Alignment

Unaligned reads

HISAT2 alignment

Fully aligned reads

Hard/Soft clips and unaligned reads

BWA mem alignment realignment

Samtools merge/sort/ index bam

Pipeline Overview

Patient DNA (bam,sam, cram,fastq)

Multi Sample (bam,sam, cram,fastq)

Variant File (one or more VCFs)

Alignment

Analysis

Annotation

Report generation

REPORT

Data Analysis

Aligned reads

Unaligned reads

Viral DB

SNV/INDELS

SVs + CNVs

Virus

SNVs Freebayes

SV calling Manta

Alignment to Viral DB HISAT2 + NCBI

INDELs GATK HC

Known Repeats

Variant Filtering Bcftools

Repeats Expan Hunter

Results Samtools idxstats

Towards annotation

Towards reports

VCF

VCF

Stats