JBrowse Basics

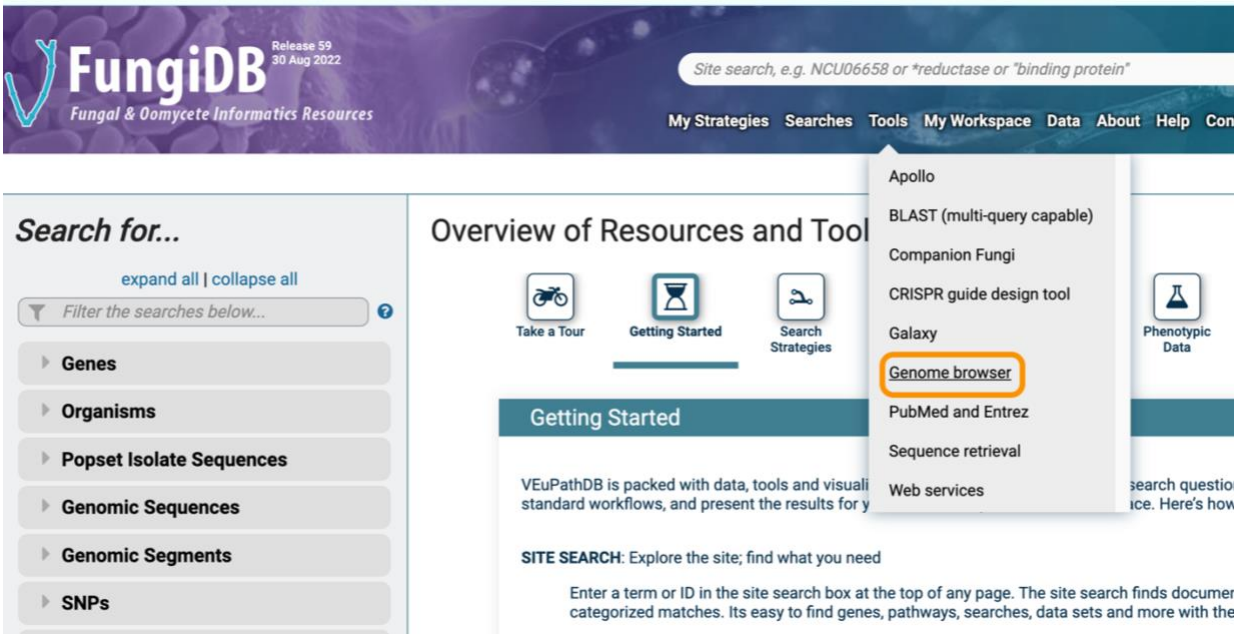
Learning objectives:

- 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. Navigate to the Genome Browser (JBrowse).

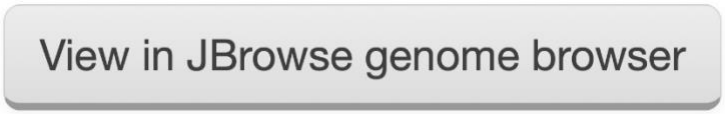
Links to the genome browser are available from multiple locations:

a. **The tools menu:**



b. **Record pages (e.g., gene, SNP or genomic sequence pages)**

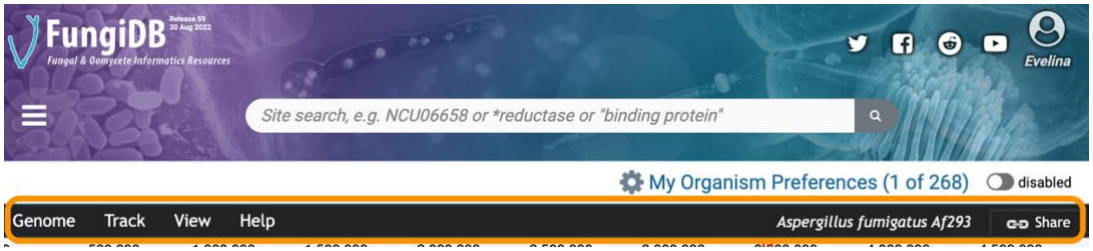
These links are usually to a specific JBrowse configuration that includes data relevant to the section on that record page. For example, a JBrowse link from a gene record page would display the gene of interest along with the default JBrowse tracks. These links are usually indicated by “View in JBrowse genome browser” button.



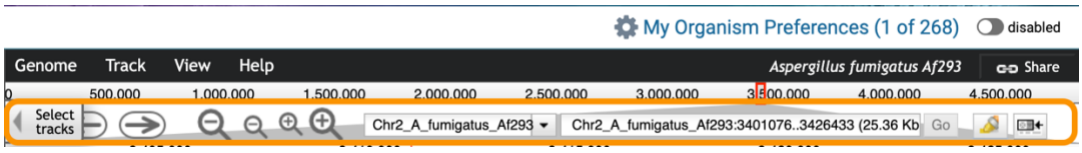
2. Getting around JBrowse.

Use the tools menu or the View in JBrowse button to open JBrowse. Once in JBrowse examine the following features:

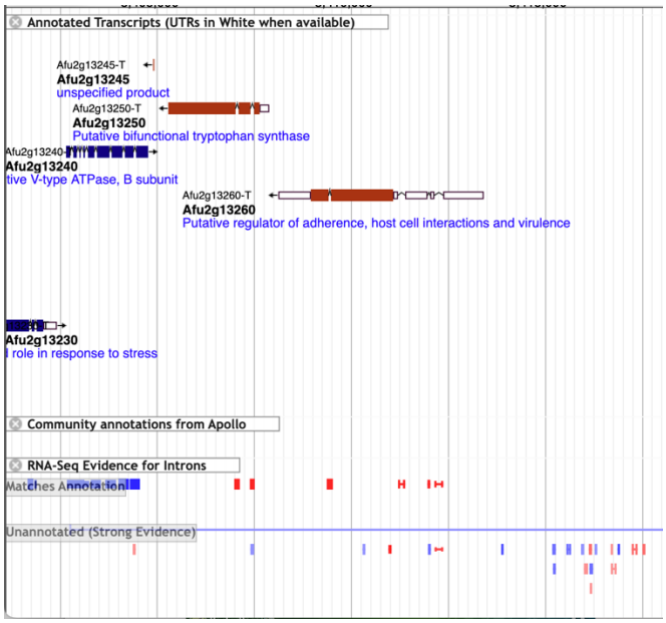
a. The **menu bar**: located at the top of the JBrowse frame.
This includes the Genome menu, Track menu, View menu, Help menu and the Sharing link that help you navigate within the JBrowse, upload your tracks, share a unique URL and get help.



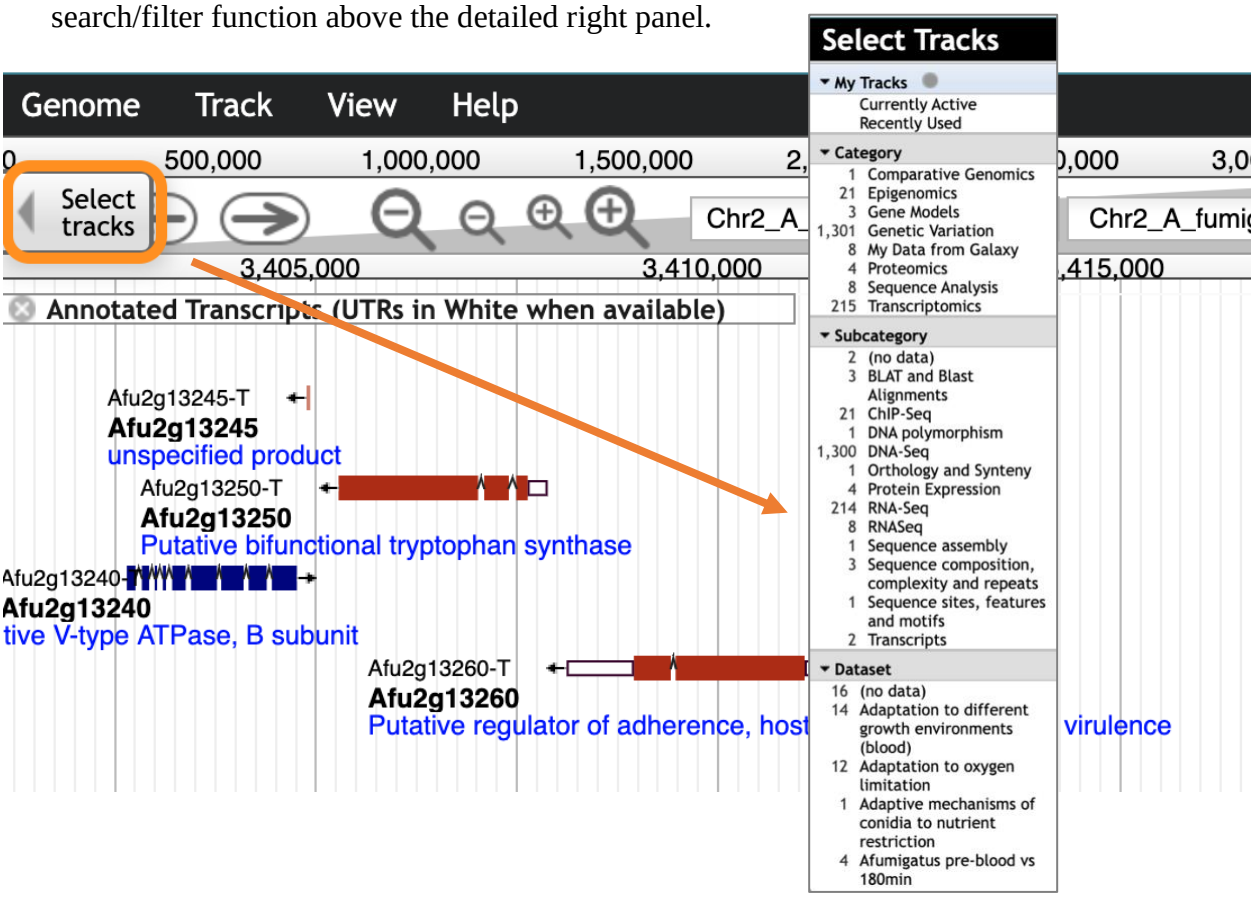
b. The **navigation bar**: located below the menu bar.
This contains zooming (magnifying glass icons), panning (left/right arrows) and highlighting (yellow highlighter) buttons, reference sequence selector (drop down with sequences from the selected genome sorted by length), a text box to search for features such as gene IDs and overview bar which shows the location of the region in view. Zoom features are also built into the scale on the top of the navigation panel.



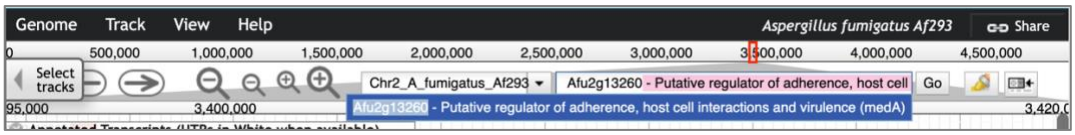
c. The **genome view**: this is where the data tracks are displayed.
When viewing the annotation track (top most track), you can move upstream and downstream by dragging the track features left or right.



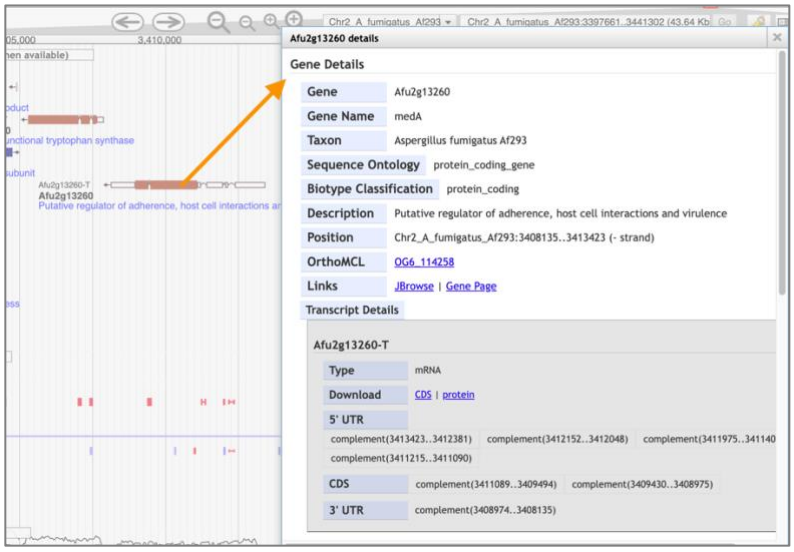
d. **Select tracks**.
This menu contains all the data tracks that are aligned to the genome that you are viewing. The list of tracks can be filtered using the 'clickable' left panel categories, or with the search/filter function above the detailed right panel.



3. **Navigate to a specific gene in JBrowse**.
   - Navigate to JBrowse
   - Click on the **Genome** menu at the top left and select ***Aspergillus fumigatus* Af293** genome from the drop down list.
   - Copy and paste this gene ID into the search box: Afu2g13260. After a few seconds you should see the gene of interest being found, select on the gene hightighted in blue to navigate to the region where it is located.. Select the gene called AGAP004707-voltage-gated sodium channel (para) from the search dropdown.



Details about most features are available in pop-up panels. Click (or control click) on the gene feature to view the details panel. You can also right click to choose the same details panel, a link to the gene page, or highlight the gene in yellow. Explore this popup to find out more about information available.



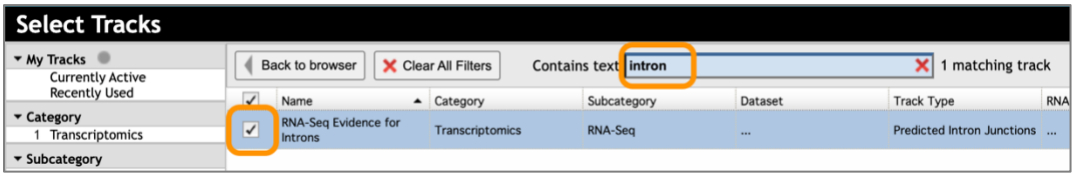
a. What genes are immediately upstream and downstream of this gene?
b. Try the zoom function. What is the difference between the small and large zoom buttons?

4. **Exploring evidence.**

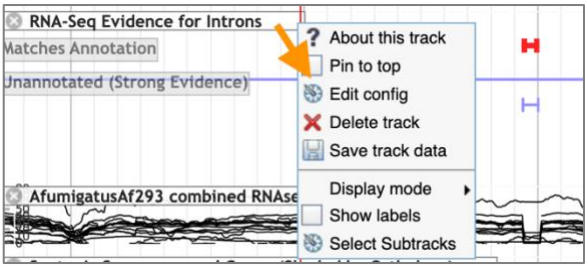
Intron evidence tracks

a. Explore the intron evidence tracks by clicking on the **Select tracks** tab and activating the **RNA-Seq Evidence for Introns**

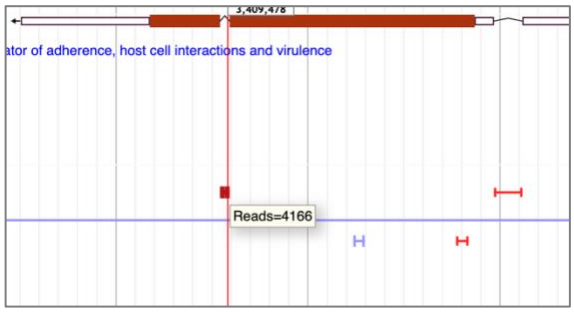
Notice there are two subtracks turned on by default: Matches Annotation and Unannotated (Strong evidence). What is the difference between these subtracks?



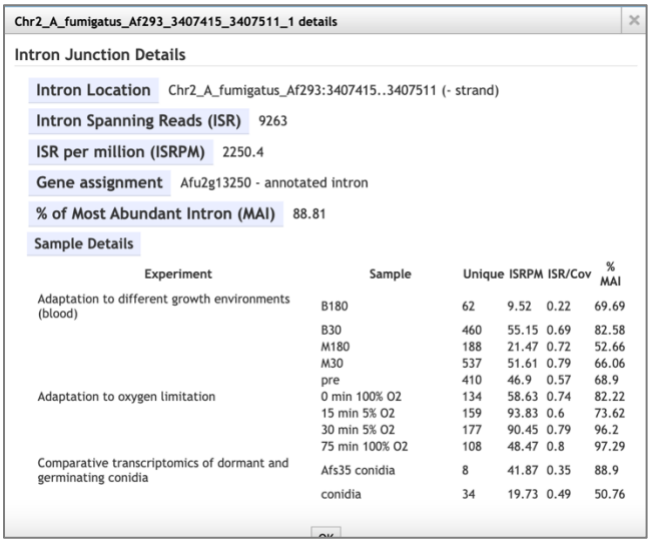
b. The track titles also contain dropdown menus with actions or information about the track. Hover over the track title and then click the down arrow that appears to access more track functions.



c. Mouse over an intron span to determine the number of reads that support that intron



d. Click on one of the intron spanning reads find the information about this intron the experiments that support it.



Experiment	Sample	Unique	ISRPM	ISR/Cov	% MAI
Adaptation to different growth environments (blood)	B180	62	9.52	0.22	69.69
	B30	460	55.15	0.69	82.58
	M180	188	21.47	0.72	52.66
	M30	537	51.61	0.79	66.06
	pre	410	46.9	0.57	68.9
Adaptation to oxygen limitation	0 min 100% O2	134	58.63	0.74	82.22
	15 min 5% O2	159	93.83	0.6	73.62
	30 min 5% O2	177	90.45	0.79	96.2
	75 min 100% O2	108	48.47	0.8	97.29
Comparative transcriptomics of dormant and germinating conidia	Afs35 conidia	8	41.87	0.35	88.9
	conidia	34	19.73	0.49	50.76

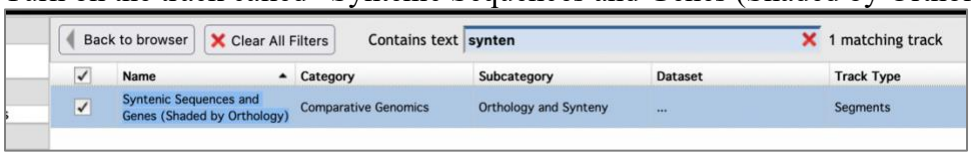
e. Notice that the track also provide evidence for currently “unannotated (strong evidence)” (the darker the color, the stronger the support).

Synteny tracks

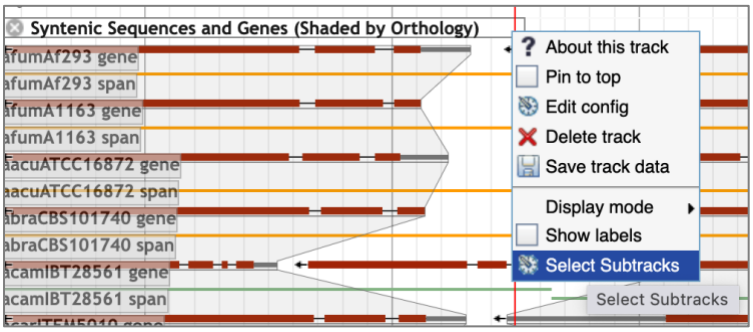
JBrowse includes a configurable track containing sequence alignment between genomes. Genes are shaded based on orthology to demonstrate the co-linearity between genomes.

Activate the Orthology and Synteny track to display synteny between *Aspergillus fumigatus Af293* and Aspergillus fumigatus AA163

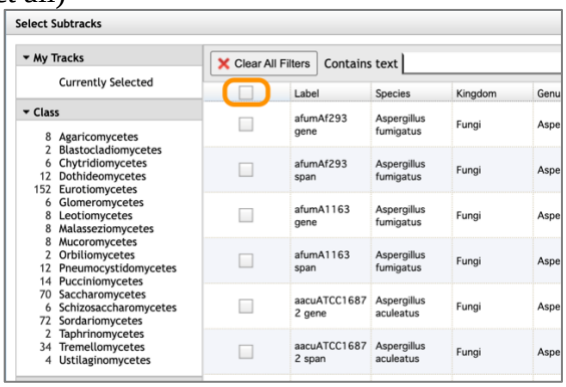
a. Turn on the track called “Syntenic Sequences and Genes (Shaded by Orthology)”



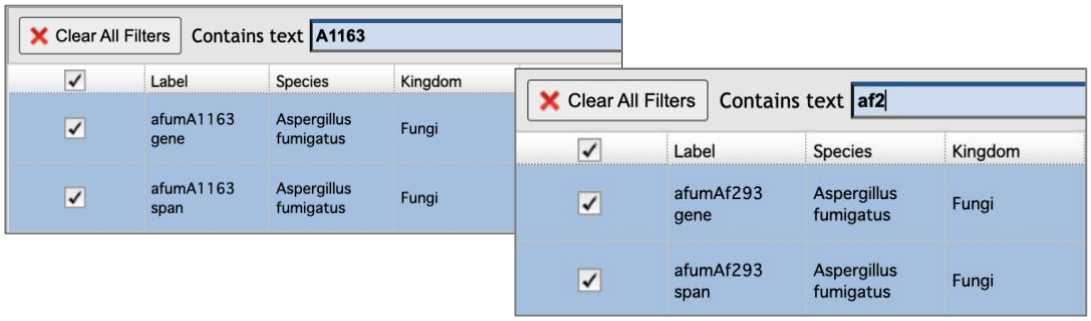
b. Select synteny subtracts by clicking on the down arrow on the track name and selecting “Select Subtracts”.



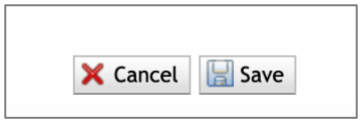
c. Unselect all the tracks (the easiest way is to use the top check box to select all then unselect all)

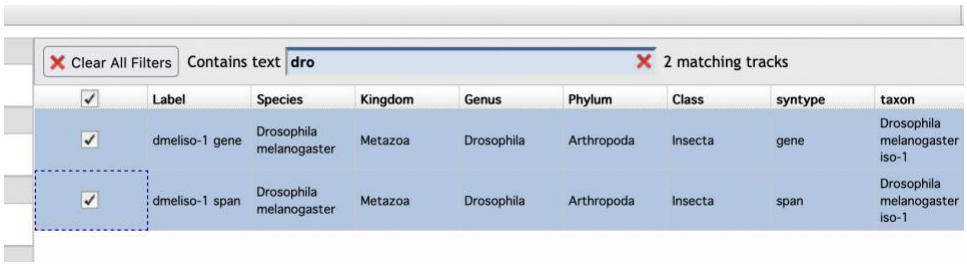


d. Select the tracks for A1163 and the reference gnome Af293

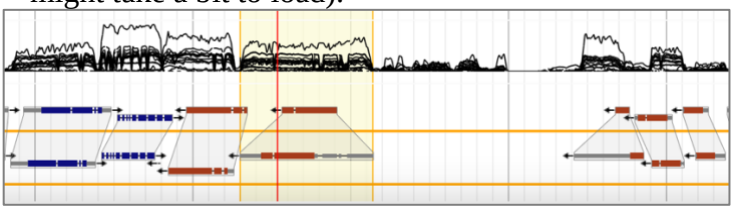


and click on the “Save” button at the bottom of the popup to modify the track selection.





e. View the track.
   i. Does A1163 have an ortholog of the Af293 gene. Take a note of the gene structure and 3' and 5' UTR annotations.
   ii. What does synteny look like around Afu2g13260? Zoom out a bit (this might take a bit to load).



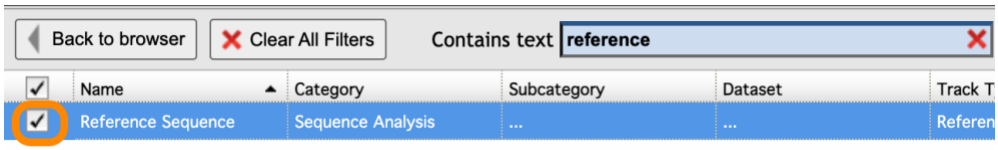
Adding more data tracks

JBrowse contains many data tracks that you can load by selecting them from the select tracks tab. Each track represents sequence data or features aligned to the genome. Depending on the data type, viewing different data tracks in concert can reveal much - transcriptomics tracks display coverage plots for the integrated RNA-Seq data; proteomics tracks display all peptides from mass spectroscopy experiments we have in the database mapped to the genome.

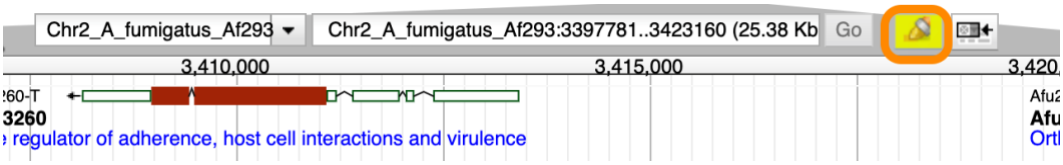
Retrieving sequence data from JBrowse

Sequence data from a region of interest can be downloaded from JBrowse in FASTA format. Download is a function of the Reference Sequence track.

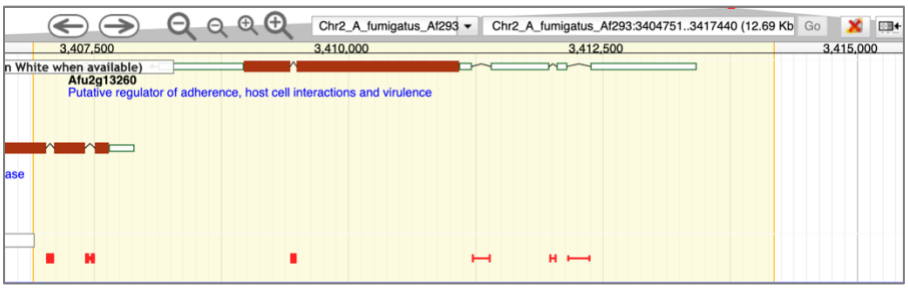
a. Make sure the "annotated transcripts" and the "reference sequence" tracks are turned on.



b. Click on the "highlight a region" button in the navigation bar. It should turn yellow when activated.



c. Click and drag in the genome view region and select the area you would like to highlight.



d. Click on the down arrow on the reference sequence track and select “Save track data”.
e. In the next popup window you can keep everything as the default and either save or view the sequence.