**RESOURCE SHARING PLAN: MOUSE GENOMIC DATA**

1. **Summary of Data to be Shared**

Single-cell datasets: All single-cell epigenomics and transcriptomics data will made available through the BRAIN Initiative Cell Data Center (BCDC) and the Neuroscience Multi-omic Archive (NeMO) after initial data processing. In addition to the deposition of data through the BCDC portal, we will also make all data available through the NCBI Gene Expression Omnibus (GEO) and Sequence Read Archive (SRA), for the mouse data sets.

Human single cell data will be deposited to NeMO.

Upon publication we will host processed data matrixes and associated metadata as compressed downloadable archives either at the BCDC or NeMO and when appropriate as supplementary information in journal publication.

1. **Description of the Standards/Data Dictionaries**

As detailed in the research strategy section, we propose the generation of a spatially-mapped single-cell atlas of the developing mouse brain and include specific deliverables. Our primary deliverable for each modality will be a matrix of cells × (counts in peaks for ATAC, UMIs in genes for RNA, or methylation status for DNAm) along with a dense metadata table with information for each cell including the animal sex, developmental time point, punch of origin with x,y,z coordinates, assigned cluster and cell type inferred, assigned subcluster and cell type inferred, as well as a number of QC metrics (total reads, passing reads, reads in peaks, TSS enrichment, cell barcode combination, date of preparation for each stage, sequencing platform, likelihood of being a doublet, and any other relevant metrics that arise during the project). We will use the standards defined by the NeMO archive.

1. **Validation Schedule**

Data will be validated using the existing pipelines at the BCDC. We will submit each dataset once we reach a specific data freeze milestone. Upon each data freeze we will perform an initial phase of analysis that will culminate in the production of the cell × property matrix and associated metadata, at which point the dataset will be released. These milestones and target timelines include:

End of 1st quarter of year 2: A full spatial single-cell ATAC-seq map of an entire mouse brain at P14.

End of 4th quarter of year 2: An accompanying spatially-mapped single-cell RNA-seq dataset for a full mouse brain at P14, integrated with the ATAC dataset.

End of 2nd quarter of year 3: A full spatial single-cell ATAC-seq map of each time point.

End of 2nd quarter of year 3: A full spatial single-cell DNA methylation map for P14, integrated with RNA and ATAC datasets.

End of 4th quarter of year 3: The complete spatial single-cell RNA-seq dataset for all time points, integrated with the ATAC data.

End of 4th quarter of year 3: A full spatial single-cell map for all modalities, ATAC, RNA, and DNA methylation, integrated across modalities.

1. **Additional Resource Sharing Plans**

We will release datasets associated with the technological advances proposed in the application once protocols are established and initial analysis performed, at which point data will be released along with a preprint prior to manuscript submission.

Software and code sharing: All code and software that will be written for this work will be deposited on GitHub for public access and be provided as Supplementary Code files for any publications.

Methods distribution: In addition to a detailed methods section for any publications associated with this work, we will provide a detailed step-by-step protocol as a Supplementary Protocol document and maintain active protocols.io protocols for each technology and workflow. We will additionally release protocol links as metadata to be associated with single-cell data deposited to NeMO.

Distribution efforts: In addition to providing detailed protocols, the laboratory has hosted visiting scientists to train on the technologies developed and deployed by the lab. We welcome the opportunity to continue these training efforts.