# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/25 23:09:29*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085036.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_SRR3085036 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085036.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Aug 25 23:09:28 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3085036.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,761,718 |
| Mapped reads | 2,509,769 / 90.88% |
| Unmapped reads | 251,949 / 9.12% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 16,942 / 0.61% |
| Read min/max/mean length | 30 / 76 / 76.21 |
| Duplicated reads (estimated) | 89,094 / 3.23% |
| Duplication rate | 2.72% |
| Clipped reads | 1,143,209 / 41.39% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 46,613,345 / 27.79% |
| Number/percentage of C's | 32,756,612 / 19.53% |
| Number/percentage of T's | 50,884,341 / 30.34% |
| Number/percentage of G's | 37,465,837 / 22.34% |
| Number/percentage of N's | 18,926 / 0.01% |
| GC Percentage | 41.86% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0542 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4058 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.72 |

## 2.5. Mismatches and indels

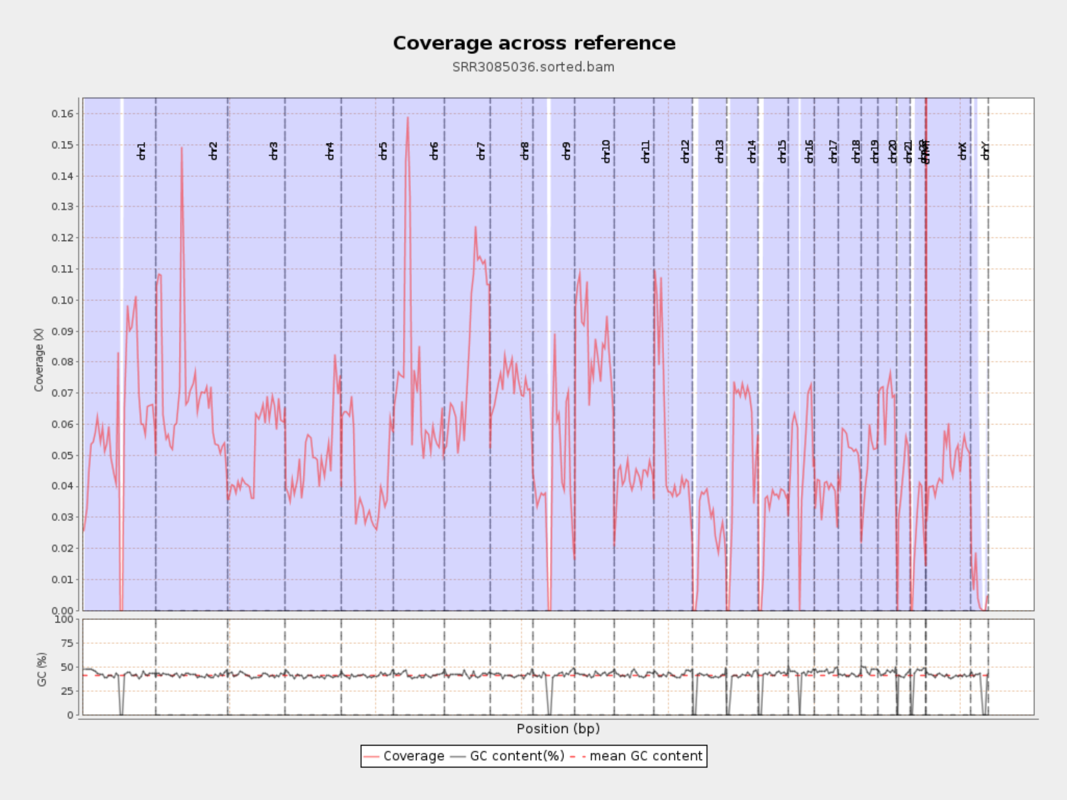
| | |
|---|---|
| General error rate | 0.89% |
| Mismatches | 1,473,178 |
| Insertions | 12,275 |
| Mapped reads with at least one insertion | 0.48% |
| Deletions | 34,682 |
| Mapped reads with at least one deletion | 1.37% |
| Homopolymer indels | 46.01% |

## 2.6. Chromosome stats

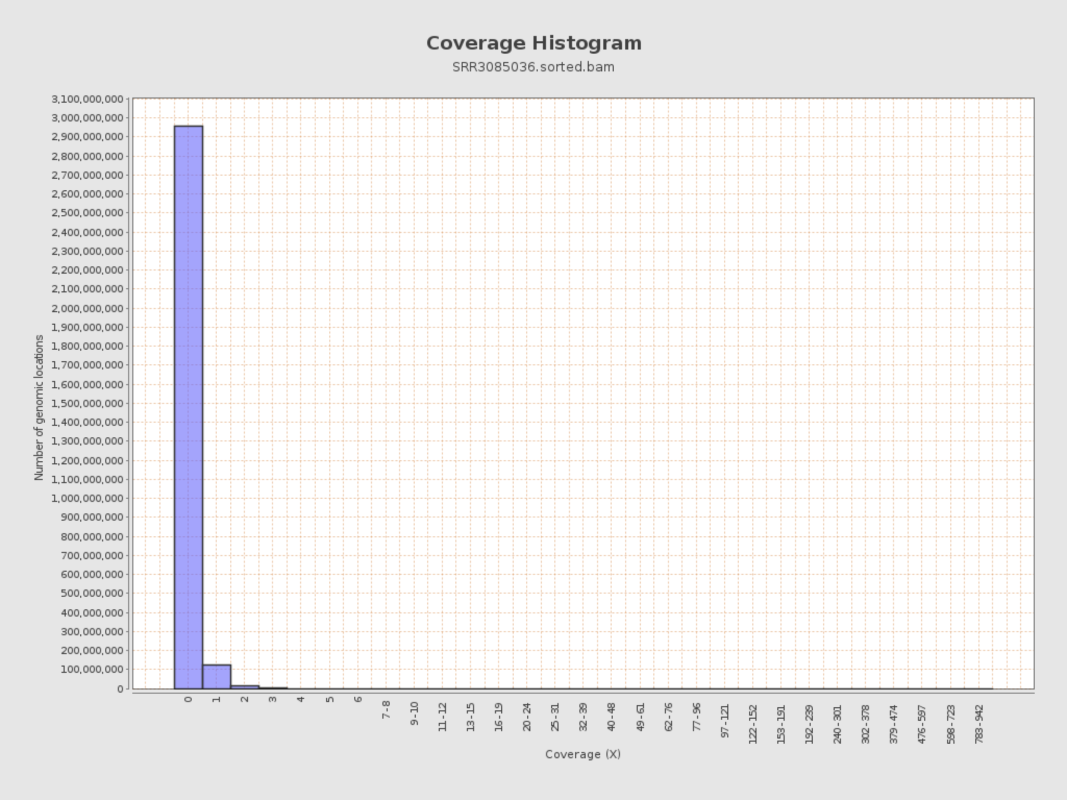
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 14569447 | 0.0585 | 0.5611 |
| chr2 | 243199373 | 17167849 | 0.0706 | 0.5705 |
| chr3 | 198022430 | 10283569 | 0.0519 | 0.2625 |
| chr4 | 191154276 | 9522178 | 0.0498 | 0.267 |
| chr5 | 180915260 | 7744830 | 0.0428 | 0.237 |
| chr6 | 171115067 | 12746055 | 0.0745 | 0.4722 |
| chr7 | 159138663 | 13260621 | 0.0833 | 0.4341 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 10565310 | 0.0722 | 0.6503 |
| chr9 | 141213431 | 6036804 | 0.0427 | 0.3848 |
| chr10 | 135534747 | 11752728 | 0.0867 | 0.5081 |
| chr11 | 135006516 | 5734782 | 0.0425 | 0.3628 |
| chr12 | 133851895 | 7305672 | 0.0546 | 0.2757 |
| chr13 | 115169878 | 2923515 | 0.0254 | 0.1802 |
| chr14 | 107349540 | 5788564 | 0.0539 | 0.282 |
| chr15 | 102531392 | 3050779 | 0.0298 | 0.2058 |
| chr16 | 90354753 | 4461640 | 0.0494 | 0.2784 |
| chr17 | 81195210 | 3096408 | 0.0381 | 0.2456 |
| chr18 | 78077248 | 4018251 | 0.0515 | 0.6827 |
| chr19 | 59128983 | 2777540 | 0.047 | 0.4326 |
| chr20 | 63025520 | 4256306 | 0.0675 | 0.3035 |
| chr21 | 48129895 | 1902393 | 0.0395 | 0.2422 |
| chr22 | 51304566 | 1229021 | 0.024 | 0.174 |
| chrMT | 16571 | 10292 | 0.6211 | 0.9936 |
| chrX | 155270560 | 7248384 | 0.0467 | 0.2841 |
| chrY | 59373566 | 346019 | 0.0058 | 0.1348 |

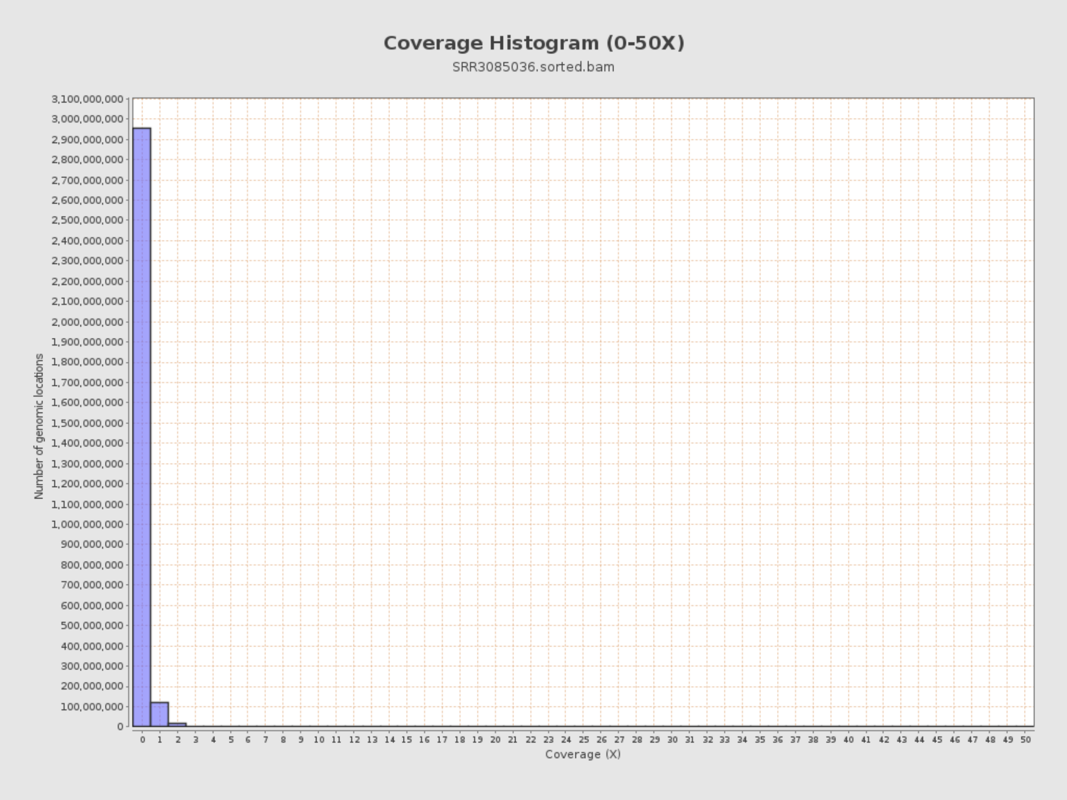
# 3. Results : Coverage across reference



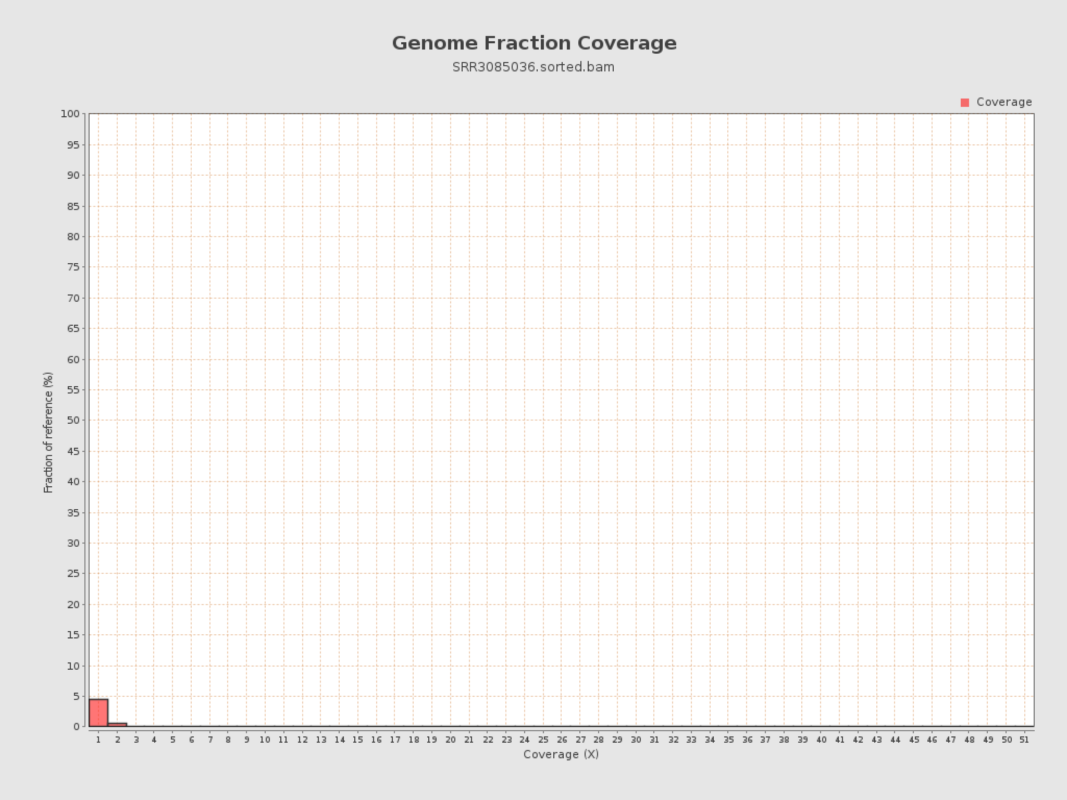
# 4. Results : Coverage Histogram



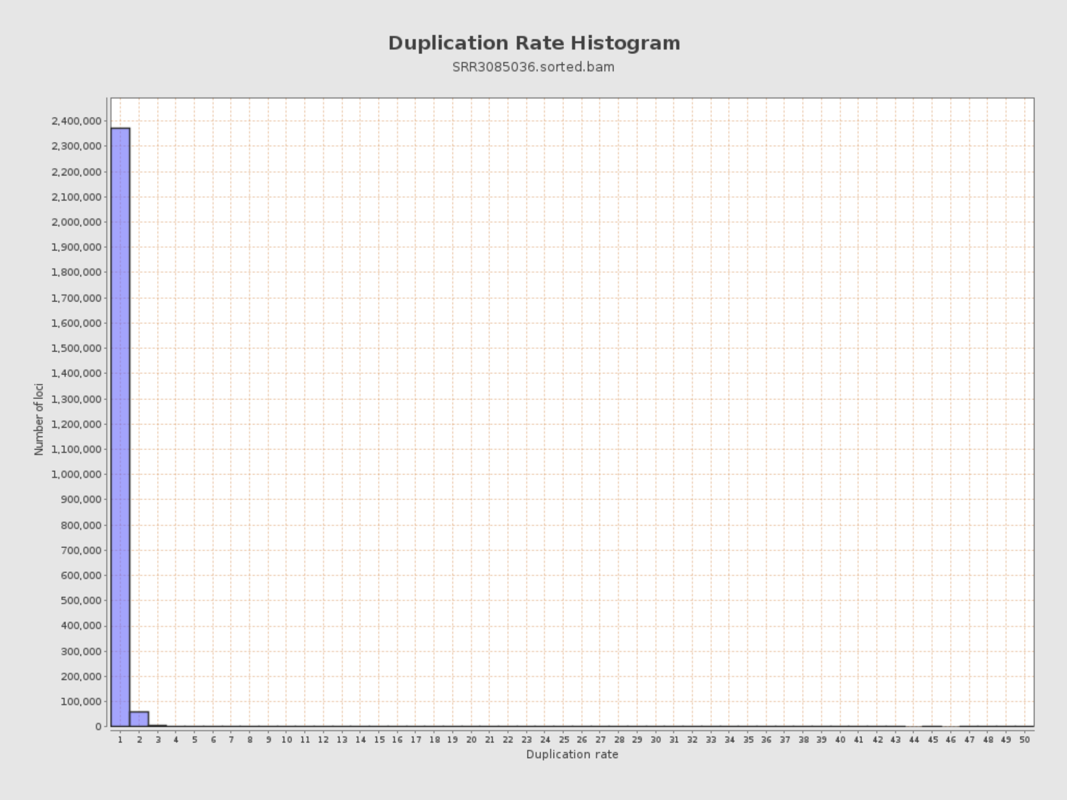
# 5. Results : Coverage Histogram (0-50X)



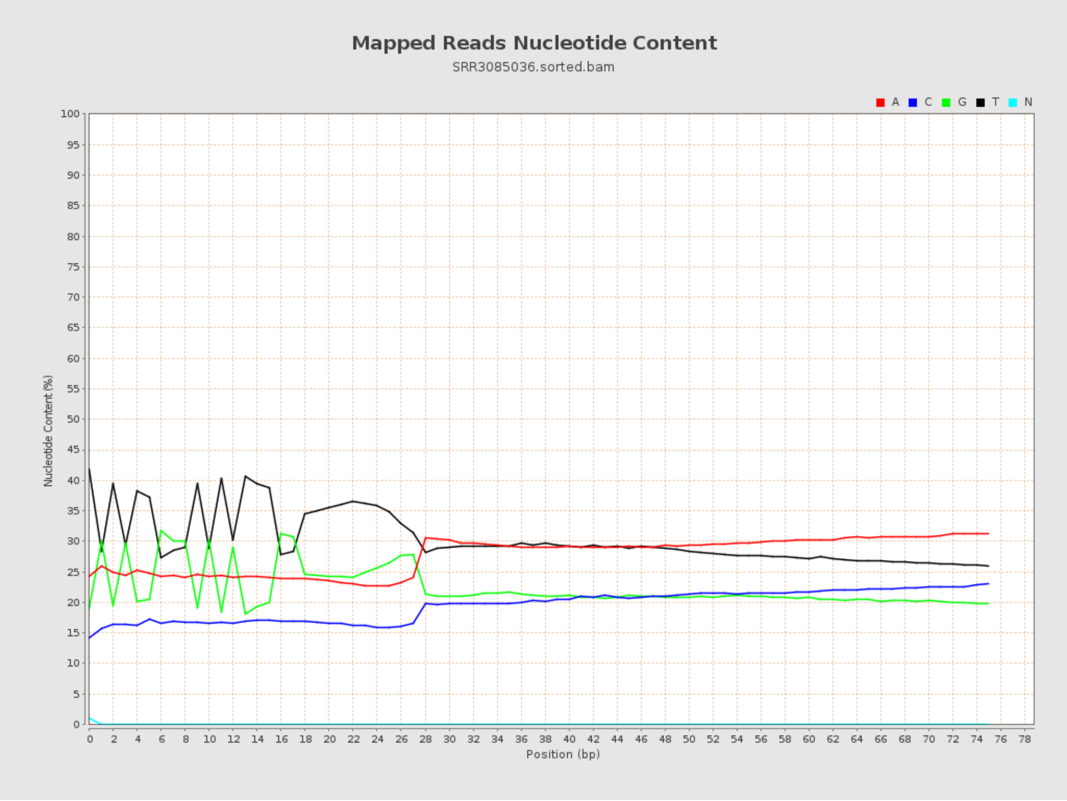
# 6. Results : Genome Fraction Coverage



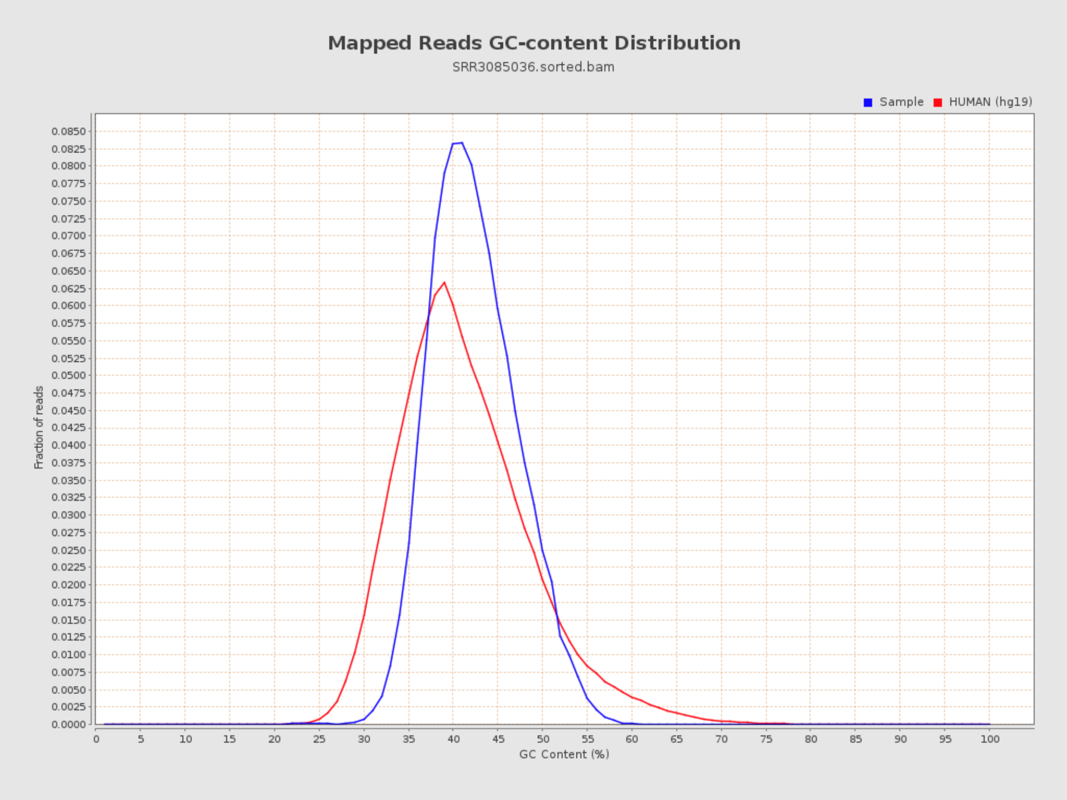
# 7. Results : Duplication Rate Histogram



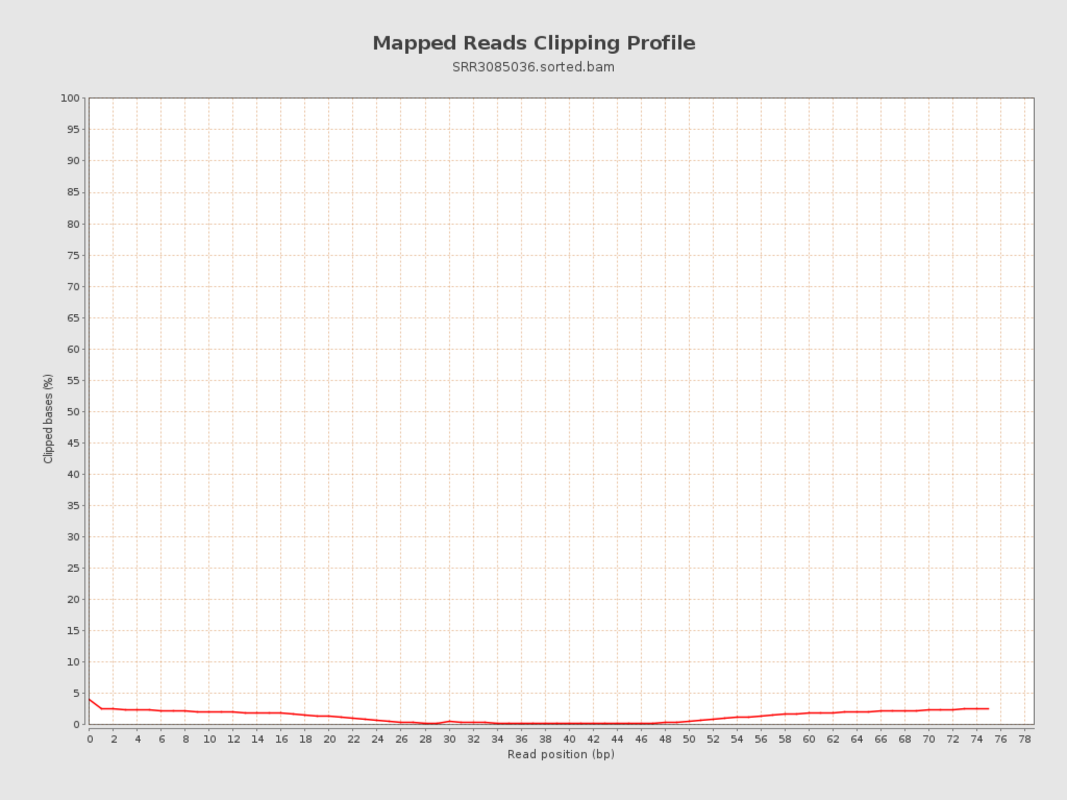
# 8. Results : Mapped Reads Nucleotide Content



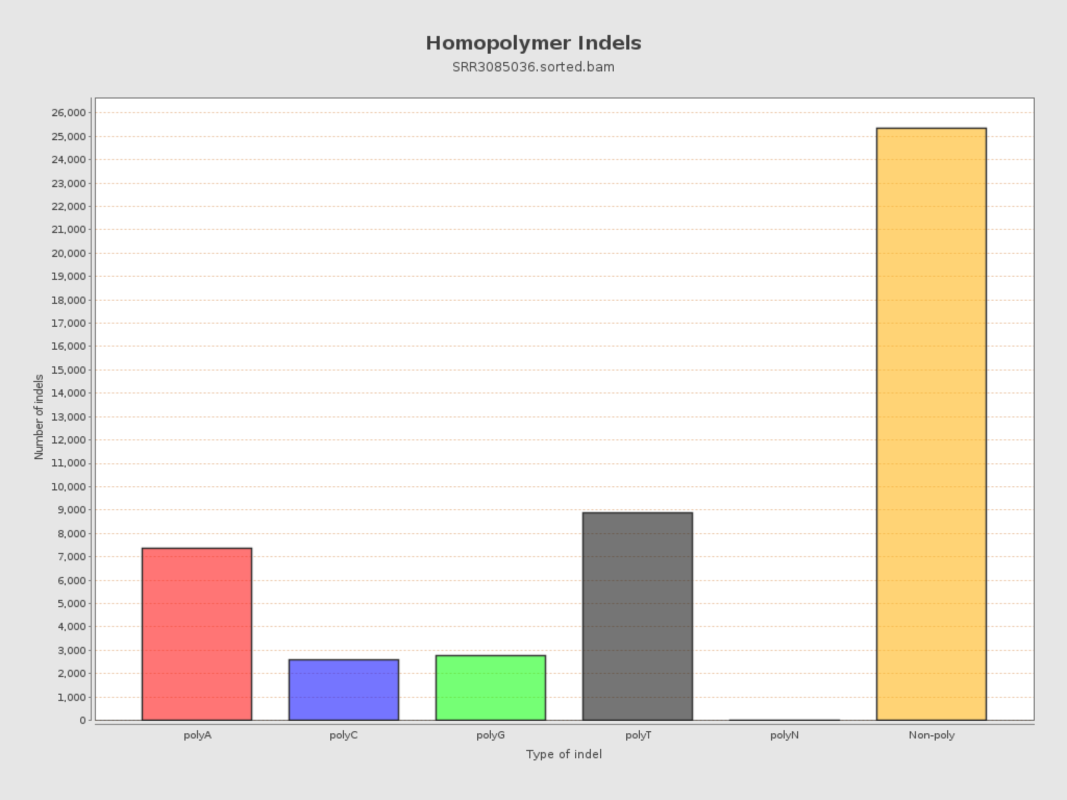
# 9. Results : Mapped Reads GC-content Distribution



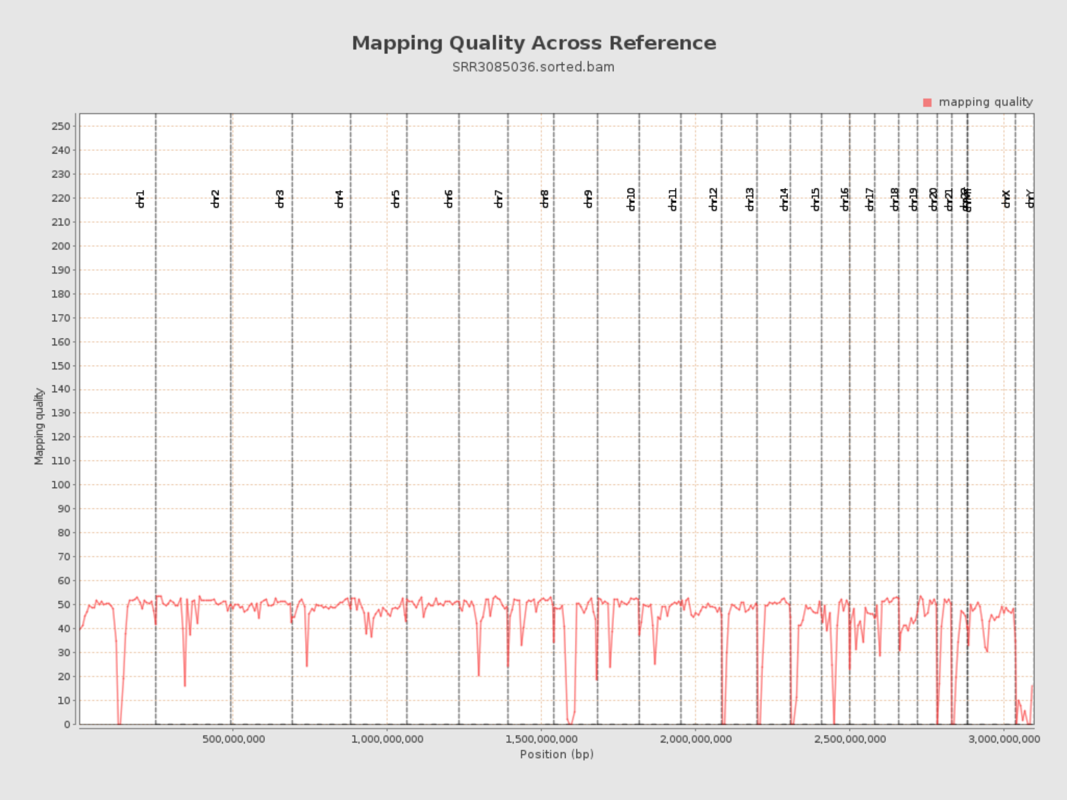
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram