



Running NVIDIA Parabricks on nf-core

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This guide shows how to run Parabricks on [nf-core](#).

What is NVIDIA Parabricks?

Parabricks is an accelerated compute framework that supports applications across the genomics industry, primarily supporting analytical workflows for DNA, RNA, and somatic mutation detection applications. With industry leading compute times, Parabricks rapidly converts a FASTQ file to a VCF using multiple, industry validated variant callers and also includes the ability to QC and annotate those variants. As Parabricks is based upon publicly available tools, results are easy to verify and combine with other publicly available data sets.

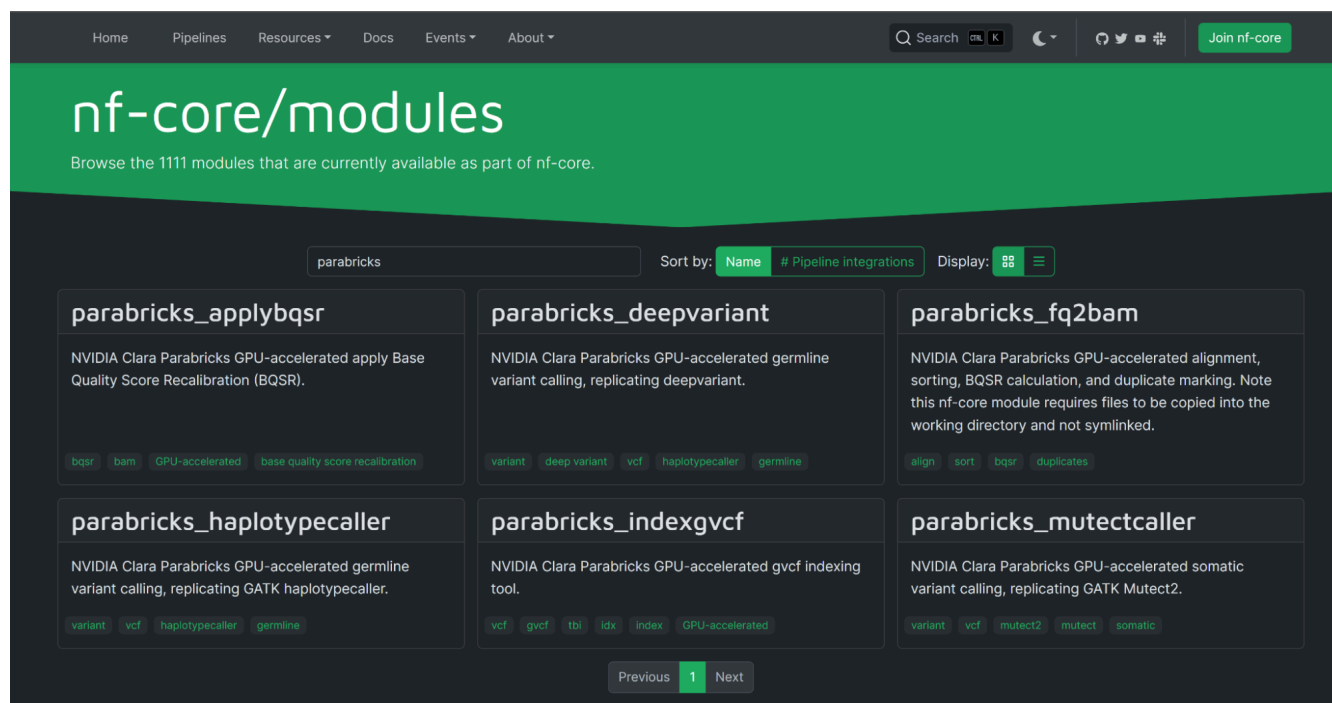
More information is available on the [Parabricks Product Page](#).

Detailed installation, usage, and tuning information is available in the [Parabricks user guide](#).

Finding the Parabricks modules on nf-core

Several Parabricks pipelines can be found on nf-core as modules. These modules can be dropped into existing workflows or used on their own. To read more about nf-core modules, see their [documentation](#).

To find the available Parabricks modules, visit the [nf-core modules](#) page and search for “Parabricks”. The following modules are available:



Running the Parabricks modules on nf-core

Clicking on any module will take you to the homepage for that module. This page shows the nf-core CLI command to install this module as well as information about the expected inputs and outputs.

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modules/parabricks_deepvariant

NVIDIA Clara Parabricks GPU-accelerated germline variant calling, replicating deepvariant.

variant deep variant vcf haplotypcaller germline

```
nf-core modules install parabricks/deepvariant
```

<https://github.com/nf-core/modules/parabricks/deepvariant>

Description

NVIDIA Clara Parabricks GPU-accelerated germline variant calling, replicating deepvariant.

Input

Name (Type)	Description	Pattern
meta (map)	Groovy Map containing tumor sample information - id must match read groups for this sample. [id:'test']	
ref_meta (map)	Groovy Map containing reference information. [id:'test']	
input (file)	bam file for sample to be variant called.	*.bam
input_index (file)	bai index corresponding to input bam file. Only necessary if intervals are provided.	*.bai
interval_file (file)	file or files containing genomic intervals for use in base quality score recalibration.	*.{bed,interval_list,picard,list,intervals}
fasta (file)	reference fasta - must be unzipped.	*.fasta

Output

Name (Type)	Description	Pattern
meta (map)	Groovy Map containing sample information. e.g. [id:'test']	
vcf (file)	Variant file.	*.vcf
versions (file)	File containing software versions.	versions.yml

Tools

parabricks custom

NVIDIA Clara Parabricks GPU-accelerated genomics tools

nvidia.com/en-us/claragenomics

docs.nvidia.com/claragenomics/4.0.1/documentation

This module can be installed by running:

```
nf-core modules install parabricks/deepvariant
```

And it can be tested locally using:

```
nf-core modules test parabricks/deepvariant
```

For more details on how to integrate this module into an existing pipeline, see the [nf-core documentation](#).

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