Application brief

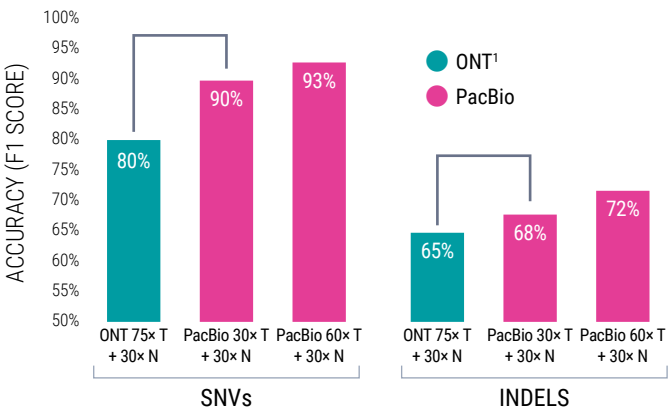
HIFI SEQUENCING ENABLES GREATER ACCURACY OF SOMATIC VARIANT CALLING

The extraordinary accuracy and long read lengths of PacBio® HiFi sequencing overcomes the challenges of detecting variation in cancer genomes faced by other technologies.

High-quality HiFi reads detect a wide range of cancer-specific somatic variation including single nucleotide variants (SNVs), structural variants (SVs), insertions and deletions (indels), copy number variations (CNVs), and methylation in a single assay.

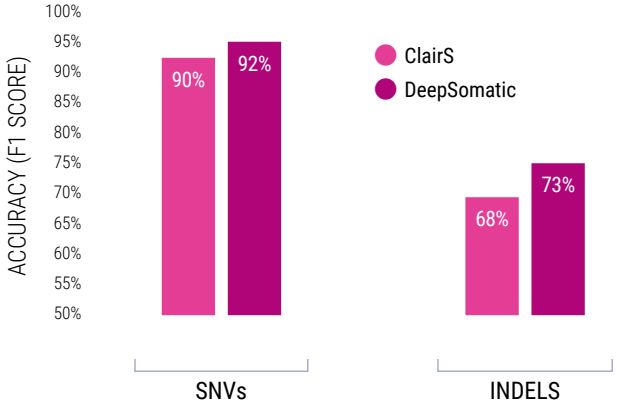
HiFi sequencing shows improved somatic variant calling accuracy with less sequencing relative to other technologies.

INCREASED ACCURACY WITH 2.5× LESS TUMOR SEQUENCING



In paired tumor/normal sequencing of the breast cancer cell line HCC1395, HiFi sequencing on the Revio® system yielded greater somatic variant calling accuracy with ClairS for SNVs and indels than Oxford Nanopore Technologies even at 2.5× less sequencing.

PACBIO HIFI SEQUENCING



Even greater accuracy can be achieved with HiFi sequencing for both SNVs and indels at 30× tumor/30× normal coverage with the DeepSomatic variant caller.

A streamlined whole genome sequencing tumor-normal workflow

Blood/tissue extraction

The Nanobind® tissue kit enables extraction of HMW DNA from blood or tissue

Library prep

Construct single WGS libraries using the SMRTbell® library prep kit 3.0

HiFi sequencing

Highly accurate whole genome sequencing on the Revio and Vega™ systems

Analysis

On-board 5mC and 6mA methylation calling and compatible callers for detection of somatic variants

For more details on detecting somatic variants with HiFi WGS, see the application note.[2]

1. ONT data sequenced on a R10.4.1 PromethION flowcell as presented in Zheng et al., 2023. 2. https://www.pacb.com/wp-content/uploads/Application-note-Robust-detection-of-somatic-variants-from-tumor-normal-samples-with-highly-accurate-long-read-whole-genome-sequencing.pdf

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