



UNC CHARLOTTE
College of Computing and Informatics

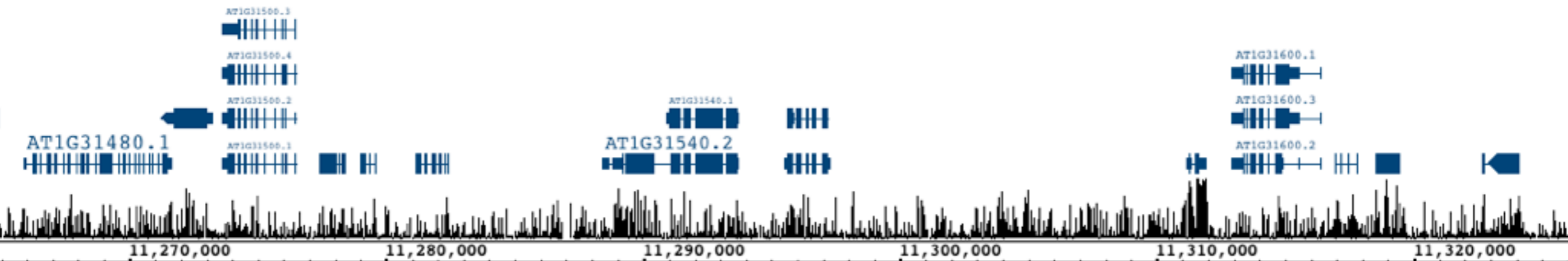
Integrated Genome Browser

Analyze, Visualize, Share

Fast

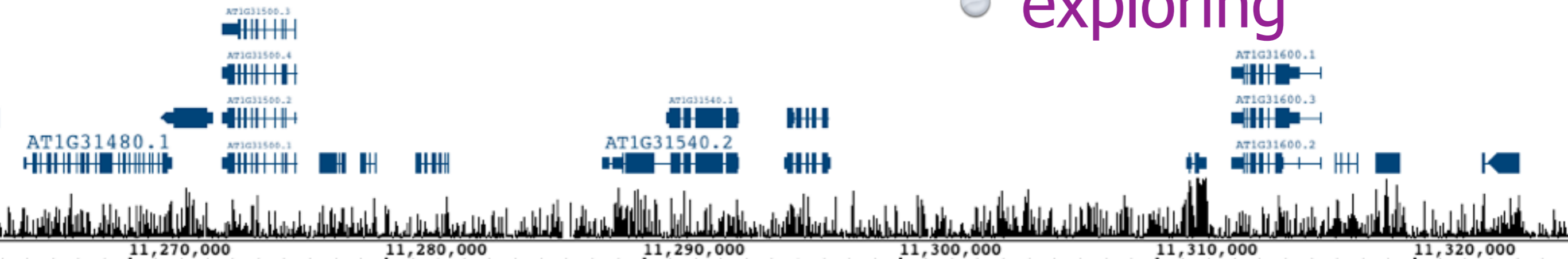
Flexible

Free

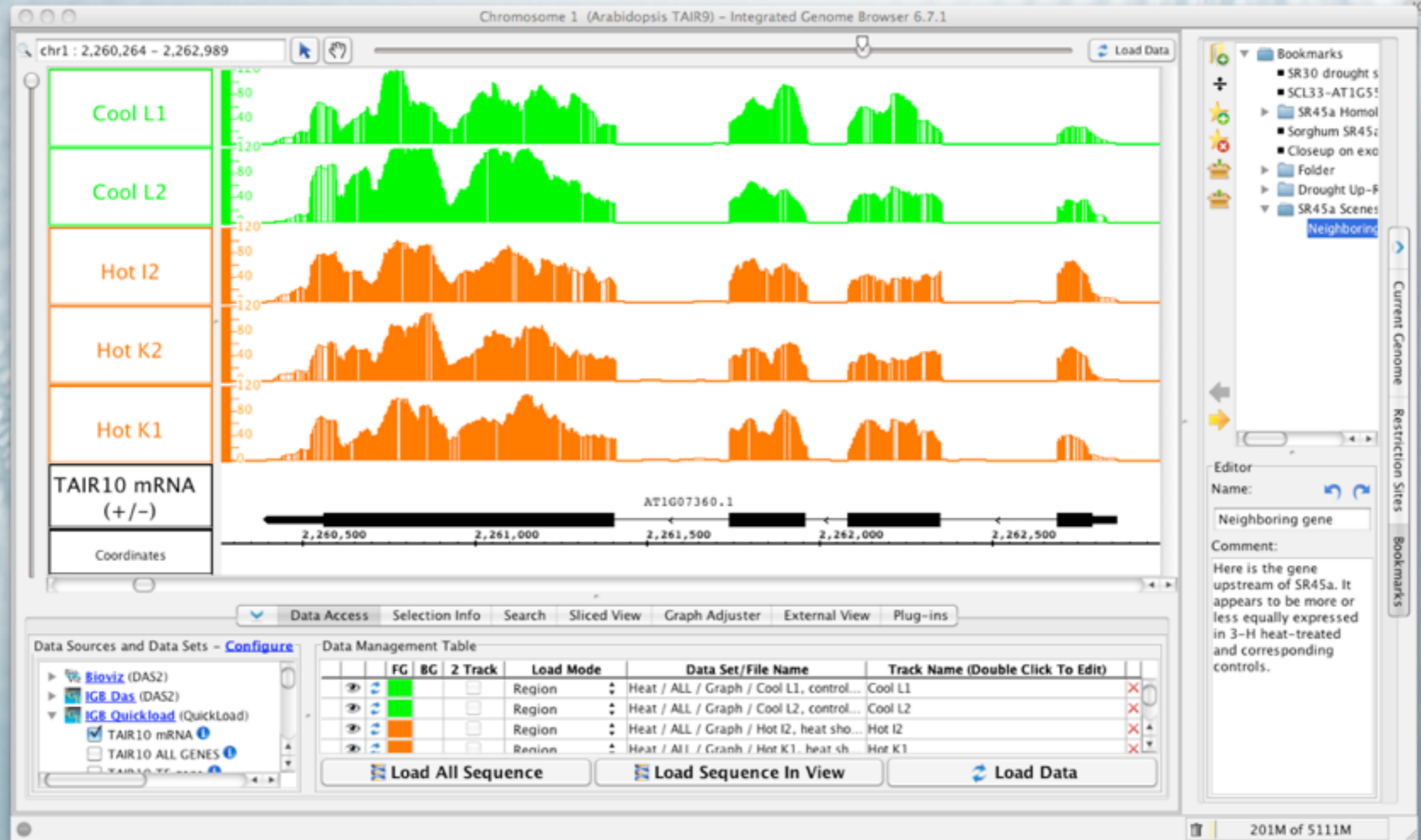


Goals

- Stimulate insight, creativity
- Support all aspects of scientific process
 - taking notes
 - making images
 - publishing data
 - exploring

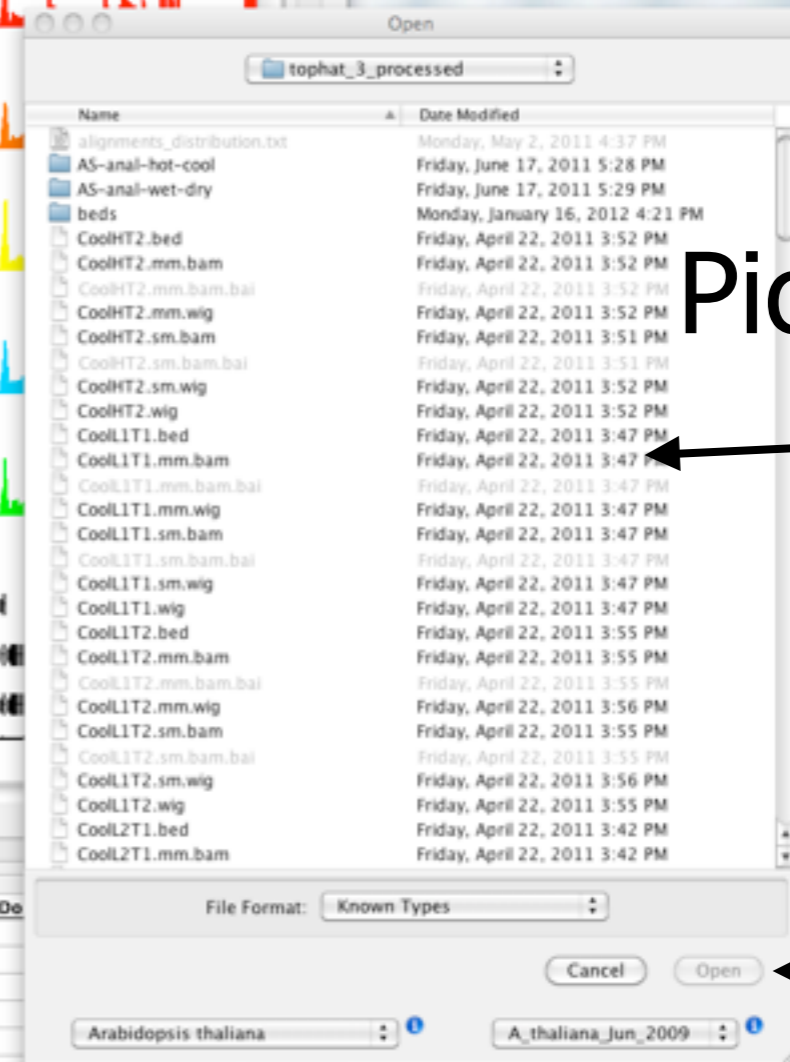


IGB is a Java desktop application

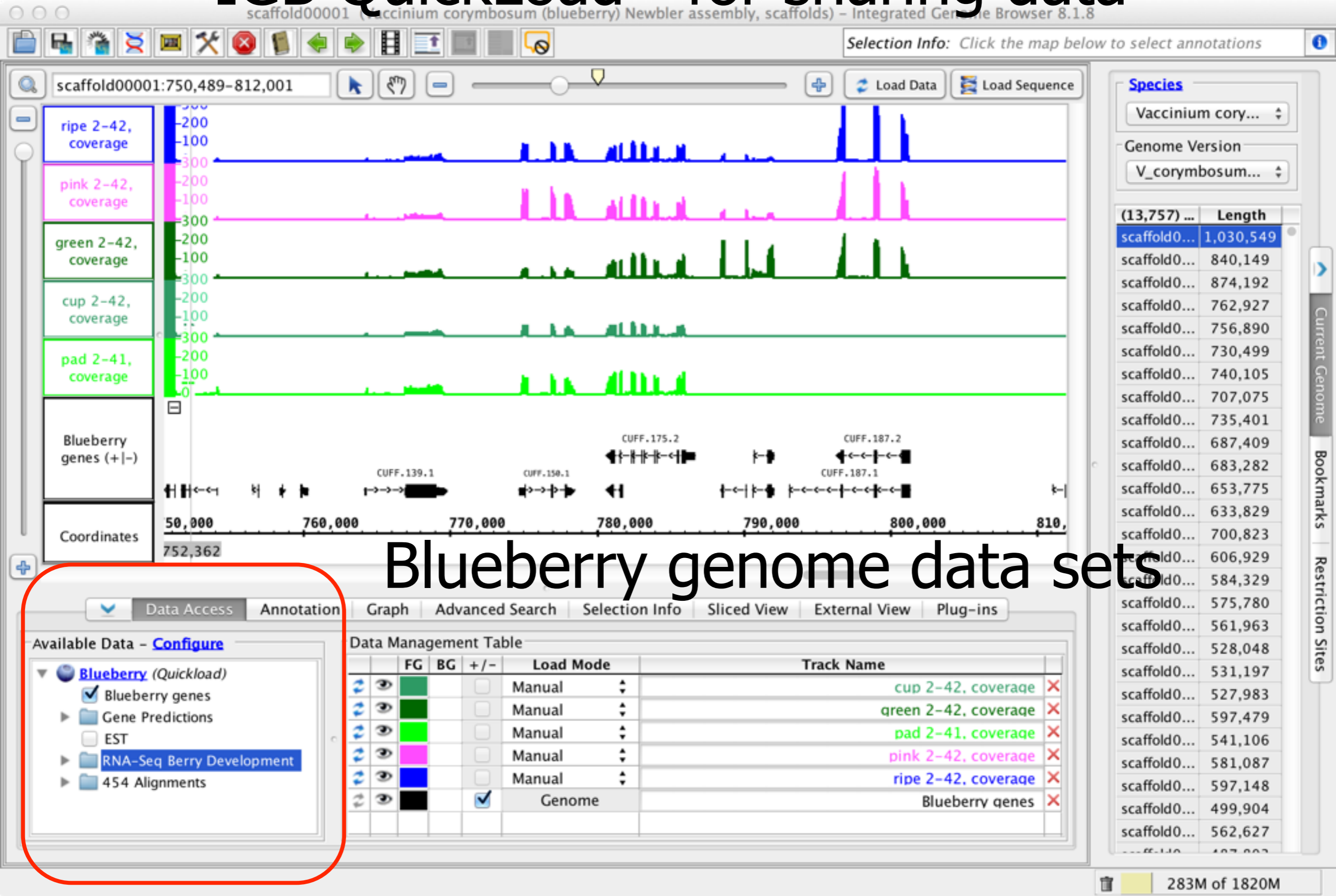


Download & run locally

Benefits: Simple. Install it. Open files.



IGB QuickLoad - for sharing data

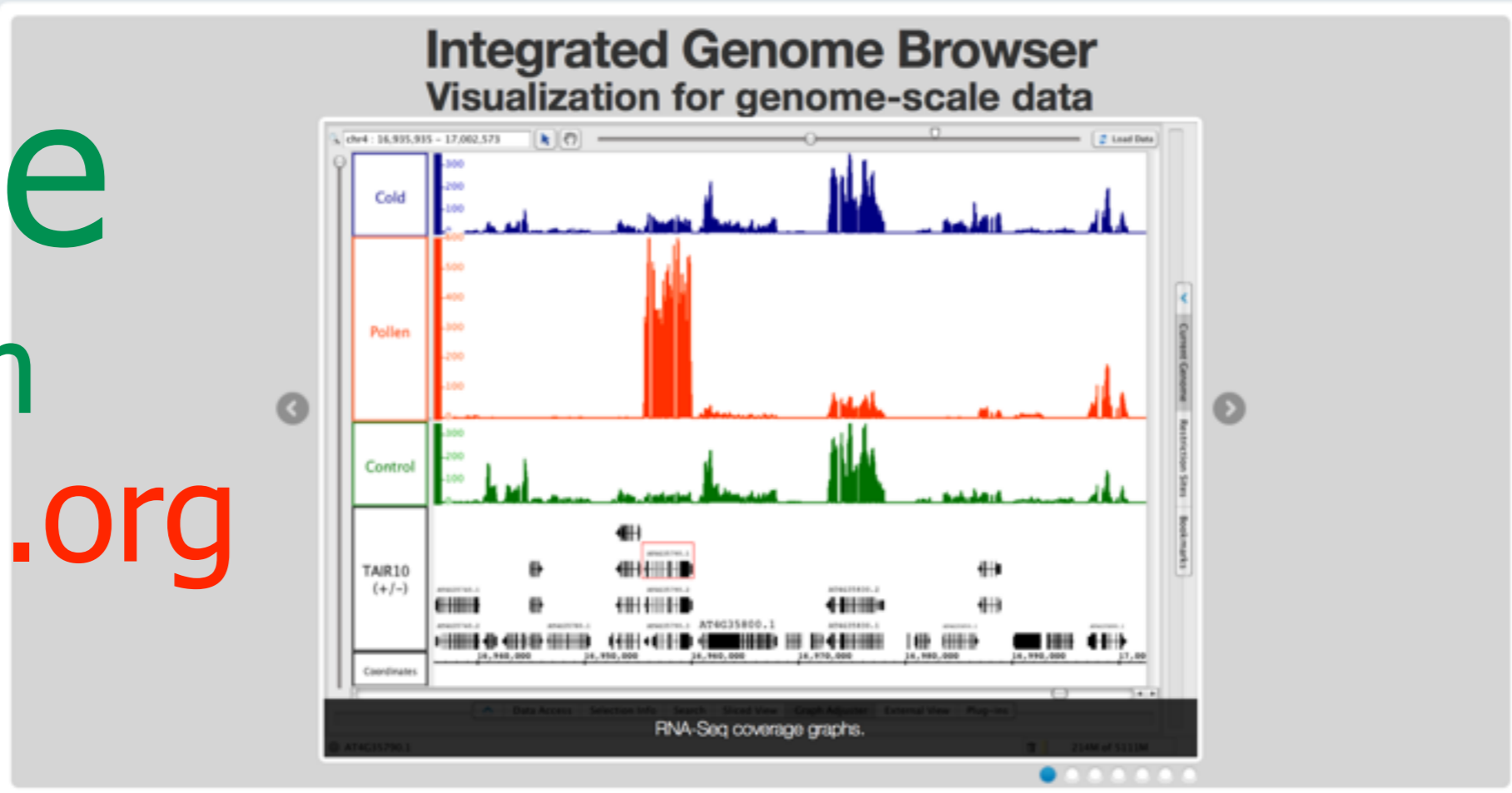


Blueberry genome data sets

Available Data - [Configure](#)

- Blueberry (Quickload)
 - Blueberry genes
 - Gene Predictions
 - EST
 - RNA-Seq Berry Development
 - 454 Alignments

Free
from
BioViz.org



What is IGB?

Integrated Genome Browser is an easy-to-use, highly customizable genome browser you can use to view and explore genomic data and annotations, especially RNA-Seq and CHIP-Seq data sets.

[Learn More »](#)

[Follow](#) [YouTube](#)

Where can I get IGB?

IGB is free and runs on Windows, Mac, and Unix computers. Visit the IGB [download page](#) to install and run IGB. The source code is hosted in a [git repository at BitBucket](#).

[Visit BioViz Download Page »](#)

Questions?

To get help, post questions to the [GenoViz Help Forum](#). Also try searching the [IGB User's Guide](#). For help with advanced features and programming IGB, visit the [IGB Developer's Guide](#).

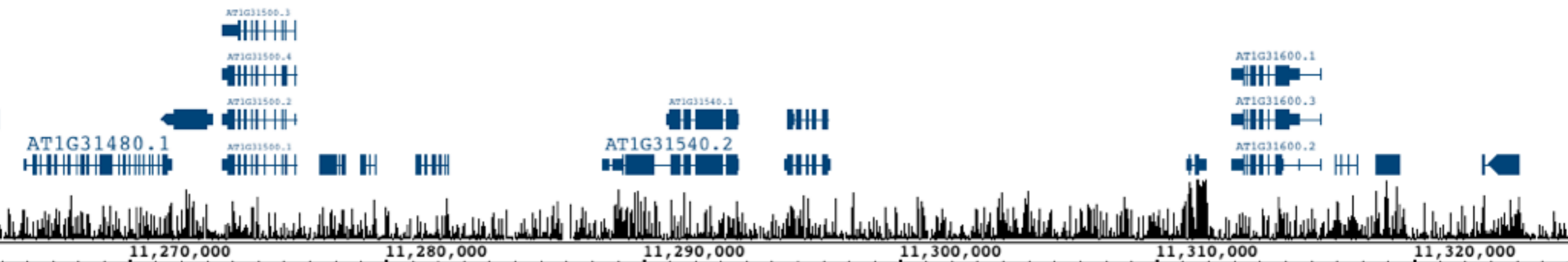
[Visit IGB User's Guide »](#)

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Genoviz is a [sourceforge](#) project

- git repository hosted on bitbucket
- public issue tracking at jira.transvar.org

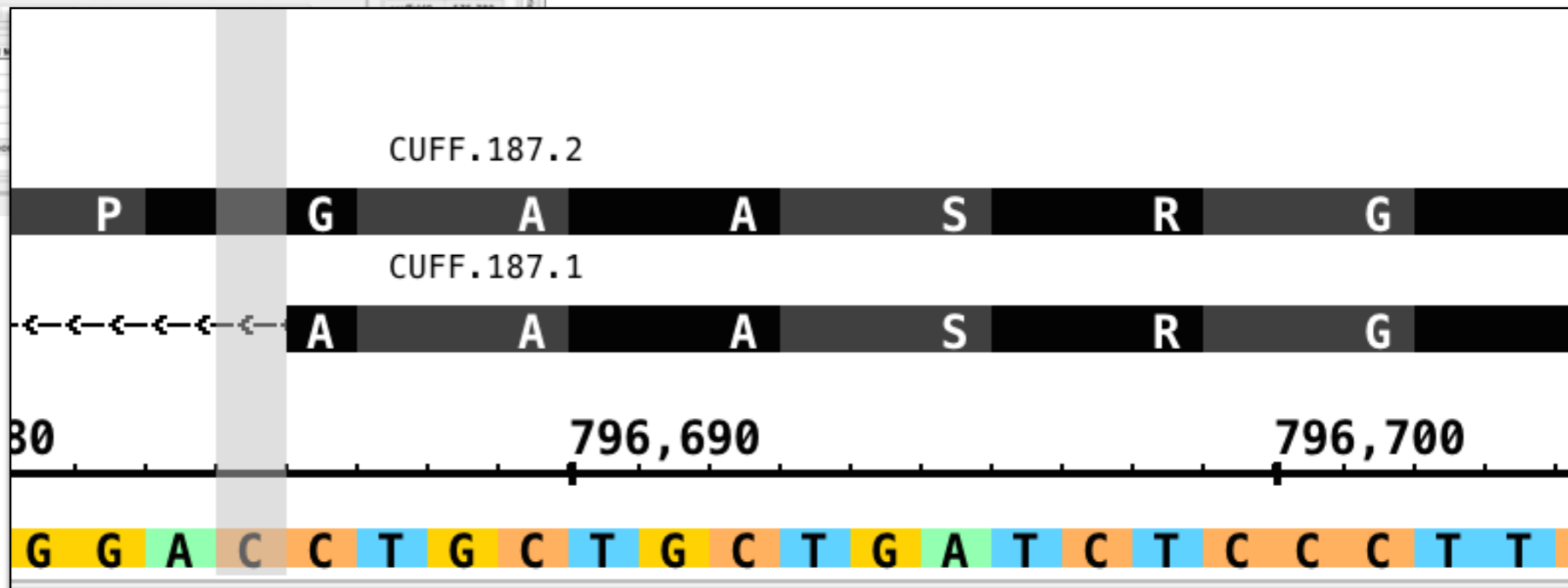
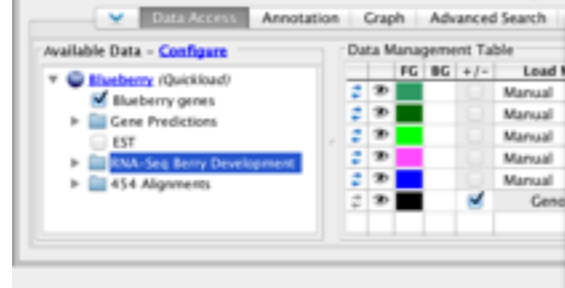
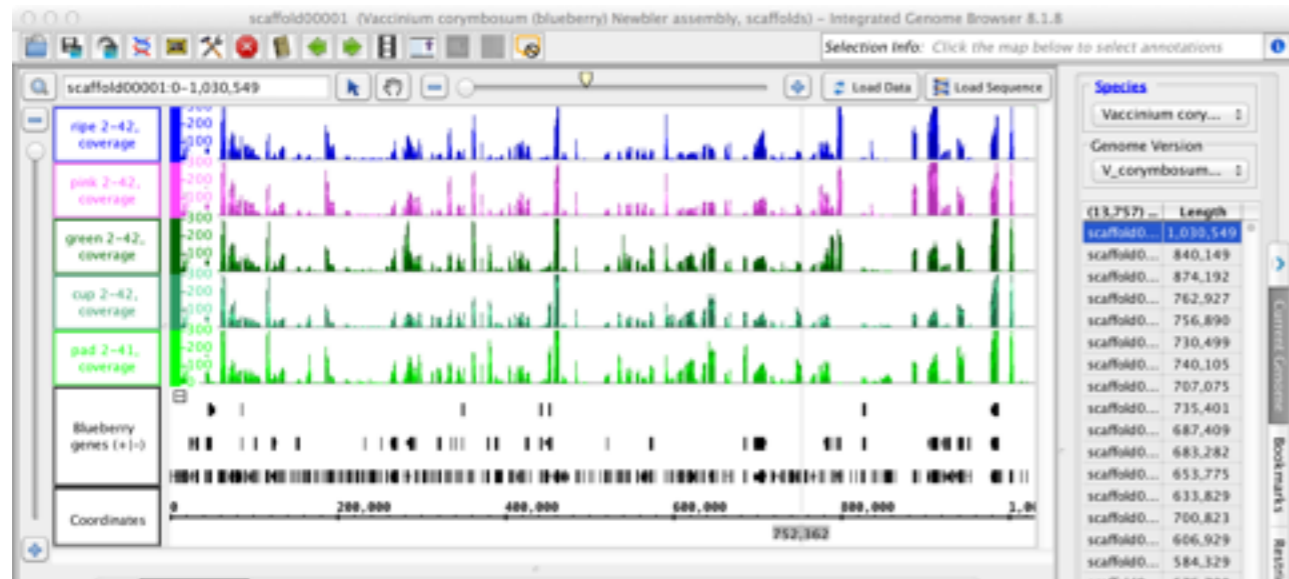
What makes IGB unique?

- fast, fluid animated zooming
- highly interactive
- dozens of features, alternative views, analytical functions, and more

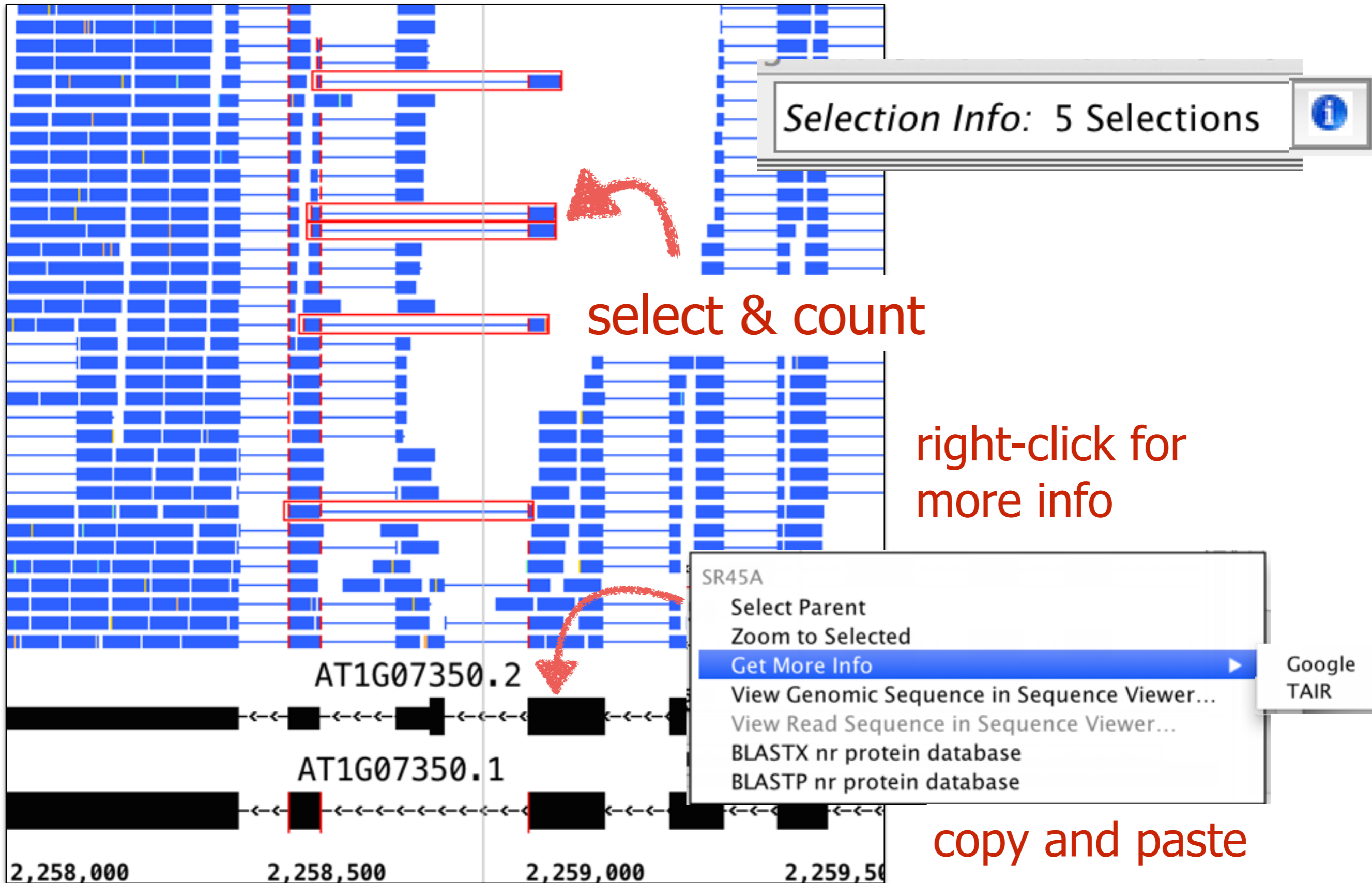


Fast, fluid animated zooming

- zoom stripe focuses zooming



You interact with data



Selection Info: 5 Selections

select & count

right-click for more info

copy and paste sequence

Google
TAIR

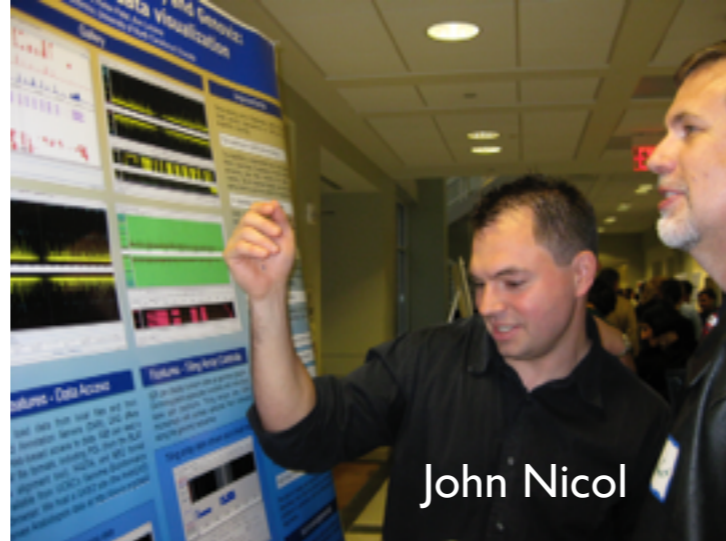
Many features, many contributors: 2002 - 2014



Gregg Helt



Ed Erwin



John Nicol



Stephen
Blanchard



Hiral Vora



Archana Raja



Richard
Linchango



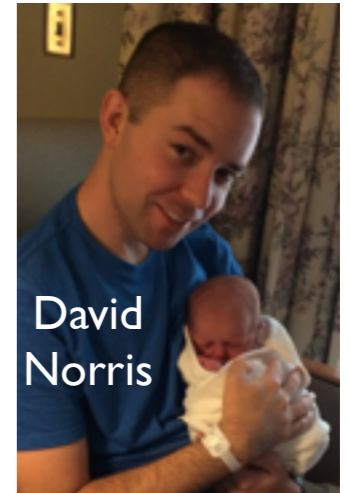
Vikram
Bishnoi



David Nix



Nick Ren



David
Norris



Neomorphic
Software



Alyssa
Gulledge



Ehsan Tabari



Ivory
Blakley



Mason
Meyer

Michael
Lawrence

Lance
Frohman

Katie
Kubiak

Ido
Tamir

Fuquan
Wang

Anuj
Puram

Nate
Watson

Shira
Stav

Max Li

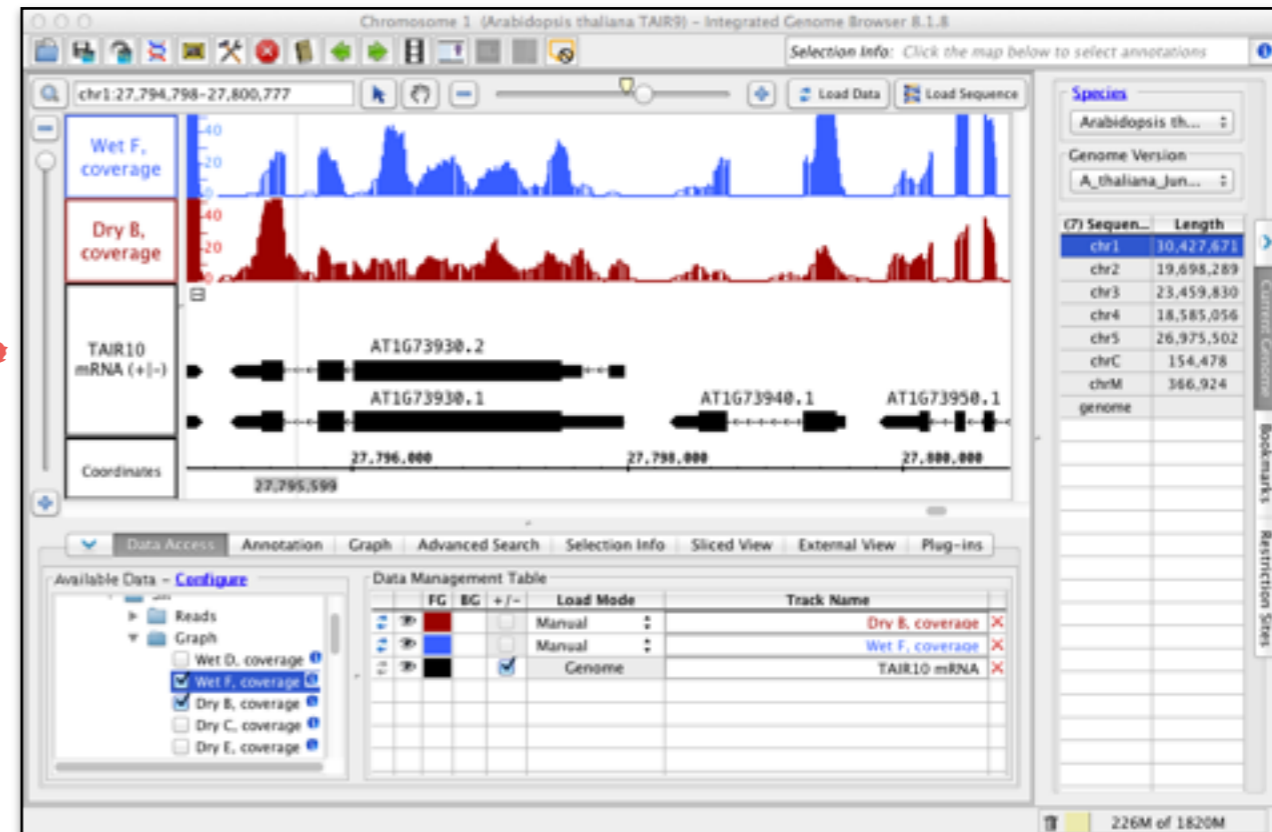
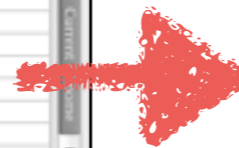
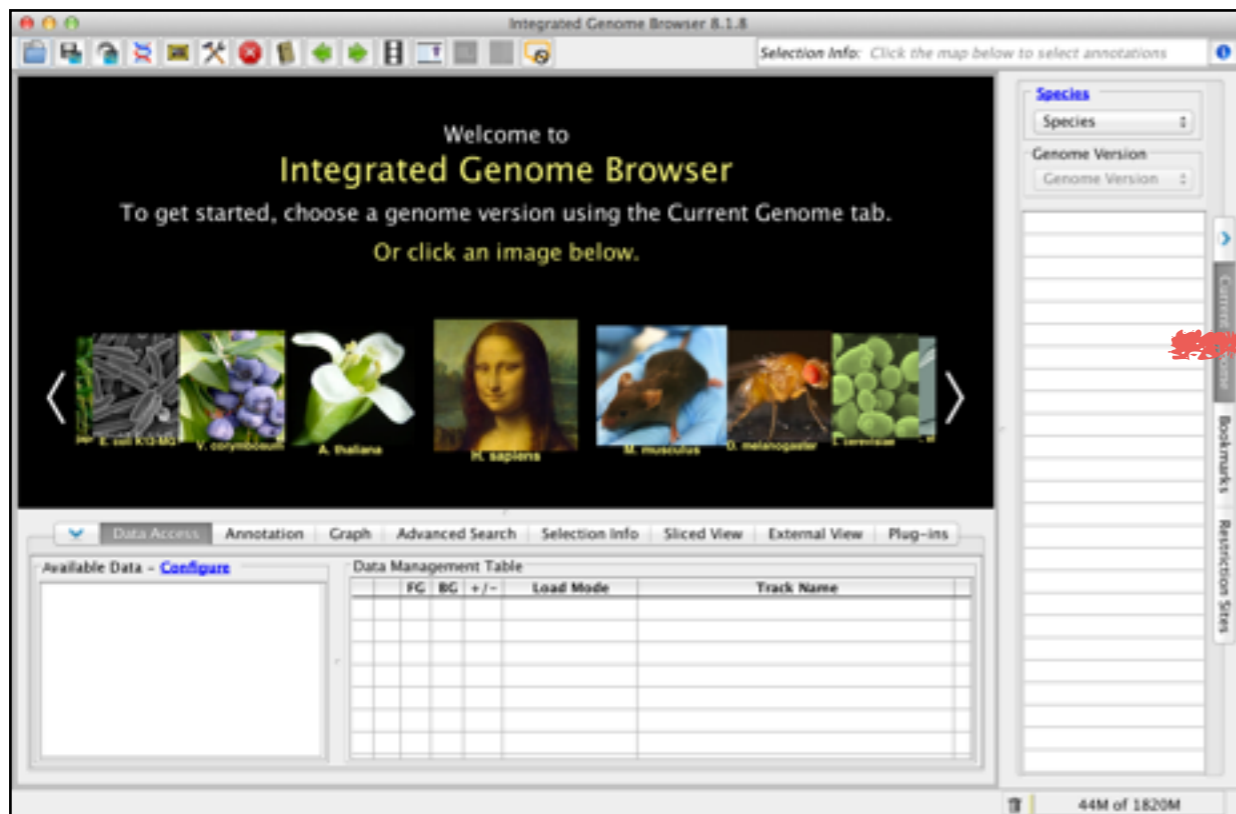
Tarun
Kanaparthi

Kyle
Suttlemyre

IGB ReST-style API

[http://localhost:7085/\[parameters\]](http://localhost:7085/[parameters])

IGB zooms to new location



for
parameters,
google
“IGB links”

Controlling IGB using IGB Links - Dashboard

<https://wiki.transvar.org/.../igbman/Controlling+IGB+using+IGB+Links>

Jan 20, 2013 - Introduction. You can control IGB by embedding IGB links in Web pages. This is useful when you need to manually inspect a large number of ...

Controlling IGB using IGB ...

IGB recognizes commonly-used synonyms for a variety of ...

[More results from transvar.org »](#)

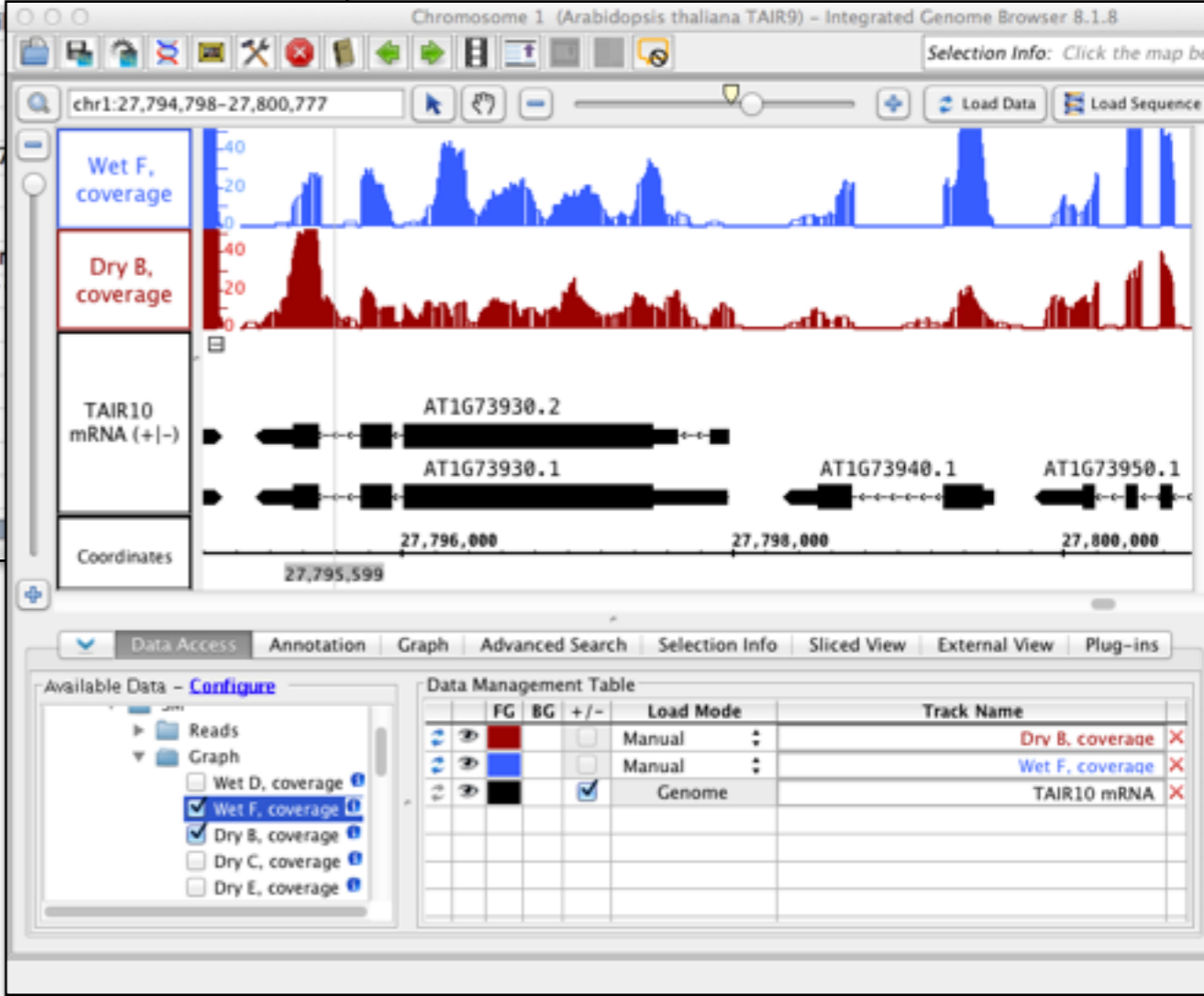
Spreadsheet with IGB links

	A	I	J	K
1	IGB link	fdr	gene	description
2	chr1:-1:27797680:27797863:RI	1.26E-05	AT1G73930	unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown funct
3	chr1:-1:2943226:2943564:AS	2.07E-04	At-SR30	RNA-binding SR protein At-SR30 subfamily SR
4	chr1:-1:182135:182252:RI	1.51E-03	AT1G01490	Heavy metal transport/detoxification superfamily protein
5	chr4:-1:13787373:13788083:RI	1.51E-03	AT4G27610	unknown protein; FUNCTIONS IN: molecular_function unknow
6	chr5:-1:9285615:9285618:AS	1.55E-03	emb1138	DEAD box RNA helicase (RH3)
7	chr1:-1:3525119:3525209:RI	1.68E-03	AT1G10650	SBP (S-ribonuclease binding protein) family protein
8	chr2:-1:12872819:12872822:AS	1.68E-03	AT2G30140	UDP-Glycosyltransferase superfamily protein
9	chr3:-1:5072959:5073040:DS/ES	4.49E-03	AT3G15070	RING/U-box superfamily protein
10	chr5:-1:26413838:26414154:RI	4.56E-03	AT5G66050	Wound-responsive family protein
11	chr2:-1:11702387:11702526:AS	4.71E-03	AT2G27350	OTU-like cysteine protease family protein
12	chr2:-1:11702449:11702526:AS	4.71E-03	AT2G27350	OTU-like cysteine protease family protein
13	chr4:-1:609857:609955:DS	5.37E-03	AT4G19110	Protein kinase superfamily protein
14	chr4:-1:13574622:13574700:AS	5.84E-03	AT4G19110	Protein kinase superfamily protein
15	chr4:-1:14535882:14536000:AS	6.79E-03	SPHK1	sphingosine kinase 1
16	chr4:-1:13574622:13574622:AS	6.79E-03	SPHK1	sphingosine kinase 1
17	chr1:-1:30411680:30411748:RI	5.37E-03	AT1G80940	unknown protein, has 30201 blast hits to 17
18	chr4:-1:10455011:10455020:AS	5.84E-03	AT4G19110	Protein kinase superfamily protein
19	chr4:-1:11461341:11461364:DS	6.79E-03	SPHK1	sphingosine kinase 1
20	chr5:-1:26275685:26275722:DS/ES	6.89E-03	AT5G65685	UDP-Glycosyltransferase superfamily protein
21	chr1:-1:9668904:9669096:RI	6.90E-03	ATSAT32 SAT32	interferon-related developmental regulator
22	chr4:-1:10455008:10455020:AS	6.90E-03	AT4G19110	Protein kinase superfamily protein
23	chr5:-1:1251501:1251564:AS	6.90E-03	R1 ATR1L BTR1	binding to TOMV RNA 1L (long form)
24	chr5:-1:1548221:1548221:AS	6.90E-03	R1 ATR1L BTR1	binding to TOMV RNA 1L (long form)
25	chr5:-1:2515000:2515000:AS	6.90E-03	R1 ATR1L BTR1	binding to TOMV RNA 1L (long form)
26	chr1:-1:2966000:2966000:AS	6.90E-03	R1 ATR1L BTR1	binding to TOMV RNA 1L (long form)
27	chr1:-1:2197900:2197900:AS	6.90E-03	R1 ATR1L BTR1	binding to TOMV RNA 1L (long form)

IGB scrolls and zooms, loads data

1. Start IGB

2. Click link



Made in R using xlsx library

IGB linked to Galaxy

Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy start here or consult our help resources.

History

36: Cold Treatment assembled transcripts
~150,000 lines
format: gtf, database: Arabidopsis_thaliana_TAIR10
cufflinks v2.1.1
cufflinks -q --no-update-check -l 5000 -F 0.100000 -j 0.150000 -p 8
display in IGB View

1. Sequence 2. Source 3. Feature 4

1. Sequence	2. Source	3. Feature	4
chr1	transcript	transcript	1
chr1	exon	exon	1
chr1	exon	exon	1
chr1	transcript	transcript	3

Running Your Own
Understanding how Galaxy

Tweets

Galaxy Project @galaxyproject
Galaxy workshops are 3 of 99 reasons to "Be in Long Beach this November" bit.ly/TT11UV

1. Click Galaxy History file

2. Click link

display in IGB View



BioViz Overview Downloads Tools News Cite IGB Get Help Credits Contact Us

Integrated Genome Browser

Visualization for genome-scale data

Welcome Galaxy User

Thank you for using IGB!

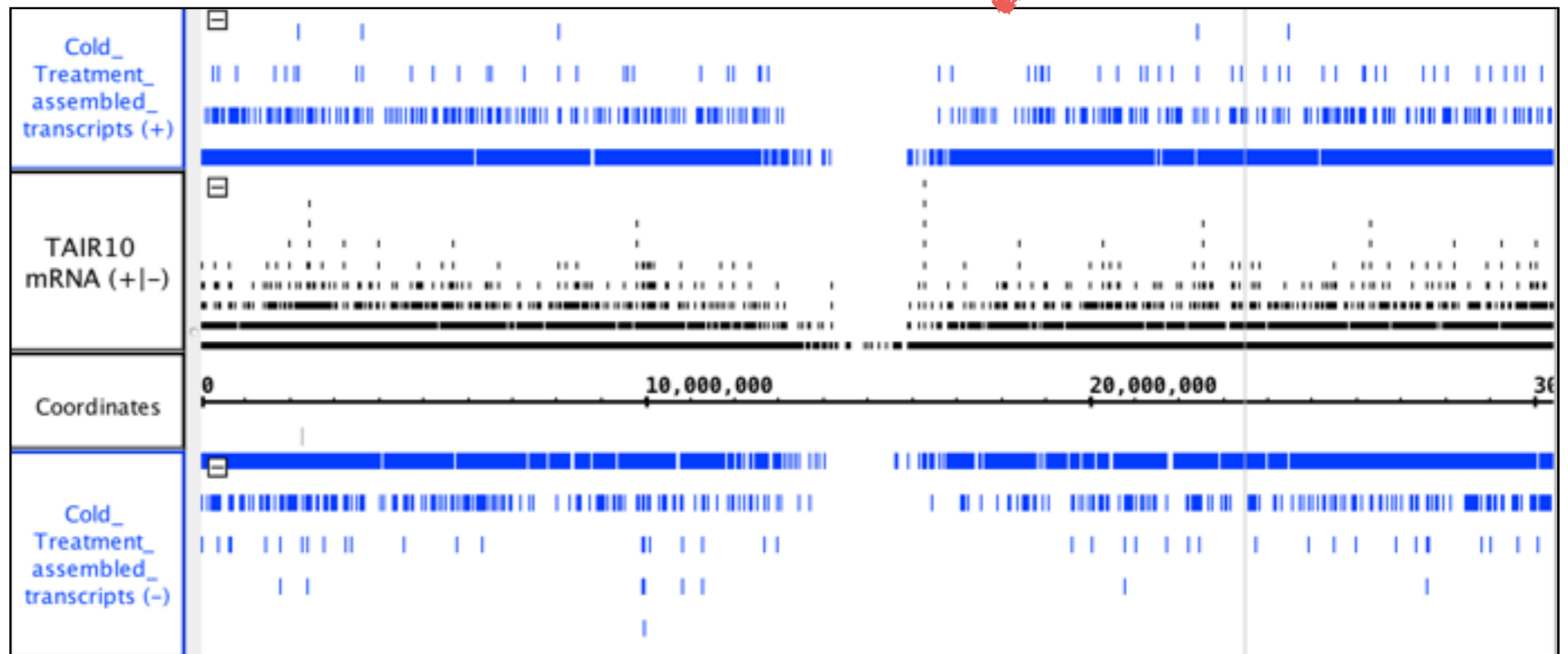
Follow YouTube

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Genoviz is a sourceforge project

3. Click Again



New Galaxy track in IGB



Save track, choose format

Chromosome 1 (Arabidopsis thaliana TAIR9) - Integrated Genome Browser 8.1.8

Selection Info: Cold_Treatment_assembled_transcripts.gtf

chr1:11,176,644-14,363,900

Save

Save As: AssembledTranscripts.bed

File Format: BED (*.bed)

Available Data - Configure

- Reads
- Graph
 - Wet D, c
 - Wet F, c
 - Dry B, c
 - Dry C, c
 - Dry E, c

(7) Sequen...	Length
chr1	30,427,671
chr2	19,698,289
chr3	23,459,830
chr4	18,585,056
chr5	26,975,502
chrC	154,478
chrM	366,924
genome	

345M of 1820M

User's Guide

Home - IGB User's Guide - Confluence

wiki.transvar.org/confluence/display/igbman/Home

Dashboard > IGB User's Guide > Home

Browse ▾ Log In ■■ Search Confluence

Search

- New in IGB 6.7
- Quick Start
- Introduction
- IGB Anatomy
- IGB Preferences
- Loading Data
 - Data Sources
 - Adding and Managing Data Sources
 - Creating QuickLoad Sites
 - File Formats
 - Converting FASTA to BNIB
 - Making BAM Files for IGB (RNA-Seq)
 - Working with .wig files
 - Removing data from a current session
 - Creating your own genome version
 - Personal Synonyms
 - Species currently recognized by IGB
- Saving and sharing data
- Bookmarks

IGB Home Tools ▾

1 Added by [Ann Loraine](#), last edited by [Ann Loraine](#) on Apr 29, 2012 ([view change](#))

https://wiki.transvar.org

About IGB

New sequencing technologies are making it much easier for labs to produce huge volumes of short- and long-read sequencing data. At the same time, more labs are using DNA microarrays to study expression patterns, identify sites bound by transcriptional factors, and explore the epigenome. To understand these new data sets, researchers need to view their data alongside other known features of the genomic landscape.

The Integrated Genome Browser (IGB, pronounced Ig-Bee) aims to meet this need. First developed at Affymetrix in 2003 for their tiling array products, IGB provides an advanced, highly customizable environment for exploring and analyzing large-scale genomic data sets.

Using IGB, you can:

- View your RNA-Seq, ChIP-chip or ChIP-seq data alongside genome annotations and sequence.
- Investigate alternative splicing, regulation of gene expression, epigenetic modifications of DNA, and other genome-scale questions.
- View results from aligning short-read sequences onto a target genome, identify SNPs, and check alignment quality.
- Copy and paste genomic sequences for further analysis into other tools, such as primer design and promoter analysis tools.
- Create high-quality images for publication in a variety of formats.

Powered by Atlassian Confluence 3.5, the Enterprise Wiki | Report a bug | Atlassian News

IGB Gallery

IGB 6.7.1 running in iPlant Atmosphere - IGB User's Guide - Confluence

transvar.org https://wiki.transvar.org/confluence/display/igbman/IGB+6.7.1+running+in+iPlant+Atmosphere

Dashboard > IGB User's Guide > ... > IGB Gallery > IGB 6.7.1 running in iPlant Atmosphere

RNASeq experiment from the Loraine lab that we deployed the the publicly-accessible IGBQuickLoad site at UNC Charlotte.

vm142-21.iplantcollaborative.org:1 (aloraine) - VNC Viewer

Applications Places System 5:19 PM

Chromosome 1 (Arabidopsis TAIR9) - Integrated Genome Browser 6.7.1

File Edit View Tools Bookmarks Help

chr1: 2,942,203 - 2,946,533

Cold (bedgraph) (0, 181.42)

Control (bedgraph) (0, 181.42)

TAIR10 mRNA (+/-)

Coordinates

AT1G09140.1

AT1G09140.2

AT1G09150.1

2,942,000 2,943,000 2,944,000 2,945,000 2,946,000

2,942,373

Data Access Selection Info Search Sliced View Graph Adjuster External View Plug-ins

Data Sources and Data Sets - Configure

RNA-Seq

Loraine Lab

Mixed Cold

SM

Reads

Graph

Control, coverage

Cold, coverage

MM

Juncs

TAIR9

Data Management Table

	FG	BG	2 Track	Load Mode	Data Set/File Name	Track Name (Double ...	
<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Region	RNA-Seq / Loraine...	Cold (bedgraph)	X
<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Region	RNA-Seq / Loraine...	Control (bedgraph)	X
<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Genome	TAIR10 mRNA	TAIR10 mRNA	X

Load All Sequence Load Sequence In View Load Data

316M of 910M

Powered by Atlassian Confluence 3.5, the Enterprise Wiki | Report a bug | Atlassian News

<http://wiki.transvar.org>

Lorraine Lab Agile Board

QUICK FILTERS: David Ivory Mason Tarun Ann Tiffany Only My Issues Recently Updated

EPICS

- All issues
- Technical Debt Reduction
- Integration with SNpedia
- Paired End Visualization
- Needs Clarification or blocked
- Issues without epics

▼ Sprint 1 15 issues Start Sprint

Issue ID	Description	Estimate
IGBF-87	Dragging and dropping an arrow from the toolbar causes constant scrolling.	1
IGBF-103	Save all the data, not just the current chromosome	2
IGBF-27	Improve right-click menu when users right-click a feature or sequence in IGB display	1
IGBF-67	External Viewer does not work.	2
IGBF-93	Help menu improvements - new link to BioStars, rewording	0.5
IGBF-59	Create a Deprecated server list that IGB applies to older user server lists	1.5
IGBF-104	Update Jira Configuration with similar "promotion" based au Technical Debt Red...	1
IGBF-62	User can not delete a track that does not contain data via context menu	1
IGBF-58	IGB gives confusing message when adding a duplicate data source and duplicates dat	1
IGBF-49	Creating a "Not" track with the coordinates track. (should this be allowed?) When delet	1
IGBF-81	Zoom in and load data message appears even when file can't be loaded	1
IGBF-47	Add context menu "copy" to bookmarks right click	0.5
IGBF-30	file choosers should recall the last directory user navigated to	0.5
IGBF-56	Update circle info icon to have a clear background instead of white background	0.25
IGBF-43	Remove RELEASES.txt from igb.zip	0.1

15 issues Estimate 14.35

Backlog 47 issues Create Sprint

jira.transvar.org

IGB 8.2 / IGBF-32

Don't replace spaces with underscore characters when viewing files from Galaxy.

Estimate: 1

Details

Status: **OPEN**

Component/s: None

Labels: None

Affects Version/s: None

Fix Version/s: None

Epic: **Galaxy Server galaxy.transvar.org**

People

Reporter: Ann Loraine

Assignee: David Norris

Dates

Created: 13/Apr/14 10:34 AM

Updated: 10/Jul/14 1:18 PM

- agile development
- 3 week sprints

- sprints, stories public
- technical debt reduction