



# Single-Nucleus Multiome Sequencing

## Product Overview

The **10x Single Cell Multiome** assay allows profiling of the transcriptome and accessible chromatin at the single nucleus level. The assay can be used with nuclei hashing for sample multiplexing reducing technical variability. 10x's Multiome kit is based on the generation of nanoliter-scale droplets in which a single nucleus will bind to a gel bead coated with oligos containing a unique barcode, UMIs and sequences to capture poly-A tails of mRNA transcripts (for GEX) and specific capture sequences to capture transposed DNA fragments (for ATAC). A unique pool of pre-amplified transposed cDNA and DNA will be the template material for both GEX and ATAC libraries.

Sequencing will be performed on the NovaSeq X Plus platform (Illumina) with tailored sequencing settings based on the project design and the user's needs.

## What is Included

- Cell sorting using FACS (optional)
- GEM generation and Single Cell library preparation
- Quality control of library
- Library pooling and sequencing on Illumina NovaSeq X Plus
- FASTQ files
- ATAC: Standard data processing using CellRanger ARC
- RNA: Standard data processing, QC, and basic bioinformatic analysis. HTO demultiplexing (if applicable).

## Input and quality requirements

### Isolation of cells or nuclei

Isolation of nuclei is the responsibility of the user. Contact [SCOP](#) to consult.

### Quality

The quality of the nuclei will reflect the downstream process – poor quality leads to poor data.

- Intact nuclei
- No to minimal debris and nuclei aggregates
- Optional quality measures: DV200 > 30% for nuclei.

SCOP strongly recommends performing a pilot experiment to assess both sample and data quality.

### Cell Hashing

Cell hashing (if applied) is the responsibility of the user, and samples should be incubated with cell hashing antibodies (Hashtags, provided by SCOP) prior to sample drop-off. Contact SCOP to consult on nucleus hashing and protocols.

### Sample drop-off

Single nuclei should be delivered at a specific concentration which depends on the assay type and the desired number of nuclei. Contact SCOP for more information.

## Data Deliverables

SCOP's preprocessing workflow includes:

- FASTQ files
- Multiome data output (CellRanger ARC)
- ATAC data output (CellRanger ARC)
- RNA: data output and preprocessed data stored in Seurat objects
- Figures visualizing the data.