Genetic Sequencer

DNBSEQ-G400*

To be used with HotMPS exclusively

Welcome HotMPS**: Bringing choice to sequencing

Strengthen your daily sequencing capabilities with the unique combination of our new sequencing chemistry and the proven performance of our DNBSEQ-G400*.

Leading Life Science Innovation

◎ About MGI

MGI Tech Co., Ltd. (referred to as MGI) is committed to building core tools and technologies to lead life science through intelligent innovation. MGI focuses on R&D, production and sales of DNA sequencing instruments, reagents, and related products to support life science research, agriculture, precision medicine and healthcare. MGI is a leading producer of clinical high-throughput gene sequencers, and its multi-omics platforms include genetic sequencing, medical imaging, and laboratory automation.

MGI, founded in 2016 in Shenzhen, China, is one of the few companies worldwide that can develop and mass-produce clinical genetic sequencers. Providing real-time, comprehensive, life-long solutions, its vision is to lead life science innovation.

At present, MGI has more than 1,800 employees and operates in more than 70 countries and regions serving more than 1,100 customers around the world, with 8 international subsidiaries including Wuhan, Qingdao, Changchun, Kunshan and Hongkong, China, Japan, UAE, Latvia, and USA.

◎ Disclaimer

DNBSEQ-G400RS (Cat.No.900-000493-00) and DNBSEQ-G400 (Cat.No.900-000492-00) whose software has been configured for HotMPS MUST be used in conjunction with MGI's HotMPS sequencing reagent, and MUST NOT be used with MGI's CoolMPS or StandardMPS reagents (or with any reagents containing a 3'O-azidomethyl blocking group). This is important because (i) such sequencers will not work effectively with MGI's CoolMPS or StandardMPS reagents (or with any reagents containing a 3'O-azidomethyl blocking group); and (ii) the use of such reagents will give rise to the risk of patent infringement proceedings. Use of MGI's CoolMPS or StandardMPS reagents (or with any reagents containing a 3'O-azidomethyl blocking group) with such sequencers will invalidate any warranty which may have been provided by MGI, and any liability for intellectual property infringement arising from the use of such reagents is excluded from any IP indemnity.

The HotMPS sequencing reagent can only be used with DNBSEQ-G400RS (Cat.No.900-000493-00) and DNBSEQ-G400 (Cat.No.900-000492-00) whose software has been configured for HotMPS, and will not work effectively with MGI's sequencer whose software has not been properly configured for HotMPS. Use of these reagents with sequencers whose software has not been configured for HotMPS will invalidate any warranty which may have been provided by MGI, and any liability for intellectual property infringement arising from the use of such reagents is excluded from any IP indemnity.

About DNBSEQ-G400*

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Flexible sequencing & analysis solution
Fluent library preparation & sequencing solution

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Flexible, high quality
Activate your daily sequencing capability

Product Introduction

DNBSEQ-G400* is a versatile benchtop sequencer, providing users with comprehensive, flexible, and efficient sequencing options.

DNBSEQ-G400* sequencer supports a wide range of applications including scientific research, clinical research, disease prevention, environment studies and agriculture, etc., increasing the popularity of high-throughput sequencing systems in medical and scientific research fields.

Multiple choices

- **Dual flow cell system**
  One or two flow cells:
  1500M~3600M reads/run

High quality

- **Proven DNBSEQ™ technology**
  No error accumulation
  Low amplification bias
  Low index hopping

High speed

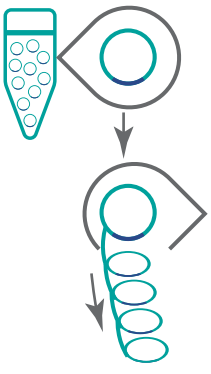
- **Short sequencing & time**
  FCL SE50 from DNB to FASTQ takes only 14 hours

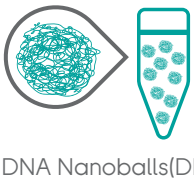
Versatile

- **Wide range of applications**
  Suitable for research and clinical applications

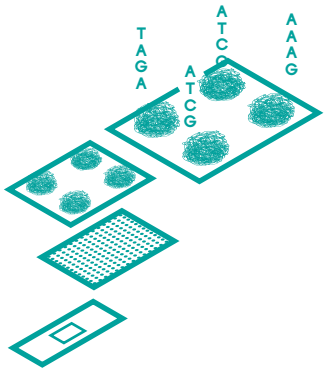
Technical Principle

MGI'S PROPRIETARY
DNBSEQ™
TECHNOLOGY





DNA Nanoballs(DNB)



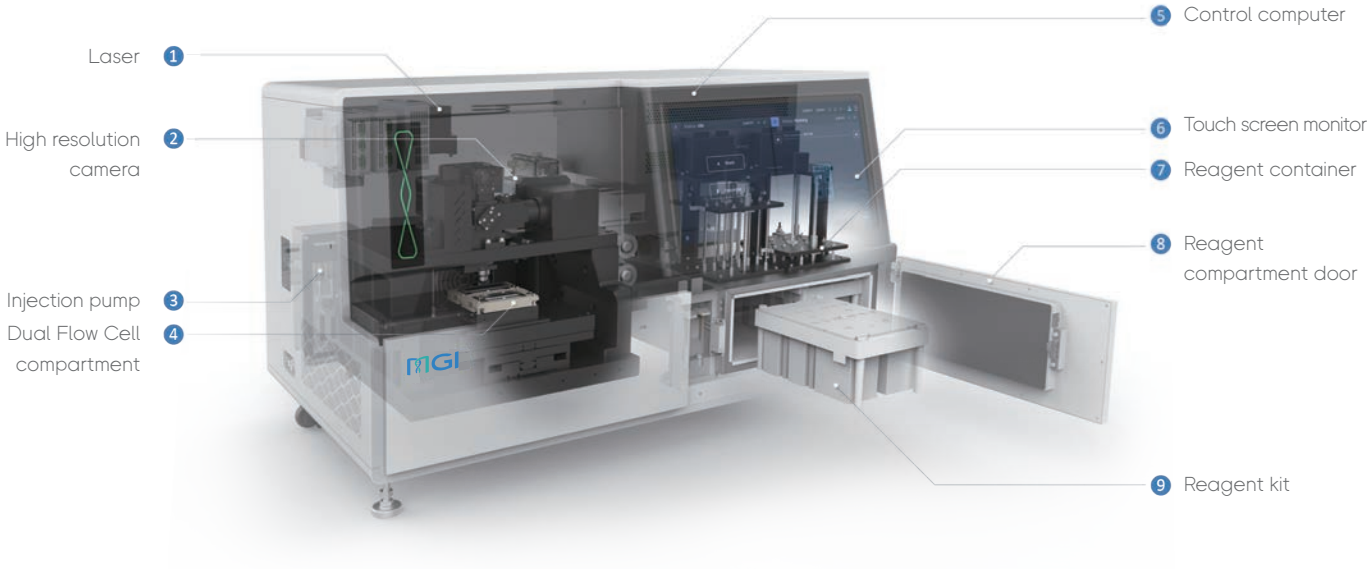
Patterned Array

- INCREASED ACCURACY
- DECREASED DUPLICATES
- REDUCED INDEX HOPPING

DNA Nanoball sequencing technology - No accumulation of amplification errors

Hardware Platform

DNBSEQ-G400* sequencer utilizes an innovative flow cell system which can support various sequencing modes and an optimized optical and biochemical system that enables the whole sequencing process to be completed within a short period of time, offering the user a simplified and streamlined sequencing experience.



Performance Parameters

Effective Reads/Flow Cell[1]	Reads Lengths	Data Output/Flow Cell[1]	Run Time[2]	Q30[3]
1500-1800M	SE50	75-90G	14H	>90%
	SE100	150-180G	22.5H	>85%
	PE50	150-180G	25.5H	>90%
	PE100	300-360G	42.5H	>85%

1. 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.
2. Run time was calculated based on dual-slides mode and takes sample loading, sequencing, base calling and data processing in account.
3. The percentage of base above Q30 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.

◎ Adapted Applications

DNBSEQ-G400* supports four read lengths, from fertility testing and rapid pathogen detection (SE50, SE100), to tumor detection, transcriptome, WGBS, WES, WGS (PE100), comprehensively cover the application needs of scientific research and clinical fields.

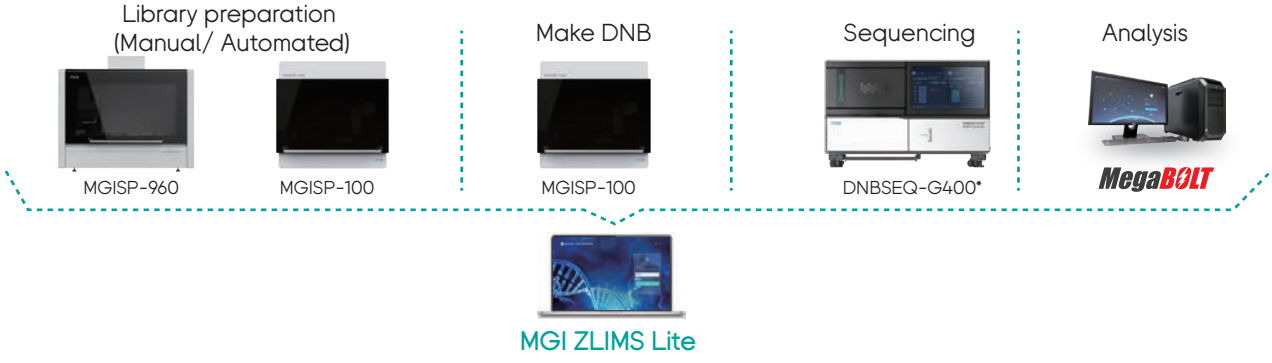
Application type	Recommended read length	Recommended data per sample	Recommended sample numbers[4] for a single run on DNBSEQ-G400*	
			1 Flow Cell	2 Flow Cell
			1500M-1800M reads	3000M-3600M reads
NIPT	SE50	5M reads/sample	300 samples	600 samples
Pathogen Fast Identification	SE50/SE100	25M reads/sample	60 samples	120 samples
Single cell RNA-Seq	PE100	5000cells，100K reads/-cell，100 Gb/sample	3 samples	6 samples
Cancer small panel		1 Gb/sample	300 samples	600 samples
Cancer large panel		5 Gb/sample	60 samples	120 samples
Transcriptome		40M reads/sample	38 samples	76 samples
WES		15 Gb/sample (100×)	20 samples	40 samples
WGS		90 Gb/sample (30×)	3 samples	6 samples

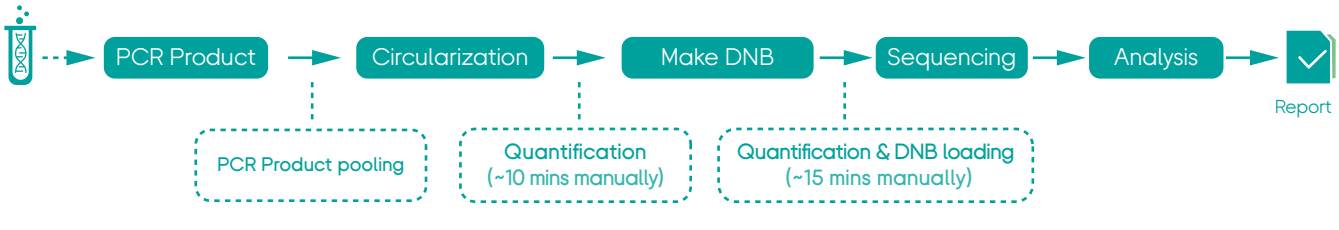
4. Theoretical sample numbers are calculated with consideration to pooling variation and applications. For reference only.

◎ Total Package

Versatile Library Prep, Sequencing & Analysis Solution

Genetic Sequencer DNBSEQ-G400* fully automated workflow (& all scenarios applicable)





automated either manual or automated

◎ Highlights

Efficient

- High efficiency with fully automated comprehensive workflow from sample to report
- Less than 30 mins of manual operations from sample to sequencing

Intelligent

- ZLIMS controls fully automated workflow from sample to report
- Compatible with multiple MGI and third-party software
- MegaBOLT is compatible with MGI and third-party data

Flexible

- Multiple sequencing and analysis options to expand application scenarios
- The above equipments can be selected according to needs

◎ Applications

Whole Genome Sequencing (WGS)

Case 1

Background

Whole genome sequencing (WGS) is designed to fully decode the genetic information of individuals and populations. With the increasing number of species with known genomic sequences, WGS is widely used in animal and plant breeding, population studies, disease research, clinical diagnosis and drug development, and has become one of the most rapid and effective sequencing methods.
In this case study the DNBSEQ-G400* was used together with the HotMPS High-throughput Sequencing Set** for whole genome sequencing.

Samples: Human Cell Line NA12878
Library kit: MGIEasy PCR-Free DNA Library Prep Set[1], MGIEasy FS PCR-Free DNA Library Prep Kit[1]
Sequencing Parameter: Genetic Sequencer DNBSEQ-G400RS* with HotMPS High-throughput Sequencing Set (G400 HM FCL PE100)**

Figure 1-1 Whole Genome Sequencing (WGS)

Result

- The Q30 ratios of the bases in all samples are over 93%.
- Low duplication rate (<3%) and high unique mapping rate (>94%) indicate higher data efficiency
- The coverage in high GC content region is even

Conclusion

DNBSEQ™ Technology can generate accurate and reliable whole-genome sequencing data, with high Q30, high unique mapping rate, and low duplication rate.

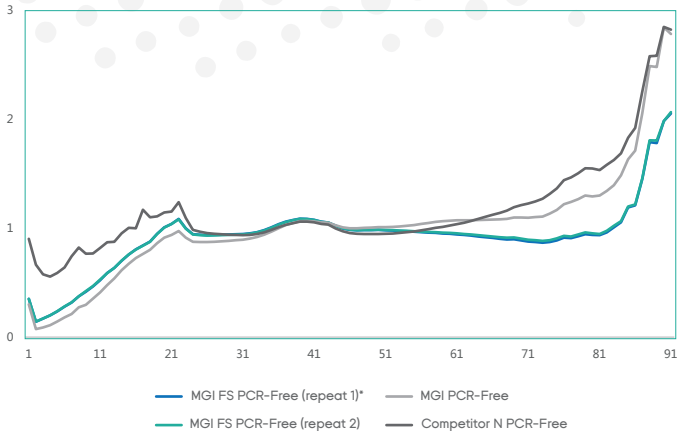


Figure 1-2 WGS GC distribution curve

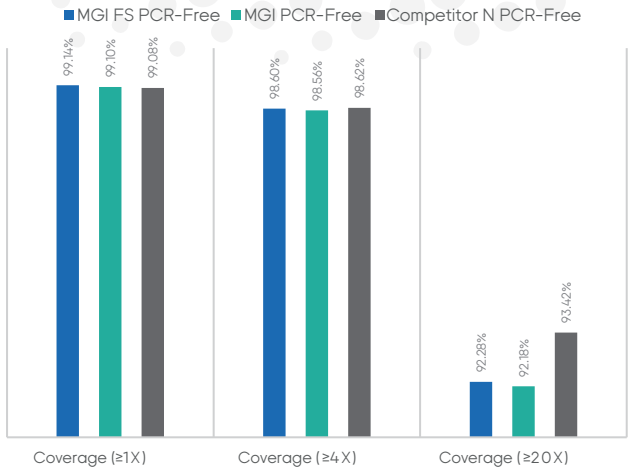


Figure 1-3 WGS coverage

1. MGIEasy FS PCR-Free DNA Library Prep Kit uses enzymatic fragmentation while MGIEasy PCR-Free DNA Library Prep Set uses mechanical fragmentation.

Table 1 WGS 30X data quality and analysis

Parameters	MGI FS PCR-Free	MGI PCR-Free	Competitor N PCR-Free
Clean Q30 (%)	93.04%	95.73%	92.19%
GC Content (%)	41.15%	41.60%	41.56%
Mapping Rate (%)	98.94%	98.92%	99.29%
Unique mapping Rate (%)	94.67%	94.45%	87.87%
Duplicate Rate (%)	2.08%	2.24%	9.46%
Mismatch Rate (%)	0.48%	0.47%	0.76%
Insert size	367.9	281.2	455.5
Average sequencing depth (rmdup)	30.12	30.62	30.52
Uniformity(>0.2f)	98.07%	98.02%	98.17%

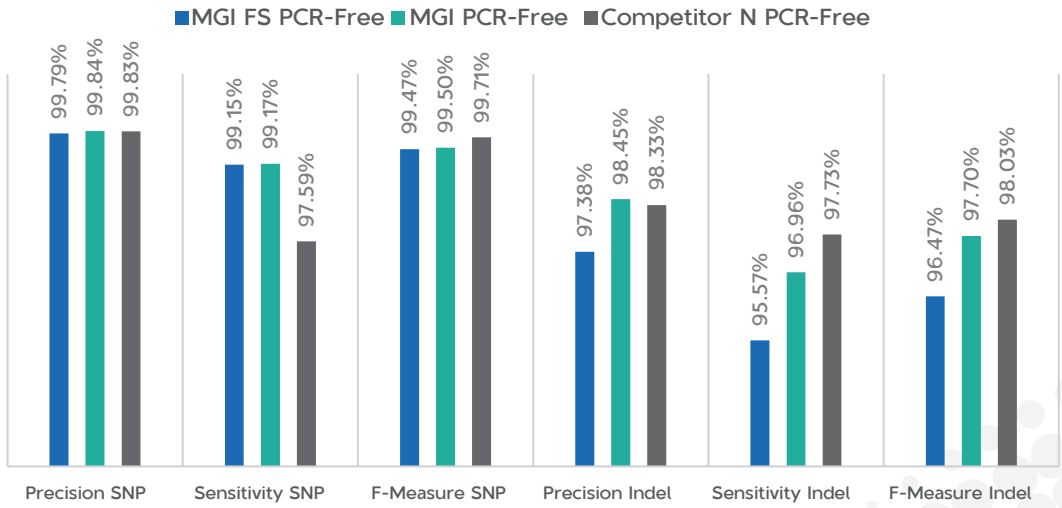


Figure 1-4 SNP' s and Indel' s detection results

Whole Exome Sequencing (WES)

Case 2

Background

With the development of precision medicine, Whole Exome Sequencing (WES) offers advantages for analysing the data of the patient's cases where the diagnoses or treatment options are unclear. For example, for many cancer types, Whole Exome Sequencing (WES) has been able to place specific types on treatments that in some cases have led to a complete cure.
MGI's Genetic Sequencer DNBSEQ-G400RS* utilizes an innovative system that can support WES sequencing

Samples: Cell lines YH and NA12878
Library kit: MGIEasy Exome Capture V4 Probe Set, MGIEasy Exome Universal Library Prep Set
Sequencing Parameter: Genetic Sequencer DNBSEQ-G400RS* with HotMPS High-throughput Sequencing Set(G400 HM FCL PE100)**
Analysis Pipeline: MGI MegaBOLT (V2.2.3.0)

Result

- Raw depth of more than 96% of the samples is above 20X;
- Average uniformity (>0.2f) is over than 92%;
- High data quality of WES ensures accurate SNP/InDel calling(>90%).

Conclusion:

High capture rate, uniformity, and good SNP/InDel calling results show DNBSEQ-G400˚ can perform well in WES application.

Table 2 WES 200X data quality and analysis

	YH-1	YH-2	NA12878
Capture_Rate_on_Reads	68.00%	69.54%	65.89%
Capture_Rate_on_Bases	57.47%	58.98%	55.63%
Average_depth(rmdup)	205.52	206.04	208.61
Coverage(>=1X)	99.27%	99.30%	99.69%
Coverage(>=20X)	96.36%	96.30%	97.32%
Coverage(>=100X)	76.01%	74.58%	74.72%
Uniformity(>0.2f)	93.03%	92.47%	92.85%

Table 2a WES 200X SNP data quality and analysis

	NA12878
Precision_SNP	99.64%
Sensitivity_SNP	98.62%
F-measure_SNP	99.12%
Precision_InDel	91.91%
Sensitivity_InDel	90.42%
F-measure_InDel	91.16%

RNA sequencing

Case 3

Background

RNA sequencing is a powerful method for comprehensive and rapid analysis of gene expression changes, examining rare and novel transcripts, discovery of alternate splicing events, gene fusions, SNPs and allele-specific expression in tissues or cells. Researchers aim to understand known or novel factors that alter gene expression during particular biological processes or development of diseases. Therefore, RNA-Seq has been widely applied to many fields such as biological research, disease research, drug development, agriculture and environmental research.

Samples: Universal Human Reference RNA (UHRR)
Library kit: MGIEasy RNA Library Prep Set
Sequencing Parameter: Genetic Sequencer DNBSEQ-G400RS* with HotMPS High-throughput Sequencing Set (G400 HM FCL PE100)**

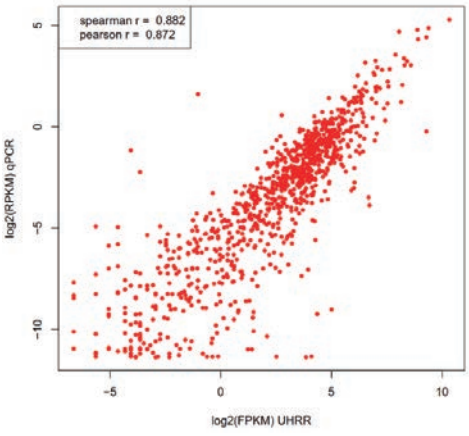


Figure 2 RNA-Seq and qPCR correlation coefficient

Result

- Q30 ratios of Clean Reads in all samples are over 96%.
- Average mapping genome ratios is over 93%;
- RNA-seq and qPCR correlation coefficient indicate good correlation (pearson r>0.87).

Conclusion

The high accuracy of DNBSEQ-G400* allows researchers to confirm and examine the transcriptome on an unprecedented scale.

Table 3 RNA-Seq data quality

	RNA-UHRR_1	RNA-UHRR_2	RNA-UHRR_3	RNA-UHRR_4	RNA-UHRR_5
Read_length	100:100	100:100	100:100	100:100	100:100
Total Raw Reads(M)	98.75	115.03	118.7	88.58	111.49
Total Clean Reads(M)	97.66	113.74	117.42	87.53	110.28
Clean Reads Ratio(%)	98.89%	98.88%	98.92%	98.82%	98.91%
Clean Reads Q30(%)	96.86%	96.76%	96.65%	96.64%	96.52%
rRNA Ratio(%)	3.25%	3.00%	3.06%	2.93%	3.28%
Mapping Genome Ratio(%)	94.05%	93.98%	93.93%	94.00%	93.93%
Mapping Gene Ratio(%)	52.98%	52.79%	52.46%	52.96%	53.42%
Gene Number	21102	21184	21219	20929	21121
Transcript Number	40918	41342	41415	40501	41209
Pearson_R	87.20%	87.00%	86.90%	87.00%	87.50%
Spearman_R	88.20%	88.30%	88.30%	88.10%	88.10%

10X Genomics Single Cell 3′ Gene Expression

Case 4

Background

The development of single-cell omics technology provides a powerful tool for the understanding of systems biology. Application of DNBSEQ-G400* with HotMPS** in 10x Genomics single-cell sequencing uses MGI library conversion technology to cooperate with 10x Genomics' Chromium system to achieve perfect compatibility between 10x Genomics single-cell sequencing technology and MGI's DNBSEQ platform*. MGI's sequencing products are compatible with the Chromium system while retaining its unique sequencing technology advantages.

Samples: Animal tissue
Library kit: Chromium Next GEM Single Cell 3' Reagent Kits v3.1 from 10X Genomics
Sequencing Parameter: Genetic Sequencer
DNBSEQ-G400RS* with HotMPS High-throughput Sequencing Set (G400 HM FCL PE100)**

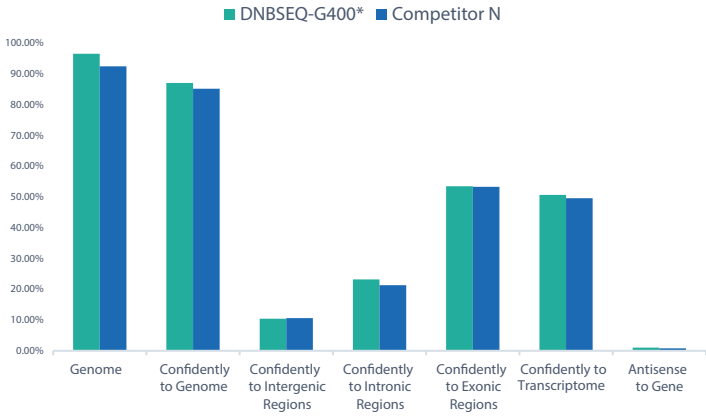


Figure 4-1 % of Reads mapped to different regions

Result

- Higher data utilization (Number of reads on DNBSEQ-G400*+ is less than competitor but estimated number of cells detected are quite similar).
- Genome mapping rate is higher than competitor.

Conclusion

The single-cell RNA sequencing data on the DNBSEQ-G400* with the HotMPS** sequencing demonstrate the openness and flexibility of MGI's DNBSEQ sequencing platform, providing single-cell researchers with more choices.

Table 4 10X Genomics 3′ RNA-Seq data quality and analysis

Parameters	DNBSEQ-G400*	Competitor N
Number of Reads	494,078,254	719,160,550
Valid Barcodes (%)	97.70%	98.30%
Valid UMIs (%)	99.90%	100%
Sequencing Saturation (%)	90.00%	92.80%
Q30 Bases in Barcode (%)	92.80%	97.50%
Q30 Bases in RNA Read (%)	93.30%	93.90%
Q30 Bases in UMI (%)	92.80%	97.40%
Estimated Number of Cells	4,687	4,714
Fraction Reads in Cells (%)	91.20%	91.20%
Mean Reads per Cell	105,415	152,558
Median Genes per Cell	1,104	1,123
Total Genes Detected	16,722	16,309
Median UMI Counts per Cell	1,959	2,042

Pathogen Sequencing - COVID-19

Case 5

Background

The identification and tracking of viral variants and lineages have rapidly become a priority in the fight against SARS-COV-2. MGI ATOPlex RNA Library Prep Set is a 2-step multiplex PCR-based library preparation set, which provides a streamlined workflow for SARS-CoV-2 whole genome enrichment and amplification. Combined with DNBSEQ-based high-throughput sequencing platform, it can obtain the full-length genome sequences of SARS-CoV-2 and achieve relative quantification of SARS-CoV-2 for population-scale virus detection, surveillance and tracing.

Samples: SARS-CoV-2 RNA QC sample from GeneWell with 4000 copy/ μL (4000cp) and 400copy / μL (400cp), NA12878, water (25% Balanced library)
Library kit: ATOPlex RNA Library Prep. Set (V1.1)
Sequencing Parameter: Genetic Sequencer DNBSEQ-G400RS* with HotMPS High-throughput Sequencing Set (G400 HM FCL PE100)**

Result

- High quality data (Q30＞96%, estimated error rate is lower than 0.1%)
- In all libraries, mapping rate can reach 99.9%
- In the positive samples, uniformity can reach 98.5%
- There is no difference between repeats
- All libraries were detected accurately(100X coverage>98%; Relative virus percentage (Pct%) >95% for 4000cp and >70% for 400cp)
- 100X coverage and relative virus percentage (Pct%) were highly consistent between repeats

Conclusion

Empowered by its multiplex PCR technology, MGI's proprietary ATOPlex ultra-high multiplex platform together with the DNBSEQ-G400* provides effective whole-genome sequencing, surveillance, and monitoring of SARS-CoV-2 variants

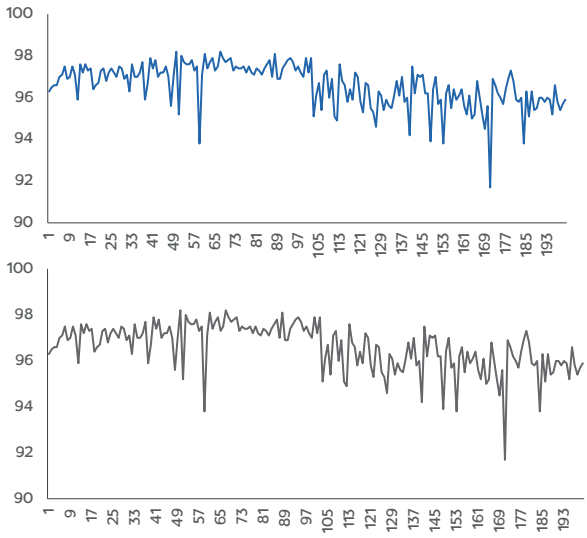


Figure 5-1 Clean Q30 curve of 2 repeats

	4000cp	400cp	NA12878	Water	Total
Number of pooled libraries	32	32	30	2	96

Table 5-1 Pooled Libraries

Samples	Total Reads (M)	Q20%	Q30%	EstErr%	SplitRate (%)
Pool 1	439.19	99.14	96.61	0.08	90.31
Pool 2	458.74	99.14	96.57	0.08	91.58

Table 5-2 SARS-CoV-2 sequencing data quality

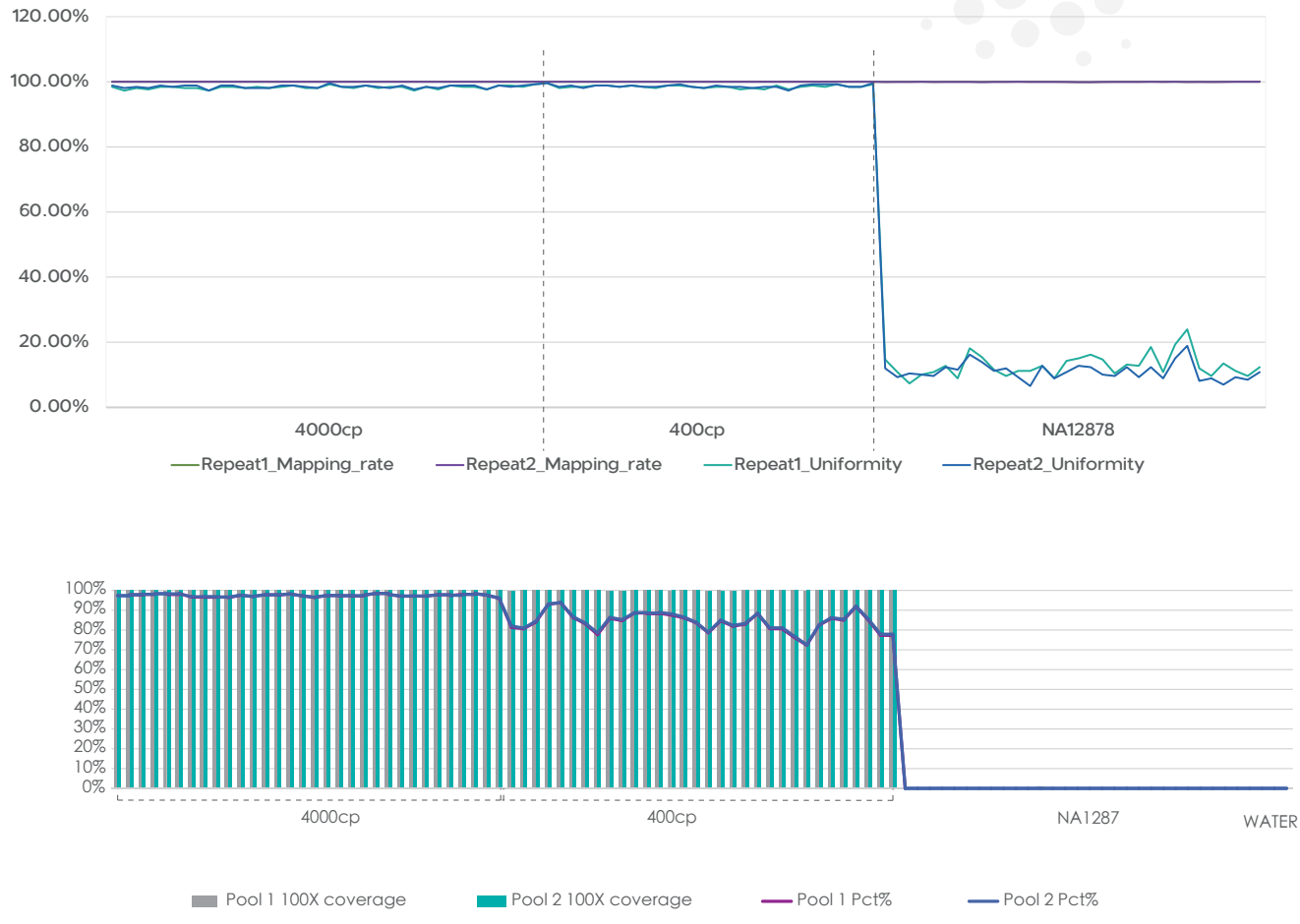


Figure 4 The mapping rate and uniformity (upper), 100X coverage and Pct% (below, Pct% refer to relative virus percentage of different samples)

Appendix

◎ Hardware Parameters

	Model[1]	Intended Market
Model[1]	DNBSEQ-G400*	IVD
	DNBSEQ-G400RS*	RUO
Dimensions	1086 mm(L)×756 mm(W)×710 mm(H)	
Net Weight	200 kg	
Power	Type	100-240 V, 50/60 Hz
	Rated Power	1200 VA
Operating Environment Requirements[2]	Temperature	19°C-25°C
	Relative Humidty	20% RH-80% RH,non-condensing
	Atmospheric Pressure	70 kPa-106 kPa
	Waterproof Rating	IPX0
Control Computer Configurations[3]	CPU	Intel Xeon E5 10Core 2 2.2GHz
	Internal Storage	256 GB RAM
	HDD	16 Tb
	SSD	480 Gb
	Operating System	Windows 10 Enterprise

1. Only for model classification
2. For indoor use only; The Flow Cells can be stored and transported at room temperature. No liquid medium is needed
3. Supporting the computer’ s configurations and system updates

◎ Ordering Information

Cat. No.	Product Name
900-000493-00	Genetic Sequencer DNBSEQ-G400RS*
900-000492-00	Genetic Sequencer (DNBSEQ-G400)*
1000028237	HotMPS High-throughput Sequencing Set (G400 HM FCL SE50)**
940-000089-00	HotMPS High-throughput Sequencing Set (G400 HM FCL SE100)**
940-000489-00	HotMPS High-throughput Sequencing Set (G400 HM FCL PE100)**
940-000491-00	HotMPS High-throughput Sequencing Set (G400 HM FCL PE50)**
1000028240	HotMPS High-throughput Sequencing Set (G400 HM FCL sRNA SE50)**
940-000492-00	Universal Sequencing Reaction Kit (G400 HM FCL PE100(CE))**
940-000493-00	Universal Sequencing Reaction Kit (G400 HM FCL PE50(CE))**
940-000094-00	Universal Sequencing Reaction Kit (G400 HM FCL SE100(CE))**
1000028239	Universal Sequencing Reaction Kit (G400 HM FCL SE50(CE))**

** This sequencer is only available in selected countries, and its software has been specially configured to be used in conjunction with MGI’ s HotMPS sequencing reagents exclusively.*

***This sequencing reagent is only available in selected countries.*

MGI Global Presence

Technical Support Globally

The technical support team has a complete global coverage including technical services centers and multiple locations in major international regions to maximize customer satisfaction.

Multiple local technical support centers around the world provide timely and effective technical support and training.

Spare part centers in Shenzhen, Wuhan, Qingdao, Tianjin, Hong Kong (China); Brisbane (Australia); and Riga (Latvia), to ensure sufficient supply of parts for machine maintenance.

Online technical support is accessible worldwide, with a fully functioning call center (Toll-Free Hotline: 4000-966-988) (9:00-12:00,13:00-18:00, Beijing time, workday) and multi-language online training courses coming soon.

Comprehensive Instrument Service and Warranty Plans Globally

Warehouses in Shenzhen, Wuhan, Qingdao, Tianjin, Hong Kong, Taipei (China), Bangkok (Thailand, Asia-Pacific); Brisbane (Australia, Oceania); Riga (Latvia, Europe); and San Jose (the USA, America) are established to ensure sufficient supply of maintenance parts for major regions.

Free installation and system verification service (including the QC reagents and consumables) are provided to turn your investment into production quickly.

MGI is responsible for any manufacturing defects or faults on the system within the warranty. Warranty covers labor, parts and travel charges.

One Free instrument preventive maintenance provided with warranty, along with a variety of available extended warranty support plans.

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