# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/02 13:15:47*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716435.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_SRR9716435 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716435.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 02 13:15:47 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716435.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,598,019 |
| Mapped reads | 1,389,245 / 86.94% |
| Unmapped reads | 208,774 / 13.06% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 7,324 / 0.46% |
| Read min/max/mean length | 30 / 76 / 76.15 |
| Duplicated reads (estimated) | 36,513 / 2.28% |
| Duplication rate | 1.82% |
| Clipped reads | 1,392,431 / 87.13% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 20,489,264 / 25.93% |
| Number/percentage of C's | 15,616,584 / 19.77% |
| Number/percentage of T's | 24,609,112 / 31.15% |
| Number/percentage of G's | 18,290,864 / 23.15% |
| Number/percentage of N's | 1,171 / 0% |
| GC Percentage | 42.92% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0255 |
| | |

| | |
|---|---|
| Standard Deviation | 0.251 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.38 |

## 2.5. Mismatches and indels

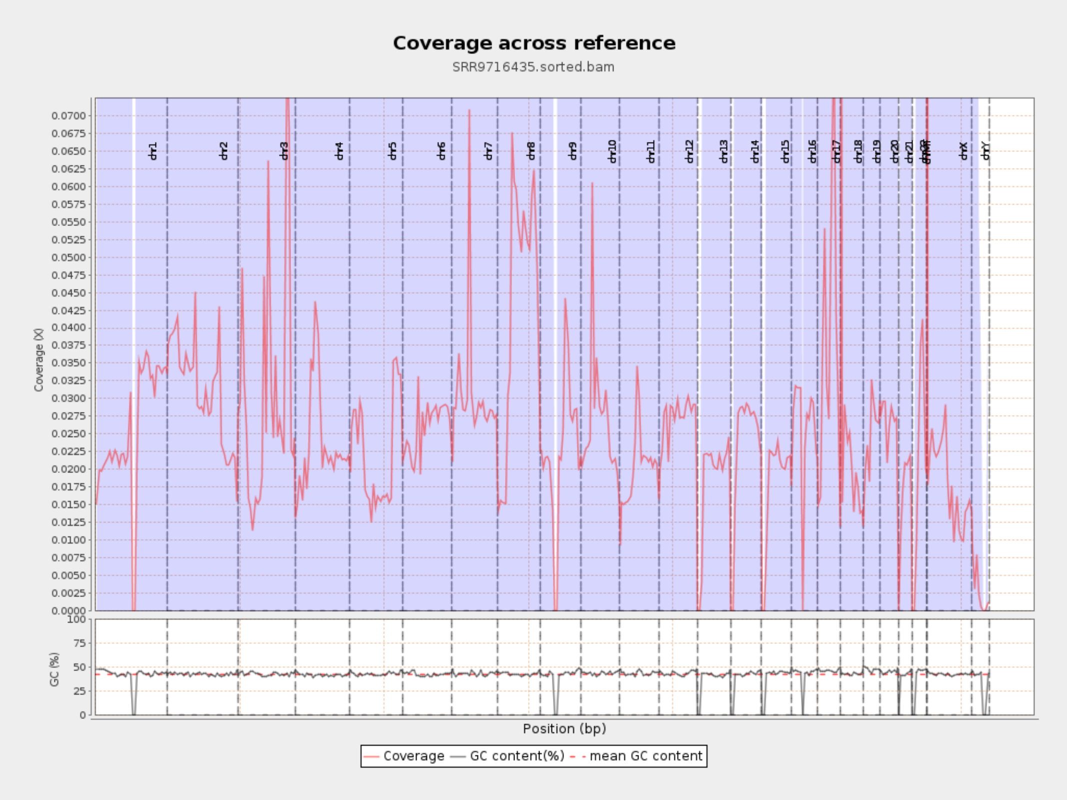
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 394,048 |
| Insertions | 6,602 |
| Mapped reads with at least one insertion | 0.47% |
| Deletions | 15,270 |
| Mapped reads with at least one deletion | 1.09% |
| Homopolymer indels | 40.25% |

## 2.6. Chromosome stats

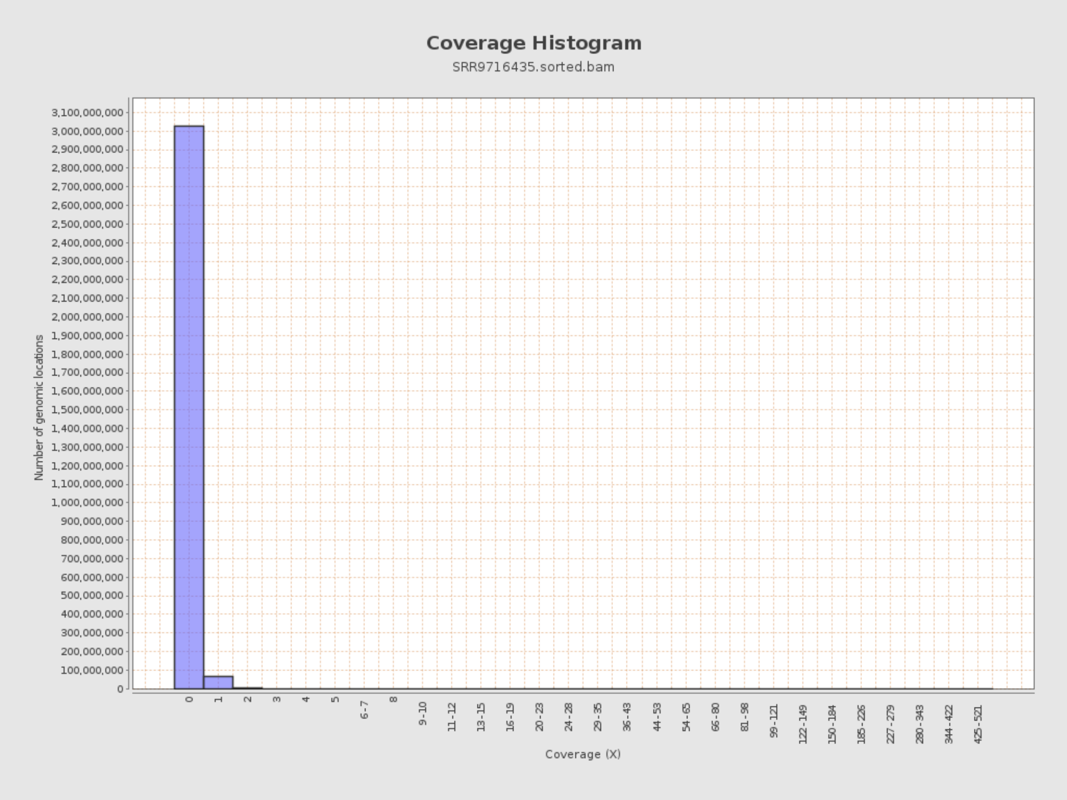
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 6311779 | 0.0253 | 0.2769 |
| chr2 | 243199373 | 7600237 | 0.0313 | 0.3011 |
| chr3 | 198022430 | 6029319 | 0.0304 | 0.2008 |
| chr4 | 191154276 | 4494720 | 0.0235 | 0.1684 |
| chr5 | 180915260 | 4006602 | 0.0221 | 0.161 |
| chr6 | 171115067 | 4437984 | 0.0259 | 0.19 |
| chr7 | 159138663 | 4887633 | 0.0307 | 0.6071 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6431374 | 0.0439 | 0.2606 |
| chr9 | 141213431 | 3167900 | 0.0224 | 0.189 |
| chr10 | 135534747 | 3648188 | 0.0269 | 0.3076 |
| chr11 | 135006516 | 2778643 | 0.0206 | 0.1869 |
| chr12 | 133851895 | 3634689 | 0.0272 | 0.1852 |
| chr13 | 115169878 | 2077724 | 0.018 | 0.1446 |
| chr14 | 107349540 | 2494091 | 0.0232 | 0.17 |
| chr15 | 102531392 | 1815058 | 0.0177 | 0.1462 |
| chr16 | 90354753 | 2285717 | 0.0253 | 0.1806 |
| chr17 | 81195210 | 3119097 | 0.0384 | 0.2186 |
| chr18 | 78077248 | 1817569 | 0.0233 | 0.2726 |
| chr19 | 59128983 | 1469959 | 0.0249 | 0.2729 |
| chr20 | 63025520 | 1667356 | 0.0265 | 0.1773 |
| chr21 | 48129895 | 783473 | 0.0163 | 0.1385 |
| chr22 | 51304566 | 1058527 | 0.0206 | 0.1552 |
| chrMT | 16571 | 51097 | 3.0835 | 2.7888 |
| chrX | 155270560 | 2800729 | 0.018 | 0.1647 |
| chrY | 59373566 | 161366 | 0.0027 | 0.0693 |

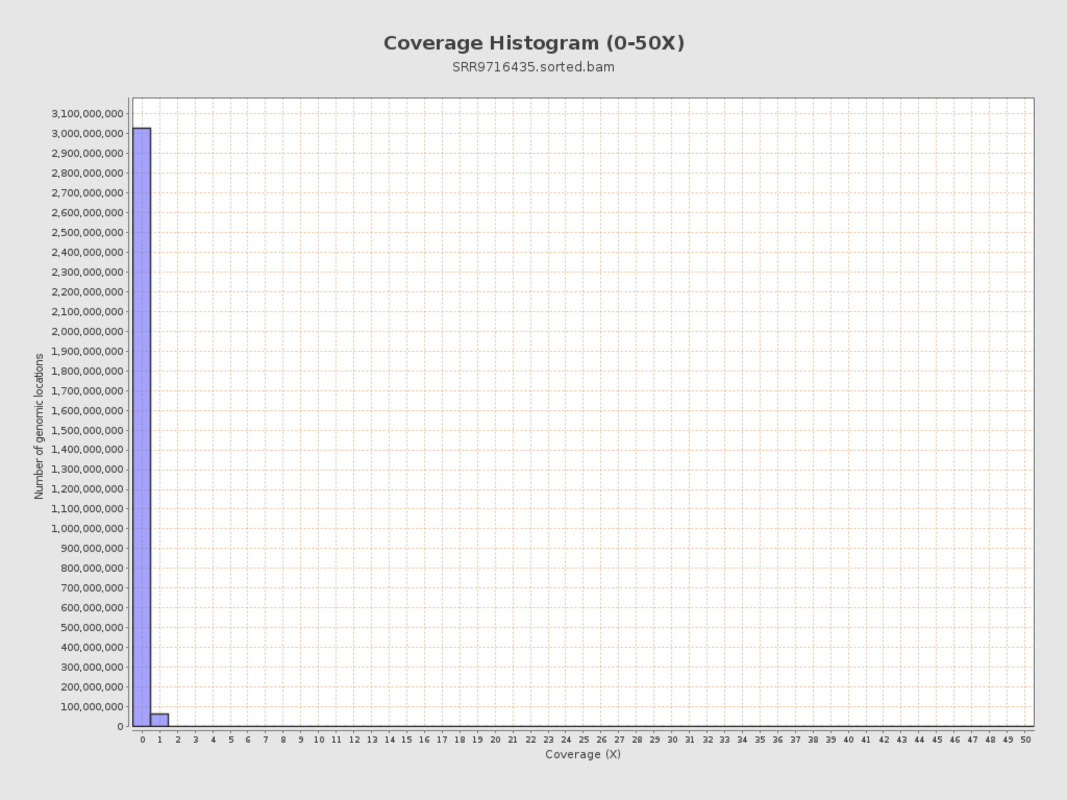
# 3. Results : Coverage across reference



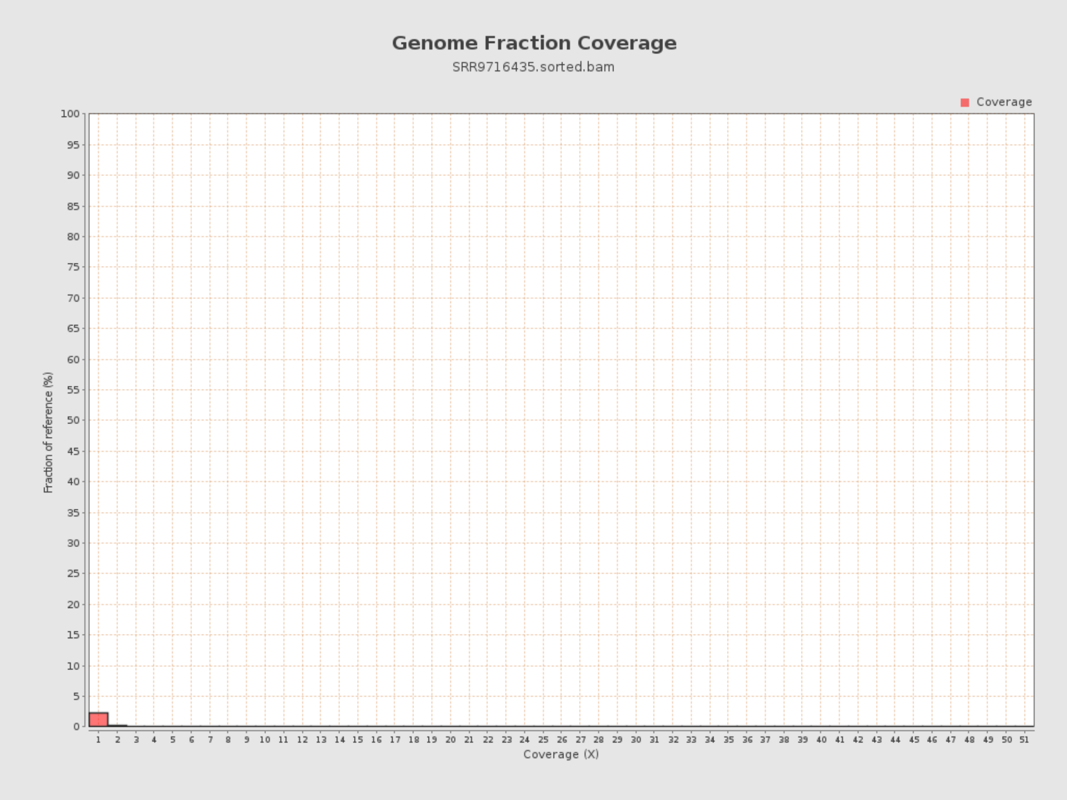
# 4. Results : Coverage Histogram



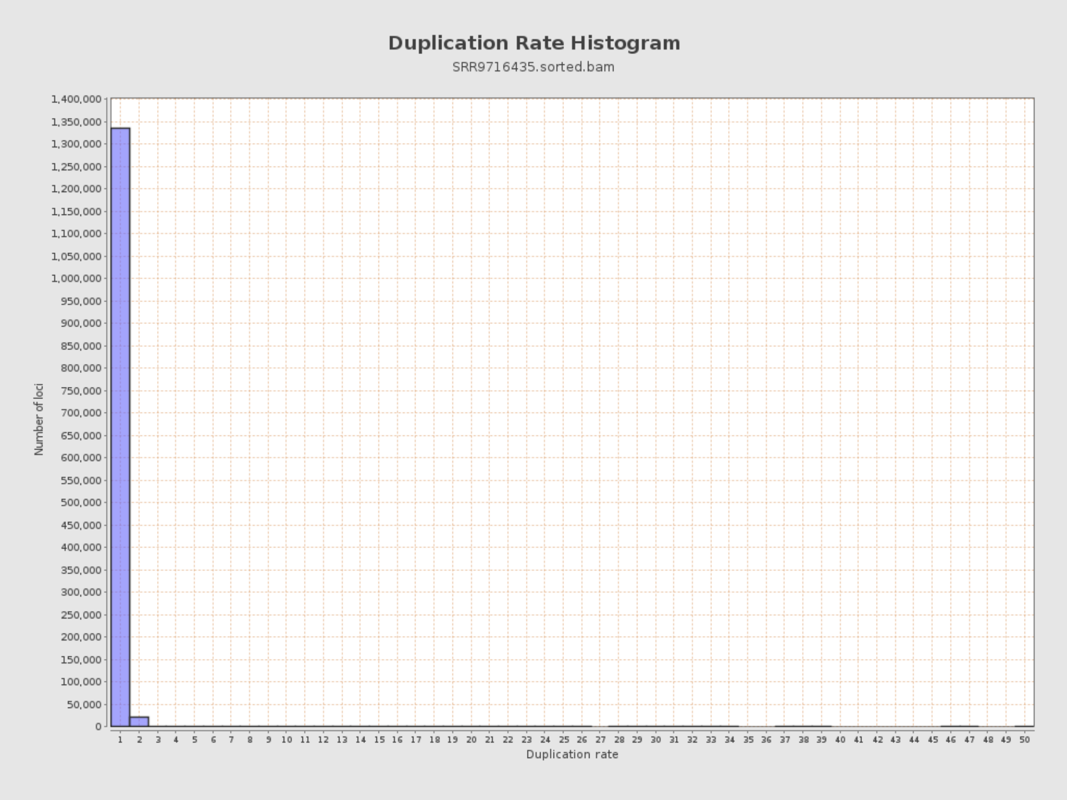
# 5. Results : Coverage Histogram (0-50X)



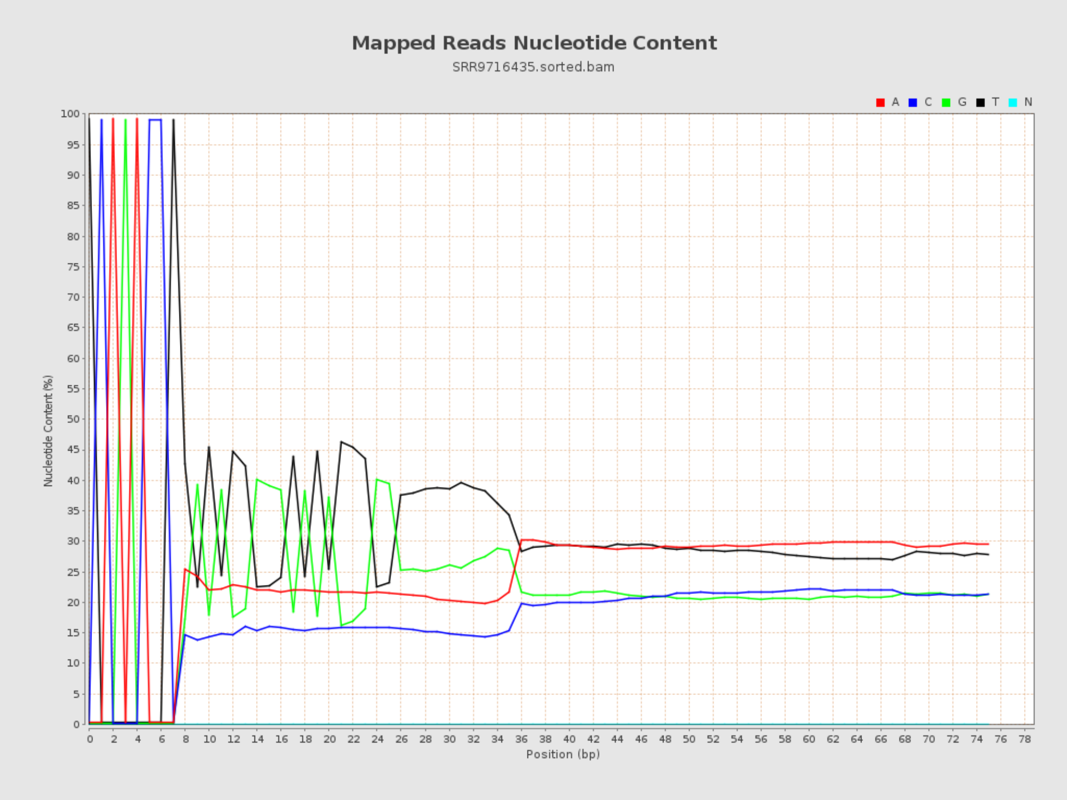
# 6. Results : Genome Fraction Coverage



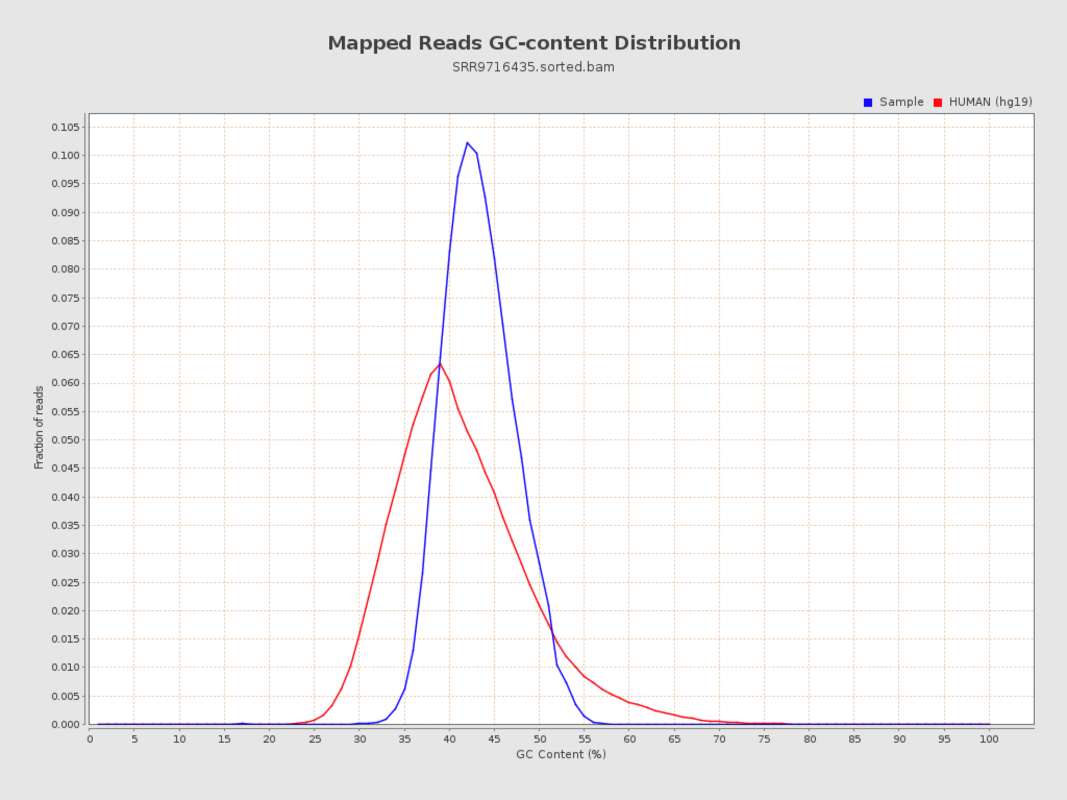
# 7. Results : Duplication Rate Histogram



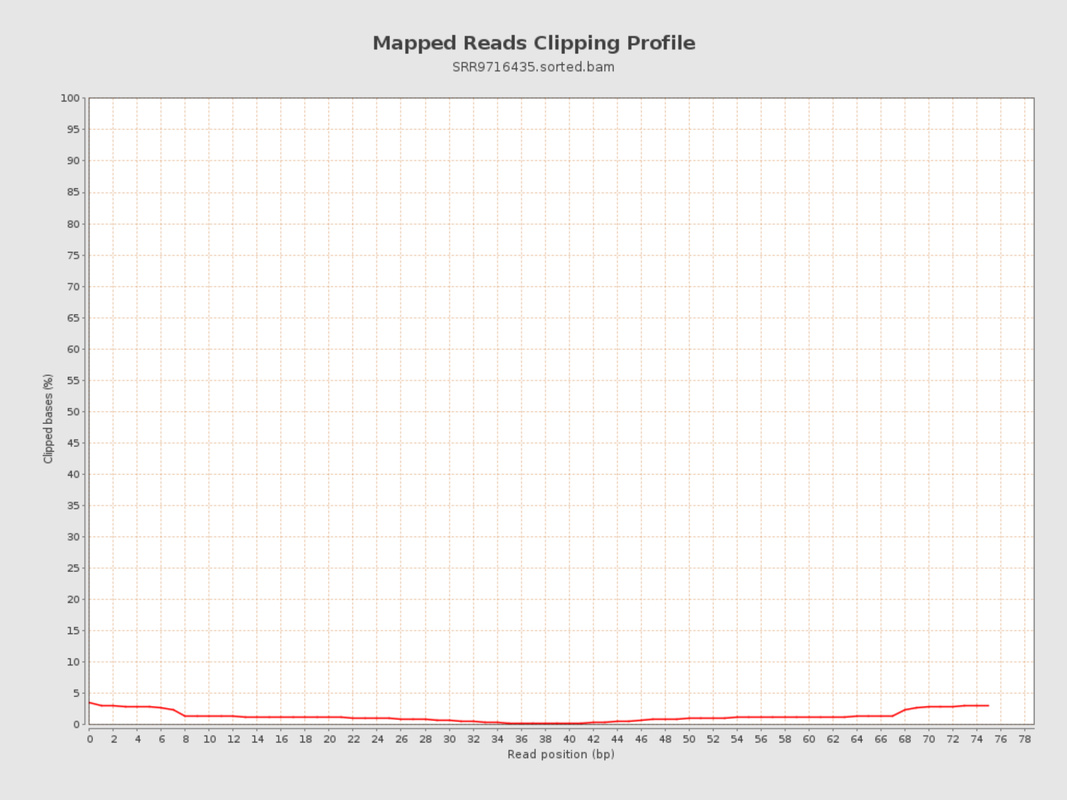
# 8. Results : Mapped Reads Nucleotide Content



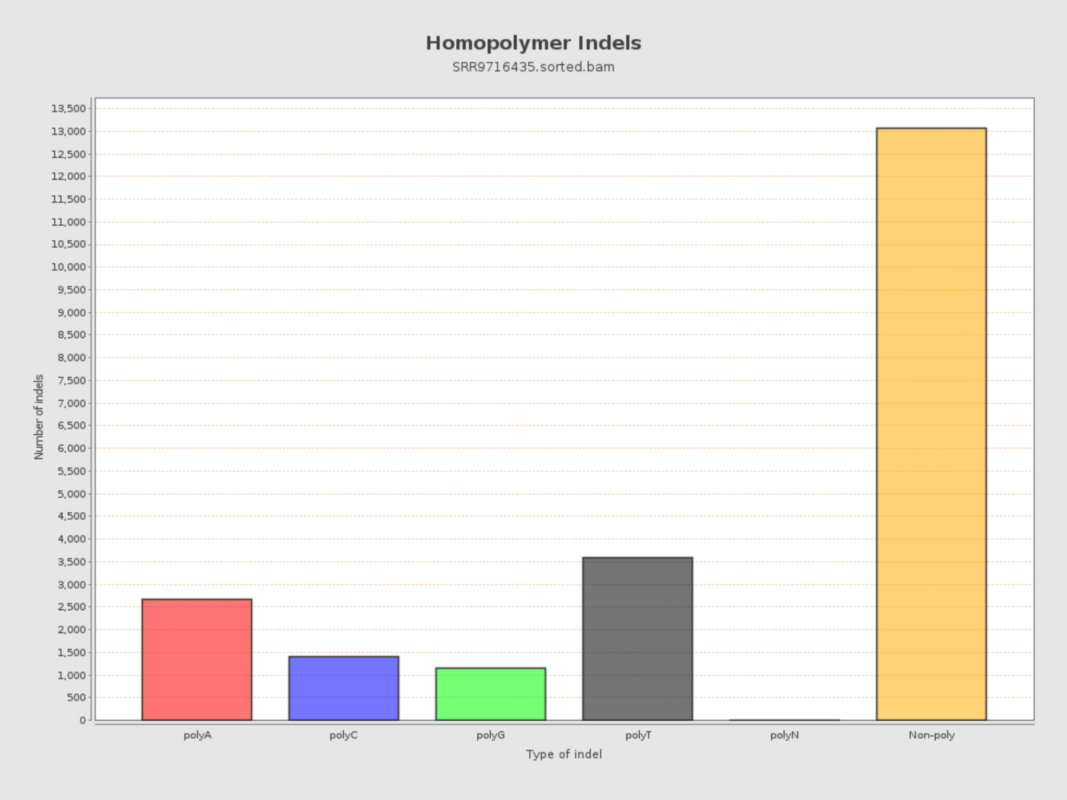
# 9. Results : Mapped Reads GC-content Distribution



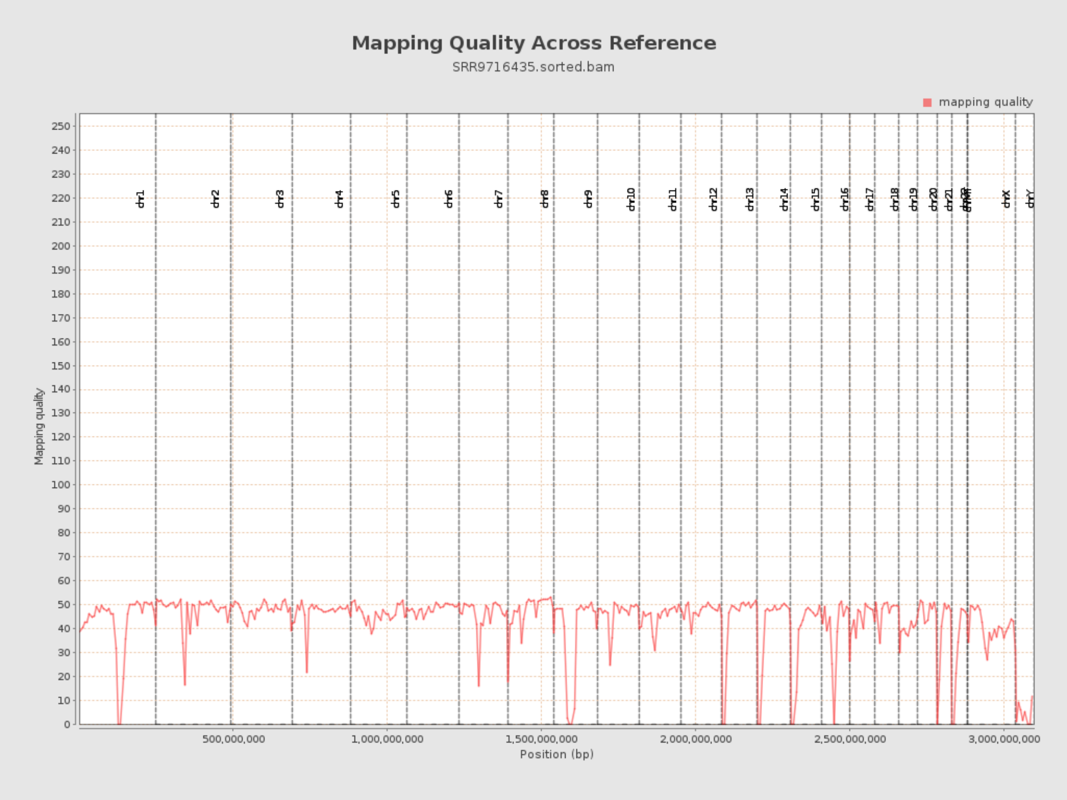
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram