# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/02 02:51:01*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716252.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_SRR9716252 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716252.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 02 02:50:54 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716252.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,895,609 |
| Mapped reads | 3,694,772 / 94.84% |
| Unmapped reads | 200,837 / 5.16% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 75,664 / 1.94% |
| Read min/max/mean length | 30 / 101 / 101.7 |
| Duplicated reads (estimated) | 304,224 / 7.81% |
| Duplication rate | 6.24% |
| Clipped reads | 3,766,788 / 96.69% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 69,468,310 / 24.09% |
| Number/percentage of C's | 59,292,774 / 20.56% |
| Number/percentage of T's | 86,073,518 / 29.85% |
| Number/percentage of G's | 73,511,811 / 25.49% |
| Number/percentage of N's | 10,731 / 0% |
| GC Percentage | 46.06% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0932 |
| | |

| | |
|---|---|
| Standard Deviation | 0.6913 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.68 |

## 2.5. Mismatches and indels

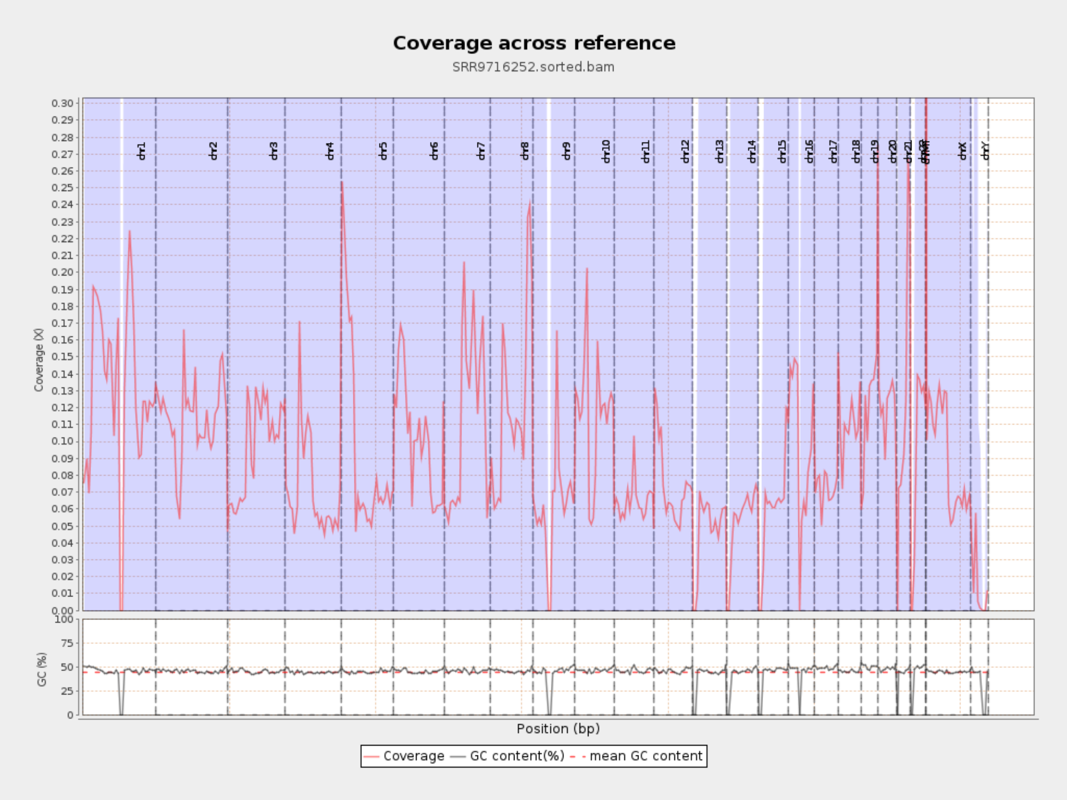
| | |
|---|---|
| General error rate | 0.68% |
| Mismatches | 1,899,541 |
| Insertions | 22,077 |
| Mapped reads with at least one insertion | 0.59% |
| Deletions | 55,269 |
| Mapped reads with at least one deletion | 1.47% |
| Homopolymer indels | 39.1% |

## 2.6. Chromosome stats

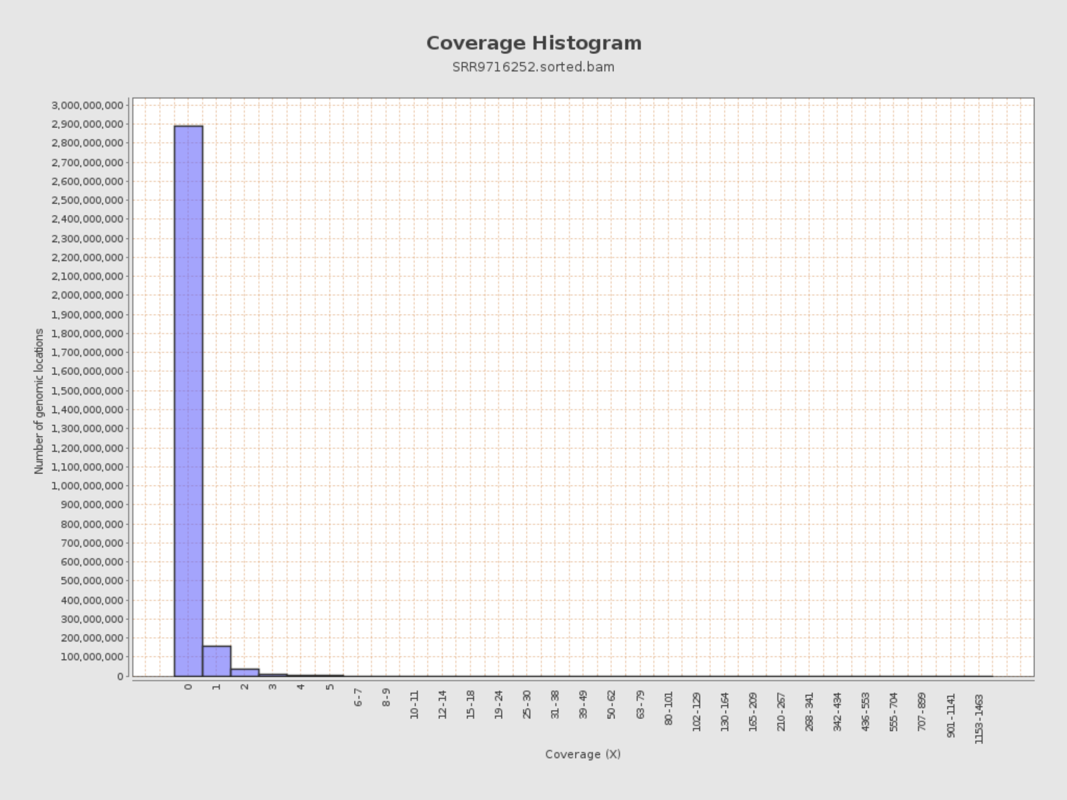
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 32838238 | 0.1317 | 1.3669 |
| chr2 | 243199373 | 27827943 | 0.1144 | 0.7488 |
| chr3 | 198022430 | 19133154 | 0.0966 | 0.4202 |
| chr4 | 191154276 | 13648729 | 0.0714 | 0.5837 |
| chr5 | 180915260 | 17501251 | 0.0967 | 0.4325 |
| chr6 | 171115067 | 17423316 | 0.1018 | 0.4651 |
| chr7 | 159138663 | 17835426 | 0.1121 | 0.9222 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 17927130 | 0.1225 | 0.7812 |
| chr9 | 141213431 | 8785275 | 0.0622 | 0.4839 |
| chr10 | 135534747 | 15610838 | 0.1152 | 0.9613 |
| chr11 | 135006516 | 8775834 | 0.065 | 0.5301 |
| chr12 | 133851895 | 10137332 | 0.0757 | 0.3722 |
| chr13 | 115169878 | 5499159 | 0.0477 | 0.2849 |
| chr14 | 107349540 | 5617923 | 0.0523 | 0.3523 |
| chr15 | 102531392 | 5957151 | 0.0581 | 0.3198 |
| chr16 | 90354753 | 8795547 | 0.0973 | 0.4666 |
| chr17 | 81195210 | 5812943 | 0.0716 | 0.4364 |
| chr18 | 78077248 | 8535216 | 0.1093 | 0.7558 |
| chr19 | 59128983 | 7358080 | 0.1244 | 0.9851 |
| chr20 | 63025520 | 7636887 | 0.1212 | 0.5049 |
| chr21 | 48129895 | 6059473 | 0.1259 | 0.6122 |
| chr22 | 51304566 | 4622230 | 0.0901 | 0.4325 |
| chrMT | 16571 | 167867 | 10.1302 | 8.2764 |
| chrX | 155270560 | 14078140 | 0.0907 | 0.454 |
| chrY | 59373566 | 886477 | 0.0149 | 0.5154 |

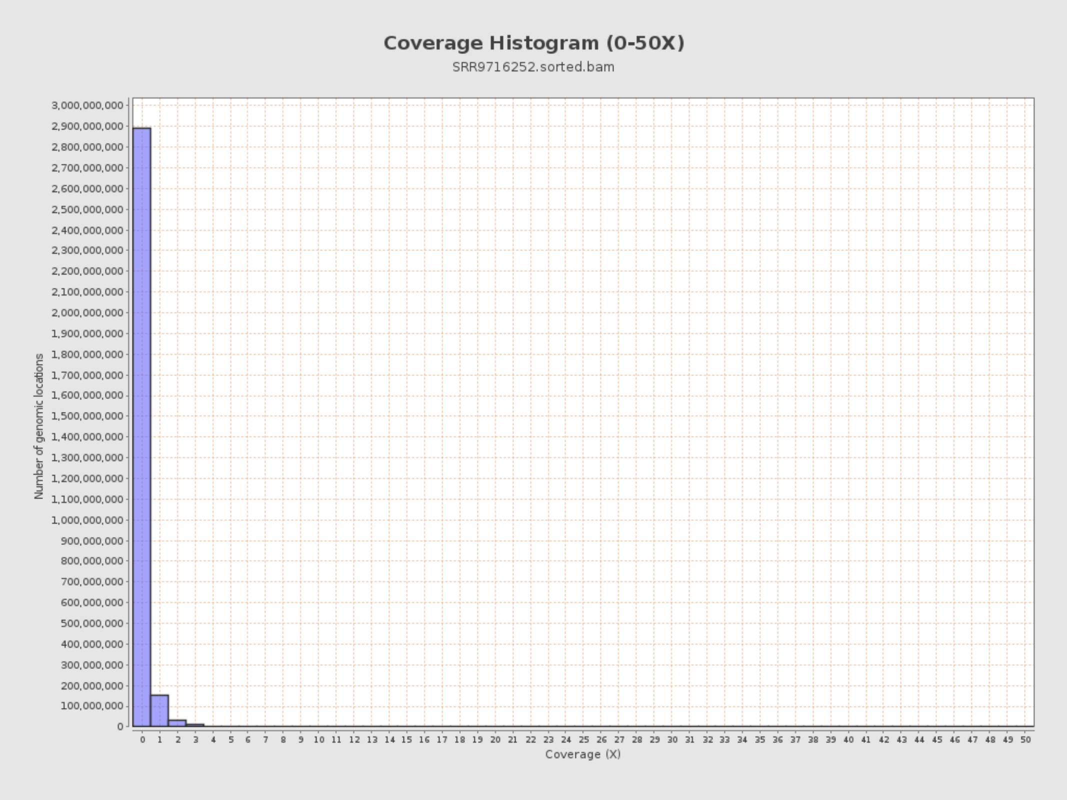
# 3. Results : Coverage across reference



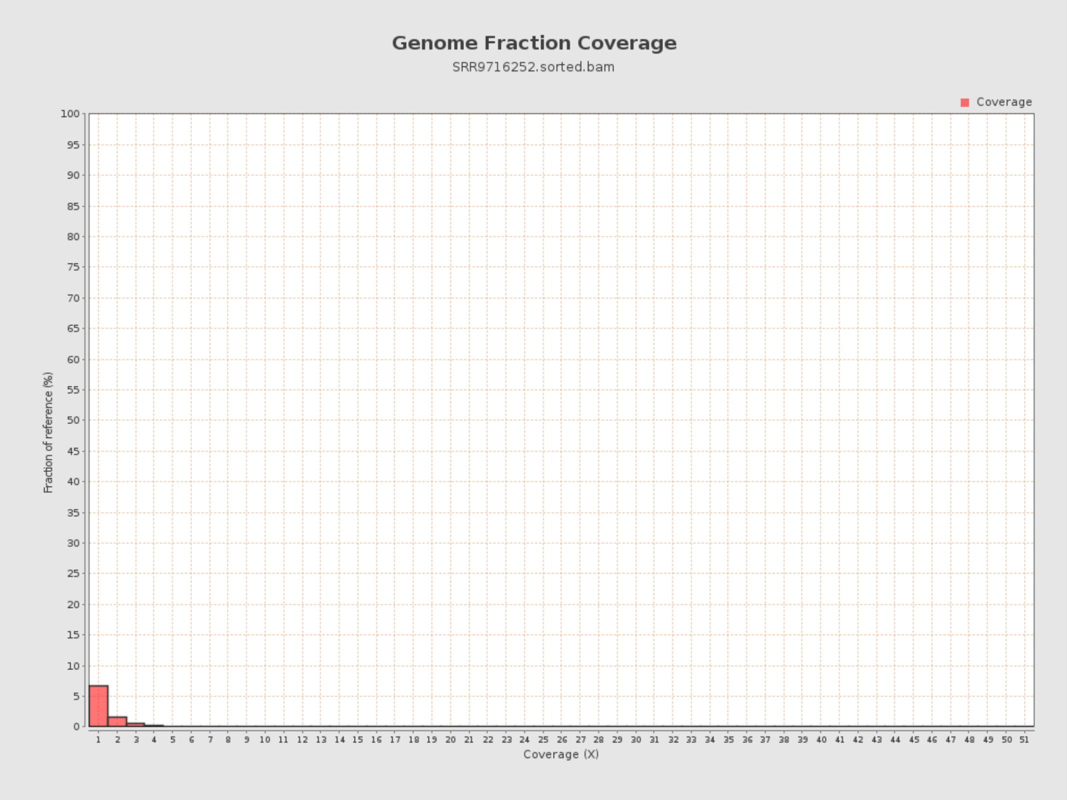
# 4. Results : Coverage Histogram



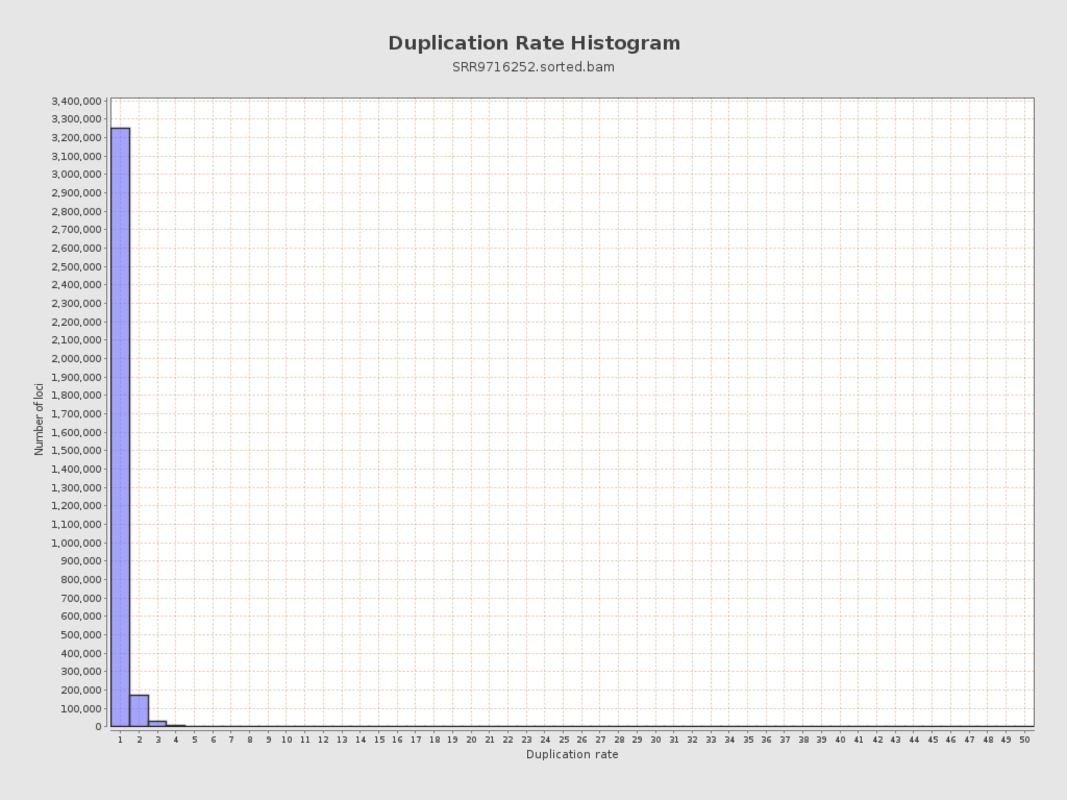
# 5. Results : Coverage Histogram (0-50X)



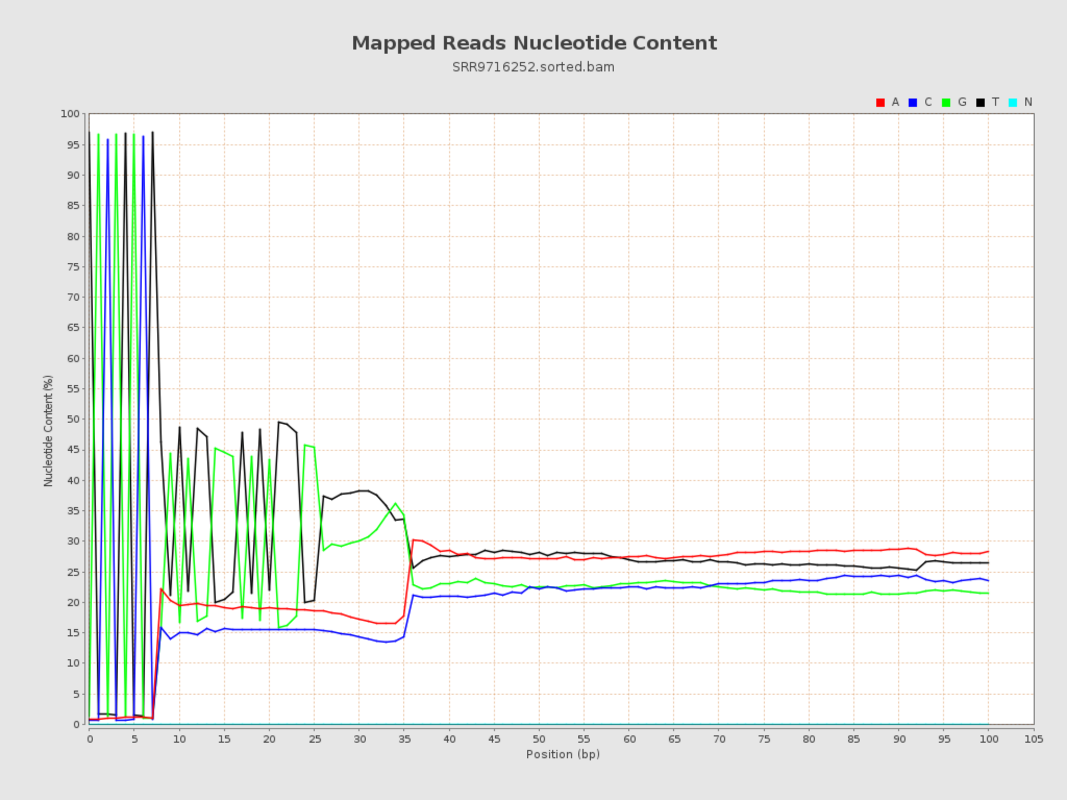
# 6. Results : Genome Fraction Coverage



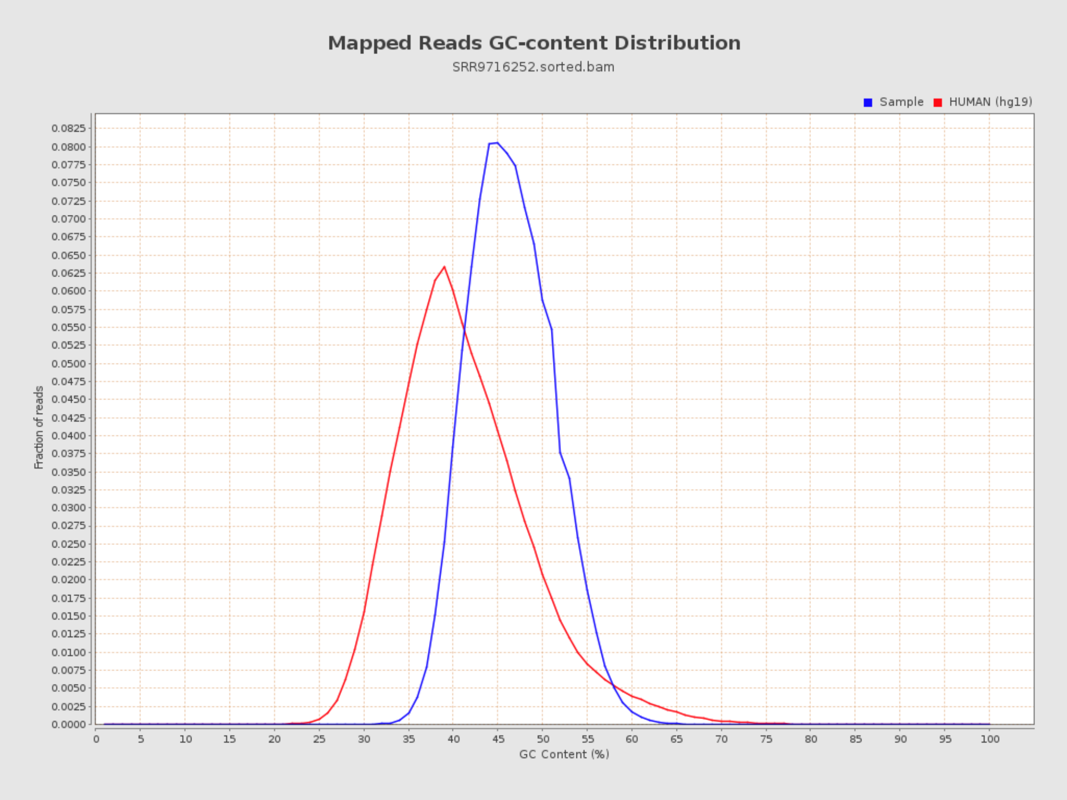
# 7. Results : Duplication Rate Histogram



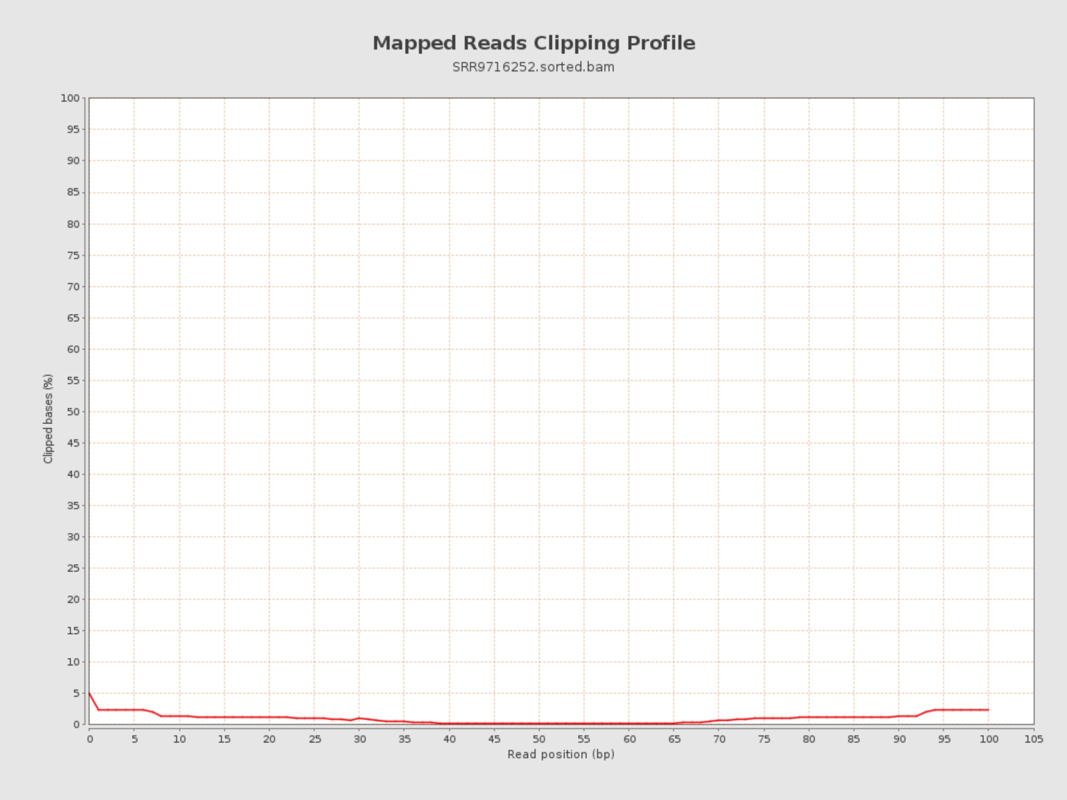
# 8. Results : Mapped Reads Nucleotide Content



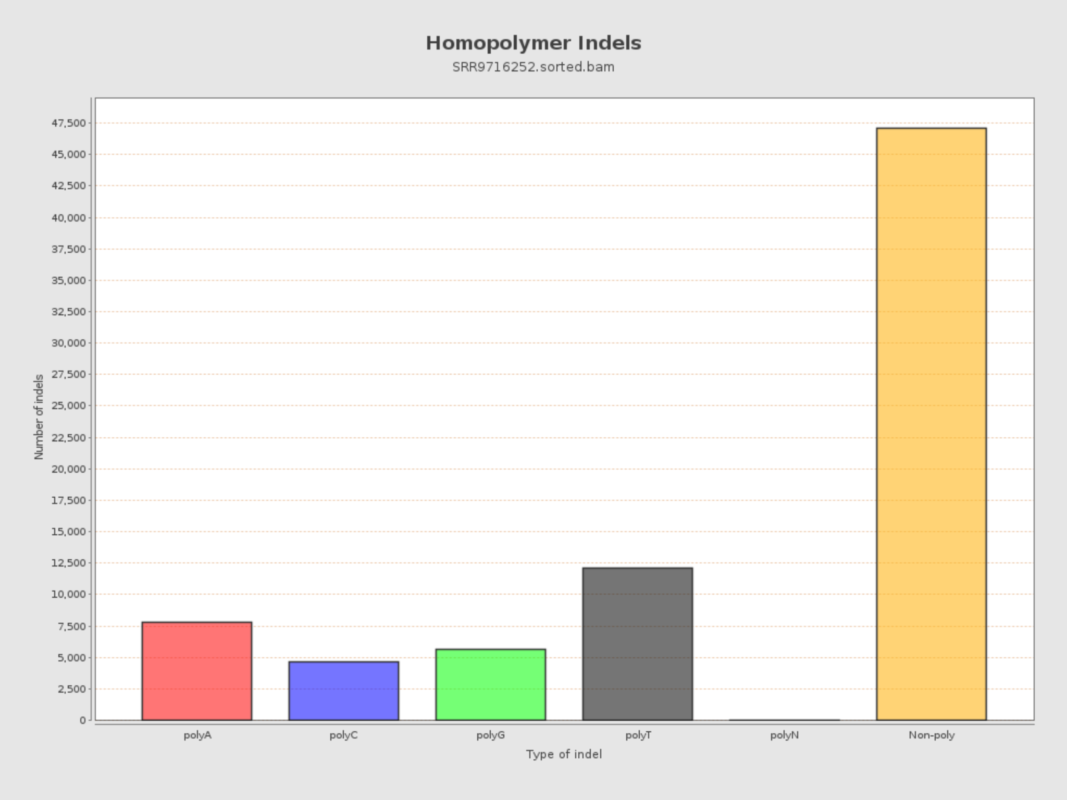
# 9. Results : Mapped Reads GC-content Distribution



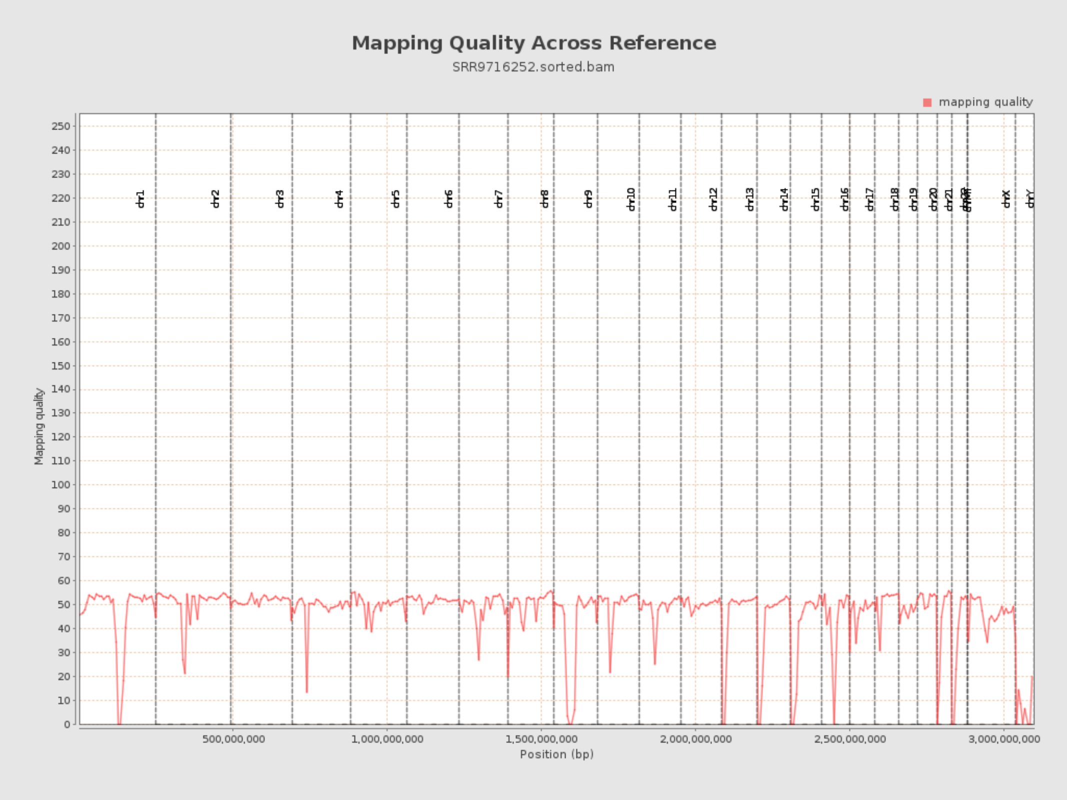
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram