



4.2.1-1 Release Notes

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Improvements

Two new beta tools have been released: [fq2bamfast](#) and [minimap2](#).

A new beta pipeline has been released: [pacbio_germline](#).

Performance improvements include [fq2bamfast](#), a faster version of the existing [fq2bam](#) and the ability to run the variant caller in [germline](#) and [deepvariant_germline](#) in parallel with BAM generation.

A number of bugs have been fixed. Most notably, [fq2bam](#) read filtering could have failed with read sizes more than ~500 basepairs.

New Tools

With this release we have added two new tools:

- [fq2bamfast](#)
- [minimap2](#)

We have also added one new pipeline:

- [pacbio_germline](#)

The new beta [fq2bamfast](#) is a re-implementation of accelerated BWA-MEM present in [fq2bam](#) to better utilize GPUs such as A100 and H100.

Improvements

Tool Updates

mutectcaller:

- Adds the following new options:
 - `--active-probability-threshold`
 - `--genotype-germline-sites`
 - `--genotype-pon-sites`
 - `--initial-tumor-lod`
 - `--mutect-bam-output`
 - `--pruning-lod-threshold`
 - `--tumor-lod-to-emit`
 - `-max-reads-per-alignment-start` (as part of the `--mutectcaller-options` option)

fq2bam and associated pipelines: germline pipeline, deepvariant_pipeline, and somatic pipeline:

- New compression options for `--gpuwrite`: use `--gpuwrite-deflate-algo 3` for more compression at slightly slower speed and `--gpuwrite-deflate-algo 0` for more speed, which continues to be the default.
- Fix edge case with FASTQ filtering.

Improvements spanning multiple tools

- Added the `--read-from-tmp-dir` option to [germline pipeline](#) and [deepvariant pipeline](#). It will run the variant caller in parallel with BAM generation. It has been tested on A100 and H100 but might cause out-of-memory on other GPUs.
- Added the `--fq2bamfast` option to [germline pipeline](#), [deepvariant pipeline](#), and [somatic pipeline](#) to use [fq2bamfast](#) for alignment.

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

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