



Single-cell RNA sequencing

Celinus

Powerful technique for improving
our understanding of human health

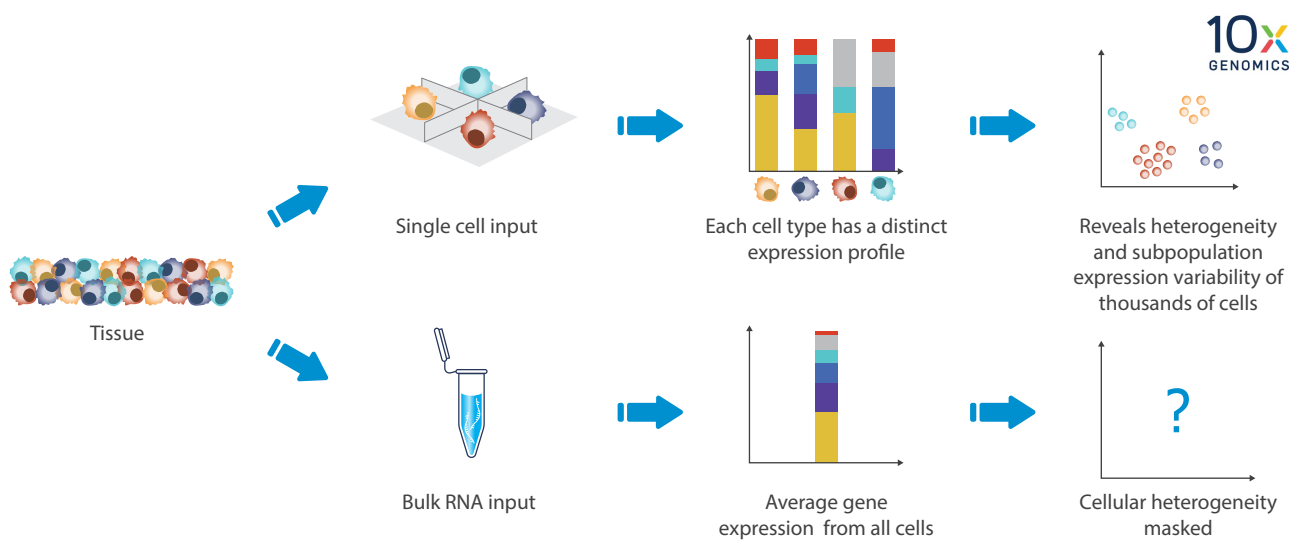


CONTENTS

01	What is Single-cell RNA sequencing?	03
02	Celinus Service	04
03	Service Workflow	05
04	What is the Analysis Process?	06
05	FAQ	08
06	Contact Us	10

What is Single-cell RNA sequencing?

Single-cell RNA sequencing allows the direct measurement of gene expression and genetic alteration at scale with single cell resolution to quantify intracellular heterogeneity and characterize cell types, states and cellular transition dynamics. Through uncovering the transcriptome diversity in heterogeneous samples, reveal novel insights and create new opportunities.



Single cell gene expression profiling reveals cellular heterogeneity that is masked by the conventional bulk RNA-sequencing methods.

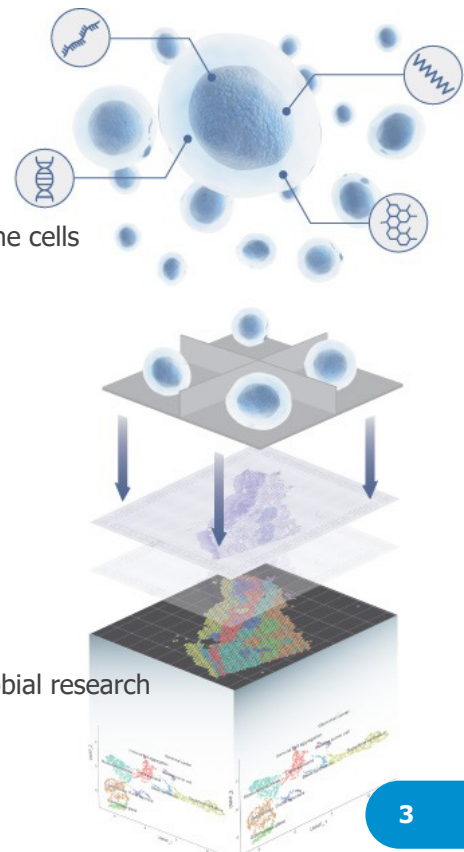
Benefits

- Possible to identify RNA expression in each of thousands of cells
- Possible to check the composition ratio of each cell including immune cells
- Possible to distinguish biomarkers in cell units

Applications



- Cancer research
- Circulating tumor cell research
- Neuroscience or stem cell research
- Metagenomics
- Infectious disease, microbial research
- Embryo genetic research



Celinus Service



Single Cell Gene Expression

- Whole transcriptome profiling for characterization of tens of thousands of single cells
- For identification of cell types, characterization of cell populations, understanding of cellular heterogeneity



Single Cell Immune Profiling

- Immune cell diversity exploration through single cell whole transcriptome analysis
- For immune repertoire profiling, antigen specificity determination, tumor microenvironment characterization



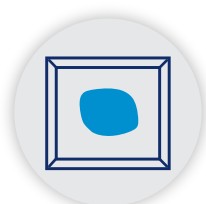
Single Nucleus Gene Expression

- Transcriptome profiling of nucleus isolated from each cell
- For transcriptome analysis in cells which are difficult to isolate, as well as frozen tissue



Single Cell Multiome ATAC (Assay for Transposase Accessible Chromatin)

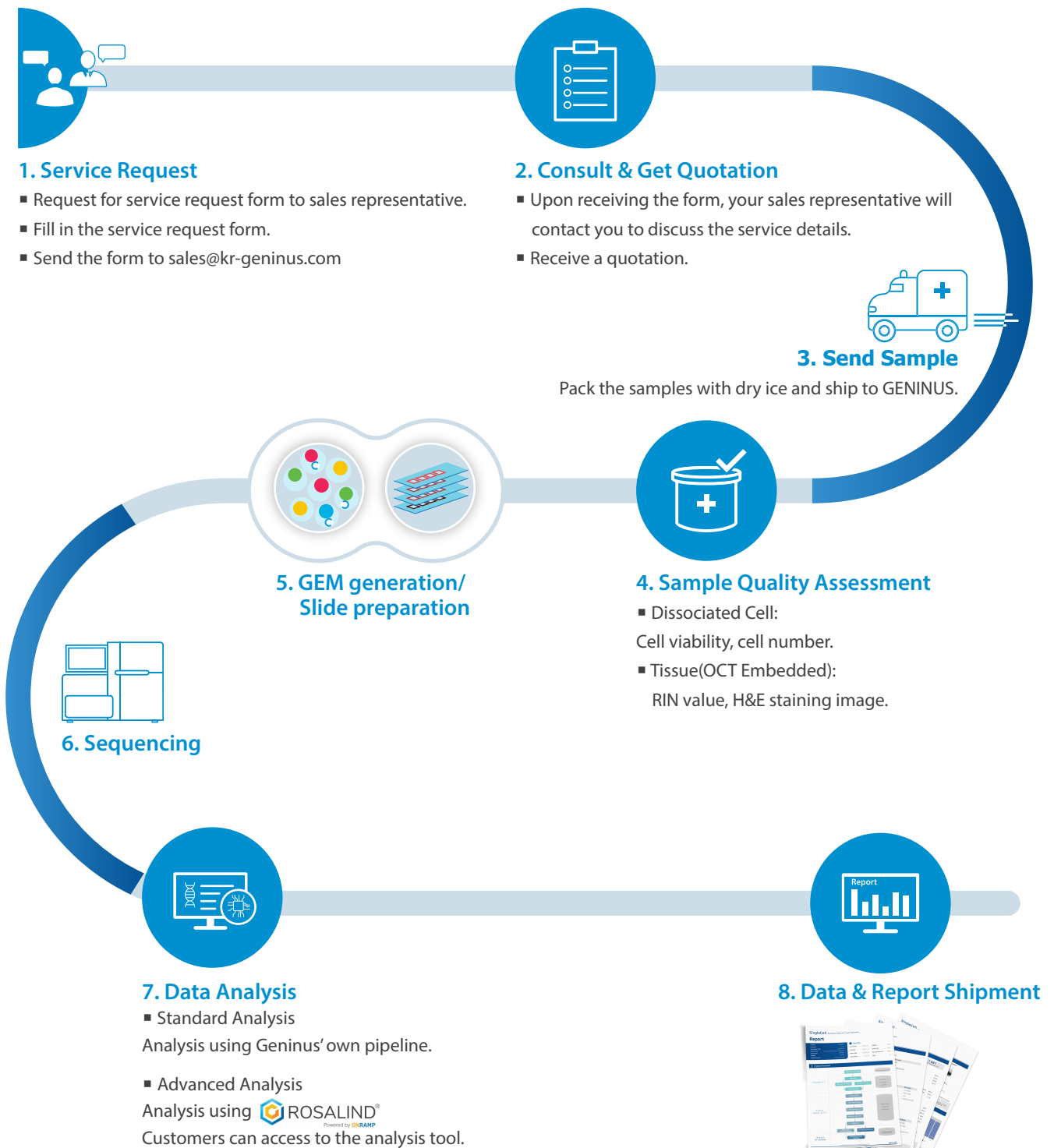
- Epigenomic analysis and whole transcriptome profiling of thousands of individual cell
- For characterization of cell types and states, and uncovering gene regulatory network



Spatial Gene Expression (Visium)

- Relationship analysis between cells and their relative locations within a tissue sample
- For gaining complete view of disease complexity, identification of spatiotemporal gene expression patterns and profiling per site expressions (up to 10 cells per spot)

Service Workflow



What is the Analysis Process?

Standard Analysis

Common Single cell RNA-sequencing



Deliverables

- Data quality measurement
- Data normalization
- Cell clustering
- tSNE analysis
- UMAP analysis
- Loupe file

Spatial Gene Expression



Deliverables

- Spot quality measurement
- Data normalization
- Cell clustering
- tSNE analysis
- UMAP analysis
- Loupe file

Advanced Analysis

Advanced single cell analysis using ONRAMP's Rosalind® Software (Spatial Gene Expression is exclusive)

Process of Analysis



Deliverables

- Data quality measurement
- Data normalization
- Cell clustering
- tSNE analysis
- UMAP analysis
- Loupe file

 ROSALIND®
Powered by ONRAMP



Features & Benefits of Advanced Analysis Tool

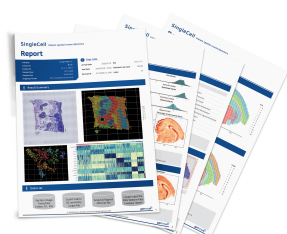
- Single cell analysis for any scientist, no bioinformatics expertise needed
- Secure, scalable cloud infrastructure to process 10X Genomics Cell Ranger data for thousands of cells in parallel
- Real-time collaboration so multiple scientists across sites can explore single cell results at once
- Compare differential expression patterns between cell clusters
- Integrate single cell data in multi-omic comparisons with bulk RNA-seq, ATAC-seq, or ChIP-seq
- Automated public data import to explore trends across public data sets
- Enterprise security with SSO and API integration to enable production informatics teams

Let's work with GENINUS

We are dedicated to support your research by offering helpful resources

Features

- Exclusive Technique for Analysis**
 Utilizing proprietary software to analyze samples.
- Streamlined Assistance with Expertise**
 Experts deliver optimized assistance.
- Customized Service for Researchers**
 Seek and apply optimized procedure for each customer.
- Exclusive Service**
 Nation's only 10X Genomics certified service provider (Spatial Gene Expression).



Research & Publications



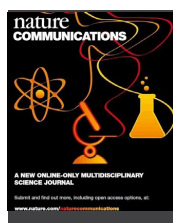
Lineage-dependent gene expression programs influence the immune landscape of colorectal cancer

(*Nature Genetics*, May 25, 2020)



Single-cell RNA sequencing reveals the tumor microenvironment and facilitates strategic choices to circumvent treatment failure in a chemorefractory bladder cancer patient

(*Genome Medicine*, May 27, 2020)



Single-cell RNA sequencing demonstrates the molecular and cellular reprogramming of metastatic lung adenocarcinoma

(*Nature Communications*, May 08, 2020)



Spatiotemporal genomic architecture informs precision oncology in glioblastoma

(*Nature genetics*, March 06, 2017)



SIDR: simultaneous isolation and parallel sequencing of genomic DNA and total RNA from single cells

(*Genome Research*, Jan 28, 2018)

+ 50 Peer-reviewed Publications

FAQ

What I can get?

- 3,000 cells with a sequencing depth of 50,000 reads per cell will be generated for single cell service.
- Sequencing depth of 50,000 reads per spot will be generated for Spatial Gene Expression service.
- Additional data generation is also available upon request.

What do I need to prepare?

For Gene Expression & Immune Profiling

- Dissociated frozen cell stock.
- Isolated PBMC.

For Spatial Gene Expression

- OCT embedded frozen tissue.
(Maximum size is 5x5 mm)
- Sample preparation guide will be provided.

For Single Nucleus Gene Expression

- Frozen tissue sample.

How long does it take to get report?

Servies	Turn Around Time	Remark
Gene Expression	6~7 weeks	
Immune Profiling	7~8 weeks	
Spatial Gene Expression	6 ~7 weeks	Can be extended if minimum number of samples are not collected.
Single Nucleus Gene Expression	7~8 weeks	

What kind of sample is needed for Spatial Gene Expression Service?

▪ Human

Skin, Heart, Kidney, Esophagus, Tonsil, Lung, Stomach, Ovary, Breast, Lymph Node

▪ Mouse

Adipose, Brain, Small Intestine, Stomach, Liver, Brain, Quadricep, Lung, Testes, Thyroid, Eyes, Tongue, Large Intestine, Spleen, Mammary Gland, Spinal Cord

▪ Rat

Brain, Kidney, Heart

*Please contact sales representative if you have samples other than above.

How can I deliver the sample?

- Deliver under -20 °C.
- Pack samples with dry ice in styrofoam box.

Do I need bioinformatician for Analysis?

- Geninus delivers basic analysis report.
- You could also perform analysis using Loupe and Rosalind platform.
(Geninus provide the Loupe input data for every service)
- If you want customized analysis, you may need bioinformatician.

FAQ

Condition of sample

Gene Expression, Immune Profiling

- Concentration of cell stock should be more than 5×10^5 cells/ml per 1 vial.
- Survival rate for total cell should be higher than 80%.

Spatial Gene Expression

- Frozen mold (OCT embedded tissue) must be stored at -80 °C.
- FFPE sample is not available for the service.
- Shipment with dry ice is recommended.
- Geninus sales representative will arrange your shipment.

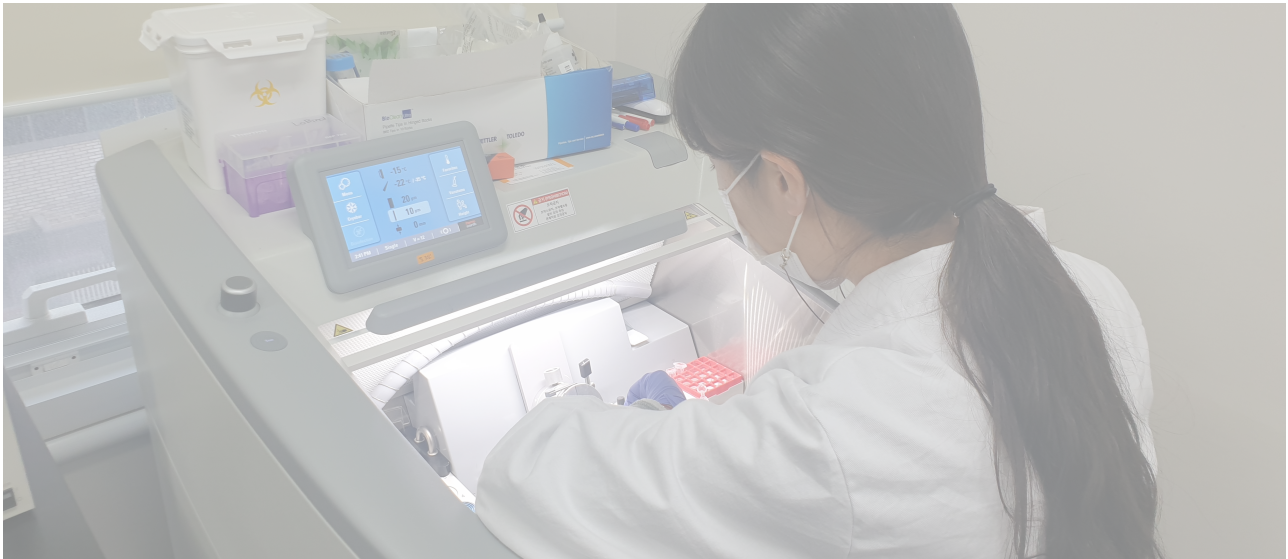
Additional services

- Immunofluorescence paired Spatial Gene Expression.
- On-call sample preparation.
(fresh tissue and whole blood)
- Cell sorting.
(BD FACSMelody™ Cell Sorter)
- High resolution H&E staining image.
(4X, 10X, 20X)
- Additional charges will be applied.
- Consult to the sales representative beforehand.

Promotion

- Discounted price can be applied if you order services with more than 4 samples.
- Collaborative research work is also available upon request.

Contact Us



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