# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/02 08:02:45*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716332.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_SRR9716332 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716332.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 02 08:02:45 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716332.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 996,179 |
| Mapped reads | 875,669 / 87.9% |
| Unmapped reads | 120,510 / 12.1% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 3,237 / 0.32% |
| Read min/max/mean length | 30 / 76 / 76.11 |
| Duplicated reads (estimated) | 24,893 / 2.5% |
| Duplication rate | 2.14% |
| Clipped reads | 875,955 / 87.93% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 11,859,478 / 24.09% |
| Number/percentage of C's | 9,301,753 / 18.89% |
| Number/percentage of T's | 16,380,568 / 33.27% |
| Number/percentage of G's | 11,687,919 / 23.74% |
| Number/percentage of N's | 743 / 0% |
| GC Percentage | 42.64% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0159 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1773 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.77 |

## 2.5. Mismatches and indels

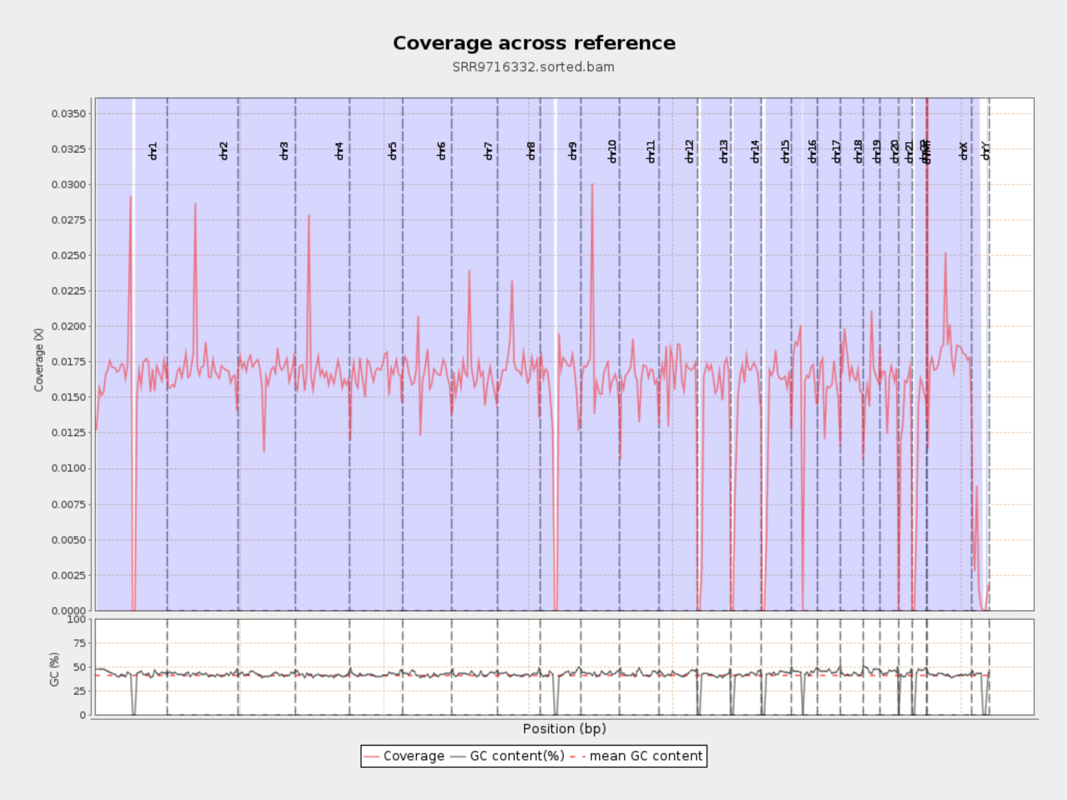
| | |
|---|---|
| General error rate | 0.57% |
| Mismatches | 273,534 |
| Insertions | 3,678 |
| Mapped reads with at least one insertion | 0.42% |
| Deletions | 8,829 |
| Mapped reads with at least one deletion | 1% |
| Homopolymer indels | 40.75% |

## 2.6. Chromosome stats

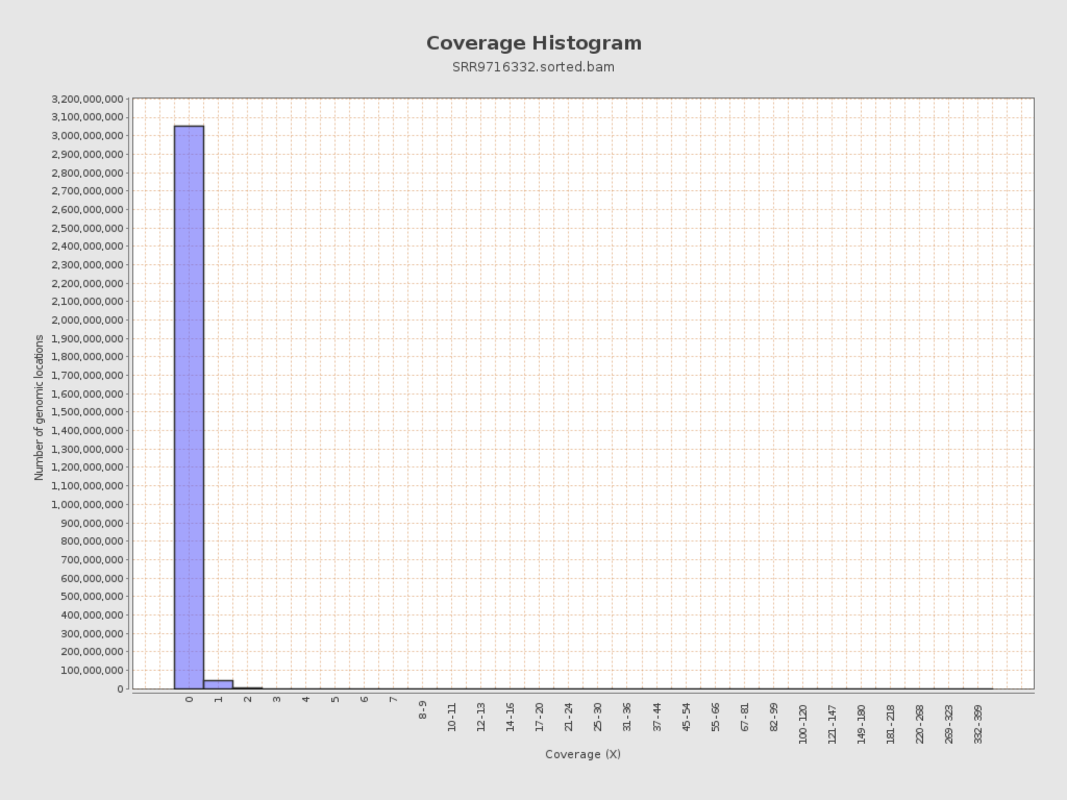
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 3963859 | 0.0159 | 0.3227 |
| chr2 | 243199373 | 4167909 | 0.0171 | 0.1805 |
| chr3 | 198022430 | 3347168 | 0.0169 | 0.1365 |
| chr4 | 191154276 | 3241668 | 0.017 | 0.1445 |
| chr5 | 180915260 | 3038144 | 0.0168 | 0.1367 |
| chr6 | 171115067 | 2854370 | 0.0167 | 0.1459 |
| chr7 | 159138663 | 2639424 | 0.0166 | 0.1778 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2524653 | 0.0172 | 0.1875 |
| chr9 | 141213431 | 2087816 | 0.0148 | 0.1709 |
| chr10 | 135534747 | 2315907 | 0.0171 | 0.178 |
| chr11 | 135006516 | 2212367 | 0.0164 | 0.1622 |
| chr12 | 133851895 | 2259757 | 0.0169 | 0.1406 |
| chr13 | 115169878 | 1587562 | 0.0138 | 0.1228 |
| chr14 | 107349540 | 1495933 | 0.0139 | 0.1332 |
| chr15 | 102531392 | 1374013 | 0.0134 | 0.1213 |
| chr16 | 90354753 | 1411658 | 0.0156 | 0.1406 |
| chr17 | 81195210 | 1273188 | 0.0157 | 0.1357 |
| chr18 | 78077248 | 1328260 | 0.017 | 0.271 |
| chr19 | 59128983 | 966692 | 0.0163 | 0.2263 |
| chr20 | 63025520 | 999318 | 0.0159 | 0.1345 |
| chr21 | 48129895 | 644120 | 0.0134 | 0.1293 |
| chr22 | 51304566 | 546113 | 0.0106 | 0.108 |
| chrMT | 16571 | 9417 | 0.5683 | 0.8117 |
| chrX | 155270560 | 2808045 | 0.0181 | 0.158 |
| chrY | 59373566 | 147836 | 0.0025 | 0.0729 |

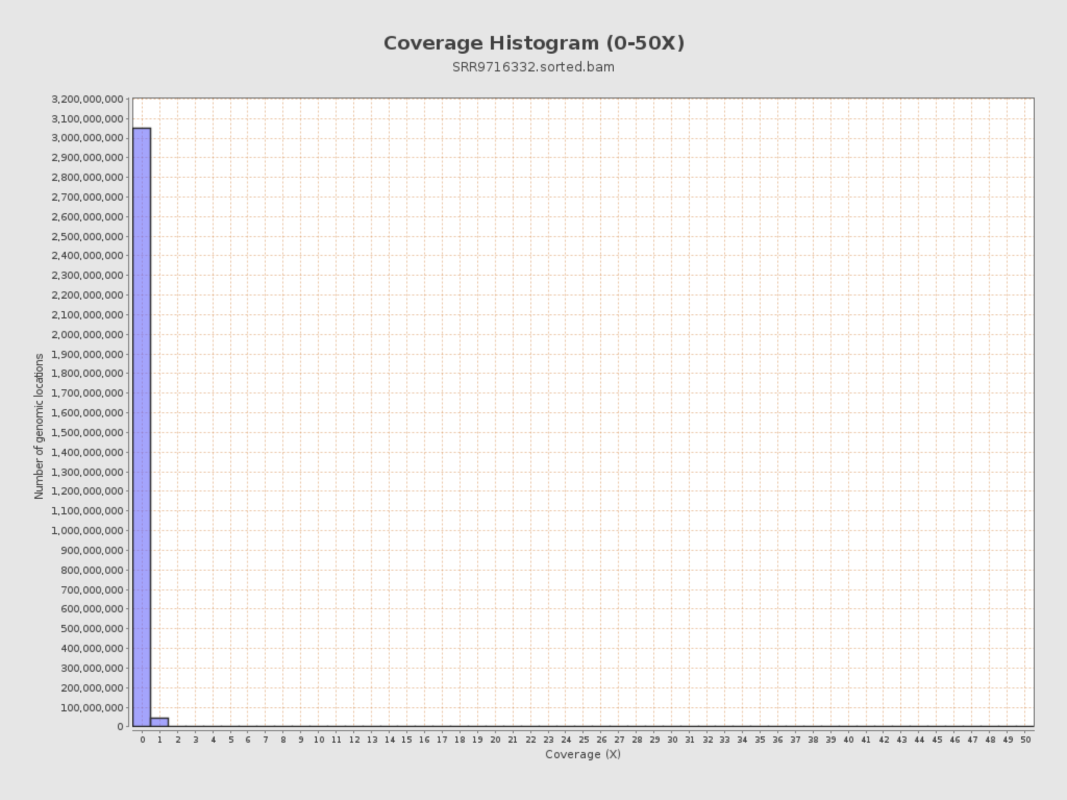
# 3. Results : Coverage across reference



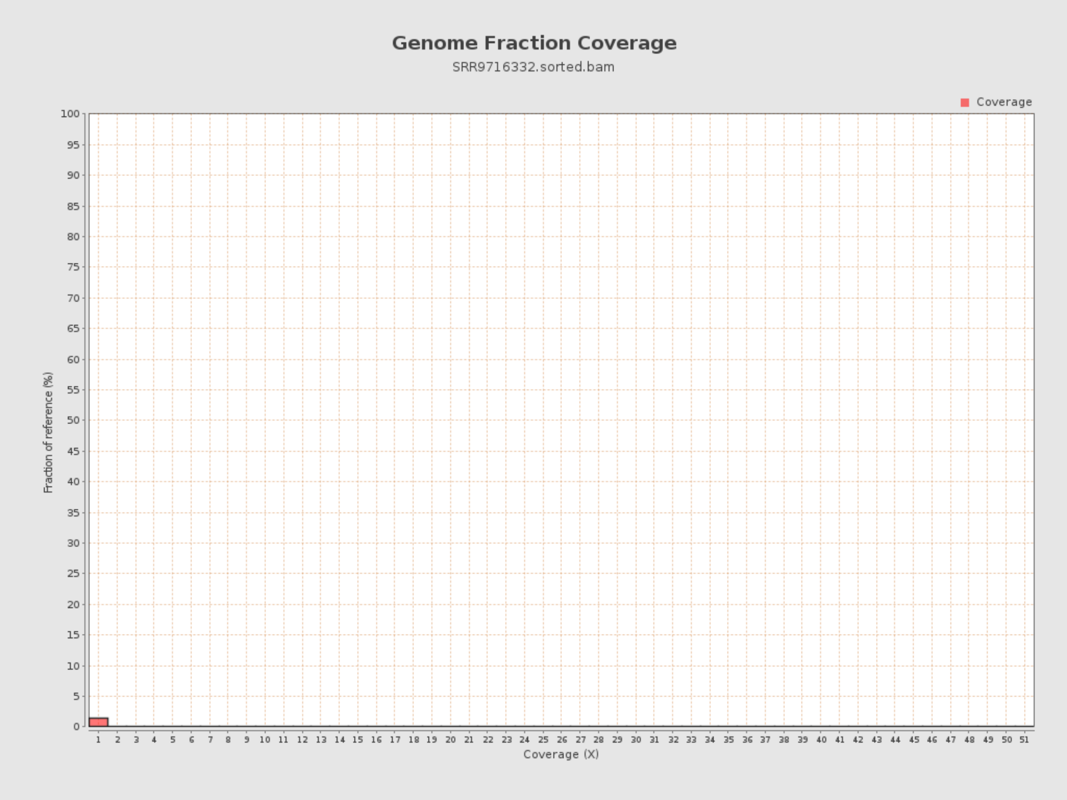
# 4. Results : Coverage Histogram



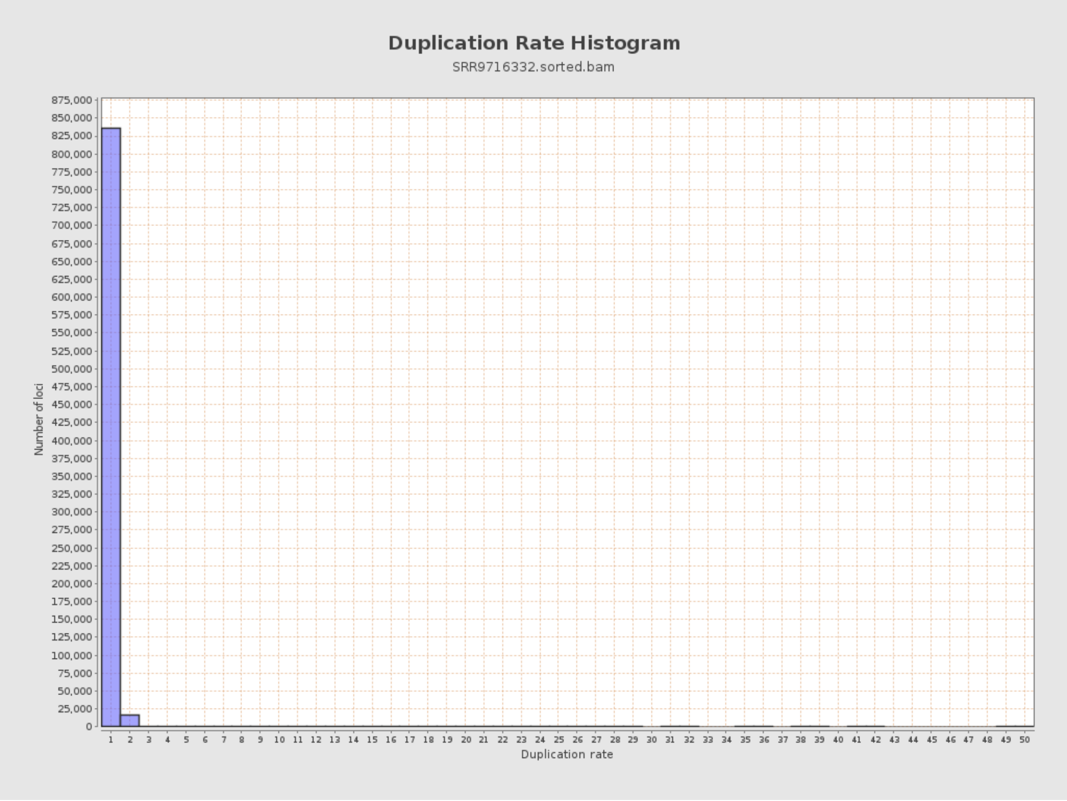
# 5. Results : Coverage Histogram (0-50X)



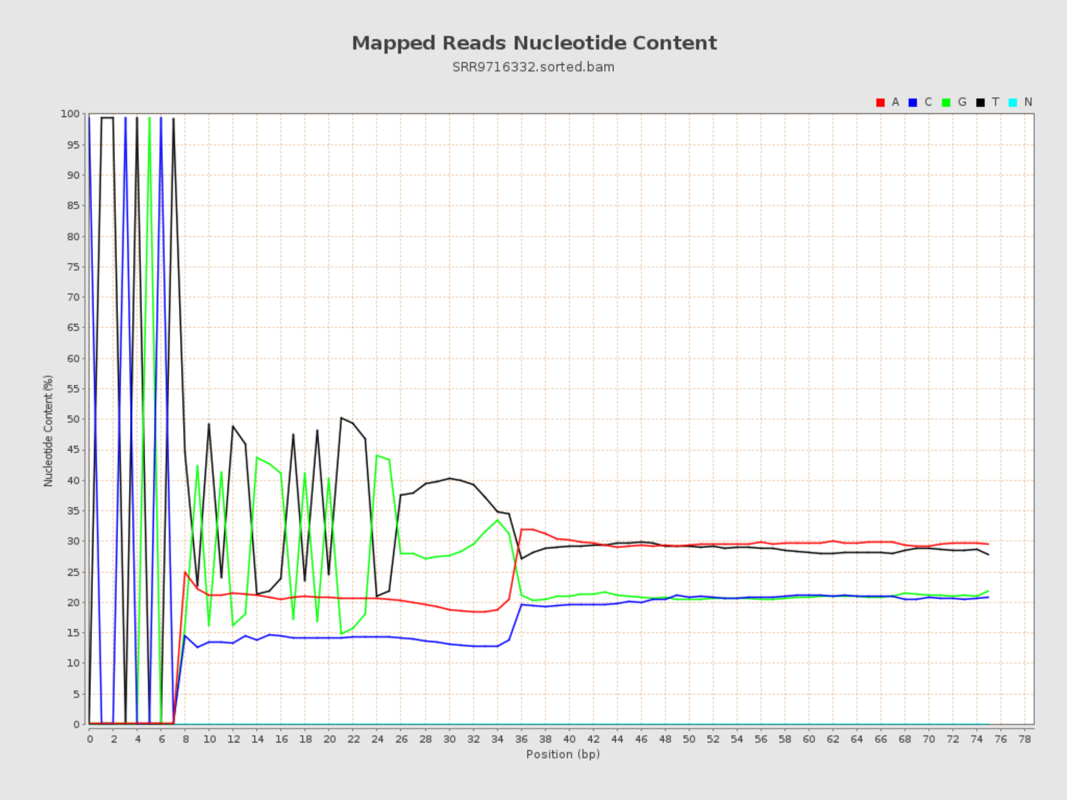
# 6. Results : Genome Fraction Coverage



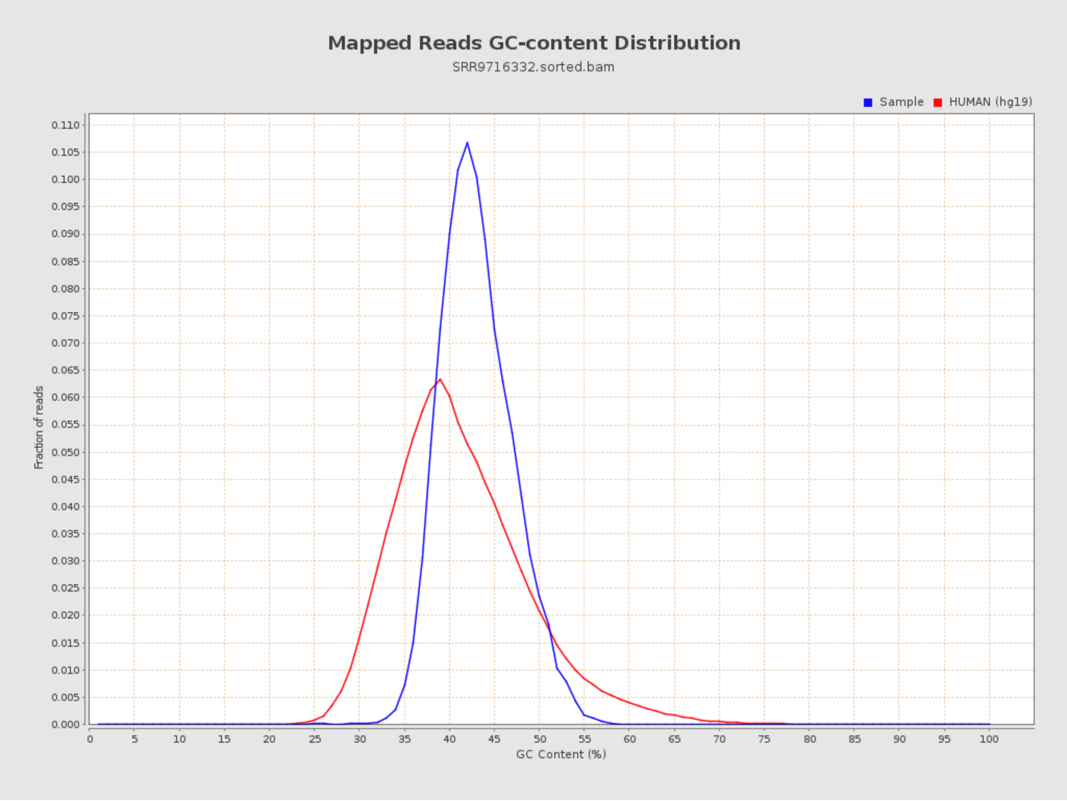
# 7. Results : Duplication Rate Histogram



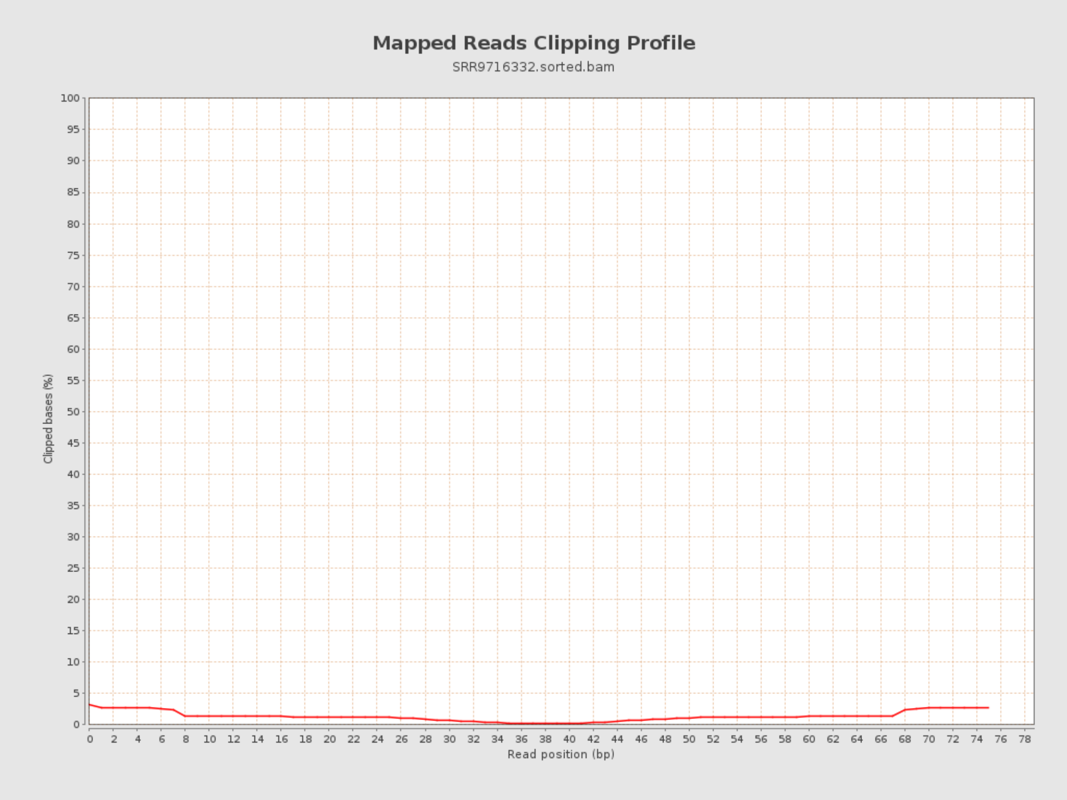
# 8. Results : Mapped Reads Nucleotide Content



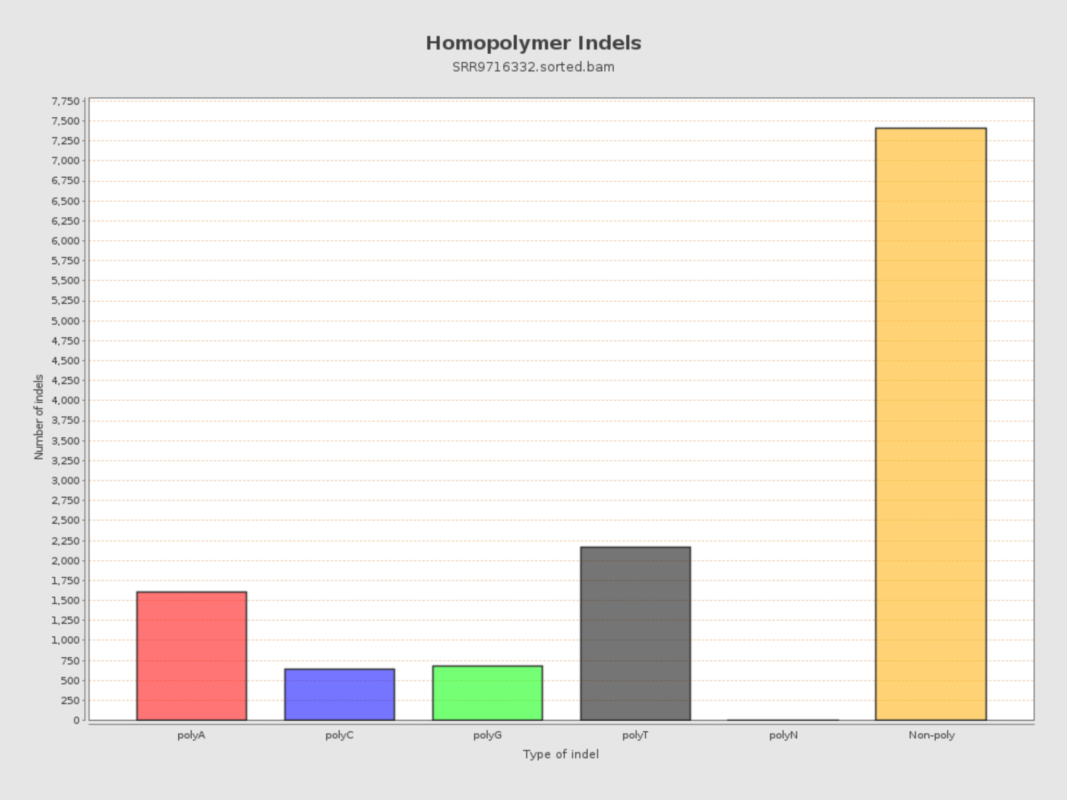
# 9. Results : Mapped Reads GC-content Distribution



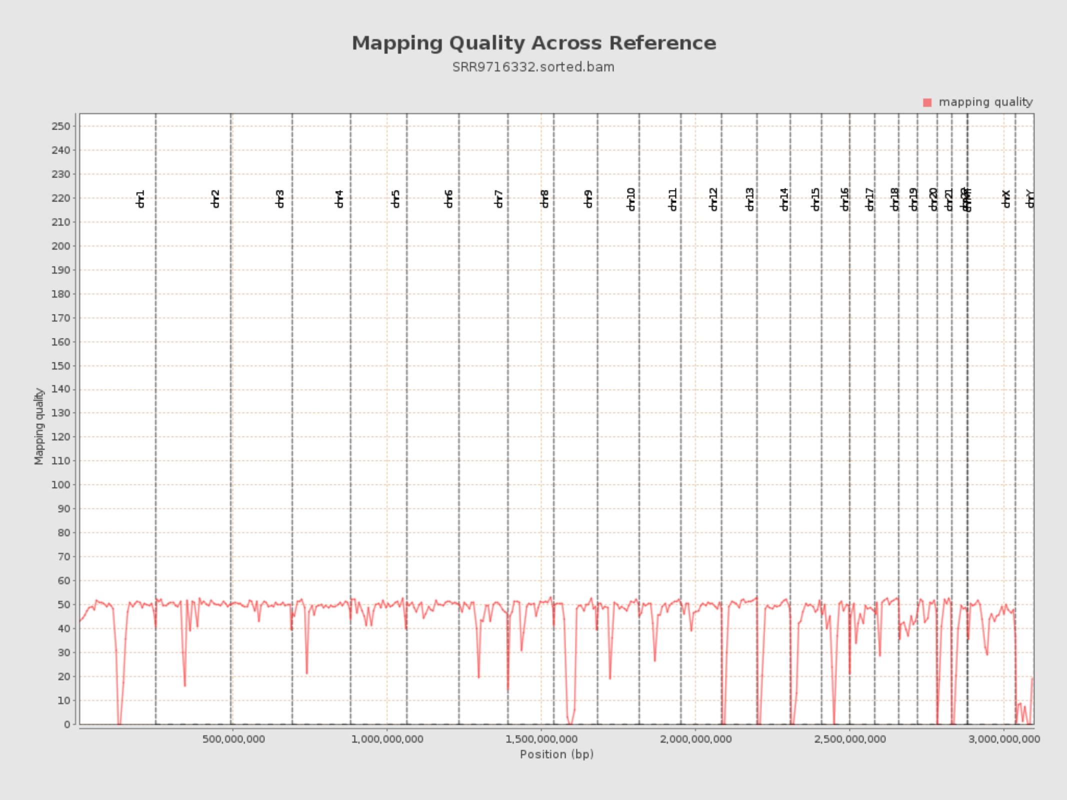
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram