



Improvements

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Tool Updates

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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).