# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 00:44:31*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081176.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_SRR3081176 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081176.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Aug 24 00:44:30 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3081176.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,359,698 |
| Mapped reads | 2,083,848 / 88.31% |
| Unmapped reads | 275,850 / 11.69% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 16,819 / 0.71% |
| Read min/max/mean length | 30 / 76 / 76.25 |
| Duplicated reads (estimated) | 88,095 / 3.73% |
| Duplication rate | 3.04% |
| Clipped reads | 923,654 / 39.14% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 38,965,934 / 27.94% |
| Number/percentage of C's | 25,646,252 / 18.39% |
| Number/percentage of T's | 43,915,692 / 31.49% |
| Number/percentage of G's | 30,904,904 / 22.16% |
| Number/percentage of N's | 41,034 / 0.03% |
| GC Percentage | 40.55% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0451 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4629 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.94 |

## 2.5. Mismatches and indels

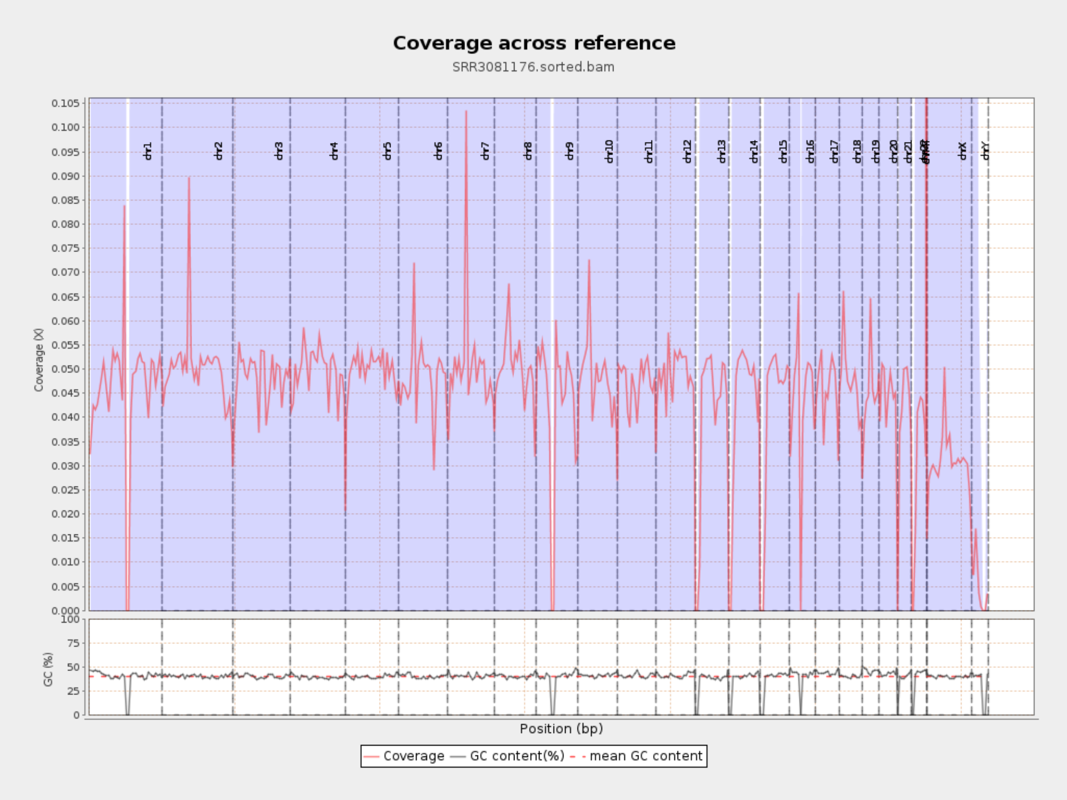
| | |
|---|---|
| General error rate | 0.89% |
| Mismatches | 1,217,827 |
| Insertions | 11,511 |
| Mapped reads with at least one insertion | 0.55% |
| Deletions | 37,791 |
| Mapped reads with at least one deletion | 1.79% |
| Homopolymer indels | 46.28% |

## 2.6. Chromosome stats

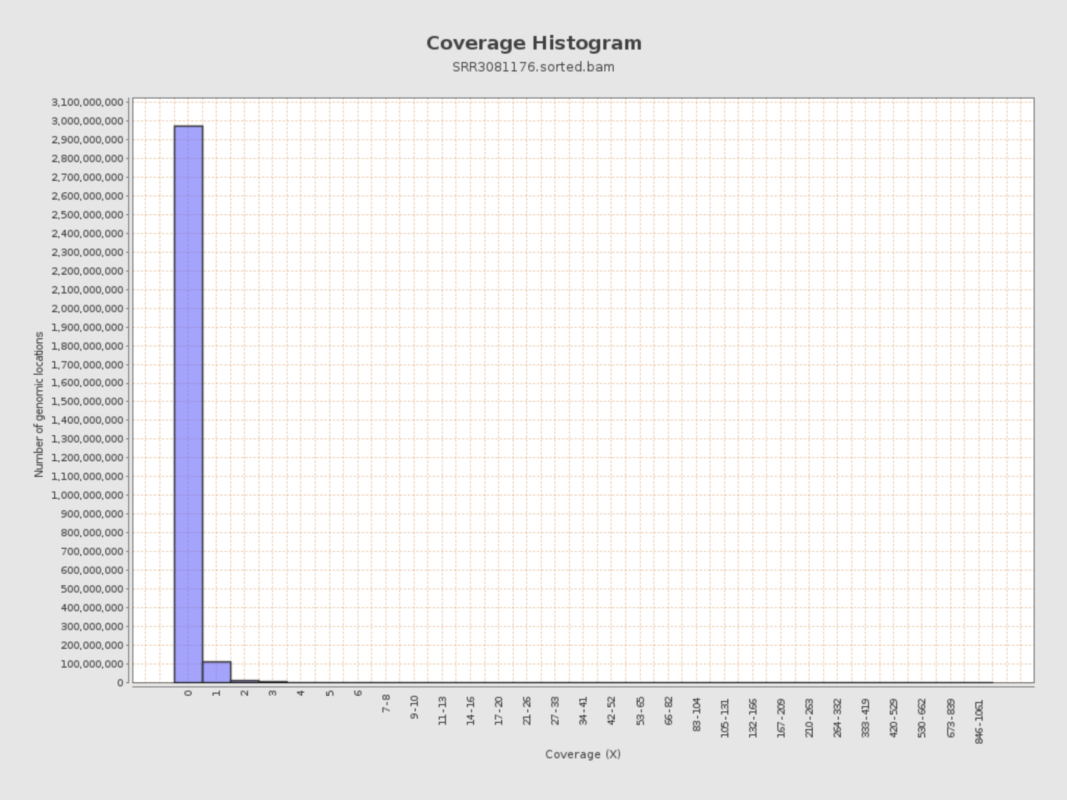
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 11403043 | 0.0457 | 0.9288 |
| chr2 | 243199373 | 12244402 | 0.0503 | 0.518 |
| chr3 | 198022430 | 9489419 | 0.0479 | 0.2389 |
| chr4 | 191154276 | 9479643 | 0.0496 | 0.2579 |
| chr5 | 180915260 | 9041699 | 0.05 | 0.2482 |
| chr6 | 171115067 | 8304819 | 0.0485 | 0.3298 |
| chr7 | 159138663 | 8140919 | 0.0512 | 0.7937 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 7333897 | 0.0501 | 0.5389 |
| chr9 | 141213431 | 6099530 | 0.0432 | 0.3965 |
| chr10 | 135534747 | 6581731 | 0.0486 | 0.3737 |
| chr11 | 135006516 | 6313575 | 0.0468 | 0.3846 |
| chr12 | 133851895 | 6555977 | 0.049 | 0.2508 |
| chr13 | 115169878 | 4576686 | 0.0397 | 0.2183 |
| chr14 | 107349540 | 4449992 | 0.0415 | 0.2487 |
| chr15 | 102531392 | 4142527 | 0.0404 | 0.2278 |
| chr16 | 90354753 | 3923707 | 0.0434 | 0.2652 |
| chr17 | 81195210 | 3690414 | 0.0455 | 0.2944 |
| chr18 | 78077248 | 3767890 | 0.0483 | 0.7756 |
| chr19 | 59128983 | 2697874 | 0.0456 | 0.5969 |
| chr20 | 63025520 | 2802366 | 0.0445 | 0.2497 |
| chr21 | 48129895 | 1912718 | 0.0397 | 0.2388 |
| chr22 | 51304566 | 1481329 | 0.0289 | 0.1844 |
| chrMT | 16571 | 28631 | 1.7278 | 1.6872 |
| chrX | 155270560 | 4783646 | 0.0308 | 0.2338 |
| chrY | 59373566 | 288793 | 0.0049 | 0.123 |

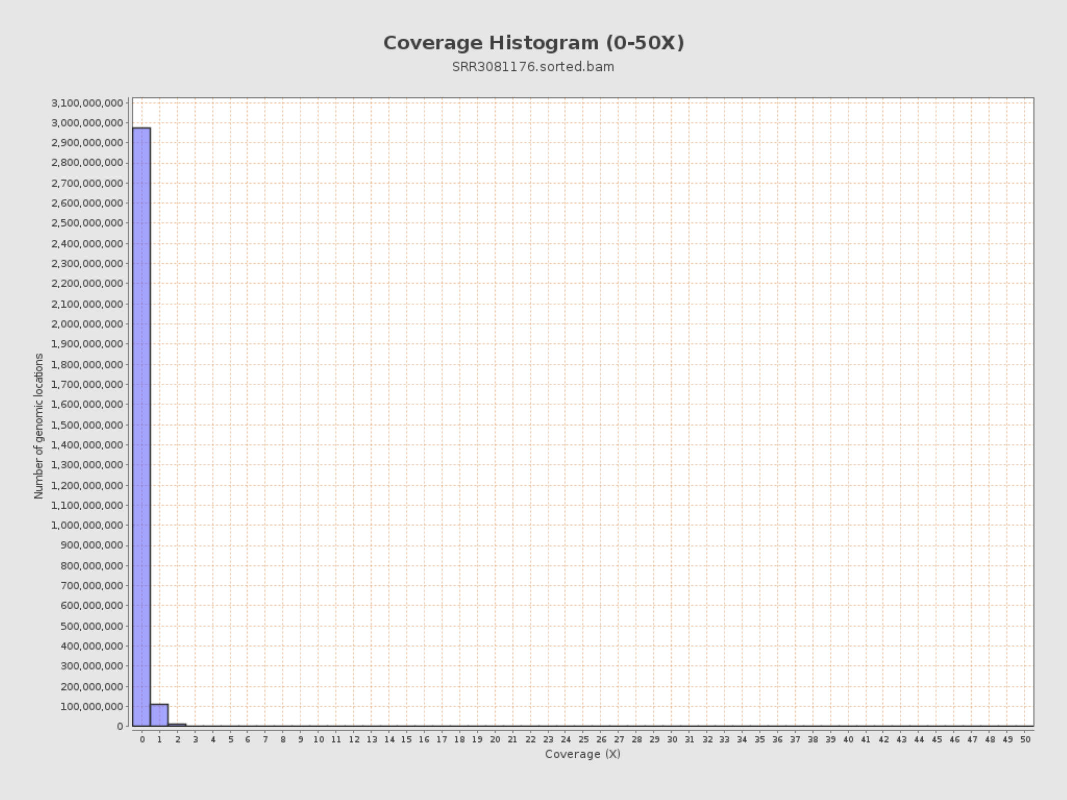
# 3. Results : Coverage across reference



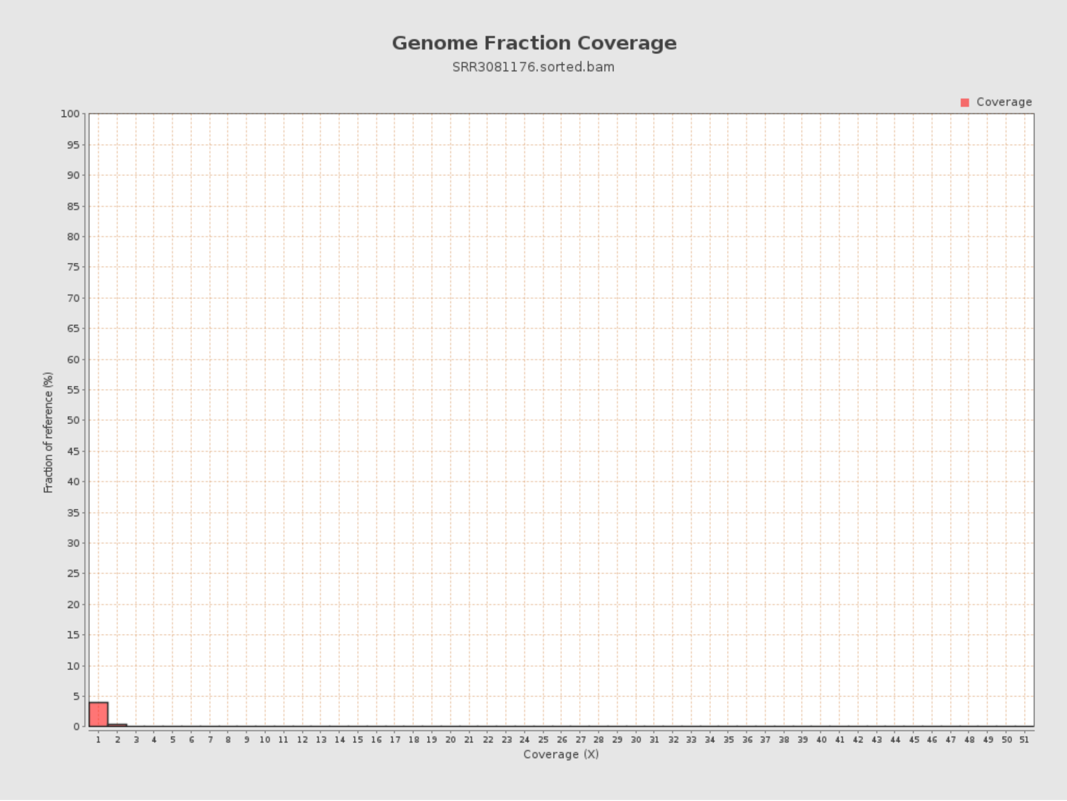
# 4. Results : Coverage Histogram



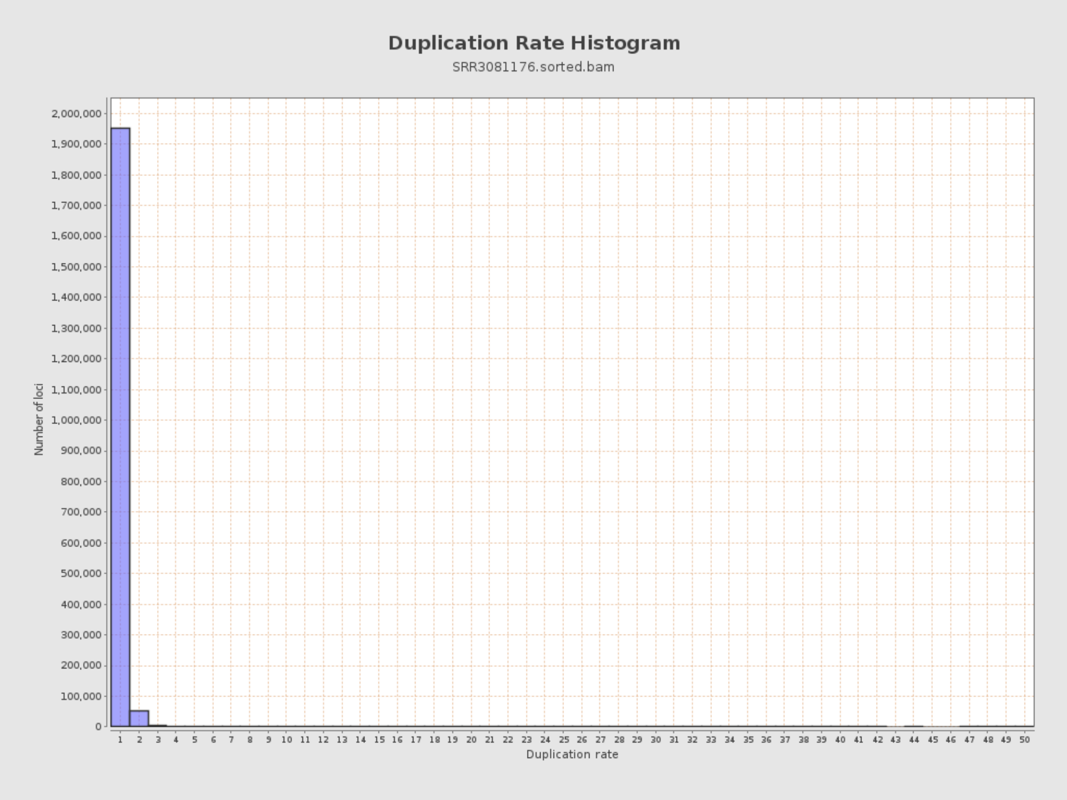
# 5. Results : Coverage Histogram (0-50X)



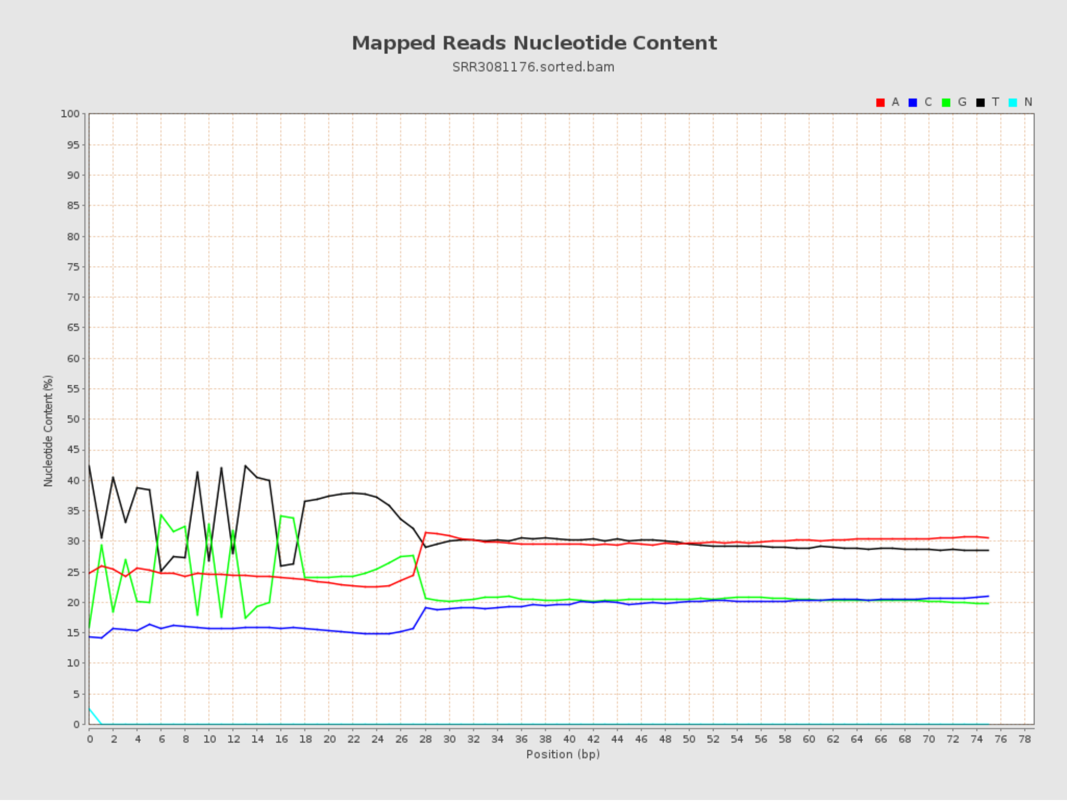
# 6. Results : Genome Fraction Coverage



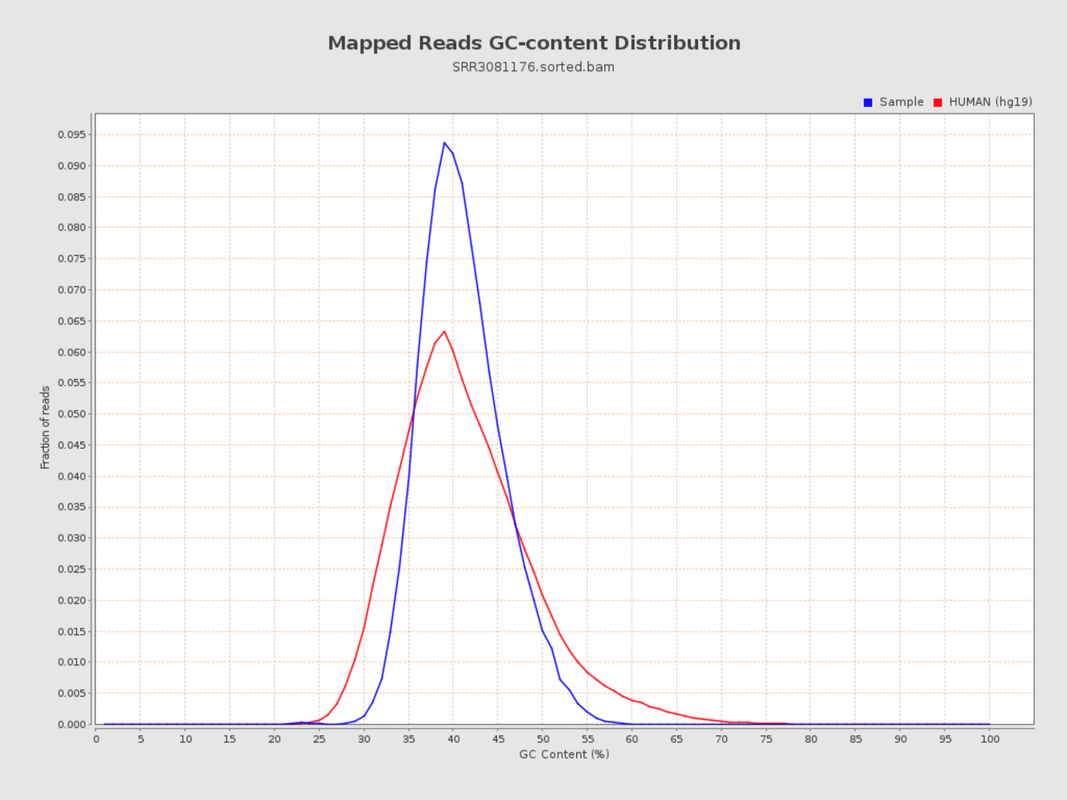
# 7. Results : Duplication Rate Histogram



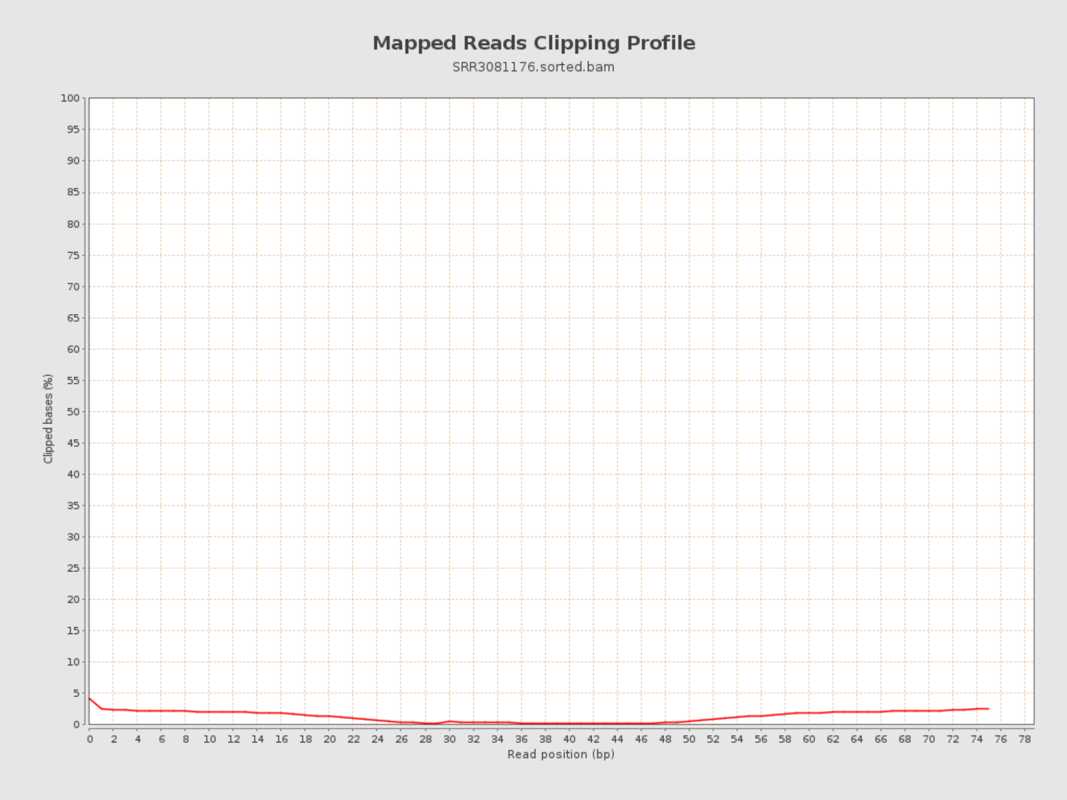
# 8. Results : Mapped Reads Nucleotide Content



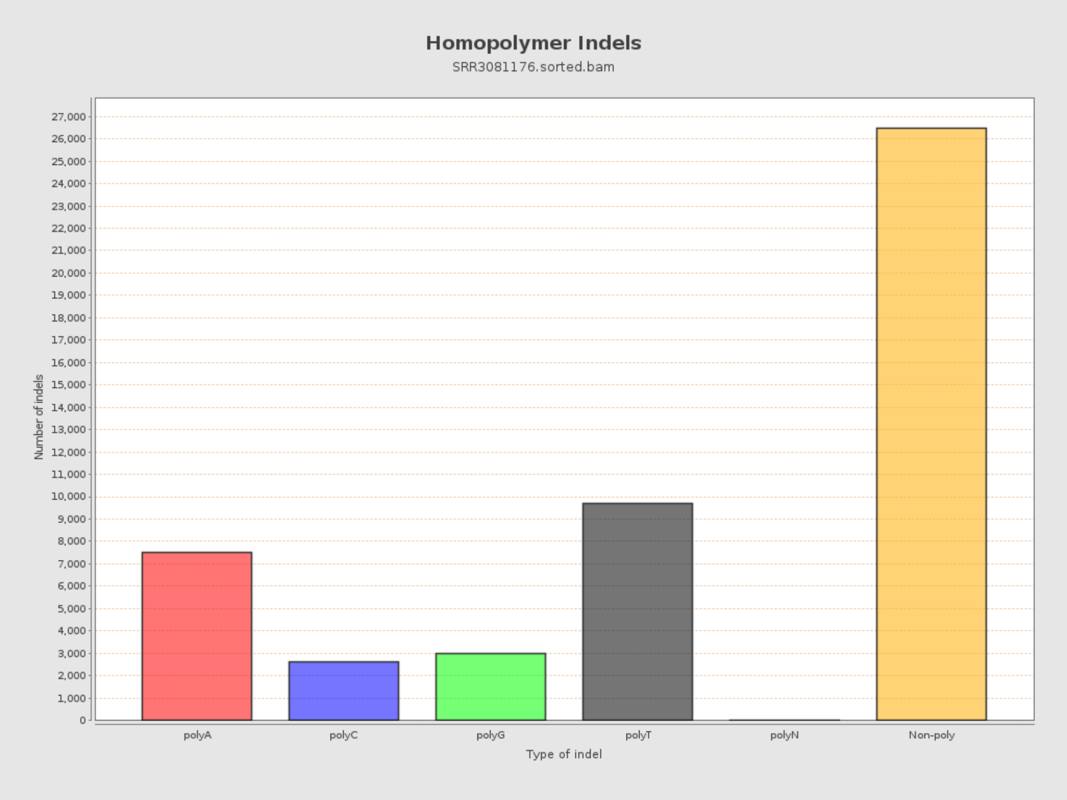
# 9. Results : Mapped Reads GC-content Distribution



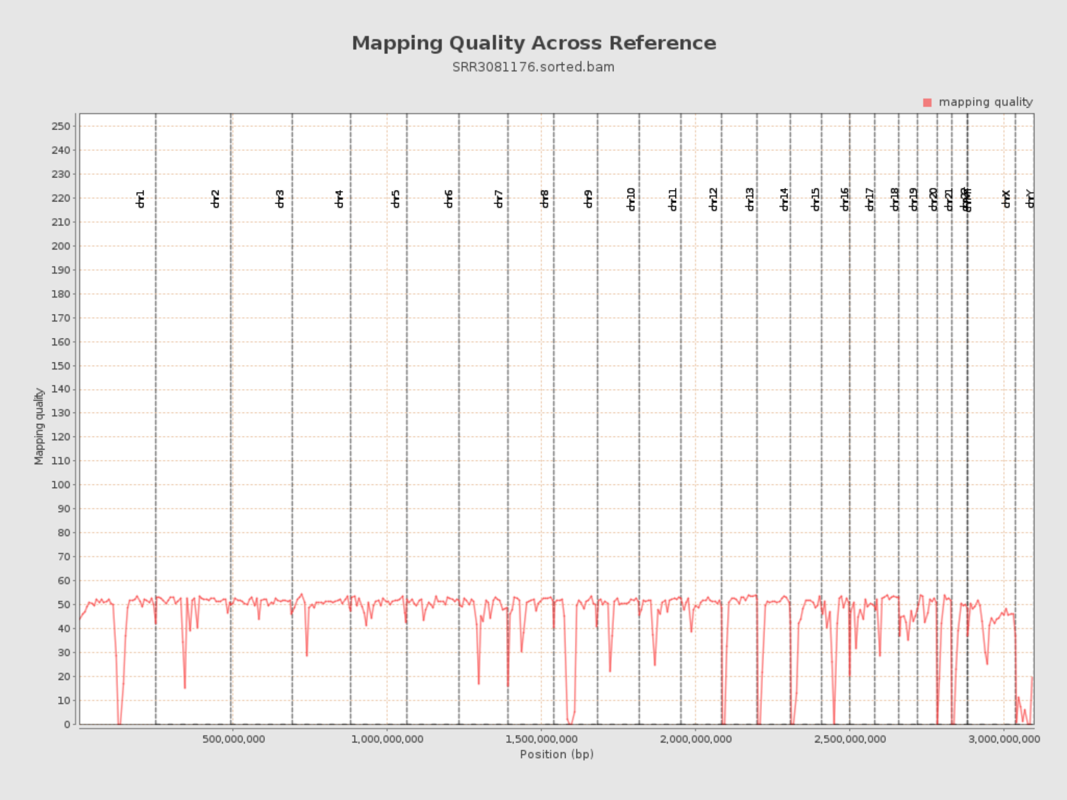
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram