



Novogene 10x single-cell RNA-seq (10x scRNA-seq)

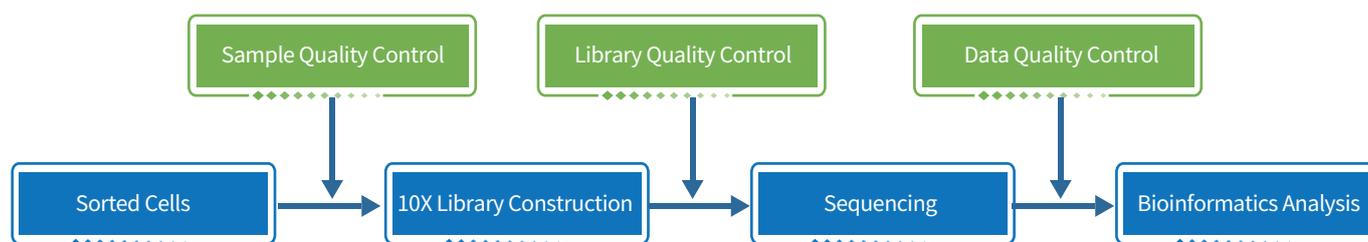
Single-cell RNA-seq can reveal cell-to-cell differences and cellular heterogeneities that have been completely obscured by bulk RNA-seq, thus enabling an exploration of the function of individual cells. Until now, it has been widely applied to multiple research areas, including the immunology, neurology, and stem cell biology, and more.

Based on the Chromium platform (powered by Next GEM technology from 10x Genomics), Novogene's 10x single-cell RNA-seq (10x scRNA-seq), from an expertise perspective, offers services from library preparation, sequencing to bioinformatic analysis at a cost-effective, competitive price and in a customer-focused manner, allowing you to explore the transcriptome and immune profiling cell-by-cell in the sea of cells.

👍 Novogene Advantages

- ✓ More than 200,000 samples successfully sequenced at an industry-leading turnaround time
- ✓ Extraordinary NGS intelligent delivery system applied to provide more efficient and reliable services
- ✓ Exceptional data quality guarantee ($Q30 \geq 85\%$, consistent with Illumina's new benchmarks)

📅 Project Workflow



★ Service Highlights



◆ Sample Requirement

Single cell suspension(cryopreserved) \geq 500K, fresh/snap-frozen tissue \geq 50mg



◆ Library Type

10x single cell 3' & 5' RNA library, 10x single cell V(D)J library, 10x single cell immune profiling library.



Sequencing Strategy

NovaSeq 6000 platform, paired-end 150 bp,
 ≥5000 cells, 150Gb raw data/sample
 (recommended)



Bioinformatic Analysis

Identify clusters of cells, differentially expression analysis between clusters, clonotypes distribution analysis.

Bioinformatics Analysis Pipeline

Pipeline 1: For Gene Expression Standard Analysis



Pipeline 2: For 10X V(D)J Standard Analysis



Novogene Powered Publications

Year	Journal	Title
2019	Cell	Stress-induced metabolic disorder in peripheral CD4+ T cells leads to anxiety-like behavior
2019	Nature Communications	B1 oligomerization regulates PML nuclear body biogenesis and leukemogenesis
2019	Cell Reports	Single-cell RNA-Seq of the developing cardiac outflow tract reveals convergent development of the vascular smooth muscle cells
2020	Nature Immunology	Single-cell transcriptome profiling reveals neutrophil heterogeneity in homeostasis and infection



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