# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/02 05:49:35*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716288.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_SRR9716288 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716288.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 02 05:49:34 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716288.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 724,812 |
| Mapped reads | 577,781 / 79.71% |
| Unmapped reads | 147,031 / 20.29% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 1,762 / 0.24% |
| Read min/max/mean length | 30 / 76 / 76.08 |
| Duplicated reads (estimated) | 9,852 / 1.36% |
| Duplication rate | 1.16% |
| Clipped reads | 578,224 / 79.78% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 7,559,136 / 23.7% |
| Number/percentage of C's | 6,234,898 / 19.55% |
| Number/percentage of T's | 9,523,065 / 29.86% |
| Number/percentage of G's | 8,579,244 / 26.9% |
| Number/percentage of N's | 900 / 0% |
| GC Percentage | 46.44% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0103 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1187 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 39.03 |

## 2.5. Mismatches and indels

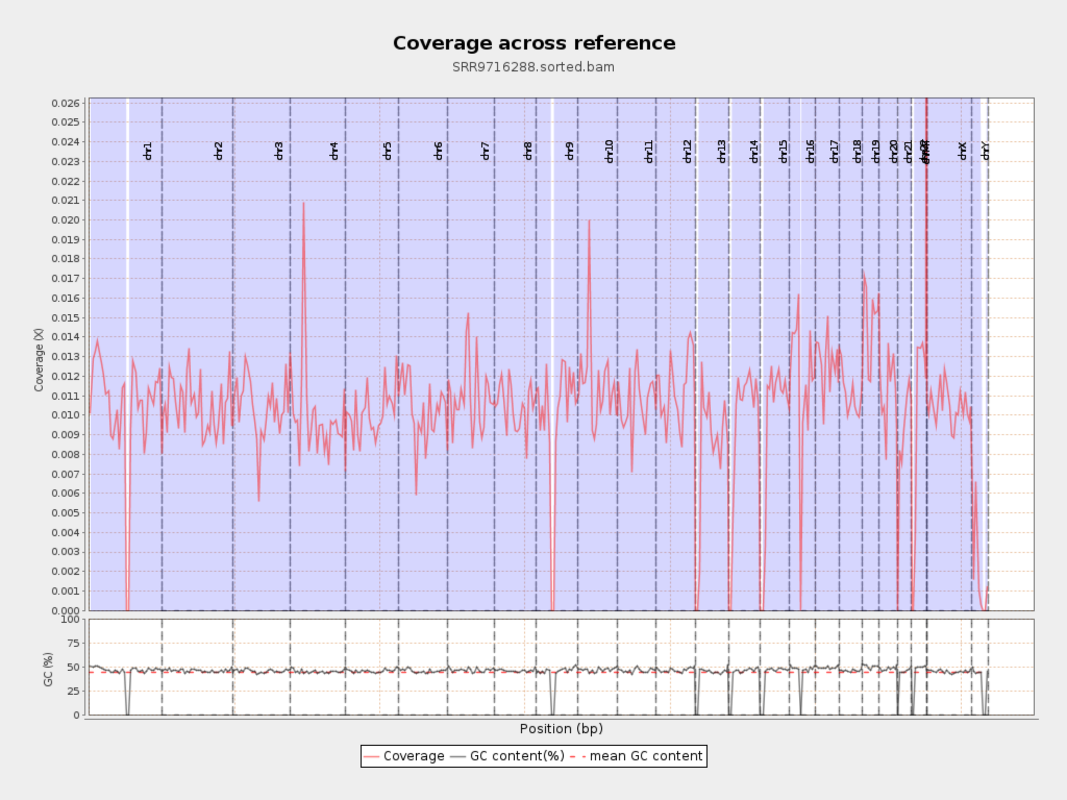
| | |
|---|---|
| General error rate | 0.55% |
| Mismatches | 170,848 |
| Insertions | 2,544 |
| Mapped reads with at least one insertion | 0.44% |
| Deletions | 5,581 |
| Mapped reads with at least one deletion | 0.96% |
| Homopolymer indels | 36.74% |

## 2.6. Chromosome stats

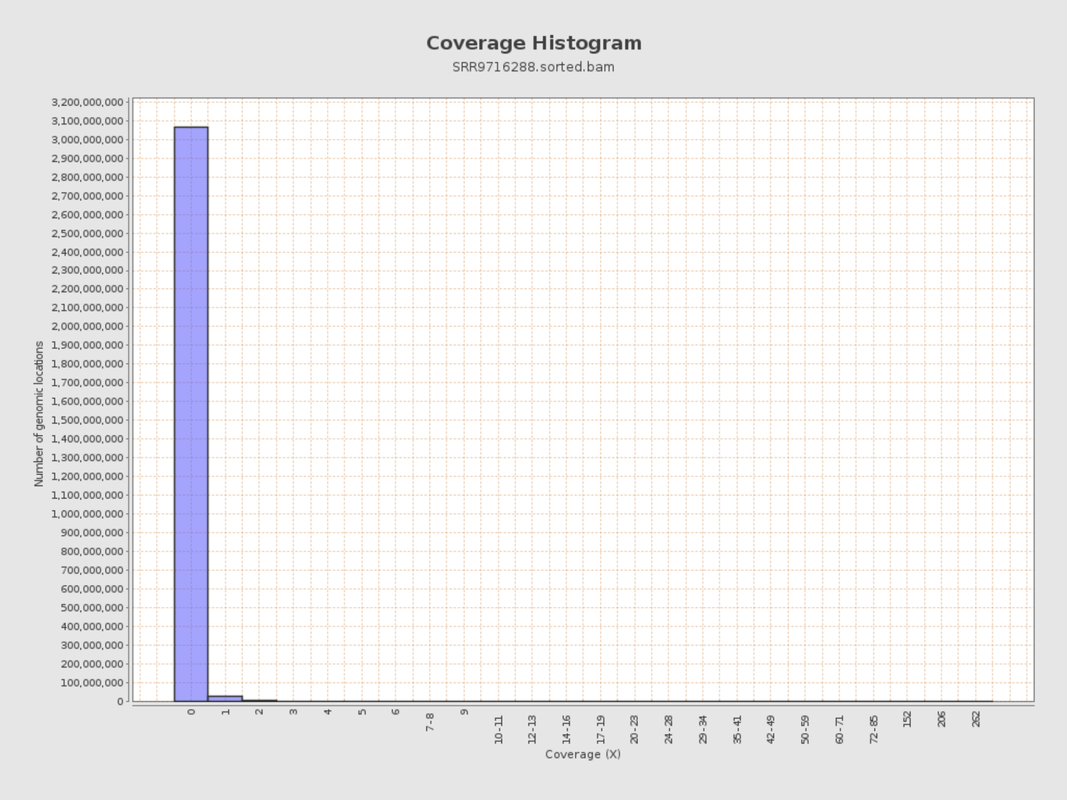
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 2577700 | 0.0103 | 0.1217 |
| chr2 | 243199373 | 2562272 | 0.0105 | 0.1542 |
| chr3 | 198022430 | 2061916 | 0.0104 | 0.1105 |
| chr4 | 191154276 | 1904519 | 0.01 | 0.1153 |
| chr5 | 180915260 | 1834105 | 0.0101 | 0.1063 |
| chr6 | 171115067 | 1756485 | 0.0103 | 0.1102 |
| chr7 | 159138663 | 1740889 | 0.0109 | 0.1275 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 1534363 | 0.0105 | 0.1141 |
| chr9 | 141213431 | 1361830 | 0.0096 | 0.1087 |
| chr10 | 135534747 | 1577615 | 0.0116 | 0.1396 |
| chr11 | 135006516 | 1439167 | 0.0107 | 0.122 |
| chr12 | 133851895 | 1516541 | 0.0113 | 0.1123 |
| chr13 | 115169878 | 927737 | 0.0081 | 0.0942 |
| chr14 | 107349540 | 1006238 | 0.0094 | 0.1039 |
| chr15 | 102531392 | 946512 | 0.0092 | 0.1026 |
| chr16 | 90354753 | 1052143 | 0.0116 | 0.1189 |
| chr17 | 81195210 | 1032727 | 0.0127 | 0.1226 |
| chr18 | 78077248 | 863408 | 0.0111 | 0.1319 |
| chr19 | 59128983 | 870721 | 0.0147 | 0.1438 |
| chr20 | 63025520 | 704947 | 0.0112 | 0.114 |
| chr21 | 48129895 | 423281 | 0.0088 | 0.1082 |
| chr22 | 51304566 | 468491 | 0.0091 | 0.1025 |
| chrMT | 16571 | 1476 | 0.0891 | 0.3043 |
| chrX | 155270560 | 1628828 | 0.0105 | 0.1144 |
| chrY | 59373566 | 112711 | 0.0019 | 0.0634 |

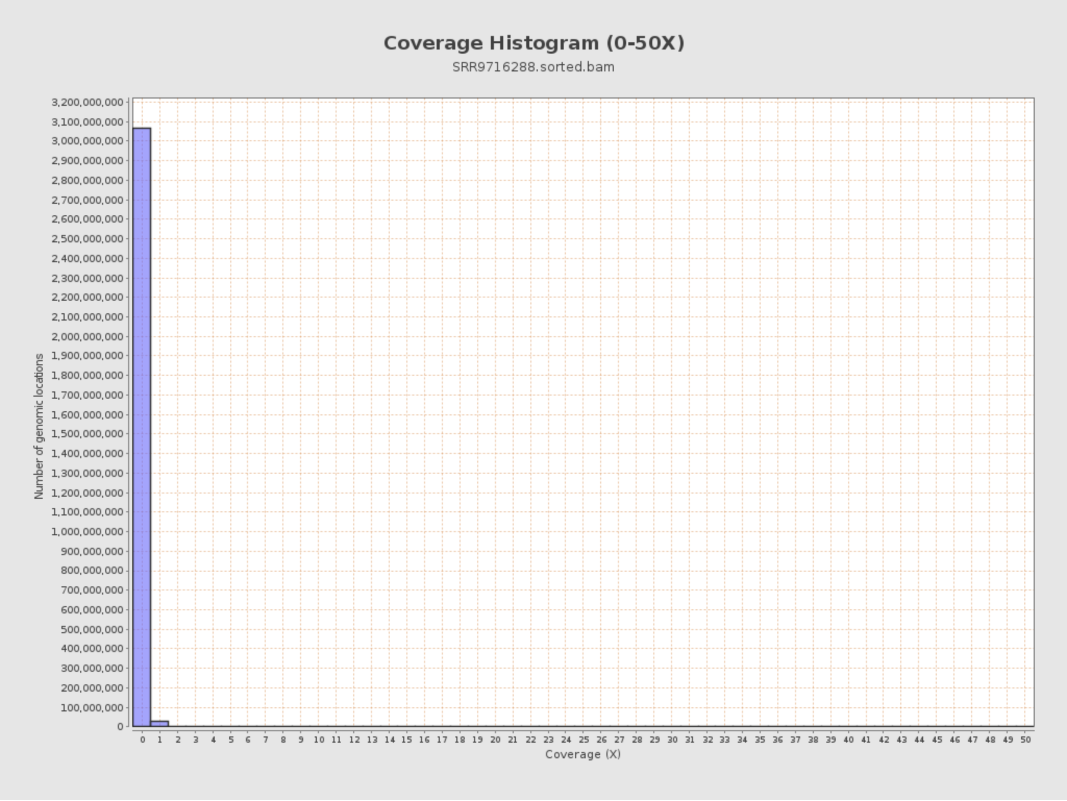
# 3. Results : Coverage across reference



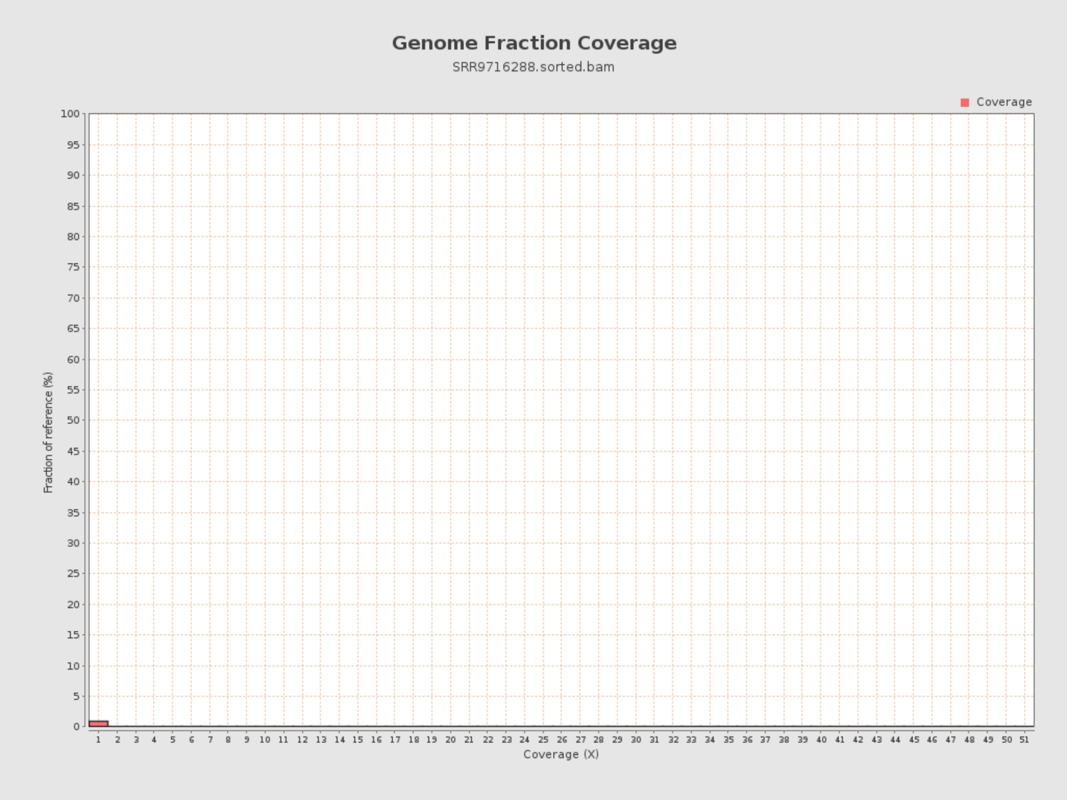
# 4. Results : Coverage Histogram



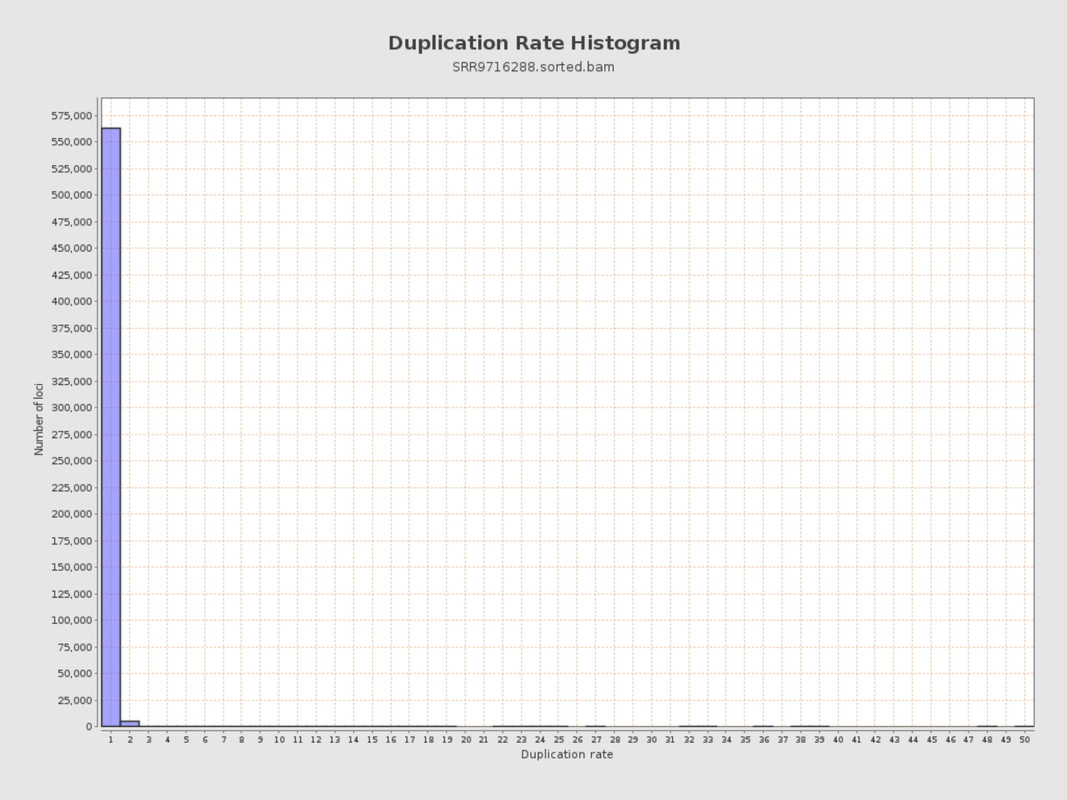
# 5. Results : Coverage Histogram (0-50X)



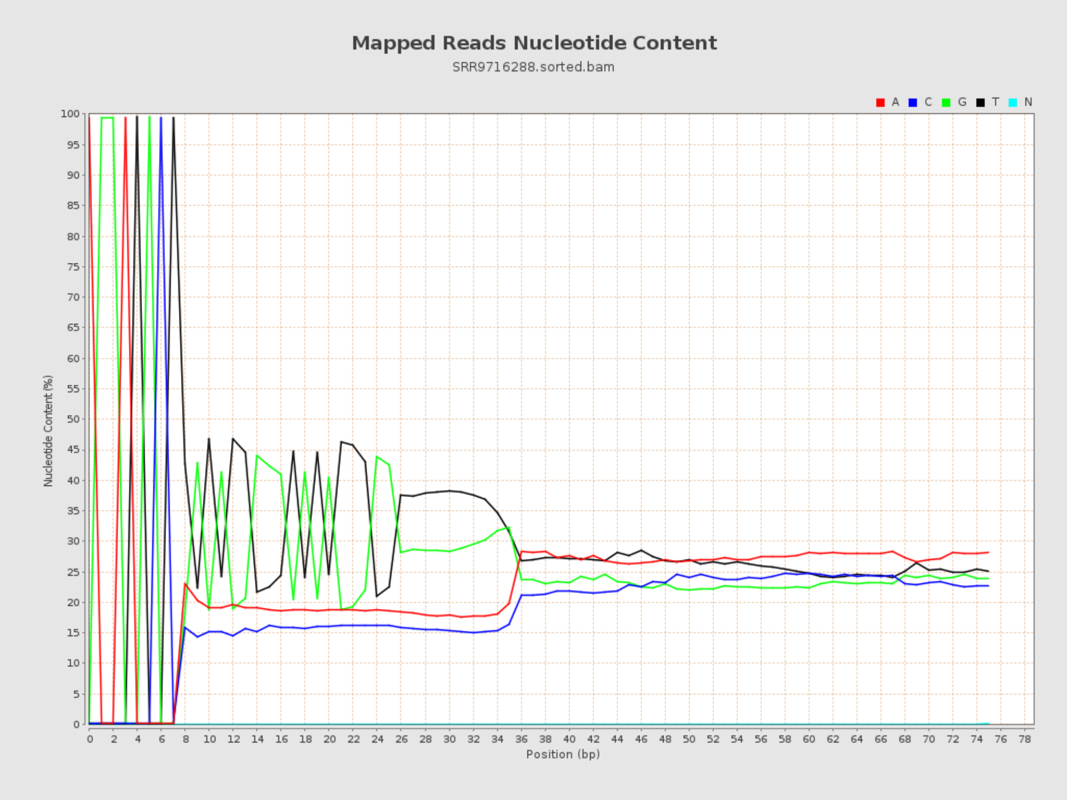
# 6. Results : Genome Fraction Coverage



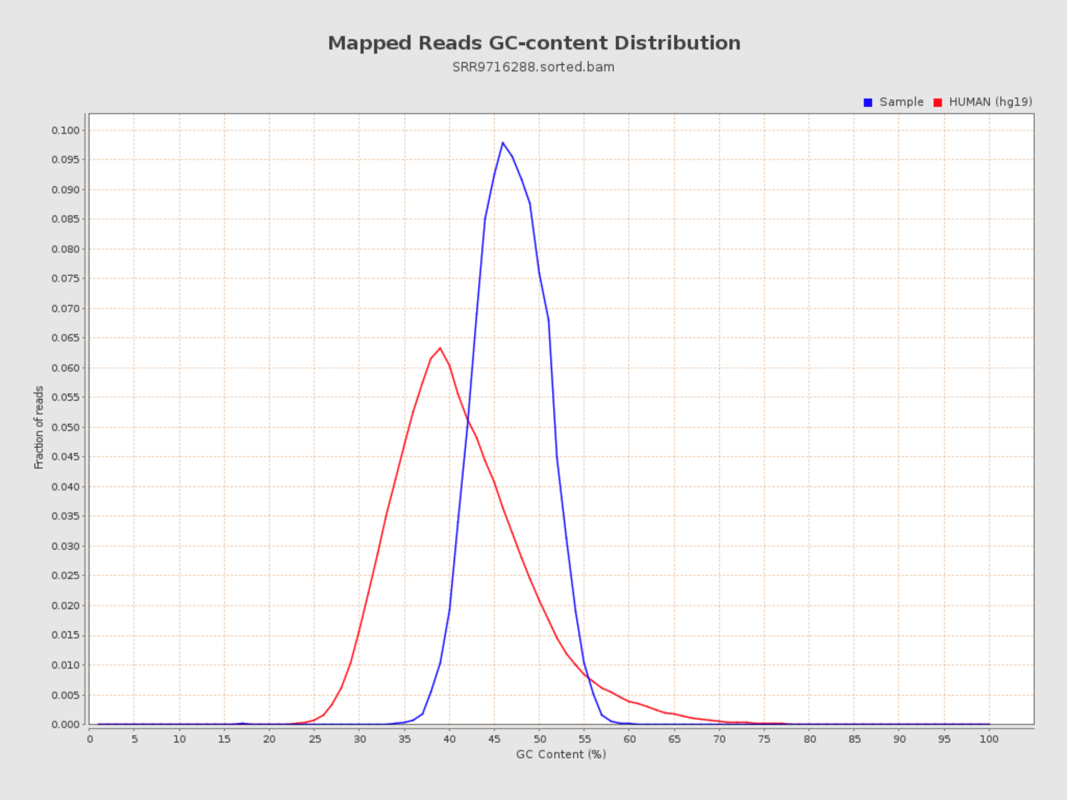
# 7. Results : Duplication Rate Histogram



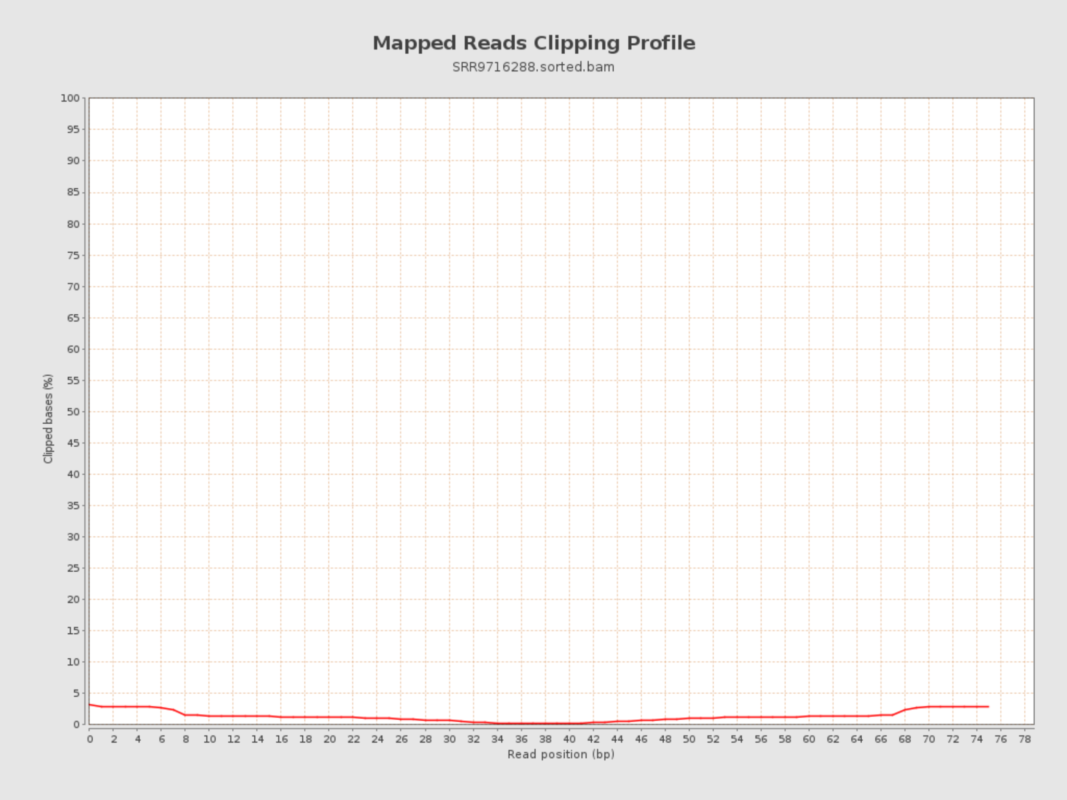
# 8. Results : Mapped Reads Nucleotide Content



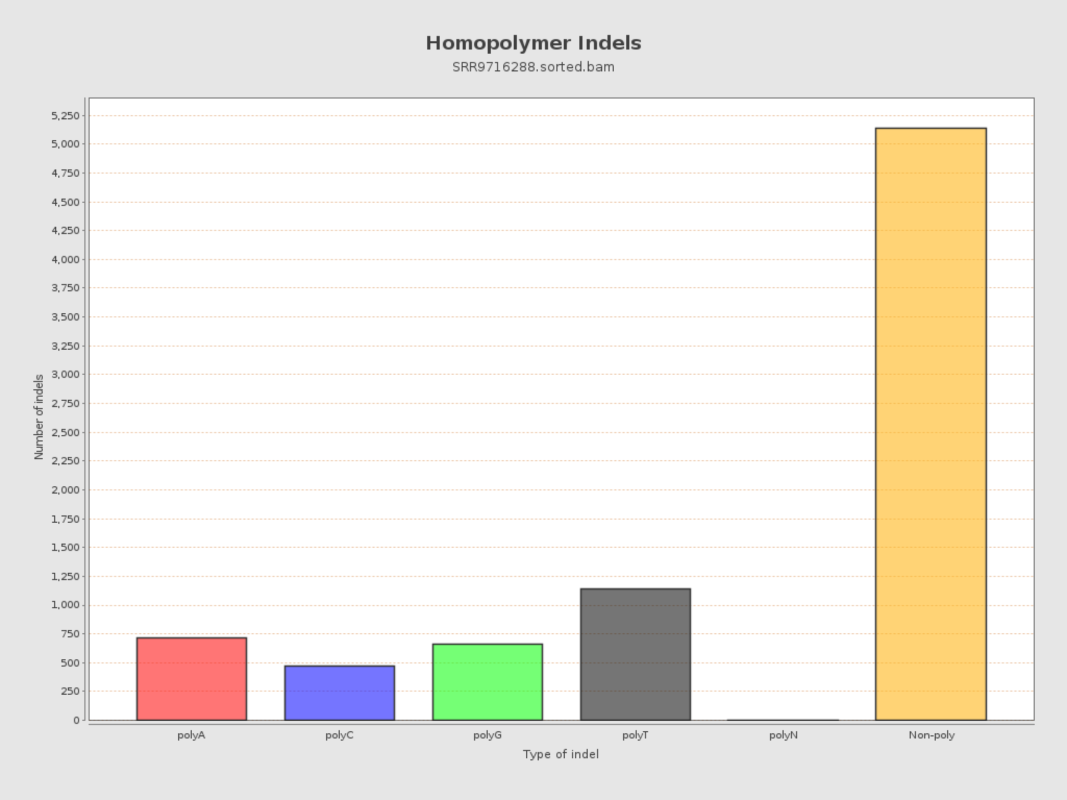
# 9. Results : Mapped Reads GC-content Distribution



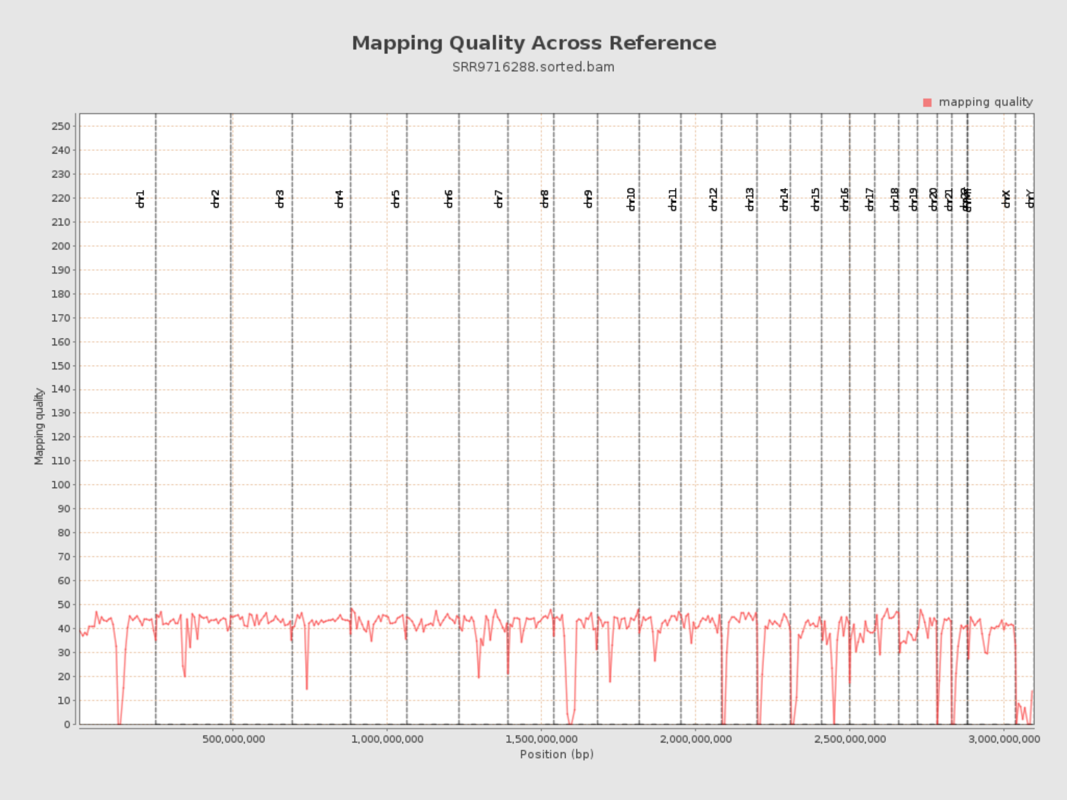
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram