# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/25 09:37:05*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084285.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_SRR3084285 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084285.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Aug 25 09:37:04 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3084285.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,501,055 |
| Mapped reads | 2,237,913 / 89.48% |
| Unmapped reads | 263,142 / 10.52% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 15,991 / 0.64% |
| Read min/max/mean length | 30 / 76 / 76.22 |
| Duplicated reads (estimated) | 70,707 / 2.83% |
| Duplication rate | 2.64% |
| Clipped reads | 1,151,421 / 46.04% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 40,860,700 / 27.86% |
| Number/percentage of C's | 28,289,691 / 19.29% |
| Number/percentage of T's | 44,656,855 / 30.45% |
| Number/percentage of G's | 32,661,124 / 22.27% |
| Number/percentage of N's | 178,417 / 0.12% |
| GC Percentage | 41.56% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0474 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3184 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.06 |

## 2.5. Mismatches and indels

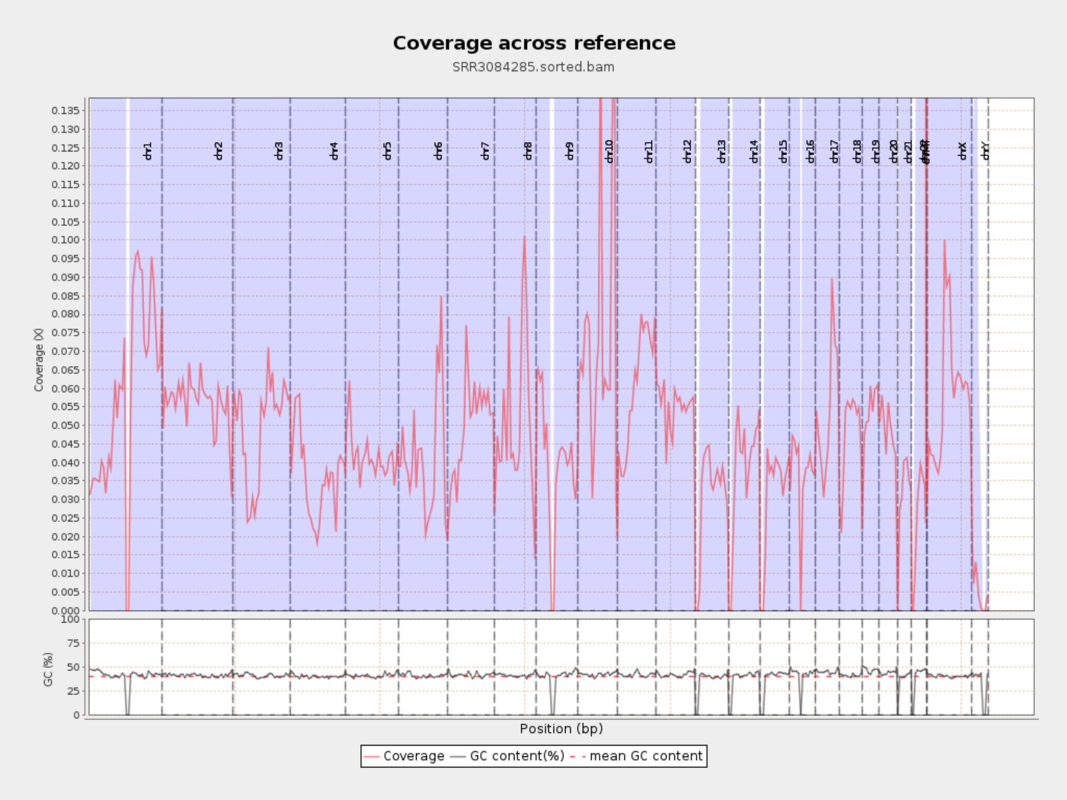
| | |
|---|---|
| General error rate | 1.05% |
| Mismatches | 1,519,218 |
| Insertions | 11,184 |
| Mapped reads with at least one insertion | 0.5% |
| Deletions | 31,106 |
| Mapped reads with at least one deletion | 1.38% |
| Homopolymer indels | 46.6% |

## 2.6. Chromosome stats

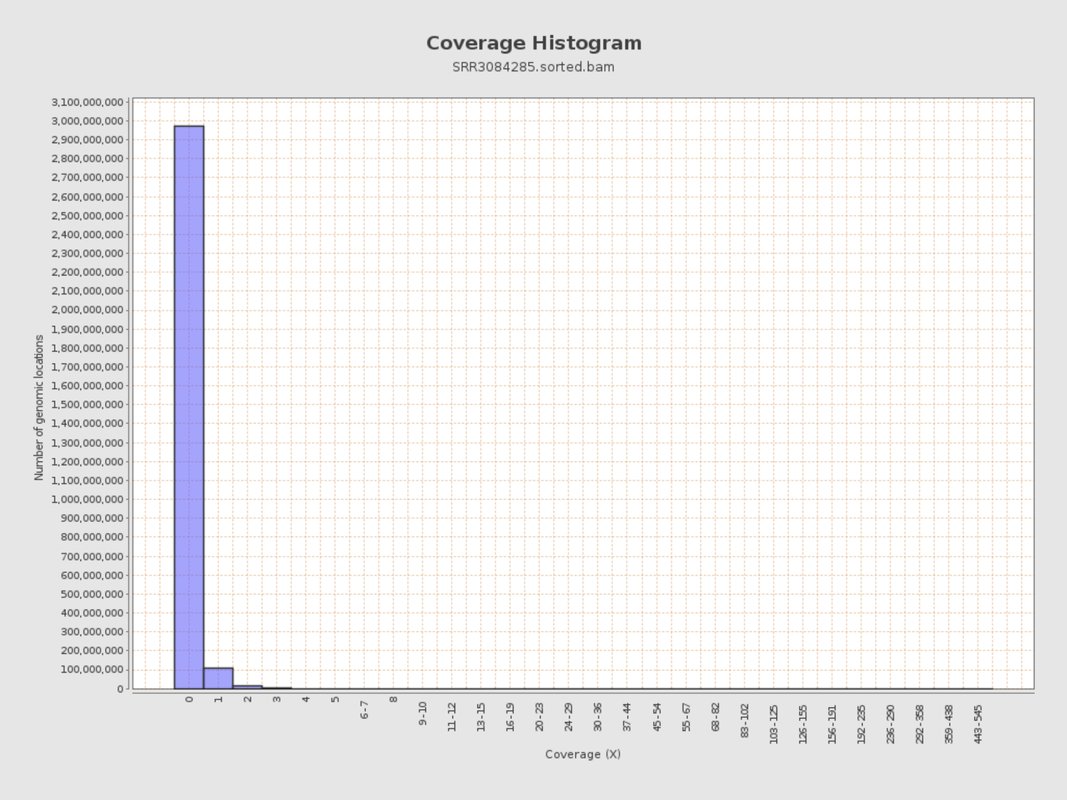
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 14421476 | 0.0579 | 0.493 |
| chr2 | 243199373 | 13671075 | 0.0562 | 0.3777 |
| chr3 | 198022430 | 9814864 | 0.0496 | 0.2557 |
| chr4 | 191154276 | 6929108 | 0.0362 | 0.2208 |
| chr5 | 180915260 | 7500405 | 0.0415 | 0.2292 |
| chr6 | 171115067 | 7044377 | 0.0412 | 0.2578 |
| chr7 | 159138663 | 8025583 | 0.0504 | 0.4443 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 7434747 | 0.0508 | 0.3077 |
| chr9 | 141213431 | 5557401 | 0.0394 | 0.2624 |
| chr10 | 135534747 | 10439920 | 0.077 | 0.4616 |
| chr11 | 135006516 | 8115505 | 0.0601 | 0.3198 |
| chr12 | 133851895 | 7330200 | 0.0548 | 0.2663 |
| chr13 | 115169878 | 3518937 | 0.0306 | 0.1974 |
| chr14 | 107349540 | 4039227 | 0.0376 | 0.2237 |
| chr15 | 102531392 | 3170098 | 0.0309 | 0.2053 |
| chr16 | 90354753 | 3324346 | 0.0368 | 0.2338 |
| chr17 | 81195210 | 4402864 | 0.0542 | 0.274 |
| chr18 | 78077248 | 3737518 | 0.0479 | 0.3882 |
| chr19 | 59128983 | 3144795 | 0.0532 | 0.3788 |
| chr20 | 63025520 | 3032631 | 0.0481 | 0.2495 |
| chr21 | 48129895 | 1509839 | 0.0314 | 0.2062 |
| chr22 | 51304566 | 1223808 | 0.0239 | 0.1743 |
| chrMT | 16571 | 33050 | 1.9944 | 1.7832 |
| chrX | 155270560 | 8975863 | 0.0578 | 0.3003 |
| chrY | 59373566 | 298434 | 0.005 | 0.1003 |

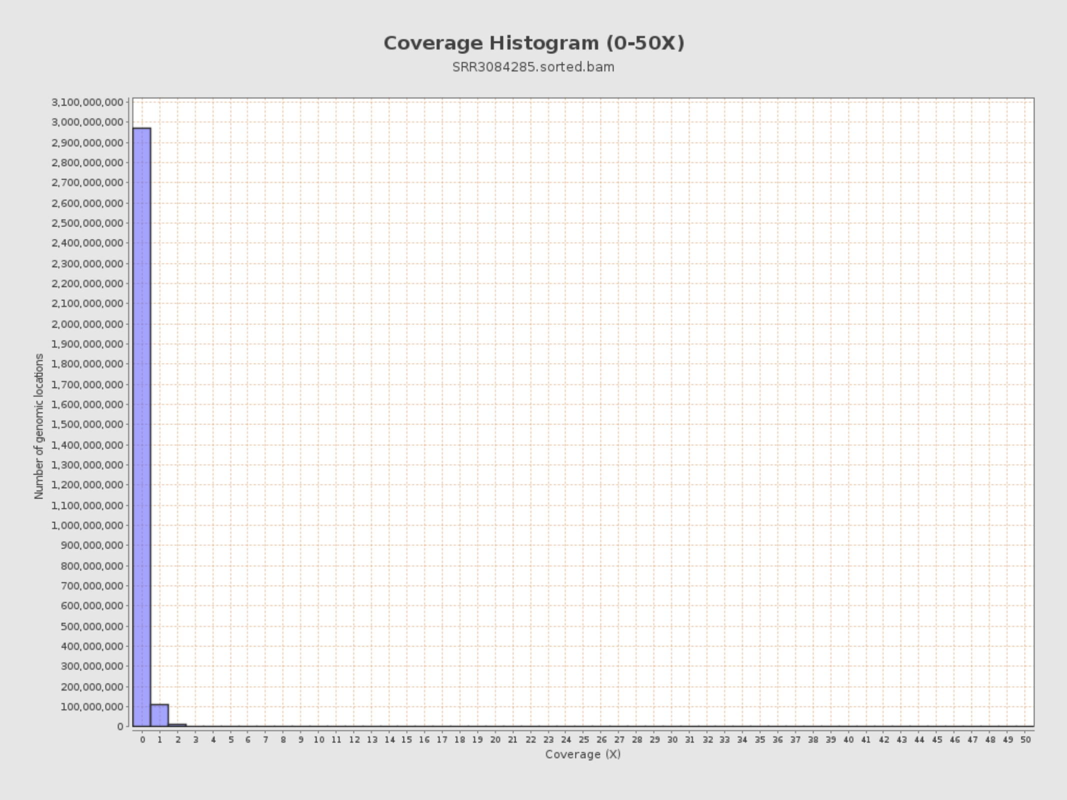
# 3. Results : Coverage across reference



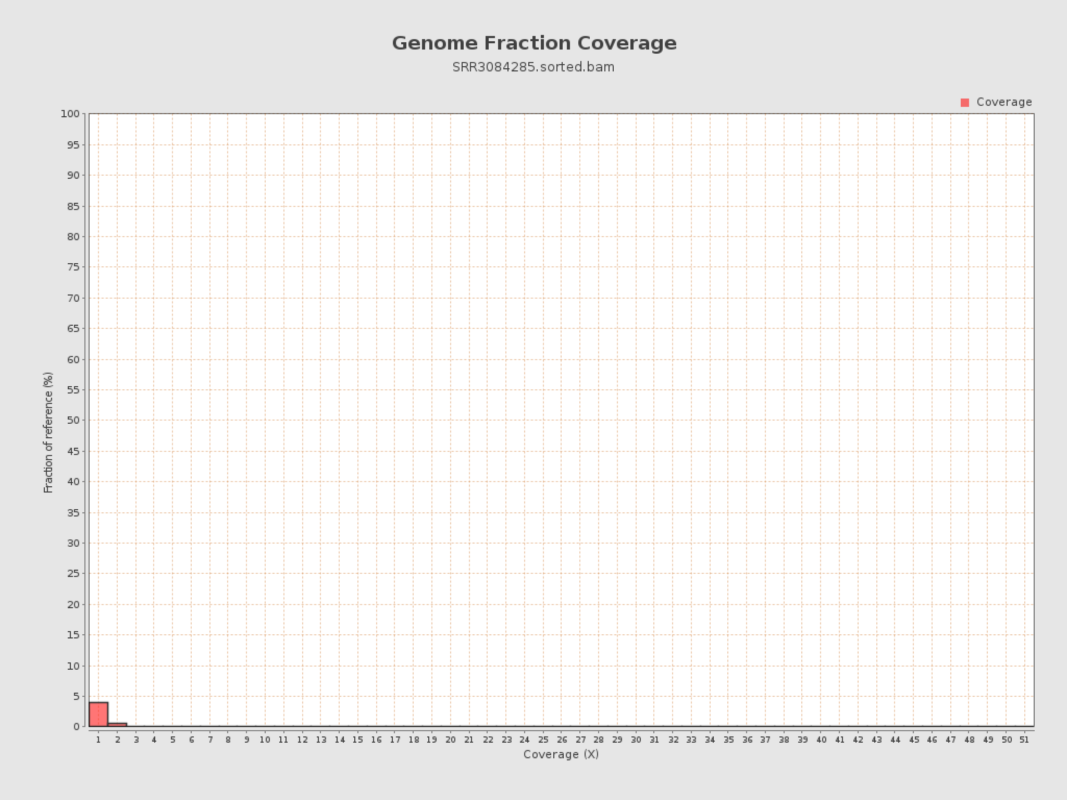
# 4. Results : Coverage Histogram



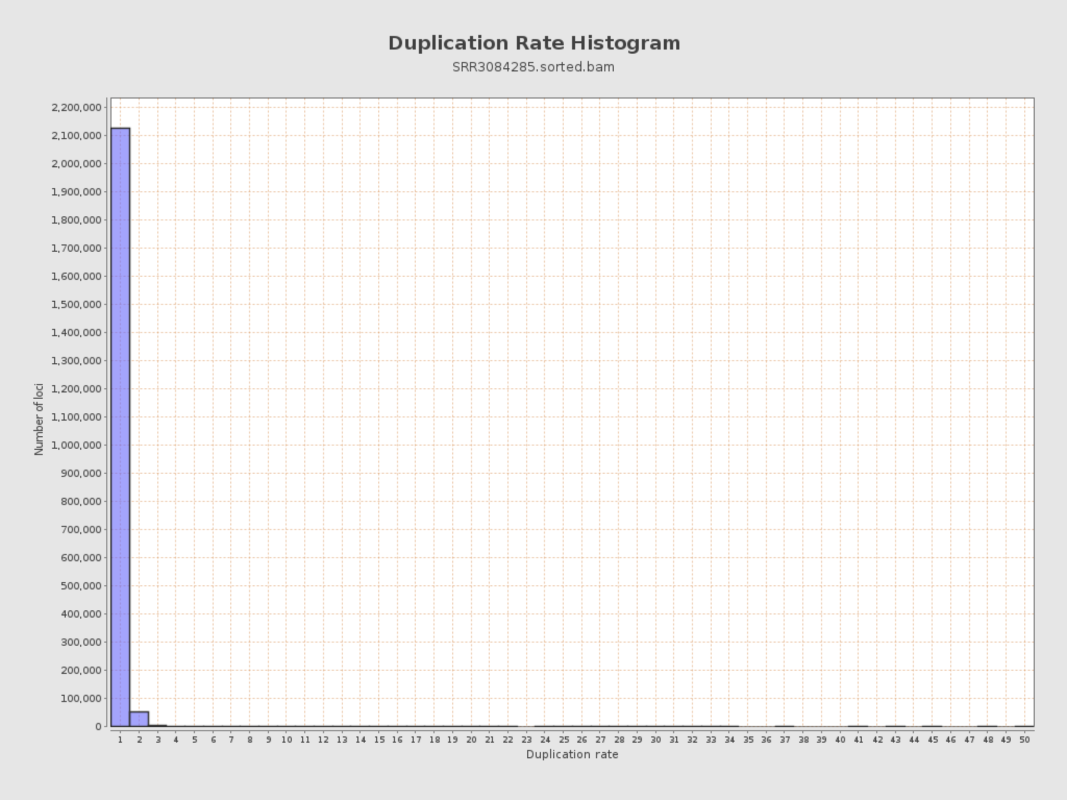
# 5. Results : Coverage Histogram (0-50X)



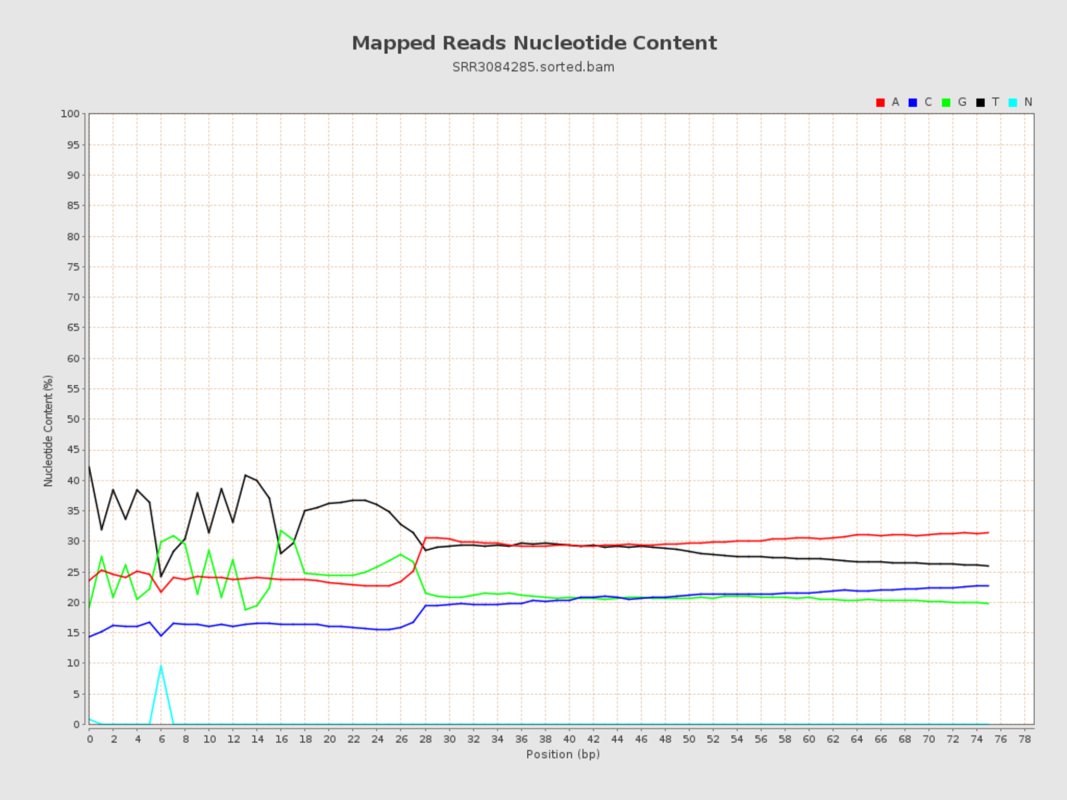
# 6. Results : Genome Fraction Coverage



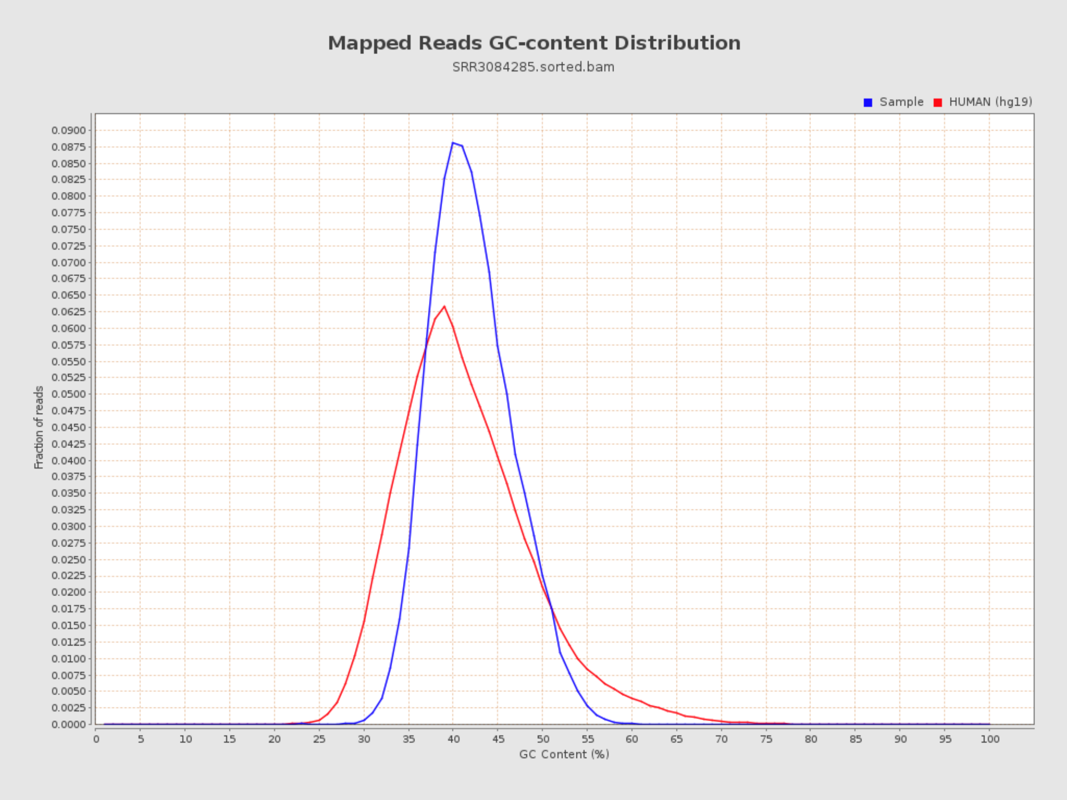
# 7. Results : Duplication Rate Histogram



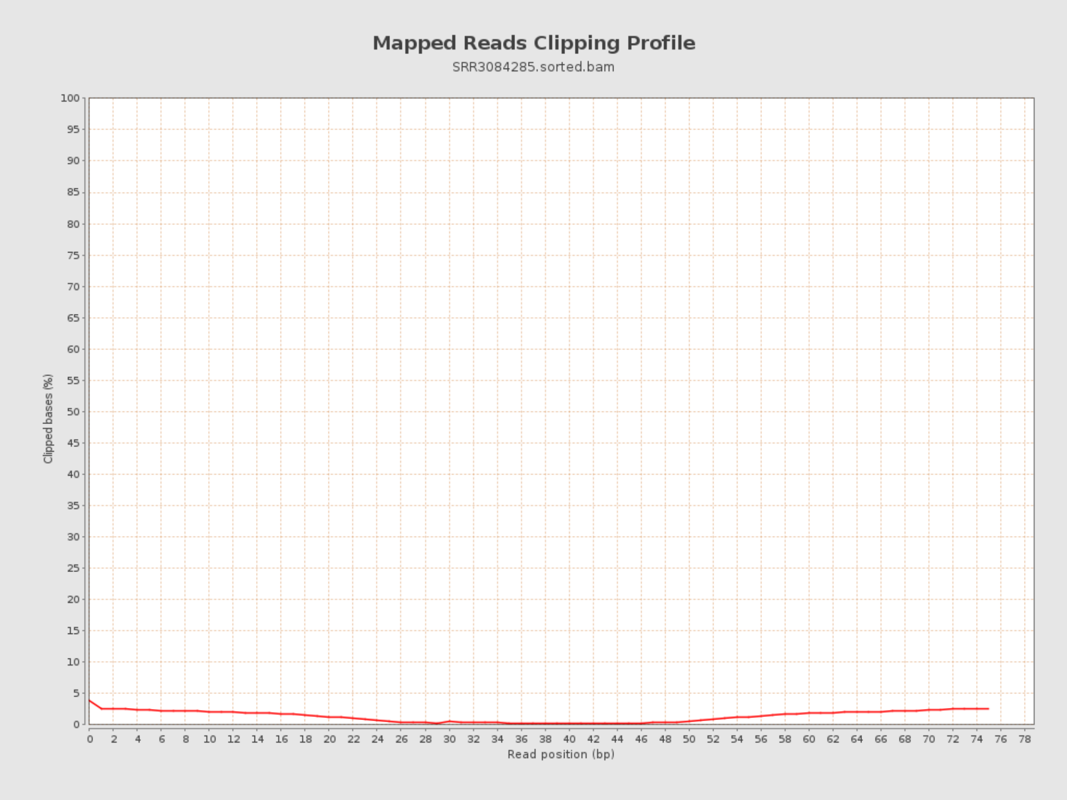
# 8. Results : Mapped Reads Nucleotide Content



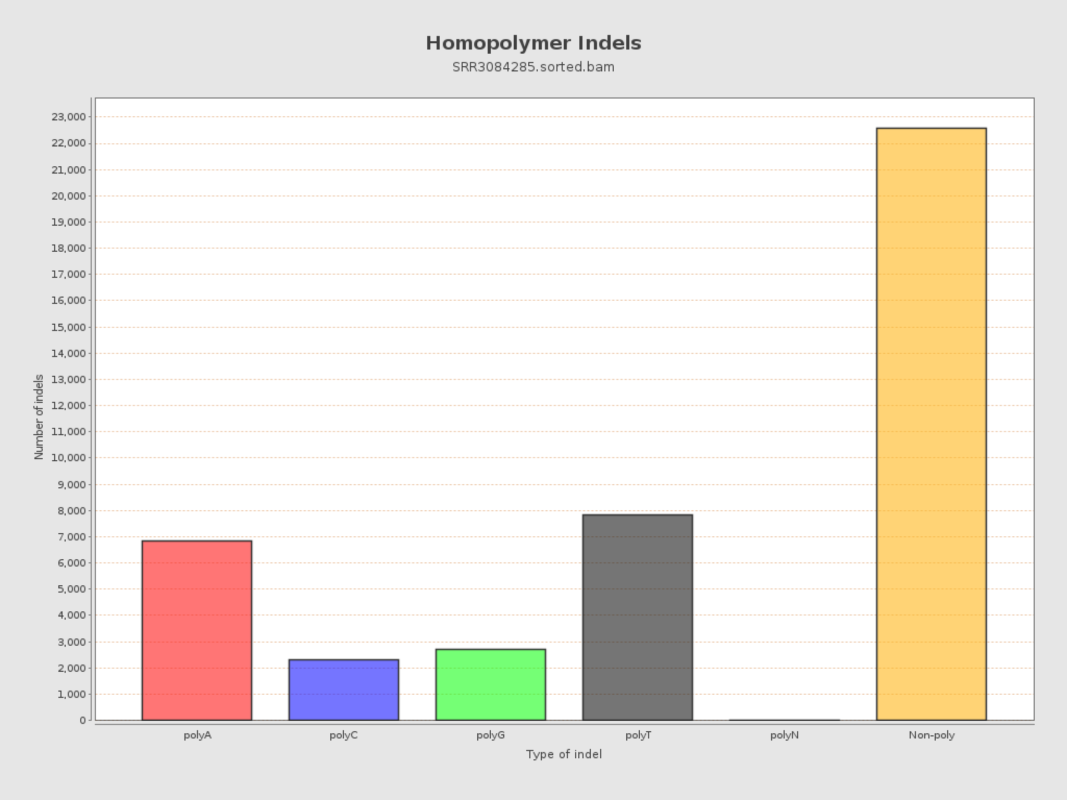
# 9. Results : Mapped Reads GC-content Distribution



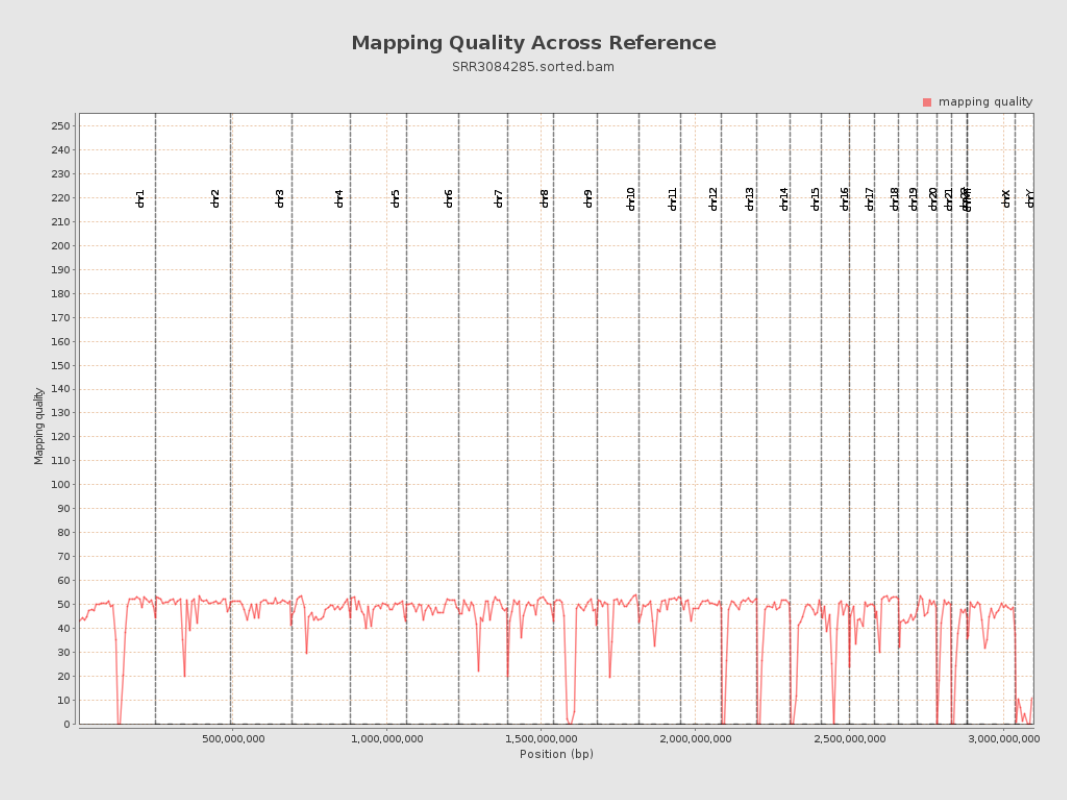
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram