BROAD
CLINICAL LABS

PRODUCT DATASHEET

10X Genomics Single Cell Multiome (ATAC-Seq + Gene Expression)

Product Overview

Broad Clinical Labs' Multiome service utilizes a kit developed by 10x Genomics that combines ATAC-seq (assay for transposase accessible chromatin) and Gene Expression, simultaneously generating transcriptomic and epigenetic information from a single source sample. This service enables customers to assess cell states and regulatory mechanisms more deeply than with single cell expression data alone.

Broad Clinical Labs' automated 10X Multiome process yields a level of data consistency and quality difficult to achieve in lower-throughput laboratories using manual sample preparation methods. Broad Clinical Labs has successfully generated data for nuclei derived from blood, tumor tissue and fresh frozen brain tissue.

What's Included

- Sample preparation, including 10X Chromium run and subsequent library preparation steps.
- Library QC and sequencing
- Data delivery to customer-owned cloud location in Google Cloud or Amazon Web Services; or Terra Workspace
- All submissions will be sequenced in units of full flowcells, with the number of flowcells dependent on the batch size submitted.

Input Requirements

- 3,000-10,000 cells or nuclei, suspended in 5uL of cell/nuclei suspension 10x "Diluted Nuclei Buffer" (available to purchase from 10X Genomics); ~60% recovery during encapsulation

Data Deliverable

- Raw BCL files; analysis available on request

Data Deliverable (cont.)

- Sequencing coverage achieved per cell will depend on the number of nuclei submitted and the flowcell type (flowcell Gb output / total number of nuclei = estimated reads/nuclei). The minimum recommended sequencing coverage for gene expression libraries is 20,000 reads/nuclei, and 25,000 reads/nuclei for ATAC-Seq.

GEX sequencing	Brain tissue	PBMC	10X PBMC reference
Sequenced read pairs	1,145,009,144	1,112,195,732	830,371,627
Valid barcodes	95.1%	93.9%	95.2%
Valid UMIs	100%	100%	100%
Q30 bases in barcodes	96.4%	96.2%	93.2%
Percent duplicates	78.9%	83.3%	89.1%

Figure 1. Representative performance of Gene Expression Profiling via the Mulitome assay. The quality summaries above show performance of two experimental samples, fresh frozen brain tissue and PBMC isolated nuclei (which have different nuclei isolation protocols and are shown in columns 1 and 2) compared to reference data from 10X genomics (column 3).

ATAC Targeting	Brain tissue	PBMC	10X PBMC reference
Number of peaks	125,019	106,710	111,857
Fraction of genome in peaks	3.4%	2.9%	3.0%
TSS enrichment score	6.40	8.01	9.83
Fraction of high-quality fragments overlapping TSS	26.9%	35.3%	50.4%
Fraction of high-quality fragments overlapping peaks	36.0%	46.9%	63.6%

Figure 2. Representative performance of ATAC-Seq via the Multiome assay. Again experimental samples perform similarly to the control. Per 10X Genomics specifications, TSS scores >5 indicate a high ratio of chromatin accessible signals to noise

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