# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 21:12:58*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524803.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_SRR10524803 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524803.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 21:12:58 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524803.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,009,502 |
| Mapped reads | 922,971 / 91.43% |
| Unmapped reads | 86,531 / 8.57% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 3,223 / 0.32% |
| Read min/max/mean length | 30 / 76 / 76.11 |
| Duplicated reads (estimated) | 29,455 / 2.92% |
| Duplication rate | 2.51% |
| Clipped reads | 923,735 / 91.5% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 12,236,227 / 23.18% |
| Number/percentage of C's | 9,287,018 / 17.59% |
| Number/percentage of T's | 17,610,075 / 33.36% |
| Number/percentage of G's | 13,654,671 / 25.86% |
| Number/percentage of N's | 6,562 / 0.01% |
| GC Percentage | 43.45% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0171 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1725 |

## 2.4. Mapping Quality

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

## 2.5. Mismatches and indels

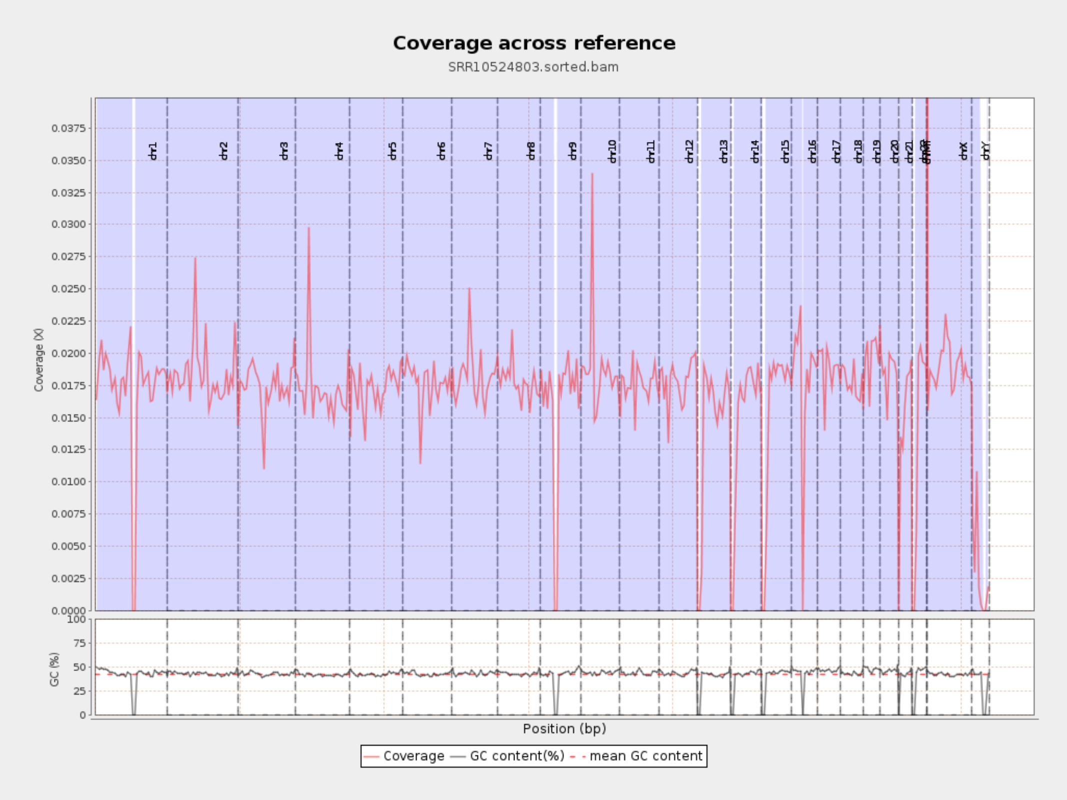
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 266,817 |
| Insertions | 3,657 |
| Mapped reads with at least one insertion | 0.39% |
| Deletions | 10,265 |
| Mapped reads with at least one deletion | 1.11% |
| Homopolymer indels | 43.71% |

## 2.6. Chromosome stats

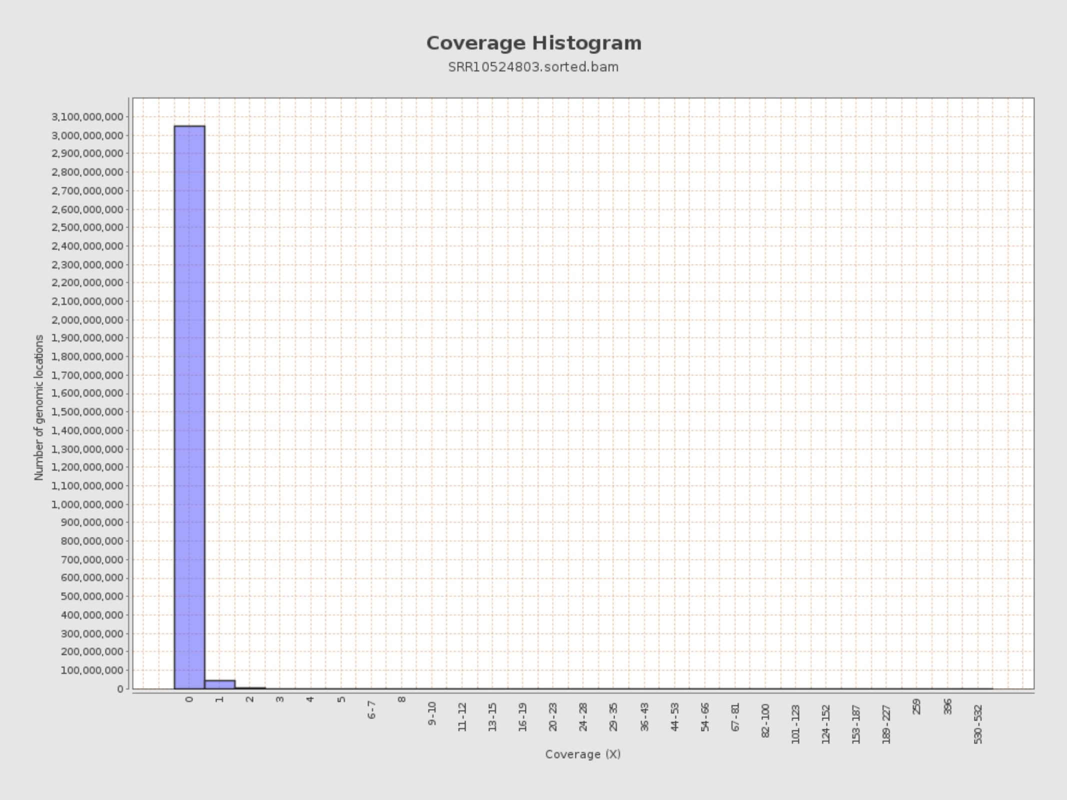
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 4271686 | 0.0171 | 0.2148 |
| chr2 | 243199373 | 4473555 | 0.0184 | 0.2645 |
| chr3 | 198022430 | 3440005 | 0.0174 | 0.1424 |
| chr4 | 191154276 | 3315747 | 0.0173 | 0.1524 |
| chr5 | 180915260 | 3147284 | 0.0174 | 0.1419 |
| chr6 | 171115067 | 3005304 | 0.0176 | 0.1526 |
| chr7 | 159138663 | 2908043 | 0.0183 | 0.1922 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2598667 | 0.0178 | 0.1667 |
| chr9 | 141213431 | 2219666 | 0.0157 | 0.1516 |
| chr10 | 135534747 | 2556719 | 0.0189 | 0.1918 |
| chr11 | 135006516 | 2384781 | 0.0177 | 0.1606 |
| chr12 | 133851895 | 2384298 | 0.0178 | 0.1447 |
| chr13 | 115169878 | 1623838 | 0.0141 | 0.1286 |
| chr14 | 107349540 | 1568860 | 0.0146 | 0.1317 |
| chr15 | 102531392 | 1544305 | 0.0151 | 0.1323 |
| chr16 | 90354753 | 1600322 | 0.0177 | 0.1529 |
| chr17 | 81195210 | 1530787 | 0.0189 | 0.1521 |
| chr18 | 78077248 | 1384673 | 0.0177 | 0.2248 |
| chr19 | 59128983 | 1165753 | 0.0197 | 0.1898 |
| chr20 | 63025520 | 1162406 | 0.0184 | 0.151 |
| chr21 | 48129895 | 706612 | 0.0147 | 0.1375 |
| chr22 | 51304566 | 691761 | 0.0135 | 0.1271 |
| chrMT | 16571 | 6952 | 0.4195 | 0.6791 |
| chrX | 155270560 | 2942261 | 0.0189 | 0.1549 |
| chrY | 59373566 | 177001 | 0.003 | 0.0942 |

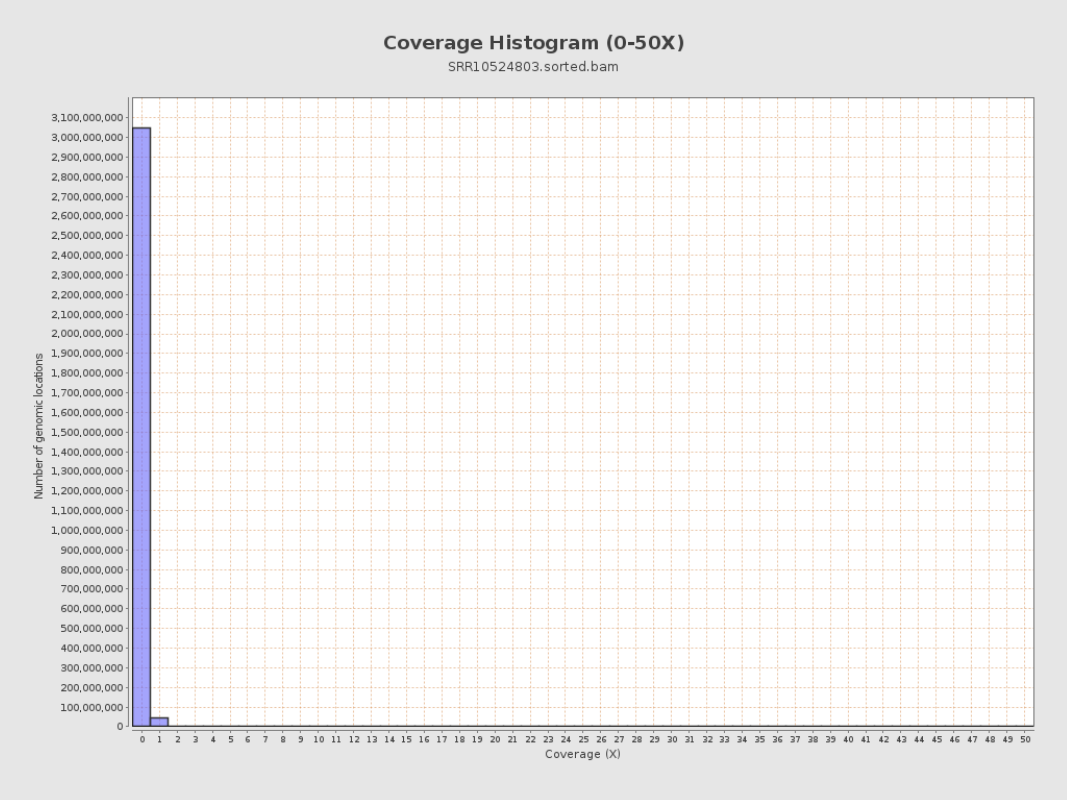
# 3. Results : Coverage across reference



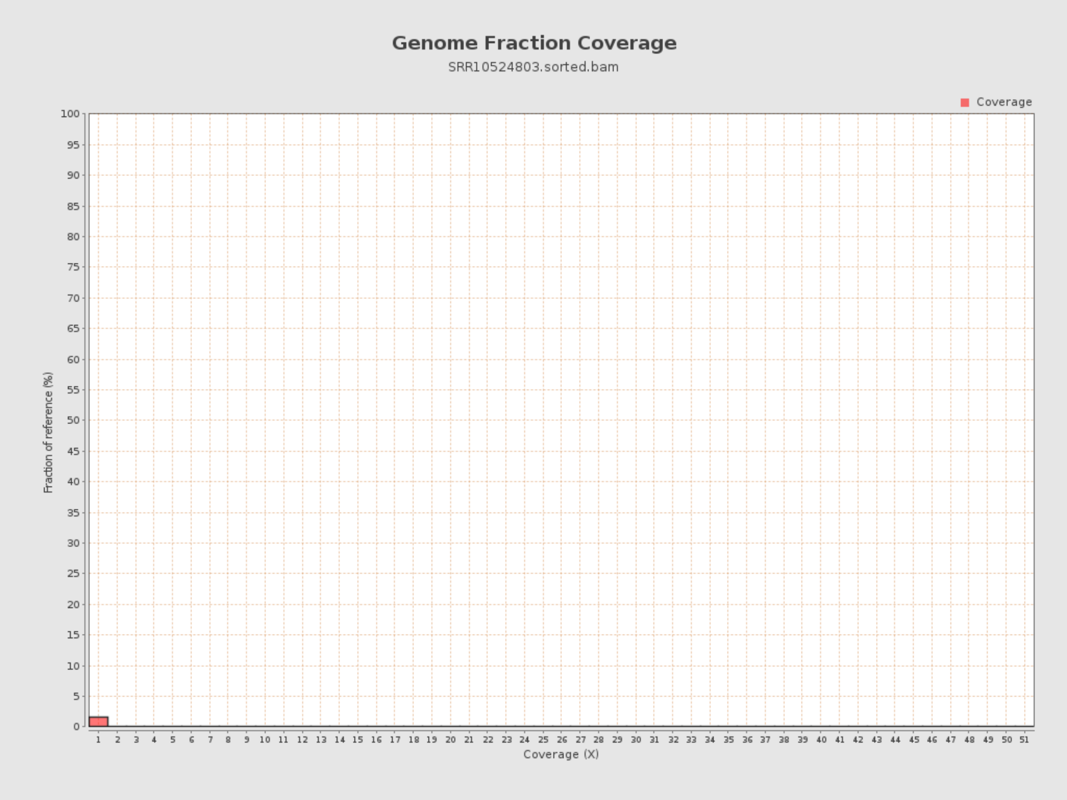
# 4. Results : Coverage Histogram



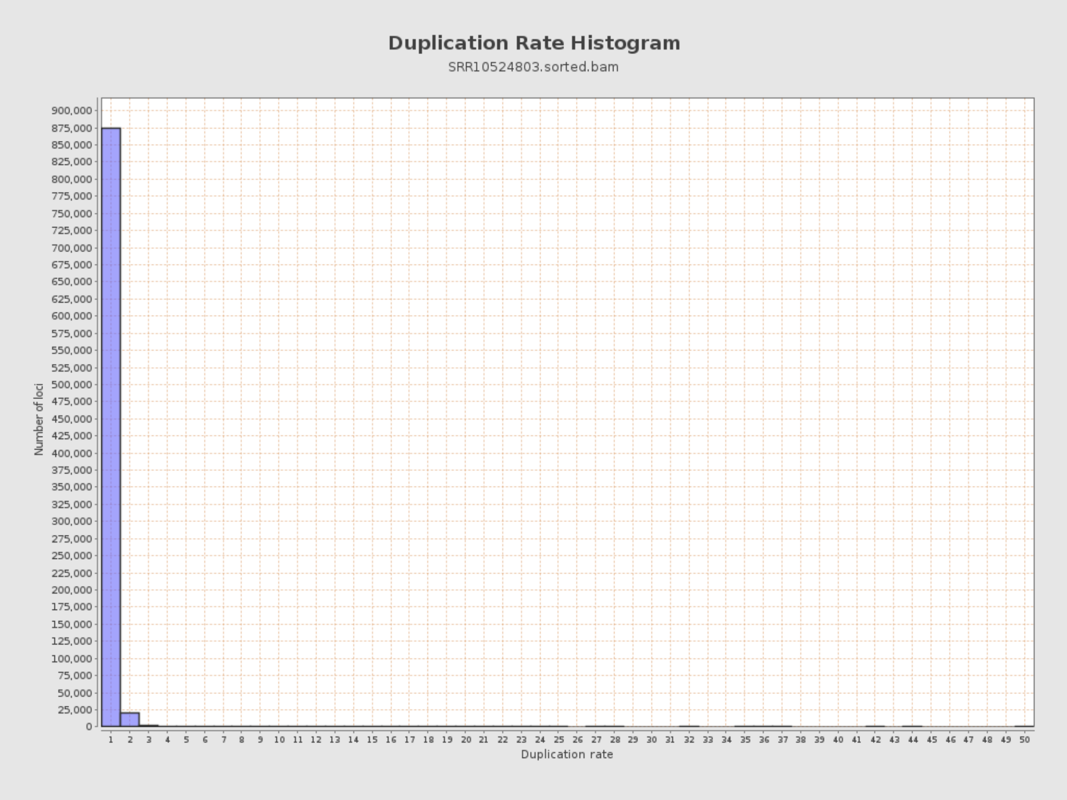
# 5. Results : Coverage Histogram (0-50X)



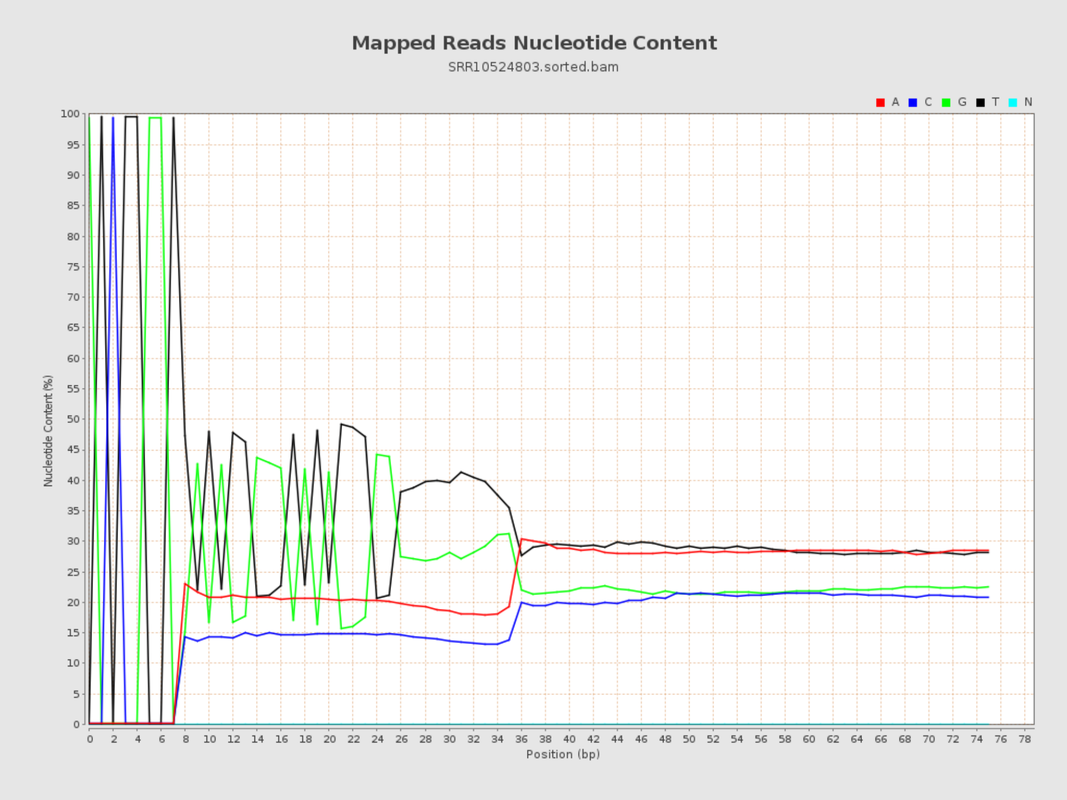
# 6. Results : Genome Fraction Coverage



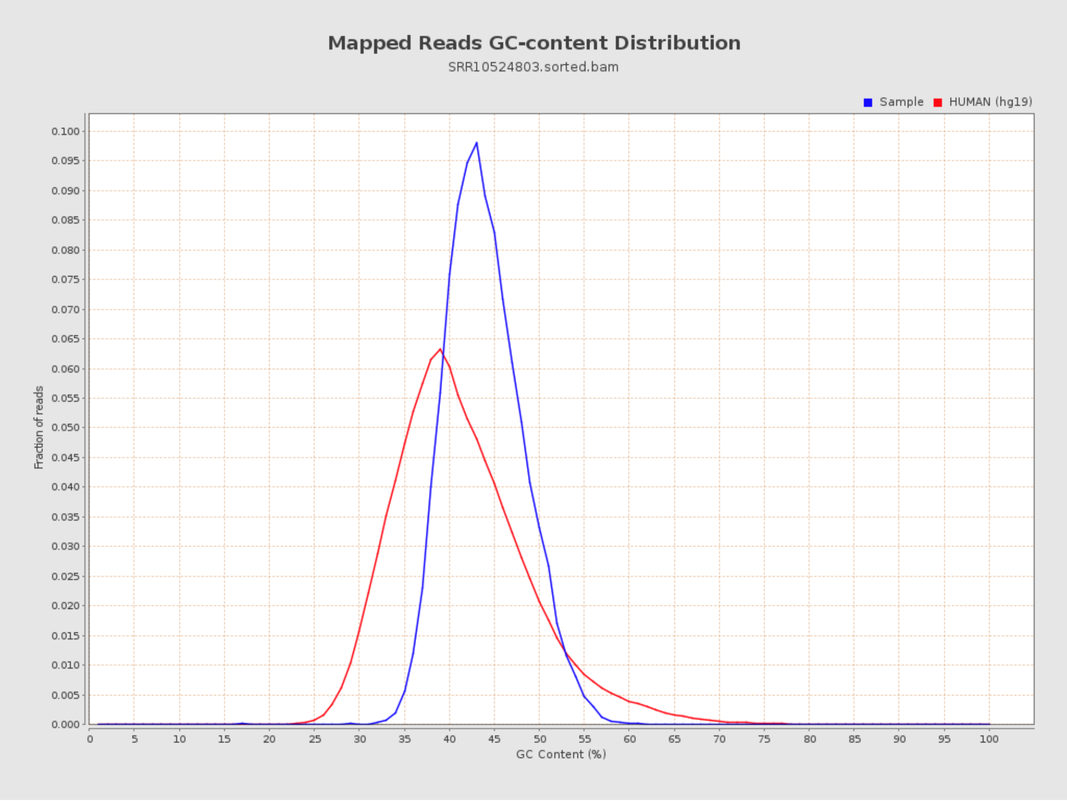
# 7. Results : Duplication Rate Histogram



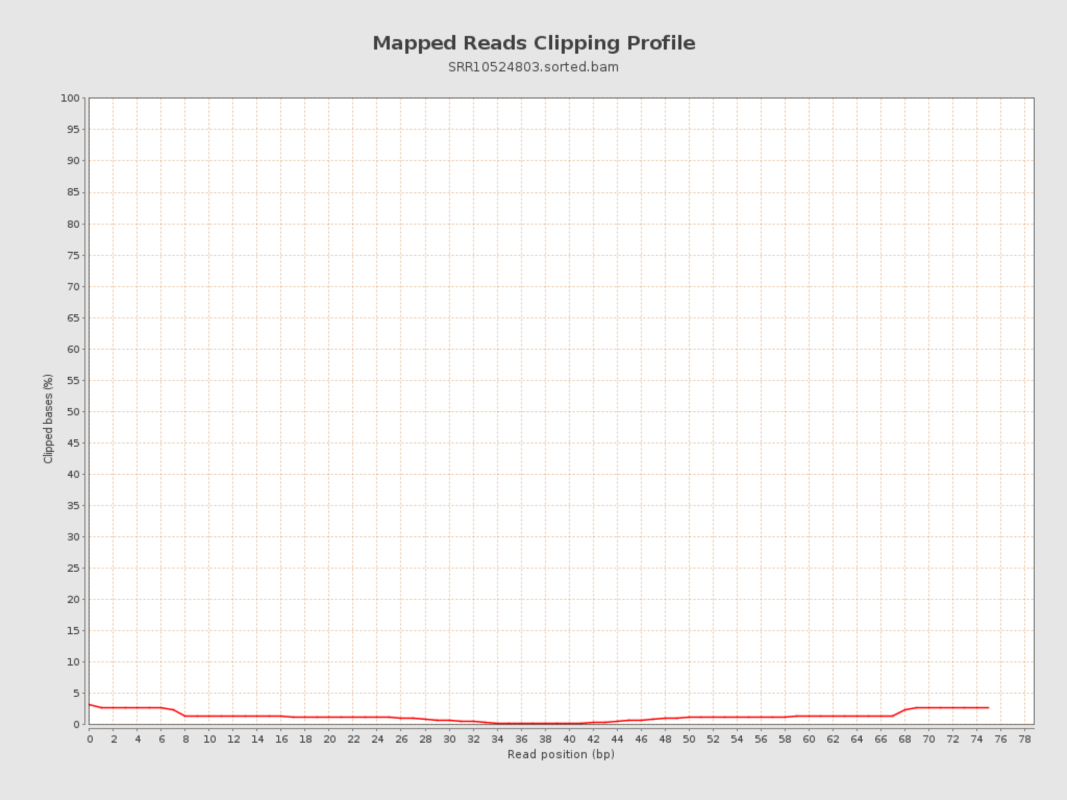
# 8. Results : Mapped Reads Nucleotide Content



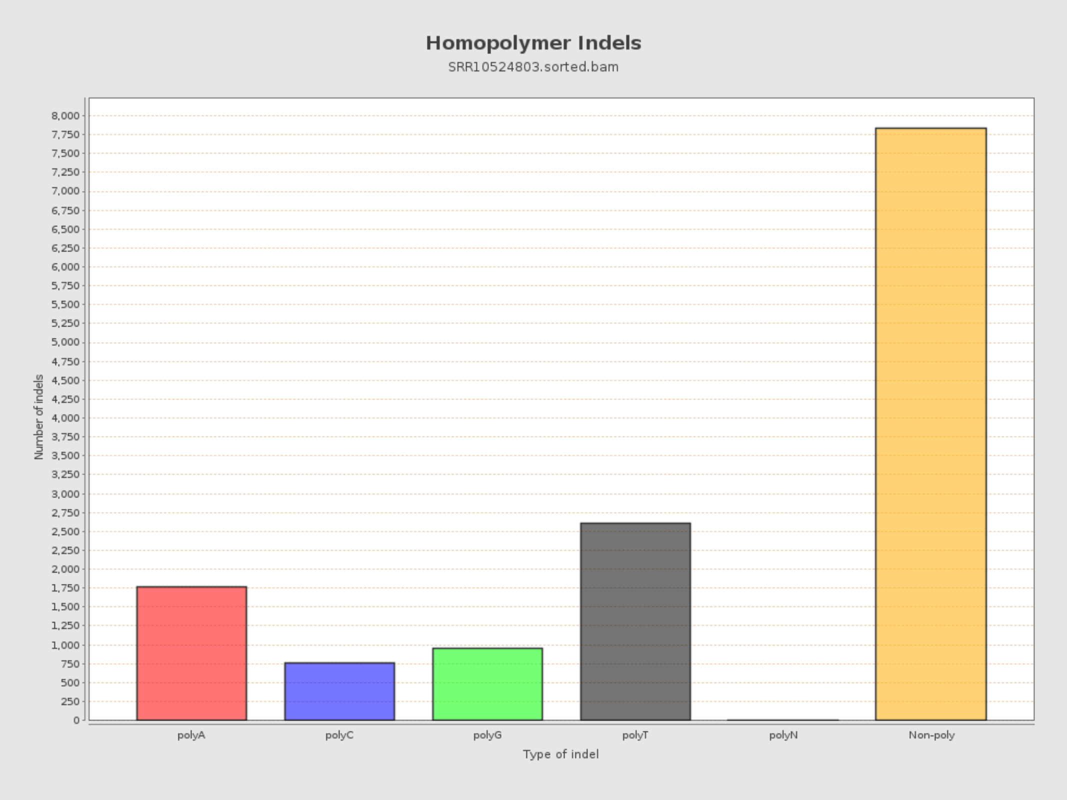
# 9. Results : Mapped Reads GC-content Distribution



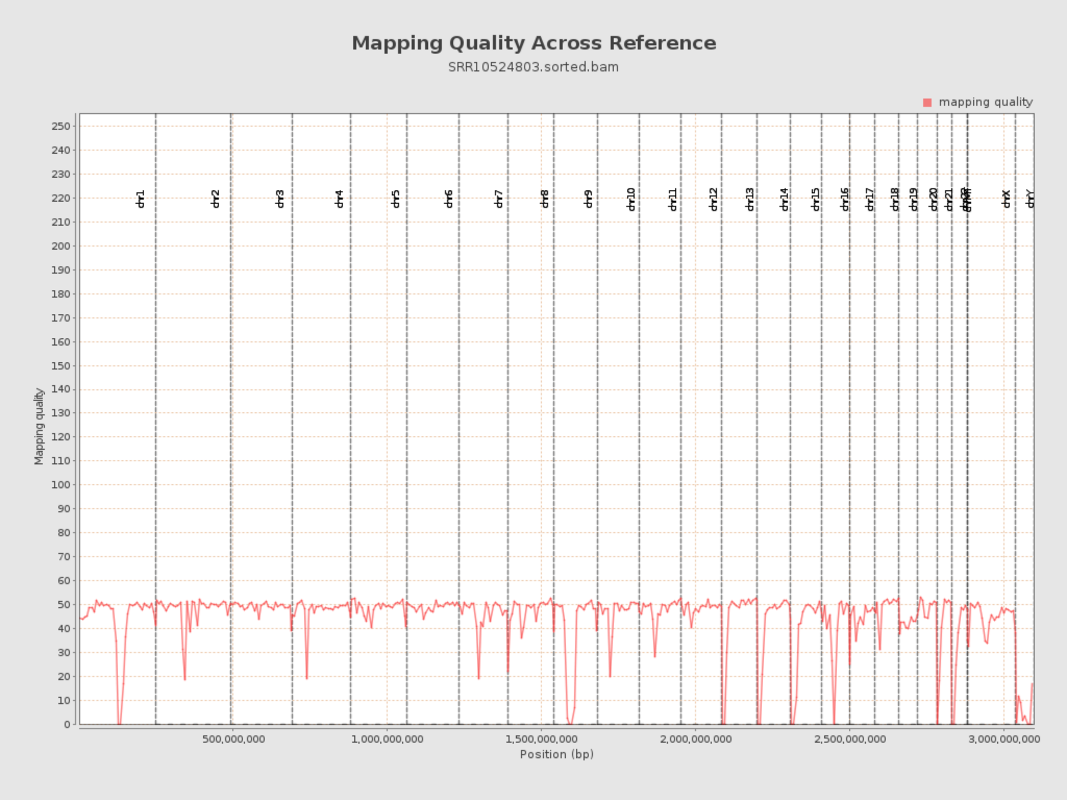
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram