# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/16 07:19:26*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231843.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_SRR6231843 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231843.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 16 07:19:25 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6231843.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 21,583 |
| Mapped reads | 4,656 / 21.57% |
| Unmapped reads | 16,927 / 78.43% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 44 / 0.2% |
| Read min/max/mean length | 30 / 76 / 76.07 |
| Duplicated reads (estimated) | 950 / 4.4% |
| Duplication rate | 2.75% |
| Clipped reads | 2,333 / 10.81% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 70,013 / 23.01% |
| Number/percentage of C's | 45,432 / 14.93% |
| Number/percentage of T's | 68,289 / 22.44% |
| Number/percentage of G's | 120,551 / 39.62% |
| Number/percentage of N's | 5 / 0% |
| GC Percentage | 54.55% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0001 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1158 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.67 |

## 2.5. Mismatches and indels

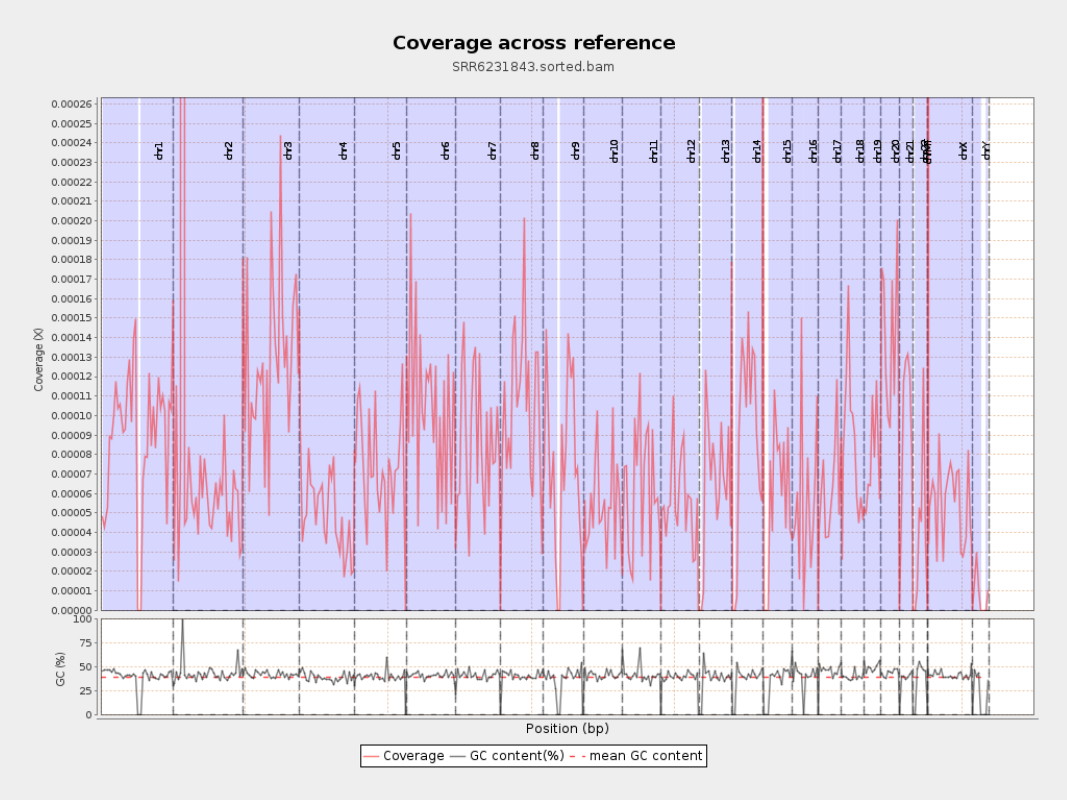
| | |
|---|---|
| General error rate | 0.97% |
| Mismatches | 2,673 |
| Insertions | 103 |
| Mapped reads with at least one insertion | 2.13% |
| Deletions | 51 |
| Mapped reads with at least one deletion | 1.1% |
| Homopolymer indels | 31.82% |

## 2.6. Chromosome stats

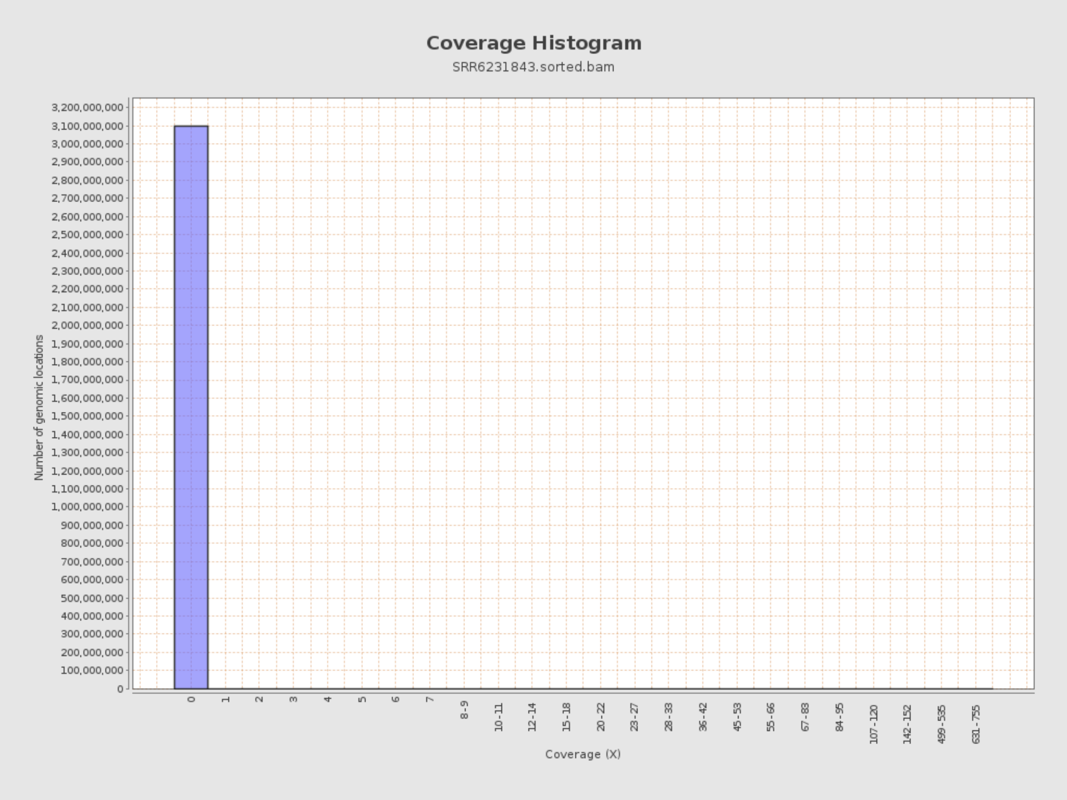
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 22490 | 0.0001 | 0.0096 |
| chr2 | 243199373 | 84035 | 0.0003 | 0.412 |
| chr3 | 198022430 | 25457 | 0.0001 | 0.0116 |
| chr4 | 191154276 | 9457 | 0 | 0.0071 |
| chr5 | 180915260 | 13294 | 0.0001 | 0.0086 |
| chr6 | 171115067 | 17836 | 0.0001 | 0.0104 |
| chr7 | 159138663 | 13724 | 0.0001 | 0.0094 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 15610 | 0.0001 | 0.0104 |
| chr9 | 141213431 | 10339 | 0.0001 | 0.0086 |
| chr10 | 135534747 | 7476 | 0.0001 | 0.0075 |
| chr11 | 135006516 | 8228 | 0.0001 | 0.0097 |
| chr12 | 133851895 | 7420 | 0.0001 | 0.0075 |
| chr13 | 115169878 | 7443 | 0.0001 | 0.0081 |
| chr14 | 107349540 | 9672 | 0.0001 | 0.0096 |
| chr15 | 102531392 | 5689 | 0.0001 | 0.0075 |
| chr16 | 90354753 | 5004 | 0.0001 | 0.0076 |
| chr17 | 81195210 | 5169 | 0.0001 | 0.008 |
| chr18 | 78077248 | 6690 | 0.0001 | 0.0093 |
| chr19 | 59128983 | 4544 | 0.0001 | 0.0087 |
| chr20 | 63025520 | 8844 | 0.0001 | 0.0121 |
| chr21 | 48129895 | 4640 | 0.0001 | 0.01 |
| chr22 | 51304566 | 2067 | 0 | 0.0063 |
| chrMT | 16571 | 168 | 0.0101 | 0.1002 |
| chrX | 155270560 | 8600 | 0.0001 | 0.0075 |
| chrY | 59373566 | 509 | 0 | 0.0029 |

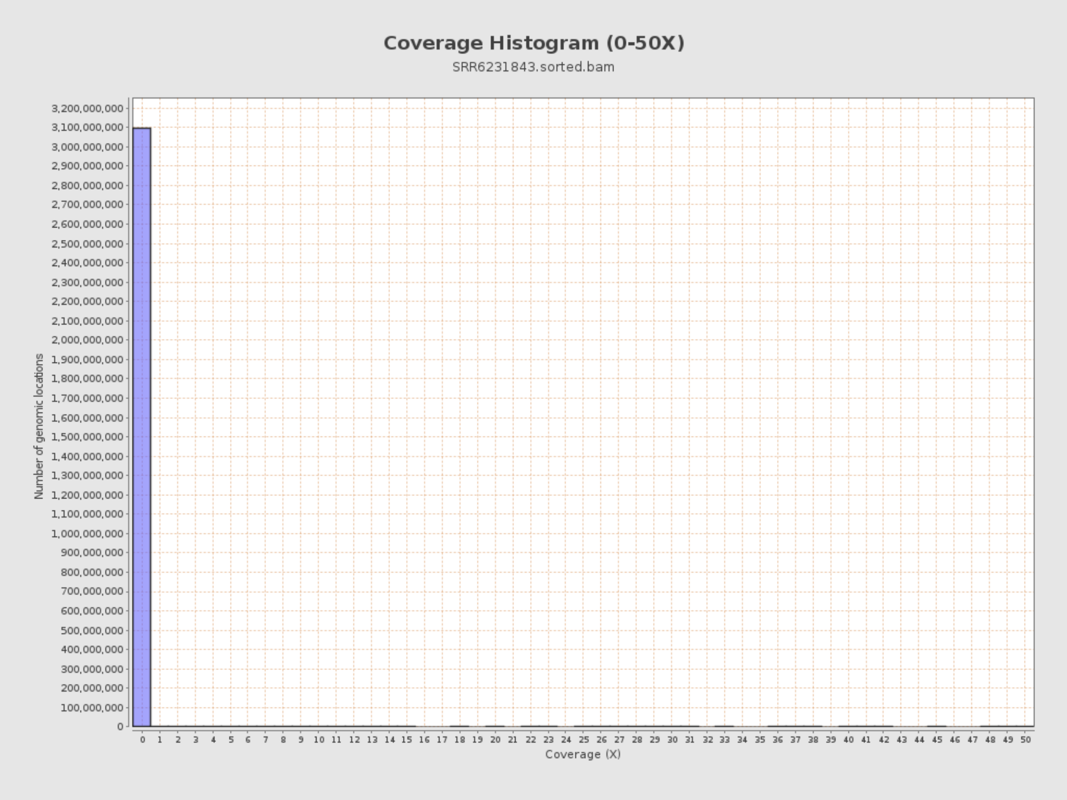
# 3. Results : Coverage across reference



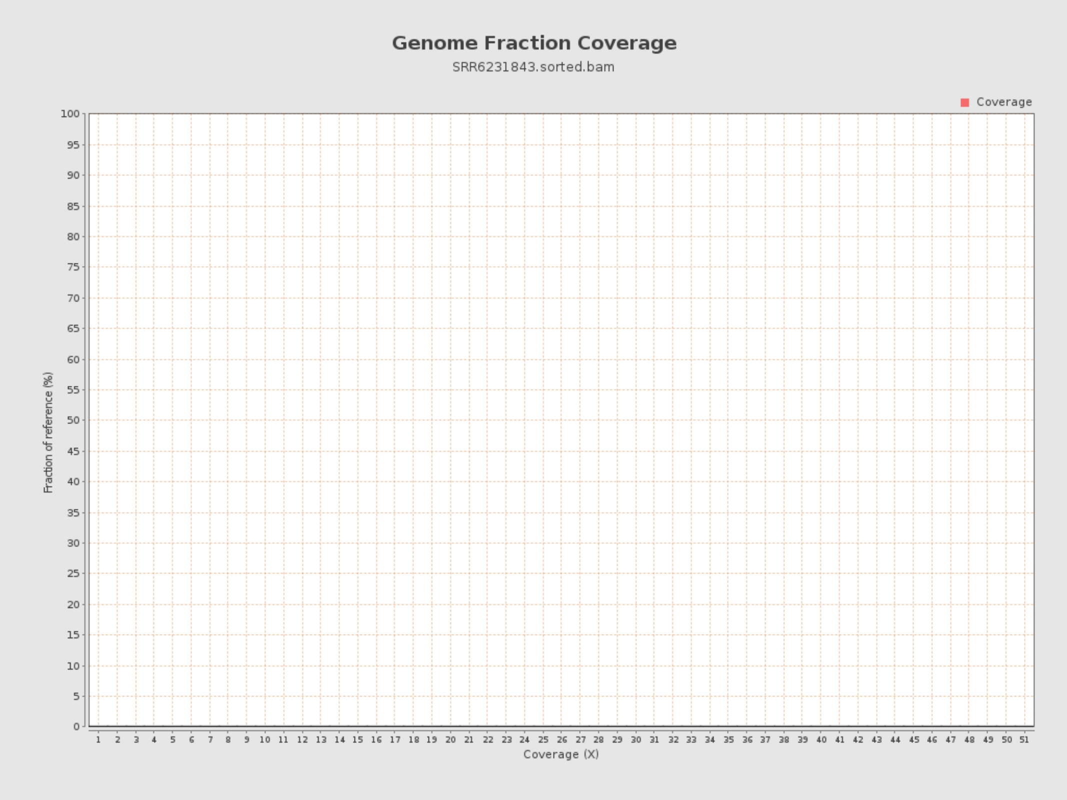
# 4. Results : Coverage Histogram



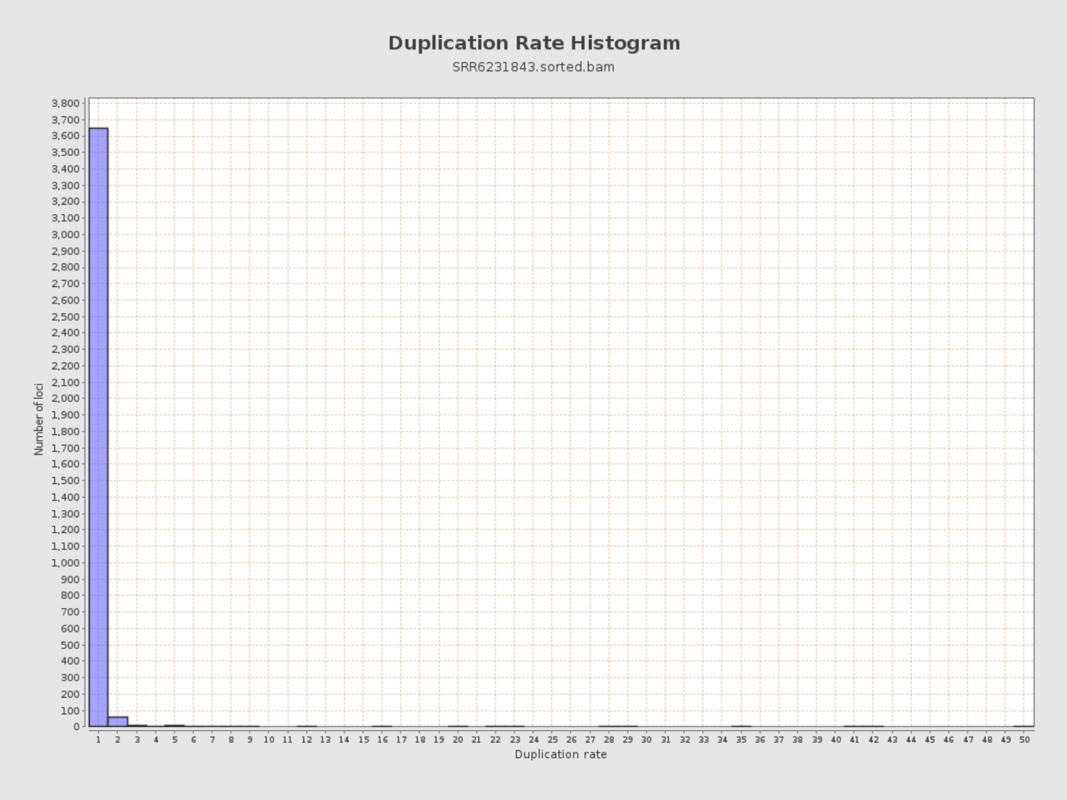
# 5. Results : Coverage Histogram (0-50X)



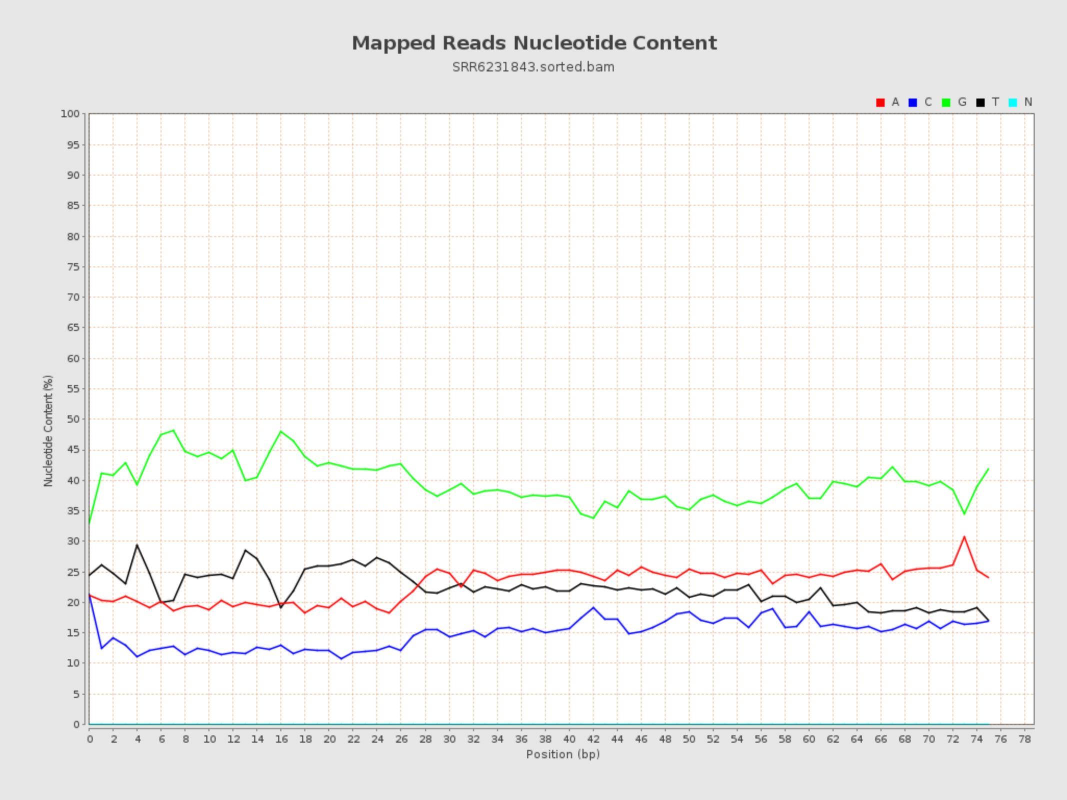
# 6. Results : Genome Fraction Coverage



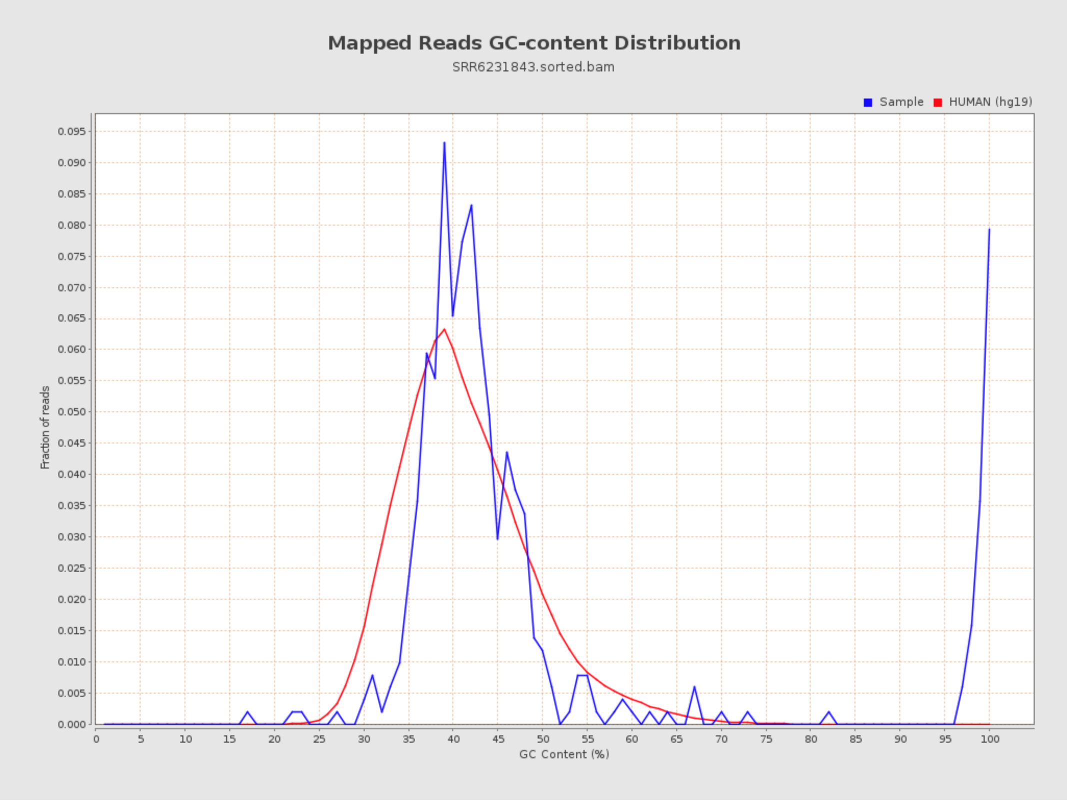
# 7. Results : Duplication Rate Histogram



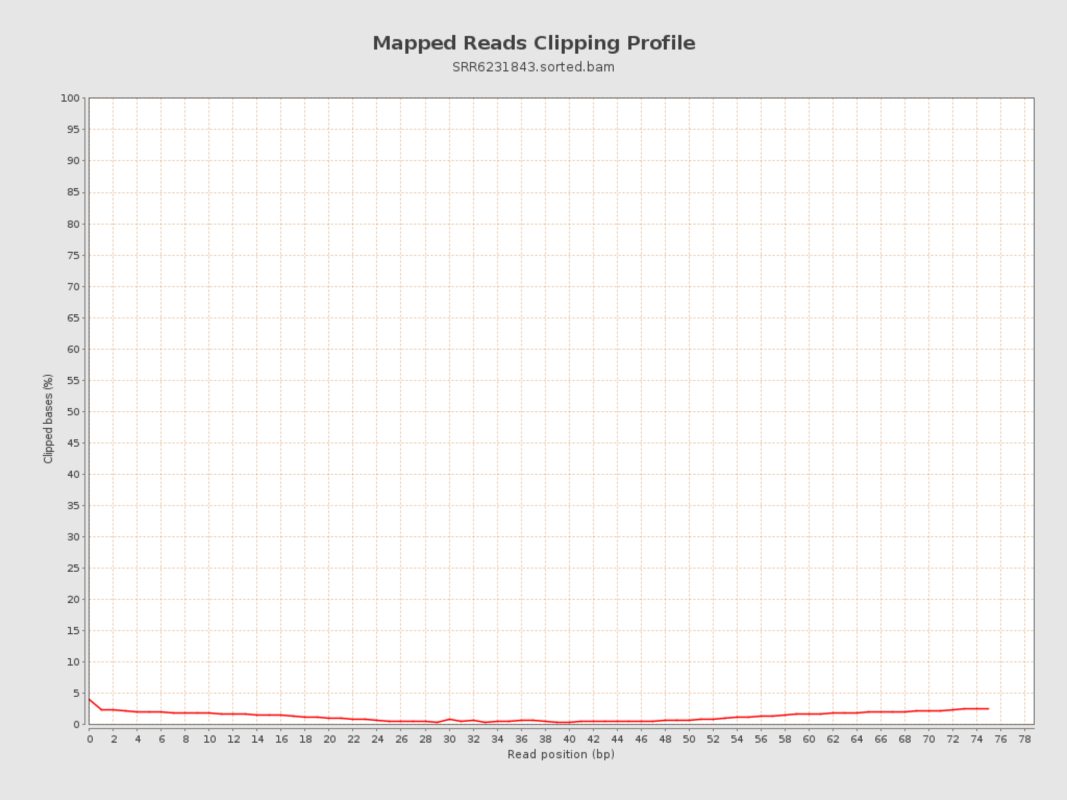
# 8. Results : Mapped Reads Nucleotide Content



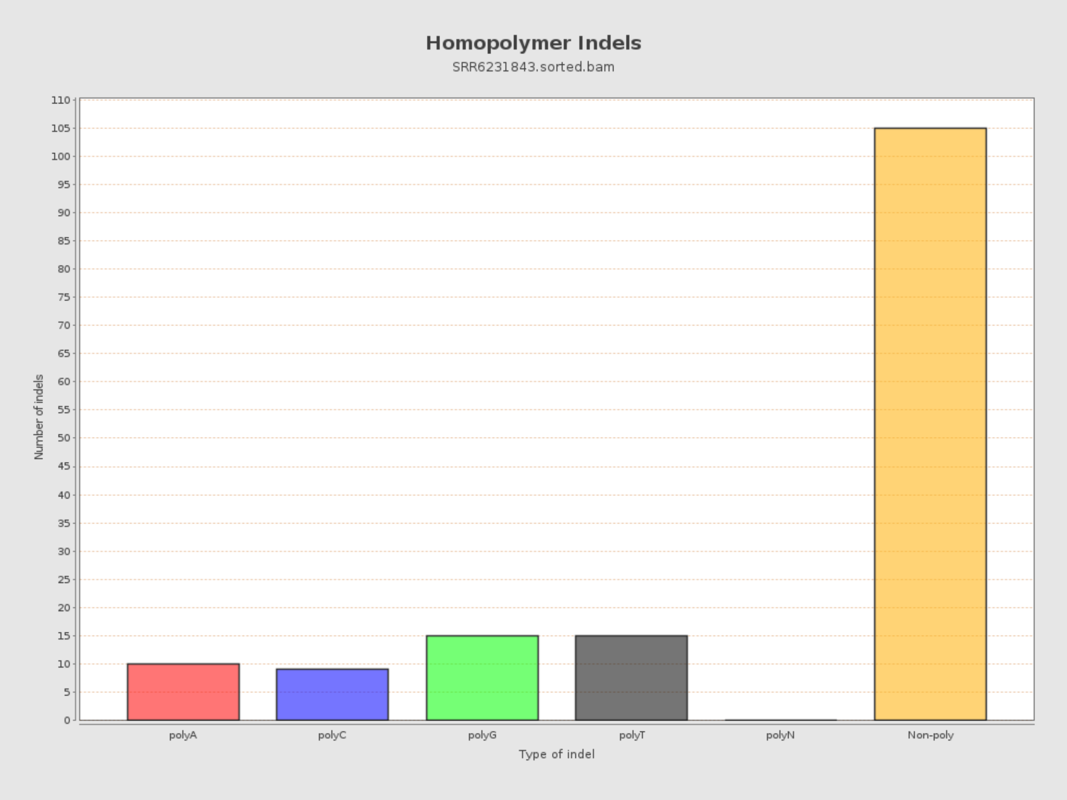
# 9. Results : Mapped Reads GC-content Distribution



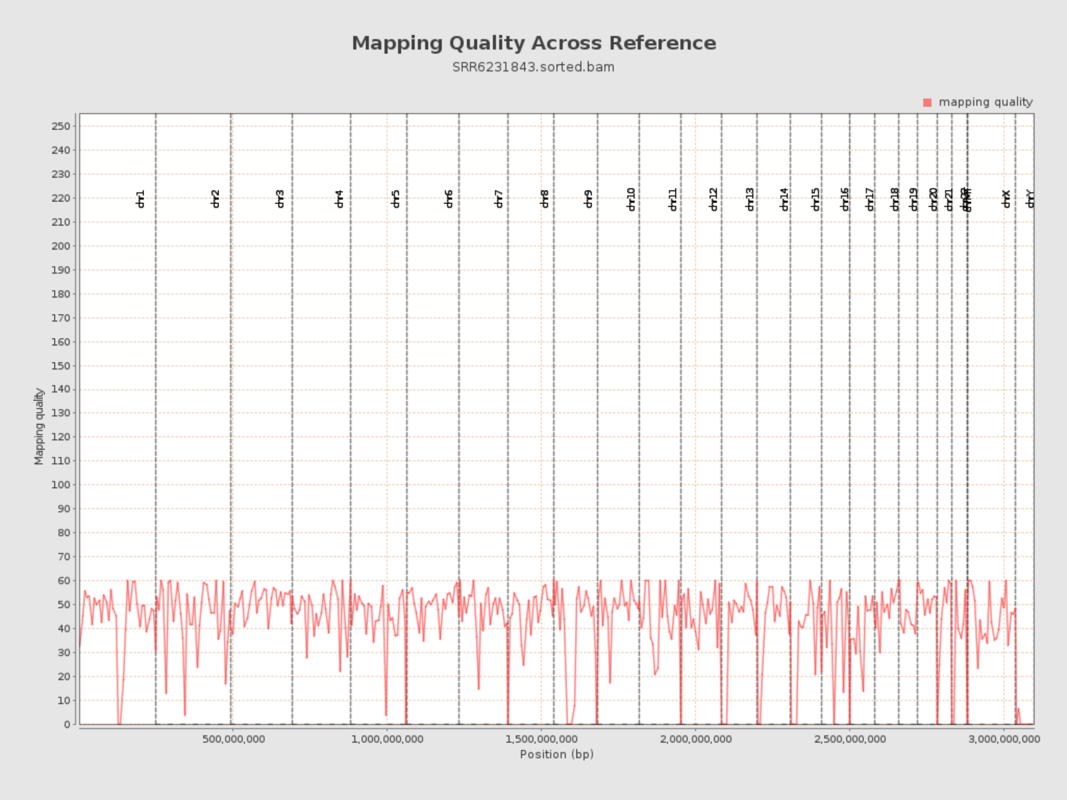
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram