# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/18 01:03:31*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238655.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_SRR6238655 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238655.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Sep 18 01:03:30 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6238655.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,595,423 |
| Mapped reads | 2,847,351 / 79.19% |
| Unmapped reads | 748,072 / 20.81% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 24,678 / 0.69% |
| Read min/max/mean length | 30 / 76 / 76.24 |
| Duplicated reads (estimated) | 1,429,986 / 39.77% |
| Duplication rate | 23.39% |
| Clipped reads | 2,005,290 / 55.77% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 43,117,773 / 25.25% |
| Number/percentage of C's | 28,796,406 / 16.86% |
| Number/percentage of T's | 58,313,093 / 34.15% |
| Number/percentage of G's | 40,542,670 / 23.74% |
| Number/percentage of N's | 3,842 / 0% |
| GC Percentage | 40.6% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0552 |
| | |

| | |
|---|---|
| Standard Deviation | 1.1925 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.28 |

## 2.5. Mismatches and indels

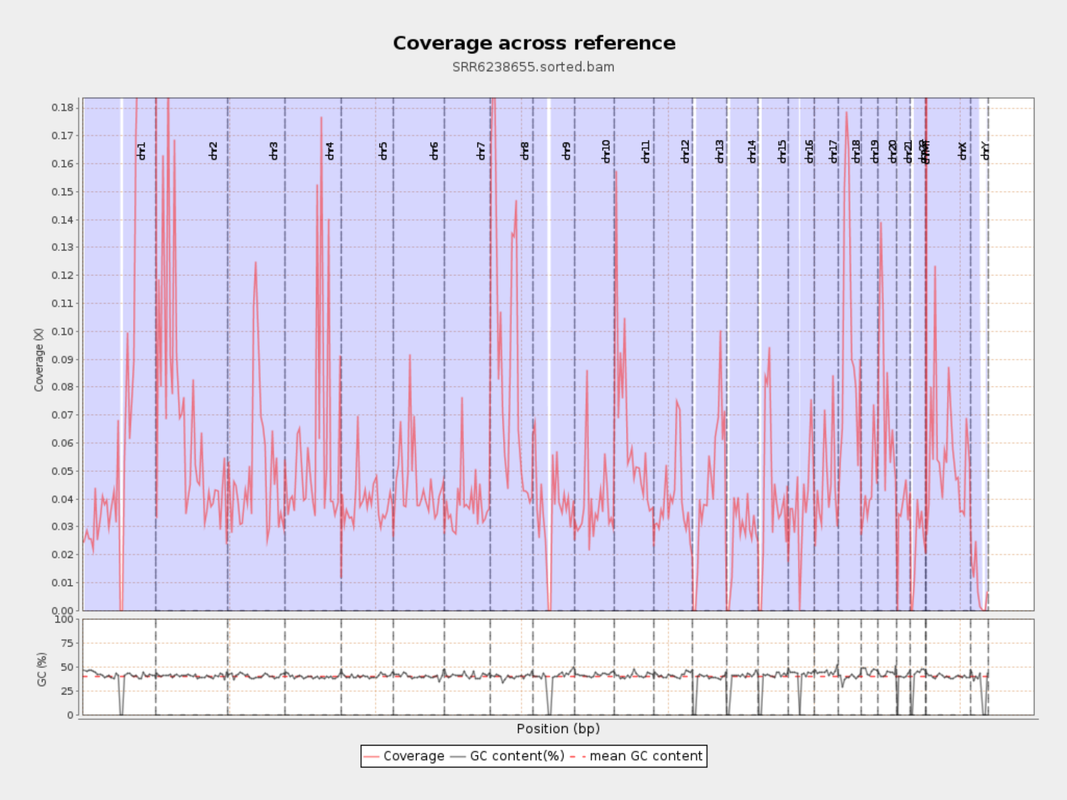
| | |
|---|---|
| General error rate | 0.6% |
| Mismatches | 996,171 |
| Insertions | 11,091 |
| Mapped reads with at least one insertion | 0.39% |
| Deletions | 47,473 |
| Mapped reads with at least one deletion | 1.65% |
| Homopolymer indels | 41.96% |

## 2.6. Chromosome stats

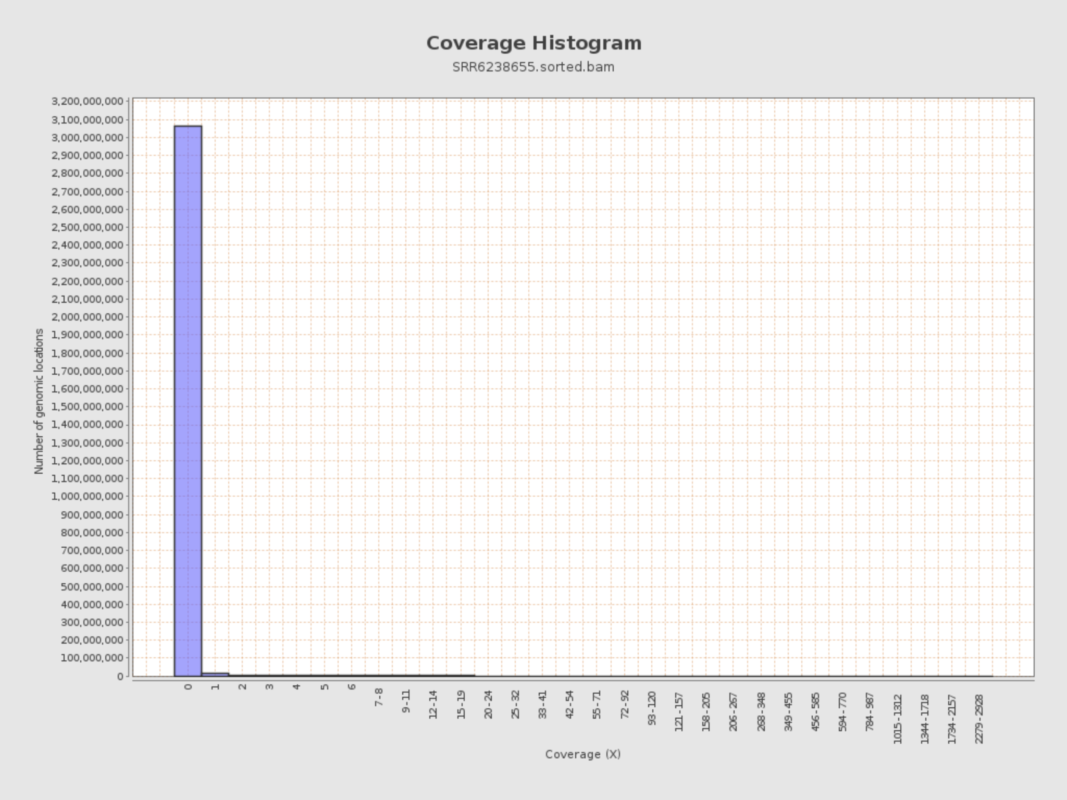
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 28372960 | 0.1138 | 1.4103 |
| chr2 | 243199373 | 16427917 | 0.0675 | 1.6779 |
| chr3 | 198022430 | 10059181 | 0.0508 | 0.879 |
| chr4 | 191154276 | 11439578 | 0.0598 | 0.9391 |
| chr5 | 180915260 | 6993722 | 0.0387 | 0.76 |
| chr6 | 171115067 | 7884136 | 0.0461 | 1.0624 |
| chr7 | 159138663 | 6104263 | 0.0384 | 0.8207 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 13036330 | 0.0891 | 1.8179 |
| chr9 | 141213431 | 5083267 | 0.036 | 0.7449 |
| chr10 | 135534747 | 5100527 | 0.0376 | 0.8455 |
| chr11 | 135006516 | 8461985 | 0.0627 | 0.9627 |
| chr12 | 133851895 | 5259248 | 0.0393 | 0.7534 |
| chr13 | 115169878 | 5222686 | 0.0453 | 1.0005 |
| chr14 | 107349540 | 2906006 | 0.0271 | 0.7339 |
| chr15 | 102531392 | 4185917 | 0.0408 | 0.8971 |
| chr16 | 90354753 | 3378955 | 0.0374 | 0.7518 |
| chr17 | 81195210 | 3717319 | 0.0458 | 0.7987 |
| chr18 | 78077248 | 7725705 | 0.0989 | 3.5447 |
| chr19 | 59128983 | 2576444 | 0.0436 | 0.8711 |
| chr20 | 63025520 | 4895421 | 0.0777 | 1.0724 |
| chr21 | 48129895 | 1676225 | 0.0348 | 0.7082 |
| chr22 | 51304566 | 1136877 | 0.0222 | 0.5639 |
| chrMT | 16571 | 43920 | 2.6504 | 6.4201 |
| chrX | 155270560 | 8677140 | 0.0559 | 0.9059 |
| chrY | 59373566 | 488513 | 0.0082 | 0.3706 |

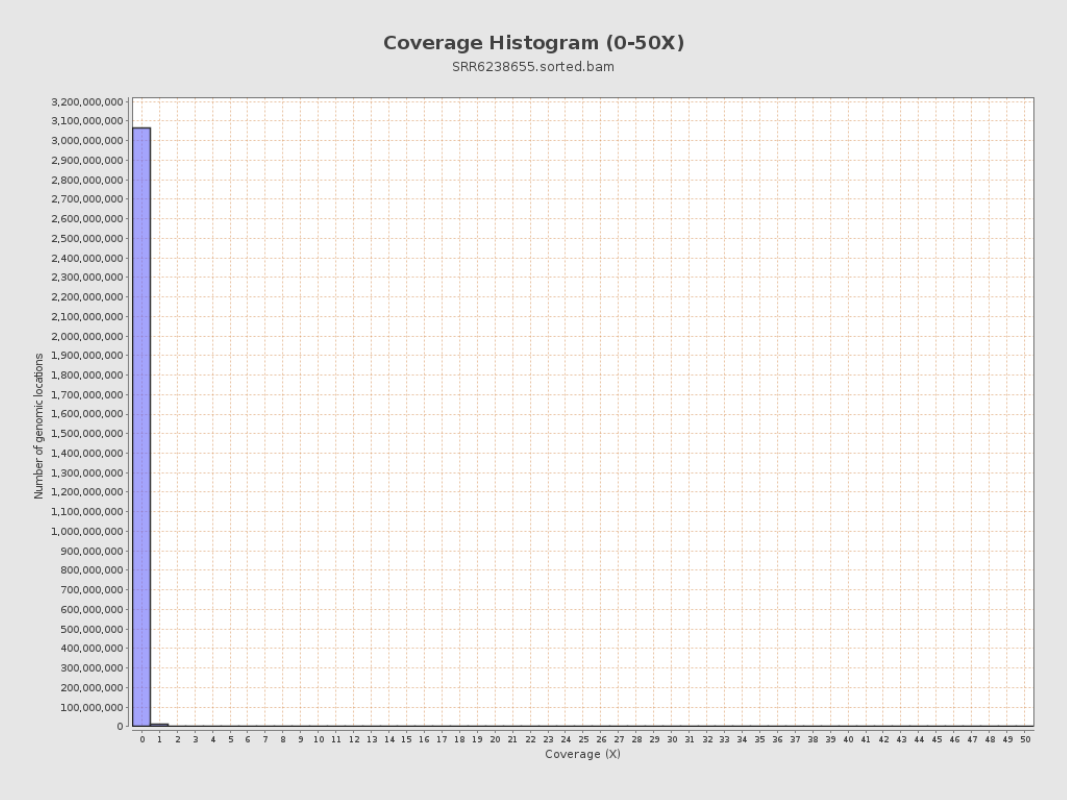
# 3. Results : Coverage across reference



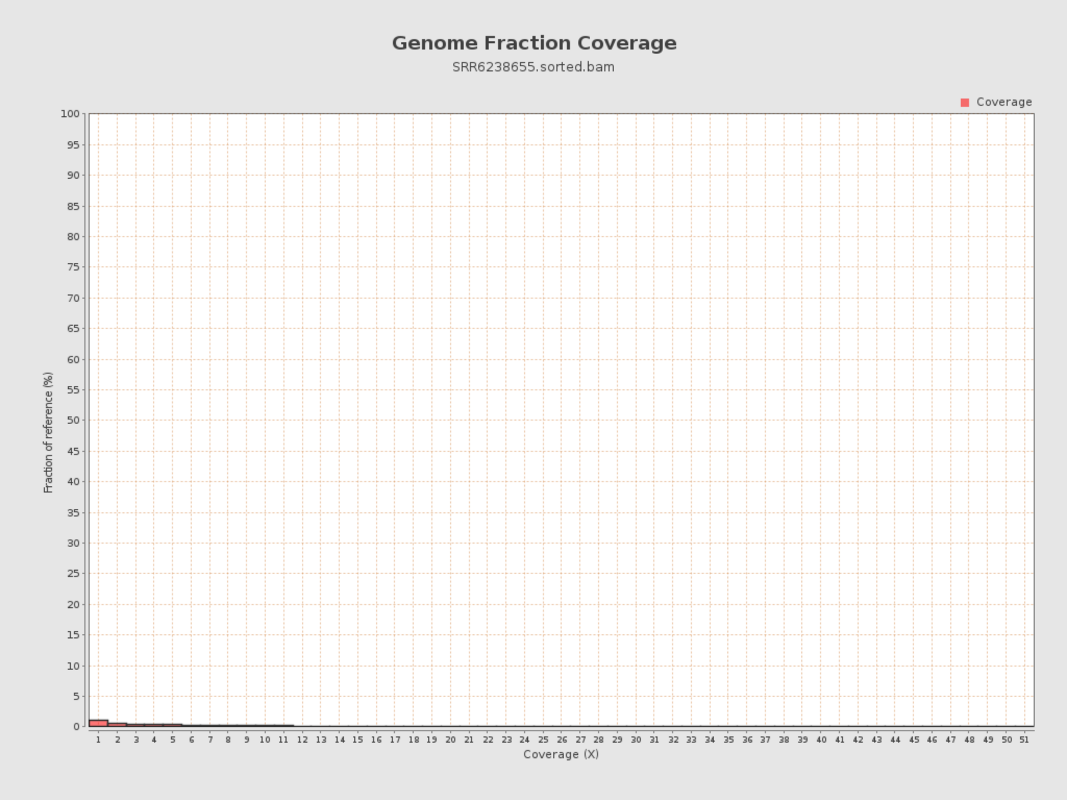
# 4. Results : Coverage Histogram



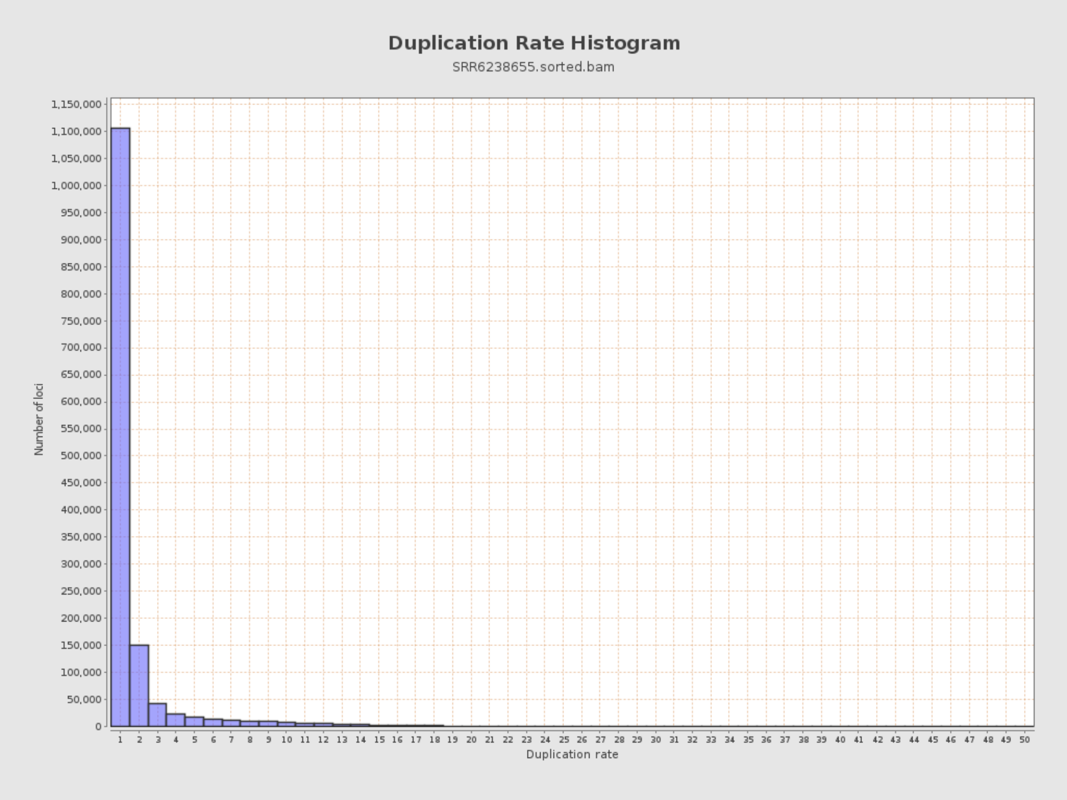
# 5. Results : Coverage Histogram (0-50X)



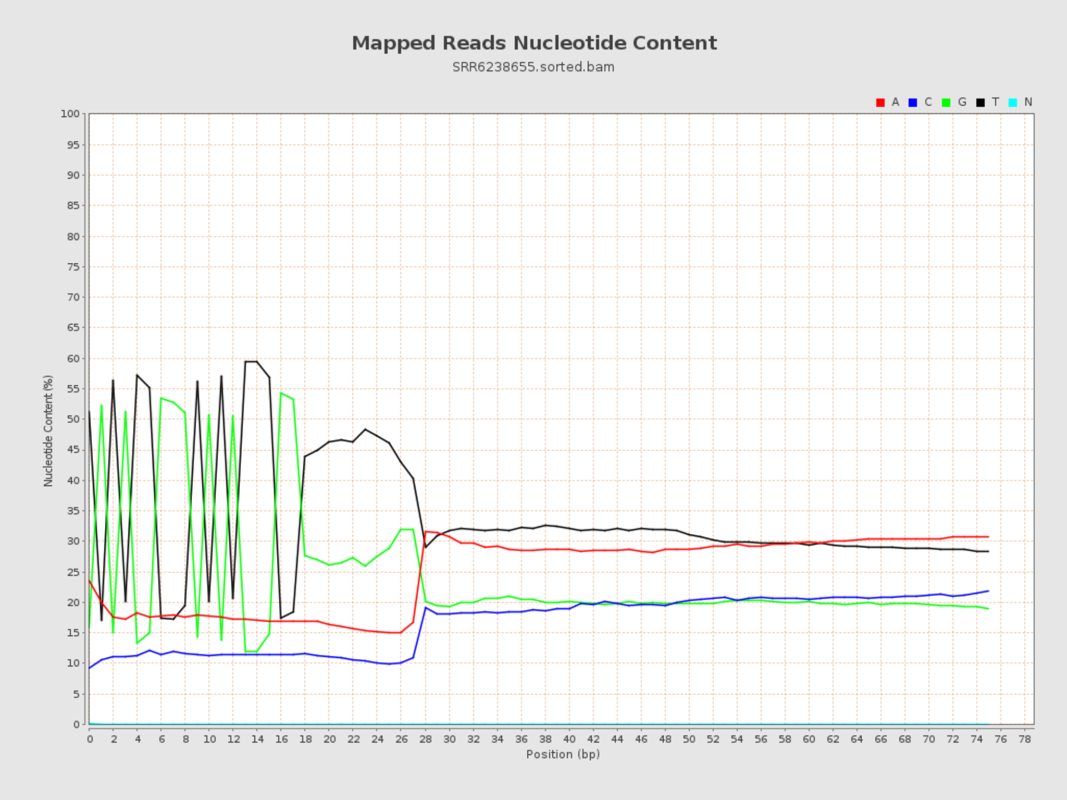
# 6. Results : Genome Fraction Coverage



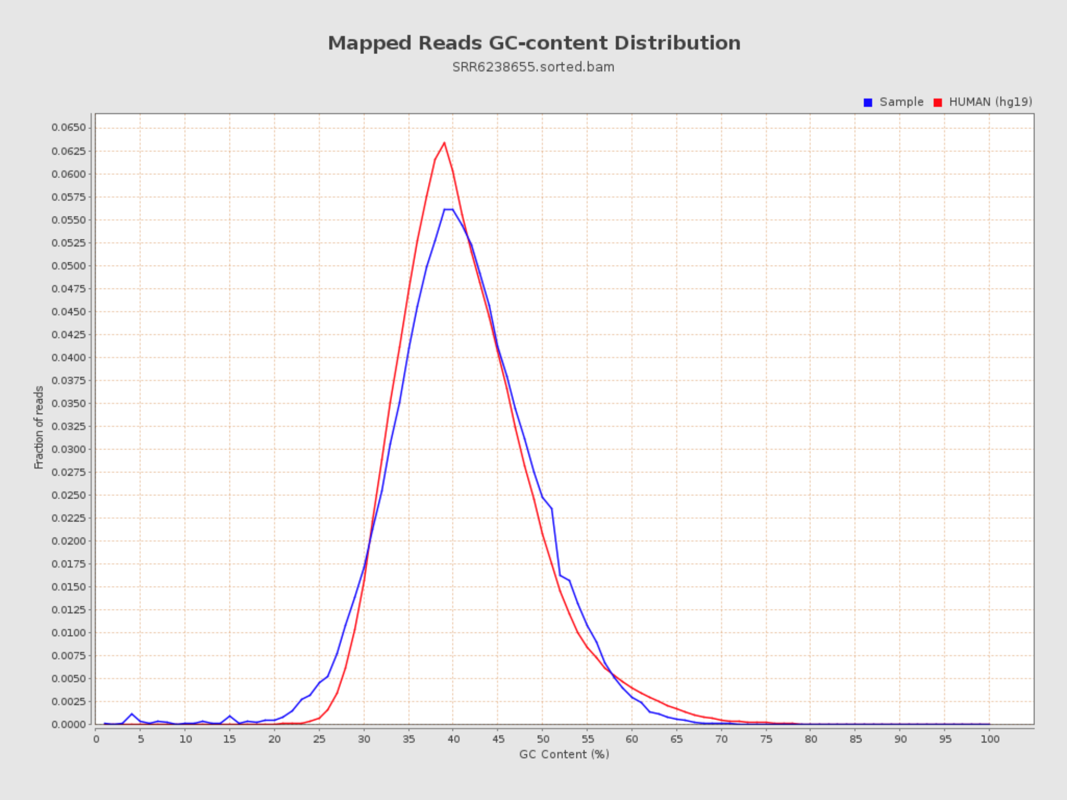
# 7. Results : Duplication Rate Histogram



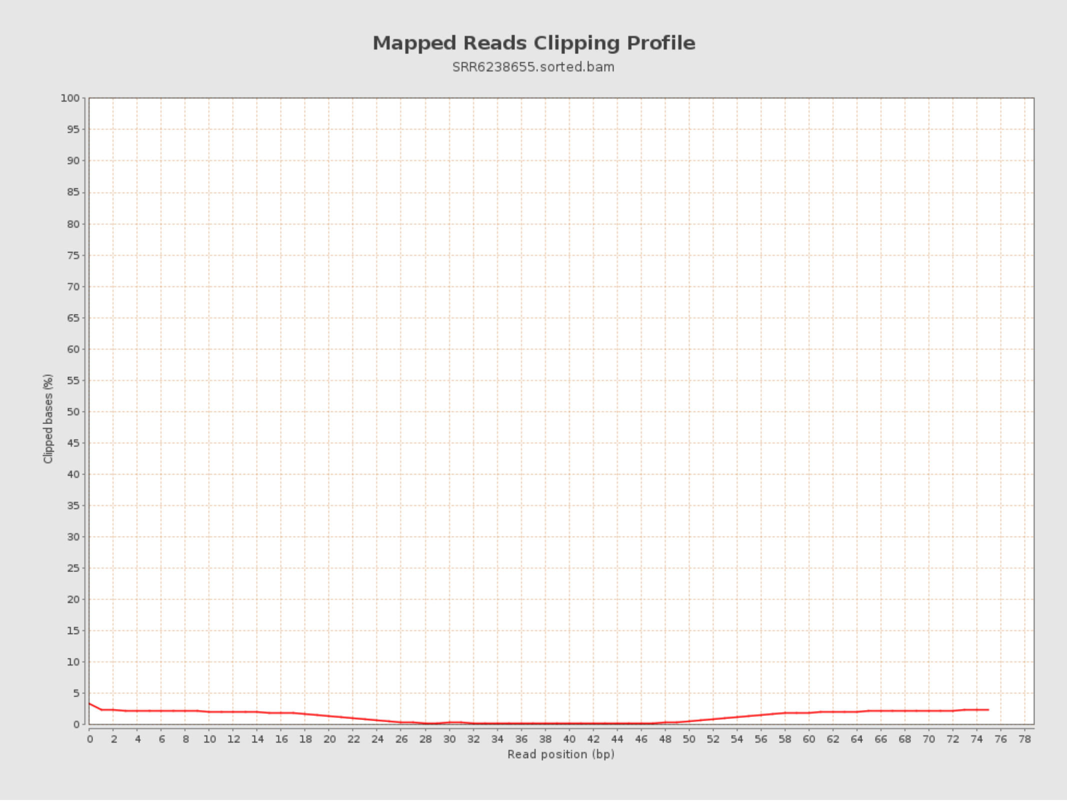
# 8. Results : Mapped Reads Nucleotide Content



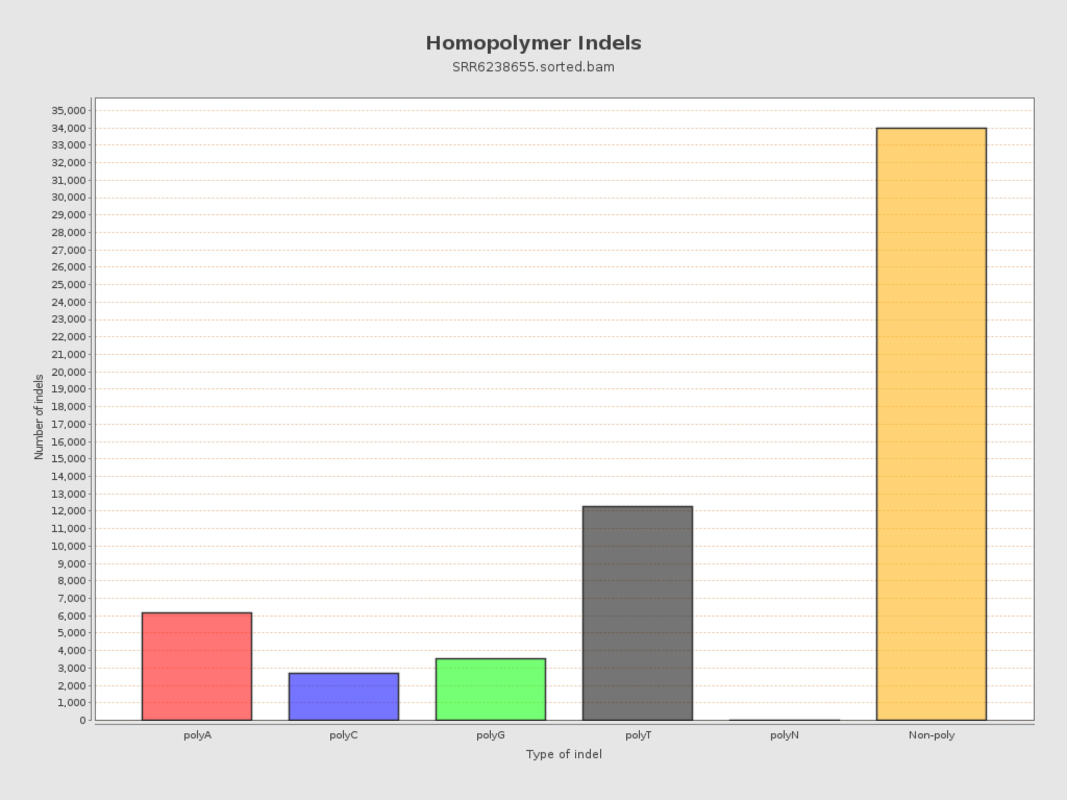
# 9. Results : Mapped Reads GC-content Distribution



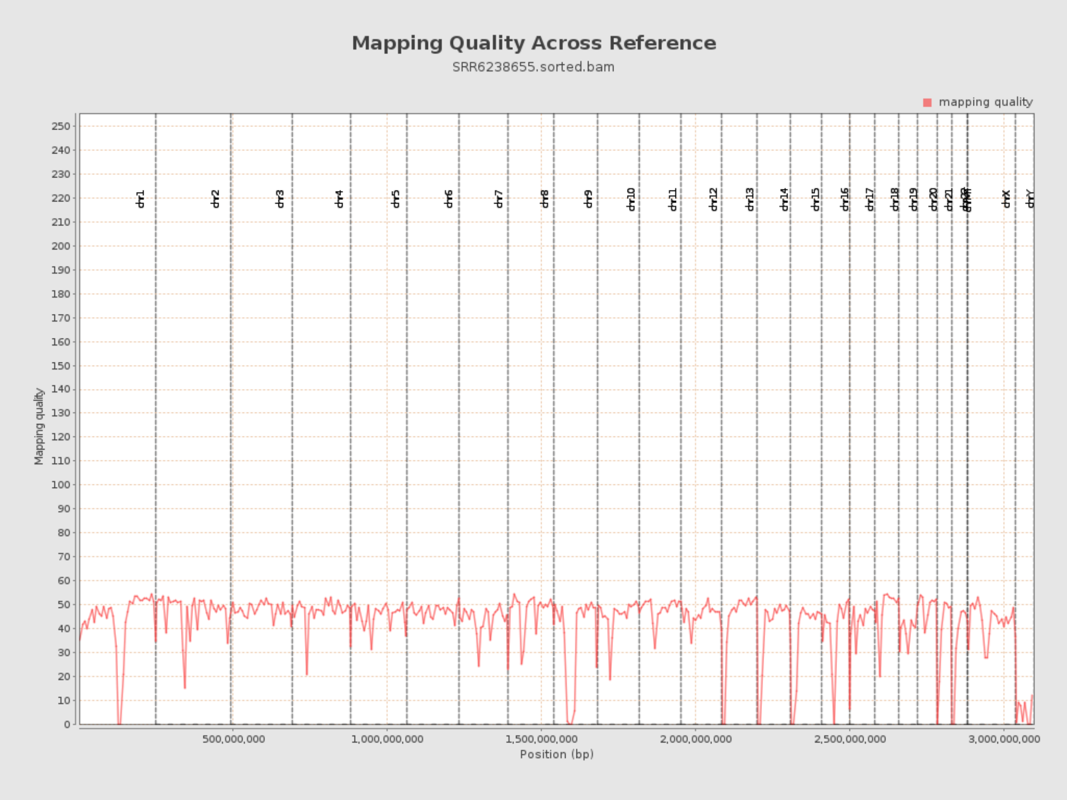
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram