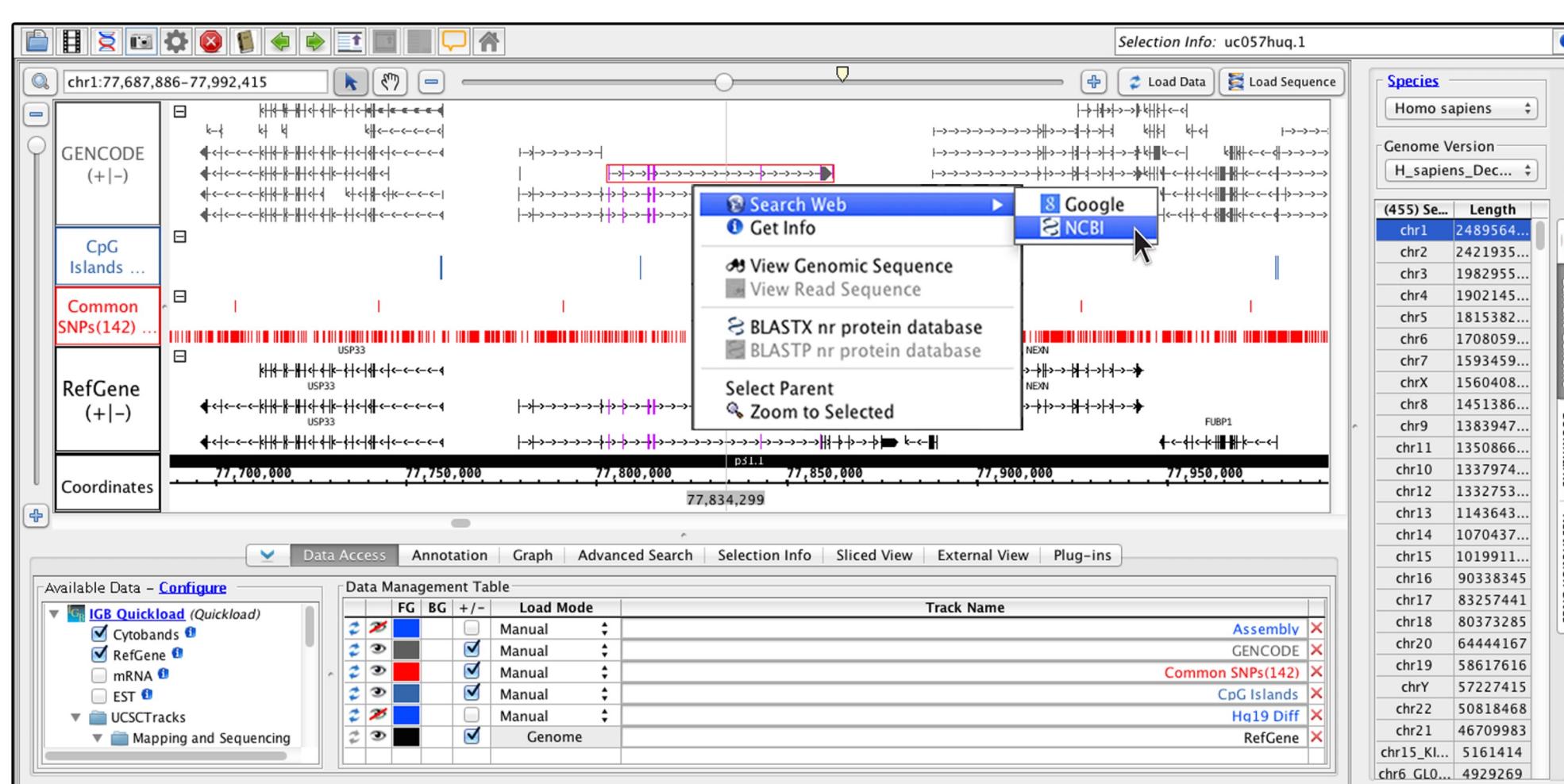


Paige Kulzer, Nowlan Freese, Karthik Raveendran, Gopu Kaushik, Jaya Sravani Sirigineedi, and Ann Loraine

Visualize biologically-interesting patterns in genomic data

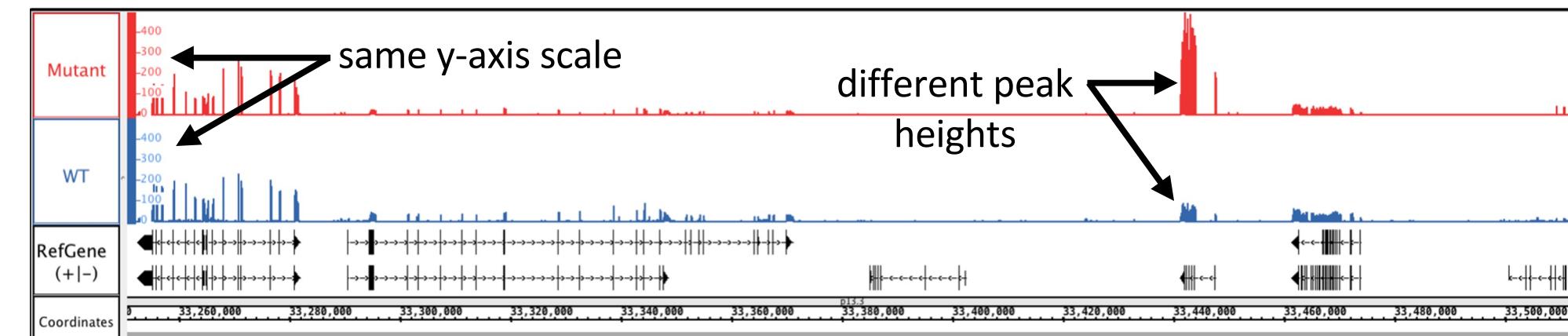
We develop and maintain Integrated Genome Browser (IGB), a highly configurable, interactive and fast open-source desktop genome browser.



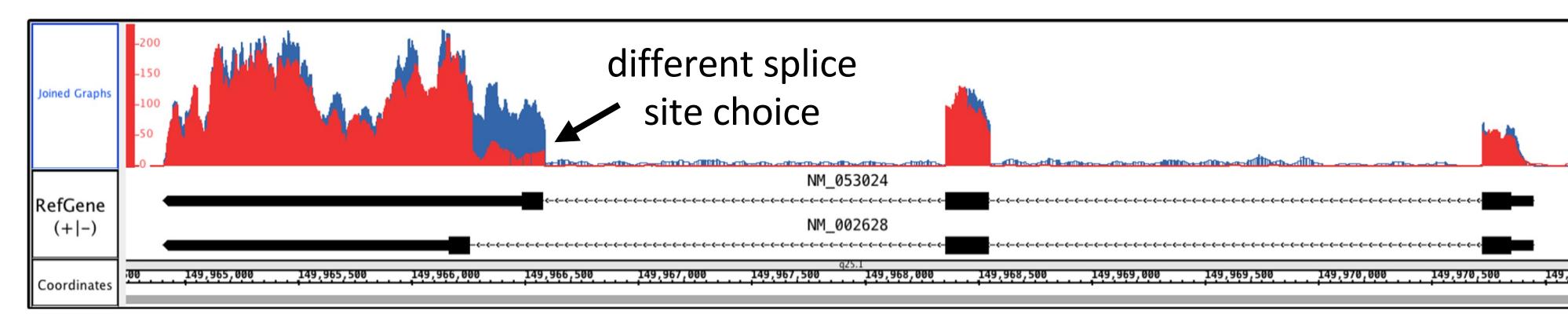
Interactively analyze a wide variety of data types

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. The image below shows depth graphs from samples bearing wild-type or mutant copies of the KRAS oncogene. One peak is taller in the mutant sample, indicating higher expression.

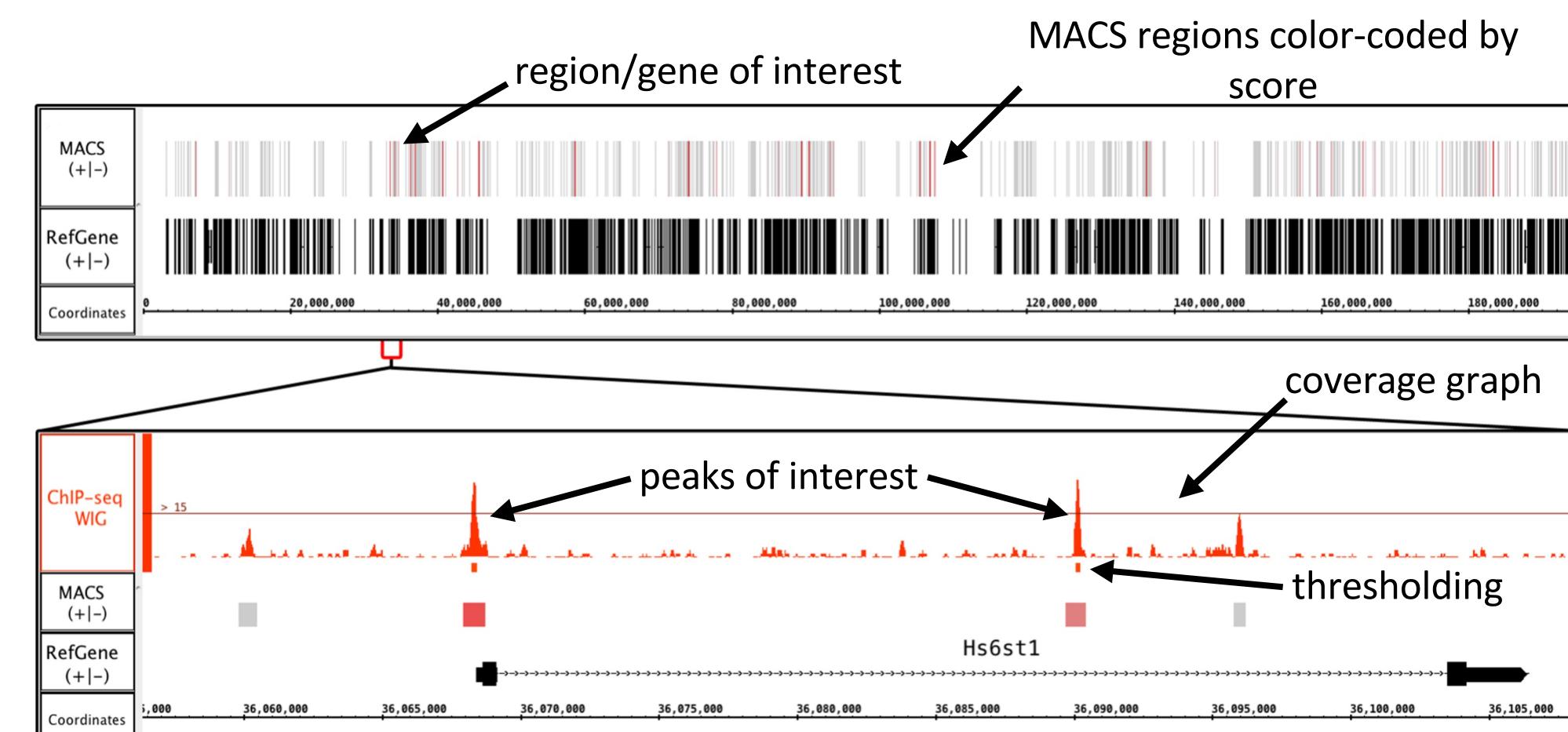


Visual analysis of RNA-seq data can also highlight alternative splicing differences. PFN2 produces two isoforms due to alternative splicing. Comparing the peak discontinuities to the gene models shows that the mutant sample favors the shorter isoform.



ChIP-Seq

Whole-genome ChIP-Seq can locate transcription factor binding sites in DNA as regions where many ChIP-Seq reads align, forming peaks. ChIP-Seq analysis tools (like MACS) produce BED files with peak locations and significance scores. IGB's "Color by score" feature makes it easy to zoom in on high scoring peaks. IGB's thresholding feature can highlight high-scoring windows in coverage graphs. Here, IGB shows SOX9 binding near Hs6st1, one of its regulatory targets.



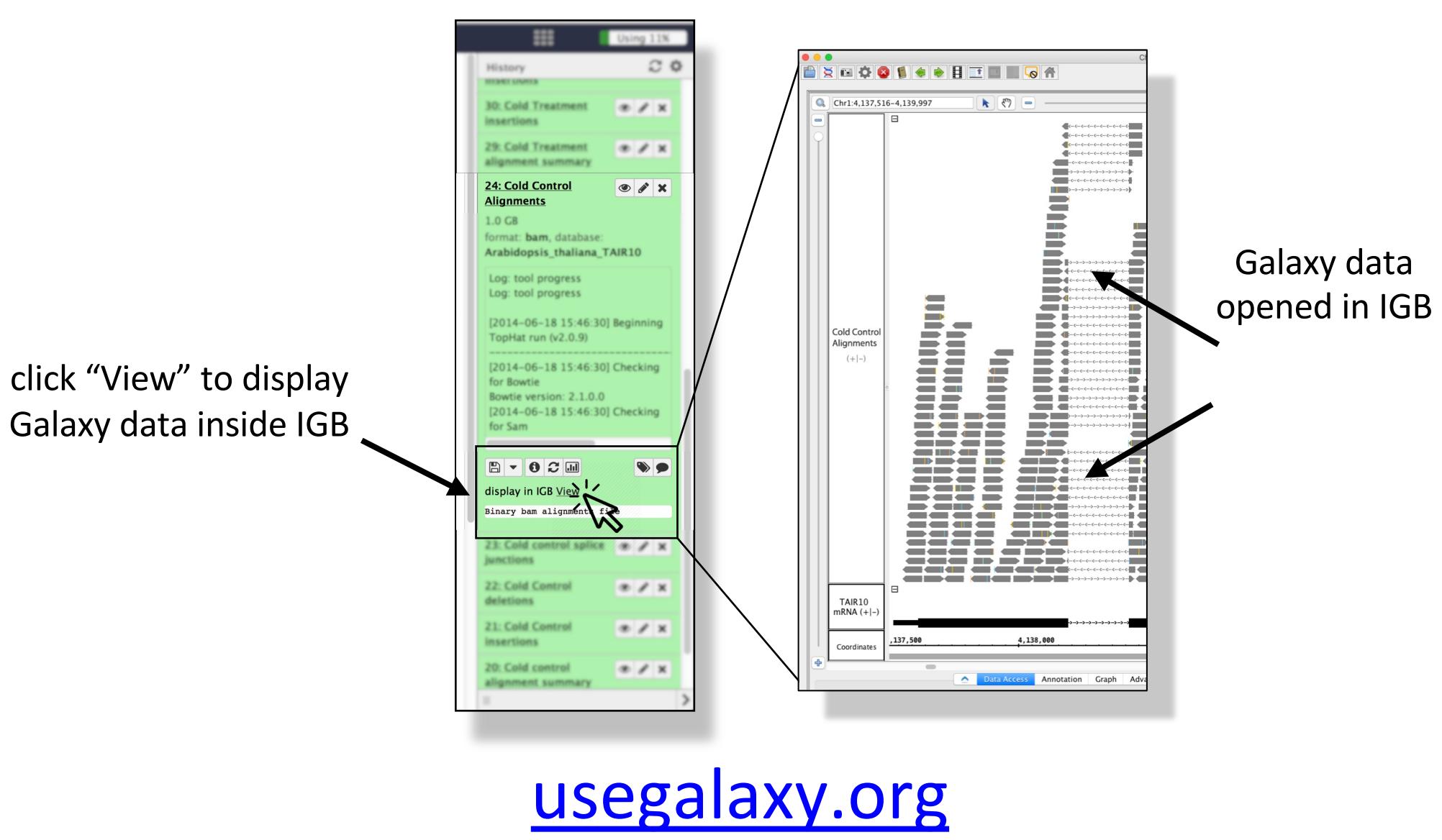
Open source software with support for Linux/Mac/Windows

[Download IGB at BioViz.org](http://BioViz.org)

Pull data from diverse sources



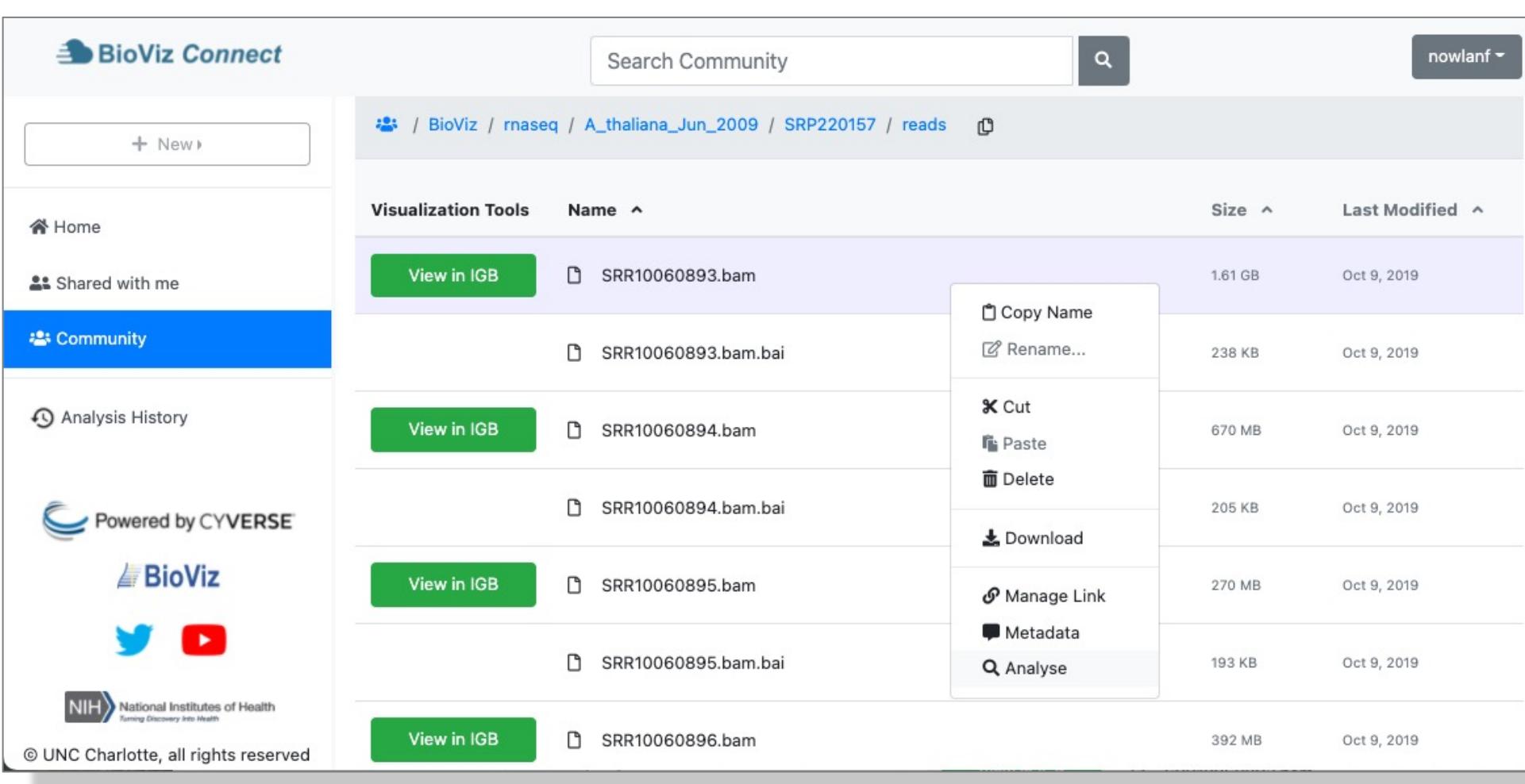
Galaxy is an open source, web-based platform for data intensive biomedical research.



usegalaxy.org

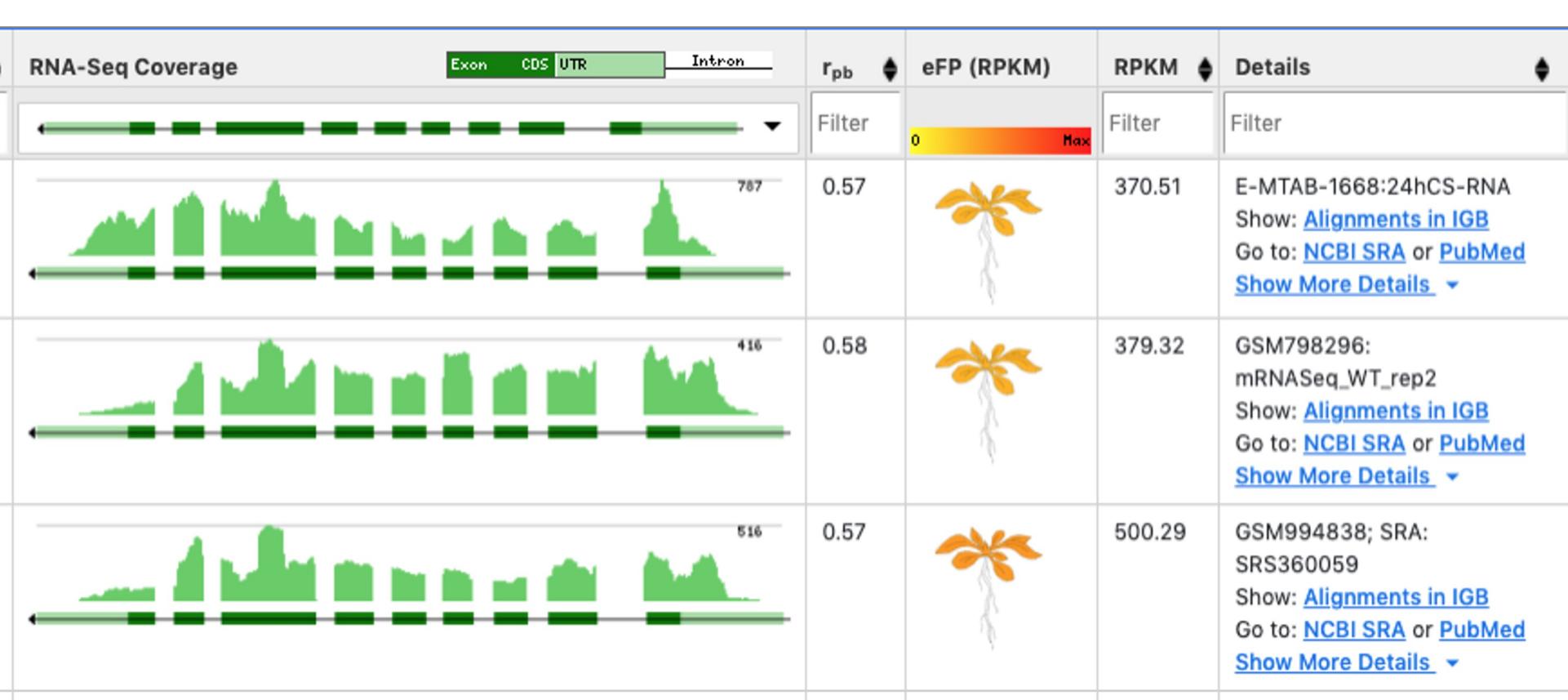
BioViz Connect

Use BioViz Connect to stream CyVerse data to IGB for visualization, add IGB specific metadata such as genome version and track appearance to data, and run visual analytics functions in the cloud to create new visualizations for IGB.



BAR 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.

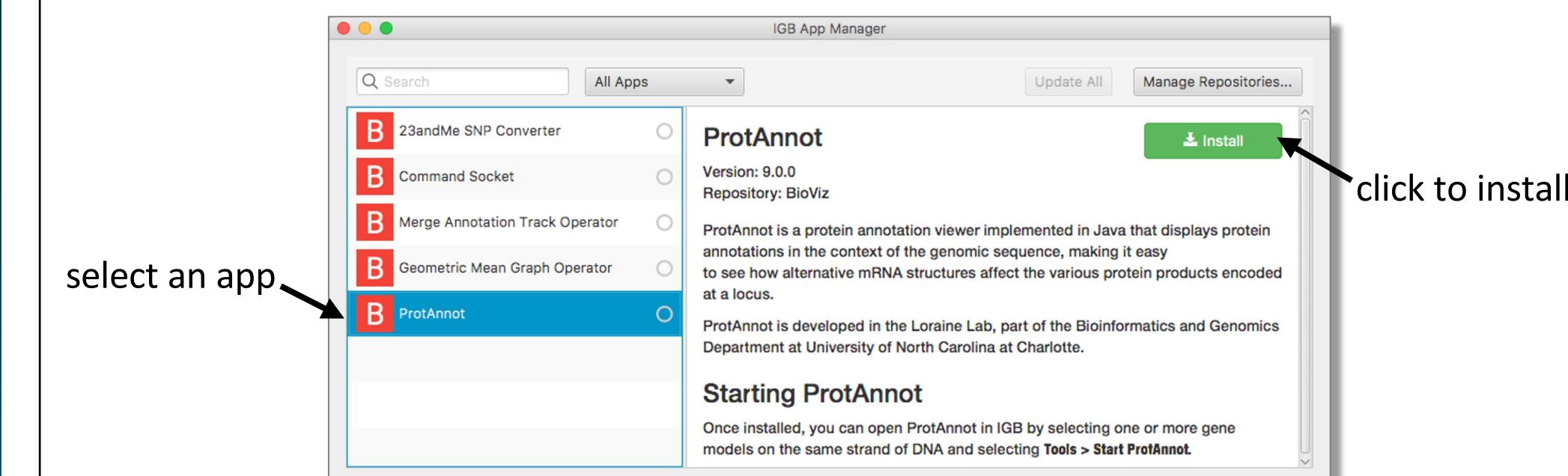


bar.utoronto.ca/efp-seq_browser

Add new functionality via plug-ins

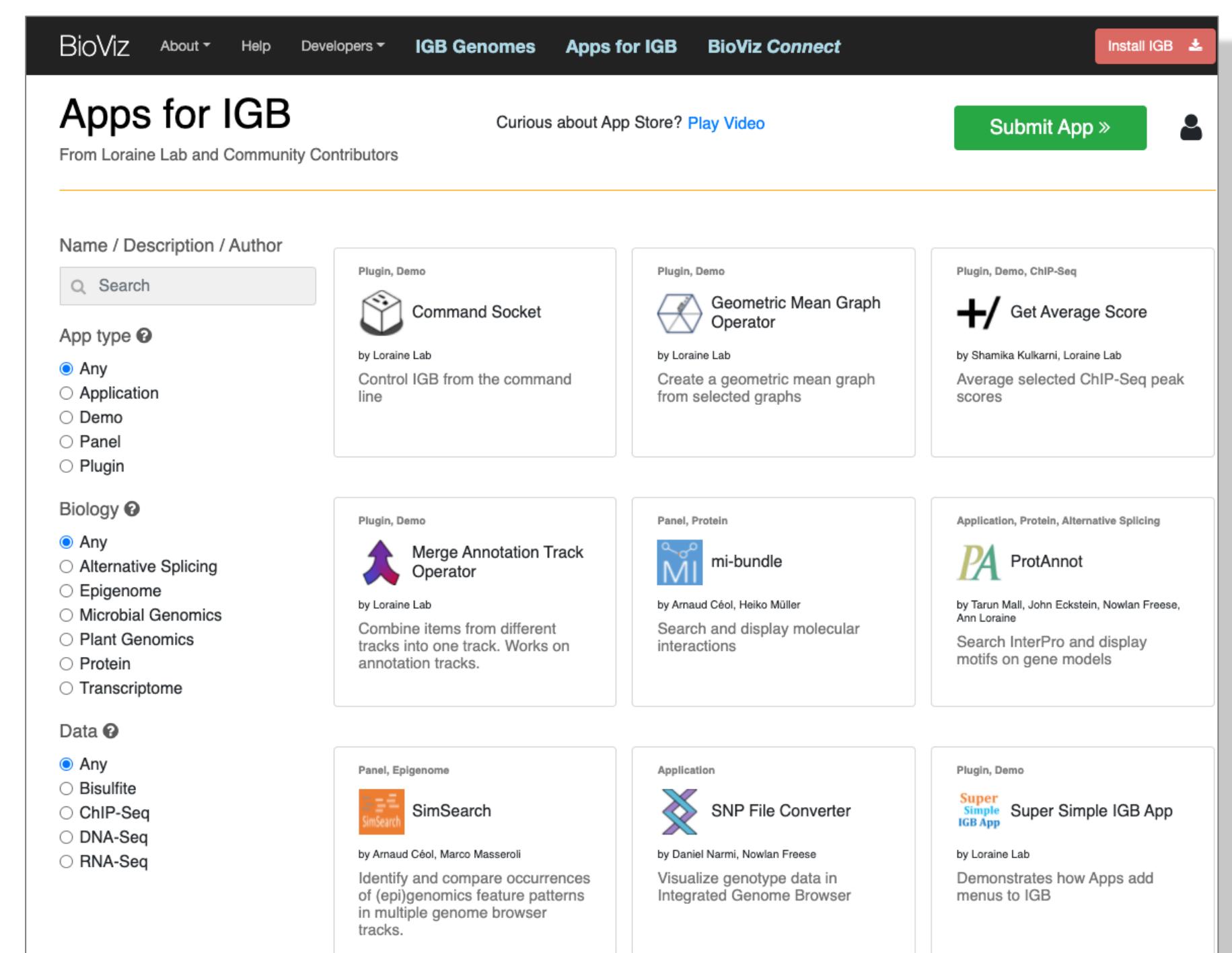
IGB Apps

For developers to easily add new visualizations of genomic data we transformed IGB into an extensible platform. The IGB architecture now supports adding new functionality via plug-ins. This new Apps API empowers community developers to contribute new functionality without needing a deep understanding of IGB systems.



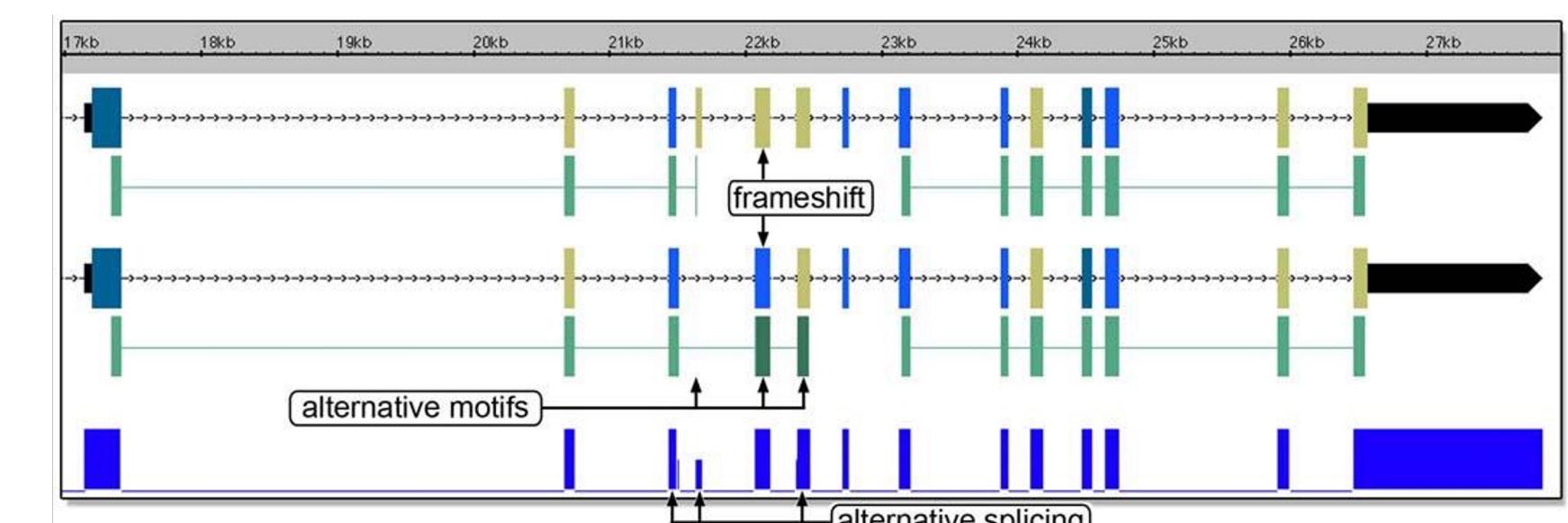
IGB App Store

Find and install apps to expand the functionality of IGB, or create your own app and upload it to the app store.



ProtAnnot App

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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