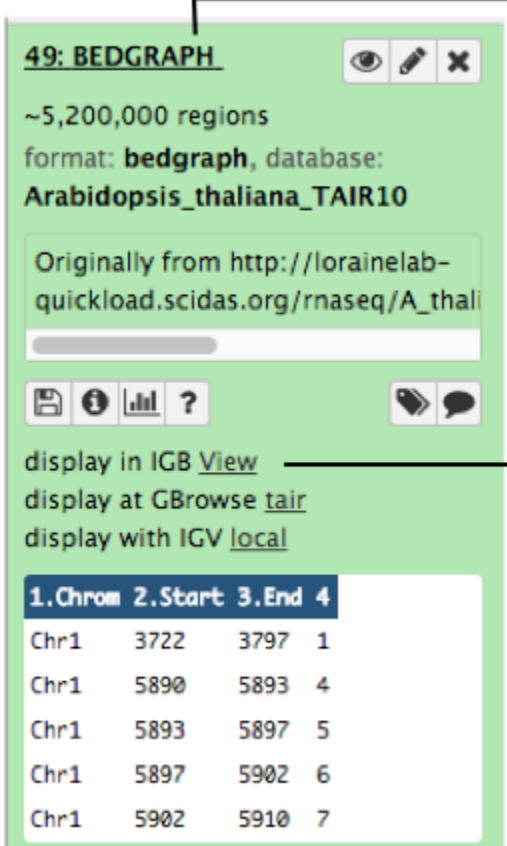


View Galaxy files in IGB

To view a Galaxy file in IGB

- start IGB
- click a file title to open the file in your Galaxy history
- click the View link to open the Galaxy bridge page at BioViz.org



1. click to open file

2. click to open Galaxy bridge page at BioViz.org

49: BEDGRAPH

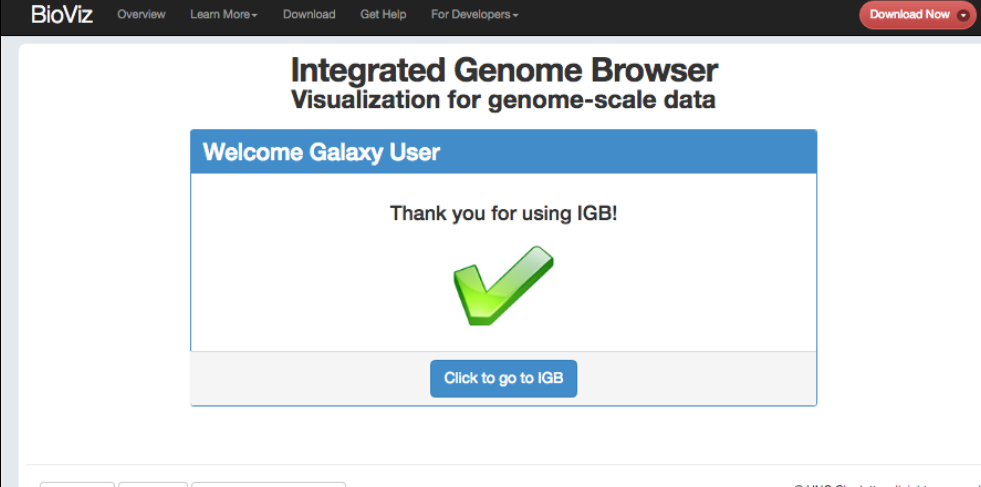
~5,200,000 regions
format: **bedgraph**, database: **Arabidopsis_thaliana_TAIR10**

Originally from http://lorainelab-quickload.scidas.org/rnaseq/A_thali

display in IGB [View](#)
display at GBrowse [tair](#)
display with IGV [local](#)

1.Chrom	2.Start	3.End	4
Chr1	3722	3797	1
Chr1	5890	5893	4
Chr1	5893	5897	5
Chr1	5897	5902	6
Chr1	5902	5910	7

Clicking **View** opens a new Web browser page at BioViz. This is the BioViz-to-Galaxy bridge page. It page contains JavaScript code that helps IGB make a new track from your Galaxy file. Once the new track appears in IGB, you will see a message like this:



BioViz Overview Learn More Download Get Help For Developers Download Now

Integrated Genome Browser

Visualization for genome-scale data

Welcome Galaxy User

Thank you for using IGB!

Click to go to IGB

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Go back to IGB to view your data. You will see a new entries in the Available Data Sets section of the Data Access tab showing your new track.

Note: IGB may show a message asking you to accept a certificate from the Galaxy site. Click Accept to continue loading data.