Capital Bio TECHNOLOGY

sCelluFlu-A® Single-cell Transcriptome Solution

Introduction to Products

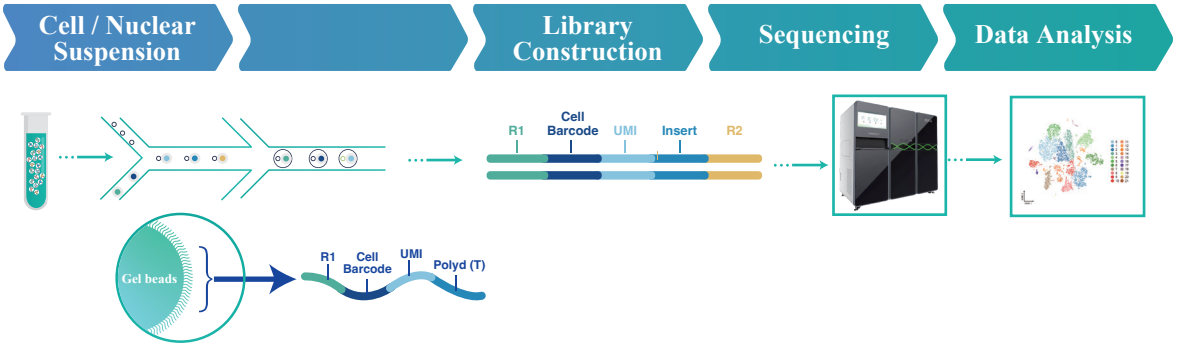
sCelluFlu-A® CapitalBiotech High-Throughput Single-Cell Transcriptome Solution is an industry-leading, stable-performance, flexible and efficient high-quality droplet microfluidic high-throughput single-cell transcriptome solution. Using the compact and simple microfluidic separation device, the water-in-oil structure containing probe gel beads and single cells can be formed quickly in 150s. Next, mRNA released by the cell lysis is captured by probe gel beads, reverse transcribed to form cDNA, and processed for recovery and library construction, obtaining gene expression data for 500-20000 cells. This solution provides the efficient, high-quality and accurate research data for fields such as tumor research, immunology, neuroscience, developmental biology, drug development and molecular diagnostics.

1-8 samples can be loaded flexibly for one time

500-20,000 captured cells

Water-in-oil structure formed in 150s

Polyploidy rate in 1000 cells: 0.3%



sCelluFlu-A® Single-cell Transcriptome Sequencing Workflow

Platform Advantages

High Quality

Stable Cell Capture

Capture rate: 50%

Median gene count: above 1,000

High repeatability and mini mized coefficient of variation

High Speed

High-speed Water-in-oil Forming, and Less Stress

Water-in-oil time: 150s

At least a two-fold reduction in mitochondrial content

Capable of capturing fragile cells like neutrophils

High Throughput

High Throughput, Low Polyploidy Rate

Sample can be loaded onto machine individually

8 channels x 20,000 cells multi-

cell rate 3% / 10,000 cells

High Values

Super-high Cost Effectiveness

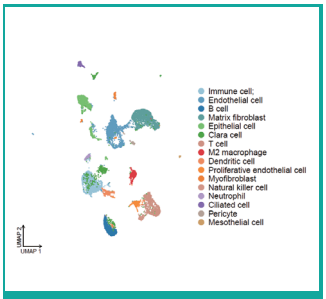
Superior performance comparable to high cost products

Significantly reduced clinical cohort costs

Data Display

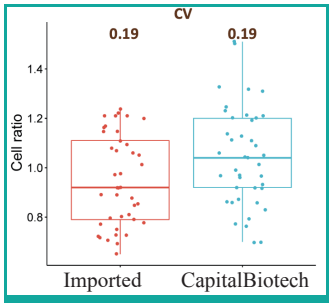
Species	Tissue	Data Volume / G	Cell count	Median gene count	Saturation percentage (%)
Mouse	Tumors	141	12003	1235	80.52
Human	293T	120	8435	3941	49.60
Human	PBMC	120	7701	1679	84.83
Human	Fetal stomach	109	10491	1395	75.07
Human	Ovary	120	11109	1924	72.33
Human	Polyps	141	8273	1470	75.89
Human	J. Dermatol.	180	13334	1334	79.73
Human	Gingiva	111	13163	1169	77.25
Human	Heart valve nuclei extraction	180	18045	1044	85.97
Mouse	Brain nuclei extraction	120	10119	2352	53.19
Mouse	Brain nuclei extraction	120	8645	2432	51.10

Human PBMC

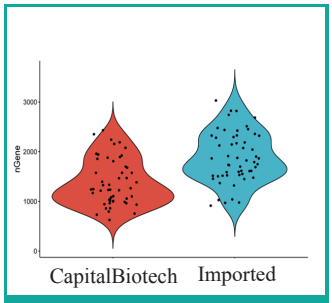


Mouse lung

1. High stability with an average cell capture count above 10,000. The ratio of actual cell capture count to expected counts ranges from 50%-150%, with the median gene count for routine sample types stabilized in 1,000-2,000.



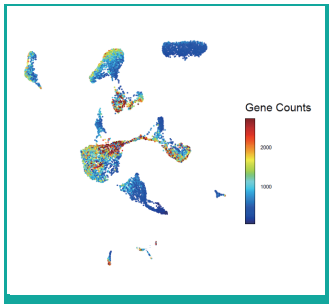
Actual / estimated cell count statistics



Median gene count comparison

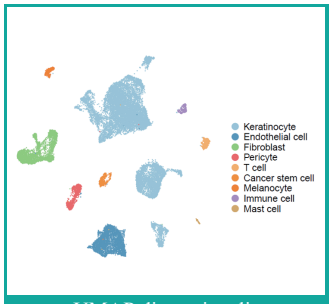
2. It is capable of capturing fragile or low-abundance cell types, such as a large quantity of nucleated red blood cells and neutrophils at various development stages in human bone marrow samples.

Cell type annotation

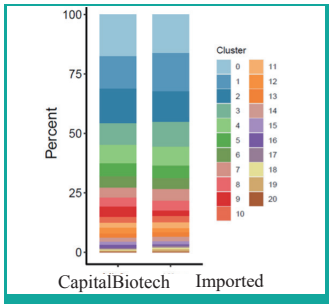


Gene count distribution

3. Comprehensive cell type identification, the high consistency is shown in cell types after combining human skin sample head-to-head data.

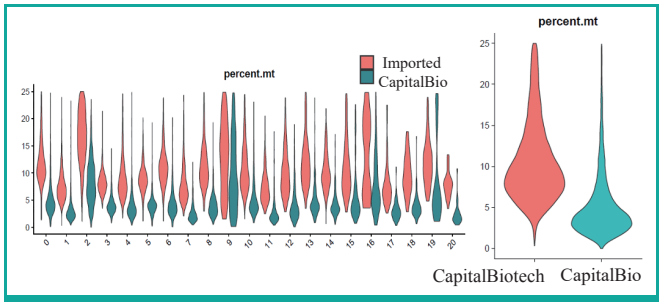


UMAP dimensionality reduction clustering



Cluster proportion

4. The mitochondrial content is reduced, with a significantly lower mitochondrial proportion across cell clusters in combined human liver cancer sample head-to-head data.



Cluster mitochondrial content distribution

Overall mitochondrial content distribution

Data Display

1. Developmental Biology
2. Neuroscience
3. Tumor Research
4. Immunology
5. Infectious Diseases
6. Degenerative Diseases
7. Agriculture and Livestock
8. Drug Screening

CapitalBiotech

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