

# Browser Exercises

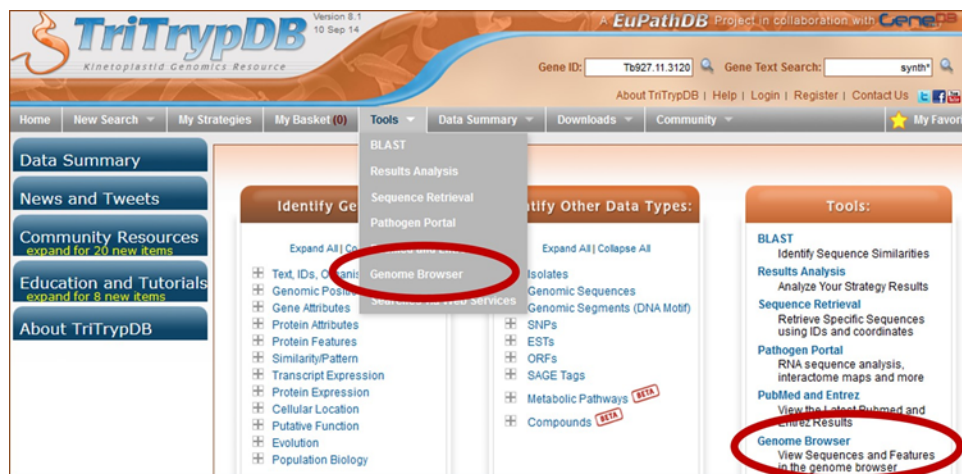
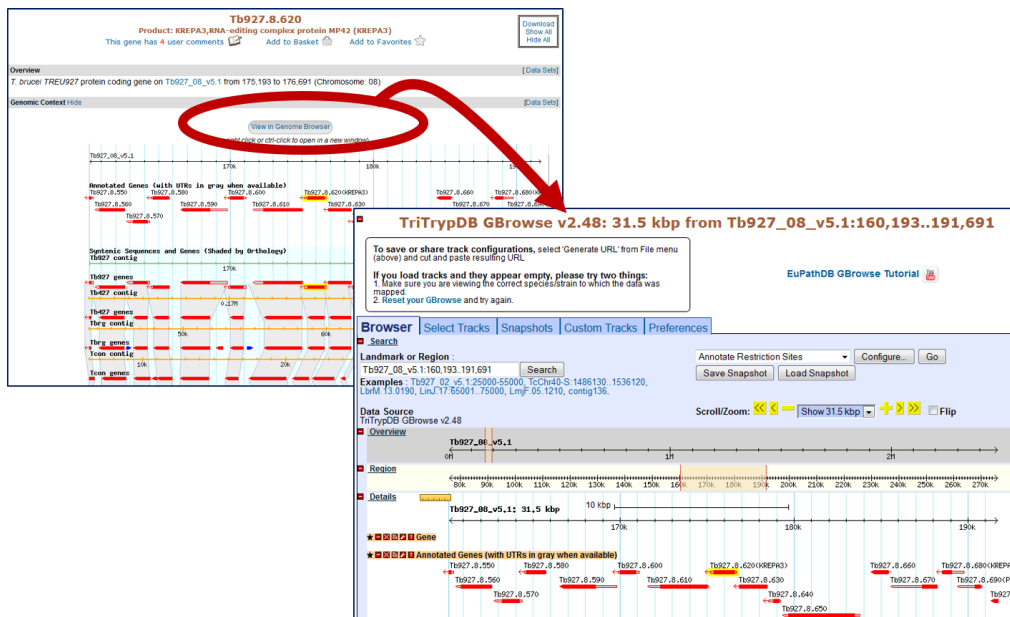
## Alignments and Comparative genomics

### 1. Navigating to the Genome Browser (GBrowse)

Note: For this exercise use <http://www.tritrypdb.org>

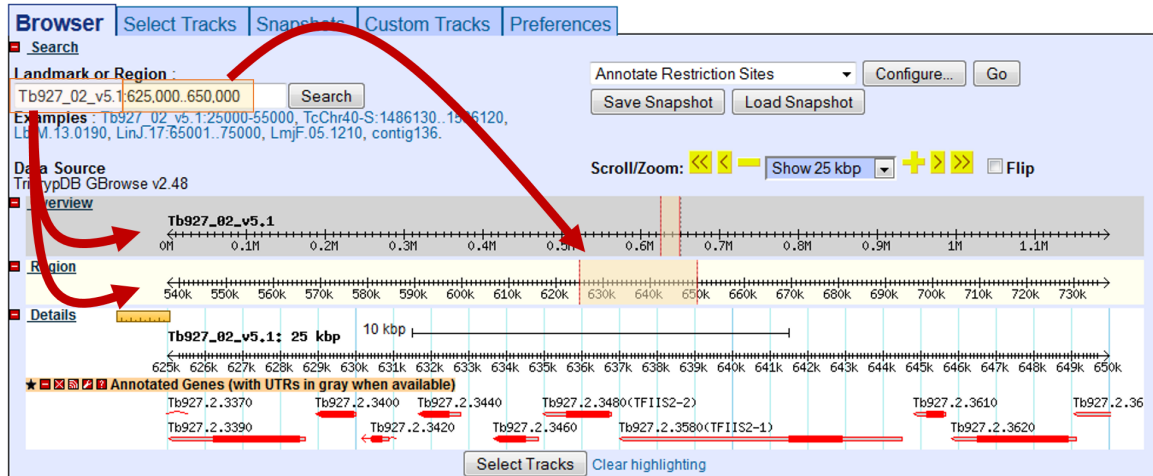
#### 1a. There are two ways to navigate to GBrowse from TriTrypDB.

- From record pages, like a gene page, genomic sequence or EST page, click on the “View in Genome Browser” link. You can also use the Tools section on the homepage or the grey toolbar in the header section

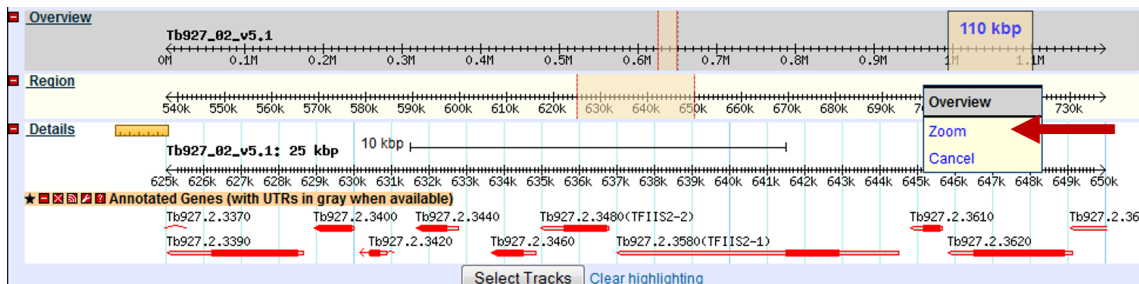


1b. Go to GBrowse from the TriTrypDB home page. Explore this page – take note of the different sections: Instructions, Search, Overview, Region, Details, Tracks, etc...

1c. Look at the “Landmark or Region” box.



- What information does the “Landmark or Region” box contain? The Landmark or Region box should read – Tb927\_02\_v5.1:625,000..650,000.
- What chromosome is displayed?
- What location of the chromosome is displayed?
- Move to a different genomic region on this chromosome – for example, visit the right arm of this chromosome.
  - Hint: change the coordinate numbers in the “landmark or region” box to correspond to an area in that region. Look at the overview to give you an indication of the total size of this chromosome, ie. 1000000..1100000).
  - OR highlight the area representing approx. 1000000-1100000 on the scale in the Overview section and then choose zoom from the popup.



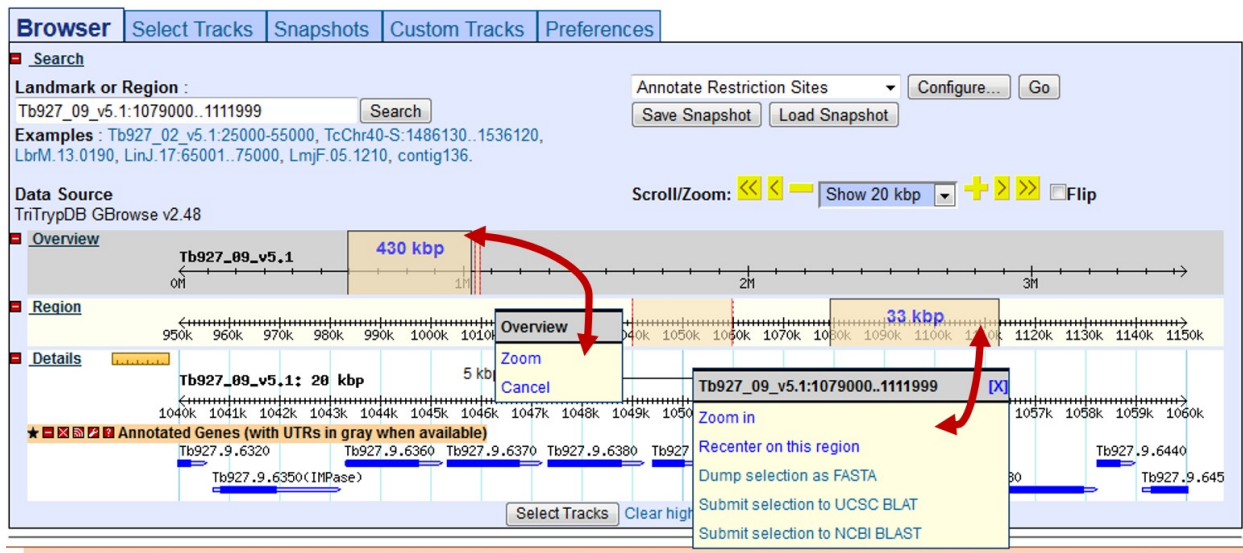
- Move to chromosome 9. How did you do this?
  - Hint: Change the chromosome number in the “landmark or region” box – it should look like this: Tb927\_09\_v5.1:1,000,000..1,100,000.

- Zoom in to a 20Kb region. Select 20Kb from the Scroll/zoom drop down menu.

The screenshot shows the GBrowse interface with the 'Scroll/Zoom' dropdown menu open. The menu options are: Show 100 kbp, Show 1 Mbp, Show 500 kbp, Show 200 kbp, Show 100 kbp, Show 50 kbp, Show 20 kbp (highlighted), Show 10 kbp, Show 5 kbp, Show 2 kbp, Show 1 kbp, Show 200 bp, and Show 100 bp. The main view displays a genomic track for Tb927\_09\_v5 with a ruler at the bottom showing coordinates from 950k to 1150k. The 'Details' section shows a zoomed-in view of the region with gene annotations and a ruler at the bottom showing coordinates from 1000k to 1100k.

- What genes are in this region? Mouse over the gene graphics and look at the popups.
- Explore the ruler tool. Click on the ruler to engage then drag it across the window. The ruler tool displays the nucleotide coordinates of the ruler's solid center line. This is very useful for comparing between the annotation data track and others that we will add later.
- There are other ways to move and zoom. Try highlighting an area along the scale in the overview, region or details sections of GBrowse.

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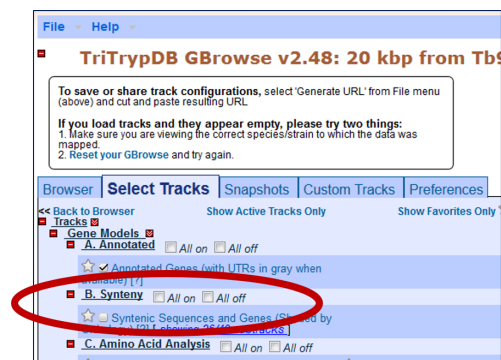


- 1d. What if you want to go to a specific gene in Gbrowse? Try to figure out how to go to this gene: Tb927.2.5800
- Type the ID in the “landmark or region” box. The landmark box has a search function that supports gene IDs. What else does it support?
  - What is this gene?

## 2. Exploring Synteny data tracks in GBrowse

- 2a. Is the region containing the sedoheptulose-1,7-bisphosphatase (SBPase) gene syntenic in all kinetoplastids?

Hint: Go to the “Select Tracks” section and turn on the track called “Syntenic Sequences and Genes”. The browser is automatically updated with tracks you select. Note that this track contains multiple subtracks.



- Return to the browser by clicking the “Browser” tab and **zoom out to 20Kb**.
- What does this region look like?
- What direction is the gene relative to the chromosome?
- What genes are upstream and downstream of the SBPase?
- Modify the subtracks to remove *Leishmania* species from the view. Click on the link ‘showing 40 of 40 subtracks’, wait for the popup and uncheck all *Leishmania* and *Crithidia* species. **Then click Change**.

Details  
Tb927\_02\_v5.1: 20 kbp 5 kbp

← 1038k 1039k 1040k 1041k 1042k 1043k 1044k 1045k 1046k 1047k 1048k 1049k 1050k 1051k 1052k 1053k 1054k 1055k 1056k 1057k →

★ [x] [x] [x] [x] Annotated Genes (with UTRs in gray when available)

Tb927.2.5760 Tb927.2.5800 (SBPase) Tb927.2.5820

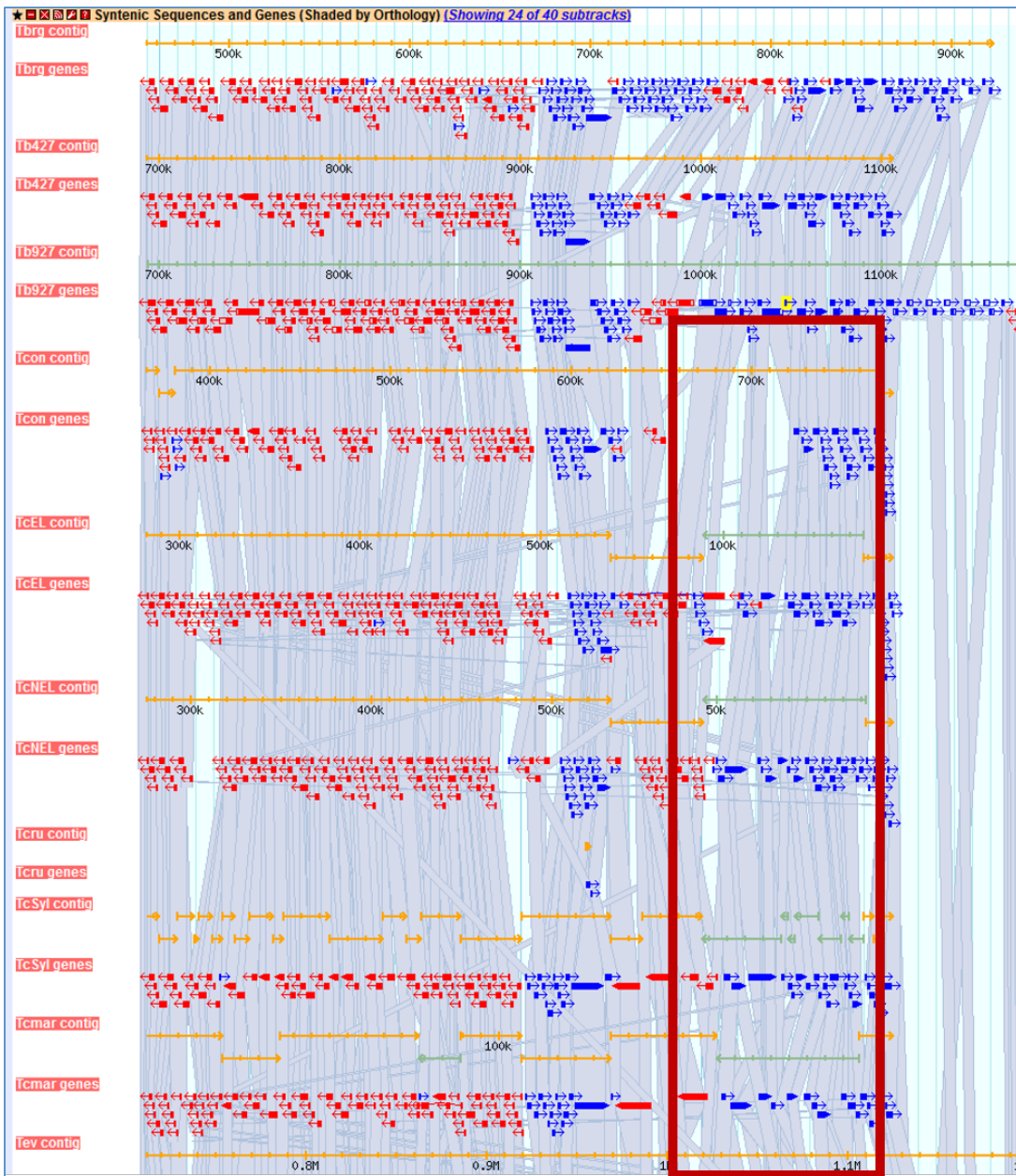
★ [x] [x] [x] [x] Syntenic Sequences and Genes (Shaded by Orthology) (Showing 40 of 40 subtracks)

Tbrq contin  
Tbrq genes  
Tb427 contin  
Tb427 genes  
Tb927 contin  
Tb927 genes  
Tcon contin  
Tcon genes  
TcEL contin  
TcEL genes  
TcNEL contin  
TcNEL genes

<input checked="" type="checkbox"/>	Trypanosoma vivax ANR4	contig
<input checked="" type="checkbox"/>	Trypanosoma grayi ANR4	genes
<input checked="" type="checkbox"/>	Trypanosoma vivax Y486	contig
<input checked="" type="checkbox"/>	Trypanosoma vivax Y486	genes
<input checked="" type="checkbox"/>	Crithidia fasciculata strain Cf-CI	contig
<input checked="" type="checkbox"/>	Crithidia fasciculata strain Cf-CI	genes
<input checked="" type="checkbox"/>	Leishmania braziliensis MHOM/BR/75/M2904	contig
<input checked="" type="checkbox"/>	Leishmania braziliensis MHOM/BR/75/M2904	genes
<input checked="" type="checkbox"/>	Leishmania br	contig
<input checked="" type="checkbox"/>	Leishmania br	genes
<input checked="" type="checkbox"/>	Leishmania do	contig
<input checked="" type="checkbox"/>	Leishmania do	genes
<input checked="" type="checkbox"/>	Leishmania inf	contig
<input checked="" type="checkbox"/>	Leishmania inf	genes
<input checked="" type="checkbox"/>	Leishmania infantum of CWS	genes
<input checked="" type="checkbox"/>	Leishmania major strain Friedlin	contig
<input checked="" type="checkbox"/>	Leishmania major strain Friedlin	genes
<input checked="" type="checkbox"/>	Leishmania mexicana MHOM/GT/2001/U1103	contig
<input checked="" type="checkbox"/>	Leishmania mexicana MHOM/GT/2001/U1103	genes
<input checked="" type="checkbox"/>	Leishmania tarentolae Parrot-Tarll	contig
<input checked="" type="checkbox"/>	Leishmania tarentolae Parrot-Tarll	genes

**Uncheck the Crithidia and Leishmania tracks to turn them off.**

- Zoom out to 500KB – what could you conclude about this region in *T. congolense*? (See image on next page if needed).
- You will also notice that some of the genomes have contigs that are not contiguous. Why is that?
- Mouse over the two contigs and look at the information in the popups – do these pieces belong to the same chromosome? What does this mean?

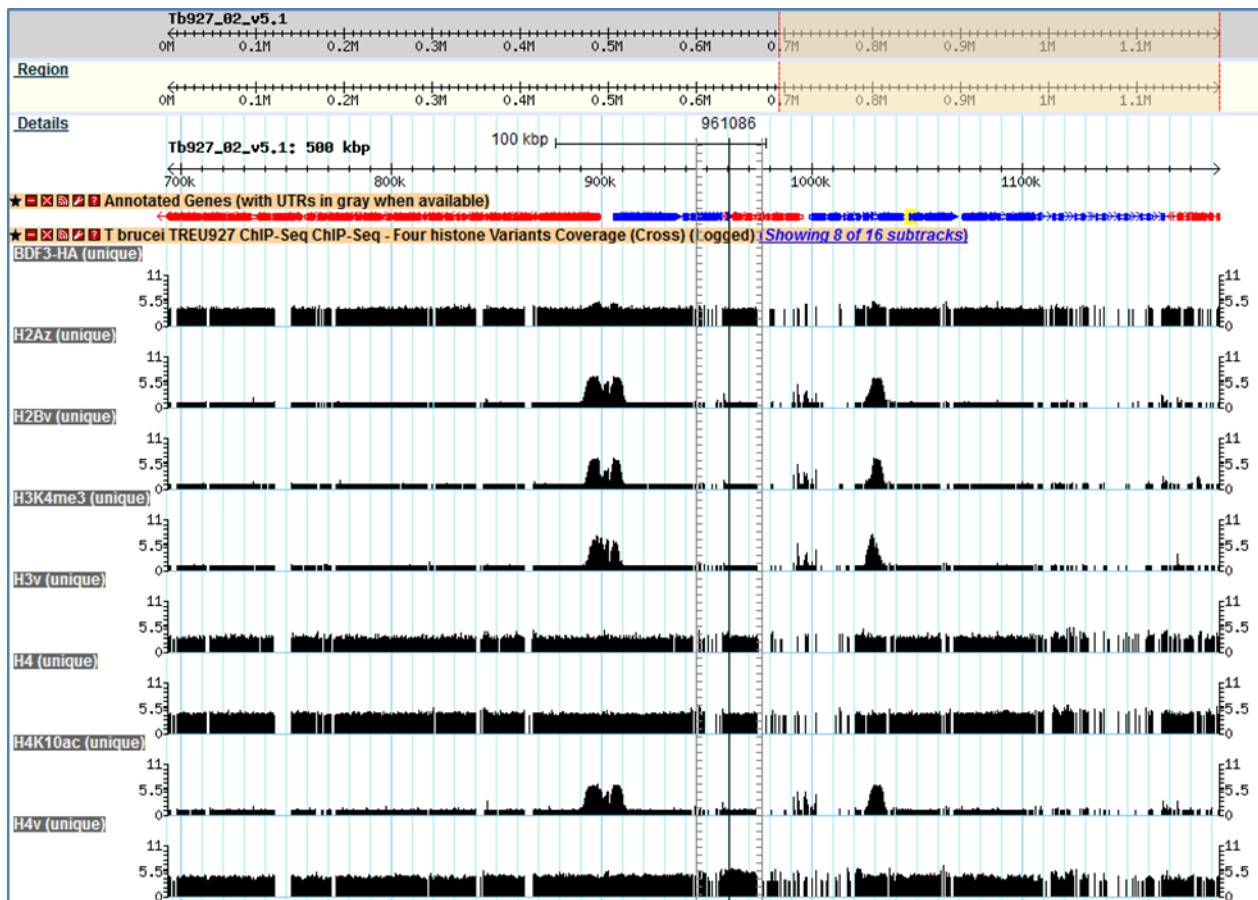


## 2b. Exploring other data tracks in Gbrowse.

In this example we are viewing *T. brucei* SBPase, so the data tracks you turn on will display data only if the data is aligned to the *T. brucei* genome.

Turn on the ChIP-seq coverage plots and turn off the syntenic gene and region tracks. The data track is called: **ChIP-Seq - Four histone Variants ChIP-Seq Coverage aligned to T brucei TREU927 (Cross) (log plot)**.

- What does this data show you?  
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 and transcription start sites.  
<http://www.ncbi.nlm.nih.gov/pubmed/19369410>
- 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)?



### 3. Uploading your own tracks to GBrowse

- **Uploading your own tracks is also possible.** One reason to upload your own tracks is if you have data that you would like to display on a chromosome or genomic segment and view it in the context of gene models and other data. To do this you have to follow some rules to ensure that the file you are uploading can be understood by GBrowse.

- Now let's load a complex graphic, a bigwig file of some RNA Sequencing data. For this we posted the file to a public site and are using the URL to direct GBrowse to the file location. In the field "Fetch track file from this URL", enter the following and click Import:

**[http://loquat.rcc.uga.edu/swfultz/bigwig/TREU927\\_Cross\\_RNASeq.bw](http://loquat.rcc.uga.edu/swfultz/bigwig/TREU927_Cross_RNASeq.bw)**

