

# Browser Exercises - I

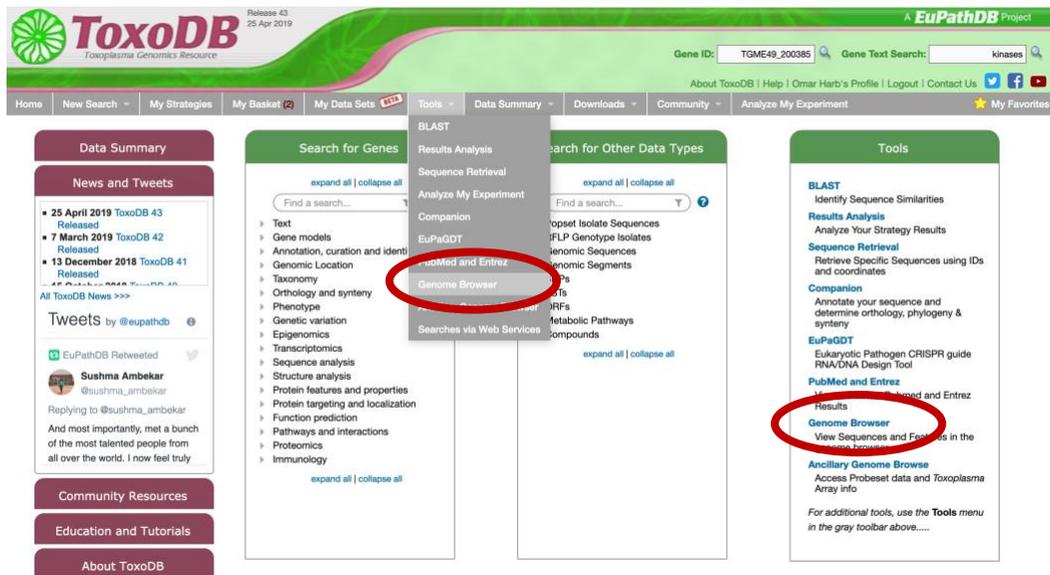
## Alignments and Comparative genomics

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

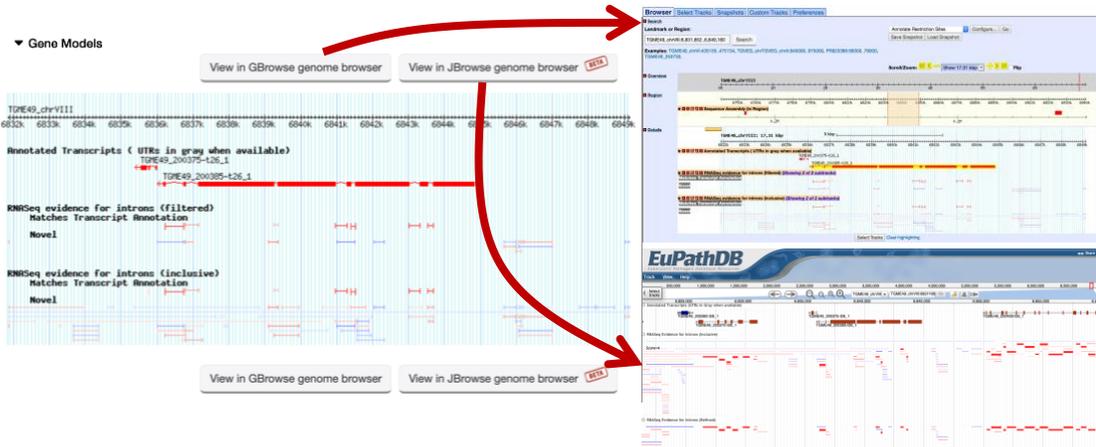
Note: For this exercise use <http://toxodb.org>

#### a. Navigate to the Genome Browser (GBrowse) from the ToxoDB home page.

- Go to GBrowse from the ToxoDB home page. You can use the Tools section on the homepage or the grey toolbar in the header section.
- Explore the browser – take note of the different sections of the browser: Search, Overview, Region, Details, Select Tracks, etc.

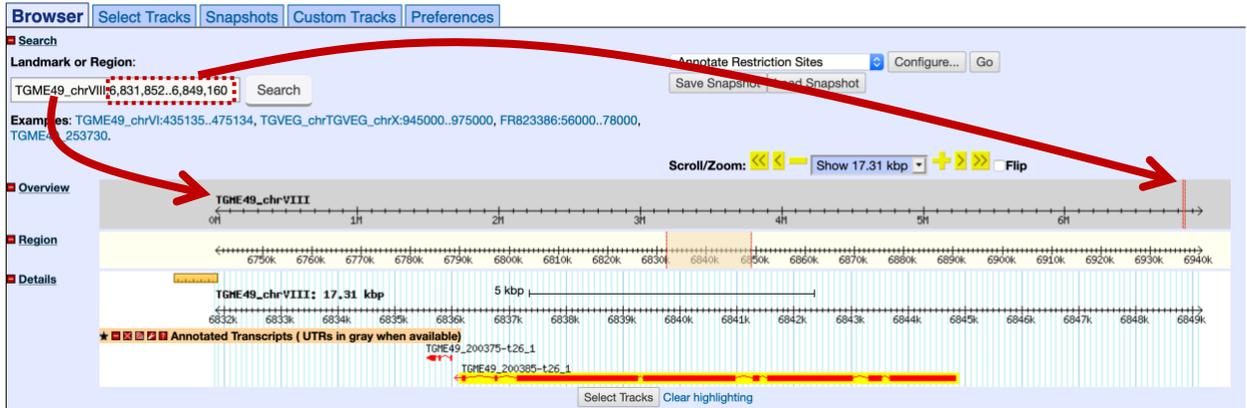


- Gene pages contain links to the GBrowse as well as JBrowse in various places. For example, the Gene Models section of the gene links to GBrowse and JBrowse. Both browsers are GMOD projects, but JBrowse is actively supported by GMOD.

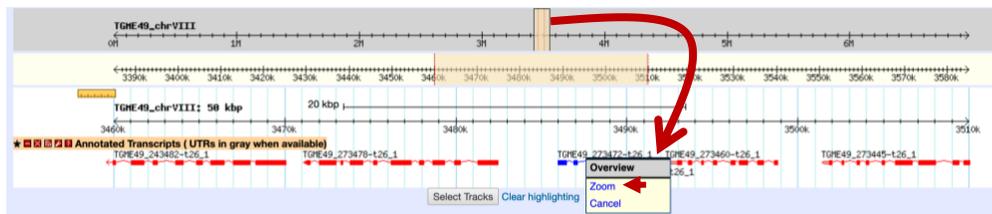


b. Explore a genomic sequence and the annotation track in GBrowse.

- Look at the “Landmark or Region” box. What information does the “Landmark or Region” box contain? The Landmark or Region box should read – TGME49\_chrVIII:6,831,852..6,849,160. If not, then cut and paste the location into the box.
- What chromosome is displayed?

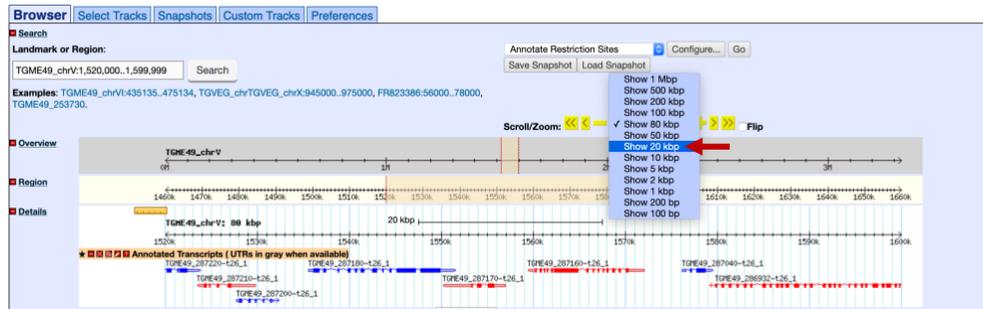


- What location of the chromosome is displayed?
- Move to a different genomic region on this chromosome. For example, visit the middle of this chromosome.
  - Hint: change the coordinate numbers in the “Landmark or Region” box to correspond to an area in that region. Look at the Overview to give you an indication of the total size of this chromosome, ie. 3,460,000..3,509,999).
  - OR highlight the area representing approx. 3,460,000..3,509,999 on the scale in the Overview section and then choose zoom from the popup.

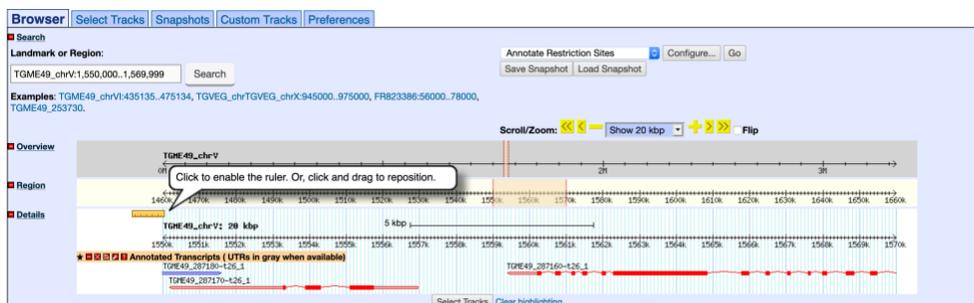


- Move to chromosome 5. How did you do this?
  - Hint: Change the chromosome number in the “landmark or region” box. Try something like this: TGME49\_chrV:1520000..1599999. The TGME49\_chrV portion is the genomic sequence ID for chromosome V (five).

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



- What genes are in this region? Mouse over a gene glyph and look at the popups that contain details of the gene model and options for downloading sequence, exploring the gene's ortholog group and navigating to the record of the gene represented in the glyph.
- 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.
- What if you want to go to a specific gene in Gbrowse? Try to figure out how to go to this gene: TGME49\_293420
  - 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 data tracks in GBrowse

- Is the region containing the major facilitator family protein (TGME49\_293420) gene syntenic in all organisms in ToxoDB, does it have orthologs in all organisms?
- Go to the "Select Tracks" tab 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 50Kb.
- What does the synteny track in this region look like?
- Does this gene have orthologs in all *Toxoplasma*? What about *Eimeria*?
- What direction is this gene relative to the chromosome?
- What genes are upstream and downstream of this gene? Are these genes syntenic?
- Modify the subtracks to remove all species except *Toxoplasma* from the view. Click on the link ‘showing 52 of 52 subtracks’, wait for the popup and select *Toxoplasma* from the genus drop-down menu. Click Change to reconfigure the track.

- Examine the gene to the right of the major facilitator protein. Hover over the gene image to find the gene name in the popup. Does this gene exist in other *Toxoplasma* strains?
- What other track would be useful to confirm the existence of this gene? (note, we will explore this further in the next exercise module).

### 3. Exploring JBrowse (optional):

EuPathDB is transitioning to using JBrowse as its main genome browser. JBrowse is a modern genome browser that continues to be developed while GBrowse is not.

- Go to the gene page for the *T. gondii* TGME49\_293420 transporter, major facilitator family protein
  - [https://toxodb.org/gene/TGME49\\_293420](https://toxodb.org/gene/TGME49_293420)
- Scroll down to the gene models section (section 1) of the gene page and click on the “View in JBrowse genome browser” button

## 1 Gene models

# Exons in Gene 1

# Transcripts 1

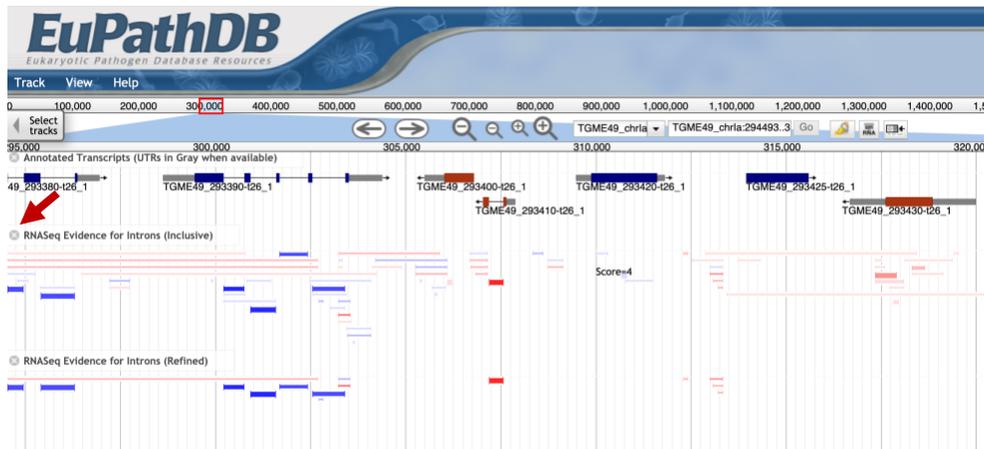
▼ Gene Models



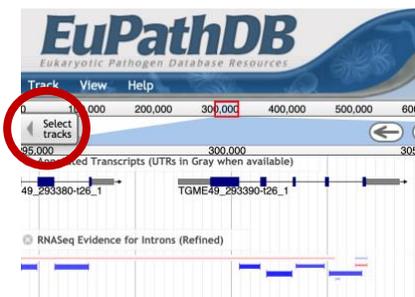
▼ Transcripts [Download](#) [Data sets](#)

Transcript	# exons	Transcript length	Protein length
TGME49_293420-126_1	1	2329	575

- In JBrowse, you can close open tracks by clicking on the 'x' symbol next to the track name. Try this by closing the track called "RNaseq Evidence for Introns (Inclusive)"



- Explore the zoom in and out options. You can zoom in and out using two mechanisms: 1. Clicking on the '+' and '-' magnifying glasses in the top center of the browser. 2. By clicking and dragging your mouse across the area you want to zoom into to.
- Adding data tracks in JBrowse is performed by clicking on the select tracks tab in the upper left hand side of the browser. Click on this tab and find the and turn on the track called "nanopore tachyzoite transcriptome"
- Finding data track in JBrowse can be done by using the search box (top center)
- Search for "nanopore tachyzoite transcriptome"



**Select Tracks** Help

My Tracks Back to browser Clear All Filters Contains text **nanopore tachyzoite transcriptome** 1 matching track

Currently Active  
Recently Used

Name	Category	Subcategory	Dataset	Track Type	RNASeq Alignment	RNASeq Strand
<input type="checkbox"/> tachyzoite transcriptome	Transcriptomics	RNASeq	nanopore tachyzoite transcriptome	Read Alignments	unique	both strands

800,000  
Select tracks  
0

- If needed, additional filtering can be done by selecting from the categories on the left.
- Once the track is selected, you can close the select tracks window by clicking on the “Back to Browser” button.

**EuPathDB** Eukaryotic Pathogen Database Resources

Track View Help

100,000 200,000 300,000 400,000 500,000 600,000 700,000 800,000 900,000 1,000,000 1,100,000 1,200,000 1,300,000 1,400,000 1,500,000 1,600,000 1,700,000 1,800,000

Select tracks TGME49\_chria TGME49\_chria.291931.3 Go

295,000 300,000 305,000 310,000 315,000 320,000

Annotated Transcripts (UTRs in Gray when available)  
 RNASeq Evidence for Introns (Refined)  
 tachyzoite transcriptome