Step 1 –

bwa index sacCer3.fa

Step 2 -

##FILE NAME quick.sh

#!/bin/bash

for i in 09 11 23 24 27 31 35 39 62 63

do

bwa mem -R "@RG\tID:A01\_${i}\tSM:A01\_$i" -o A01\_$i.sam sacCer3.fa A01\_$i.fastq

done

[~/qbb2020-answers/QUANT2020/data/Lab2]chmod +x quick.sh

[~/qbb2020-answers/QUANT2020/data/Lab2] ./quick.sh

Step 3 –

SORTING BASH SCRIPT

#!/bin/bash

for i in 09 11 23 24 27 31 35 39 62 63

do

samtools view -S -b A01\_$i.sam > A01\_$i.bam

samtools sort A01\_$i.bam -O BAM -o output\_01\_$i.bam

done

[~/qbb2020-answers/QUANT2020/data/Lab2]chmod +x make\_bam.sh

[~/qbb2020-answers/QUANT2020/data/Lab2] ./make\_bam.sh

Step 4 –

[~/qbb2020-answers/QUANT2020/data/Lab2]freebayes -f sacCer3.fa output\*.bam -p 1 --genotype-qualities > var.vcf

Step 5 –

[~/qbb2020-answers/QUANT2020/data/Lab2] cat var.vcf |vcffilter -f "QUAL > 20" > ofilter.vcf

Step 6 –

[~/qbb2020-answers/QUANT2020/data/Lab2]vcfallelicprimitives -k -g ofilter.vcf > decomposed.vcf

Step 7 –

[~/qbb2020-answers/QUANT2020/data/Lab2]snpeff ann R64-1-1.86 decomposed.vcf > snpeff.vcf

Step 8 – On Python script in same folder in repository