



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_fq2bam](#): 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 <= 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.

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