# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/02 08:41:28*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716350.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_SRR9716350 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716350.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 02 08:41:27 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716350.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 478,504 |
| Mapped reads | 432,488 / 90.38% |
| Unmapped reads | 46,016 / 9.62% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 9,039 / 1.89% |
| Read min/max/mean length | 30 / 101 / 101.68 |
| Duplicated reads (estimated) | 7,571 / 1.58% |
| Duplication rate | 1.22% |
| Clipped reads | 440,729 / 92.11% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 8,841,855 / 26.23% |
| Number/percentage of C's | 6,514,226 / 19.33% |
| Number/percentage of T's | 10,450,979 / 31.01% |
| Number/percentage of G's | 7,893,305 / 23.42% |
| Number/percentage of N's | 2,402 / 0.01% |
| GC Percentage | 42.75% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0109 |
| | |

| | |
|---|---|
| Standard Deviation | 0.137 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 47.04 |

## 2.5. Mismatches and indels

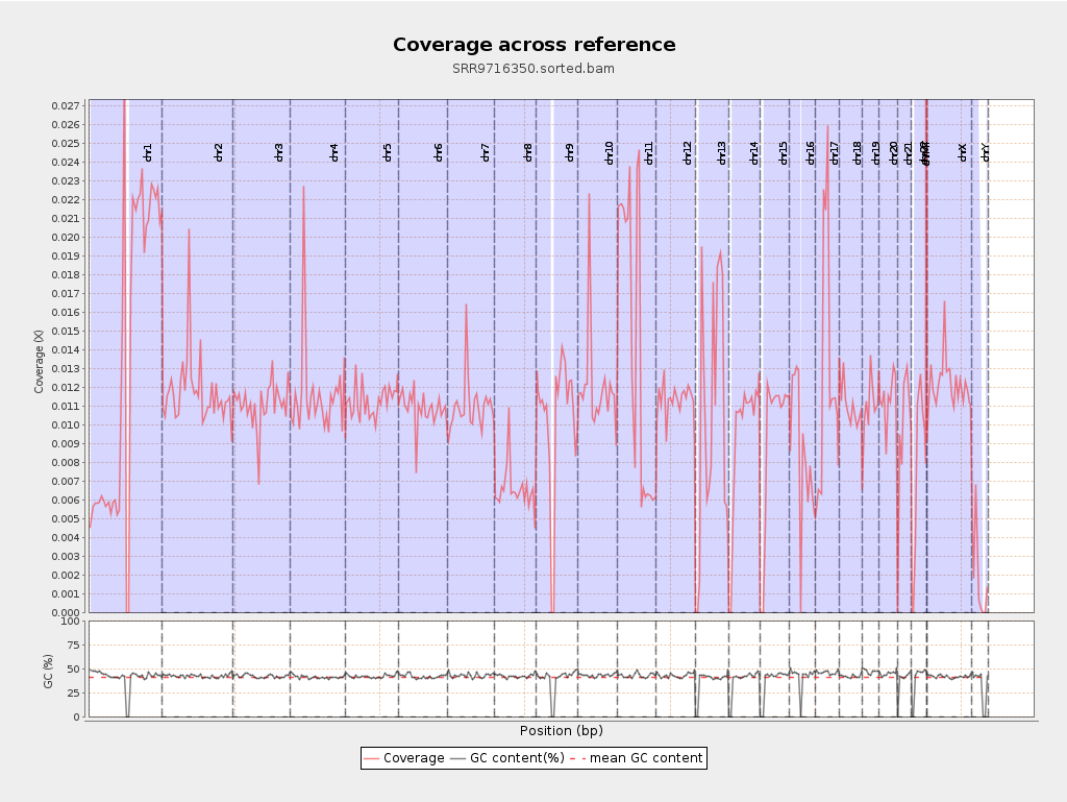
| | |
|---|---|
| General error rate | 0.72% |
| Mismatches | 235,267 |
