# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/02 13:47:23*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716439.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_SRR9716439 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716439.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 02 13:47:22 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716439.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,133,371 |
| Mapped reads | 1,002,626 / 88.46% |
| Unmapped reads | 130,745 / 11.54% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 5,932 / 0.52% |
| Read min/max/mean length | 30 / 76 / 76.18 |
| Duplicated reads (estimated) | 25,053 / 2.21% |
| Duplication rate | 1.77% |
| Clipped reads | 1,007,875 / 88.93% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 14,972,544 / 25.65% |
| Number/percentage of C's | 10,745,018 / 18.41% |
| Number/percentage of T's | 17,983,614 / 30.81% |
| Number/percentage of G's | 14,666,932 / 25.13% |
| Number/percentage of N's | 849 / 0% |
| GC Percentage | 43.54% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0189 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1979 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.43 |

## 2.5. Mismatches and indels

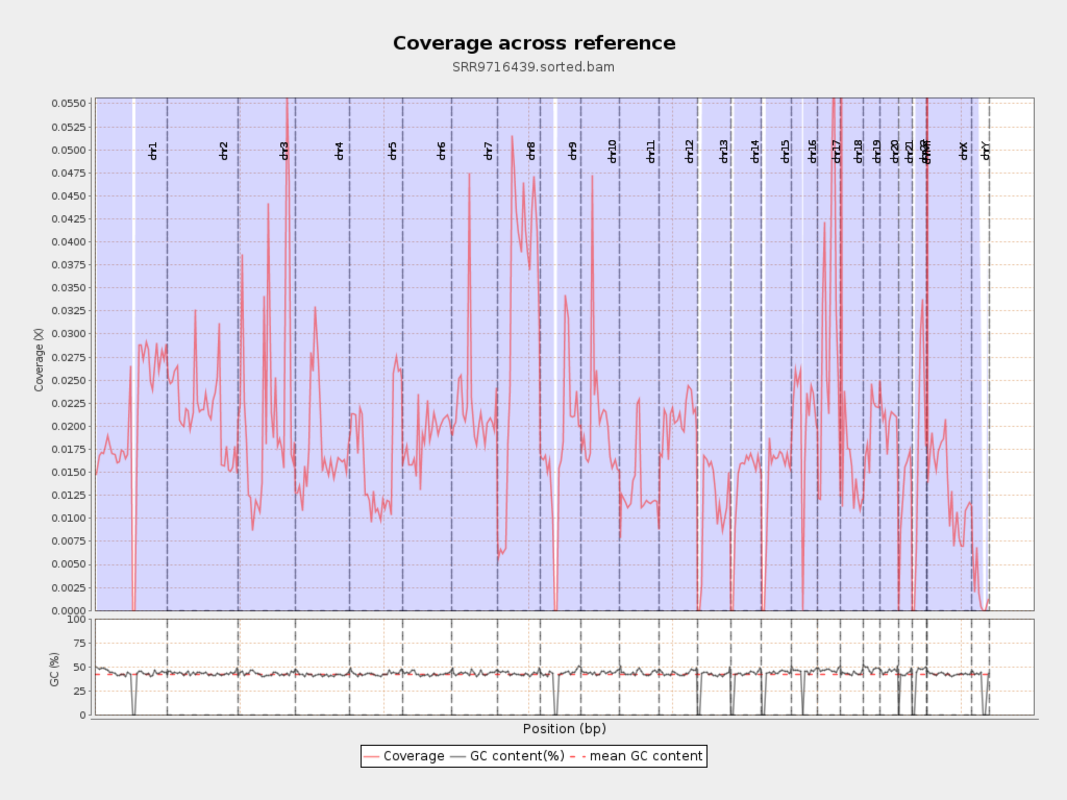
| | |
|---|---|
| General error rate | 0.49% |
| Mismatches | 282,090 |
| Insertions | 3,202 |
| Mapped reads with at least one insertion | 0.32% |
| Deletions | 10,096 |
| Mapped reads with at least one deletion | 1% |
| Homopolymer indels | 43.27% |

## 2.6. Chromosome stats

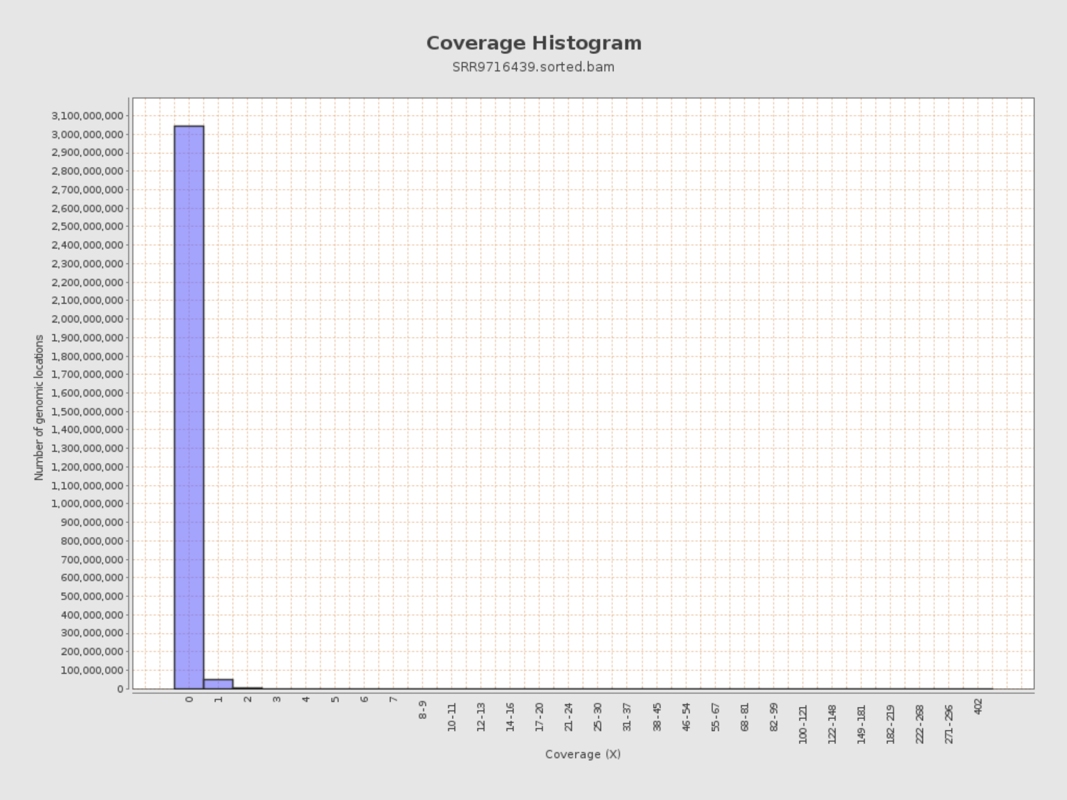
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5112136 | 0.0205 | 0.2736 |
| chr2 | 243199373 | 5254910 | 0.0216 | 0.2297 |
| chr3 | 198022430 | 4357492 | 0.022 | 0.1627 |
| chr4 | 191154276 | 3361666 | 0.0176 | 0.1468 |
| chr5 | 180915260 | 2996452 | 0.0166 | 0.1362 |
| chr6 | 171115067 | 3215582 | 0.0188 | 0.1506 |
| chr7 | 159138663 | 3540182 | 0.0222 | 0.392 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 4744650 | 0.0324 | 0.2334 |
| chr9 | 141213431 | 2465555 | 0.0175 | 0.1528 |
| chr10 | 135534747 | 2778568 | 0.0205 | 0.2422 |
| chr11 | 135006516 | 1784009 | 0.0132 | 0.1354 |
| chr12 | 133851895 | 2777385 | 0.0207 | 0.1633 |
| chr13 | 115169878 | 1275987 | 0.0111 | 0.111 |
| chr14 | 107349540 | 1449352 | 0.0135 | 0.1245 |
| chr15 | 102531392 | 1392055 | 0.0136 | 0.127 |
| chr16 | 90354753 | 1864435 | 0.0206 | 0.156 |
| chr17 | 81195210 | 2481522 | 0.0306 | 0.1899 |
| chr18 | 78077248 | 1374371 | 0.0176 | 0.2133 |
| chr19 | 59128983 | 1178227 | 0.0199 | 0.2498 |
| chr20 | 63025520 | 1295379 | 0.0206 | 0.1569 |
| chr21 | 48129895 | 611726 | 0.0127 | 0.1232 |
| chr22 | 51304566 | 873265 | 0.017 | 0.1379 |
| chrMT | 16571 | 5015 | 0.3026 | 0.5901 |
| chrX | 155270560 | 2063801 | 0.0133 | 0.1327 |
| chrY | 59373566 | 131534 | 0.0022 | 0.0647 |

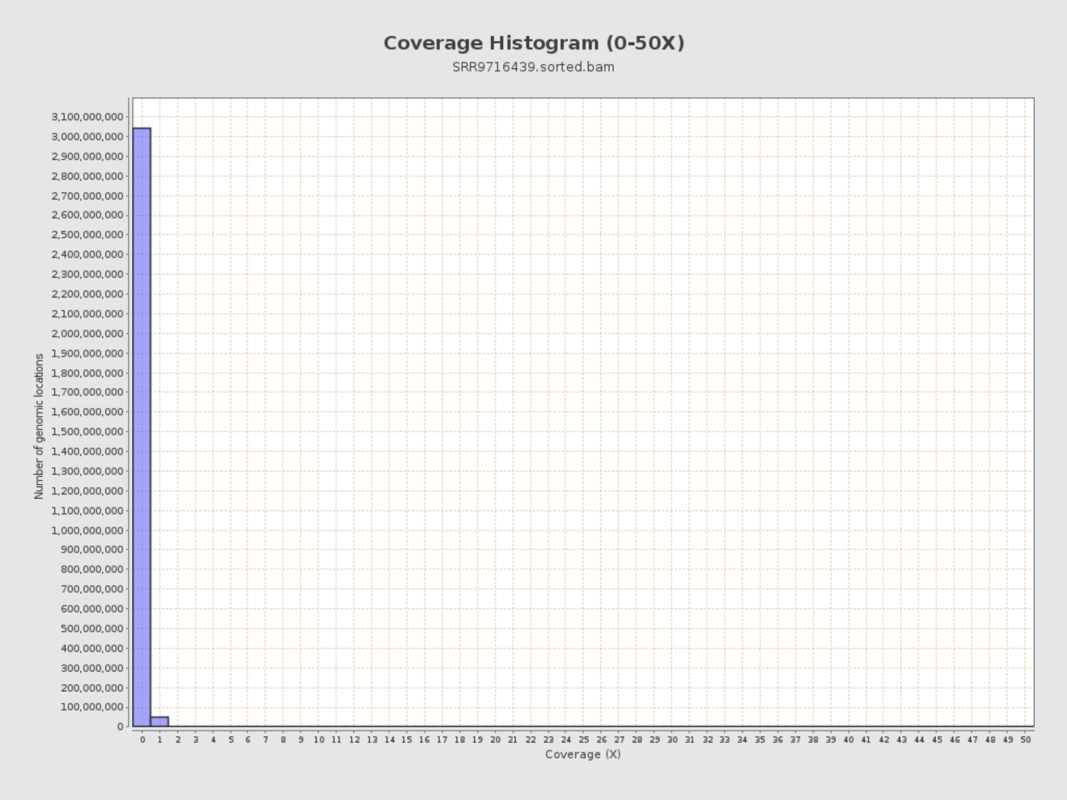
# 3. Results : Coverage across reference



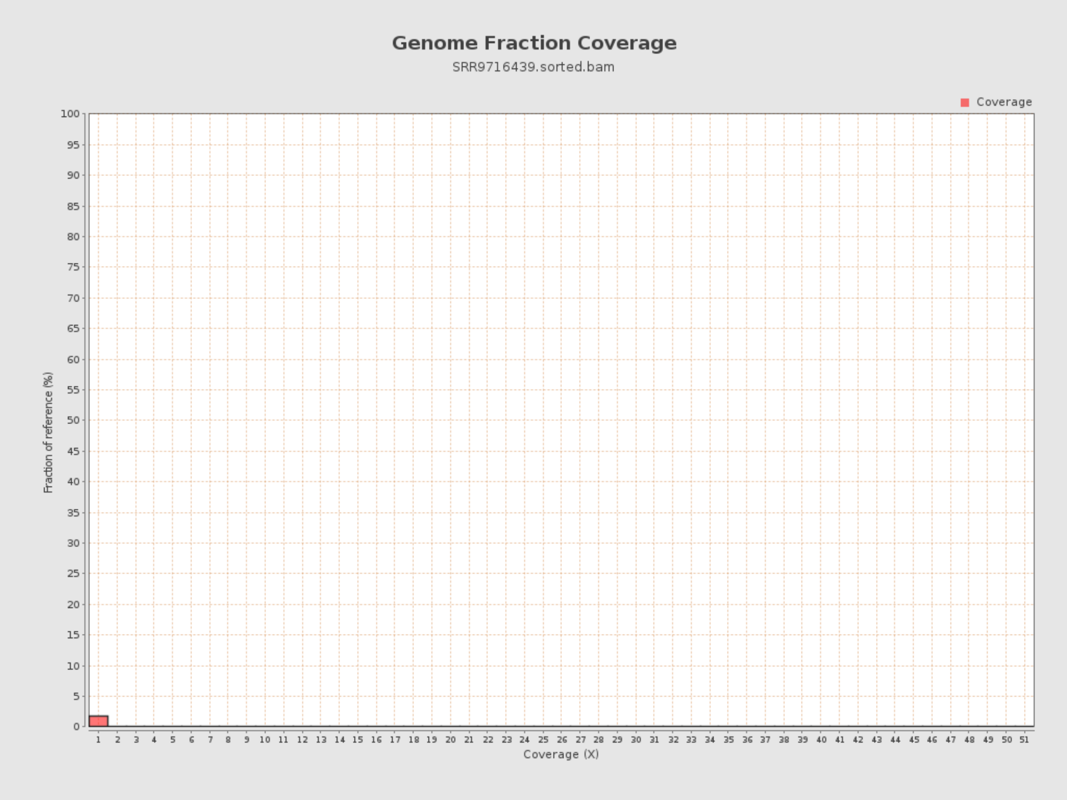
# 4. Results : Coverage Histogram



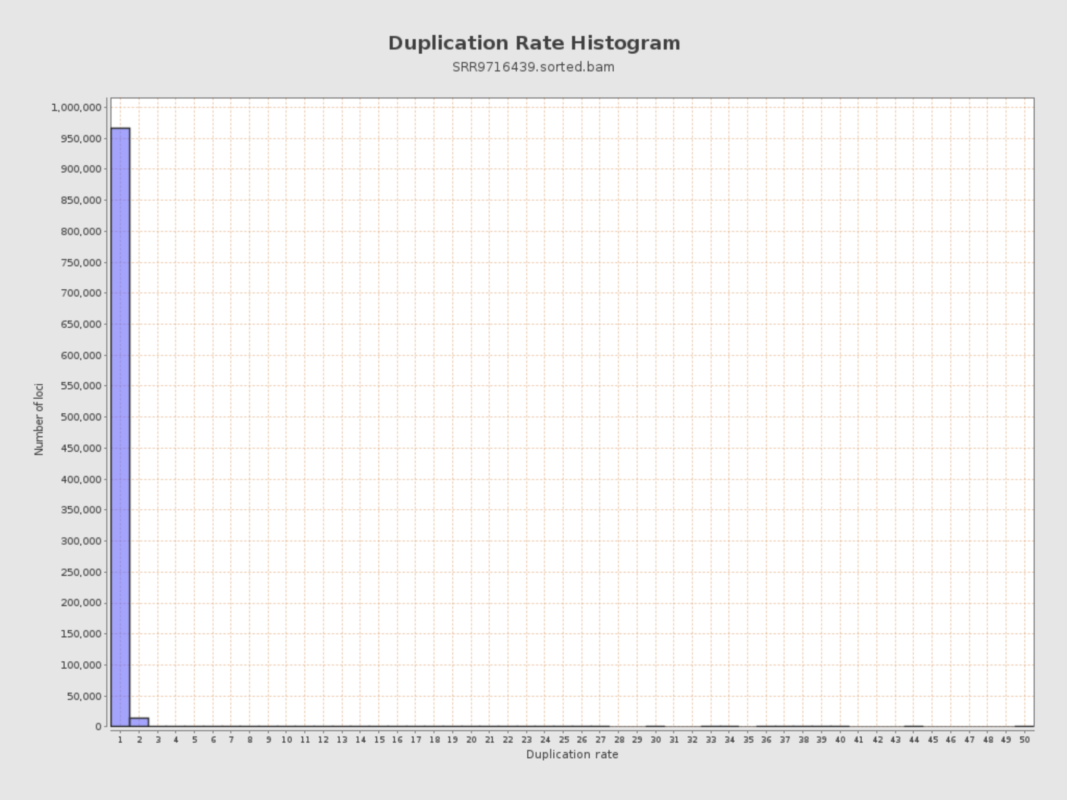
# 5. Results : Coverage Histogram (0-50X)



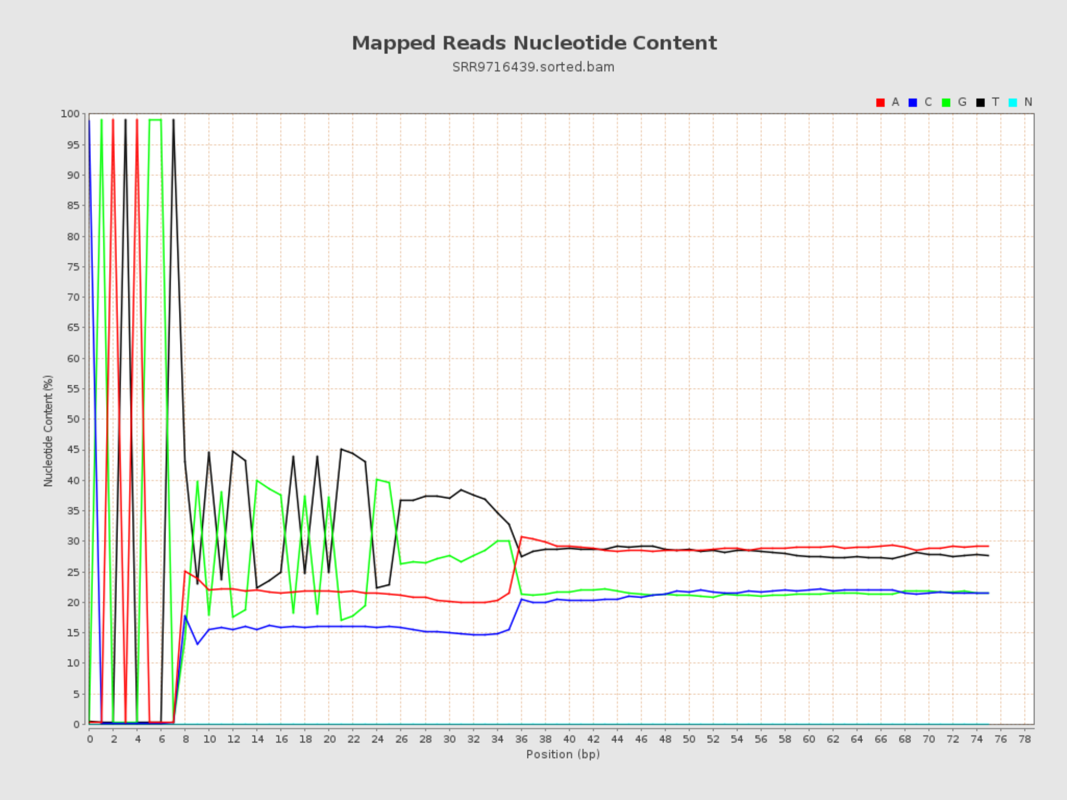
# 6. Results : Genome Fraction Coverage



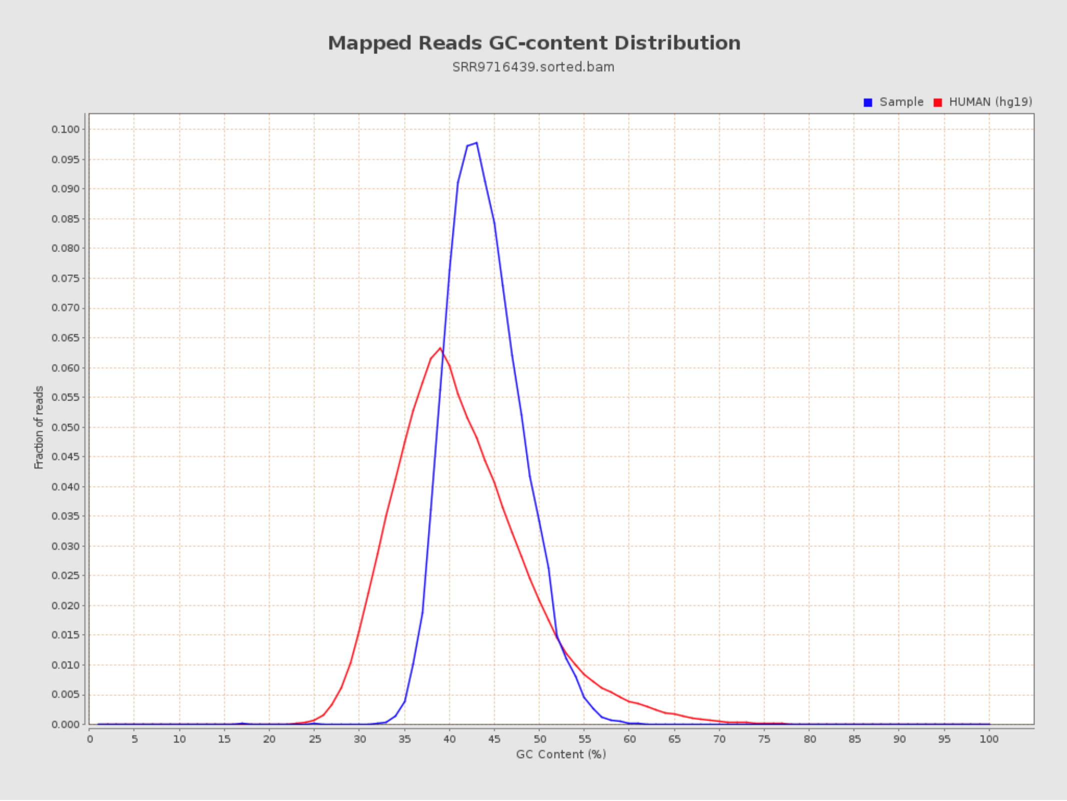
# 7. Results : Duplication Rate Histogram



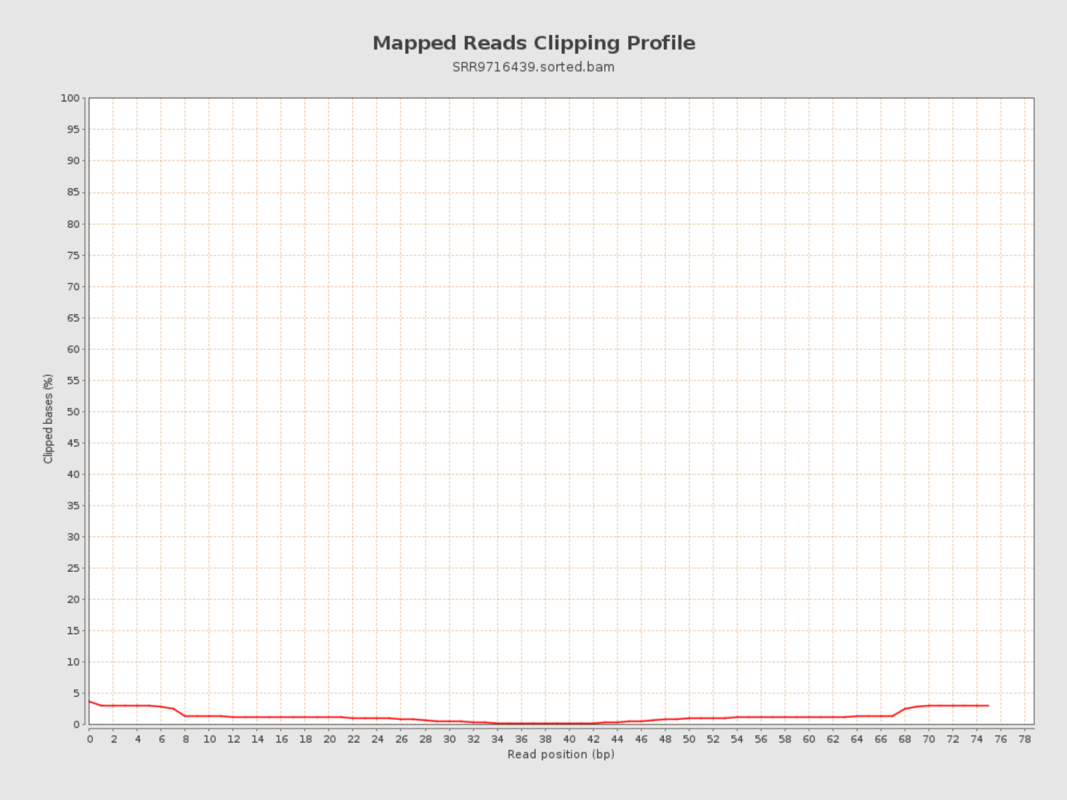
# 8. Results : Mapped Reads Nucleotide Content



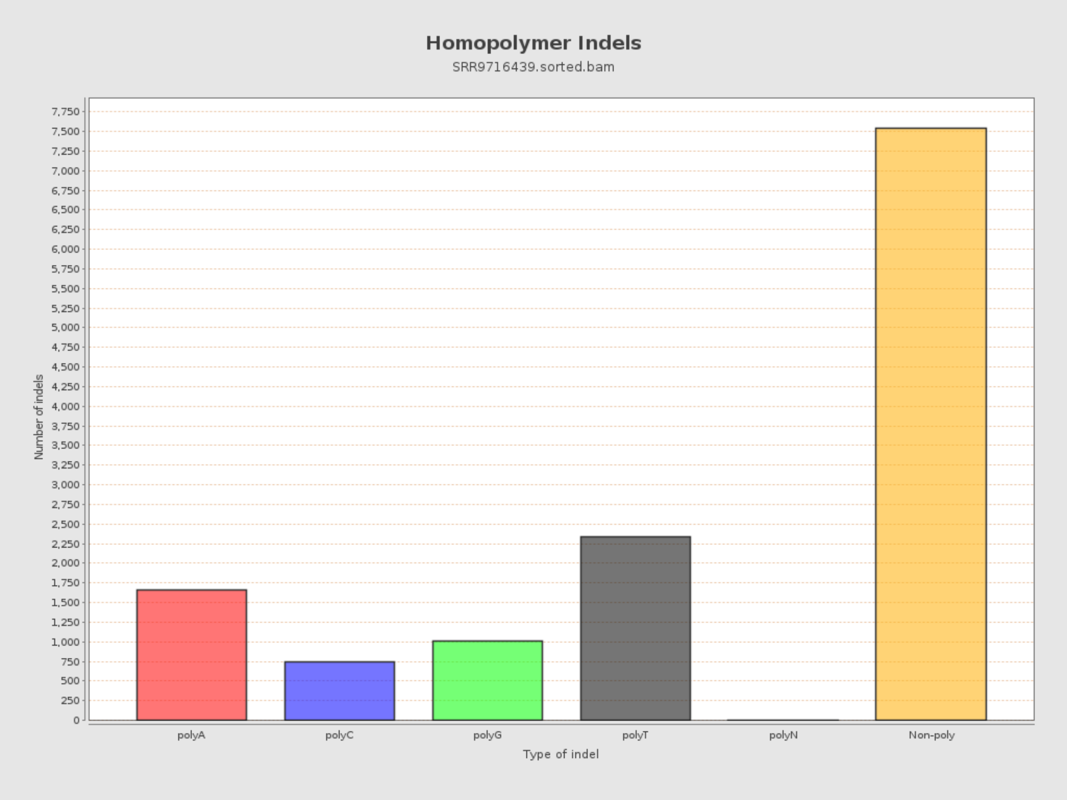
# 9. Results : Mapped Reads GC-content Distribution



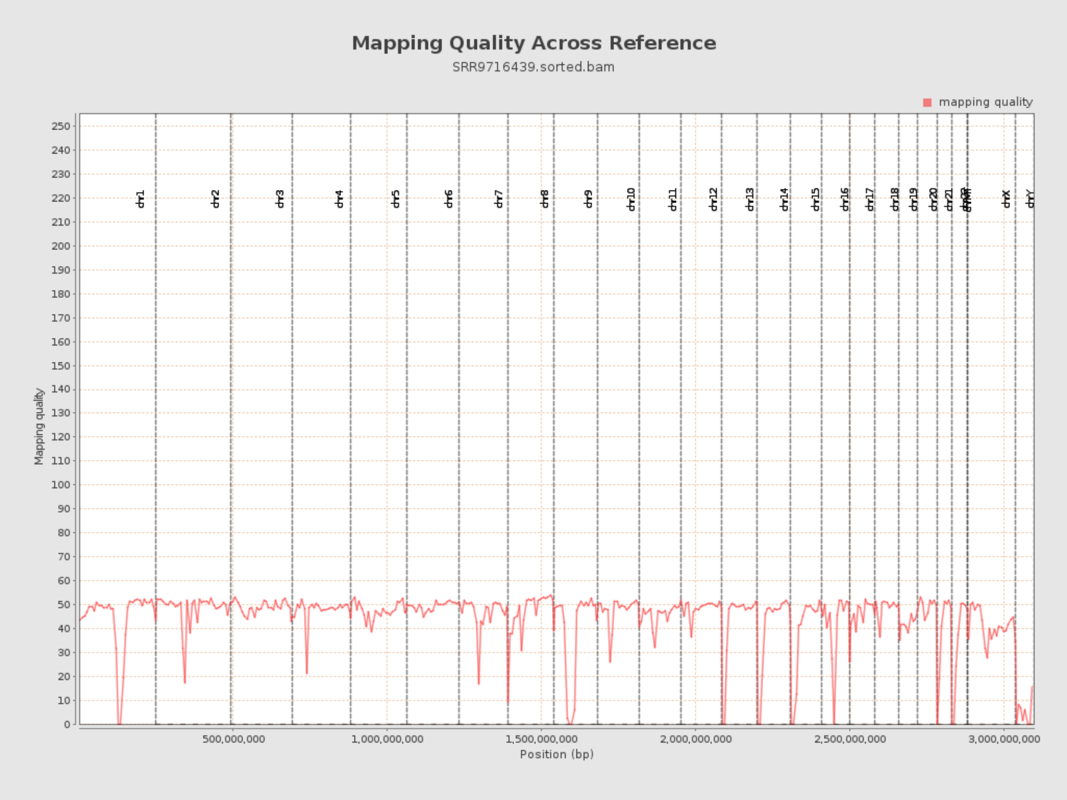
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram