# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 04:53:28*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081244.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_SRR3081244 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081244.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Aug 24 04:53:27 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3081244.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,786,982 |
| Mapped reads | 1,598,142 / 89.43% |
| Unmapped reads | 188,840 / 10.57% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 16,945 / 0.95% |
| Read min/max/mean length | 30 / 76 / 76.33 |
| Duplicated reads (estimated) | 57,190 / 3.2% |
| Duplication rate | 2.91% |
| Clipped reads | 900,858 / 50.41% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 30,172,152 / 29.24% |
| Number/percentage of C's | 19,774,865 / 19.17% |
| Number/percentage of T's | 31,614,302 / 30.64% |
| Number/percentage of G's | 21,595,713 / 20.93% |
| Number/percentage of N's | 13,399 / 0.01% |
| GC Percentage | 40.1% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0333 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2834 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.38 |

## 2.5. Mismatches and indels

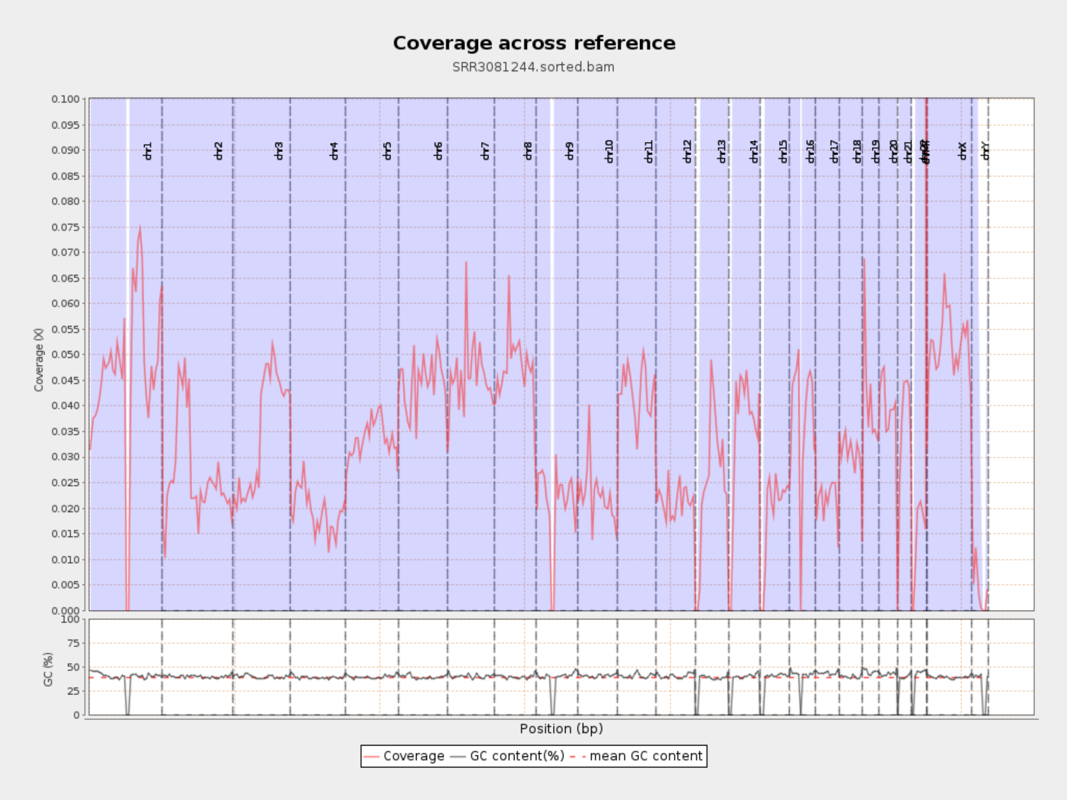
| | |
|---|---|
| General error rate | 0.94% |
| Mismatches | 955,489 |
| Insertions | 7,963 |
| Mapped reads with at least one insertion | 0.49% |
| Deletions | 24,894 |
| Mapped reads with at least one deletion | 1.54% |
| Homopolymer indels | 47.99% |

## 2.6. Chromosome stats

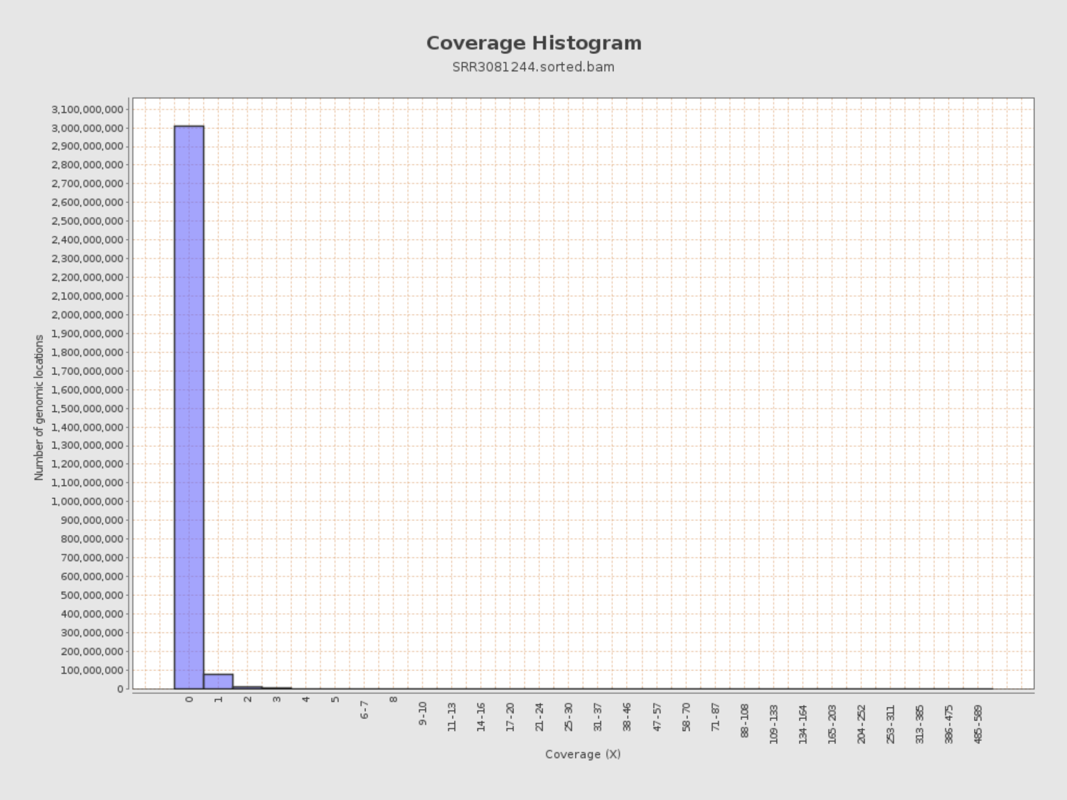
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 11631089 | 0.0467 | 0.4313 |
| chr2 | 243199373 | 6533197 | 0.0269 | 0.2848 |
| chr3 | 198022430 | 6873281 | 0.0347 | 0.2105 |
| chr4 | 191154276 | 3711794 | 0.0194 | 0.1638 |
| chr5 | 180915260 | 6104481 | 0.0337 | 0.2062 |
| chr6 | 171115067 | 7661434 | 0.0448 | 0.2731 |
| chr7 | 159138663 | 7398073 | 0.0465 | 0.4358 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6959937 | 0.0476 | 0.4448 |
| chr9 | 141213431 | 2966552 | 0.021 | 0.2115 |
| chr10 | 135534747 | 3071413 | 0.0227 | 0.2408 |
| chr11 | 135006516 | 5749220 | 0.0426 | 0.3465 |
| chr12 | 133851895 | 2860175 | 0.0214 | 0.1656 |
| chr13 | 115169878 | 2904966 | 0.0252 | 0.1803 |
| chr14 | 107349540 | 3635715 | 0.0339 | 0.2115 |
| chr15 | 102531392 | 1921645 | 0.0187 | 0.1586 |
| chr16 | 90354753 | 3446278 | 0.0381 | 0.2244 |
| chr17 | 81195210 | 1734330 | 0.0214 | 0.1877 |
| chr18 | 78077248 | 2437269 | 0.0312 | 0.3449 |
| chr19 | 59128983 | 2406856 | 0.0407 | 0.369 |
| chr20 | 63025520 | 2505616 | 0.0398 | 0.2263 |
| chr21 | 48129895 | 1664537 | 0.0346 | 0.2153 |
| chr22 | 51304566 | 698275 | 0.0136 | 0.1277 |
| chrMT | 16571 | 40508 | 2.4445 | 2.3898 |
| chrX | 155270560 | 8027492 | 0.0517 | 0.2743 |
| chrY | 59373566 | 267042 | 0.0045 | 0.0906 |

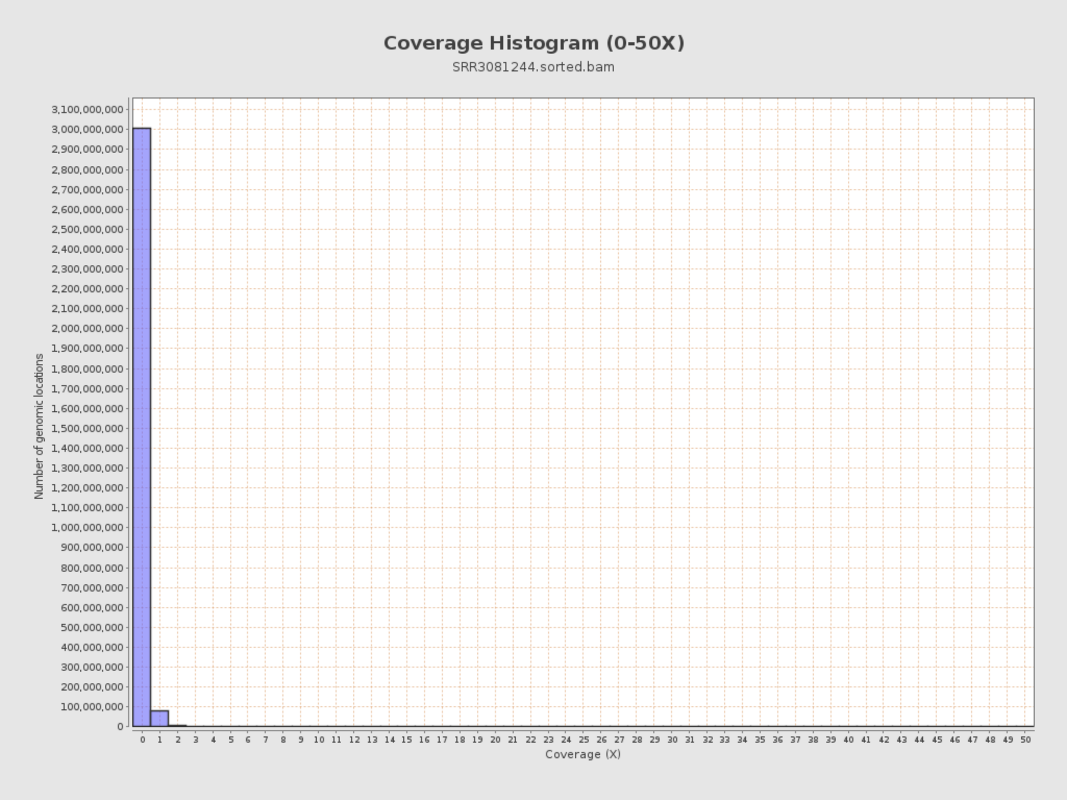
# 3. Results : Coverage across reference



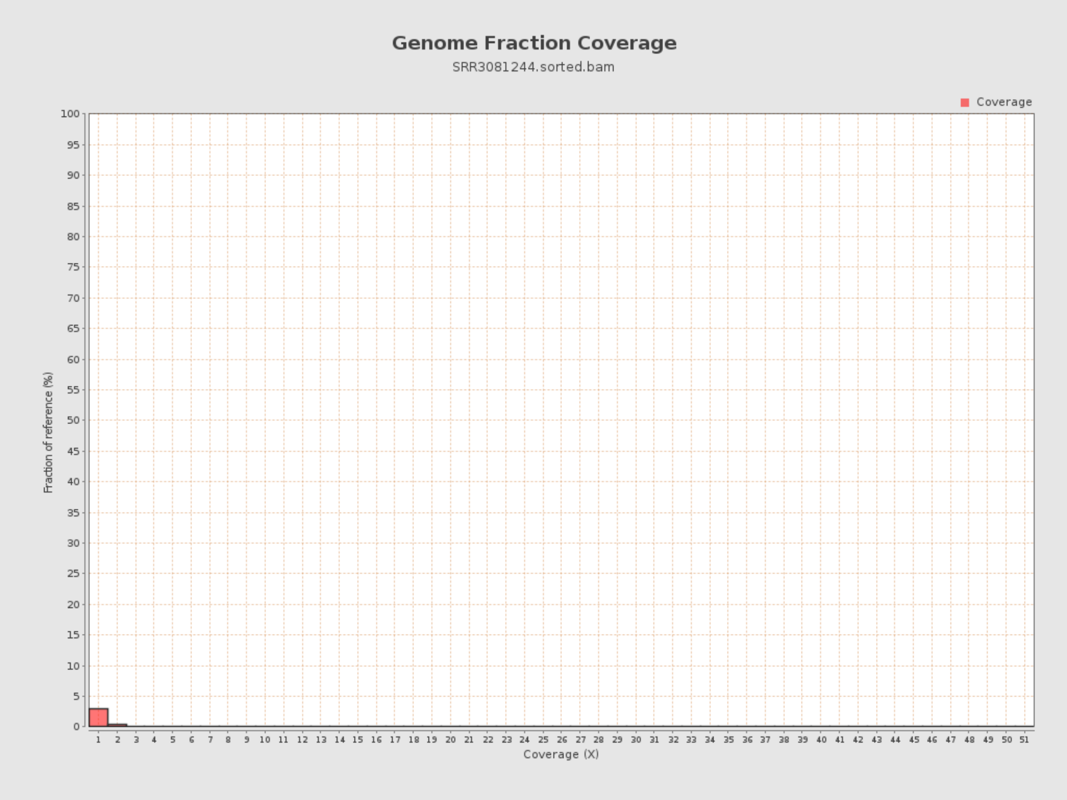
# 4. Results : Coverage Histogram



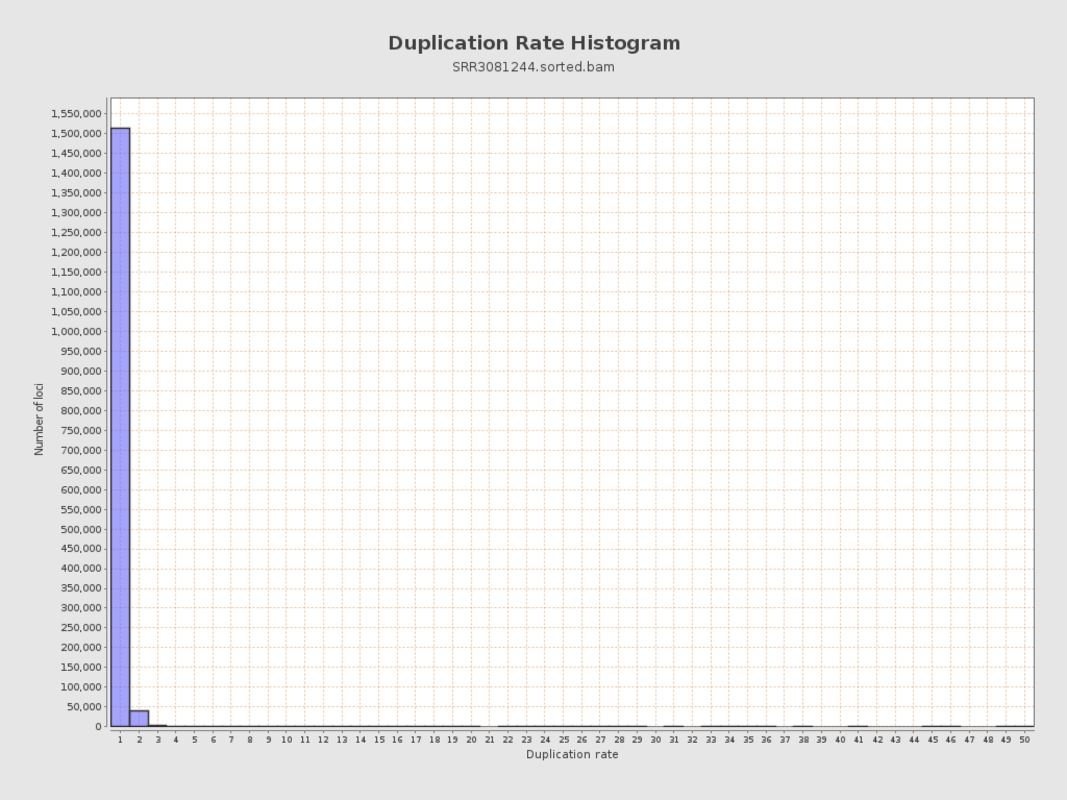
# 5. Results : Coverage Histogram (0-50X)



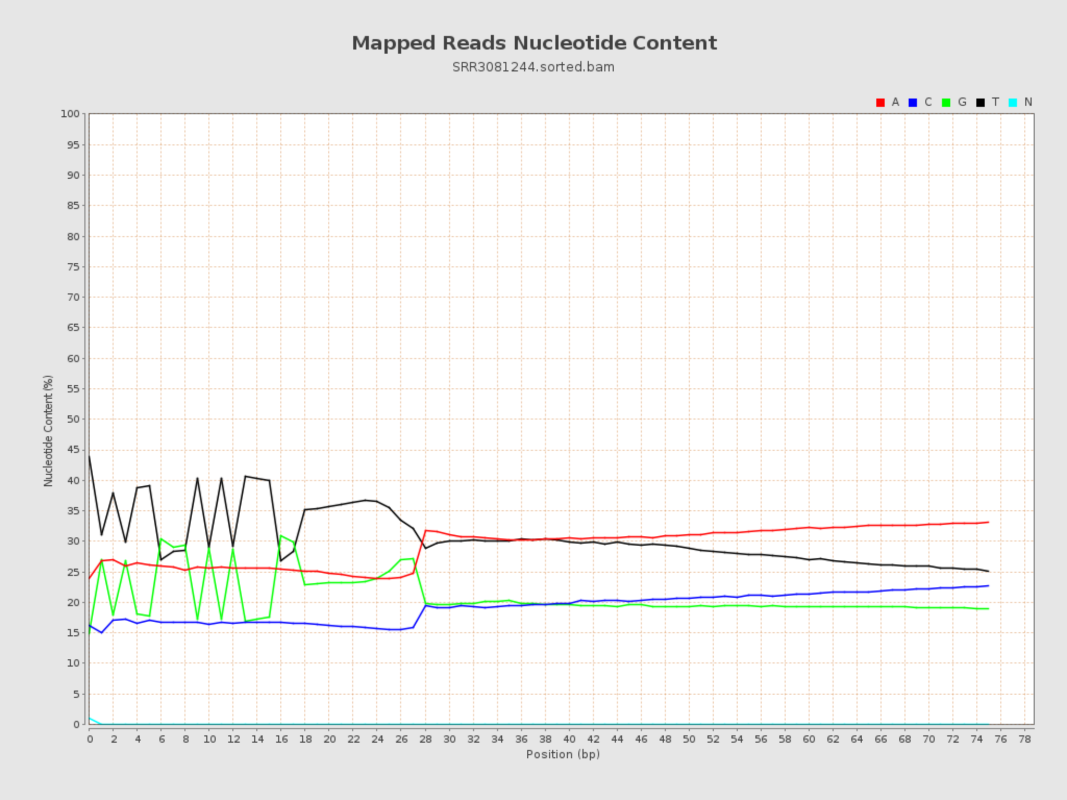
# 6. Results : Genome Fraction Coverage



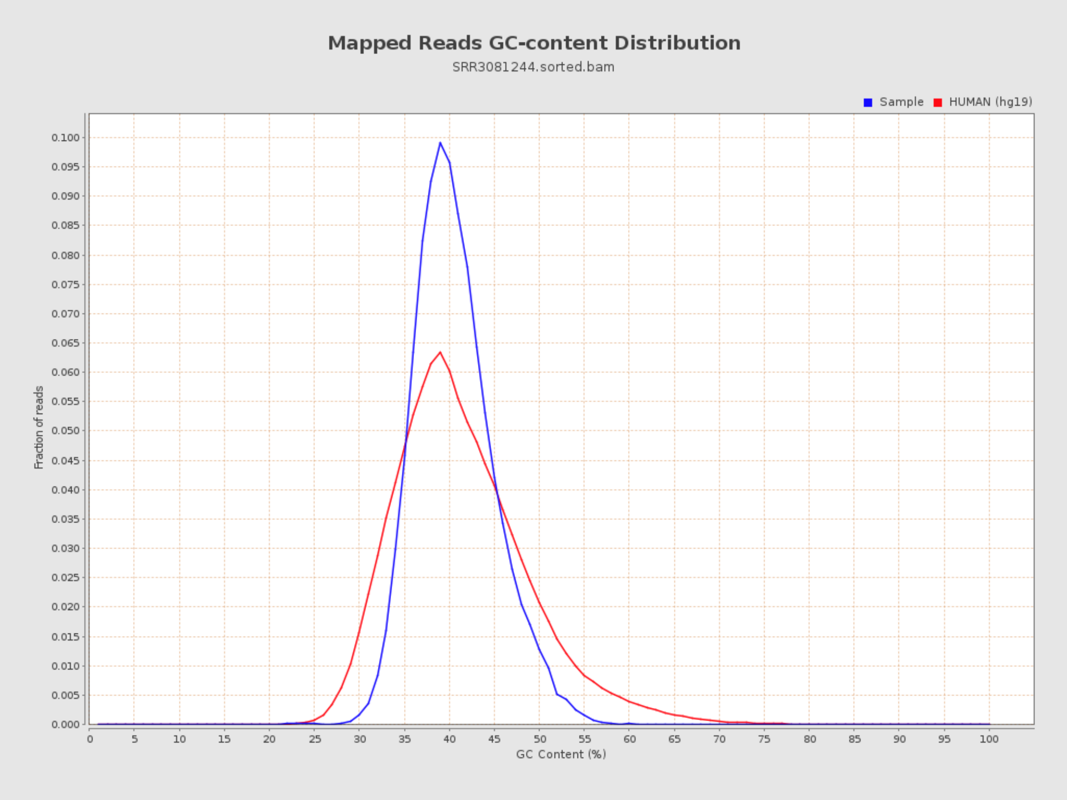
# 7. Results : Duplication Rate Histogram



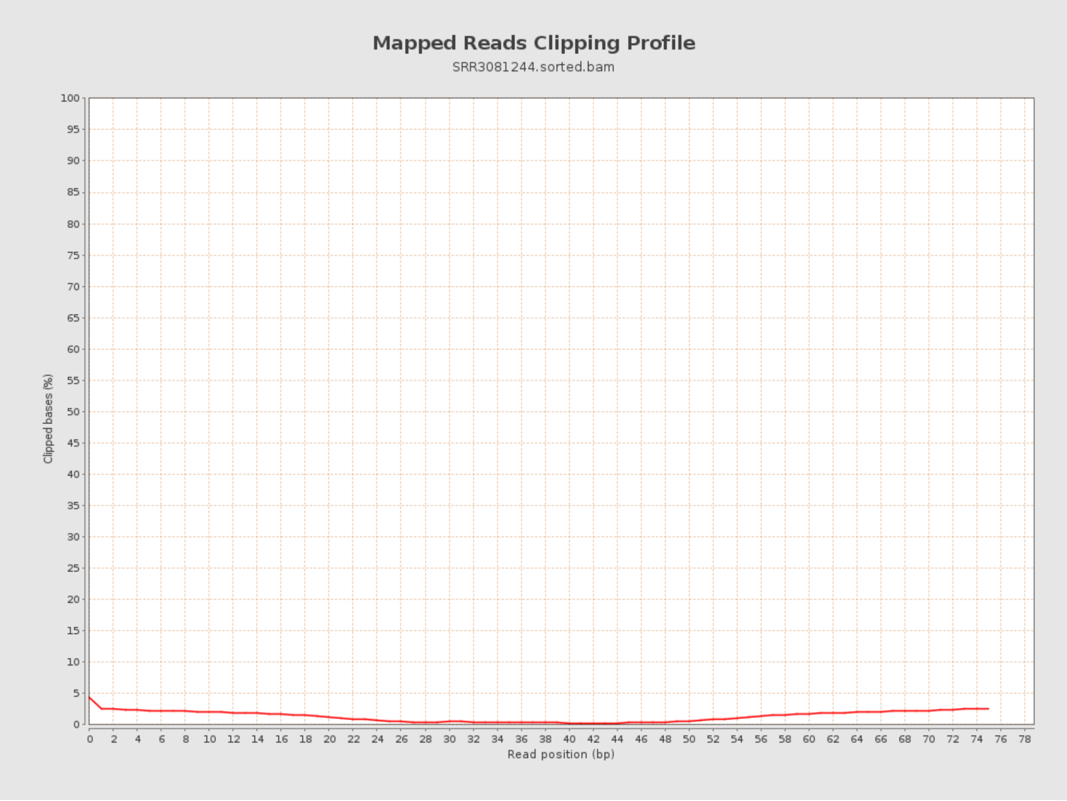
# 8. Results : Mapped Reads Nucleotide Content



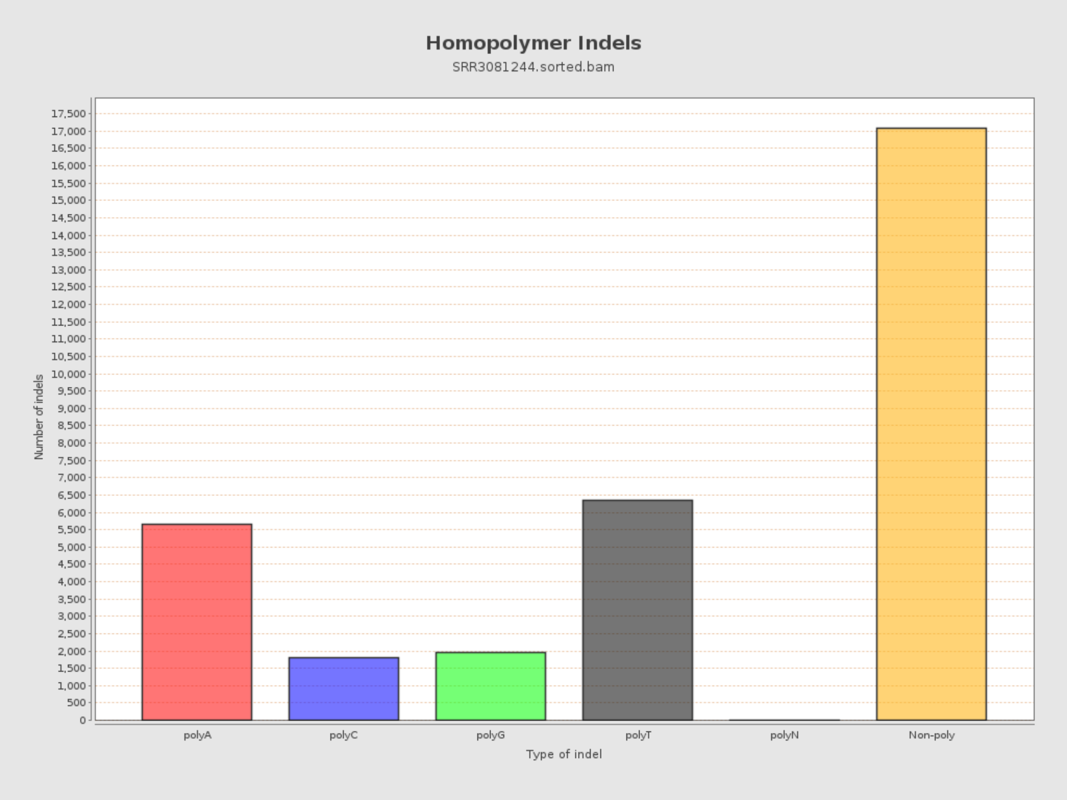
# 9. Results : Mapped Reads GC-content Distribution



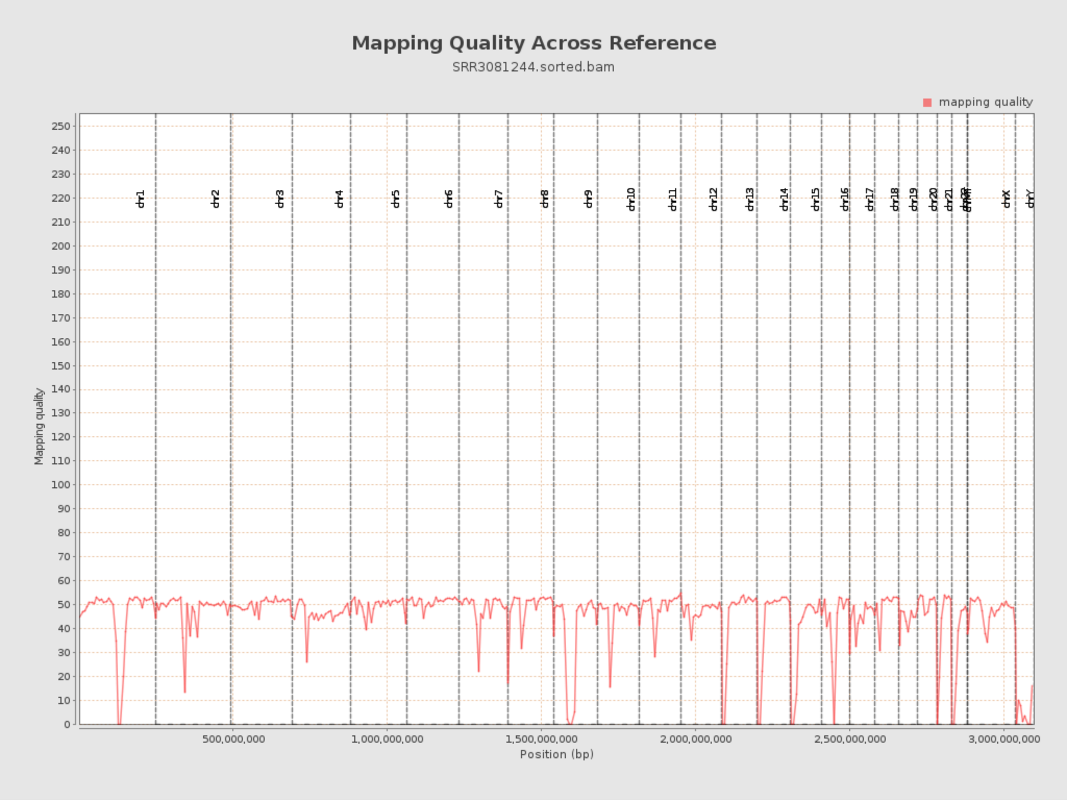
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram