# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/16 20:29:26*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236098.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_SRR6236098 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236098.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 16 20:29:26 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6236098.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,749,792 |
| Mapped reads | 3,212,015 / 85.66% |
| Unmapped reads | 537,777 / 14.34% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 21,758 / 0.58% |
| Read min/max/mean length | 30 / 76 / 76.2 |
| Duplicated reads (estimated) | 237,504 / 6.33% |
| Duplication rate | 5.84% |
| Clipped reads | 2,056,265 / 54.84% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 56,495,254 / 28.34% |
| Number/percentage of C's | 35,584,583 / 17.85% |
| Number/percentage of T's | 63,874,354 / 32.04% |
| Number/percentage of G's | 43,348,899 / 21.74% |
| Number/percentage of N's | 70,131 / 0.04% |
| GC Percentage | 39.59% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0644 |
| | |

| | |
|---|---|
| Standard Deviation | 0.6381 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.14 |

## 2.5. Mismatches and indels

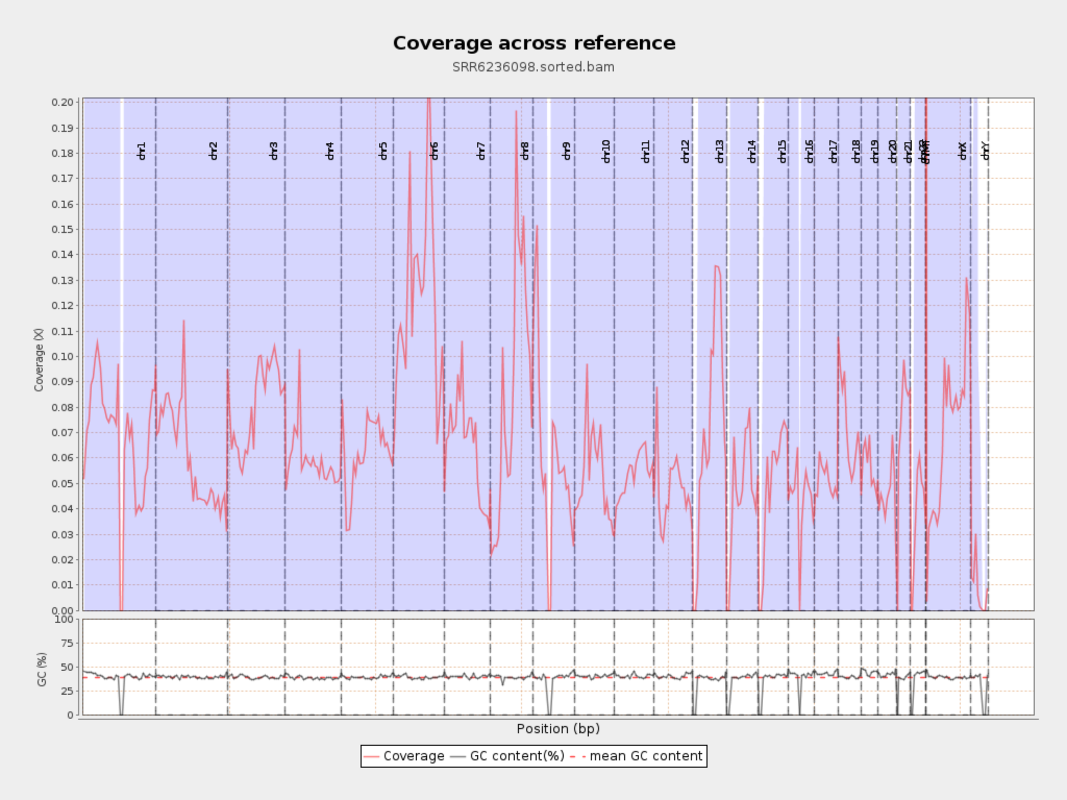
| | |
|---|---|
| General error rate | 0.89% |
| Mismatches | 1,745,331 |
| Insertions | 15,257 |
| Mapped reads with at least one insertion | 0.47% |
| Deletions | 56,911 |
| Mapped reads with at least one deletion | 1.75% |
| Homopolymer indels | 44.96% |

## 2.6. Chromosome stats

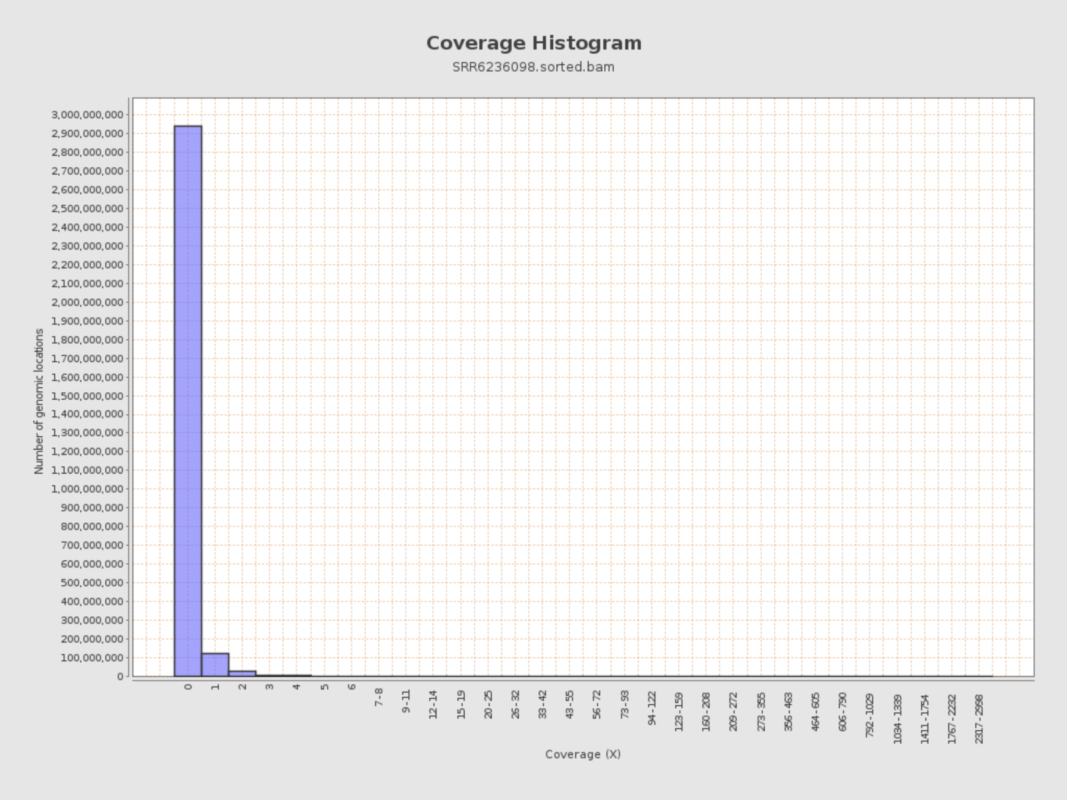
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 16954253 | 0.068 | 0.8064 |
| chr2 | 243199373 | 14705493 | 0.0605 | 0.6506 |
| chr3 | 198022430 | 16124501 | 0.0814 | 0.3595 |
| chr4 | 191154276 | 11254005 | 0.0589 | 0.3848 |
| chr5 | 180915260 | 11341234 | 0.0627 | 0.3171 |
| chr6 | 171115067 | 21322664 | 0.1246 | 0.6618 |
| chr7 | 159138663 | 10327833 | 0.0649 | 0.6505 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 12745934 | 0.0871 | 1.9083 |
| chr9 | 141213431 | 8406878 | 0.0595 | 0.4507 |
| chr10 | 135534747 | 7246215 | 0.0535 | 0.4911 |
| chr11 | 135006516 | 7252276 | 0.0537 | 0.4136 |
| chr12 | 133851895 | 6433563 | 0.0481 | 0.2893 |
| chr13 | 115169878 | 8402228 | 0.073 | 0.3516 |
| chr14 | 107349540 | 4978591 | 0.0464 | 0.298 |
| chr15 | 102531392 | 4939961 | 0.0482 | 0.2936 |
| chr16 | 90354753 | 3894100 | 0.0431 | 0.2928 |
| chr17 | 81195210 | 4141972 | 0.051 | 0.3219 |
| chr18 | 78077248 | 5680229 | 0.0728 | 0.7575 |
| chr19 | 59128983 | 3371124 | 0.057 | 0.5434 |
| chr20 | 63025520 | 2948066 | 0.0468 | 0.2869 |
| chr21 | 48129895 | 3553874 | 0.0738 | 0.3783 |
| chr22 | 51304566 | 1902559 | 0.0371 | 0.2334 |
| chrMT | 16571 | 84864 | 5.1212 | 4.2229 |
| chrX | 155270560 | 10937097 | 0.0704 | 0.3686 |
| chrY | 59373566 | 519138 | 0.0087 | 0.2393 |

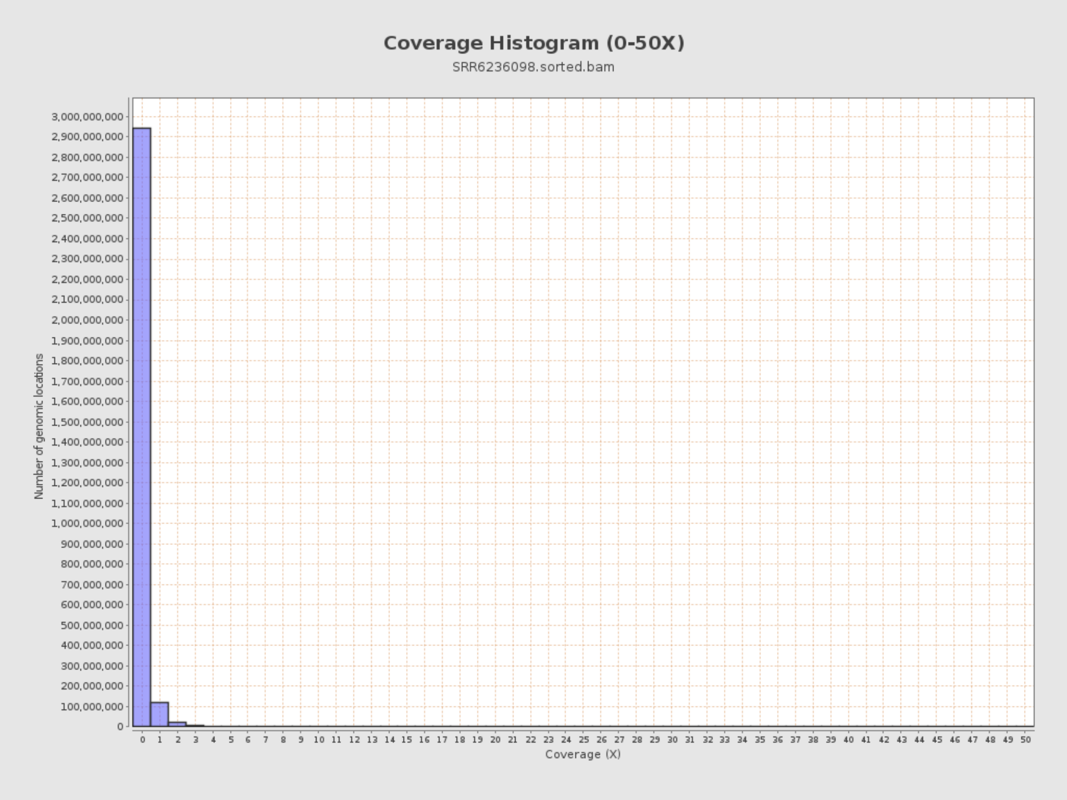
# 3. Results : Coverage across reference



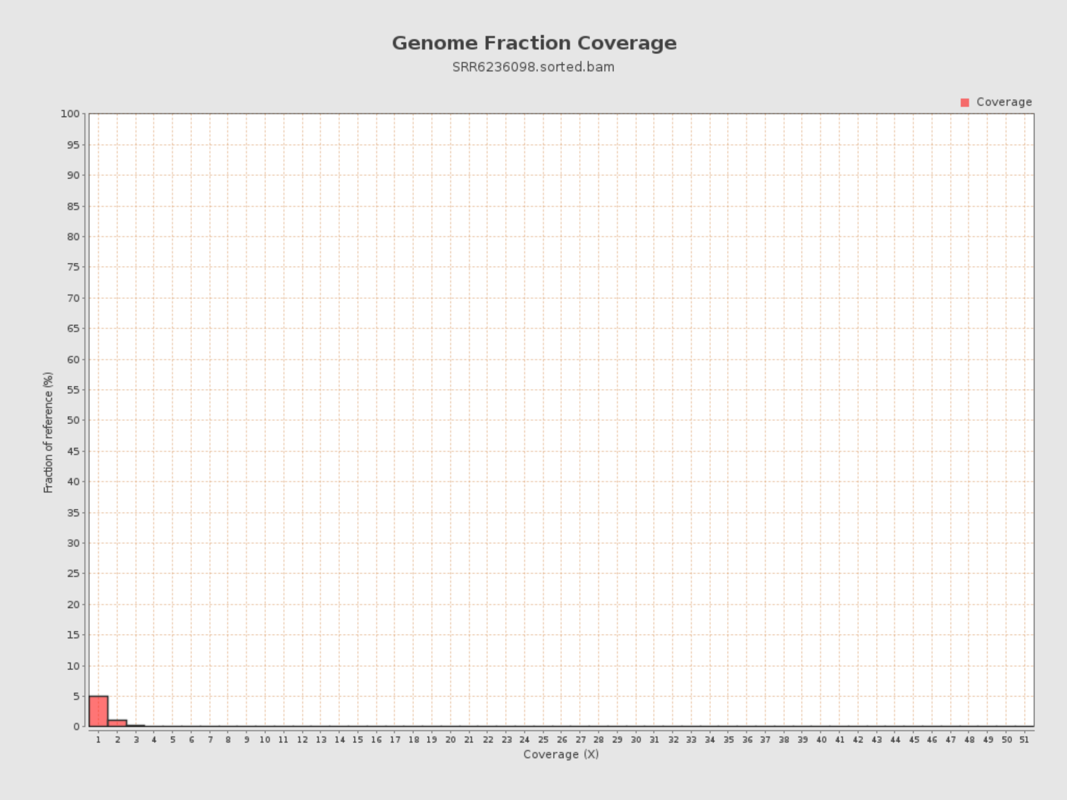
# 4. Results : Coverage Histogram



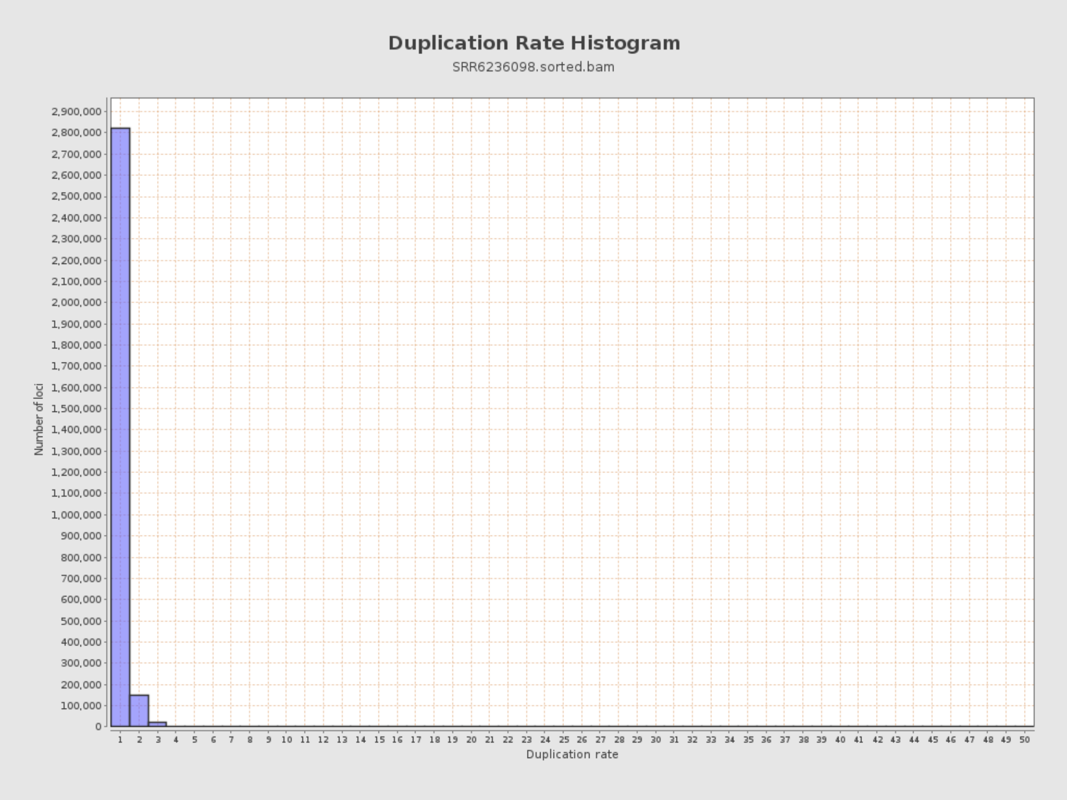
# 5. Results : Coverage Histogram (0-50X)



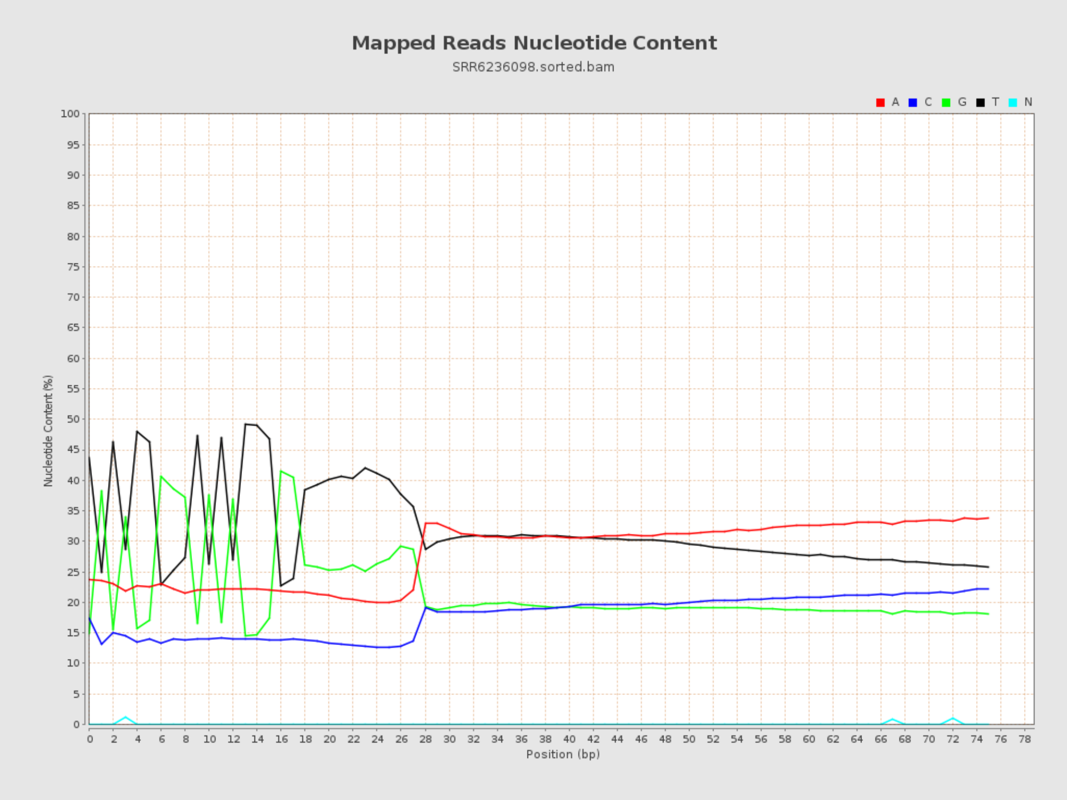
# 6. Results : Genome Fraction Coverage



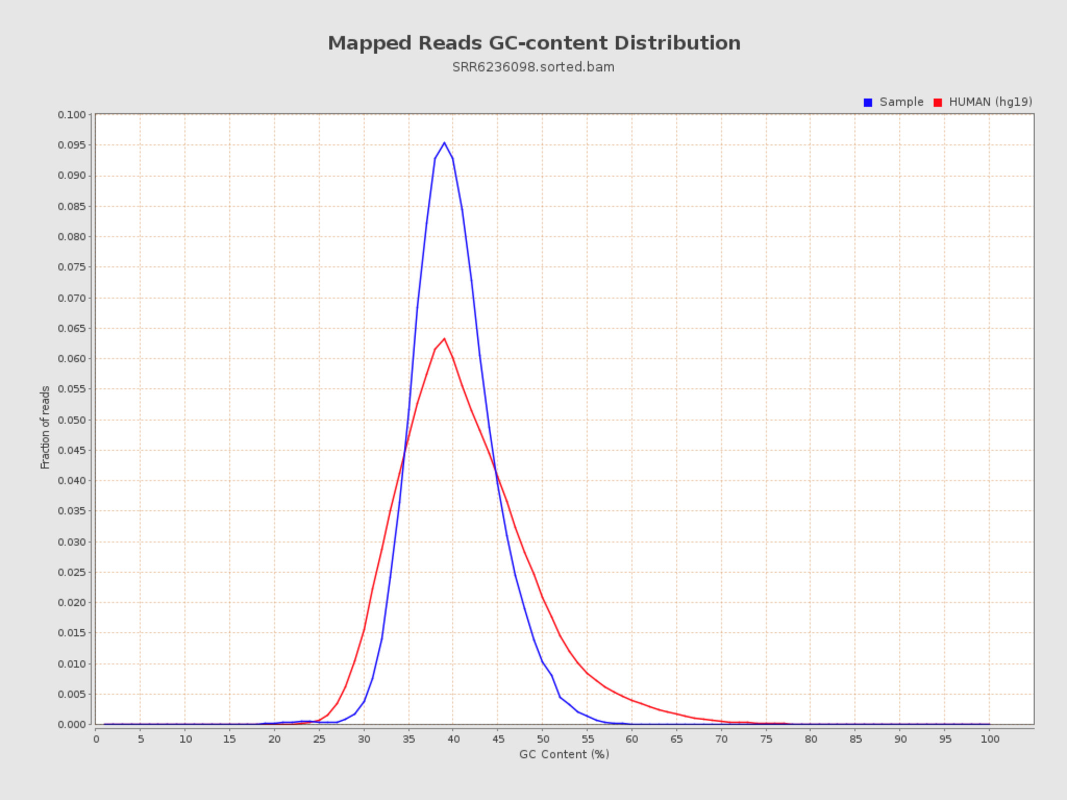
# 7. Results : Duplication Rate Histogram



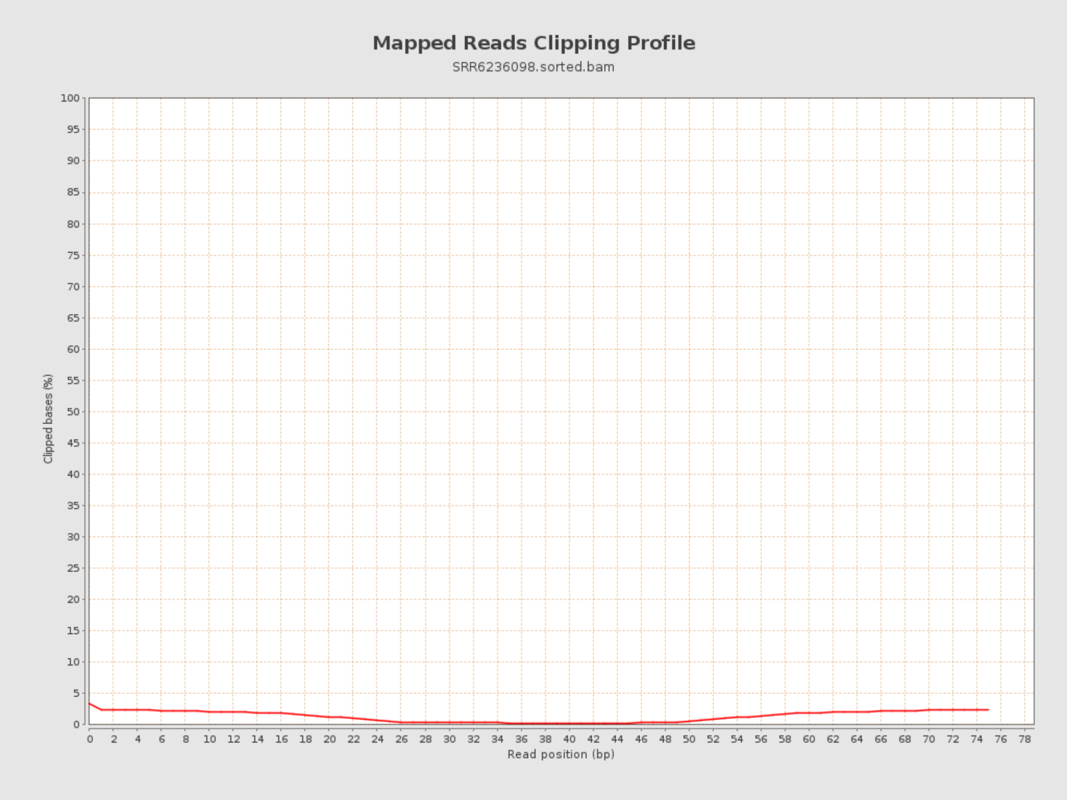
# 8. Results : Mapped Reads Nucleotide Content



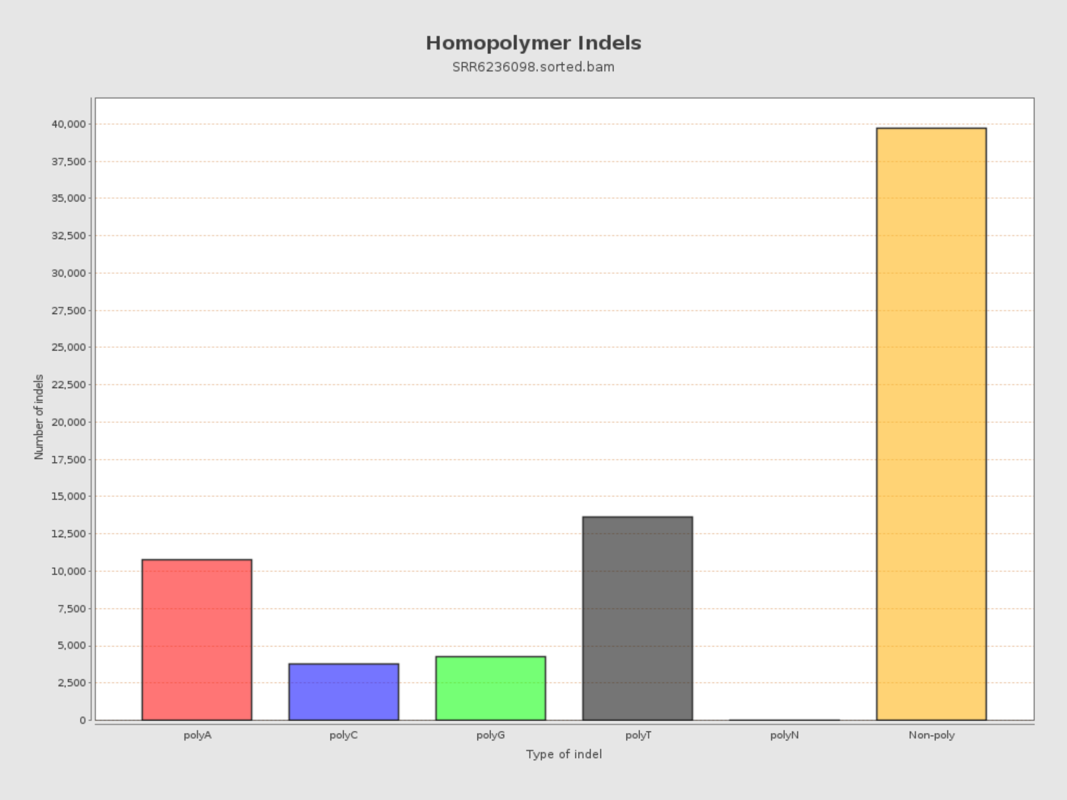
# 9. Results : Mapped Reads GC-content Distribution



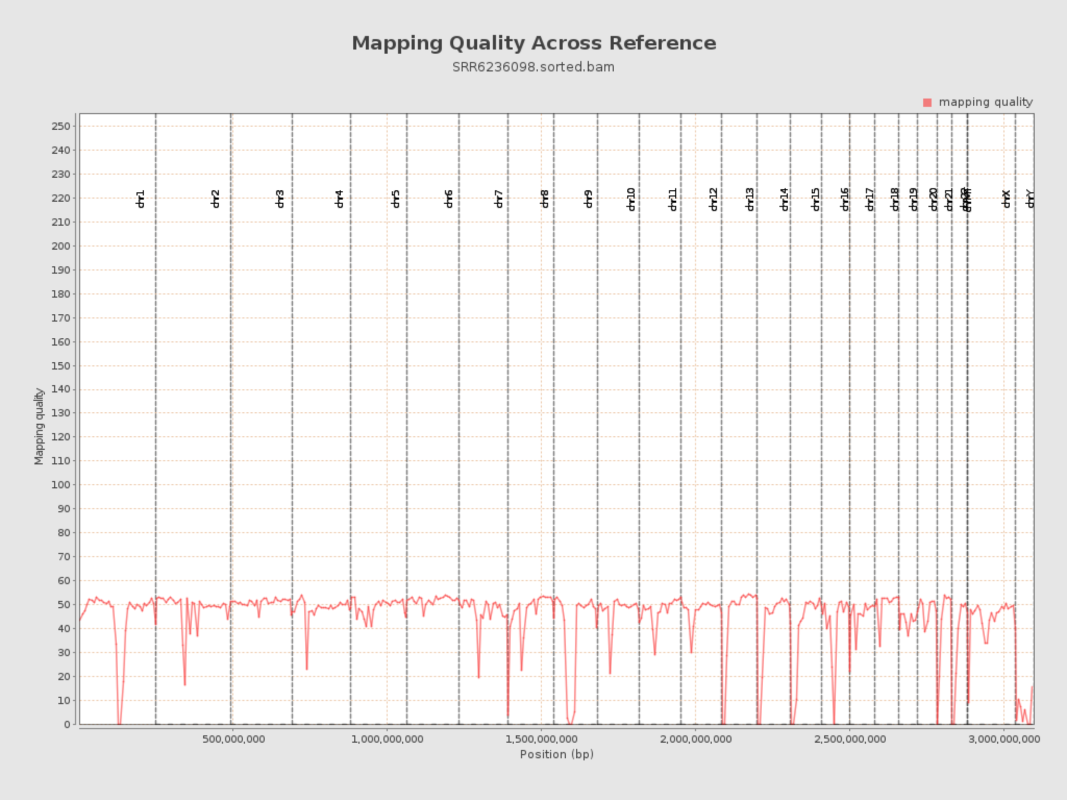
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram