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The NIDA Center for Genetic Studies at SAMPLED Develops Novel Multiomic Solutions for NIDA Investigators: A Case Study

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SAMPLED established a number of resources for NIH agencies, among them the NIDA Center for Genetic Studies (NGCS) and the biobank for the HEALthy Brain and Child Development (HBCD) Study. While the NGCS was conceived as a cell, DNA and clinical data resource designed to facilitate cost-effective sample sharing among NIH researchers, it has surpassed that original mandate by providing services beyond sample processing and including Whole Genome and Single Cell sequencing, ATAC-Sequencing and Proteomics.

We will present a study that exemplifies our approach in collaborating with investigators to develop innovative solutions to achieve their scientific goals while maximizing the utility of the precious biospecimens in the collection. Dr. Yasmin Hurd designed a study to interrogate the transcriptome and chromatin accessibility related to opioid dependence through RNA-sequencing and ATAC-sequencing, respectively. This study leverages the PBMC biospecimens that have been collected as blood samples, along with critical clinical and phenotypic data, for more than 20 years by participating NIDA studies, followed by processing and cryopreserved of the PBMCs at SAMPLED. These cells are a limited non-renewable resource making it imperative to develop a novel workflow for performing ATAC- and RNA-Seq, as well as MS-based proteomic analysis, from a single vial. In this presentation, we will describe the development of the workflow and its impact on specimen and data quality. This case study highlights the critical role of biorepository, as guardian of precious genetic resources, in designing processing strategies that take present and future applications into account.

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