

Ordering Information



	Product Name	Product Name of Component Kits	Catalogue Number	Storage Temperature
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°C~8°C
		Droplet Reagent	940-001929-00	-25°C~-15°C
		Lib Prep Reagent	940-001925-00	-25°C~-15°C
		Flow Cell(TaiM 4)	940-001928-00	10°C~30°C
		Sample Labeling Reagent	940-001926-00	-25°C~-15°C
	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°C~8°C
		Droplet Reagent	940-001819-00	-25°C~-15°C
		Lib Prep Reagent	940-001821-00	-25°C~-15°C
		Flow Cell(TaiM 4)	940-001822-00	10°C~30°C
		Sample Labeling Reagent	940-001920-00	-25°C~-15°C
			900-000637-00 (China)	10°C~30°C
			900-000780-00 (CE)	
			900-000781-00 (EAC)	
			900-000782-00 (UKCA)	

DNBelab C Series

High-throughput Single-cell RNA

Library Preparation Set V3.0



For Research Use Only. Not for use in diagnostic procedures.

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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

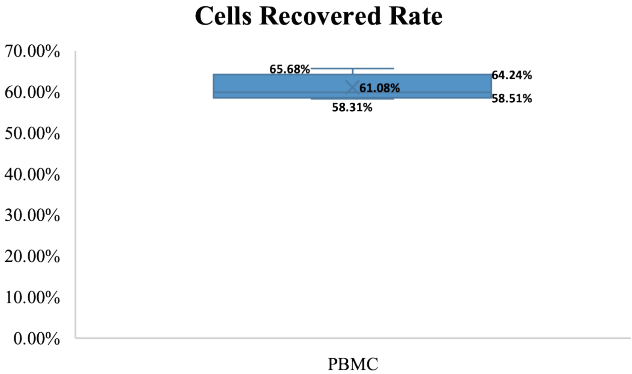
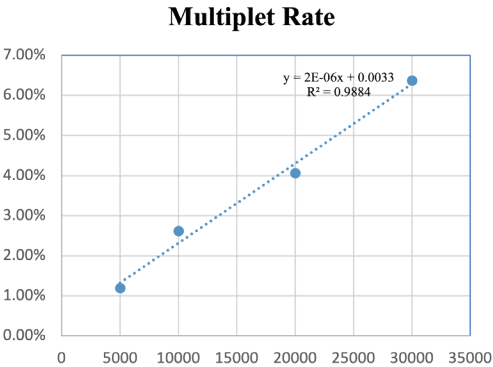


Advantages

- 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

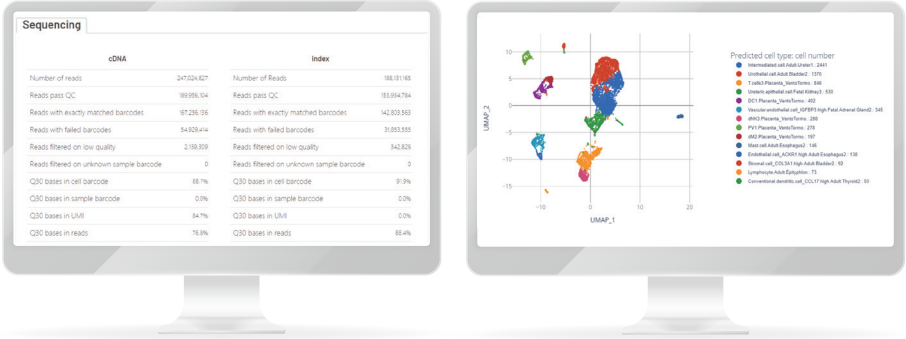
Data Analysis



One-click Deployment & Operation

Rich Visual Content

Excellent System Compatibility



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 so different species 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 sequencerS-DNBSEQ-G400, DNBSEQ-T7, and DNBSEQ-T20×2 complete sequencing of different amounts of libraries. The data quality control analysis platform DNBC4Tools can 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°C~8°C, 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

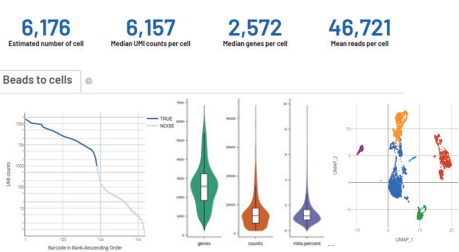
Tested Data

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.

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.

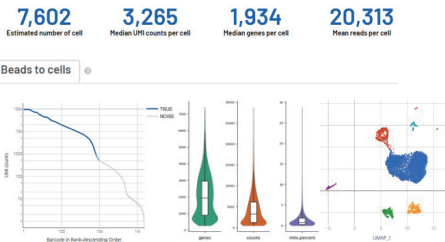
Human Bladder Cancer

Input cells: 10,000



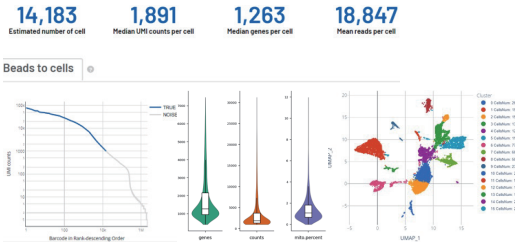
Human PBMC

Input cells: 10,000



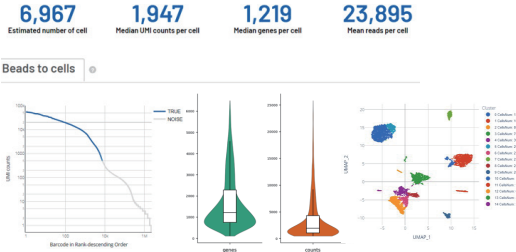
Peanut Protoplasts

Input cells: 20,000



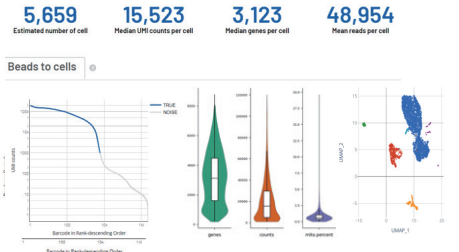
Mouse Lymph Node

Input cells: 10,000



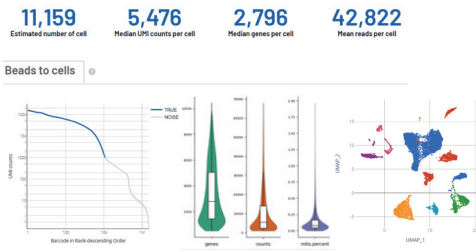
Human Kidney Cancer

Input cells: 10,000



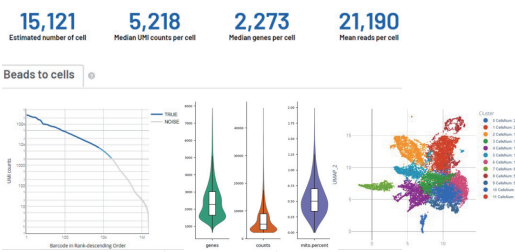
Mouse Brain Nuclei

Input cells: 20,000



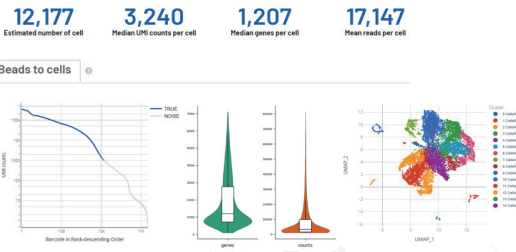
Mouse Lung

Input cells: 10,000



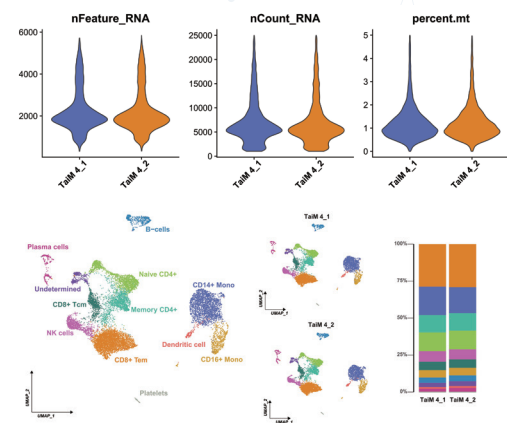
Mouse Spleen

Input cells: 20,000

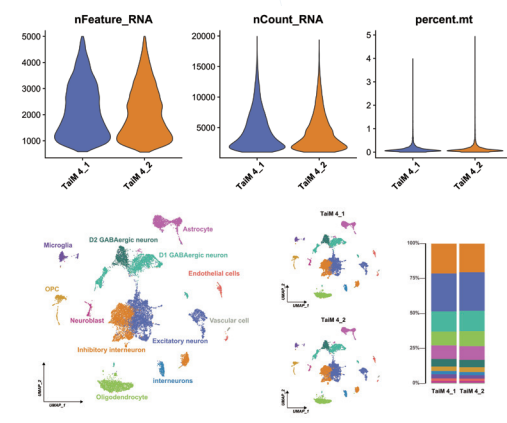


Data Performance

Repeatability test- PBMC



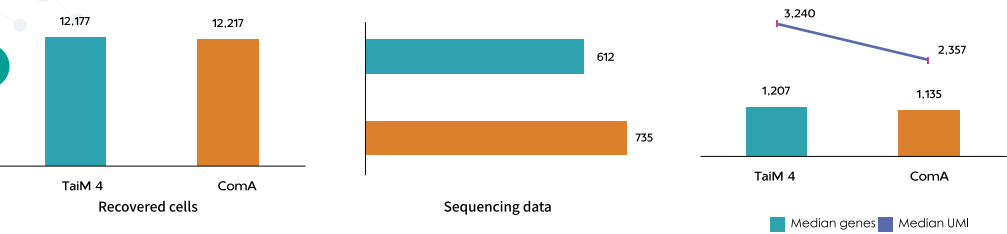
Repeatability test- Mouse brain nucleus



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

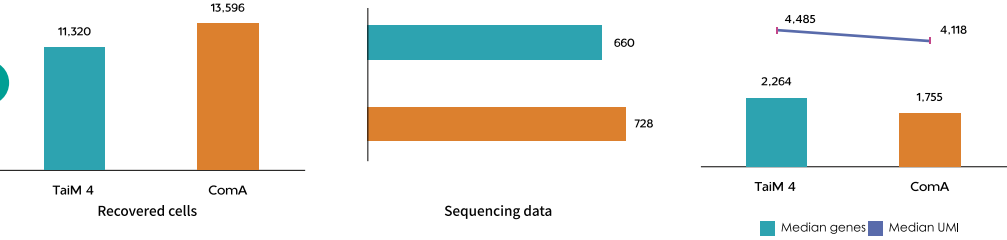
Protoplast

Input Cells: 20,000

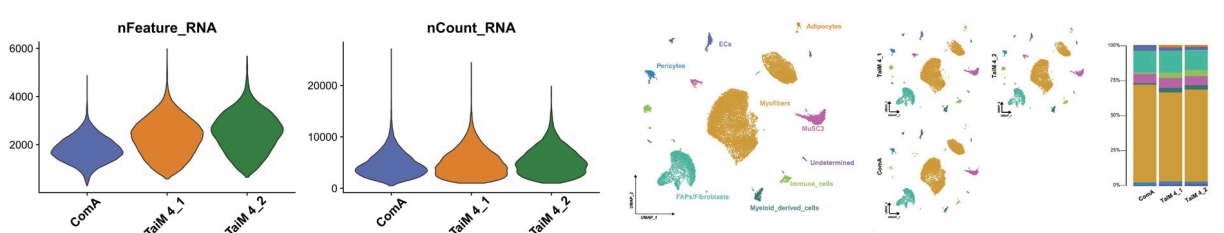
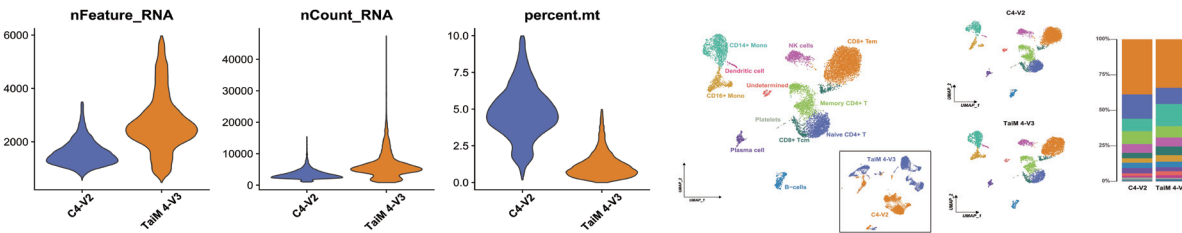


Muscle nucleus

Input Cells: 20,000

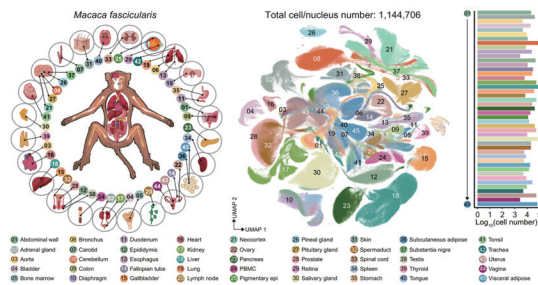


Comparison of different versions - PBMC



Application Cases

Case 1 Single-cell atlas of *Macaca fascicularis*



Han, L. et al, Nature 2022

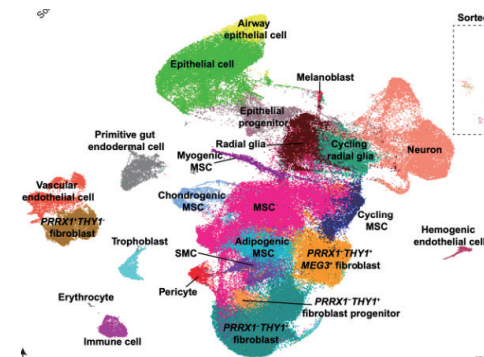
Samples

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

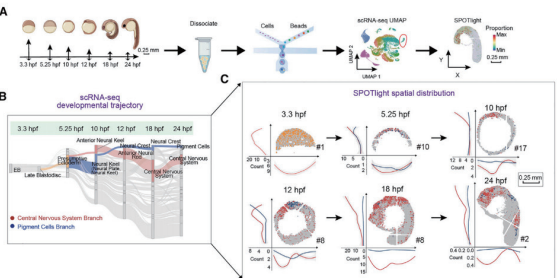
Samples

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

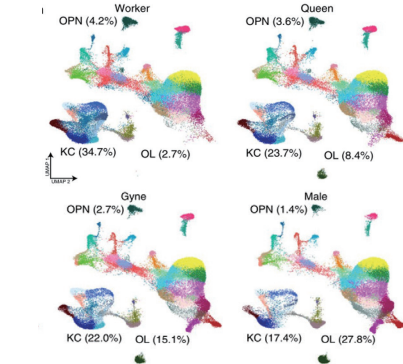
Samples

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 official 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.