# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/02 10:30:23*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716379.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_SRR9716379 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716379.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 02 10:30:23 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716379.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,259,399 |
| Mapped reads | 1,117,422 / 88.73% |
| Unmapped reads | 141,977 / 11.27% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 4,304 / 0.34% |
| Read min/max/mean length | 30 / 76 / 76.11 |
| Duplicated reads (estimated) | 20,871 / 1.66% |
| Duplication rate | 1.31% |
| Clipped reads | 1,120,261 / 88.95% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 15,977,859 / 24.78% |
| Number/percentage of C's | 12,592,203 / 19.53% |
| Number/percentage of T's | 19,209,850 / 29.8% |
| Number/percentage of G's | 16,690,152 / 25.89% |
| Number/percentage of N's | 434 / 0% |
| GC Percentage | 45.42% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0208 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1891 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 42.86 |

## 2.5. Mismatches and indels

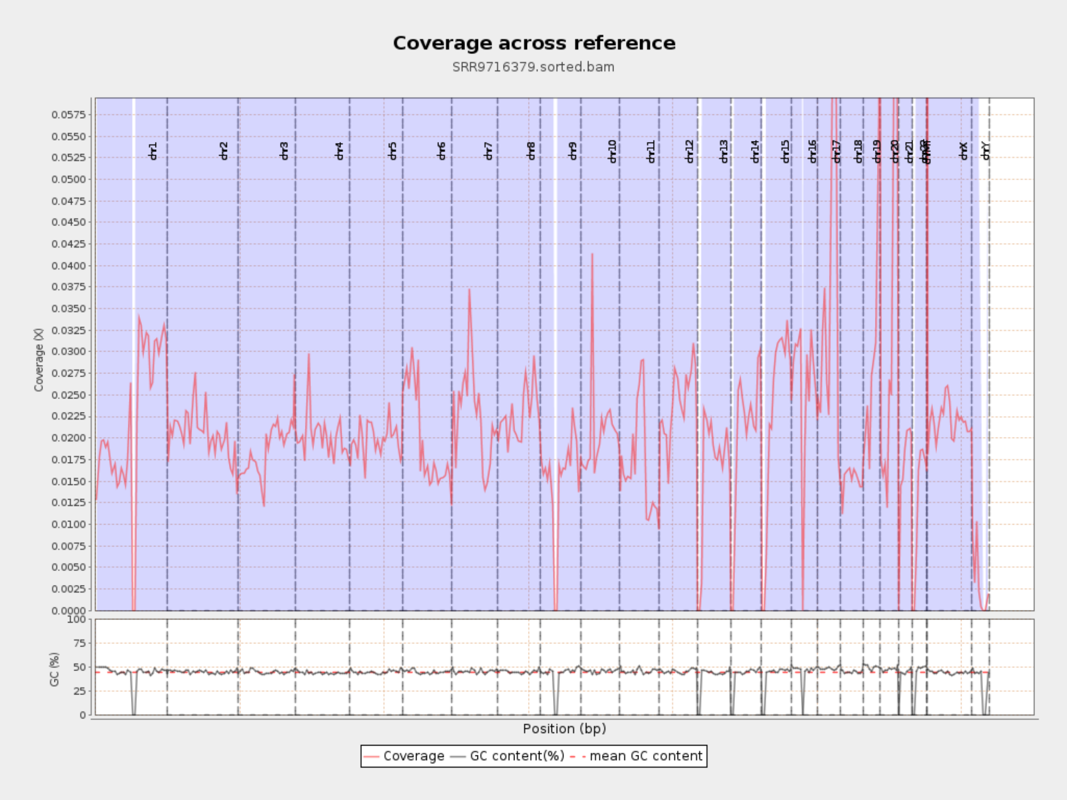
| | |
|---|---|
| General error rate | 0.55% |
| Mismatches | 347,104 |
| Insertions | 3,896 |
| Mapped reads with at least one insertion | 0.35% |
| Deletions | 11,873 |
| Mapped reads with at least one deletion | 1.06% |
| Homopolymer indels | 43.86% |

## 2.6. Chromosome stats

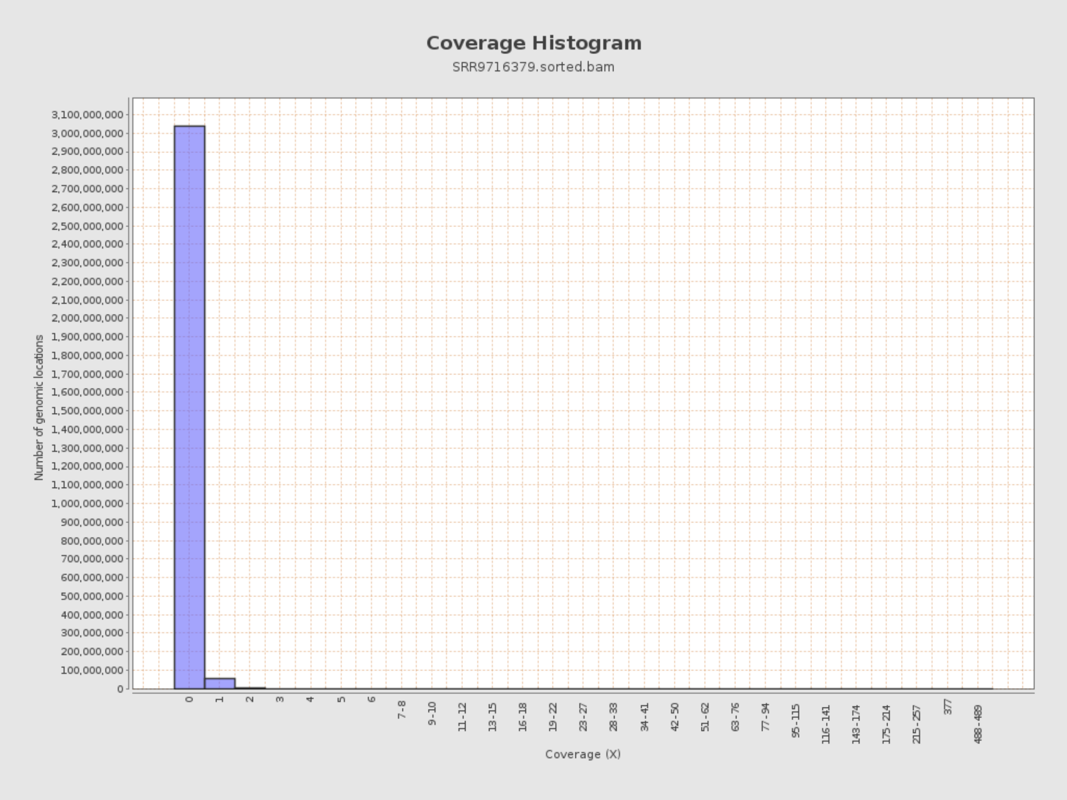
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5486102 | 0.022 | 0.2304 |
| chr2 | 243199373 | 4981214 | 0.0205 | 0.2517 |
| chr3 | 198022430 | 3658494 | 0.0185 | 0.1461 |
| chr4 | 191154276 | 3884730 | 0.0203 | 0.1576 |
| chr5 | 180915260 | 3608081 | 0.0199 | 0.1482 |
| chr6 | 171115067 | 3407302 | 0.0199 | 0.1708 |
| chr7 | 159138663 | 3641599 | 0.0229 | 0.2634 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3329896 | 0.0228 | 0.1822 |
| chr9 | 141213431 | 2156391 | 0.0153 | 0.1456 |
| chr10 | 135534747 | 2813685 | 0.0208 | 0.2389 |
| chr11 | 135006516 | 2318342 | 0.0172 | 0.1625 |
| chr12 | 133851895 | 3221262 | 0.0241 | 0.1651 |
| chr13 | 115169878 | 1883594 | 0.0164 | 0.1351 |
| chr14 | 107349540 | 2179699 | 0.0203 | 0.1548 |
| chr15 | 102531392 | 2355316 | 0.023 | 0.1613 |
| chr16 | 90354753 | 2312146 | 0.0256 | 0.1785 |
| chr17 | 81195210 | 3055988 | 0.0376 | 0.2147 |
| chr18 | 78077248 | 1179478 | 0.0151 | 0.216 |
| chr19 | 59128983 | 1805987 | 0.0305 | 0.242 |
| chr20 | 63025520 | 2159101 | 0.0343 | 0.2035 |
| chr21 | 48129895 | 799635 | 0.0166 | 0.1455 |
| chr22 | 51304566 | 631220 | 0.0123 | 0.1172 |
| chrMT | 16571 | 12053 | 0.7274 | 1.0561 |
| chrX | 155270560 | 3423559 | 0.022 | 0.1643 |
| chrY | 59373566 | 184656 | 0.0031 | 0.0928 |

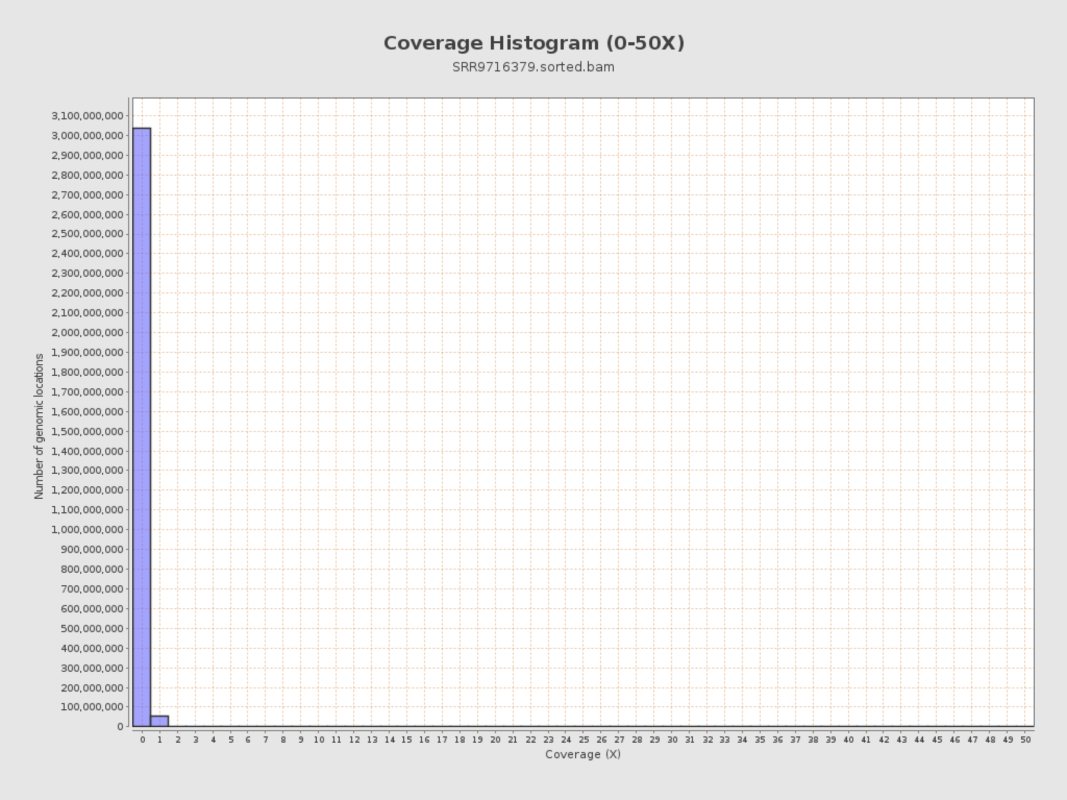
# 3. Results : Coverage across reference



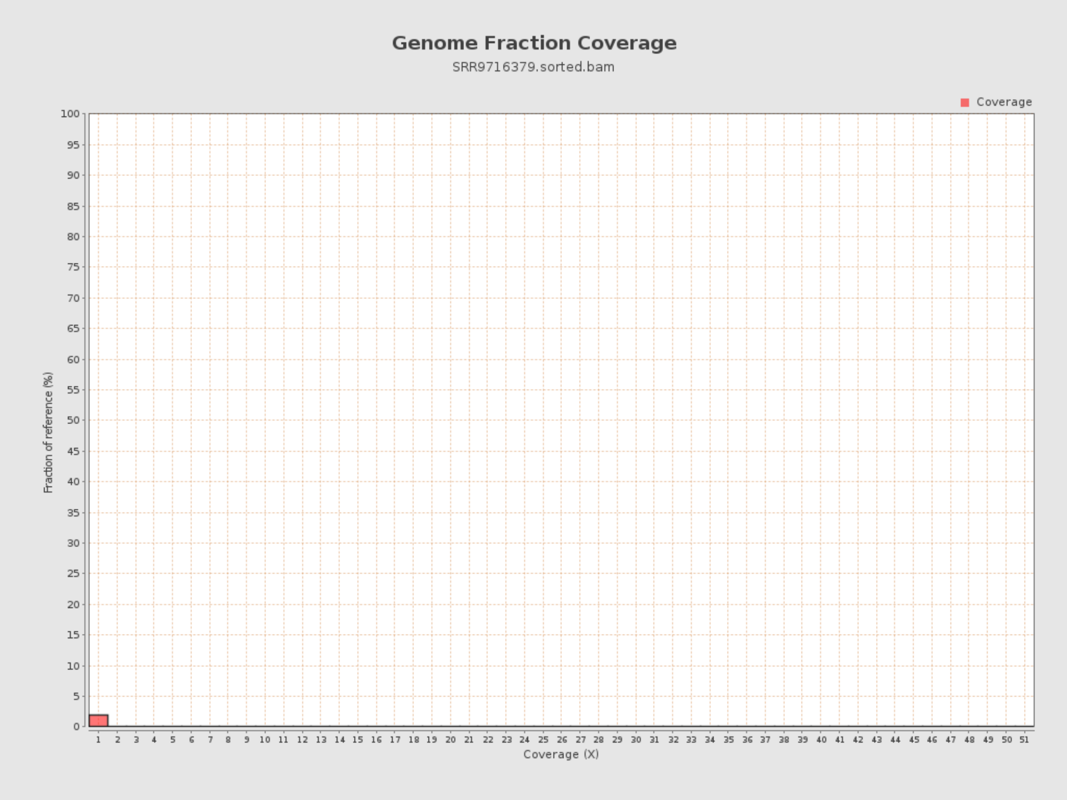
# 4. Results : Coverage Histogram



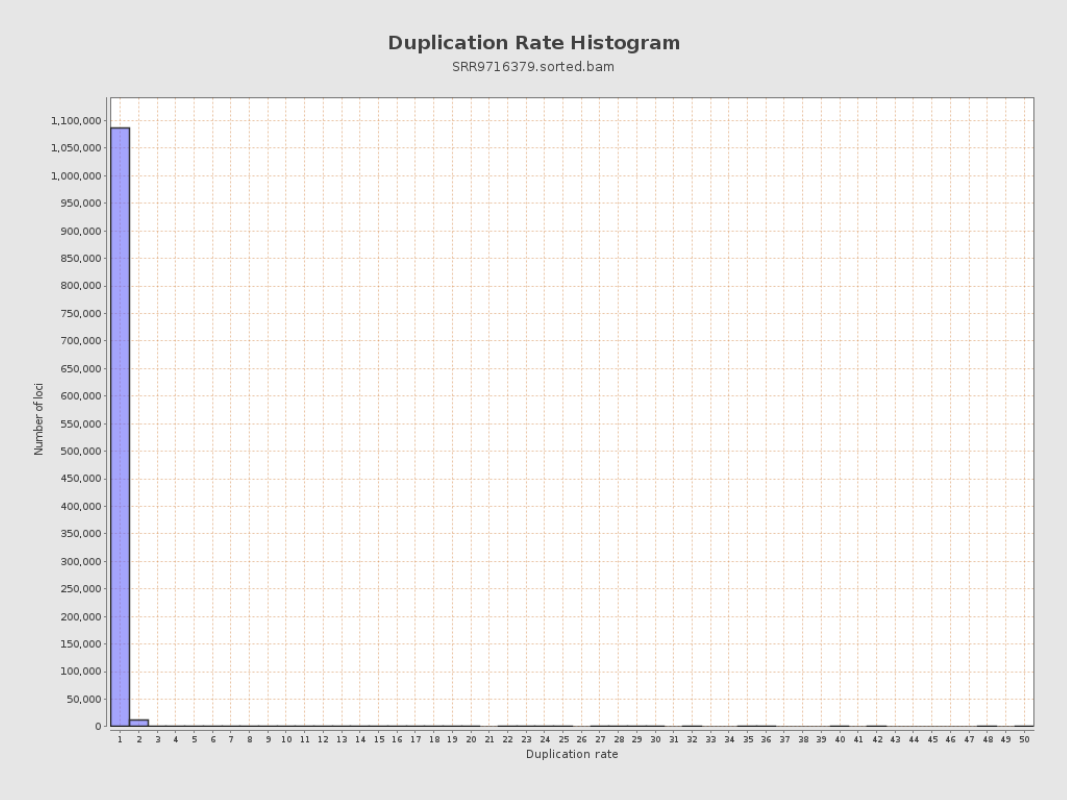
# 5. Results : Coverage Histogram (0-50X)



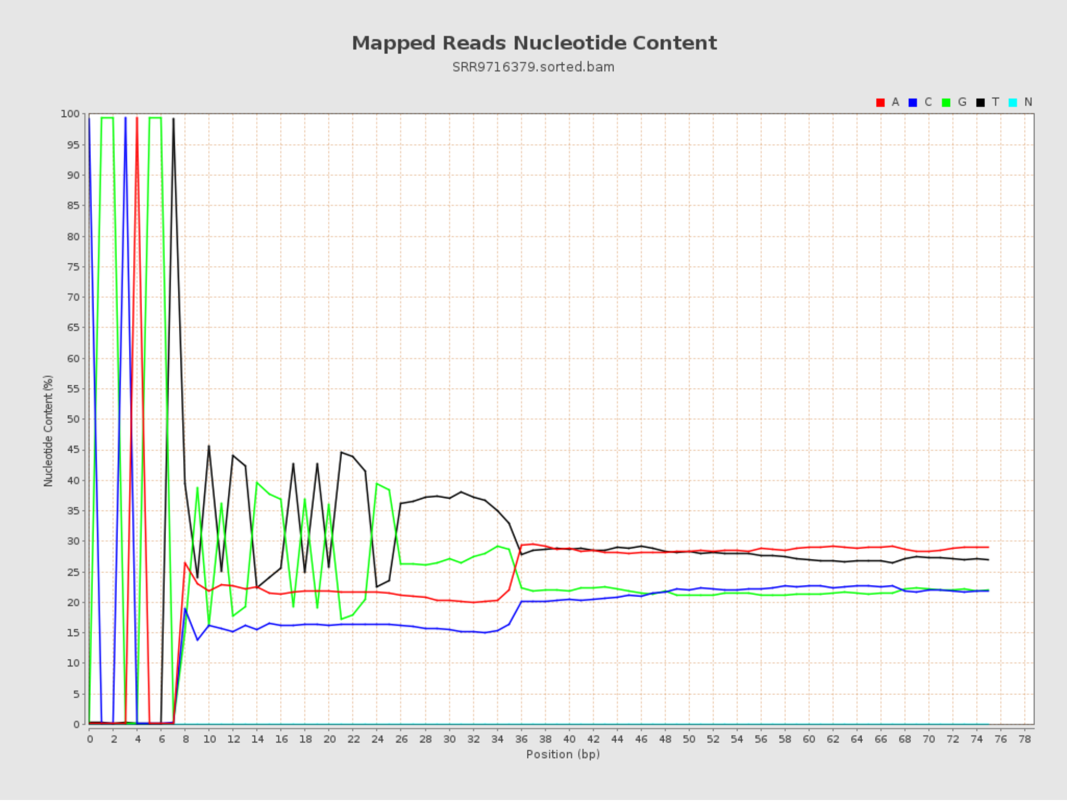
# 6. Results : Genome Fraction Coverage



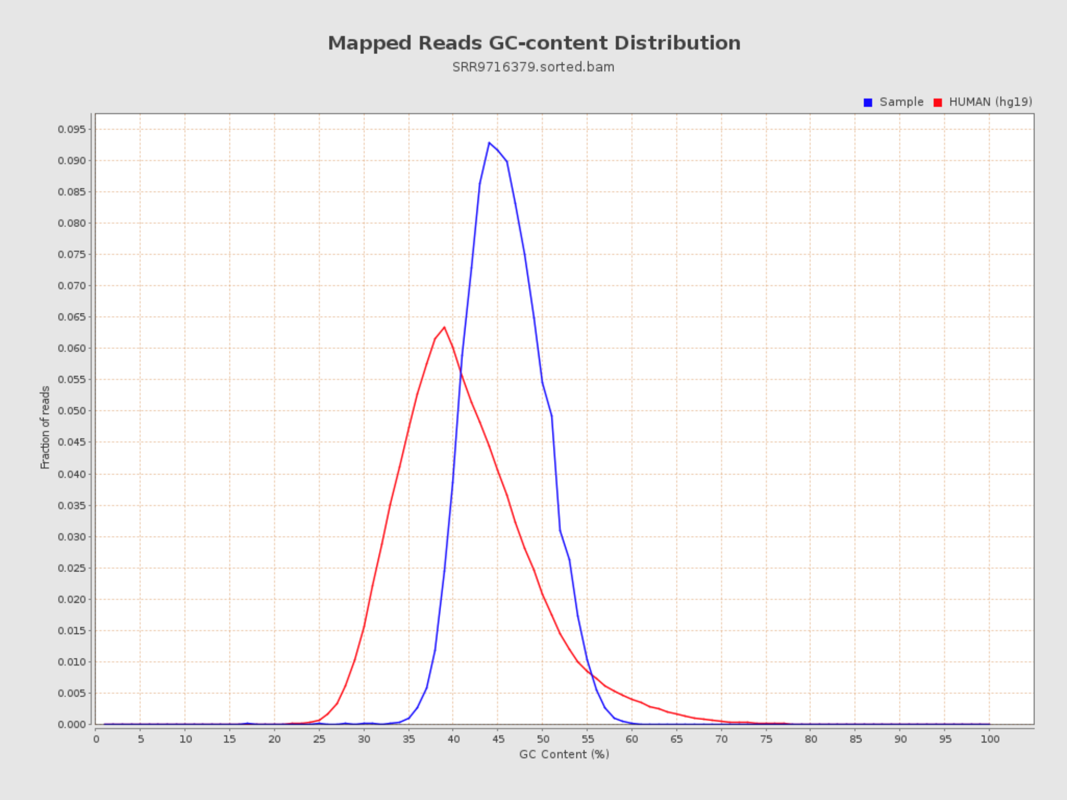
# 7. Results : Duplication Rate Histogram



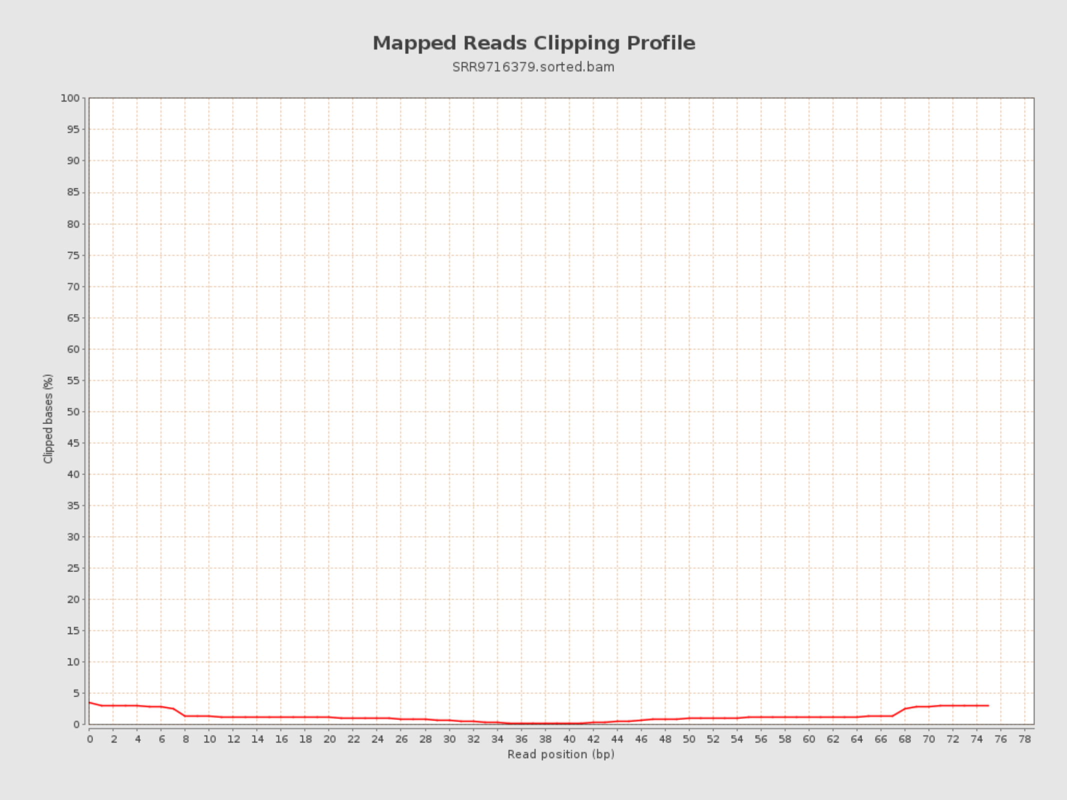
# 8. Results : Mapped Reads Nucleotide Content



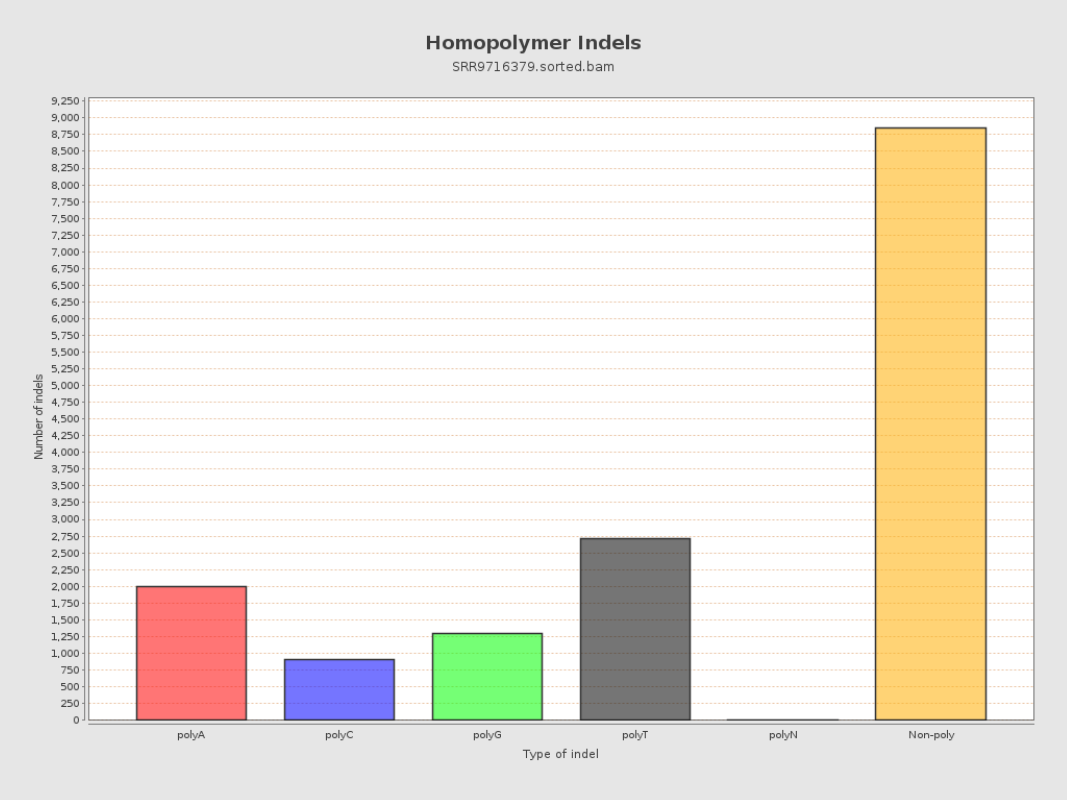
# 9. Results : Mapped Reads GC-content Distribution



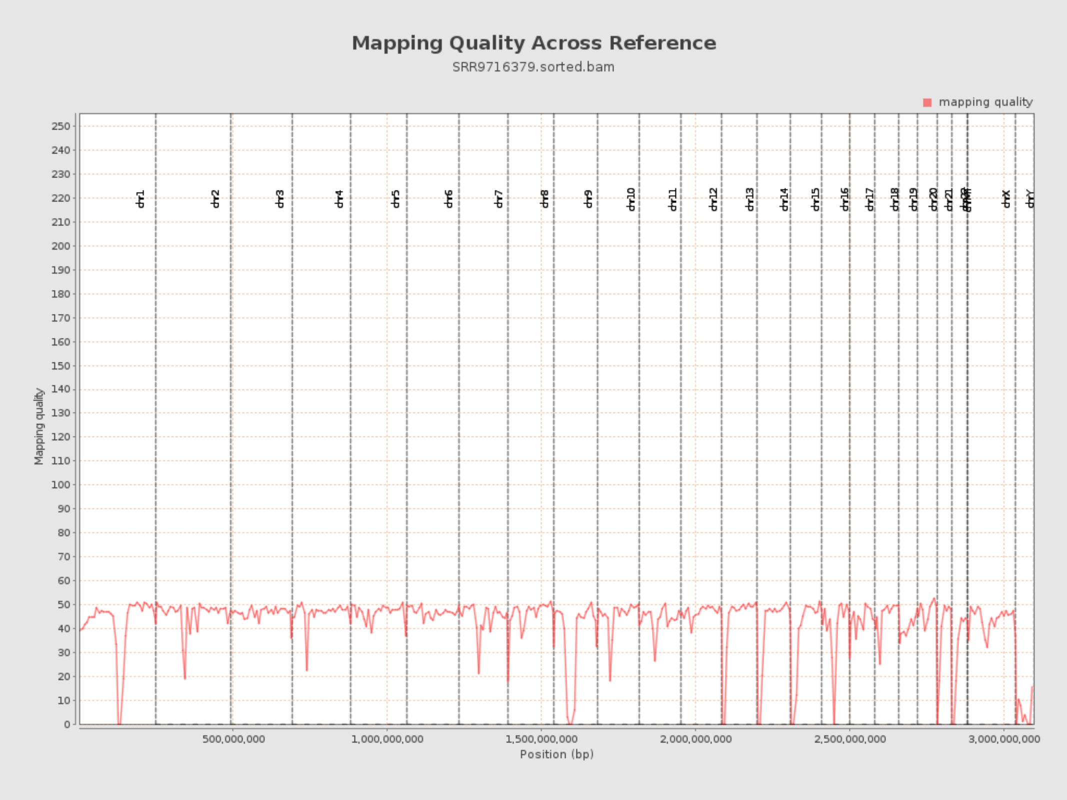
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram