



## **4.3.1-1 Release Notes**

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## Highlights:

- New tool, [deepsomatic](#) for somatic variant calling.
- The latest Parabricks toolkit (v4.3.1) is now fully supported on Grace Hopper, see [Grace Hopper Superchip](#).
- [deepvariant](#) version 1.6.1 updated, new option added.
- [haplotypcaller](#) bug fixes and 3 new options added.
- [mutectcaller](#) a few bug fixes.
- [rna\\_fq2bam](#) bug fixes and feature added in wrapper.
- [minimap2 \(Beta\)](#) bug fixes, version update, and improved support for ONT data.
- [fq2bamfast](#) and [fq2bam](#): Bug fixes and performance improvements. Additional option to monitor approximate CPU utilization and host memory usage during execution (`--monitor-usage`).

## New Tools

With Parabricks 4.3.1 we are releasing an accelerated [deepsomatic](#) tool. DeepSomatic builds on the deep learning-based variant caller DeepVariant. It processes aligned reads from tumor and normal samples (in BAM or CRAM format), generates pileup image tensors, classifies these tensors using a convolutional neural network, and outputs somatic variants in standard VCF or gVCF files.

## Improvements

### Tool Updates

[haplotypcaller](#):

- Adds the following new options:
  - `--minimum-mapping-quality`
  - `--mapping-quality-threshold-for-genotyping`
  - `--enable-dynamic-read-disqualification-for-genotyping`
- Improved performance by leveraging AVX512 instructions for CPU-based PairHMM computation.

#### mutectcaller:

- Improved performance by leveraging AVX512 instructions for CPU-based PairHMM computation.

#### deepvariant:

- Updates to match the baseline version v1.6.1.
- Adds the new option `--haploid-contigs`
- Improved performance for short-read mode through increased GPU utilization and kernel optimizations.

#### rna\_fq2bam:

- Supports passing `--out-chim-type` multiple times.

#### fq2bamfast:

- Improved alignment performance on Hopper GPUs through increased use of [DPX instructions](#).
- Improved performance on multi-GPU runs; for example, on [DGX H100](#).
- Improved error detection for improper FASTQ inputs through `--in-fq` or `--in-se-fq`. Previously recorded a utf-8 decode error.
- Additional option to monitor approximate CPU utilization and host memory usage during execution (`--monitor-usage`).

#### [fq2bam](#):

- Improved error detection for improper FASTQ inputs through `--in-fq` or `--in-se-fq`. Previously recorded a utf-8 decode error.
- Additional option to monitor approximate CPU utilization and host memory usage during execution (`--monitor-usage`).

#### [minimap2](#):

- Updated map-pbmm2 preset to match the updated versions of minimap2 (v2.26) and pbmm2 (v1.13.0).

## Bug Fixes

- [mutectcaller](#) and [haplotypcaller](#): Fixed a wrong alignment offset value in smith-waterman algorithm.
- [mutectcaller](#) and [haplotypcaller](#): Fixed a crash on GPU when running in low memory mode.
- [mutectcaller](#): Fixed the wrong active probability value when the pileup size is 0.
- [mutectcaller](#): Fixed a max coverage overflow bug.

- [rna\\_fg2bam](#): Fixed an error when passing "WithinBAM\_SoftClip" or "WithinBAM\_HardClip" to `--out-chim-type`.
- [minimap2 \(Beta\)](#): Fixed support for Oxford Nanopore Technologies (ONT) data with minimap2.
- [fq2bamfast](#): Fix rare erroneous assertion (`Workspace not big enough, expected desiredSize &lt;= cubWorkspaceSize, exiting`). Case will now be handled correctly and fall back to CPU recovery if needed.
- [deepvariant](#): Fixed bug related to Smith-Waterman computation on CPU.

For further information see the [Parabricks datasheet](#).

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