# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 06:50:53*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524505.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_SRR10524505 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524505.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 06:50:52 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524505.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 522,516 |
| Mapped reads | 483,924 / 92.61% |
| Unmapped reads | 38,592 / 7.39% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 1,220 / 0.23% |
| Read min/max/mean length | 30 / 76 / 76.08 |
| Duplicated reads (estimated) | 9,302 / 1.78% |
| Duplication rate | 1.48% |
| Clipped reads | 483,814 / 92.59% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 7,360,344 / 25.92% |
| Number/percentage of C's | 5,543,394 / 19.52% |
| Number/percentage of T's | 8,808,917 / 31.02% |
| Number/percentage of G's | 6,681,973 / 23.53% |
| Number/percentage of N's | 466 / 0% |
| GC Percentage | 43.05% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0092 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1173 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.45 |

## 2.5. Mismatches and indels

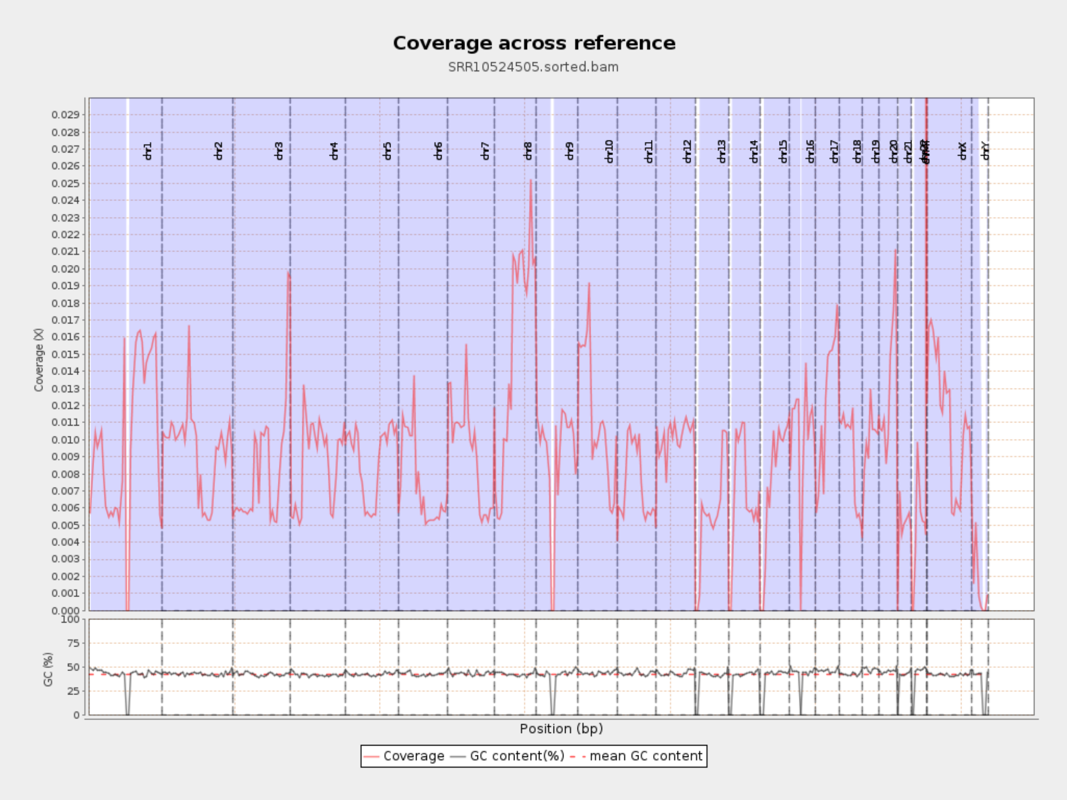
| | |
|---|---|
| General error rate | 0.47% |
| Mismatches | 130,540 |
