



4.0.0-1 Release Notes

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Figure 0.

Clara Parabricks 4.0.0-1 is a major release with many significant changes. It streamlines how users get and set up the software and simplifies deployment on different platforms. If you are an existing Parabricks user, review this section to understand the major changes.

Licensing Changes

There is no license required to use NVIDIA Parabricks. The container works out of the box once downloaded.

Users who would like Enterprise Support can purchase NVIDIA AI Enterprise licenses, which provides full-stack support for Parabricks and many other NVIDIA software offerings.

To inquire about Enterprise Support for Parabricks, please reach out to the NVIDIA genomics team at <https://www.nvidia.com/en-gb/clara/genomics/> 

Supported Tools

Starting with v4.0.0-1 the Clara Parabricks toolset focused primarily on those tools that benefit most from GPU acceleration.

If you would like access to one or more of the tools that are no longer available, please contact us in the [developer forum](#).

WDL/Nextflow Workflows

Clara Parabricks containers are compatible with WDL and NextFlow for building customized workflows, intertwining GPU- and CPU-powered tasks with different compute requirements, and deploying at scale.

These enable workflows to be deployed on cloud batch services as well as local clusters (e.g. SLURM) in a well managed process, pulling from a combination of Parabricks and third-party containers and running these on pre-defined nodes.

 ../_images/Workflow%20diagram.png

For further information on running these workflows, and to see the open-source reference workflows, which can be easily forked/edited, visit the [Clara Parabricks Workflows repository](#). This repository includes recommended instance configurations for deploying the GPU-based tools on cloud and can be easily forked/edited for your own purposes.

Improvements

- [deepvariant](#) now implements DeepVariant v1.5.
- [haplotypcaller](#) supports additional original HaplotypeCaller options.
- [deepvariant](#) and [deepvariant_germline](#) support the `--channel-insert-size` option.
- [starfusion](#) now adds `PG:Z:MarkDuplicates` to each output BAM record.

Bug Fixes

- Corrected rna_fq2bam sample code. The `--read-files-command zcat`, while not a required parameter, is needed for correct operation with compressed FASTQ files.
- Updated the list of supported haplotypcaller options.
- Corrected GATK sample code.
- Fixed an fq2bam bug that occurred when many Ns are present in the fastq files.
- General deepvariant performance improvements.

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

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