# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/02 09:28:56*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716368.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_SRR9716368 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716368.fastq.gz` |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 02 09:28:55 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716368.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,850,026 |
| Mapped reads | 1,698,441 / 91.81% |
| Unmapped reads | 151,585 / 8.19% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 30,980 / 1.67% |
| Read min/max/mean length | 30 / 101 / 101.6 |
| Duplicated reads (estimated) | 70,032 / 3.79% |
| Duplication rate | 3.03% |
| Clipped reads | 1,725,889 / 93.29% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 34,603,269 / 25.96% |
| Number/percentage of C's | 25,600,267 / 19.21% |
| Number/percentage of T's | 41,461,515 / 31.11% |
| Number/percentage of G's | 31,610,915 / 23.72% |
| Number/percentage of N's | 9,058 / 0.01% |
| GC Percentage | 42.92% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0431 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3701 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 47.39 |

## 2.5. Mismatches and indels

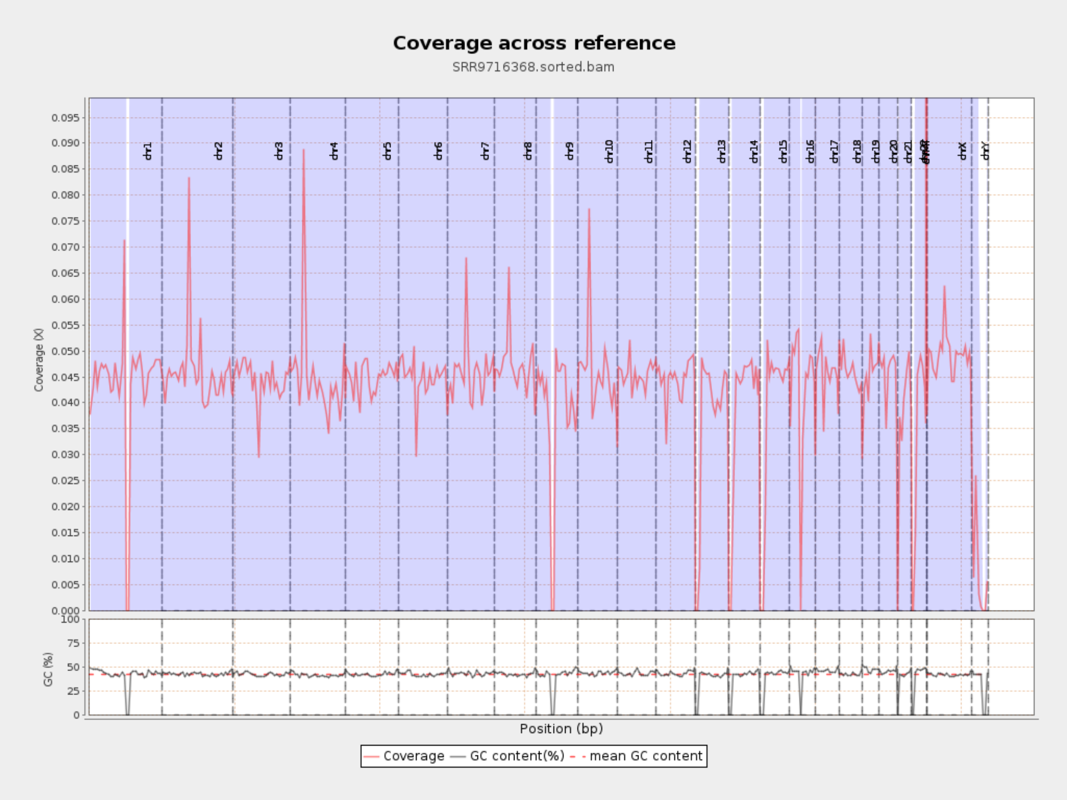
| | |
|---|---|
| General error rate | 0.72% |
| Mismatches | 931,923 |
| Insertions | 12,162 |
| Mapped reads with at least one insertion | 0.7% |
| Deletions | 32,794 |
| Mapped reads with at least one deletion | 1.9% |
| Homopolymer indels | 42.76% |

## 2.6. Chromosome stats

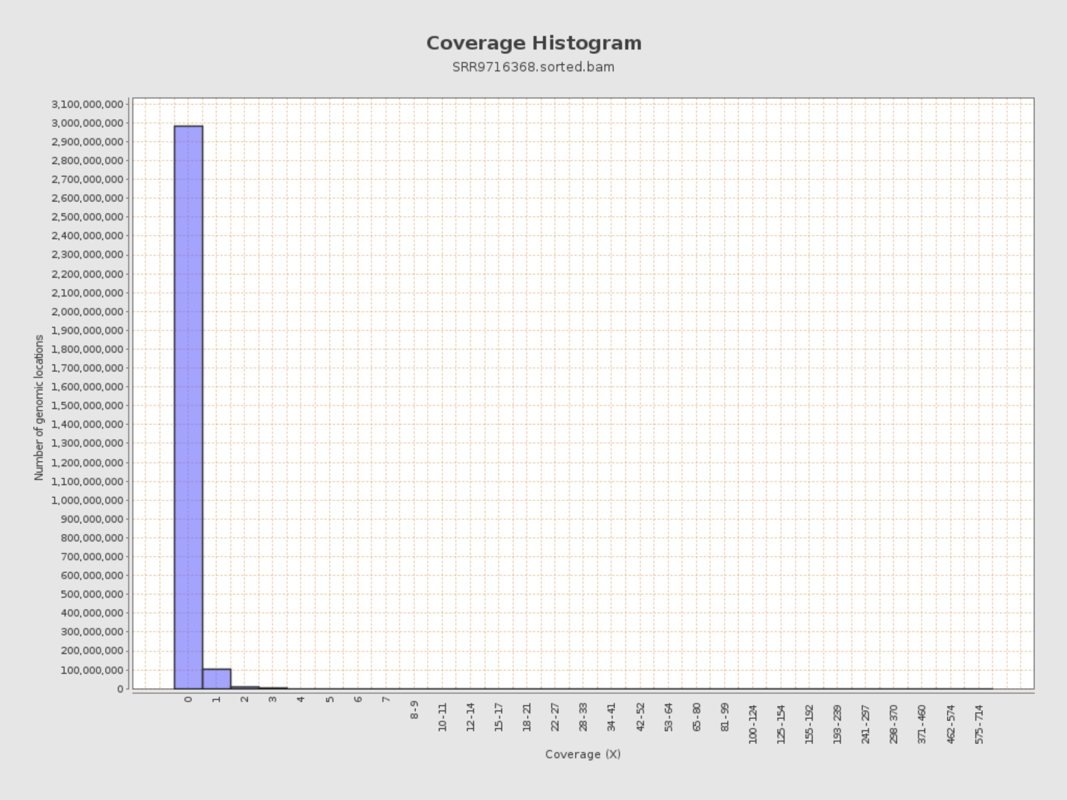
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 10841593 | 0.0435 | 0.6404 |
| chr2 | 243199373 | 11221389 | 0.0461 | 0.451 |
| chr3 | 198022430 | 8770042 | 0.0443 | 0.2342 |
| chr4 | 191154276 | 8562447 | 0.0448 | 0.3003 |
| chr5 | 180915260 | 8106127 | 0.0448 | 0.2381 |
| chr6 | 171115067 | 7686133 | 0.0449 | 0.2576 |
| chr7 | 159138663 | 7323658 | 0.046 | 0.4985 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6903139 | 0.0472 | 0.4688 |
| chr9 | 141213431 | 5319240 | 0.0377 | 0.3529 |
| chr10 | 135534747 | 6245682 | 0.0461 | 0.3825 |
| chr11 | 135006516 | 6103196 | 0.0452 | 0.3487 |
| chr12 | 133851895 | 5960897 | 0.0445 | 0.2372 |
| chr13 | 115169878 | 4158550 | 0.0361 | 0.2109 |
| chr14 | 107349540 | 4065560 | 0.0379 | 0.235 |
| chr15 | 102531392 | 3890587 | 0.0379 | 0.2173 |
| chr16 | 90354753 | 3852575 | 0.0426 | 0.2476 |
| chr17 | 81195210 | 3699761 | 0.0456 | 0.2697 |
| chr18 | 78077248 | 3608566 | 0.0462 | 0.533 |
| chr19 | 59128983 | 2688337 | 0.0455 | 0.4945 |
| chr20 | 63025520 | 2881573 | 0.0457 | 0.2539 |
| chr21 | 48129895 | 1796222 | 0.0373 | 0.2484 |
| chr22 | 51304566 | 1612958 | 0.0314 | 0.1999 |
| chrMT | 16571 | 10263 | 0.6193 | 0.9478 |
| chrX | 155270560 | 7628116 | 0.0491 | 0.2879 |
| chrY | 59373566 | 410714 | 0.0069 | 0.2429 |

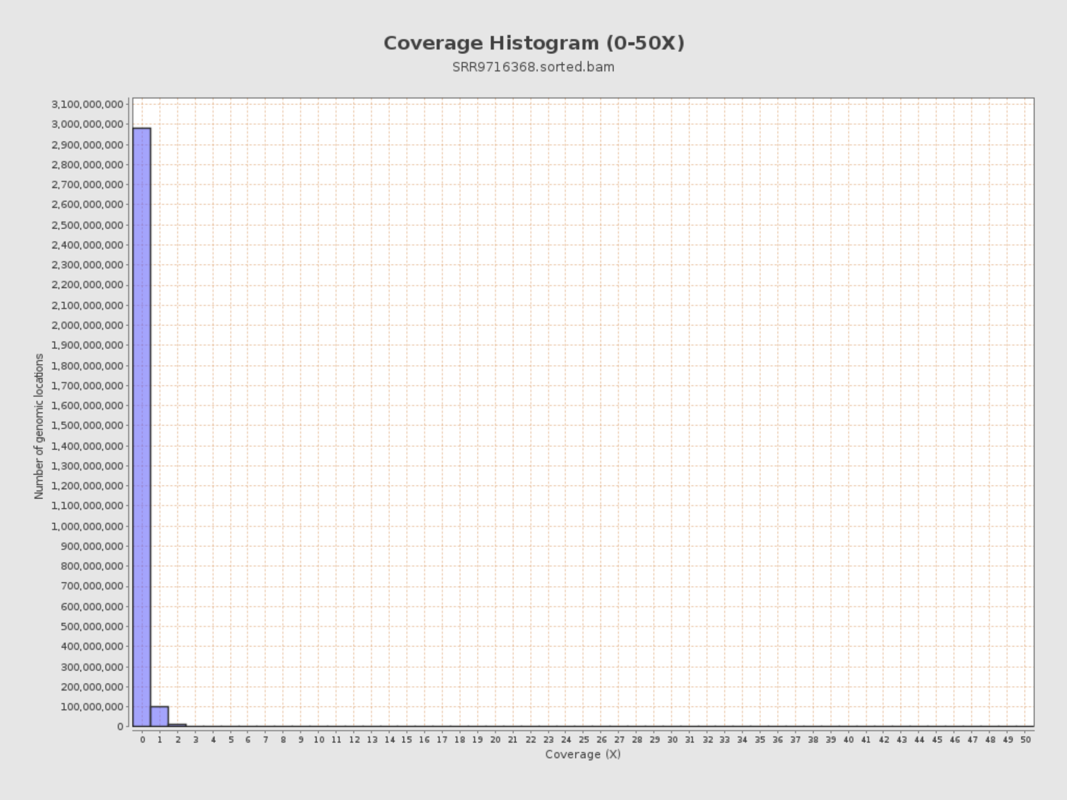
# 3. Results : Coverage across reference



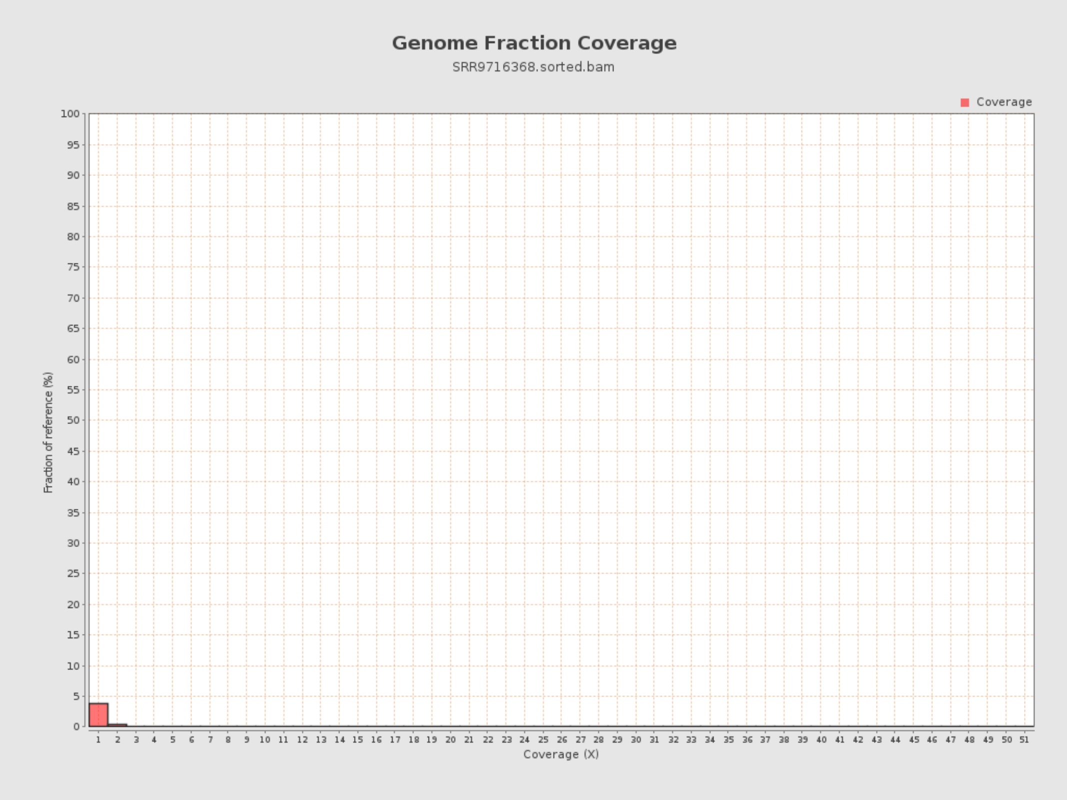
# 4. Results : Coverage Histogram



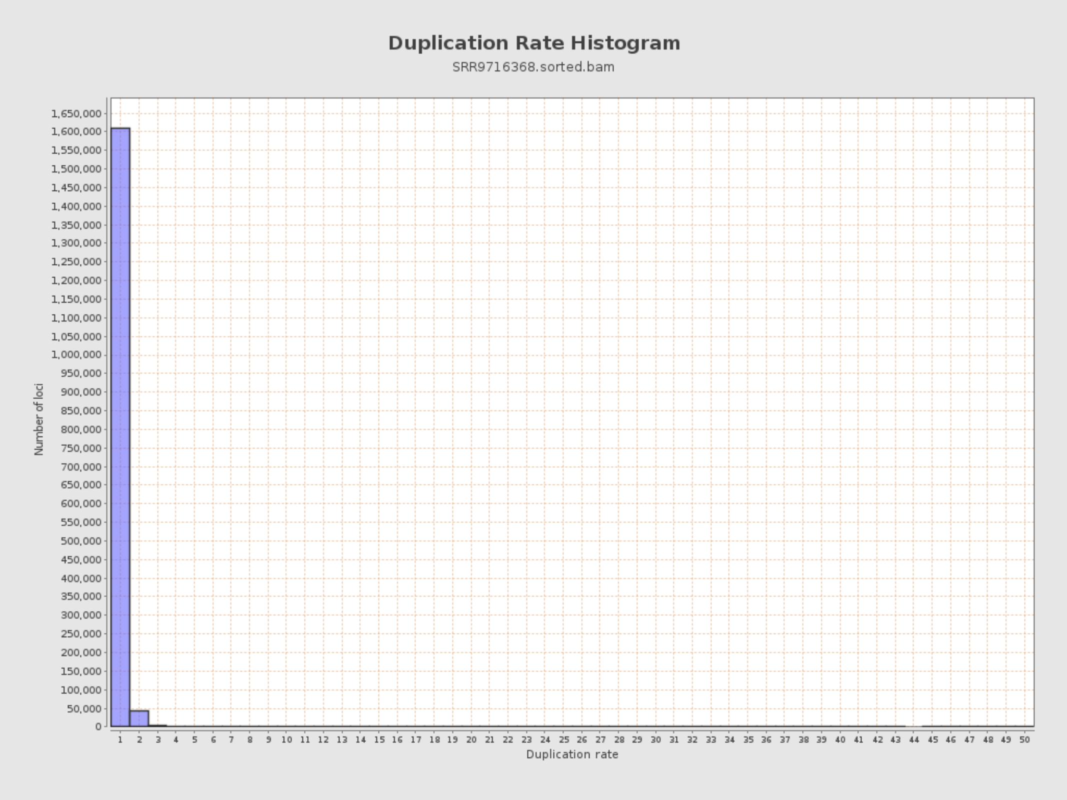
# 5. Results : Coverage Histogram (0-50X)



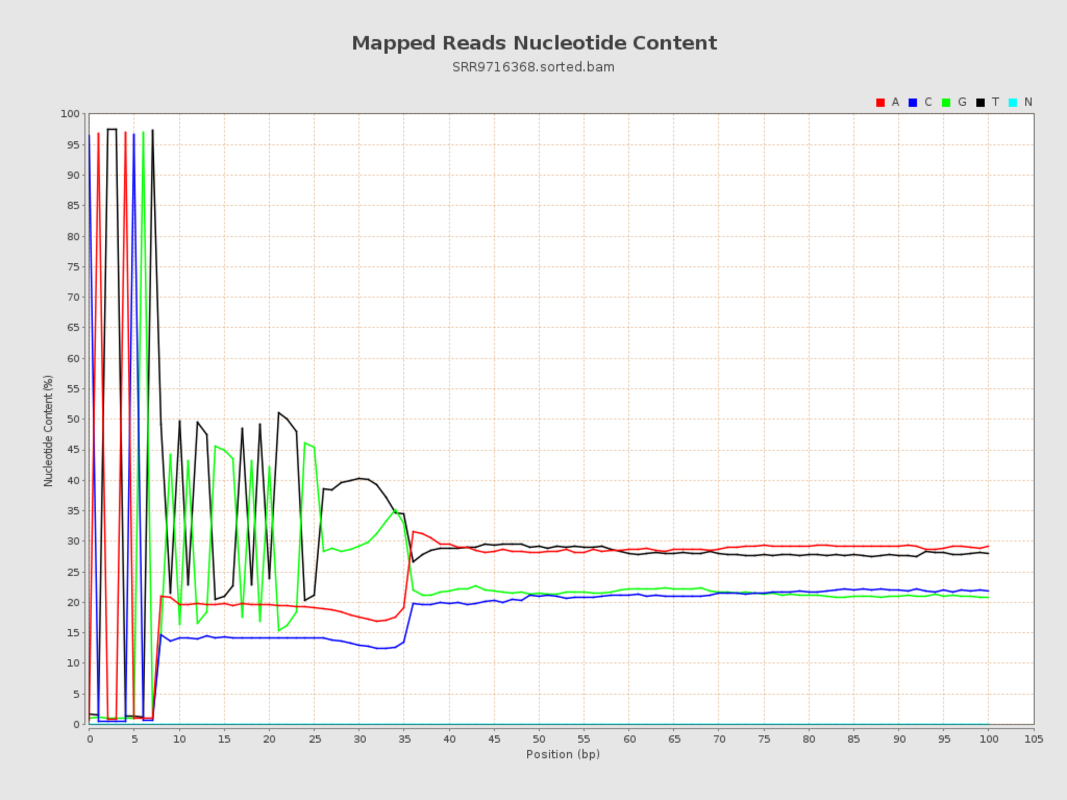
# 6. Results : Genome Fraction Coverage



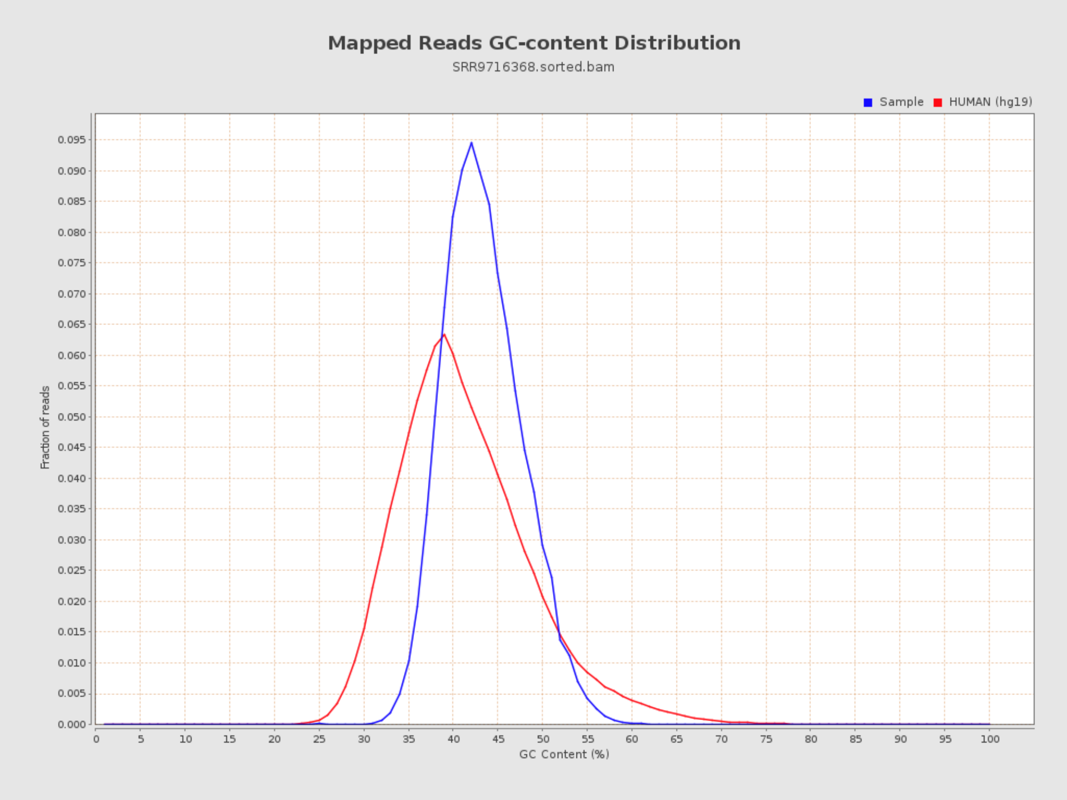
# 7. Results : Duplication Rate Histogram



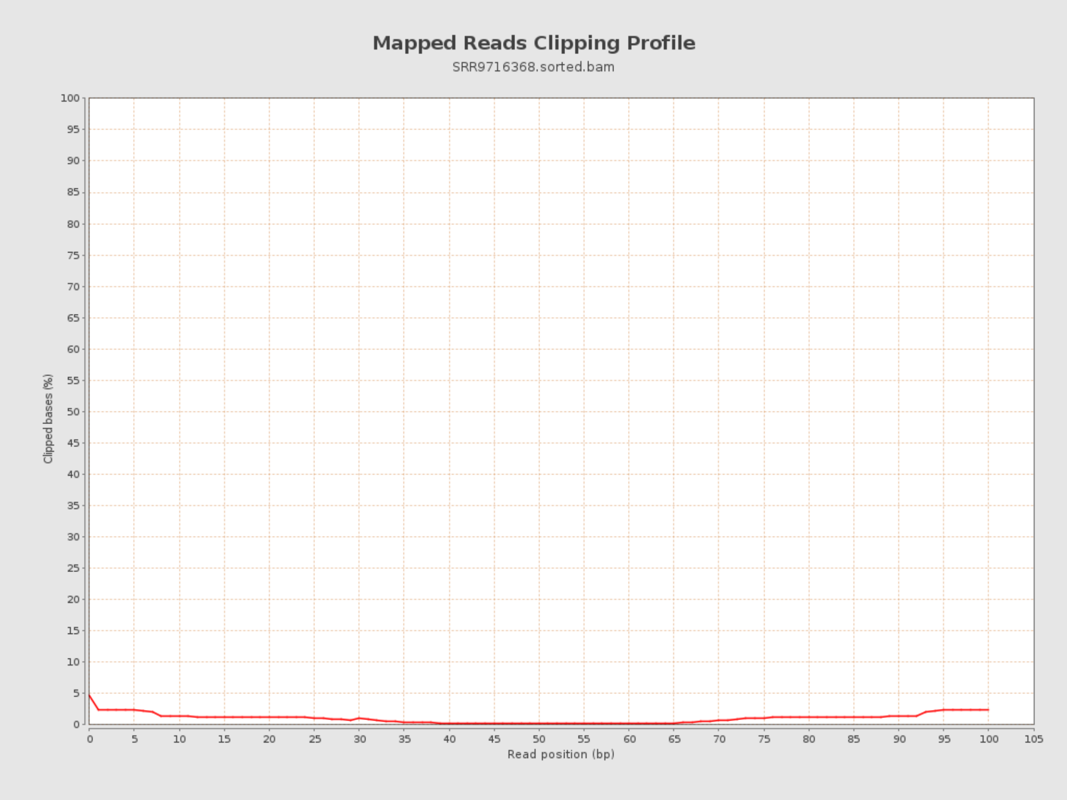
# 8. Results : Mapped Reads Nucleotide Content



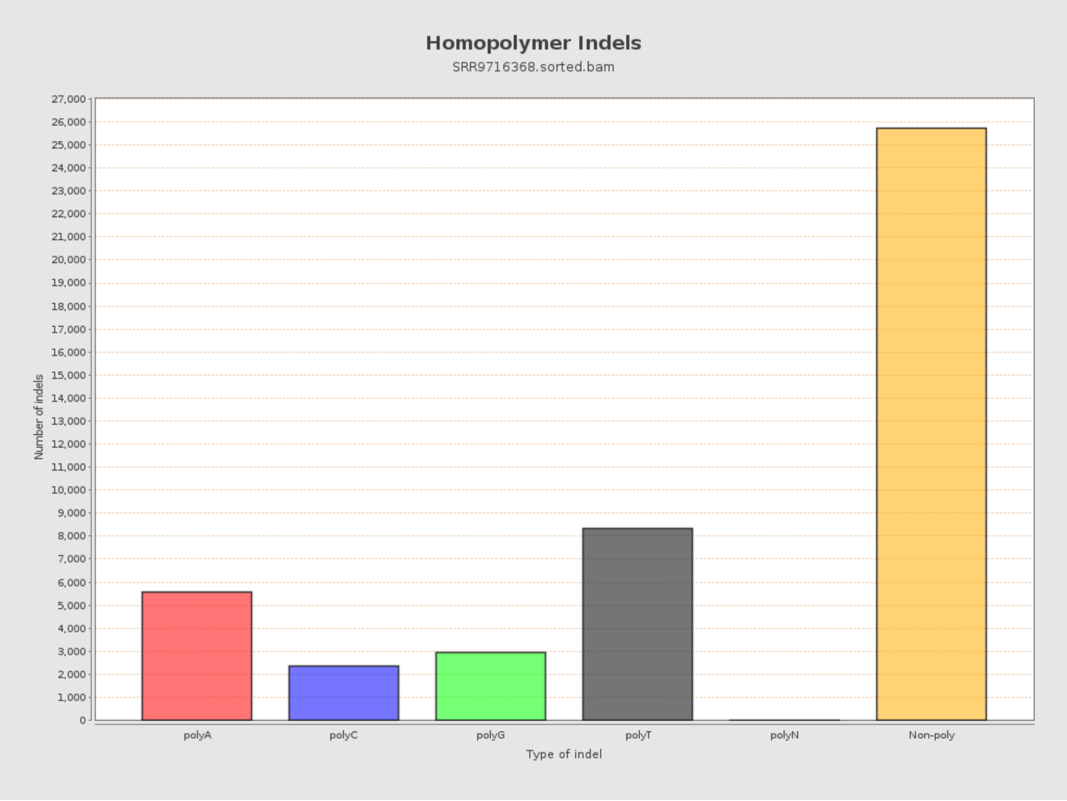
# 9. Results : Mapped Reads GC-content Distribution



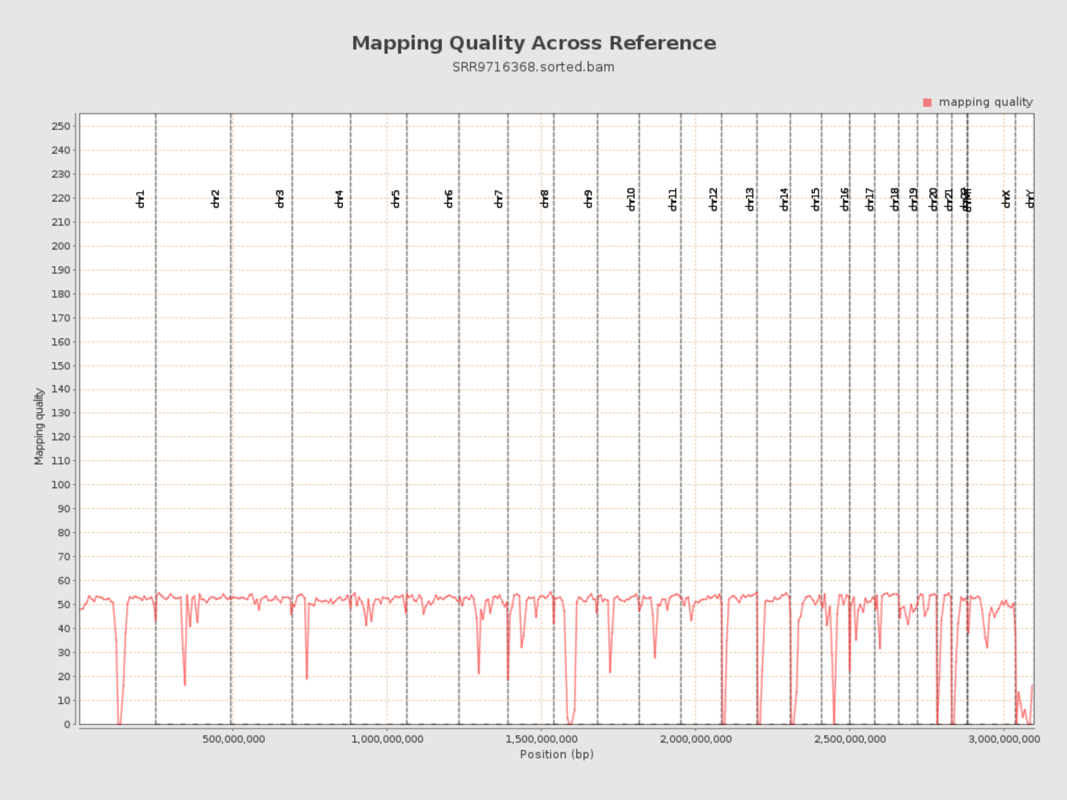
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram