# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/16 01:13:08*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231764.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_SRR6231764 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231764.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 16 01:13:07 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6231764.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 5,833,588 |
| Mapped reads | 5,477,203 / 93.89% |
| Unmapped reads | 356,385 / 6.11% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 41,152 / 0.71% |
| Read min/max/mean length | 30 / 76 / 76.25 |
| Duplicated reads (estimated) | 520,147 / 8.92% |
| Duplication rate | 4.41% |
| Clipped reads | 1,993,406 / 34.17% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 101,113,054 / 26.92% |
| Number/percentage of C's | 69,297,270 / 18.45% |
| Number/percentage of T's | 109,590,449 / 29.17% |
| Number/percentage of G's | 95,591,561 / 25.45% |
| Number/percentage of N's | 82,839 / 0.02% |
| GC Percentage | 43.89% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1214 |
| | |

| | |
|---|---|
| Standard Deviation | 31.9598 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.19 |

## 2.5. Mismatches and indels

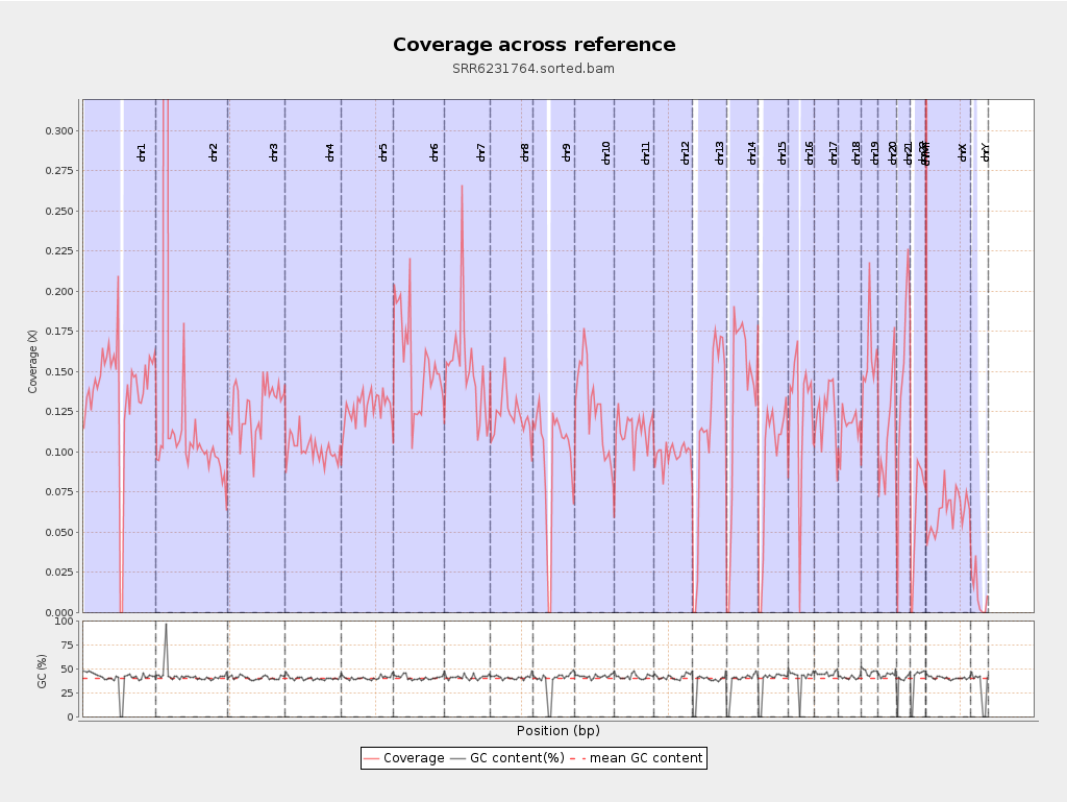
| | |
|---|---|
| General error rate | 0.65% |
| Mismatches | 2,414,184 |
| Insertions | 25,776 |
| Mapped reads with at least one insertion | 0.47% |
| Deletions | 83,639 |
| Mapped reads with at least one deletion | 1.51% |
| Homopolymer indels | 47.55% |

## 2.6. Chromosome stats

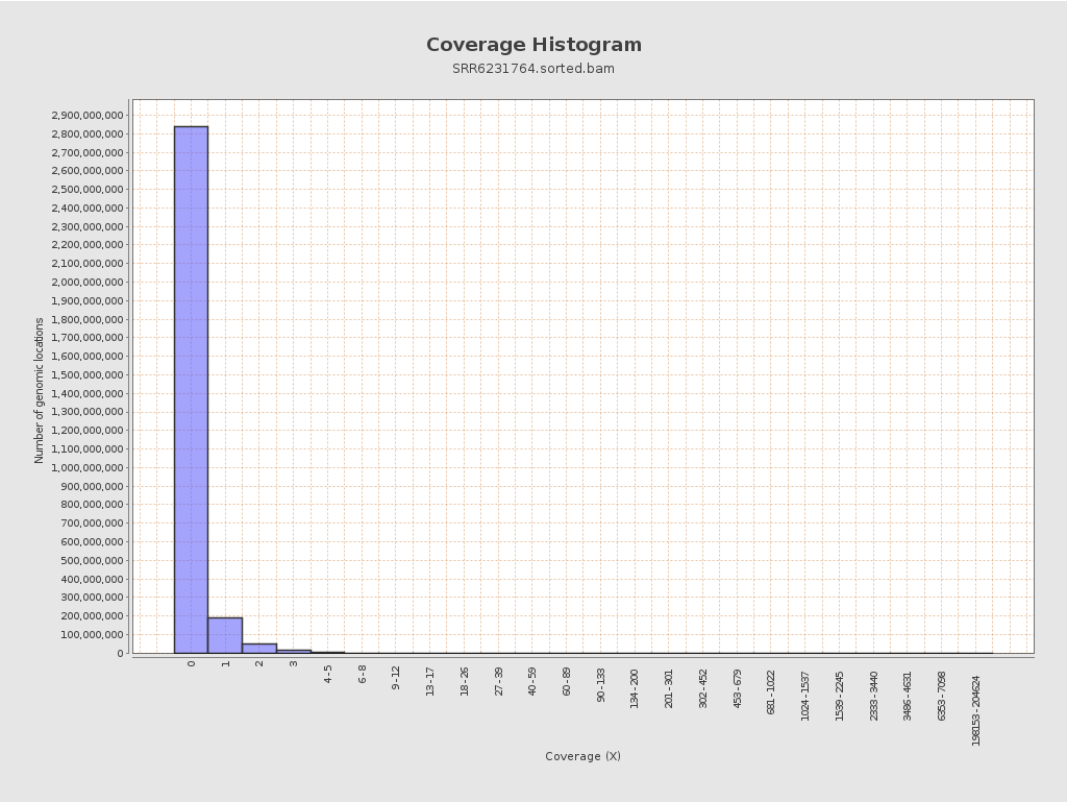
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 34315663 | 0.1377 | 1.7942 |
| chr2 | 243199373 | 41149755 | 0.1692 | 113.9787 |
| chr3 | 198022430 | 25152632 | 0.127 | 0.4676 |
| chr4 | 191154276 | 19423118 | 0.1016 | 0.4528 |
| chr5 | 180915260 | 22923723 | 0.1267 | 0.4769 |
| chr6 | 171115067 | 26612077 | 0.1555 | 0.7497 |
| chr7 | 159138663 | 23972937 | 0.1506 | 1.9253 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 17940749 | 0.1226 | 1.1482 |
| chr9 | 141213431 | 13735563 | 0.0973 | 0.7255 |
| chr10 | 135534747 | 17159031 | 0.1266 | 0.7051 |
| chr11 | 135006516 | 15225013 | 0.1128 | 0.979 |
| chr12 | 133851895 | 13191762 | 0.0986 | 0.429 |
| chr13 | 115169878 | 13350330 | 0.1159 | 0.4522 |
| chr14 | 107349540 | 14482394 | 0.1349 | 0.6226 |
| chr15 | 102531392 | 9602935 | 0.0937 | 0.4043 |
| chr16 | 90354753 | 11097504 | 0.1228 | 0.5266 |
| chr17 | 81195210 | 10248094 | 0.1262 | 0.6436 |
| chr18 | 78077248 | 9064340 | 0.1161 | 1.5425 |
| chr19 | 59128983 | 9314309 | 0.1575 | 1.2638 |
| chr20 | 63025520 | 7078816 | 0.1123 | 0.4682 |
| chr21 | 48129895 | 7183659 | 0.1493 | 0.5685 |
| chr22 | 51304566 | 3211153 | 0.0626 | 0.3207 |
| chrMT | 16571 | 36989 | 2.2322 | 2.366 |
| chrX | 155270560 | 9664493 | 0.0622 | 0.4338 |
| chrY | 59373566 | 674433 | 0.0114 | 0.2156 |

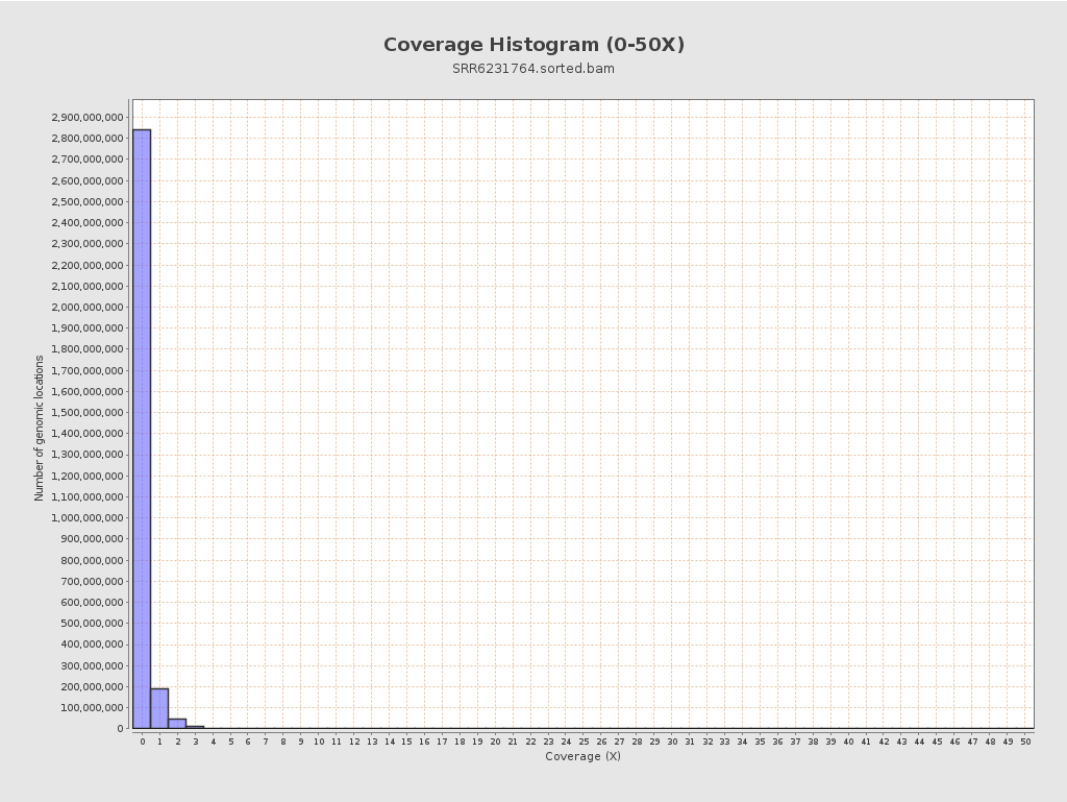
# 3. Results : Coverage across reference



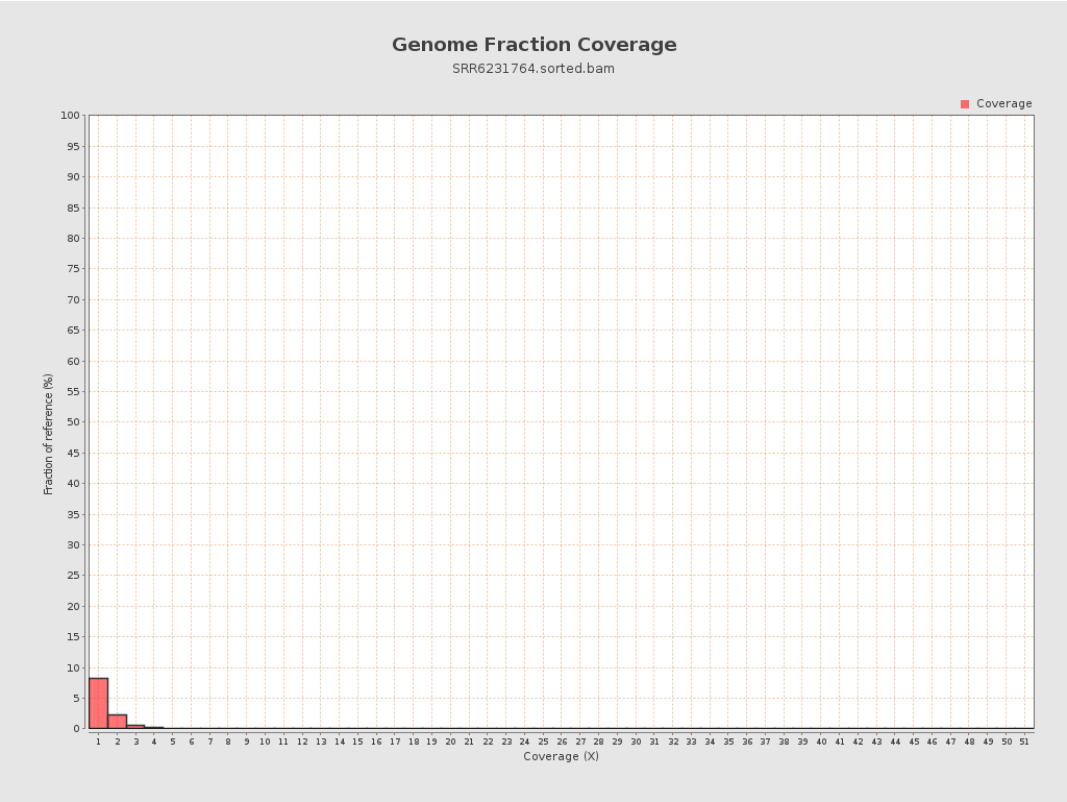
# 4. Results : Coverage Histogram



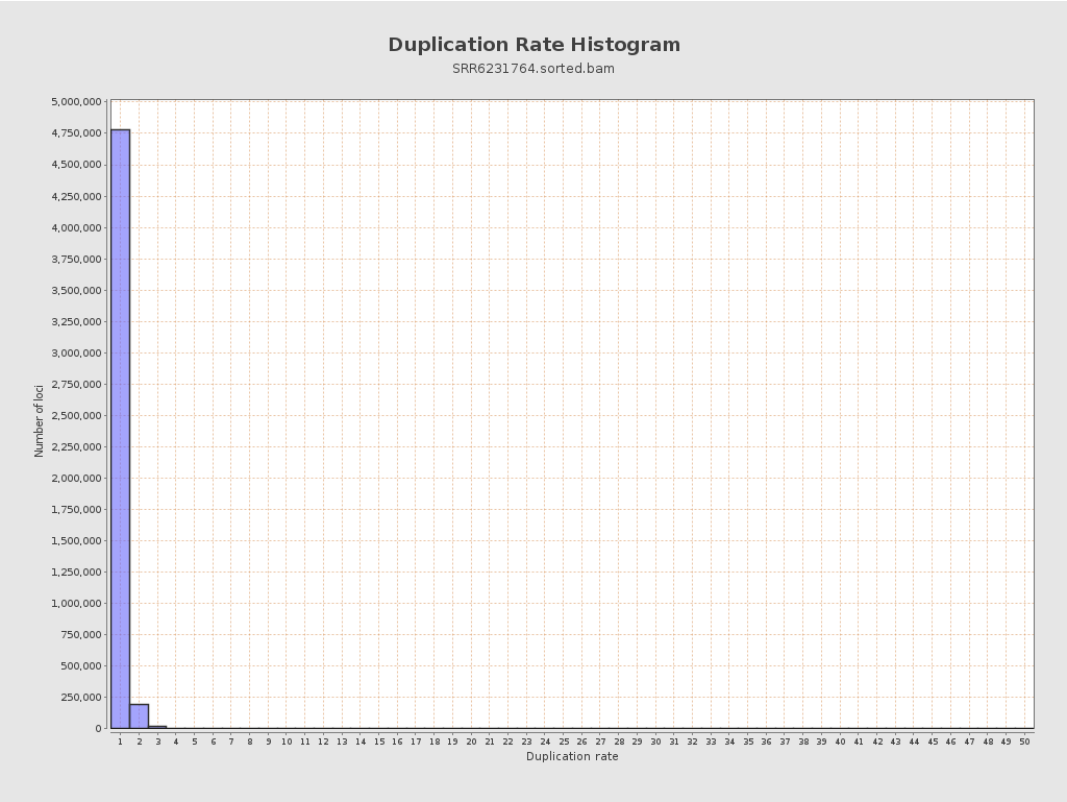
# 5. Results : Coverage Histogram (0-50X)



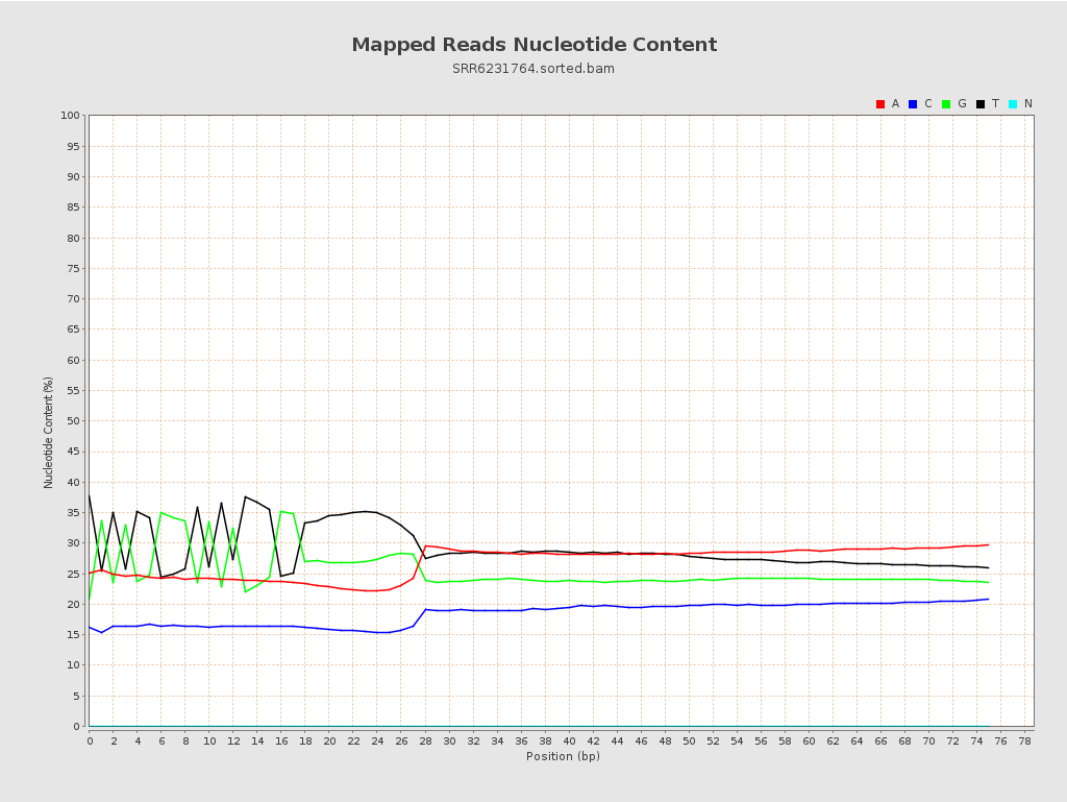
# 6. Results : Genome Fraction Coverage



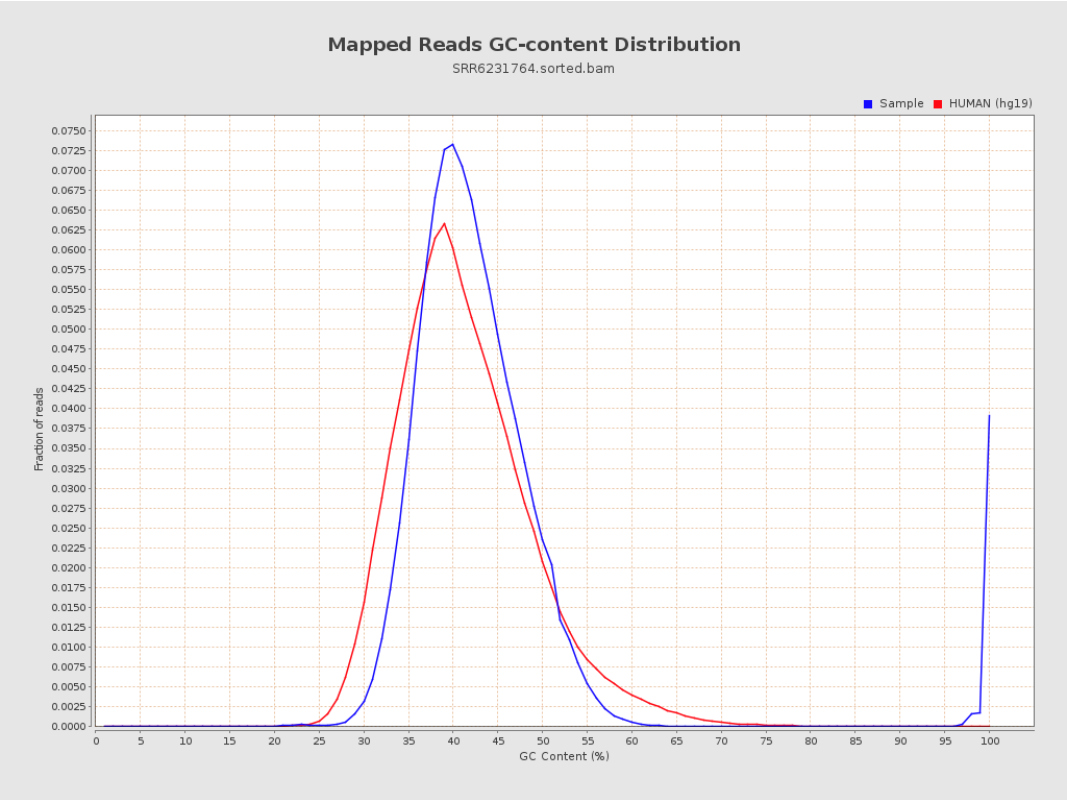
# 7. Results : Duplication Rate Histogram



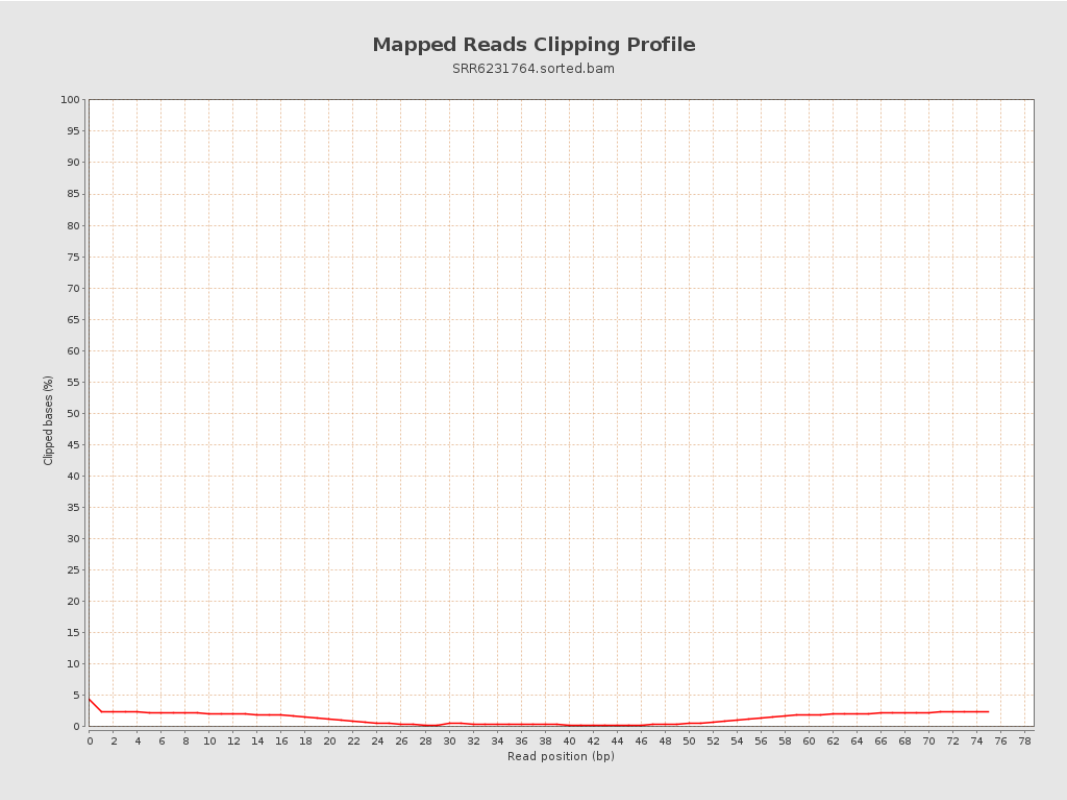
# 8. Results : Mapped Reads Nucleotide Content



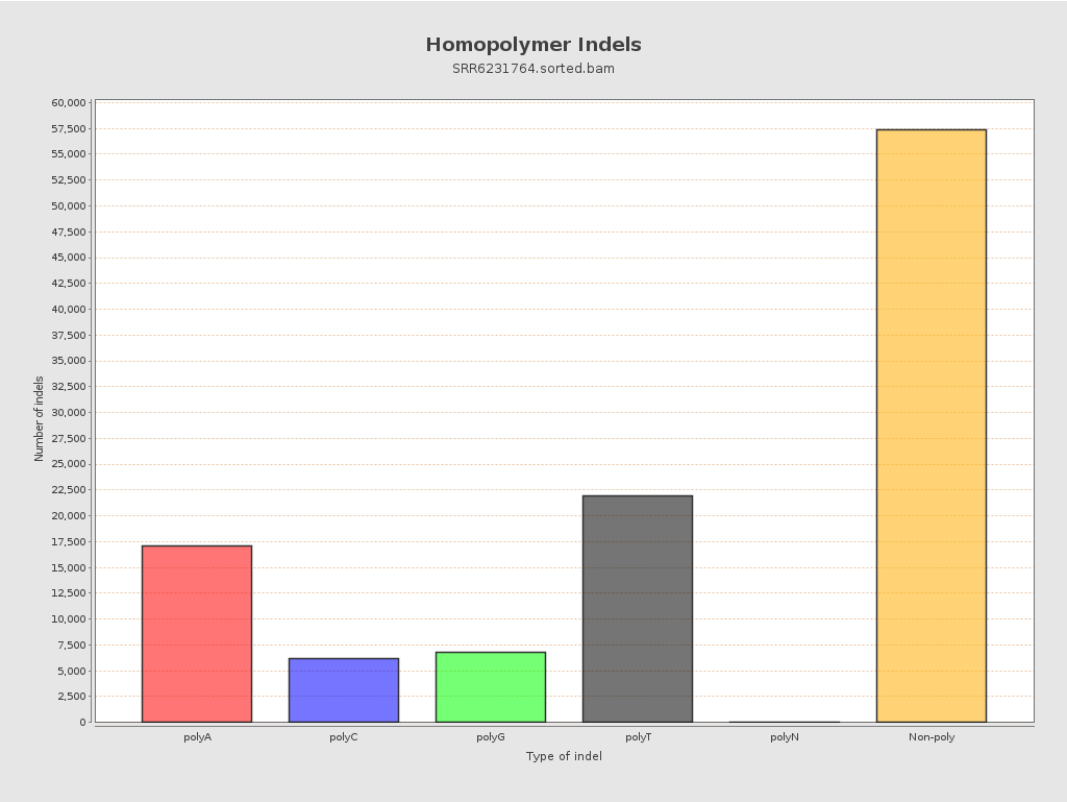
# 9. Results : Mapped Reads GC-content Distribution



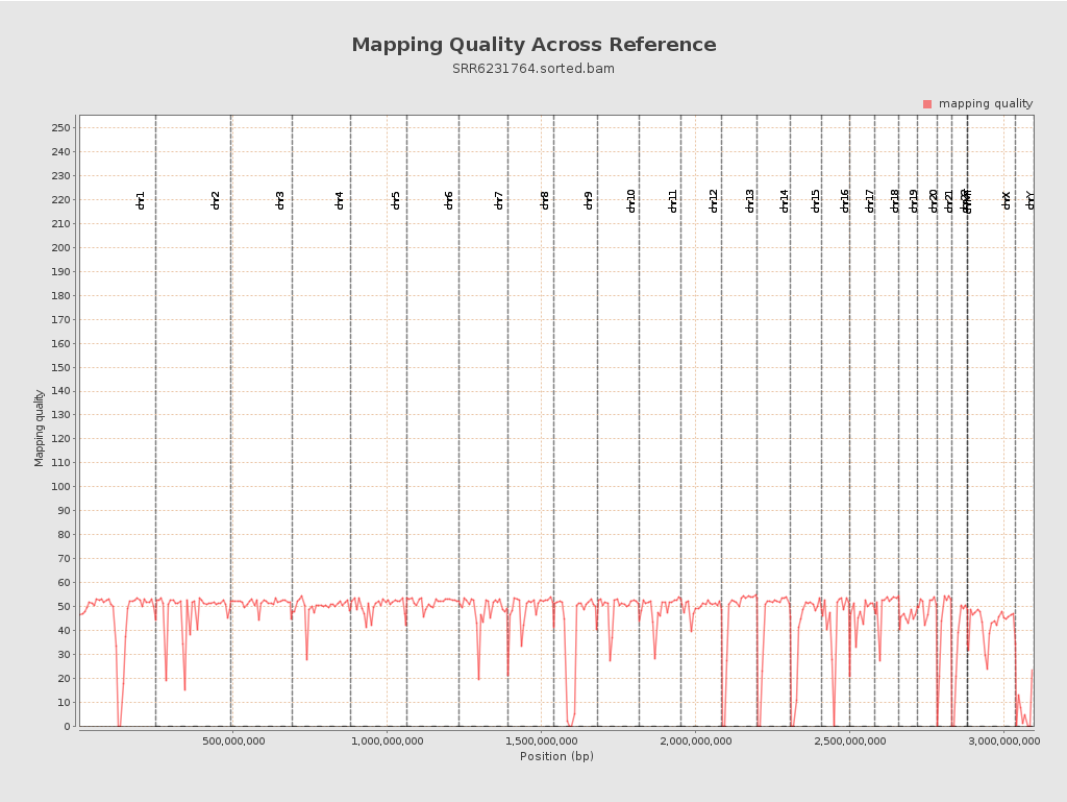
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram