Quick start

If you are new to IGB, use this **Quick Start Guide** get started.

Step 1: Get and start IGB

- Go to BioViz.org and click the **Download** button
- Select and download the installer for your platform

If you have trouble starting IGB, visit the help page on BioViz.org for assistance.

Step 2: Choose species and genome version

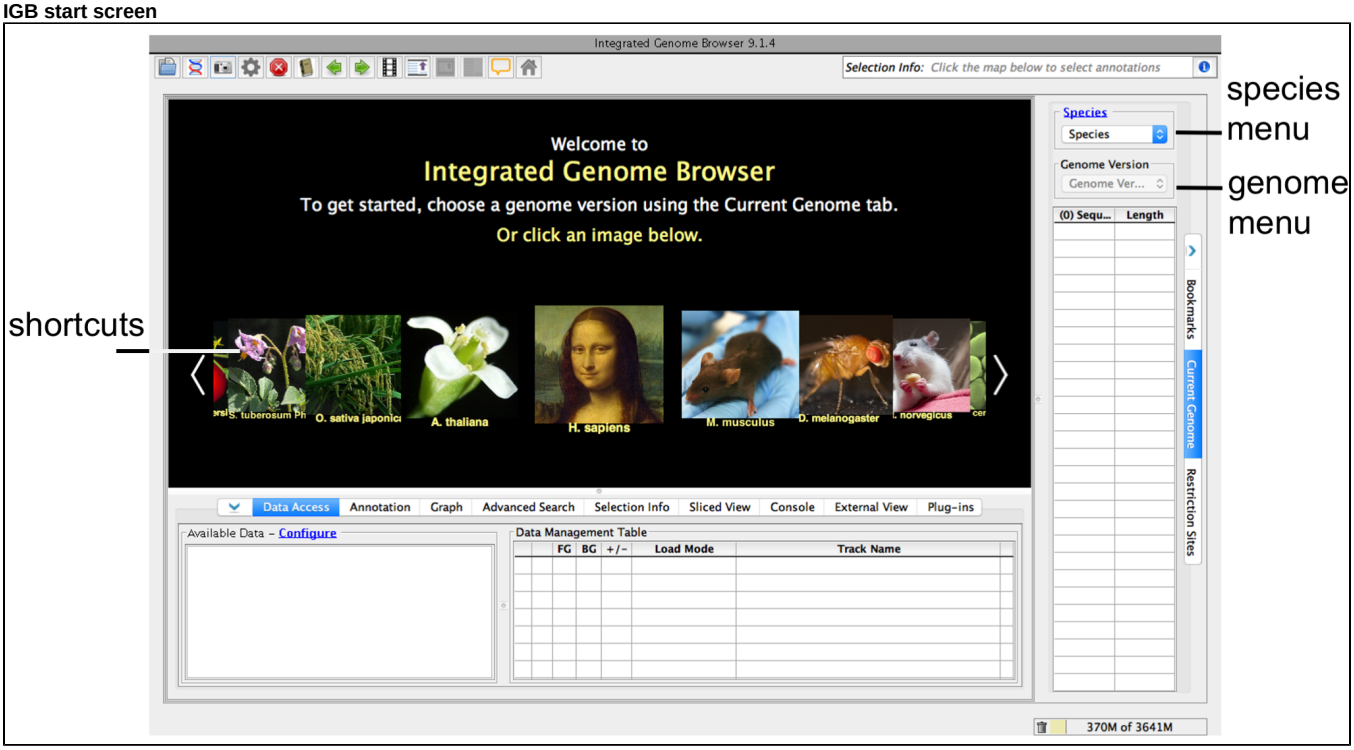
To choose a species and genome version

- Click a shortcut image (loads most recent genome)

or

- Choose **Species** and **Genome Version** using the **Current Genome** tab.

IGB start screen



If your species or genome version is not listed, you can view it if you have a fasta or 2bit file with sequence data. See Custom Genomes

Step 3. Open data sets

Open data sets from remote data sources (**Data Access** tab) or by opening local files.

To open a data set from an IGB Quickload data source (see About IGB Quickload)

1. Select **Data Access**

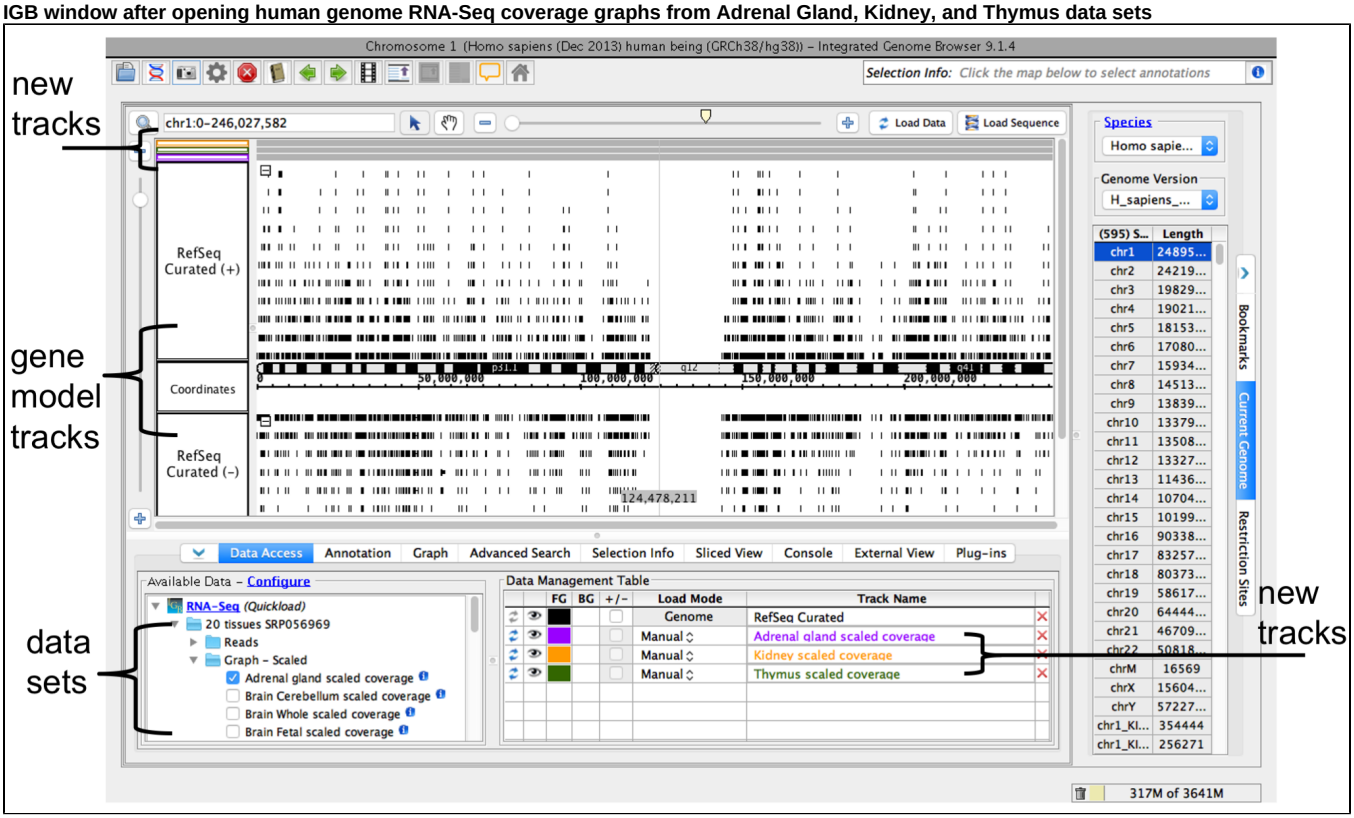
2. Select data sets in the **Available Data** section

To open local files on your computer

1. Select **File > Open File...** or **File > Open URL...**
2. Enter file name or URL

When you select a data sets or a file, IGB adds a new empty track to the main view and lists it in the **Data Management** table. Empty regions in the new track that do not have data loaded are gray.

IGB window after opening human genome RNA-Seq coverage graphs from Adrenal Gland, Kidney, and Thymus data sets



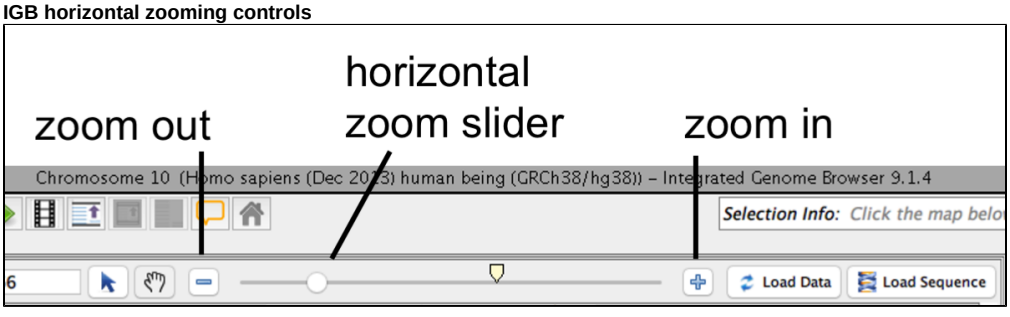
Step 4: Zoom in

Because many data files contain too much data to view all at once, IGB does not load data into the viewer until you click the **Load Data** button.

Before loading data, zoom in to a region.

1. Click a location in the main view
2. Drag the horizontal zoom slider or use plus and minus buttons

IGB horizontal zooming controls



Other ways to zoom

Other ways to zoom include

- Search for a gene by name or keyword (For example, **TBATA** or **thymus**)
- Double-click an exon or gene model to zoom in on it
- Click-drag the coordinate axis to zoom in on a region

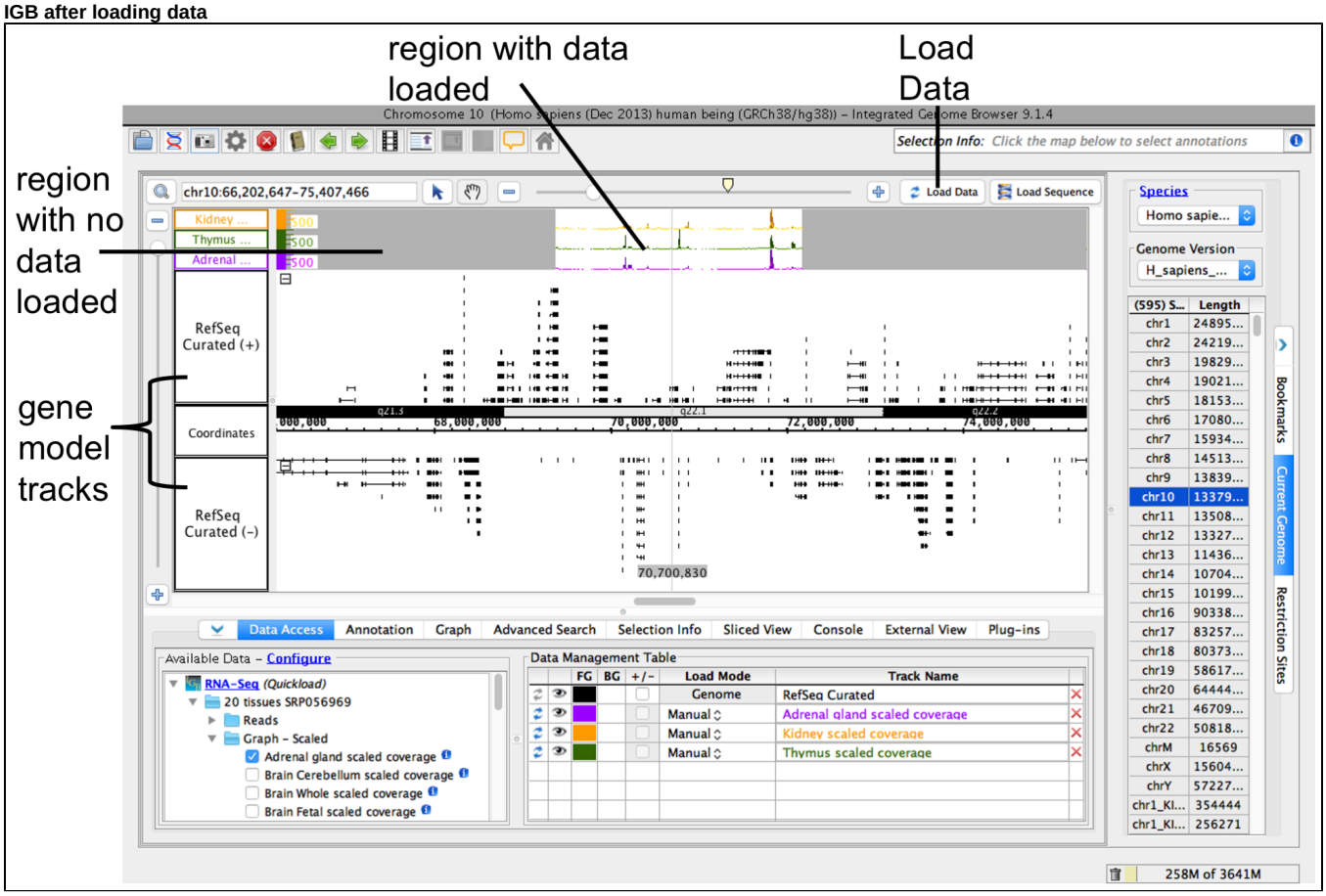
See also:

- Zooming
- Panning the display

Step 5: Load data

To load data, click **Load Data** button. Regions with loaded data show the selected background color; areas without loaded data appear darker.

IGB after loading data



See also:

- Main View
- Loading Data

Step 6: Configure tracks

You can reorder the tracks by dragging the **Track Label** (the **Data Management Table** reflect changes).

To change style elements of a track, click the track label and use the **Annotation** or **Graph** tab to change to change color, track height, annotation label, amount of data shown (stack height), and other options.

See also:

- Customizing tracks
- Preferences
- Annotation tab
- Graph Tab