Pipeline for Variant Calling

```
Raw Reads (Fastq)
        |
        v
Quality Check (Fastqc)
        |
        v
Trimming (Fastp)
        |
        v
Map to References (SAM)       BWA-MEM
        |
        v
Sort by Coordinate
Convert to BAM
        |
        v
Marked Duplicates (BAM)
```

gatk

Build BAM Index (Bai)

Base Quality Score Recalibration (recali-data table)

Apply Recalibration (BAM)

Variant Calling (VCF)

Extract SNPs   Extract indels

Filter SNPs   Filter indels

Predict Variant Effects (VCF, Txt, HTML)