

Loading data

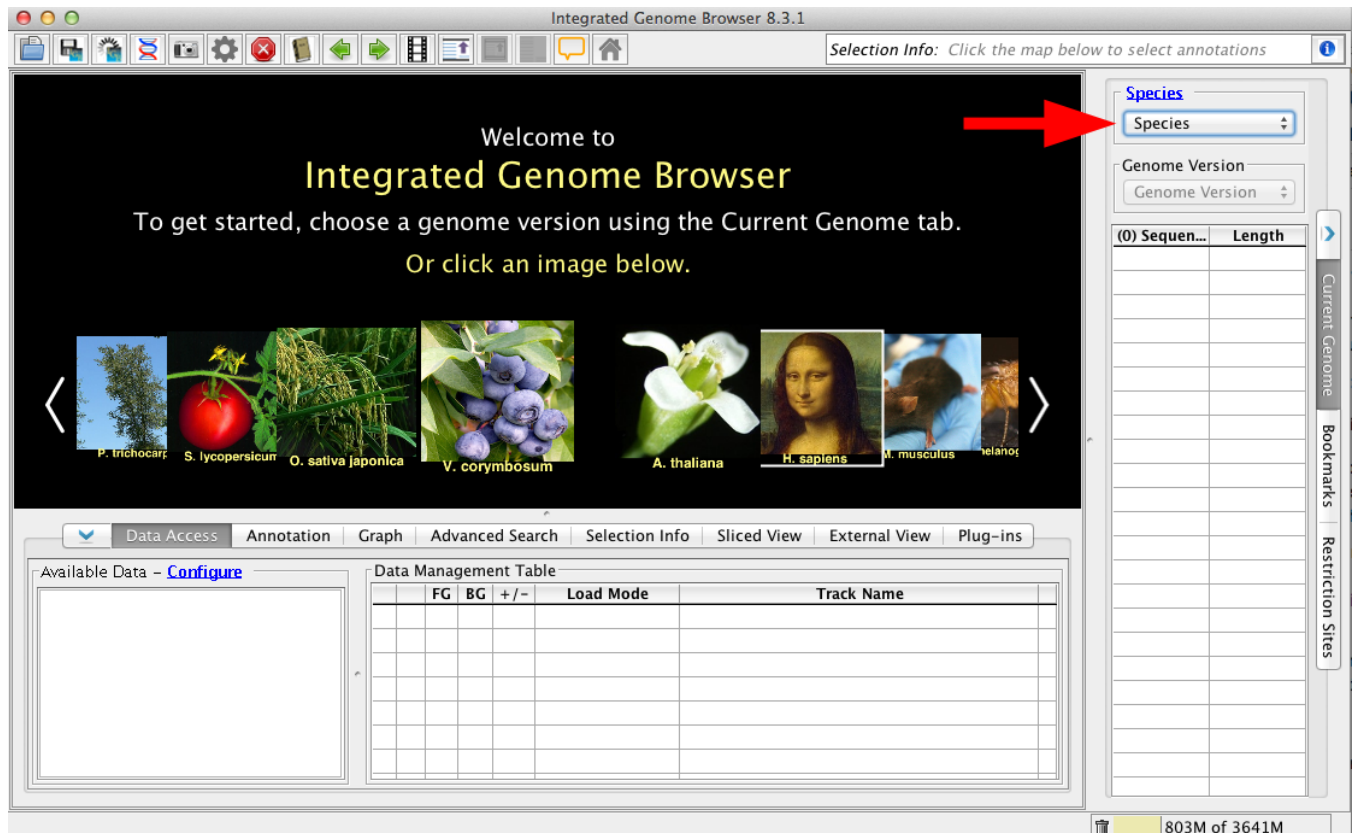
IGB can integrate and merge data from multiple sources in the same view. These includes data sets loaded from your computer, from URL sites, or from various public (and private) DAS, DAS2 and Quickload servers.

To load data:

- [Choose Species and Genome Version](#)
- [Open data sets](#) - from files, Quickload sites, URLs, or other sources
- [Use Data Management Table](#) to configure data loading settings (optional)
- [Click Load Data](#) or [Load Sequence](#) buttons

Choose Species and Genome Version

Use the **Current Genome** tab to select a **Species** and **Genome Version**. Or select an image on the Start Screen.



You can also open custom genomes not already available in IGB. See [Custom Genomes \(Genomes not in IGB\)](#).

Open data sets - from files, Quickload sites, URLs, or other sources

Once you select a species and genome version, publicly accessible data sets hosted on IGB Quickload sites or other sources will appear in the Available Data section of the Data Access tab. Select these data sets to open them in IGB.

You can also open files. To open a file, select **File > Open File...** or **File > Open URL...**

Once a file is opened, IGB adds it to the **Data Management Table** in the **Data Access** tab.



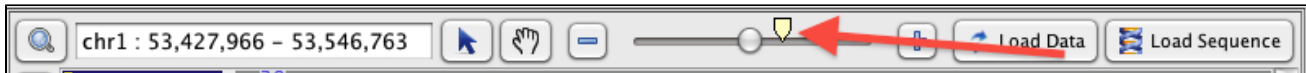
Opening a file does not automatically cause IGB to start showing data in the file. Because some data files are very large, you must first zoom in and click the **Load Data** button load the data into IGB.

Use Data Management Table to configure data loading settings (optional)

To change how and when IGB loads data into a track, open the **Data Access** panel and change settings under **Load Mode** in the **Data Management Table**.

Options include:

- **Don't Load** means no data will load when you click the **Load Data** button.
- **Genome** triggers automatic loading of all data from a file.
- **Manual** means that only data overlapping for the currently displayed region will load when you click **Load Data**. This is the default setting.
- **Auto** means that moving or zooming to a new location triggers data loading, but only when the zoom threshold is lower than the mark shown on the horizontal zoomer. Change the threshold by selecting **View > Set AutoLoad Threshold to Current View**.



Click Load Data or Load Sequence buttons

To load data for all visible tracks with load mode setting **Manual**, click the **Load Data** button.

To load reference sequence, click the **Load Sequence** button.

To load all data for a data set, change its **Load Mode** in the **Data Management Table** to **Genome**.

Regions where data have not yet been loaded have gray background color.

region with no data yet loaded region with loaded data click to load data click to load sequence

A screenshot of the IGB interface showing the Data Management Table and the tracks. The tracks show a gray bar indicating genomic sequence is loaded. The Data Management Table shows the Load Mode for the tracks.

gray bar indicates genomic sequence is loaded

	FG	BG	+/-	Load Mode	Track Name
				Genome	RefSeq Curated
				Manual	Adrenal gland scaled coverage

