# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/06 22:28:36*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR975294.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_SRR975294 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975294_1.fastq.gz SRR975294_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Sep 06 22:28:35 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR975294.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 5,187,088 |
| Mapped reads | 5,152,065 / 99.32% |
| Unmapped reads | 35,023 / 0.68% |
| Mapped paired reads | 5,152,065 / 99.32% |
| Mapped reads, first in pair | 2,575,537 / 49.65% |
| Mapped reads, second in pair | 2,576,528 / 49.67% |
| Mapped reads, both in pair | 5,139,996 / 99.09% |
| Mapped reads, singletons | 12,069 / 0.23% |
| Secondary alignments | 0 |
| Supplementary alignments | 23,390 / 0.45% |
| Read min/max/mean length | 30 / 101 / 101.18 |
| Duplicated reads (estimated) | 263,798 / 5.09% |
| Duplication rate | 3.27% |
| Clipped reads | 2,987,696 / 57.6% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 142,545,887 / 29.14% |
| Number/percentage of C's | 98,311,622 / 20.1% |
| Number/percentage of T's | 146,249,051 / 29.9% |
| Number/percentage of G's | 102,086,062 / 20.87% |
| Number/percentage of N's | 13,201 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 40.96% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1581 |
| Standard Deviation | 1.3211 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.15 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 69,678.32 |
| Standard Deviation | 2,555,621.5 |
| P25/Median/P75 | 148 / 183 / 235 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.86% |
| Mismatches | 4,058,999 |
| Insertions | 76,929 |
| Mapped reads with at least one insertion | 1.47% |
| Deletions | 178,523 |
| Mapped reads with at least one deletion | 3.4% |
| Homopolymer indels | 48.62% |

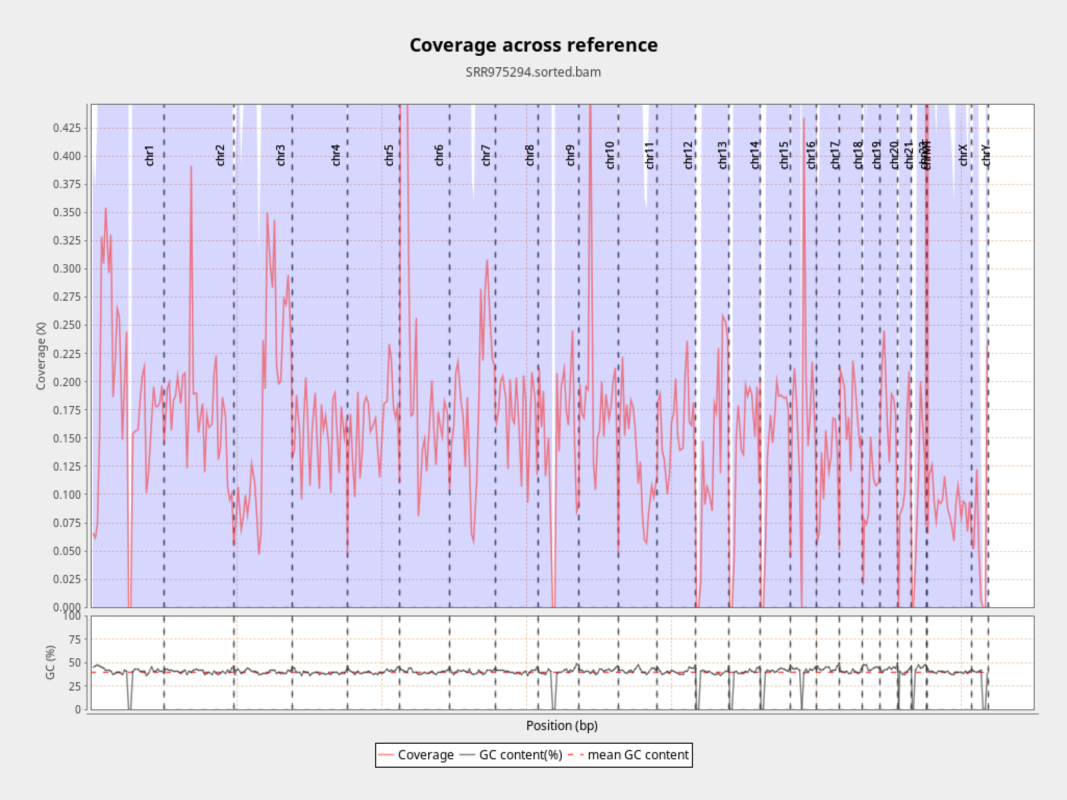
## 2.7. Chromosome stats

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

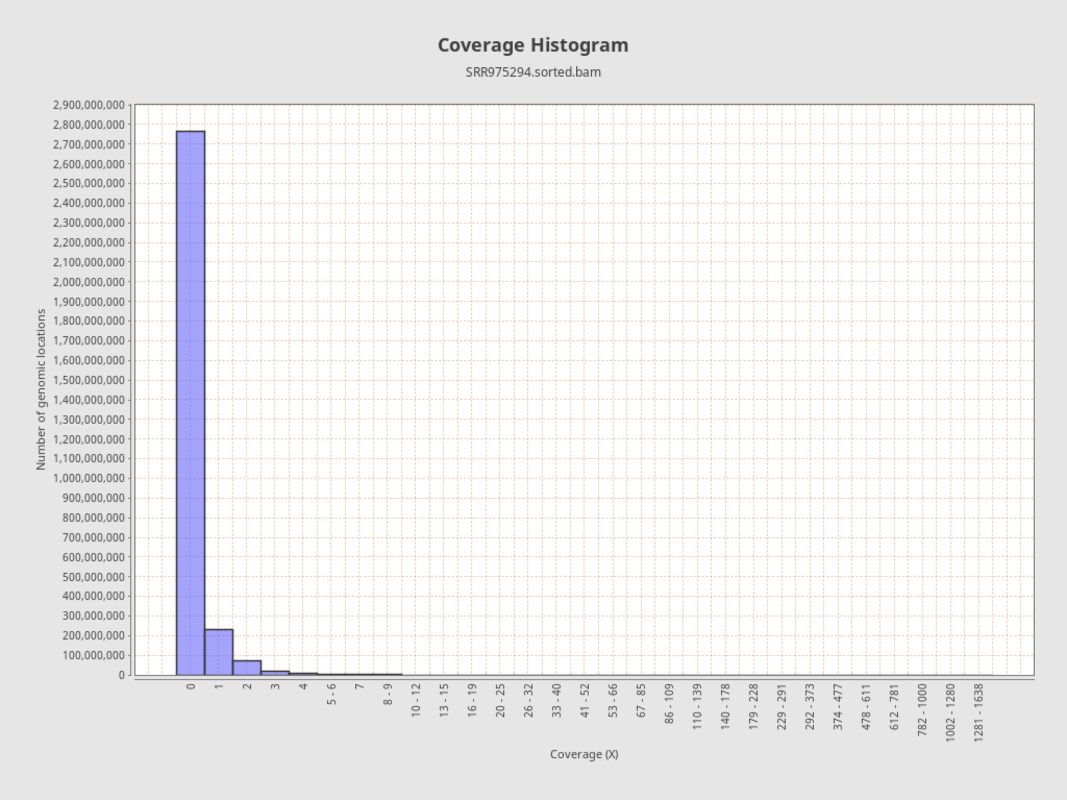
|  |  | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 45631047 | 0.1831 | 1.6347 |
| chr2 | 243199373 | 42084250 | 0.173 | 1.4462 |
| chr3 | 198022430 | 35059537 | 0.177 | 0.5757 |
| chr4 | 191154276 | 29392532 | 0.1538 | 0.7076 |
| chr5 | 180915260 | 29317384 | 0.1621 | 0.5182 |
| chr6 | 171115067 | 39357161 | 0.23 | 1.276 |
| chr7 | 159138663 | 29134920 | 0.1831 | 1.4132 |
| chr8 | 146364022 | 24703366 | 0.1688 | 0.6607 |
| chr9 | 141213431 | 20929472 | 0.1482 | 2.1879 |
| chr10 | 135534747 | 25586470 | 0.1888 | 3.0229 |
| chr11 | 135006516 | 17425868 | 0.1291 | 1.4291 |
| chr12 | 133851895 | 21677138 | 0.1619 | 0.5239 |
| chr13 | 115169878 | 15694206 | 0.1363 | 0.4778 |
| chr14 | 107349540 | 14663270 | 0.1366 | 0.517 |
| chr15 | 102531392 | 14187487 | 0.1384 | 0.4828 |
| chr16 | 90354753 | 15780016 | 0.1746 | 1.7864 |
| chr17 | 81195210 | 9824264 | 0.121 | 1.1766 |
| chr18 | 78077248 | 13556264 | 0.1736 | 2.2457 |
| chr19 | 59128983 | 5836891 | 0.0987 | 0.9752 |
| chr20 | 63025520 | 11101815 | 0.1761 | 0.5639 |
| chr21 | 48129895 | 5480485 | 0.1139 | 0.509 |
| chr22 | 51304566 | 5135013 | 0.1001 | 0.418 |
| chrMT | 16571 | 120791 | 7.2893 | 9.9155 |
| chrX | 155270560 | 13971525 | 0.09 | 0.6405 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 3843452 | 0.0647 | 1.2321 |

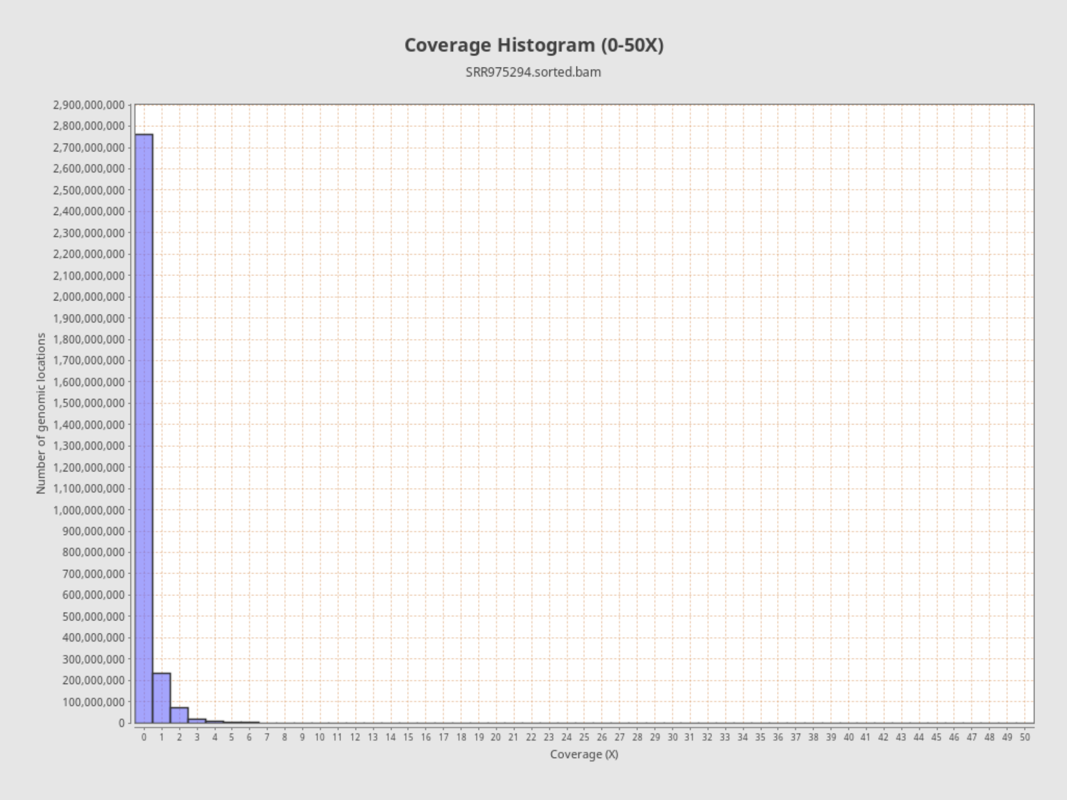
# 3. Results : Coverage across reference



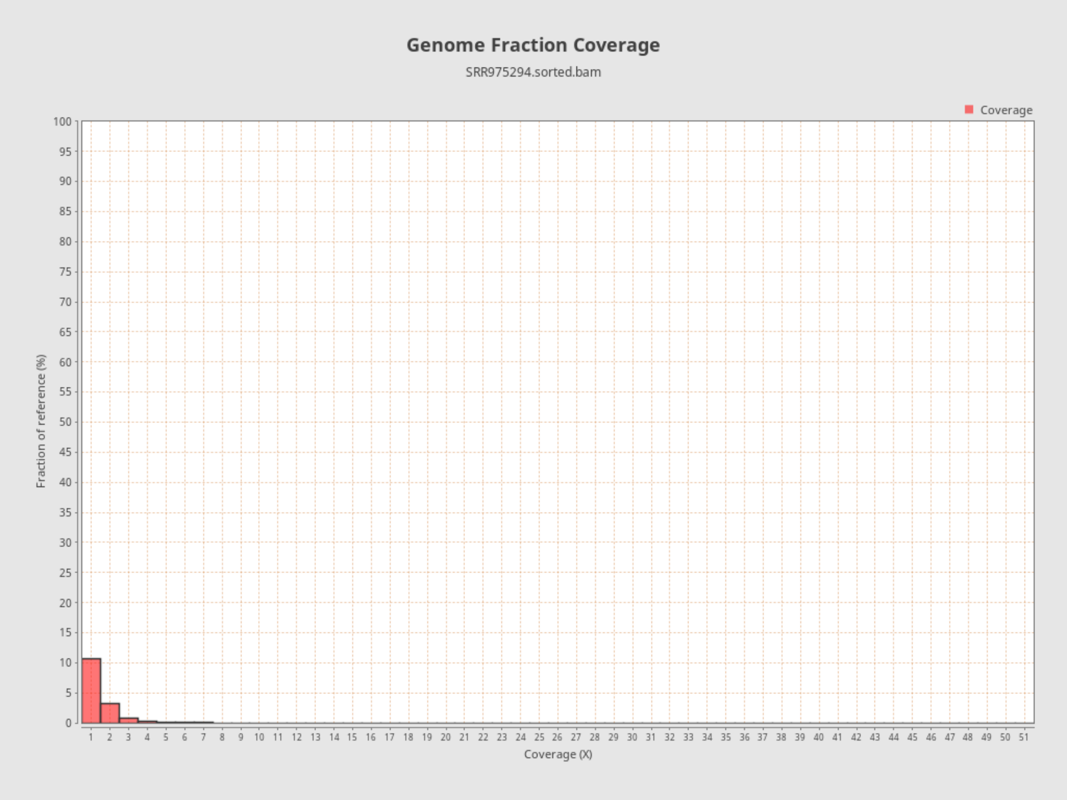
# 4. Results : Coverage Histogram



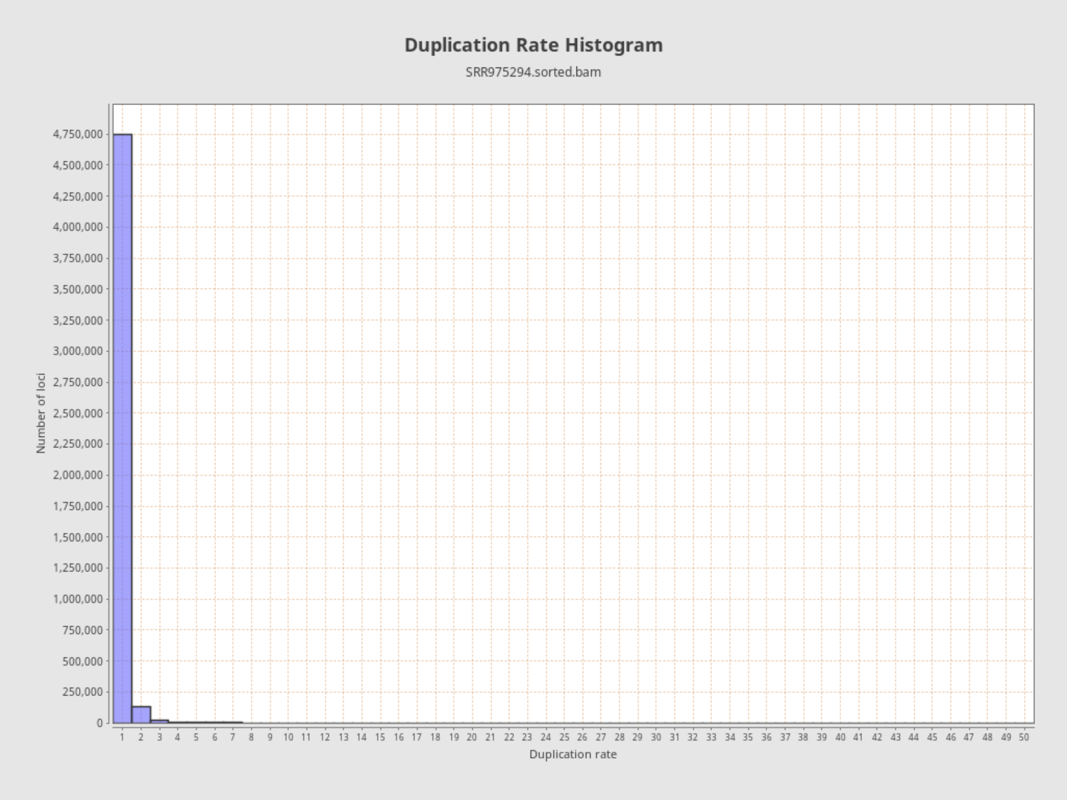
# 5. Results : Coverage Histogram (0-50X)



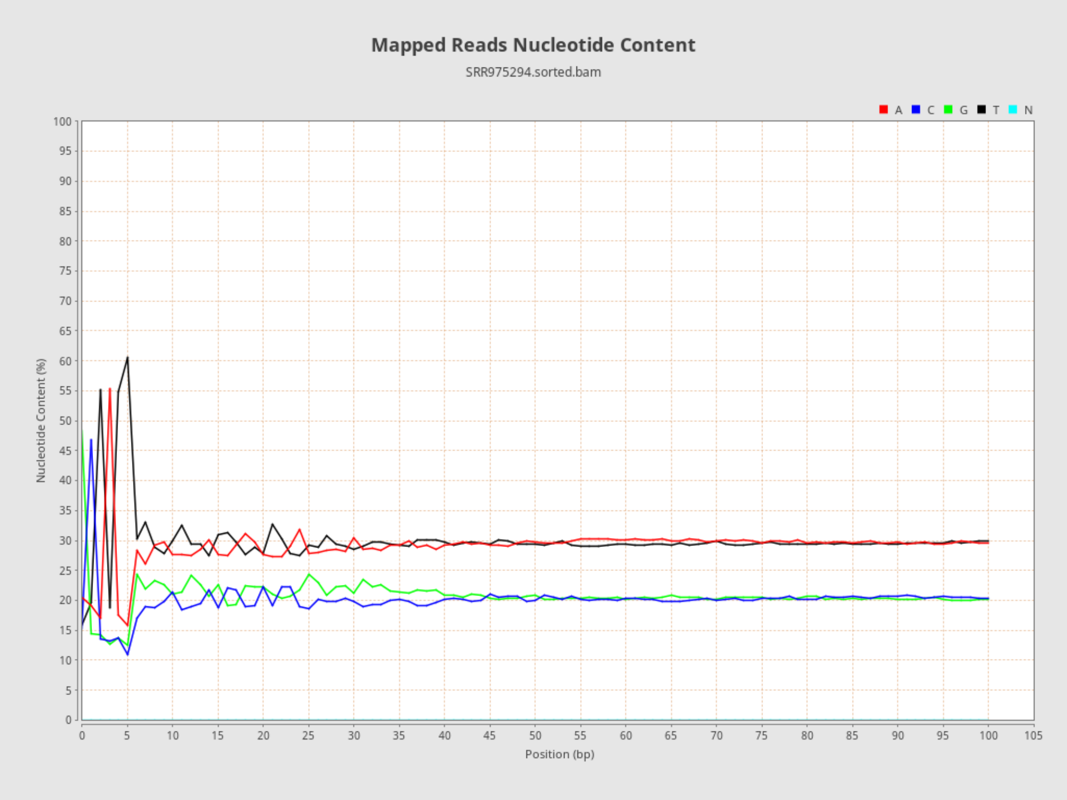
# 6. Results : Genome Fraction Coverage



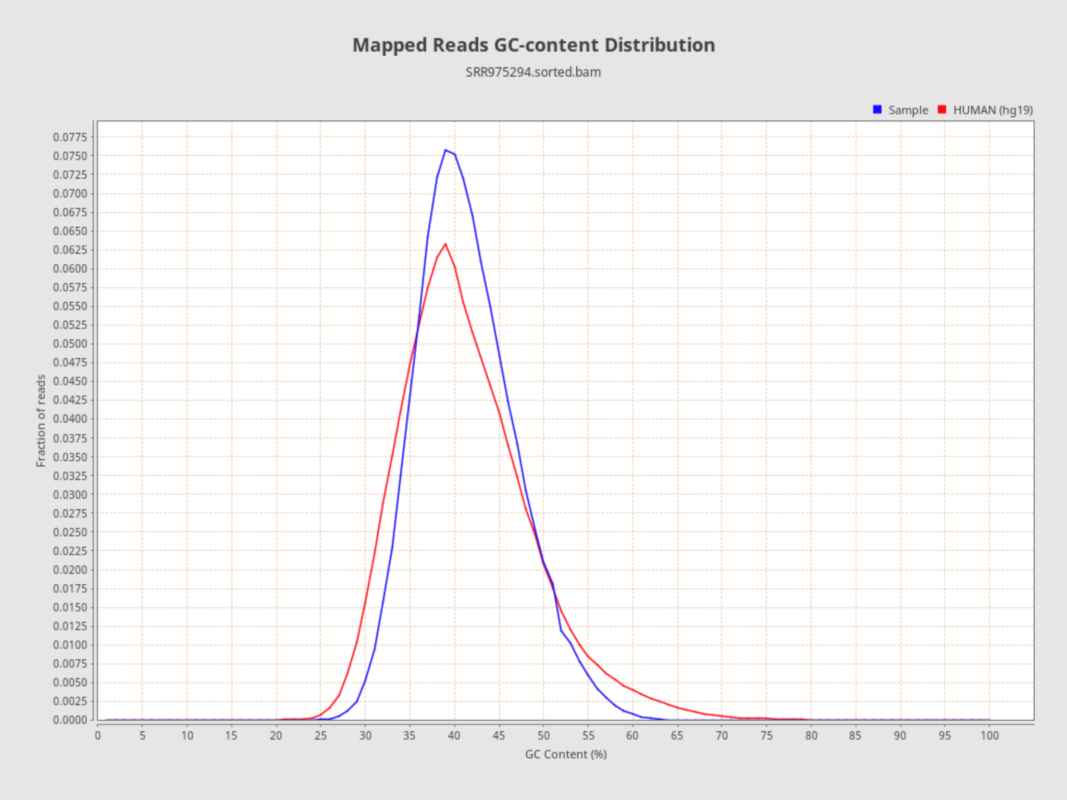
# 7. Results : Duplication Rate Histogram



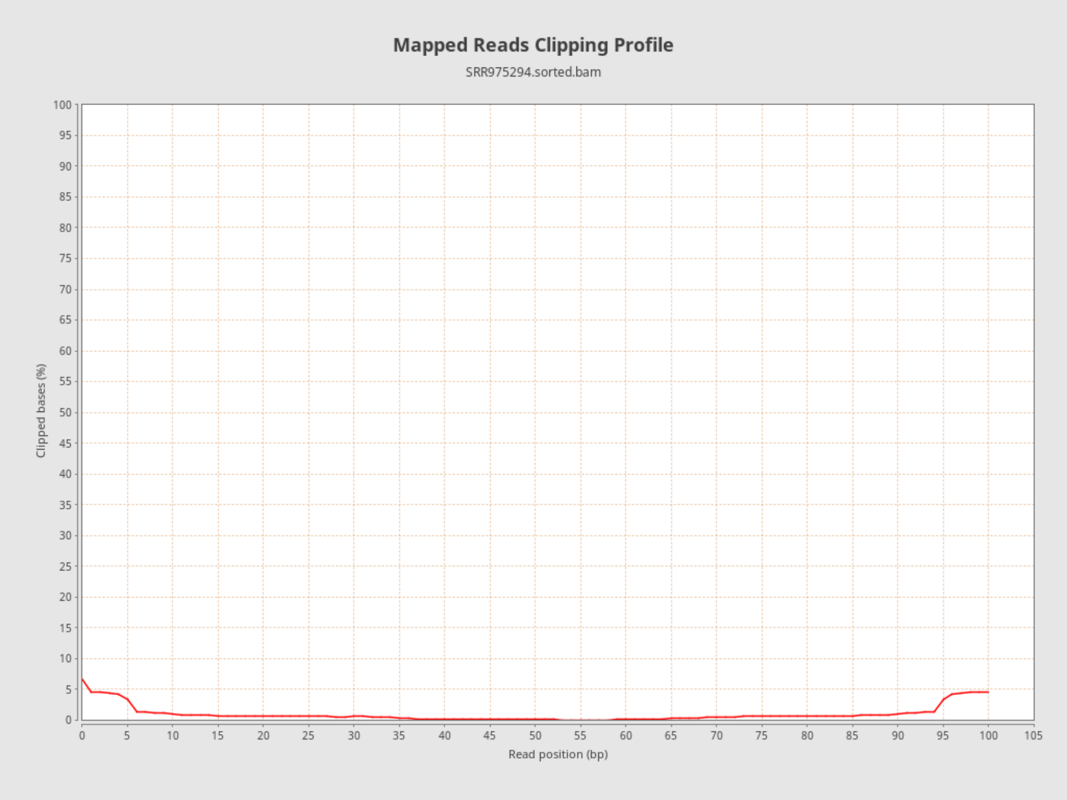
# 8. Results : Mapped Reads Nucleotide Content



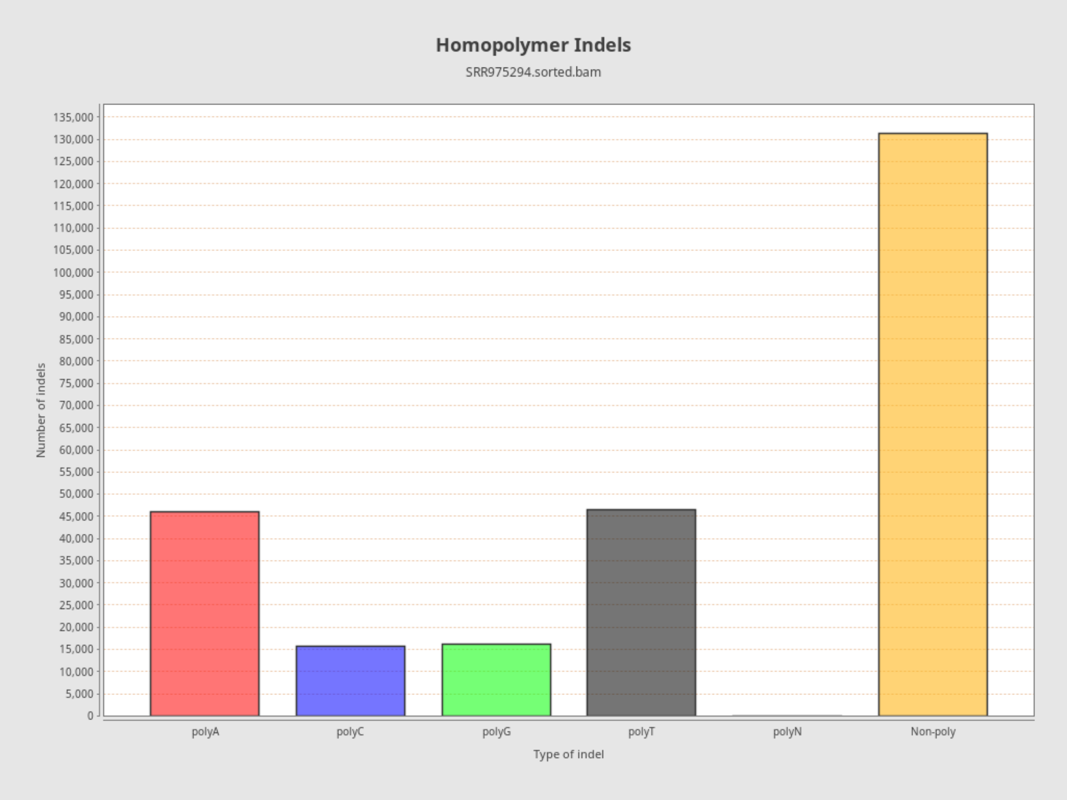
# 9. Results : Mapped Reads GC-content Distribution



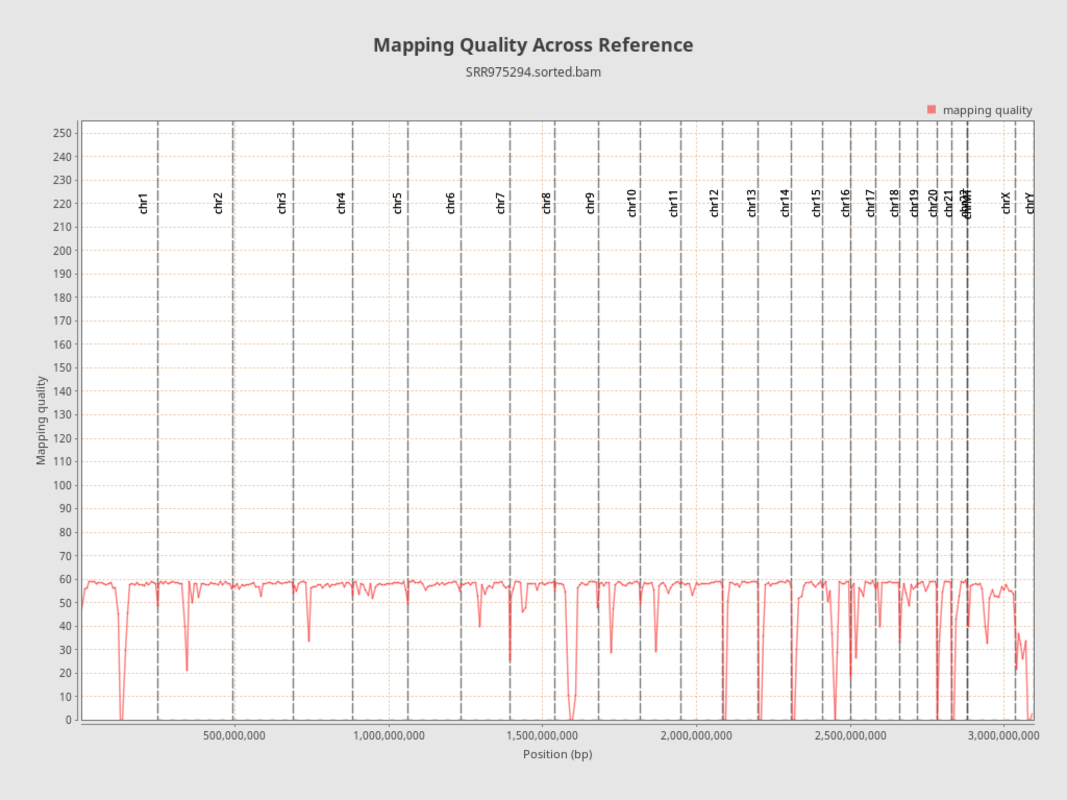
# 10. Results : Mapped Reads Clipping Profile



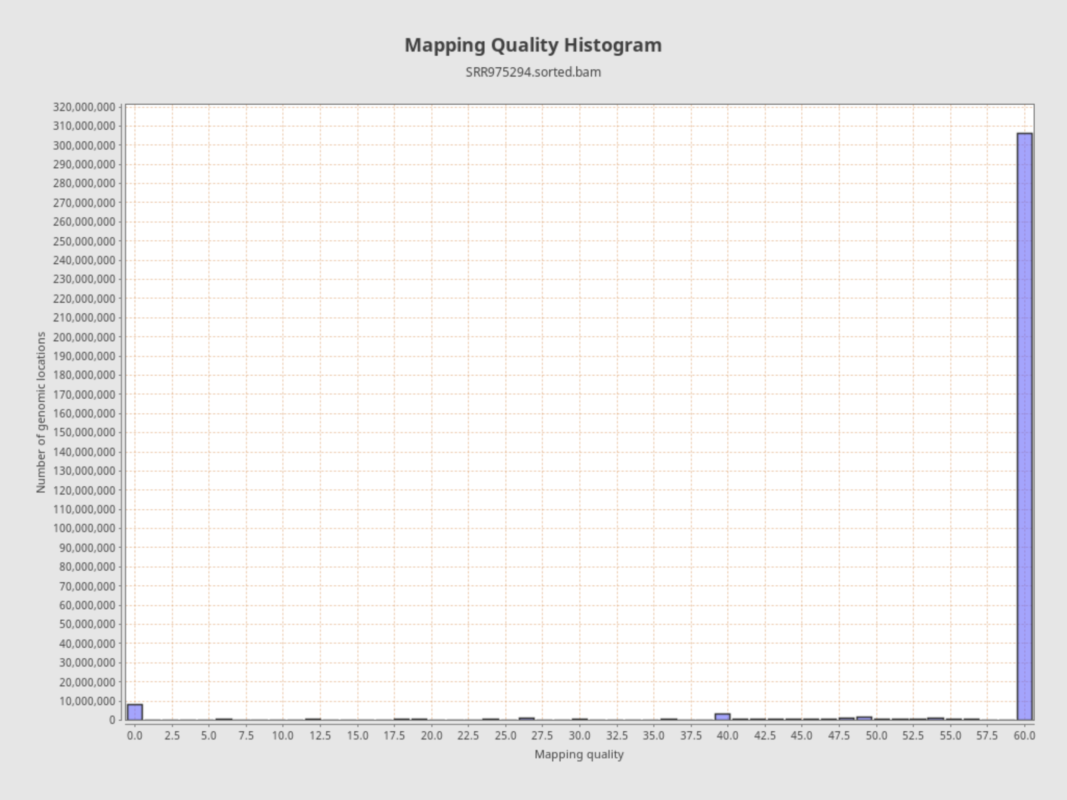
# 11. Results : Homopolymer Indels



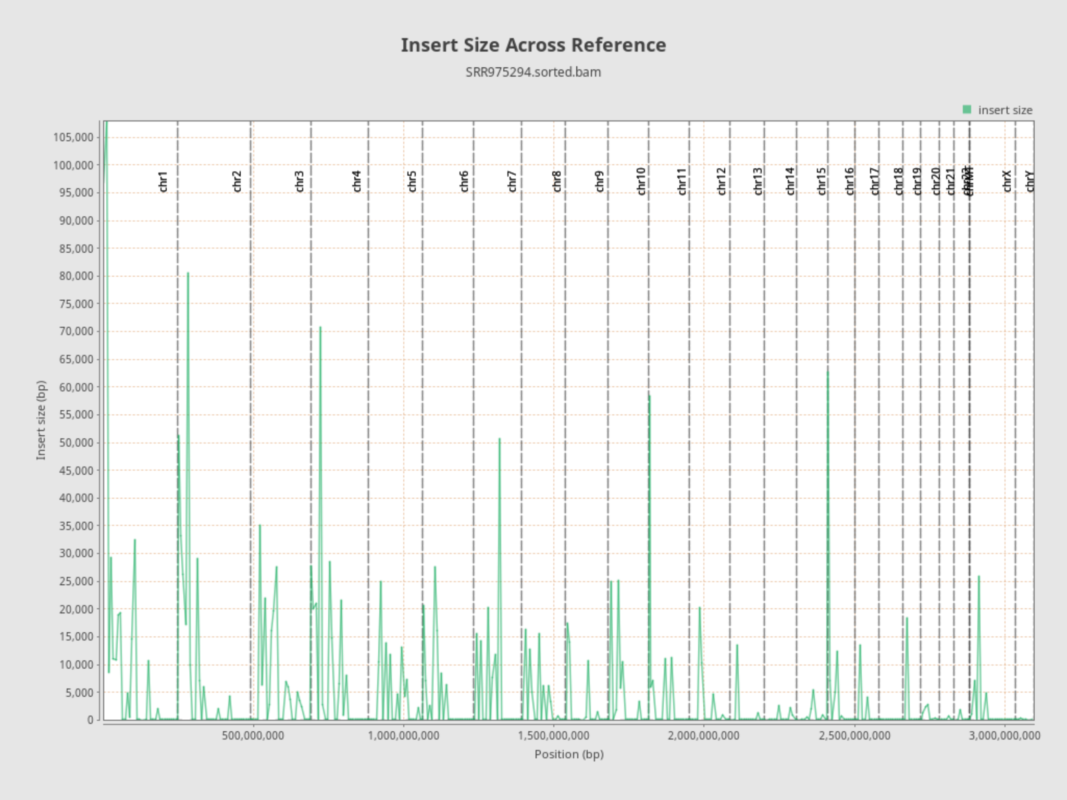
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram