Software Tools

The following tools are available in the NVIDIA Parabricks software. Click on a tool name for tool-specific options.

The Parabricks somatic (Somatic Variant Caller), germline (GATK Germline Pipeline) and deepvariant_germline tools are collections of several other individual tools that are commonly used together, all wrapped up as a single tool. For example, the deepvariant_germline takes FASTA and FASTQ files as input and produces a VCF and BAM file as output. Internally, it runs BWA mem alignment, performs coordinate sorting, marks duplicates, and then runs DeepVariant.

Tool	Details
applybqsr	Apply BQSR report to a BAM file and generate a new BAM file
bam2fq	Convert a BAM file to FASTQ
bammetrics	Collect WGS Metrics on a BAM file
bamsort	Sort a BAM file
bqsr	Collect BQSR report on a BAM file
collectmultiplemetrics	Collect multiple classes of metrics on a BAM file
dbsnp	Annotate variants based on a dbsnp
deepsomatic	Run GPU-DeepSomatic for calling somatic variants
deepvariant	Run GPU-DeepVariant for calling germline variants
deepvariant_germline	Run the germline pipeline from FASTQ to VCF using a deep neural network analysis
fq2bam (BWA-MEM + GATK)	Run bwa mem, co-ordinate sorting, marking duplicates, and Base Quality Score Recalibration
fq2bam_meth	Run GPU-accelerated bwa-meth compatible alignment, co-ordinate sorting, marking duplicates, and Base Quality Score Recalibration
fq2bamfast (BWA-MEM + GATK)	Run newly optimized version of bwa mem, co-ordinate sorting, marking duplicates, and Base Quality Score Recalibration

genotypegvcf	Convert a GVCF to VCF
germline (GATK Germline Pipeline)	Run the germline pipeline from FASTQ to VCF
haplotypecaller	Run GPU-HaplotypeCaller for calling germline variants
indexgvcf	Index a GVCF file
markdup	Identifies duplicate reads
minimap2 (Beta)	Align long read sequences against a large reference database to convert FASTQ to BAM/CRAM
mutectcaller	Run GPU-Mutect2 for tumor-normal analysis
pacbio_germline (Beta)	Run the germline pipeline from FASTQ to VCF by aligning long read sequences with minimap2 and using a deep neural network analysis
postpon	Generate the final VCF output of doing mutect pon
prepon	Build an index for PON file, which is the prerequisite to performing mutect pon
rna_fq2bam	Run RNA-seq data through the fq2bam pipeline
somatic (Somatic Variant Caller)	Run the somatic pipeline from FASTQ to VCF
starfusion	Identify candidate fusion transcripts supported by Illumina reads