

# FPGA-ACCELERATED GENOMIC DATA ANALYSIS WITH HUGENOMIC NANOPOLISH

## INTRODUCTION

Analyze more than 800,000 long reads of genomic data (about 102 GB) in 3 hours thanks to Huxelerate Hugenomic Nanopolish<sup>1</sup>.

## PRODUCT OVERVIEW

Huxelerate Hugenomic Nanopolish enables **ultra-fast signal-level analysis of large datasets** of Oxford Nanopore Sequencing data.

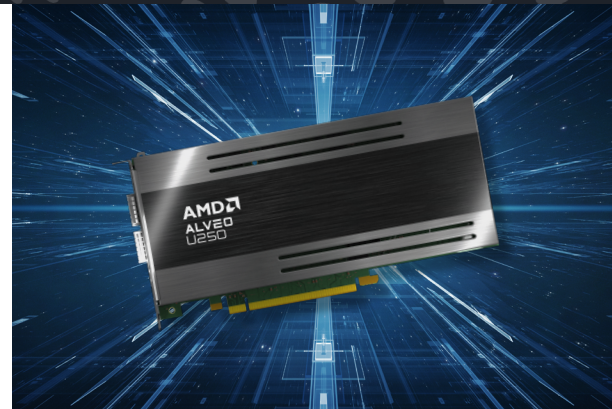
The software is based on Nanopolish ( [github.com/jts-nanopolish](https://github.com/jts-nanopolish) ) and can calculate an improved consensus sequence for a draft genome assembly, detect base modifications, call SNPs and indels with respect to a reference genome and more.

The **accelerated implementation** exploits **FPGAs to accelerate the computation and provide high performance and faster time to result**.

Current implementation allows to accelerate the eventalign tool, **reducing computational time from days to hours when compared to software only executions**.

The functionalities provided in this release, mirror Nanopolish v0.13.2.

Huxelerate supports academic research. If you are willing to use Hugenomic Nanopolish for your academic research, please contact us at [info@huxelerate.it](mailto:info@huxelerate.it).

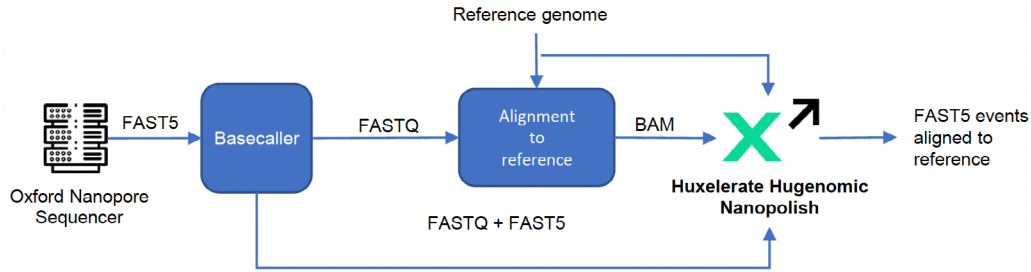


## HIGHLIGHTS

- Ultra-fast genomic analysis
- Faster time to results
- 10x performance improvement

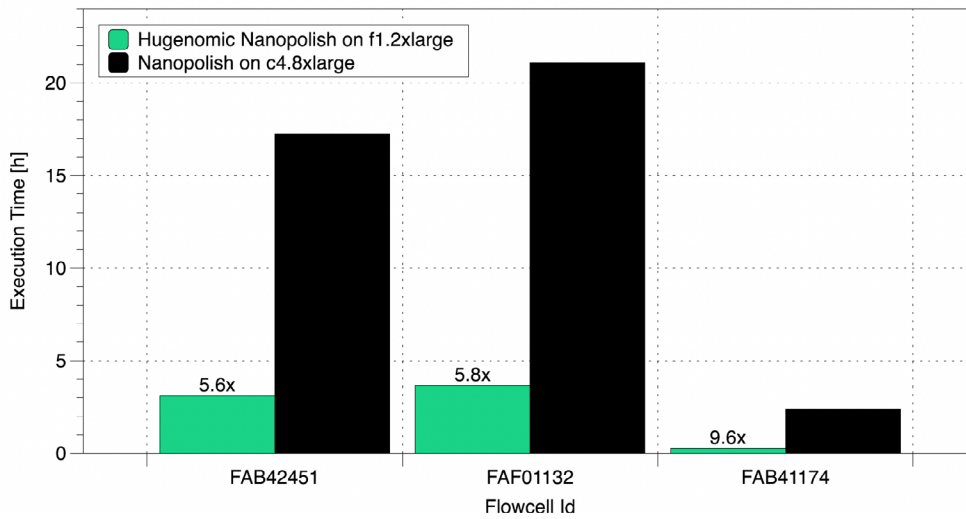
<sup>1</sup> Dataset taken from WGS Consortium: <https://github.com/nanopore-wgsconsortium/NA12878/blob/master/Genome.md>  
flowcell\_id : FAB42451

## SOLUTION OVERVIEW



## SOLUTION BENCHMARKS

**Huxelerate Hugenomic Nanopolish Performance vs Original Nanopolish**



Dataset WGS Consortium: <https://github.com/nanopore-wgs-consortium/NA12878/blob/master/Genome.md>  
 Software equivalent tested on c4.8xlarge (2.9 GHz Intel Xeon E5 2666 v3) using 36 cores

## NEXT STEPS

- Learn more about [Huxelerate](#)
- Learn more about [Huxelerate Hugenomic Nanopolish](#)
- Reach out [Huxelerate Sales](#)

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