# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/16 11:08:20*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234027.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_SRR6234027 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234027.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 16 11:08:20 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6234027.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 7,626,735 |
| Mapped reads | 4,249,010 / 55.71% |
| Unmapped reads | 3,377,725 / 44.29% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 27,725 / 0.36% |
| Read min/max/mean length | 30 / 76 / 76.13 |
| Duplicated reads (estimated) | 547,375 / 7.18% |
| Duplication rate | 9.04% |
| Clipped reads | 1,639,551 / 21.5% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 81,446,890 / 28.39% |
| Number/percentage of C's | 51,890,520 / 18.09% |
| Number/percentage of T's | 92,770,092 / 32.34% |
| Number/percentage of G's | 60,671,172 / 21.15% |
| Number/percentage of N's | 71,560 / 0.02% |
| GC Percentage | 39.24% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0927 |
| | |

| | |
|---|---|
| Standard Deviation | 1.1229 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 41.14 |

## 2.5. Mismatches and indels

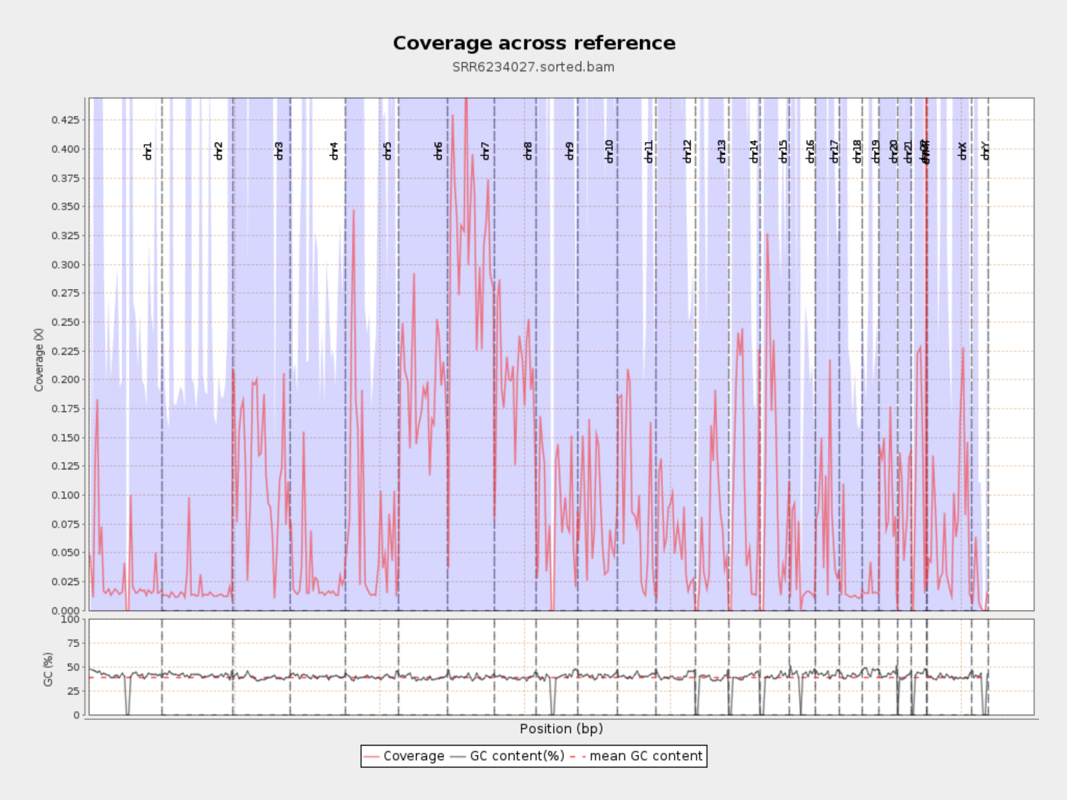
| | |
|---|---|
| General error rate | 0.83% |
| Mismatches | 2,315,747 |
| Insertions | 25,912 |
| Mapped reads with at least one insertion | 0.6% |
| Deletions | 78,044 |
| Mapped reads with at least one deletion | 1.81% |
| Homopolymer indels | 45.48% |

## 2.6. Chromosome stats

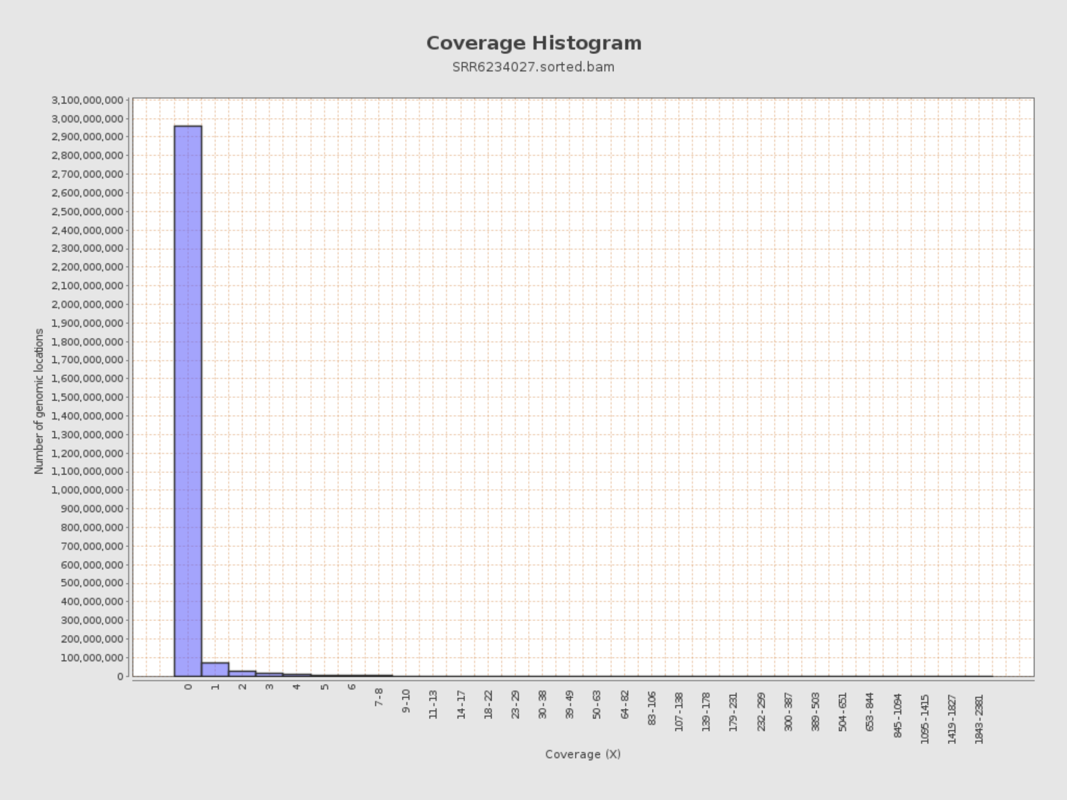
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 8040566 | 0.0323 | 0.5131 |
| chr2 | 243199373 | 4219202 | 0.0173 | 0.8554 |
| chr3 | 198022430 | 25148422 | 0.127 | 0.6785 |
| chr4 | 191154276 | 5446984 | 0.0285 | 0.4611 |
| chr5 | 180915260 | 14535141 | 0.0803 | 0.5477 |
| chr6 | 171115067 | 32525993 | 0.1901 | 1.0265 |
| chr7 | 159138663 | 51836806 | 0.3257 | 3.3183 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 29707303 | 0.203 | 1.6557 |
| chr9 | 141213431 | 11767172 | 0.0833 | 1.0031 |
| chr10 | 135534747 | 11053919 | 0.0816 | 0.9079 |
| chr11 | 135006516 | 12958377 | 0.096 | 0.9023 |
| chr12 | 133851895 | 8384673 | 0.0626 | 0.484 |
| chr13 | 115169878 | 8060979 | 0.07 | 0.5142 |
| chr14 | 107349540 | 10395047 | 0.0968 | 0.625 |
| chr15 | 102531392 | 11733200 | 0.1144 | 0.643 |
| chr16 | 90354753 | 2865021 | 0.0317 | 0.5414 |
| chr17 | 81195210 | 6683288 | 0.0823 | 0.6188 |
| chr18 | 78077248 | 1775231 | 0.0227 | 2.297 |
| chr19 | 59128983 | 1119094 | 0.0189 | 0.4548 |
| chr20 | 63025520 | 6655208 | 0.1056 | 0.6197 |
| chr21 | 48129895 | 4604273 | 0.0957 | 0.656 |
| chr22 | 51304566 | 5564571 | 0.1085 | 0.6352 |
| chrMT | 16571 | 55646 | 3.358 | 3.5365 |
| chrX | 155270560 | 10973699 | 0.0707 | 0.5964 |
| chrY | 59373566 | 880015 | 0.0148 | 0.4104 |

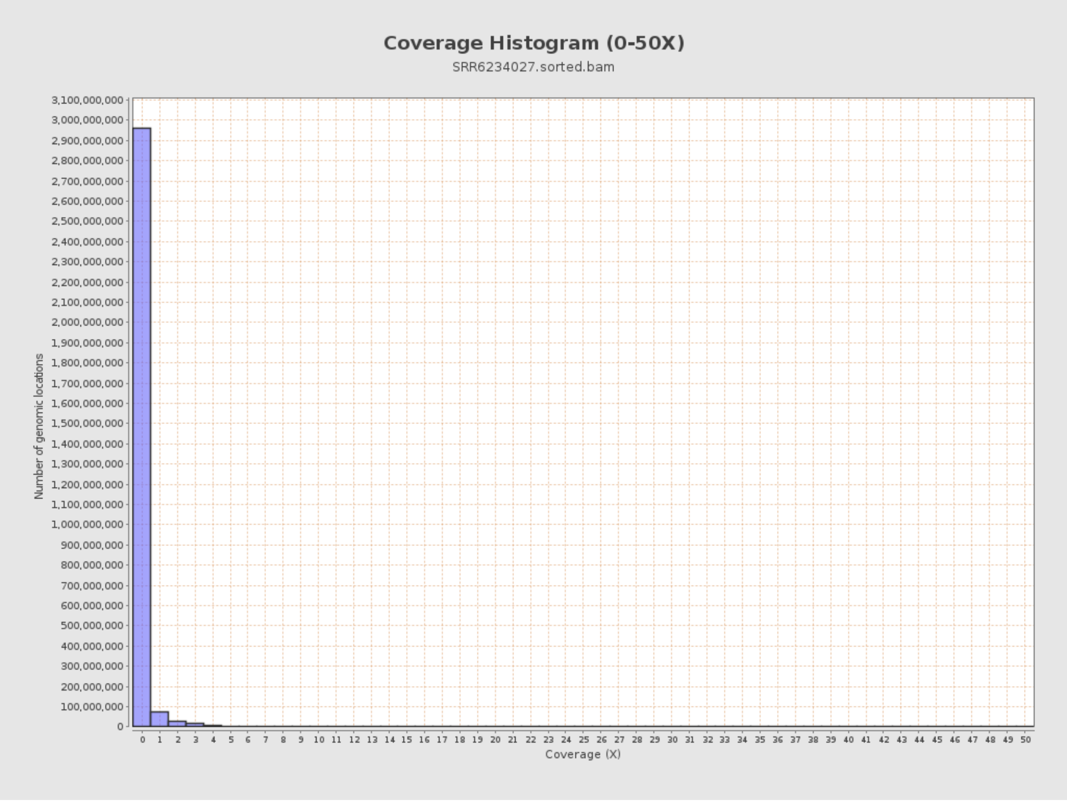
# 3. Results : Coverage across reference



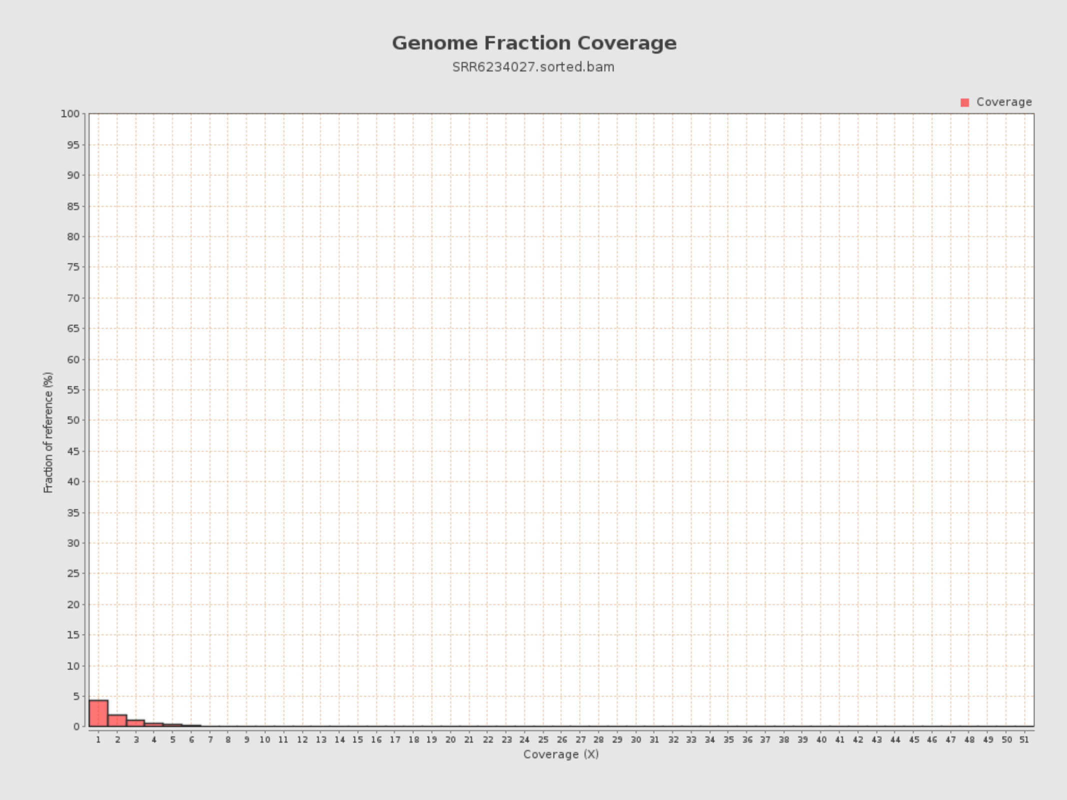
# 4. Results : Coverage Histogram



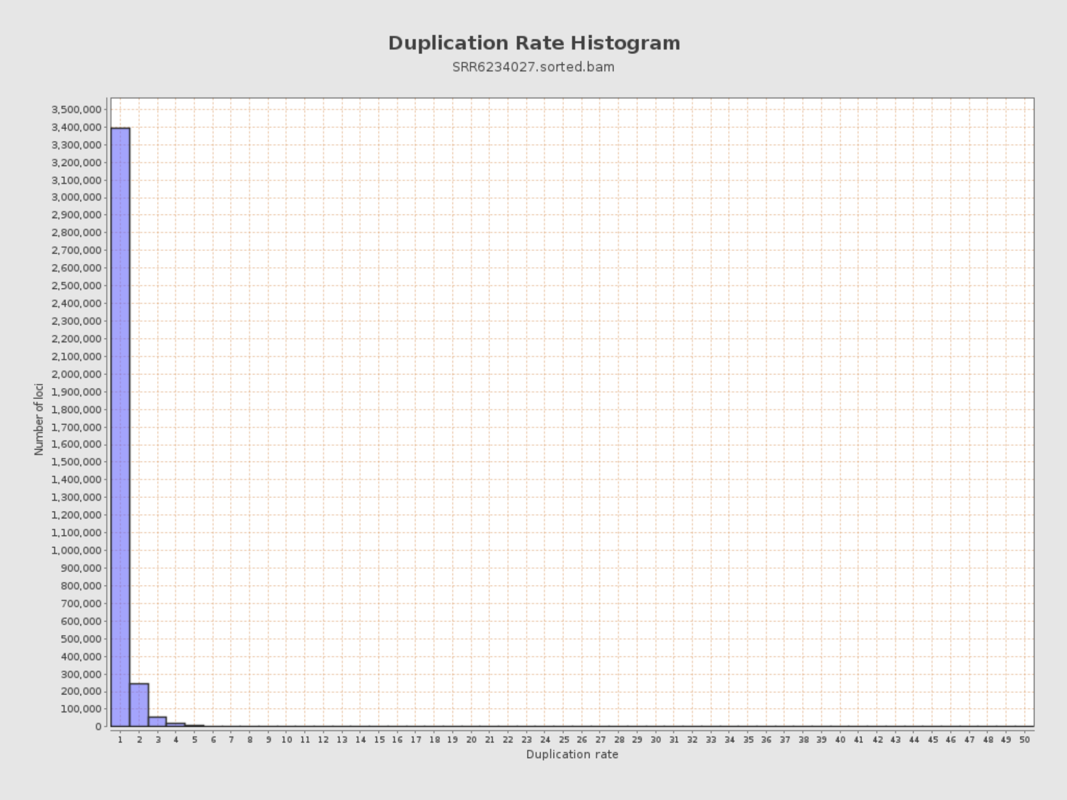
# 5. Results : Coverage Histogram (0-50X)



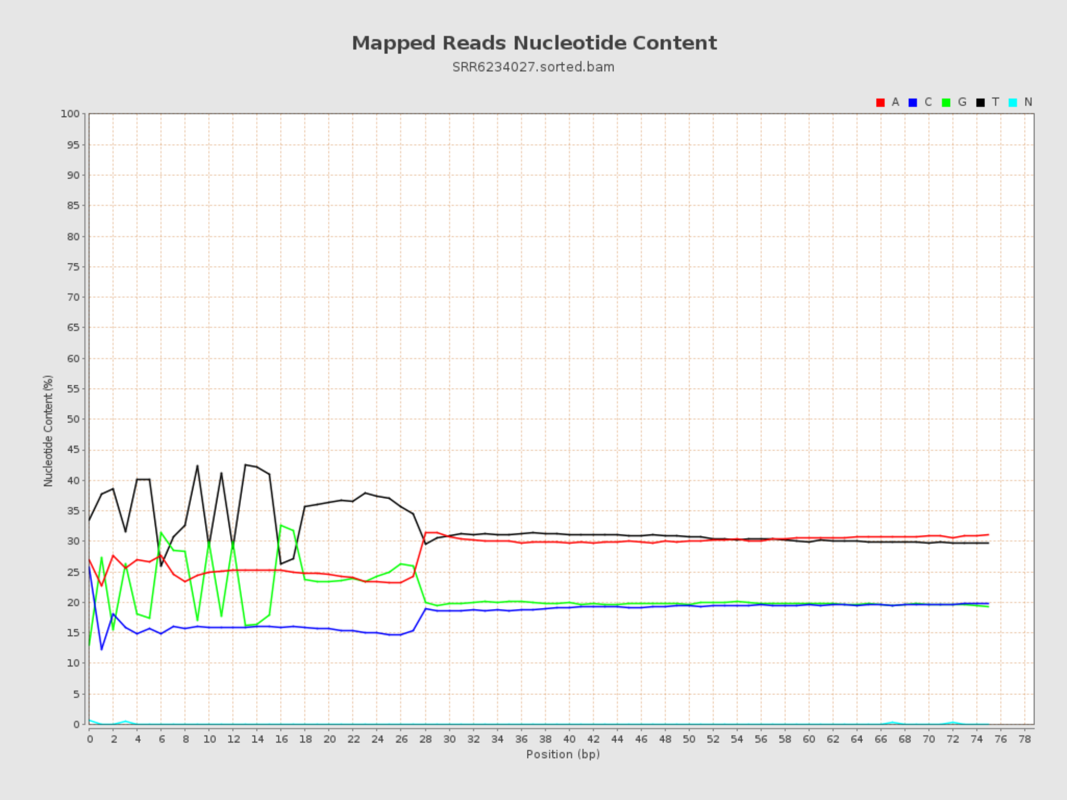
# 6. Results : Genome Fraction Coverage



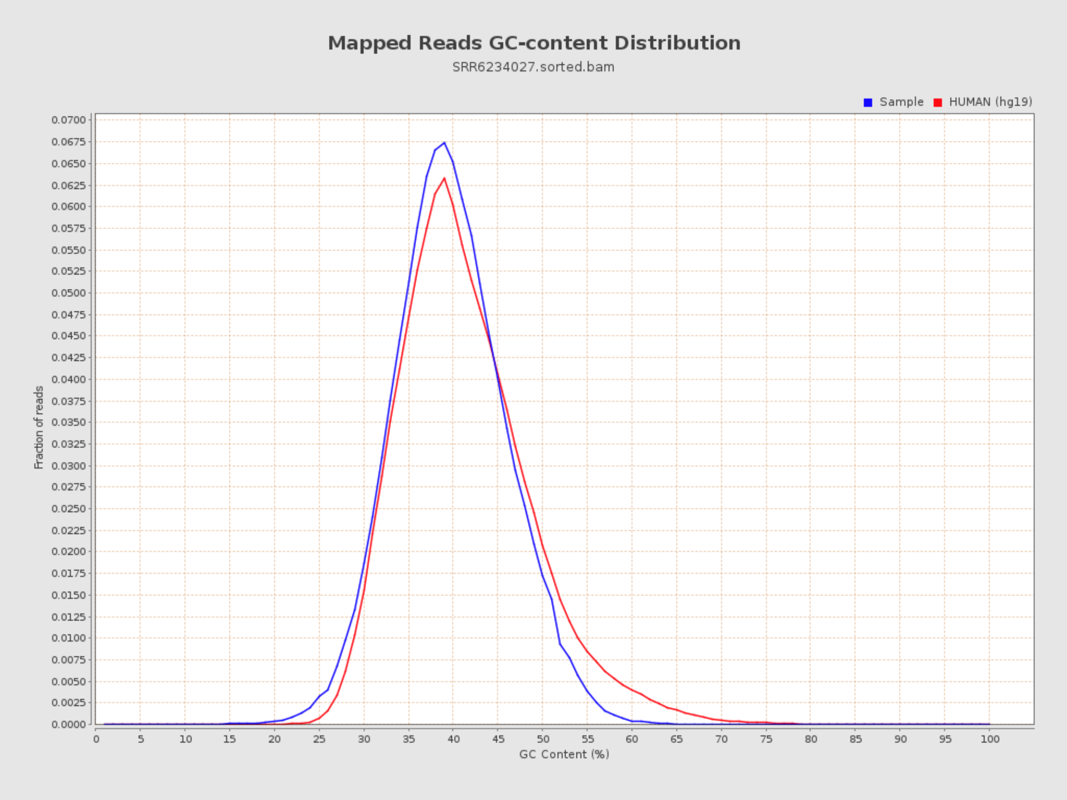
# 7. Results : Duplication Rate Histogram



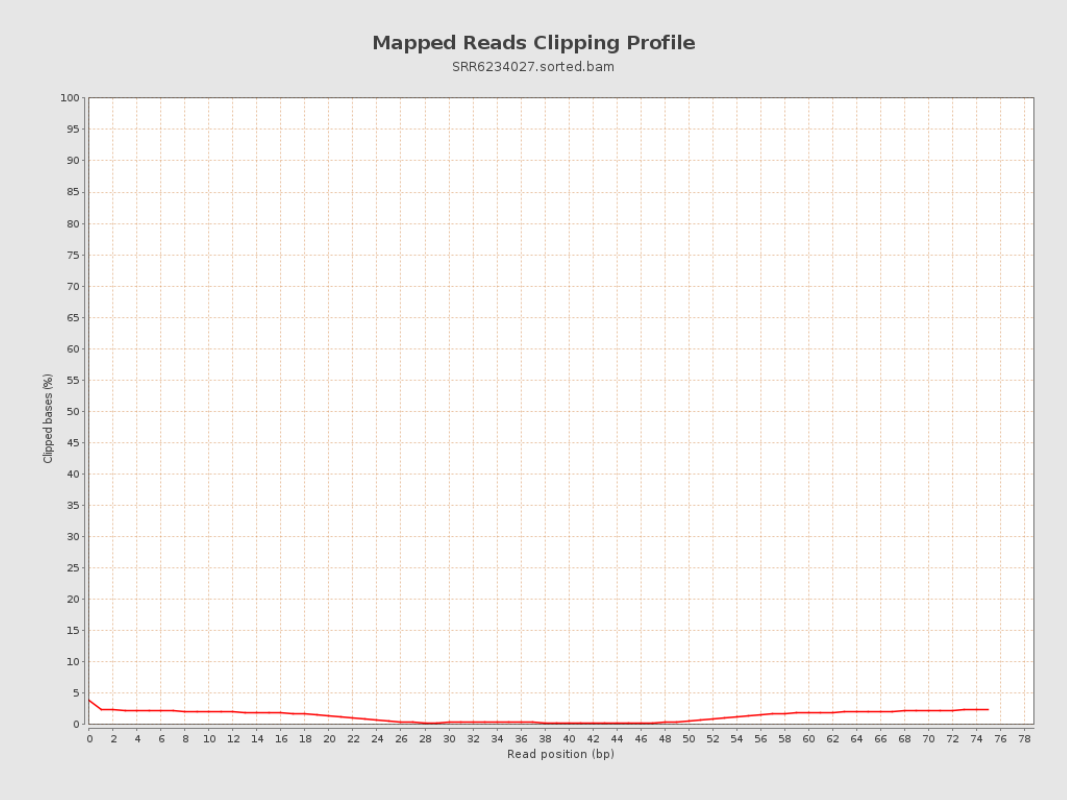
# 8. Results : Mapped Reads Nucleotide Content



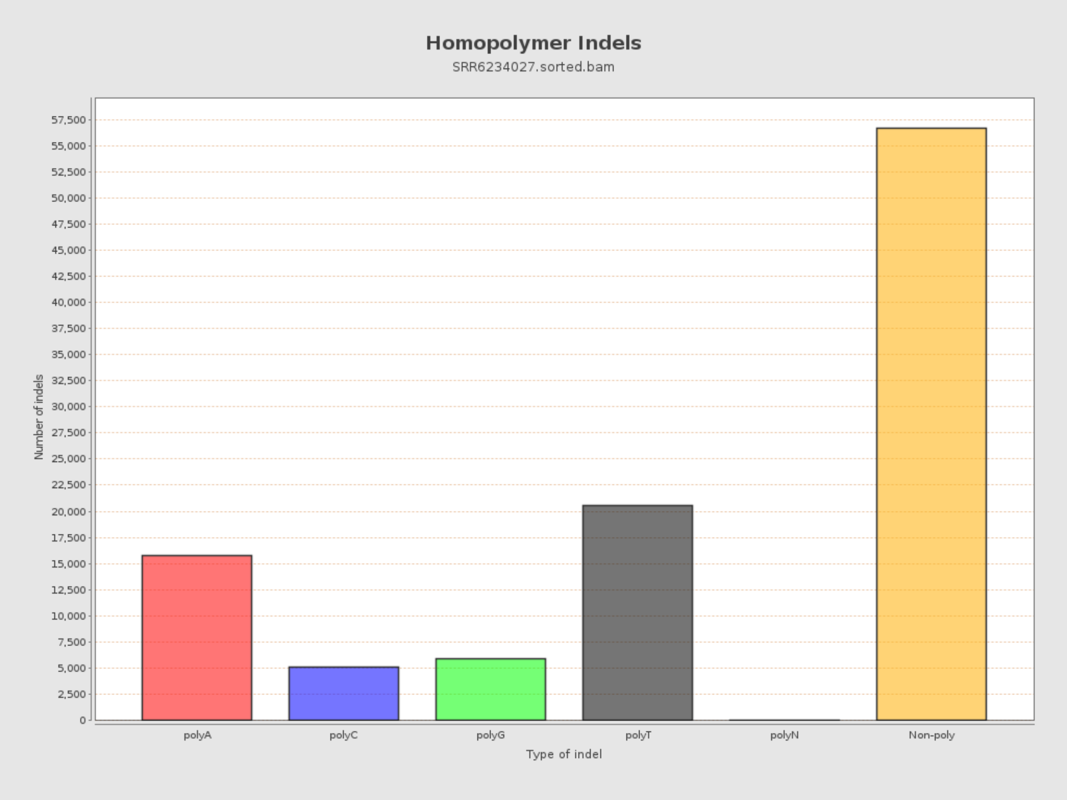
# 9. Results : Mapped Reads GC-content Distribution



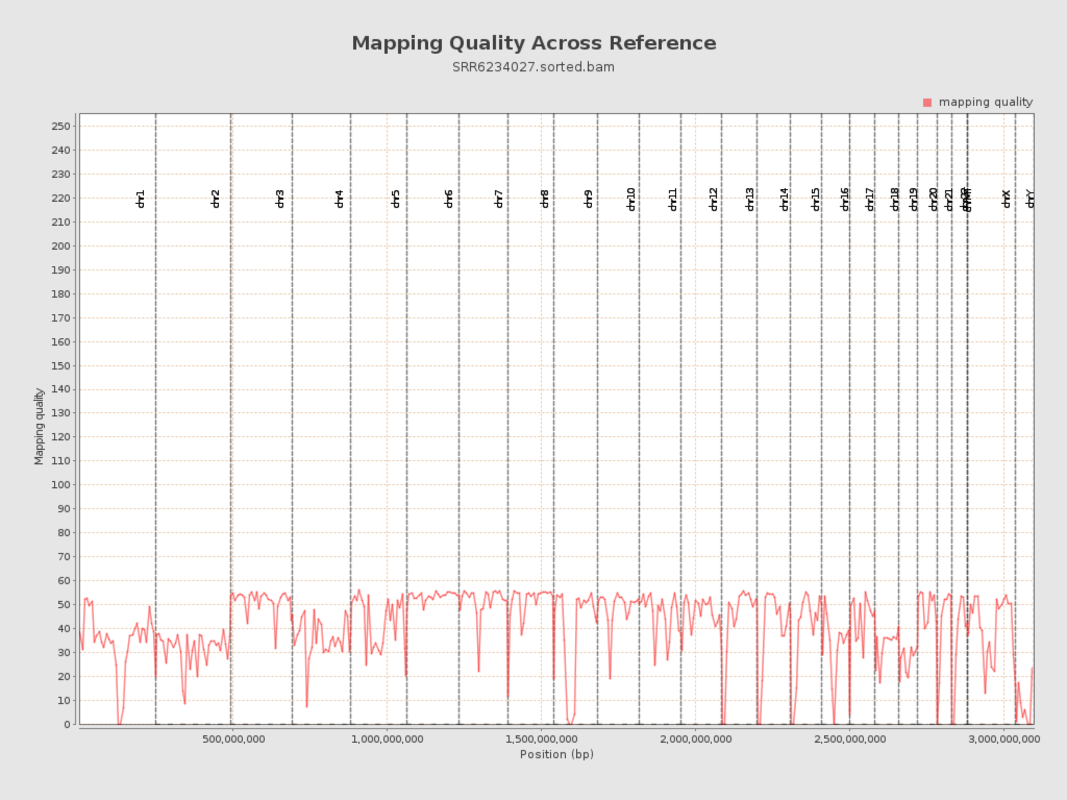
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram