

# CHRD 2024: Abstract Submission Form

**Presenter Name**

Alana Lamont

**Presenter Status**

Non-Trainee

**Role in the project**

Write Abstract

**Research Category**

Basic Science

**Title**

Development of the Precision Genomics Suite for Investigating Biological Pathways at the Single-Cell Level

**Background**

Advances in single-cell RNA sequencing (scRNA-seq) have opened new avenues to dissect biological pathways at a resolution that was not previously possible. However, the high cost of specialized instruments for single-cell experiments can be a barrier. Therefore, we established the local Precision Genomics Suite, to allow for the development of an integrated workflow for single-cell multi-omics (Chromium iX) and spatial transcriptomics (Visium/Xenium workflows).

**Objective**

Here, we describe using this suite to generate snRNA-seq data to examine the genetic basis of an adverse drug reaction: cisplatin-induced ototoxicity (CIO) in pediatric cancer patients.

**Methods**

6-day-old CBA/CaJ mice were treated with cisplatin (n=6, 3 mg/kg) or saline (n=6), both administered intraperitoneally. Four-hours post treatment with cisplatin or saline, whole cochlear ducts were dissected, nuclei isolated using the Chromium Nuclei Isolation Kit, and libraries were prepared using the Chromium iX. Sequencing was performed on an external NovaSeq X Plus, and data was processed locally using CellRanger, Seurat and MiloR.

**Results**

After applying minor modifications to the nuclei isolation protocol, snRNA-seq libraries were successfully generated. In total, RNA from 15,510 control nuclei and 12,194 treated nuclei were sequenced. Preliminary data revealed that treatment with cisplatin led to a reduction in the proportion of specialized auditory cells, supporting cells, and bone cells in the inner ear and an increase in the proportion of macrophages (MILO-R: LogFC<=-3, SpatialFDR<0.1).

**Conclusion**

Single-cell sequencing has identified novel insights into the biology of CIO. These technologies represent a cutting-edge approach that can be applied to an abundance of biological questions. The single-cell field is evolving quickly, and new technologies such as GEM-X and spatial transcriptomics promise to produce data with even higher throughput and sensitivity. The Precision Genomics Suite offers the opportunity for labs who have an interest in single-cell assays to generate these state-of-the-art data.

**Do you have a table/figure to upload?**

No

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