

Advanced genome browsers: Integrated Genome Browser and others

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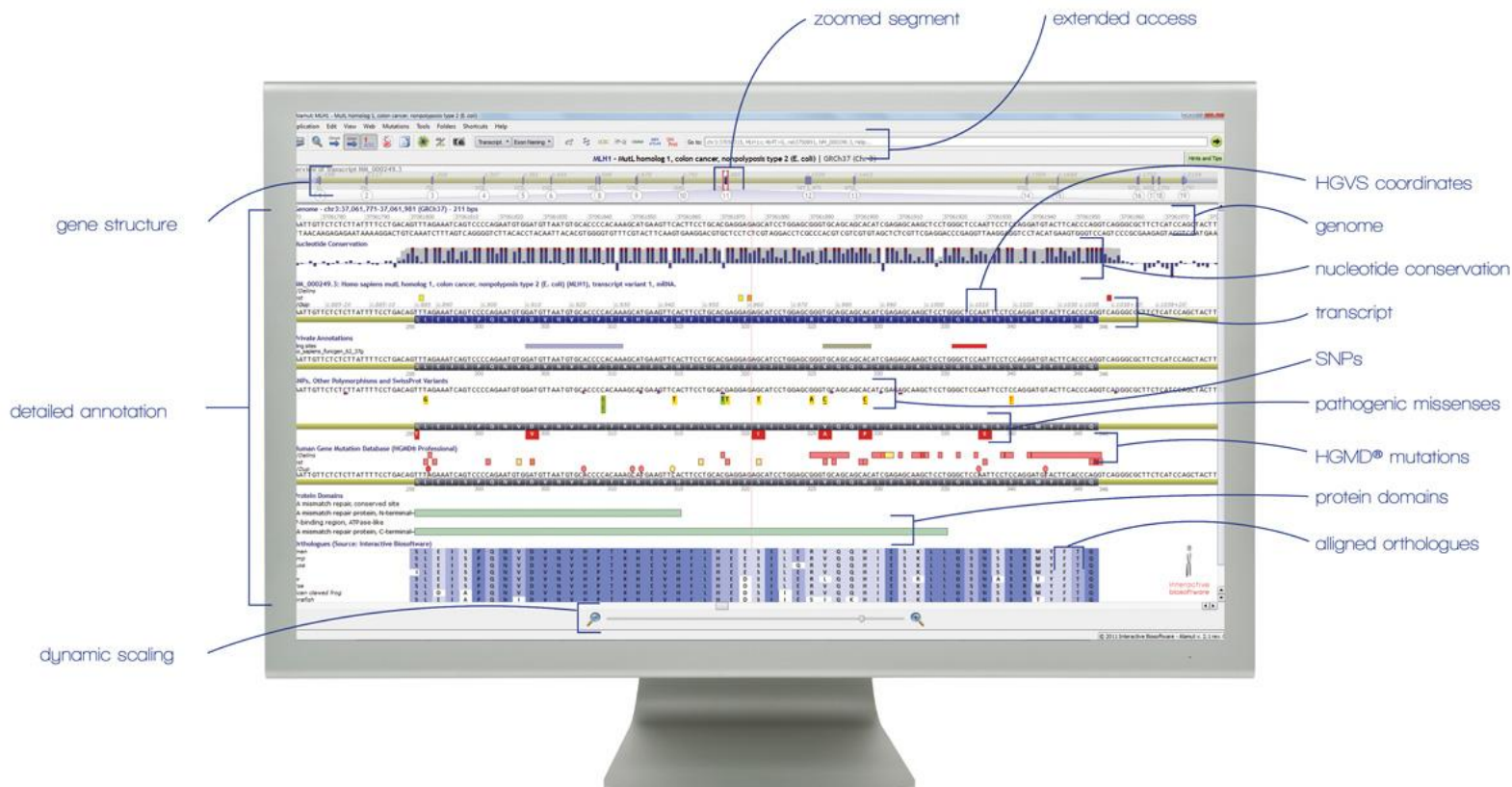
List of Genome Browsers

Alamut
Annmap
Apollo Genome Annotation Curation Tool
Argo Genome Browser
Artemis Genome Browser
Avadis NGS
BugView
Celera Genome Browser
Dalliance Javascript-based genome browser
DiProGB
DNAnexus Flash-based interactive genome browser
Ensembl The Ensembl Genome Browser
Gaggle Genome Browser
GBrowse
Genome Wowser
The Genomic HyperBrowser
Integrative Genomics Viewer
Genostar GenoBrowser
Geniverse interactive genome browser
GenPlay
Golden Helix GenomeBrowse
Integrated Genome Browser
Integrated Microbial Genomes
JBrowse
MGV - Microbial Genome Viewer
MochiView Genome Browser
NextBio Genome Browser
Pathway Tools Genome Browser
Savant Genome Browser
SEED viewer
UCSC Genome Bioinformatics Genome Browser
Viral Genome Organizer (VGO)
VISTA genome browser
WashU Genome Browser

Genome Browser screenshots and brief description (Alamut)

Alamut

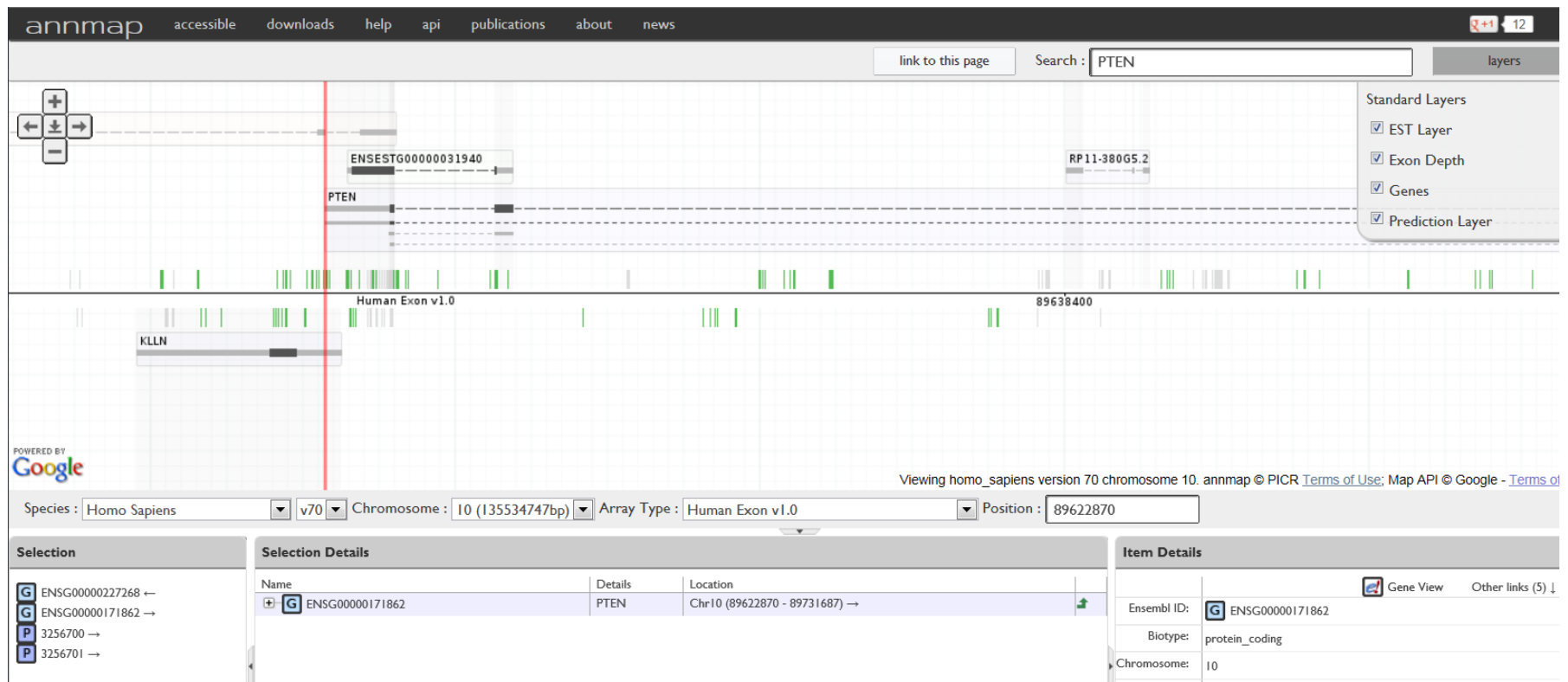
A gene browser that handles HGVS nomenclature and integrates missense and splicing prediction tools for mutation interpretation (commercial), HGVS = Human Genome Variation Society
<http://www.interactive-biosoftware.com/software/alamut/features>



Annmap

A genome browser that shows Affymetrix Exon Microarray hit locations alongside the gene, transcript and exon data on a Google Maps API (free)

<http://annmap.picr.man.ac.uk/>



The screenshot displays the Annmap genome browser interface. At the top, there is a navigation bar with links for accessible, downloads, help, api, publications, about, and news. A search bar contains the text "PTEN". Below the search bar, a map view shows the genomic region on chromosome 10. The map includes tracks for genes (PTEN, KLLN), transcripts (ENSESTG00000031940, RP11-38065.2), and exons (Human Exon v1.0). A red vertical line indicates the current position at 89622870. A sidebar on the right shows the "Standard Layers" menu with checkboxes for EST Layer, Exon Depth, Genes, and Prediction Layer. At the bottom, there is a selection table and an item details panel.

Viewing homo_sapiens version 70 chromosome 10. annmap © PICR [Terms of Use](#); Map API © Google - [Terms of Use](#)

Species: Homo Sapiens v70 Chromosome: 10 (135534747bp) Array Type: Human Exon v1.0 Position: 89622870

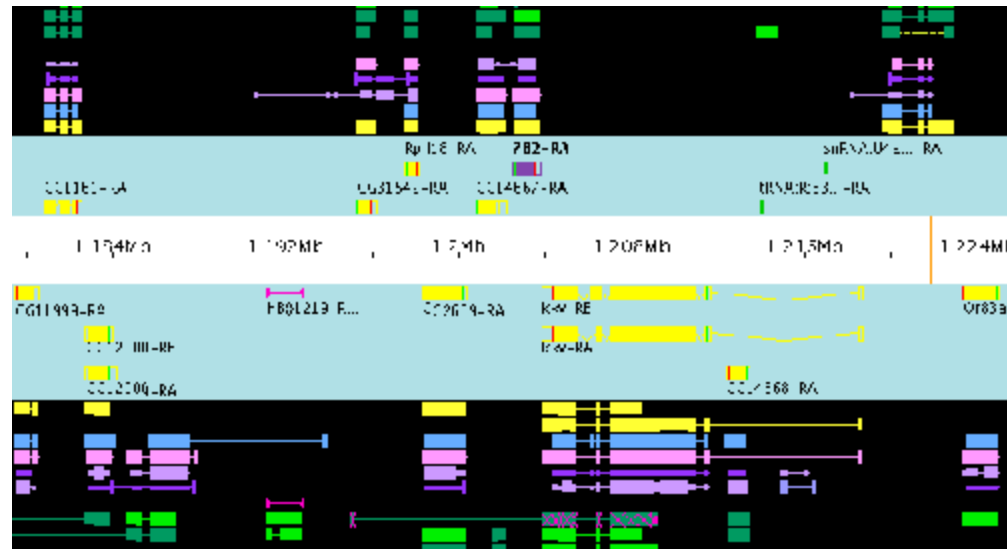
Selection		Selection Details		Item Details	
<input type="checkbox"/>	ENSG00000227268 ←				
<input type="checkbox"/>	ENSG00000171862 →				
<input type="checkbox"/>	3256700 →				
<input type="checkbox"/>	3256701 →				
<input checked="" type="checkbox"/>	ENSG00000171862	PTEN	Chr10 (89622870 - 89731687) →	Ensembl ID:	ENSG00000171862
				Biotype:	protein_coding
				Chromosome:	10

Apollo

Genome Annotation Curation Tool A cross-platform, Java-based standalone genome viewer with enterprise-level functionality and customizations.

The standard for many model organism databases. (free)

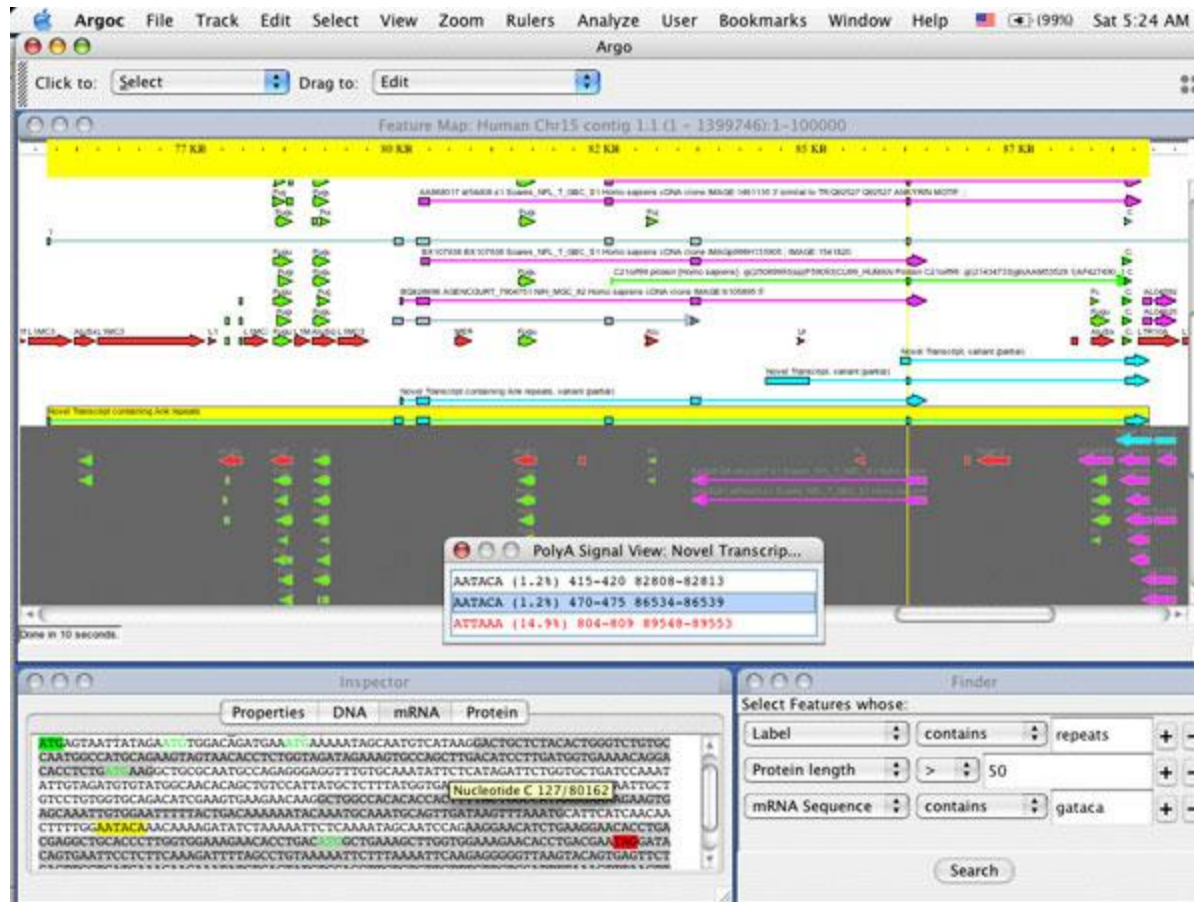
<http://apollo.berkeleybop.org/current/index.html>



Genome Browser screenshots and brief description (Argo)

Argo Genome Browser

A free and open source standalone Java-based genome browser for visualizing and manually annotating whole genomes. (free)
<http://www.broadinstitute.org/annotation/argo/>



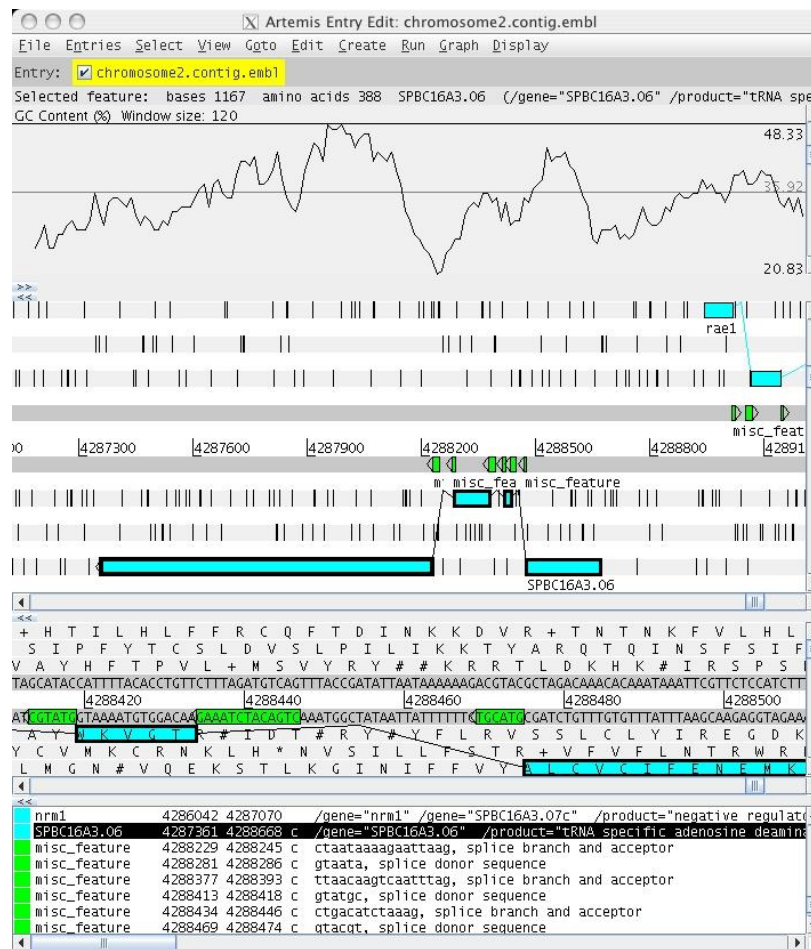
Genome Browser screenshots and brief description (Artemis)

Artemis Genome Browser

A free and open source standalone genome browser (Wellcome Trust Sanger Institute) for visualizing and manually annotating whole genomes.

It can also be used to visualize next generation data.

<http://www.sanger.ac.uk/resources/software/artemis/>



Genome Browser screenshots and brief description (Avadis)

Avadis NGS

combines a genome browser and set of data analysis tools for CHIP-Seq, RNA-Seq, and genomic variation experiments, developed by Strand Life Sciences (commercial)
http://www.avadis-ngs.com/features/genome_browser

The screenshot displays the Avadis Genome Browser interface. The top toolbar includes navigation and search icons. The main area is divided into several tracks:

- Chromosome View:** Shows a chromosome map with a red callout pointing to the current region.
- Genome View:** Shows a detailed view of the current region with a red callout.
- Region View:** Shows aligned reads for the current region with a red callout.
- Transcripts / Ensembl Transcripts (Transcripts):** Shows the gene structure for the current region.
- Spreadsheet View:** Shows a table of transcript data with a red callout.

Red callouts identify the following components:

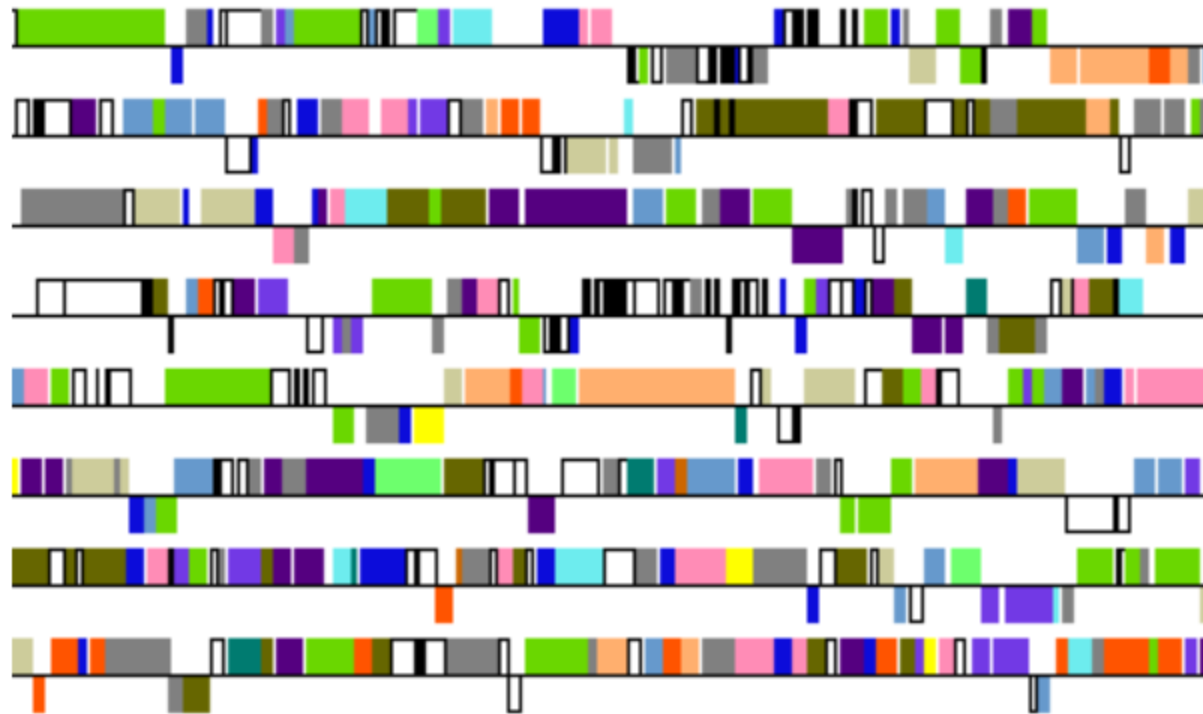
- Genome Browser Toolbar
- Chromosome View
- Genome View
- Region View
- Spreadsheet View

Start	End	Transcript Name	Strand	Cds Start	Cds End	Exon Count	Gene Name	Gene ID
21006863	21007325	ENST000003902...	+	21006863	21007325	2	D87018.1-1	ENSG000002116...
21011708	21012174	ENST000003902...	+	21011708	21012174	2	D87018.1-2	ENSG000002116...

BugView

Free cross-platform desktop browser for visualizing genomes, especially suited for comparing prokaryotic genomes.

<http://doolittle.ibls.gla.ac.uk/leader/BugView/index.html>

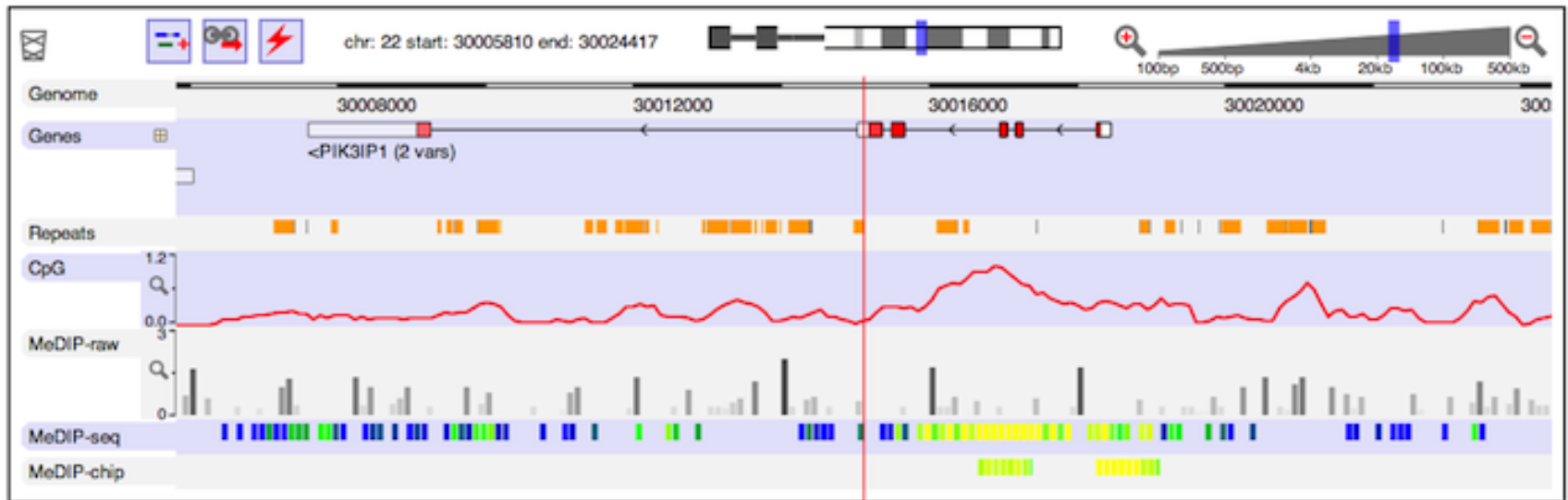


Horizontal presentation of genes colour-coded by COG category

Dalliance

Javascript-based genome browser. Talks DAS.

<http://www.biodalliance.org/docs.html>



DiProGB:

The Dinucleotide Properties Genome Browser

<http://diprogb.fli-leibniz.de/>

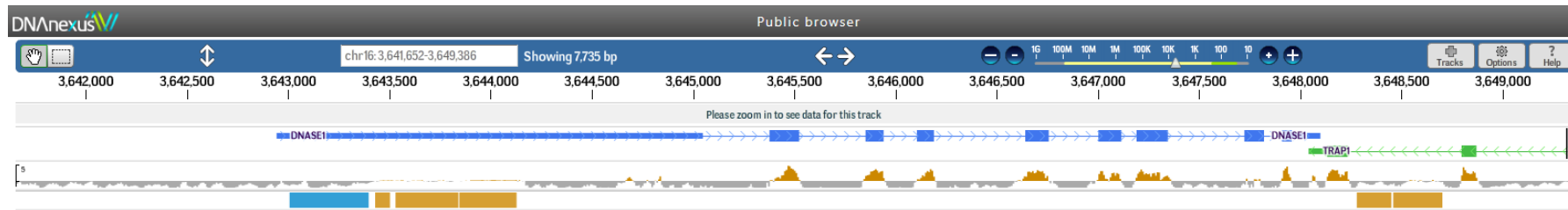
DiProGB



DNANexus

Flash-based interactive genome browser, as well as next-gen sequence analysis and visualization. Commercial

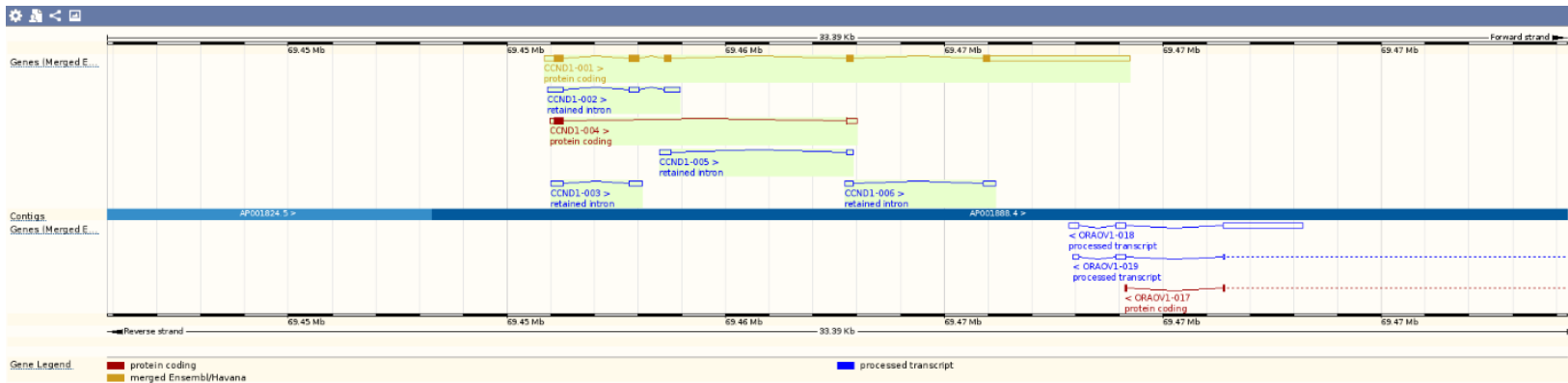
https://dnanexus.com/genomes/hg18/public_browse



Ensembl

The Ensembl Genome Browser (Wellcome Trust Sanger Institute and EBI)

<http://www.ensembl.org/>



Gaggle Genome Browser

A java-based genome browser developed at Institute for Systems Biology (ISB) for high-throughput data integration.

<http://gaggle.systemsbiology.net/docs/geese/genomebrowser/>

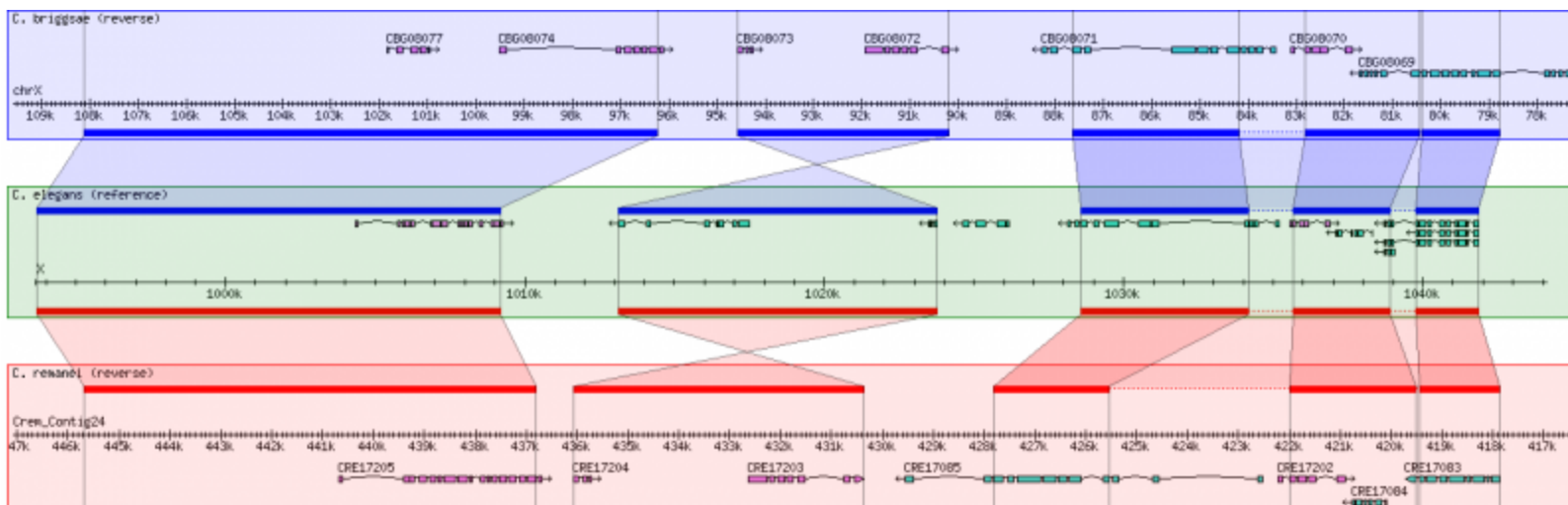


Genome Browser screenshots and brief description (Gbrowse)

GBrowse

The GMOD GBrowse Project

<http://gmod.org/wiki/GBrowse>

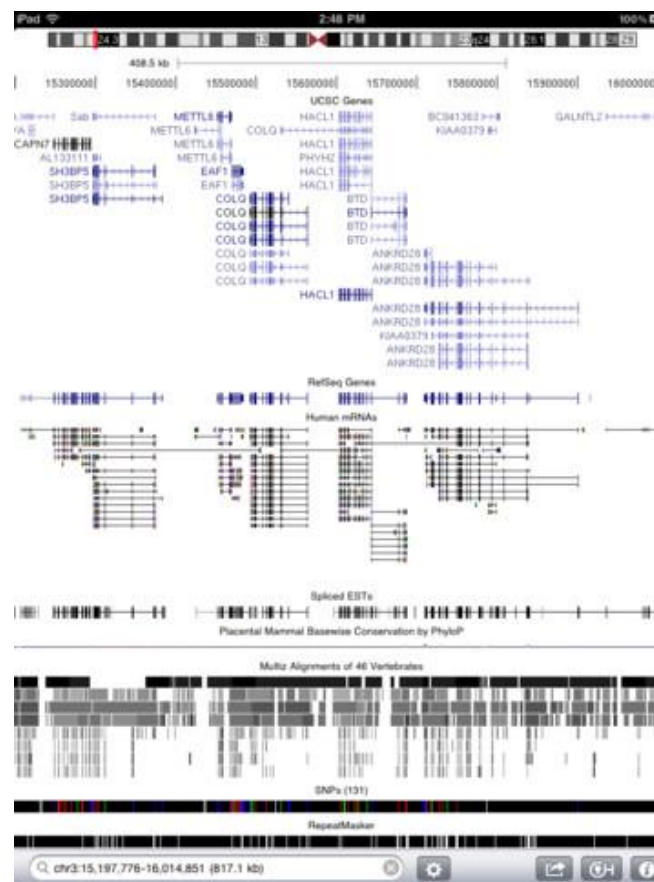


Genome Wowser

An iPad-enabled view of the human genome.

The app, developed by the Center for Biomedical Informatics (CBMi) at The Children's Hospital of Philadelphia, provides a functional presentation of the popular UCSC Genome Browser.

http://gmod.org/wiki/GBrowse_syn



The Genomic HyperBrowser

focuses on statistical analysis of elements along the genome.

Embedded in Galaxy.

<http://hyperbrowser.uio.no/hb/>

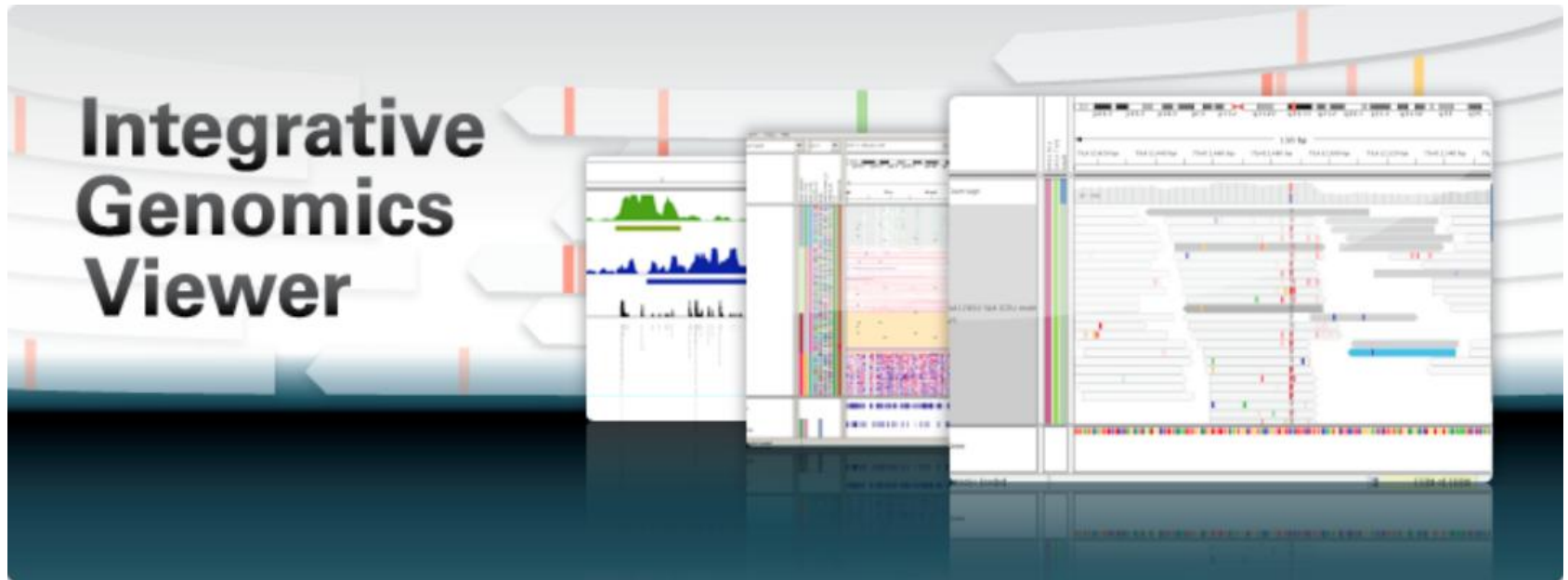
The screenshot displays the Galaxy web interface with 'The Genomic HyperBrowser' tool selected. The top navigation bar includes 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User', with a 'Using 0 bytes' indicator on the right. The left-hand menu is titled 'Tools' and contains a search bar and a list of tool categories: 'HYPERBROWSER TOOLS' and 'GALAXY TOOLS'. Under 'HYPERBROWSER TOOLS', the selected tool 'The Genomic HyperBrowser' is expanded to show sub-items: 'Perform analysis', 'Help', 'Export / import', 'Create tracks', 'Edit tracks', 'Create and edit GTrack files', 'Advanced analysis of tracks', 'Analyze nmers', 'Transcription factor analysis', 'Create and view regulomes', 'MCFDR tools', 'Admin of genomes and tracks', and 'Restricted tools'. The main content area features a large graphic with a yellow Greek letter sigma (Σ) and a DNA double helix, followed by the text 'The Genomic HyperBrowser'. Below this, a yellow box contains the message: 'If you have a *genomic track*, this is the place to analyze it!'. Underneath, it says 'To analyze a track, simply:' followed by a numbered list: '1. Click [The Genomic Hyperbrowser: Perform analysis](#) in the left-hand menu.' and '2. Select tracks from your Galaxy history of browse our collection...'. The right-hand panel is titled 'History' and shows '0 bytes' and a message: 'Your history is empty. Click 'Get Data' on the left pane to start'.

Integrative Genomics Viewer (IGV)

Integrative Genomics Viewer

Java based thick client application, communicates with DAS servers

<http://www.broadinstitute.org/igv/>

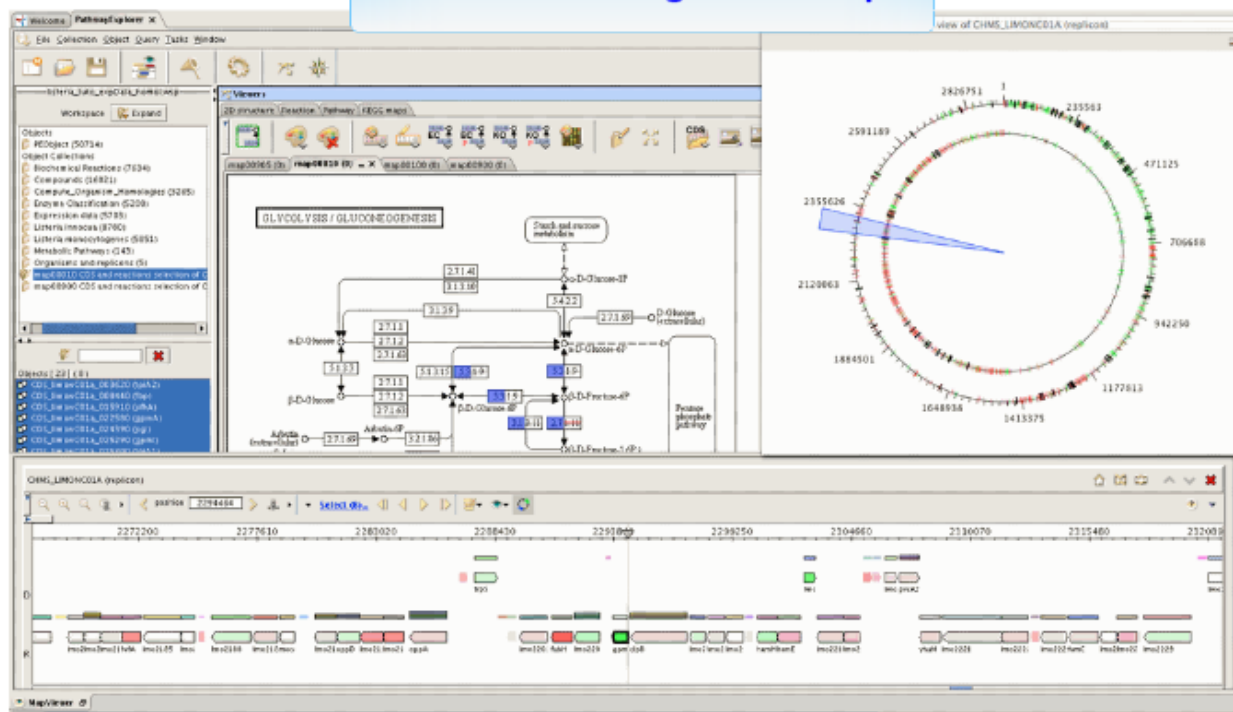


Genostar **GenoBrowser**:

a standalone application to display and explore genomic data from any kind of file (EMBL, GenBank, Fasta, GFF...), commercial

<http://www.genostar.com/en/>

Visualize expression data on
metabolic and genomic maps

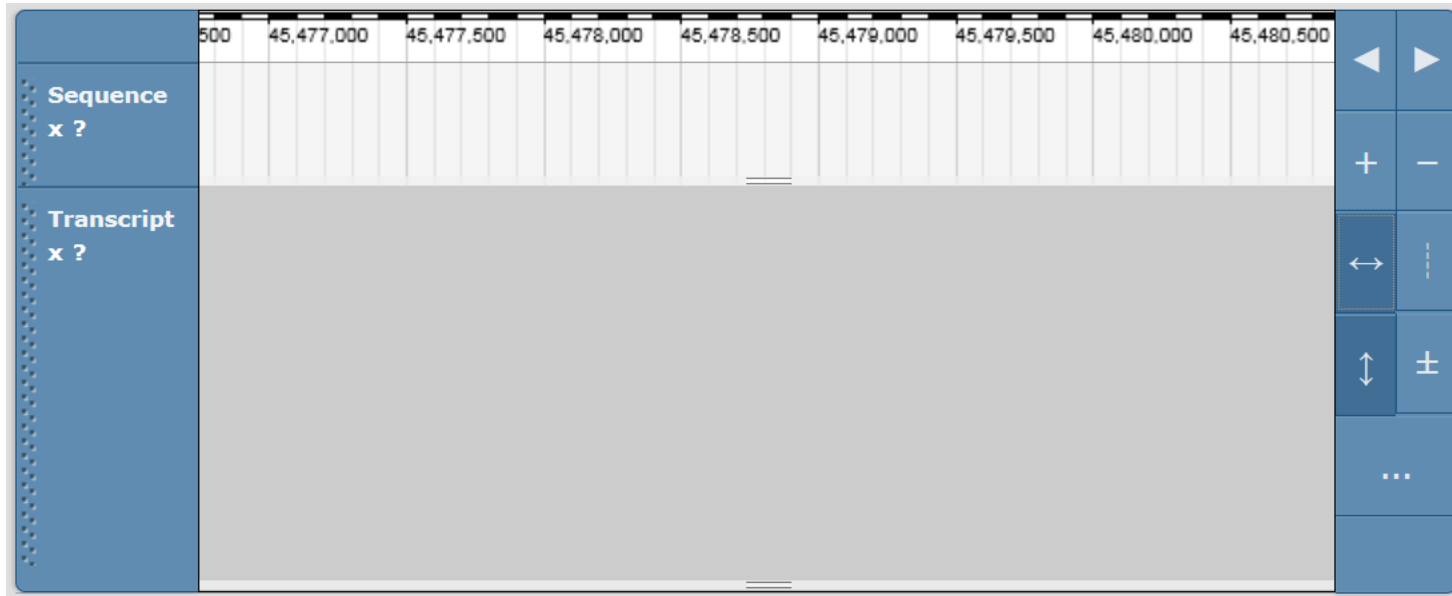


Genome Browser screenshots and brief description (Genoverse)

Genoverse interactive genome browser:

web-based, scrollable genome browser, developed to be easily integrated into any website with a few strings of javascript. Loads data dynamically via AJAX and visualizes via HTML5 canvas element

<http://eugenebragin.github.com/Genoverse/>



GenPlay

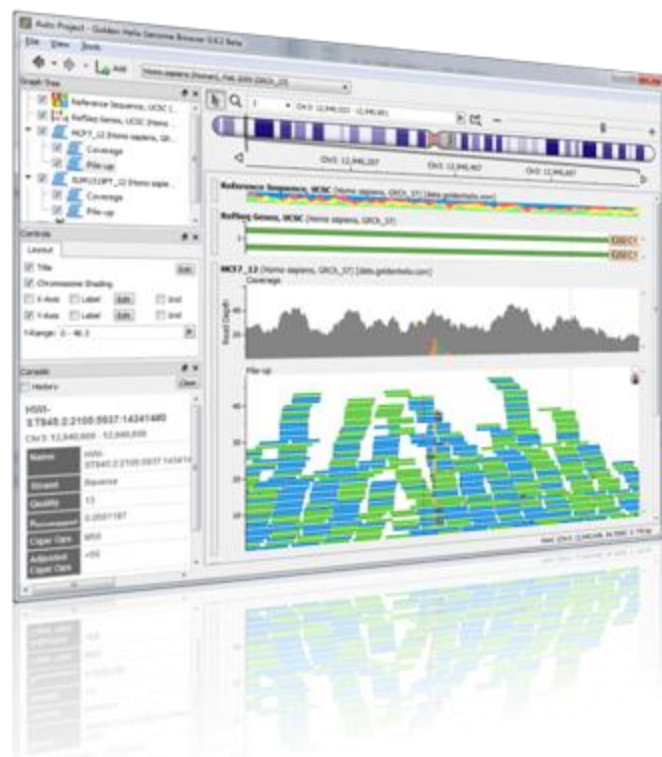
A genome viewer and analyzer developed in Java at Albert Einstein College of Medicine.

<http://genplay.einstein.yu.edu/>



Golden Helix GenomeBrowse

A free genome browser for exploring sequencing pile-up and coverage data with numerous annotation tracks hosted on the cloud. Commercial
<http://www.goldenhelix.com/GenomeBrowse/index.html>

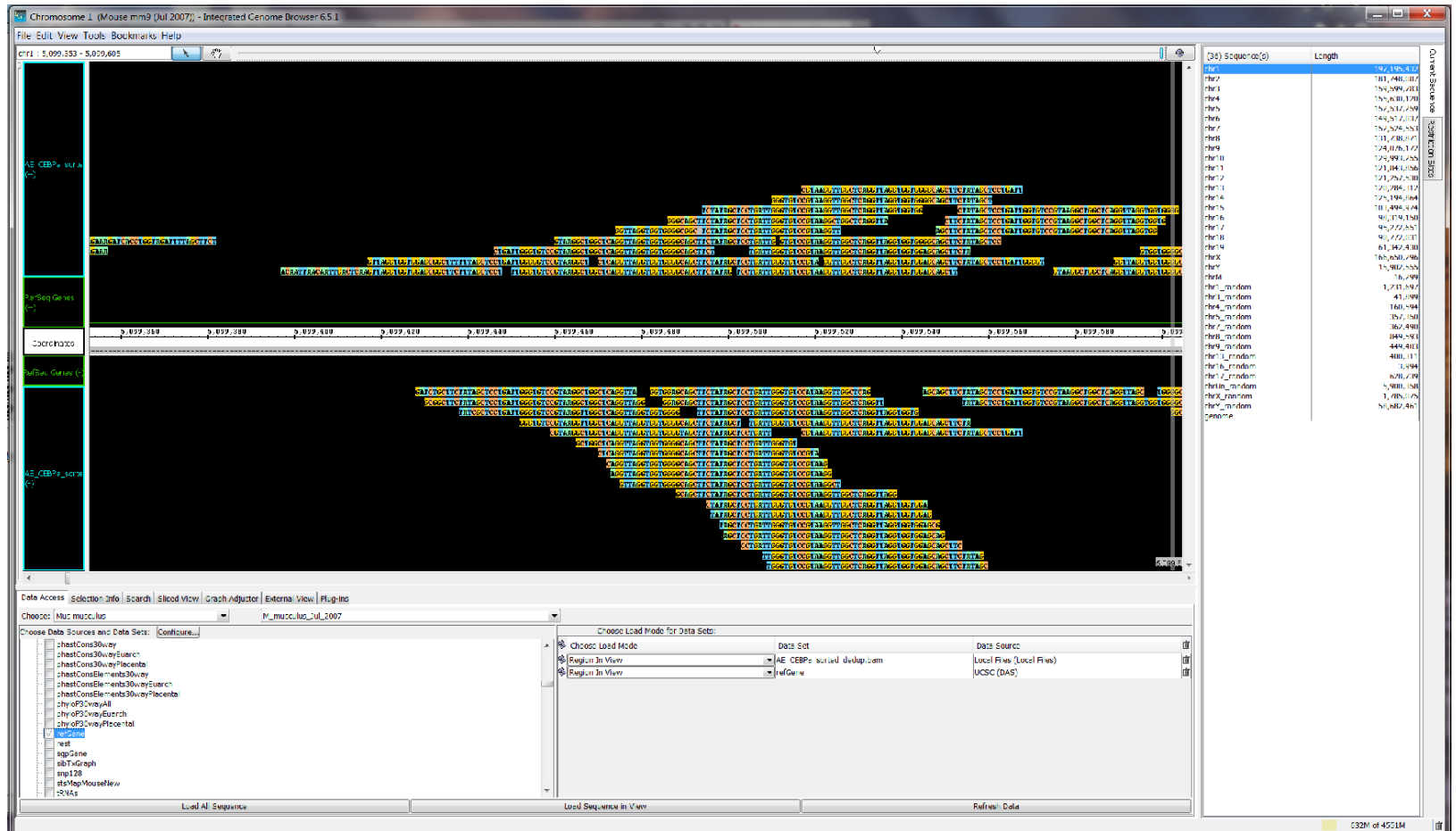


Genome Browser screenshots and brief description (IGB)

Integrated Genome Browser (IGB)

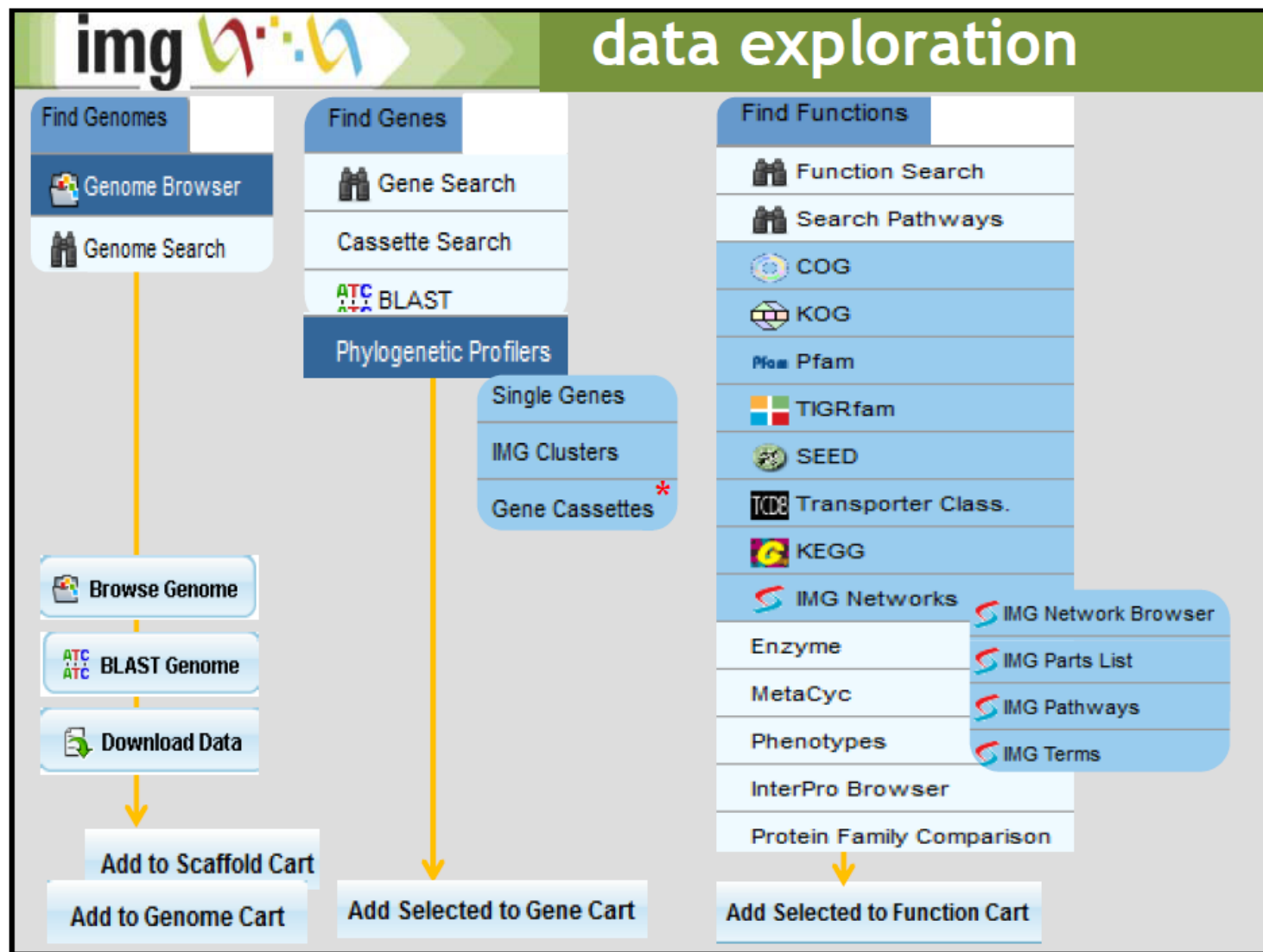
Open source and free Java-based desktop genome viewer for visualizing next-gen sequence and microarray data.

<http://bioviz.org/igb/download.html>



Genome Browser screenshots and brief description (IMG)

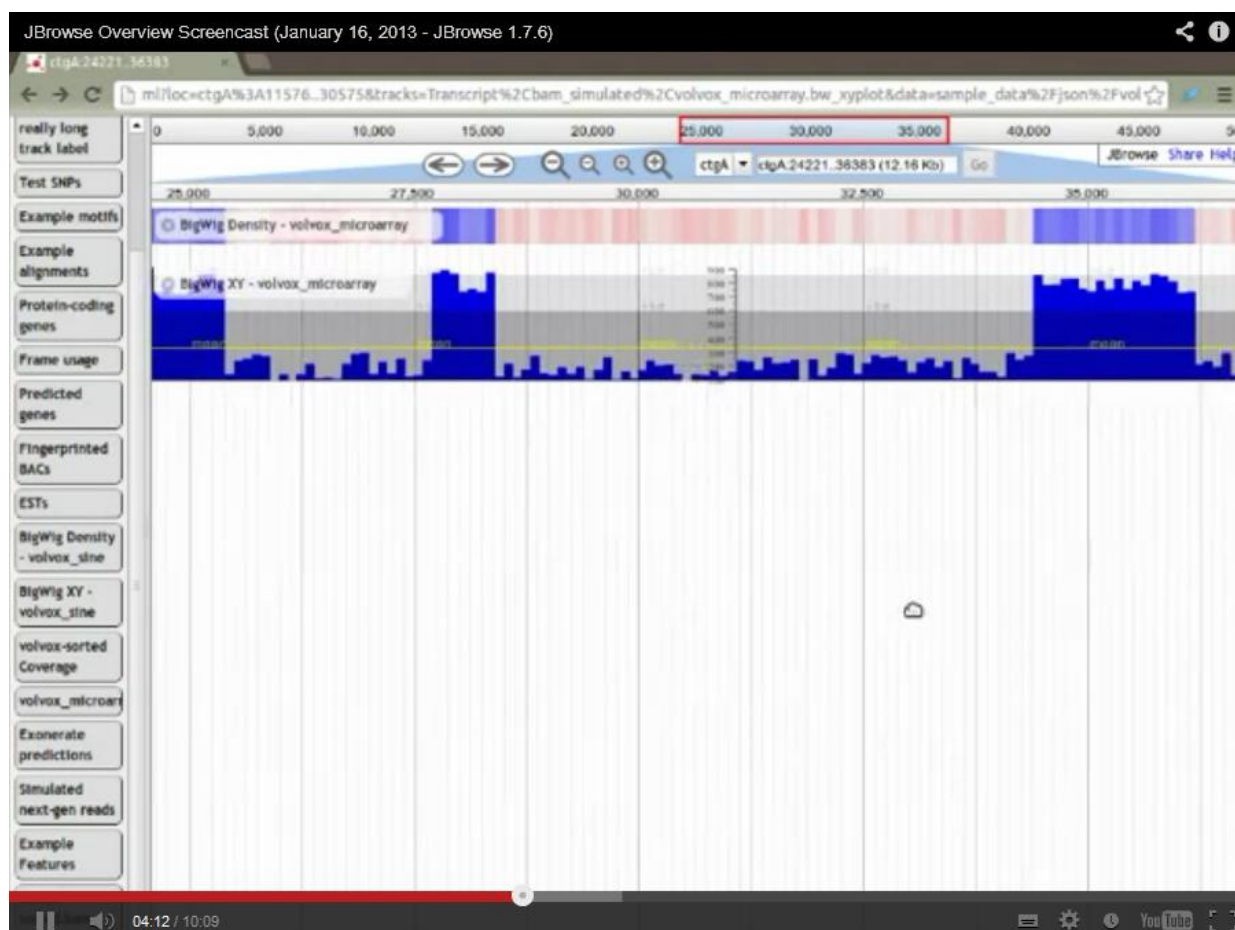
Integrated Microbial Genomes (IMG) system by the DOE-Joint Genome Institute



Genome Browser screenshots and brief description (JBrowse)

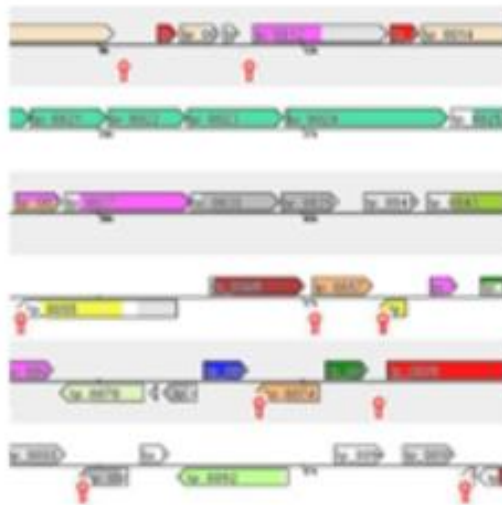
JBrowse

a JavaScript genome browser by the open source
Generic Model Organism Database project.
<http://jbrowse.org/>

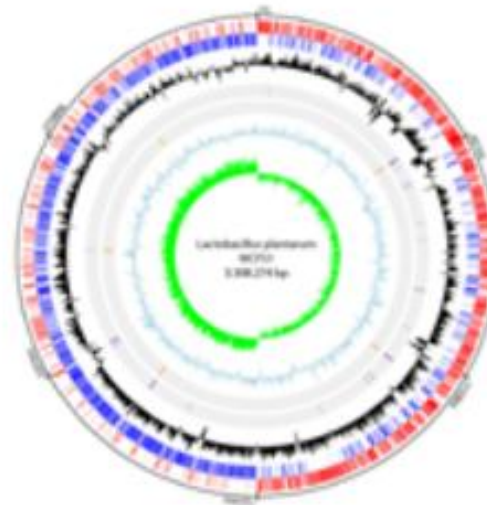


MGV - Microbial Genome Viewer

Linear genome maps



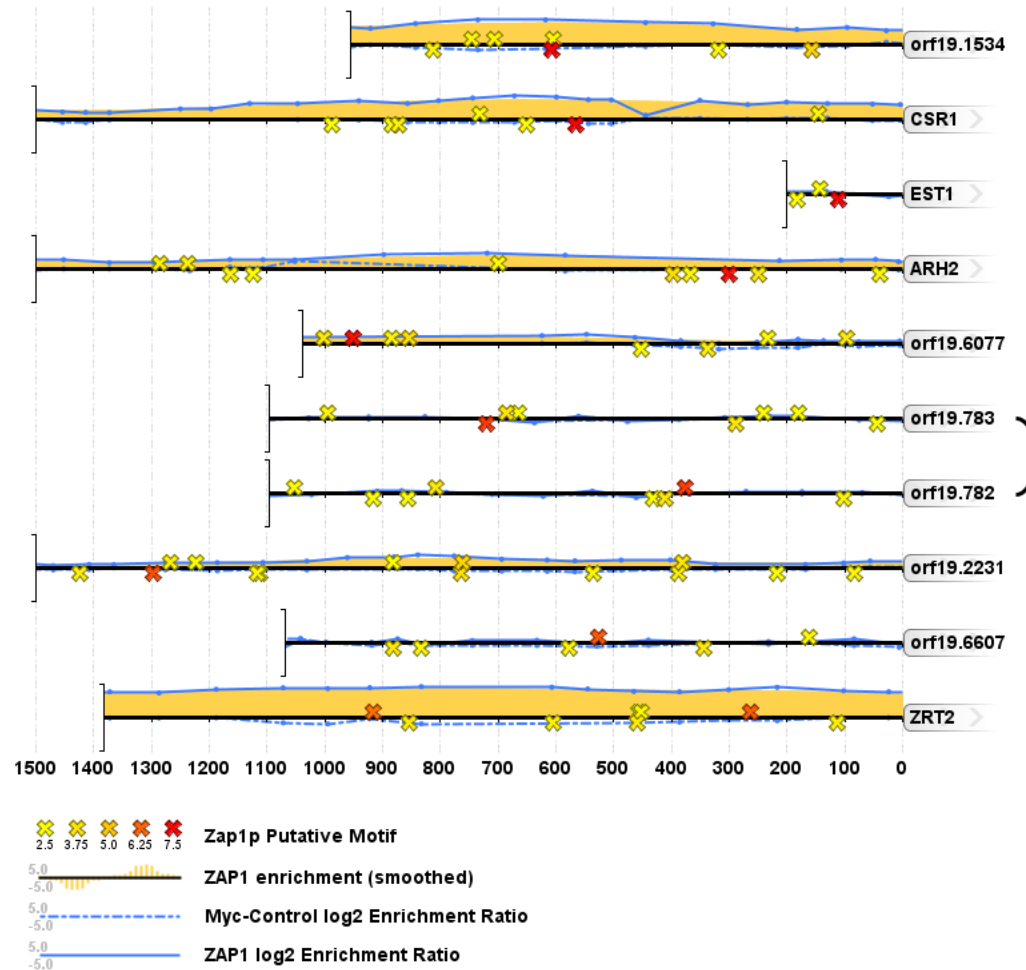
Circular genome maps



Microbial Genome Viewer 2.0: explore, analyze and export.
Consult the **quick overview** to learn about the layout. Example figures can be found in this **pdf document**.

MochiView Genome Browser

<http://johnsonlab.ucsf.edu/sj/mochiview-start>



NextBio Genome Browser

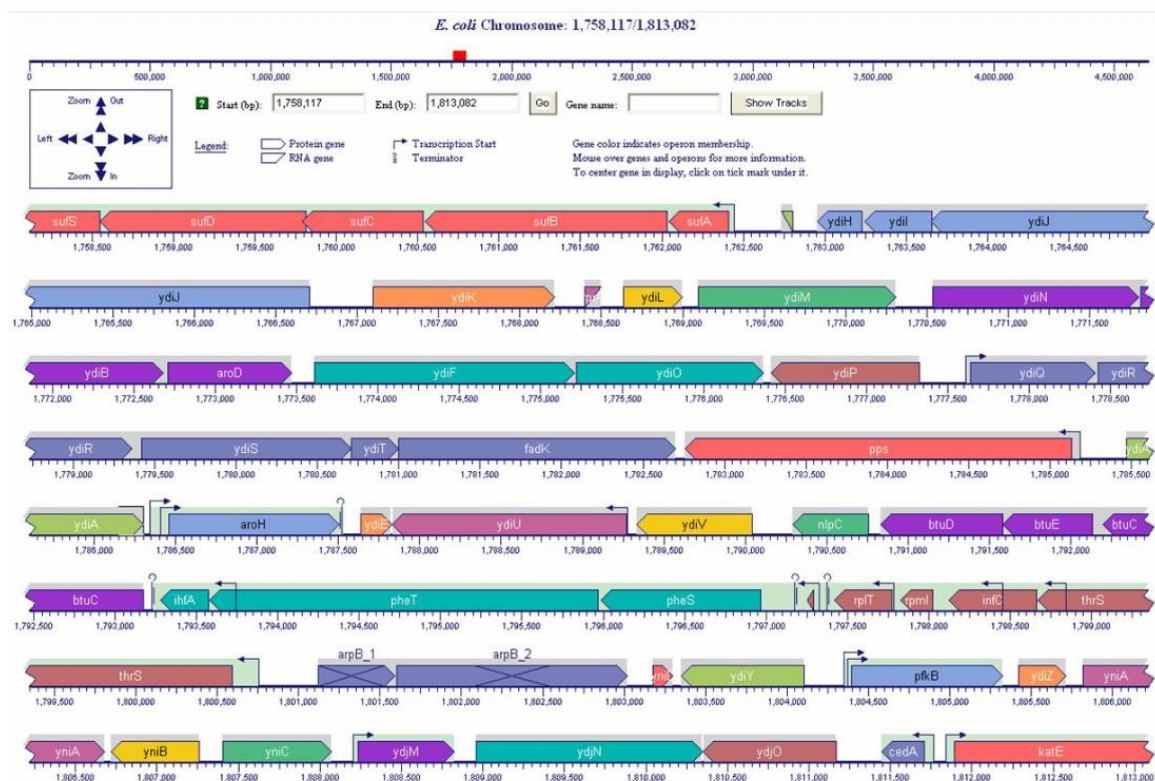
an interactive application that lets visualization of physical relationship between private or public biosets and different types of genomic elements, including genes, miRNA targets, CNVs, CpG islands, SNPs, GWAS associations, and LD blocks
<https://www.nextbio.com/b/gb/genomeBrowser.nb>

You need to sign in to access Genome Browser

Genome Browser screenshots and brief description (Pathway Tools)

Pathway Tools Genome Browser, commercial

<http://bioinformatics.ai.sri.com/ptools/>

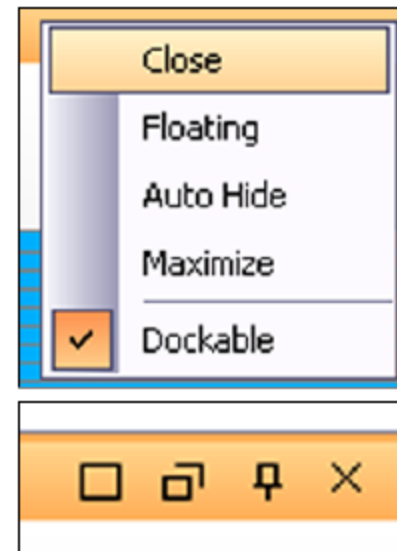
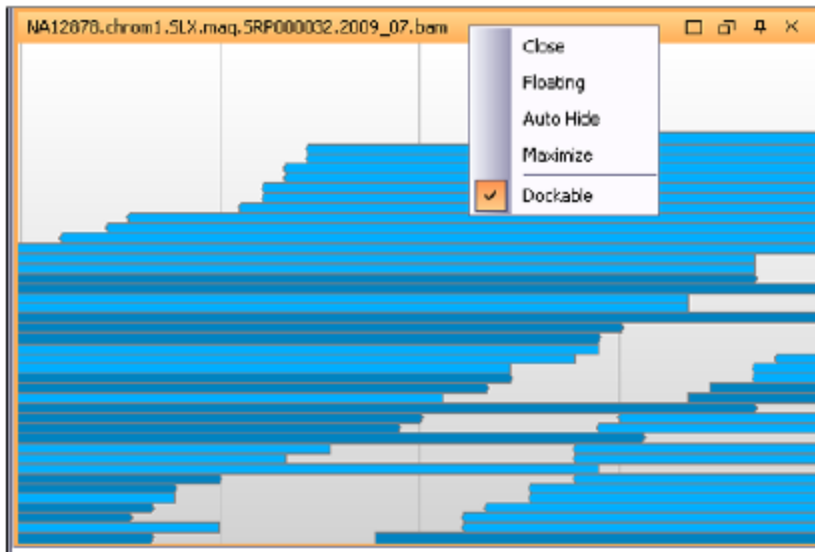


Genome Browser screenshots and brief description (Savant)

Savant Genome Browser

for visual analytics of high-throughput sequencing data, commercial

<http://www.genomesavant.com/>



Genome Browser screenshots and brief description (UCSC)

UCSC Genome Bioinformatics Genome Browser and Tools (UCSC)

<http://genome.ucsc.edu>



Genome Browser screenshots and brief description (VISTA)

VISTA genome browser

a comprehensive suite of programs and databases for comparative analysis of genomic sequences. There are two ways of using VISTA - you can submit your own sequences and alignments for analysis (VISTA servers) or examine pre-computed whole-genome alignments of different species.

<http://genome.lbl.gov/vista/index.shtml>

Region	Coding SNPs		Non-Coding SNPs			ICFs	Conservation
	Genes	Total coding	Deleterious	Total non-coding	Splice Sites		
chr11:118988000-118988000	0	40	10	4,007	0	10	
chr11:118988040-118988040	0	40	10	4,007	0	10	
chr11:118988080-118988080	0	10	0	4,000	0	0	
chr11:118988120-118988120	0	10	0	3,970	0	10	
chr11:118988160-118988160	0	10	0	3,960	0	10	

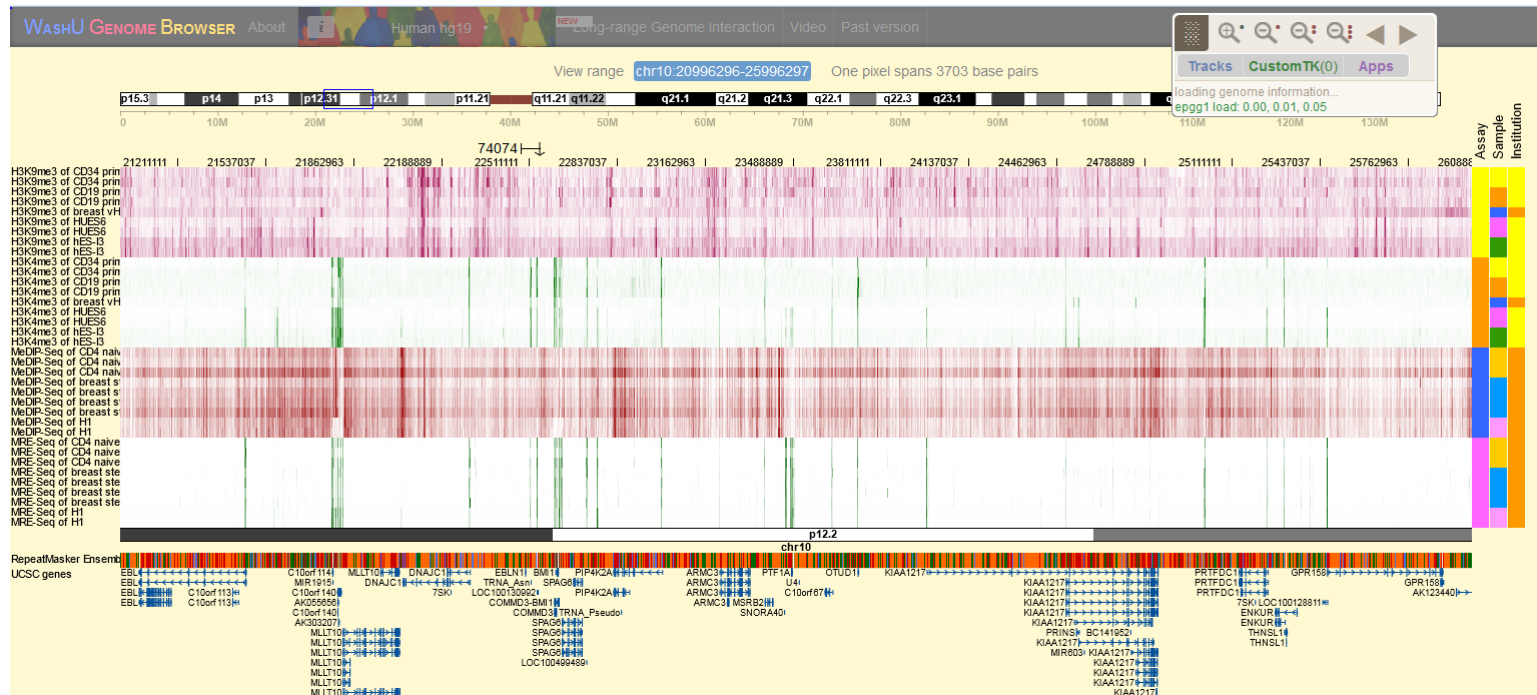
Simple Nucleotide Polymorphisms												
Details: The table contains SNP information from dbSNP (build 131) for both coding and non-coding SNPs. In addition, Conservation scores when available, is presented for coding non-synonymous (missense) SNPs, while enhancers, ICFs, along with other data are shown for non-coding SNPs.												
Chr	dbSNP name	Strand	Observed	Class	Insulation	Function	Strand type			Pop		
								all	pop	all	all	
chr11	rs2274007	-	A/T	single	By-cluster/By-frequency/By-2	coding-synon	genomic			0	0	
chr11	rs2274007	-	G/T	single	By-cluster/By-frequency/By-4	coding-synon	genomic			0	0	
chr11	rs7943704	-	G/T	single	unknown	coding-synon	genomic			0	0	
chr11	rs7200124	-	A/G	single	By-cluster/By-1000genomes	missense	genomic	DBPOL		400	A	0

Genome Browser screenshots and brief description (WashU)

WashU Genome Browser

web-based visual exploration of genomics and epigenomics data sets

<http://epigenomegateway.wustl.edu/browser>



IGB: Integrated Genome Browser (<http://www.bioviz.org/igb/>)

The Integrated Genome Browser (IGB, pronounced Ig-Bee) is an interactive, zoomable, scrollable software program you can use to visualize and explore genome-scale data sets, such as tiling array data, next-generation sequencing results, genome annotations, microarray designs, and the sequence itself. IGB is implemented using the Java programming language and should run on any computer.

IGB is an open source, publicly-funded project, but it did not start out that way. Initial development of the software was largely funded by Affymetrix, Inc., which donated the IGB software to the community in 2005. Since then, community developers have continued to contribute their time and efforts to improving the software. In 2008, funding from National Science Foundation has allowed us to speed up the pace of development.

IGB interacts with DAS (distributed annotation system servers)

DAS (http://www.biodas.org/wiki/Main_Page)

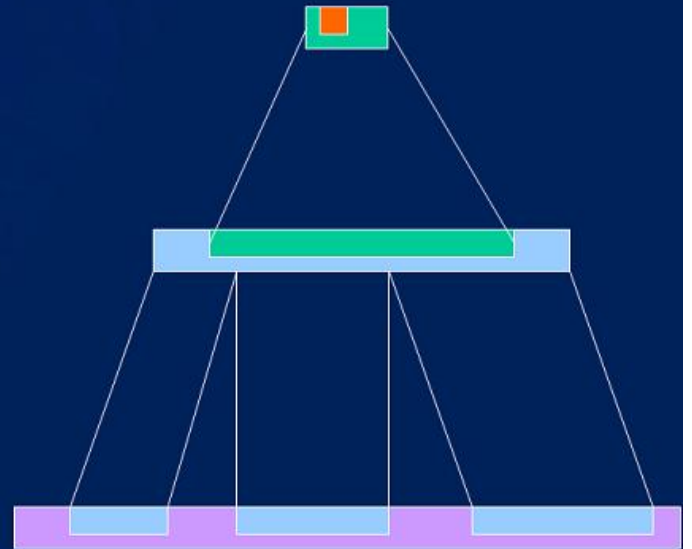
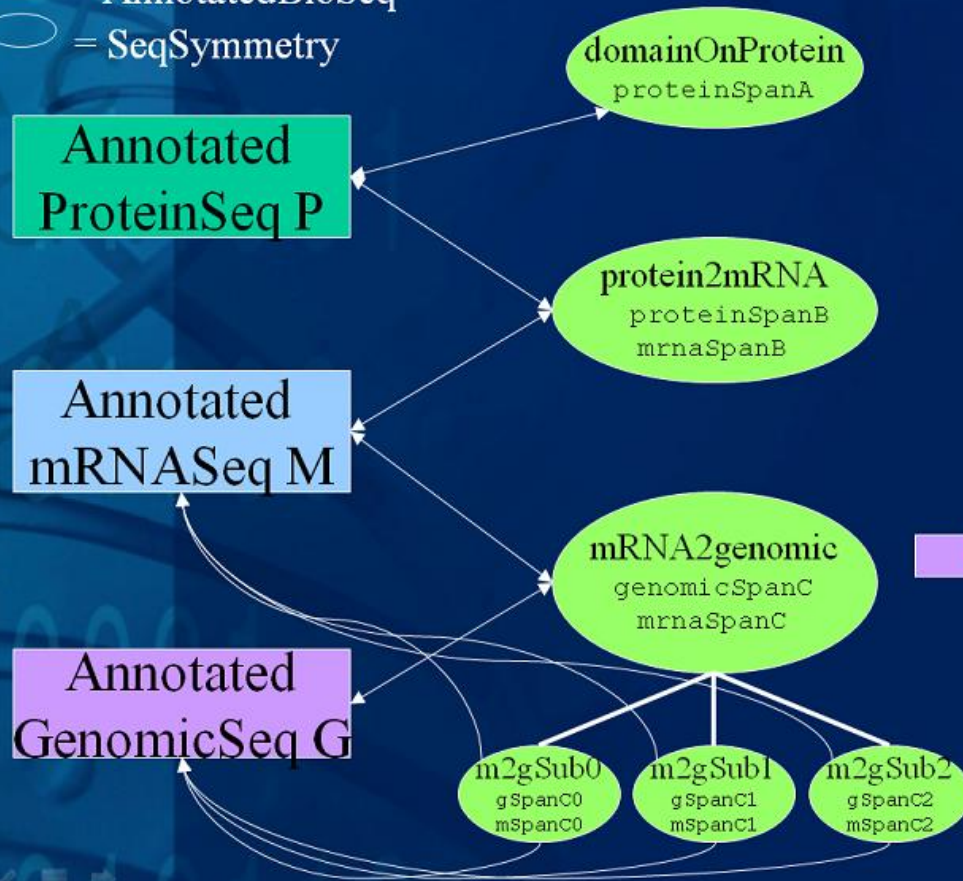
(DAS) defines a communication protocol used to exchange annotations on genomic or protein sequences. It is motivated by the idea that such annotations should not be provided by single centralized databases, but should instead be spread over multiple sites.

DAS/2 built to address the needs of distributing massive genomic data sets derived from high density microarray applications and Next (and Next Next) Generation Sequencing. Unlike DAS/1, DAS/2 does not require data exchange through text based XML but allows for data distribution using any text or binary format.

Annotation Networks

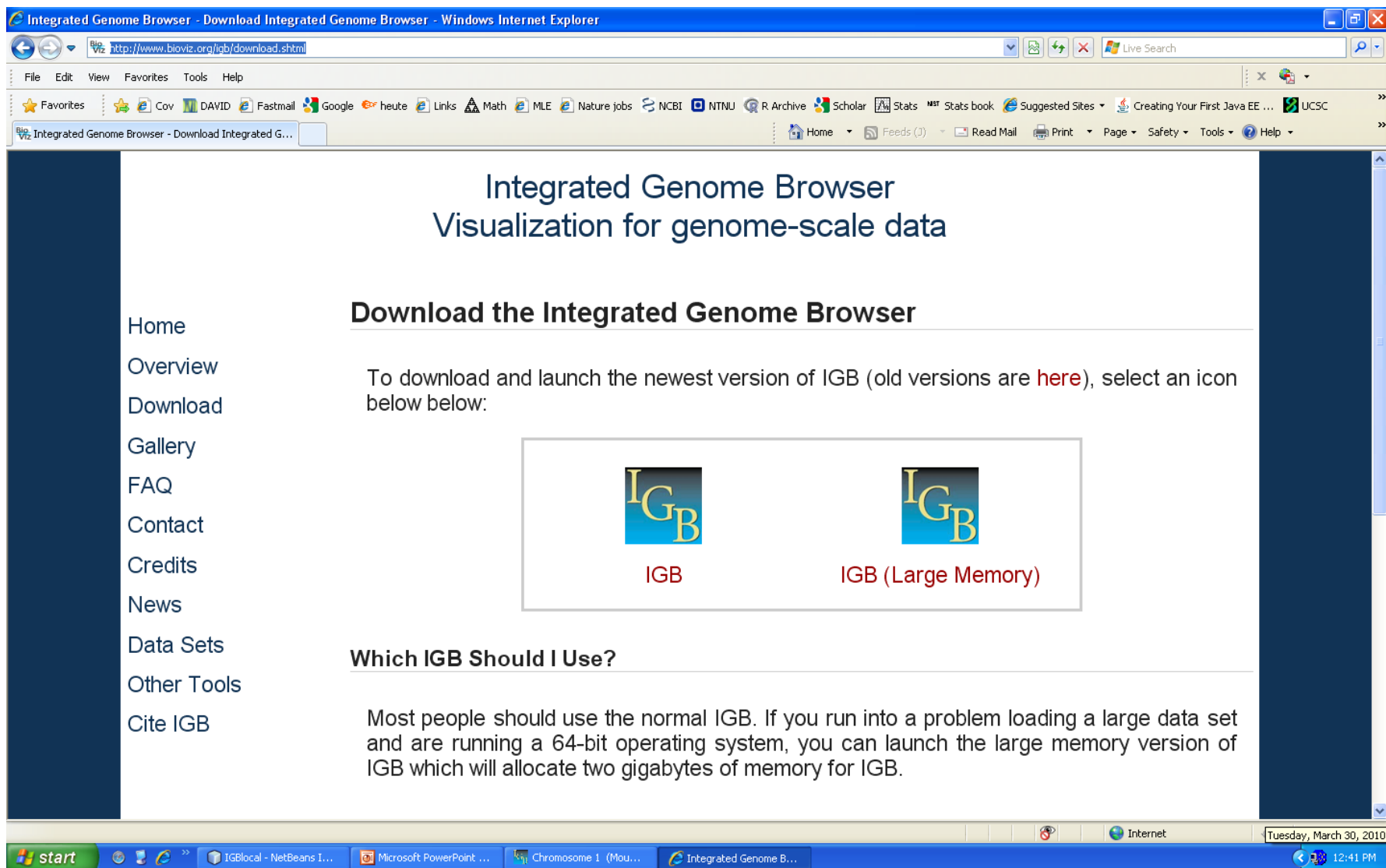
- Can traverse networks of annotations, alternating between AnnotatedBioSeqs and SeqSymmetries

 = AnnotatedBioSeq
 = SeqSymmetry



How to launch IGB

URL: <http://www.bioviz.org/igb/download.shtml>




The screenshot shows a Windows Internet Explorer browser window with the address bar displaying <http://www.bioviz.org/igb/download.shtml>. The page content is as follows:

Integrated Genome Browser Visualization for genome-scale data

Download the Integrated Genome Browser

To download and launch the newest version of IGB (old versions are [here](#)), select an icon below below:



The image shows two IGB logos side-by-side. The first logo is labeled 'IGB' and the second is labeled 'IGB (Large Memory)'. Both logos consist of the letters 'IGB' in a stylized font, with 'I' and 'G' in blue and 'B' in yellow, set against a dark blue square background.

Which IGB Should I Use?

Most people should use the normal IGB. If you run into a problem loading a large data set and are running a 64-bit operating system, you can launch the large memory version of IGB which will allocate two gigabytes of memory for IGB.

The browser window also shows a sidebar on the left with the following navigation links: Home, Overview, Download, Gallery, FAQ, Contact, Credits, News, Data Sets, Other Tools, and Cite IGB. The Windows taskbar at the bottom shows the Start button and several open applications: IGBlocal - NetBeans I..., Microsoft PowerPoint ..., Chromosome 1 (Mou..., and Integrated Genome B... The system tray shows the date and time as Tuesday, March 30, 2010, 12:41 PM.

IGB after startup

The screenshot displays the Integrated Genome Browser (IGB) interface for Chromosome 1 (Mouse mm8, Mar 2006). The main view shows a genomic track with RefSeq annotations (green vertical lines) and cytoband annotations (black and white bars) along the chromosome. The coordinates range from 0 to 180,000,000. The interface includes a menu bar (File, Edit, View, Bookmarks, Tools, Help), a search bar, and a toolbar with various view options (Data Access, Selection Info, Search, Sliced View, Graph Adjuster, Restriction Sites, External View). The bottom panel shows the 'Choose Data Sources and Data Sets' section, where 'NetAffx (DAS2)' is selected as the data source for 'refseq' and 'cytobands'. The 'Current Sequence' table is also visible.

Sequence	Length
chr1	197069962
chr2	181976762
chr3	159872112
chr4	155029701
chr5	152003063
chr6	149525685
chr7	145134094
chr8	132085098

Refseq and cytoband annotations automatically loaded from NetAffx DAS2

Data access tab

Data Access | Selection Info | Search | Sliced View | Graph Adjuster | Restriction Sites | External View

Choose: Mus musculus | M_musculus_Mar_2006

Choose Data Sources and Data Sets: [Configure...](#)

Choose Load Mode for Data Sets:

Choose Load Mode	Data Set	Data Source
Region In View	Amati/Giovanni_...	localDAS2 (DAS2)
Don't Load	__cytobands	NetAffx (DAS2)
Region In View	refseq	NetAffx (DAS2)
Whole Chromosome		

Current Sequence

Sequence	Length
chr1	197069962
chr2	181976762
chr3	159872112
chr4	155029701
chr5	152003063
chr6	149525685
chr7	145134094
chr8	132085098
chr9	124000669
chr10	129959148
chr11	121798632
chr12	120463159
chr13	120614378
chr14	123978870
chr15	103492577
chr16	98252459
chr17	95177420

NetAffx (DAS2) | NetAffx (QuickLoad) | UCSC (DAS) | local (QuickLoad) | localDAS2 (DAS2)

- Amati
 - Giovanni_Faga
 - mycC_peak ⓘ
 - mycC_track ⓘ
 - mycP_peak ⓘ
 - mycP_track ⓘ
 - mycT_peak ⓘ
 - mycT_track ⓘ

Load All Sequence
Load Sequence In View
Refresh Data

Search tab

refseq (+)

Coordinates

refseq (-)

Gluld1

4931428L18Rik

qA5
 1,137,700 31,137,720 31,137,740 31,137,760 31,137,780 31,137,800

ataatgc atgtataaac tgc cagtgc atacc gagg tca tggg acaca tagag atc agatc agatg gaga acttt ggag agtctc tttcca tttt ggggt aagg agatc caaact

31,137,773

Data Access
Selection Info
Search
Sliced View
Graph Adjuster
Restriction Sites
External View

Find Annotations For *M_musculus_Mar_2006*

Search Matching residues in chr1 for cacatagaga
Search
 also search remotely (2 servers)

ID	Tier	Start	End	Chromosome	Strand
Matching IDs					
Matching residues					

Search for cacatagaga on chr1: Working...

Selection info tab

Data Access Selection Info Search Sliced View Graph Adjuster Restriction Sites External View		
property	http://localhost:8080/genopub/genome/M_musculus_Mar_2006/Amati/Giova...	NM_153601
gene name		Glud1
id	http://localhost:8080/genopub/genome/M_musculus_Mar_2006/Amati/Giova...	NM_153601
chromosome	chr1	chr1
start	0	31,120,980
end	197,069,962	31,149,270
length	197,069,962	28,290
min score	0.0	
max score	11.0	
type		http://netaffxdas.affymetrix.com/das2/genome/M_musculus_Mar_2006/refseq
cds min		31120996
cds max		31149076
originatingDataSource	C:\quickload\useq\mycC.bedGraph4	
dataType	graph	
archiveCreationDate	Mon Mar 22 13:08:33 CET 2010	
Graph Strand	2	
forward		true
initialGraphStyle	Stairstep	
versionedGenome	M_musculus_Mar_2006	
useqArchiveVersion	1.0	

Sliced view tab

The screenshot displays the Integrated Genome Browser (IGB) interface for Chromosome 1 (Mouse mm8, Mar 2006). The main window shows the gene structure of the *Ugt1a* gene family, including exons and introns, with a coordinate scale from 89,861,556 to 90,217,546. The sliced view tab is active, showing a zoomed-in view of the gene structure with a coordinate scale from 0 to 3,308. The sliced view displays alternative splice variants and ORF analysis, with a coordinate scale from 0 to 3,308. The sliced view shows the gene structure with exons and introns, and a coordinate scale from 0 to 3,308. The sliced view displays alternative splice variants and ORF analysis, with a coordinate scale from 0 to 3,308.

Chromosome 1 (Mouse mm8 (Mar 2006)) - Integrated Genome Browser 6.1

File Edit View Bookmarks Tools Help

89,861,556 : 90,217,546 Refresh data

refseq (+)

Coordinates 000 89,900,000 89,950,000 90,000,000 90,050,000 90,100,000 90,150,000 90,200,000

refseq (-)

90,086,684

Data Access Selection Info Search Sliced View Graph Adjuster Restriction Sites External View

0 : 3,308 Refresh data

refseq (+)

Coordinates 0 500 1,000 1,500 2,000 2,500 3,000

1,654

Slice By Selection Slice Buffer: 10 Analyze ORFs Min ORF Length: 300

244.4 MB / 966.7 MB 12:48 PM

Sliced view to interrogate alternative splice variants, ORF analysis.

Graph adjuster tab

Data Access Selection Info Search Sliced View **Graph Adjuster** Restriction Sites External View

Select All Graphs Save Selected Graphs... Delete Selected Graphs Graph Thresholding...

Style

Color

Bar Line
 Dot Min/Max/Avg
 Heat Map Stairstep

Black/White

Y-Axis Scale

By Value (together) By Percentile (individually)

Min: 0
Max: 11

Height

Advanced

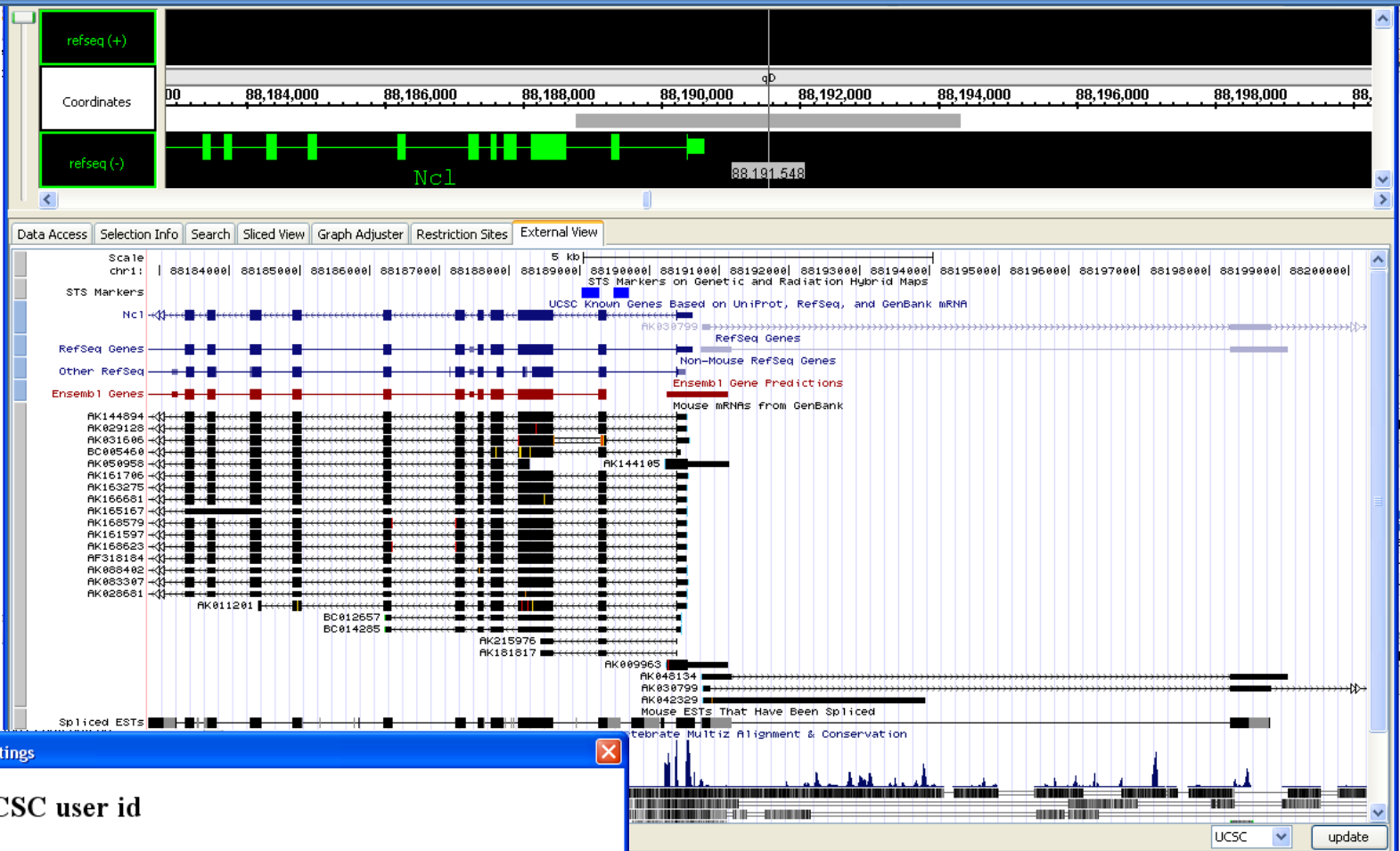
Label Y Axis Floating

Transformation:
Copy

Join Split

Combine: $A + B$ $A - B$ $A * B$ A / B

External view tab



Customize UCSC settings

Setting the UCSC user id

Using the UCSC user id you can customize the UCSC Viewer settings with your browser.

1. Obtain your user id by clicking on the "UCSC info" button.
Or open <http://genome.ucsc.edu/cgi-bin/cartDump> in your browser
2. Then scroll down in the opened window and copy the value of hguid into the "UCSC user id" field.
3. Click the submit button.
4. Your IGB UCSC View is now synchronized with you browser track configuration. The settings in your browser now change the view.

UCSC info UCSC user id (hguid): 154684160

submit

Data access tab

Data Access Selection Info Search Sliced View Graph Adjuster Restriction Sites External View

Choose: Mus musculus M_musculus_Mar_2006

Choose Data Sources and Data Sets: Configure...

- NetAffix (DAS2)
- NetAffix (QuickLoad)
- UCSC (DAS)
- local (QuickLoad)
- localDAS2 (DAS2)
 - Amati
 - Giovanni_Faga
 - mycC_peak
 - mycC_track
 - mycP_peak
 - mycP_track
 - mycT_peak
 - mycT_track

Choose Load Mode for Data Sets:

Choose Load Mode	Data Set	Data Source
Region In View	Amati/Giovanni_...	localDAS2 (DAS2)
Don't Load	__cytobands	NetAffix (DAS2)
Region In View	refseq	NetAffix (DAS2)
Whole Chromosome		

Current Sequence

Sequence	Length
chr1	197069962
chr2	181976762
chr3	159872112
chr4	155029701
chr5	152003063
chr6	149525685
chr7	145134094
chr8	132085098
chr9	124000669
chr10	129959148
chr11	121798632
chr12	120463159
chr13	120614378
chr14	123978870
chr15	103492577
chr16	98252459
chr17	95177420

Load All Sequence Load Sequence In View Refresh Data

To load data:

**Click desired data set, choose region in view or whole chromosome,
Click refresh data.**

Load Affy probesets in View

Chromosome 1 (Mouse mm8 (Mar 2006)) - Integrated Genome Browser 6.1

File Edit View Bookmarks Tools Help

89,861,556 : 90,217,546 Refresh data

afly/Mouse430_2

refseq (+)

Coordinates

refseq (-)

afly/Mouse430_2

Data Access Selection Info Search Sliced View Graph Adjuster Restriction Sites External View

Choose: Mus musculus M_musculus_Mar_2006

Choose Data Sources and Data Sets: Configure...

Choose Load Mode for Data Sets:

Choose Load Mode	Data Set	Data Source
Region In View	afly/Mouse430_2 netaffx consensus	NetAffx (DAS2)
Whole Genome	__cytobands	NetAffx (DAS2)
Whole Genome	refseq	NetAffx (DAS2)

Load All Sequence Load Sequence In View Refresh Data

Current Sequence

Sequence	Length
chr1	197069962
chr2	181976762
chr3	159872112
chr4	155029701
chr5	152003063
chr6	149525685
chr7	145134094
chr8	132085098
chr9	124000669

75.4 MB / 966.7 MB

start IGBlocal - NetBeans I... Microsoft PowerPoint ... Chromosome 1 (Mou... Integrated Genome B... 1:09 PM

NetAffx and UCSC mm8 annotations

- NetAffx (DAS2)
 - _cytobands
 - affy
 - MOE430A netaffx consensus
 - MoGene-1_0-st-v1-Probes
 - MoGene-1_0-st-v1-Transcripts
 - Mouse430A_2 netaffx consensus
 - Mouse430_2 netaffx consensus
 - genscan
 - knownGene
 - miRNA
 - refseq

- NetAffx (QuickLoad)
 - knownGene
 - refseq
 - mrna
 - mgcGenes
 - genscan
 - cytoBand
 - miRNA

- UCSC (DAS)
 - NIAGene
 - affyAllExonProbes
 - affyExonTissues
 - affyGnf1m
 - affyGnfU74A
 - affyGnfU74B
 - affyGnfU74C
 - affyMOE430
 - affyU74
 - allenBrainAli
 - bacEndPairs
 - broadStemChipHmmSitesH3K20me3Es
 - broadStemChipHmmSitesH3K27me3Es
 - broadStemChipHmmSitesH3K36me3Es
 - broadStemChipHmmSitesH3K4me3Es
 - broadStemChipHmmSitesH3K9me3Es
 - broadStemChipSignalH3Es
 - broadStemChipSignalH3K27Es
 - broadStemChipSignalH3K27Mef
 - broadStemChipSignalH3K27Np
 - broadStemChipSignalH3K27me3Brain
 - broadStemChipSignalH3K36Es
 - broadStemChipSignalH3K36EsHyb
 - broadStemChipSignalH3K36Mef
 - broadStemChipSignalH3K36Np
 - broadStemChipSignalH3K4Es
 - broadStemChipSignalH3K4EsHyb
 - broadStemChipSignalH3K4Mef
 - broadStemChipSignalH3K4Np
 - broadStemChipSignalH3K4me1Es
 - broadStemChipSignalH3K4me1Np
 - broadStemChipSignalH3K4me2Brain
 - broadStemChipSignalH3K4me2Es
 - broadStemChipSignalH3K4me2Np
 - broadStemChipSignalH3K4me3Brain
 - broadStemChipSignalH3K9Es

- broadStemChipWinSitesH3K9me3Np
- ccdsGene
- cgapSage
- est
- intronEst
- mrna
- contrastGene
- cpgIslandExt
- cytoBand
- cytoBandIdeo
- ensGene
- gc5Base
- geneid
- genomicSuperDups
- genscan
- gnfAtlas2
- igtc
- jaxAllele
- jaxPhenotype
- jaxQtl
- jaxRepTranscript
- knownGene
- mgcFullMrna
- miRNA
- microsat
- multiz17way
- nscanGene
- phastConsElements17way
- refGene
- regPotential7X
- rinnSex
- sgpGene
- sibGene
- sibTxGraph
- snp126
- stsMapMouseNew
- wssdCoverage
- xenoMrna
- xenoRefGene

NetAffx and UCSC mm9 annotations

NetAffx (DAS2)

- __cytobands
- acembly
- affy
 - MG_U74A netaffx consensus
 - MG_U74Av2 netaffx consensus
 - MG_U74B netaffx consensus
 - MG_U74Bv2 netaffx consensus
 - MG_U74C netaffx consensus
 - MG_U74Cv2 netaffx consensus
 - MOE430A netaffx consensus
 - MOE430B netaffx consensus
 - MoEx-1_0-st-v1-Probes
 - MoEx-1_0-st-v1-Transcripts
 - MoGene-1_0-st-v1-Probes
 - MoGene-1_0-st-v1-Transcripts
 - Mouse430A_2 netaffx consensus
 - Mouse430_2 netaffx consensus
 - Mu11KsubA netaffx consensus
 - Mu11KsubB netaffx consensus
- geneid
- genscan
- knownGene
- mgcGenes
- miRNA
- mrna
- refseq

NetAffx (QuickLoad)

- knownGene
- refseq
- mrna
- mgcGenes
- genscan
- cytoBand
- miRNA
- acembly
- ensGene
- geneid

UCSC (DAS)

- NIAGene
- acembly
- affyAllExonProbes
- affyExonTissues
- affyGnf1m
- affyGnfU74A
- affyGnfU74B
- affyGnfU74C
- affyMOE430
- affyU74
- agilentCgh105a
- agilentCgh244a
- agilentCgh44k
- allenBrainAli
- bacEndPairs
- blastHg18KG
- ccdsGene
- est
- intronEst
- mrna
- cpgIslandExt
- cytoBand
- cytoBandIdeo
- ensGene
- exoniphy
- gc5Base
- geneid
- genscan
- gnfAtlas2
- igt
- jaxAllele
- jaxPhenotype
- jaxQtl
- jaxRepTranscript
- knownAlt

Additional Annotations

- knownAlt
- knownGene
- komp
- mgcFullMrna
- miRNA
- microsat
- multiz30way
- nscanGene
- oregonno
- phastConsElements30way
- phastConsElements30wayEuarch
- phastConsElements30wayPlacental
- refGene
- rest
- sgpGene
- sibTxGraph
- snp128
- stsMapMouseNew
- transMapAlnMRna
- transMapAlnRefSeq
- transMapAlnSplicedEst
- transMapAlnUcscGenes
- transcriptome
- vegaGene
- vegaPseudoGene
- wgEncodeNhgrBip
- xenoMrna
- xenoRefGene

NetAffx and UCSC hg18 annotations

HughesLab (QuickLoad) ← **new server**

- ucsc-genes
- 014841-features
- NetAffx** (DAS2)
- NetAffx** (QuickLoad)
- UCSC** (DAS)
 - hInvGeneMrna
 - acembly
 - acescan
 - affyAllExonProbes
 - affyExonTissues
 - affyGnf1h
 - affyRatio
 - affyTxnPhase3FragHDF
 - affyTxnPhase3FragHeLaBottomStrand
 - affyTxnPhase3FragHeLaCyto
 - affyTxnPhase3FragHeLaNuclear
 - affyTxnPhase3FragHeLaTopStrand
 - affyTxnPhase3FragHepG2BottomStrand
 - affyTxnPhase3FragHepG2Cyto
 - affyTxnPhase3FragHepG2Nuclear
 - affyTxnPhase3FragHepG2TopStrand
 - affyTxnPhase3FragJurkat
 - affyTxnPhase3FragNCCIT
 - affyTxnPhase3FragPC3
 - affyTxnPhase3FragSK_N_AS
 - affyTxnPhase3FragU87MG
 - affyTxnPhase3HDF
 - affyTxnPhase3HeLaBottomStrand
 - affyTxnPhase3HeLaCyto
 - affyTxnPhase3HeLaNuclear
 - affyTxnPhase3HeLaTopStrand
 - affyTxnPhase3HepG2BottomStrand
 - affyTxnPhase3HepG2Cyto
 - affyTxnPhase3HepG2Nuclear
 - affyTxnPhase3HepG2TopStrand
 - affyTxnPhase3Jurkat
 - affyTxnPhase3NCCIT
 - affyTxnPhase3PC3
 - affyTxnPhase3SK_N_AS
 - affyTxnPhase3U87MG
 - affyU133
 - affyU133Plus2
 - affyU95

- affyU95
- agilentCgh105a
- agilentCgh1x1m
- agilentCgh244a
- agilentCgh2x400k
- agilentCgh44k
- agilentCgh4x180k
- agilentCgh8x60k
- agilentCnv2x105k
- agilentCnv2x400k
- agilentHrd1x1m
- allenBrainAli
- augustusAbinitio
- augustusHints
- augustusXRA
- bacEndPairs
- ccdsGene
- cgapSage
- est
- intronEst
- mrna
- rmskRM327
- cnpIafrate2
- cnpLocke
- cnpRedon
- cnpSebat2
- cnpSharp2
- cnpTuzun
- consIndelsHgMmCanFam
- contrastGene
- cpGISlandExt
- cytoBand
- cytoBandIdeo
- delConrad2
- delHinds2
- delMcCarroll
- dgv
- ecoresTetNig1
- eioJcviNASNeg
- eioJcviNASPos
- encodeAffyChIpHl60PvalBrg1Hr00
- encodeAffyChIpHl60PvalBrg1Hr02
- encodeAffyChIpHl60PvalBrg1Hr08

- encodeAffyChIpHl60PvalCebpeHr08
- encodeAffyChIpHl60PvalCebpeHr32
- encodeAffyChIpHl60PvalCtcfHr00
- encodeAffyChIpHl60PvalCtcfHr02
- encodeAffyChIpHl60PvalCtcfHr08
- encodeAffyChIpHl60PvalCtcfHr32
- encodeAffyChIpHl60PvalH3K27me3Hr00
- encodeAffyChIpHl60PvalH3K27me3Hr02
- encodeAffyChIpHl60PvalH3K27me3Hr08
- encodeAffyChIpHl60PvalH3K27me3Hr32
- encodeAffyChIpHl60PvalH4Kac4Hr00
- encodeAffyChIpHl60PvalH4Kac4Hr02
- encodeAffyChIpHl60PvalH4Kac4Hr08
- encodeAffyChIpHl60PvalH4Kac4Hr32
- encodeAffyChIpHl60PvalP300Hr00
- encodeAffyChIpHl60PvalP300Hr02
- encodeAffyChIpHl60PvalP300Hr08
- encodeAffyChIpHl60PvalP300Hr32
- encodeAffyChIpHl60PvalPu1Hr00
- encodeAffyChIpHl60PvalPu1Hr02
- encodeAffyChIpHl60PvalPu1Hr08
- encodeAffyChIpHl60PvalPu1Hr32
- encodeAffyChIpHl60PvalRaraHr00
- encodeAffyChIpHl60PvalRaraHr02
- encodeAffyChIpHl60PvalRaraHr08
- encodeAffyChIpHl60PvalRaraHr32
- encodeAffyChIpHl60PvalRnapHr00
- encodeAffyChIpHl60PvalRnapHr02
- encodeAffyChIpHl60PvalRnapHr08
- encodeAffyChIpHl60PvalRnapHr32
- encodeAffyChIpHl60PvalSirt1Hr00
- encodeAffyChIpHl60PvalSirt1Hr02
- encodeAffyChIpHl60PvalSirt1Hr08
- encodeAffyChIpHl60PvalSirt1Hr32
- encodeAffyChIpHl60PvalStrictH3K9K14Dhr00
- encodeAffyChIpHl60PvalStrictH3K9K14Dhr02
- encodeAffyChIpHl60PvalStrictH3K9K14Dhr08
- encodeAffyChIpHl60PvalStrictH3K9K14Dhr32
- encodeAffyChIpHl60PvalStrictHisH4Hr00
- encodeAffyChIpHl60PvalStrictHisH4Hr02
- encodeAffyChIpHl60PvalStrictHisH4Hr08
- encodeAffyChIpHl60PvalStrictHisH4Hr32
- encodeAffyChIpHl60PvalStrictPol2Hr00

ChIPchip
 ChIPseq
 Exon array
 DNaseI
 RNA seq
 ChIP pet
 RNA pet
 Methyl seq
 Cage tags
 .
 .
 .
 Km of data

Server registration (data source) tab

Preferences Help

Tiers Shortcuts Graphs Other Options **Data Sources**

Data Sources

Name ▲	Type	URL	Enabled
Bioviz	DAS2	http://bioviz.org/das2/genome	<input checked="" type="checkbox"/>
Bioviz	QuickLoad	http://bioviz.org/quickload/	<input checked="" type="checkbox"/>
Ensembl	DAS	http://www.ensembl.org/das/dsn	<input type="checkbox"/>
HughesLab	QuickLoad	http://hugheslab.ccb.utoronto.ca/igb/	<input checked="" type="checkbox"/>
local	QuickLoad	file:///C:/quickload/	<input checked="" type="checkbox"/>
localDAS2	DAS2	http://localhost:8080/genopub/genome	<input checked="" type="checkbox"/>
NetAffx	DAS2	http://netaffxdas.affymetrix.com/das2/genome	<input checked="" type="checkbox"/>
NetAffx	QuickLoad	http://netaffxdas.affymetrix.com/quickload_data	<input checked="" type="checkbox"/>
UCSC	DAS	http://genome.cse.ucsc.edu/cgi-bin/das/dsn	<input checked="" type="checkbox"/>

Add... Authentication... Remove

Personal Synonyms

Synonyms File ...

Cache Settings

Cache Behavior ▼

Empty Cache

Data sources: Quickload, DAS, DAS2

Four types of data sources (files)

1. Single files

file type	extension
BAM	.bam
BED	.bed
Binary	.bps, .bgn, .brs, .bsnp, .brpt, .bnib, .bp1, .bp2, .ead, .useq
GFF	.gff, .gtf, .gff3
FASTA	.fa, .fasta, .fas
PSL	.psl, .psl3
DAS	.das, .dasxml, .das2xml
Graph	.gr, .bgr, .sgr, .bar, .chp, .wig
Scored Interval	.sin, .egr, .egr.txt
Copy number	.cnt
Copy number chp	.cnchp, .lohchp
Genomic variation (Toronto DB)	.var
Region (genotype console segmenter)	SegmenterRptParser.CN_REGION_FILE_EXT, SegmenterRptParser.LOH_REGION_FILE_EXT
FishClones	.fsh, FishClonesParser.FILE_EXT
Scored map	.map

2. Quickload (local directory with auxiliary files)

example <http://www.bioviz.org/quickload/>

Address: C:\quickload\M_musculus_Jul_2007

Name	Size	Type	Date Modified
annotations.txt	1 KB	Text Document	3/16/2010 11:36 AM
cytoBand.cyt	14 KB	CYT File	3/12/2010 6:03 PM
das_entry_response.xml	4 KB	XML Document	3/12/2010 6:03 PM
Gio_Affy.egr	2,345 KB	EGR File	3/16/2010 11:39 AM
knownGene.bgn	5,269 KB	BGN File	3/12/2010 6:06 PM
miRNA.bed	24 KB	BED File	3/12/2010 6:04 PM
mod_chromInfo.txt	2 KB	Text Document	3/12/2010 6:04 PM
mrna.bps	34,356 KB	BPS File	3/12/2010 6:13 PM
refseq.brs	2,895 KB	BRS File	3/12/2010 6:06 PM
sintest.sin	8 KB	SIN File	3/12/2010 7:28 PM

Easy to set up but can load data only into entire genome.

Four types of data sources (servers)

3. DAS(1) (example UCSC), (software <http://code.google.com/p/mydas/>)

Can load data into view of interest
response XML (problematic for large datasets)

4. DAS2 (example NetAffx), (software <http://genoviz.sourceforge.net/>)

Unlike DAS1, DAS2 does not require data exchange through text based XML but allows for data distribution using any text or binary format. The two versions are not natively compatible.

Can load data into view of interest in a range of different formats.

Loading BAM files from http listing (no need to move them)

Chromosome 1 (Mouse mm8 (Mar 2006)) - Integrated Genome Browser 6.1

File Edit View Bookmarks Tools Help

30,836,465 : 30,836,634

Refresh data Close

/ga-data/Analysis/M (+)

refseq (+)

Coordinates

refseq (-)

/ga-data/Analysis/M (-)

ILLUMINA-F3E58E:2:29:645:1142#0

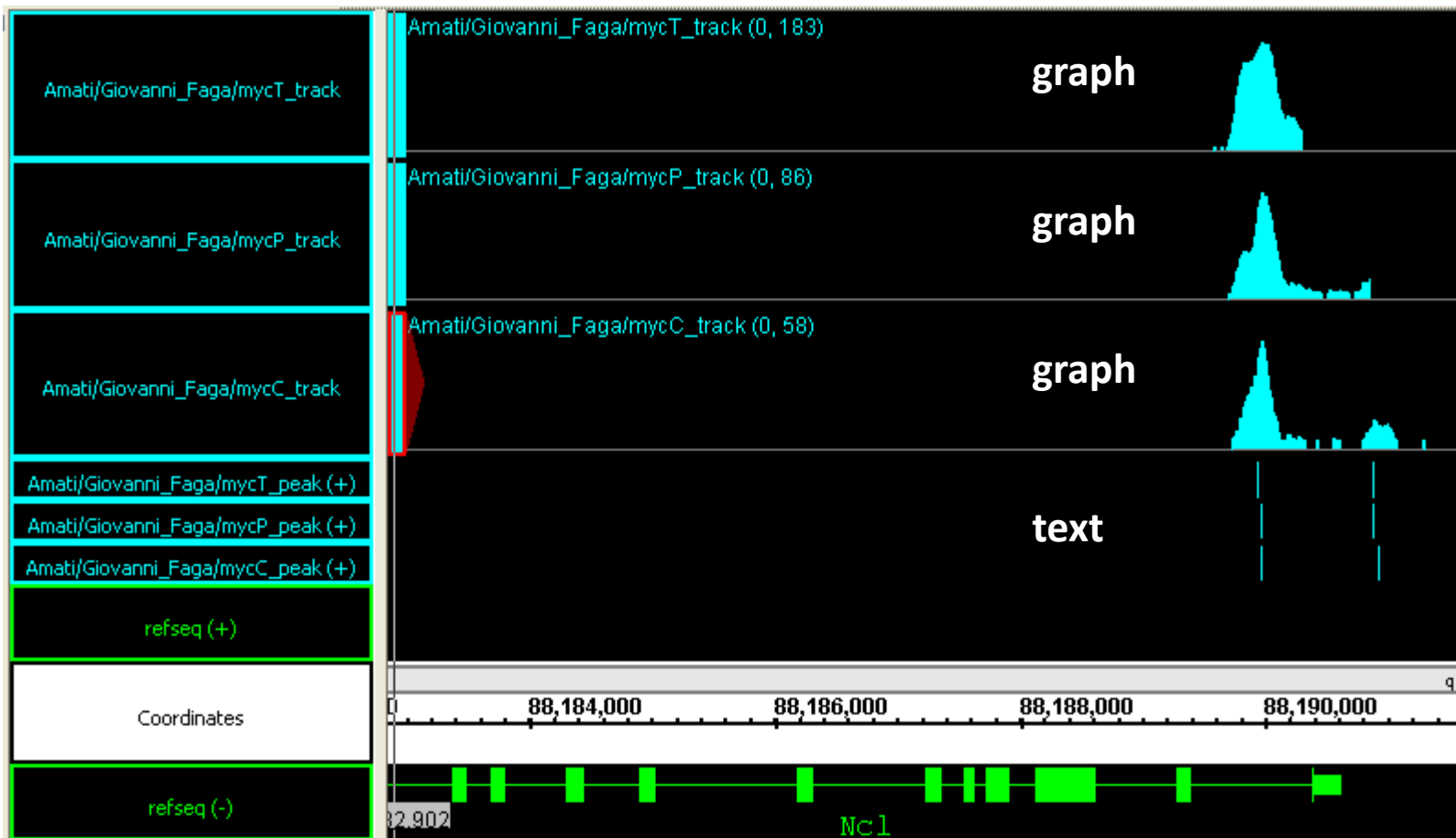
209.6 MB / 966.7 MB

start IGBlocal - NetBea... Microsoft Power... untitled - Paint C:\softwaredownl... Microsoft Excel - ... Tabbed Panes Chromosome 1 (... url.txt - Notepad 4:38 PM

The screenshot displays the Integrated Genome Browser interface. The main window shows a genomic track for Chromosome 1 (Mouse mm8) with read alignments. The tracks are labeled 'refseq (+)' and 'refseq (-)'. The coordinate scale at the bottom indicates positions from 30,836,460 to 30,836,620. The read alignments are color-coded by base pair (A, C, G, T) and show various alignment patterns, including mismatches and indels. The interface includes a menu bar (File, Edit, View, Bookmarks, Tools, Help) and a status bar at the bottom showing system information and open applications.

Two basic types of annotation

1. Graph based annotations (.gr, .bgr, .sgr, .bar, .chp, .wig, .sin, .egr, .egr.txt)
2. Text based annotations (e.g. .bed, .bam, .psl, .gff, .fasta files)



Permit different types of operations

Operations on text based annotations

Logical: intersect, union, A not B, B not A, Xor, Not

The screenshot shows the Integrated Genome Browser 6.1 interface. The main window displays a genomic track for Chromosome 1 (Mouse mm8, Mar 2006). The track is divided into several sections: 'all transcribed regions' (cyan bars), 'antisense transcription' (green bars), and 'refseq (+)' (red bars). A context menu is open over the 'refseq (+)' track, showing options: 'Combine Selected Tiers', 'Customize', 'Hide', 'Show...', 'Show All Types', 'Strands...', 'Select All Tiers', 'Change...', 'Collapse', 'Expand', 'Adjust Max Expand', 'Save Annotations', 'Make Annotation Depth Graph', and 'Make Annotation Coverage Track'. The 'Combine Selected Tiers' sub-menu is open, showing options: 'Intersect', 'Union', 'A not B', 'B not A', 'Xor', and 'Not'. The browser title is 'Chromosome 1 (Mouse mm8 (Mar 2006)) - Integrated Genome Browser 6.1'. The browser address bar shows '0 : 197,069,962'. The browser status bar shows 'Choose: Mus musculus' and 'M_musculus_Mar_2006'. The browser tabs include 'Data Access', 'Selection', 'Restriction Sites', and 'External View'. The browser current sequence is 'Current Sequence'.

Select tracks, right-click to access context-menu

Operations on graph based annotations

Scale: filter displayed values by value or by percentile

Height: adjust display height

Style: bar, line, dot, min/max/avg. heatmap, stairstep, color

transform: \log_{10} , \log_2 , \log_e , and inverses thereof

Join/split: display all graphs as one

arithmetic (requires identical X-values): sum, difference, product, division

Thresholding: transforms regions meeting given criterion into text-based annotation
(can then be used in logical operations)

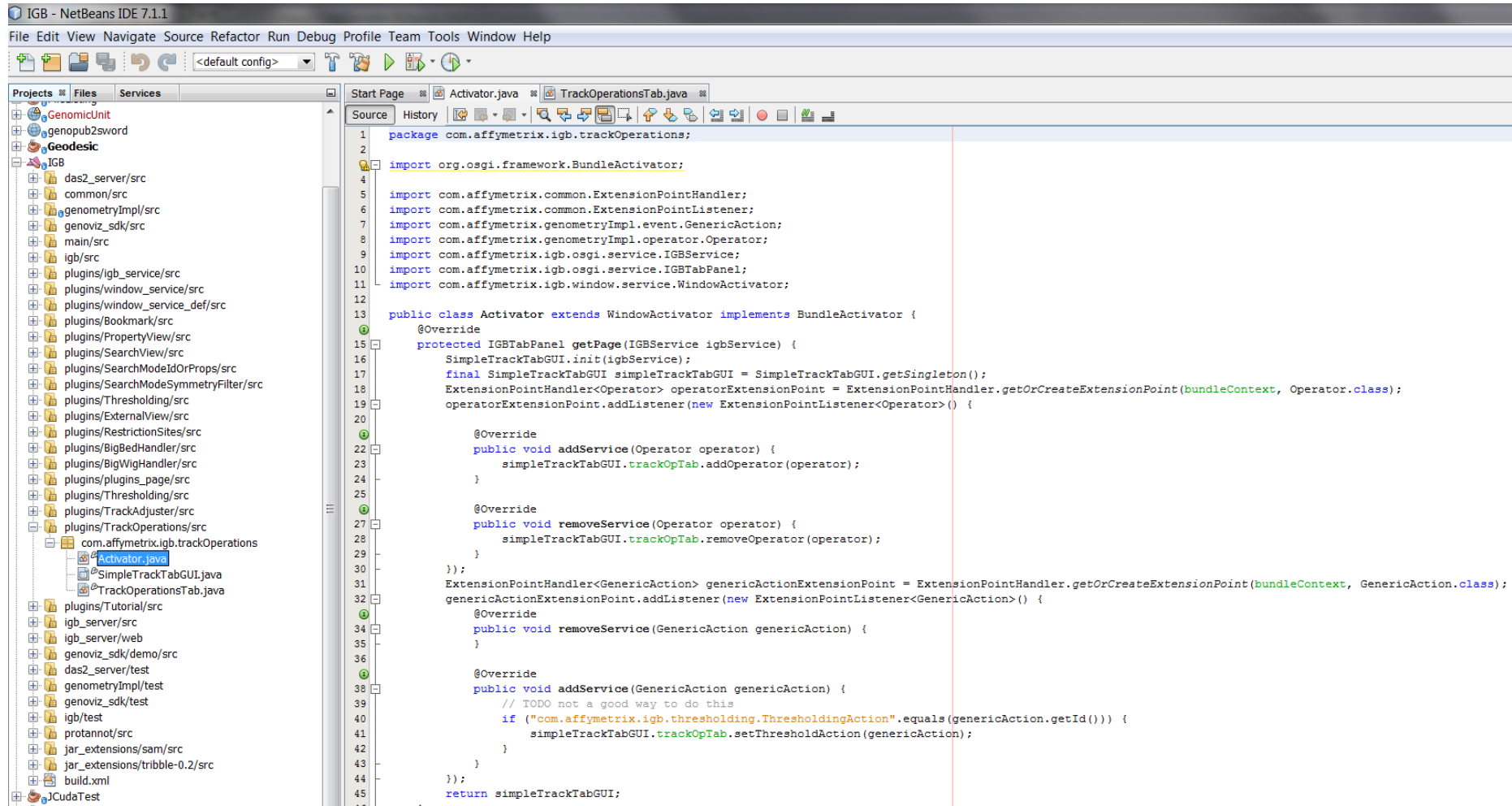
The screenshot shows the 'Graph Adjuster' tab in a software interface. The top navigation bar includes 'Data Access', 'Selection Info', 'Search', 'Sliced View', 'Graph Adjuster', 'Restriction Sites', and 'External View'. Below the navigation bar are several buttons: 'Select All Graphs', 'Save Selected Graphs...', 'Delete Selected Graphs', and 'Graph Thresholding...'. The main area is divided into several sections:

- Style:** Includes a 'Color' button and radio buttons for 'Bar', 'Line', 'Dot', 'Min/Max/Avg', 'Heat Map', and 'Stairstep' (which is selected). There is also a 'Black/White' dropdown menu.
- Y-Axis Scale:** Features two radio buttons: 'By Value (together)' (selected) and 'By Percentile (individually)'. Below these are input fields for 'Min:' (0) and 'Max:' (11), each with a corresponding slider.
- Height:** A slider control for adjusting the display height.
- Advanced:** Contains checkboxes for 'Label' (checked), 'Y Axis', and 'Floating'. Below this is a 'Transformation:' section with a dropdown menu set to 'Copy' and a 'Go' button. Further down are 'Join' and 'Split' buttons, and a 'Combine:' section with buttons for 'A + B', 'A - B', 'A * B', and 'A / B'.

Based on Open Services Gateway initiative (OSGI)

Data Access Selection Info Search Sliced View Track Adjuster Track Operations External View Plug-ins					
Installed	Name	Description	Version	Repository	
<input type="checkbox"/>	SampleSelection ⓘ	tab to allow the user to select sample data	1.0.0	Genentech	
<input type="checkbox"/>	TallyHandler ⓘ	plugin to allow the user to load tally files	1.0.0	Genentech	
<input type="checkbox"/>	FindAnnotations ⓘ	a simple search panel that uses all search modes.	0.1.9	Genentech development	
<input type="checkbox"/>	OverlapAnnotationOperator ⓘ	plugin to allow the user to find symmetries that overlap on two selected annotation tracks	0.0.9	Genentech development	
<input type="checkbox"/>	PythonScript	plugin to allow the user to run Python scripts in IGB	1.0.0	Genentech development	
<input type="checkbox"/>	RubyScript	plugin to allow the user to run Ruby scripts in IGB	1.0.0	Genentech development	
<input type="checkbox"/>	SearchModeLength ⓘ	search mode to allow searching on length of annotation	1.9.1	Genentech development	
<input type="checkbox"/>	SearchModeLucene ⓘ	plugin to allow the user to do a search using lucene indexes	0.1.9	Genentech development	
<input type="checkbox"/>	TranscriptIsoform ⓘ	BETA release of transcript isoform evidence visualization	0.0.9	Genentech development	

Implement Activator interface



The screenshot displays the NetBeans IDE interface with the following components:

- Projects View:** Shows a project structure for 'IGB' with various sub-projects and source folders. The 'com.affymetrix.igb.trackOperations' package is expanded, showing 'Activator.java' selected.
- Source Editor:** Displays the code for 'Activator.java'. The code implements the 'BundleActivator' interface and includes several imports and methods.

```
1 package com.affymetrix.igb.trackOperations;
2
3
4 import org.osgi.framework.BundleActivator;
5
6 import com.affymetrix.common.ExtensionPointHandler;
7 import com.affymetrix.common.ExtensionPointListener;
8 import com.affymetrix.genometryImpl.event.GenericAction;
9 import com.affymetrix.genometryImpl.operator.Operator;
10 import com.affymetrix.igb.osgi.service.IGBService;
11 import com.affymetrix.igb.osgi.service.IGBTabPanel;
12 import com.affymetrix.igb.window.service.WindowActivator;
13
14
15 public class Activator extends WindowActivator implements BundleActivator {
16     @Override
17     protected IGBTabPanel getPage(IGBService igbService) {
18         SimpleTrackTabGUI.init(igbService);
19         final SimpleTrackTabGUI simpleTrackTabGUI = SimpleTrackTabGUI.getSingleton();
20         ExtensionPointHandler<Operator> operatorExtensionPoint = ExtensionPointHandler.getOrCreateExtensionPoint(bundleContext, Operator.class);
21         operatorExtensionPoint.addListener(new ExtensionPointListener<Operator>() {
22
23             @Override
24             public void addService(Operator operator) {
25                 simpleTrackTabGUI.trackOpTab.addOperator(operator);
26             }
27
28             @Override
29             public void removeService(Operator operator) {
30                 simpleTrackTabGUI.trackOpTab.removeOperator(operator);
31             }
32         });
33         ExtensionPointHandler<GenericAction> genericActionExtensionPoint = ExtensionPointHandler.getOrCreateExtensionPoint(bundleContext, GenericAction.class);
34         genericActionExtensionPoint.addListener(new ExtensionPointListener<GenericAction>() {
35             @Override
36             public void removeService(GenericAction genericAction) {
37             }
38
39             @Override
40             public void addService(GenericAction genericAction) {
41                 // TODO not a good way to do this
42                 if ("com.affymetrix.igb.thresholding.ThresholdingAction".equals(genericAction.getId())) {
43                     simpleTrackTabGUI.trackOpTab.setThresholdAction(genericAction);
44                 }
45             }
46         });
47         return simpleTrackTabGUI;
48     }
49 }
```

Needed to display plugin in tab

Access tracks from Genometry model

IGB - NetBeans IDE 7.1.1

File Edit View Navigate Source Refactor Run Debug Profile Team Tools Window Help

<default config>

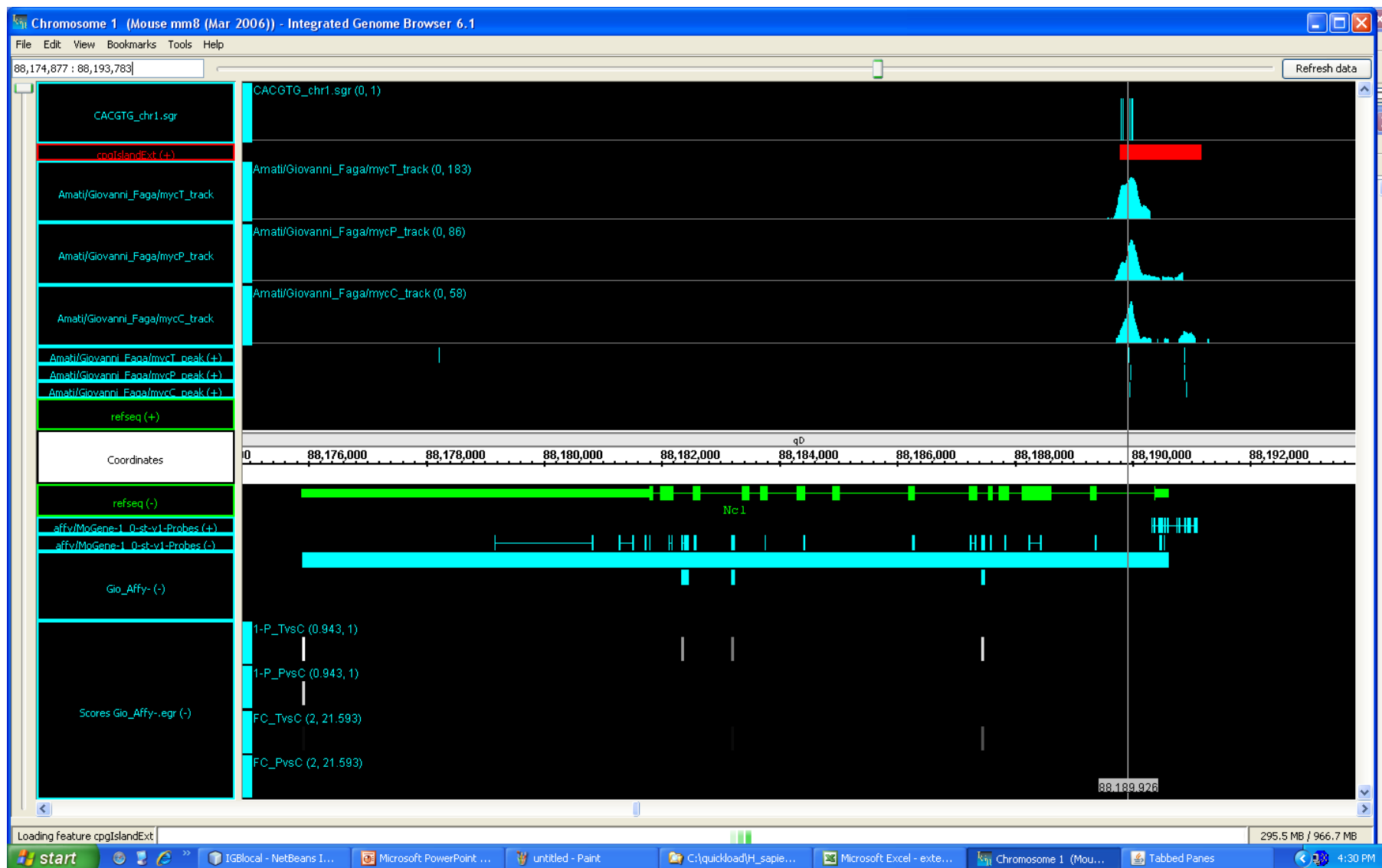
Projects Files Services

Start Page Activator.java TrackOperationsTab.java

```
48 boolean is_listening = true; // used to turn on and off listening to GUI events
49 boolean DEBUG_EVENTS = false;
50 public final List<GraphSym> grafs = new ArrayList<GraphSym>();
51 public final List<AbstractGraphGlyph> glyphs = new ArrayList<AbstractGraphGlyph>();
52 public final JRPCheckBox labelCB = new JRPCheckBox("SimpleGraphTab_hidden_labelCB", BUNDLE.getString("labelCheckBox"));
53 public final JRPCheckBox yaxisCB = new JRPCheckBox("SimpleGraphTab_hidden_yaxisCB", BUNDLE.getString("yAxisCheckBox"));
54 public final JRPCheckBox floatCB = new JRPCheckBox("SimpleGraphTab_hidden_floatCB", BUNDLE.getString("floatingCheckBox"));
55 public final JRPButton threshB = new JRPButton("SimpleGraphTab_threshB");
56 public final JRPTextField paramT = new JRPTextField("SimpleGraphTab_paramT", "", 2);
57 public final JRPButton combineB = new JRPButton("SimpleGraphTab_combineB", BUNDLE.getString("combineButton"));
58 public final JRPButton splitB = new JRPButton("SimpleGraphTab_splitB", BUNDLE.getString("splitButton"));
59 private IGBService igbService;
60 public AdvancedGraphPanel advanced_panel;
61
62 public void setThresholdAction(GenericAction thresholdAction) {
63     threshB.setAction(thresholdAction);
64 }
65
66 public static void init(IGBService igbService) {
67     singleton = new TrackOperationsTab(igbService);
68 }
69
70 public static synchronized TrackOperationsTab getSingleton() {
71     return singleton;
72 }
73
74 public TrackOperationsTab(IGBService igbS) {
75     igbService = igbS;
76     advanced_panel = new TrackOperationsTab.AdvancedGraphPanel();
77     resetSelectedGraphGlyphs(Collections.EMPTY_LIST);
78     gmodel = GenometryModel.getGenometryModel();
79     gmodel.addSeqSelectionListener(this);
80     gmodel.addSymSelectionListener(this);
81 }
82
83 public boolean isTierGlyph(GlyphI glyph) {
84     return glyph instanceof TierGlyph;
85 }
86
87 public void addOperator(Operator operator) {
88     advanced_panel.loadOperators();
89 }
90
91 public void removeOperator(Operator operator) {
92     advanced_panel.loadOperators();
93 }
```

Can perform arbitrary manipulations on tracks

Example: myc bound and differentially regulated gene



External view

Chromosome 1 (Mouse mm8 (Mar 2006)) - Integrated Genome Browser 6.1

File Edit View Bookmarks Tools Help

88,174,877 : 88,193,783 Refresh data

CACGTG_chr1.sgr CACGTG_chr1.sgr (0, 1)

Amati/Giovanni_Faga/mycT_track Amati/Giovanni_Faga/mycT_track (0, 183)

Amati/Giovanni_Faga/mycP_track Amati/Giovanni_Faga/mycP_track (0, 86)

Amati/Giovanni_Faga/mycC_track Amati/Giovanni_Faga/mycC_track (0, 58)

Amati/Giovanni_Faga/mycT_peak (A)

Amati/Giovanni_Faga/mycP_peak (A)

Amati/Giovanni_Faga/mycC_peak (A)

refseq (+)

Coordinates 0 88,176,000 88,178,000 88,180,000 88,182,000 88,184,000 88,186,000 88,188,000 88,190,000 88,192,000

refseq (-)

ssr/McGene_1_0_2chr1_Drsbc (1)

ssr/McGene_1_0_2chr1_Drsbc (2)

Gio_Affy (-)

1-P_TvsC (0.943, 1)

1-P_PvsC (0.943, 1)

FC_TvsC (2, 21.593)

FC_PvsC (2, 21.593)

88,189,926

Data Access Selection Info Search Sliced View Graph Adjuster Restriction Sites External View

STS Markers

RefSeq Genes

Other RefSeq

Ensembl Genes

Mouse mRNAs

Spliced ESTs

Conservation

UCSC Known Genes Based on UniProt, RefSeq, and GenBank mRNA

RefSeq Genes

Non-Mouse RefSeq Genes

Ensembl Gene Predictions

Mouse mRNAs from GenBank

Mouse ESTs That Have Been Spliced

Vertebrate Multiz Alignment & Conservation

human

mouse

opossum

chicken

X_tropicalis

tetraodon

settings

loading feature cpGIslandExt

CAMPUS update

269.2 MB / 966.7 MB

start IGBlocal - NetBeans I... Microsoft PowerPoint ... untitled - Paint C:\quickload\H_saple... Microsoft Excel - exte... Chromosome 1 (Mou... 4:29 PM

IGB summary

Highly interactive

Excellent logarithmic zooming around hairline

Integrated with UCSC/campus browser

Can do logical/arithmetic operations on annotations

Can create custom annotations on the fly

Can incorporate distributed annotations

Easily customizable display options

Open-source: new features can be added according to our needs