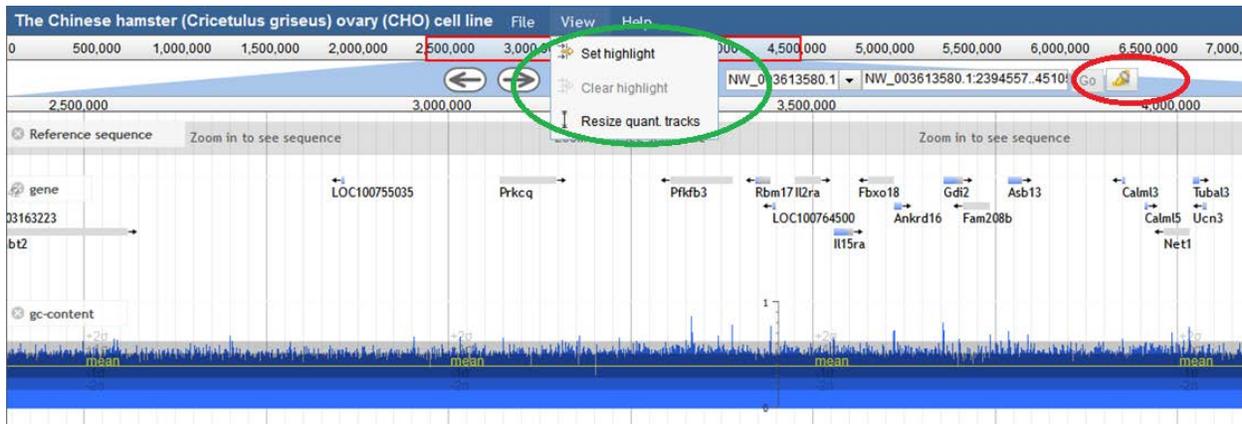
The user can select a file from their computer or use a remote URL to access the track. The track can be opened immediately on the browser or added to the tracks.

A user can also create a combination track by clicking File>Combination tracks. A new track is then added to the browser where the user can click and drag the tracks they want to combine. The following box appears:



A user can choose how they want the tracks to be combined. In the image above, the intersection of the exon features and the gene features will be shown once the user chooses “Combine tracks”.

Highlighting Regions –There are two ways a user can highlight a specified region on the browser. The first option is to go to the View menu (circled in green) and select “Set highlight”. A text box appears where the user can fill in the genome coordinates they want highlighted. The default region specified is the complete region that is visible in the browser. The highlight can then be cleared using “Clear highlight”. The third item on this menu, “Resize quant tracks”, enables the user to change the height of the quantitative tracks.



The second method to highlight regions is to click on the highlighter button (circled in red). The user can then select the region they want highlighted by clicking and dragging the mouse over the region directly on the browser.

5) CH Genome Viewer

The chromosomes from the Chinese hamster genome is also viewed using the JBrowse tool. The user must choose which chromosome they want to view first.

