



# Linking Galaxy and Integrated Genome Browser (BioViz.org)

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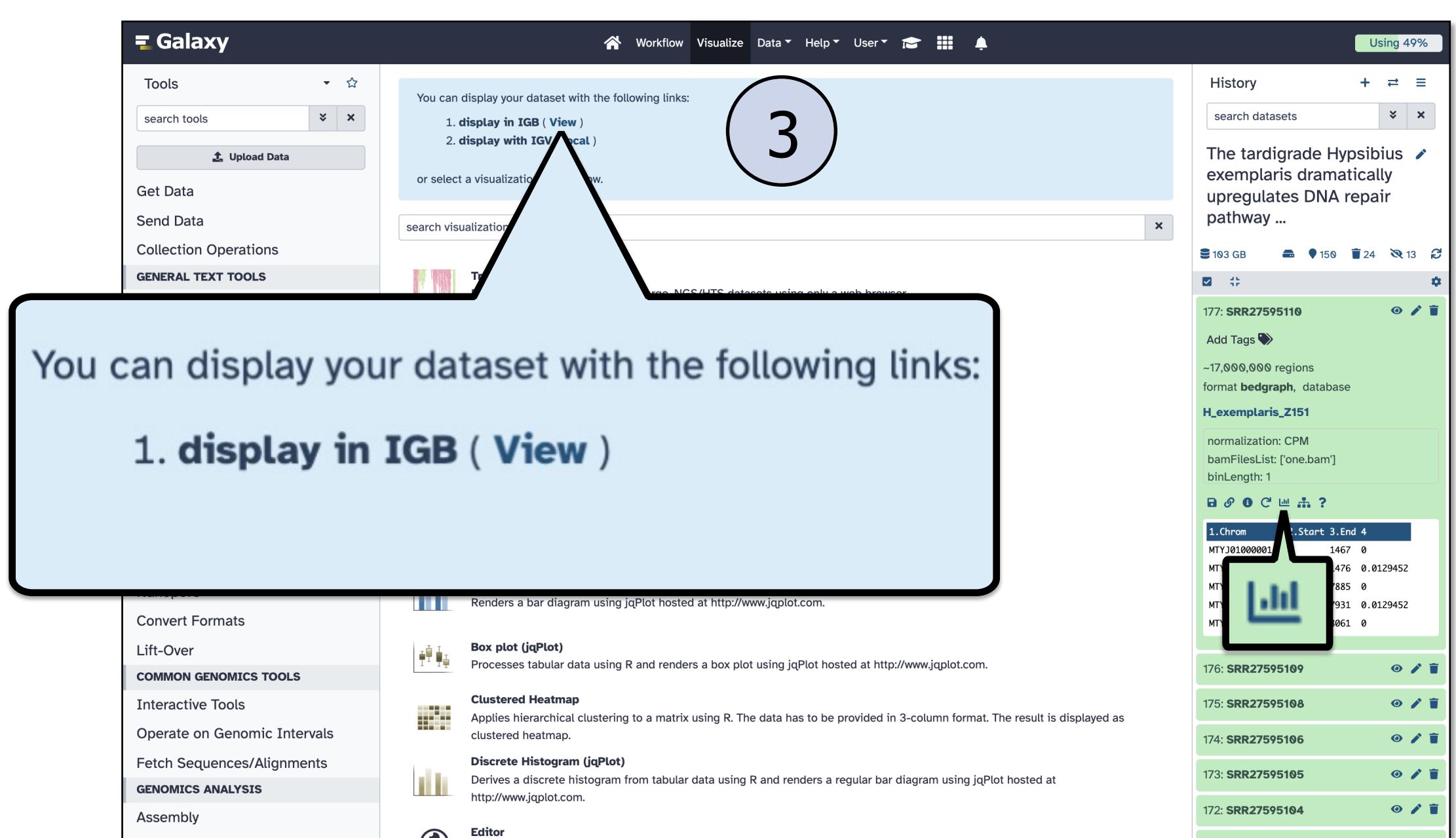
## Abstract

Integrated Genome Browser (IGB) is a fast, flexible and free Java-based desktop software tool that enables interactive exploration of genomic data sets. To promote sharing of large data sets, IGB features a ReST-style interface which allows data to be loaded from local or remote files. We leveraged this ReST-style interface to integrate IGB into Galaxy as an External Display Application. When Galaxy users create compatible data files, they now see a link labeled "View in IGB" upon clicking data file links in their Galaxy History. Clicking this link triggers delivery of data to IGB for display. This is a simple interaction from the user's perspective, but from an engineering point of view, it highlights a key extension point for Galaxy that enables integration with IGB or other visualization tools. By enabling access to data sets in a user-friendly, web-based interface, Galaxy offers many possibilities to enhance user interactions for data analysis and sharing.

## Benefits

- Galaxy makes it easy for biologists to process, analyze, store and share data.
- They can store & curate datasets using **Histories**, then share them with collaborators or the public.
- IGB links in Galaxy Histories make it easy for users to directly import data from Galaxy into IGB.

## How it works from a user's point of view



1. Click a dataset in your History

2. Click the Visualize icon

3. Click View next to "display in IGB"

A new webpage opens at BioViz.org

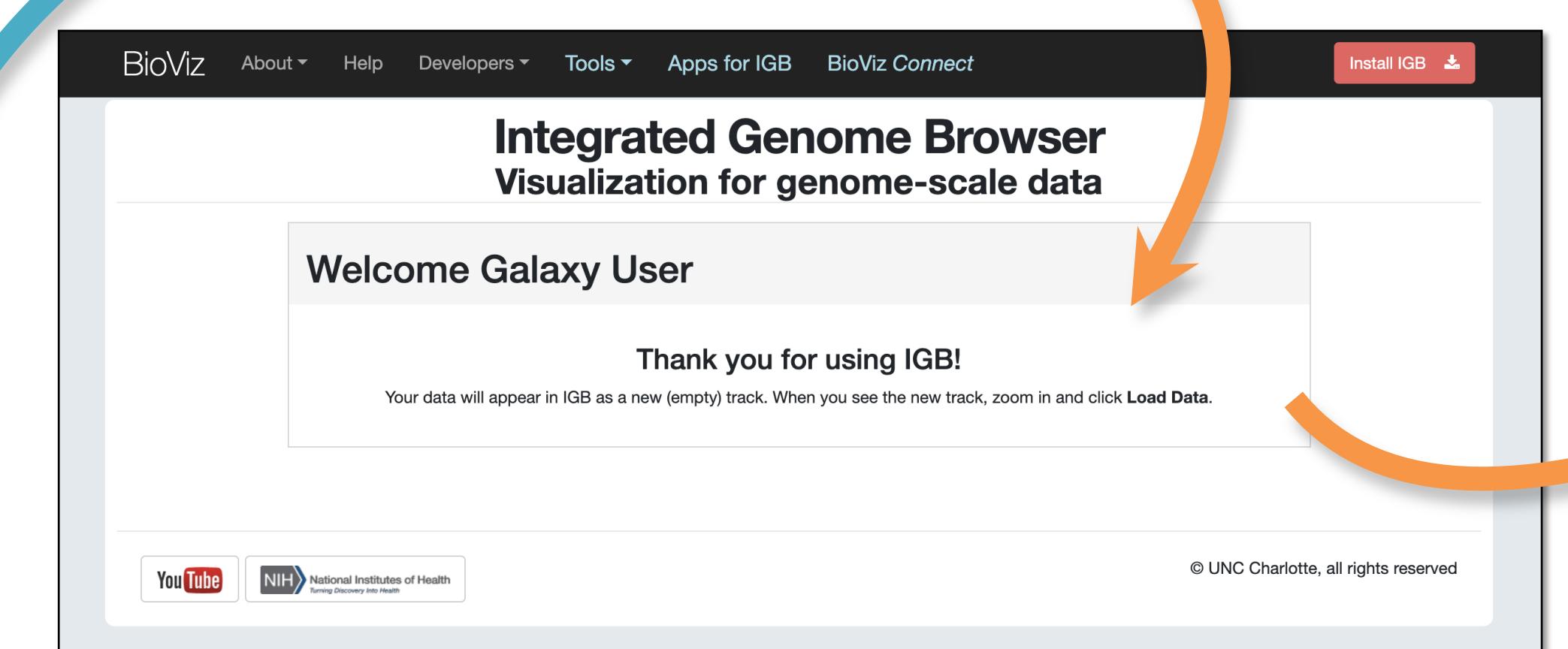
## BioViz.org

This new page at BioViz.org contains JavaScript code that looks for IGB, asking...

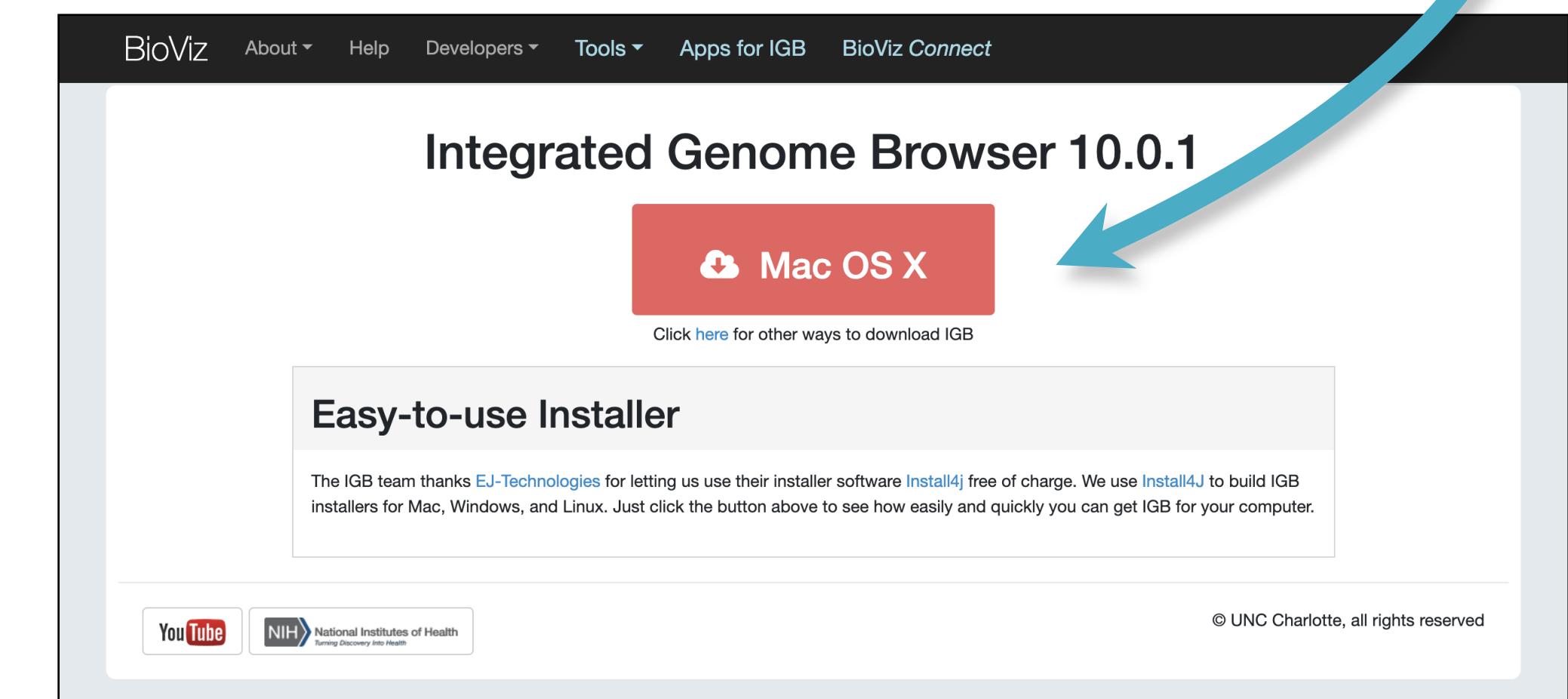
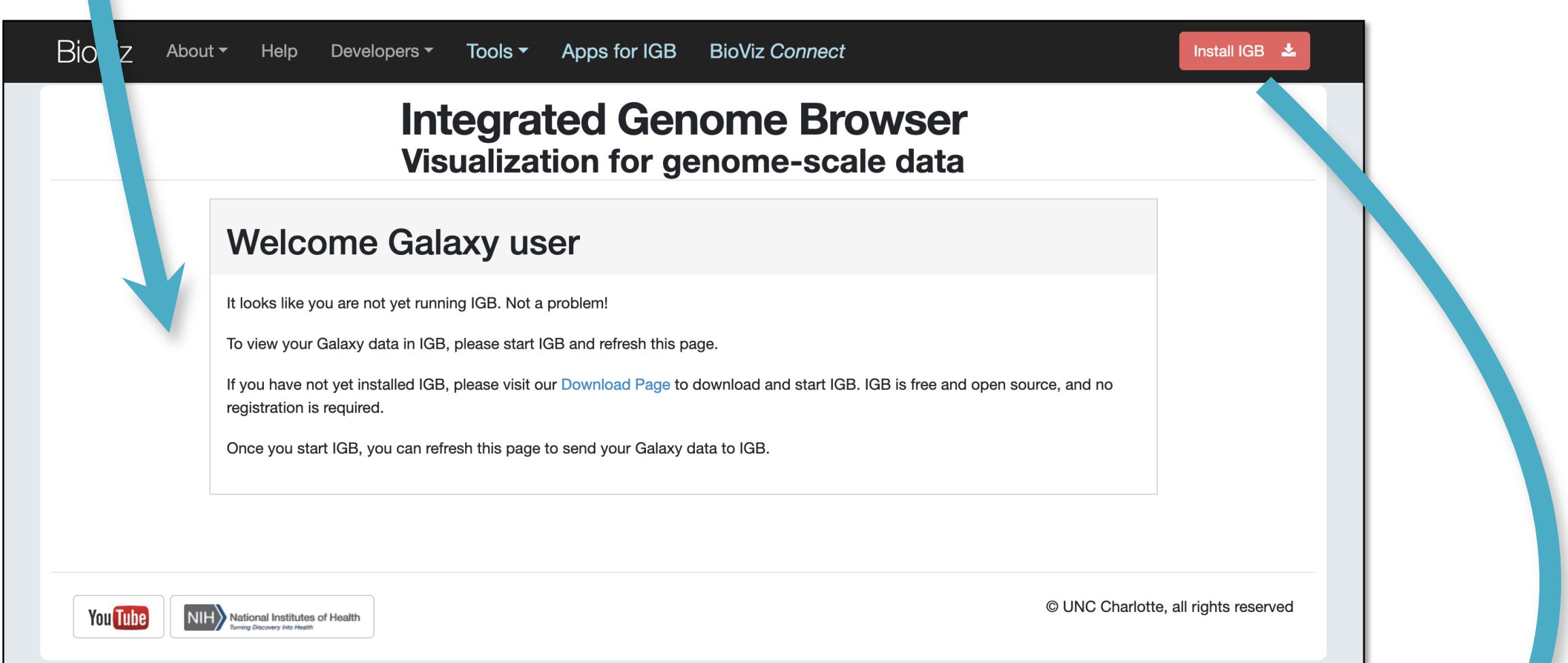
**Is IGB running?**

No

Yes



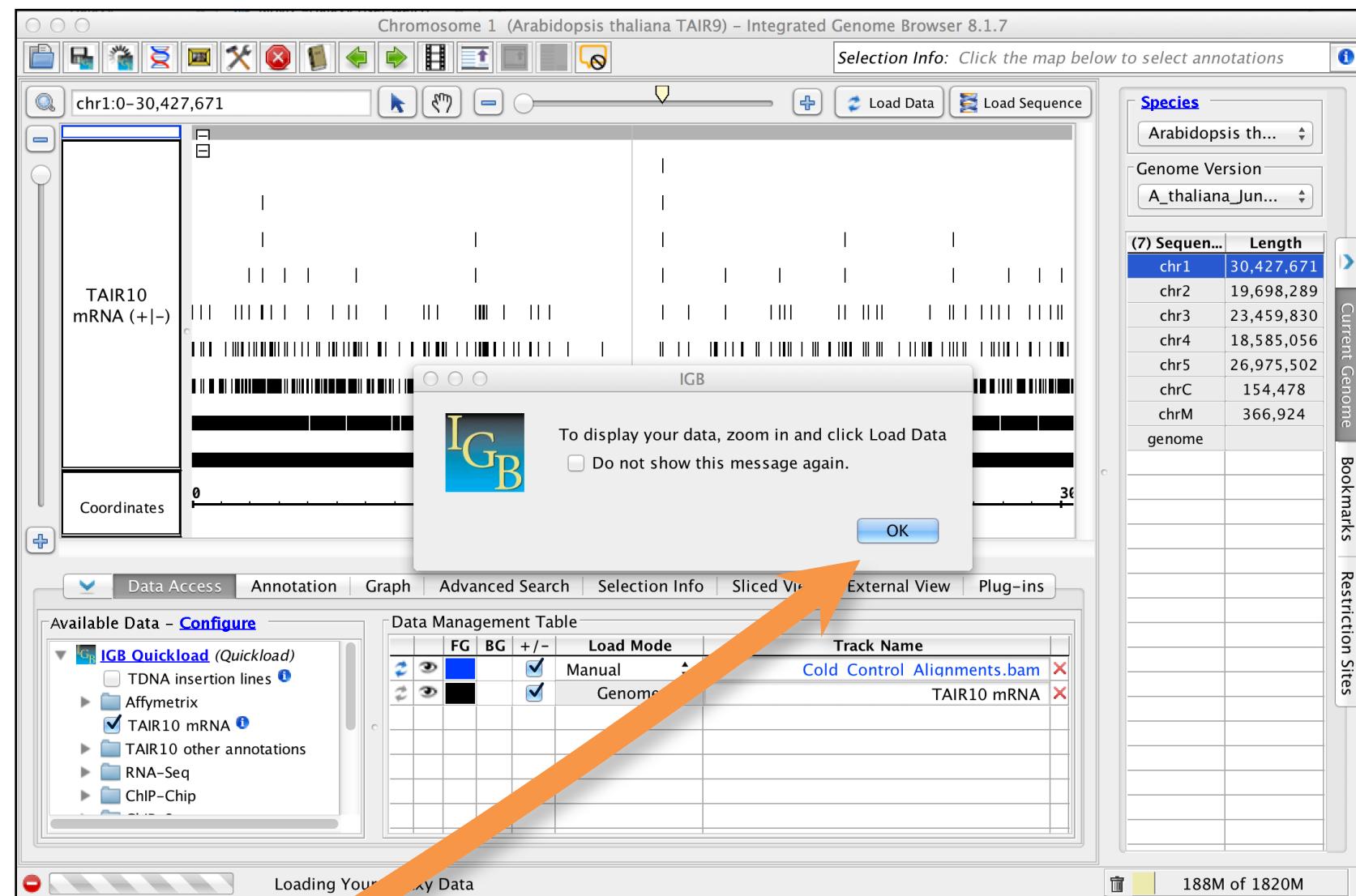
4a. Start IGB or download it from BioViz.org



4b. After starting IGB, refresh the BioViz page

## Acknowledgements

Data are sent directly to IGB - no downloads necessary



## Integrated Genome Browser

**Find Junctions**  
shows read support for splice junctions. In this case, cold increases inclusion of an alternative exon.

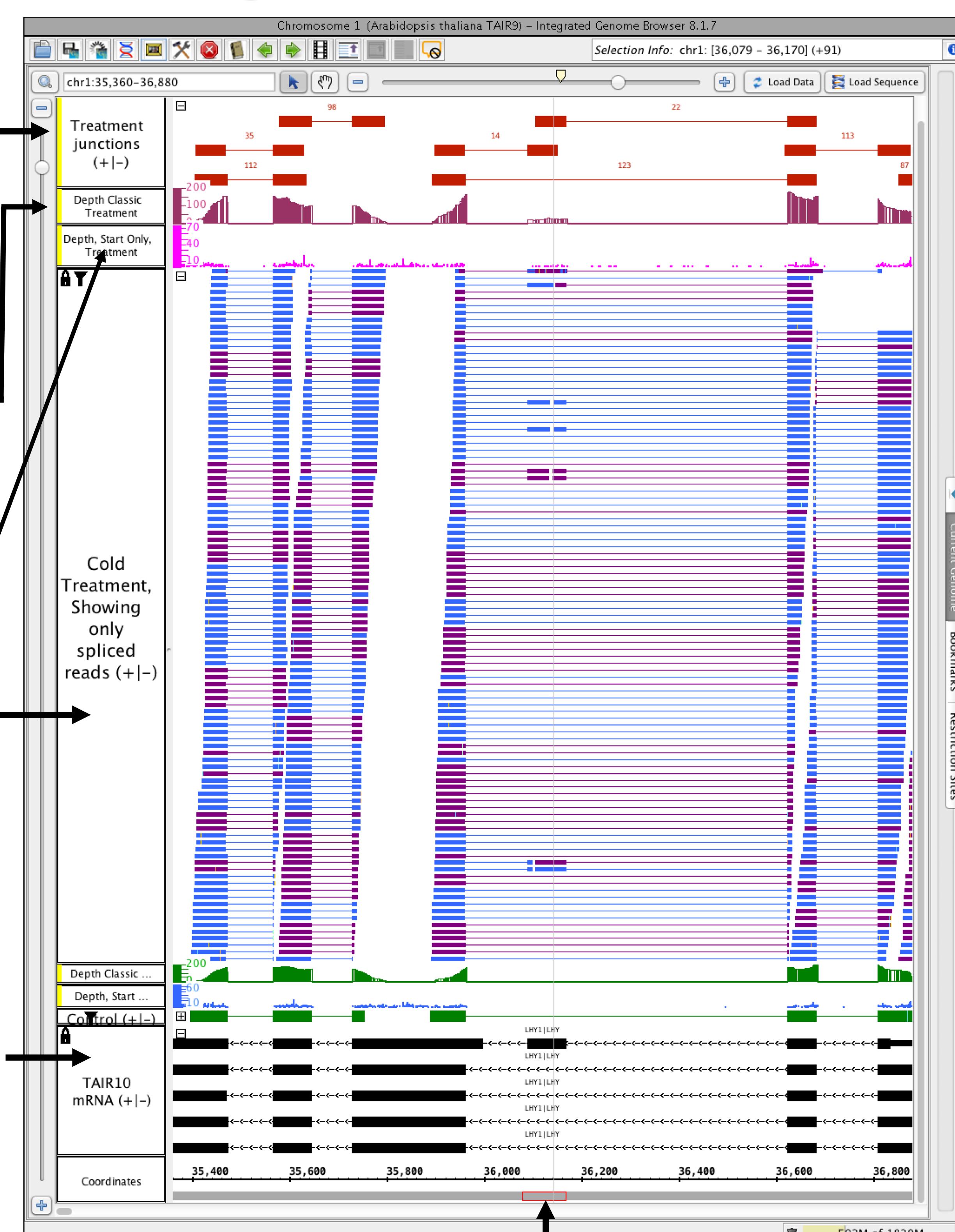
**Classic depth**  
graphs count all reads that overlap a position.

**Start only depth**  
graphs count reads that start at a position.

**Filters** hide or show reads based on their properties. Here, only reads with gaps (spliced reads) are shown.

**Gene model** tracks load automatically. Right-click a gene to search google, run BLAST, or view sequence in a new window.

**Click-drag to select sequence** and right-click to copy to external tools, like blast search or primer design.



This image shows cold-induced alternative splicing of Arabidopsis LHY, a circadian clock regulator. In plants, many genes that regulate the circadian clock are highly alternatively spliced and their pattern of splicing changes in response to temperature.

## How it works from a programmer's point of view

IGB leverages the Galaxy External Display Applications interface. Within Galaxy, IGB XML files define URLs that link to BioViz.org, which brokers interactions between Galaxy and IGB.

5. Load data and explore using IGB's visual analytics functions.