Ordering Information

	Product Name	Product Name of Component Kits	Catalogue Number	Storage Tempearture
DNBelab C Series High-throughput Single-cell RNA Library Preparation Set V3.0 	DNBelab C Series High-throughput Single-cell RNA Library Preparation Set V3.0(TaiM 4) -4RXNS/SET 940-001924-00	Droplet Reagent	940-001927-00	2℃~8℃
		Droplet Reagent	940-001929-00	-25℃~-15℃
		Lib Prep Reagent	940-001925-00	-25℃~-15℃
		Flow Cell(TaiM 4)	940-001928-00	10℃~30℃
		Sample Labeling Reagent	940-001926-00	-25℃~-15℃
	DNBelab C Series High-throughput Single-cell RNA Library Preparation Set V3.0（TaiM 4）-16RXNS/SET 940-001818-00	Droplet Reagent	940-001820-00	2℃~8℃
		Droplet Reagent	940-001819-00	-25℃~-15℃
		Lib Prep Reagent	940-001821-00	-25℃~-15℃
		Flow Cell(TaiM 4)	940-001822-00	10℃~30℃
		Sample Labeling Reagent	940-001920-00	-25℃~-15℃
	DNBelab C-TaiM 4 Single-cell Droplet Generator		900-000637-00 (China) 900-000780-00 (CE) 900-000781-00 (EAC) 900-000782-00 (UKCA)	10℃~30℃

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MGI

DNBelab C Series

High-throughput Single-cell RNA

Library Preparation Set V3.0

Efficient Multi-beads Capture

Four Independent Microfluidic Channels

Product Introduction

As one of MGI ‘s single cell series products, DNBelab C series high-throughput single-cell RNA library preparation set V3.0 consists of droplet generation reagents, high-throughput library preparation reagents and sample loading flow cell; Droplet generation instrument—TaiM 4 can run 1 to 4 samples per run; Data quality control analysis package—DNBC4 tools is free.

Single-cell Droplet Generator

Single-cell Library Prep Reagents

Data Analysis Package

Lib Prep Reagent
Box 3 (-20℃)

Droplet Reagent
Box 2 (-20℃)

Sample Barcode Reagent
Box 5 (-20℃)

Droplet Reagent
Box 1 (4℃)

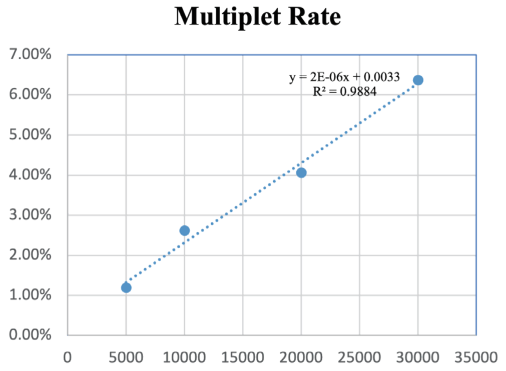
Flow Cell
Box 4 (10~30℃)

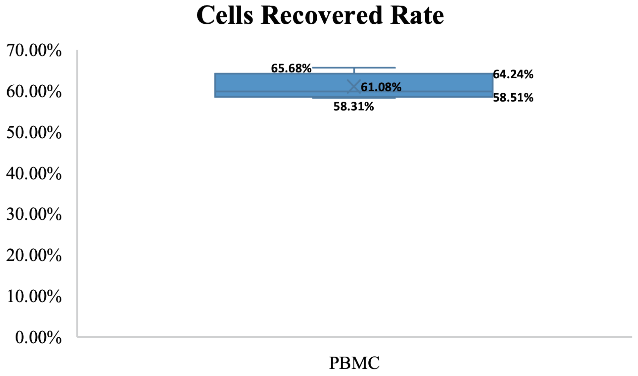
Advantages

- Sensitive detection of genes
- Efficient and stable cells recovered
- Accurately identifying multiple cell beads
- 1-4 samples per run to choose from flexibly
- Fast droplet generation

Performance Parameters

Input cells	5,000 - 30,000
Estimated number of cells	Up to 20,000
Cells Recovered Rate	⩾ 50 %
Multiplet rate	1,000 cells/0.4%
Median UMI counts per cell	>5,000 (PBMC)
Median genes per cell	>2,000 (PBMC)





cDNA Library Sequencing

Number of Target Cells	Recommended Input Cells	Raw Data (M Reads/ Sample)	DNBSEQ-G400 Sequencing (4 Lanes/Flow Cell, 2 Flow Cells/Run)	DNBSEQ-T7 Sequencing (4 Flow Cells/Run)	DNBSEQ-T20×2 Sequencing (6 Flow Cells/Run)
5,000	10,000	250+	6 Samples/Flow Cell, 12 Samples/Run	16 Samples/Flow Cell, 64 Samples/Run	96 Samples/Flow Cell, 576 Samples/Run
10,000	20,000	500+	3 Samples/Flow Cell, 6 Samples/Run	9 Samples/Flow Cell, 36 Samples/Run	53 Samples/Flow Cell, 318 Samples/Run
15,000	30,000	750+	2 Samples/Flow Cell, 4 Samples/Run	6 Samples/Flow Cell, 24 Samples/Run	35 Samples/Flow Cell, 210 Samples/Run

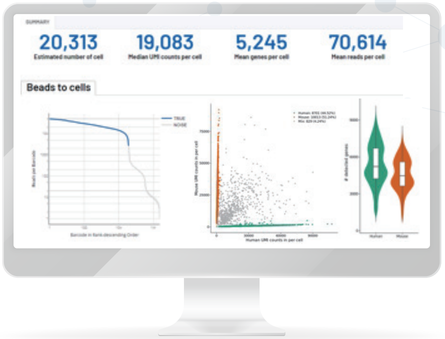
Oligo Library Sequencing

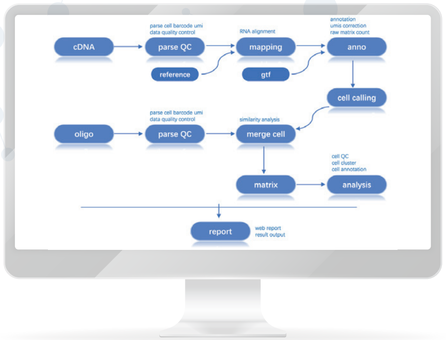
Raw Data (M Reads/Sample)	DNBSEQ-G400 Sequencing (4 Lanes/Flow Cell, 2 Flow Cells/Run)	DNBSEQ-T7 Sequencing (4 Flow Cells/Run)	DNBSEQ-T20×2 Sequencing (6 Flow Cells/Run)
50+	6 Samples/Flow Cell, 48 Samples/Run	80 Samples/Flow Cell, 320 Samples/Run	96 Samples/Flow Cell, 576 Samples/Run

Simultaneous Sequencing Of Mixed cDNA And Oligo Libraries

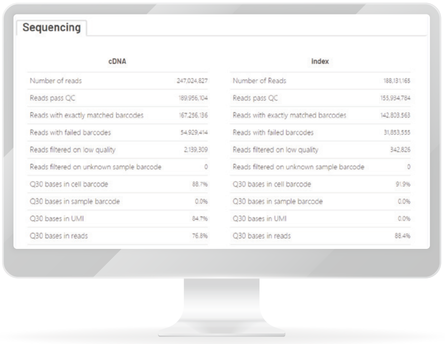
Number of Target Cells	Recommended Input Cells	Raw Data (M Reads /Sample)	DNBSEQ-G400 Sequencing (4 Lanes/Flow Cell, 2 Flow Cells/Run)	DNBSEQ-T7 Sequencing (4 Flow Cells/Run)	DNBSEQ-T20×2 Sequencing (6 Flow Cells/Run)
5,000	10,000	350+	4 Samples/Flow Cell, 8 Samples/Run	12 Samples/Flow Cell, 48 Samples/Run	80 Samples/Flow Cell, 480 Samples/Run
10,000	20,000	600+	2 Samples/Flow Cell, 4 Samples/Run	8 Samples/Flow Cell, 32 Samples/Run	46 Samples/Flow Cell, 276 Samples/Run
15,000	30,000	800+	2 Samples/Flow Cell, 4 Samples/Run	5 Samples/Flow Cell, 20 Samples/Run	32 Samples/Flow Cell, 192 Samples/Run

Data Analysis





One-click Deployment & Operation	Rich Visual Content	Excellent System Compatibility



Sequencing

cDNA		index	
Number of reads	247,024,827	Number of Reads	188,131,165
Reads pass QC	189,956,104	Reads pass QC	155,934,784
Reads with exactly matched barcodes	167,256,136	Reads with exactly matched barcodes	142,803,563
Reads with failed barcodes	54,929,414	Reads with failed barcodes	31,853,555
Reads filtered on low quality	2,139,309	Reads filtered on low quality	342,826
Reads filtered on unknown sample barcode	0	Reads filtered on unknown sample barcode	0
Q30 bases in cell barcode	88.7%	Q30 bases in cell barcode	91.9%
Q30 bases in sample barcode	0.0%	Q30 bases in sample barcode	0.0%
Q30 bases in UMI	84.7%	Q30 bases in UMI	0.0%
Q30 bases in reads	76.8%	Q30 bases in reads	88.4%

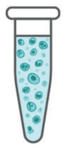
One-stop Platform

MGI provides a one-stop platform for single-cell research, including tissue preservation reagents to maintain the freshness of samples within 72 hours to prevent mRNA degradation. MGI also provides a single sample preparation protocol for more than 50 different species. Single-cell sorting droplet microfluidic platform-TaiM 4 can run 1~4 flexible samples. Automated library preparation platform MGISP-100 completes1~8 single-cell libraries preparation. Gene sequencer DNBSEQ-G400, DNBSEQ-T7, and DNBSEQ-T20×2 complete sequencing of different amounts of libraries. The data quality control analysis platform DNBC4Tools convert sequencing data into single-cell data matrix files.

Storage & Transport → Samples Prep → Samples labeling & Library Prep (Automation is optional) → High-throughput Sequencing → Data Analysis

Tissue Storage Reagent
(2℃~8℃, 72h)

MGICLab-LN55K
22,000~55,000 Tubes



Sample adaptation whitelist (200+)
Sample preparation protocols (50+)

3' RNA, ATAC, Cut&Tag

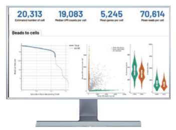
DNBelab C-TaiM 4

MGISP-100
1~8 Samples/run

DNBSEQ-G400
≤8 Samples/run (32h)

DNBSEQ-T7
≤48 Samples/run (16h)

DNBSEQ-T20×2
≤480 Samples/run



C4Tools

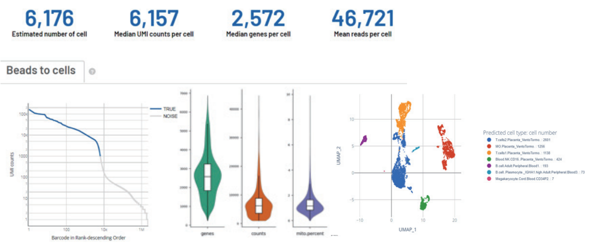
ZTRON Series

Tested Data

Currently, research or applications based on MGI's DNBelab C series single-cell 3’ RNA library preparation kit covers a wide range of sample types, including more than 300 samples from more than 50 species of animals such as human, mouse, plants, etc.

Human Bladder Cancer

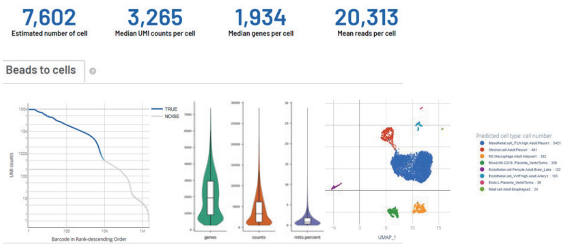
Input cells: 10,000


6,176 Estimated number of cell
6,157 Median UMI counts per cell
2,572 Median genes per cell
46,721 Mean reads per cell

Beads to cells

Human PBMC

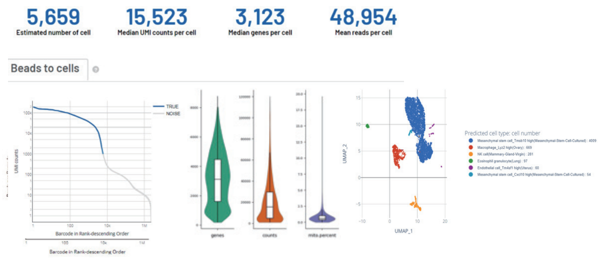
Input cells: 10,000


7,602 Estimated number of cell
3,265 Median UMI counts per cell
1,934 Median genes per cell
20,313 Mean reads per cell

Beads to cells

Human Kidney Cancer

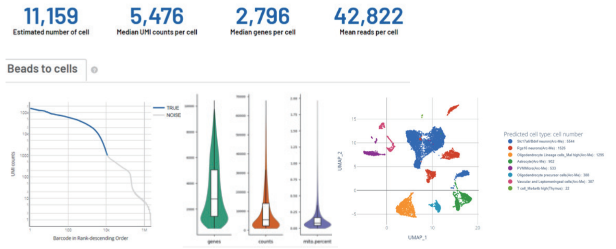
Input cells: 10,000


5,659 Estimated number of cell
15,523 Median UMI counts per cell
3,123 Median genes per cell
48,954 Mean reads per cell

Beads to cells

Mouse Brain Nuclei

Input cells: 20,000

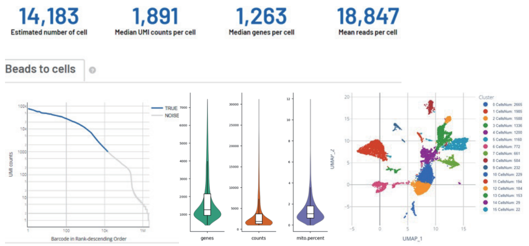

11,159 Estimated number of cell
5,476 Median UMI counts per cell
2,796 Median genes per cell
42,822 Mean reads per cell

Beads to cells

The tested data shows that the cell recovered rate of sample types such as human PBMC cells, brain cell nuclei, adipocyte nuclei, and mouse lung cancer cells is more than 50%, and the median number of genes detection is more than 2,000 or close to 2,000; complex sample types such as OCT-embedded samples, birds, and plants all have good data performance.

Peanut Protoplasts

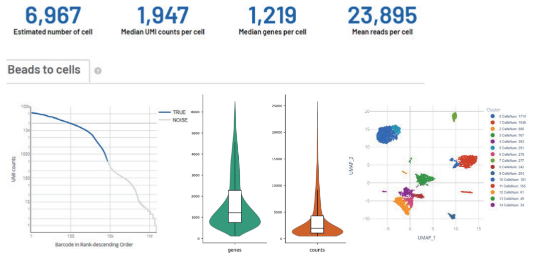
Input cells: 20,000


14,183 Estimated number of cell
1,891 Median UMI counts per cell
1,263 Median genes per cell
18,847 Mean reads per cell

Beads to cells

Mouse Lymph Node

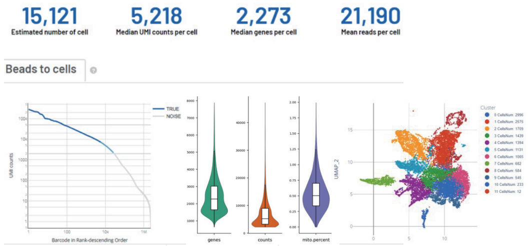
Input cells: 10,000


6,967 Estimated number of cell
1,947 Median UMI counts per cell
1,219 Median genes per cell
23,895 Mean reads per cell

Beads to cells

Mouse Lung

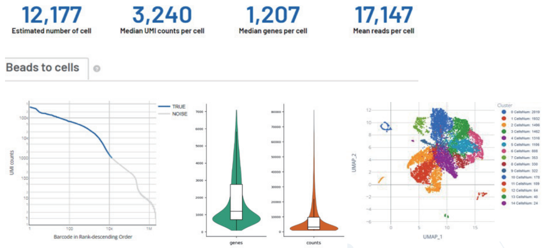
Input cells: 10,000


15,121 Estimated number of cell
5,218 Median UMI counts per cell
2,273 Median genes per cell
21,190 Mean reads per cell

Beads to cells

Mouse Spleen

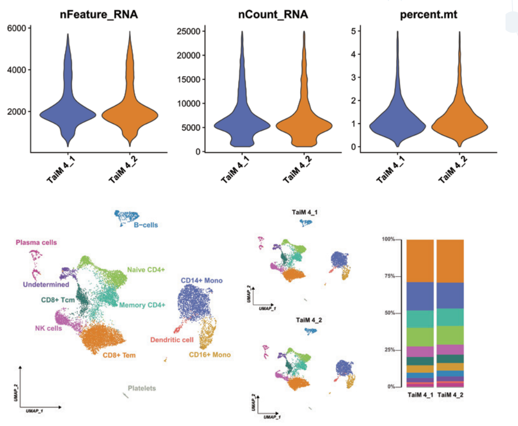
Input cells: 20,000


12,177 Estimated number of cell
3,240 Median UMI counts per cell
1,207 Median genes per cell
17,147 Mean reads per cell

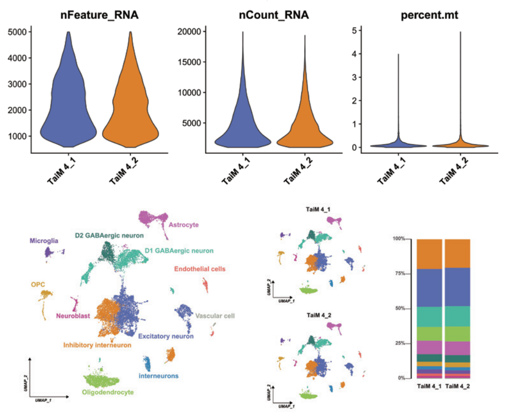
Beads to cells

Data Performance

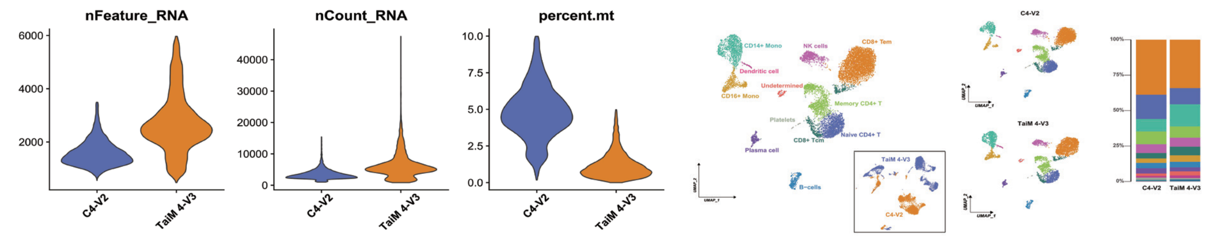
◎ Repeatability test- PBMC



◎ Repeatability test- Mouse brain nucleus



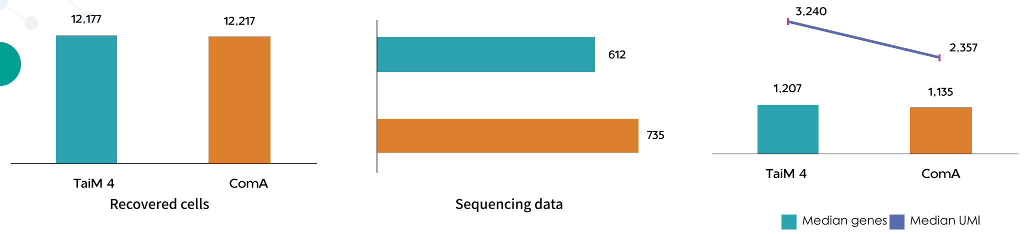
◎ Comparison of different versions - PBMC



◎ Comparison of different platforms - TaiM 4 V3.0 VS ComA

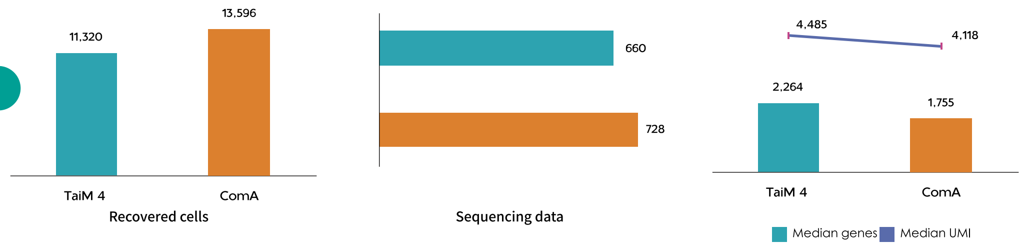
Protoplast

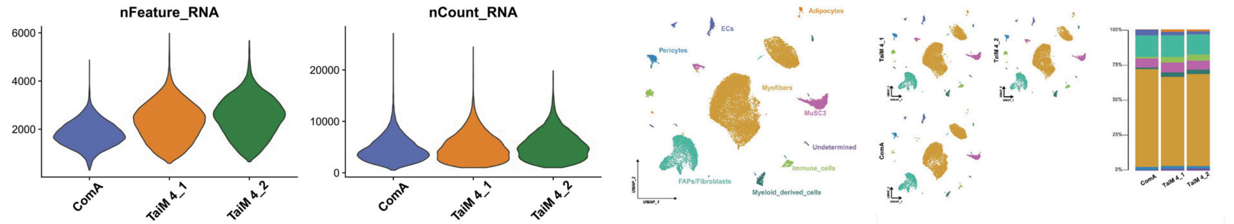
Input Cells: 20,000



Muscle nucleus

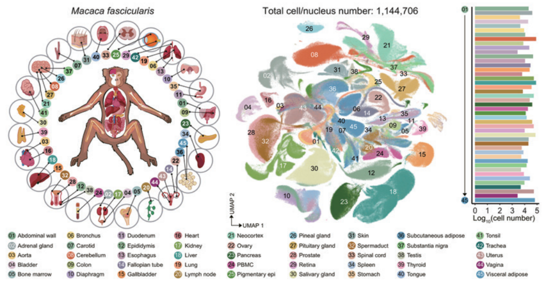
Input Cells: 20,000





Application Cases

Case 1 Single-cell atlas of Macaca fascicularis



Han, L. et al, Nature 2022

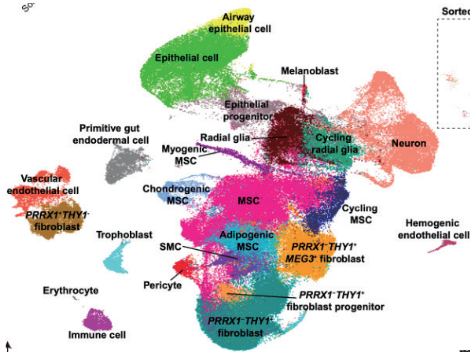
Samples

45 organs or tissues of *Macaca fascicularis*

Methods

Using DNBelab C4 scRNA library preparation system and DNBSEQ sequencing platforms, single-cell transcriptome sequencing was performed on the main tissues and organs (lung, kidney, liver, pancreas, brain, aorta, thyroid, parotid gland, and blood) of cynomolgus monkeys, and established single cell transcriptome database of Macaca fascicularis.The transcriptome database has identified 44 main cell types of cynomolgus monkeys, and completed the construction of non-human primate single-cell map V1.0 for the first time in the world, which has an important guiding role in the development of new crown drugs and vaccines.

Case 2 Human totipotent stem cell



Mazid, MA. et al, Nature 2022

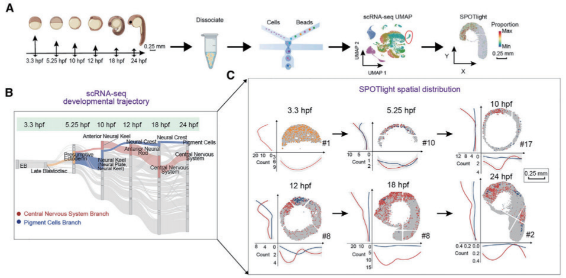
Samples

Human embryonic-like cells at the 8-cell stage (8CLC)

Methods

Using DNBelab C4 and DNBSEQ sequencing platforms, single-cell transcriptome (scRNA-seq) and chromatin accessibility sequencing(scATAC-seq) were performed on 8CLC-induced cell samples, and the characteristics of the 8CLC population were analyzed in detail. The four induction time points delineate the dynamic changes of transcriptome and chromatin opening during 8CLC induction, providing an important platform and resource for studying zygotic genome activation and developmental regulation at the human 8-cell stage.

Case 3 Zebrafish development and differentiation



Liu, C. et al, Developmental Cell 2022

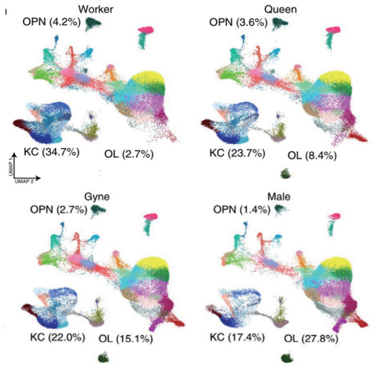
Samples

Zebrafish embryo

Methods

The experiment was performed at six key developmental time points within 24 h of fertilization in zebrafish embryos, using Stereo-seq technology to analyze a total of 91 sagittal frozen sections, and draw a spatiotemporal transcriptome map of zebrafish early embryonic development. Stereo-seq and scRNA-seq data were integrated at each key developmental time point to construct the spatio-temporal developmental trajectory of cell fate transition and cell molecular changes during zebrafish embryonic development, and to explore the relationship between cell space microenvironment and differentiation direction associated.

Case 4 Ant brain nuclei



Li, Q. et al. Nature Ecology & Evolution 2022

Samples

Ant brain

Methods

This study constructed brain cell atlases of four different castes of ants, revealing the neural basis for brain specialization and caste-specific behavioral differences that emerge with social organization. The study also demonstrated the plasticity changes that occur in the brain during the maturation process of ant queens and identified key cell groups that regulate their fecundity and longevity.

Selected Publications

【1】Mazid MA. et al. Rolling back human pluripotent stem cells to an eight-cell embryo-like stage. Nature. (2022)

【2】Han L. et al. Cell transcriptomic atlas of the non-human primate Macaca fascicularis. Nature. (2022)

【3】Chen. A. et al. Single-cell spatial transcriptome reveals cell-type organization in macaque cortex. Cell. (2023)

【4】Cao J. et al. Live birth of chimeric monkey with high contribution from embryonic stem cells. Cell. (2023)

【5】Zhao Z. et al. Evolutionarily conservative and non-conservative regulatory networks during primate interneuron development revealed by single-cell RNA and ATAC sequencing. Cell research. (2022)

【6】Wu L. et al. An invasive zone in human liver cancer identified by Stereo-seq promotes hepatocyte-tumor cell crosstalk, local immunosuppression and tumor progression. Cell research. (2023)

【7】Zhu L. et al. Single-Cell Sequencing of Peripheral Mononuclear Cells Reveals Distinct Immune Response Landscapes of COVID-19 and Influenza Patients. Immunity. (2020)

【8】Yin J. et al. Single-cell transcriptome sequencing reveals the immune response and homeostasis mechanism following administration of BBIBP-CorV SARS-CoV-2 inactivated vaccine. Innovation (Cambridge (Mass.)). (2022)

【9】LI Q. et al. A single-cell transcriptomic atlas tracking the neural basis of division of labor in an ant superorganism. Nature Ecology & Evolution. (2022)

【10】Wang F. et al. Endothelial cell heterogeneity and microglia regulons revealed by a pig cell landscape at single-cell level. Nature communications. (2022)

【11】Lei Y. et al. Spatially resolved gene regulatory and disease-related vulnerability map of the adult Macaque cortex. Nature communications. (2022)

【12】Sui Q. et al. Inflammation promotes resistance to immune checkpoint inhibitors in high microsatellite instability colorectal cancer. Nature communications. (2022)

【13】Zhang R. et al. A single-cell atlas of West African lungfish respiratory system reveals evolutionary adaptations to terrestrialization. Nature communications. (2023)

【14】Wang Y. et al. Interferon stimulated immun eprofile changes in a humanized mouse model of HBV infection. Nature communications. (2023)

【15】Wang D. et al. GDF11 slows excitatory neuronal senescence and brain ageing by repressing p21. Nature communications. (2023)

【16】Zhu Q. et al. Single cell multi-omics reveal intra-cell-line heterogeneity across human cancer cell lines. Nature communications. (2023)

【17】Zhu Q. et al. Single-cell multi-omics analysis of human testicular germ cell tumor reveals its molecular features and microenvironment. Nature communications. (2023)

【18】Yang Y. et al. VGLL1 cooperates with TEAD4 to control human trophectoderm lineage specification. Nature communications. (2024)

【19】Wang Y. et al. Loss-of-Function of p21-Activated Kinase 2 Links BMP Signaling to Neural Tube Patterning Defects. Advanced Science. (2024)

【20】Liu K. et al. Bilineage embryo-like structure from EPS cells can produce live mice with tetraploid trophectoderm. Protein & Cell. (2023)

*To learn more about published articles, please visit offcial website: https://www.mgitech.cn/Home/Products/new_bussiness_info/id/28.html

About MGI Tech Co., Ltd.

MGI Tech Co., Ltd. (referred to as MGI) is committed to building core tools and technology to lead life science through intelligent innovation. With a focus on R&D, production and sales of DNA sequencing instruments, reagents, and related products, MGI provides real-time, panoramic, and life course equipment and systems for precision medicine, precision agriculture, precision healthcare and other relevant industries. MGI is a leading producer of clinical high-throughput gene sequencers, and its multi-omics platforms include genetic sequencing, medical imaging, and laboratory automation. As of September 30, 2023, MGI has more than 2,900 employees, and 36% of whom are R&D personnel. Founded in 2016, MGI operates in more than 100 countries and regions, serving more than 2,600 customers. It has established scientific research and production bases, global training and service network in many countries and regions around the world. MGI is one of the few companies in the world that can independently develop and mass-produce low-, medium- and high-throughput clinical gene sequencers from GB to TB. Providing real-time, comprehensive, life course solutions, its vision is to lead life science innovation.