# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/25 22:13:40*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085021.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_SRR3085021 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085021.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Aug 25 22:13:39 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3085021.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,394,338 |
| Mapped reads | 2,170,548 / 90.65% |
| Unmapped reads | 223,790 / 9.35% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 17,642 / 0.74% |
| Read min/max/mean length | 30 / 76 / 76.26 |
| Duplicated reads (estimated) | 85,625 / 3.58% |
| Duplication rate | 3.17% |
| Clipped reads | 980,564 / 40.95% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 40,711,572 / 28.07% |
| Number/percentage of C's | 27,787,305 / 19.16% |
| Number/percentage of T's | 44,836,871 / 30.92% |
| Number/percentage of G's | 31,684,831 / 21.85% |
| Number/percentage of N's | 3,753 / 0% |
| GC Percentage | 41.01% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0469 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3573 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.8 |

## 2.5. Mismatches and indels

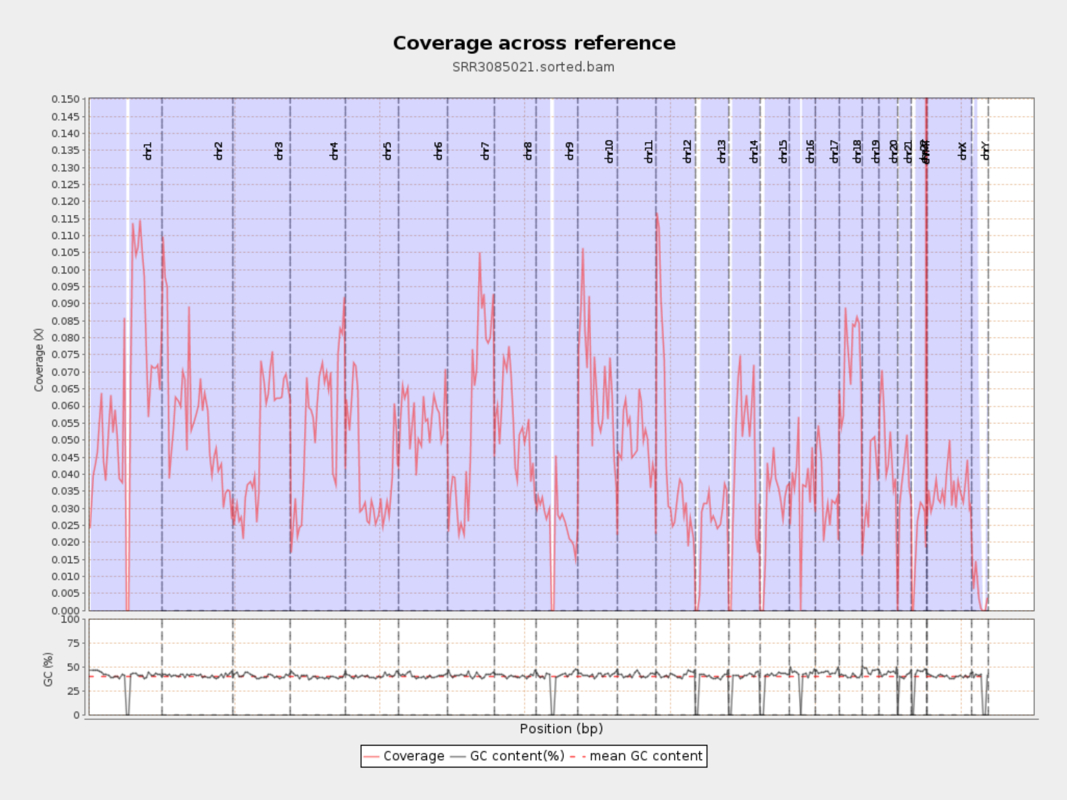
| | |
|---|---|
| General error rate | 0.84% |
| Mismatches | 1,207,813 |
| Insertions | 10,035 |
| Mapped reads with at least one insertion | 0.46% |
| Deletions | 29,826 |
| Mapped reads with at least one deletion | 1.36% |
| Homopolymer indels | 46.84% |

## 2.6. Chromosome stats

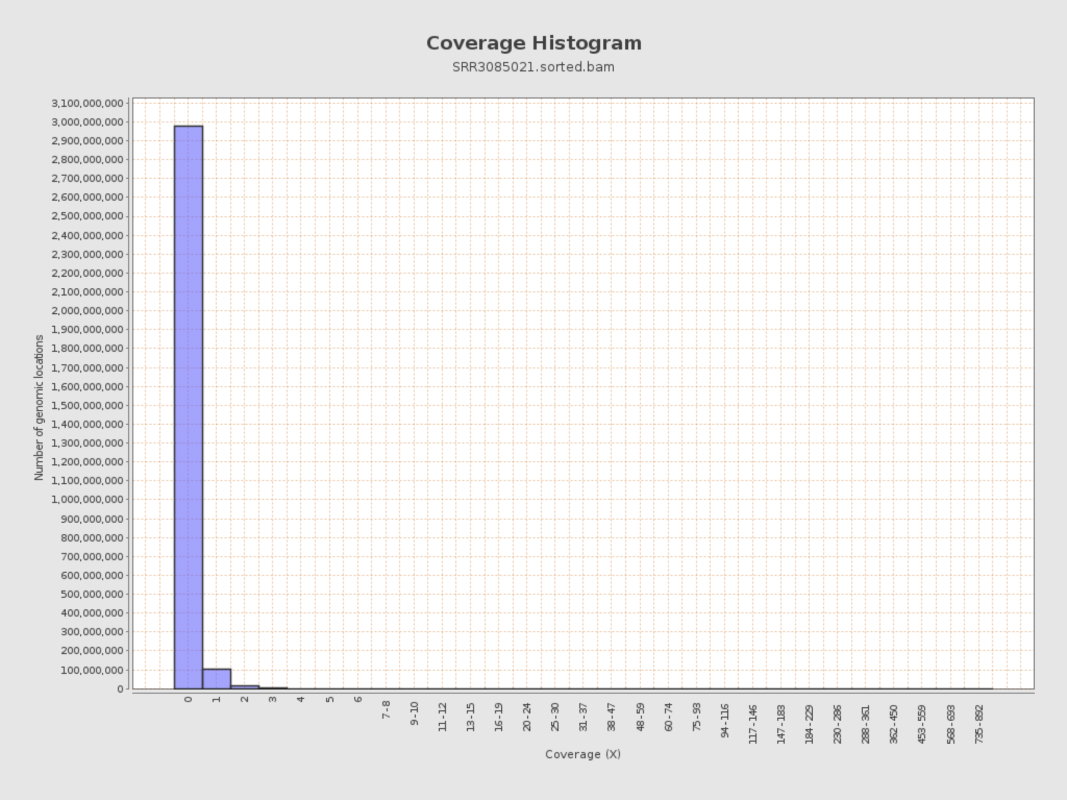
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 15549850 | 0.0624 | 0.5172 |
| chr2 | 243199373 | 13667453 | 0.0562 | 0.4809 |
| chr3 | 198022430 | 9781741 | 0.0494 | 0.2664 |
| chr4 | 191154276 | 10433150 | 0.0546 | 0.2754 |
| chr5 | 180915260 | 7407469 | 0.0409 | 0.2348 |
| chr6 | 171115067 | 9549106 | 0.0558 | 0.3206 |
| chr7 | 159138663 | 9025420 | 0.0567 | 0.3175 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 7954644 | 0.0543 | 0.6046 |
| chr9 | 141213431 | 3440407 | 0.0244 | 0.2938 |
| chr10 | 135534747 | 9221896 | 0.068 | 0.467 |
| chr11 | 135006516 | 6729118 | 0.0498 | 0.3541 |
| chr12 | 133851895 | 6034023 | 0.0451 | 0.253 |
| chr13 | 115169878 | 2849589 | 0.0247 | 0.1801 |
| chr14 | 107349540 | 4822327 | 0.0449 | 0.2572 |
| chr15 | 102531392 | 3080983 | 0.03 | 0.2034 |
| chr16 | 90354753 | 3253590 | 0.036 | 0.2368 |
| chr17 | 81195210 | 2743505 | 0.0338 | 0.2345 |
| chr18 | 78077248 | 5824972 | 0.0746 | 0.5867 |
| chr19 | 59128983 | 2223234 | 0.0376 | 0.3931 |
| chr20 | 63025520 | 3018001 | 0.0479 | 0.2582 |
| chr21 | 48129895 | 1696102 | 0.0352 | 0.2248 |
| chr22 | 51304566 | 1056790 | 0.0206 | 0.163 |
| chrMT | 16571 | 19869 | 1.199 | 1.3195 |
| chrX | 155270560 | 5410450 | 0.0348 | 0.2462 |
| chrY | 59373566 | 281891 | 0.0047 | 0.1012 |

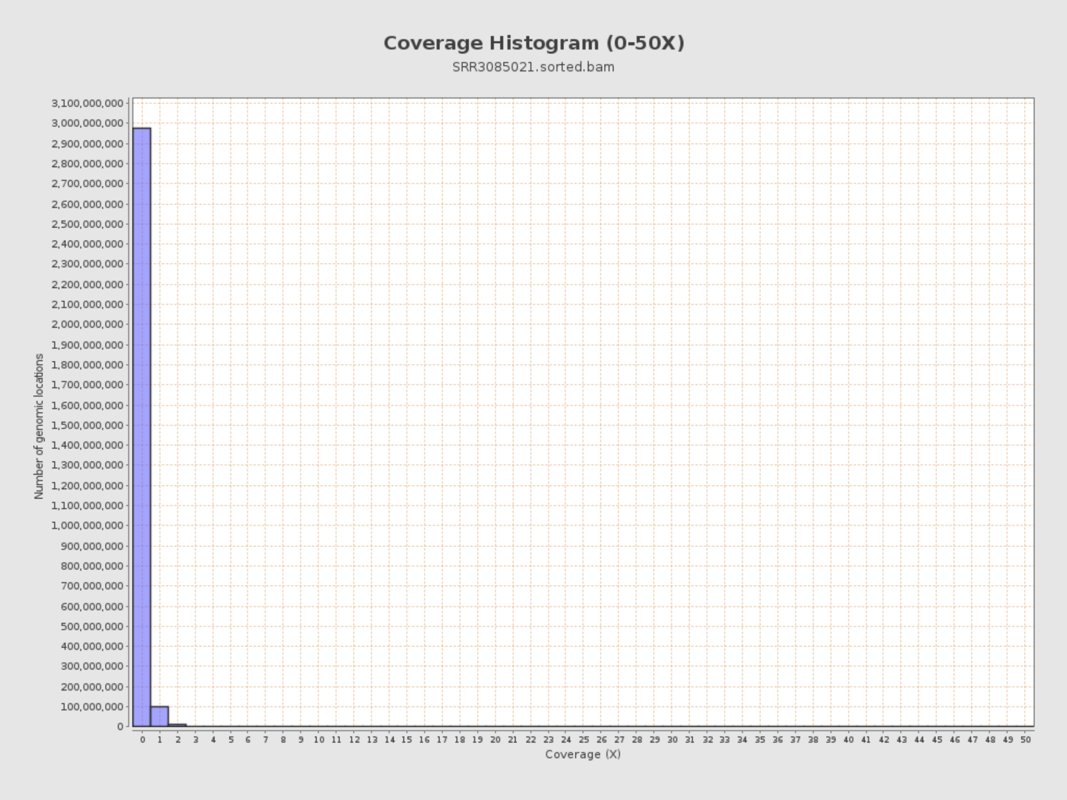
# 3. Results : Coverage across reference



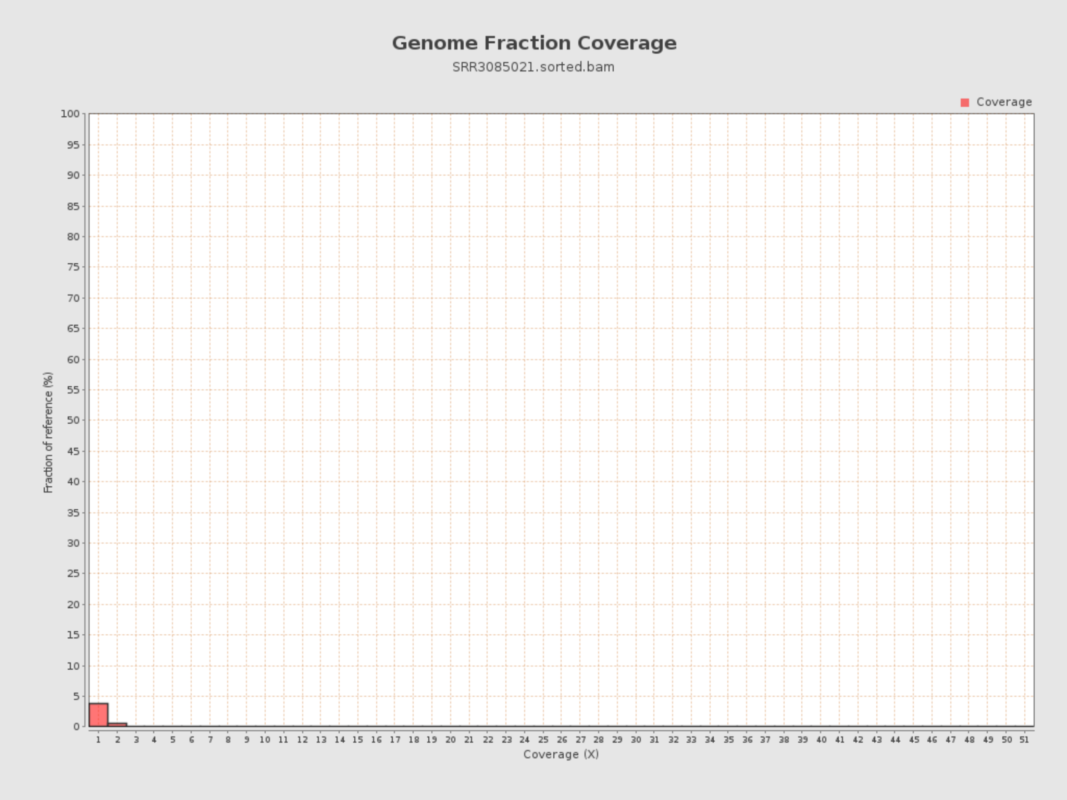
# 4. Results : Coverage Histogram



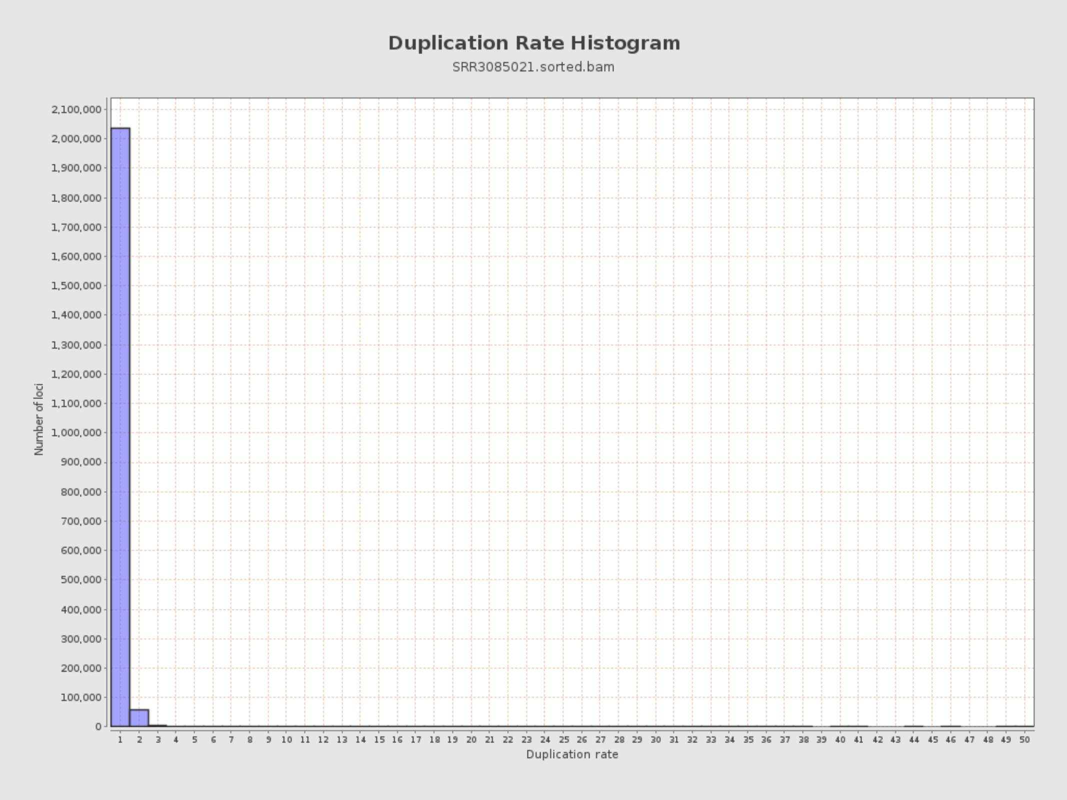
# 5. Results : Coverage Histogram (0-50X)



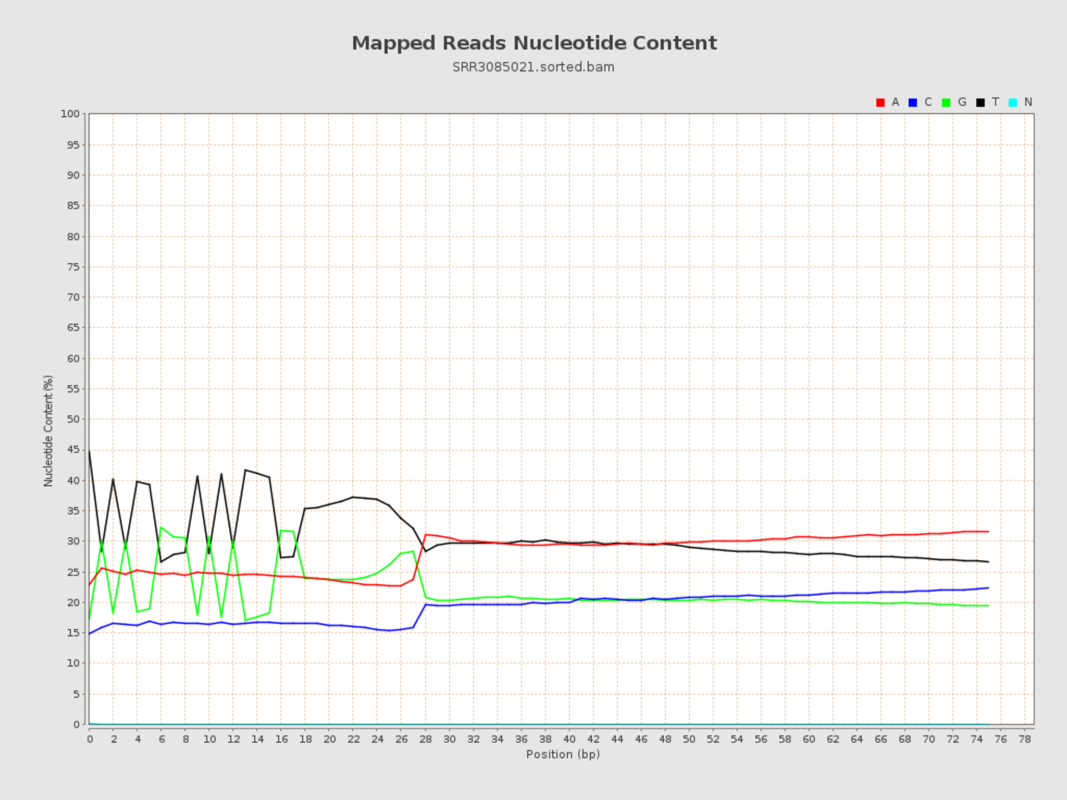
# 6. Results : Genome Fraction Coverage



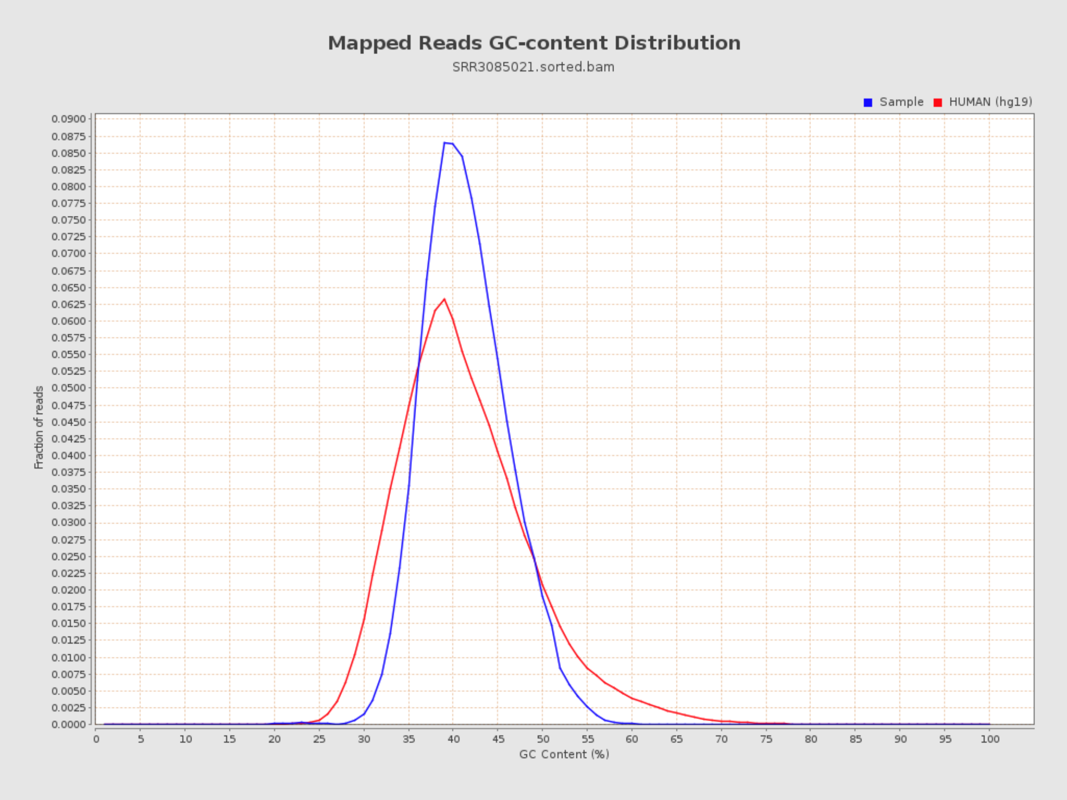
# 7. Results : Duplication Rate Histogram



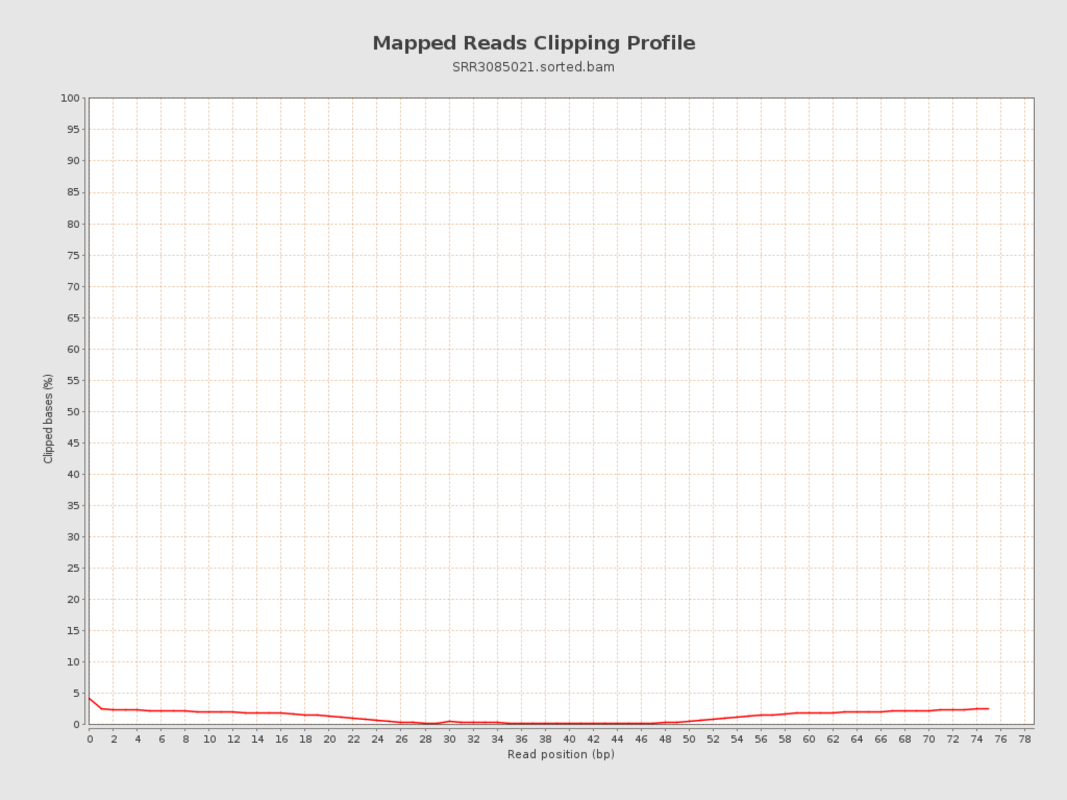
# 8. Results : Mapped Reads Nucleotide Content



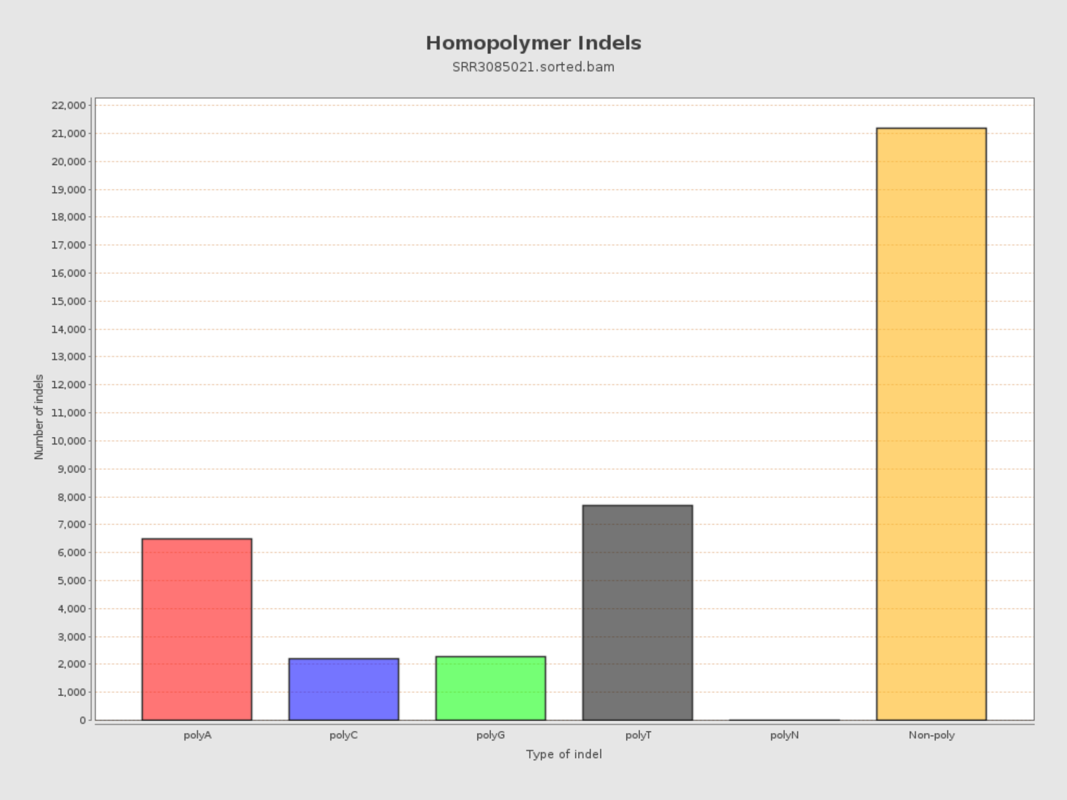
# 9. Results : Mapped Reads GC-content Distribution



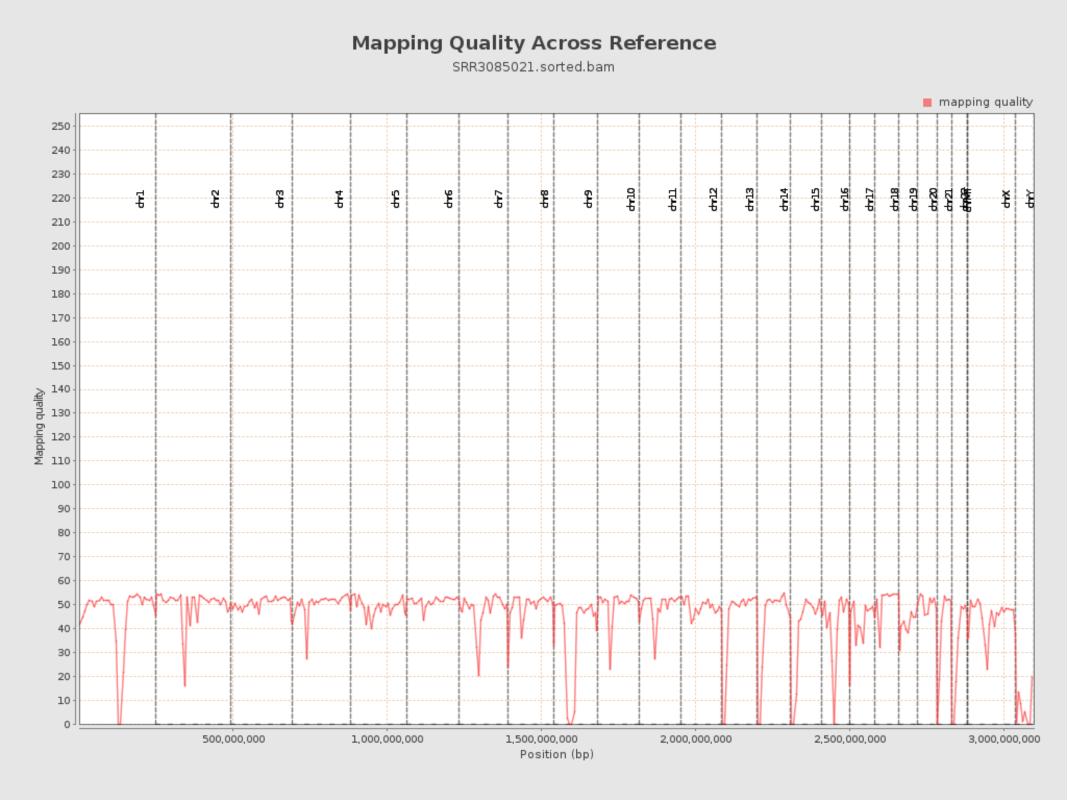
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram