



4.3.0-1 Release Notes

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Highlights:

- New tool, [fq2bam_meth](#) for accelerated DNA methylation analysis.
- Germline resource mode and force calling mode are supported in [mutectcaller](#).
- Support for writing CRAM files using queryname-based sorting has been added into [bamsort](#).
- Parabricks toolkit (v4.2) is now fully supported on Grace Hopper, see [Grace Hopper Superchip](#).
- Performance improvements in [germline](#) and [deepvariant_germline](#) running on DGX H100.
- [deepvariant](#) version 1.6 updated.
- [minimap2](#) performance improvements and bug fixes.
- [fq2bamfast](#) performance improvements and bug fixes.

New Tools

New tool for bisulfite sequencing data [fq2bam_meth](#) based on [bwa-meth](#). Our tool, [fq2bam_meth](#), implements compatible pre- and post-processing around BWA MEM for DNA methylation analysis. It uses the same accelerated alignment code as is used in [fq2bamfast](#) to produce fast and accurate alignment.

Improvements

Tool Updates

[bamsort](#):

- Supports CRAM file write on queryname-based sorting. It auto-detects cram file extension on output file.

mutectcaller:

- Adds the following new options:
 - `--mutect-germline-resource`
 - `--mutect-alleles`
 - `--force-call-filtered-alleles`

deepvariant:

- Updates to match the baseline version v1.6.

minimap2 (Beta):

- Reduced reader buffer size to shorten the time it takes to start processing.

fq2bamfast:

- Speed improvements.
- Added support for BWA MEM options: `-B` (values up to 15), `-T`, `-L`, and `-U`.
- Added support for reads longer than 500 bp using CPU recovery mode (note that speed will be slower and memory usage will be higher). Set `--max-read-length` to the desired max read length for the FASTQ filter.

Improvements spanning multiple tools

- Better messaging in filehandle when reading index files to avoid user confusion.
- Better error checking when reading FASTQ files: checks that *each* FASTQ read name line starts with '@'.

Bug Fixes

- [mutectcaller](#) and [haplotypcaller](#): Fixed a random segfault in bamOut mode.
- [haplotypcaller](#): Fixed an "allele out of index" bug in gvcf mode.
- [haplotypcaller](#): Fixed an GPU shared memory overflow bug in gvcf mode.
- [haplotypcaller](#), [mutectcaller](#) and [deepvariant](#): Fixed a wrong return value 0 when the run fails.
- [minimap2 \(Beta\)](#): Corrected banner name when running minimap2.
- [minimap2 \(Beta\)](#): Fixed overflow issue in postsort.
- [minimap2 \(Beta\)](#): Removed max read size requirement that made some inputs unable to run.
- [fq2bamfast](#): Fix for edge case (related to multiple hits) with `-C` option in BWA MEM to copy auxiliary tags from FASTQ comments.

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

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