

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 19:00:23*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081106.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_SRR3081106 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081106.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Fri Aug 23 19:00:22 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR3081106.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 2,489,775          |
| Mapped reads                 | 2,259,884 / 90.77% |
| Unmapped reads               | 229,891 / 9.23%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 21,937 / 0.88%     |
| Read min/max/mean length     | 30 / 76 / 76.31    |
| Duplicated reads (estimated) | 95,069 / 3.82%     |
| Duplication rate             | 3.35%              |
| Clipped reads                | 979,304 / 39.33%   |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 41,852,849 / 27.52% |
| Number/percentage of C's | 28,924,309 / 19.02% |
| Number/percentage of T's | 47,154,623 / 31%    |
| Number/percentage of G's | 34,163,272 / 22.46% |
| Number/percentage of N's | 1,708 / 0%          |
| GC Percentage            | 41.48%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0491 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.3786 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 45.05 |
|----------------------|-------|

## 2.5. Mismatches and indels

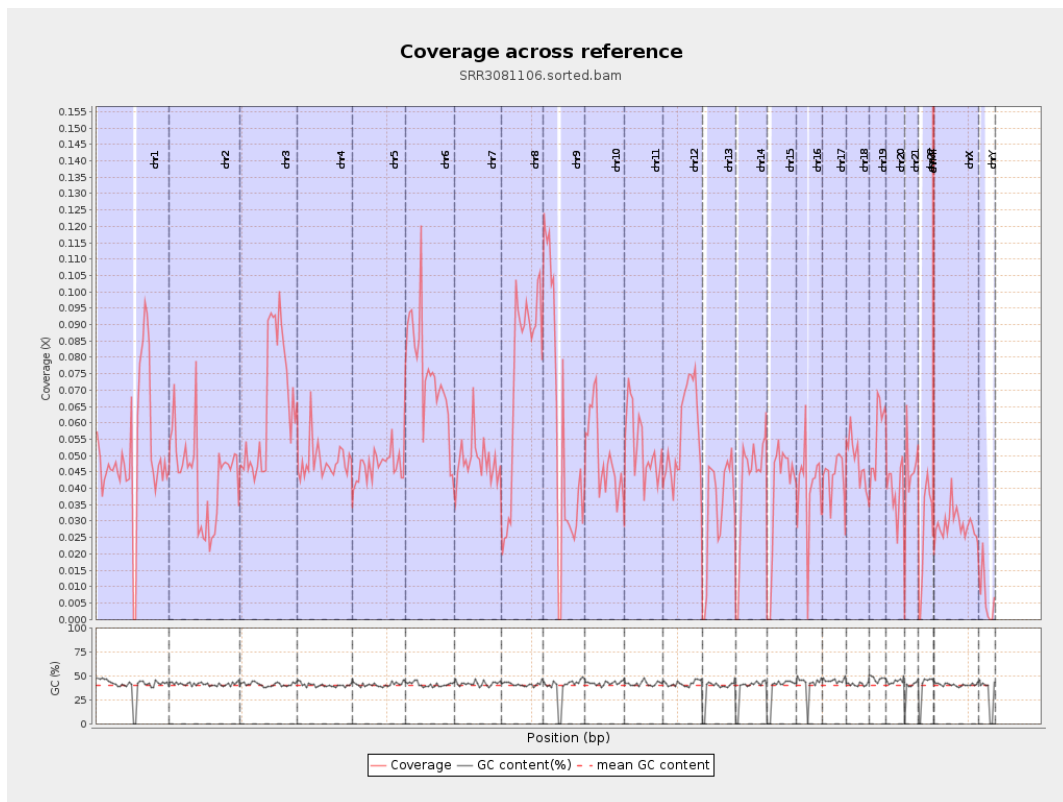
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.92%     |
| Mismatches                               | 1,371,713 |
| Insertions                               | 12,013    |
| Mapped reads with at least one insertion | 0.53%     |
| Deletions                                | 33,450    |
| Mapped reads with at least one deletion  | 1.46%     |
| Homopolymer indels                       | 46.42%    |

## 2.6. Chromosome stats

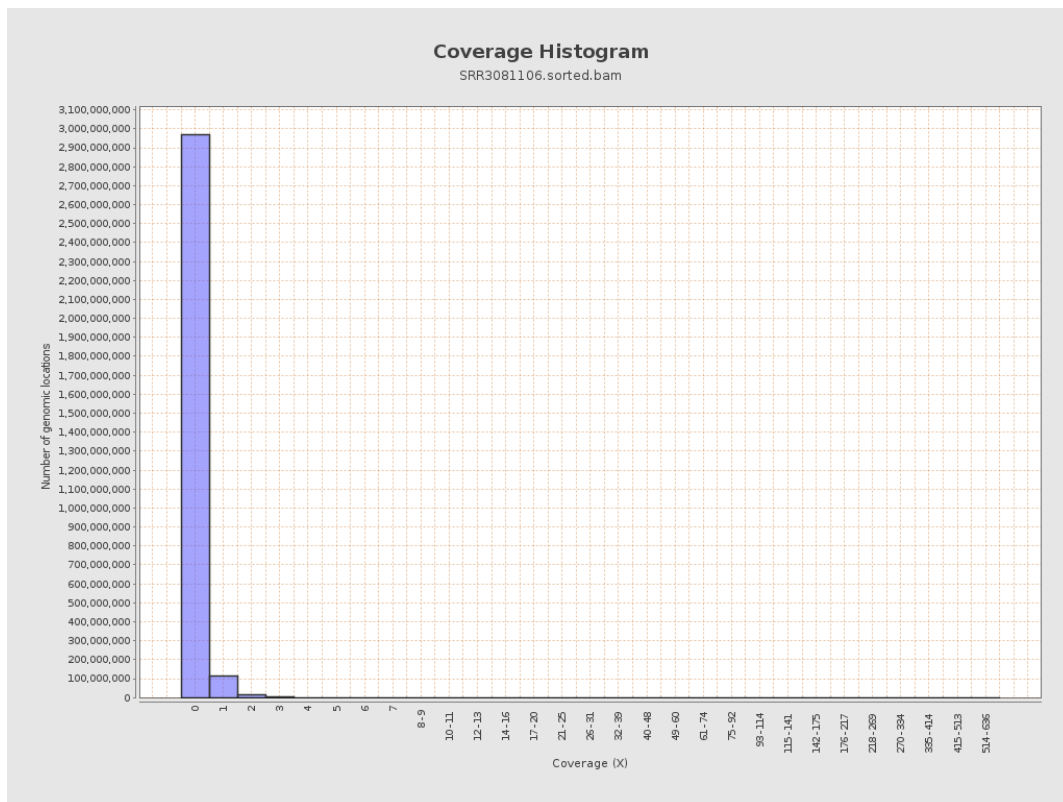
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 12615151     | 0.0506        | 0.567              |
| chr2 | 243199373 | 10688766     | 0.044         | 0.4474             |
| chr3 | 198022430 | 12788231     | 0.0646        | 0.2904             |
| chr4 | 191154276 | 9201350      | 0.0481        | 0.2715             |
| chr5 | 180915260 | 8515592      | 0.0471        | 0.2485             |
| chr6 | 171115067 | 12679027     | 0.0741        | 0.435              |
| chr7 | 159138663 | 7766592      | 0.0488        | 0.3468             |
|      |           |              |               |                    |

|       |           |          |         |         |
|-------|-----------|----------|---------|---------|
| chr8  | 146364022 | 10835474 | 0.074   | 0.4443  |
| chr9  | 141213431 | 7804833  | 0.0553  | 0.4608  |
| chr10 | 135534747 | 6795793  | 0.0501  | 0.3601  |
| chr11 | 135006516 | 7065949  | 0.0523  | 0.3848  |
| chr12 | 133851895 | 7619748  | 0.0569  | 0.2858  |
| chr13 | 115169878 | 3926898  | 0.0341  | 0.2108  |
| chr14 | 107349540 | 4424163  | 0.0412  | 0.299   |
| chr15 | 102531392 | 3981255  | 0.0388  | 0.224   |
| chr16 | 90354753  | 3643153  | 0.0403  | 0.2905  |
| chr17 | 81195210  | 3517572  | 0.0433  | 0.25    |
| chr18 | 78077248  | 3783508  | 0.0485  | 0.7254  |
| chr19 | 59128983  | 3302304  | 0.0558  | 0.4416  |
| chr20 | 63025520  | 2500285  | 0.0397  | 0.2394  |
| chr21 | 48129895  | 2126112  | 0.0442  | 0.2989  |
| chr22 | 51304566  | 1367059  | 0.0266  | 0.1845  |
| chrMT | 16571     | 345899   | 20.8738 | 10.2311 |
| chrX  | 155270560 | 4474227  | 0.0288  | 0.2285  |
| chrY  | 59373566  | 382353   | 0.0064  | 0.1631  |

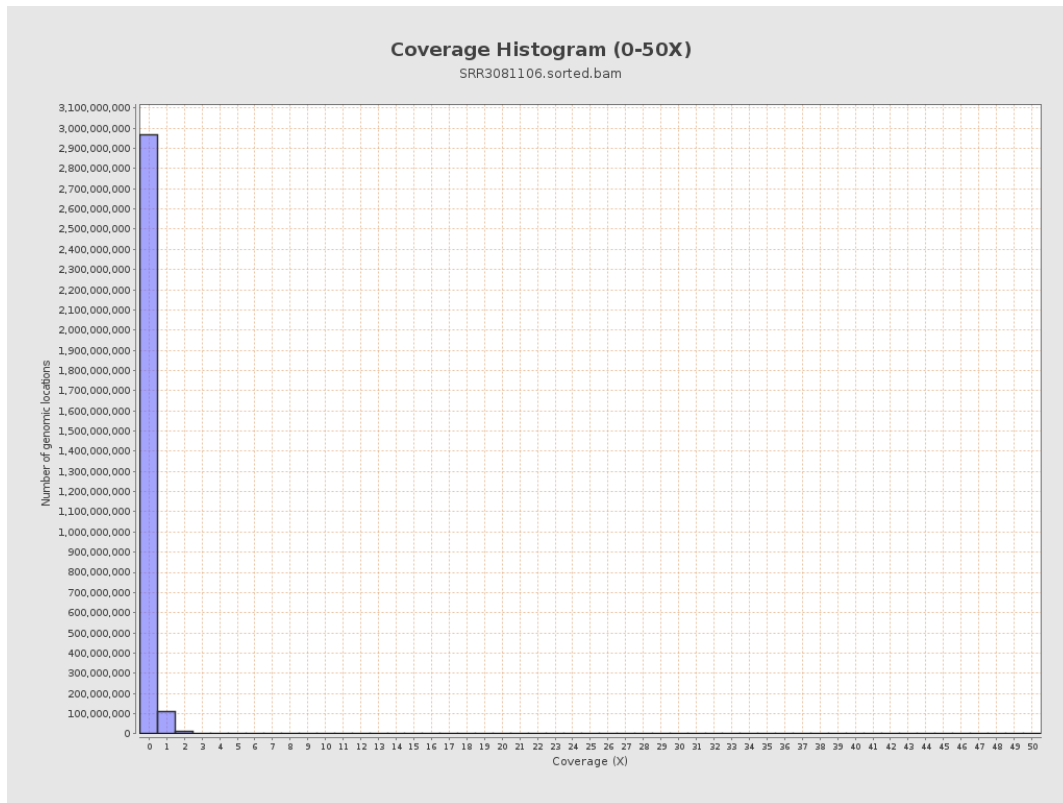
### 3. Results : Coverage across reference



