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. This hands-on workshop will show you how to visually analyze RNA-seq, ChIP-seq, and whole genome bisulfite sequencing data, and how to turn that visual analysis into publication quality images.

Questions?

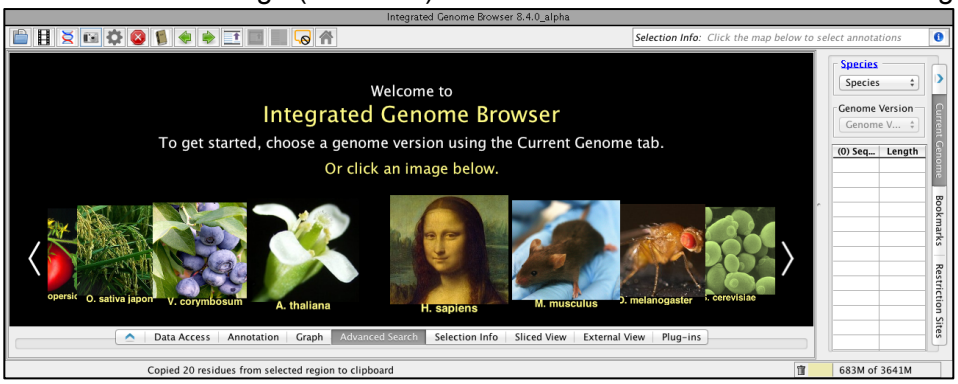
Visit the IGB user's guide for more information on IGB (https://wiki.transvar.org/display/igbman/Home). Or contact the IGB team: Ann Loraine - ann.loraine@uncc.edu or Nowlan Freese - nfreese@uncc.edu

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.

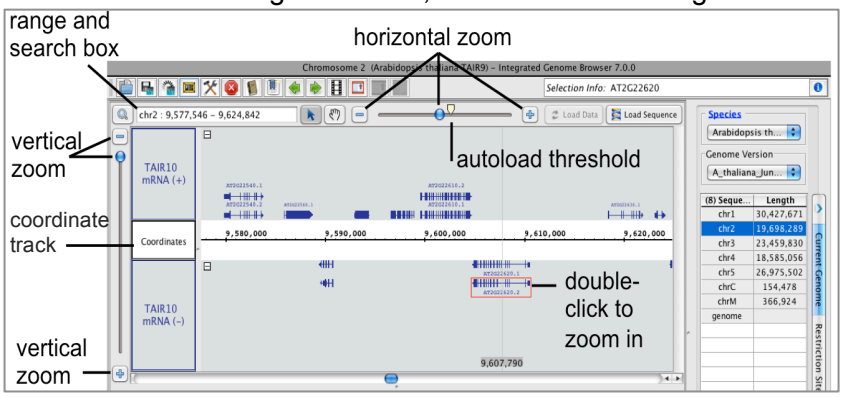
Selecting a genome

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.

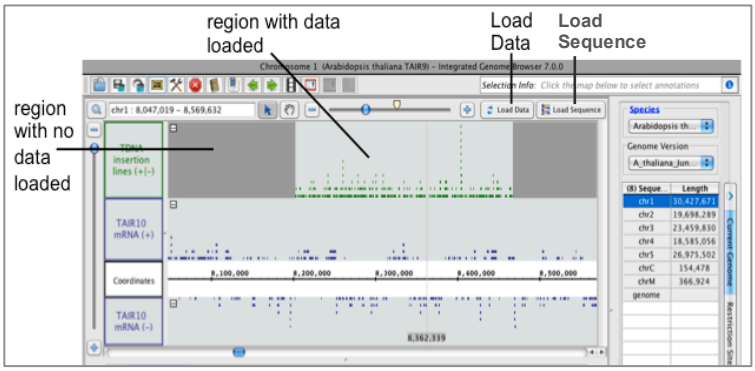


Importing example data

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/demo
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

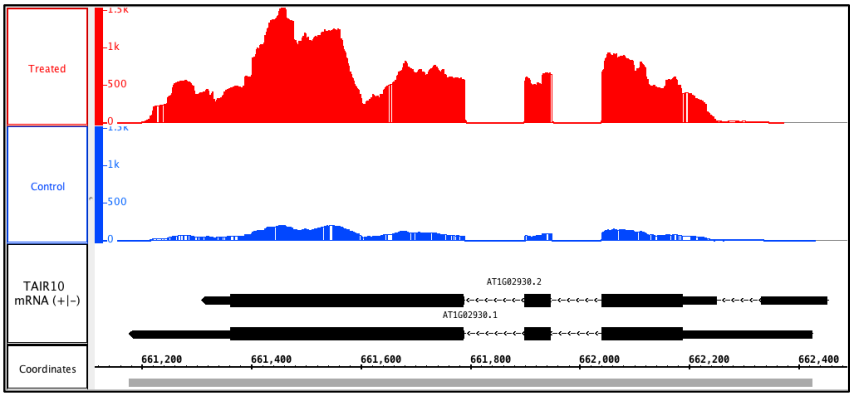
18. Right-click on the control_reads track, select **Track Operations** > **Depth Graph (All)**.

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 WGB-seq data

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

Thresholding data

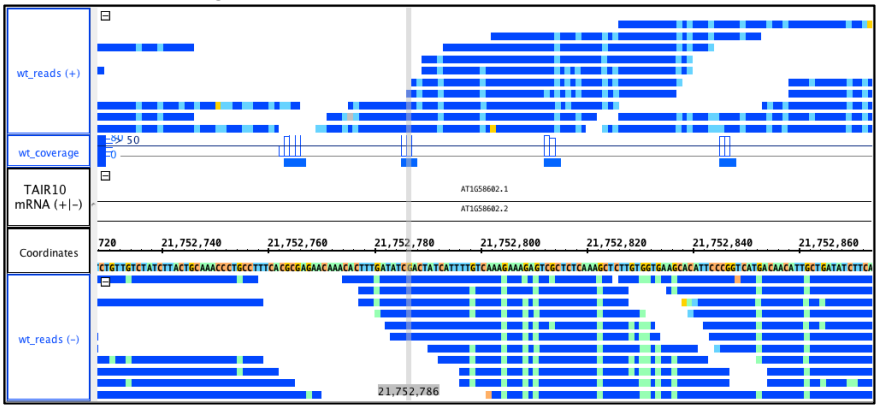
36. In the **search box** in the upper left, type in AT1G58602 and hit Enter.
37. Select the wt_coverage track.
38. Under the **Graph** tab, click on **Thresholding**.
39. Turn on **Visibility**.
40. Change **By Value** to 70, **Max Gap** to 0, and **Min Run** to 0.

Viewing WGB-seq reads

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

Saving an image

44. Save an image as before.



Removing data

45. Under the **Data Management** Table, click on the red X to remove all tracks except for the TAIR10 mRNA.

Changing genomes

46. Click on the **Home** icon to go back to the main window.
47. Click on the image (**shortcut**) of **M. musculus** to change to the mouse genome.

Loading ChIP-seq data

48. In the **Available Data** box, click the arrow next to demo, then the arrows next to ChIP-seq, then click the checkbox next to peaks.
49. Click **Load Data**.
50. In the **Data Management Table**, select the **+/-** for both the peaks and the RefGene files.

Coloring data by score

51. Right click on the peaks track, and select **Color by…**
52. Select **Score** in the dropdown menu.

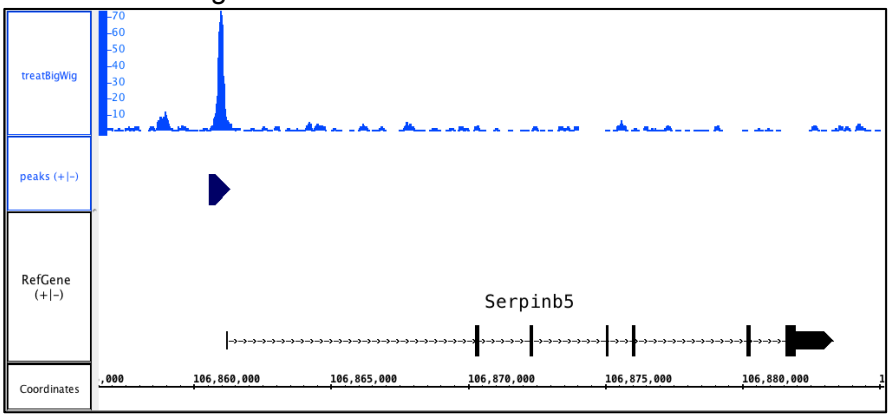
53. Click **Edit** next to heatmap.
54. Double-click on the arrows to change their color - light blue for the leftmost two arrows, and dark blue for the rightmost arrows.
55. Click on **Set Range**, and change the **Min** to 50, and the **Max** to 250.
56. Click **OK**.

Viewing ChIP-seq peaks

57. In the **search box** in the upper left, enter serpinb5 and hit Enter.
58. Right-click on the RefGene track and click **Optimize Stack Height**.
59. Zoom out just enough to see the predicted peak at the 5' end of the gene.
60. In the **Available Data** box, click the checkbox next to treatBigWig.
61. Click **Load Data**.

Saving an image

62. Save an image as before.



Loading data via Dropbox

63. Click on **File** > **Open URL**.
64. Enter https://dl.dropboxusercontent.com/u/33652246/workshop/ChIP-seq_reads.bam and click **OK** (Click yes to trust certificate).
65. Click **Load Data**.

Creating Bookmarks

66. Click on the **Bookmarks** tab on the right.
67. Click on **Bookmark icon** to add a new bookmark.
68. Enter a name and any comments for the bookmark.

Searching for motifs

69. Click on the **Advanced Search** tab.
70. In the dropdown menu next to **Search**, select **Residues**.
71. Search for the motif: AGAACAATGG

Searching for CRISPR-cas sites

72. Double-click on the second exon of serpinb5.
73. In the **Advanced Search** tab, search for: .GG (make sure to include the period before GG)
74. Select a .GG site, and highlight the 20bp upstream of the site in the coordinates sequence.
75. Right-click on the sequence and select **BLASTX nr protein database** to check for potential off-target effects.