# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/16 15:50:15*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234100.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_SRR6234100 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234100.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 16 15:50:14 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6234100.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 5,526,190 |
| Mapped reads | 5,246,438 / 94.94% |
| Unmapped reads | 279,752 / 5.06% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 36,975 / 0.67% |
| Read min/max/mean length | 30 / 76 / 76.23 |
| Duplicated reads (estimated) | 655,449 / 11.86% |
| Duplication rate | 10.44% |
| Clipped reads | 2,642,883 / 47.82% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 88,777,310 / 25.99% |
| Number/percentage of C's | 62,988,685 / 18.44% |
| Number/percentage of T's | 109,220,866 / 31.97% |
| Number/percentage of G's | 80,622,338 / 23.6% |
| Number/percentage of N's | 34,113 / 0.01% |
| GC Percentage | 42.04% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1104 |
| | |

| | |
|---|---|
| Standard Deviation | 1.0559 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.14 |

## 2.5. Mismatches and indels

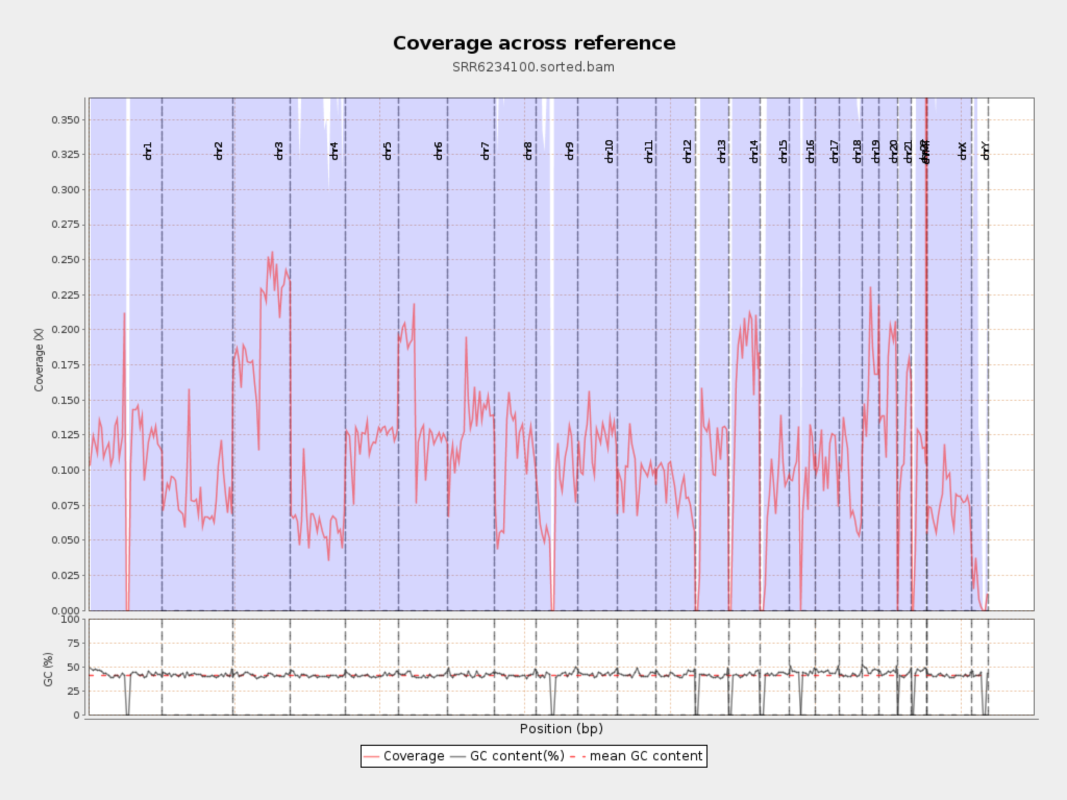
| | |
|---|---|
| General error rate | 0.54% |
| Mismatches | 1,808,777 |
| Insertions | 22,410 |
| Mapped reads with at least one insertion | 0.42% |
| Deletions | 78,943 |
| Mapped reads with at least one deletion | 1.49% |
| Homopolymer indels | 44.43% |

## 2.6. Chromosome stats

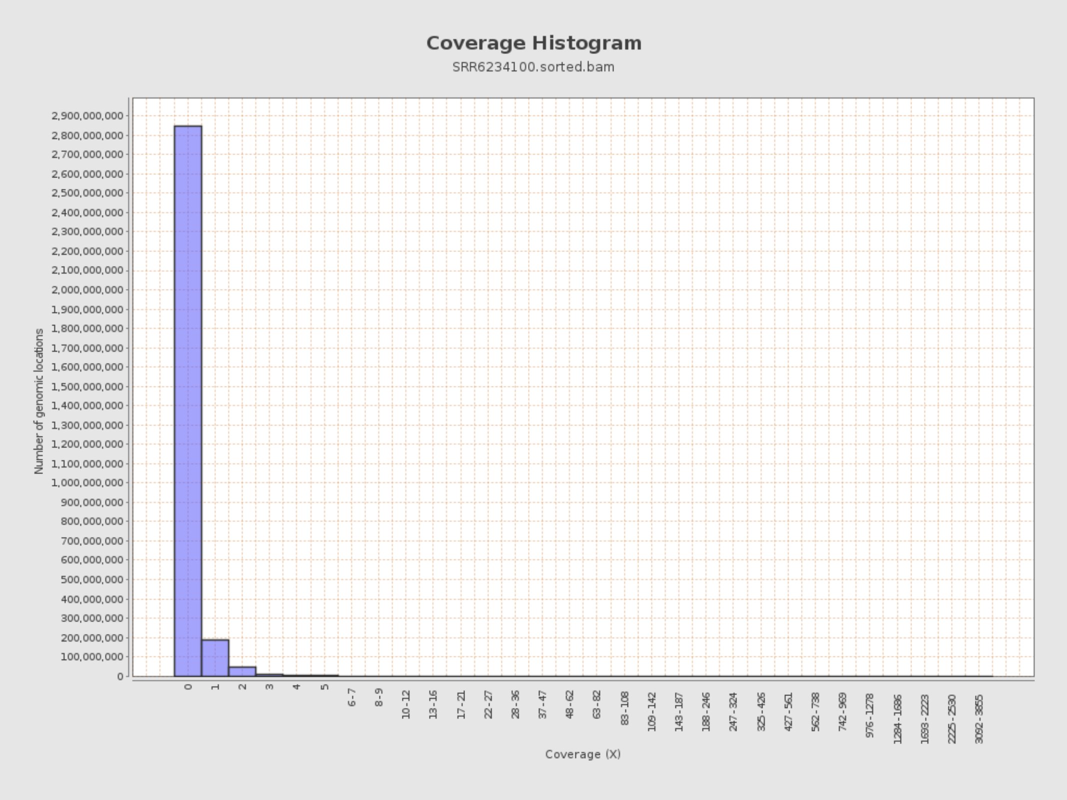
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 29130558 | 0.1169 | 2.171 |
| chr2 | 243199373 | 20035363 | 0.0824 | 1.8068 |
| chr3 | 198022430 | 40211098 | 0.2031 | 0.5983 |
| chr4 | 191154276 | 11829063 | 0.0619 | 0.4167 |
| chr5 | 180915260 | 22069880 | 0.122 | 0.4687 |
| chr6 | 171115067 | 24997642 | 0.1461 | 0.7673 |
| chr7 | 159138663 | 21216324 | 0.1333 | 1.139 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 15777670 | 0.1078 | 1.2521 |
| chr9 | 141213431 | 11096154 | 0.0786 | 0.6874 |
| chr10 | 135534747 | 16547422 | 0.1221 | 0.7666 |
| chr11 | 135006516 | 13256975 | 0.0982 | 0.9353 |
| chr12 | 133851895 | 11792277 | 0.0881 | 0.4076 |
| chr13 | 115169878 | 11928254 | 0.1036 | 0.4739 |
| chr14 | 107349540 | 16861855 | 0.1571 | 0.5548 |
| chr15 | 102531392 | 7769973 | 0.0758 | 0.3943 |
| chr16 | 90354753 | 8489431 | 0.094 | 0.5072 |
| chr17 | 81195210 | 8613471 | 0.1061 | 0.5306 |
| chr18 | 78077248 | 6811037 | 0.0872 | 1.6611 |
| chr19 | 59128983 | 9956225 | 0.1684 | 1.1768 |
| chr20 | 63025520 | 10288210 | 0.1632 | 0.5647 |
| chr21 | 48129895 | 5761911 | 0.1197 | 0.4824 |
| chr22 | 51304566 | 4310326 | 0.084 | 0.3721 |
| chrMT | 16571 | 335982 | 20.2753 | 11.8364 |
| chrX | 155270560 | 11987958 | 0.0772 | 0.5175 |
| chrY | 59373566 | 705260 | 0.0119 | 0.2555 |

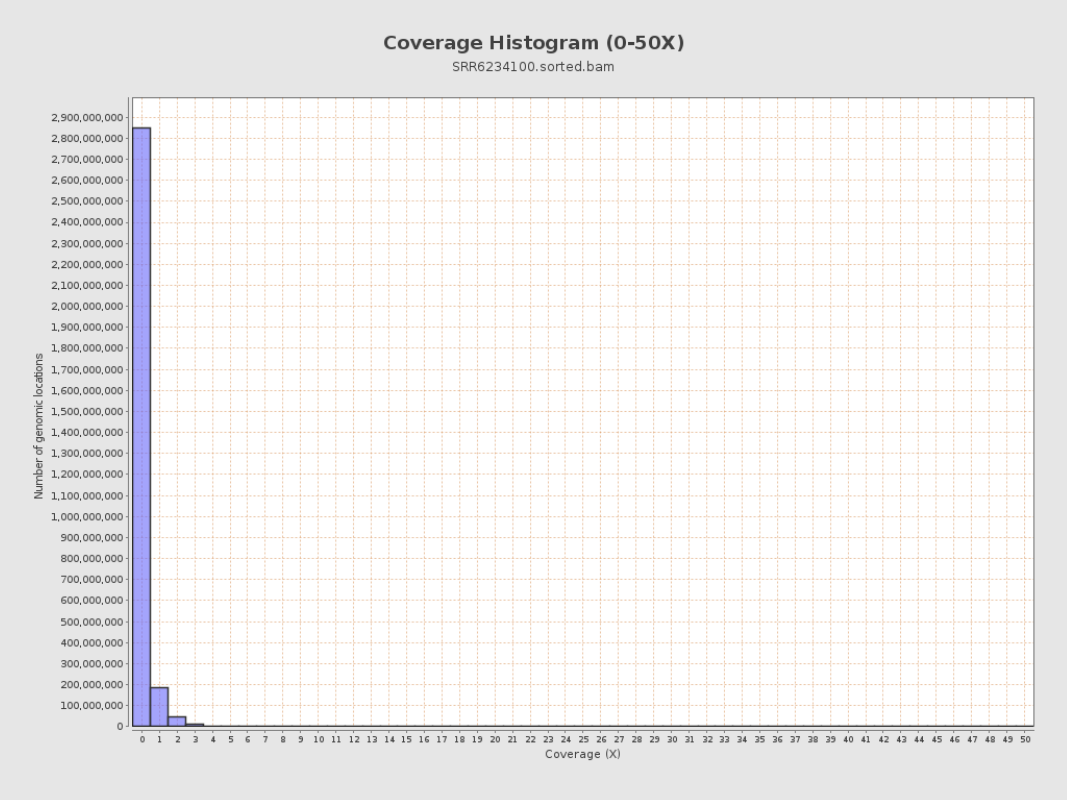
# 3. Results : Coverage across reference



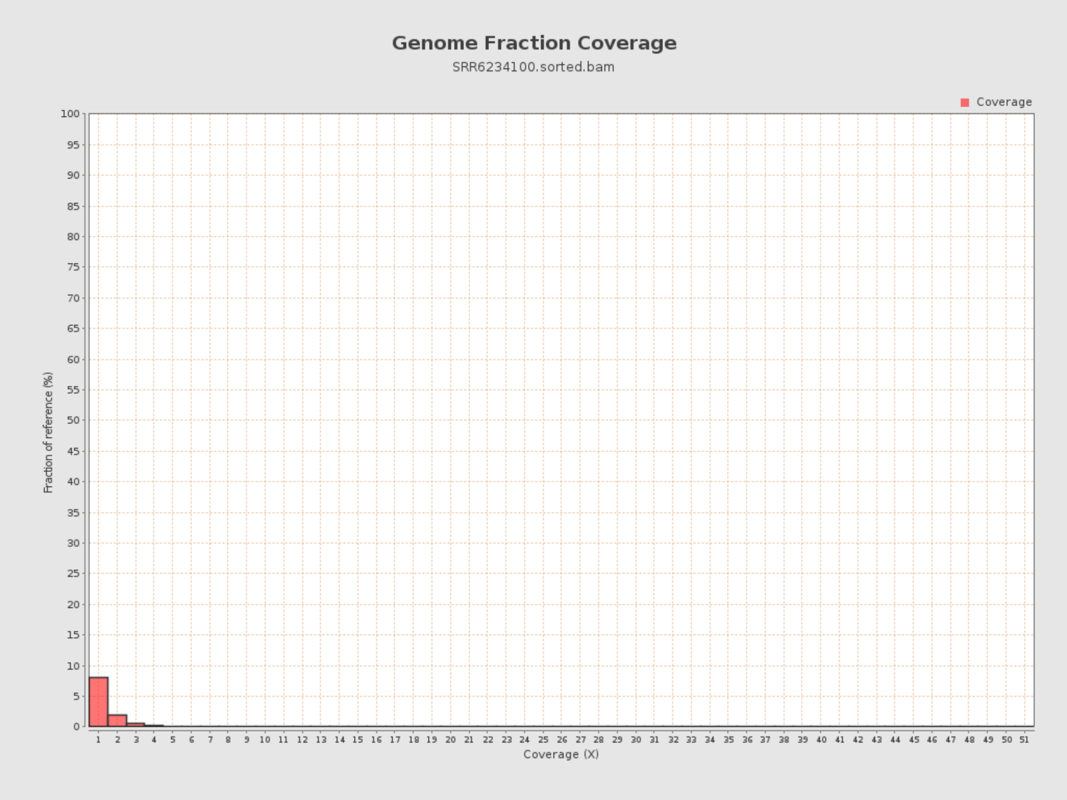
# 4. Results : Coverage Histogram



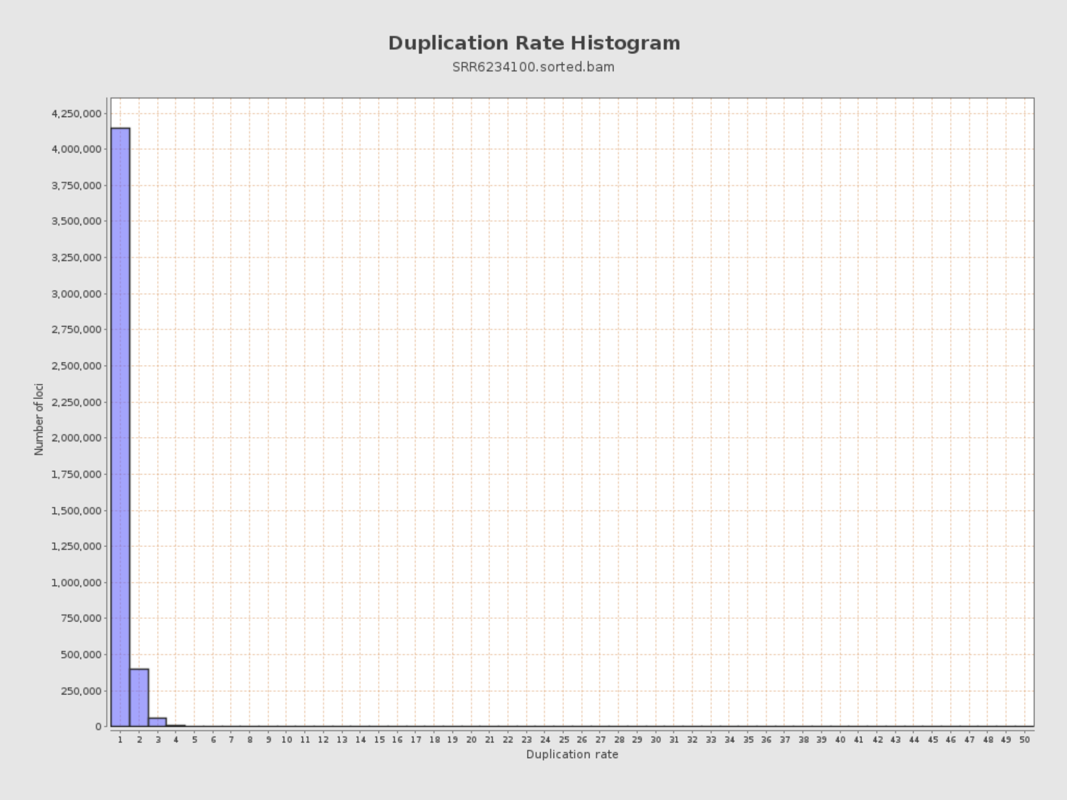
# 5. Results : Coverage Histogram (0-50X)



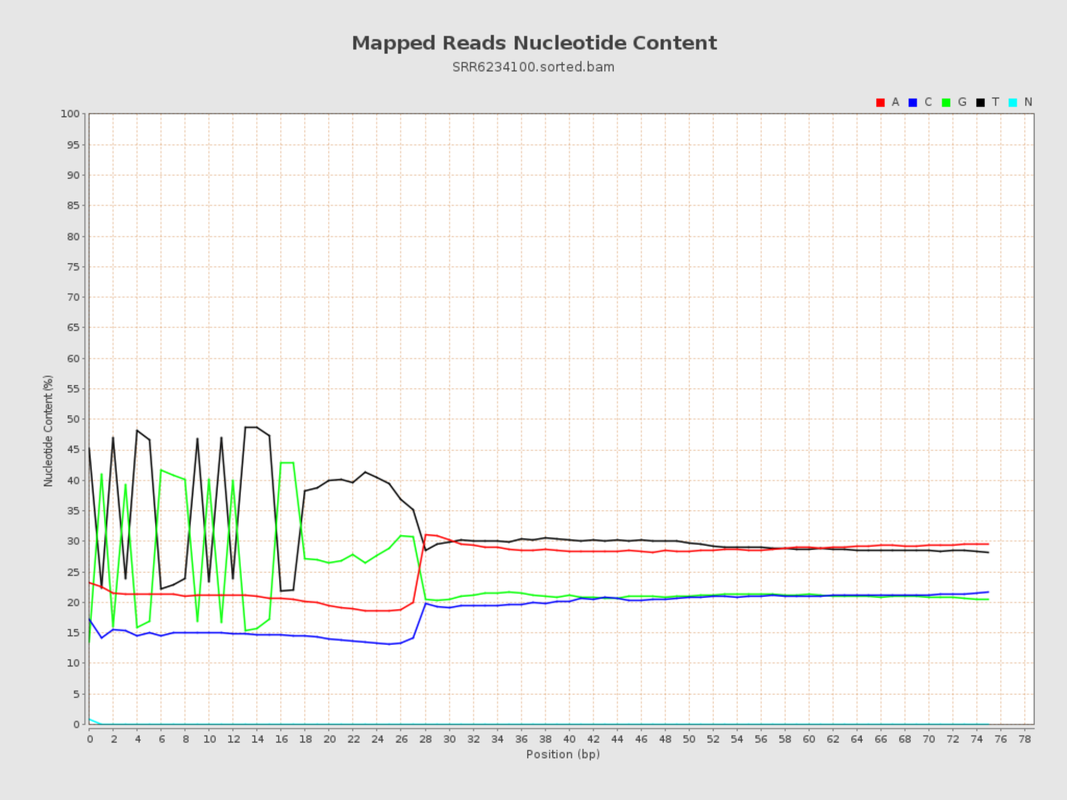
# 6. Results : Genome Fraction Coverage



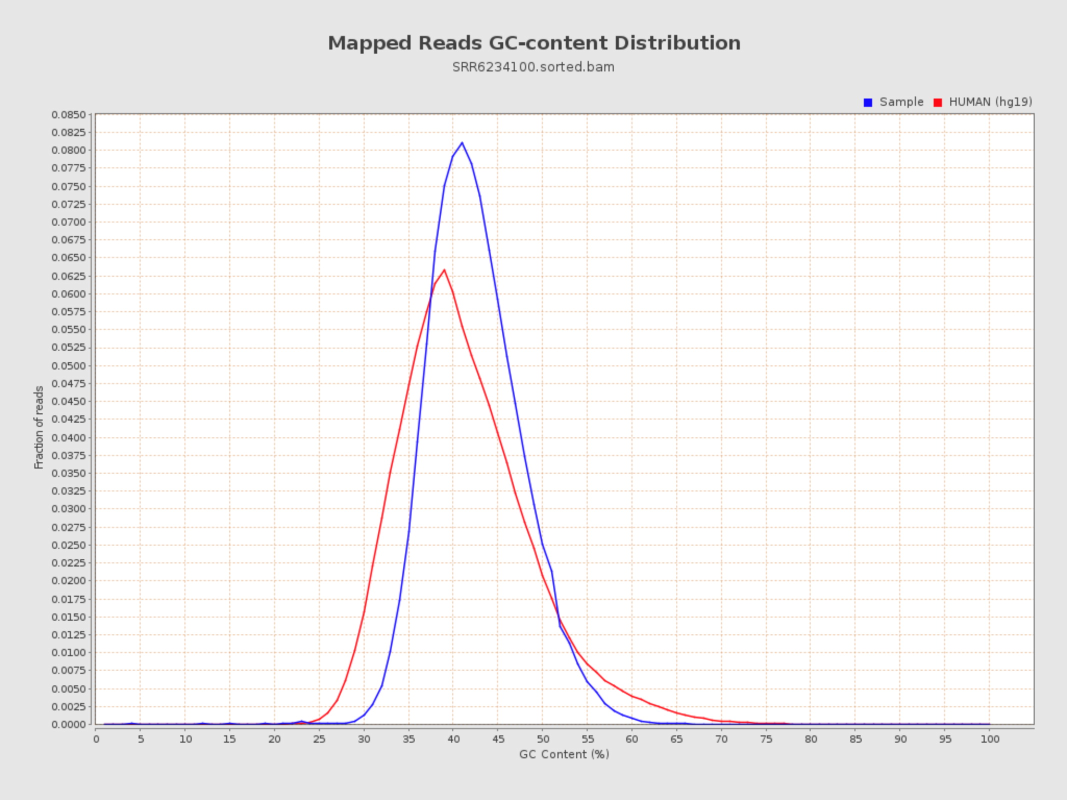
# 7. Results : Duplication Rate Histogram



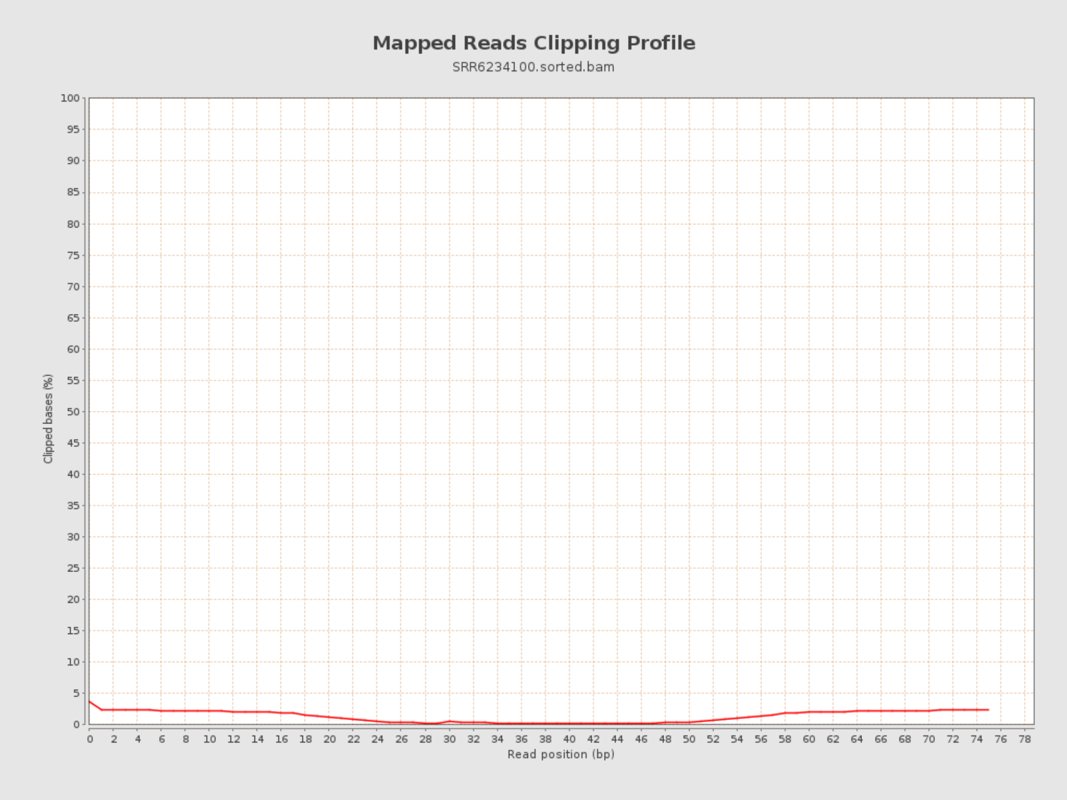
# 8. Results : Mapped Reads Nucleotide Content



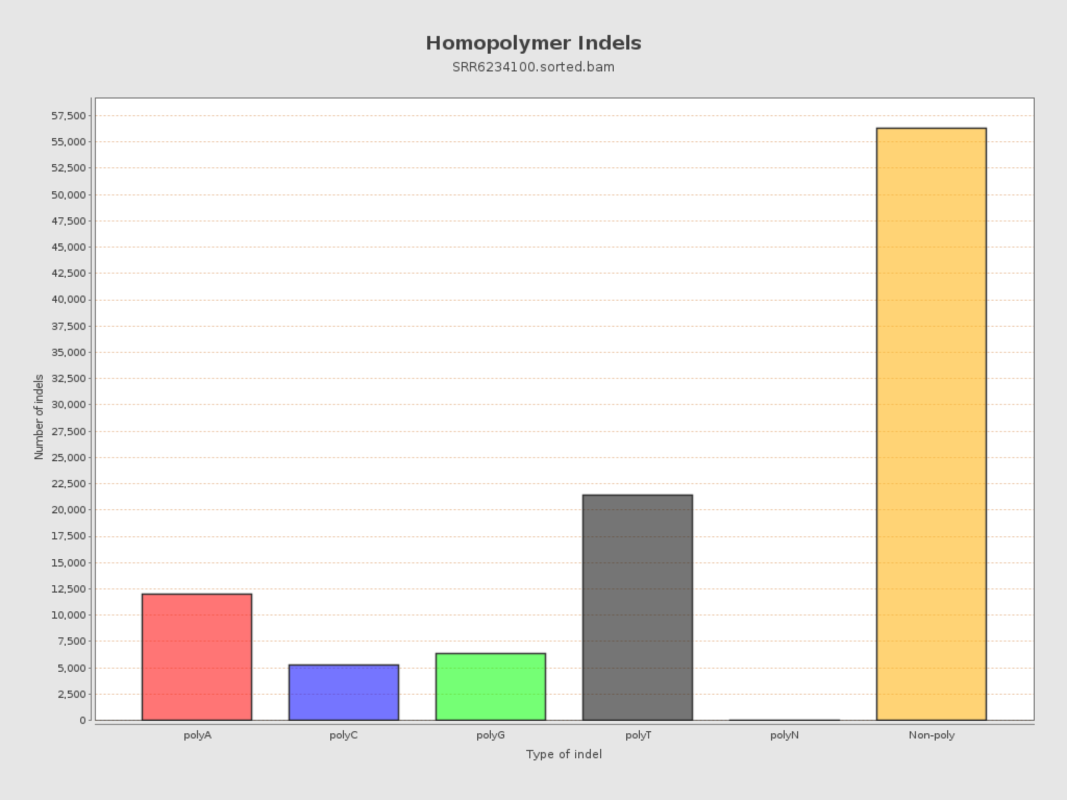
# 9. Results : Mapped Reads GC-content Distribution



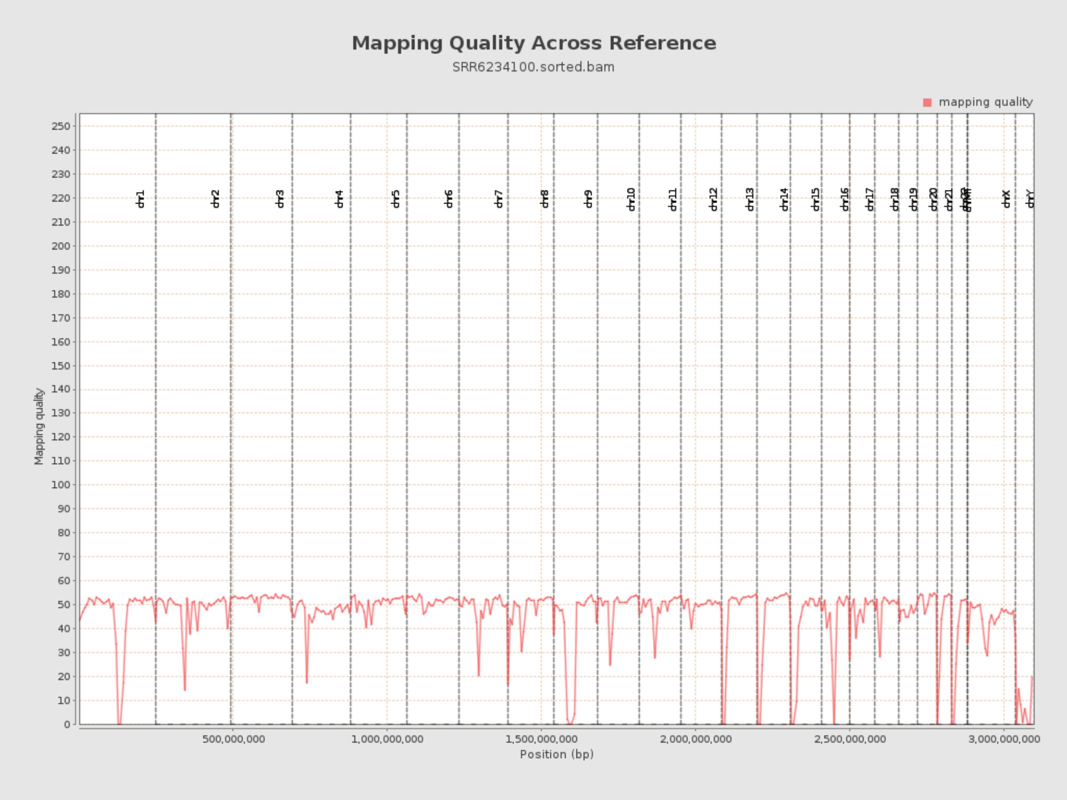
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram