



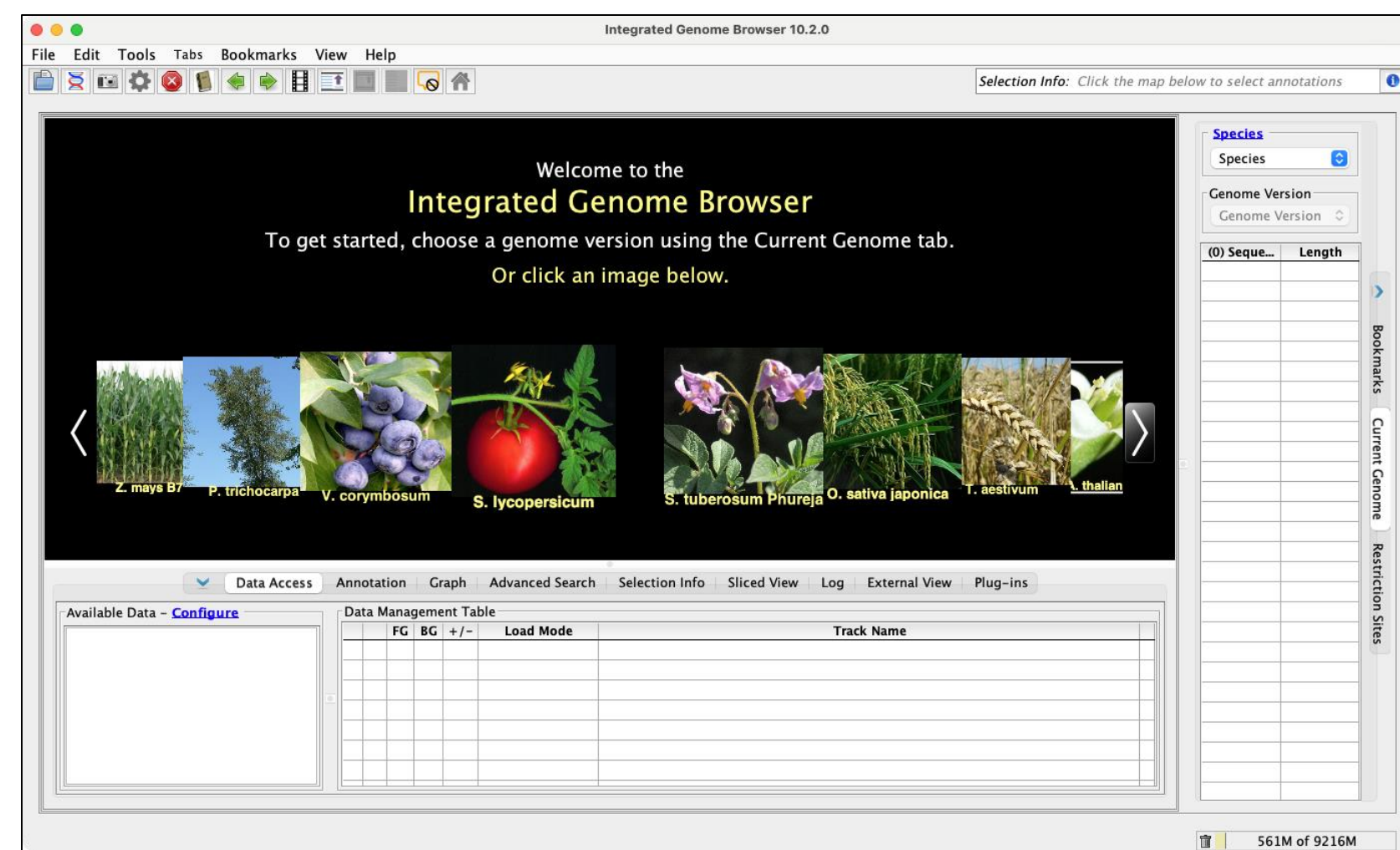
Integrated Genome Browser: software for visualizing and quality-checking genomic data

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Free to use Genome Browser with support for Linux/Mac/Windows

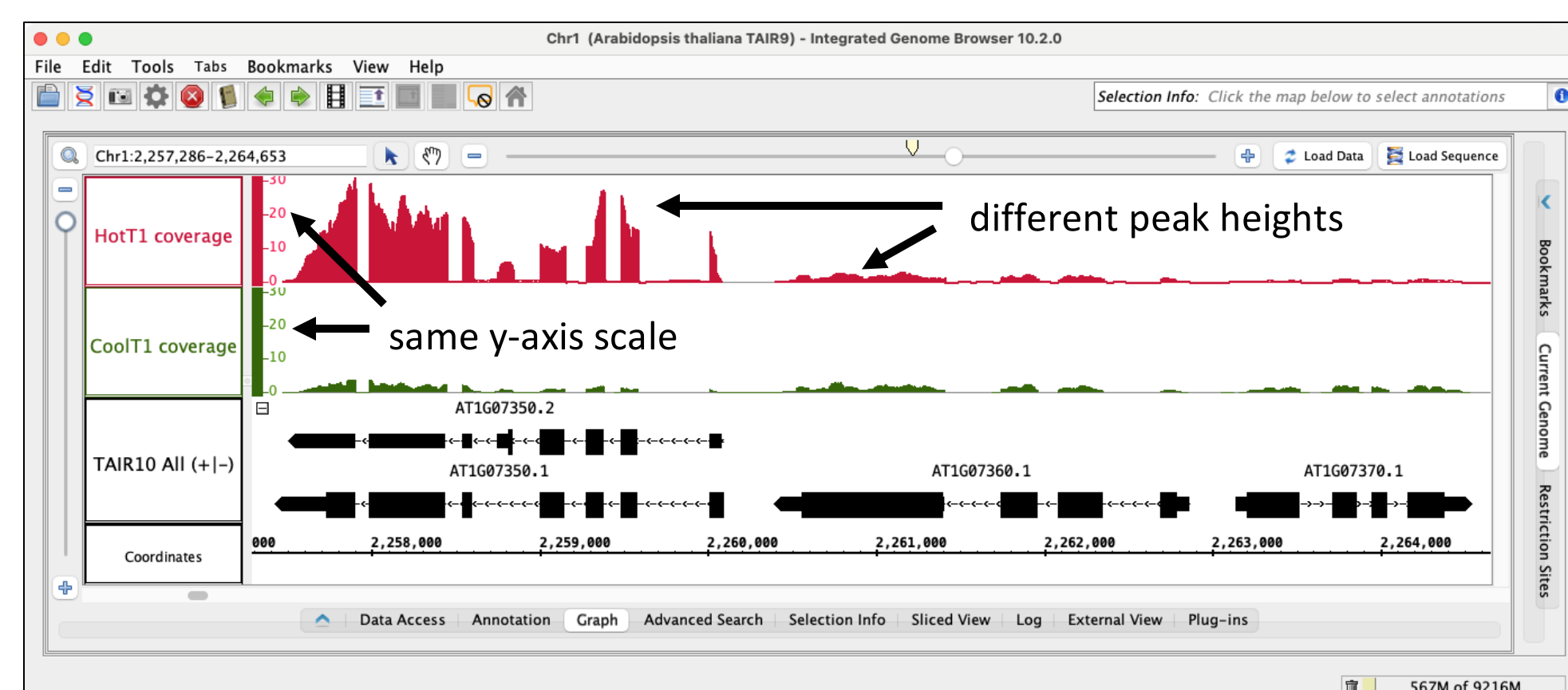
We develop and maintain the Integrated Genome Browser (IGB), a highly configurable, interactive, and fast open-source desktop genome browser. IGB supports visualization of data from many sequencing experiments, such as bulk RNA-Seq, ChIP-Seq, ATAC-Seq, whole exome sequencing, and single cell RNA-Seq. IGB is **free** to use.



Visualize biologically-interesting patterns in genomic data

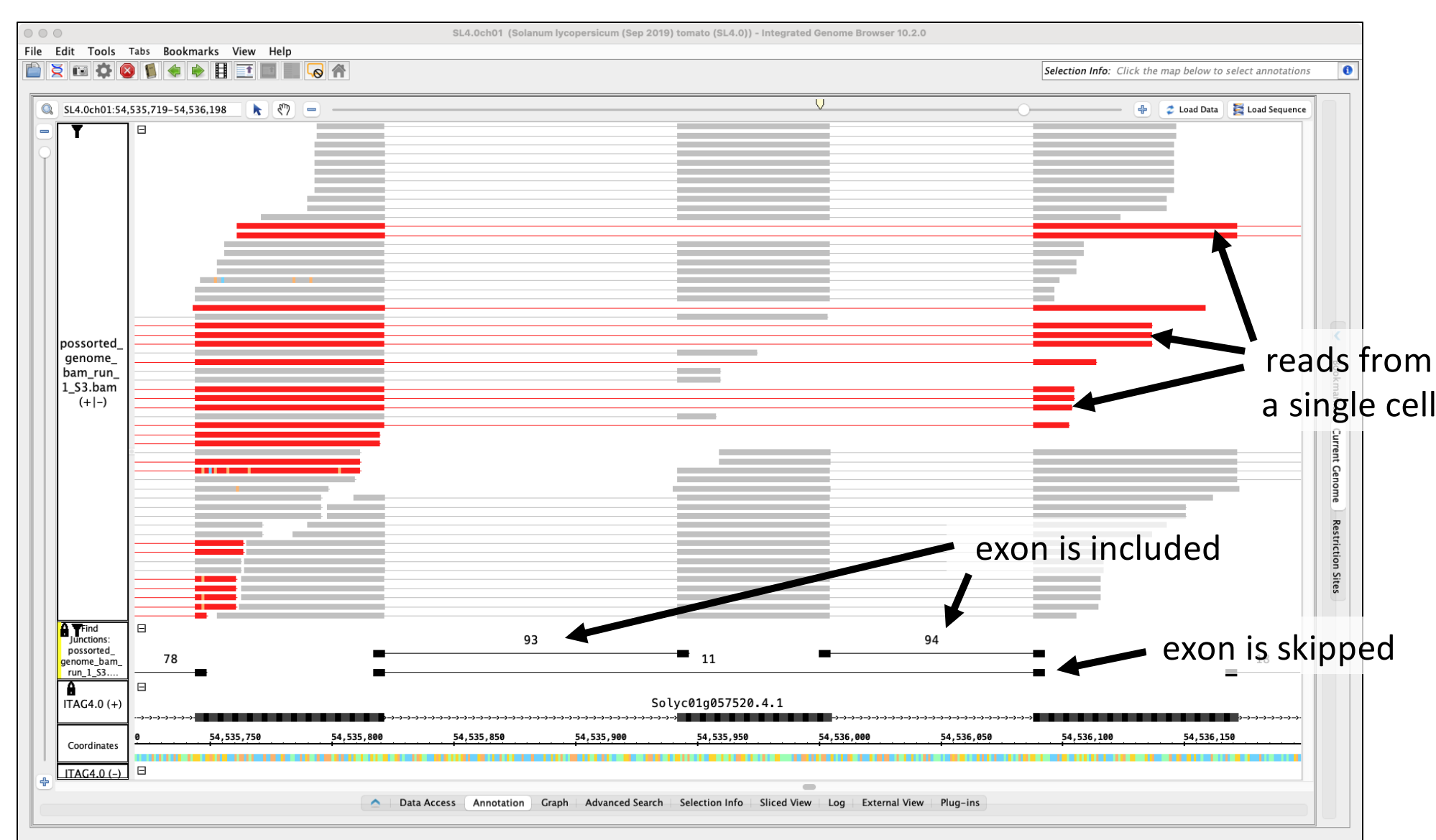
RNA-Seq

RNA-Seq analysis produces large read alignment (BAM) files. To aid in visual analysis, IGB can create depth (coverage) graphs from these BAM files. By comparing depth graphs for multiple samples, users can easily identify differences in transcript levels.



scRNA-Seq

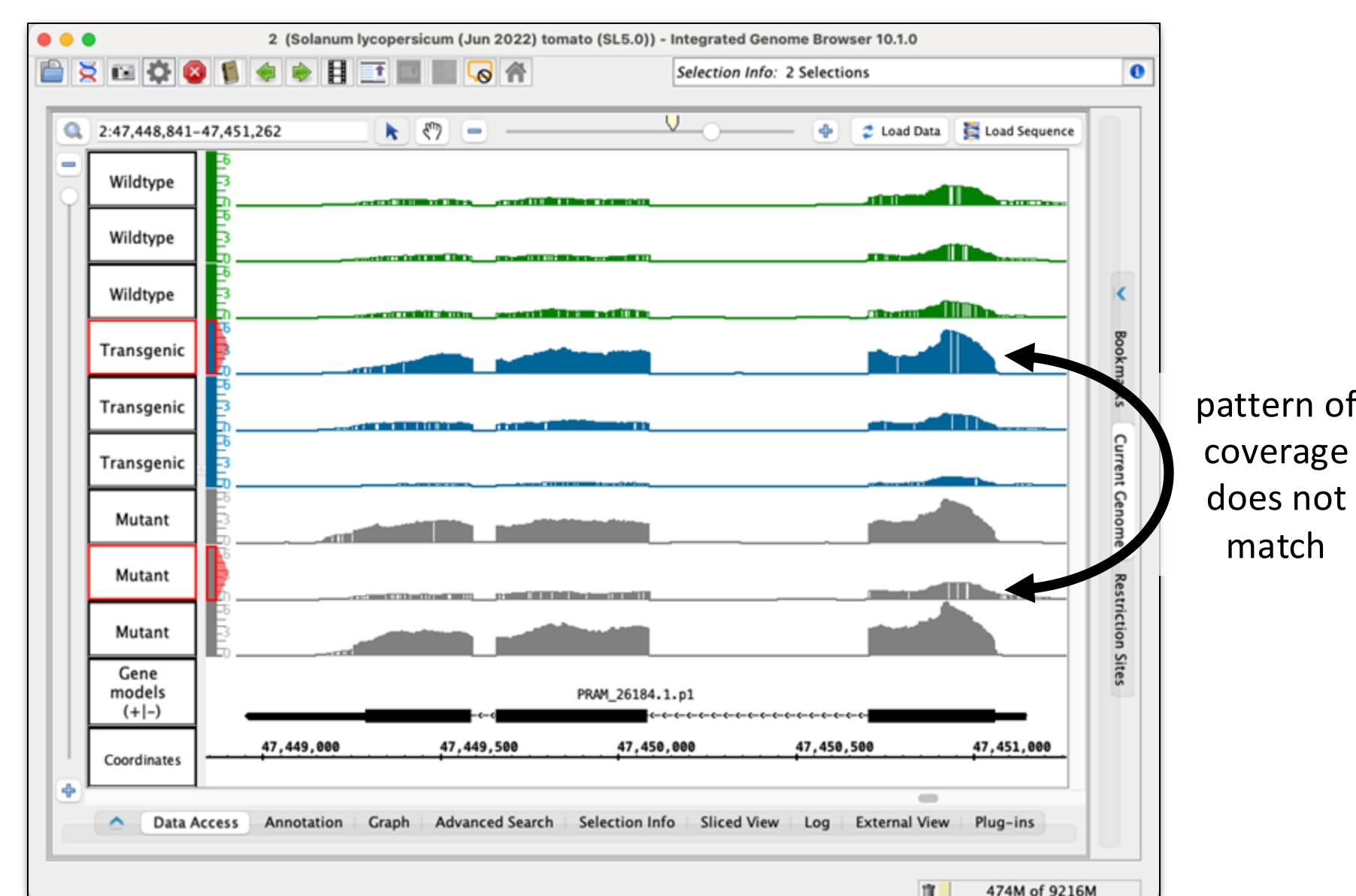
Single-cell RNA-Seq (scRNA-Seq) detects and quantifies RNA in individual cells. IGB can display these RNA sequences and color them by their SAMtag cell or molecular barcode. The image below shows IGB's "Color by" feature highlighting reads from a single cell in **red** that supports an exon skipping event, while the other cell's reads support the inclusion of the exon.



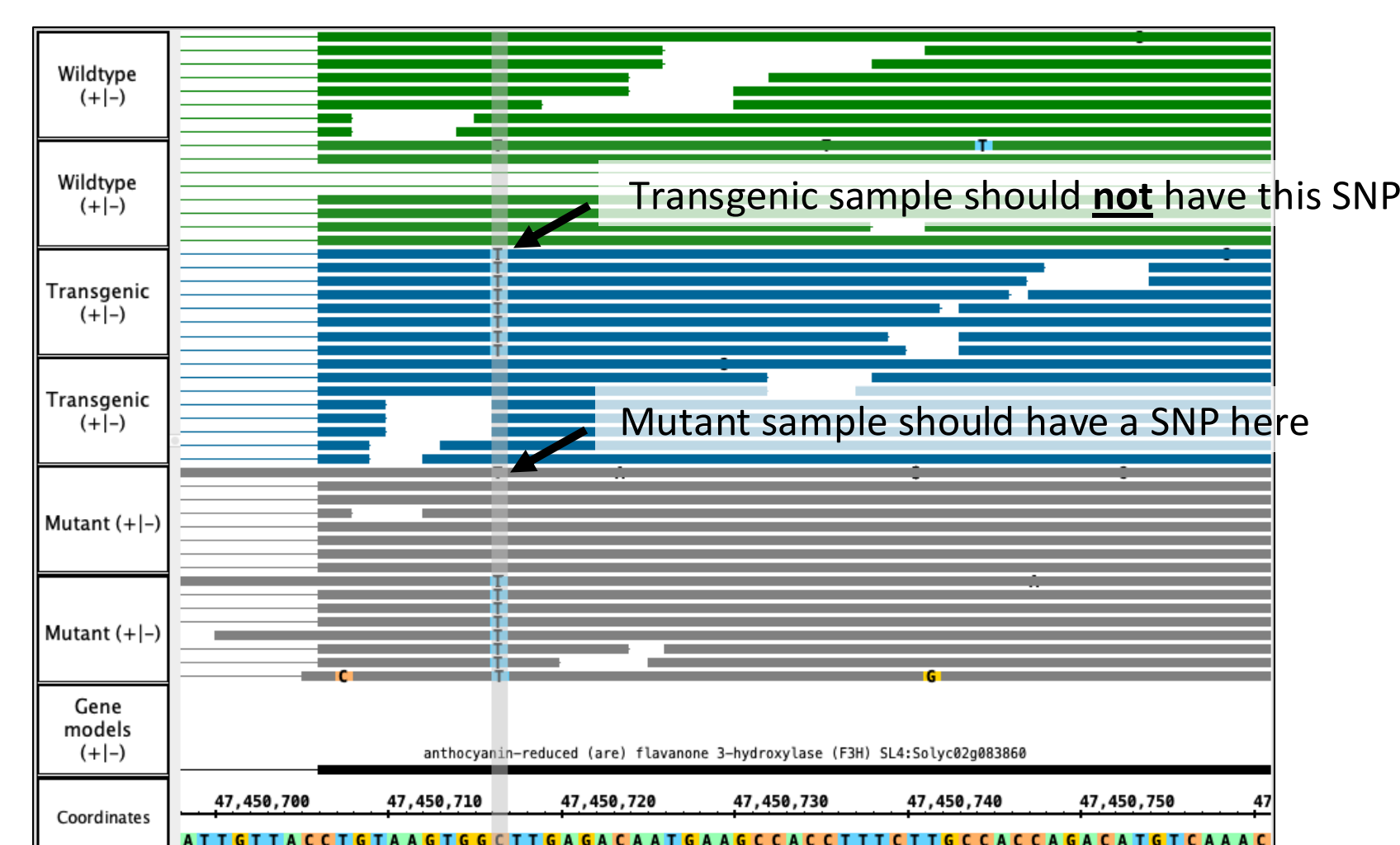
Download IGB at [BioViz.org](https://www.bioviz.org)

Sample Switching

Sample switching can occur in a variety of places, whether that's in the lab or at the sequencing facility. Visualizing the data in IGB is one way to catch sample switching before data are used in downstream analyses. The image below shows coverage graphs in IGB where the pattern appears switched for two samples.

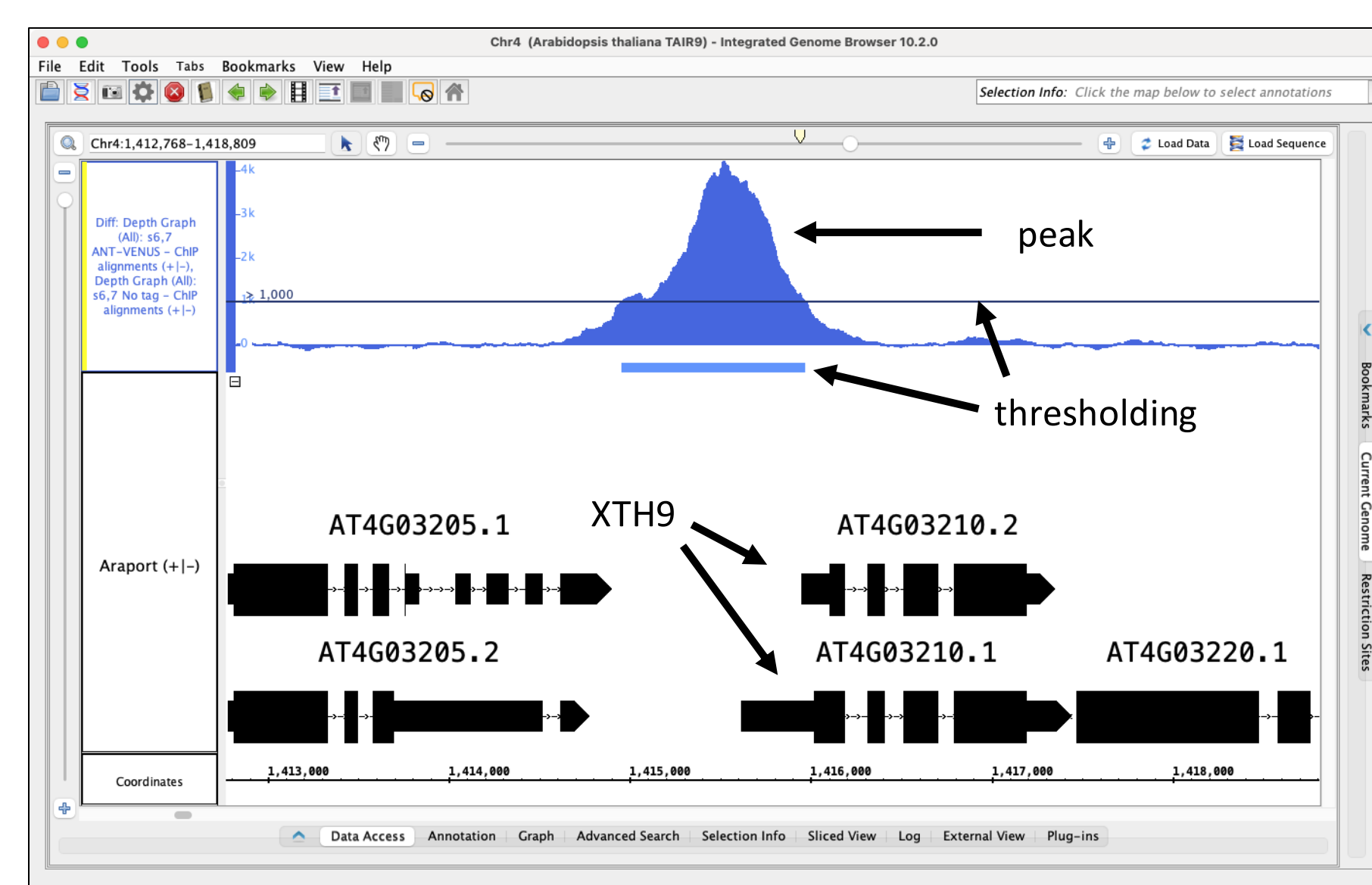


The tomato *anthocyanin reduced* (*are*) mutant has a mutation in the *F3H* gene that is not present in wildtype or transgenic lines. In the image below, the mutation is present in a transgenic sample and absent from a mutant sample, further supporting sample switching.



ChIP-Seq

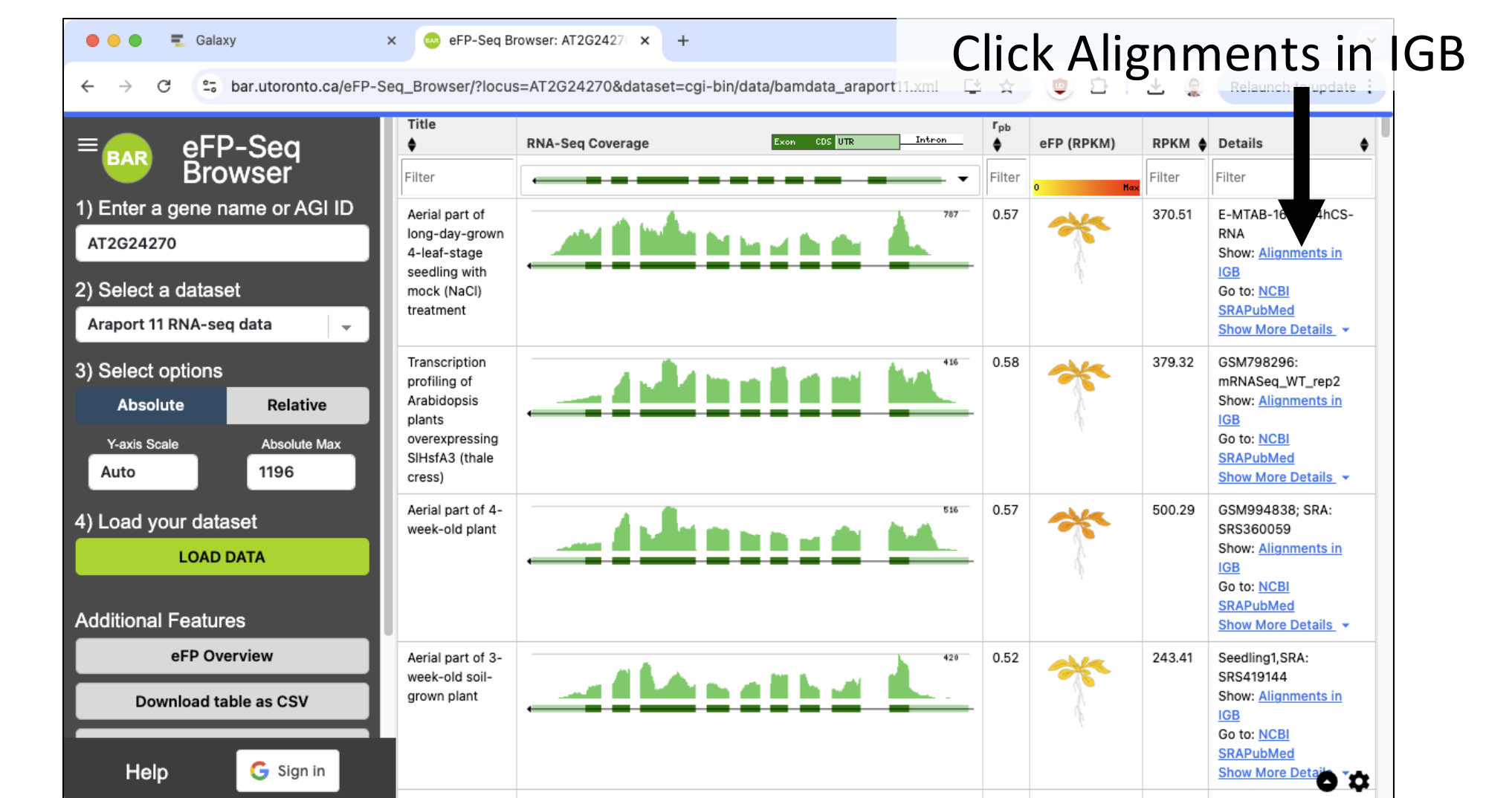
ChIP-Seq can locate transcription factor binding sites in DNA. Peaks appear as regions where many ChIP-Seq reads align. Below, IGB shows ANT binding upstream of the gene *XTH9*. A difference coverage graph was generated in IGB by subtracting coverage graphs of the untagged sample from the tagged sample. IGB's thresholding feature was then used to highlight peaks.



Pull data from diverse sources

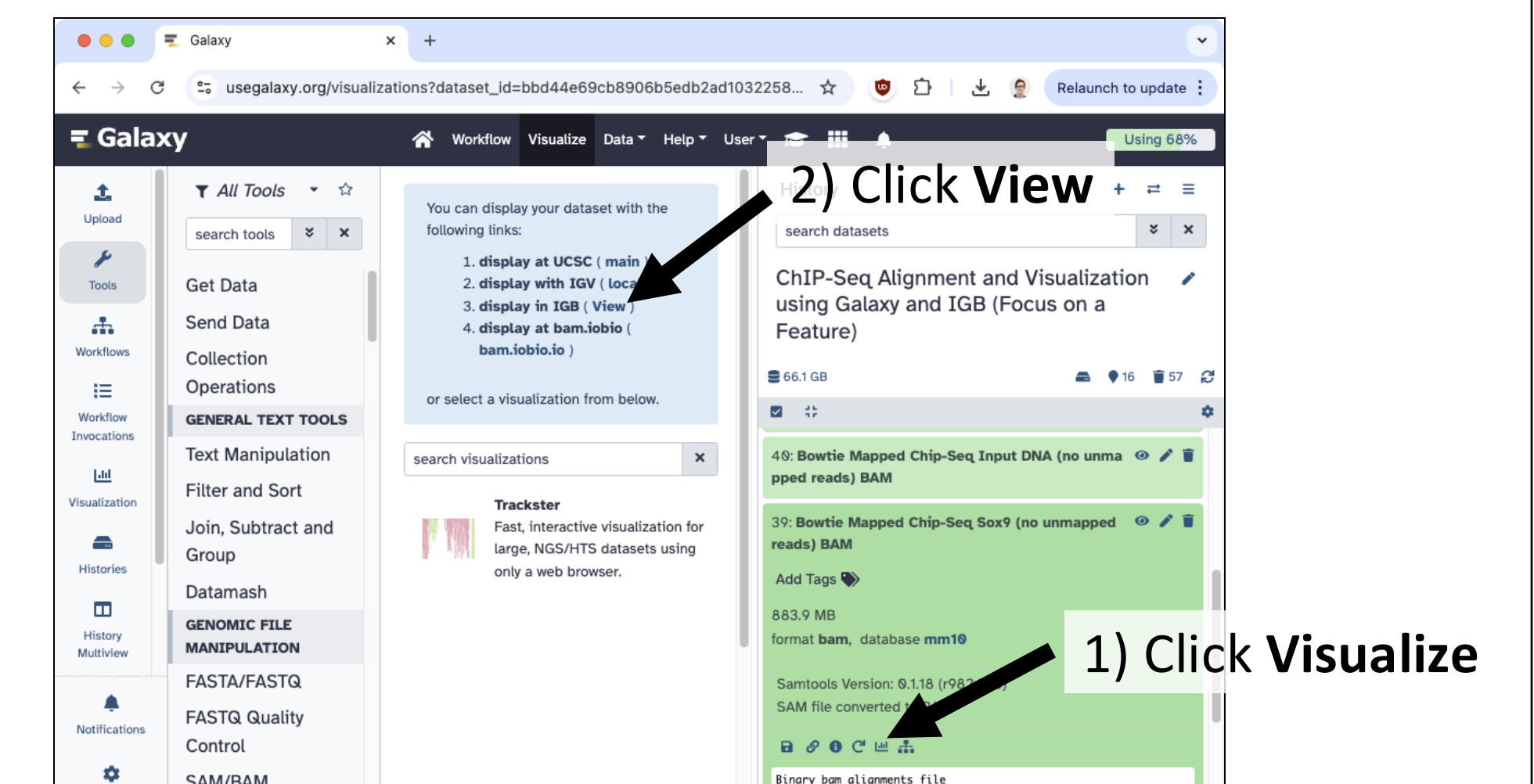
eFP-Seq Browser

The **eFP-Seq Browser** allows you to explore RNA-seq-based gene expression levels for your gene of interest in expression datasets. Data from the eFP-Seq browser can be viewed in IGB by clicking on [Alignments in IGB](#).



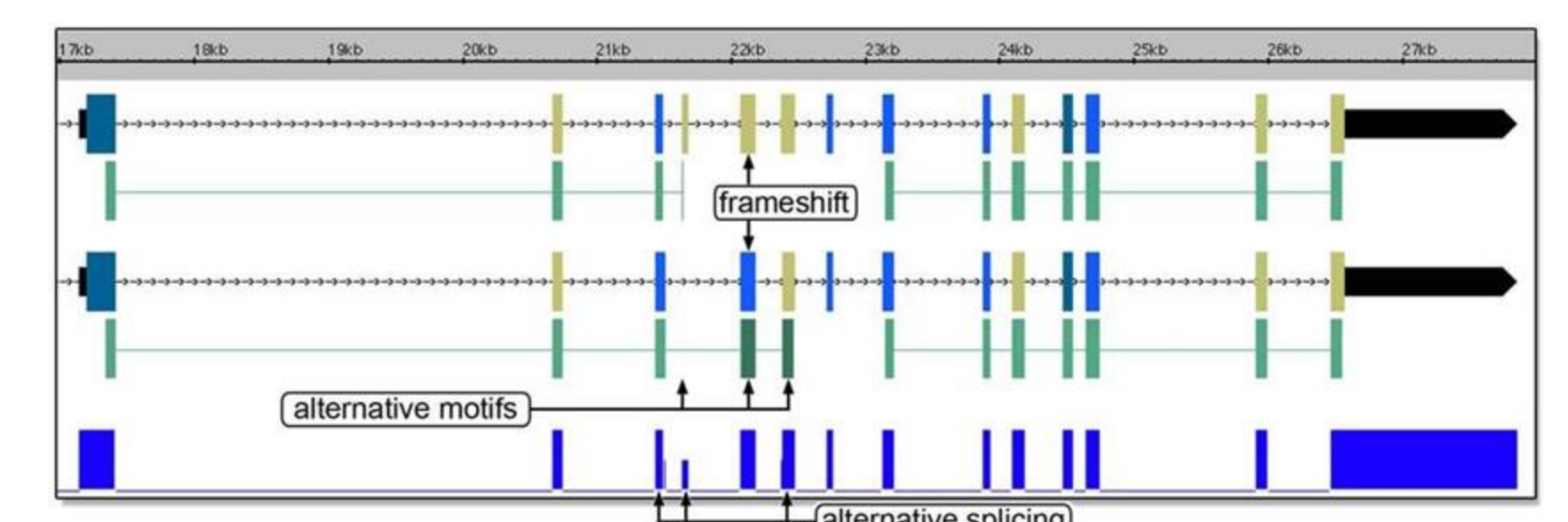
Galaxy PROJECT

Galaxy is an open-source, web-based platform for data intensive biomedical research. Data stored in Galaxy, such as BAM files, can be viewed in IGB by clicking on the **Visualize** button and then clicking **View** next to **display in IGB**.



InterPro

ProtAnnot is an **IGB App** that shows protein annotations in the context of genomic sequence. ProtAnnot searches **InterPro** and displays profile matches (protein annotations) alongside gene models, exposing how alternative promoters, splicing and 3' end processing add, remove, or remodel functional motifs.



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