

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/25 13:36:54*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084785.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_SRR3084785 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084785.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Sun Aug 25 13:36:53 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR3084785.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 1,759,277          |
| Mapped reads                 | 1,589,299 / 90.34% |
| Unmapped reads               | 169,978 / 9.66%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 15,751 / 0.9%      |
| Read min/max/mean length     | 30 / 76 / 76.31    |
| Duplicated reads (estimated) | 75,389 / 4.29%     |
| Duplication rate             | 3.97%              |
| Clipped reads                | 692,347 / 39.35%   |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 29,469,712 / 27.68% |
| Number/percentage of C's | 19,642,921 / 18.45% |
| Number/percentage of T's | 33,839,730 / 31.78% |
| Number/percentage of G's | 23,472,634 / 22.05% |
| Number/percentage of N's | 40,742 / 0.04%      |
| GC Percentage            | 40.5%               |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0344 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.2799 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 46.97 |
|----------------------|-------|

## 2.5. Mismatches and indels

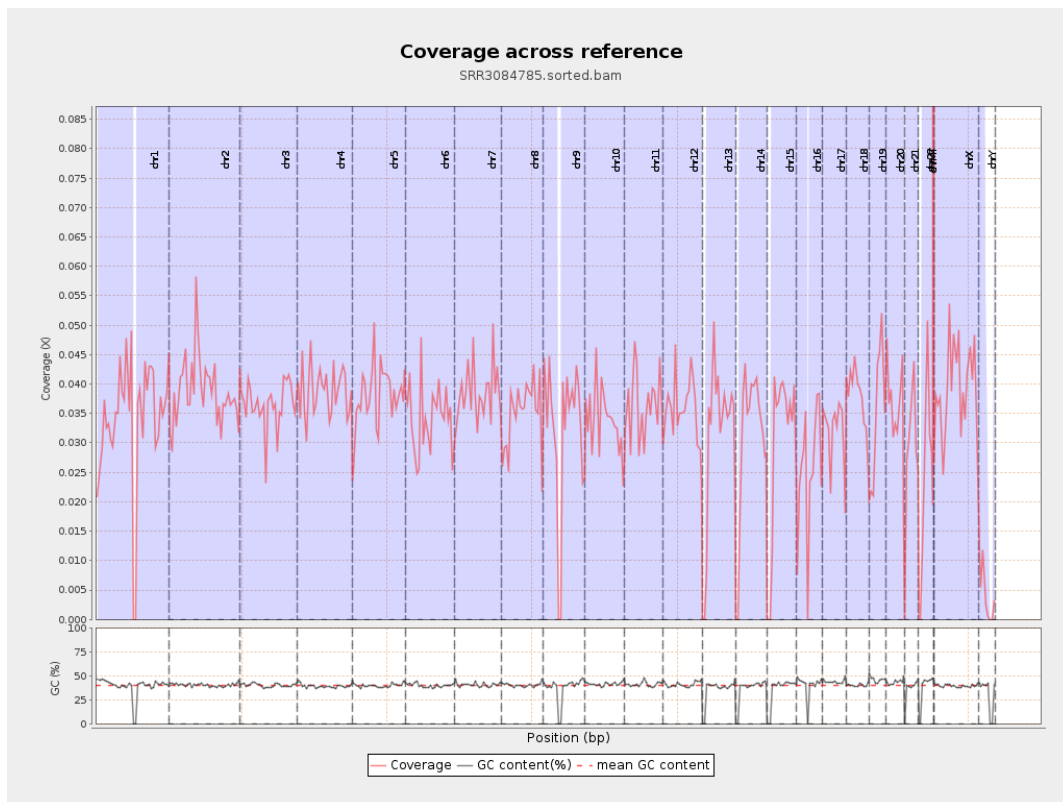
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 0.86%   |
| Mismatches                               | 898,942 |
| Insertions                               | 8,141   |
| Mapped reads with at least one insertion | 0.51%   |
| Deletions                                | 24,595  |
| Mapped reads with at least one deletion  | 1.53%   |
| Homopolymer indels                       | 47.81%  |

## 2.6. Chromosome stats

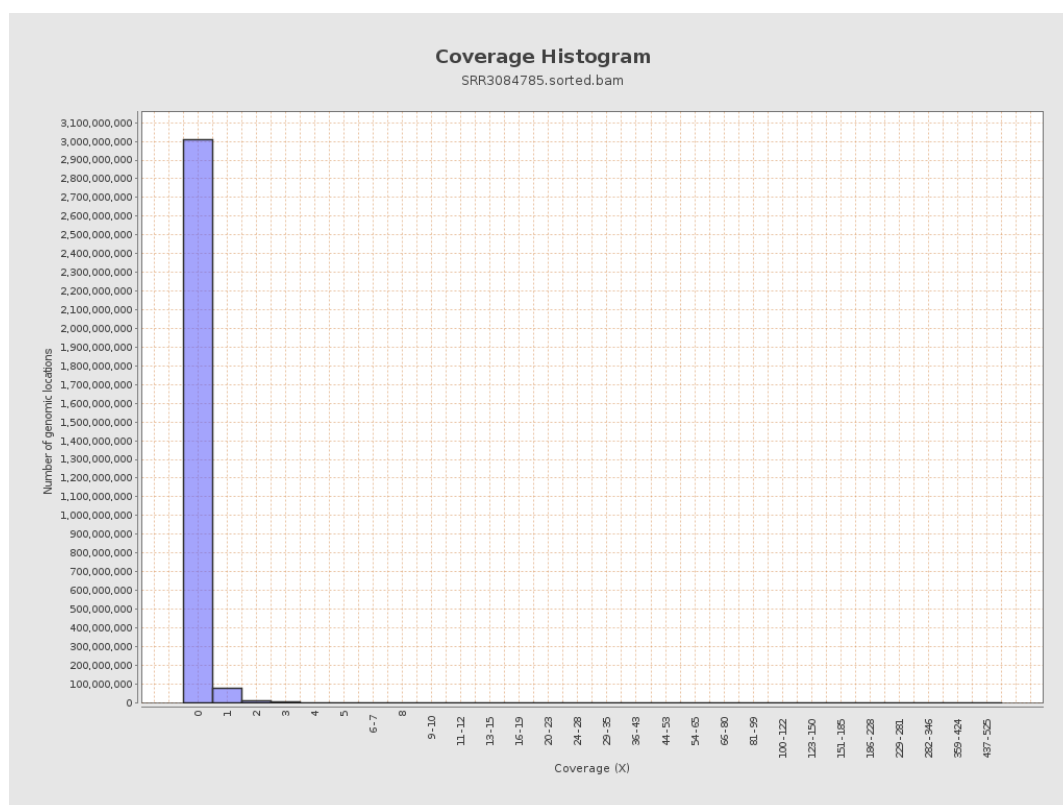
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 8496455      | 0.0341        | 0.3445             |
| chr2 | 243199373 | 9390986      | 0.0386        | 0.3574             |
| chr3 | 198022430 | 7235480      | 0.0365        | 0.2221             |
| chr4 | 191154276 | 7414462      | 0.0388        | 0.2361             |
| chr5 | 180915260 | 6895536      | 0.0381        | 0.2279             |
| chr6 | 171115067 | 5853952      | 0.0342        | 0.2487             |
| chr7 | 159138663 | 6133157      | 0.0385        | 0.366              |
|      |           |              |               |                    |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr8  | 146364022 | 5103956 | 0.0349 | 0.3477 |
| chr9  | 141213431 | 4549408 | 0.0322 | 0.2851 |
| chr10 | 135534747 | 4621970 | 0.0341 | 0.2634 |
| chr11 | 135006516 | 4898919 | 0.0363 | 0.2598 |
| chr12 | 133851895 | 4814217 | 0.036  | 0.2236 |
| chr13 | 115169878 | 3579646 | 0.0311 | 0.2058 |
| chr14 | 107349540 | 3294134 | 0.0307 | 0.2184 |
| chr15 | 102531392 | 3069246 | 0.0299 | 0.2093 |
| chr16 | 90354753  | 2311956 | 0.0256 | 0.2039 |
| chr17 | 81195210  | 2566507 | 0.0316 | 0.2275 |
| chr18 | 78077248  | 2967987 | 0.038  | 0.5137 |
| chr19 | 59128983  | 2086925 | 0.0353 | 0.3162 |
| chr20 | 63025520  | 2308238 | 0.0366 | 0.2298 |
| chr21 | 48129895  | 1401201 | 0.0291 | 0.2064 |
| chr22 | 51304566  | 1184153 | 0.0231 | 0.1748 |
| chrMT | 16571     | 11996   | 0.7239 | 1.0026 |
| chrX  | 155270560 | 6075235 | 0.0391 | 0.2449 |
| chrY  | 59373566  | 239732  | 0.004  | 0.0895 |

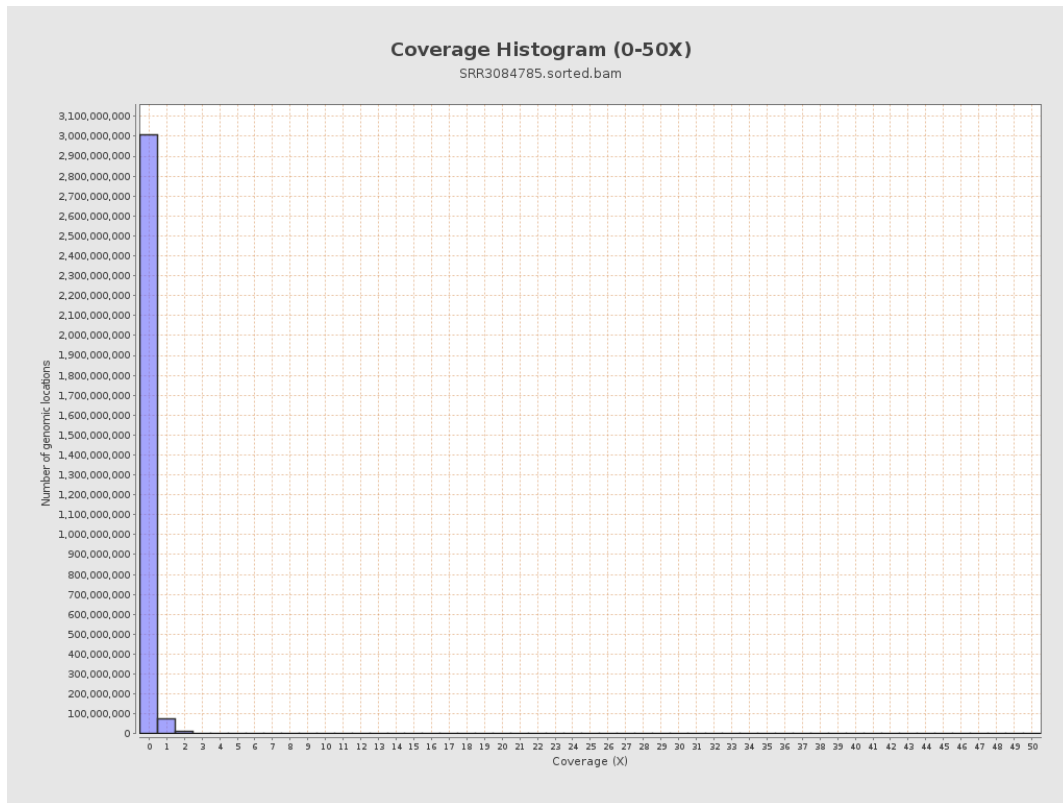
### 3. Results : Coverage across reference



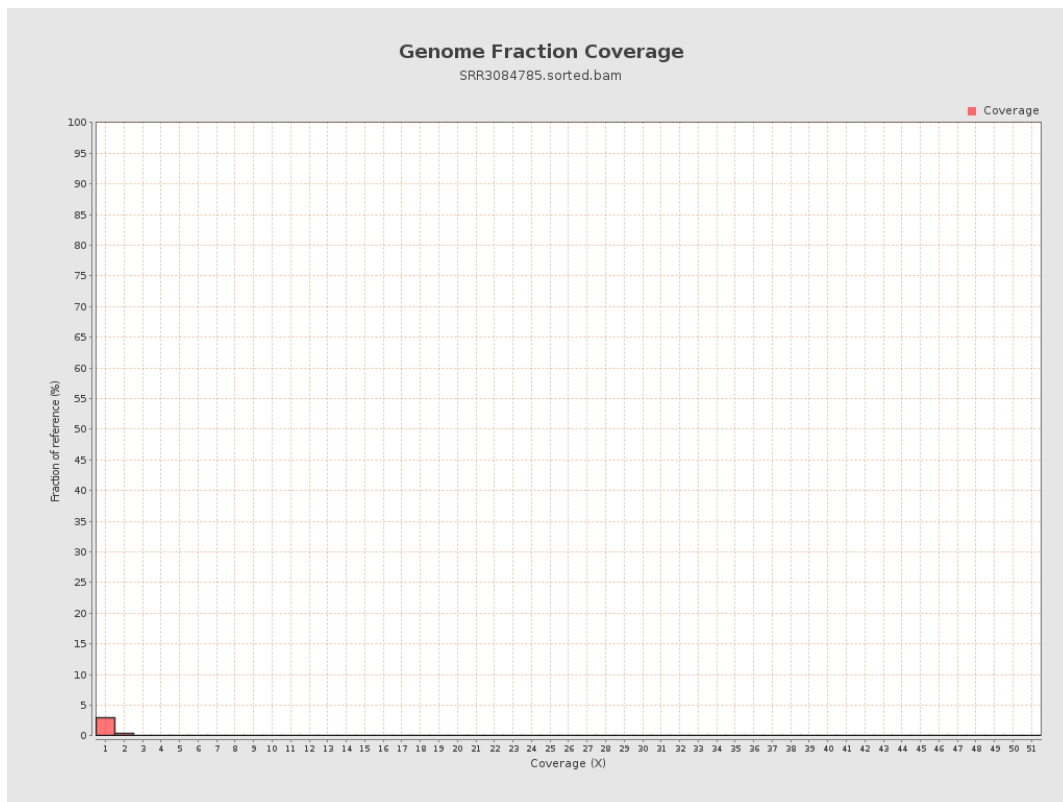
## 4. Results : Coverage Histogram



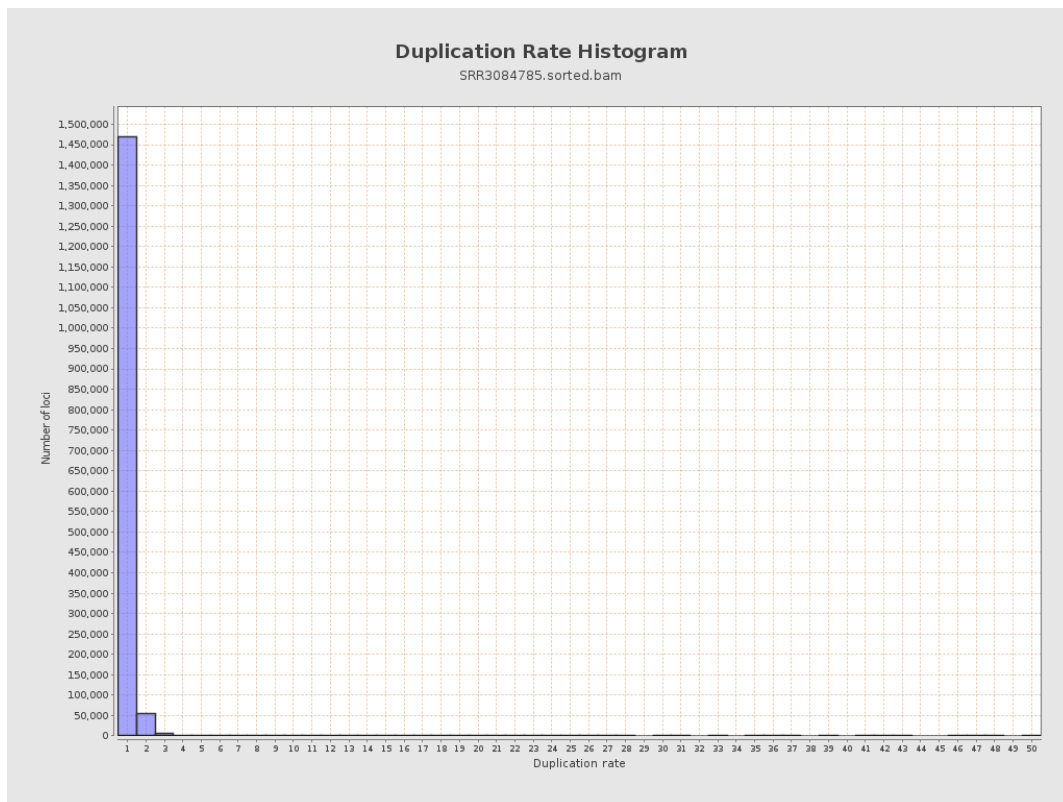
## 5. Results : Coverage Histogram (0-50X)



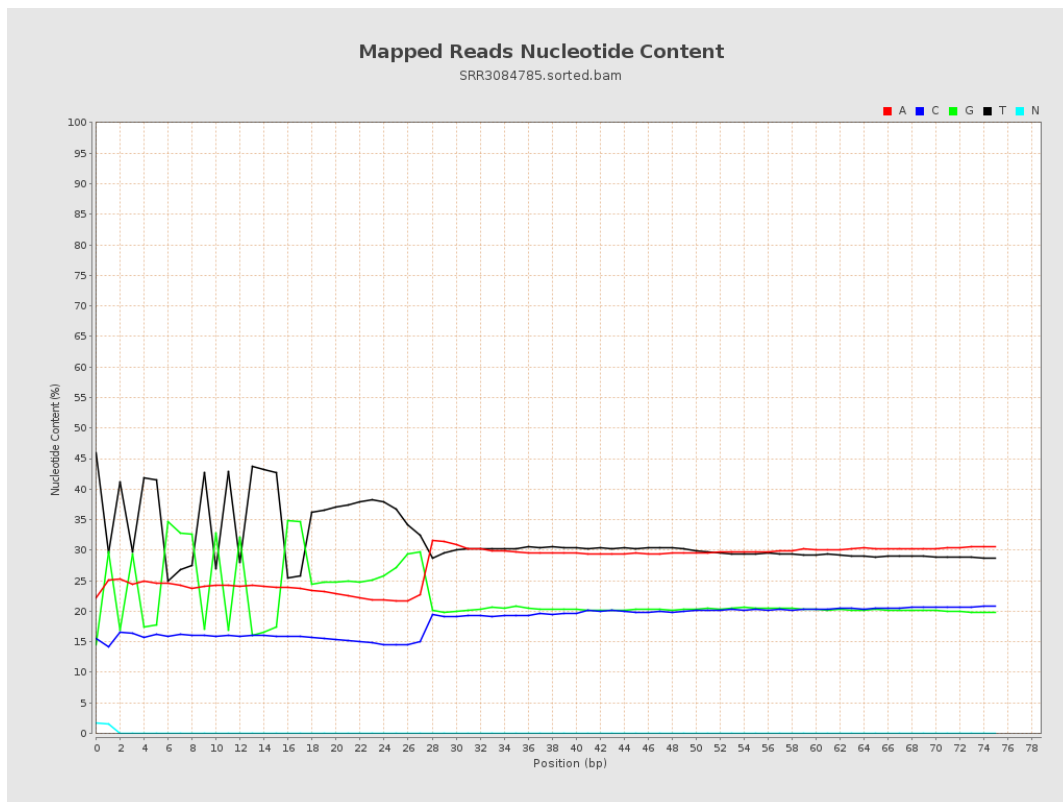
## 6. Results : Genome Fraction Coverage



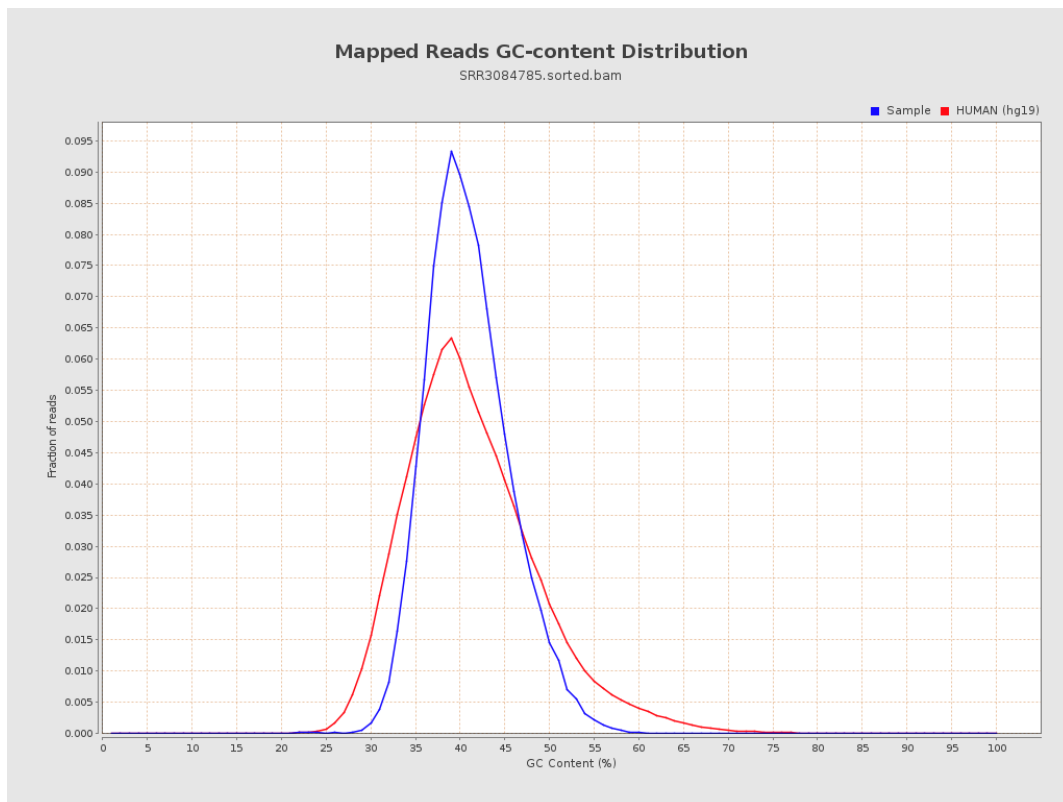
## 7. Results : Duplication Rate Histogram



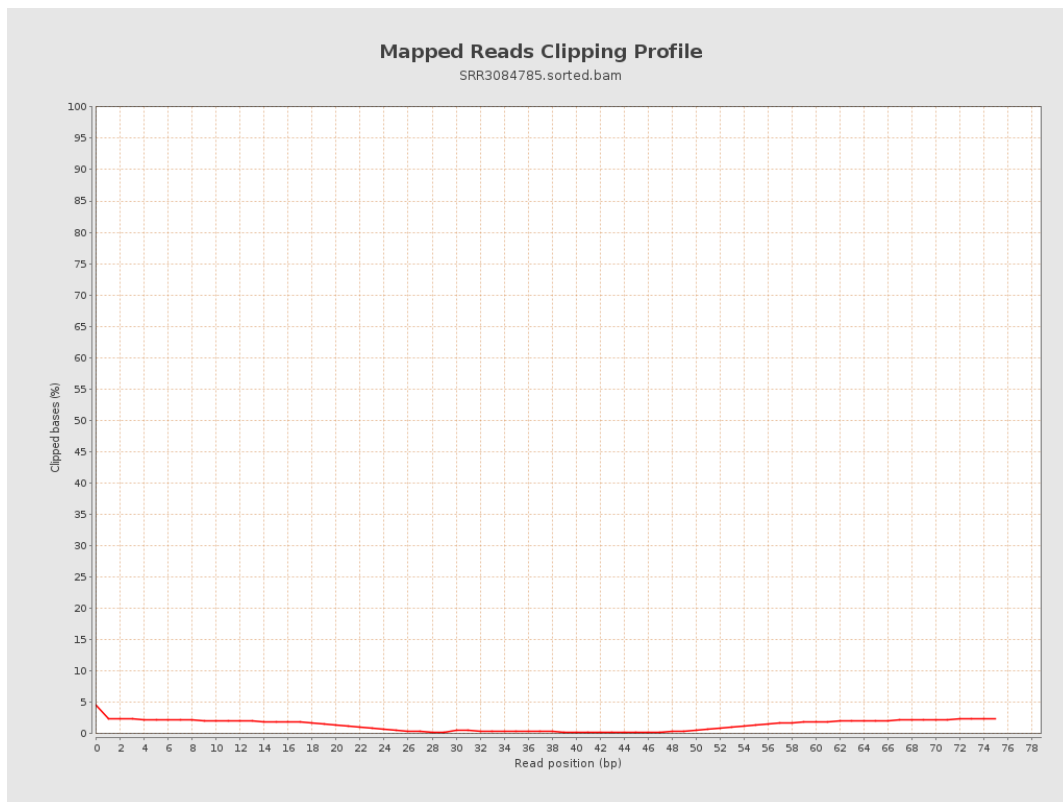
## 8. Results : Mapped Reads Nucleotide Content



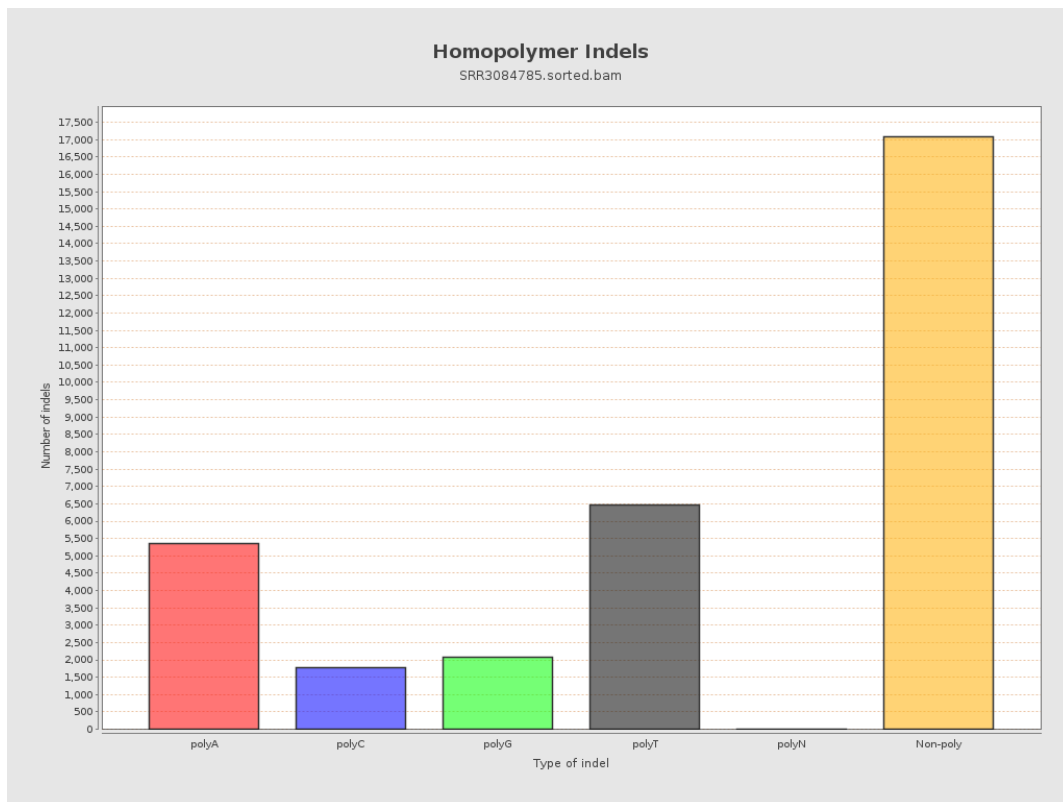
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

