

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/14 10:51:01*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008771.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_SRR6008771 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008771.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Sat Sep 14 10:51:01 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6008771.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 7,286,491          |
| Mapped reads                 | 6,676,107 / 91.62% |
| Unmapped reads               | 610,384 / 8.38%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 30,257 / 0.42%     |
| Read min/max/mean length     | 30 / 76 / 76.14    |
| Duplicated reads (estimated) | 494,348 / 6.78%    |
| Duplication rate             | 5.63%              |
| Clipped reads                | 2,933,415 / 40.26% |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 122,628,447 / 27.64% |
| Number/percentage of C's | 80,812,169 / 18.21%  |
| Number/percentage of T's | 140,383,820 / 31.64% |
| Number/percentage of G's | 99,801,192 / 22.49%  |
| Number/percentage of N's | 81,689 / 0.02%       |
| GC Percentage            | 40.71%               |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.1434 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 1.0543 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 46.08 |
|----------------------|-------|

## 2.5. Mismatches and indels

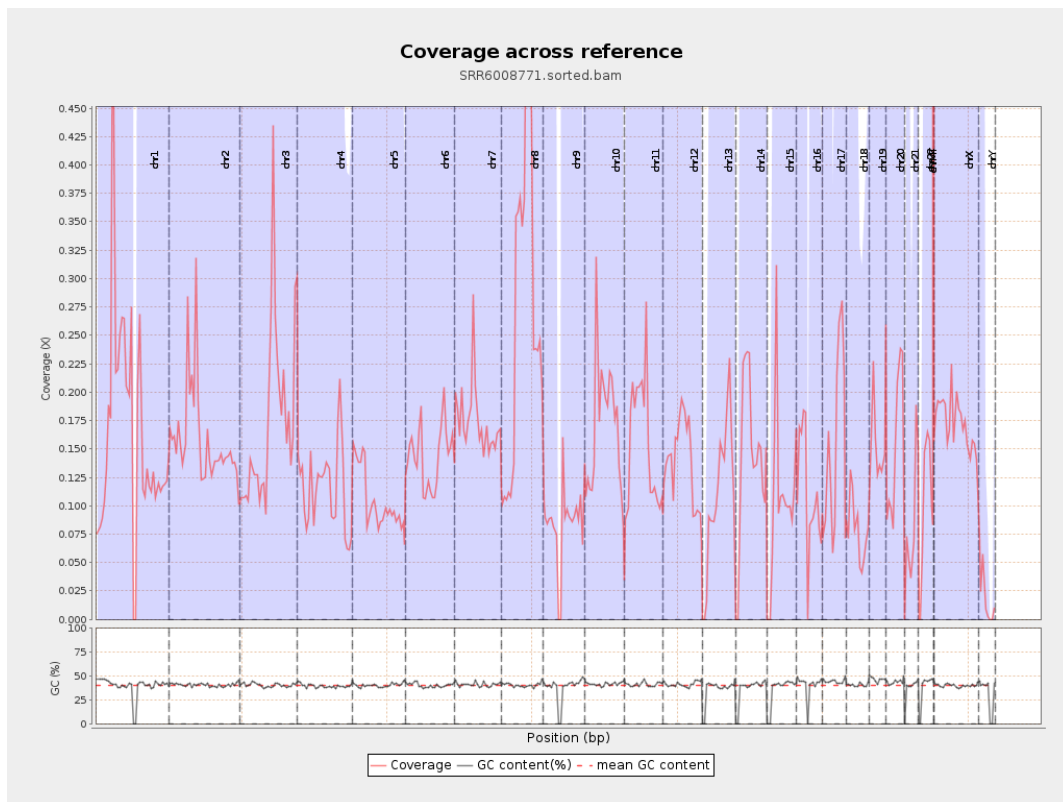
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.71%     |
| Mismatches                               | 3,060,674 |
| Insertions                               | 37,835    |
| Mapped reads with at least one insertion | 0.56%     |
| Deletions                                | 109,207   |
| Mapped reads with at least one deletion  | 1.62%     |
| Homopolymer indels                       | 48.62%    |

## 2.6. Chromosome stats

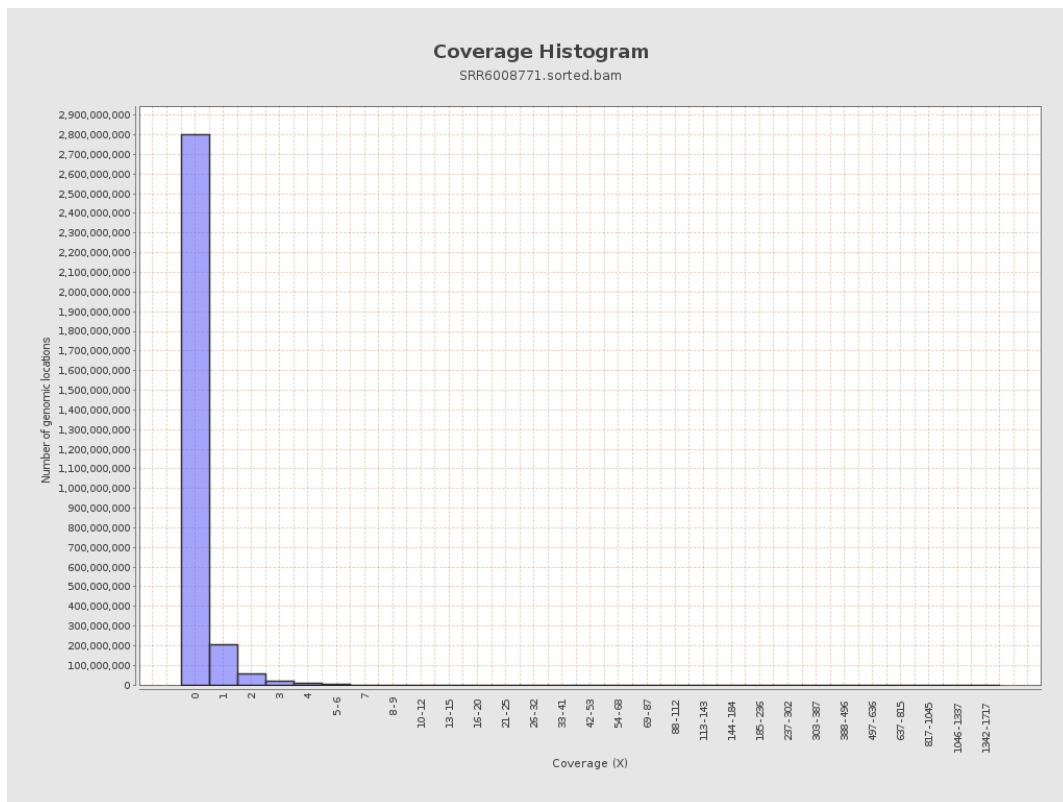
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 40478802     | 0.1624        | 1.7324             |
| chr2 | 243199373 | 38871844     | 0.1598        | 1.2833             |
| chr3 | 198022430 | 34062972     | 0.172         | 0.6181             |
| chr4 | 191154276 | 21810612     | 0.1141        | 0.5375             |
| chr5 | 180915260 | 18925981     | 0.1046        | 0.4498             |
| chr6 | 171115067 | 24426068     | 0.1427        | 0.7134             |
| chr7 | 159138663 | 27864853     | 0.1751        | 1.7218             |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr8  | 146364022 | 39960415 | 0.273  | 1.1822 |
| chr9  | 141213431 | 11731179 | 0.0831 | 0.9896 |
| chr10 | 135534747 | 23063269 | 0.1702 | 1.309  |
| chr11 | 135006516 | 20677591 | 0.1532 | 1.3166 |
| chr12 | 133851895 | 18637027 | 0.1392 | 0.5312 |
| chr13 | 115169878 | 12756603 | 0.1108 | 0.456  |
| chr14 | 107349540 | 15361764 | 0.1431 | 0.5665 |
| chr15 | 102531392 | 10825371 | 0.1056 | 0.4558 |
| chr16 | 90354753  | 10050785 | 0.1112 | 0.6833 |
| chr17 | 81195210  | 12358480 | 0.1522 | 0.9208 |
| chr18 | 78077248  | 6125885  | 0.0785 | 1.9605 |
| chr19 | 59128983  | 9250758  | 0.1565 | 1.1301 |
| chr20 | 63025520  | 9563489  | 0.1517 | 0.5822 |
| chr21 | 48129895  | 3999918  | 0.0831 | 0.485  |
| chr22 | 51304566  | 5020774  | 0.0979 | 0.4278 |
| chrMT | 16571     | 105950   | 6.3937 | 4.8064 |
| chrX  | 155270560 | 26790680 | 0.1725 | 0.767  |
| chrY  | 59373566  | 1167464  | 0.0197 | 0.4538 |

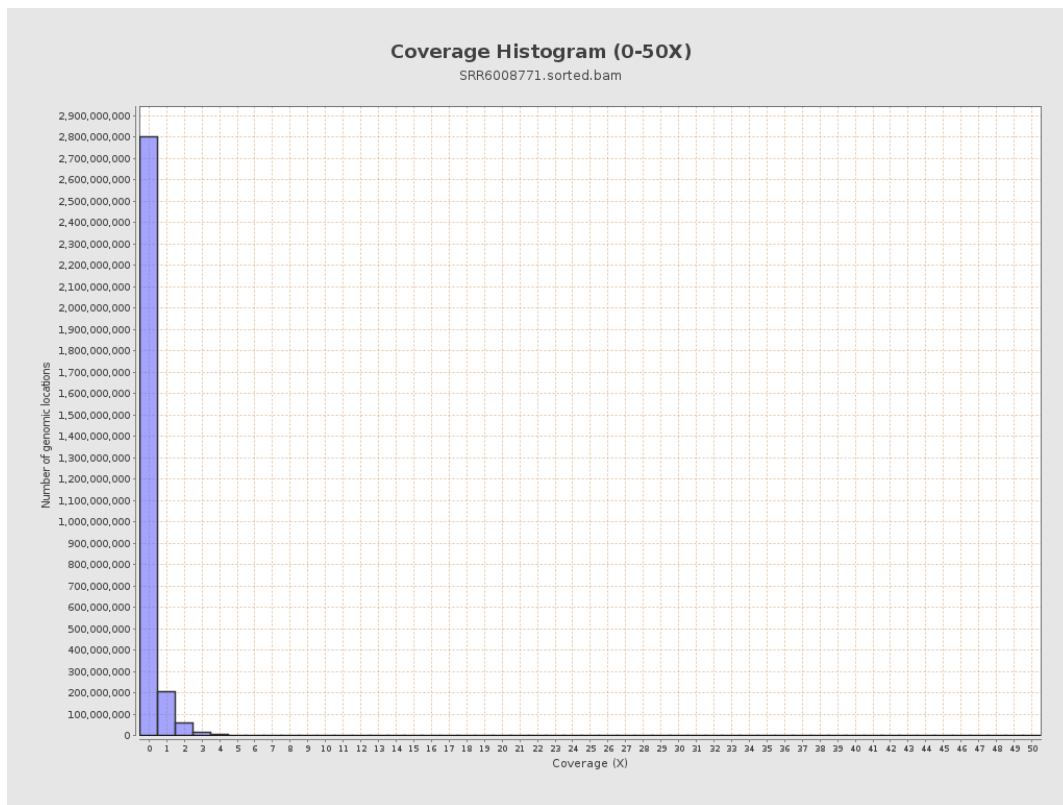
### 3. Results : Coverage across reference



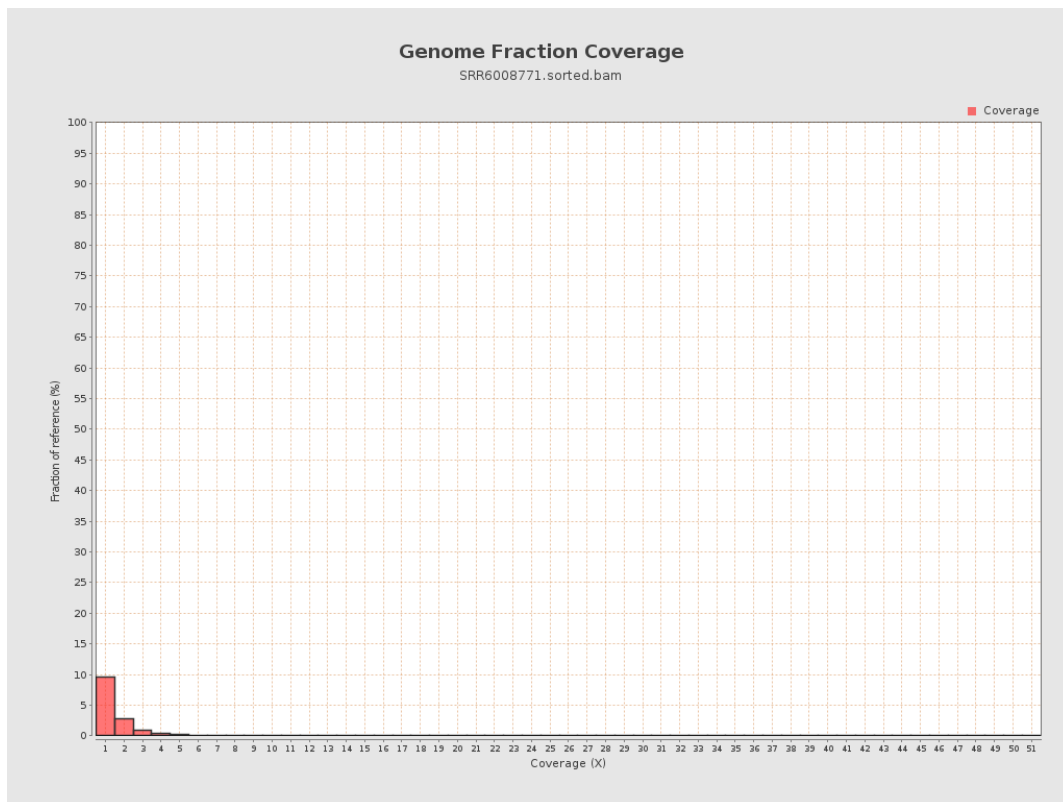
## 4. Results : Coverage Histogram



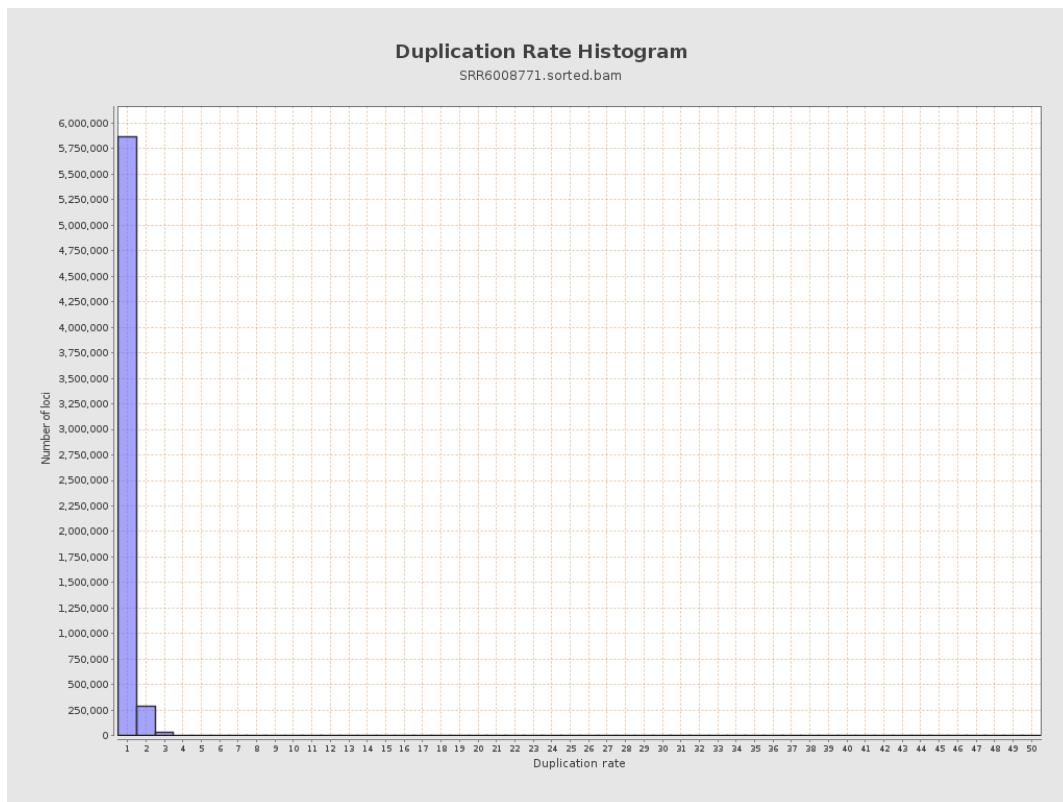
## 5. Results : Coverage Histogram (0-50X)



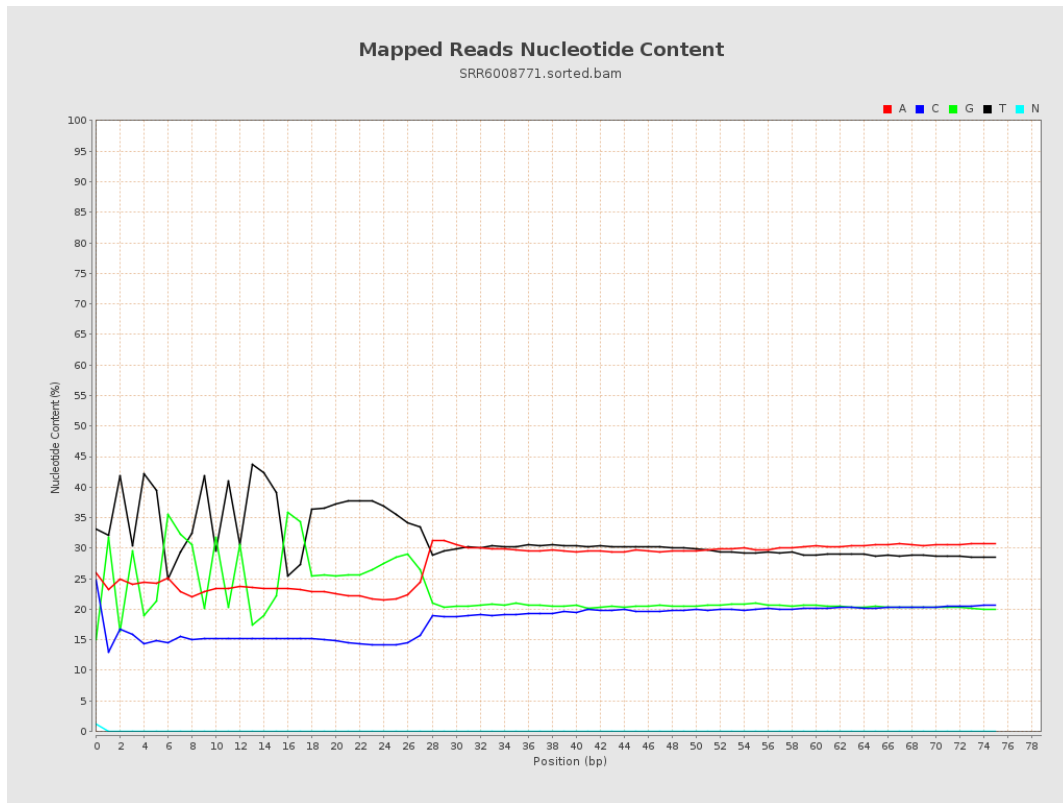
## 6. Results : Genome Fraction Coverage



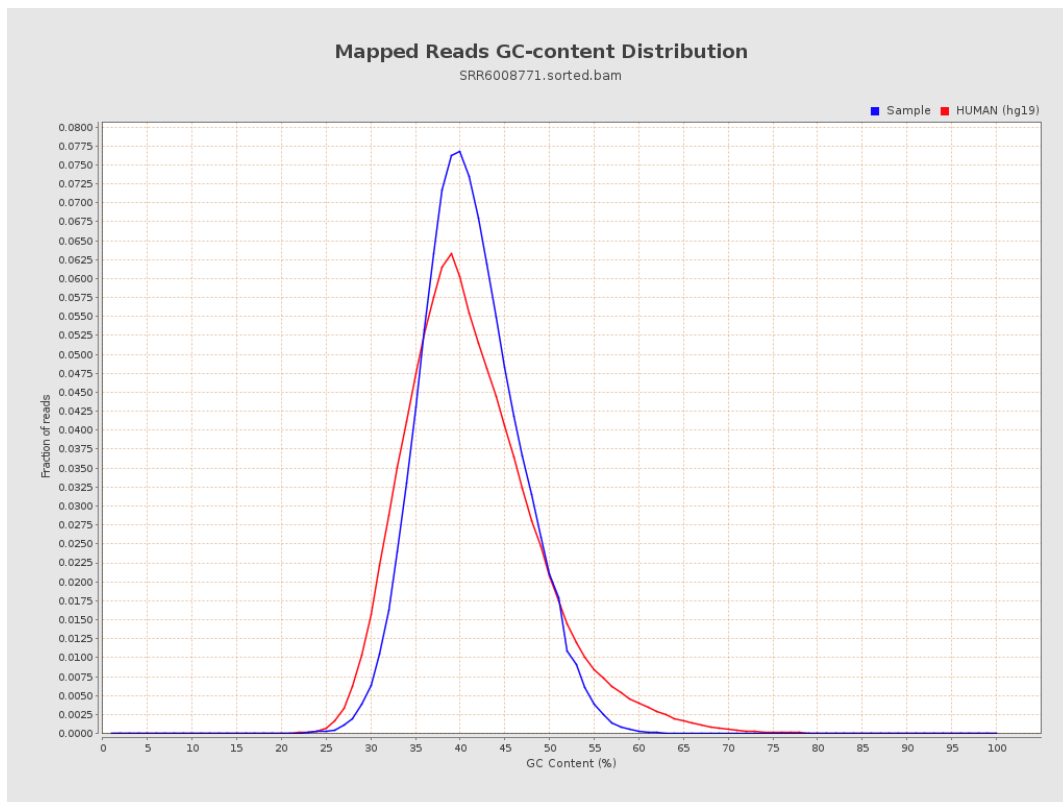
## 7. Results : Duplication Rate Histogram



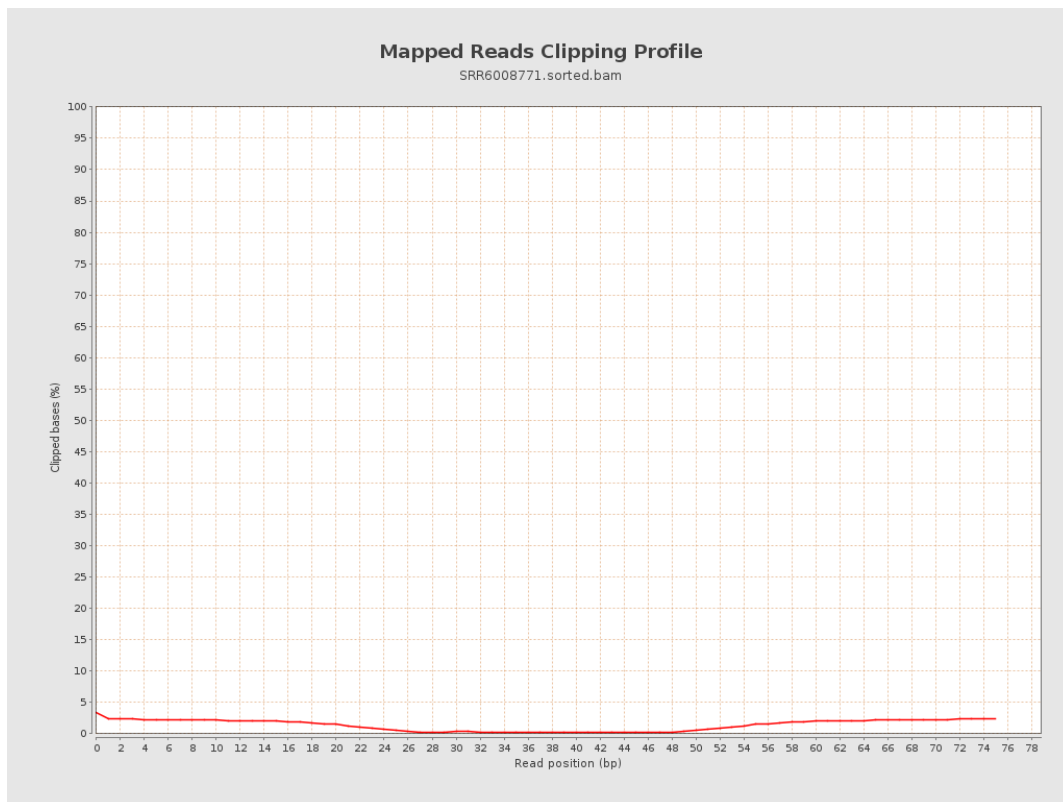
## 8. Results : Mapped Reads Nucleotide Content



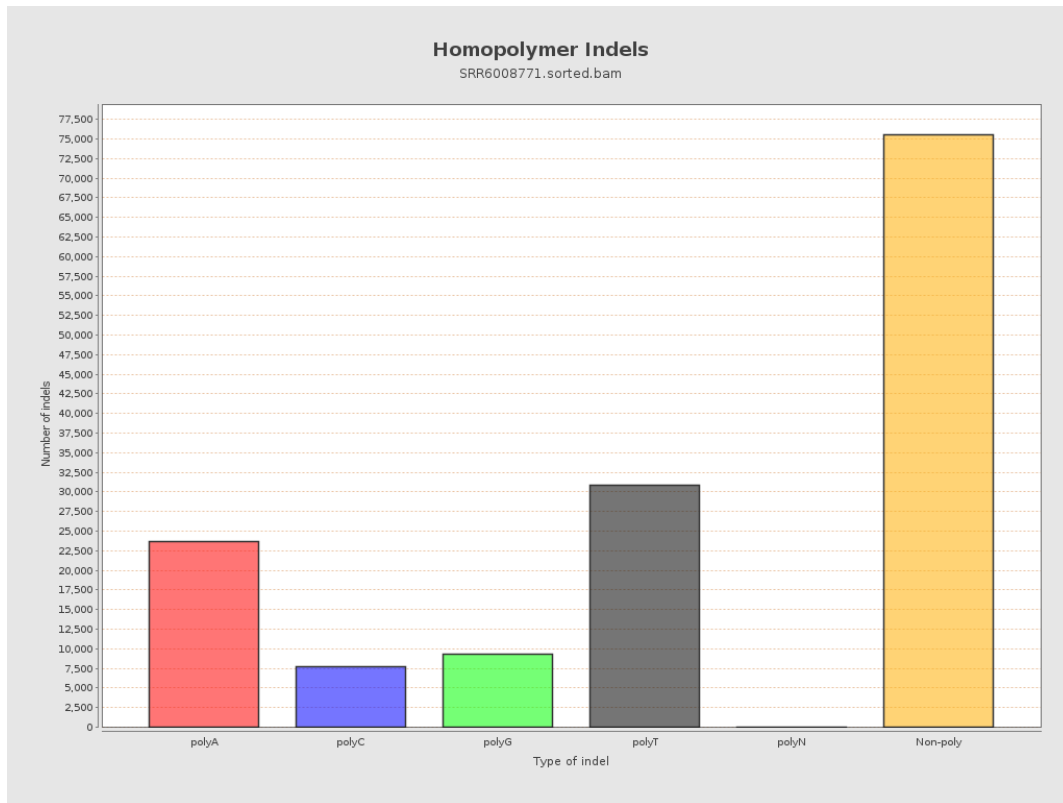
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