| Insertions | 2,030 |
| Mapped reads with at least one insertion | 0.42% |
| Deletions | 5,227 |
| Mapped reads with at least one deletion | 1.07% |
| Homopolymer indels | 44.52% |

## 2.6. Chromosome stats

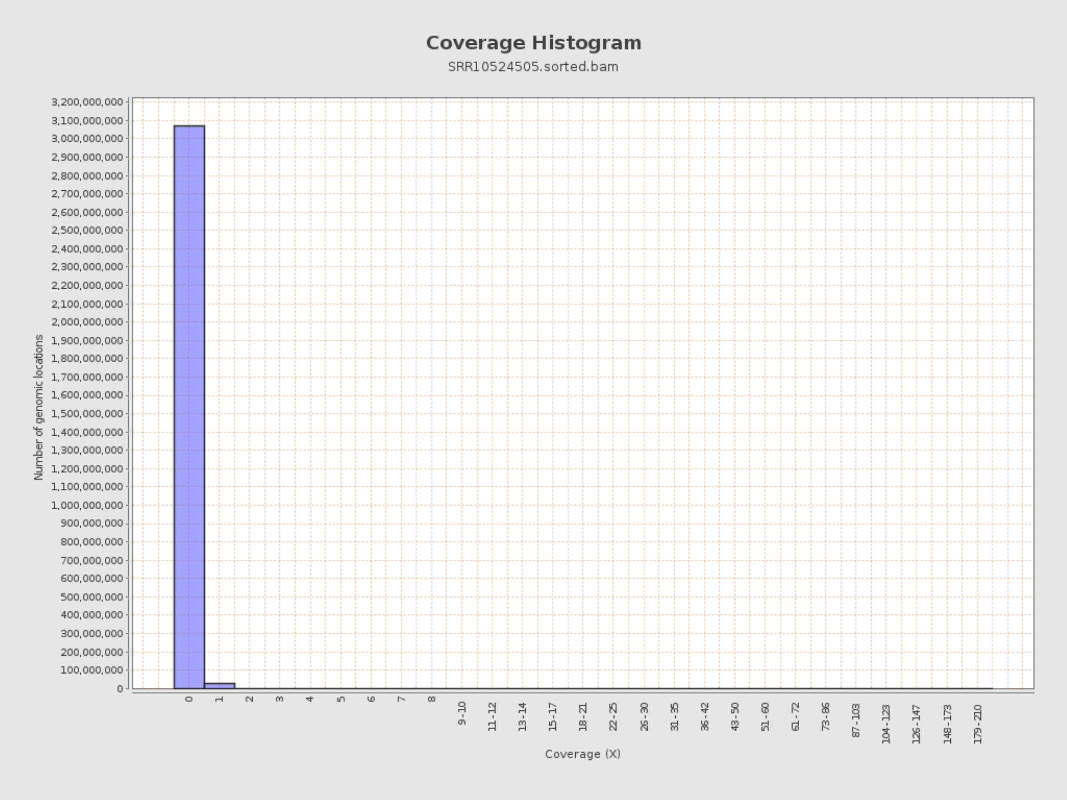
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 2472252 | 0.0099 | 0.1788 |
| chr2 | 243199373 | 2293617 | 0.0094 | 0.1253 |
| chr3 | 198022430 | 1619024 | 0.0082 | 0.0938 |
| chr4 | 191154276 | 1669128 | 0.0087 | 0.1011 |
| chr5 | 180915260 | 1600181 | 0.0088 | 0.0974 |
| chr6 | 171115067 | 1262613 | 0.0074 | 0.0984 |
| chr7 | 159138663 | 1472374 | 0.0093 | 0.1322 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2264298 | 0.0155 | 0.1364 |
| chr9 | 141213431 | 1260671 | 0.0089 | 0.11 |
| chr10 | 135534747 | 1541554 | 0.0114 | 0.1294 |
| chr11 | 135006516 | 1002747 | 0.0074 | 0.1096 |
| chr12 | 133851895 | 1366927 | 0.0102 | 0.1045 |
| chr13 | 115169878 | 657327 | 0.0057 | 0.0783 |
| chr14 | 107349540 | 712573 | 0.0066 | 0.0851 |
| chr15 | 102531392 | 766526 | 0.0075 | 0.0898 |
| chr16 | 90354753 | 925039 | 0.0102 | 0.1085 |
| chr17 | 81195210 | 1009758 | 0.0124 | 0.1173 |
| chr18 | 78077248 | 713407 | 0.0091 | 0.1503 |
| chr19 | 59128983 | 588869 | 0.01 | 0.1371 |
| chr20 | 63025520 | 837013 | 0.0133 | 0.1199 |
| chr21 | 48129895 | 236133 | 0.0049 | 0.0751 |
| chr22 | 51304566 | 236341 | 0.0046 | 0.07 |
| chrMT | 16571 | 35131 | 2.12 | 1.8253 |
| chrX | 155270560 | 1772687 | 0.0114 | 0.115 |
| chrY | 59373566 | 87976 | 0.0015 | 0.0502 |

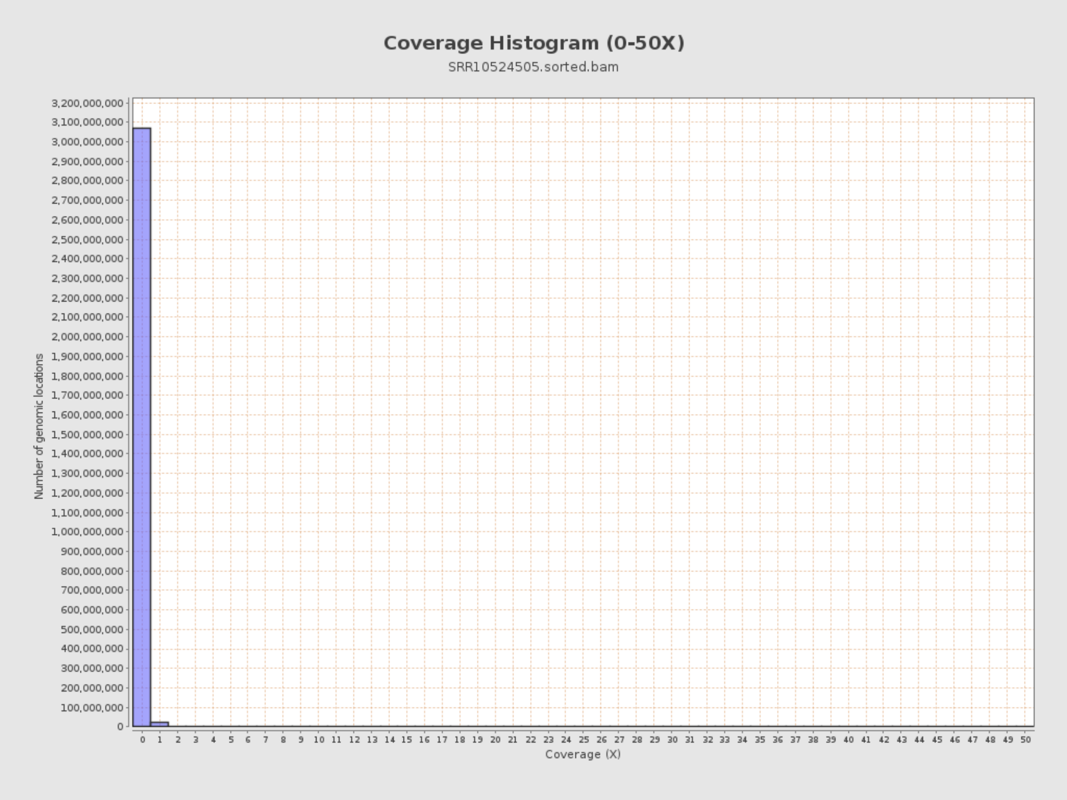
# 3. Results : Coverage across reference



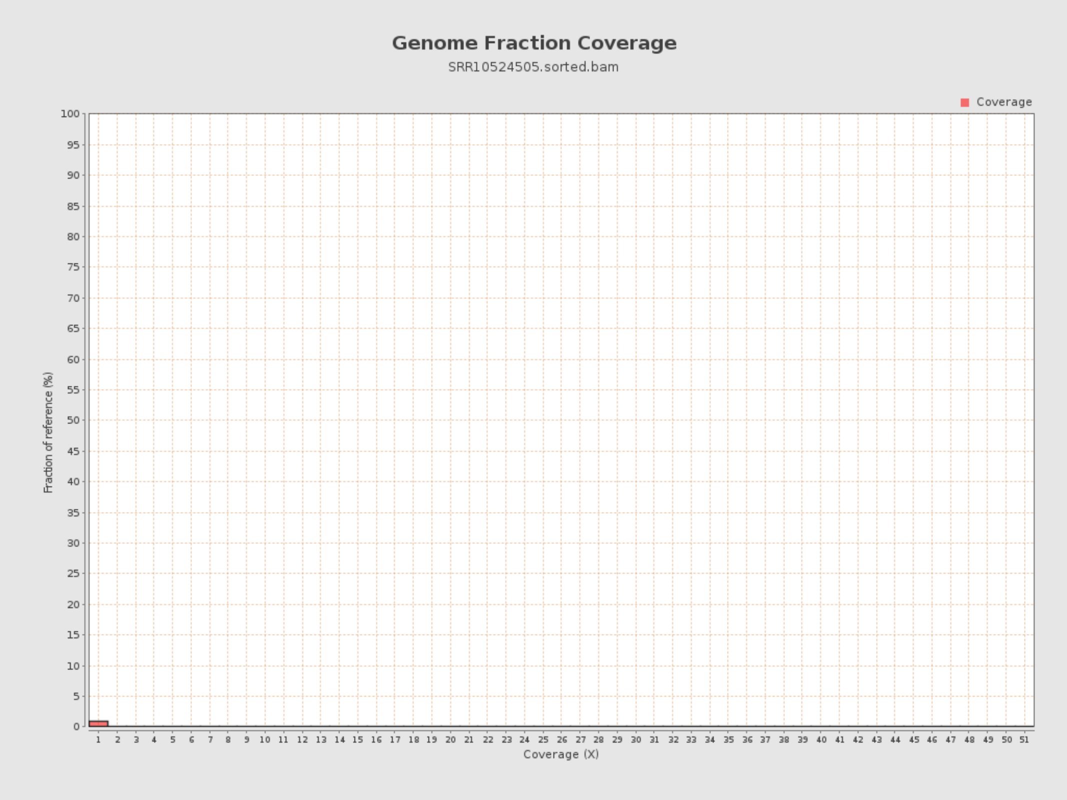
# 4. Results : Coverage Histogram



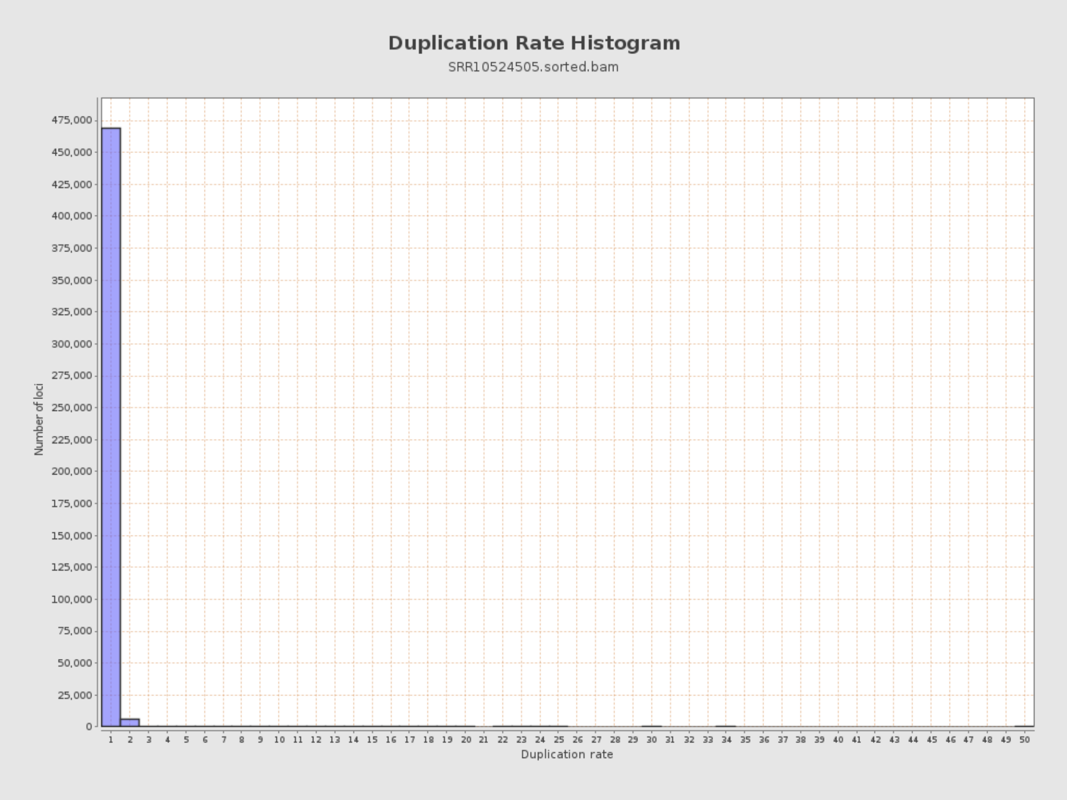
# 5. Results : Coverage Histogram (0-50X)



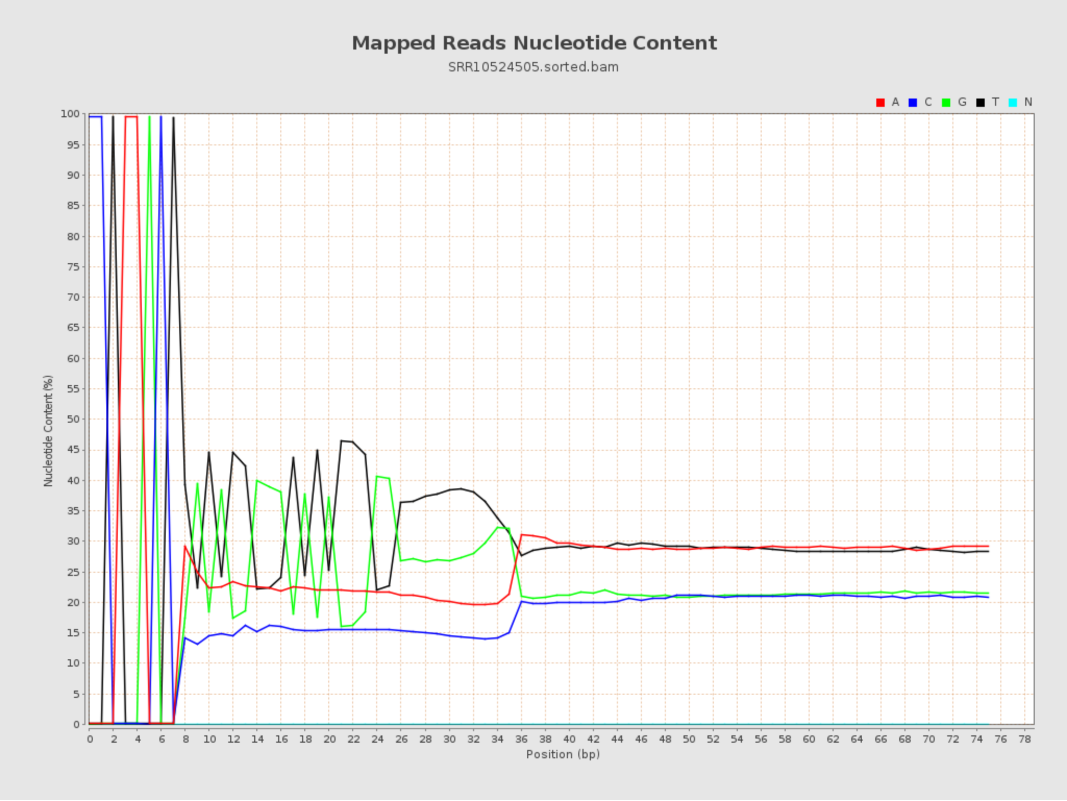
# 6. Results : Genome Fraction Coverage



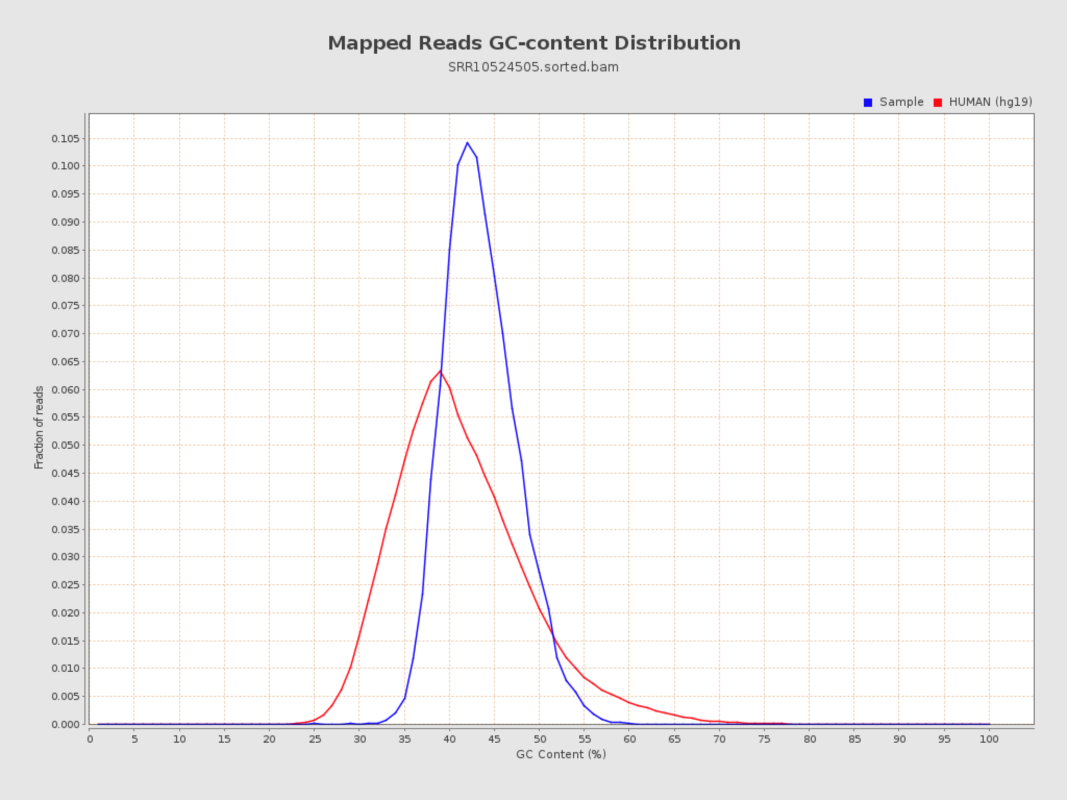
# 7. Results : Duplication Rate Histogram



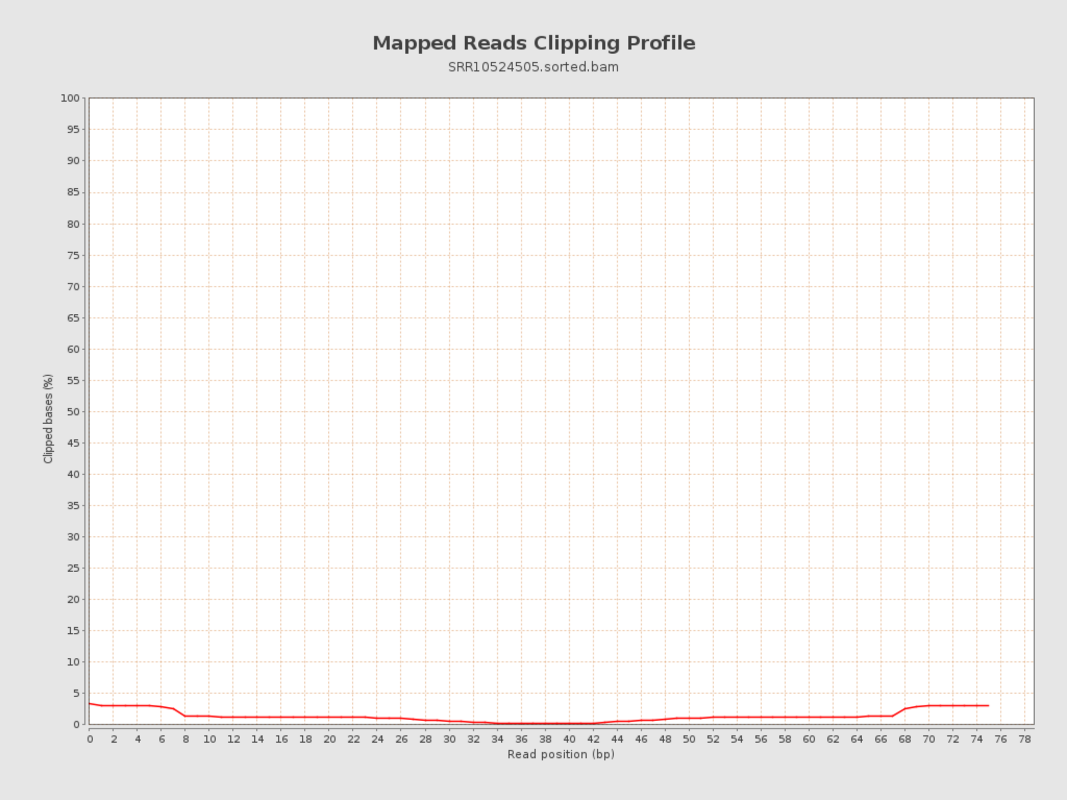
# 8. Results : Mapped Reads Nucleotide Content



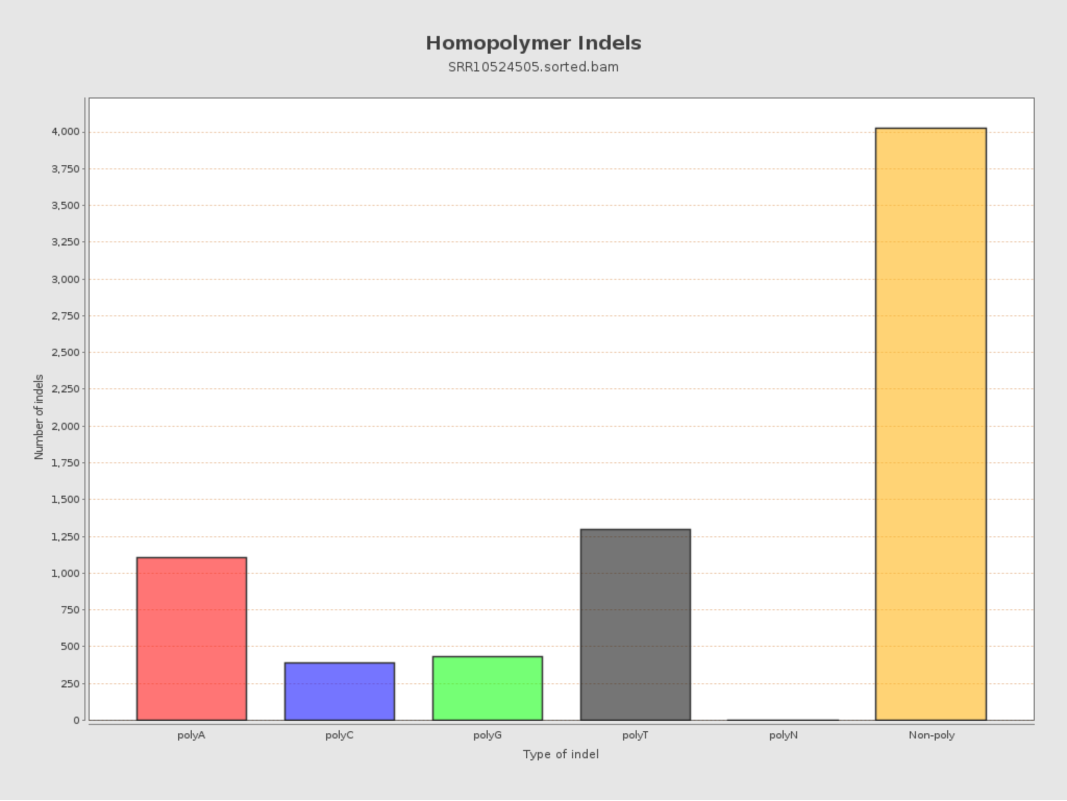
# 9. Results : Mapped Reads GC-content Distribution



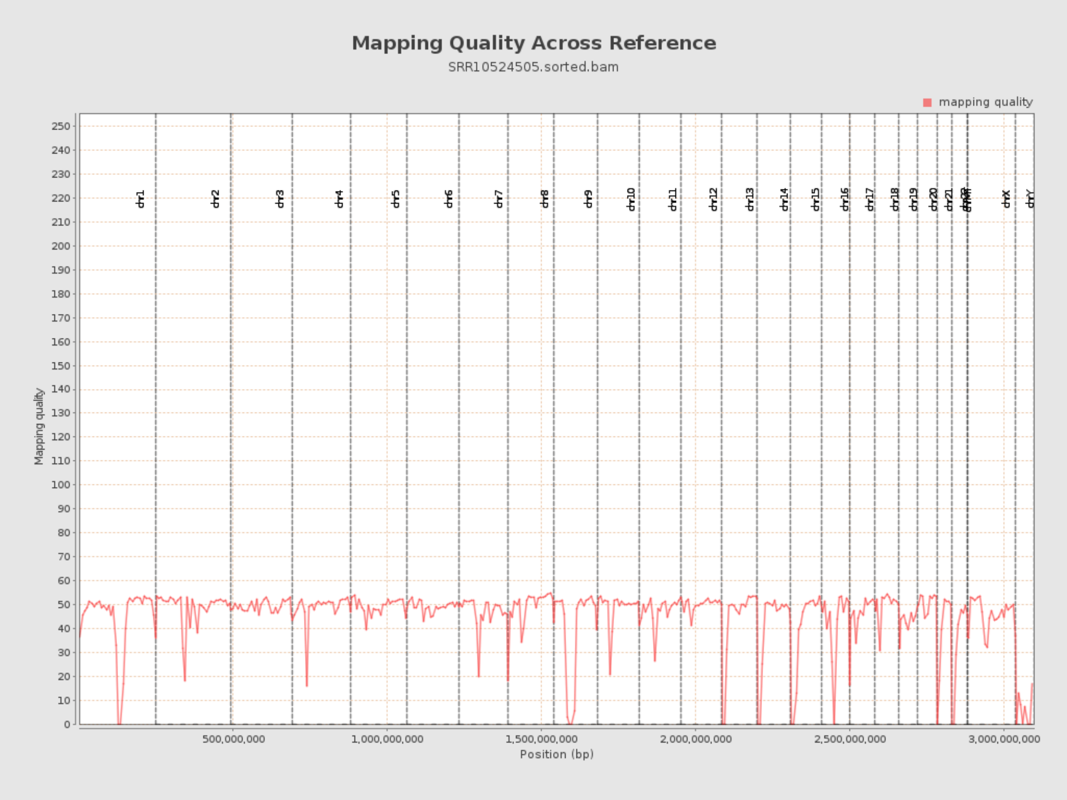
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram