# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/26 02:10:39*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085120.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_SRR3085120 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085120.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Aug 26 02:10:38 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3085120.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,213,323 |
| Mapped reads | 2,000,799 / 90.4% |
| Unmapped reads | 212,524 / 9.6% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 19,350 / 0.87% |
| Read min/max/mean length | 30 / 76 / 76.3 |
| Duplicated reads (estimated) | 69,651 / 3.15% |
| Duplication rate | 2.71% |
| Clipped reads | 851,437 / 38.47% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 37,958,859 / 28.11% |
| Number/percentage of C's | 25,206,908 / 18.66% |
| Number/percentage of T's | 42,205,222 / 31.25% |
| Number/percentage of G's | 29,655,535 / 21.96% |
| Number/percentage of N's | 31,630 / 0.02% |
| GC Percentage | 40.62% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0436 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3565 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.31 |

## 2.5. Mismatches and indels

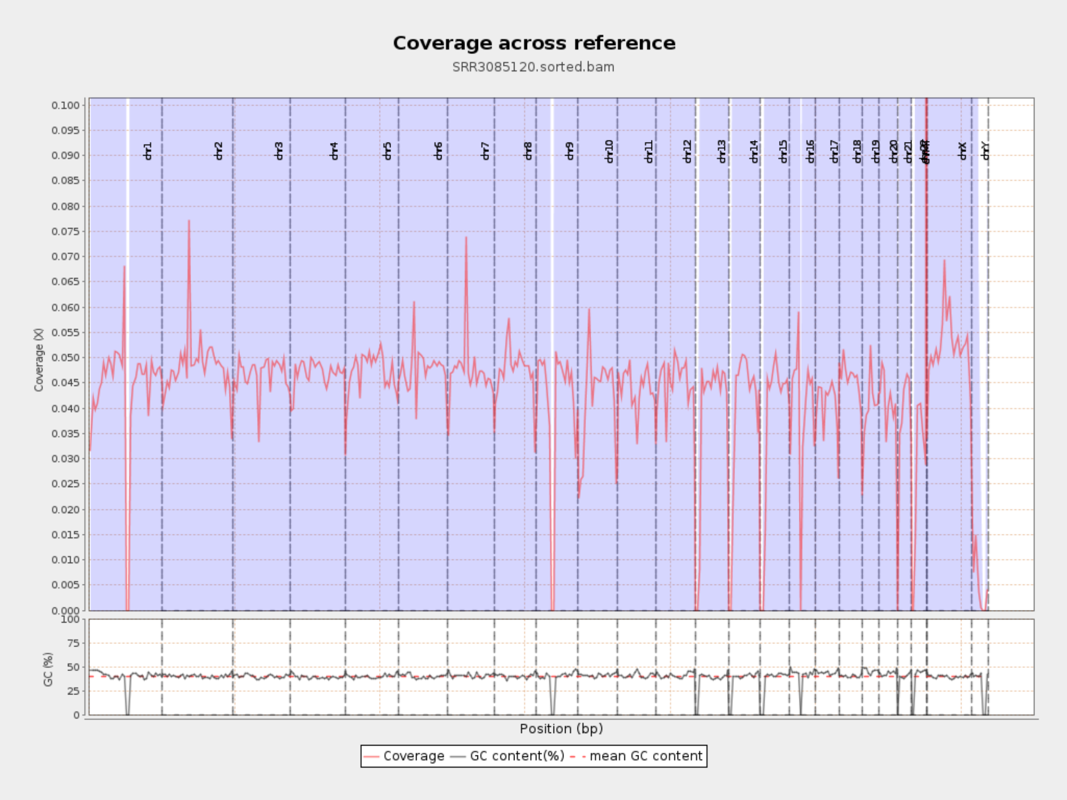
| | |
|---|---|
| General error rate | 0.87% |
| Mismatches | 1,159,063 |
| Insertions | 10,531 |
| Mapped reads with at least one insertion | 0.52% |
| Deletions | 29,930 |
| Mapped reads with at least one deletion | 1.48% |
| Homopolymer indels | 47.59% |

## 2.6. Chromosome stats

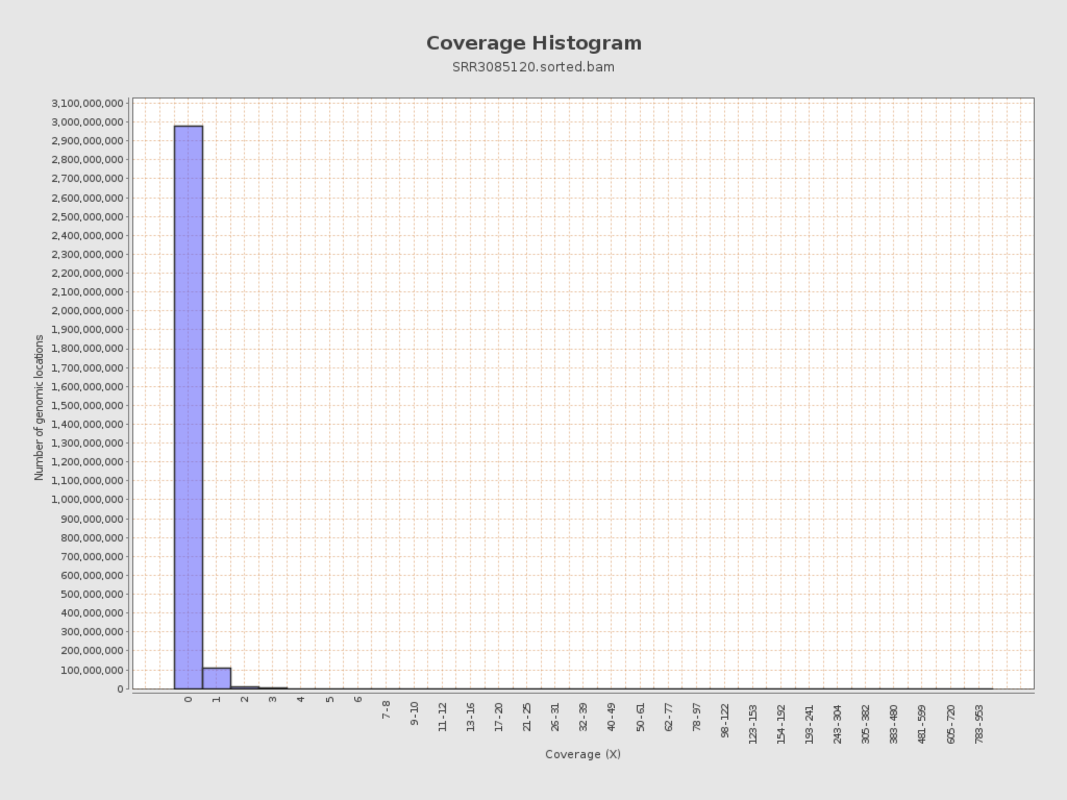
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 10908753 | 0.0438 | 0.5852 |
| chr2 | 243199373 | 11848919 | 0.0487 | 0.4344 |
| chr3 | 198022430 | 9249774 | 0.0467 | 0.2362 |
| chr4 | 191154276 | 8987967 | 0.047 | 0.2444 |
| chr5 | 180915260 | 8579251 | 0.0474 | 0.2396 |
| chr6 | 171115067 | 8195787 | 0.0479 | 0.2836 |
| chr7 | 159138663 | 7608780 | 0.0478 | 0.4853 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6953558 | 0.0475 | 0.6113 |
| chr9 | 141213431 | 5756578 | 0.0408 | 0.3223 |
| chr10 | 135534747 | 5701003 | 0.0421 | 0.3125 |
| chr11 | 135006516 | 5921226 | 0.0439 | 0.2901 |
| chr12 | 133851895 | 6051269 | 0.0452 | 0.2353 |
| chr13 | 115169878 | 4360823 | 0.0379 | 0.2145 |
| chr14 | 107349540 | 4120283 | 0.0384 | 0.228 |
| chr15 | 102531392 | 3787383 | 0.0369 | 0.216 |
| chr16 | 90354753 | 3612126 | 0.04 | 0.238 |
| chr17 | 81195210 | 3300128 | 0.0406 | 0.2372 |
| chr18 | 78077248 | 3616001 | 0.0463 | 0.5057 |
| chr19 | 59128983 | 2403977 | 0.0407 | 0.4355 |
| chr20 | 63025520 | 2588294 | 0.0411 | 0.2263 |
| chr21 | 48129895 | 1779426 | 0.037 | 0.2216 |
| chr22 | 51304566 | 1316102 | 0.0257 | 0.174 |
| chrMT | 16571 | 12585 | 0.7595 | 0.9238 |
| chrX | 155270560 | 8125296 | 0.0523 | 0.279 |
| chrY | 59373566 | 321140 | 0.0054 | 0.1126 |

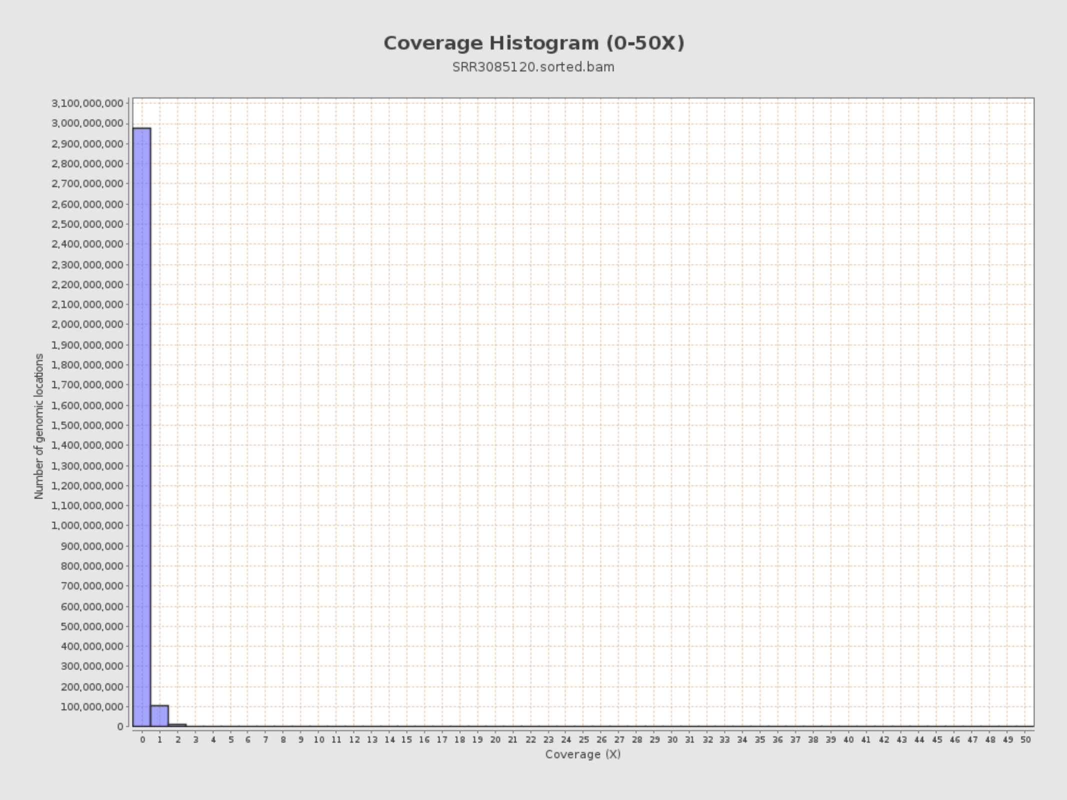
# 3. Results : Coverage across reference



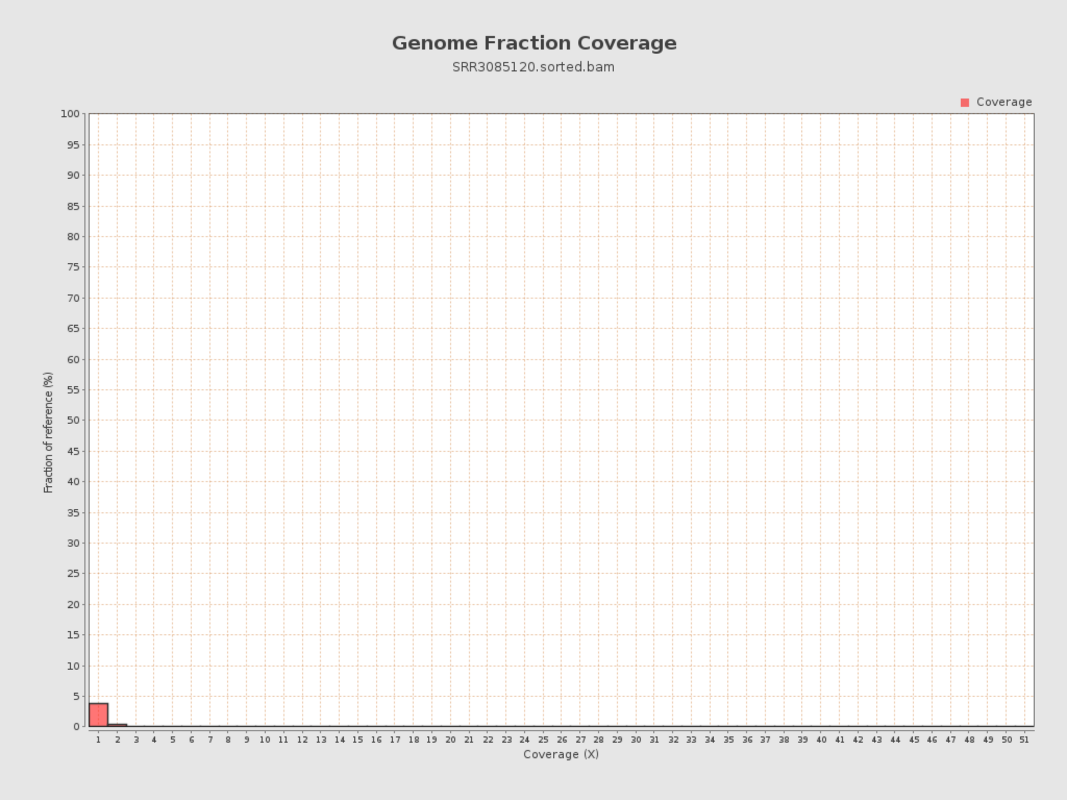
# 4. Results : Coverage Histogram



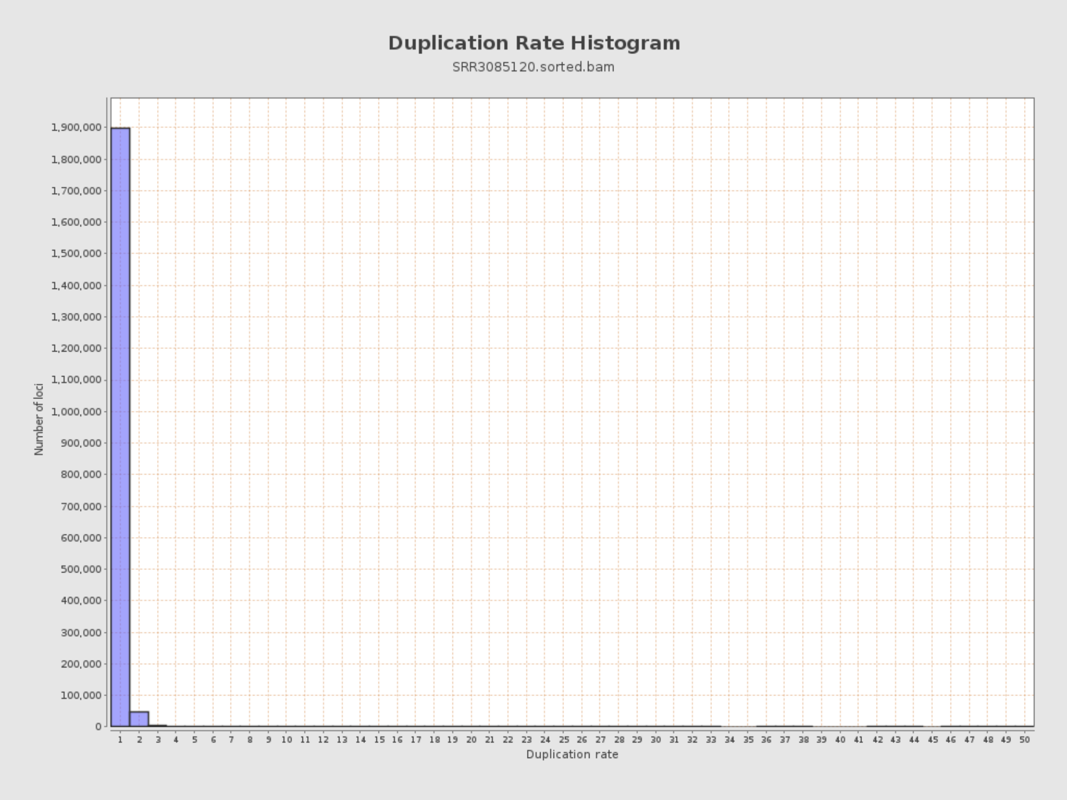
# 5. Results : Coverage Histogram (0-50X)



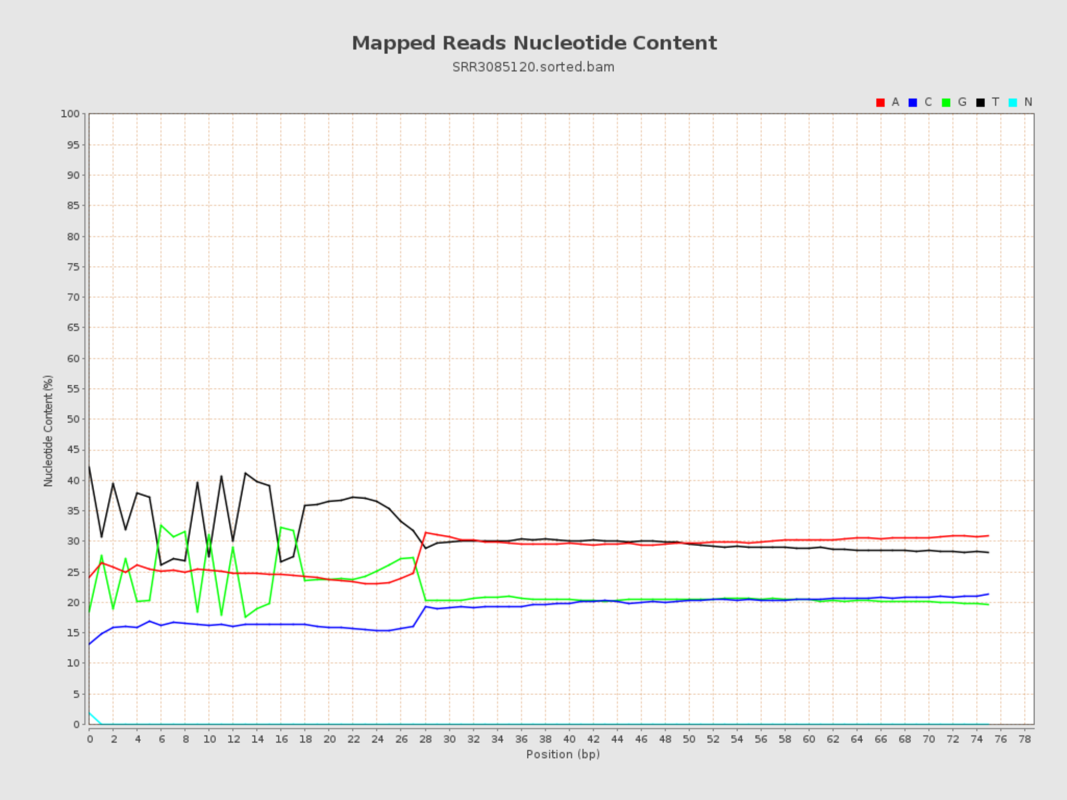
# 6. Results : Genome Fraction Coverage



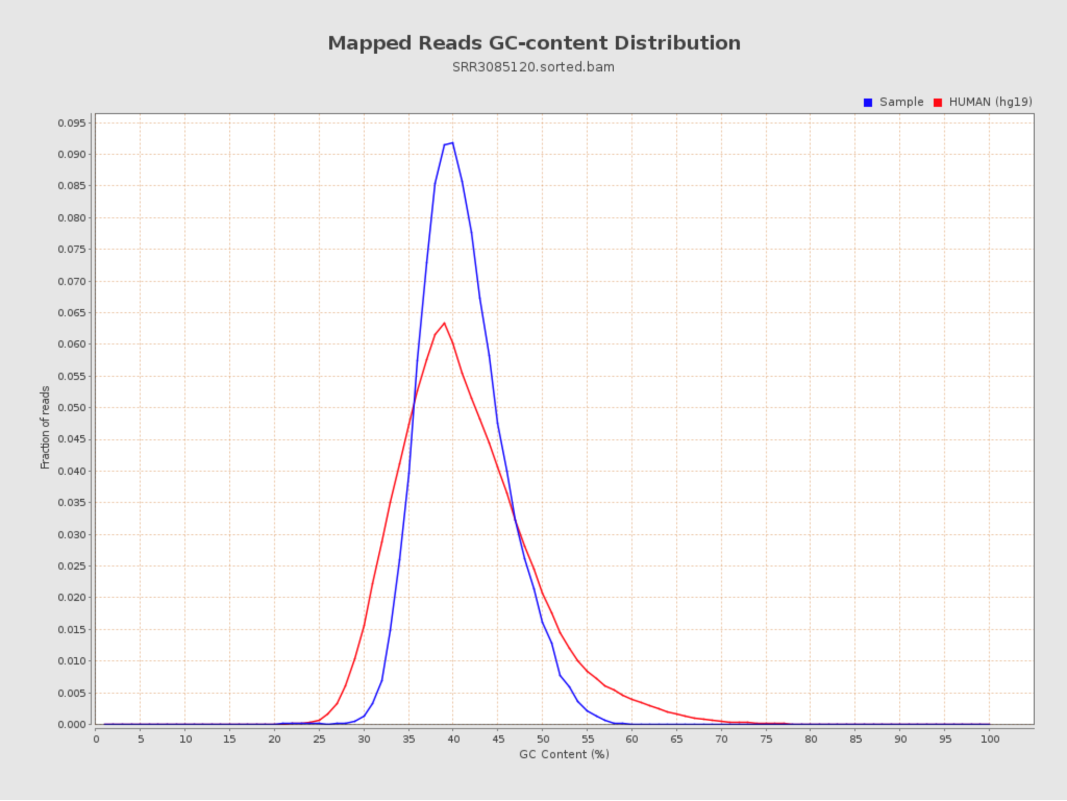
# 7. Results : Duplication Rate Histogram



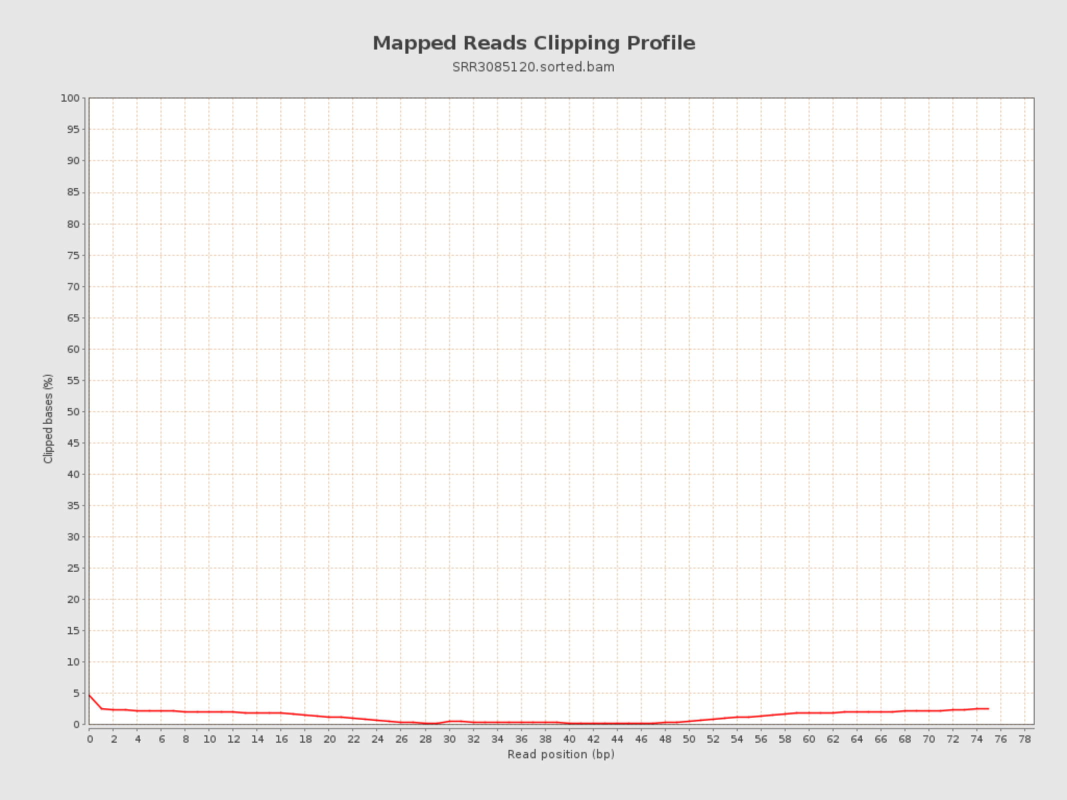
# 8. Results : Mapped Reads Nucleotide Content



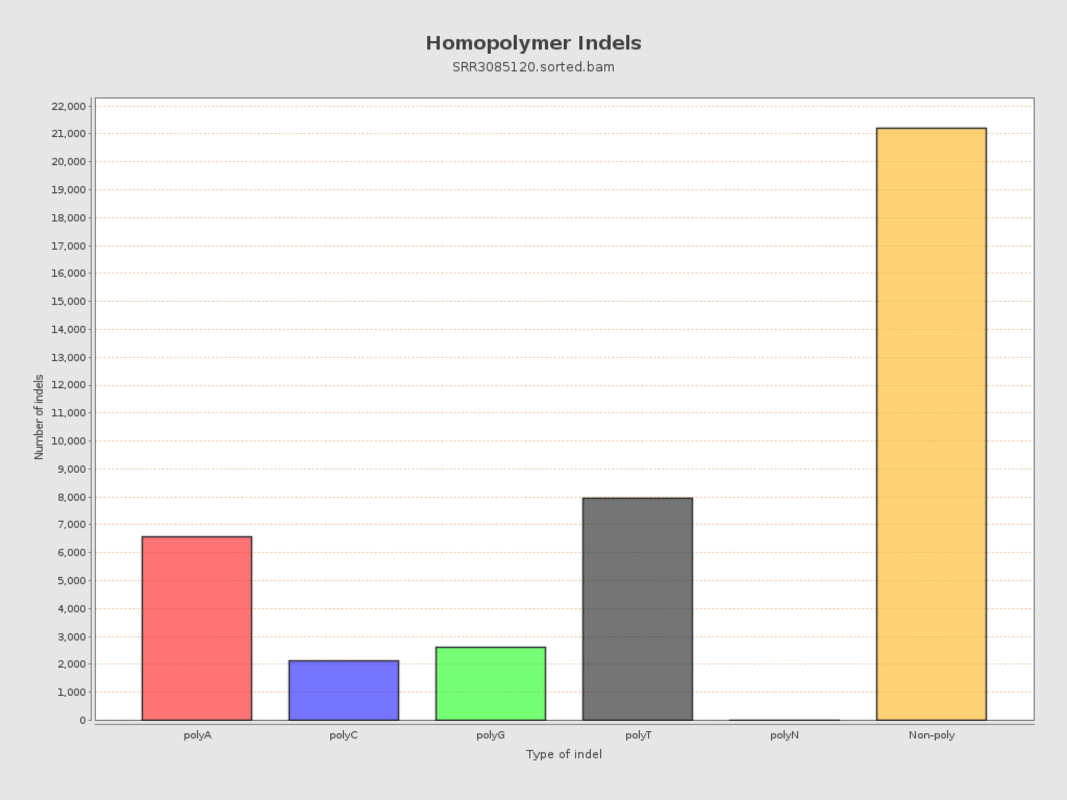
# 9. Results : Mapped Reads GC-content Distribution



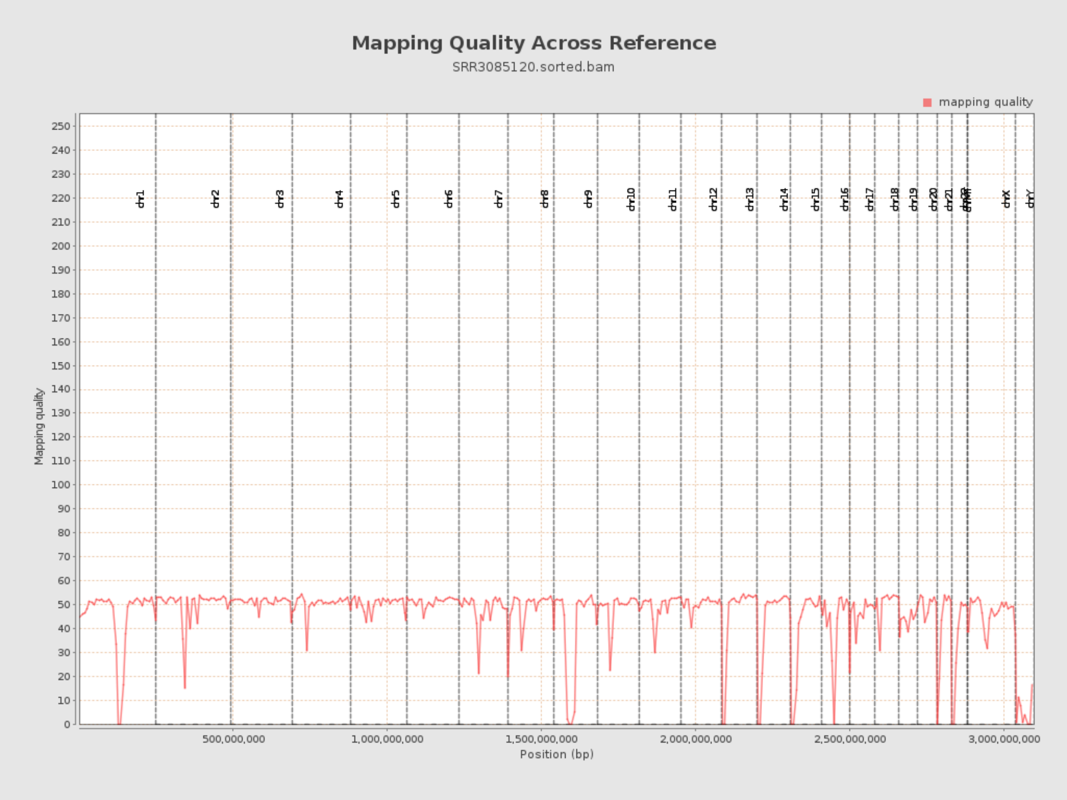
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram