# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/22 04:10:43*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080617.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_SRR3080617 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080617.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 22 04:10:40 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3080617.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,567,638 |
| Mapped reads | 1,790,107 / 69.72% |
| Unmapped reads | 777,531 / 30.28% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 15,095 / 0.59% |
| Read min/max/mean length | 30 / 76 / 76.21 |
| Duplicated reads (estimated) | 118,821 / 4.63% |
| Duplication rate | 5.83% |
| Clipped reads | 854,476 / 33.28% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 32,514,699 / 27.5% |
| Number/percentage of C's | 20,718,282 / 17.53% |
| Number/percentage of T's | 39,080,858 / 33.06% |
| Number/percentage of G's | 25,812,933 / 21.83% |
| Number/percentage of N's | 92,063 / 0.08% |
| GC Percentage | 39.36% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0382 |
| | |

| | |
|---|---|
| Standard Deviation | 0.278 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 47.32 |

## 2.5. Mismatches and indels

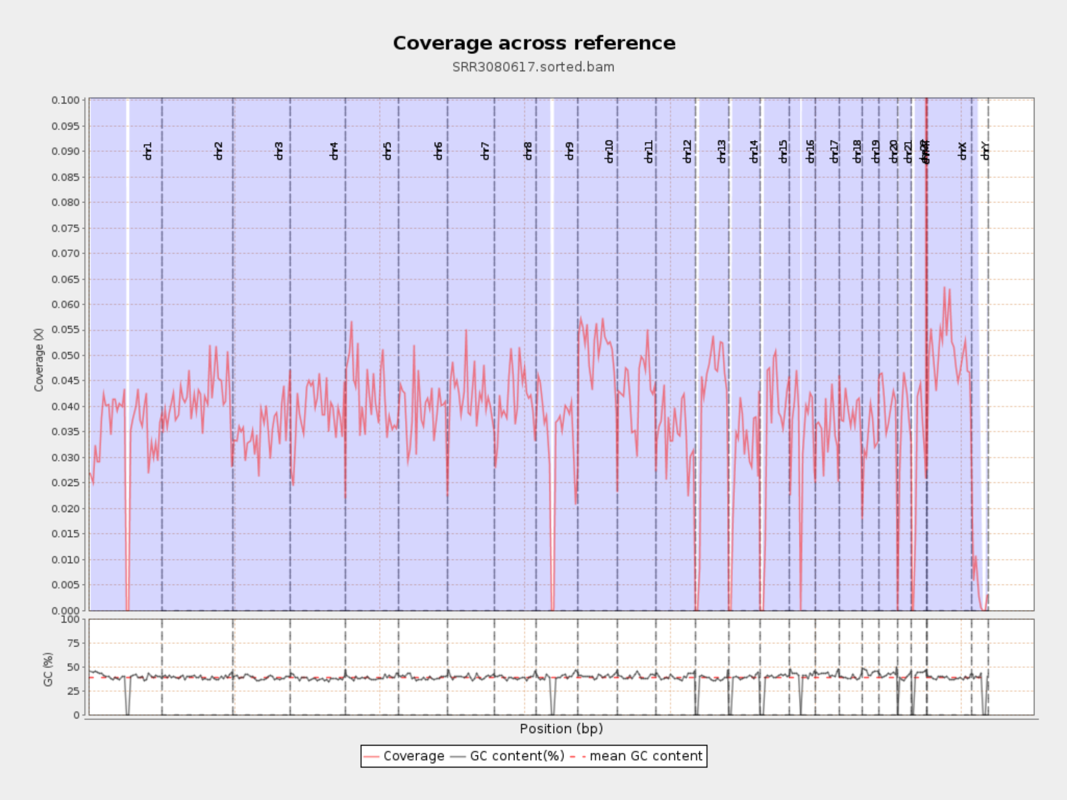
| | |
|---|---|
| General error rate | 0.93% |
| Mismatches | 1,084,553 |
| Insertions | 9,825 |
| Mapped reads with at least one insertion | 0.54% |
| Deletions | 28,031 |
| Mapped reads with at least one deletion | 1.55% |
| Homopolymer indels | 49.24% |

## 2.6. Chromosome stats

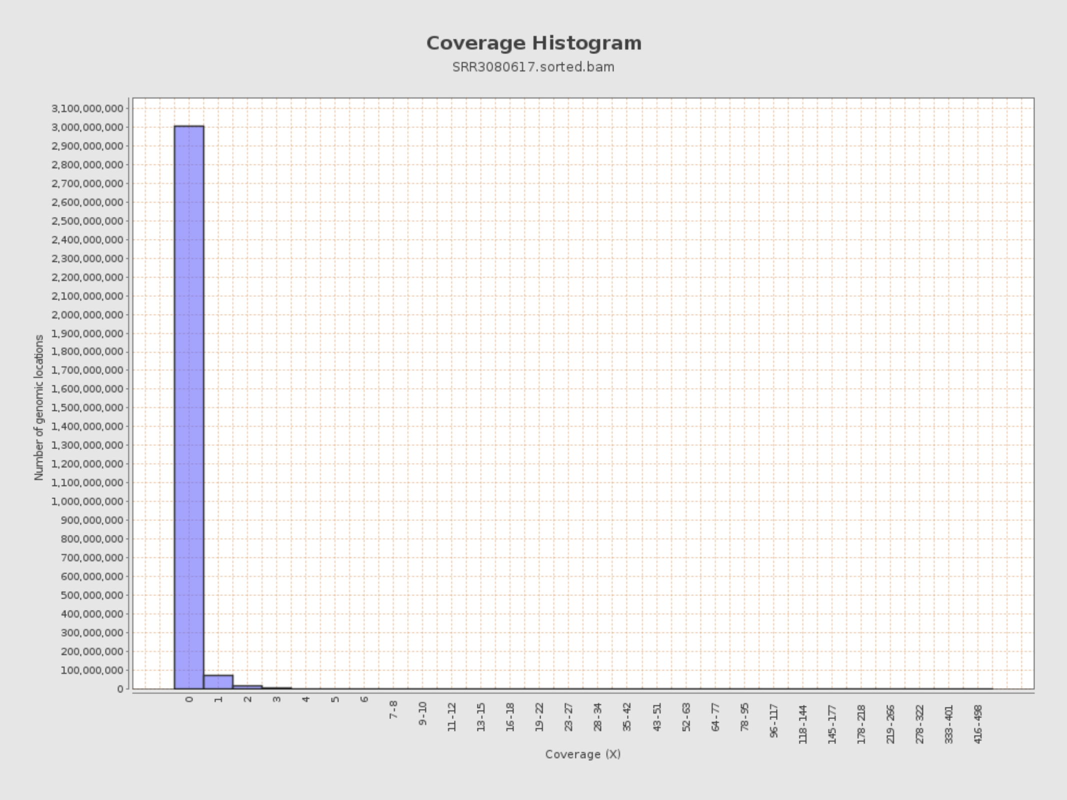
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 8464446 | 0.034 | 0.2973 |
| chr2 | 243199373 | 10165021 | 0.0418 | 0.3061 |
| chr3 | 198022430 | 6988816 | 0.0353 | 0.235 |
| chr4 | 191154276 | 7443812 | 0.0389 | 0.2476 |
| chr5 | 180915260 | 7653821 | 0.0423 | 0.2568 |
| chr6 | 171115067 | 6735832 | 0.0394 | 0.281 |
| chr7 | 159138663 | 6766306 | 0.0425 | 0.3747 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6013867 | 0.0411 | 0.386 |
| chr9 | 141213431 | 4662179 | 0.033 | 0.2546 |
| chr10 | 135534747 | 7041575 | 0.052 | 0.3004 |
| chr11 | 135006516 | 5835068 | 0.0432 | 0.2715 |
| chr12 | 133851895 | 4612092 | 0.0345 | 0.233 |
| chr13 | 115169878 | 4581283 | 0.0398 | 0.2519 |
| chr14 | 107349540 | 3079448 | 0.0287 | 0.2136 |
| chr15 | 102531392 | 3542018 | 0.0345 | 0.231 |
| chr16 | 90354753 | 3114070 | 0.0345 | 0.2381 |
| chr17 | 81195210 | 2838952 | 0.035 | 0.2386 |
| chr18 | 78077248 | 3053676 | 0.0391 | 0.3336 |
| chr19 | 59128983 | 2007059 | 0.0339 | 0.2811 |
| chr20 | 63025520 | 2532121 | 0.0402 | 0.253 |
| chr21 | 48129895 | 1651856 | 0.0343 | 0.2339 |
| chr22 | 51304566 | 1351649 | 0.0263 | 0.1995 |
| chrMT | 16571 | 48756 | 2.9422 | 4.2085 |
| chrX | 155270560 | 7823218 | 0.0504 | 0.289 |
| chrY | 59373566 | 257386 | 0.0043 | 0.0911 |

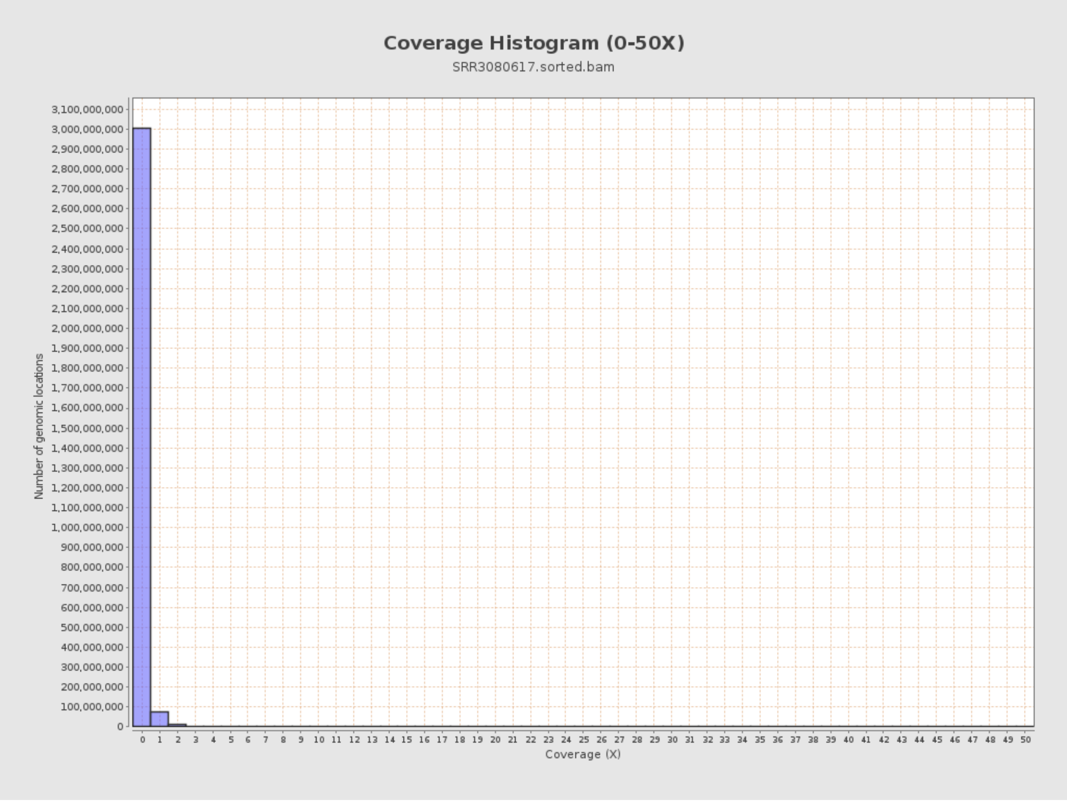
# 3. Results : Coverage across reference



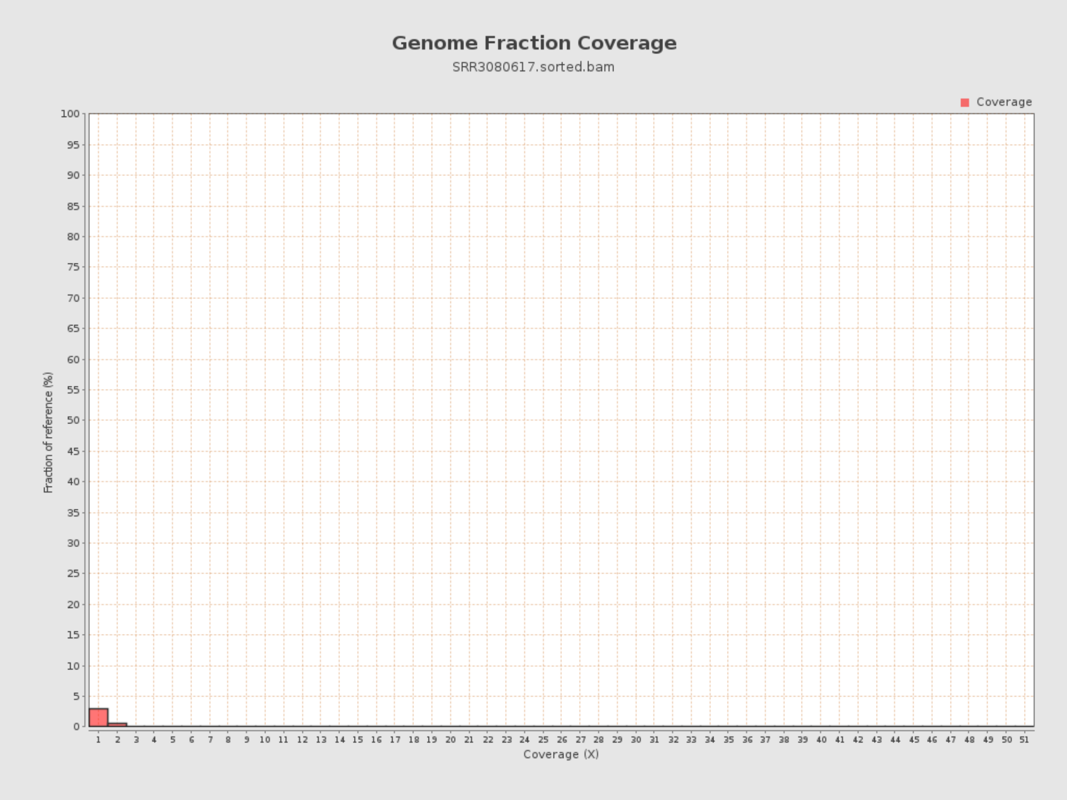
# 4. Results : Coverage Histogram



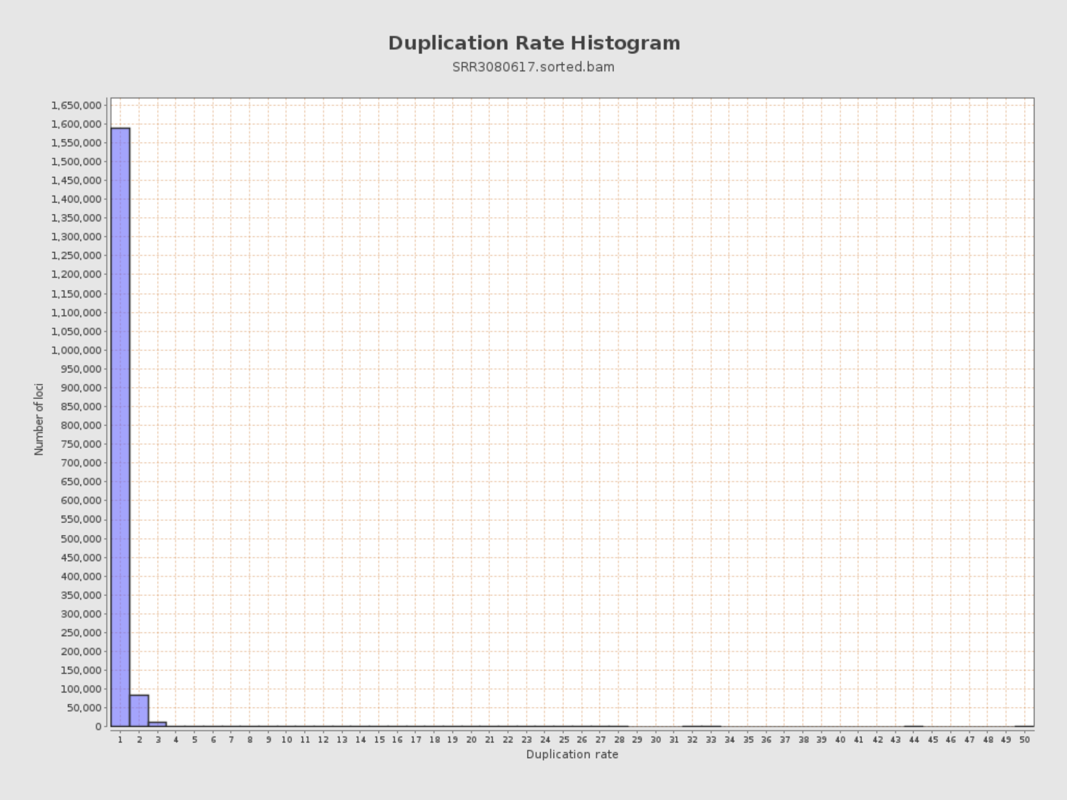
# 5. Results : Coverage Histogram (0-50X)



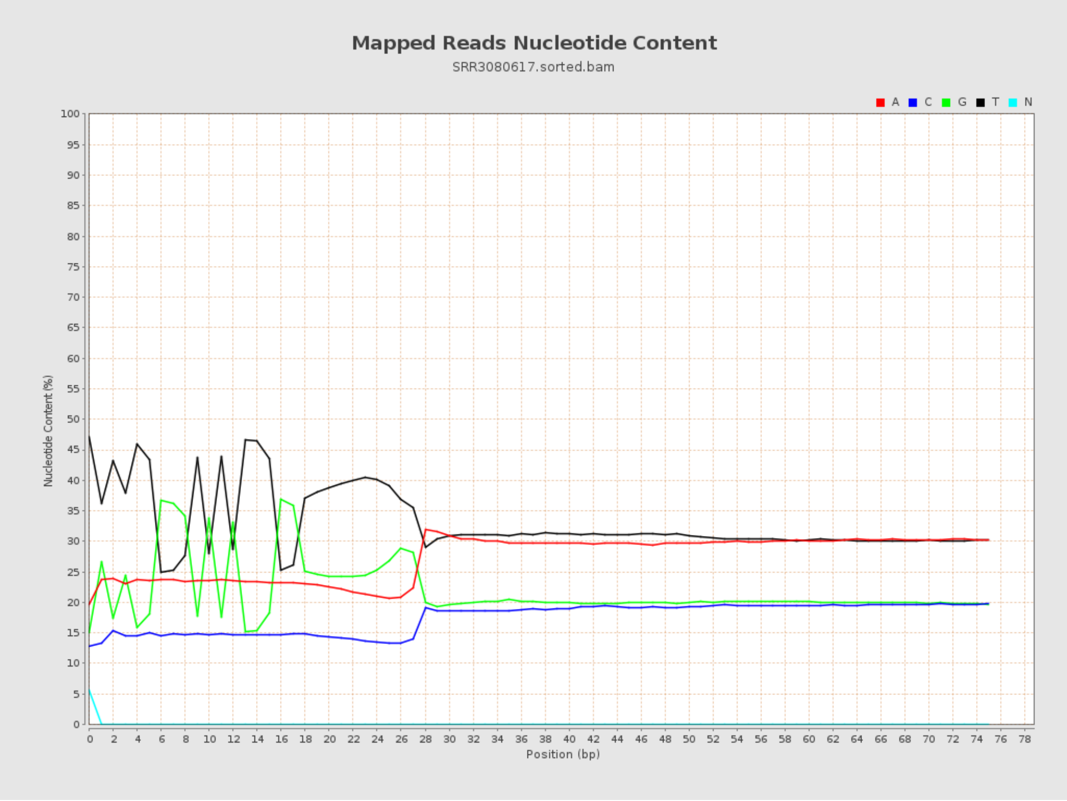
# 6. Results : Genome Fraction Coverage



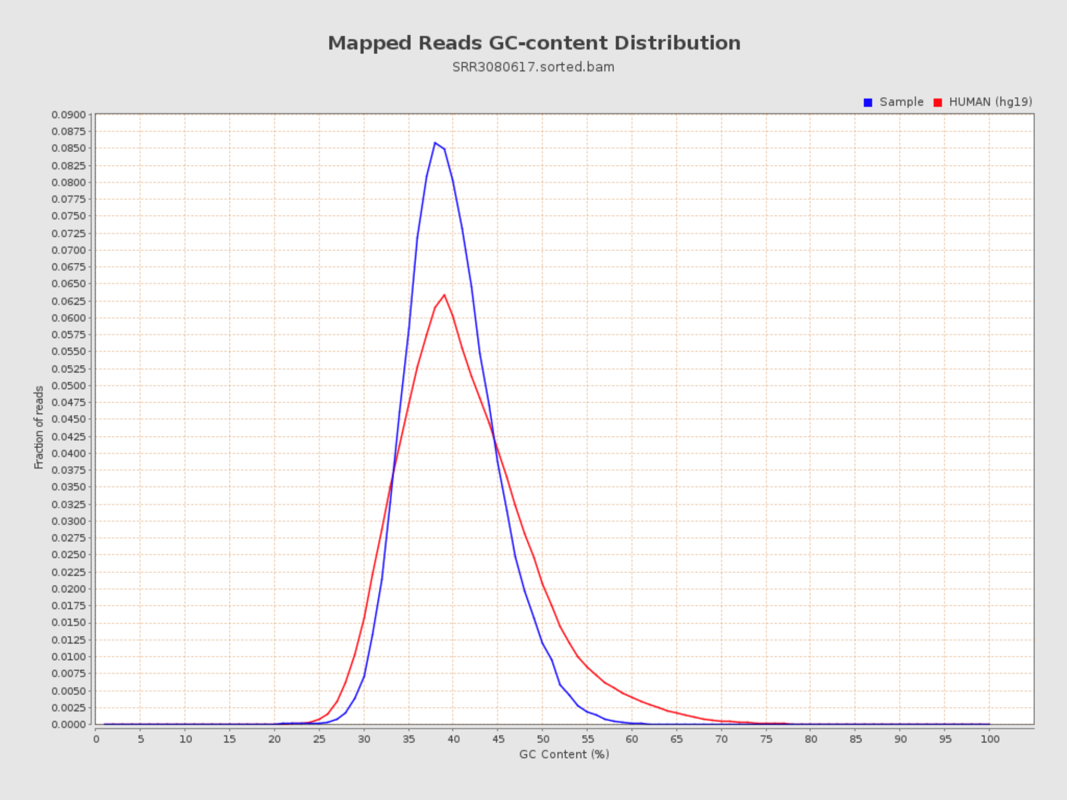
# 7. Results : Duplication Rate Histogram



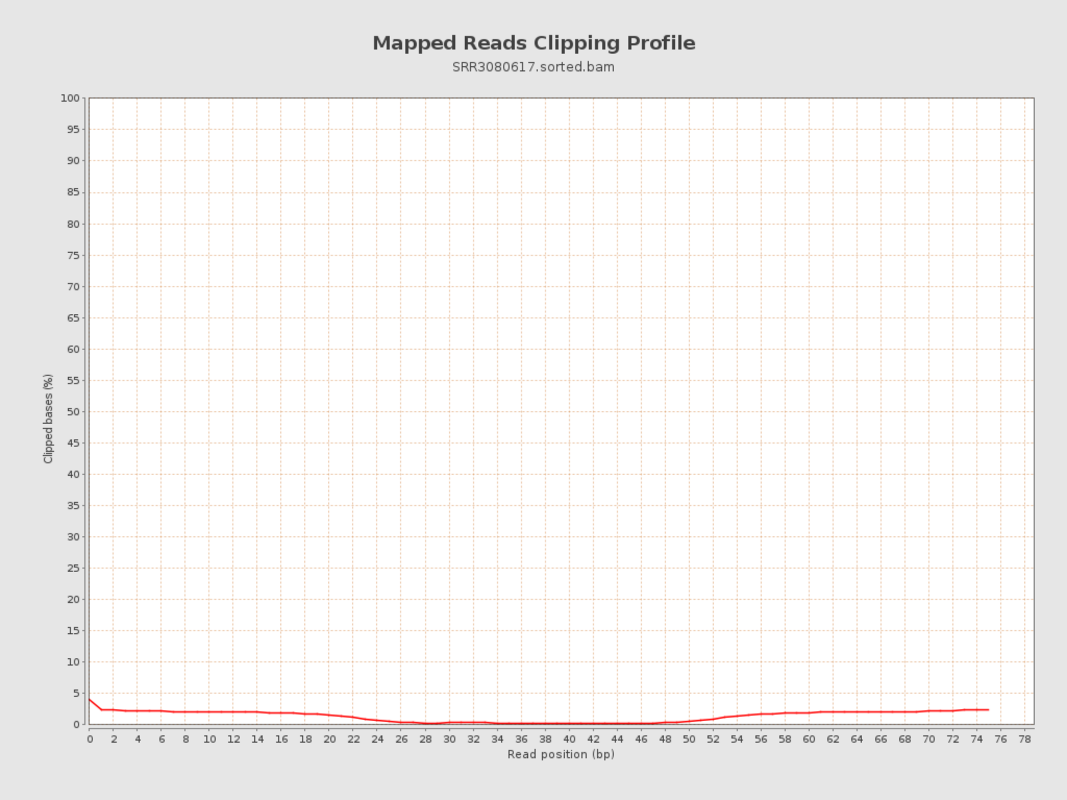
# 8. Results : Mapped Reads Nucleotide Content



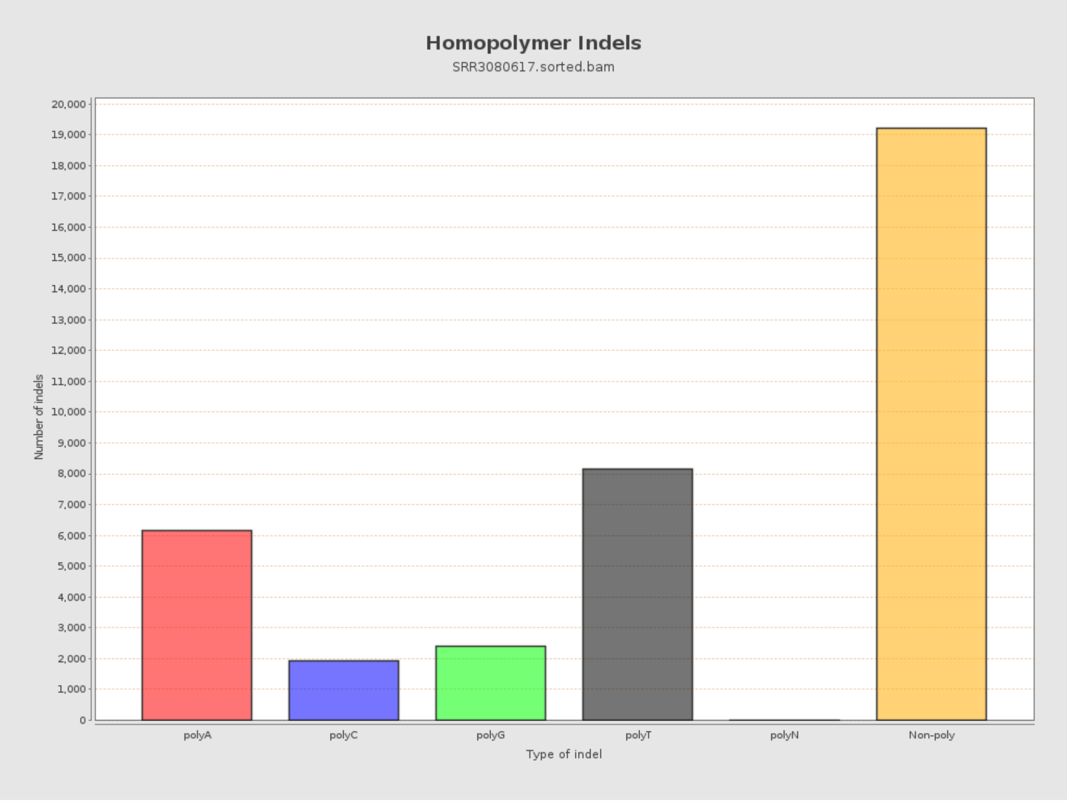
# 9. Results : Mapped Reads GC-content Distribution



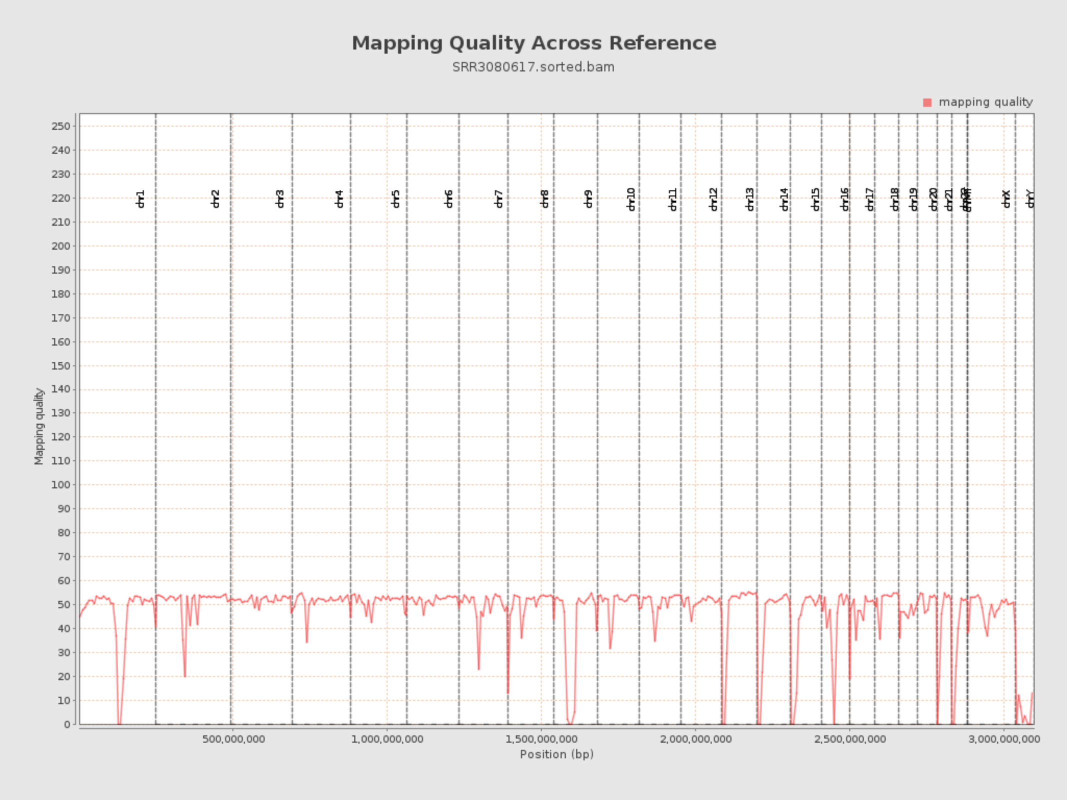
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram