# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 08:43:53*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716720.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_SRR9716720 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716720.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 08:43:52 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716720.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,243,499 |
| Mapped reads | 1,066,650 / 85.78% |
| Unmapped reads | 176,849 / 14.22% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 5,250 / 0.42% |
| Read min/max/mean length | 30 / 76 / 76.14 |
| Duplicated reads (estimated) | 30,547 / 2.46% |
| Duplication rate | 1.93% |
| Clipped reads | 1,068,889 / 85.96% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 15,815,576 / 25.87% |
| Number/percentage of C's | 10,860,970 / 17.76% |
| Number/percentage of T's | 19,240,656 / 31.47% |
| Number/percentage of G's | 15,219,278 / 24.89% |
| Number/percentage of N's | 764 / 0% |
| GC Percentage | 42.66% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0198 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2244 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.76 |

## 2.5. Mismatches and indels

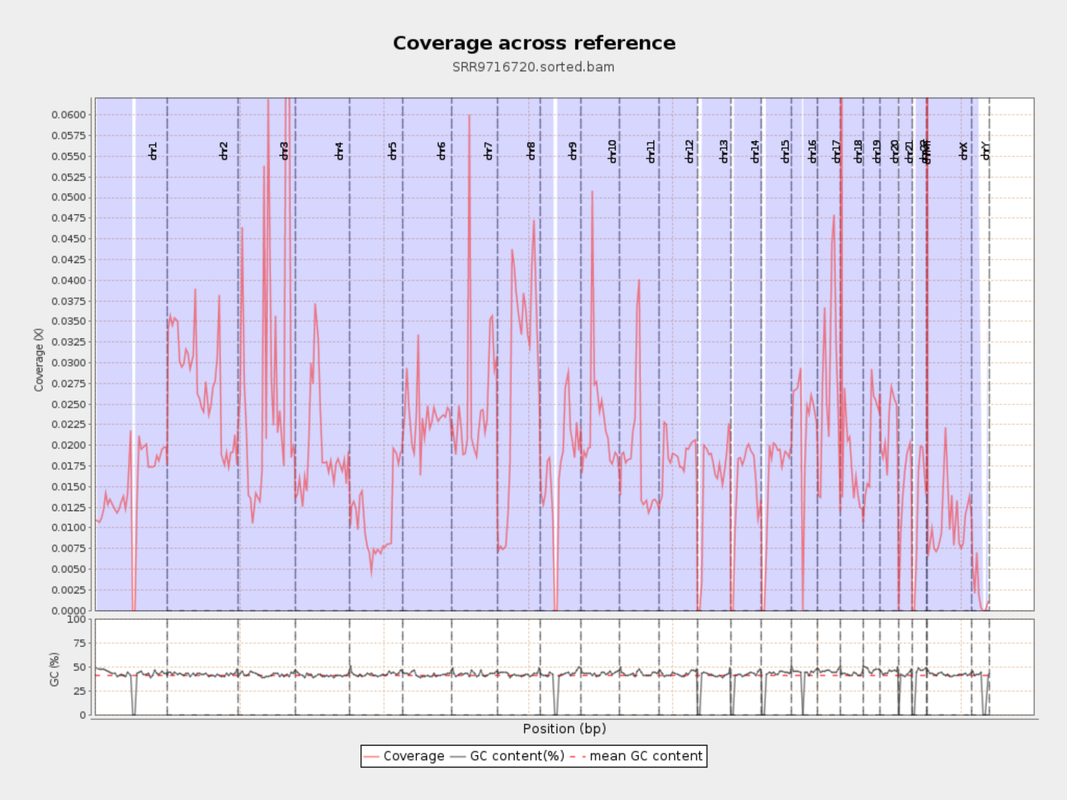
| | |
|---|---|
| General error rate | 0.53% |
| Mismatches | 315,336 |
| Insertions | 4,278 |
| Mapped reads with at least one insertion | 0.4% |
| Deletions | 11,692 |
| Mapped reads with at least one deletion | 1.09% |
| Homopolymer indels | 41.49% |

## 2.6. Chromosome stats

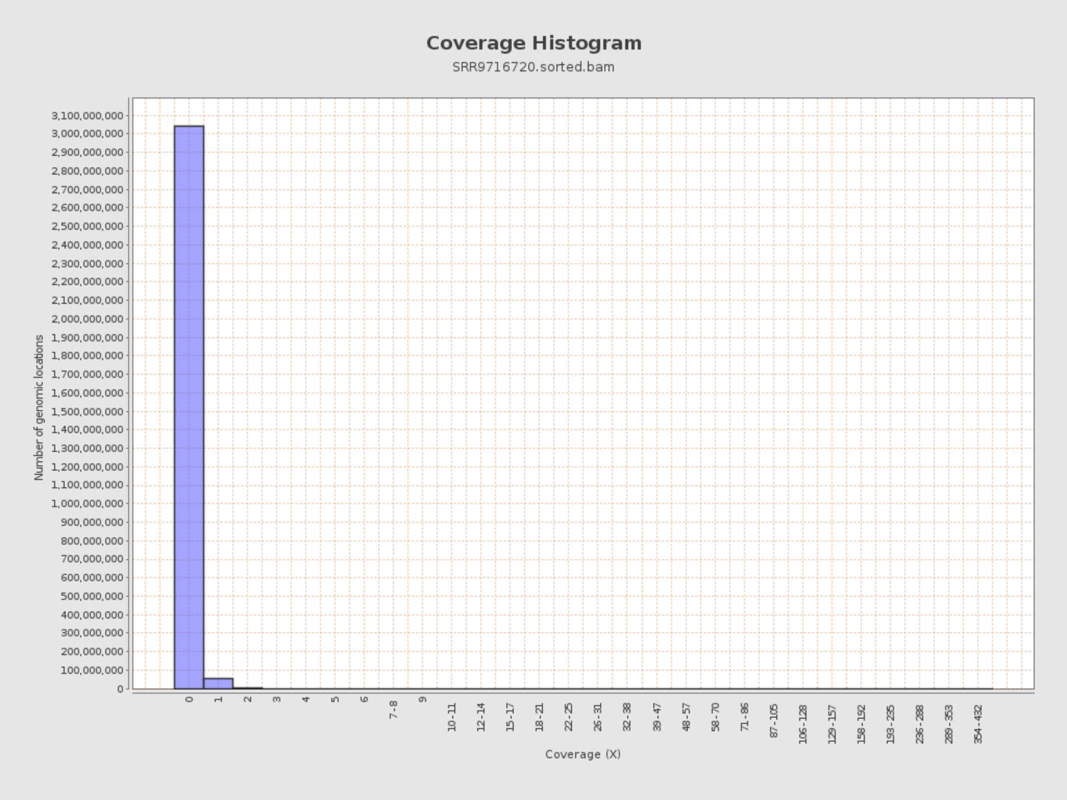
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 3658599 | 0.0147 | 0.2363 |
| chr2 | 243199373 | 6681678 | 0.0275 | 0.2559 |
| chr3 | 198022430 | 5722809 | 0.0289 | 0.198 |
| chr4 | 191154276 | 3733839 | 0.0195 | 0.1571 |
| chr5 | 180915260 | 1978731 | 0.0109 | 0.1127 |
| chr6 | 171115067 | 4000943 | 0.0234 | 0.1729 |
| chr7 | 159138663 | 4041570 | 0.0254 | 0.5444 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 4174371 | 0.0285 | 0.2293 |
| chr9 | 141213431 | 2370085 | 0.0168 | 0.1513 |
| chr10 | 135534747 | 3080764 | 0.0227 | 0.3307 |
| chr11 | 135006516 | 2511372 | 0.0186 | 0.1676 |
| chr12 | 133851895 | 2496788 | 0.0187 | 0.1686 |
| chr13 | 115169878 | 1766857 | 0.0153 | 0.1305 |
| chr14 | 107349540 | 1560874 | 0.0145 | 0.1308 |
| chr15 | 102531392 | 1595591 | 0.0156 | 0.1371 |
| chr16 | 90354753 | 2036093 | 0.0225 | 0.1681 |
| chr17 | 81195210 | 2263852 | 0.0279 | 0.1816 |
| chr18 | 78077248 | 1694156 | 0.0217 | 0.2232 |
| chr19 | 59128983 | 1239823 | 0.021 | 0.2694 |
| chr20 | 63025520 | 1387647 | 0.022 | 0.1718 |
| chr21 | 48129895 | 702545 | 0.0146 | 0.1348 |
| chr22 | 51304566 | 628706 | 0.0123 | 0.1166 |
| chrMT | 16571 | 5369 | 0.324 | 0.6068 |
| chrX | 155270560 | 1695568 | 0.0109 | 0.1319 |
| chrY | 59373566 | 126750 | 0.0021 | 0.0643 |

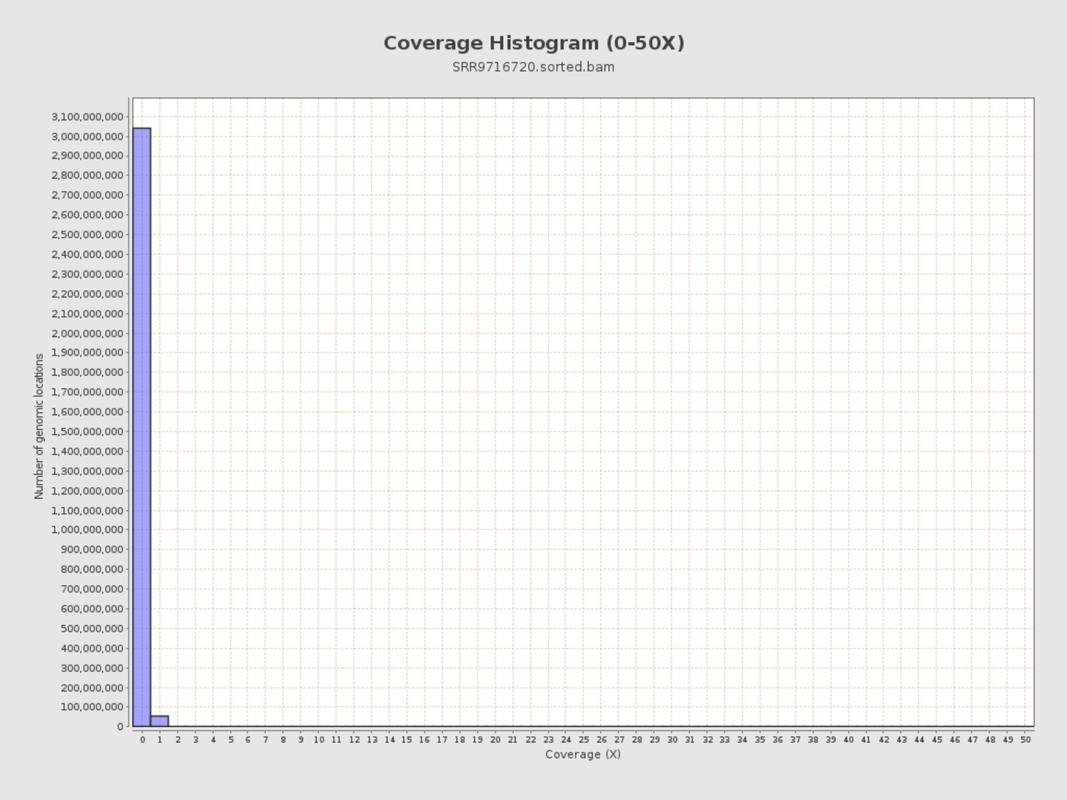
# 3. Results : Coverage across reference



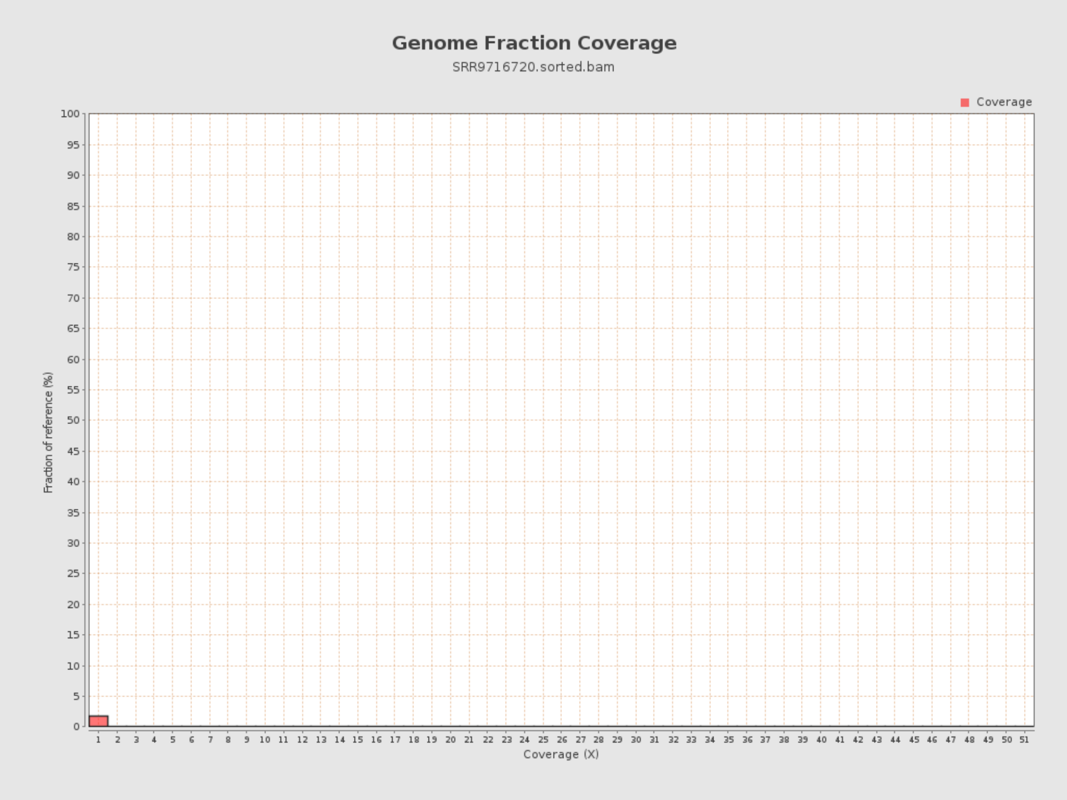
# 4. Results : Coverage Histogram



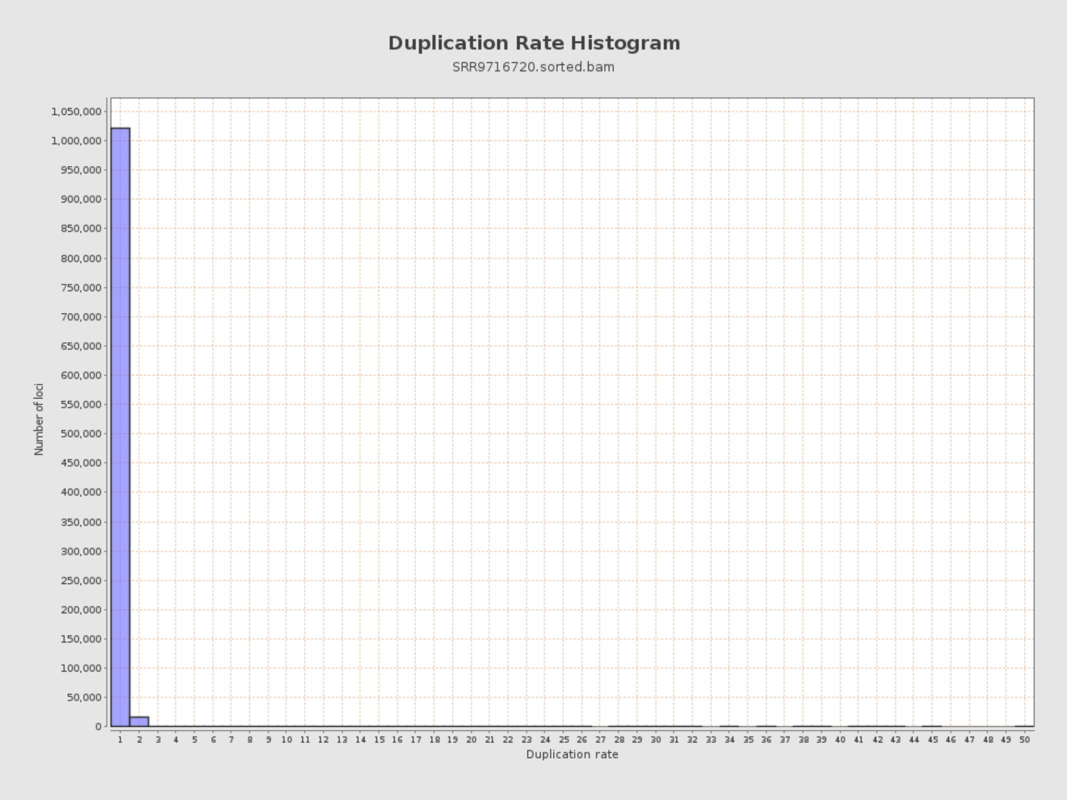
# 5. Results : Coverage Histogram (0-50X)



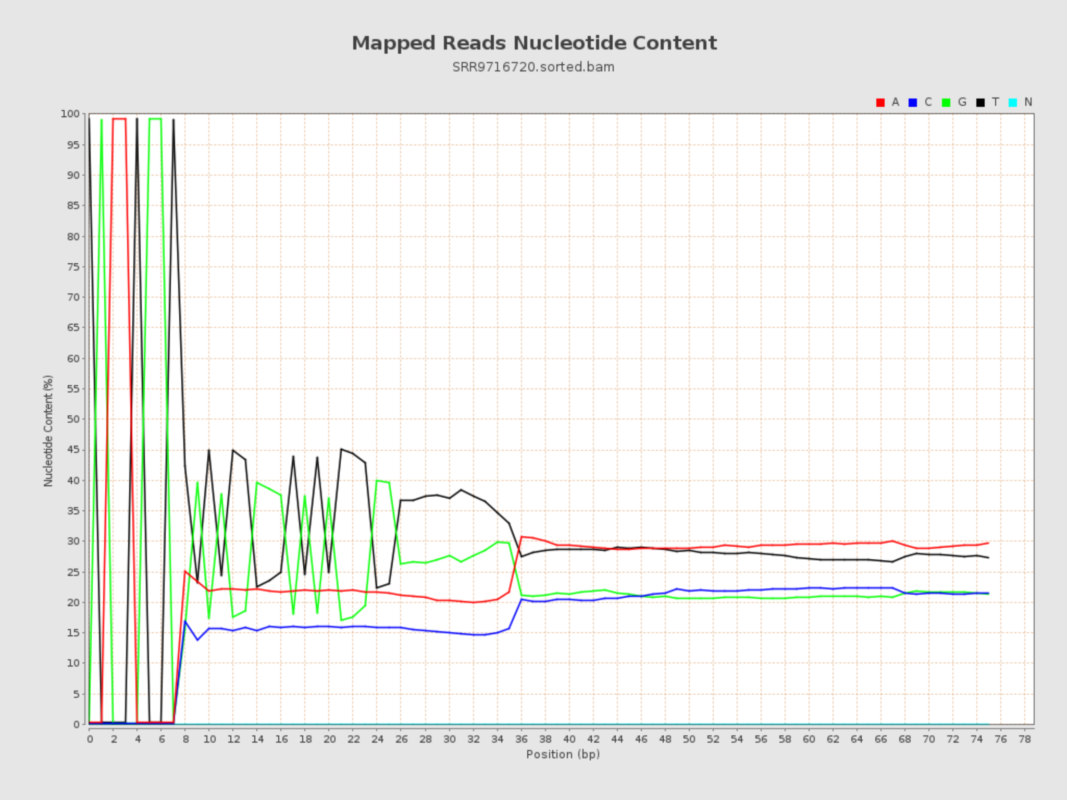
# 6. Results : Genome Fraction Coverage



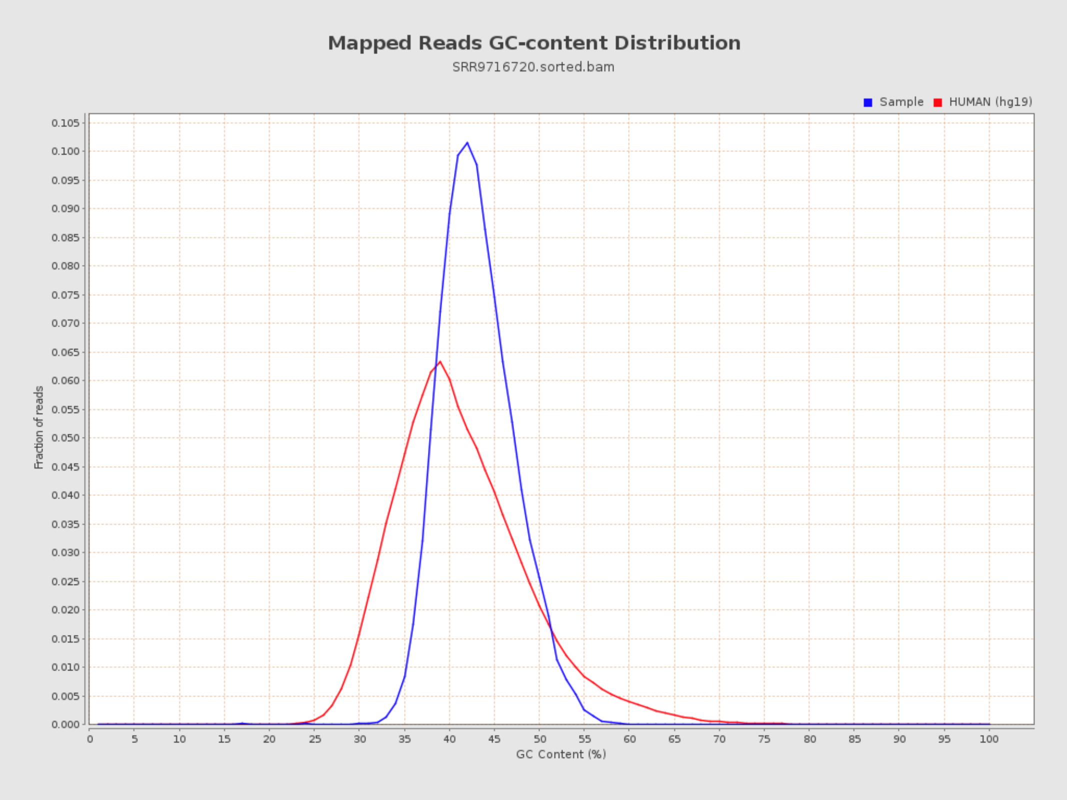
# 7. Results : Duplication Rate Histogram



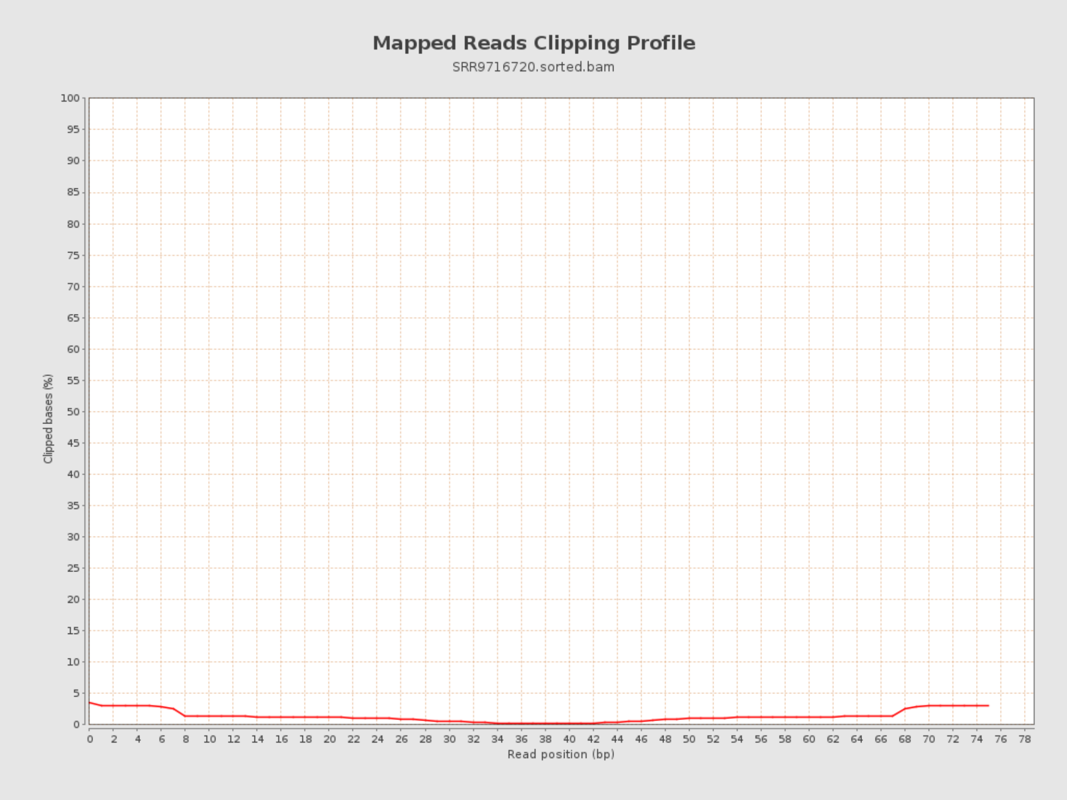
# 8. Results : Mapped Reads Nucleotide Content



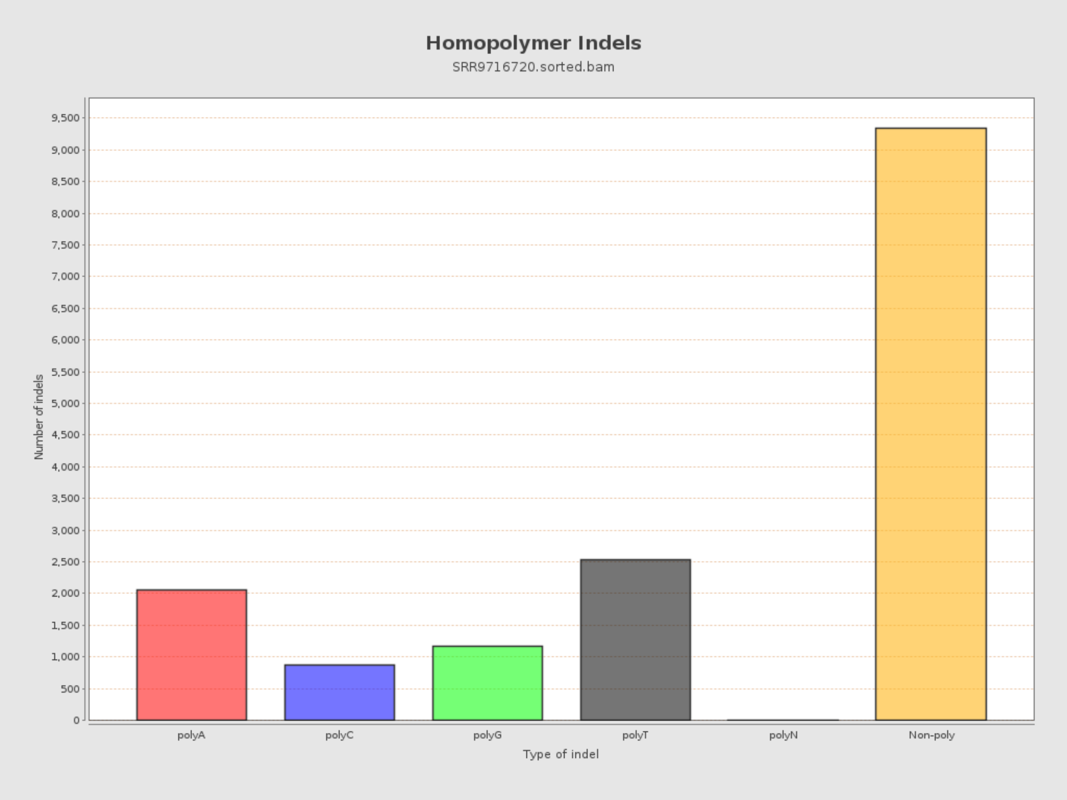
# 9. Results : Mapped Reads GC-content Distribution



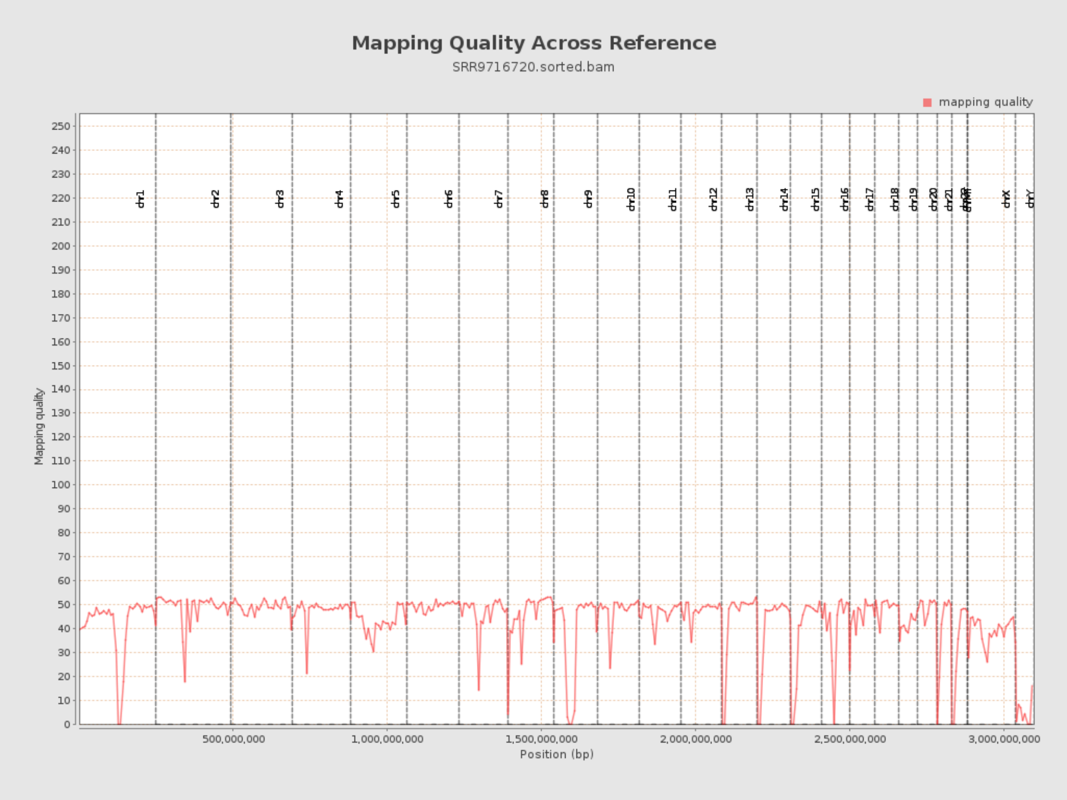
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram