# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 06:19:09*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716690.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_SRR9716690 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716690.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 06:19:08 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716690.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 487,577 |
| Mapped reads | 448,599 / 92.01% |
| Unmapped reads | 38,978 / 7.99% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 1,893 / 0.39% |
| Read min/max/mean length | 30 / 76 / 76.13 |
| Duplicated reads (estimated) | 11,593 / 2.38% |
| Duplication rate | 2.01% |
| Clipped reads | 450,072 / 92.31% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 6,615,082 / 25.36% |
| Number/percentage of C's | 5,128,803 / 19.66% |
| Number/percentage of T's | 8,159,012 / 31.28% |
| Number/percentage of G's | 6,178,196 / 23.69% |
| Number/percentage of N's | 517 / 0% |
| GC Percentage | 43.35% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0084 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1121 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.9 |

## 2.5. Mismatches and indels

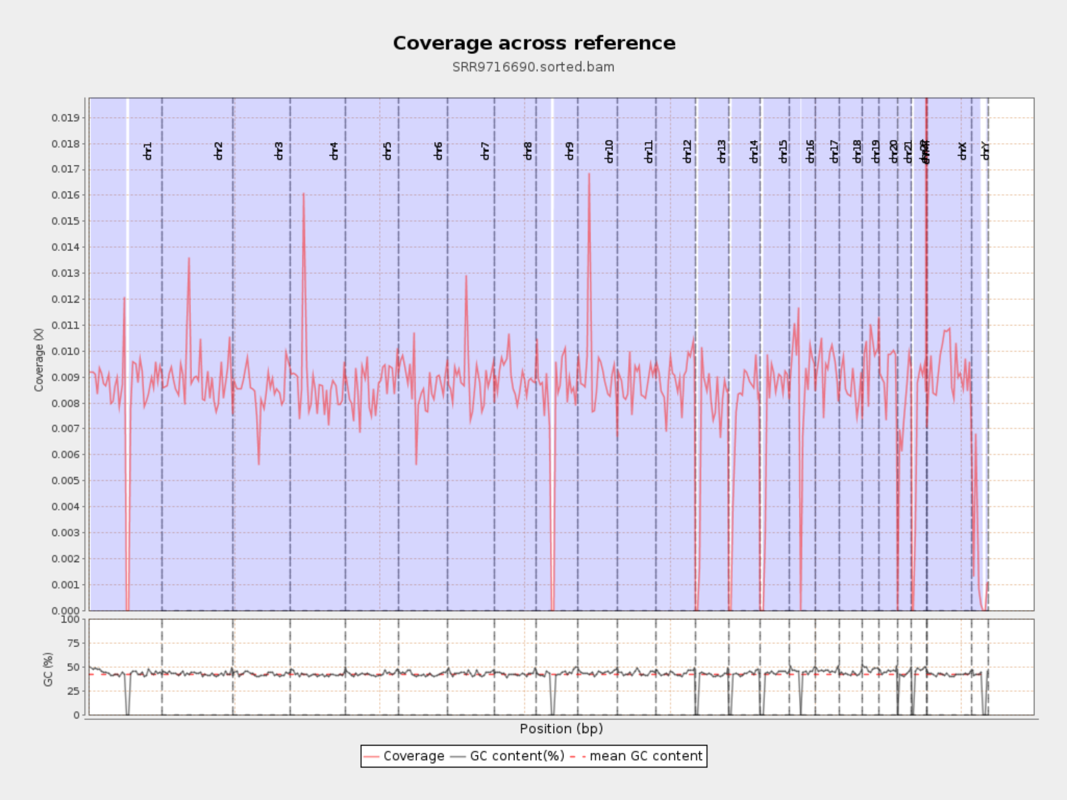
| | |
|---|---|
| General error rate | 0.5% |
| Mismatches | 128,264 |
| Insertions | 1,664 |
| Mapped reads with at least one insertion | 0.37% |
| Deletions | 4,543 |
| Mapped reads with at least one deletion | 1% |
| Homopolymer indels | 44.42% |

## 2.6. Chromosome stats

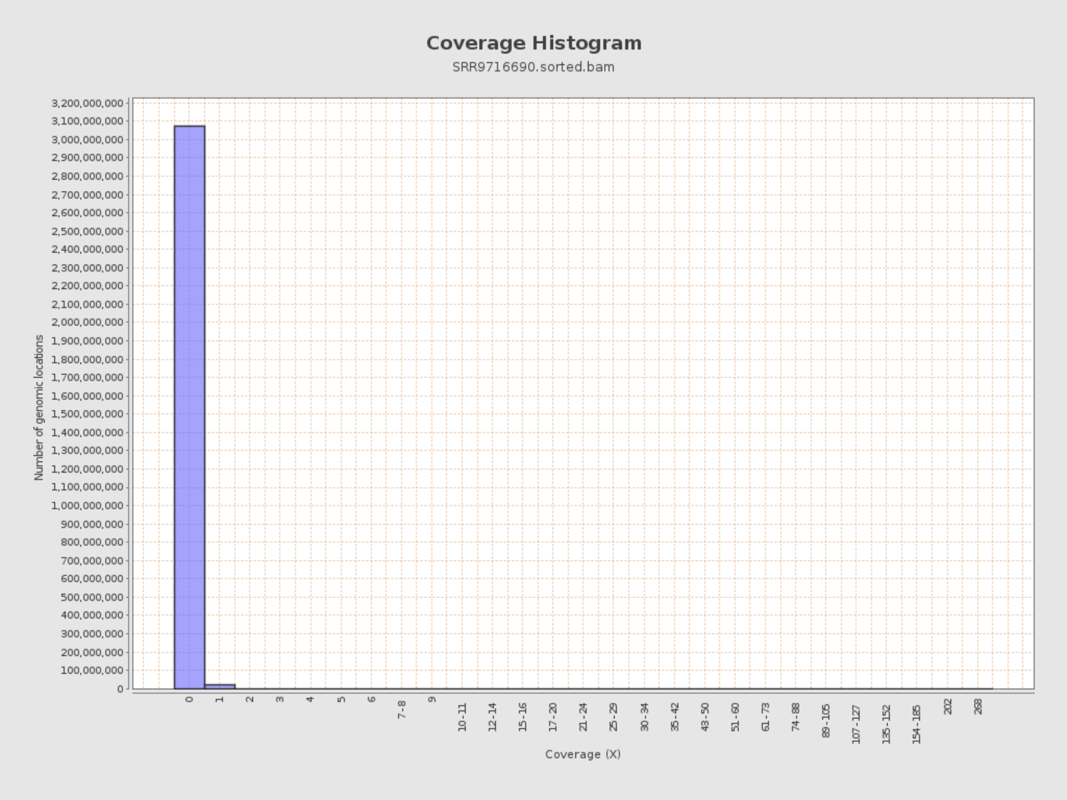
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 2084987 | 0.0084 | 0.1442 |
| chr2 | 243199373 | 2196205 | 0.009 | 0.1514 |
| chr3 | 198022430 | 1686377 | 0.0085 | 0.0963 |
| chr4 | 191154276 | 1670685 | 0.0087 | 0.105 |
| chr5 | 180915260 | 1561270 | 0.0086 | 0.0973 |
| chr6 | 171115067 | 1487234 | 0.0087 | 0.1013 |
| chr7 | 159138663 | 1417518 | 0.0089 | 0.1189 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 1311710 | 0.009 | 0.121 |
| chr9 | 141213431 | 1091944 | 0.0077 | 0.1014 |
| chr10 | 135534747 | 1261054 | 0.0093 | 0.1216 |
| chr11 | 135006516 | 1184116 | 0.0088 | 0.1051 |
| chr12 | 133851895 | 1200704 | 0.009 | 0.0995 |
| chr13 | 115169878 | 811185 | 0.007 | 0.0877 |
| chr14 | 107349540 | 778038 | 0.0072 | 0.0901 |
| chr15 | 102531392 | 742856 | 0.0072 | 0.0893 |
| chr16 | 90354753 | 794609 | 0.0088 | 0.1 |
| chr17 | 81195210 | 757352 | 0.0093 | 0.104 |
| chr18 | 78077248 | 675421 | 0.0087 | 0.1293 |
| chr19 | 59128983 | 583213 | 0.0099 | 0.1228 |
| chr20 | 63025520 | 574822 | 0.0091 | 0.1009 |
| chr21 | 48129895 | 348778 | 0.0072 | 0.0978 |
| chr22 | 51304566 | 325049 | 0.0063 | 0.084 |
| chrMT | 16571 | 1419 | 0.0856 | 0.2966 |
| chrX | 155270560 | 1441327 | 0.0093 | 0.1032 |
| chrY | 59373566 | 101260 | 0.0017 | 0.0806 |

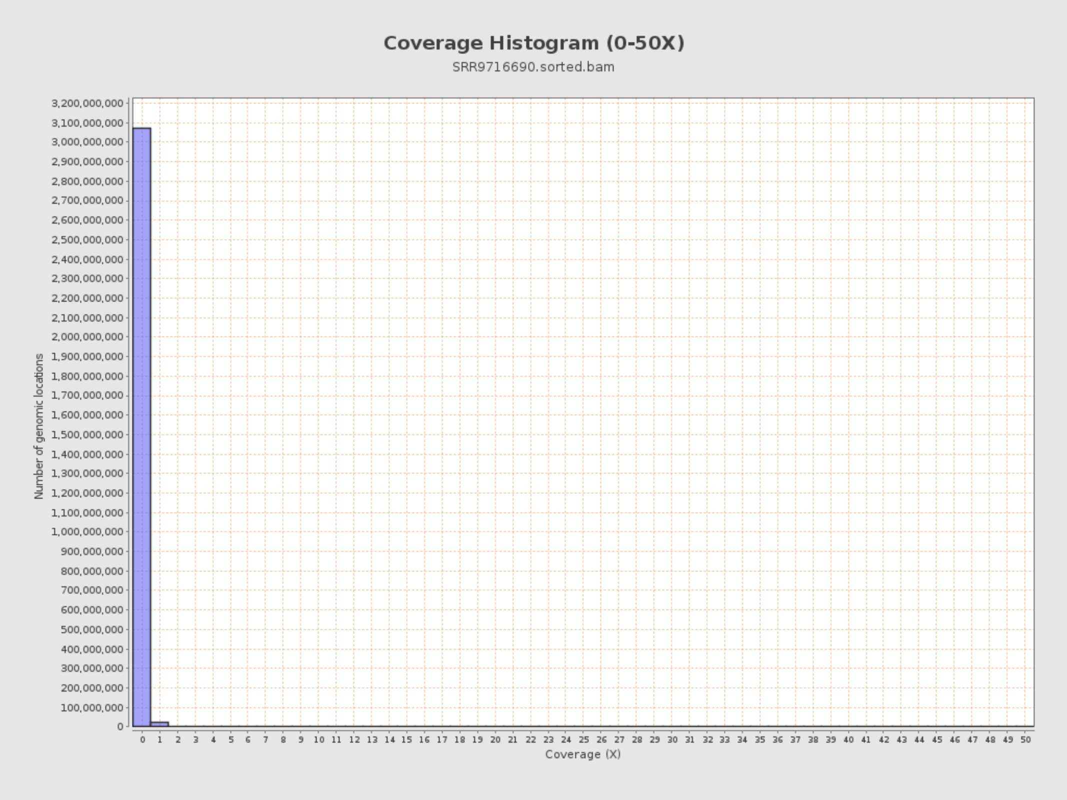
# 3. Results : Coverage across reference



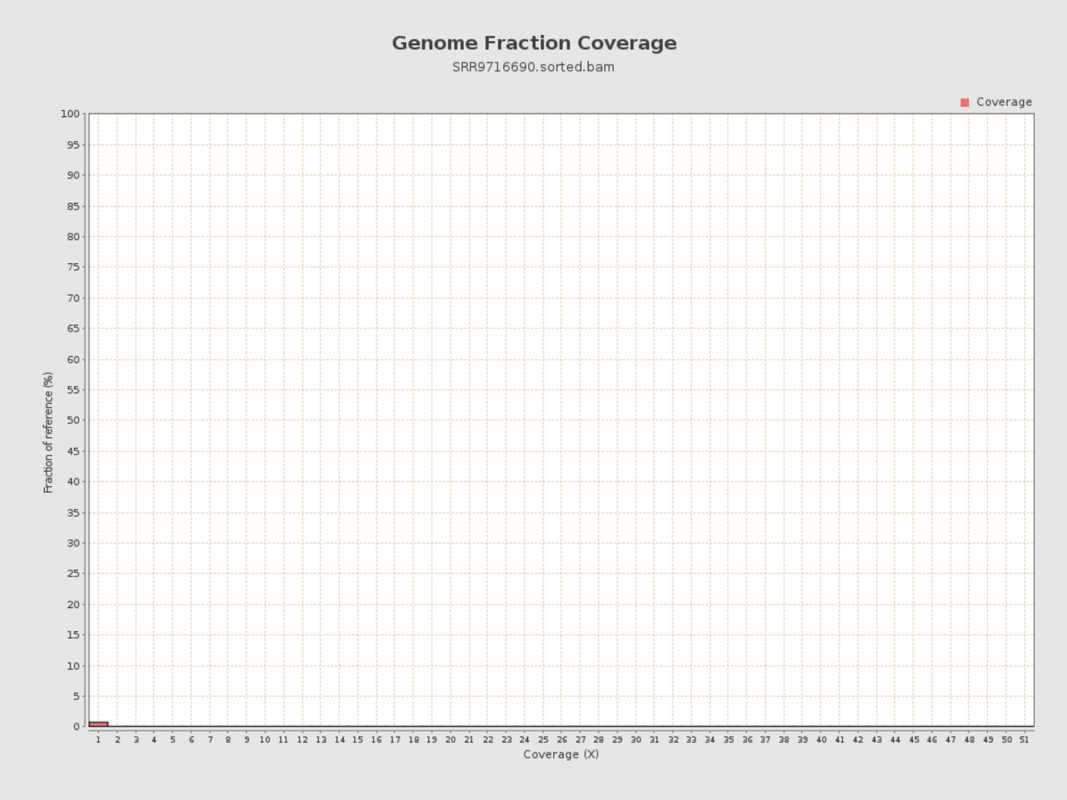
# 4. Results : Coverage Histogram



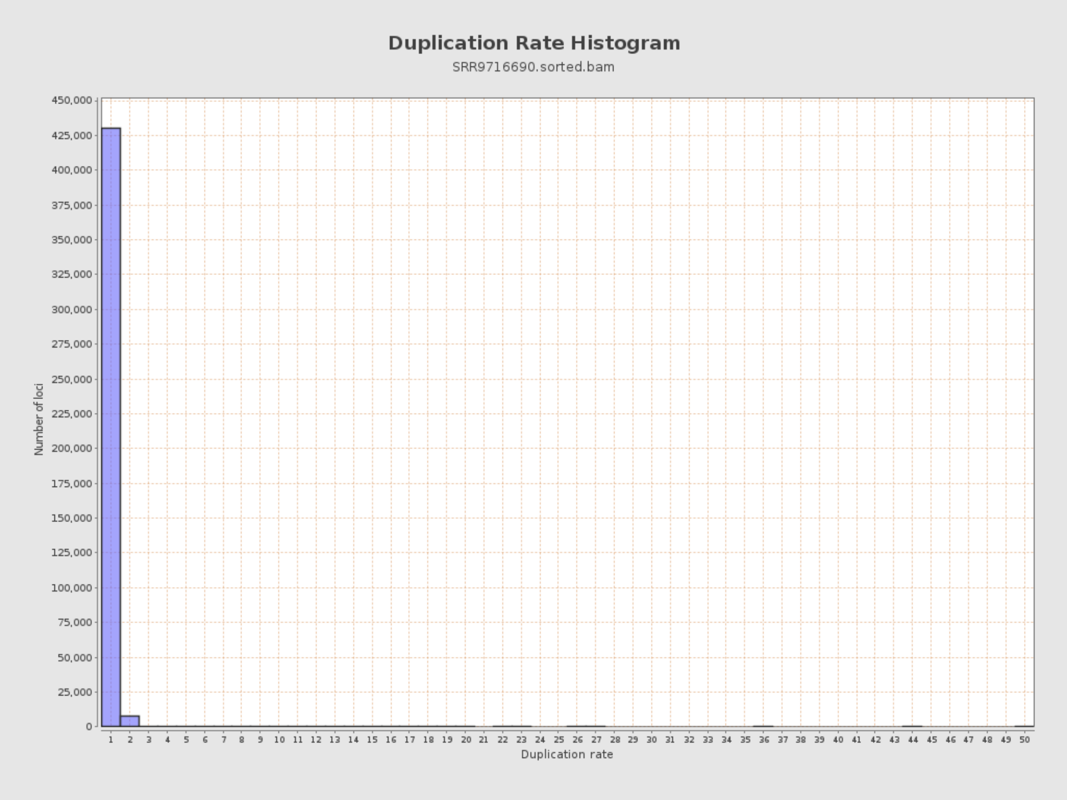
# 5. Results : Coverage Histogram (0-50X)



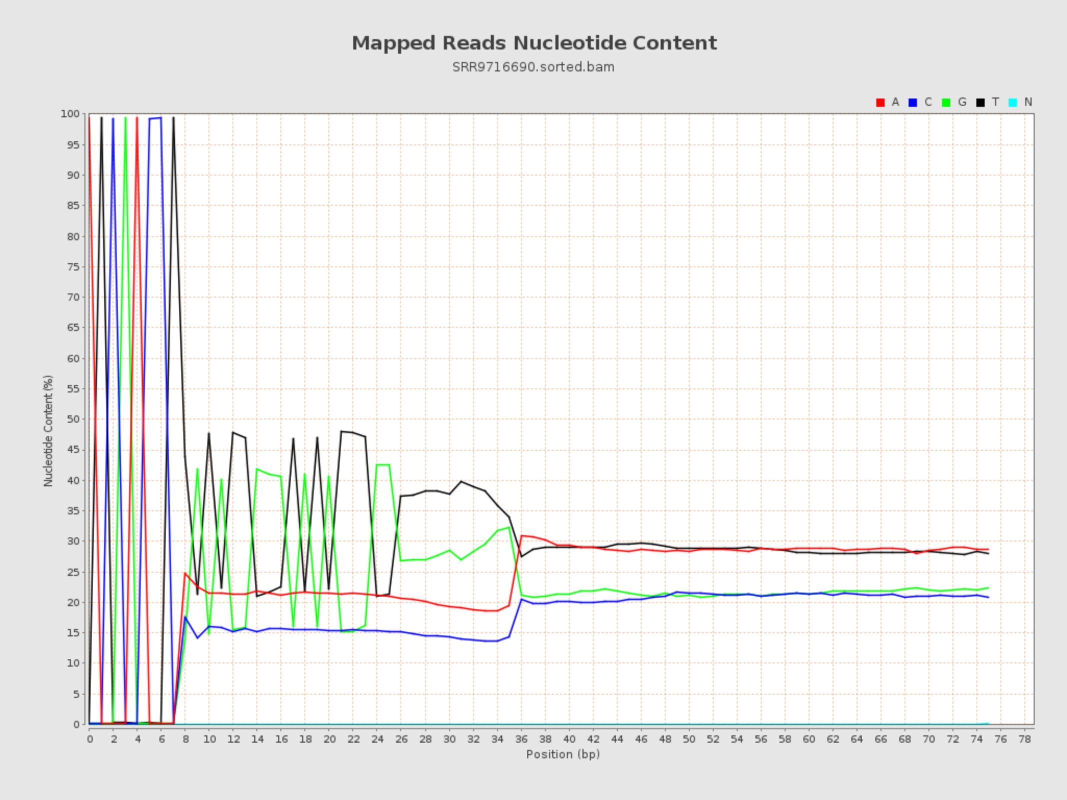
# 6. Results : Genome Fraction Coverage



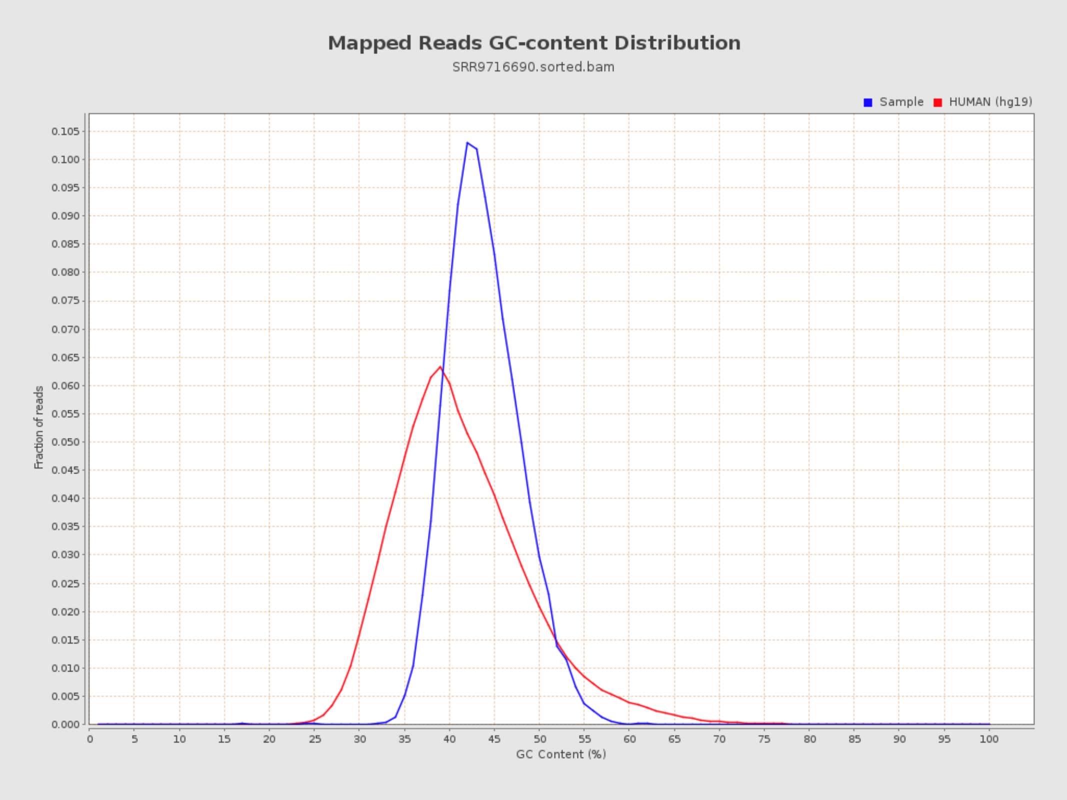
# 7. Results : Duplication Rate Histogram



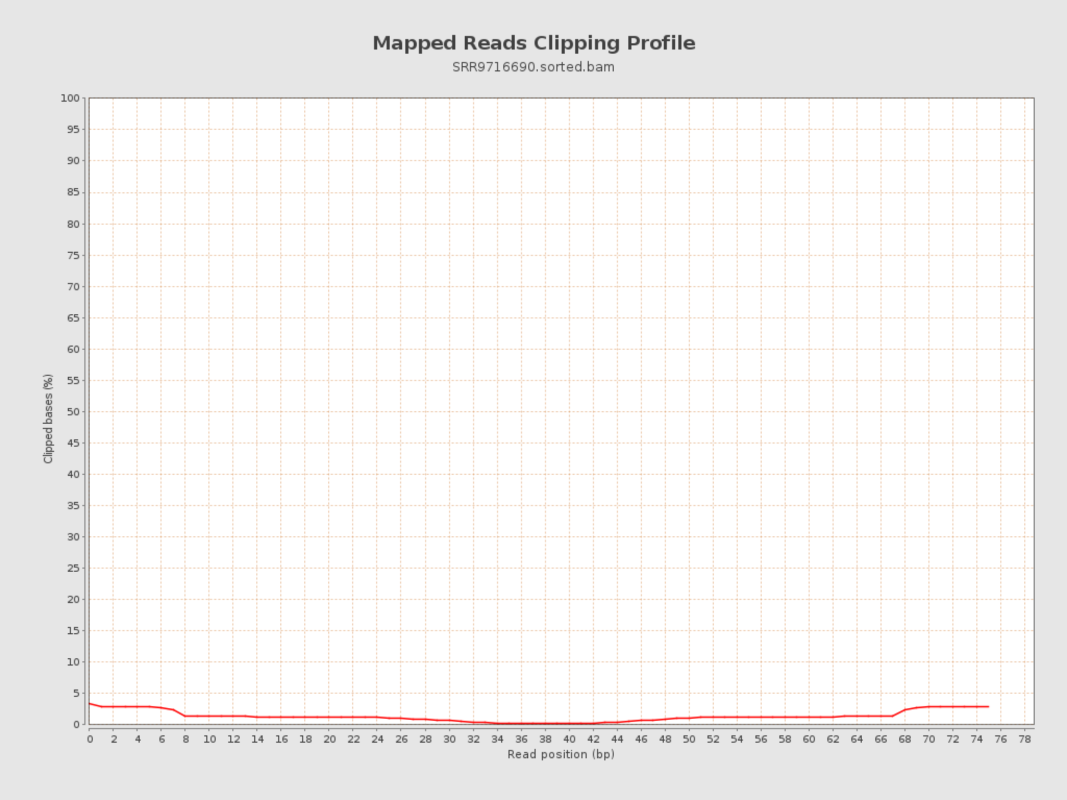
# 8. Results : Mapped Reads Nucleotide Content



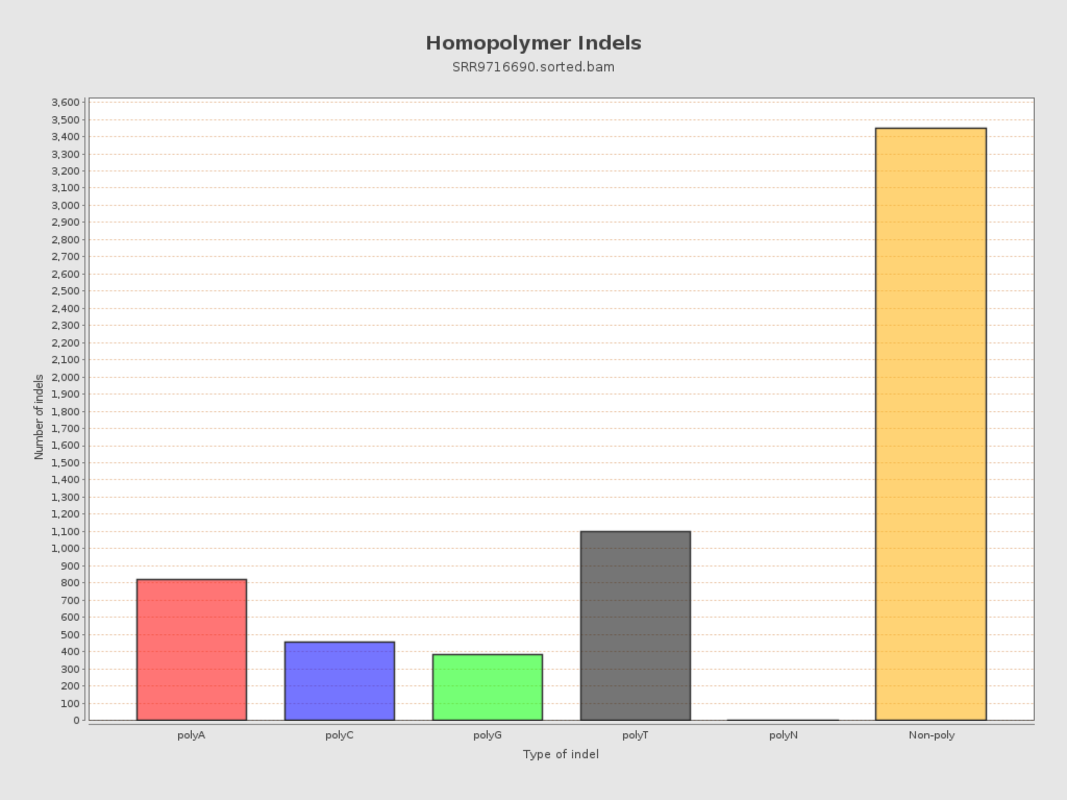
# 9. Results : Mapped Reads GC-content Distribution



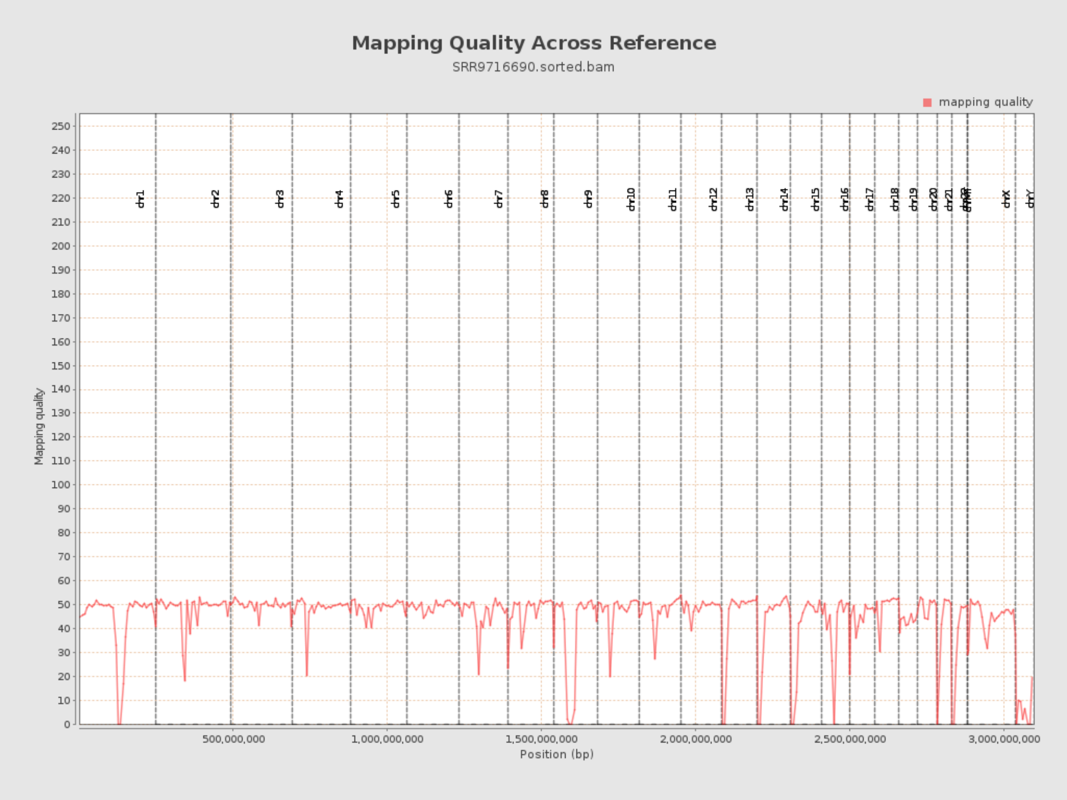
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram