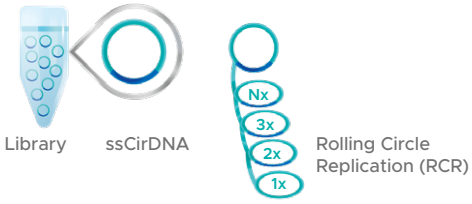
How does DNBSEQ™ sequencing technology work?

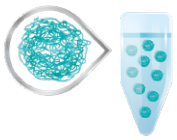
DNBSEQ™, a cutting-edge sequencing technology developed by MGI and built around DNA nanoballs (DNBs), enables highly accurate and efficient DNA sequencing.

1 LIBRARY PREPARATION



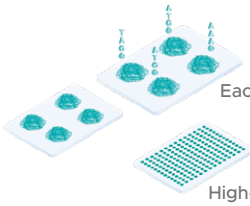
DNBSEQ technology utilizes a versatile library prep process. First, double-stranded DNA is fragmented and equipped with adapter sequences at both ends. These fragments are then converted into single-stranded circles (ssCirDNA) through splint oligonucleotide hybridization and nick repair. Next, a technique called rolling circle replication (RCR) efficiently amplifies the ssCirDNA, generating billions of identical copies in a single reaction. Unlike PCR, RCR minimizes bias and errors. Finally, under proprietary conditions, the long strand of amplified DNA (concatemer) folds into compact, spherical structures called DNA nanoballs (DNBs), ready for sequencing.

2 DNB MAKING



300-500 template copies fold into a tiny DNA nanoball ~200 nm in diameter

3 DNB LOADING

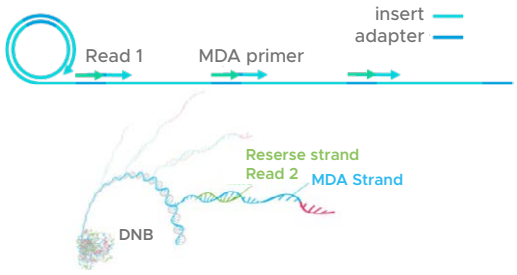


DNBs are loaded onto a flow cell etched with a pattern of uniformly spaced ~200nm binding sites at submicron distances. Proprietary loading buffers ensure DNBs stick to the same spots for multiple sequencing, cycles maintaining strong signals. These refinements enable exceptional sequencing accuracy with minimal reagent consumption.

Combinatorial probe-anchor synthesis (cPAS) chemistry hybridizes sequencing primers to the DNBs and fluorescently labeled reversibly terminated probes are incorporated by a proprietary DNA polymerase in consecutive sequencing cycles. The fluorescent probes are then excited by laser light and the DNB array is imaged using advanced cameras.

After completing the first strand, the second, complementary strand attached to the original DNB is synthesized by controlled multiple displacement amplification (MDA) and sequenced. This generates a stronger second strand signal with high sequencing accuracy.

4 SEQUENCING



5 ANALYSIS

DNBSEQ technology utilizes signal intensities from the fluorescent probes to determine base calls and assigns a quality score. MGI's proprietary sub-pixel registration algorithm extracts precise fluorescent intensity at the sub-pixel level for each DNB. This unique approach significantly enhances the precision of base call determination, contributing to faster data processing and highly accurate sequencing results.

Higher Accuracy | **Rapid Speed and Scalability** | **Lower Cost**

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