# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 02:59:00*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716657.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_SRR9716657 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716657.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 02:58:59 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716657.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,641,950 |
| Mapped reads | 1,518,922 / 92.51% |
| Unmapped reads | 123,028 / 7.49% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 9,286 / 0.57% |
| Read min/max/mean length | 30 / 76 / 76.19 |
| Duplicated reads (estimated) | 47,574 / 2.9% |
| Duplication rate | 2.3% |
| Clipped reads | 1,526,964 / 93% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 21,357,641 / 24.02% |
| Number/percentage of C's | 17,961,610 / 20.2% |
| Number/percentage of T's | 27,166,470 / 30.55% |
| Number/percentage of G's | 22,441,516 / 25.24% |
| Number/percentage of N's | 1,103 / 0% |
| GC Percentage | 45.43% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0287 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2561 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.64 |

## 2.5. Mismatches and indels

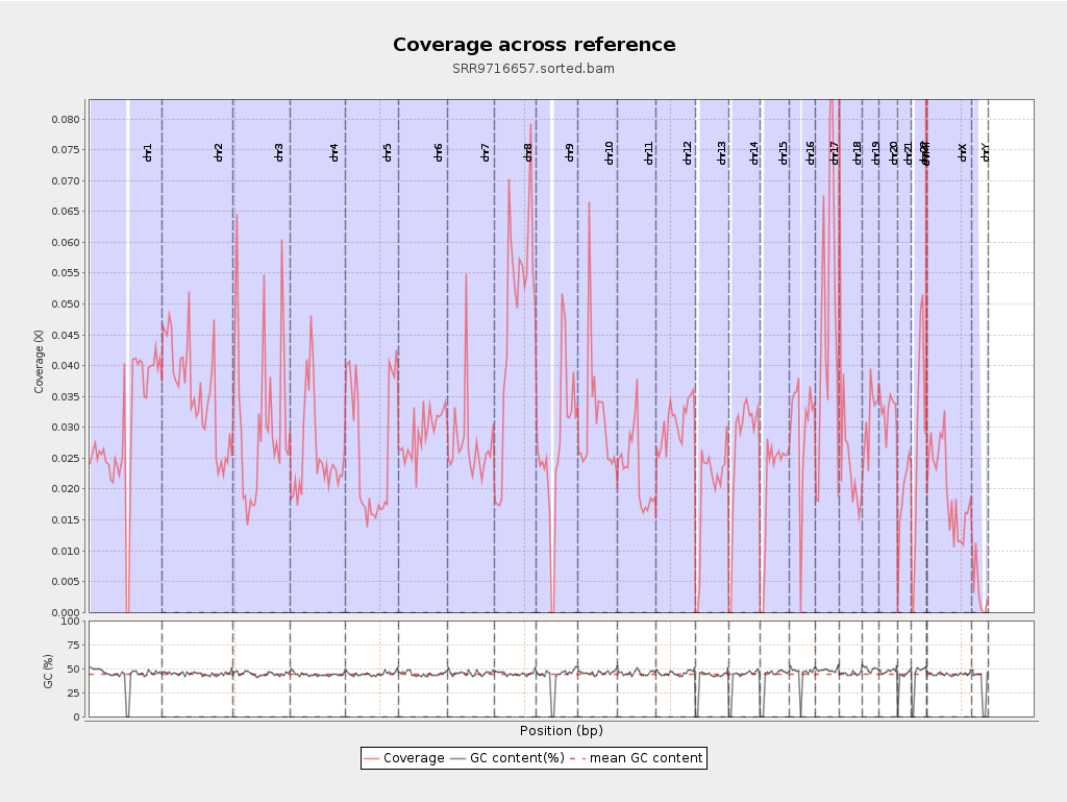
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 441,211 |
| Insertions | 5,032 |
| Mapped reads with at least one insertion | 0.33% |
| Deletions | 16,679 |
| Mapped reads with at least one deletion | 1.09% |
| Homopolymer indels | 41.81% |

## 2.6. Chromosome stats

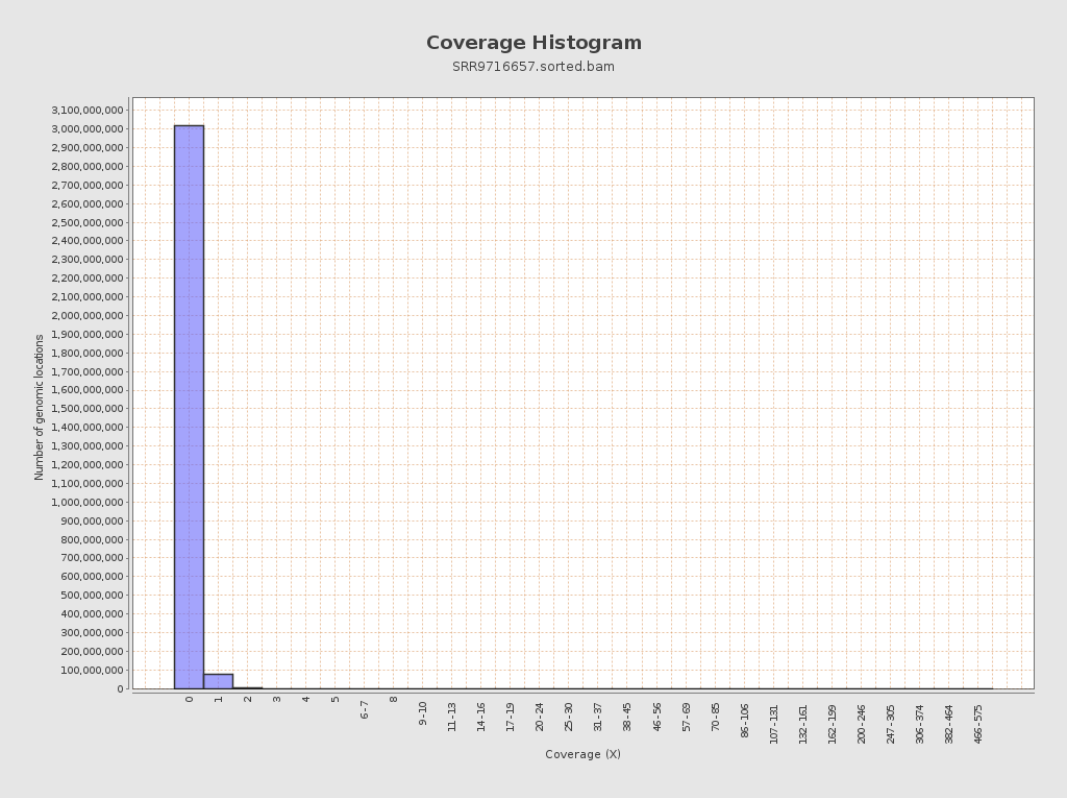
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 7422382 | 0.0298 | 0.4004 |
| chr2 | 243199373 | 8699875 | 0.0358 | 0.3269 |
| chr3 | 198022430 | 6057426 | 0.0306 | 0.1918 |
| chr4 | 191154276 | 4934701 | 0.0258 | 0.1926 |
| chr5 | 180915260 | 4785490 | 0.0265 | 0.1761 |
| chr6 | 171115067 | 4983409 | 0.0291 | 0.1967 |
| chr7 | 159138663 | 4352559 | 0.0274 | 0.3865 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6978075 | 0.0477 | 0.3158 |
| chr9 | 141213431 | 3765075 | 0.0267 | 0.1985 |
| chr10 | 135534747 | 4184323 | 0.0309 | 0.3055 |
| chr11 | 135006516 | 3071762 | 0.0228 | 0.2024 |
| chr12 | 133851895 | 4114642 | 0.0307 | 0.1989 |
| chr13 | 115169878 | 2293405 | 0.0199 | 0.152 |
| chr14 | 107349540 | 2867397 | 0.0267 | 0.18 |
| chr15 | 102531392 | 2144266 | 0.0209 | 0.1572 |
| chr16 | 90354753 | 2739692 | 0.0303 | 0.1961 |
| chr17 | 81195210 | 3853047 | 0.0475 | 0.2459 |
| chr18 | 78077248 | 2055183 | 0.0263 | 0.3094 |
| chr19 | 59128983 | 1865675 | 0.0316 | 0.3438 |
| chr20 | 63025520 | 2064843 | 0.0328 | 0.2014 |
| chr21 | 48129895 | 906875 | 0.0188 | 0.1595 |
| chr22 | 51304566 | 1393920 | 0.0272 | 0.1794 |
| chrMT | 16571 | 93884 | 5.6656 | 3.7995 |
| chrX | 155270560 | 3121854 | 0.0201 | 0.1709 |
| chrY | 59373566 | 205310 | 0.0035 | 0.1005 |

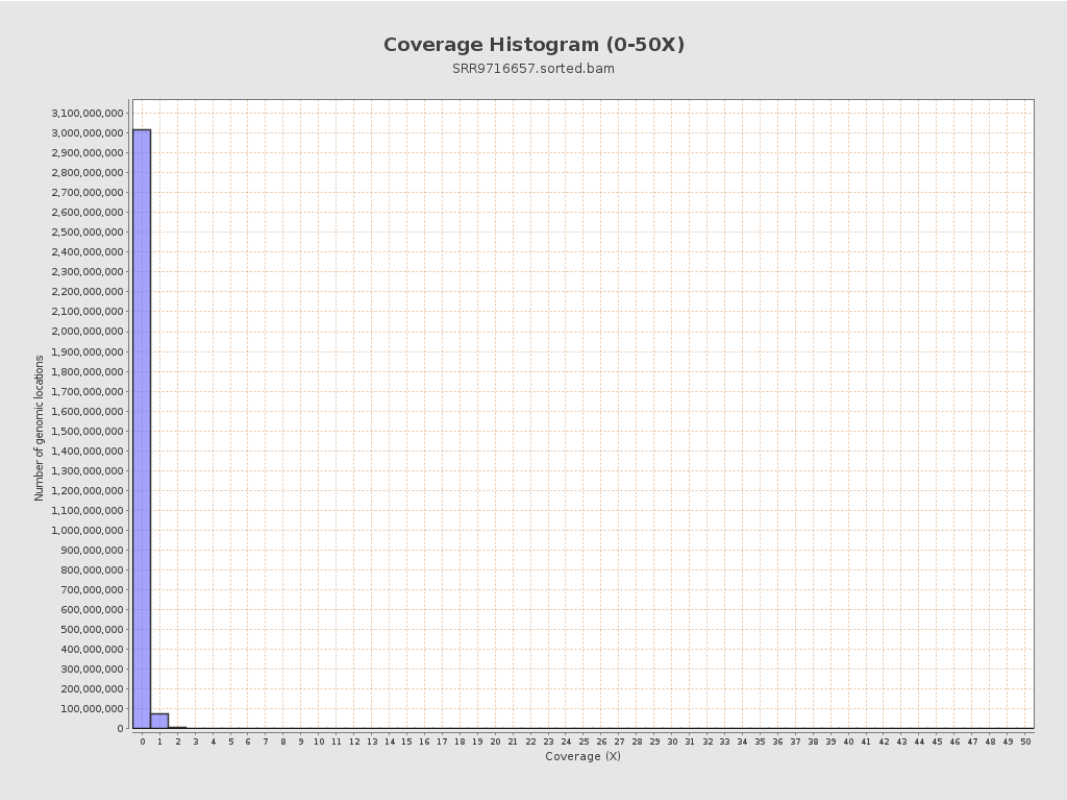
# 3. Results : Coverage across reference



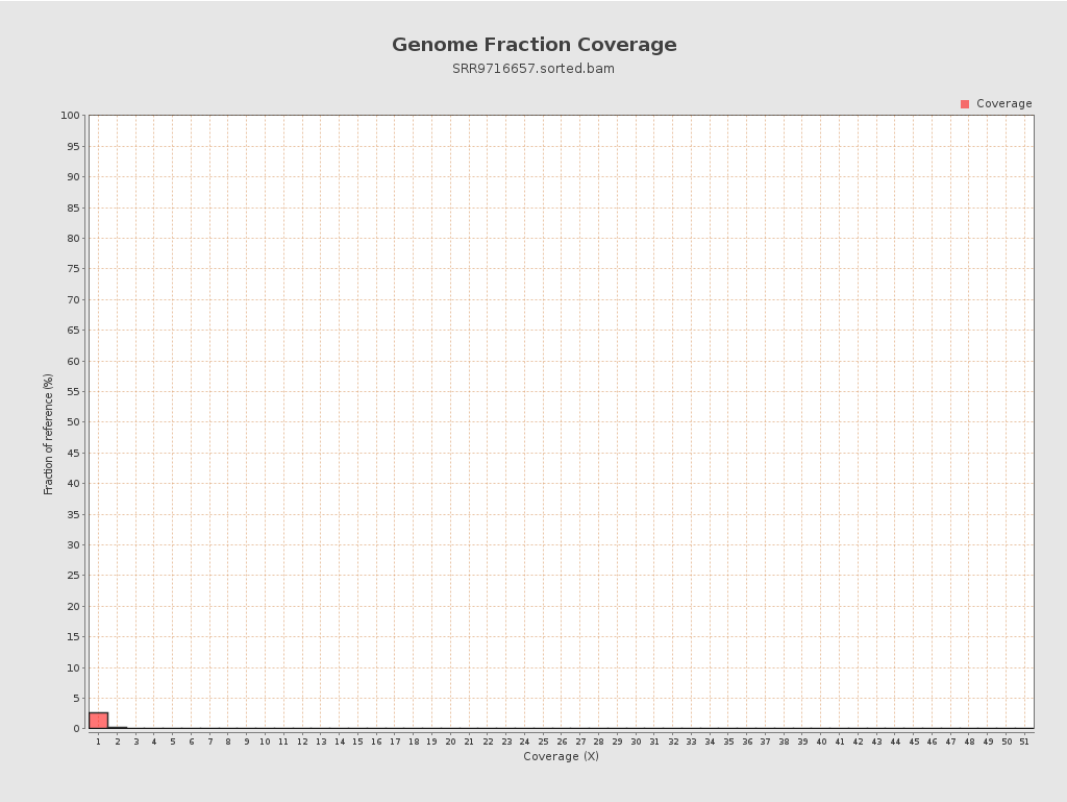
# 4. Results : Coverage Histogram



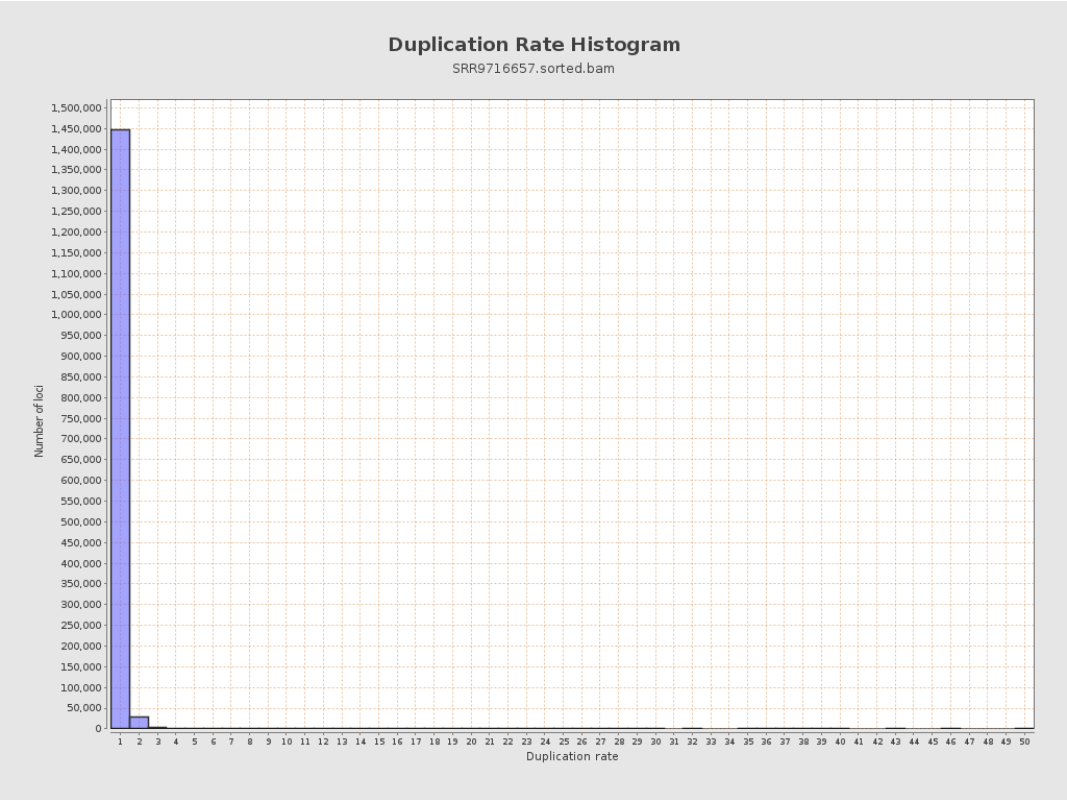
# 5. Results : Coverage Histogram (0-50X)



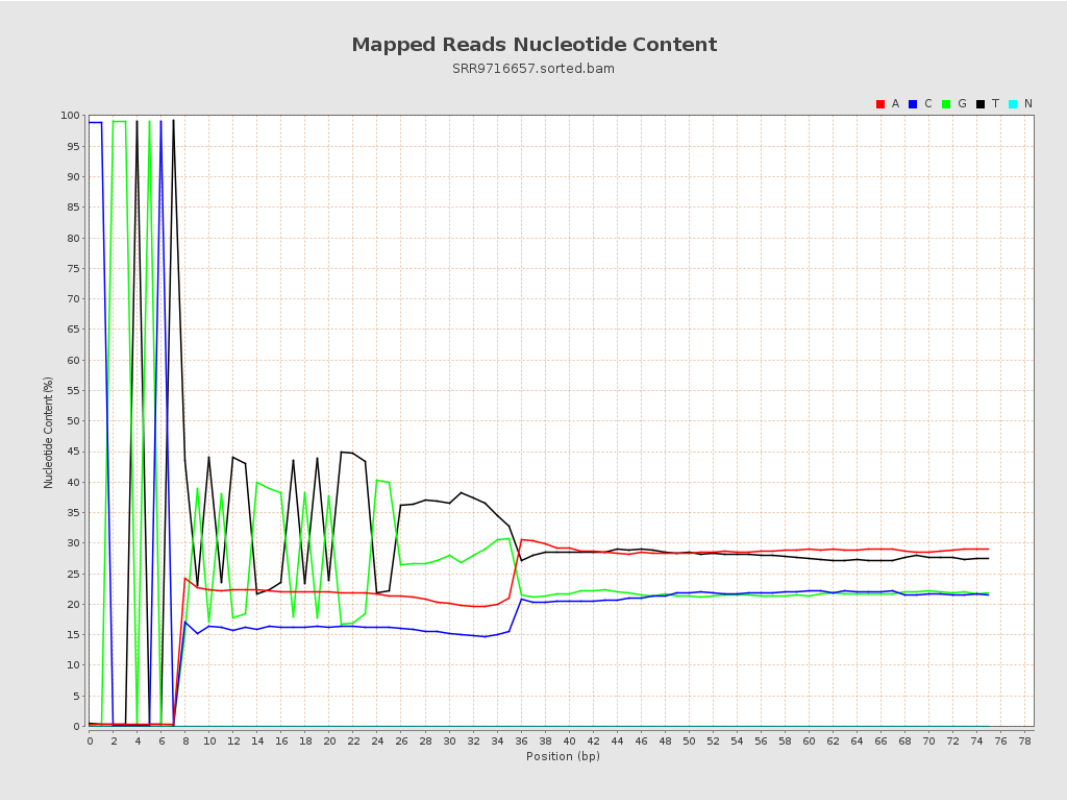
# 6. Results : Genome Fraction Coverage



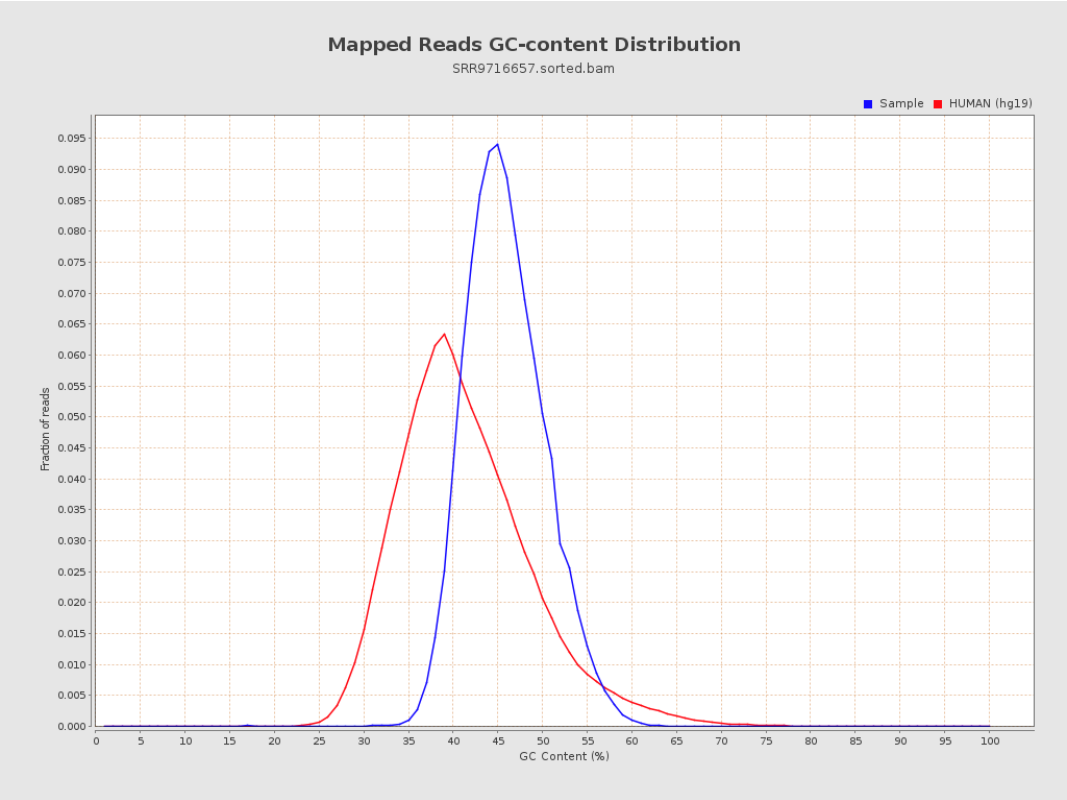
# 7. Results : Duplication Rate Histogram



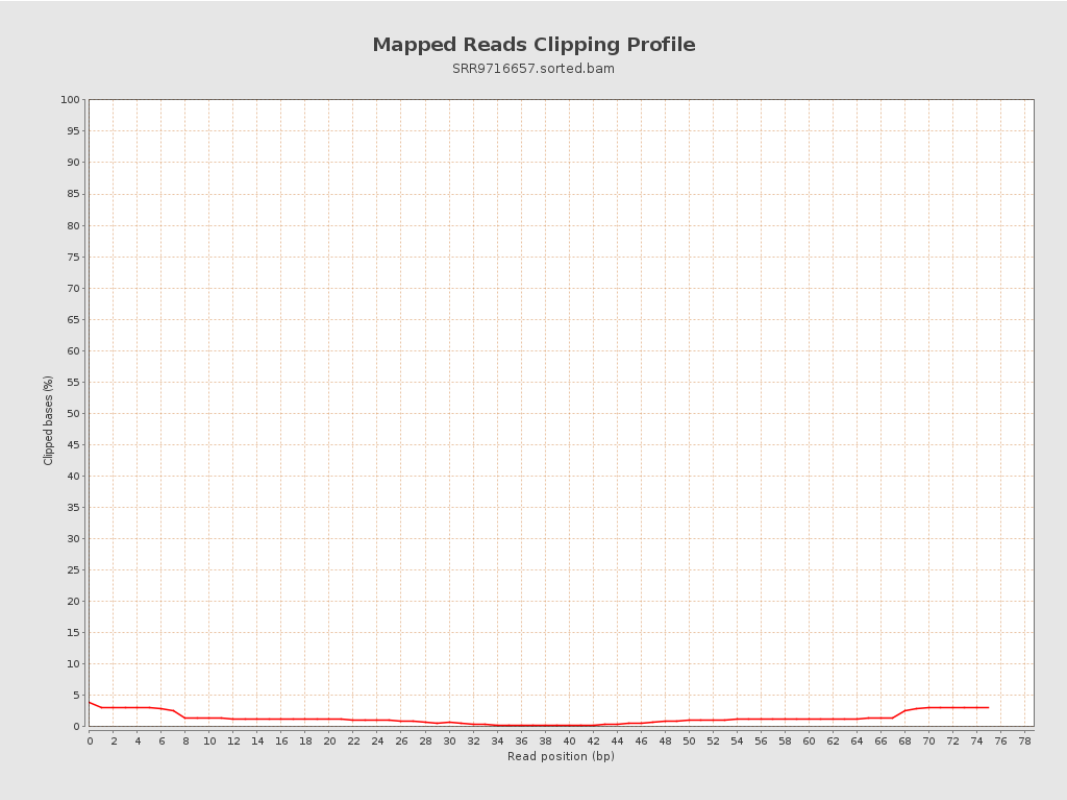
# 8. Results : Mapped Reads Nucleotide Content



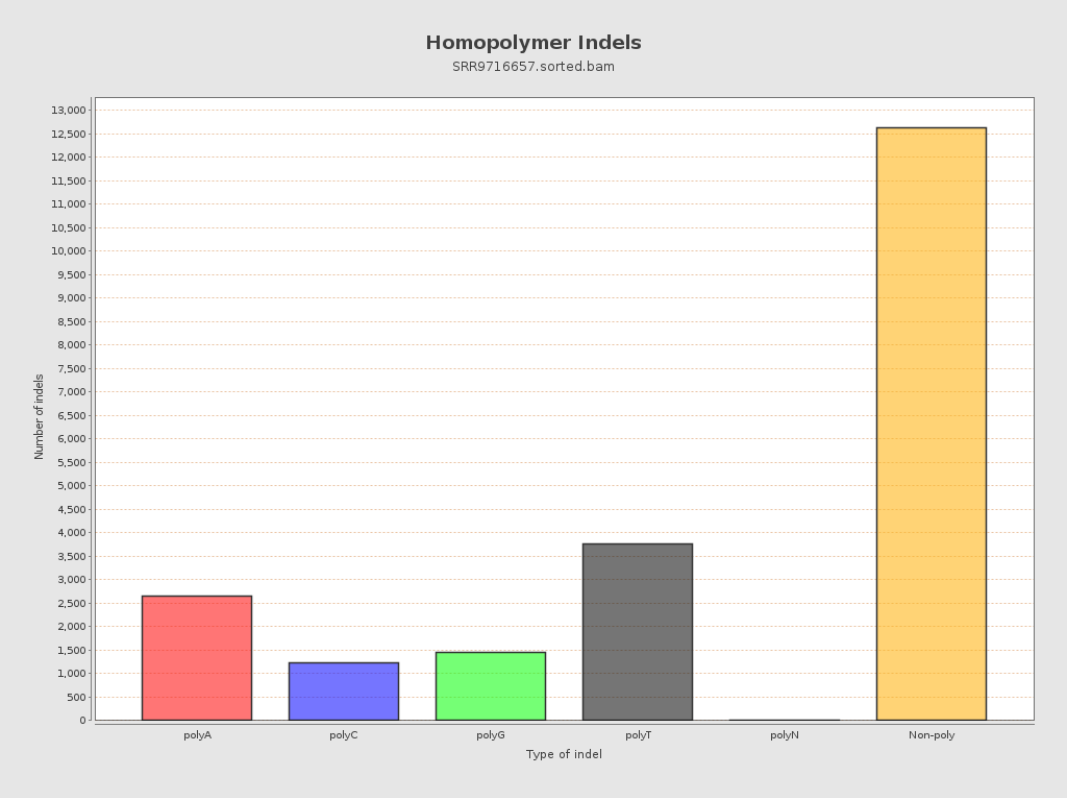
# 9. Results : Mapped Reads GC-content Distribution



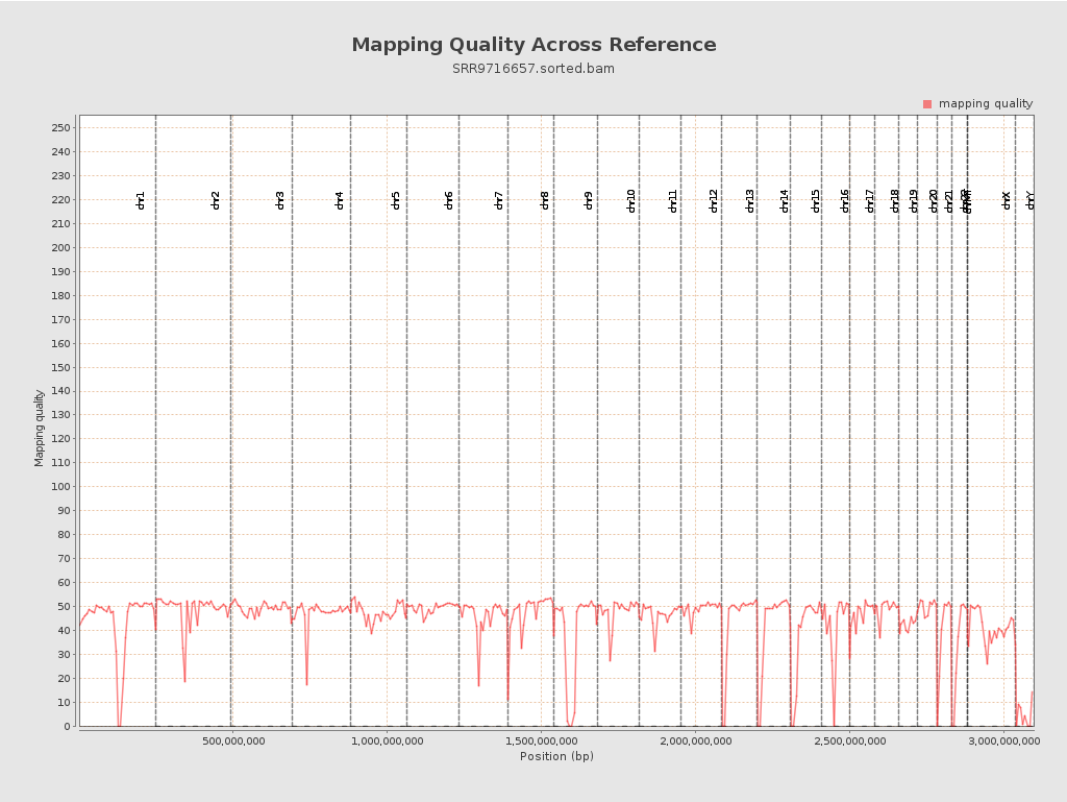
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram