# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/08 20:23:50*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR975301.sorted.bam -c -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| Command line: | /home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR975301 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975301_1.fastq.gz SRR975301_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Sep 08 20:23:49 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR975301.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 67,987,954 |
| Mapped reads | 67,889,933 / 99.86% |
| Unmapped reads | 98,021 / 0.14% |
| Mapped paired reads | 67,889,933 / 99.86% |
| Mapped reads, first in pair | 33,954,362 / 49.94% |
| Mapped reads, second in pair | 33,935,571 / 49.91% |
| Mapped reads, both in pair | 67,842,456 / 99.79% |
| Mapped reads, singletons | 47,477 / 0.07% |
| Secondary alignments | 0 |
| Supplementary alignments | 105,273 / 0.15% |
| Read min/max/mean length | 30 / 101 / 101.06 |
| Duplicated reads (estimated) | 41,712,617 / 61.35% |
| Duplication rate | 48.81% |
| Clipped reads | 37,599,773 / 55.3% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 1,690,525,816 / 26.58% |
| Number/percentage of C's | 1,422,094,274 / 22.36% |
| Number/percentage of T's | 1,741,433,682 / 27.38% |
| Number/percentage of G's | 1,504,961,146 / 23.67% |
| Number/percentage of N's | 278,978 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 46.03% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 2.0549 |
| Standard Deviation | 26.9959 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 56.08 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 67,613.81 |
| Standard Deviation | 2,566,028.49 |
| P25/Median/P75 | 151 / 187 / 235 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.61% |
| Mismatches | 37,731,447 |
| Insertions | 511,682 |
| Mapped reads with at least one insertion | 0.75% |
| Deletions | 1,380,550 |
| Mapped reads with at least one deletion | 2.01% |
| Homopolymer indels | 48.44% |

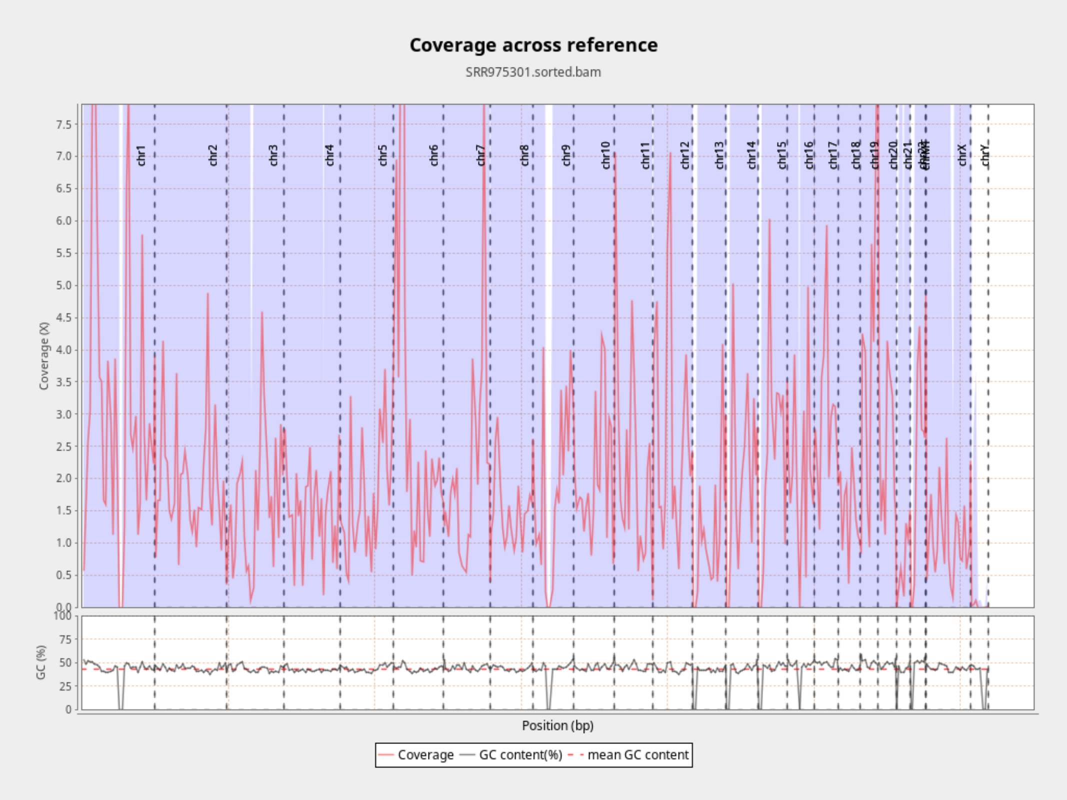
## 2.7. Chromosome stats

| **Name** | **Length** | **Mapped** | **Mean** | **Standard** |
|---|---|---|---|---|

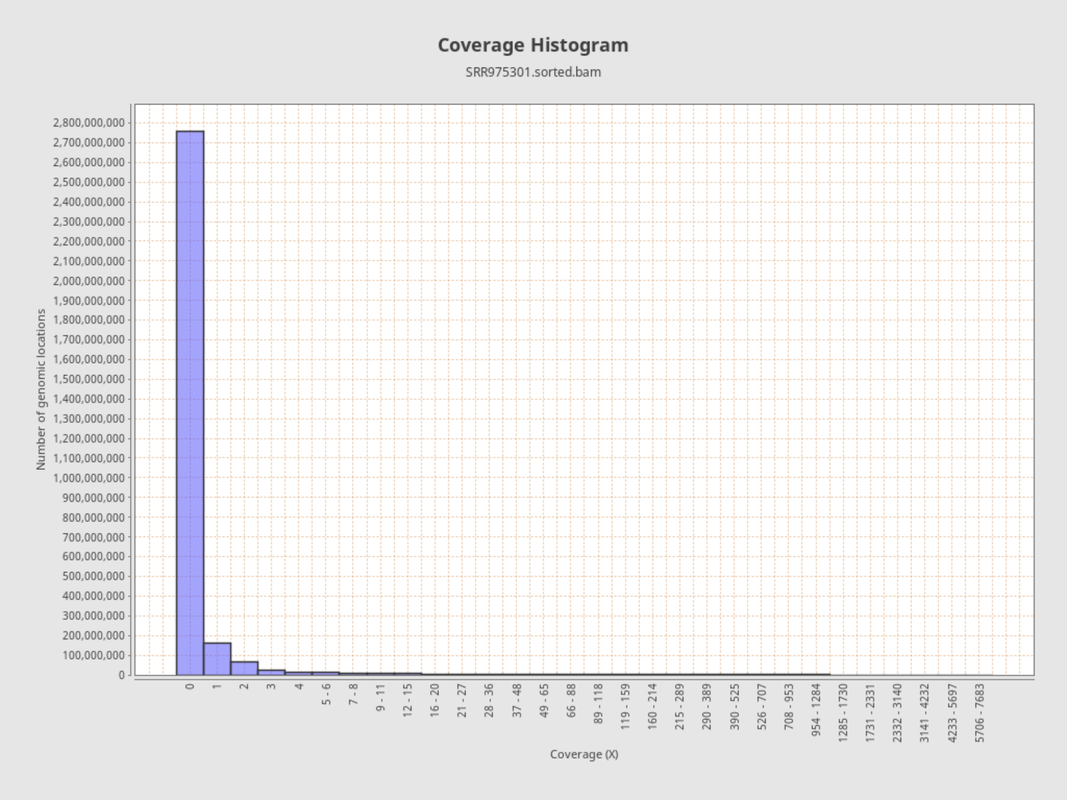
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 775294004 | 3.1105 | 36.1901 |
| chr2 | 243199373 | 473626489 | 1.9475 | 23.6939 |
| chr3 | 198022430 | 324621063 | 1.6393 | 21.4183 |
| chr4 | 191154276 | 286394015 | 1.4982 | 21.9813 |
| chr5 | 180915260 | 308819960 | 1.707 | 22.6351 |
| chr6 | 171115067 | 588767364 | 3.4408 | 46.0822 |
| chr7 | 159138663 | 338910051 | 2.1297 | 29.1215 |
| chr8 | 146364022 | 218480099 | 1.4927 | 20.3489 |
| chr9 | 141213431 | 259580065 | 1.8382 | 23.5381 |
| chr10 | 135534747 | 279197126 | 2.06 | 26.4772 |
| chr11 | 135006516 | 296578801 | 2.1968 | 24.9197 |
| chr12 | 133851895 | 358553907 | 2.6787 | 28.296 |
| chr13 | 115169878 | 128757675 | 1.118 | 20.0902 |
| chr14 | 107349540 | 208505773 | 1.9423 | 24.7445 |
| chr15 | 102531392 | 244769407 | 2.3873 | 27.7592 |
| chr16 | 90354753 | 194942818 | 2.1575 | 25.4885 |
| chr17 | 81195210 | 246712994 | 3.0385 | 29.6213 |
| chr18 | 78077248 | 119501709 | 1.5306 | 25.7992 |
| chr19 | 59128983 | 235445828 | 3.9819 | 35.6217 |
| chr20 | 63025520 | 158132814 | 2.509 | 30.7009 |
| chr21 | 48129895 | 34178260 | 0.7101 | 12.2222 |
| chr22 | 51304566 | 113592013 | 2.2141 | 26.0647 |
| chrMT | 16571 | 80287 | 4.845 | 13.0003 |
| chrX | 155270560 | 166208917 | 1.0704 | 16.5364 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 1590162 | 0.0268 | 1.6361 |

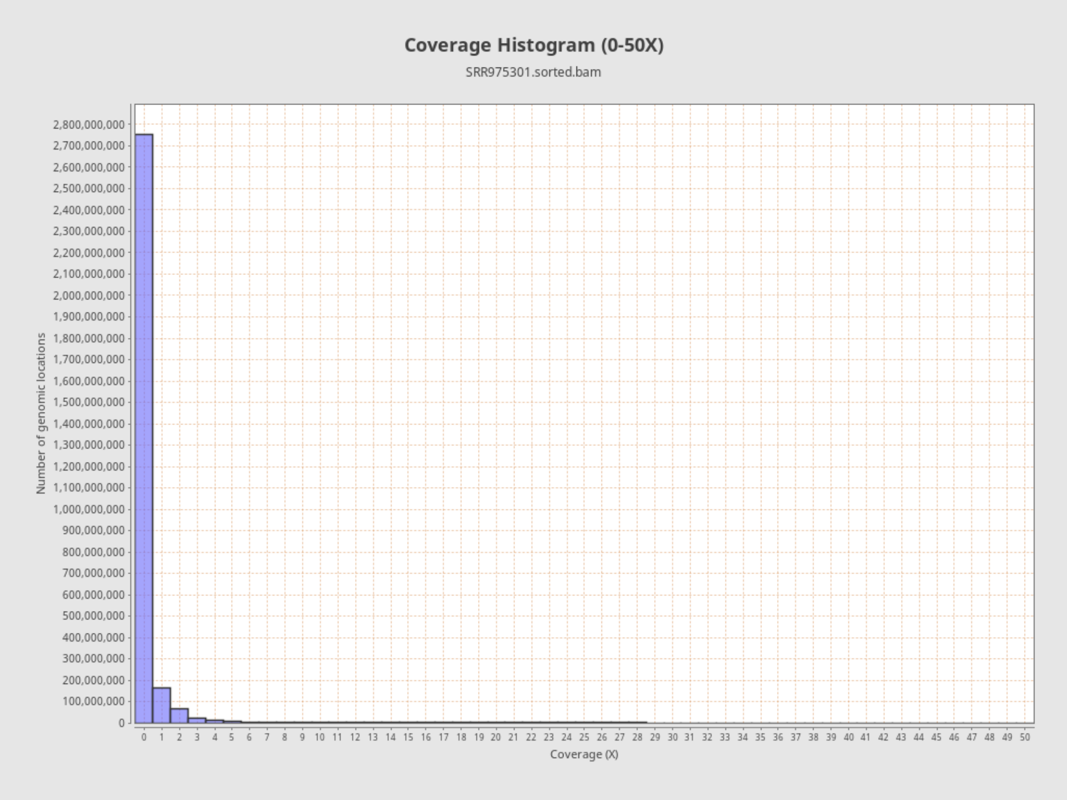
# 3. Results : Coverage across reference



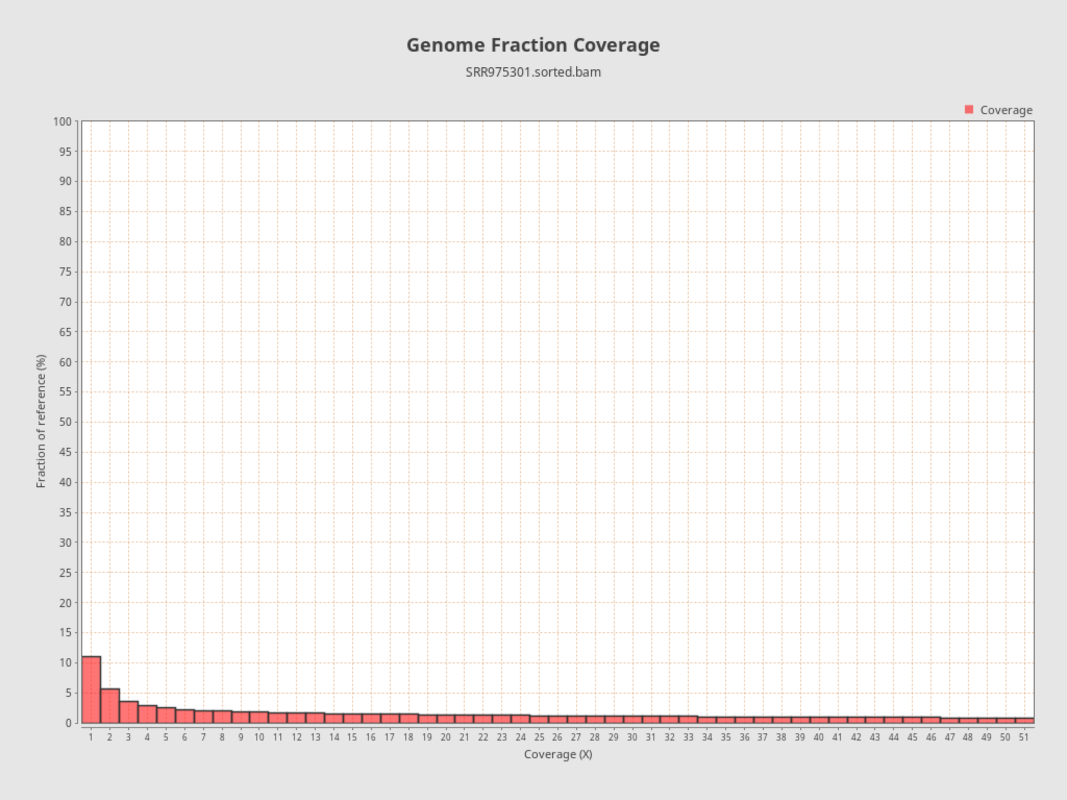
# 4. Results : Coverage Histogram



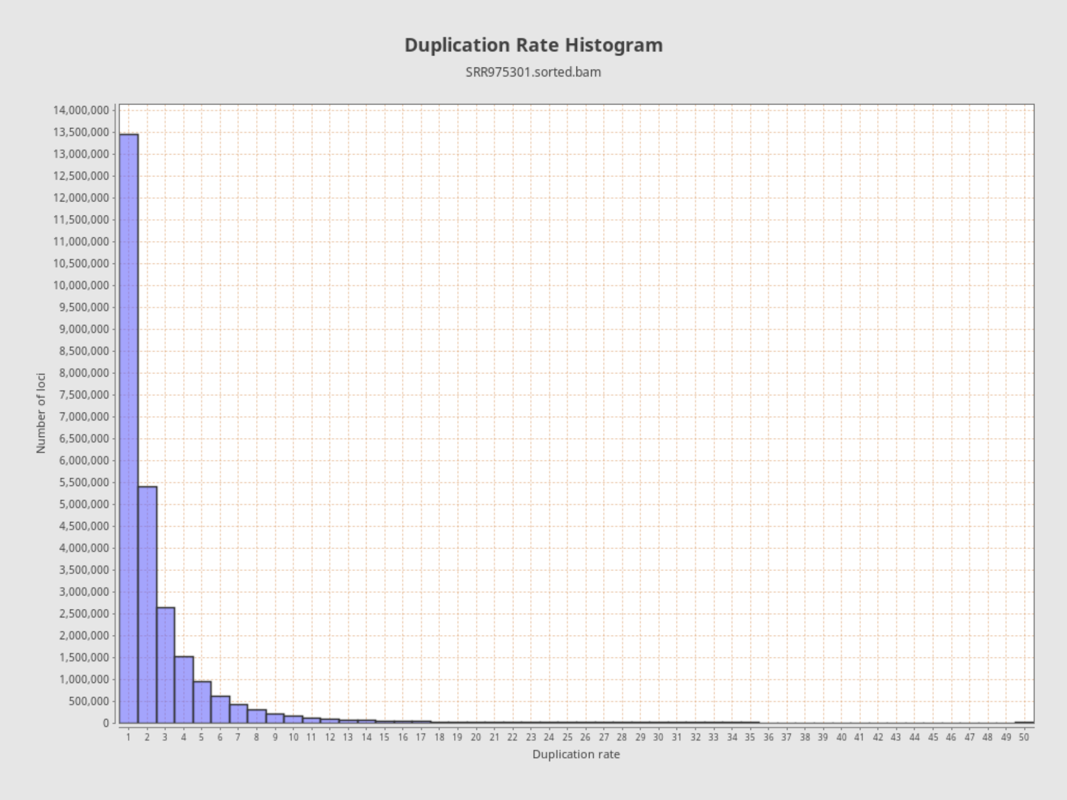
# 5. Results : Coverage Histogram (0-50X)



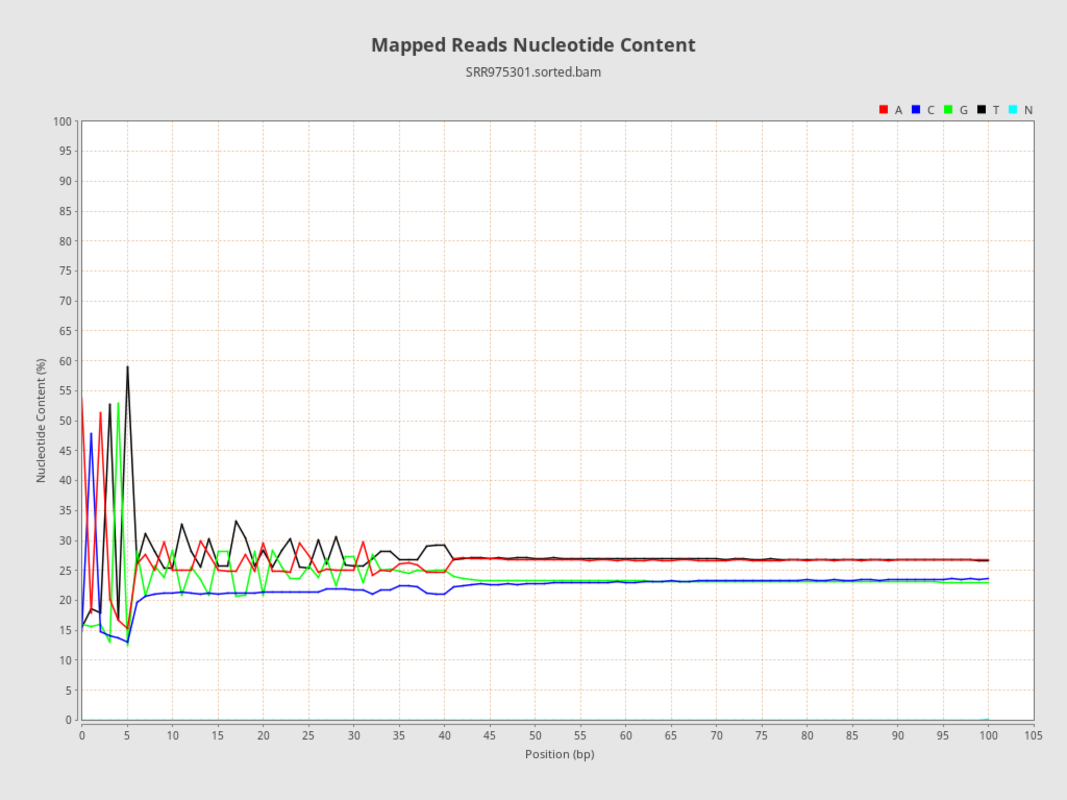
# 6. Results : Genome Fraction Coverage



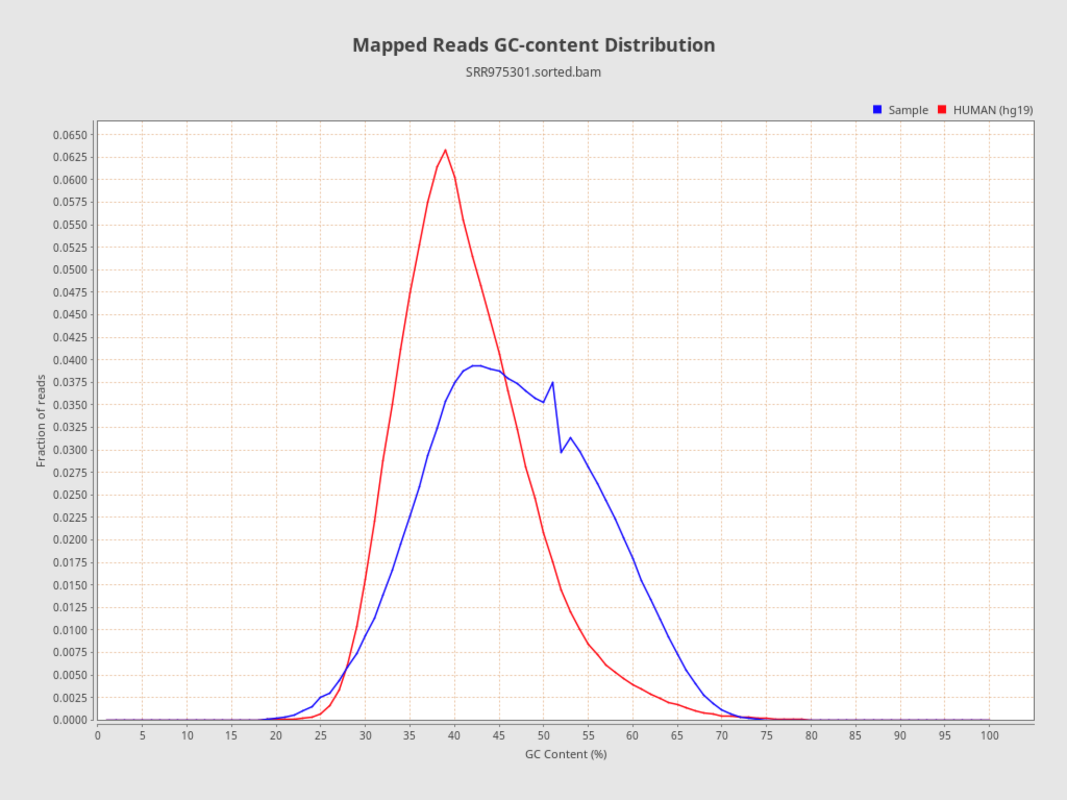
# 7. Results : Duplication Rate Histogram



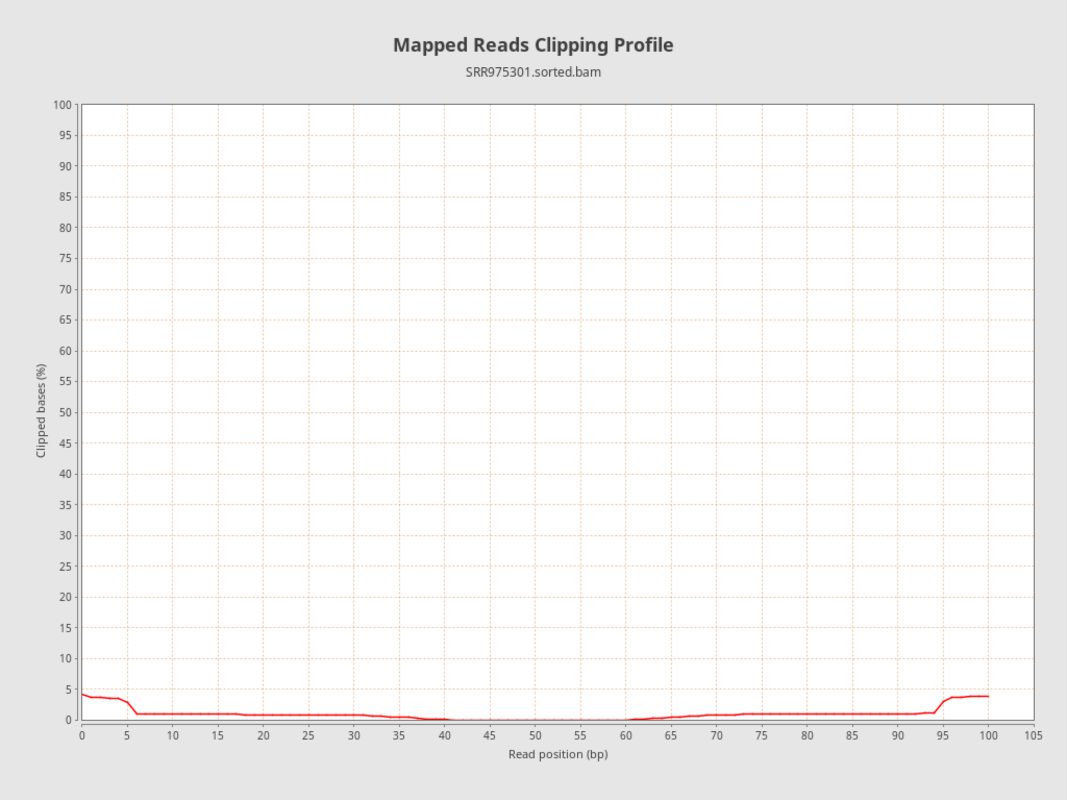
# 8. Results : Mapped Reads Nucleotide Content



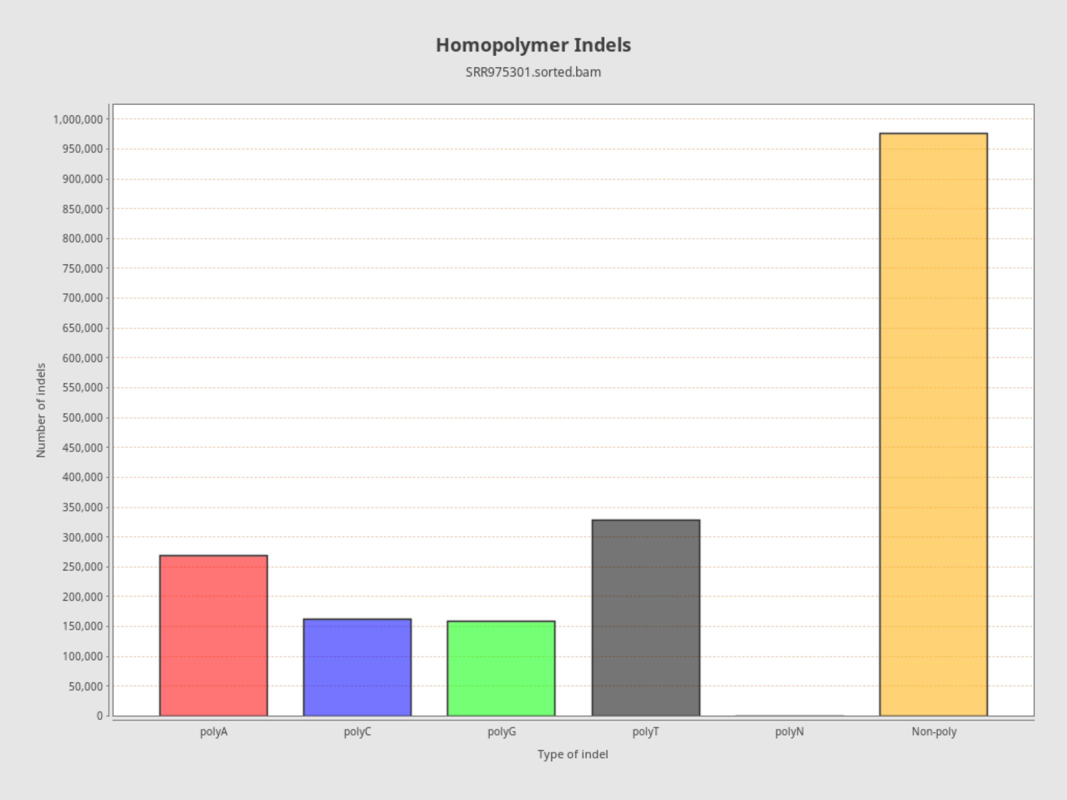
# 9. Results : Mapped Reads GC-content Distribution



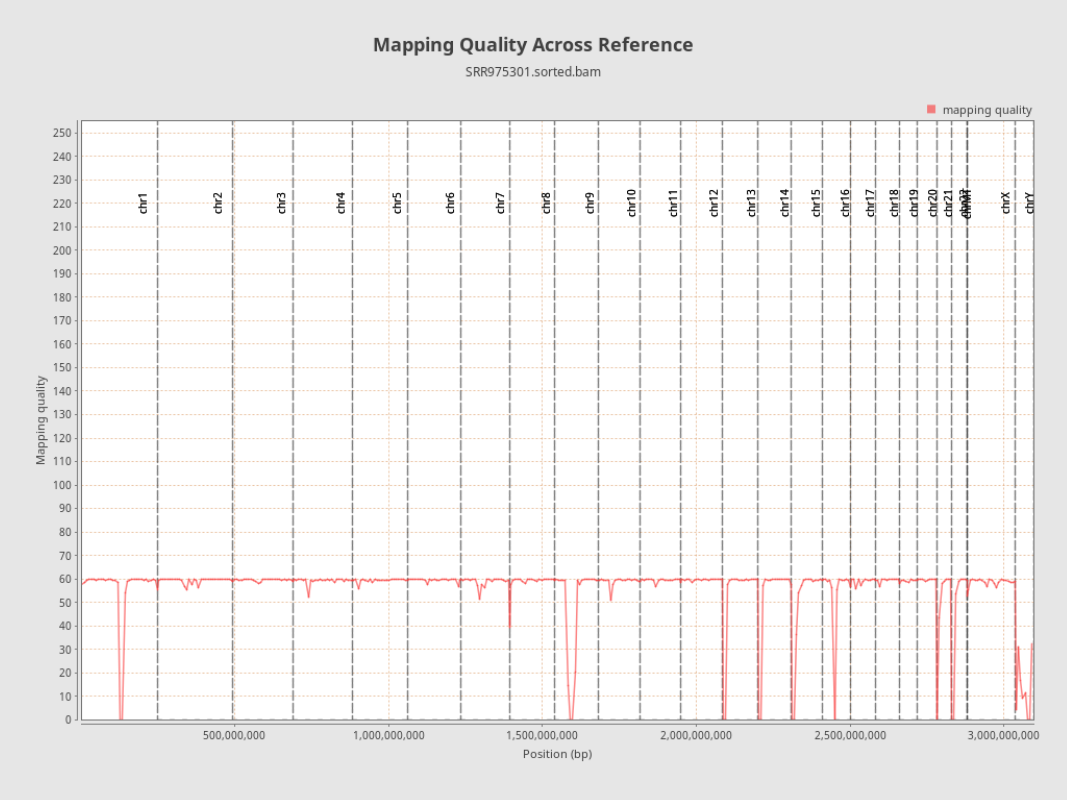
# 10. Results : Mapped Reads Clipping Profile



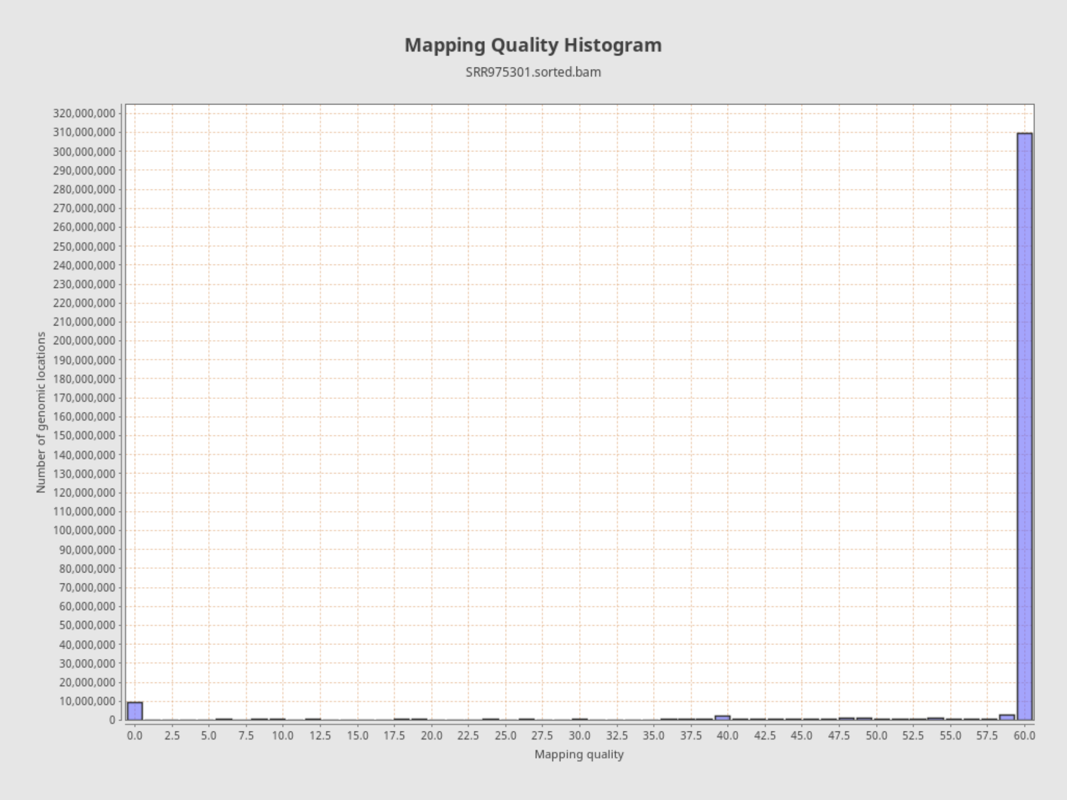
# 11. Results : Homopolymer Indels



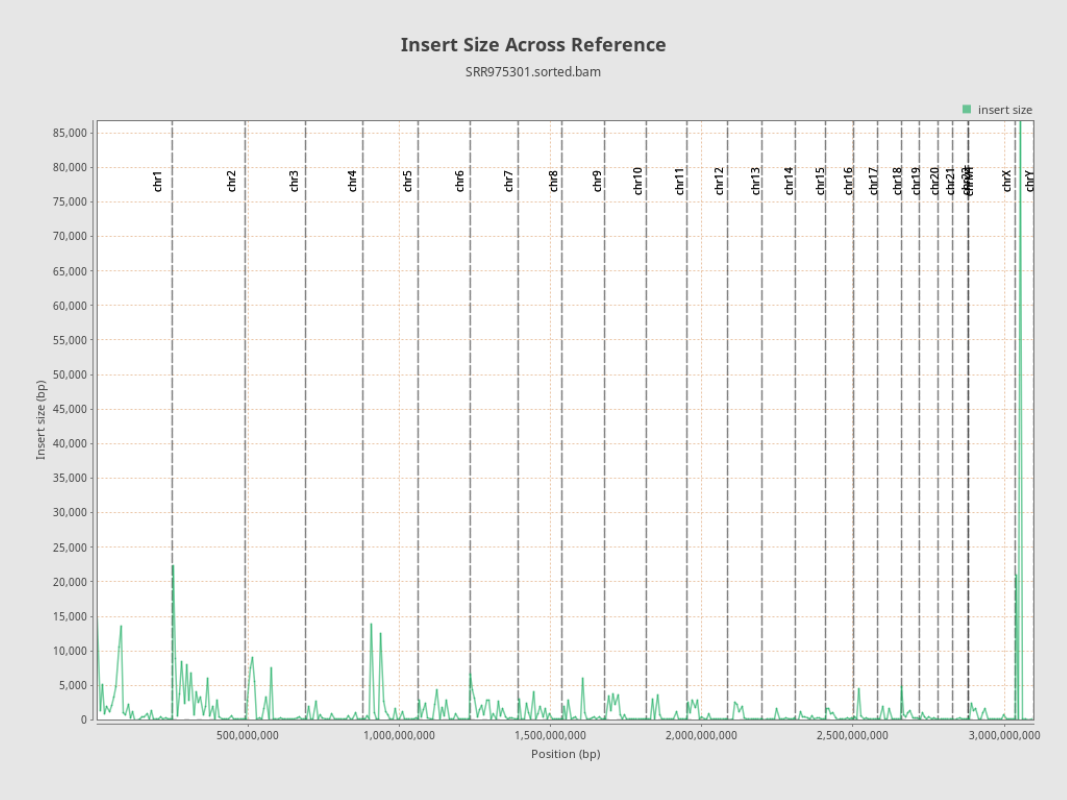
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram