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A Multiomic Genetic Resource for Analysis of Gene Function and SUD in the Rat CNS

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MOTIVATION. The mu opioid receptor (OPRM1) is a key mediator of pain, reward, and hedonic drive. We generated whole brain multiomics to enable unbiased surveys of molecular traits and phenotypes that may be downstream of polymorphisms in the rat *OPRM1* locus, or other polymorphic regions.

MATERIAL, METHODS, FAIR Data. We generated data for whole brains of both sexes across 20–30 HXB/BXH strains segregating for ~3 million variants at MAF >0.3. The HXB are fully inbred and sequenced progeny of crosses between SHR (RRID:RGD_631848) and BN (RRID:RGD_61117) by MPra. We generated the following data:

1. Transcriptomes (whole brain, *n* = 18K RNAseq assays) by LS and BT; hippocampus (*n* = 616K exon array assays) by LL, RWW, SS, PP, MPra
2. Proteomics by TMT-based MS (whole brain, *n* = 9K proteins, 99K peptides) by XW, JPe, MPra
3. Metabolite levels (whole brain, *n* = 150) by MPu, HS, HC, MPra, RWW
4. Physiological, anatomical, and pharmacological traits (*n* = 234) by MPra, RWW

All data are FAIR+ compliant in *GeneNetwork.org*. This link, *https://bit.ly/multiomic*, will fetch a table listing all protein assays. Key results and data can be exported, sorted by expression, by LOD, or by location of peak eQTLs. We sorted for trans-eQTLs with peaks near *OPRM1*.

RESULTS. *OPRM1* has a weak cis eQTL in the 5' UTR of exon 2. There is compelling evidence of a polymorphism since over 200+ highly expressed CNS proteins map to the *OPRM1* region with LODs >6 (e.g. SYT7, SYT9, and SYT13). We point readers to a detailed narrative with key results and methodology related to ORPM1 at *https://tinyurl.com/oprmprimer* .

CONCLUSION. These deep omic data are invaluable for efficient open analyses of molecular processes linked to SUDs in any species. Mapping, PheWAS, and translation to human data are practical with tools in *GeneNetwork*, *PhenoGen*, and *GeneWeaver*.

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