

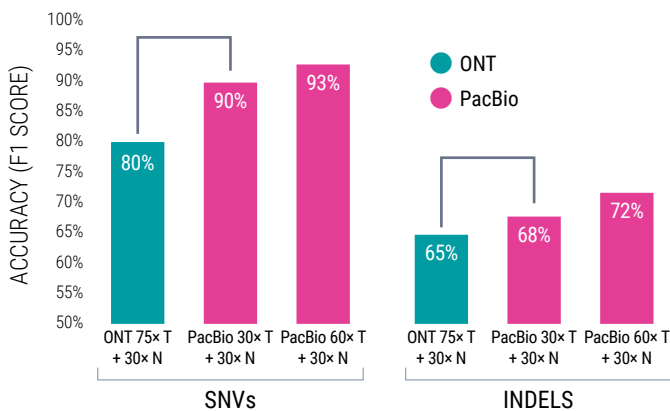
# HIFI SEQUENCING ENABLES GREATER ACCURACY OF SOMATIC VARIANT CALLING

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

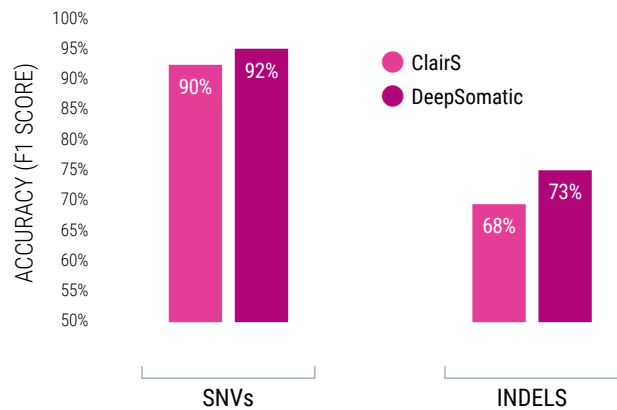
High-quality HiFi reads detect a wide range of cancer-specific somatic variation including single nucleotide variants (SNVs), structural variants (SVs), insertions and deletions (indels), copy number variations (CNVs), and methylation in a single assay.

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

## INCREASED ACCURACY WITH 2.5× LESS TUMOR SEQUENCING



## PACBIO HIFI SEQUENCING



In paired tumor/normal sequencing of the breast cancer cell line HCC1395,<sup>1</sup> 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.

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



For more details on detecting somatic variants with HiFi WGS, [see the application note.](#)<sup>2</sup>

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>