High Throughput Single Cell RNA-Seq

PRODUCT CATALOG

BGI

What Is High Throughput Single Cell RNA Sequencing

1 10x Genomics Chromium System

10x Genomics Single Cell RNA Sequencing is based on an integrated service for high throughput single cell processing, providing sample preparation, cell sorting, droplet different, library construction, sequencing and bioinformatics in one service. By analyzing gene expression among single cells, 10x Genomics high throughput single cell RNA-Seq describes the heterogeneity between cells and facilitates the study of biological interactions.

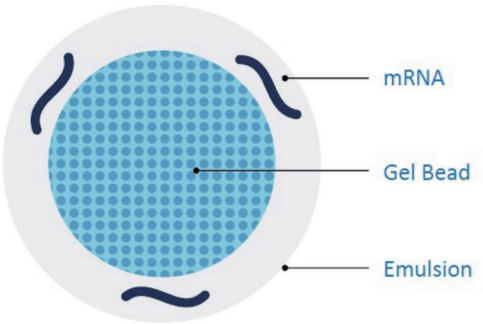

Fig 1. GEM (Gel in Emulsion) Structure

By using microfluidic chip technology and beads with unique barcodes, cell and enzymes are encapsulated by oil to form a Gel in Emulsion (GEM).(See Fig 1) In the GEM, the single cell is lysed to release mRNA, which is then ligated by oligos on the bead, followed by the melt down of the bead, RT PCR, and GEM rupture to form cDNA library.(See Fig 2)

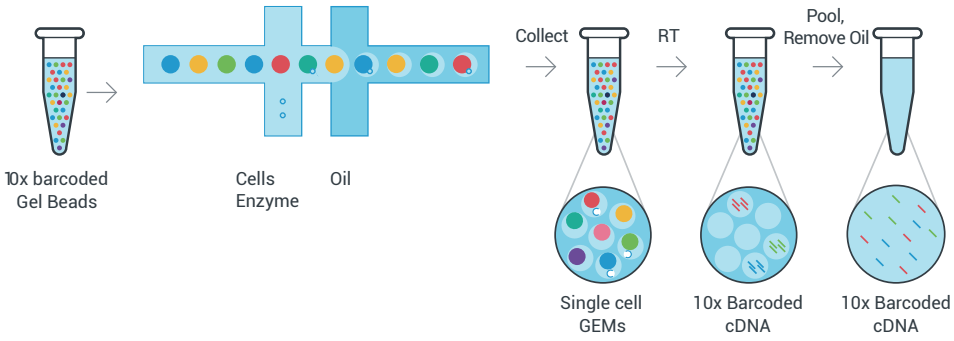

Fig 2. 10x Genomics Library Construction Mechanism

The reverse transcription takes place in droplet to generate cDNA. The emulsion is subsequently broken down to release cDNA for library construction. By identifying the cell barcode on each library, it can be recognized which cell the target region from. Each sequence has its own index to identify which sample it comes from. (See Fig 3)

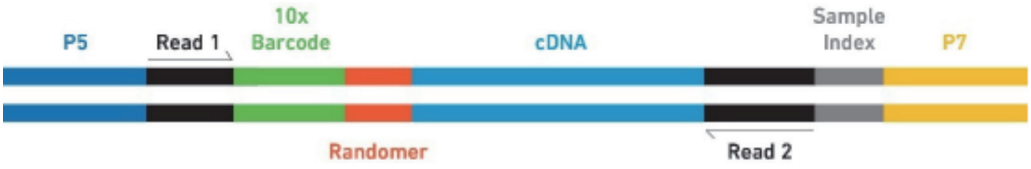

Fig 3. 10x Genomics Library Sequence Paradigm

Why Choose Us for High-Throughput Single Cell RNA Sequencing

2

Advantages

Dr. Tom: A proven convenient intuitive web-based data visualization system.
High throughput processing ability, up to 80,000 cells processed at one time.
Highly automated processing platform, able to complete thousands of cells partitioning within 10 minutes; Amplification and library construction are done in the reaction system; Cell Ranger pipelines provide direct analysis result.
Lower cost for each individual cell.

High Throughput Single Cell RNA Sequencing Workflow

3

Our Service

You can send in the frozen sample to our lab. We will check the cell viability rate. If the rate is less than 80%, then we will perform a cell debris removal to ensure sample quality. Then, the sample is loaded on to the 10x Genomics Chromium System to construct the library. The library will then go through QC and after go into sequencing.(See Fig 4)

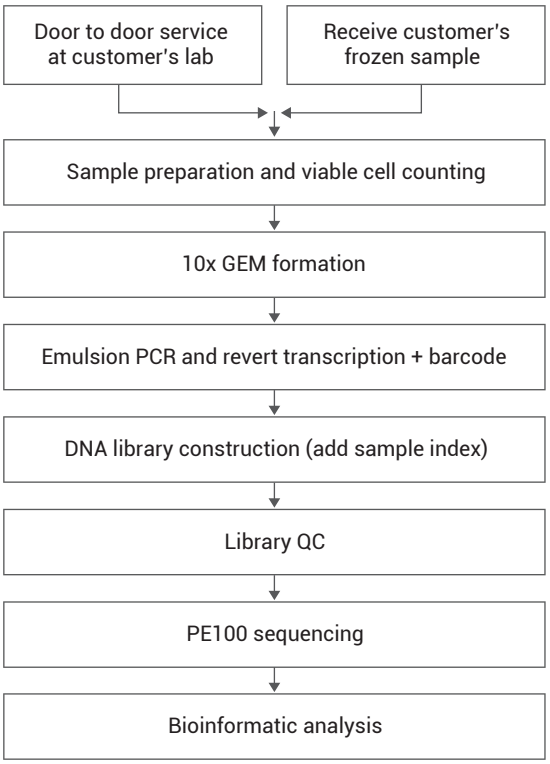

Fig 4. Service Workflow

4 Sample Requirements

Sample Requirements	Sample Type	Tissue	Fresh/Frozen Tissue
		Cell	Tumor Cell, Germ Cell, Embryonic Cell, Immune Cell, PBMC, Cell Line, etc.
	Cell Condition	Cell diameter <40 μm, Cell viability rate>80%, Cell number >5*10^5 cells/sample; Clear background of suspension, no large clumps and debris, no Ca^{2+} and Mg^{2+}	
Turnaround Time	28~45 working days(Case by case)		

5 Bioinformatics Workflow

You can choose from two kinds of bioinformatics analysis service: Cell Ranger analysis, standard Dr. Tom analysis or customized bioinformatics analysis performed according to customers' needs. (See Fig 5) Your standard bioinformatics analysis result will be delivered with our revolutionary easy-to-use web-based bioinformatics analysis system Dr. Tom. (See Fig 6A&6B&6C)

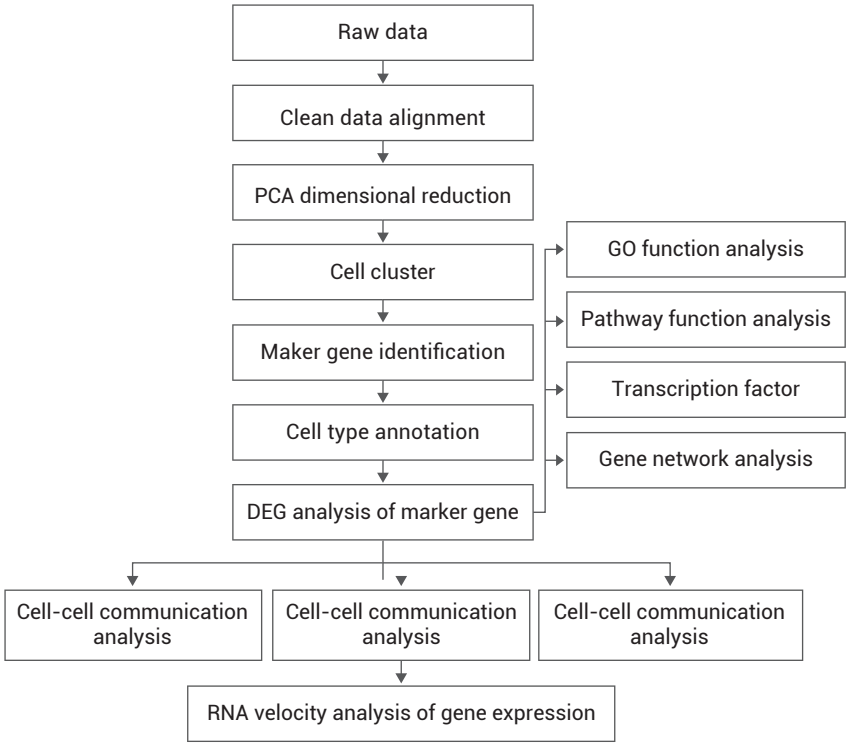

Fig 5. Bioinformatics Workflow

Bioinformatics Analysis	Bioinformatics Analysis Contents
Standard Bioinformatics Analysis	1,Sequencing Result; 2,Comparison Result; 3, Quantitative Analysis; 4, Data QC; 5, Cell Cluster; 6, Differential Gene Identification Between Samples; 7, Cell Cluster Annotation; 8, Marker Gene/Differentially Expressed Gene GO Pathway; 9, Marker Gene/Differentially Expressed Gene KEGG Pathway Fnrichment; 10, RNA Velocity; 11, CellPhone DB; 12, Pseudotemporal Ordering; 13, Customized Cell Cluster Analysis; 14, Customized Cell Cluster Annotation By Database of your choice; 15, Gene-Protein Interaction Analysis; 16, Gene Function Enrichment Analysis; 17, Dynamic Interactive Analysis of Cell Type And Cell Trajectory Analysis; 18, Different Dimension Analysis of Differential Gene Between Cell Types/ Samples;
Customized Bioinformatics Analysis	Customized according to client's needs

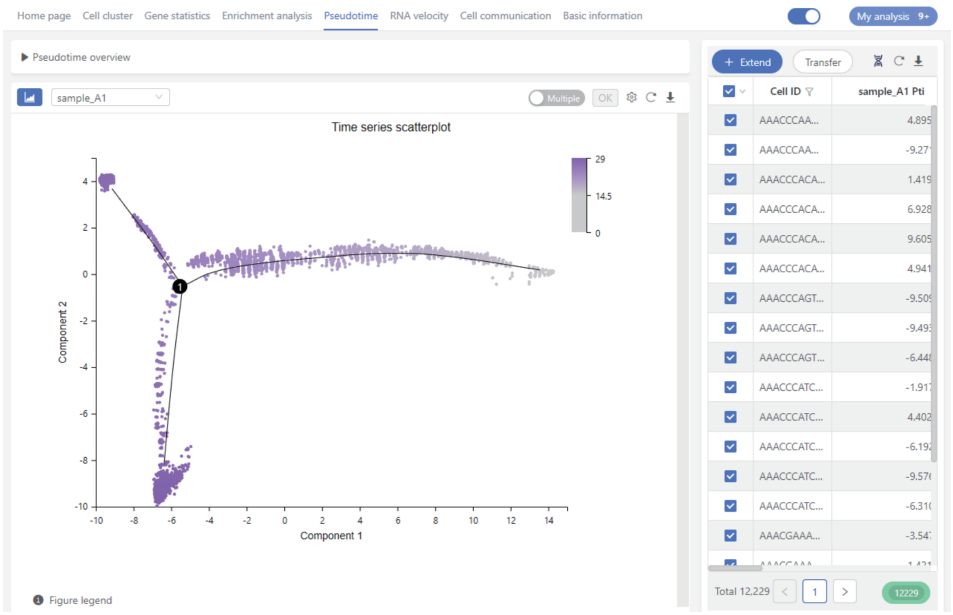

Fig 6A. Pseudotime Overview in Dr. Tom

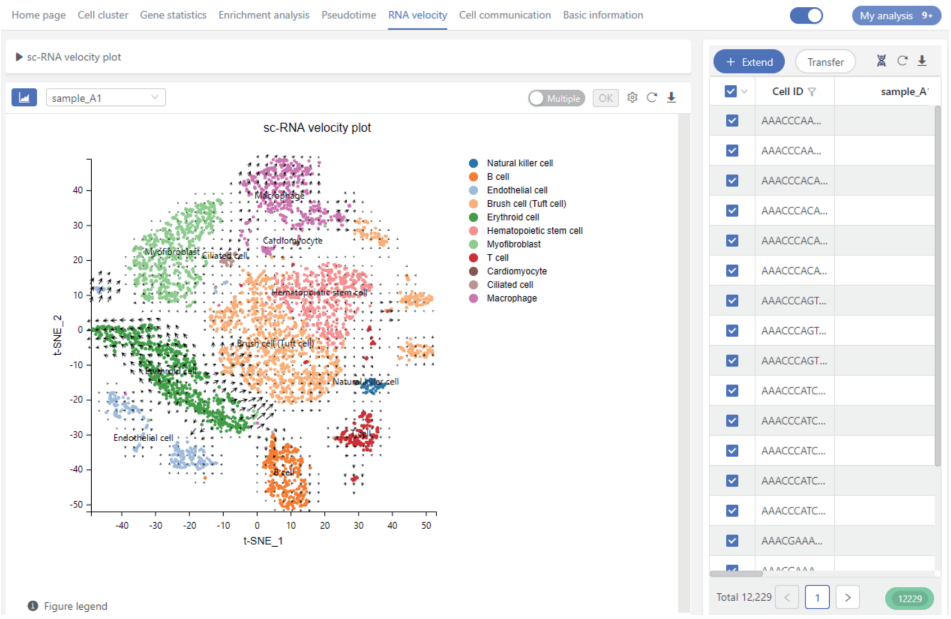

Fig 6B. SC-RNA Velocity Plot in Dr. Tom

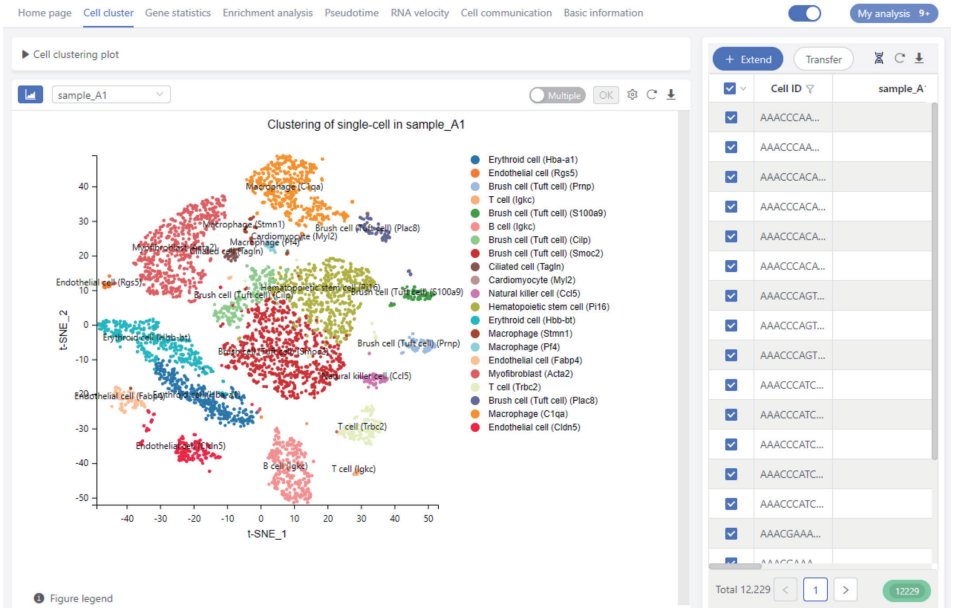

Fig 6C. Cluster Specific Marker Gene Expression Heatmap in Dr. Tom.

6 Case Study 1

LYMPHATIC-LOCALIZED TREG-MREGDC CROSSTALK LIMITS ANTIGEN TRAFFICKING AND RESTRAINS ANTI-TUMOR IMMUNITY

YOU, S., ET AL. (2024). ***CANCER CELL***

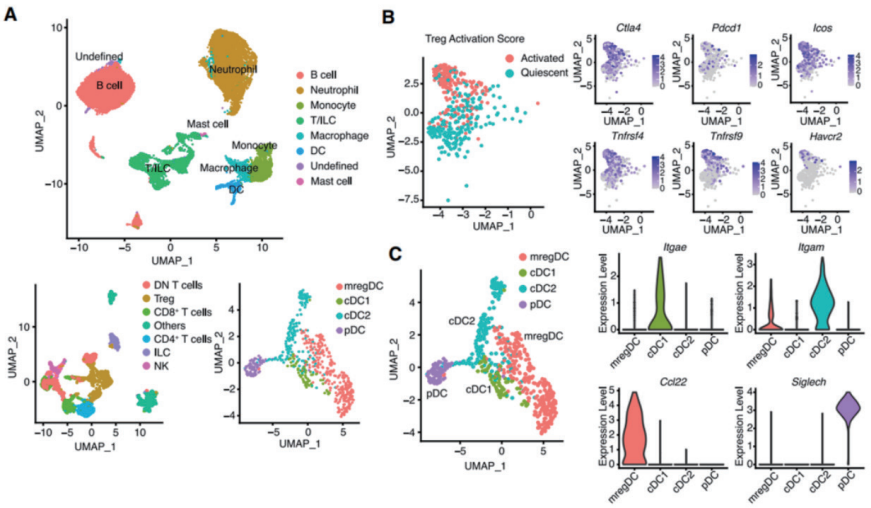

Fig 7 Clusters of T cells and dendritic cells in the tumor microenvironment (TME).

Single Cell RNA-Seq reveals activated and quiescent states of Treg cells in the tumor microenvironment (TME)
(Fig 7B). Dendritic cells (DCs) were grouped into four clusters: mregDC, cDC1, cDC2, and pDC (Fig 7C).

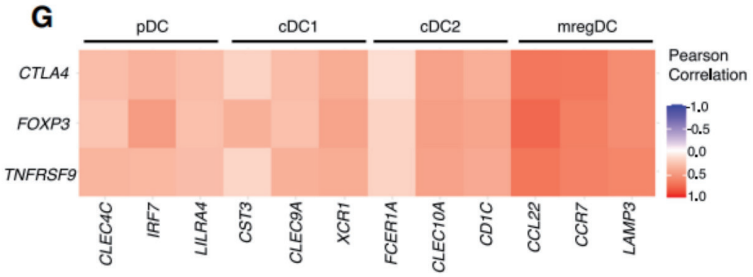

Fig 8 Treg-mregDC-lymphatic niche in tumor stroma

Treg and mature dendritic cells enriched in immunoregulatory molecules (mregDCs) had extremely high ligand-receptor interactions (Fig 8). Immunofluorescence staining further verified that Treg and mregDC co-aggregated around lymphatic vessels. This spatial distribution feature is named Treg-mregDC-lymphatic niche.

Case Study 2

GROWTH HORMONE PROMOTES MYELIN REPAIR AFTER CHRONIC HYPOXIA VIA TRIGGERING PERICYTE-DEPENDENT ANGIOGENESIS.

REN, XIA ET AL. (2024) *NEURON*

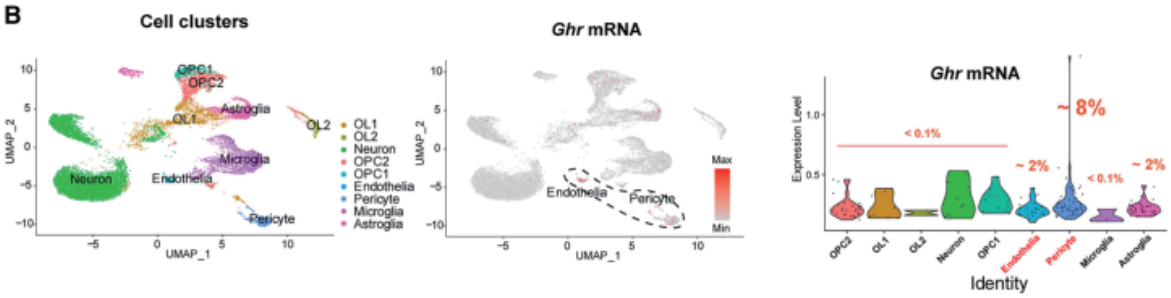

Fig 9 Ghr mRNA was highly enriched in vascular cells, especially in pericytes (~8%) and Endothelia (~2%) (Fig 9).

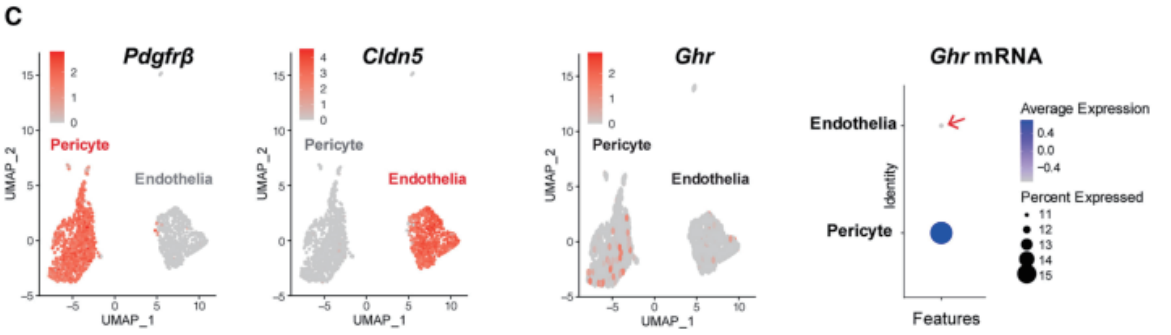

Fig 10 The expression rate and level of Ghr mRNA in pericytes were significantly higher than those in endothelial cells (Fig 10). This cluster is named pericyte tip cells (PTC) according to its morphological characteristics.

www.bgi.com
info@bgi.com

www.bgi.com BGI Genomics