# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 14:19:56*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524637.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_SRR10524637 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524637.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 14:19:52 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524637.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 870,362 |
| Mapped reads | 797,255 / 91.6% |
| Unmapped reads | 73,107 / 8.4% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 3,435 / 0.39% |
| Read min/max/mean length | 30 / 76 / 76.13 |
| Duplicated reads (estimated) | 24,835 / 2.85% |
| Duplication rate | 2.46% |
| Clipped reads | 797,830 / 91.67% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 11,844,330 / 25.45% |
| Number/percentage of C's | 8,391,469 / 18.03% |
| Number/percentage of T's | 14,562,198 / 31.29% |
| Number/percentage of G's | 11,746,006 / 25.24% |
| Number/percentage of N's | 429 / 0% |
| GC Percentage | 43.27% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.015 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1617 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.87 |

## 2.5. Mismatches and indels

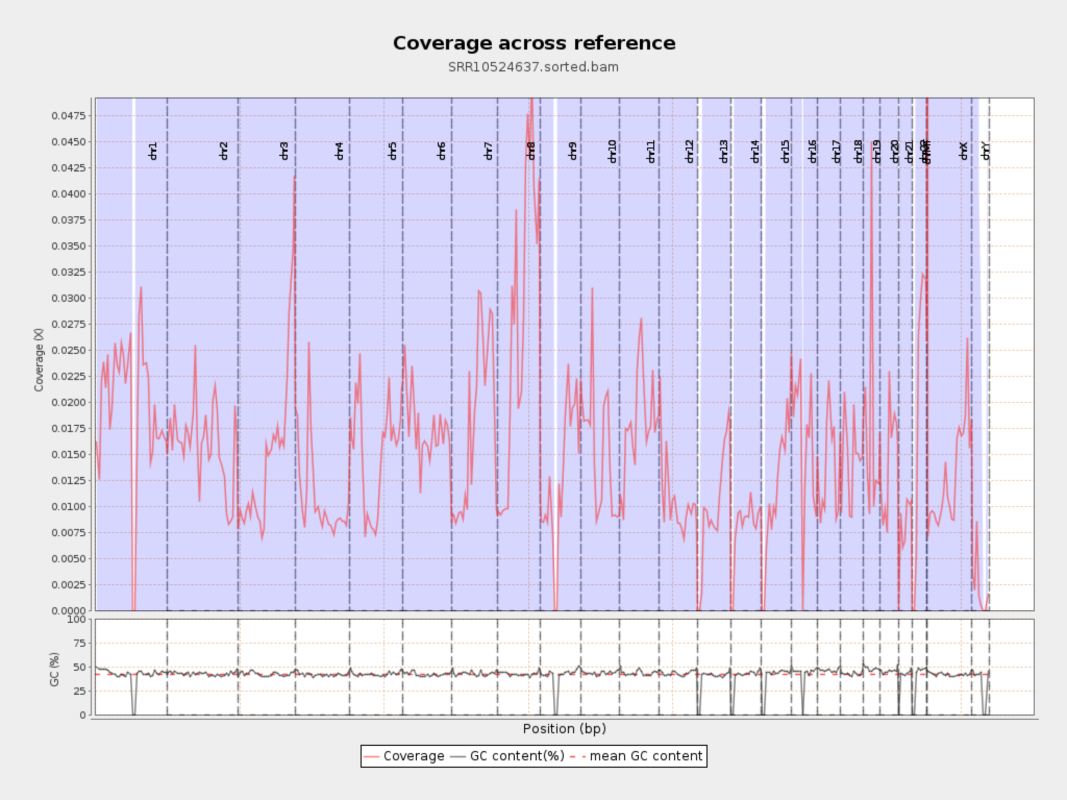
| | |
|---|---|
| General error rate | 0.5% |
| Mismatches | 225,526 |
| Insertions | 3,750 |
| Mapped reads with at least one insertion | 0.47% |
| Deletions | 9,115 |
| Mapped reads with at least one deletion | 1.13% |
| Homopolymer indels | 40.47% |

## 2.6. Chromosome stats

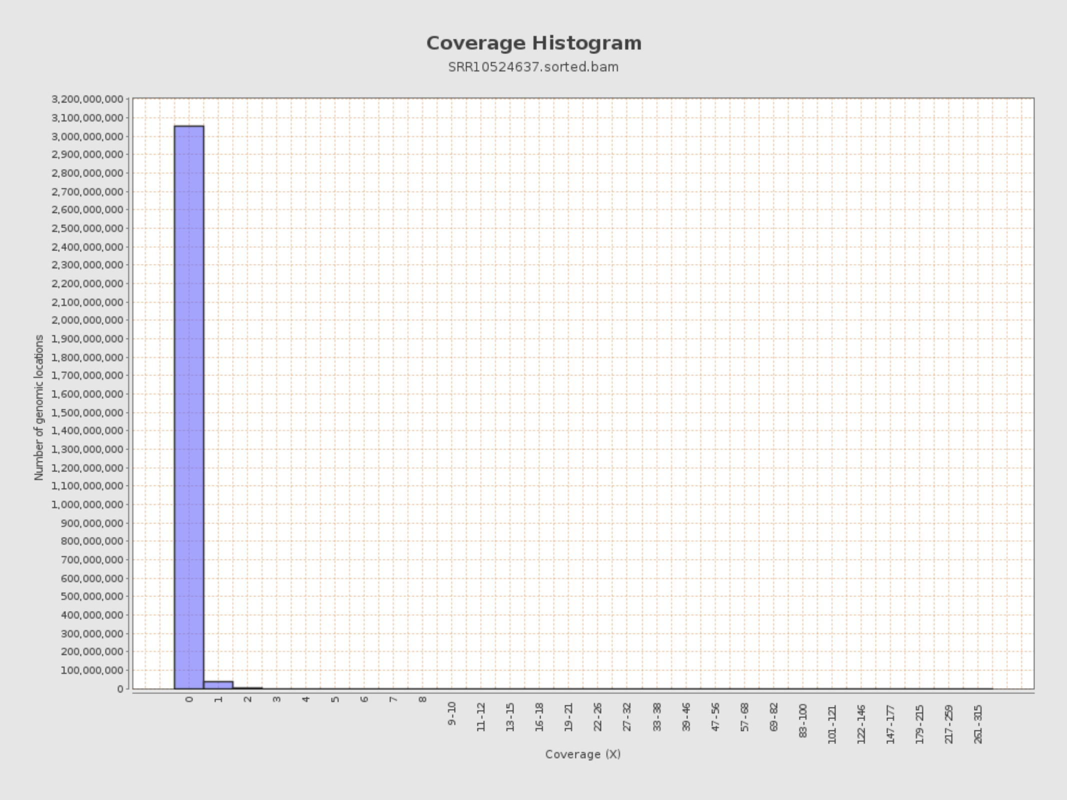
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 4882310 | 0.0196 | 0.2643 |
| chr2 | 243199373 | 3873752 | 0.0159 | 0.1842 |
| chr3 | 198022430 | 2970980 | 0.015 | 0.1307 |
| chr4 | 191154276 | 2107099 | 0.011 | 0.1245 |
| chr5 | 180915260 | 2723109 | 0.0151 | 0.13 |
| chr6 | 171115067 | 2994638 | 0.0175 | 0.1452 |
| chr7 | 159138663 | 2841801 | 0.0179 | 0.1903 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 4100825 | 0.028 | 0.2154 |
| chr9 | 141213431 | 1782215 | 0.0126 | 0.1357 |
| chr10 | 135534747 | 2106251 | 0.0155 | 0.177 |
| chr11 | 135006516 | 2450667 | 0.0182 | 0.1548 |
| chr12 | 133851895 | 1423160 | 0.0106 | 0.1113 |
| chr13 | 115169878 | 1118463 | 0.0097 | 0.1042 |
| chr14 | 107349540 | 841554 | 0.0078 | 0.0987 |
| chr15 | 102531392 | 1149873 | 0.0112 | 0.1134 |
| chr16 | 90354753 | 1470318 | 0.0163 | 0.1393 |
| chr17 | 81195210 | 1101542 | 0.0136 | 0.1263 |
| chr18 | 78077248 | 1132050 | 0.0145 | 0.1977 |
| chr19 | 59128983 | 1045222 | 0.0177 | 0.2055 |
| chr20 | 63025520 | 905056 | 0.0144 | 0.1295 |
| chr21 | 48129895 | 383432 | 0.008 | 0.1079 |
| chr22 | 51304566 | 1027547 | 0.02 | 0.1511 |
| chrMT | 16571 | 7876 | 0.4753 | 0.7713 |
| chrX | 155270560 | 1993704 | 0.0128 | 0.1269 |
| chrY | 59373566 | 126523 | 0.0021 | 0.0844 |

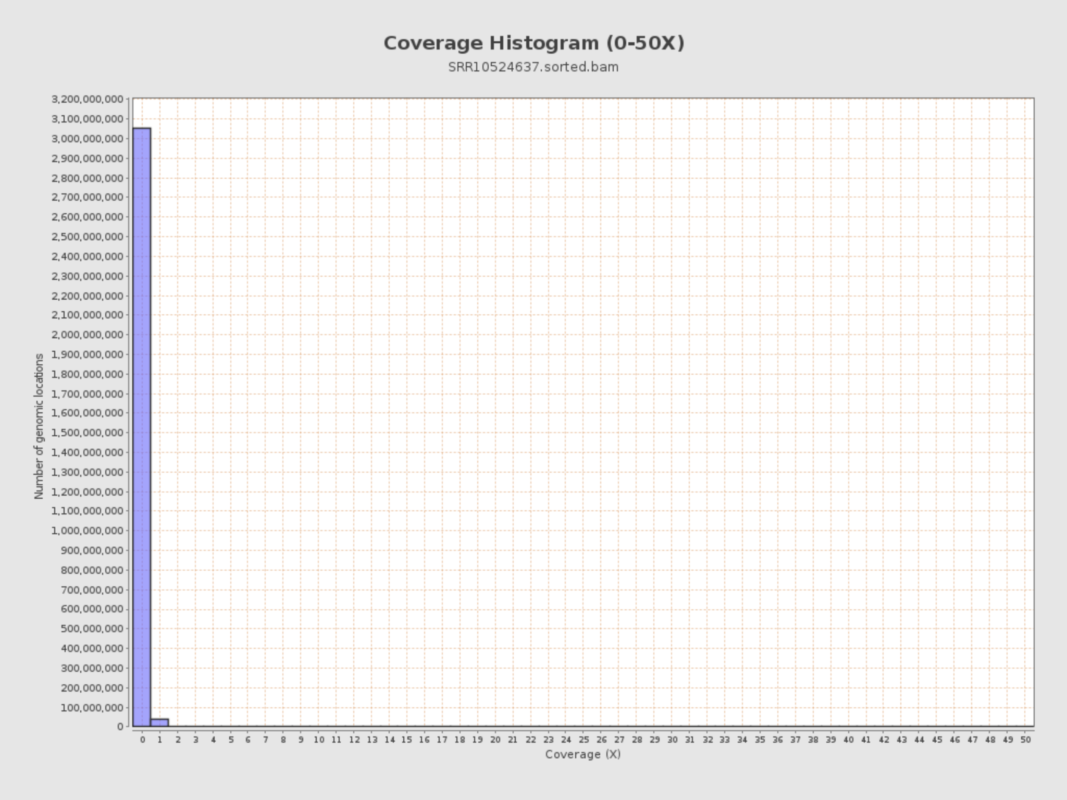
# 3. Results : Coverage across reference



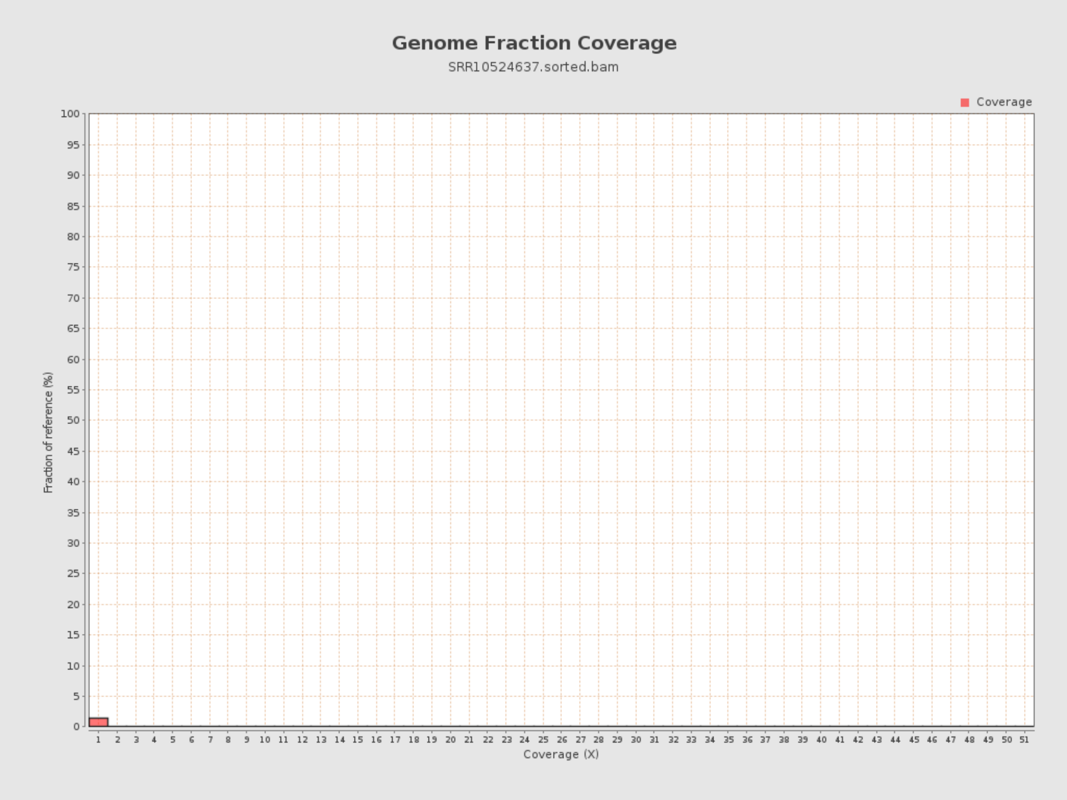
# 4. Results : Coverage Histogram



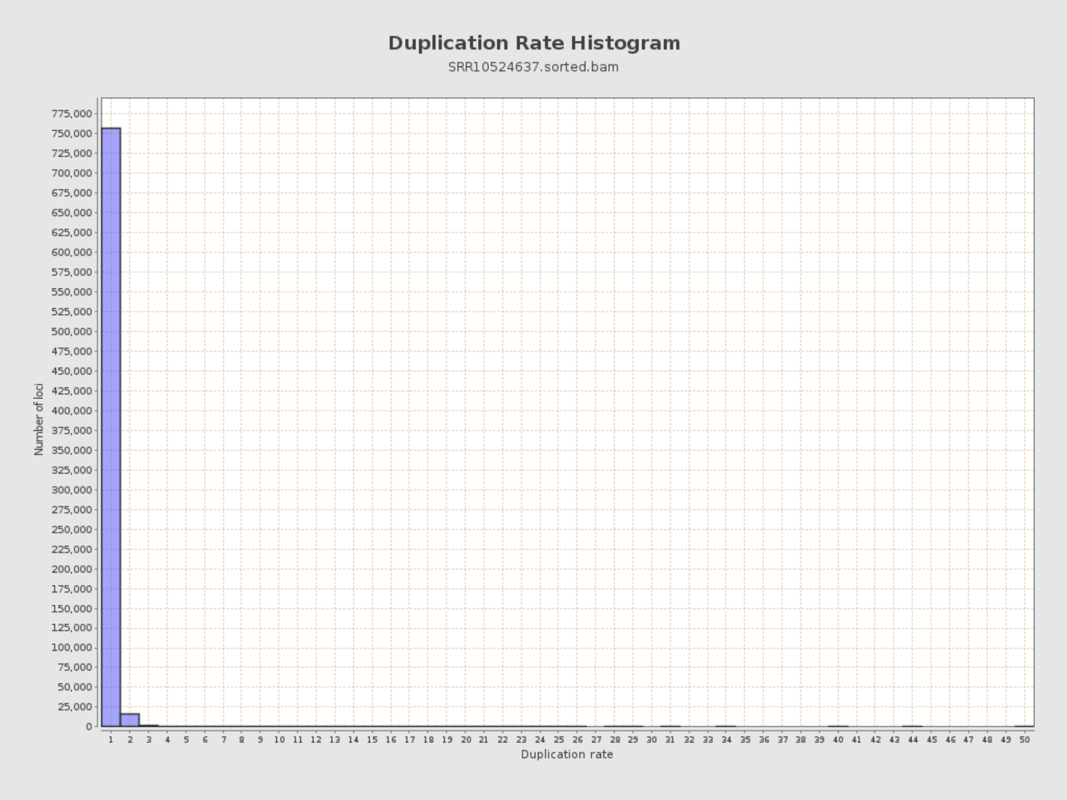
# 5. Results : Coverage Histogram (0-50X)



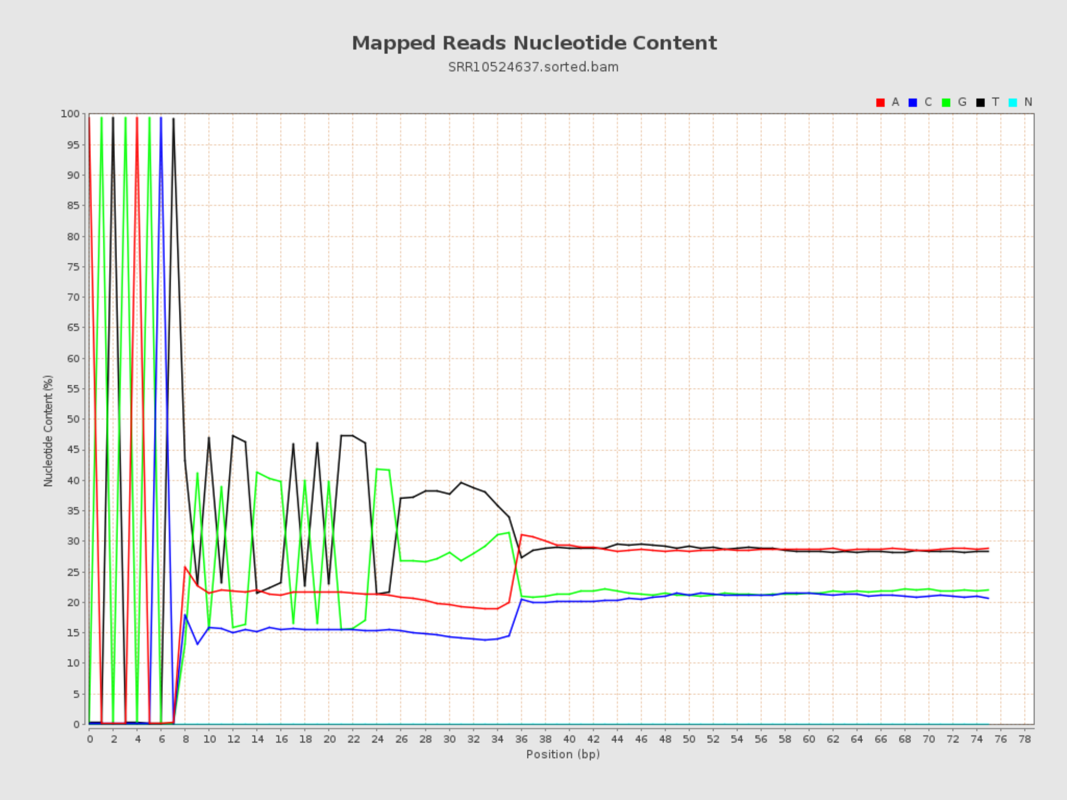
# 6. Results : Genome Fraction Coverage



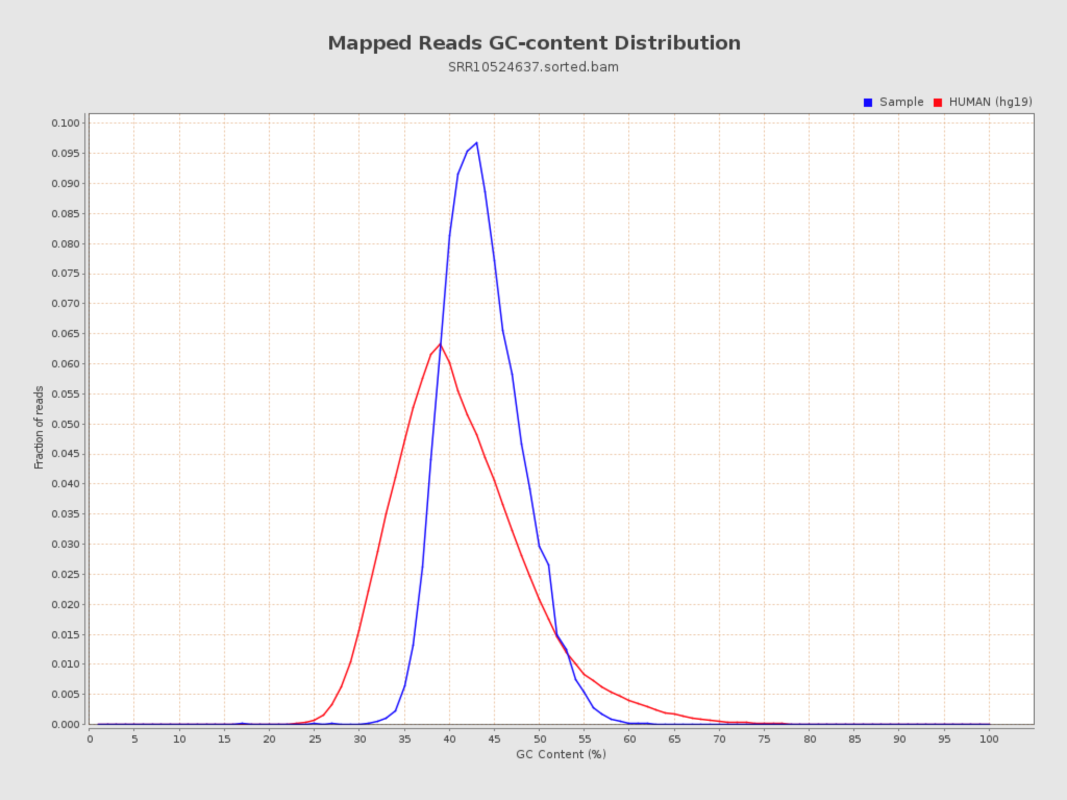
# 7. Results : Duplication Rate Histogram



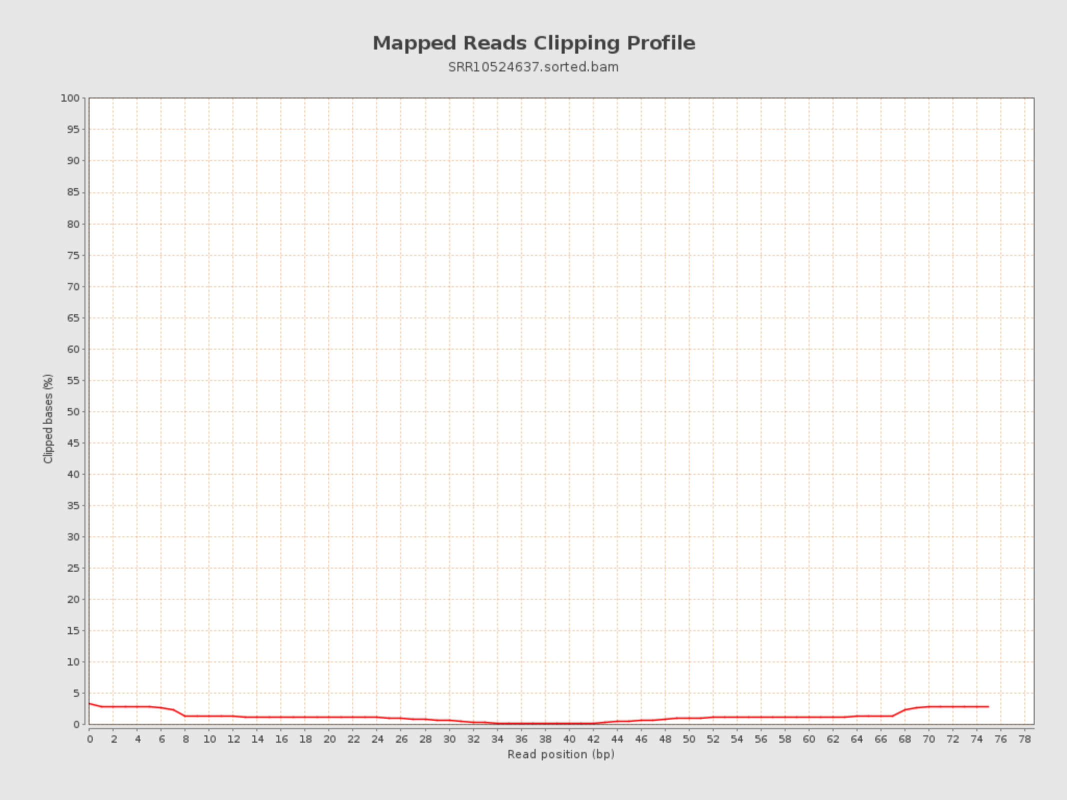
# 8. Results : Mapped Reads Nucleotide Content



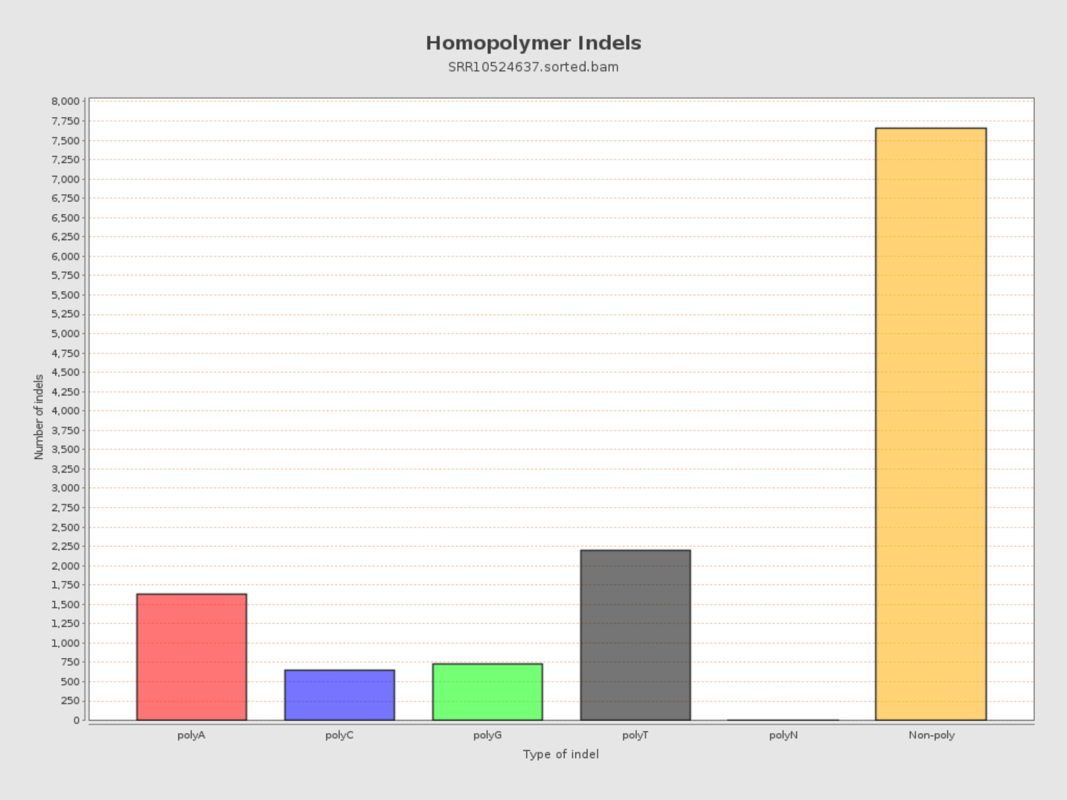
# 9. Results : Mapped Reads GC-content Distribution



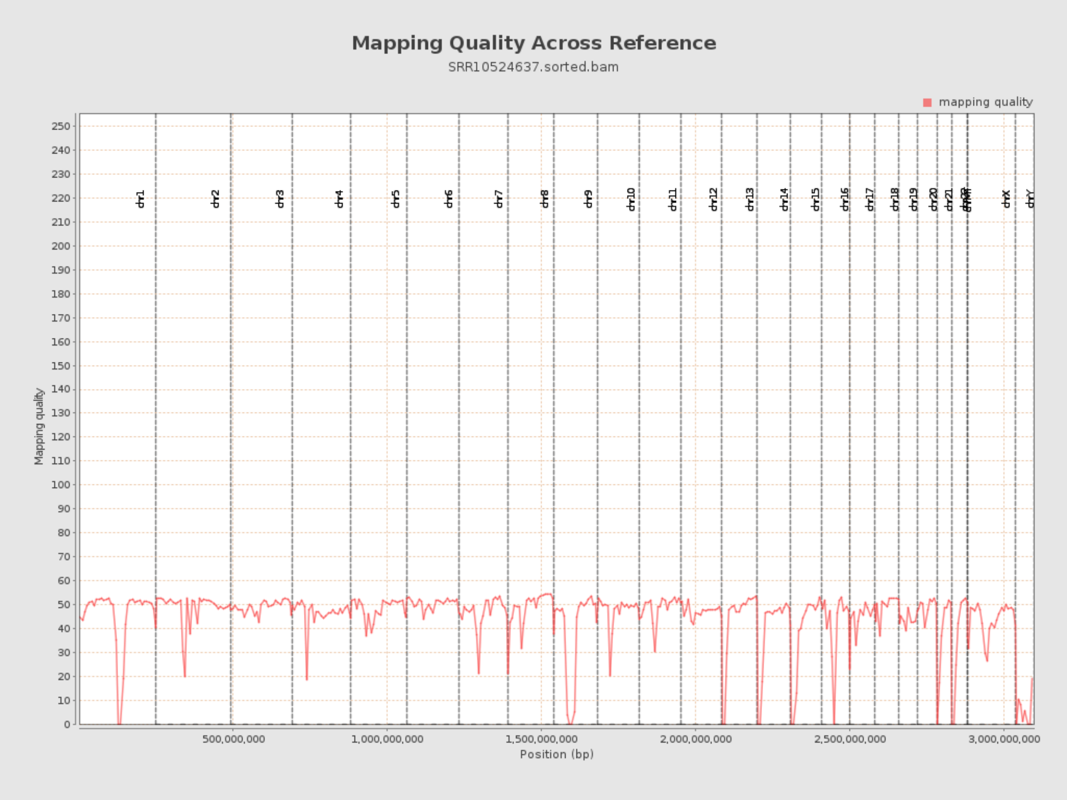
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram