Quickload Saver

General Function Checklist

- 1. Download and unzip the following folder: test genomes.zip
- Download and anzip the following foldar: leaf genomes.zip
 The folder "test genomes" should contain the following files:

 a. E_unicornis_Jul_2043.bed.gz.tbi
- b. E_unicornis_Jul_2043.bed.gz.
 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.

- Select the Plug-ins tab.
 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.

	Add Plugin Repository
Name:	Quickload Saver Repo
URL:	https://bitbucket.org/lorainelab/guickload-saver/downloads/
	Choose local folder
	Cancel Submit

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- Checkpoint:
- ✓ mac
- linux
- windows
- In the Plug-ins tab, click Launch App Manager.
 Select the Quickload Saver app.
 Click Install.



- · 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.
- Select File > Open File...
 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.

ChrXVI (E_unicornis_Jui_2043) - Integrated Genome Browser 9.1.8				
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- Checkpoint:
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- 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.



- mac
- linux
- windows

In the Data Access tab at the bottom of IGB:

- Change the Load Mode to Genome for S_cerevisiae_Apr_2011_ncbiRefSeq.bed.gz
- Change the color of the foreground (FG) to green.



- · Checkpoint:
- ~ mac
- linux
- windows
- 1. Select File > Save Custom Genome to Local Quickload Site.
- Select your desktop as the destination and rex as the name. 2.
- 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:	unicorn
Type:	Quickload
URL:	file:/Users/lorainelab/Desktop/unicorn/
	Choose local folder
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1. Close the **Preferences** window.

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

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

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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).

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

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

- There are no errors in the Log.
- mac
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