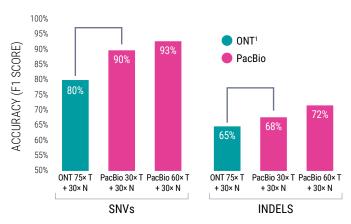
## HIFI SEQUENCING ENABLES GREATER ACCURACY OF SOMATIC VARIANT CALLING

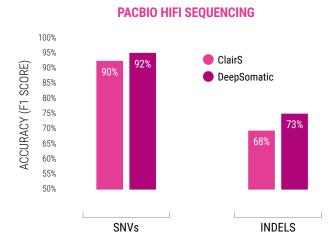
The extraordinary accuracy and long read lengths of PacBio® HiFi sequencing overcomes the challenges of detecting variation in cancer genomes faced by other technologies.

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**

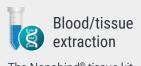




In paired tumor/normal sequencing of the breast cancer cell line HCC1395, HiFi sequencing on the Revio $^{\circ}$  system yielded greater somatic variant calling accuracy with ClairS for SNVs and indels than Oxford Nanopore Technologies even at 2.5× less sequencing.

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



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



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



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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