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

Jennifer R. Smith

MEDICAL COLLEGE OF WISCONSIN

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/

RGD 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

OPEN FACETED SELECTOR

- Tracks ...
  - ☐ Reference sequence (mRatBN7.2 (rn7)) ...
  - ▶ 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 (rn7) Genes and Transcripts ...
      - ☐ Rat mRatBN7.2 (rn7) Genes Only ...
      - ☐ Rat mRatBN7.2 (rn7) 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 ...

▶ ChIP-Seq ...

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

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

▼ Synteny ...

- ☐ rn7.2 to canFam3 Synteny ...
- ☐ rn7.2 to hg38 Synteny ...
- ☐ rn7.2 to mm39 Synteny ...
- ☐ rn7.2 to rn3.4 Synteny ...
- ☐ rn7.2 to rn5 Synteny ...
- ☐ rn7.2 to rn6 Synteny ...
- ☐ rn7.2 to susScr11 Synteny ...
- ☐ rn7.2 to UTH_Rnor_SHR_Utx Synteny ...
- ☐ rn7.2 to UTH_Rnor_SHRSP_BbbUtx_1.0 Synteny ...
- ☐ rn7.2 to UTH_Rnor_WKY_Bbb_1.0 Synteny ...
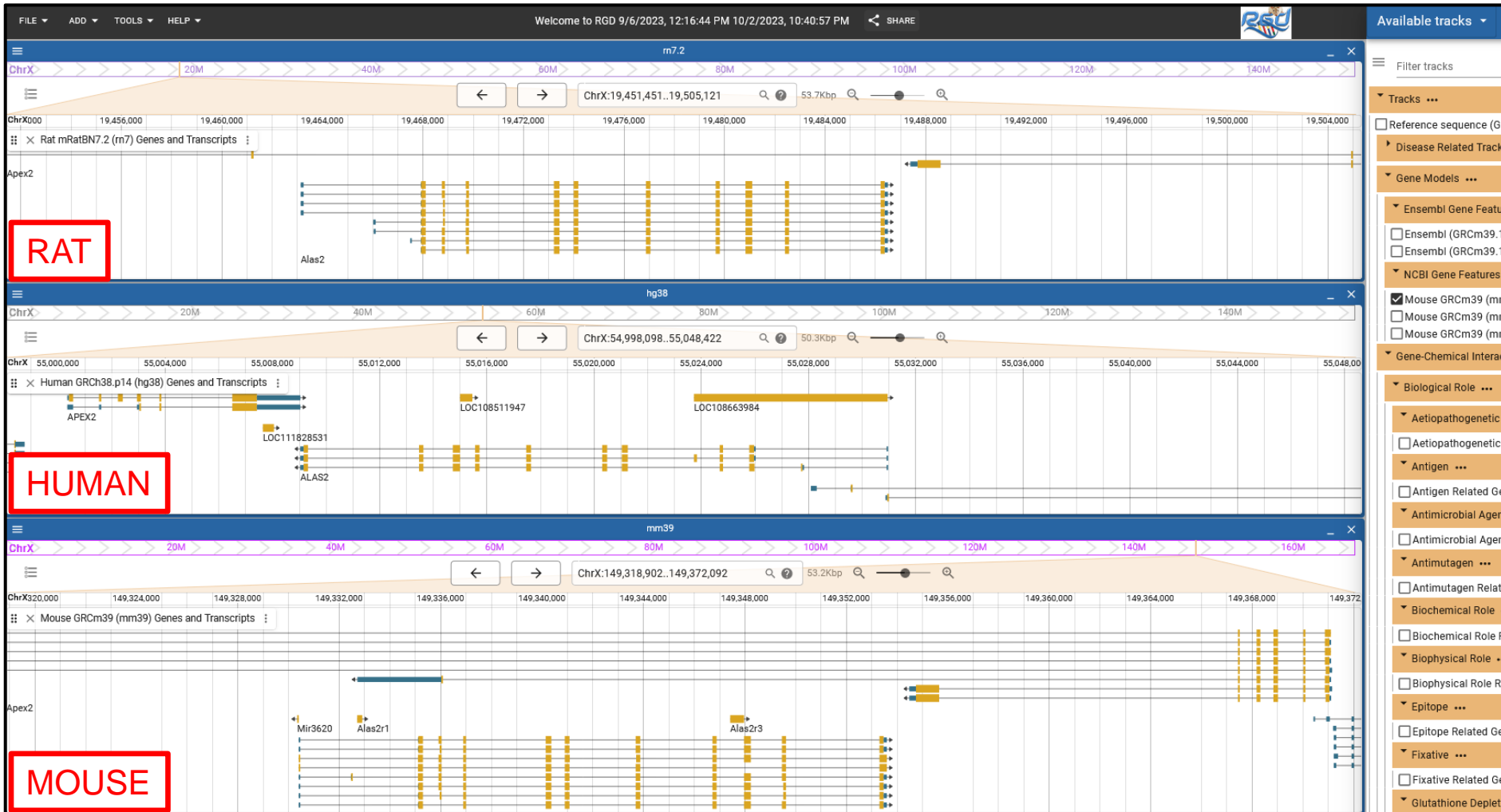
New data types in JBrowse 2

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

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.

Synteny view: mRatBN7.2 vs. SHRSP/BbbUtx *de novo* assembly

Dotplot View : mRatBN7.2 vs. SHRSP/BbbUtx *de novo* assembly
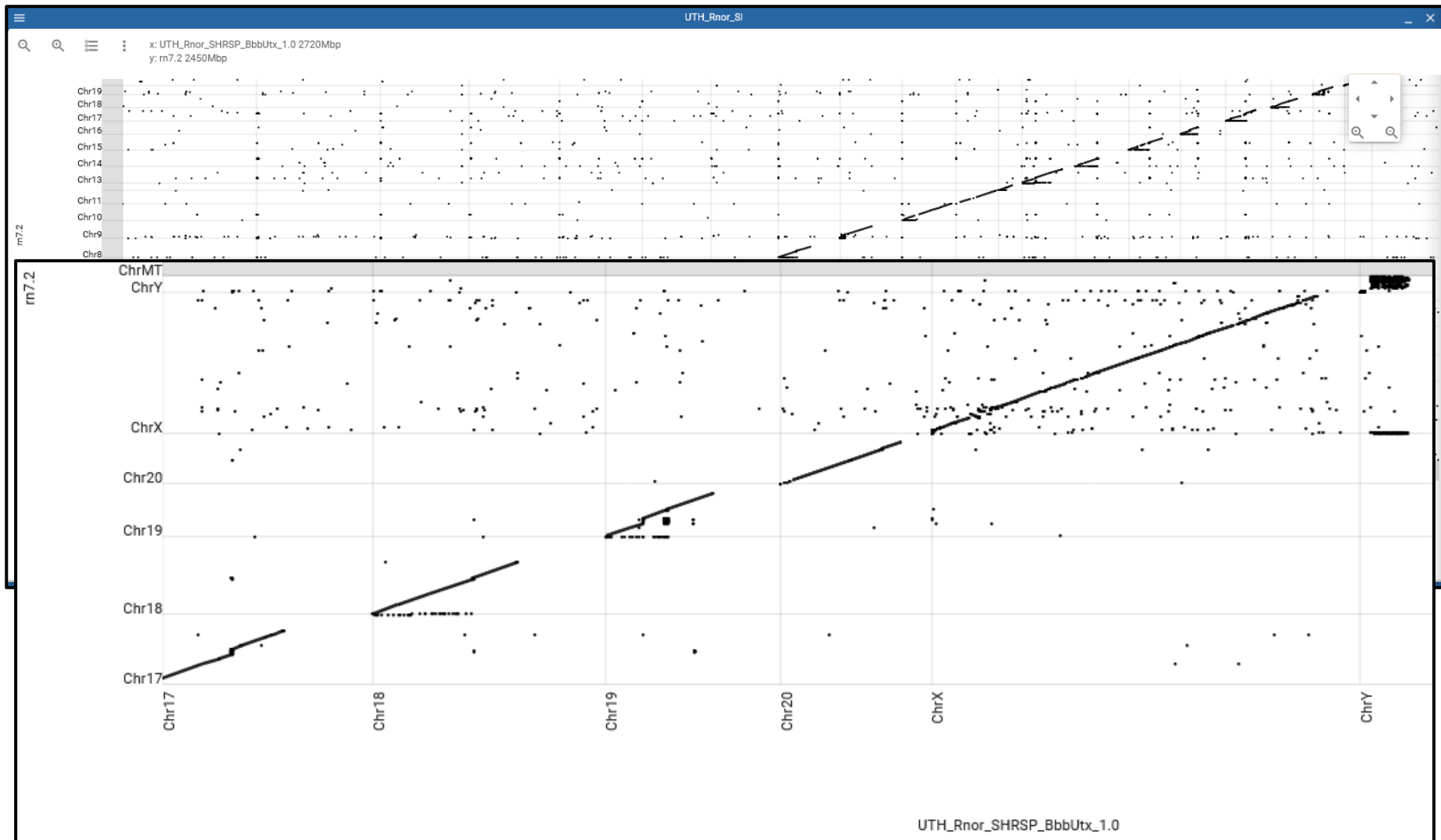
Breakpoint Split View and Circular Plot
(aka the Structural Variant inspector, image from the JBrowse website)
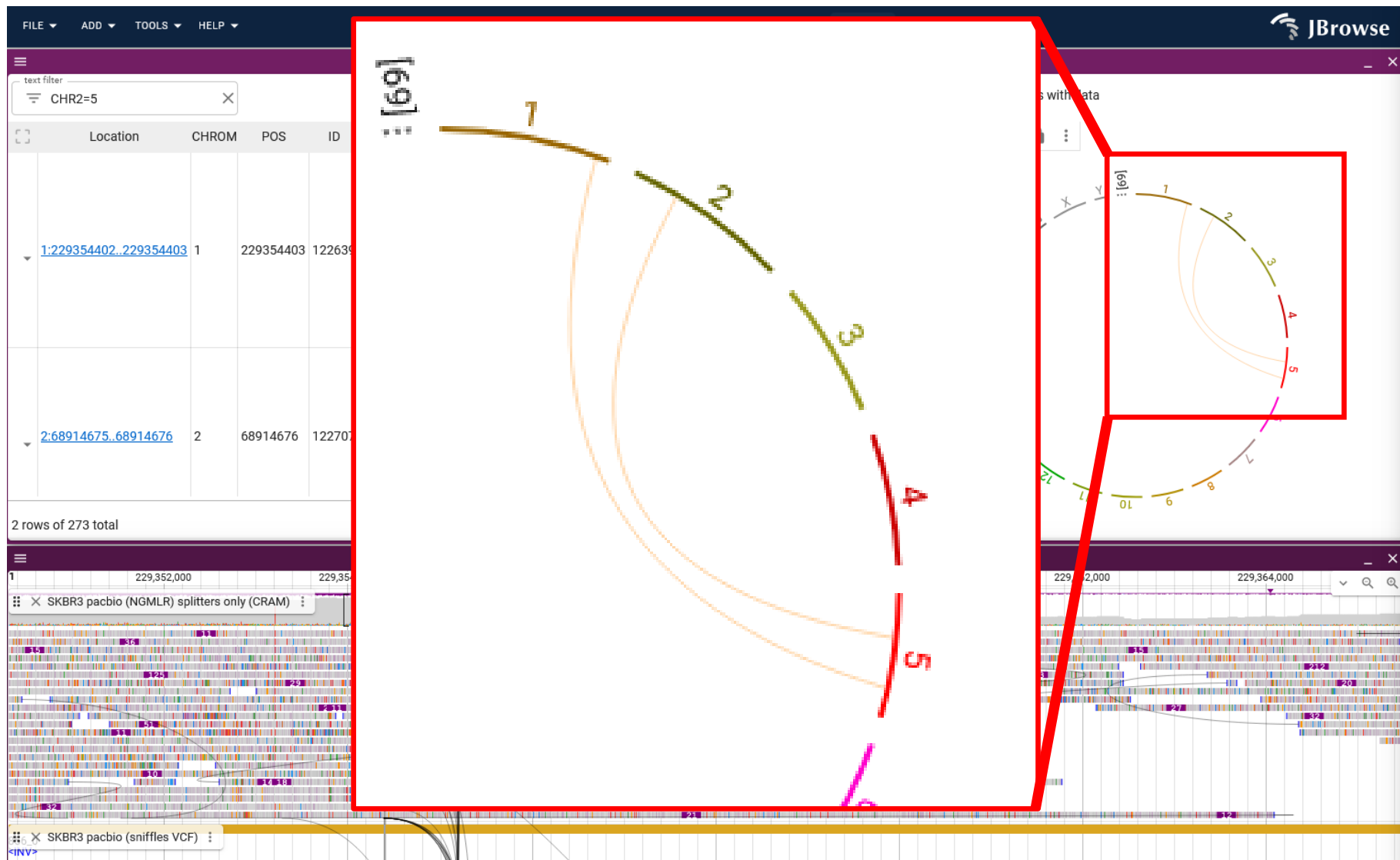
Viewing synteny using VCMap

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

Viewing synteny using VCMap

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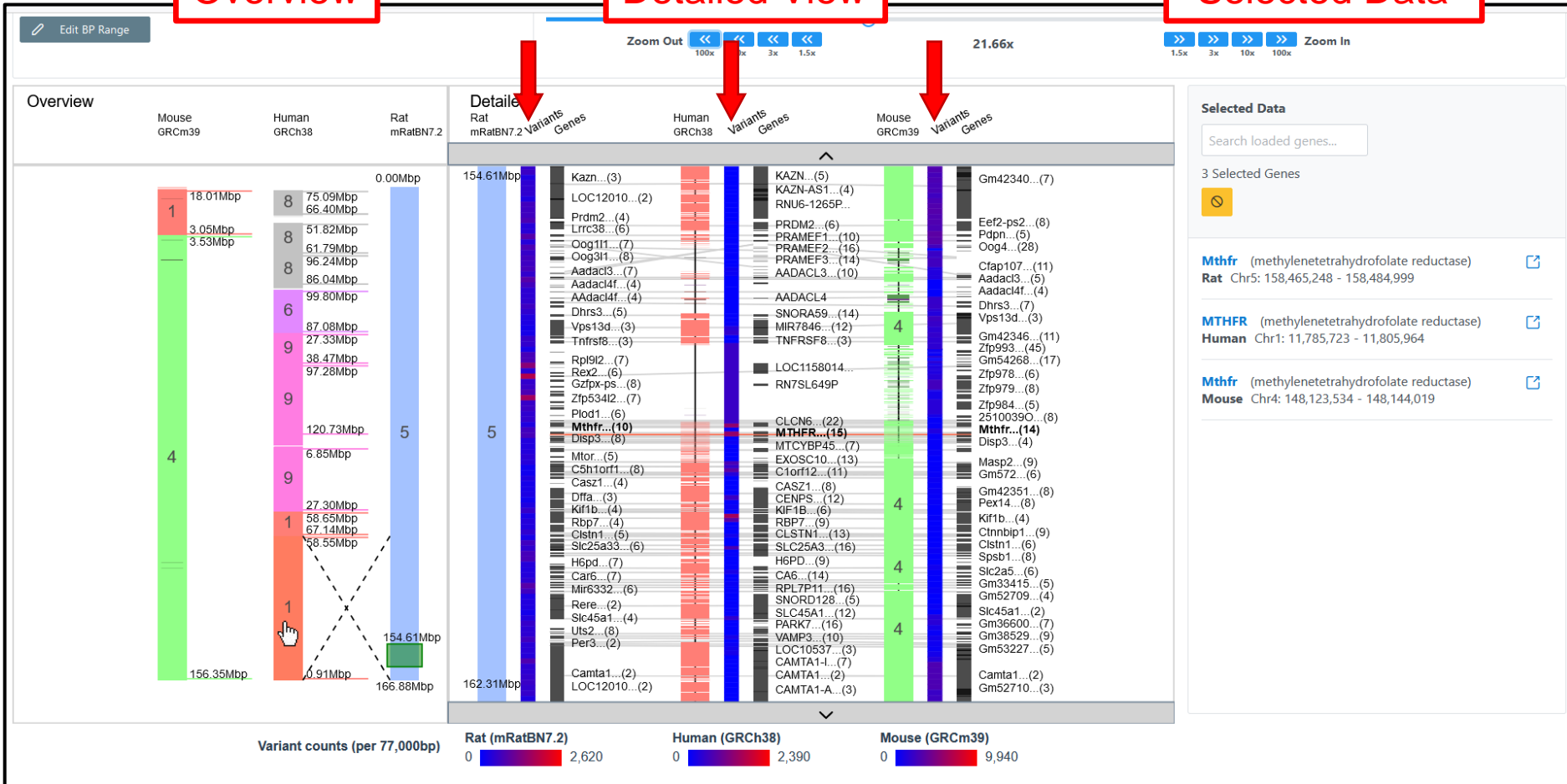
Heatmap tracks for variant density in the three species are currently available. Variants are binned, with bin sizes dependent on the zoom level and colors determined by the number of variants in the bin. Heatmaps for epigenome data are coming soon.

Thank you!

jrsmith@mcw.edu

https://rgd.mcw.edu

The RGD Team:

Principal Investigator:
Anne Kwitek, PhD

Co-Investigator:
Mindy Dwinell, PhD

Curation Team:
Jennifer Smith, MSc
Stan Laulederkind, PhD
Tom Hayman, PhD
Shur-Jen Wang, PhD
Monika Tutaj, PhD
Mary Kaldunski, MSc
Mahima Vedi, PhD
Wendy Demos, MSc

Development Team:
Jeff De Pons, BSc
Marek Tutaj, MSc
Jyothi Thota, MSc
Logan Lamers, BA
Adam Gibson, BSc
Akhil Kundurthi, MSc

Systems Administrator:
Kent Brodie, MSMI

Database Administrator:
Stacy Zacher, MSc

JBrowse and JBrowse 2 were developed by The JBrowse Consortium
(*https://jbrowse.org/*; *https://github.com/GMOD/jbrowse-components*)

Thank you!

jrsmith@mcw.edu

https://rgd.mcw.edu

The RGD Team:

Principal Investigator:
    Anne Kwitek, PhD

Co-Investigator:
    Mindy Dwinell, PhD

Curation Team:
    Jennifer Smith, MSc
    Stan Laulederkind, PhD
    Tom Hayman, PhD
    Shur-Jen Wang, PhD
    Monika Tutaj, PhD
    Mary Kaldunski, MSc
    Mahima Vedi, PhD
    Wendy Demos, MSc

Development Team:
    Jeff De Pons, BSc
    Marek Tutaj, MSc
    Jyothi Thota, MSc
    Logan Lamers, BA
    Adam Gibson, BSc
    Akhil Kundurthi, MSc

Systems Administrator:
    Kent Brodie, MSMI

Database Administrator:
    Stacy Zacher, MSc

JBrowse and JBrowse 2 were developed by The JBrowse Consortium
(*https://jbrowse.org/*; *https://github.com/GMOD/jbrowse-components*)

MEDICAL COLLEGE OF WISCONSIN

ALLIANCE of GENOME RESOURCES *FOUNDING MEMBER*

GBC GLOBAL CORE BIODATA RESOURCE
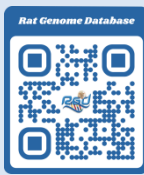
NIH National Heart, Lung, and Blood Institute

Rat Genome Database