# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/01 18:20:49*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524390.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_SRR10524390 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524390.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Sep 01 18:20:49 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524390.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,236,983 |
| Mapped reads | 3,873,536 / 91.42% |
| Unmapped reads | 363,447 / 8.58% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 14,323 / 0.34% |
| Read min/max/mean length | 30 / 76 / 76.11 |
| Duplicated reads (estimated) | 273,909 / 6.46% |
| Duplication rate | 5.24% |
| Clipped reads | 3,872,896 / 91.41% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 56,045,791 / 24.81% |
| Number/percentage of C's | 45,647,898 / 20.2% |
| Number/percentage of T's | 72,764,793 / 32.21% |
| Number/percentage of G's | 51,449,951 / 22.77% |
| Number/percentage of N's | 28,248 / 0.01% |
| GC Percentage | 42.98% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.073 |
| | |

| | |
|---|---|
| Standard Deviation | 0.665 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.71 |

## 2.5. Mismatches and indels

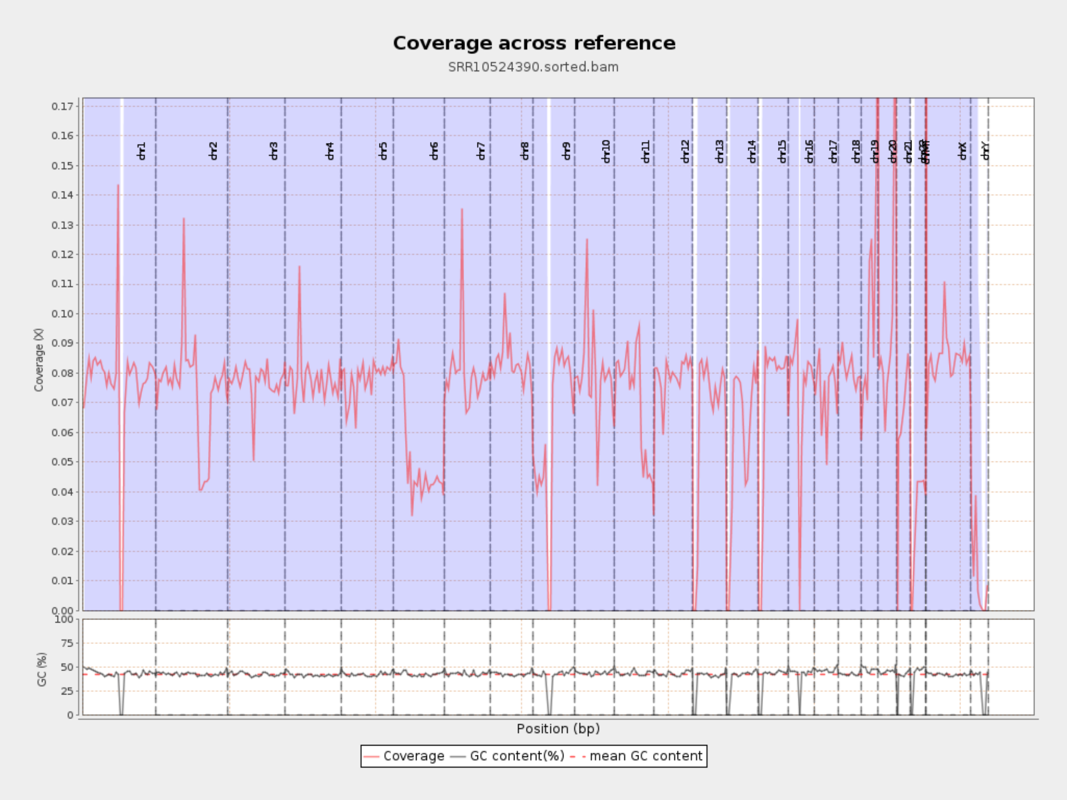
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 1,106,933 |
| Insertions | 19,085 |
| Mapped reads with at least one insertion | 0.49% |
| Deletions | 41,241 |
| Mapped reads with at least one deletion | 1.06% |
| Homopolymer indels | 42.25% |

## 2.6. Chromosome stats

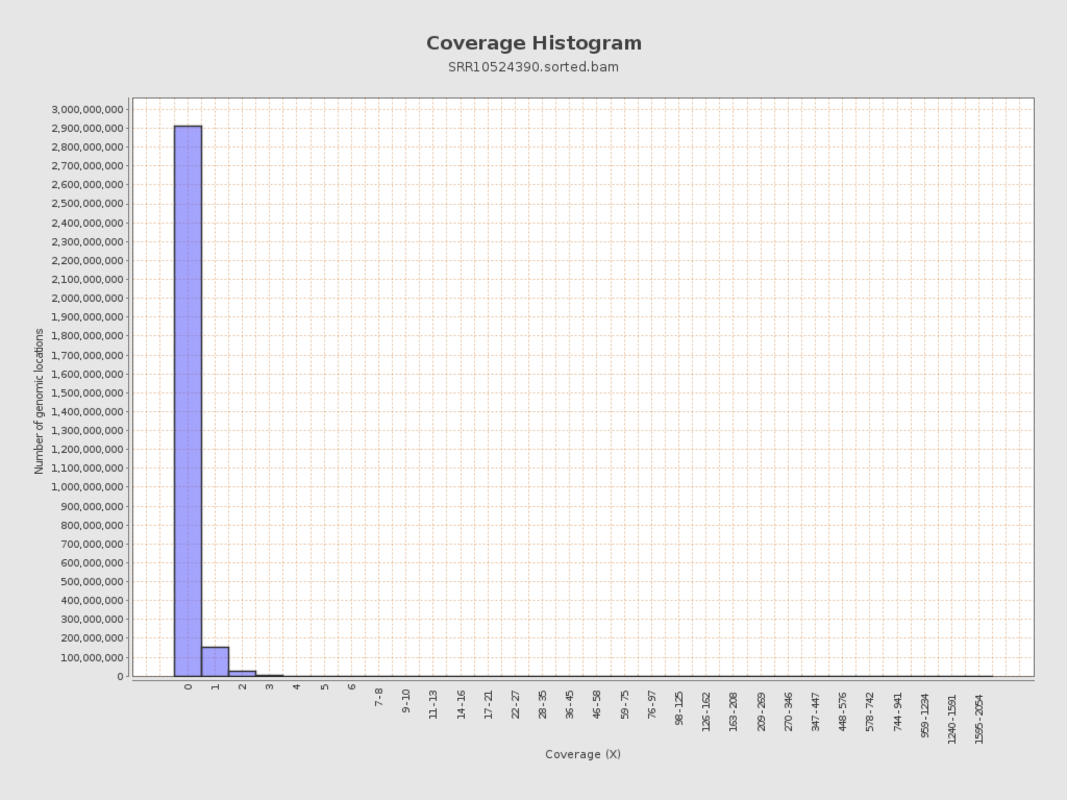
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 18997962 | 0.0762 | 1.5448 |
| chr2 | 243199373 | 18222325 | 0.0749 | 0.7382 |
| chr3 | 198022430 | 15258297 | 0.0771 | 0.3299 |
| chr4 | 191154276 | 15016791 | 0.0786 | 0.4025 |
| chr5 | 180915260 | 14122213 | 0.0781 | 0.333 |
| chr6 | 171115067 | 8954753 | 0.0523 | 0.3244 |
| chr7 | 159138663 | 12808429 | 0.0805 | 0.9631 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 12270761 | 0.0838 | 0.592 |
| chr9 | 141213431 | 8601416 | 0.0609 | 0.4594 |
| chr10 | 135534747 | 10833961 | 0.0799 | 0.552 |
| chr11 | 135006516 | 9494848 | 0.0703 | 0.5038 |
| chr12 | 133851895 | 10651165 | 0.0796 | 0.3544 |
| chr13 | 115169878 | 7413856 | 0.0644 | 0.3029 |
| chr14 | 107349540 | 6243283 | 0.0582 | 0.308 |
| chr15 | 102531392 | 7026637 | 0.0685 | 0.3136 |
| chr16 | 90354753 | 6622380 | 0.0733 | 0.3571 |
| chr17 | 81195210 | 6030640 | 0.0743 | 0.3845 |
| chr18 | 78077248 | 6368081 | 0.0816 | 0.8904 |
| chr19 | 59128983 | 6277495 | 0.1062 | 1.0121 |
| chr20 | 63025520 | 6214292 | 0.0986 | 0.3989 |
| chr21 | 48129895 | 3081858 | 0.064 | 0.3696 |
| chr22 | 51304566 | 1569634 | 0.0306 | 0.2041 |
| chrMT | 16571 | 69479 | 4.1928 | 3.1572 |
| chrX | 155270560 | 13173618 | 0.0848 | 0.4266 |
| chrY | 59373566 | 677328 | 0.0114 | 0.2938 |

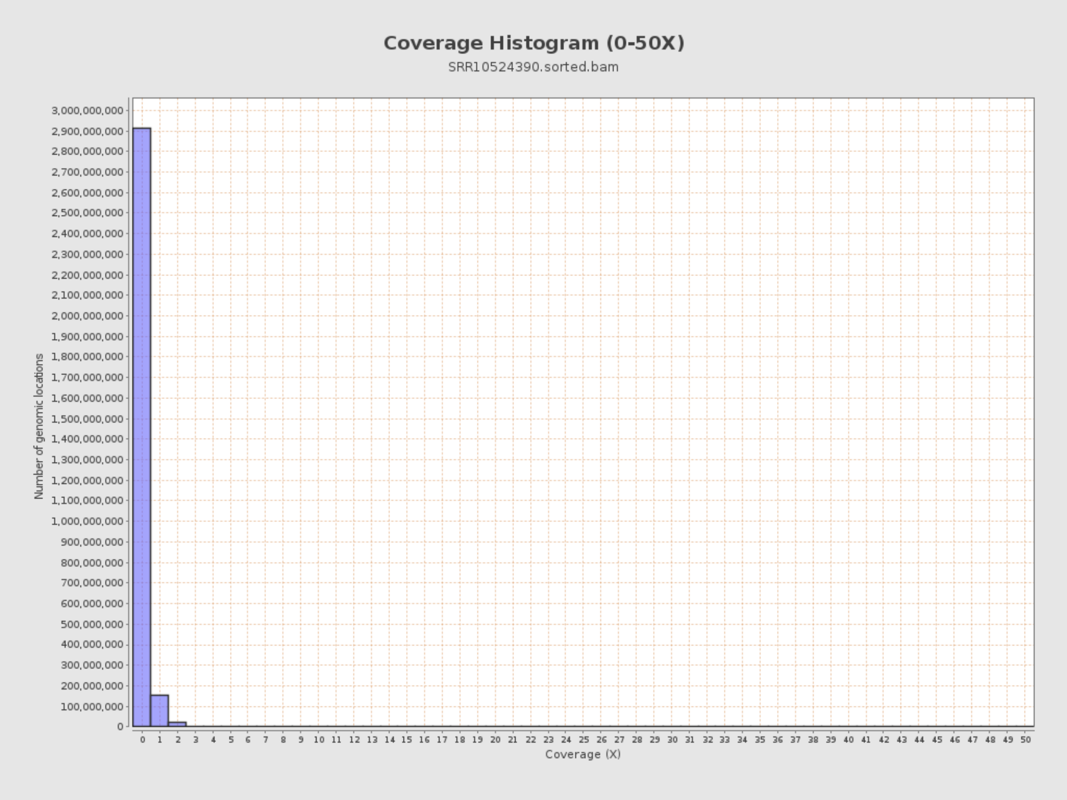
# 3. Results : Coverage across reference



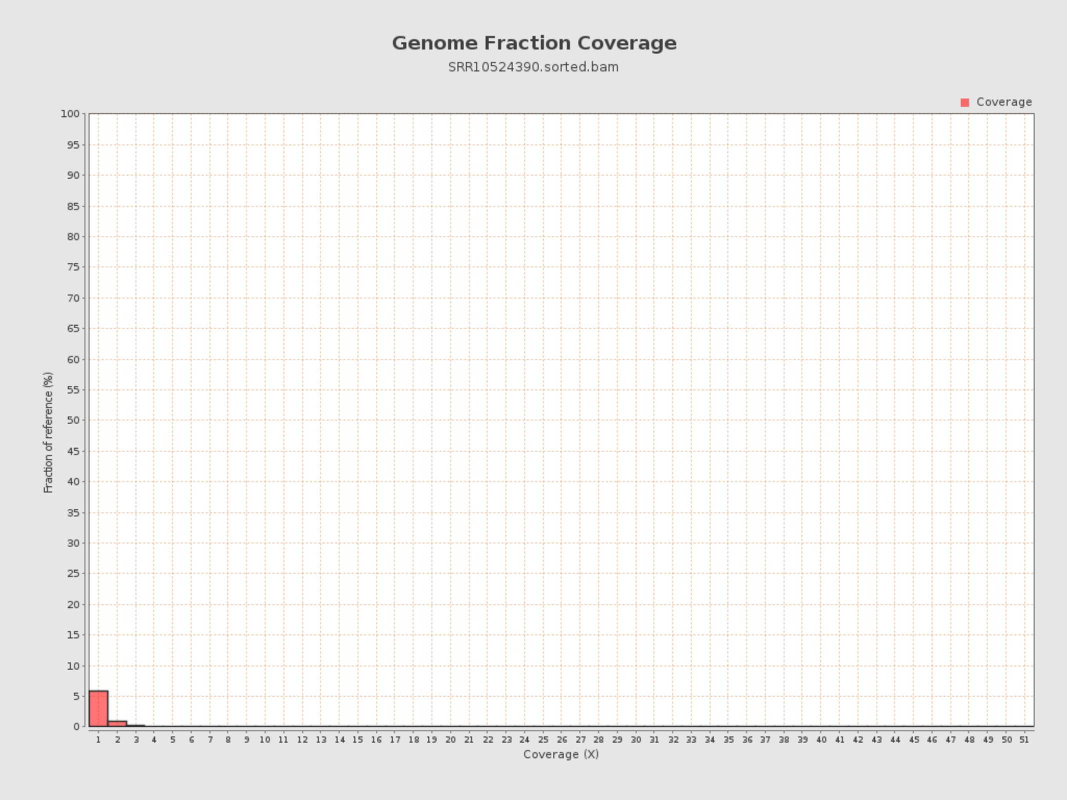
# 4. Results : Coverage Histogram



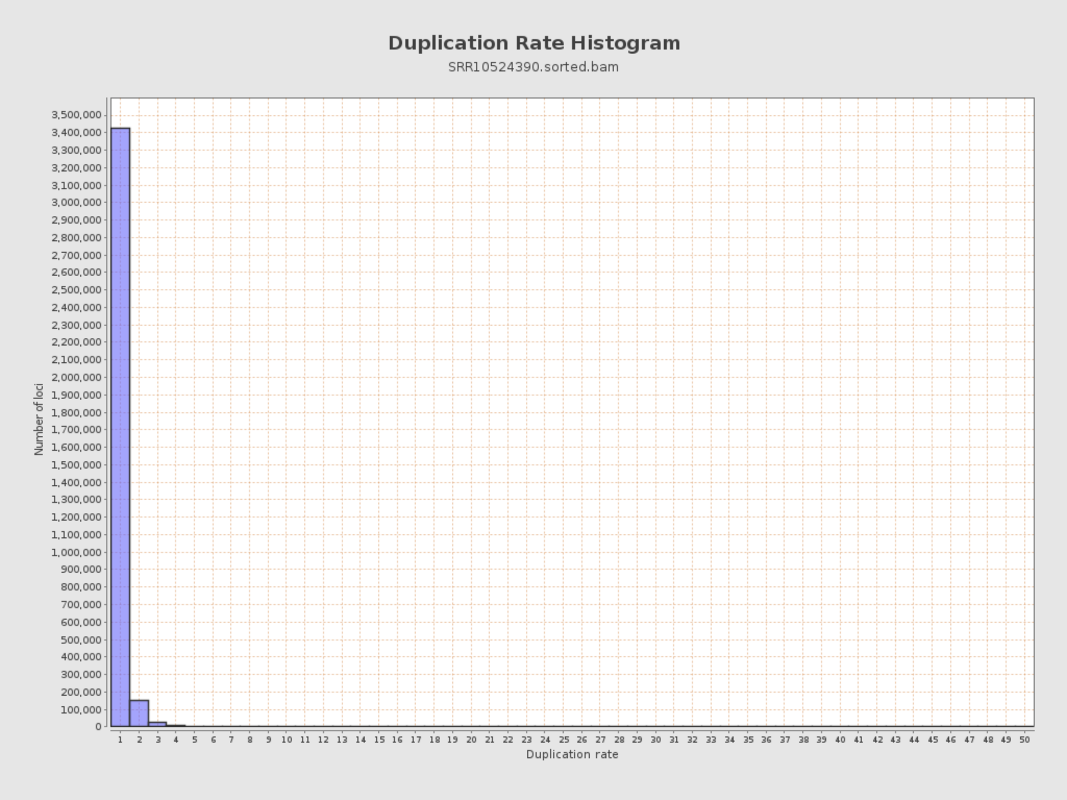
# 5. Results : Coverage Histogram (0-50X)



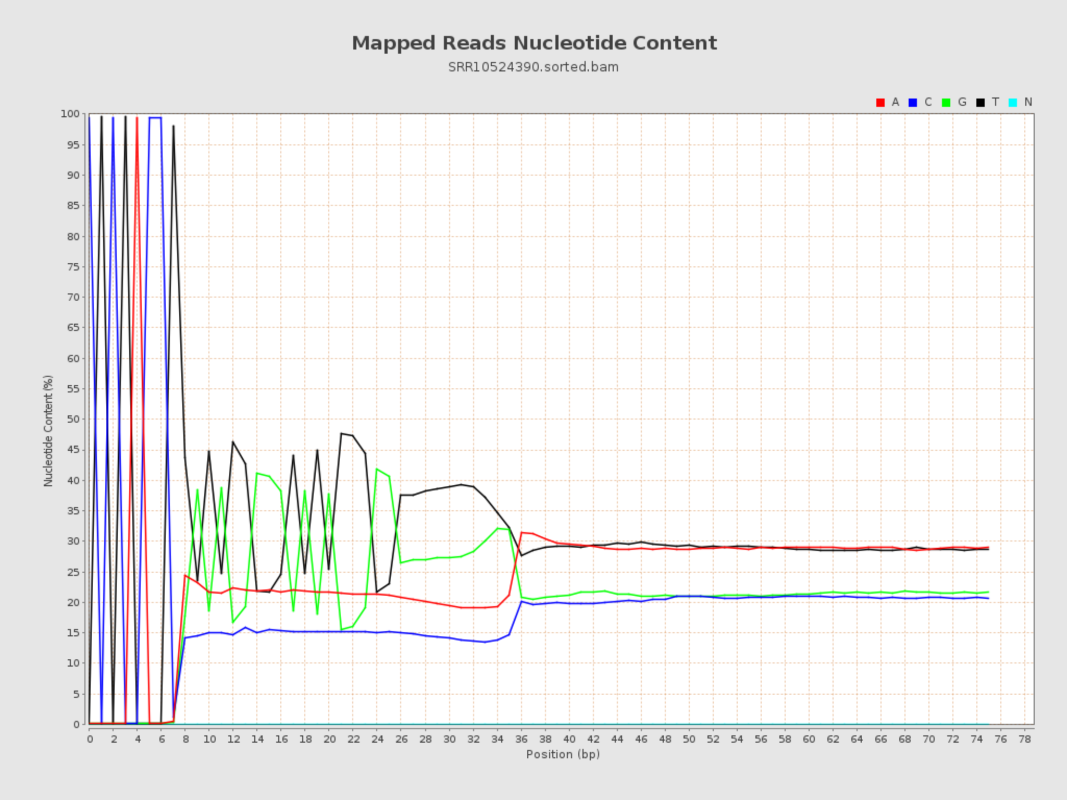
# 6. Results : Genome Fraction Coverage



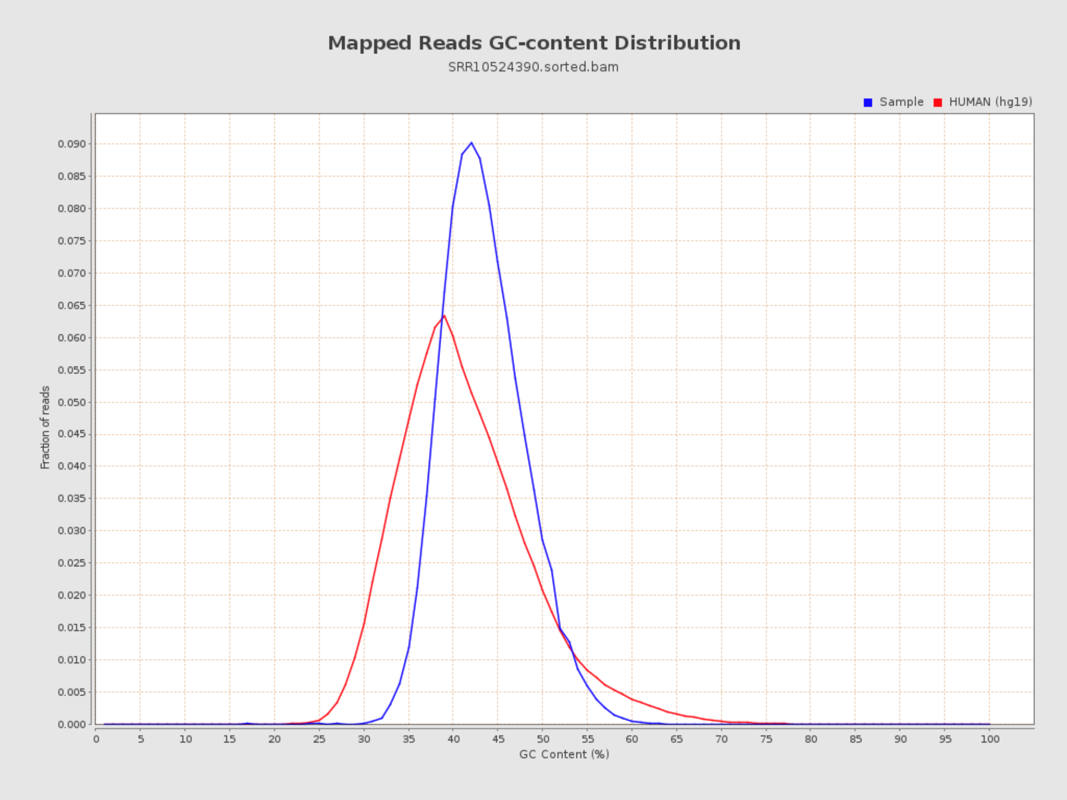
# 7. Results : Duplication Rate Histogram



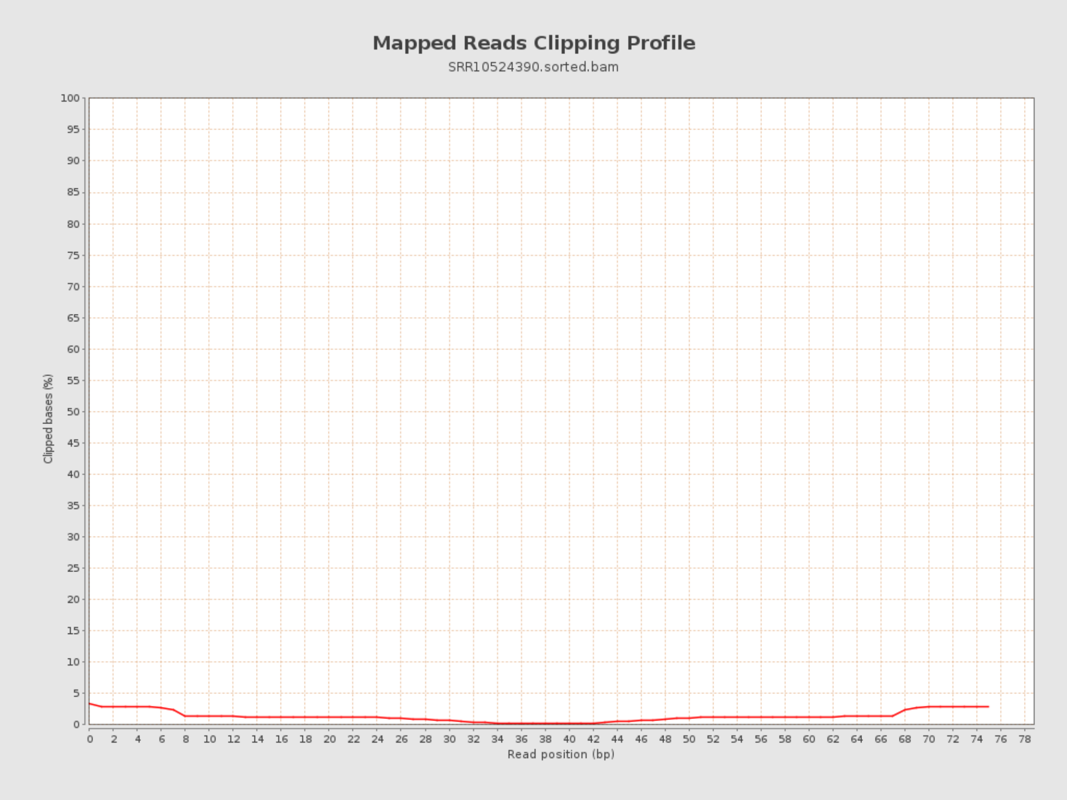
# 8. Results : Mapped Reads Nucleotide Content



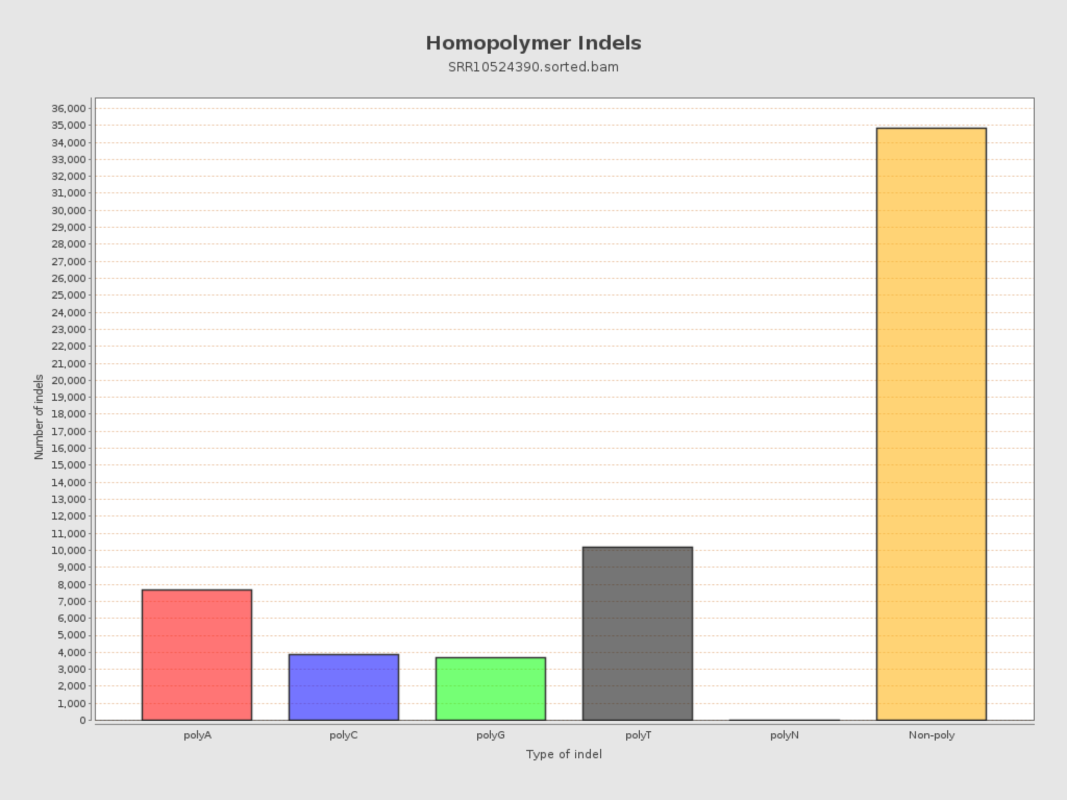
# 9. Results : Mapped Reads GC-content Distribution



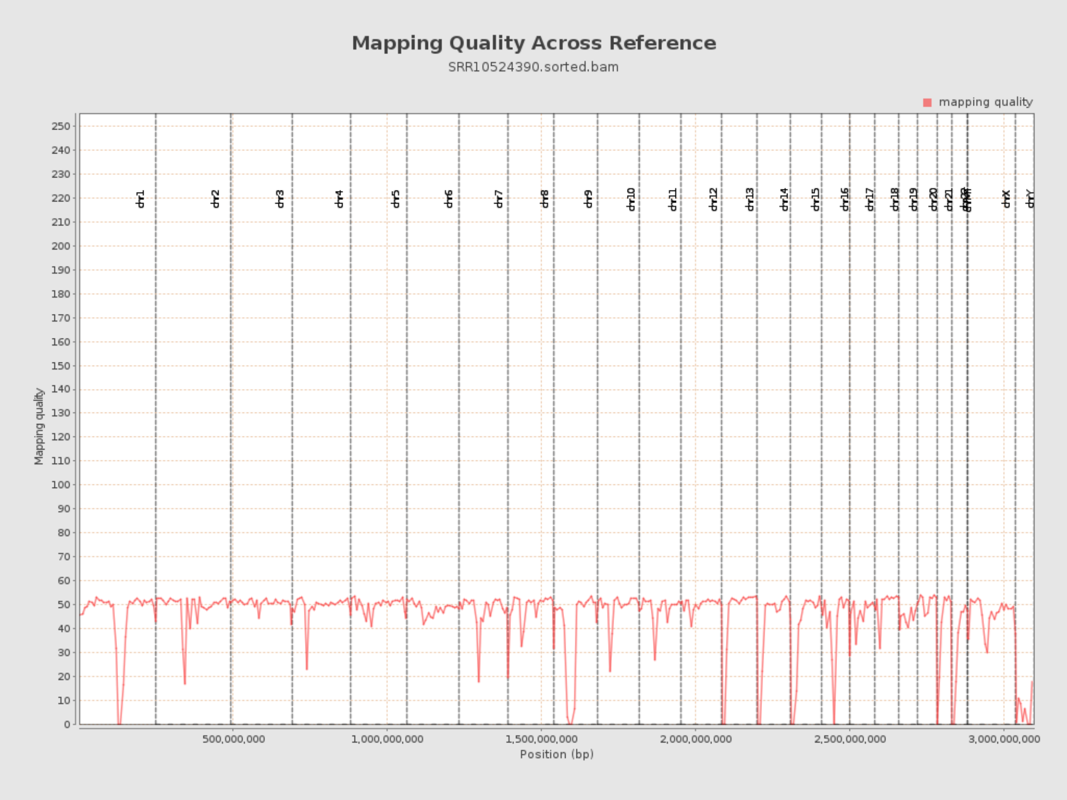
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram