

Genetic Sequencer DNBSEQ-G50

Our Most Accessible Sequencer For You











- PE100 sequencing in only 48 hours, up to 60 Gb yield per run
- Applicable in a wide range of areas: scientific research, clinical applications
- High quality data available at high-altitude and marine environment



Introduction

DNBSEQ-G50: versatile yet intuitive sequencing workflows in one dedicated integrated instrument

A wide range of throughput and flexible turnaround time satisfies various clinical and research applications such as targeted DNA&RNA sequencing, pathogen identification, copy number variation detection, etc

DNBSEQ[™] technology, an cutting-edge Nanoarray Sequencing Technology, delivers multiple read lengths and optimized sequencing time, enabling you to complete sequencing in a short period of time with high quality yield in standard FASTQ format.



Applications

Scientific Research

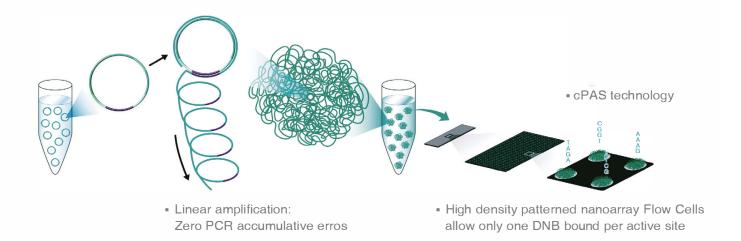
- Whole Genome Sequencing
- Targeted DNA/RNA Sequencing
- Whole Exome Sequencing
- Transcriptome Sequencing
- RNA-Seq
- Small RNA Sequencing
- ChIP-Seq
- Single Cell Sequencing (DNA , RNA)

Clinical Application

- NIPT
- PGS/PGD
- Chromo-Seq/CNV-Seq
- Metagenomic Sequencing
- Rapid Pathogenic & Microbial Testing
- Cancer Panels
- Monogenic Disorder Detection
- Targeted Gene Sequencing



MGI'S PROPRIETARY DNBSEQ TM TECHNOLOGY



INCREASED ACCURACY

No PCR amplification required. Our unique Rolling Circle Replication (RCR) technology employed in DNBSEQ ™ library construction eliminates errors associated with PCR. Only the original template DNA is used to generate copies and therefore amplification errors do not accumulate, resulting in greater accuracy for detection of significant mutations such as Indels and SNPs.

DECREASED DUPLICATES

Optimized Patterned Array ensures that only one single DNB is attached at each spot, which results in greater saturation of DNB on the Flow Cell with unprecedented uniformity. This enables an industry-leading with reduced duplicate rate.

REDUCED INDEX HOPPING

MGI platform's unique library preparation method and RCR amplification results in much lower index hopping rates compared with other platforms, at a rate of 0.0001%~0.0004%.

Features

Flexible

Various read length options & Compatible with different sample types

- Read length available: SE50, PE50, SE100, PE100
- Compatible with samples from human, plant, animal, bacteria, etc

Accessible

Cost-effective & Adaptable in different operating environment

- Sequencing even under low pressure at high altitude or marine environment
 - ▶ Improved Flow-Cell platform
 - ► Microfluidic technology
- Small footprint, low consumable cost, affordable instrument price

Intelligent

Fully-automated operation & Integrated analysis software

- Sample loading, sequencing and data analysis in a single instrument
- Integrated DNB loading system providing accurate genetic analysis with minimal hands-on time and effort
- The built-in analysis software providing basic analysis of sequencing data in FASTQ format and calculating quality scores across all bases
- Allowing installation of third-party software locally or in the cloud

DNBSEQ-G50 Specifications

Flow Cell Parameters

Flow Cell											
No. of Lanes	1 lane	Read Lengths	Single-end	SE50 / SE100	Sequencing Time*	12-48h					
			Paired-end	PE50 / PE100							
Max. Effective Reads	300M	Data Output	10.5 - 60G / run		Date Quality**	SE50 Q30 ≥ 85% SE100 Q30 ≥ 80% PE50 Q30 ≥ 80% PE100 Q30 ≥ 75%					

^{*} 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.

Complete Solution

Sample preparation

► Available MGI Sample Preparation Kit Series

Basic Research Clinical Applications

Input Requirement: As low pg level Standardized Procedure

▶ The Automated Sample Preparation System MGISP-100

Fully-Automated Accurate, Reproducible



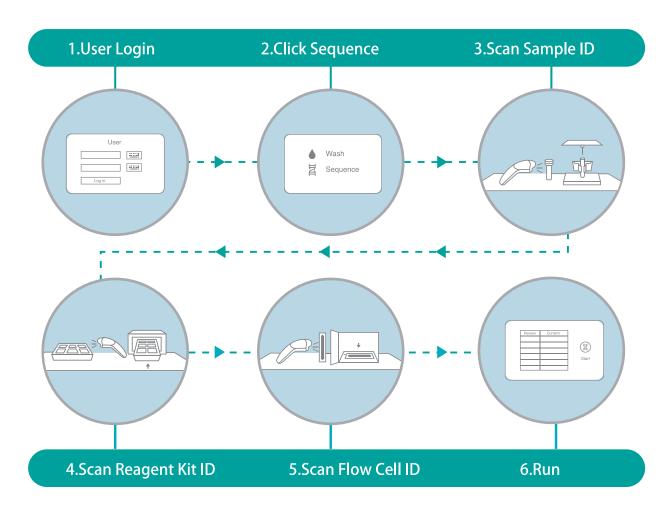








Gene Sequencing





ZLIMS

Zebra LIMS (Laboratory Information Management System)

The system enables real-time sample tracking throughout the workflow. With integrated data analysis platform, DNBSEQ-G50 can download, store and manage sequencing data and offer an end-to-end solution from sample to sequencing report.

Compatible Analysis Softwares

- Pathogen Fast Identification System
- Whole Exome Sequencing Analysis System
- Single Cell Copy Number Variation Analysis System
- Chromosome Copy Number Variation Analysis System





