# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/15 23:04:25*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231734.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_SRR6231734 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231734.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Sep 15 23:04:24 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6231734.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,125,177 |
| Mapped reads | 997,827 / 88.68% |
| Unmapped reads | 127,350 / 11.32% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 3,600 / 0.32% |
| Read min/max/mean length | 30 / 76 / 76.11 |
| Duplicated reads (estimated) | 396,153 / 35.21% |
| Duplication rate | 3.85% |
| Clipped reads | 460,439 / 40.92% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 9,503,110 / 14.41% |
| Number/percentage of C's | 6,396,317 / 9.7% |
| Number/percentage of T's | 12,609,112 / 19.12% |
| Number/percentage of G's | 37,421,552 / 56.75% |
| Number/percentage of N's | 6,833 / 0.01% |
| GC Percentage | 66.45% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0213 |
| | |

| | |
|---|---|
| Standard Deviation | 55.4632 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.54 |

## 2.5. Mismatches and indels

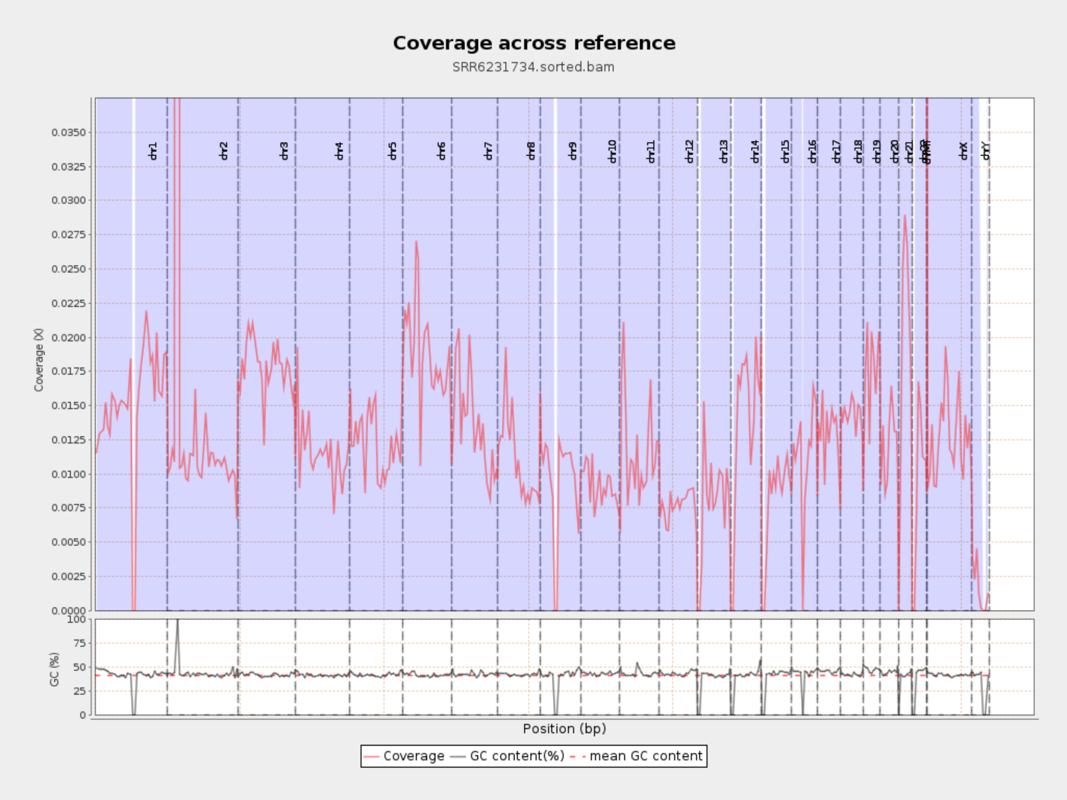
| | |
|---|---|
| General error rate | 0.67% |
| Mismatches | 433,825 |
| Insertions | 3,644 |
| Mapped reads with at least one insertion | 0.36% |
| Deletions | 8,552 |
| Mapped reads with at least one deletion | 0.85% |
| Homopolymer indels | 43.46% |

## 2.6. Chromosome stats

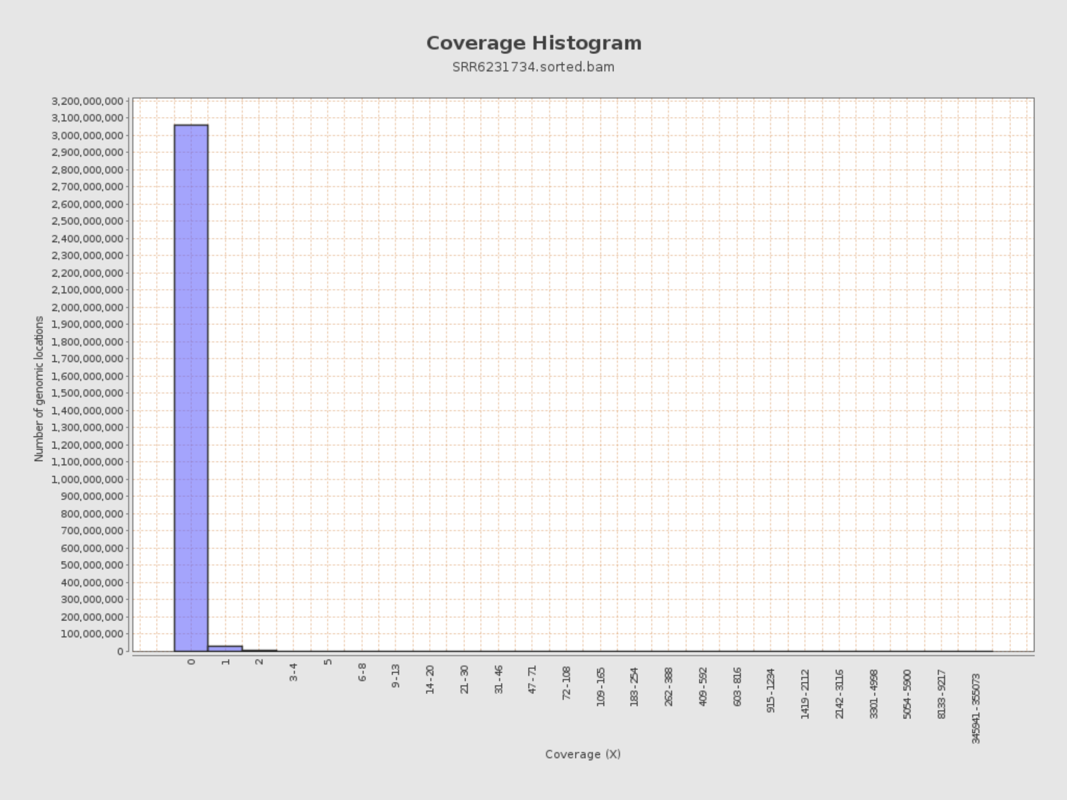
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 3769473 | 0.0151 | 0.1727 |
| chr2 | 243199373 | 30343189 | 0.1248 | 197.8794 |
| chr3 | 198022430 | 3545114 | 0.0179 | 0.1483 |
| chr4 | 191154276 | 2202168 | 0.0115 | 0.1249 |
| chr5 | 180915260 | 2201060 | 0.0122 | 0.1217 |
| chr6 | 171115067 | 3206938 | 0.0187 | 0.1672 |
| chr7 | 159138663 | 2165002 | 0.0136 | 0.2041 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 1606327 | 0.011 | 0.1353 |
| chr9 | 141213431 | 1333829 | 0.0094 | 0.1233 |
| chr10 | 135534747 | 1237478 | 0.0091 | 0.1141 |
| chr11 | 135006516 | 1604264 | 0.0119 | 0.2915 |
| chr12 | 133851895 | 1029217 | 0.0077 | 0.0973 |
| chr13 | 115169878 | 899178 | 0.0078 | 0.0976 |
| chr14 | 107349540 | 1492079 | 0.0139 | 0.4368 |
| chr15 | 102531392 | 820602 | 0.008 | 0.1014 |
| chr16 | 90354753 | 1001820 | 0.0111 | 0.1206 |
| chr17 | 81195210 | 1052332 | 0.013 | 0.1306 |
| chr18 | 78077248 | 1126911 | 0.0144 | 0.2018 |
| chr19 | 59128983 | 1041849 | 0.0176 | 0.1691 |
| chr20 | 63025520 | 764704 | 0.0121 | 0.126 |
| chr21 | 48129895 | 947680 | 0.0197 | 0.159 |
| chr22 | 51304566 | 484560 | 0.0094 | 0.107 |
| chrMT | 16571 | 959 | 0.0579 | 0.2517 |
| chrX | 155270560 | 1979717 | 0.0128 | 0.1324 |
| chrY | 59373566 | 93717 | 0.0016 | 0.0467 |

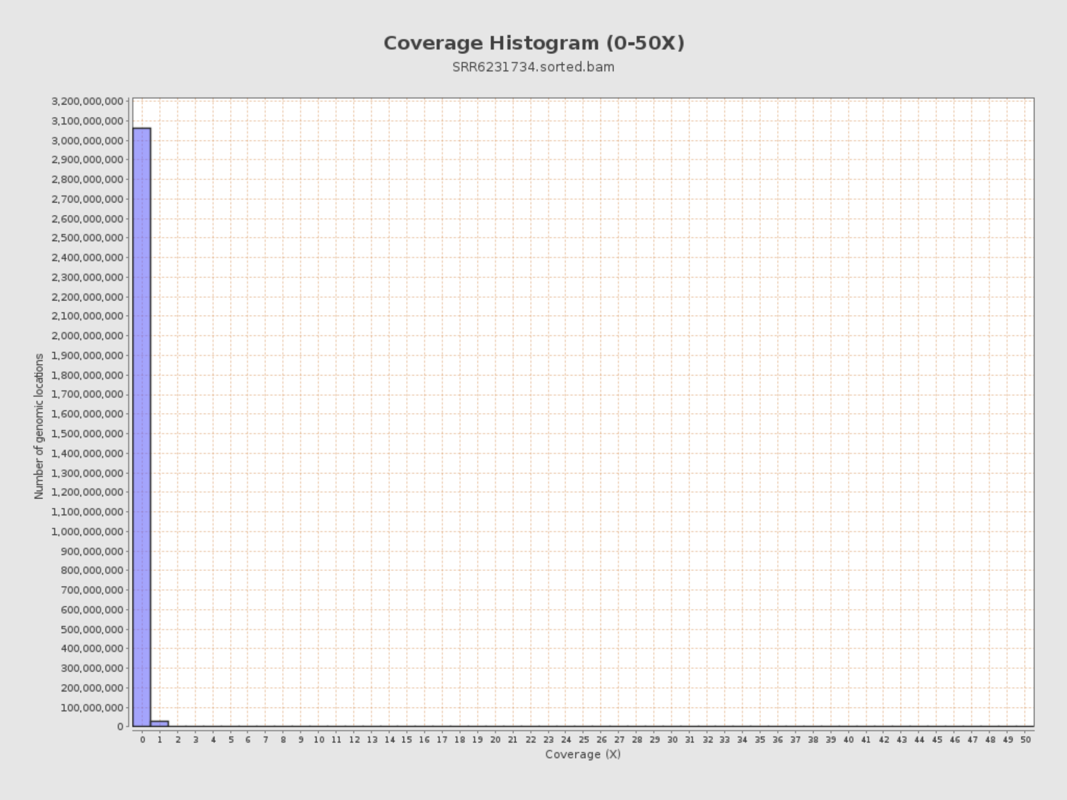
# 3. Results : Coverage across reference



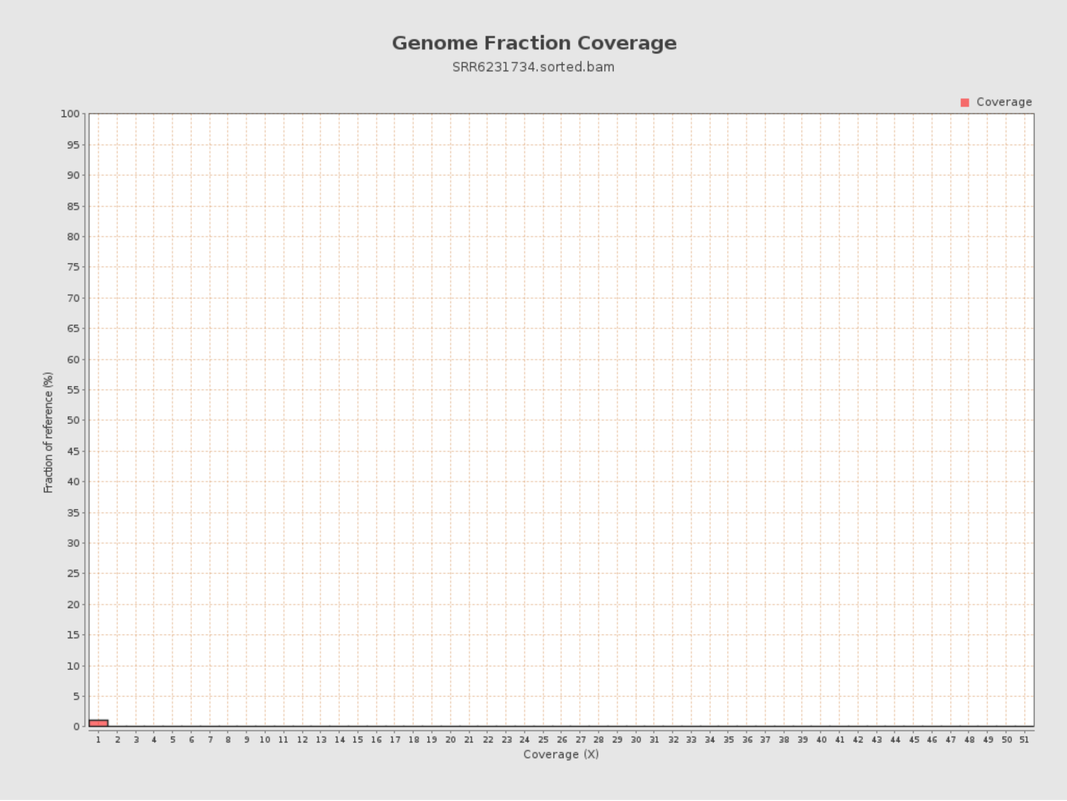
# 4. Results : Coverage Histogram



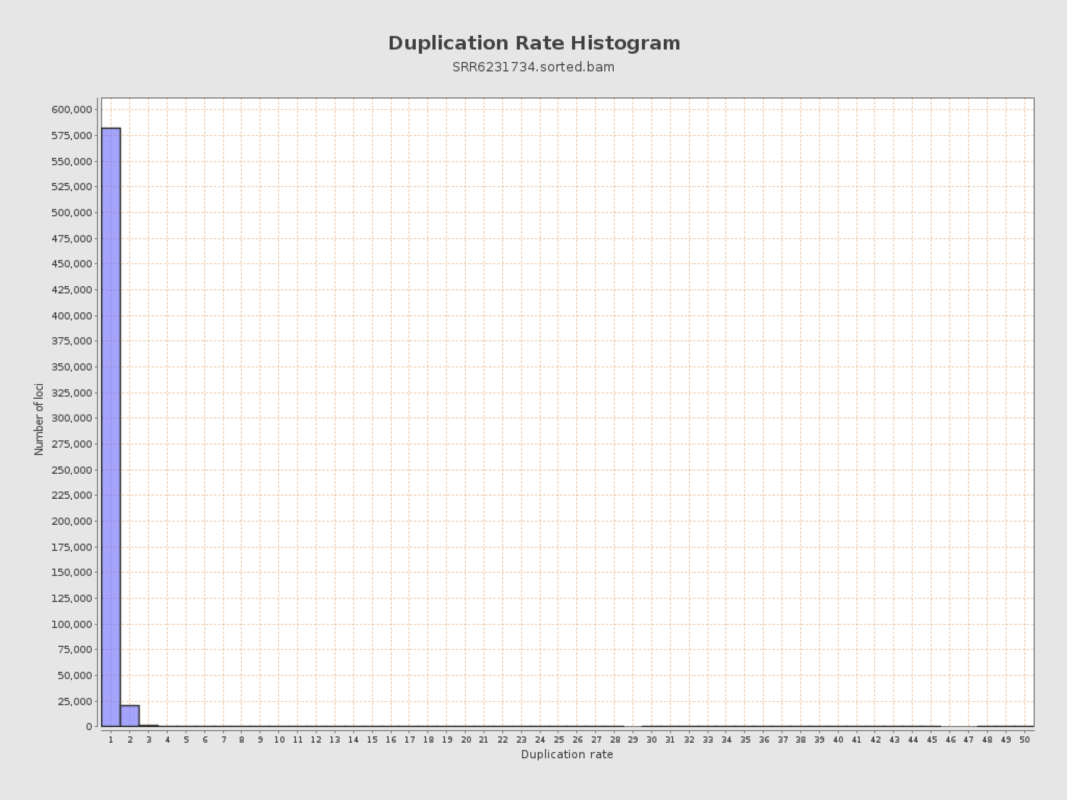
# 5. Results : Coverage Histogram (0-50X)



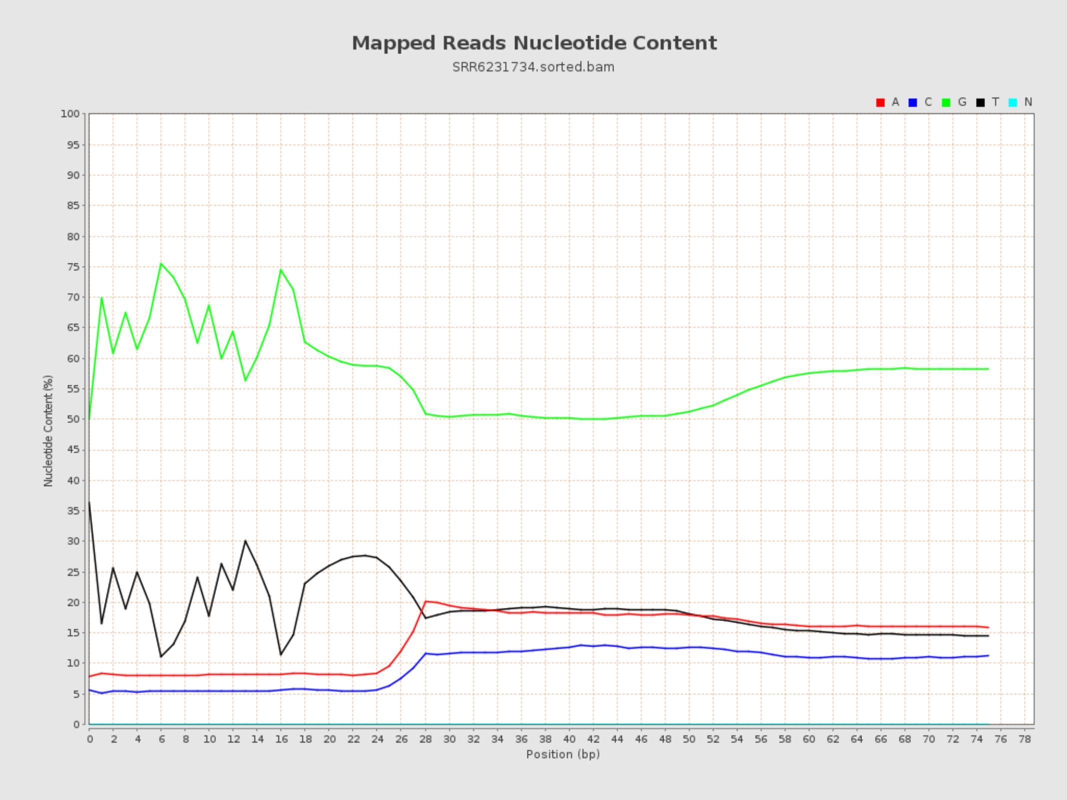
# 6. Results : Genome Fraction Coverage



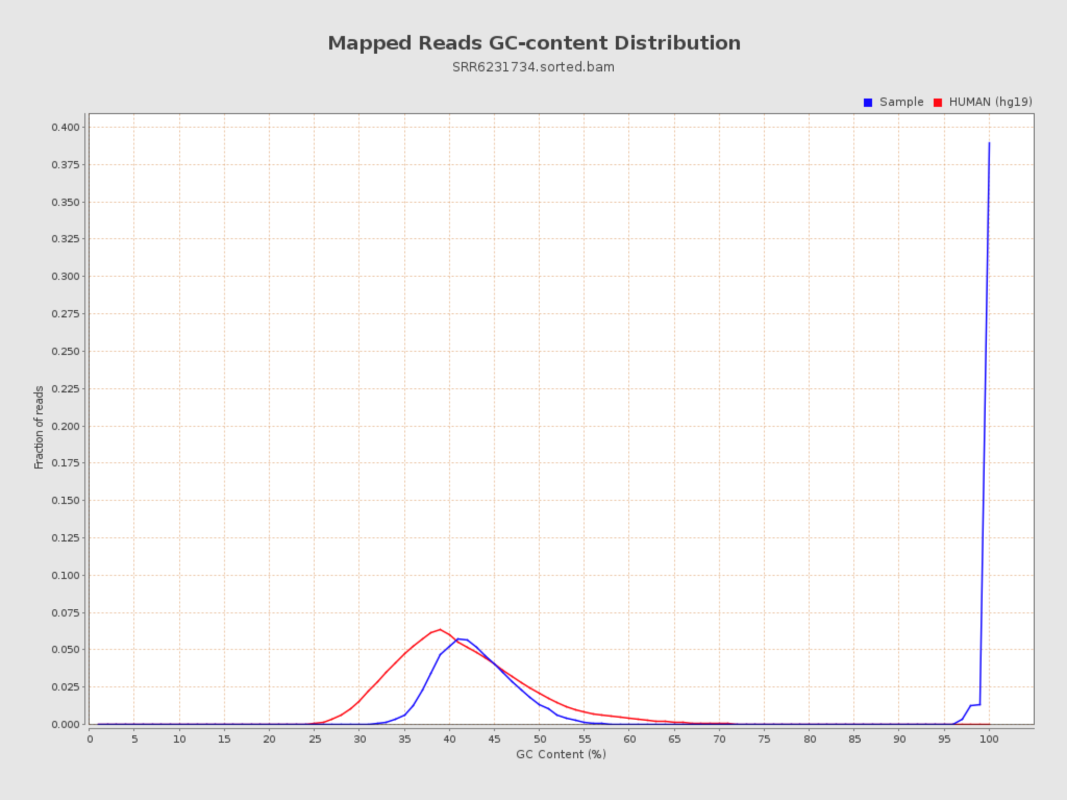
# 7. Results : Duplication Rate Histogram



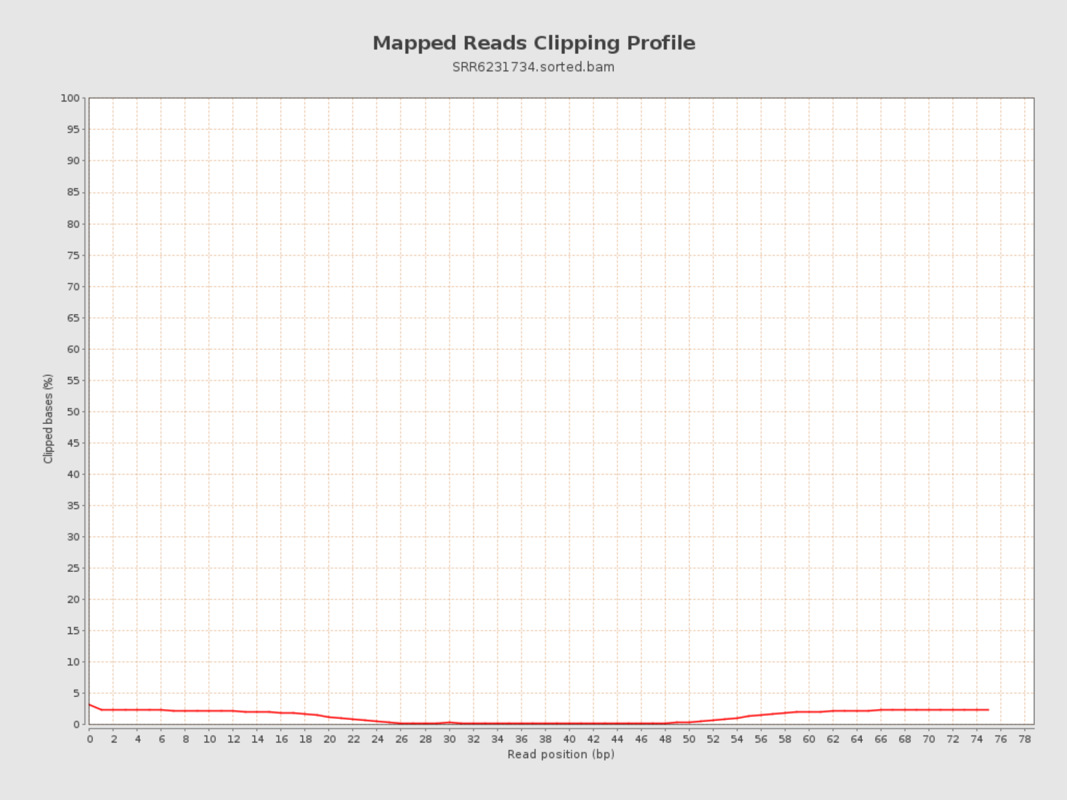
# 8. Results : Mapped Reads Nucleotide Content



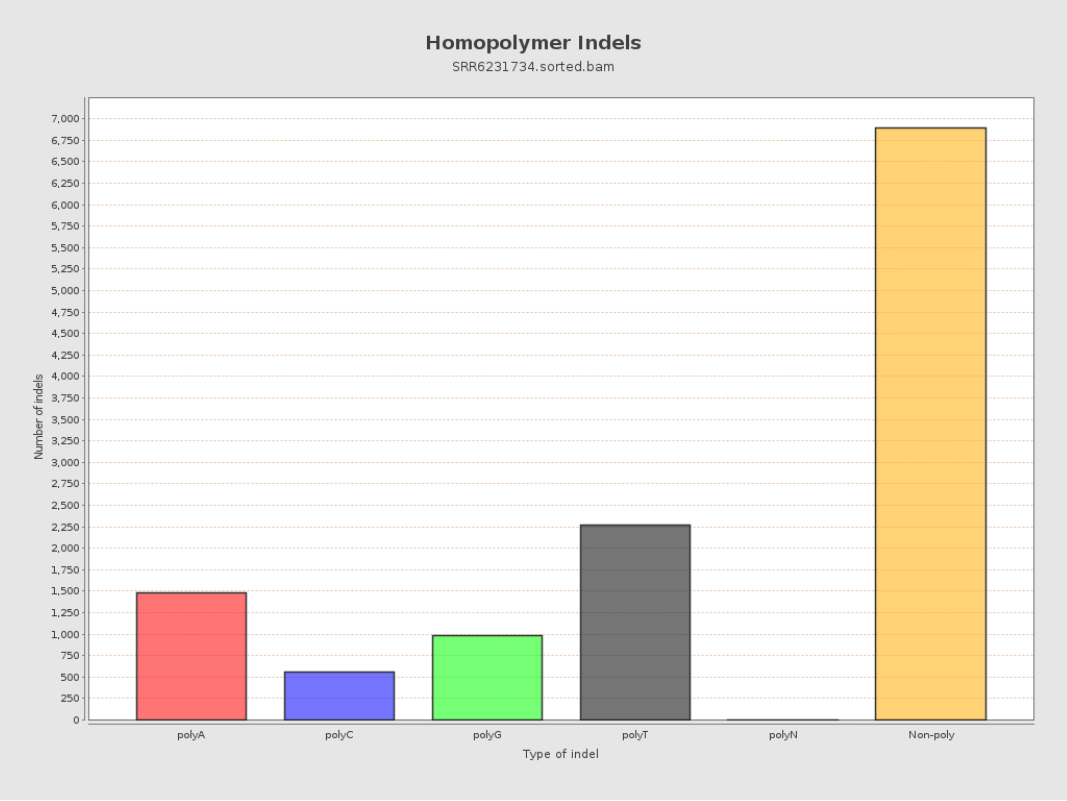
# 9. Results : Mapped Reads GC-content Distribution



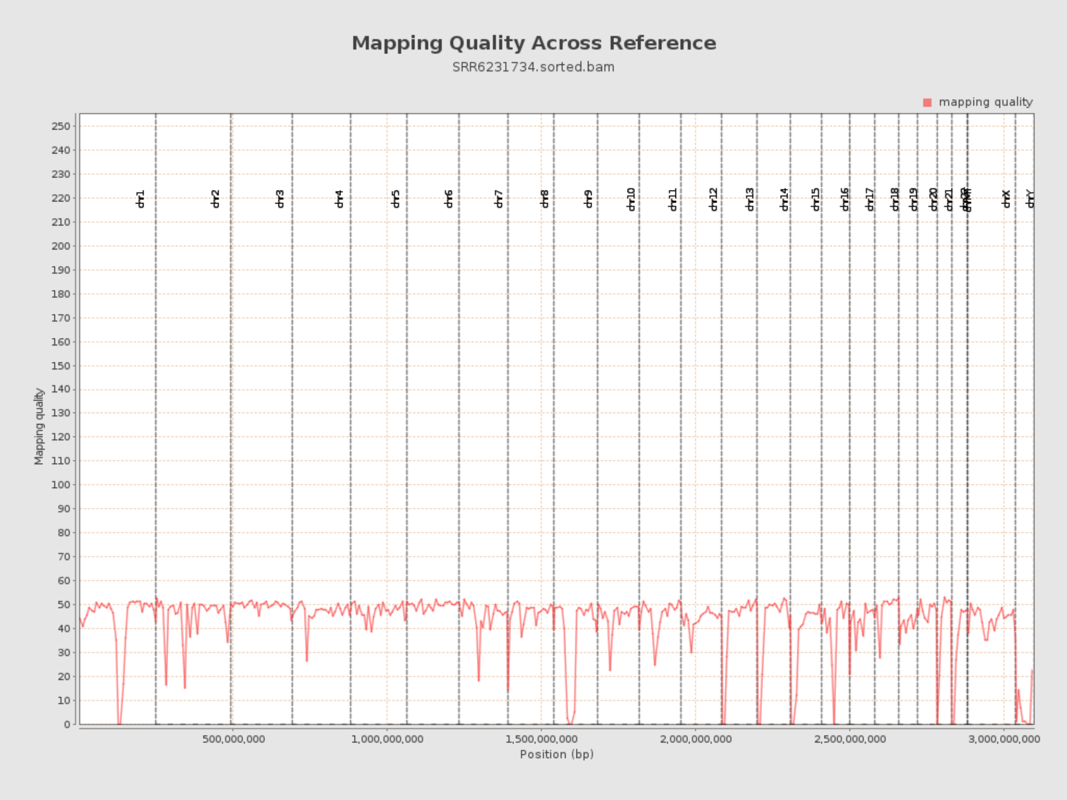
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram