

JBrowse Basics

Note: this exercise uses *TriTrypDB* (<https://TriTrypDB.org>) as an example database, but the same functionality is available on all VEuPathDB resources.

Learning objectives:

- Navigate to the genome browser
- Use the menu and navigation bars
- Run searches
- Add pre-loaded data tracks
- Upload your own data tracks
- Configure tracks
- Download track data

1. Navigating to the Genome Browser (JBrowse)

JBrowse is a fast and full-featured genome browser built with JavaScript and HTML5.

You can read more about JBrowse and its features here:

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4830012/>

Links to the genome browser are available from multiple locations:

a. The tools menu in the banner of any page.

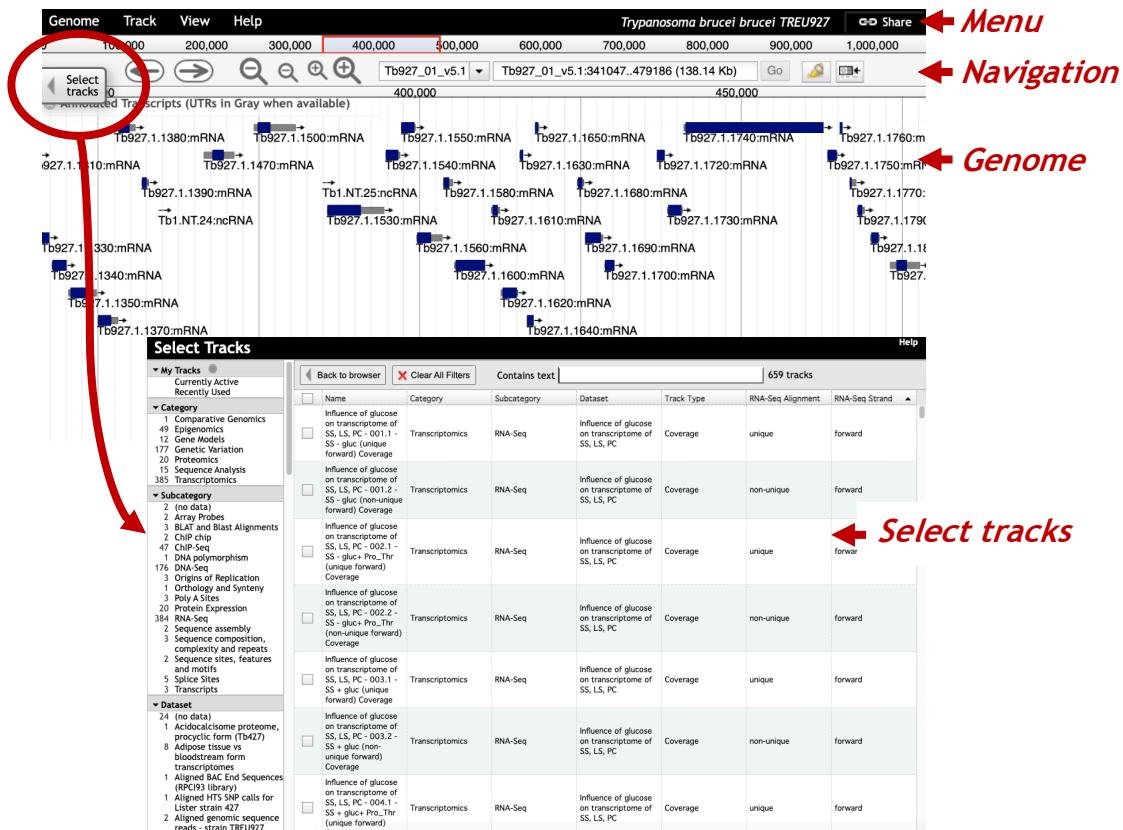
The screenshot shows the TriTrypDB homepage. At the top, there's a search bar and a menu bar with links like 'My Strategies', 'Searches', 'Tools', 'My Workspace', 'Data', 'About', 'Help', and 'Contact Us'. Below the menu, there's a section titled 'Overview of Resources available' with various links: 'Take a Tour', 'Sustainability and Future' (which is highlighted with a red arrow), 'Funding', 'BLAST (multi-query capable)', 'Companion', 'Apollo', 'CRISPR guide design tool', 'Genome browser' (also highlighted with a red arrow), 'LeishGEedit', 'NCBI Primer3', 'PubMed and Entrez', and 'Sequence retrieval'. To the right, there's a sidebar for 'My Organism Preferences' and a 'News and Trends' section.

b. From record pages such as gene, SNP or genomic sequence pages – these links are usually to a specific JBrowse configuration that includes data relevant to the section on that record page. For example, a JBrowse link from an RNAseq dataset on the gene page would display the gene of interest along with the RNAseq data as density or coverage plots. These links are usually indicated by “View in JBrowse genome browser” button.

[View in JBrowse genome browser](#)

2. Getting around JBrowse.

- Use any of the above described JBrowse linking strategies to get to the genome browser.
- Once in JBrowse examine the following features:
 - The **menu bar**: located at the top of the JBrowse frame. This includes the Genome menu, Track menu, View menu, Help menu and the Sharing link on the right side of the screen. What do each of these do/provide?
 - The **navigation bar**: located below the menu bar. This contains zooming (magnifying glass icons), panning (left/right arrows) and highlighting (yellow highlighter) buttons, reference sequence selector (drop down with sequences from the selected genome sorted by length), a text box to search for features such as gene IDs and overview bar which shows the location of the region in view.
 - The **genome view**: this is where the data tracks are displayed.

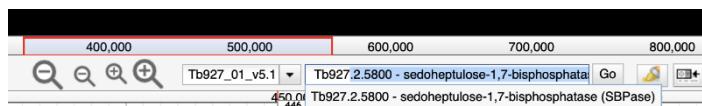


- Selecting tracks: click on the “select track” button (top left). You can search/filter for tracks and then select them for display by checking the check box next to the track name.

3. Navigate to a specific gene in JBrowse.

The goal of this step is to navigate to the sedoheptulose-1,7-bisphosphatase (SBPase) gene of *T. brucei* 927.

- Make sure the *Trypanosoma brucei brucei* TREU927 genome is selected from the genome menu.
- Start typing the word sedoheptulose in the search box. After a few seconds you should see the result of the search (do not hit enter). Select the gene from the search dropdown and press GO. This will take you to Tb927.2.5800.

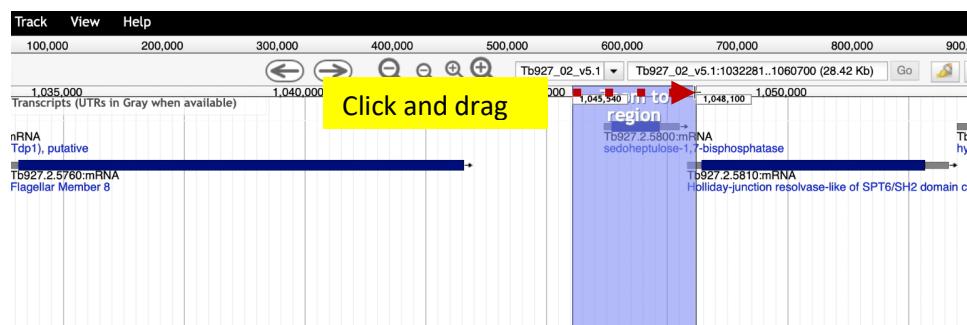


- You can get information about any feature in the genome view window by clicking on it. Click on the gene. What information is in the popup?
 - You can also right click (or control click) on a feature to display a menu which provides quick links to highlight a feature, go to the feature page (like the gene page) or get the info popup (the same one you get when you click on the feature).
- View Details
 - View Gene Page
 - Highlight this gene
- What genes are immediately upstream and downstream of SBP? (Hint: use the zoom out button in the navigation bar). What is the difference between the small and large zoom buttons? (*Tip1*: another way to zoom in and out is by clicking on shift and the up or down arrows. What happens if you click shift and left or right arrows? *Tip2*: you can also zoom in by clicking and dragging your cursor in the location ruler in the navigation bar).

Genome Track View Help

Leishmania panamensis strain mRNAs v0.1

- Leishmania sp. Ghana MHOM/GH/2012/GH5
- Leishmania sp. Namibia MPRO/NA/1975/252/LV425
- Leishmania tarentolae Parrot Tar II 2019
- Leishmania tarentolae Parrot-TarII
- Leishmania tropica L590
- Leishmania turanica strain LEM2300
- Leptomonas pyrrhocoris H10
- Leptomonas seymouri ATCC 30220
- Paratrypanosoma confusum CUL13
- Porcisia hertigi MC0E/PA/1965/C1129
- Trypanosoma brucei EATRO1125
- Trypanosoma brucei Lister strain 427
- Trypanosoma brucei Lister strain 427 2018
- Trypanosoma brucei brucei TREU927
- Trypanosoma brucei gambiense DAL972
- Trypanosoma congolense IL3000
- Trypanosoma congolense IL3000 2019
- Trypanosoma congolense Tc1/148
- Trypanosoma cruzi Berenice
- Trypanosoma cruzi Brazil A4
- Trypanosoma cruzi Bug2148
- Trypanosoma cruzi CL Brener Esmeraldo-like
- Trypanosoma cruzi CL Brener Non-Esmeraldo-like

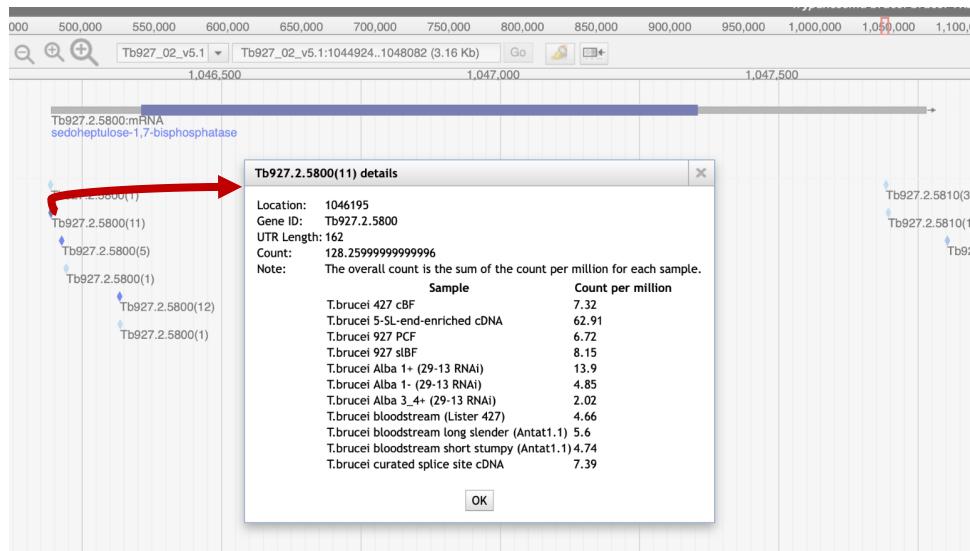


4. Explore transcription start sites.

Are you confident about the gene transcription start? (Note: gene features are in blue (left to right) or red (right to left) while untranslated regions (UTRs) are white). What additional data track would be useful for you to assess the transcription start site? (hint: Click on the “Select Tracks” button to reveal all available tracks. Now type the word “splice” in the “contains text” box. This will filter all tracks that contain the word splice. Find the one called “Unified Splice Leader Addition Sites” and select it. Click on the “Back to browser” button).

Category	Subcategory	Dataset	Track Type	RNASeq Alignment	RNASeq Strand
Bloodstream and procyclic for spliced leader transcriptions (927, 427)(2014) - Splice Sites	Gene Models	Splice Sites	Segments
Bloodstream and procyclic form spliced leader transcriptions (427, Antat) (2010) - Splice Sites	Gene Models	Splice Sites	Segments
Curated Poly A Sites from bloodstream and procyclic forms	Gene Models	Poly A Sites	Segments
Procyclic form spliced leader transcriptome - Poly A Sites	Gene Models	Poly A Sites	Segments
Procyclic form spliced leader transcriptome - Splice Sites	Gene Models	Splice Sites	Segments
Spliced Leader and Poly A Sites from bloodstream and procyclic forms - Splice Sites	Gene Models	Splice Sites	Segments
Unified Spliced Leader Addition Sites	Gene Models	Splice Sites	Segments

What do the different diamond colors mean? Each track title has a drop-down menu that contains a link to an ABOUT popup. Click on this to see what the colors mean. Click on the diamonds to see information about that specific feature. Which color provides the most evidence for a splice junction?



5. Explore synteny between genomes.

Synteny helps define conservation of homologous genes and gene order between genomes.

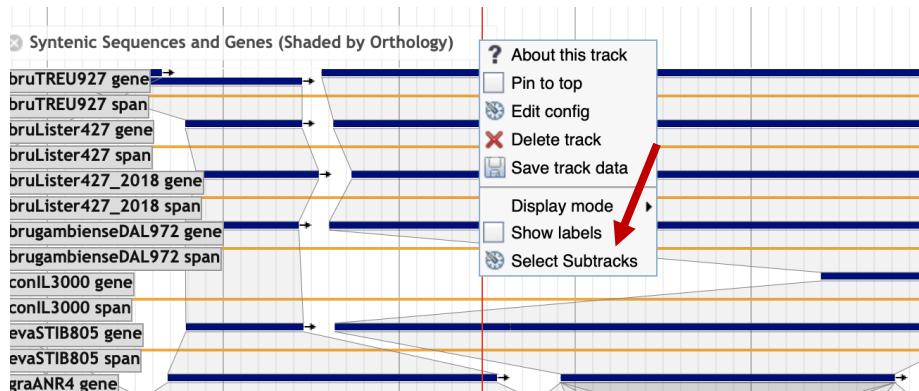
- Go to the “Select Tracks” tab on the left of the page and turn on the track called “Syntenic Sequences and Genes”. How did you find this track? One option is to click on the “Comparative Genomics” category on the left side to filter the tracks.

The screenshot shows the 'Select Tracks' interface. On the left, there's a sidebar with 'My Tracks' (Currently Active, Recently Used) and a 'Category' section where 'Comparative Genomics' is expanded, showing sub-options like Epigenomics, Gene Models, Genetic Variation, Proteomics, Sequence Analysis, and Transcriptomics. The main area is a table titled '1 matching track' with columns: Name, Category, Subcategory, Dataset, Track Type, RNASeq Alignment, and RNASeq Strand. A single row is selected: 'Syntenic Sequences and Genes (Shaded by Orthology)' under 'Comparative Genomics' > 'Orthology and Synteny'. The 'Track Type' is listed as 'Segments'.

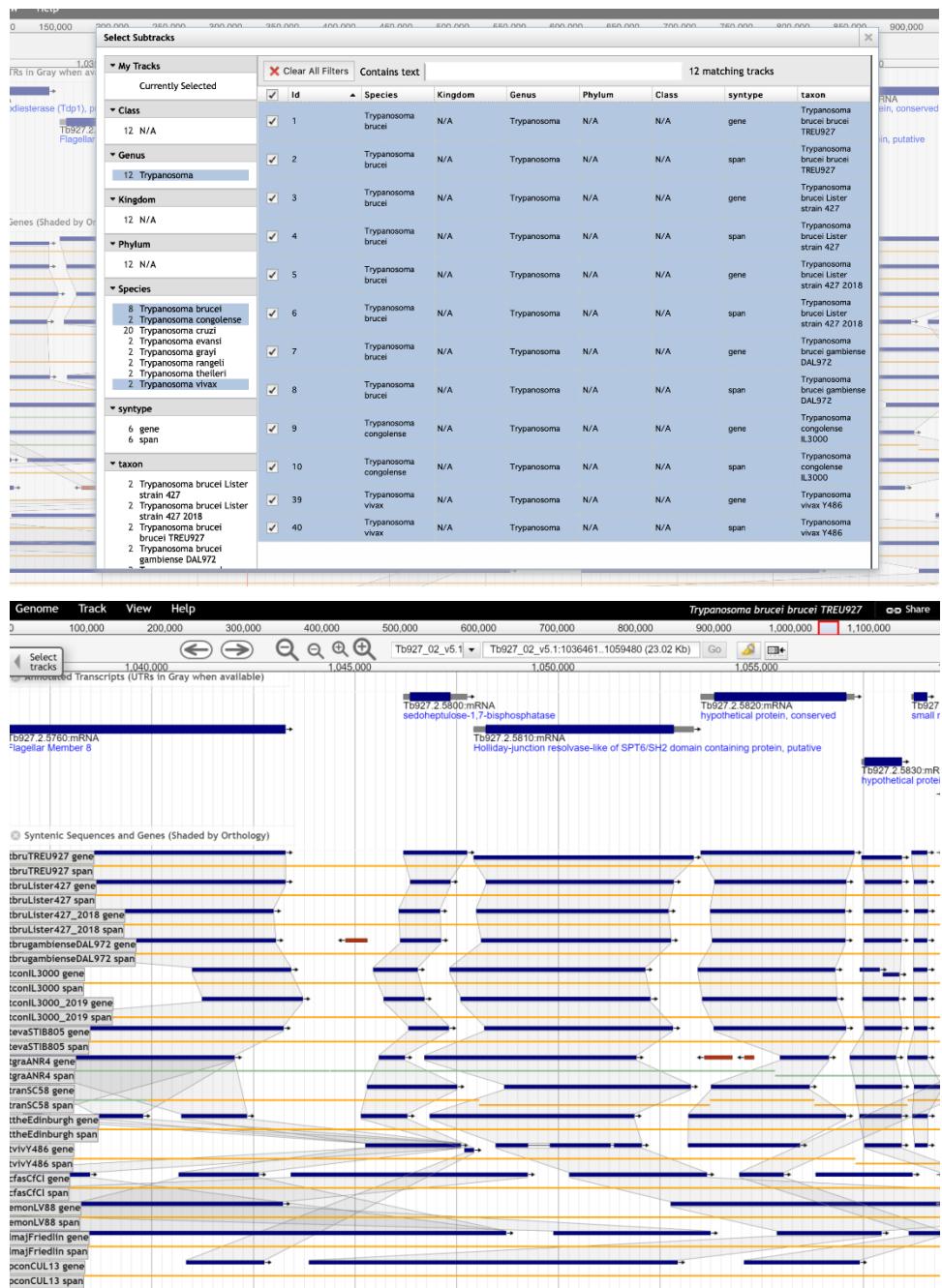
- Return to the browser by clicking “Back to Browser” and zoom out so you can see a couple of genes on either side of SBP (does not have to be exact)
- Configure the synteny track to include the following species subtracks: *Trypanosoma brucei* 927, *T. brucei* 427, *T. brucei gambiense*, *T. congolense*, *T. evansi*, *T. theileri* and *T. grayi*, *Crithidia fasciculata*, *Leishmania amazonensis*, *L. braziliensis*, *L. donovani*, *L. infantum*.
 - To configure the subtracks:
 - Click on the down arrow in the track name



- Select the option called “Select Subtracks” from the menu



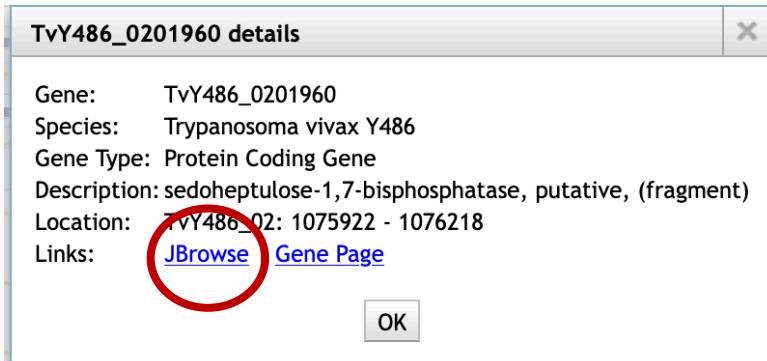
- In the next popup first uncheck all organisms, second use the filters on the left to select Trypanosoma, third select the species of interest (note that you should select both the gene and span subtracks for each species and that there may be two genome versions for an organism), fourth **click on the save button at the bottom of the popup**.



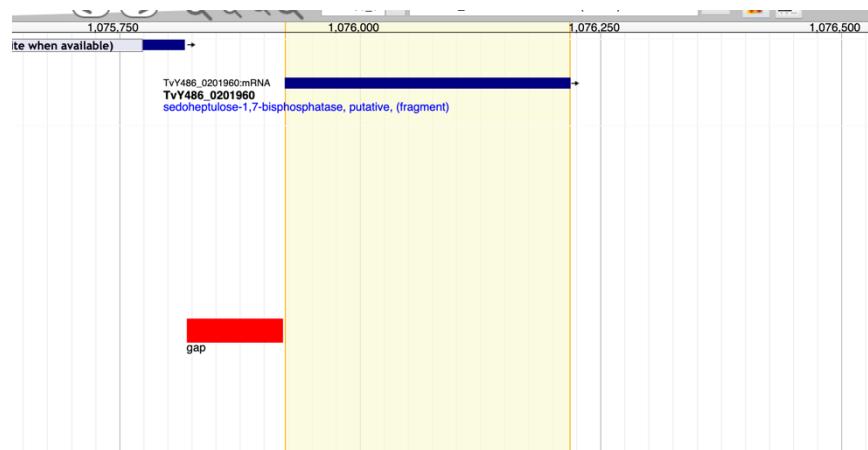
- What does the synteny track in this region look like? Feel free to zoom out some more. Are genes (in general) similarly organized between these species? What does the shading between genes mean?
- What direction is the SBPase gene relative to the chromosome?
- What genes are upstream and downstream of the SBPase? Are these genes synteny?
- What does synteny look like if you add more distantly related species? Does SBPase appear to have orthologs in *Leishmania* species or *Cryptosporidium*?
- Add a synteny subtract for *T. vivax*. Examine the gene corresponding to the *T. vivax* SBPase in the synteny track. Hover over the gene image to find the gene name in the

popup. Does this gene appear to be a fragment? What could be some possible reasons for this?

- Click on the Jbrowse link in the *T. vivax* SBPase (fragment) popup.



- Add the track called “scaffolds and Gaps”



- What does this track tell you about the sequence in that area? Based on this do you expect *T. vivax* to contain a full SBPase sequence?

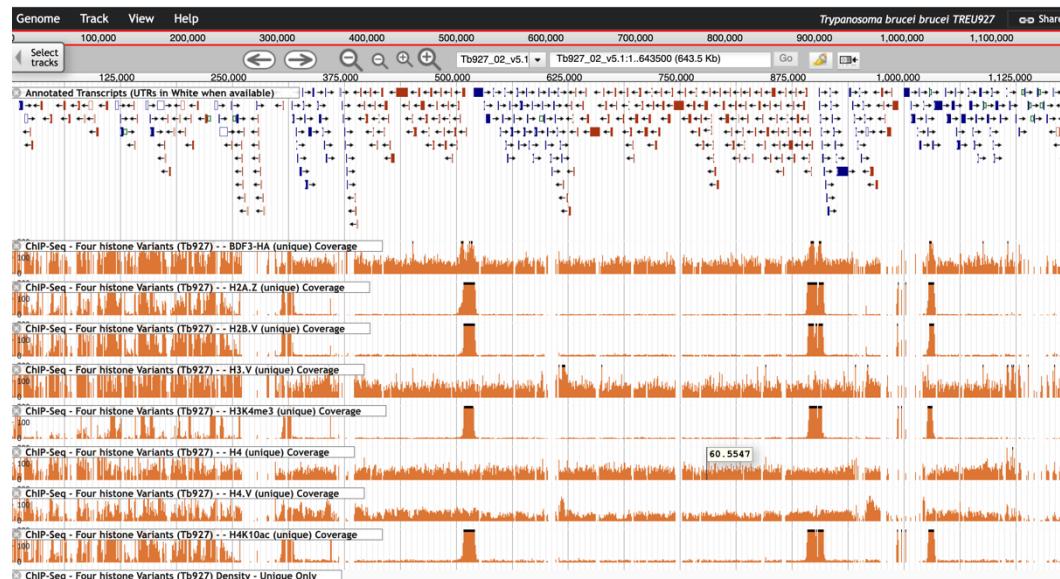
6. Explore other data tracks in JBrowse.

For this example, we will view *T. brucei* TREU927 data, so the data tracks you turn on will display data only if the data is aligned to the *T. brucei* genome. Return to the SBPase gene in *T. brucei* by searching for the gene ID in the (Tb927.2.5800) in ‘Landmark or Region’ to redirect the browser.

Turn on the ChIP-seq coverage plots and turn off the syntenic gene and region tracks. The data tracks are from an experiment called: **ChIP-Seq - Four Histone Variants ChIP-Seq Coverage aligned to *T brucei* TREU927 (Cross) (linear plot)**. For this experiment, chromatin was immunoprecipitated using several different histone antibodies. The DNA that precipitated with the histone was sequenced and aligned to the *T. brucei* TREU927 genome. Peaks in the sequence coverage plots represent areas of histone binding. Different histone variants can be associated with start and termination sites for transcription (<http://www.ncbi.nlm.nih.gov/pubmed/19369410>).

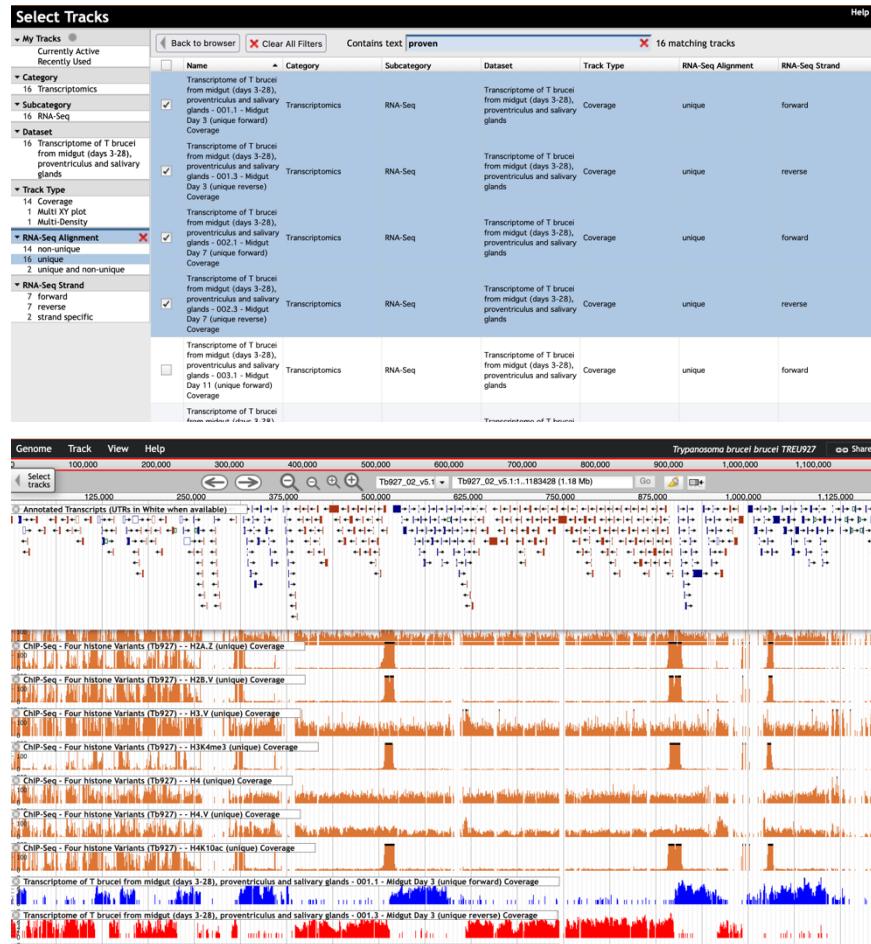
Name	Category	Subcategory	Dataset	Track Type	RNASeq Alignment	RNASeq Strand
BDF3-HA (unique) Coverage	Epigenomics	ChIPSeq	ChIP-Seq - Four histone Variants	Coverage
ChIP-Seq - Four histone Variants		ChIPSeq	ChIP-Seq - Four histone Variants	Multi-Density
H2A.Z (unique) Coverage	Epigenomics	ChIPSeq	ChIP-Seq - Four histone Variants	Coverage
H2B.V (unique) Coverage	Epigenomics	ChIPSeq	ChIP-Seq - Four histone Variants	Coverage
H3K4me3 (unique) Coverage	Epigenomics	ChIPSeq	ChIP-Seq - Four histone Variants	Coverage
H3v (unique) Coverage	Epigenomics	ChIPSeq	ChIP-Seq - Four histone Variants	Coverage
H4 (unique) Coverage	Epigenomics	ChIPSeq	ChIP-Seq - Four histone Variants	Coverage
H4K10ac (unique) Coverage	Epigenomics	ChIPSeq	ChIP-Seq - Four histone Variants	Coverage
H4v (unique) Coverage	Epigenomics	ChIPSeq	ChIP-Seq - Four histone Variants	Coverage

- Zoom out to display the entire chromosome. What does this data show you?
- Roughly how many polycistronic units does this chromosome have? Zoom out to the entire chromosome.



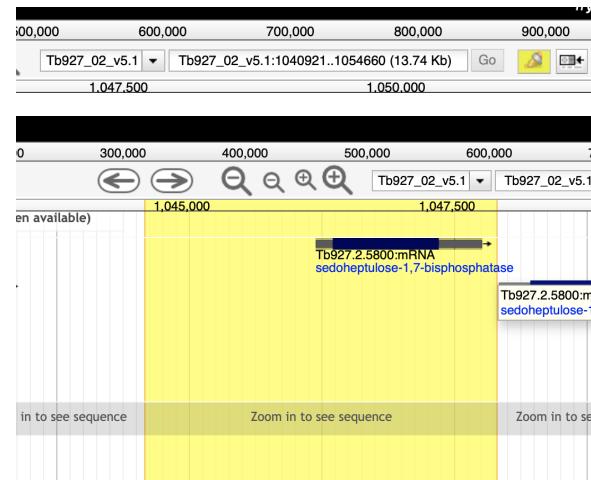
- Do the ChIP-seq peaks correlate with the direction of gene transcription (blue vs. red)?

- What if you turn on a strand-specific RNAseq dataset – for example, turn on some of the uniquely mapped forward and reverse coverage tracks from the experiment:
“Transcriptome of *T brucei* from midgut (days 3-28), proventriculus and salivary glands”.



7. Retrieve data from JBrowse and upload your own tracks to JBrowse

- Download sequence in FASTA format from the SBPase gene (your region of interest):
 - Make sure the “**annotated transcripts**” and the “**reference sequence**” tracks are turned on.
 - Click on the “highlight a region” button in the navigation bar. The button should turn yellow when activated.
 - Click and drag in the genome view region (in the Annotated Transcripts track) and select the area you would like to highlight.
 - Click on the down arrow on the reference sequence track and select “Save track data”.
 - In the next popup window you can keep everything as the default and either save or view the sequence.



b. *Uploading data to JBrowse:*

JBrowse can accept several standard-format data files by direct upload or through a URL if the data is stored remotely. Some file formats like BAM and VCF require indexing before uploading. In this exercise we will download a bigwig file from GEO and then upload it to JBrowse:

- Go to this GEO sample record:

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM2407365>

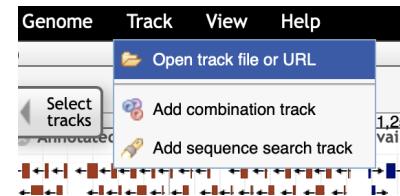
- Scroll down to the bottom of the page and download the bigwig file with the http link.

- Once the file is downloaded go to JBrowse and

Supplementary file	Size	Download	File type/resource
GSM2407365_BF_WT_HNI_VO2_rep2-T_brucei_427.bigwig	12.4 Mb	(ftp)(http)	BIGWIG

select ***Trypanosoma brucei* Lister strain 427** as the reference genome (hint: use the Genome link in the menu panel, top left).

- Turn on the track for annotated transcripts if it is not on already.



- Click on the Tracks menu item and select “Open track file or URL”.

In the popup click on select file then select the file you just downloaded. JBrowse should automatically recognize that the file is in bigwig format.

- Click on the Open button. The bigwig output should appear very quickly in your browser.