GENO1®: A NOVEL CIRCULAR LIBRARY PREP FOR RAPID AND UNIVERSAL NGS ANALYSIS

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LIBRARY PREP – BOTTLENECK OF LIQUID BIOPSIES

Traditional library prep methods are **slow, labor-intensive and complex**, increasing operational demands and negatively impacting decentralised laboratories.

Unnecessary complexity **introduces errors and reduces data quality**, thereby limiting clinical utility.

GENO1® REMOVES THE BOTTLENECK

RAPID & SIMPLE

Streamlined library prep from the very first step, with **minimal hands-on time** and **fast turnaround**. Eliminates the need for specialized equipment, supporting use in diverse settings.

EXTREMELY SENSITIVE

Detects rare mutations, enabling **early cancer detection** and **minimal residual disease** monitoring.

COST-EFFICIENT

Simplified workflow and integration of **early sample indexing** lower overall costs.

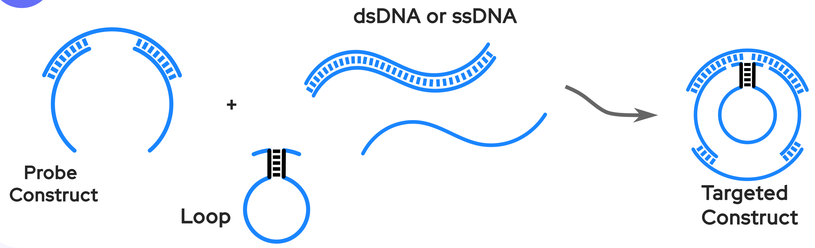
PLATFORM AGNOSTIC

The **PCR-free workflow generates multiple library formats**, allowing seamless integration across a wide range of NGS platforms.

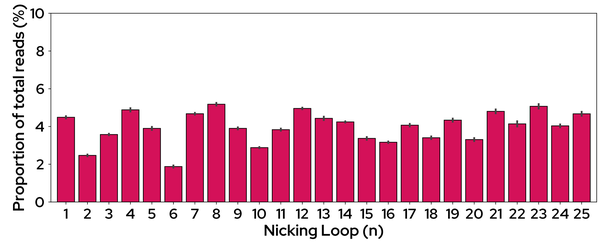
FIND FULL DETAIL

IN RECENT STUDIES

1 DNA CIRCULARIZATION WITH EARLY SAMPLE INDEXING

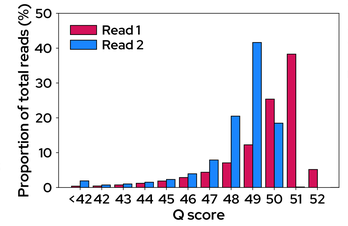


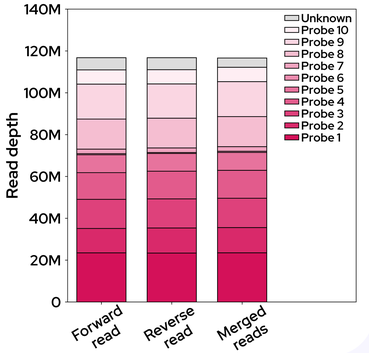
Twenty-five different Loops competed for their incorporation into Converted Circular DNA. The Loops performed comparably with **no preferential enrichment**, demonstrating feasibility of early sample indexing.



2 DIRECT SEQUENCING OF CIRCULAR LIBRARIES

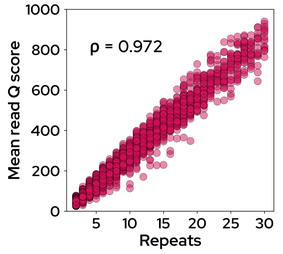
Direct circular sequencing on **PacBio Onso™** yielded **high Q scores** and **uniform read composition** across ten probes for both forward and reverse reads.

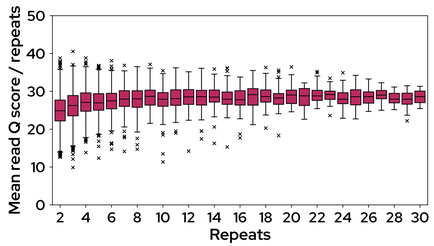




3 SHORT-READ NANOPORE SEQUENCING

Concatemers composed of **short-read repeats** form Nanopore-compatible libraries. Alignment of repeats into **consensus sequence** improves accuracy with repeat count, reaching unprecedented **Q scores (up to 1000)**.

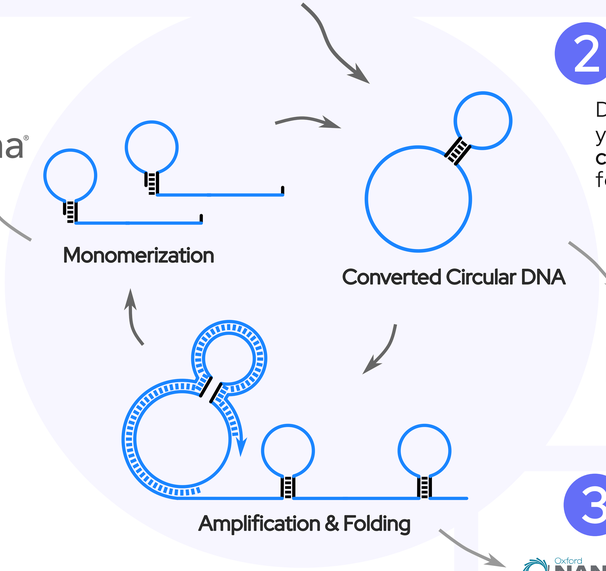




4 CLINICAL VALIDATION

Serial plasma samples (n = 80) from ten colorectal cancer patients with **known KRAS variant** were analyzed. **Geno1®** showed **substantial and perfect agreement** with **ddPCR** and **Idylla**, and with **Ion AmpliSeq CHPv2**, respectively (Cohen's Kappa).

	GENO1® +	GENO1® −	Cohen's Kappa
ddPCR (n = 80)	35	4	0.70
	8	33	
Idylla (n = 58)	31	4	0.79
	2	21	
Ion AmpliSeq (n = 10)	7	0	1.0
	0	3	



Matched KRAS variant detected by Geno1® (violet) and by reference method ddPCR (red). Geno1® revealed also **previously undetected variants (grey)**, analysed with a 282-probe panel.