

JointCaller reference 38 documentation

<https://git.gimr.garvan.org.au/CCG/nextflow-kccg-gatk4/-/blob/master/jointcaller/JointCaller.nf>

Process	Tools	What it achieves
Dynamically CombineIntervals	Python scripts	Get intervals
getIntervalLength	Shell script	Get interval length
CombineGenotypeSitesOnlyGVCf	Gatk GenomicsDBImport Gatk GenotypeGVCFs Gatk VariantFiltration Gatk MakeSitesOnlyVcf	Import single-sample VCFs into GenomicsDB before join genotyping (GenomicsDBImport – GATK) Perform joint genotyping on one or more samples pre-called with HaplotypeCaller (GenotypeGVCFs – GATK) Filter variant calls based on INFO and/or FORMAT annotations (VariantFiltration – GATK) Reads a VCF/VCF.gz/BCF and removes all genotype information from it while retaining all site level information, including annotations based on genotypes (MakeSitesOnlyVcf (Picard) – GATK)
ImportGVCFs	CombineGVCFs	Merges one or more HaplotypeCaller GVCf files into a single GVCf with appropriate annotations (CombineGVCFs – GATK)
GenotypeGVCFs	Gatk GenotypeGVCFs	Perform joint genotyping on one or more samples pre-called with HaplotypeCaller (GenotypeGVCFs – GATK)
VariantFiltration	Gatk VariantFiltration	Filter variant calls based on INFO and/or FORMAT annotations (VariantFiltration – GATK)
MakeSitesOnlyVcf	Gatk MakeSitesOnlyVcf	Reads a VCF/VCF.gz/BCF and removes all genotype information from it while retaining all site level information, including annotations based on genotypes (MakeSitesOnlyVcf (Picard) – GATK)
GatherSiteOnlyVCFs	Gatk GatherVcfsCloud	Gathers multiple VCF files from a scatter operation into a single VCF file (GatherVcfsCloud (BETA) – GATK)

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	tabix	Indexes a TAB-delimited genome position file in tab.bgz and creates an index file when region is absent from the command-line (tabix · bio.tools)
IndelsVariantRecalibrator	Gatk VariantRecalibrator	Build a recalibration model to score variant quality for filtering purposes (VariantRecalibrator – GATK) Having -mode INDEL in the script which specifically recalibrate INDELS in the data
SNPsVariantRecalibratorClassic	Gatk VariantRecalibrator	Build a recalibration model to score variant quality for filtering purposes (VariantRecalibrator – GATK) Having -mode SNPs in the script which specifically recalibrate SNPs in the data
ApplyRecalibration	Gatk ApplyVQSR	Apply a score cutoff to filter variants based on recalibration table (ApplyVQSR – GATK)
FinalGather	Gatk GatherVcfsCloud tabix	((same tools used with GatherSiteOnlyVCFs process))