



Trimmomatic



> Input FASTQ file

☒ fastq_out



BWA-MEM



> Select first set of reads

> Select second set of reads

☒ BWA-MEM on input dataset(s) (mapped reads in BAM format) (bam)



FreeBayes



> BAM c

☒ Free
dataset

Tool recommendations

- bcftools norm
- VcfAllelicPrimitives:
- CustomProDB
- Filter
- bedtools Intersect intervals
- Remove beginning
- VCFtoTab-delimited:
- SnpEff eff:
- VCFfilter:
- GEMINI load
- Select last
- bcftools consensus