Achieving Q40 (85%*): Improved Data Quality on DNBSEQ™ Platforms**

Experience Improved Sensitivity and Precision in Detection

With a quality score exceeding 85%* at Q40, coupled with a low duplication rate and reduced index hopping, there an improvement in the accuracy and sensitivity of SNPs (Single Nucleotide Polymorphism) and InDels (Insertion-Deletion) detection.

Explore the Lower Limit of Detection

Experience increased sensitivity and reduce the detection limit to 0.1% VAF, enabling the identification of variants overlooked by other sequencing platforms. This increased sensitivity is especially beneficial for applications requiring high sensitivity such as liquid biopsy and MRD (minimal residual disease).

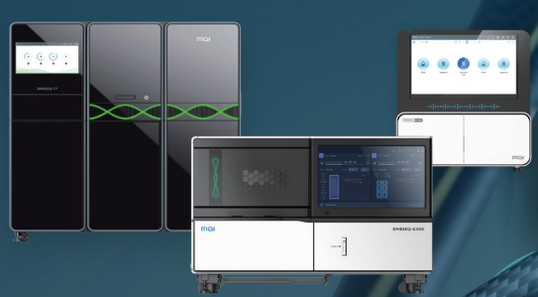
Elevate Your Sequencing Efficiency with Less Raw Data

Achieve high-quality results with Q40 even at lower amount of raw data, facilitating scalable sequencing and simultaneously reducing time and cost.

Streamline Your Workflow with Our One-Stop Solution

Integrated cartridges accommodate different types of adapter libraries, eliminating the need for hands-on time when to replace sequencing primers.

By adopting the DNBSEQ™ technology with the innovative StandardMPS 2.0 sequencing reagents, this upgrade delivers an impressive proportion of 85% or higher for base quality scores reaching or exceeding Q40 during the sequencing process. Users can leverage this high-quality sequencing data to identify Single Nucleotide Polymorphisms (SNPs) and Insertion-Deletion variations (InDels) with better accuracy and sensitivity. The StandardMPS 2.0 reagents provide a reliable and efficient solution for both research and clinical applications, allowing users to get access to highly accurate genomic data in their studies.



*Q40 (>85%) refers to the sequencing quality for read length of PE150 and below.

**This version of brochure shows the Q40 performance from DNBSEQ-G99, DNBSEQ-G400 and DNBSEQ-T7. If you have questions on Q40 for other DNBSEQ™ platforms, please kindly contact our local sales representatives.

StandardMPS 2.0 Reagent

Technical Features

DNA Polymerase and MDA Enzyme Optimization

By selecting DNA polymerase mutants with better sequencing polymerization efficiency, and MDA (Multiple Displacement amplification) enzyme with better second strand displacement capabilities, the signal intensity and stability have been improved.

dNTP Optimization

The dNTP fluorescent dyes have been optimized to reduce crosstalk between bases, which improves base recognition accuracy, and reduces sequencing errors.

Algorithm Optimization

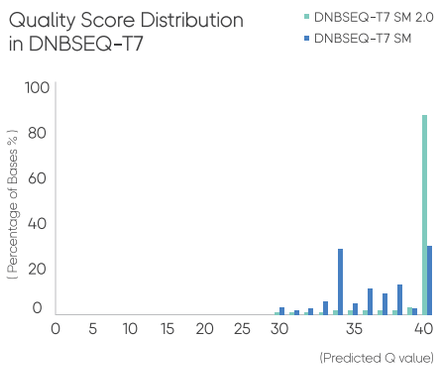
Q-value table is trained with data more closely reflects actual qualities by unitilizing high-fidelity enzyme and PCR-Free library preparation method to reduce the bias introduced by errors in upstream experiments. With more accurate model training, the precision of data interpretation has been improved, ensuring that the sequencing results more closely match empirical base calling accuracies.

DNBSEQ-G99
DNBSEQ-G400
DNBSEQ-T7

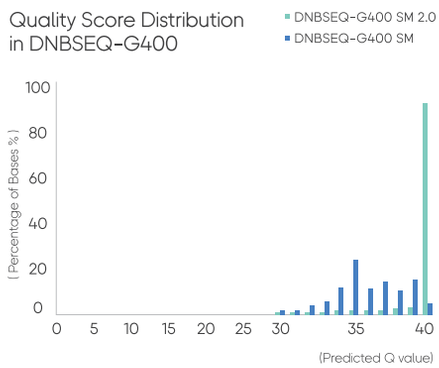
Q40 > 85%*

MGI Platforms

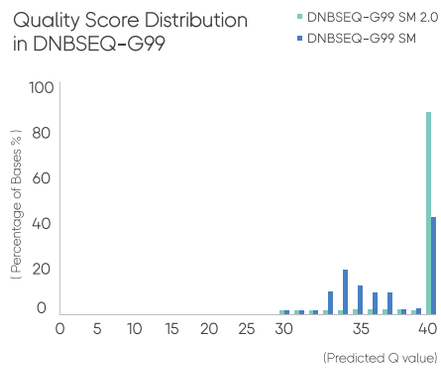
Performance



Sample: NA12878
Library Prep Kit: MGIEasy PCR-Free DNA Library Prep Set
Sequencing platform and read length: DNBSEQ-T7 PE150



Sample: NA12878
Library Prep Kit: MGIEasy PCR-Free DNA Library Prep Set
Sequencing platform and read length: DNBSEQ-G400 PE150



Sample：E.coli
Library Prep Kit: MGIEasy Universal DNA Library Prep Set
Sequencing platform and read length: DNBSEQ-G99 PE150

By comparing the Q-value distribution charts of different DNBSEQ™ platforms, we found that StandardMPS 2.0 (SM 2.0) has significantly improved sequencing quality compared to StandardMPS (SM). Specifically, in SM 2.0, the percentage of bases with a Q score greater than or equal to Q40 exceeds 85%. This result further highlights the outstanding performance of StandardMPS 2.0 (SM 2.0) in sequencing quality.

*Q40 (>85%) refers to the sequencing quality for read length of PE150 and below.

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