| Insertions | 2,807 |
| Mapped reads with at least one insertion | 0.64% |
| Deletions | 7,844 |
| Mapped reads with at least one deletion | 1.79% |
| Homopolymer indels | 42.15% |

## 2.6. Chromosome stats

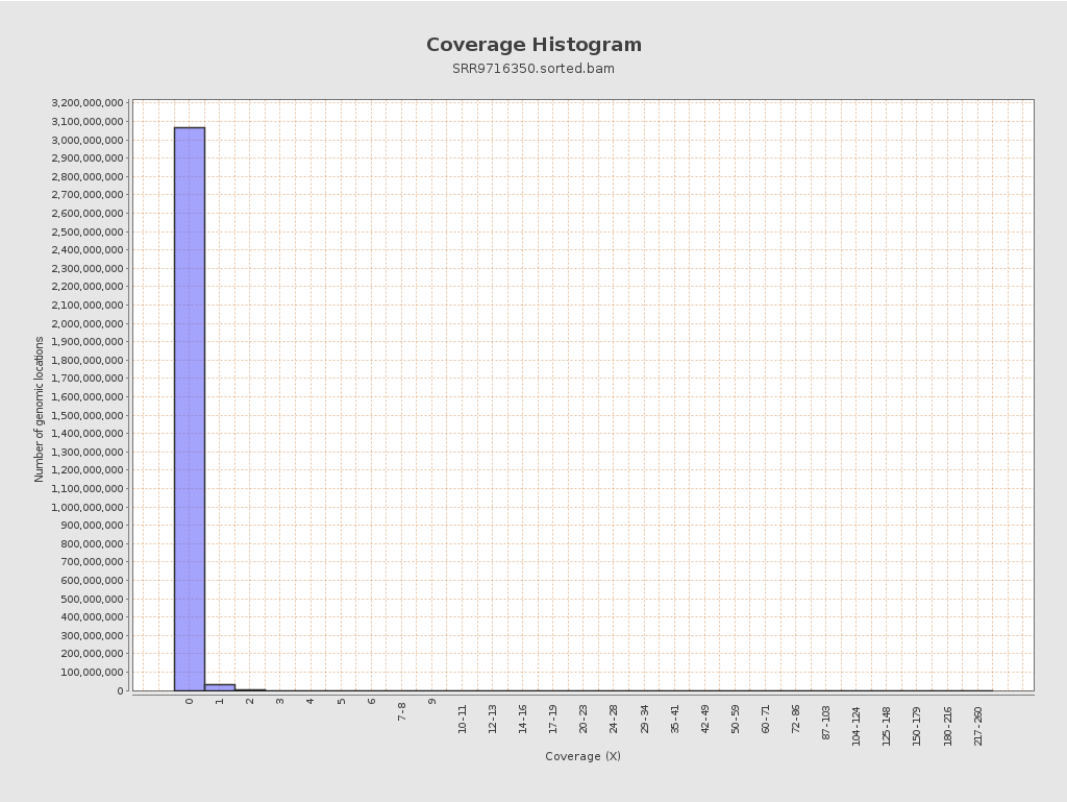
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 3319784 | 0.0133 | 0.2462 |
| chr2 | 243199373 | 2867170 | 0.0118 | 0.1431 |
| chr3 | 198022430 | 2196100 | 0.0111 | 0.1085 |
| chr4 | 191154276 | 2209635 | 0.0116 | 0.1222 |
| chr5 | 180915260 | 2035408 | 0.0113 | 0.1098 |
| chr6 | 171115067 | 1859455 | 0.0109 | 0.1108 |
| chr7 | 159138663 | 1757489 | 0.011 | 0.1514 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 960341 | 0.0066 | 0.1208 |
| chr9 | 141213431 | 1440050 | 0.0102 | 0.1208 |
| chr10 | 135534747 | 1620803 | 0.012 | 0.1424 |
| chr11 | 135006516 | 1915338 | 0.0142 | 0.1451 |
| chr12 | 133851895 | 1515350 | 0.0113 | 0.11 |
| chr13 | 115169878 | 1173128 | 0.0102 | 0.1045 |
| chr14 | 107349540 | 994212 | 0.0093 | 0.1015 |
| chr15 | 102531392 | 955609 | 0.0093 | 0.0995 |
| chr16 | 90354753 | 771048 | 0.0085 | 0.0973 |
| chr17 | 81195210 | 1056077 | 0.013 | 0.1253 |
| chr18 | 78077248 | 862941 | 0.0111 | 0.1622 |
| chr19 | 59128983 | 656818 | 0.0111 | 0.1657 |
| chr20 | 63025520 | 708605 | 0.0112 | 0.1119 |
| chr21 | 48129895 | 466435 | 0.0097 | 0.1064 |
| chr22 | 51304566 | 385605 | 0.0075 | 0.0896 |
| chrMT | 16571 | 3608 | 0.2177 | 0.4519 |
| chrX | 155270560 | 1881819 | 0.0121 | 0.1201 |
| chrY | 59373566 | 105049 | 0.0018 | 0.0749 |

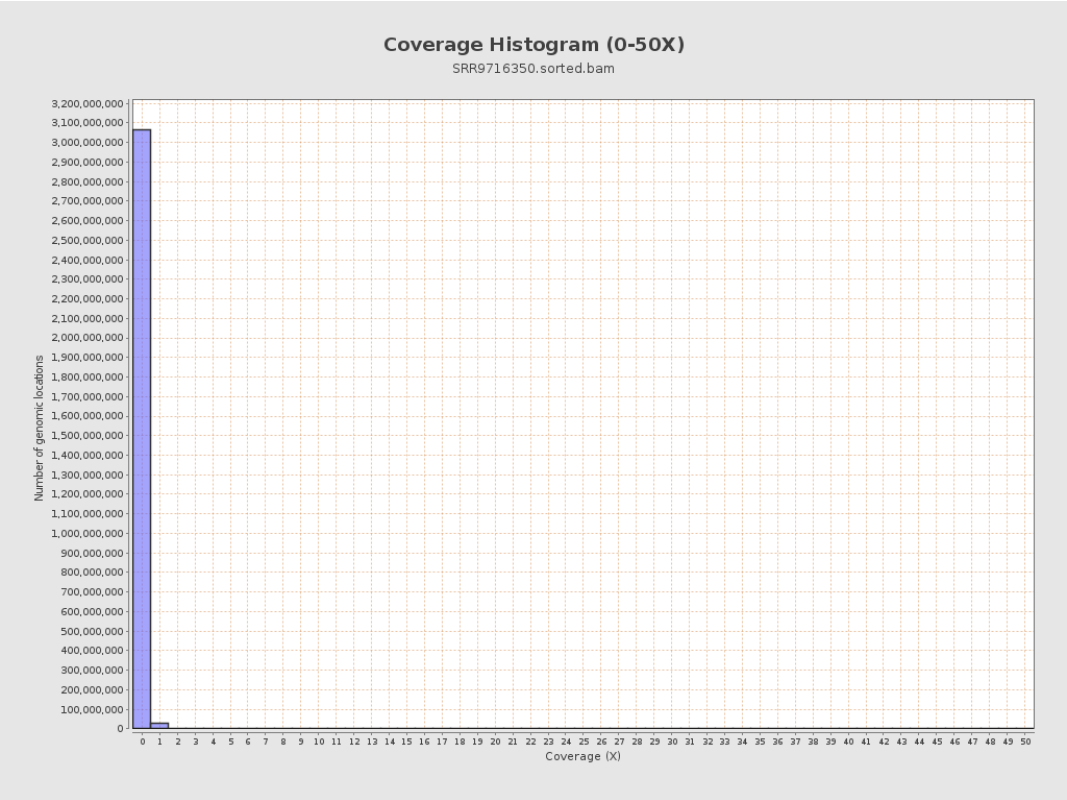
# 3. Results : Coverage across reference



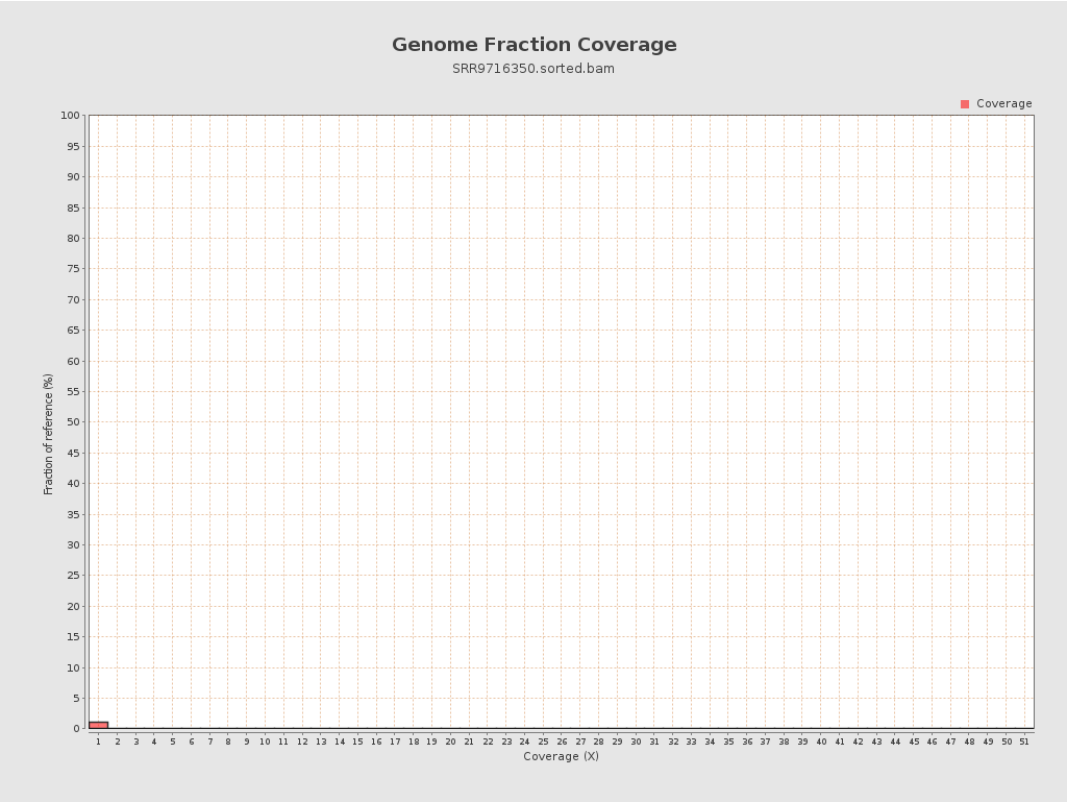
# 4. Results : Coverage Histogram



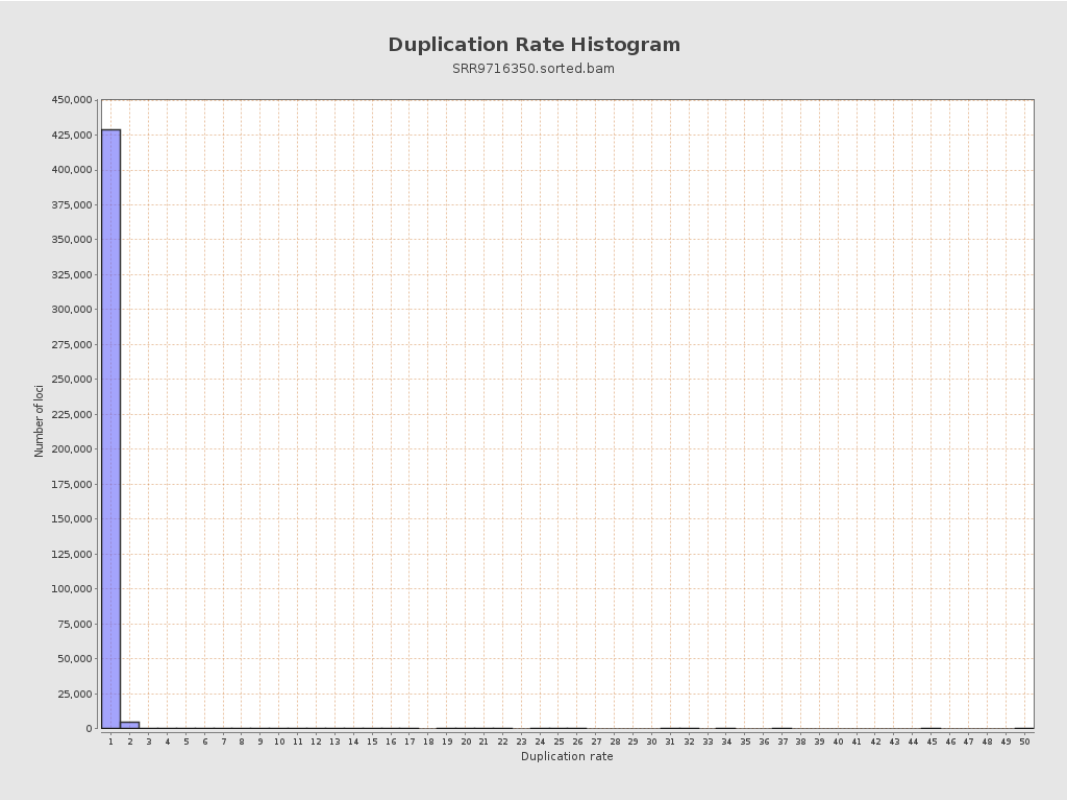
# 5. Results : Coverage Histogram (0-50X)



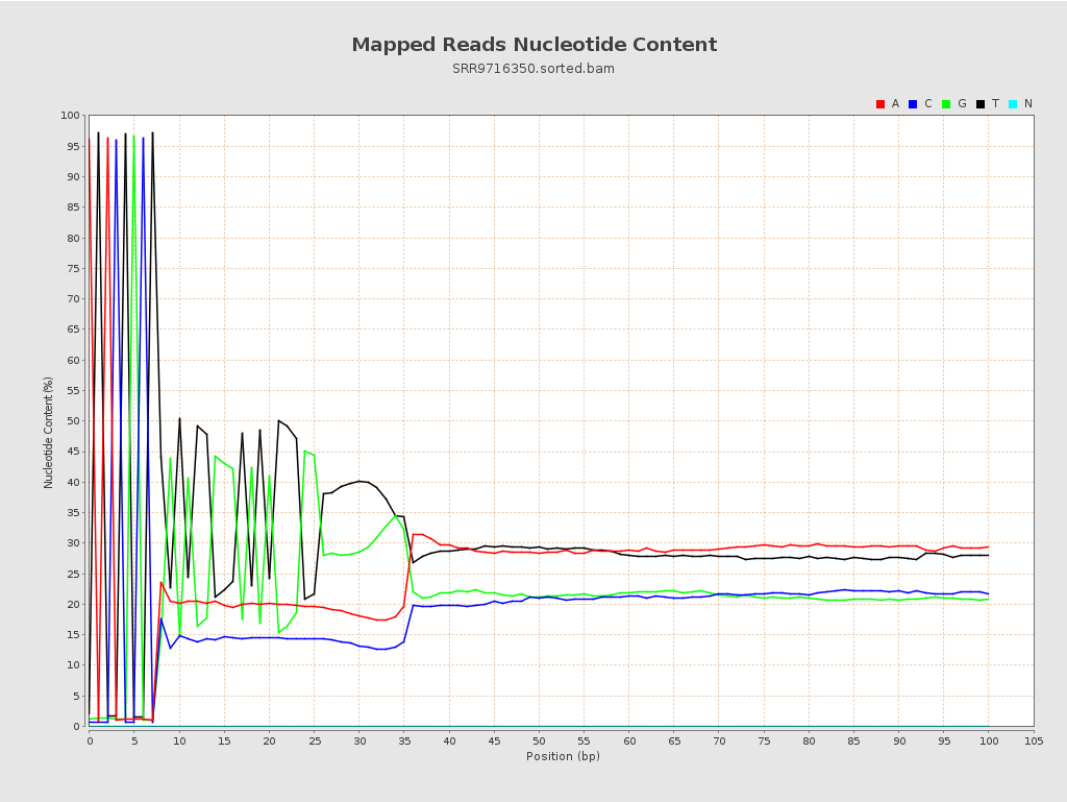
# 6. Results : Genome Fraction Coverage



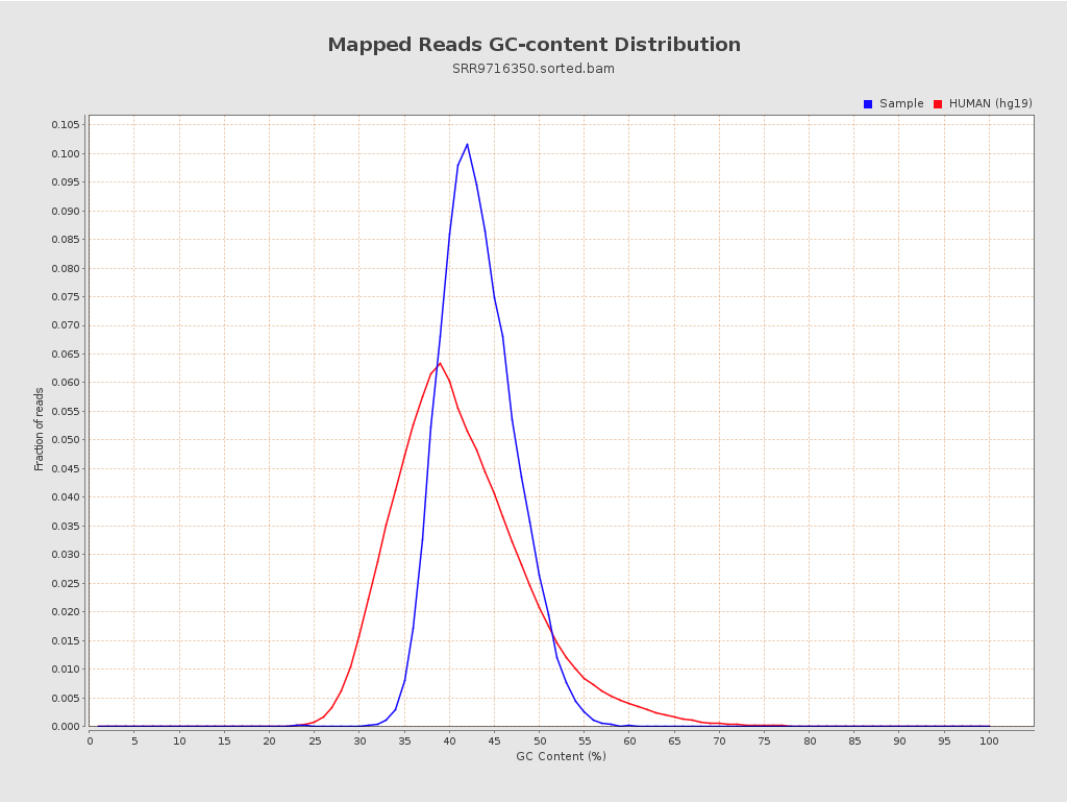
# 7. Results : Duplication Rate Histogram



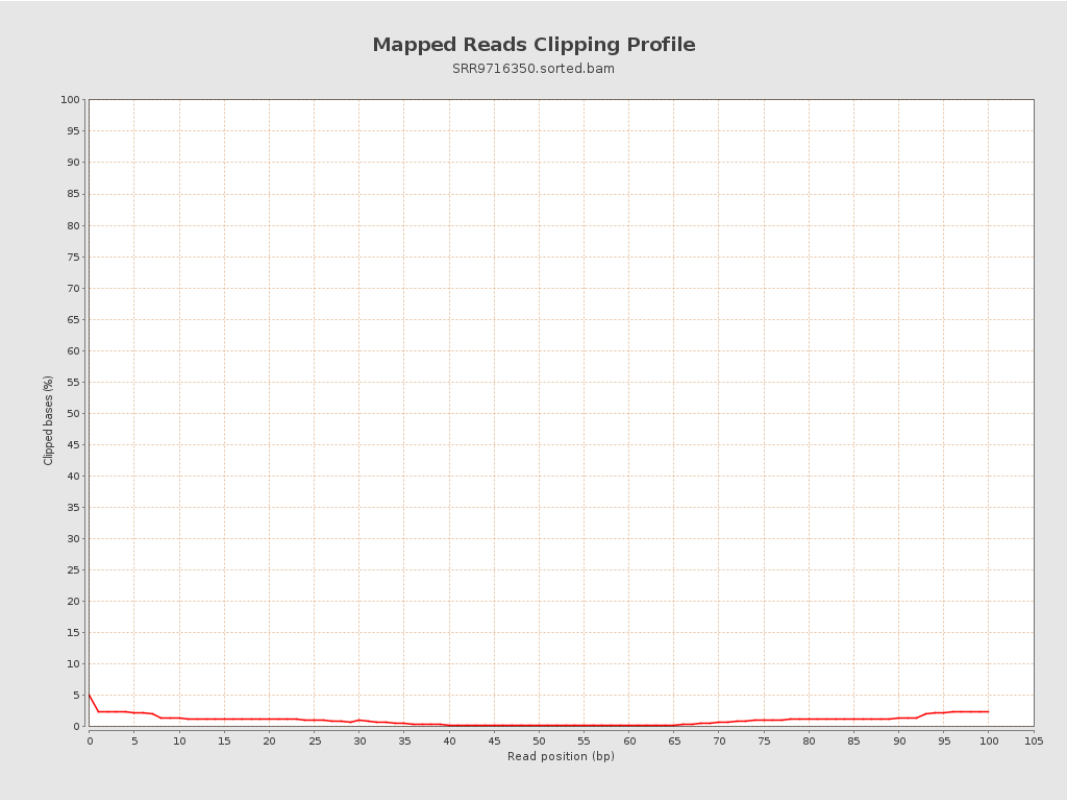
# 8. Results : Mapped Reads Nucleotide Content



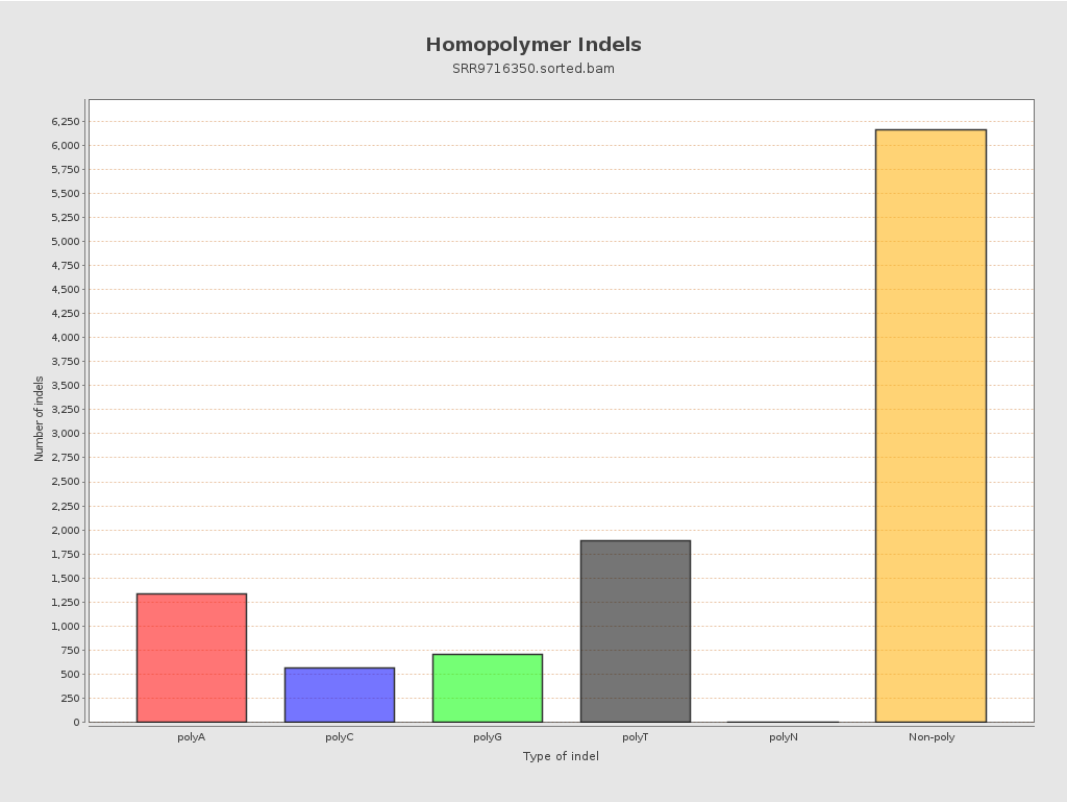
# 9. Results : Mapped Reads GC-content Distribution



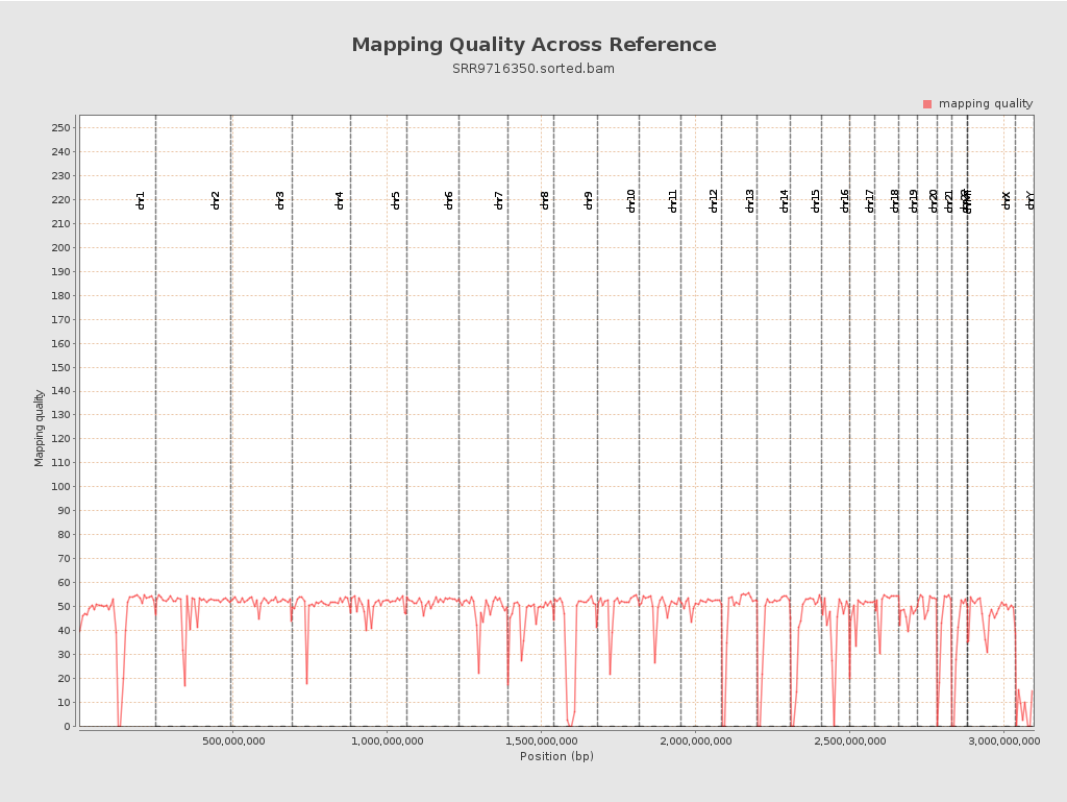
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram