Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2021/01/24 23:56:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/mnt/1TB_0/Data/RaTG13/BBmap/Sars_SL3_R2_171127_sorted.sam -c -nw
400 -hm 3
```

1.2. Alignment

Command line:	java -ea -Xmx129862m -Xms129862m align2.BBMap build=1 overwrite=true fastareadlen=500 in=/mnt/1TB_0/Data/RaTG13/Sars_SL3_R2_171127.fastq out=Sars_SL3_R2_171127_mapped.sam
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	BBMap (38.87)
Analysis date:	Sun Jan 24 23:55:13 AWST 2021
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/mnt/1TB_0/Data/RaTG13/BBmap/Sars_SL3_R2_171127_sorted.sam

2. Summary

2.1. Globals

Reference size	29,855
Number of reads	11,604,666
Mapped reads	870 / 0.01%
Unmapped reads	11,603,796 / 99.99%
Mapped paired reads	0 / 0%
Read min/max/mean length	35 / 151 / 142.04
Duplicated reads (estimated)	145 / 0%
Duplication rate	16.41%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	37,889 / 29.4%
Number/percentage of C's	24,555 / 19.06%
Number/percentage of T's	39,871 / 30.94%
Number/percentage of G's	24,827 / 19.27%
Number/percentage of N's	2 / 0%
GC Percentage	38.32%

2.3. Coverage

Mean	5.2599
Standard Deviation	3.2874

2.4. Mapping Quality

Mean Mapping Quality	30.91

2.5. Mismatches and indels

| General error rate	19.04%
Insertions	3
Mapped reads with at least one insertion	0.34%
Deletions	2
Mapped reads with at least one deletion	0.23%
Homopolymer indels	40%

2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
MN996532.2	29855	157033	5.2599	3.2874

3. Results : Coverage across reference

Coverage across reference
Sars_SL3_R2_171127_sorted.sam
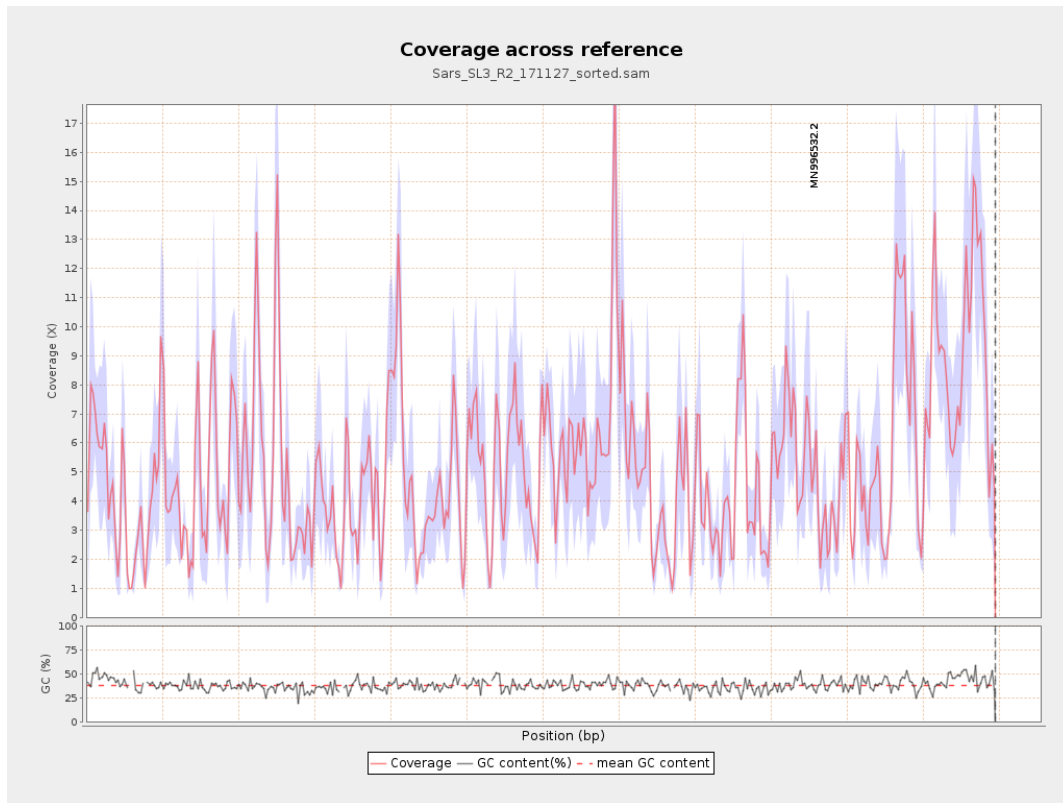
4. Results : Coverage Histogram

5. Results : Coverage Histogram (0-50X)
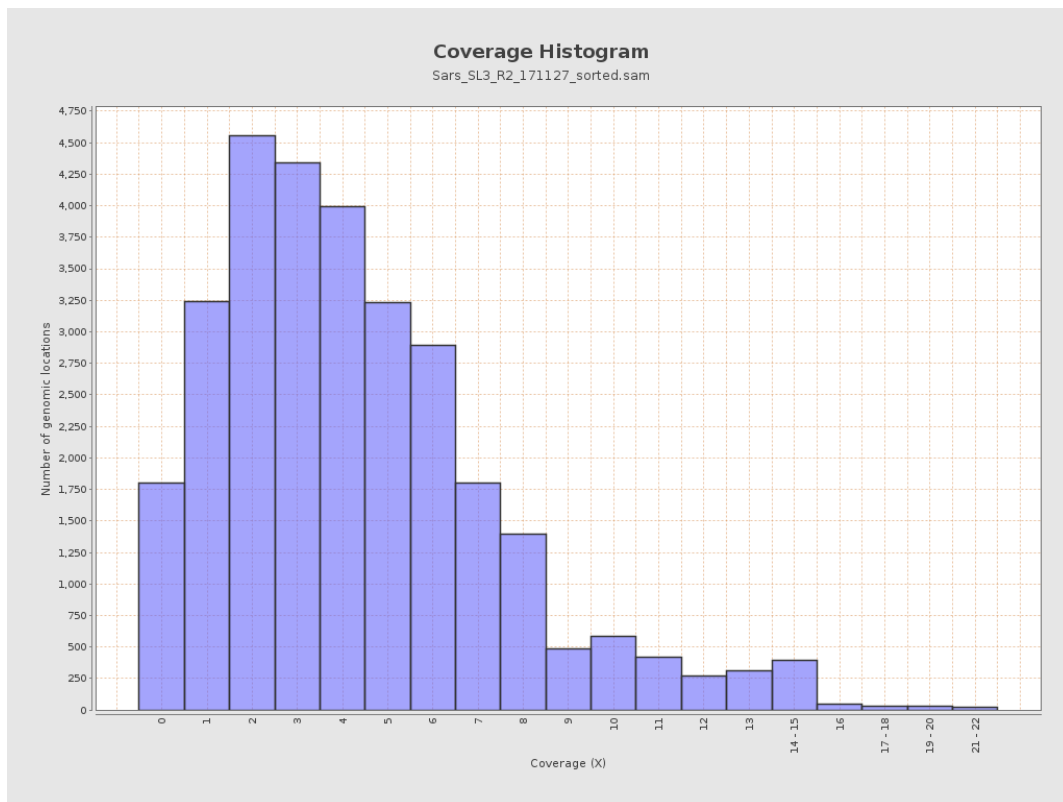
Coverage Histogram (0-50X)
Sars_SL3_R2_171127_sorted.sam
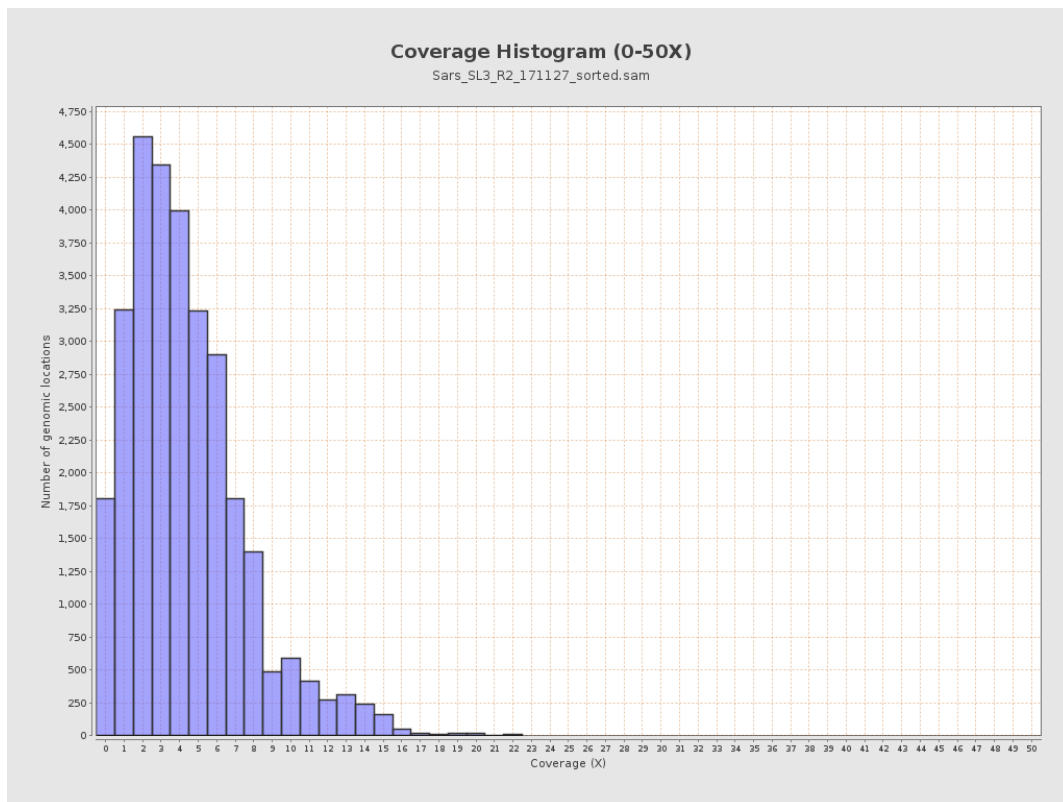
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
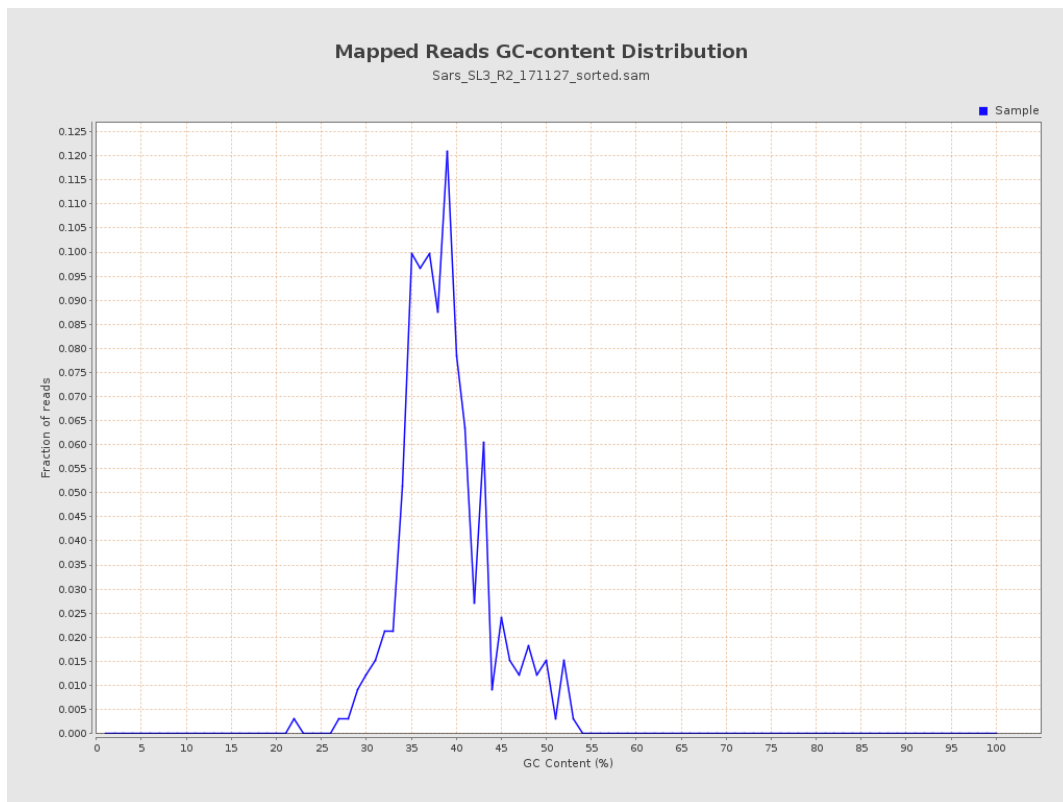Sars_SL3_R2_171127_sorted.sam
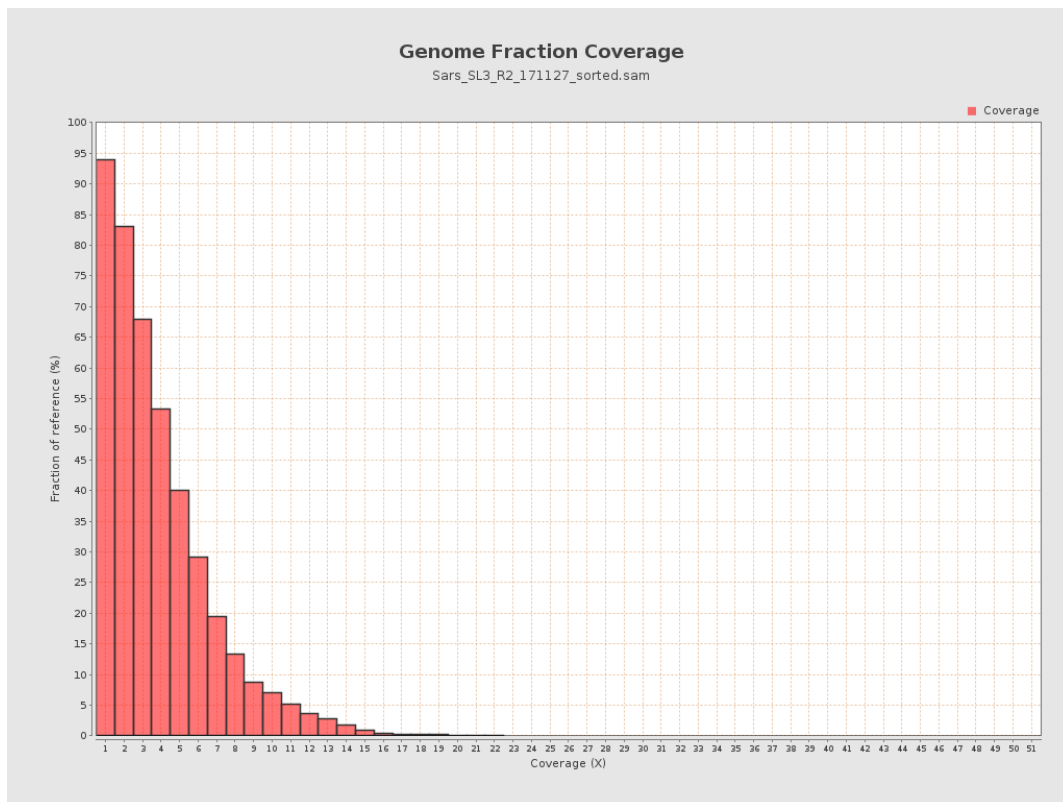
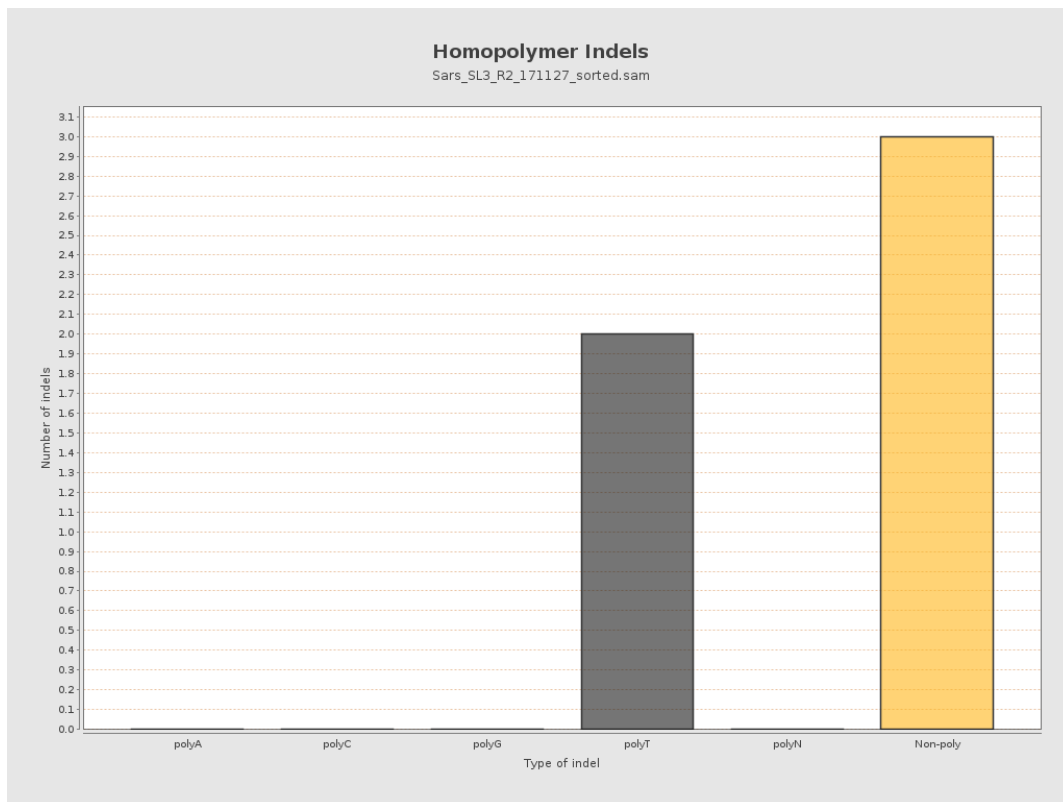# 7. Results : Duplication Rate Histogram
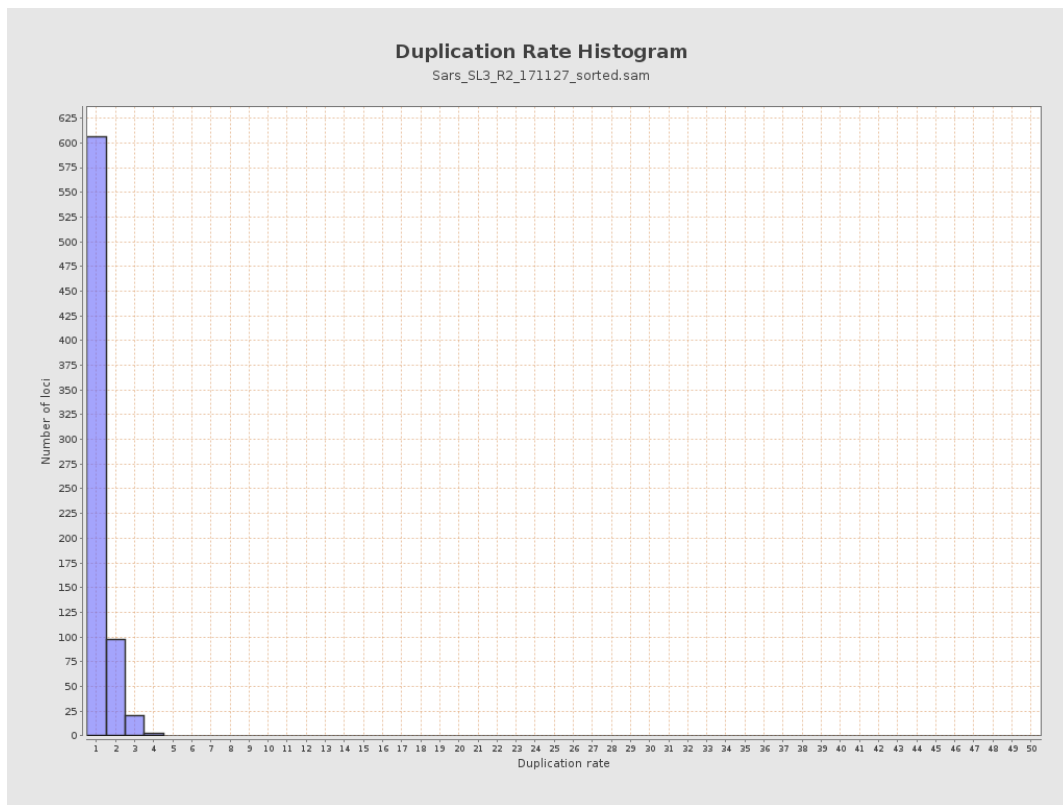
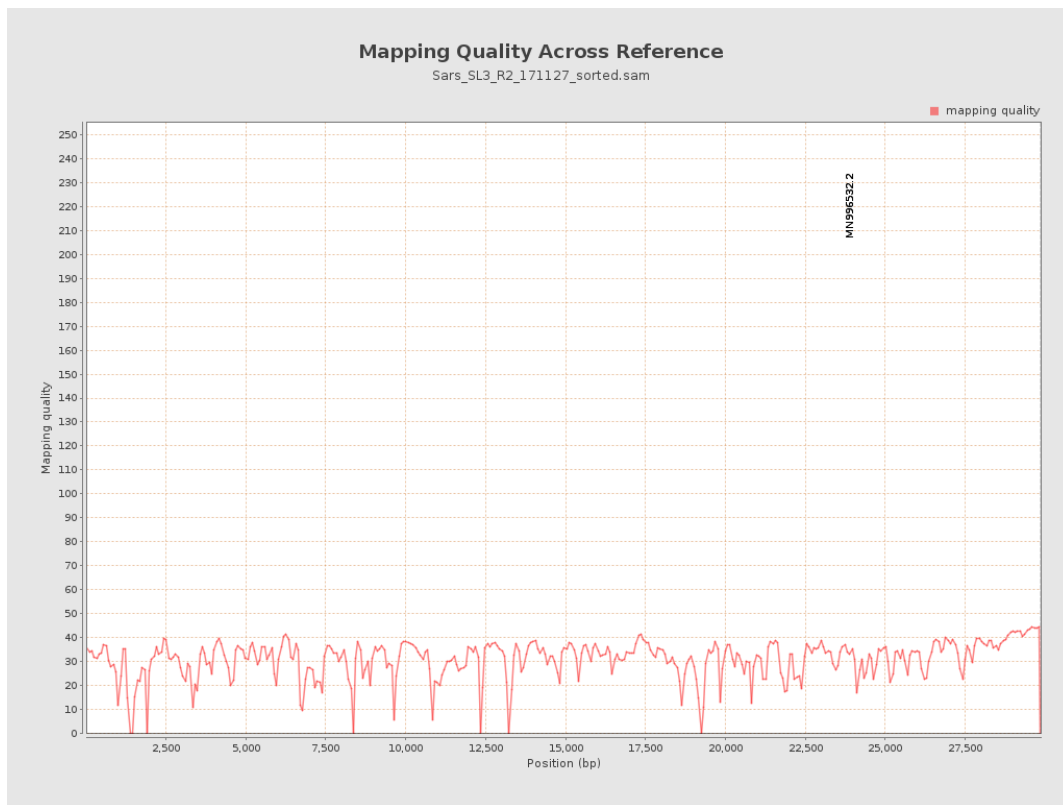# 8. Results : Mapped Reads Nucleotide Content
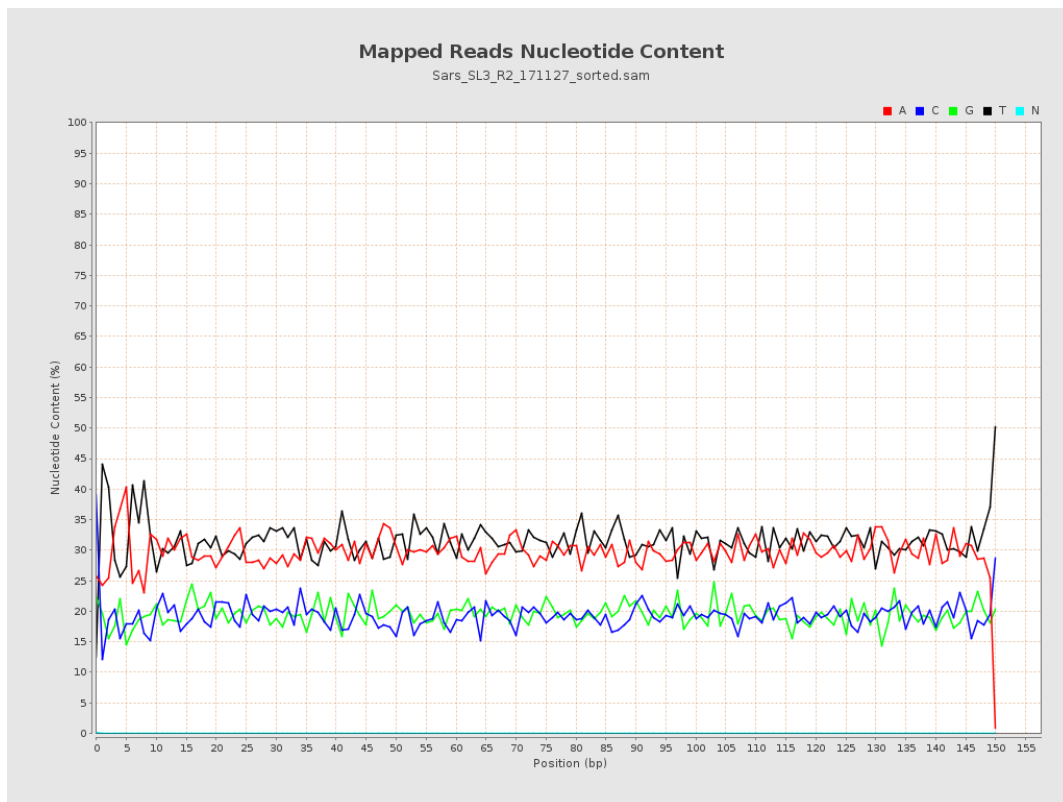
9. Results : Mapped Reads GC-content Distribution

10. Results : Homopolymer Indels

11. Results : Mapping Quality Across Reference

12. Results : Mapping Quality Histogram

Mapping Quality Histogram
Sars_SL3_R2_171127_sorted.sam