# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 01:17:04*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716628.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_SRR9716628 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716628.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 01:17:03 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716628.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 946,913 |
| Mapped reads | 854,861 / 90.28% |
| Unmapped reads | 92,052 / 9.72% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 4,282 / 0.45% |
| Read min/max/mean length | 30 / 76 / 76.15 |
| Duplicated reads (estimated) | 19,979 / 2.11% |
| Duplication rate | 1.75% |
| Clipped reads | 858,017 / 90.61% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 12,728,473 / 25.67% |
| Number/percentage of C's | 10,351,342 / 20.88% |
| Number/percentage of T's | 14,800,621 / 29.85% |
| Number/percentage of G's | 11,697,674 / 23.59% |
| Number/percentage of N's | 684 / 0% |
| GC Percentage | 44.47% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.016 |
| | |

| | |
|---|---|
| Standard Deviation | 0.167 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.31 |

## 2.5. Mismatches and indels

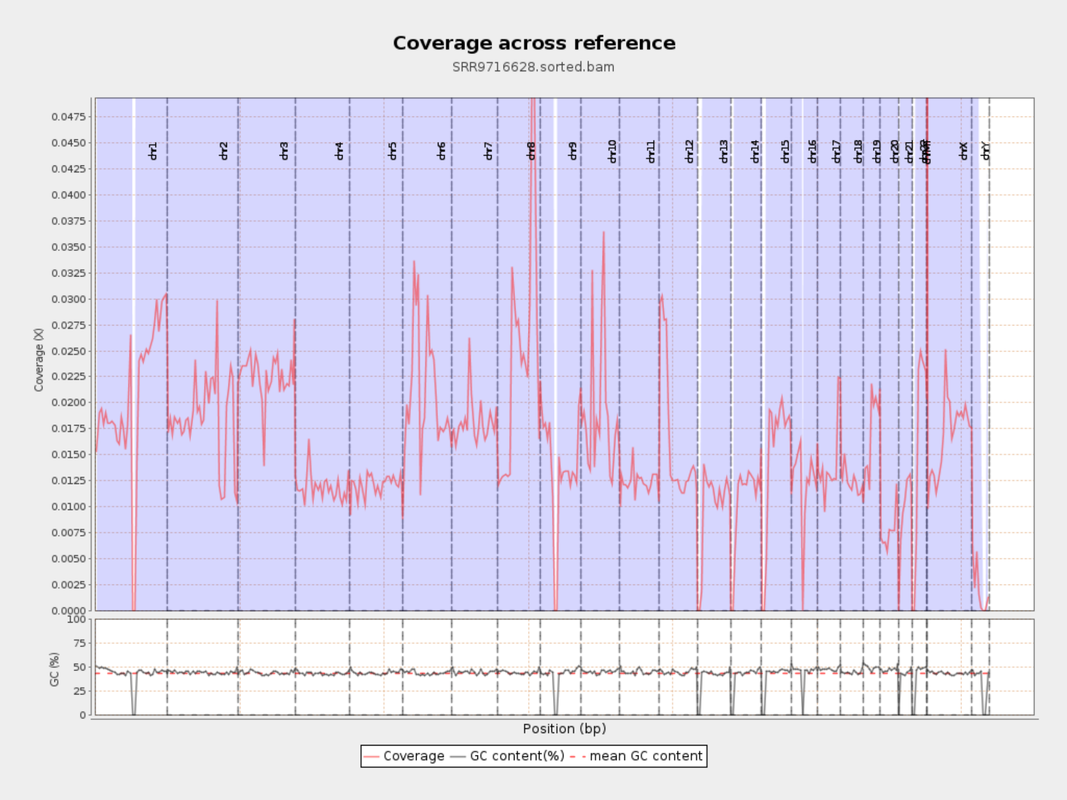
| | |
|---|---|
| General error rate | 0.49% |
| Mismatches | 236,992 |
| Insertions | 2,962 |
| Mapped reads with at least one insertion | 0.34% |
| Deletions | 8,609 |
| Mapped reads with at least one deletion | 1% |
| Homopolymer indels | 42.31% |

## 2.6. Chromosome stats

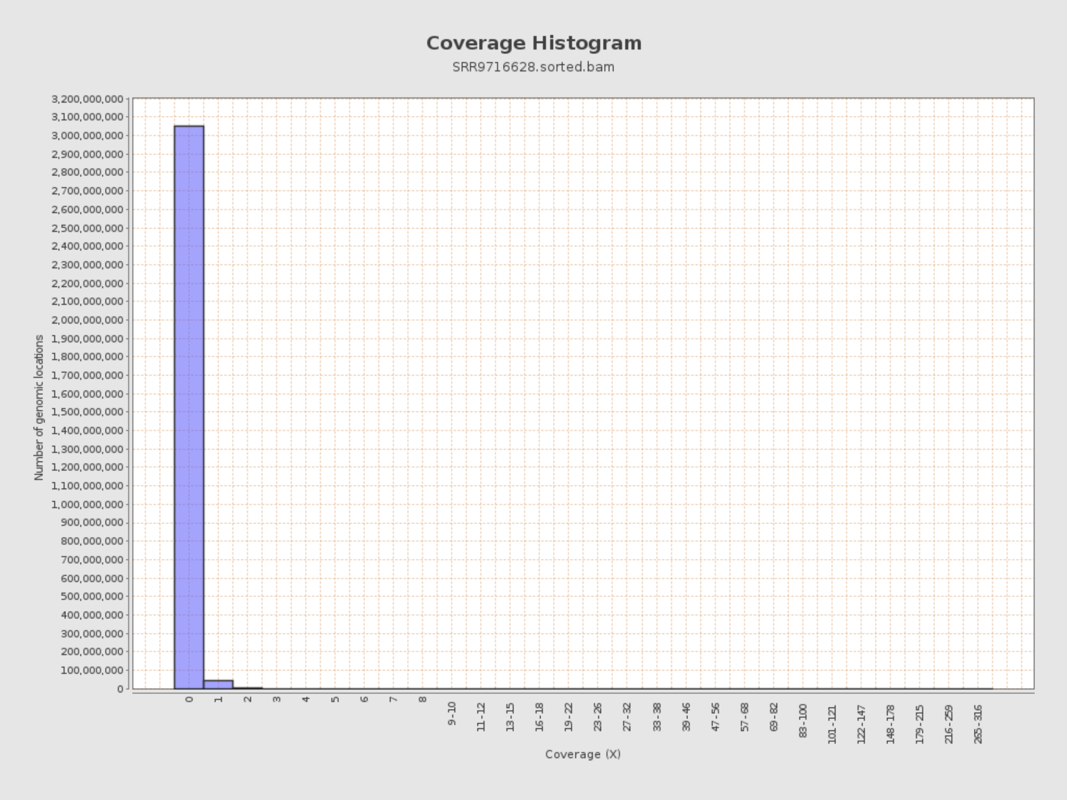
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5113508 | 0.0205 | 0.2657 |
| chr2 | 243199373 | 4546100 | 0.0187 | 0.1992 |
| chr3 | 198022430 | 4467404 | 0.0226 | 0.1593 |
| chr4 | 191154276 | 2271370 | 0.0119 | 0.118 |
| chr5 | 180915260 | 2208256 | 0.0122 | 0.1167 |
| chr6 | 171115067 | 3567645 | 0.0208 | 0.1902 |
| chr7 | 159138663 | 2901070 | 0.0182 | 0.2014 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3598319 | 0.0246 | 0.1743 |
| chr9 | 141213431 | 1892903 | 0.0134 | 0.1419 |
| chr10 | 135534747 | 2604673 | 0.0192 | 0.1799 |
| chr11 | 135006516 | 1687945 | 0.0125 | 0.1437 |
| chr12 | 133851895 | 2229985 | 0.0167 | 0.138 |
| chr13 | 115169878 | 1123656 | 0.0098 | 0.1043 |
| chr14 | 107349540 | 1117271 | 0.0104 | 0.1146 |
| chr15 | 102531392 | 1523159 | 0.0149 | 0.129 |
| chr16 | 90354753 | 1094638 | 0.0121 | 0.1231 |
| chr17 | 81195210 | 1140791 | 0.014 | 0.1275 |
| chr18 | 78077248 | 964827 | 0.0124 | 0.2287 |
| chr19 | 59128983 | 1007085 | 0.017 | 0.2017 |
| chr20 | 63025520 | 490789 | 0.0078 | 0.0925 |
| chr21 | 48129895 | 464696 | 0.0097 | 0.1071 |
| chr22 | 51304566 | 831118 | 0.0162 | 0.1341 |
| chrMT | 16571 | 3827 | 0.2309 | 0.5145 |
| chrX | 155270560 | 2624393 | 0.0169 | 0.1478 |
| chrY | 59373566 | 116824 | 0.002 | 0.0575 |

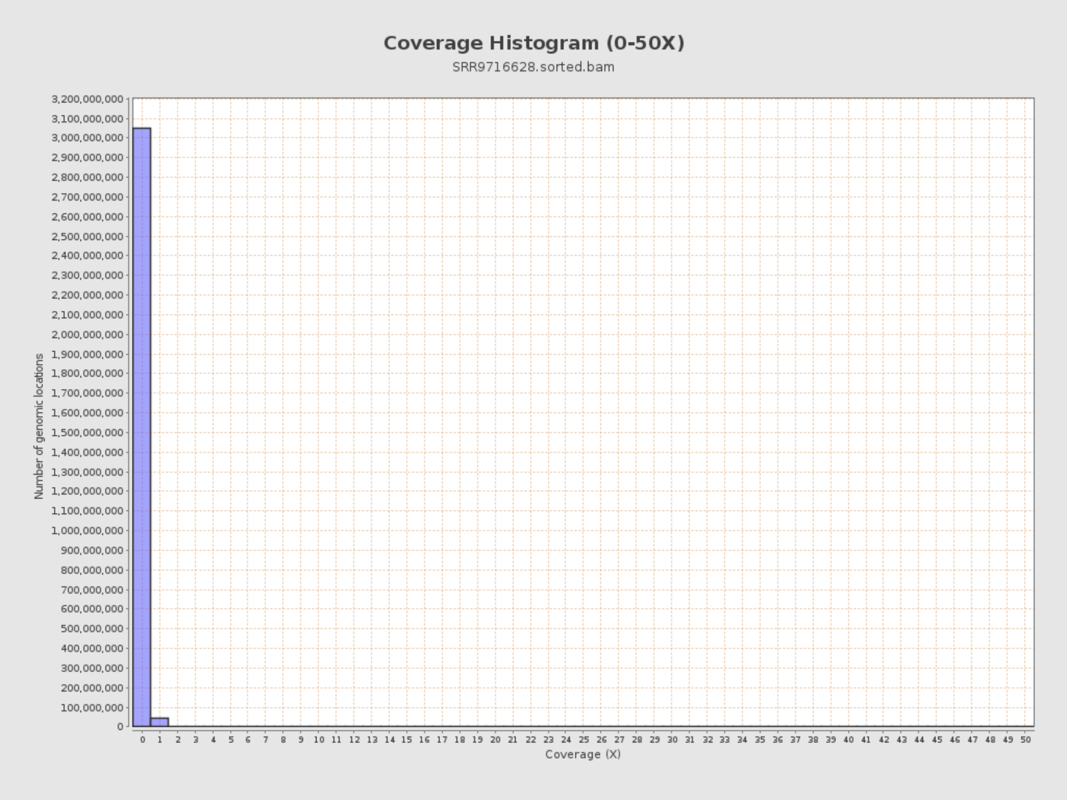
# 3. Results : Coverage across reference



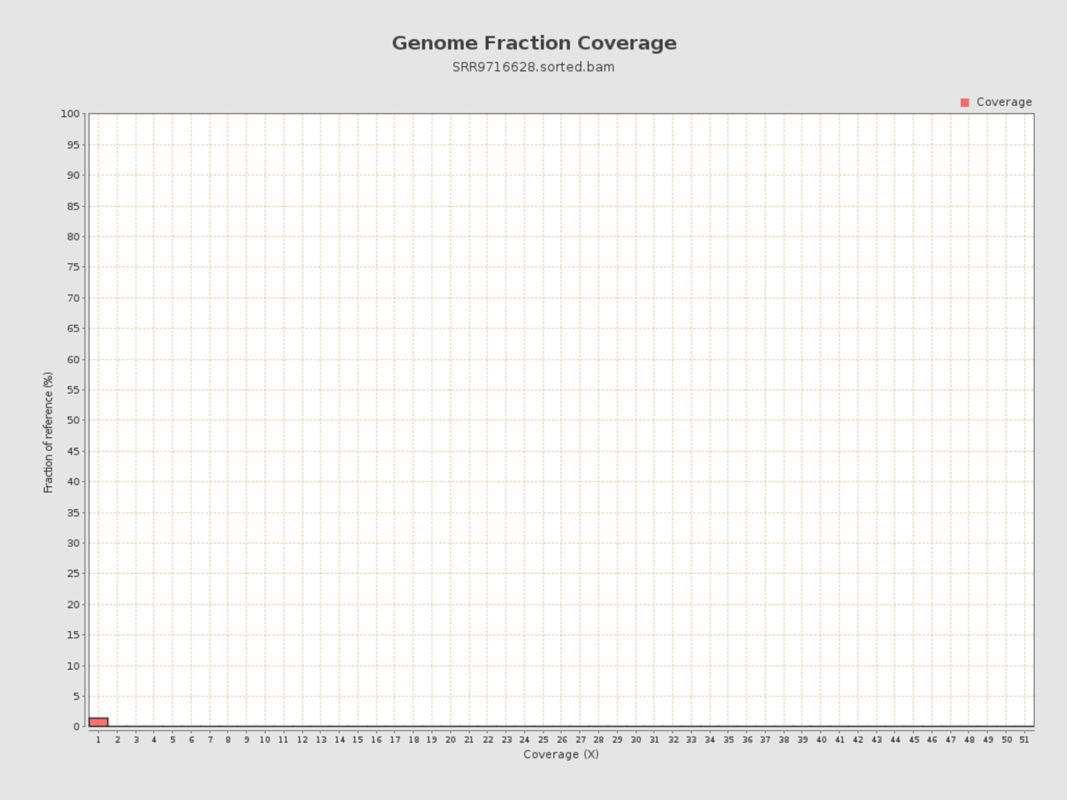
# 4. Results : Coverage Histogram



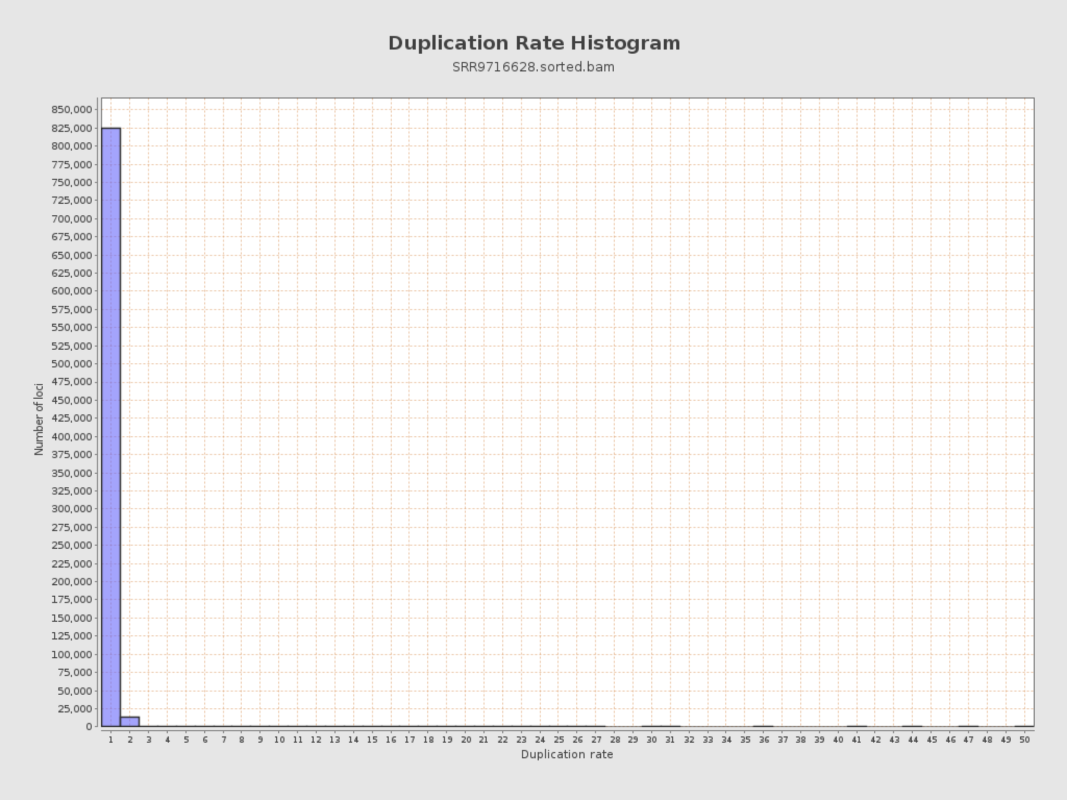
# 5. Results : Coverage Histogram (0-50X)



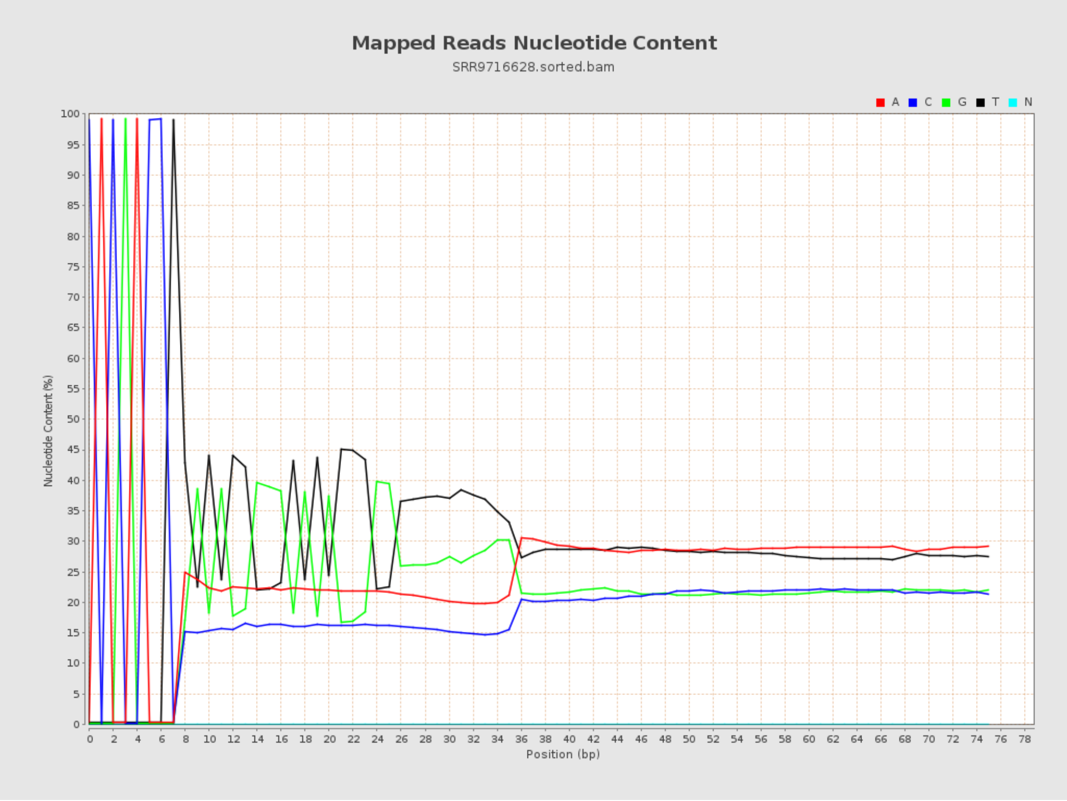
# 6. Results : Genome Fraction Coverage



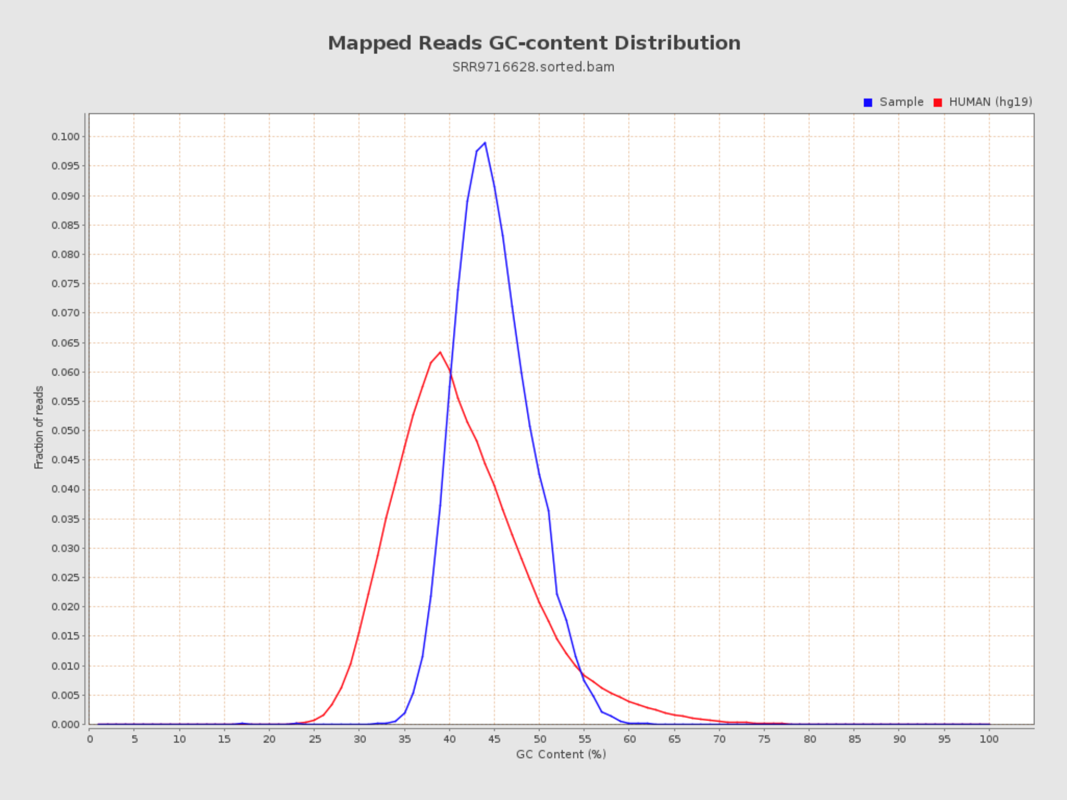
# 7. Results : Duplication Rate Histogram



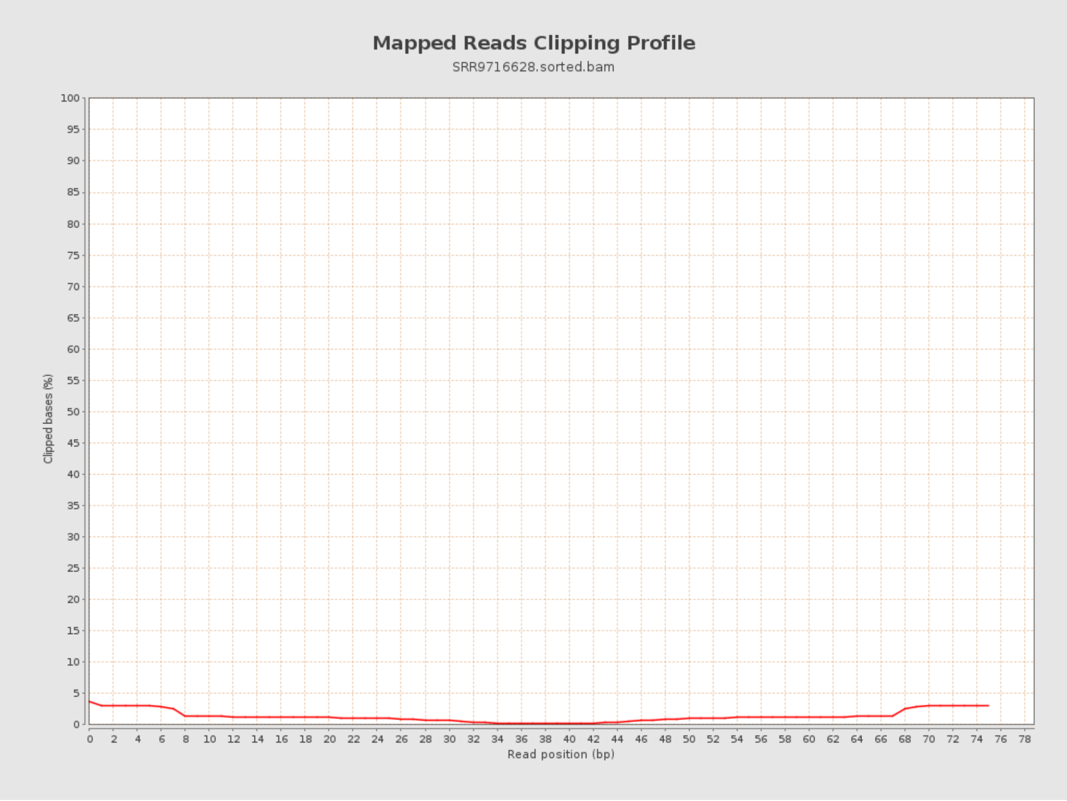
# 8. Results : Mapped Reads Nucleotide Content



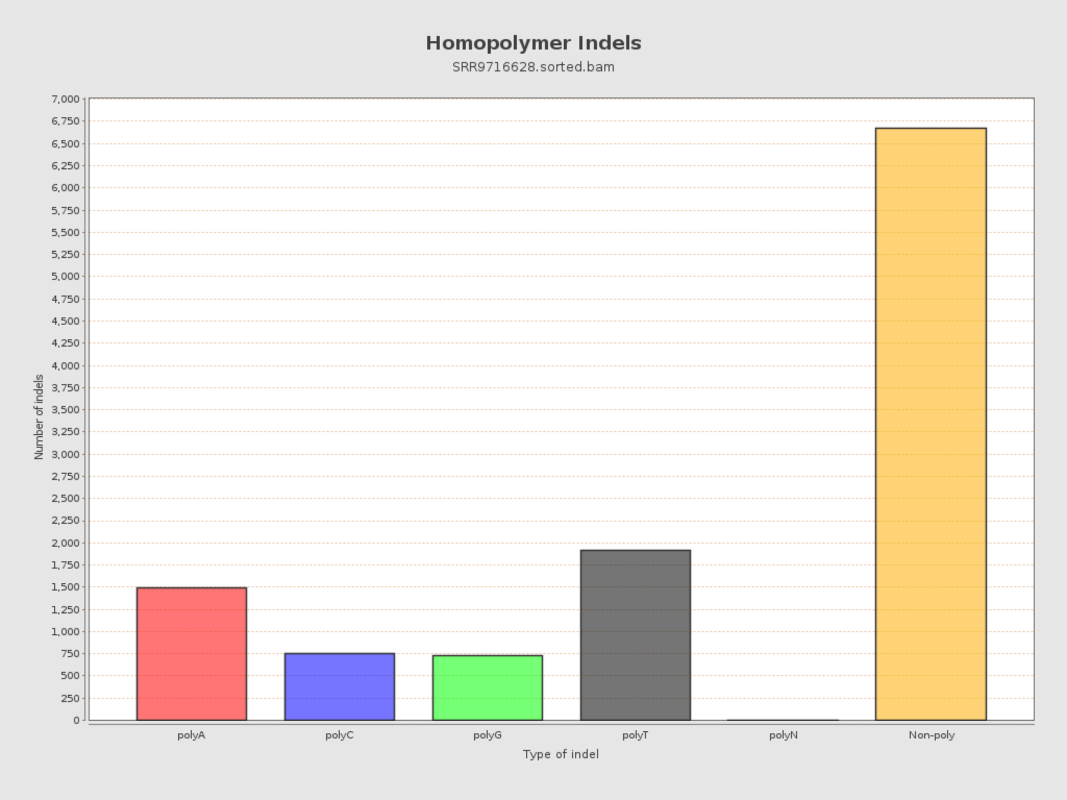
# 9. Results : Mapped Reads GC-content Distribution



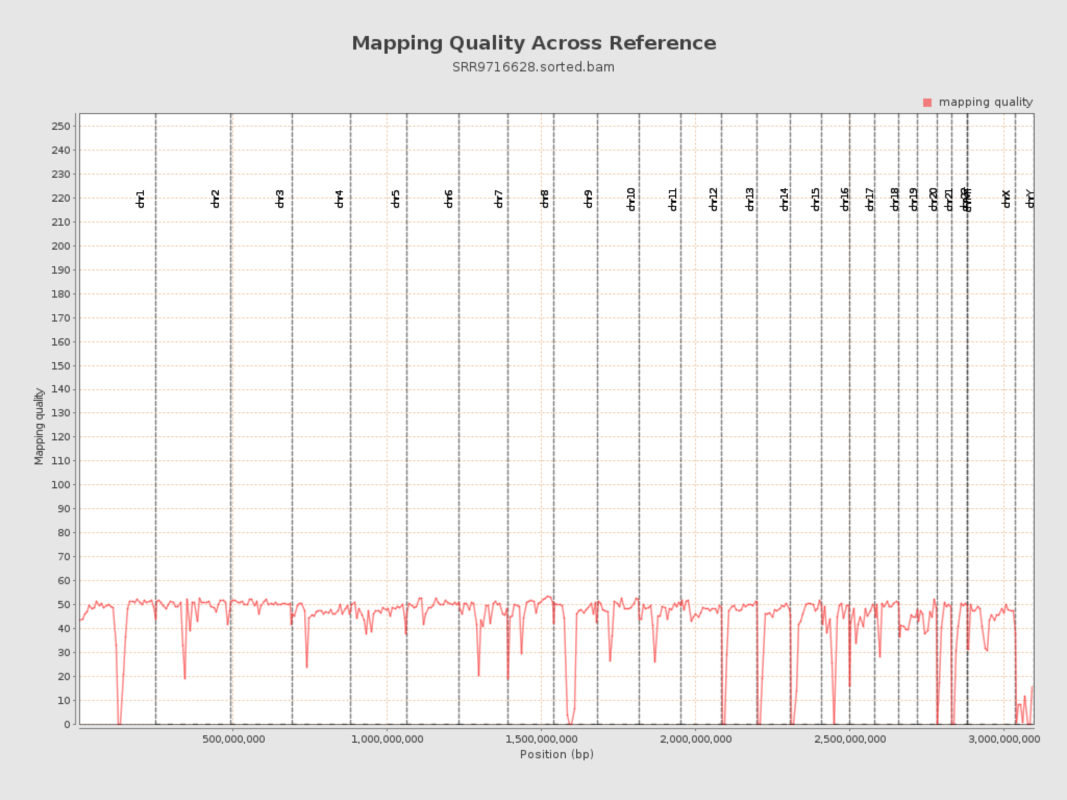
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram