# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 13:42:11*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716823.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_SRR9716823 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716823.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 13:42:10 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716823.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 760,685 |
| Mapped reads | 598,497 / 78.68% |
| Unmapped reads | 162,188 / 21.32% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 664 / 0.09% |
| Read min/max/mean length | 30 / 76 / 76.03 |
| Duplicated reads (estimated) | 37,251 / 4.9% |
| Duplication rate | 5.58% |
| Clipped reads | 598,047 / 78.62% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 6,913,509 / 22.04% |
| Number/percentage of C's | 6,051,547 / 19.29% |
| Number/percentage of T's | 9,941,725 / 31.7% |
| Number/percentage of G's | 8,458,044 / 26.97% |
| Number/percentage of N's | 595 / 0% |
| GC Percentage | 46.26% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0101 |
| | |

| | |
|---|---|
| Standard Deviation | 0.12 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43 |

## 2.5. Mismatches and indels

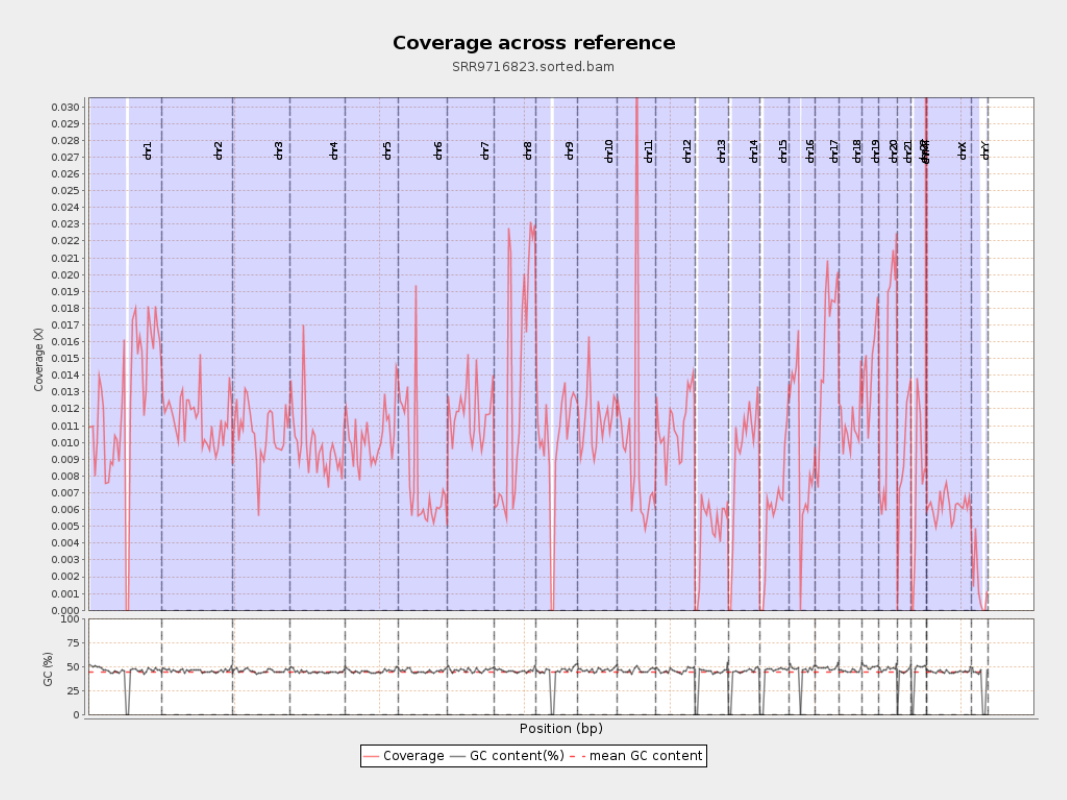
| | |
|---|---|
| General error rate | 0.65% |
| Mismatches | 198,983 |
| Insertions | 1,940 |
| Mapped reads with at least one insertion | 0.32% |
| Deletions | 4,398 |
| Mapped reads with at least one deletion | 0.73% |
| Homopolymer indels | 41.51% |

## 2.6. Chromosome stats

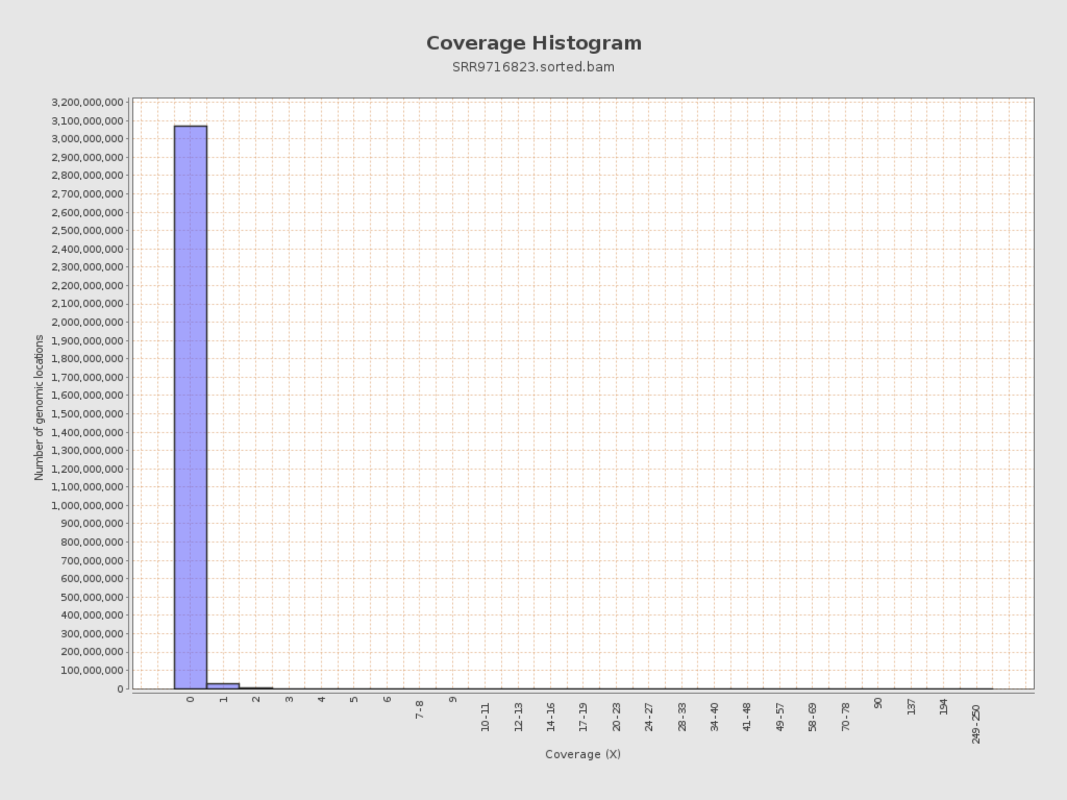
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 3042764 | 0.0122 | 0.1356 |
| chr2 | 243199373 | 2770840 | 0.0114 | 0.156 |
| chr3 | 198022430 | 2091294 | 0.0106 | 0.114 |
| chr4 | 191154276 | 1877146 | 0.0098 | 0.1132 |
| chr5 | 180915260 | 1872544 | 0.0104 | 0.1128 |
| chr6 | 171115067 | 1387455 | 0.0081 | 0.1052 |
| chr7 | 159138663 | 1866818 | 0.0117 | 0.1315 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 1976380 | 0.0135 | 0.1317 |
| chr9 | 141213431 | 1392615 | 0.0099 | 0.1133 |
| chr10 | 135534747 | 1533671 | 0.0113 | 0.1281 |
| chr11 | 135006516 | 1323429 | 0.0098 | 0.1165 |
| chr12 | 133851895 | 1479721 | 0.0111 | 0.117 |
| chr13 | 115169878 | 543298 | 0.0047 | 0.0768 |
| chr14 | 107349540 | 971042 | 0.009 | 0.1056 |
| chr15 | 102531392 | 614309 | 0.006 | 0.0857 |
| chr16 | 90354753 | 848582 | 0.0094 | 0.1111 |
| chr17 | 81195210 | 1294596 | 0.0159 | 0.1428 |
| chr18 | 78077248 | 857738 | 0.011 | 0.1268 |
| chr19 | 59128983 | 860601 | 0.0146 | 0.1553 |
| chr20 | 63025520 | 871735 | 0.0138 | 0.1355 |
| chr21 | 48129895 | 446647 | 0.0093 | 0.1118 |
| chr22 | 51304566 | 364565 | 0.0071 | 0.0959 |
| chrMT | 16571 | 36633 | 2.2107 | 2.2661 |
| chrX | 155270560 | 964054 | 0.0062 | 0.0889 |
| chrY | 59373566 | 84302 | 0.0014 | 0.049 |

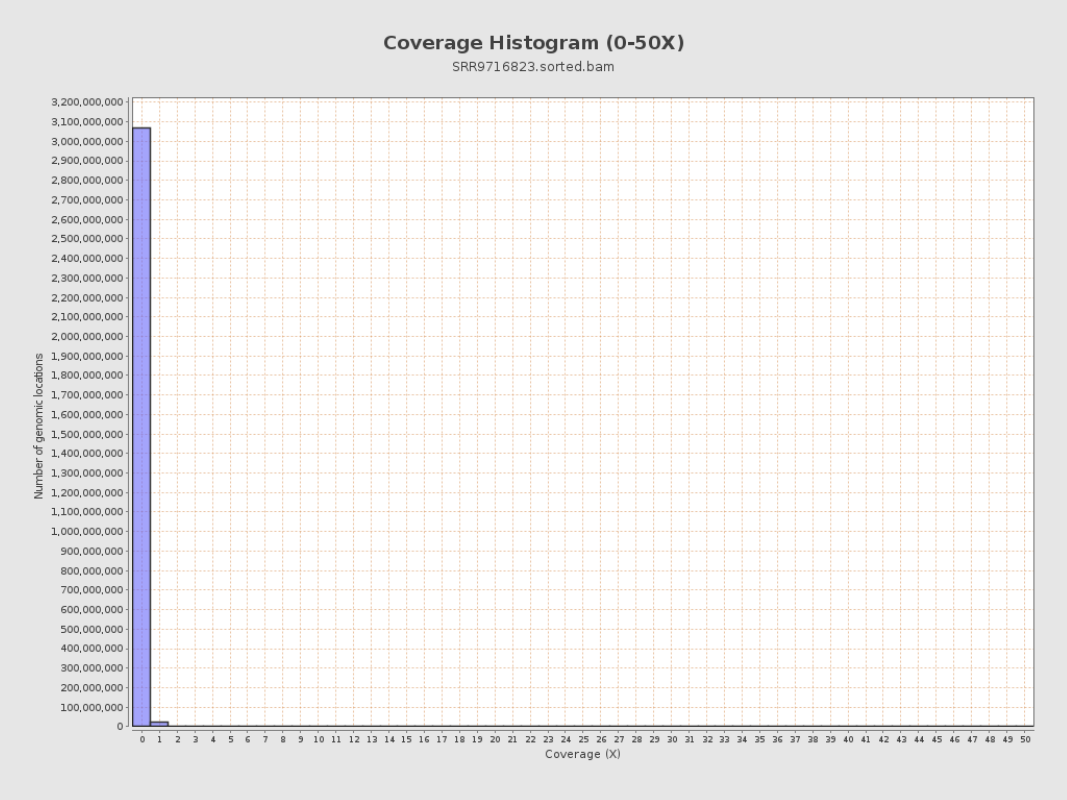
# 3. Results : Coverage across reference



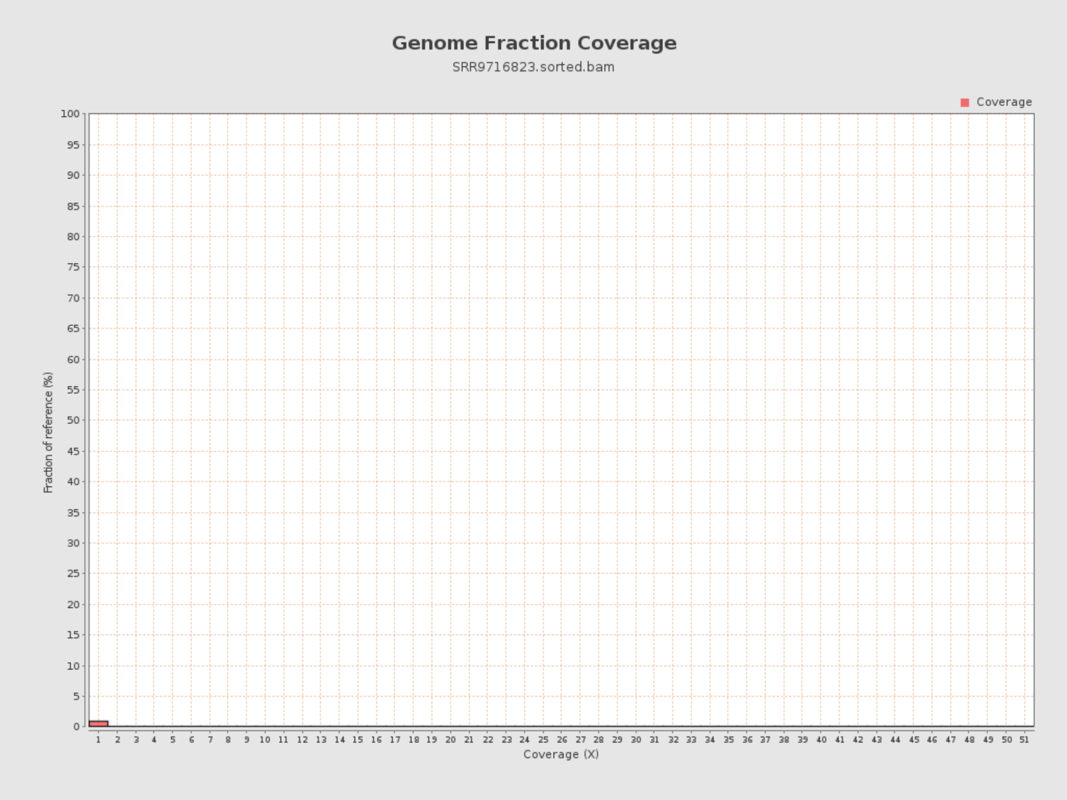
# 4. Results : Coverage Histogram



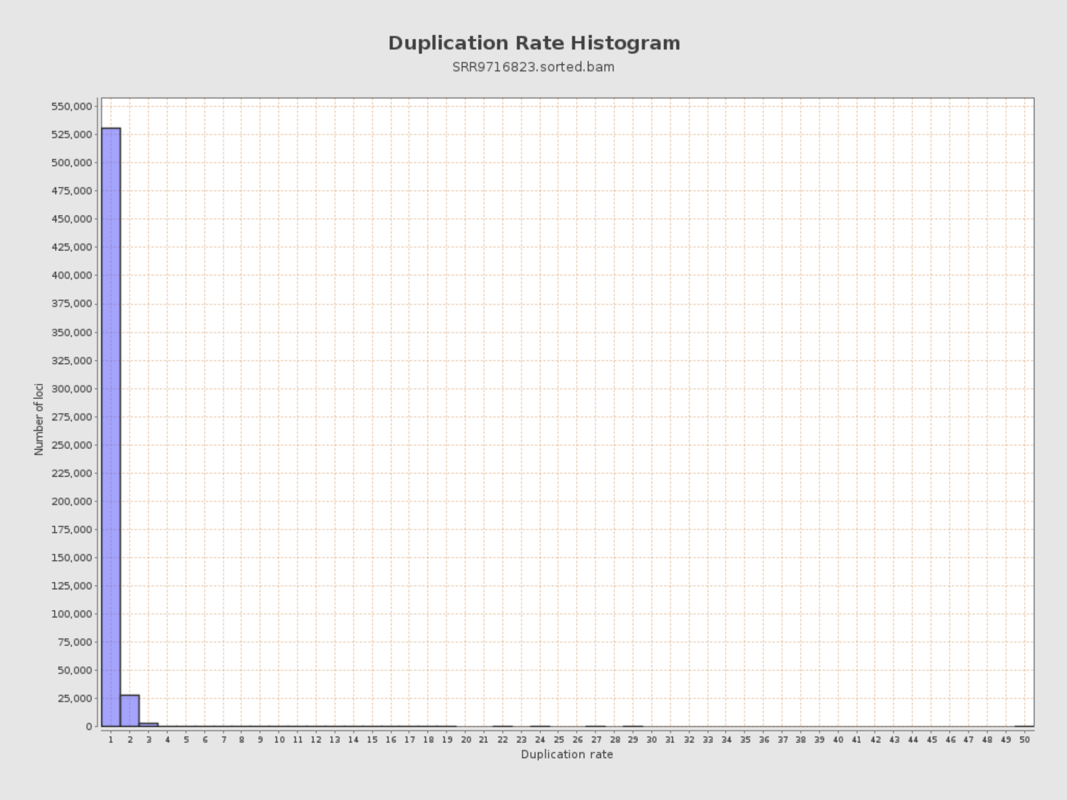
# 5. Results : Coverage Histogram (0-50X)



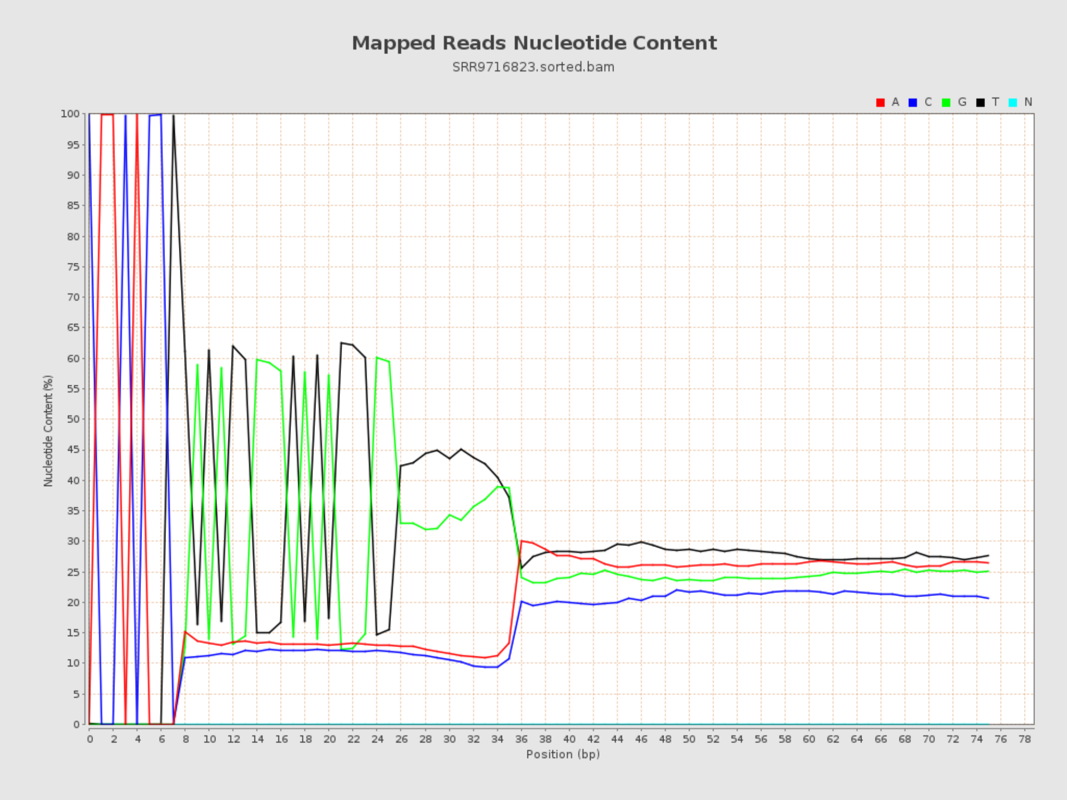
# 6. Results : Genome Fraction Coverage



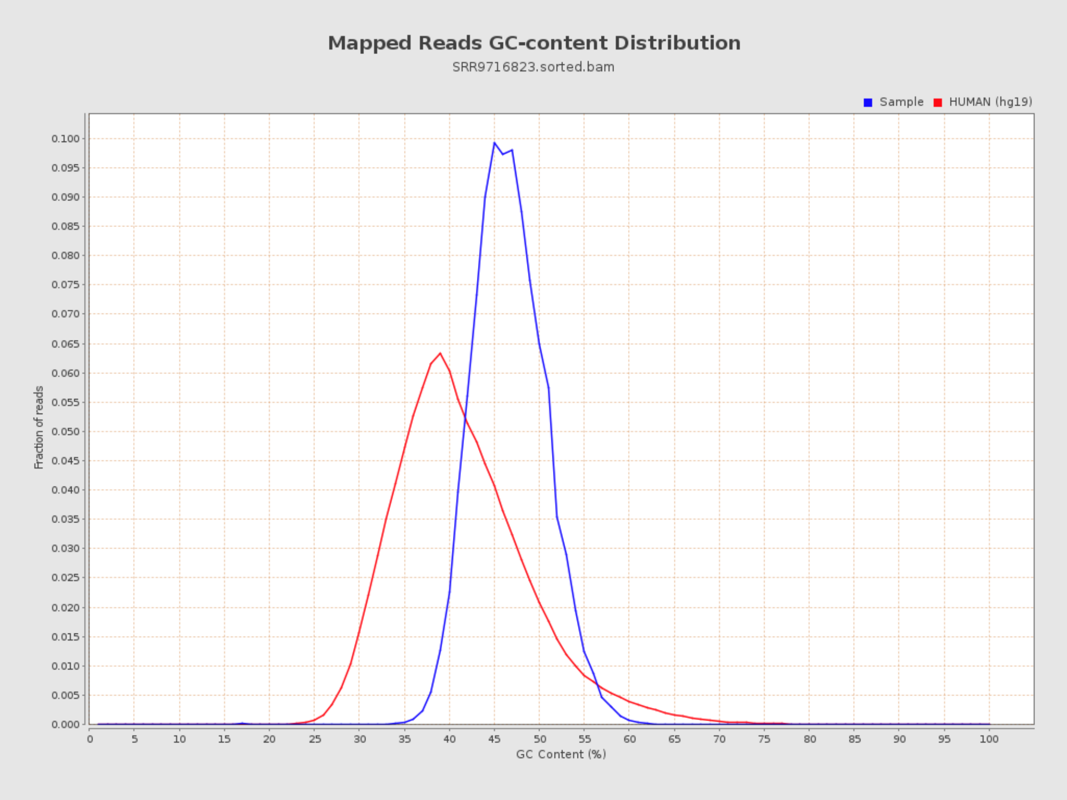
# 7. Results : Duplication Rate Histogram



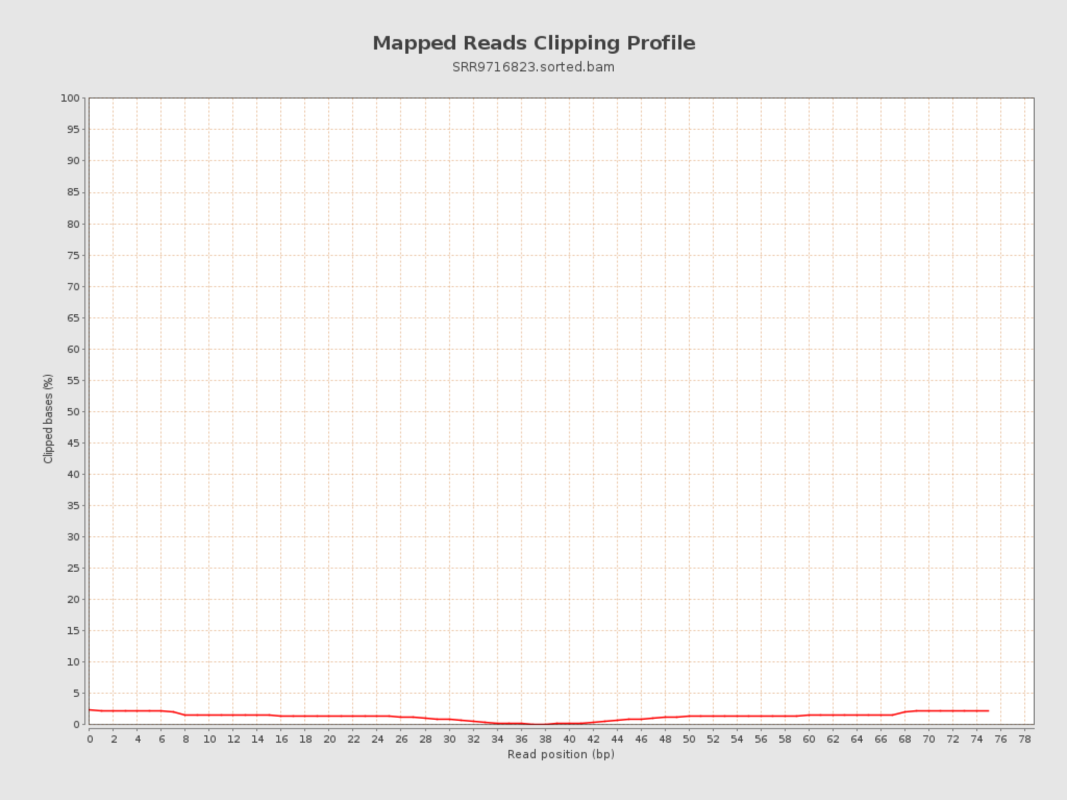
# 8. Results : Mapped Reads Nucleotide Content



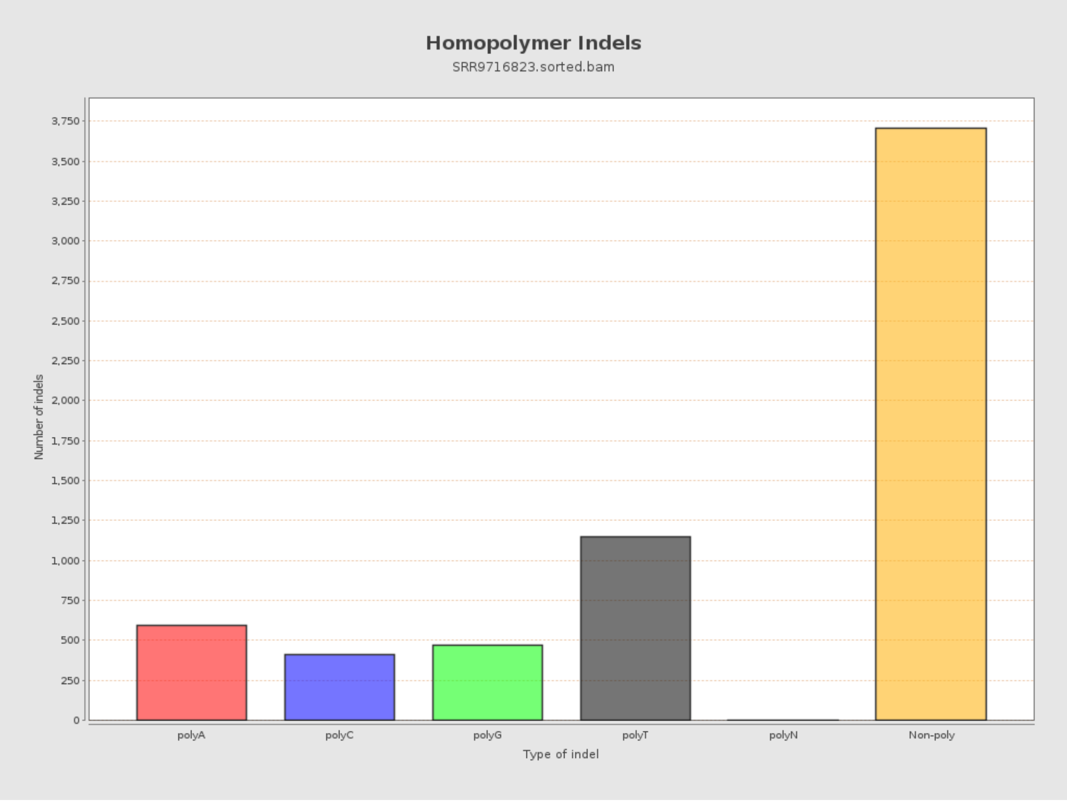
# 9. Results : Mapped Reads GC-content Distribution



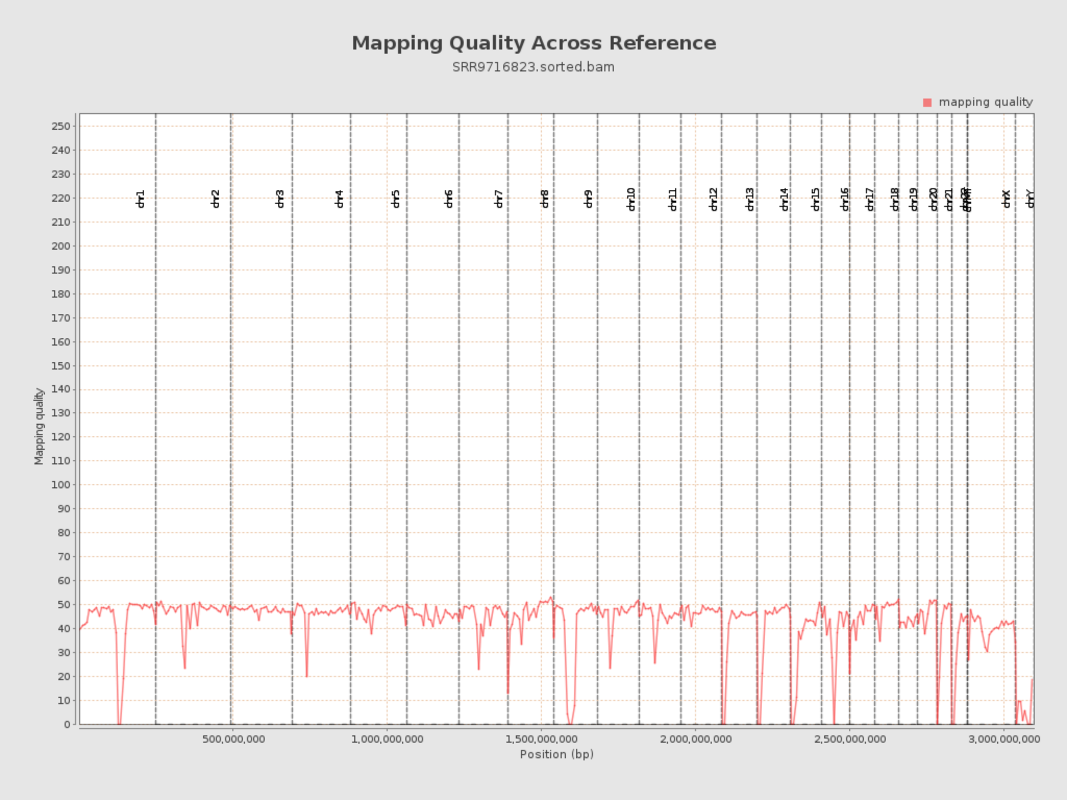
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram