# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/07 06:35:55*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR975338.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_SRR975338 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975338_1.fastq.gz SRR975338_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Sep 07 06:35:54 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR975338.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,585,282 |
| Mapped reads | 4,520,834 / 98.59% |
| Unmapped reads | 64,448 / 1.41% |
| Mapped paired reads | 4,520,834 / 98.59% |
| Mapped reads, first in pair | 2,259,779 / 49.28% |
| Mapped reads,  second in pair | 2,261,055 / 49.31% |
| Mapped reads, both in pair | 4,508,234 / 98.32% |
| Mapped reads, singletons | 12,600 / 0.27% |
| Secondary alignments | 0 |
| Supplementary alignments | 16,602 / 0.36% |
| Read min/max/mean length | 30 / 101 / 101.14 |
| Duplicated reads (estimated) | 177,609 / 3.87% |
| Duplication rate | 2.74% |
| Clipped reads | 2,821,521 / 61.53% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 117,839,221 / 28.74% |
| Number/percentage of C's | 81,987,411 / 20% |
| Number/percentage of T's | 120,311,597 / 29.35% |
| Number/percentage of G's | 89,809,246 / 21.91% |
| Number/percentage of N's | 8,619 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 41.91% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1325 |
| Standard Deviation | 0.8636 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.14 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 83,693.6 |
| Standard Deviation | 2,809,620.26 |
| P25/Median/P75 | 134 / 166 / 211 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.82% |
| Mismatches | 3,221,280 |
| Insertions | 69,275 |
| Mapped reads with at least one insertion | 1.5% |
| Deletions | 149,787 |
| Mapped reads with at least one deletion | 3.25% |
| Homopolymer indels | 47.03% |

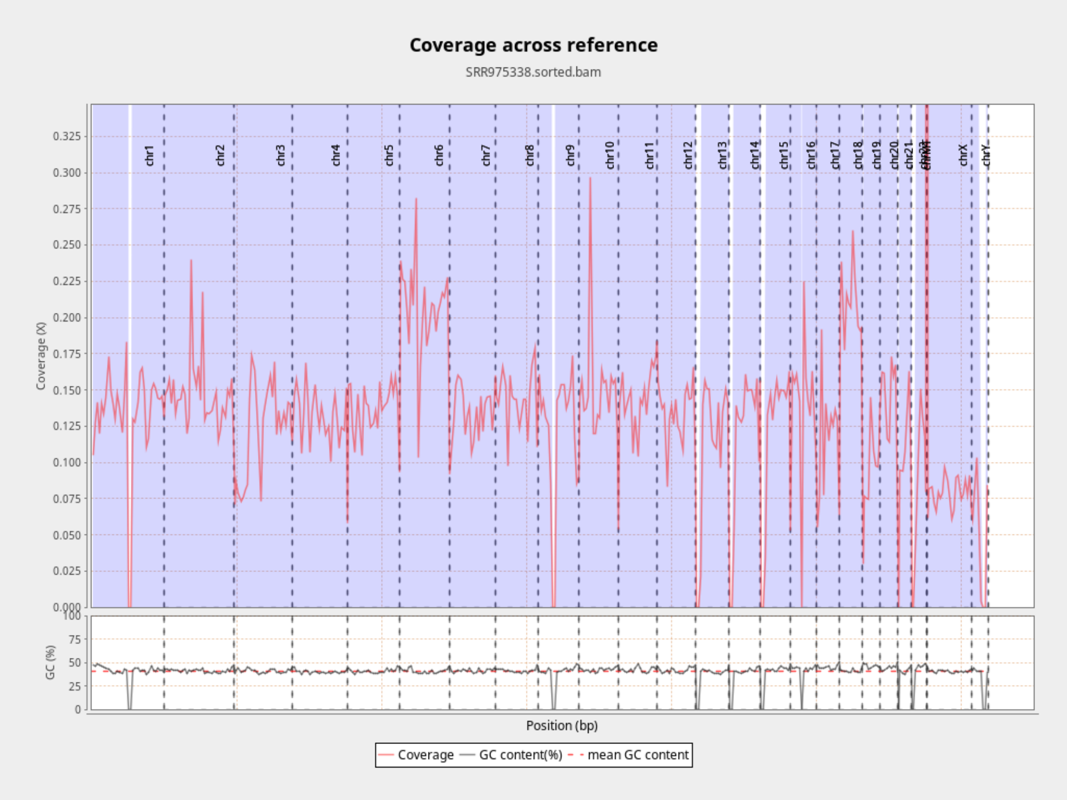
## 2.7. Chromosome stats

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

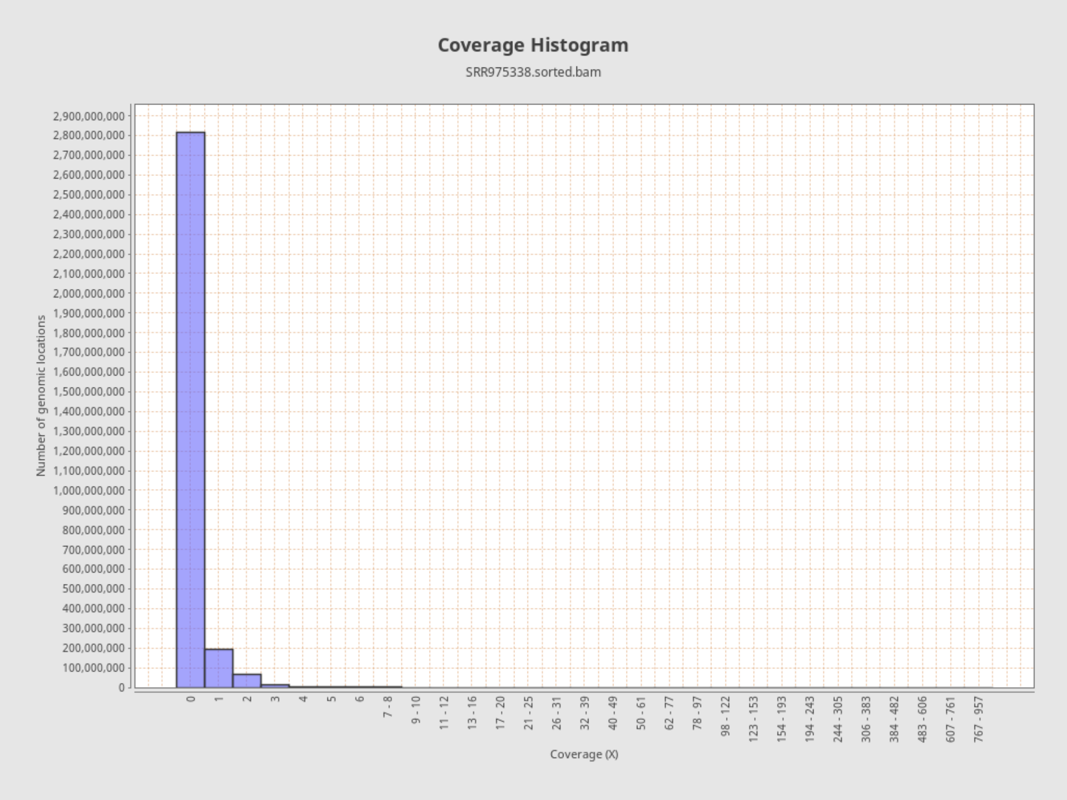
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 33005290 | 0.1324 | 0.9131 |
| chr2 | 243199373 | 35821969 | 0.1473 | 1.1552 |
| chr3 | 198022430 | 24345826 | 0.1229 | 0.4613 |
| chr4 | 191154276 | 25237549 | 0.132 | 0.6305 |
| chr5 | 180915260 | 24922117 | 0.1378 | 0.4952 |
| chr6 | 171115067 | 35154717 | 0.2054 | 1.1409 |
| chr7 | 159138663 | 21144116 | 0.1329 | 0.8489 |
| chr8 | 146364022 | 20939498 | 0.1431 | 0.5524 |
| chr9 | 141213431 | 17153389 | 0.1215 | 1.0921 |
| chr10 | 135534747 | 20587070 | 0.1519 | 1.645 |
| chr11 | 135006516 | 19132182 | 0.1417 | 0.6734 |
| chr12 | 133851895 | 18057222 | 0.1349 | 0.4823 |
| chr13 | 115169878 | 12675064 | 0.1101 | 0.4333 |
| chr14 | 107349540 | 12487314 | 0.1163 | 0.466 |
| chr15 | 102531392 | 12008044 | 0.1171 | 0.4509 |
| chr16 | 90354753 | 12324372 | 0.1364 | 0.9973 |
| chr17 | 81195210 | 9380593 | 0.1155 | 1.333 |
| chr18 | 78077248 | 16566706 | 0.2122 | 1.3374 |
| chr19 | 59128983 | 5523373 | 0.0934 | 0.5985 |
| chr20 | 63025520 | 9130111 | 0.1449 | 0.5127 |
| chr21 | 48129895 | 5024666 | 0.1044 | 0.5524 |
| chr22 | 51304566 | 4406738 | 0.0859 | 0.4081 |
| chrMT | 16571 | 114640 | 6.9181 | 38.1569 |
| chrX | 155270560 | 12243315 | 0.0789 | 0.4189 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 2808260 | 0.0473 | 0.9055 |

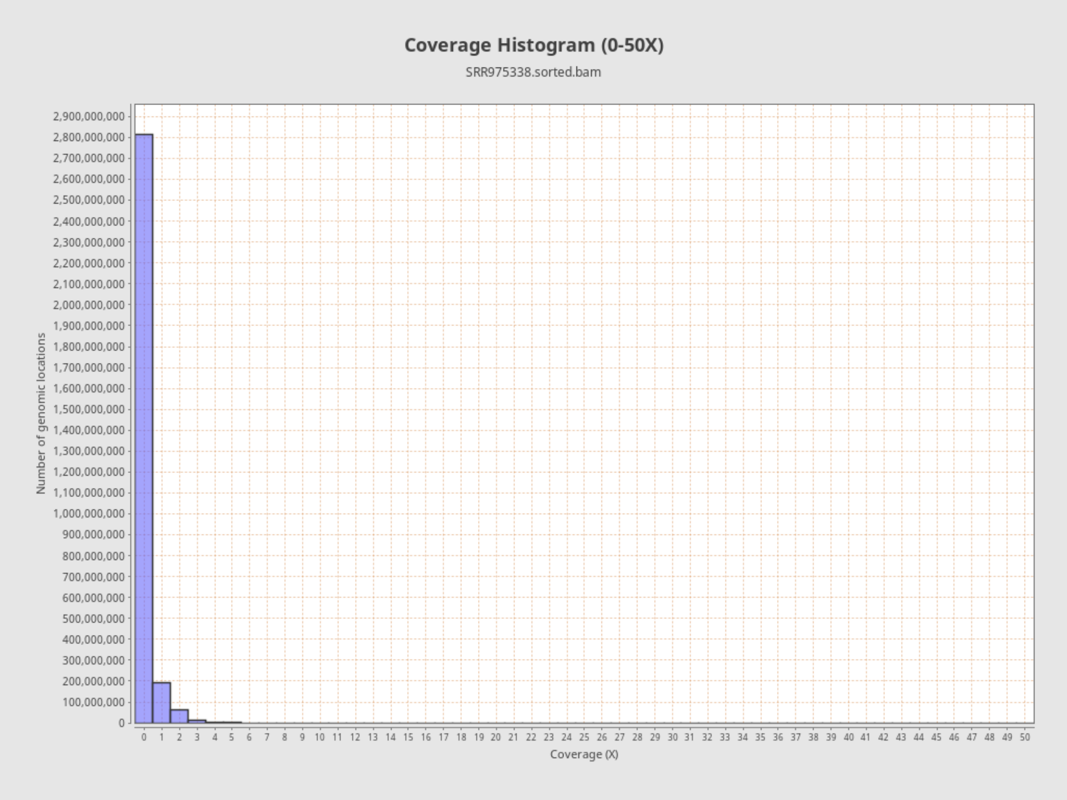
# 3. Results : Coverage across reference



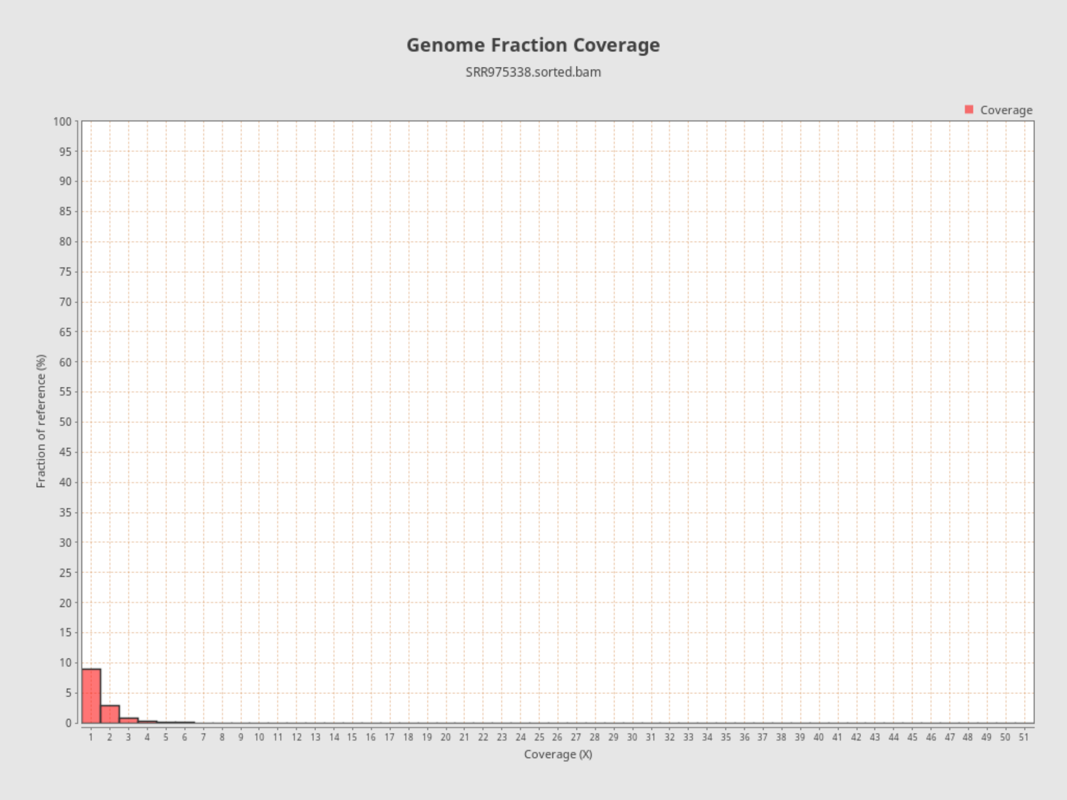
# 4. Results : Coverage Histogram



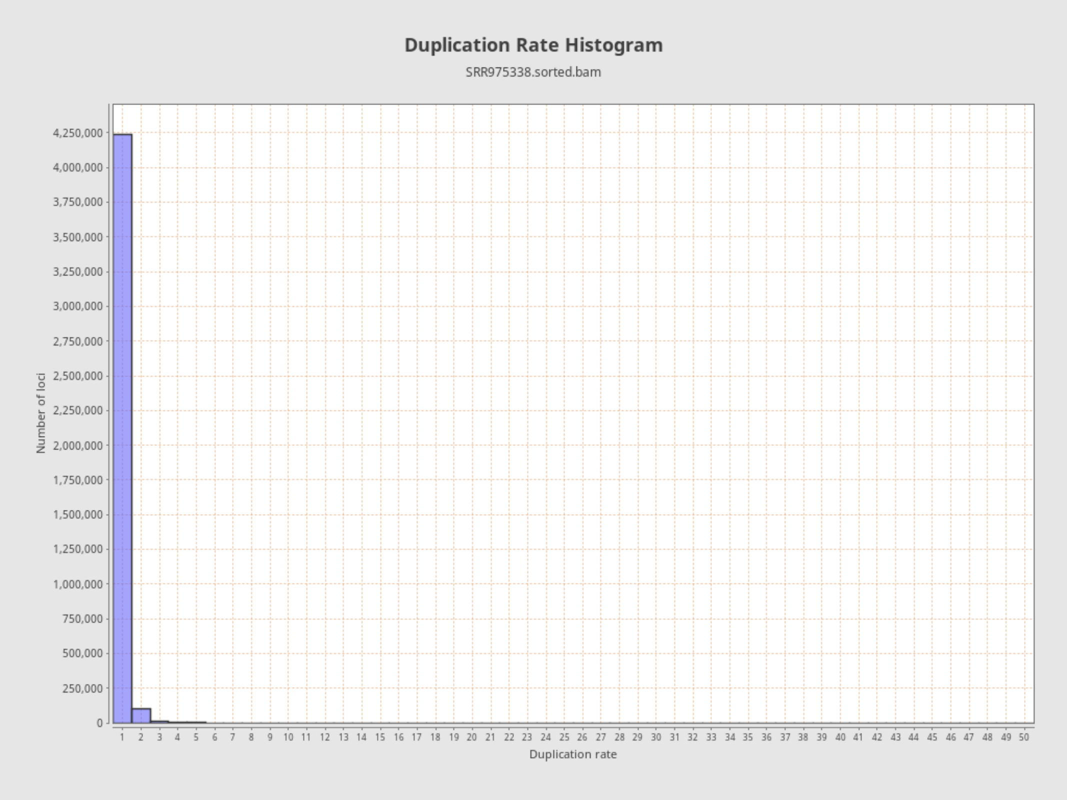
# 5. Results : Coverage Histogram (0-50X)



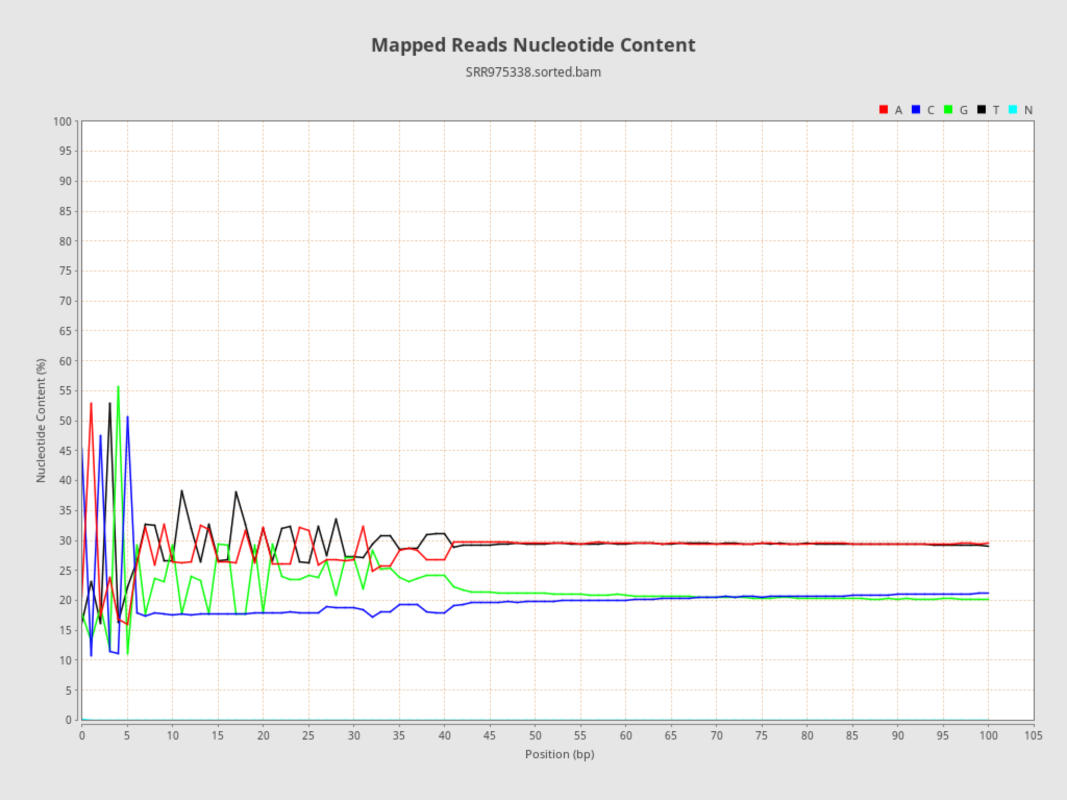
# 6. Results : Genome Fraction Coverage



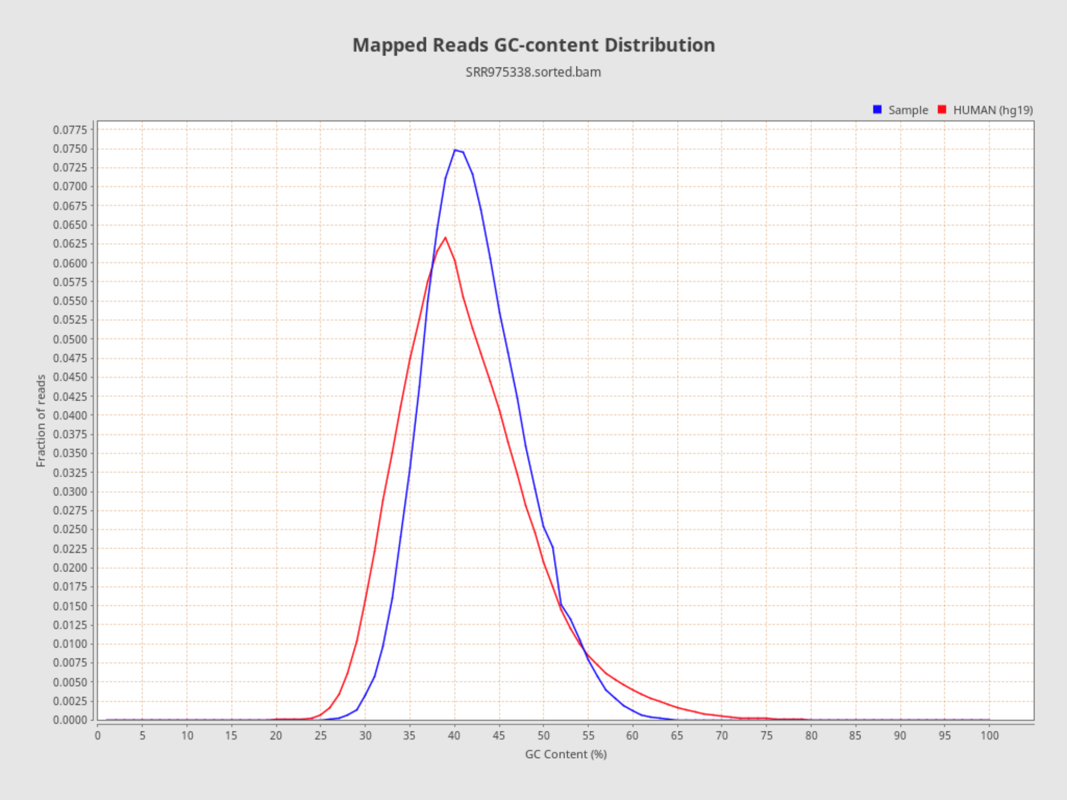
# 7. Results : Duplication Rate Histogram



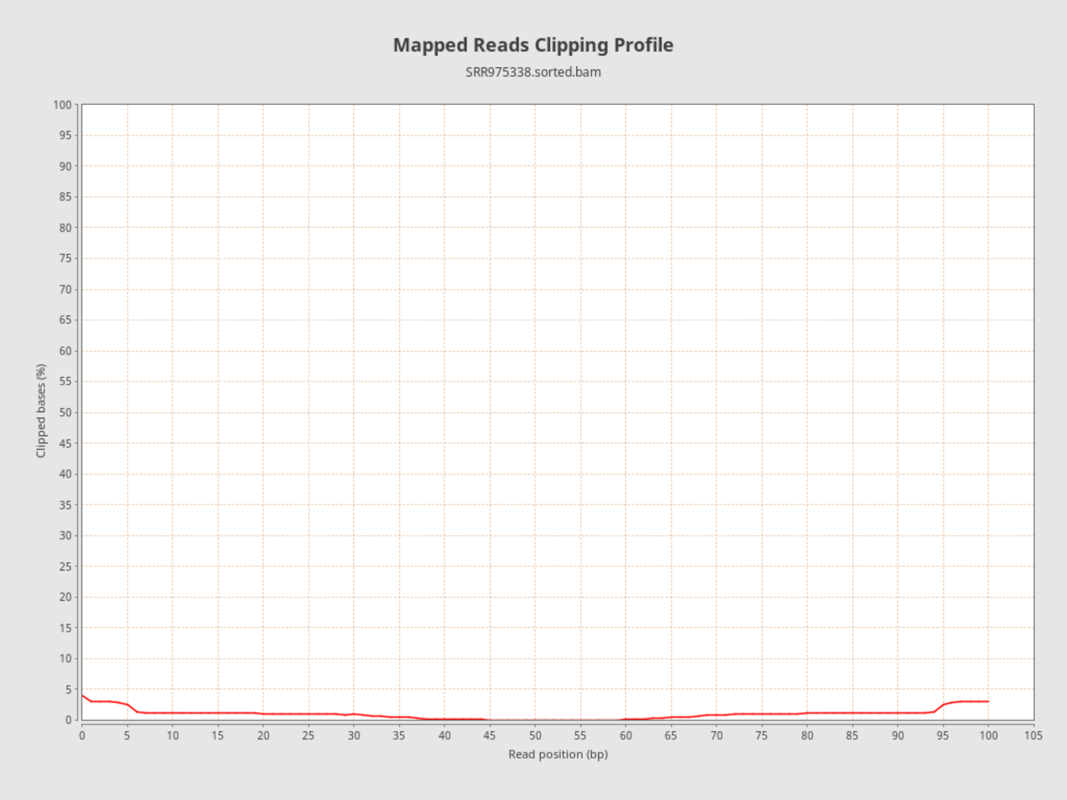
# 8. Results : Mapped Reads Nucleotide Content



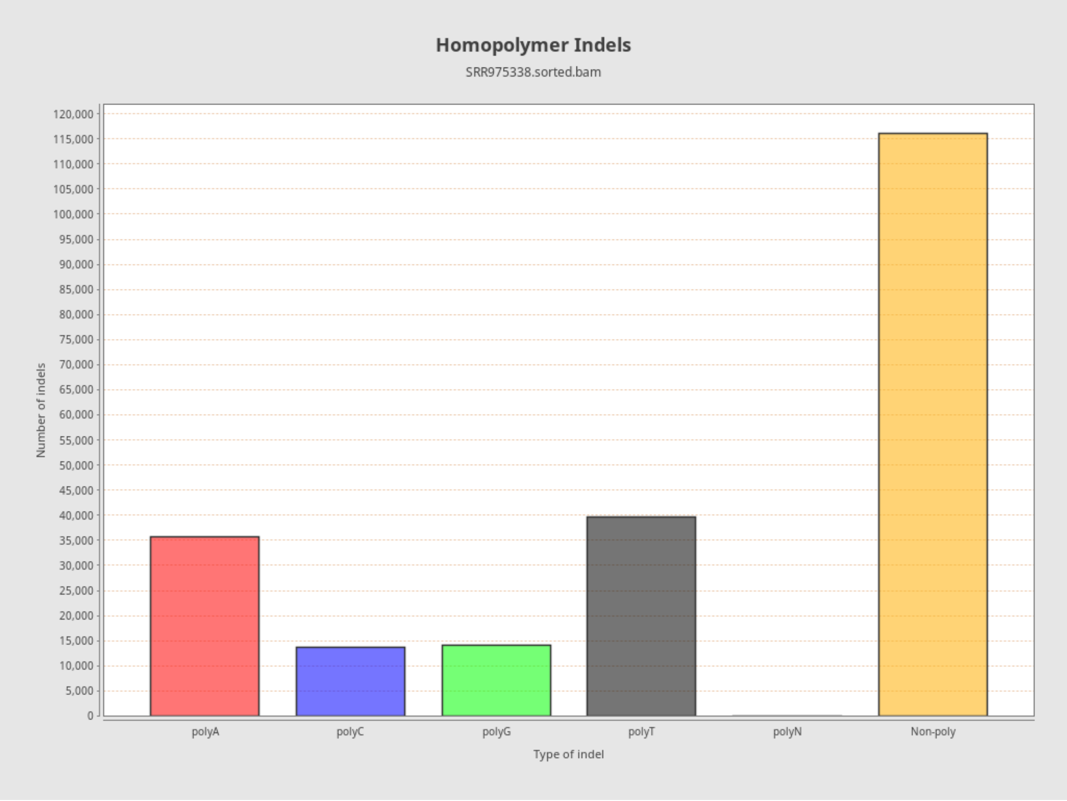
# 9. Results : Mapped Reads GC-content Distribution



# 10. Results : Mapped Reads Clipping Profile

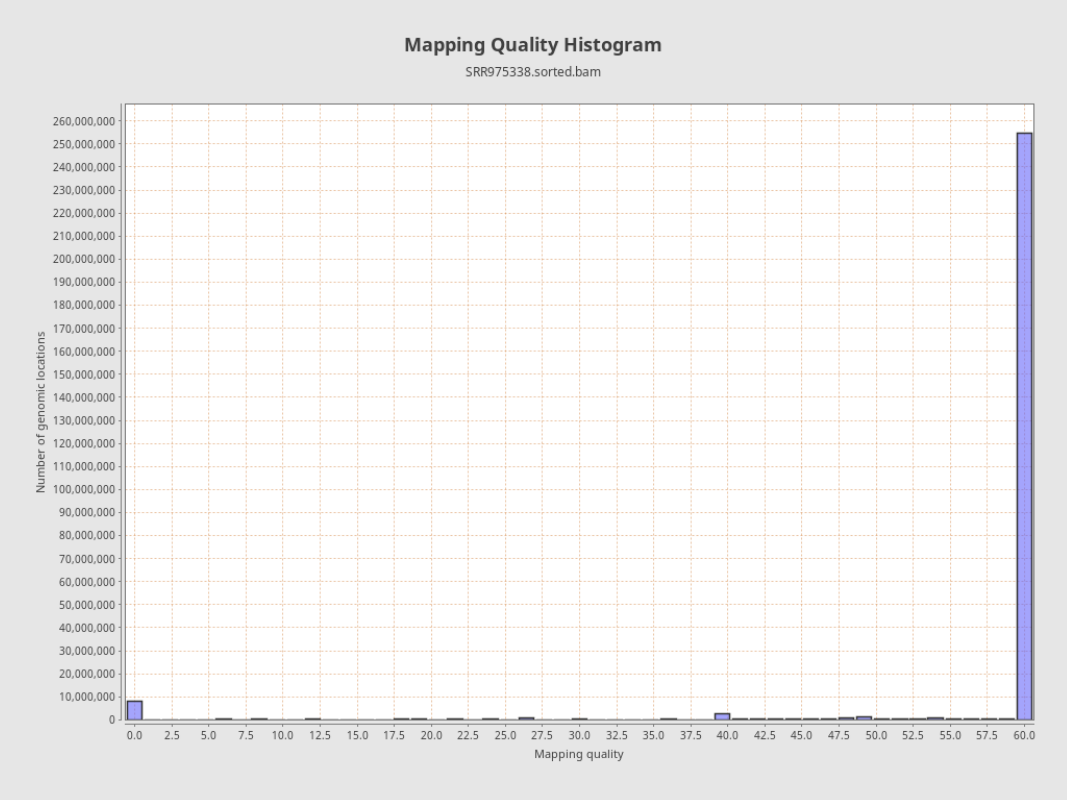


# 11. Results : Homopolymer Indels

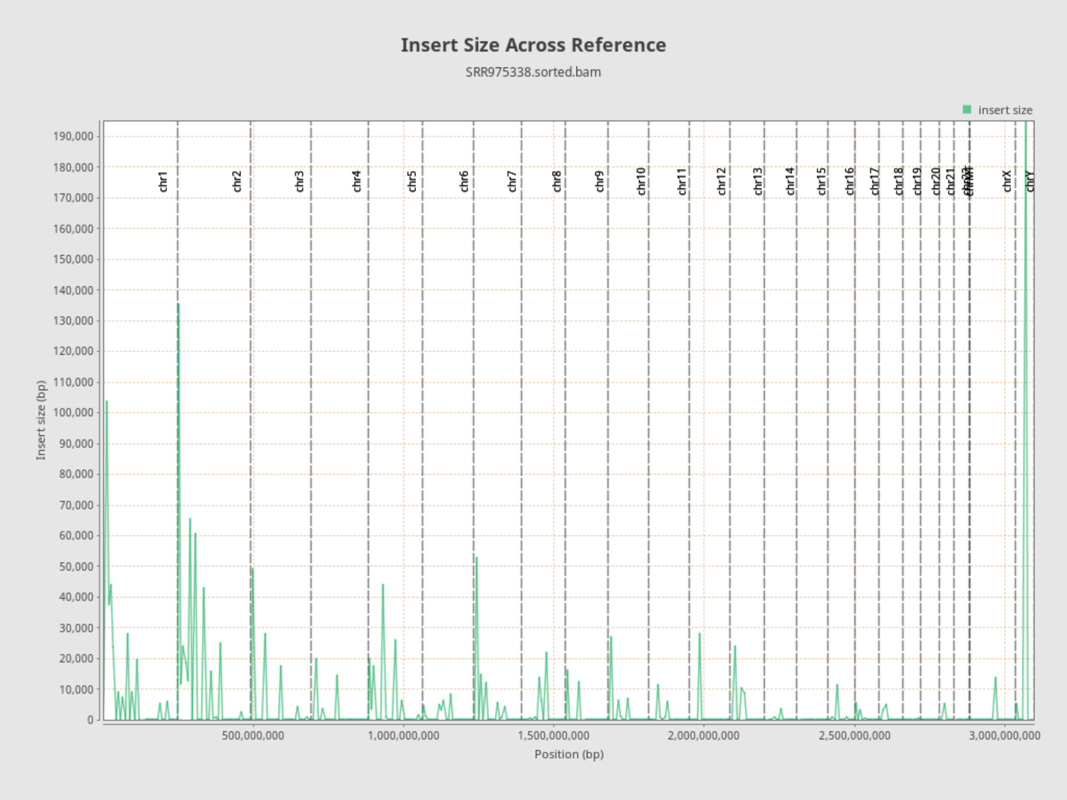


# 12. Results : Mapping Quality Across Reference

# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram