Building a Comparative Genomic Atlas of Epigenetic Variation in Rat Tissues

Monika Tutaj [1,2], Pengyuan Liu[3], Jennifer R Smith[1,2], Stanley JF Laulederkind[1,2], G Thomas Hayman[1,2], Shur-Jen Wang[1,2], Mary L Kaldunski[1,2], Mahima Vedi[1,2], Wendy M Demos[1,2], Jeffrey L De Pons[1,2], Marek A Tutaj[1,2], Jyothi Thota[1,2], Logan Lamers[1,2], Adam C Gibson[1,2], Akhilanand Kundurthi[1,2], Varun Reddy Gollapally[1,2], Kent C Brodie[1], Stacy Zacher[1], Sridhar Rao[4], Melinda R Dwinell[1,2], Aron Geurts[2], Anne E Kwitek[1,2]

[1] Rat Genome Database, [2] Department of Physiology, Medical College of Wisconsin, Milwaukee, WI, [3] University of Arizona, Tucson, AZ, [4] Versiti, Milwaukee, WI

1. Introduction

- Human epigenomic research, driven by major initiatives, has advanced our understanding of complex diseases. Mouse epigenomic research has benefited from extensive genetic resources. In contrast, rats, despite their importance in physiology and pharmacology research, still lack similar resources.
- With recent advancements in reference genome assembly and gene model annotations, along with the assembly of additional rat strain genomes, comprehensive genomic and epigenomic resources for rats could be developed.

2. Methods

- Rat Genome Database (RGD) is updating, integrating, and expanding rat genomic and epigenomic datasets to ameliorate comparability with human data, thereby facilitating more effective cross-species comparisons.

3. Results

- We are harmonizing multi-level, genome-wide ENCODE data from human tissues with publicly available **RNA-seq, ATAC-seq**, and **ChIP-seq** data from rats, enriched with RGD rat information, including strain variations, gene sequences, QTLs, and ontology-based gene annotations.
- Using **JBrowse2** and **VCMap** tools, we have created **syntenic genome maps** and organized data into multilevel tracks by analysis method, grouped by organ (e.g., liver, kidney), allowing for the comparison of genes associated with cardiovascular diseases across species.

4. Discussion

- Comparative genome visualization helps researchers identify critical factors associated with diseases. It improves the selection and engineering of model organisms for studying disease mechanisms, testing therapies and increases the utility of genomic databases.
- Ultimately, the **synteny-orthology based genomic atlas** will improve the effectiveness of translational research by providing a robust comparative framework (deeper insight into gene function or disease mechanisms).

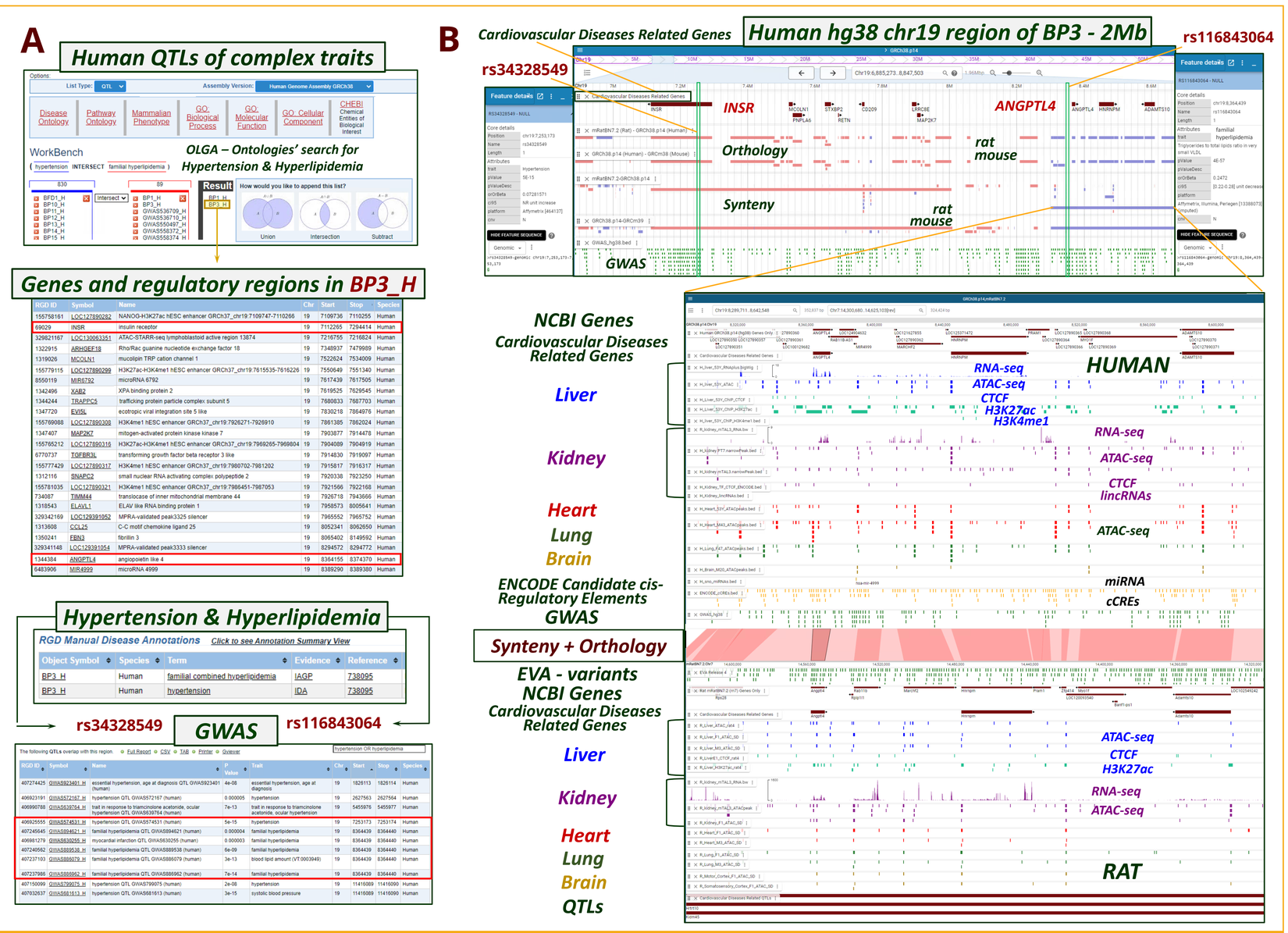

*Figure 1. (A) Human blood pressure QTL3, located on chromosome 19, contains genes with experimental evidence and annotations linked to both hypertension and hyperlipidemia. (B) Synteny and orthology comparison between human and rat data in JBrowse2, highlighting the **INSR** and **ANGPTL4** genes. The detailed figure shows gene expression, epigenetic and variant data across liver, kidney, heart, lung, and brain in a 353 kb human region and a 324 kb rat region, respectively.*

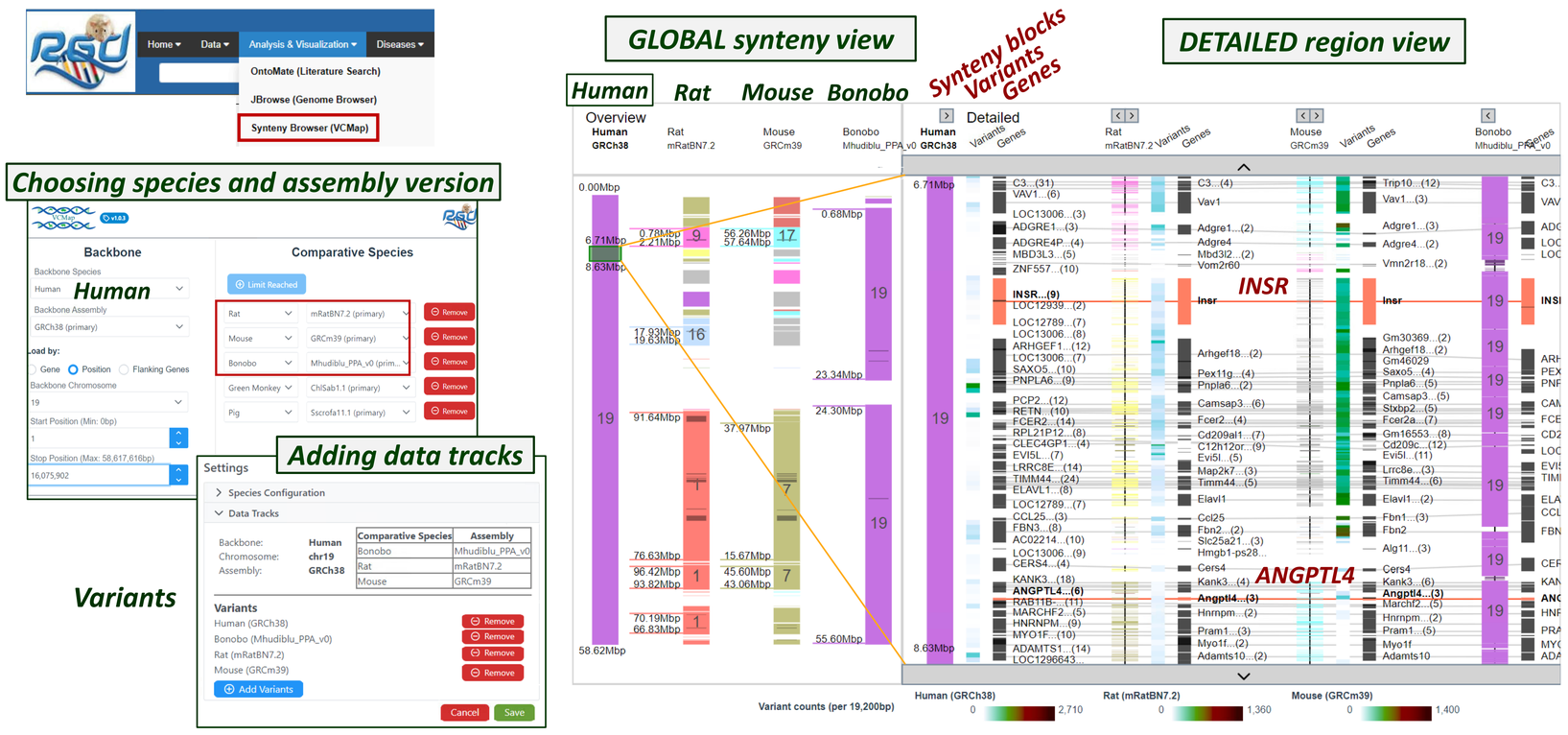

*Figure 2. Synteny view of the human **chromosome 19 region** across rat, mouse, and bonobo species using the RGD Virtual Comparative Map (VCMap). This tool allows exploration of gene order, genome conservation, and data annotations across **multiple species**. VCMap can integrate **various genomic datasets**, including genome assemblies, gene annotations, QTL data, variants, and epigenomic markers, facilitating connections between phenotypic traits and genomic regions.*

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Monika Tutaj, PhD
Rat Genome Database, MCW
motutaj@mcw.edu
rgd.mcw.edu

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See RGD JBrowse2 & VCMap