# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/16 08:51:28*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231867.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_SRR6231867 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231867.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 16 08:51:28 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6231867.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 5,754,586 |
| Mapped reads | 5,132,548 / 89.19% |
| Unmapped reads | 622,038 / 10.81% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 46,498 / 0.81% |
| Read min/max/mean length | 30 / 76 / 76.28 |
| Duplicated reads (estimated) | 314,815 / 5.47% |
| Duplication rate | 4.13% |
| Clipped reads | 2,465,414 / 42.84% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 99,450,675 / 29.39% |
| Number/percentage of C's | 64,589,769 / 19.09% |
| Number/percentage of T's | 101,585,491 / 30.02% |
| Number/percentage of G's | 72,690,434 / 21.48% |
| Number/percentage of N's | 26,105 / 0.01% |
| GC Percentage | 40.57% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1093 |
| | |

| | |
|---|---|
| Standard Deviation | 3.89 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.75 |

## 2.5. Mismatches and indels

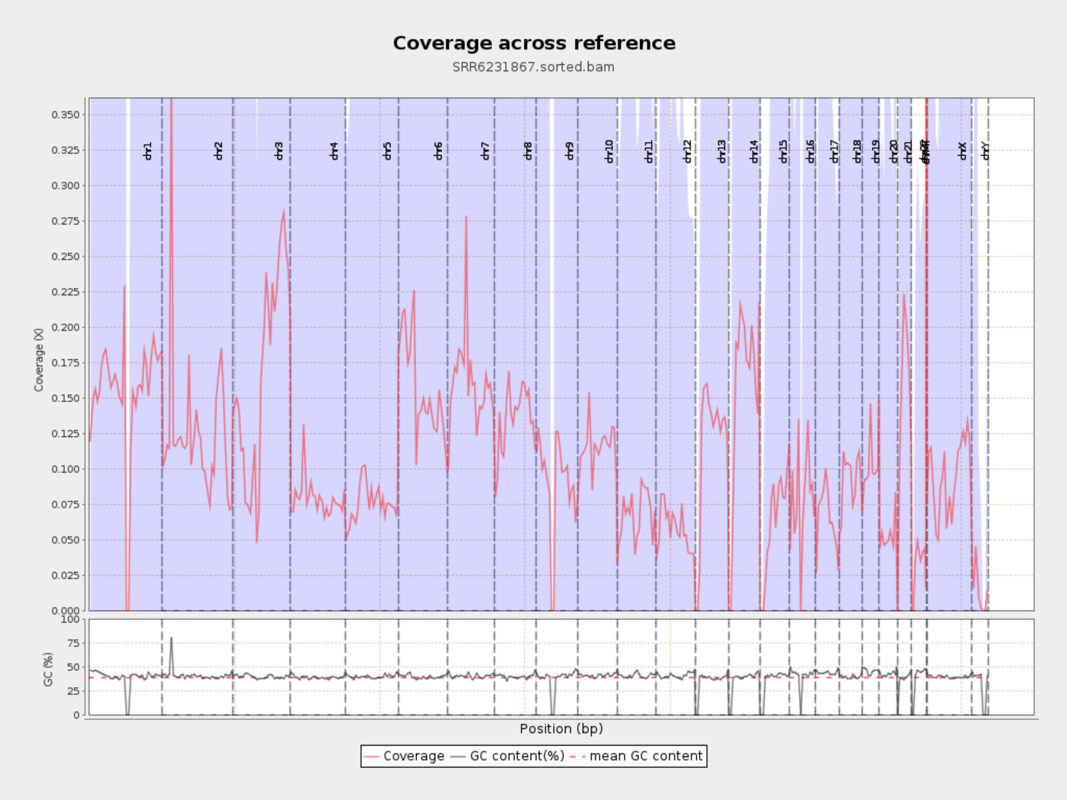
| | |
|---|---|
| General error rate | 0.63% |
| Mismatches | 2,080,505 |
| Insertions | 23,615 |
| Mapped reads with at least one insertion | 0.46% |
| Deletions | 85,730 |
| Mapped reads with at least one deletion | 1.65% |
| Homopolymer indels | 45.67% |

## 2.6. Chromosome stats

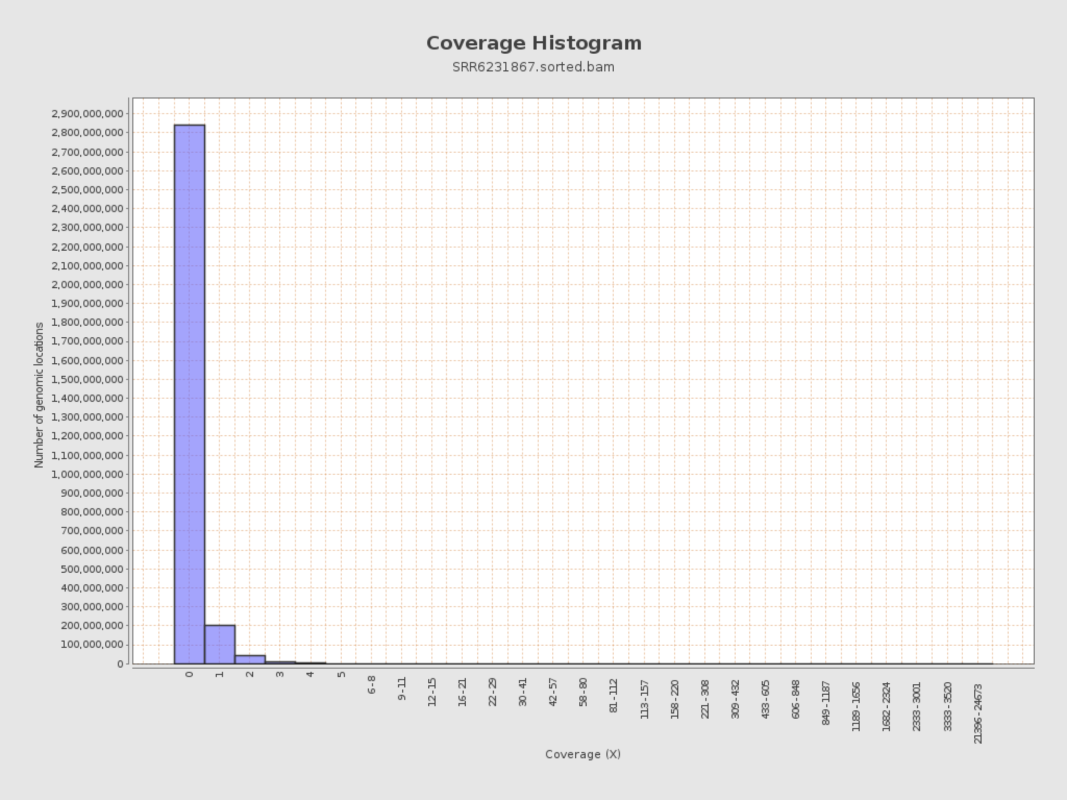
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 38351581 | 0.1539 | 2.293 |
| chr2 | 243199373 | 30521192 | 0.1255 | 13.4145 |
| chr3 | 198022430 | 33217395 | 0.1677 | 0.512 |
| chr4 | 191154276 | 15068057 | 0.0788 | 0.3898 |
| chr5 | 180915260 | 13638441 | 0.0754 | 0.3524 |
| chr6 | 171115067 | 26898587 | 0.1572 | 0.7203 |
| chr7 | 159138663 | 25950104 | 0.1631 | 1.9059 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 19776509 | 0.1351 | 1.4745 |
| chr9 | 141213431 | 12647328 | 0.0896 | 0.667 |
| chr10 | 135534747 | 15680628 | 0.1157 | 0.7518 |
| chr11 | 135006516 | 9146952 | 0.0678 | 0.5854 |
| chr12 | 133851895 | 7682924 | 0.0574 | 0.3139 |
| chr13 | 115169878 | 13353289 | 0.1159 | 0.4192 |
| chr14 | 107349540 | 16422997 | 0.153 | 0.5641 |
| chr15 | 102531392 | 6348938 | 0.0619 | 0.3093 |
| chr16 | 90354753 | 7155061 | 0.0792 | 0.4888 |
| chr17 | 81195210 | 5273416 | 0.0649 | 0.3735 |
| chr18 | 78077248 | 7252239 | 0.0929 | 1.6016 |
| chr19 | 59128983 | 6082495 | 0.1029 | 1.389 |
| chr20 | 63025520 | 3345543 | 0.0531 | 0.3445 |
| chr21 | 48129895 | 7286735 | 0.1514 | 0.5151 |
| chr22 | 51304566 | 1617962 | 0.0315 | 0.212 |
| chrMT | 16571 | 253701 | 15.3099 | 8.4131 |
| chrX | 155270560 | 14716465 | 0.0948 | 0.4681 |
| chrY | 59373566 | 799939 | 0.0135 | 0.258 |

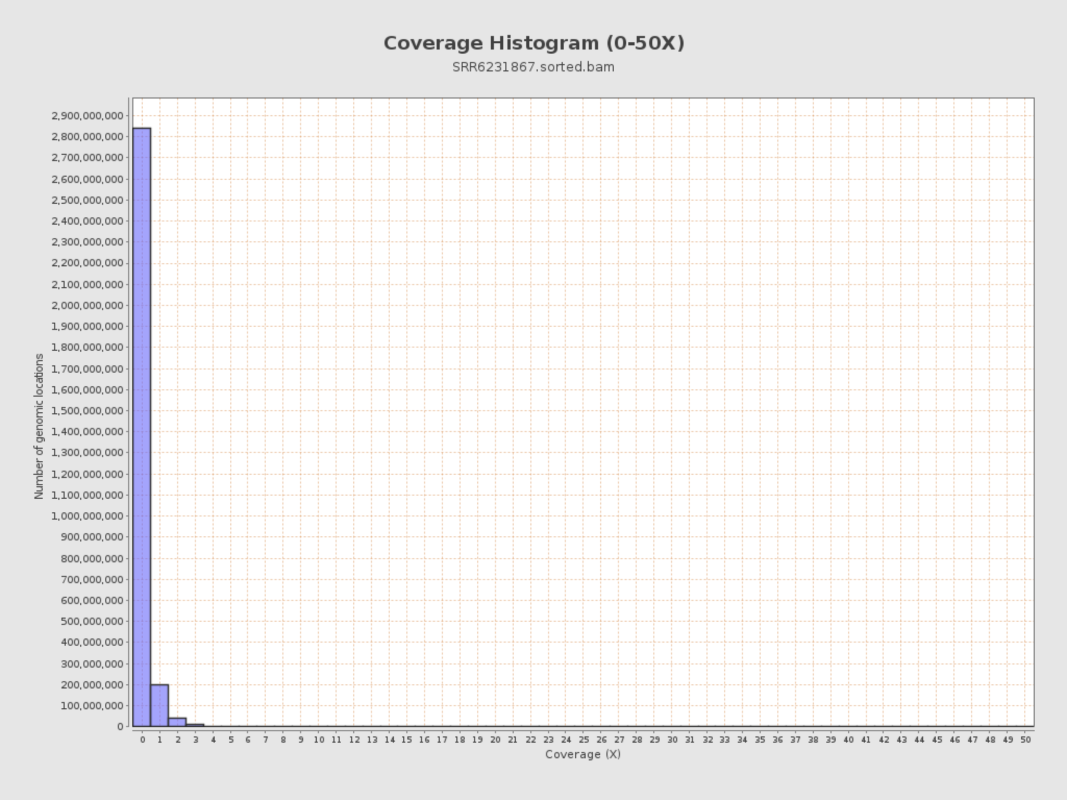
# 3. Results : Coverage across reference



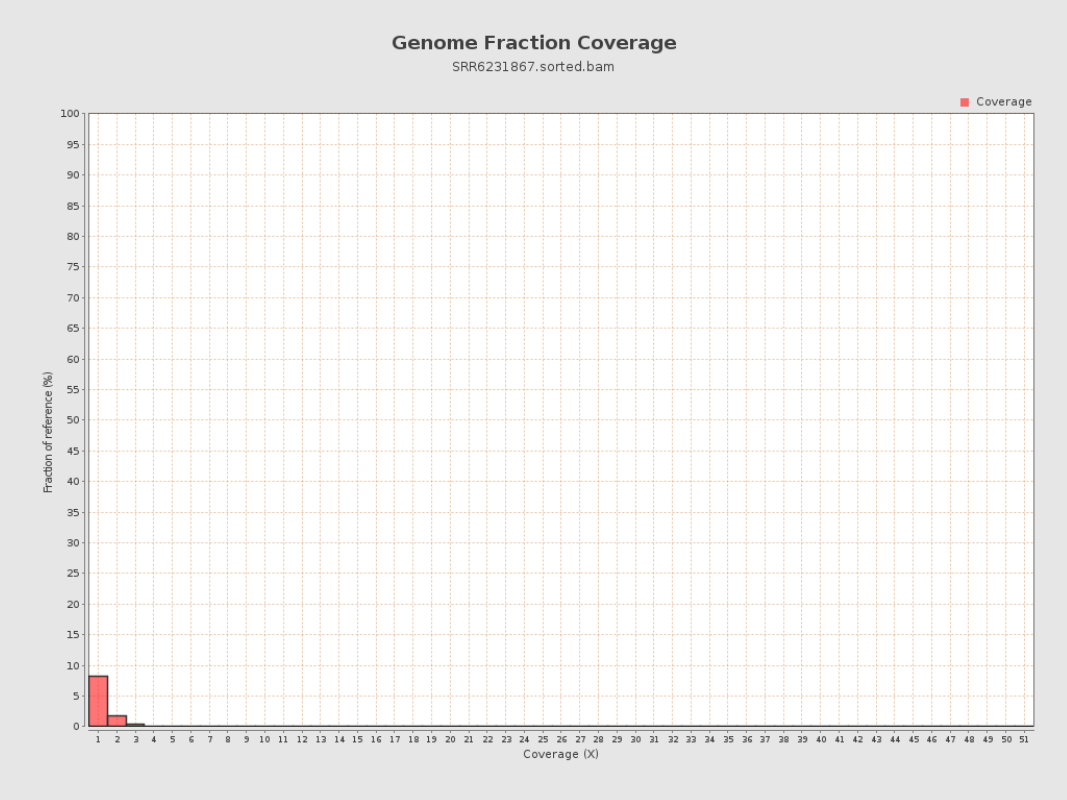
# 4. Results : Coverage Histogram



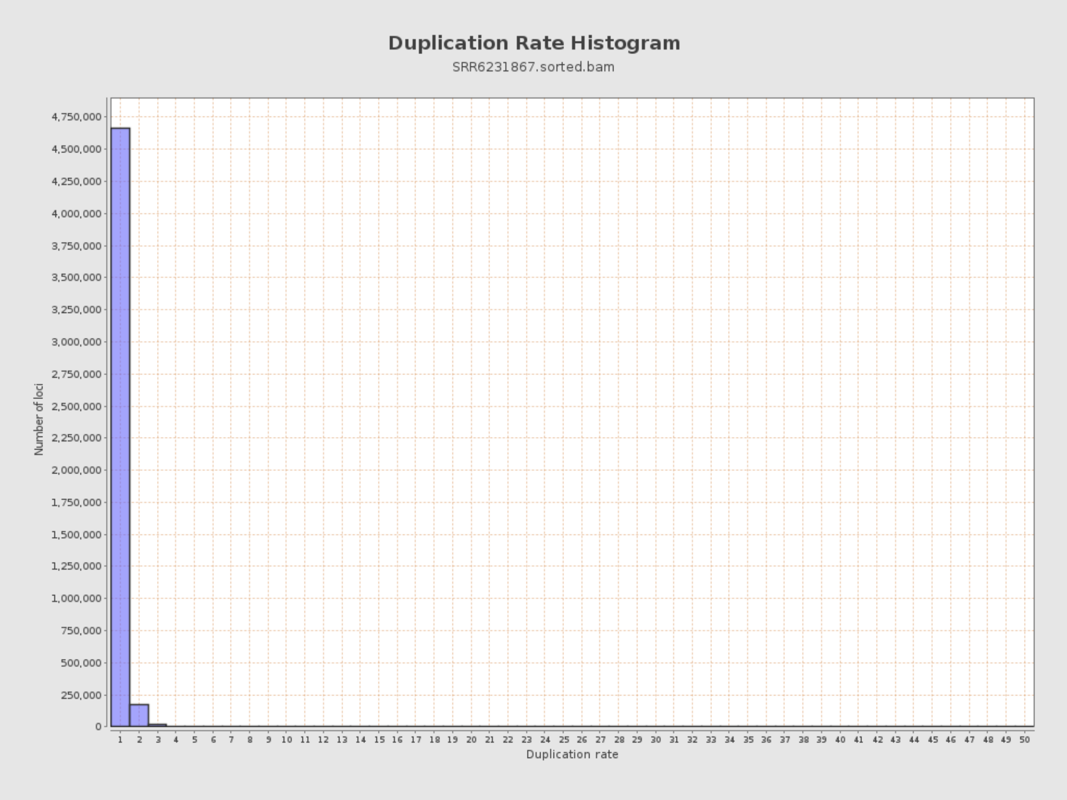
# 5. Results : Coverage Histogram (0-50X)



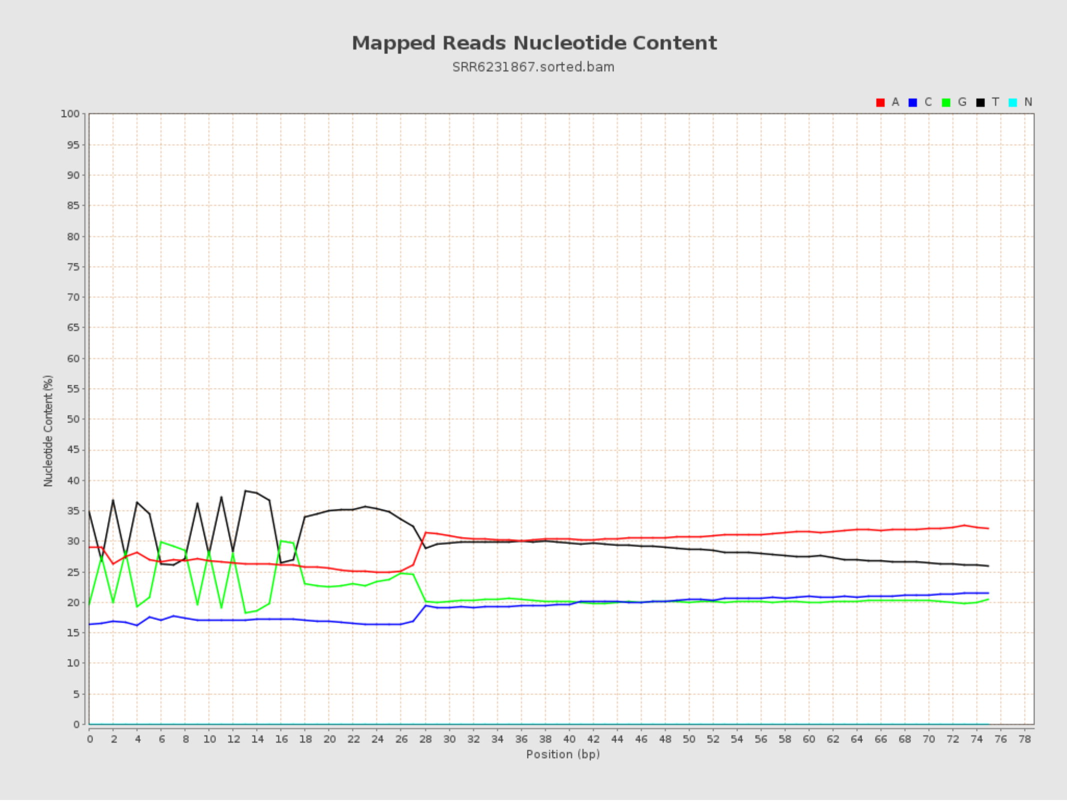
# 6. Results : Genome Fraction Coverage



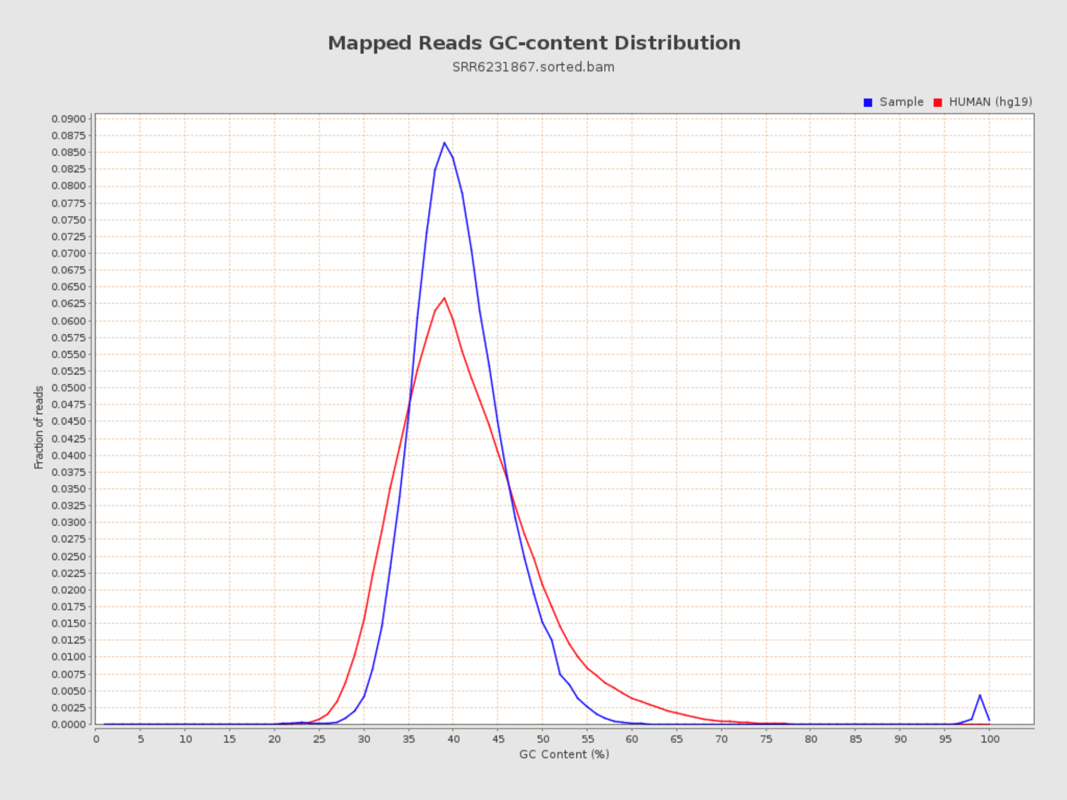
# 7. Results : Duplication Rate Histogram



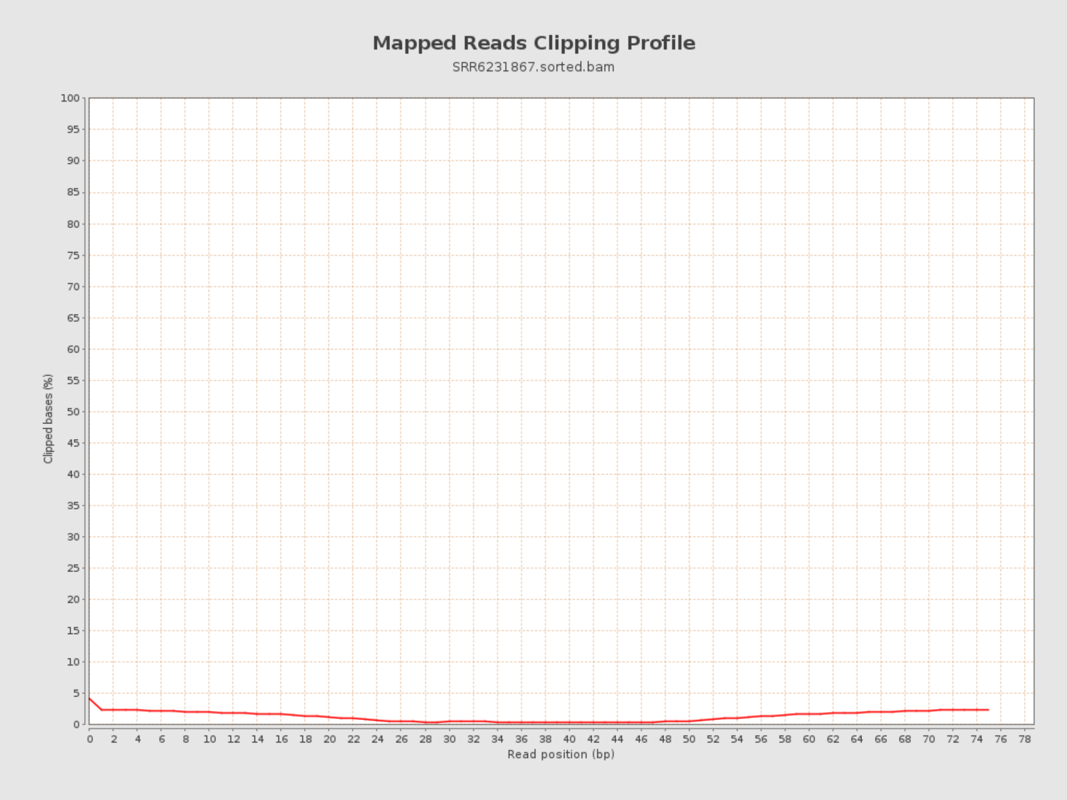
# 8. Results : Mapped Reads Nucleotide Content



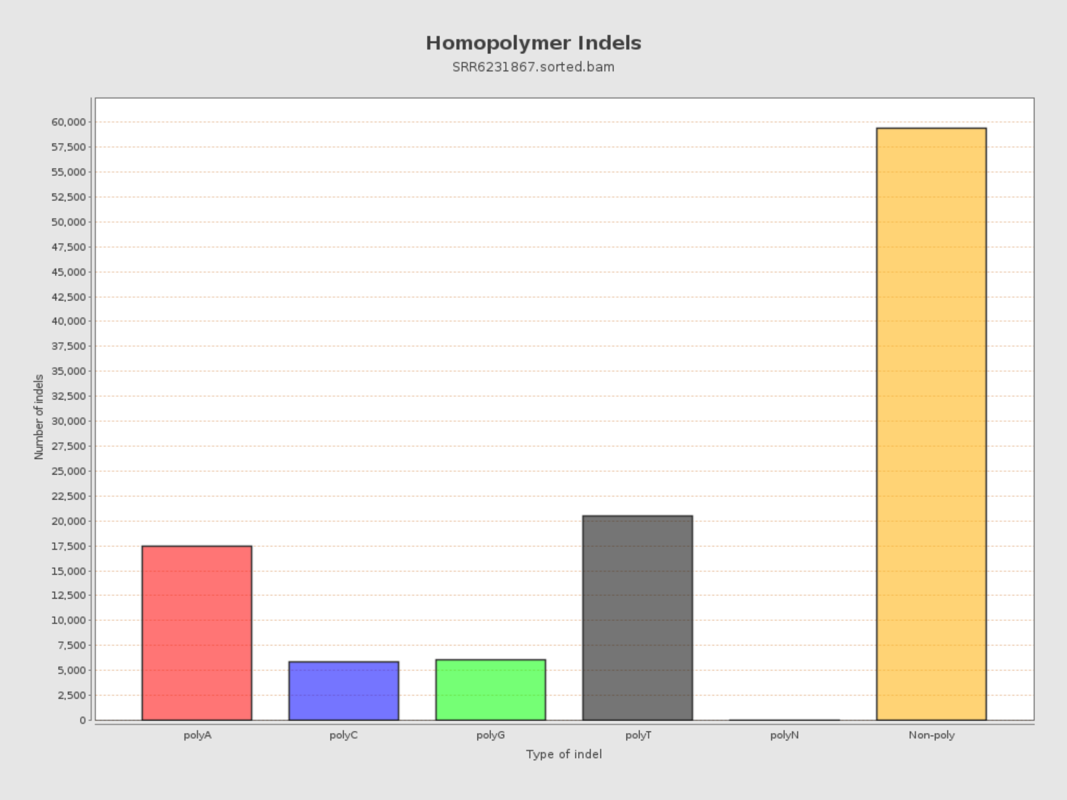
# 9. Results : Mapped Reads GC-content Distribution



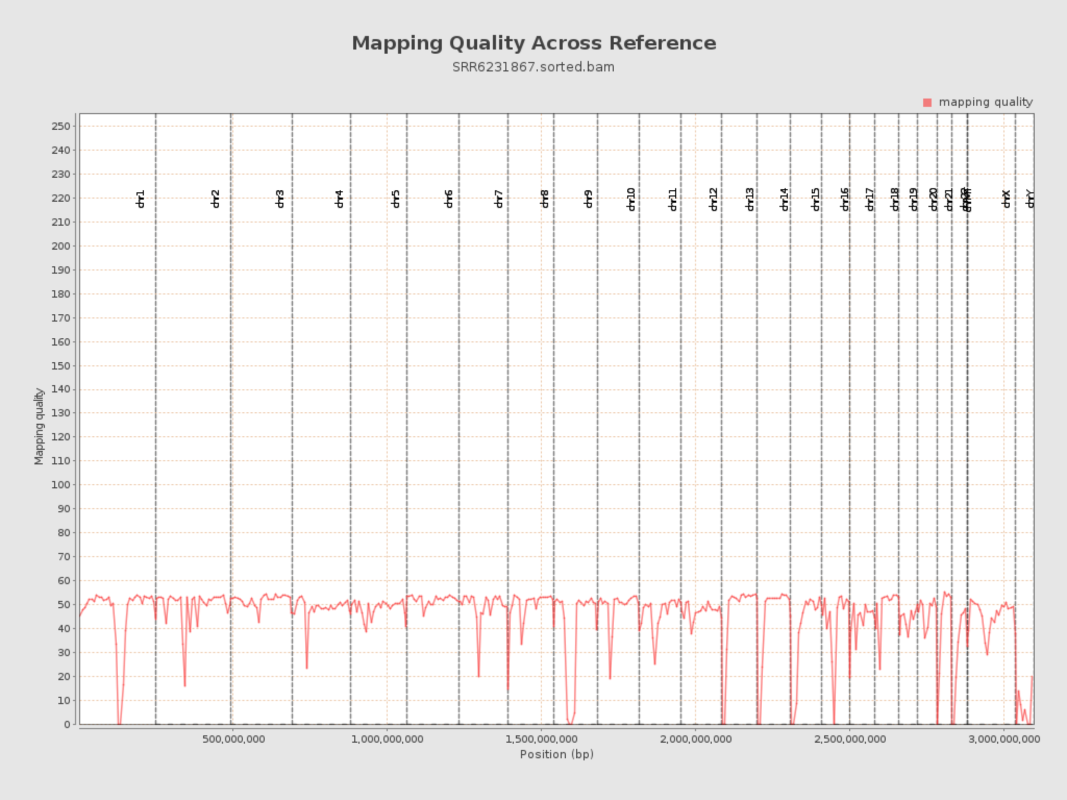
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram