

Building a Comparative Genomic Atlas of Epigenetic Variation in Rat Tissues

Monika Tutaj^{1,2}, Pengyuan Liu³, 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 Brodie¹, Stacy Zacher¹, Sridhar Rao⁴, Melinda R Dwinell^{1,2}, Aron Geurts², Anne E Kwitek^{1,2}

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

The rat is a vital model organism particularly in cardiovascular, toxicology, and neurobiology research. Despite recent improvements in genome assembly and gene model annotations, the rat's genomic and epigenomic data remain underdeveloped. To confront this challenge, the Rat Genome Database (RGD) is updating, integrating, and expanding these datasets to ameliorate comparability with human data, thereby facilitating more effective cross-species comparisons.

Human epigenomic research, driven by initiatives like the Human Epigenome Project, ENCODE, and the NIH Roadmap Epigenomics Mapping Consortium, has significantly advanced our understanding of complex diseases through detailed DNA methylation maps, histone modification profiles, and RNA expression data. Similarly, research using mice has benefited from extensive resources, such as the Mouse Genome Informatics (MGI) and the mouse ENCODE project, establishing this species as versatile models for genetic manipulation. In contrast, rats, despite their crucial role in physiology and pharmacology, have lacked comparable genetic resources, though advancements in gene-editing technologies like CRISPR are beginning to close this gap.

Our project aims to build a comprehensive comparative genomic atlas of epigenetic variation in rat tissues. 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 comprehensive RGD rat information, including strain variations, gene sequences, QTLs, and ontology-based gene annotations. Using advanced visualization tools like JBrowse2 and VCMAP, we create syntenic genome maps to enhance cross-species comparisons. This approach harnesses the utility of genomic databases to aid researchers in identifying critical factors associated with diseases, thereby improving the selection and engineering of model organisms for studying disease mechanisms and testing therapies. Ultimately, the atlas will improve the effectiveness of translational research by providing a robust comparative framework.