# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/25 11:33:17*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084386.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_SRR3084386 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084386.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Aug 25 11:33:15 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3084386.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,665,810 |
| Mapped reads | 1,533,815 / 92.08% |
| Unmapped reads | 131,995 / 7.92% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 7,818 / 0.47% |
| Read min/max/mean length | 30 / 76 / 76.16 |
| Duplicated reads (estimated) | 47,035 / 2.82% |
| Duplication rate | 2.58% |
| Clipped reads | 623,713 / 37.44% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 29,399,723 / 28.32% |
| Number/percentage of C's | 19,441,586 / 18.73% |
| Number/percentage of T's | 32,589,948 / 31.39% |
| Number/percentage of G's | 22,249,601 / 21.43% |
| Number/percentage of N's | 138,587 / 0.13% |
| GC Percentage | 40.16% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0335 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2598 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.74 |

## 2.5. Mismatches and indels

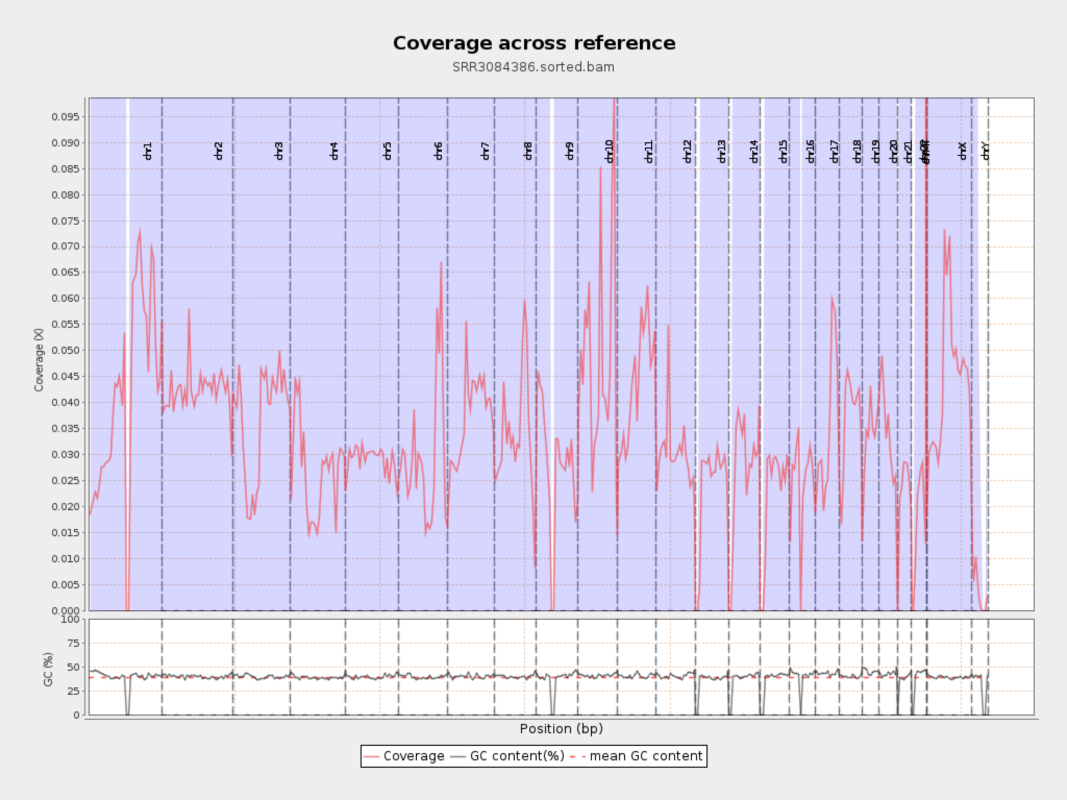
| | |
|---|---|
| General error rate | 0.99% |
| Mismatches | 1,014,556 |
| Insertions | 7,295 |
| Mapped reads with at least one insertion | 0.47% |
| Deletions | 20,491 |
| Mapped reads with at least one deletion | 1.32% |
| Homopolymer indels | 47.71% |

## 2.6. Chromosome stats

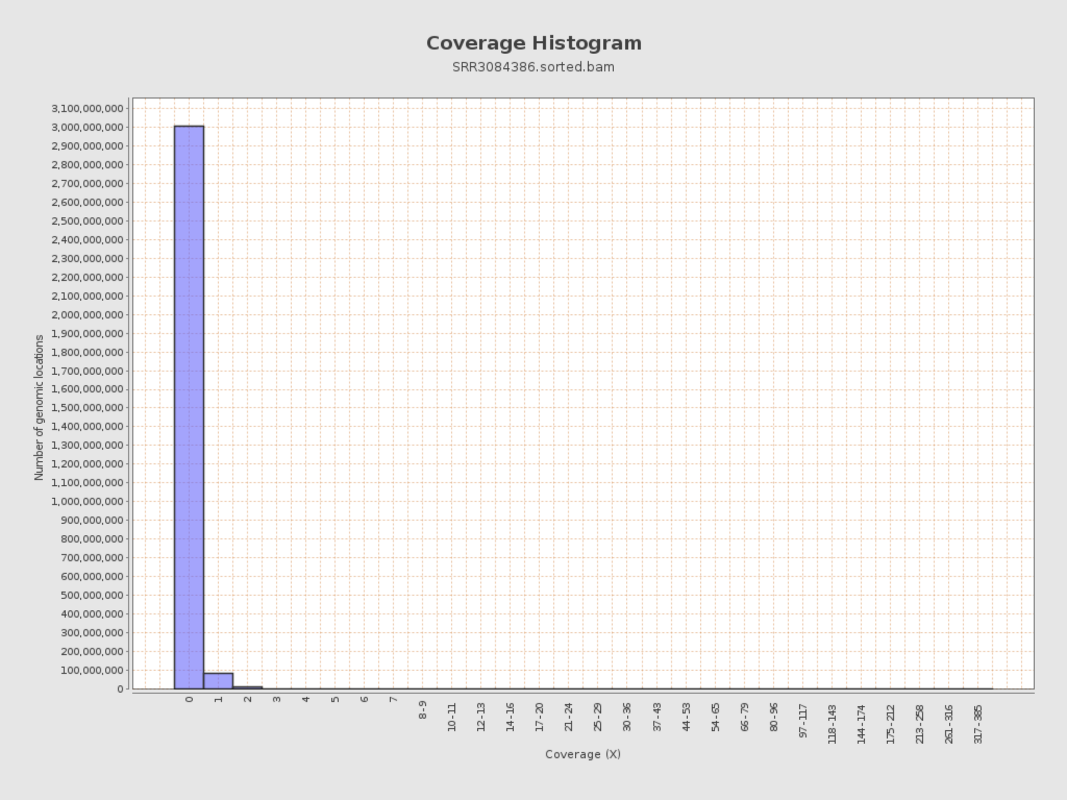
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 10297791 | 0.0413 | 0.4054 |
| chr2 | 243199373 | 10290383 | 0.0423 | 0.2925 |
| chr3 | 198022430 | 7270493 | 0.0367 | 0.2145 |
| chr4 | 191154276 | 5150529 | 0.0269 | 0.1894 |
| chr5 | 180915260 | 5259231 | 0.0291 | 0.1886 |
| chr6 | 171115067 | 5048073 | 0.0295 | 0.2104 |
| chr7 | 159138663 | 5971290 | 0.0375 | 0.3466 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 4928936 | 0.0337 | 0.2448 |
| chr9 | 141213431 | 3954335 | 0.028 | 0.2328 |
| chr10 | 135534747 | 6772146 | 0.05 | 0.3744 |
| chr11 | 135006516 | 5851139 | 0.0433 | 0.2701 |
| chr12 | 133851895 | 4076824 | 0.0305 | 0.1941 |
| chr13 | 115169878 | 2683619 | 0.0233 | 0.1687 |
| chr14 | 107349540 | 2855977 | 0.0266 | 0.1854 |
| chr15 | 102531392 | 2291980 | 0.0224 | 0.1661 |
| chr16 | 90354753 | 2255371 | 0.025 | 0.187 |
| chr17 | 81195210 | 2857462 | 0.0352 | 0.2189 |
| chr18 | 78077248 | 2878398 | 0.0369 | 0.3555 |
| chr19 | 59128983 | 2013752 | 0.0341 | 0.301 |
| chr20 | 63025520 | 2155909 | 0.0342 | 0.2059 |
| chr21 | 48129895 | 1079545 | 0.0224 | 0.1738 |
| chr22 | 51304566 | 830460 | 0.0162 | 0.1394 |
| chrMT | 16571 | 20011 | 1.2076 | 1.3868 |
| chrX | 155270560 | 6841592 | 0.0441 | 0.2515 |
| chrY | 59373566 | 219322 | 0.0037 | 0.0865 |

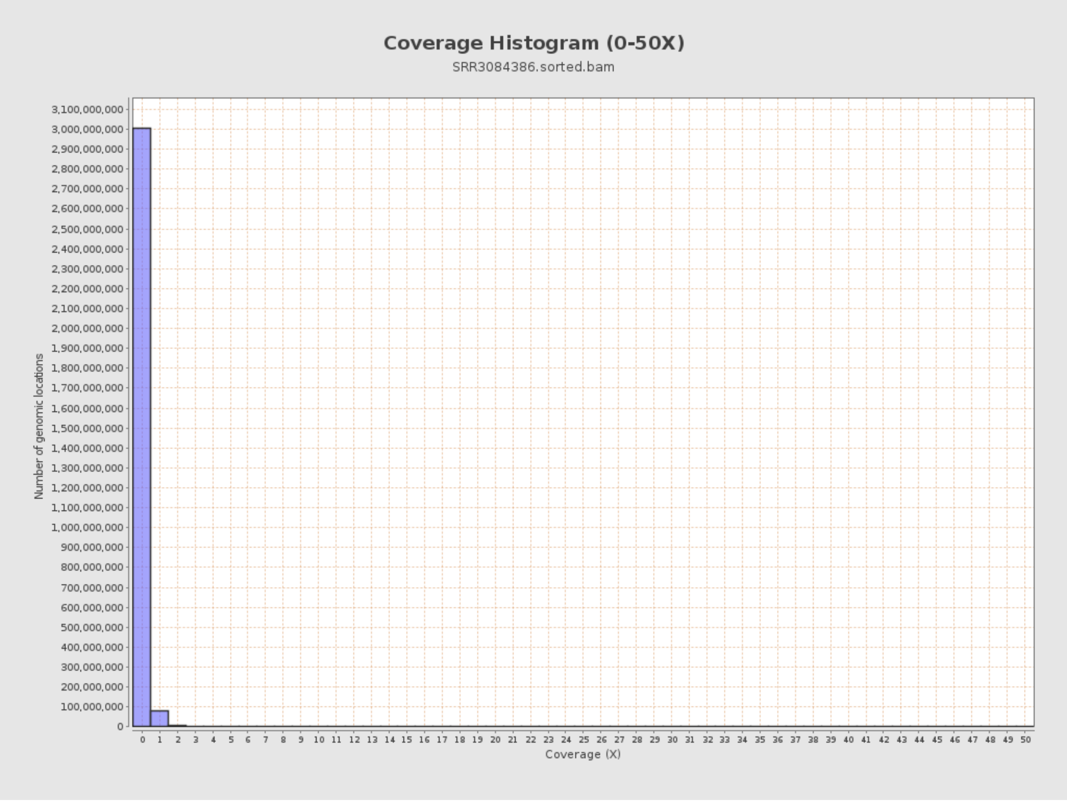
# 3. Results : Coverage across reference



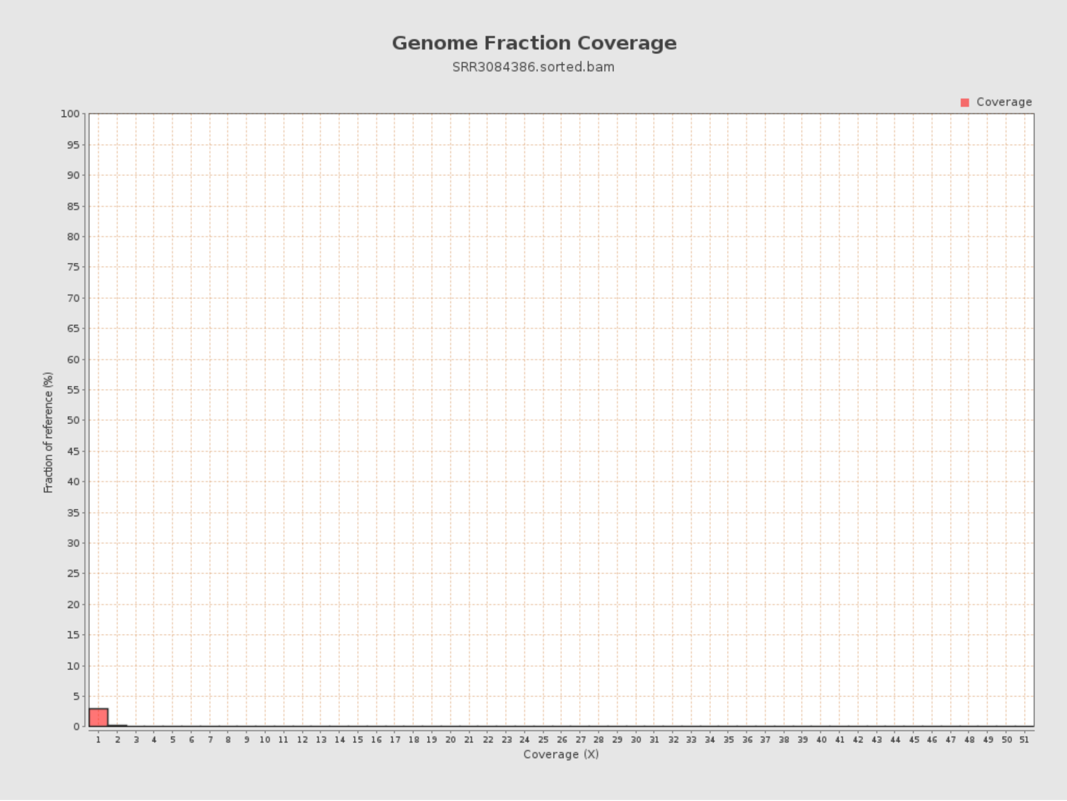
# 4. Results : Coverage Histogram



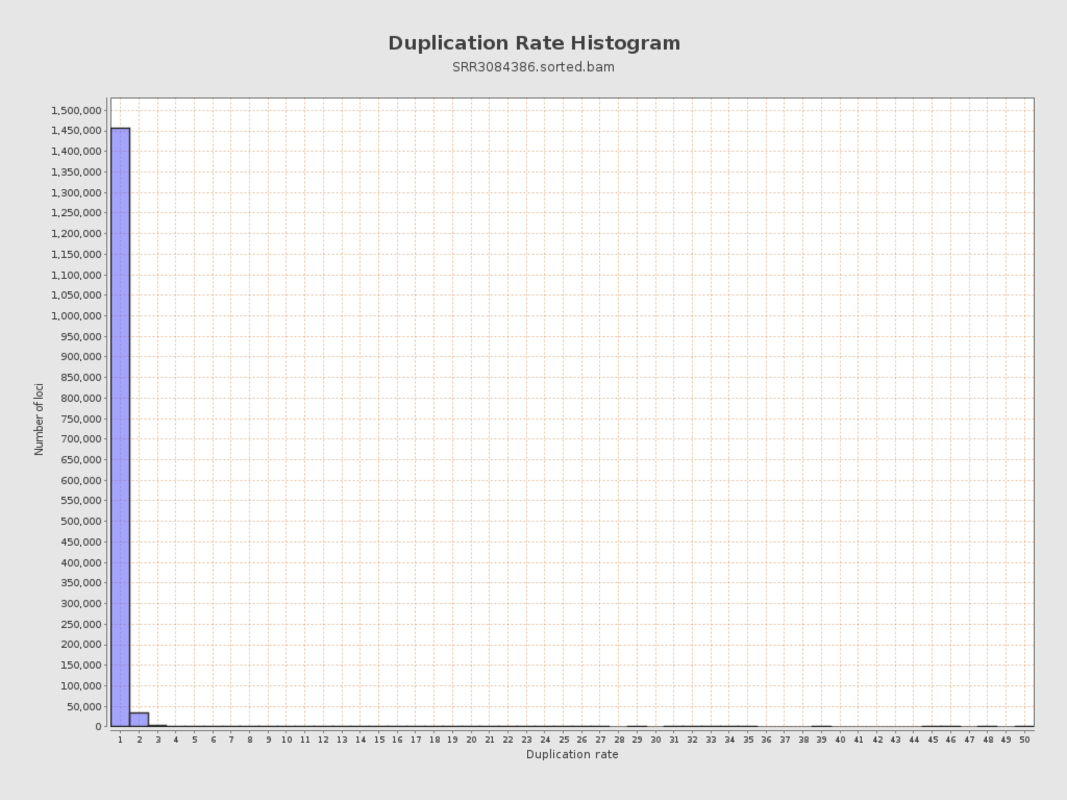
# 5. Results : Coverage Histogram (0-50X)



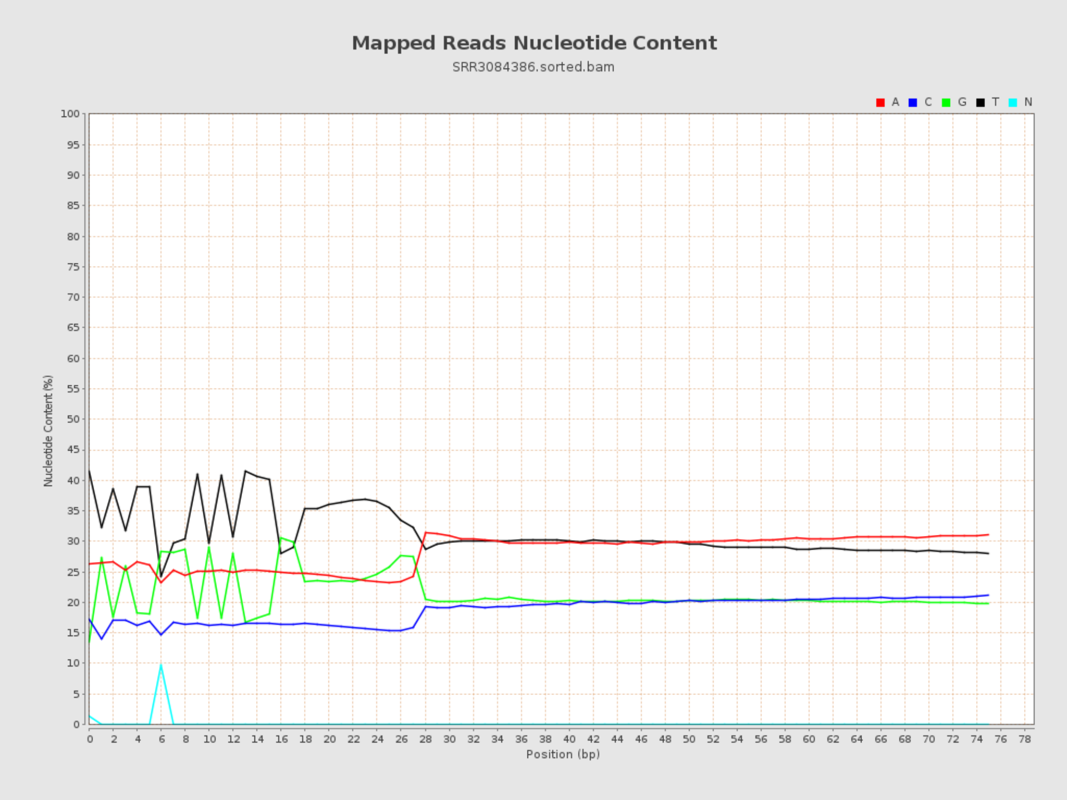
# 6. Results : Genome Fraction Coverage



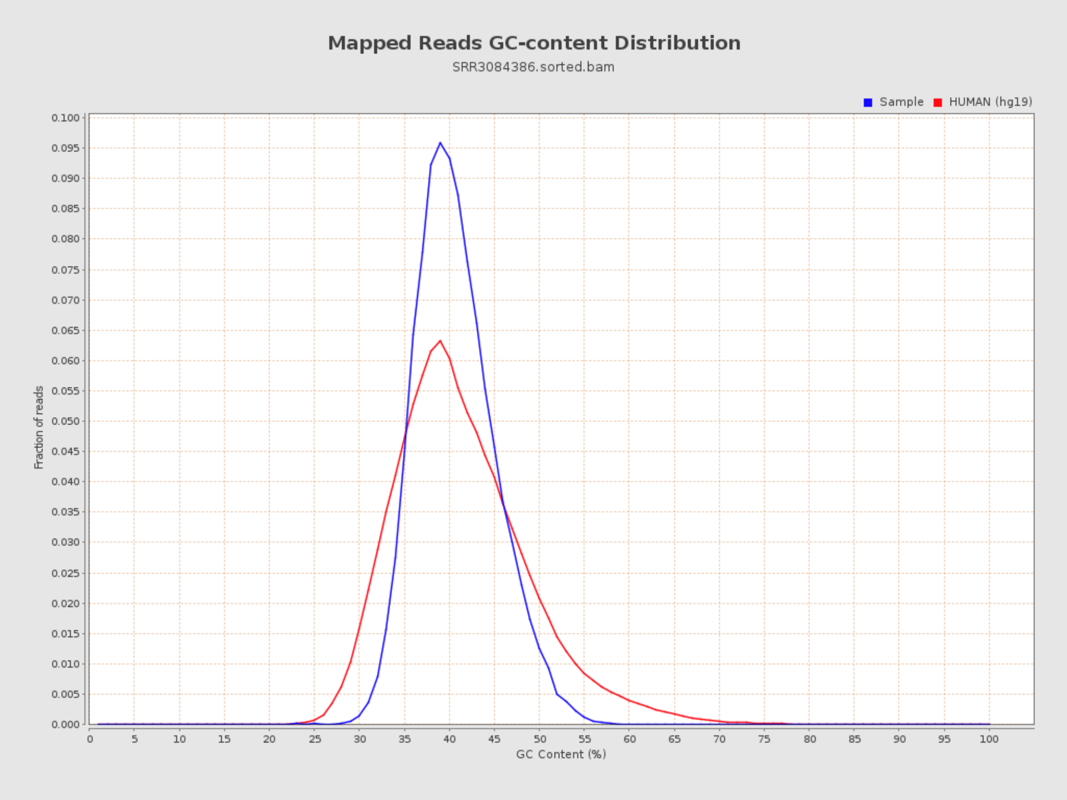
# 7. Results : Duplication Rate Histogram



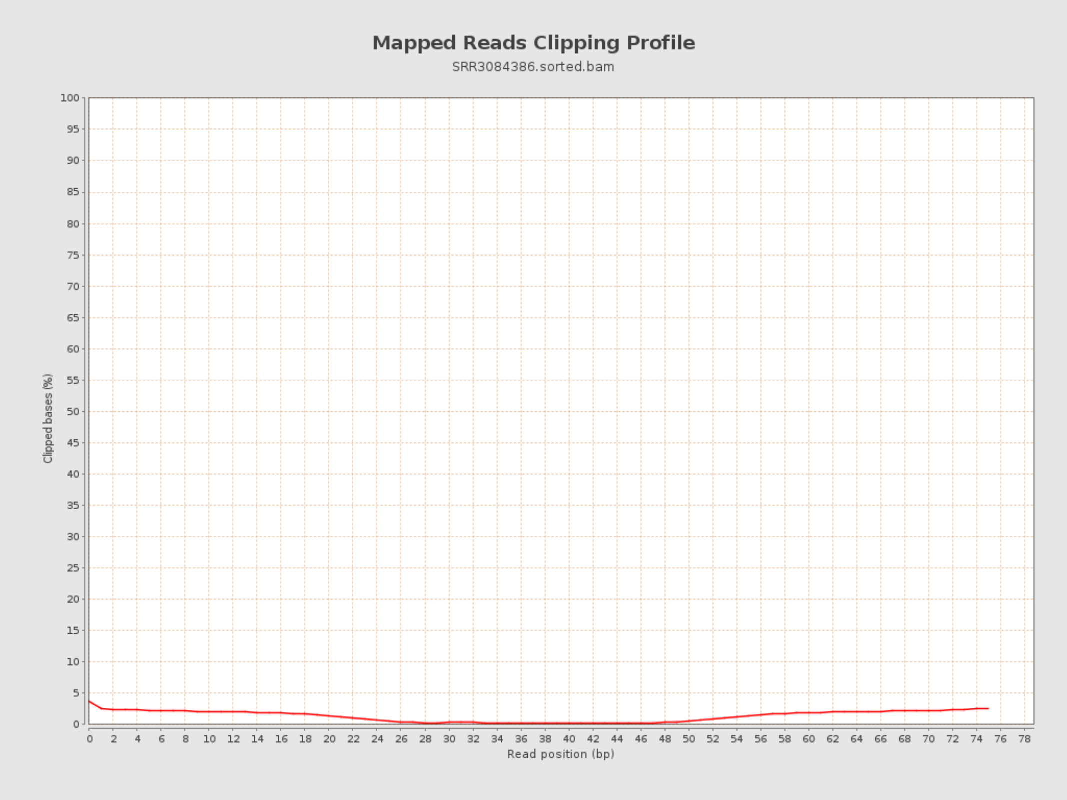
# 8. Results : Mapped Reads Nucleotide Content



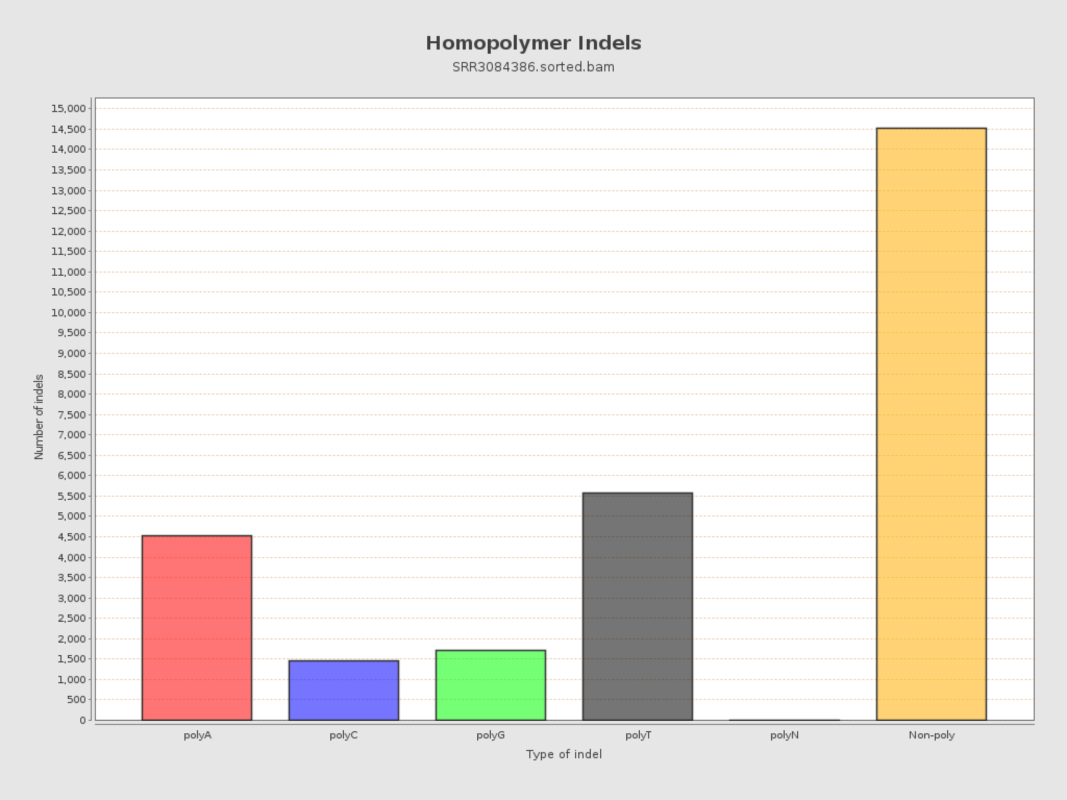
# 9. Results : Mapped Reads GC-content Distribution



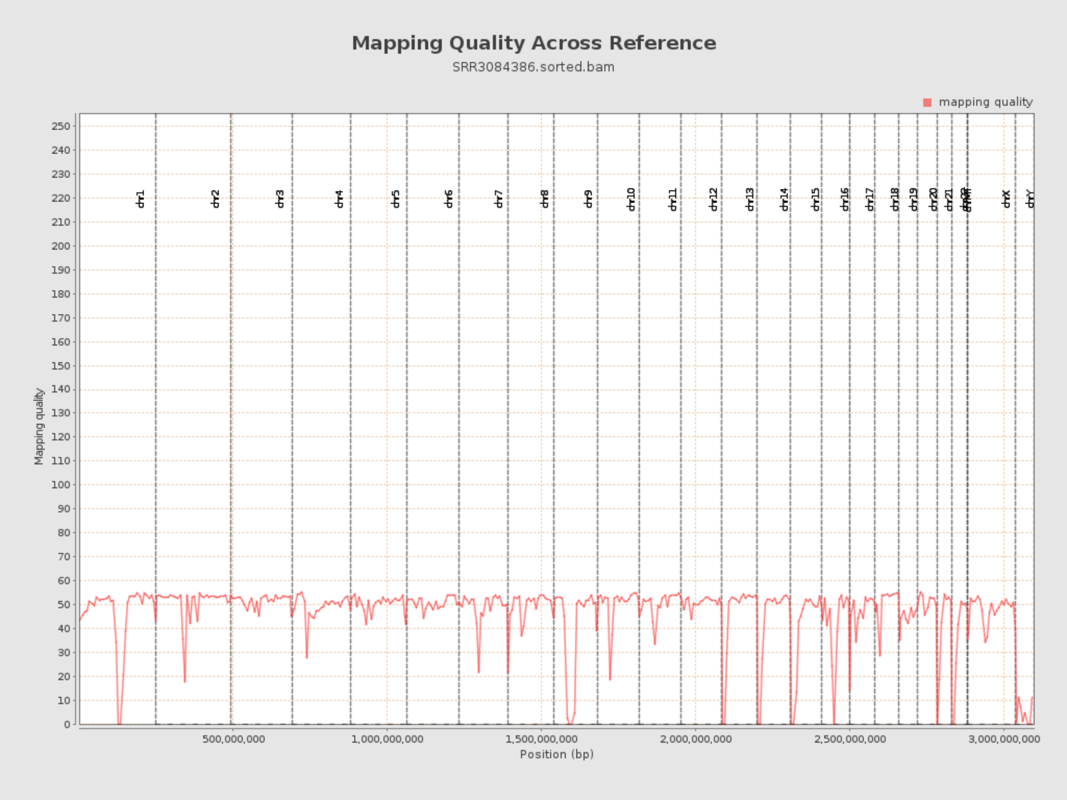
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram