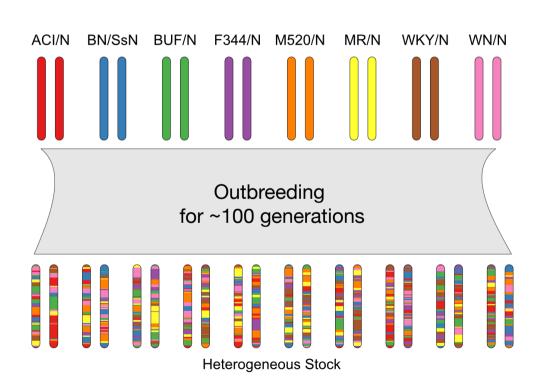
Genome-wide association of adiposity in Heterogeneous Stock rats

Apurva S. Chitre

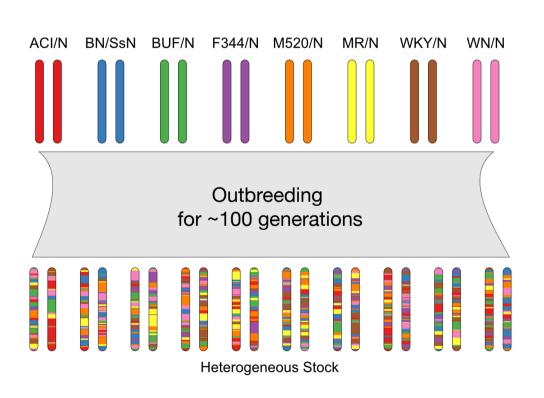
PhD student in Bioinformatics and Systems Biology program Palmer Lab, UC San Diego

Utilizing Heterogeneous Stock Rats for Genetic Mapping



In 1984, at the NIH, 8 inbred rat strains were interbred to develop an outbred population enriched with alleles from these diverse founders.

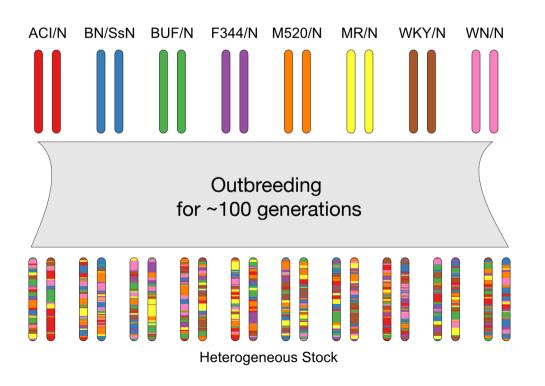
Utilizing Heterogeneous Stock Rats for Genetic Mapping



- In this population, at any given locus, a given individual might have inherited their alleles from different strains, contributing to a diverse
- Each animal is genetically and phenotypically distinct.

genetic makeup.

Heterogenous stock (HS) rats







Dr. Leah Solberg Woods



Aiming to link genotype and phenotype through GWAS in HS rats

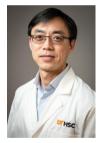


- Lead collaborative efforts in studying genetics of drug abuse in HS rats.
- Distributes HS rats to various research groups for targeted phenotyping.
- Conducts genotyping and GWAS.



Genes and Addiction NIDA Center for GWAS in Outbred Rats





Hao Chen

Socially-acquired nicotine self-administration





Shelly Flagel

Genetic Studies of Incentive Salience









Paul Meyer

Association between behavioral regulation and cocaine cue preference

Post-Behavioral Phenotyping Trait Measurements







- Fasting Period: 17 ± 2 hours
- Measured Traits:
 - Body Weight
 - Body Length (with/without tail)
 - Fasting Glucose Levels
- Visceral Fat Pads:
 - Retroperitoneal Fat
 - Epididymal Fat (Males)
 - Parametrial Fat (Females)

Study Scale and Demographics

Center	Age at Euthanasia	Sample Size		Drug Treatment	Drug Dose	Diet
University of Tennessee - Experimental	73 +/- 12 days	2,766	Pairs	Nicotine	Variable (self- administration)	_Tektad LM-485 Mouse/Rat Diet
University of Tennessee - Breeders	169 +/- 34 days	1,032	-	-	-	
University at Buffalo - Dietz lab	198 +/- 13 days	2,726	Pairs	Cocaine	10 mg/kg	_Envigo Tektad 18% Protein Rodent Diet
University at Buffalo - Meyer lab	164 +/- 14 days	707	Pairs	-	-	
University of Michigan	89 +/- 6 days	1,626	Trios	Cocaine	15 mg/kg	Labdiet Picolab Rodent Diet Irradiated

Total sample size = 8,857 male and female Heterogenous Stock rats

Genotyping

- Spleen tissue from the phenotyped rats were shipped to the Palmer lab at UC San Diego.
- Through low-coverage whole-genome sequencing (lcWGS), we accurately identified 7.32 million SNPs with a 99.8% accuracy rate.



Khai Nguyen



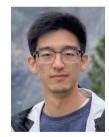
Clara Ortez



Yizhi Wang



Benjamin Johnson



Denghui Chen

GWAS pipeline

- <u>Phenotyping center differences</u> accounted for as covariates, mitigating site-specific variations such as diet and housing.
- SNP heritability (h²) estimated with GCTA-GREML.
- Genetic correlations via bivariate GREML (GCTA).
- GWAS employed GCTA's linear mixed model with a GRM to account for complex HS population relationships.
- Significance thresholds established through permutation.

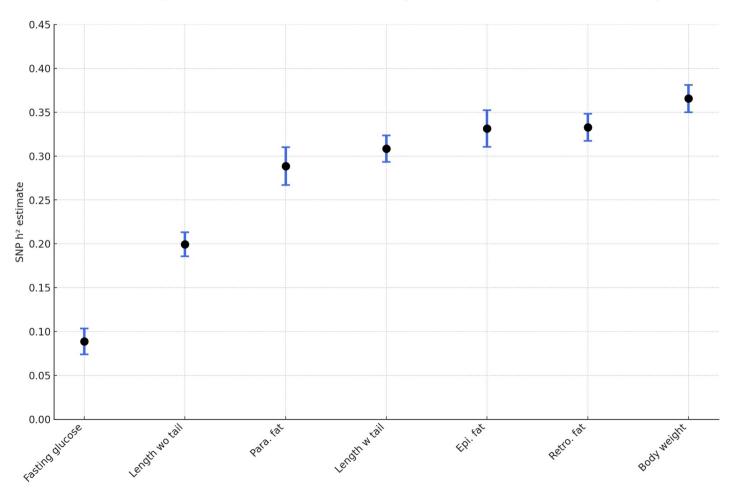


Thiago Sanches

Apurva Chitre

Are the adiposity traits heritable?

Adiposity traits exhibit high SNP heritability



Phenotypic and Genetic Correlation

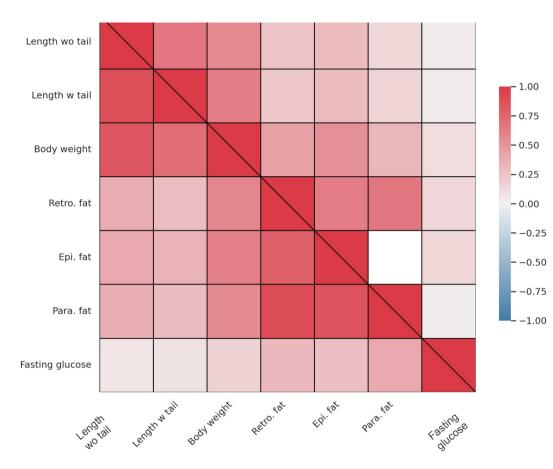
Phenotypic Correlation:

How one phenotype relates to another in observed values.

Genetic Correlation:

- Shared variance between two traits due to genetics.
- Can be estimated even if traits aren't measured in the same individuals.

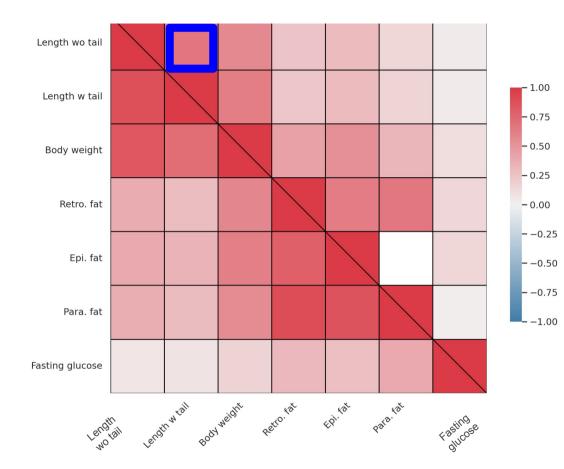
Upper triangle displays phenotypic correlations, while the lower triangle shows genetic correlations.



Upper triangle displays phenotypic correlations, while the lower triangle shows genetic correlations.

Phenotypic correlations:

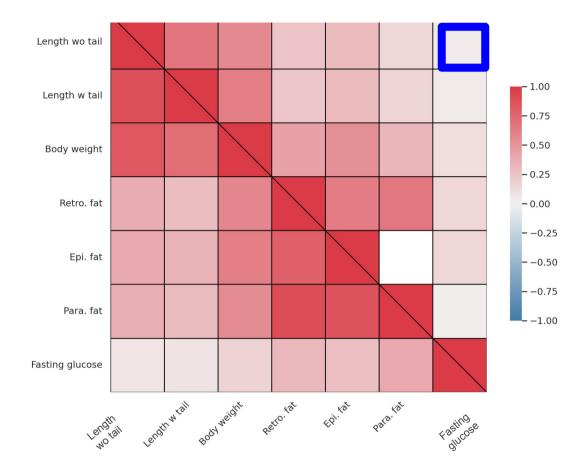
- Strongest estimate was between length with tail and length without tail.
- Weakest phenotypic correlation was between parametrial fat weight and fasting glucose.



Upper triangle displays phenotypic correlations, while the lower triangle shows genetic correlations.

Phenotypic correlations:

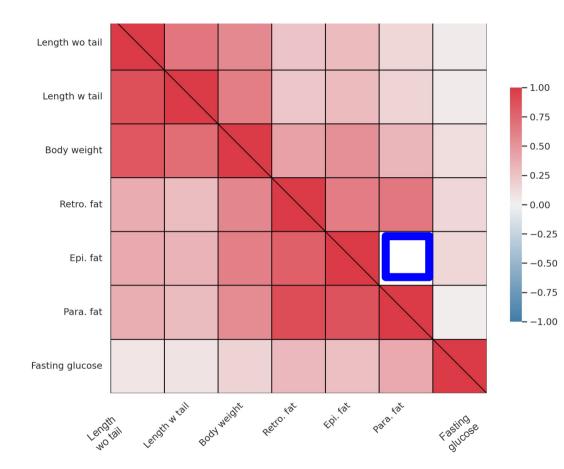
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Phenotypic correlations:

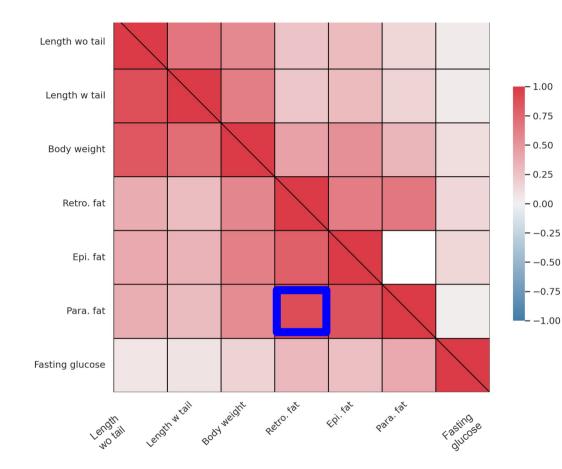
- Strongest estimate was between length with tail and length without tail.
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Upper triangle displays phenotypic correlations, while the lower triangle shows genetic correlations.

Genetic correlations:

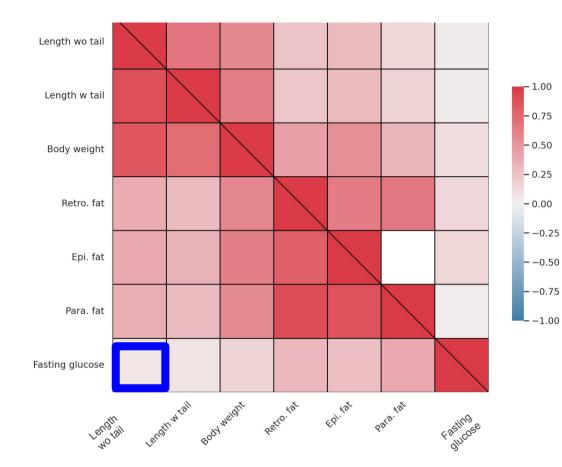
- Highest genetic correlation observed was between parametrial fat weight and retroperitoneal fat weight.
- Lowest genetic correlation was between length without tail and fasting glucose.



Upper triangle displays phenotypic correlations, while the lower triangle shows genetic correlations.

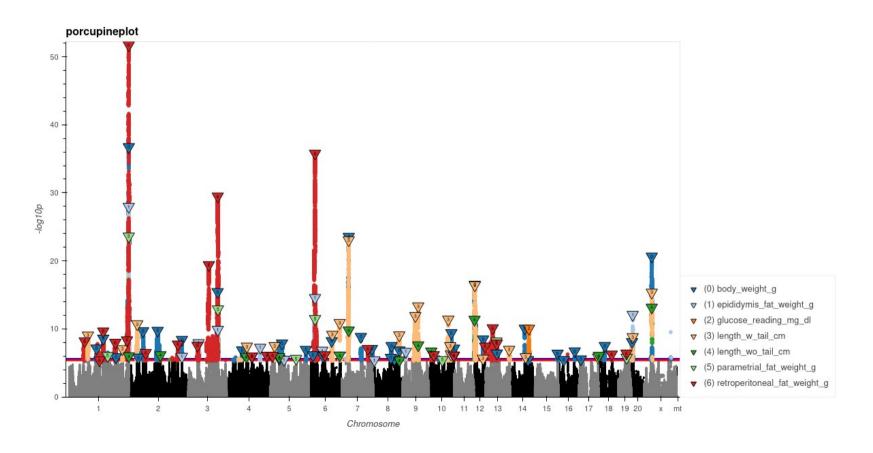
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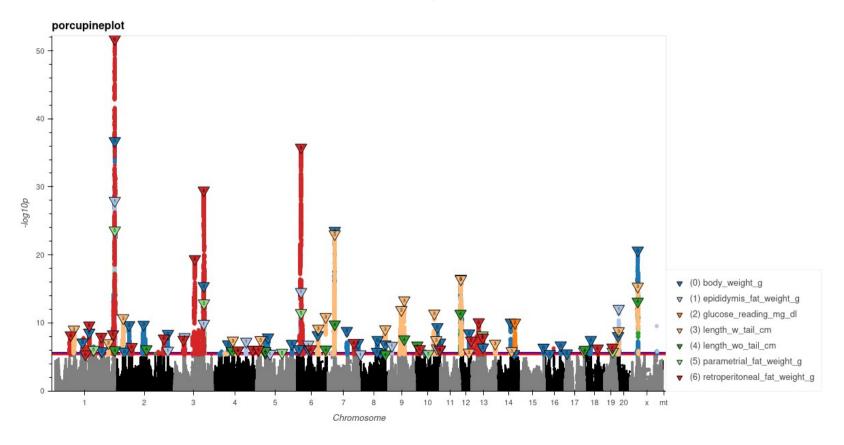


Are there specific chromosomal locations associated with adiposity traits in our HS rat population?

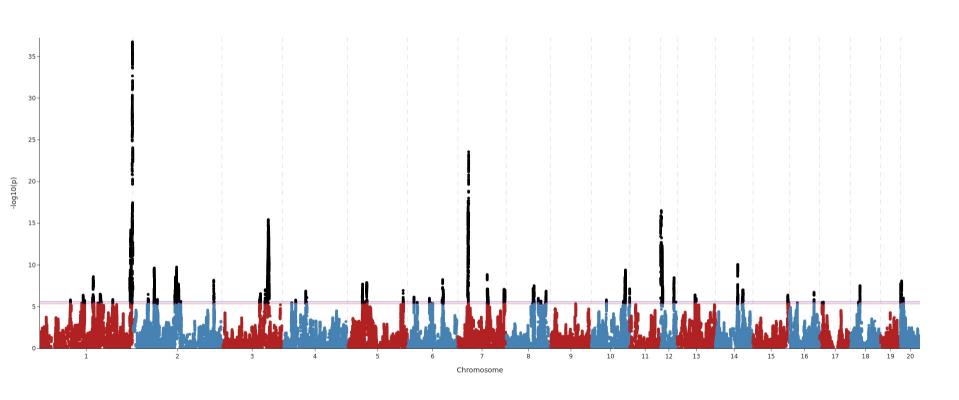
Identification of multiple GWAS hits, N= 8,857



Identification of 116 independent QTLs for 7 adiposity traits



37 independent QTLs for Body weight, N= 8,857 SNP heritability: 0.37 ± 0.02

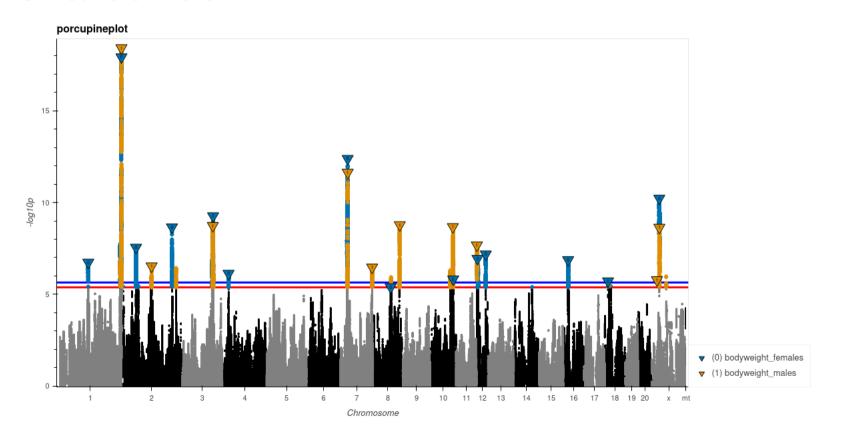


Are Body Weight QTLs Sex-Specific?

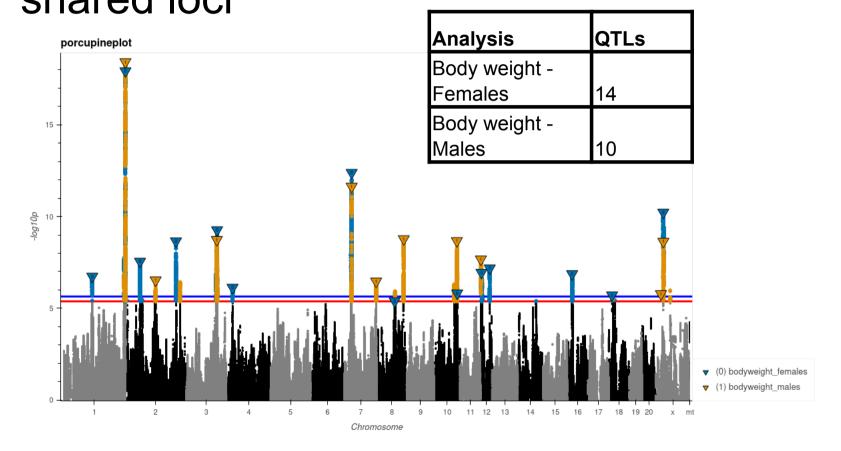
Sex-stratified GWAS analysis for body weight

- Dataset division :
 - Females: n = 4,173
 - Males: n = 4,285
- Applied standard GWAS pipeline separately to each sex
- Sex was not included as a covariate

Sex-specific GWAS reveals distinct and shared loci

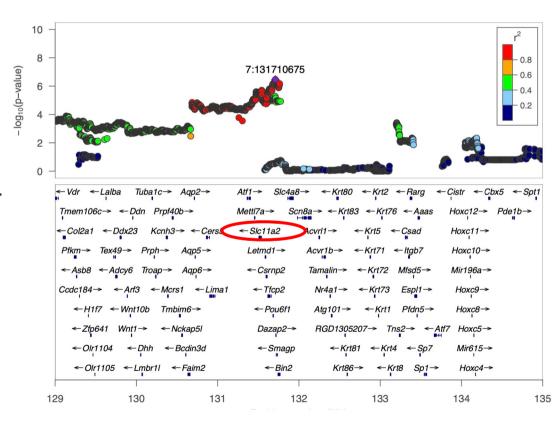


Sex-specific GWAS reveals distinct and shared loci



Chr7: 131.71Mb locus specific to males

- Identified a high-impact splice donor variant in gene Slc11a2 potentially altering mRNA splicing.
- SLC11A2 gene linked to obesity and iron accumulation in skeletal muscle. (González-Domínguez et al. 2020)

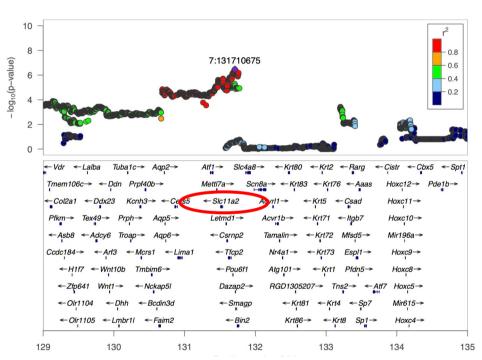


What other traits also show association at this locus?

Chr7: 131.71Mb locus specific to males

Results from PheWAS

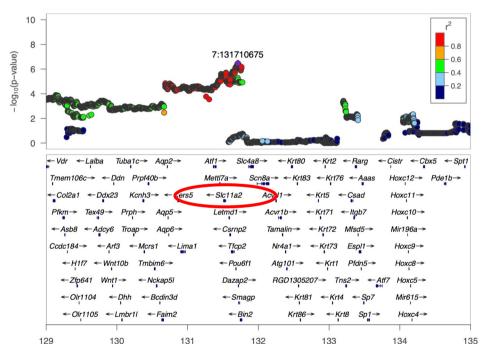
Category	Trait	Significance (-log ₁₀ P- value)
Muscle Phenotypes	Tibialis Anterior Weight (grams)	4.47
[Lionikas Lab]	Extensor Digitorum Longus Weight (grams)	6.105
Bone Phenotypes [Adams Lab]	Bone Stiffness	6.291
ili damo Labj	Bone Surface Area	4.391



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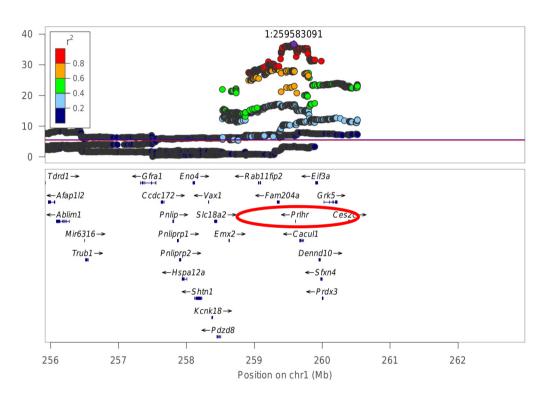


Variation at this locus may influence multiple related traits through common biological pathways

Shared locus in male and female body weight GWAS

- Within this QTL, we've identified a 'HIGH' impact 'start_lost' coding variant in *Prlhr* gene.
- Loss of start codon likely disrupts protein translation and function

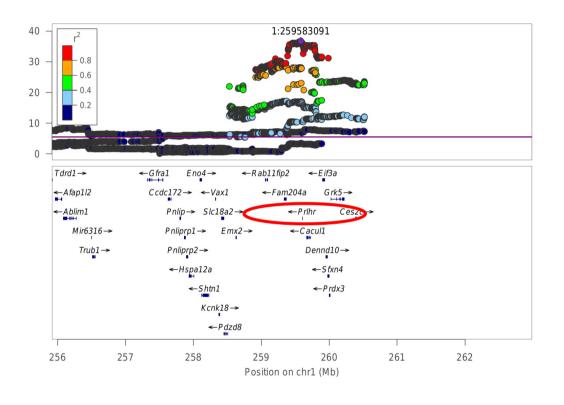
Chr1: 259.61 Mb locus for bodyweight



Shared locus in male and female body weight GWAS

- Talbot et al. 2023 identified multiple rare variants in PRLHR (GPR10) linked to severe obesity, impairing ligand binding and G protein signaling, supporting GPR10's role in energy homeostasis and potential as a weight-loss therapeutic target.
- Keele et al.'s 2018 (PMID: 29193816) GWAS on a different HS rat cohort also highlighted this locus, supporting our results.

Chr1: 259.61 Mb locus for bodyweight



Conclusions

- This is the largest GWAS ever conducted in rodents.
- We performed sex stratified GWAS and identified male- and female-specific loci for body weight.
- Some loci found to be common in both males and females.
- We replicated previously identified loci (Keele et. al. 2018) and identified numerous novel loci for multiple adiposity traits.
- This result demonstrates the importance of large sample sizes for genetic dissection of complex traits

Future directions

- Ongoing phenotyping by partner labs will significantly increase our dataset.
- Anticipate re-analysis with ~1000 additional animals to strengthen our findings.
- Perform sex as an interaction term GWAS.

Acknowledgements



Genes and Addiction
NIDA Center for GWAS in Outbred Rats



References

- Keele GR, et al. Genetic Fine-Mapping and Identification of Candidate Genes and Variants for Adiposity Traits in Outbred Rats. Obesity. 2018;26(1):213-222. doi: 10.1002/oby.22075.
- González-Domínguez Á, et al. Iron Metabolism in Obesity and Metabolic Syndrome. Int J Mol Sci. 2020;21(15):5529. doi: 10.3390/ijms21155529.
- Talbot F, et al. A rare human variant that disrupts GPR10 signalling causes weight gain in mice. Nat Commun. 2023;14:1450. doi: 10.1038/s41467-023-36966-3.