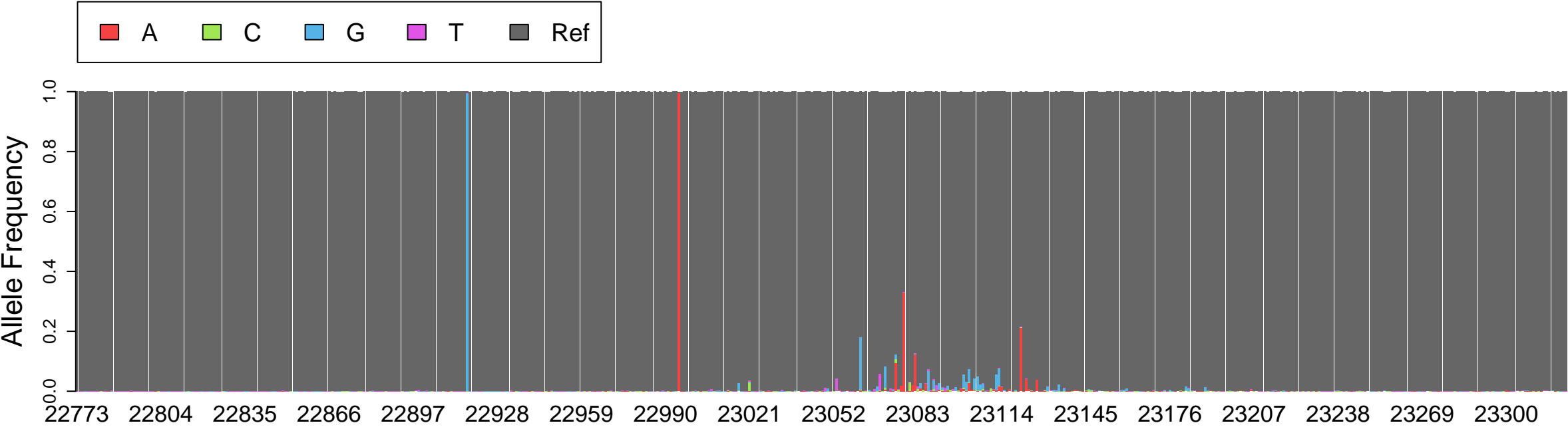
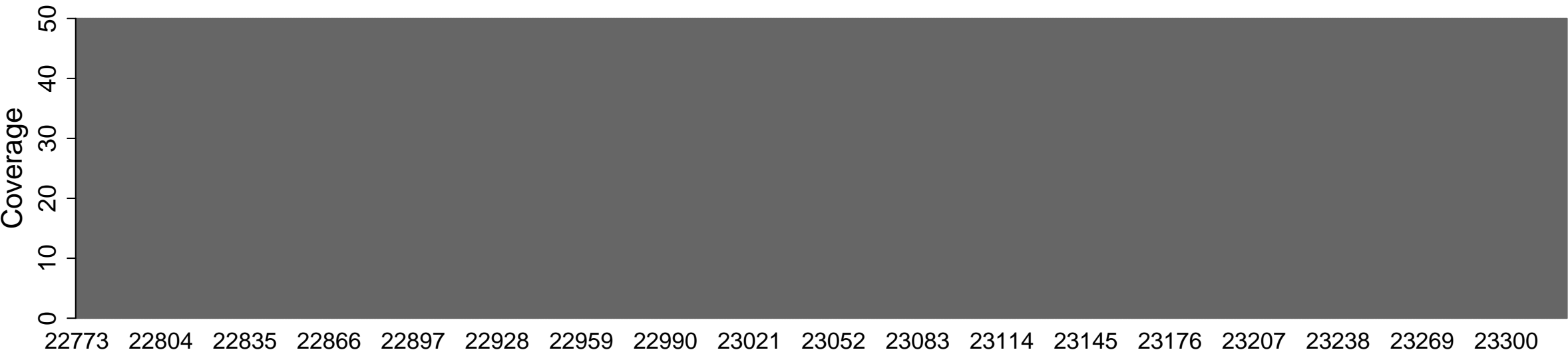
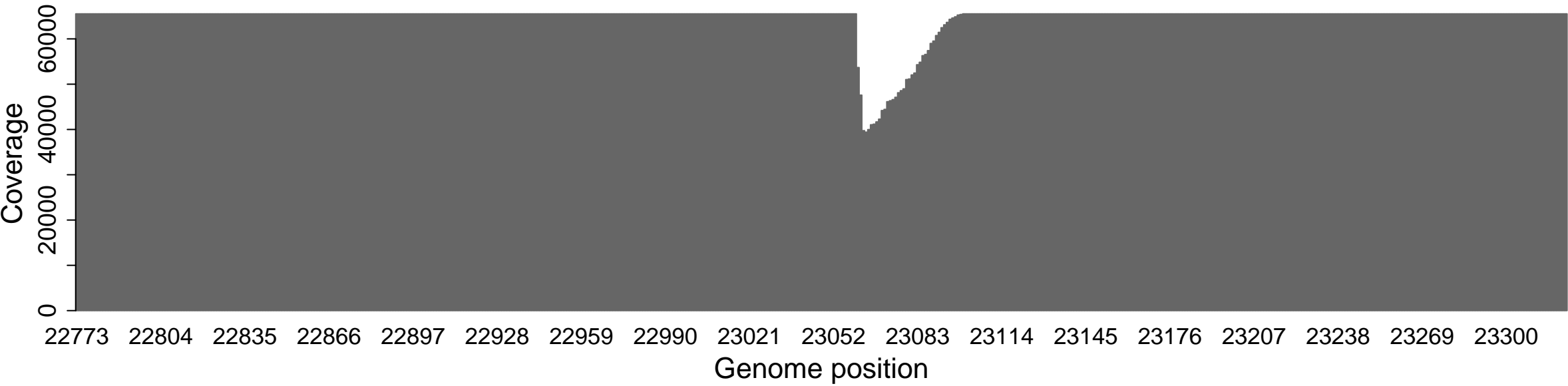


HiCt Sample Report	
vsp	VSP3607
sample_id	VSP3607-h1
sample_date	
report_date	4/3/2022
files	VSP3607-h1_S35_RX_001.fastq.gz
filter	y
reads_aligned	76257
percent_aligned	100
average_coverage	74363.89
percent50x_coverage	100
error	
command_sam	bwa mem -M nc_045512.2_rbd.fasta 00_Raw-Data/VSP3607-h1_S35_R1_001.fastq.gz 00_Raw-Data/VSP3607-h1_S35_R2_001.fastq.gz > ./temp_Sam-Files/VSP3607-h1_genome.sam
command_bam	samtools view -S -b -h ./temp_Sam-Files/VSP3607-h1_genome.sam > ./01_Bam-Files/VSP3607-h1_genome.bam
command_filt1	samtools view -F 8 -h ./01_Bam-Files/VSP3607-h1_genome.bam awk 'length(\$10) > 280 && length(\$10) < 300 \$1 ~ /^[^@/]' samtools view -b -h > ./01_Bam-Files/VSP3607-h1_genome.filt.bam
command_qual	samtools view -h -q 30 -b ./01_Bam-Files/VSP3607-h1_genome.filt.bam > ./01_Bam-Files/VSP3607-h1_genome.filt.qual.bam
command_sort	samtools sort -o ./01_Bam-Files/VSP3607-h1_genome.filt.qual.sorted.bam ./01_Bam-Files/VSP3607-h1_genome.filt.qual.bam
command_index	samtools index ./01_Bam-Files/VSP3607-h1_genome.filt.qual.sorted.bam
command_pileup1	./Bin/bbmap/pileup.sh in=./01_Bam-Files/VSP3607-h1_genome.filt.qual.sorted.bam ref=nc_045512.2_rbd.fasta out=./02_Variant-Calling/VSP3607-h1_covstats.txt basecov=./02_Variant-Calling/VSP3607-h1_basecov.txt countgc=f overwrite=t 2> temp.txt
command_pileup2	samtools mpileup ./01_Bam-Files/VSP3607-h1_genome.filt.qual.sorted.bam -f ./nc_045512.2_rbd.fasta > ./02_Variant-Calling/VSP3607-h1_pileup.tsv
command_var1	./Bin/bbmap/callvariants.sh in=./01_Bam-Files/VSP3607-h1_genome.filt.qual.sorted.bam ref=nc_045512.2_rbd.fasta out=./02_Variant-Calling/VSP3607-h1_allVariants.vcf shist=./02_Variant-Calling/VSP3607-h1_variantQualityHisto.txt rarity=0 overwrite=t clearfilters
command_var2	bcftools index ./02_Variant-Calling/VSP3607-h1_filteredVariants.vcf.gz
command_consensus	cat nc_045512.2_rbd.fasta bcftools consensus ./02_Variant-Calling/VSP3607-h1_filteredVariants.vcf.gz > ./03_Consensus/VSP3607-h1_consensus.fasta
version_bwa	0.7.17-r1188
version_samtools	1.10 (using htplib 1.10.2-3)
version_bcftools	1.10.2 (using htplib 1.10.2-3)
version_bbmap	38.96



Mutations

nt_mutation	gene	aa_mutation	top_lineages (propotion)
T22917G	S	S_L452R	AY.25 (0.17); AY.103 (0.17); AY.3 (0.1)
C22995A	S	S_T478K	AY.25 (0.17); AY.103 (0.16); AY.3 (0.09)