

SINGLE CELL OMICS

| Capture and Library Preparation | | | | |
|---|---------------------------------------|---|--|--|
| Application | Platform | Capture Range | Optimal Cell Concentration | Deliverables |
| 3' scRNA-Seq • Optional: With cell surface protein expression and/or sample multiplexing | 10x Genomics Chromium | 500 – 10,000 cells | 700 – 1,200 cells/ μ l | Outputs from CellRanger, FASTQ files |
| 3' scRNA-Seq + CRISPR screening | 10x Genomics Chromium | 500 – 10,000 cells | 700 – 1,200 cells/ μ l | |
| scATAC-Seq | 10x Genomics Chromium | 500 – 10,000 nuclei (nuclei isolation from 100,000 – 1,000,000) | NA | |
| scCNV | 10x Genomics Chromium | 250 – 5,000 cells or nuclei | 200 – 4000 cells/ μ l, dependent on targeted cell recovery | |
| scV(D)J, B or T cell enrichment • Optional: With 5' scRNA-Seq • Optional: With cell surface protein expression and/or sample multiplexing | 10x Genomics Chromium | 500 – 10,000 cells | 700 – 1,200 cells/ μ l | |
| Cell lysis, RT, cDNA amplification, cDNA QC | Plate-based full transcript scRNA-Seq | Minimum 94 cells | NA | Gene count matrix (TPM/COUNT), QC summary table, MultiQC report, FASTQ files |
| Library preparation and QC | | | | |
| Library preparation only for any 10x Genomics application | | | | |
| Processing of cryopreserved cells | | | | |
| Dead cell removal | | | | |

SINGLE CELL OMICS

| Sequencing | | | | | | |
|-------------------------------------|----------|-----------------------|--------------------------|-----------------|--|--------------------------------------|
| Application | Platform | Read Length | Maximum Output | Sample Minimum* | Sample Requirements | Deliverables |
| 10x Genomics 3' scRNA-Seq libraries | NovaSeq | 91 bp transcript read | 400M | 2 | <ul style="list-style-type: none"> • Pooled, multiplexed libraries • Sample names with letters, numbers, dashes, and underscores only • Library preparation kit name • Index kit name • Index names and sequences | Outputs from CellRanger, FASTQ files |
| 10x Genomics scATAC-Seq libraries | NextSeq | 2 x 70 bp | 2 x 130M, 2 x 400M reads | 1 | | |
| | NovaSeq | 2 x 50 bp | 2 x 400M | 2 | | |
| 10x Genomics scCNV libraries | NovaSeq | 2 x 100 bp | 2 x 1.6B | 1 | | |
| | NovaSeq | 2 x 150 bp | 2 x 800M | 1 | | |
| 10x Genomics scV(D)J libraries | MiSeq | 2 x 150 bp | 2 x 15M | 1 | | |
| | NovaSeq | 2 x 150 bp | 2 x 400M | 2 | | |
| 10x Genomics 5' scRNA-Seq libraries | NovaSeq | 91 bp transcript read | 400M | 2 | | |

* Turnaround time of 3-5 business days if sample minimum is met. If sample minimum is not met, please allow for extra lead time. Alternatively, samples may be processed sooner for an additional cost. Contact genomics@cshs.org for more information.