# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 14:29:18*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524640.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_SRR10524640 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524640.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 14:29:17 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524640.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,560,866 |
| Mapped reads | 912,659 / 58.47% |
| Unmapped reads | 648,207 / 41.53% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 3,297 / 0.21% |
| Read min/max/mean length | 30 / 76 / 76.07 |
| Duplicated reads (estimated) | 35,960 / 2.3% |
| Duplication rate | 3.07% |
| Clipped reads | 914,933 / 58.62% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 12,428,767 / 23.55% |
| Number/percentage of C's | 10,742,351 / 20.35% |
| Number/percentage of T's | 17,032,320 / 32.27% |
| Number/percentage of G's | 12,578,193 / 23.83% |
| Number/percentage of N's | 451 / 0% |
| GC Percentage | 44.18% |

## 2.3. Coverage

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

| | |
|---|---|
| Standard Deviation | 0.1853 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.46 |

## 2.5. Mismatches and indels

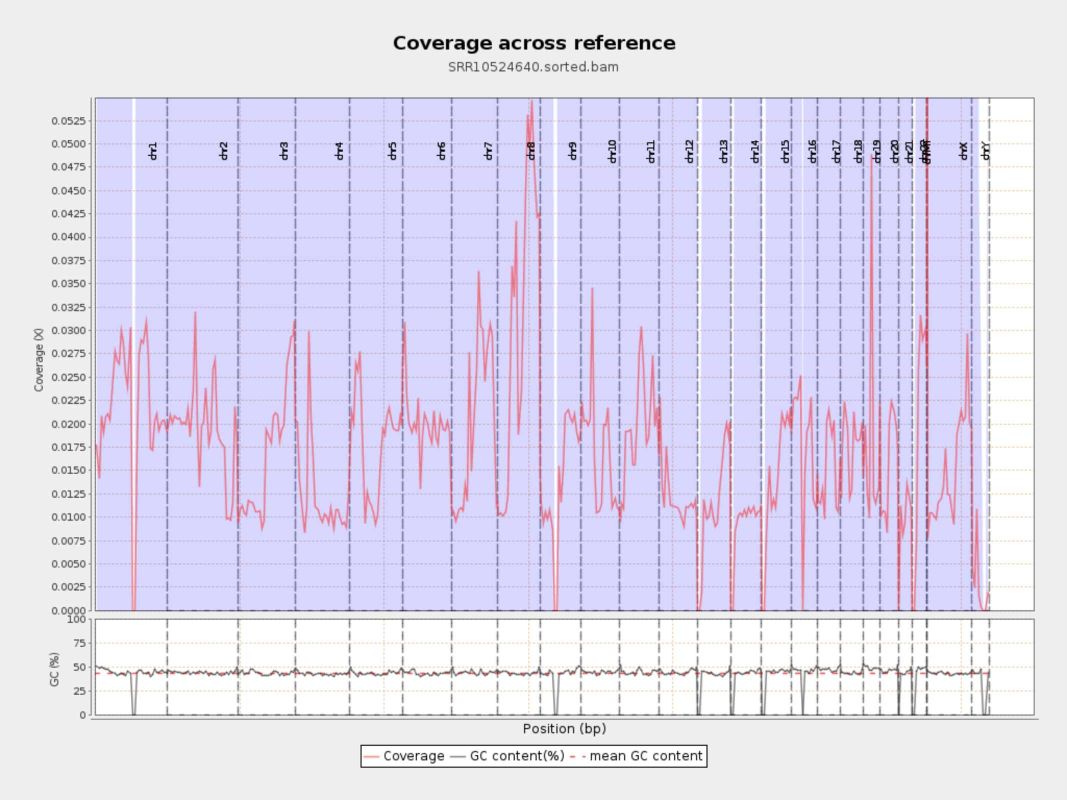
| | |
|---|---|
| General error rate | 0.53% |
| Mismatches | 272,828 |
| Insertions | 3,167 |
| Mapped reads with at least one insertion | 0.34% |
| Deletions | 10,316 |
| Mapped reads with at least one deletion | 1.12% |
| Homopolymer indels | 44.29% |

## 2.6. Chromosome stats

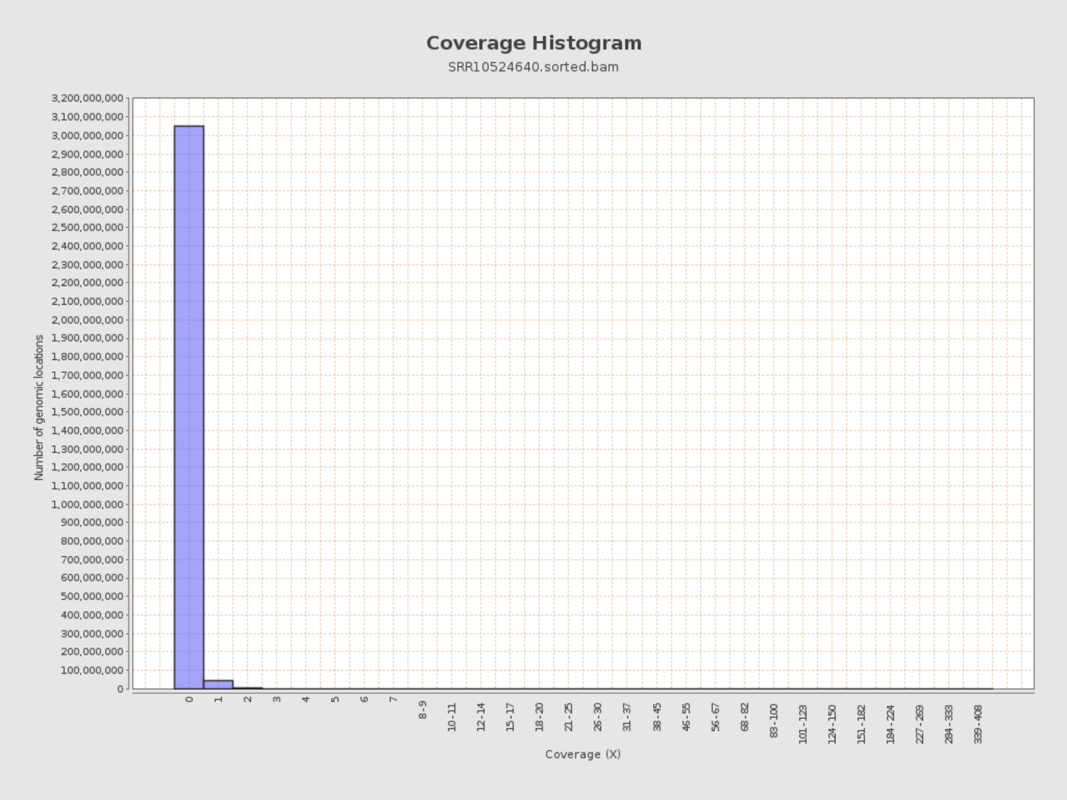
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5383327 | 0.0216 | 0.3212 |
| chr2 | 243199373 | 4714960 | 0.0194 | 0.2265 |
| chr3 | 198022430 | 3308218 | 0.0167 | 0.1396 |
| chr4 | 191154276 | 2387091 | 0.0125 | 0.1399 |
| chr5 | 180915260 | 3253691 | 0.018 | 0.1449 |
| chr6 | 171115067 | 3437716 | 0.0201 | 0.1611 |
| chr7 | 159138663 | 3207730 | 0.0202 | 0.2149 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 4618867 | 0.0316 | 0.2466 |
| chr9 | 141213431 | 1923865 | 0.0136 | 0.15 |
| chr10 | 135534747 | 2343045 | 0.0173 | 0.1889 |
| chr11 | 135006516 | 2697548 | 0.02 | 0.1725 |
| chr12 | 133851895 | 1634658 | 0.0122 | 0.1225 |
| chr13 | 115169878 | 1282641 | 0.0111 | 0.1157 |
| chr14 | 107349540 | 970668 | 0.009 | 0.1087 |
| chr15 | 102531392 | 1388290 | 0.0135 | 0.1269 |
| chr16 | 90354753 | 1589995 | 0.0176 | 0.1489 |
| chr17 | 81195210 | 1212282 | 0.0149 | 0.1369 |
| chr18 | 78077248 | 1387607 | 0.0178 | 0.2297 |
| chr19 | 59128983 | 1078231 | 0.0182 | 0.2187 |
| chr20 | 63025520 | 987202 | 0.0157 | 0.1375 |
| chr21 | 48129895 | 471496 | 0.0098 | 0.1231 |
| chr22 | 51304566 | 1010122 | 0.0197 | 0.1523 |
| chrMT | 16571 | 3867 | 0.2334 | 0.5123 |
| chrX | 155270560 | 2348759 | 0.0151 | 0.1412 |
| chrY | 59373566 | 157497 | 0.0027 | 0.1121 |

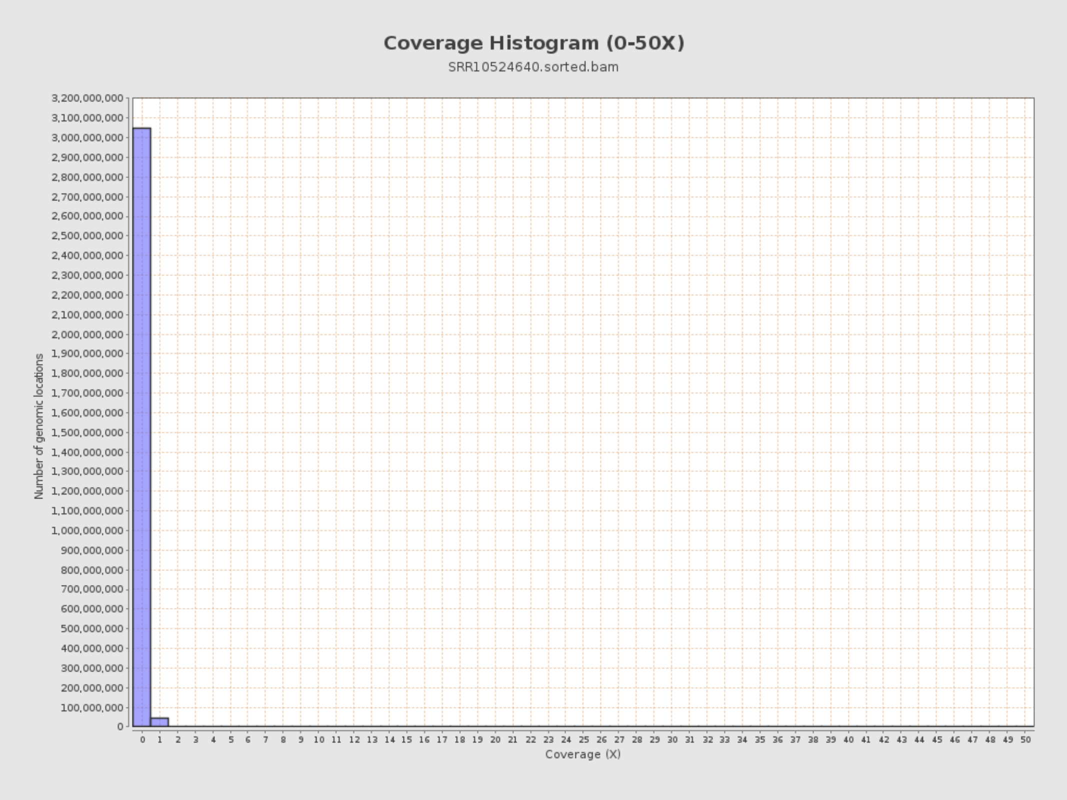
# 3. Results : Coverage across reference



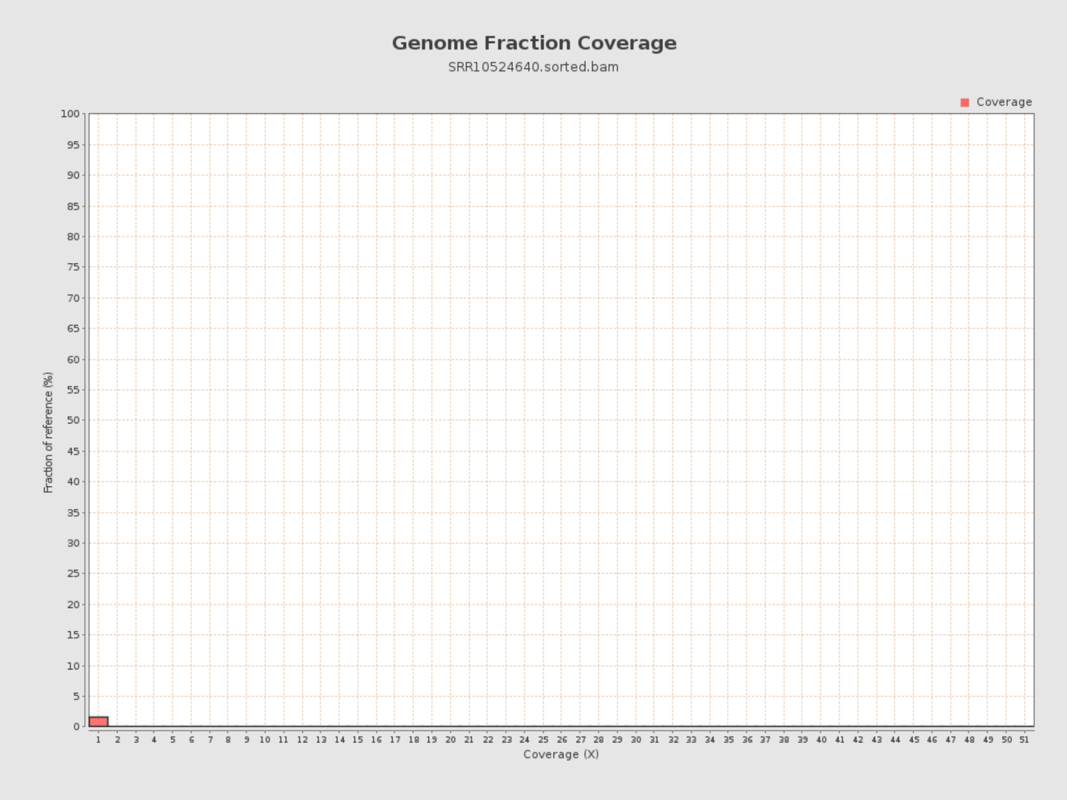
# 4. Results : Coverage Histogram



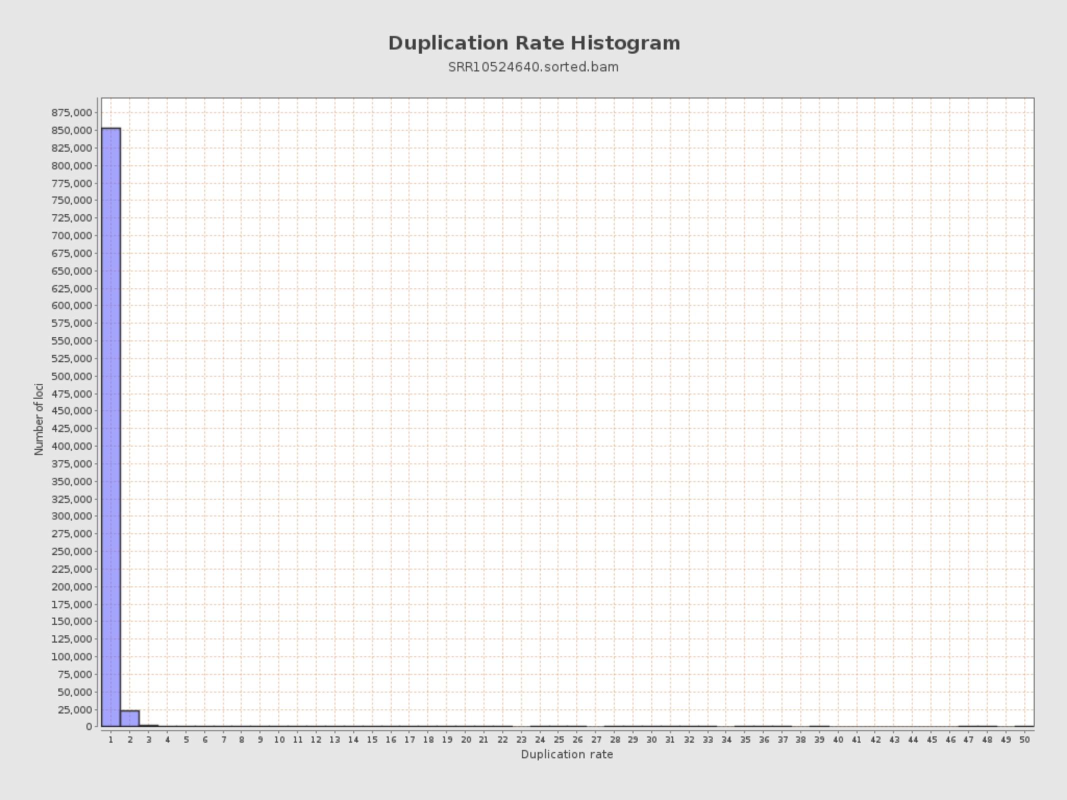
# 5. Results : Coverage Histogram (0-50X)



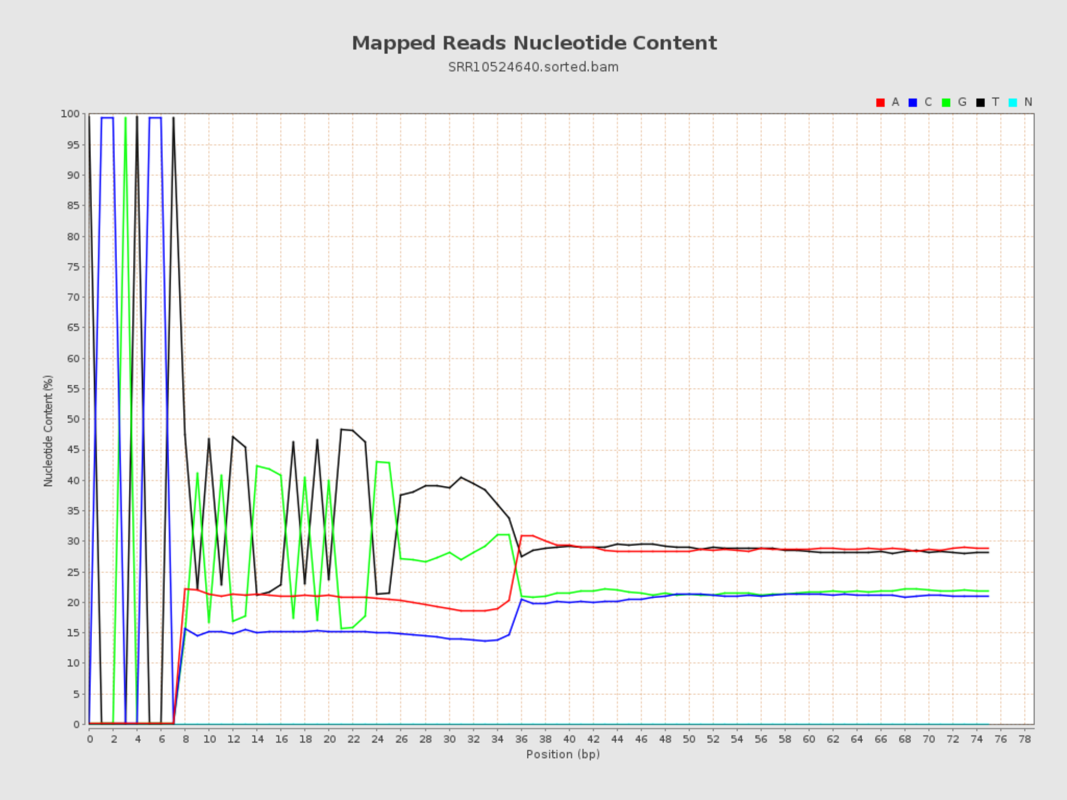
# 6. Results : Genome Fraction Coverage



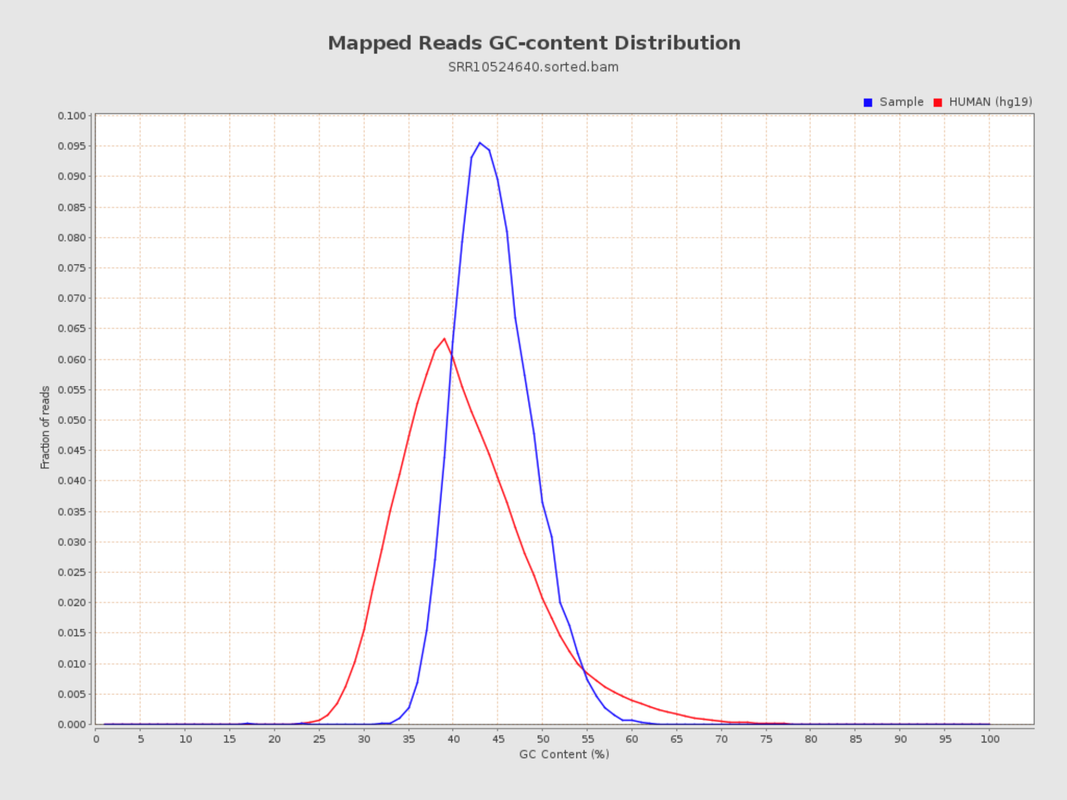
# 7. Results : Duplication Rate Histogram



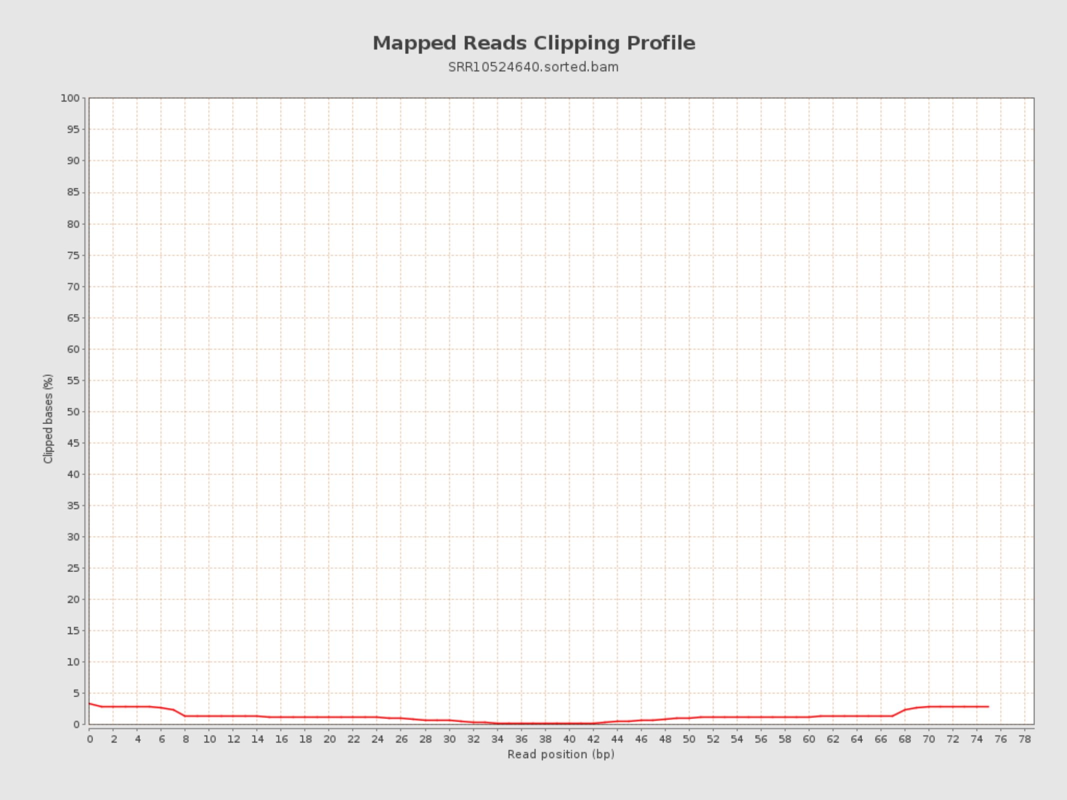
# 8. Results : Mapped Reads Nucleotide Content



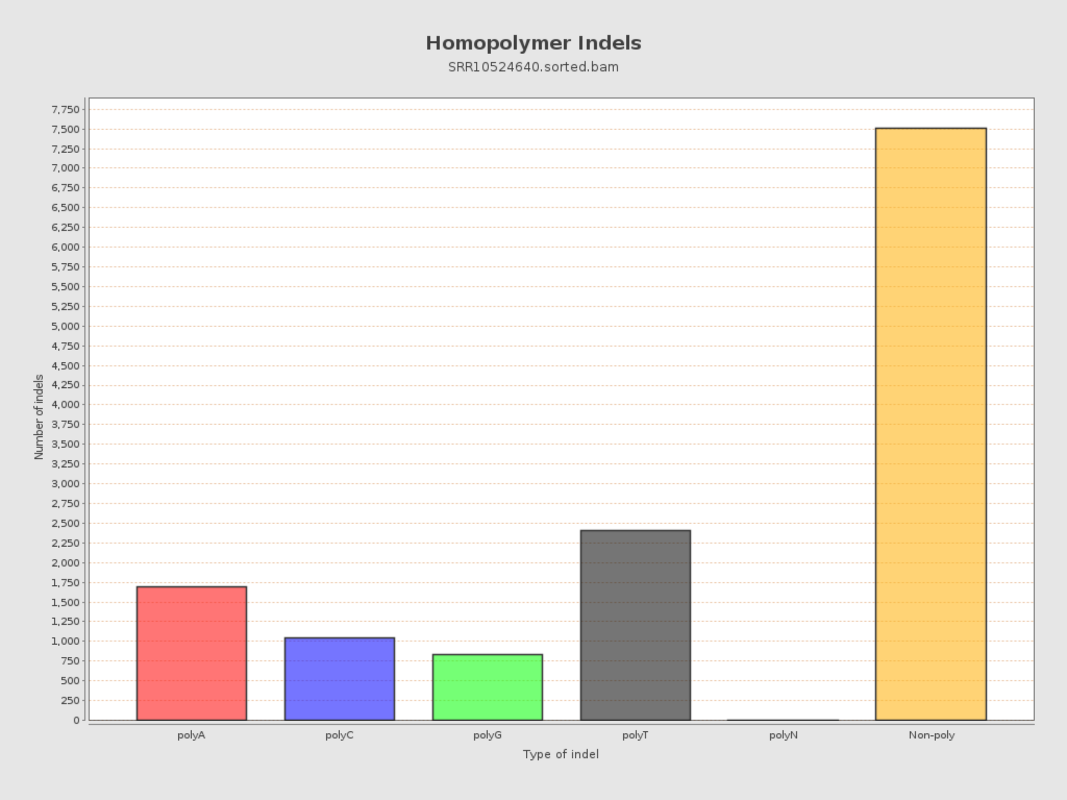
# 9. Results : Mapped Reads GC-content Distribution



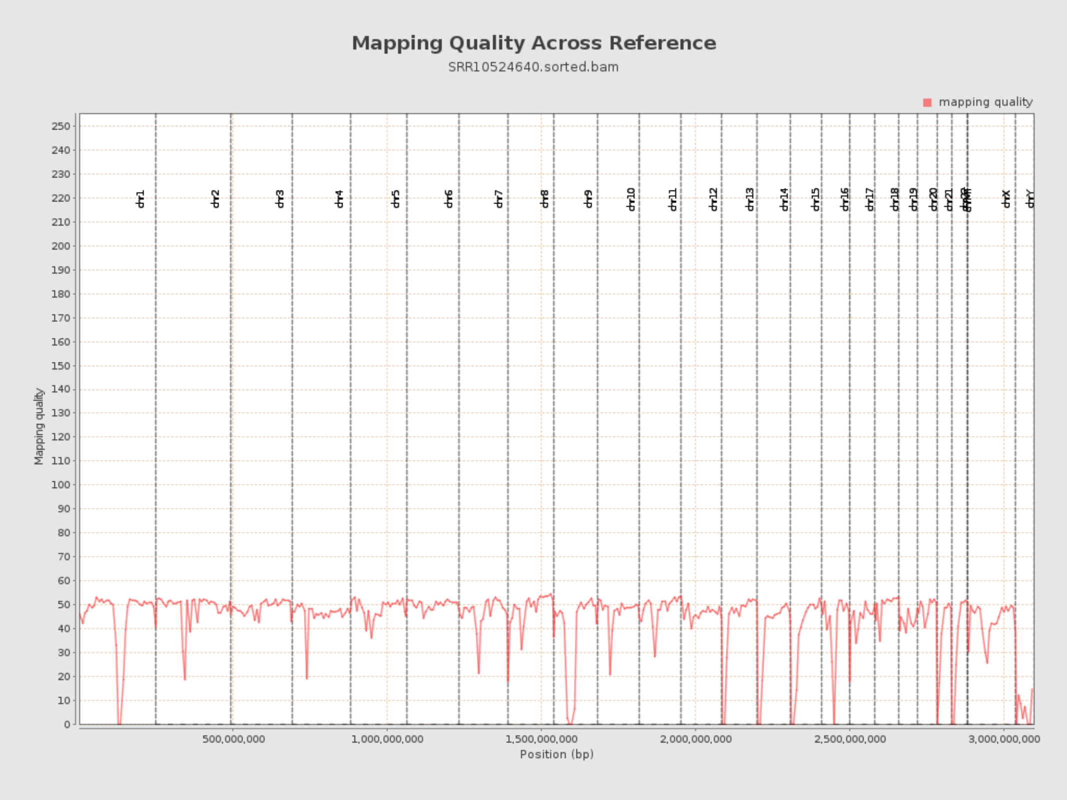
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram