# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/02 20:21:11*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716555.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_SRR9716555 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716555.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 02 20:21:10 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716555.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 635,854 |
| Mapped reads | 576,558 / 90.67% |
| Unmapped reads | 59,296 / 9.33% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 2,157 / 0.34% |
| Read min/max/mean length | 30 / 76 / 76.11 |
| Duplicated reads (estimated) | 8,617 / 1.36% |
| Duplication rate | 1.16% |
| Clipped reads | 577,408 / 90.81% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 7,931,808 / 24.18% |
| Number/percentage of C's | 6,610,186 / 20.15% |
| Number/percentage of T's | 10,033,176 / 30.59% |
| Number/percentage of G's | 8,227,432 / 25.08% |
| Number/percentage of N's | 798 / 0% |
| GC Percentage | 45.23% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0106 |
| | |

| | |
|---|---|
| Standard Deviation | 0.117 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.9 |

## 2.5. Mismatches and indels

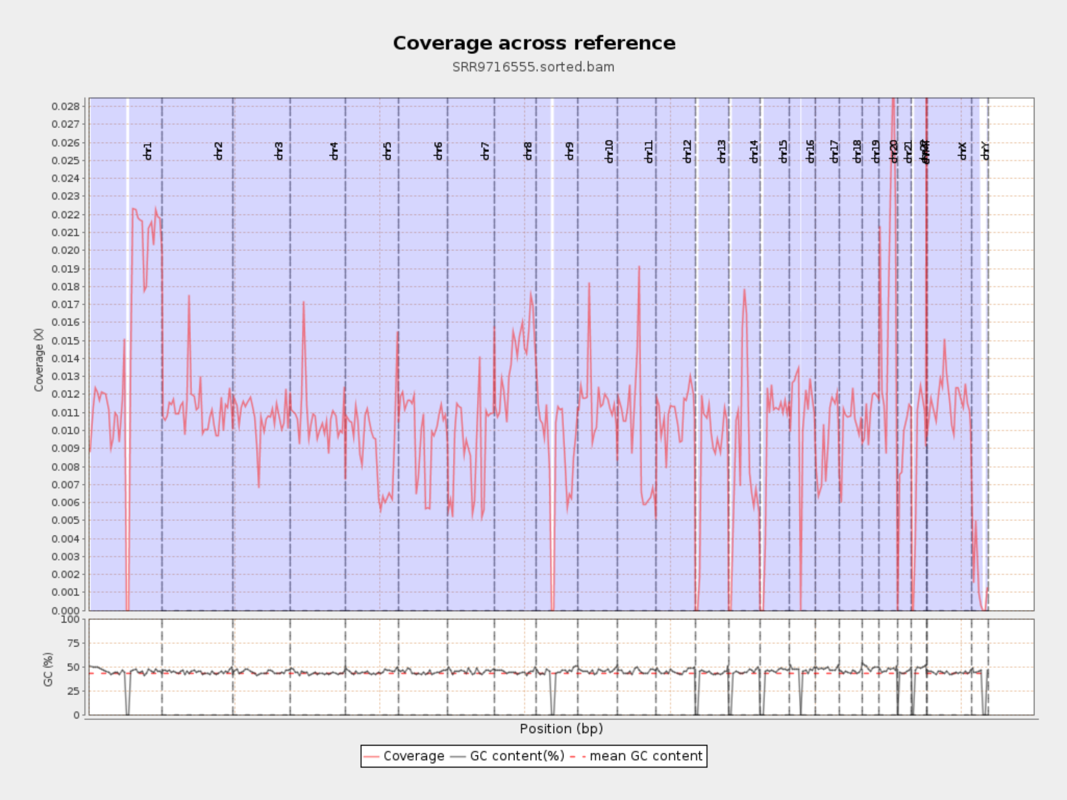
| | |
|---|---|
| General error rate | 0.5% |
| Mismatches | 161,563 |
| Insertions | 2,078 |
| Mapped reads with at least one insertion | 0.36% |
| Deletions | 5,277 |
| Mapped reads with at least one deletion | 0.91% |
| Homopolymer indels | 40.57% |

## 2.6. Chromosome stats

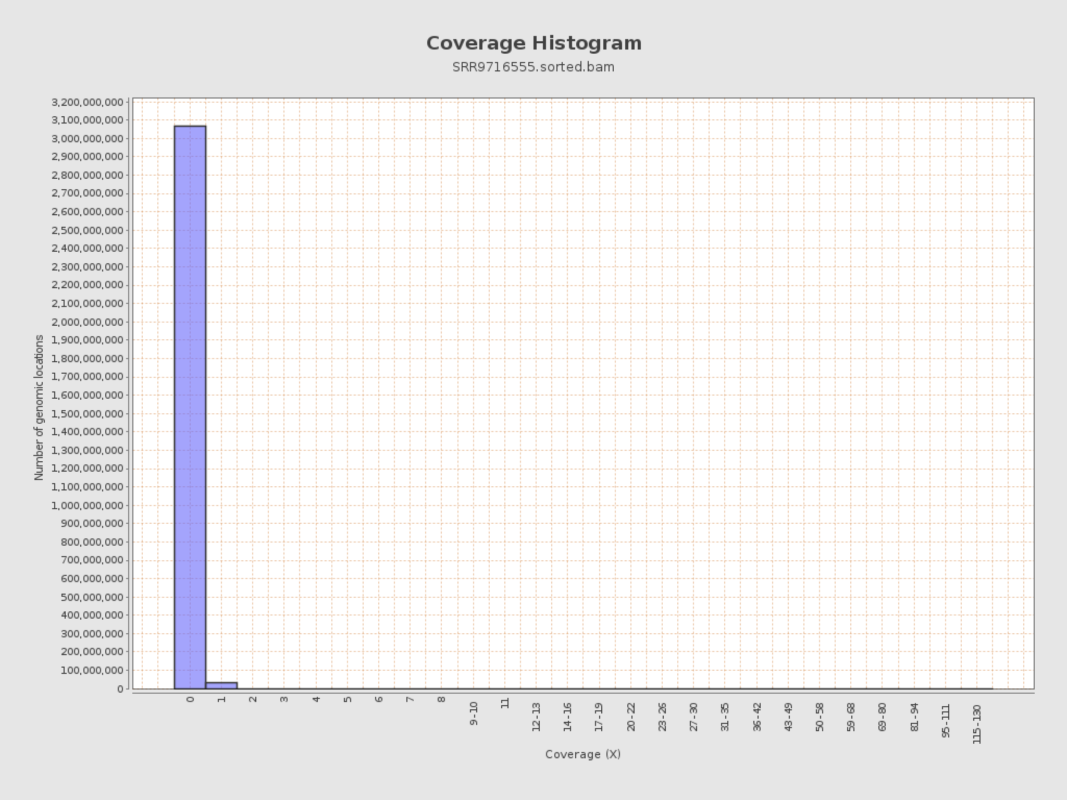
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 3659452 | 0.0147 | 0.1519 |
| chr2 | 243199373 | 2733489 | 0.0112 | 0.1268 |
| chr3 | 198022430 | 2128426 | 0.0107 | 0.1072 |
| chr4 | 191154276 | 2051473 | 0.0107 | 0.1112 |
| chr5 | 180915260 | 1645878 | 0.0091 | 0.0989 |
| chr6 | 171115067 | 1694041 | 0.0099 | 0.1062 |
| chr7 | 159138663 | 1423250 | 0.0089 | 0.1089 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2039553 | 0.0139 | 0.1279 |
| chr9 | 141213431 | 1184765 | 0.0084 | 0.1086 |
| chr10 | 135534747 | 1581526 | 0.0117 | 0.1276 |
| chr11 | 135006516 | 1310080 | 0.0097 | 0.1201 |
| chr12 | 133851895 | 1465930 | 0.011 | 0.1087 |
| chr13 | 115169878 | 982556 | 0.0085 | 0.0955 |
| chr14 | 107349540 | 899622 | 0.0084 | 0.0958 |
| chr15 | 102531392 | 949432 | 0.0093 | 0.0996 |
| chr16 | 90354753 | 989638 | 0.011 | 0.1115 |
| chr17 | 81195210 | 770475 | 0.0095 | 0.1022 |
| chr18 | 78077248 | 796072 | 0.0102 | 0.1692 |
| chr19 | 59128983 | 649409 | 0.011 | 0.1246 |
| chr20 | 63025520 | 1115136 | 0.0177 | 0.1399 |
| chr21 | 48129895 | 422050 | 0.0088 | 0.1026 |
| chr22 | 51304566 | 408364 | 0.008 | 0.0925 |
| chrMT | 16571 | 813 | 0.0491 | 0.2418 |
| chrX | 155270560 | 1818889 | 0.0117 | 0.1179 |
| chrY | 59373566 | 92113 | 0.0016 | 0.048 |

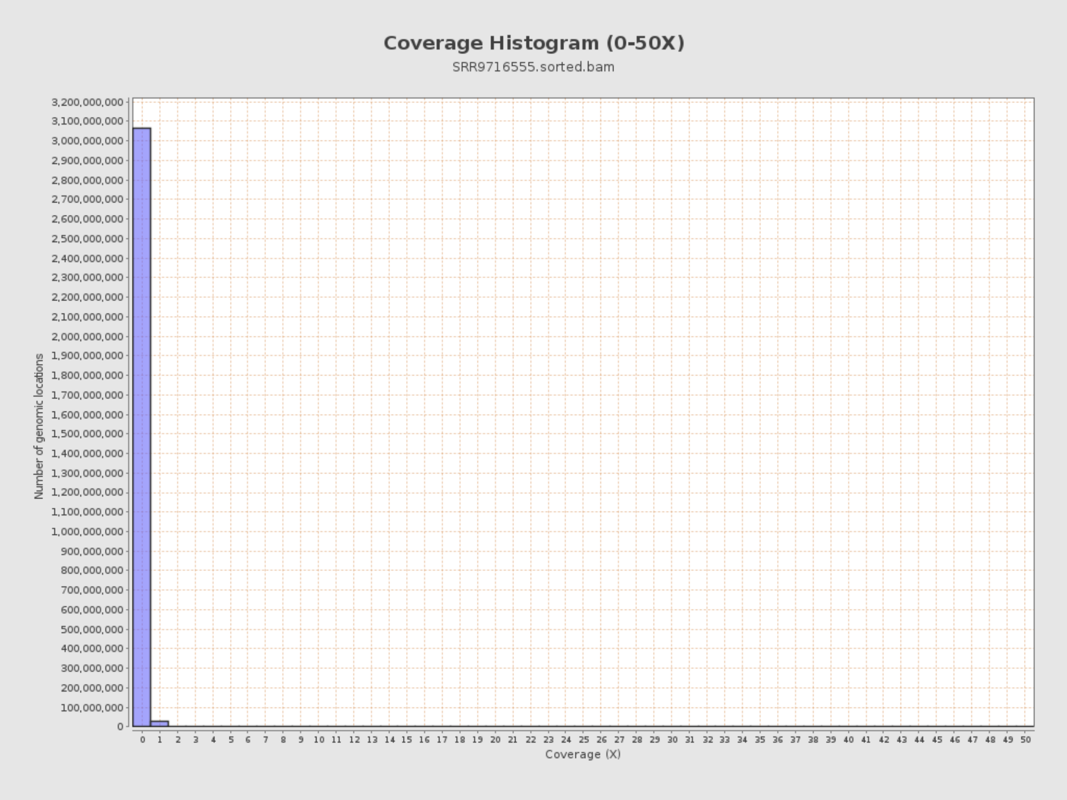
# 3. Results : Coverage across reference



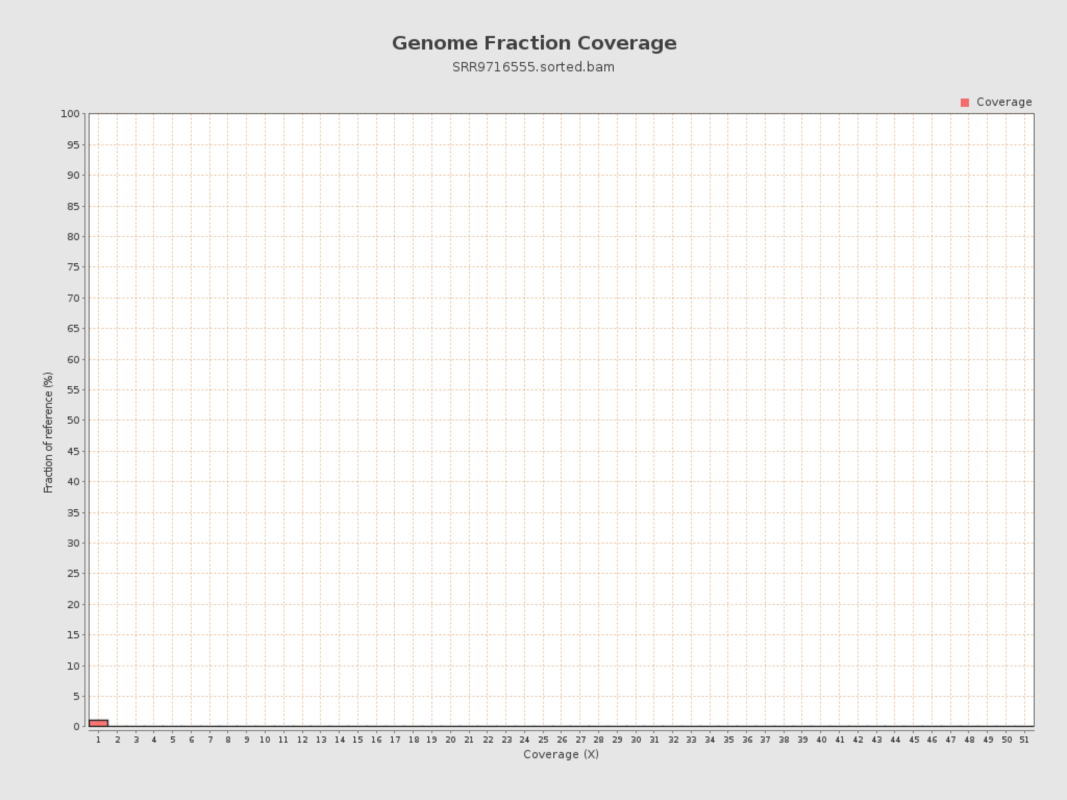
# 4. Results : Coverage Histogram



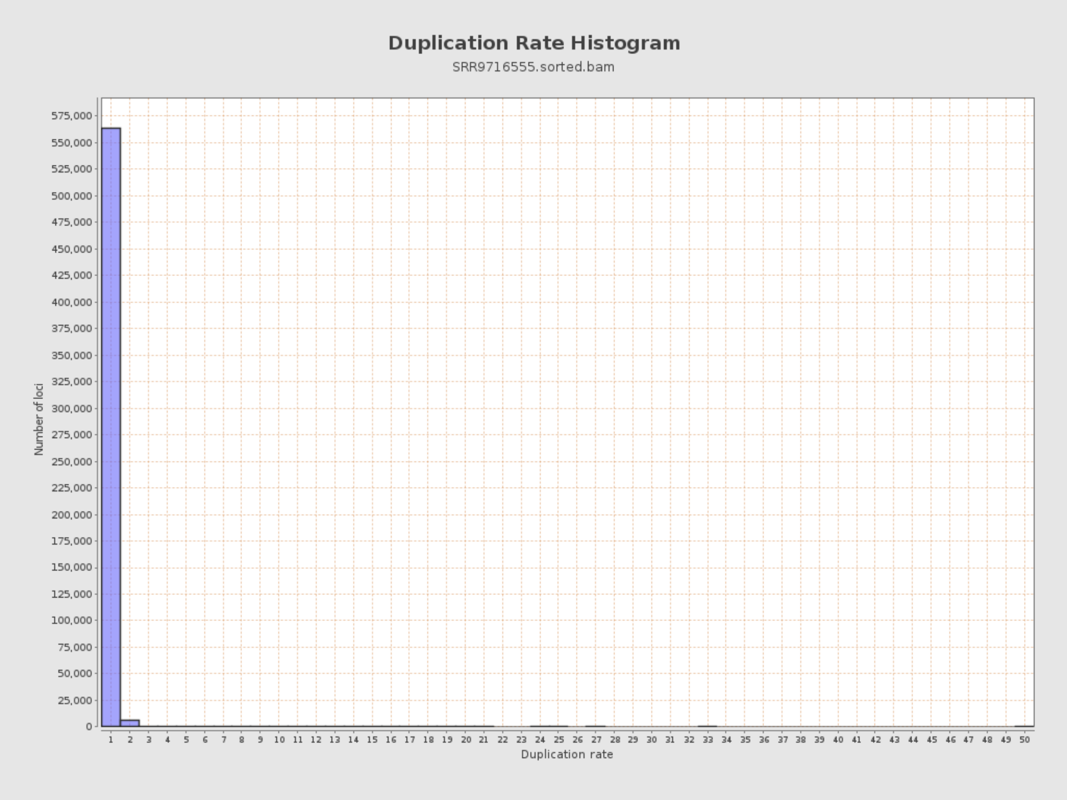
# 5. Results : Coverage Histogram (0-50X)



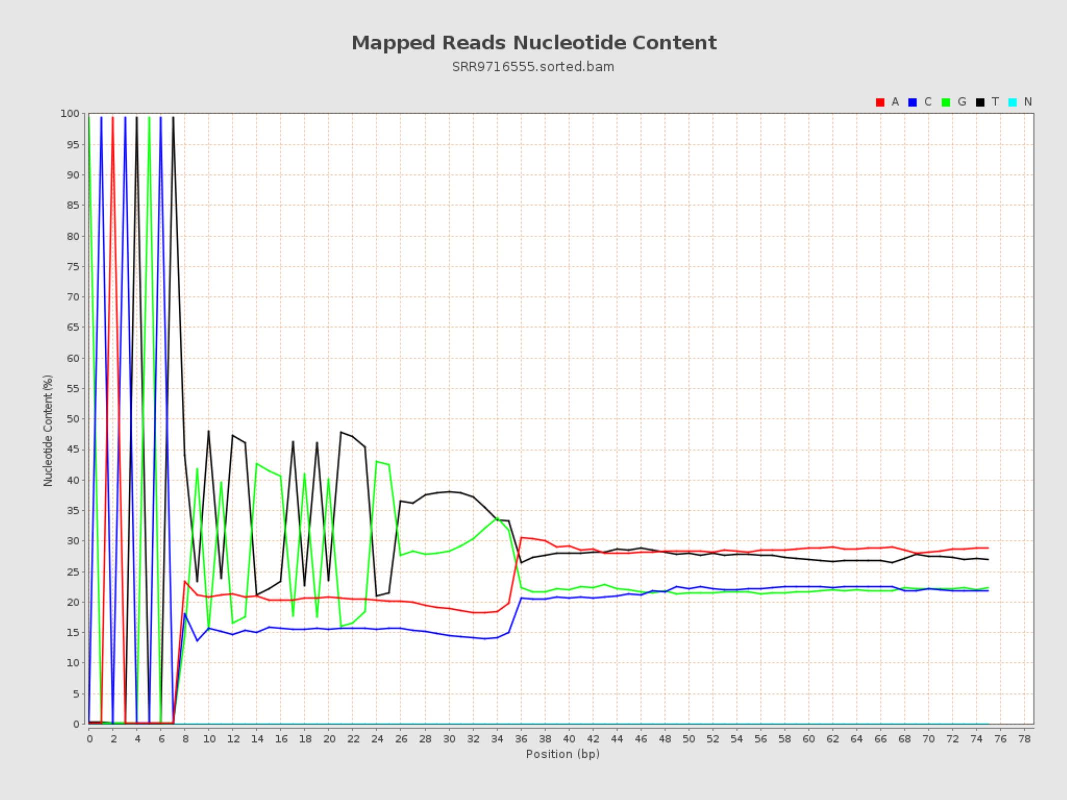
# 6. Results : Genome Fraction Coverage



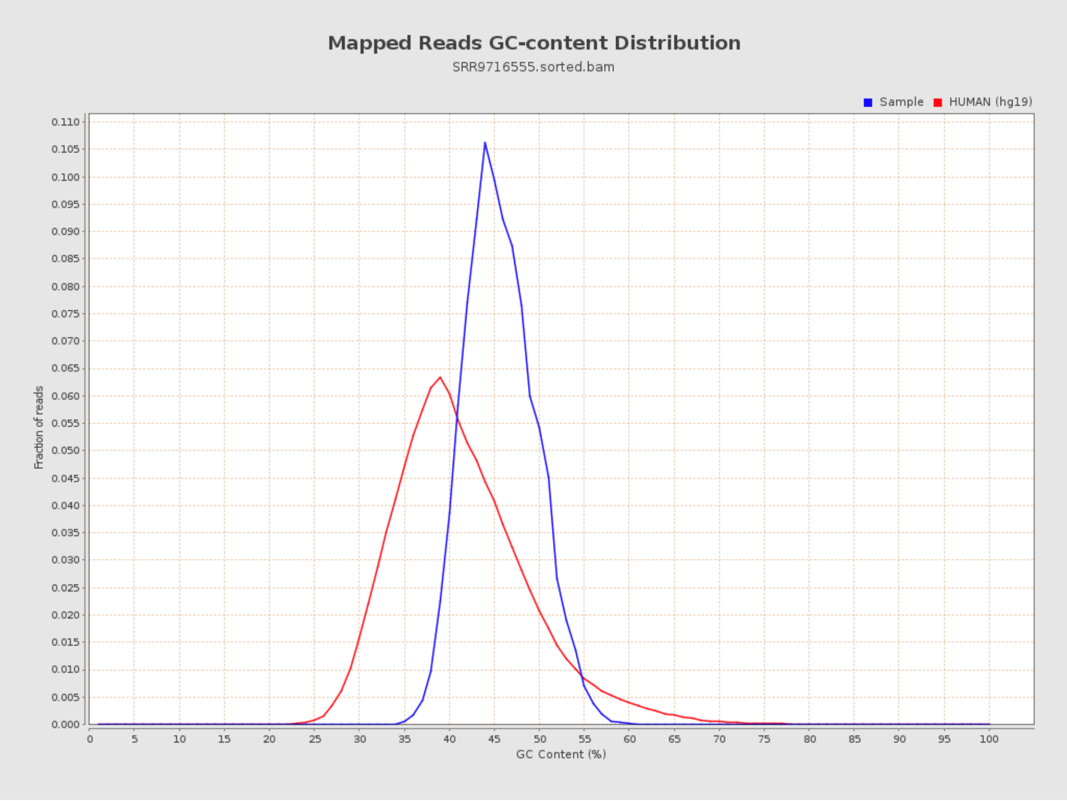
# 7. Results : Duplication Rate Histogram



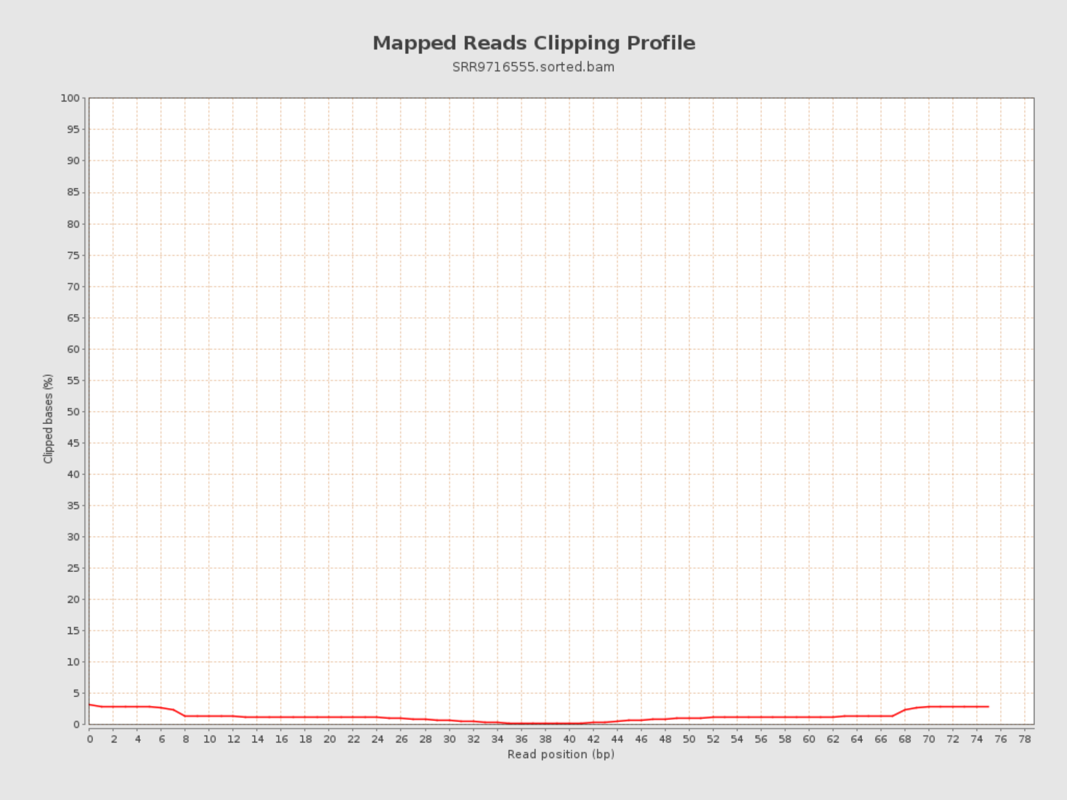
# 8. Results : Mapped Reads Nucleotide Content



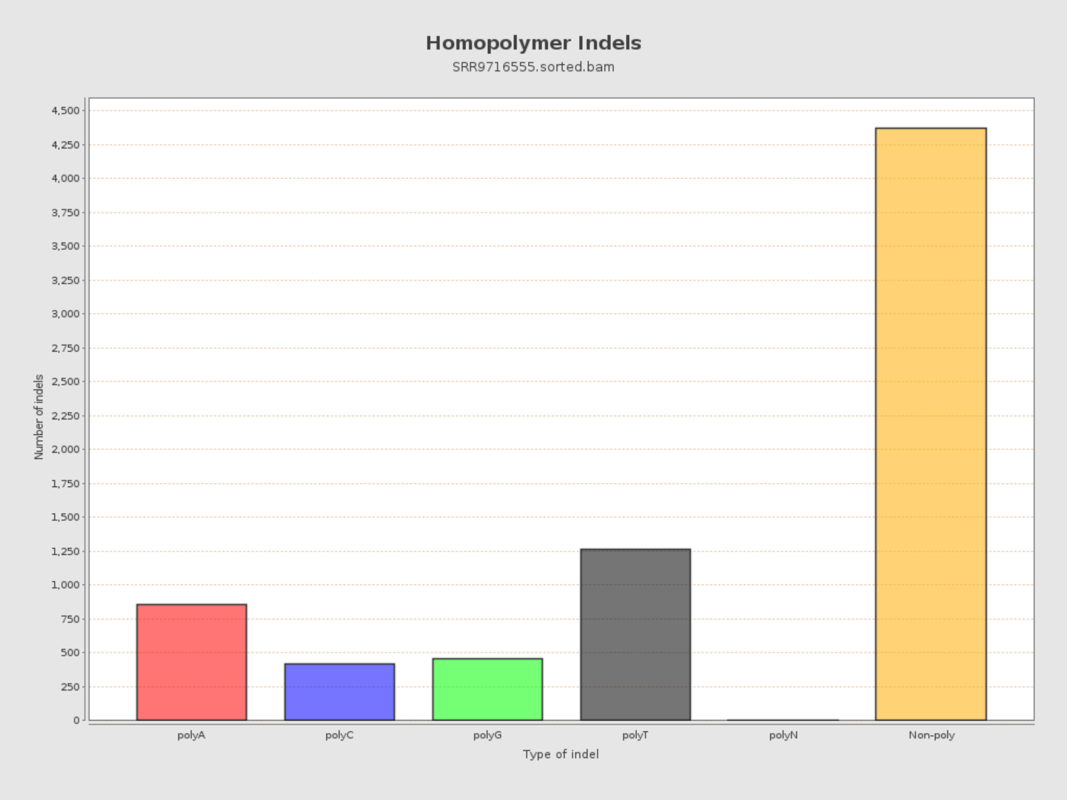
# 9. Results : Mapped Reads GC-content Distribution



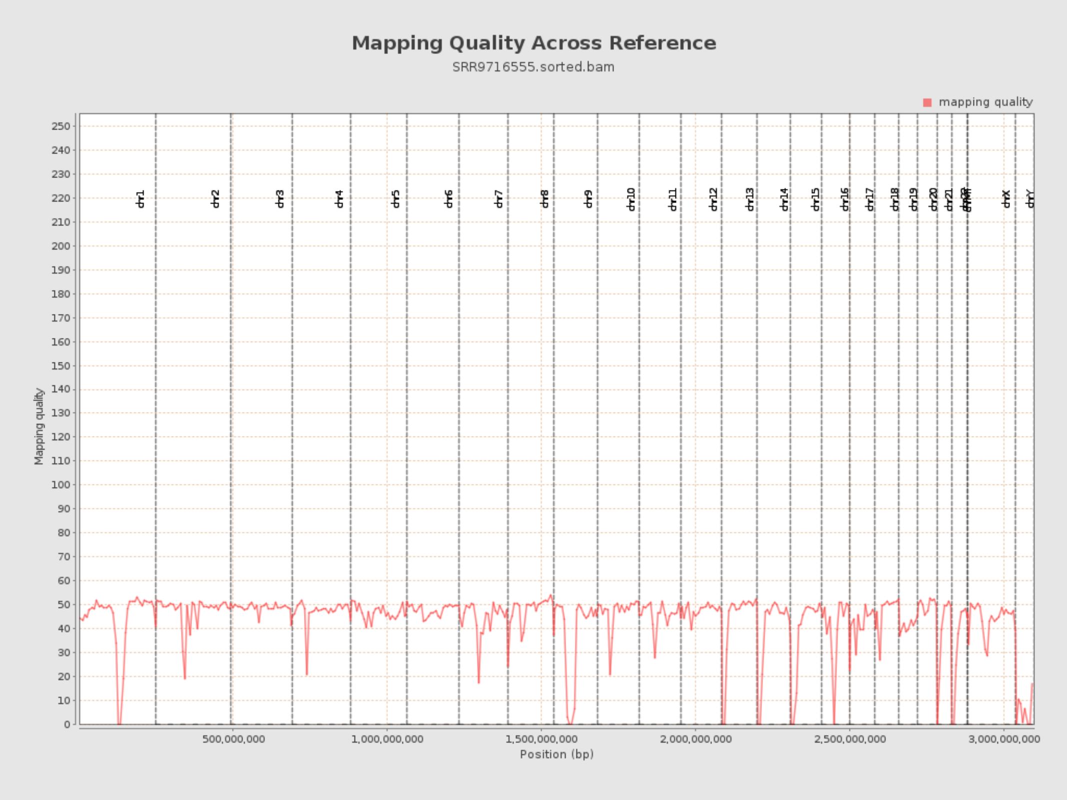
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram