# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/02 11:28:05*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716395.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_SRR9716395 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716395.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 02 11:28:04 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716395.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,964,153 |
| Mapped reads | 1,801,670 / 91.73% |
| Unmapped reads | 162,483 / 8.27% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 28,333 / 1.44% |
| Read min/max/mean length | 30 / 101 / 101.53 |
| Duplicated reads (estimated) | 84,935 / 4.32% |
| Duplication rate | 2.86% |
| Clipped reads | 1,826,979 / 93.02% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 35,678,478 / 25.04% |
| Number/percentage of C's | 27,832,363 / 19.53% |
| Number/percentage of T's | 44,351,749 / 31.12% |
| Number/percentage of G's | 34,642,959 / 24.31% |
| Number/percentage of N's | 8,809 / 0.01% |
| GC Percentage | 43.84% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0461 |
| | |

| | |
|---|---|
| Standard Deviation | 0.5295 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.2 |

## 2.5. Mismatches and indels

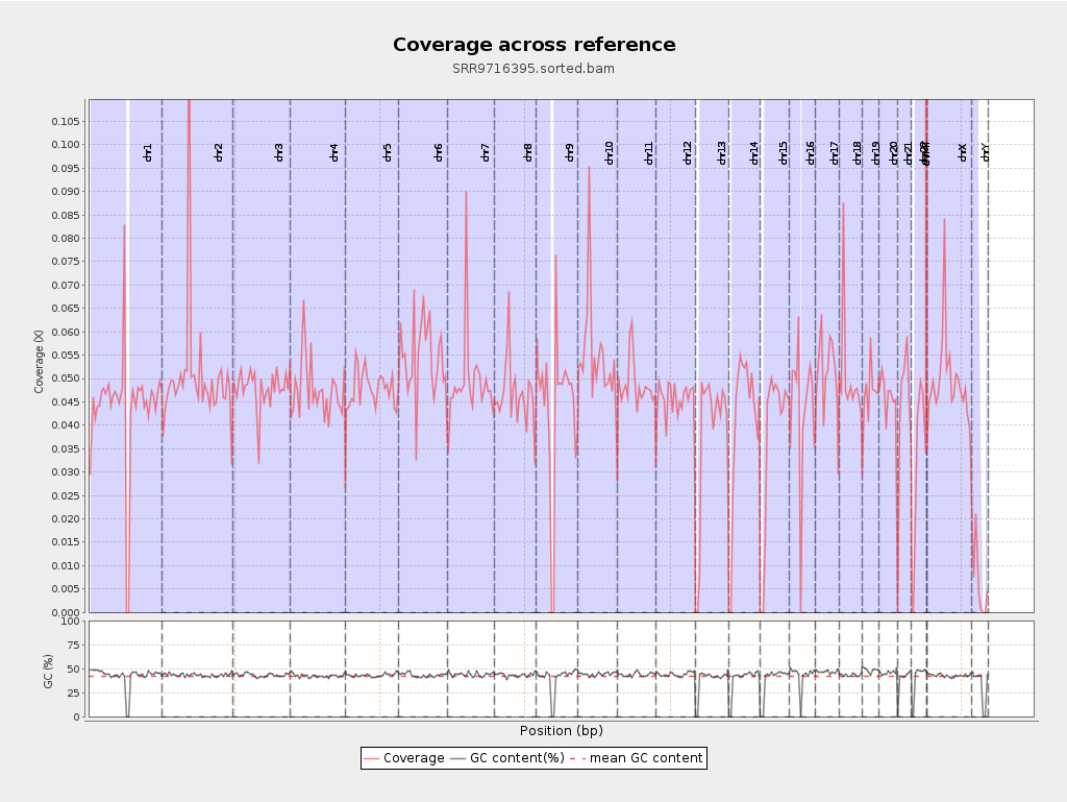
| | |
|---|---|
| General error rate | 0.87% |
| Mismatches | 1,213,745 |
| Insertions | 13,146 |
| Mapped reads with at least one insertion | 0.72% |
| Deletions | 36,150 |
| Mapped reads with at least one deletion | 1.98% |
| Homopolymer indels | 43.78% |

## 2.6. Chromosome stats

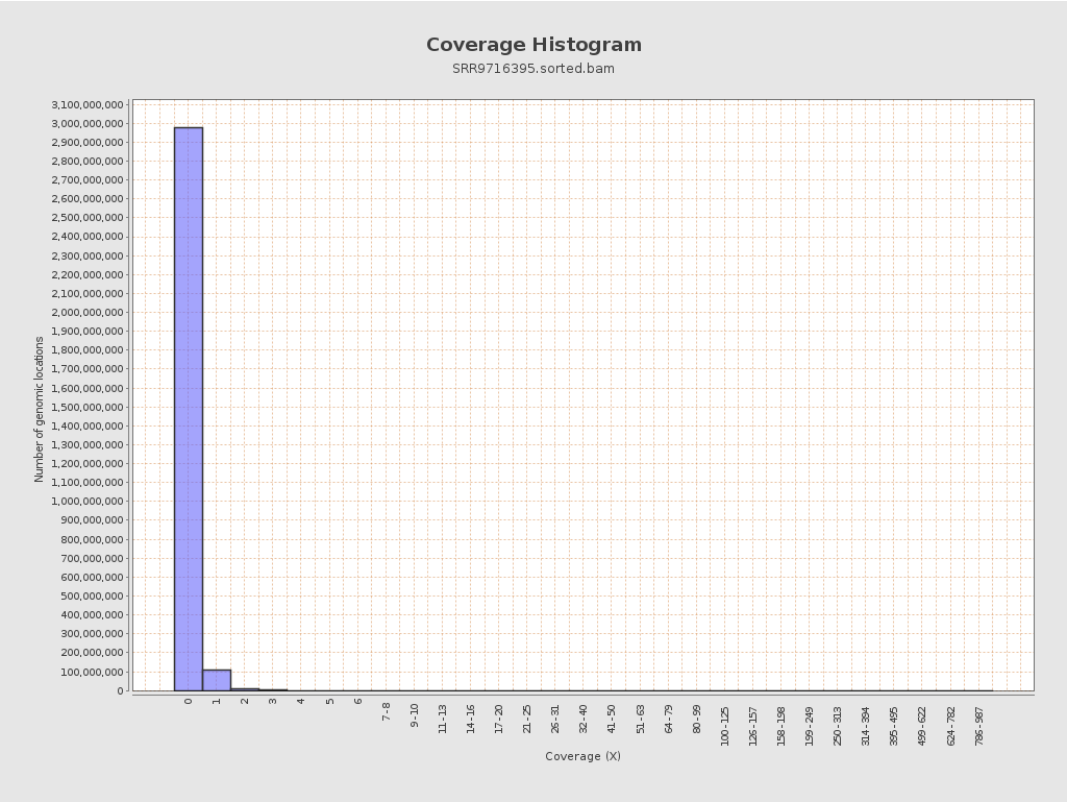
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 10896196 | 0.0437 | 0.8163 |
| chr2 | 243199373 | 12336639 | 0.0507 | 0.7717 |
| chr3 | 198022430 | 9464352 | 0.0478 | 0.2485 |
| chr4 | 191154276 | 9067115 | 0.0474 | 0.2737 |
| chr5 | 180915260 | 8656673 | 0.0478 | 0.2561 |
| chr6 | 171115067 | 9301587 | 0.0544 | 0.3307 |
| chr7 | 159138663 | 7881853 | 0.0495 | 0.6893 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6797722 | 0.0464 | 0.722 |
| chr9 | 141213431 | 6157732 | 0.0436 | 0.6324 |
| chr10 | 135534747 | 7440401 | 0.0549 | 0.4829 |
| chr11 | 135006516 | 6501722 | 0.0482 | 0.5715 |
| chr12 | 133851895 | 6093962 | 0.0455 | 0.2521 |
| chr13 | 115169878 | 4337194 | 0.0377 | 0.2166 |
| chr14 | 107349540 | 4360458 | 0.0406 | 0.3332 |
| chr15 | 102531392 | 3855012 | 0.0376 | 0.2222 |
| chr16 | 90354753 | 3959875 | 0.0438 | 0.2934 |
| chr17 | 81195210 | 4141298 | 0.051 | 0.3171 |
| chr18 | 78077248 | 3961069 | 0.0507 | 1.1958 |
| chr19 | 59128983 | 2790065 | 0.0472 | 0.6088 |
| chr20 | 63025520 | 2875566 | 0.0456 | 0.2773 |
| chr21 | 48129895 | 2079922 | 0.0432 | 0.2587 |
| chr22 | 51304566 | 1599009 | 0.0312 | 0.1999 |
| chrMT | 16571 | 23064 | 1.3918 | 1.5795 |
| chrX | 155270560 | 7632280 | 0.0492 | 0.3853 |
| chrY | 59373566 | 366567 | 0.0062 | 0.1781 |

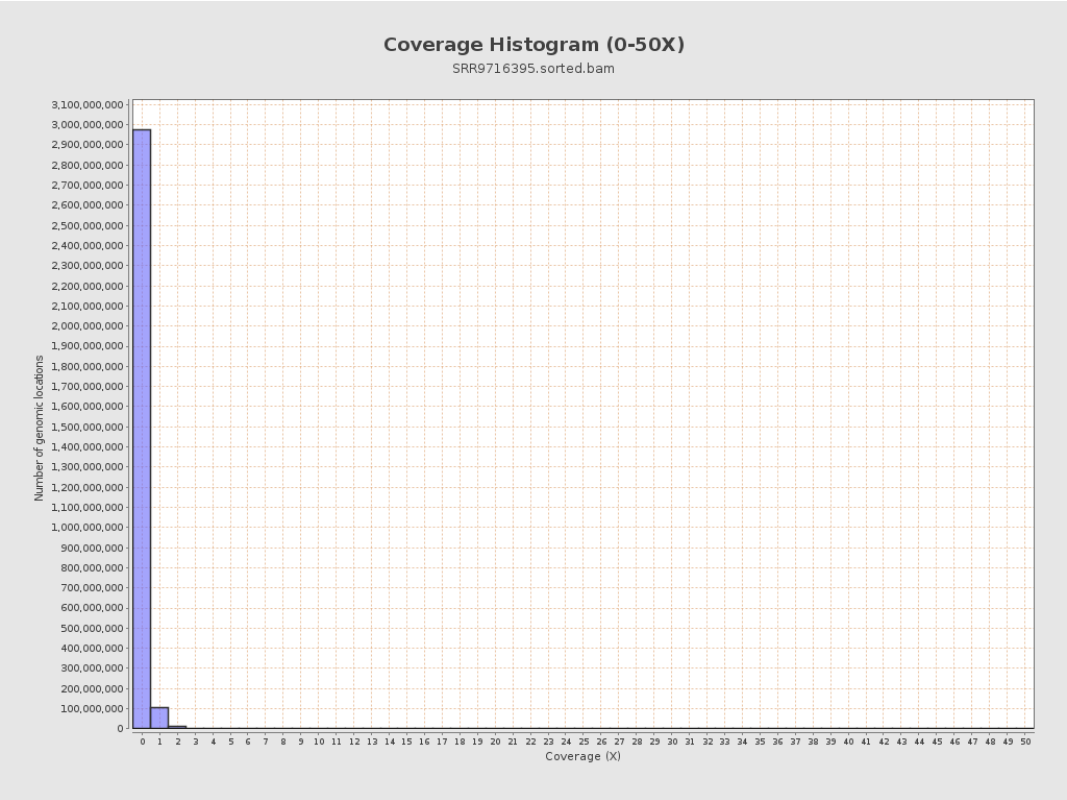
# 3. Results : Coverage across reference



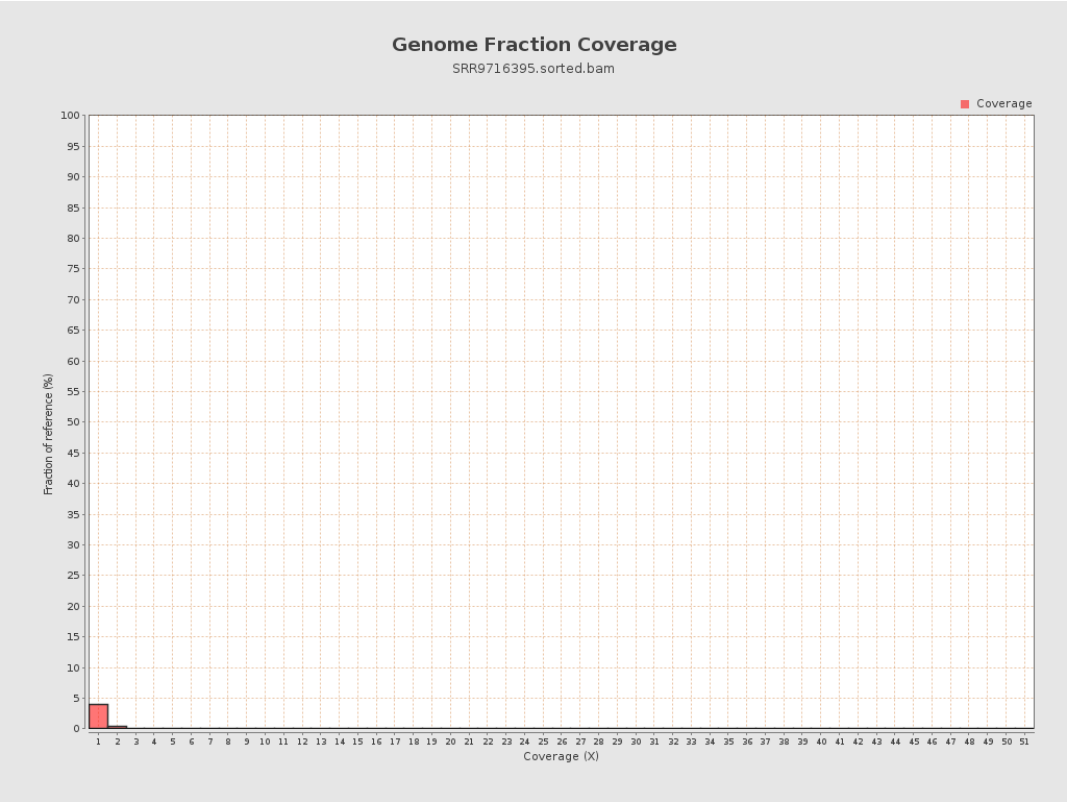
# 4. Results : Coverage Histogram



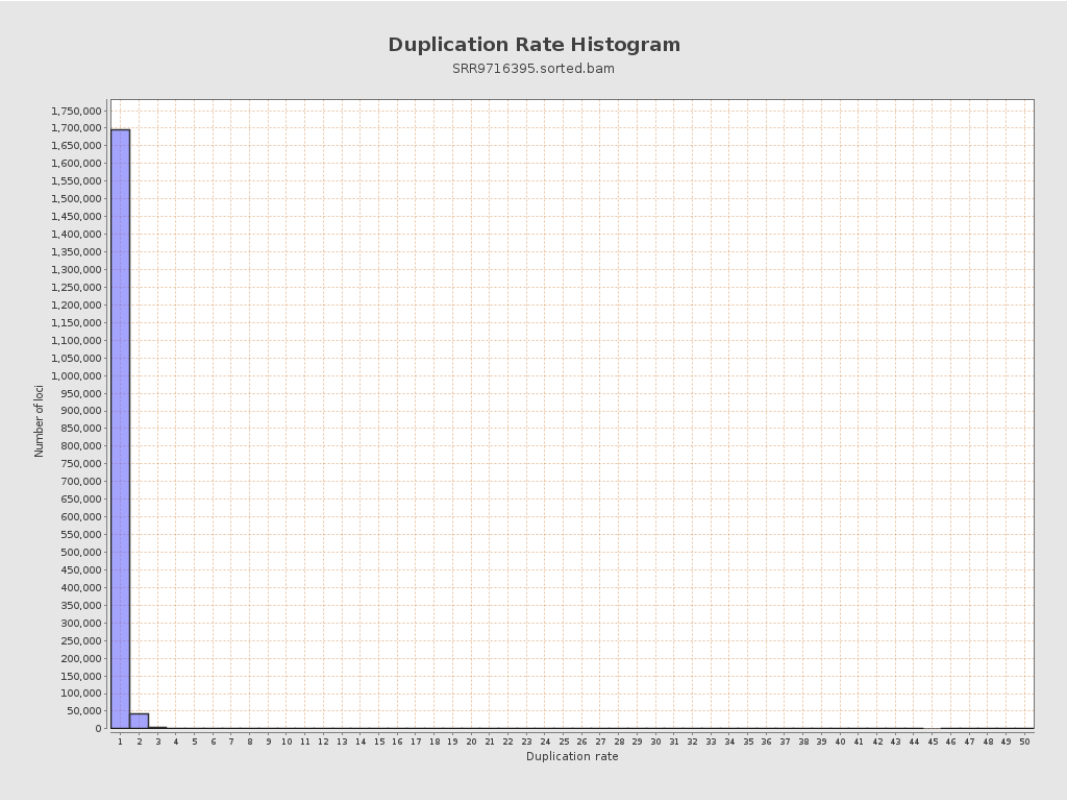
# 5. Results : Coverage Histogram (0-50X)



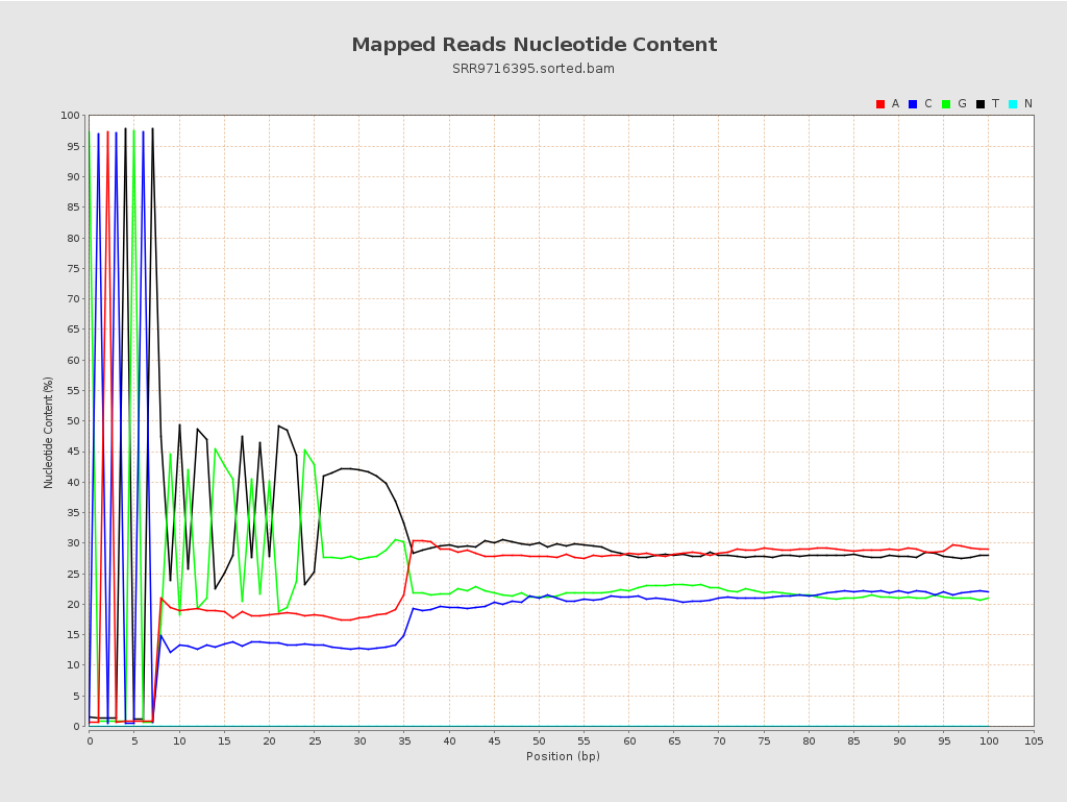
# 6. Results : Genome Fraction Coverage



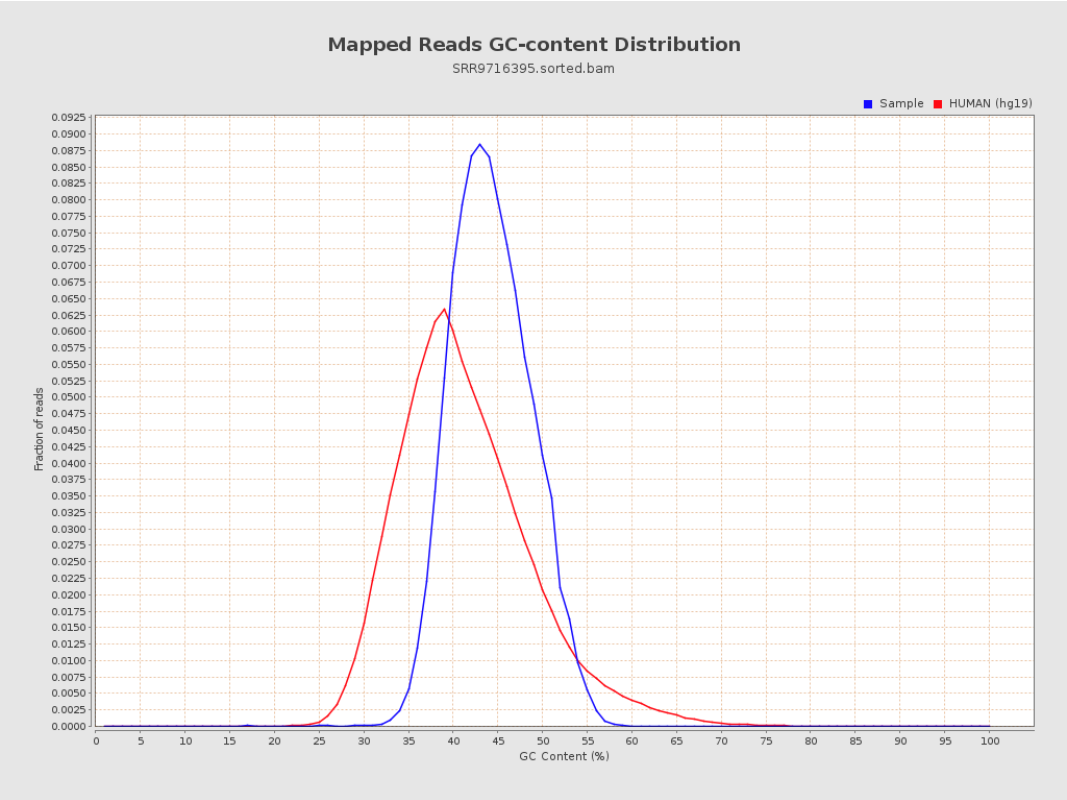
# 7. Results : Duplication Rate Histogram



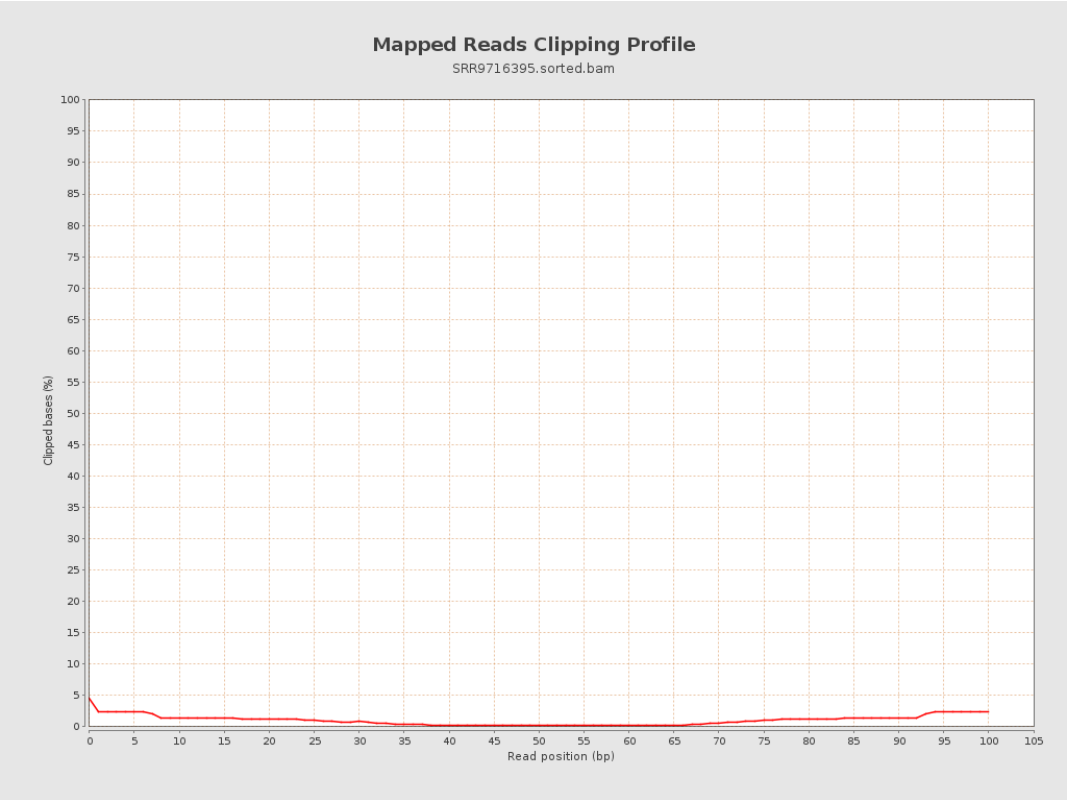
# 8. Results : Mapped Reads Nucleotide Content



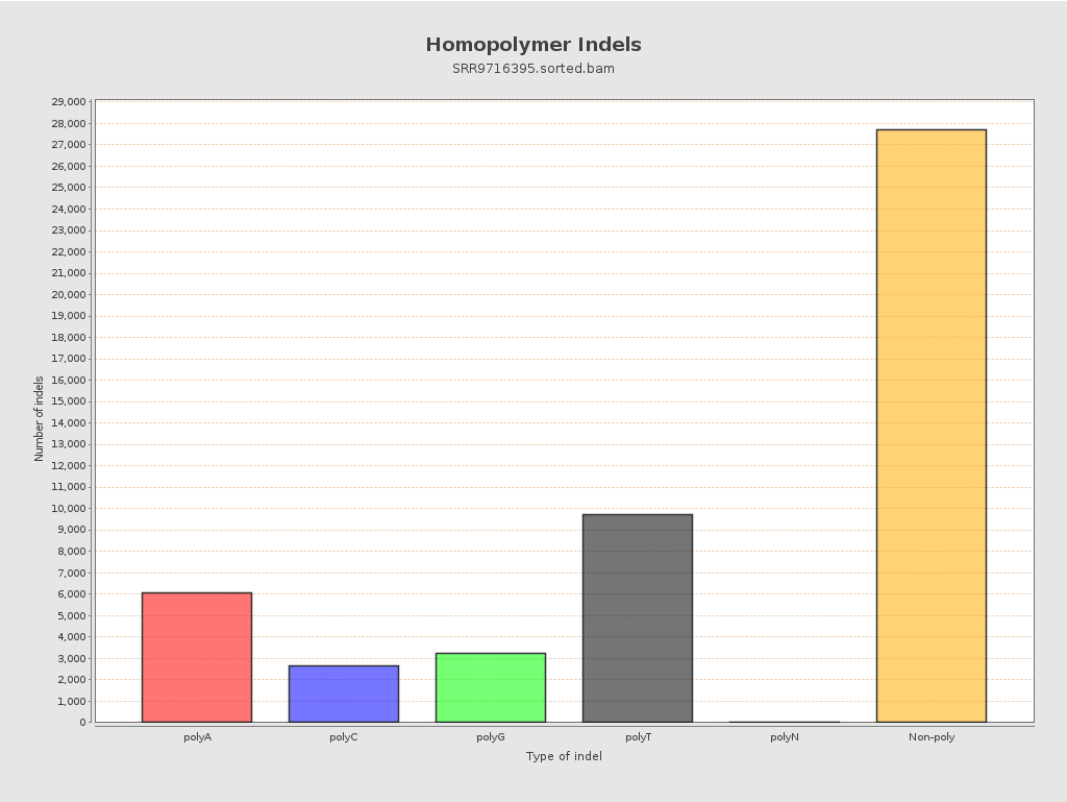
# 9. Results : Mapped Reads GC-content Distribution



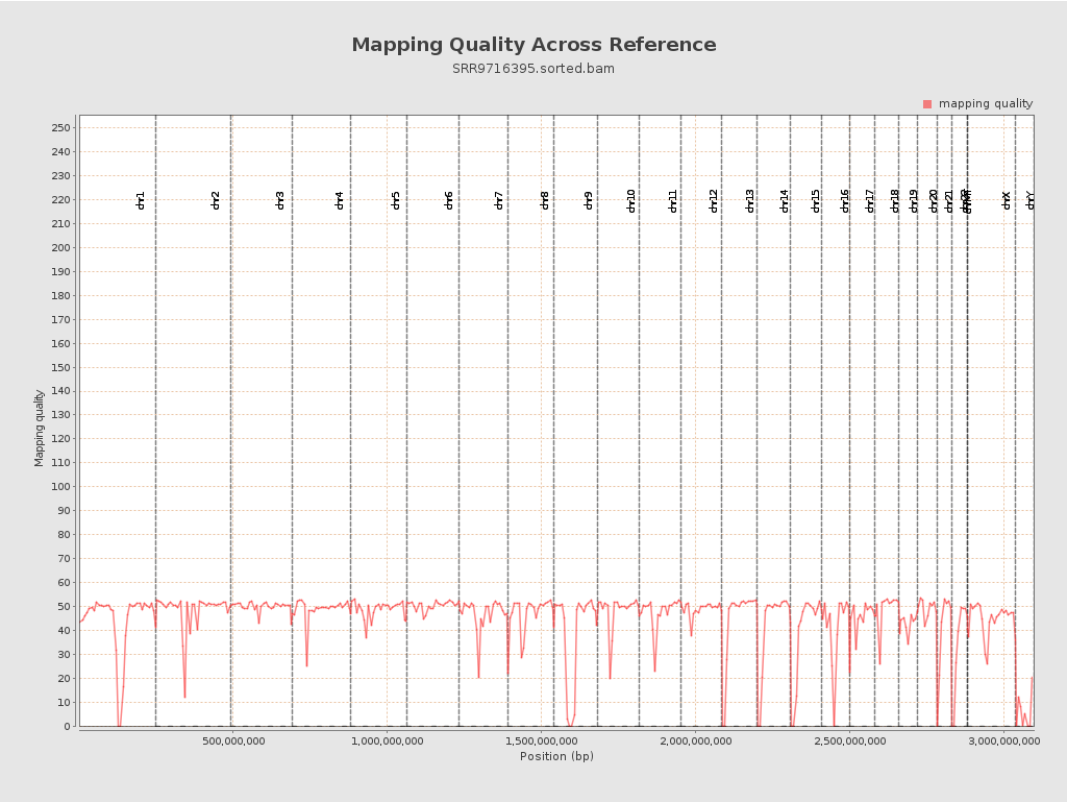
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram