# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/02 06:14:13*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716298.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_SRR9716298 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716298.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 02 06:14:12 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716298.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 983,283 |
| Mapped reads | 822,471 / 83.65% |
| Unmapped reads | 160,812 / 16.35% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 3,363 / 0.34% |
| Read min/max/mean length | 30 / 76 / 76.11 |
| Duplicated reads (estimated) | 21,992 / 2.24% |
| Duplication rate | 2.07% |
| Clipped reads | 823,602 / 83.76% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 12,075,934 / 25.12% |
| Number/percentage of C's | 9,099,684 / 18.93% |
| Number/percentage of T's | 15,295,267 / 31.81% |
| Number/percentage of G's | 11,605,750 / 24.14% |
| Number/percentage of N's | 1,323 / 0% |
| GC Percentage | 43.07% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0155 |
| | |

| | |
|---|---|
| Standard Deviation | 0.166 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.37 |

## 2.5. Mismatches and indels

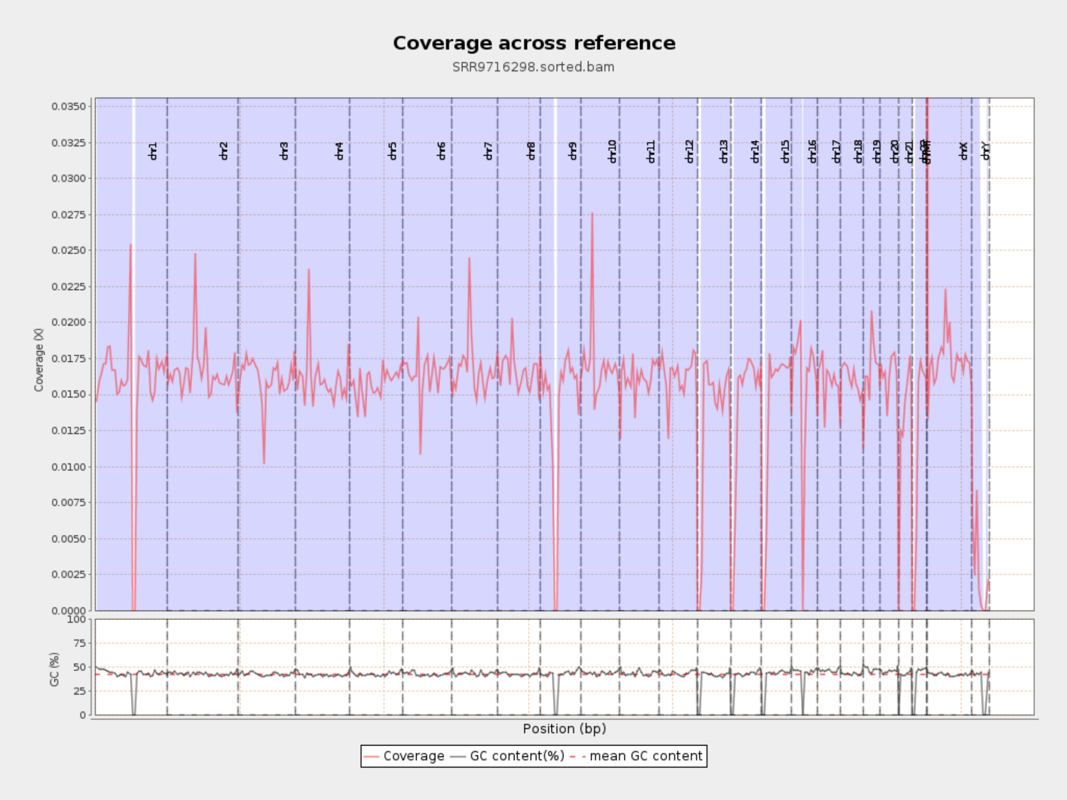
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 236,916 |
| Insertions | 3,647 |
| Mapped reads with at least one insertion | 0.44% |
| Deletions | 9,075 |
| Mapped reads with at least one deletion | 1.09% |
| Homopolymer indels | 43.14% |

## 2.6. Chromosome stats

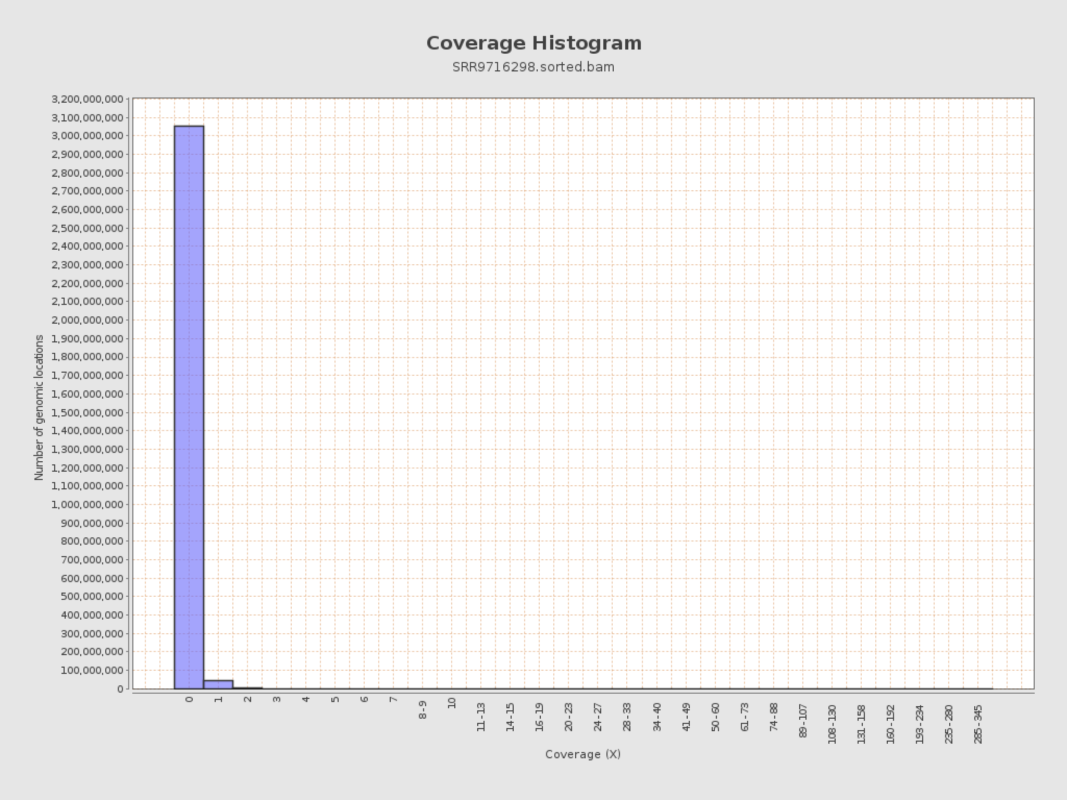
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 3914658 | 0.0157 | 0.2784 |
| chr2 | 243199373 | 4039601 | 0.0166 | 0.1984 |
| chr3 | 198022430 | 3185149 | 0.0161 | 0.1341 |
| chr4 | 191154276 | 3083516 | 0.0161 | 0.1396 |
| chr5 | 180915260 | 2856224 | 0.0158 | 0.1334 |
| chr6 | 171115067 | 2825933 | 0.0165 | 0.1509 |
| chr7 | 159138663 | 2676192 | 0.0168 | 0.1834 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2427063 | 0.0166 | 0.1559 |
| chr9 | 141213431 | 1983196 | 0.014 | 0.1435 |
| chr10 | 135534747 | 2319428 | 0.0171 | 0.1661 |
| chr11 | 135006516 | 2184028 | 0.0162 | 0.1506 |
| chr12 | 133851895 | 2185312 | 0.0163 | 0.1366 |
| chr13 | 115169878 | 1503466 | 0.0131 | 0.1215 |
| chr14 | 107349540 | 1462633 | 0.0136 | 0.1262 |
| chr15 | 102531392 | 1394763 | 0.0136 | 0.1242 |
| chr16 | 90354753 | 1400765 | 0.0155 | 0.1358 |
| chr17 | 81195210 | 1294716 | 0.0159 | 0.1374 |
| chr18 | 78077248 | 1256915 | 0.0161 | 0.2183 |
| chr19 | 59128983 | 999855 | 0.0169 | 0.2103 |
| chr20 | 63025520 | 1024225 | 0.0163 | 0.1366 |
| chr21 | 48129895 | 637488 | 0.0132 | 0.1296 |
| chr22 | 51304566 | 579080 | 0.0113 | 0.1122 |
| chrMT | 16571 | 3606 | 0.2176 | 0.4697 |
| chrX | 155270560 | 2705886 | 0.0174 | 0.1469 |
| chrY | 59373566 | 148524 | 0.0025 | 0.0755 |

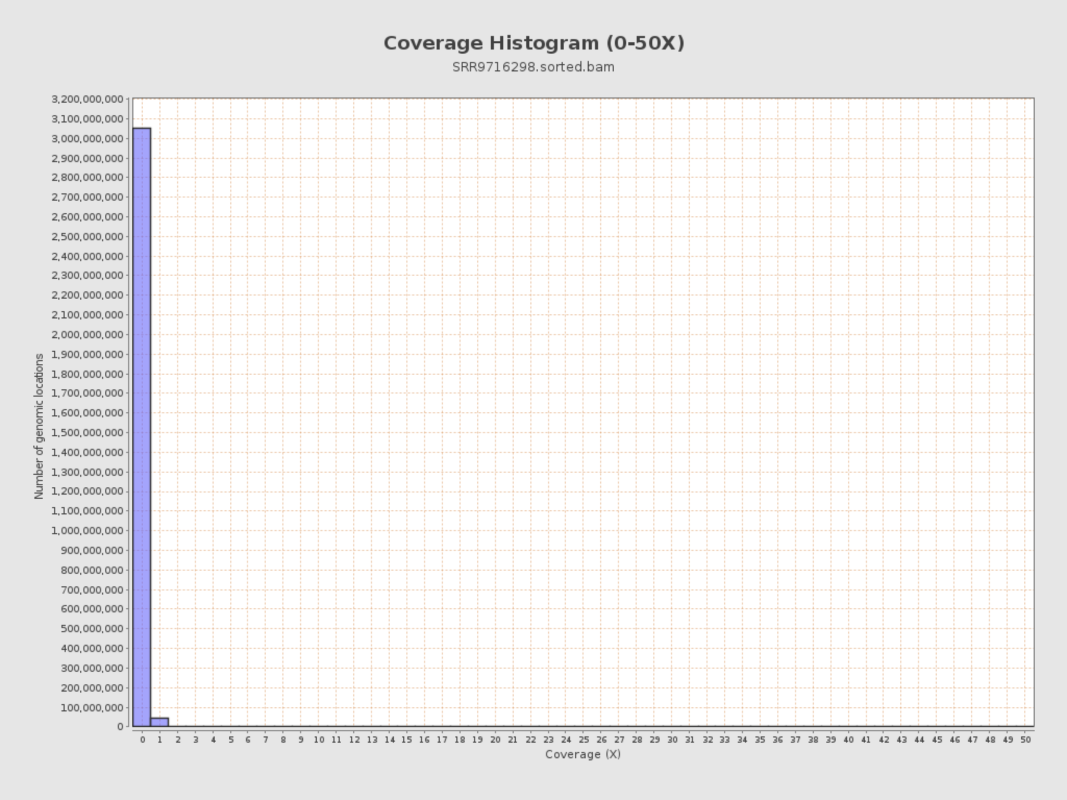
# 3. Results : Coverage across reference



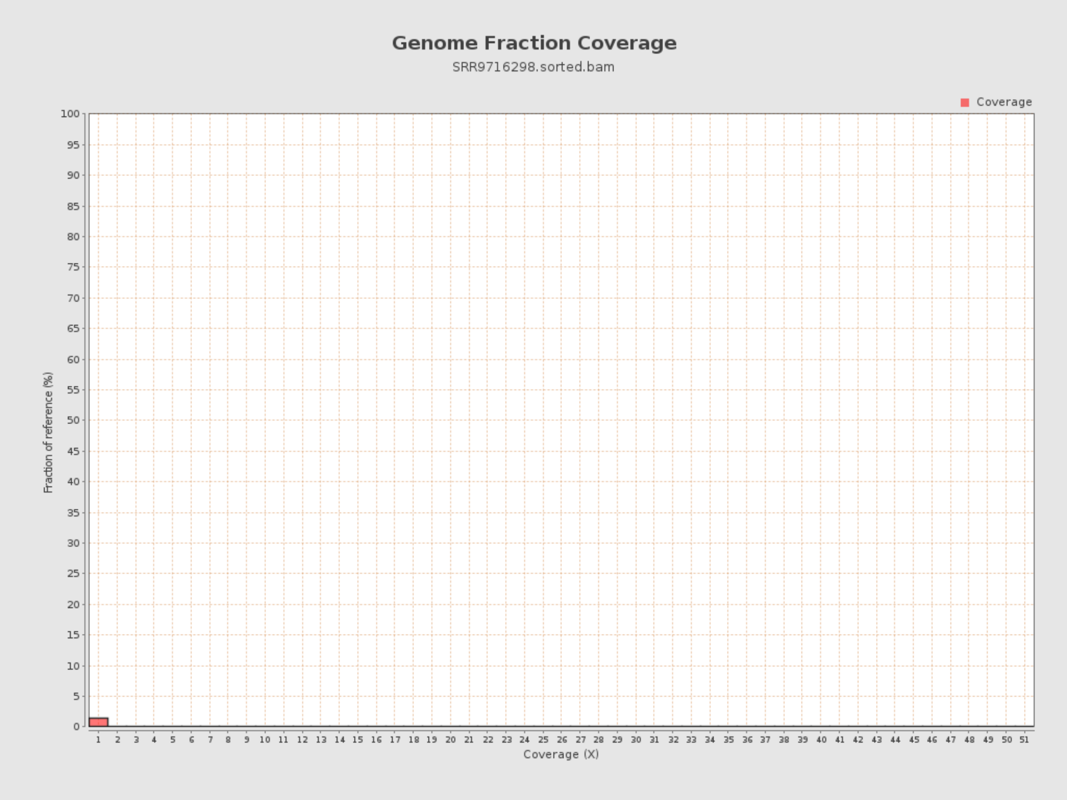
# 4. Results : Coverage Histogram



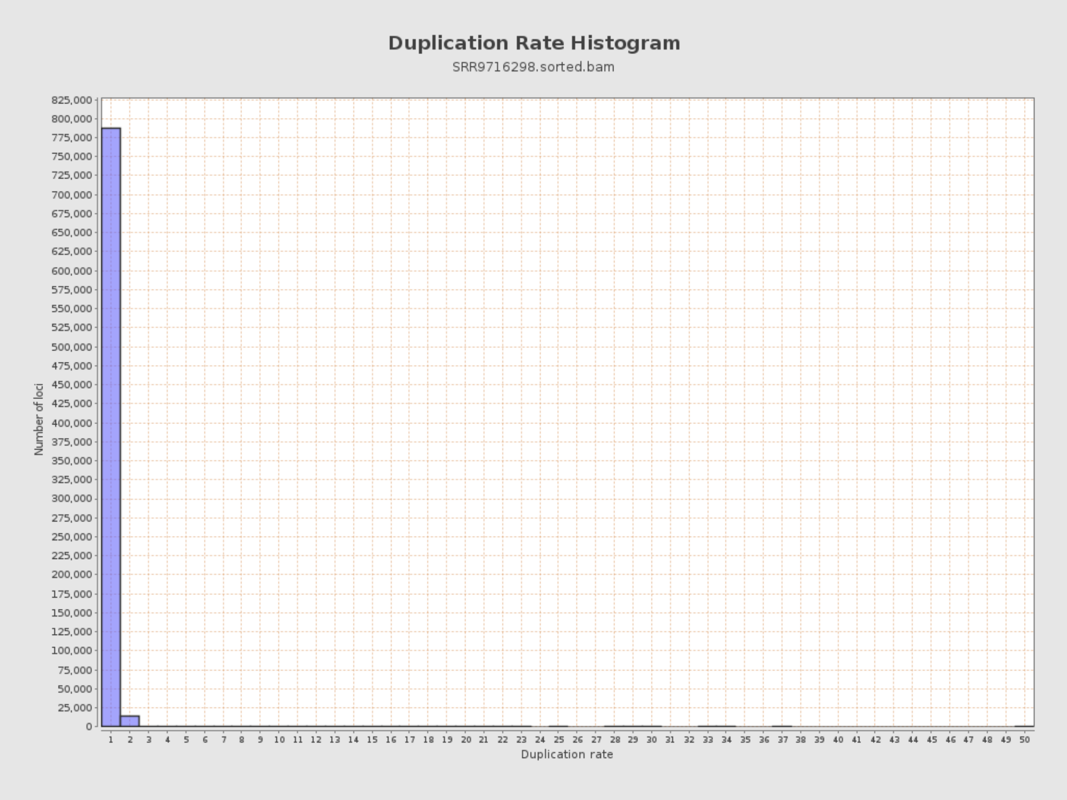
# 5. Results : Coverage Histogram (0-50X)



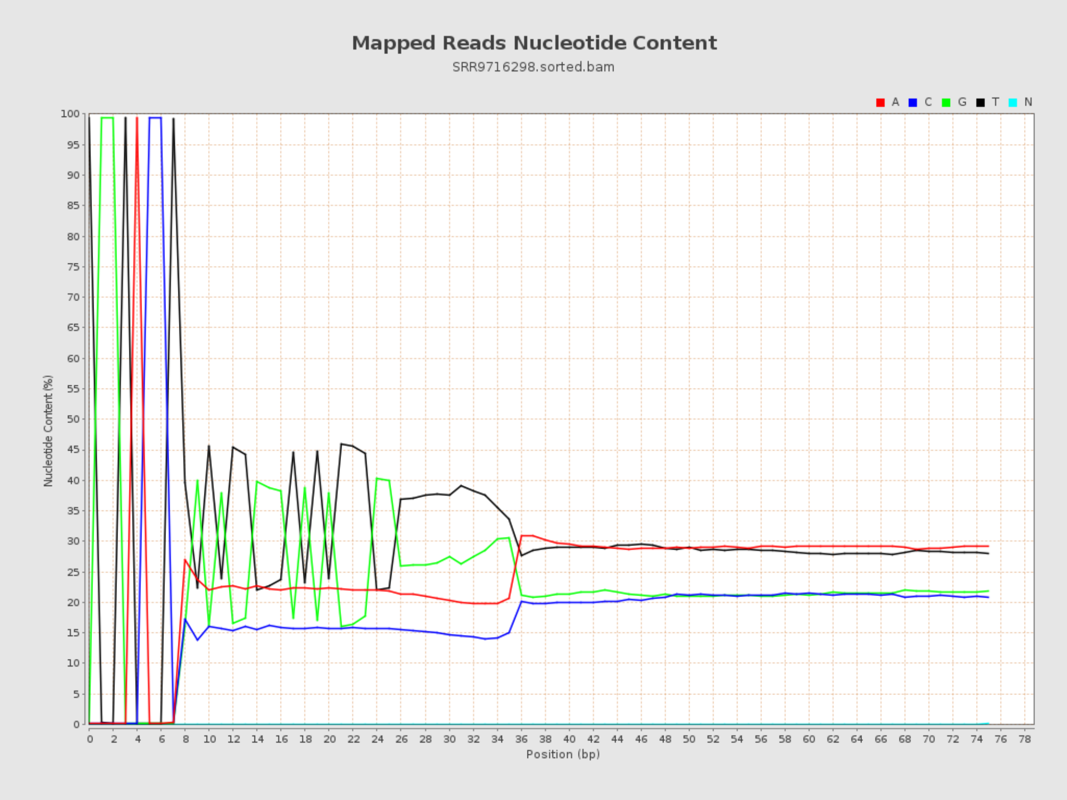
# 6. Results : Genome Fraction Coverage



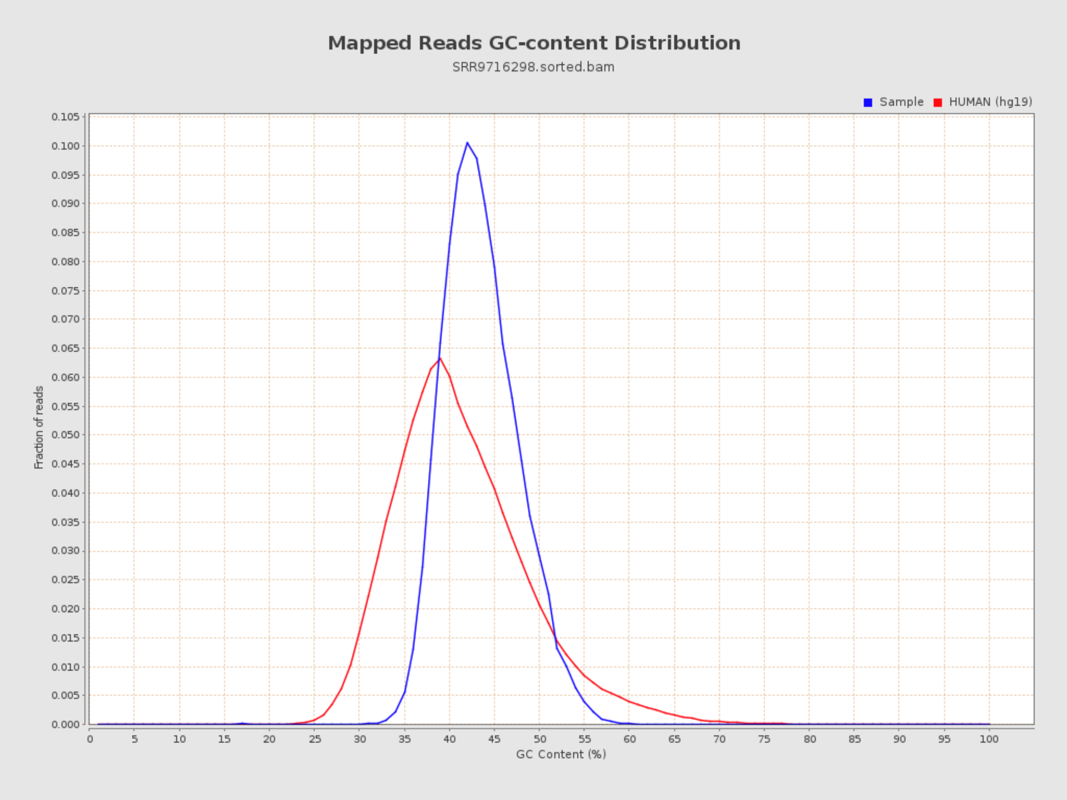
# 7. Results : Duplication Rate Histogram



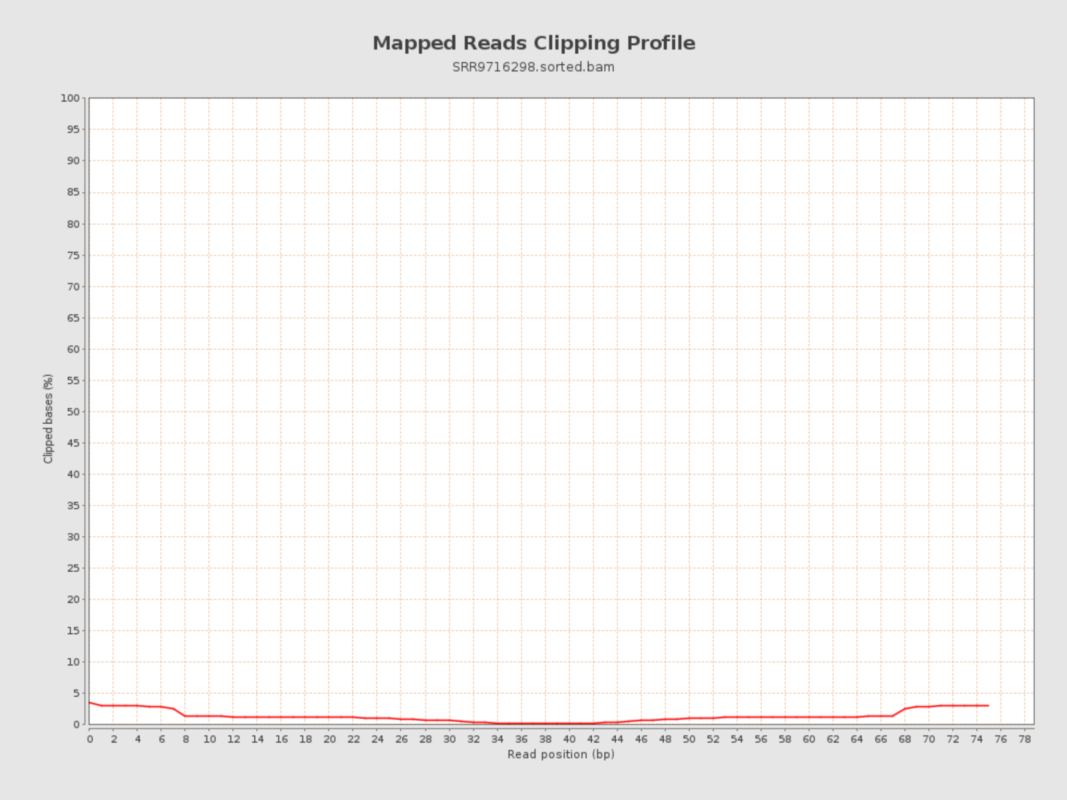
# 8. Results : Mapped Reads Nucleotide Content



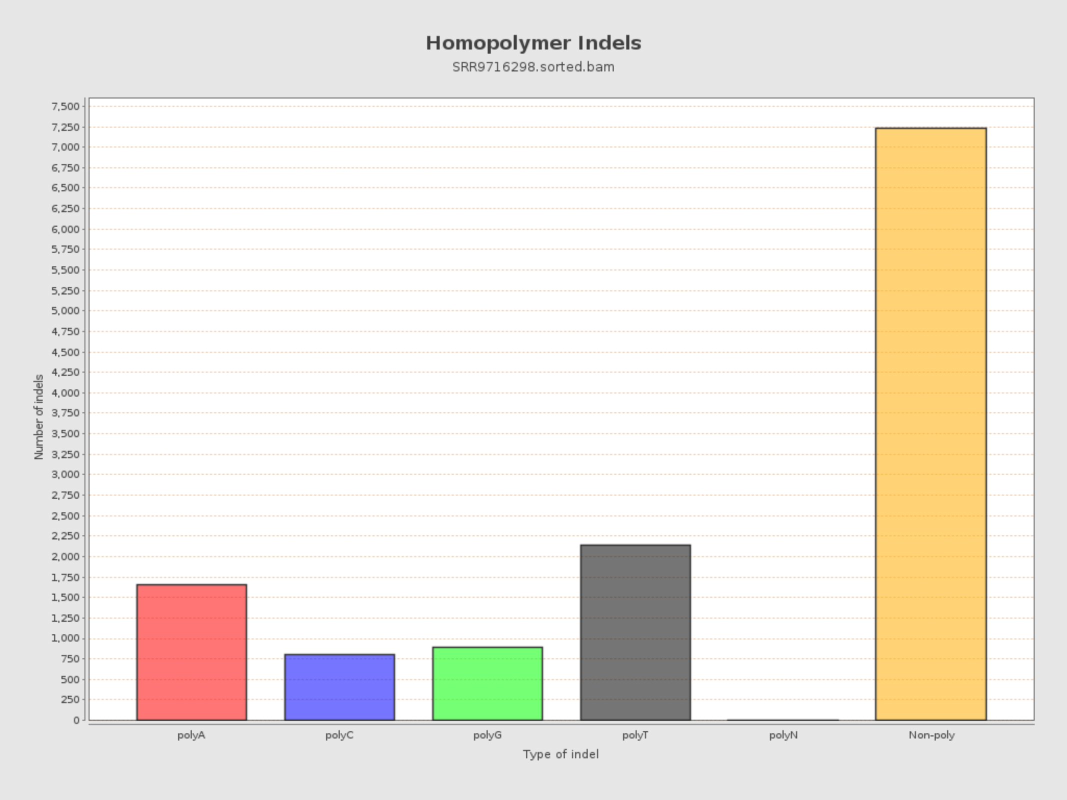
# 9. Results : Mapped Reads GC-content Distribution



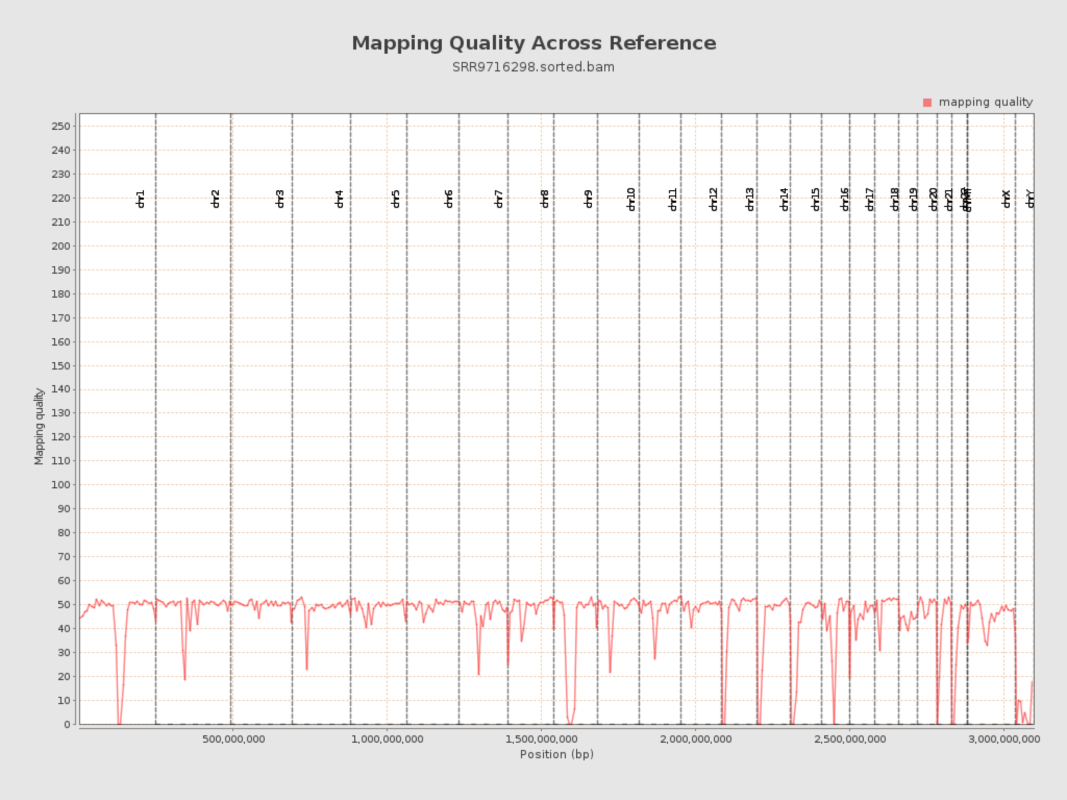
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram