# Genetic Sequencer

## DNBSEQ-G400*

CB CE NMPA

Strengthen your daily sequencing capability


**Flexible, stable, and well-qualified, offering more choices**

**2** sequencing technologies
DNBSEQ™ + CoolMPS™ technologies

**2** Flow Cell Types

**5** Sequencing Modes

**6** Sequencing Lengths

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.

Founded in 2016, MGI has 1578 employees, 34% of whom are R&D personnel. MGI operates in more than 50 countries and regions, serving more than 1000 customers. It has established scientific research and production bases, global training and service network in many countries and regions around the world. MGI is one of the companies in the world that have the ability to independently develop and mass-produce clinical high-throughput gene sequencers. Providing real-time, comprehensive, life-long packages, its vision is to lead life science innovation.

# About DNBSEQ-G400

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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. In addition to the high-throughput sequencing reagents (StandardMPS), the CoolMPS high-throughput sequencing reagents provide more choices for users in pursuing higher sequencing quality. With stable high-intensity signals and random low sequencing error rate, CoolMPS reagents exhibit excellent performance in scientific and clinical applications, especially in the detection of low-frequency mutations in tumors.

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.

Multipl choices

- **Two flow cell types**
  FCL 1800M reads, FCS 550M reads
- **Dual flow cell system**
  One or two flow cells covering 550M~3600M reads/run

High quality

- **Advantages of DNBSEQ™ technology**
  Zero error accumulation, low amplification bias, low index hopping
- **Advantages of CoolMPS™ technology**
  MGI'S proprietary CoolMPS sequencing reagents make low-frequency mutation detection in cancer more accurate

High speed

- **Short sequencing & time**
  FCS SE100 from DNB to FASTQ takes only 13 hours

Various applica-tions

- **Wide range of application fields**
  Satisfy both scientific research and clinical test

DNBSEQ-G400 is built with a dual flow cell system that can perform different types of flow cell individually in a single run, giving users a more flexible and streamlined sequencing experience.

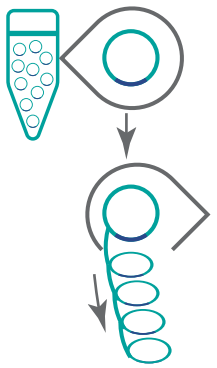
| Sequencer | Reagent type | FCS | FCL |
|---|---|---|---|
| DNBSEQ-G400RS | StandardMPS | ● | ● |
| | CoolMPS | | ● |
| DNBSEQ-G400 | StandardMPS | ● | ● |
| | CoolMPS | | ● |

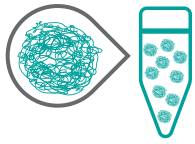
# Technical principle

MGI'S PROPRIETARY

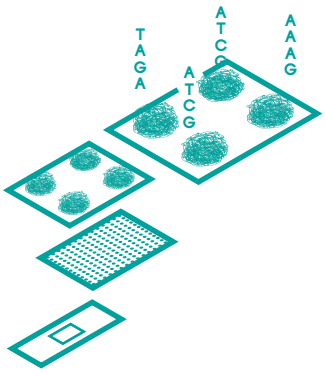
**DNBSEQ™**

TECHNOLOGY





DNA Nanobolls(DNB)




Patterned Array

INCREASED ACCURACY

DECREASED DUPLICATES

REDUCED INDEX HOPPING

DNA Nanoball sequencing technology - No accumulation of amplification errors

## CoolMPS™ Sequencing Reagent--- Natural bases make base recognition clearer

CoolMPS is the first antibody based massively parallel sequencing chemistry for DNBSEQ platforms produced by MGI. The dNTPs of CoolMPS are not fluorescent labeled (called cold dNTPs) and they are incorporated into the sequencing strand by DNA polymerase, where base calling is achieved by specific binding of fluorescently labeled antibodies. During this process, the incorporated bases are unmodified, ultimately resulting in clearer base calling.

CoolMPS High-throughput Sequencing Set is a novel antibody-based sequencing product based on this method, adapted to the MGI DNBSEQ sequencing platform, and compatible with conventional library preparation methods.

## CoolMPS™ chemistry principles

The CoolMPS is the sequencing method used in DNBSEQ technology (Fig 1). It uses

- Four cold dNTPs with an extension block (Fig 2)
- Four antibodies that are both base specific and block dependent (Fig 3). The A, T, G and C specific antibodies have almost zero cross reactivity. Each antibody has a specific dye (label) molecules attached to it.

The CoolMPS chemistry is compatible with all commonly used library preparation methods

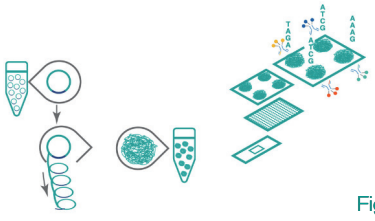



Fig 1

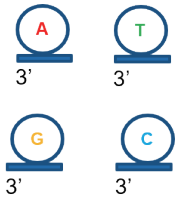



Fig 2

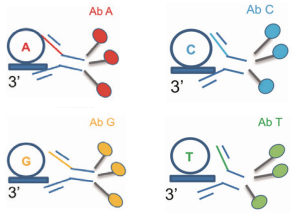



Fig 3

## CoolMPS sequencing steps

- The cold unlabeled dNTPs are polymerized using DNA polymerase on the flow cell
- The incorporated base is recognized by a fluorescently labeled antibody that binds specifically to the incorporated cold dNTP
- The flow cell is imaged
- A regeneration agent then cleanly removes the block and the antibody. No scarring of bases.
- The newly added bases are completely natural without any modification
- The sequencing cycles are repeated for necessary read length

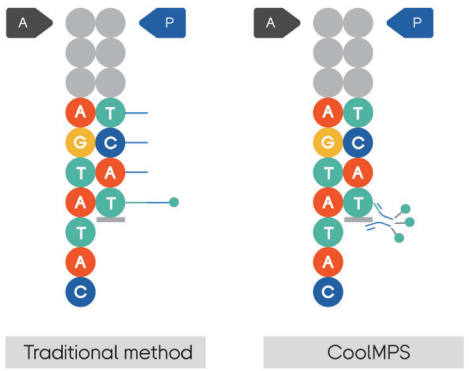



Fig 4

Shows four discrete steps of the chemistry

## Lower mismatch rate of CoolMPS reagent

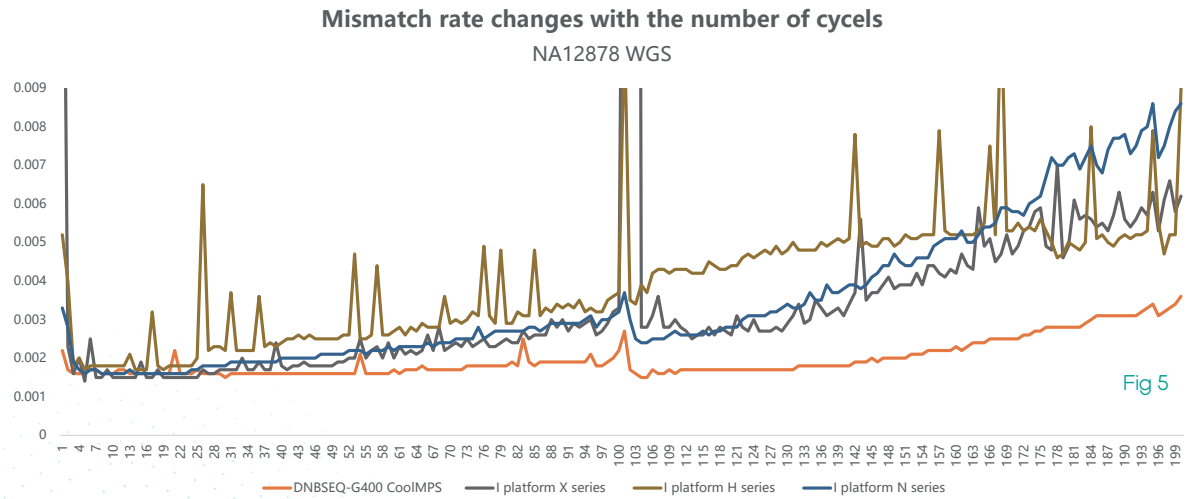
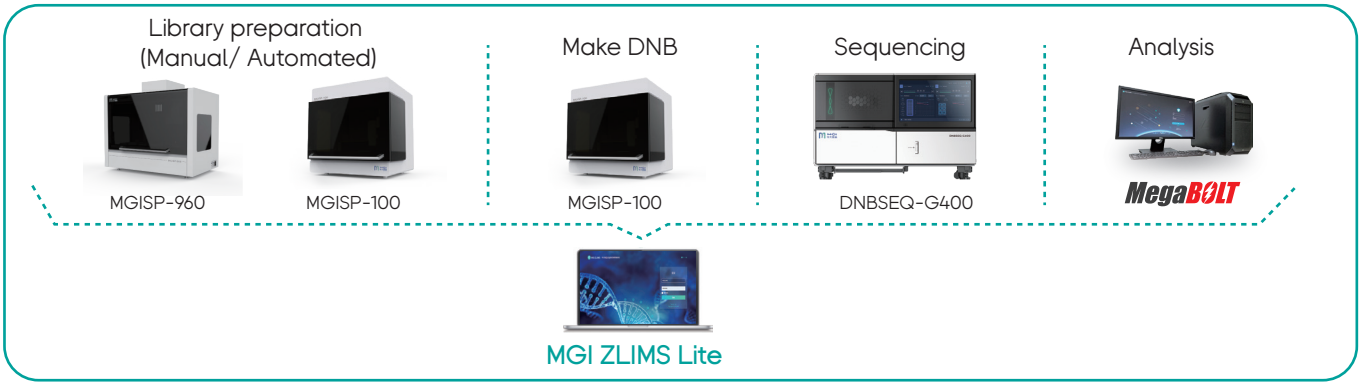


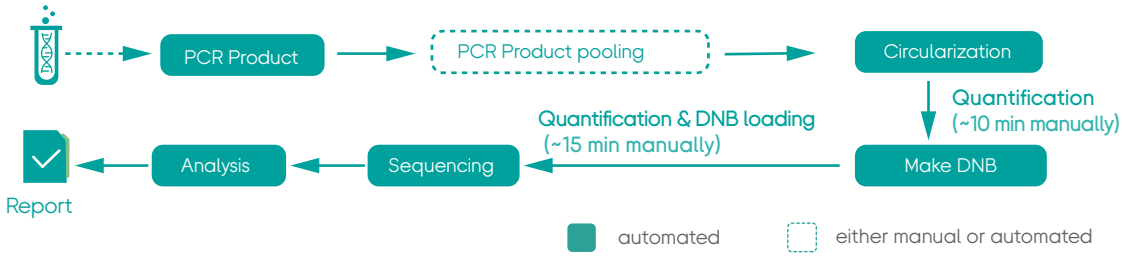

Fig 5

# Total Packages

## Versatile Library Prep,Sequencing & Analysis Package

Genetic Sequencer DNBSEQ-G400RS 2006A Fully automated workflow & all scenarios applicable




# ◎ Highlights

## Efficient

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

## Intelligent

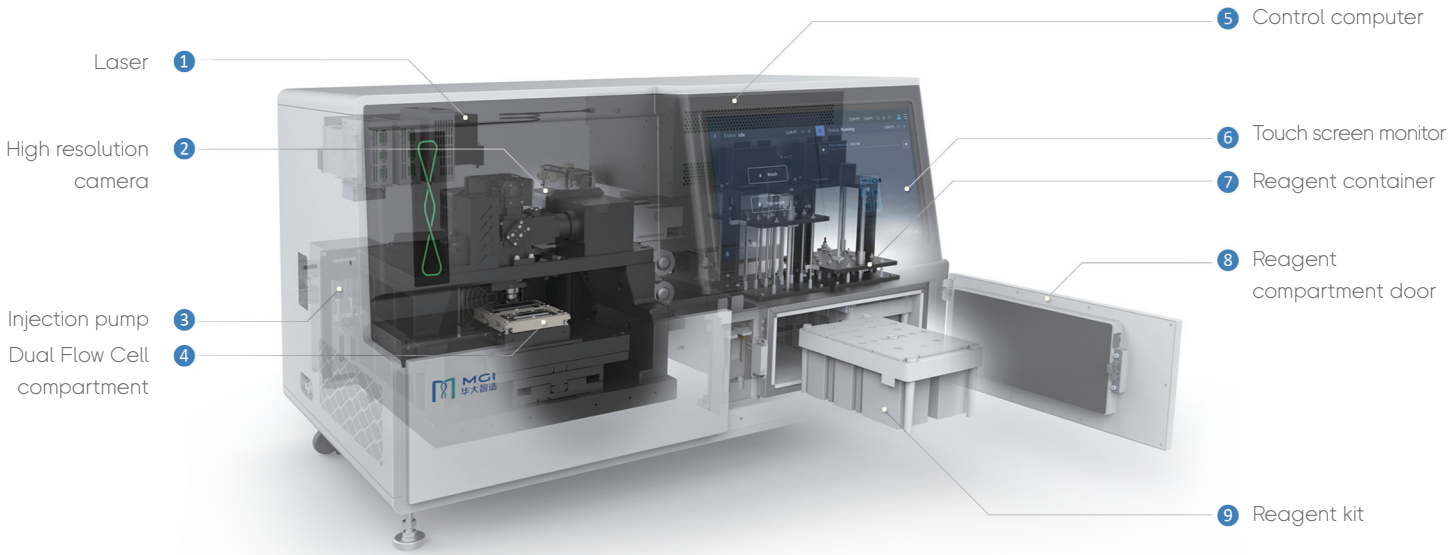
- ZIIMS controls fully automated workflow from sample to report
- Compatible with multiple MGI and third-party software
- MegaBOLT compatible with MGI and third-party data

## Flexible

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

# ◎ 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

| Reagent Type | Flow Cell Type | Effective Reads /Flow Cell* | Reads Lengths | Data Output /Flow Cell | Run Time** | Q30*** |
|---|---|---|---|---|---|---|
| StandardMPS | FCS | 550M | SE100 | 55G | 13H | >85% |
| | | | PE100 | 110G | 26H | >85% |
| | | | PE150 | 165G | 37H | >75% |
| | FCL | 1500-1800M | SE50 | 75-90G | 14H | >85% |
| | | | SE100 | 150-180G | 25H | >85% |
| | | | PE100 | 300-360G | 48H | >85% |
| | | | PE150 | 450-540G | 66H | >75% |
| | | | SE400 | 600-720G | 109H | >70% |
| | | | PE200 | 600-720G | 107H | >75% |
| CoolMPS | | 1500-2000M | SE50 | 75-100G | 17H | >90% |
| | | | SE100 | 150-200G | 30H | >90% |
| | | | PE100 | 300-400G | 58H | >90% |

* 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.

** Run time was calculated based on dual-slides mode and takes sample loading, sequencing, base calling and data processing in account.

*** 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 6 read lengths, from fertility testing and rapid pathogen detection (SE50, SE100), to tumor detection, transcriptome, WGBS, WES, WGS (PE100, PE150), to individual identification (SE400) and plants and animal genome sequencing (PE200), comprehensively covers the application needs of scientific research and clinical fields.

| Application type | Recommended read length | Recommended sample numbers for a single run on DNBSEQ-G400* | | | | |
|---|---|---|---|---|---|---|
| | | 1*FCS | 2*FCS | 1*FCL | 1*FCL+1*FCS | 2*FCL |
| | | 550M reads | 1100M reads | 1800M reads | 2350M reads | 3600M reads |
| NIPT<br>5M reads/sample | SE50 | 85 samples | 170 samples | 275 samples | 360 samples | 550 samples |
| Pathogen Fast Identification<br>25M reads/sample | SE50/SE100 | 17 samples | 34 samples | 55 samples | 72 samples | 110 samples |
| Single cell RNA-Seq<br>5000cells，100K reads/cell，100 Gb/sample | PE100 | 1 sample | 2 samples | 4 samples | 5 samples | 8 samples |
| Cancer small panel<br>1 Gb/sample | | 85 samples | 170 samples | 275 samples | 360 samples | 550 samples |
| Cancer large panel<br>5 Gb/sample | | 17 samples | 34 samples | 55 samples | 72 samples | 110 samples |
| Transcriptome<br>40M reads/sample | PE150 | 11 samples | 22 samples | 35 samples | 46 samples | 70 samples |
| WES<br>100×average sequencing depth，15 Gb/sample | | 8 samples | 16 samples | 28 samples | 36 samples | 56 samples |
| WGS<br>30×average sequencing depth，100 Gb/sample | | 1 sample | 2 samples | 4 samples | 5 samples | 8 samples |
| Individual identification<br>1M reads/sample | SE400 | / | / | 1500 samples | / | 3000 samples |

* Sample numbers are calculated with consideration to pooling variation and applications. For reference only.

# Application Cases

## Pathogen detection

### Case 1: Pathogen detection - COVID-19

Sample: 6 serial dilutions of extracted RNA from isolated culture were subjected to ATOPlex Sequencing and RT-qPCR.
Sequencing Platform: DNBSEQ-G400
Results:

Table 1 Summary of ATOPlex Sequencing

| ID | Raw reads | SARS-CoV-2 mean depth | 100XSARS-CoV-2 coverage | Ct value of RT-qPCR | SAS-CoV-2%# |
|---|---|---|---|---|---|
| Dilution $10^{-1}$ | 9,455,876 | 61102.3 | 99.8% | 24.3 | 99.95% |
| Dilution $10^{-2}$ | 10,232,235 | 59012.7 | 99.8% | 27.1 | 99.43% |
| Dilution $10^{-3}$ | 9,122,357 | 31140.3 | 99.8% | 30.6 | 94.82% |
| Dilution $10^{-4}$ | 5,965,846 | 2951.4 | 99.8% | 33.5 | 63.13% |
| Dilution $10^{-5}$ | 4,536,254 | 1036.6 | 95.3% | 36.9 | 15.36% |
| Dilution $10^{-6}$ | 17,563,253 | 206.9 | 75.4% | NO CT | 1.87% |
| Negative control | 5,245,547 | 0.3 | 0.0% | NO CT | 0.00% |

#SARS-CoV-2 detection; SARS-CoV-2% < 0.05%,negative; SARS-CoV-2% > 0.1%,positive; SARS-CoV-2% = 0.05-0.1%, gray zone.

**Conclusion:**

ATOPlex Sequencing can detect SARS-CoV-2 with 10 gradient dilutions (about 10~100 copies per ml) and assemble nearly full-length genome with 10 gradient dilutions (about 100~1000 copies per ml).

# WGS

## Case 2: Human WGS

Sample: 1025 DNA samples of Han Chinese in the Central Plains
Library: MGIEasy PCR-Free DNA Library Preparation Set
Sequencing Strategy: DNBSEQ-G400 PE150
Results:

Table 2-1 Sequencing data quality

| | | Min | Median | Mean | Max | High quality | PASS |
|---|---|---|---|---|---|---|---|
| Total Reads | | 601727956 | 726056164 | 726494436 | 952285662 | / | / |
| Mean Reads Length | | 150 | 150 | 150 | 150 | / | / |
| Reads* | R1 | 100% | 100% | 100% | 100% | =100% | =100% |
| | R2 | 100% | 100% | 100% | 100% | =100% | =100% |
| Q30 | R1 | 87.21% | 90.43% | 90.34% | 92.91% | >=85% | >=80% |
| | R2 | 84.22% | 89.79% | 89.56% | 92.00 % | >=85% | >=80% |

*passed filter

Table 2-2 Key indicators of sequencing data analysis

| | Min | Median | Mean | Max | High quality | PASS |
|---|---|---|---|---|---|---|
| Properly Paired | 96.38% | 98.27% | 98.26% | 98.88% | >=95% | >=90% |
| Raw Depth (GRCh38) | 29.23 | 35.27 | 35.29 | 46.25 | >=30 | >=10 |
| Mapping Rate | 97.81% | 99.99% | 99.99% | 100.00% | >=99% | >=95% |
| Duplication | 0.25% | 0.88% | 0.99% | 3.22% | / | / |
| Mean Insert Size | 262.38 | 329.40 | 332.64 | 382.18 | / | / |
| Insert Size SD | 51.23 | 71.40 | 71.75 | 82.80 | / | / |

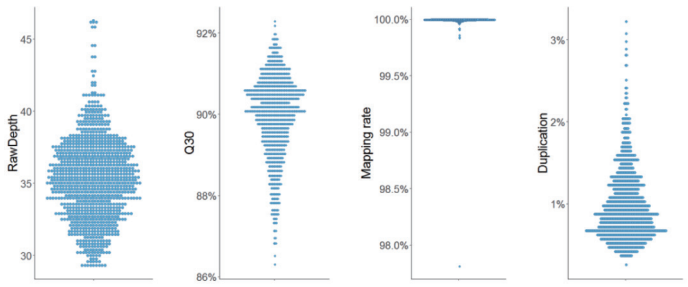



Figure 2. Excellent overall sequencing quality

Conclusion:

1) The raw depth of more than 98% of the samples is above 30X, with a lowest raw depth of 29.226X;

2) The Q30 ratios of the bases in all samples are over 85%;

3) Except for one sample (97%), the mapping rates of all other samples are greater than 99.5%

4) More than 95% of the samples have a duplication rate of less than 2%, with the highest rate also less than 4%;

The DNBSEQ-G400 platform can produce high-quality WGS sequencing data with high Q30 and mapping rate, and low duplication rate, which can generate accurate and reliable whole-genome sequencing data.

# Single Cell sequencing

## Case3: DNBelab C4 RNA sequencing

DNBelab C Series Single-Cell Omics Package is comprised of DNBelab C4 Pocket Single-Cell Lab, DNBelab C Series Single-Cell Library Preparation Set, DNBSEQTM sequencing platform and Single-Cell Analysis Suite, all as part of a portable, instant, and one-stop single-cell research workflow.

Sample: Human 293T cell line :Murine 3T3 cell line =1:1
Library Preparation: DNBelab C Series Single-Cell Library Preparation Set
Sequencing Strategy: DNBSEQ-G400 PE100
Data Results:

Table 3-1 Cell data results

| | |
|---|---|
| Estimated Number of Cells | 2,544 |
| Estimated Number of Human Cells | 1,309 |
| Estimated Number of Mouse Cells | 1,155 |
| Fraction Reads in Cells | 79.70% |
| Fraction Reads in Human Cells | 80% |
| Fraction Reads in Mouse Cells | 79.30% |
| Mean Reads per Cell | 40,882 |
| Mean Reads per Human Cell | 41,485 |
| Mean Reads per Mouse Cell | 39,518 |
| Median UMI Counts per Human Cell | 28,915 |
| Median UMI Counts per Mouse Cell | 26,411 |
| Median Genes per Human Cell | 6,168 |
| Median Genes per Mouse Cell | 5,395 |

Table 3-2 Sequencing data results

| | |
|---|---|
| Number of Reads | 172,491,759 |
| Reads Pass QC | 148,377,085 |
| Reads with Valid Barcodes | 148,377,085 |
| Filtered Reads with Failed Barcodes | 23,040,453 |
| Filtered Reads with Low Quality | 1,074,221 |
| Filtered Reads with Unknown Sample Barcodes | 0 |
| Q30 Bases in Cell Barcode | 89.30% |
| Q30 Bases in Sample Barcode | 0.00% |
| Q30 Bases in UMI | 86.50% |
| Q30 Bases in RNA Read | 79.80% |

Table 3-3 Mapping results

| | |
|---|---|
| Reads Mapped Confidently to Genome | 95.20% |
| Reads Mapped Confidently to Gene | 95.10% |
| Reads Mapped Confidently to Exonic Regions | 66.30% |
| Reads Mapped Confidently to Intronic Regions | 2.80% |
| Reads Mapped Antisense to Gene | 5.70% |

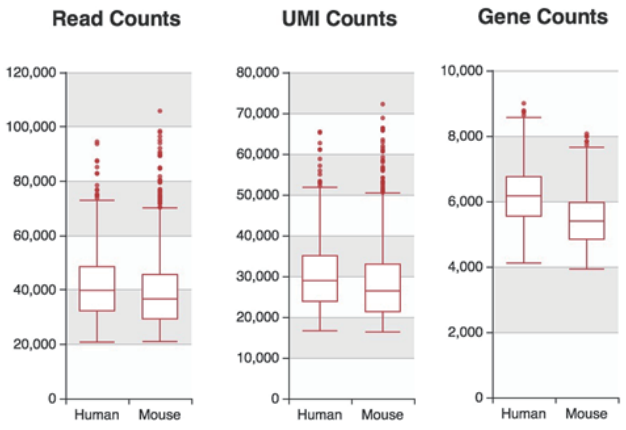



Figure 3. Data distribution

### Conclusion:

The data output and quality performance of MGI DNBelab C4 single-cell library preparation products on the DNBSEQ-G400 platform meet expectations.

# Oncology

## Case 4: CoolMPS detects low frequency mutations

Sample: GeneWell Pancancer 800 gDNA Reference Standard
Library Preparation: WES (IDT probe)
Sequencing Strategy: Illumina X10 PE150, DNBSEQ-G400RS CoolMPS PE100
Sequencing Depth: 700X (filter duplication)
Data Results:

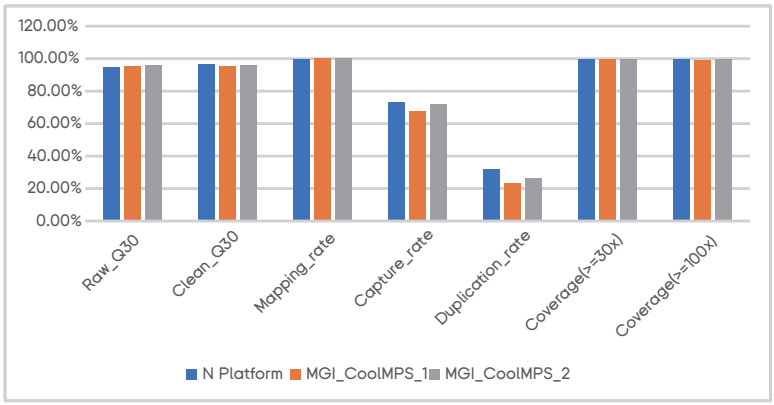



Figure 4. Comparison of quality data on different platforms

Table 4 Detection of specific site mutations on different platform

| Gene | AA | STD_FREQ | N 平台 | MGI_1 | MGI_2 |
|---|---|---|---|---|---|
| EGFR | V769_D770insASV | 3% | 1.73% | 1.27% | 2.32% |
| EGFR | L858R | 1% | 1.44% | 0.62% | 1% |
| EGFR | T790M | 2% | 2.00% | 0.53% | 1.49% |
| **EGFR** | **E746_A750del** | **2%** | **NA** | **NA** | **1.03%** |
| KRAS | G12D | 2% | 1.29% | 1.93% | 1.62% |
| KRAS | G13D | 4% | 3.67% | 4.66% | 2.60% |
| **KRAS** | **A146T** | **1%** | **NA** | **2.02%** | **NA** |
| **NRAS** | **Q61K** | **1%** | **NA** | **1.26%** | **1.02%** |
| KIT | D816V | 2% | 2.21% | 2.61% | 2.56% |
| FLT3 | I836del | 2% | 2.16% | 1.51% | 1.75% |
| EGFR | G719S | 4% | 4.23% | 2.86% | 2.97% |
| BRAF | V600E | 7% | 4.34% | 4.72% | 5.47% |
| PIK3CA | H1047R | 7% | 7.76% | 4.91% | 10.14% |

## Conclusion:

The performance of Q30, mapping rate and coverage of the two platform is consistent, but the duplication rate of CoolMPS reagent on DNBSEQ-G400 platform is lower;

In the 13 loci of the low-frequency mutation standard with a preset mutation rate of 1%-7%, the detection rate of N platform was 76.9% (10/13), which is lower compared to the 92.3% of DNBSEQ-G400 CoolMPS reagent (12/13).

# Appendix

## ◎ Hardware Parameters

| | Model* | Intended Market |
|---|---|---|
| Model* | 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** | 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*** | CPU | Intel Xeon E5 10Core * 2 2.2GHz |
| | Internal Storage | 256 GB RAM |
| | HDD | 16 Tb |
| | SSD | 480 Gb |
| | Operating System | Windows 10 Enterprise |

* Only for model classification

** For indoor use only; The Flow Cells can be stored and transported at room temperature. No liquid medium is needed

*** Supporting the computer’ s configurations and system updates

# ◎ Ordering Information

Table: DNBSEQ-G400 Series products

| Cat. No. | Product Name |
|---|---|
| 900-000168-00 | Genetic Sequencer DNBSEQ-G400 |
| 900-000170-00 | Genetic Sequencer DNBSEQ-G400RS |
| 1000016941 | DNBSEQ-G400RS High-throughput Sequencing Set (FCL SE50) |
| 1000016943 | DNBSEQ-G400RS High-throughput Sequencing Set (FCL SE100) |
| 1000016946 | DNBSEQ-G400RS High-throughput Sequencing Set (FCL SE400) |
| 1000016950 | DNBSEQ-G400RS High-throughput Sequencing Set (FCL PE100) |
| 1000016952 | DNBSEQ-G400RS High-throughput Sequencing Set (FCL PE150) |
| 1000016955 | DNBSEQ-G400RS High-throughput Sequencing Set (FCL PE200) |
| 1000016978 | DNBSEQ-G400RS High-throughput Rapid Sequencing Set (FCS SE100) |
| 1000016980 | DNBSEQ-G400RS High-throughput Rapid Sequencing Set (FCS PE100) |
| 1000016982 | DNBSEQ-G400RS High-throughput Rapid Sequencing Set (FCS PE150) |
| 1000016984 | DNBSEQ-G400RS High-throughput Sequencing Set (stLFR FCL PE100) |
| 1000016993 | DNBSEQ-G400RS High-Throughput Sequencing Set (App-A FCL SE50) |
| 1000016994 | DNBSEQ-G400RS High-Throughput Sequencing Set (App-A FCL PE100) |
| 1000016995 | DNBSEQ-G400RS High-Throughput Sequencing Set (App-A FCL PE150) |
| 1000016998 | DNBSEQ-G400RS High-throughput Sequencing Set (Small RNA FCL SE50) |
| 1000023783 | DNBSEQ-G400RS High-throughput Rapid Sequencing Set (App-A FCS SE100) |
| 1000023784 | DNBSEQ-G400RS High-throughput Rapid Sequencing Set (App-A FCS PE100) |
| 1000023785 | DNBSEQ-G400RS High-throughput Rapid Sequencing Set (App-A FCS PE150) |
| 1000017992 | CoolMPS High-throughput Sequencing Set (DNBSEQ-G400RS FCL SE50) |
| 1000019478 | CoolMPS High-throughput Sequencing (DNBSEQ-G400RS Small RNA FCL SE50) |
| 1000016933 | CoolMPS High-throughput Sequencing (DNBSEQ-G400RS FCL SE100) |
| 1000016935 | CoolMPS High-throughput Sequencing (DNBSEQ-G400RS FCL PE100) |
| 1000022483 | Universal Sequencing Reaction Kit (G400 SM FCS SE100) (CE-IVD) |
| 1000022484 | Universal Sequencing Reaction Kit (G400 SM FCS PE100) (CE-IVD) |
| 1000022485 | Universal Sequencing Reaction Kit (G400 SM FCS PE150) (CE-IVD) |
| 1000022477 | Universal Sequencing Reaction Kit (G400 SM FCL SE35) (CE-IVD) |
| 1000022478 | Universal Sequencing Reaction Kit (G400 SM FCL SE50) (CE-IVD) |
| 1000022479 | Universal Sequencing Reaction Kit (G400 SM FCL SE100) (CE-IVD) |
| 1000022480 | Universal Sequencing Reaction Kit (G400 SM FCL PE50) (CE-IVD) |
| 1000022481 | Universal Sequencing Reaction Kit (G400 SM FCL PE100) (CE-IVD) |
| 1000022482 | Universal Sequencing Reaction Kit (G400 SM FCL PE150) (CE-IVD) |
| 1000022466 | Universal Sequencing Reaction Kit (G400 CM FCL SE50) (CE-IVD) |
| 1000022467 | Universal Sequencing Reaction Kit (G400 CM FCL SE100) (CE-IVD) |
| 1000022468 | Universal Sequencing Reaction Kit(G400 CM FCL PE100) (CE-IVD) |
| 1000022549 | Universal Sequencing Reaction Kit (G400 SM FCS SE100) (IVD for Vietnam and Thailand) |
| 1000022550 | Universal Sequencing Reaction Kit (G400 SM FCS PE100) (IVD for Vietnam and Thailand) |
| 1000022551 | Universal Sequencing Reaction Kit (G400 SM FCS PE150) (IVD for Vietnam and Thailand) |
| 1000017811 | Universal Sequencing Reaction Kit(G400 SM FCL SE35) (IVD for Vietnam and Thailand) |
| 1000017812 | Universal Sequencing Reaction Kit (G400 SM FCL SE35) (IVD for Vietnam and Thailand) |
| 1000017813 | Universal Sequencing Reaction Kit (G400 SM FCL SE100) (IVD for Vietnam and Thailand) |
| 1000017814 | Universal Sequencing Reaction Kit (G400 SM FCL PE50) (IVD for Vietnam and Thailand) |
| 1000017815 | Universal Sequencing Reaction Kit (G400 SM FCL PE100) (IVD for Vietnam and Thailand) |
| 1000017816 | Universal Sequencing Reaction Kit (G400 SM FCL PE150) (IVD for Vietnam and Thailand) |

# 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 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, Bangkok (Thailand,Asia-Pacific); Brisbane (Australia, Oceania); Riga (Latvia, Europe); and San Jose (the USA, Americas) are established to ensure sufficient supply of maintenance parts for major regions.

Free installation and system verification services (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.

*Unless otherwise informed, all sequencers and sequencing reagents are not available in Germany, USA, Spain, UK, Hong Kong, Sweden and Belgium.

# All products

## High, medium and low throughput, all included

### DNBSEQ-G50

Compact and flexible sequencers for small whole genome and targeted sequencing offered as part of total packages.

### DNBSEQ-G400

Stable and flexible sequencer, for medium to large genome sequencing projects.

### DNBSEQ-T7

Fast and flexible ultra-high-throughput sequencer, for large genome sequencing projects and population studies.


**MGI Tech Co., Ltd.**

Building 11, Beishan Industrial Zone,
Yantian District, Shenzhen.CHINA
518083

en.mgi-tech.com MGI-service@mgi-tech.com

**4000-966-988**



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