# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 22:07:40*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716978.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_SRR9716978 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716978.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 22:07:37 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716978.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,794,909 |
| Mapped reads | 1,649,972 / 91.93% |
| Unmapped reads | 144,937 / 8.07% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 8,920 / 0.5% |
| Read min/max/mean length | 30 / 76 / 76.17 |
| Duplicated reads (estimated) | 72,050 / 4.01% |
| Duplication rate | 3.32% |
| Clipped reads | 1,656,958 / 92.31% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 22,887,403 / 23.87% |
| Number/percentage of C's | 19,786,368 / 20.63% |
| Number/percentage of T's | 30,421,697 / 31.73% |
| Number/percentage of G's | 22,791,503 / 23.77% |
| Number/percentage of N's | 657 / 0% |
| GC Percentage | 44.4% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.031 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2897 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.39 |

## 2.5. Mismatches and indels

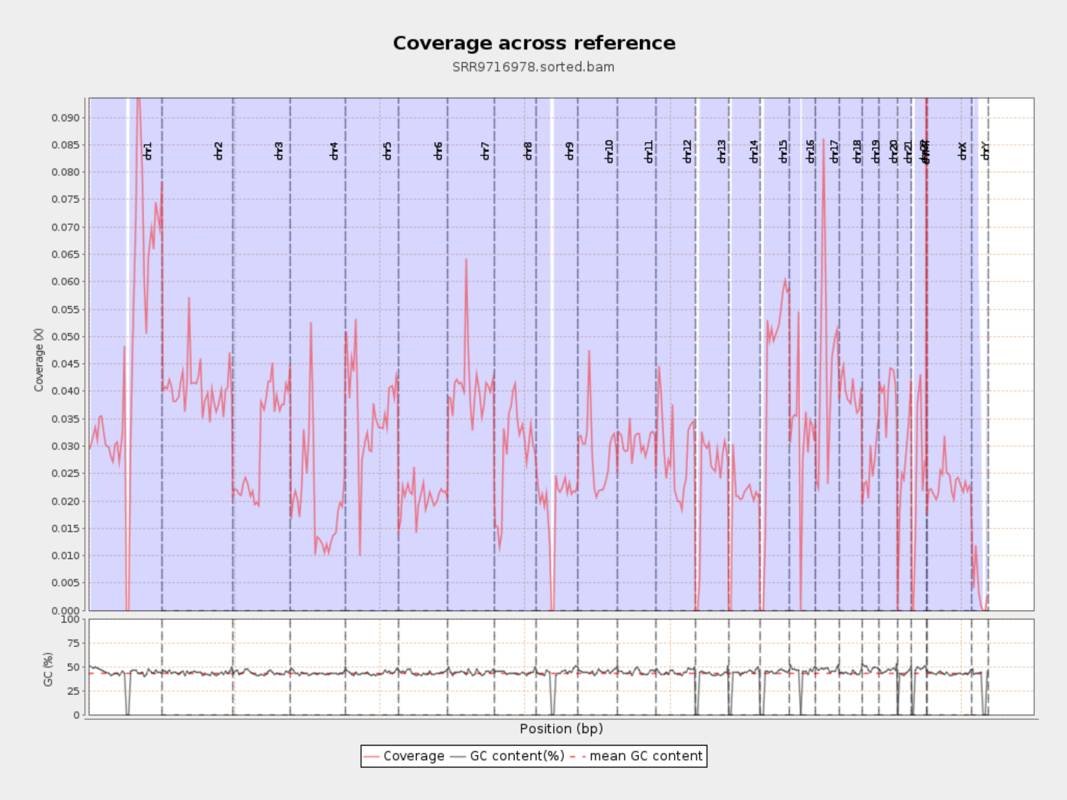
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 481,284 |
| Insertions | 5,567 |
| Mapped reads with at least one insertion | 0.34% |
| Deletions | 17,261 |
| Mapped reads with at least one deletion | 1.04% |
| Homopolymer indels | 44.33% |

## 2.6. Chromosome stats

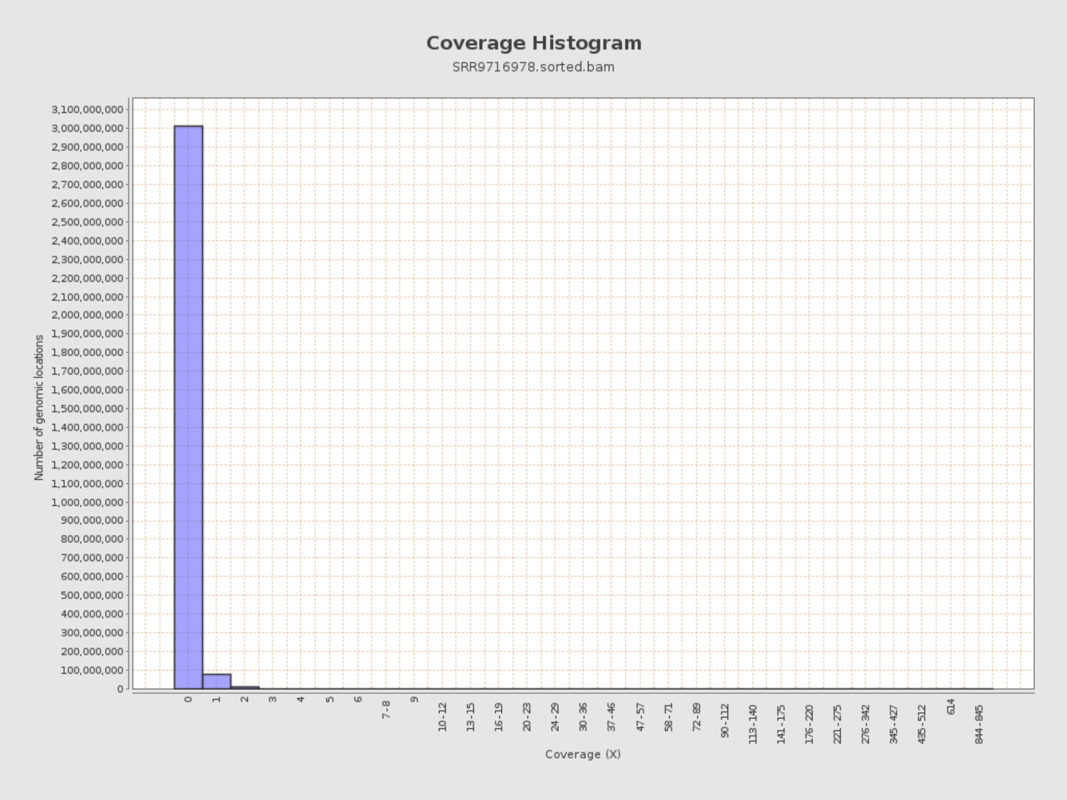
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 11478225 | 0.0461 | 0.4622 |
| chr2 | 243199373 | 9851667 | 0.0405 | 0.4284 |
| chr3 | 198022430 | 6089227 | 0.0308 | 0.1946 |
| chr4 | 191154276 | 3823874 | 0.02 | 0.1769 |
| chr5 | 180915260 | 6578337 | 0.0364 | 0.2115 |
| chr6 | 171115067 | 3523548 | 0.0206 | 0.1856 |
| chr7 | 159138663 | 6534897 | 0.0411 | 0.4696 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 4280336 | 0.0292 | 0.2456 |
| chr9 | 141213431 | 2689151 | 0.019 | 0.2207 |
| chr10 | 135534747 | 3859602 | 0.0285 | 0.2371 |
| chr11 | 135006516 | 4148016 | 0.0307 | 0.2797 |
| chr12 | 133851895 | 3844815 | 0.0287 | 0.189 |
| chr13 | 115169878 | 2752591 | 0.0239 | 0.1735 |
| chr14 | 107349540 | 2057534 | 0.0192 | 0.1635 |
| chr15 | 102531392 | 4424758 | 0.0432 | 0.2326 |
| chr16 | 90354753 | 2891563 | 0.032 | 0.209 |
| chr17 | 81195210 | 3710797 | 0.0457 | 0.2574 |
| chr18 | 78077248 | 3100064 | 0.0397 | 0.5023 |
| chr19 | 59128983 | 1544230 | 0.0261 | 0.342 |
| chr20 | 63025520 | 2527654 | 0.0401 | 0.2253 |
| chr21 | 48129895 | 1236489 | 0.0257 | 0.1883 |
| chr22 | 51304566 | 1156232 | 0.0225 | 0.1658 |
| chrMT | 16571 | 5133 | 0.3098 | 0.6426 |
| chrX | 155270560 | 3580043 | 0.0231 | 0.192 |
| chrY | 59373566 | 226409 | 0.0038 | 0.0959 |

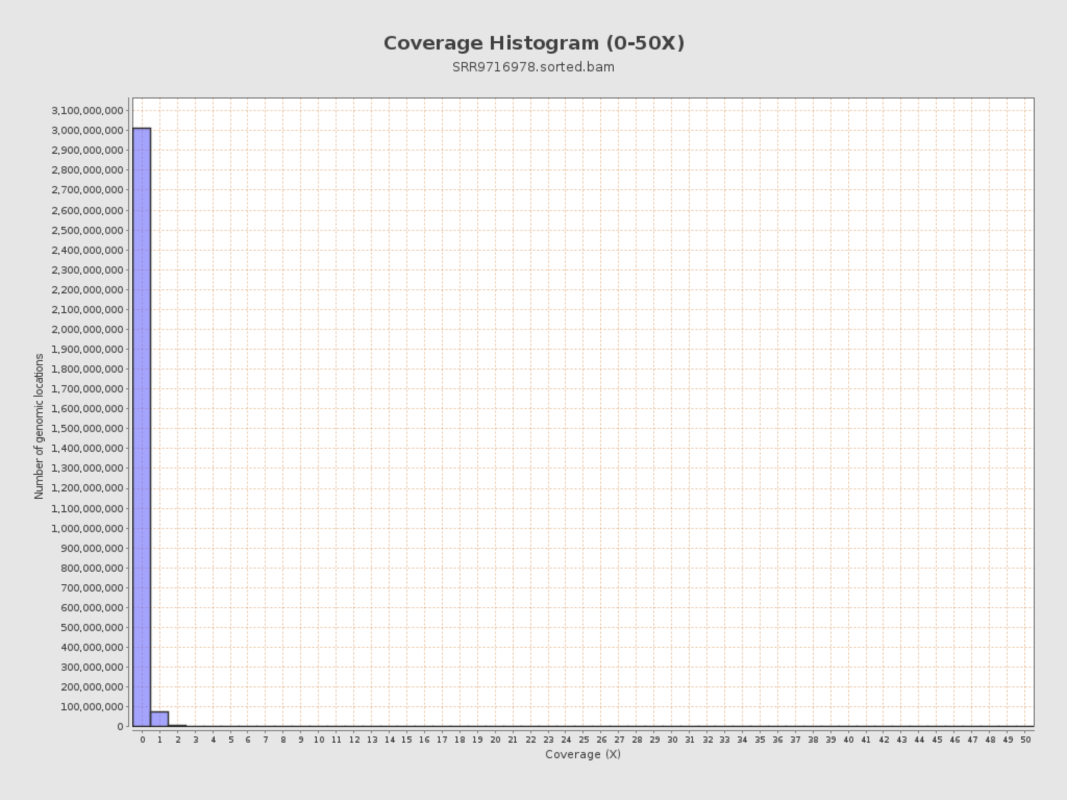
# 3. Results : Coverage across reference



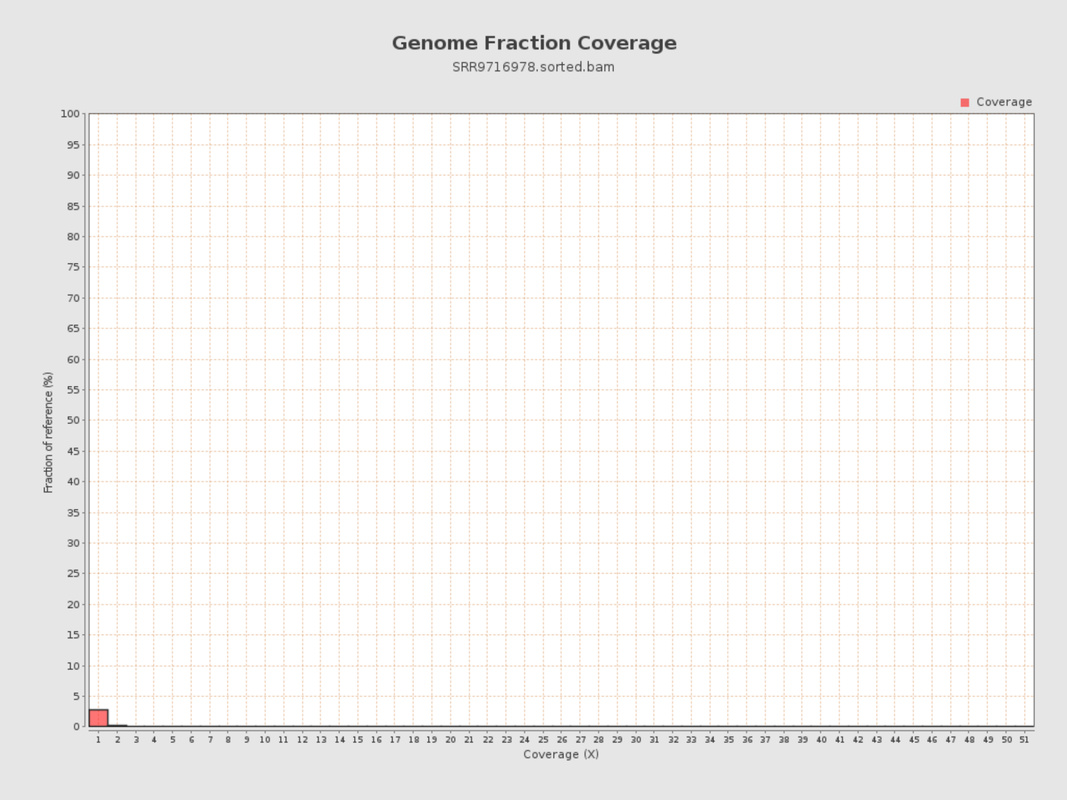
# 4. Results : Coverage Histogram



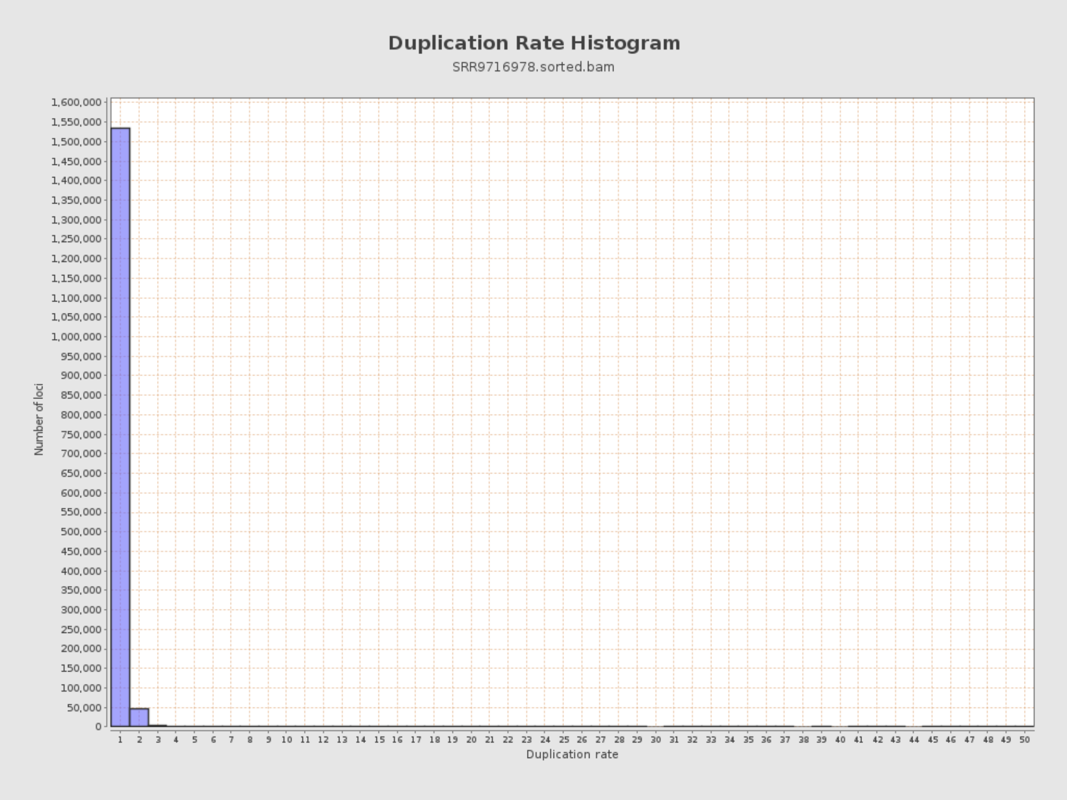
# 5. Results : Coverage Histogram (0-50X)



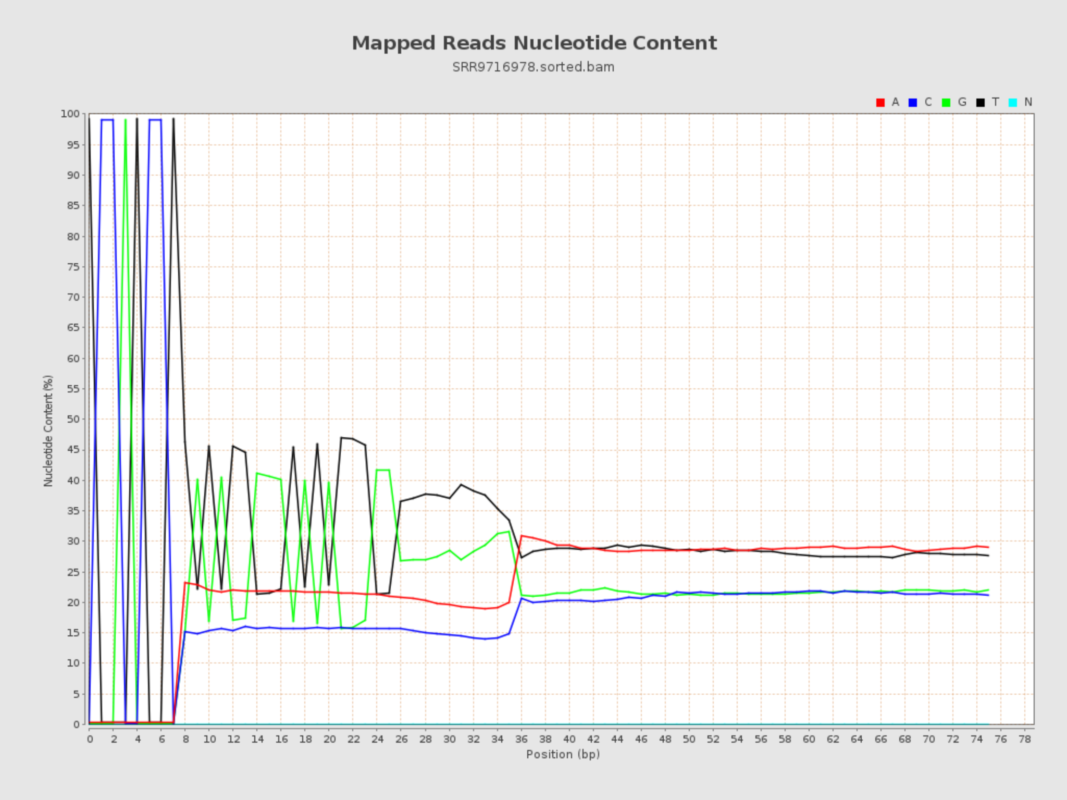
# 6. Results : Genome Fraction Coverage



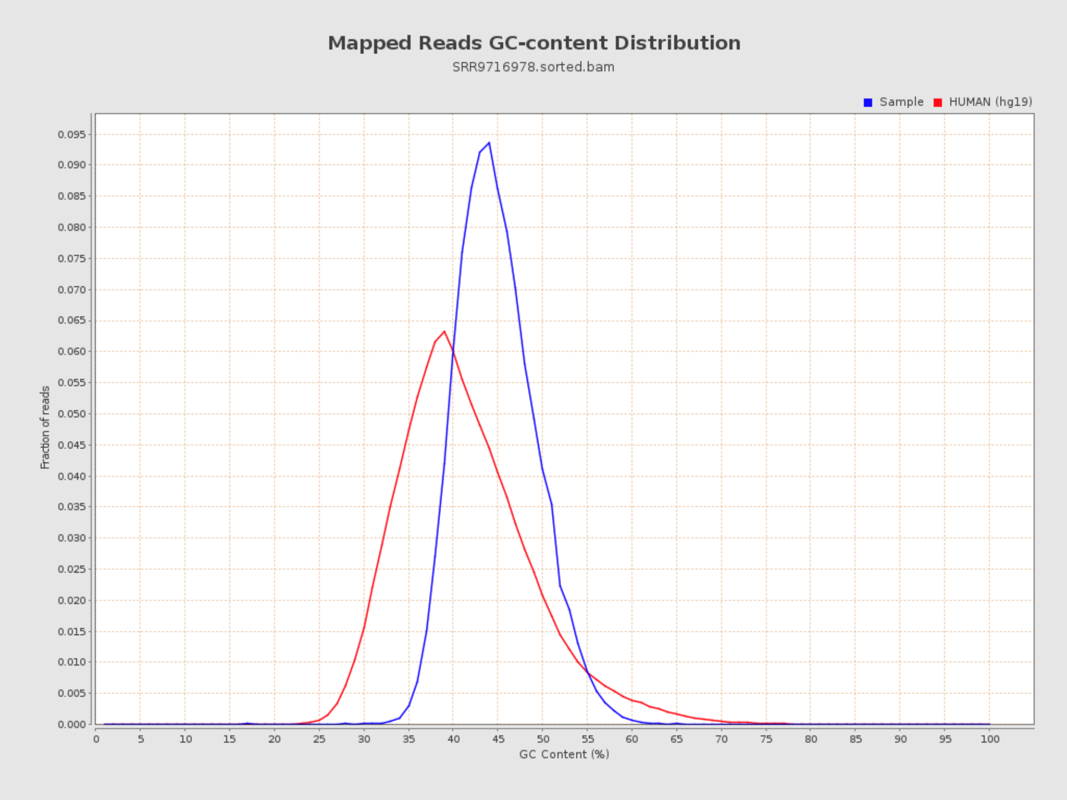
# 7. Results : Duplication Rate Histogram



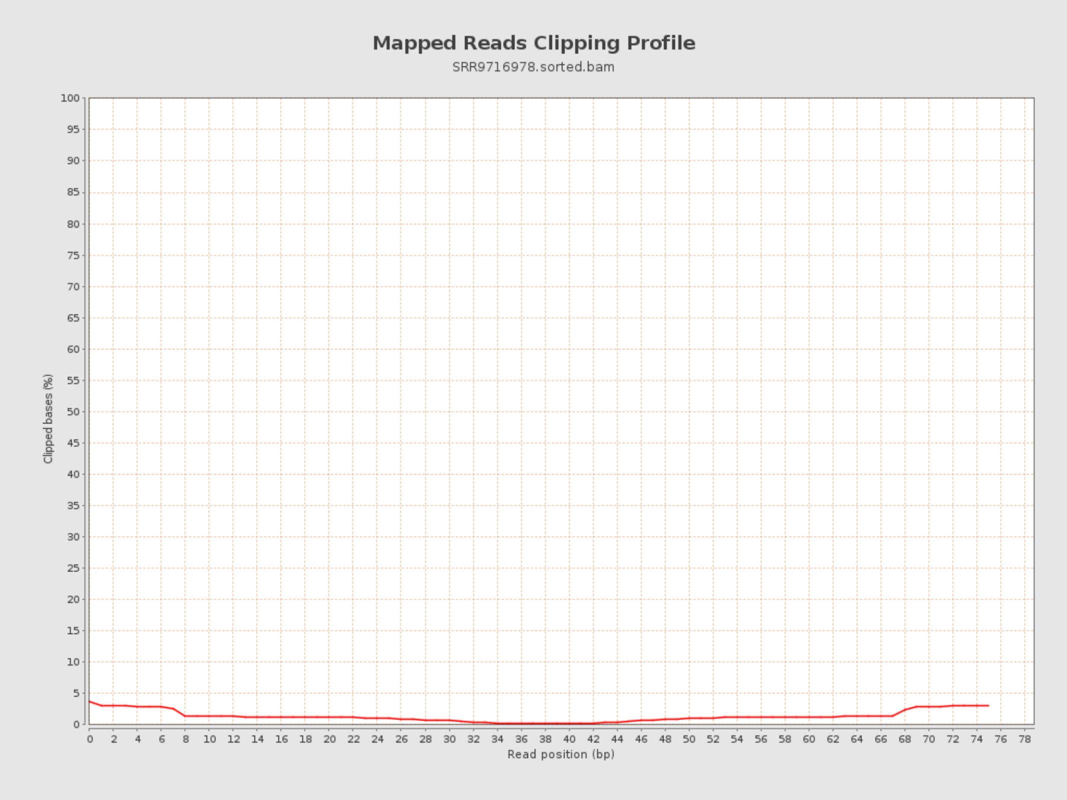
# 8. Results : Mapped Reads Nucleotide Content



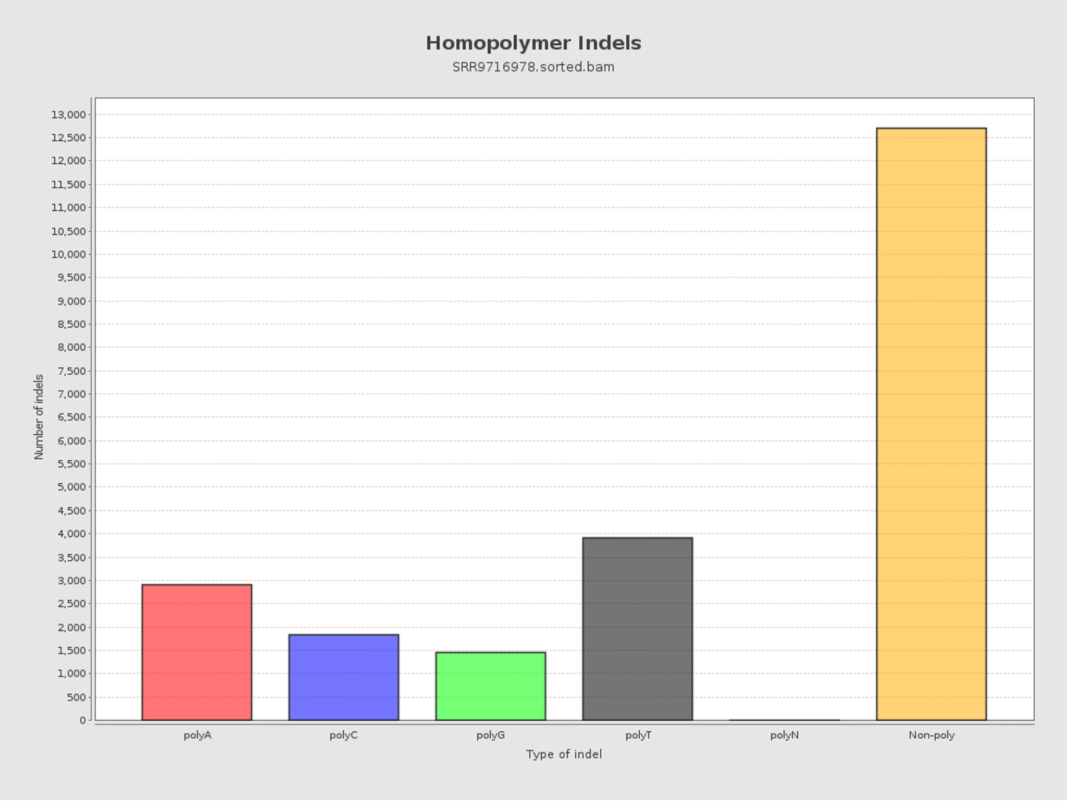
# 9. Results : Mapped Reads GC-content Distribution



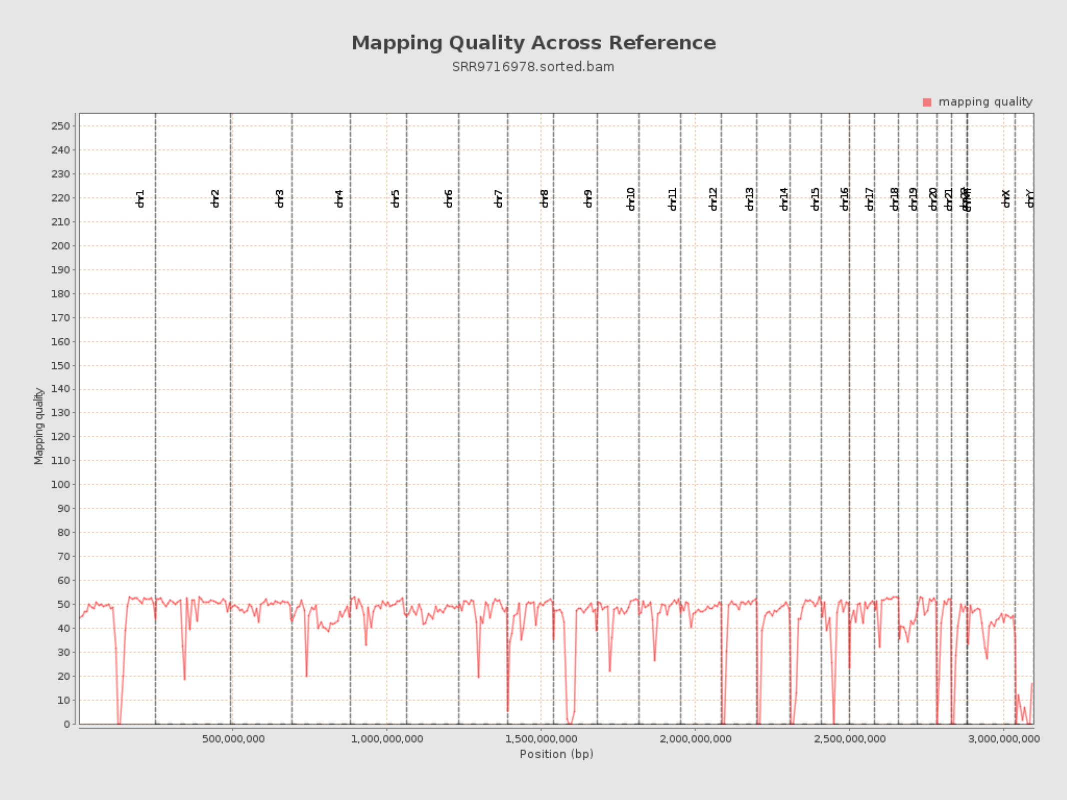
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram