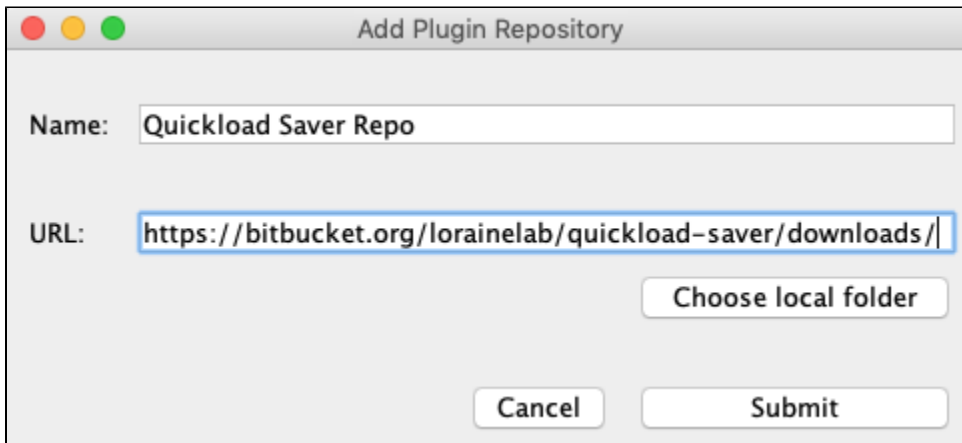


# Quickload Saver

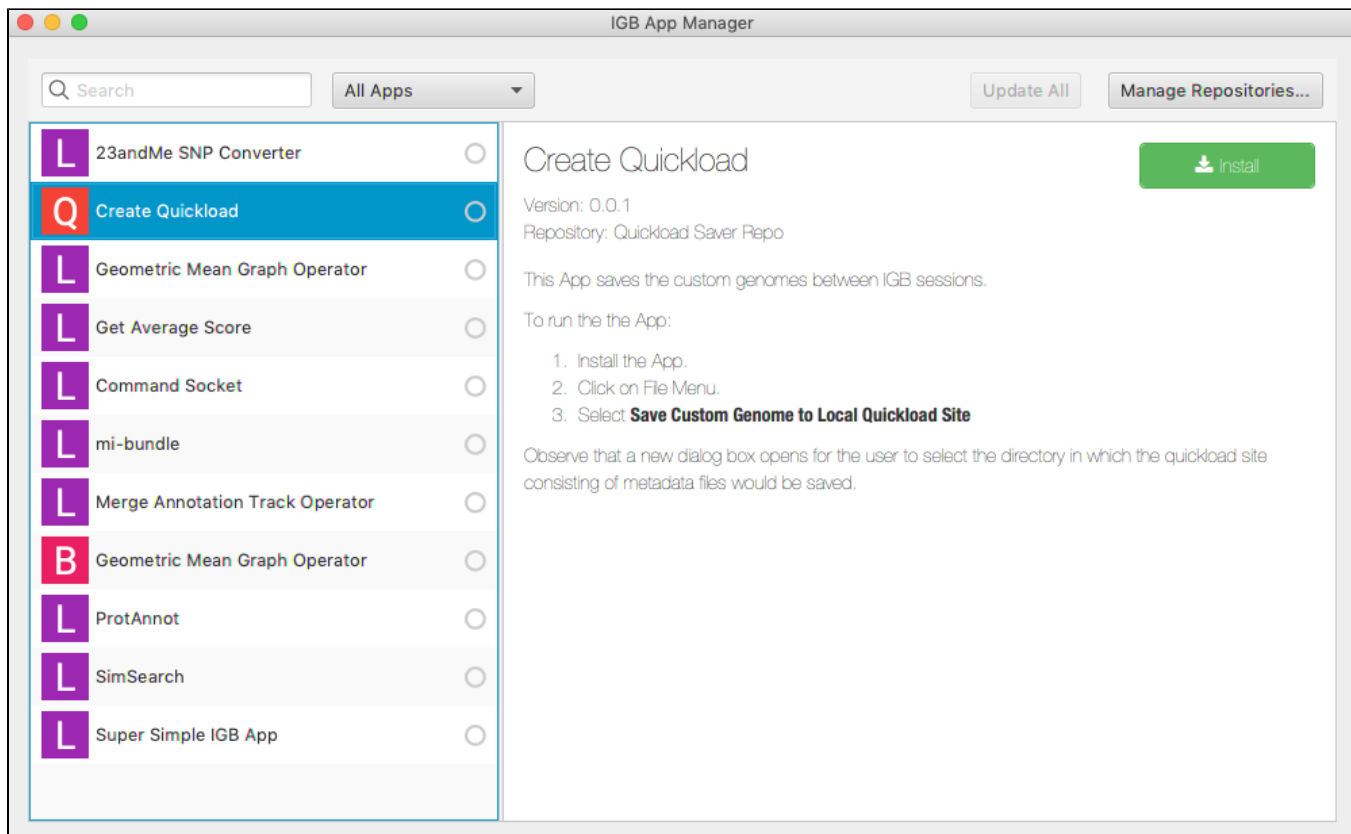
## General Function Checklist

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".

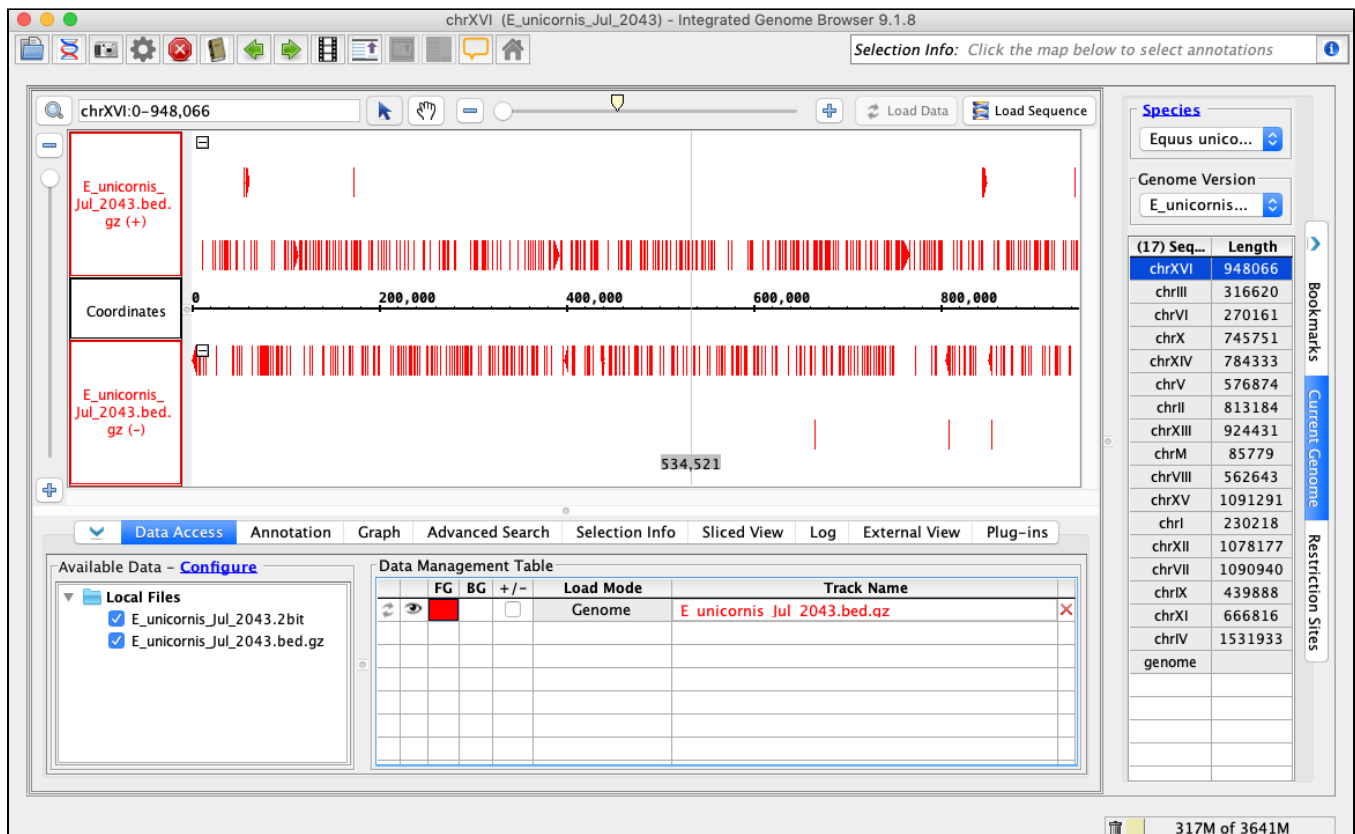




- Checkpoint:

- ☒ mac
- ☐ linux
- ☐ windows

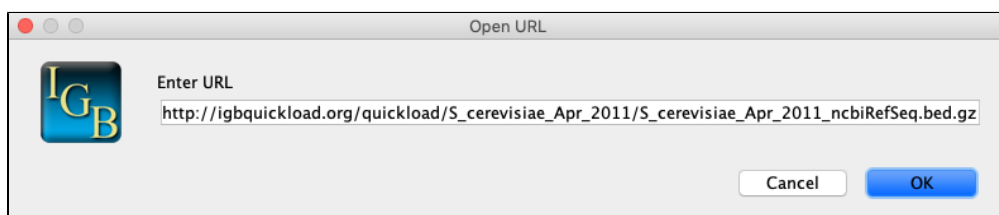
1. Close the IGB App Manager window.
2. Select **File > Open Genome from File...**
  - a. Reference Sequence: Click **Choose File...** and select **E\_unicornis\_Jul\_2043.2bit**
  - b. Genus: **Equus**
  - c. Species: **unicornis**
  - d. Variety: **(leave blank)**
  - e. Genome release date: **July 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](http://igbquickload.org/quickload/S_cerevisiae_Apr_2011/S_cerevisiae_Apr_2011_ncbiRefSeq.bed.gz)
8. Click **OK**.



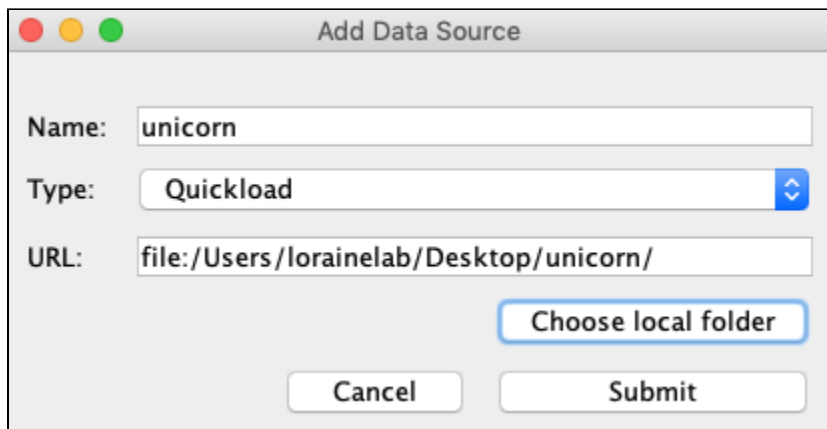
- Checkpoint:

- ☒ 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**



**Add Data Source**

Name:

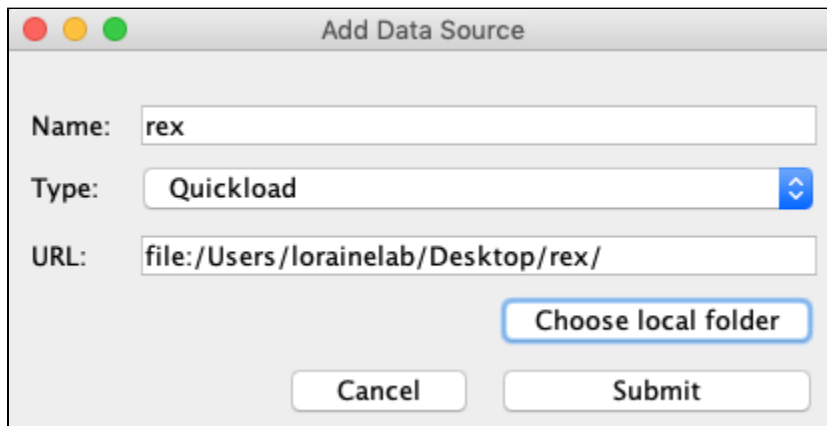
Type:

URL:

- 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**.

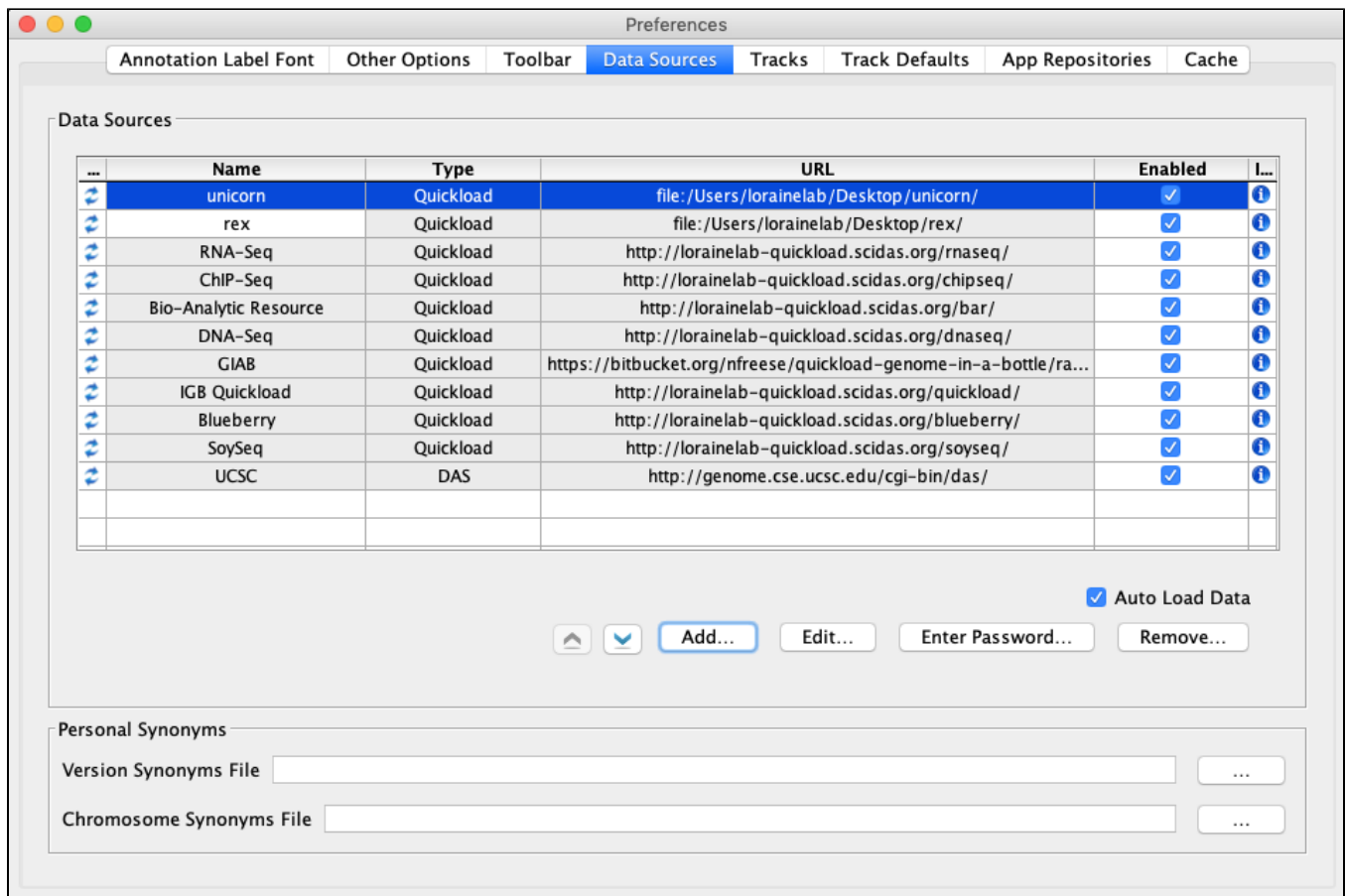


**Add Data Source**

Name:

Type:

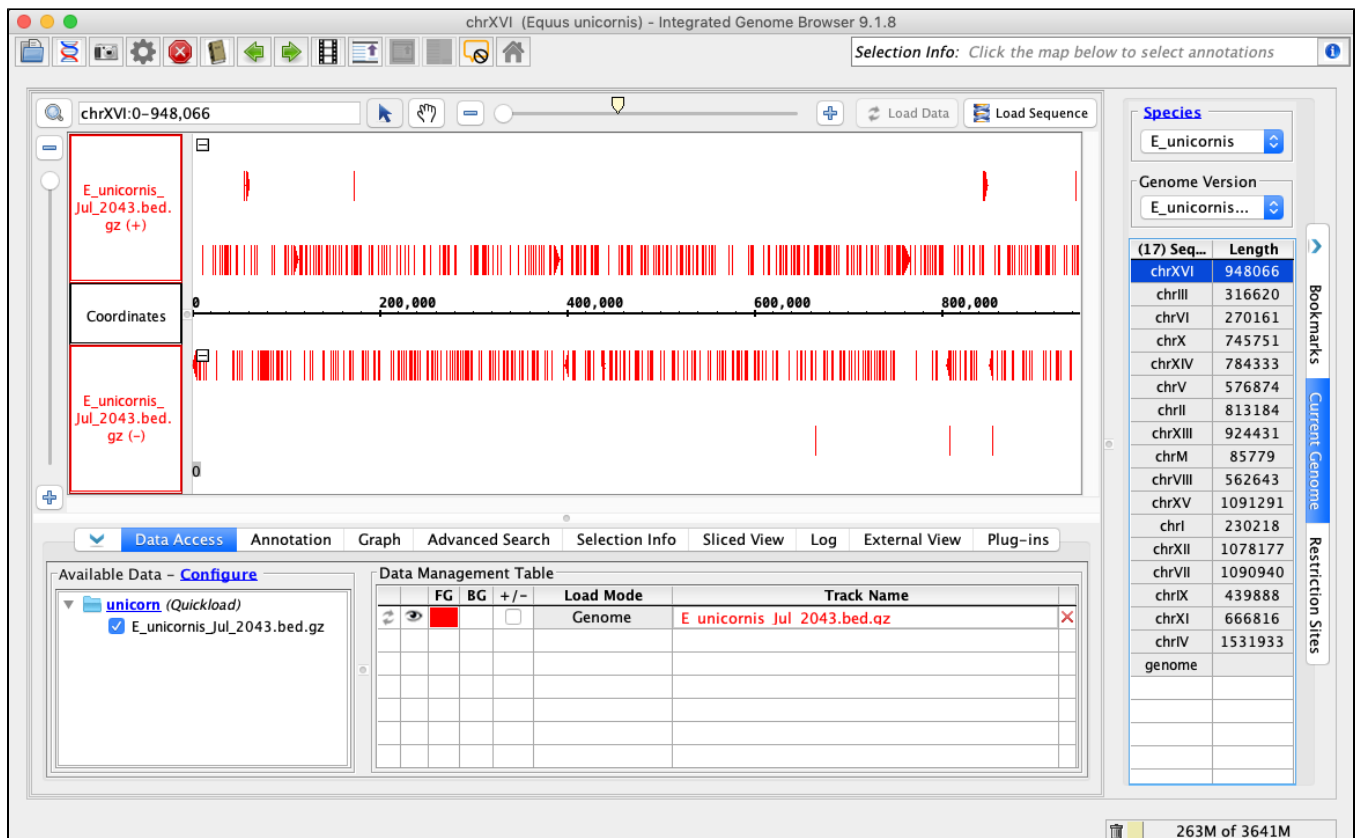
URL:



- 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).

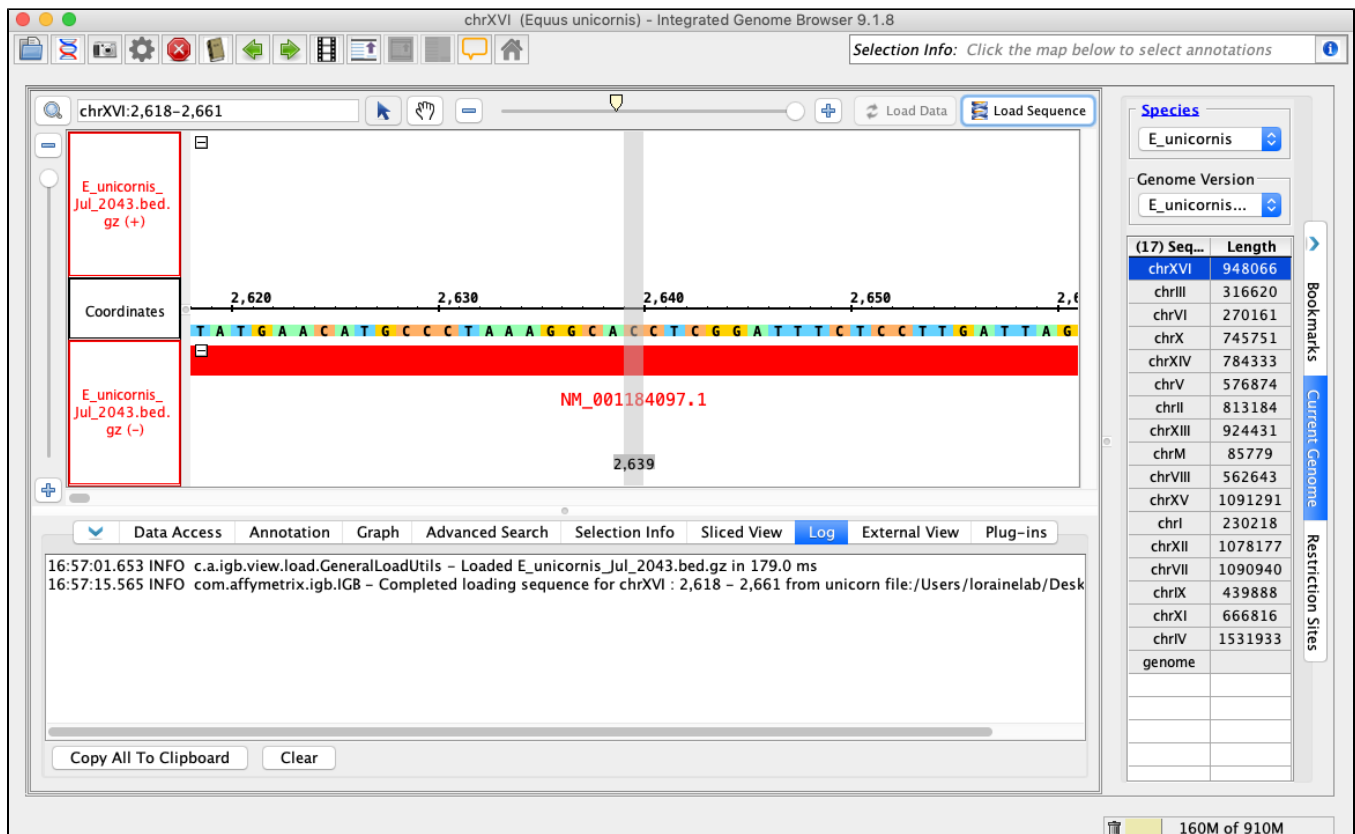


- Your IGB appears to look the same as the above image.

- ☒ mac
- ☐ linux
- ☐ windows

1. Navigate to: chrXVI:2,618-2,661
2. Click **Load Sequence**.





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

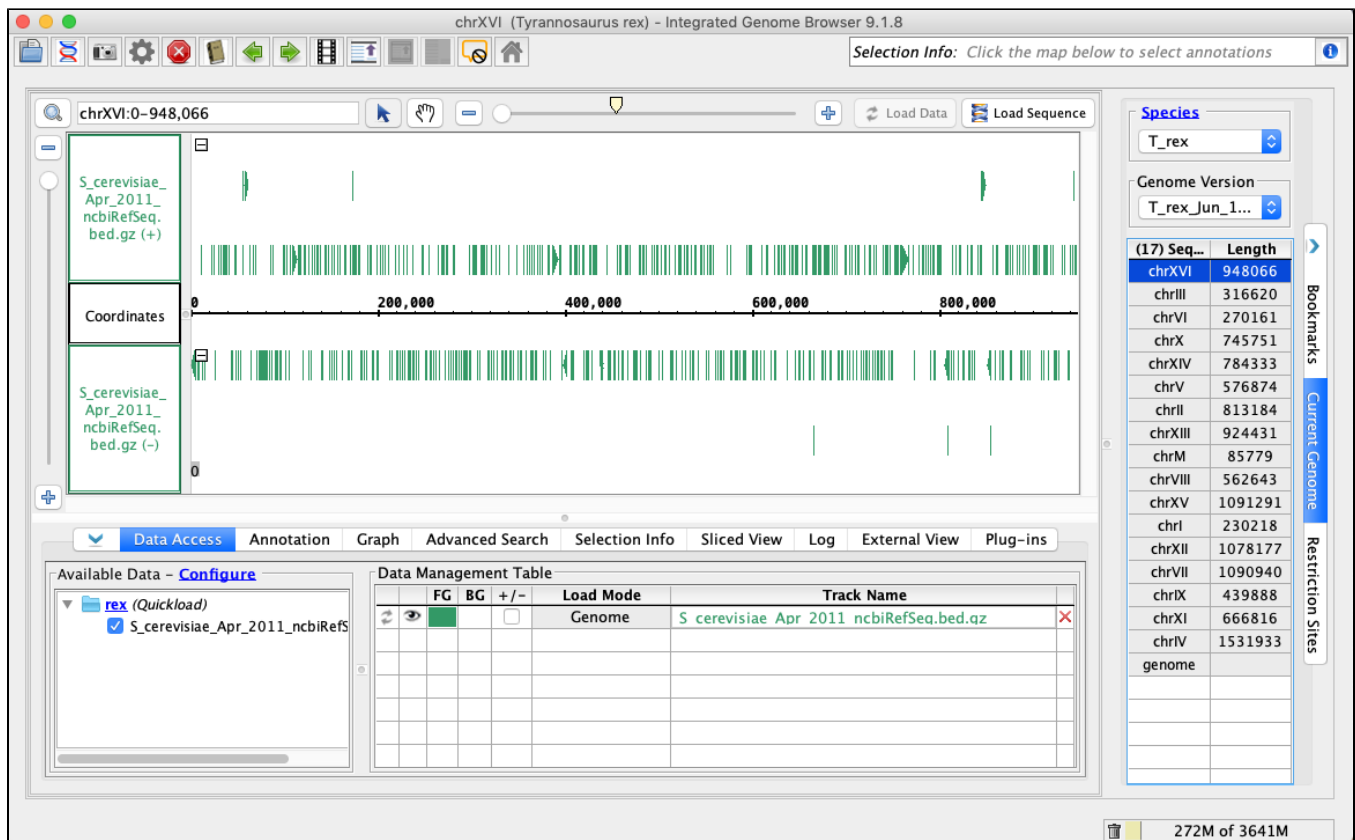
- ☒ mac
- ☐ linux
- ☐ windows

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

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

- ☒ mac
- ☐ linux
- ☐ windows

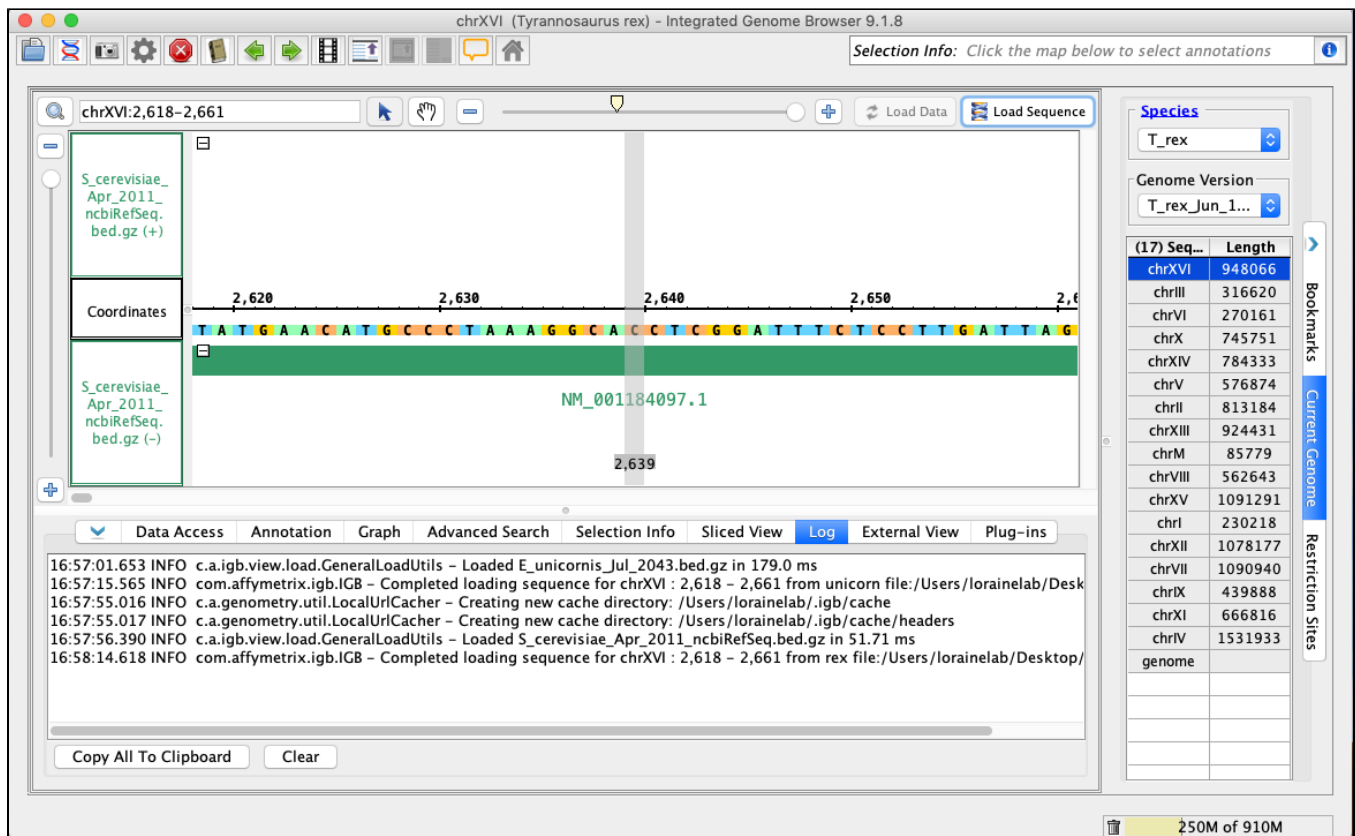
1. Click **Clear** in the **Log** tab.
2. Open the **T\_rex\_Jun\_1993** genome.
3. In the **Data Access** tab, **S\_cerevisiae\_Apr\_2011\_ncbiRefSeq.bed.gz** should be set to Load Mode **Genome** and should be **green** (FG).



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

- ☒ mac
- ☐ linux
- ☐ windows

1. Navigate to: chrXVI:2,618-2,661
2. Click **Load Sequence**.



- 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