## 4. Results : Coverage Histogram

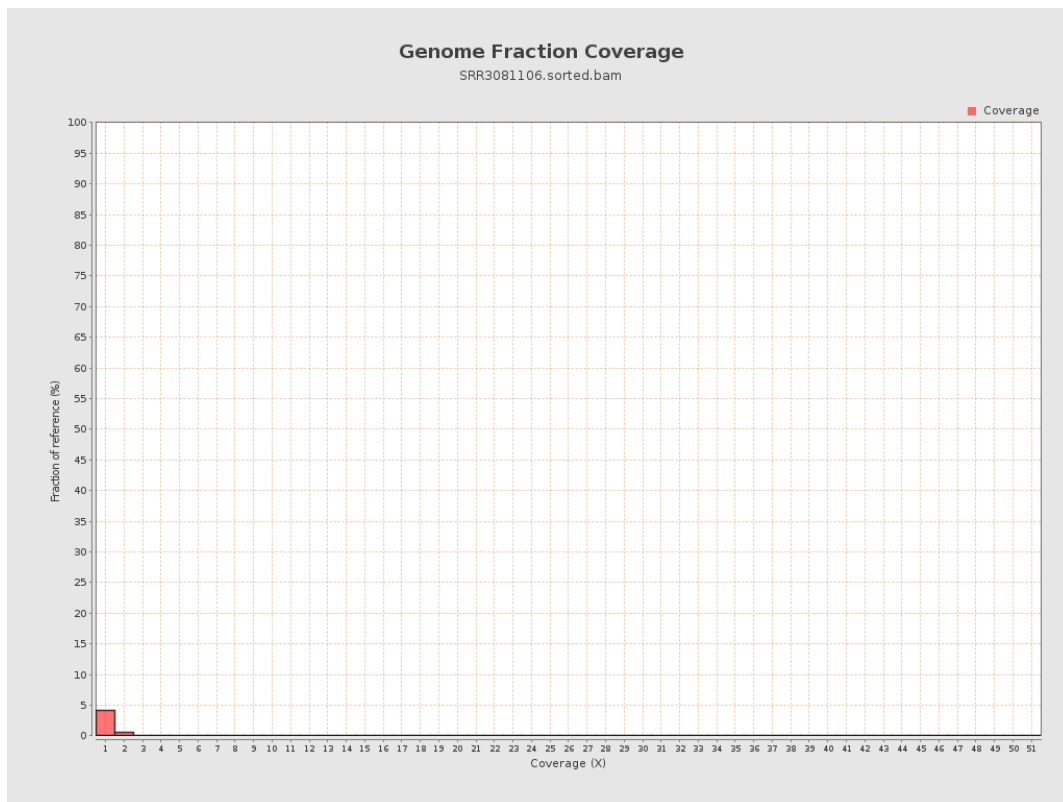


## 5. Results : Coverage Histogram (0-50X)

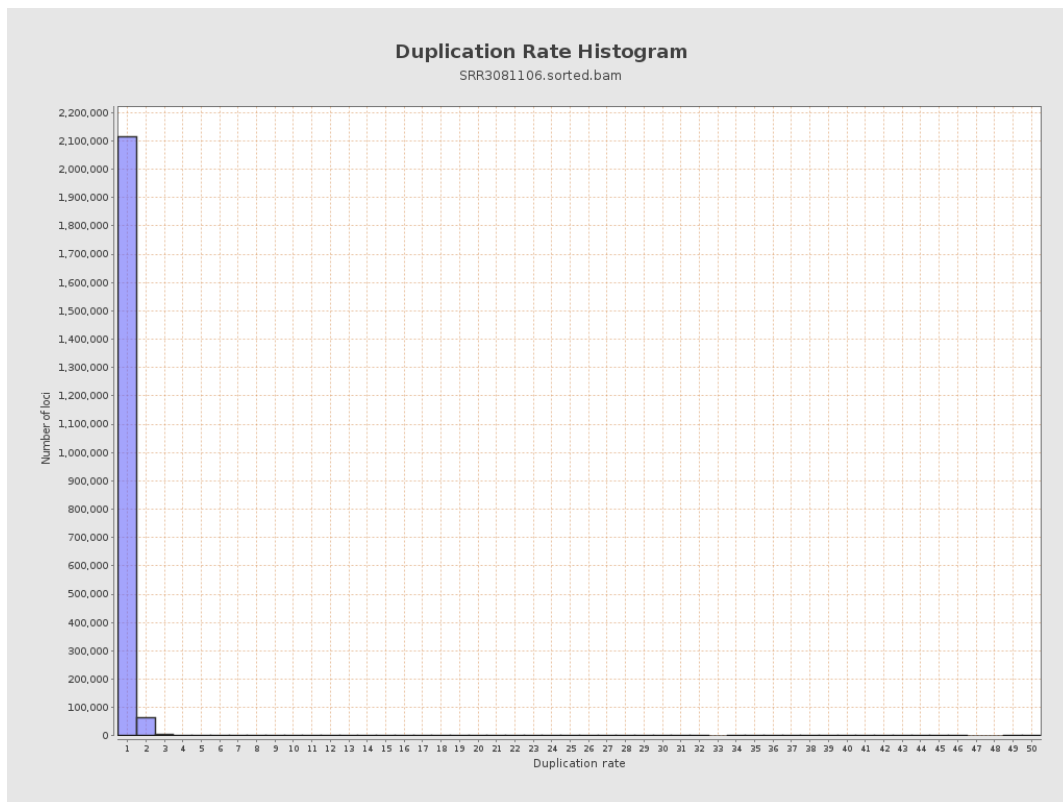




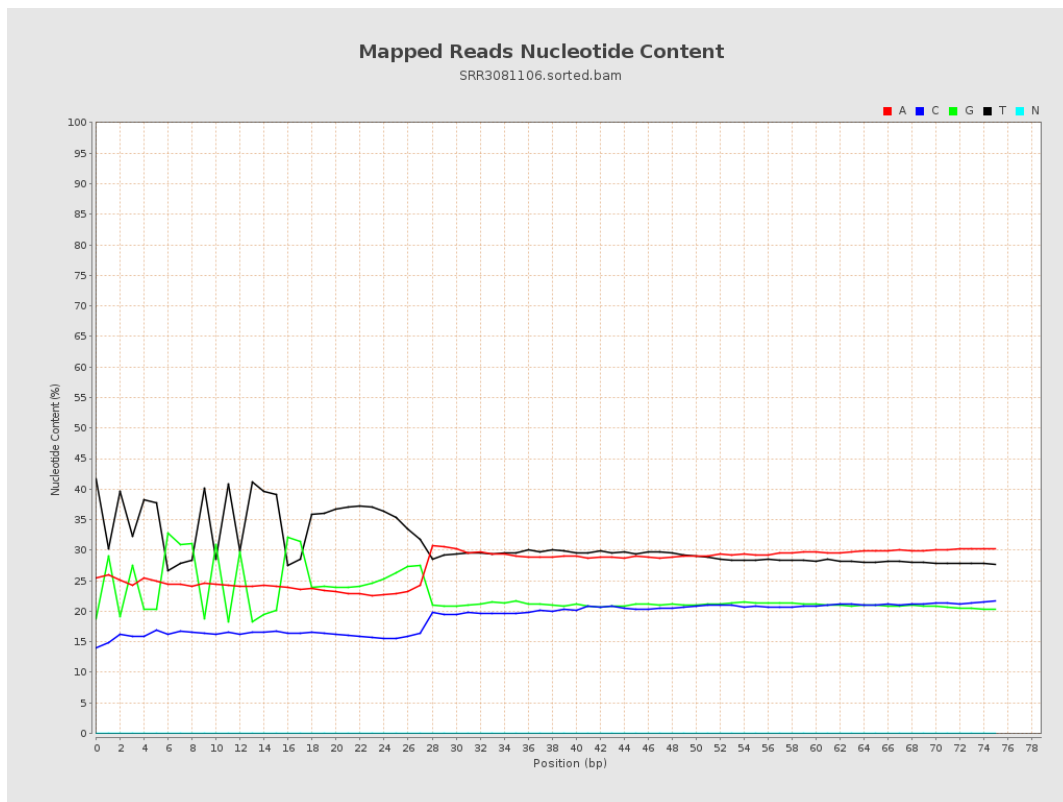
## 6. Results : Genome Fraction Coverage



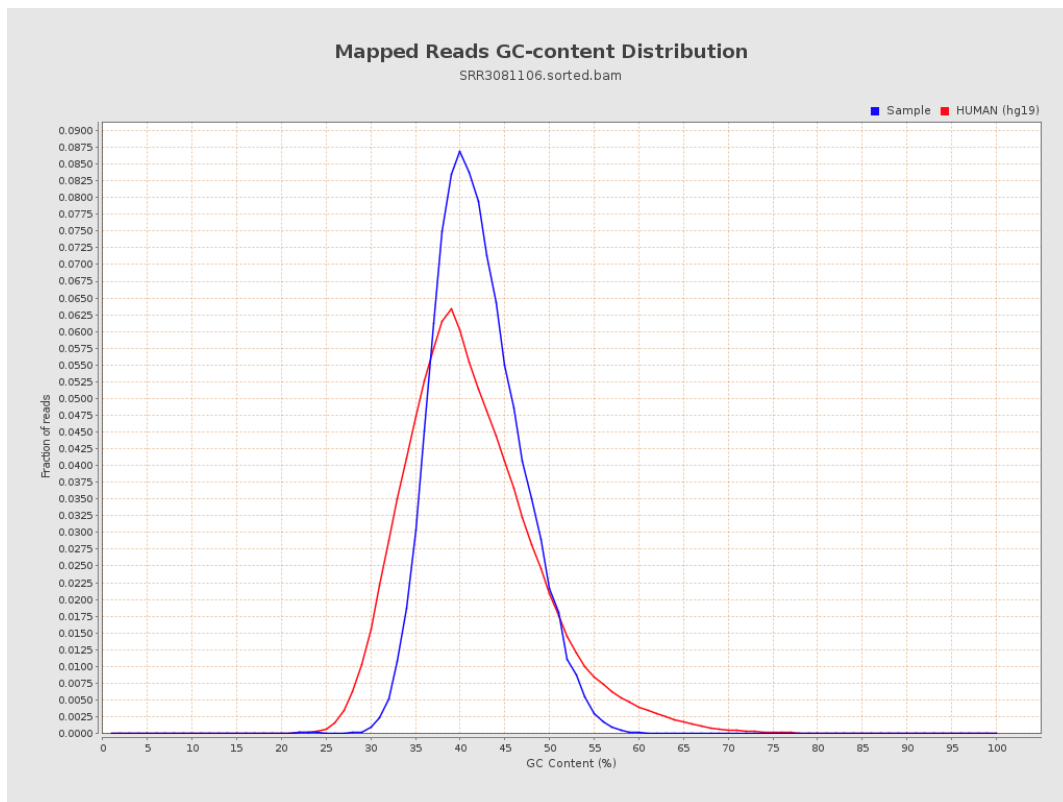
## 7. Results : Duplication Rate Histogram



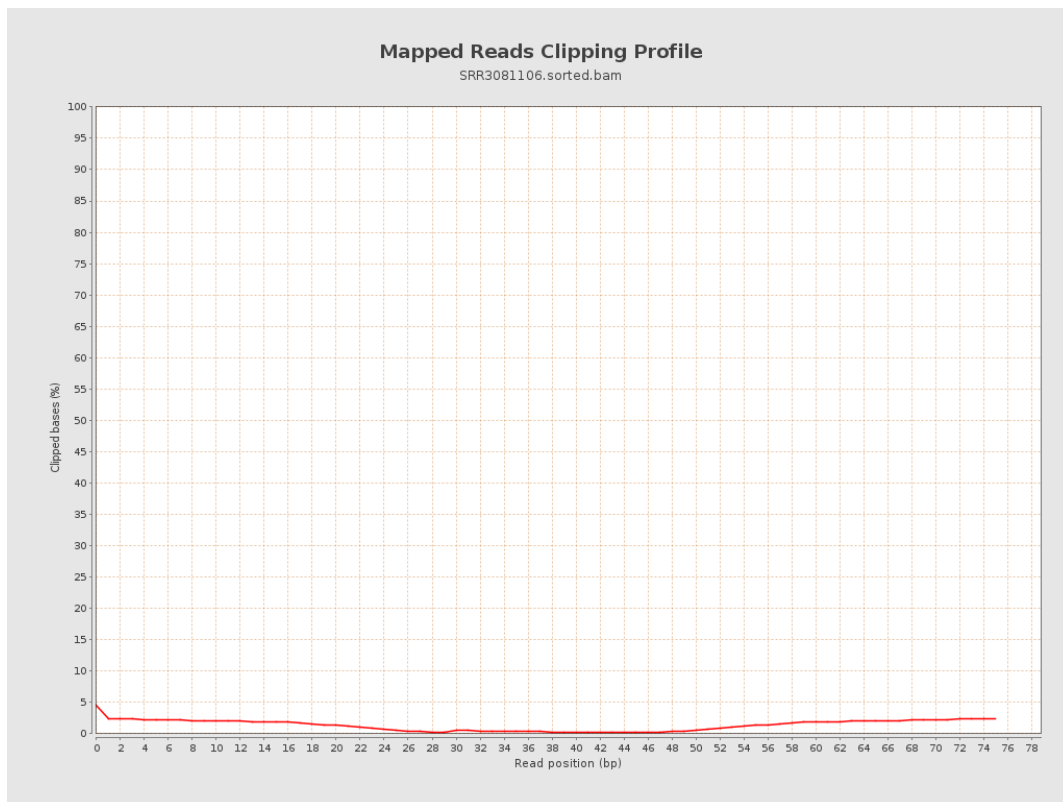
## 8. Results : Mapped Reads Nucleotide Content



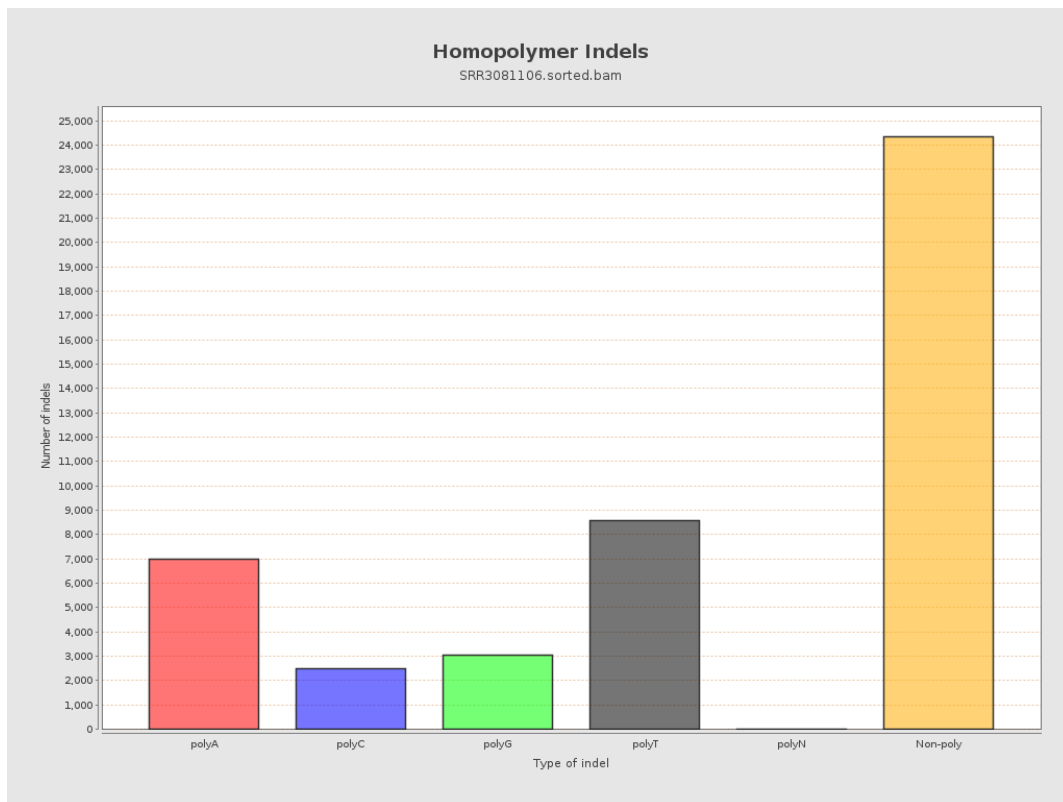
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

