# Integrated Genome Browser

The Integrated Genome Browser is an easy-to-use, easy-to-install, highly customizable genome browser you can use to view and explore genomic data and annotations. IGB supports visualization of data from RNA-seq, ChIP-seq, and more, and can load all of the major file types (BAM, SAM, BED, VCF, WIG, GTF, etc.).

## Questions?

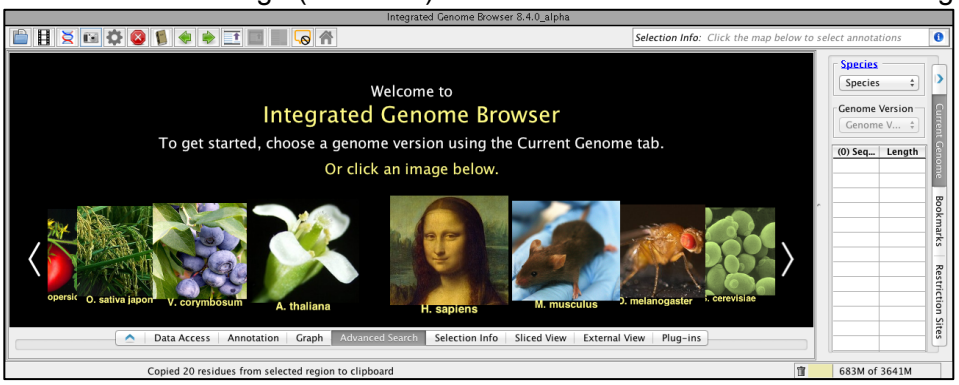
Visit the IGB user's guide for more information on IGB (https://wiki.transvar.org/display/igbman/Home), post questions to biostars.org with the IGB tag, or watch tutorials on the IGB YouTube page.
To contact the IGB team: Ann Loraine - ann.loraine@uncc.edu or Nowlan Freese - nfreese@uncc.edu

## Downloading IGB

1. Go to http://bioviz.org, select Downloads and download the IGB installer.
2. Double-click the installer to install IGB. A shortcut will appear on your desktop.
3. Double-click on the desktop shortcut (IGB icon) to launch IGB.

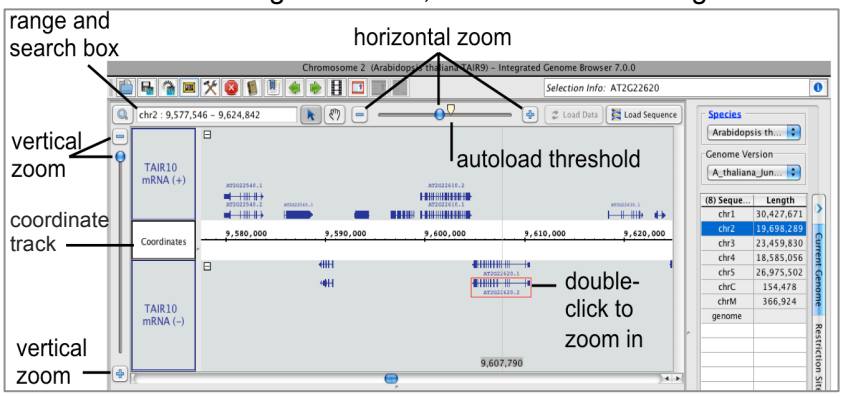
## Selecting a genome

4. Click on the image (**shortcut**) of **A. thaliana** to load the most recent genome version.




## Navigating a genome

5. Use the **horizontal zoom** slider, or highlight an area of interest in the **Coordinates** track.
6. To zoom in on a gene model, double-click on the gene itself.

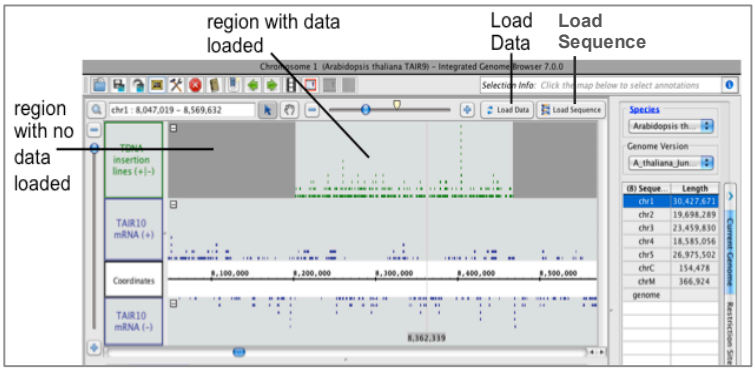



## Importing example data

7. In the **Data Access** tab, click on **Configure**, next to **Available Data**.
8. Click on **Add…**
9. In the **Name:** box, type in Demo.
10. For the **URL**, type in: http://igbquickload.org/aspb
11. Click **Submit**.

## Loading RNA-seq data

12. In the **search box** in the upper left, type in **ERD11** and hit Enter.
13. In the **Available Data** box, click the arrow next to Demo, then the arrow next to RNA-seq, then click the checkbox next to control_reads.
14. Click on **Load Data** in the top right.
15. In the **Data Management Table**, select the **+/-** for TAIR10 mRNA.
16. Right-click on the TAIR10 mRNA track and click **Optimize Stack Height**.




## Loading sequence

17. Click on **Load Sequence** in the top right.

## Creating coverage graph

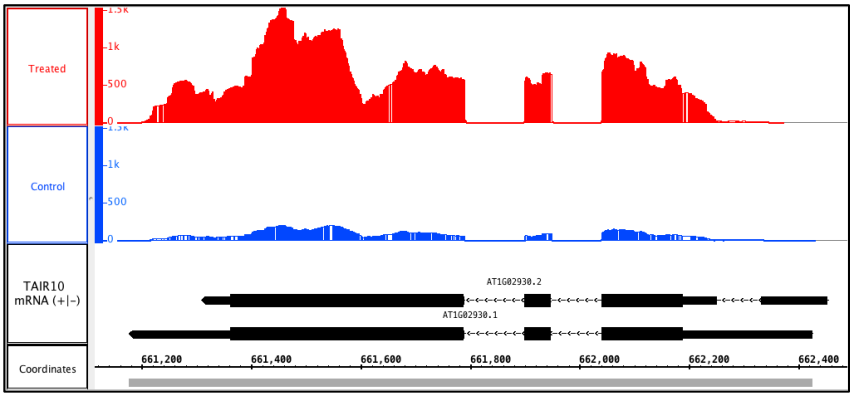
18. Right-click on the control_reads track, select **Track Operations** > **Depth Graph (All)**.

## Comparing coverage graphs

19. In the **Available Data** box, select the checkbox next to treated_reads.
20. Click on **Load Data** in the top right.
21. Right-click on the treated_reads track, select **Track Operations** > **Depth Graph (All)**.
22. Click on the treated_reads depth graph, and change the **Foreground** to red in the **Graph** tab.
23. Shift click and select the treated depth graph, and then the control depth graph.
24. In the **Graph** tab, adjust the **Y Axis Scale** slider all the way to the right.

## Saving an image

25. In the **Data Management Table**, click the eye icon for the control_reads and treated_reads.
26. Click on **View** > **Hide Visual Tools**.
27. Click on the camera icon.
28. Select png, and a resolution of 300.
29. Select **Main View (with labels)**.
30. Click **Save As…** to select the destination, name the file and save.
31. Click on **View** > **Show All Visual Tools** to turn the visual tools back on.



## Removing data

32. In the **Data Access** tab, within the **Data Management Table**, click on the red X to remove all tracks except for the TAIR10 mRNA.

## Loading ChIP-seq data

33. In the **Available Data** box, click the arrow next to ChIP-seq, then click the checkbox next to ChIP_coverage.
34. In the **search box** in the upper left, type in **chr1:6,322,560-6,431,706** and hit Enter.
35. Click **Load Data**.

## Thresholding data

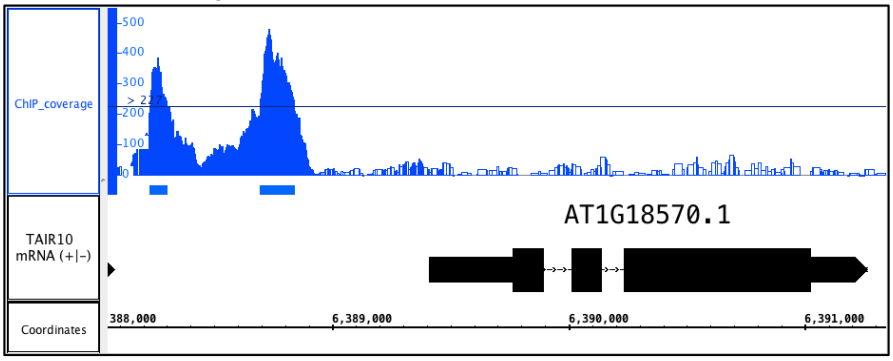
36. Select the ChIP_coverage track, and then click on the **Graph** tab.
37. Click **Thresholding…**
38. Turn on **Visibility**.
39. Change **By Percentile** to 95.

## Viewing ChIP-seq peaks

40. In the **search box** in the upper left, enter **AT1G18570.1** and hit Enter.
41. Right-click on the RefGene track and click **Optimize Stack Height**.
42. Zoom out just enough to see the predicted peak at the 5’ end of the gene.
43. In the **Graph** tab, change the Y Axis scale so the peaks fill the track.

## Saving an image

44. Save an image as before.




## Creating Bookmarks

45. Click on the **Bookmarks** tab on the right.
46. Click on **Bookmark icon** to add a new bookmark.
47. Enter a name and any comments for the bookmark.

## Searching for motifs

48. Click on the **Advanced Search** tab.
49. In the dropdown menu next to **Search**, select **Residues**.
50. Search for the motif: CTTTG[GT]AC

## Searching for CRISPR-cas sites

51. Double-click on the second exon of AT1G18570.15.
52. In the **Advanced Search** tab, search for: .GG (make sure to include the period before GG)
53. Select a .GG site, and highlight the 20bp upstream of the site in the coordinates sequence.
54. Right-click on the sequence and select **BLASTX nr protein database** to check for potential off-target effects.

## Removing data

1. In the **Data Access** tab, within the **Data Management Table**, click on the red X to remove all tracks except for the TAIR10 mRNA.

## Loading WGB-seq data

1. Zoom out so that all of chromosome 1 is visible.
2. In the **Available Data** box, click the arrow next to WGB-seq, then click the checkbox next to WGB_coverage.
3. Click on **Load Data** in the top right.

## Thresholding data

4. In the **search box** in the upper left, type in **AT1G58602** and hit Enter.
5. Select the WGB_coverage track.
6. Under the **Graph** tab, click on **Thresholding**.
7. Turn on **Visibility**.
8. Change **By Value** to 70, **Max Gap** to 0, and **Min Run** to 0.

## Viewing WGB-seq reads

9. In the **Data Access** tab, within the **Available Data** box, click the checkbox next to WGB_reads.
10. Click on **Load Data** and **Load Sequence** in the upper right.
11. In the **search box** in the upper left, enter **chr1:21,752,728-21,752,874** and hit Enter.

## Saving an image

12. Save an image as before.