# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/07 00:24:37*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR975303.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_SRR975303 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975303_1.fastq.gz SRR975303_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Sep 07 00:24:36 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR975303.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 50,248,508 |
| Mapped reads | 50,082,060 / 99.67% |
| Unmapped reads | 166,448 / 0.33% |
| Mapped paired reads | 50,082,060 / 99.67% |
| Mapped reads, first in pair | 25,033,660 / 49.82% |
| Mapped reads, second in pair | 25,048,400 / 49.85% |
| Mapped reads, both in pair | 50,007,202 / 99.52% |
| Mapped reads, singletons | 74,858 / 0.15% |
| Secondary alignments | 0 |
| Supplementary alignments | 96,821 / 0.19% |
| Read min/max/mean length | 30 / 101 / 101.08 |
| Duplicated reads (estimated) | 29,195,749 / 58.1% |
| Duplication rate | 42.91% |
| Clipped reads | 31,559,533 / 62.81% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 1,200,752,443 / 26.38% |
| Number/percentage of C's | 1,027,375,294 / 22.57% |
| Number/percentage of T's | 1,228,486,958 / 26.98% |
| Number/percentage of G's | 1,095,840,461 / 24.07% |
| Number/percentage of N's | 83,159 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 46.64% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 1.4711 |
| Standard Deviation | 23.0622 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 55.57 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 32,684.52 |
| Standard Deviation | 1,774,537.87 |
| P25/Median/P75 | 148 / 185 / 236 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.63% |
| Mismatches | 27,951,742 |
| Insertions | 389,773 |
| Mapped reads with at least one insertion | 0.77% |
| Deletions | 1,074,075 |
| Mapped reads with at least one deletion | 2.11% |
| Homopolymer indels | 47.17% |

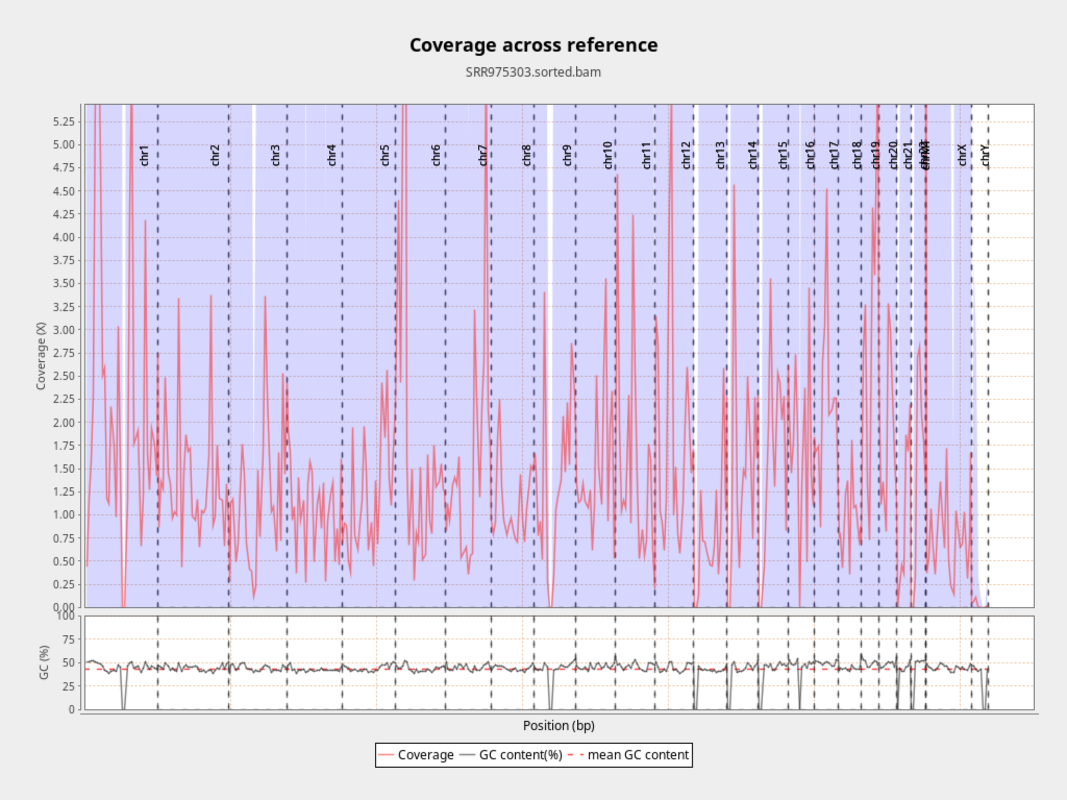
## 2.7. Chromosome stats

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

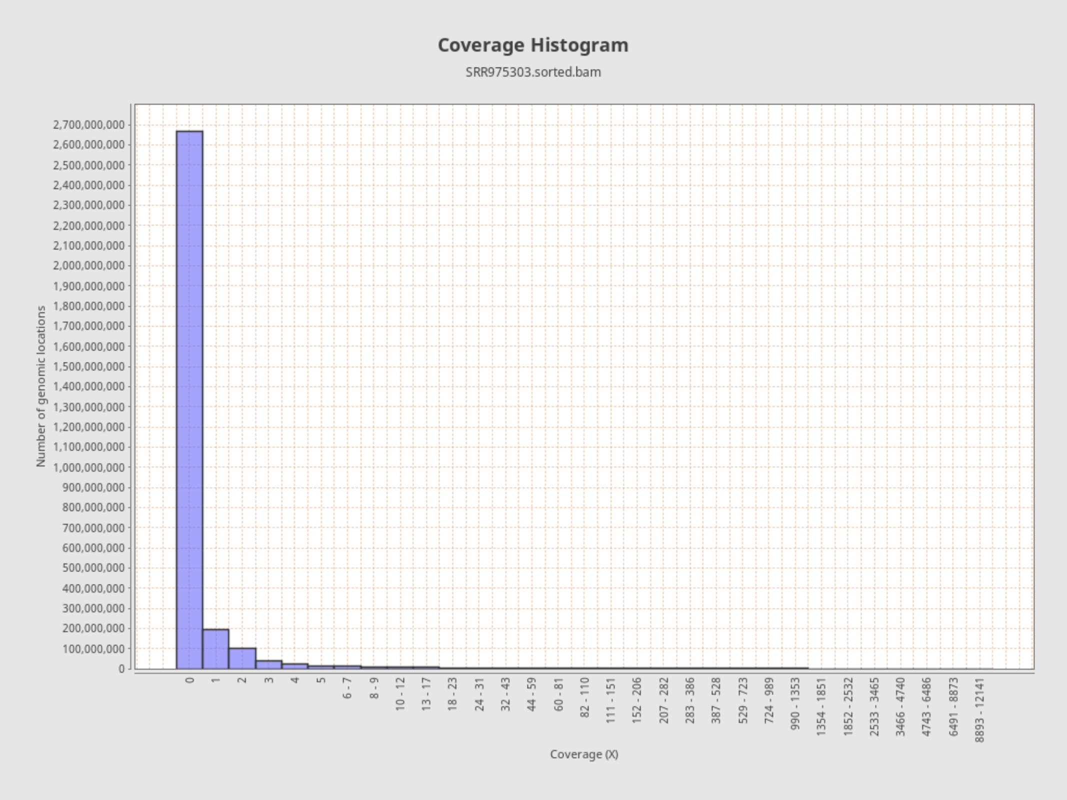
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 554858348 | 2.2261 | 31.8157 |
| chr2 | 243199373 | 329471959 | 1.3547 | 19.9301 |
| chr3 | 198022430 | 237927028 | 1.2015 | 18.5212 |
| chr4 | 191154276 | 200477080 | 1.0488 | 17.877 |
| chr5 | 180915260 | 221440236 | 1.224 | 19.3963 |
| chr6 | 171115067 | 353373317 | 2.0651 | 33.4649 |
| chr7 | 159138663 | 254238132 | 1.5976 | 27.5033 |
| chr8 | 146364022 | 164568840 | 1.1244 | 17.2962 |
| chr9 | 141213431 | 187883949 | 1.3305 | 20.4122 |
| chr10 | 135534747 | 207692182 | 1.5324 | 23.2867 |
| chr11 | 135006516 | 219052380 | 1.6225 | 23.1538 |
| chr12 | 133851895 | 256309264 | 1.9149 | 27.076 |
| chr13 | 115169878 | 89750944 | 0.7793 | 13.4303 |
| chr14 | 107349540 | 154892013 | 1.4429 | 21.1284 |
| chr15 | 102531392 | 166373219 | 1.6227 | 23.0934 |
| chr16 | 90354753 | 150617616 | 1.667 | 22.8084 |
| chr17 | 81195210 | 184380288 | 2.2708 | 27.2348 |
| chr18 | 78077248 | 75546190 | 0.9676 | 17.176 |
| chr19 | 59128983 | 179414374 | 3.0343 | 34.3133 |
| chr20 | 63025520 | 122578055 | 1.9449 | 27.1906 |
| chr21 | 48129895 | 46646501 | 0.9692 | 18.4105 |
| chr22 | 51304566 | 77901064 | 1.5184 | 22.7753 |
| chrMT | 16571 | 147617 | 8.9082 | 13.2387 |
| chrX | 155270560 | 116780996 | 0.7521 | 13.4509 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 1807541 | 0.0304 | 1.6734 |

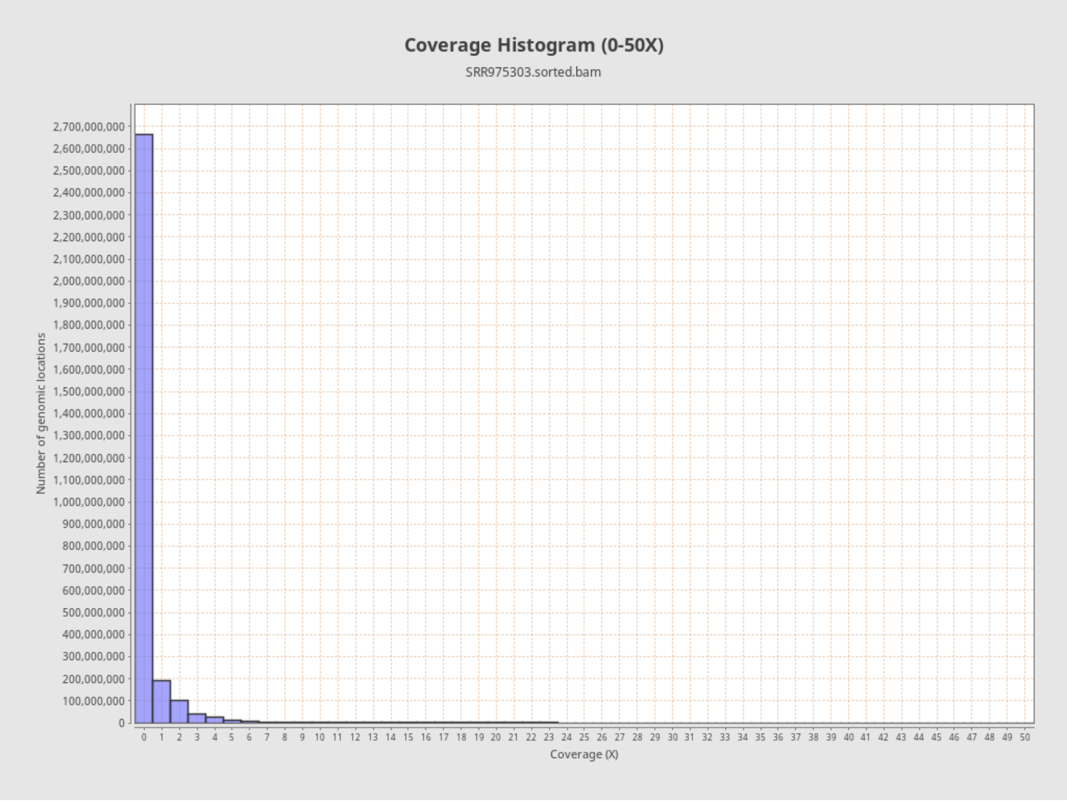
# 3. Results : Coverage across reference



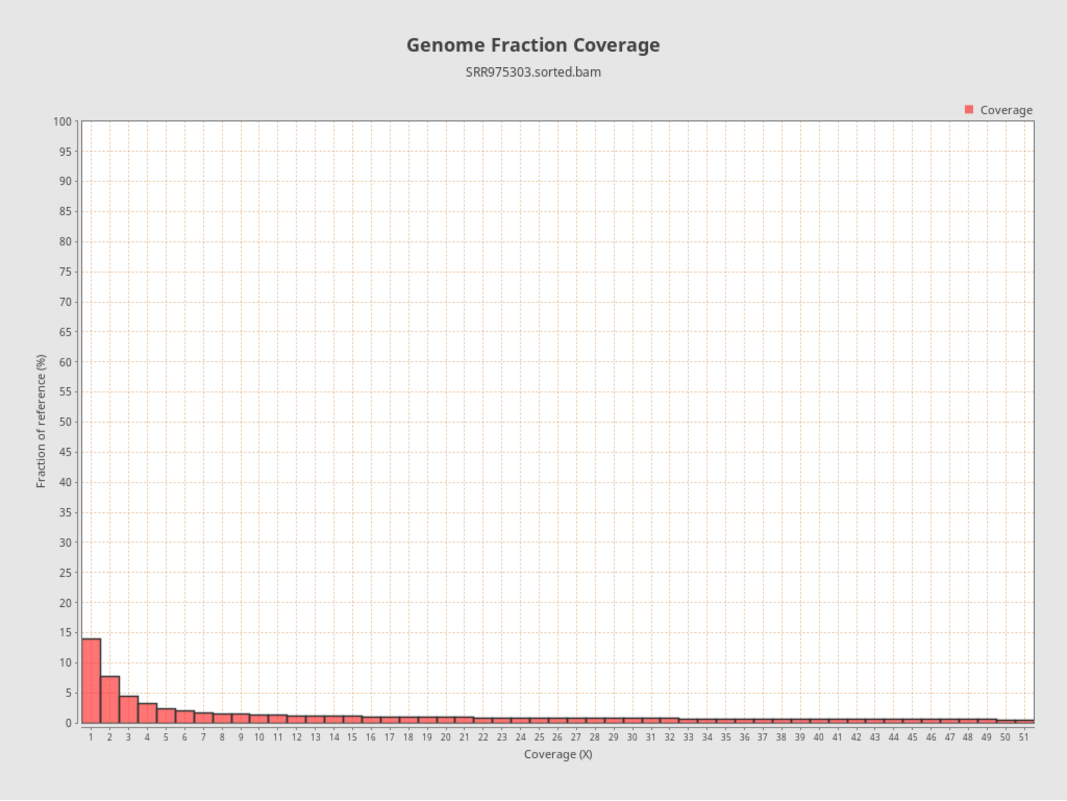
# 4. Results : Coverage Histogram



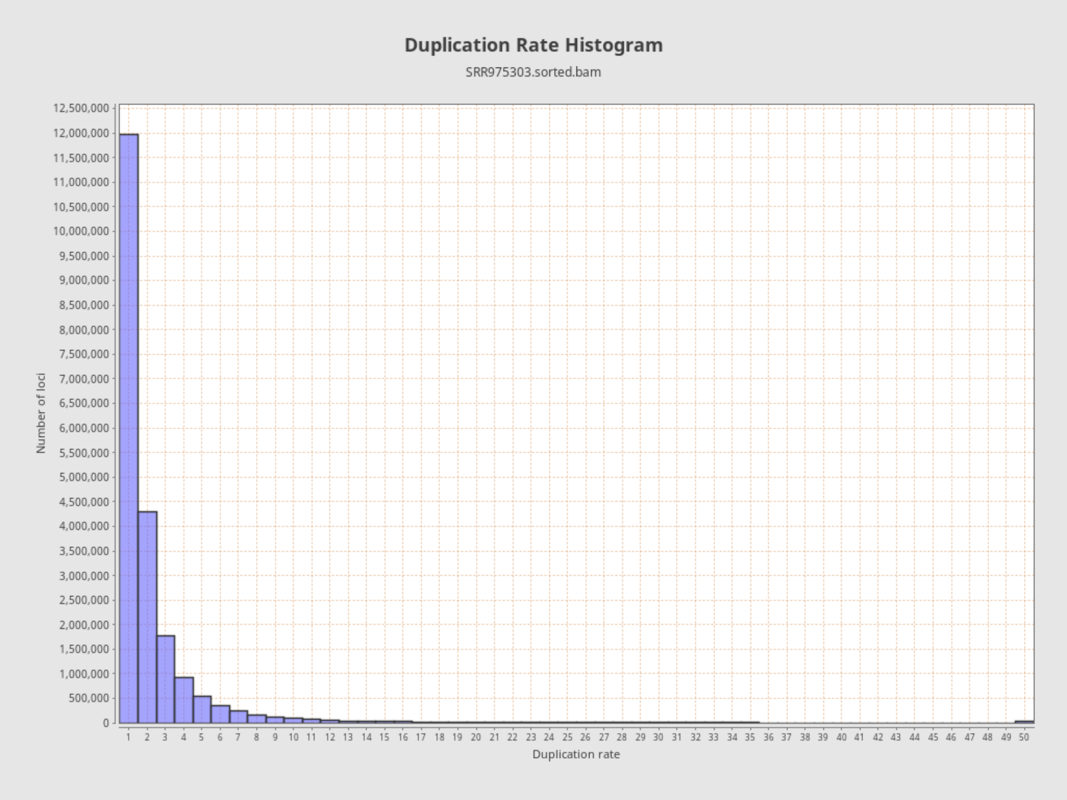
# 5. Results : Coverage Histogram (0-50X)



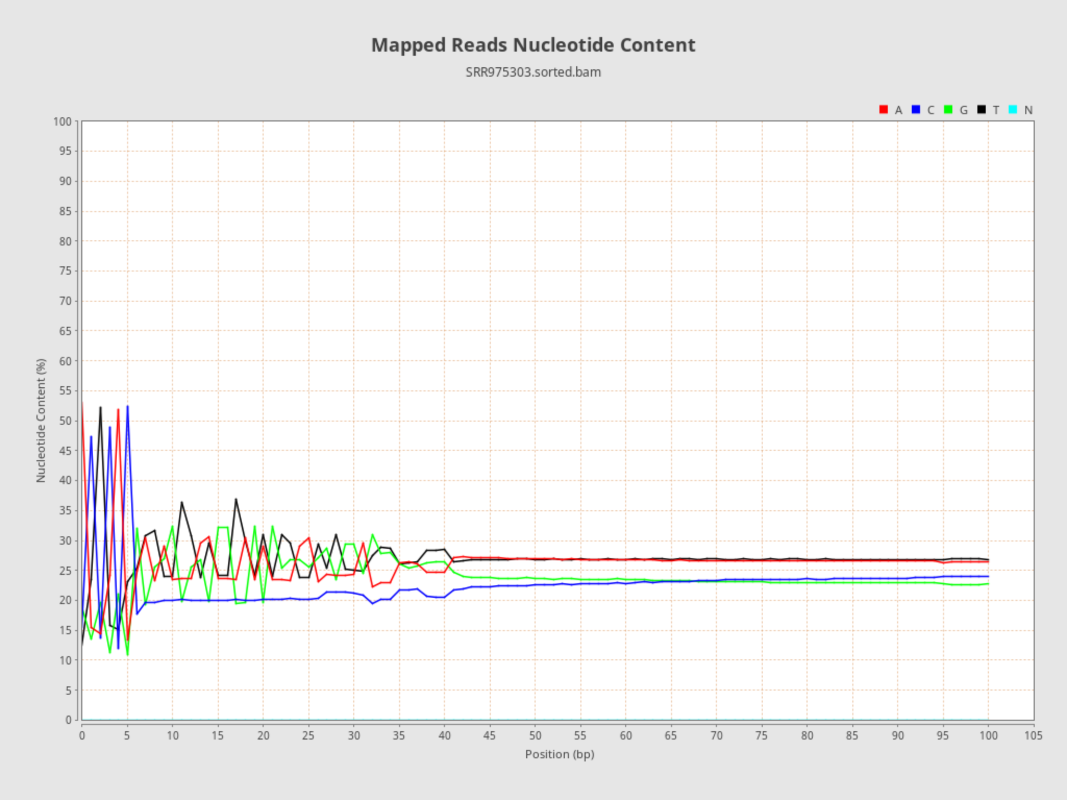
# 6. Results : Genome Fraction Coverage



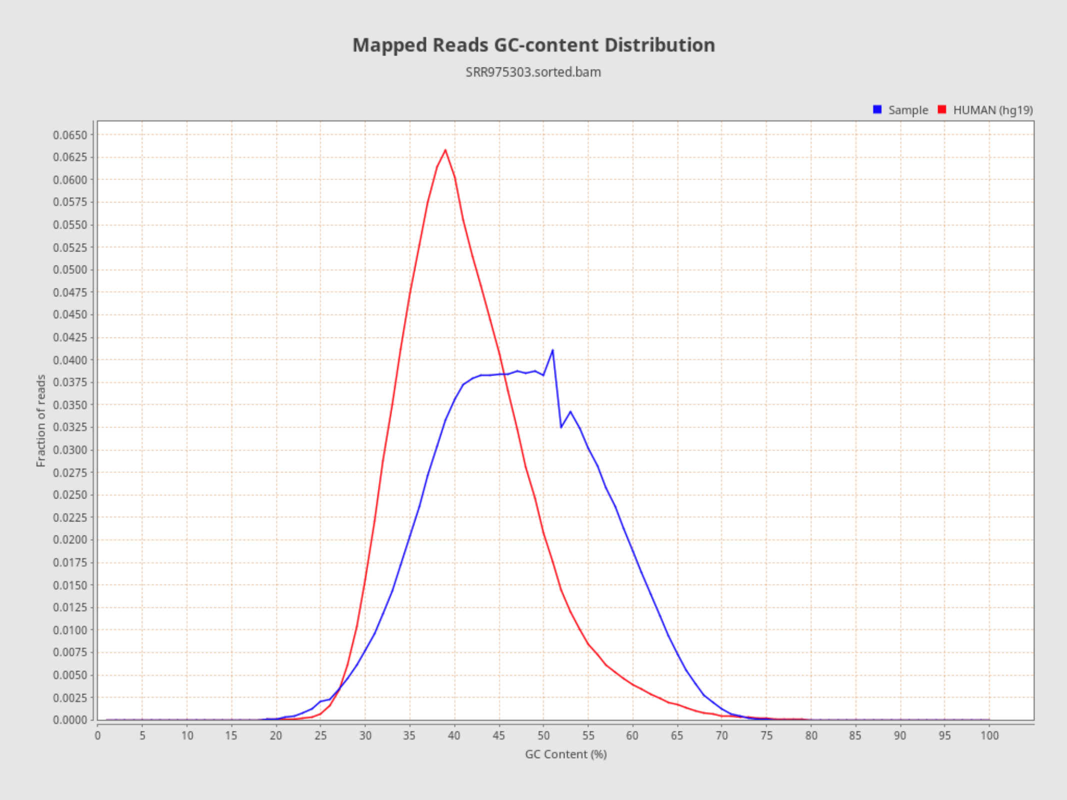
# 7. Results : Duplication Rate Histogram



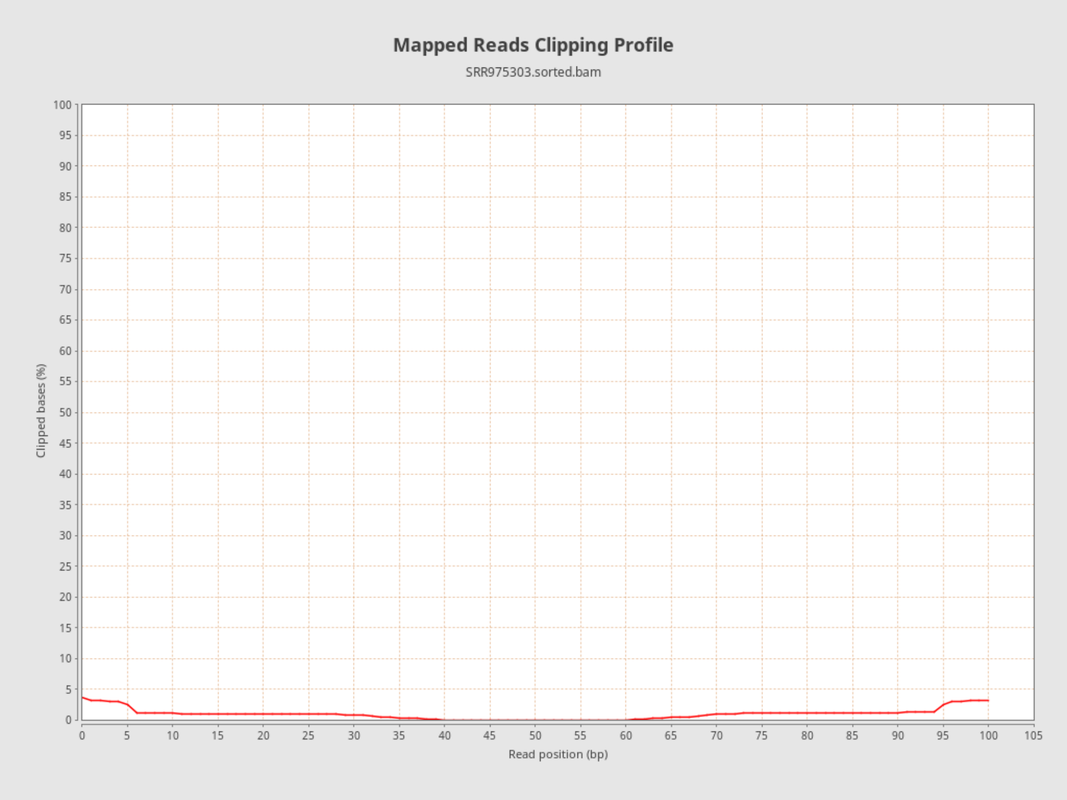
# 8. Results : Mapped Reads Nucleotide Content



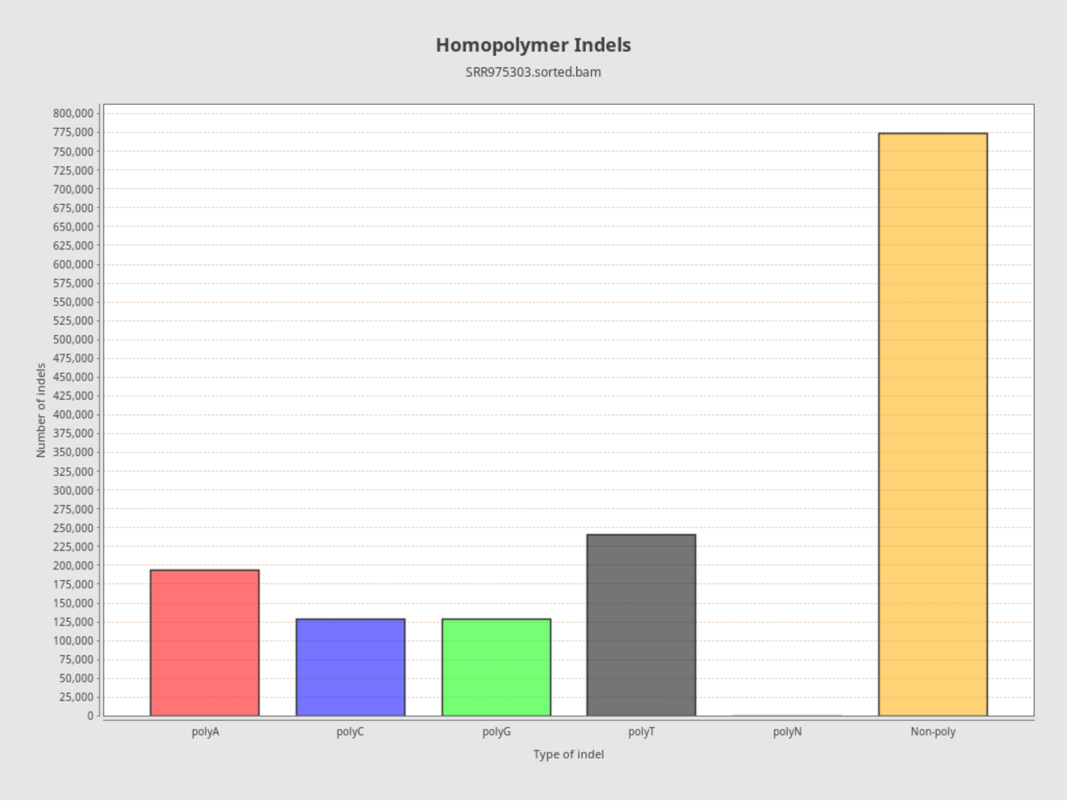
# 9. Results : Mapped Reads GC-content Distribution



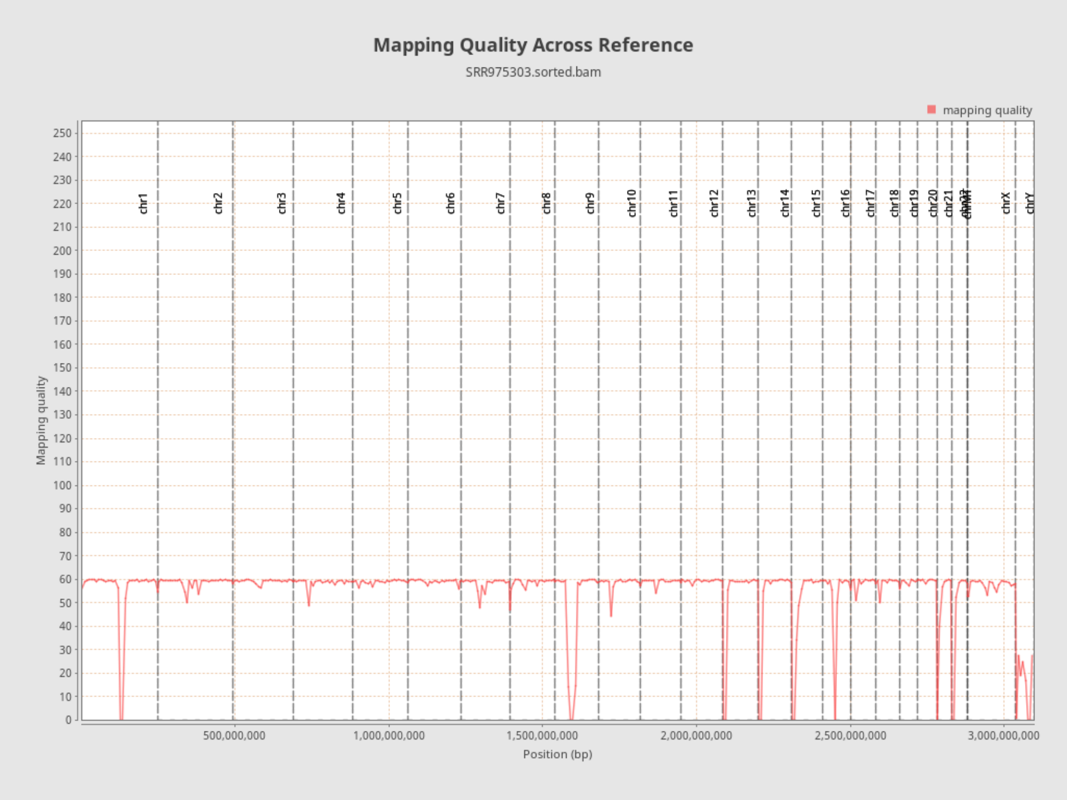
# 10. Results : Mapped Reads Clipping Profile



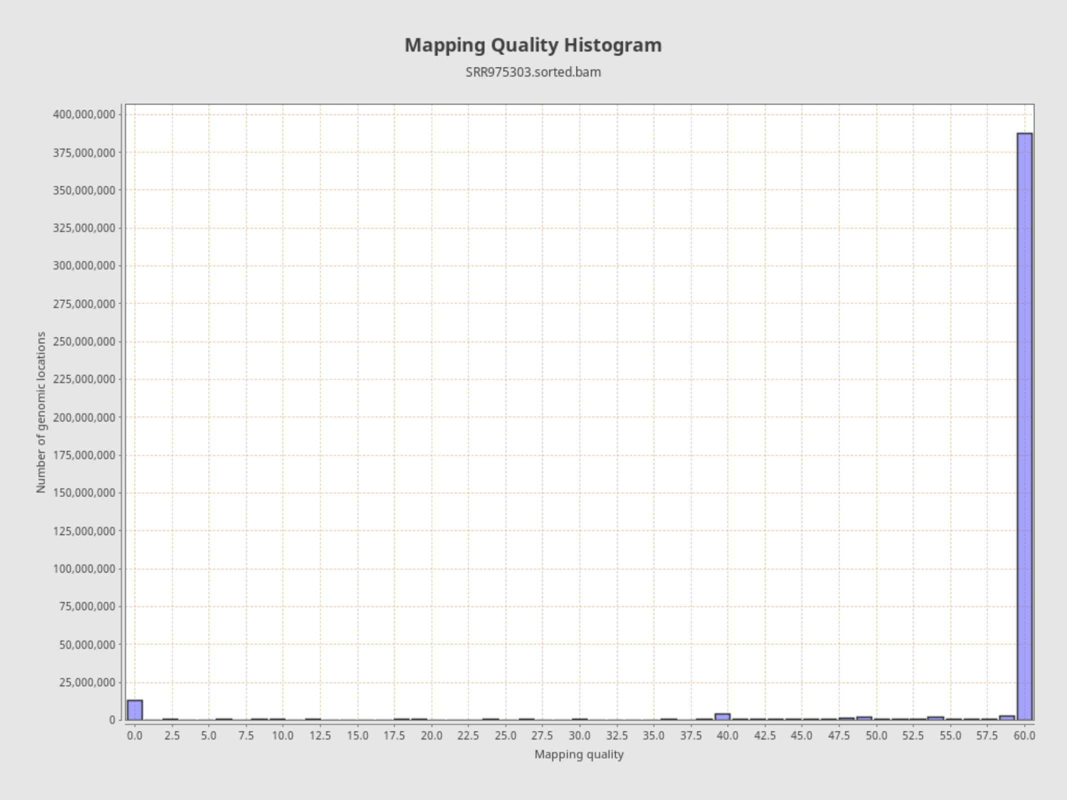
# 11. Results : Homopolymer Indels



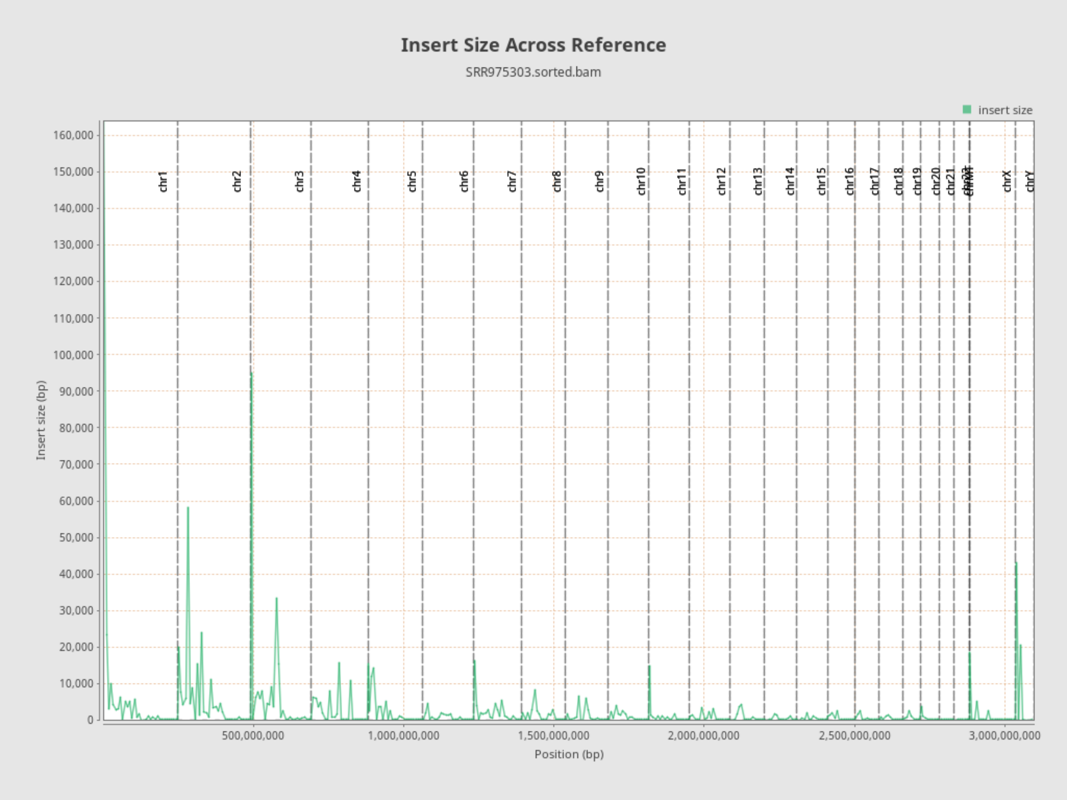
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram