# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/25 08:28:23*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084261.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_SRR3084261 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084261.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Aug 25 08:28:20 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3084261.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,784,822 |
| Mapped reads | 1,666,983 / 59.86% |
| Unmapped reads | 1,117,839 / 40.14% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 7,238 / 0.26% |
| Read min/max/mean length | 30 / 76 / 76.09 |
| Duplicated reads (estimated) | 51,313 / 1.84% |
| Duplication rate | 2.49% |
| Clipped reads | 1,040,030 / 37.35% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 29,027,020 / 28.53% |
| Number/percentage of C's | 19,874,231 / 19.53% |
| Number/percentage of T's | 30,173,843 / 29.65% |
| Number/percentage of G's | 22,679,179 / 22.29% |
| Number/percentage of N's | 1,129 / 0% |
| GC Percentage | 41.82% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0329 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2591 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.16 |

## 2.5. Mismatches and indels

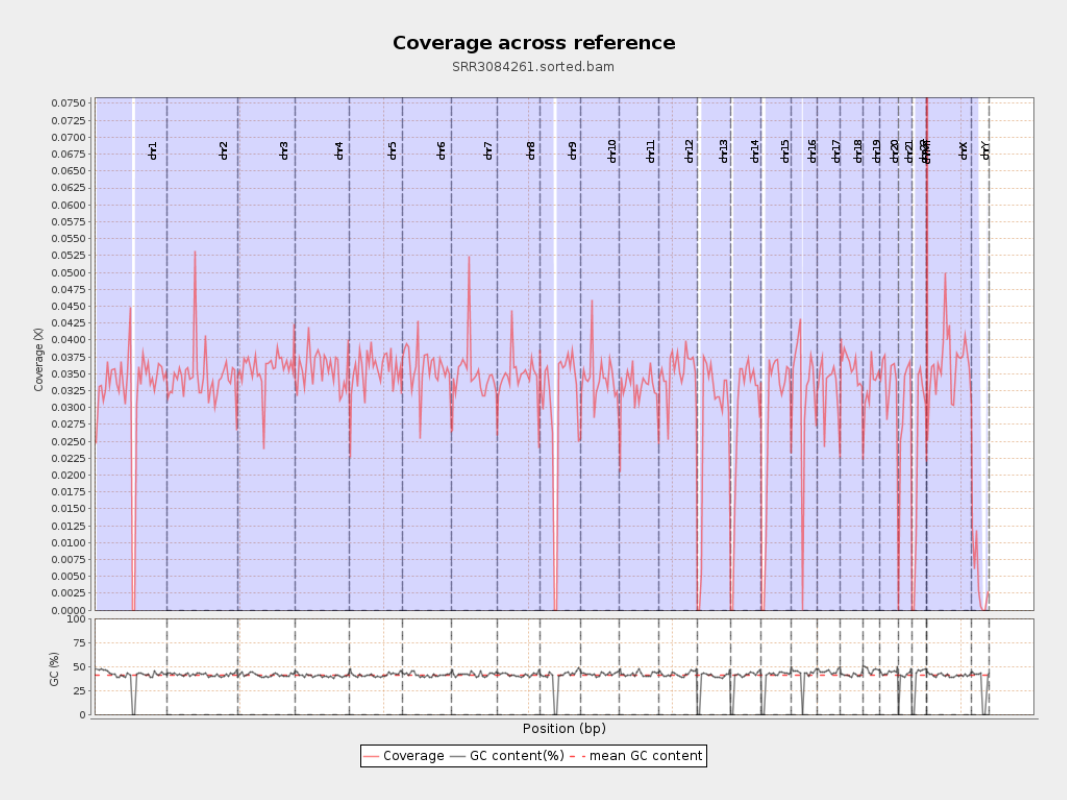
| | |
|---|---|
| General error rate | 0.82% |
| Mismatches | 823,699 |
| Insertions | 7,189 |
| Mapped reads with at least one insertion | 0.43% |
| Deletions | 20,532 |
| Mapped reads with at least one deletion | 1.22% |
| Homopolymer indels | 45.56% |

## 2.6. Chromosome stats

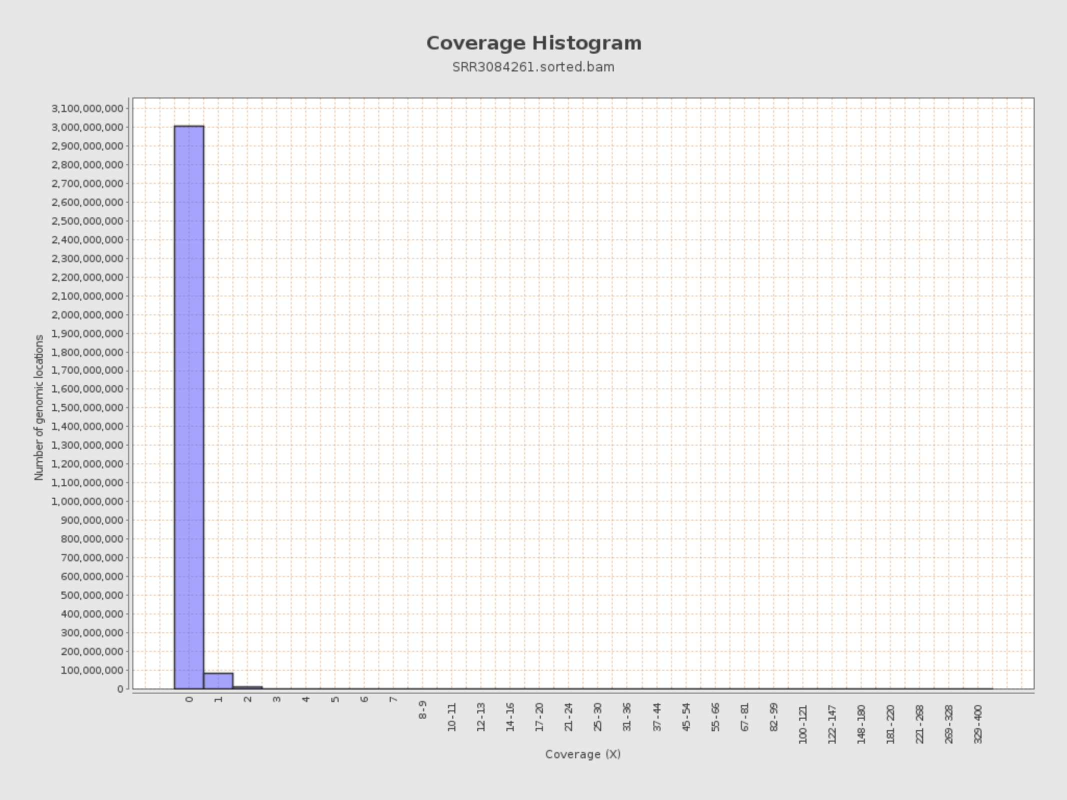
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 8012382 | 0.0321 | 0.3678 |
| chr2 | 243199373 | 8399278 | 0.0345 | 0.3182 |
| chr3 | 198022430 | 7073074 | 0.0357 | 0.2055 |
| chr4 | 191154276 | 6826898 | 0.0357 | 0.2131 |
| chr5 | 180915260 | 6479023 | 0.0358 | 0.2057 |
| chr6 | 171115067 | 6129383 | 0.0358 | 0.2323 |
| chr7 | 159138663 | 5569143 | 0.035 | 0.3417 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 5077135 | 0.0347 | 0.264 |
| chr9 | 141213431 | 4281499 | 0.0303 | 0.2506 |
| chr10 | 135534747 | 4637661 | 0.0342 | 0.2536 |
| chr11 | 135006516 | 4474338 | 0.0331 | 0.2322 |
| chr12 | 133851895 | 4740080 | 0.0354 | 0.207 |
| chr13 | 115169878 | 3178720 | 0.0276 | 0.1808 |
| chr14 | 107349540 | 3048502 | 0.0284 | 0.1953 |
| chr15 | 102531392 | 2915107 | 0.0284 | 0.1895 |
| chr16 | 90354753 | 2858414 | 0.0316 | 0.2105 |
| chr17 | 81195210 | 2669172 | 0.0329 | 0.2166 |
| chr18 | 78077248 | 2822398 | 0.0361 | 0.4652 |
| chr19 | 59128983 | 1956893 | 0.0331 | 0.2974 |
| chr20 | 63025520 | 2126924 | 0.0337 | 0.2082 |
| chr21 | 48129895 | 1383750 | 0.0288 | 0.1916 |
| chr22 | 51304566 | 1170021 | 0.0228 | 0.1634 |
| chrMT | 16571 | 22634 | 1.3659 | 1.4597 |
| chrX | 155270560 | 5686091 | 0.0366 | 0.2281 |
| chrY | 59373566 | 249787 | 0.0042 | 0.0931 |

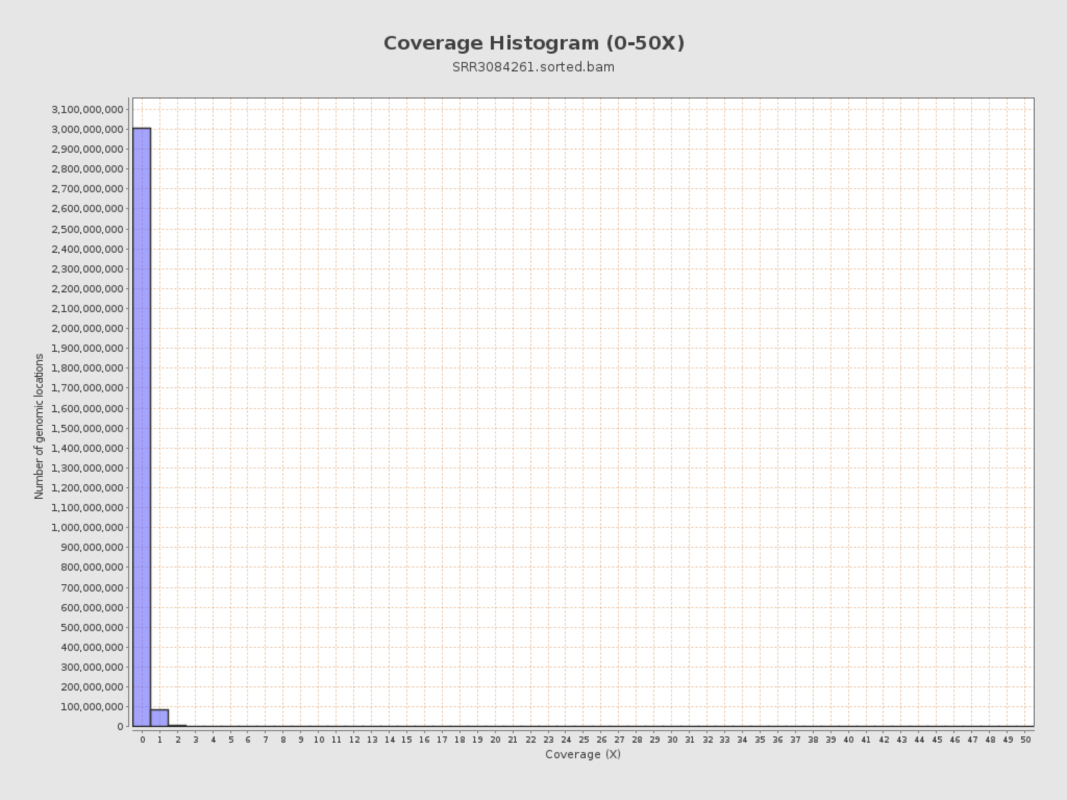
# 3. Results : Coverage across reference



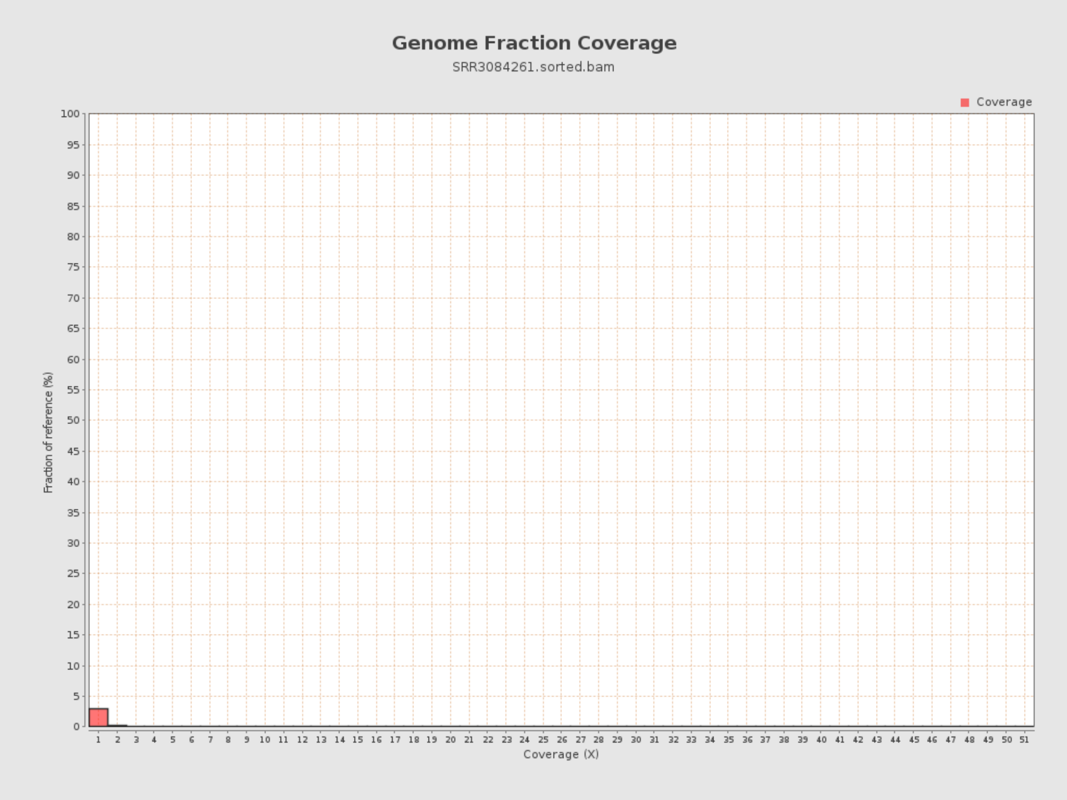
# 4. Results : Coverage Histogram



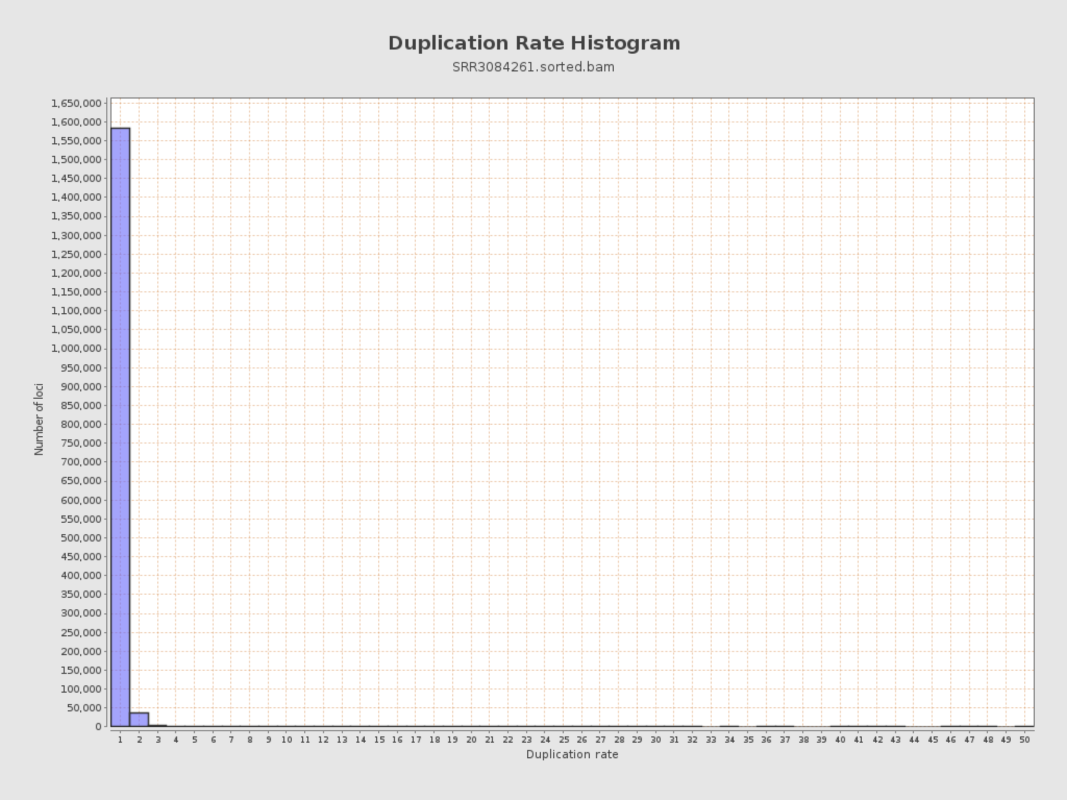
# 5. Results : Coverage Histogram (0-50X)



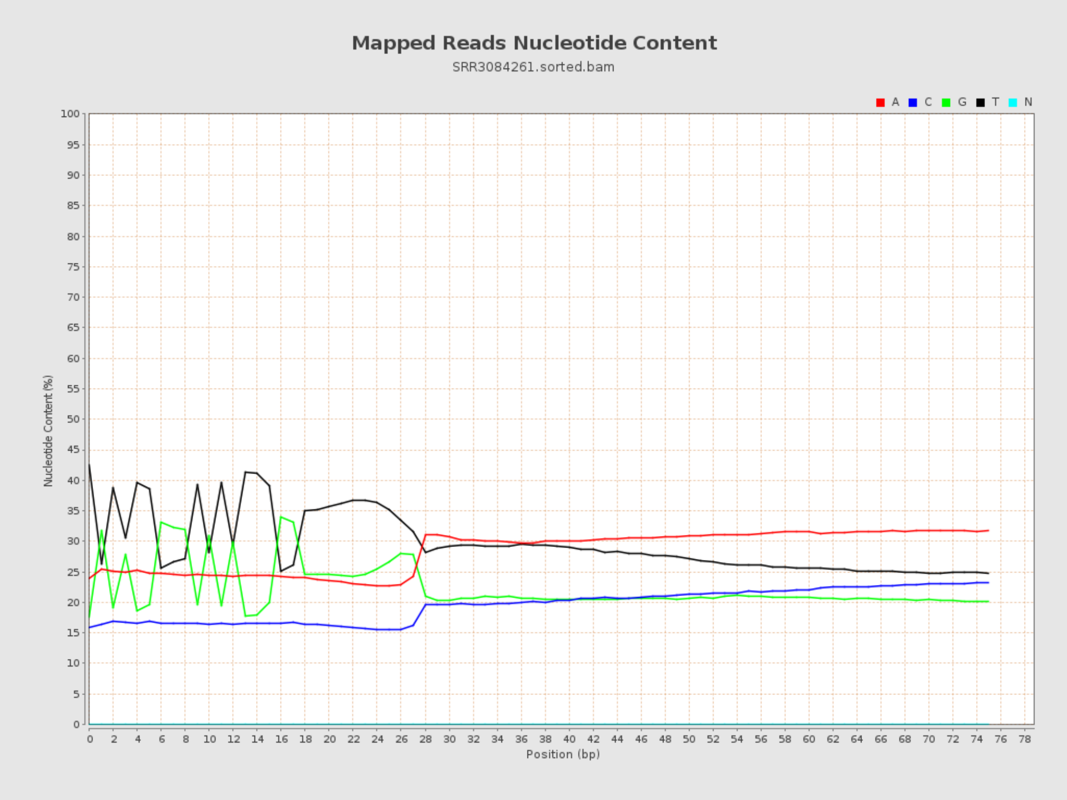
# 6. Results : Genome Fraction Coverage



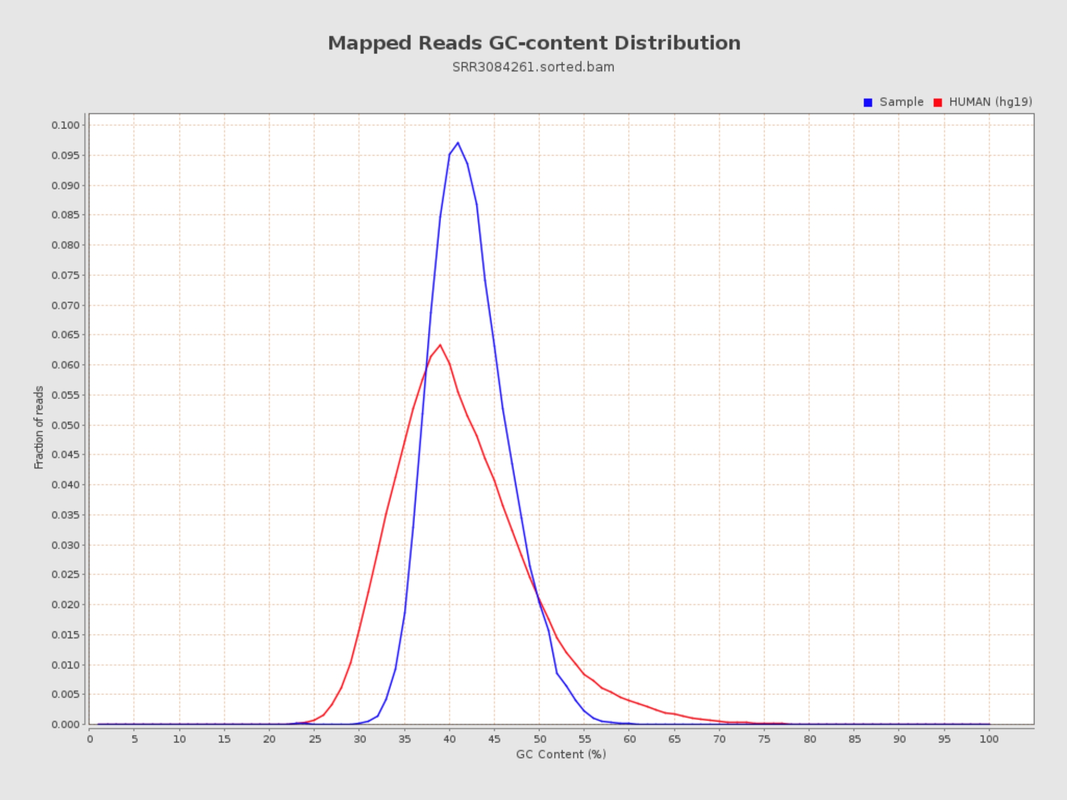
# 7. Results : Duplication Rate Histogram



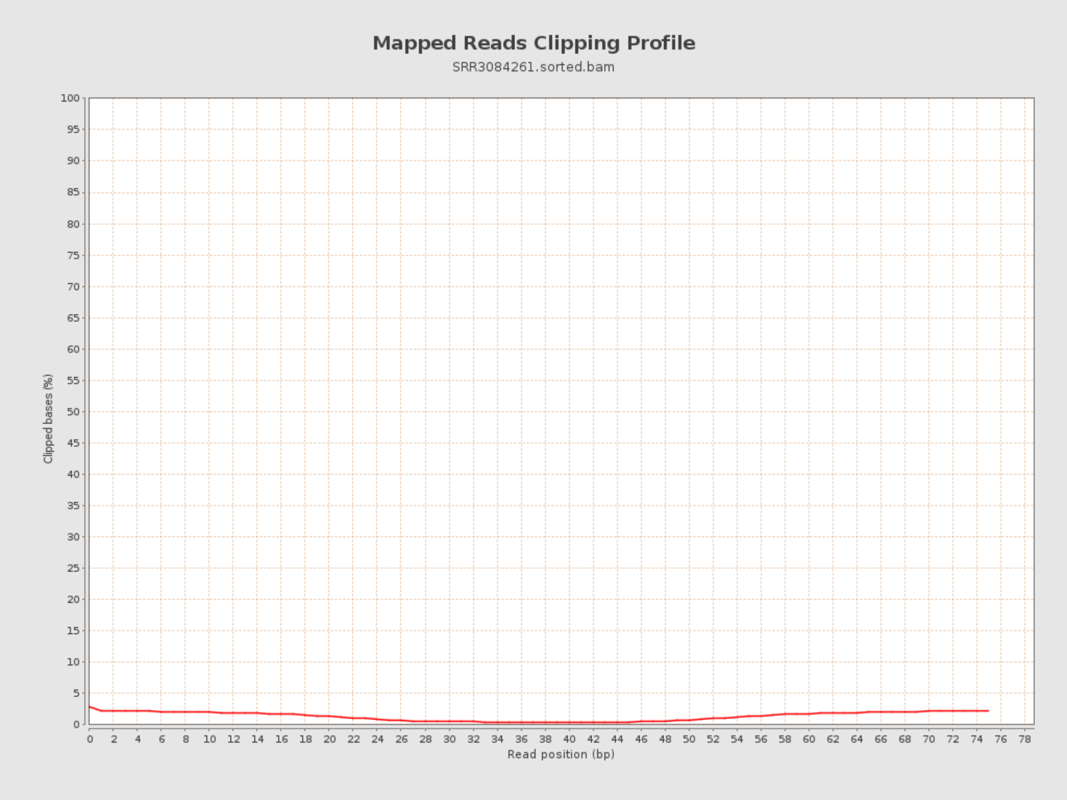
# 8. Results : Mapped Reads Nucleotide Content



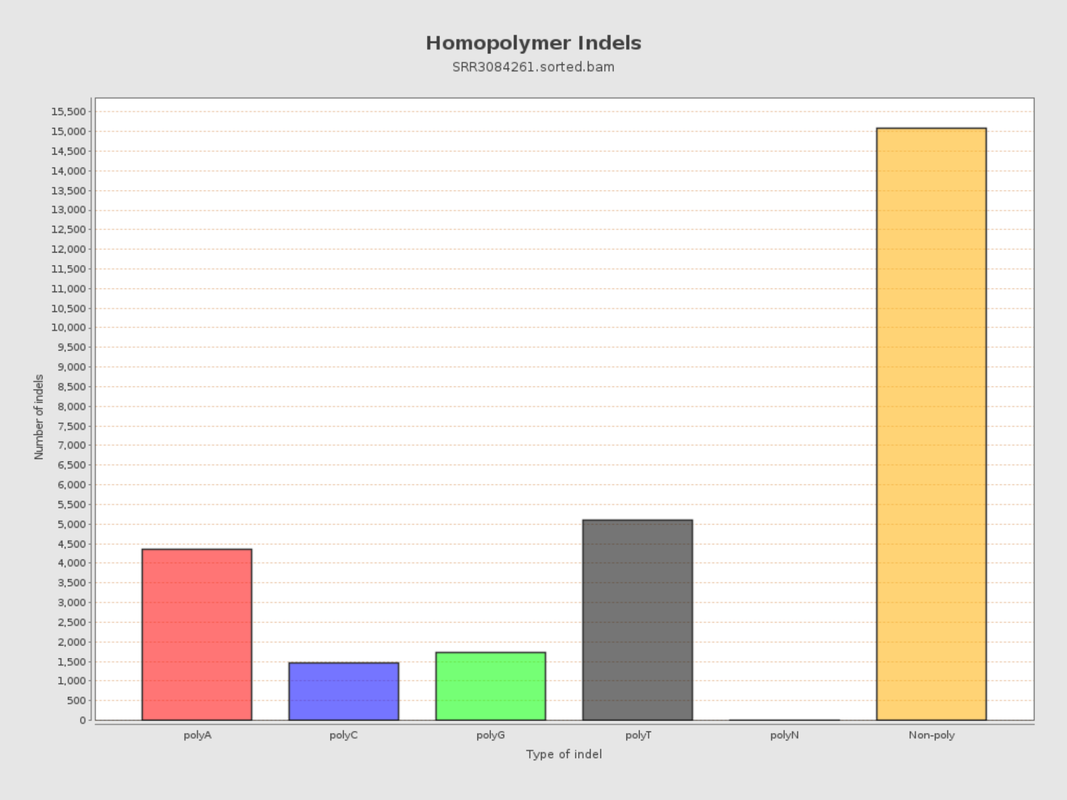
# 9. Results : Mapped Reads GC-content Distribution



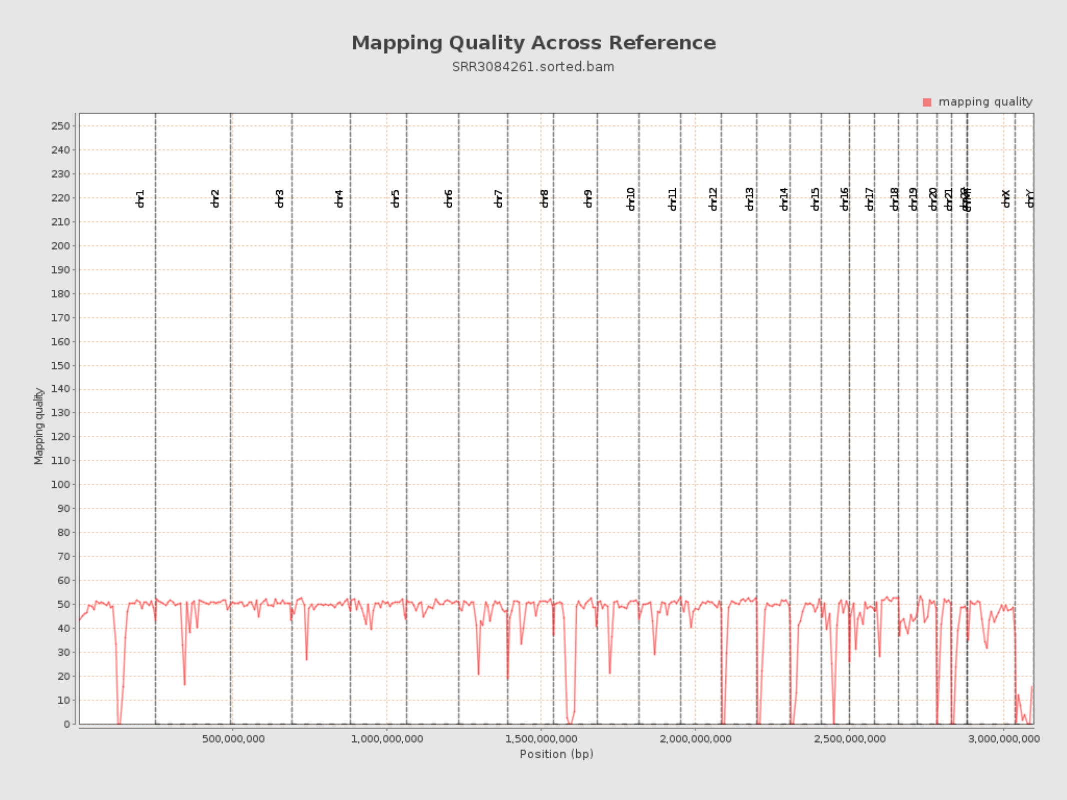
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram