# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 14:33:15*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524642.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_SRR10524642 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524642.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 14:33:11 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524642.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,105,434 |
| Mapped reads | 1,005,648 / 90.97% |
| Unmapped reads | 99,786 / 9.03% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 3,721 / 0.34% |
| Read min/max/mean length | 30 / 76 / 76.11 |
| Duplicated reads (estimated) | 34,584 / 3.13% |
| Duplication rate | 2.65% |
| Clipped reads | 1,006,100 / 91.01% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 14,760,327 / 25.35% |
| Number/percentage of C's | 9,821,279 / 16.86% |
| Number/percentage of T's | 18,843,067 / 32.36% |
| Number/percentage of G's | 14,809,821 / 25.43% |
| Number/percentage of N's | 470 / 0% |
| GC Percentage | 42.3% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0188 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1933 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.6 |

## 2.5. Mismatches and indels

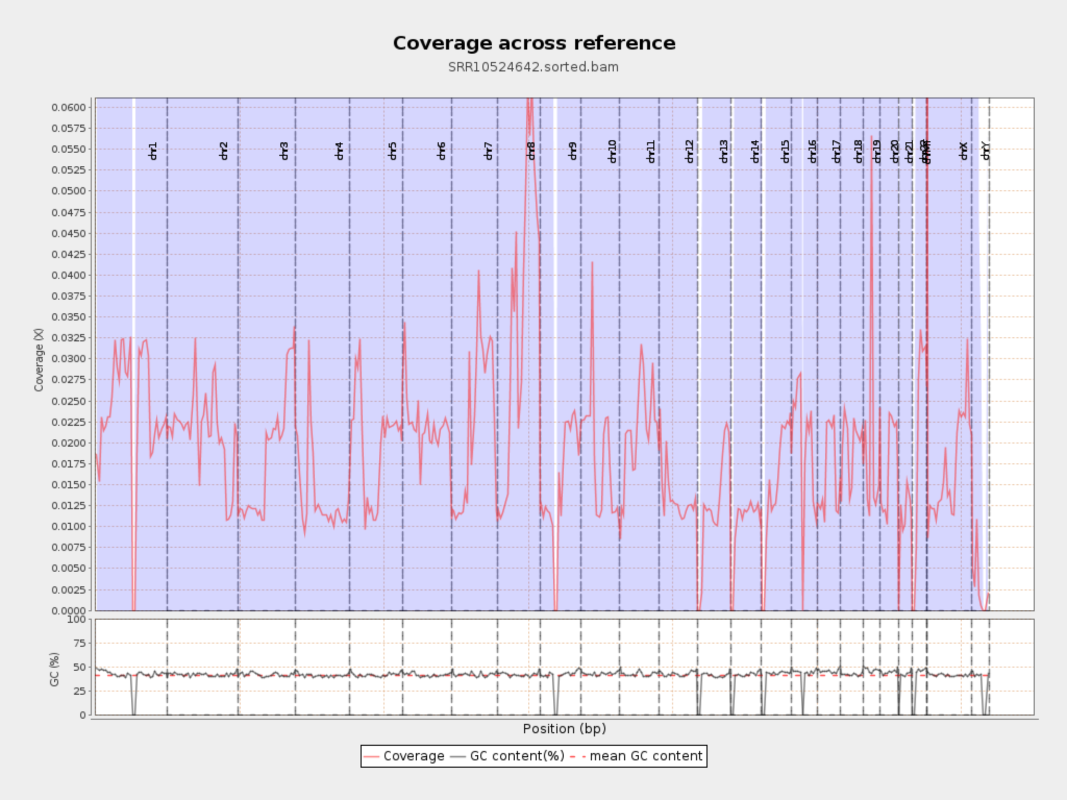
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 295,088 |
| Insertions | 4,012 |
| Mapped reads with at least one insertion | 0.4% |
| Deletions | 11,612 |
| Mapped reads with at least one deletion | 1.14% |
| Homopolymer indels | 43.31% |

## 2.6. Chromosome stats

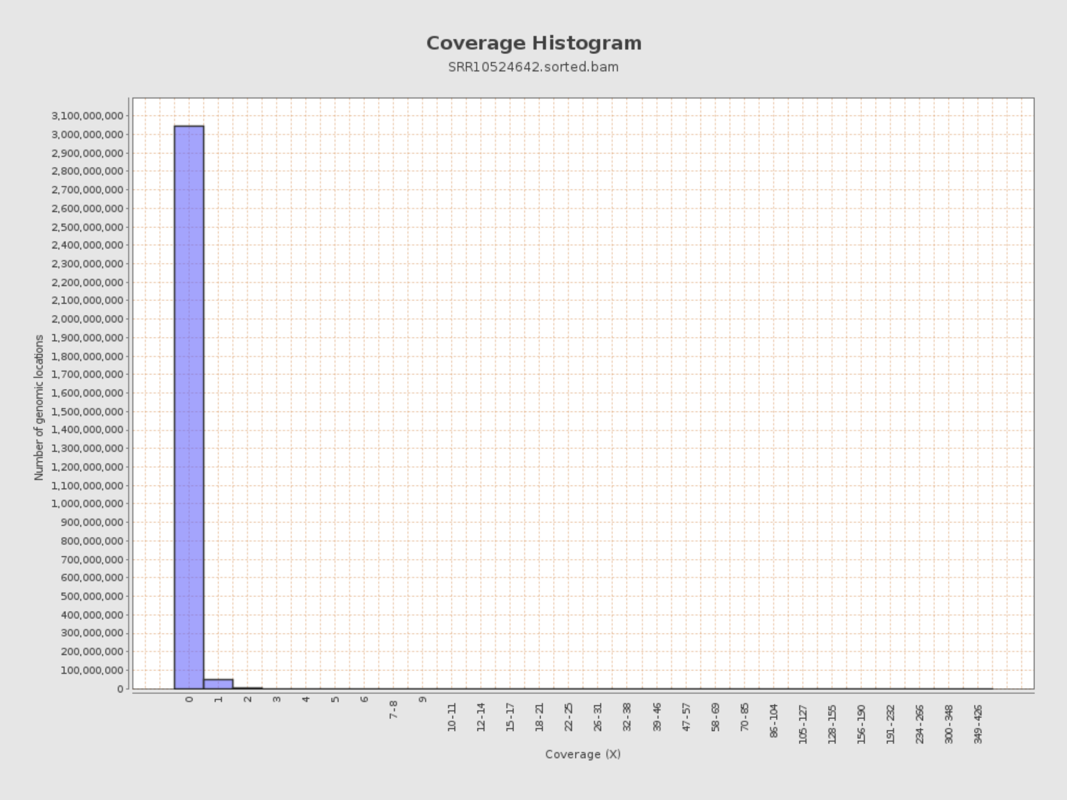
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5898693 | 0.0237 | 0.3285 |
| chr2 | 243199373 | 5175978 | 0.0213 | 0.2322 |
| chr3 | 198022430 | 3625894 | 0.0183 | 0.1462 |
| chr4 | 191154276 | 2648312 | 0.0139 | 0.1439 |
| chr5 | 180915260 | 3602040 | 0.0199 | 0.1509 |
| chr6 | 171115067 | 3792464 | 0.0222 | 0.1678 |
| chr7 | 159138663 | 3536249 | 0.0222 | 0.2326 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 5180571 | 0.0354 | 0.244 |
| chr9 | 141213431 | 2113291 | 0.015 | 0.1574 |
| chr10 | 135534747 | 2572807 | 0.019 | 0.2145 |
| chr11 | 135006516 | 2921730 | 0.0216 | 0.1797 |
| chr12 | 133851895 | 1824818 | 0.0136 | 0.1291 |
| chr13 | 115169878 | 1419173 | 0.0123 | 0.1189 |
| chr14 | 107349540 | 1096023 | 0.0102 | 0.1114 |
| chr15 | 102531392 | 1496800 | 0.0146 | 0.1298 |
| chr16 | 90354753 | 1755498 | 0.0194 | 0.1557 |
| chr17 | 81195210 | 1319476 | 0.0163 | 0.1404 |
| chr18 | 78077248 | 1536174 | 0.0197 | 0.2511 |
| chr19 | 59128983 | 1220737 | 0.0206 | 0.2567 |
| chr20 | 63025520 | 1098886 | 0.0174 | 0.144 |
| chr21 | 48129895 | 530484 | 0.011 | 0.1286 |
| chr22 | 51304566 | 1070375 | 0.0209 | 0.1559 |
| chrMT | 16571 | 4129 | 0.2492 | 0.4884 |
| chrX | 155270560 | 2647927 | 0.0171 | 0.1504 |
| chrY | 59373566 | 166050 | 0.0028 | 0.0979 |

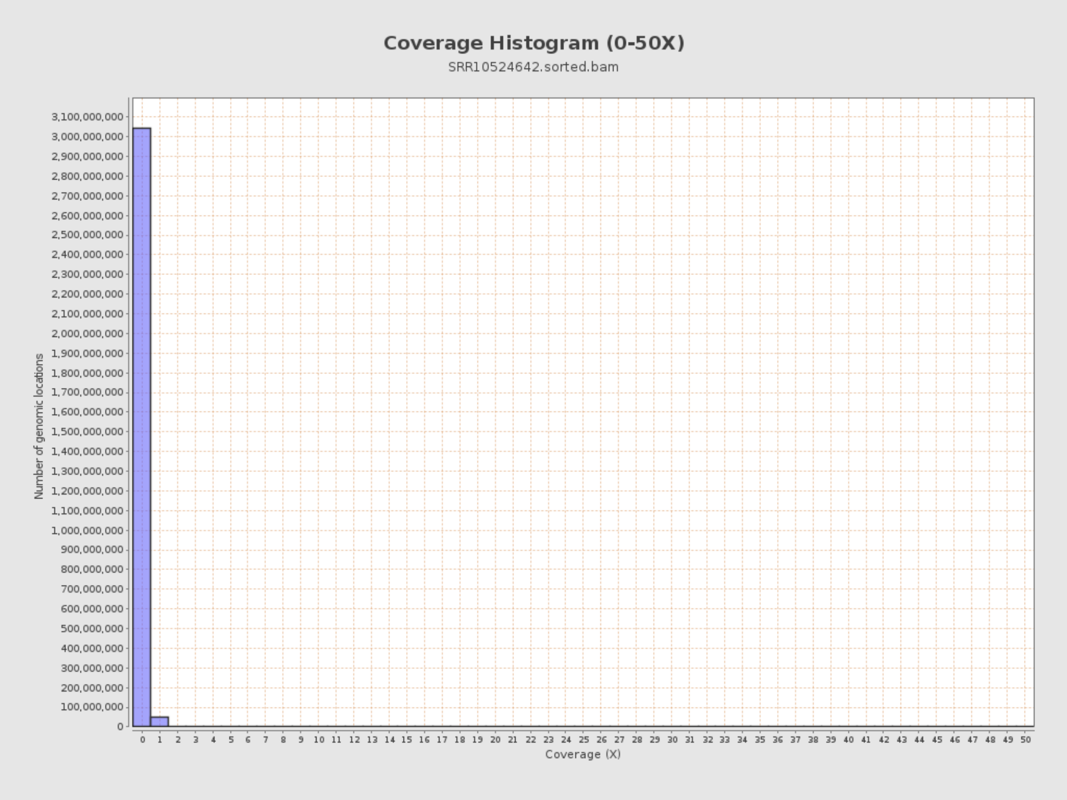
# 3. Results : Coverage across reference



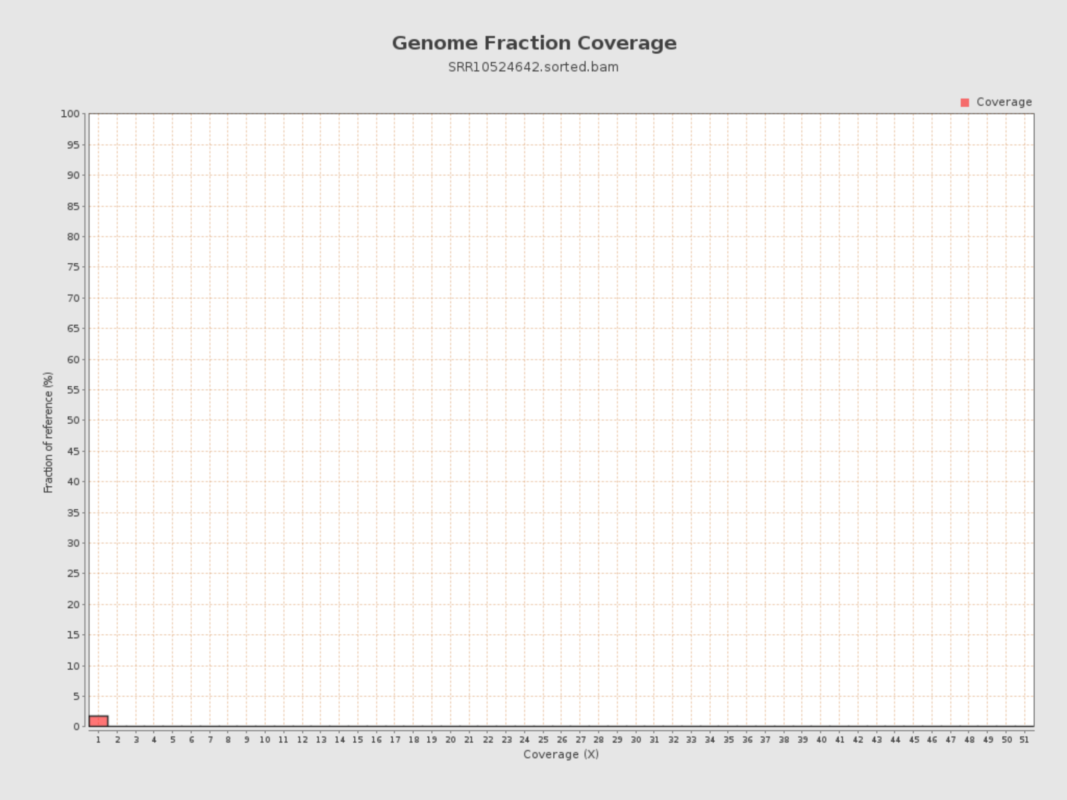
# 4. Results : Coverage Histogram



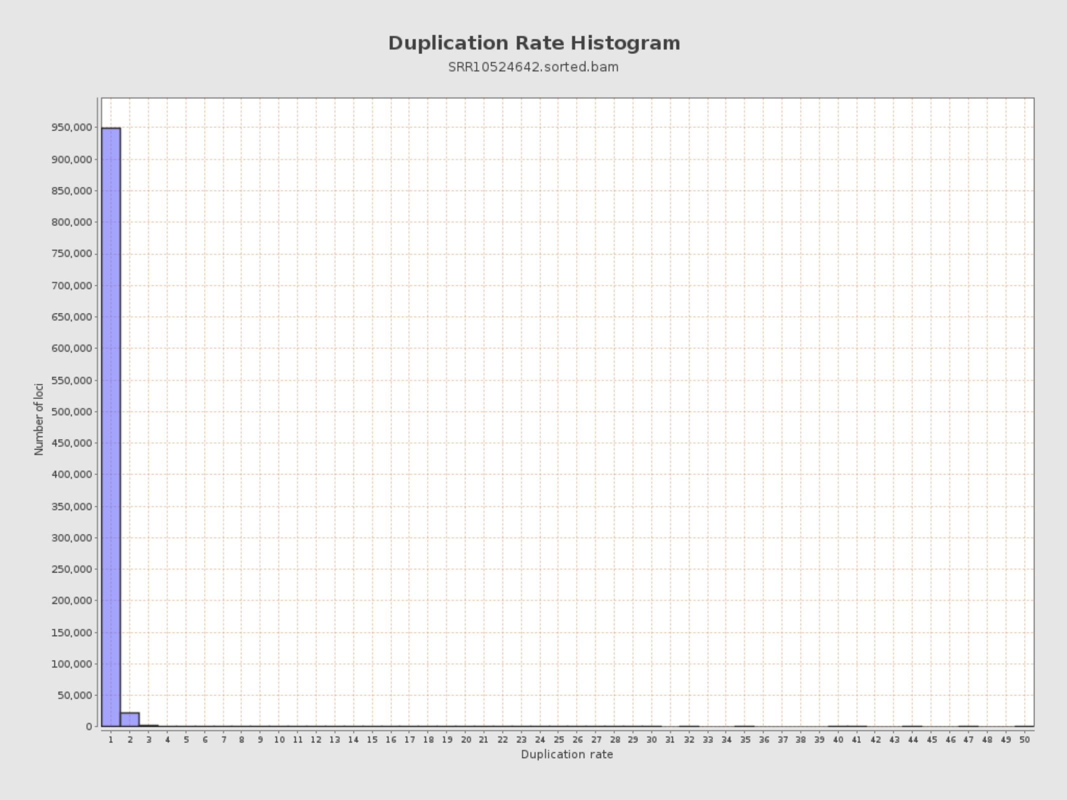
# 5. Results : Coverage Histogram (0-50X)



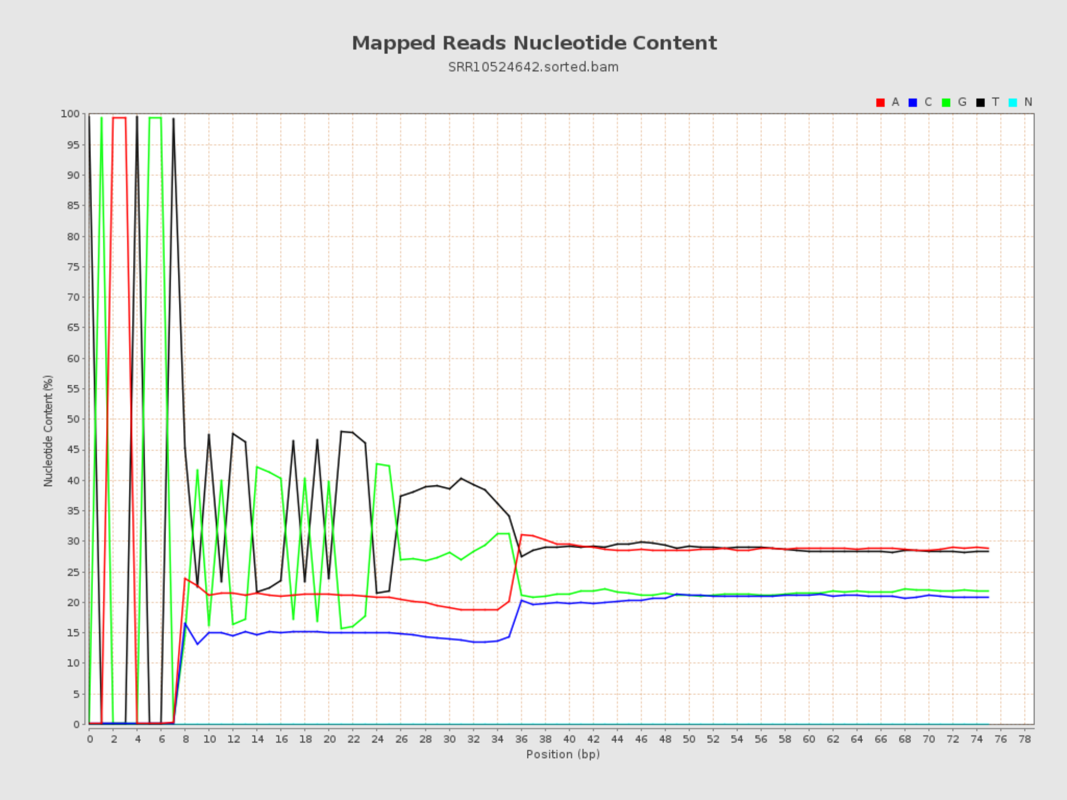
# 6. Results : Genome Fraction Coverage



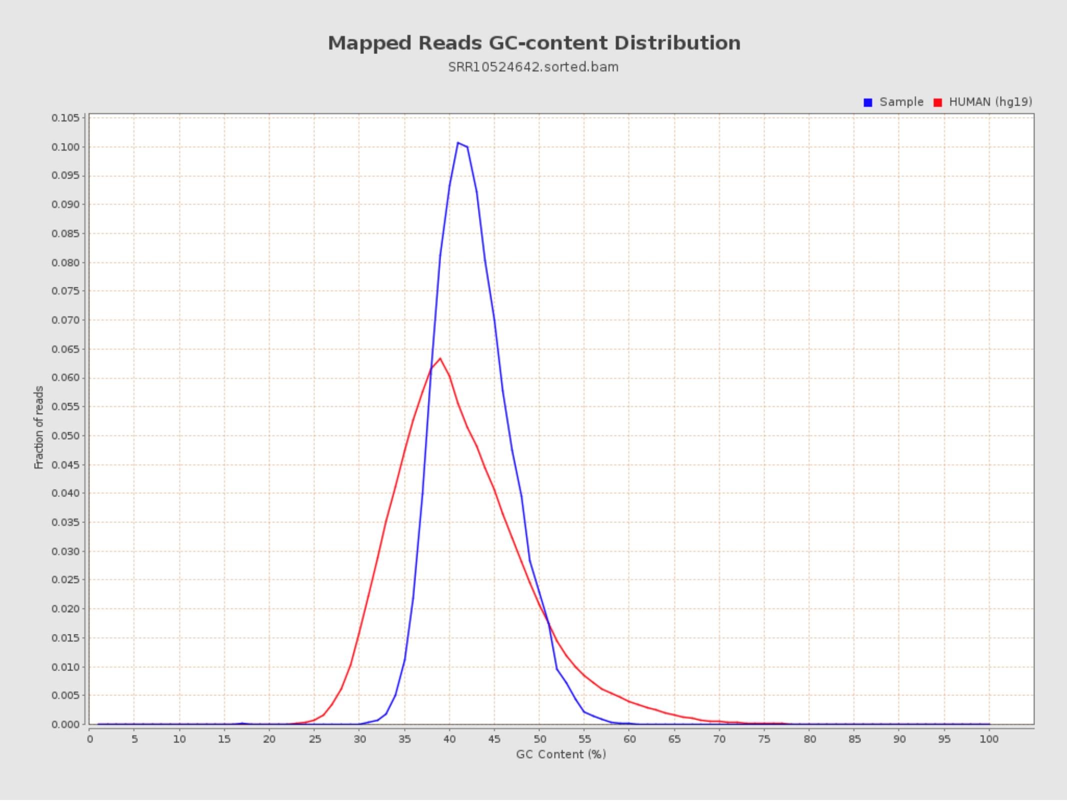
# 7. Results : Duplication Rate Histogram



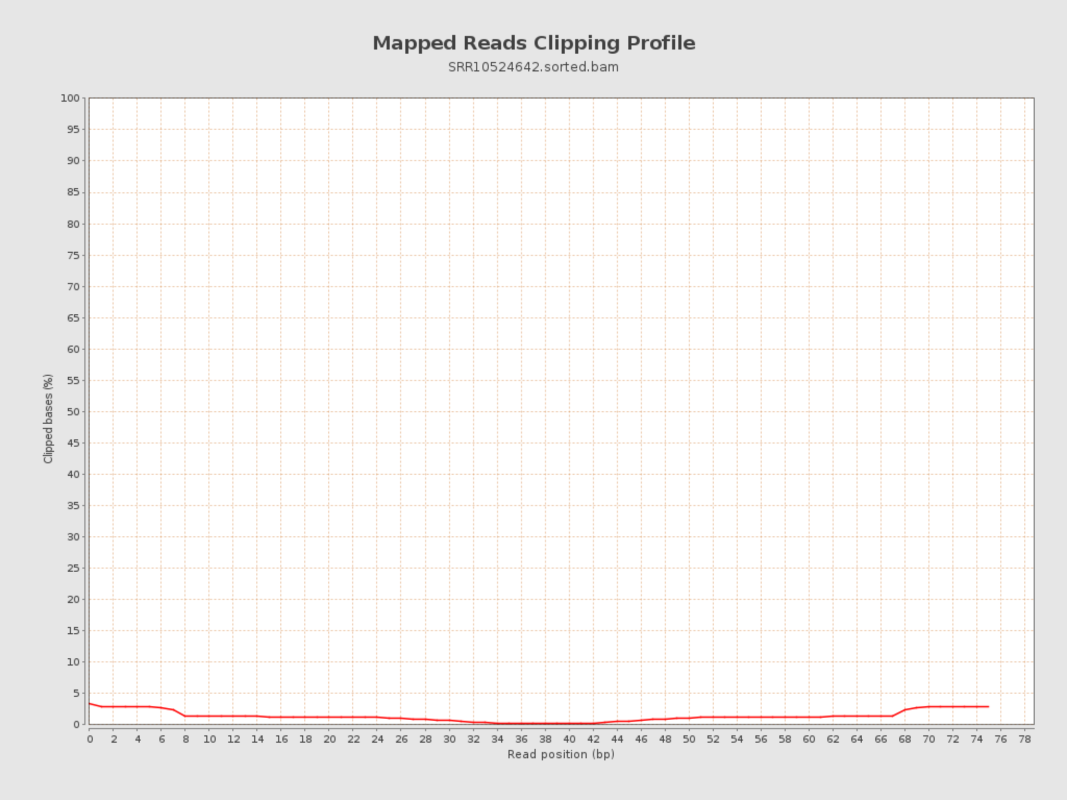
# 8. Results : Mapped Reads Nucleotide Content



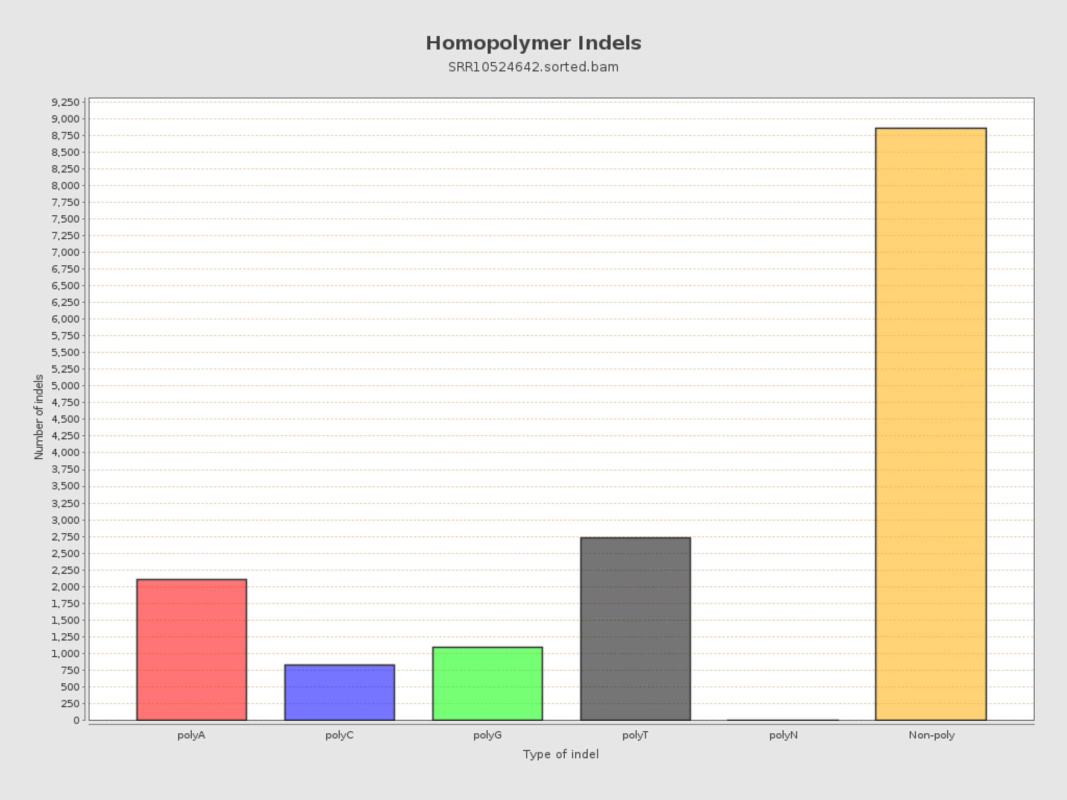
# 9. Results : Mapped Reads GC-content Distribution



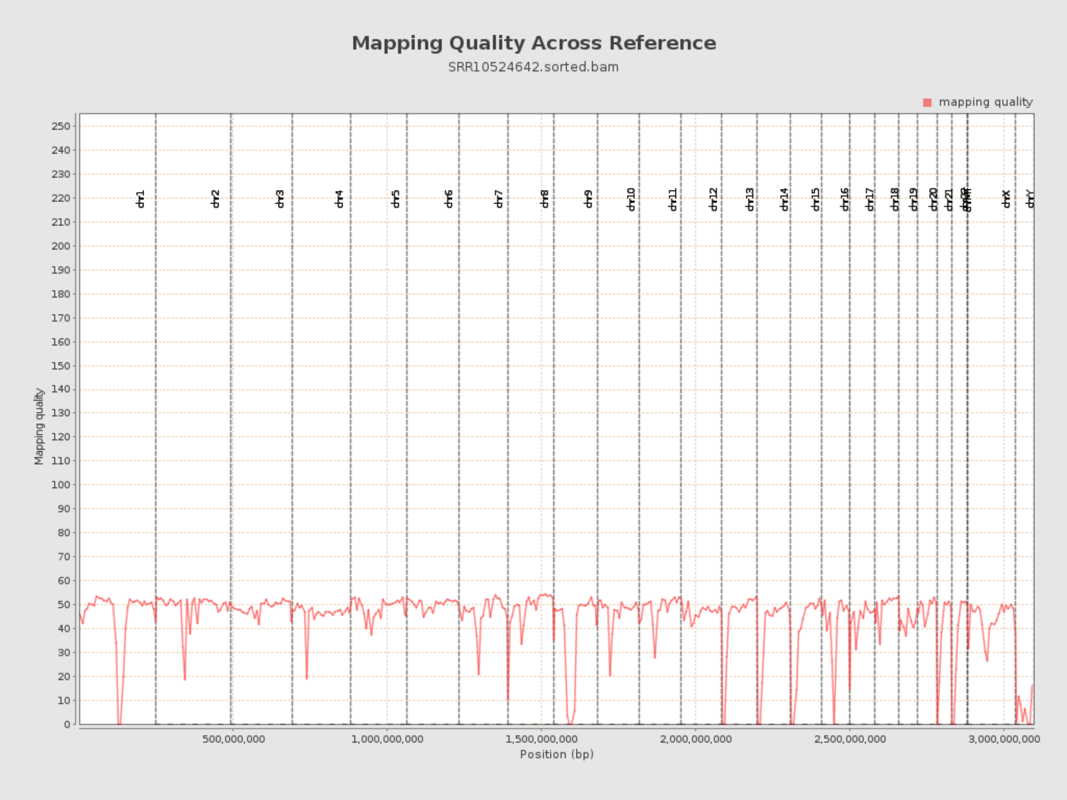
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram