# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/16 18:21:10*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234140.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_SRR6234140 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234140.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 16 18:21:10 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6234140.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 893,417 |
| Mapped reads | 372,217 / 41.66% |
| Unmapped reads | 521,200 / 58.34% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 1,735 / 0.19% |
| Read min/max/mean length | 30 / 76 / 76.07 |
| Duplicated reads (estimated) | 10,658 / 1.19% |
| Duplication rate | 2.37% |
| Clipped reads | 233,968 / 26.19% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 6,362,867 / 27.71% |
| Number/percentage of C's | 3,989,279 / 17.37% |
| Number/percentage of T's | 7,397,019 / 32.21% |
| Number/percentage of G's | 5,211,160 / 22.69% |
| Number/percentage of N's | 2,913 / 0.01% |
| GC Percentage | 40.07% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0074 |
| | |

| | |
|---|---|
| Standard Deviation | 0.107 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.76 |

## 2.5. Mismatches and indels

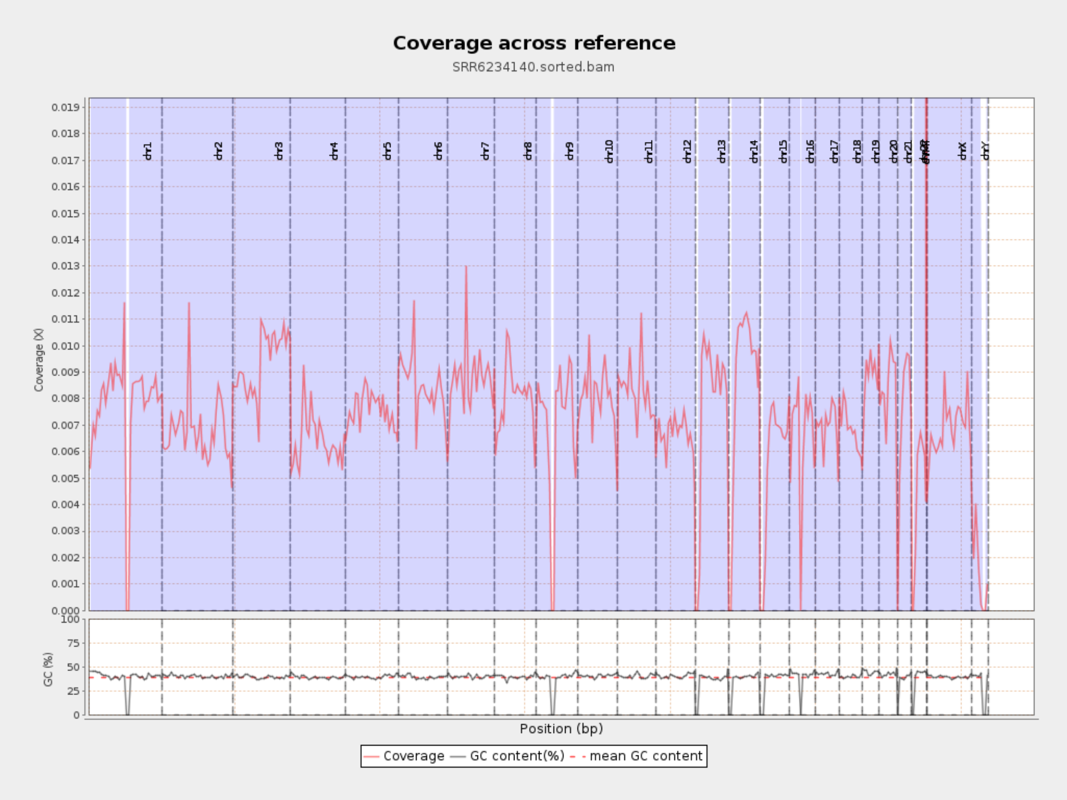
| | |
|---|---|
| General error rate | 1.12% |
| Mismatches | 253,005 |
| Insertions | 2,064 |
| Mapped reads with at least one insertion | 0.55% |
| Deletions | 9,142 |
| Mapped reads with at least one deletion | 2.42% |
| Homopolymer indels | 46.56% |

## 2.6. Chromosome stats

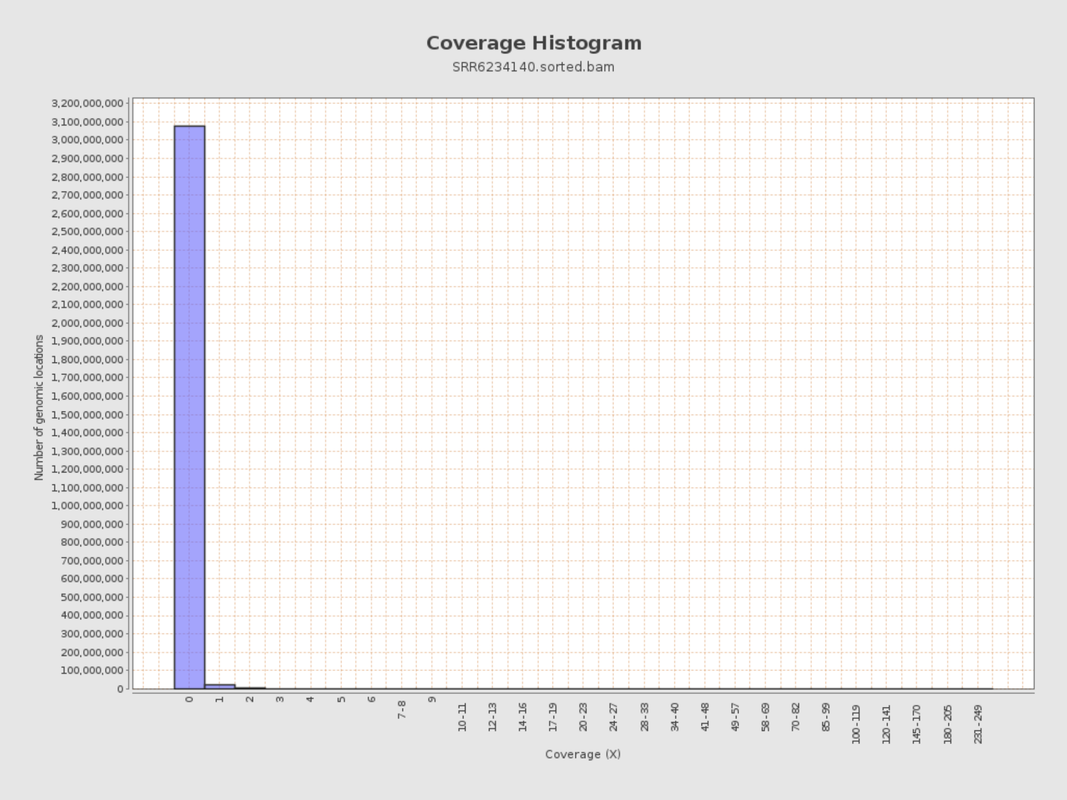
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 1931288 | 0.0077 | 0.1268 |
| chr2 | 243199373 | 1652340 | 0.0068 | 0.11 |
| chr3 | 198022430 | 1850981 | 0.0093 | 0.1044 |
| chr4 | 191154276 | 1221693 | 0.0064 | 0.0875 |
| chr5 | 180915260 | 1369637 | 0.0076 | 0.0938 |
| chr6 | 171115067 | 1455576 | 0.0085 | 0.1042 |
| chr7 | 159138663 | 1404254 | 0.0088 | 0.126 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 1172515 | 0.008 | 0.1722 |
| chr9 | 141213431 | 974977 | 0.0069 | 0.1014 |
| chr10 | 135534747 | 1101459 | 0.0081 | 0.1021 |
| chr11 | 135006516 | 1115018 | 0.0083 | 0.1086 |
| chr12 | 133851895 | 897100 | 0.0067 | 0.0881 |
| chr13 | 115169878 | 873317 | 0.0076 | 0.0947 |
| chr14 | 107349540 | 913877 | 0.0085 | 0.1017 |
| chr15 | 102531392 | 568053 | 0.0055 | 0.0793 |
| chr16 | 90354753 | 594748 | 0.0066 | 0.0899 |
| chr17 | 81195210 | 560815 | 0.0069 | 0.0914 |
| chr18 | 78077248 | 540135 | 0.0069 | 0.1346 |
| chr19 | 59128983 | 521768 | 0.0088 | 0.1093 |
| chr20 | 63025520 | 528574 | 0.0084 | 0.0991 |
| chr21 | 48129895 | 352624 | 0.0073 | 0.0923 |
| chr22 | 51304566 | 216220 | 0.0042 | 0.0692 |
| chrMT | 16571 | 15731 | 0.9493 | 1.2613 |
| chrX | 155270560 | 1064933 | 0.0069 | 0.0916 |
| chrY | 59373566 | 81469 | 0.0014 | 0.0417 |

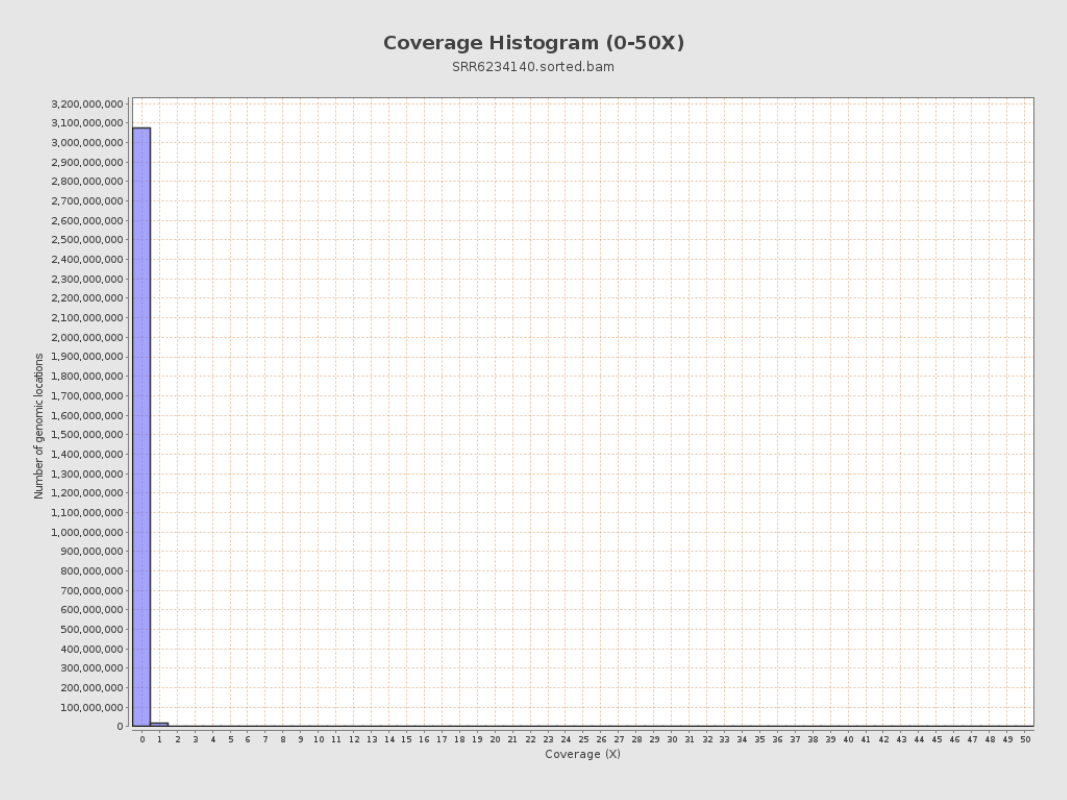
# 3. Results : Coverage across reference



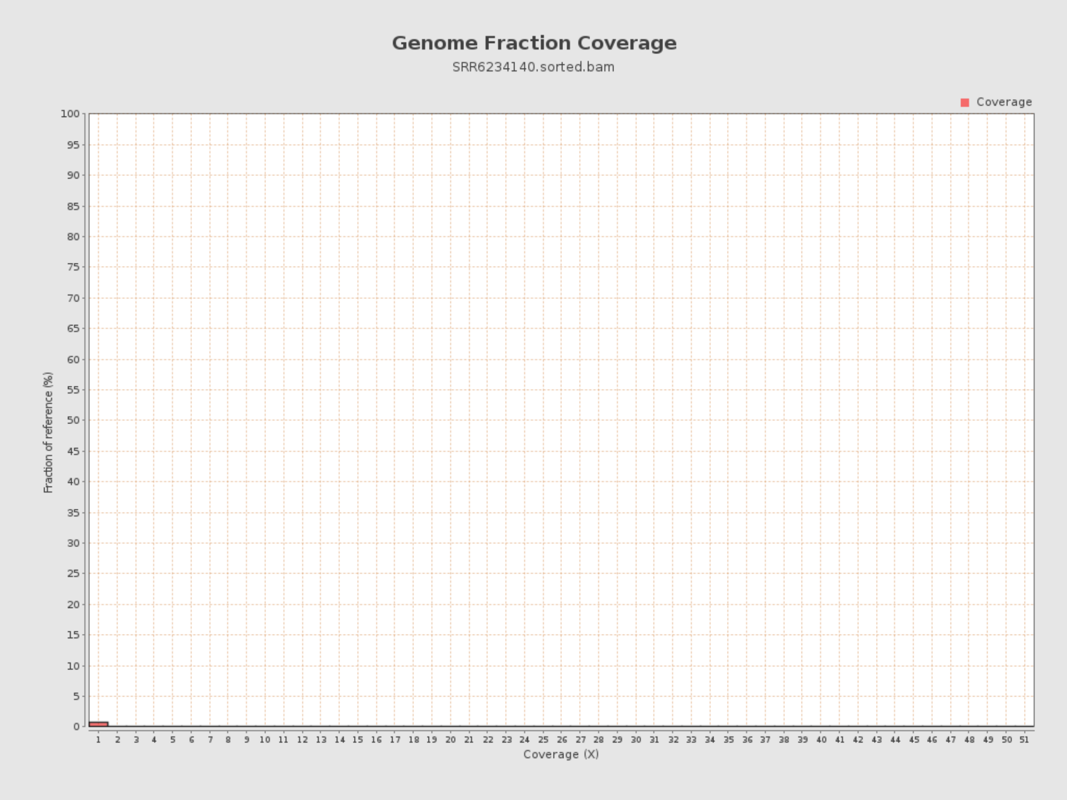
# 4. Results : Coverage Histogram



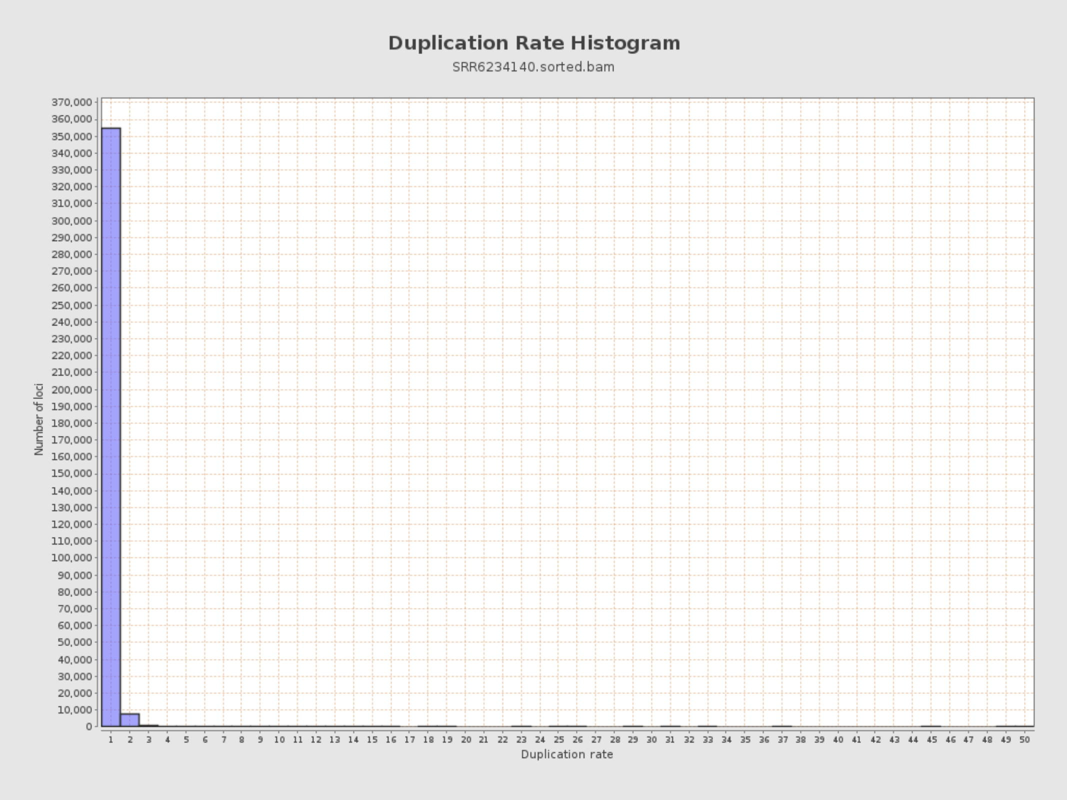
# 5. Results : Coverage Histogram (0-50X)



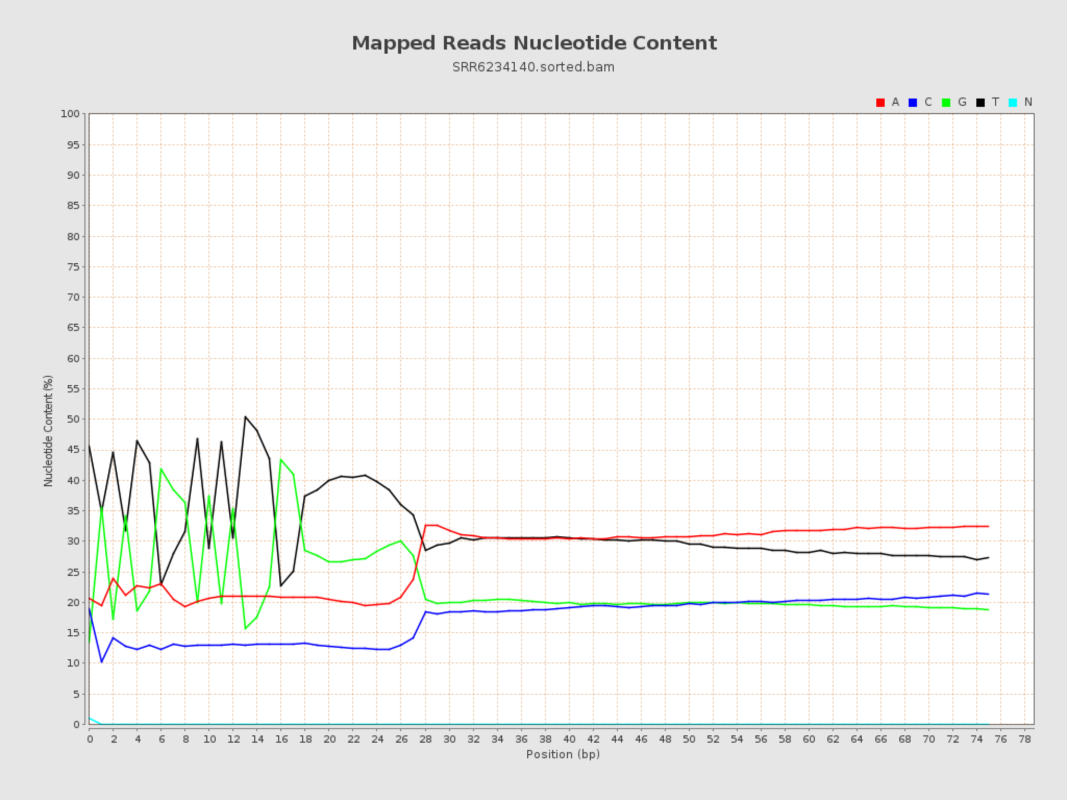
# 6. Results : Genome Fraction Coverage



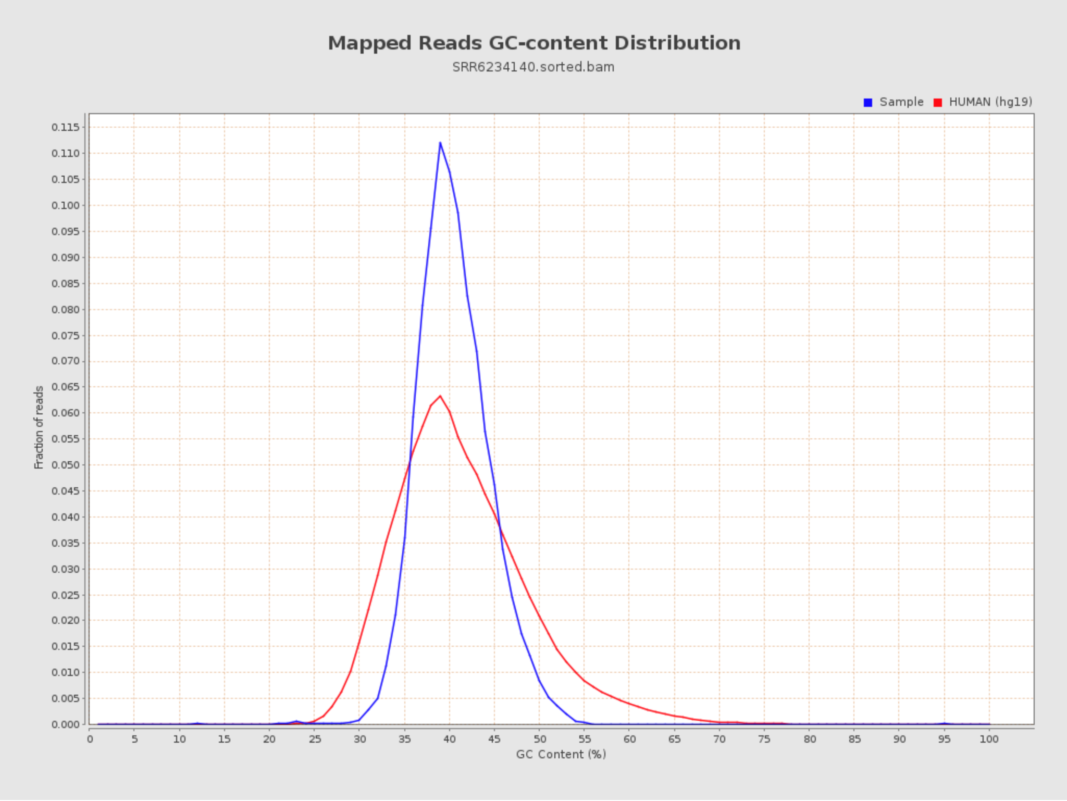
# 7. Results : Duplication Rate Histogram



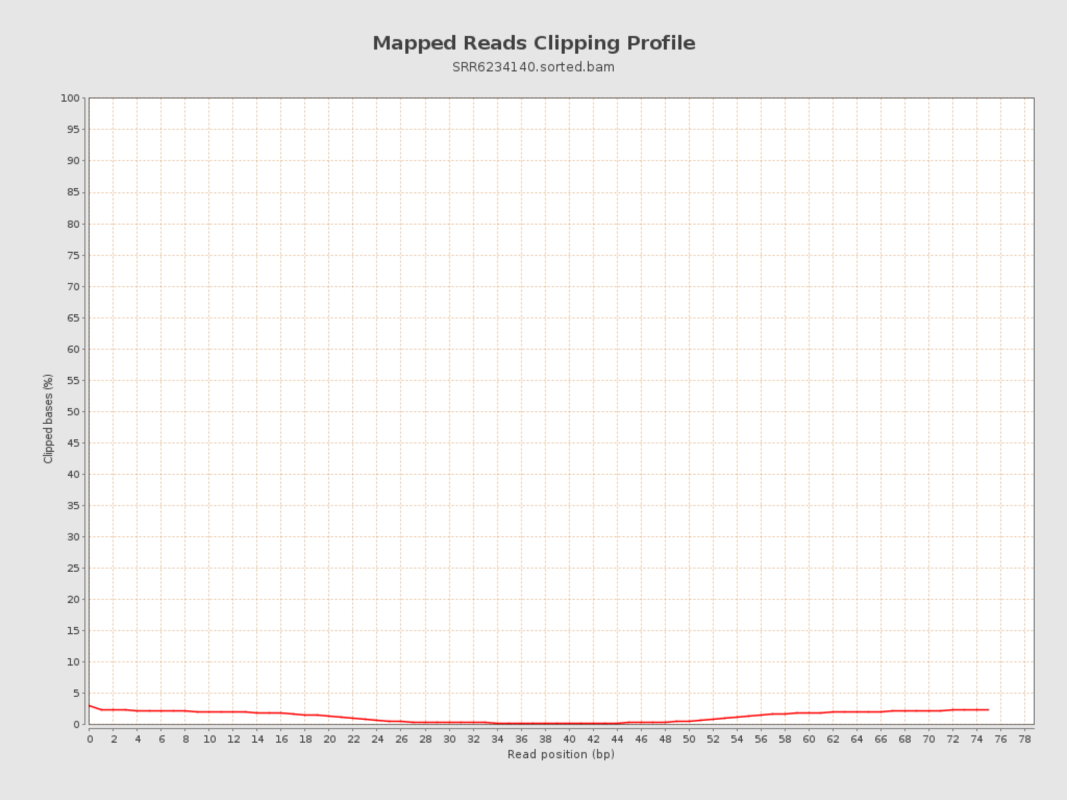
# 8. Results : Mapped Reads Nucleotide Content



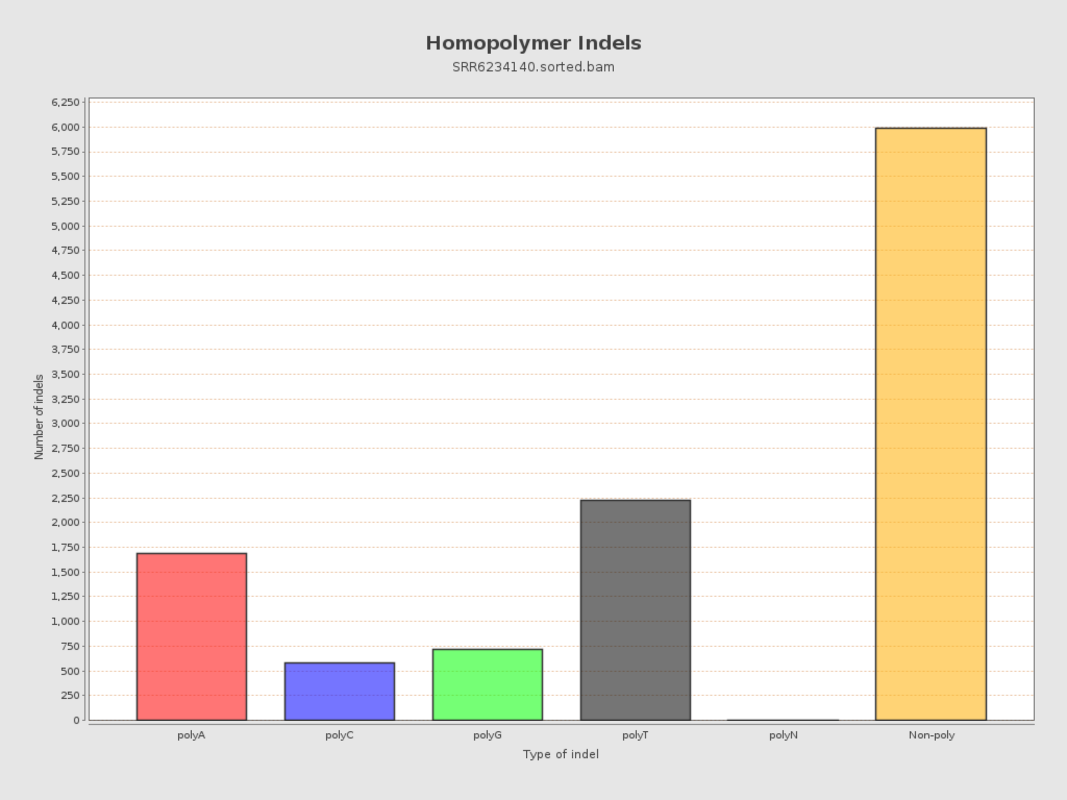
# 9. Results : Mapped Reads GC-content Distribution



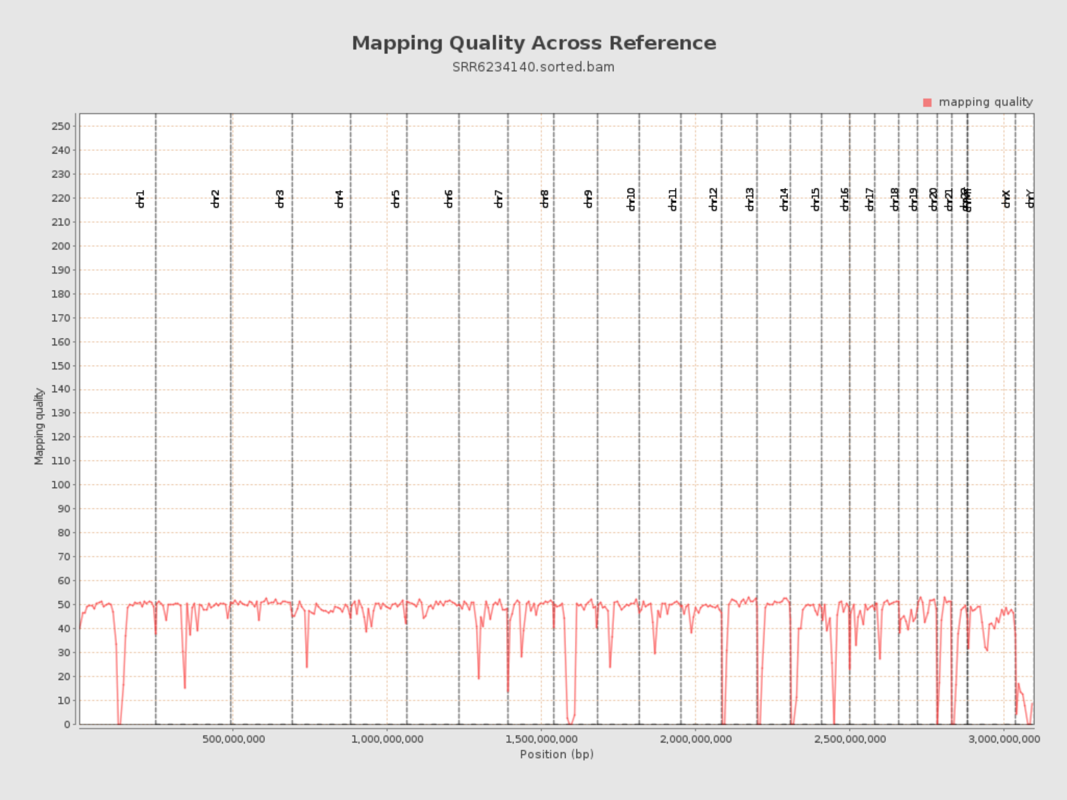
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram