# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/15 19:14:23*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230358.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_SRR6230358 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230358.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Sep 15 19:14:22 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6230358.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,879,205 |
| Mapped reads | 2,638,231 / 91.63% |
| Unmapped reads | 240,974 / 8.37% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 22,100 / 0.77% |
| Read min/max/mean length | 30 / 76 / 76.27 |
| Duplicated reads (estimated) | 135,210 / 4.7% |
| Duplication rate | 3.75% |
| Clipped reads | 905,845 / 31.46% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 56,203,385 / 30.27% |
| Number/percentage of C's | 37,524,898 / 20.21% |
| Number/percentage of T's | 54,455,468 / 29.33% |
| Number/percentage of G's | 37,379,603 / 20.14% |
| Number/percentage of N's | 80,464 / 0.04% |
| GC Percentage | 40.35% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.06 |
| | |

| | |
|---|---|
| Standard Deviation | 0.6921 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 40.1 |

## 2.5. Mismatches and indels

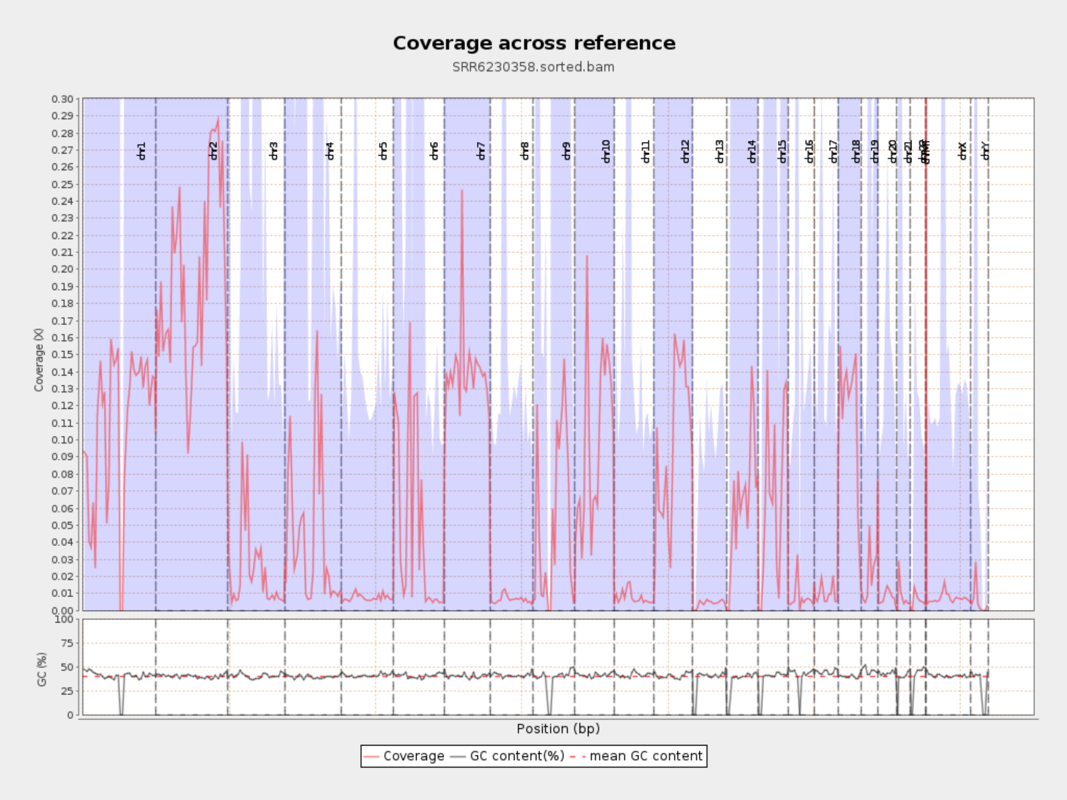
| | |
|---|---|
| General error rate | 0.85% |
| Mismatches | 1,539,122 |
| Insertions | 15,066 |
| Mapped reads with at least one insertion | 0.57% |
| Deletions | 45,619 |
| Mapped reads with at least one deletion | 1.71% |
| Homopolymer indels | 46.59% |

## 2.6. Chromosome stats

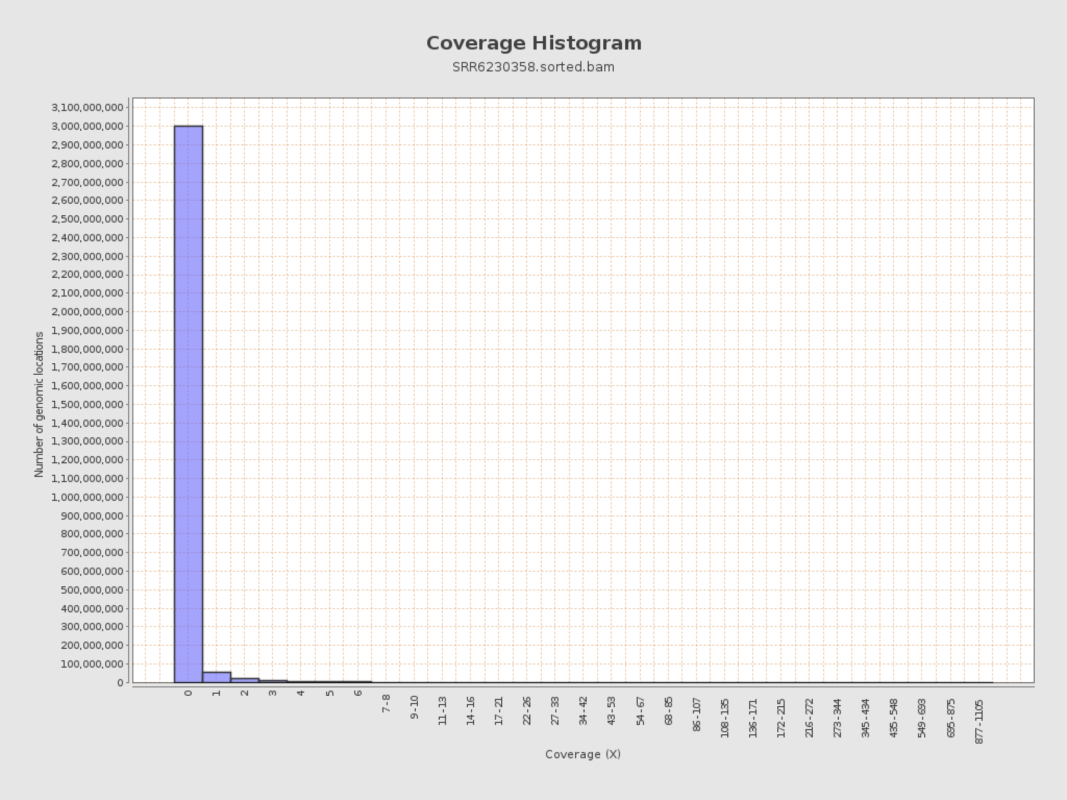
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 26891037 | 0.1079 | 0.7681 |
| chr2 | 243199373 | 47945992 | 0.1971 | 0.9058 |
| chr3 | 198022430 | 4683641 | 0.0237 | 0.345 |
| chr4 | 191154276 | 8764574 | 0.0459 | 0.411 |
| chr5 | 180915260 | 1372509 | 0.0076 | 0.155 |
| chr6 | 171115067 | 8438111 | 0.0493 | 0.483 |
| chr7 | 159138663 | 22321666 | 0.1403 | 1.8461 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 969898 | 0.0066 | 0.166 |
| chr9 | 141213431 | 7699694 | 0.0545 | 0.575 |
| chr10 | 135534747 | 13355528 | 0.0985 | 1.1645 |
| chr11 | 135006516 | 1044871 | 0.0077 | 0.2417 |
| chr12 | 133851895 | 13218256 | 0.0988 | 0.5493 |
| chr13 | 115169878 | 490584 | 0.0043 | 0.0962 |
| chr14 | 107349540 | 7041411 | 0.0656 | 0.4603 |
| chr15 | 102531392 | 6703697 | 0.0654 | 0.4364 |
| chr16 | 90354753 | 658527 | 0.0073 | 0.2833 |
| chr17 | 81195210 | 777735 | 0.0096 | 0.1725 |
| chr18 | 78077248 | 9328892 | 0.1195 | 1.2609 |
| chr19 | 59128983 | 1300156 | 0.022 | 0.4278 |
| chr20 | 63025520 | 498243 | 0.0079 | 0.1476 |
| chr21 | 48129895 | 435551 | 0.009 | 0.2424 |
| chr22 | 51304566 | 293700 | 0.0057 | 0.11 |
| chrMT | 16571 | 10710 | 0.6463 | 1.1723 |
| chrX | 155270560 | 1121623 | 0.0072 | 0.1637 |
| chrY | 59373566 | 353953 | 0.006 | 0.2504 |

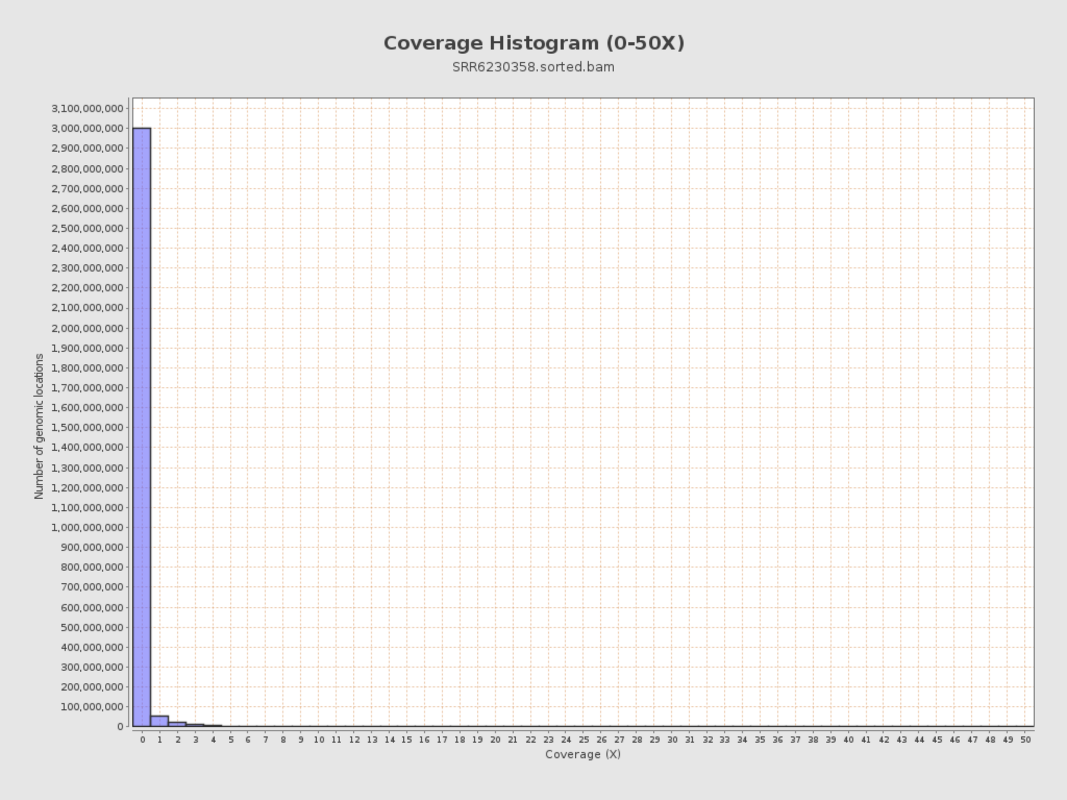
# 3. Results : Coverage across reference



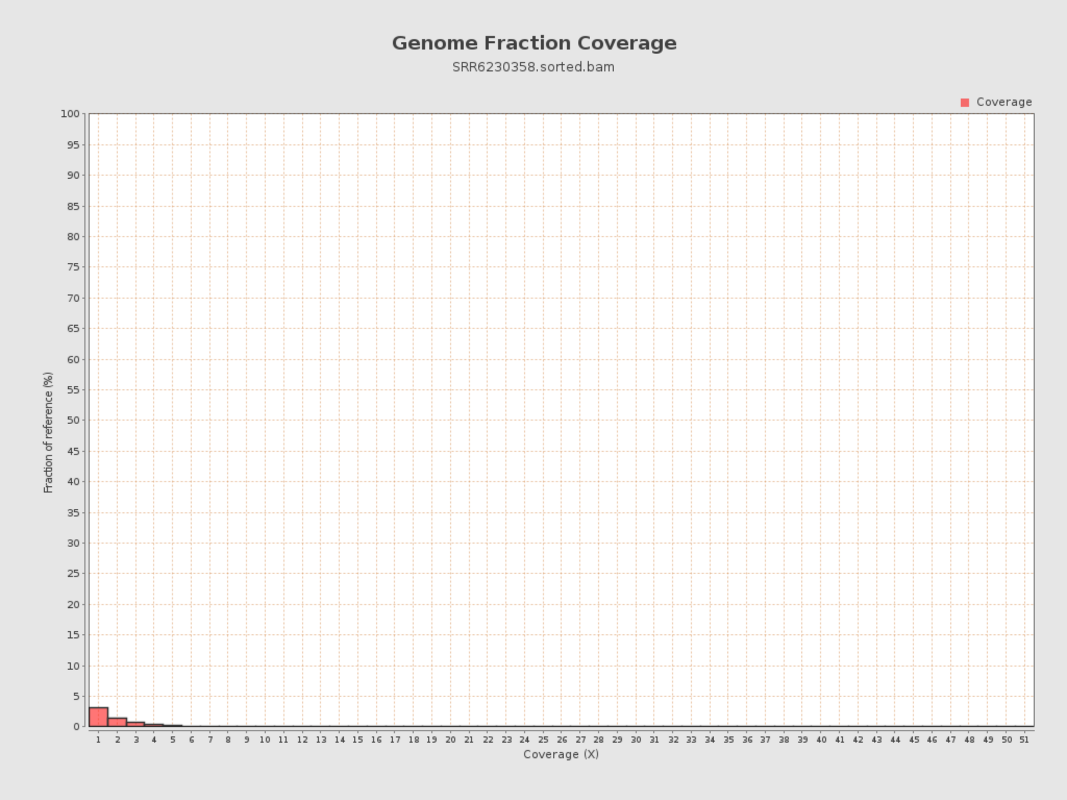
# 4. Results : Coverage Histogram



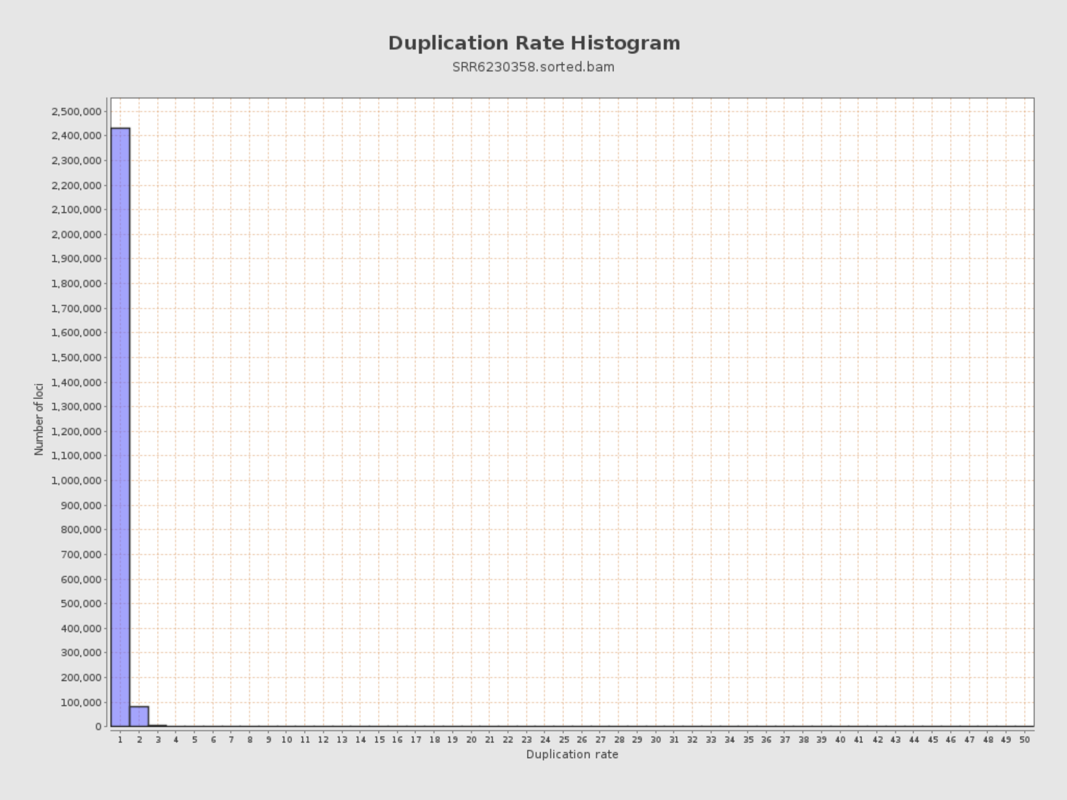
# 5. Results : Coverage Histogram (0-50X)



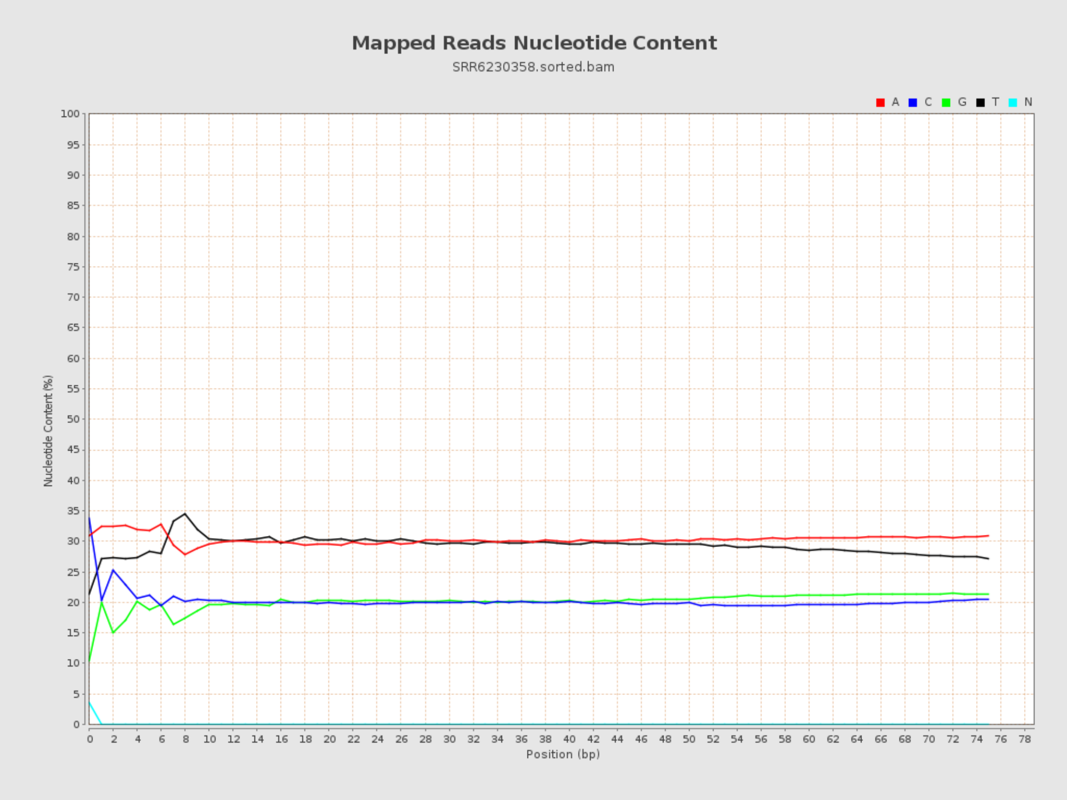
# 6. Results : Genome Fraction Coverage



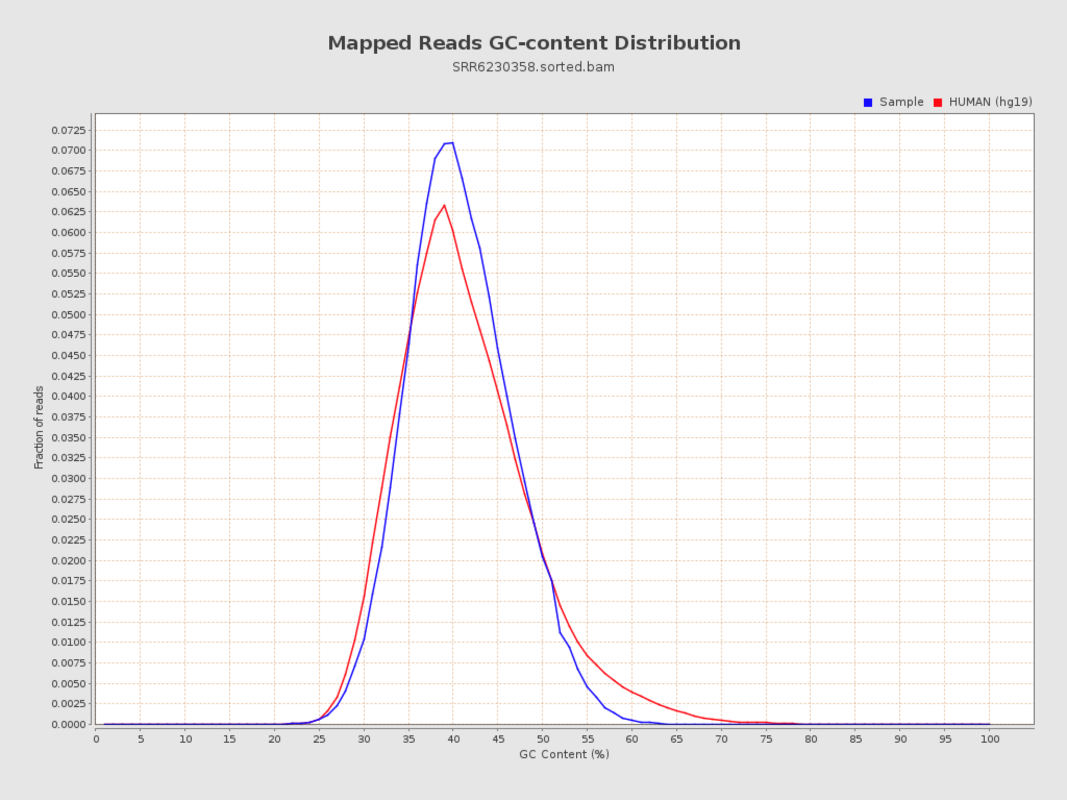
# 7. Results : Duplication Rate Histogram



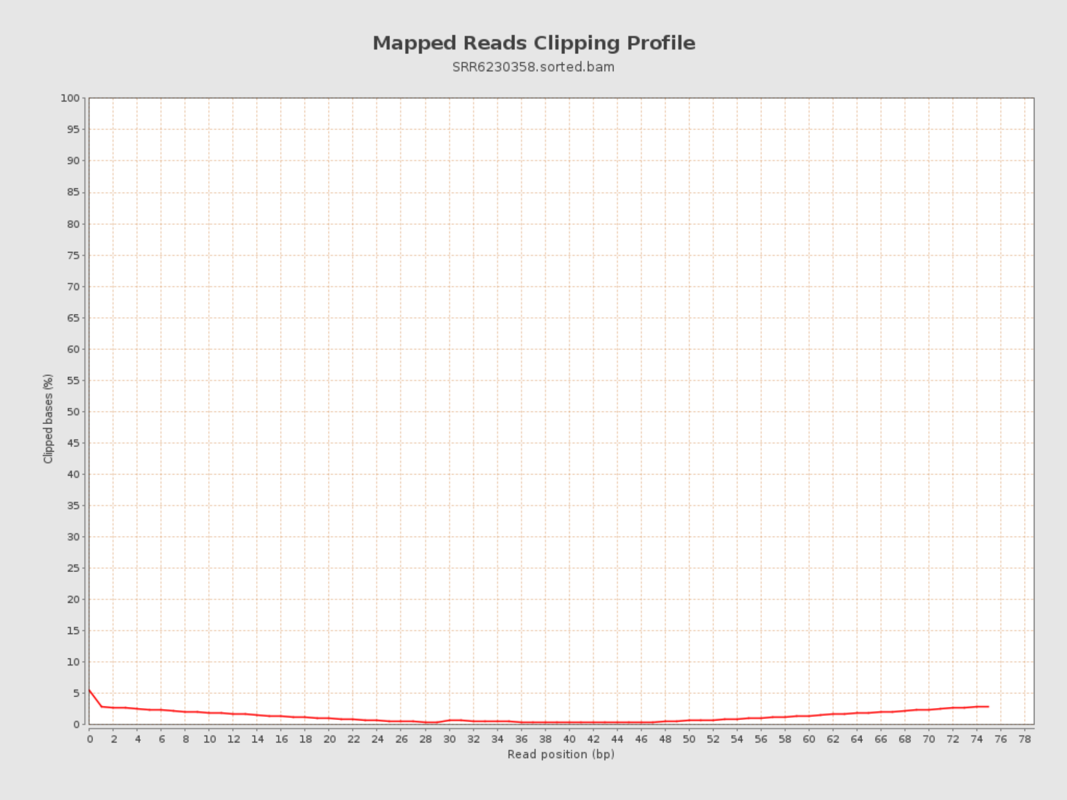
# 8. Results : Mapped Reads Nucleotide Content



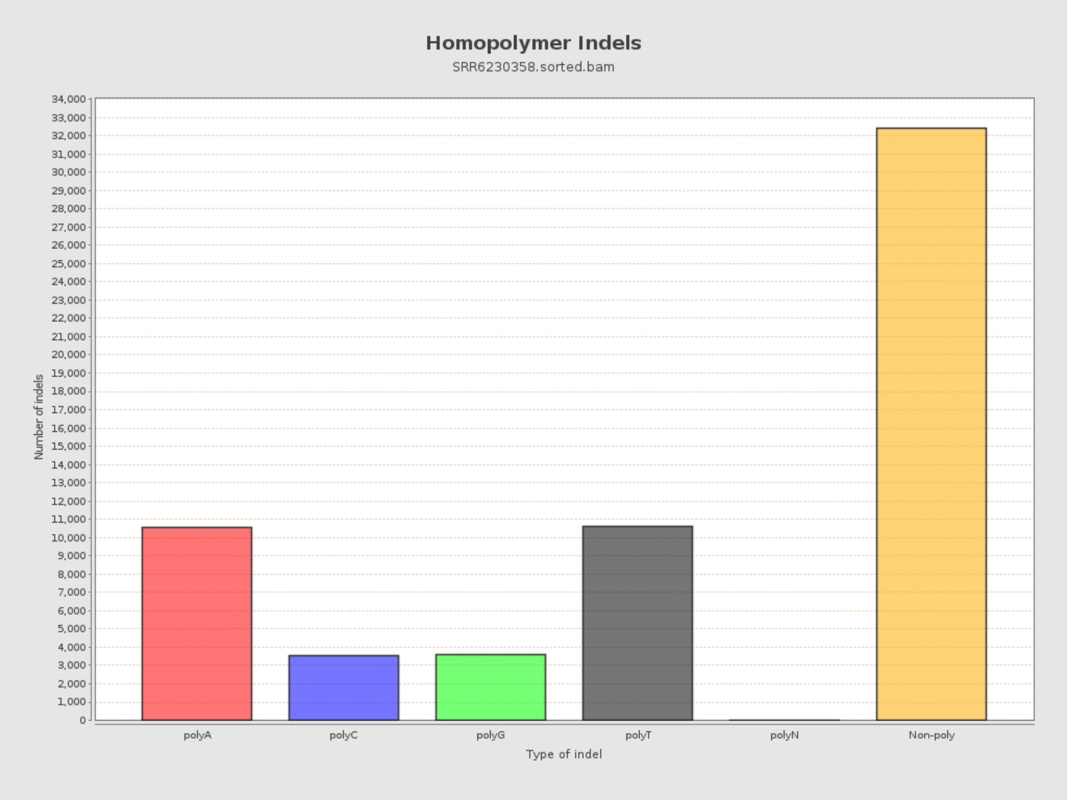
# 9. Results : Mapped Reads GC-content Distribution



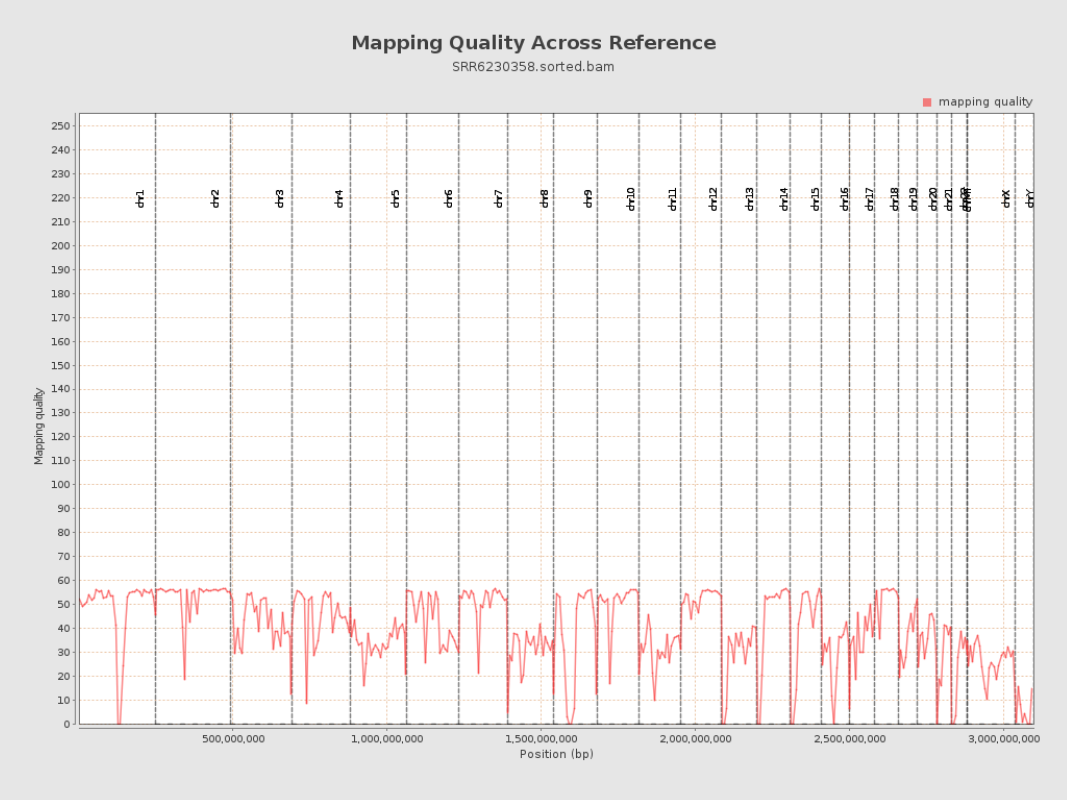
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram