

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/26 12:01:14*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251071.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_SRR10251071 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251071.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                            |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                             |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                             |
| Analysis date:                        | Mon Aug 26 12:01:14 CST 2024                                                                                                                                                                   |
| Size of a homopolymer:                | 3                                                                                                                                                                                              |
| Skip duplicate alignments:            | no                                                                                                                                                                                             |
| Number of windows:                    | 400                                                                                                                                                                                            |
| BAM file:                             | SRR10251071.sorted.bam                                                                                                                                                                         |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 4,435,807          |
| Mapped reads                 | 4,172,178 / 94.06% |
| Unmapped reads               | 263,629 / 5.94%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 32,557 / 0.73%     |
| Read min/max/mean length     | 30 / 80 / 80.26    |
| Duplicated reads (estimated) | 969,646 / 21.86%   |
| Duplication rate             | 20.65%             |
| Clipped reads                | 549,180 / 12.38%   |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 94,387,823 / 29.13% |
| Number/percentage of C's | 64,750,925 / 19.98% |
| Number/percentage of T's | 95,815,956 / 29.57% |
| Number/percentage of G's | 69,093,491 / 21.32% |
| Number/percentage of N's | 2,687 / 0%          |
| GC Percentage            | 41.3%               |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.1047 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.9913 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 48.27 |
|----------------------|-------|

## 2.5. Mismatches and indels

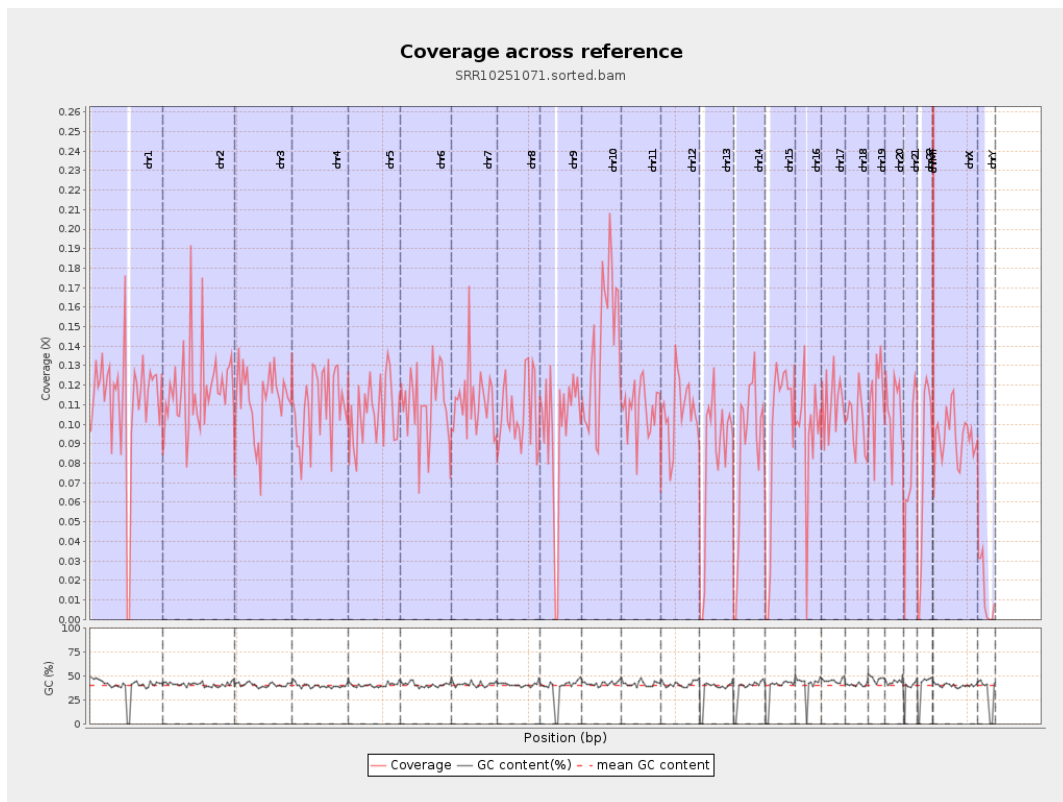
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.59%     |
| Mismatches                               | 1,836,147 |
| Insertions                               | 39,340    |
| Mapped reads with at least one insertion | 0.92%     |
| Deletions                                | 115,818   |
| Mapped reads with at least one deletion  | 2.73%     |
| Homopolymer indels                       | 45.42%    |

## 2.6. Chromosome stats

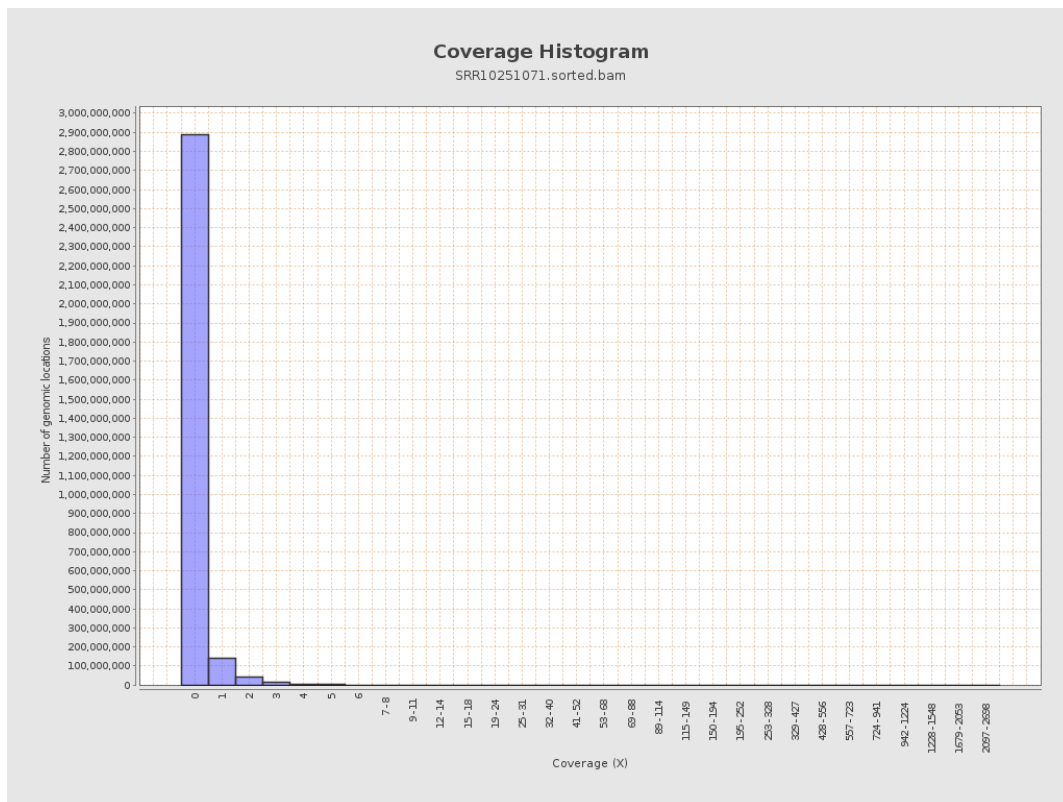
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 27755446     | 0.1114        | 1.9408             |
| chr2 | 243199373 | 28832052     | 0.1186        | 1.3408             |
| chr3 | 198022430 | 22237233     | 0.1123        | 0.4872             |
| chr4 | 191154276 | 20939829     | 0.1095        | 0.5488             |
| chr5 | 180915260 | 19264064     | 0.1065        | 0.4874             |
| chr6 | 171115067 | 18827330     | 0.11          | 0.6042             |
| chr7 | 159138663 | 17782232     | 0.1117        | 1.4483             |
|      |           |              |               |                    |

|       |           |          |        |         |
|-------|-----------|----------|--------|---------|
| chr8  | 146364022 | 15480287 | 0.1058 | 0.6534  |
| chr9  | 141213431 | 13720401 | 0.0972 | 1.0227  |
| chr10 | 135534747 | 18912120 | 0.1395 | 1.0053  |
| chr11 | 135006516 | 14531685 | 0.1076 | 0.6732  |
| chr12 | 133851895 | 14416232 | 0.1077 | 0.4905  |
| chr13 | 115169878 | 9509924  | 0.0826 | 0.4095  |
| chr14 | 107349540 | 9431644  | 0.0879 | 0.6627  |
| chr15 | 102531392 | 9570585  | 0.0933 | 0.4394  |
| chr16 | 90354753  | 8689594  | 0.0962 | 0.8117  |
| chr17 | 81195210  | 9091599  | 0.112  | 0.5927  |
| chr18 | 78077248  | 7892848  | 0.1011 | 1.1781  |
| chr19 | 59128983  | 6780163  | 0.1147 | 1.9834  |
| chr20 | 63025520  | 6705642  | 0.1064 | 0.5217  |
| chr21 | 48129895  | 3868536  | 0.0804 | 0.4413  |
| chr22 | 51304566  | 4022908  | 0.0784 | 0.4353  |
| chrMT | 16571     | 651903   | 39.34  | 21.2092 |
| chrX  | 155270560 | 14536737 | 0.0936 | 0.5159  |
| chrY  | 59373566  | 805670   | 0.0136 | 0.9604  |

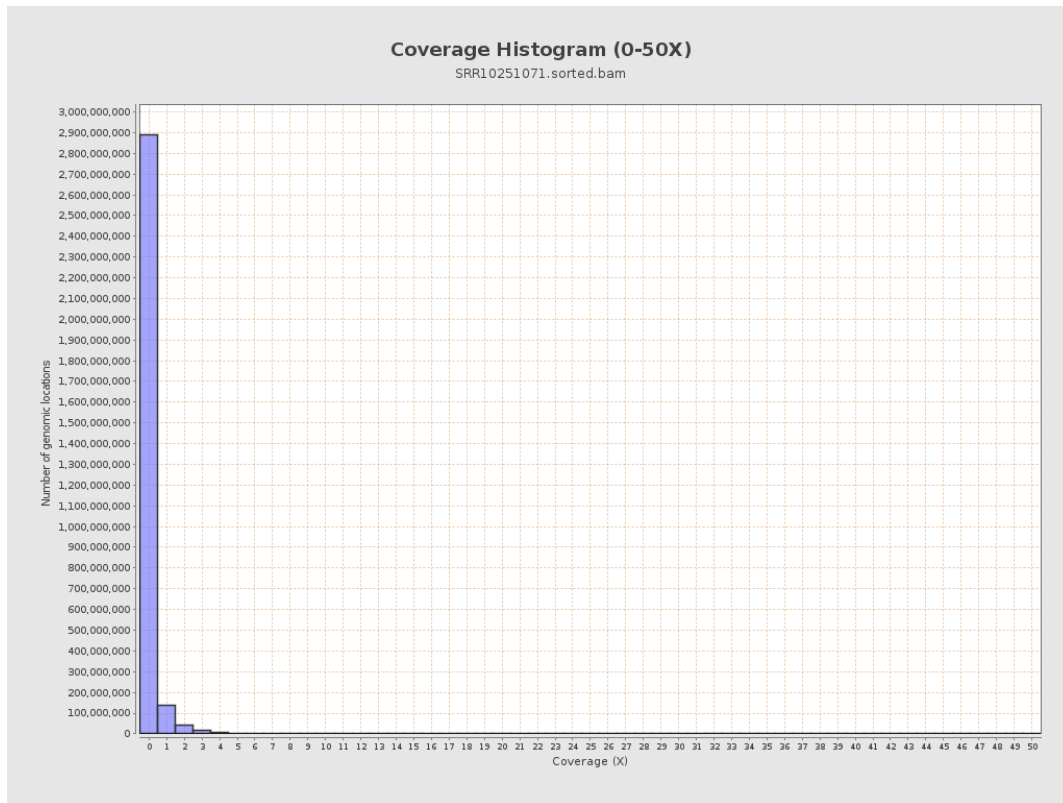
### 3. Results : Coverage across reference



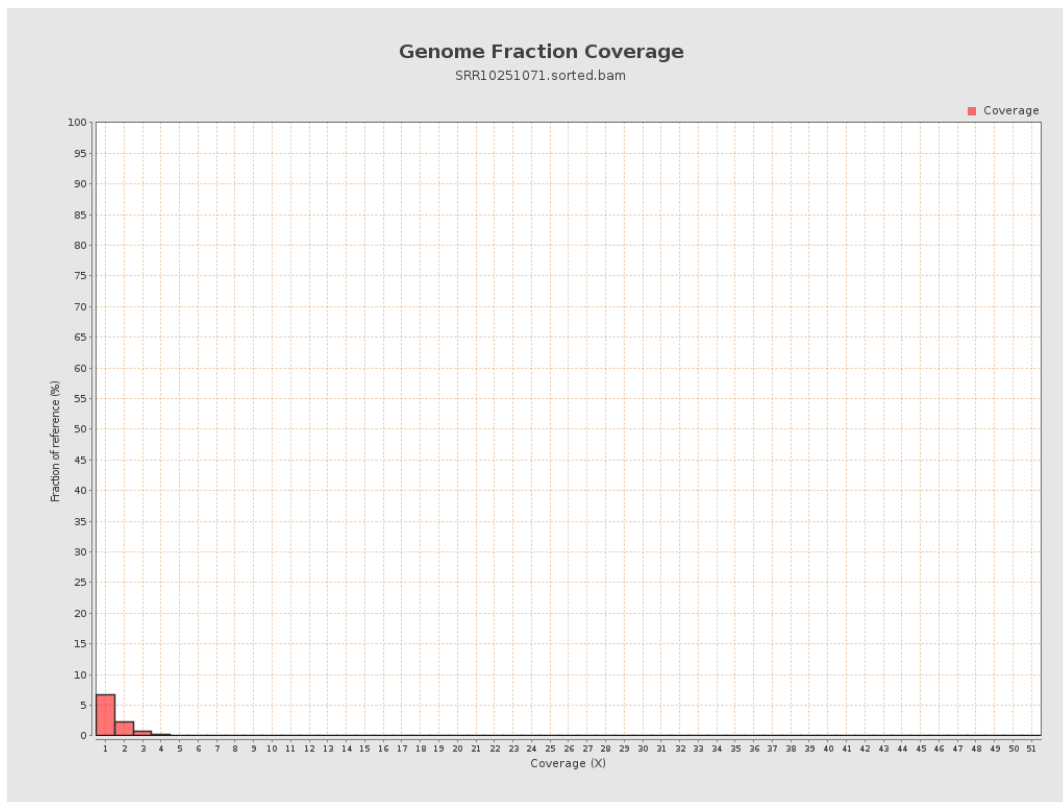
## 4. Results : Coverage Histogram



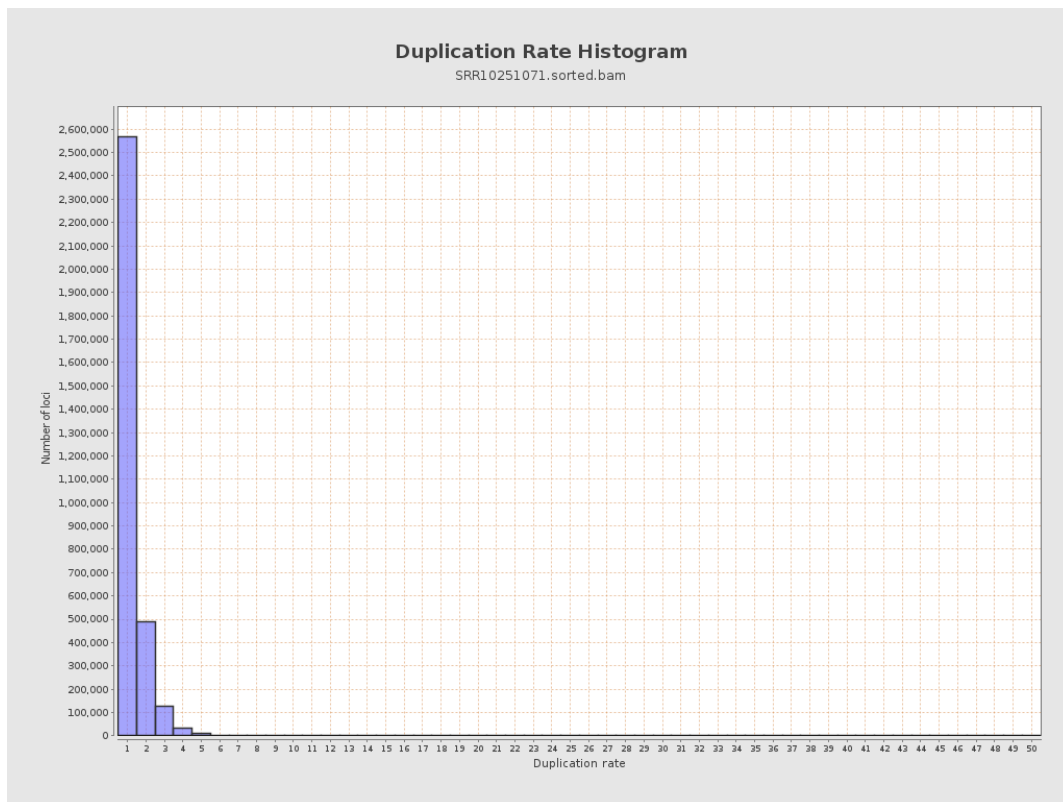
## 5. Results : Coverage Histogram (0-50X)



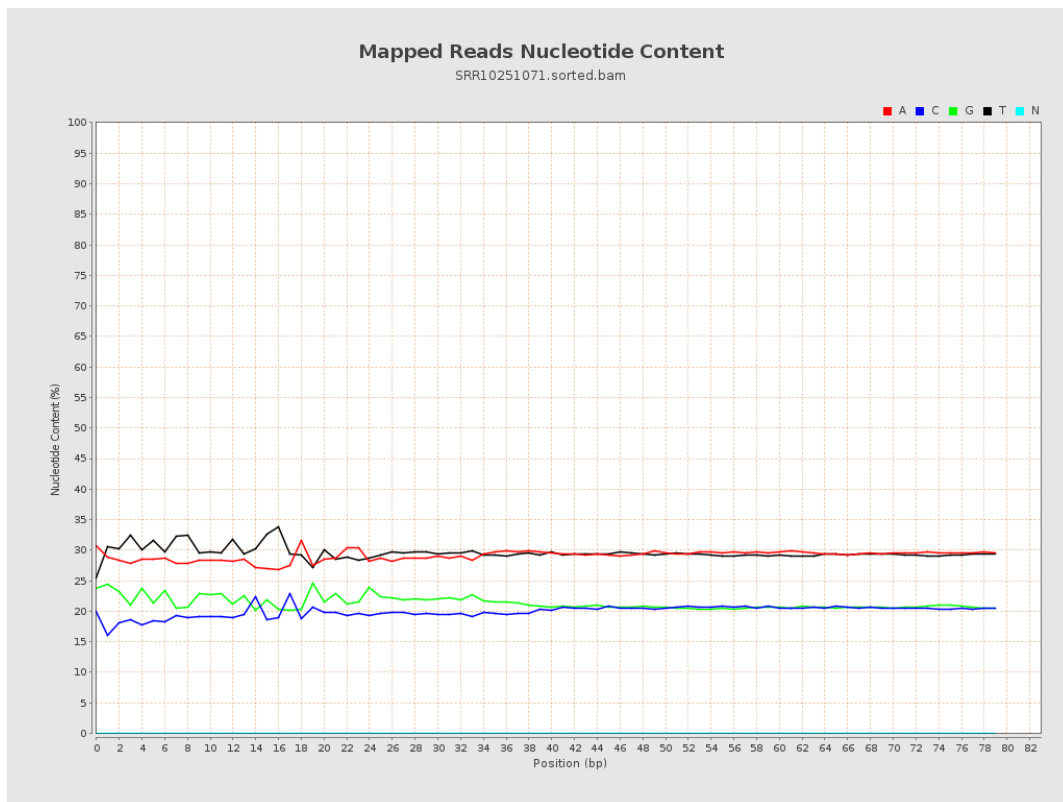
## 6. Results : Genome Fraction Coverage



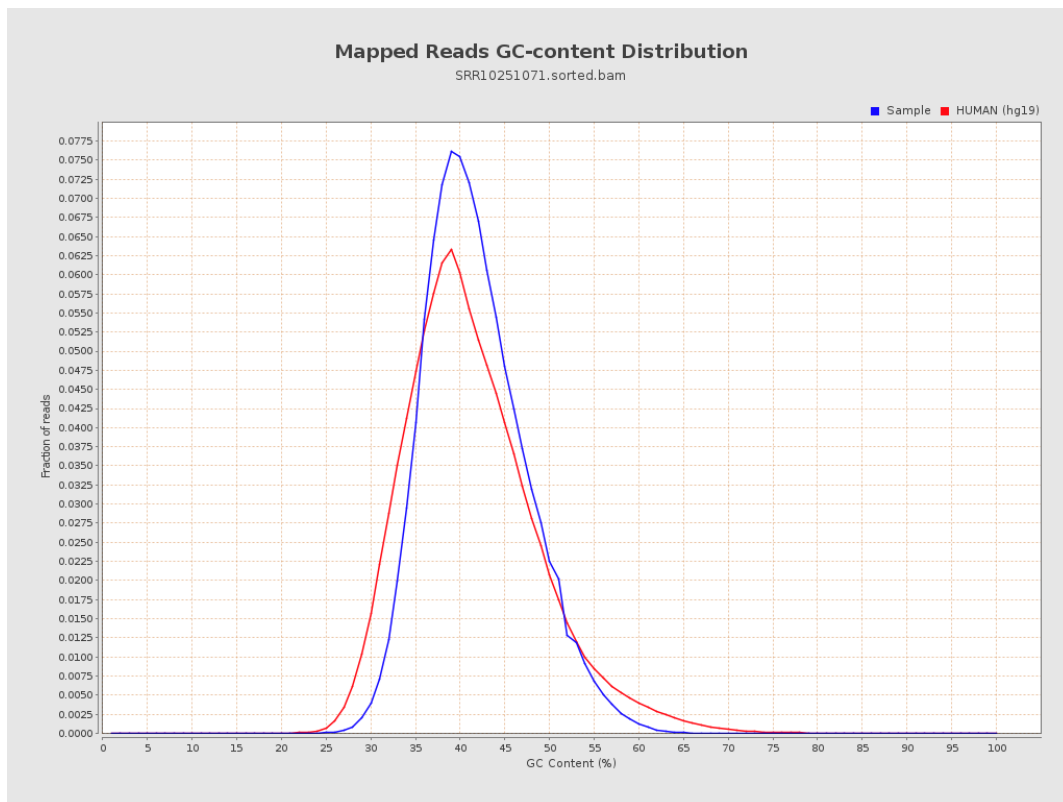
## 7. Results : Duplication Rate Histogram



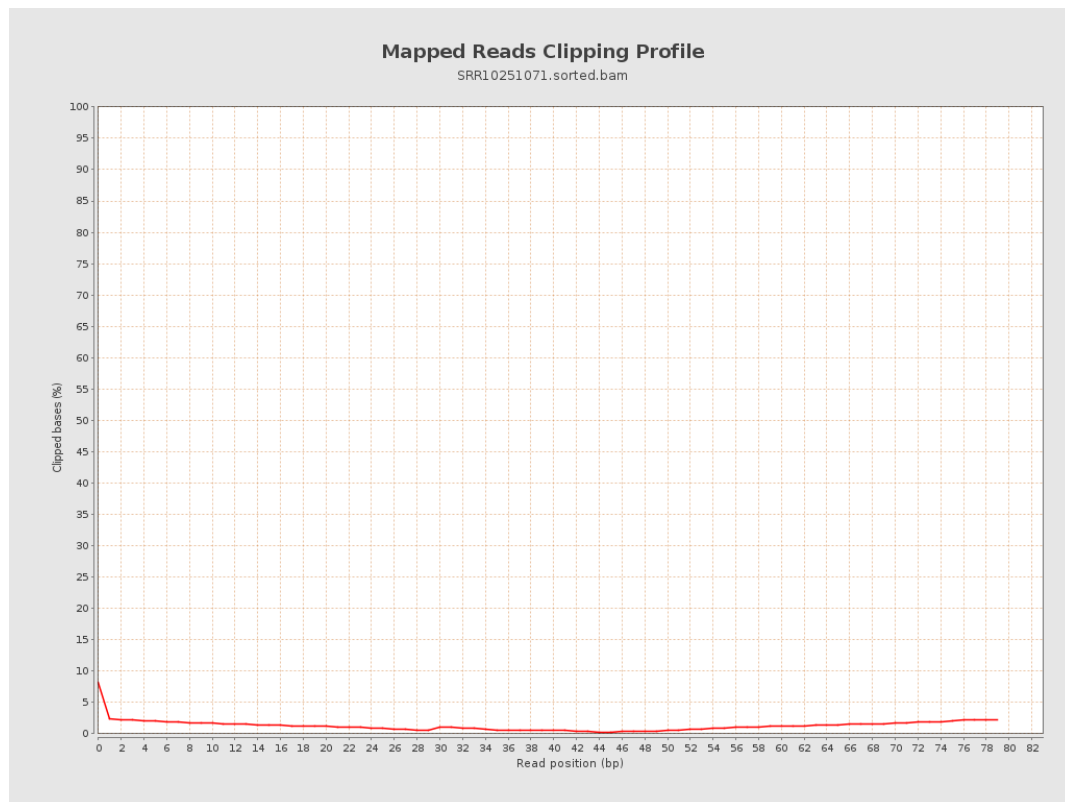
## 8. Results : Mapped Reads Nucleotide Content



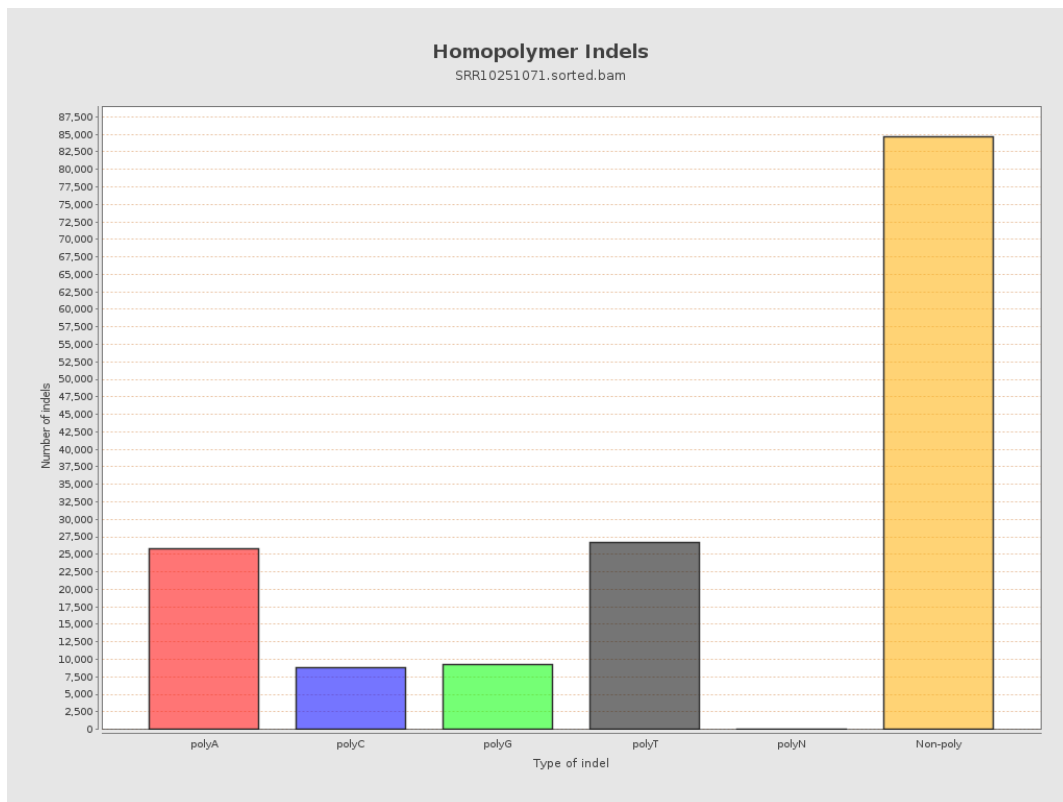
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

