# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/16 17:32:57*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234125.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_SRR6234125 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234125.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 16 17:32:57 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6234125.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,424,356 |
| Mapped reads | 1,165,349 / 48.07% |
| Unmapped reads | 1,259,007 / 51.93% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 6,861 / 0.28% |
| Read min/max/mean length | 30 / 76 / 76.1 |
| Duplicated reads (estimated) | 654,960 / 27.02% |
| Duplication rate | 10.04% |
| Clipped reads | 285,411 / 11.77% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 10,722,055 / 12.97% |
| Number/percentage of C's | 8,103,242 / 9.8% |
| Number/percentage of T's | 11,459,667 / 13.86% |
| Number/percentage of G's | 52,384,845 / 63.36% |
| Number/percentage of N's | 13,755 / 0.02% |
| GC Percentage | 73.16% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0267 |
| | |

| | |
|---|---|
| Standard Deviation | 87.9918 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.55 |

## 2.5. Mismatches and indels

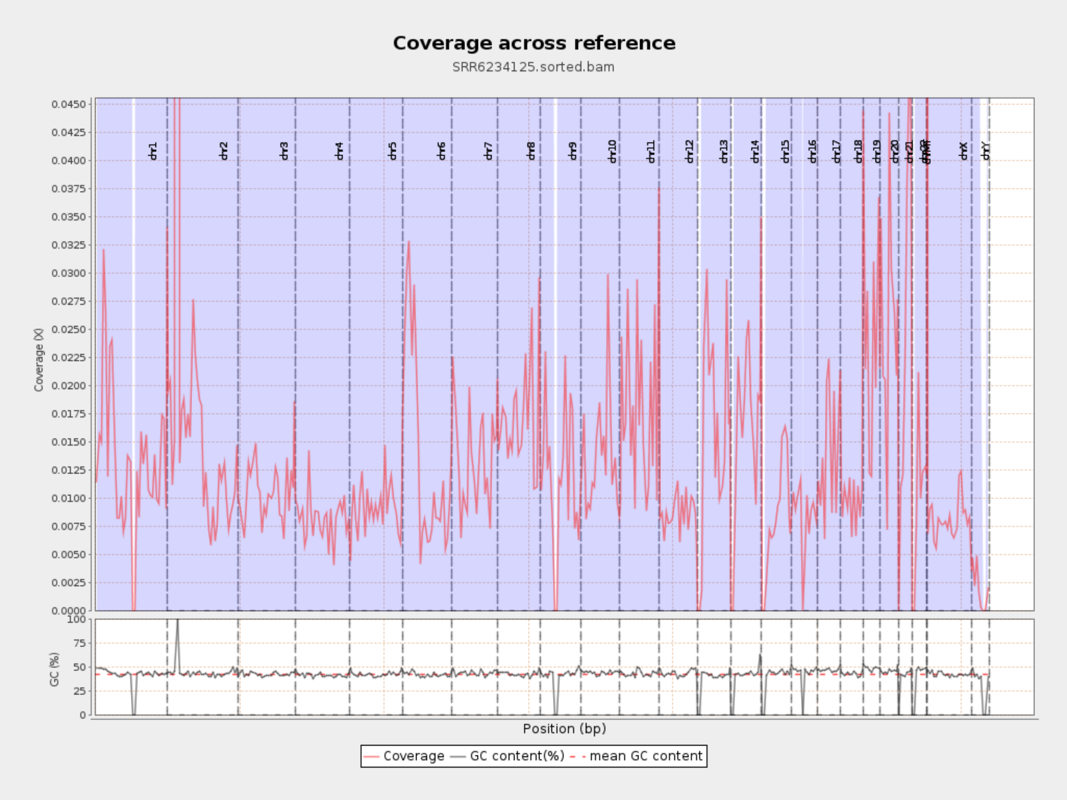
| | |
|---|---|
| General error rate | 0.44% |
| Mismatches | 358,716 |
| Insertions | 4,115 |
| Mapped reads with at least one insertion | 0.35% |
| Deletions | 8,622 |
| Mapped reads with at least one deletion | 0.73% |
| Homopolymer indels | 42.64% |

## 2.6. Chromosome stats

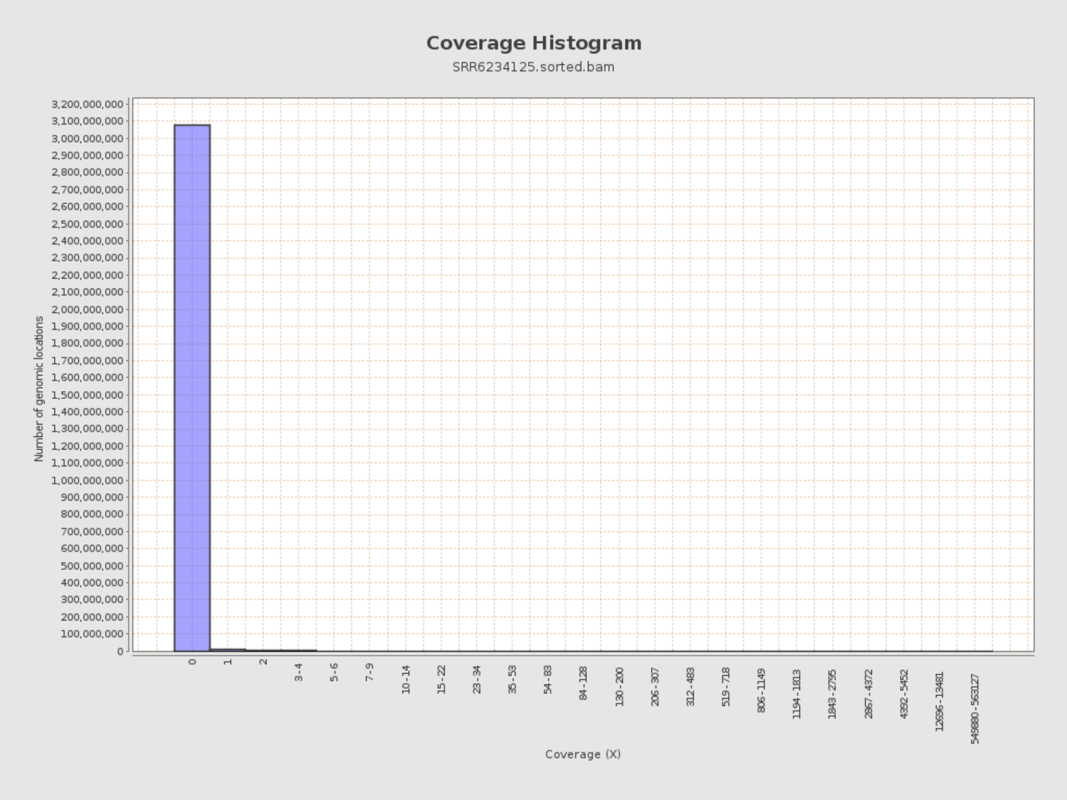
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 3276624 | 0.0131 | 0.255 |
| chr2 | 243199373 | 46831561 | 0.1926 | 313.9335 |
| chr3 | 198022430 | 2051197 | 0.0104 | 0.2183 |
| chr4 | 191154276 | 1568350 | 0.0082 | 0.1884 |
| chr5 | 180915260 | 1667204 | 0.0092 | 0.2155 |
| chr6 | 171115067 | 2342106 | 0.0137 | 0.2652 |
| chr7 | 159138663 | 2146924 | 0.0135 | 0.2891 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2545153 | 0.0174 | 0.2804 |
| chr9 | 141213431 | 1641035 | 0.0116 | 0.2249 |
| chr10 | 135534747 | 1878231 | 0.0139 | 0.2521 |
| chr11 | 135006516 | 2391943 | 0.0177 | 0.3549 |
| chr12 | 133851895 | 1156715 | 0.0086 | 0.2002 |
| chr13 | 115169878 | 1833534 | 0.0159 | 0.2611 |
| chr14 | 107349540 | 1693352 | 0.0158 | 0.7476 |
| chr15 | 102531392 | 835277 | 0.0081 | 0.2047 |
| chr16 | 90354753 | 736336 | 0.0081 | 0.1958 |
| chr17 | 81195210 | 1143594 | 0.0141 | 0.2563 |
| chr18 | 78077248 | 745045 | 0.0095 | 0.2423 |
| chr19 | 59128983 | 1423580 | 0.0241 | 0.3337 |
| chr20 | 63025520 | 1605824 | 0.0255 | 0.341 |
| chr21 | 48129895 | 1230606 | 0.0256 | 0.336 |
| chr22 | 51304566 | 520655 | 0.0101 | 0.2003 |
| chrMT | 16571 | 68606 | 4.1401 | 4.7042 |
| chrX | 155270560 | 1255759 | 0.0081 | 0.1898 |
| chrY | 59373566 | 109020 | 0.0018 | 0.0706 |

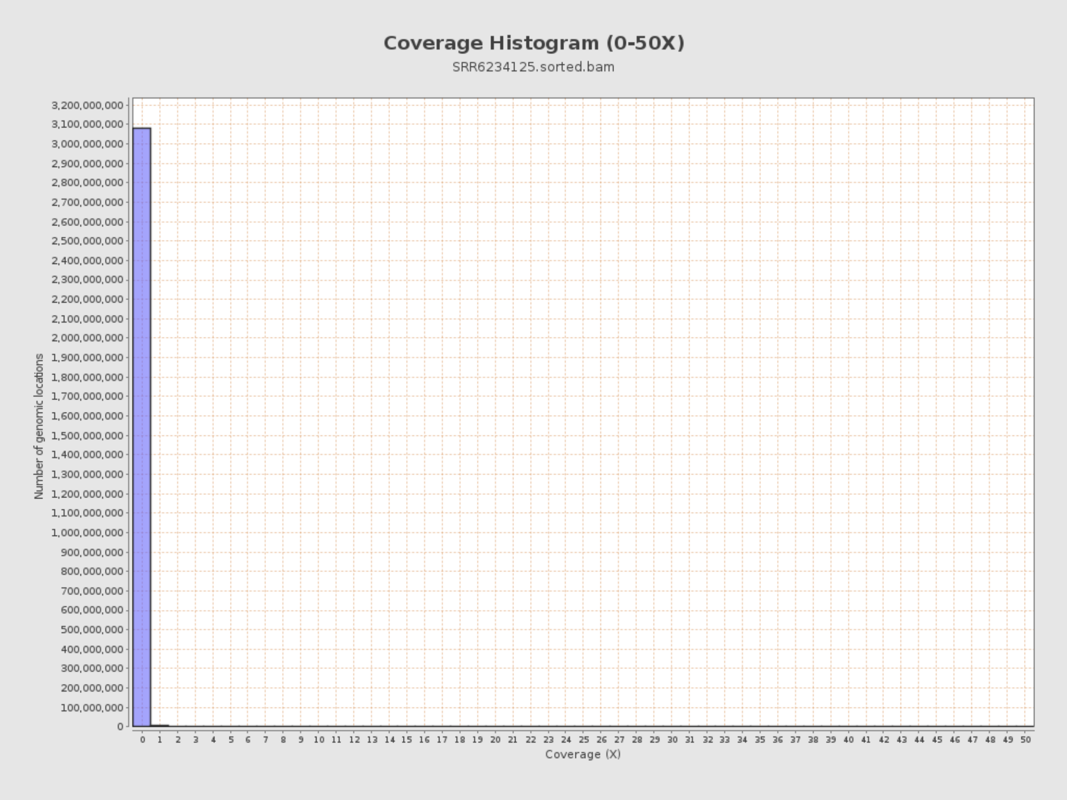
# 3. Results : Coverage across reference



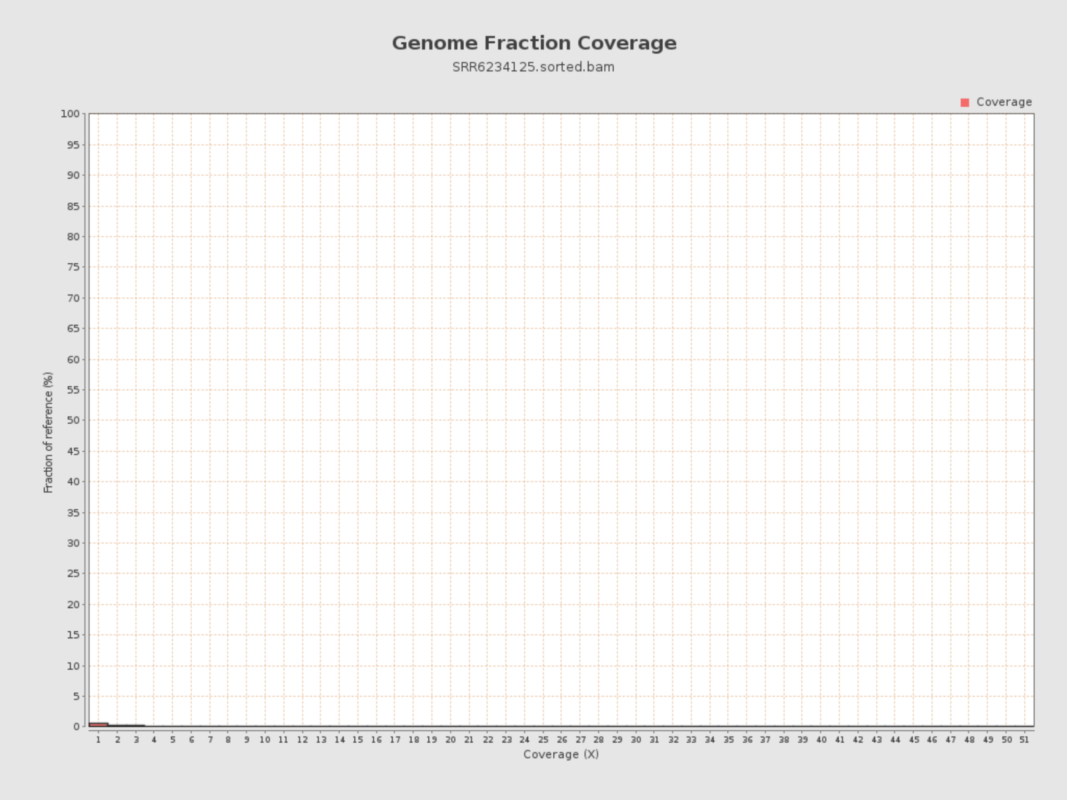
# 4. Results : Coverage Histogram



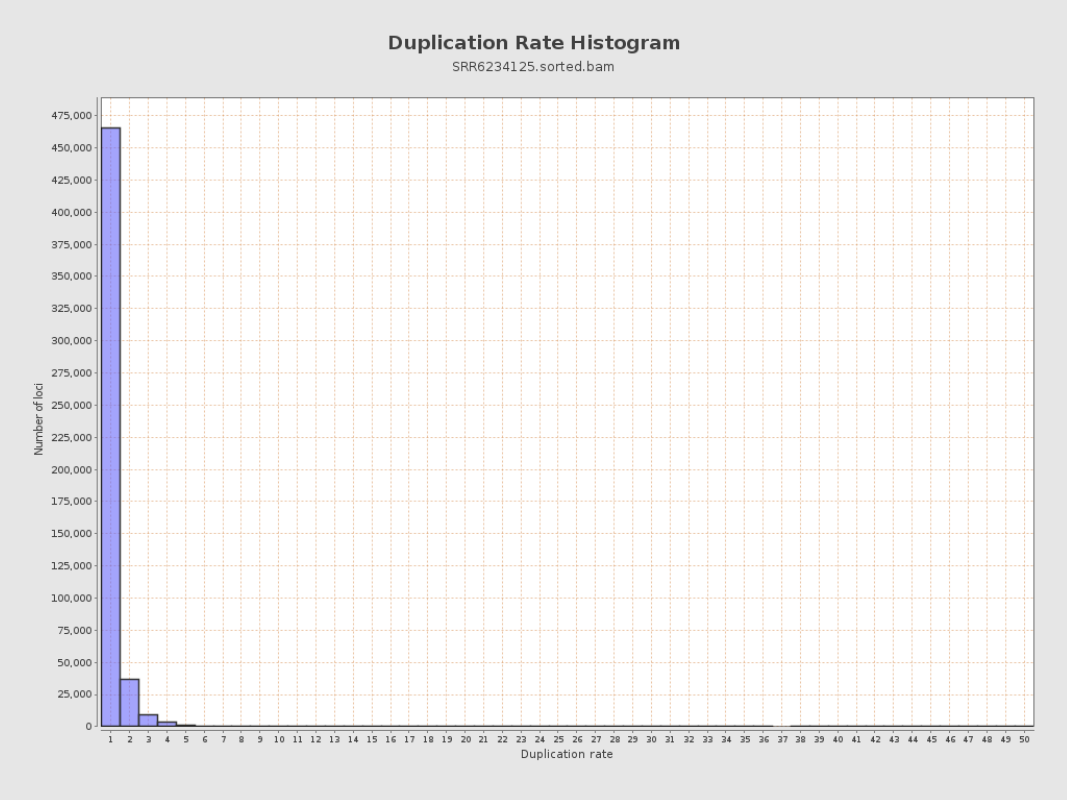
# 5. Results : Coverage Histogram (0-50X)



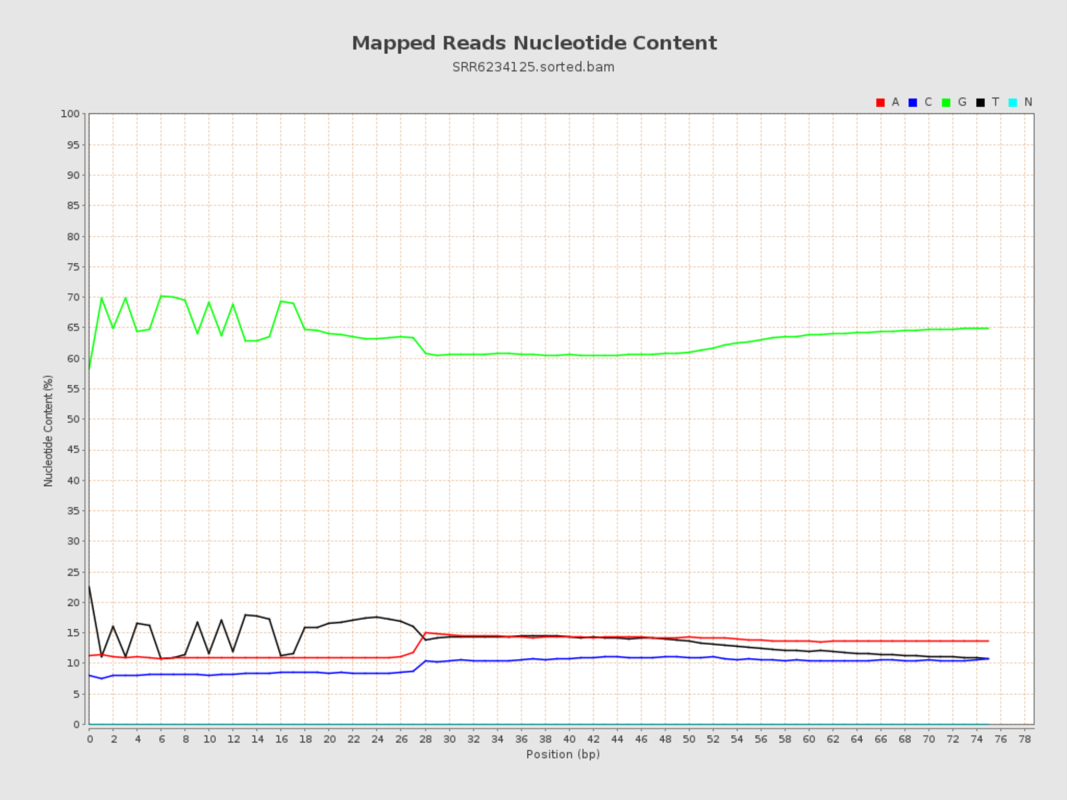
# 6. Results : Genome Fraction Coverage



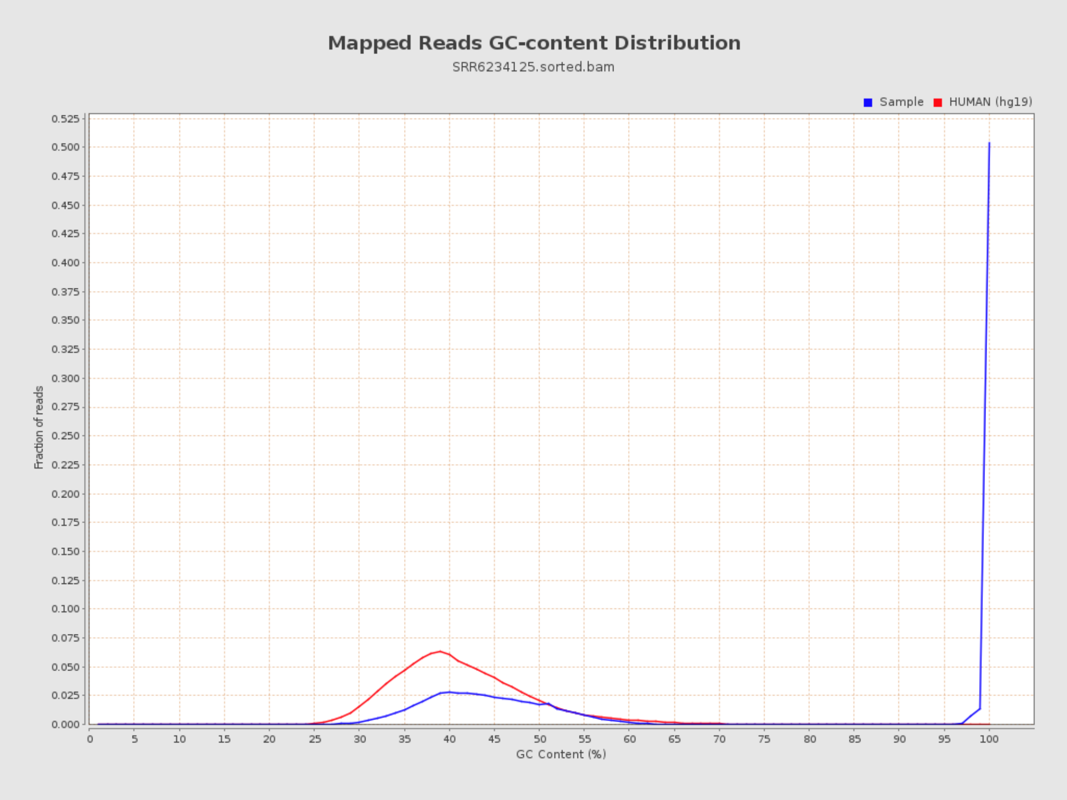
# 7. Results : Duplication Rate Histogram



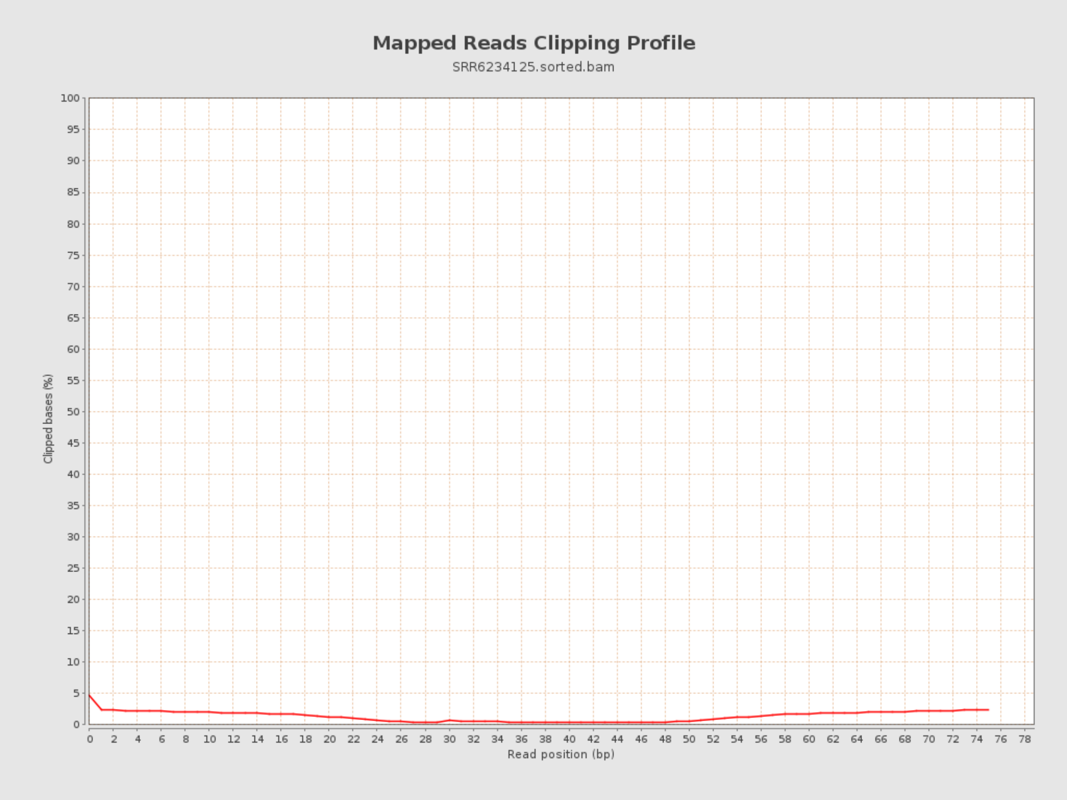
# 8. Results : Mapped Reads Nucleotide Content



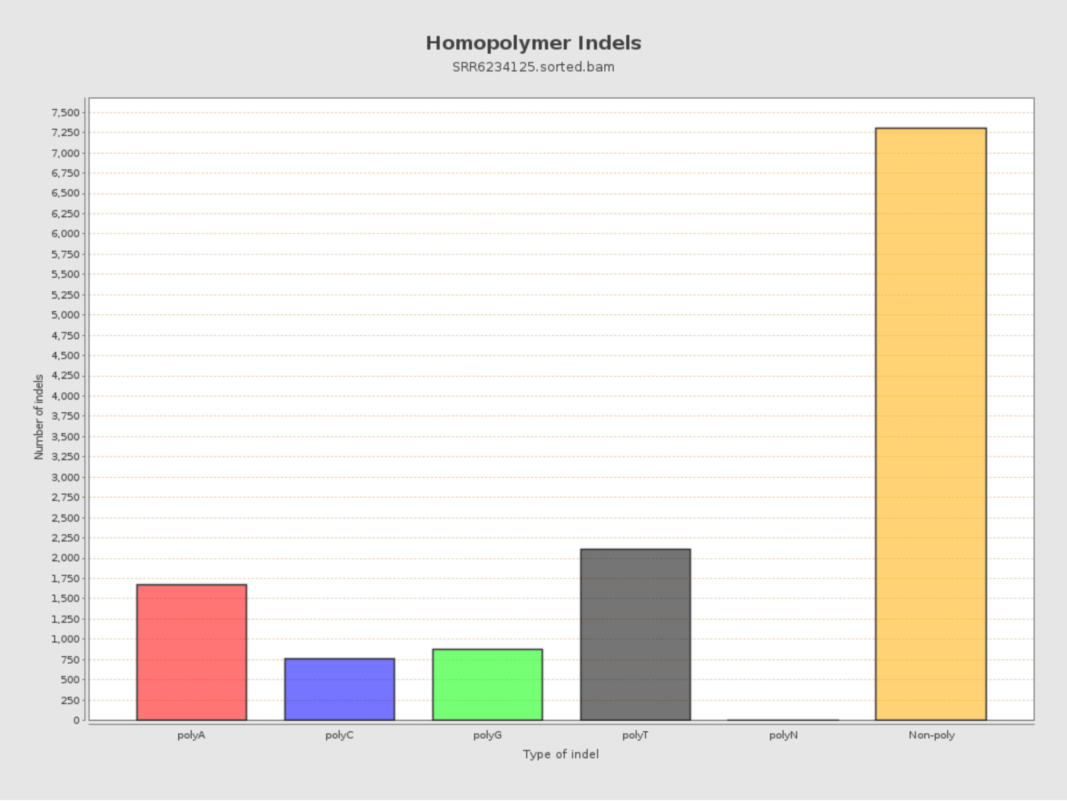
# 9. Results : Mapped Reads GC-content Distribution



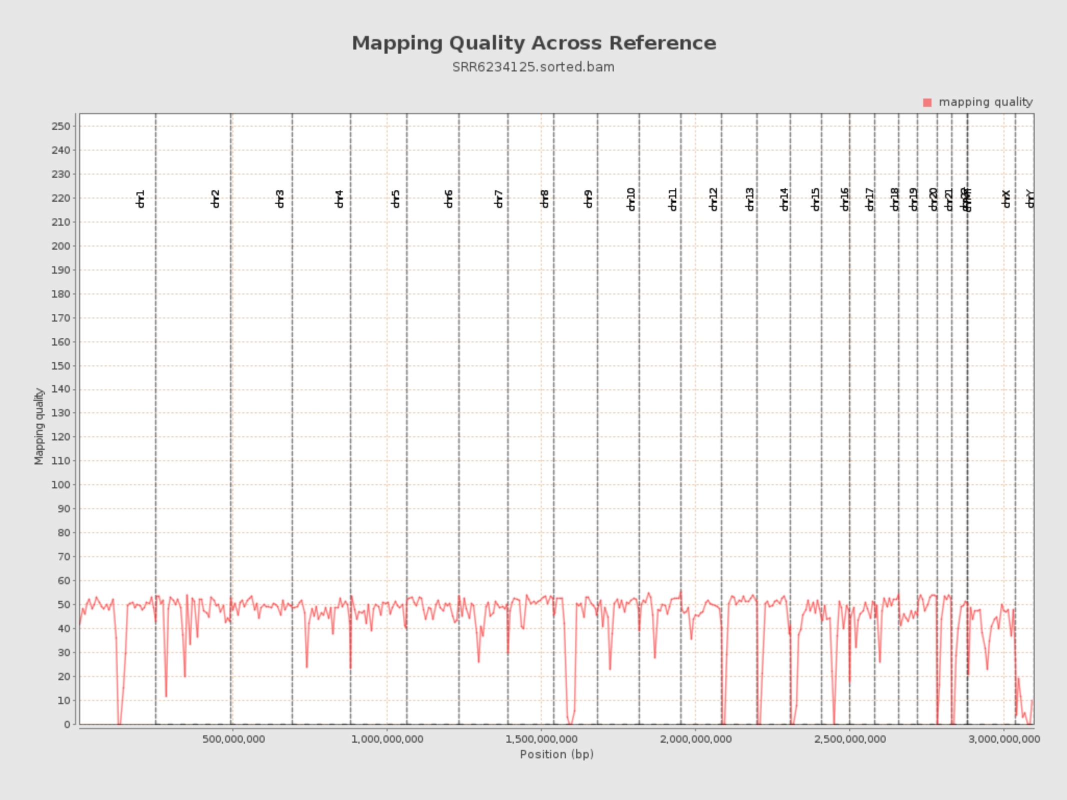
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram