# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 10:21:50*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716759.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_SRR9716759 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716759.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 10:21:49 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716759.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,636,156 |
| Mapped reads | 1,375,672 / 84.08% |
| Unmapped reads | 260,484 / 15.92% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 4,071 / 0.25% |
| Read min/max/mean length | 30 / 76 / 76.08 |
| Duplicated reads (estimated) | 29,788 / 1.82% |
| Duplication rate | 1.58% |
| Clipped reads | 1,376,215 / 84.11% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 17,552,895 / 22.96% |
| Number/percentage of C's | 16,644,022 / 21.77% |
| Number/percentage of T's | 22,156,095 / 28.98% |
| Number/percentage of G's | 20,101,545 / 26.29% |
| Number/percentage of N's | 2,038 / 0% |
| GC Percentage | 48.06% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0247 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2017 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 39.24 |

## 2.5. Mismatches and indels

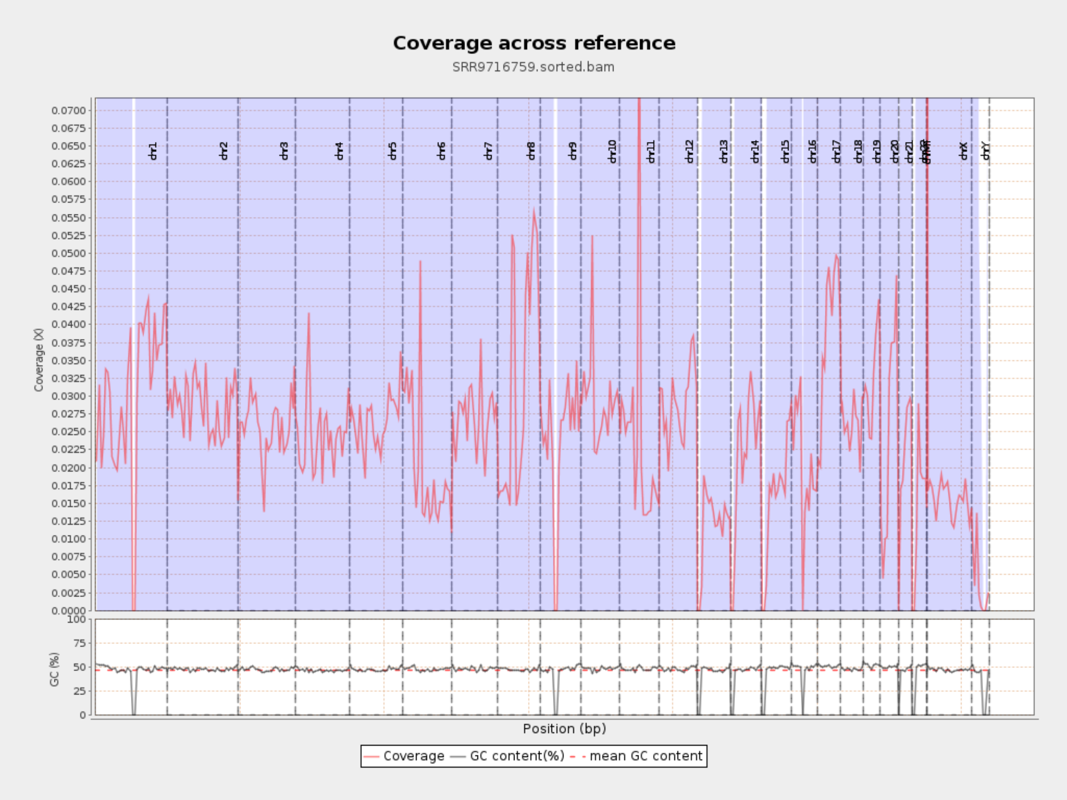
| | |
|---|---|
| General error rate | 0.54% |
| Mismatches | 399,394 |
| Insertions | 5,937 |
| Mapped reads with at least one insertion | 0.43% |
| Deletions | 11,972 |
| Mapped reads with at least one deletion | 0.86% |
| Homopolymer indels | 35.27% |

## 2.6. Chromosome stats

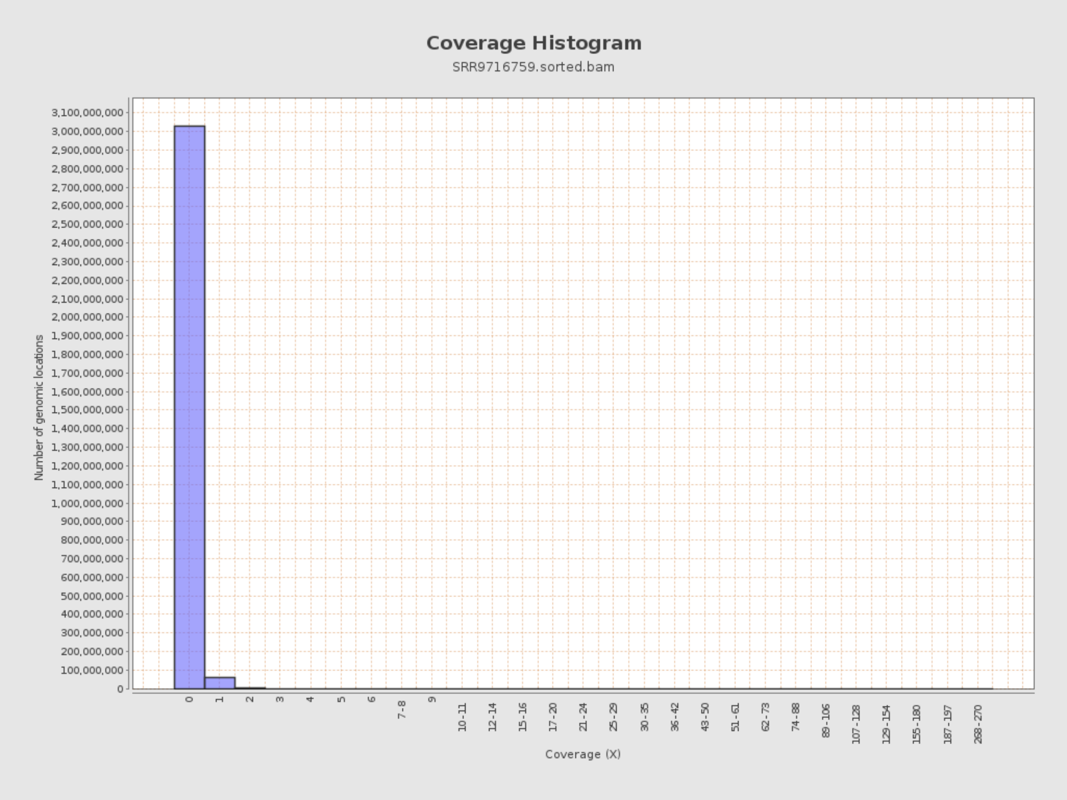
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 7493939 | 0.0301 | 0.2494 |
| chr2 | 243199373 | 6974071 | 0.0287 | 0.2404 |
| chr3 | 198022430 | 5077697 | 0.0256 | 0.1809 |
| chr4 | 191154276 | 4740605 | 0.0248 | 0.1975 |
| chr5 | 180915260 | 4816379 | 0.0266 | 0.1785 |
| chr6 | 171115067 | 3512730 | 0.0205 | 0.1632 |
| chr7 | 159138663 | 4316631 | 0.0271 | 0.2355 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 4732339 | 0.0323 | 0.2079 |
| chr9 | 141213431 | 3344617 | 0.0237 | 0.1845 |
| chr10 | 135534747 | 4005518 | 0.0296 | 0.2874 |
| chr11 | 135006516 | 3345784 | 0.0248 | 0.209 |
| chr12 | 133851895 | 3890623 | 0.0291 | 0.1889 |
| chr13 | 115169878 | 1358565 | 0.0118 | 0.1204 |
| chr14 | 107349540 | 2305621 | 0.0215 | 0.1635 |
| chr15 | 102531392 | 1597459 | 0.0156 | 0.1428 |
| chr16 | 90354753 | 1804312 | 0.02 | 0.1693 |
| chr17 | 81195210 | 3194257 | 0.0393 | 0.2315 |
| chr18 | 78077248 | 2032433 | 0.026 | 0.2367 |
| chr19 | 59128983 | 1906913 | 0.0323 | 0.2417 |
| chr20 | 63025520 | 1547366 | 0.0246 | 0.1816 |
| chr21 | 48129895 | 1047910 | 0.0218 | 0.1775 |
| chr22 | 51304566 | 761405 | 0.0148 | 0.1361 |
| chrMT | 16571 | 8240 | 0.4973 | 0.7587 |
| chrX | 155270560 | 2436895 | 0.0157 | 0.1488 |
| chrY | 59373566 | 224236 | 0.0038 | 0.1136 |

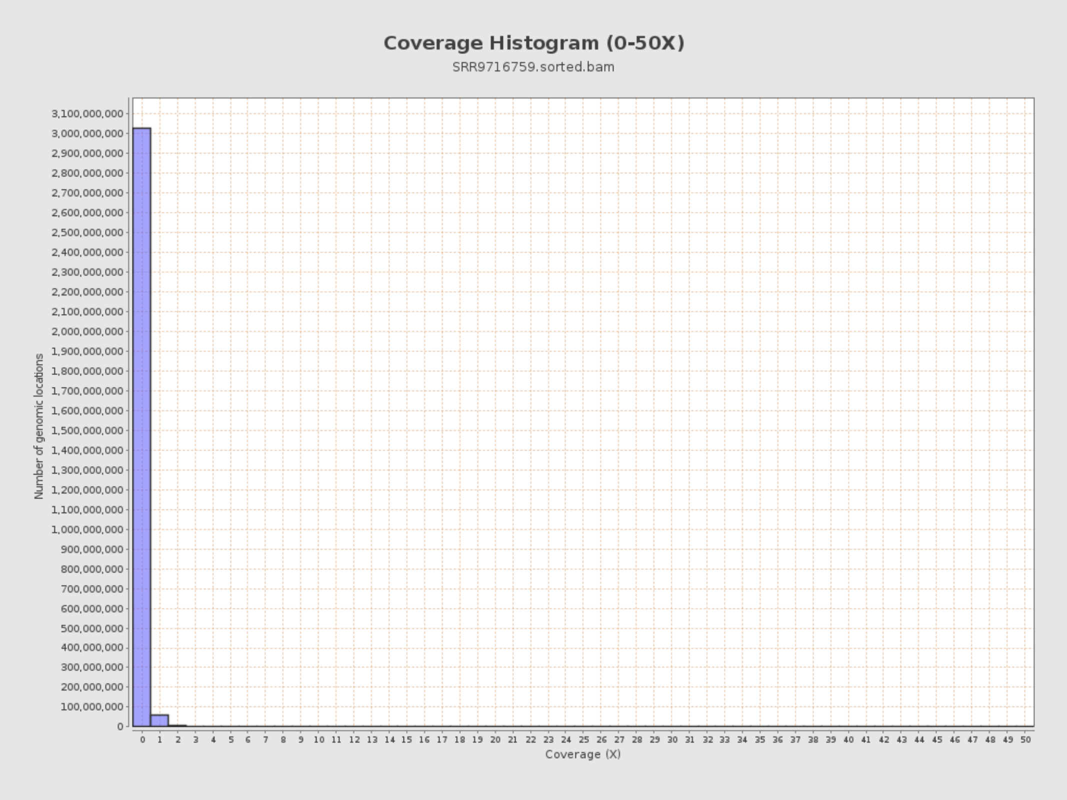
# 3. Results : Coverage across reference



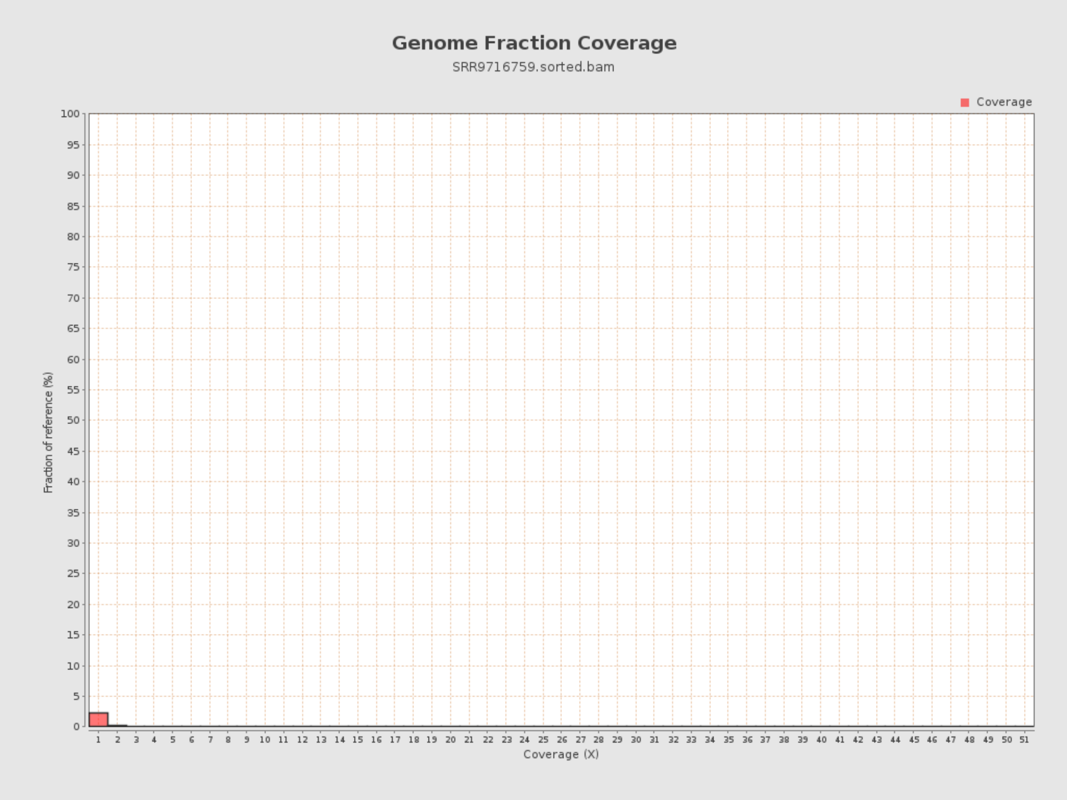
# 4. Results : Coverage Histogram



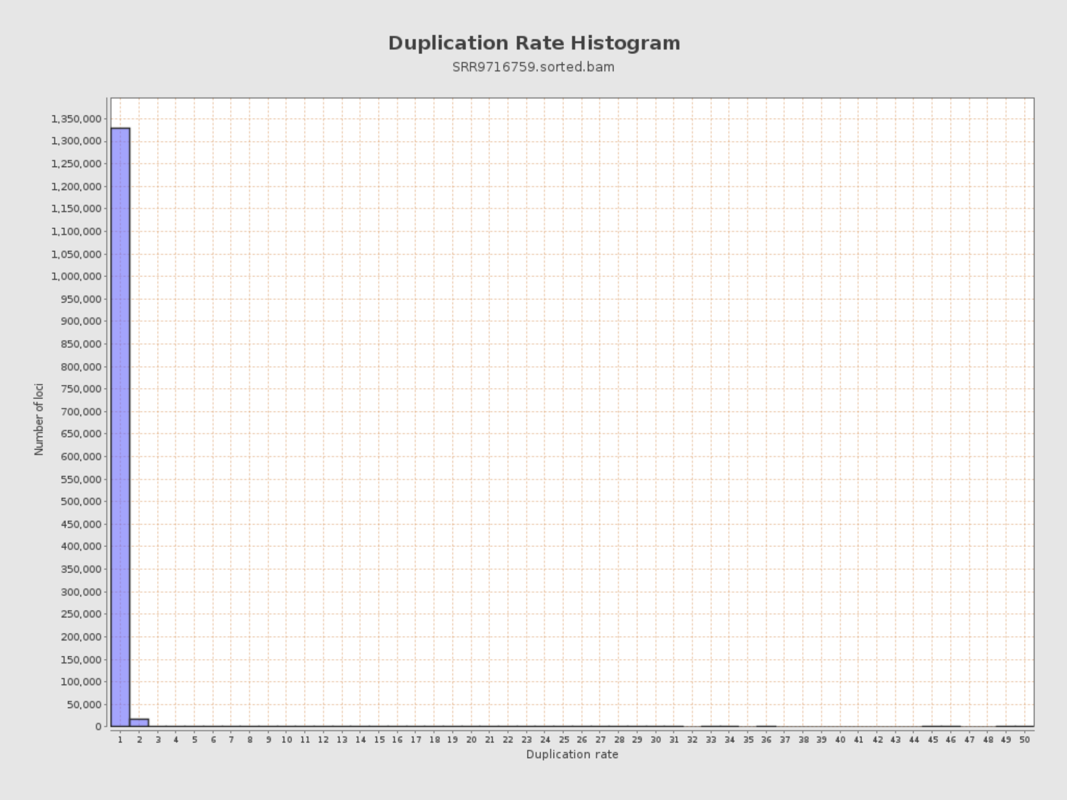
# 5. Results : Coverage Histogram (0-50X)



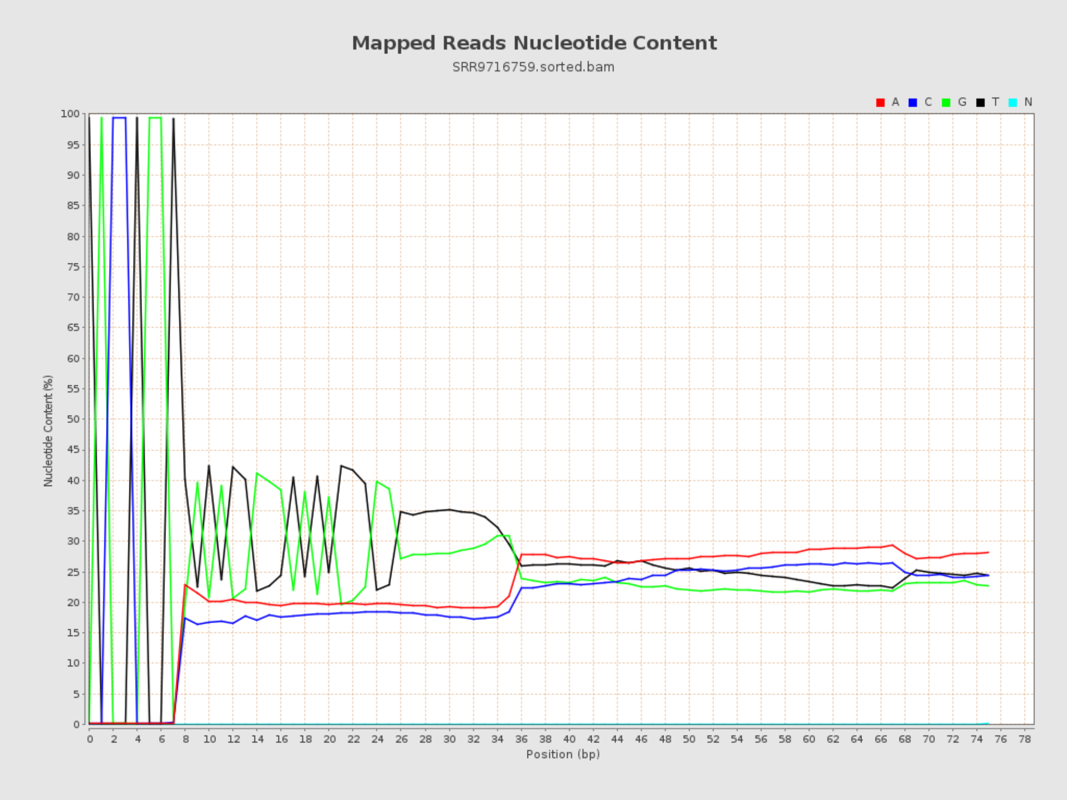
# 6. Results : Genome Fraction Coverage



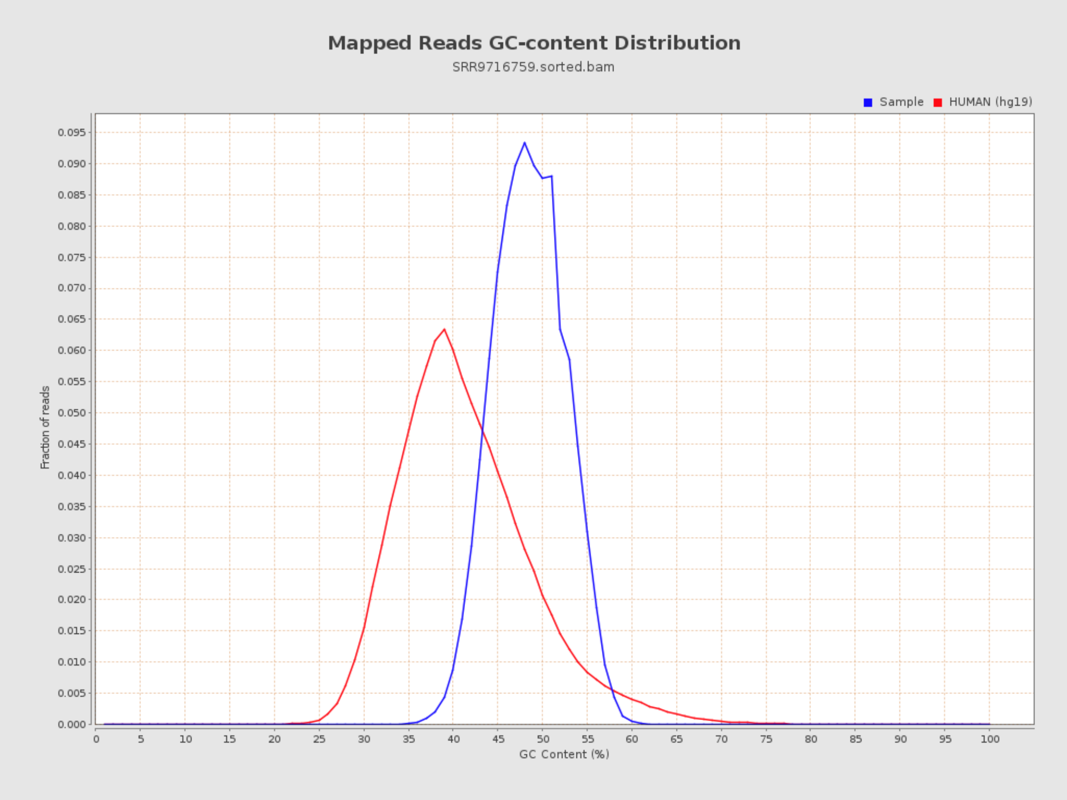
# 7. Results : Duplication Rate Histogram



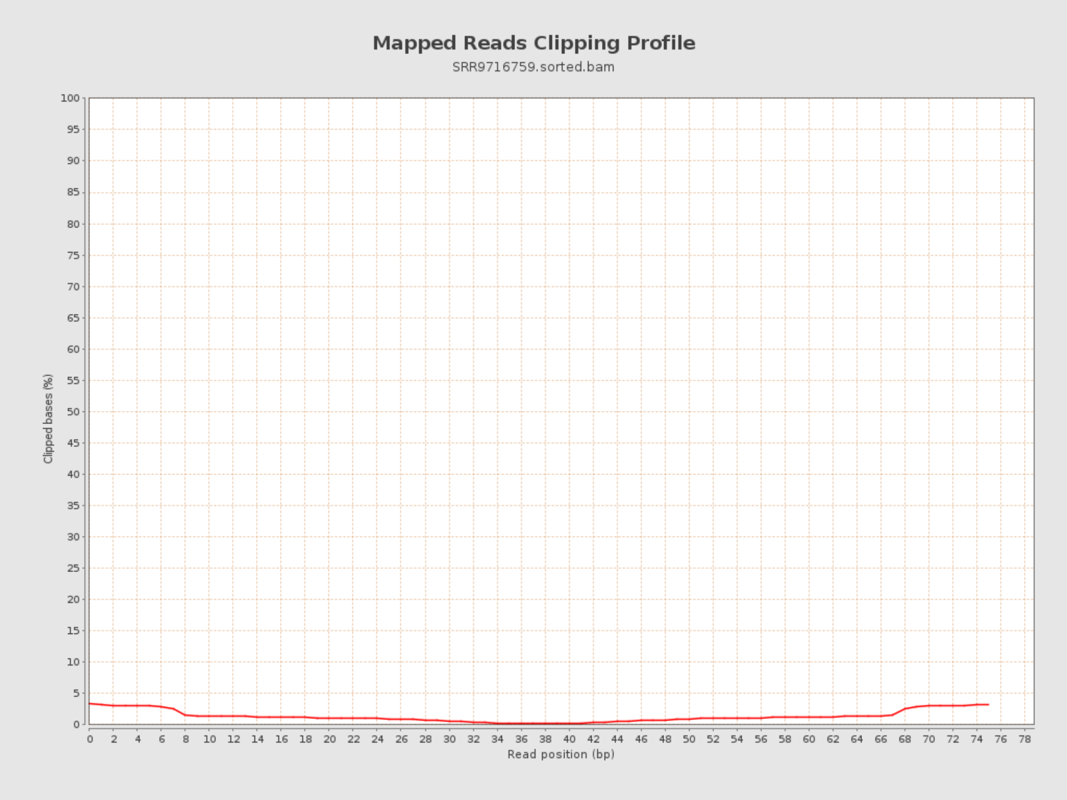
# 8. Results : Mapped Reads Nucleotide Content



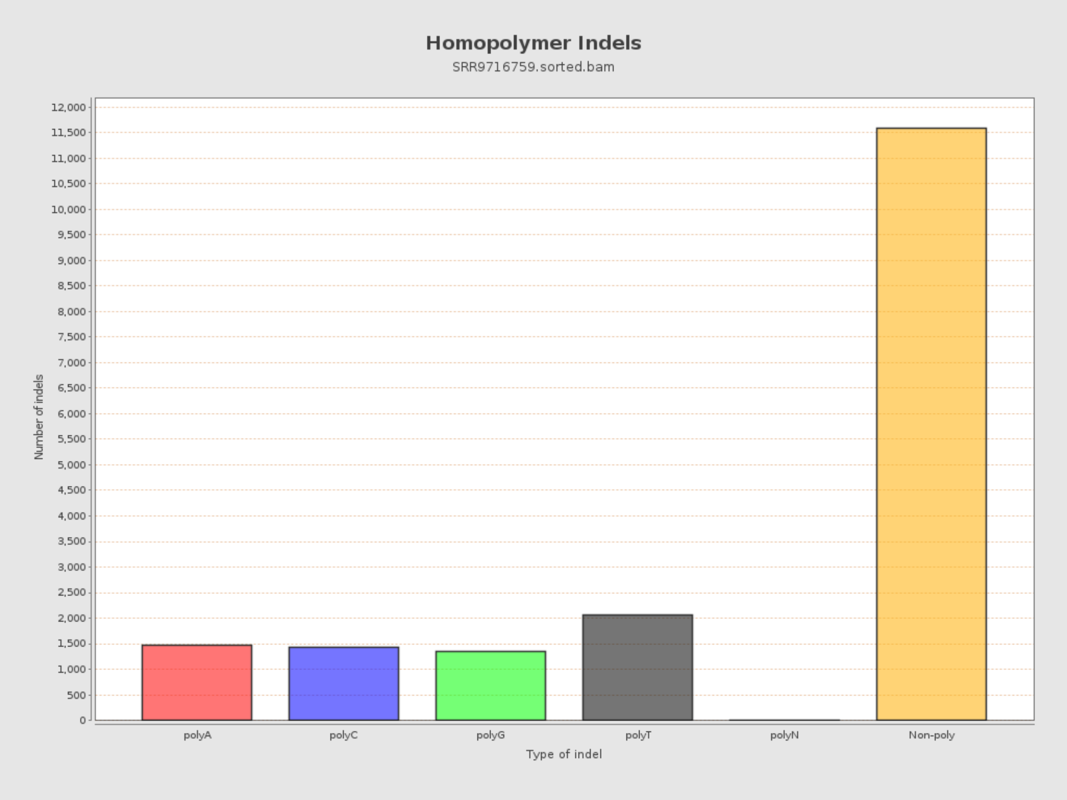
# 9. Results : Mapped Reads GC-content Distribution



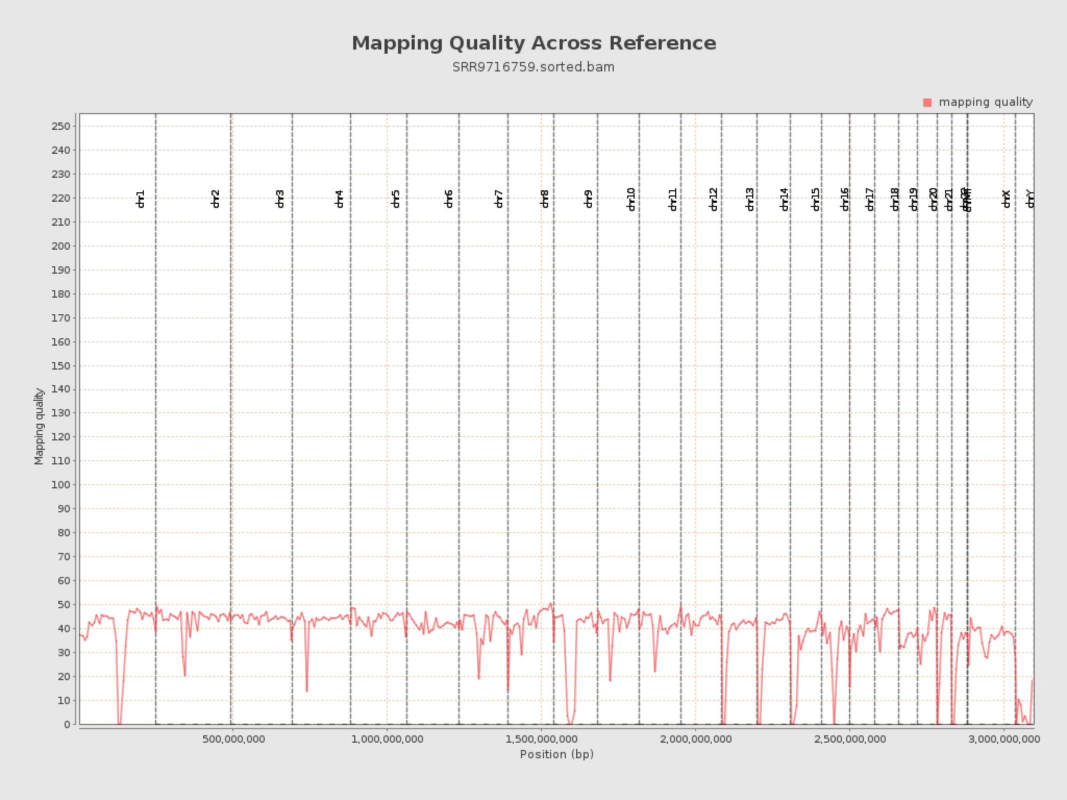
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram