

Get started with Illumina single-cell sequencing

Find the right kit configuration to achieve high-quality single-cell sequencing results



Illumina Single Cell 3' RNA Prep at a glance

Consideration	Details
Input type	Fresh cells, nuclei from fresh or frozen tissues, or DSP-methanol fixed samples
Input quantity	100s to 200,000 cells per reaction
Cell quality	Ideal cell viability > 90% but tolerant of lower viability and debris
Sample multiplexing	Up to 96 unique dual indexed sample libraries per sequencing run
Sequencing platform	NextSeq 1000, NextSeq 2000, NovaSeq 6000, NovaSeq X, NovaSeq X Plus Systems
Analysis	DRAGEN Single Cell RNA App, Illumina Connected Multiomics
DSP, dithiobis (succinimidyl propionate).	

Illumina Single Cell 3' RNA Prep provides fast, flexible single-cell processing that captures up to five times the number of cells per reaction at half the cost per cell as leading alternatives.* Powered by PIPseq™ chemistry, this solution creates barcoded partitions for single-cell RNA sequencing (scRNA-Seq) without the need for complex microfluidics and labor-intensive protocols. Characterize diverse and challenging sample types for a comprehensive, high-resolution view of complex tissues.

*Data calculations on file. Illumina, Inc. 2026.

Flexible workflow that can be customized to your needs

Illumina Single Cell 3' RNA Prep is available as a comprehensive workflow for researchers who value convenience or as individual products that separate cell capture and library preparation for users seeking a modular, customizable workflow.

Optional accessory products further customize the workflow, including:

Illumina Single Cell Nuclei Isolation Kit

For nuclei isolation from large cells or fresh frozen tissue

Illumina Single Cell Supplemental Enrichment and Amplification Kit

For targeted amplicon sequencing

Illumina Single Cell Unique Dual Indexes (UDIs)

For high-plex pooling of libraries for high-throughput sequencing applications

Multiplex sequencing libraries with Illumina Single Cell UDIs

- Save reagent costs and instrument run time
- Enable high-throughput studies without increasing turnaround time
- Ensure accurate sample identification and minimize index hopping

Multiple kit configurations to match your sample type, study scale, and research goals

Illumina Single Cell 3' RNA Prep easily scales from hundreds to hundreds of thousands of cells to support various research application needs.

Kit	No. of cells per reaction	Ideal for	Example sample types
T2	up to ~2000	Enriched cell populations, pilot studies, or limited sample availability	Organoids, low-diversity samples, enriched populations of primary cells
T10	up to ~10,000	Cell type identification in tissues	PBMCs, tumor biopsies, mixed cell cultures, heterogenous tissues
T20	up to ~20,000	Diverse cell population profiling, timed studies	Dissociated tissue from biopsies, whole blood, or PBMCs
T100	up to ~100,000	Large projects and maximum resolution	Dissociated tissue, rare cell identification without pre-enrichment

PBMCs, peripheral blood mononuclear cells.

Single-cell applications



Cancer cell heterogeneity analysis

Identify rare immune cell populations in drug-resistant samples from DSP-methanol fixed cells from breast cancer tissue with the T100 kit and sequence on the NovaSeq™ X Plus System.



Immune cell type profiling

Investigate gene expression changes from interacting cells with lung fibroblasts cocultured with macrophages with the T2 kit and sequence on the NextSeq™ 2000 System.



Developmental lineage tracing

Measure cell type expression differences between individuals using nuclei from frozen liver or heart tissue with the T20 kit and sequence on the NovaSeq X Plus System.



Drug response characterization

Profile target markers for novel treatments using intestinal organoids under drug treatment with the T2 kit and sequence on the NextSeq 2000 System.

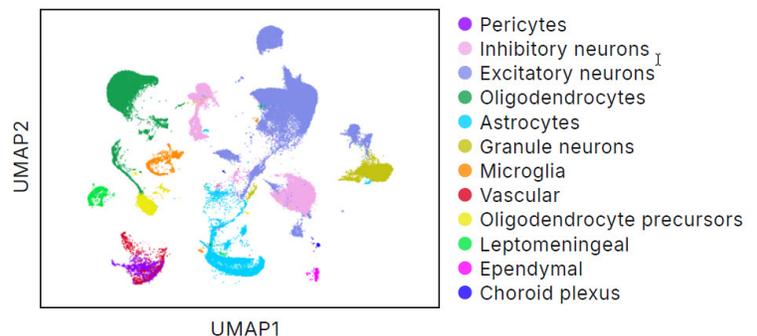
Enable single-cell insights with Illumina bioinformatics software

DRAGEN™ Single Cell RNA App

Analyze and visualize scRNA-Seq data, including summary metrics, clustering plots, differential gene expression tables, and standard feature-barcode matrixes.

Illumina Connected Multiomics

Integrate scRNA-Seq data with spatial transcriptomics, proteomics, methylation data, and more to streamline analysis and unlock deeper biological insights.



Learn more →

Explore Illumina Single Cell 3' RNA Prep kits
Contact your Illumina representative for more information.