# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/16 08:42:06*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231865.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_SRR6231865 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231865.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 16 08:42:06 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6231865.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,261,358 |
| Mapped reads | 944,359 / 74.87% |
| Unmapped reads | 316,999 / 25.13% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 5,245 / 0.42% |
| Read min/max/mean length | 30 / 76 / 76.14 |
| Duplicated reads (estimated) | 44,136 / 3.5% |
| Duplication rate | 4.01% |
| Clipped reads | 499,234 / 39.58% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 16,719,333 / 27.45% |
| Number/percentage of C's | 10,457,281 / 17.17% |
| Number/percentage of T's | 20,163,463 / 33.1% |
| Number/percentage of G's | 13,565,840 / 22.27% |
| Number/percentage of N's | 2,690 / 0% |
| GC Percentage | 39.44% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0197 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2118 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.7 |

## 2.5. Mismatches and indels

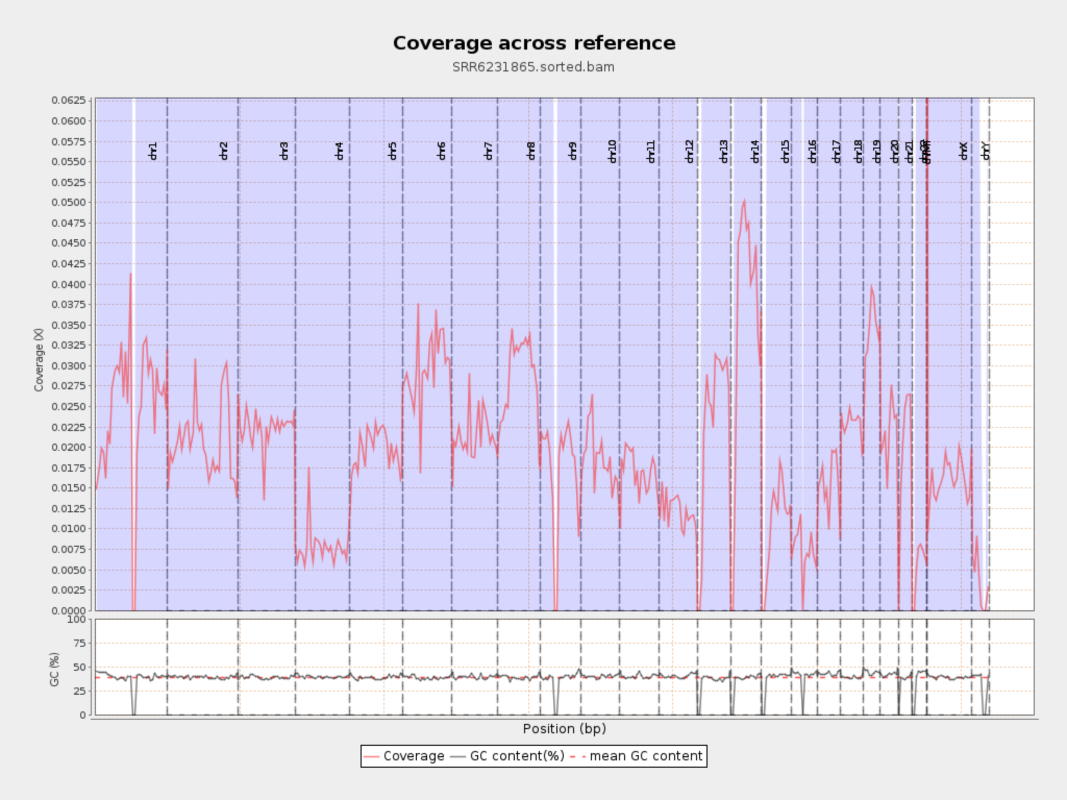
| | |
|---|---|
| General error rate | 0.81% |
| Mismatches | 486,585 |
| Insertions | 4,956 |
| Mapped reads with at least one insertion | 0.52% |
| Deletions | 22,888 |
| Mapped reads with at least one deletion | 2.39% |
| Homopolymer indels | 45.91% |

## 2.6. Chromosome stats

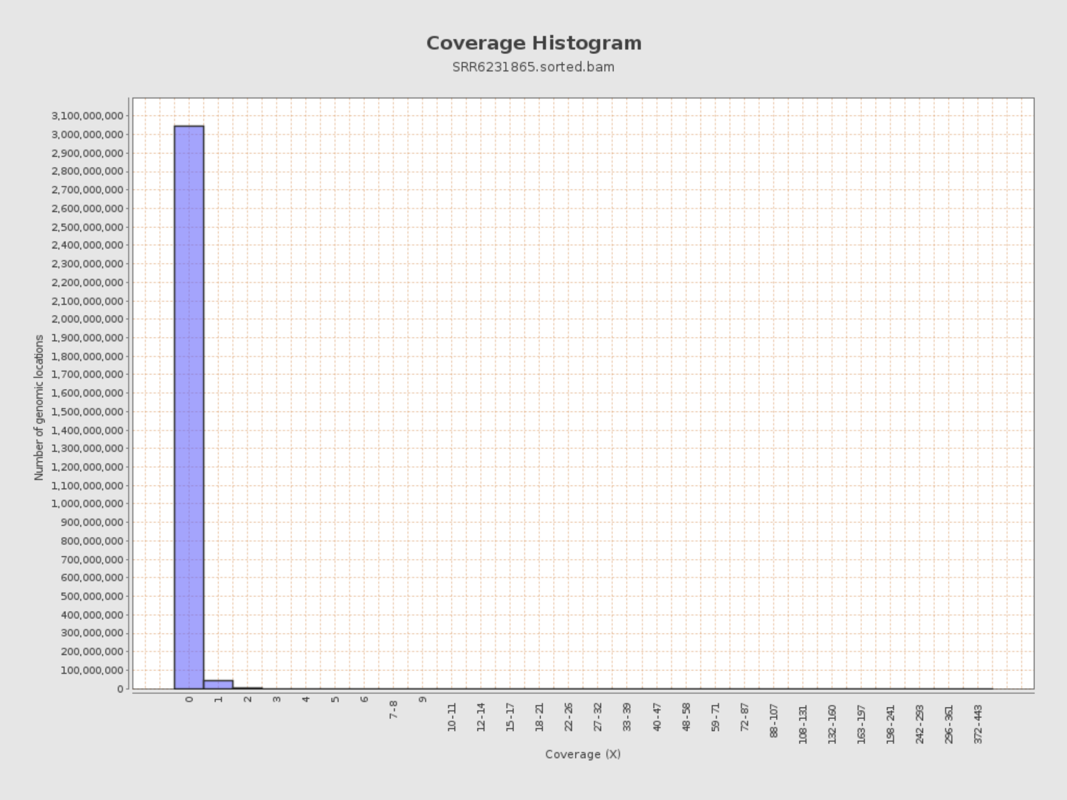
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 6122796 | 0.0246 | 0.387 |
| chr2 | 243199373 | 5047680 | 0.0208 | 0.2239 |
| chr3 | 198022430 | 4418489 | 0.0223 | 0.1703 |
| chr4 | 191154276 | 1492237 | 0.0078 | 0.1081 |
| chr5 | 180915260 | 3590954 | 0.0198 | 0.1604 |
| chr6 | 171115067 | 5092444 | 0.0298 | 0.2204 |
| chr7 | 159138663 | 3430450 | 0.0216 | 0.2308 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 4243339 | 0.029 | 0.3444 |
| chr9 | 141213431 | 2413806 | 0.0171 | 0.1656 |
| chr10 | 135534747 | 2528692 | 0.0187 | 0.1775 |
| chr11 | 135006516 | 2311294 | 0.0171 | 0.1696 |
| chr12 | 133851895 | 1625970 | 0.0121 | 0.1266 |
| chr13 | 115169878 | 2646190 | 0.023 | 0.174 |
| chr14 | 107349540 | 3835954 | 0.0357 | 0.2173 |
| chr15 | 102531392 | 1081141 | 0.0105 | 0.1189 |
| chr16 | 90354753 | 649769 | 0.0072 | 0.1048 |
| chr17 | 81195210 | 1281432 | 0.0158 | 0.1464 |
| chr18 | 78077248 | 1805395 | 0.0231 | 0.2315 |
| chr19 | 59128983 | 2023699 | 0.0342 | 0.2622 |
| chr20 | 63025520 | 1352674 | 0.0215 | 0.1682 |
| chr21 | 48129895 | 974789 | 0.0203 | 0.1641 |
| chr22 | 51304566 | 280607 | 0.0055 | 0.0836 |
| chrMT | 16571 | 8544 | 0.5156 | 0.7728 |
| chrX | 155270560 | 2486791 | 0.016 | 0.1484 |
| chrY | 59373566 | 203389 | 0.0034 | 0.0721 |

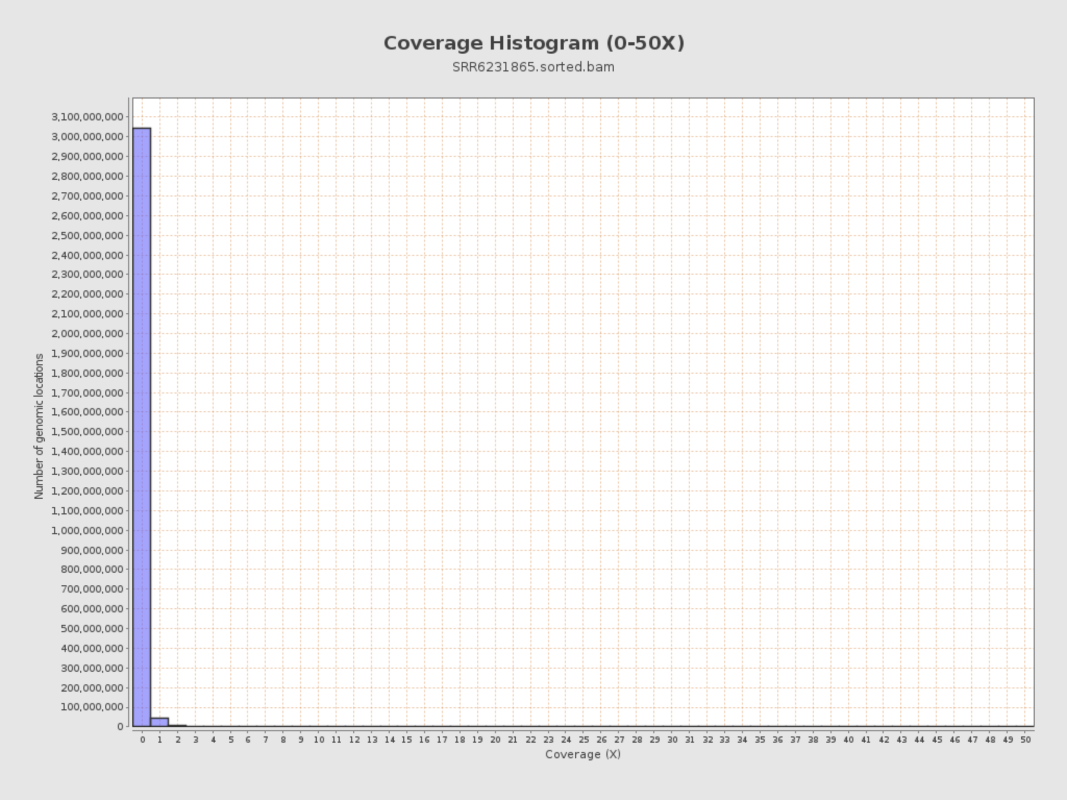
# 3. Results : Coverage across reference



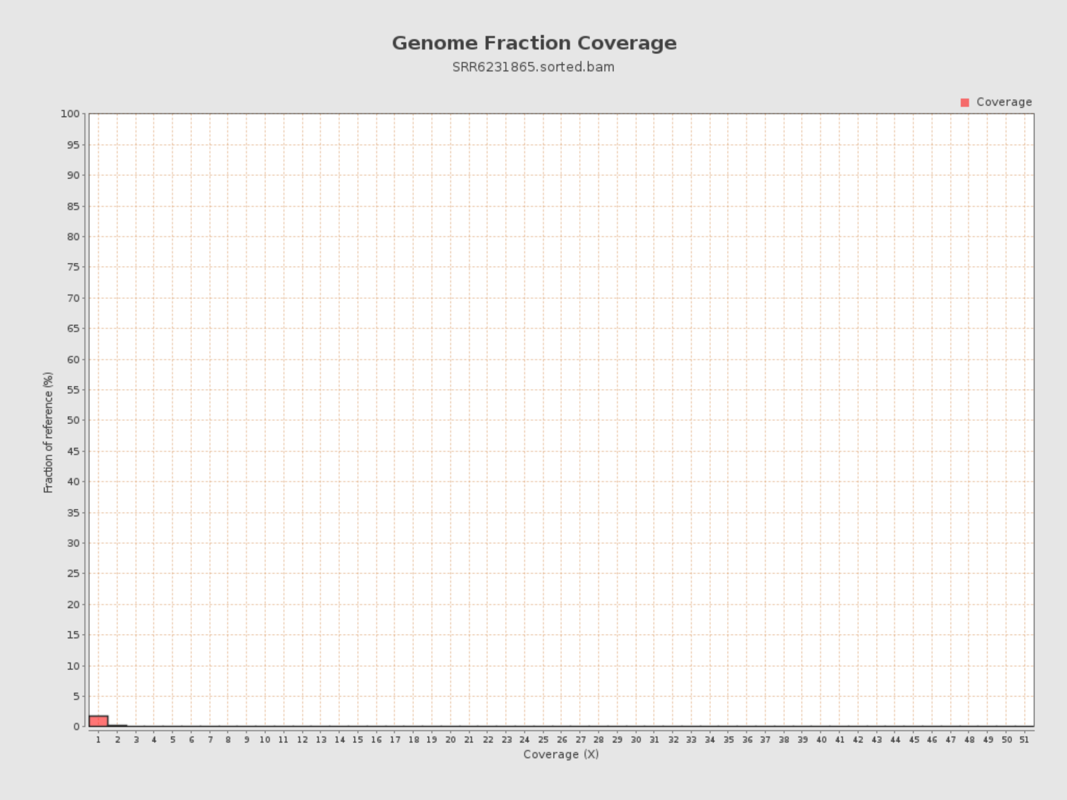
# 4. Results : Coverage Histogram



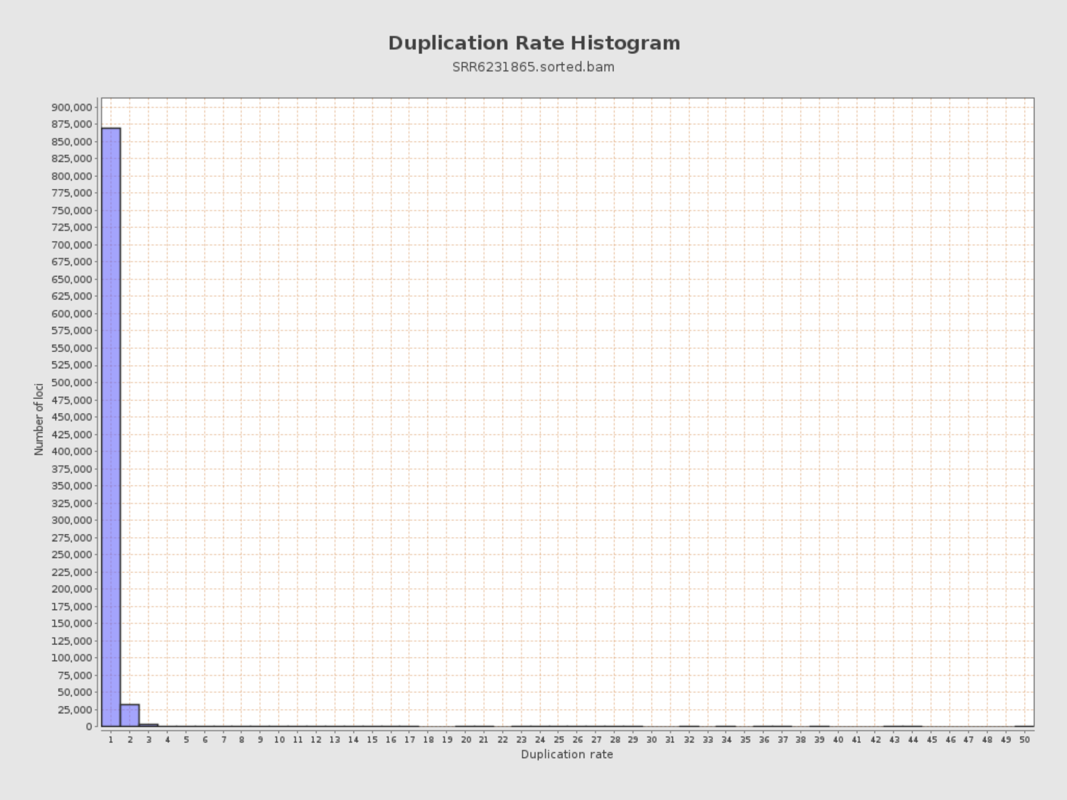
# 5. Results : Coverage Histogram (0-50X)



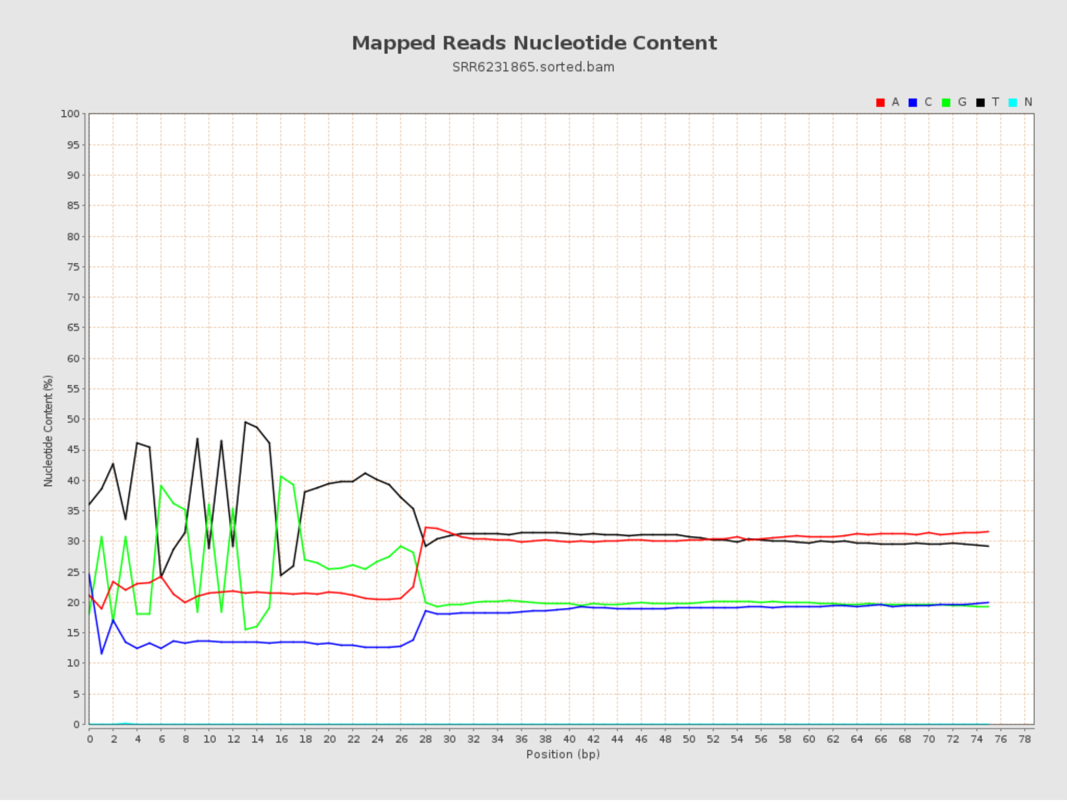
# 6. Results : Genome Fraction Coverage



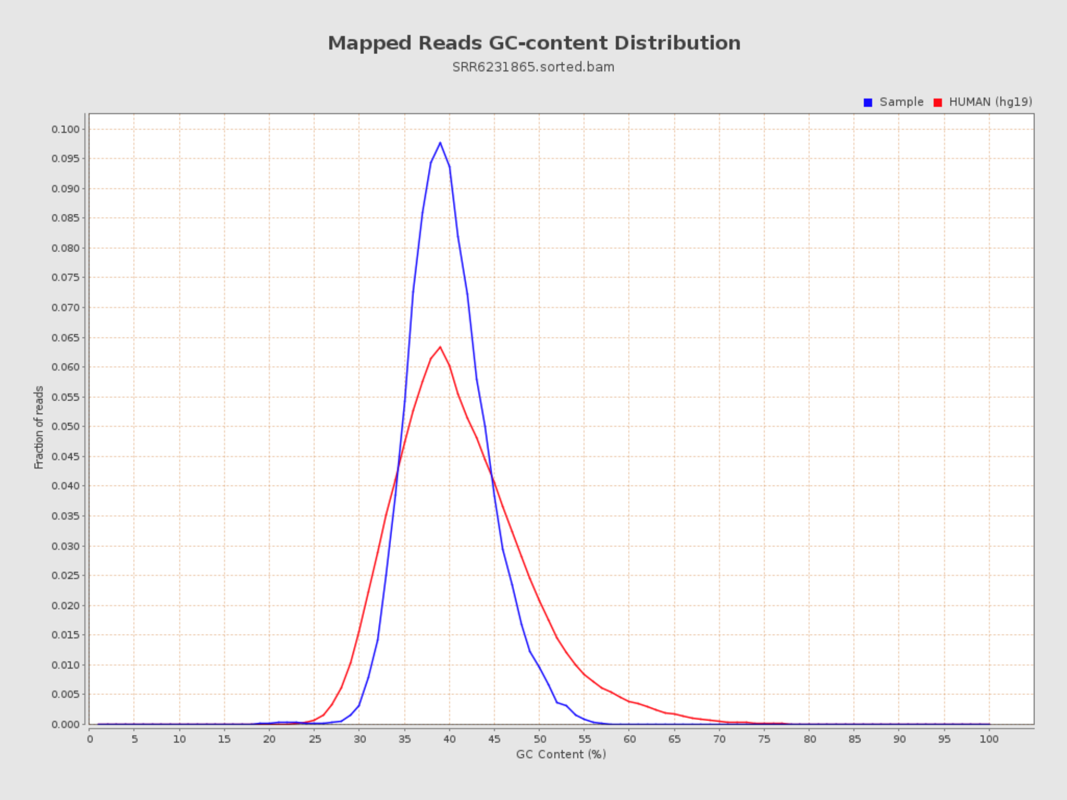
# 7. Results : Duplication Rate Histogram



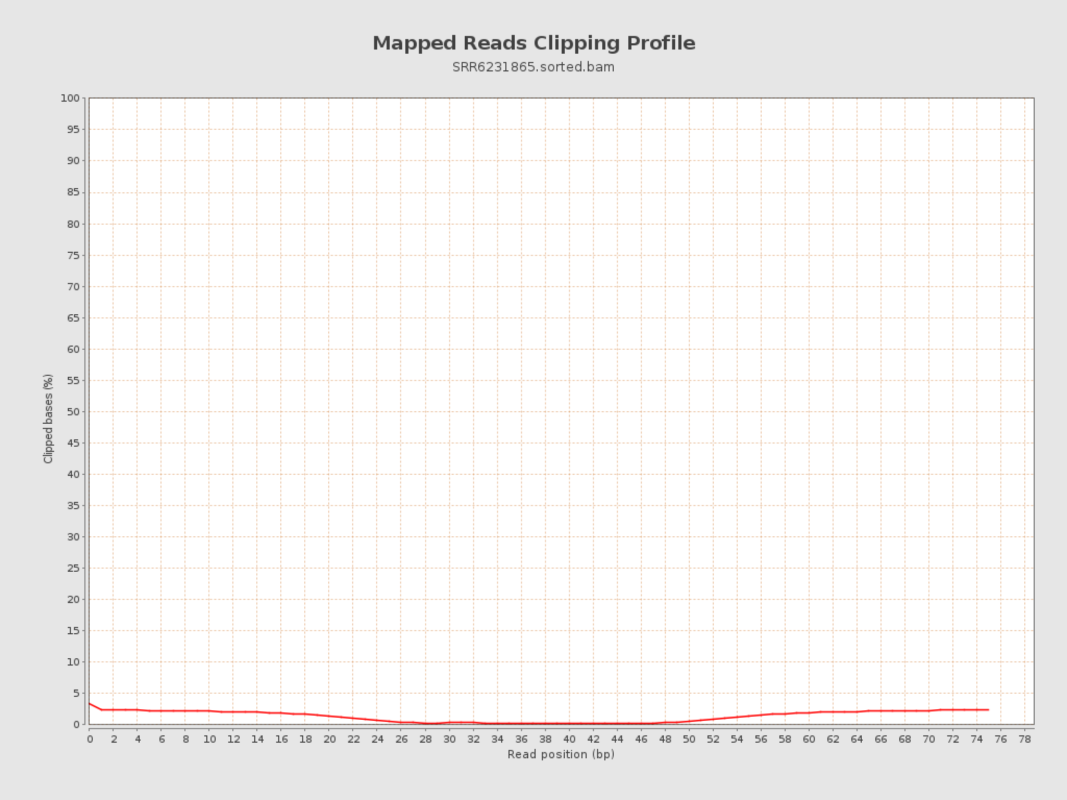
# 8. Results : Mapped Reads Nucleotide Content



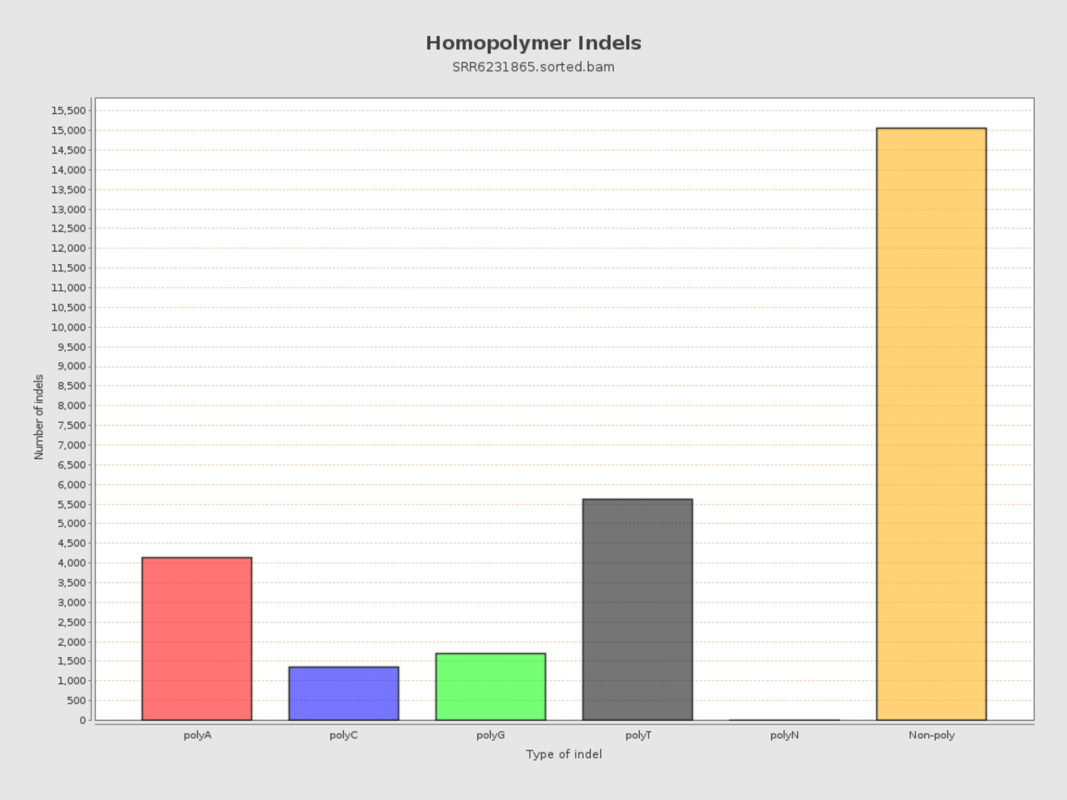
# 9. Results : Mapped Reads GC-content Distribution



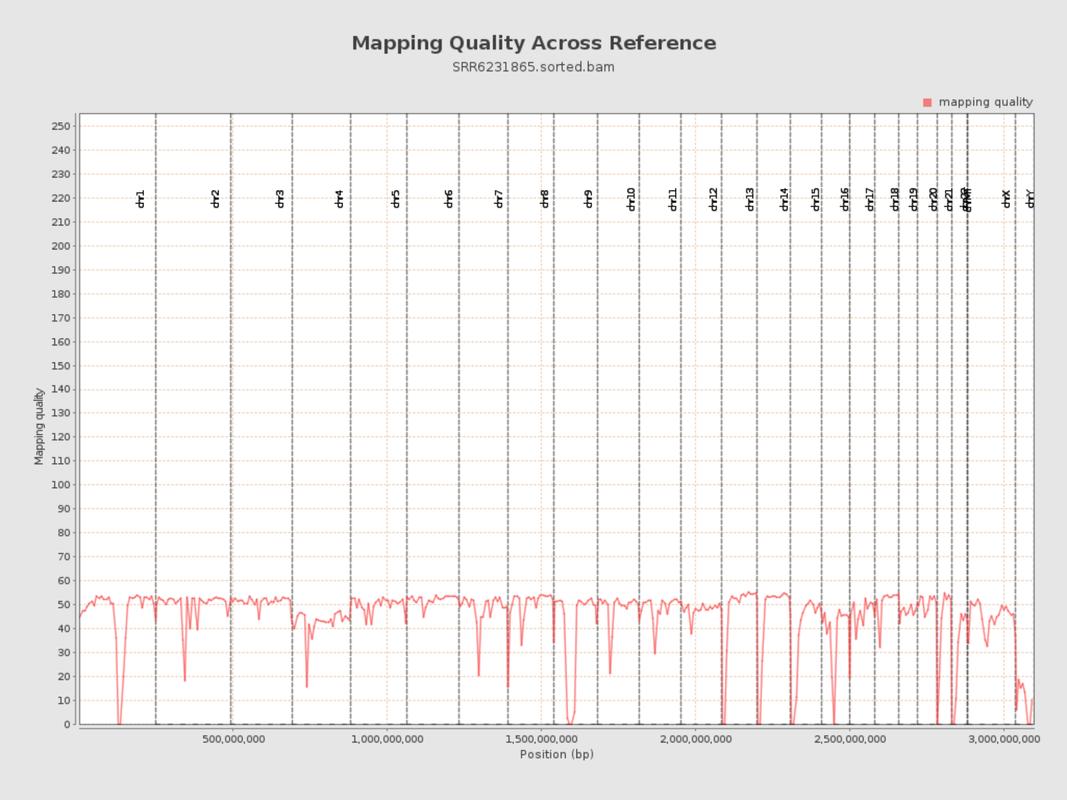
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram