

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/15 16:48:31*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068947.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_SRR6068947 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068947.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Sun Sep 15 16:48:30 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6068947.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 2,287,506          |
| Mapped reads                 | 1,751,365 / 76.56% |
| Unmapped reads               | 536,141 / 23.44%   |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 13,370 / 0.58%     |
| Read min/max/mean length     | 30 / 76 / 76.2     |
| Duplicated reads (estimated) | 90,834 / 3.97%     |
| Duplication rate             | 4.18%              |
| Clipped reads                | 774,982 / 33.88%   |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 32,283,778 / 27.71% |
| Number/percentage of C's | 20,256,373 / 17.39% |
| Number/percentage of T's | 38,527,734 / 33.07% |
| Number/percentage of G's | 25,142,874 / 21.58% |
| Number/percentage of N's | 284,548 / 0.24%     |
| GC Percentage            | 38.97%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0376 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.3707 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 43.61 |
|----------------------|-------|

## 2.5. Mismatches and indels

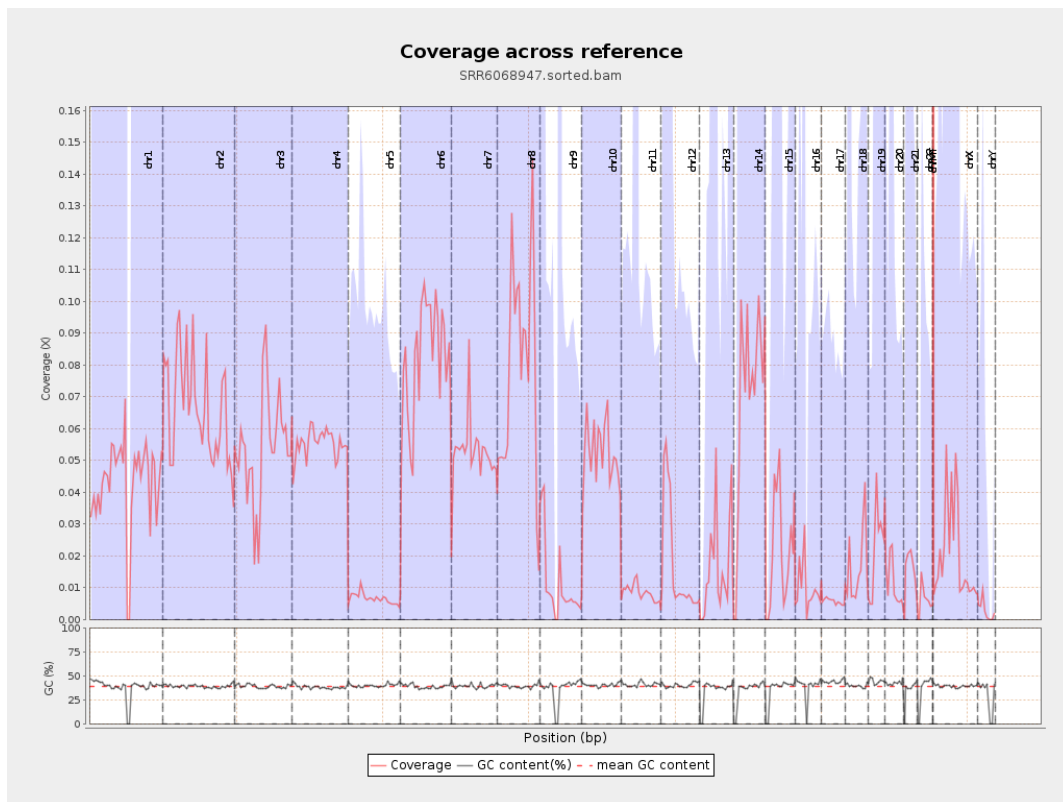
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.99%     |
| Mismatches                               | 1,133,311 |
| Insertions                               | 9,980     |
| Mapped reads with at least one insertion | 0.57%     |
| Deletions                                | 30,650    |
| Mapped reads with at least one deletion  | 1.73%     |
| Homopolymer indels                       | 47.9%     |

## 2.6. Chromosome stats

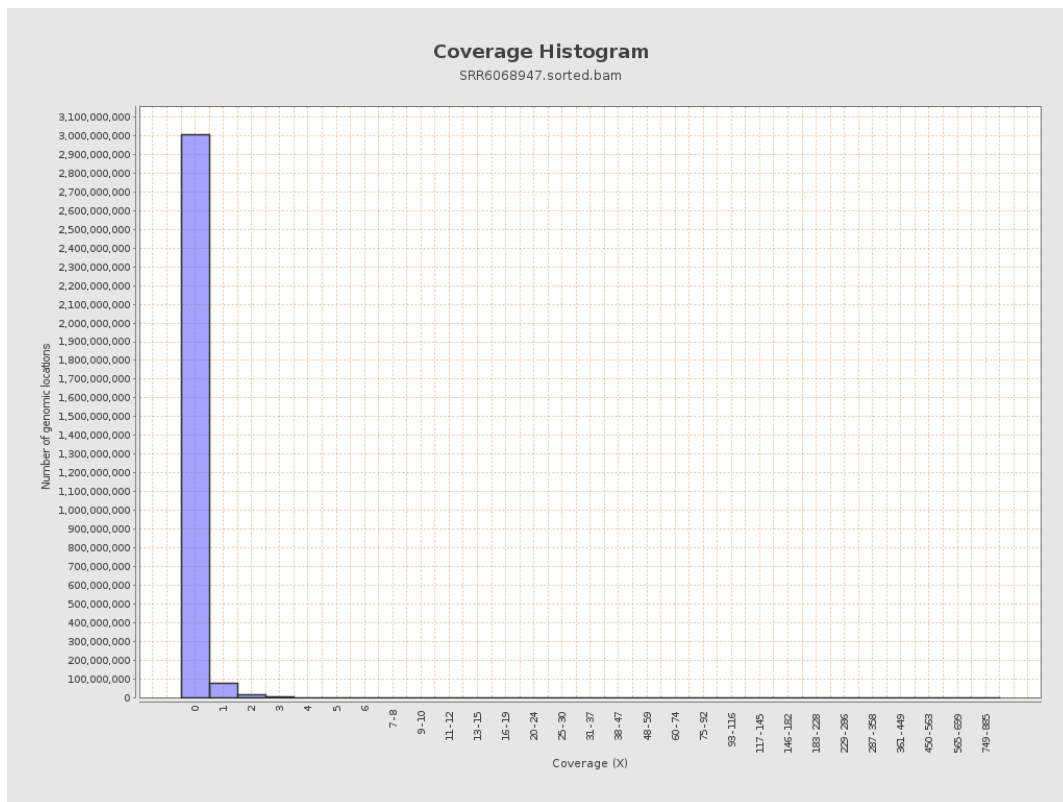
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 10722552     | 0.043         | 0.6276             |
| chr2 | 243199373 | 16239520     | 0.0668        | 0.381              |
| chr3 | 198022430 | 10629586     | 0.0537        | 0.2814             |
| chr4 | 191154276 | 10578143     | 0.0553        | 0.2871             |
| chr5 | 180915260 | 1196973      | 0.0066        | 0.0927             |
| chr6 | 171115067 | 14206511     | 0.083         | 0.4201             |
| chr7 | 159138663 | 8392055      | 0.0527        | 0.7232             |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr8  | 146364022 | 11689315 | 0.0799 | 0.6518 |
| chr9  | 141213431 | 1495655  | 0.0106 | 0.2197 |
| chr10 | 135534747 | 7095971  | 0.0524 | 0.3419 |
| chr11 | 135006516 | 1144496  | 0.0085 | 0.1771 |
| chr12 | 133851895 | 2258695  | 0.0169 | 0.1575 |
| chr13 | 115169878 | 1956419  | 0.017  | 0.157  |
| chr14 | 107349540 | 7593911  | 0.0707 | 0.3327 |
| chr15 | 102531392 | 2105649  | 0.0205 | 0.1738 |
| chr16 | 90354753  | 860559   | 0.0095 | 0.1277 |
| chr17 | 81195210  | 461337   | 0.0057 | 0.0825 |
| chr18 | 78077248  | 1327934  | 0.017  | 0.4536 |
| chr19 | 59128983  | 1367743  | 0.0231 | 0.3177 |
| chr20 | 63025520  | 722168   | 0.0115 | 0.129  |
| chr21 | 48129895  | 731135   | 0.0152 | 0.1504 |
| chr22 | 51304566  | 308827   | 0.006  | 0.0935 |
| chrMT | 16571     | 113879   | 6.8722 | 4.6528 |
| chrX  | 155270560 | 3179848  | 0.0205 | 0.1797 |
| chrY  | 59373566  | 166440   | 0.0028 | 0.075  |

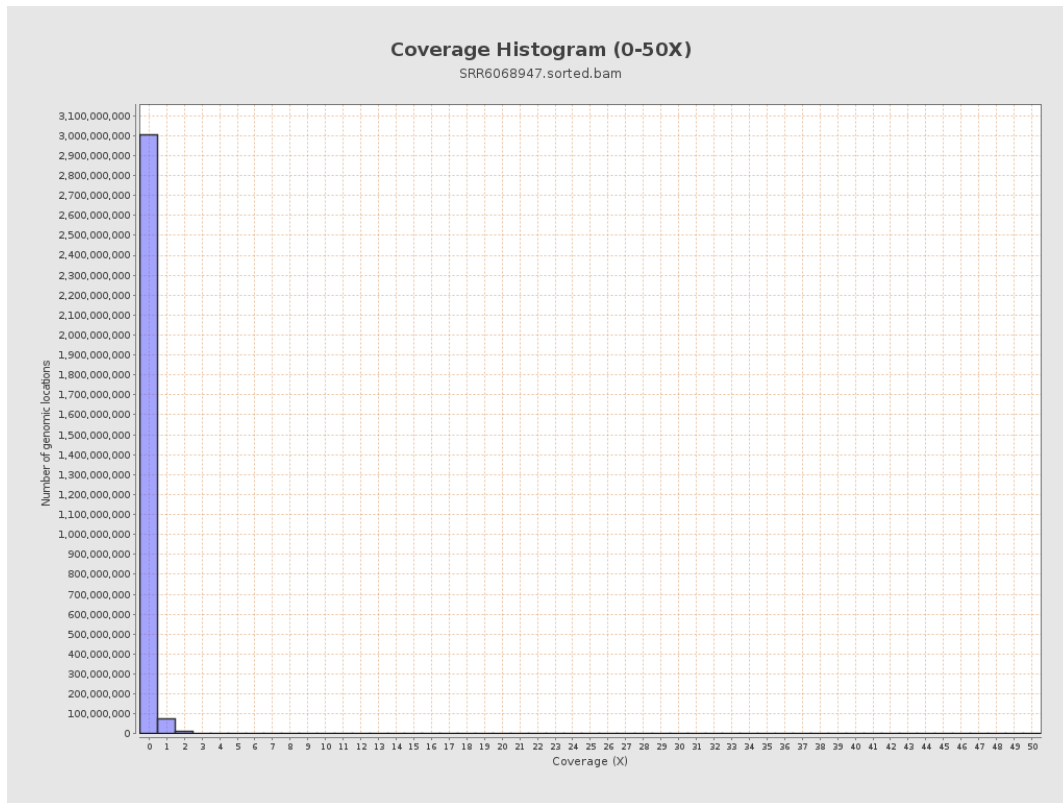
### 3. Results : Coverage across reference



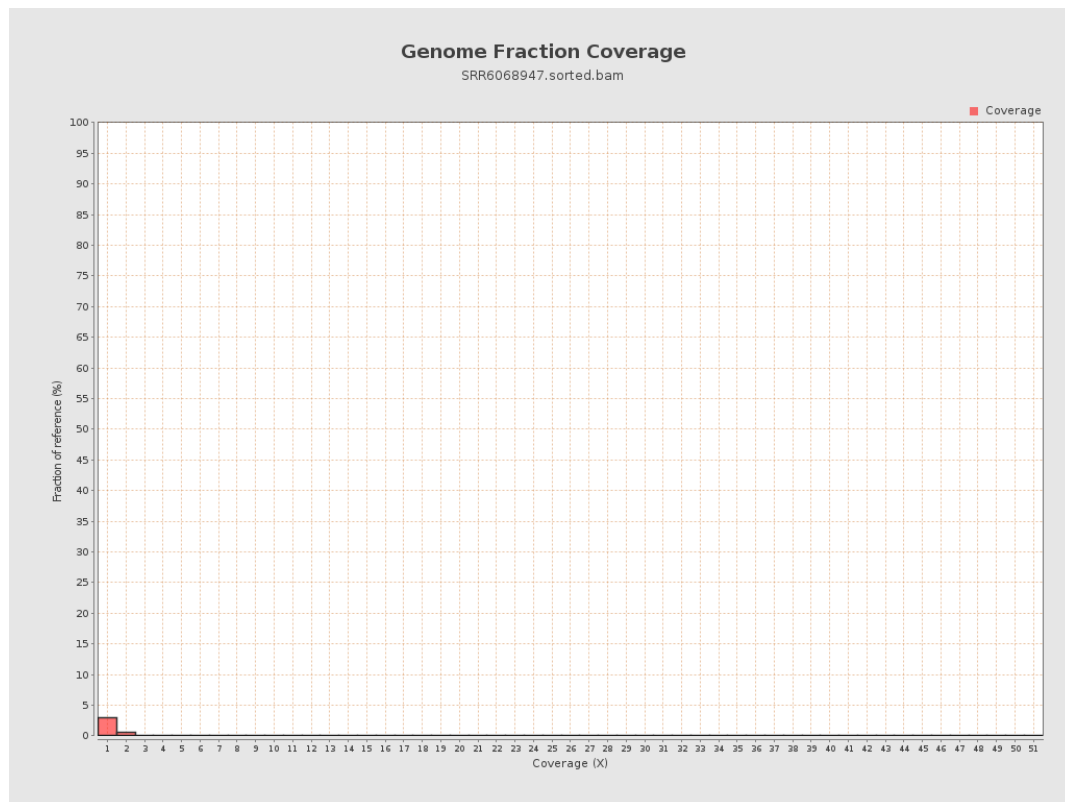
## 4. Results : Coverage Histogram



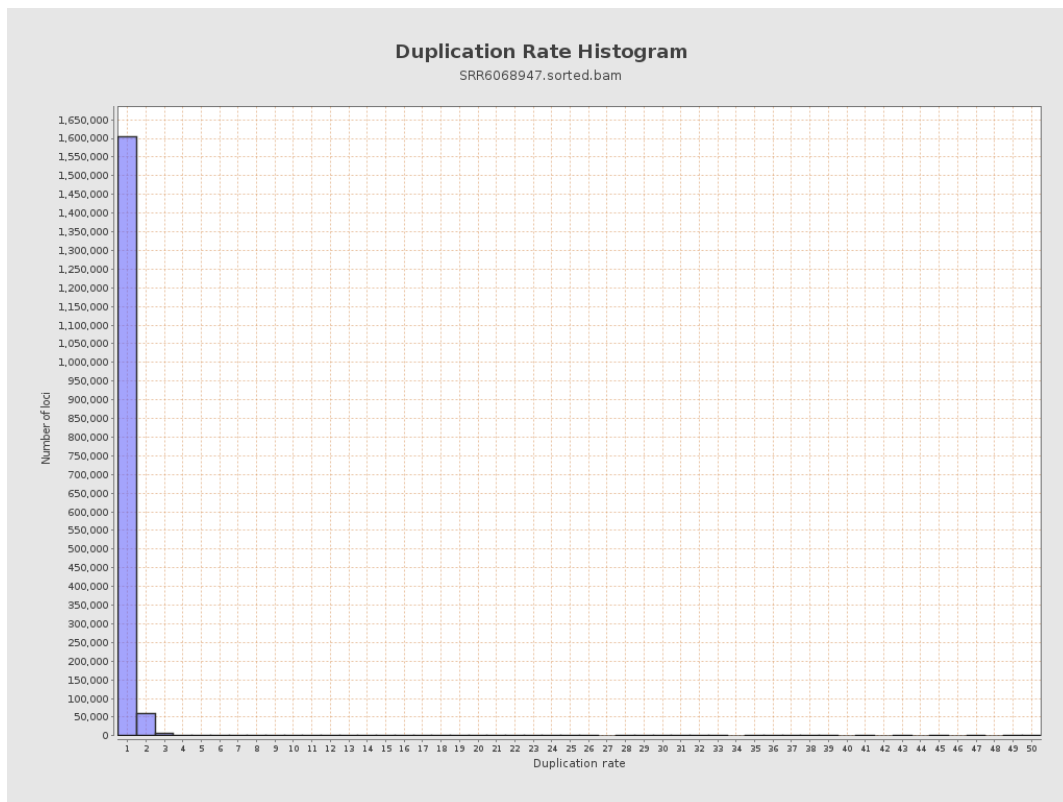
## 5. Results : Coverage Histogram (0-50X)



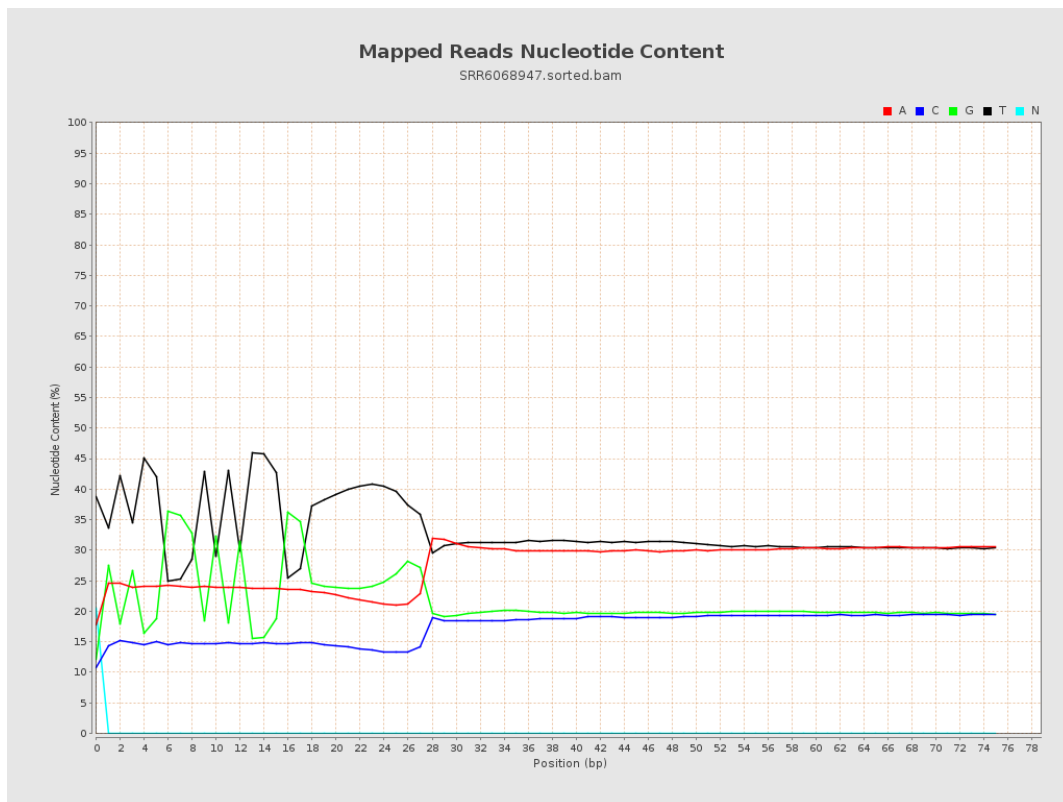
## 6. Results : Genome Fraction Coverage



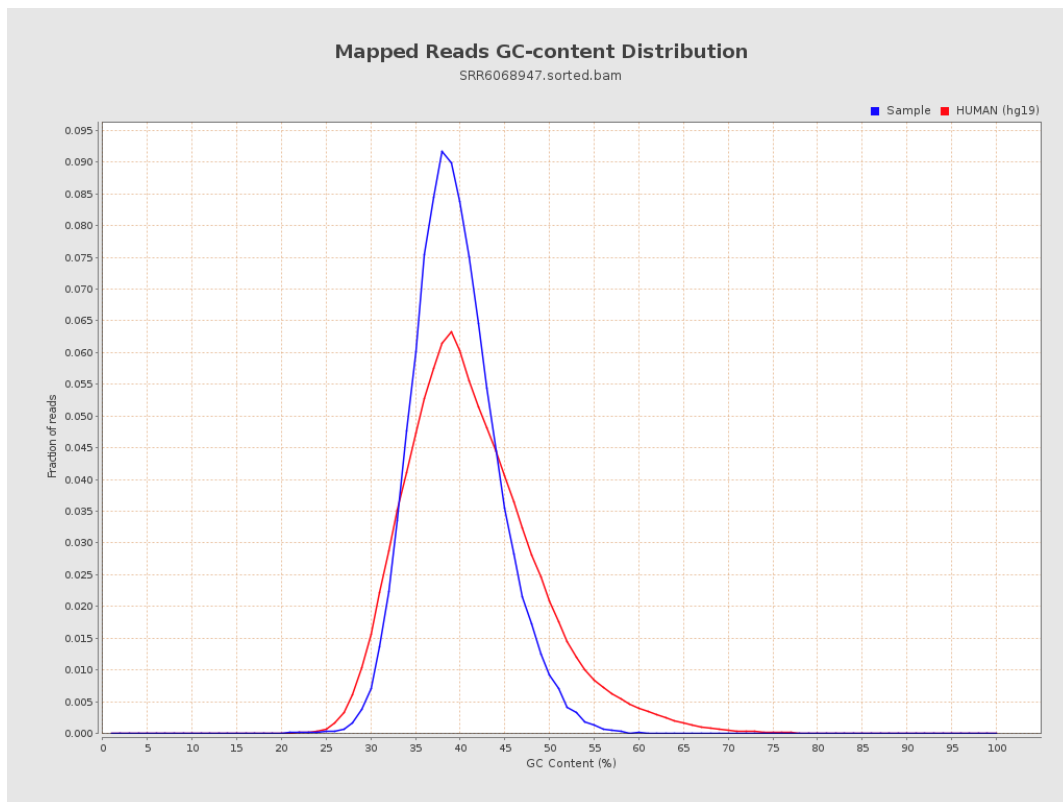
## 7. Results : Duplication Rate Histogram



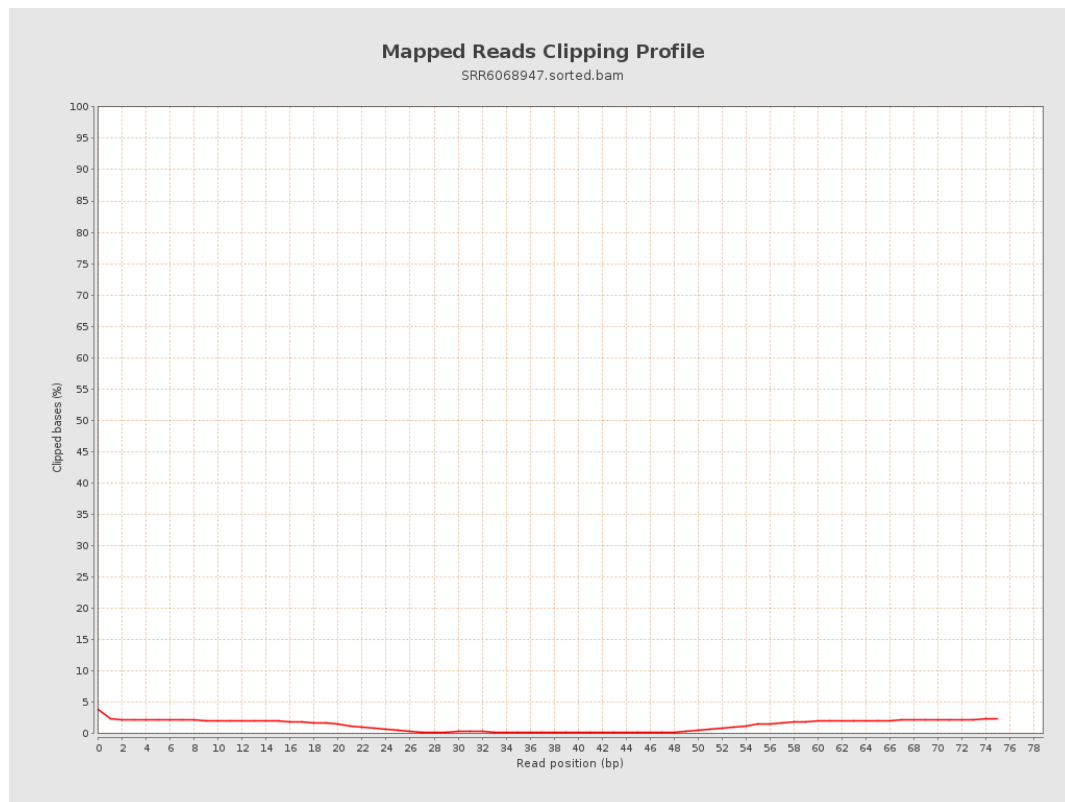
## 8. Results : Mapped Reads Nucleotide Content



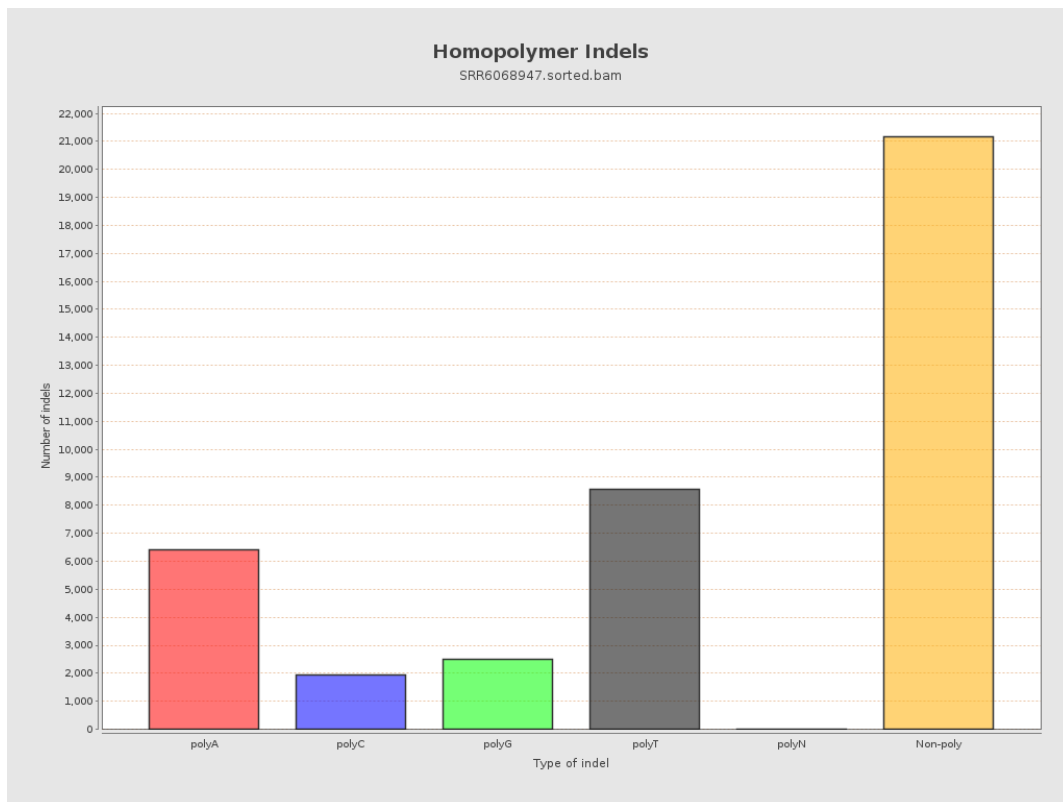
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

