Accelerating WGS Insights

with GPU-Powered Parabricks® and DNBSEQ™

Accurate
>99% concordance with truth set

Fast
Variant calling as fast as 6 mins

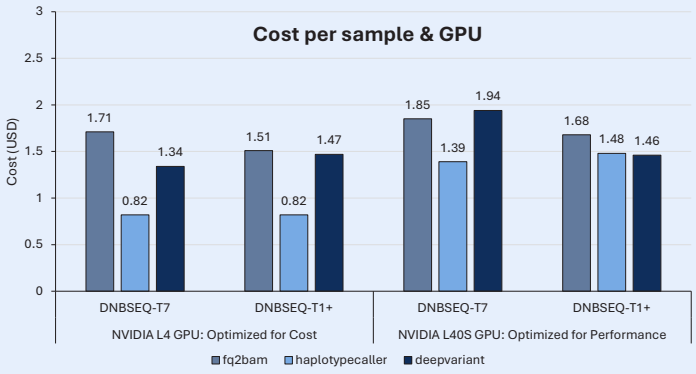
Cost Effective
As low as $1 per sample analysis

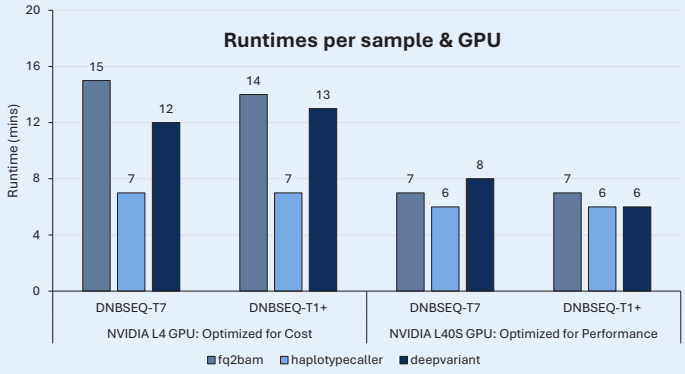
High-throughput sequencers like Complete Genomics DNBSEQ-T7 and DNBSEQ-T1+ can generate terabytes of data, enabling projects that span whole-genome disease cohorts, tumor-normal comparisons, and the discovery of germline variants. In most cases, the rate-limiting step is no longer the sequencing, but the analysis. FASTQ files need to be converted into BAM and VCF results for interpretation. Traditional CPU-based workflows can require tens of hours per sample, limiting the pace of discovery and clinical utility.

NVIDIA® Parabricks®, a scalable genomics software suite for secondary analysis, addresses this bottleneck by providing GPU-accelerated versions of open-source tools—including HaplotypeCaller and DeepVariant. As a result, Parabricks increases speed with faster runtimes and reduces costs—while enhancing accuracy and maintaining concordance with established truth sets.

From sequencing to variant calling in minutes and under $2

- Optimized for performance, the NVIDIA L40S GPU enables alignment (fq2bam) in as little as 7 minutes and variant calling (HaplotypeCaller or DeepVariant) in 6–8 minutes for 30× WGS datasets generated by DNBSEQ-T1+ or DNBSEQ-T7.
- Optimized for cost, the NVIDIA L4 GPU performs alignment for under $1 and variant calling for under $2 per 30× WGS dataset generated by DNBSEQ-T1+ or DNBSEQ-T7.





Variant calling performance on DNBSEQ-T7 sequenced WGS datasets processed using Parabricks achieved F1-scores >0.99, with recall and precision consistently above 98% and 99% respectively, demonstrating both accuracy and reliability in high-throughput clinical and research workflows.

To learn more, visit completegenomics.com

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DNBSEQ-T7 DNBSEQ-T1+ Parabricks