

Upgraded genome browsers at the Rat Genome Database support comparative and translational studies

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RGD is a multi-species knowledgebase

- Ten species: Human plus nine species used as models for human disease
- Standardized annotations for disease, qualitative and quantitative phenotypes, pathway, gene ontology, and gene-chemical interactions
- RGD has developed a suite of tools for finding and analyzing these data

RGD is upgrading to JBrowse 2

- Currently released as a beta version
- Implemented for all RGD species
- Shares many features with other browsers
 - Search for the name or ID of a genome feature and go directly to that region
 - Select and view multiple data types in a single view
 - Easy zooming and navigation across a chromosome
- Provides expanded functionality designed to facilitate comparative studies
- <https://rgd.mcw.edu/jbrowse2/>



Comparison of JBrowse 1 and JBrowse 2

Gene Tracks (Gene Models from both NCBI and Ensembl)

Disease-related tracks based on RGD's Disease annotations

Strain-specific variant tracks, plus new European Variant Archive consolidated variant track

All of the data types available in RGD's JBrowse 1 browsers are available in JBrowse 2...and more

New data types in JBrowse 2

Available tracks

Filter tracks

Tracks ...

- Reference sequence (mRatBN7.2 (r7)) ...
- ▶ Disease Related Tracks ...
- Epigenetics ...
 - ▶ ATAC-Seq ...
 - ▶ CHIP-Seq ...
- Gene Models ...
 - Ensembl Gene Features ...
 - Ensembl (mRatBN7.2.110) Features ...
 - Ensembl (mRatBN7.2.110) Model ...
 - NCBI Gene Features ...
 - Rat mRatBN7.2 (r7) Genes and Transcripts ...
 - Rat mRatBN7.2 (r7) Genes Only ...
 - Rat mRatBN7.2 (r7) Protein Domains ...
- ▶ Gene-Chemical Interaction Tracks ...
- ▶ QTLs ...
- ▶ RNA-Seq ...
- ▶ Strains ...
- ▶ Synteny ...
- Variants ...
 - ▶ Damaging Variants ...
 - ▶ European Variation Archive ...
 - ▶ Micro Satellite Markers ...
 - ▶ Phenotypic Alleles Variants ...
 - ▶ Strain Specific Variants ...

Epigenetics ...

▶ ATAC-Seq ...

ATAC-Seq peaks and alignments for liver and peaks for an additional 24 organs

▶ CHIP-Seq ...

ChIP-Seq peaks for methylation and acetylation marks and TF binding sites in liver and denervated and non-denervated gastrocnemius muscle

Synteny ...

- m7.2 to canFam3 Synteny ...
- m7.2 to hg38 Synteny ...
- m7.2 to mm39 Synteny ...
- m7.2 to rn3.4 Synteny ...
- m7.2 to rn5 Synteny ...
- m7.2 to rn6 Synteny ...
- m7.2 to susScr11 Synteny ...
- m7.2 to UTH_Rnor_SHR_Utx Synteny ...
- m7.2 to UTH_Rnor_SHRSP_BbbUtx_1.0 Synteny ...
- m7.2 to UTH_Rnor_WKY_Bbb_1.0 Synteny ...

New data types in JBrowse 2



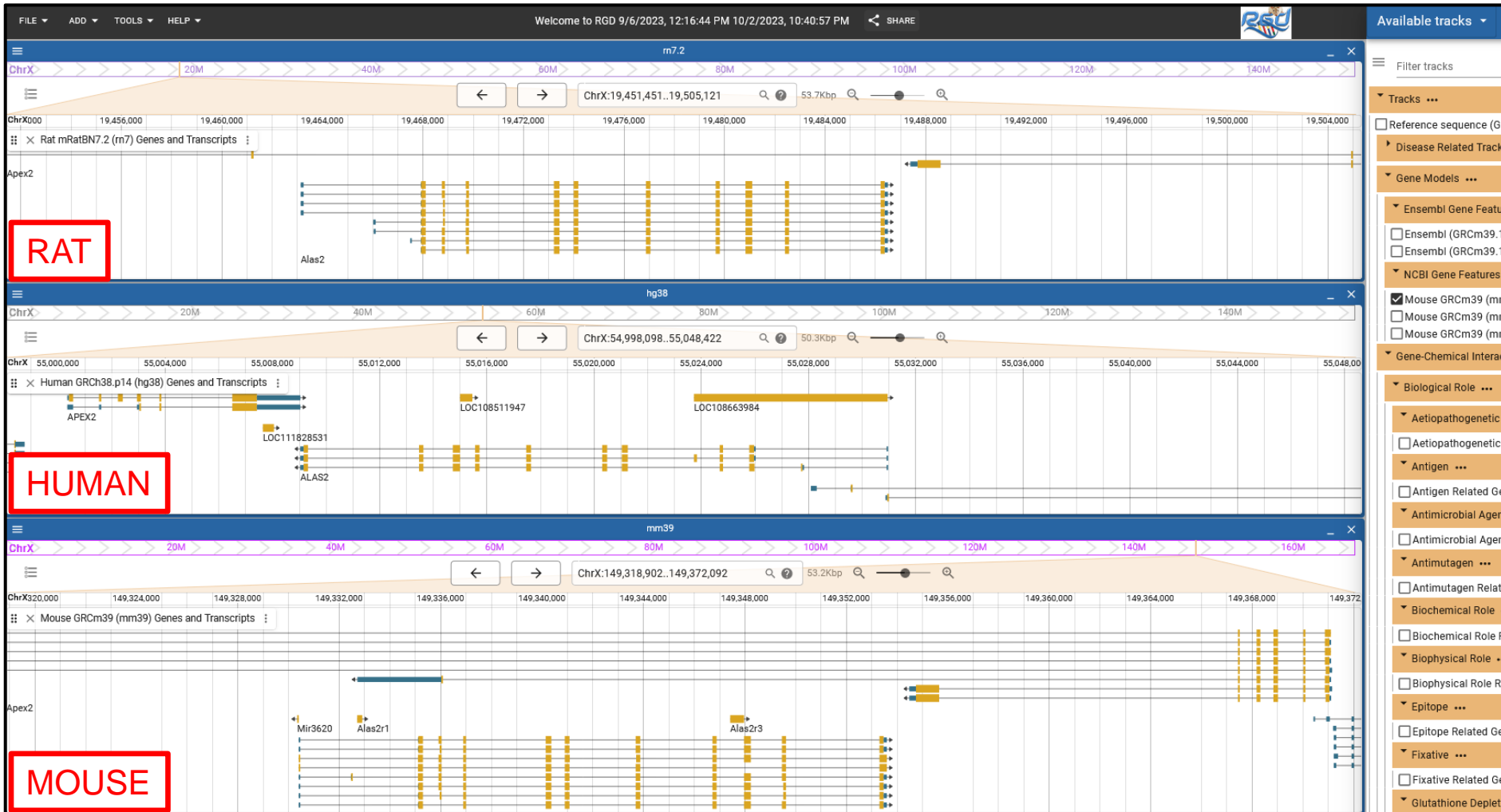
The right sidebar can display either a track selector or feature details, in this case, it shows information about the Mthfr gene. The sidebar is on the right by default but can be moved to the left of the main genome browser subwindow.

Multiple linear genome views

The screenshot displays the RGD web interface. At the top, a navigation bar includes 'FILE', 'ADD', 'TOOLS', and 'HELP'. A status bar shows the date and time: 'Welcome to RGD 9/6/2023, 12:16:44 PM 10/2/2023, 10:40:57 PM'. A 'SHARE' button is also present. On the right, there is an 'Available tracks' dropdown menu. The main content area is a grid of tracks, with a search bar and 'OPEN' and 'SHOW ALL REGIONS IN ASSEMBLY' buttons. A dropdown menu is open, listing various genome assemblies for Rat and Human. A red box highlights the 'R' in the 'Rat' column of the dropdown menu.

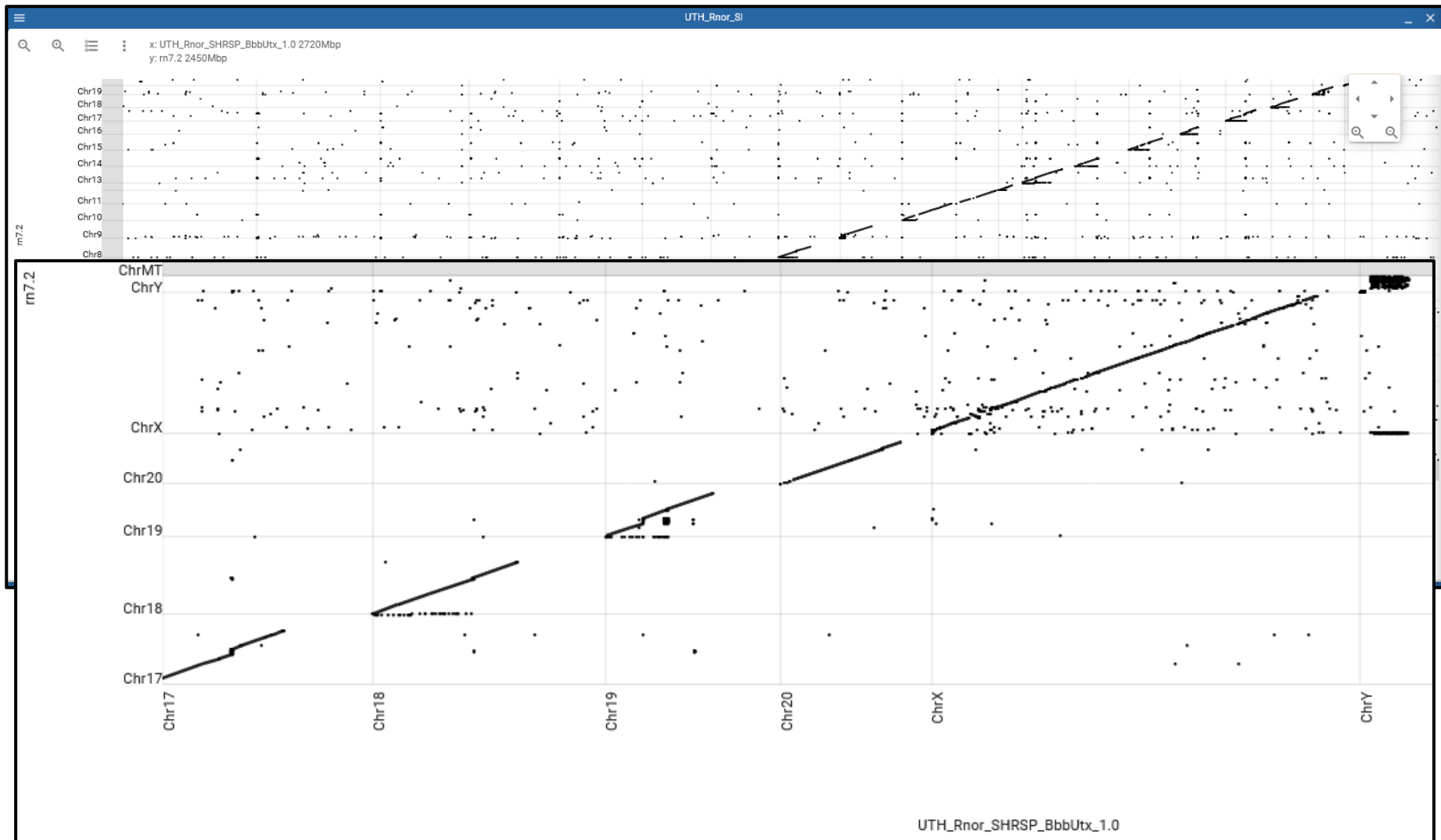
- mRatBN7.2 (Rat)
- Rnor_6.0 (Rat)
- Rnor_5.0 (Rat)
- RGSC_v3.4 (Rat)
- UTH_Rnor_SHR_Utx (Rat)
- UTH_Rnor_SHRSP_BbbUtx_1.0 (Rat)
- UTH_Rnor_WKY_Bbb_1.0 (Rat)
- hg38 (Human)
- hg19 (Human)
- hg18 (Human)
- GRCm39 (Mouse)
- GRCm38 (Mouse)
- GRCm37 (Mouse)
- canFam3.1 (Domestic Dog)
- susScr11 (Pig)
- susScr3 (Pig)
- chISab2 (Green Monkey/Vervet)
- veroWho (Green Monkey/Vervet)

Multiple linear genome views



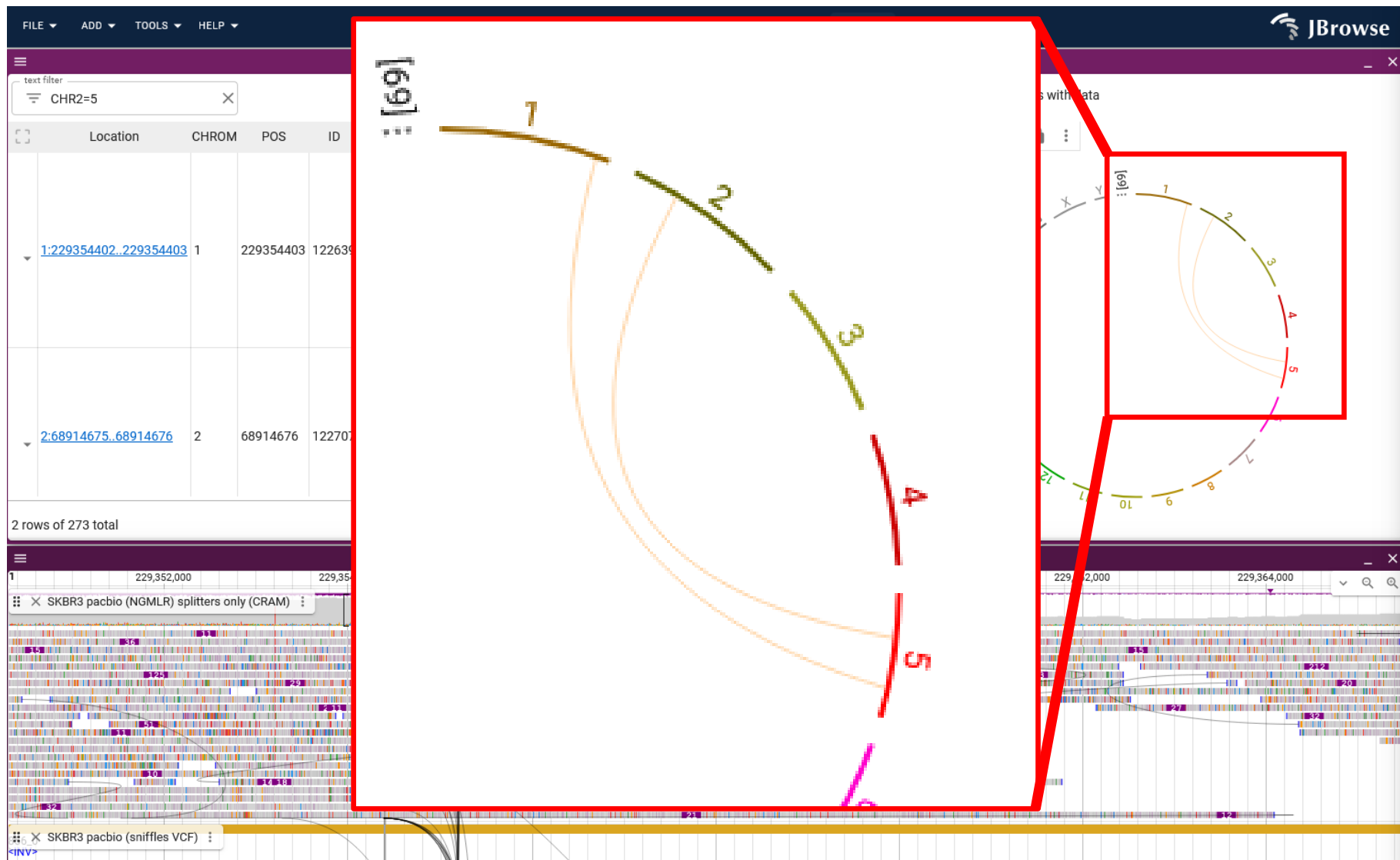
The stacked linear genome views make it easy to see that in mouse and rat, *Alas2* overlaps *Apex2* whereas in human *ALAS2* is downstream of *APEX2*.

Dotplot View : mRatBN7.2 vs. SHRSP/BbbUtx *de novo* assembly



Breakpoint Split View and Circular Plot

(aka the Structural Variant inspector, image from the JBrowse website)



Viewing synteny using VMap

RGD virtual office hours are available by appointment. Contact us to schedule a time.

VMap Synteny Browser (beta)

Search: Genes, Strains

Analysis and Visualization: JBrowse Genome Browser

OLGA Gene List Generator: hypertension INTERSECT synaptic signal

Disease Portals

Phenotypes and Models

Rat Genome Database

VMap is a synteny viewer that allows comparisons across multiple species or assemblies.

Viewing synteny using VCMMap

Overview

Detailed View

"Selected Data"



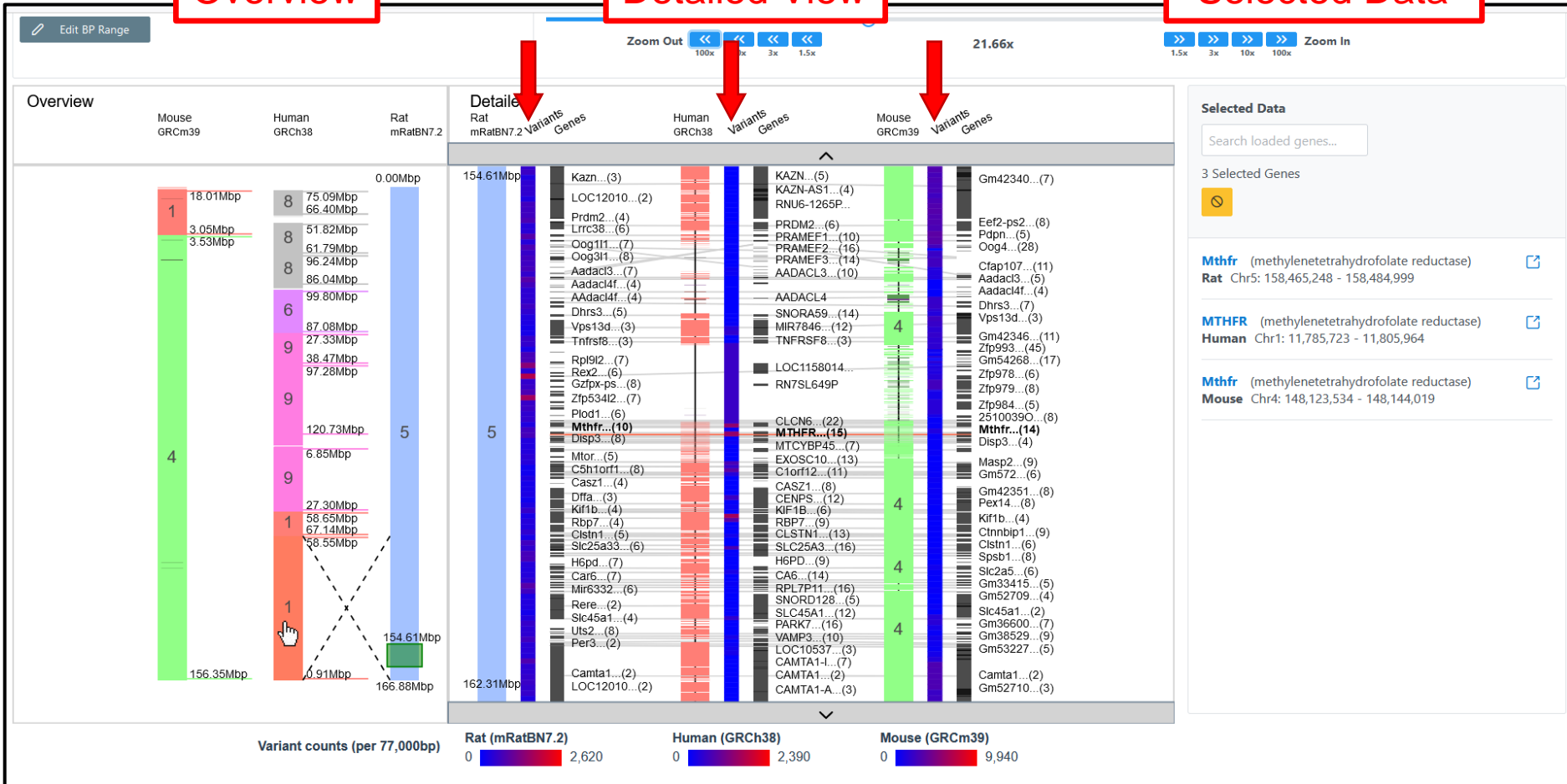
The overview panel gives a chromosome-wide view of the syntenic blocks. The detailed view shows blocks and gaps with a genes track for each species. When a gene or gene group is selected, the orthology is indicated by a red line and information is displayed in the "Selected Data" panel with links to gene records in RGD.

Viewing synteny using VCMMap

Overview

Detailed View

"Selected Data"



Heatmap tracks for variant density in the three species are currently available. Variants are binned, with bin sizes dependent on the zoom level and colors determined by the number of variants in the bin. Heatmaps for epigenome data are coming soon.

The RGD Team:

Principal Investigator:

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Thank you!

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RGD is funded by the National Heart, Lung, and Blood Institute (NHLBI; R01HL064541), and the National Human Genome Research Institute (NHGRI) as part of the Alliance of Genome Resources (U24HG010859).

Many thanks to our collaborators:

Dr. Melinda Dwinell and colleagues in The Hybrid Rat Diversity Program (*grant 5R24OD024617 from the NIH Office of the Director*),

Dr. Mingyu Liang, Dr. Aron Geurts, Dr. Pengyuan Liu and colleagues for generous provision of epigenomics data

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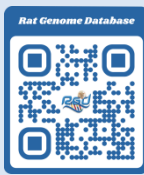
And to the researchers who contribute data and who faithfully use our website and data!

JBrowse and JBrowse 2 were developed by The JBrowse Consortium

(<https://jbrowse.org/>; <https://github.com/GMOD/jbrowse-components>)



GLOBAL
CORE
BIODATA
RESOURCE



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