# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 05:30:14*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716678.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_SRR9716678 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716678.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 05:30:13 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716678.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,480,719 |
| Mapped reads | 3,124,558 / 89.77% |
| Unmapped reads | 356,161 / 10.23% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 20,137 / 0.58% |
| Read min/max/mean length | 30 / 76 / 76.19 |
| Duplicated reads (estimated) | 217,719 / 6.26% |
| Duplication rate | 5.4% |
| Clipped reads | 3,135,042 / 90.07% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 43,937,163 / 24.07% |
| Number/percentage of C's | 33,837,907 / 18.54% |
| Number/percentage of T's | 58,681,627 / 32.14% |
| Number/percentage of G's | 46,095,427 / 25.25% |
| Number/percentage of N's | 1,370 / 0% |
| GC Percentage | 43.79% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.059 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4688 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.68 |

## 2.5. Mismatches and indels

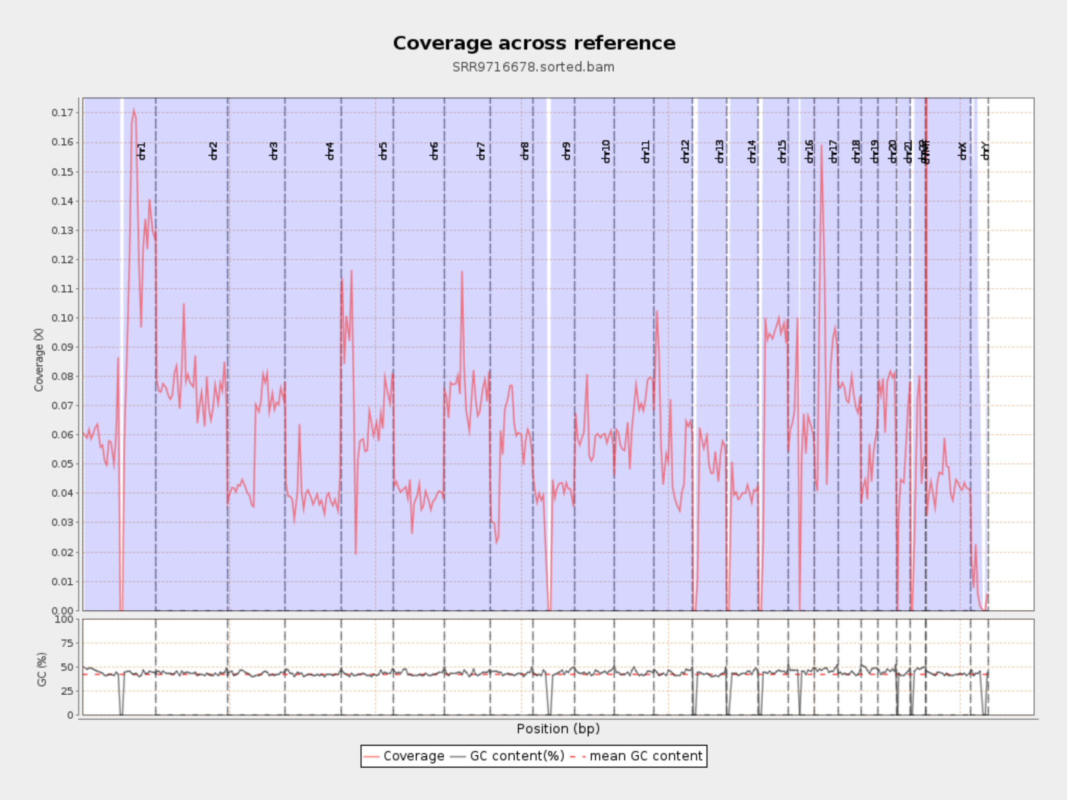
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 903,453 |
| Insertions | 13,037 |
| Mapped reads with at least one insertion | 0.42% |
| Deletions | 32,728 |
| Mapped reads with at least one deletion | 1.04% |
| Homopolymer indels | 42.48% |

## 2.6. Chromosome stats

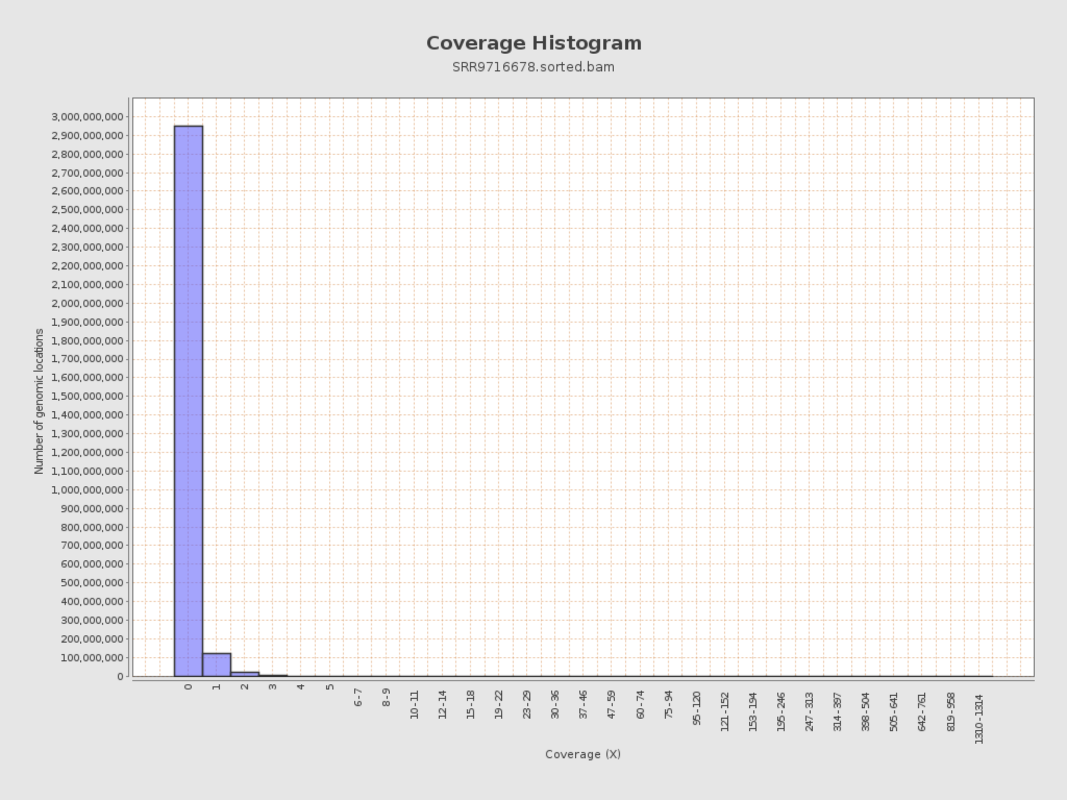
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 21332223 | 0.0856 | 0.777 |
| chr2 | 243199373 | 18516119 | 0.0761 | 0.6762 |
| chr3 | 198022430 | 11354493 | 0.0573 | 0.2917 |
| chr4 | 191154276 | 7500014 | 0.0392 | 0.2884 |
| chr5 | 180915260 | 12870110 | 0.0711 | 0.3262 |
| chr6 | 171115067 | 6684014 | 0.0391 | 0.2811 |
| chr7 | 159138663 | 12126532 | 0.0762 | 0.7915 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 8068993 | 0.0551 | 0.4078 |
| chr9 | 141213431 | 4981096 | 0.0353 | 0.3417 |
| chr10 | 135534747 | 8101651 | 0.0598 | 0.3844 |
| chr11 | 135006516 | 8903385 | 0.0659 | 0.4654 |
| chr12 | 133851895 | 7644295 | 0.0571 | 0.2934 |
| chr13 | 115169878 | 5183553 | 0.045 | 0.2586 |
| chr14 | 107349540 | 3834420 | 0.0357 | 0.2458 |
| chr15 | 102531392 | 7880231 | 0.0769 | 0.3417 |
| chr16 | 90354753 | 5375138 | 0.0595 | 0.3182 |
| chr17 | 81195210 | 6930946 | 0.0854 | 0.4069 |
| chr18 | 78077248 | 5767487 | 0.0739 | 0.794 |
| chr19 | 59128983 | 2893993 | 0.0489 | 0.5566 |
| chr20 | 63025520 | 4789798 | 0.076 | 0.3428 |
| chr21 | 48129895 | 2301548 | 0.0478 | 0.2913 |
| chr22 | 51304566 | 2201269 | 0.0429 | 0.2506 |
| chrMT | 16571 | 235857 | 14.2331 | 10.0545 |
| chrX | 155270560 | 6708334 | 0.0432 | 0.2937 |
| chrY | 59373566 | 419543 | 0.0071 | 0.165 |

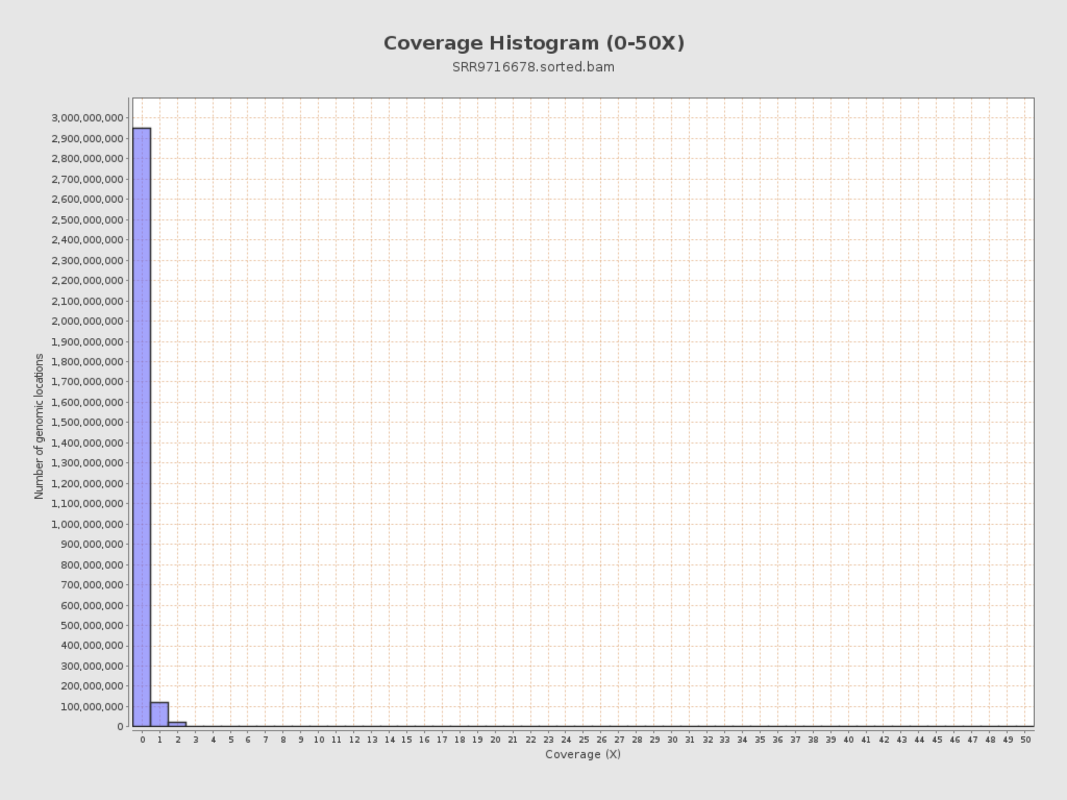
# 3. Results : Coverage across reference



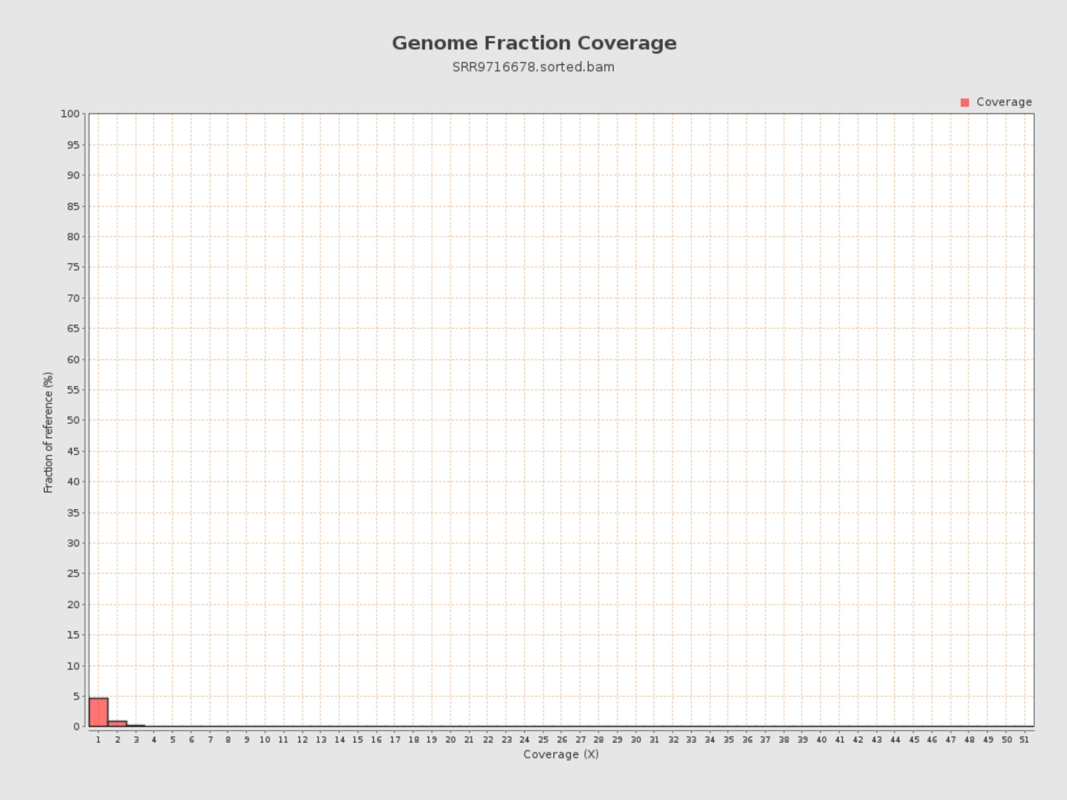
# 4. Results : Coverage Histogram



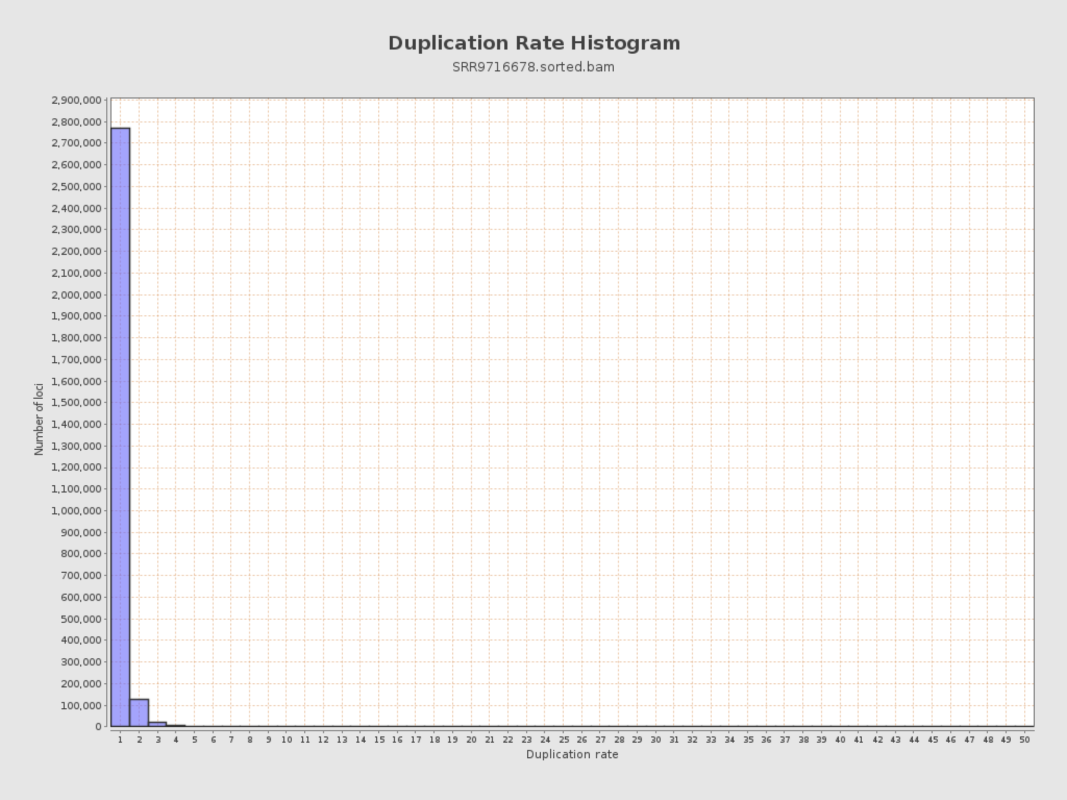
# 5. Results : Coverage Histogram (0-50X)



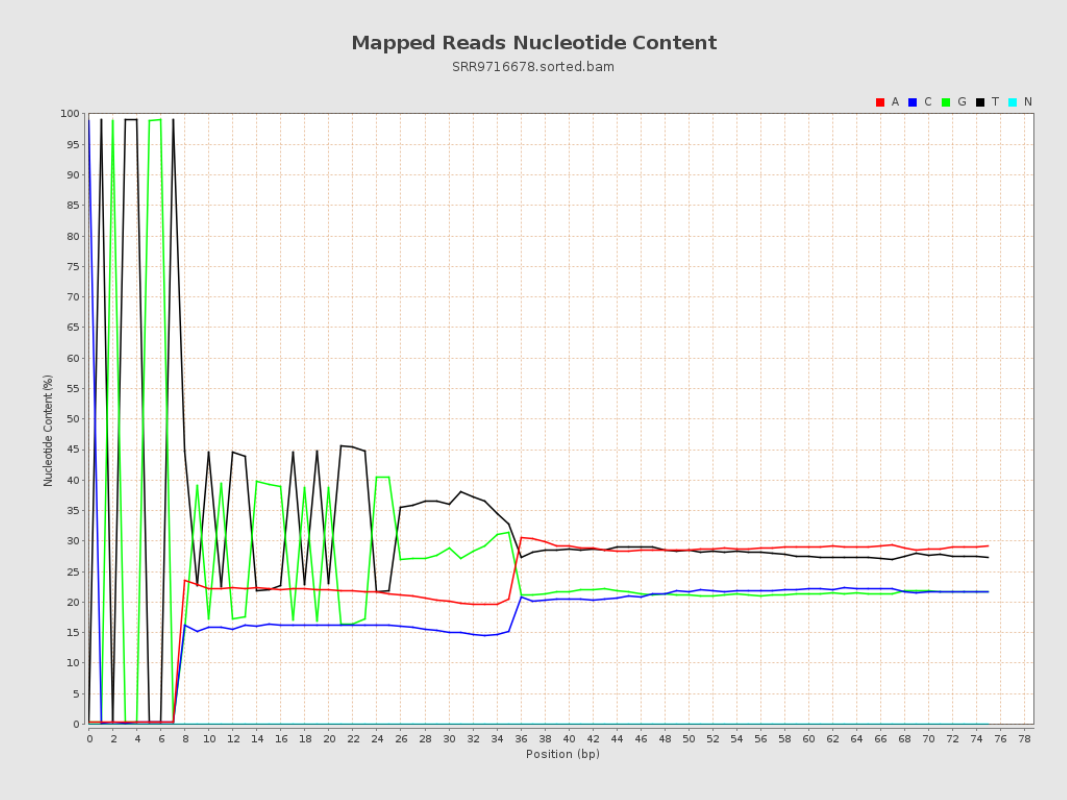
# 6. Results : Genome Fraction Coverage



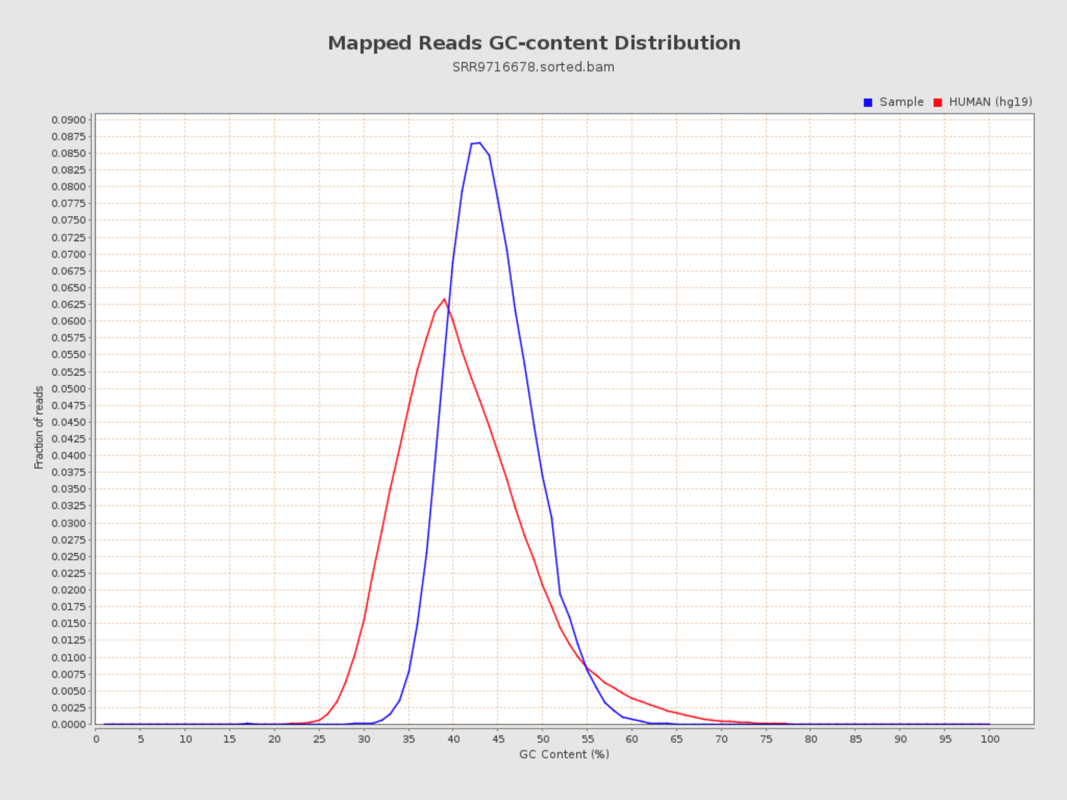
# 7. Results : Duplication Rate Histogram



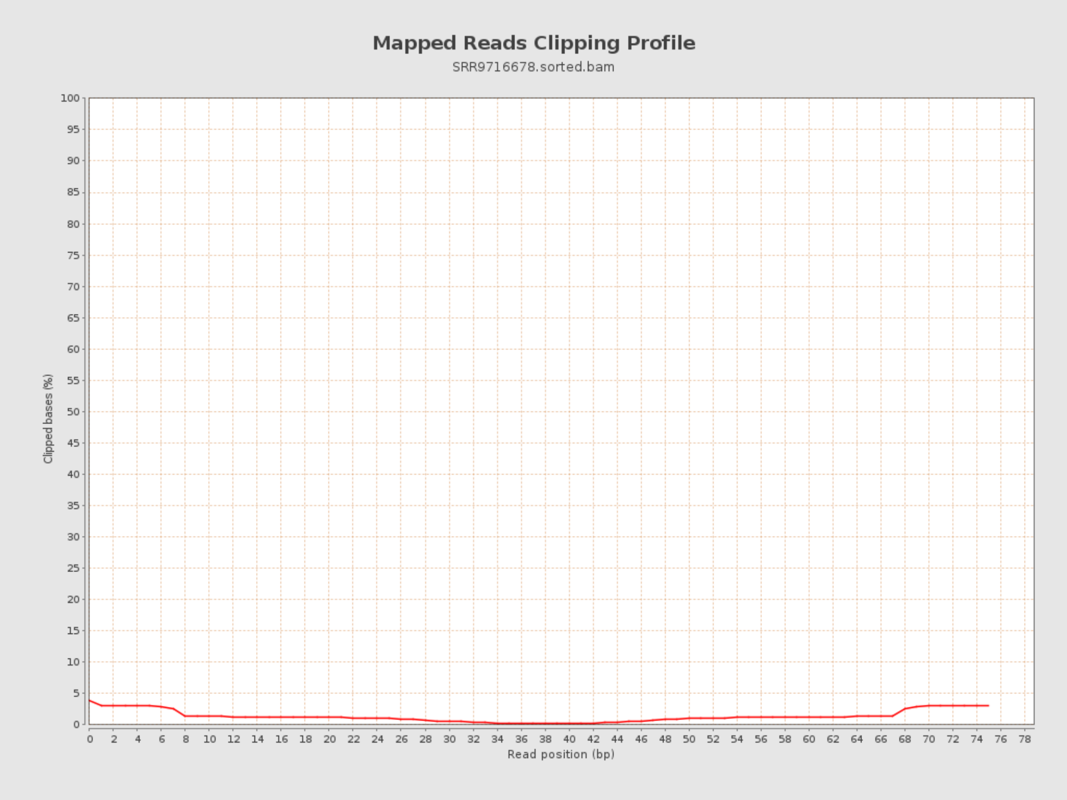
# 8. Results : Mapped Reads Nucleotide Content



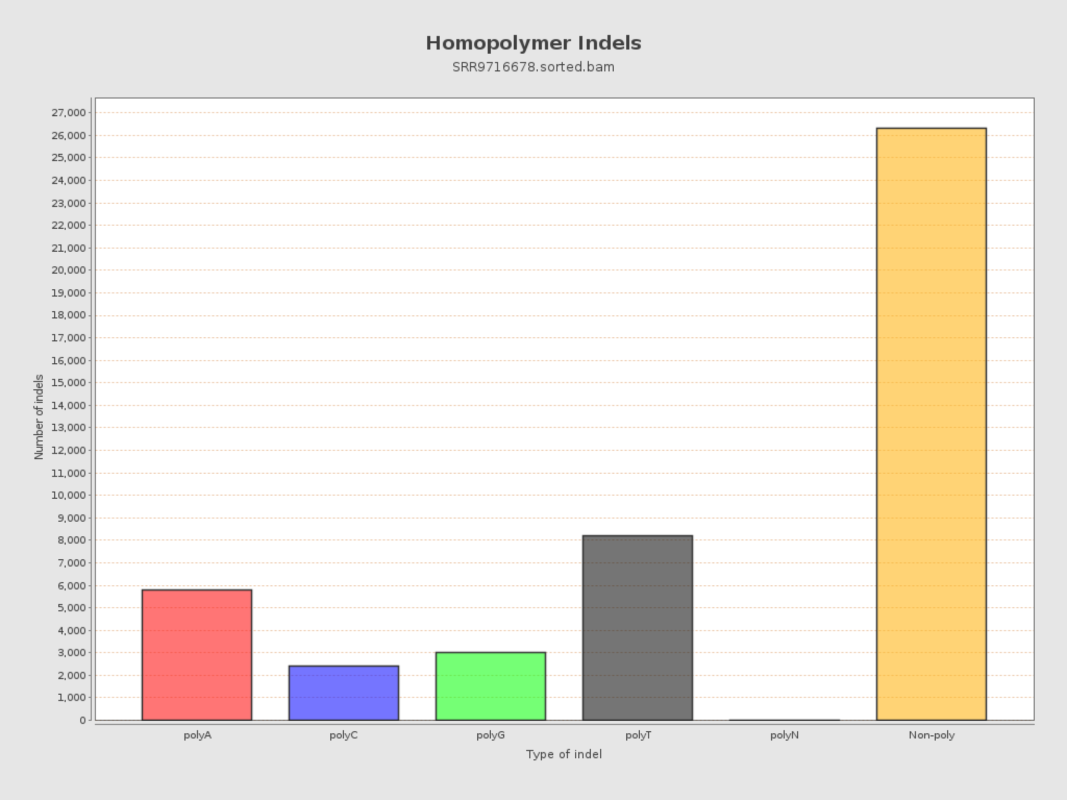
# 9. Results : Mapped Reads GC-content Distribution



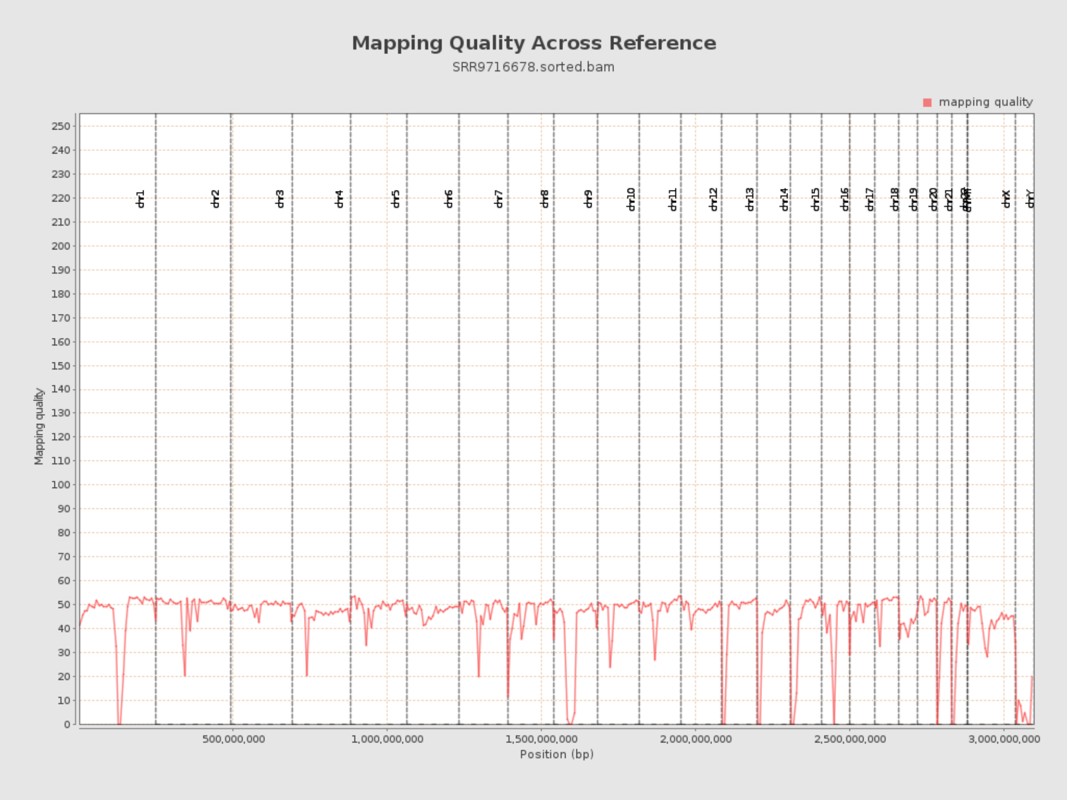
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram