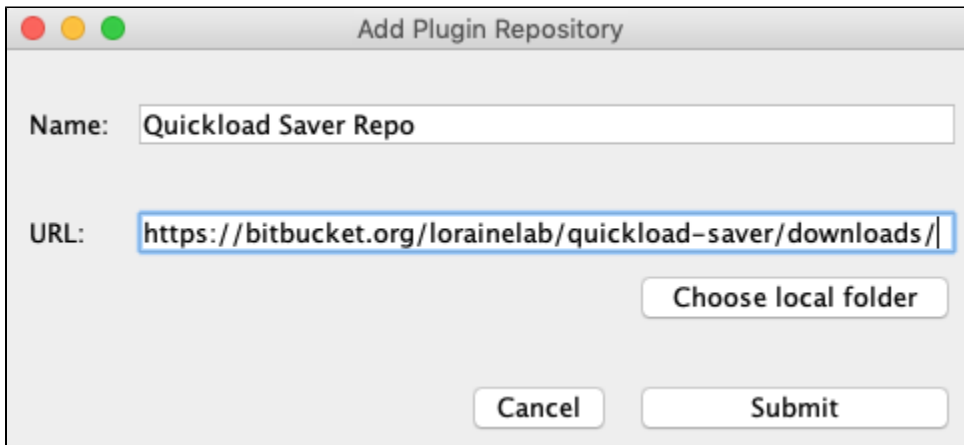


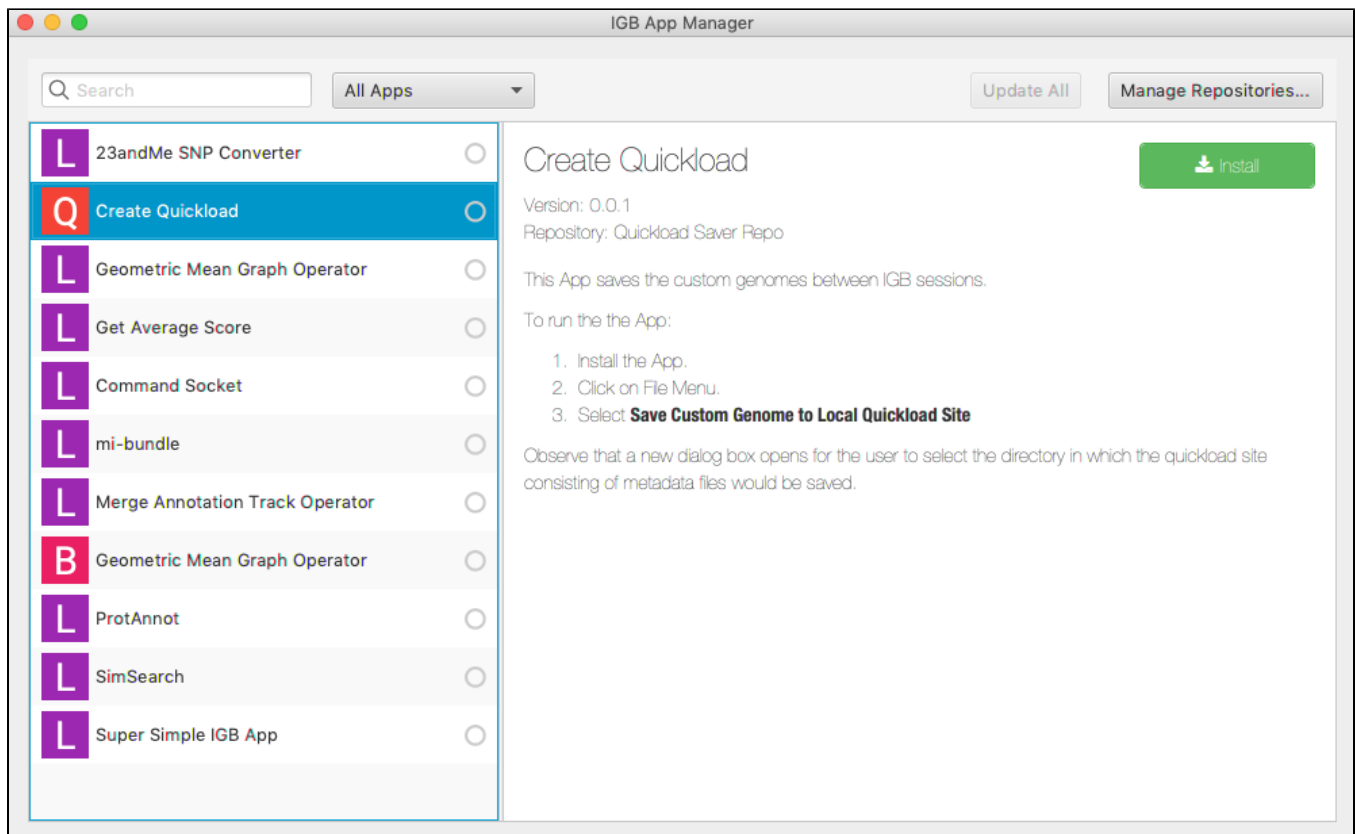
Quickload Saver

General Function Checklist

1. Download and unzip the following folder: [test genomes.zip](#)
2. The folder "test genomes" should contain the following files:
 - a. E_unicornis_Jul_2043.bed.gz.tbi
 - b. E_unicornis_Jul_2043.bed.gz
 - c. E_unicornis_Jul_2043.2bit
 - d. T_rex_Jun_1993.2bit
3. Start IGB 9.1.8 or later.
4. Select the **Plug-ins** tab.
5. Click **Launch App Manager**.
6. Select **Manage Repositories...**
7. Click **Add...**
 - a. Name: Quickload Saver Repo
 - b. URL: <https://bitbucket.org/lorainelab/quickload-saver/downloads/>
8. Click **Submit**.
9. Click **Done**.



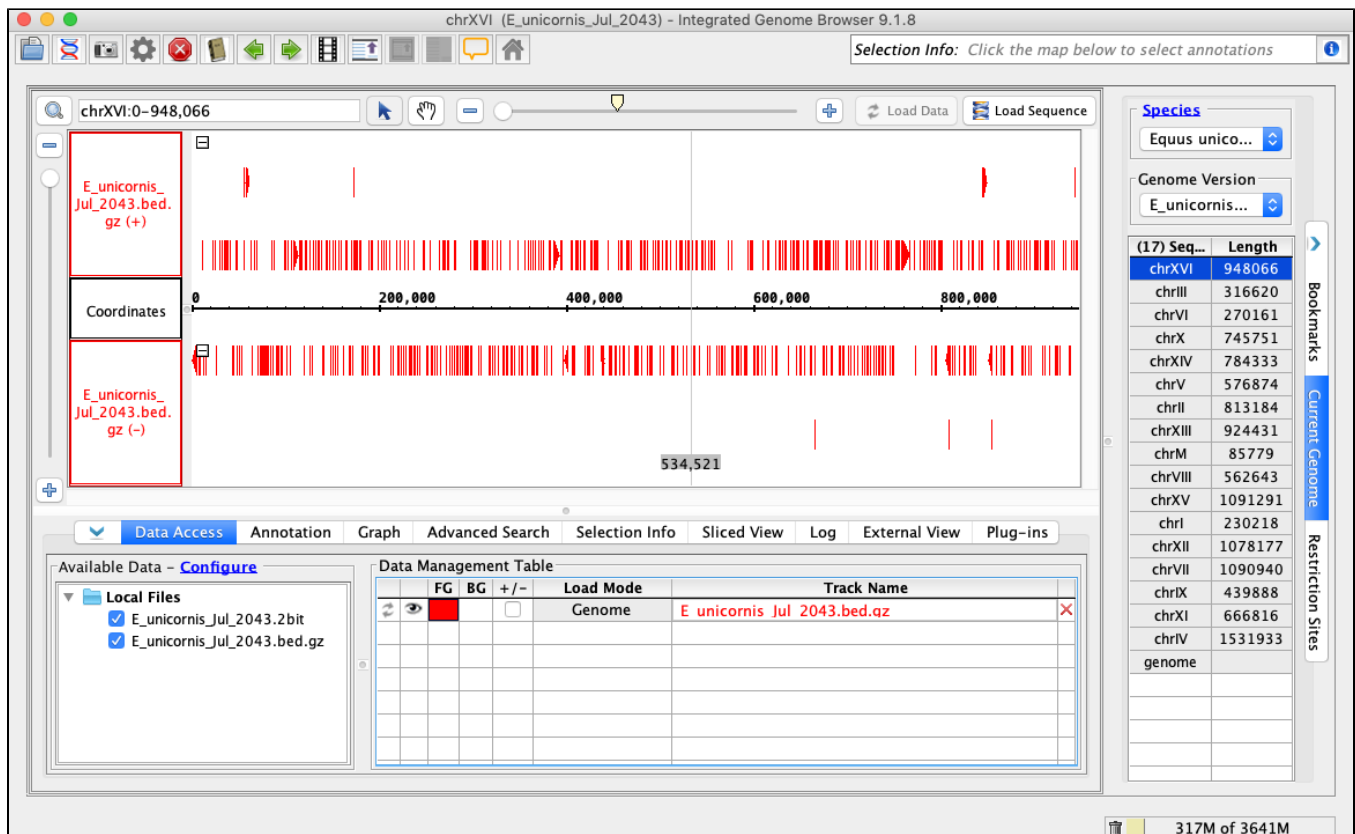
The screenshot shows a macOS-style dialog box titled "Add Plugin Repository". It has two text input fields: "Name:" with the value "Quickload Saver Repo" and "URL:" with the value "https://bitbucket.org/lorainelab/quickload-saver/downloads/". The URL field is currently selected. Below the URL field is a button labeled "Choose local folder". At the bottom of the dialog are two buttons: "Cancel" and "Submit".



- Checkpoint:

- ☒ mac
- ☐ linux
- ☐ windows

1. Close the IGB App Manager window.
2. Select **File > Open Genome from File...**
 - a. Reference Sequence: Click **Choose File...** and select **E_unicornis_Jul_2043.2bit**
 - b. Genus: **Equus**
 - c. Species: **unicornis**
 - d. Variety: **(leave blank)**
 - e. Genome release date: **July 2043**
3. Click **OK**.
4. Select **File > Open File...**
5. Select **E_unicornis_Jul_2043.bed.gz**
6. Click **Open**.
7. In the Data Access tab at the bottom of IGB,
 - a. Change the Load Mode to **Genome** for E_unicornis_Jul_2043.bed.gz
 - b. Change the color of the foreground (**FG**) to **red**.



- Checkpoint:

- ☒ mac
- ☐ linux
- ☐ windows

1. Select **File > Save Custom Genome to Local Quickload Site**
2. Select your **desktop** as the destination and **unicorn** as the name.
3. Click **Save**.
4. Select **File > Open Genome from File...**
 - a. Reference Sequence: Click **Choose File...** and select the **T_rex_Jun_1993.2bit**
 - b. Genus: **Tyrannosaurus**
 - c. Species: **rex**
 - d. Variety: **(leave blank)**
 - e. Genome release date: **June 1993**
5. Click **OK**.
6. Select **File > Open URL...**
7. Enter URL: http://igbquickload.org/quickload/S_cerevisiae_Apr_2011/S_cerevisiae_Apr_2011_ncbiRefSeq.bed.gz
8. Click **OK**.

Open URL

Enter URL

http://igbquickload.org/quickload/S_cerevisiae_Apr_2011/S_cerevisiae_Apr_2011_ncbiRefSeq.bed.gz

Cancel OK

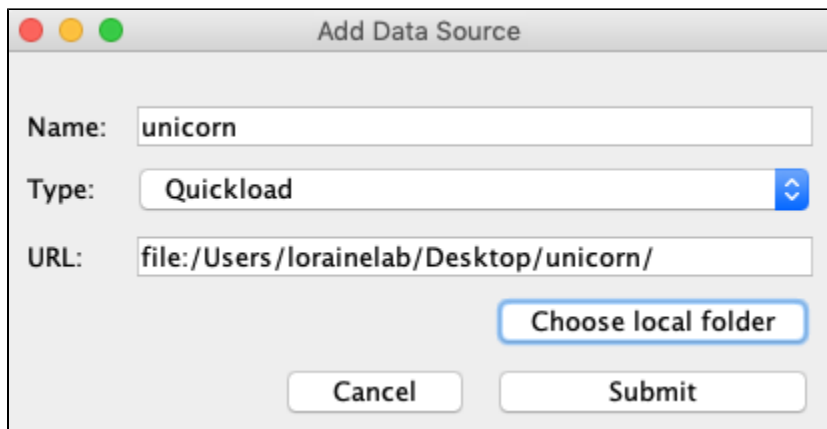
- Checkpoint:

- ☒ mac
- ☐ linux
- ☐ windows

[illegible]

- ☒ mac
- ☐ linux
- ☐ windows

1. Select **File > Save Custom Genome to Local Quickload Site**.
2. Select your **desktop** as the destination and **rex** as the name.
3. Select **File > Preferences...**
4. In the **Preferences** window select the **Other Options** tab.
5. Click **Reset Preference to Defaults** and then click **Yes**. IGB will close.
6. Start IGB.
7. Select **File > Preferences**.
8. Select the **Data Sources** tab.
9. Click **Add...**
 - a. Name: unicorn
 - b. Type: Quickload
 - c. Click Choose local folder
10. Select the **unicorn** folder on your desktop and click **Open**.
11. Click **Submit**

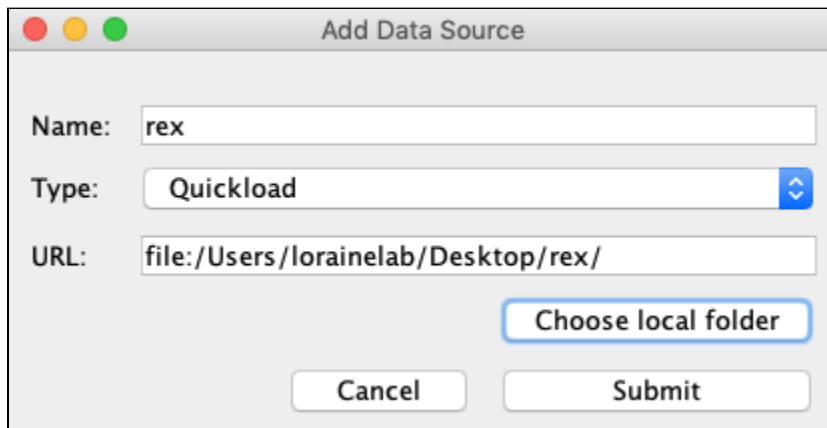


The dialog box is titled "Add Data Source". It contains three input fields: "Name" with the value "unicorn", "Type" with a dropdown menu showing "Quickload", and "URL" with the value "file:/Users/lorainelab/Desktop/unicorn/". Below the URL field is a button labeled "Choose local folder". At the bottom are two buttons: "Cancel" and "Submit".

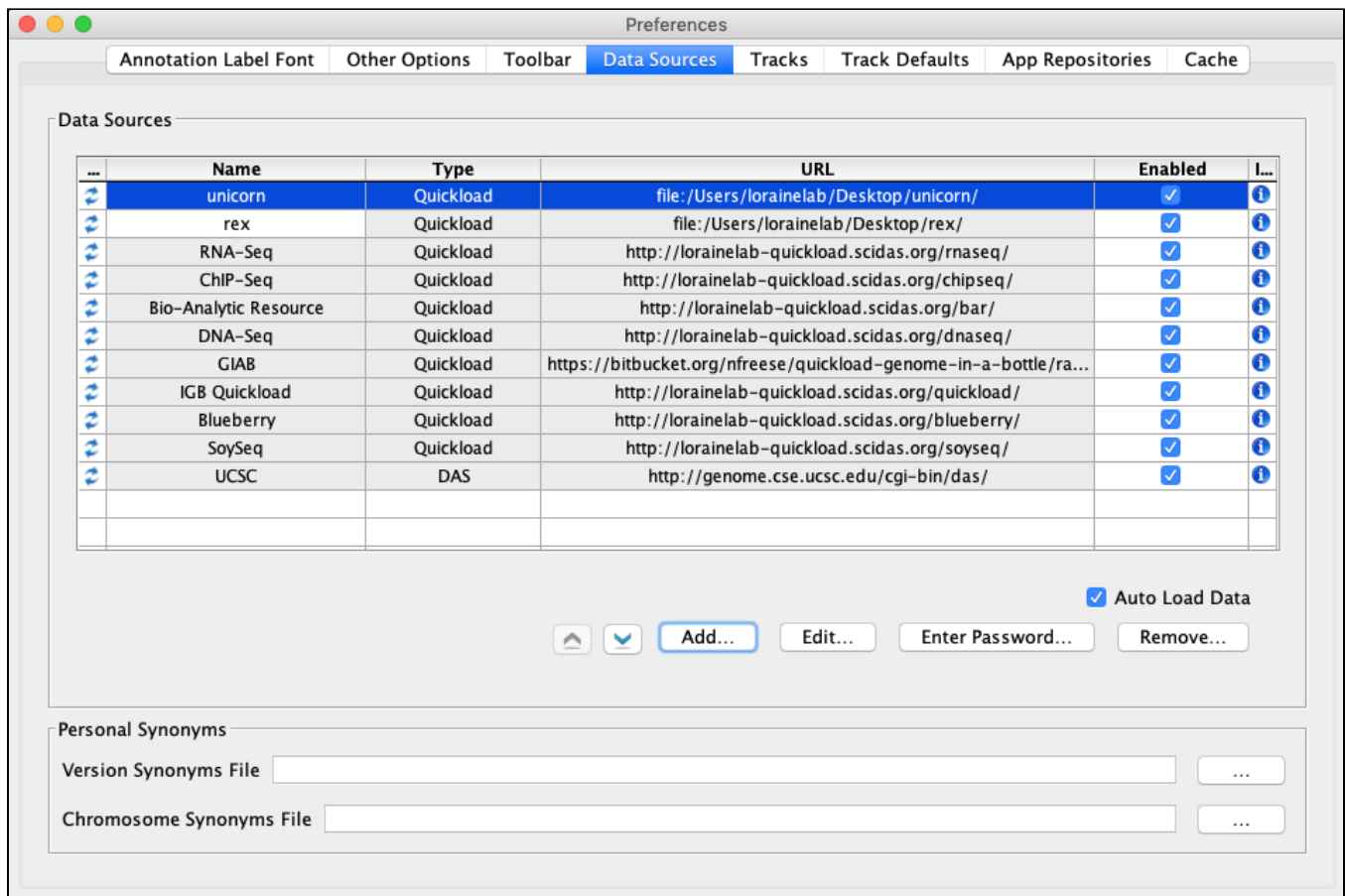
- Checkpoint:

- ☒ mac
- ☐ linux
- ☐ windows

1. Click **Add...**
 - a. Name: rex
 - b. Type: Quickload
2. Click **Choose local folder**.
3. Select the **rex** folder on your desktop and click **Open**.
4. Click **Submit**.



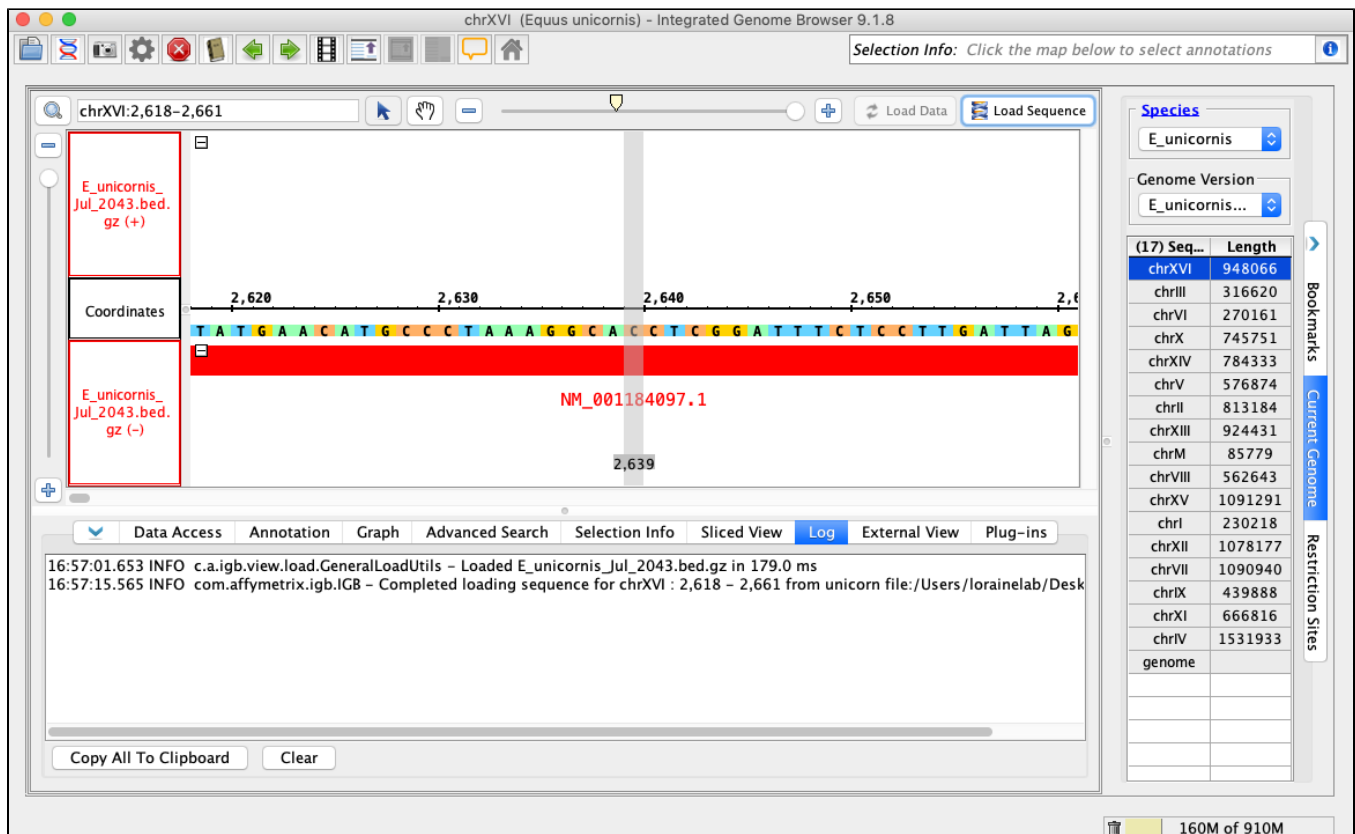
The dialog box is titled "Add Data Source". It contains three input fields: "Name" with the value "rex", "Type" with a dropdown menu showing "Quickload", and "URL" with the value "file:/Users/lorainelab/Desktop/rex/". Below the URL field is a button labeled "Choose local folder". At the bottom are two buttons: "Cancel" and "Submit".



- Checkpoint:

- ☒ mac
- ☐ linux
- ☐ windows

1. Close the **Preferences** window.
2. Select the **Log** tab and click **Clear**.
3. Open the **E_unicornis_Jul_2043** genome.
4. In the **Data Access** tab, **E_unicornis_Jul_2043.bed.gz** should be set to Load Mode **Genome** and should be **red** (FG).



- Your IGB appears to look the same as the above image.

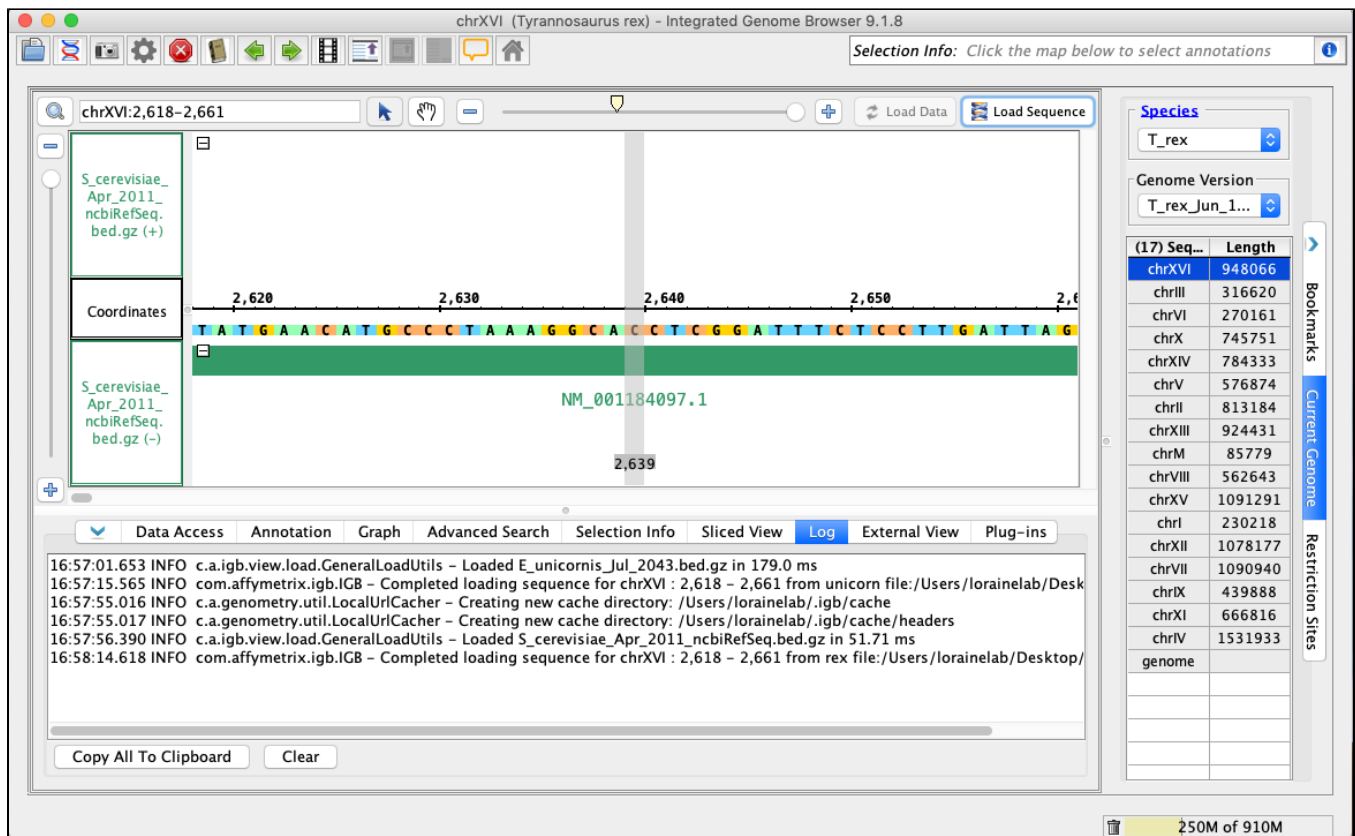
- ☒ mac
- ☐ linux
- ☐ windows

Select the **Log** tab and check for errors.

- There are no errors in the **Log**.

- ☒ mac
- ☐ linux
- ☐ windows

- Click **Clear** in the **Log** tab.
- Open the **T_rex_Jun_1993** genome.
- In the **Data Access** tab, **S_cerevisiae_Apr_2011_ncbiRefSeq.bed.gz** should be set to Load Mode **Genome** and should be **green** (FG).



- Your IGB appears to look the same as the above image.

- ☒ mac
- ☐ linux
- ☐ windows

- Select the **Log** tab and check for errors.
- Click **Clear** in the **Log** tab.

- There are no errors in the **Log**.

- ☒ mac
- ☐ linux
- ☐ windows