# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/25 23:59:21*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085051.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_SRR3085051 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085051.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Aug 25 23:59:20 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3085051.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,867,505 |
| Mapped reads | 1,693,197 / 90.67% |
| Unmapped reads | 174,308 / 9.33% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 14,534 / 0.78% |
| Read min/max/mean length | 30 / 76 / 76.27 |
| Duplicated reads (estimated) | 52,918 / 2.83% |
| Duplication rate | 2.39% |
| Clipped reads | 812,980 / 43.53% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 32,661,180 / 29.13% |
| Number/percentage of C's | 21,131,913 / 18.85% |
| Number/percentage of T's | 34,805,133 / 31.04% |
| Number/percentage of G's | 23,513,145 / 20.97% |
| Number/percentage of N's | 12,667 / 0.01% |
| GC Percentage | 39.82% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0362 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3296 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.89 |

## 2.5. Mismatches and indels

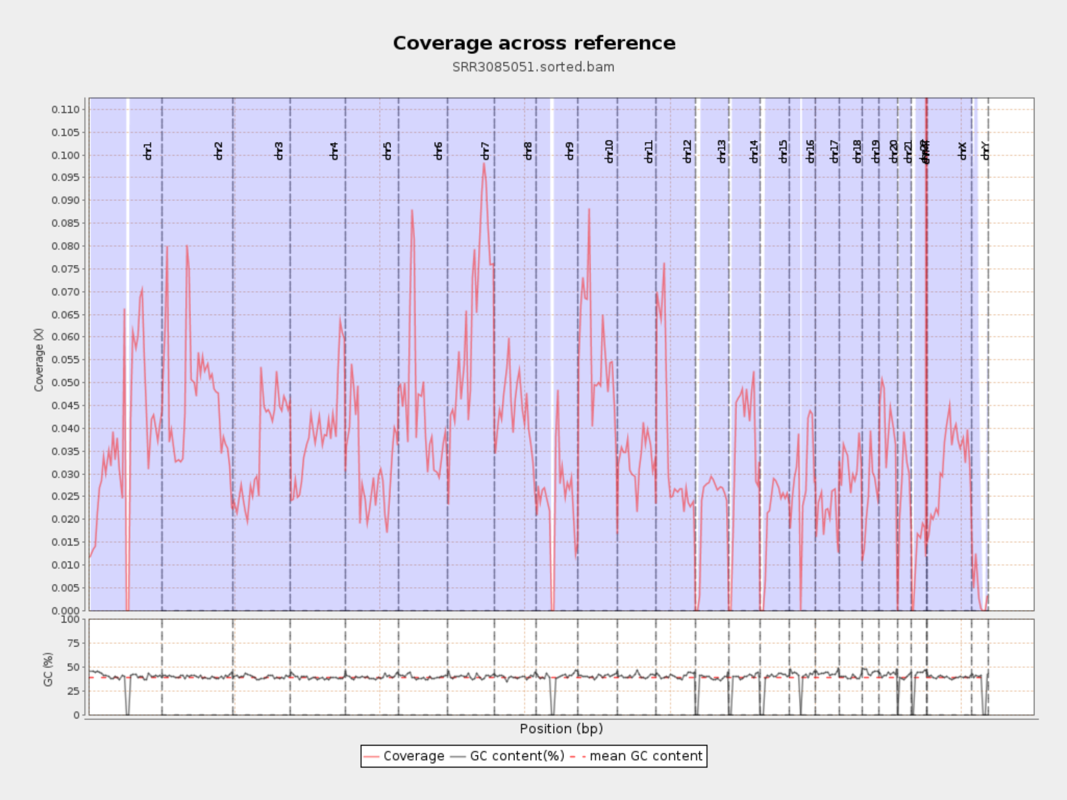
| | |
|---|---|
| General error rate | 0.91% |
