MGI

Portable and Easy-to-use Genetic Sequencer

Gene sequencer
DNBSEQ-E25

Easy installation

Easy-to-use cartridge
No environmental requirement

Simple sequencing

Ready to use in 10 minutes
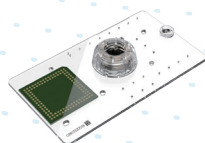Built-in bioinformatics enables full work-flow from sample to report

DNBSEQ-E25 is a small-sized and light-weighted genetic sequencer that can achieve high-speed and highly flexible sequencing. Meanwhile, the easy-to-operate feature lowers the operation threshold of a genetic sequencer.

DNBSEQ™ Core Technology + Interagted Sequecning Chip

Integrated signal acquisition module
Nanoscale array site

High speed
High precision
No signal interference

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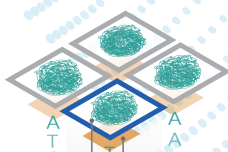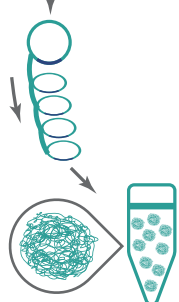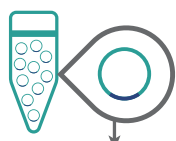
Microfluidic sequencing chip

Sequencing reagent can directly enter the chip without passing through the instrument

Signal acquisition module

Integrated signal acquisition module directly reads the base signal
No need for traditional optical system

Self-luminous biochemical system

Signal can be generated without external excitation light source
Making the instrument more portable and stable for multiple scenarios

Performance parameters

Number of Reads*	Sequencing Reagent	Data Output	Turnaround Time	Q30[§]
25M	SE100 (fast version)	2.5GB	~5 hour	>90%
25M	SE100 (standard version)	2.5GB	~8 hour	>90%
25M	PE150	7.5GB	~20 hour	>80%

[*] The maximum number of valid reads is obtained by running a specific standard library, and the actual application library will fluctuate by the sample type and library construction method.

[†] SE100 consumables can be used for SE50 sequencing, PE150 consumables can be used for PE100 sequencing, and read lengths can be customized in the sequencer user interface.

[‡] Turnaround times include DNB loading and FASTQ generation time, excluding tag sequencing time.

[§] The percentage of bases above Q30 and the running time are averaged over the entire run for a specific standard library, and the actual application performance is affected by sample type, library quality, insert length, etc.

Standard model (DNBSEQ-E25)
stable data output

Sequencer host + Calculation module (standard)

Standard model computing module
Process the original data efficiently collected by the host and output FASTQ data in standard format.

Extended model (DNBSEQ-E25A)
More room for adaptation and expansion

Sequencer host + High configuration + Plus

Scalable Computing Module
On the basis of the standard model, the bioinformatics process can also be integrated to realize the combination of sequencing and analysis