# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 00:36:12*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716613.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_SRR9716613 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716613.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 00:36:11 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716613.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 583,138 |
| Mapped reads | 525,047 / 90.04% |
| Unmapped reads | 58,091 / 9.96% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 1,816 / 0.31% |
| Read min/max/mean length | 30 / 76 / 76.1 |
| Duplicated reads (estimated) | 11,391 / 1.95% |
| Duplication rate | 1.75% |
| Clipped reads | 525,458 / 90.11% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 7,874,346 / 25.82% |
| Number/percentage of C's | 5,639,565 / 18.49% |
| Number/percentage of T's | 9,428,951 / 30.92% |
| Number/percentage of G's | 7,551,653 / 24.76% |
| Number/percentage of N's | 310 / 0% |
| GC Percentage | 43.26% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0099 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1172 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.76 |

## 2.5. Mismatches and indels

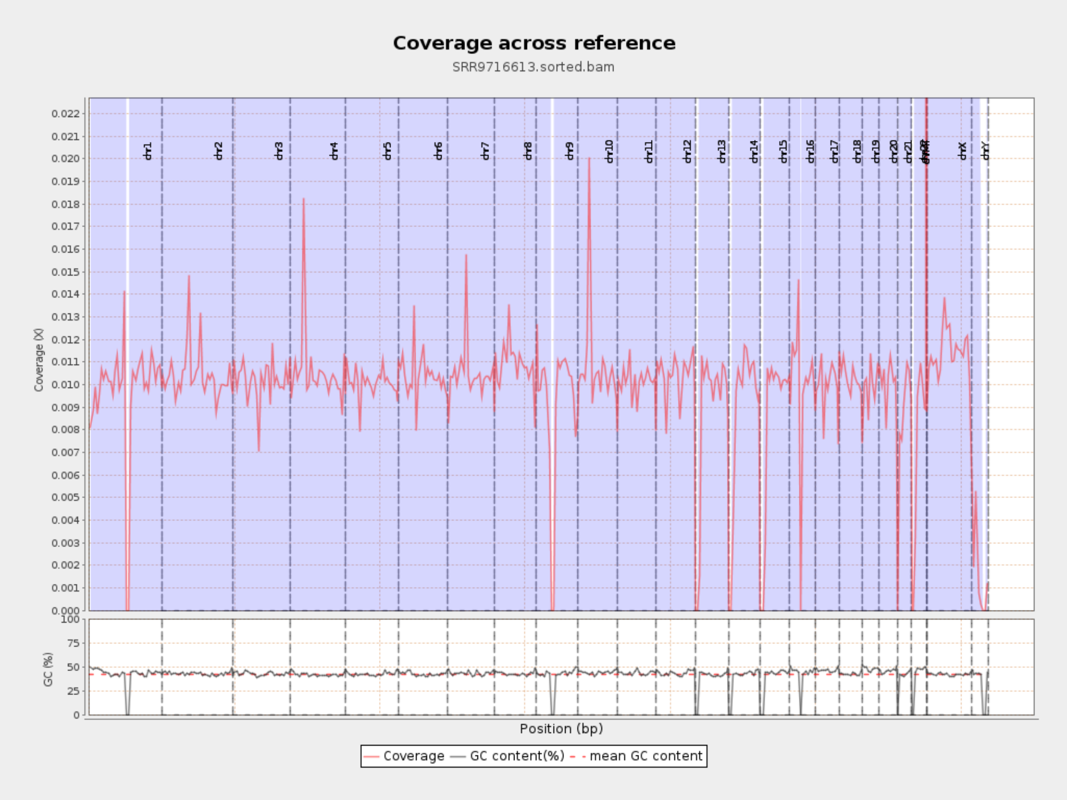
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 150,495 |
| Insertions | 2,230 |
| Mapped reads with at least one insertion | 0.42% |
| Deletions | 6,294 |
| Mapped reads with at least one deletion | 1.19% |
| Homopolymer indels | 41.93% |

## 2.6. Chromosome stats

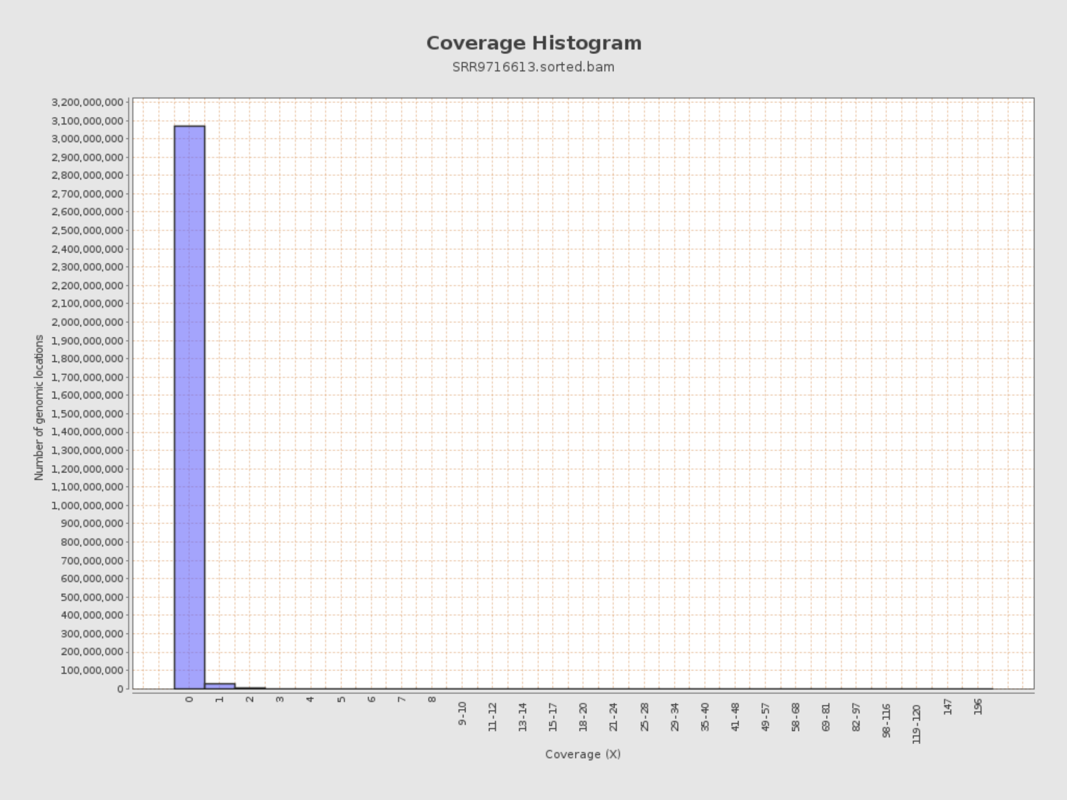
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 2410277 | 0.0097 | 0.1419 |
| chr2 | 243199373 | 2543594 | 0.0105 | 0.1411 |
| chr3 | 198022430 | 2014189 | 0.0102 | 0.1051 |
| chr4 | 191154276 | 2017895 | 0.0106 | 0.112 |
| chr5 | 180915260 | 1825532 | 0.0101 | 0.1045 |
| chr6 | 171115067 | 1786333 | 0.0104 | 0.1145 |
| chr7 | 159138663 | 1677795 | 0.0105 | 0.1368 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 1594497 | 0.0109 | 0.1248 |
| chr9 | 141213431 | 1259377 | 0.0089 | 0.1043 |
| chr10 | 135534747 | 1477549 | 0.0109 | 0.1316 |
| chr11 | 135006516 | 1367471 | 0.0101 | 0.1141 |
| chr12 | 133851895 | 1392664 | 0.0104 | 0.1065 |
| chr13 | 115169878 | 988609 | 0.0086 | 0.0965 |
| chr14 | 107349540 | 930609 | 0.0087 | 0.0977 |
| chr15 | 102531392 | 851238 | 0.0083 | 0.0947 |
| chr16 | 90354753 | 904256 | 0.01 | 0.1098 |
| chr17 | 81195210 | 804697 | 0.0099 | 0.1054 |
| chr18 | 78077248 | 809931 | 0.0104 | 0.1483 |
| chr19 | 59128983 | 589433 | 0.01 | 0.1266 |
| chr20 | 63025520 | 634142 | 0.0101 | 0.1055 |
| chr21 | 48129895 | 403520 | 0.0084 | 0.0989 |
| chr22 | 51304566 | 347142 | 0.0068 | 0.0856 |
| chrMT | 16571 | 13478 | 0.8133 | 1.0324 |
| chrX | 155270560 | 1764744 | 0.0114 | 0.1142 |
| chrY | 59373566 | 95978 | 0.0016 | 0.0547 |

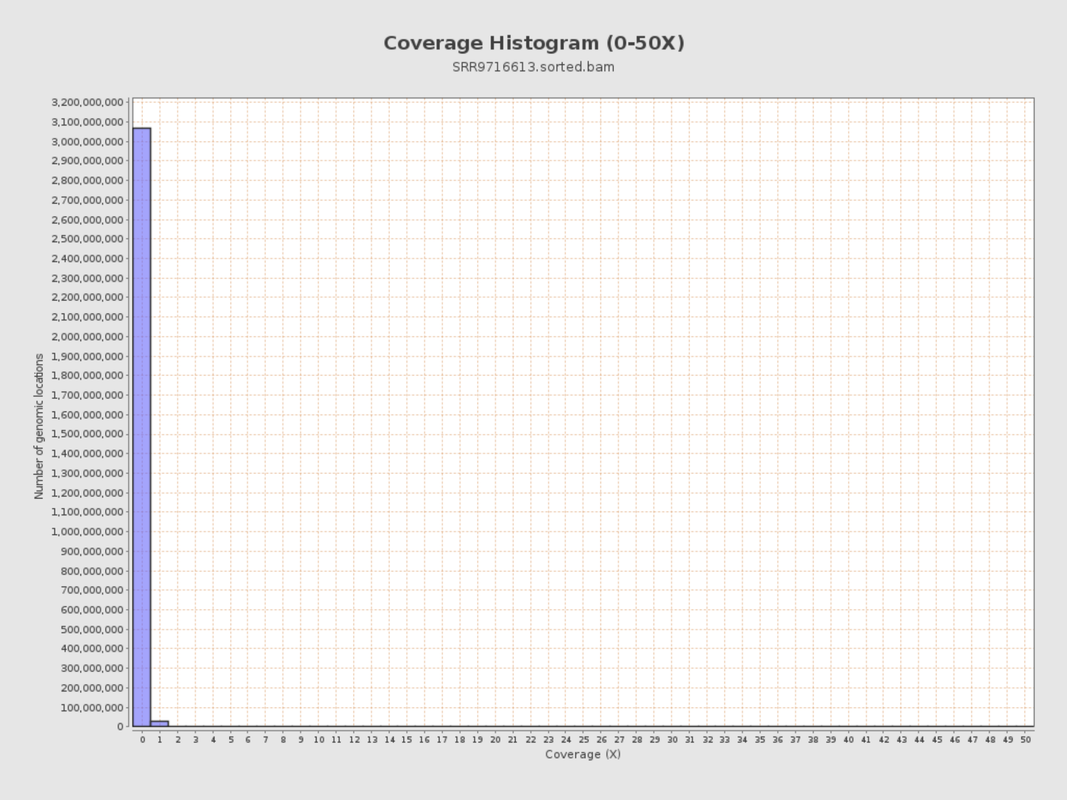
# 3. Results : Coverage across reference



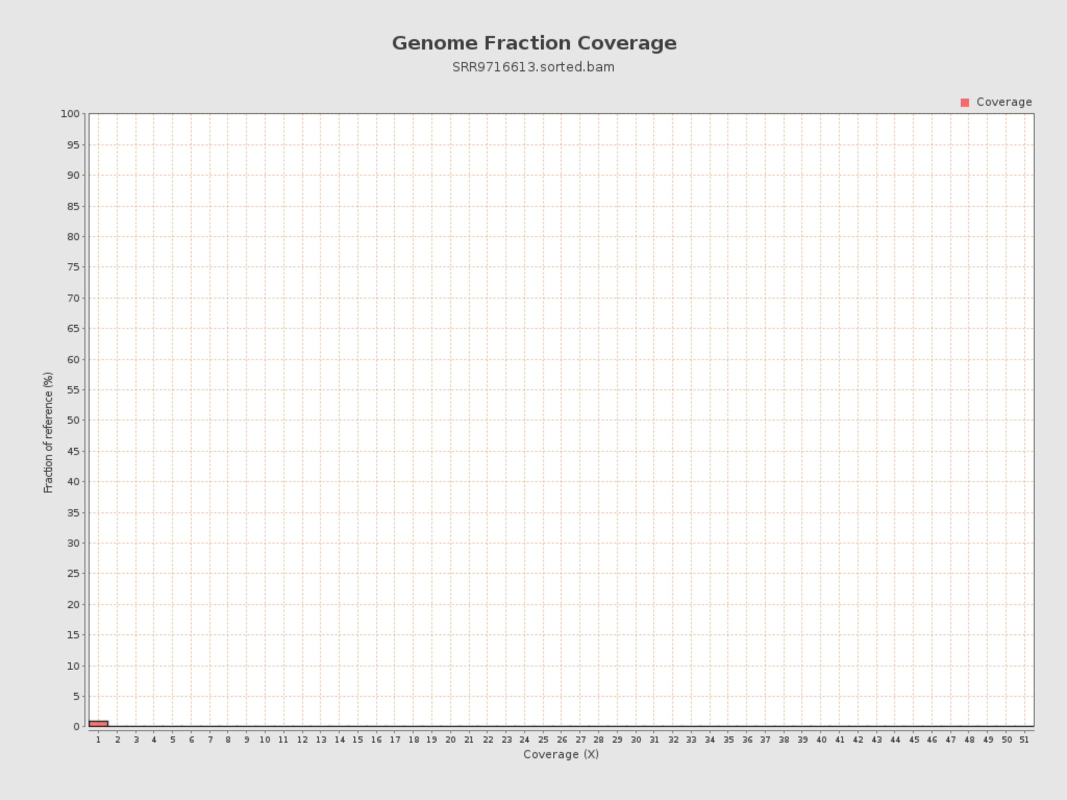
# 4. Results : Coverage Histogram



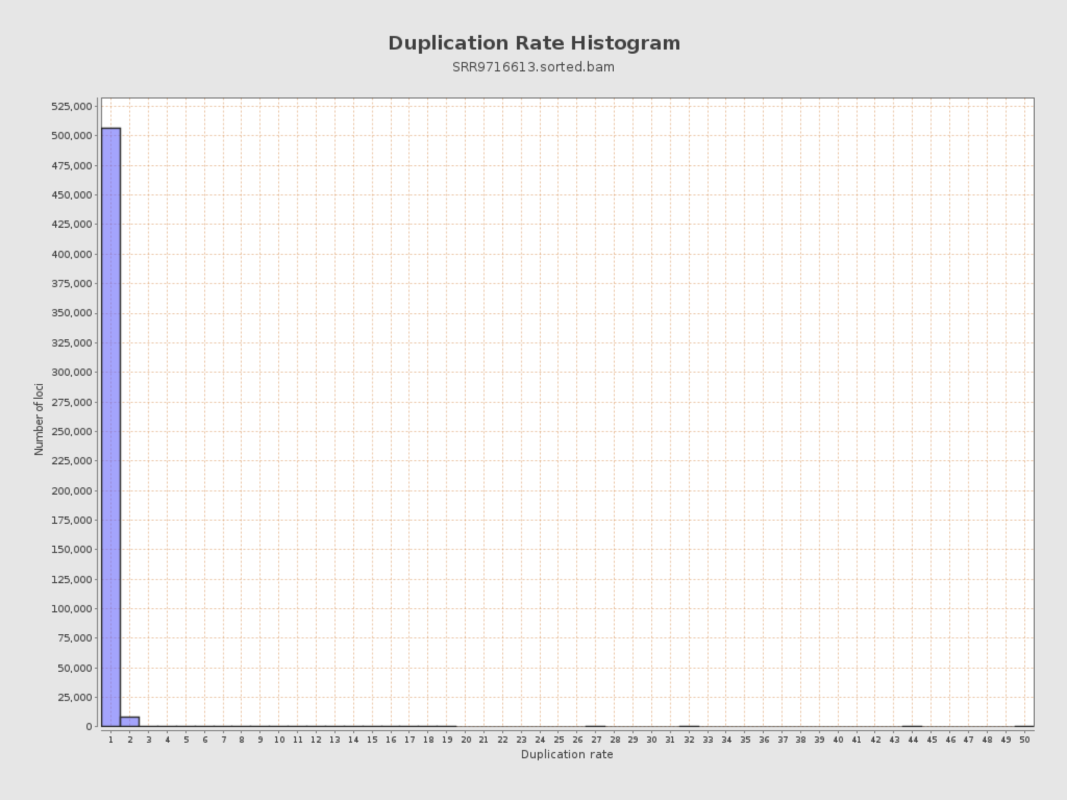
# 5. Results : Coverage Histogram (0-50X)



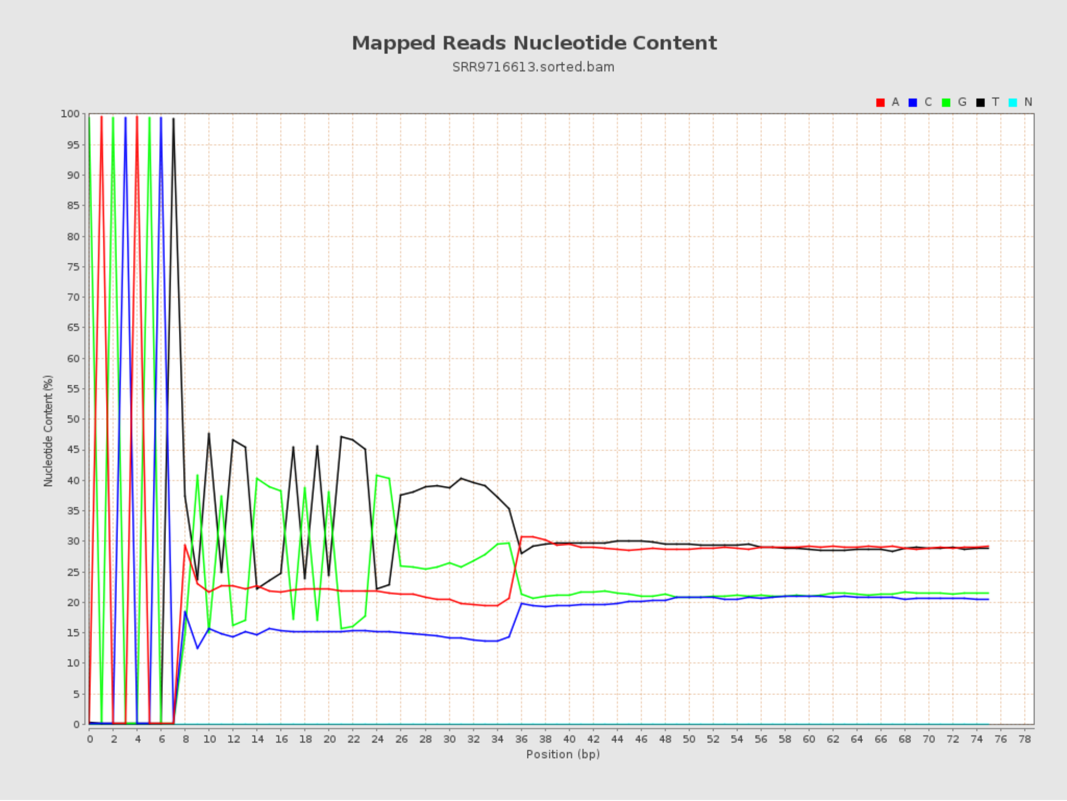
# 6. Results : Genome Fraction Coverage



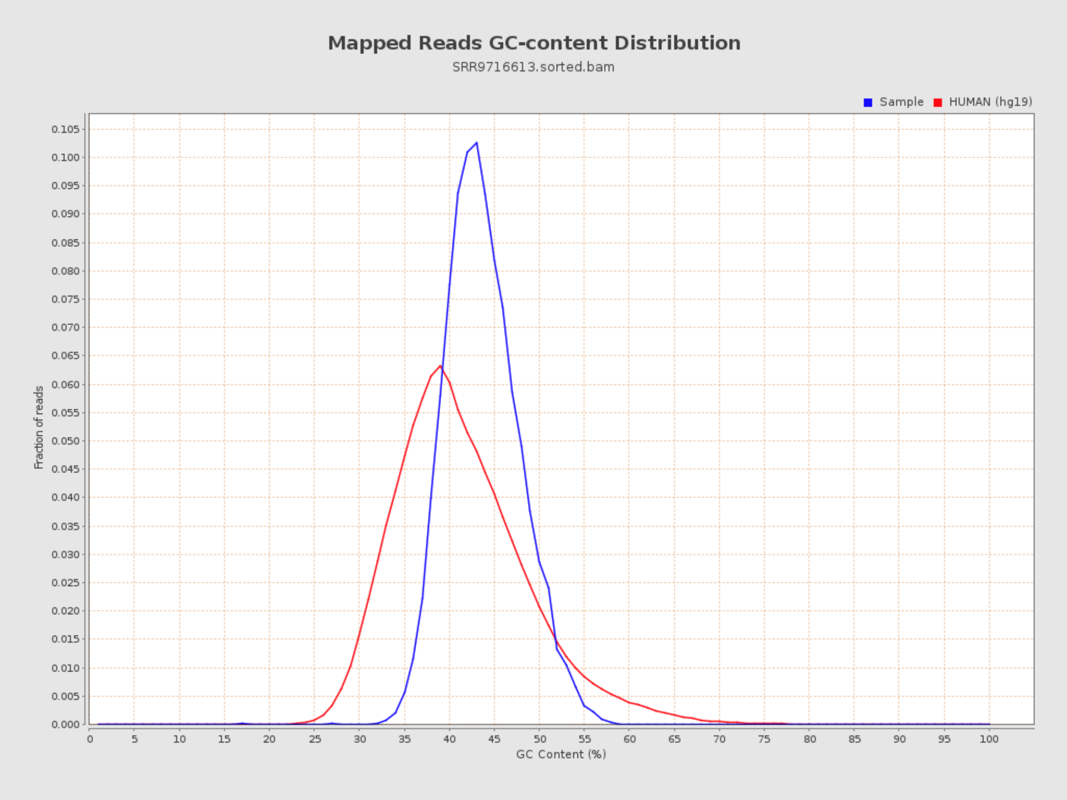
# 7. Results : Duplication Rate Histogram



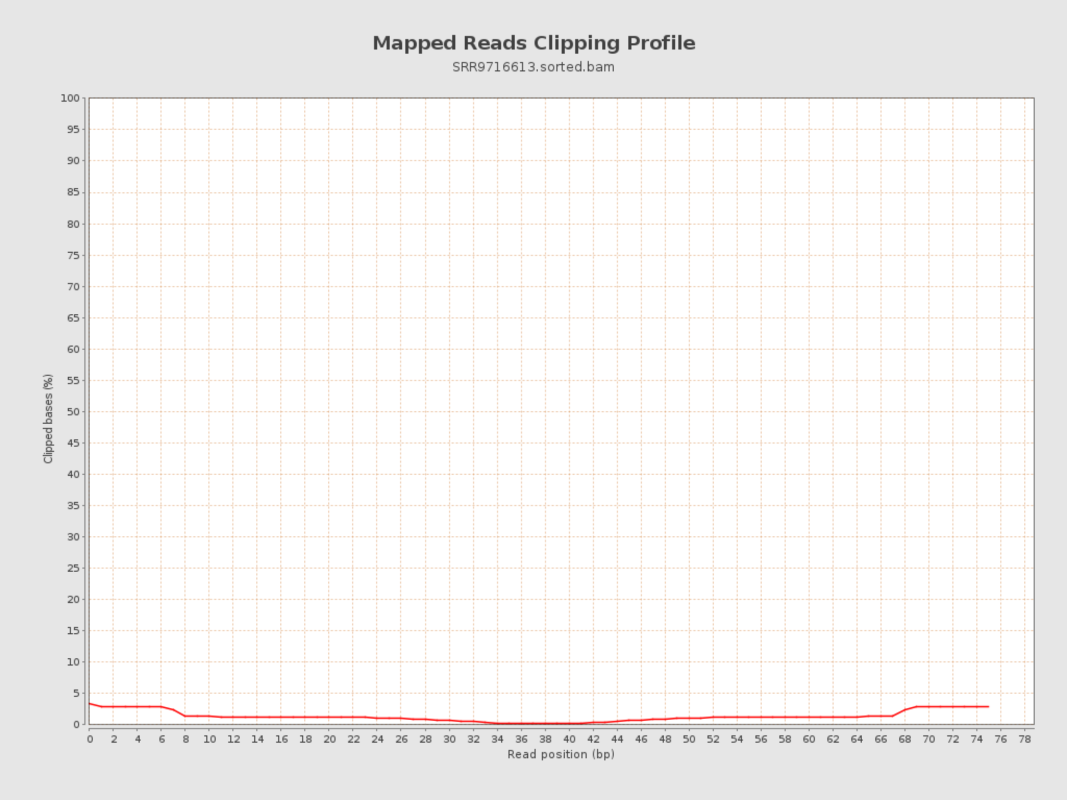
# 8. Results : Mapped Reads Nucleotide Content



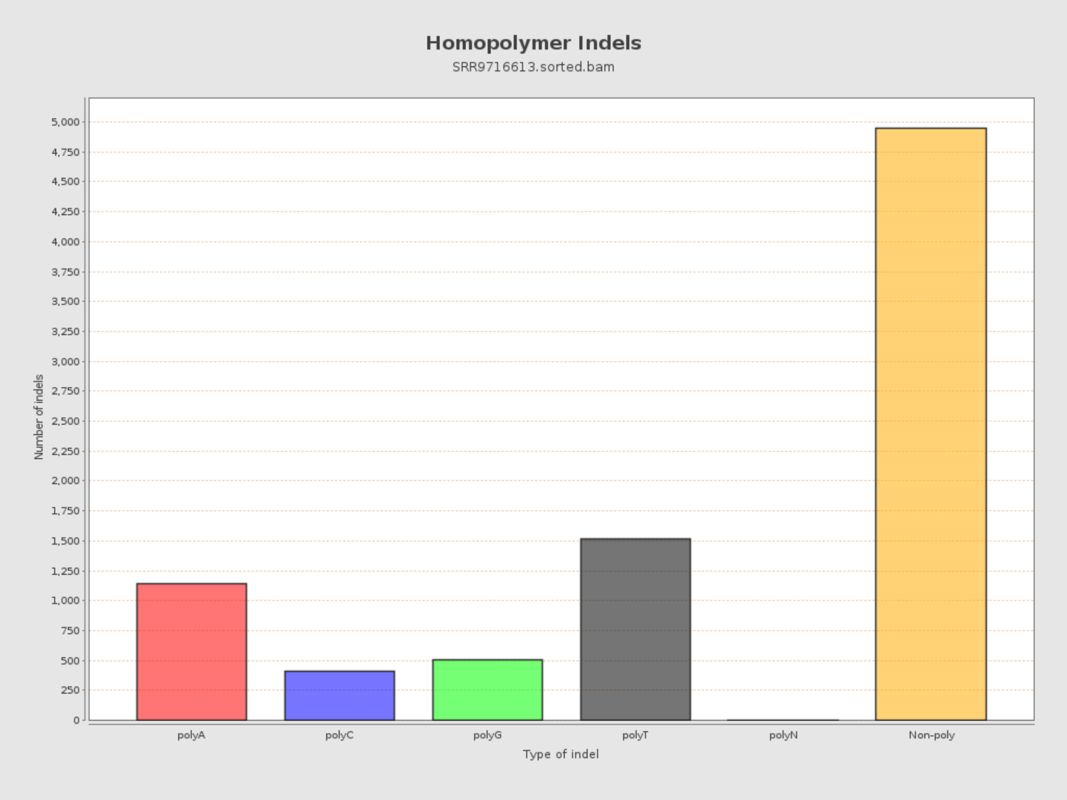
# 9. Results : Mapped Reads GC-content Distribution



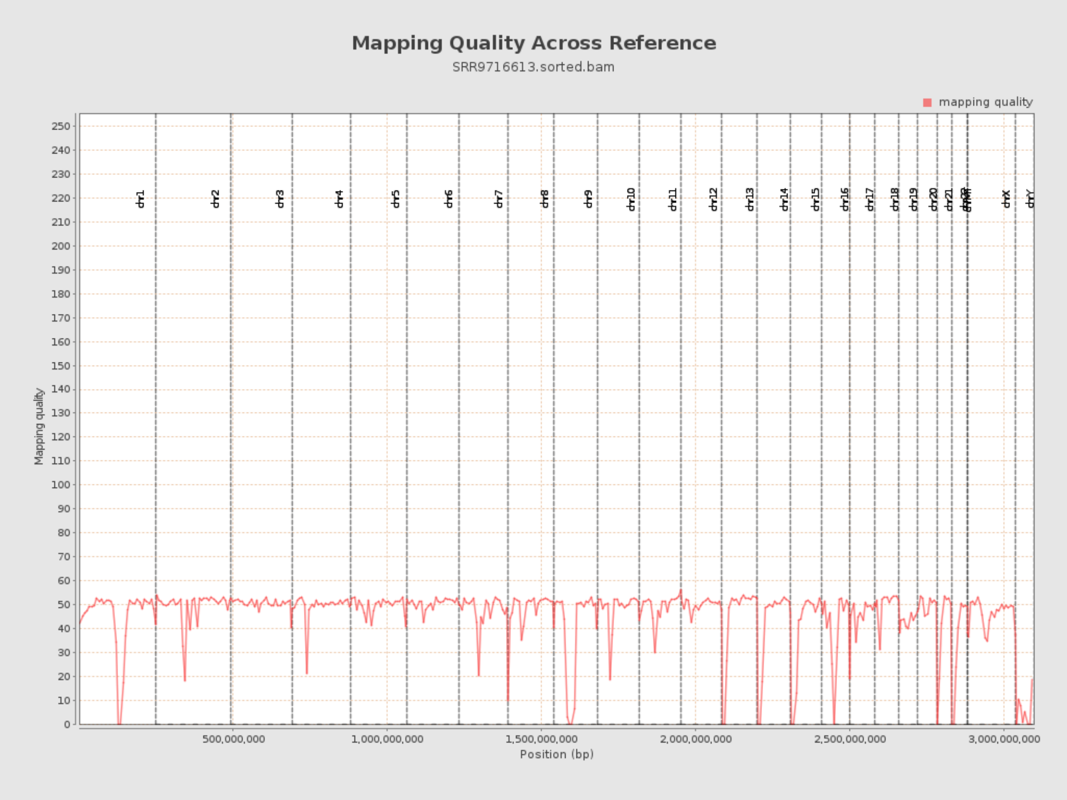
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram