

🔧 Trimmomatic



➤ Input FASTQ file

fastq\_out



🔧 Bowtie2



➤ FASTA/Q file

Bowtie2 on input dataset(s):

alignments (bam,



qname\_input\_sorted.bam, sam)

🔧 FreeBayes



➤ Sample BAM file 1 > BAM file

FreeBayes on input dataset(s)

(variants) (vcf)



## Recommended tools

🔧 Filter (100%)

🔧 VCFfilter: (85%)

🔧 VcfAllelicPrimitives: (83%)

🔧 Remove beginning (80%)

🔧 SnpEff eff: (80%)

🔧 Select last (65%)

🔧 SnpSift Filter (62%)

🔧 SnpSift Annotate (56%)

🔧 VCF-VCFintersect: (44%)

🔧 VCFcombine: (40%)

🔧 Merge (33%)

🔧 VCF-BEDintersect: (27%)

🔧 bcftools norm (17%)

Close