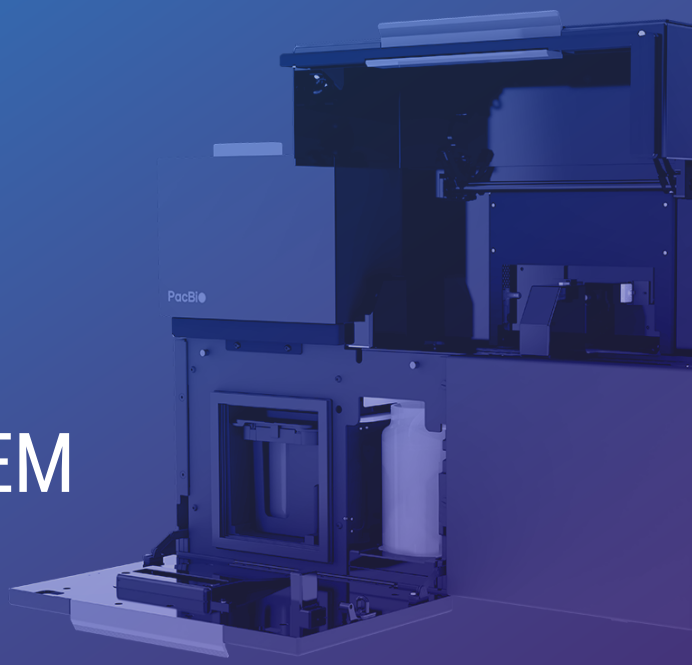
Product note

SEQUENCING BY BINDING (SBB) ON THE ONSO SYSTEM



Introduction

SBB employs an innovative sequencing chemistry that delivers extraordinary accuracy due to ultra-low levels of sequencing noise. By incorporating native nucleotides, optimizing chemistry at each step, and minimizing molecular scarring, SBB provides significantly higher quality data than existing technologies.

Sequencing by binding (SBB)

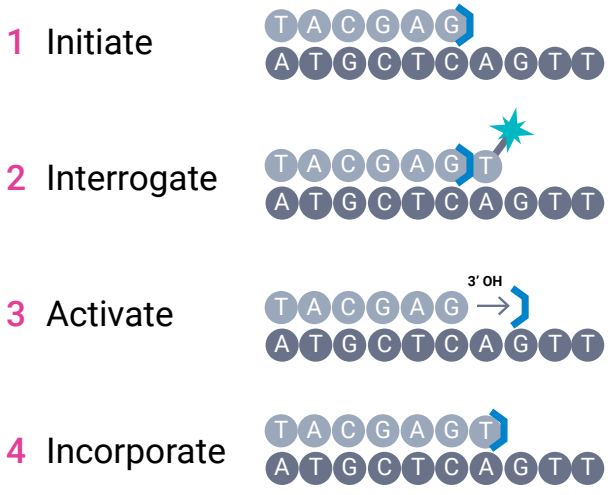


Figure 1. Conceptual diagram of SBB sequencing.

Key features of SBB

- Extraordinary accuracy — 90% of bases ≥Q40
- Ultra-low sequencing noise
- High-confidence sequencing through repetitive regions
- Negligible duplication rate
- Minimal index-hopping

(1) Each cycle initiates with a 3' reversible blocked nucleotide. (2) Fluorescently labelled nucleotides are then flowed over the flow cell allowing for the appropriate base to bind. Unbound nucleotides are washed away so that the base can be interrogated with reduced background signal. (3) The 3' end of the nucleotide is activated via removal of the reversible terminator. (4) Native, unlabeled, reversible blocked nucleotides are flowed over the flow cell and the cognate base can incorporate into the growing strand. The process is then repeated for each new sequenced base.

By separating the interrogation and incorporation steps, and optimizing chemistries for each step, SBB chemistry enables high signal-to-noise levels to be achieved. Moreover, the lack of molecular scarring from the use of native nucleotides for incorporation drives industry-leading accuracy.

	Sample applications		
	WGS[1] (2x150bp)	scRNA-Seq[2] (28x90bp)	Exome[2] (2x100bp)
Number of paired-end reads	1,033 M	1,000 M	1,062 M
Total yield	151 Gb	58 Gb	116 Gb
Q score (≥90% of bases)	50	46	49

1. Sequenced with Onso native library prep kit
2. Sequenced using converted libraries

Table 1. Sample output metrics from the Onso™ sequencing system.

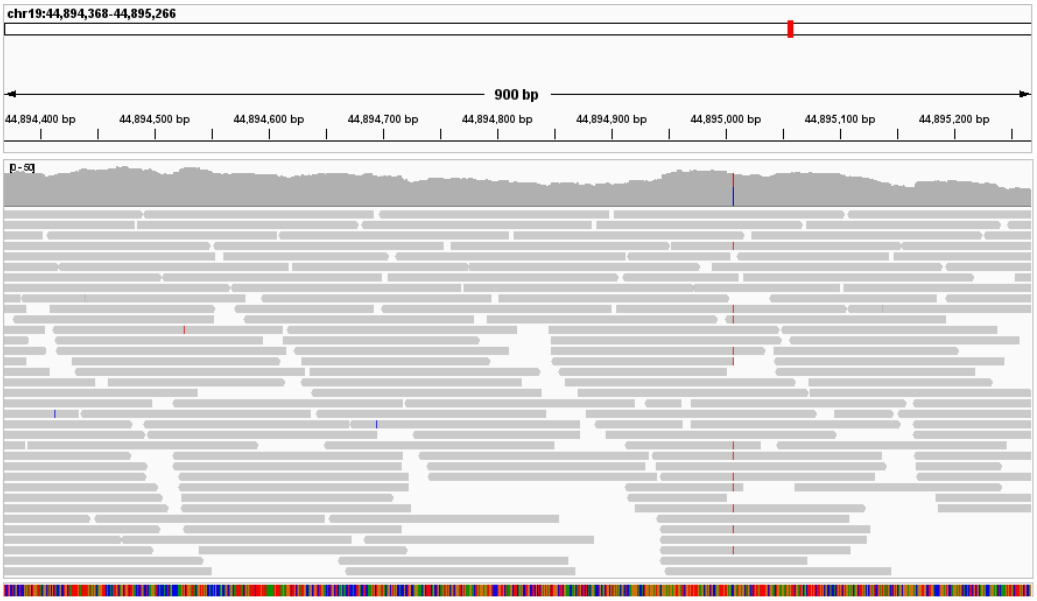


Figure 2. SBB sequencing delivers near perfect reads with >90% of bases above Q40, low duplication rates, minimal index-hopping, and sequencing through difficult and repetitive regions.

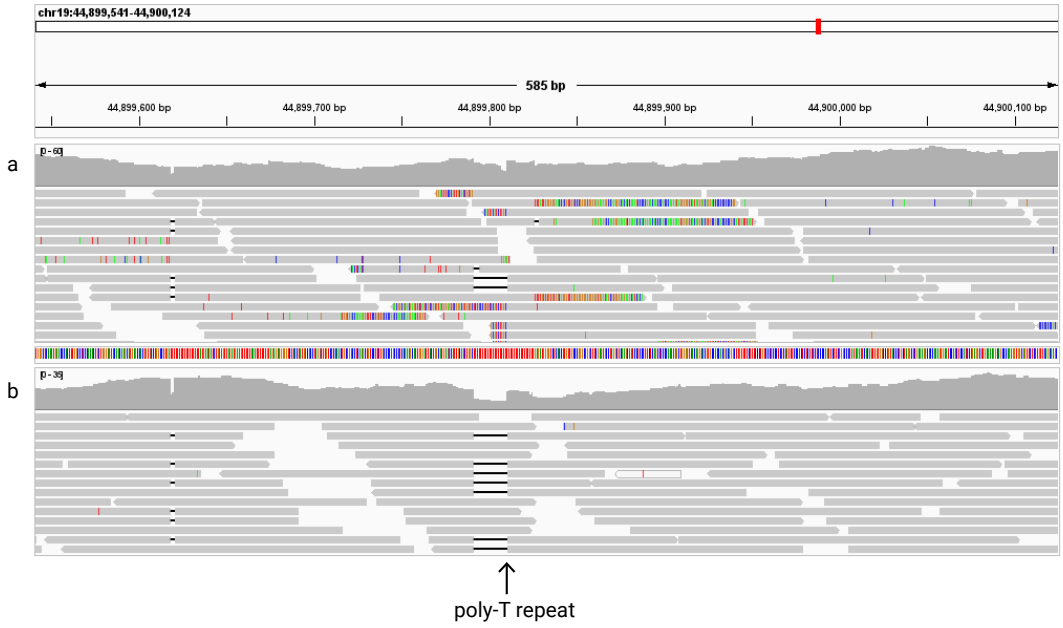


Figure 3. The Onso sequencing system produces near perfect reads through the variable poly-T region within the *TOMM40* gene. (a) SBS sequencing was unable to fully resolve the low-complexity region, with many false positive calls. (b) SBB sequencing was able to fully sequence through and confidently resolve this region, resulting in a call of T16 vs the original estimate of T35.

SBB complete workflow

Onso library prep

- Employ standardized NGS library prep optimized for SBB sequencing
- Create Onso libraries directly from samples
- Adapt existing P5/P7 libraries to an Onso-compatible format

Onso sequencing

- Easily implement workflow into new and existing NGS labs
- Produce highly accurate reads with SBB chemistry
- Individually addressable flow cell lanes

Data analysis

- Generate industry-standard FASTQ output
- Easily integrate with currently available secondary analysis tools

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