# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/02 12:28:32*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716418.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_SRR9716418 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716418.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 02 12:28:31 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716418.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 987,940 |
| Mapped reads | 887,616 / 89.85% |
| Unmapped reads | 100,324 / 10.15% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 4,197 / 0.42% |
| Read min/max/mean length | 30 / 76 / 76.14 |
| Duplicated reads (estimated) | 22,534 / 2.28% |
| Duplication rate | 1.96% |
| Clipped reads | 890,144 / 90.1% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 12,368,872 / 24.11% |
| Number/percentage of C's | 9,860,704 / 19.22% |
| Number/percentage of T's | 16,173,005 / 31.52% |
| Number/percentage of G's | 12,902,682 / 25.15% |
| Number/percentage of N's | 699 / 0% |
| GC Percentage | 44.37% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0166 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1667 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.32 |

## 2.5. Mismatches and indels

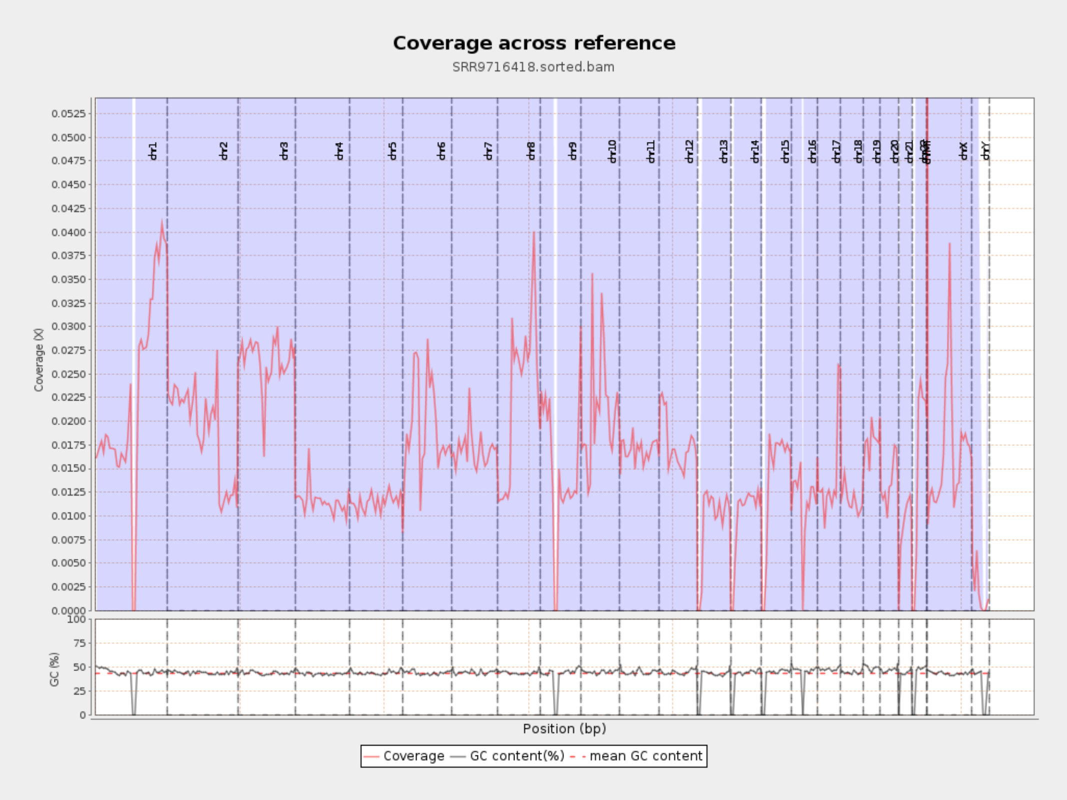
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 254,828 |
| Insertions | 3,319 |
| Mapped reads with at least one insertion | 0.37% |
| Deletions | 8,968 |
| Mapped reads with at least one deletion | 1% |
| Homopolymer indels | 43.88% |

## 2.6. Chromosome stats

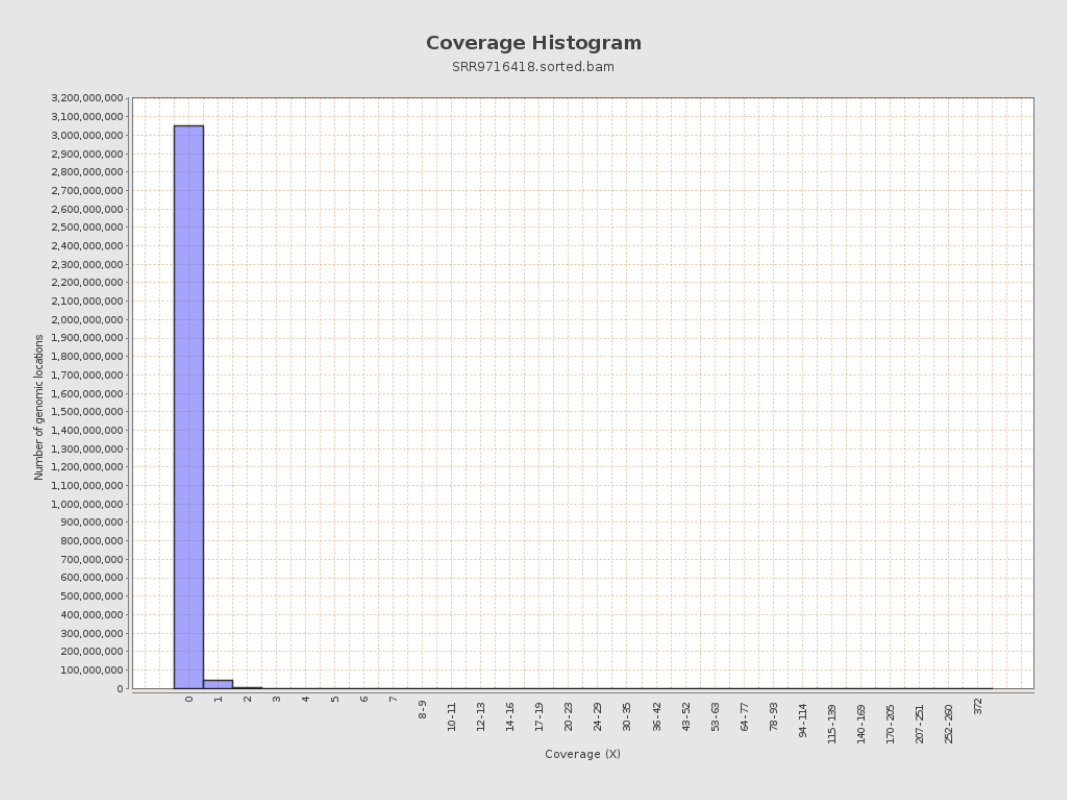
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5724429 | 0.023 | 0.2523 |
| chr2 | 243199373 | 4599589 | 0.0189 | 0.211 |
| chr3 | 198022430 | 5230957 | 0.0264 | 0.1726 |
| chr4 | 191154276 | 2206094 | 0.0115 | 0.1193 |
| chr5 | 180915260 | 2081029 | 0.0115 | 0.1146 |
| chr6 | 171115067 | 3309177 | 0.0193 | 0.1702 |
| chr7 | 159138663 | 2717019 | 0.0171 | 0.1872 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3373687 | 0.023 | 0.172 |
| chr9 | 141213431 | 2026667 | 0.0144 | 0.1503 |
| chr10 | 135534747 | 2881005 | 0.0213 | 0.1868 |
| chr11 | 135006516 | 2298474 | 0.017 | 0.1634 |
| chr12 | 133851895 | 2367857 | 0.0177 | 0.1429 |
| chr13 | 115169878 | 1076837 | 0.0093 | 0.1029 |
| chr14 | 107349540 | 1049637 | 0.0098 | 0.1122 |
| chr15 | 102531392 | 1419748 | 0.0138 | 0.1276 |
| chr16 | 90354753 | 1016151 | 0.0112 | 0.119 |
| chr17 | 81195210 | 1134547 | 0.014 | 0.1307 |
| chr18 | 78077248 | 909085 | 0.0116 | 0.2261 |
| chr19 | 59128983 | 1052427 | 0.0178 | 0.1915 |
| chr20 | 63025520 | 850923 | 0.0135 | 0.1239 |
| chr21 | 48129895 | 435158 | 0.009 | 0.1081 |
| chr22 | 51304566 | 793246 | 0.0155 | 0.1322 |
| chrMT | 16571 | 4878 | 0.2944 | 0.5697 |
| chrX | 155270560 | 2644463 | 0.017 | 0.1483 |
| chrY | 59373566 | 116924 | 0.002 | 0.0577 |

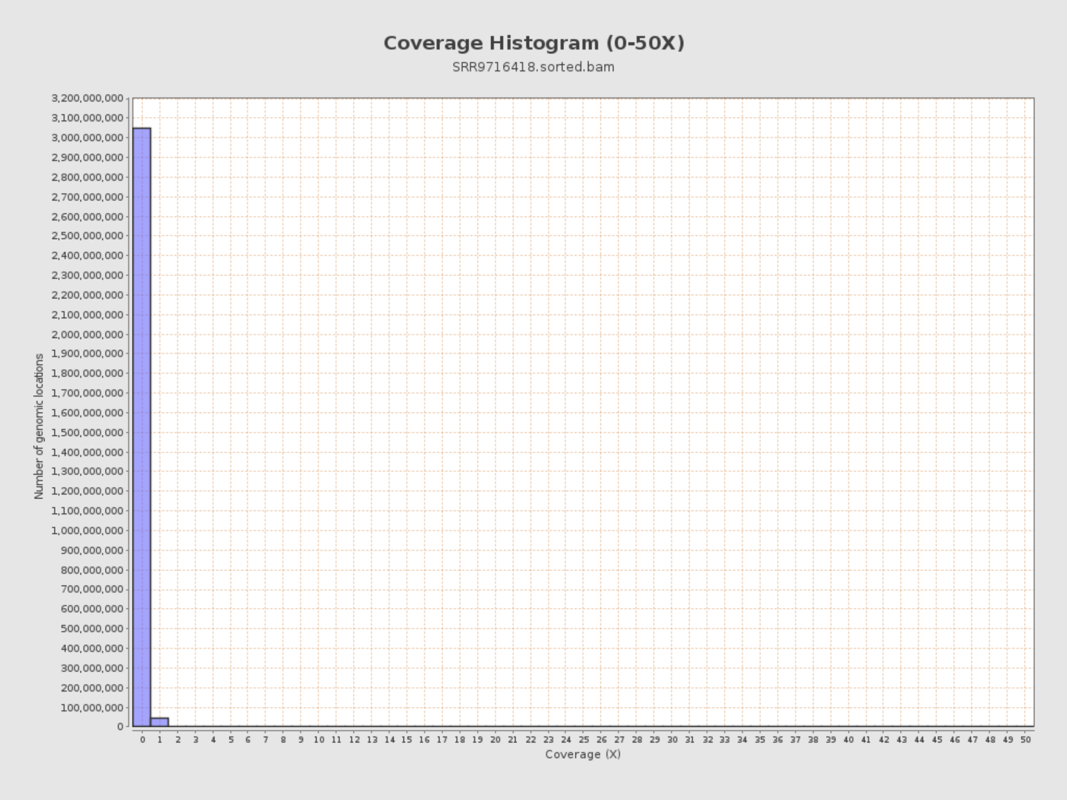
# 3. Results : Coverage across reference



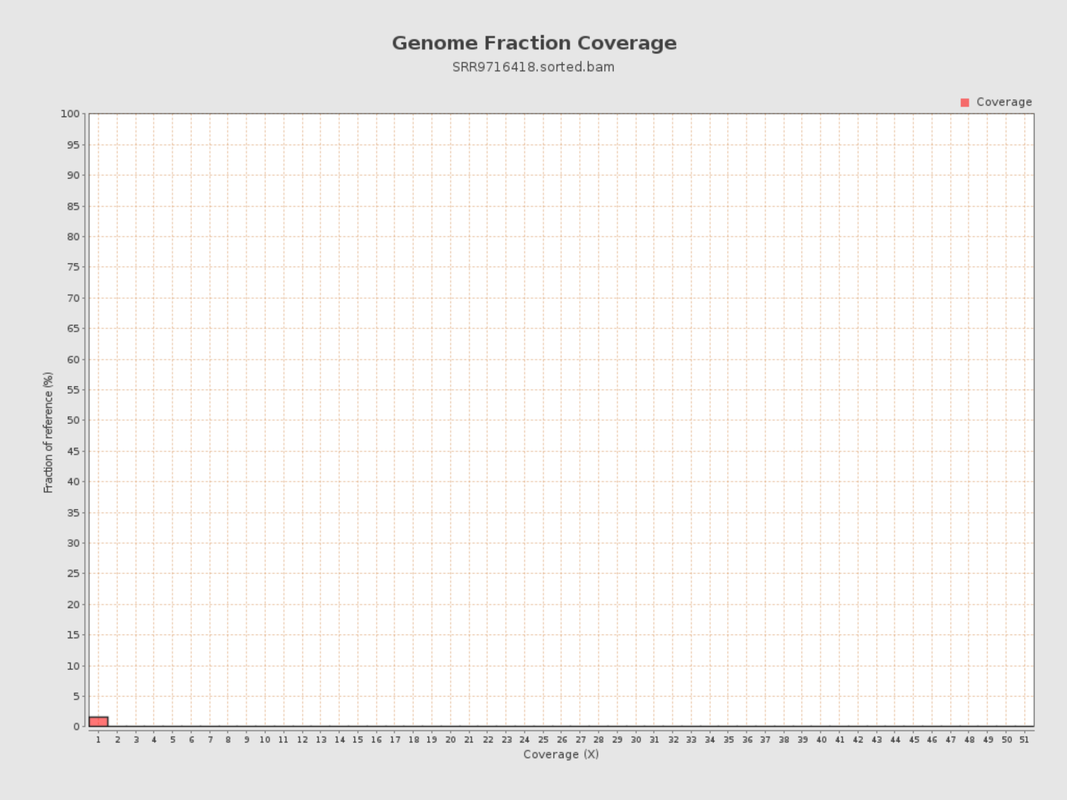
# 4. Results : Coverage Histogram



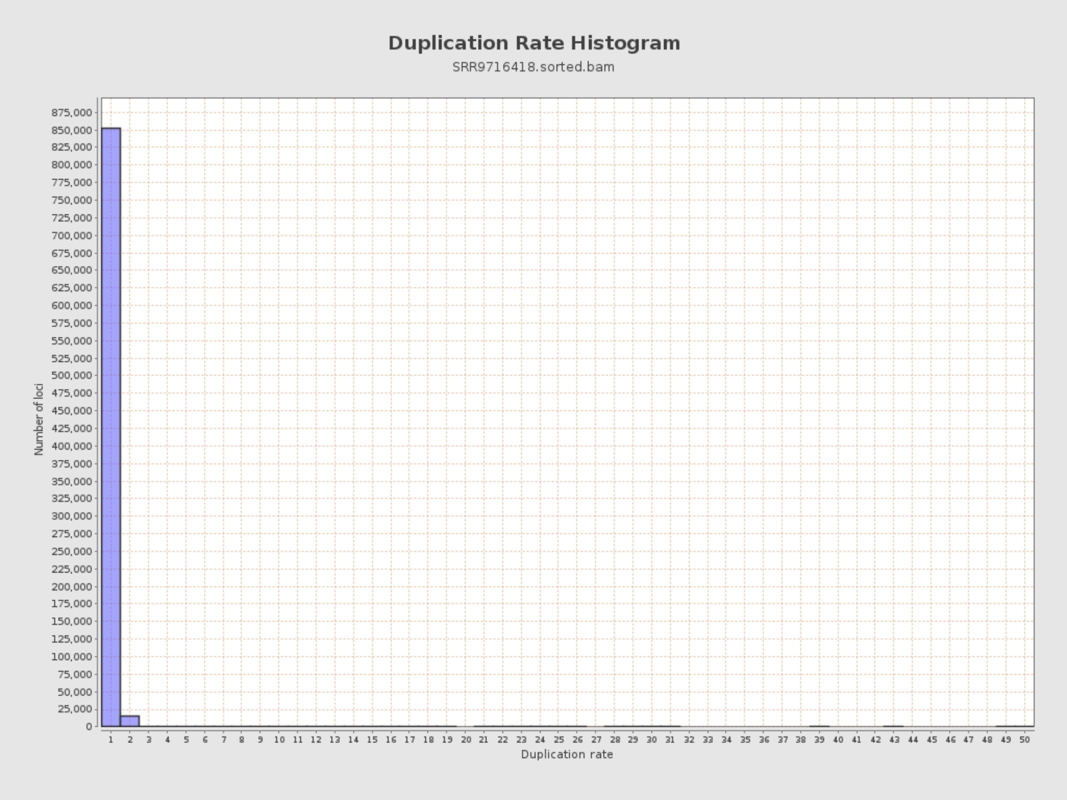
# 5. Results : Coverage Histogram (0-50X)



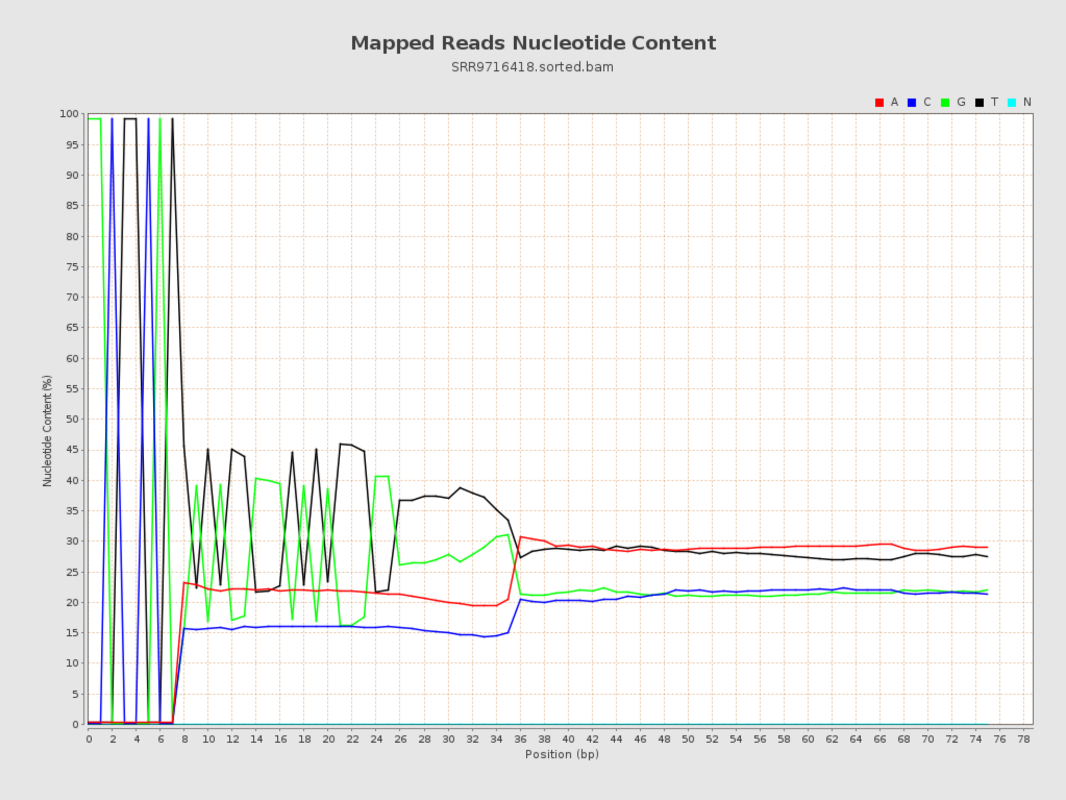
# 6. Results : Genome Fraction Coverage



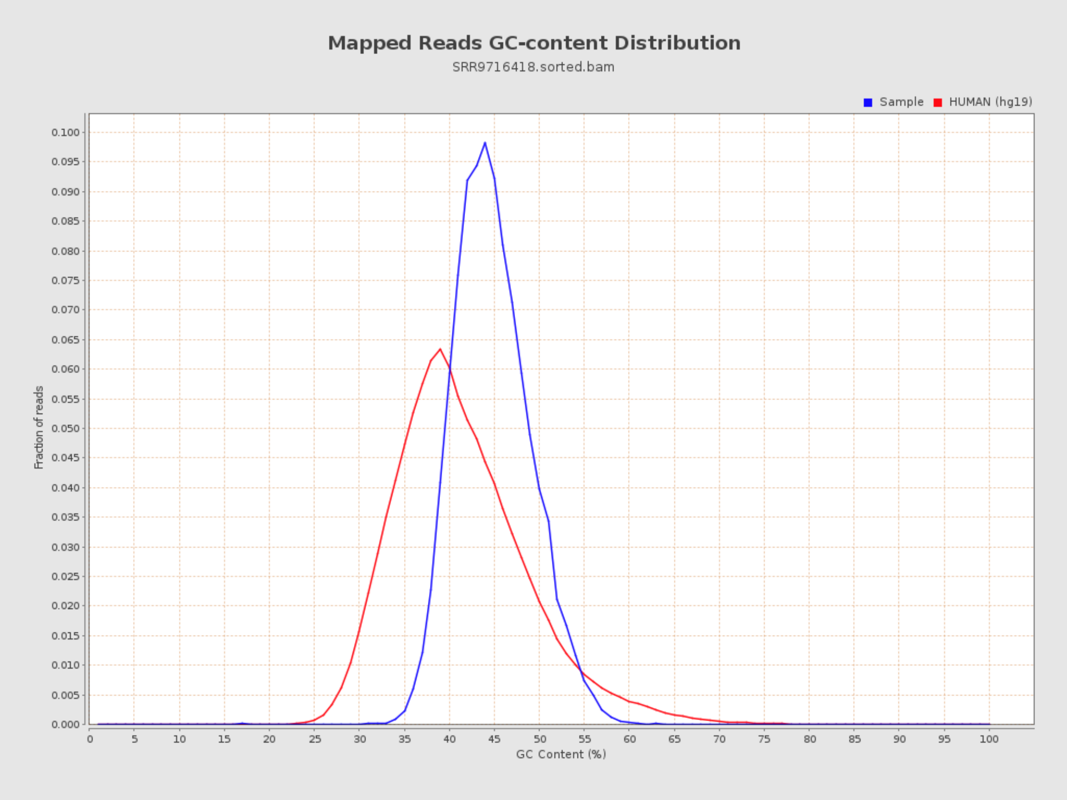
# 7. Results : Duplication Rate Histogram



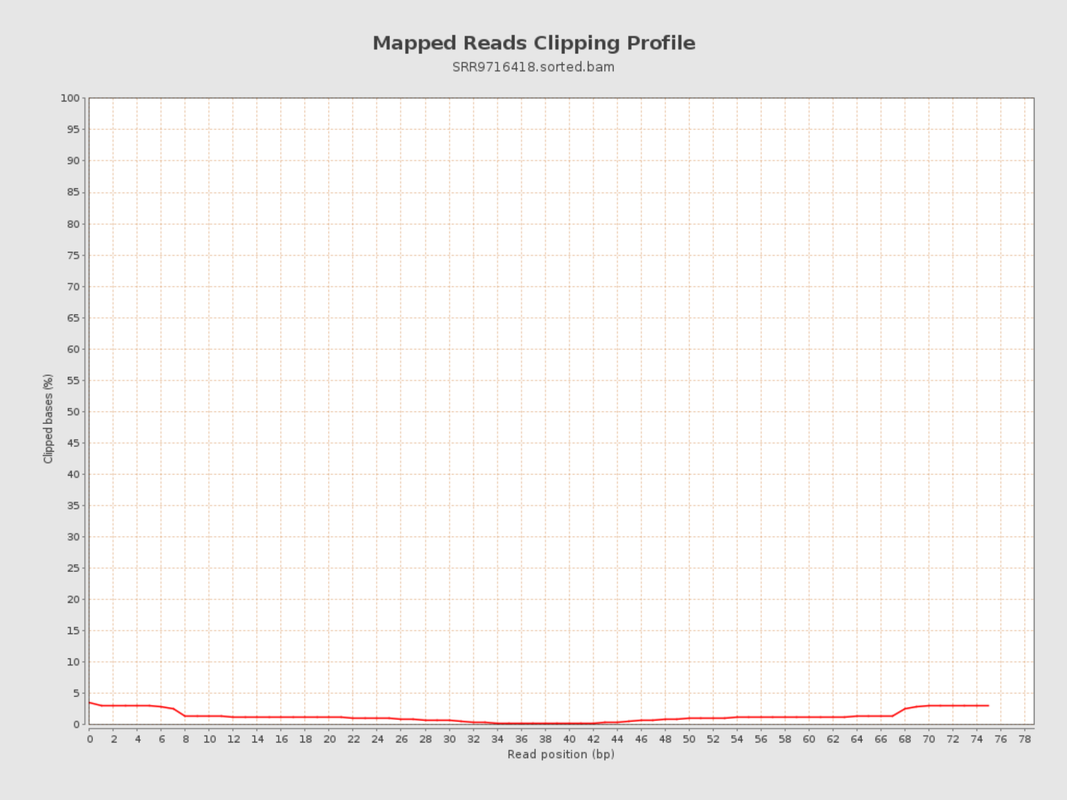
# 8. Results : Mapped Reads Nucleotide Content



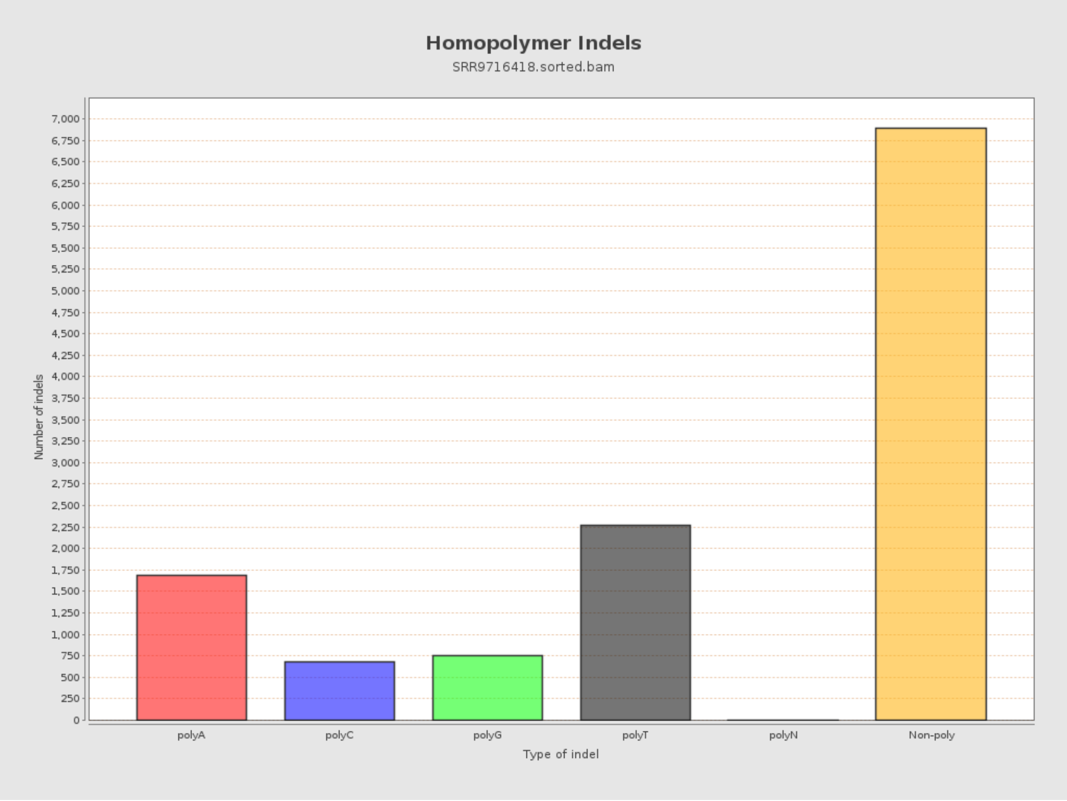
# 9. Results : Mapped Reads GC-content Distribution



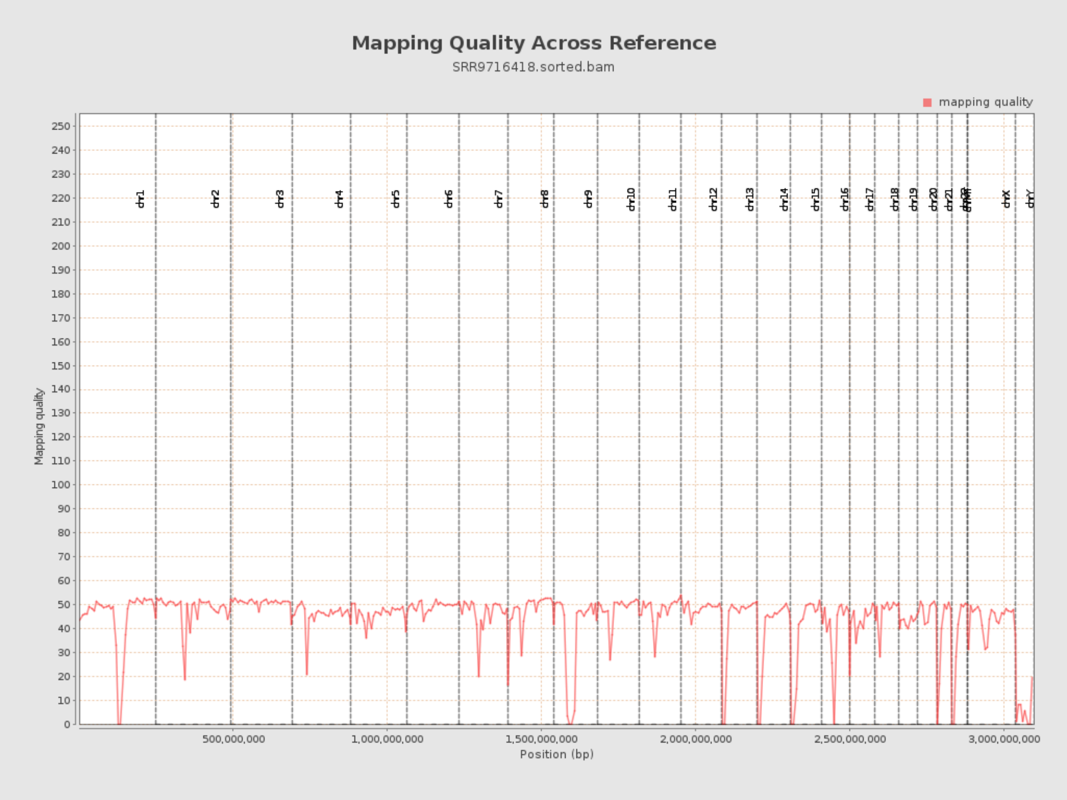
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram