# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 19:09:40*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716931.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_SRR9716931 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716931.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 19:09:39 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716931.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,112,521 |
| Mapped reads | 898,413 / 80.75% |
| Unmapped reads | 214,108 / 19.25% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 3,123 / 0.28% |
| Read min/max/mean length | 30 / 76 / 76.09 |
| Duplicated reads (estimated) | 18,813 / 1.69% |
| Duplication rate | 1.45% |
| Clipped reads | 898,721 / 80.78% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 13,156,297 / 25.9% |
| Number/percentage of C's | 9,296,779 / 18.3% |
| Number/percentage of T's | 15,816,067 / 31.14% |
| Number/percentage of G's | 12,522,305 / 24.65% |
| Number/percentage of N's | 727 / 0% |
| GC Percentage | 42.96% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0164 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1809 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 42.95 |

## 2.5. Mismatches and indels

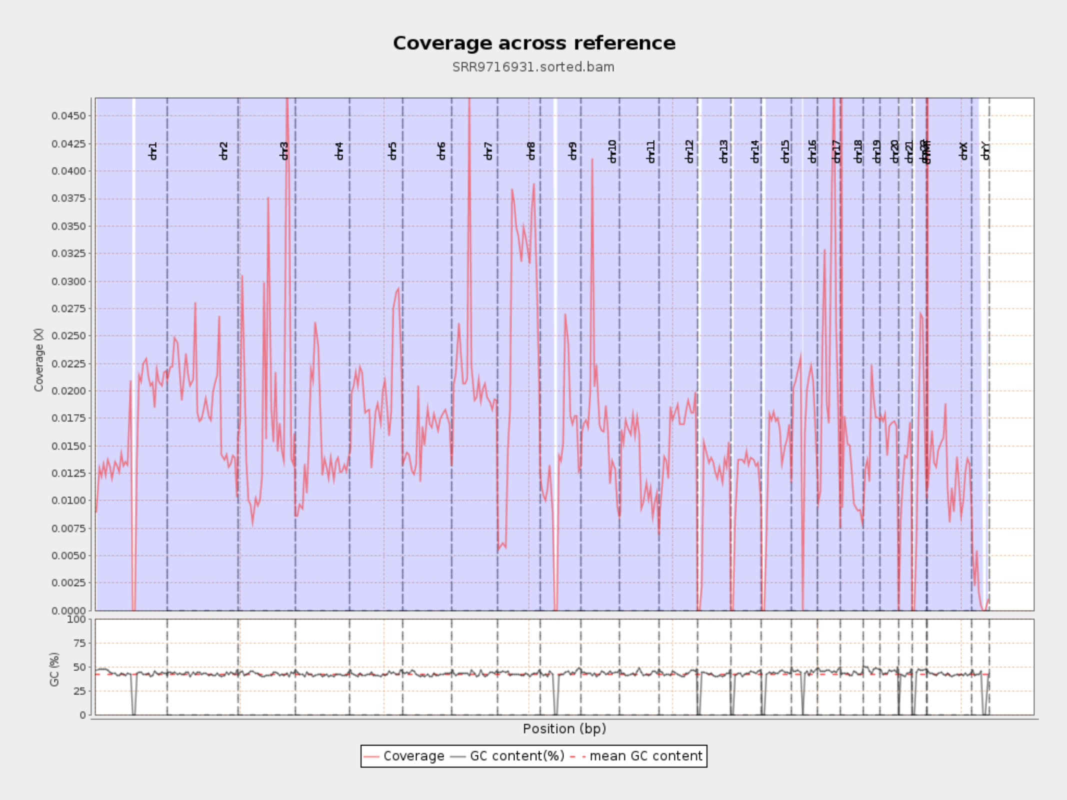
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 256,383 |
| Insertions | 4,463 |
| Mapped reads with at least one insertion | 0.49% |
| Deletions | 10,025 |
| Mapped reads with at least one deletion | 1.11% |
| Homopolymer indels | 37.15% |

## 2.6. Chromosome stats

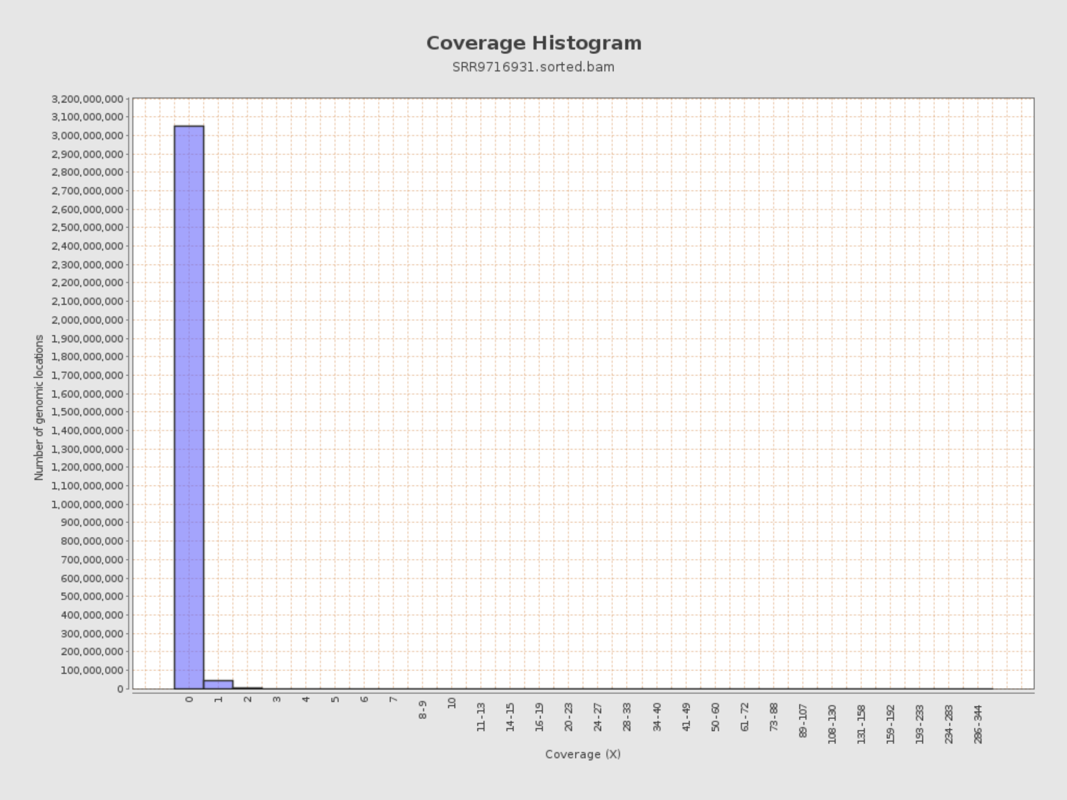
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 3925200 | 0.0157 | 0.201 |
| chr2 | 243199373 | 4677110 | 0.0192 | 0.2072 |
| chr3 | 198022430 | 3687947 | 0.0186 | 0.1502 |
| chr4 | 191154276 | 2734363 | 0.0143 | 0.1284 |
| chr5 | 180915260 | 3675793 | 0.0203 | 0.1493 |
| chr6 | 171115067 | 2719129 | 0.0159 | 0.1408 |
| chr7 | 159138663 | 3455229 | 0.0217 | 0.4129 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3779511 | 0.0258 | 0.1918 |
| chr9 | 141213431 | 1898793 | 0.0134 | 0.1376 |
| chr10 | 135534747 | 2373586 | 0.0175 | 0.2131 |
| chr11 | 135006516 | 1812189 | 0.0134 | 0.1426 |
| chr12 | 133851895 | 2175729 | 0.0163 | 0.1383 |
| chr13 | 115169878 | 1295078 | 0.0112 | 0.1118 |
| chr14 | 107349540 | 1216251 | 0.0113 | 0.1141 |
| chr15 | 102531392 | 1373297 | 0.0134 | 0.1242 |
| chr16 | 90354753 | 1618109 | 0.0179 | 0.1447 |
| chr17 | 81195210 | 1936975 | 0.0239 | 0.1678 |
| chr18 | 78077248 | 1093617 | 0.014 | 0.1765 |
| chr19 | 59128983 | 952513 | 0.0161 | 0.2121 |
| chr20 | 63025520 | 1036719 | 0.0164 | 0.136 |
| chr21 | 48129895 | 569043 | 0.0118 | 0.1161 |
| chr22 | 51304566 | 706379 | 0.0138 | 0.1234 |
| chrMT | 16571 | 8224 | 0.4963 | 0.7488 |
| chrX | 155270560 | 1976135 | 0.0127 | 0.1282 |
| chrY | 59373566 | 110836 | 0.0019 | 0.0529 |

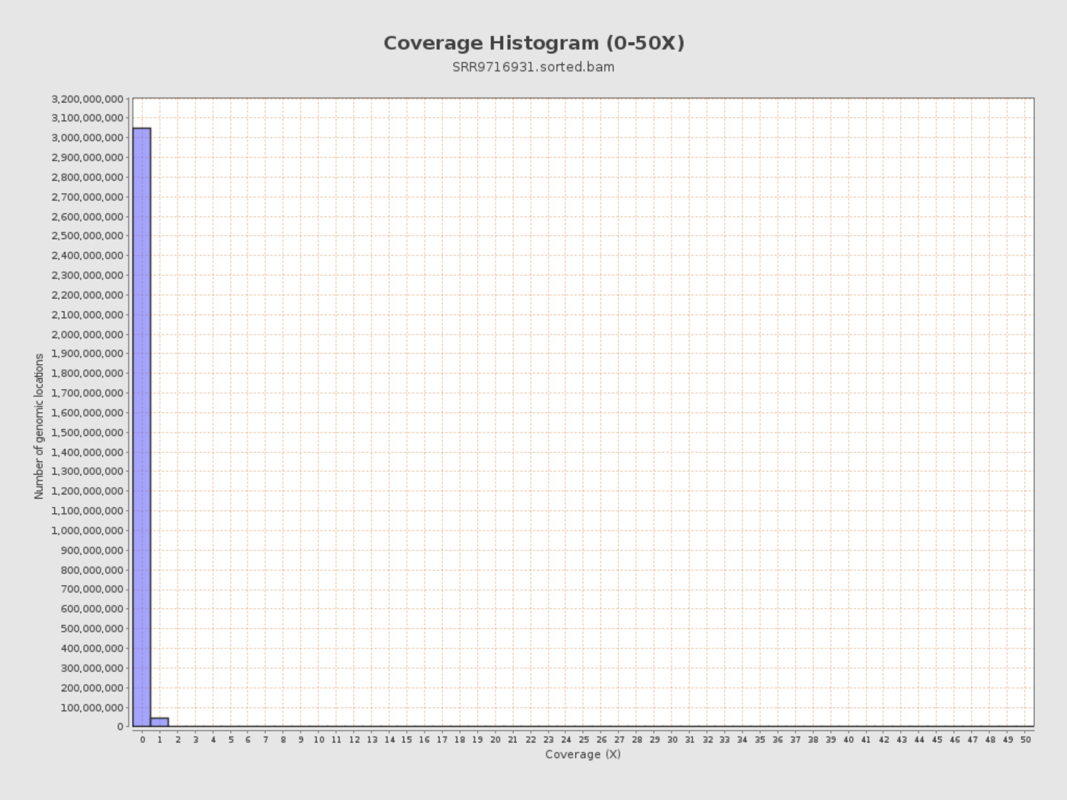
# 3. Results : Coverage across reference



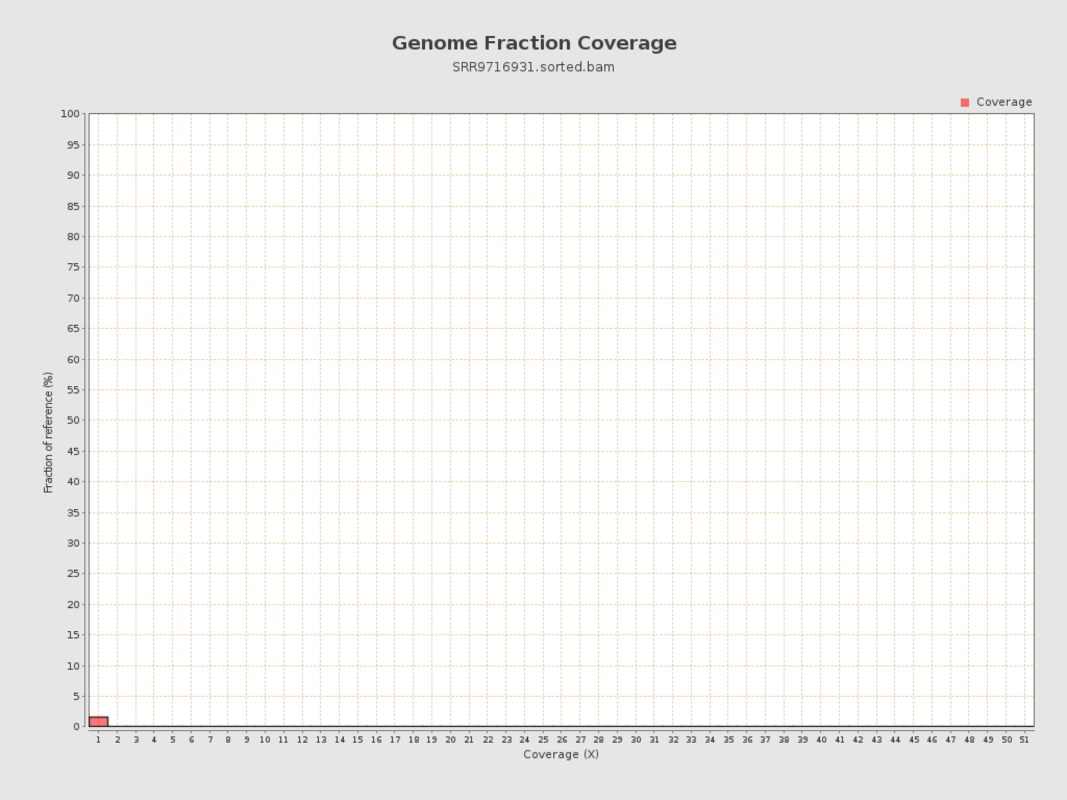
# 4. Results : Coverage Histogram



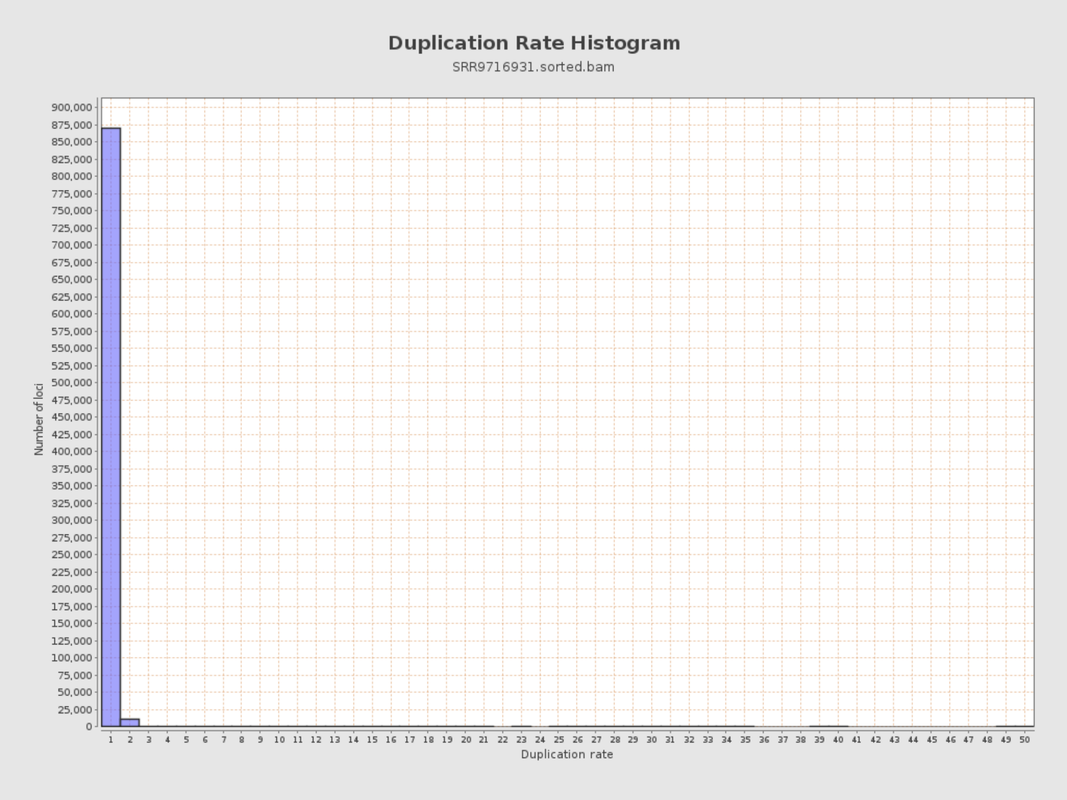
# 5. Results : Coverage Histogram (0-50X)



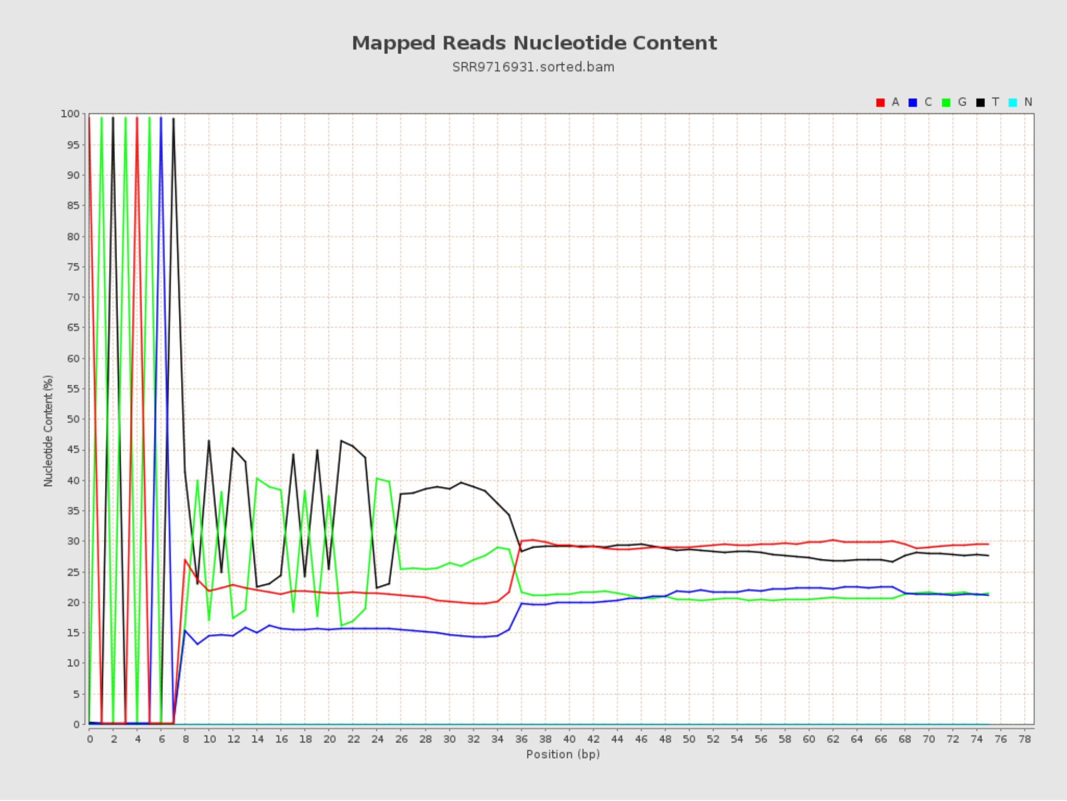
# 6. Results : Genome Fraction Coverage



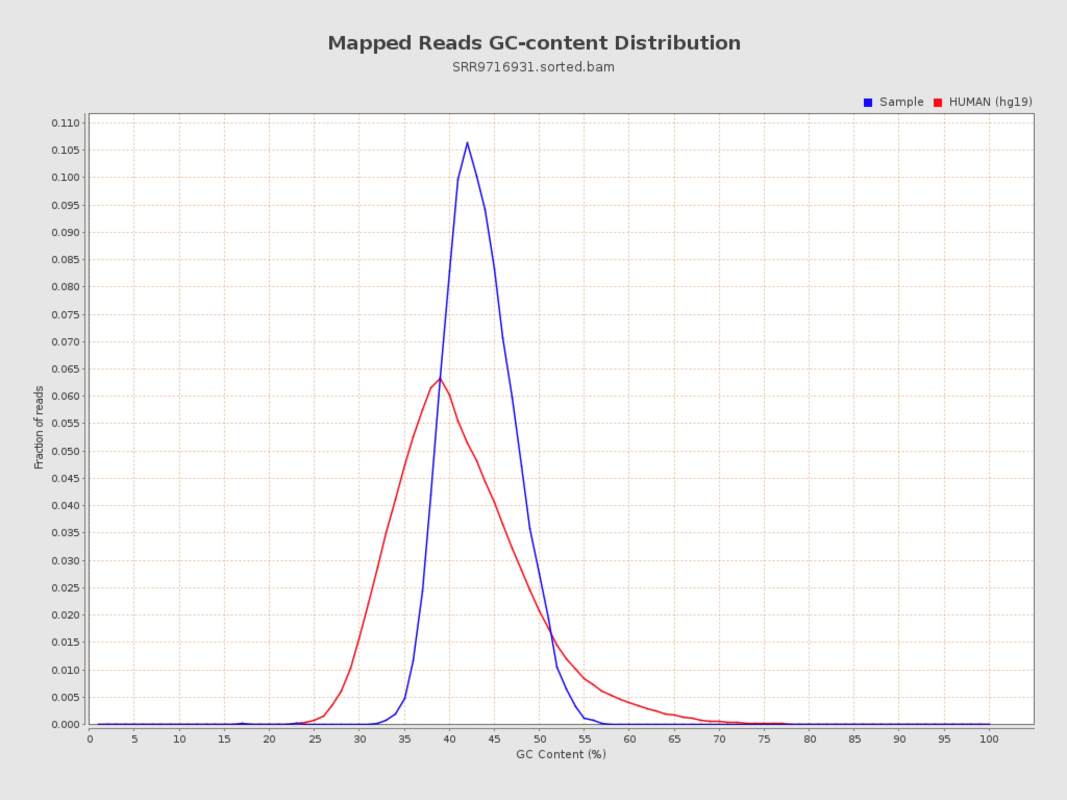
# 7. Results : Duplication Rate Histogram



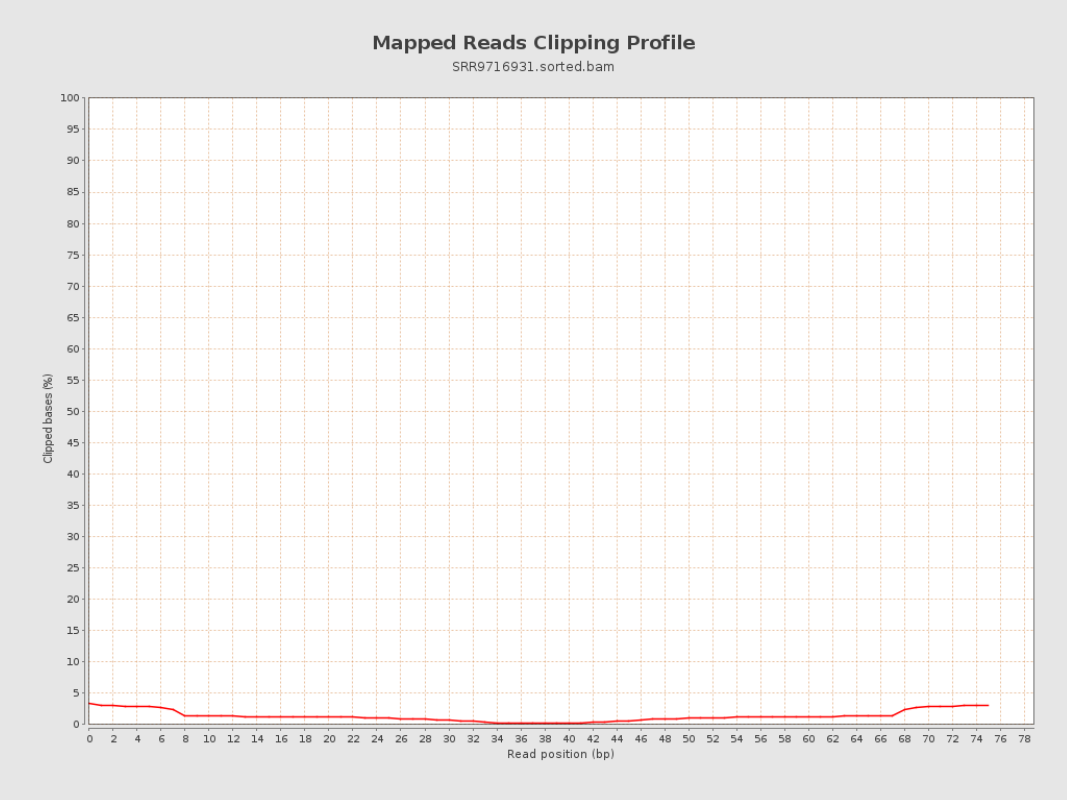
# 8. Results : Mapped Reads Nucleotide Content



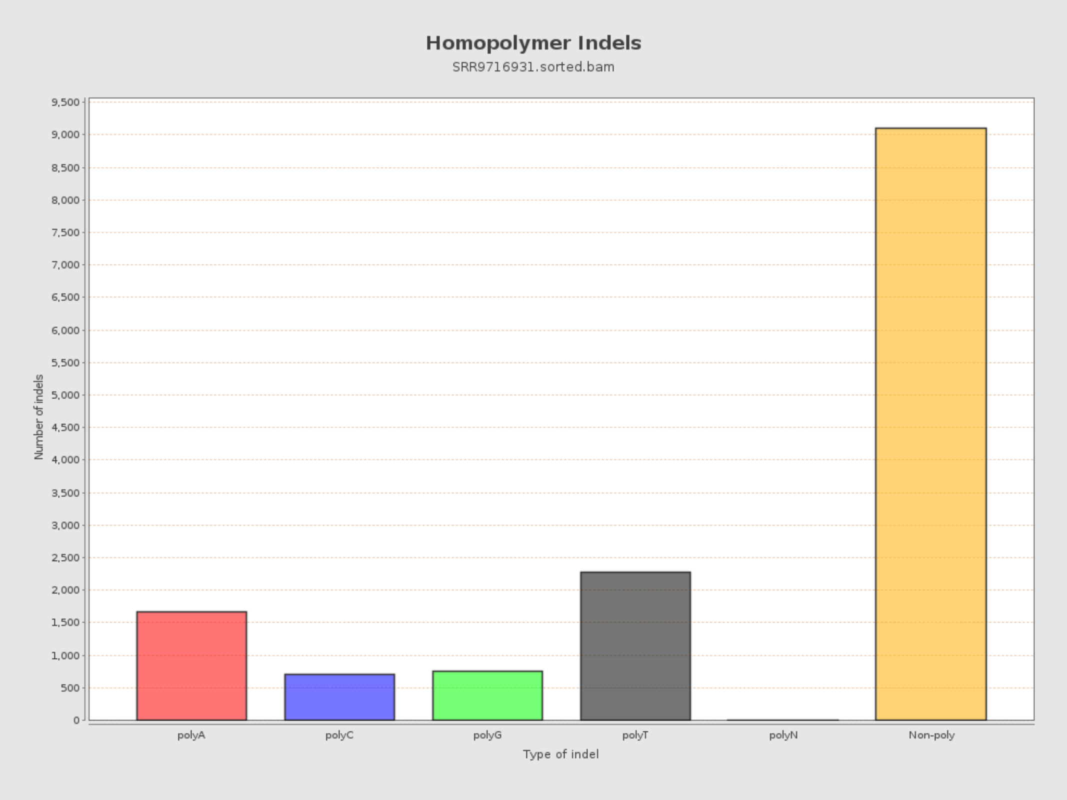
# 9. Results : Mapped Reads GC-content Distribution



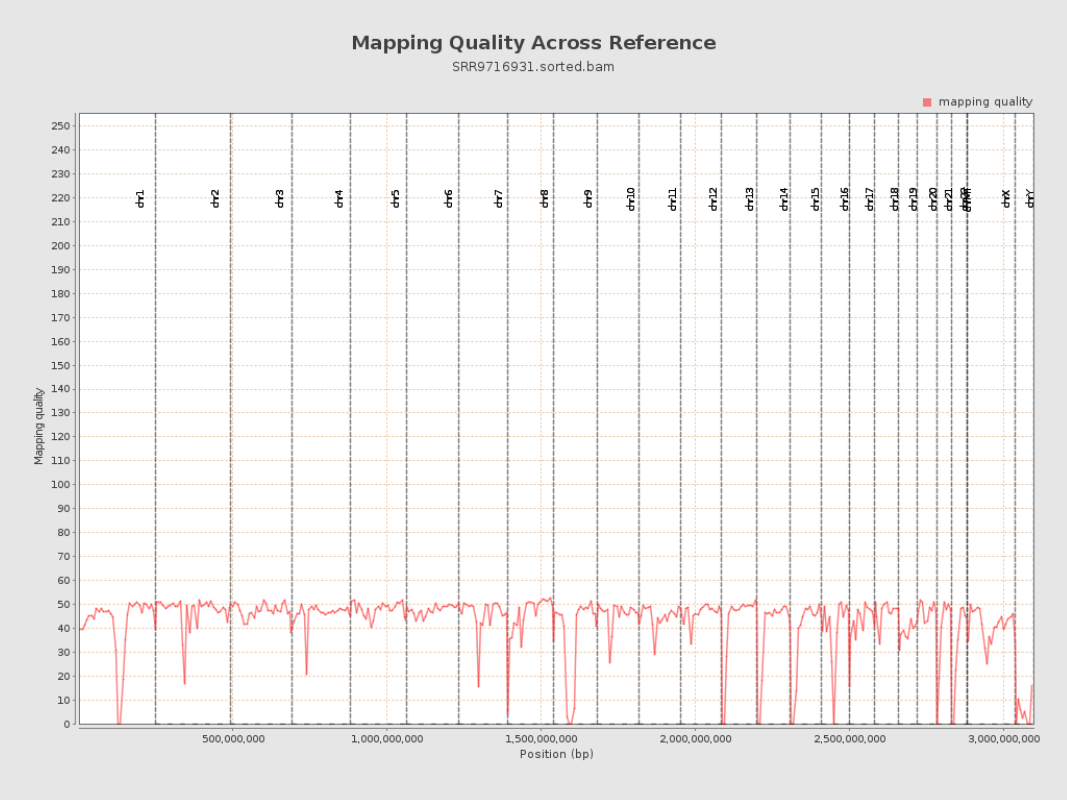
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram