# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/30 19:16:10*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716132.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_SRR9716132 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716132.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 30 19:16:09 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716132.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 991,713 |
| Mapped reads | 862,407 / 86.96% |
| Unmapped reads | 129,306 / 13.04% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 4,876 / 0.49% |
| Read min/max/mean length | 30 / 76 / 76.17 |
| Duplicated reads (estimated) | 23,641 / 2.38% |
| Duplication rate | 2% |
| Clipped reads | 863,905 / 87.11% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 13,182,558 / 26.73% |
| Number/percentage of C's | 8,912,963 / 18.07% |
| Number/percentage of T's | 15,172,031 / 30.76% |
| Number/percentage of G's | 12,056,910 / 24.44% |
| Number/percentage of N's | 779 / 0% |
| GC Percentage | 42.51% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0159 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1773 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.27 |

## 2.5. Mismatches and indels

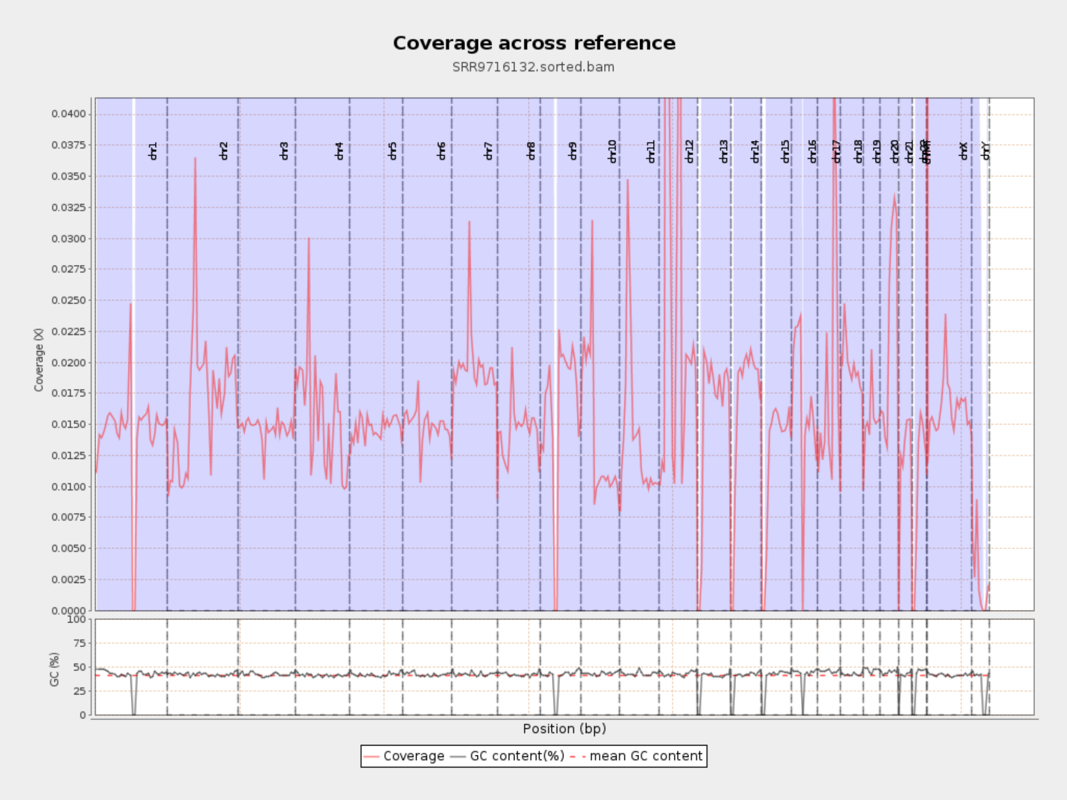
| | |
|---|---|
| General error rate | 0.57% |
| Mismatches | 273,779 |
| Insertions | 4,184 |
| Mapped reads with at least one insertion | 0.48% |
| Deletions | 8,686 |
| Mapped reads with at least one deletion | 1% |
| Homopolymer indels | 40.77% |

## 2.6. Chromosome stats

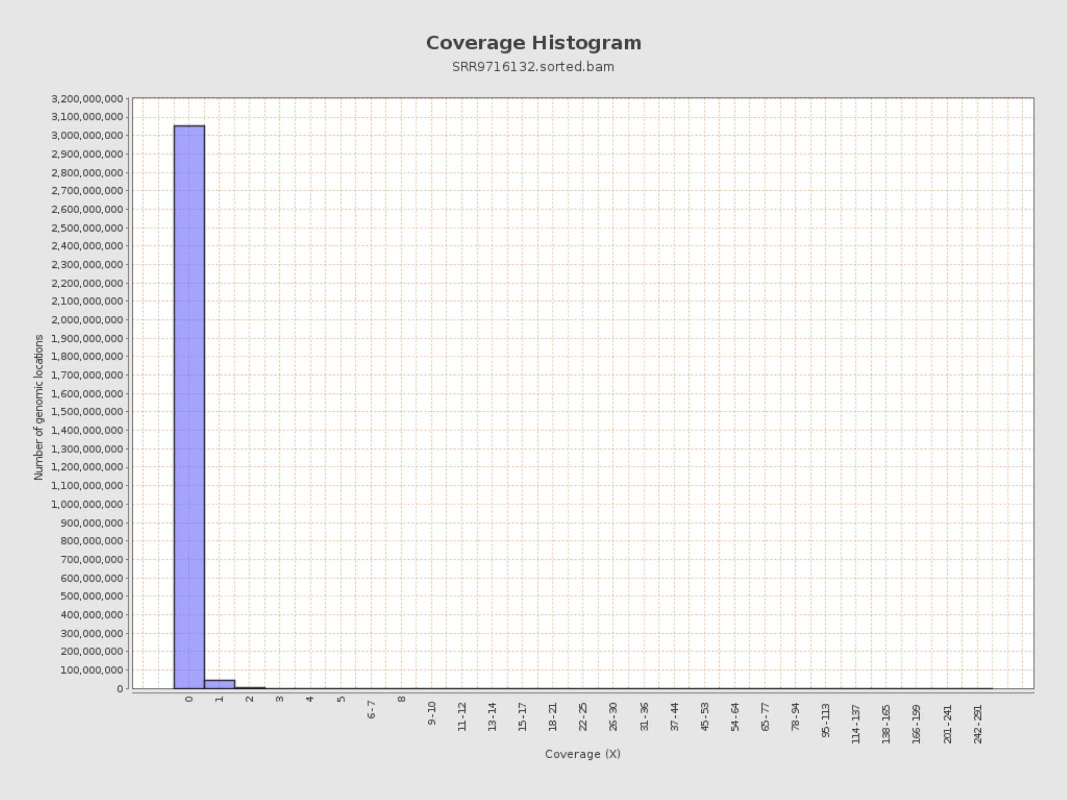
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 3546638 | 0.0142 | 0.2607 |
| chr2 | 243199373 | 4097329 | 0.0168 | 0.204 |
| chr3 | 198022430 | 2903973 | 0.0147 | 0.1267 |
| chr4 | 191154276 | 3006327 | 0.0157 | 0.1431 |
| chr5 | 180915260 | 2677039 | 0.0148 | 0.1285 |
| chr6 | 171115067 | 2552769 | 0.0149 | 0.1375 |
| chr7 | 159138663 | 3148853 | 0.0198 | 0.2243 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2140491 | 0.0146 | 0.1562 |
| chr9 | 141213431 | 2288871 | 0.0162 | 0.1933 |
| chr10 | 135534747 | 1938512 | 0.0143 | 0.1842 |
| chr11 | 135006516 | 1894413 | 0.014 | 0.1572 |
| chr12 | 133851895 | 3624663 | 0.0271 | 0.1847 |
| chr13 | 115169878 | 1792990 | 0.0156 | 0.13 |
| chr14 | 107349540 | 1758997 | 0.0164 | 0.1487 |
| chr15 | 102531392 | 1258514 | 0.0123 | 0.1167 |
| chr16 | 90354753 | 1463947 | 0.0162 | 0.1426 |
| chr17 | 81195210 | 1549173 | 0.0191 | 0.1483 |
| chr18 | 78077248 | 1540863 | 0.0197 | 0.3261 |
| chr19 | 59128983 | 920176 | 0.0156 | 0.2213 |
| chr20 | 63025520 | 1436361 | 0.0228 | 0.1636 |
| chr21 | 48129895 | 588897 | 0.0122 | 0.1295 |
| chr22 | 51304566 | 510783 | 0.01 | 0.1042 |
| chrMT | 16571 | 4082 | 0.2463 | 0.5127 |
| chrX | 155270560 | 2543052 | 0.0164 | 0.1525 |
| chrY | 59373566 | 151865 | 0.0026 | 0.0749 |

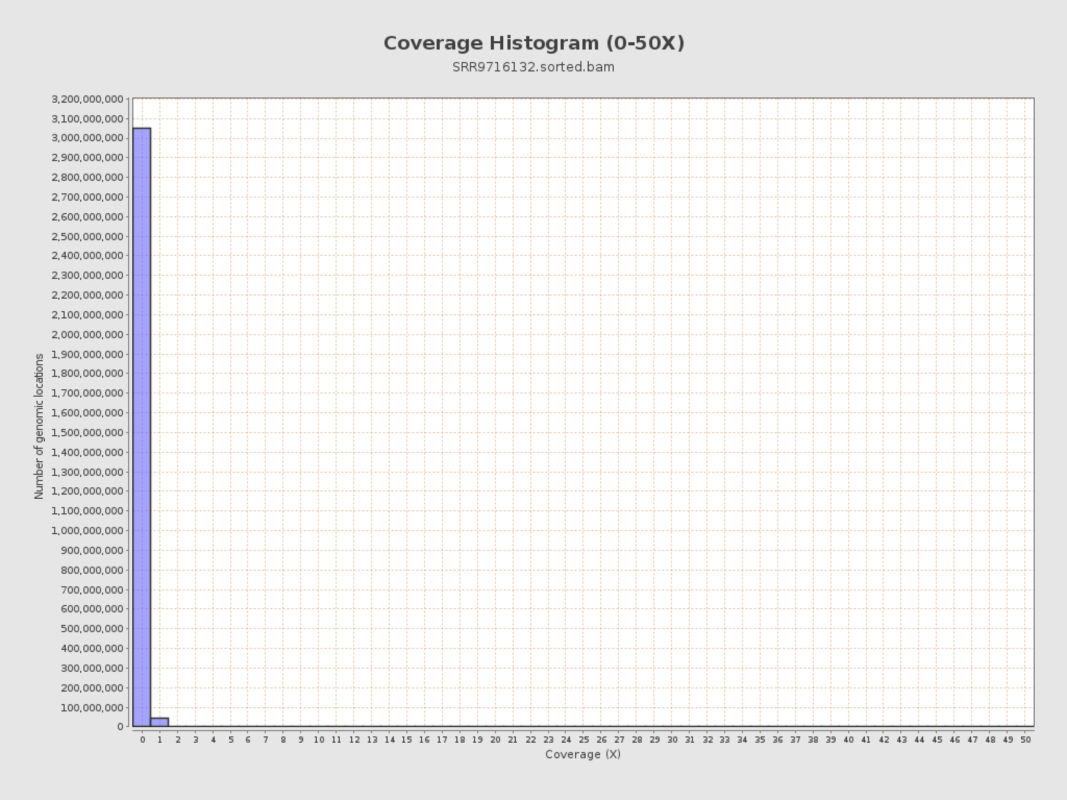
# 3. Results : Coverage across reference



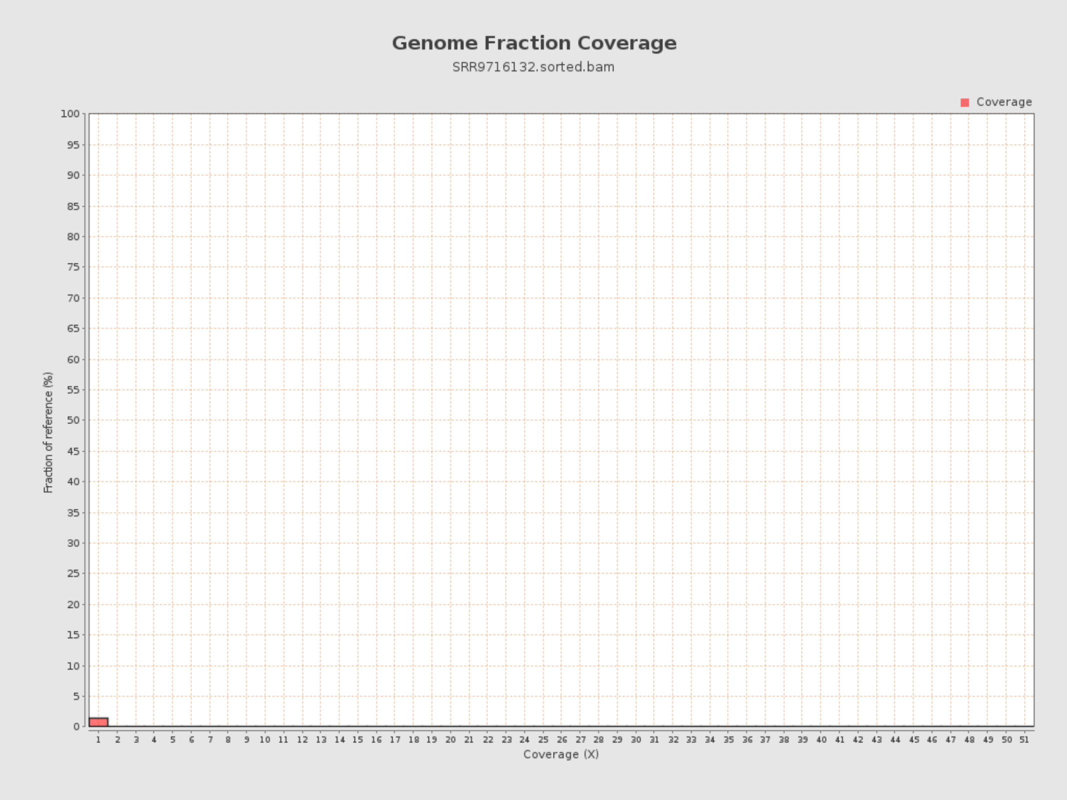
# 4. Results : Coverage Histogram



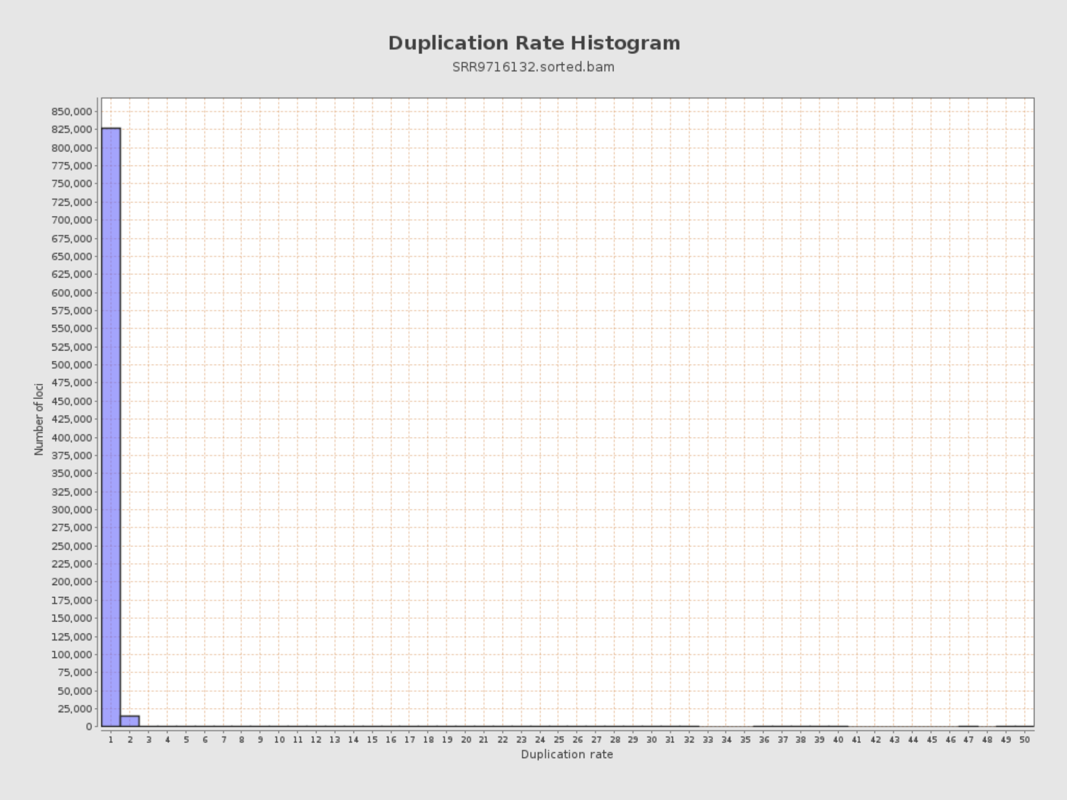
# 5. Results : Coverage Histogram (0-50X)



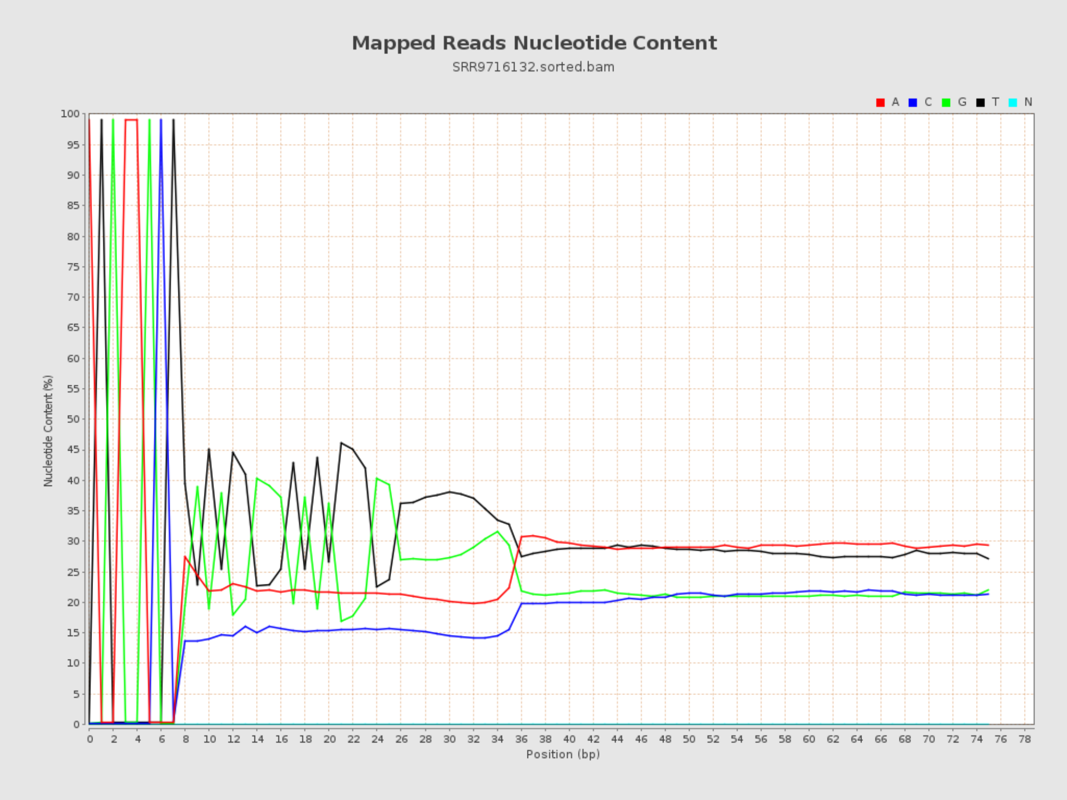
# 6. Results : Genome Fraction Coverage



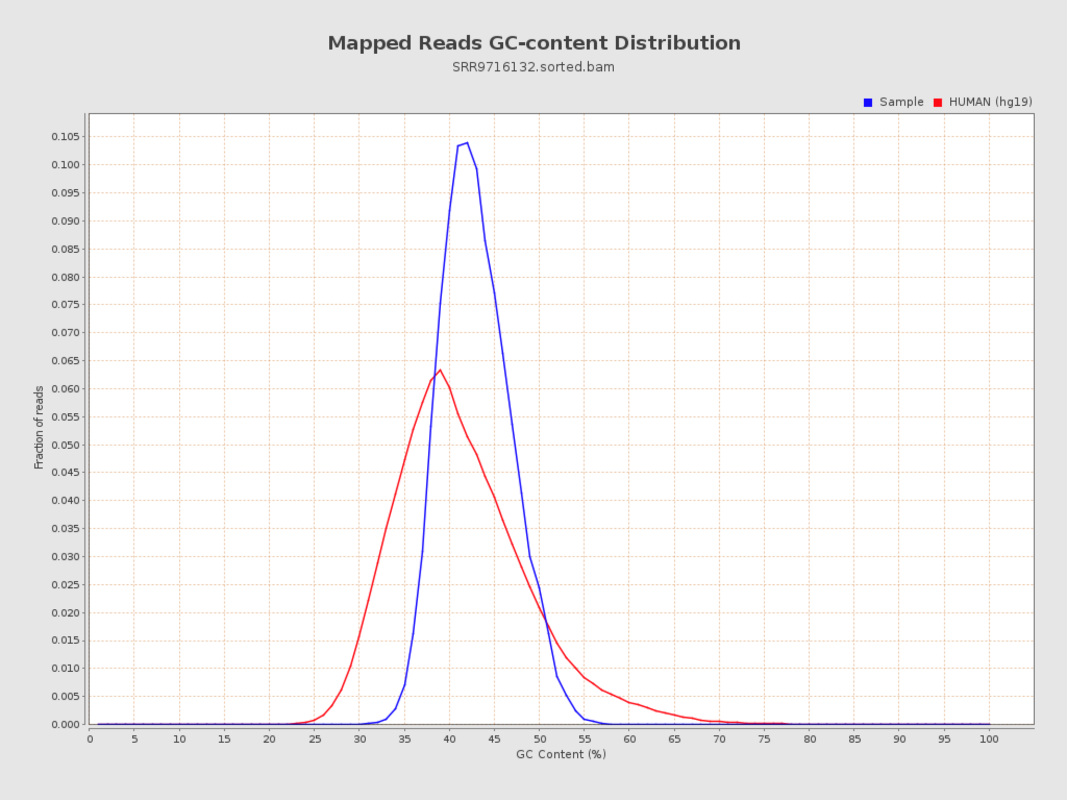
# 7. Results : Duplication Rate Histogram



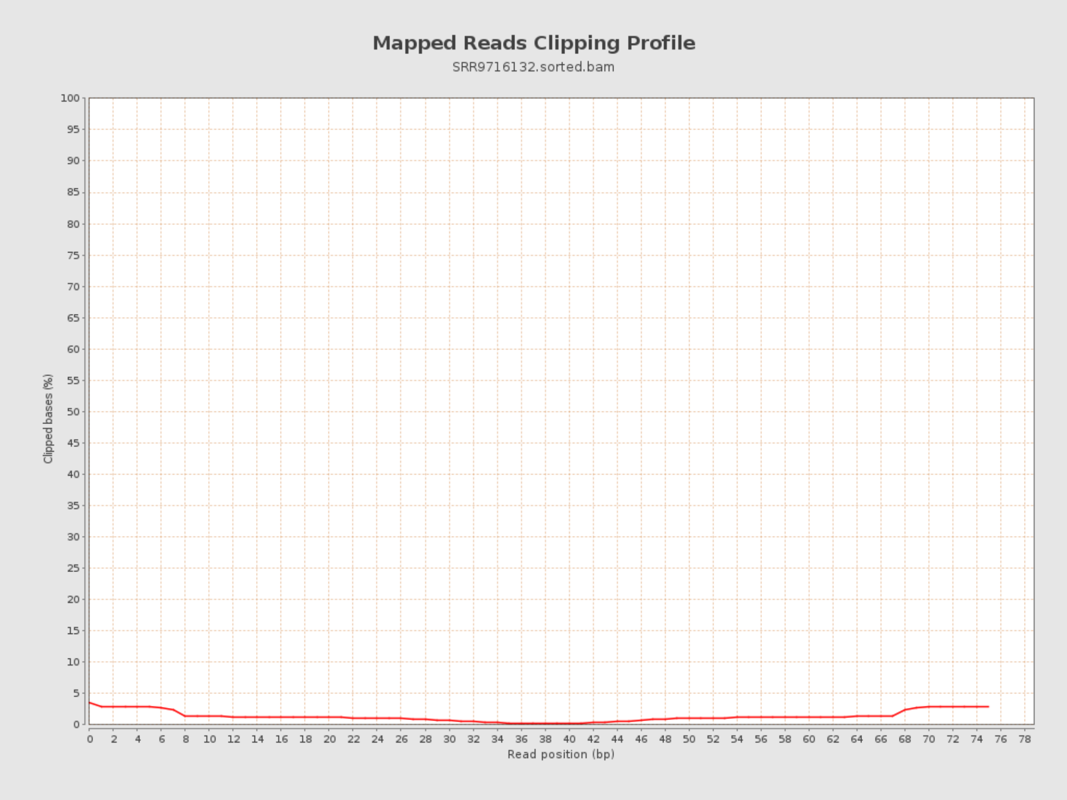
# 8. Results : Mapped Reads Nucleotide Content



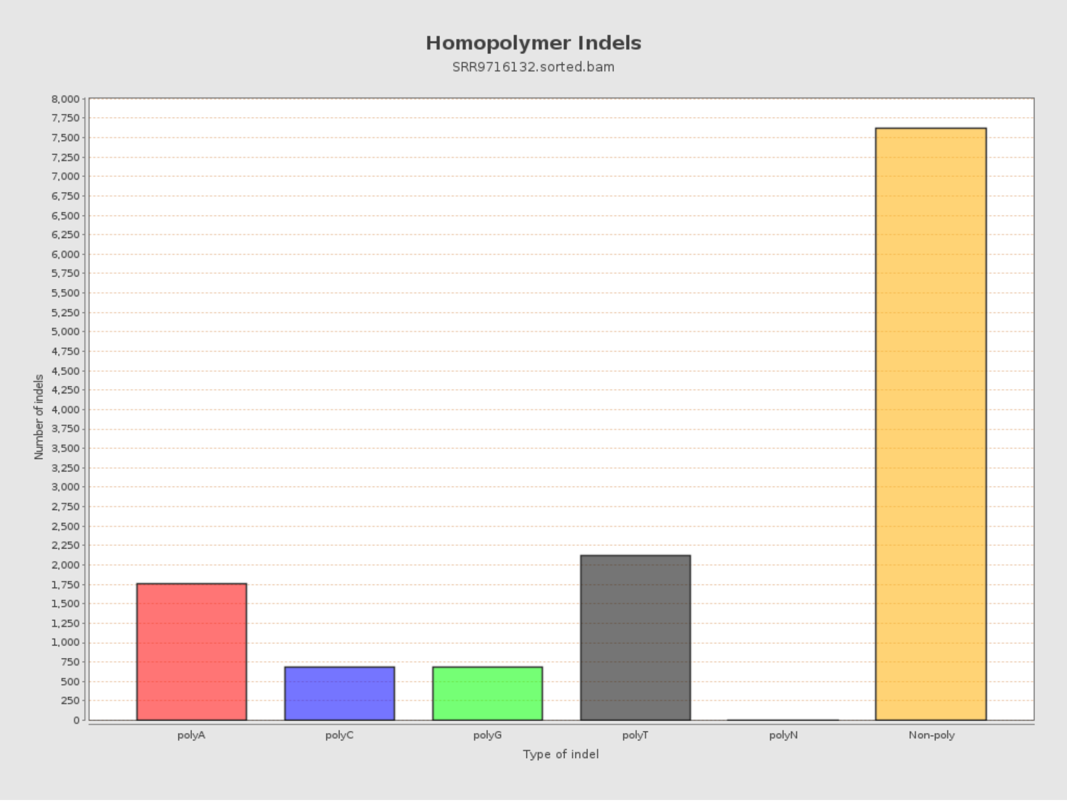
# 9. Results : Mapped Reads GC-content Distribution



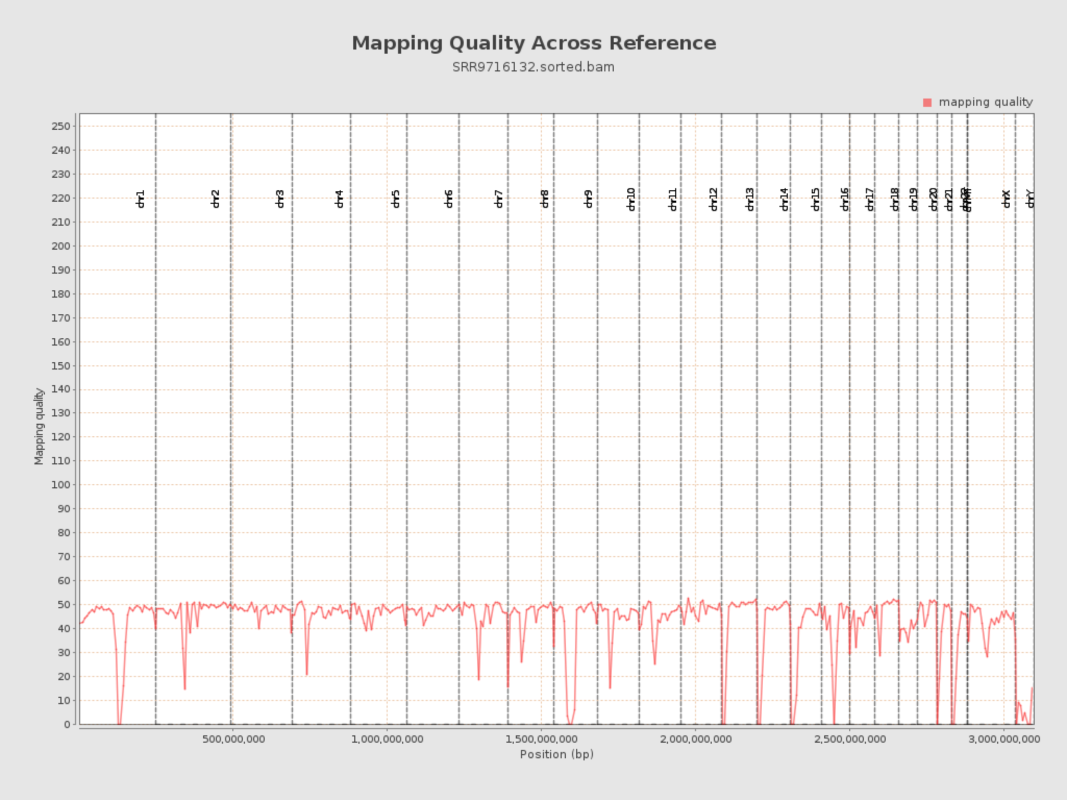
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram