

Local Quickload

General Function Checklist

This page tests local QuickLoads using relative file paths.

(To test absolute file paths see QuickLoad Saver release testing documentation)

Add files to your computer

1. Download the following file: [relative space.zip](#)
2. Extract it to where you would like your local QuickLoad to be stored. (Desktop, C drive, etc.)









- Files were extracted to local machine:

- ☐ mac
- ☐ linux
- ☐ windows



Add the QuickLoad to IGB

1. Open the **Data Sources** tab in **Preferences**.
2. Click **Add...** to open the **Add Data Source** window.
3. Click **Choose local folder**.
4. Choose the unzipped QuickLoad folder "relative space".
5. Click **Submit**.

Data Sources

	Name	Type	URL	Enab...
	IGB Quickload	Quickload	http://igbquickload.org/quickload/	<input checked="" type="checkbox"/>
	Pollen	Quickload	http://www.igbquickload.org/pollen/	<input checked="" type="checkbox"/>
	Cytokinin	Quickload	http://www.igbquickload.org/cyto/	<input checked="" type="checkbox"/>
	Blueberry	Quickload	http://www.igbquickload.org/blueberry/	<input checked="" type="checkbox"/>
	UCSC	DAS	http://genome.cse.ucsc.edu/cgi-bin/das/	<input checked="" type="checkbox"/>
	UofUtahBioinfoCore	DAS2	http://bioserver.hci.utah.edu:8080/DAS2DB/	<input type="checkbox"/>
				

☒ Auto Load Data

Add Data Source

Name:

Type:

URL:

Preferences

Preferences Help

Annotation Label Font Other Options Toolbar **Data Sources** Tracks Track Defaults App Repositories Cache

Data Sources

...	Name	Type	URL	Enabled	...
	Your server name	Quickload	file:/C:/relative space/relative space/	<input checked="" type="checkbox"/>	
	RNA-Seq	Quickload	http://lorainelab-quickload.scidas.org/rnaseq/	<input checked="" type="checkbox"/>	
	ChIP-Seq	Quickload	http://lorainelab-quickload.scidas.org/chipseq/	<input checked="" type="checkbox"/>	
	Bio-Analytic Resource	Quickload	http://lorainelab-quickload.scidas.org/bar/	<input checked="" type="checkbox"/>	
	DNA-Seq	Quickload	http://lorainelab-quickload.scidas.org/dnaseq/	<input checked="" type="checkbox"/>	
	GIAB	Quickload	https://bitbucket.org/nfreese/quickload-genome-in-a-bottl...	<input checked="" type="checkbox"/>	
	IGB Quickload	Quickload	http://lorainelab-quickload.scidas.org/quickload/	<input checked="" type="checkbox"/>	
	Blueberry	Quickload	http://lorainelab-quickload.scidas.org/blueberry/	<input checked="" type="checkbox"/>	
	SoySeq	Quickload	http://lorainelab-quickload.scidas.org/soyseq/	<input checked="" type="checkbox"/>	
	UCSC	DAS	http://genome.cse.ucsc.edu/cgi-bin/das/	<input checked="" type="checkbox"/>	

☒ Auto Load Data

Personal Synonyms

Version Synonyms File

Chromosome Synonyms File

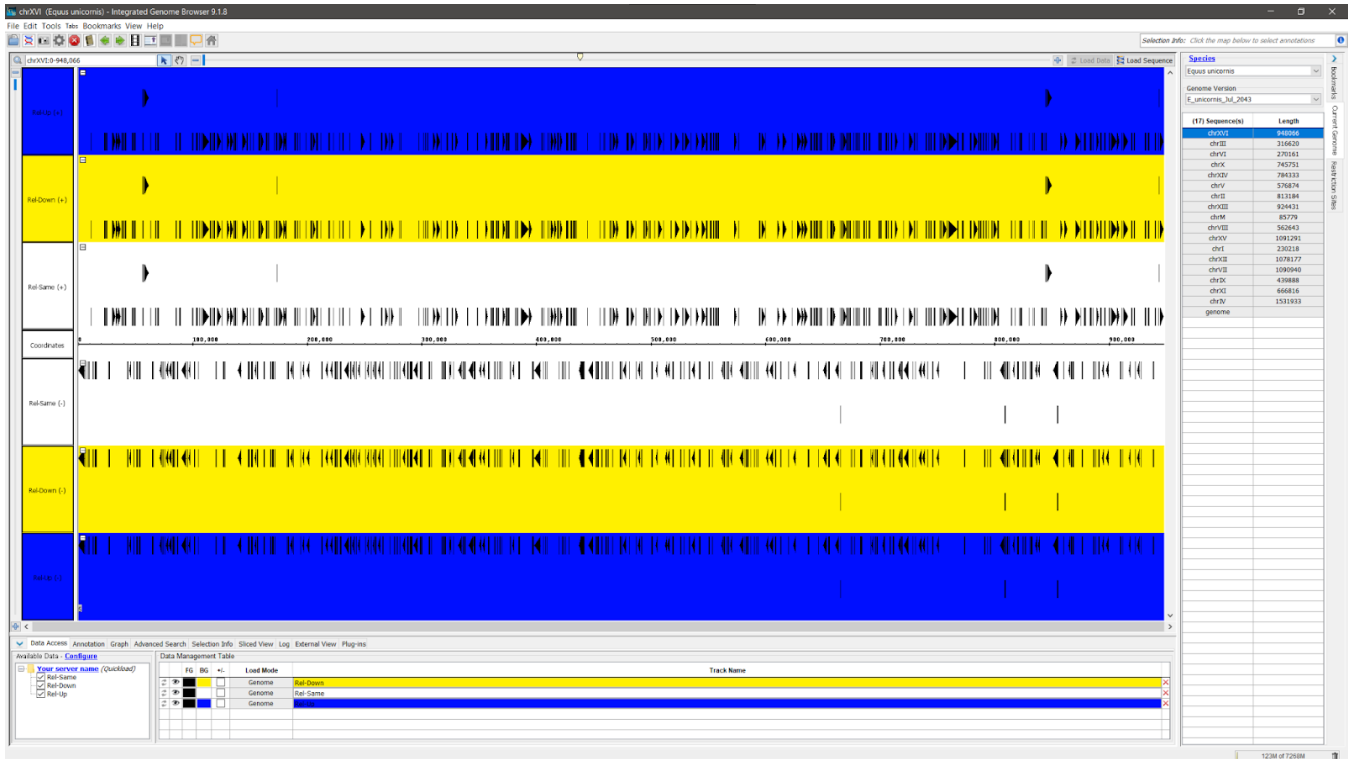
- The data on your QuickLoad is reachable by IGB and not highlighted in Red, Yellow, or Greyed out.

- ☐ mac
- ☐ linux
- ☐ windows

Access local QuickLoad data

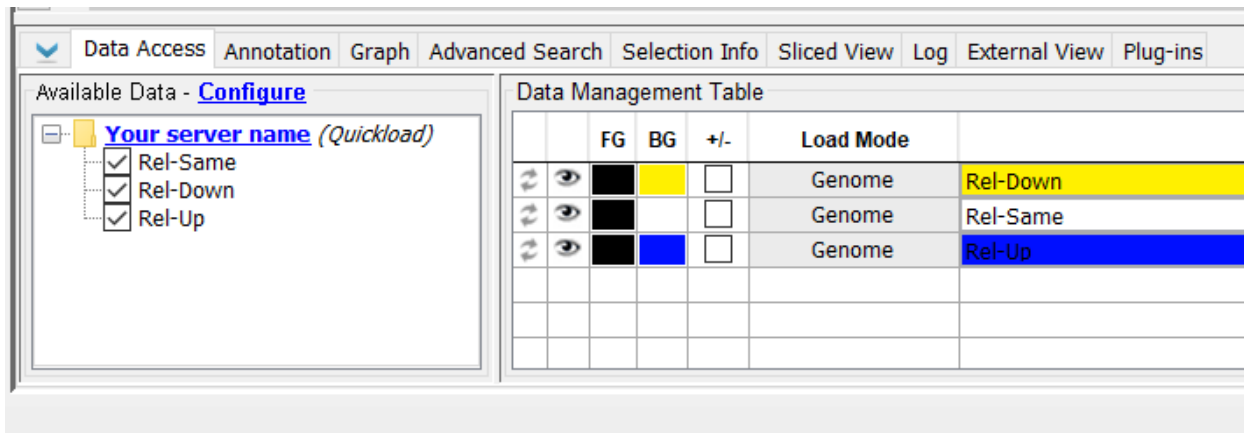
1. Close the **Preferences** window.
 2. Open the **E_unicornis_Jul_2043** genome.
- The correct **Species** (E_unicornis) and **Genome Version** (Jul_2043) loaded.

- ☐ mac
- ☐ linux
- ☐ windows



- Data loads automatically and appears the same as the above image.

- ☐ mac
- ☐ linux
- ☐ windows

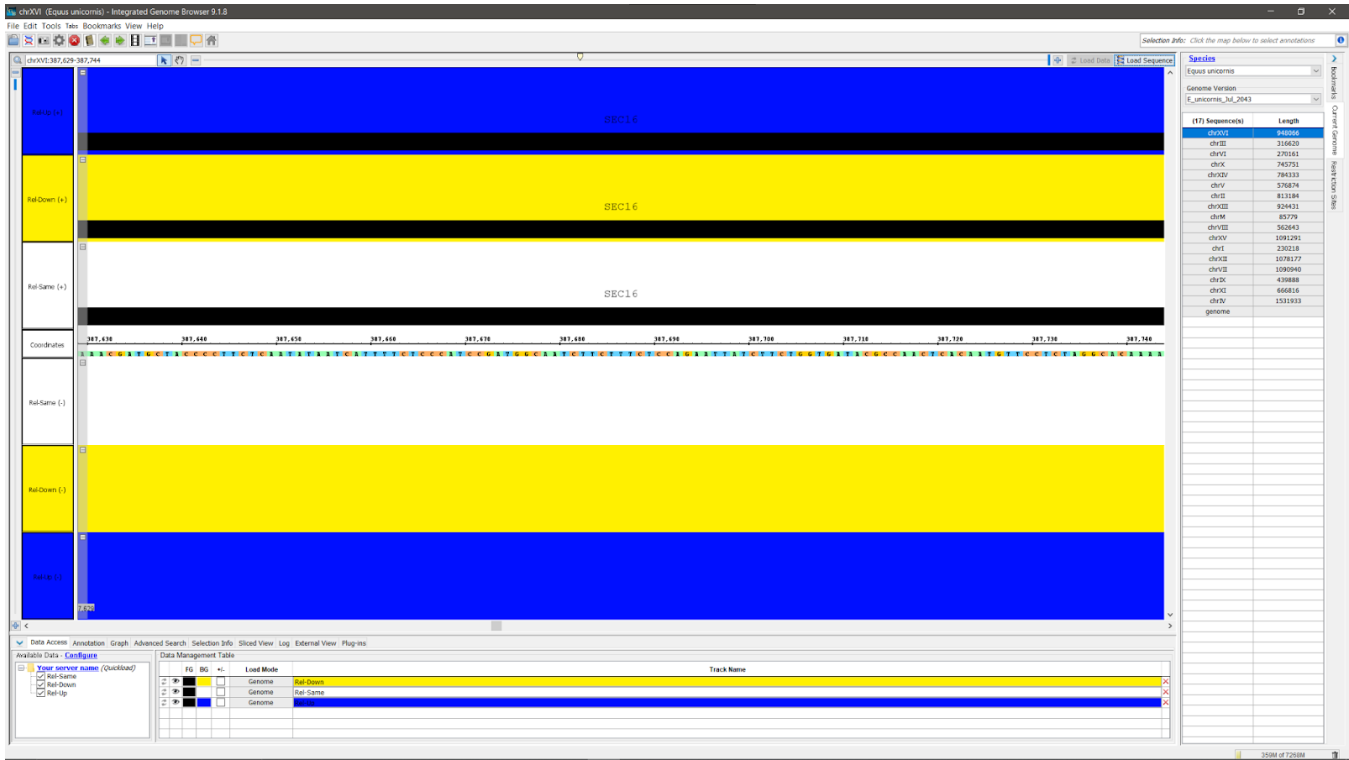


- Your QuickLoad appears in the **Available Data** section.

- ☐ mac

- ☐ linux
- ☐ windows

Zoom to the following coordinates, then click **Load Sequence: chrXVI:387,629-387,744**



- The sequence data loads along the coordinates track.

- ☐ mac
- ☐ linux
- ☐ windows