# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/02 01:15:18*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716221.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_SRR9716221 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716221.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 02 01:15:17 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716221.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,931,949 |
| Mapped reads | 1,765,182 / 91.37% |
| Unmapped reads | 166,767 / 8.63% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 7,950 / 0.41% |
| Read min/max/mean length | 30 / 76 / 76.14 |
| Duplicated reads (estimated) | 77,125 / 3.99% |
| Duplication rate | 3.41% |
| Clipped reads | 1,768,074 / 91.52% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 26,656,615 / 26.07% |
| Number/percentage of C's | 19,984,052 / 19.54% |
| Number/percentage of T's | 31,812,453 / 31.11% |
| Number/percentage of G's | 23,794,527 / 23.27% |
| Number/percentage of N's | 1,655 / 0% |
| GC Percentage | 42.82% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.033 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2965 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.44 |

## 2.5. Mismatches and indels

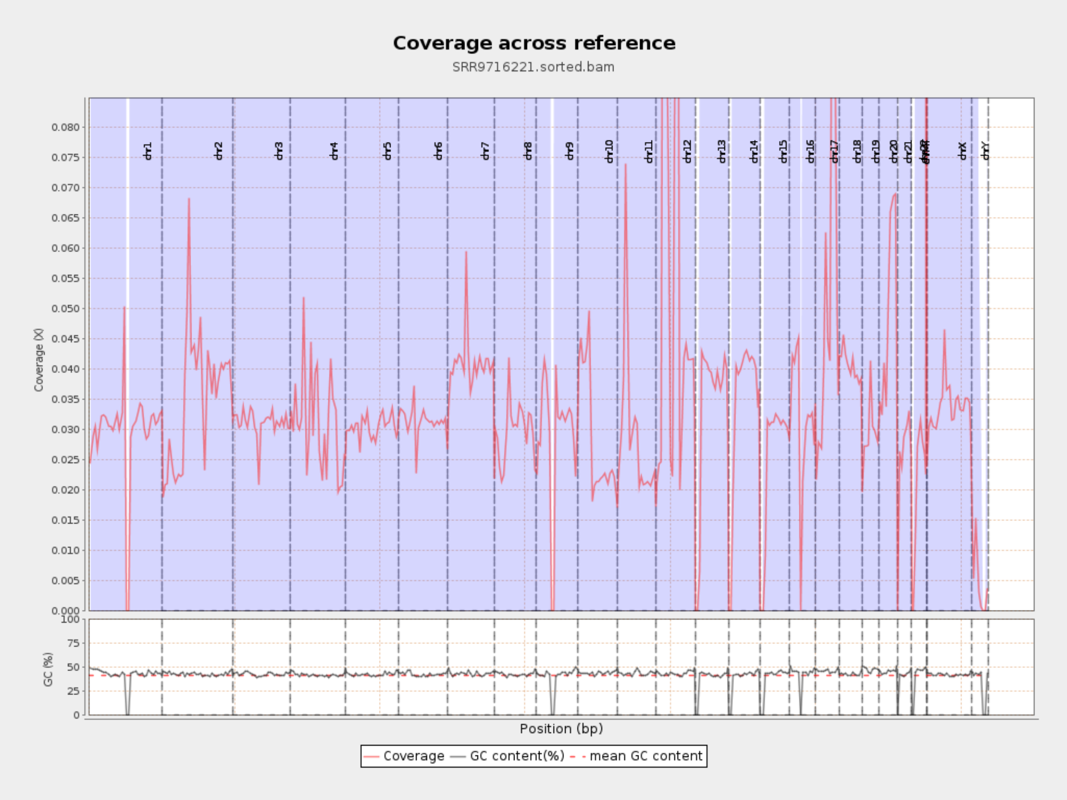
| | |
|---|---|
| General error rate | 0.53% |
| Mismatches | 529,481 |
| Insertions | 7,730 |
| Mapped reads with at least one insertion | 0.44% |
| Deletions | 16,688 |
| Mapped reads with at least one deletion | 0.94% |
| Homopolymer indels | 41.26% |

## 2.6. Chromosome stats

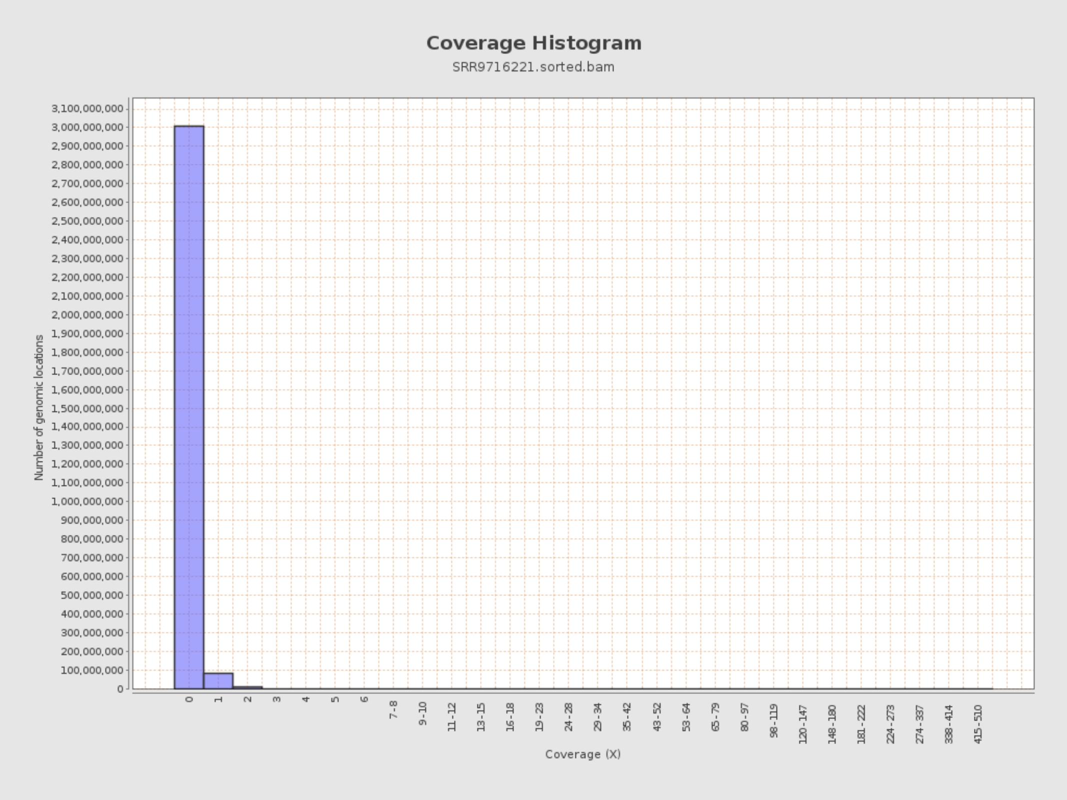
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 7347964 | 0.0295 | 0.4745 |
| chr2 | 243199373 | 8614012 | 0.0354 | 0.3469 |
| chr3 | 198022430 | 6149124 | 0.0311 | 0.1933 |
| chr4 | 191154276 | 5943674 | 0.0311 | 0.2167 |
| chr5 | 180915260 | 5503470 | 0.0304 | 0.1945 |
| chr6 | 171115067 | 5370930 | 0.0314 | 0.2154 |
| chr7 | 159138663 | 6543519 | 0.0411 | 0.4067 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 4359028 | 0.0298 | 0.2933 |
| chr9 | 141213431 | 4085083 | 0.0289 | 0.3081 |
| chr10 | 135534747 | 3918971 | 0.0289 | 0.2807 |
| chr11 | 135006516 | 3949285 | 0.0293 | 0.2466 |
| chr12 | 133851895 | 7665089 | 0.0573 | 0.2988 |
| chr13 | 115169878 | 3789163 | 0.0329 | 0.1989 |
| chr14 | 107349540 | 3626659 | 0.0338 | 0.2199 |
| chr15 | 102531392 | 2572926 | 0.0251 | 0.1748 |
| chr16 | 90354753 | 2864550 | 0.0317 | 0.2121 |
| chr17 | 81195210 | 4144555 | 0.051 | 0.2644 |
| chr18 | 78077248 | 3179135 | 0.0407 | 0.5538 |
| chr19 | 59128983 | 1756900 | 0.0297 | 0.3775 |
| chr20 | 63025520 | 3133758 | 0.0497 | 0.2538 |
| chr21 | 48129895 | 1229151 | 0.0255 | 0.2059 |
| chr22 | 51304566 | 1006657 | 0.0196 | 0.1523 |
| chrMT | 16571 | 8635 | 0.5211 | 0.7977 |
| chrX | 155270560 | 5237863 | 0.0337 | 0.2424 |
| chrY | 59373566 | 276651 | 0.0047 | 0.1101 |

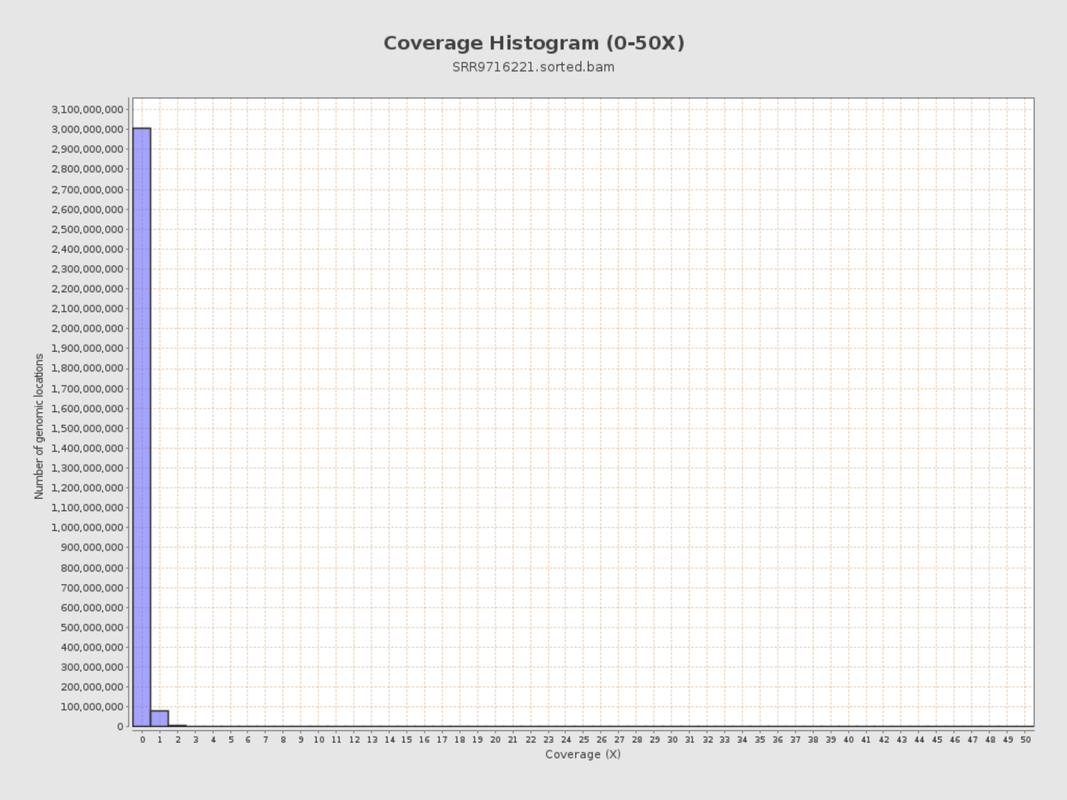
# 3. Results : Coverage across reference



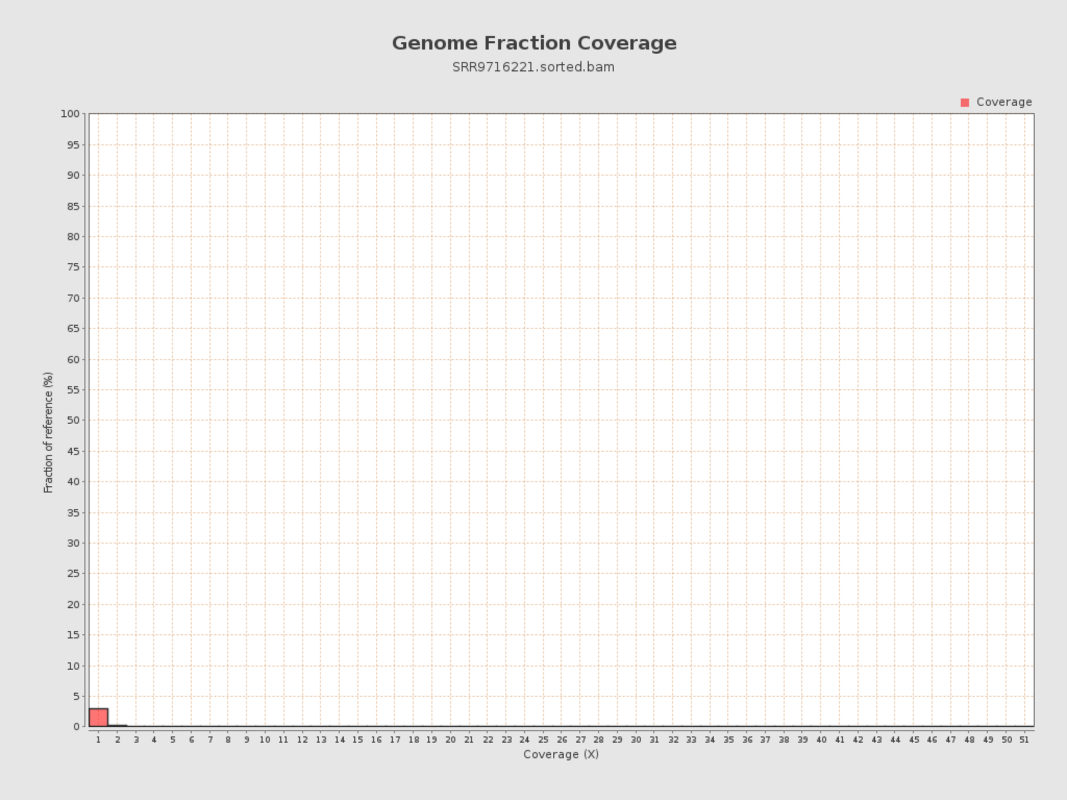
# 4. Results : Coverage Histogram



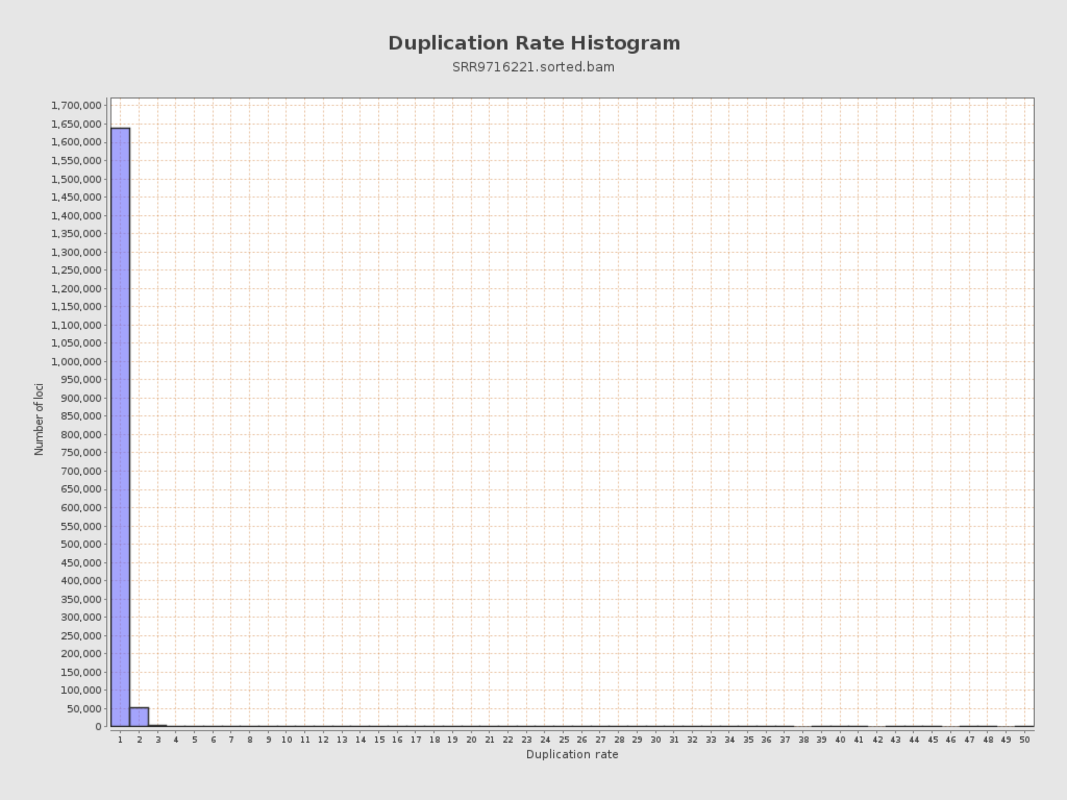
# 5. Results : Coverage Histogram (0-50X)



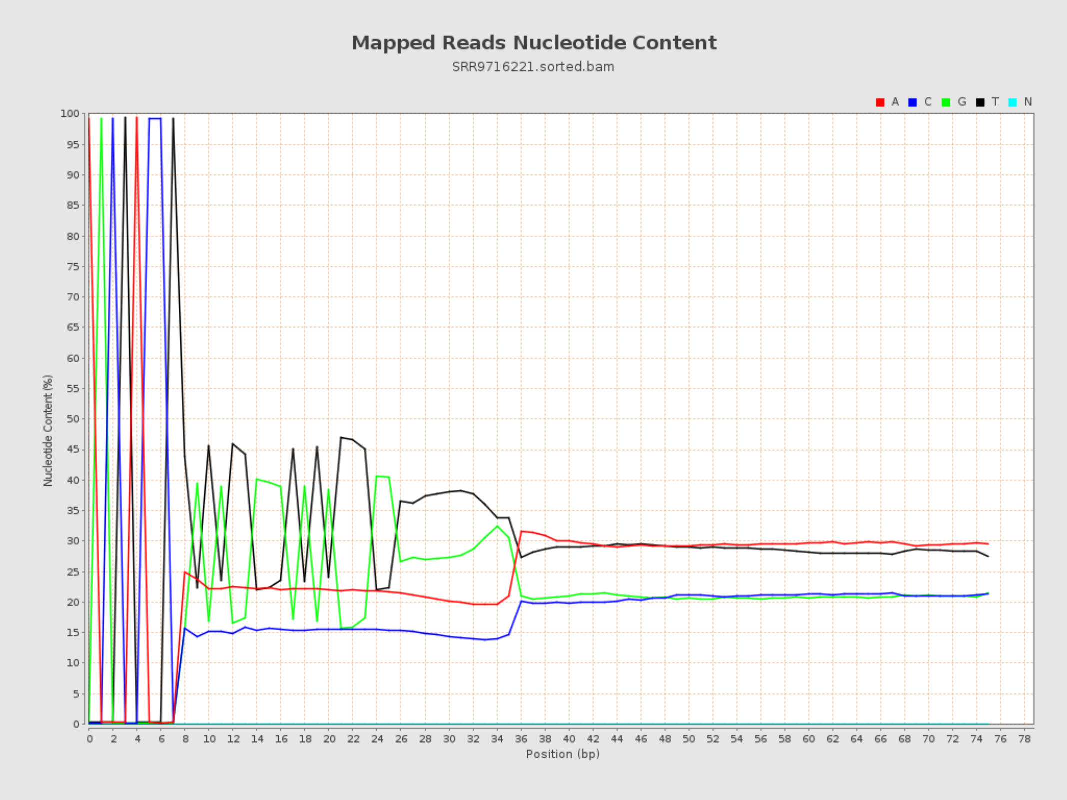
# 6. Results : Genome Fraction Coverage



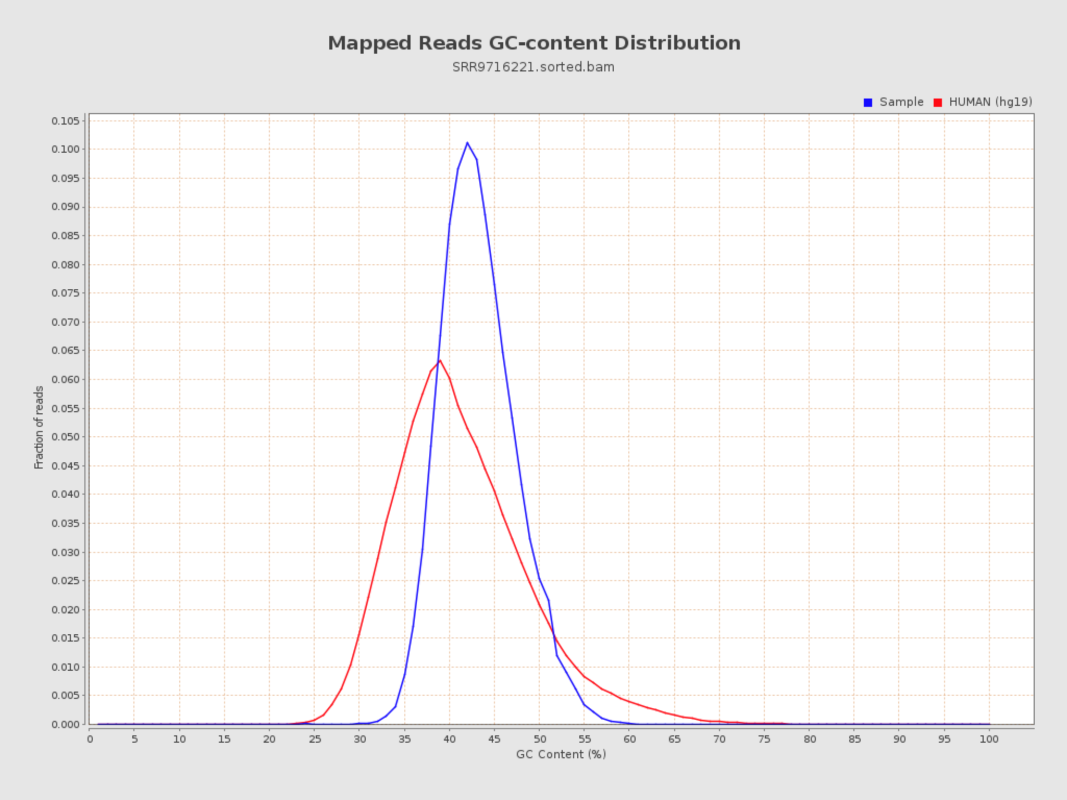
# 7. Results : Duplication Rate Histogram



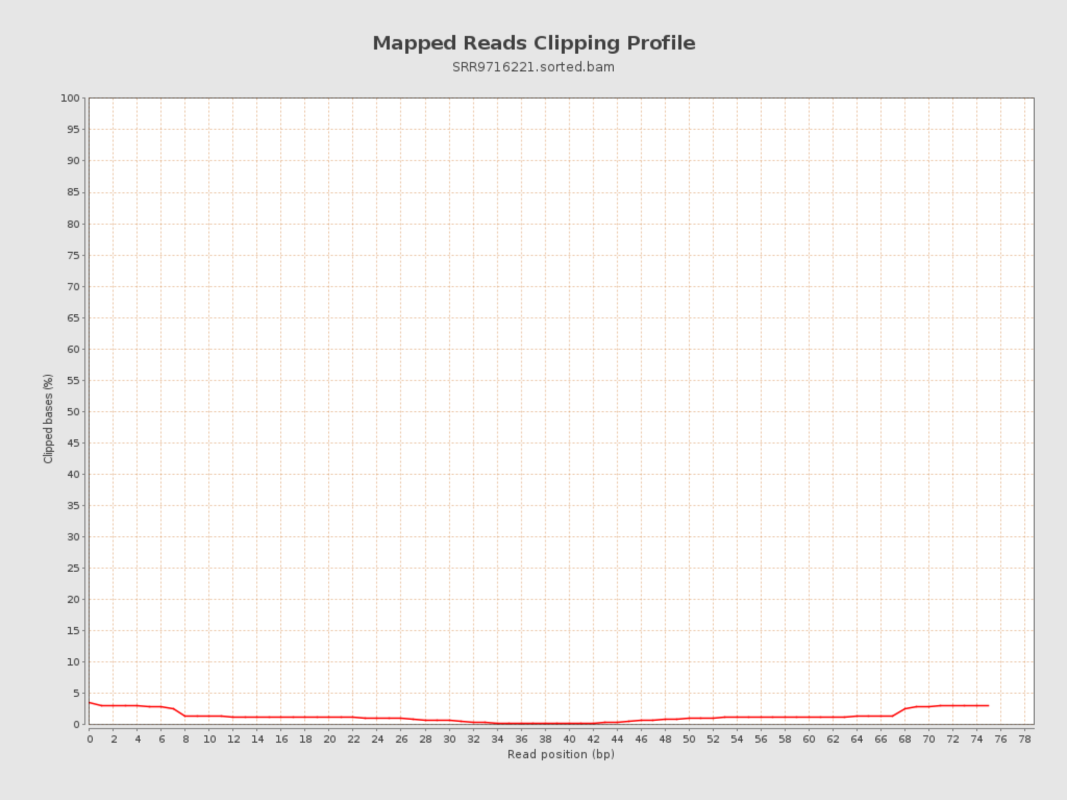
# 8. Results : Mapped Reads Nucleotide Content



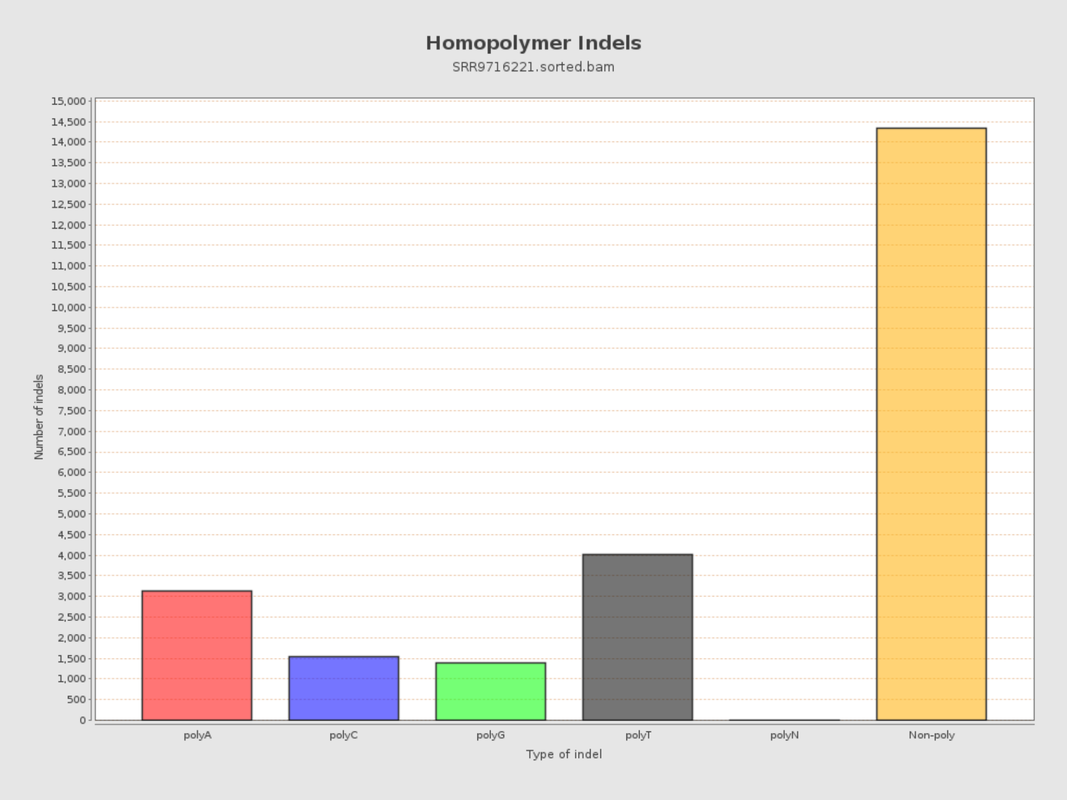
# 9. Results : Mapped Reads GC-content Distribution



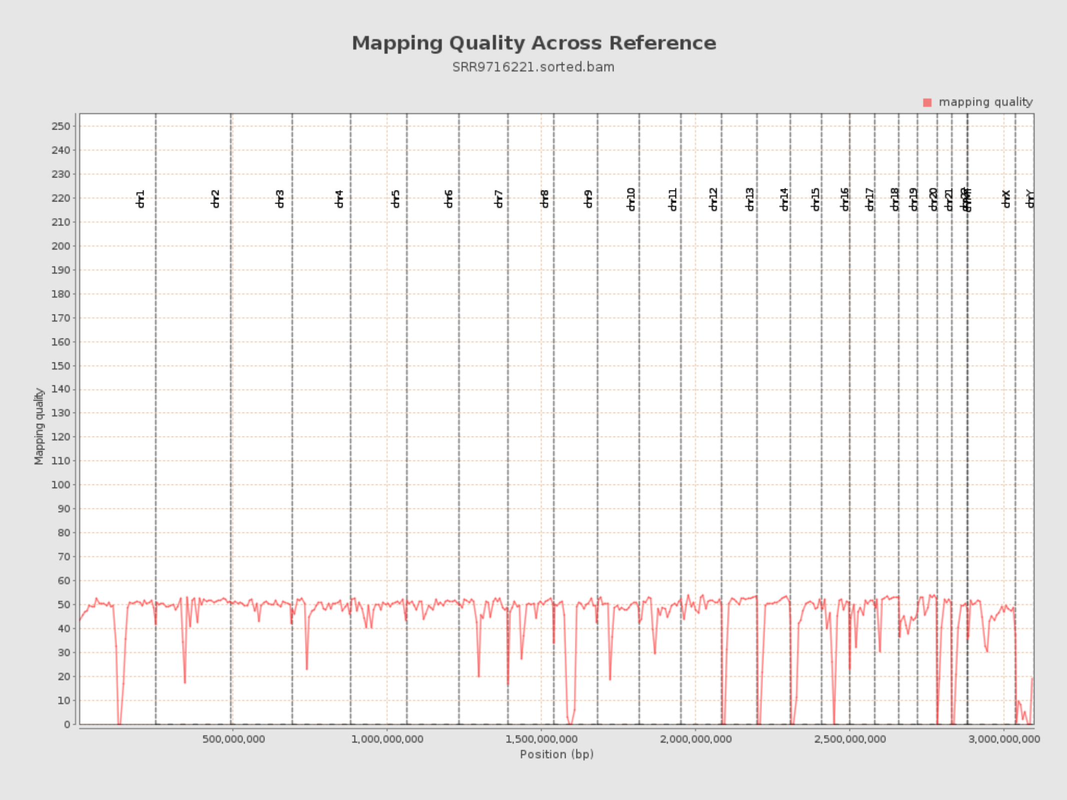
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram