# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/15 22:47:32*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231730.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_SRR6231730 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231730.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Sep 15 22:47:31 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6231730.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,096,206 |
| Mapped reads | 3,552,061 / 86.72% |
| Unmapped reads | 544,145 / 13.28% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 35,706 / 0.87% |
| Read min/max/mean length | 30 / 76 / 76.31 |
| Duplicated reads (estimated) | 839,608 / 20.5% |
| Duplication rate | 9.92% |
| Clipped reads | 1,249,836 / 30.51% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 59,948,947 / 24.52% |
| Number/percentage of C's | 41,037,343 / 16.78% |
| Number/percentage of T's | 64,646,410 / 26.44% |
| Number/percentage of G's | 78,837,810 / 32.24% |
| Number/percentage of N's | 53,086 / 0.02% |
| GC Percentage | 49.02% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.079 |
| | |

| | |
|---|---|
| Standard Deviation | 65.9568 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 42.96 |

## 2.5. Mismatches and indels

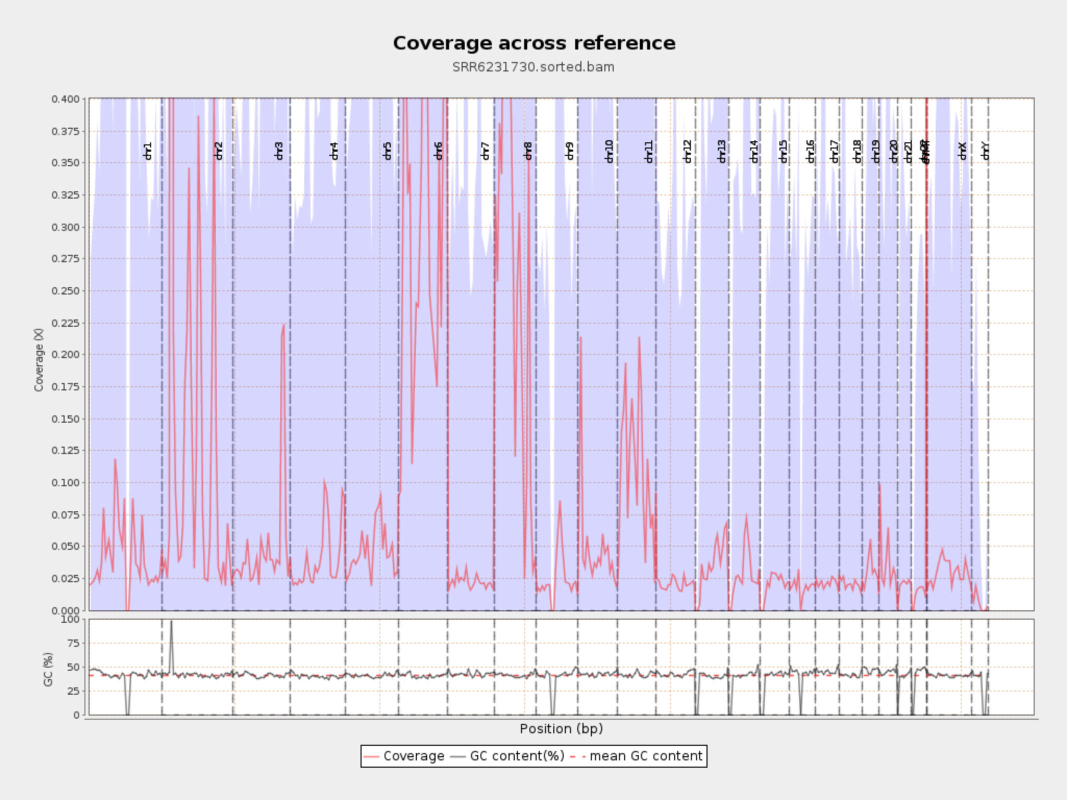
| | |
|---|---|
| General error rate | 0.57% |
| Mismatches | 1,364,096 |
| Insertions | 14,029 |
| Mapped reads with at least one insertion | 0.39% |
| Deletions | 45,511 |
| Mapped reads with at least one deletion | 1.27% |
| Homopolymer indels | 47.46% |

## 2.6. Chromosome stats

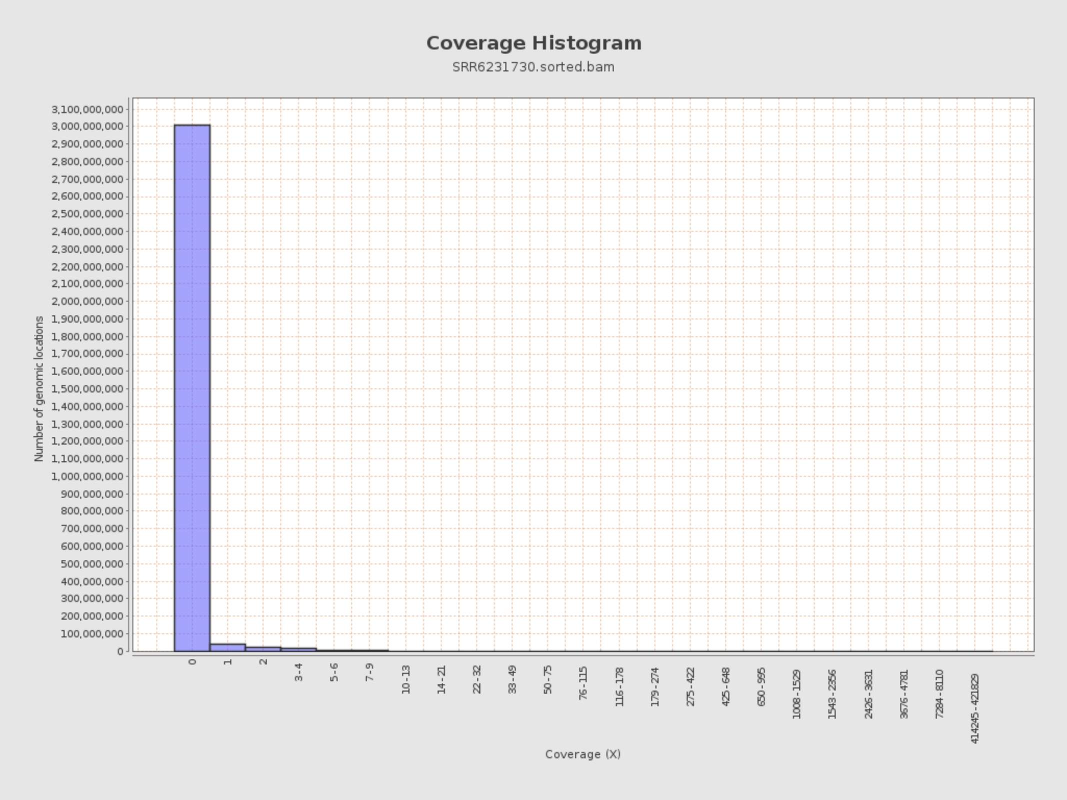
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 10404408 | 0.0417 | 0.9248 |
| chr2 | 243199373 | 61023884 | 0.2509 | 235.3068 |
| chr3 | 198022430 | 10177679 | 0.0514 | 0.4545 |
| chr4 | 191154276 | 7965526 | 0.0417 | 0.3959 |
| chr5 | 180915260 | 8390238 | 0.0464 | 0.4246 |
| chr6 | 171115067 | 51734660 | 0.3023 | 1.3263 |
| chr7 | 159138663 | 3549870 | 0.0223 | 0.3864 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 38308882 | 0.2617 | 1.3369 |
| chr9 | 141213431 | 3665095 | 0.026 | 0.3302 |
| chr10 | 135534747 | 6852811 | 0.0506 | 0.4881 |
| chr11 | 135006516 | 14670498 | 0.1087 | 1.4012 |
| chr12 | 133851895 | 2793232 | 0.0209 | 0.2932 |
| chr13 | 115169878 | 4099553 | 0.0356 | 0.3865 |
| chr14 | 107349540 | 2960784 | 0.0276 | 0.4404 |
| chr15 | 102531392 | 2050427 | 0.02 | 0.3032 |
| chr16 | 90354753 | 1647887 | 0.0182 | 0.2694 |
| chr17 | 81195210 | 1736733 | 0.0214 | 0.5729 |
| chr18 | 78077248 | 1628806 | 0.0209 | 0.3413 |
| chr19 | 59128983 | 1853170 | 0.0313 | 0.6305 |
| chr20 | 63025520 | 2391528 | 0.0379 | 0.3996 |
| chr21 | 48129895 | 942184 | 0.0196 | 0.2889 |
| chr22 | 51304566 | 647468 | 0.0126 | 0.2118 |
| chrMT | 16571 | 32529 | 1.963 | 3.1924 |
| chrX | 155270560 | 4719666 | 0.0304 | 0.4212 |
| chrY | 59373566 | 348937 | 0.0059 | 0.1332 |

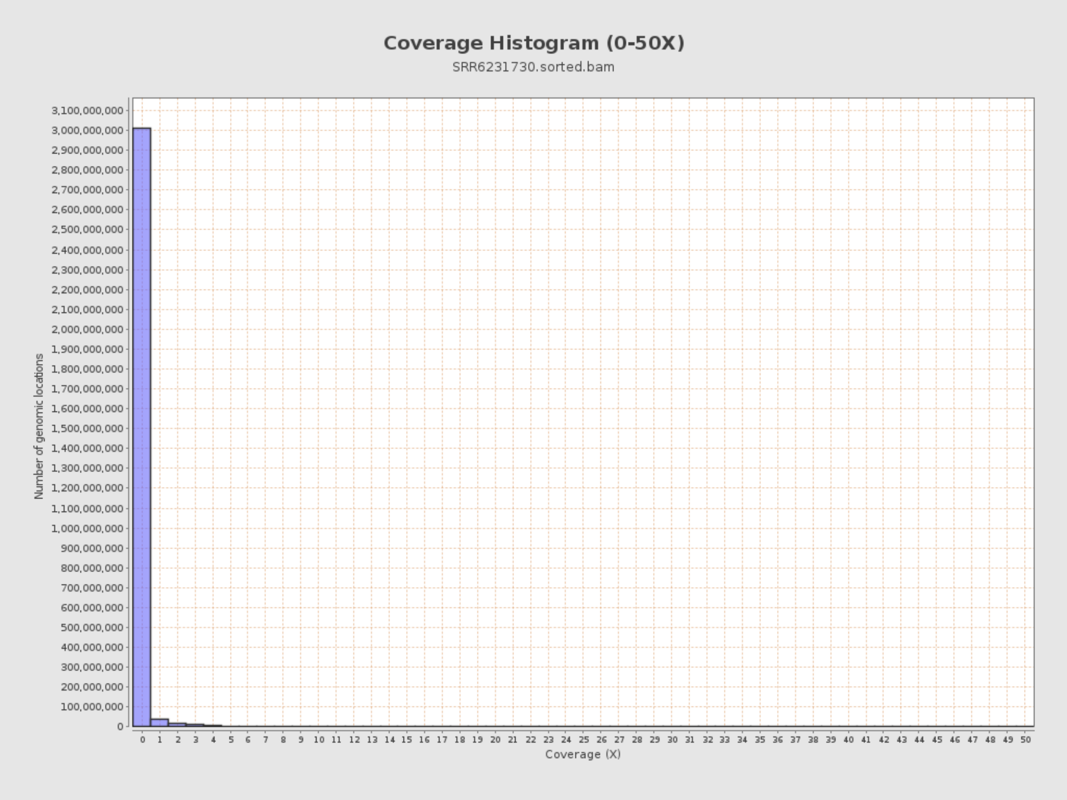
# 3. Results : Coverage across reference



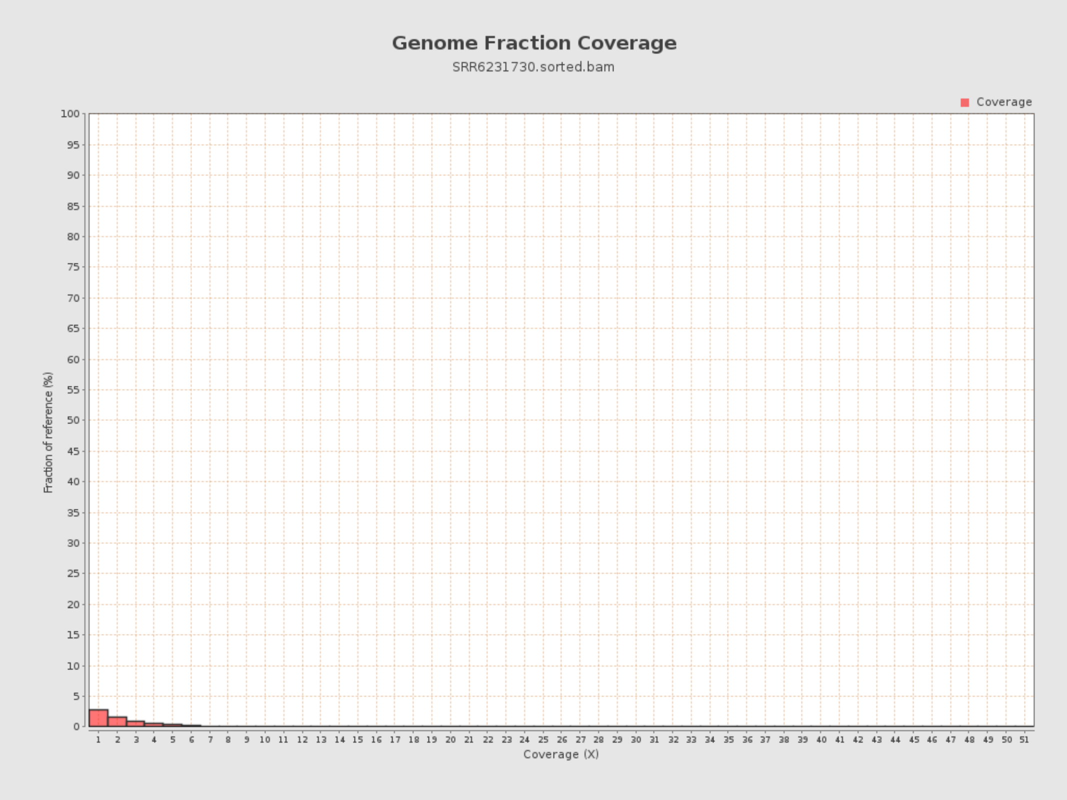
# 4. Results : Coverage Histogram



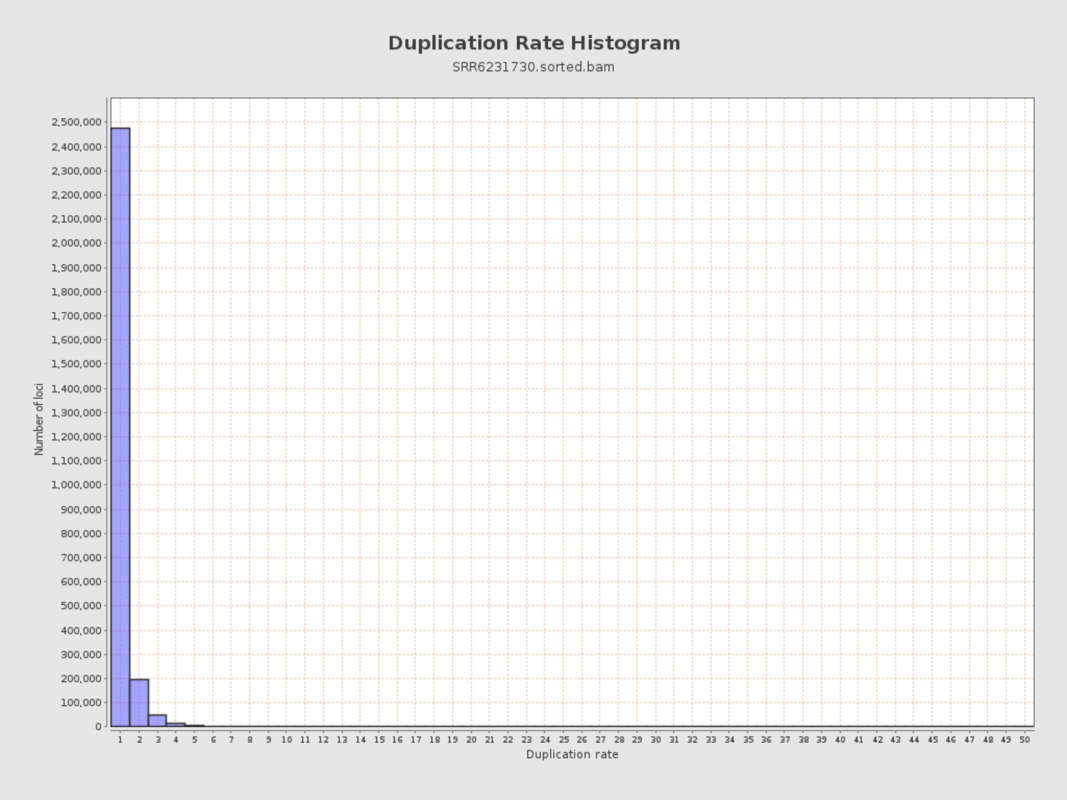
# 5. Results : Coverage Histogram (0-50X)



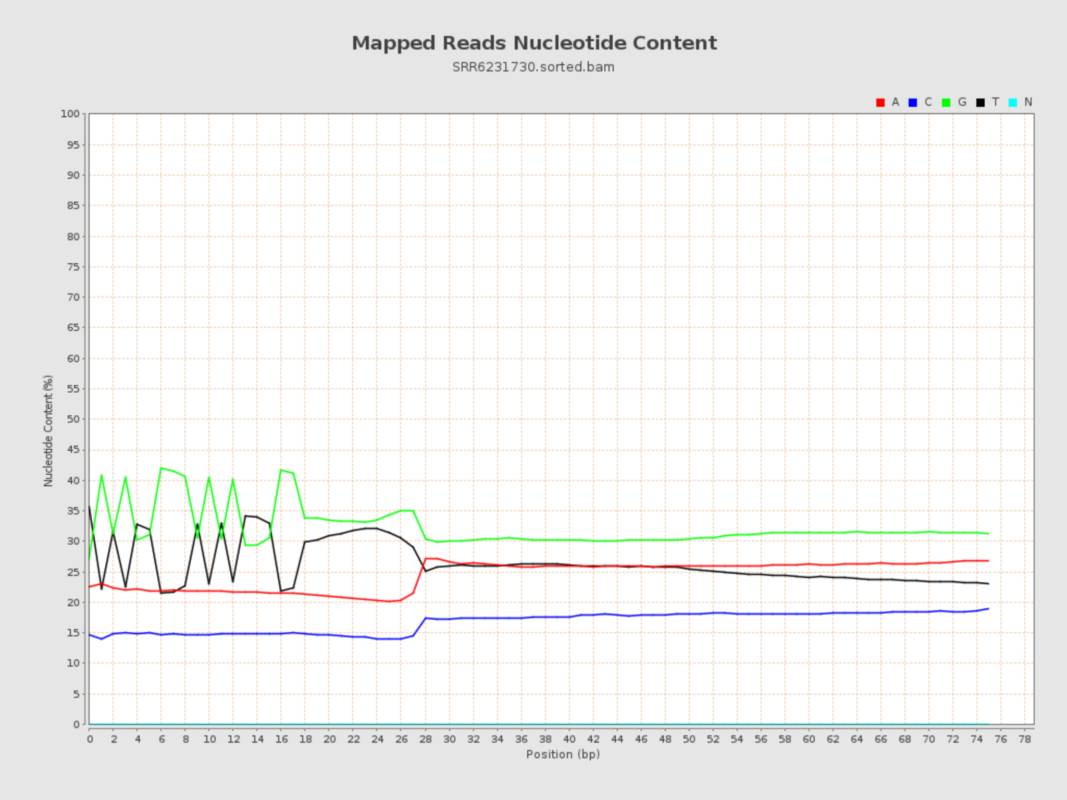
# 6. Results : Genome Fraction Coverage



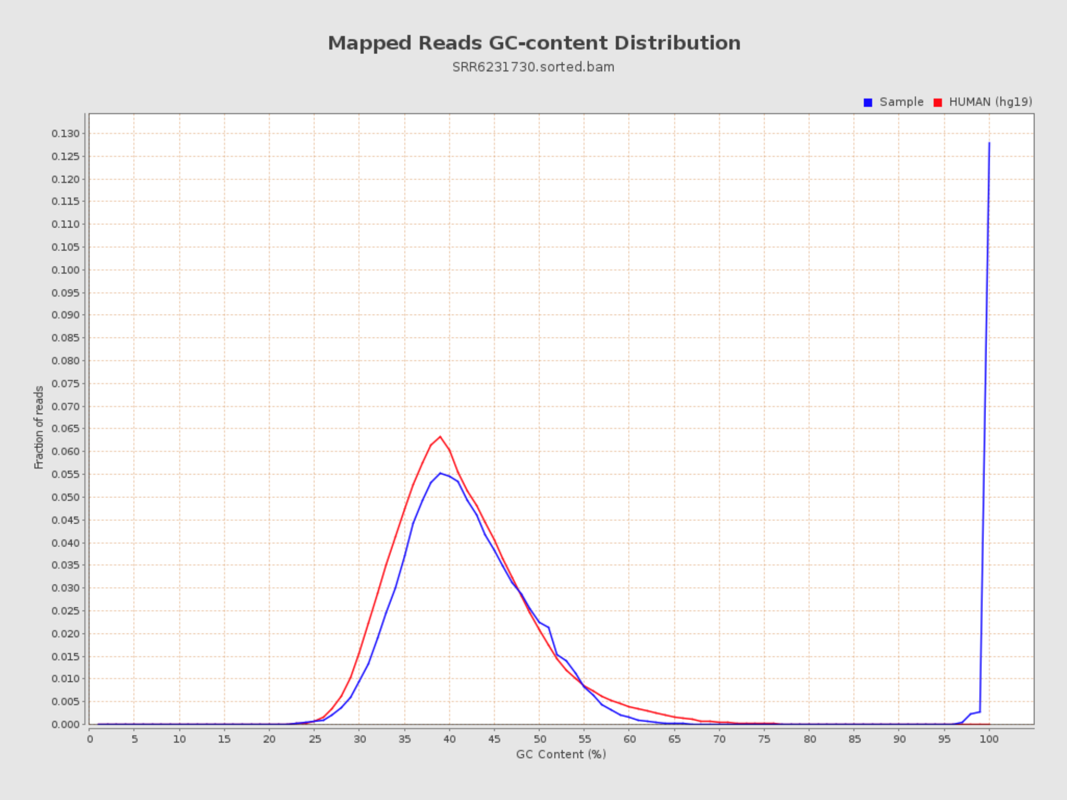
# 7. Results : Duplication Rate Histogram



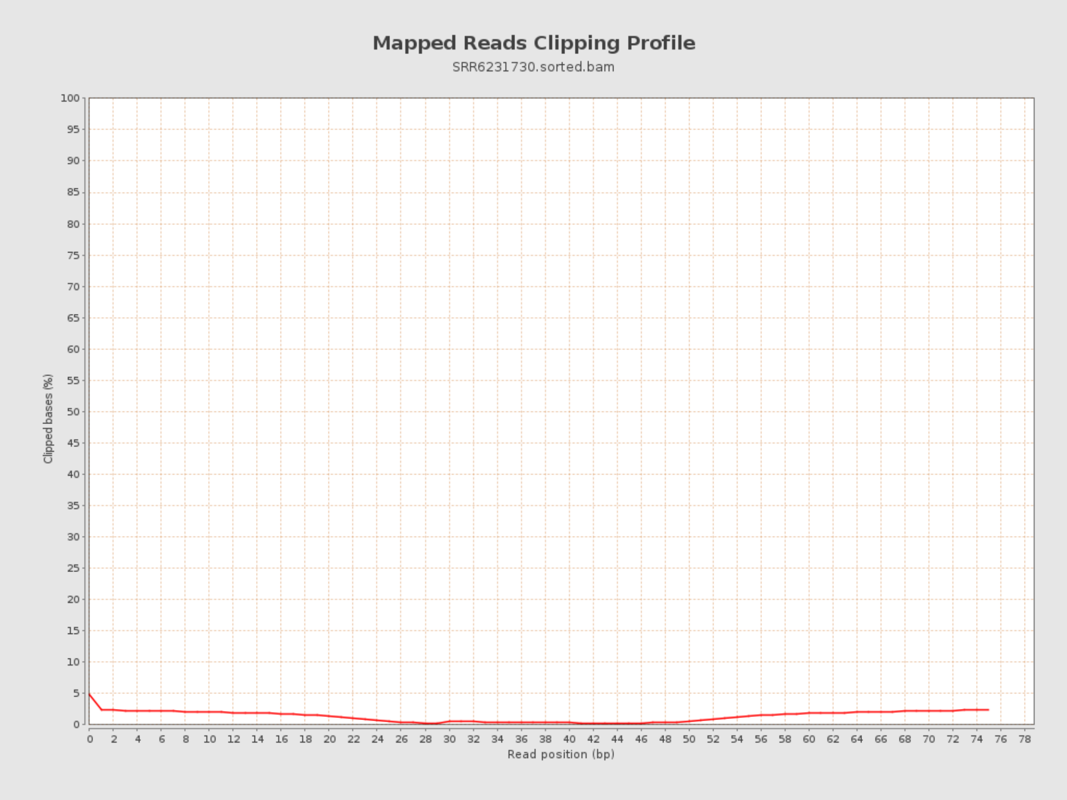
# 8. Results : Mapped Reads Nucleotide Content



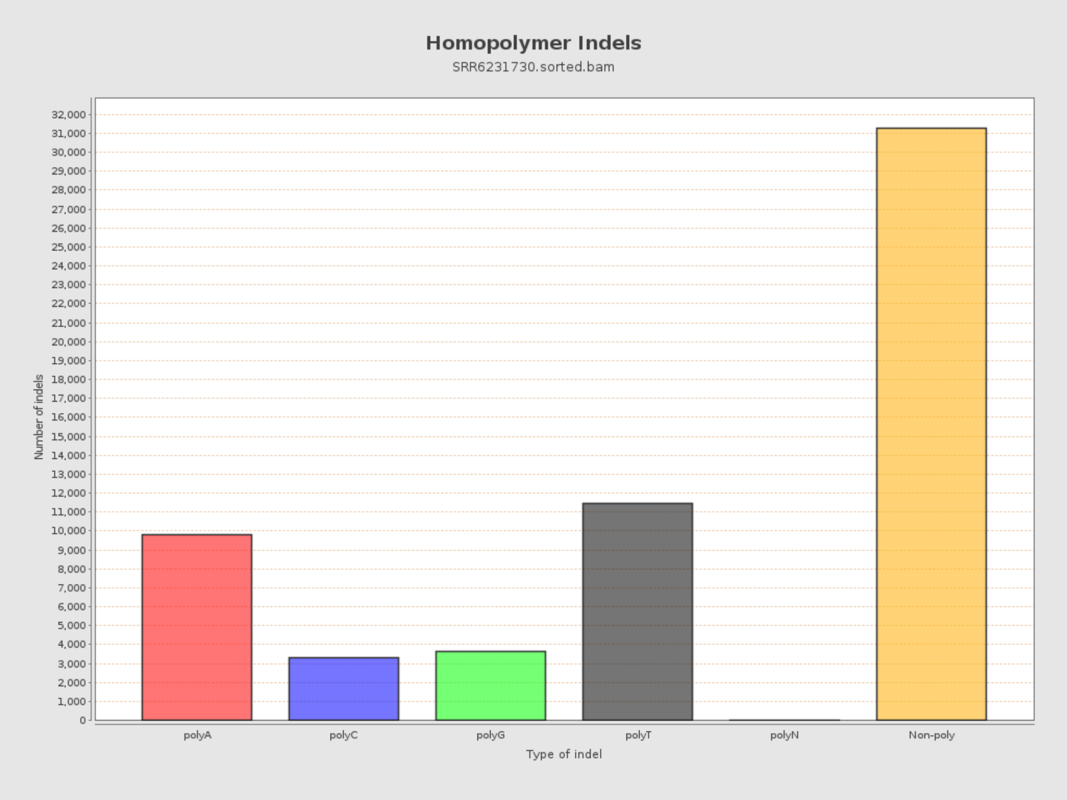
# 9. Results : Mapped Reads GC-content Distribution



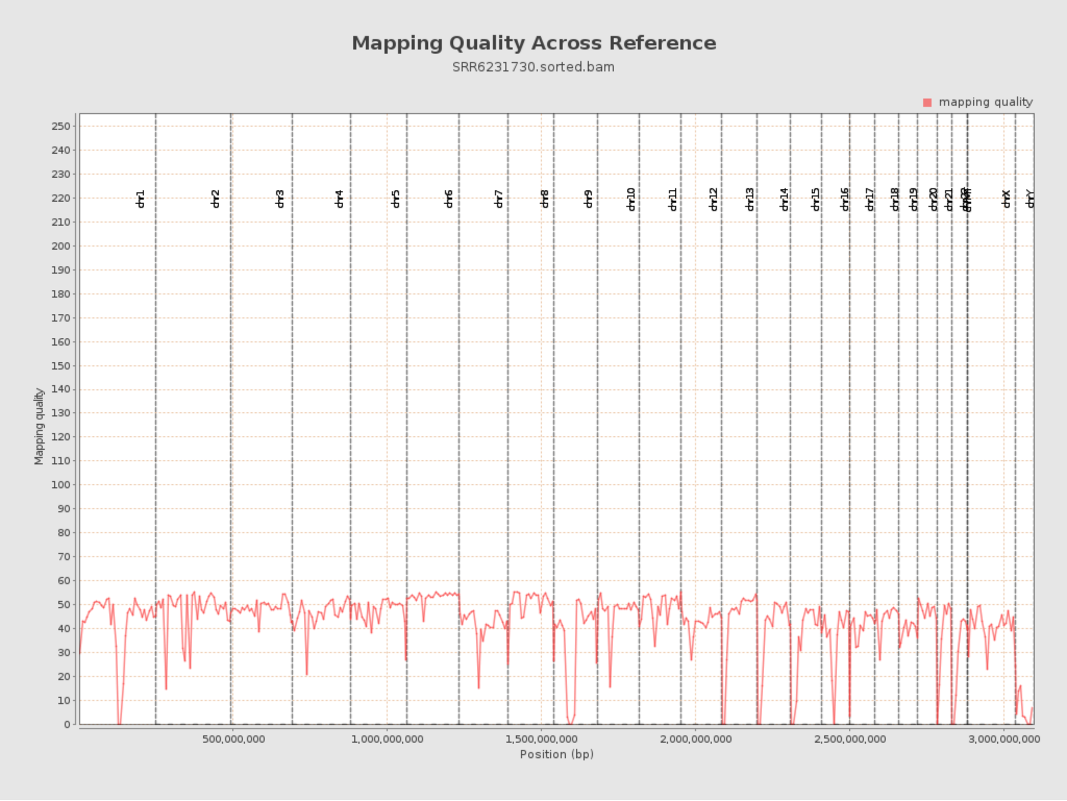
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram