The Rat Genome Database – Genome Browser

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RGD Rat Genome Database

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Abstract

The Rat Genome Database has enhanced the Generic Genome Browser (GBrowse), an open-source genome browser developed as part of the Generic Model Organism Database project (GMOD) (Stein et al., 2002) to provide a comprehensive research platform for its diverse research community. The genome browser at RGD (http://rgd.mcw.edu/gb/gbrowse/rgd_904/) is utilized by researchers not only for the visualization of rat genomic features such as genes and sequence variants, but also for visualization of Comparative Genomics data.

In order to support human/rat comparative analyses, RGD provides both a rat and a human GBrowse, allowing users to view genomic features in the human, rat, and mouse genomes with either the rat or human genome as the reference. Synteny tracks are provided on both references to provide visualization of synteny, and the relative positions of orthologs in these three species. Data is updated on a regular basis. Tracks representing diverse data types are available including: protein coding and RNA genes, single nucleotide polymorphisms (SNPs), copy number variants (CNVs), and simple sequence length polymorphisms (SSLPs). A number of international collaborations are in the process of sequencing and assembling a handful of additional rat strains; the RGD GBrowse is being modified to accommodate these emerging strain genomes and to provide visualizations of the identified strain specific differences. This will provide users with the opportunity to compare strain data for detailed analysis of trait-specific conserved genes. The availability of this sequence data and this type of analysis tools will further the users' insight into the relationship between genotype and phenotype.

Fig 1.
Users may click on any of the 'SYNTENY' tracks in order to view the features of interest. They can link-out into the Human Genome browser by clicking on Features on the Rat genome browser such that they may simultaneously view features on the rat and human. This provides a more intuitive view for comparative analysis between species.
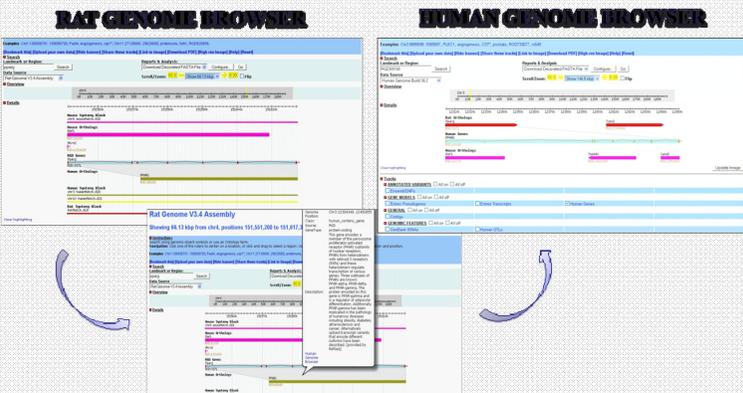

Fig 2.
Users may mouse over QTLs for details about each QTL and links to its report pages. Users can compare data to find specific differences across species. Here, we find that the Pparg human ortholog has Body Weight QTLs that the rat ortholog doesn't.

Fig 3.
Variation data between the two orthologs allows users to look at the synteny between regions at the nucleotide level. Users may then be able to link out to Ensembl report pages or the SNP report pages. This information can be used in the development of knock-out strains.
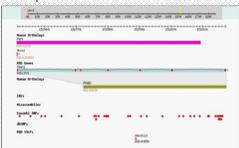

Fig 4.
Users may be able to generate genotype-phenotype relationships by linking out to the various metabolic pathway pages that a particular feature is involved in.
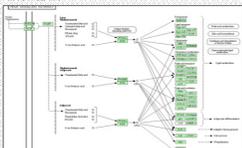

Fig 5.
ESTs and UNISTS data for the respective features will provide further insight into genomic features and functions. Clicking on each feature provides direct access to its report page at NCBI.
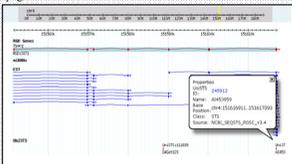

Fig 6.
Users may also be able to view contig information mapped onto the chromosome. This will allow users to have an intuitive view of features mapped on a chromosome and their position on the corresponding contig.
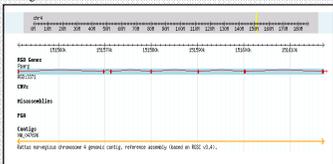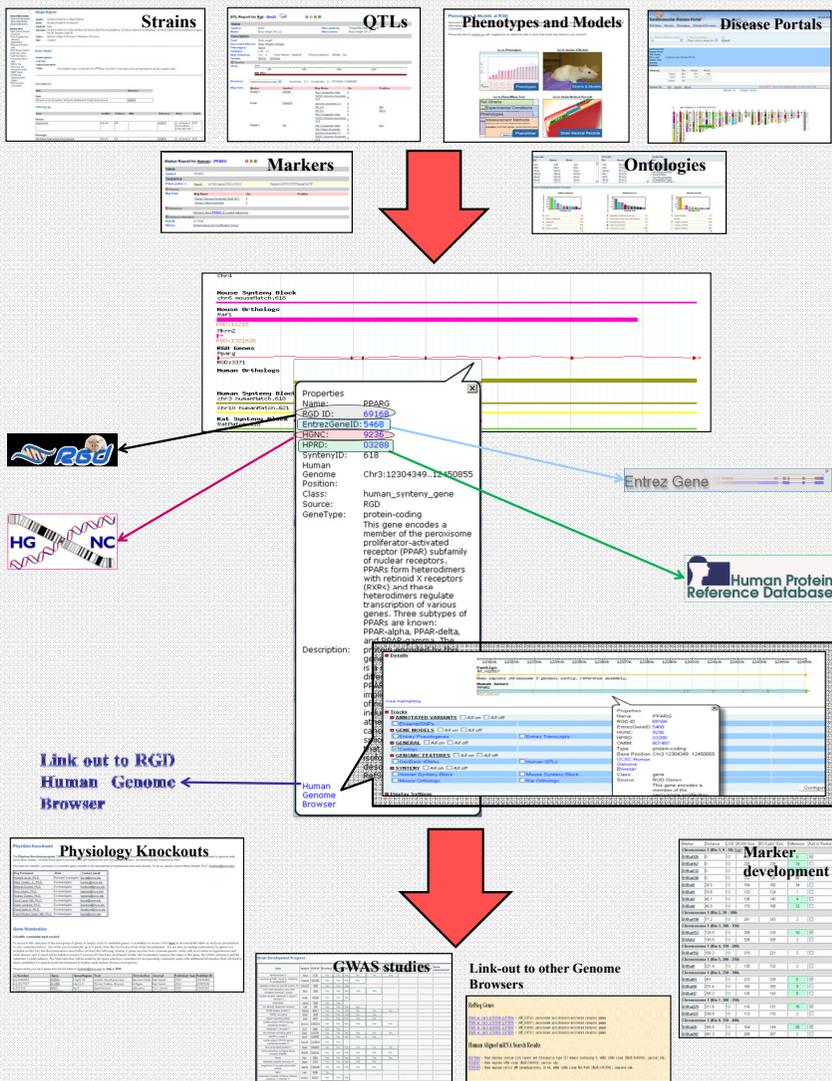

Fig7.
The below figure portrays how the Rat Genome Browser acts as an integral tool to link Genotype and Phenotype. Users may access the Browser through any of the report pages or the portals. The resulting information can be valuable for creating PhysGen knock-out strains or conducting genome-wide association studies. Apart from linking out to the Human genome Browser at RGD, users can analyze their features of interest by linking out to the UCSC browser from the bubble.

Strains

QTLs

Phenotypes and Models

Disease Portals

Markers

Ontologies

Link out to RGD Human Genome Browser

Physiology Knockouts

GWAS studies

Link-out to other Genome Browsers

Marker development

Salient features of the Rat and Human Genome Browser:

- Rat and Human Genome Browser with ability to navigate between the two browsers through a feature.(Fig1)
- Available tracks include: RGD Gene models, PGA data, annotated variants and genomic features such as ESTs, QTLs, DNA/GC Content and miRNAs.(Fig2-Fig6)
- Synteny between Rat/Mouse and Human Orthologs.(Fig1)
- Bubble tooltip provides links to above features.(Fig1,2,5)

Forthcoming features of the new Rat and Human Genome Browser:

- Feature Density Tracks showing histogram view when the number of features are high. e.g. SNPs
- Improved speed and rendering due to multiple database back-ends and slave processors.
- Sub-tracks within each track depending on certain select feature conditions.
- Ontology Tracks.