

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

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1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/mnt/1TB_0/Data/RaTG13/BBmap/Sars_SL3_R1_171127_sorted.sam -c -nw
400 -hm 3
```

1.2. Alignment

Command line:	java -ea -Xmx129944m -Xms129944m align2.BBMap build=1 overwrite=true fastareadlen=500 in=/mnt/1TB_0/Data/RaTG13/Sars_SL3_R1_171127.fastq out=Sars_SL3_R1_171127_mapped.sam
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	BBMap (38.87)
Analysis date:	Sun Jan 24 23:50:41 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_R1_171127_sorted.sam

2. Summary

2.1. Globals

Reference size	29,855
Number of reads	11,604,666
Mapped reads	891 / 0.01%
Unmapped reads	11,603,775 / 99.99%
Mapped paired reads	0 / 0%
Read min/max/mean length	35 / 151 / 142.04
Duplicated reads (estimated)	275 / 0%
Duplication rate	25.65%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	39,335 / 30.05%
Number/percentage of C's	25,009 / 19.11%
Number/percentage of T's	39,878 / 30.47%
Number/percentage of G's	25,872 / 19.77%
Number/percentage of N's	1,398 / 1.07%
GC Percentage	38.87%

2.3. Coverage

Mean	4.4323
Standard Deviation	4.4706

2.4. Mapping Quality

Mean Mapping Quality	39.56
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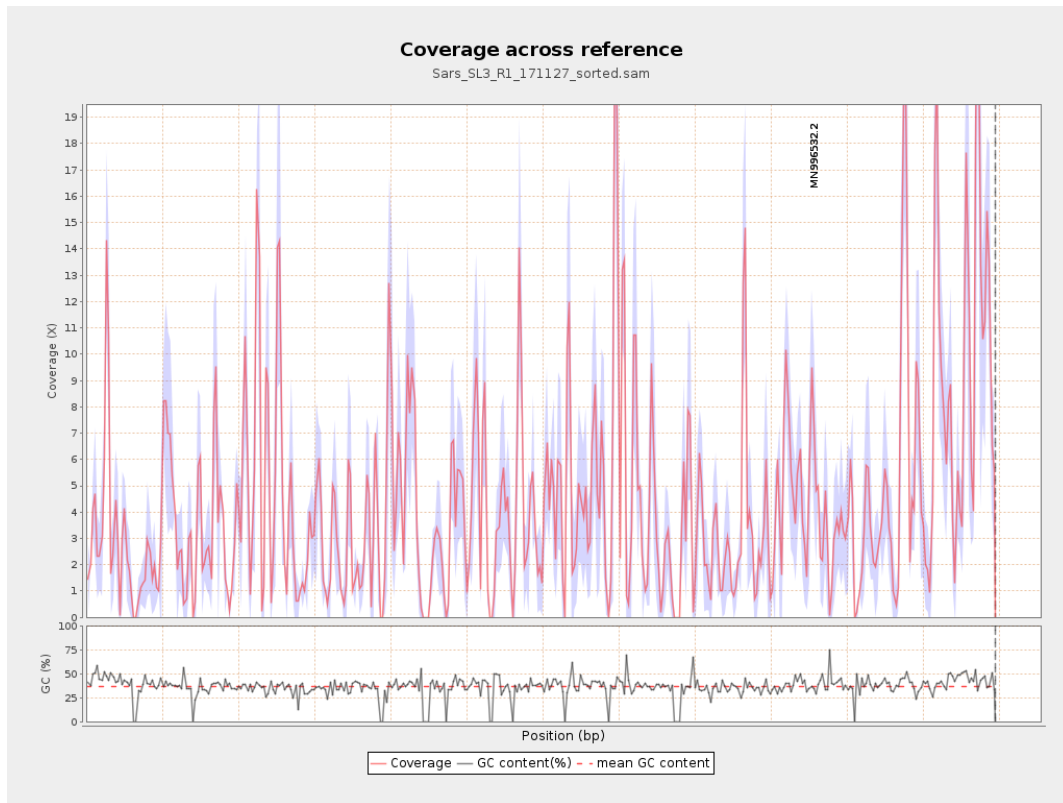
2.5. Mismatches and indels

General error rate	1.72%
Insertions	7
Mapped reads with at least one insertion	0.79%
Deletions	3
Mapped reads with at least one deletion	0.34%
Homopolymer indels	20%

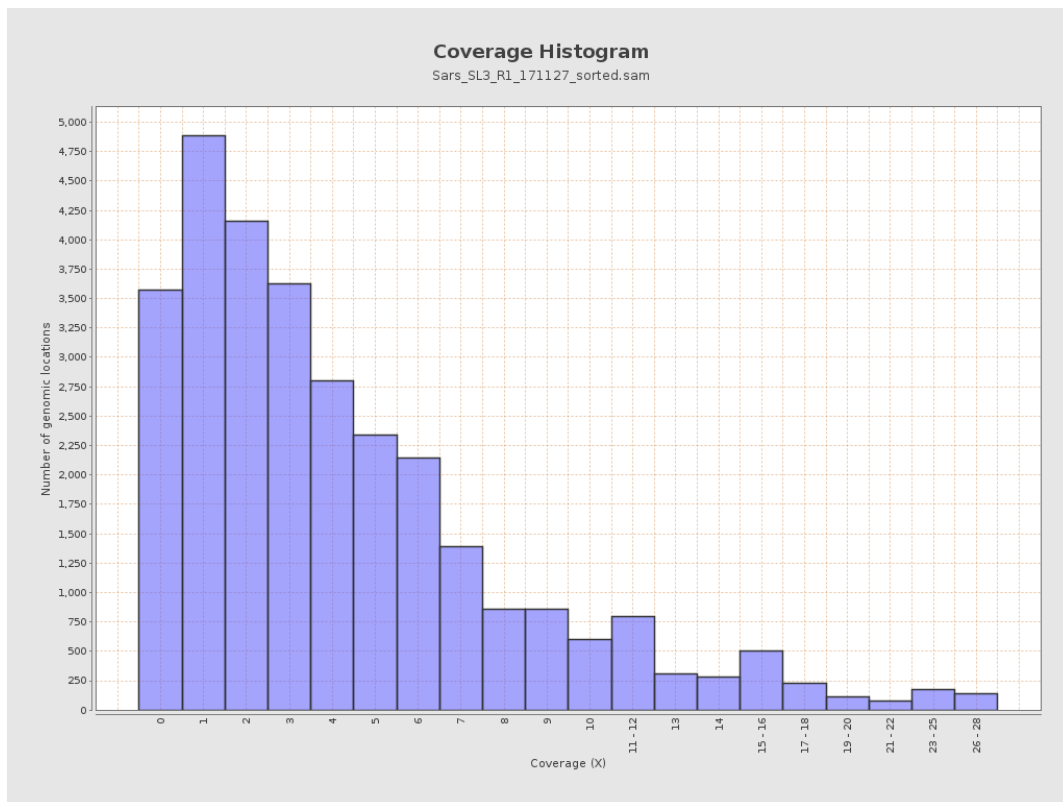
2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
MN996532.2	29855	132325	4.4323	4.4706

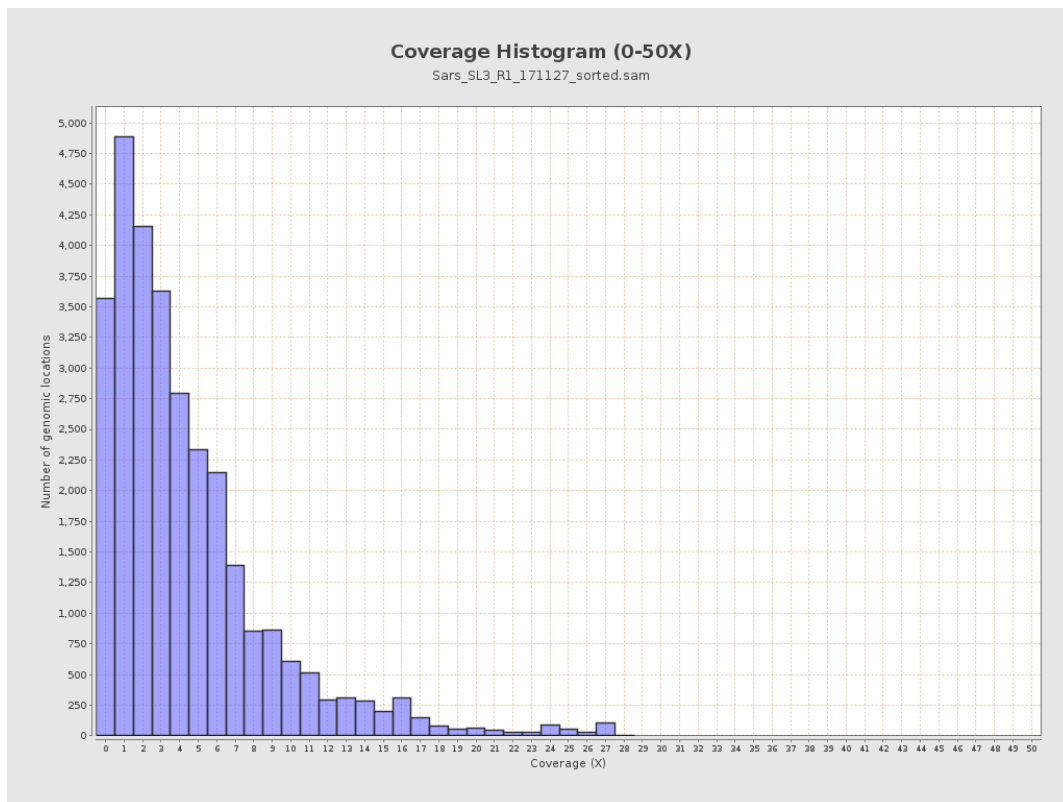
3. Results : Coverage across reference



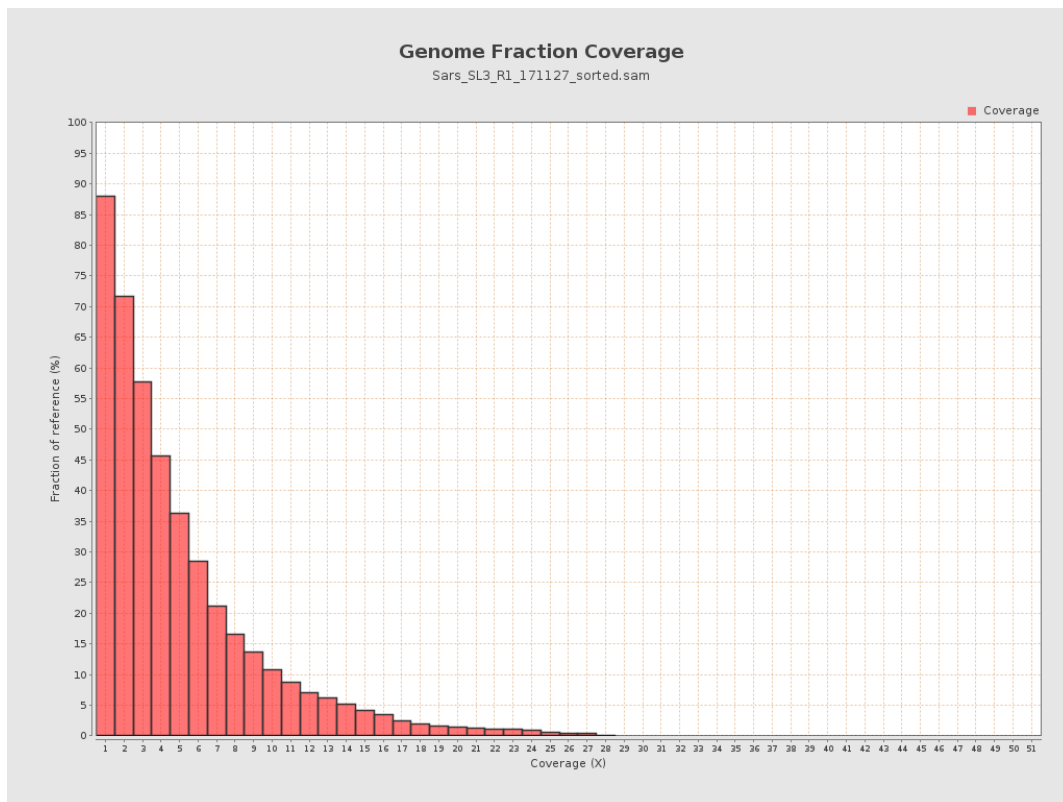
4. Results : Coverage Histogram



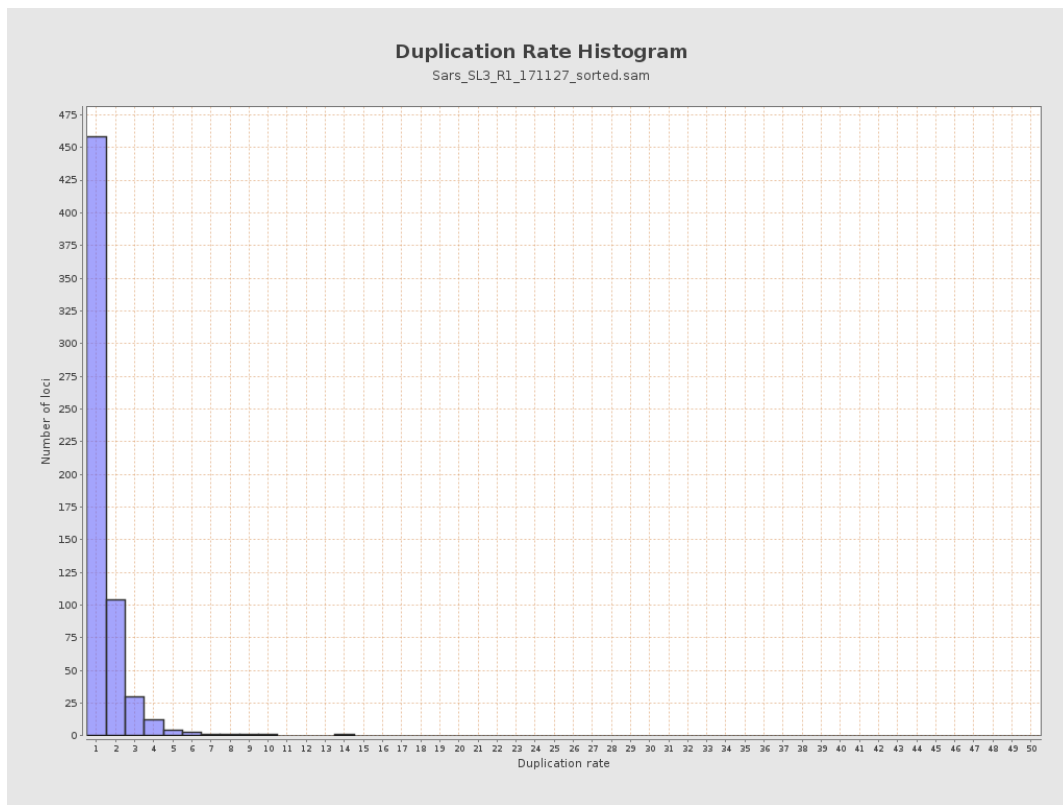
5. Results : Coverage Histogram (0-50X)



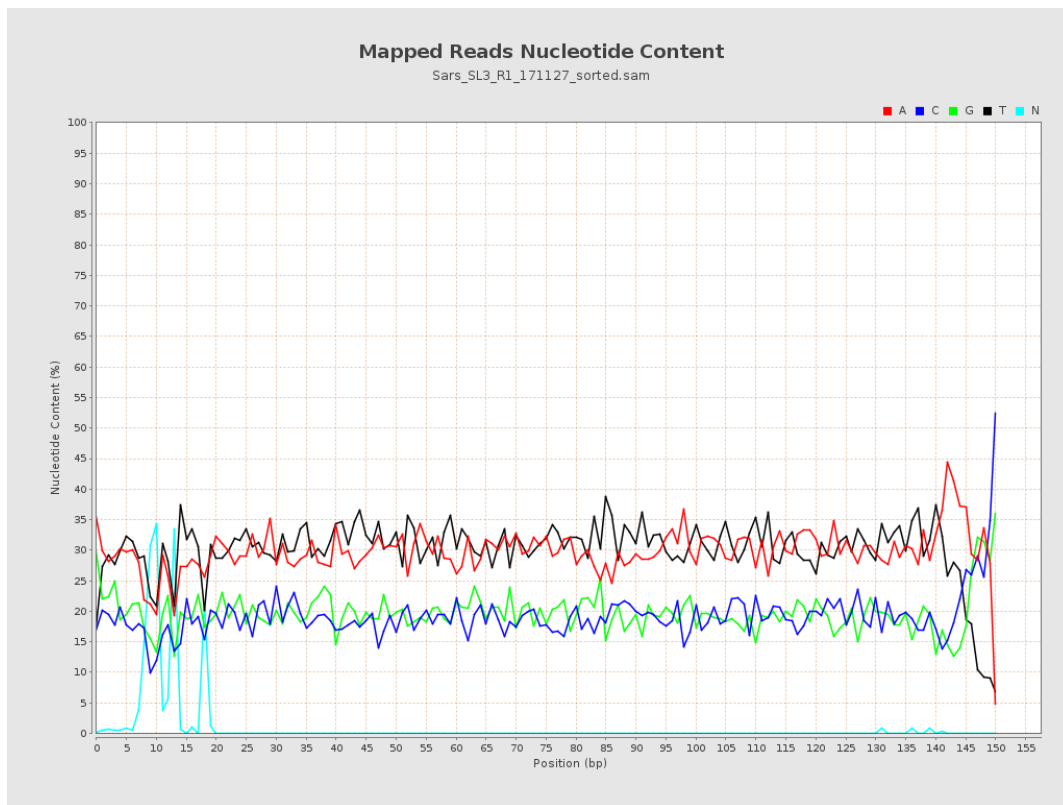
6. Results : Genome Fraction Coverage



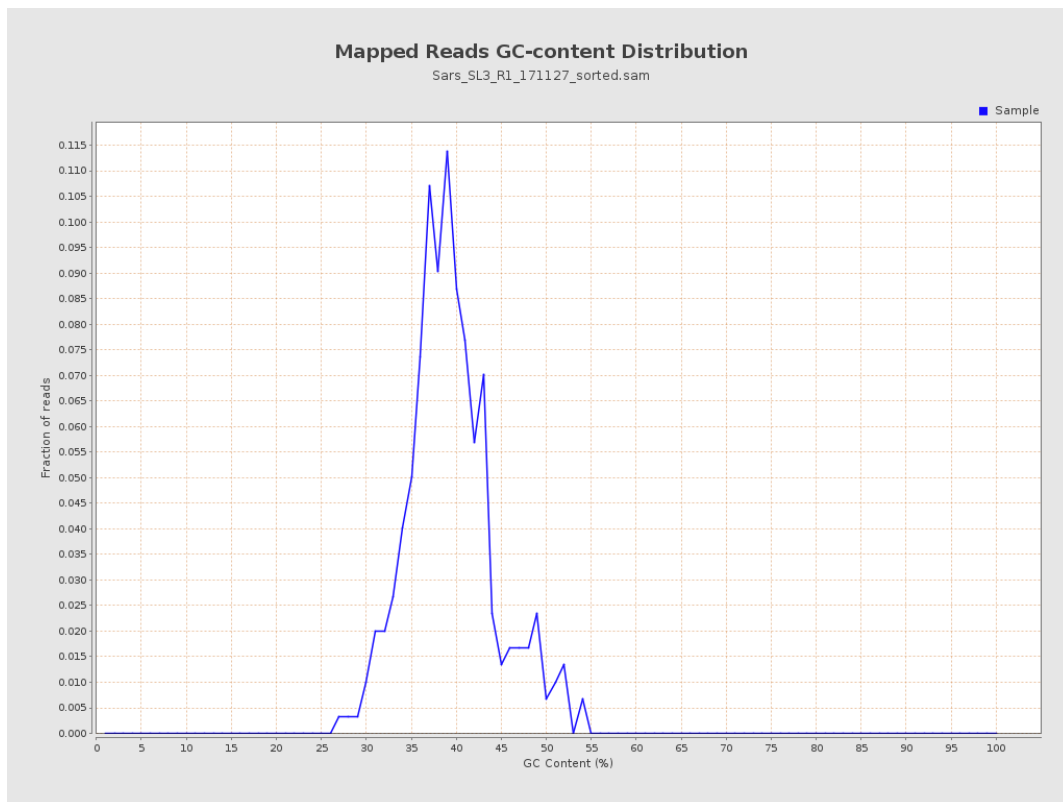
7. Results : Duplication Rate Histogram



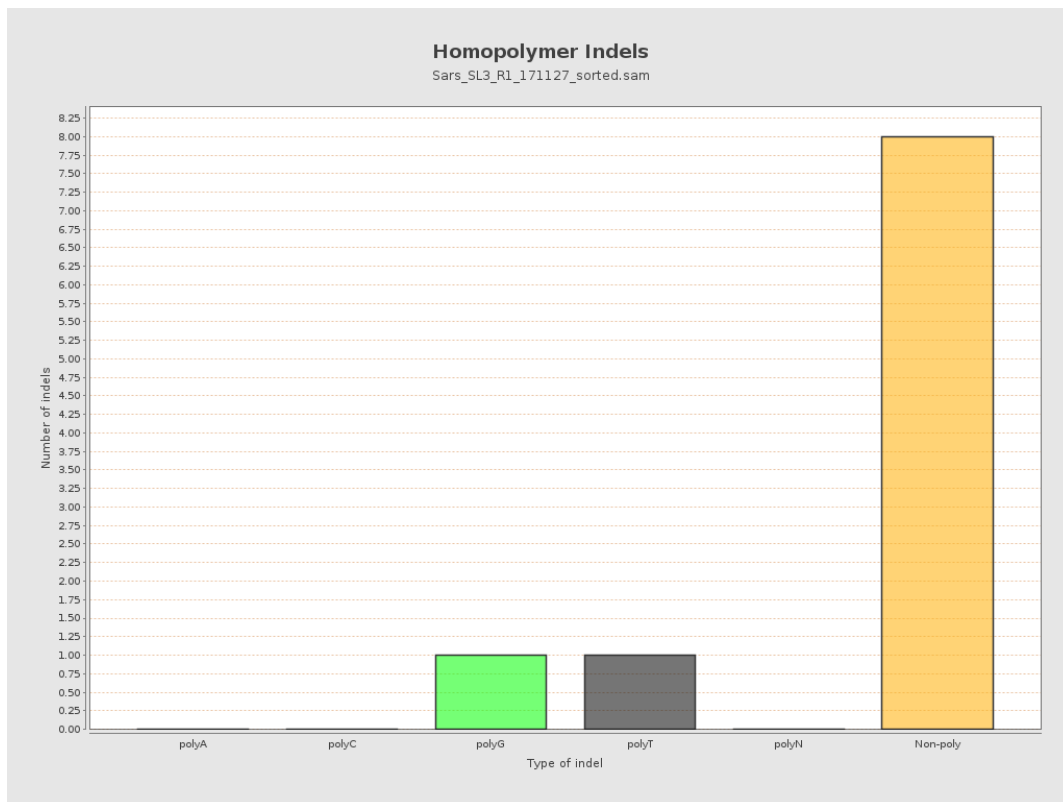
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



10. Results : Homopolymer Indels



11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram

