

Leading Life Science Innovation

MGI
Product Catalog
2026 • SEQ ALL • GLI • OMICS

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*Unless otherwise informed, this StandardMPS sequencing reagent is not available in Germany, UK, Sweden, and Switzerland.



MGI Latvia Branch



About MGI Tech Co., Ltd.

MGI Tech Co., Ltd. (or its subsidiaries, together referred to MGI), is committed to building core tools and technologies that drive innovation in life science. Our focus lies in research & development, manufacturing, and sales of instruments, reagents, and related products in the field of life science and biotechnology. We provide real-time, multi-omics, and full spectrum of digital equipment and systems for precision medicine, agriculture, healthcare and various other industries.

Founded in 2016, MGI has grown into a leader in life science, serving customers across six continents and have established research, manufacturing, training, and after-sales service facilities globally. MGI stands out as one of the few companies capable of independently developing and mass-producing clinical-grade gene sequencers with varying throughput capacities, ranging from Gb to Tb levels. With unparalleled expertise, cutting-edge products, and a commitment to global impact, MGI continues to shape the trajectory of life sciences into the future.

As of June 30, 2025, MGI has a team over 2,277 employees, with research and development personnel accounting for approximately 29.21%. Our business spans over 110 countries and regions worldwide, serving more than 3,560 users.

2,277

Employees

29.21%

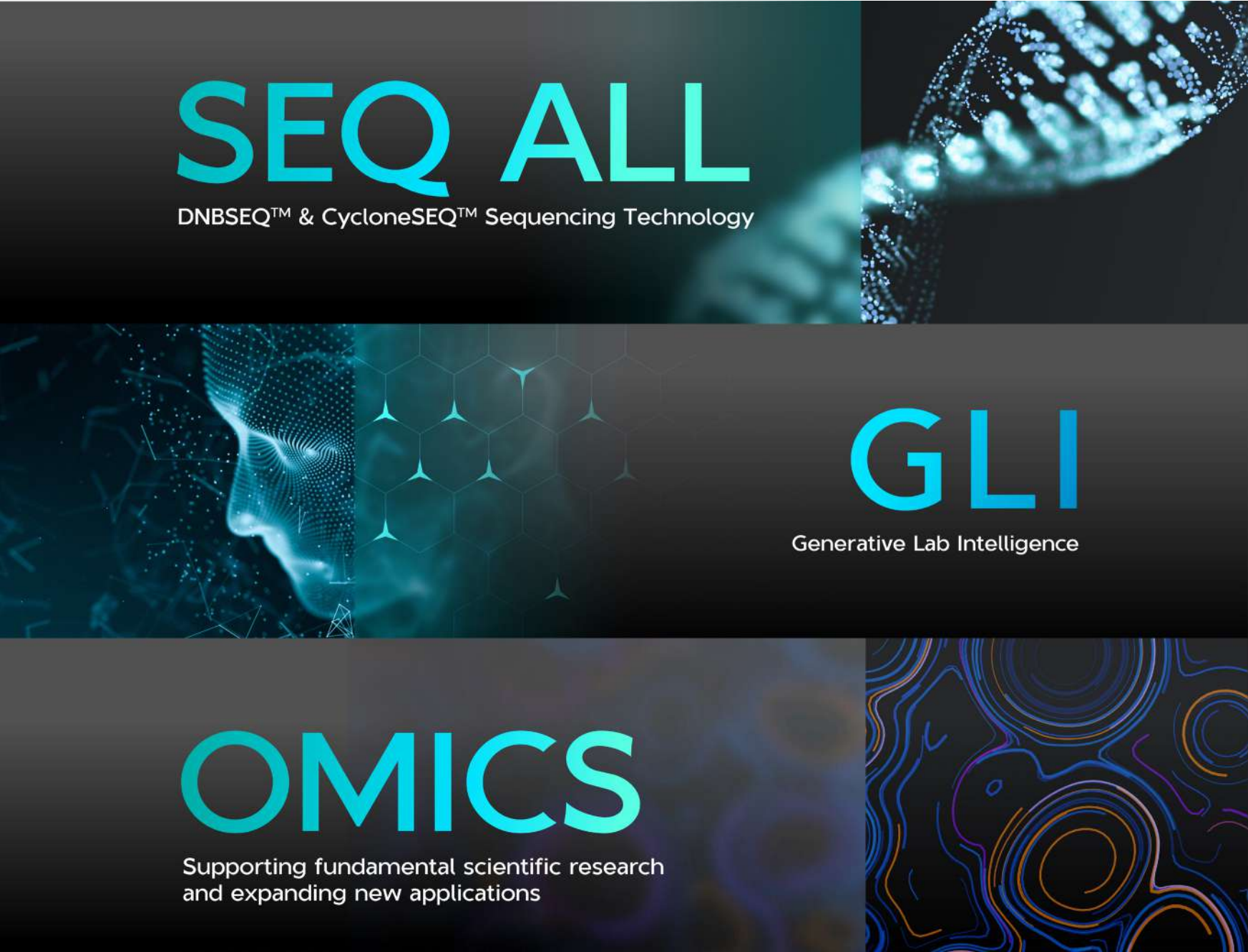
R&D Personnel

3,560+

Customers

110+

Countries & Regions



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SEQ ALL

Core Sequencing Technologies

MGI's DNA sequencing instruments incorporate the cutting-edge core technology known as DNBSEQ™. DNBSEQ™ encompasses all technologies related to DNA nanoballs (DNB), including DNA single-strand circularization, patterned array, cPAS (combinatorial probe anchor synthesis), and more. This has been widely adopted across various sequencing platforms such as the E25, G99, G50, G400, T1+, T7 and T20×2.

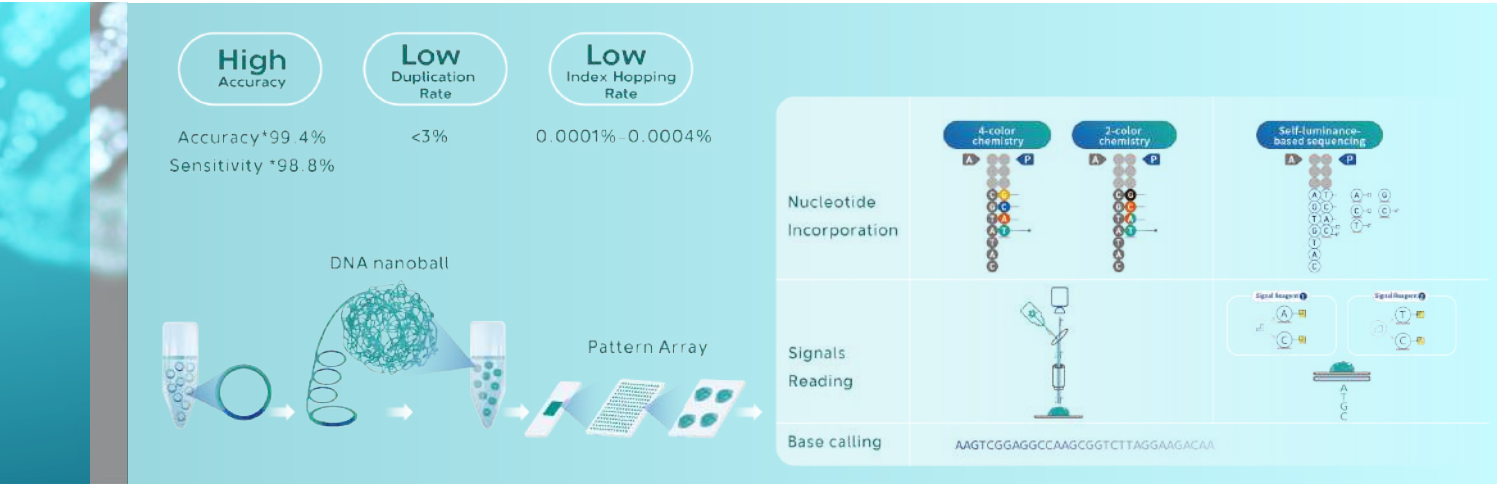
Building on this foundation, MGI has recently introduced CycloneSEQ™ technology, representing a breakthrough in long-read sequencing. CycloneSEQ™ harnesses innovative nanopore-based detection mechanisms and advanced base-calling algorithms to enable direct, real-time sequencing of native DNA and RNA molecules up to Mb level in length. CycloneSEQ™ is currently deployed across G100-ER and G400-ER sequencing platforms.

With the ability of sequencing both short reads and long reads, now MGI can provide a comprehensive product portfolio to 'SEQ ALL'.



DNBSEQ™ sequencing technology

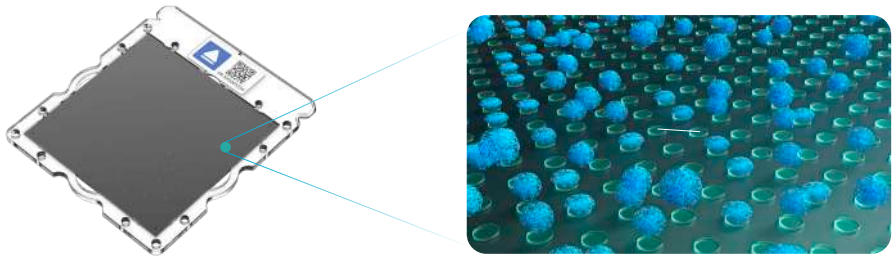
DNB is the unique technology that allows DNA linear amplification in a single-tube solution. The workflow includes DNA fragmentation, adapter ligation and single-stranded circulation to produce DNB.



- **High intensity of fluorescent signals and high sequencing accuracy**
Rolling Circle Amplification (RCA) increases the quantity of “DNA fragments (to be processed)” and thus enhance the intensity of fluorescent signals and accuracy.
- **Zero-error accumulation using RCA**
RCA enables each copy to be amplified from the original template and generates no accumulated replication errors, delivering high sequencing accuracy.
- **Maximized efficiency of DNA loading on patterned array**

Patterned array

Patterned array is the key in DNB loading technology. The coating surface of the semiconductor chip makes each loading spot positively charged. Therefore, the negatively charged DNB can easily attach to the positively charged chip surface through electrostatic adhesion. Patterned array ensures each spot is attached to a single DNB and thus prevents the signal interference. Overall, patterned array enables high sequencing accuracy and high chip utilization.

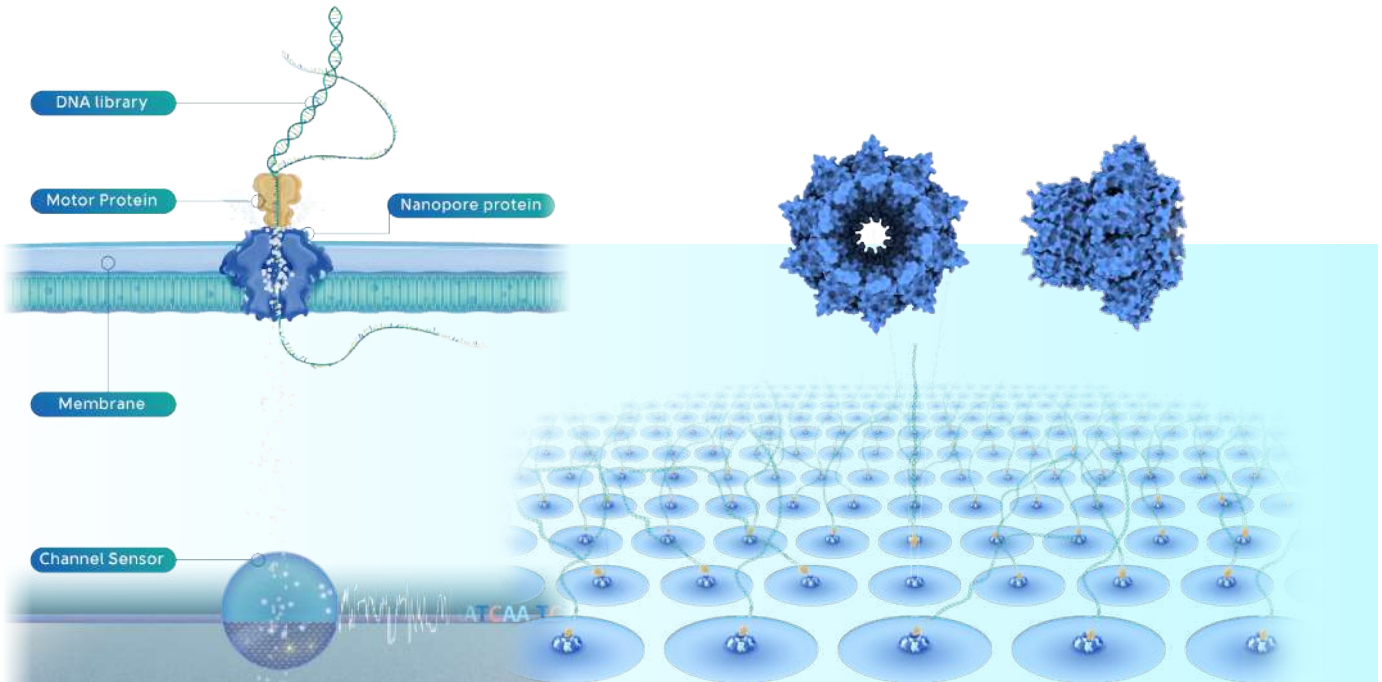


- **Enhancing sequencing signals using nanoscale patterned chip**
The patterned array of spots on flow cells prevents cross interference between fluorescent signals and enables high intensity of signals.

- **Precision machined semiconductor chip enhances the attachment of DNB to chip**
The size of DNB matches the area of effective spot on the chip. Thus, each spot is only attached to a single DNB, avoiding signal interference.
- **Precise pattern enables efficient imaging system and DNB loading**
Patterned array and DNB technology maximize the utilization of imaging system and chip surface area, increasing sequencing accuracy.
- **Low duplication no index hopping**
DNB is amplified in solution and loaded without PCR reagents. Hence the duplicate rate is extremely low using DNB technology and patterned array.

CycloneSEQ™ sequencing technology

CycloneSEQ™ sequencing technology refers to the process in which, during the sequencing of CycloneSEQ platform, the DNA library molecules linked to the motor proteins approach the entrance of the nanopore protein under the influence of an electric field. When the motor proteins reach the nanopore entrance, they are activated, effectively and rapidly unwinding the DNA, allowing the library to pass through the nanopore protein as single-stranded molecules. As different DNA bases and their arrangements obstruct the current to varying degrees, fluctuations in the current occur as the DNA passes through the nanopore. The channel sensors on the sequencing flow cell capture these current signals, which are then analyzed by the control software to obtain real-time information about the base sequence of the sample being tested.



CycloneSEQ™ sequencing technology enables full-length sequencing detection from ultra-short to ultra-long sequences, which is crucial for applications such as genome assembly and structural variation detection. In areas like new pathogen detection and rapid diagnosis, its feature of real-time sequencing also offers significant advantages. This technology allows direct sequencing and can be extended to multi-omics application scenarios such as RNA sequencing and epigenetics research. Meanwhile, in non-sequencing directions, such as being directionally modified into selective molecular transport channels, it helps explore more cutting-edge fields.

Sequencing Product Portfolio

Lead in achieving R&D and mass production of clinical-grade genetic sequencers that cover different throughput levels from low, medium, to high, as well as full read lengths.

Excited luminous sequencing

Self-luminous sequencing

Non-luminous sequencing



WGS, spatio-temporal omics, cell-omics, proteomics, epigenomics, transcriptomics, cancer research, agriculture

WGS, WES, targeted sequencing, transcriptome sequencing, single cell sequencing, methylation sequencing, spatial sequencing, proteomics

WGS, WES, targeted sequencing, transcriptome sequencing, single cell sequencing, methylation sequencing, spatial sequencing

Small WGS, low-pass WGS, targeted sequencing, 16s sequencing, gene expression profiling

Small WGS, targeted sequencing, 16s sequencing, transcriptome sequencing

Targeted sequencing, small WGS, gene expression profiling

Plasmid sequencing, Targeted disease detection, Microbial genome research, Amplicon microbial detection, Small-genome research, Bulk full-length transcriptome sequencing, Methylation sequencing

Genome resequencing, Genome assembly, Metagenomics sequencing, Single-cell full-length transcriptome sequencing, Methylation sequencing, Chromatin interaction detection, Targeted disease detection, Microbial genome research, Amplicon microbial detection, Small-genome research, Bulk full-length transcriptome sequencing



Product Model	T20x2	T7+	T7	T1+			G400		G50		G99			E25	G100-ER	G400-ER
Certification																
Dimensions	4200x4800 x2000	1370 × 848 × 1760	1656 x 903 x 1815	1150 x 750 x 810			1086 x 756x 710		654 x 489 x 545		607 × 689 × 657			348 x 312 x 257	160 x 165 x 127	155 × 140 × 148
Flow Cells/Run	6	4	4	2			2		1		2			1	2	1
Flow Cell Type	Slide	FCL	FCL	FCS	FCM	FCL	FCS	FCL	FCS	FCL	FCS	FCL	FCU	FCL	/	/
Lanes/Flow Cell	1	1	1	2	2	4	2	4	1	1	1	1	1	1	2	1
Effective Reads/Flow Cell	40,000M	12,000M	5,800M	500M	1,000M	2,000M	300M, 550M	1,500 - 1,800M	100M	500M	40M	80M	200M	25M	4,096 Pore Proteins	30,000+ Pore Proteins
Max Read Length	PE150	PE150	PE150	PE300	PE150	PE150	PE300	SE400 PE200	PE150	PE150	PE150	PE300	PE300	PE150	≥2 Mbp	≥2 Mbp
Min Read Length	PE100	PE75	PE100	SE100	SE100	SE50	SE100	SE50	SE100	SE50	PE150	PE100	SE100	SE100	100 bp	100 bp
Max. Throughput/Run	72Tb	14.4Tb	7Tb	1.2Tb			1.44Tb		150 Gb		12 Gb~ 24 Gb	8 Gb~ 96 Gb	20 Gb~ 240 Gb	7.5 Gb	85 Gb	400Gb
Sequencing Quality (PE150)	>85%	>85%	>85%	Q40>90%			Q30>85%	Q40>85%	Q30>80%		Q40>85%			Q30>80%	/	/
Run Time	60-80h	14~24h	16-24h	7.5-35h	8.5-20h	7-24h	13-98h	14-109h	10-28h	7-40h	~11 h	5 h~30 h	7h~35 h	5-20h	0 - 72h	0 - 72h
*L×W×H (mm)															As of Dec 2025	

Sequencers

T20×2
An Ultra-High Throughput Sequencer

T20×2 is designed to meet the most challenging sequencing scenarios. It aims to empower large population genome projects around the world, and revolutionize healthcare with OMICS technologies. T20×2 is a fully automated sequencer comprising all components of a genetic sequencer integrated by robotics to process six slides per run. It covers all high-throughput sequencing needs in scientific research and clinical research including: WGS, WES, Meta, Single-cell sequencing, Stereo-seq, and more.

Features

- Achievable for 50k high-depth WGS per year.
- Support the simultaneous operation of 6 flow cells.
- Innovation-packed to maximize the efficiency of sequencing.
- Automation from sample to report.

Performance parameters

Effective reads/Slide*	40 B	40 B
Read Length	PE100	PE150
Data output	~48 Tb	~72 Tb
Run time**	~60 h	~80 h
Data quality Q30***	≥ 85%	≥ 85%

* The maximum number of effective reads are based on a specific standard library, and the actual application library will fluctuate depending on the sample type and library construction method.
** The run time includes sequencing, generation of Cal. File. Cal. File is a binary file format generated by MGI sequencer basecall software.
*** The percentage of bases above Q30 is obtained by averaging metrics for runs using standard library. Actual performance is influenced by sample type, library quality and type, insert length among other factors.

Applications

Application type	Recommended read length	Requirements	Recommended sample numbers for a single run on T20×2
WGS	PE100	500M	432
		700M	336
WGS	PE150	334M	576
		467M	480
Meta	PE150	20M	5760
Single cell	PE100	500M(10000 cells/sample)	360
Spatial Omics	PE100	1000M	144



T7+
The End of Compromise

As a highly efficient integrated ultra-high-throughput sequencer designed for large-scale sequencing scenarios, powered by MGI's DNBSEQ™ Technology and SM2.0 biochemistry, T7+ can deliver over 14Tb of high-quality data within 24 hours. Its 7-in-1 modular design enables full automation from sample to report, ensuring a streamlined sequencing experience. With an annual capacity of up to 35,000 whole-genome sequencing (WGS), there is no need for compromise between throughput and speed.

Features

- Ultrafast Breakthrough:** 14.4 Tb/24 h
- 7 in 1 Highly-Integrated:**Provide a one-stop process, covering DNB making, DNB loading, sequencing, pure water container, waste container, data analysis (including FASTQ files generation and bioinformatic analysis) and data compression software.
- 1-4 Flow Cells:**QUAD-Flow Cell Sequencing Independently. PE150, PE100 and PE75 at the same time.
- High-Quality Data Output:**Q40 > 90%
- Friendly in Use:**Ergonomically design, adjustable screen angle, and the reagent cartridge features a modular design, making the preparation process straightforward.
- Smart System Management :** Equipped with comprehensive system sensing,real-time diagnostics, proactive fault detection, and self-healing capabilities.
- Smart Interaction:**Omni-smart hub; Smart IP assistant guides workflows.

Product specifications

No. of flow cell per run	Flow cell type	Supported read lengths*	Reads/flow cell**	Data output per run	Q30***	Run time per run****
4	FCL	PE75	10,000M~12,000M	/	> 90%	/
		PE100	12,000 M	2.4 Tb~9.6 Tb	> 90%	< 20 h
		PE150		3.6 Tb~14.4 Tb	> 90%	< 24 h

* The instrument is equipped with PE150, PE100 and PE75 sequencing modes, and the existing reagent kits support PE150, PE100 and PE75 read length sequencing.
** The maximum number of effective reads are based on a specific standard library, and the actual application library will fluctuate depending on the sample type and library construction method.
*** The percentage of bases above Q30 is obtained by averaging metrics for runs using standard library. Actual performance is influenced by sample type, library quality and type, insert length among other factors.
**** 24-hour run time is from DNB making to cal. files generation (including automated wash).

Applications

Application type	Requirements	Recommended read length	Recommended sample numbers for a single run on T7+*			
			1*FC	2*FC	3*FC	4*FC
Single cell RNA-Seq	600 M/sample (C4: 10K cells, 50K reads/cell)	PE100	20	40	60	80
Cancer large panel	10 Gb/ sample (5,000X, 1Mb panel)	PE100/PE150	288	576	864	1,152
Transcriptome	6 Gb/ sample	PE150	480	960	1,440	1,920
WGS	100 Gb/ sample (30× average sequencing depth)		28	56	84	112
WGBS	110 Gb/ sample (30× average sequencing depth)		24	48	72	96
Stereo-seq	3,000 M/sample (FFPE)	PE75	3	6	9	12
	1,000 M/sample (FF)		12	24	36	48

* Sample numbers are calculated considering pooling variation and applications. For reference only.



T7

Turbocharge your sequencing

T7 can generate 1-7 Tb of high quality data per day, for a wide range of applications. Powered by DNBSEQ™ Technology.

T7 makes sequencing more efficient and productive with advances in biochemical, fluidics, and optical systems.

Features

- High-speed:** 22 to 24 HOURS for PE150 sequencing[†]
 - High-flexibility:** 4 FLOW CELLS, PE150 and PE100 at the same time
 - Ultra-high Throughput:** up to 7 Tb/DAY, High quality data 24/7
- [†] 24H sequencing time is based on using T7 High-throughput Sequencing Reagent Kit V3.0 and FPGA server.

Performance parameters

Read Lengths	Effective Reads / Flow cell*	Data Output	Q30**	Run Time***
SE50****	5800 M	290~1160 Gb	>85%	5.5-6 h
PE100	5800 M	1.16-4.64 Tb	>85%	16-18 h
PE150	5800 M	1.75-7 Tb	>85%	22-24 h

*The maximum number of effective reads are based on the sequencing of an internal standard library. Actual output may vary depending on sample type and library preparation method.

**The percentage of base above Q30 is the average of an internal standard library over the entire run. The actual performance is affected by factors such as sample type, library quality, and insert fragment length.

***Run time includes Flow Cell loading, sequencing, and outputting cal. File. Cal. is a binary file format generated by MGI sequencer basecall software.

**** Customized product.

Applications

Application type	Requirements	Recommended read length	Recommended sample numbers for a single run on T7			
			1*FC	2*FC	3*FC	4*FC
			5800M reads	11,600M reads	17,400M reads	23,200M reads
Single cell RNA-Seq	C4: 10K cells, 50K reads/cell 500M/sample	PE100	9	18	27	36
Cancer large panel	10 Gb/ sample(5000X, 1Mb panel)	PE100/PE150	139	278	417	556
Transcriptome	6Gb/ sample	PE150	232	464	696	928
WGS	100× average sequencing depth 15 Gb/ sample		92	184	276	368
WGBS	30× average sequencing depth 100 Gb/ sample		14	28	42	56
Stereo-seq	30× average sequencing depth 100 Gb/ sample		12	24	36	48
	FFPE: 3000M/sample	PE75	1	2	3	4



T1+

T-level Benchtop Sequencer

T1+ is one of the fastest T-level benchtop sequencers globally, developed with MGI's core DNBSEQ™ technology. T1+ supports dual flow cell concurrent operation, generating up to 1.2 Tb of sequencing data within 24 hours(600 Gb per flow cell, totaling 1.2 Tb for two flow cells). Additionally, T1+ offers an optional built-in bioinformatics module, enabling automated advanced analysis immediately after the sequencing run. This facilitates a tremendously efficient and simple workflow, thus accelerating the application of omics technology to advance global life sciences and clinical research.

Features

- Rapid:** PE 150 < 24 Hours, 1.2Tb/Run, Q40 > 90%
- Simple:** Integrated DNB Make & Load Module, Reagent Kit One-step Operation, Integrated Sequencing and Cleaning
- Flexible:** Individually Addressable Lanes, Dual-Flow Cell, Dual-Configuration

Function Modules

- Built-in Bioinformatics Module
- DNB Make & Load Module
- Dynamic Island
- Elevating Touchscreer Monitor
- Flow Cell Receptacle
- Reagent Cartridge Receptacle

Product specifications

Flow Cell Type	Read Lengths	Data Output/Flow Cell	Run Time***	Q30**	Q40**
FCL 2000M	SE50/App-D SE50	100Gb~200Gb	7h	>93%	>90%
	SE100/App-D SE100	200Gb~400Gb	9.5h	>93%	>90%
	PE150/App-D PE150	600Gb~1.2Tb	24h	>93%	>90%
FCM**** 1000M	App-D SE100	100Gb~200Gb	7h	>93%	>90%
	App-D PE150	300Gb~600Gb	19.5h	>93%	>90%
FCS**** 500M	App-D SE100	50Gb~100Gb	6.5h	>93%	>90%
	App-D PE150	150Gb~300Gb	19h	>93%	>90%
	App-D PE300	300Gb~600Gb	35h	>85%	>75%

* The effective reads are based on the sequencing of an internal standard library. Actual output may vary depending on sample type and library preparation method.

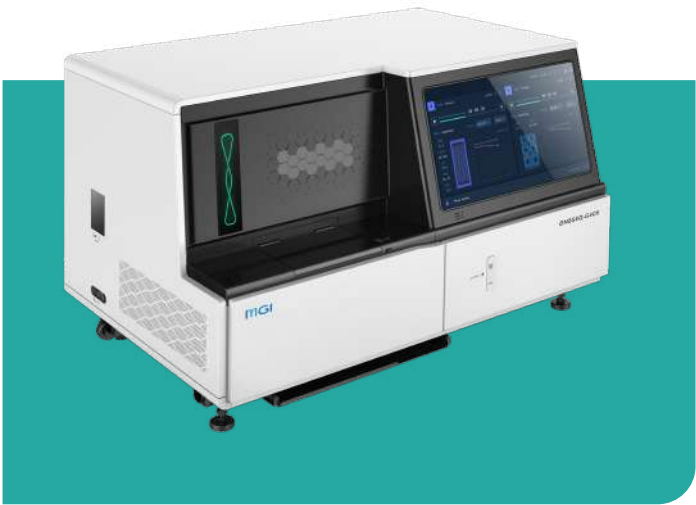
** The percentage of bases above Q30, Q40 and run time is the average of an internal standard library over the entire run. Actual performance is affected by factors such as sample type, library quality, and insert fragment length.

***The sequencing time is the statistical duration from ssCirDNA library to Fastq. FCM and FCS are theoretical estimates of duration.

**** FCS: Available in H2 2025, FCS PE300 and FCM: Available in H1 2026.

Applications

Application type	Requirements	Recommended read length	Recommended sample numbers for a single run on T1+		
			1*FCS	1*FCM	1*FCL
WGS	30X average sequencing depth 100Gb/sample	PE150	500M Reads	1000M Reads	2000M Reads
WGBS	30X average sequencing depth 120Gb/sample		288	576	864
RNA	6 Gb/ sample		480	960	1,440
Single Cell RNA-seq	10k cells (50K reads/cell, 500M reads/sample)		28	56	84
Spatital Transcriptomics	0.5cm × 0.5cm chip(300-600M reads/sample)	PE75	24	48	72
Clinical WGS	40X average sequencing depth 135Gb/sample	PE150	3	6	9
	10Gb/sample (5000X, 1Mb panel)		12	24	36



G400

Versatile and flexible large-scale sequencer

The G400 provides cost-effective solutions for exome, transcriptome and whole-genome sequencing. Its dual flow cell (FC) system supports two FC and several different read lengths to meet a wide range of sequencing needs.

Features

- Competitive pricing and low running cost
- Various read lengths, short turnaround time, a wide range of applications
- Multiple throughput modes support different sequencing project needs

Performance parameters

	Flow Cell Type	Flow Cell No.	Effective Reads /Flow Cell*	Lane No./ Flow Cell	Read Lengths	Data Output /Flow Cell	Run Time***	Q30**	Q40**
Standard MPS	FCS	2	550M	2	SE100	55 Gb	~13 h	>85%	/
					PE100	110 Gb	~22 h****/26 h	>85%	
			300M	2	PE150	165 Gb	~31 h****/37 h	>85%	
					PE300	180 Gb	~98 h	>80%	
	FCL	2	1500-1800M	4	SE35*****	52.5-63 Gb	~11 h	>90%	
					SE50	75-90 Gb	~14 h	>90%	
					SE100	150-180 Gb	~25 h	>90%	
					SE400	600-720 Gb	~109 h	>70%	
					PE100	300-360 Gb	~35 h****/38 h	>85%	
					PE150	450-540 Gb	~50 h****/56 h	>85%	
Standard MPS 2.0	FCL	2	1500-1800M	4	SE50	75-90G	~14h	> 90%	> 85%
					SE100	150-180G	~25h	> 90%	> 85%
					SE100	300-360G	~35h	> 85%	> 85%
					SE150	450-540G	~50h	> 85%	> 85%

* The maximum number of effective reads are based on the sequencing of an internal standard library. Actual output may vary depending on the sample type and library preparation method.
** The percentage of base above Q30 is the average of an internal standard library over the entire run. The actual performance may vary depending on the sample type, library quality and insert fragment length.
*** Run time is calculated based on dual-slide mode including sample loading, sequencing, base calling, and data processing. Only StandardMPS 2.0 (SM 2.0) reagents support the output of Q40 data.
**** This time is the run time after upgrading to the latest version.

Applications

Application type	Requirements	Recommended read length	Recommended sample numbers for a single run on G400	
			1 Flow Cell	2 Flow Cell
			1500M-1800M reads	3000M-3600M reads
NIPT	5M reads/sample	SE50	300	600
Pathogen Fast Identification	25M reads/sample	SE50/SE100	60	120
Single cell RNA-Seq	5000 cells, 100K reads/cell100 Gb/sample	PE100	3	6
Cancer small panel	1 Gb/sample		300	600
Cancer large panel	5 Gb/sample		60	120
Transcriptome	40M reads/sample	PE150	38	76
WES	15 Gb/sample (100×)		30	60
WGS	90 Gb/sample (30×)		5	10



G50

Compact flexible genetic sequencer

G50 is a dedicated benchtop sequencer with 2 different flow cells which meets different requirements of read length time and output. Its key applications are low-pass WGS, targeted sequencing, small whole genome sequencing, RNA sequencing and WES.

Features

- Various read length options and short turnaround time
- Perfect balance between speed and affordability
- Support sequencing solutions for research, clinical, agriculture, etc.

Performance parameters

Flow Cell Type	Flow Cell No.	Effective Reads /Flow Cell*	Lane No./ Flow Cell	Read Lengths	Data Output /Flow Cell	Run Time***	Q30**
FCS	1	100M	1	SE100	~10 G	~13 h	>80%
				PE100	~20 G	~22 h****/26 h	>85%
				PE150	~30 G	~31 h****/37 h	>80%
FCL	1	500M	1	SE50	~25 G	~11 h	>85%
				SE100	~50 G	~14 h	>85%
				PE50	~50 Gb	~25 h	>85%
				PE100	~100 G	~109 h	>85%
				PE150	~150 G	~35 h****/38 h	>80%

* The maximum number of effective reads are based on the sequencing of an internal standard library. Actual output may vary depending on the sample type and library preparation method.
** The percentage of base above Q30 is the average of an internal standard library over the entire run. The actual performance may vary depending the sample type, library quality and insert fragment length.
*** Run time is calculated over the entire run including sample loading, sequencing, base calling, and data processing.

Applications

Application type	Requirements	Recommended read length	Recommended sample numbers for a single run on G50			
			1*FCL	1*FCS	2*FCL	2*FCS
Single cell RNA-Seq	Meta: ~20M reads/sample	PE100	25	5	6,250	1,250
Cancer large panel	Isolated Bacteria: ~1Gb/sample	PE100/PE150	100~150	20~23	12,500	2,500-3,000
Transcriptome	NIPT/PGS: ~10M reads/sample	PE150	50	10	12,500	2,500
WGS	NIPT plus/CNV: ~25M reads/sample		20	4	5,000	1,000
WGBS	Large panel: ~10Gb/sample	PE100, PE150	10~15	2~3	2,500	500~800
	Small panel: ~1Gb/sample		100~150	20~23	25,000	5,000~6,000
Stereo-seq	Expression: ~25M reads/sample	PE75	20	4	~5,000	1,000
	Transcriptome: ~6Gb/sample	PE150	25	5	~6,300	1,250



G99

Unleash your ultimate sequencing speed

As one of the sequencers with the fastest speed among mid-low throughput in the world, G99 is developed based on MGI's core **DNBSEQ™** sequencing technology, enabled by innovations in biochemistry, optics, fluidics, temperature control, and other core systems. G99 is especially applicable for multiple sequencing methods and it only needs 12 hours to finish PE150 sequencing.

Features

- **High-speed:** 8~96GB per run, Only 12 hrs for PE150 (from loading to FASTQ)
- **FSupports** multiple read lengths, including PE50, SE100, PE150, PE300, SE400
- Applicable to multiple sequencing methods

Performance parameters

Maximum number of Flow Cells	Lanes / Flow Cell	Effective Reads/ Flow Cell*	Supported Reads	Data Output	Q30**	Q40**	Run Time***
2	1	80M	Lengths	8-16G	>90%	>85%	5h
			PE150	24-48G	>90%	>85%	12h
			APP-D SE100	8-16G	>90%	>85%	5h
			APP-D PE150	24-48G	>85%	>85%	12h
			APP-D PE300	48-96G	>85%	>80%	30h
			SE400	32-64G	>75%	>70%	20h

*Minimum effective reads is determined using a standard library. Actual output may vary depending on sample type and library preparation method.
** The percentage of bases above Q30 and run time is the average of an internal standard library over the entire run. The actual performance is affected by factors such as sample type, library quality, and insert fragment length. Only StandardMPS 2.0(SM 2.0) reagents support the generation of Q40 data.
***The sequencing time is the statistical duration for single flow cell sequencing and dual flow cell simultaneous sequencing.
+The instrument is equipped with SE50 and PE100 sequencing modes, and the existing reagent kits support SE50 and PE100 read length sequencing.
Note: APP-D has built-in Illumina's Truseq, Nextera adapters, and MGI adapter, which supporting mixed testing of Illumina's Truseq, Nextera adapters, and MGI adapter libraries.

Applications

Application type	Requirements	Recommended read length	Recommended sample numbers for a single run on G99	
Onco panel	Small panel: ~1Gb/sample	PE100/PE150	1 Flow Cell	2 Flow Cell
Single cell RNA-Seq	Meta: ~20M reads/sample	PE150	4	8
Cancer large panel	Isolated Bacteria: ~1Gb/sample		400	800
ATOPlex panel (Respiratory, COVID-19, etc.)	Respiratory panel: 5M reads/sample COVID-19 panel: 5M reads/sample	PE100/PE150	16	32
WES	15Gb/sample	PE150	1-2	2-4
Onco targeted methylation panel	~5Gb/sample	PE150	4	8
Metagenomics for pathogen detection	Meta: 20M reads/sample	SE50/SE100	4	8
Microbial WGS sequencing	Single bacterium: ~1Gb/sample	PE100/PE150	16-24	32-48
NIPT	NIPT/PGS: ~10M reads/sample	SE50	8	16
PGS		SE50		
RNA-Seq	Expression profiling: ~25M/sample	SE50/PE150	3	6
	Transcriptome: ~6Gb/sample		4	8



E25

Unleash your ultimate sequencing speed

As one of the sequencers with the fastest speed among mid-low throughput in the world, G99 is developed based on MGI's core **DNBSEQ™** sequencing technology, enabled by innovations in biochemistry, optics, fluidics, temperature control, and other core systems. G99 is especially applicable for multiple sequencing methods and it only needs 12 hours to finish PE150 sequencing.

Features

- **Easy installation:** Easy-to-use cartridge, no environmental requirement
- **Simple sequencing:** Ready to use in 10 minutes Built-in bioinformatics enables full workflow from sample to report
- Supports MGI and App-C libraries and requires no primer substitutions

Performance parameters

Read Lengths	Effective Reads*	Data Output	Run Time	Q30**
SE100	25M	2.5GB	~5h	>90%
PE150	25M	7.5GB	~20h	>80%
APP-C SE100***	20-25M	2.0 Gb	~5h	>90%
App-C PE150***	20-25M	6.0 Gb	~20h	>80%

* The effective reads value is obtained according to the operation of a specific standard library, and the actual application library will fluctuate according to the sample type and library construction method.
** The percentage of bases above Q30 and the running time are averaged over the entire run for a particular standard library. The practical application performance is affected by sample type, library quality, insert length and other factors.
*** The App-C Sequencing Set includes the invertase module, eliminating the need to purchase additional conversion reagents.
+ The existing kit supports SE50 and PE100 reads, and the instrument does not have SE50 and PE100 sequencing modes.

Applications

Application	Recommended data size	Recommended read length	Recommended sample numbers for a single run on E25
ATOPlex pan (Respiratory)	Respiratory panel: ~5M reads/sample	PE150	4
ATOPlex panel (COVID-19, HIV, TB, MPXV)	COVID-19: ~1M reads/sample	SE100	24
	MPXV: 5M reads/sample or 20M reads/sample		4 (5M) /1 (20M)
	HIV: ~1M reads/sample	PE150	16
	TB: ~3M reads/sample		4~8
	MPXV: 1.5M reads/sample or 6M reads/sample		16 (1.5M) /4 (6M)
Infectious Diseases Identification	0.5M~1M reads/sample	SE50	16~32
Small cancer panels	2-5M/sample	PE150	4
eDNA	65K reads/sample	PE150	72
16S sequencing	~ 0.3M reads/sample	PE150	72
Metagenomics for pathogen detection	Meta: 20M reads/sample	SE100/PE150	1
Microbial WGS sequencing	Single bacterium: 20M reads/sample	SE100	1
Bacteriophage	~ 5M reads/sample	SE100	4
DNA Trait for Genomics Education	~0.3M reads/sample	SE100	48
STR	~1M reads/sample	SE400 (Customized Developing)	10
Synthetic Strand Verification	0.5M~1M/sample	SE100	24-48
DNA Storage	12~96 pool oligo	PE150	/

G100-ER

Nano Gates to the Macro Cosmos

G100-ER, a nanopore genetic sequencer features a dual flow cell architecture that enables independent operation simultaneously. With flexible throughput options and exceptional capabilities such as broad coverage, rapid sequencing, and flexible testing. It effectively addresses the challenges of complex sequences, meeting the diverse sequencing needs across various applications, such as microbial genome research, microbial metagenomes, amplicon-based microbial detection, targeted disease testing, small whole-genome sequencing and whole transcriptome study, etc.



G400-ER

Sequence More, Discover More

The G400-ER nanopore genetic sequencer, a self-developed product based on the CycloneSEQplatform, integrates a high-throughput and high-density flow cell. This instrument combines longread lengths, high data output, and real-time sequencing capabilities, enabling efficient andprecise analysis of complex genomes while simultaneously detecting base modifications. Itsupports diverse applications including whole-genome resequencing, de novo genome assembly.full-length transcriptome sequencing, and epigenomic sequencing, ensuring accuracy across theentire genomic research spectrum.

Features

Rapid Sequencing

- Sequencing speed 350 nt/s - 420 nt/s
- Obtain 100 Mb data s10 min
- Read 100 Kb long fragment ≤ 5 min

Broad Coverage

- bp -Mbp read length
- Broad genome coverage
- Expandable to multi-omics sequencing

Flexible Testing

- Get FASTQ results in real-time
- Random access and easy to operate
- Low start-up cost

Performance parameters

Number of Nanopore Proteins

- 4096/Flow Cell

Sequencing Acquisition Time

- Real-time

Maximum Throughput / Flow Cell*

- ≥ 60 Gb (Designed throughput is 50 Gb)

* in Real Laboratory Experiments

Number of Nanopore Proteins	4096 / Flow Cell
Sequencing Speed	350 nt/s - 420 nt/s
Sequencing Time	10 mins - 72 hrs
Sequencing Acquisition Time	Real-time
Read Length	100 bp - Mbp Level
Maximum Throughput / Flow Cell (in Real Laboratory Experiments)	50 Gb
Data Output Rate / Flow Cell	10 Mb / min
Single Time Accuracy	97%
Consensus Accuracy	99.99% (40X)

Applications

Application	Recommended read length	Recommended sample numbers for a single run on G100-ER
Full-length 16S rRNA Gene Amplicon Sequencing	According to the hope that the analysis of the lower limit of the lower abundance of measurement: in the multiple samples pooling the total data volume measurement need to take into account the loss caused by splitting, can be calculated according to the limit of 70% ~ 80% of the value of the more extreme. For example, 0.1 M reads/sample, 24 samples require 150Mb *24/0.7=5.14Gb of data.	Customizable (no less than 24 samples recommended), self-selectable based on barcode combination
Bacterial Isolates WGS and Assembly case	Minimum 50X recommended for general genomes, <10 Mb genome size, 24 sample mixes, ≥ 17 Gb of data recommended.(complex genomes need to be reassessed)	< 24
	10 Mb~15 Mb genome size, 12 samples mixed, recommended data volume ≥ 13 Gb (complex genomes need to be reassessed)	< 12
Whole Plasmid Sequencing and Assembly	Single sample 10M~20M, not less than 10M; customized according to the number of samples	Customizable (no less than 24 samples recommended), self-selectable based on barcode combination (24xN, e.g. 24x24 or 24x96)
Bulk full-length transcriptome sequencing	Sequencing of 2 mixed samples, total sequencing throughput is recommended to be not less than 40G	≤ 2

Features

- Plasmid sequencing
- Targeted disease detection
- Microbial genome research
- Amplicon microbial detection
- Small-genome research
- Bulk full-length transcriptome sequencing

Performance parameters

Number of Nanopore Proteins	30,000+/Flow Cell
Maximum Throughput / Flow Cell (in Real Laboratory Experiments)	400 Gb
Data Output Rate / Flow Cell	100 Mb/min
Read Length	100 bp - Mbp Level
Sequencing Time*	10 mins - 72 hrs
Sequencing Acquisition Time	Real-time
Sequencing Speed	350 nt/s - 420 nt/s
Single Time Accuracy	≥ 97%
Consensus Accuracy	≥ 99.99% (40x)

Applications

Application	Recommended read length	Recommended sample numbers for a single run on G400-ER
Human genome resequencing (90 Gb/30x)	Recommended depth for human genome resequencing is 30×, if used for assembly, 50× depth is recommended. Complex genome needs reassessment	1
		2
Human genome resequencing (15x)	It is recommended to a general genome analysis at least 15X for combining DNBSEQ Data and CycloneSEQ Data Analysis	1
		4
Sequencing and assembly of animal and plant genomes (3 Gb/50x)	It is recommended to assemble a general genome at least 50X for regular assembly. Complex genome needs reassessment	1
Bulk transcriptome sequencing (20 Gb)		8
Single-cell full-length transcriptome sequencing (200 Gb)	It is recommended to a general analysis at least 20Gb data for analysis. Complex genome needs reassessment	1
Microbial metagenomic sequencing and assembly (20 Gb/sample)		1
	It is recommended to a general sequencing at least 10Gb data for Microbial metagenomic. It is recommended to a general assembly at least 20Gb data for Microbial metagenomic.	8

Library Preparation Kits

Universal Library Prep

Whole Genome Sequencing

- MGIEasy Fast FS Library Prep Set V2.0
- MGIEasy Fast PCR-FREE FS Library Prep Set V2.0
- MGIEasy UDB Universal Library Prep Set
- MGIEasy Universal DNA Library Prep Set
- MGIEasy PCR-free DNA Library Prep Set

Whole Exome Sequencing

- MGIEasy Exome Capture V5 Probe Set
- MGIEasy Fast Hybridization and Wash Kit
- MGIEasy Exome Capture Accessory Kit
- MGIEasy Dual Barcode Exome Capture Accessory Kit
- MGIEasy Duplex UMI Universal Library Prep Set

Methylation Sequencing

- MGIEasy Whole Genome Methylation Sequencing Library Prep Kit V3.0

RNA Sequencing

- MGIEasy Fast RNA Library Prep Set
- MGIEasy rRNA Depletion Kit V1.3
- MGIEasy rRNA & Globin Depletion Kit V1.3
- MGIEasy Small RNA Library Prep Kit

Library preparation modules

- MGIEasy Universal Library Conversion Kit (App-A)
- MGIEasy Circularization Kit
- MGIEasy Dual Barcode Circularization Kit
- MGIEasy DNA Adapters-96 (Plate) Kit
- MGIEasy UDB Primers Adapter Kit A/B/C
- MGIEasy DNA Clean Beads
- Standard Library Reagent
- ...

Specific Library Prep

Library Prep for Forensic Genomics

- MGIEasy Pa-SNPs Genotyping Kit
- MGIEasy Signature Identification Library Prep Kit

cfDNA

- MGIEasy Cell-free DNA Library Prep Set

ATOPlex Library Prep series

- ATOPlex customized products
- ATOPlex RNA Multiplex PCR-based Library Preparation Set V3.1 (for SARA-CoV-2 sequencing)
- ATOPlex RNA Library Preparation Set (for SARA-CoV-2 sequencing)
- MGIEasy Respiratory Microorganisms Genome Library Preparation Set
- ATOPlex MTB Library Preparation Set
- ATOPlex HIV-1 Library Preparation Set
- ATOPlex DNA Panels (16SV3V4 rDNA / 18SV4 rDNA / ITS1 rDNA / Ac12S mtDNA / COI mtDNA / MiFish / MPXV / DENV1-4)
- ...

Sequencing Modular Reagents

APP Series Products

- High-Throughput Pair-End Sequencing Primer Kit (App-D)
- High-Throughput Single-End Sequencing Primer Kit (App-D)
- High-Throughput Sequencing Primer Kit (App-C) *
- High-Throughput Pair-End sequencing Primer Kit (App-A)+High-Throughput Barcode Primer 3 Reagent Kit (App-A)
- High-Throughput Single End sequencing Primer Kit (App-A)

OneStep DNB Make Reagent Kit

DNB Make Reagent Kit V1.0

- DNBSEQ OneStep DNB Make Reagent Kit (OS-App-A)
- DNBSEQ OneStep DNB Make Reagent Kit (OS-DB)
- DNBSEQ OneStep DNB Make Reagent Kit (OS-SB)
- DNBSEQ DNB Make Reagent Kit (SD)
- DNBSEQ DNB Make Reagent Kit (SD-App-A)

DNB Make Reagent Kit V4.0

- DNBSEQ OneStep DNB Make Reagent Kit V4.0
- DNBSEQ OneStep DNB Make Reagent Kit V4.0
- DNBSEQ OneStep DNB Make Reagent Kit V4.0
- DNBSEQ OneStep DNB Make Reagent Kit V4.0 (Single Barcode)
- DNBSEQ OneStep DNB Make Reagent Kit V4.0 (Dual Barcode)

Whole Genome Sequencing

Whole-Genome Sequencing (WGS) is the process by which an organism’s entire genome, both nuclear and cytoplasmic, is unraveled and read. It is useful in elucidating the underlying genomic details in studies at either an individual or population scale. WGS has applications in selective breeding, population evolution, disease research, clinical diagnosis and drug developments. The DNBSEQ-based WGS solutions can accurately and rapidly identify the distribution of SNPs across the genome and annotate the variants based on the genome database.

Recommended MGI Process for different applications

Application	Sample	Library perp	Sequencing	Data analysis
Large genome& Human / Animal / Plant				
Human WGS (National genome project, LargePopulation Genomex clinical rapidWGS, Genetic disease research, etc)	50ng-900ng gDNAblood/ saliva/ oral swabs/tissue	■ SP-960/SP-100/SP-Smart8 ■ MGIEasy Fast PCR-FREE FS Library Prep Set V2.0 ■ MGIEasy Dual Barcode Circularization Kit	G400/T1+/T7/ T20x2	■ MegaBOLT ■ WGS Germline variant calling pipeline ■ WGS Somatic variant calling pipeline
Animal/Plant (WGSGenetic and breeding researchpopulation genetic evolution,genetic map construction, etc)	50ng-900ng gDNAor 25ng-1ug gDNAblood/ tissue	■ SP-960/SP-100/SP-Smart8 ■ MGIEasy Fast PCR-FREE FS Library Prep Set V2.0or ■ MGEasy Fast FS Library Prep Set V2.0M GIEasy Dual Barcode Circularization Kit	G400/T1+/T7/ T20x2	/
Low-pass WGS (DTC, Agricultural breeding, etc)	25ng-200ng gDNAblood/ saliva	■ SP-960 ■ MGIEasy Fast PCR-FREE FS Library Prep Set V2.0(1152customized UDBs) ■ DNBSQ OneStep DNB Make Reagent Kit V2.0(OS-DB)	G400/T1+/T7/ T20x2	/
Smallgenomex Micorbe/Meta/Amplicon				
Microbial WGS/ Metagenomic sequencing (Microbial genome research,Pathogensor bacteria identification, etc)	1ng-200ng gDNAMicrobial culture/ saliva/ oralswabs/Meta DNA	■ SP-960 /SP-100/SP-Smart8 ■ MGI E.sy Fast FS Library Prep Set V2.0(1152customized UDBs) ■ DNBSQ OneStep DNB Make Reagent Kit V2.0(OS-DB)	G99/G50/ E25G400/T1+/ T7/T20x2	■ Platform of Microorganisms Fast identification, PFI ■ Microbial Genome Analysis Pipeline,MGAP ■ Bacteria Fast identification, BFI
Amplicon sequencing (Pathogens or bacteriaidentification, etc	25ng-200ng DNAATOPlex amplicons	■ SP-960/SP-100/SP-Smart8 ■ MGIE.sy Fast PCR-FREE FS Library Prep Set V2.0 ■ DNBSEQ OneStep DNB Make Reagent Kit V2.0(OS-DB)	G99/G50/ E25G400/T1+/ T7	A series of bioinformatics analysis productsspecifically designed for the ATOPlex technologyplatform

WGS library preparation

MGI has developed a series of DNA library preparation kits for WGS to meet the needs of various sample types and applications.

- **MGIEasy Fast FS Library Prep Set V2.0**
The MGIEasy Fast FS Library Prep Set provides flexible workflow to be compatible with 1 ng~1 µg DNA input, supporting variety sample types, including blood, saliva, oral swabs FFPE and precious samples with low starting amount suitable for microbial sequencing, metagenomics sequencing, WGS and WES.
- **MGIEasy Fast PCR-FREE FS Library Prep Set V2.0**
The MGIEasy Fast PCR-FREE FS Library Prep Set V2.0 is optimized to convert 25 ng~900 ng genomic DNA (gDNA) into a special library and uses high quality fast fragmentase to combine the fragmentation, end-repair and add A into one step, to simplify the preparation process and significantly shorten the duration of DNA library preparation.
- **MGIEasy UDB Universal Library Prep Set**
The MGIEasy UDB Universal Library Prep Set is specifically designed for creating WGS libraries for the MGI high-throughput sequencing platform series. This library prep set is optimized to convert 1-1000ng of fragmented DNA into a customized library. Unique dual barcode supported double checked barcode split method ensuring sequencing homogeneity and accuracy.
- **MGIEasy Duplex UMI Universal Library Prep Set**
The MGIEasy Duplex UMI Universal Library Prep Set is designed for cancer applications. It incorporates duplex-UMI (unique-molecule-identifier) to obtain higher sensitivity and precision. Duplex barcodes reduce label hopping and contamination between samples, while the UMI is used to reduce PCR and sequencing errors.

- **MGIEasy Universal DNA Library Prep Set**
The MGIEasy Universal DNA Library Prep Set provides an efficient and universal library construction solution for various DNA sample types such as fragmented gDNA, FFPE DNA, Meta DNA , cfDNA, ChIP DNA and capture DNA.
- **MGIEasy PCR-Free DNA Library Prep Set**
The MGIEasy PCR-Free DNA Library Prep Set is used for broad application of WGS library without PCR amplification. The removal of PCR amplification during library preparation does not result in error or bias. It has the advantages of no error accumulation, high coverage uniformity and excellent performance of variation detection.

Product specifications

Products	MGIEasy Fast FS Library Prep Set	MGIEasy Universal DNA Library Prep Set	MGIEasy PCR-Free DNA Library Prep Set	MGIEasy Fast PCR-FREE FS Library Prep Set	MGIEasy Duplex UMI Universal Library Prep Set	MGIEasy UDB Universal Library Prep Set
Method	Enzymatic Fragmentation, PCR method	Covaris Fragmentation, PCR method	Covaris Fragmentation, PCR-free method	Enzymatic Fragmentation, PCR-free method	Covaris Fragmentation, PCR method	Covaris Fragmentation, PCR method
Barcode	288 standard UDBs; 1152 customized UDBs for Metagenomic sequencing	96 Single BCs	96 Single BCs	384 standard UDBs; 1152 customized UDBs for low-pass WGS	192 UDBs	96 UDBs
Assay time	~2 h	<4.5 h	~3.5 h	~1.3-1.4 h	~7 h	~4.5 h
Input quantity	1 ng~200 ng gDNA for small genomes (e.g. microbial, meta),25 ng~1 µg gDNA for large genomes (e.g. human, plant, animal)	0.5-50 ng fragmented DNA	80-200 ng fragmented DNA	25-900 ng gDNA	10 ng cfDNA	1-1000 ng fragmented DNA
Sample types	gDNA from blood, saliva, oral swabs, tissue, Microbial gDNA, Meta DNA, FFPE DNA	gDNA, FFPE DNA, cfDNA, ChIP DNA, etc.	gDNA	gDNA, Virus long amplicons	Blood, tissue, FFPE DNA, cfDNA	gDNA, FFPE, cfDNA, ChIP DNA, etc.
Species compatibility	Human, animals, plants, fungi, bacteria, and meta				Human	Human, mice, rice, Arabidopsis, yeast, E. coli, meta, FFPE, etc.
Automation option	Automation-friendly: SP-100, SP-960				SP-100, SP-960, s eminar probes	N/A
Applications	Human WGS, Plants & Animals WGS, Microbial WGS, Metagenomics sequencing, WES	WGS, WES, target capture sequencing, Microbial WGS, Metagenomics sequencing	Human WGS sequencing (high depth)	Human WGS, Plants & animals WGS, Low-pass WGS, Microbial WGS, Metagenomics sequencing, Virus long amplicons sequencing	Target capture sequencing, such as cancer screening, drug selection	WGS, WES, target capture sequencing, Microbial WGS, Metagenomics sequencing
Platform Compatibility	G400, G50, G99, E25, T7, T10×4, T20×2	G400, G50, T7		G400, G50, T7, T10×4, T20×2, G99, E25	G400, G50, T7	
Recommended Read Length	SE100, PE100, PE150	PE100, PE150	PE100, PE150	SE100, PE100, PE150	PE100, PE150	PE100/PE150

MGIEasy Fast FS Library Prep Set V2.0

The MGIEasy Fast FS Library Prep Set V2.0 is designed to prepare WGS libraries for MGI high-throughput sequencing platforms and combines the high-quality fast fragmentase to simplify the preparation process and significantly shorten the DNA library preparation time. This library prep set provides flexible workflow to be compatible with 1 ng~1 µg DNA input, supporting a variety sample types, including blood, saliva, oral swabs, FFPE and precious samples with low starting amounts, suitable for microbial sequencing, metagenomics sequencing, WGS and WES.

Features

- Fast library prep workflow: combining the DNA fragmentation, end repair and add A into one step, significantly reducing the library prep time in 1.3 hours
- Flexible workflow to accommodate variations in sample type, DNA input amount and applications
- High uniform and consistent insert sizes across a wide DNA input range and sample types
- Efficient automatable workflow

Product specifications

Assay Time	~2 hrs (from gDNA to PCR library)
Input Quantity	1 ng~200 ng gDNA for small genomes (e.g. microbial, meta), 25 ng~1 µg gDNA for large genomes (e.g. human, plant, animal)
Barcode	~288 Unique Dual Barcodes
Sample types	gDNA from blood, saliva, oral swabs, tissue, Microbial gDNA, Meta DNA, FFPE DNA
Species Compatibility	Human, Animal, Plant, Microbe
Applications	Human WGS Plants & Animals WGS, Microbial WGS, Metagenomics sequencing, WES
Platform Compatibility	G400, G50, G99, E25, T7, T10×4, T20×2
Recommended Read Length	SE100/PE100/PE150
Adaptation automation platform	SP-100(16RXN), SP-960(96RXN)

Performance

- Normalized coverage of three different bacterial species with varying GC content

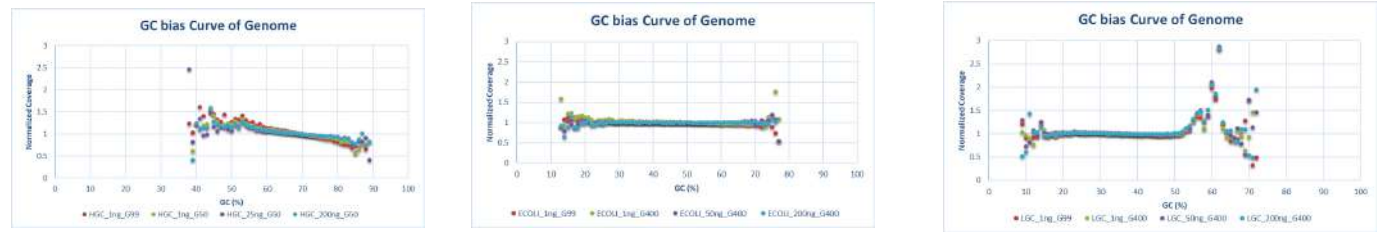
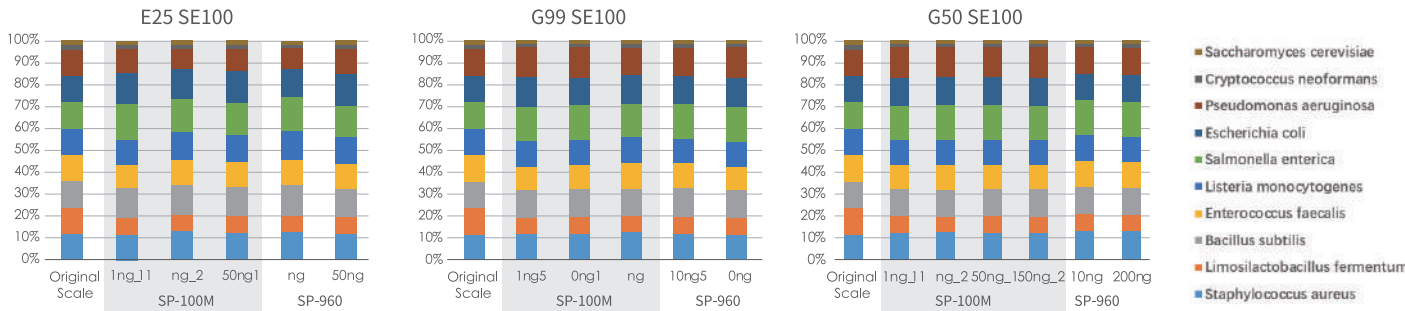


Fig. a Normalized coverage of HGC (68%) Fig. b Normalized coverage of Ecoli (50%) Fig. c Normalized coverage of LGC (38%)

Libraries were prepared from the gDNA from three different bacterial species varying GC content (HGC (68%), LGC (38%), Ecoli (50%)), with starting amount of 1 ng, 50 ng and 200 ng DNA, by using the MGIEasy Fast FS Library Prep Set V2.0 combined with the MGI OneStep DNB kits. Sequencing was performed on G400, G99 and G50.

- Highly concordant bacterial species identification and distribution



Libraries were prepared from the gDNA from Meta standard ranging from 1-200ng using the MGIEasy Fast FS Library Prep Set V2.0 combined with the MGI OneStep DNB kits. Sequencing was performed on G50 SE100, G99 SE100 and E25 PE150. MGI PFI software was used for the bacterial species identification and distribution evaluation.

MGIEasy Fast PCR-FREE FS Library Prep Set V2.0

The MGIEasy Fast PCR-FREE FS Library Prep Set V2.0 is designed to prepare WGS PCR-Free library for MGI high-throughput sequencing platforms. This library prep set is significantly shorten the DNA library preparation time by using high quality fast fragmentase. The PCR-free method and optimized library prep make it perform well in genome coverage uniformity and mutation detection precision and sensitivity. The set combined with the SP-100 and SP-960, could provide automatic library preparation workflows. This library prep set is suitable for WGS with fast, easy-to-use, and excellent performance and is the preferred recommendation for the large genome sequencing project.

Features

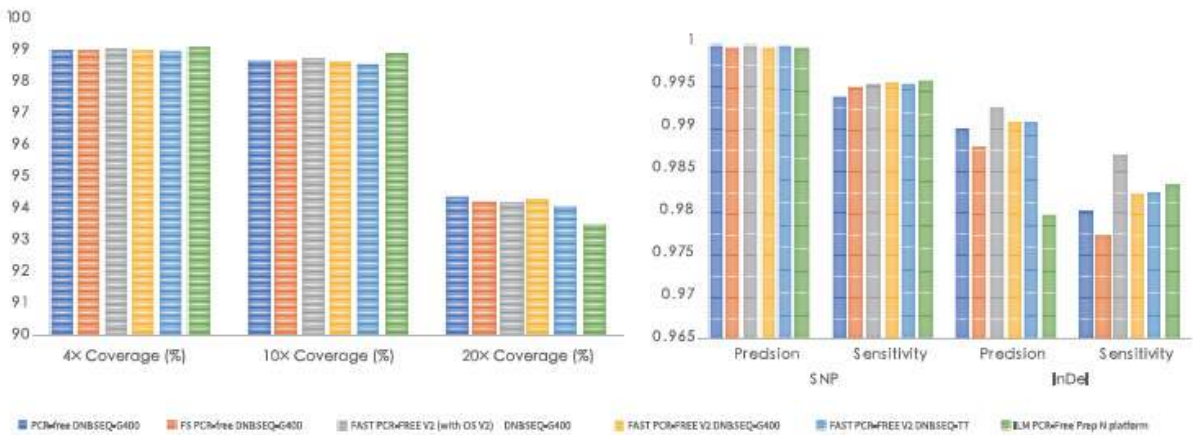
- Fast, simple and automated workflow
- Flexible workflow to accommodate variations in sample type, DNA input amount, applications
- Excellent performances in genome coverage uniformity and variation detection.

Product specifications

Version	V2.0
Assay Time	~ 1.3 hrs -1.4 hrs
Hands-On Time	~20 min
Input Quantity	25 ng ~900 ng gDNA
Barcode	~384 Unique Dual Barcodes
Insert size	Two sides beads purification: 400 bp~600 bp, One side beads purification: 600 bp~850 bp
Sample types	gDNA from blood, saliva, oral swabs, tissue, Microbial gDNA, Meta DNA, Virus long amplicons
Species Compatibility	Human, Animal, Plant, Microbe
Applications	Human WGS, Plants & animals WGS, Low-pass WGS, Microbial WGS, Metagenomics sequencing, Virus long amplicons sequencing
Platform Compatibility	G400, G50, T7, T10×4, T20×2, G99, E25
Recommended Read Length	SE100/PE100/PE150
Adaptation automation platform	SP-100(16RXN), SP-960(96RXN, 384RXN)

Performance

- Excellent performance in genome coverage uniformity and mutation detection precision and sensitivity



PCR-free libraries were constructed using different library prep kits and were sequenced on MGI sequencers and another sequencing platform. The results showed that the MGIEasy Fast PCR-FREE FS Library Prep Set V2.0 have better genome coverage uniformity, and excellent t mutation detection precision and sensitivity.

MGIEasy UDB Universal Library Prep Set

MGIEasy UDB Universal Library Prep Set is specifically designed for creating WGS libraries for the MGI high-throughput sequencing platform series. When sample multiplexing is performed for sequencing, the dual barcode adapter design, which helps mitigate barcode contamination and hopping, effectively reduces barcode swapping within samples. In addition, allowing for the mixing of libraries prior to targeted capture or DNB preparation simplifies sample preparation and reduces the cost of sequencing.

Features

- Unique dual barcode to avoid contamination between samples
 - Suitable for FFPE samples
- Good sample compatibility
 - Suitable for different commercial probe

Performance

Unique dual barcode to avoid contamination between samples

The adaptors and incomplete PCR product in the reaction may introduce wrong barcode information and cause inter-sample contamination. Figure 1a shows the effect of dual barcode removal and capture library contamination(16 plex). It can be seen from the figure that cross-contamination data in the 16 sample pooling captured library data are real (red area). the dual barcode,which helps mitigate barcode contamination and hopping.

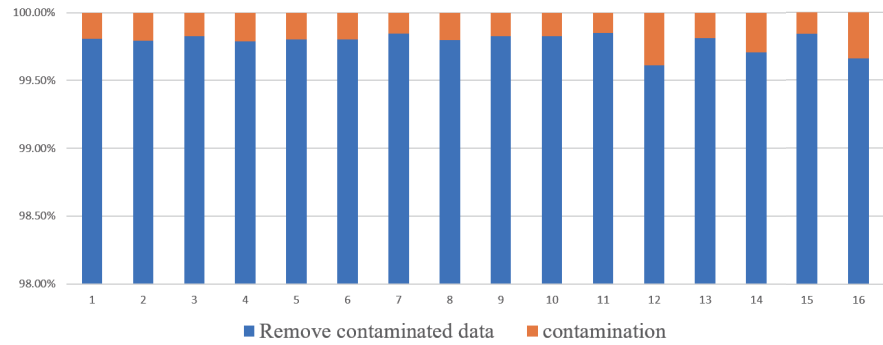


Figure 1a Dual barcode remove capture library contamination (16 plex)

If there is a strong positive sample in the same lane and weak positive samples mixed with a large number of contaminated samples, it is impossible to detect the weak positivie samples because of the contamination between samples. The dual barcode technology could reduce contamination, which will improve the sensitivity and accuracy of weak positive sample detection.

Figure 1b When there are strong positive samples (reach to 100,000-200,000 reads) in the same lane, combined with dual barcode, the contamination rate can be reduced, so as to avoid the contamination of negative samples as far as possible. It can be seen from the figure that, even if mixed sequencing is performed with strong positive samples, the contaminated sequence of negative samples will be reduced to below ten reads.

Figure 1c shows low contamination rate can effectively improve the discrimination of target bacteria/background bacteria. When the contamination rate is 0.001%, the weak positive samples can be distinguished from background bacteria even if the read number less than 10. Thus the sensitivity and accuracy of the detection of weak positive samples are significantly improved.

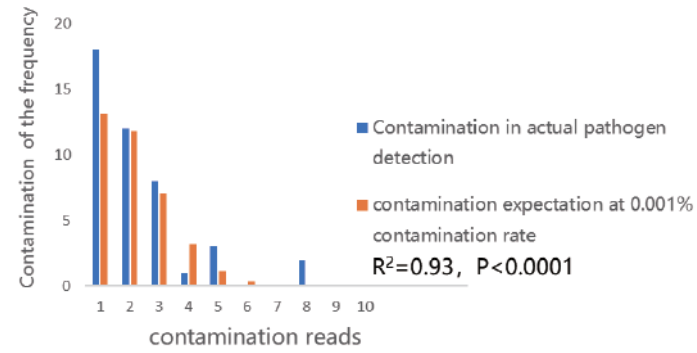


Figure 1b Actual and simulated distribution of contamination between samples

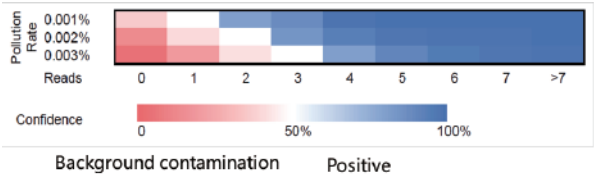


Figure 1c Positive bacteria determination confidence simulation (when strongly positive samples are less than 200,000 reads)

MGIEasy Universal DNA Library Prep Set

Features

- Use as low as 0.5 ng fragmented DNA per sample
 - Compatible with different DNA fragmentation methods
 - Accepts gDNA, FFPE, cfDNA, CHIP DNA, and other samples with varying degrees of degradation
- Compatible with many sample types, such as human, animals, plants, high and low GC bacteria, and fungi
 - Library preparation can be completed in as little as 4.5 hours

Performance

Good consistency of library yield

PCR library preparations with selected samples from five species, including human, mouse, soybeans, E. coli and meta, each with an initial amount of 50 ng fragmented DNA, result in consistent yields above 400 ng. This indicates that MGIEasy Universal DNA Library Prep Set obtains sufficient PCR library yield for subsequent circularization and sequencing for samples of different species and different genome size.

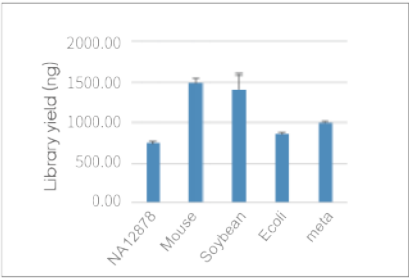


Fig.1a PCR yield of library preparation for different species

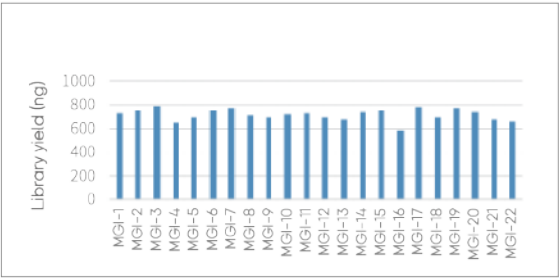


Fig 1b PCR yield of library preparation for NA 12878 standard

22 repetitions of PCR library preparation were performed using NA12878 stanard as a template. The mean library yield was 718.9 ng with a CV value of 6%. This indicates that the MGI easy Universal DNA Library Prep set is capable of producing stable library yields.

Compatible with different GC content microbial library preparation

Using single bacterial strains with different GC contents as templates, a PCR library yield above 40 ng can be achieved consistently at various starting amounts of gDNA, which meets the requirements of subsequent circularization and sequencing. The GC content of single strains below from left to right are 64%, 50%, and 37% respectively. The gDNA initial amounts used are 50 ng, 5 ng, and 0.5 ng. The PCR reaction is carried out for the corresponding number of amplification cycles.

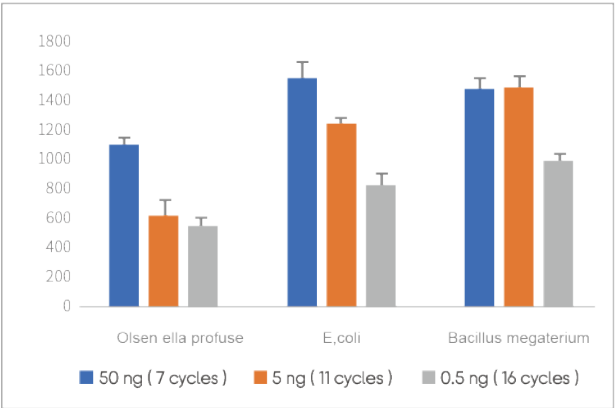


Fig.2 Library preparation of different GC content for single bacterial strains

Whole Exome Sequencing

Whole Exome Sequencing (WES) is a targeted sequencing technology that focuses on only 2% of an entire region's genome, but covers most of the gene coding regions and >99% of variations in the ClinGen database. Data from WES can be used to detect SNVs, indels, gene arrangements and copy number variations (CNVs). The decreasing cost of DNA sequencing has made WES more accessible, resulting in widespread adoption of the technology for genetic disease scanning, tumor molecular diagnosis and immunotherapy. The DNBSEQ-based WES solutions deliver full coverage of coding regions and help identify the exomes with the most significant phenotypic impact.

Recommended MGI Process

	Library construction	Capture	Sequencing	Analysis
Traditional overnight hybridization	· MGIEasy Fast FS Library Prep Set V2.0 · or MGIEasy UDB Universal Library Prep Set · or MGIEasy Duplex UMI Universal Library Prep Set	WES Probe: MGI V5 Probes (with traditional overnight hybridization reagents) + Block and Post PCR: MGIEasy Dual Barcode Exome Capture Accessory Kit	G99/ G400/ T7	MegaBOLT - WES pipeline
Fast hybridization	· MGIEasy Fast FS Library Prep Set V2.0 · + MGIEasy Dual Barcode Circularization Kit · or MGIEasy UDB Universal Library Prep Set · or MGIEasy Duplex UMI Universal Library Prep Set	WES Probes: Third-party commercial DNA probes + Hybridization: MGIEasy Fast Hybridization and Wash Kit + Block and Post PCR: MGIEasy Dual Barcode Exome Capture Accessory Kit	G99/ G400/ T7	MegaBOLT - WES pipeline

WES library preparation

MGIEasy Exome Capture V5 Probe Set

The MGIEasy Exome Capture V5 Probe Set provides comprehensive coverage beyond traditional exome probes, targeting coding sequences associated with a wide range of diseases, including reproductive, neonatal, cardiovascular, cerebrovascular, hereditary tumours, deafness, monogenic disorders, medication safety, immunodeficiency, personal genome analysis, and mitochondrial defects. With a design size of 69 Mb, the primary targets include CCDS, GENCODE, RefSeq, miRBase, and the MGI Clinical Database. As a universal exome capture solution, this probe set is compatible with MGI and other NGS platforms, making it an ideal choice for researchers seeking high-quality, clinically relevant exome sequencing.

MGIEasy Fast Hybridization and Wash Kit

MGIEasy Fast Hybridization and Wash Kit is designed for targeted capture with rapid hybridization elution steps of DNA probes and includes hybridization elution reagents and streptavidin magnetic beads. It has broad compatibility, standardizing the hybridization process for DNA probes, and reduces hybridization time to within 2 hours while ensuring data quality, significantly shortening the liquid-phase probe hybridization capture time. By flexibly pairing with the MGIEasy series of library preparation kits, it can be used for the construction and targeted enrichment of exome libraries and panel capture libraries on the MGI high-throughput sequencing platform.

MGIEasy Dual Barcode Exome Capture Accessory Kit

MGIEasy Dual Barcode Exome Capture Accessory Kit contains universal dual blocker for MGI dual barcodes and the post-PCR reagents. It enables flexible throughput for 4-288 samples multiplexing when used with MGI dual barcode library kits MGIEasy Fast FS Library Prep Set V2.0, MGIEasy UDB Universal Library Prep Set and MGIEasy Universal DNA Library Prep Set.

MGIEasy Exome Capture Accessory Kit

MGIEasy Exome Capture Accessory Kit contains contains 16 unique blockers for MGI 16 single barcodes, only support 16 samples multiplexing.

MGIEasy Fast Hybridization and Wash Kit

MGIEasy Fast Hybridization and Wash Kit is designed for targeted capture with rapid hybridization elution steps of DNA probes and includes hybridization elution reagents and streptavidin magnetic beads. It has broad compatibility, standardizing the hybridization process for DNA probes, and reduces hybridization time to within 2 hours while ensuring data quality, significantly shortening the liquid-phase probe hybridization capture time. By flexibly pairing with the MGIEasy series of library preparation kits, it can be used for the construction and targeted enrichment of exome libraries and panel capture libraries on the MGI high-throughput sequencing platform.

Features

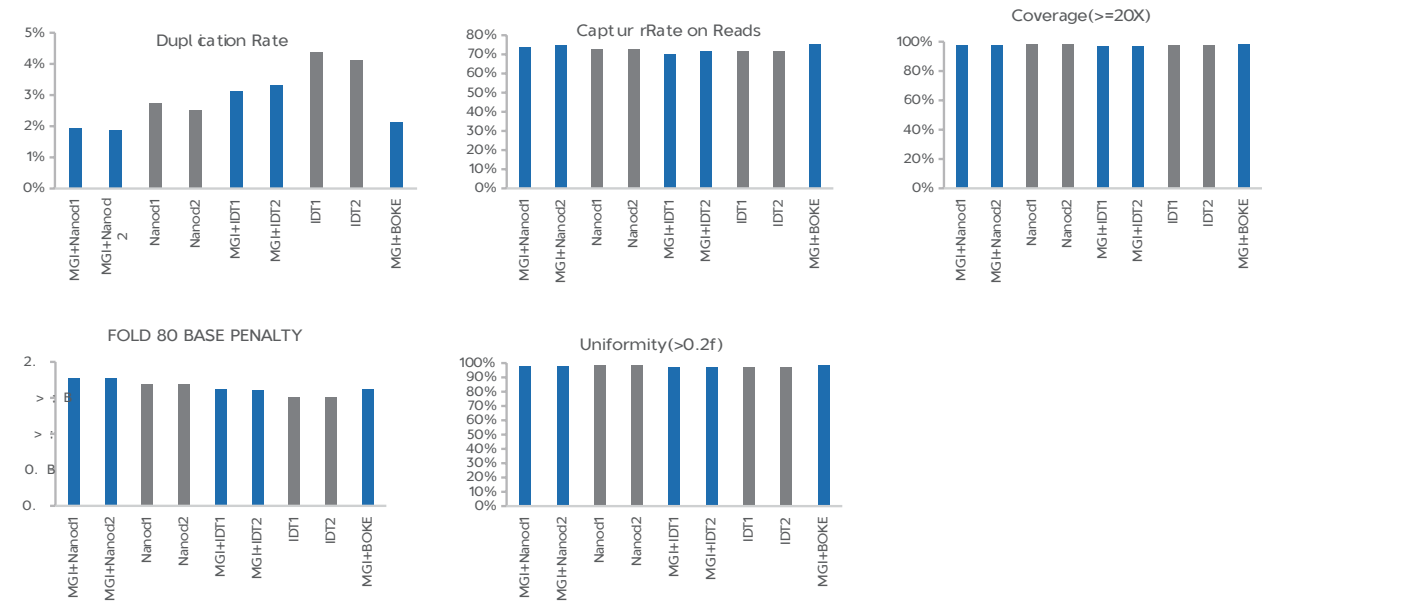
- Fast hybridization within 2 hours while ensuring data quality.
- Flexible hybridization selection between 0.5-2hours fast hybridization and traditional overnight hybridization.
- Broad compatibility with multiple commercial DNA probes
- Flexibly pairing with the MGI library prep kits for the exome libraries construction
- Simplify the operation to minimize the possibility of human errors

Product specifications

Application	Human whole exome sequencing, target capture sequencing.
Compatible probes	Commercial DNA probes (such as IDT, Twist, Nanod, BOKE)
Sample type	Huamn gDNA, FFPE DNA, cfDNA
Hybridization time	0.5h ~24h
Platform Compatibility	G99, G400, T7
multi-plex hybridization	Compatible with single-plex and multi-plex samples hybridization (supports multi-hybridization of up to 12 samples)
Circularization	MGI universal circularization

Performance

Compatible with multiple commercial DNA probes and good performance with low duplication rate, high capture rate and uniform coverage of target regions.



MGIEasy Fast Hybridization and Wash Kit was paired with three commercial Exome DNA probes to perform 2 hours fast hybridization capture under a unified hybridization capture process following the MGIEasy Fast Library Preparation and Capture Application Operation Guide, and was compared with the original fast hybridization reagents of these Exome DNA probes. The results showed that the MGIEasy Fast Hybridization and Wash Kit was comparable or superior to the original hybridization reagent of these probes.

MGIEasy Duplex UMI Universal Library Prep Set

Features

- Mitigates barcode swapping and contamination
- Uses a minimum of 10 ng DNA input for library construction
- Over 200+ UMI supports ultra-low frequency variant detection

Performance

Duplex barcode mitigates barcode swapping

Residuary adaptors or incomplete PCR amplification during the library construction may bring in false barcode information, leading to contamination between samples. These kinds of contamination are more likely to occur in multiple sample pooling hybridization (Fig.1A). Duplex barcode supports double-checked barcode split method and mitigates barcode swapping.

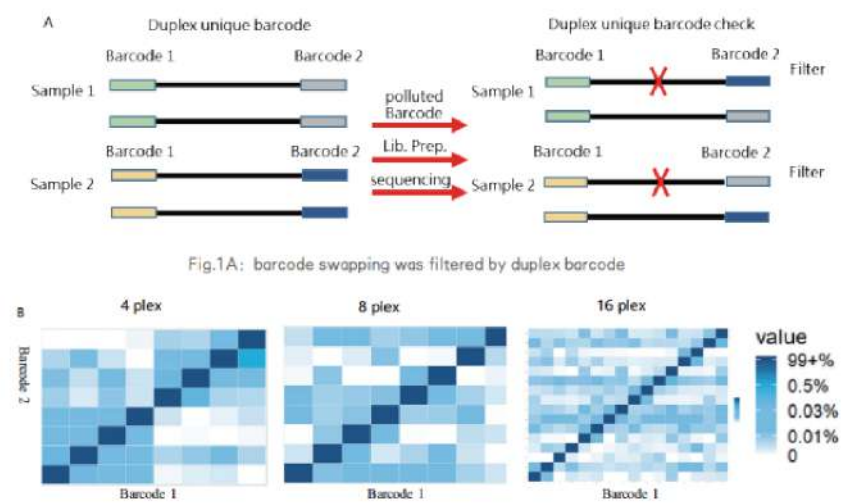


Fig.1A: barcode swapping was filtered by duplex barcode

Fig.1B : Duplex barcode combine with MGI Exome Probe

Excellent conversion rate

MGI duplex barcode product combine with special designed bubble adapter and newly released library construction module provides maximum conversion rate. DNA input requirement is minimized to 10 ng cfDNA (Fig. 2A). Over 3000 sequencing depth is reached when imputing 20 ng cfDNA (Fig. 2B).

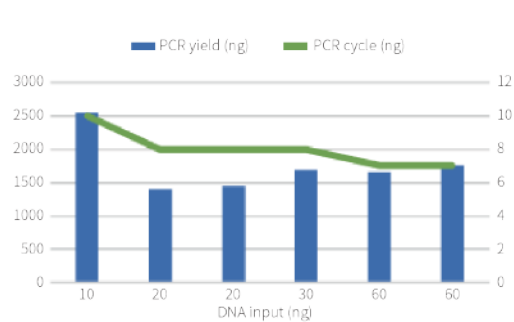


Fig.2A PCR Yield when different DNA input

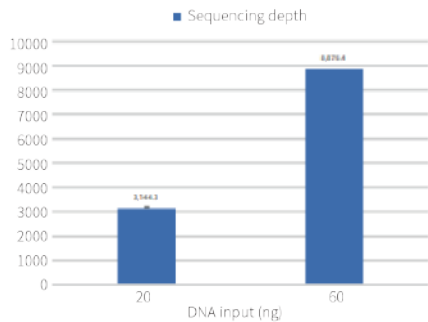
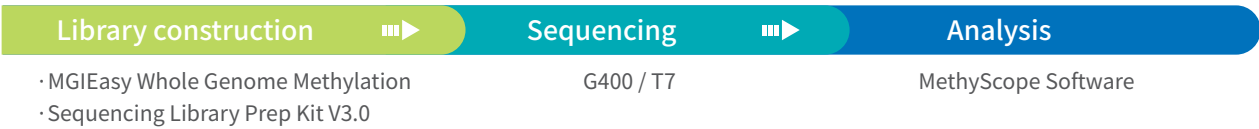


Fig.2B maximum depth of different DNA input

MGIEasy Whole Genome Methylation Sequencing Library Prep Kit V3.0

MGIEasy Whole Genome Methylation Sequencing Library Prep Kit V3.0 (WGMS V3.0) is specifically designed for preparing WGMS libraries for MGI high-throughput sequencing platform from 100ng-1μg gDNA or 5ng - 20ng cfDNA. This kit adopts the dsDNA library construction method to perform library construction from the size-selected fragmented DNA (by Covaris fragmentation) through end repair, "A" tailing, and adapter ligation. And then combines with enzymatic conversion method to convert unmethylated C to U. Paired with the upgraded algorithm of the G400 and T7 platforms, it can greatly reduce the mixing ratio of balanced library and even achieve without adding any balanced library when sequencing. WGMS V3.0 provides an efficient and accurate method for genome-wide methylation sequencing.

Recommended MGI Process



Features

- Compatible with human, animal and plant samples with high integrity DNA or degraded DNA such as FFPE and plasma samples
- Larger library insert size to support PE150 sequencing
- Low duplication rate and high mapping rate enable high usability of sequencing data
- High genome coverage and high consistency of methylation detection
- No need to add balanced library when sequencing on upgraded G400 and T7 platform.

Product specifications

Application	Genome-wide methylation sequencing
Sample types	Human gDNA extracted from blood, fresh tissue and cells samples and FFPE samples, cell free DNA; gDNA from common plant and animal (such as mouse, Arabidopsis, etc.)
Input Quantity	100ng-1μg gDNA, 5ng - 20ng cfDNA
Conversion method	Adapted to enzymatic conversion method to convert unmethylated C to U
Fragmentation method	Covaris (no fragmentation for cfDNA)
Barcode	~96 single barcodes
Assay Time	~10.5 hours (from gDNA to ssCir DNA)
Sequencing compatibility	· G400 (ECR 7.0 and later), PE100/ PE150 · T7 (ECR5.0 and later), T7RS High-throughput Methylation Sequencing Set (T7 Methylation FCL PE150)
Recommended sequencing data per sample	40X raw data (e.g. human DNA sample: 120G raw data per sample)

High usability of sequencing data

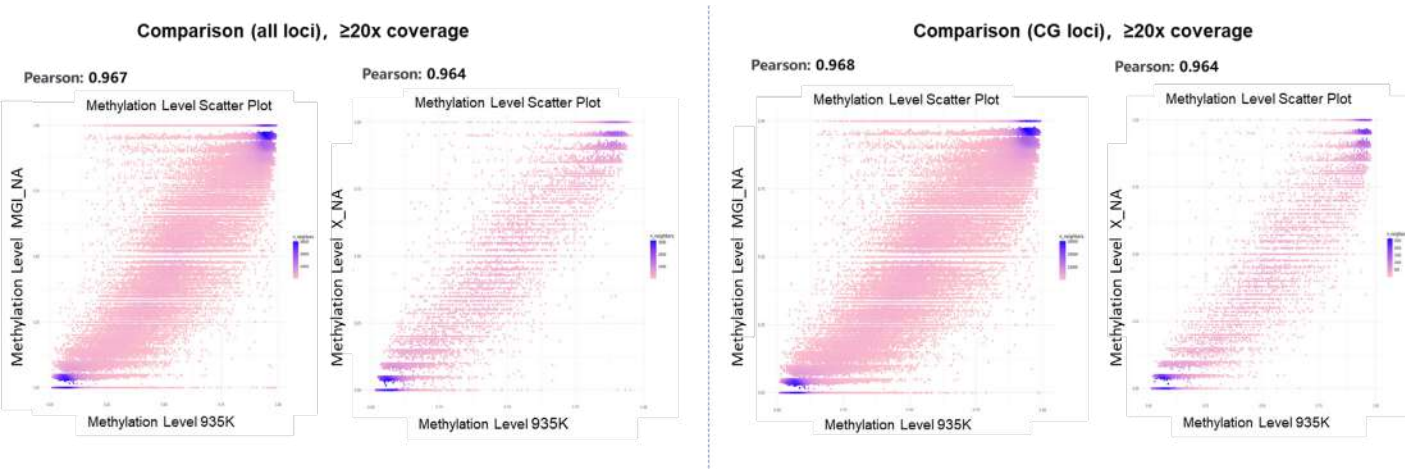
WGMS libraries were prepared from NA12878 gDNA using the MGIEasy Whole Genome Methylation Sequencing Library Prep Kit V3.0 and sequenced on T7 ECR5.0 without adding balanced libraries. About 100 Gb raw data per library were used for analysis by using MethyScope Software.

Sample	NA12878			
gDNA input (ng)	200	200	150	100
Clean_Rate(%)	99.6	99.6	99.6	99.58
Uniquely Mapped Rate(%)	92.81	92.88	92.79	92.68
Duplication Rate(%)	2.68	2.82	3.29	4.47
Average_sequencing_depth	31.25	31.22	30.99	30.46
≥ 4× coverage (%)	97.741	97.723	97.74	97.737
≥ 10× coverage (%)	96.344	96.304	96.377	96.223
Conversion_rate(%)	99.83	99.81	99.84	99.87

High CpG coverage

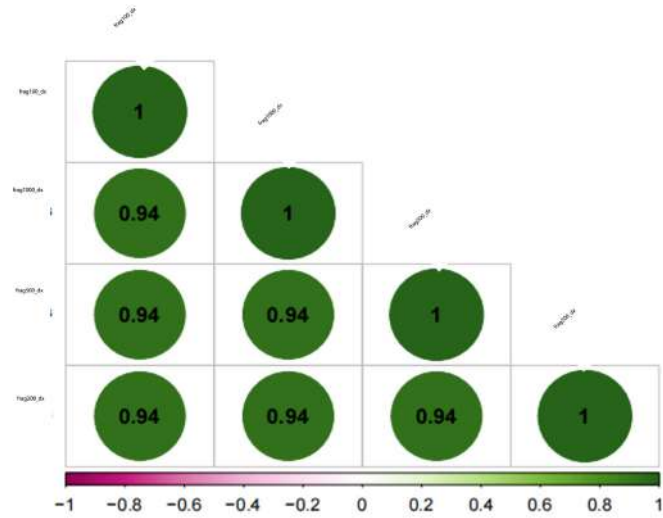
Data produced from NA12878 DNA using Infinium® MethylationEPIC BeadChip was used to compare the CpG coverage between MGI_NA and X_NA. The result shows that MGI_NA data has higher concordance of CpG coverage with microarray compared with X_NA and detects more CpG loci with sequencing depth at 4X, 10X and 20X.

Proportion of detected loci	Comparison (detected loci)	≥ 4X	≥ 10X	≥ 20X
	MGI_NA loci / 935K Microarray	95.14%	73.90%	14.29%
	X_NA loci / 935K Microarray	90.78%	42.36%	1.25%
Pearson correlation coefficient of methylation level about all loci	Comparison (all loci)	≥ 4X	≥ 10X	≥ 20X
	935K Microarray vs MGI_NA	0.959	0.962	0.967
	935K Microarray vs X_NA	0.944	0.953	0.964
Pearson correlation coefficient of methylation level about CG loci	Comparison (CG loci)	≥ 4X	≥ 10X	≥ 20X
	935K Microarray vs MGI_NA	0.959	0.962	0.968
	935K Microarray vs X_NA	0.945	0.953	0.964



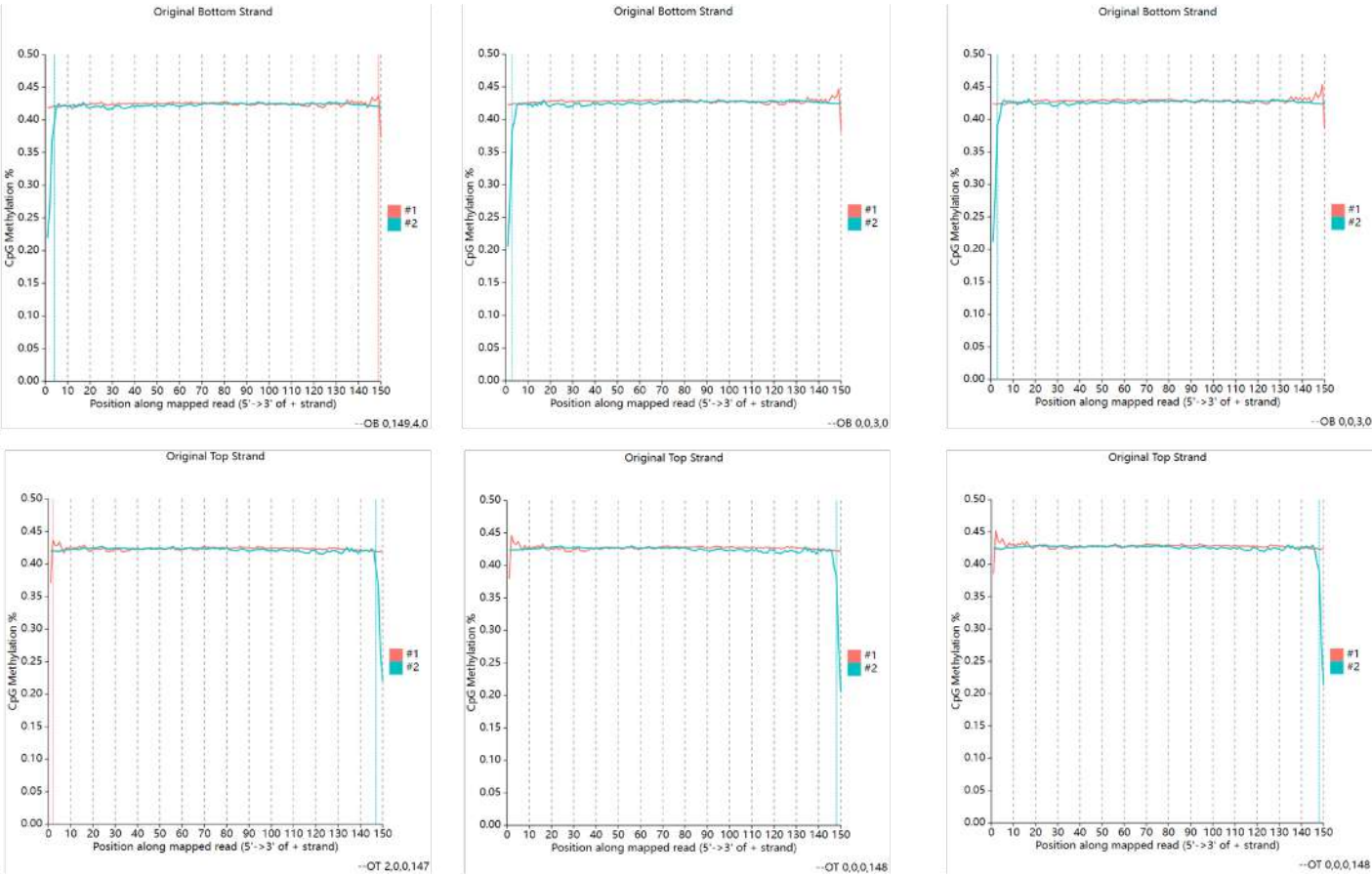
High consistency of methylation detection at different gDNA input amounts

WGMS libraries were prepared from NA12878 gDNA under different input amount and sequenced on G400 PE150. The pearson correlation coefficient is 0.94 of genome CG methylation level between different libraries under 4x coverage.



No obvious M-bias.

WGMS libraries were prepared from NA12878 gDNA and sequenced on G400 PE150.



RNA Sequencing

RNA sequencing is a powerful method for comprehensive and rapid analysis of gene expression changes, examination of rare and novel transcripts, and discovery of alternate splicing events, gene fusions, SNPs and allele-specific expression in tissues or cells. It has been widely applied to many research fields, including biological, disease, drug development, agriculture and environmental studies.

Recommended MGI Process for different applications

Application	Sample	Library perp	Sequencing	Data analysis
Whole transcriptome sequencing/Long noncoding RNA Sequencing (Human/Mouse /Rat)	10ng-1ug total RNAblood/ tissue/ FFPE	■ SP-960/SP-00/SP-Smart8 ■ MGIEasy rRNA Depletion Kit V1.3 or MGIEasyRNA & Globin Depletion Kit V1.3 ■ MGIEasy Fast RNA Library Prep Set ■ MGIEasy Dual Barcode Circularization Kit	G99/G50/G400/ T1+/T7/T20x2	■ MegaBOLT RN-seq basic pipeline
Whole transcriptome sequencing/Long noncoding RNA Sequencing (othereukaryotes,such as animalsplant, fungi, etc)	10ng-1ug total RNAblood/ tissue / FFPE/fungi	■ SP-960/SP100/SP-Smart8 ■ rRNA Depletion for corresponding species ■ MGIEasy Fast RNA Library Prep Set ■ MGIEasy Dal Barcode Circularization Kit	G99/G50 /G400/ T1+/T7/T20x2	■ MeJaBOLT RN-seq basic pipeline
mRNA sequencing /RNA-seg (Eukaryotes)	10ng-1ug totalRNAblood/ tissue / FFPE/fungi	■ SP-960/SP-00/SP-Smart8 ■ mRNA enriched by oligo (dT)beads ■ MGIEasy Fat RNA Library Prep set ■ MGIEasy DUal Barcode Circularization Kit	G99/G50/G400 / T1+/T7/T20x2	■ MegaBOLT RNA-seg basic pipeline
Microbial transcriptom esequencing (Prokaryotes)	10ng-1ug total RNAProkaryotic total RNA	■ SP960/SP-Smart8 ■ rRNA Depletion for Prokaryotes ■ MGIEasy Fast RNA Library Prep set ■ DNBSEQ OeStep DNB Make Reagent Kit V2.0 (OS-DB)	G99/G50G400 / T1+/ T7	Platform of Microorganisms Fast identification,PFI
Meta transcriptome sequencing (Pathogens or bacteria identification,etc 𐄂)	10ng-1ug total RNAmicrobial culture/ saliva /oral swabs/Meta RNA	■ SP-960/SP100/SP-Smart8 ■ MGIEasy rRNA Depletion Kit V1.3 (used for removinghuman bacground rRNA in meta RNA samples) ■ MGIEasy Fast RNA Library Prep set ■ DNBSEO OneStep DNB Make Reagent Kit V2.0(OS-DB)	G99/G50G400/ T1+/ T7	Platform of Microorganisms Fast identification,PFI

MGIEasy Fast RNA Library Prep Set

The MGIEasy Fast RNA Library Prep Set is a specifically designed RNA rapid library prep product for MGI high-throughput sequencing platforms. This kit is optimized with high-quality enzyme and buffer system to combine cDNA second strand synthesis and end repair steps, which greatly shortens the time of library construction. The second strand synthesis is equipped with two kinds of buffers that can be used to prepare a common or directional libraryaccording to your needs.

Features

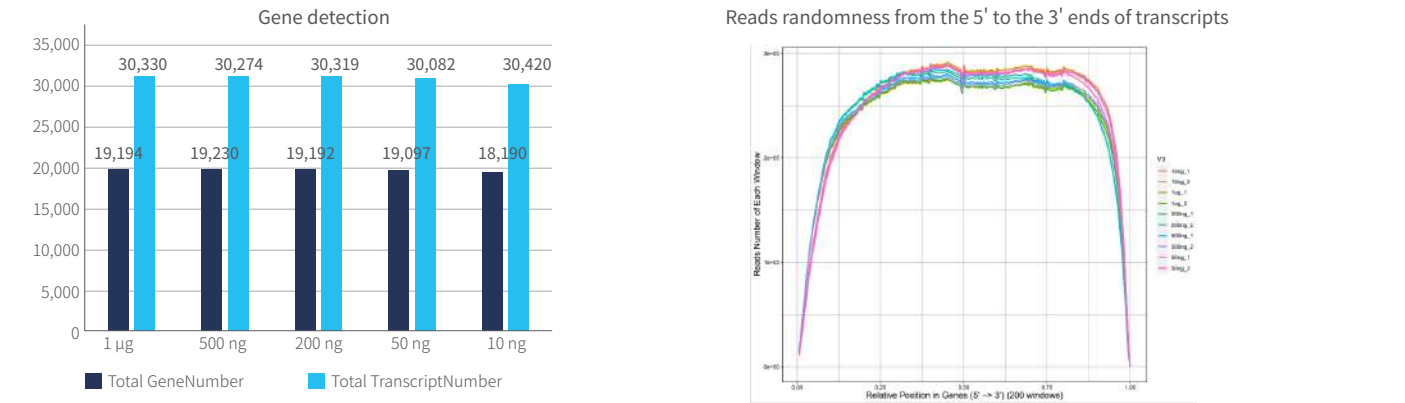
- Fast workflow with one-step cDNA second strand synthesis, end repair and dA-tailing
- Flexible library prep with two optional library types, directional RNA library or non-directional RNA library
- Wide range of total RNA input and various sample types
- High uniformity coverage across transcripts from the 5' to the 3' ends
- Flexible solutions

Product specifications

Assay time	~ 4 hrs (from gDNA to PCR library)
Hands-On Time	~ 1 hrs
Input quantity	10 ng~1 μg total RNA
Barcode	~288 Unique Dual Barcodes
Sample types	Total RNA from blood, saliva, fresh tissue, FFPE RNA, Plant total RNA, Animal total RNA, Microbial total RNA, Meta RNA
Species compatibility	Human, Animal, Plant, Microbe
Applications	Whole-Transcriptome Sequencing, mRNA Sequencing, Long non-coding RNA Sequencing, RNA-Seq, Metatranscriptome Sequencing
Strand specificity	Support strand-specificity library prep or regular library prep. The second strand synthesis module is equipped with two buffers (dNTP buffer, dUTP buffer) to meet the need for a conventional library or strand-specific library.
Platform compatibility	G400, G50, G99, T7, T10×4
Recommended read length	SE50/PE100/PE150
Adaptation automation platform	SP-100(16RXN), SP-960(96RXN), SP-Smart8

Performance

Abundant gene detection and high uniformity coverage across transcripts



Libraries were prepared from an input of UHRR ranging from 10 ng -1 μg using the MGIEasy Fast RNA Library Prep Set and sequenced on G400. The results demonstrate that the MGIEasy Fast RNA Library Prep Set had abundant genes detection and achieve high uniformity coverage across transcripts, which is helpful for gene structure analysis.

MGIEasy rRNA Depletion Kit V1.3

MGIEasy rRNA Depletion Kit V1.3 can efficiently remove rRNA from total RNA and keep mRNA and non-coding RNA to increase the proportion of useful data. It depletes rRNA from human, mouse and rat total RNA with an input of total RNA ranging from 10 ng to 1 µg. This kit is compatible with both intact and degraded RNA (e.g. FFPE RNA). The library prepared by using this kit with RNA Library Prep Kit (e.g. MGIEasy Fast RNA Library Prep Set) is suitable for transcriptome or non-coding RNA research applications.

Features

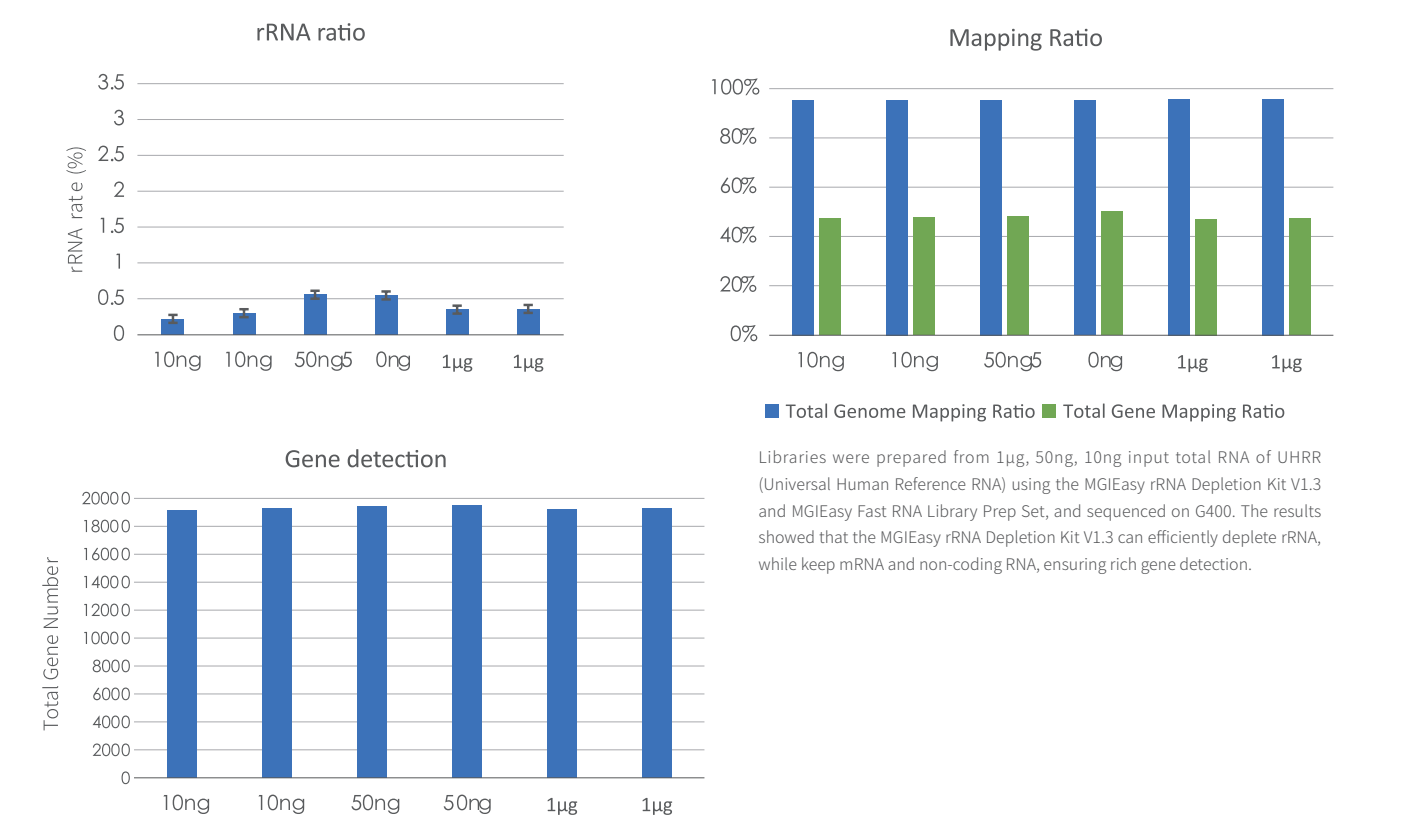
- Efficient elimination of rRNA
- Compatible with degraded sample
- Efficient automatable workflow
- Flexible solutions

Product specifications

Assay time	~2 hours
Hands-On Time	~12 min
Input quantity	10 ng – 1 µg total RNA
Sample types	blood, fresh tissue, FFPE RNA
Species compatibility	Human, Mouse, Rat
Applications	Whole-Transcriptome Sequencing, Long non-coding RNA Sequencing
Adaptation automation platform	SP-100(16RXN), SP-960(96RXN)
Removed rRNA types	cytoplasmic 5 S rRNA, 5.8 S rRNA, 18 S rRNA, 28 S rRNA, mitochondrial ribosomal RNA 12 S rRNA, 16 S rRNA and 45 S pre-ribosomal RNA

Performance

High efficiency on rRNA depletion



■ Total Genome Mapping Ratio ■ Total Gene Mapping Ratio

Libraries were prepared from 1µg, 50ng, 10ng input total RNA of UHRR (Universal Human Reference RNA) using the MGIEasy rRNA Depletion Kit V1.3 and MGIEasy Fast RNA Library Prep Set, and sequenced on G400. The results showed that the MGIEasy rRNA Depletion Kit V1.3 can efficiently deplete rRNA, while keep mRNA and non-coding RNA, ensuring rich gene detection.

MGIEasy rRNA & Globin Depletion Kit V1.3

MGIEasy rRNA & Globin Depletion Kit V1.3 can efficiently deplete rRNA and Globin mRNA from Human blood total RNA and keep other mRNA and non-coding RNA to increase the proportion of useful data. It depletes rRNA and Globin mRNA from human blood total RNA with an input of total RNA ranging from 10 ng to 1 µg. The library prepared by using this kit with RNA Library Prep Kit (e.g. MGIEasy Fast RNA Library Prep Set) is suitable for transcriptome or non-coding RNA research applications.

Features

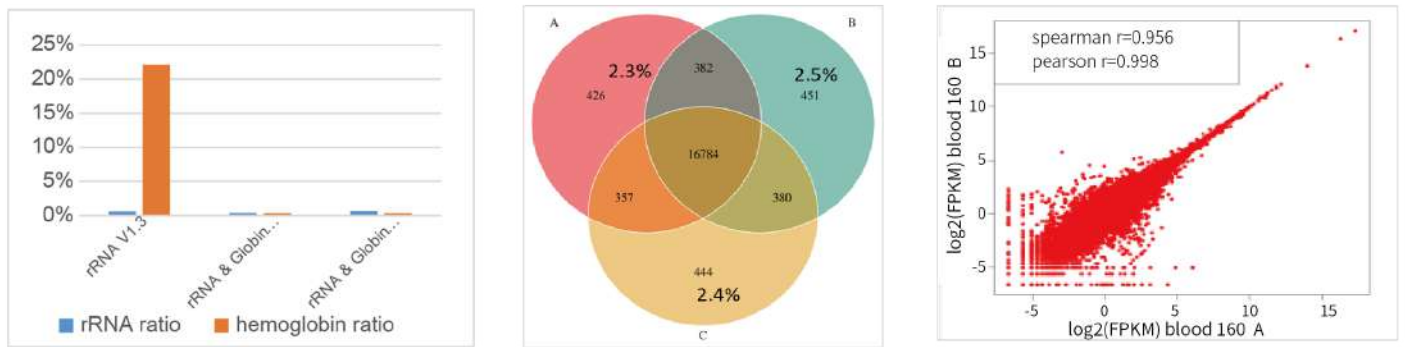
- Efficiently remove both rRNA and hemoglobin mRNA simultaneously from human blood total RNA samples
- Efficient automatable workflow
- Flexible solutions

Product specifications

Assay time	~2 hours
Hands-On Time	~12 min
Input quantity	10 ng – 1 µg total RNA
Sample types	Human blood total RNA
Applications	Whole-Transcriptome Sequencing, Long non-coding RNA Sequencing
Adaptation automation platform	SP-100 (16RXN), SP-960 (96RXN)
Removed rRNA types	cytoplasmic 5 S rRNA, 5.8 S rRNA, 18 S rRNA, 28 S rRNA, mitochondrial ribosomal RNA 12 S rRNA, 16 S rRNA and 45 S pre-ribosomal RNA Removed human Globin mRNA types HBA1/2, HBB, HBD, HBG1/2, HBM, HBE1, HBQ1, HBZ
Removed human Globin mRNA types	HBA1/2, HBB, HBD, HBG1/2, HBM, HBE1, HBQ1, HBZ

Performance

Efficiently remove both rRNA and hemoglobin mRNA

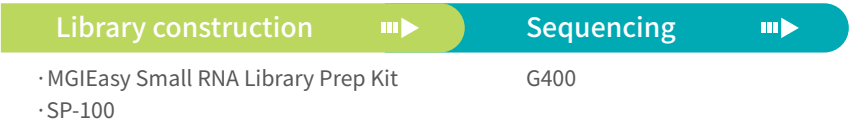


Human blood total RNA samples were treated with MGIEasy rRNA Depletion V1.3 (sample A) and MGIEasy rRNA & Globin Depletion V1.3 (samples B and C) , respectively. Subsequently, libraries were constructed using the MGIEasy Fast RNA Library Prep Set and sequenced on G50. The results showed that the MGIEasy rRNA & Globin Depletion Kit V1.3 can efficiently deplete both rRNA and hemoglobin mRNA simultaneously, while keep mRNA and non-coding RNA, ensuring rich gene detection.

MGIEasy Small RNA Library Prep Kit

Small RNAs are endogenous non-coding single-stranded RNA molecules formed of 20-24 nucleotides and include miRNAs, siRNA and piRNA, snRNA and snoRNA. Small RNAs are involved in gene silencing and post-transcriptional regulation of gene expression through RNA-RNA interactions. They are crucial regulators in cell growth and differentiation in development processes. Small RNA Sequencing is a technique used to isolate and sequence small RNA for biological, disease, drug development, plant and animal research. The DNBSEQ-based Small RNA sequencing solution uses supported kits to prepare single-stranded circularized cDNA libraries from total RNA, sequences those libraries, and generates base calling sequencing data of hundreds of small RNA sequences. MGIEasy Small RNA Library Prep Kit provides an efficient solution for generating libraries suitable for MGI high-throughput sequencing platforms with a broad range of input amounts (10 ng - 1 µg) of total RNA.

Recommended MGI Process



Product specifications

Assay time	~13 hours
Input quantity	10 ng - 1 µg of total RNA
Sample types	Tissues
Species compatibility	Human, animals and plants, such as mouse, rice and Arabidopsis
Applications	Small RNA Sequencing
Platform compatibility	G400
Recommended read length	FCL SE50
Recommended sequencing data per sample	25 M raw reads

Features

- Use as low as 10 ng total RNA per sample
- Compatible with various species (human, animal and plant) samples
- Provides two options of size selection based on either bead or gel purification to meet a wide range of library needs

Library preparation modules

In addition to high quality library preparation kits, MGI offers flexible library preparation modules and reagents. Library preparation modules are used in a single step or multiple steps. They can be used with other kits to meet the requirements of the workflow. A variety of reagents are available to meet the full range of project needs.

Library preparation module

Type	Products	Configuration	Version	Catalog No.
Purification Beads	MGIEasy DNA Clean Beads	50 mL	V1.0	1000005279
Circularization Kits	Universal Cyclization Reaction Kit(SD-SB)	16 Test		940-000141-00
	Universal Cyclization Reaction Kit (SD-App-A)	16 Test		940-000143-00
	Universal Cyclization Reaction Kit (SD-DB)	16 Test		940-000142-00
	MGIEasy Dual Barcode Circularization Kit	16RXN	V1.0	1000020570
	MGIEasy Dual Barcode Circularization Module	96 RXN	V1.0	1000018650
	MGIEasy App Library Circularization Kit	16RXN		940-000915-00
	MGIEasy Circularization Kit	16 RXN	V2.0	1000005259
	MGIEasy Circularization Module	96 RXN	V2.0	1000017573
Conversion Kit	MGIEasy Rapid Circularization Module	16 RXN	V1.0	1000005258
	MGIEasy Universal Library Conversion Kit (App-A)	16 RXN	V1.0	1000004155
Adapters Kit	MGIEasy DNA Adapters-96 (Plate) Kit	96 × 10 µL	V1.0	1000005282
	MGIEasy Duplex UMI Adapters Kit V1.0 (96RXN)			1000018646
	MGIEasy UDB Primers Adapter Kit A	96RXN		940-001763-00
	MGIEasy UDB Primers Adapter Kit B	96RXN		940-001762-00
	MGIEasy UDB Primers Adapter Kit C	96RXN		940-001748-00
Standard Library	Standard library reagent V3.0, 26ng, Barcode 97-104		V3.0	1000005033
	Standard Library Reagent(PCR Product) V3.0, 1500 ng, Barcode 97-104		V3.0	1000005038
	Standard Library Reagent V4.0, 26 ng/EA, Barcode 73-81-80-88	26ng	V4.0	1000025115
	Standard Library Reagent (PCR Product) V4.0 ,1500 ng, Barcode 73-81-80-88	1500ng	V4.0	1000027585
	Standard library reagent-TP(PCR Product) V5.0	1500ng	V5.0	940-001276-00
	Standard library reagent-TP V5.0	42ng	V5.0	940-001278-00
	Standard library reagent-NP(PCR Product) V6.0	1500ng	V6.0	940-001279-00
	Standard library reagent-NP V6.0	42ng	V6.0	940-001280-00
Onestep DNB Make	DNBSEQ Onestep DNB Make Reagent Kit (OS-SB)	4 RXN		1000020563
	DNB Make	4 RXN	V1.0	1000026466
	DNBSEQ OneStep DNB Make Reagent Kit (OS-DB)	4 RXN	V2.0	940-000036-00
DNB Make	DNBSEQ DNB Make Reagent Kit (SD-APP-A)			1000027738
	DNB Make			1000027737
Sequencing Primer Kits	CPAS Barcode Primer 3 Reagent Kit	1 kit		1000020834
	Primer Kits			1000014048
	High-Throughput Barcode Primer 3 Reagent Kit(App-A)	/	V1.0	1000014047
	High-Throughput Pair-End Sequencing Primer Kit (App-A)	1 kit		1000020832
	High-Throughput Single-End Sequencing Primer Kit(App-A)	1 kit		1000020835
	High-throughput Sequencing Primer Kit (StereOmics)			940-000037-00
	High-Throughput Sequencing Primer Kit (App-C)	1 RXN/kit		1000027472
	High-Throughput Paired-End Sequencing Primer Kit (App-D)	1 RXN/Kit		1000028550
	High-Throughput Single-End Sequencing Primer Kit (App-D)			940-000857-00
	High-throughput Sequencing Primer Kit (App-D)	576 Rxn/Kit		940-000714-00

Library Prep for Forensic Genomics

MGEasy Pa-SNPs Genotyping kit

The MGEasy Pa-SNPs Genotyping Kit is suitable for individual characteristic identification. Based on the ATOplex multiplex PCR technology, this kit can be used to detect 2010 high-frequency single nucleotide polymorphisms (SNPs). It is applicable to multiple sample types, such as plasma cfDNA, and gDNA from blood, saliva, tissues, hair, or semen. It is used in forensic genomics research applications, including non-invasive prenatal paternity testing, paternity testing, individual identification, etc.

Features

- Wide applicability, amplify 2010 SNPs in one tube
- Easy to operate, two-step PCR method
- Fast detection, from DNA to analysis results within 1 day
- High accuracy, accurate detection of sample with fetal fraction of 2% and above
- Short amplicon size of 60~90bp, suitable for highly degraded samples

Product specifications

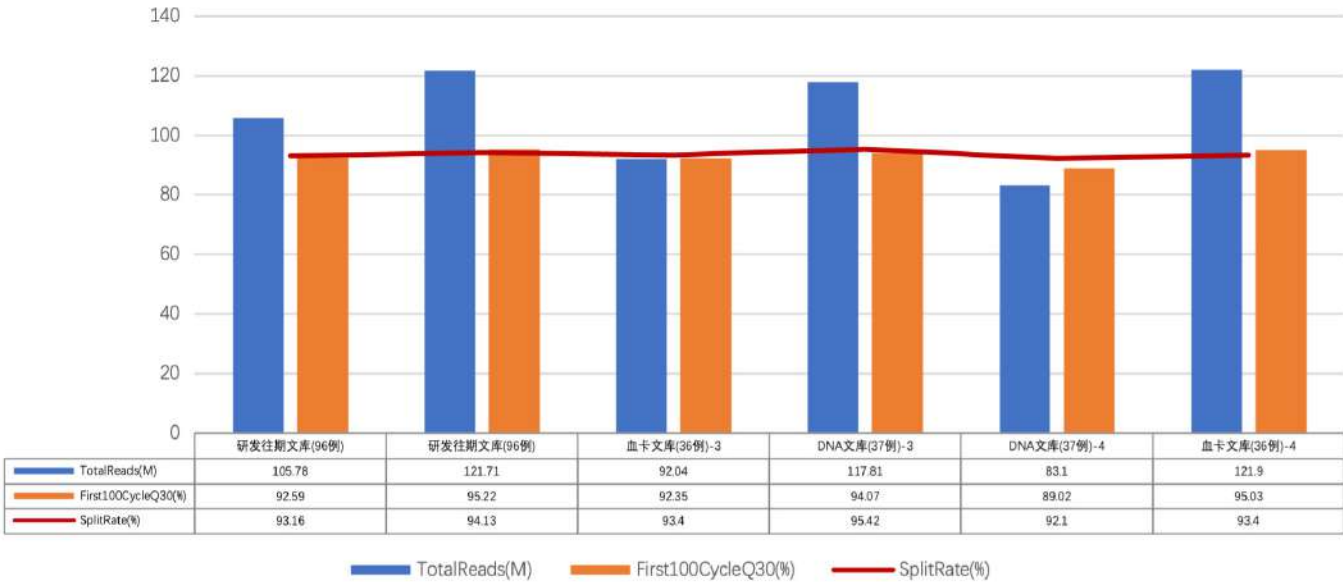
Product Name	MGEasy Pa-SNPs Typing Kit
Target Region	2,010 human SNP loci
Amplicon Size	60–90 bp
Total Library Prep Time	6.5 hours
Sample Types	Plasma cell-free DNA (cfDNA) and genomic DNA (gDNA) from blood cells, tissues, dried blood spots, saliva, buccal swabs, semen, hair, and nails
Nucleic Acid Input	cfDNA: Recommended input 8–20 ng, concentration ≥ 0.4 ng/μL;
gDNA: Recommended input 1–20 ng	Small RNA Sequencing
Automation Compatibility	D4
Hands-on Time	~3 hours
Sequencing Platform	G400RS / G50RS / -G99RS
Application	Non-invasive Paternity, Paternity, Individual identification

Performance

Stable output and quality

- Experimental materials: blood card; standard product gDNA; saliva, oral swab, blood extraction, blood card extraction DNA.
- Experimental equipment: SP-100RS+G99RS/ARS
- Experimental scheme: "DNA Feature Identification Combination Product (G99&G99RS) Quick Operation Guide".
- Experimental results: TotalReads ≥ 80M, First100CycleQ30 ≥ 88%, Split rate ≥ 90%, Detection rate ≥ 99.70%, Consistency rate ≥ 99.90%. The library concentration, sequencing data, and analysis results are all qualified.

	STR Loci Detection Rate	STR Loci Consistency Rate	SNP Loci Detection Rate
Past R&D Library (96 cases)	99.97%	100.00%	100.00%
Past R&D Library (96 cases)	99.95%	99.99%	100.00%
Blood Card Library (36 cases)-3	100.00%	100.00%	100.00%
DNA Library (37 cases)-3	100.00%	100.00%	100.00%
DNA Library (37 cases)-4	100.00%	100.00%	100.00%
Blood Card Library (36 cases)-4	100.00%	99.97%	100.00%



MGIEasy Signature Identification Library Prep Kit

The MGIEasy Signature Identification Library Prep Kit is a library preparation kit tailored for human individual identification genetic marker detection on the MGI high-throughput sequencing platform. This kit can directly prepare pretreated dried blood spot samples or gDNA samples into libraries dedicated to the MGI high-throughput sequencing platform through a two-step PCR method. Through optimized multiplex PCR technology, the reagent completes the preparation of high-throughput sequencing libraries for 131 STR loci, 227 SNP loci and mitochondrial hypervariable regions in a single reaction, significantly improving the detection efficiency of various application scenarios in the forensic field. The reagent uses dual-end molecular tagging technology to improve the sample detection throughput of single sequencing.

Features

Easy to operate, Detection of STR, SNP and mitochondrial hypervariable regions can be completed in a single tube.

Short library construction cycle, Library construction operation only takes 6.5 hours.

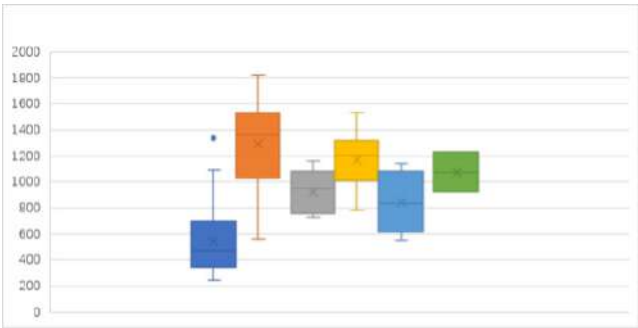
High sensitivity, Samples with an input amount of more than 200pg can be accurately detected.

Product specifications

Product Name	MGIEasy Signature Identification Library Prep Kit V2.1
Product Specifications	48 RXN
Total Library Preparation Time	4.5 hours
Amplicon Length	60-382 bp
Detection Range	132 STRs+215 SNPs+3 mitochondrial hypervariable region+ 2 gender determination loci
Detection Principle	Multiplex PCR+High Throughput Sequencing
Sample Types	gDNA of blood, blood spot, tissue, swab, saliva, sperm, hair with follicles, nail
Nucleic Acid Input	1~10ngDNA or 1~1.2mm Diameter Dried Blood card
Compatible Sequencer and Read Length	G400 / G99 SE400
G50/E25 SE50 (for SNPs only)	Non-invasive Paternity, Paternity, Individual identification
Automation Compatibility	SP-960RS、 SP-100RS

Performance

MGIEasy Pa-SNPs typing Kit V1.0 can support the construction of different types of samples. Using this kit, different types of samples (plasma, blood, saliva, semen, hair follicle and nails) were invested with 8~20ng DNA to construct libraries, and the library yield of different types of samples was stable.



Plasma(n=60) Blood(n=71) semen(n=5) hair(n=10) nail(n=4) saliva(n=4)

Non-invasive prenatal paternity test

- cfDNA from 1mL maternal plasma, gDNA from maternal WBC and gDNA from suspected father were recruited for testing
- Twenty-three families were tested for non-invasive paternity test, and the results of all families were consistent with the comparison results.
- Among them, 20 pedigrees were affirmative paternity, and the minimum fetal concentration detected was 2.12% (2.12% ~ 15.08%); 3 pedigrees were negative paternity.

#Family	week	Fetal%	Err	lg(CPI)	RCP	MGI result	Comparison result	Concordance
F37	18	7.30%	0.44%	152.05	100.00%	Affirmative	Affirmative	Concordant
F38	19	6.73%	0.41%	157.16	100.00%	Affirmative	Affirmative	Concordant
F39	16	5.63%	0.44%	137.56	100.00%	Affirmative	Affirmative	Concordant
F40	7	5.68%	0.47%	149.35	100.00%	Affirmative	Affirmative	Concordant
F41	32	15.08%	0.45%	188.33	100.00%	Affirmative	Affirmative	Concordant
F42	22	3.91%	0.39%	136.33	100.00%	Affirmative	Affirmative	Concordant
F43	12	6.63%	0.47%	150.11	100.00%	Affirmative	Affirmative	Concordant
F44	31	13.90%	0.46%	168.73	100.00%	Affirmative	Affirmative	Concordant
F45	18	4.82%	0.47%	139.81	100.00%	Affirmative	Affirmative	Concordant
F46	7	4.87%	0.48%	131.04	100.00%	Affirmative	Affirmative	Concordant
F47	7	7.25%	0.47%	152.72	100.00%	Affirmative	Affirmative	Concordant
F48	14	4.63%	0.38%	149.65	100.00%	Affirmative	Affirmative	Concordant
F49	7	7.23%	0.47%	151.18	100.00%	Affirmative	Affirmative	Concordant
F50	7	5.93%	0.42%	157.9	100.00%	Affirmative	Affirmative	Concordant
F51	12	3.89%	0.32%	124.82	100.00%	Affirmative	Affirmative	Concordant
F52	26	12.25%	0.39%	166.56	100.00%	Affirmative	Affirmative	Concordant
F57	6+	2.98%	0.39%	101.96	100.00%	Affirmative	Affirmative	Concordant
F58	6	2.12%	0.69%	14.01	100.00%	Affirmative	Affirmative	Concordant
F59	6	1.14%	0.59%	-11.67	0.00%	Negative	Negative	Concordant
F60	7	4.06%	0.44%	106.41	100.00%	Affirmative	Affirmative	Concordant
F61	7	4.37%	0.37%	119.71	100.00%	Affirmative	Affirmative	Concordant
F62	7	1.38%	0.66%	-17.29	0.00%	Negative	Negative	Concordant
F63	7+	1.03%	0.55%	-5.04	0.00%	Negative	Negative	Concordant

*Data originated by G400RS
*Fetal%:Fetal fraction; Err: Error rate; lg(CPI): combined paternity index ; RCP: Relative patriarchal probability

ATOPlex Library Prep series

The ATOPlex eDNA Library Preparation Set is a set of library preparation kits designed for environmental DNA sequencing. It comprises eight distinct kits targeting specific genetic markers: MiFish, 16S V4 rDNA, 16S V3V4 rDNA, Ac12S mtDNA, COI mtDNA, 18S V4 rDNA, ITS1 rDNA, ITS2 rDNA. Work for eDNA extracted from environmental samples such as soil, water, and sediment. When used in combination with the E25 and G99 sequencing platforms and the MetaSIS analysis software, it enables the characterization of biological community structures within environmental samples. This solution finds applications in diverse fields including Biodiversity monitoring, Invasive species surveillance, Aquatic environmental monitoring, Fisheries management.

Features

- The monitored species cover bacteria, fungi, algae, plants, planktonic animals, benthic animals, and fish, meeting various application needs.
- Automation friendly-Combined with automated sample preparation systems, to achieve automated sample preparation and data analysis, save labor.
- Up to 4608 barcodes can be provided for library preparation, meeting the demands of ultra-high-throughput sequencing.
- Library preparation can be completed in one reaction tube through two steps of PCR, which is simple and efficient.

Product specifications

Product Name	ATOPlex eDNA Library Preparation Set
Target Region	MiFish/16S V4 rDNA/16S V3V4 rDNA/Ac12S mtDNA/COI mtDNA/18S V4 rDNA/ITS1 rDNA/ITS2 rDNA
Amplicon Size	300–650 bp
Total Library Prep Time	~6 hours
Sample Types	eDNA extracted from soil, water, and sediment
Nucleic Acid Input	1-50ng for 16SV4、16SV3V4、18SV4、ITS1、ITS2 and COI kits 10-100ng for Ac12S and MiFish kits.
Automation Compatibility	SP-100 / SP-960
Sequencing Platform	E25 / G99
Application	Biodiversity monitoring, Invasive species surveillance, Aquatic environmental monitoring, Fisheries management.

Performance

The following three sets of data were to evaluate the performance of the solution, such as repeatability, species detection rate, and quantitative assessment of species abundance, using simulated samples with known species composition and abundance. Samples S1-S3 are three replicates of mixed samples containing 8 bacterial DNA standards. The samples were prepared to 16S V3V4 library, sequenced and analyzed on the G99. The results are shown in Table 2 and Figure 2. all expected species were detected, and the measured abundance similar with the theoretical abundance. The three replicates showed minimal deviation.

Species	Theoretical abundance	S1 Measured abundance	S2 Measured abundance	S3 Measured abundance
Pseudomonas	4.20%	6.83%	7.86%	6.94%
Escherichia	10.10%	12.62%	9.15%	13.29%
Salmonella	10.40%	11.48%	8.12%	9.97%
Lactobacillus	18.40%	16.24%	20.45%	16.58%
Enterococcus	9.90%	10.63%	11.14%	13.02%
Staphylococcus	15.50%	12.44%	18.34%	12.58%
Listeria	14.10%	15.40%	12.56%	13.97%
Bacillus	17.40%	14.36%	12.37%	13.64%

Table 2 Species abundance analysis results

Samples S4-S6 are three replicates of mixed samples containing 10 species fish tissue. The samples were prepared to MiFish library, sequenced on the E25 platform and analysis. The results are shown in Table 3 and Figure 3. From the results, we can see all expected species were detected, and the measured abundance closely matched the theoretical abundance. Additionally, the three replicates showed excellent reproducibility.

Species	Theoretical abundance	S4 Measured abundance	S5 Measured abundance	S6 Measured abundance
Acanthopagrus	15%	21%	21%	21%
Carassius cuvieri	3%	2%	2%	2%
Channa maculata	6%	8%	8%	8%
Ctenopharyngodon idella	10%	12%	12%	13%
Hypophthalmichthys nobilis/molitrix	5%	4%	4%	4%
Larimichthys crocea	16%	14%	15%	15%
Lateolabrax japonicus/Laterolabrax maculatus	17%	15%	15%	14%
Oreochromis niloticus	5%	3%	3%	3%
Sciaenops ocellatus	12%	9%	9%	9%
Sebastiscus marmoratus	12%	12%	12%	12%

Table 3 Species abundance analysis results

Samples S7 and S8 are mixed samples containing 10 fish tissue species but with different proportions. The samples were prepared to AC12S library, sequenced and analyzed on the G99. The results are shown in Table 4 and Figure 4. we can see all expected species were detected, and the measured abundance closely matched the theoretical abundance.

Species	S7 Theoretical abundance	S7 Measured abundance	S8 Theoretical abundance	S8 Measured abundance
Acanthopagrus	3.79%	6.81%	1.94%	1.76%
Carassius cuvieri	21.00%	21.97%	17.19%	19.01%
Channa maculata	14.73%	19.70%	15.92%	23.68%
Ctenopharyngodon idella	10.32%	8.65%	13.03%	13.35%
Hypophthalmichthys nobilis / molitrix	11.47%	14.86%	9.88%	14.36%
Larimichthys crocea	4.01%	4.30%	2.01%	1.31%
Lateolabrax maculatus	4.24%	3.48%	6.13%	5.41%
Oreochromis niloticus	18.49%	11.52%	15.98%	8.49%
Sciaenops ocellatus	3.97%	2.32%	5.95%	3.39%
Sebastiscus marmoratus	7.99%	6.39%	11.97%	9.25%

Table 4 Species abundance analysis results

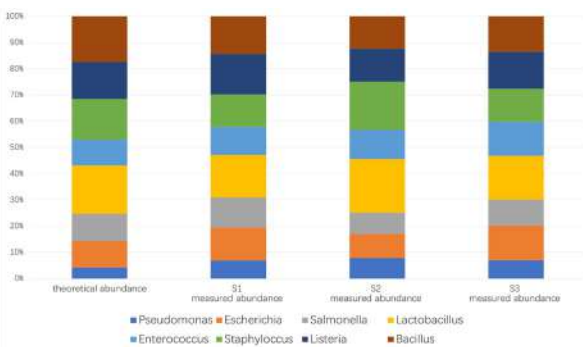


Figure 2 Species composition and abundance stacked histogram

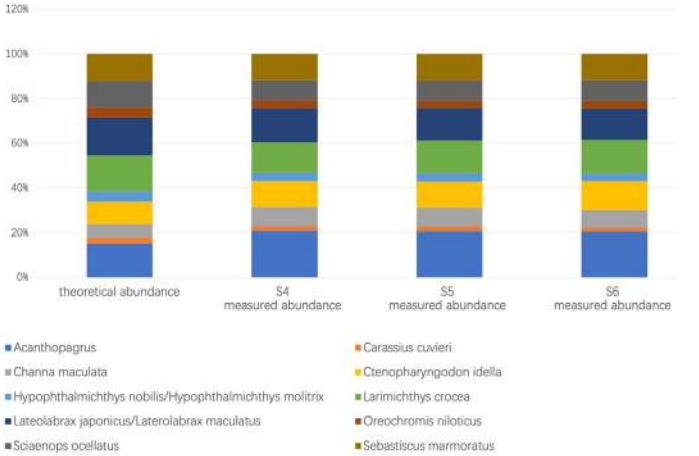


Figure 3 Species composition and abundance stacked histogram

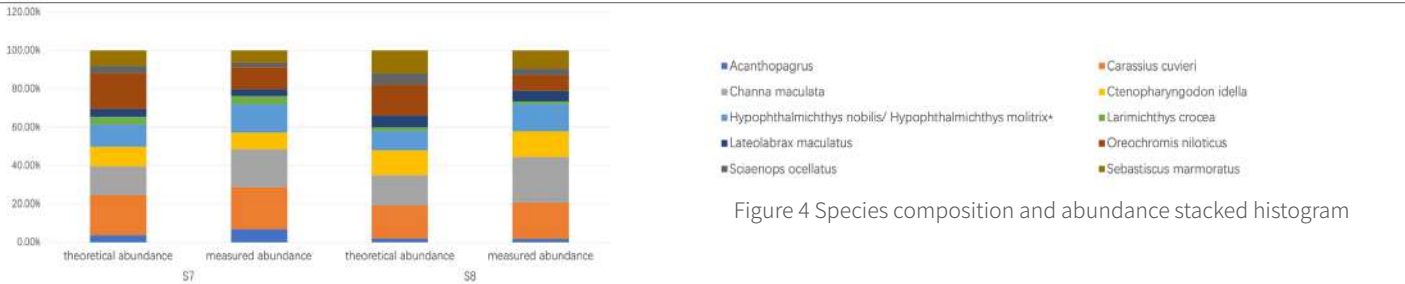
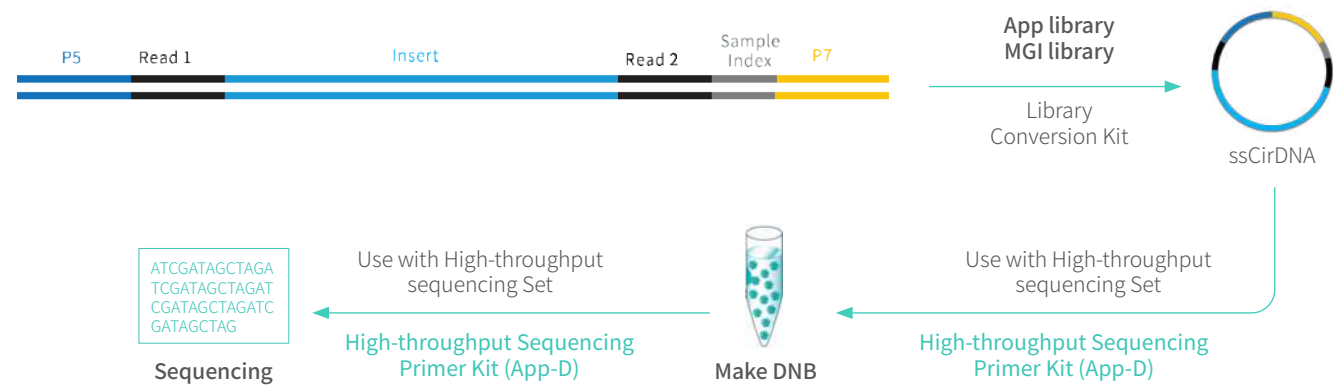


Figure 4 Species composition and abundance stacked histogram

APP Series Products

The App series products produced by MGI include App-A, App-C, App-D, etc. The main function of the App series of products is to convert the third-party company's library products, the converted library products can be sequenced on the MGI sequencing platform



Step One-Library adapter conversion:

The library products constructed by third-party library preparation kits are generally linear double-stranded DNA, and the library conversion kit is used to convert the linear dsDNA library into a single-stranded circular DNA library compatible with the MGI sequencing platform.

Step Two- Sequencing primer replacement:

According to the library type, select the appropriate App-A/C/D series sequencing primer kit. Follow the user manuals to directly replace the sequencing primers in the MGI high-throughput sequencing kit, then the converted library can be sequenced on MGI sequencer.

OneStep DNB Make Reagent Kit

MGI OneStep Method Series Product includes OS-SB, OS-DB, and OS-APP*. The primary function of the OneStep Method Product is to enable the production of DNBs directly from dsDNA libraries in a single reaction system,eliminating the need for separate steps of single-strand circularization and DNB preparation,thereby simplifying the workflow.
*OS-SB: OneStep-Single Barcode ,OS-DB: OneStep-Dual Barcode, OS-APP: OneStep-App.

Features



Faster dsDNA → DNB
Directly generate DNB using dsDNA as the library, thus eliminating the cyclization step after library preparation.



Better coverage
DNBSEQ OneStep DNB Make Reagent Kit V4.0 can effectively retain more fragments, with targeted optimization and enhancement of the coverage for genes in simple repeat sequences and high-GC regions.



Lower input
The one-step OS-SB and OS-DB protocols require a lower input amount of dsDNA compared with the conventional cyclization method (except for T7), thus providing a targeted solution for customers with limited sample volumes.



Conventional method VS One-step method

GLI

Generative Lab Intelligence

MGI will continue to provide users with comprehensive, efficient, and flexible automated solutions to meet the diverse needs in different application scenarios, achieving Prep ALL and empowering Seq ALL.

Unlock the infinite potential of "AI + life sciences" and empower the intelligent paradigm shift in life sciences from "manual experience - based" to "data - driven" decision - making.

From "centimeter-scale" laboratory to "factory-scale" production laboratory, it covers all scenarios.

Automated Liquid Handling Platform

Intelligent Digital Platform

Integrated Platform

Automated Devices and Consumables

Customize Platform



GLI Product Portfolio

Unlock the infinite potential of "AI + life sciences" and empower the intelligent paradigm shift in life sciences from "manual experience - based" to "data - driven" decision - making
From "centimeter-scale" laboratory to "factory-scale" production laboratory, it covers all scenarios.

Lab on Chip

Lab on Desk

Lab on cube

Lab as Factory



STP-7000



STP-B1000



SP-NE32



SP-NEX



SP-NE384



Sample Pretreatment

Nucleic acid extraction

Sample Preparation

Universal Pipetting



D4



SP-100



SP-960



SP-Smart 8



PrepALL



AlphaTool

Automated Liquid Handling Platform



αCube



α Lab Studio/ZLims/ZSM



MegaBOLT



OmicsNest

Intelligent Digital Platform



FLP



AIO

Integrated Platform



Bloomics™



Portable Smart Water Sampler



Consumables

Automated Devices and Consumables



CDMO



Integrated Solution

Customized Platform

Automated Liquid Handling Platform



STP-7000
Ultra-high throughput
Sample Transfer Processing
System

STP-7000 integrates tube decapping, tube recapping, barcode identification, automated liquid transfer, and negative pressure protection. It can transfer 192 samples from tubes to 96-well microplates in 40 minutes.

Features

- Throughput:** 192 samples in 40min
- Automated:** Touch screen, complete tedious sample pre-processing with just one step.
- Safe:** HEPA protection with negative pressure and UV light
- Reliability:** Automatic barcode scanning and recording
- Compatibility:** 5-30mL virus sampling tube, 4-10mL blood collection tube, cryopreservation tube, feces collection tube, saliva collection tube.

Performance parameters

Pipetting Method	Based on the principle of air displacement, liquid level detection
Volume Range	2 μL-1000 μL
Accuracy	10 μL<±10%; 100 μL< ±5%; 1000 μL<±2%
CV	10 μL<5%; 100 μL< 2%; 1000 μL<1%
Robot Arm Accuracy	X-Y-Z: ±0.1mm
Barcode Scanner	Four 1D Scanner Sensors
UV Light	36W
Supply/Exhaust Air Filter	HEPA 99.995% at 0.3 μm, Negative Pressure System



STP-B1000
Specialized in blood
component transfer

The STP-B1000 can precisely identify and automatically transfer blood components in centrifuged blood collection tubes, including plasma, the buffy coat, and red blood cells. Additionally, it can automatically complete information traceability management to prevent information mismatch.

Features

- Flexible Sample Loading:** Automatic sampling of blood collection tubes, supporting 1~192 samples for free loading, meeting various sample processing needs.
- Efficient Buffy Coat Recovery:** High-precision camera recognition of different components of blood samples, and multipoint spiral aspiration for high buffy coat recovery rate.
- Simple Operation:** Users only need to fill in essential parameters such as components,volume, and transfer numbers, and can start transfer with a single click.
- Full Process Traceability:** Supports scanning of blood collection tubes, the bottom of cryotubes, cryotube boxes, and 96-well plates, enabling comprehensive tracking of sample information throughout the process, and supports information output.

Performance parameters

Pipettor	Pipette Range	1 μL - 1000 μL
	Pipette Accuracy	1 μL: CV ≤ 8%, accuracy: ±10%
		50 μL: CV ≤ 1%, accuracy: ±2%
		200 μL: CV ≤ 1%, accuracy: ±2%
		1000 μL: CV ≤ 1%, accuracy: ±1%
Independent 8-channel Pipettor		
Detection Mode	pLLD, cLLD	
Throughput	1 - 192 samples/run	
UV System	The dose of irradiation is higher than 100,000 μW.s/cm ²	
Size (L × W × H)	1420 × 1010 × 1120 mm (without door handle)	
Weight	~250 kg	



The AIO is currently a custom-built product offered on an ODM basis and is not a standard catalog item. Current ODM applications include areas such as blood typing, oncology genetic testing, and rapid pathogen detection (supporting both targeted and metagenomics approaches).

AIO

The AIO (All-In-One) integrated sequencer is a fully integrated system that combines all essential modules required for sequencing library preparation—including liquid handling (pipetting), thermal cycling (PCR), magnetic bead-based purification, and quantification—with the sequencing module necessary for data output. This consolidated instrument is designed to automate the complete workflow from input sample to final report, capable of processing either extracted nucleic acids or even raw samples (e.g., FFPE tissues), thereby enabling true end-to-end sequencing based testing within a single platform.

Features

Integrated "Sample-to-Answer" Workflow

Performs automated library preparation, sequencing, and analysis in one continuous, unattended process.

Minimal Hands-on Time

Requires only minutes of manual setup (e.g., ~10 minutes), significantly reducing operator intervention and potential for error.

Flexible Throughput

Supports processing of 4, 8, 12, or 16 samples per run to match varying workflow demands.

Rapid Turnaround

Delivers from library construction to analyzed report within approximately 11 hours (SE100 sequencing) with AI driven self-luminous sequencing.

Smart Design

Library preparation throughput is optimized to align with sequencer capacity, and intelligent library pooling strategies help mitigate barcode-induced sequence bias.

Customizable Module	Diagram	Customizable Module	Diagram
8-Channel Pipette		Temperature Control Module	
1-Channel Pipette		Temperature Controlled Vibration Module	
Gripper		Magnetic Block	
Fluorometric Quantification Module		Tube Transferring Module	
Thermocycler Module		Flat Bottom Block	
E25 Genetic Sequencer		Fixed Modules	



SP-NE384 High-throughput Extraction Tool

SP-NE384 is a high-throughput automated nucleic acid extractor adopting magnetic rod technology. Together with nucleic acid extraction kit, SP-NE384 can extract and purify nucleic acid from 96/192/288/384 samples. HEPA filtration system and UV lamp ensure a safe working environment for lab technicians. Ultra high-throughput extraction tool, with a daily throughput of over 10000 samples.

Features

- Mixing and magnetic module Z axis independent control
- 1-4 modules running choices for 96/192/288/384 samples
- Equipped with HEPA filtration system and UV lamp, ISO Class 5
- Extract and purify nucleic acid from 384 samples within 30 minutes
- Reliable hardware design, with 96-well plate reagent and disposable tip
- Prevent cross contamination, minimize operational errors.

Applications

Ultra high-throughput, capable of meeting various high-throughput nucleic acid extraction applications, such as molecular breeding, large scale disease testing, cancer screening and so on.

Performance parameters

Capacity	384 samples
Turnaround time	30 min (virus extraction)
Processing volume	20-1000 μ L
Temperature precision	$\leq \pm 1^{\circ}\text{C}$
UV lamp	$> 100,000\mu\text{W}\cdot\text{s}/\text{cm}^2$
HEPA filtration system	99.995% at 0.3 μm

Performance

Test Method

SP-NE384 VS Liquid handling method

Evaluation Standard

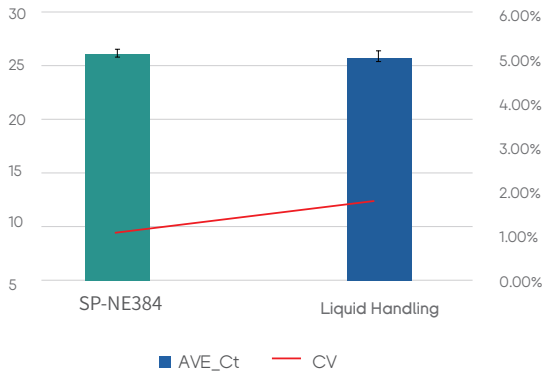
RT-PCR

Test Samples

Simulated throat swab samples with SARS-CoV-2 RNA, diluted in different concentrations

Test Results

Ct values of fluorescent RT-PCR are almost equal, showing that the yield of virus RNA is coincident between SP-NE384 and liquid handling method. Great reproducibility





SP-NE32

Compact extraction tool

SP-NE32 is an automated nucleic acid extractor adopting magnetic rod technology. Together with nucleic acid extraction kit, SP-NE32 can extract and purify nucleic acid from 16/32 samples in approximately 10 minutes.

Features

- Adjustable mixing module with multiple modes & gears
- Compatible with different magnetic particles and reagents
- Extract and purify nucleic acid from 16/32 samples in approximately 10 minutes
- Equipped with UV lamp, 96-well pre-packed plate, and disposable tips, avoiding cross-contamination by minimizing contact with sample
- Specially designed heating block for 96-well plate, ensuring even heating

Applications

Due to the small size, SP-NE32 able to meet various low flux nucleic acid extraction application such as scientific research, tumor prevention and treatment, infectious disease detection and so on.

Performance parameters

Capacity	16/32 samples
Turnaround time	~ 10 min (virus DNA/RNA extraction)
Processing volume	20-1000 μL
Magnetic particles collection efficiency	≥ 98%
Temperature precision	≤ ±1°C

Performance

Test Method

SP-NE32 VS Liquid handling method

Evaluation Standard

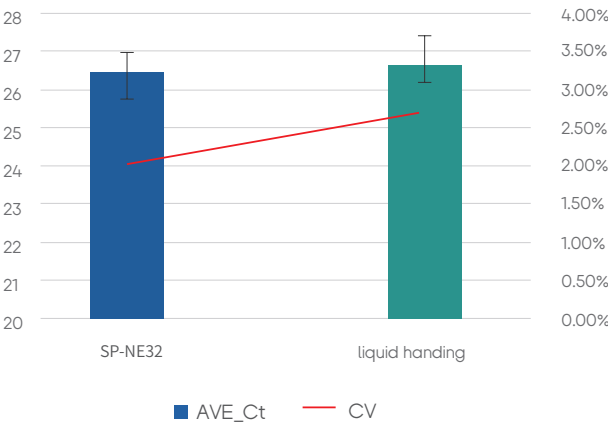
RT-PCR

Test Samples

Simulated throat swab samples with SARS-CoV-2 RNA, diluted in different concentrations

Test Results

Ct values of fluorescent RT-PCR are almost equal, showing that the yield of virus RNA is coincident between SP-NE32 and liquid handling method. Great reproducibility with the CV less than 2.5%.



SP-NEX

Complex sample extraction tool, fully automatic without manual intervention

SP-NEX is a versatile automated nucleic acid extractor independently developed by MGI. It is equipped with an independent 8-channel pipetting module and magnetic rod extraction module. The independent 8-channel pipetting can perform liquid transferring, which reduces manual intervention and achieves a higher degree of automation. The magnetic rod extraction module has two types of magnetic rods: one with 24 magnetic rod heads and another with 96 magnetic rod heads, which can be flexibly interchanged.

Features

- The independent 8-channel pipetting performing liquid transferring
- The flexible interchangeable magnetic rod module meeting the needs of different scenarios
- The triple anti-pollution design ensuring sample safety and reduces cross-contamination

Applications

SP-NEX is an automated nucleic acid extractor with dual functions of liquid handling workstation and nucleic acid extractor. It supports multiple application fields, such as oncology field, infectious field, reproductive health research field, etc.

Performance parameters

Capacity	1~24 samples or 1~96 samples
24 Magnetic Rod Heads Processing Volume	50 μL~5000 μL
96 Magnetic Rod Heads Processing Volume	20 μL~1000 μL
Pipette Range	1 μL~1000 μL
Robot Arm Positioning Accuracy	±0.1 mm
UV Lamp	Radiation dose higher than 100,000 μW.s/cm2
HEPA	99.995% at 0.3 μm



D4

Fully automated digital sample preparation system

With D4, as little as 1 μL of droplet can be controlled. This precise and versatile reagent manipulation, along with temperature, magnet and quantification modules, fulfill the requirement for most of the complex biological processes on a single instrument.

Features

- Portable:** Occupies only 0.1m² of bench space and weighs only 15 kg
 - Fully automated:** Set up each run with only 15 min hands-on time and no intervention needed afterwards
 - Streamlined:** User friendly interface allows seamless experience from sample to results
 - Enclosed system:** Enclosed system with no cross contamination between samples, no aerosols produced during the whole process
 - Fast:** Achieve DNA in and DNB out with DNB quantification within 2.5h
- Using DNBelab-D4RS Fast PCR-FREE FS Library Prep Set V2.0

Performance parameters

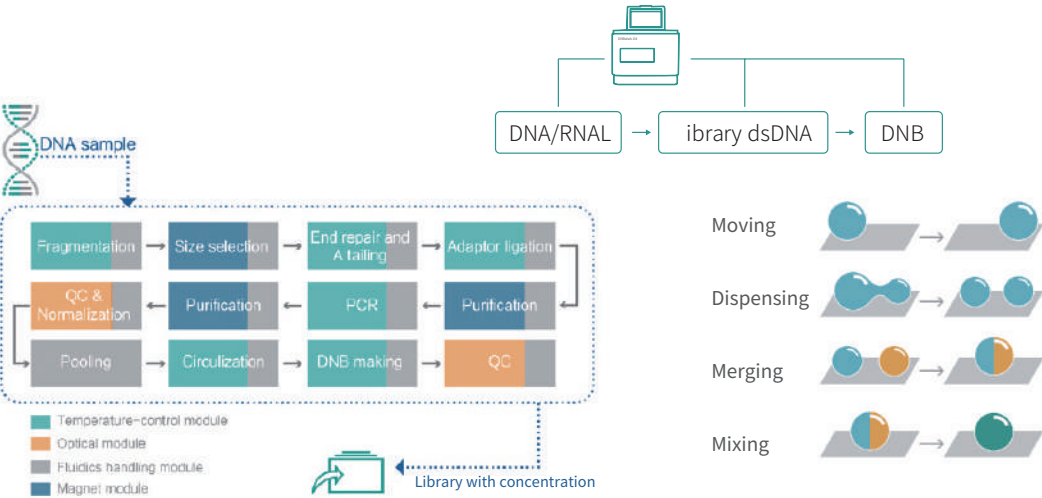
No. of samples/Run	1-4
Hands-on time	15 min
Library Quantification	Built-in
Compatible Sequencer	DNBSEQ E series
Temperature precision	DNBSEQ G series

Applications

- FS DNA library preparation
- Multiplexed-PCR-based enrichment library preparation
- Library conversion
- Support customization of third-party library construction kits

Workflow

Nucleic acid in (without extraction process), library/DNB out



SP-100

SP-100 Automated Sample Preparation System is an automated workstation specialized for high-throughput sequencing library preparation. SP-100 integrated 8- channel pipettes, processes samples in batches, eliminates operators from repetitive processing procedures, increases the stability of library preparation, reduces total costs, and significantly enhances the overall efficiency in the laboratory.

Function

- Integrated the different function modules, including PCR machine, magnetic rack, temp. modules and so on.
- Supports a wide range of library preparation kits, including WGS, WES, RNA, etc.

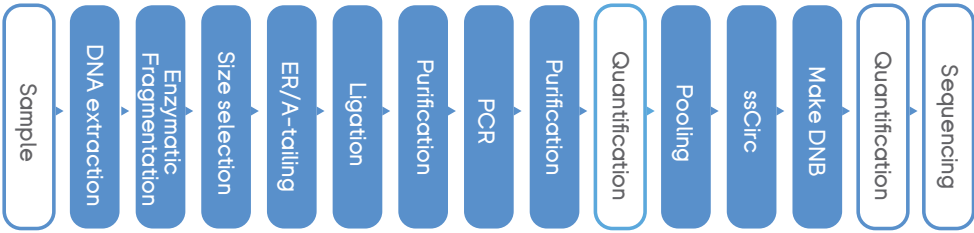
Features

- Simplified library preparation on a single instrument. Minimal labor requirement and human errors
- Cost-effective, short turnaround time. Batch operation is ideal for small and medium laboratories
- Simple-to-follow interface and instruction
- Integrated UV lamp and laminar flow hood, comprehensive pollution prevention design
- Open platform and customizable system setting

Performance parameters

Throughput	16 samples/run
Pipette Type	Fixed 8 channel
Pipette Range	1 μL-200 μL
Pipette CV	1->2μL: <5%, 200 μL: 1%
Pipette Accuracy	1->2μL: <±10%, 200 μL: <±1%
Temperature Control Module Temp. Range	4~99°C
HEPA System	99.99% at 0.3 μm

Automated WGS library preparation workflow



Note: white shows manual operation and blue shows automated steps.

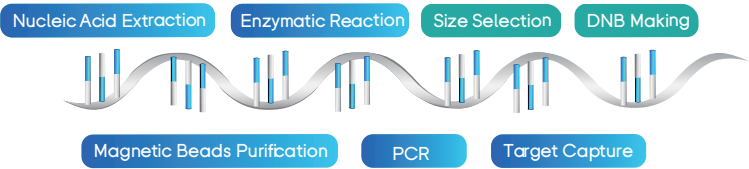


SP-960

SP-960 High-throughput Automated Sample Preparation System is a flexible, fully automated workstation with 96-channel pipette. SP-960 has validated lots of library kits, including WES/WGS/RNA and so on. SP-960 has fully automatic operation design, realizes walk-away process, and can be customized according to customer needs. It is an efficient and widely used automated sample preparation system.

Function

- Supports a wide range of library preparation kits, including WGS, WES, RNA, etc.



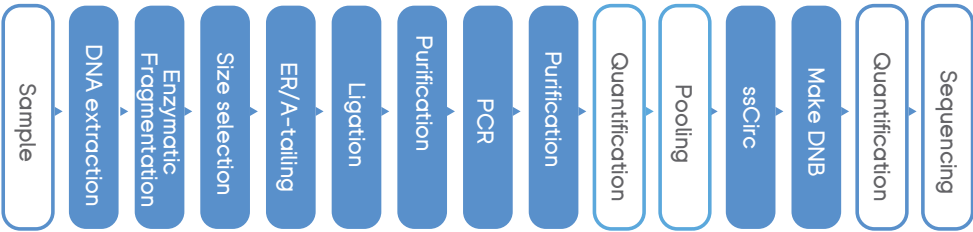
Features

- One stop solution integrating PCR, temperature control, shaker, magnetic rack and many functional modules
- Simplified library preparation on a single instrument. Minimal labor requirement and human errors
- Integrated UV lamp and laminar flow hood, comprehensive pollution prevention design.
- Open platform and customizable system setting

Performance parameters

Throughput	Standard: 96 samples/run
Pipette Type	Fixed 96 channel
Pipette Range	2 μL-200 μL
Pipette CV	2 μL: <5%, 200 μL: 1%
Pipette Accuracy	2 μL: <±10%, 200 μL: <±1%
Temperature Control Module Temp. Range	4~99°C
HEPA System	99.995% at 0.3 μm

Automated WGS library preparation workflow



Note: white shows manual operation and blue shows automated steps.



SP-Smart 8 Independent 8-channel pipetting robot

SP-Smart 8 is a professional automated pipetting robot, equipped with an independent 8 pipetting channel. The pipetting volume range is from 1 μL to 1000 μ L. SP-Smart 8 is adaptable to microplates as well as reservoirs and tubes. It saves valuable time and reduces errors inherent in complex, repetitive liquid handling protocols. SP-Smart 8 supports customization. It can integrate different functional modules, like PCR machine, shaker, magnetic rack, temperature control module, etc.

Function

- Cherry Picking Workstation
- Nucleic Acid Extraction Workstation
- Library Preparation Workstation

Features

- Integrated Pipetting Robot Arm Flexible and Efficient: Independent 8-channel pipettes for cherry picking; Integrated rotatable gripper
- Slide Track Deck Design High Compatibility: Consumables; Carriers
- Sensing and Barcode Scanning Function Intelligent and Informationalized: Sensing Function; Barcode Scanner

Performance parameters

Throughput	8-96 samples/run as Nucleic Acid Extraction Workstation, 1-48 samples/run as Library Preparation Workstation
Pipette Type	Independent 8 pipetting channel
Pipette Range	1 μL-1000 μL
Pipette CV	1 μL: <8%, 200 μL: <1%, 1000 μL: <1%
Pipette Accuracy	1 μL: <±10%, 200 μL: <±2%, 1000 μL: <±1%
HEPA System	99.995% at 0.3 μm



AlphaTool

Modular Intelligent Pipetting Platform

AlphaTool delivers automated solutions across multiple fields through high-precision hardware and an open ecosystem. Equipped with 8-channel and single-channel pipetting modules (with an error margin of $\pm 0.5\%$), it supports expansion with various modules such as magnetic attraction and PCR modules, while maintaining compatibility with mainstream equipment. Its software integrates the AI-driven α Lab Studio platform, enabling voice interaction, script generation, and data visualization. With open APIs, it allows flexible customization of automated workflows to meet diverse needs. AlphaTool facilitates the development of a full-chain intelligent laboratory ecosystem, accelerating advancements in research and industrial upgrading.

Features

Rapid pipetting

It can fill a 96-well plate in as fast as 22 seconds, equipped with both single-channel and 8-channel pipettes, meeting precise pipetting needs ranging from 1 to 1000 μL .

Flexible configuration

12 plate positions, modular hardware, flexible and customizable tabletop.

User friendly

The visual interface is simple and easy to understand. One-click to complete a variety of complex experimental processes via the customized script editing.

High compatibility

Compatible with many reagents and consumables on the market and compatible with standard SBS utensils. Standard API interface that supports being integrated as a unit of work.

Performance parameters

Pipette property	$1\mu\text{L} \pm 10\%$; $\text{CV} \leq 5.0\%$
	$1000\mu\text{L} \pm 1\%$; $\text{CV} \leq 0.5\%$
Robotic Arm Positioning Accuracy	$\leq \pm 0.1\text{mm}$
Overall dimensions (L x W x H)	$747 \times 695 \times 972\text{ mm}$
Weight	77 Kg
Power	200 VA
Rated voltage	AC100 V - 240 V
Voltage frequency	50/60 Hz
Fuse (A)	F10AL250 V

Application Scenarios

Life Sciences: Integrates with sequencers to handle experimental system configuration, aliquoting, and pre-loading pooling.

Education & Research: Breaks down disciplinary barriers across biology, chemistry, programming, and automation, fostering interdisciplinary talent development.



PrepALL

Flexible Pipetting Accessible to All

Flexible liquid handling is essential for high-throughput and complex laboratory workflows. Yet, traditional independent 8 channel liquid handling workstations are often expensive, complicated, and oversized—making them inaccessible to many labs.

PrepALL is designed to change that. It’s an flexible, affordable, compact, and intuitive solution that empowers more labs to adopt automation—no engineers or advanced training required. Built-in AI and vision technologies ensure simple, fast, and safe operation.

Biosynthesis

- Hit Picking
- Sample plating
- Plasmid construction

Genomics

- PCR Setup
- Pooling
- Normalization
- Nucleic acid extraction
- Quantitative preparation

Proteomics

- ELISA
- Immunoprecipitation
- MS pretreatment
- Protein extraction quantification
- Universal Liquid Handling
- Reagent preparation
- Sample transfer
- Plate replicate
- Serial dilution

Performance parameters

Pipetting range	0.5-1200 μL	
Pipetting accuracy	1-5 μL	$\text{CV} < 6\%$
	5-50 μL	$\text{CV} < 3\%$
	50-200 μL	$\text{CV} < 1\%$
	200-1000 μL	$\text{CV} < 1\%$
Pipetting precision	1-5 μL	$< \pm 8\%$
	5-50 μL	$< \pm 5\%$
	50-200 μL	$< \pm 2\%$
	200-1000 μL	$< \pm 1\%$



For operator and lab manager

Remote monitoring enables unattended operation and reduces operational costs



For operator

The operation tablet that comes with the machine has a friendly interface and low operation difficulty



For engineer

Plug-and-play PC-end control, supporting scripting and testing

Integrated Platform



FLP-L

The FLP-L Automated Sequencing Library Preparation System fully automates the entire process including sample extraction, library preparation, pooling, make DNB, and quality control. With a user-friendly interface and preset application programs, FLP-L supports one-click start, walk-away automation that enables the "sample in, DNB out" seamless end-to-end process.

Function

- Integration of all functional modules enables end-to-end unattended automation
- Manual setup in under 30 minutes with preset application programs
- Minimal training with user-friendly control software

Features1:

Sample in, DNB out

Pre-set application programs, supporting abundant library preparation scenarios

- Equipped with a “fixed 8-channel + independent single-channel” pipette to support complex pipetting operations / combined operations.
- Integrated quantitative module to record data during the experiment process and automatically calculate the input reaction.
- Pre-set selectable application programs, while providing a graphical editor to support user customization.

Features2:

Guarantee safety and reliability

Offer flexible "one-stop" library preparation plans

- UV and HEPA high-efficiency filtration system ensures biosafety
- Real-time process monitoring ensures dependable results, while comprehensive recording aids risk detection.

FLP series products	Product feature	Application	Recommended No. of samples /RUN*
FLP-L Standalone version + G99	Use in combination Create more possibilities	mNGS	4~8 samples
		Onco panel	4~32 samples
		ATOPlex panel (respiratory pathogens)	4~32 samples
FLP-L Interconnected version + G50	Back the on-site upgrade of G50 (RUO)at the user end.	mNGS	4~32 samples
FLP-L50	One-click to start the sequencing experiment: samples in, results out.	Onco panel	
		ATOPlex panel(respiratory pathogens)	



FLP-L50

FLP-L50 is a modular sequencing workstation independently developed by MGI. FLP-L50 focuses on creating a new sequencing model, and integrates the whole sequencing workflow into one machine, creating a fully automated solution from sample to report with just one click.

Features

Less than 24h per experiment, 4~32 samples per run

3 Labs → 1 Lab: minimizing the footprint of the instrument, consolidating the traditional 3 laboratory spaces into a modular sequencing workstation occupying less than 2 m²

Intelligent Experiment: Sample Barcode Scanning; Sample & Result Life-cycle Tracing; Intelligent Device Monitoring; Experimental Process Monitoring

Pre-defined Workflow: providing new-standard operation-simplicity to conduct sequencing experiments

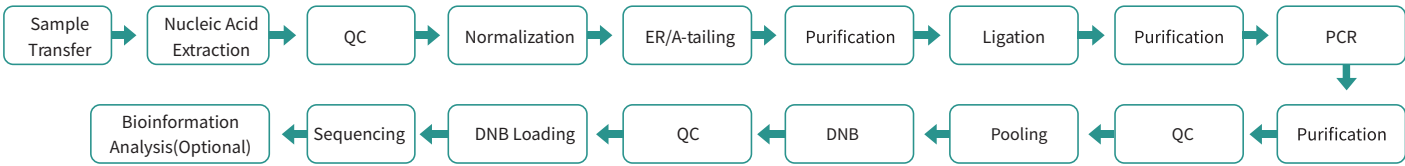
Disinfection System: HEPA system: 99.995% at 0.3 μm; UV system: Higher than 100,000 μW.s/cm²

Performance parameters

Dimensions (L x W x H)	1840 x 851.5 x 1821 mm
Sample Type	Plasma, full-blood, cerebrospinal fluid, swab preservation fluid, saliva, nucleic acid, etc.
Throughput	4 ~32 samples/run
Read Length	SE50, SE100, PE50, PE100, PE150
HEPA System	99.995% at 0.3 μm

Applications

- Pathogenic microorganism detection
- eg. Automated mNGS workflow



Intelligent Digital Platform



MegaBOLT

MegaBOLT bioinformatics analysis accelerator series (including MegaBOLT/ZBOLT/ZBOLT Pro, hereinafter called MegaBOLT) is an MGI self-developed and MPS-concentrated hardware accelerating system for bioinformatics analysis. MegaBOLT supports analysis of Whole Genome Sequencing (WGS), Whole Exome Sequencing (WES) and Panel Sequencing on Germline or Somatic data. It is up to 300 times faster than the classical algorithm. Fast, integrated, easy to use, and economic are MegaBOLT's most prominent features. MegaBOLT products series include the workstation (MegaBOLT) and rack server (ZBOLT/ZBOLT Pro), which can be applied to various scenarios of all scales.

Features

- Fast with Multi-task Scheduling System
- High Precision
- Deep Learning Making Sequencing More Cost-effective
- Highly Integrated Functions

Performance parameters

Analysis time comparison	Classical Algorithm	MegaBOLT	ZBOLT	ZBOLT Pro
Germline WGS 30X Basic	42.82 h	1.50 h	0.52 h	0.12 h
Germline WGS 30X Full	44.00 h	1.94 h	0.64 h	0.16 h
Germline WES 100X Basic	4.9 h	0.26 h	0.09 h	0.02 h
Germline WES 100X Full	5.04 h	0.32 h	0.11 h	0.03 h
Somatic WGS 40X Tumor + 40X Normal	58.20 h	5.17 h	1.74 h	0.44 h
Somatic WES400X Tumor + 400X Normal	9.53 h	0.86 h	0.29 h	0.07 h

* Basic: Includes the analysis steps from clean data after quality control to variant calls, taking the average time of multiple tasks.
* Full: Includes extra steps of quality control and report generating in addition to the Basic workflow.
* The time consumed is measured by taking the average of completing 4 identical tasks (MegaBOLT)/ 12 (ZBOLT) / 48 (ZBOLT Pro).



αCube
Data Center Appliance

αCube Data Center Appliance is an innovative genetic data center solution that integrates biotechnology (BT), information technology (IT) and artificial intelligence (AI) from MGI. It integrates bioinformatics computing acceleration, massive data storage and intelligent analysis, supports independent offline deployment and horizontal expansion, and takes into account security and low operation and maintenance costs.

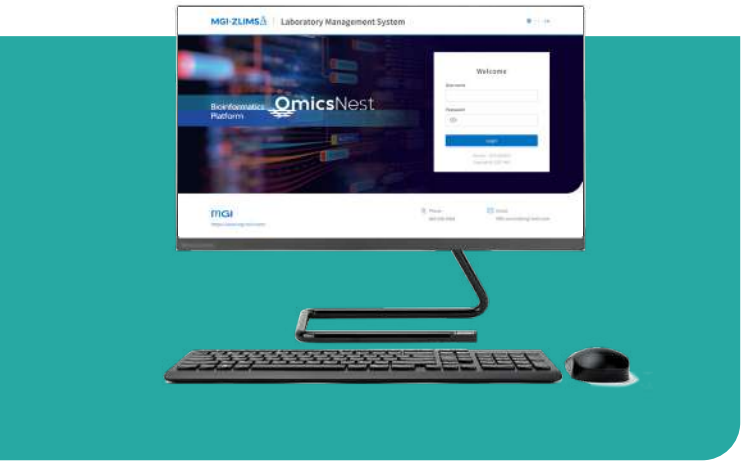
Features

- **Extreme Computing Power**
High-performance heterogeneous computing architecture
- **AI Empowerment**
A new era of intelligent bioinformatics analysis
- **High-performance Storage**
Large capacity and high density storage
- **Flexible Customization**
Elastic scalability and easy expansion

Performance

- **Peak AI computing power**
391.5TFlops (CPU+GPU Total AI computing power)
- **Write Fastq Time**
45min/T7 Slide
- **WGS Analysis Time**
About 10min/30X human sample
- **Available storage**
1.3PiB

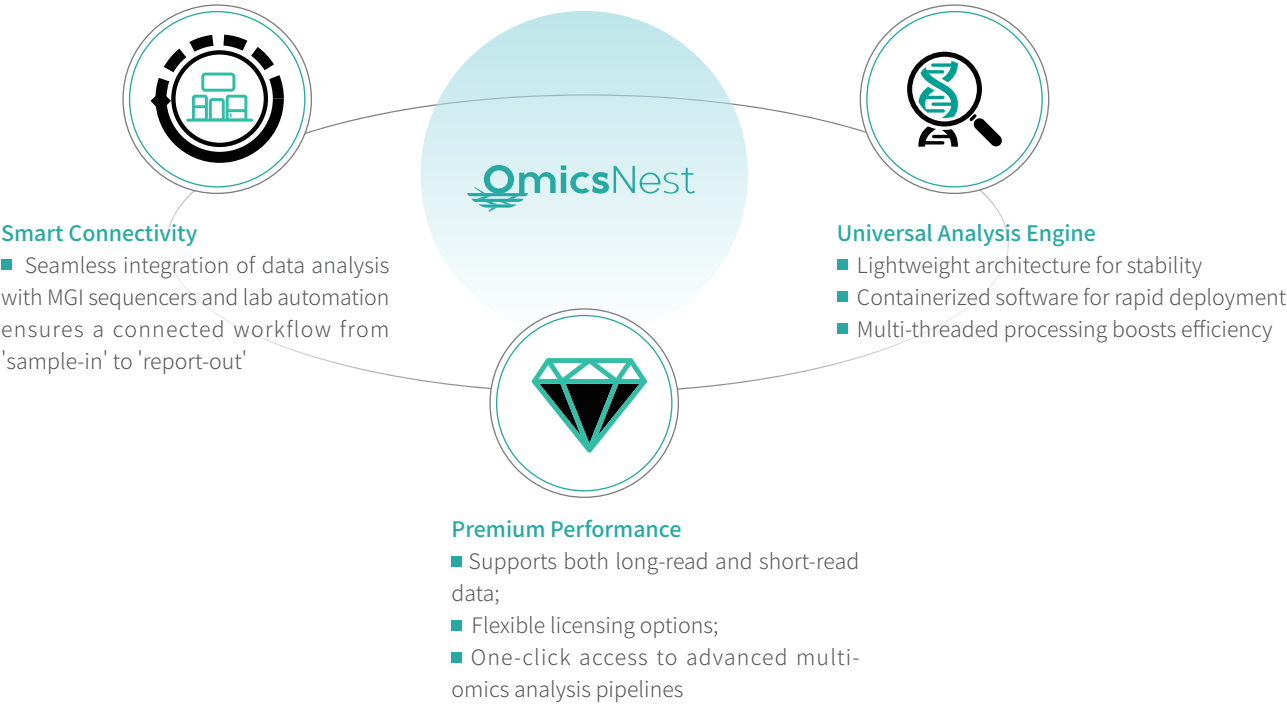
Component	αCube 650D	αCube 1300D
Compute Nodes (2 nodes each)		
CPU	AMD EPYC 9654 × 2	AMD EPYC 9654 × 2
RAM	512GB DDR5	512GB DDR5
System Disk	480GB SSD (Read-intensive) × 2	480GB SSD (Read-intensive) × 2
Data Disk	3.84TB NVMe SSD × 2	3.84TB NVMe SSD × 2
GPU	NVIDIA RTX A4500 20GB × 2	NVIDIA RTX A4500 20GB × 2
Network	Dual-port 25GbE × 2, Quad-port Gigabit × 1	Dual-port 25GbE × 2, Quad-port Gigabit × 1
IO Nodes (2 nodes each)		
CPU	Intel Xeon Silver 4314 × 2	Intel Xeon Silver 4314 × 2
RAM	128GB	128GB
System Disk	480GB SSD × 2	480GB SSD × 2
Acceleration Disk	3.84TB NVMe × 1	3.84TB NVMe × 1
Network	Dual-port 100GbE × 1, Dual-port Gigabit × 1	Dual-port 100GbE × 1, Dual-port Gigabit × 1
Disk Enclosure (2 units each)		
Metadata	800GB SAS SSD(DWPD=3) × 4	1.6TB SAS SSD(DWPD=3) × 4
Data Disk	8TB NL-SAS HDD × 55	16TB NL-SAS HDD × 55
Performance	7 GB/s	7 GB/s+
Effective Capacity	650 TiB	1,300 TiB
Networking Equipment		
Data Switch	24 × 25GbE SFP28 ports, 4 × 100GbE QSFP28 ports	
Management Switch	48 × 1G ports, 4 × 10G SFP+ ports, 2 × 100G QSFP28 ports	
System Software		
LIMS	Laboratory Information Management System — Dashboard, sample entry, task management, sequencing management, real-time monitoring, message centre	
Multi-omics Platform	Automated bioinformatics analysis — 200+ built-in workflows, graphical/script interface, automated scheduling, lifecycle data management, automated governance, sample/project/workflow-level tracking	
Physical	1 × 22U cabinet (1,200 × 600 × 1,200 mm) + 2 PDUs (32A industrial plugs)	



OmicsNest Bioinformatics Platform

OmicsNest Bioinformatics Platform is specifically designed for multi-omics analysis, offering a one-stop solution that integrates sequencing task management with bioinformatics analysis. By deeply interfacing with the ZLIMS/PaaZ laboratory management system and seamlessly connecting to MGI sequencing devices, the platform supports end-to-end software, including metagenomics, whole genome sequencing, and targeted sequencing. Compatible with both long-read and short-read sequencing technologies, OmicsNest delivers efficient and stable analysis services, catering to diverse application scenarios worldwide.

Features



Performance parameters

Module	Function	Sequencing Length	Single Sample Analysis Data Volume/Sequencing Depth	Analysis Time
Targeted Genome Analysis	Drug Resistance Analysis of Mycobacterium tuberculosis	PE150	3M reads	32min
	MPXV Genome Assembly and Phylogenetic Tracing	SE100	20M reads	11min
	Covid Genome Assembly and Phylogenetic Tracing	PE150	2.5M reads	11min
	Influenza Typing, Subtyping and Phylogenetic Tracing	PE100	5M reads	37min
Metagenomics Analysis	Microorganisms Fast Identification	SE50	25M reads (4 samples)	35min
	Antibiotic Resistance Gene (ARG) Annotation and Quantitative Classification	PE150	34M reads	35min
Whole Genome Analysis	Mycobacterium tuberculosis Identification, Mutation Detection and Genotyping	PE150	10M reads	19m
	Escherichia coli Long-Read Assembly	Long reads	50X	19min
	MPXV Short-Read Assembly and Phylogenetic Tracing	SE100	1.5M reads	4min

Product Configuration

Product Name	OmicsNest Bioinformatics Platform	OmicsNest Lite Bioinformatics Platform
Model	OmicsNest	OmicsNest Lite
Zlims Version	ZlimsV3.0.3.250627 and above	ZlimsV3.0.3.250627 and above
PaaZ Version	PaaZ4.0.2.250604 and above	PaaZ4.0.2.250604 and above
CPU	Intel Xeon Gold 6430 × 2	Intel Xeon 4514Y × 2
CPU threads	128	64
Memory	256 GB	128GB
Storage(HDD)	28TB (RAID5)	7.3TB (RAID5)
Storage(SSD)	2.5 TB	1.5 TB

Adapted Bioinformatics Software

Application	Software
Public Health	HIV-GenomePro Software
	HIVLongSeq(HIVLS)
	Platform of microorganisms Fast Identification software(PFI)
	MGI MGAP
	Microbial Genome Assembler(MGA)
	Vector Identification Software(VIS)
	MGI FluTrack software
	MGI metatargetCOVID software
	MTB-Explorer Software
	ATOPlex MultiPCR Microbiome Research Software(ATOPlex MMRS)
	Virus Identification for Rapid and Universal Screening Software(VIRUS)
Environment and Biodiversity	Metabarcoding Species Identification Software(MetaSIS)
Agriculture and Food Safety	Low-pass Whole Genome Sequencing Software(BOLT Low-pass)
	ATOPlex MultiPCR Explorer Software(ATOPlex MES)
Forensic Science and Impartial Testing	DNA Signature Identification Software Suite(FIS Suite)



αLab™ Studio

αLab™ Studio Laboratory Intelligent Management Platform deeply integrates large AI models with automation technologies. Through intelligent decision - making, dynamic scheduling, and data management, it achieves digital,unmanned, and standardized management of the entire experimental process in the field of AI + life sciences driving a leap - forward improvement in scientific research efficiency and accuracy. It comprehensively improves research efficiency and accuracy in one - stop, enabling researchers to focus on innovation.

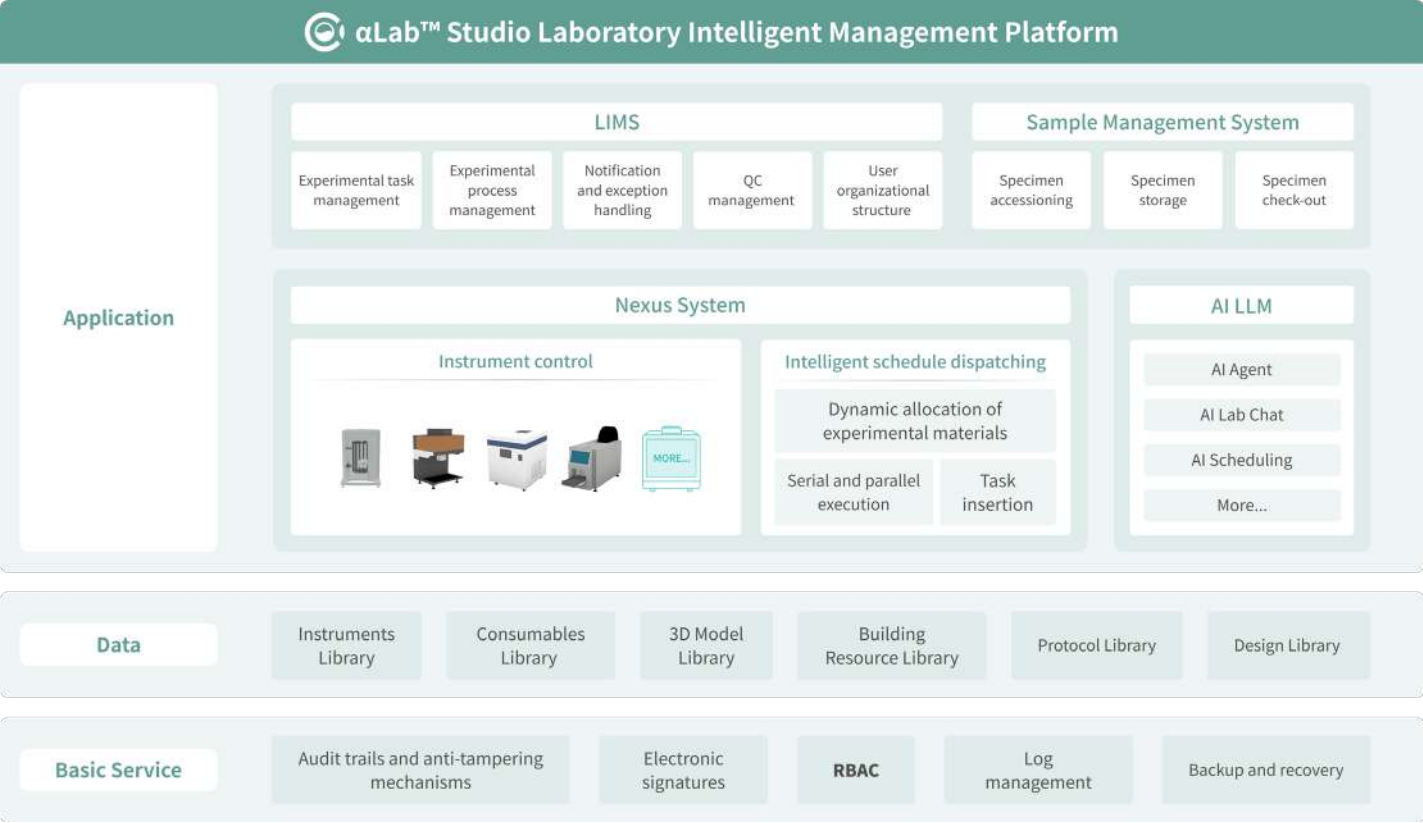
Nexus System

- Process Design:** Graphically design experimental protocols by modularizing actions and flexibly adjusting parameter details.
- Intelligent Scheduling:** Maintain full visibility and control over experiment execution, monitor instrument utilization in real time, and optimize scheduling with precision and efficiency.
- Standard Communication:** Coordinate instruments through a unified control system, enabling seamless interoperability across multiple instruments.
- Open API:** Provide stable API interfaces, detailed getting-started guides, and complete execution examples to support deep customization of experimental program.



- AI-assisted Scientific Research:** Enable automated protocol generation and optimized advice with demand-based configuration to accelerate experimental design.
- Digital Twin–Driven Automation** Create real-time digital twins of laboratory and experimental processes, supporting second-level monitoring, virtual dry runs, and predictive validation, which significantly reduces trial and error costs.

αLab Studio Laboratory Intelligent Management Platform



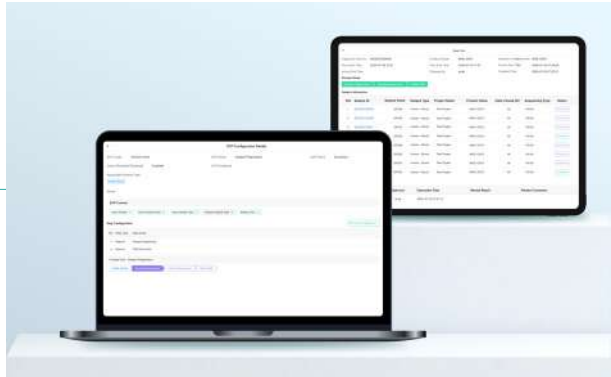
Sample Management System



- Intelligent Visualization:** An interactive dashboard displays visualized sample container hierarchies and clear sample positioning.
- Standardized and Secure:** Role-based access control, complete audit logs, and full lifecycle traceability ensure data integrity and regulatory compliance.
- Flexible Customization:** Customize information of samples and projects enables to adapt to diverse experimental and research scenarios.

LIMS

- Flexible Configuration with High Expandability:** Build experimental workflows instantly with no coding required. Freely combine predefined logic blocks to construct efficient workflows, and choose from a wide range of templates to support multi-purpose laboratory use cases.
- Safe, Reliable and Quality - Controlled with Early Warning Mechanism:** Fine-grained role permissions, complete operation logs, and full-process traceability ensure quality compliance and regulatory readiness. Automated alerts are triggered based on predefined quality thresholds to proactively manage experimental risks.



- Comprehensive Management with Precise Traceability:** Flexibly define experimental plans and approval processes, monitor task progress in real time, and seamlessly integrate with the sample library. Gain full situational awareness of laboratory operations with real-time dashboards and intelligent Prediction.

Automated Devices and Consumables



Portable Smart Water Sampler

To solve sewage sampling challenges in confined spaces (e.g., manholes, pipes)—including unattended 24h sampling, high-temperature spoilage, and flammable gas risks—our Portable Smart Water Sampler integrates precision temperature control, gas sensors, and Bluetooth-enabled APP automation for safe, fresh, automated collection in harsh environments like sewers and ditches, serving environmental monitoring, research, and toxic/viral analysis.

Features

- Precision Cryogenic Sample Preservation**
 - Integrates precision thermal algorithms and advanced insulation for portable, low-temperature sample preservation in confined spaces.
- Real-time Hazardous Gas Monitoring**
 - Built-in sensors monitor hazardous gases (CH₄, H₂S) for safety.
- Automated Intelligent Sampling**
 - Enables 24-hour automated sampling via Bluetooth app scheduling.

Specifications

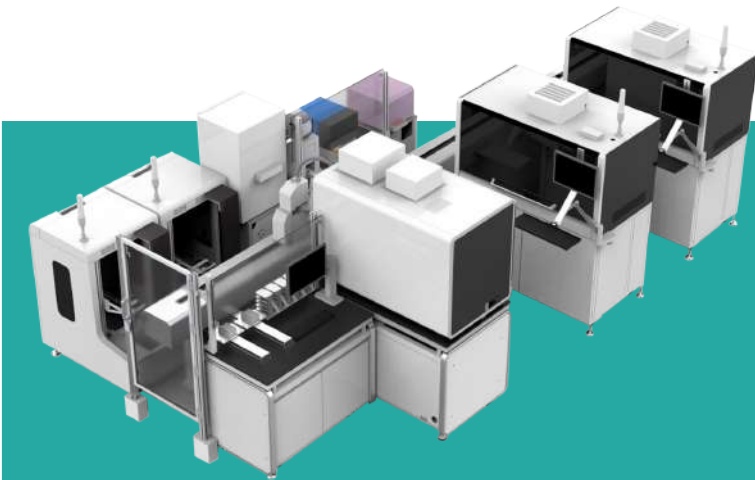
Parameter	Detail
Sampling Method	Automatic, timed sampling
Volume	4.6 L
Frequency	Customizable
Accuracy	±5%
Communication	Bluetooth
Operating Temperature	5° C to 50° C
Sample Storage Temperature	4° C to 10° C
Power Supply	AC 220V 50Hz / Rechargeable
Material	Stainless Steel
Weight	5.5 kg
Dimensions	16 × 20 × 50 cm
Max Vertical Sampling Depth	7 m

Applications

The portable smart water sampler, when integrated with MGI's reagent kits, automated sample preparation systems, and analysis software, provides end-to-end coverage from sewage collection to data analysis. This system enables rapid and accurate identification of pathogens in wastewater, delivers actionable epidemiological intelligence, and empowers:

- Real-time infectious disease surveillance & early warning
- Outbreak investigation support
- Disease control efficacy evaluation

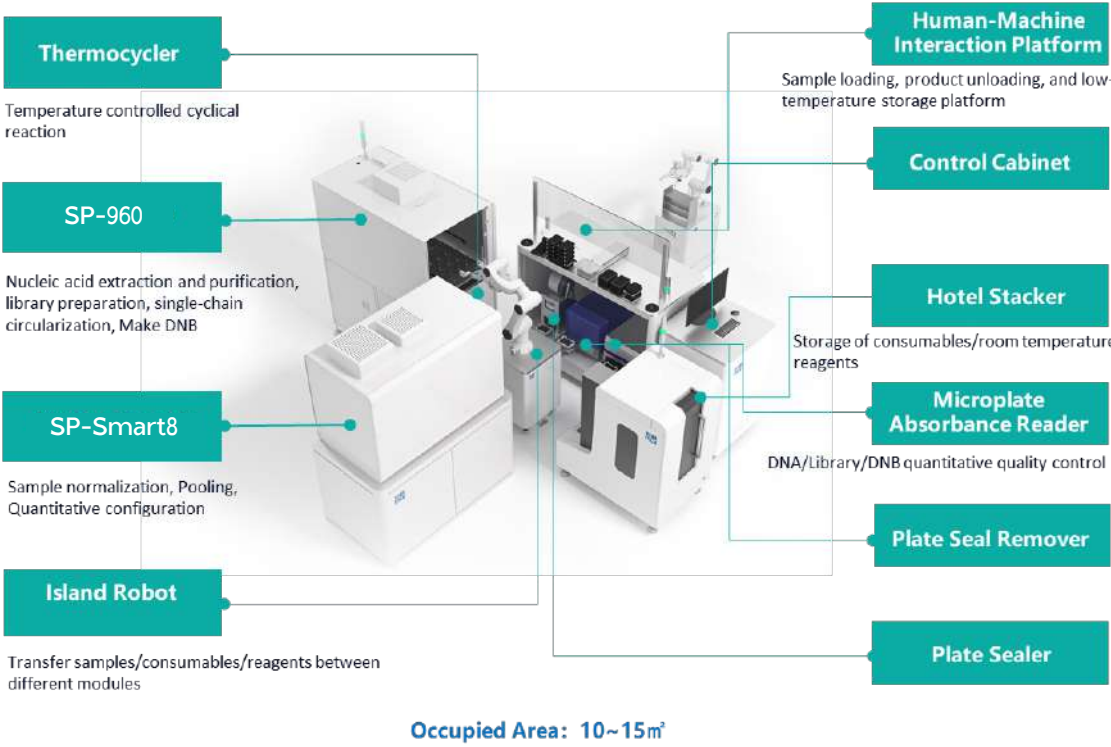
Customized Platform



GLab-50KRS



GLab-50KRS revolutionizes NGS production with ultra-compact 10-15m² design, integrating the Island Intelligence Chain System to synchronize six core modules for fully automated, contact-free operation—from sample processing to DNB synthesis. Delivering 50,000 samples/year industrial-scale throughput, it accelerates large-scale genomic



Features

- More Flexible**: Flexible Robotic Scheduling & Intelligent Unmanned Operations
- More Intelligent & Affordable**: Compact Footprint: Requires Only 10-15m²
- More Stable**: 24-Hour High-Performance Operation
- More Efficiency**: Deployment and Delivery at Client Sites Within 2-4 Weeks



Bloomics® Disposable Capillary Blood Collection System

The Bloomics Blood Collection Kit is mainly composed of one-time blood collection devices and blood collection tube. It is exquisitely designed and provide customer with a virtually painless, easy-to-use blood collection method, The whole Capillary blood sampling can be achieved simply and only one step by attaching the blood collection device to the upper arm and inserting the blood collection tube.

The Bloomics Blood Collection Kit is a user-centric blood collection solution. It can realize a new mode of blood collection for detection and analysis by connecting decentralized clinical blood samples with any laboratories in seamless integration.

One-step blood collection and transfer solution

Easy-to-use

Yield up to a 98% collection success rate

Virtually painless

90% of end-users claim they would repeat this blood collection method

Consumer-preferred

Produce clinical grade blood sampling and Enhance your data density and fidelity

Cost-Saving

Self-blood collection without nurse involvement

Blood collection device Specification

Item	Descripiton
Classification	Clinical Medical Devices II
Dimension	58 × 38 × 38mm
Weight	40g
Use/Storage	Use/Storage temperature range: 15℃ ~30℃ ; Relative humidity: 15%~85% Atmospheric pressure range: 80Kpa~106Kpa; Use site: indoor use
Transport Environment	Transport temperature range: 15℃ ~30℃ ; Relative humidity: 15%~85%,RH Atmospheric pressure range: 80Kpa~106Kpa
Penetration Depth	1mm~4mm
Collection time	≤ 90s
Blood collection volume	≥ 200 μL
Duration	1 year

Blood collection Tube Specification

Tube type	K2EDTA	Serum Gel
Additives	K2EDTA	Clot Activator & Separator Gel
Sample type	Whole blood / plasma	Serum
Hemolysis (%)	<5%	<5%

Application



OMICS

Omnidirectional Multi-omics Coverage throughout Biological Life Cycles

Multi-Omics integrates genomic, epigenomic, transcriptomic, metagenomic, single-cell sequencing, spatial transcriptomics, image data, and applications to provide a holistic view of biological systems.

Powered by MGI's advanced sequencing and automation platforms, it enables researchers to uncover complex biological relationships and drive insights across diverse applications, from basic science research to clinical applications. Empower your discovery with Multi-Omics—the key to understanding the full spectrum of life sciences.

POP Omics . Cell Omics . STOmics . Proteomics
Radiomics . Innovative Applications . Extended Solutions

Reading

POP Omics		Cell Omics	STOmics	Proteomics	Radiomics
 DNA & RNA Library preparation kits	 Methylation library reagent and analysis software	 Single cell library reagent and equipment	 Stereo reagents and instruments	 Olink library circualization kit  FluoXpert Multiplex Immunofluorescence Staining Set	 Handheld ultrasound  Remote ultrasound system  Mobile ultrasound cart

Storage

4°C & -20°C		-80°C		-196°C				
 CLab-EG	 CLab-LT	 CLab-FZ	 CLab-LT	 CLab-LN 55K	 CLab-LN 55K Pro	 CLab-Capper	 Sample transport robot	 ZSM Pro

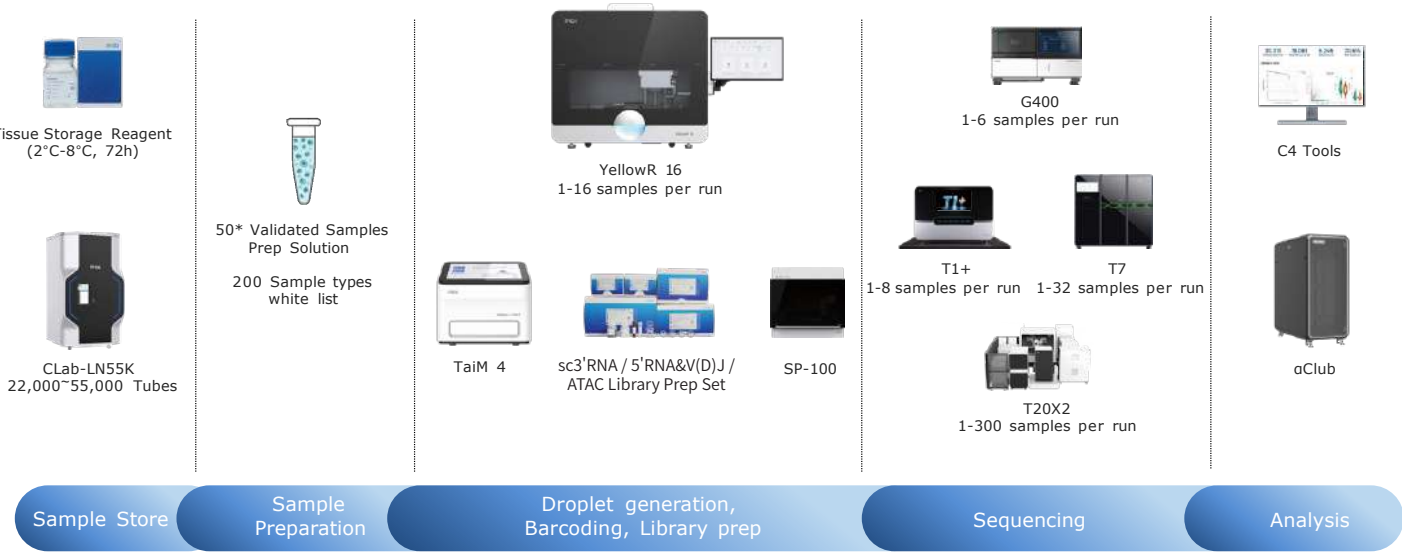
Innovative Applications

	Sample Collection	Nucleic acid Extraction	Library Preparation Reagent	Analysis Software	Customized Targeted-Seq Platform
Public Health					
Environment and Biodiversity					
Agriculture and Food Safety					
Forensic Science and Impartial Testing					

OMICS-DCSP

Complete Single-Cell Workflow Solution

MGI's single-cell whole workflow related products include tissue storage reagent, which maintains tissue freshness within 72 hours at 2-8°C , providing a buffer time for sample preservation when immediate experimentation is not possible; the droplet instrument TaiM 4 is used to complete droplet encapsulation of cells, achieving cell separation and molecular labeling; the automated instrument SP100 can perform semi-automated library preparation steps; the integrated single-cell library preparation workstation YellowR 16 can process from cell or nucleus suspension to pre-sequencing DNB preparation, replacing over 90% of manual experimental steps; single-cell multiomics library preparation kits include 3'RNA, 5'RNA and ATAC; the prepared single-cell libraries can be sequenced on sequencers with different throughputs including G400, T1+, T7 and T20; the sequencing data can be analyzed using C4Tools for single-cell matrix analysis, and the software analysis package is supported on aClub.



Features

- Maintain the cell activity of fresh tissue stably at 2-8°C within 72h
- Solve the problem of batch differences in processing multiple samples which improve the flexibility of experiments;
- Quickly penetrate fresh tissue to reduce the changes of cell gene expression after ex vivo
- Suitable for single cell RNA sequencing

Performance

- Maintain the cell viability of various mouse tissues at 2-8°C for up to 72 hours

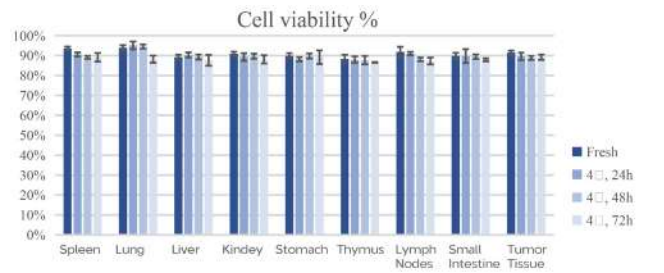


Fig.1. Various mouse tissue samples were stored by MGEasy tissue storage reagent at 4° C for 24 h, 48 h and 72 h, then dissociated and calculated the cell viability of singe cell. The cell viability of single cell was just slightly reduced while compared with the fresh tissue.

	Cell Viability	Live Cell Count (cells/mL)	Cell Clumping Rate
0h	93.52%	2.57E+07	1.84%
24h	90.56%	1.89E+07	2.01%
48h	89.09%	1.74E+07	1.75%
72h	89.13%	1.35E+07	1.28%

Table 1 Mouse spleen tissues were stored by MGEasy tissue storage reagent at 4° C for 0h, 24h, 48h, and 72h, then dissociated to single cell and calculated the cell viability, live cell count and cell clumping rate.

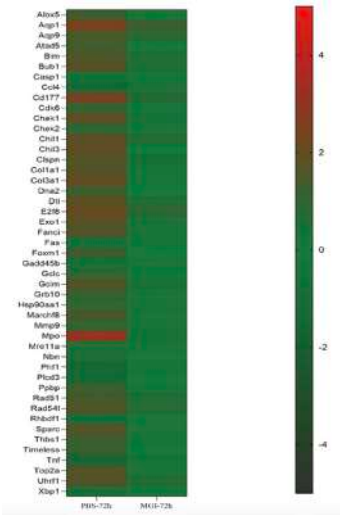
MGEasy Tissue Storage Reagent

This product can effectively preserve isolated animal tissue samples in the short term to maintain the cell activity and stabilize the gene expression levels. The samples can be used for downstream applications such as single cell RNA sequencing.

Product Information

Product Name	MGEasy Tissue Storage Reagent
Model	TSR-100
Product Specification	100 mL/bottle
Product Expiration Date	2-8° C for up to 12 months
Product transport condition	2-8° C for up to 15 days
Sample transport condition	2-8° C for up to 72 hours
Adaptable sample types	Fresh animal tissue
Adaptable application	Single cell RNA sequencing

- Maintain stable gene expression level in MGEasy tissue storage reagent



- **Stress-related genes:** Casp1, Chek1, Fas, Tnf, et al.
- **DNA damage-related genes:** Atad5, Blm, Cdk6, Chek1, et al.
- **Immune-related genes:** Cd177, Marchf8, Timeless, et al.

Fig.2. Gene expression from fresh and stored mouse spleen tissues in PBS and MGEasy tissue storage reagent. RNA was isolated from fresh and stored tissues and differential gene expression was analyzed. The heatmap shows the express differences between fresh tissue and stored tissues in PBS and MGEasy tissue storage reagent for 72 hours.



TaiM 4 Single-cell Droplet Generator

TaiM 4 Single-cell Droplet Generator provides stable and precise cell and cell nucleus separation and labeling. This instrument equips with four independent microfluidic channels, supporting single-cell ATAC,3’ RNA and 5’ RNA&V(D)J library preparation. TaiM 4 is compact, lightweight, and plug-and-play, it can operate at altitudes of 2.5 km or below, with the flexibility to handle 1-4 samples at once.

Features

- Four independent microfluidic channels, enabling 1-4 samples' cell separation and labelling.
- 6 minutes for cell nucleus separation and labelling during single-cell ATAC library prep.
- 10 minutes for cell or nucleus separation and labelling during single-cell 3’ and 5' RNA&&V(D)J RNA library prep.

Performance

Input Cells	5,000~30,000
Estimated Number of Cells	≤ 20,00 0
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)



YellowR 16 Revolution in Single-Cell RNAseq Library Prep

YellowR 16 is capable of seamlessly transitioning from cell&nucleus suspension input to the output of DNA nanoballs (DNBs) ready for sequencing. YellowR 16 is equipped with multiple built-in functional modules, enabling a fully automated workflow without tester intervention. The integrated 8-channel independent pipetting module handles plate transfer and pipetting throughout the entire process. The Single-cell Droplet Generation module performs cell sorting and labeling, while the PCR instrument, Magnetic Bead Purification Module, and Shaker modules facilitate high-throughput library preparation. Additionally, the DNA Concentration Detection module is used for library quality control (QC). These truly achieve an unattended workflow encompassing cell sorting, library preparation, and library QC, hands-free, ensuring stability and reliability. This revolutionary solution addresses the drawbacks of manual single-cell operations, such as complexity, low throughput, and data variability, paving the way for single-cell sequencing technology to enter a new era of scalability and standardization.

Features

- Unattended:** < 5% Manual Time
- High-throughput:**16 Samples/Run
- Flexibility:**Any step starts or ends
- Consistent:**High data consistency

Unmanned Workflow

Automated high throughput end-to-end workflow reducing human intervention by 90%.

Flexible

Flexibly design experimental workflows with1-16 samples per batch

High Throughput

Up to 16 libraries in 17 hours and maximum 1 week for 2.4M reads scRNA Seq data using T7.

Stable

Reduces human errors with up to 99% inter-batch reproducibility.

Performance

Throughput	1-16 Samples/Run, 5K~20K Cells/ Sample, 320K Cells/Run
Running Time	8 Samples: 14h 16 Samples: 17h
Cells Recovery Rate	> 50% （PBMC）
Median Genes Per cell	> 2,000 （PBMC）
Median UMI Counts Per Cell	> 5,000 （PBMC）
Multiplet Rate	0.4%/1,000 Cells

3’RNA Reagent Series

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.



5’RNA Reagent Series

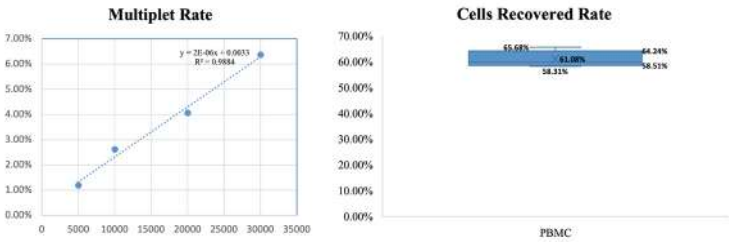
DNBelab C series high-throughput single-cell 5' RNA & V(D)J library preparation set is used in combination with the TaiM 4 single-cell droplet generator to complete the single-cell 5' RNA and TCR/BCR library preparation processes. The DNBElab C series analysis package DNBC4Tools can be used to achieve data processing, quality control, and basic analysis.

Features

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

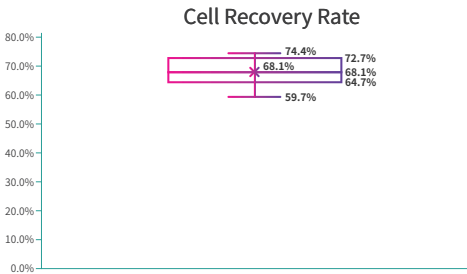
Performance

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)

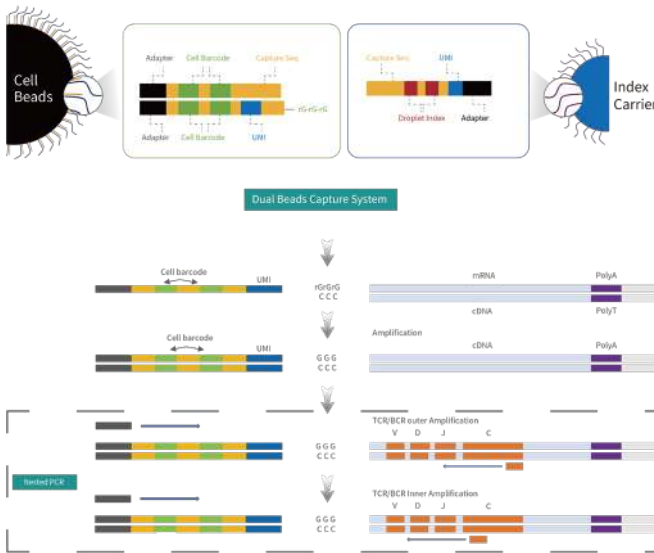


Performance

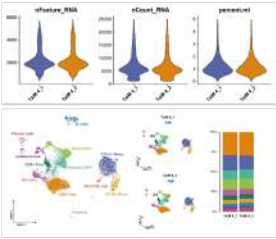
- Number of Input Cells: 5,000 ~ 30,000
- Estimated Number of Cells: < 20,000
- Recovery Rate of Cells: > 50%
- Multiplet Rate of Cells: < 0.4%/1,000 Cells
- Median Genes Per Cell: > 1,500 (PBMC)
- Cell with TRA and TRB: > 65% (PBMC)
- Reads mapped to any V(D)J gene: > 85% (PBMC)



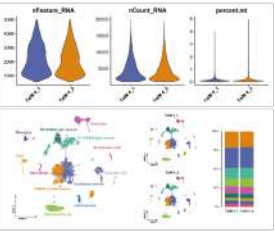
Core Technology



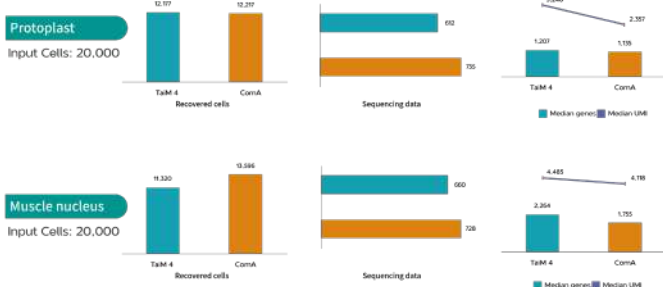
© Repeatability test- PBMC



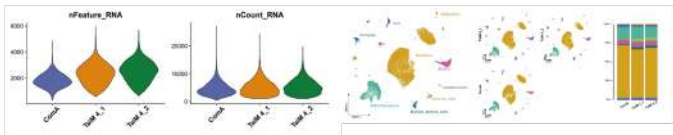
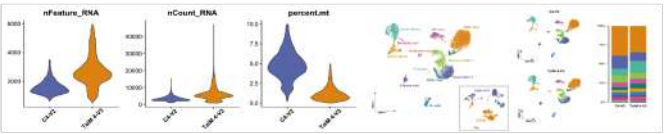
© Repeatability test- Mouse brain nucleus



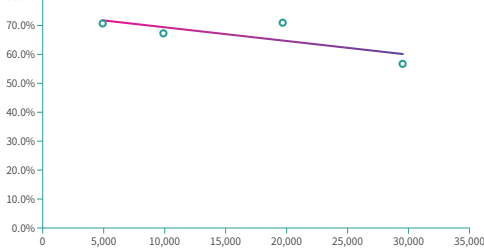
© Comparison of different platforms - TaiM 4 V3.0 VS ComA



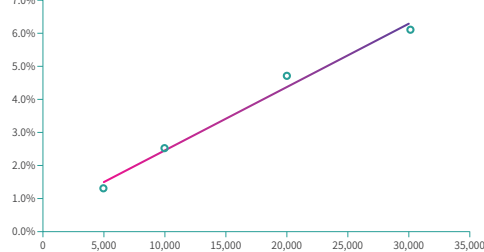
© Comparison of different versions - PBMC



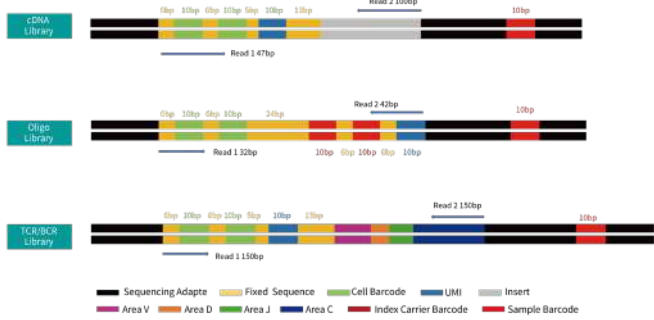
Cell Recovery Rate of Different Input Cells



Multiplet Rate of Different Input Cells



SEQ Strategy



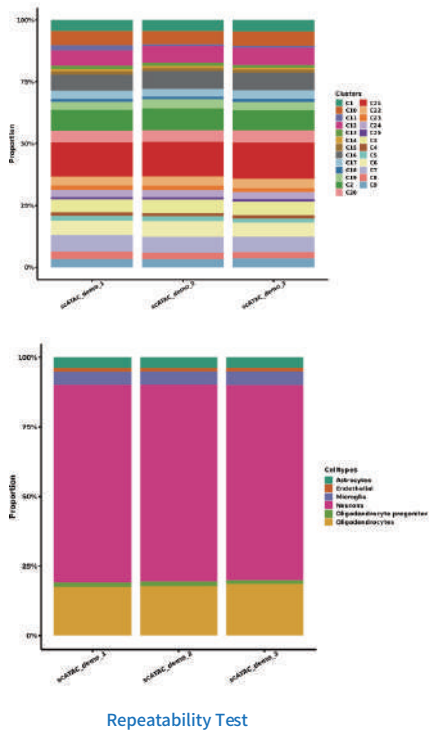
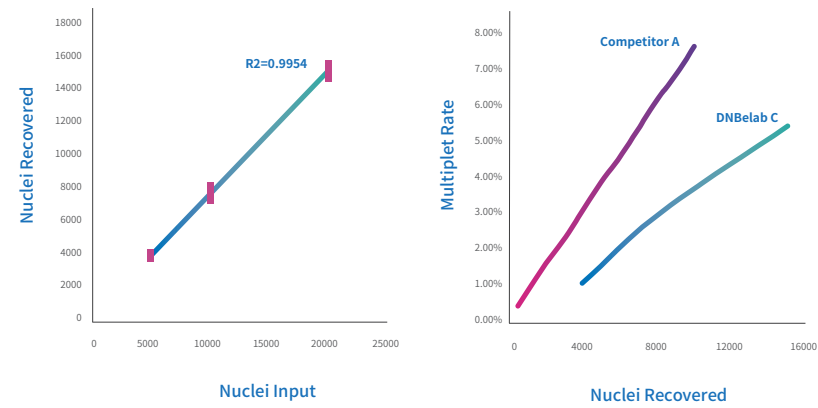


ACTC Reagent Series

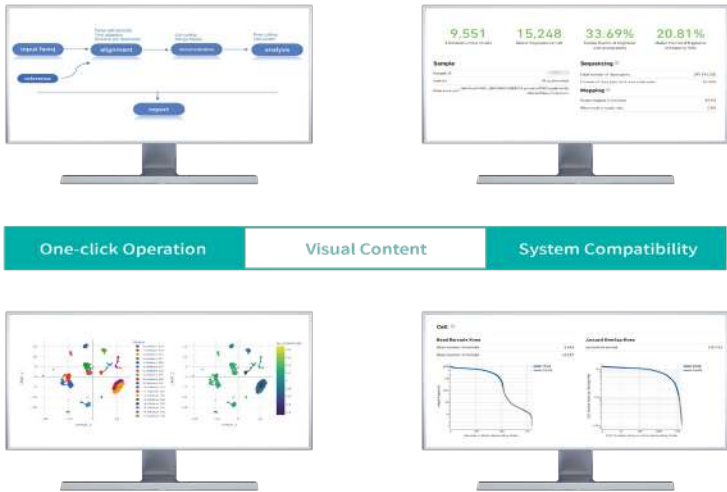
By utilizing the TaiM 4 single-cell droplet generator in conjunction with the DNBelab C series high-throughput single-cell ATAC library preparation set and the C4Tools data analysis process, input nuclei range from 5,000 to 20,000. The recovered nuclei typically fall within the range of 3,000 to 15,000, with a capture rate exceeding 60%. Additionally, the median fragment per cell count exceeds 10,000 (mouse brain), and the multiplet rate remains below 6%.

Features

- Nuclei Input: 5,000~20,000
- Nuclei Recovered: 3,000~15,000
- Median Fragment per cells: > 10,000
- Droplet Generation Time: ~6 min
- Capture Rate: > 60 %
- Multiplet Rate: < 6 %



Performance

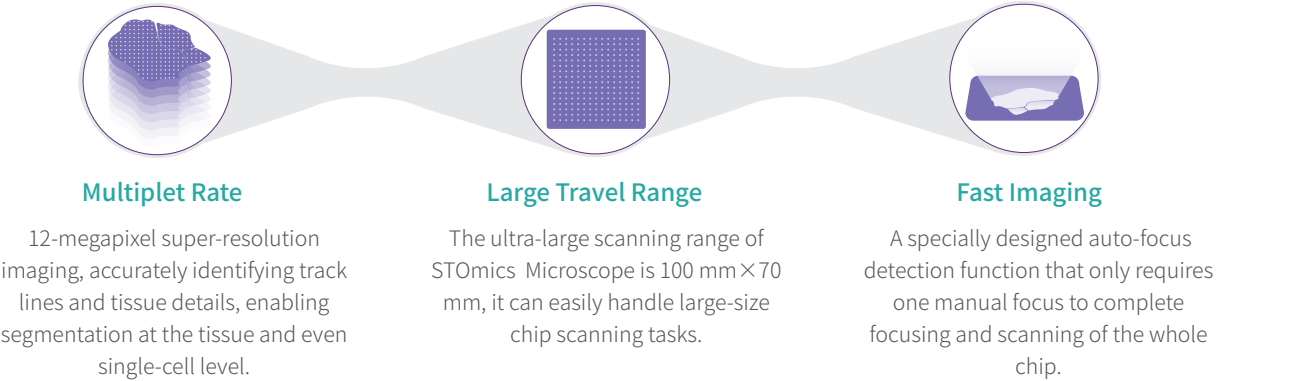


Go Optical

Providing Unprecedented Field of View

Go Optical is the STOmics microscope designed for stereo-seq. It can fully meet the imaging needs in various experimental processes of stereo-seq. Integrating high-resolution imaging with the advanced algorithms of stereo-seq technology achieves a precise position of gene expression matrices in the tissue section and satisfies the multi-scenario application needs.

Features



Performance parameters

Parameter	Description
Optical system	Positive scanning microscope
Objective lens	4X, 10X, 20X, 40X(optional) universal motorized objective lens converter, support expansion
Observation Methods	Epi-fluorescence, Epi-bright field, Transmitted bright field
Fluorescent channel	Standard configuration: DAPI, FITC, TRITC, CY5, and supports optional configuration of other dye filter blocks
Travel range X&Y	100 × 70mm
Camera resolution	High image resolution: 3008 pixels (height) and 4112 pixels (width)
Auto-focusing	Two optional modes——Photoelectric focus detection, map point selection
Work efficiency	≤ 70 seconds for a 10 mm × 10 mm chip (10X)
Operating mode	Manual operation by human eye observation; fully automatic scanning and imaging.



Go Spatial

Go Spatial provides fully automated intelligent solution going from post-imaging tissue sections to cDNA library, achieving high-throughput to 8 FFPE samples per run and 12 FF samples per run. By automating repetitive and tedious manual operation, it minimizes batch-to-batch effects, ensuring effective and standardized Stereo-seq results output.



Post-imaging to cDNA



Flexible Throughput



With low hands-on time

Features

High automated, achieves automation of post-imaging biochemical reactions built around Stereo-seq slide cassettes, reducing manual intervention steps and batch-to-batch variability.

Consistent and reliable performance, percision pipetting and temperature control deliver high reproducible, standardized results.

User Friendly, an intuitive graphical interface that simplifies user training and streamlines experimental workflow.

Performance parameters

Application	Stereo-seq Transcriptomics solution and Stereo-seq OMNI for FFPE solution
Sample type	Compatible with FFPE and FF samples
Throughput	FFPE: 2~8 samples per run FF: 2~12 samples per run
Pipetting range	20μL to 1000μL
Pipetting precision and accuracy	20μL to 50μL: CV<2%, accuracy<±5%; 50μL to 1000μL: CV<1%, accuracy<±2%; 1000μL: CV<1%, accuracy<±1%;
Dimensions * (Width× Depth× Height)	1450 × 812 × 918 mm (without supporting feet)
Net Weight *	Approximately 220 kg (485 lb) (only includes structural frame)
Supply Voltage	200-240 V~, 50/60 Hz

*(Main Unit)



G400RS FluoXpert

Boost Your Multi-Omics Research

G400RS FluoXpert is a multifunctional instrument that integrates high-throughput sequencing technology and multiplex immunofluorescence technology (mIF). Given that the same equipment may be used for multiple tasks, it is suitable for a wide range of applications in tumor classifications, disease prognosis, tissue microenvironment analysis etc. With FluoXpert, you can obtain both cellular morphological information and molecular information from the exact same platform.

Features

High Resolution: Subcellular resolution 20× (360nm/pixel)

Robust Reproducibility: Efficient fluid exchange, mild elution reagents, tissue remains intact after multiple rounds of staining

Seamless Stitching: High performance and seamless stitching

Software

Visualization: Multi-channel overlay and navigation. Interactive tools for ROI selection

Quantification: Provide different cell segmentaion tools. Positive cell quantification with threshold selection

Phenotyping: Colocalization of multiple markers provide visualization of different cell types

Spatial analysis: Spatial neighbor analysis of different cell populations

Registration: 3D reconstruction of serial sections. Comparative analysis of IF and IHC images

Performance parameters

Technology	FluoXpert™ Multiplex Immunofluorescence	DNBSEQ™ Sequencing
Flow Cells	SS, SL, DL	FCS, FCL
Flow Cells/Run	Two Flow Cells/Run	Two Flow Cells/Run
Throughput*	20 Sections/Week (SS, SL), 40 Sections/Week (DL)	55-180 Gb (FCS), 75-720 Gb (FCL)
Time/Run	4-5 h (6-plex), 10.5-12.8 h (24-plex)	31 h (FCS, PE150), 50 h (FCL, PE150)
Sample Type	Compatible with FFPE and Frozen Sections	DNA/RNA
Applications	Tumor Microenvironment, Translational Research, Immune Checkpoint Blockade, Drug Screening	Fertility Testing, Pathogen Rapid Testing, Tumor Detection, Transcriptome, WGBS, WES, WGS, Individual Screen, Genome Sequencing of Animals and Plants, Microbial Sequencing
Software Suite	FluoXpert Program FluoXpert Vision Image Analysis Solution (Optional)	G400 Sequencing Program

* *Calcualted according to standard staining kit and standard sequencing kit.

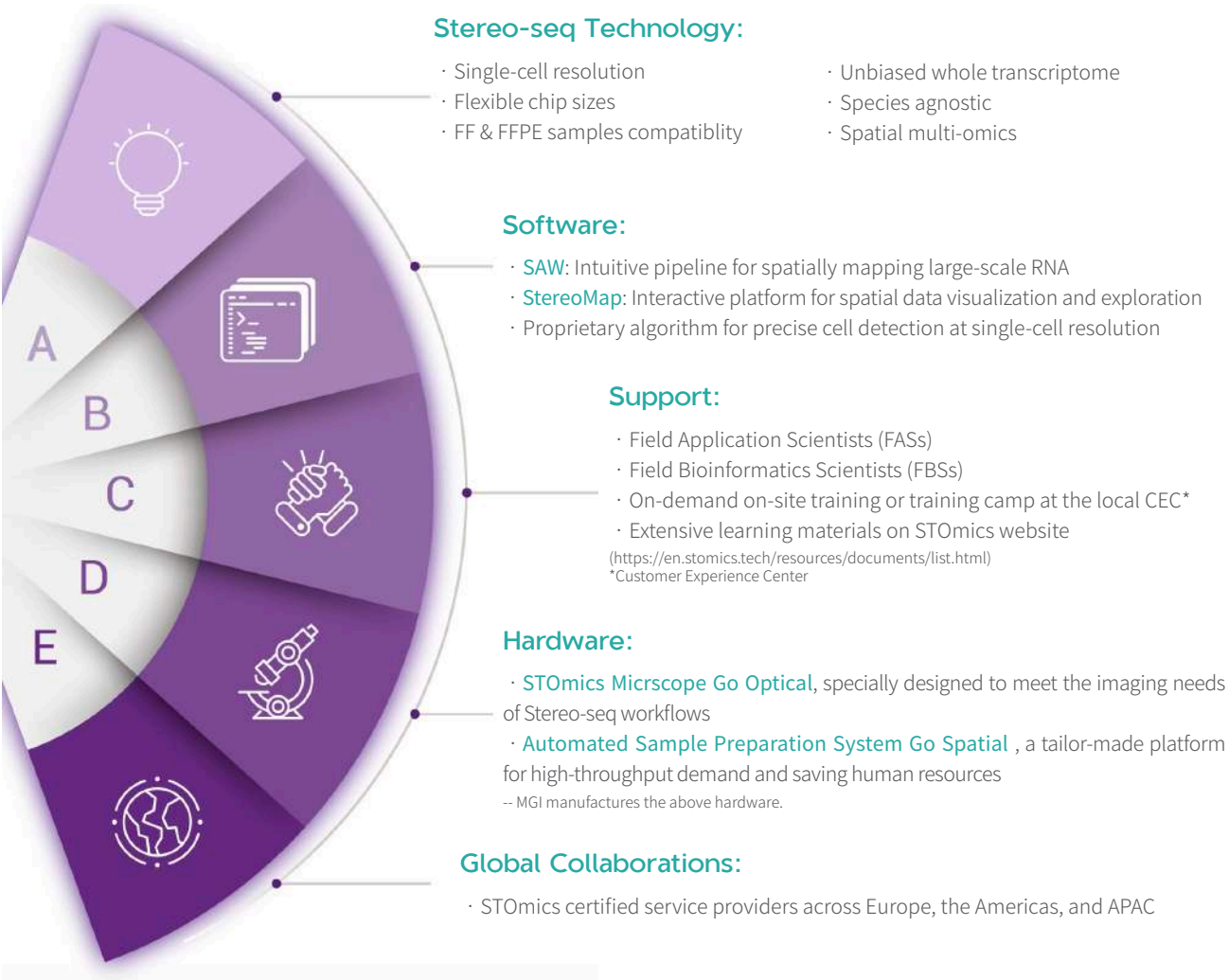
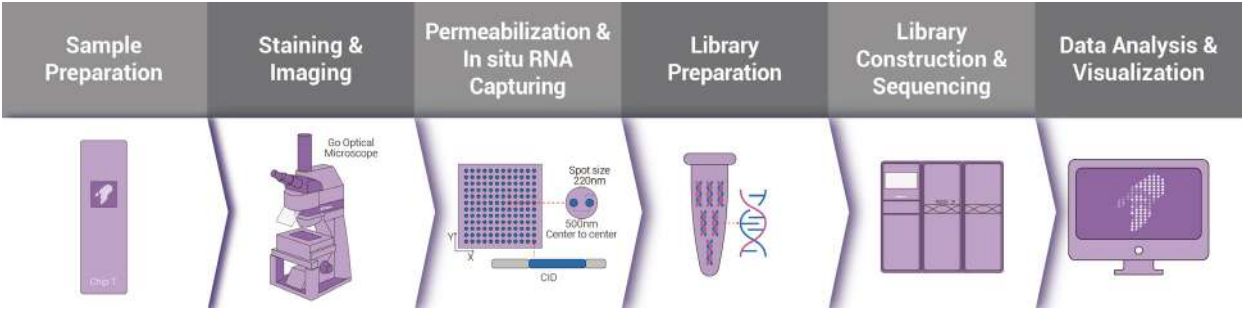
FluoXpert Staining Flow Cell

Solo Small (SS)	Solo Large (SL)	Dual Large (DL)
Suitable for small tissue samples such as percutaneous biopsy. Even faster staining speed.	Suitable for larger tissue samples such as tonsils, tumor samples. Larger scanning area for larger view.	Suitable for two tissue sections on one slide. Batch staining for less reagent used.
Imaging Area: 15mm×15mm	Imaging Area: 15mm×20mm	Imaging Area: 15mm×20mm×2

Stereo-seq

Complete STOmics Workflow Solution

Stereo-seq is built on a silicon-based chip patterned with a dense array of DNA Nanoball (DNB) , each marked with spatial coordinates(CID). A standard 1cm × 1cm Stereo-seq Chip contains approximately 400 million DNBs. Approximately 400 DNBs can capture the area of a single 10 μm cell, delivering nanometer-scale spatial resolution across extensive tissue sections. Upon interaction with a tissue section on a Stereo-seq Chip, cDNA is synthesized in situ from mRNA captured by the chip probes. Sequencing the cDNA with their spatial coordinates allows in silico reconstitution of the spatial transcriptomic profile of the tissue section, allowing easy visualization and analysis.



Stereo-seq

STOmics related reagent products

STOmics encompass kits, software, and hardware, providing powerful, robust, and user-friendly end-to-end spatial omics product solutions. STOmics enables a “tissue-to-data” experience through the in situ capture of the whole transcriptome at nanoscale resolution and a centimeter-sized field of view.

STOmics Solution	Stereo-seq Transcriptomics Solution	Stereo-seq OMNI Transcriptomics Solution	Stereo-seq OMNI Transcriptomics Solution for Large Chip Design (LCD)	Stereo-CITE Proteo-Transcriptomics Solution
Application Highlights	Unbiased spatial single-cell transcriptomics analysis, integration of tissue morphological data with high-resolution spatial transcriptome profiling, and simultaneous detection of RNA with multiplex IF (mIF) proteins	Enables true single-cell level spatial gene expression profiling on FFPE samples for various applications, including host-microorganism RNA co-detection	Unbiased spatial single-cell transcriptomics analysis for large sized tissue samples	Simultaneous profiling of unbiased whole transcriptome and high-plex proteins (100+)
Detection Scope	RNA	RNA	RNA	RNA + Protein
Capturing Method	Poly-A	Random Probe	Poly-A	Poly-A
Sample Type	Fresh Frozen (FF) with RIN value ≥ 4.0	Formalin-fixed Paraffin-embedded (FFPE) with DV200 ≥ 30%	Fresh Frozen (FF) with RIN value ≥ 6.0	Fresh Frozen (FF) with RIN value ≥ 4.0
Staining Method on the Same Section	ssDNA or H&E or immunofluorescence staining (mIF)	ssDNA or H&E	ssDNA or H&E	DAPI
Chip Size	0.5cm x 0.5cm, 1cm x 1cm	0.5cm x 0.5cm (coming soon), 1cm x 1cm	1cm x 2cm, 2cm x 2cm, 2cm x 3cm Other large-size chips can be customized (up to 13cm x 13cm)	1cm x 1cm
Compatible Species	Species agnostic	Species agnostic	Species agnostic	Human and mouse
Analysis Software	SAW & StereoMap			

Innovative Applications

Nucleic Acid Testing Total Solution

For a temporary shortage of testing facilities in an epidemic or the need to quickly increase the nucleic acid detection capacity, MGI’ s Automatic & Integrated Mobile Laboratory offers a total solution. The laboratory provides one-stop service with an entire set of equipment, reagents, and consumables for nucleic acid testing. It comes in multiple designs to suit various testing needs, including size and testing capacity. It is integrated, automated, flexible, and mobile all at the same time.

Variants

Automated & Integrated Container Laboratory FLP-C3000 / C6000

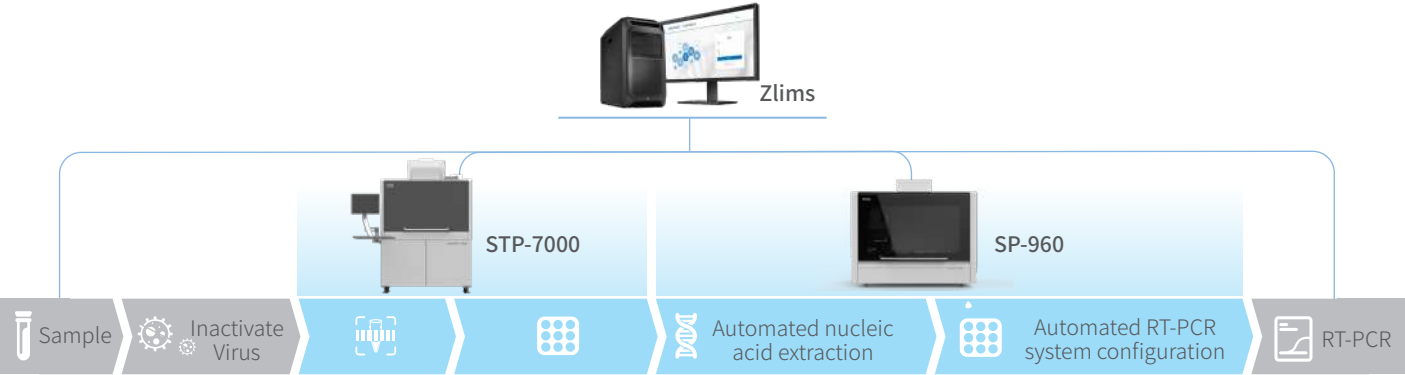
This version serves as a long-term, durable testing site, yet its modular structure also facilitates assembly, disassembly, and transportation. It comes in two variants to realize different throughputs. It is divided into three functional areas, each isolated to avoid contamination. The design is standardized, allowing for custom size and flexible combination of containers.

Fast Setup Modular Negative Pressure Laboratory MGIFLP-HW

This version offers ultra-high throughput and can be set up within 6 hours, including equipment. It is highly customizable and suitable for spacious areas such as stadiums or parks. It comes with three interconnected tents per set, along with antimicrobial and anti-aging PVDF membranes. Its PVC film and metallic frame also prepare it well for harsh environments.

	Variant // Suggested Size	Core Instruments
	FLP-C3000 / 12*2.45*2.89 m³	STP-7000 ×1、 SP-960 ×1
6,000 samples	FLP-C6000 / 13.5*2.45*2.89 m³	STP-7000 ×1、 SP-960 ×2
10,000 samples	FLP-C6000 / 16.5*4.9*2.89 m³	STP-7000 ×2、 SP-960 ×4
30,000 samples	FLP-HW / 25*25 m2 **	STP-7000 ×5、 SP-960 ×9

Workflow

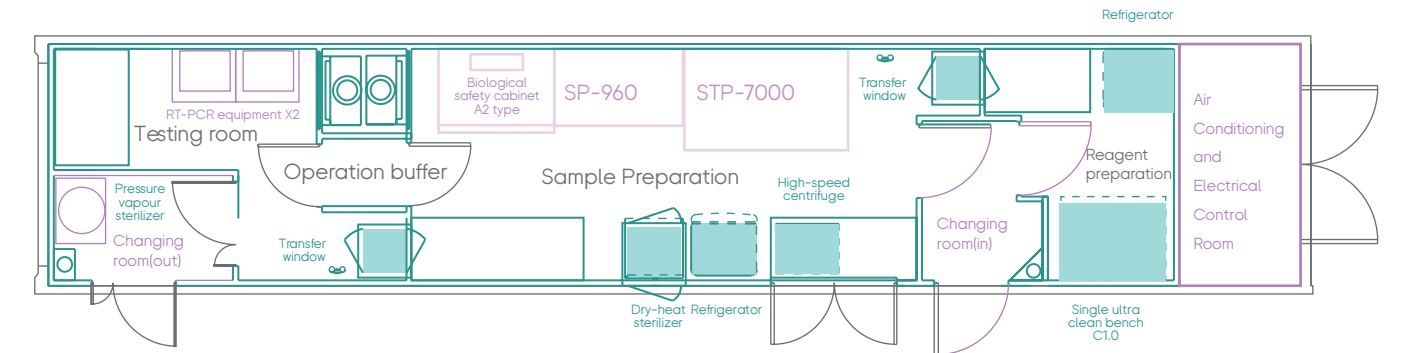


	 STP-7000	 SP-960		
Sample Collection	Sample Transfer	RNA Extraction	RT-PCR Testing	ZLIMS
A sample is obtained from the patient and the virus is inactivated manually.	STP-7000 automatically scans sample codes and transfers the samples to the 96-tube rack.	SP-960 performs RNA extraction on the samples and configures them for the RT-PCR system.	RT-PCR instrument checks each of the extracted RNA samples for the virus.	ZLIMS oversees the entire workflow. It records the instruments’ status, evaluates test results and generates reports.

Interior Design

Performance Parameters	Standards (Container)	Standards (Tent)
Cleanliness	Class 100,000	
Noise Level (dB)	≤ 60	
Temperature (°C)	18-26	
Relative Humidity	30-70%	
Ventilation Rate (times / hour)	≥ 12	15-20
Illuminance (lx)	Main room ≥ 200, auxiliary room ≥ 150	300
RPA* Pressure (Pa)	+5	+10
SPA Pressure (Pa)	-15	-10
TA Pressure (Pa)	-25	-20

Interior Design



Population Genomics Total Solution

MGI's total solution for population genomics integrates sample pretreatment, library preparation, high-throughput sequencing, genetic data management, and more. Each sequencing laboratory will be able to achieve an annual throughput of 50,000 to 1 million whole genome sequencing (WGS), with a fully automated process from sample to report.

Main Features

- Achievable for 50k 30× WGS per year per set
- Flexible customization for the full workflow from 50k to 1 million genomes sequenced annually
- Innovation-packed to maximize the efficiency of sequencing
- Automation from sample to report

Innovative Sequencing Technologies

Different from ordinary sequencing slide and closed reaction systems used in most platforms, T20×2RS uses dip-immersion biochemistry and open systems to achieve the best balance among sequencing read length, throughput, data quality and cost.



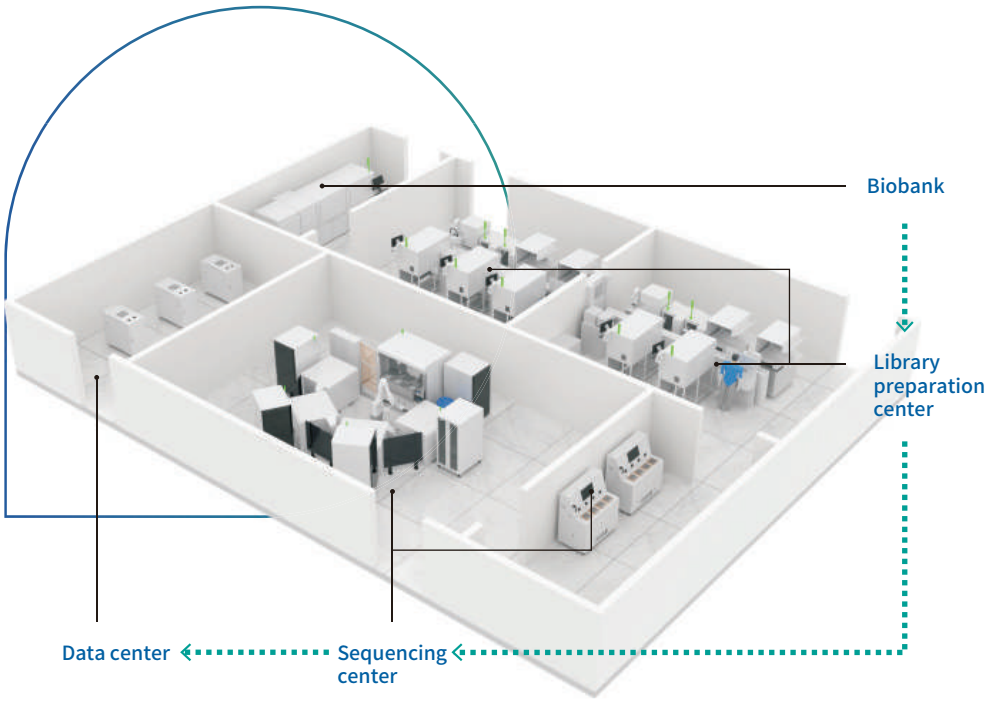
The dip-immersion biochemistry, which ensures more uniform biochemical reaction of sequencing slide with larger size, as well as significantly saves the cost of reagents.



Sequencing slide, DNB loading density is up to 4 million/mm2, and one slide can load 70 Gb DNB spots.

3D Layout of Sequencing Laboratory Total Solution

The sequencing laboratory can be customized with an annual output of ≥ 50,000 WGS.



Workflow

Original sample	Total Solution - Basic	Total Solution - Advanced
Automated Sample Pretreatment 1	SP-960, a high-throughput automated workstation, can easily complete 192 nucleic acid extraction per day, which will be used in library construction process.	SP-NE384, a high-throughput automated nucleic acid extractor, can complete 384 nucleic acid extraction in one run.
Nucleic acid Automated Library Production Line 2	SP-960 and SP-Smart 8, automated sample preparation systems, are designed for fully automation of high-throughput sequencing library construction process. Three sets of SP-960 and two sets of SP-Smart 8 are capable to realize annual preparation of 50,000 samples.	GLab-L, an automated library preparation production line, integrates different MGI and third-party instruments with robot. It adopts the concept of workstation assembly line, to accomplish automated sequencing library preparation with the capability of 300,000~500,000 samples annually.
Sequencing libraries High Throughput Sequencing 3	One T20×2RS can produce 50,000 WGS* per year.	More T20×2RS sequencing systems can be deployed for >50,000 WGS sequencing per year.
Sequencing raw data Automated Data Processing and LIMS System 4	ZTRON: a buddy to high-throughput sequencers, is applied to automatic bioinformatics analysis, storage and governance of massive sequencing data. It also contains a software system for data management in the whole cycle, from biosample management, laboratory production, bioinformatics analysis to data governance. Network Computing node Management node Storage node Hardware System ZTRON software system Primary analysis Software System ZTRON architecture - Basic	Scalability 1. Storage upgradable to 1PB, support ≥ 100,000 WGS sequencing; 2. Three-level data analysis: Write FQ, alignment and variant detection, third-party analysis and application; 3. ZLIMS could be upgraded to ZLIMS Elite, to support larger sequencing center. Network Computing node Management node Storage node Hardware System ZTRON software system Primary analysis Secondary analysis Tertiary analysis Optional Software System ZTRON architecture - Advanced
Report		

* Calculation is based on human WGS sequenced at 30× depth.

MGI Public Health Solutions

MGI's Public Health Solutions encompass a diverse array of applications, including metagenomics sequencing, whole-genome sequencing (WGS) for isolated bacterial cultures, targeted sequencing for various pathogens such as SARS-CoV-2, Flu A and B, Mycobacterium tuberculosis (MTB), monkeypox virus (MPXV), HIV-1, dengue virus (DEVN),chikungunya Virus (CHIKV) and respiratory syncytial virus (RSV). Additionally, our offerings include 16S rDNA sequencing for microbial community study. The Vector and Microorganism Identification (VMI) product package utilizes metagenomic sequencing strategy, simultaneously detecting vector species and their carrying pathogen microorganisms. Furthermore, with our ATOplex multiplex PCR-based library preparation kit customized platform, customized target sequencing panels for other pathogens or microorganisms of interest can be designed.

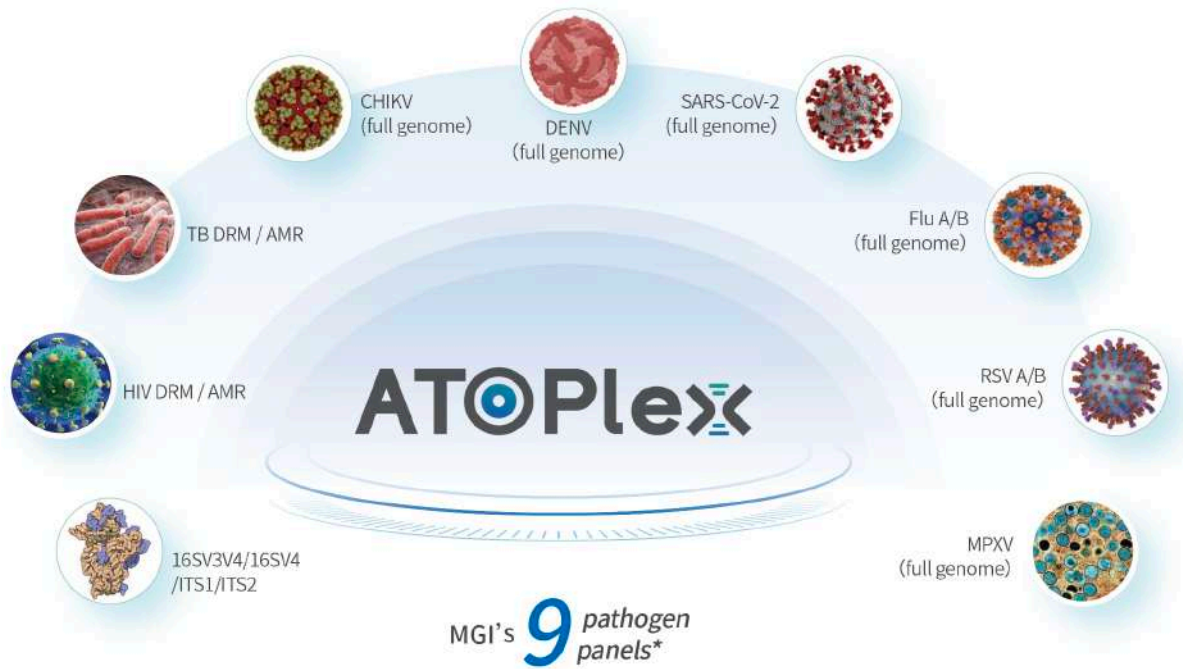
Technical route	Application	Intended use	Library preparation kits	Sequencing Platform	Bioinformatics Analysis software
Metagenomic sequencing	DNA/RNA metagenomic sequencing	Unknown pathogen detection	MGIEasy Fast FS Library Prep Set V2.0 MGIEasy Fast RNA Library Prep Set	DNBSEQ	MGAP
	Identification of vector species and pathogens carried (Meta)	Vector species and pathogen identification	MGIEasy Fast FS Library Prep Set V2.0 MGIEasy Fast RNA Library Prep Set	DNBSEQ	VMI
Whole-genome sequencing	Microbial whole genome sequencing	Genome assembly, typing and annotation, and traceability analysis	MGIEasy Fast FS Library Prep Set V2.0 MGIEasy DNA Fast Library Prep Set (for CycloneSEQ)	DNBSEQ CycloneSEQ	MGAP MGA
	MTB (WGS)	Genome assembly, drug resistance and virulence gene prediction	MGIEasy Fast FS Library Prep Set V2.0 MGIEasy DNA Fast Library Prep Set (for CycloneSEQ)	DNBSEQ CycloneSEQ	MTB- Explorer_ WGS
Targeted sequencing	MTB (ATOplex)	Drug resistance mutation detection, genotyping and identification	ATOplex MTB Library Preparation Set	DNBSEQ	MTB- Explorer_ ATOplex
	HIV-1 (ATOplex)	Drug resistance monitoring, genotyping and traceability	ATOplex HIV-1 Library Prep Set ATOplex HIV-1 FL Amplification Set MGIEasy DNA Fast Library Prep Set (for CycloneSEQ)	DNBSEQ CycloneSEQ	HIV- GenomePro
	SARS-CoV-2 (ATOplex)	Variant monitoring, genotyping, and traceability	ATOplex RNA Multiplex PCR-based Library Preparation Set V3.1 ATOplex RNA Multiplex PCR Amplification Set V3.1 MGIEasy DNA Fast Library Prep Set (for CycloneSEQ)	DNBSEQ CycloneSEQ	MGI metargetCOVID ATOplex MMRS
	Influenza A/B (ATOplex)	Variant monitoring, genotyping, and traceability	MGIEasy Respiratory Microorganisms Genome Library Preparation Set	DNBSEQ CycloneSEQ	MGI FluTrack
	MPXV (ATOplex)	Variant monitoring, genotyping, and traceability	ATOplex MPXV Library Prep Set ATOplex MPXV Amplification Set MGIEasy DNA Fast Library Prep Set (for CycloneSEQ)	DNBSEQ CycloneSEQ	MGI MPXV ATOplex MMRS
	DENV (ATOplex)	Variant monitoring, genotyping, and traceability	ATOplex DENV1-4 Library Prep Set ATOplex DENV1-4 Amplification Set MGIEasy DNA Fast Library Prep Set (for CycloneSEQ)	DNBSEQ CycloneSEQ	ATOplex MMRS
	CHIKV (ATOplex)	Variant monitoring, genotyping, and traceability	ATOplex Fast CHIKV Full-length Library Prep Set	DNBSEQ CycloneSEQ	ATOplex MMRS
	RSV (ATOplex)	Variant monitoring, genotyping, and traceability	ATOplex Fast RSV A/B Library Prep Set	DNBSEQ CycloneSEQ	ATOplex MMRS
	16SV3V4/16SV4/ITS1/ITS2 (ATOplex)	Microbial community research	ATOplex 16SV3V4/16SV4/ITS1/ITS2 rDNA Library Prep Set	DNBSEQ	MetaSIS

Metagenomic sequencing
Suitable for monitoring infection with unknown /mixed pathogens.

Targeted sequencing
Suitable for routine, rapid monitoring of known pathogens.

Whole-genome sequencing
Suitable for comprehensive genome analysis of potential pathogens to obtain more accurate and complete genetic maps

In the field of public health, MGI is committed to tailoring complete solutions from sample storage to reporting for different scenariosso any lab, even those new to sequencing, can start easily.



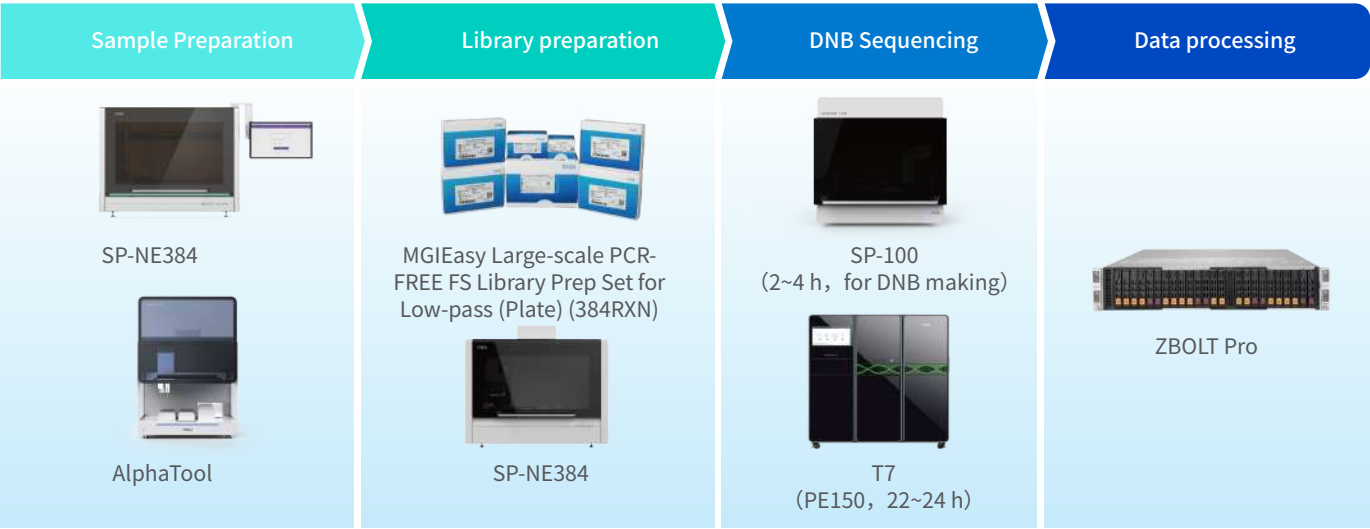
*If none of the ready-to-use panels fit your project, ATOplex custom platform (ATOplex.mgi-tech.com) can let you design one that does.

Agricultural Breeding Total Solution

MGI has established an international platform to support farmers, breeders, and researchers in identifying genetic loci linked to desirable traits. Utilizing sequencing-based technologies, MGI provides flexible and attractive solutions that facilitate the acceleration of research, breeding, and cultivation programs.

Molecular breeding by Low-pass WGS

The AgriHigh Low-pass Whole Genome Sequencing (WGS) Package is designed for agricultural breeding applications using DNBSEQ™ technology. This package provides an efficient and comprehensive solution tailored for low-pass WGS, offering flexibility, scalability, and adaptability to meet various operational demands. It is a versatile, efficient, and scalable solution for agricultural breeding. Leveraging DNBSEQ™ technology, it provides a comprehensive end-to-end workflow that can adapt to various operational needs, from small labs to large factories. Its flexible and automated capabilities ensure it can handle both off-season and peak season demands, making it an ideal choice for diverse agricultural breeding applications.

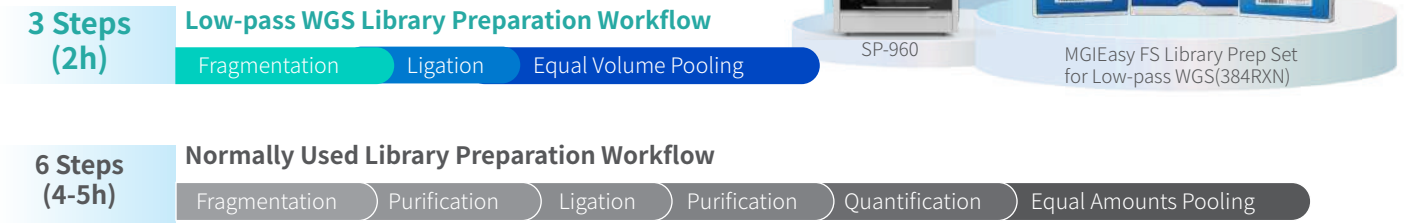


Prepacked Library Preparation

AgriHigh Low-pass WGS Package provides a revolutionary library preparation method based on the DNBSEQ™ platform. Brand-new 3-step library preparation without purification, combined with OneStep DNB Making, offering an ultra-simple and fast library preparation. The new plate-version reagent kit is friendly to automation.

Simplified 3-Step Library Preparation

384 Samples:



T7 can generate 1-7 Tb of high-quality data per day with DNBSEQ™ technology, it can unlock insights for molecular breeding by generating 1536 pigs sequencing data (~1.5× WGS) in 22~24 h. With T7, AgriHigh Low-pass WGS Package recommends low-pass whole genome sequencing application in livestock and poultry molecular breeding. Average 0.5×~2× depth WGS is provided.

Features

Brand-new 3+1

Brand-new 3-step library preparation without purification, combined with OneStep DNB Making, offering an ultra-simple and fast library preparation.

Flexible automation combination

Including sample preparation, library preparation, and pre-sequencing. Both module-style order and end-to-end workflow installation are welcomed.

100 K~1000K samples per year

A customizable solution is provided based on your request throughput.

Point-and-shoot operation

MegaBOLT: 198 samples within 24 h,
ZBOLT Pro: 1536 samples within 24 h.

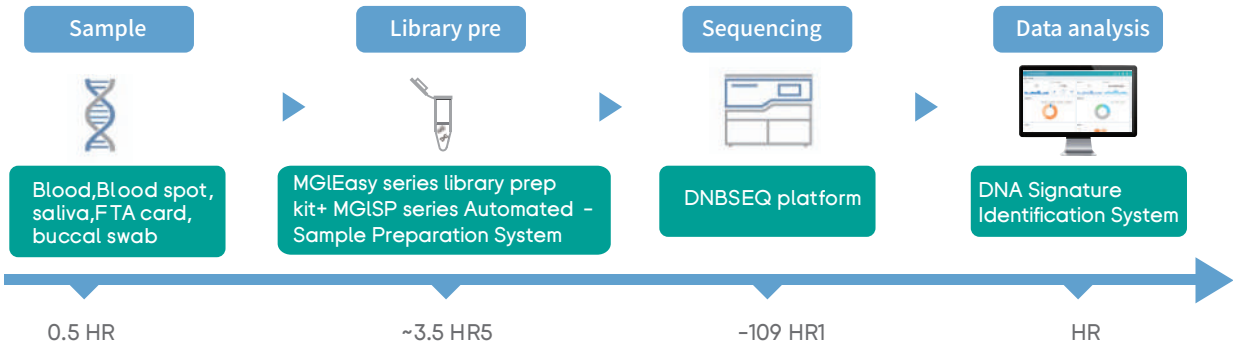
Performance parameters

Specification	AgriHigh Low-pass WGS Package (Standard Version)	AgriHigh Low-pass WGS Package (Basic Version)
Sample requirements	Tissue, Blood	Tissue, Blood
Nucleic acid	gDNA	gDNA
gDNA Input	200ng (260/230, 260/280>1.8)	200ng (260/230, 260/280>1.8)
Throughput	384-1,536 samples/day; 96,000-384,000 samples/year*	48-96 samples/day; 12,000-24,000 samples/year*
Sequencing platform	T7RS	G400RS
Data Analysis	ZBOLT Pro	MegaBOLT
Numbers of SNP marker	30,475,252	30,475,252
Numbers of InDel marker	4,123,565	4,123,565
Turn Around Time	4-6 Days	4-5 Days
Manpower	3-5	1-2

Package for forensic genetics

Providing a complete, efficient and advanced set of core tools from nucleic acid extraction, library preparation, high-throughput sequencing to analysis, which are widely used in individual identification, paternity testing, analysis of difficult samples and construction of related databases, and provide powerful tools to support the pursuit of justice.

MGI's Solution Workflow



Features

MGEasy Pa-SNPs Genotyping Kit / DNBelab-D4RS Pa-SNPs Library Prep Set

- Wide range of applications, amplifying 2010 SNPs in one tube.
- Easy to operate with a two-step PCR.
- Fast detection: from DNA to analysis results within 26h.
- High accuracy: detectable fetal content of 2% or above.
- Suitable for highly degraded samples: amplicon size of 60-90bp.

MGEasy Signature Identification Library Prep Kit

- 347 loci (STRs or SNPs) from 8 categories were included, covering the latest CODIS core loci and new loci, ranking NO.1 in loci number among all commercial kits
- The kit exhibits excellent performance in specificity, sensitivity, stability and repeatability
- A total solution is provided with the implementation of automated library preparation platform and automated data analyzing software.

Recommendation for Forensic Application of MGI High-throughput Sequencing Platform

Application	Marker	Recommended read length	Library prep kit	Automated machine	Sequencing platform
Individual identification DNA database	STR+SNP+mtDNA	SE400	MGEasy Signature Identification Library Prep Kit	SP-960 & SP-100	G400RS G99RS E25
Individual identification Sample QC	SNPs	SE50	MGEasy Signature Identification Library Prep Kit	SP-960/ SP-100	G400RS G50RS G99RS E25
Non-invasive prenatal paternity test Individual identification Mixture detection	SNPs	SE50	MGEasy Pa-SNPs Genotyping Kit / DNBelab-D4RS Pa-SNPs Library Prep Set	SP-960 D4	G400RS G50RS G99RS

High-throughput Sequencing Education Package

Stimulate students' interest in learning, provide teachers with tools for professional growth, enhance the quality of teaching and reputation of schools, and collectively promote education innovation and quality talent cultivation.

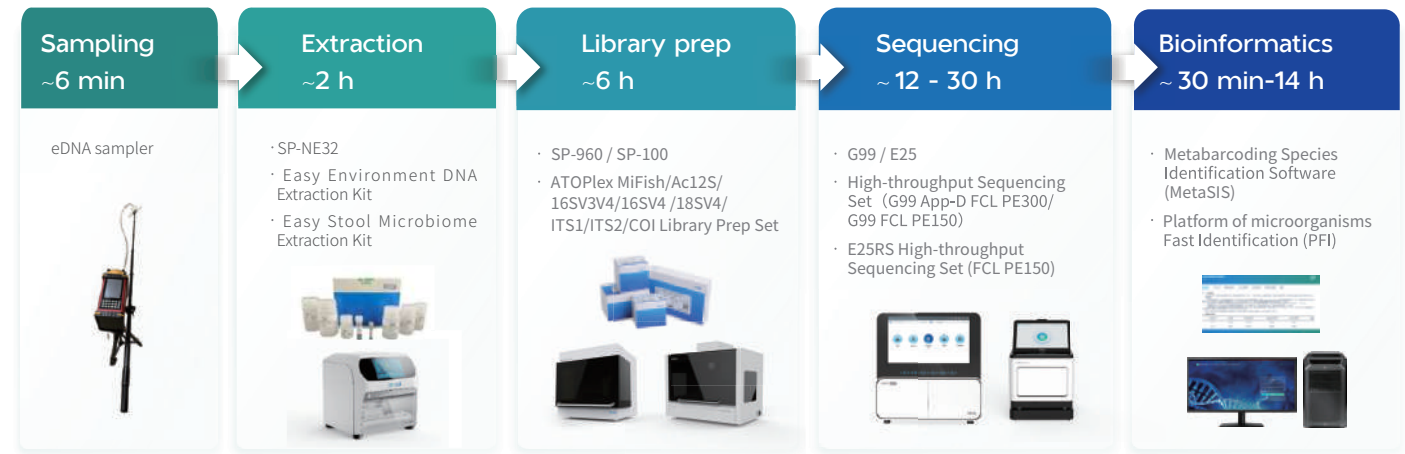
Workflow



Using MGI High-Throughput Sequencing Education Package, the course is a combination of wet and dry labs. Students will collect samples, complete the process from nucleic acid extraction, targeted library construction, and use the E25 sequencer and the corresponding analysis process for genetic testing and analysis. The package not only allowed students to understand the relationship between genotype and phenotype, but also mastered high-throughput sequencing technology and its application, while the course was permeated with experiential ethics education, increasing the interesting nature of the experimental classroom.

Environmental DNA Metabarcoding Sequencing Package

MGI Environmental DNA metabarcoding sequencing package is a combination of self-developed reagents for nucleic acid extraction, ATOPlex multiplex PCR library preparation, eDNA sampler, SP-960 automated sample preparation system, G99 and E25 sequencers, and MetaSIS analysis software. This comprehensive solution covers the entire process from sampling to reporting. It enables rapid and accurate analysis of the biological community structure in environmental sample, It provides a tool for ecological environmental monitoring and environmental scientific research.



Features

One-stop product solution

Integrated sampling, sample treatment, library preparation,sequencing, and analysis, a true one-stop product solution

Wide range of species covered

The monitored species cover bacteria, fungi,algae, plants, planktonic animals, benthic animals, and fish, meeting various application needs.

Automation friendly

Combined with automated nucleic acid extraction instruments, automated sample preparation systems and analysis software, to achieve automated sample preparation and data analysis, save labor.

Powerful analysis function

Self-developed software provides various analysis functions, such as OTU analysis, species composition analysis, alpha diversity analysis, beta diversity analysis, biomarker analysis, and more.

Panel	Applicable species types	Recommended read length	Recommended data per sample	Sequencer	Recommended sample number /FC
MiFish	fish	PE150	≥65K reads	G99 / E25	500/72
16S V4	bacteria				
Ac12S	fish				
16S V3V4	bacteria	PE300		G99 / E25	300
COI	benthic animals, zooplankton				
18S V4	algae, invertebrates				
ITS1	Fungus				
ITS2	Fungus				

Microbiome Metabarcoding Sequencing Package

MGI's Microbiome Metabarcoding Sequencing Package is based on self-developed nucleic acid extraction reagents, ATOPlex library preparation reagents, SP-960 automated sample preparation systems, G99 and E25 sequencers, and MetaSIS analysis software. It covers the entire process from sample processing to analytical reporting, enabling rapid and accurate analysis of biological community composition in environmental, human, industrial, and agricultural samples, providing a tool for microbiome research.

Features

Widely Application Scenarios

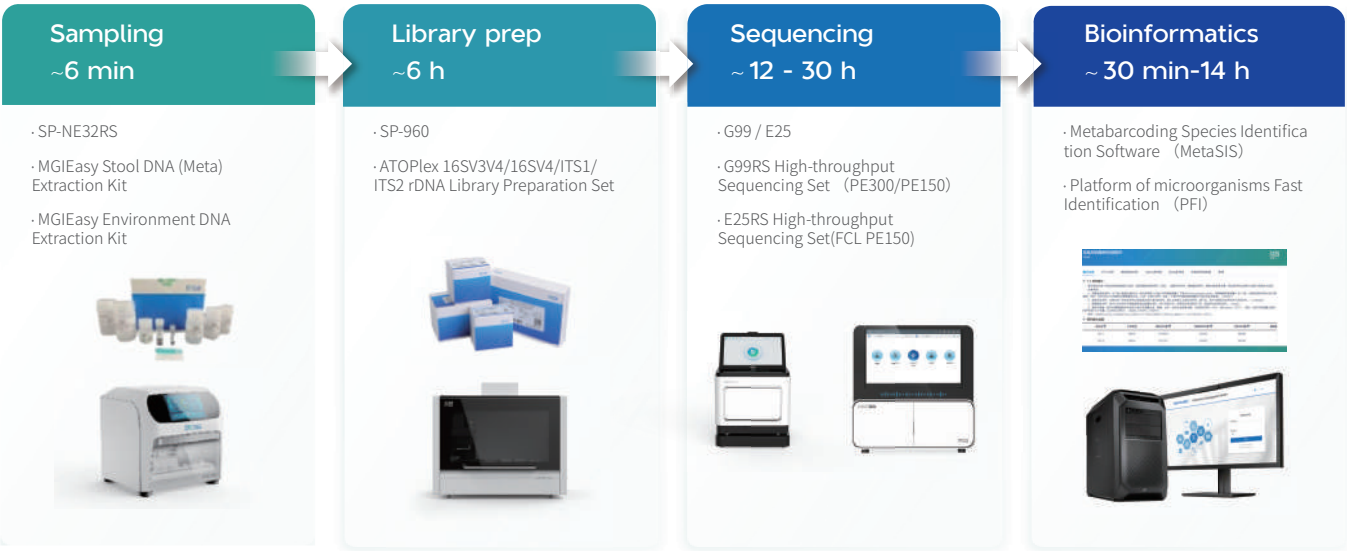
Designed based on the popular variable regions of rDNA, compatible with various sample types, fully meeting the needs of microbiome research in human,industrial, agricultural, and environmental scenarios;

One-stop Product Solution

Integrated nucleic acid extraction, library preparation, sequencing, and analysis products, meeting customer needs in one stop;

Powerful Analysis functions

Self-developed analysis software offers a wealth of analytical functions, such as OTU analysis, species composition analysis, Alpha diversity analysis, Beta diversity analysis, biomarker analysis, etc., and support for customized databases;



Recommended Sample Types	Feces, oral swabs, skin swabs, tongue coating swabs, saliva, rhizo-sphere soil, leaf surfaces, fermented grains, yogurt, sediment, etc.
Applicable Species	Bacteria, Fungi
Recommended Sample Input	DNA:10 ng
Recommended Sequencing Read Length	16SV3V4/ITS1/ITS2:PE300; 16SV4:PE150
Recommended Data Volume	≥65K reads per sample G99 PE150:500 Samples / FC
Recommended Maximum Sequencing Throughput	G99 PE300: 300 Samples / FC E25 PE150: 72 Samples / FC
Shortest Reporting Period	20.5 hrs

Wastewater-based microbial sequencing Package

MGI Wastewater-based microbial sequencing Package, based on self-developed reagents, instruments, and software, covers the entire workflow from sampling to data analysis. It rapidly and accurately identifies pathogens in wastewater, offering valuable epidemiological information. Supports for infectious disease surveillance, outbreak investigation, and disease control effectiveness evaluation, providing tools for public health policy development, implementation, and assessment

Features

All-in-One Solution

Integrates sampling, nucleic acid extraction, library preparation, high-throughput sequencing, and data analysis, offering a true end-to-end solution.

Automation friendly

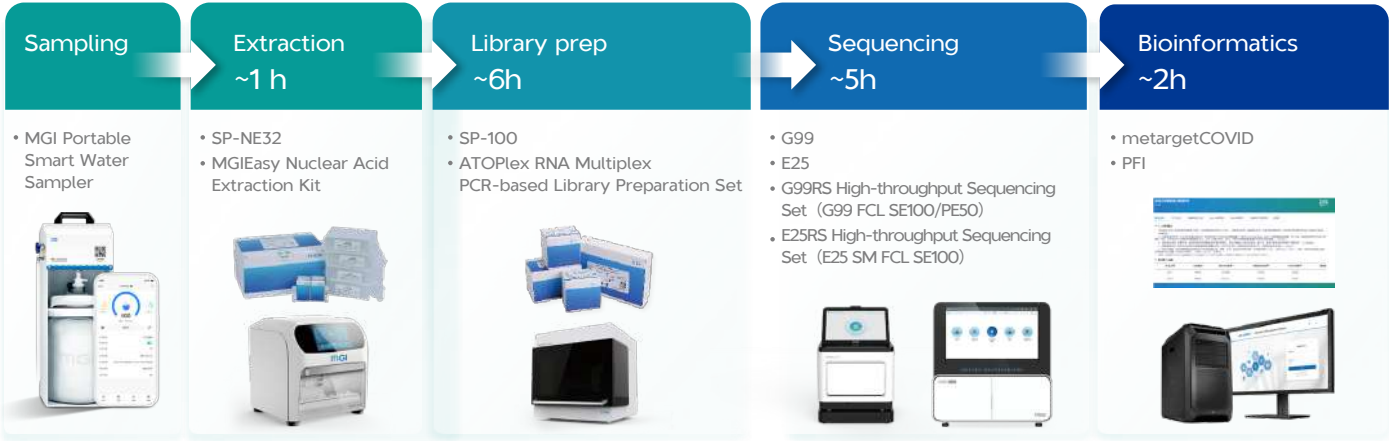
Equipped with portable intelligent water samplers, automated library preparation systems, and analysis software, it enables automated sampling, library preparation, and data analysis, minimizing manual intervention.

Comprehensive Antimicrobial Resistance Database

Features a structured ARGs-OAP database to analyze resistance genes from metagenomic sequencing data, enabling standardized analysis of ARG types and quantities in samples.

Diverse Applications

Offers both targeted and metagenomic sequencing solutions to meet the needs of identifying known and emerging unknown infectious pathogens.



	Wastewater-based COVID-19 Targeted Sequencing Package	Wastewater-based Metagenomic Sequencing Package
Sample Type	Wastewatersamples collected from wastewater treatment plants, medical institutions, aircraft, livestock farms, and agriculturamarkets	
Recommended Sequencing Platform	G99	G99/T7
Recommended Sequencing Read Length	SE100	PE150
Recommended Data Volume	5 M Reads	34 M Reads
Theoretical Sample Throughput	16 Samples/FC	2 Samples / G99 FC; 170 Samples/T7 FC
Recommended Software	metargetCOVID	PFI

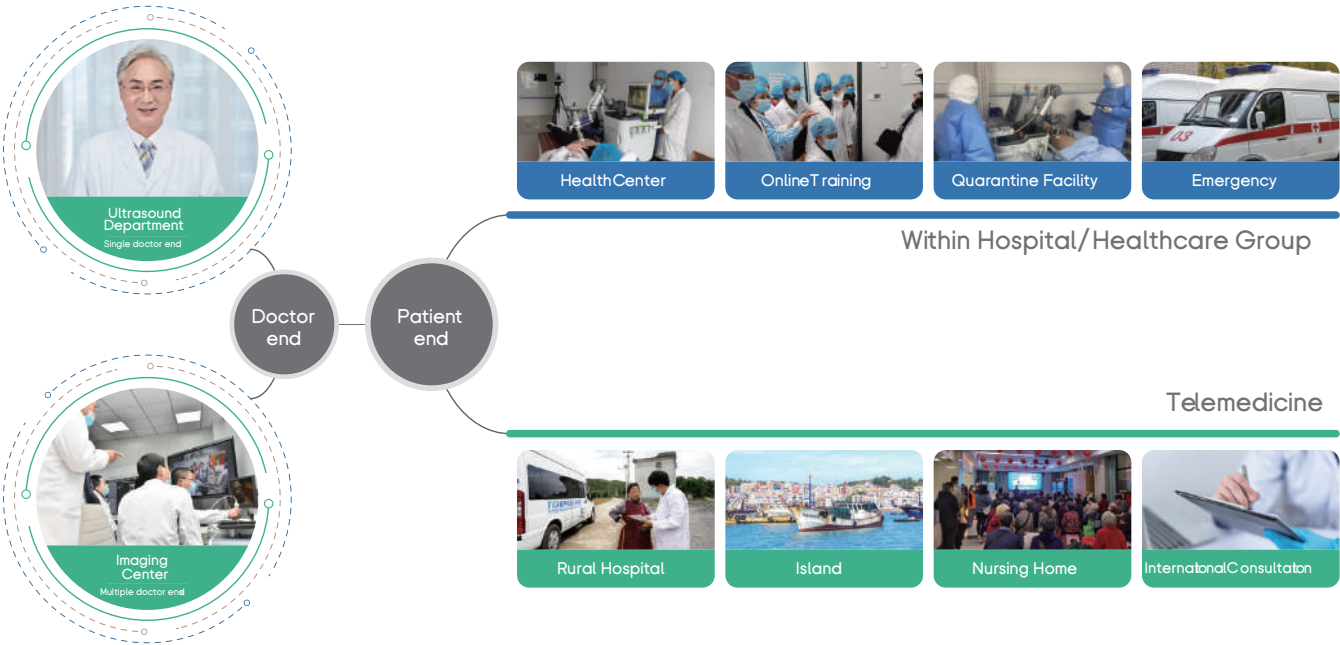
Ultrasound Platform

US-R3

US-R3, developed independently by MGI, solves the problem of shortage of ultrasound doctors in rural areas and heavy workload for current doctors. It integrates robotics, teleoperation, and ultrasound imaging technology. Breaking through the limitations of traditional ultrasound scanning method, bridging the gap between time and space, and improving the uneven distribution of medical resources, it provides the best medical service to all. It also has officially obtained CE and NMPA certification.

Features

- Remote scanning and real-time diagnoses
- Built-in intelligent workstation
- Multiple safety protection
- Integrated design



EF6-CL
Intelligent Handheld
Ultrasound

The handheld wireless color doppler ultrasound diagnostic system (EF6-CL) is a lightweight, portable, and powerful ultrasound device. Featuring a dual-probe design (convex + linear array), it meets diverse examination needs for abdominal organs, superficial tissues, and peripheral vasculature. Ideal for diverse mobile scenarios, both in-hospital and field setting. It provides an efficient and convenient solution for medical diagnostics.



The device is optimized for superficial tissue imaging, suitable for detailed examinations of blood vessels, muscles, thyroid, and other areas.

L-Linear Probe



C-Convex Probe

Offers greater penetration, ideal for comprehensive scanning of deep tissues such as the abdomen and obstetrics.

Compact Size, Expansive Vision

- C-Convex Array Probe + L-Linear Array Probe
- Supports multiple examinations with one-touch probe switching for rapid adaptation to diverse clinical needs.

Probe Design	Dual probes in one (Convex + Linear)	Waterproof Rating	Fully enclosed design, IPX7 waterproof level
Device Weight	275g	Frequency Range	Convex: 2-5 MHz Linear: 4-13 MHz
Imaging Modes	Dual probes in one (Convex + Linear)	Charging Method	Wireless fast charging, 6W, 1 hour to complete 20% to 80% charge
Battery Capacity	B/M/C/PW/PDI	Battery Life	Continuous scanning time ≥ 2.5 hours (B mode)

Sample Storage Platform

CLab-LT
Sample Storage Platform

Ultra-low temperature automated Biorepository MGICLab-LT series, as a highly customized -80 °C lift-up automatic sample storage equipment, can realize large-scale, safe and stable preservation of blood, tissue, nucleic acid, protein, microorganism and other sample resources.



Function

- Robotic vertical sample storage rooms at an ultra-low temperature of -80°C
- Scientific design, stable operation
- Multiple backups to ensure safety
- Energy-saving & efficiency-enhancing
- Intelligent management, efficient access

Product specifications

Product Model	Cabinet Area (L×D×H)	Site Area (m²)	0.5mL SBS (96-well plates)	0.75mL SBS (96-well plates)	1mL SBS (96-well plates)	2mL SBS (48-well plates)	5mL SBS (24-well plates)
CLab-LT 50	6688 x 4000 x 2900	52.34	500,000	500,000	360,000	180,000	90,000
CLab-LT 100a	10262 x 4000 x 2900	72.45	1,000,000	1,000,000	720,000	360,000	180,000
CLab-LT 100b	8843 x 4000 x 3520	67.00	1,000,000	1,000,000	760,000	380,000	190,000
CLab-LT 200	13377 x 4000 x 3520	97.26	2,000,000	2,000,000	1,520,000	760,000	380,000
CLab-LT 300	10000 x 5500 x 5020	87.77	3,010,000	3,010,000	2,260,000	1,130,000	560,000

CLab-LN55K
Sample Storage Platform

The CLab-LN55K automated liquid nitrogen storage system is a storage-type solution that offers temperature stability, large capacity, and compatibility with various sample consumables. It effectively stores samples and meets the deep low-temperature storage requirements of various applications in all fields.



Function

- Lower than -180°C stable storage temperature, sample capacity of 55,000 tubes, able to accommodate SBS standard format 0.5ml, 0.75ml,1ml, 2ml, and 5ml cryobox consumables
- Full-scope safeguards to protect samples from human or non-human damage
- Intelligent system with user-friendly human-machine interaction design
- Standard SBS cryobox full-board storage and retrieval, allowing continuous entry and exit

Product specifications

Categorization	Name	Performance indicators
Product Attributes	Storage Capacity	0.75ml SBS
		55,000 Tubes
	Storage Temperature	Internal Tank Temperature ≤ -180° C
Product Performance	Static Liquid Nitrogen Consumption	≤ 15L/D
	In-Out Units	Achieve Whole-Box Access of Cryoboxes in SBS Standard Format
	Remote Alarms	Send Real-time Tank Temperature and Liquid Level Information via Email, SMS,or Phone
	Liquid Nitrogen Usage Time	Duration Between Each Refill ≥ 12D
	Storage Capacity Management	Real-time Display of Capacity and Space, Automatic Inventory of Cryobox Storage Status
Equipment Installation	Software Data Integration	Can be Integrated with LIMS/HIS and Other Third-party Systems
	Voltage/Frequency	220V/50Hz
	Weight	Empty Weight of Liquid Nitrogen Tank not exceeding 900kg,Loaded Weight not exceeding 1200kg
	Equipment Dimensions (Width× Depth× Height)	1500× 2000× 2700 mm



CLab-LN55K Pro Sample Storage Platform

CLab-LN55K PRO automated liquid nitrogen storage system has the features of single-tube retrieval, temperature stability, large-capacity storage, and consumable multi-specification compatibility, ensuring efficient and stable sample storage, and meeting the deep low-temperature storage requirements of various fields in all aspects.

Function

- Through the hot gas bypass function, only ultra-low temperature liquid nitrogen can be injected into the tank, ensuring the temperature stability inside the tank.
- One-key automated sample access, supporting multiple sampling operation scenarios such as whole-plate/tube-picking.
- Full-process deep low-temperature protection, ensuring the sample quality is not affected by repeated freezing and thawing, guaranteeing the sample safety.
- Integrated sample management system, realizing comprehensive management of sample information such as temperature

Product specifications

Classification	Item	Performance indicators
Key Specifications	Storage Consumables	Compatible with SBS standard format 0.5ml,0.75ml,1ml, 2ml, 5ml cryogenic tubes in cryogenic box
	Storage Capacity	0.5 mL ≥ 55K tubes, 2 mL ≥ 22K tubes
Key Components	Storage Temperature	he top of the tank is< -180° C,and the tube-picking area is ≤ -150° C
	Liquid Nitrogen Consumption	One-time injection usage time ≥ 12Days, Static liquid nitrogen consumption 15L/Day
	In-out Warehouse Unit	Can perform whole-box or single-tube sample in-out warehouse tasks
	Remote Alarm System	Has remote communication function,sends real-time device status via WeChat, SMS
	Fragment Sorting	The system can sort the scattered sample tubes according to the sample information and a certain logic
	Sample Protection	Has timeout return function,time can be set.
	Monitoring System	The system is equipped with monitoring cameras, can see the internal environment in 360°
	Cryogenic Transfer	Equipped with cryogenic transfer barrels, can maintain -150° C for ≥ 4hours,sample access are in -150° C environment.
	Voltage/Frequency	220V/50Hz
Equipment Installation	Installation Conditions	Minimum door width ≥ 1.4 meters
	Device Height	Device height<2.7m
	Liquid Nitrogen Replenishment	Equipped with standard interface for liquid nitrogen tower pipeline docking



CLab-Capper

CLab-Capper series is an automatic device specifically designed for SBS format cryogenic storage tubes. Compact and lightweight, it seamlessly fits into fully automated workflows. With flexible adaptability. Simple interface allows for one-touch operations, making cap rotation effortless. Each cap opening or closing takes only 20 seconds, providing laboratory technicians with a more efficient working experience.

Function

One-touch Operation

Full SBS cryogenic tube rack can be easily manipulated with one-touch operation, offering high levels of automation and user convenience.

Flexible Adaptation

Can accept customized adaptation, accommodate various types of screw caps and different configurations of SBS cryogenic racks.

Precise Control

Precision control of the cap opening/closing action is achieved through multi-axis coordination, ensuring an effective sealing while preserving the integrity of the tube.

Program Control

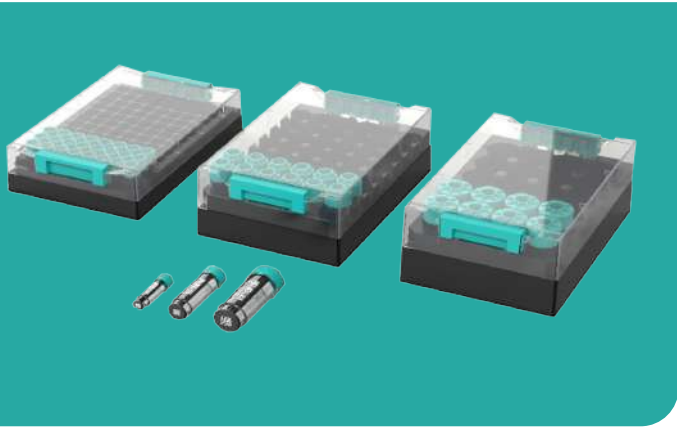
The system can be integrated via external communication ports, enabling effortless unmanned operation

Product specifications

Dimensions	295mm(W)x450mm(D)x445mm(H)	
Power	Voltage	100 -240V
	Frequency	50/60Hz
	Rated Power	350W
Operating Conditions	Temperature	10° C-40° C
	Humidity	20% RH - 80% RH (without condensation)
	Working Air Pressure	80 kPa-106 kPa
Application	SBS 96/48 wells racks	
Connector	RJ45 Ethernet Port	
Safety	Equipped with an emergency stop switch, processes can also be terminated through control software	
Efficiency	The cap opening period for the full SBS rack is s20 seconds	

SBS Cryovials

This product is suitable for various scenarios. It can be used in fields such as biological sample storage, clinical testing, sample testing, species preservation, compound screening and etc. The bottom QR code, tube wall barcode, and digital clear code are combined into one, enabling tracking of both vials and racks. Dual tracking system enables automated high-throughput sample processing at a large-scale.



Function

Strictly Selected Tube Materials

Made of USP Class VI PP material, which can withstand a temperature range of -196°C to 121°C .

Exquisitely Designed Structure

Featured an external thread tube design without silicone ring, effectively avoiding leakage caused by silicone aging and reducing the risk of sample contamination.

Stable and Reliable Quality

Produced on an automated production line in a GMP 100,000 class clean workshop to ensure the product is free of DNA enzymes, RNA enzymes, and pyrogens.

Specs	Triple-coded SBS cryovials		
	0.5ml	1ml	1.9ml
Thread	External thread		
Vial material	PP		
Heigh (mm)	29.6	49.3	43.1
Rack barcode	Slide + bottom		
Operating temperature	-196°C to 121°C		
Sterllization	Sterile		
Rack Configuration	8 × 12	8 × 12	6 × 8

Gencase - 2

This product is a portable sequencer that utilize its proprietary SNP Anchor Sequencing technology, enabling the rapid genotyping of a small number of specific SNPs under routine field conditions. It uses polymerases to amplify target nucleic acids in real time under constant temperature. During the amplification process, fluorescence signals are detected to precisely identify the SNP information. Based on the detected genotype, users can accurately determine the corresponding biological characteristics.



Function

Ultra-accuracy

≥99.3%

Super convenience

two-minute operation

Super fast

15-20 minutes

- Sample collection completed in 1 minute
- Sample processing completed in 1 minute
- Unlock the results in 15-20 minutes
- The first "on-site" experience product for genetic technology. With it, experience genetic technology for the first time. With it, learn about healthy living from a genetic perspective.

	SNP Anchor Sequencing	Whole Genome Sequencing	Traditional PCR
Accuracy	99.30%	99.90%	99.80%
Detection time	15-20 min	1-3 Day	2 hours
Results delivery cycle	20 min	5-10 Day	2h-1 Day
Cost	Low	High	Low
Operator requirements	No professional training required	professional training required	professional training required
Environmental requirements	No professional laboratory required	Professional laboratory required	Professional laboratory required

Type	GenCase-2
Power Source	Type-C 5V, ≥ 2A
Maximum Power	10W
Size	94mm(diameter)×52mm(height)
Net Weight	246g±10g
Instrument Reaction Wells	Dual wells detection
Fluorescence Channels	FAM or ROX fluorescence
Operating Temperature and Humidity	10-30°C ; 20-80%
Overall Performance	Lifespan ≤ 3 years
	Results display: Result indicator or WeChat applet
	Detection time ≤ 20 min

Extended Solutions

In collaboration with selected industry partners, we offer third-party products that have undergone rigorous compatibility validation. These products are designed to work effectively with MGI core platforms, enabling more comprehensive and flexible laboratory solutions to better address specific research and technical requirement.

Consumables Laboratory supplies

High-quality reagents and dedicated consumables form the foundation for precise, reproducible experiments. This product portfolio is designed to deliver a complete consumables solution that seamlessly integrates with MGI instrumentation platforms, covering the entire workflow from sample collection and nucleic acid extraction to reaction and detection.

Core Products

1. Pipettes & Pipette Tips: Pipettes from 0.1 μ L to 5 mL (single-channel, 8/12 channel) ; Pipette tips (manual & automated)



MicroPette Plus



HiPette



Pipette Tips

2. Reagent Reservoirs: 4, 8, 12, 96, and 384 channels



Reagent Reservoir

3. Magnetic Racks: 6, 24, 32, and 96-well



Magnetic Rack

4. Centrifuge Tubes: 0.5 mL, 1.5mL, 2.0mL, 5.0mL, 10.0mL, 15.0mL,50 mL (conical bottom, round bottom, screw cap, snap cap, and self-standing)



Centrifuge Tubes

5. Cryogenic Vials: 0.5 mL, 1.0 mL, 1.5mL, 2.0mL, 5.0mL



Cryogenic vials

6. cfDNA Preservation Tubes: 5mL , 10mL



cfDNA Preservation Tubes

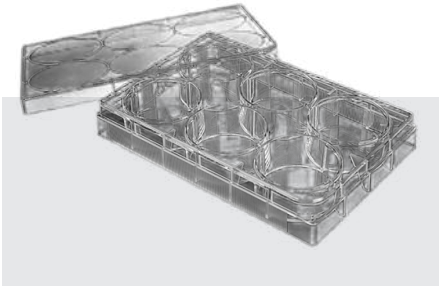
7. Cell Culture Consumables



Cell Culture Treated Dishes



Cell Culture Treated Flasks



Cell Culture Well Plates

8. PCR & Chemiluminescence Reaction Consumables

· **PCR Tubes & Plates:** 0.2mL tubes, 8-tube strips, 96-/384-well plates with clear/white frames and full/semi/no-skirt



PCR Single Tube

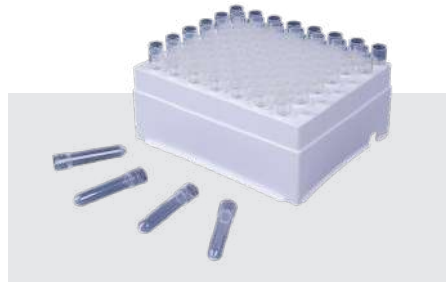


8-Strip PCR tubes



PCR Plates

· **Chemiluminescence Reaction Tube:** 33mm/44mm



Chemiluminescence Reaction Tube

9. Detection & High-Throughput Processing Consumables

· **Immuno plates:** non-removable/ removable, high-binding, black, U-bottom/ V-bottom



Immuno Plates

· **Deep-Well Plates:** 1.2mL, 2.2mL, 10mL 96-well deep-well plates (square/round wells, U-bottom/V-bottom)well



Deep Well Plates

· **Tip combs:** 96-well or 24-well



Tip combs

10. Nucleic Acid Extraction Kits

· **Plant Nucleic Acid Extraction Kits :**

FastClean Plant Genomic DNA Kit – 50 preps / 200 preps

Magbead Plant DNA Kit – 96 preps

OminiPlant RNA Kit (DNase I) – 50 preps

Magbead Plant RNA Kit – 96 preps

· **High Molecular Weight (HMW) DNA Extraction Kit :**

Monarch HMW DNA Extraction Kit for Cells & Blood – 10 preps / 50 preps

· **FFPE Sample Nucleic Acid Extraction Kits :**

FFPE DNA/RNA Kit – 50 preps/box

· **Single Cell Whole Genome Amplification Kit :**

Single Cell WGA Kit – 24 reactions/ 96 reactions



Nucleic Acid Extraction Kits

Sample Preparation

Laboratory supplies

High-quality reagents and dedicated consumables form the foundation for precise, reproducible experiments. This product portfolio is designed to deliver a complete consumables solution that seamlessly integrates with MGI instrumentation platforms, covering the entire workflow from sample collection and nucleic acid extraction to reaction and detection.

Equipment

Sample preparation is the critical first step to obtaining reliable results in molecular biology, cell biology, and omics research. This portfolio includes core instruments designed for rapid micro-sample handling, precise temperature-controlled incubation, and efficient disruption of complex samples. It provides stable and efficient solutions for workflows such as nucleic acid extraction, protein preparation, and NGS library construction.

1. Centrifuge Series:

· Palm Micro Centrifuges (TG10K,D1008, D1012UA,D2012S):



TG10K

D1008

D1012UA

D2012S

- * Positioning: Quick-spin assistants at the bench for collecting liquid from tube walls or small pellets.
- * Key Parameters: Max speed 7,000-15,000 rpm; Compatible with PCR tubes and microtubes; Compact and easy to use.
- * Core Applications: Pre-PCR collection, quick spin of reagents, rapid sedimentation post-homogenization.

· Benchtop Centrifuges (TG16.5, H17.5R/H17.5):



H17.5R/H17.5

TGL-17M/TGL-16.5M

TG16.5

- * Positioning: Workhorse centrifuges offering higher Relative Centrifugal Force (RCF) and versatile rotor compatibility.
- * Key Parameters: Max speed 15,000-17,500 rpm; Max RCF up to 29,302 xg; Multiple rotors (0.2mL to 100mL); Refrigerated models available (e.g., H17.5R).
- * Core Applications: Plasmid preparation, nucleic acid precipitation, protein purification, cell/subcellular fractionation.

2. Mixing & Incubation Series:

· Vortex Mixers (MX-E,MX-F, MX-S, , MX-S+,MX-Pro):



MX-E

MX-F

MX-S

MX-S+



MX-Pro

- * Positioning: Standard tools for rapid mixing and resuspension.
- * Key Parameters: Adjustable speed (0-3,000 rpm); Multiple heads for tubes, plates, flasks; Advanced models (MX-Pro) feature digital control and IR sensing.
- * Core Applications: Cell/reagent resuspension, thorough reaction mixing, plate washing in immunoassays.

· Dry Baths / Thermo-Shakers (HB-202/CHB-202, MB-102, MB-202):



MB-202

MB-102

HB-202 & CHB-202

- * Positioning: Provide accurate, uniform temperature control for enzymatic digestion, incubation, denaturation, etc.
- * Key Parameters: Temperature range (e.g.0-105° C); Interchangeable blocks for PCR tubes, centrifuge tubes, microplates; Shaking models (MB series) combine temperature and agitation for efficiency.
- * Core Applications: Restriction digestion, ligation, reverse transcription; Cell lysis; Hybridization.

3. Ultrasonic Disruptors:

• Focused Ultrasonicator (BoFU-80, BoFU-100, BoFU-1600):



BoFU-80 BoFU-100 BoFU-1600

- * Positioning: Non-contact and precise instruments for sample disruption and nucleic acid shearing.
- * Key Parameters: Utilizes high-frequency focused ultrasound; Concentrated energy with minimal heat generation; Programmable control (power, time, cycles); Single-sample or multi-sample processing.
- * Core Applications: Microbe ID, NGS Library Prep, Chromatin Shearing.

Laboratory Clean Environment Laboratory supplies

Water Systems

MGI provides a comprehensive portfolio of laboratory environmental control solutions, including Clean Benches, Biosafety Cabinets, and Water Purification Systems. These products deliver reliable sterile work areas, critical biological safety containment, and high-purity laboratory water for life science research, clinical testing, and industrial production, forming the foundation for experimental accuracy and personnel safety.

1. Clean Bench (HHS / HVS / SW-CJ):

The Clean Bench provides **ISO Class 5 (Class 100)** vertical or horizontal unidirectional clean air through HEPA filters, creating a local dust-free and sterile working environment to protect samples from contamination. The product line includes Horizontal Flow (HHS Series), Vertical Flow (HVS Series), and the cost-effective SW-CJ Series. The working area width ranges from 1 meter to 1.8 meters, meeting needs from routine aliquoting to high throughput operations.

2. Biosafety Cabinet (BSC II A2):

The Biosafety Cabinet is essential for operations involving biohazardous materials, such as microbiology and cell culture. BSC Series are **Class II, Type A2** cabinets, providing triple protection for the operator, the sample, and the environment. The products are certified to major international standards (NSF 49, EN12469, YY0569) and feature high filtration efficiency, intelligent airflow control, and safety alarms.

3. Water Purification System (UNIQ/RODI/GOKU):

Water Purification Systems produce laboratory-grade pure and ultrapure water directly from tap water, compliant with international standards. The product line includes the modular and intelligent UNIQ Series, the integrated dual-stage reverse osmosis RODI Series, and the GOKU Series for pre-treated water sources. Systems support multiple dispensing outlets, quantitative water delivery, and remote monitoring, providing a stable and reliable high-quality water source for analytical instruments and critical experiments.



Clean Bench Biosafety Cabinet GOKU RODI



UNIQ

Key Specifications

Category	Series	Core Parameters	Key Features
Clean Bench	HHS Series (Horizontal Flow)	Cleanliness: ISO Class 5 Air Velocity: 0.28 – 0.36 m/s Working Width: 1.0 – 1.8 m	Dual-person operation, color display, ECO mode, full-coverage airflow.
	HHS Series (Horizontal Flow)	Cleanliness: ISO Class 5 Air Velocity: 0.26 – 0.38 m/s Working Width: 1.0 – 1.8 m	Liftable front window, double side windows, low vibration, imported fan system.
	SW-CJ Series (Economic)	Cleanliness: ISO Class 5 Air Velocity: ≥ 0.45 m/s	Compact design, simple operation, ideal for basic aseptic techniques.
Biosafety Cabinet	BSC II A2 Series	Classification: Class II, Type A2	Personnel, product, and environmental protection; ULPA filters; intelligent airflow compensation; audible/visual alarms for sash position, airflow, and filter life.
		Downflow Velocity: 0.33 – 0.35 m/s	
		Inflow Velocity: 0.53 – 0.65 m/s	
		Filtration Efficiency: ≥ 99.9995% (0.12μm)	
Water System	UNIQ Series	Water Quality: Resistivity ≥ 18.2 MΩ·cm, TOC <5 ppb	Modular design, integrated EZ-DSP dispenser, bag-style tank (no cleaning), optional online TOC monitor.
		Feed Water: Tap water	
		Storage Capacity: 25L (expandable)	
	RODI Series	Output Water: RO + Ultrapure	Dual-stage RO membrane, smart cartridge management, color touchscreen, supports quantitative dispensing and foot pedal.
		Ultrapure Water Quality: Resistivity ≥ 18.2 MΩ·cm	
		Feed Water: Tap water	
		Storage Capacity: 40L	
	GOKU Series	Water Quality: Resistivity ≥ 18.2 MΩ·cm, TOC <5 ppb	Chip-based cartridge recognition, up to 3 remote dispensers (6m max), high cost-effectiveness.
		Feed Water: RO/Deionized/Distilled	

Typical Applications

Clean Bench

- Preparation and aliquoting of in vitro diagnostic reagents.
- Aseptic techniques in cell culture, such as cell seeding and passaging.
- Microbiological procedures including plate streaking and colony picking.

Biosafety Cabinet

- Nucleic acid extraction and handling of viral or bacterial pathogens.
- Culture and manipulation of stem cells or primary cells.
- Processing of clinical infectious samples.

Water Purification System

- Preparation of mobile phases and blanks for analytical instruments (HPLC, GC-MS, ICP-MS).
- Water for molecular biology applications (PCR, qPCR, NGS).
- Preparation of cell culture media, buffers, and other biological reagents.

Automated Purification,

Detection,Concentration and Sealing

Laboratory supplies

Auto-Pure Mini / Vacuum Centrifugal Concentrator / Sealer

MGI’s sample preparation portfolio provides a complete workflow solution, integrating automated nucleic acid purification, sample concentration, and microplate sealing. These instruments standardize critical pre-analytical steps to enhance efficiency, ensure reproducibility, and safeguard sample integrity for reliable downstream analysis.

1. Auto-Pure Mini Nucleic Acid Purification System:

The **Auto-Pure Mini** Nucleic Acid Purification System is a compact, versatile instrument for automated magnetic bead-based nucleic acid extraction. It features an open system design, allowing customization of protocols, and supports both single-tube and 96-deep well plate formats. Ideal for small-to-medium throughput labs and field applications, it offers precise temperature control and UV sterilization between runs.



Auto-Pure Mini

2. Vacuum Centrifugal Concentrator:

Vacuum Centrifugal Concentrator efficiently removes solvents or aqueous solutions from multiple samples simultaneously through a combination of vacuum, heat, and centrifugal force. The line includes refrigerated and non-refrigerated models, designed to handle a wide variety of tube formats while protecting sensitive samples from degradation.



AutoR1

Auto R3

MC-1

3. Automated Plate Sealer (BMF-R300, SealBio-1, SealBio-2) :

Automated Plate Sealer provides consistent, airtight sealing for PCR plates, deep-well plates, and other standard microplates to prevent evaporation and contamination. The range includes models from fully automatic, high-throughput systems to compact semi-automatic units, supporting a variety of sealing films to meet diverse experimental needs for sample storage and assay integrity.



BMF-R300

SealBio-1

SealBio-2

Key Specifications

Category	Model	Core Parameters	Key Features
Automated Extraction	Auto-Pure Mini	Throughput: 1-16 samples/run	Open protocol system, mobile app control, optional battery operation, UV sterilization.
		Processing Volume: 50-1000 µL	
		Consumables: Single strips & 96-deep well plates	
		Time-to-Result: ≤ 60 minutes	
		Multiplexing: Up to 48 targets/chip	
Vacuum Concentrator	Auto R1 (Non-Refrigerated)	Speed: 800-2000 rpm	Programmable vacuum control, corrosion-resistant chamber, imaging function for progress monitoring.
		Max Capacity: 180 x 1.5/2.0 mL	
		Temp. Range: RT+5° C to 100° C	
Vacuum Concentrator	Auto R1-Plus (Refrigerated)	Speed: 800-2000 rpm	Refrigerated concentration, automatic vacuum release, sample chamber pre-cooling function.
		Max Capacity: 180 x 1.5/2.0 mL	
		Temp. Range: -5° C to 100° C	
Integrated Concentrator	Auto R3	Speed: 800-2000 rpm	Space-saving all-in-one design, one-button operation, Teflon-coated chamber for corrosion resistance.
		Max Capacity: 90 x 1.5 mL	
		Vacuum Pump: Integrated diaphragm pump	
Automated Sealing	BMF-R300, SealBio-1, SealBio-2	Sealing Tech: Thermal Compatible Plates: 96-well PCR, deep-well, ELISA plates Sealing Time: <10-30 sec/plate	BMF-R300: Fully automatic, roll film, motorized lid. SealBio-1: Automated, continuous operation. SealBio-2: Semi-automatic, cost-effective.

Typical Applications

Auto-Pure Mini Nucleic Acid Purification System

- Genomic DNA/RNA extraction from blood, tissues, or cells for downstream analysis
- Viral nucleic acid purification in clinical and research settings.
- Provide reliable nucleic acid purification support in outdoor, mobile or resource-limited scenarios.

Centrifugal Concentrators (Auto R1 / R1-Plus / R3)

- Concentrating DNA/RNA samples after enzymatic reactions or purification.
- Drying protein or peptide samples prior to mass spectrometry analysis.
- Solvent evaporation in natural product research or pharmaceutical analysis.

Automated Plate Sealer (BMF-R300, SealBio-1, SealBio-2)

- Sealing PCR plates prior to thermal cycling to prevent evaporation and cross-contamination.
- Long-term storage of samples in 96-deep well plates at ultra-low temperatures.
- Securing assay plates during incubation or transportation steps.

MGI FragQ Series

Lab

Instrument

The MGI FragQ series represents a new generation of fully automated capillary electrophoresis systems designed for rapid, high-resolution quality control of DNA and RNA samples. It completely replaces cumbersome traditional agarose gel electrophoresis by integrating gel preparation, loading, electrophoresis, imaging, and analysis into a simple, automated workflow. It provides precise and reliable solutions for applications such as NGS library preparation, PCR product analysis, genomic DNA, and RNA integrity assessment.



FragQ-S18



FragQ-S100

Product Comparison

Aspect	FragQ-S18 (Portable)	FragQ-S100 (Benchtop)
Positioning	A compact, portable system for flexible, on-demand QC in labs with lower throughput needs or limited space.	A high-throughput, fully automated benchtop system for standardized, high-volume QC in core labs.
Core Specifications	Dimensions: 24 x 21 x 30 cm	Dimensions: 38 x 30 x 40 cm
	Weight: 5.5 kg	Weight: 15 kg
	Throughput: 1-18 samples/run	Throughput: 1-100 samples/run
	Size Range: 1 bp – 60 kbp	Size Range: 20 bp – 60 kbp (detectable to 165 kbp)
	Sensitivity: ≥ 5 pg/μL (dsDNA)	Sensitivity: ≥ 0.1 ng/μL (dsDNA)
Key Technologies & Features	Ready-to-use Cartridge: Integrated capillary and gel matrix, eliminating manual gel prep.	Full Automation: Automated sample handling for 1-100 samples, enabling walkaway operation.
	Rapid Analysis: Complete run (1-18 samples) in 3-10 minutes.	High Resolution: Distinguishes fragments with 1-4 bp differences for precise sizing.
	Portable Design: Small footprint and light weight for easy placement or transport.	Superior Sensitivity: Optimized for low-abundance samples like cfDNA and diluted NGS libraries.
	Basic NGS QC: Library quality check for small-scale sequencing projects.	Core Lab Workflow: Standardized QC for core facilities and diagnostic labs.

Primary Applications

- NGS Workflow QC: Sheared DNA fragment distribution, library fragment size and concentration analysis.
- Nucleic Acid Integrity Assessment: Genomic DNA degradation check, Total RNA Integrity Number (RQN/RIN) calculation.
- Routine Fragment Analysis: PCR/CRISPR product sizing, Plasmid DNA topology analysis, Oligonucleotide analysis.
- Liquid Biopsy & Rare Samples: Cell-free DNA (cfDNA) fragment profile analysis.

Nucleic Acid Test

Laboratory

Instrument

GeneExplorer / LineGene 9600 Plus / QuantGene 9600 / DcentriGene 160 / CentriDx ™

Product Overview

MGI's portfolio provides a complete suite of solutions for nucleic acid analysis, ranging from fundamental amplification tools (conventional PCR, qPCR, dPCR) to fully integrated, sample-to-answer detection systems. This caters to diverse needs from basic research and assay development to precise quantification and rapid molecular diagnostics.

• **The GeneExplorer series** Thermal Cycler enables flexible experiment optimization through its precise temperature control and gradient functionality, providing robust support for assay development and qualitative analysis.

• **The LineGene 9600 Plus** Fluorescent Quantitative Detection System delivers exceptional performance with high sensitivity and a broad dynamic range, making it a reliable platform for gene expression analysis and pathogen quantitative detection.

• **The QuantGene 9600** Fluorescent Quantitative Detection System delivers high-throughput, precise multiplex qPCR for demanding applications. It integrates top-side whole-plate imaging, six-zone independent temperature control, and mobile connectivity for superior performance and efficiency.

• **The DcentriGene 160** Droplet Chip DigitalPCR Analysis System, as the core of the digital PCR analysis system, achieves absolute quantification of nucleic acid molecules, demonstrating high sensitivity and accuracy in applications such as trace detection and copy number variation analysis.

• **The CentriDx ™** Automated Nucleic Acid Detection Analyzer is a fully integrated microfluidic system that automates the entire diagnostic process within one disposable cartridge. Starting with nucleic acid extraction, it carries out amplification and multi-target detection, delivering results in under 60 minutes. This offers a simple, rapid, and contamination-free solution for molecular diagnostics and pathogen screening.



GeneExplorer



LineGene 9600 Plus



QuantGene 9600



DcentriGene 160



CentriDx ™

Product Comparison

Aspect	GeneExplorer GE-96G	LineGene 9600 Plus	QuantGene 9600	DcentriGene 160	CentriDx 200
Product Category	Conventional PCR	Real-time quantitative PCR (qPCR)	High Performance Real-time quantitative PCR (qPCR)	Digital PCR (dPCR)	Fully Integrated Sample-to-Answer System
Detection Principle	End-point detection of amplified products	Real-time fluorescence monitoring (Ct-based quantification)	Real-time fluorescence monitoring (Ct-based quantification)	Droplet partitioning + end-point fluorescence counting (absolute quantification)	Integrated nucleic acid extraction, amplification & detection in a closed microfluidic chip
Primary Use	Qualitative Analysis & Assay Optimization	Routine Accurate Quantification	High-throughput, High-precision Quantification for demanding applications	Absolute Quantification for rare targets, CNV, etc.	Rapid, hands-free syndromic pathogen detection
Sensitivity	Routine	High	High	Extremely high	High
Throughput	48 or 96 wells/run	96 wells/run	96 wells/run	1-16 chips/run	48 targets/chip
Detection Channels	None	5 fluorescence channels	6 fluorescence channels	6 fluorescence channels	4-6 fluorescence channels
Thermal Performance	Ramp rate: 3.5° C/s heating, 2.5° C/s cooling; Uniformity: ≤ ±0.3° C	Ramp rate: 4.0° C/s heating; Uniformity: ≤ ±0.4° C; Gradient PCR supported (1-36° C)	Ramp rate: 6.0° C/s heating, 5.5° C/s cooling; Uniformity: ≤ ±0.3° C; Six-zone independent temperature control	Ramp rate: 2.5° C/s heating; Accuracy: ≤ 0.1° C	Fully automated temperature control within the integrated chip
Key Features	Gradient PCR, Mobile App monitoring, Large touchscreen	Top-side imaging for uniform signal acquisition	6-zone independent temperature control, LED light source & high-sensitivity CMOS detector	Wide dynamic range, integrated automated analysis software	Disposable cartridge, ≤ 60 min turnaround, CE-IVDR certified, minimal hands-on time
System Positioning	Cost-effective & flexible platform for assay development and routine amplification	Reliable & efficient platform for routine quantification	High-end & precise platform for quantitative analysis	Highly sensitive & absolute quantification core of a complete system	Walkaway, integrated solution for clinical diagnostics and screening

Applications

- Pathogen Detection & Typing: Viral load quantification, bacterial/fungal identification.
- Gene Expression Analysis: mRNA expression level quantification, microRNA analysis.
- Genotyping & Mutation Detection: SNP genotyping, allele discrimination, cancer gene mutation screening.
- Copy Number Variation (CNV) Analysis: Gene dosage determination, chromosomal aneuploidy detection.
- Absolute Quantification of Trace Nucleic Acids: Liquid biopsy (ctDNA), GMO copy number determination, precise quantification of NGS libraries.
- Microbiome Research: Quantification of amplicons prior to 16S rRNA gene sequencing.

Cell Counter Cytometer

Laboratory Instrument

Leap-Count / LongCyte & FongCyte / CytoStellar

MGI offers a complete portfolio for the entire cell analysis workflow. From routine cell culture monitoring to clinical-grade multicolor detection and cutting-edge high-dimensional research, we provide precise, reliable, and intelligent tools to help you acquire trustworthy data efficiently and accelerate scientific discovery.

• The **Leap-Count** Automated Cell Counter delivers objective, reproducible concentration and viability results within seconds using only 10µL of sample and AI-driven imaging, making it the efficient choice for daily lab analysis.



Leap-Count



LongCyte/FongCyte



CytoStellar

• The **LongCyte / FongCyte** Conventional Flow Cytometers provide a reliable, efficient, and standardized solution for clinical immunophenotyping and routine multicolor analysis, featuring exceptional stability and a one-touch automated workflow.

• The **CytoStellar™** Full-Spectrum Flow Cytometer unlocks ultra-high-dimensional single-cell analysis with up to 78 parameters through revolutionary spectral technology, empowering cutting-edge research in immunology and tumor microenvironment.

Key Product Specifications

Aspect	Leap-Count Series (100, 100A)	LongCyte / FongCyte Series	CytoStellar™ Series
Product Category	Cell Counter	Conventional Flow Cytometer	Full-Spectrum Flow Cytometer
Product Positioning	Automated, intelligent cell counting and viability analysis	Stable, reliable, and high-throughput platform for routine multicolor flow cytometry	Ultra-high-parameter, full-spectrum analysis research platform
Core Technology	AI-powered image recognition algorithm; High-resolution CMOS imaging	Dual-temperature-controlled optical system (lasers & APD detectors)	"Y"-shaped reflective optical path; Multi-channel APD array detector; Full spectral unmixing
Detection Principle	Optical imaging, identification and counting based on morphology and staining	Laser-excited fluorescence with filter-based detection	Laser excitation with full spectrum acquisition and mathematical unmixing
Key Parameters	· Concentration Range: 1 × 10 ⁴ – 1 × 10 ⁹ cells/mL · Sample Volume: 10 µL · Reproducibility: CV ≤ 5% · Models: Leap-Count 100 (Standalone) / 100A (PC-connected)	· Laser Config: Up to 3 lasers (488nm, 638nm, 405nm, etc.) · Fluorescence Channels: Up to 14 colors · Carryover: < 0.05%	· Laser Config: Scalable up to 5 lasers (incl. 349nm, 405nm, 488nm, 561nm, 638nm) · Fluorescence Channels: Up to 78 · Sensitivity: VSSC channel detects particles <80nm · Automation: Supports auto-loading
Key Advantages	Minimal sample volume; Simple & fast operation; Objective, traceable results; Ideal for frequent daily use	High system stability; One-touch maintenance; Compatible with clinical absolute counting; User-friendly operation	Unparalleled multicolor analysis capability; Exceptional weak signal sensitivity; Flexible and scalable; Supports automated & standardized workflows

Applications

- Leap-Count: Routine cell culture monitoring, cell therapy quality control, drug screening toxicity testing.
- LongCyte / FongCyte: Clinical lymphocyte subset analysis, leukemia immunophenotyping, CD34+ stem cell enumeration.
- CytoStellar™: Ultra-high-dimensional immune profiling, deep tumor microenvironment dissection, advanced multicolor panel development.

Molecular Detection

Laboratory Instrument

Quantification products

Fluo-200/800 / Nano-300/500 / AMR-100 / Feyond-A300

MGI’s detection and microplate reader portfolio offers a complete suite of instruments for precise and reliable analysis, covering applications from micro-volume sample quality control to high-performance multi-mode assays.

- **Fluo-200 / 800** Fluorometers enable ultra-sensitive, dedicated fluorescence quantification of DNA, RNA, and protein.
- **Nano-300/500** Micro-spectrophotometer provides rapid, accurate sample quality assessment with minimal sample volume, ideal for initial QC in molecular workflows.
- **AMR-100** Microplate Reader delivers stable, economical filter-based absorbance detection, designed for high-throughput routine colorimetric applications.
- **Feyond-A300** Multi-Mode Microplate Reader is a flexible, scalable system supporting absorbance, fluorescence, and luminescence detection for advanced research and complex assays.



Fluo-200/800



Nano-300/500



AMR-100



Feyond-A300

Key Product Specifications

Feature	Fluo-200/800	Nano-300/500	AMR-100	Feyond-A300
Detection Modes	Fluorescence Intensity	UV/Vis Full Spectrum Scan (200-800 nm)	Filter-based Absorbance (340-750 nm)	Absorbance (Monochromator), Fluorescence (Filters), Luminescence
Key Parameters	· Sensitivity: <0.1 pg/μL (Fluo-200) / <1 pg/μL (Fluo-800) · Throughput: 1 sample / 8 samples · Read Time: ≤ 5 s/sample / ≤ 6 s/8 samples	· Volume: 0.5-2 μL; · Detection Range: 2-15000 ng/μL (dsDNA); · Pathlength: 0.05/0.2/1.0 mm	· Filter Wheel: 8-position, 4 filters standard; · Abs. Range: 0-4.0 OD; · Read Speed: ≤ 6s (96-well)	· Abs. Wavelength: 200-1000 nm; · Fluo. Sensitivity: ≤ 1 pM; · Lumi. Sensitivity: 15 amol/well; · Incubation: Ambient to 45° C
Key Advantages	Ultra-high sensitivity, open reagent system, flexible throughput	Minimal sample consumption, fast measurement, simple operation	High stability, simple and intuitive operation, fast reading speed	Comprehensive and flexible functionality, high detection sensitivity, supports spectrum scanning & incubation

Primary Application Areas

- Fluo-200 / 800: High-sensitivity quantification for NGS library QC, cDNA yield analysis, and protein assays; ideal for applications requiring precise measurement at low concentrations.
- Nano-300/500: Concentration and purity (A260/A280, A260/A230) measurement of plasmid DNA, genomic DNA, RNA, and protein samples; Bacterial culture density (OD600) measurement.
- AMR-100: Enzyme-Linked Immunosorbent Assay (ELISA); Cell proliferation and cytotoxicity assays (e.g., MTT, CCK-8); Other routine colorimetric protein quantification assays.
- Feyond-A300: Advanced cell-based assays (proliferation, cytotoxicity, reporter gene); High-sensitivity nucleic acid/protein quantification; Kinase and GPCR assays in drug screening; ATP detection and calcium flux assays.