# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/08 17:00:30*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR975293.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_SRR975293 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975293_1.fastq.gz SRR975293_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Sep 08 17:00:29 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR975293.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 55,580,498 |
| Mapped reads | 55,296,177 / 99.49% |
| Unmapped reads | 284,321 / 0.51% |
| Mapped paired reads | 55,296,177 / 99.49% |
| Mapped reads, first in pair | 27,738,268 / 49.91% |
| Mapped reads, second in pair | 27,557,909 / 49.58% |
| Mapped reads, both in pair | 55,065,216 / 99.07% |
| Mapped reads, singletons | 230,961 / 0.42% |
| Secondary alignments | 0 |
| Supplementary alignments | 101,153 / 0.18% |
| Read min/max/mean length | 30 / 101 / 101.07 |
| Duplicated reads (estimated) | 38,798,650 / 69.81% |
| Duplication rate | 59.39% |
| Clipped reads | 32,134,030 / 57.82% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 1,438,629,134 / 27.28% |
| Number/percentage of C's | 1,145,493,427 / 21.72% |
| Number/percentage of T's | 1,503,444,682 / 28.51% |
| Number/percentage of G's | 1,184,112,483 / 22.46% |
| Number/percentage of N's | 1,153,868 / 0.02% |
| | |

| | |
|---|---|
| GC Percentage | 44.18% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 1.7039 |
| Standard Deviation | 25.8421 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 56.41 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 109,940.51 |
| Standard Deviation | 3,289,205.76 |
| P25/Median/P75 | 201 / 248 / 305 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.91% |
| Mismatches | 47,080,741 |
| Insertions | 546,399 |
| Mapped reads with at least one insertion | 0.98% |
| Deletions | 1,474,258 |
| Mapped reads with at least one deletion | 2.62% |
| Homopolymer indels | 49.52% |

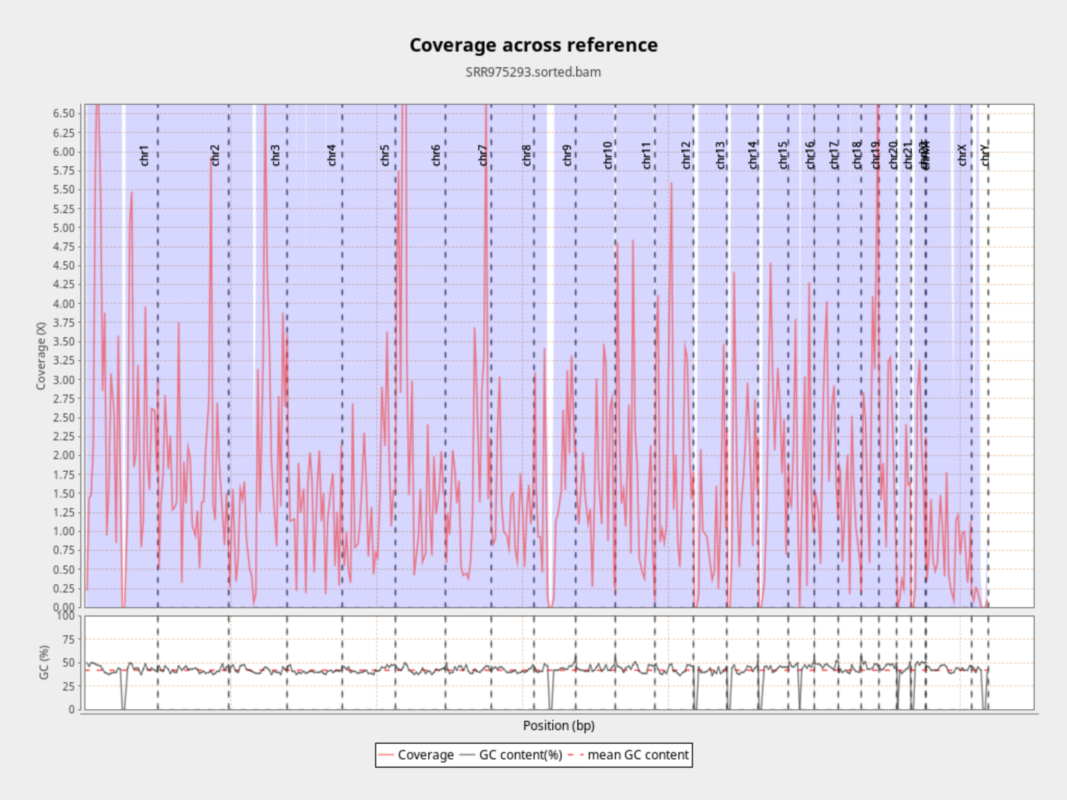
## 2.7. Chromosome stats

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

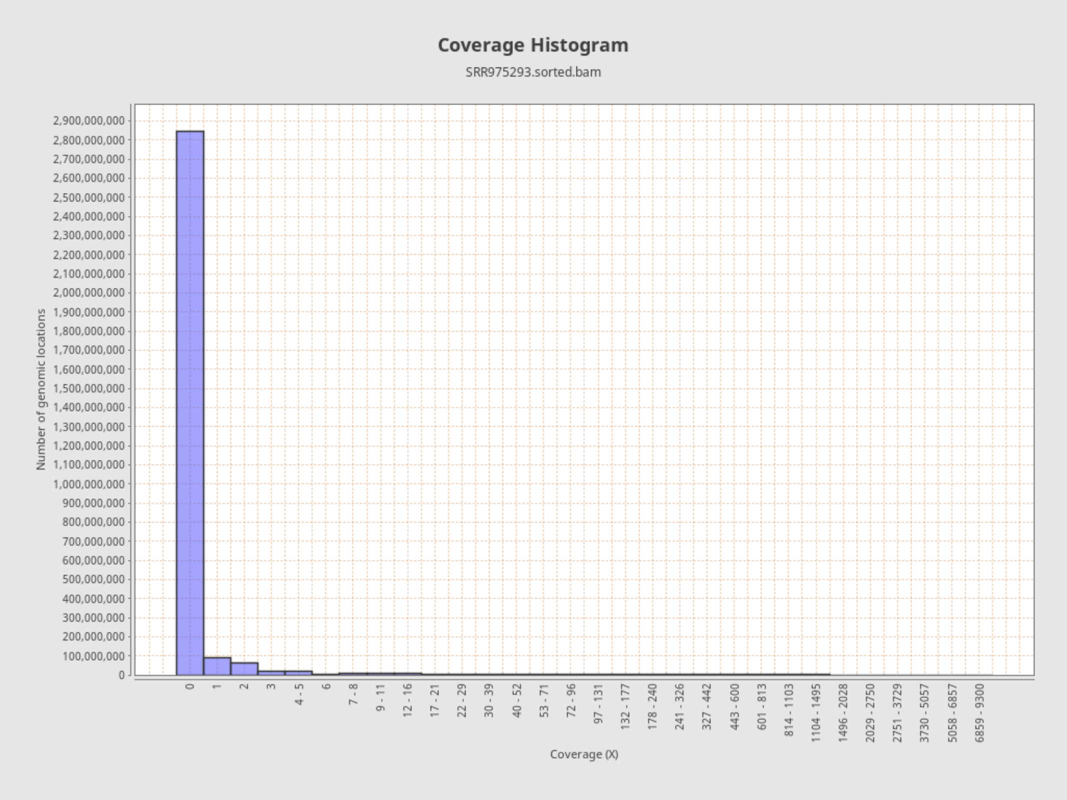
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 623988150 | 2.5035 | 31.5466 |
| chr2 | 243199373 | 420620523 | 1.7295 | 23.5735 |
| chr3 | 198022430 | 371246621 | 1.8748 | 28.1069 |
| chr4 | 191154276 | 240646948 | 1.2589 | 20.8598 |
| chr5 | 180915260 | 250361816 | 1.3839 | 20.5329 |
| chr6 | 171115067 | 434554584 | 2.5395 | 41.0461 |
| chr7 | 159138663 | 290530587 | 1.8256 | 29.1086 |
| chr8 | 146364022 | 189075060 | 1.2918 | 19.8914 |
| chr9 | 141213431 | 207426549 | 1.4689 | 22.2185 |
| chr10 | 135534747 | 236089307 | 1.7419 | 24.7714 |
| chr11 | 135006516 | 235670180 | 1.7456 | 23.843 |
| chr12 | 133851895 | 295395946 | 2.2069 | 29.1498 |
| chr13 | 115169878 | 113653356 | 0.9868 | 18.5354 |
| chr14 | 107349540 | 175110457 | 1.6312 | 22.7648 |
| chr15 | 102531392 | 196413708 | 1.9156 | 24.6617 |
| chr16 | 90354753 | 162781370 | 1.8016 | 26.6751 |
| chr17 | 81195210 | 174927448 | 2.1544 | 30.5894 |
| chr18 | 78077248 | 101802241 | 1.3039 | 21.2901 |
| chr19 | 59128983 | 170444273 | 2.8826 | 36.9922 |
| chr20 | 63025520 | 132261348 | 2.0985 | 29.4825 |
| chr21 | 48129895 | 44942416 | 0.9338 | 15.741 |
| chr22 | 51304566 | 78026805 | 1.5209 | 23.9911 |
| chrMT | 16571 | 37150 | 2.2419 | 4.4206 |
| chrX | 155270560 | 123070293 | 0.7926 | 14.2635 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 5822607 | 0.0981 | 4.0624 |

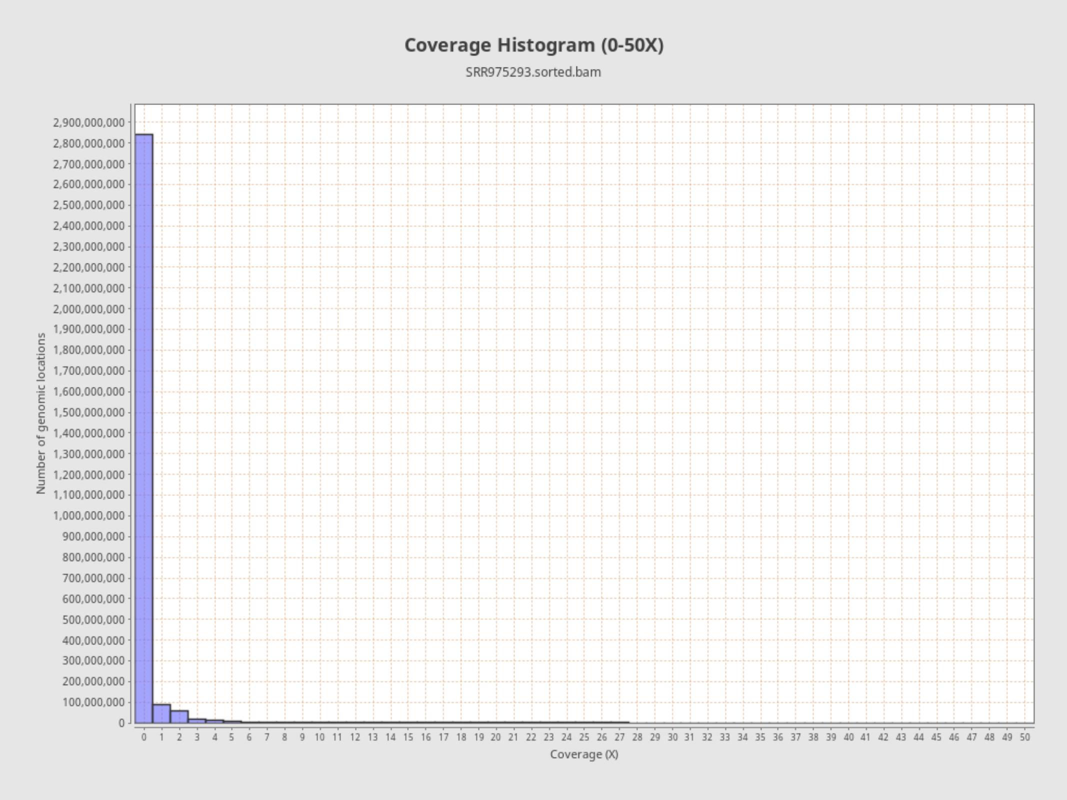
# 3. Results : Coverage across reference



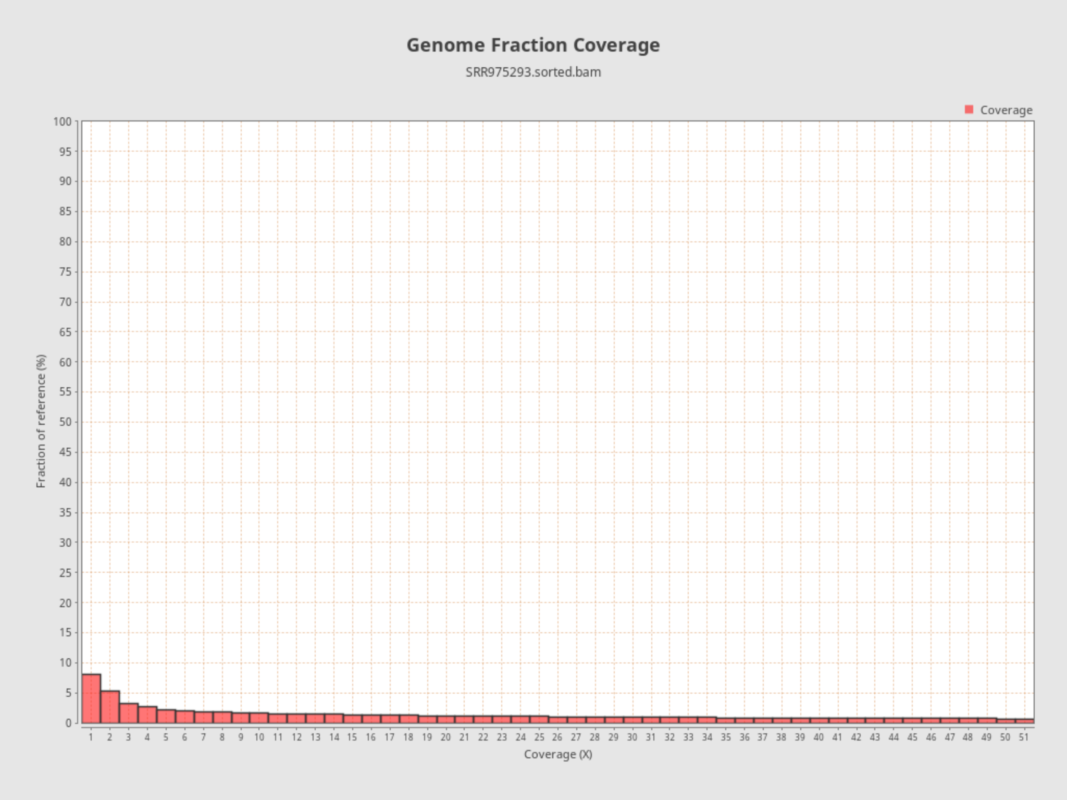
# 4. Results : Coverage Histogram



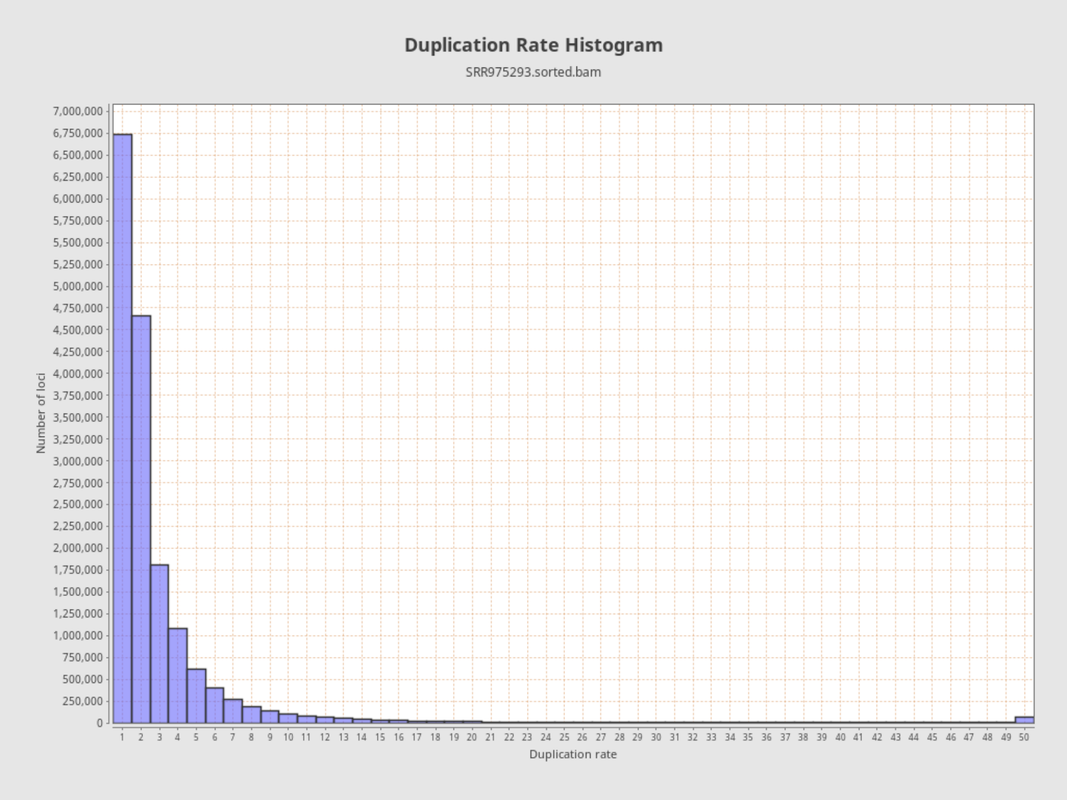
# 5. Results : Coverage Histogram (0-50X)



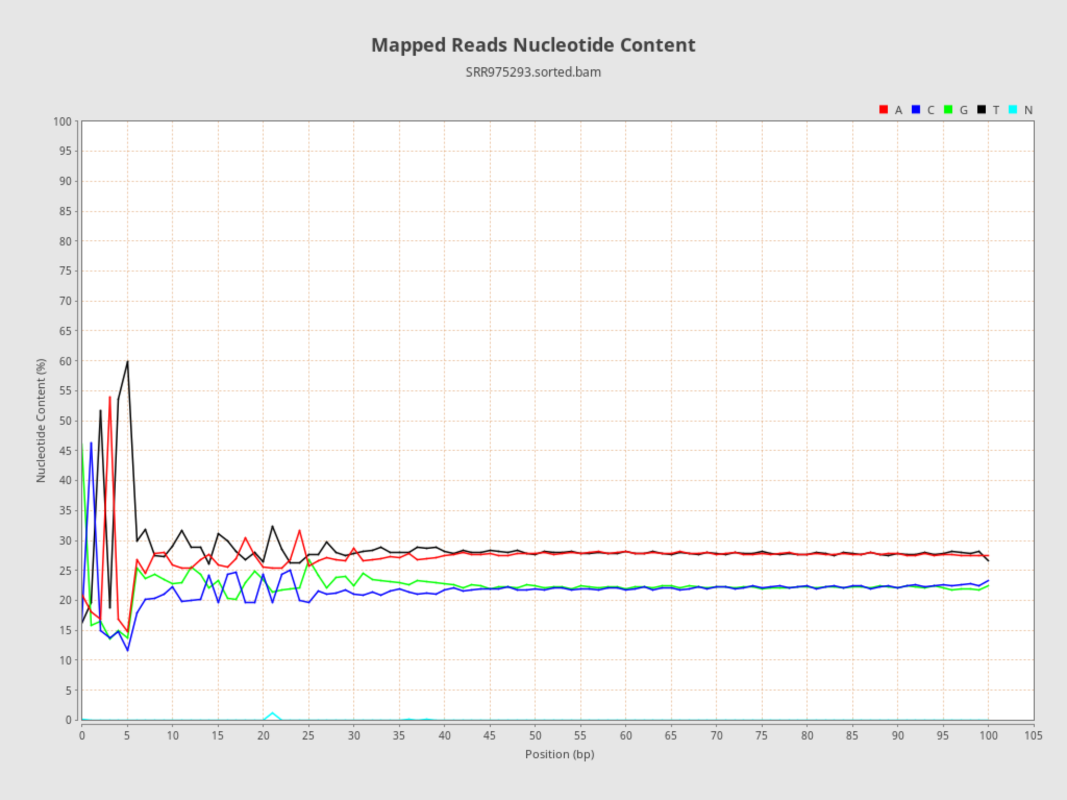
# 6. Results : Genome Fraction Coverage



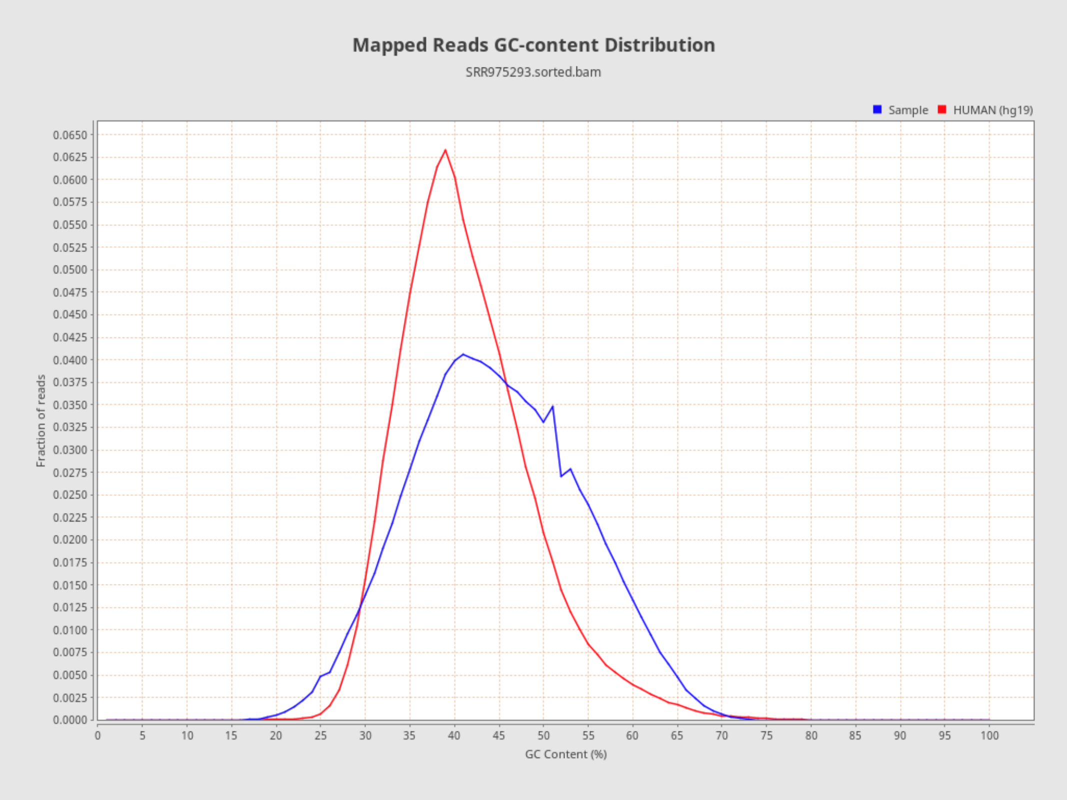
# 7. Results : Duplication Rate Histogram



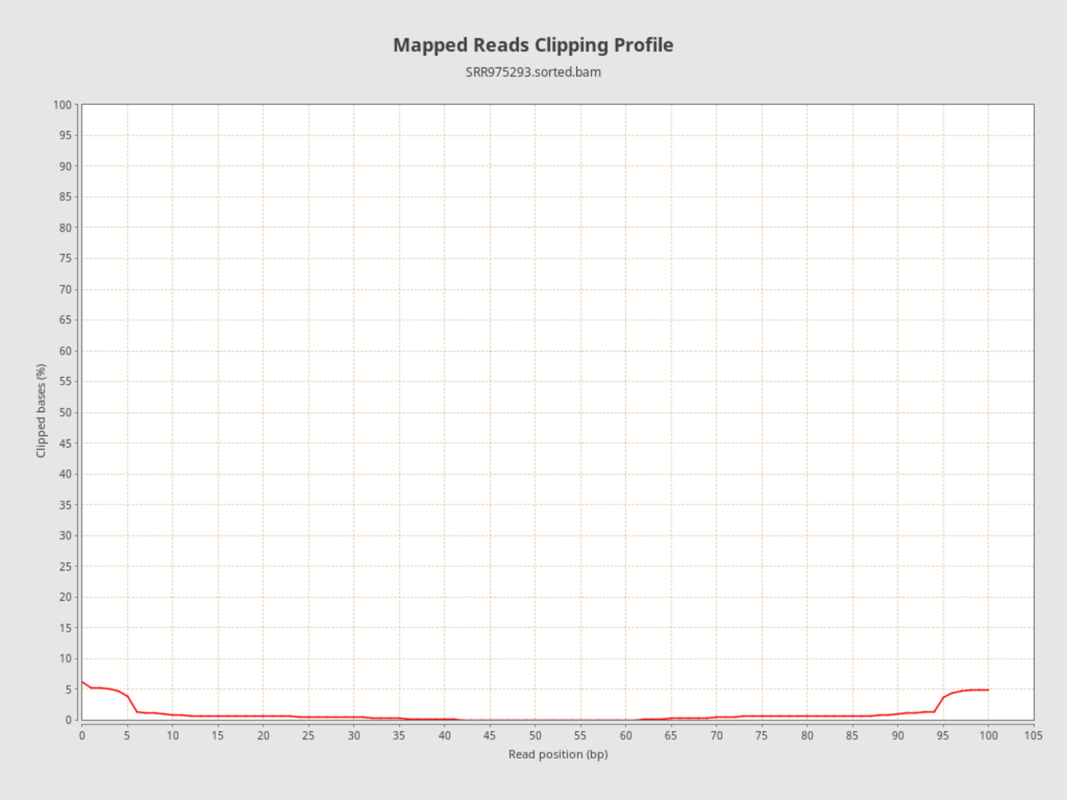
# 8. Results : Mapped Reads Nucleotide Content



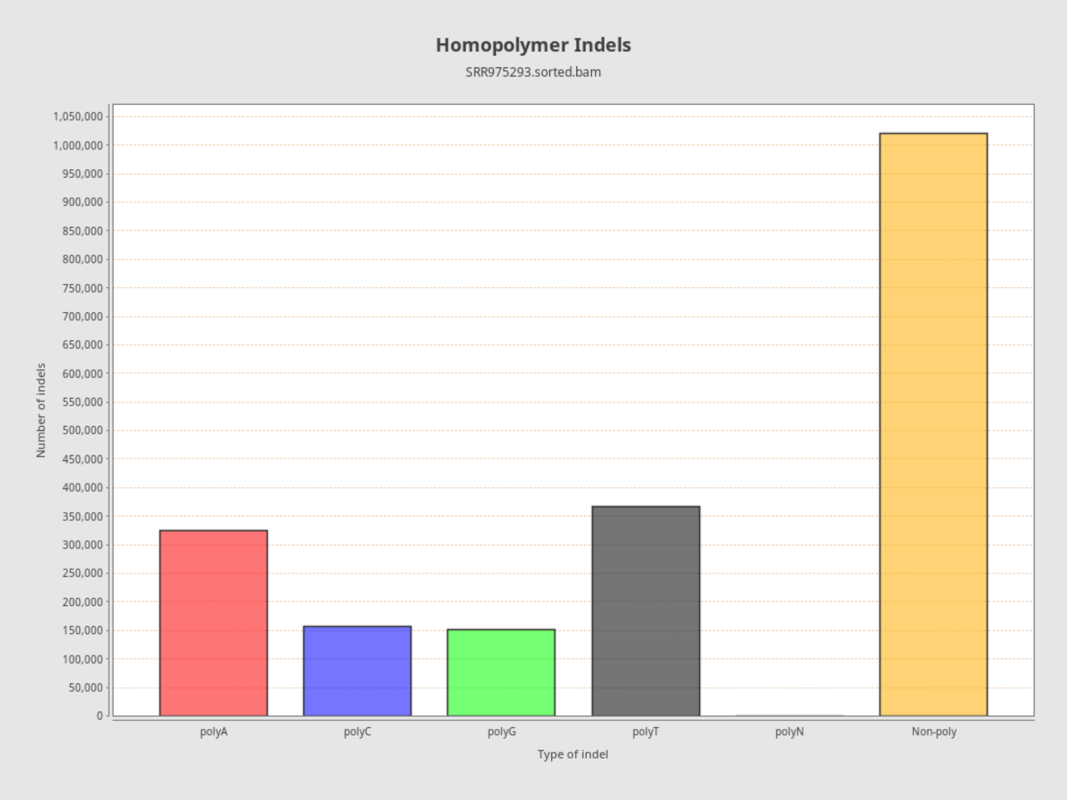
# 9. Results : Mapped Reads GC-content Distribution



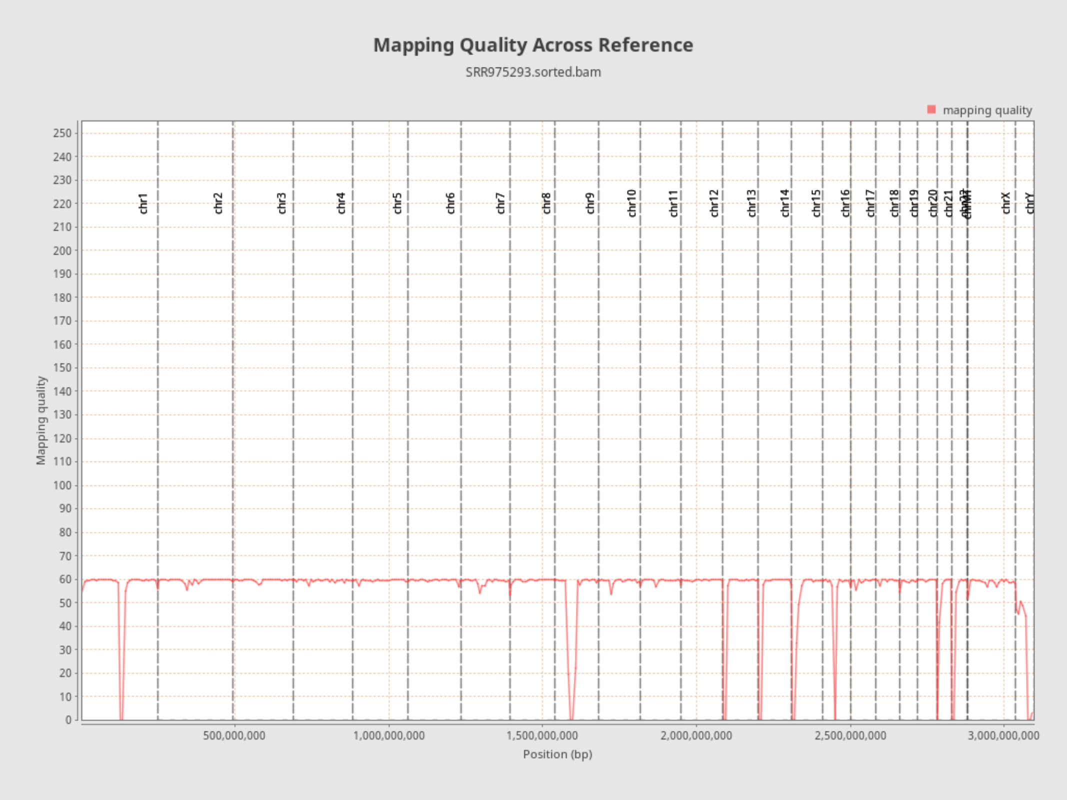
# 10. Results : Mapped Reads Clipping Profile



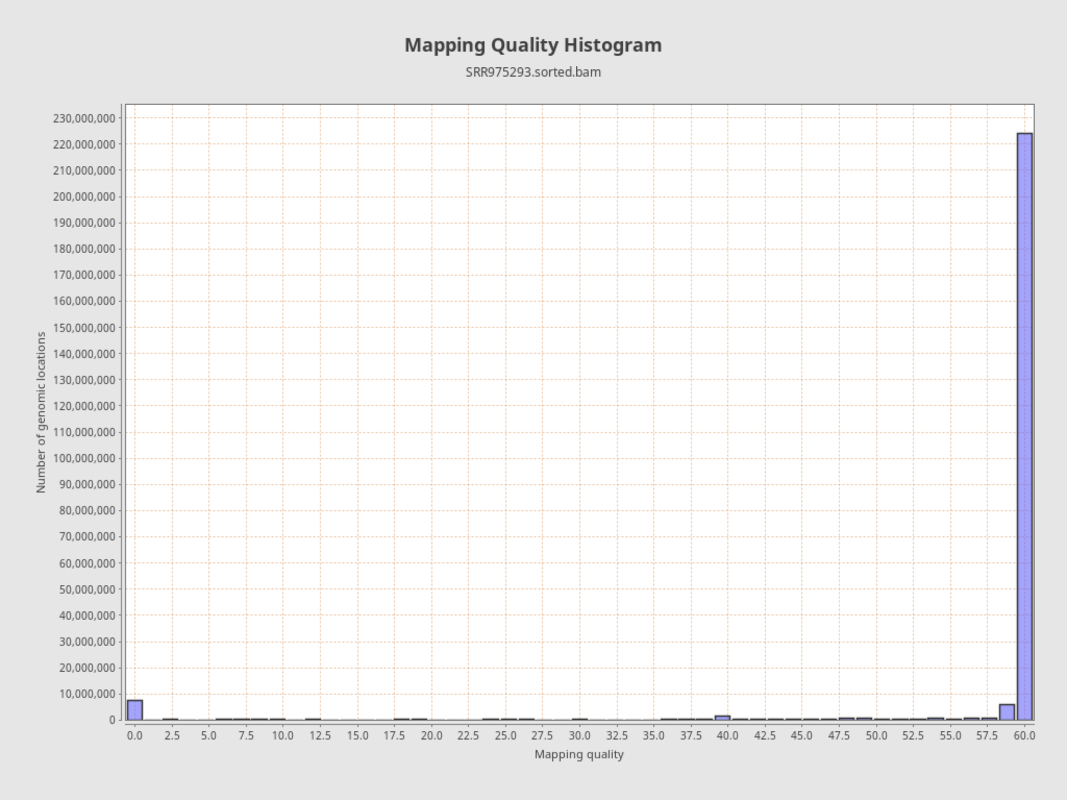
# 11. Results : Homopolymer Indels



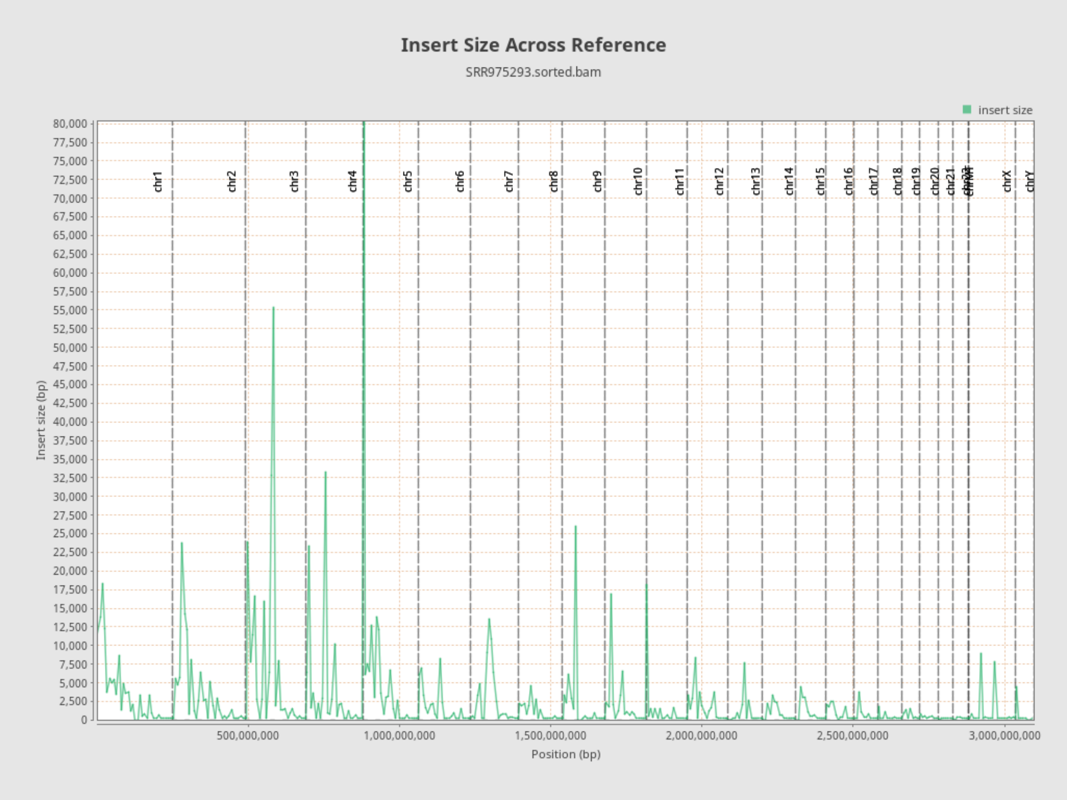
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram