# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/02 04:49:57*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716273.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_SRR9716273 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716273.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 02 04:49:57 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716273.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 475,712 |
| Mapped reads | 403,503 / 84.82% |
| Unmapped reads | 72,209 / 15.18% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 1,623 / 0.34% |
| Read min/max/mean length | 30 / 76 / 76.11 |
| Duplicated reads (estimated) | 7,113 / 1.5% |
| Duplication rate | 1.37% |
| Clipped reads | 403,882 / 84.9% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 6,117,846 / 26.03% |
| Number/percentage of C's | 4,014,364 / 17.08% |
| Number/percentage of T's | 7,539,976 / 32.09% |
| Number/percentage of G's | 5,825,884 / 24.79% |
| Number/percentage of N's | 657 / 0% |
| GC Percentage | 41.88% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0076 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1038 |

## 2.4. Mapping Quality

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

## 2.5. Mismatches and indels

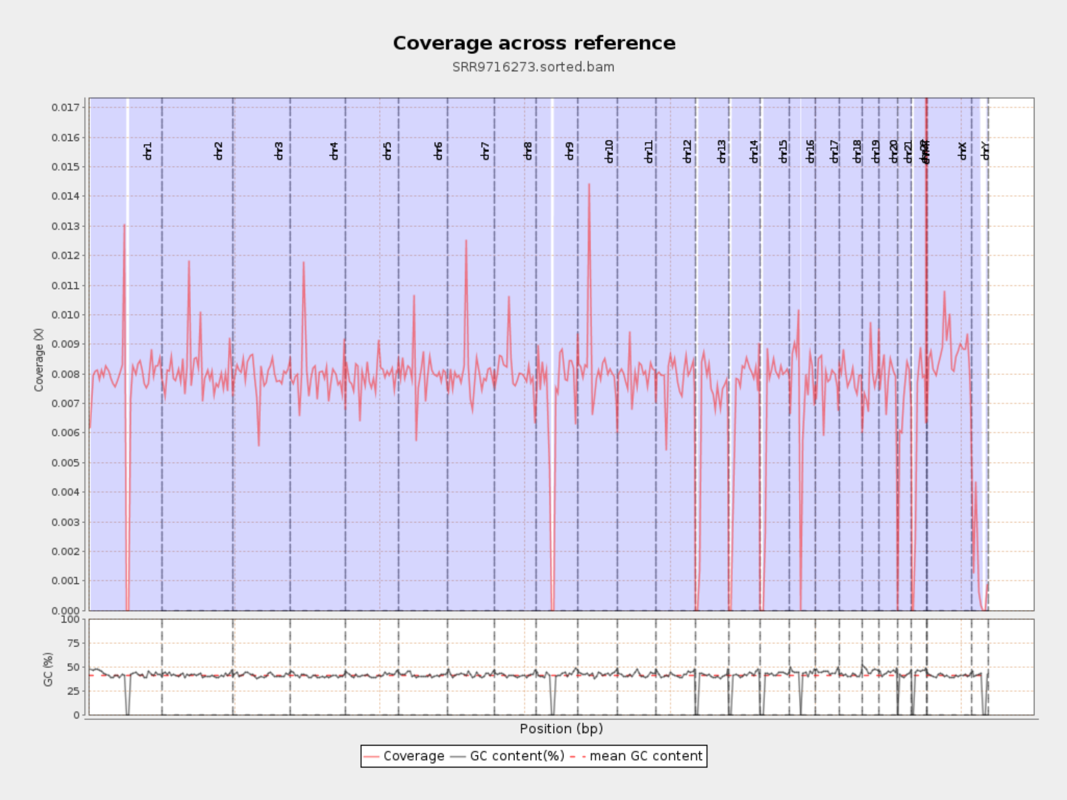
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 119,174 |
| Insertions | 1,772 |
| Mapped reads with at least one insertion | 0.44% |
| Deletions | 4,620 |
| Mapped reads with at least one deletion | 1.14% |
| Homopolymer indels | 42.32% |

## 2.6. Chromosome stats

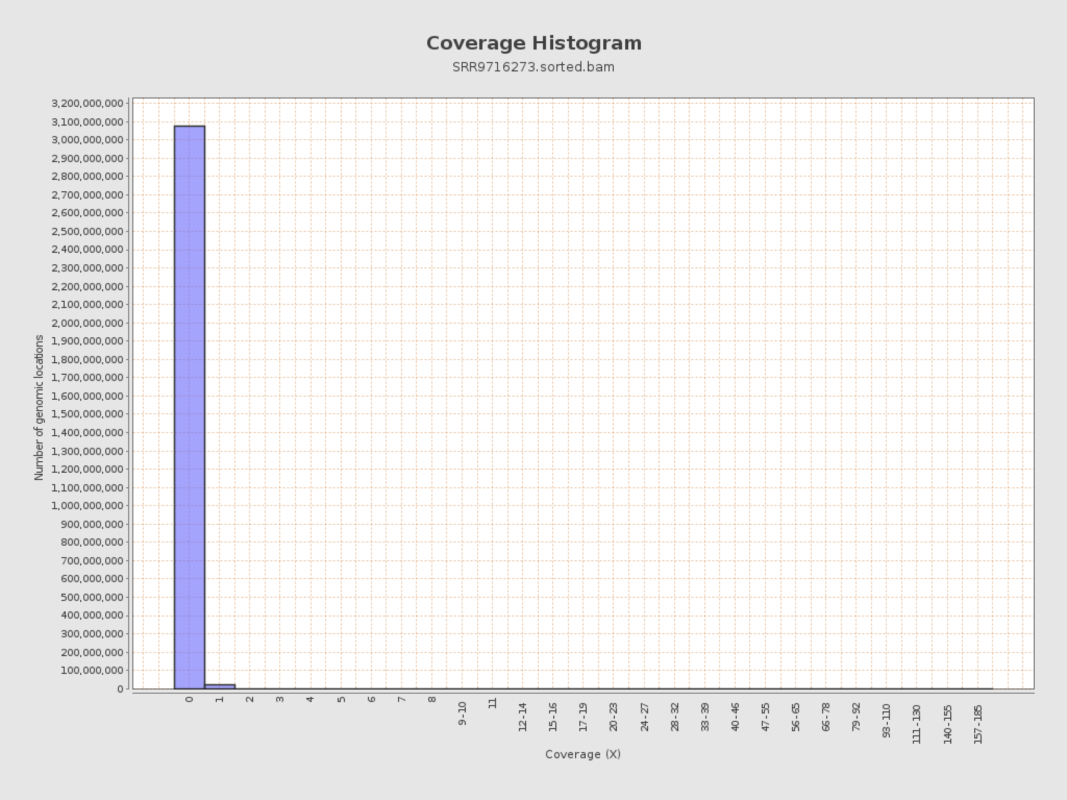
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 1898995 | 0.0076 | 0.1564 |
| chr2 | 243199373 | 1975990 | 0.0081 | 0.1162 |
| chr3 | 198022430 | 1574528 | 0.008 | 0.0922 |
| chr4 | 191154276 | 1525581 | 0.008 | 0.0945 |
| chr5 | 180915260 | 1431980 | 0.0079 | 0.0917 |
| chr6 | 171115067 | 1378272 | 0.0081 | 0.0986 |
| chr7 | 159138663 | 1282868 | 0.0081 | 0.1134 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 1183334 | 0.0081 | 0.1059 |
| chr9 | 141213431 | 983618 | 0.007 | 0.0931 |
| chr10 | 135534747 | 1126031 | 0.0083 | 0.1058 |
| chr11 | 135006516 | 1076476 | 0.008 | 0.0975 |
| chr12 | 133851895 | 1058634 | 0.0079 | 0.0921 |
| chr13 | 115169878 | 738886 | 0.0064 | 0.0827 |
| chr14 | 107349540 | 715751 | 0.0067 | 0.0847 |
| chr15 | 102531392 | 676283 | 0.0066 | 0.0838 |
| chr16 | 90354753 | 666110 | 0.0074 | 0.0901 |
| chr17 | 81195210 | 625592 | 0.0077 | 0.091 |
| chr18 | 78077248 | 620766 | 0.008 | 0.1224 |
| chr19 | 59128983 | 460801 | 0.0078 | 0.122 |
| chr20 | 63025520 | 490736 | 0.0078 | 0.0907 |
| chr21 | 48129895 | 311995 | 0.0065 | 0.0867 |
| chr22 | 51304566 | 282398 | 0.0055 | 0.0765 |
| chrMT | 16571 | 1658 | 0.1001 | 0.3156 |
| chrX | 155270560 | 1346082 | 0.0087 | 0.0987 |
| chrY | 59373566 | 72801 | 0.0012 | 0.0465 |

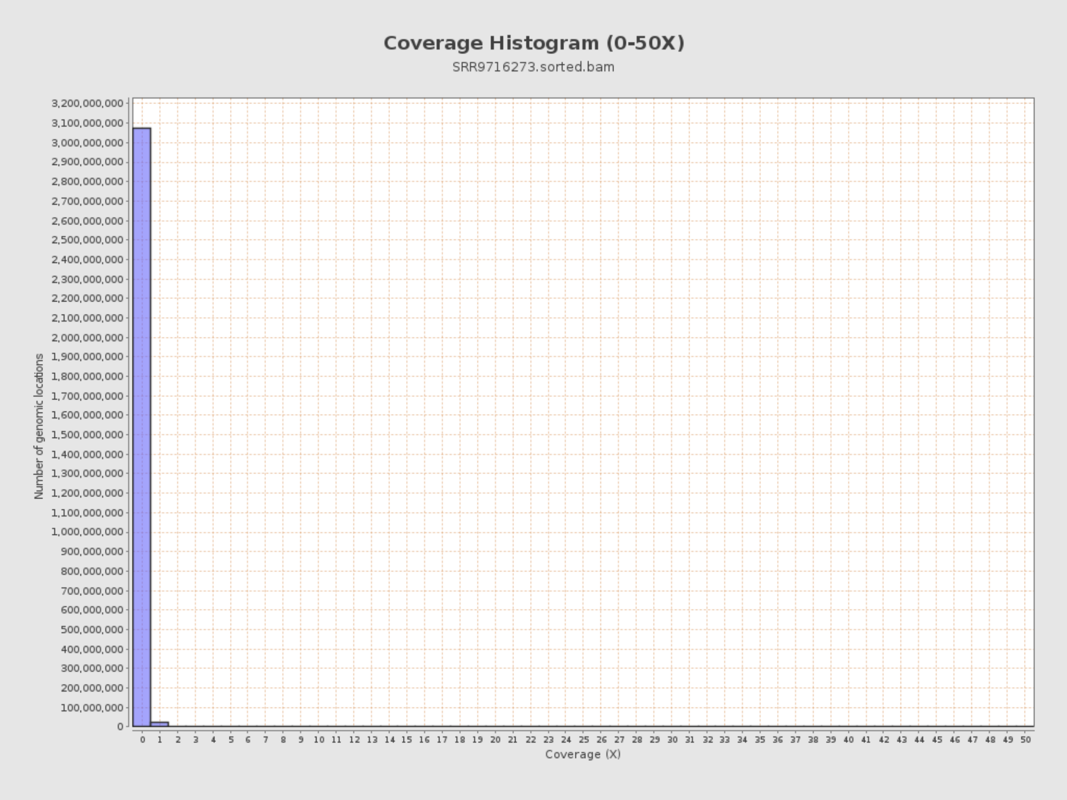
# 3. Results : Coverage across reference



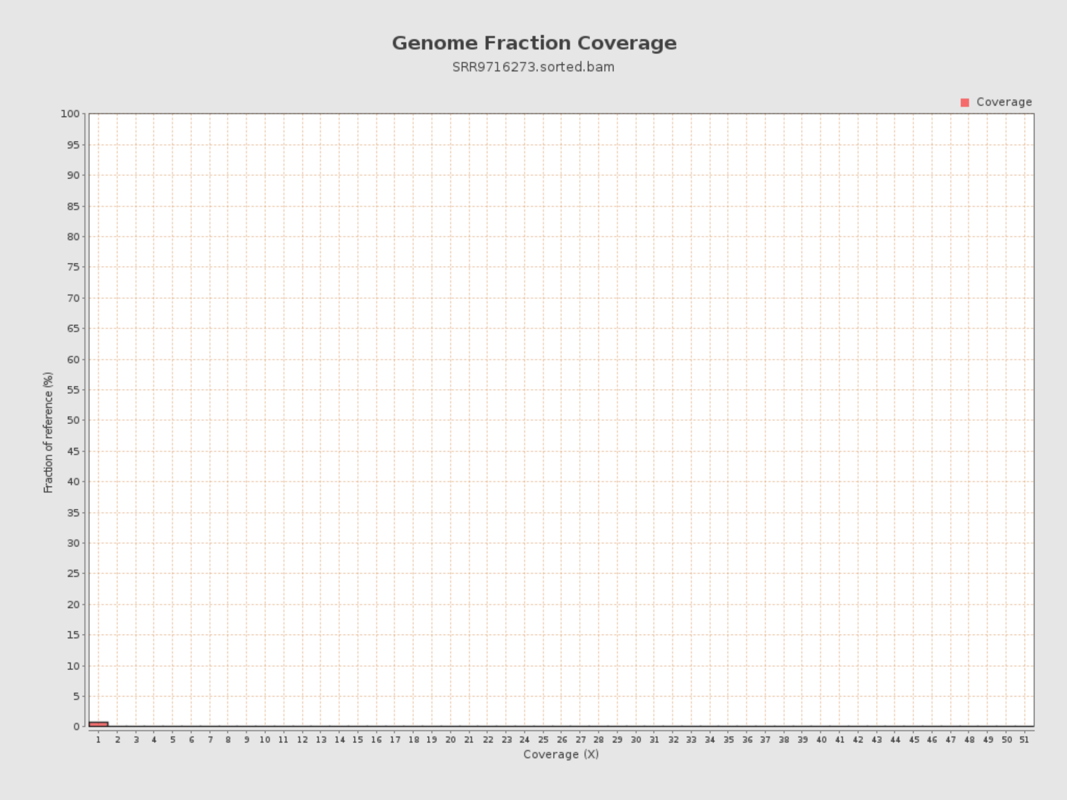
# 4. Results : Coverage Histogram



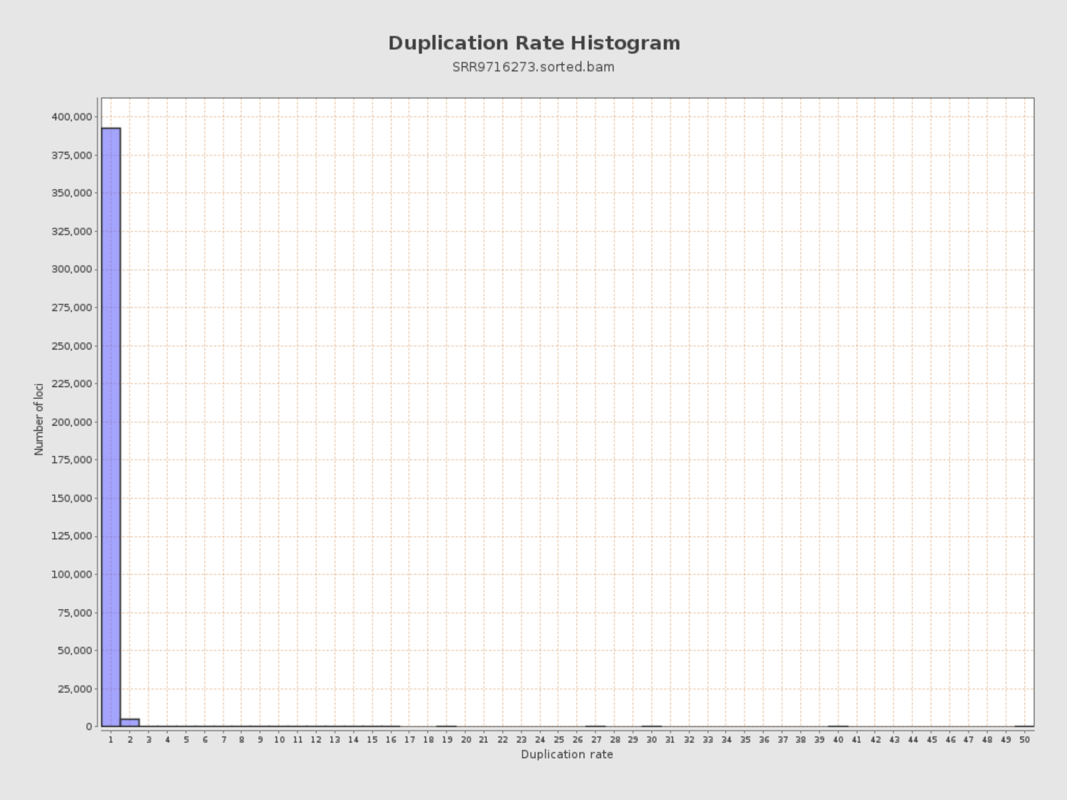
# 5. Results : Coverage Histogram (0-50X)



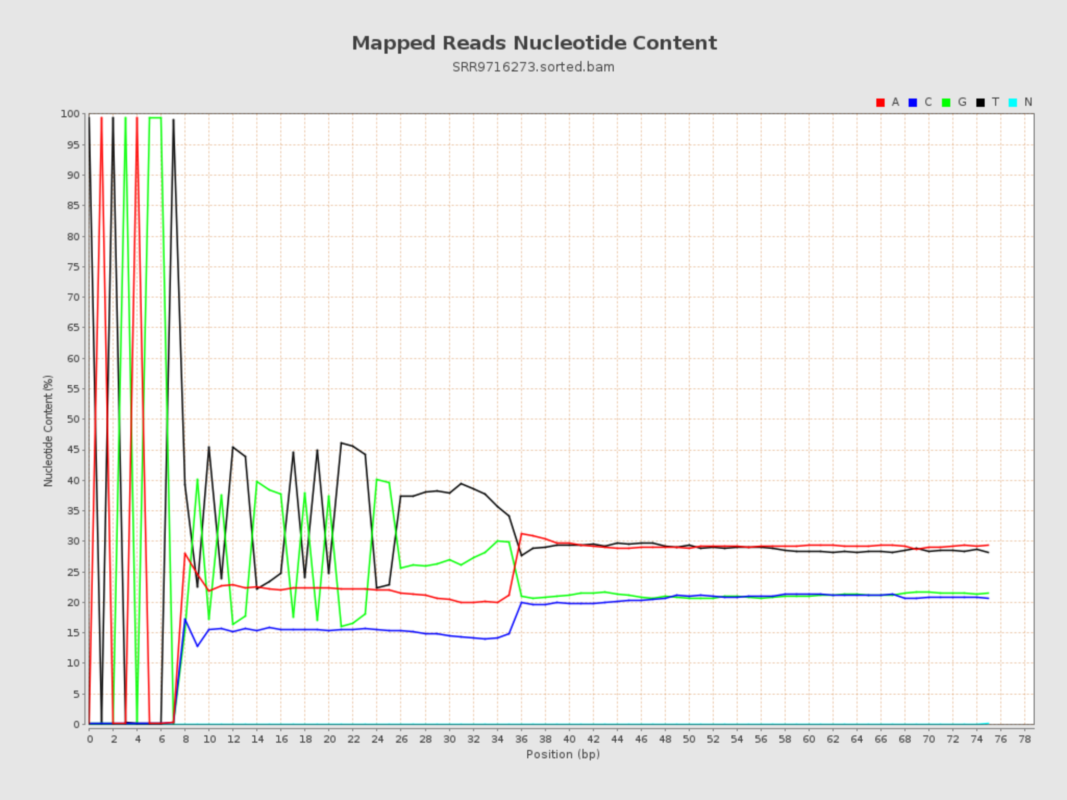
# 6. Results : Genome Fraction Coverage



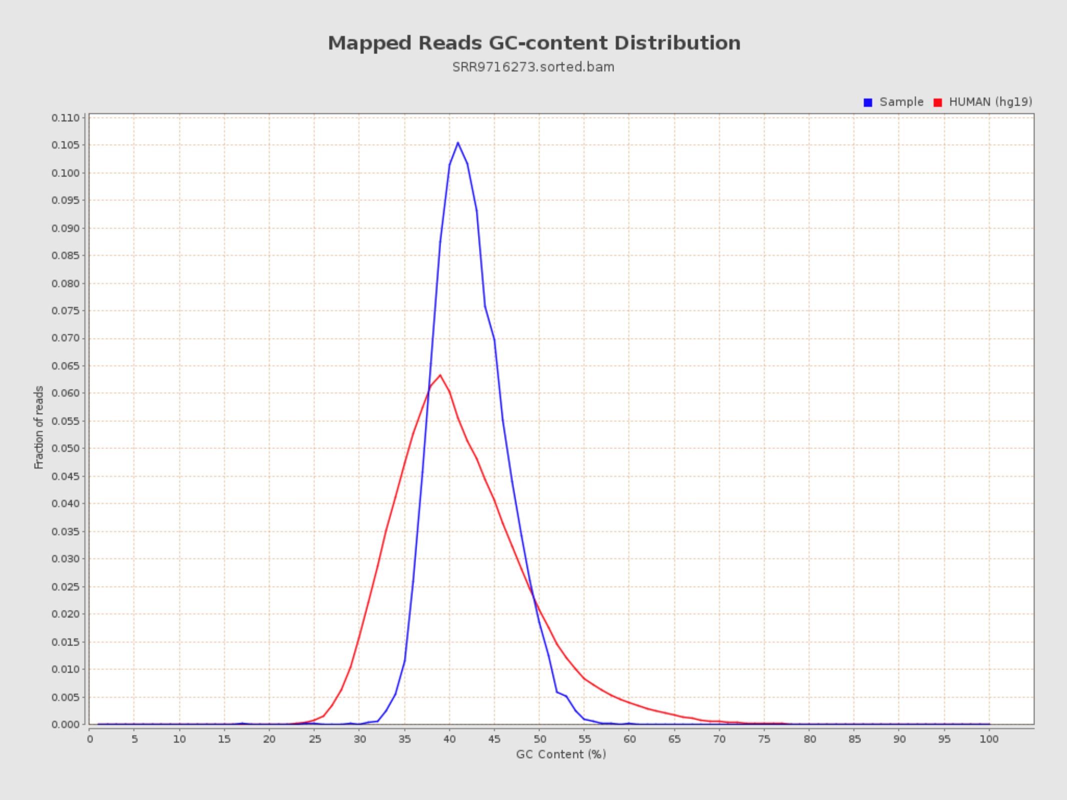
# 7. Results : Duplication Rate Histogram



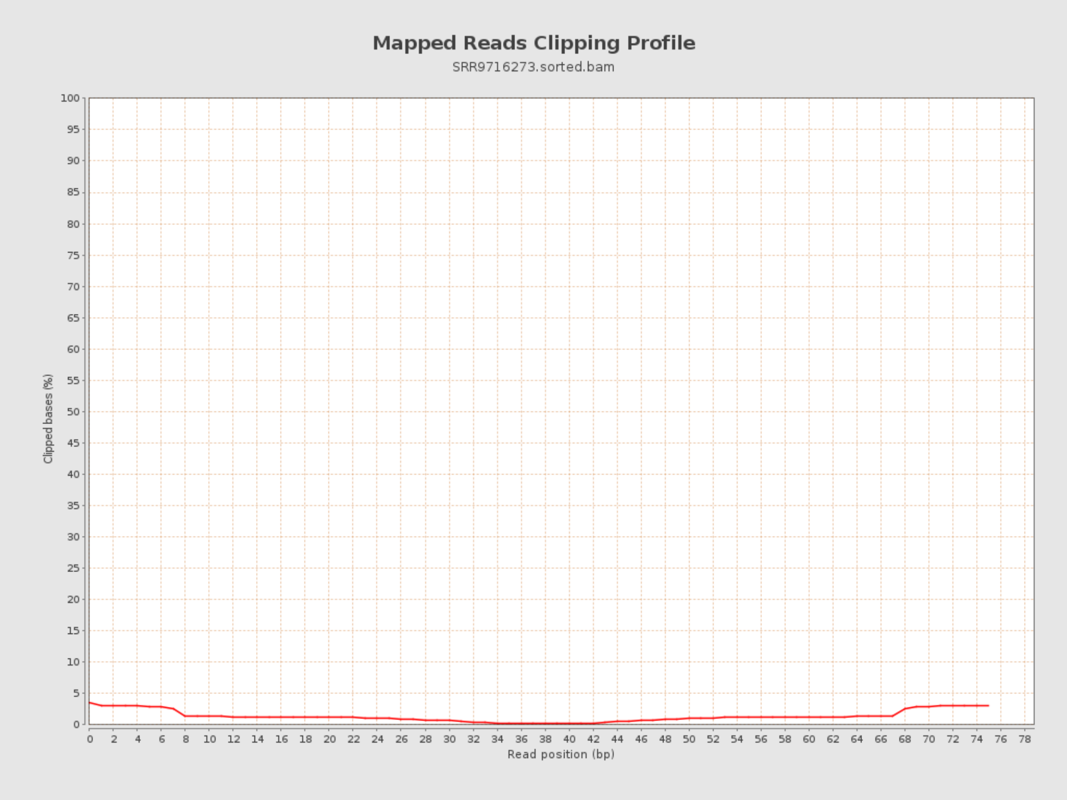
# 8. Results : Mapped Reads Nucleotide Content



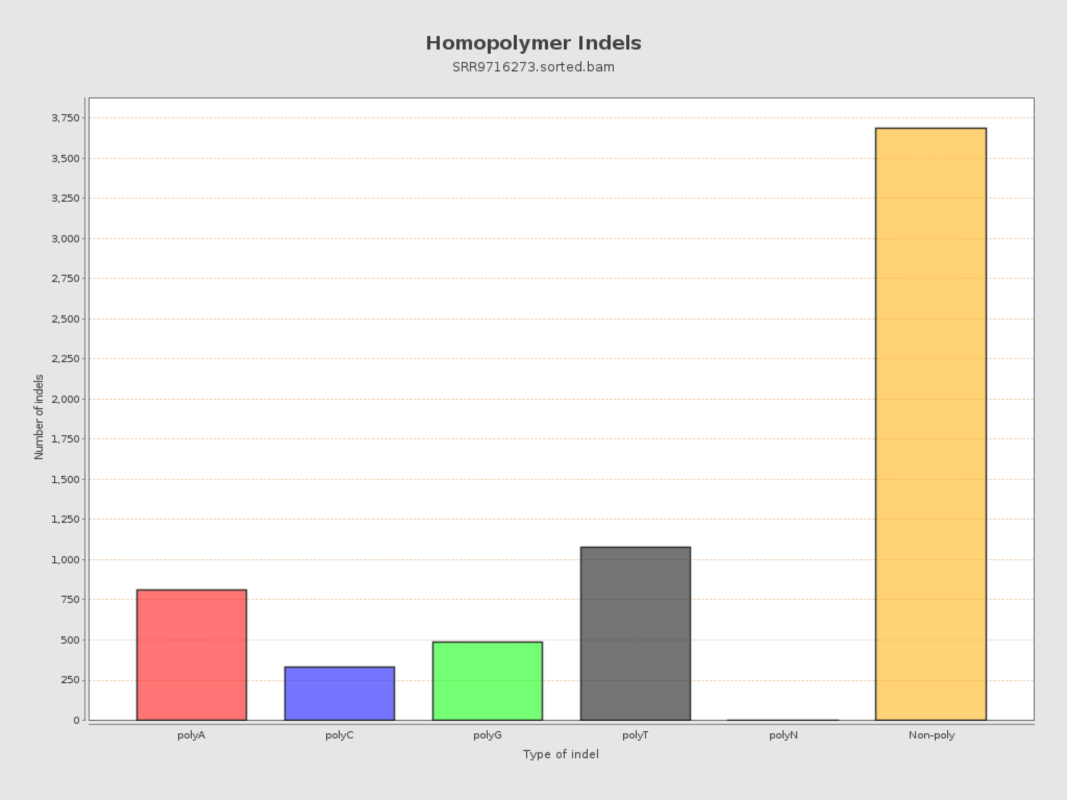
# 9. Results : Mapped Reads GC-content Distribution



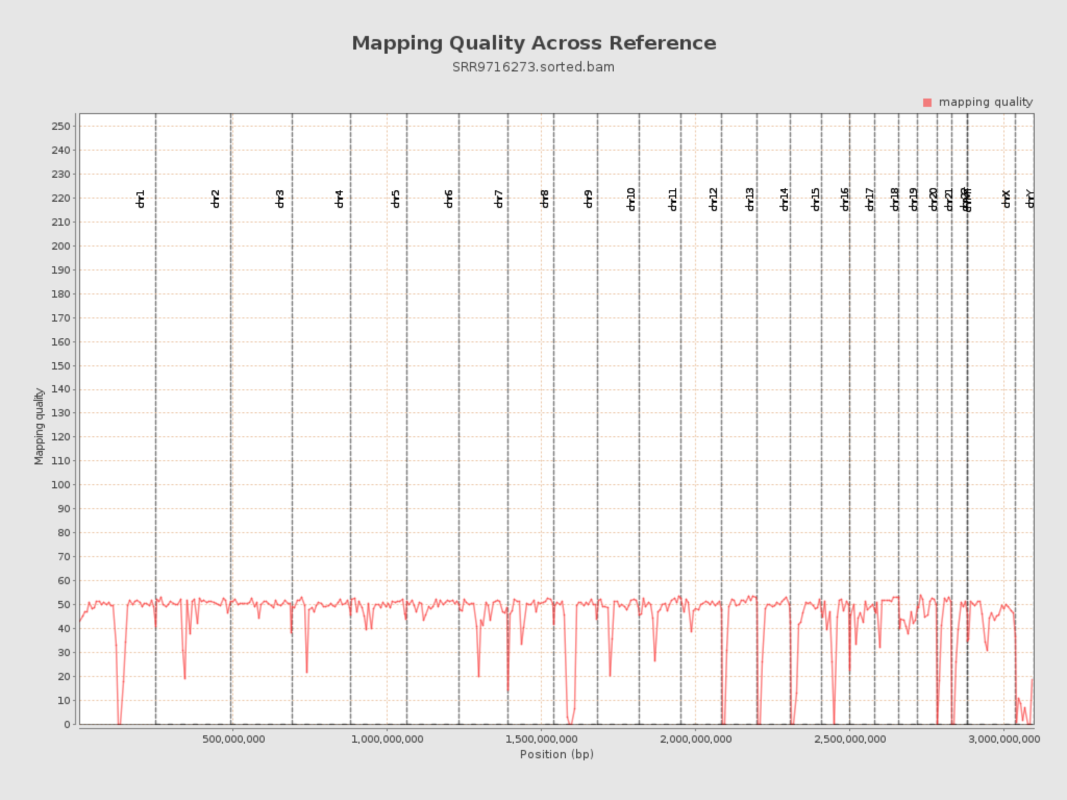
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram