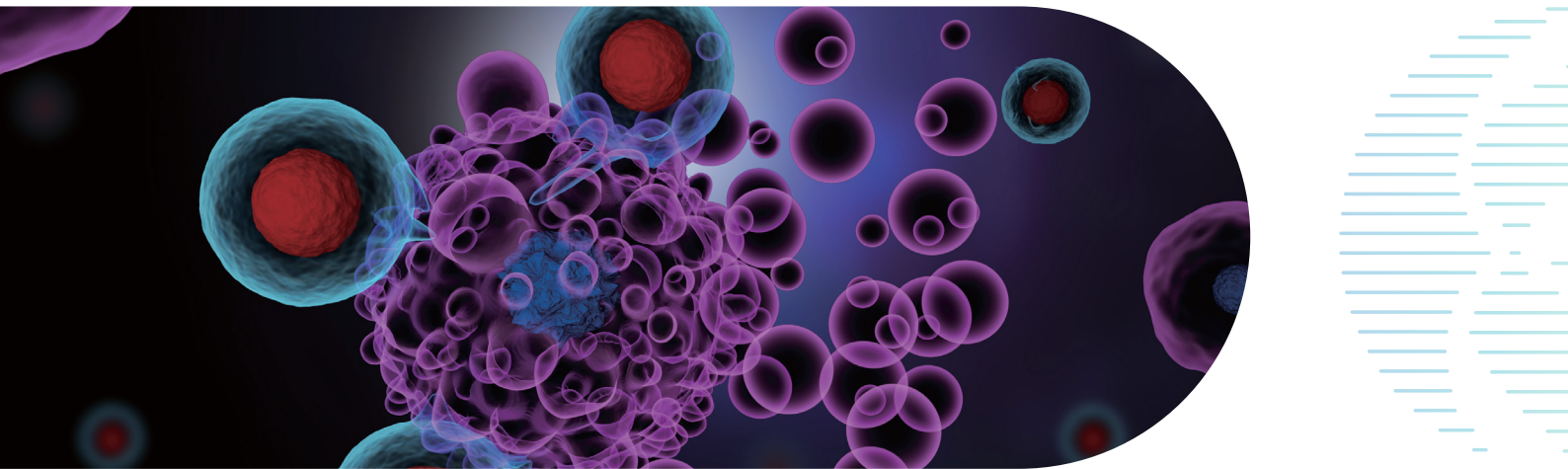


# Single Cell Gene Expression Sequencing



In contrast to whole tissue RNA sequencing, single cell gene expression sequencing has emerged as a promising tool for addressing challenges associated with studying rare cell types, cell lineage relationships, and heterogeneous samples. This technique facilitates the analysis of individual cell functions, enabling researchers to efficiently discover new targets and biomarkers.

Our single cell gene expression services offer comprehensive end-to-end support for your projects. This includes experimental design consultation, onsite services\*, library preparation, Next Generation Sequencing, and bioinformatics analysis.

## Our Key Features and Advantages



### Diverse Sample Type and Project Expertise

- Our expertise and access to multiplatform technologies provide the flexibility to run any experiment.



### No Regional Limitations

- We provide frozen cell services with no scheduling constraints and minimal batch effects for “longitudinal” experiments involving sample collection at different timepoints.



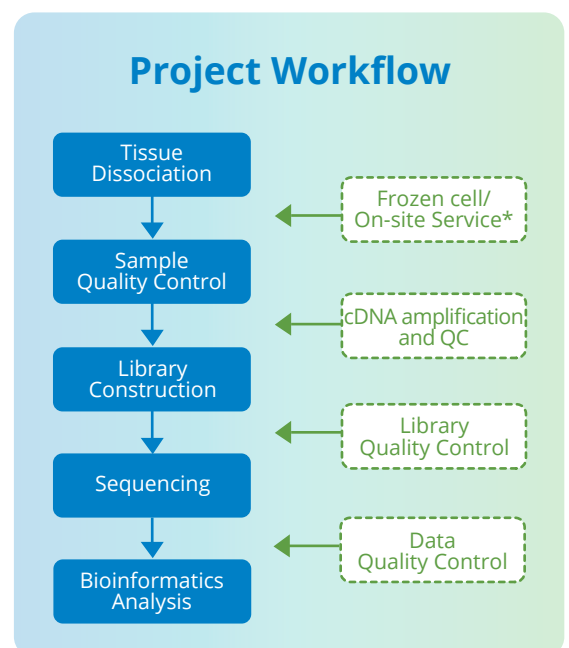
### Onsite Service for Quality Data

- We process single cell samples in your lab, ensuring high viability and quality data.



### Fast Turnaround Time

- Onsite processing of your samples reduces transportation time between each crucial step of single cell sequencing.



\*Applicable for Singapore & Japan customers only.

# Sample Requirements and Data Suggestion

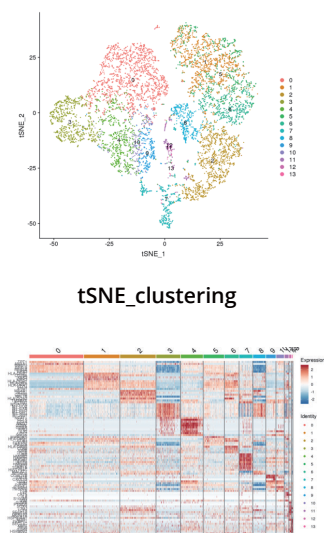
Sample Type	Sample Amount	Cell Viability	Data Suggestion
Fresh Single cell suspension Fresh Single nuclei suspension*	≥ 100,000 cells in 100 µL	Viability ≥ 80%, Cell diameter: 5-30 µm	Sequence Platform: NovaSeq6000 PE150; NovaSeq X plus PE150; 1. Single cell 3'/5' gene expression library: 100 - 120Gb/sample 2. Single cell VDJ library: 15Gb/sample
Frozen single cell	≥ 1,000,000 cells Recommend two 1.5 mL cryovials	Cell viability >85% before freezing Cell diameter: 5-30 µm	

\*Single nuclei suspension – on-site service only. Single nuclei cannot be frozen or shipped by ice.

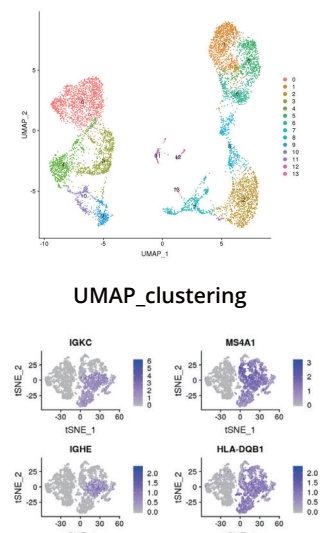
## Analysis Content

Cell Ranger (10x single cell 3' gene expression)	Standard Analysis Pipeline (10x single cell 3'/5' gene expression)
<ol style="list-style-type: none"> <li>Demultiplex BCL files from a sequencer into FASTQs</li> <li>Summary metrics (sequencing quality, number of cells detected, the mean reads per cell, and the median genes detected per cell et al.)</li> <li>Alignment of reads to genome</li> <li>Gene expression quantification</li> <li>Clustering analysis</li> <li>Differentially expression analysis between clusters</li> <li>Visualization</li> </ol>	<ol style="list-style-type: none"> <li>Demultiplex BCL files from a sequencer into FASTQs</li> <li>Alignment, UMI counting, Metrics summary</li> <li>Identification of highly variable gene (HVGs)</li> <li>Cell Subpopulation Identification Principal component analysis (PCA) Identify clusters of cells Dimensionality reduction and Visualization</li> <li>Marker gene detection (Differentially expression analysis between clusters)</li> <li>GO/KEGG/Reactome Enrichment Functional Annotation of Transcription Factor Protein-Protein Interaction Network Analysis</li> </ol>

## Demo Analysis Results



Heatmap showing relative expression of top 10 marker genes exhibiting differential expression across clusters



Expression levels of four representative marker genes of first cluster are color coded (blue) on t-SNE and UMAP plot

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