# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 15:18:14*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524658.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_SRR10524658 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524658.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 15:18:12 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524658.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,986,737 |
| Mapped reads | 1,847,069 / 92.97% |
| Unmapped reads | 139,668 / 7.03% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 8,361 / 0.42% |
| Read min/max/mean length | 30 / 76 / 76.14 |
| Duplicated reads (estimated) | 79,660 / 4.01% |
| Duplication rate | 3.17% |
| Clipped reads | 1,851,641 / 93.2% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 26,548,141 / 24.29% |
| Number/percentage of C's | 20,619,404 / 18.86% |
| Number/percentage of T's | 34,918,016 / 31.94% |
| Number/percentage of G's | 27,209,190 / 24.89% |
| Number/percentage of N's | 14,104 / 0.01% |
| GC Percentage | 43.76% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0353 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3271 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.86 |

## 2.5. Mismatches and indels

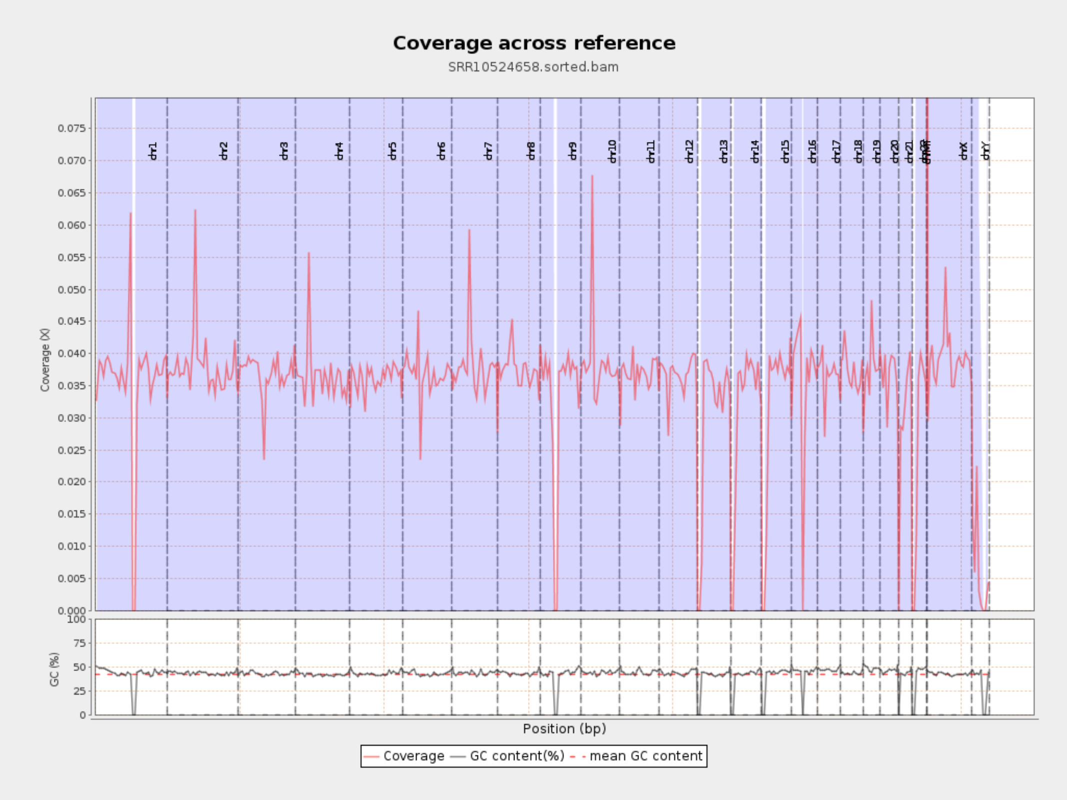
| | |
|---|---|
| General error rate | 0.5% |
| Mismatches | 535,874 |
| Insertions | 7,221 |
| Mapped reads with at least one insertion | 0.39% |
| Deletions | 20,260 |
| Mapped reads with at least one deletion | 1.09% |
| Homopolymer indels | 43.72% |

## 2.6. Chromosome stats

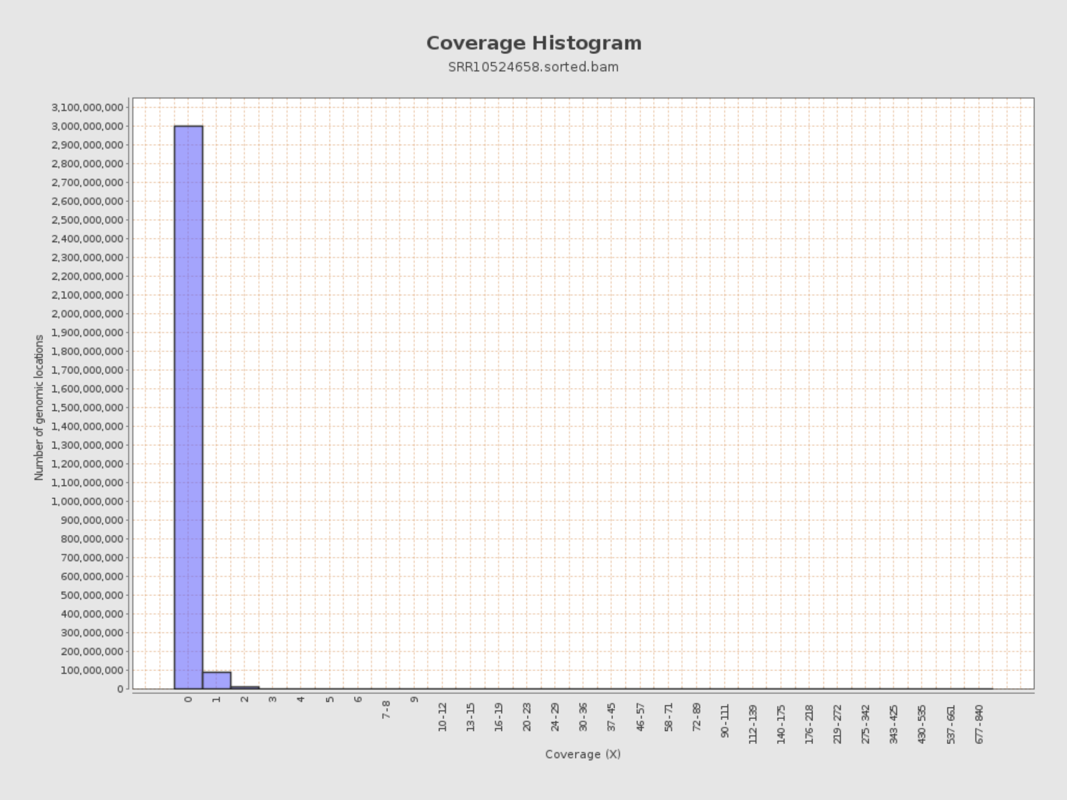
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 8846163 | 0.0355 | 0.607 |
| chr2 | 243199373 | 9262521 | 0.0381 | 0.4369 |
| chr3 | 198022430 | 7271098 | 0.0367 | 0.2095 |
| chr4 | 191154276 | 7001335 | 0.0366 | 0.237 |
| chr5 | 180915260 | 6584023 | 0.0364 | 0.2095 |
| chr6 | 171115067 | 6287062 | 0.0367 | 0.2453 |
| chr7 | 159138663 | 6084959 | 0.0382 | 0.4013 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 5509552 | 0.0376 | 0.3355 |
| chr9 | 141213431 | 4619341 | 0.0327 | 0.2686 |
| chr10 | 135534747 | 5255275 | 0.0388 | 0.3295 |
| chr11 | 135006516 | 4999382 | 0.037 | 0.2785 |
| chr12 | 133851895 | 4918393 | 0.0367 | 0.2119 |
| chr13 | 115169878 | 3428771 | 0.0298 | 0.1903 |
| chr14 | 107349540 | 3279011 | 0.0305 | 0.2011 |
| chr15 | 102531392 | 3150645 | 0.0307 | 0.1912 |
| chr16 | 90354753 | 3168744 | 0.0351 | 0.2235 |
| chr17 | 81195210 | 2972594 | 0.0366 | 0.2266 |
| chr18 | 78077248 | 2909099 | 0.0373 | 0.502 |
| chr19 | 59128983 | 2252837 | 0.0381 | 0.4587 |
| chr20 | 63025520 | 2299530 | 0.0365 | 0.2122 |
| chr21 | 48129895 | 1450770 | 0.0301 | 0.2188 |
| chr22 | 51304566 | 1310783 | 0.0255 | 0.1757 |
| chrMT | 16571 | 30794 | 1.8583 | 1.7279 |
| chrX | 155270560 | 6089763 | 0.0392 | 0.2387 |
| chrY | 59373566 | 358821 | 0.006 | 0.2216 |

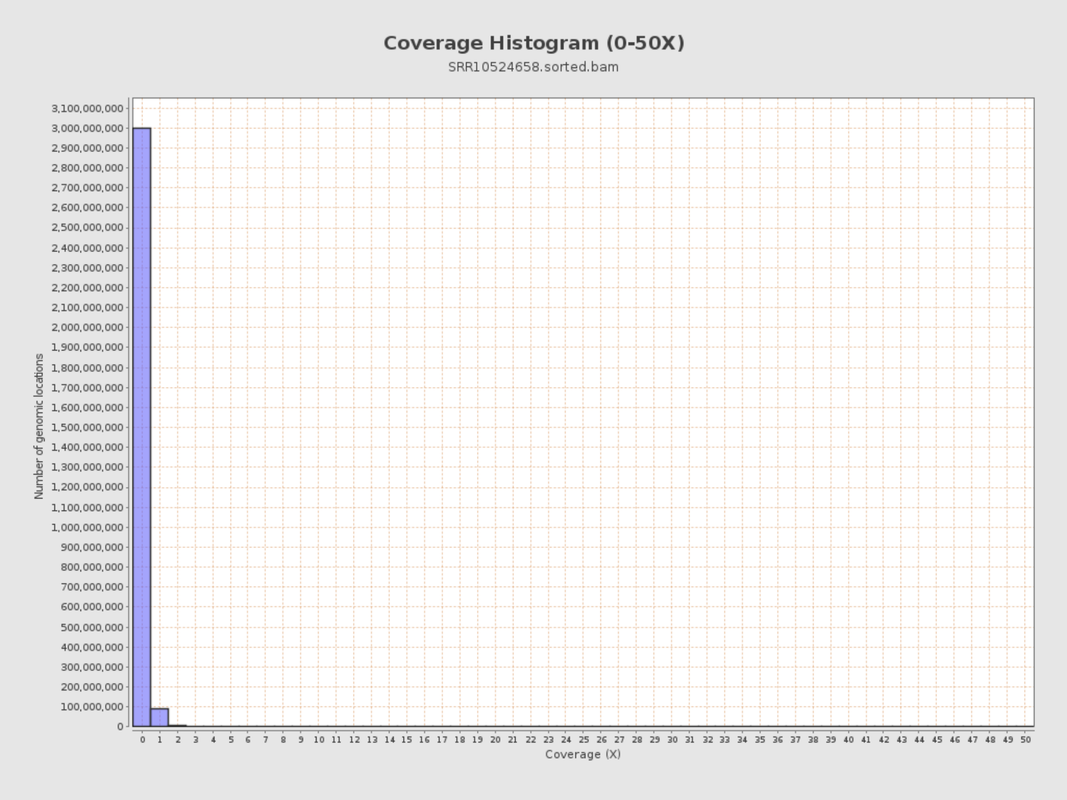
# 3. Results : Coverage across reference



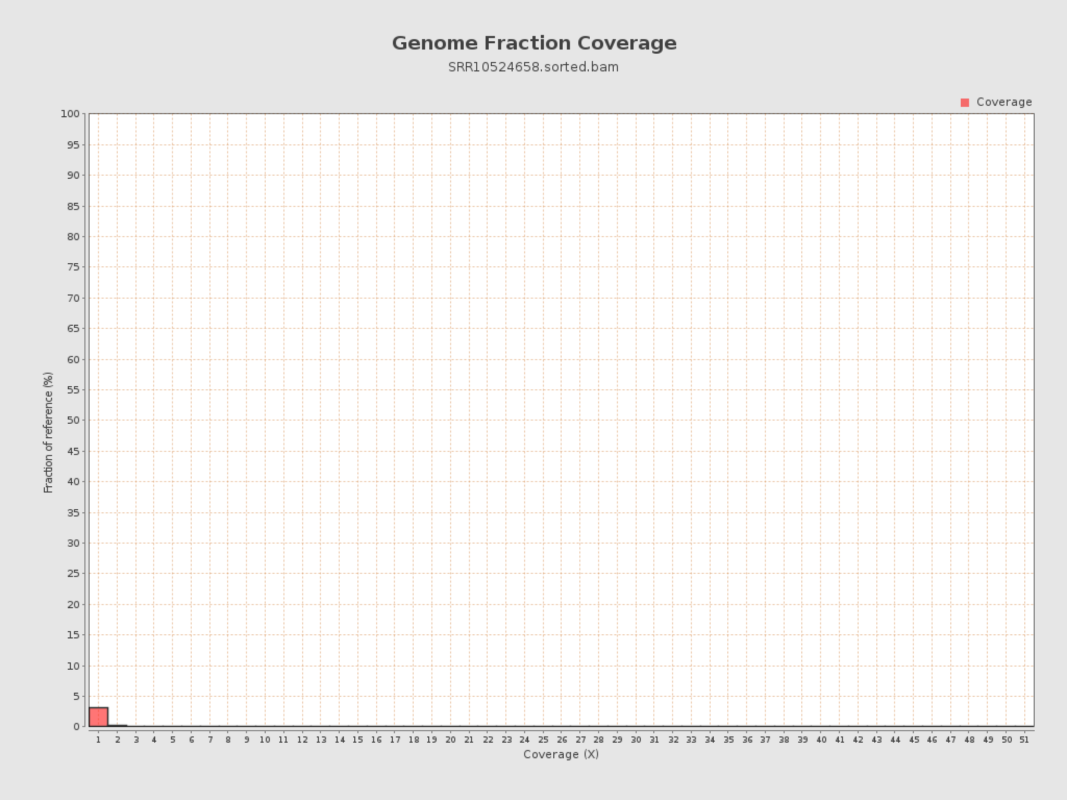
# 4. Results : Coverage Histogram



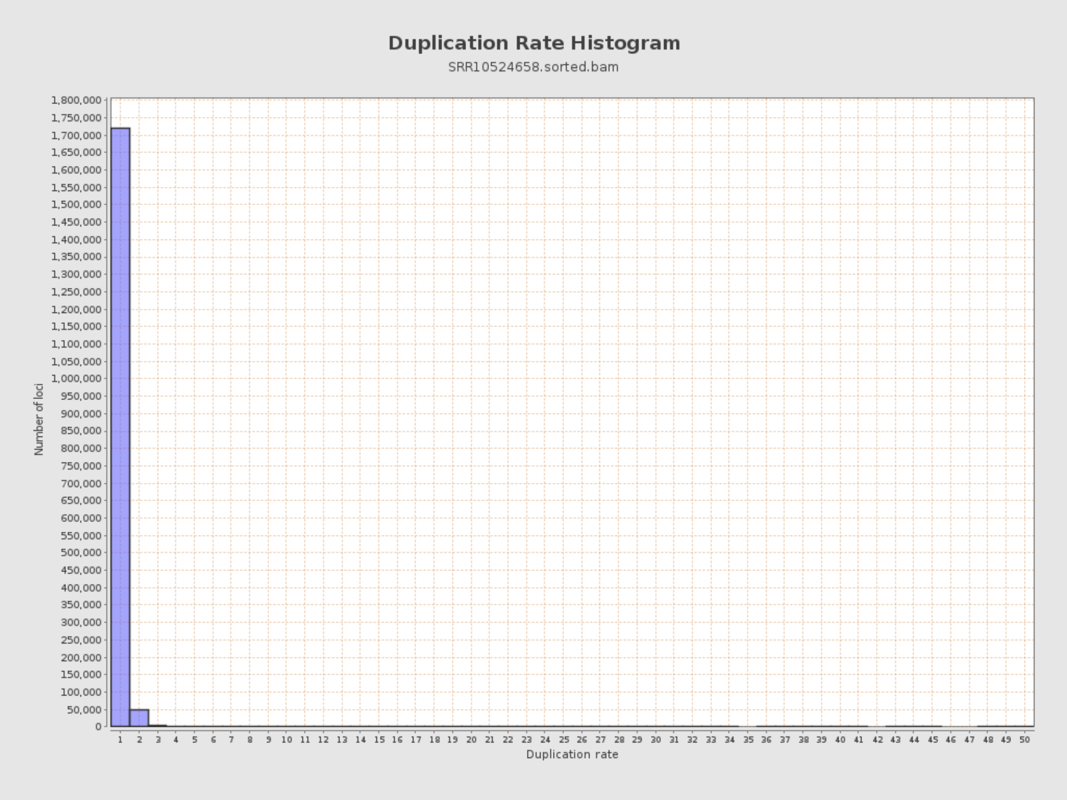
# 5. Results : Coverage Histogram (0-50X)



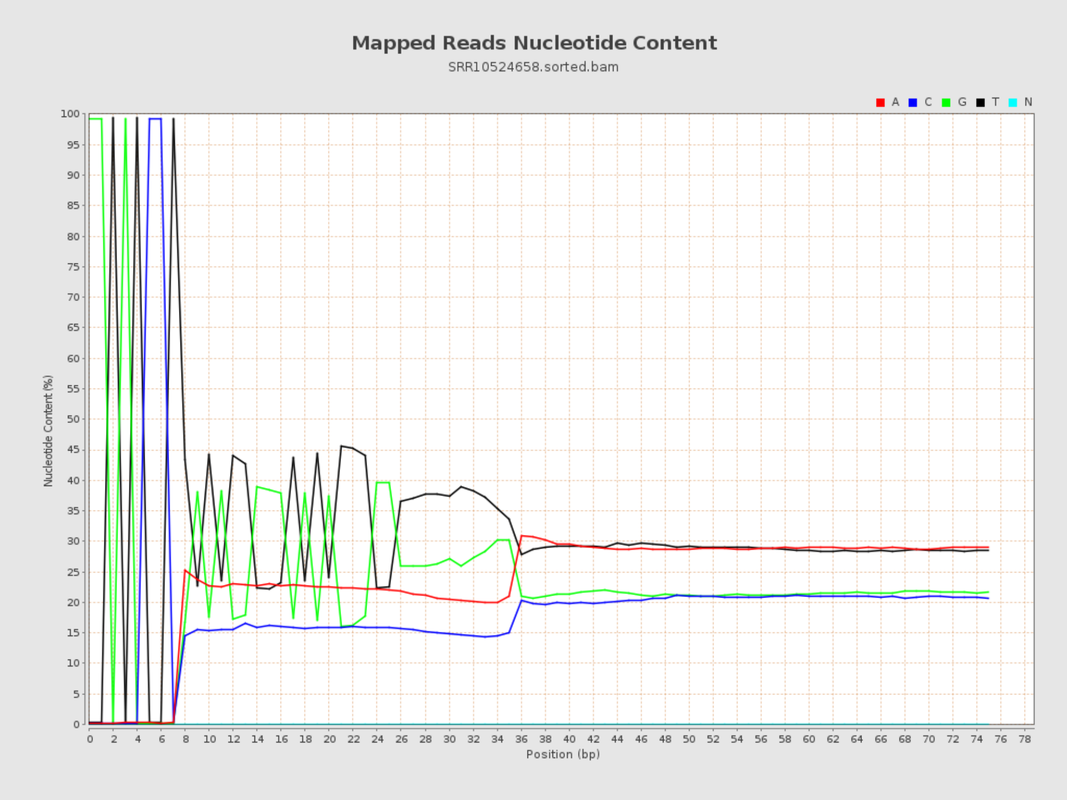
# 6. Results : Genome Fraction Coverage



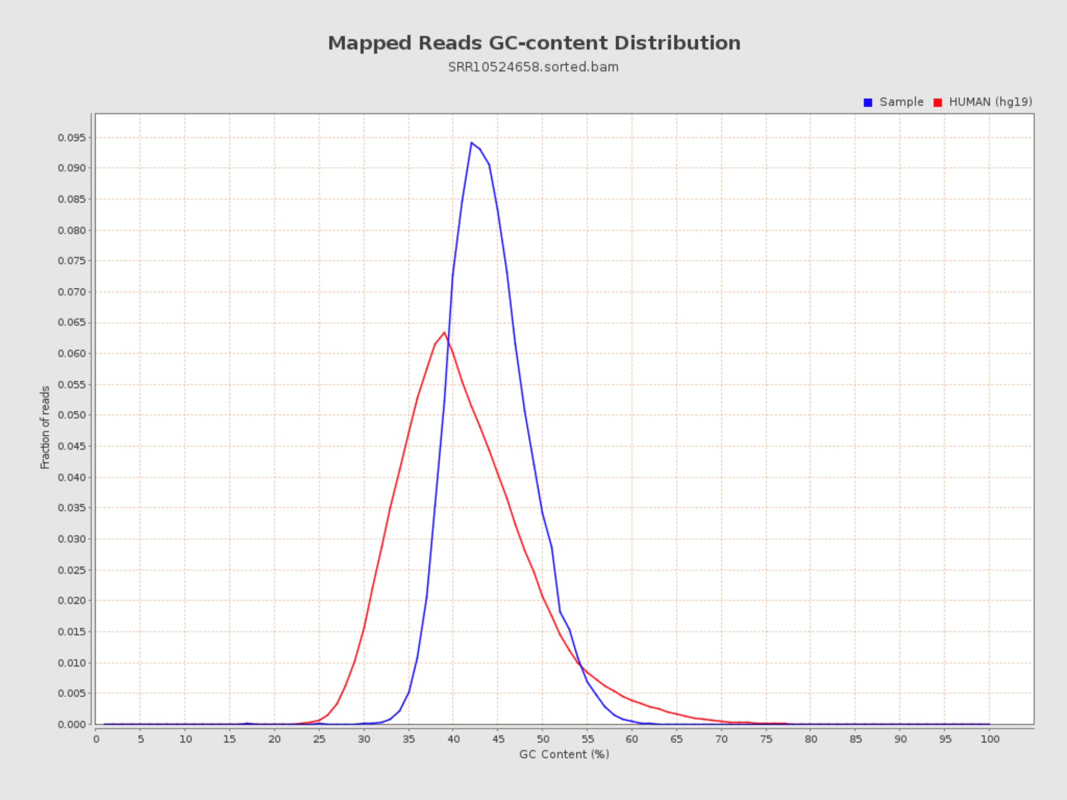
# 7. Results : Duplication Rate Histogram



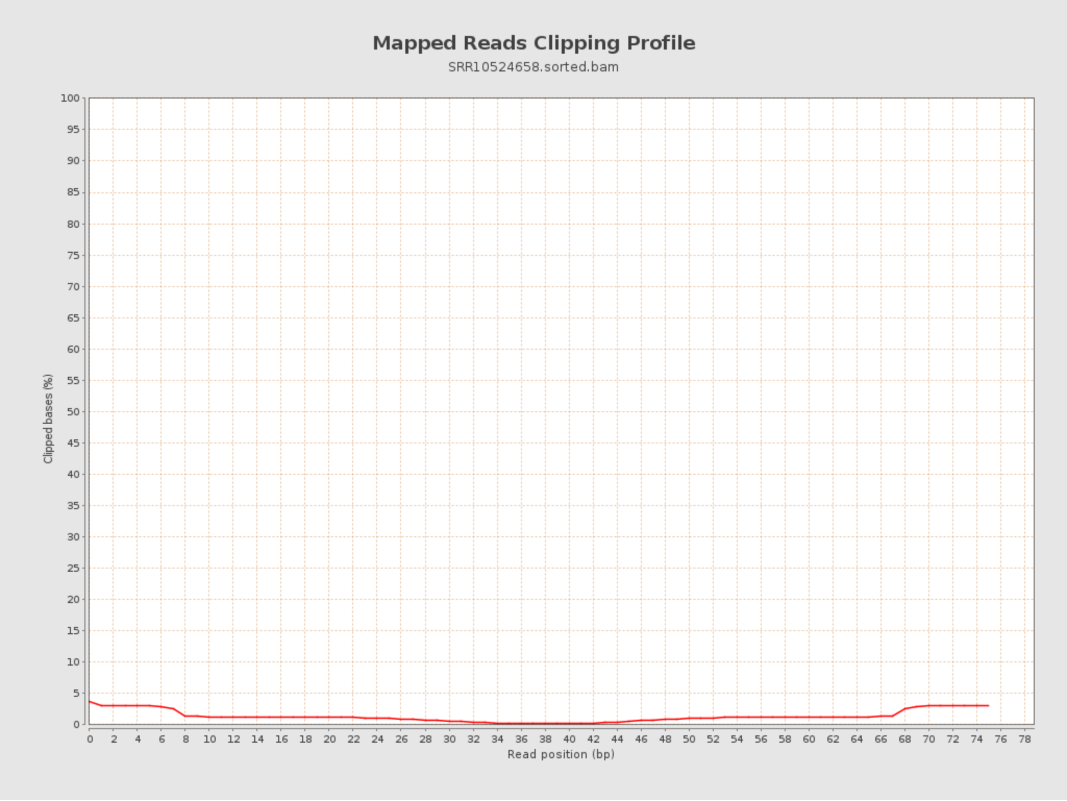
# 8. Results : Mapped Reads Nucleotide Content



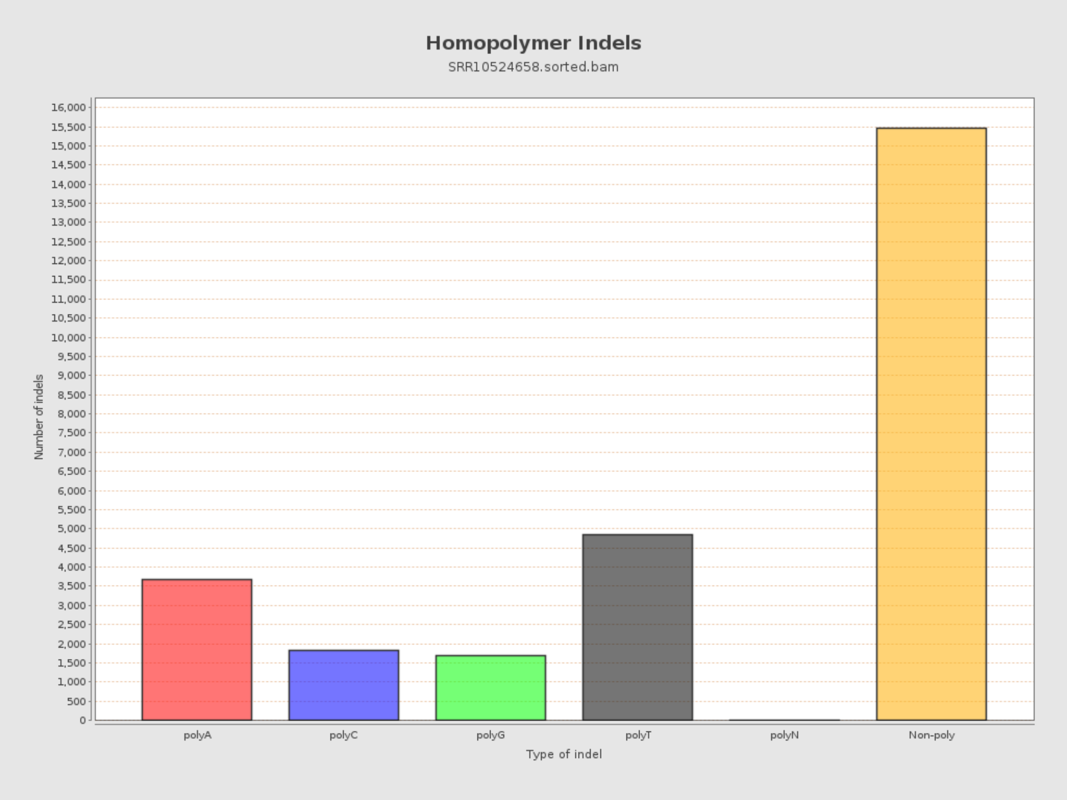
# 9. Results : Mapped Reads GC-content Distribution



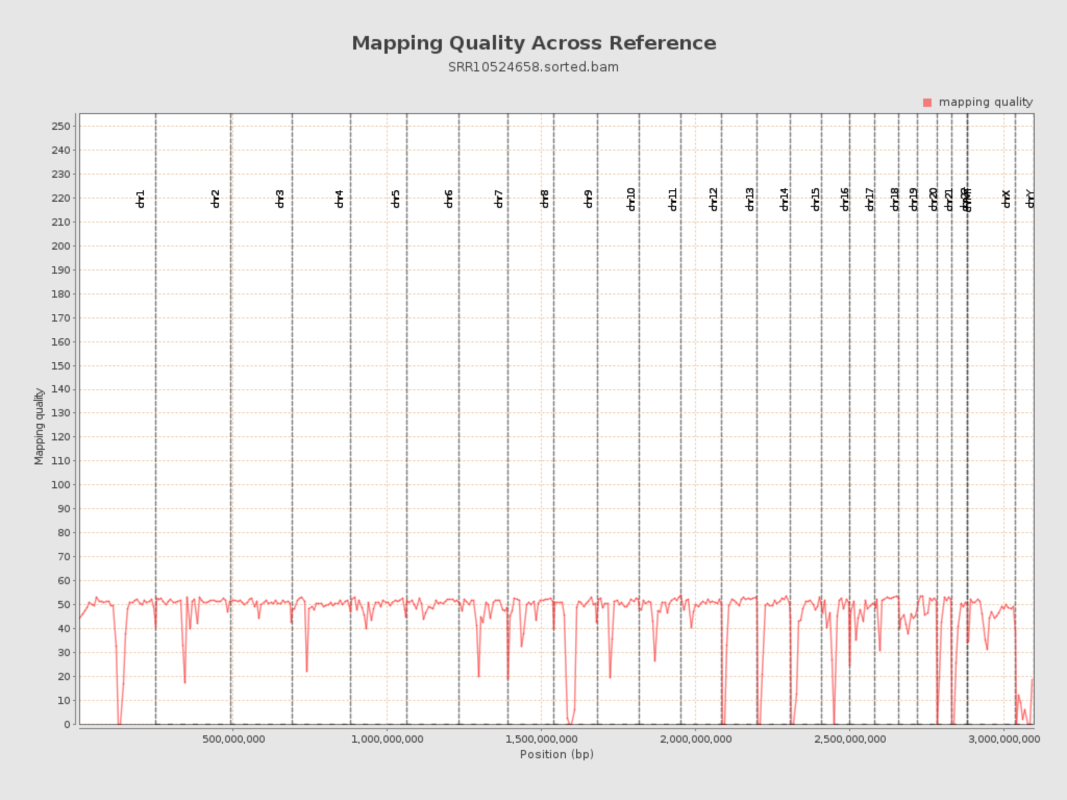
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram