# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/06 23:29:12*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR975296.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_SRR975296 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975296_1.fastq.gz SRR975296_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Sep 06 23:29:11 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR975296.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,351,676 |
| Mapped reads | 3,324,789 / 99.2% |
| Unmapped reads | 26,887 / 0.8% |
| Mapped paired reads | 3,324,789 / 99.2% |
| Mapped reads, first in pair | 1,661,601 / 49.58% |
| Mapped reads,  second in pair | 1,663,188 / 49.62% |
| Mapped reads, both in pair | 3,313,598 / 98.86% |
| Mapped reads, singletons | 11,191 / 0.33% |
| Secondary alignments | 0 |
| Supplementary alignments | 13,029 / 0.39% |
| Read min/max/mean length | 30 / 101 / 101.15 |
| Duplicated reads (estimated) | 138,252 / 4.12% |
| Duplication rate | 2.52% |
| Clipped reads | 2,015,204 / 60.13% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 89,373,099 / 29.5% |
| Number/percentage of C's | 58,709,474 / 19.38% |
| Number/percentage of T's | 89,717,206 / 29.61% |
| Number/percentage of G's | 65,203,858 / 21.52% |
| Number/percentage of N's | 6,413 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 40.89% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0979 |
| Standard Deviation | 0.9239 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.02 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 65,874.69 |
| Standard Deviation | 2,453,257.91 |
| P25/Median/P75 | 136 / 169 / 214 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.85% |
| Mismatches | 2,484,571 |
| Insertions | 48,310 |
| Mapped reads with at least one insertion | 1.42% |
| Deletions | 106,503 |
| Mapped reads with at least one deletion | 3.14% |
| Homopolymer indels | 47.26% |

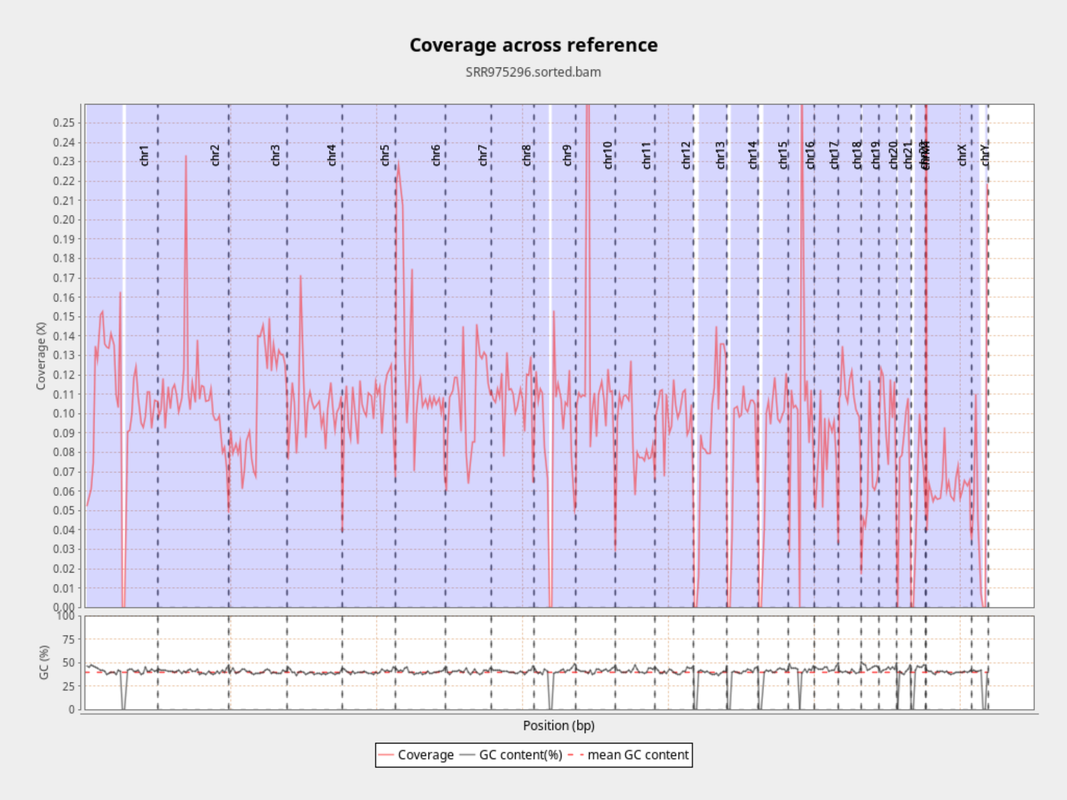
## 2.7. Chromosome stats

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

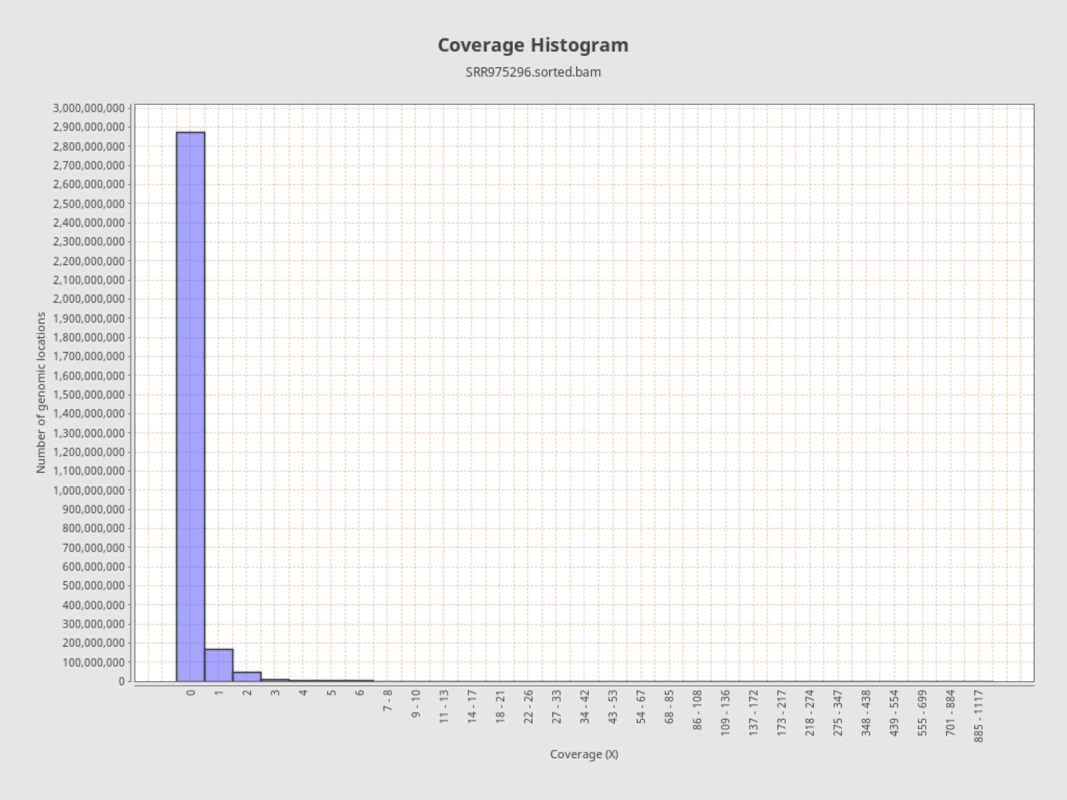
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 25825330 | 0.1036 | 1.0307 |
| chr2 | 243199373 | 26327563 | 0.1083 | 0.9472 |
| chr3 | 198022430 | 21147913 | 0.1068 | 0.4203 |
| chr4 | 191154276 | 19800367 | 0.1036 | 0.6273 |
| chr5 | 180915260 | 19032819 | 0.1052 | 0.3993 |
| chr6 | 171115067 | 21695810 | 0.1268 | 0.8225 |
| chr7 | 159138663 | 17059322 | 0.1072 | 1.0963 |
| chr8 | 146364022 | 15823800 | 0.1081 | 0.4922 |
| chr9 | 141213431 | 12825756 | 0.0908 | 1.3804 |
| chr10 | 135534747 | 16355517 | 0.1207 | 2.2594 |
| chr11 | 135006516 | 11985732 | 0.0888 | 0.9158 |
| chr12 | 133851895 | 13383033 | 0.1 | 0.3966 |
| chr13 | 115169878 | 10124814 | 0.0879 | 0.3633 |
| chr14 | 107349540 | 8937504 | 0.0833 | 0.3912 |
| chr15 | 102531392 | 8683467 | 0.0847 | 0.3612 |
| chr16 | 90354753 | 9458866 | 0.1047 | 1.282 |
| chr17 | 81195210 | 6476994 | 0.0798 | 0.9097 |
| chr18 | 78077248 | 8588901 | 0.11 | 1.4104 |
| chr19 | 59128983 | 3631968 | 0.0614 | 0.6884 |
| chr20 | 63025520 | 6305252 | 0.1 | 0.4112 |
| chr21 | 48129895 | 3770510 | 0.0783 | 0.4457 |
| chr22 | 51304566 | 2782757 | 0.0542 | 0.2957 |
| chrMT | 16571 | 45404 | 2.74 | 5.8804 |
| chrX | 155270560 | 9585795 | 0.0617 | 0.4486 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 3528634 | 0.0594 | 1.1712 |

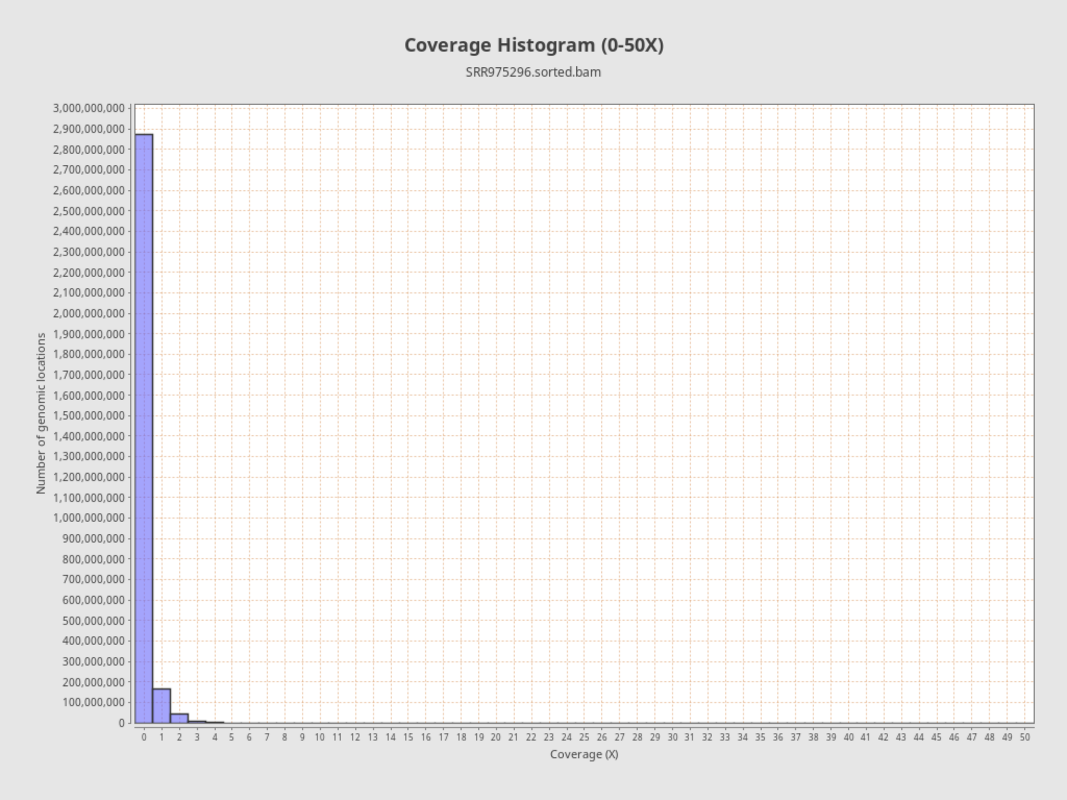
# 3. Results : Coverage across reference



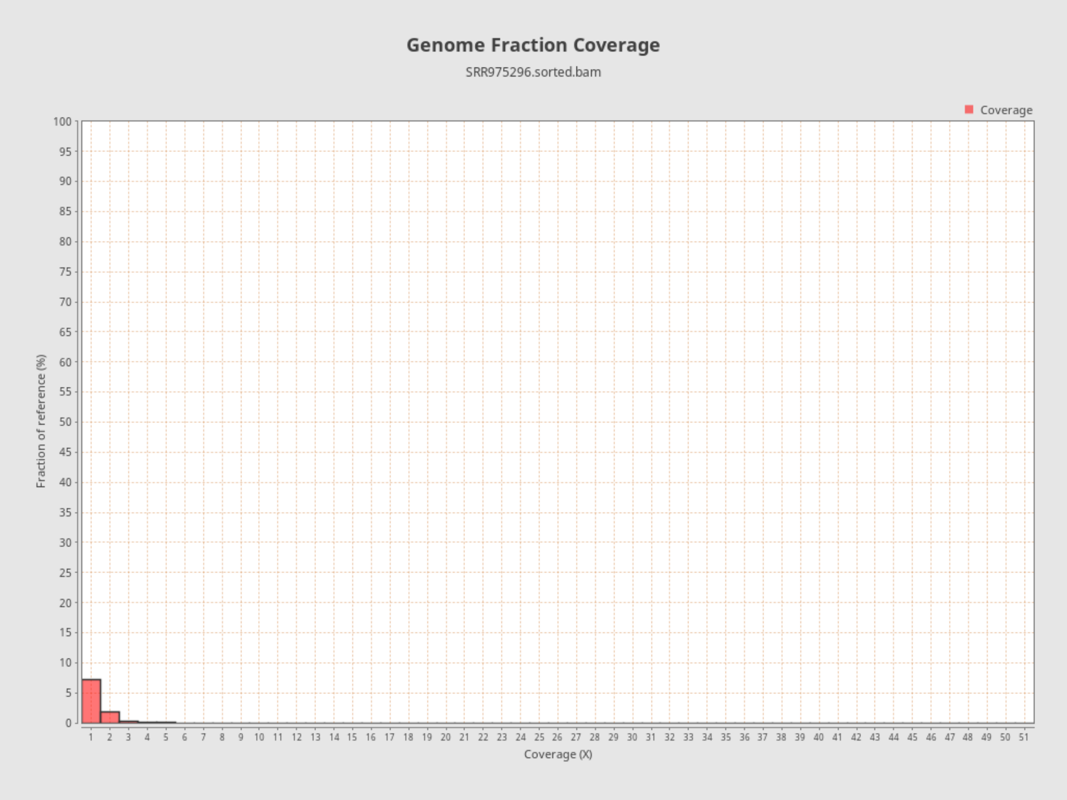
# 4. Results : Coverage Histogram



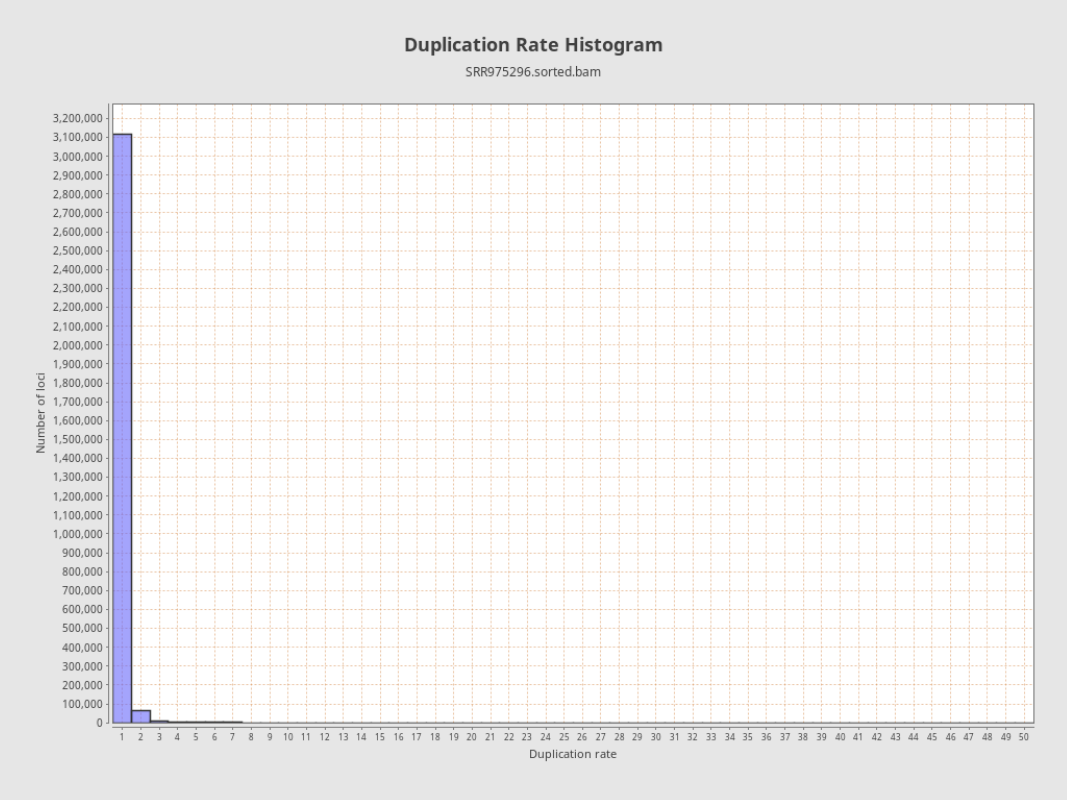
# 5. Results : Coverage Histogram (0-50X)



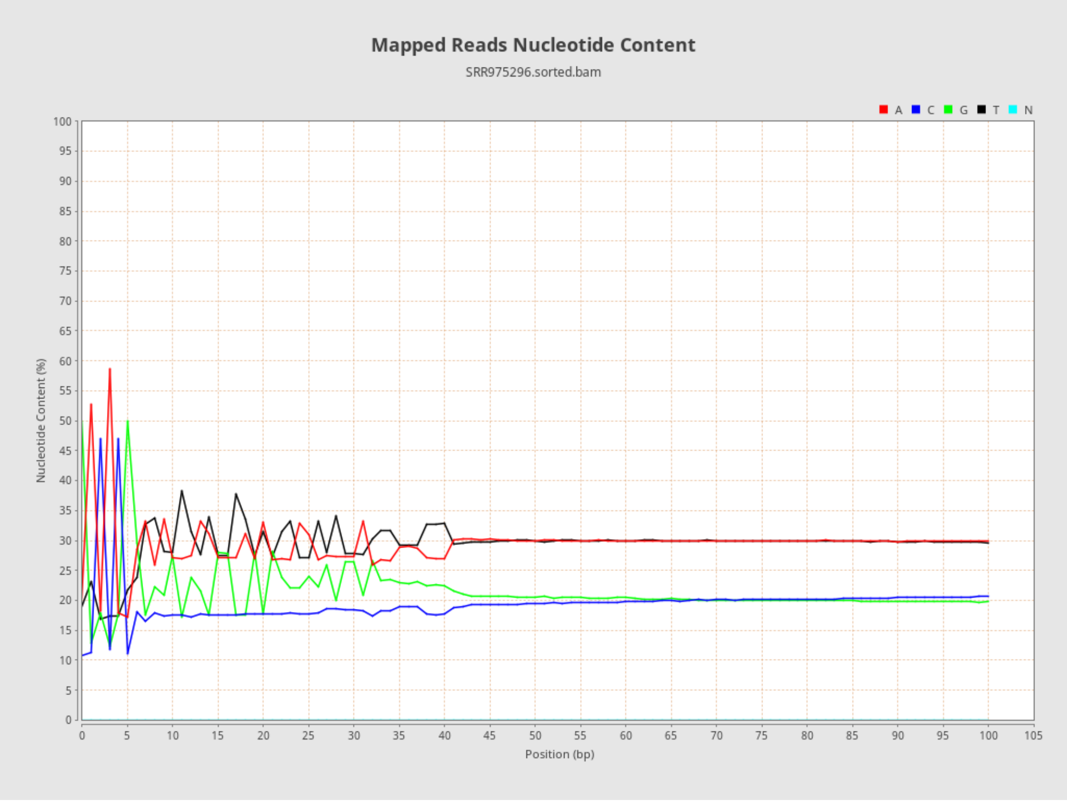
# 6. Results : Genome Fraction Coverage



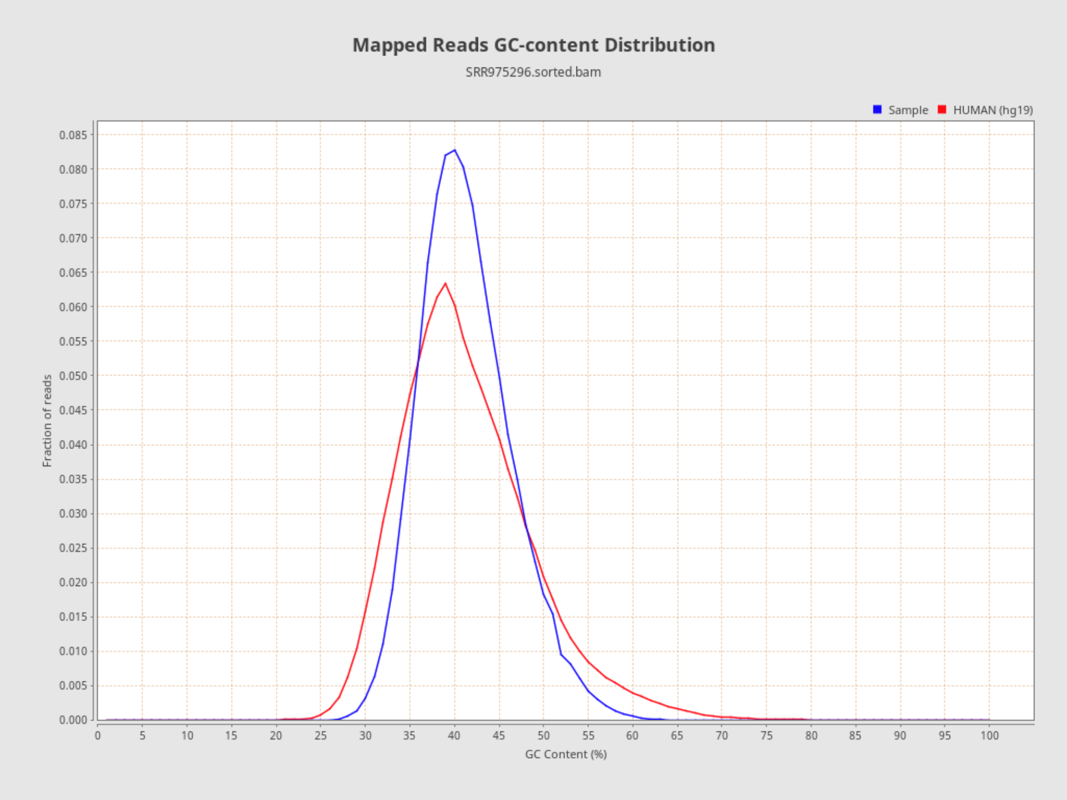
# 7. Results : Duplication Rate Histogram



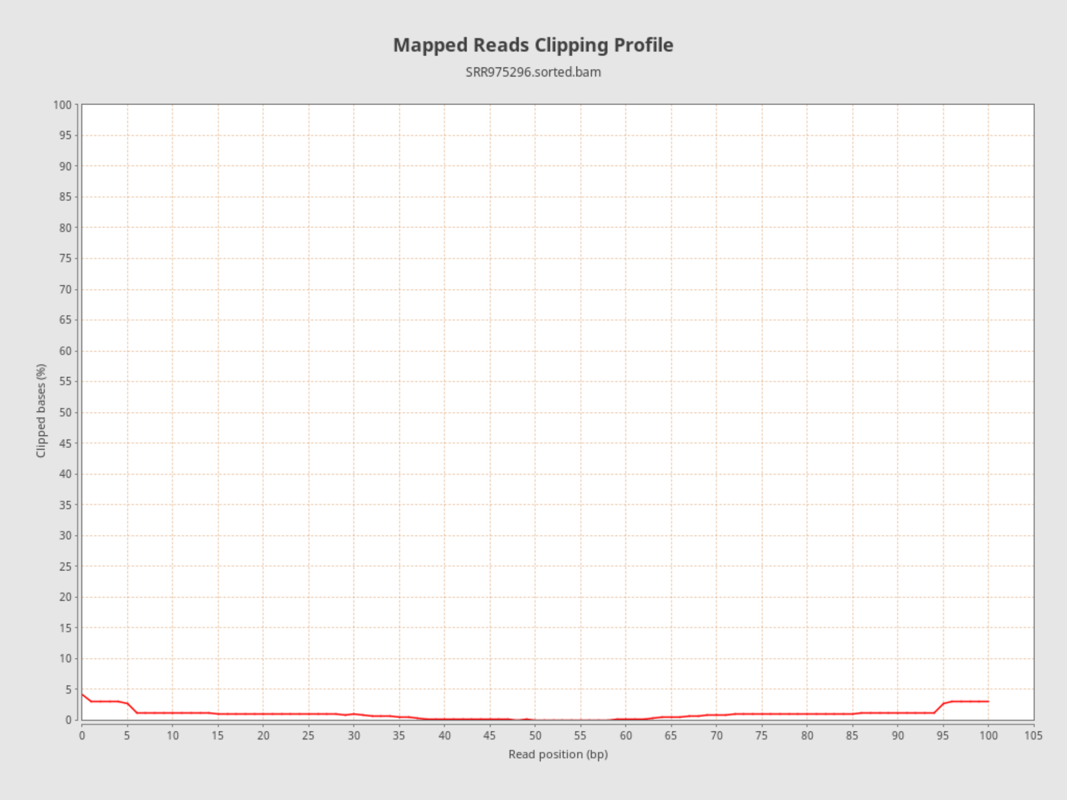
# 8. Results : Mapped Reads Nucleotide Content



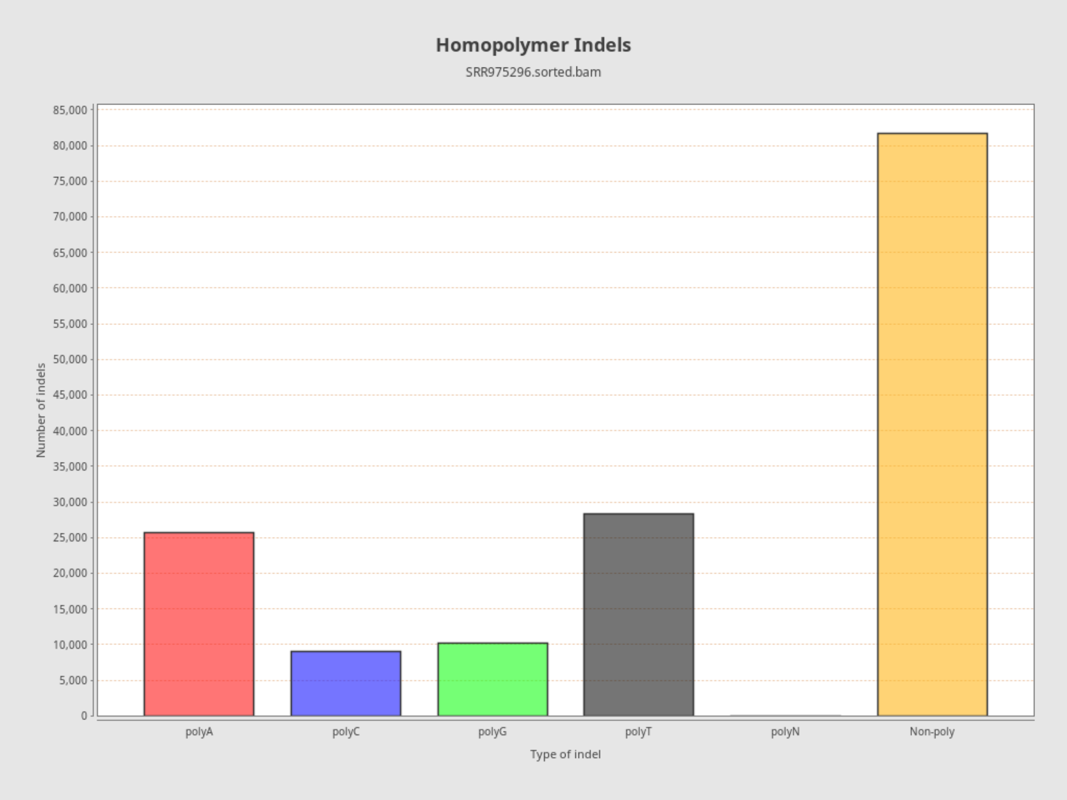
# 9. Results : Mapped Reads GC-content Distribution



# 10. Results : Mapped Reads Clipping Profile

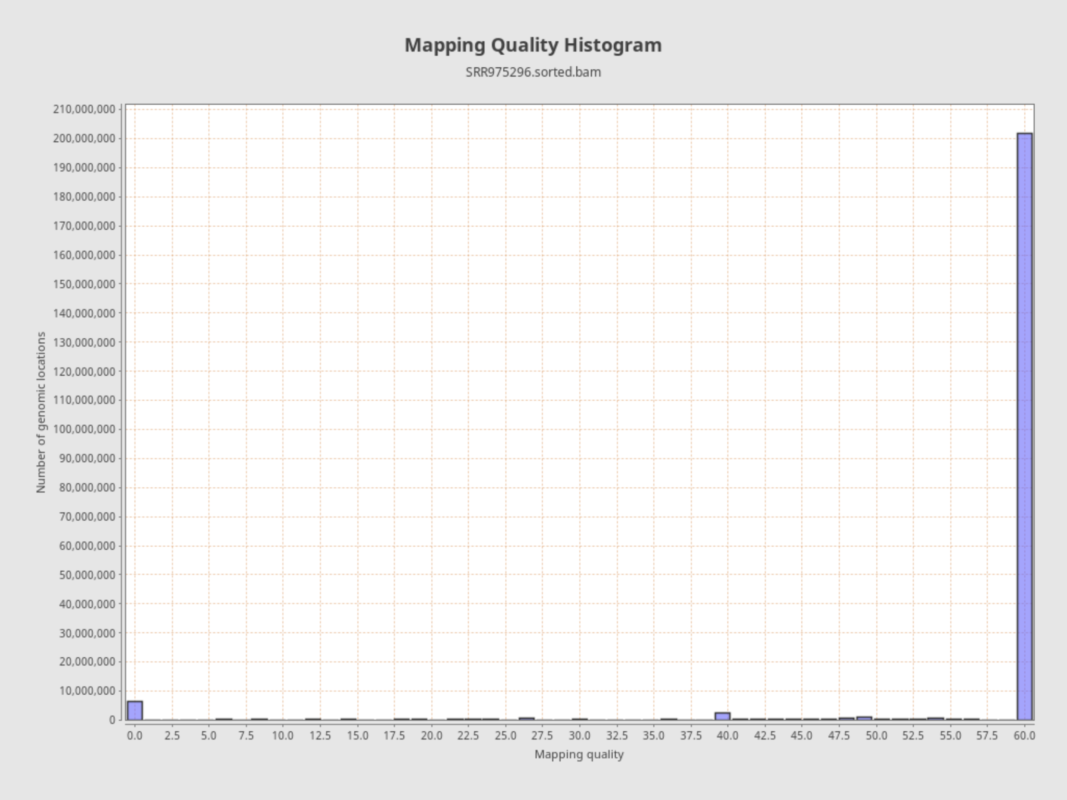


# 11. Results : Homopolymer Indels

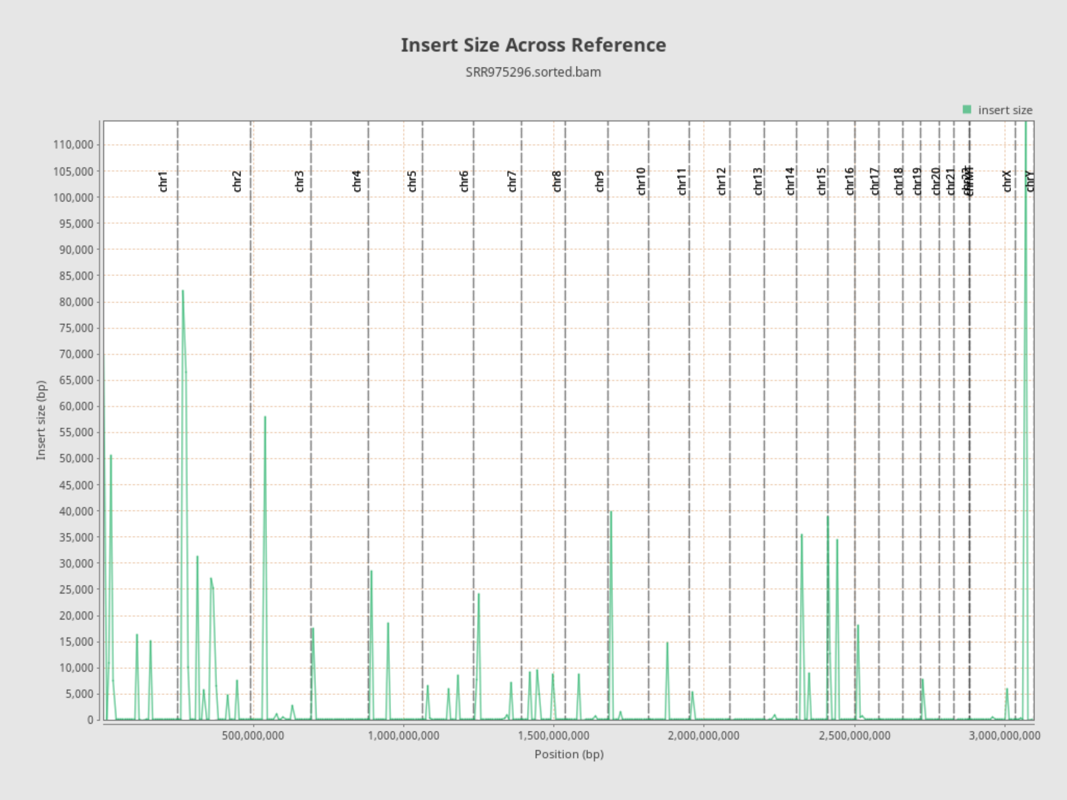


# 12. Results : Mapping Quality Across Reference

# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram