# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/25 08:38:34*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084264.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_SRR3084264 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084264.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Aug 25 08:38:33 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3084264.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,693 |
| Mapped reads | 918 / 24.86% |
| Unmapped reads | 2,775 / 75.14% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 9 / 0.24% |
| Read min/max/mean length | 30 / 76 / 76.08 |
| Duplicated reads (estimated) | 1 / 0.03% |
| Duplication rate | 0.11% |
| Clipped reads | 496 / 13.43% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 17,015 / 28.78% |
| Number/percentage of C's | 10,839 / 18.34% |
| Number/percentage of T's | 18,220 / 30.82% |
| Number/percentage of G's | 13,038 / 22.06% |
| Number/percentage of N's | 0 / 0% |
| GC Percentage | 40.39% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0 |
| | |

| | |
|---|---|
| Standard Deviation | 0.0044 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 39.03 |

## 2.5. Mismatches and indels

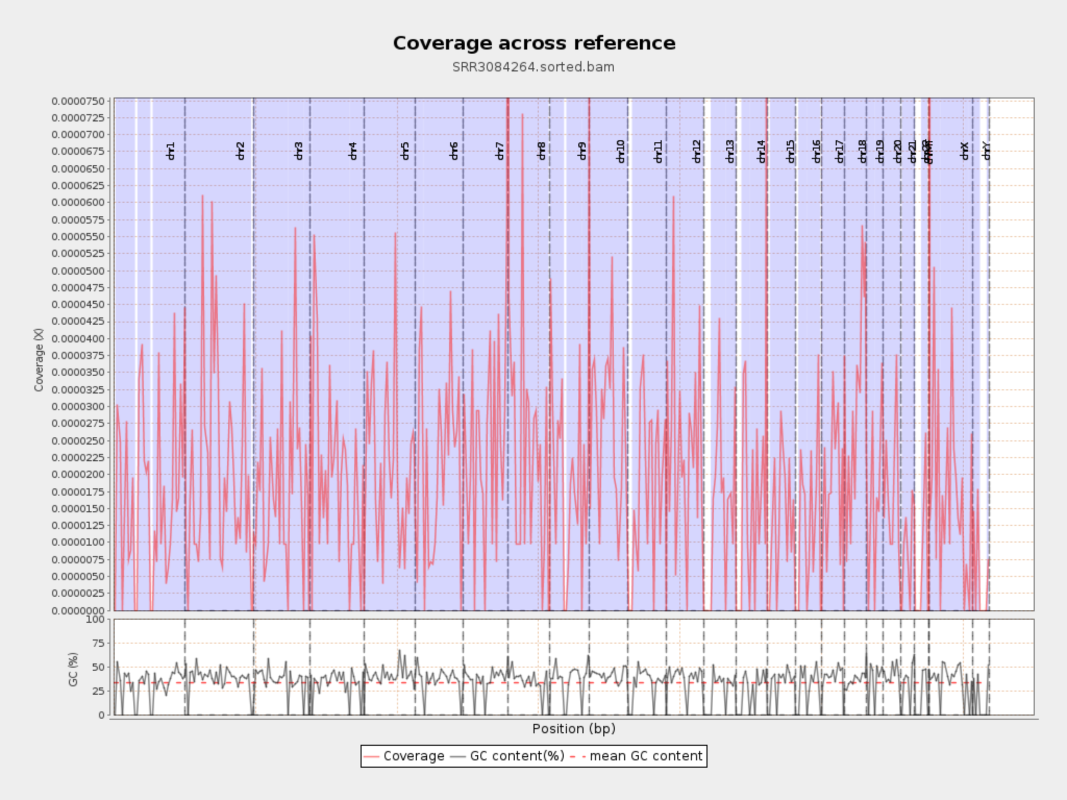
| | |
|---|---|
| General error rate | 0.87% |
| Mismatches | 511 |
| Insertions | 3 |
| Mapped reads with at least one insertion | 0.22% |
| Deletions | 12 |
| Mapped reads with at least one deletion | 1.31% |
| Homopolymer indels | 33.33% |

## 2.6. Chromosome stats

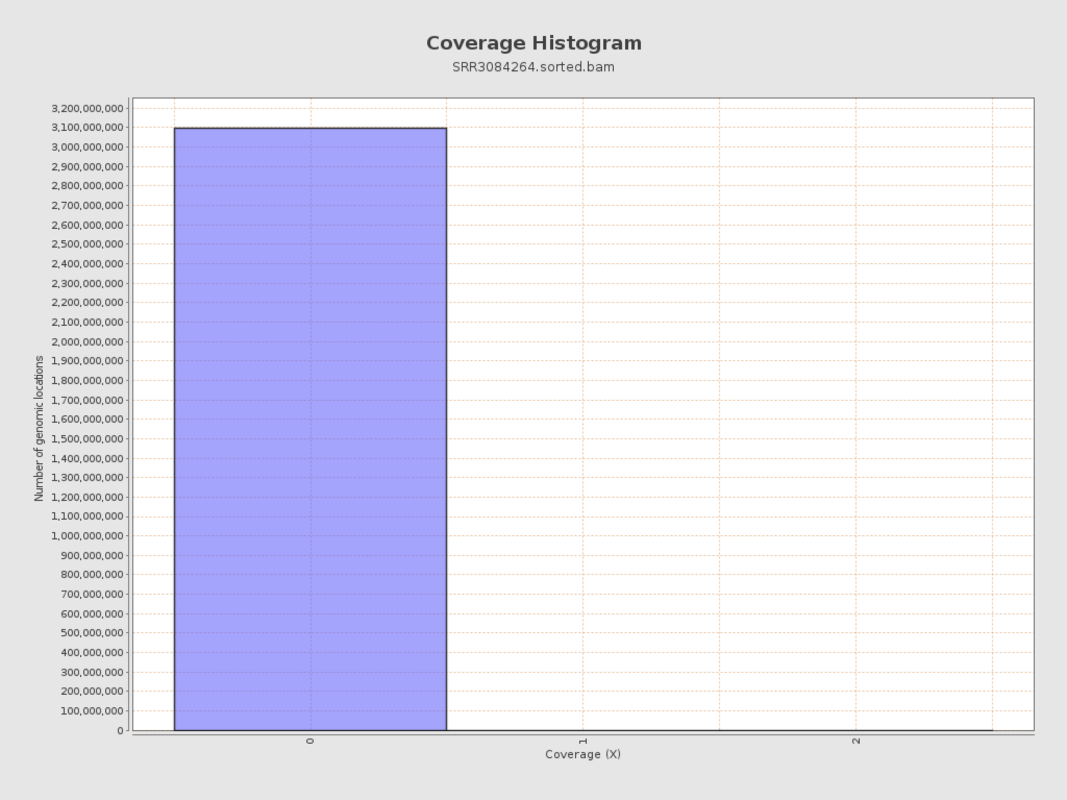
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 4096 | 0 | 0.0041 |
| chr2 | 243199373 | 5009 | 0 | 0.0045 |
| chr3 | 198022430 | 3673 | 0 | 0.0043 |
| chr4 | 191154276 | 3764 | 0 | 0.0044 |
| chr5 | 180915260 | 3989 | 0 | 0.0047 |
| chr6 | 171115067 | 3632 | 0 | 0.0046 |
| chr7 | 159138663 | 3899 | 0 | 0.005 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3478 | 0 | 0.0049 |
| chr9 | 141213431 | 2782 | 0 | 0.0044 |
| chr10 | 135534747 | 3708 | 0 | 0.0052 |
| chr11 | 135006516 | 2331 | 0 | 0.0042 |
| chr12 | 133851895 | 3253 | 0 | 0.0049 |
| chr13 | 115169878 | 1699 | 0 | 0.0038 |
| chr14 | 107349540 | 1580 | 0 | 0.0038 |
| chr15 | 102531392 | 1315 | 0 | 0.0036 |
| chr16 | 90354753 | 1171 | 0 | 0.0036 |
| chr17 | 81195210 | 1485 | 0 | 0.0043 |
| chr18 | 78077248 | 2384 | 0 | 0.0056 |
| chr19 | 59128983 | 981 | 0 | 0.0041 |
| chr20 | 63025520 | 1099 | 0 | 0.0042 |
| chr21 | 48129895 | 450 | 0 | 0.0031 |
| chr22 | 51304566 | 278 | 0 | 0.0023 |
| chrMT | 16571 | 76 | 0.0046 | 0.0676 |
| chrX | 155270560 | 2721 | 0 | 0.0042 |
| chrY | 59373566 | 273 | 0 | 0.0021 |

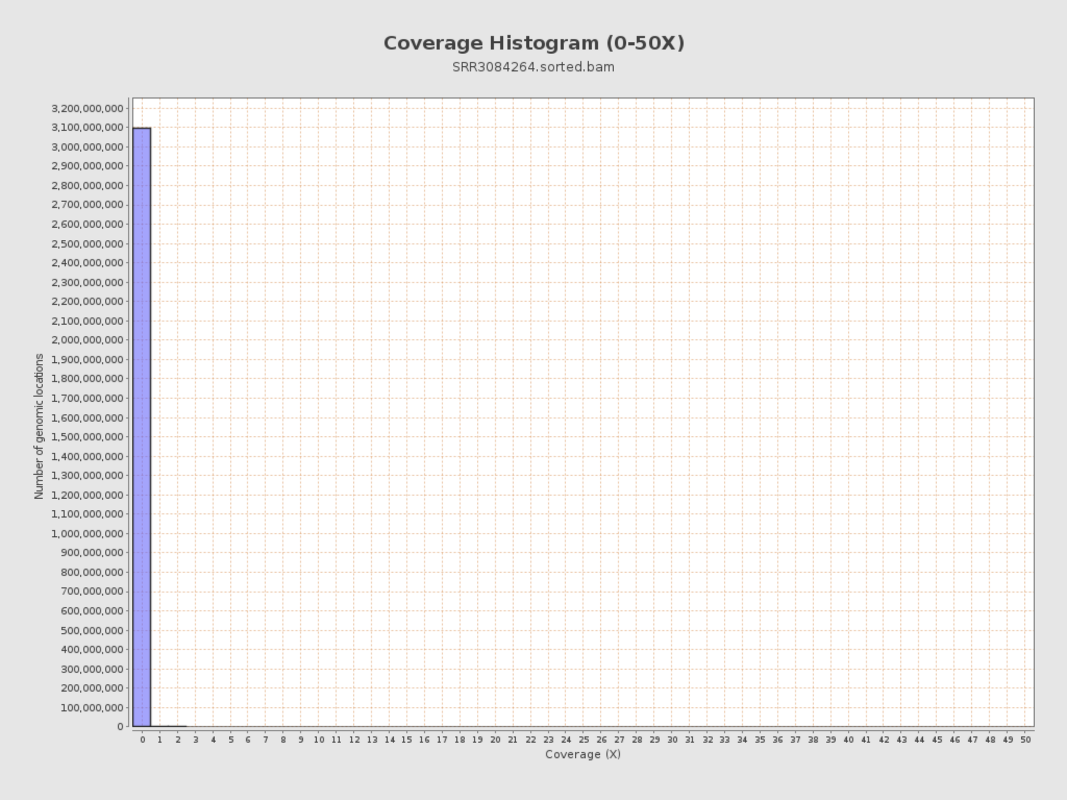
# 3. Results : Coverage across reference



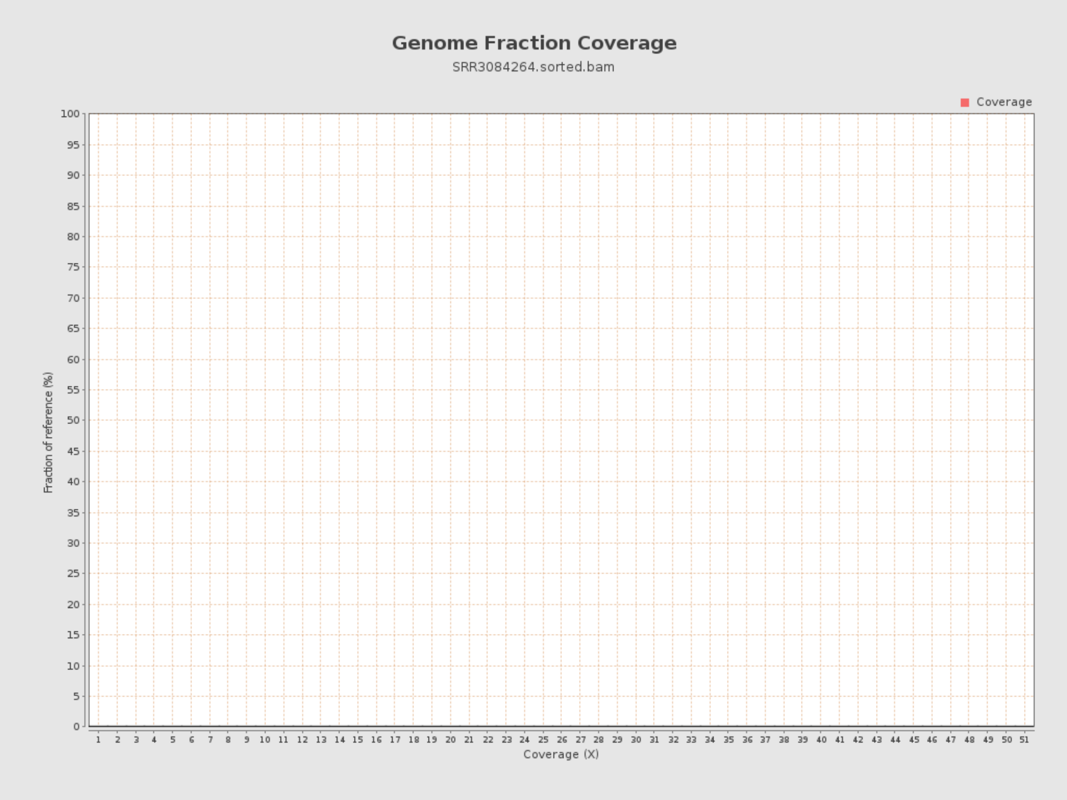
# 4. Results : Coverage Histogram



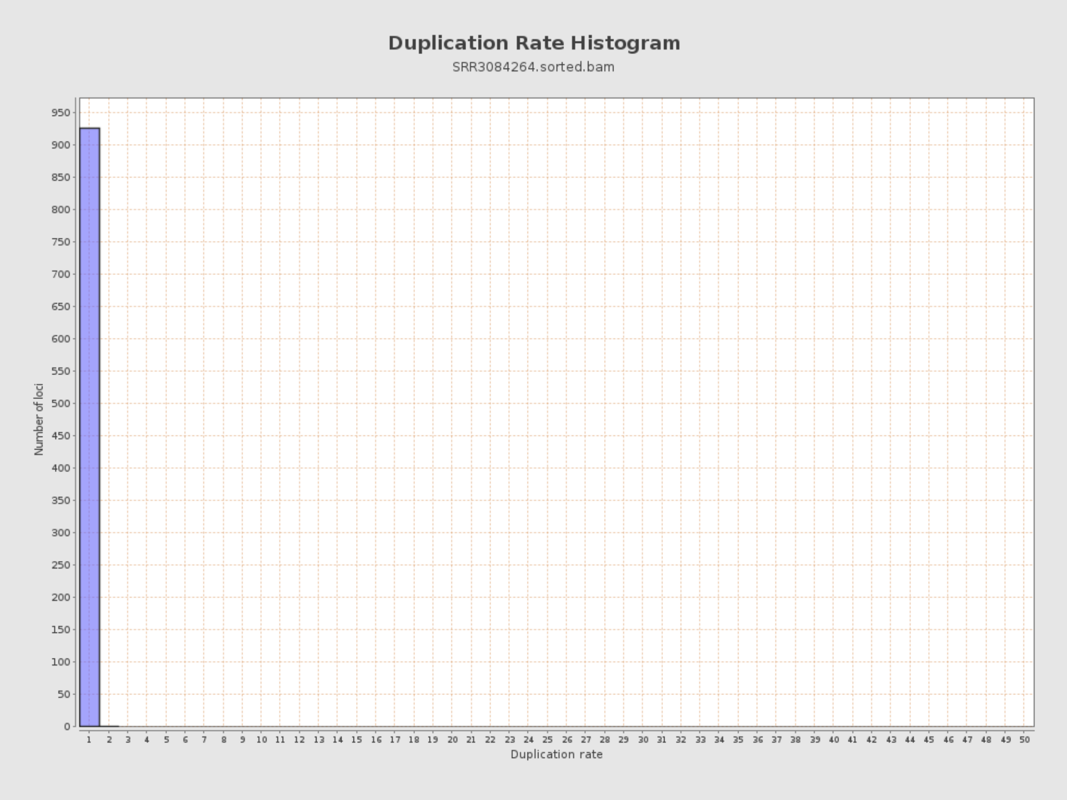
# 5. Results : Coverage Histogram (0-50X)



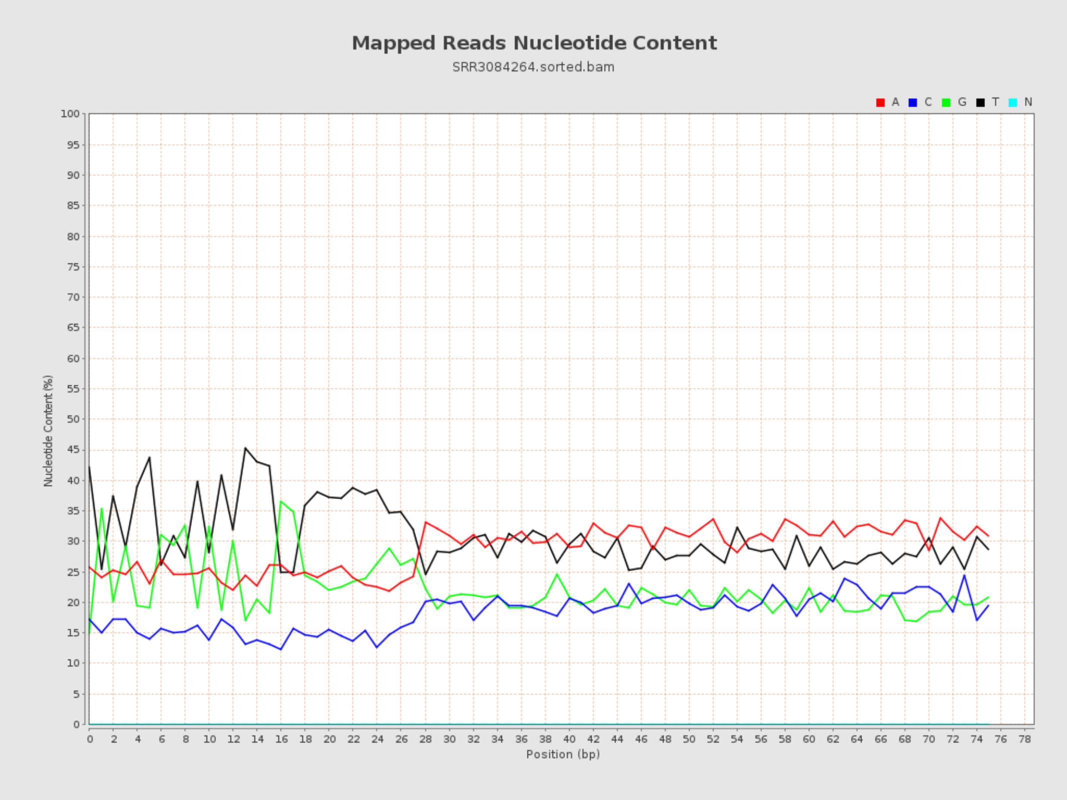
# 6. Results : Genome Fraction Coverage



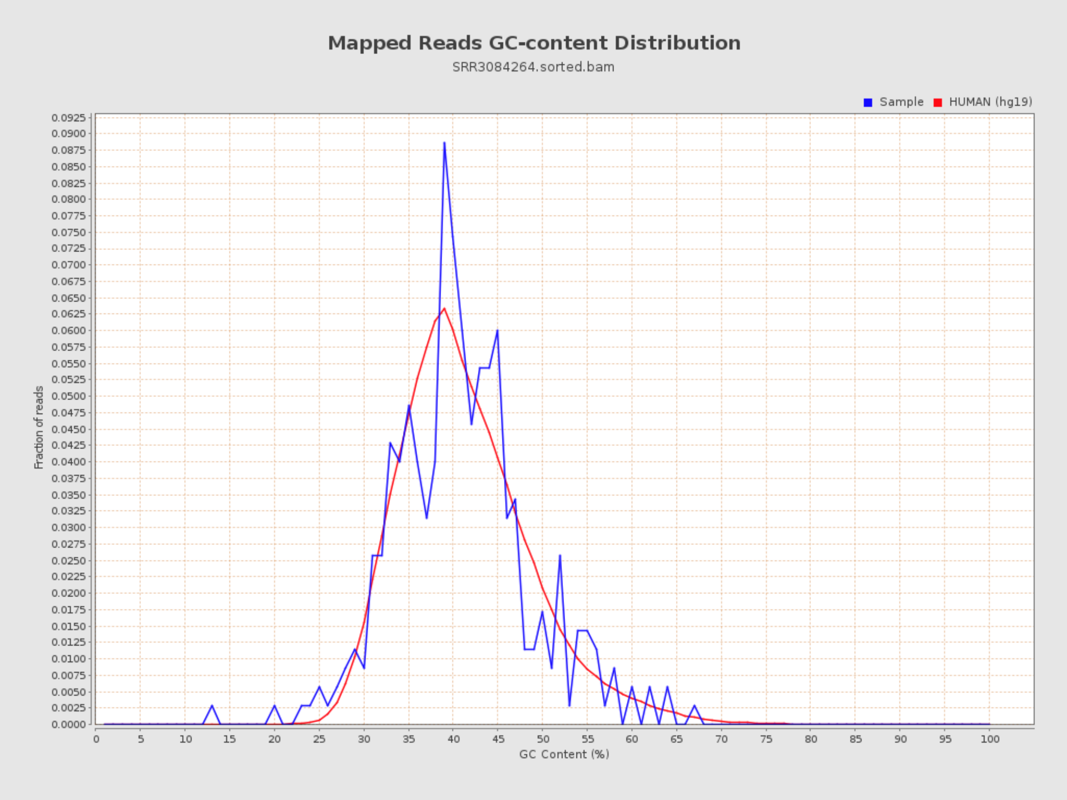
# 7. Results : Duplication Rate Histogram



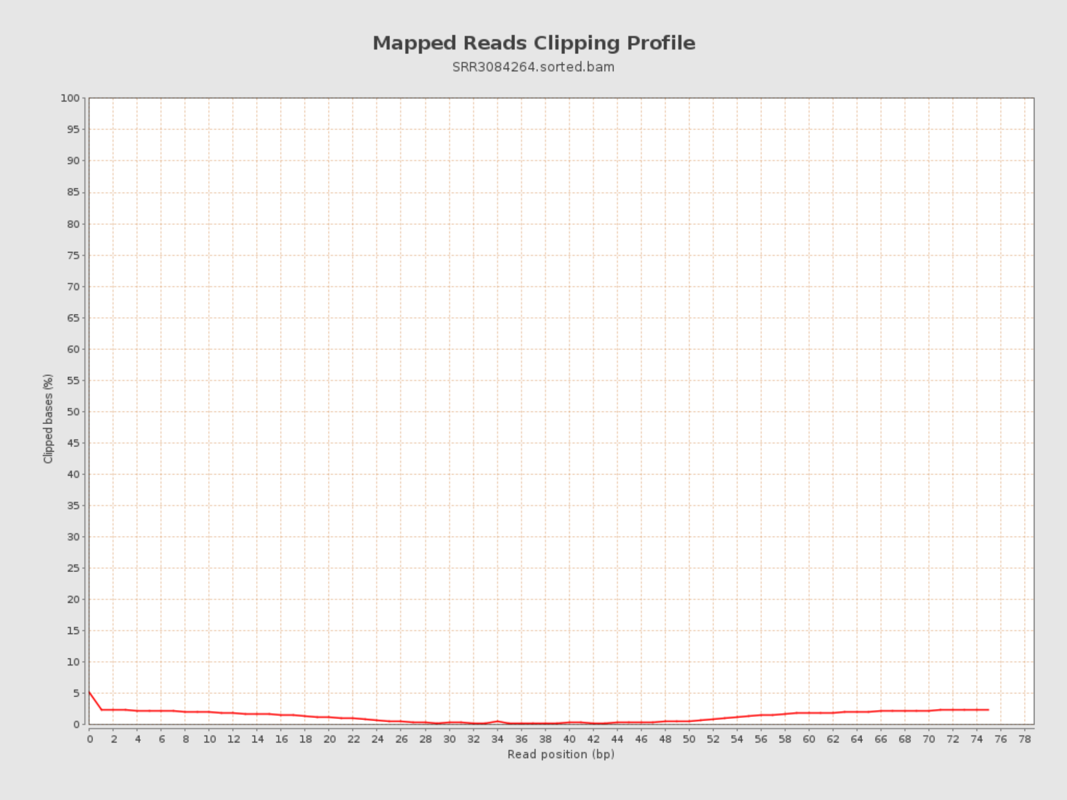
# 8. Results : Mapped Reads Nucleotide Content



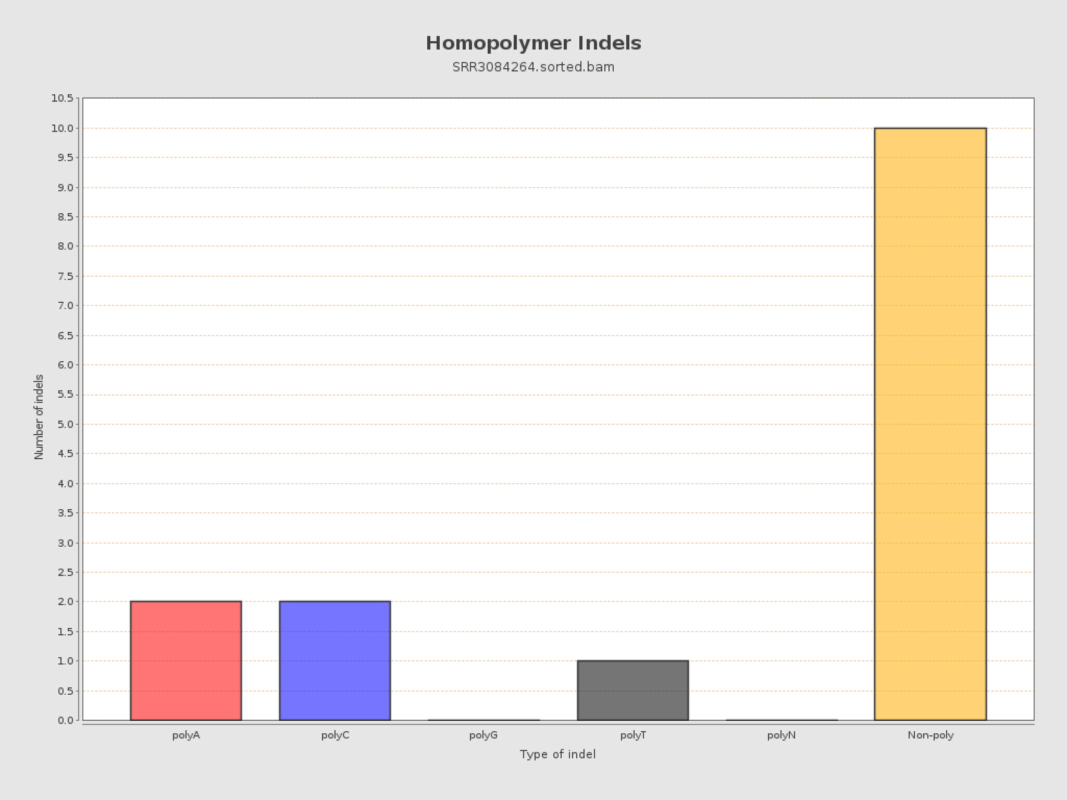
# 9. Results : Mapped Reads GC-content Distribution



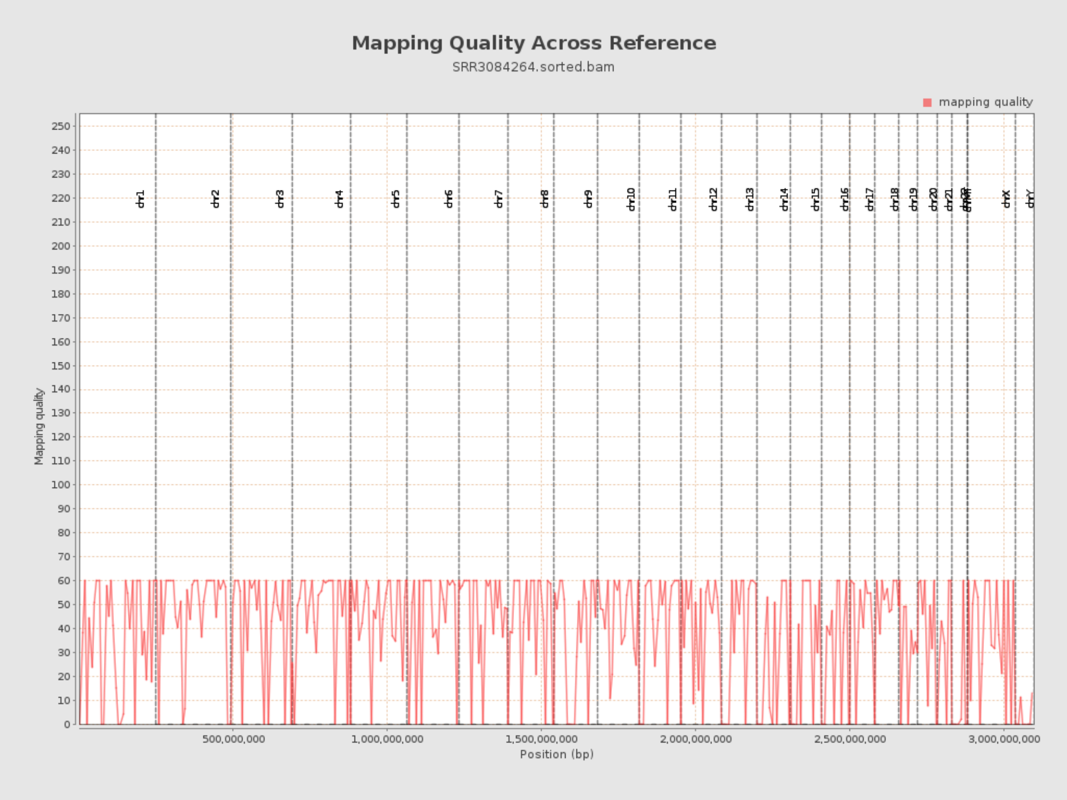
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram