

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/15 14:36:23*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068172.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_SRR6068172 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068172.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Sun Sep 15 14:36:23 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6068172.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 3,494,777          |
| Mapped reads                 | 3,299,879 / 94.42% |
| Unmapped reads               | 194,898 / 5.58%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 27,770 / 0.79%     |
| Read min/max/mean length     | 30 / 76 / 76.28    |
| Duplicated reads (estimated) | 404,172 / 11.57%   |
| Duplication rate             | 10.48%             |
| Clipped reads                | 1,749,651 / 50.06% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 55,417,937 / 26.15% |
| Number/percentage of C's | 37,959,827 / 17.91% |
| Number/percentage of T's | 69,132,867 / 32.62% |
| Number/percentage of G's | 49,386,146 / 23.3%  |
| Number/percentage of N's | 24,288 / 0.01%      |
| GC Percentage            | 41.22%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0685 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.6864 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 45.75 |
|----------------------|-------|

## 2.5. Mismatches and indels

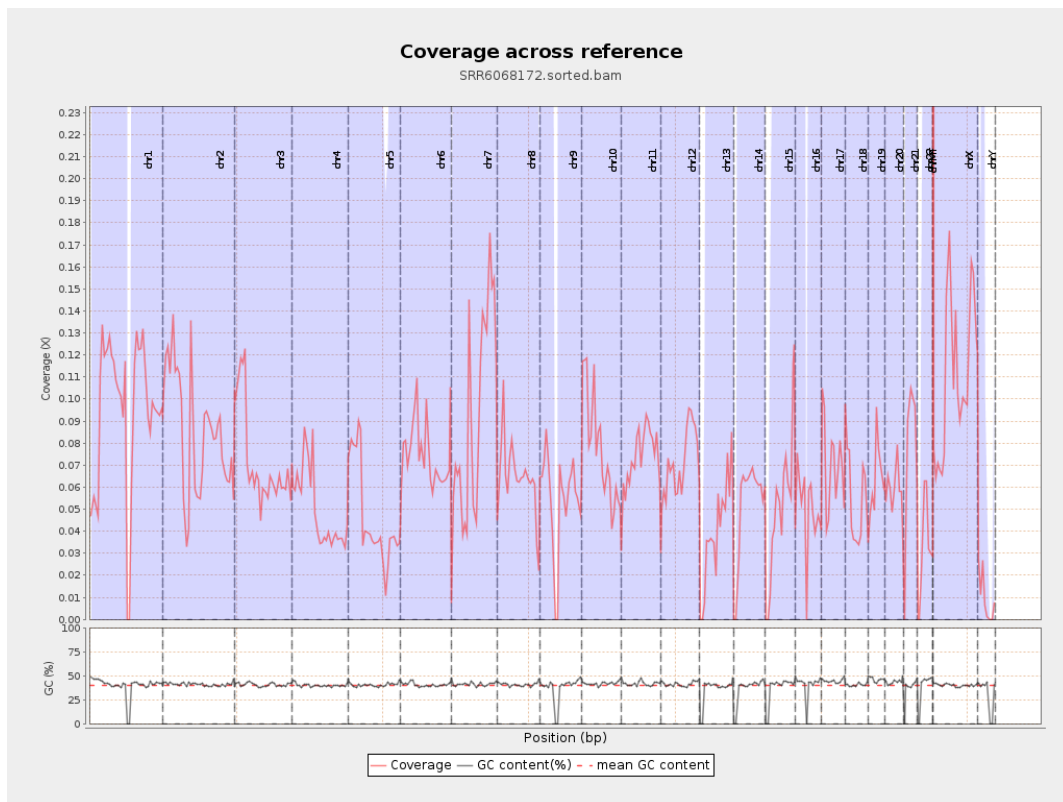
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.58%     |
| Mismatches                               | 1,200,885 |
| Insertions                               | 13,135    |
| Mapped reads with at least one insertion | 0.39%     |
| Deletions                                | 53,929    |
| Mapped reads with at least one deletion  | 1.62%     |
| Homopolymer indels                       | 44.8%     |

## 2.6. Chromosome stats

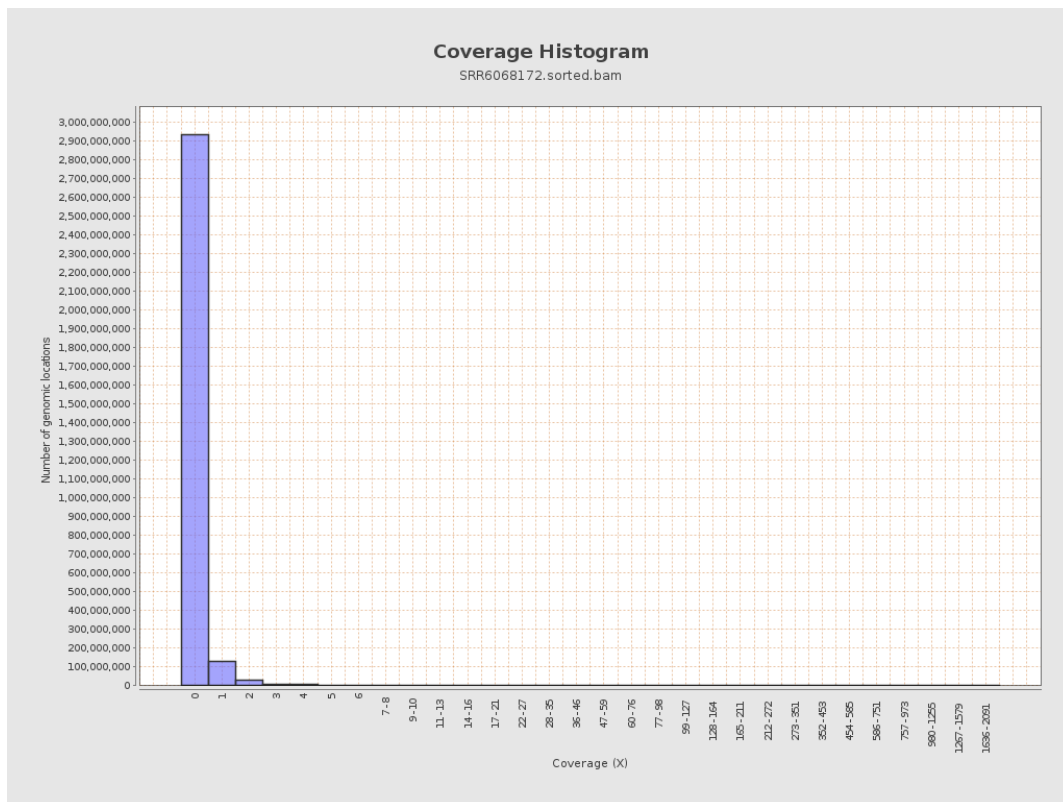
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 23541187     | 0.0944        | 1.4082             |
| chr2 | 243199373 | 20840402     | 0.0857        | 1.0509             |
| chr3 | 198022430 | 14248678     | 0.072         | 0.3397             |
| chr4 | 191154276 | 9590808      | 0.0502        | 0.3052             |
| chr5 | 180915260 | 8328200      | 0.046         | 0.2794             |
| chr6 | 171115067 | 12896898     | 0.0754        | 0.4737             |
| chr7 | 159138663 | 14811894     | 0.0931        | 1.0105             |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr8  | 146364022 | 9399807  | 0.0642 | 0.7467 |
| chr9  | 141213431 | 7768016  | 0.055  | 0.5125 |
| chr10 | 135534747 | 10495352 | 0.0774 | 0.5351 |
| chr11 | 135006516 | 9970581  | 0.0739 | 0.4755 |
| chr12 | 133851895 | 9563722  | 0.0715 | 0.3728 |
| chr13 | 115169878 | 4683429  | 0.0407 | 0.2894 |
| chr14 | 107349540 | 5615526  | 0.0523 | 0.3491 |
| chr15 | 102531392 | 5116801  | 0.0499 | 0.3125 |
| chr16 | 90354753  | 4490653  | 0.0497 | 0.3118 |
| chr17 | 81195210  | 5734187  | 0.0706 | 0.3674 |
| chr18 | 78077248  | 4259449  | 0.0546 | 0.9372 |
| chr19 | 59128983  | 3782476  | 0.064  | 0.9154 |
| chr20 | 63025520  | 3748450  | 0.0595 | 0.3324 |
| chr21 | 48129895  | 3616771  | 0.0751 | 0.361  |
| chr22 | 51304566  | 1667934  | 0.0325 | 0.2235 |
| chrMT | 16571     | 149186   | 9.0028 | 5.8069 |
| chrX  | 155270560 | 17145132 | 0.1104 | 0.5055 |
| chrY  | 59373566  | 549770   | 0.0093 | 0.2587 |

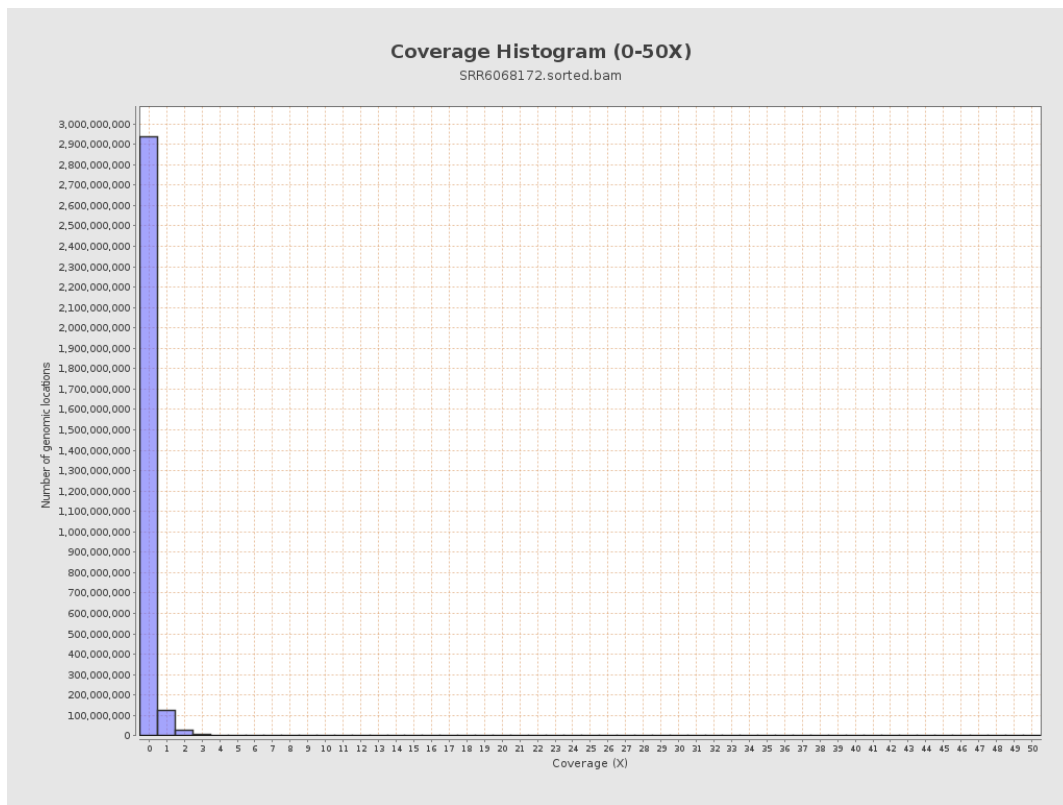
### 3. Results : Coverage across reference



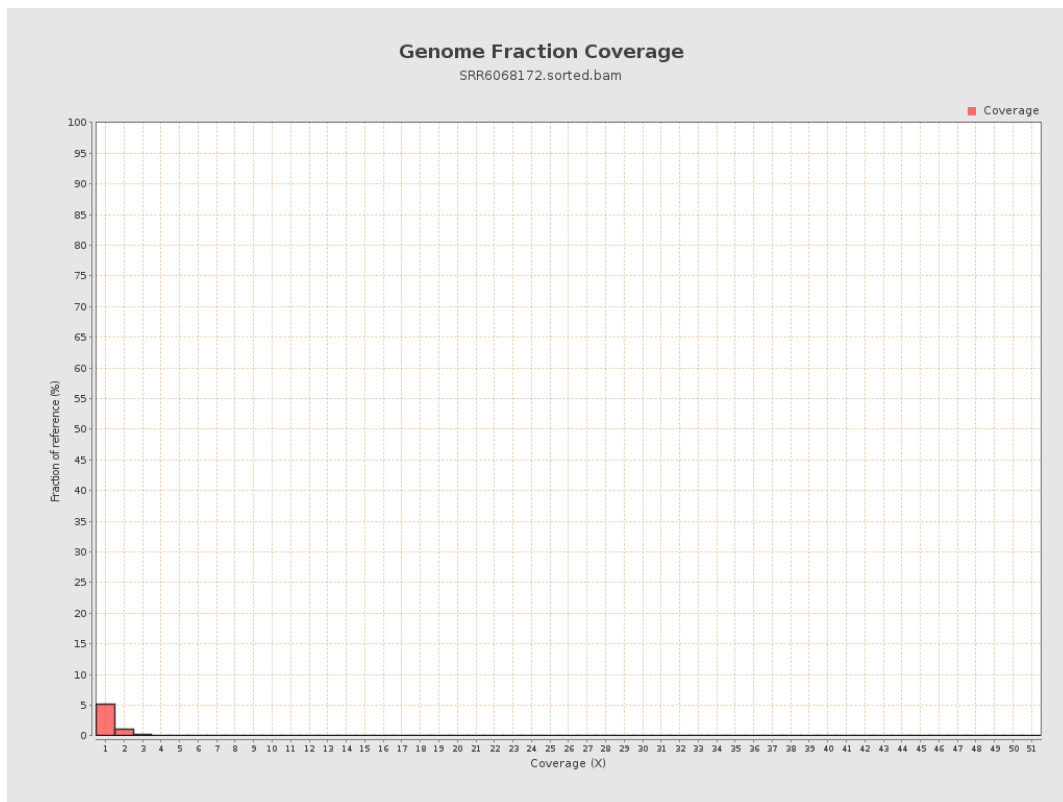
## 4. Results : Coverage Histogram



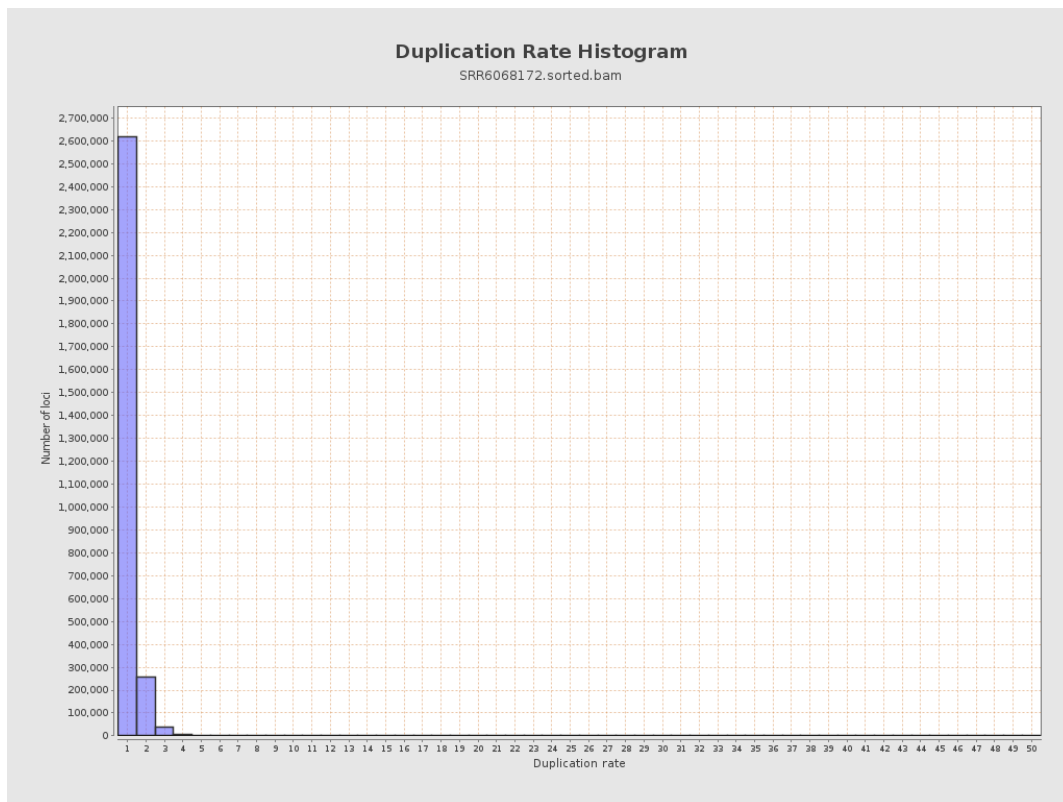
## 5. Results : Coverage Histogram (0-50X)



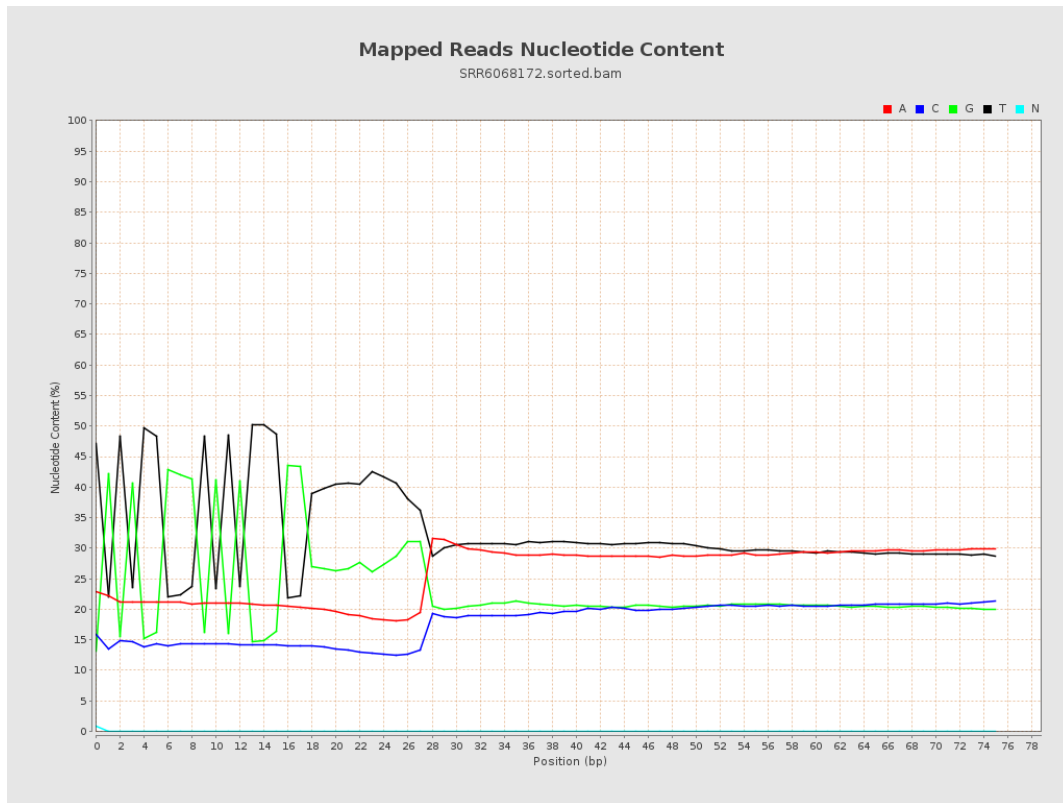
## 6. Results : Genome Fraction Coverage



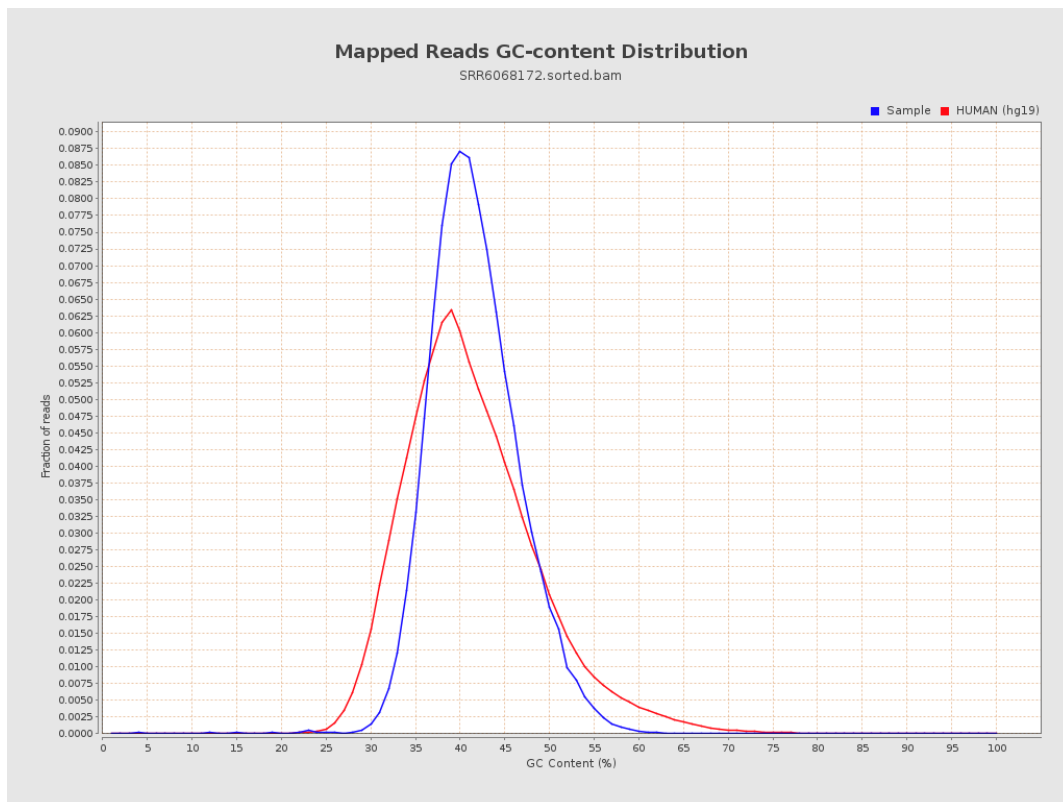
## 7. Results : Duplication Rate Histogram



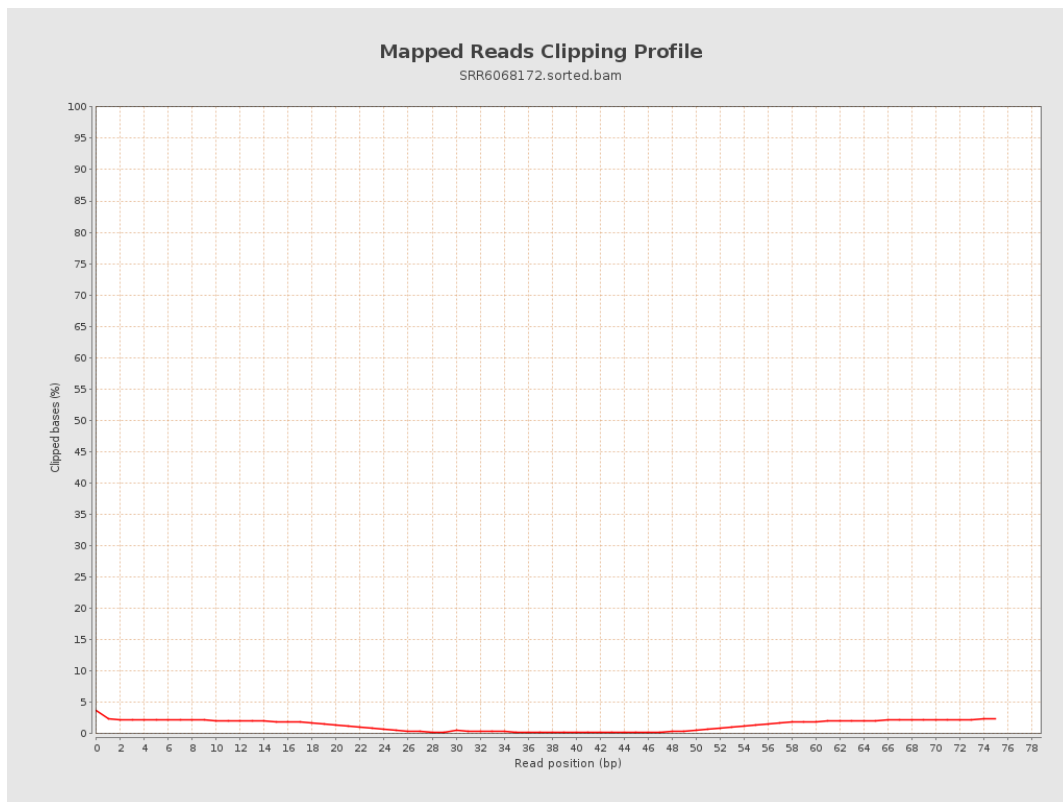
## 8. Results : Mapped Reads Nucleotide Content



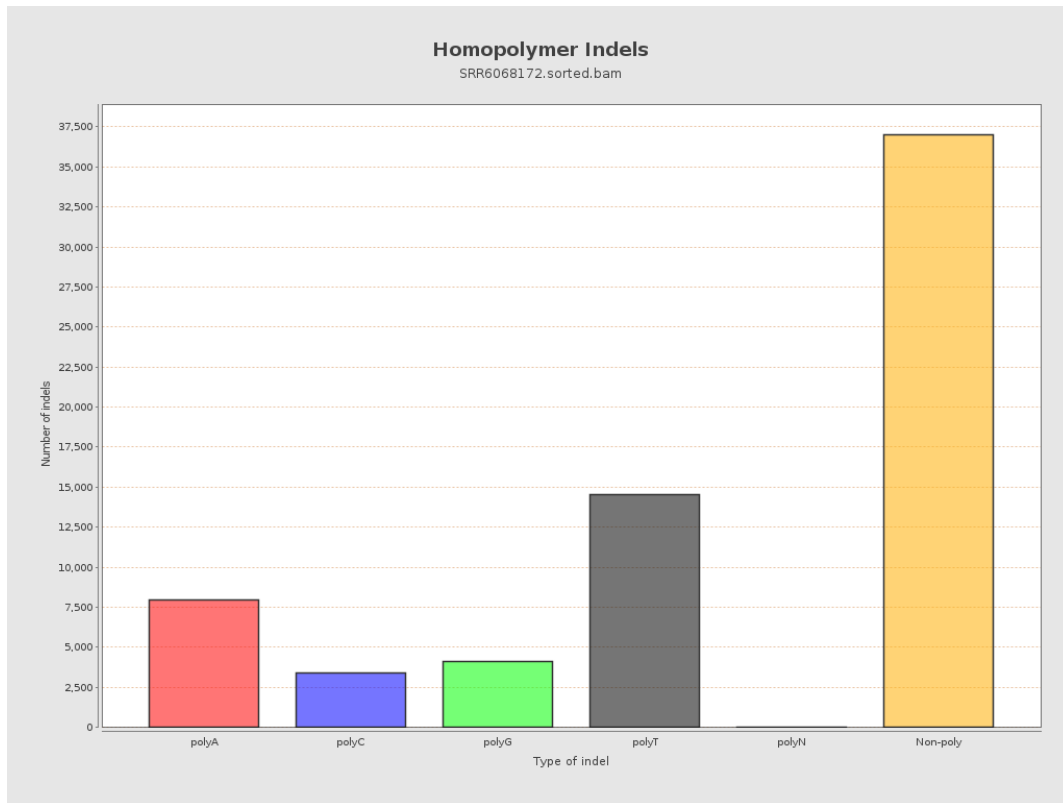
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

