

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/22 14:22:14*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080675.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_SRR3080675 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080675.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Thu Aug 22 14:22:12 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR3080675.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 1,548,396          |
| Mapped reads                 | 1,405,582 / 90.78% |
| Unmapped reads               | 142,814 / 9.22%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 12,421 / 0.8%      |
| Read min/max/mean length     | 30 / 76 / 76.28    |
| Duplicated reads (estimated) | 50,143 / 3.24%     |
| Duplication rate             | 3.07%              |
| Clipped reads                | 696,159 / 44.96%   |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 24,692,733 / 26.79% |
| Number/percentage of C's | 17,157,285 / 18.62% |
| Number/percentage of T's | 28,933,337 / 31.39% |
| Number/percentage of G's | 21,371,908 / 23.19% |
| Number/percentage of N's | 4,256 / 0%          |
| GC Percentage            | 41.81%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0298 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.2363 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 44.49 |
|----------------------|-------|

## 2.5. Mismatches and indels

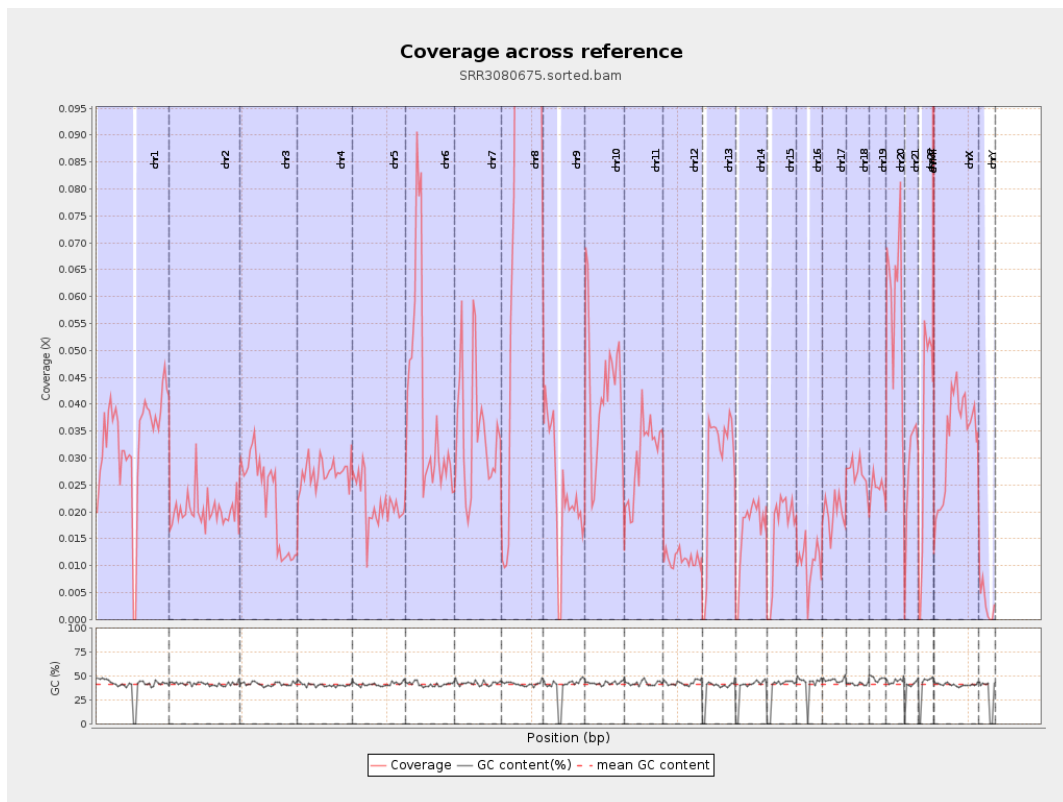
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 0.71%   |
| Mismatches                               | 642,720 |
| Insertions                               | 6,729   |
| Mapped reads with at least one insertion | 0.47%   |
| Deletions                                | 21,538  |
| Mapped reads with at least one deletion  | 1.52%   |
| Homopolymer indels                       | 47.81%  |

## 2.6. Chromosome stats

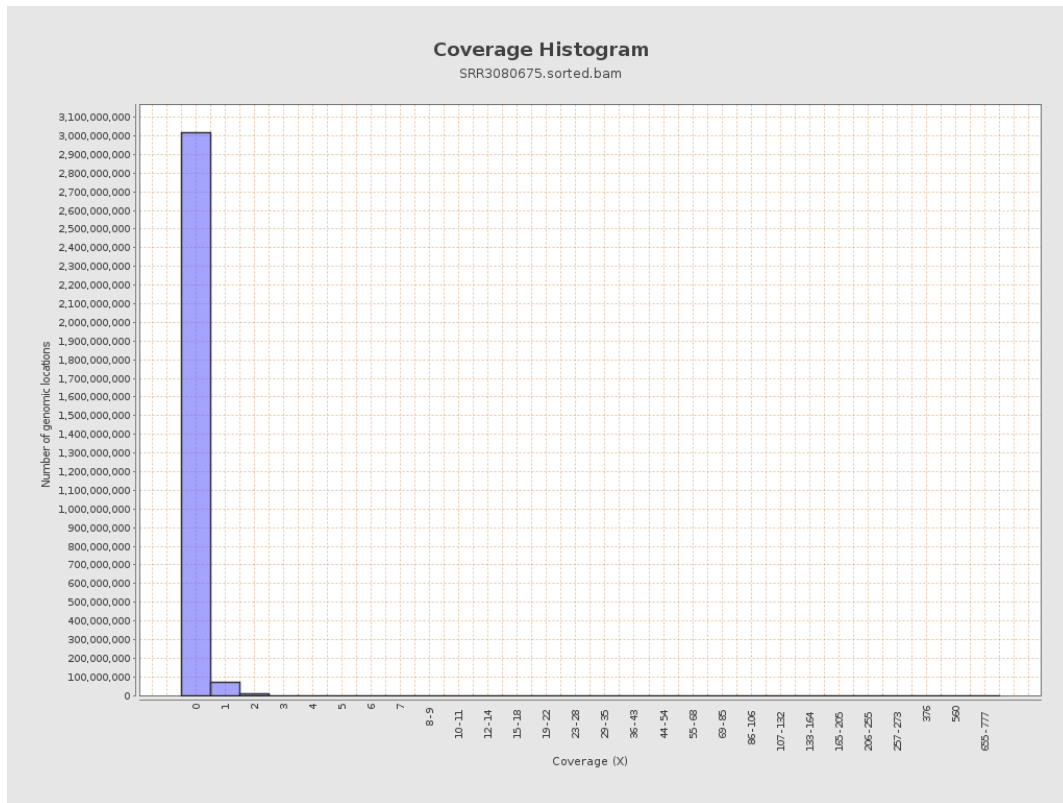
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 8256848      | 0.0331        | 0.2335             |
| chr2 | 243199373 | 4919902      | 0.0202        | 0.3715             |
| chr3 | 198022430 | 4390240      | 0.0222        | 0.1645             |
| chr4 | 191154276 | 5230300      | 0.0274        | 0.1866             |
| chr5 | 180915260 | 3885741      | 0.0215        | 0.1616             |
| chr6 | 171115067 | 6750714      | 0.0395        | 0.2544             |
| chr7 | 159138663 | 5570646      | 0.035         | 0.3643             |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr8  | 146364022 | 13442766 | 0.0918 | 0.3765 |
| chr9  | 141213431 | 3339509  | 0.0236 | 0.1996 |
| chr10 | 135534747 | 5773561  | 0.0426 | 0.2331 |
| chr11 | 135006516 | 4041177  | 0.0299 | 0.2026 |
| chr12 | 133851895 | 1497218  | 0.0112 | 0.1202 |
| chr13 | 115169878 | 3319669  | 0.0288 | 0.1886 |
| chr14 | 107349540 | 1760239  | 0.0164 | 0.1467 |
| chr15 | 102531392 | 1672810  | 0.0163 | 0.1526 |
| chr16 | 90354753  | 948524   | 0.0105 | 0.1208 |
| chr17 | 81195210  | 1592183  | 0.0196 | 0.1581 |
| chr18 | 78077248  | 2133055  | 0.0273 | 0.2415 |
| chr19 | 59128983  | 1444030  | 0.0244 | 0.1881 |
| chr20 | 63025520  | 3679321  | 0.0584 | 0.2744 |
| chr21 | 48129895  | 1351965  | 0.0281 | 0.1894 |
| chr22 | 51304566  | 1799179  | 0.0351 | 0.2106 |
| chrMT | 16571     | 10906    | 0.6581 | 0.9352 |
| chrX  | 155270560 | 5198246  | 0.0335 | 0.2097 |
| chrY  | 59373566  | 185440   | 0.0031 | 0.0676 |

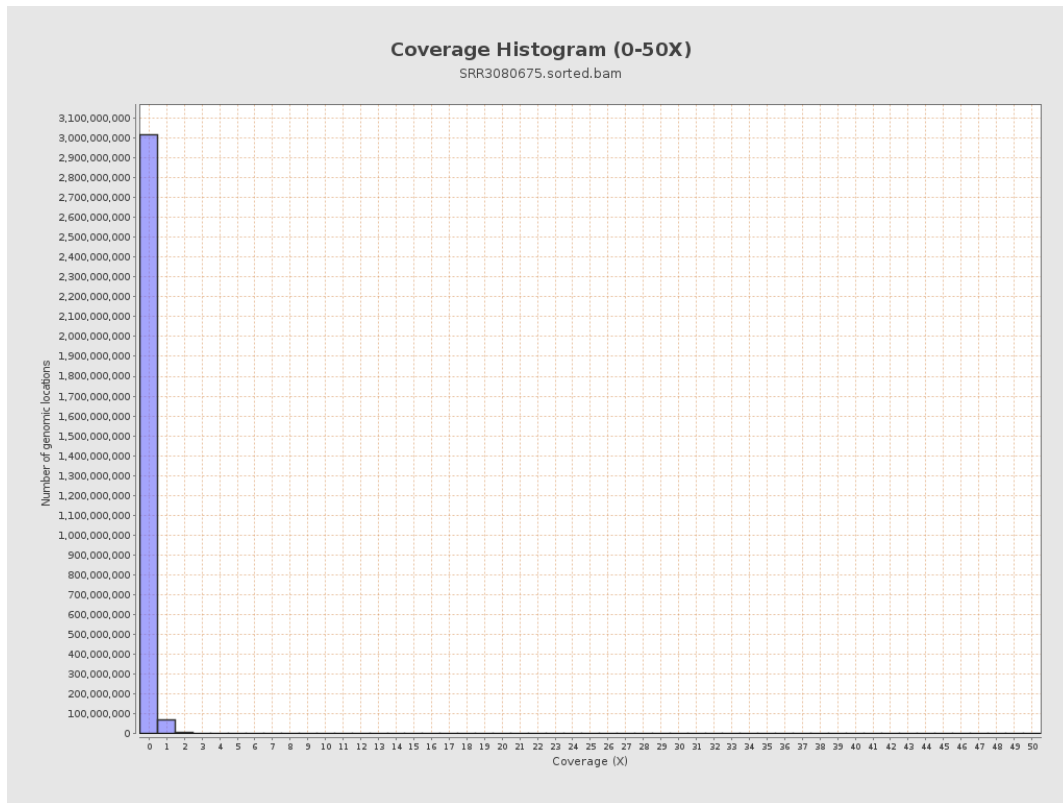
### 3. Results : Coverage across reference



## 4. Results : Coverage Histogram

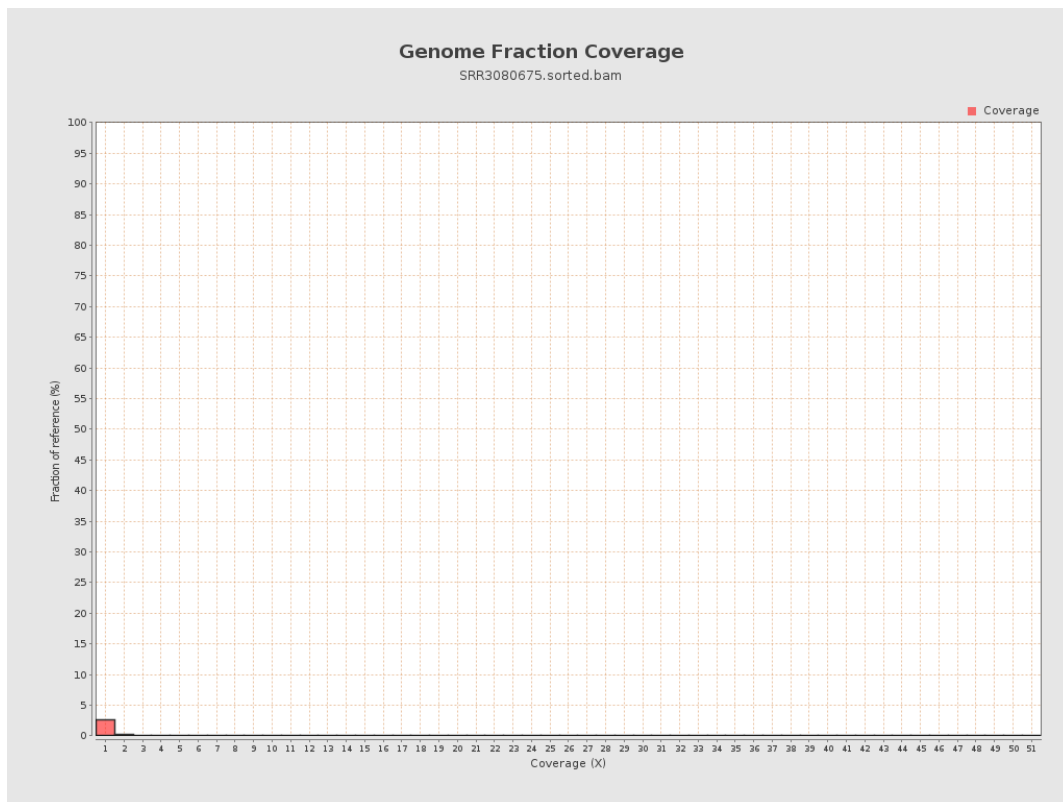


## 5. Results : Coverage Histogram (0-50X)

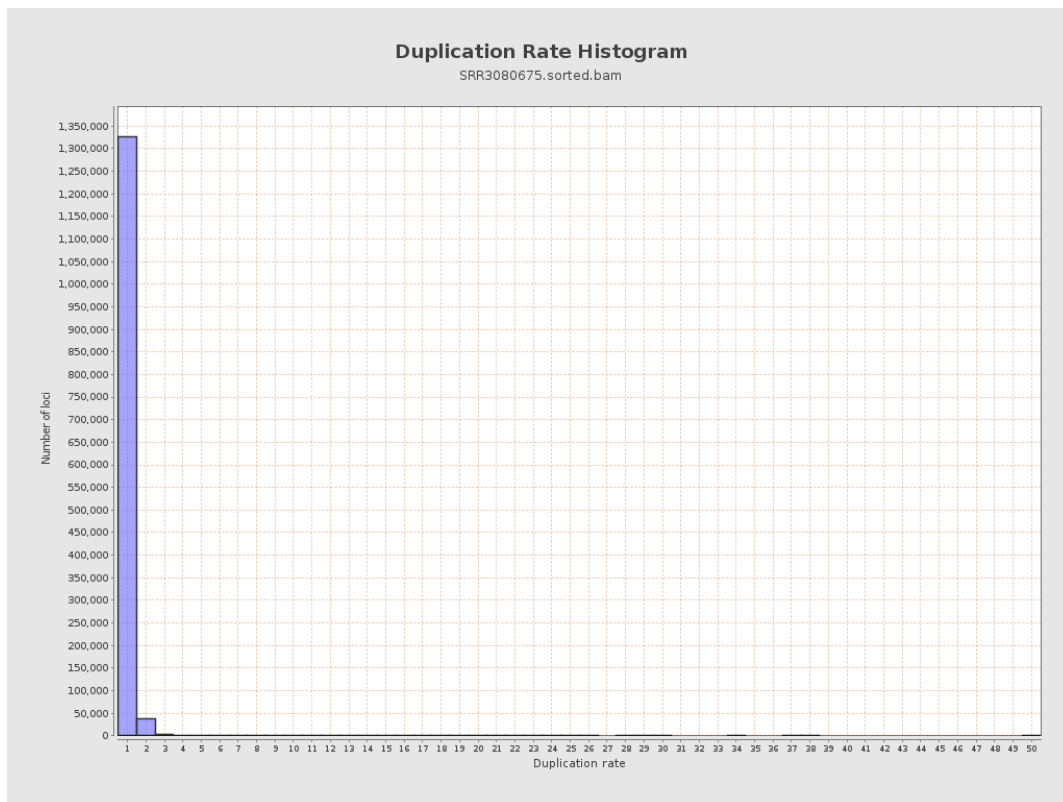




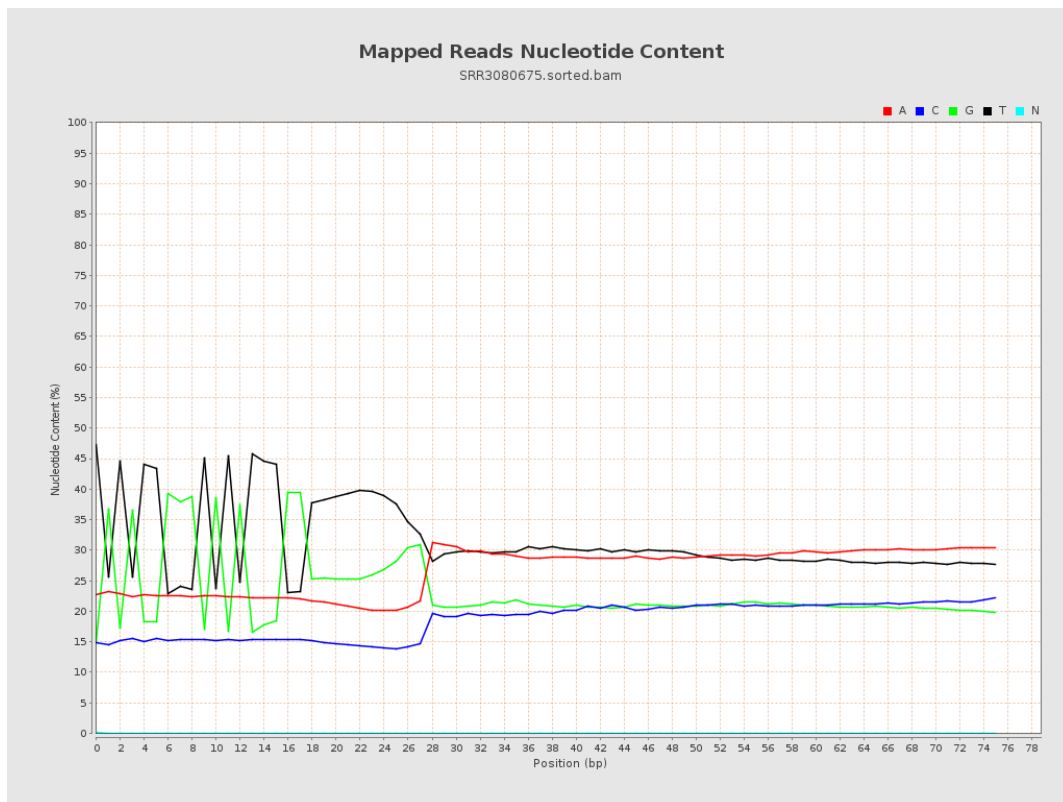
## 6. Results : Genome Fraction Coverage



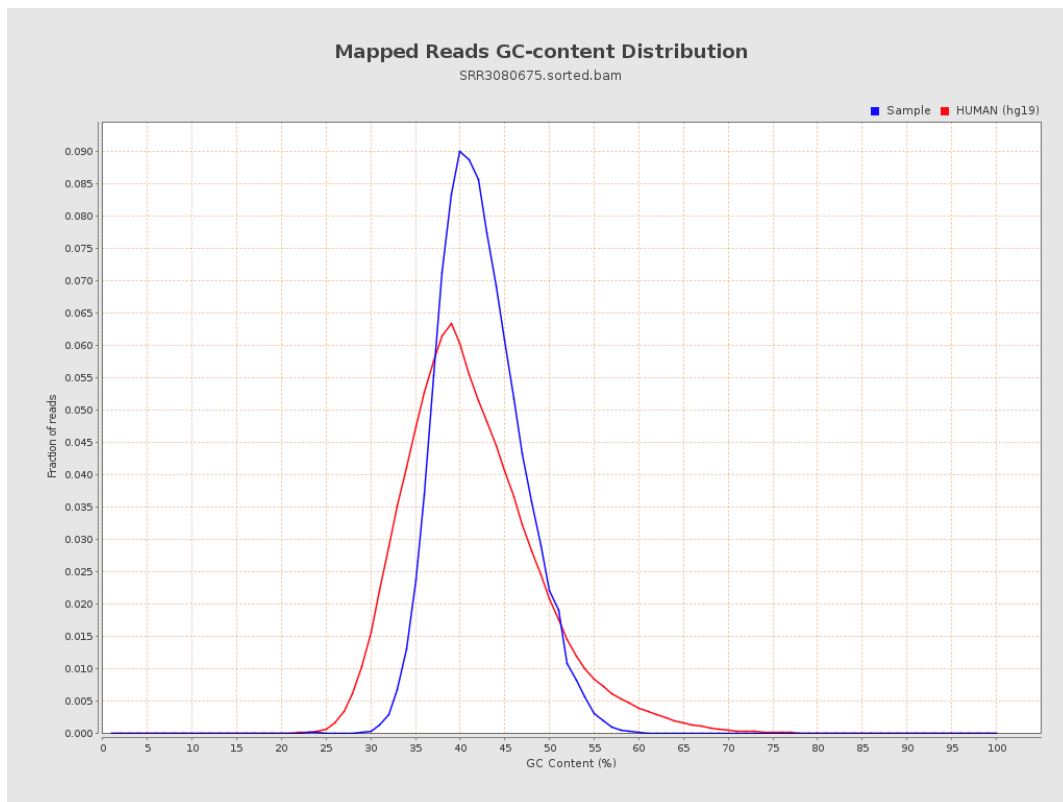
## 7. Results : Duplication Rate Histogram



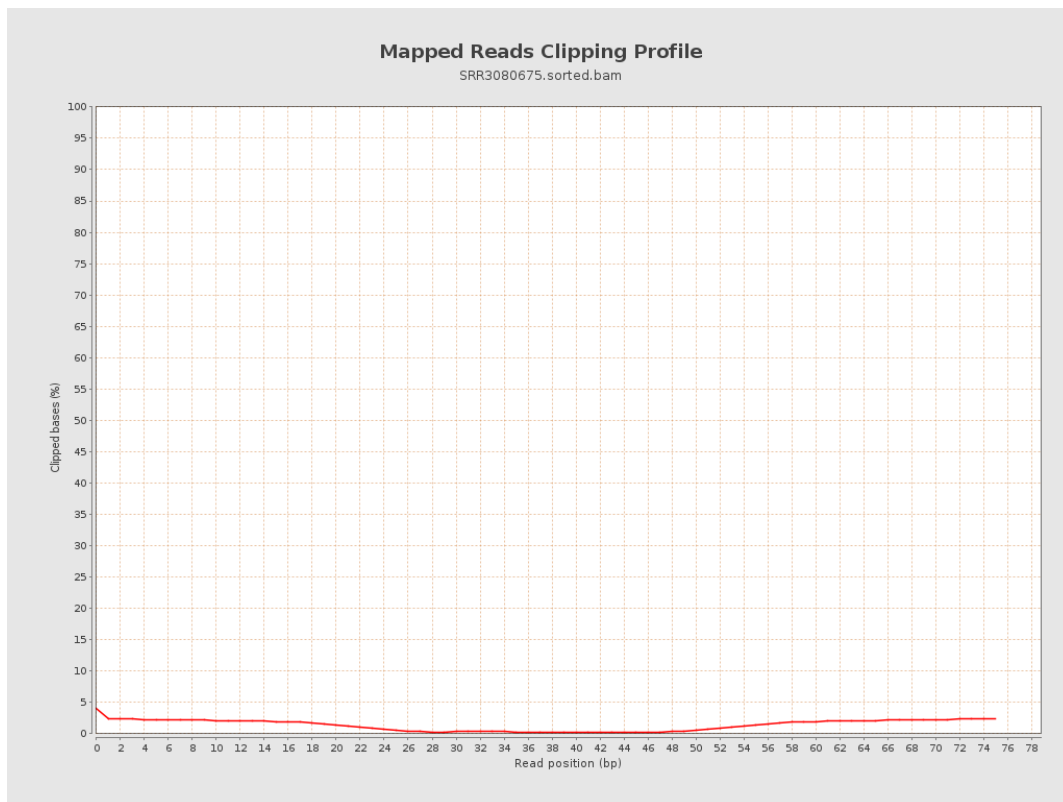
## 8. Results : Mapped Reads Nucleotide Content



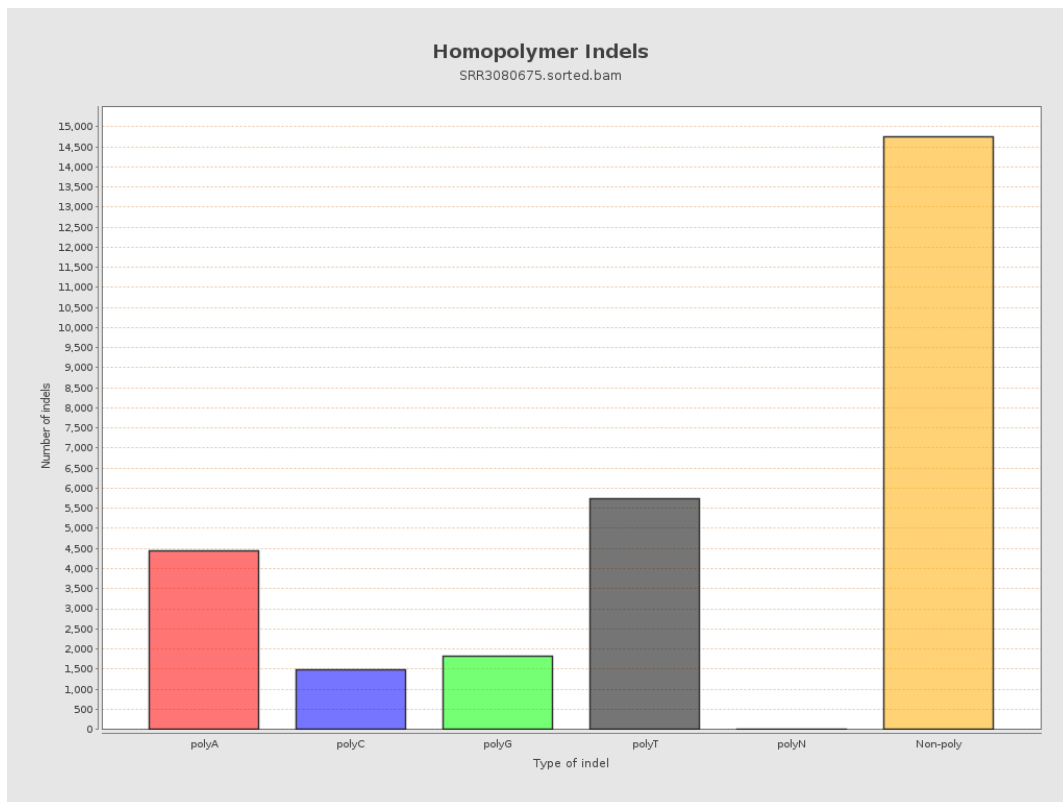
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