| Mismatches | 1,001,648 |
| Insertions | 7,886 |
| Mapped reads with at least one insertion | 0.46% |
| Deletions | 23,328 |
| Mapped reads with at least one deletion | 1.36% |
| Homopolymer indels | 45.92% |

## 2.6. Chromosome stats

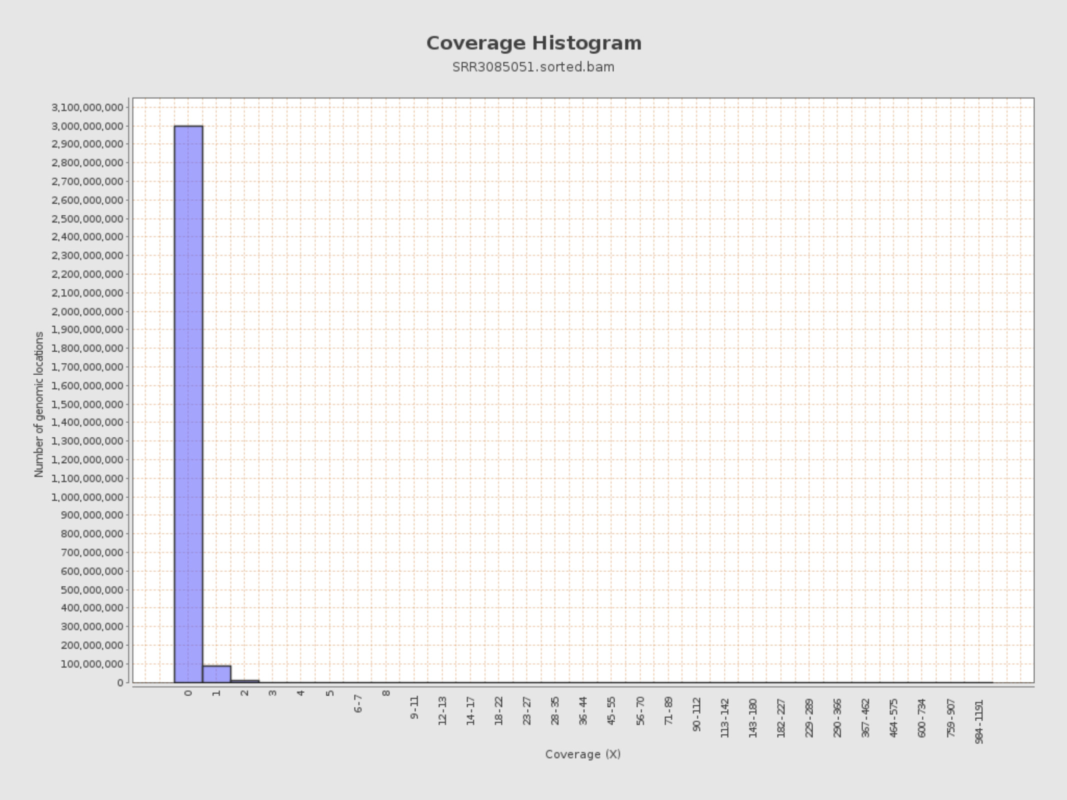
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 9154297 | 0.0367 | 0.4763 |
| chr2 | 243199373 | 11476411 | 0.0472 | 0.3638 |
| chr3 | 198022430 | 7044711 | 0.0356 | 0.2175 |
| chr4 | 191154276 | 7486064 | 0.0392 | 0.2218 |
| chr5 | 180915260 | 5730716 | 0.0317 | 0.1952 |
| chr6 | 171115067 | 7666412 | 0.0448 | 0.2993 |
| chr7 | 159138663 | 10233434 | 0.0643 | 0.3808 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6346776 | 0.0434 | 0.7219 |
| chr9 | 141213431 | 3434040 | 0.0243 | 0.2649 |
| chr10 | 135534747 | 7734450 | 0.0571 | 0.466 |
| chr11 | 135006516 | 4475258 | 0.0331 | 0.2444 |
| chr12 | 133851895 | 4897828 | 0.0366 | 0.2144 |
| chr13 | 115169878 | 2554565 | 0.0222 | 0.1622 |
| chr14 | 107349540 | 3849771 | 0.0359 | 0.2244 |
| chr15 | 102531392 | 2087425 | 0.0204 | 0.1583 |
| chr16 | 90354753 | 2663323 | 0.0295 | 0.2046 |
| chr17 | 81195210 | 1719948 | 0.0212 | 0.1812 |
| chr18 | 78077248 | 2496598 | 0.032 | 0.4381 |
| chr19 | 59128983 | 1500172 | 0.0254 | 0.3545 |
| chr20 | 63025520 | 2552488 | 0.0405 | 0.223 |
| chr21 | 48129895 | 1255810 | 0.0261 | 0.184 |
| chr22 | 51304566 | 633849 | 0.0124 | 0.1202 |
| chrMT | 16571 | 15551 | 0.9384 | 1.1311 |
| chrX | 155270560 | 4924389 | 0.0317 | 0.2183 |
| chrY | 59373566 | 229706 | 0.0039 | 0.0865 |

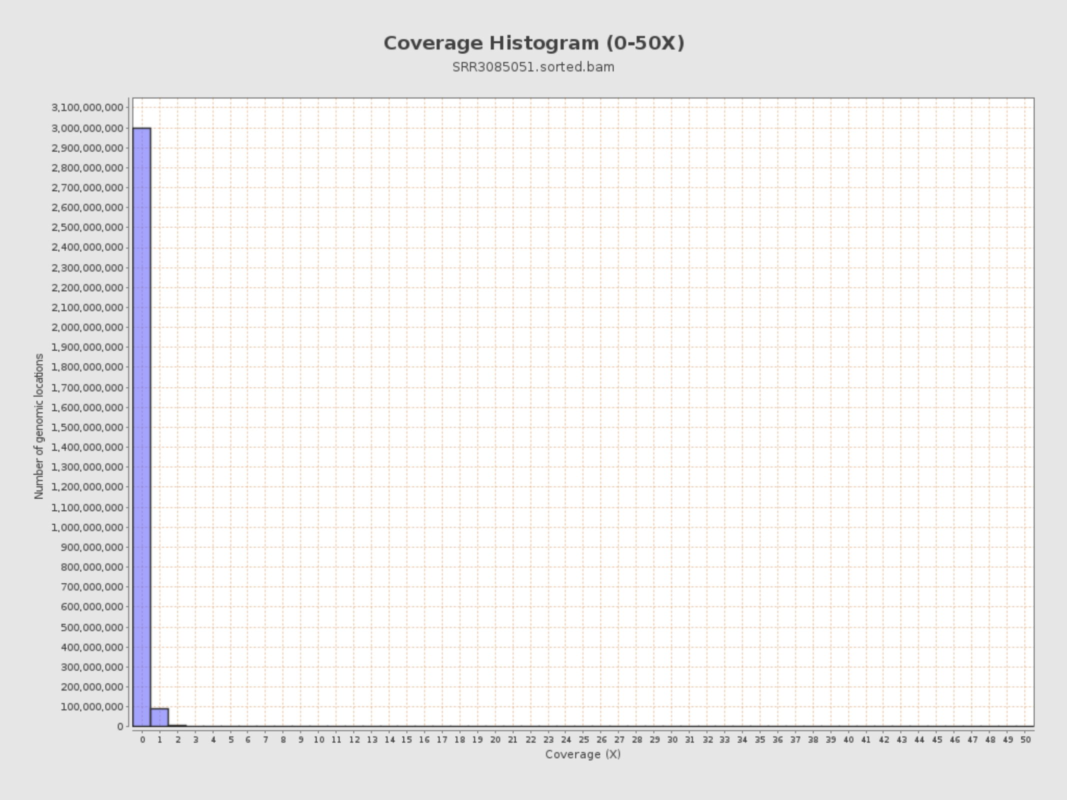
# 3. Results : Coverage across reference



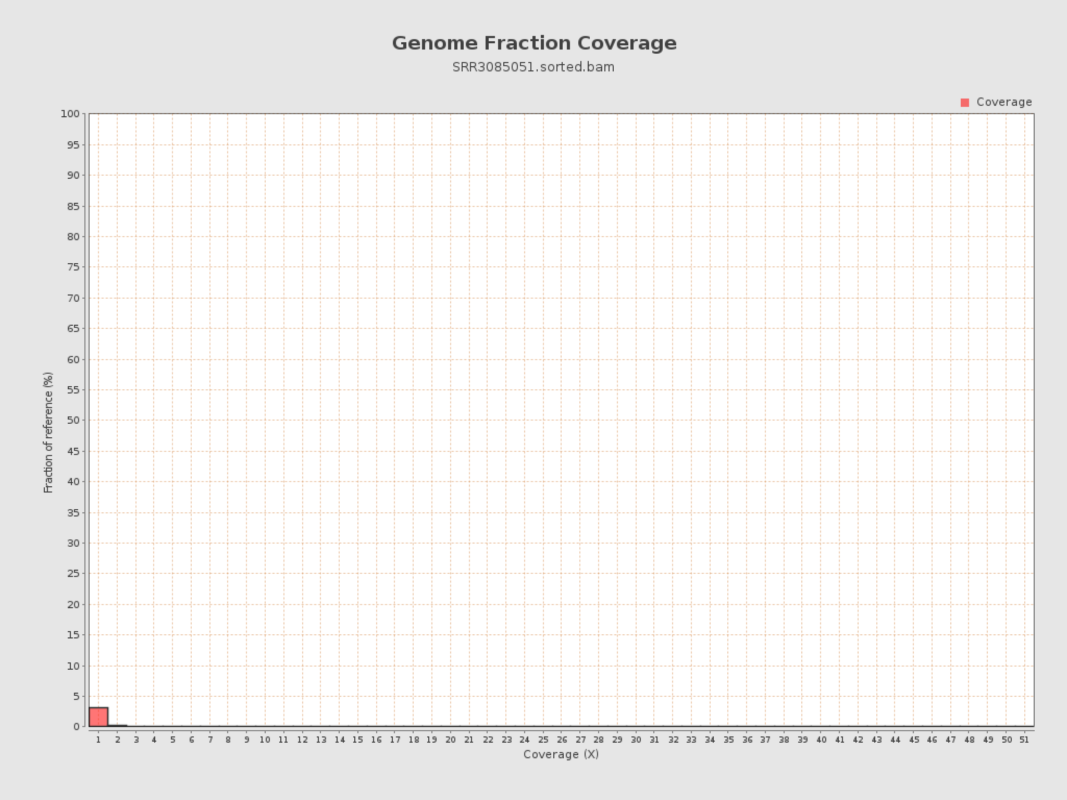
# 4. Results : Coverage Histogram



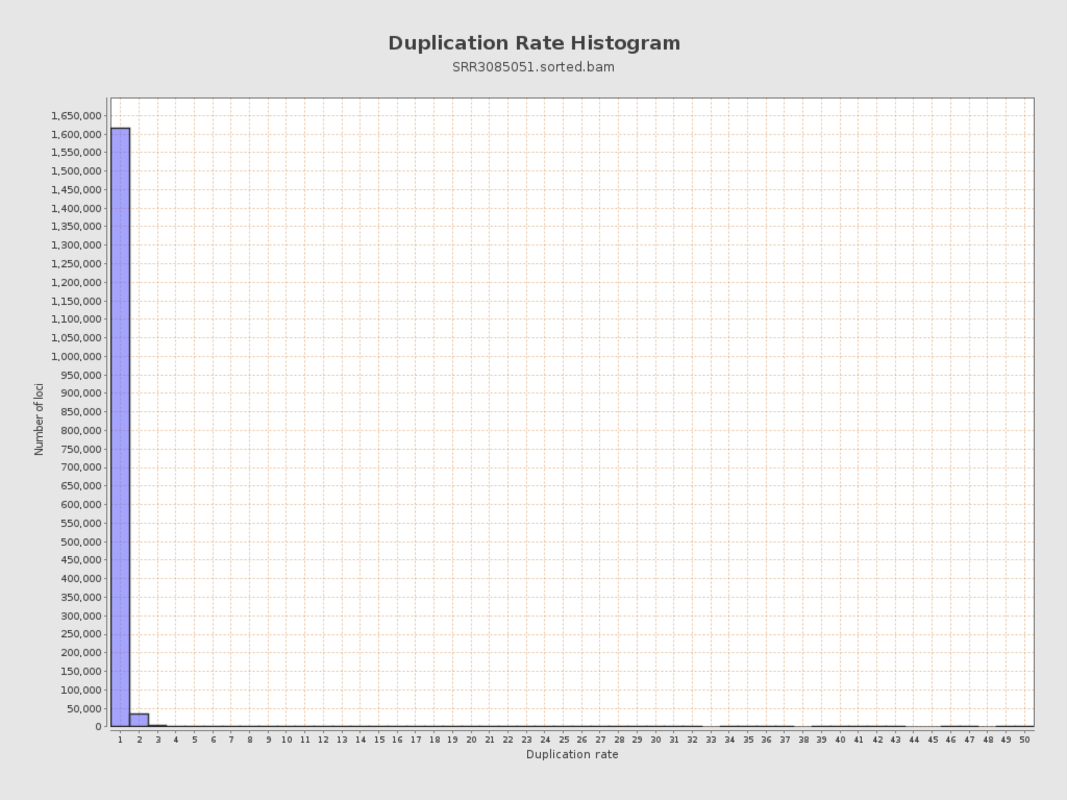
# 5. Results : Coverage Histogram (0-50X)



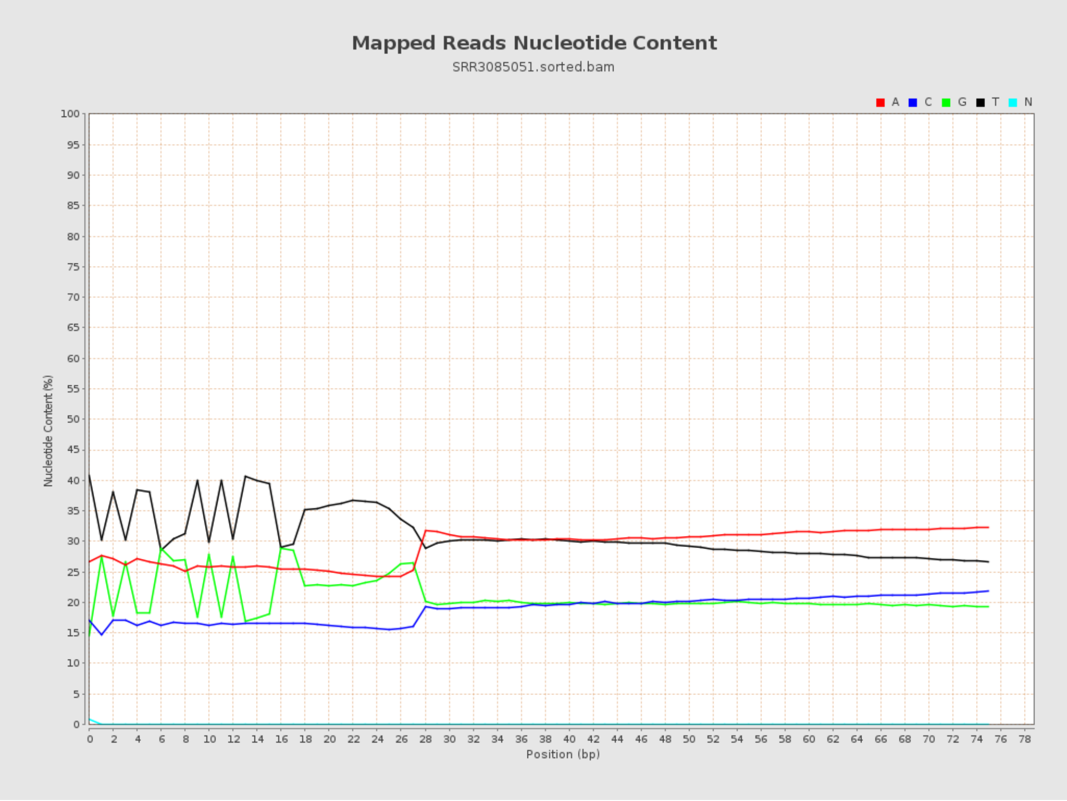
# 6. Results : Genome Fraction Coverage



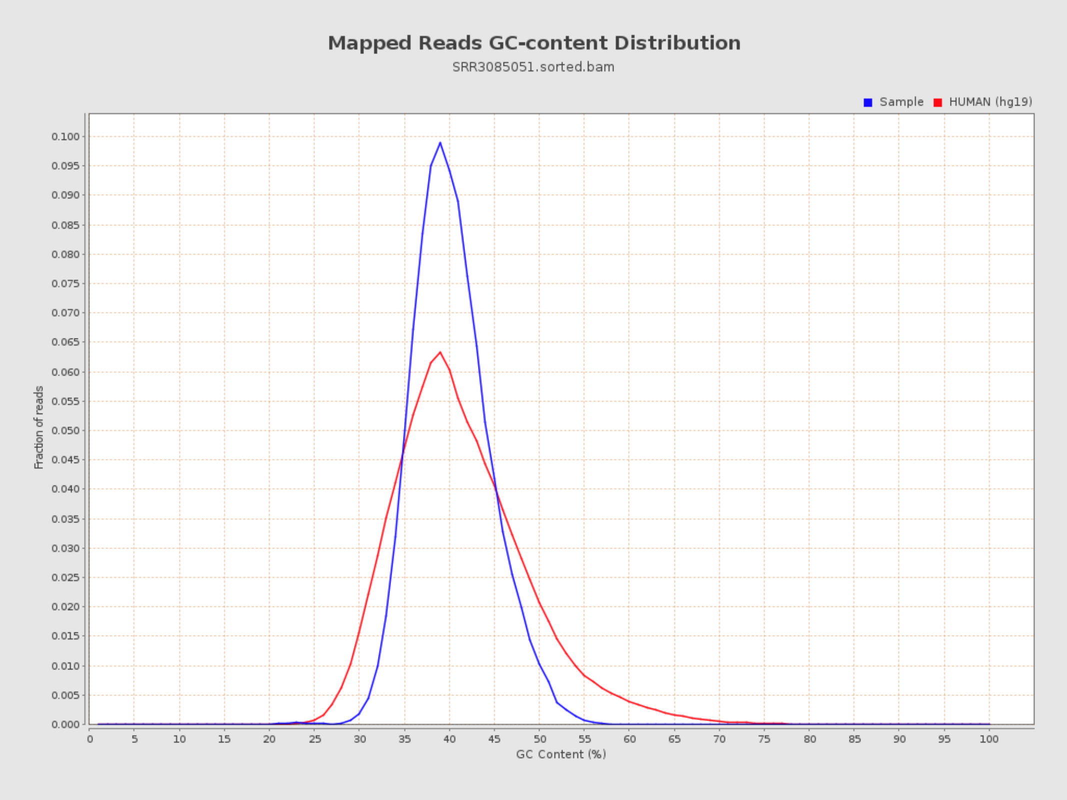
# 7. Results : Duplication Rate Histogram



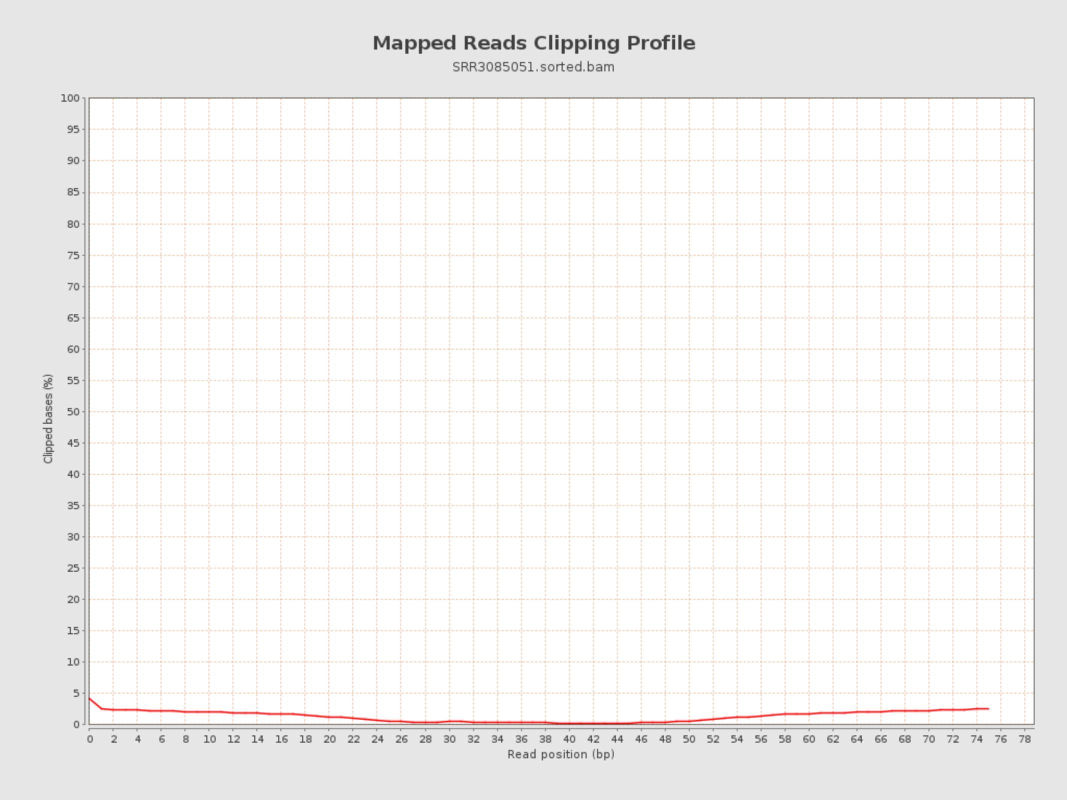
# 8. Results : Mapped Reads Nucleotide Content



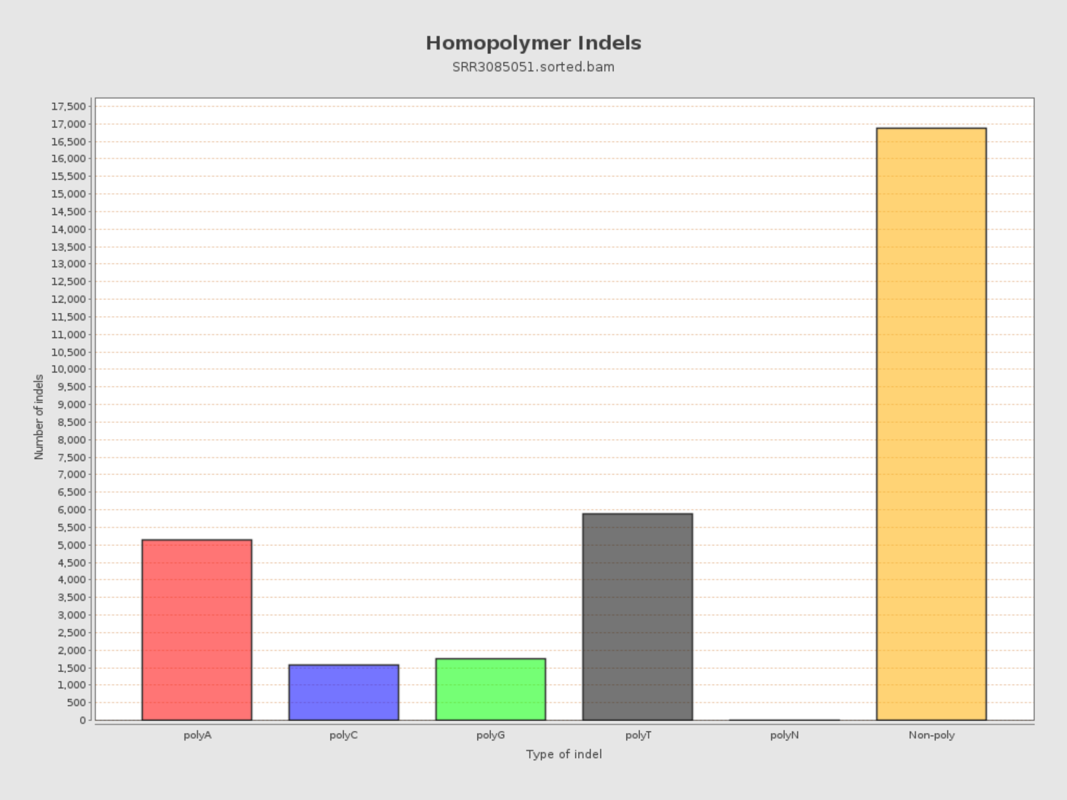
# 9. Results : Mapped Reads GC-content Distribution



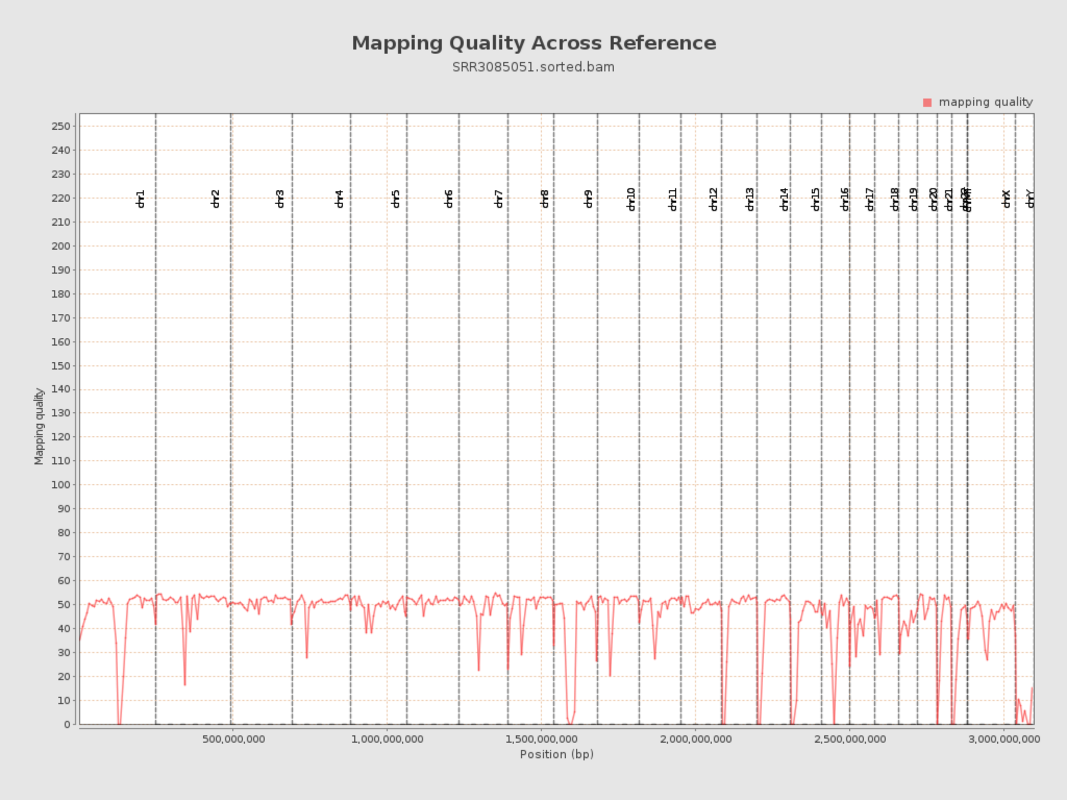
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram