```
# Use fastp for adapter trimming and quality pruning
fastp -i $sample_R1.fastq.gz -o $sample_clean_R1.fastq.gz -I $sample_R2.fastq.gz -O $sample_clean_R2.fastq.gz -h $sample_clean.html -j $sample_clean.json > $sample_clean.log &
# Extract microbial reads by filtering human reads.
bwa mem -R "@RG\tID:$sample\tLB:$sample\tPL:$sample\tSM:$sample" -t 8 -k 32 -M $path/bwaindex/hg19.fa $sample_clean_R1.fastq.gz $sample_clean_R2.fastq.gz | sentieon util sort -o $sample.hg19.sort.bam -t 8 --sam2bam -i -
samtools view -b -f 12 -F 256 $sample.hg19.sort.bam > $sample.hg19.bothEndsUnmapped.bam
samtools sort -@ 8 -n $sample.hg19.bothEndsUnmapped.bam -o $sample.hg19.bothEndsUnmapped.sorted.bam
bamToFastq -i $sample.hg19.bothEndsUnmapped.sorted.bam -fq $sample.rmhost.clean.1.fq -fq2 $sample.rmhost.clean.2.fq
# Remove Ribosomal RNA (rRNA) reads
bwa mem -R "@RG\tID:$sample\tLB:$sample\tPL:$sample\tSM:$sample" -t 8 -k 32 -M $path/rRNA_fa/sequence.fa $sample.rmhost.clean.1.fq $sample.rmhost.clean.2.fq | sentieon util sort -o $sample.rRNA.sort.bam -t 8 --sam2bam -i -
samtools view -b -f 12 -F 256 $sample.rRNA.sort.bam > $sample.rRNA.bothEndsUnmapped.bam
samtools sort -@ 8 -n $sample.rRNA.bothEndsUnmapped.bam -o $sample.rRNA.bothEndsUnmapped.sorted.bam
bamToFastq -i $sample.rRNA.bothEndsUnmapped.sorted.bam -fq $sample.rmrRNA.clean.1.fq -fq2 $sample.rmrRNA.clean.2.fq
# Align reads to the SARS-CoV-2 genome, remove duplicates, and calculated the coverage.
bwa mem -R "@RG\tID:$sample\tLB:$sample\tPL:$sample\tSM:$sample" -t 8 -k 32 -M $path/bwaindex/SARS-CoV-2.fa $sample.rmrRNA.clean.1.fq $sample.rmrRNA.clean.2.fq | sentieon util sort -o $sample.sort.bam -t 8 --sam2bam -i -
gencore -i $sample.sort.bam -o $sample.gencore.sort.bam -r $path/bwaindex/SARS-CoV-2.fa -j $sample.gencore.json -h $sample.gencore.html
samtools index $sample.gencore.sort.bams
samtools depth -aa $sample.gencore.sort.bam > $sample.gencore.sort.depth
samtools mpileup -AB -Q 25 -q 30 -d 100000 -f $path/bwaindex/SARS-CoV-2.fa $sample.gencore.sort.bam > $sample.gencore.sort.mpileup
# Determine the result by SARS-CoV-2 genome coverage, >= 20% means positive.
genome_length=$(awk '{print NR}' $sample.gencore.sort.depth | tail -n1)
coverd_base=$(awk '{print NR}' $sample.gencore.sort.mpileup | tail -n1)
percent=$(awk 'BEGIN{printf "%0.2f",('$coverd_base'/'$genome_length')*100}')
if [ "$percen" -ge "20" ];then
    echo "POSITIVE"
else
    echo "NEGATIVE"
fi
```