

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/25 21:37:27*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085012.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_SRR3085012 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085012.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Sun Aug 25 21:37:26 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR3085012.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 3,328,184          |
| Mapped reads                 | 3,081,272 / 92.58% |
| Unmapped reads               | 246,912 / 7.42%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 14,422 / 0.43%     |
| Read min/max/mean length     | 30 / 76 / 76.15    |
| Duplicated reads (estimated) | 82,119 / 2.47%     |
| Duplication rate             | 1.91%              |
| Clipped reads                | 1,017,852 / 30.58% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 62,535,323 / 28.98% |
| Number/percentage of C's | 43,368,812 / 20.1%  |
| Number/percentage of T's | 63,355,858 / 29.36% |
| Number/percentage of G's | 46,510,331 / 21.55% |
| Number/percentage of N's | 9,010 / 0%          |
| GC Percentage            | 41.65%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0697 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.4978 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 46.47 |
|----------------------|-------|

## 2.5. Mismatches and indels

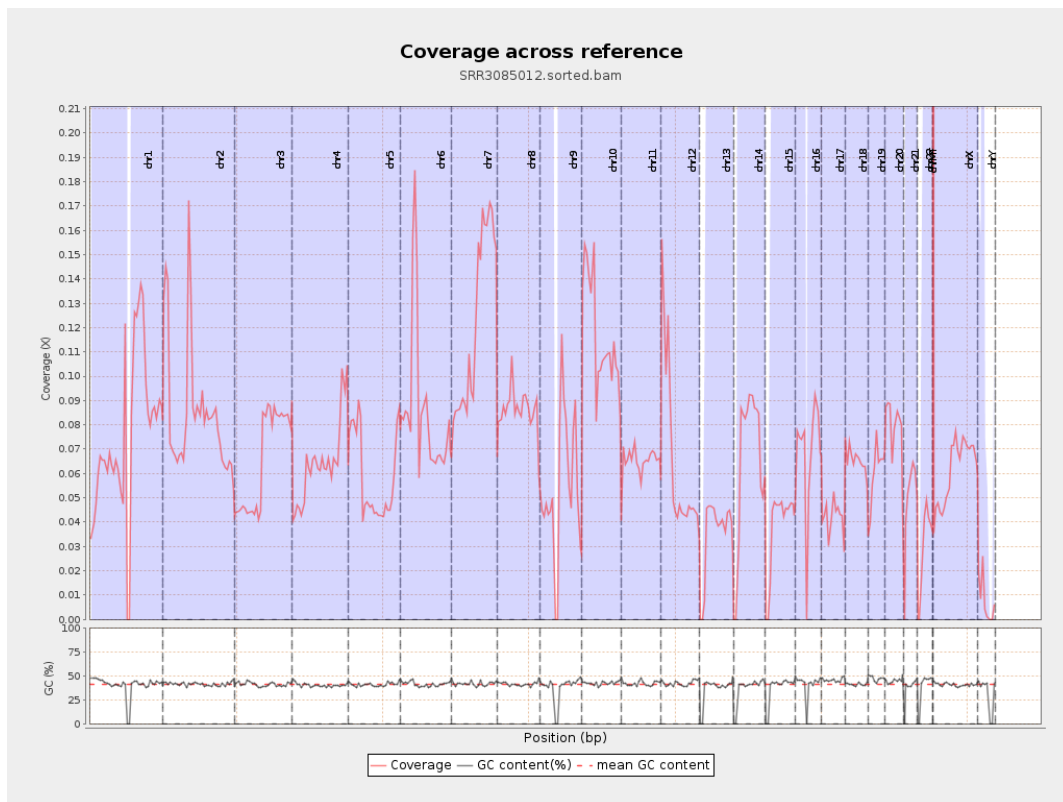
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.91%     |
| Mismatches                               | 1,934,809 |
| Insertions                               | 15,561    |
| Mapped reads with at least one insertion | 0.5%      |
| Deletions                                | 47,085    |
| Mapped reads with at least one deletion  | 1.51%     |
| Homopolymer indels                       | 48.3%     |

## 2.6. Chromosome stats

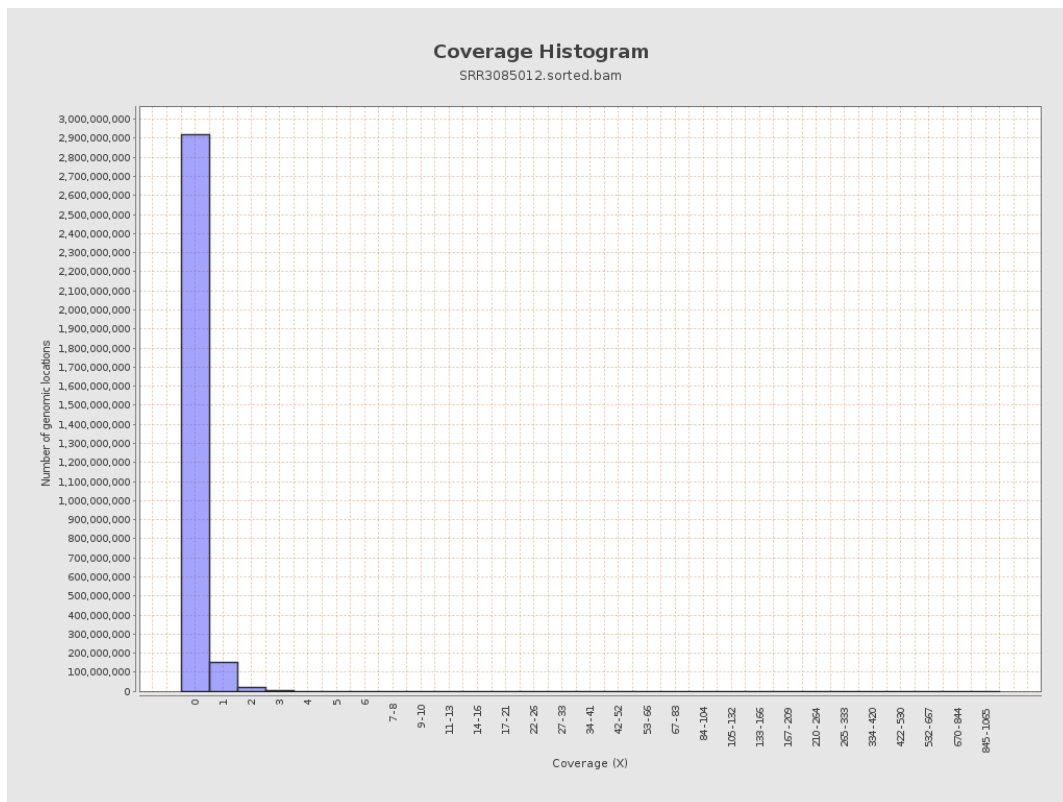
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 18795828     | 0.0754        | 0.8806             |
| chr2 | 243199373 | 20887184     | 0.0859        | 0.5626             |
| chr3 | 198022430 | 12873592     | 0.065         | 0.3078             |
| chr4 | 191154276 | 12273866     | 0.0642        | 0.3187             |
| chr5 | 180915260 | 10675300     | 0.059         | 0.2824             |
| chr6 | 171115067 | 14856953     | 0.0868        | 0.4838             |
| chr7 | 159138663 | 19402591     | 0.1219        | 0.6184             |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr8  | 146364022 | 12621526 | 0.0862 | 0.6834 |
| chr9  | 141213431 | 7750721  | 0.0549 | 0.461  |
| chr10 | 135534747 | 15831822 | 0.1168 | 0.6658 |
| chr11 | 135006516 | 8835859  | 0.0654 | 0.4616 |
| chr12 | 133851895 | 8814492  | 0.0659 | 0.3072 |
| chr13 | 115169878 | 4064043  | 0.0353 | 0.2134 |
| chr14 | 107349540 | 7170924  | 0.0668 | 0.326  |
| chr15 | 102531392 | 3829204  | 0.0373 | 0.2227 |
| chr16 | 90354753  | 6067777  | 0.0672 | 0.3347 |
| chr17 | 81195210  | 3445516  | 0.0424 | 0.285  |
| chr18 | 78077248  | 5115705  | 0.0655 | 0.8053 |
| chr19 | 59128983  | 3585969  | 0.0606 | 0.5988 |
| chr20 | 63025520  | 5043368  | 0.08   | 0.3358 |
| chr21 | 48129895  | 2394007  | 0.0497 | 0.291  |
| chr22 | 51304566  | 1533140  | 0.0299 | 0.1981 |
| chrMT | 16571     | 29688    | 1.7916 | 1.5868 |
| chrX  | 155270560 | 9511836  | 0.0613 | 0.3238 |
| chrY  | 59373566  | 454193   | 0.0076 | 0.1804 |

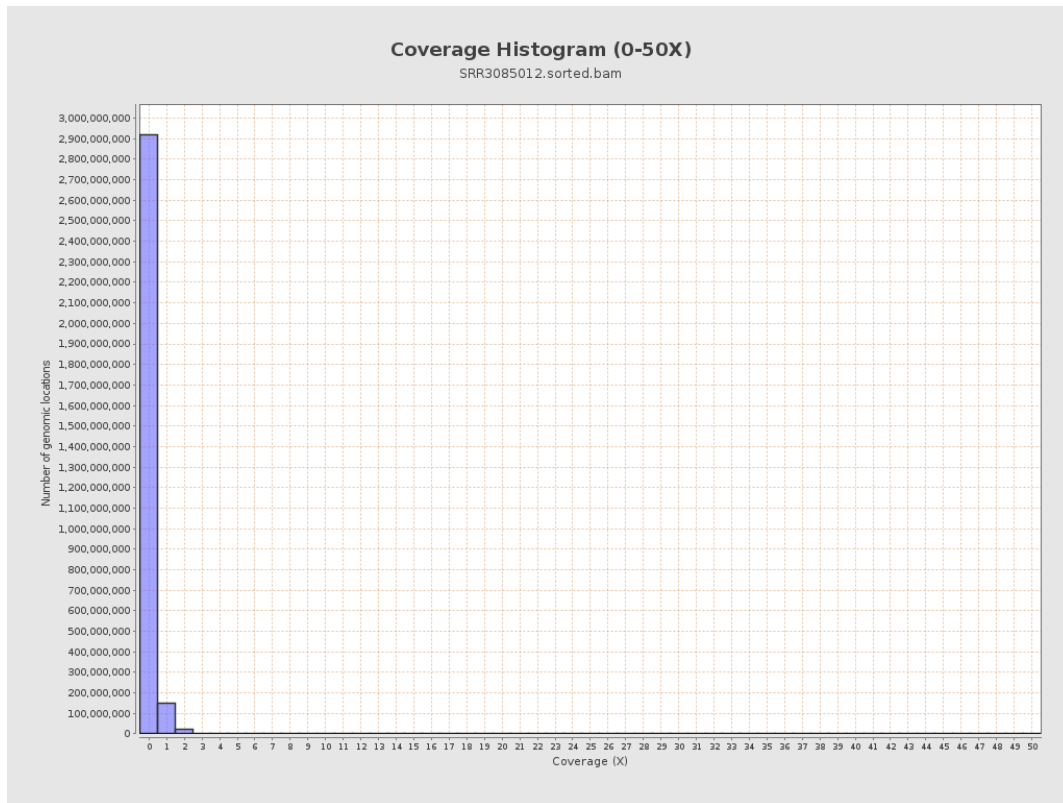
### 3. Results : Coverage across reference



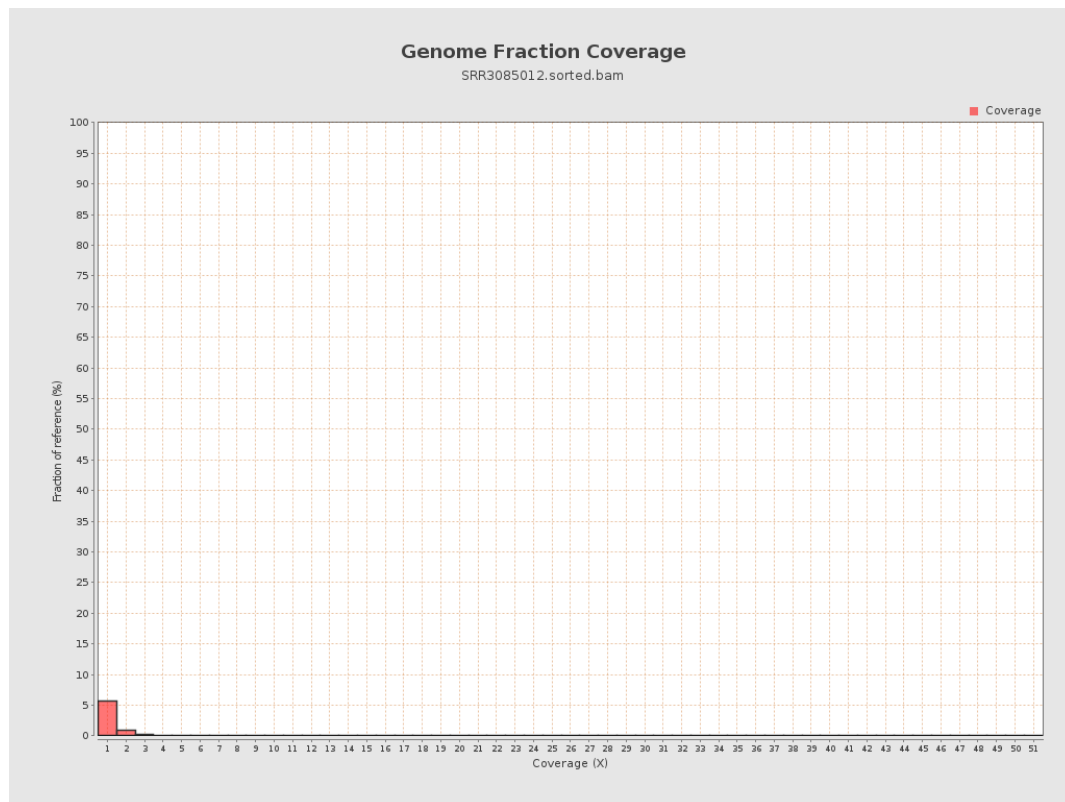
## 4. Results : Coverage Histogram



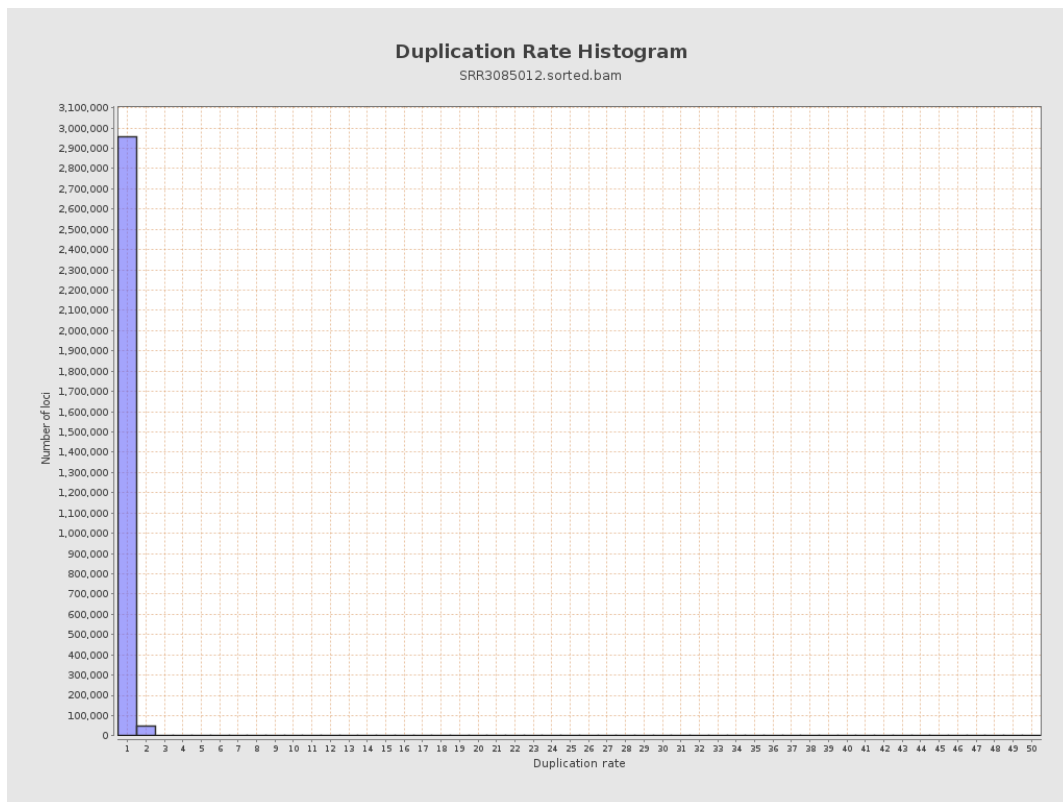
## 5. Results : Coverage Histogram (0-50X)



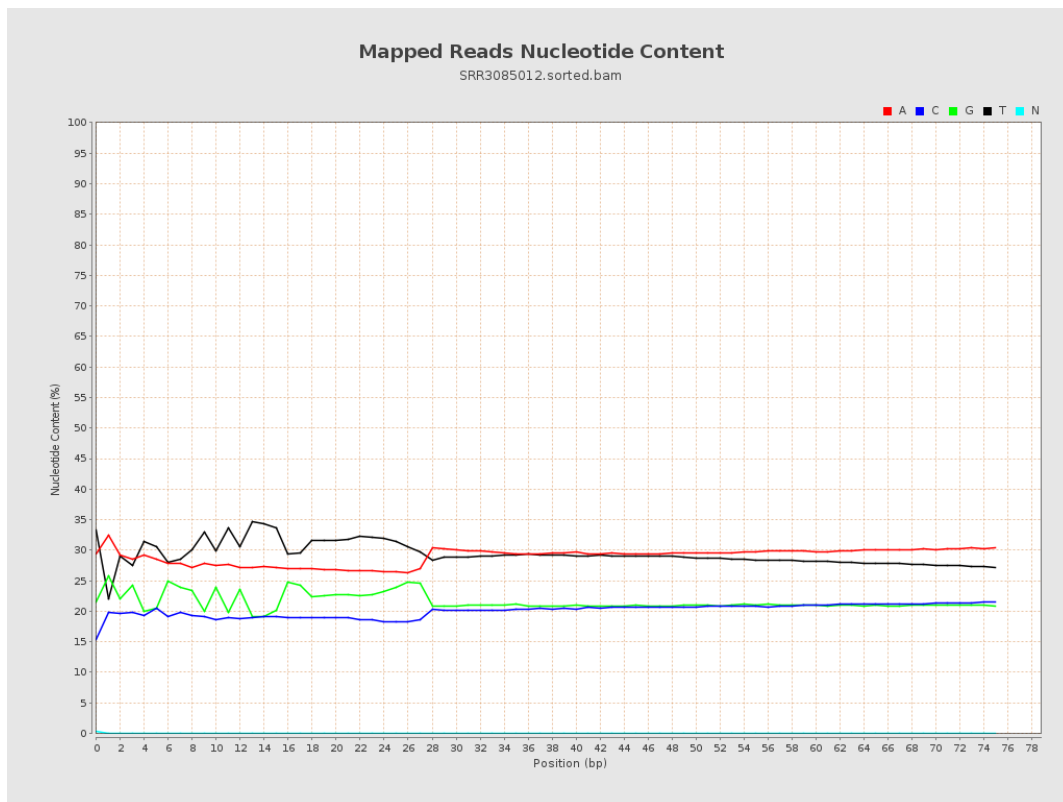
## 6. Results : Genome Fraction Coverage



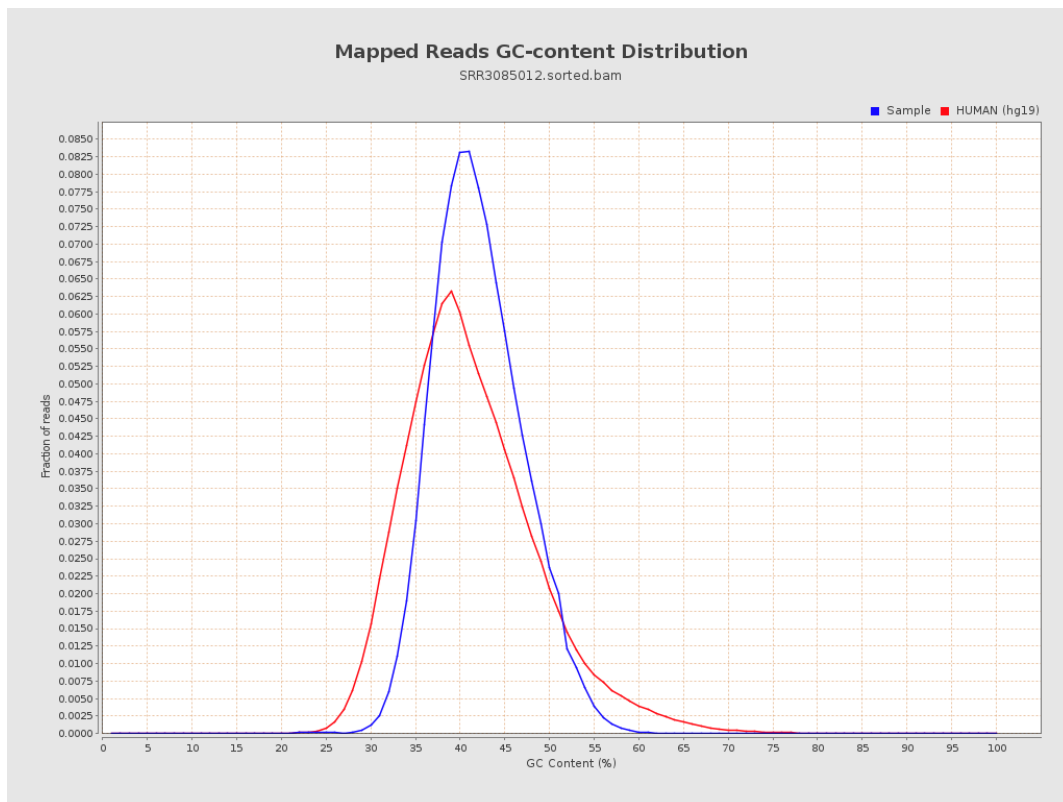
## 7. Results : Duplication Rate Histogram



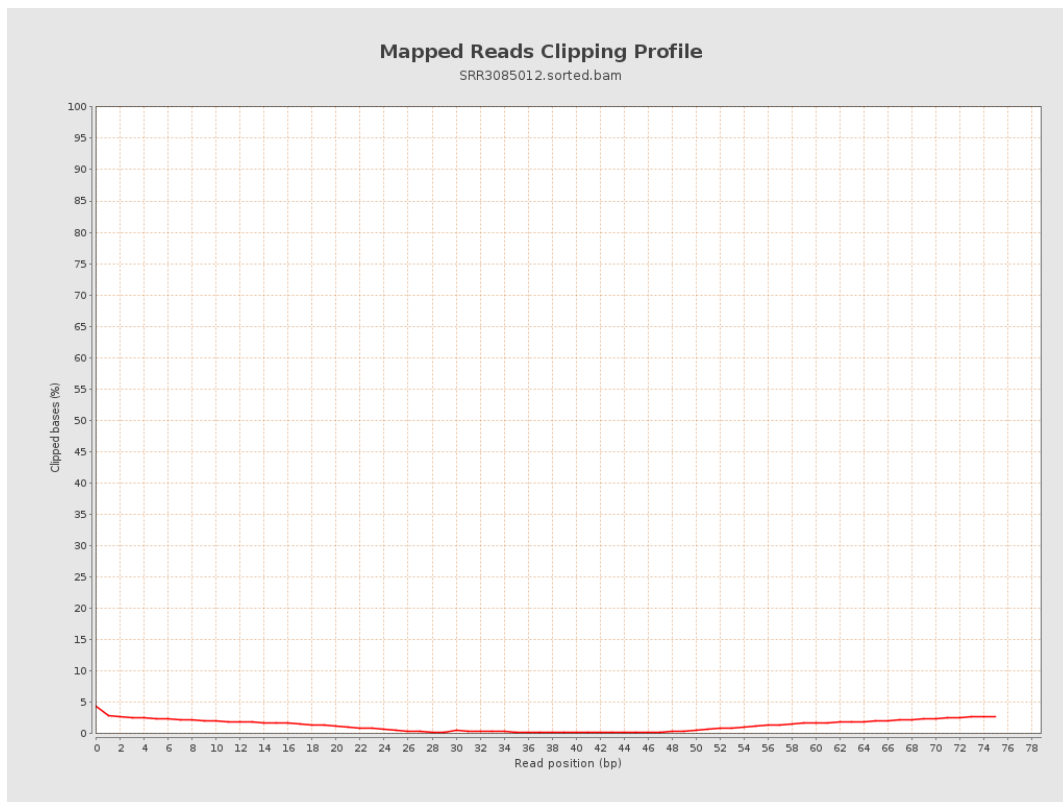
## 8. Results : Mapped Reads Nucleotide Content



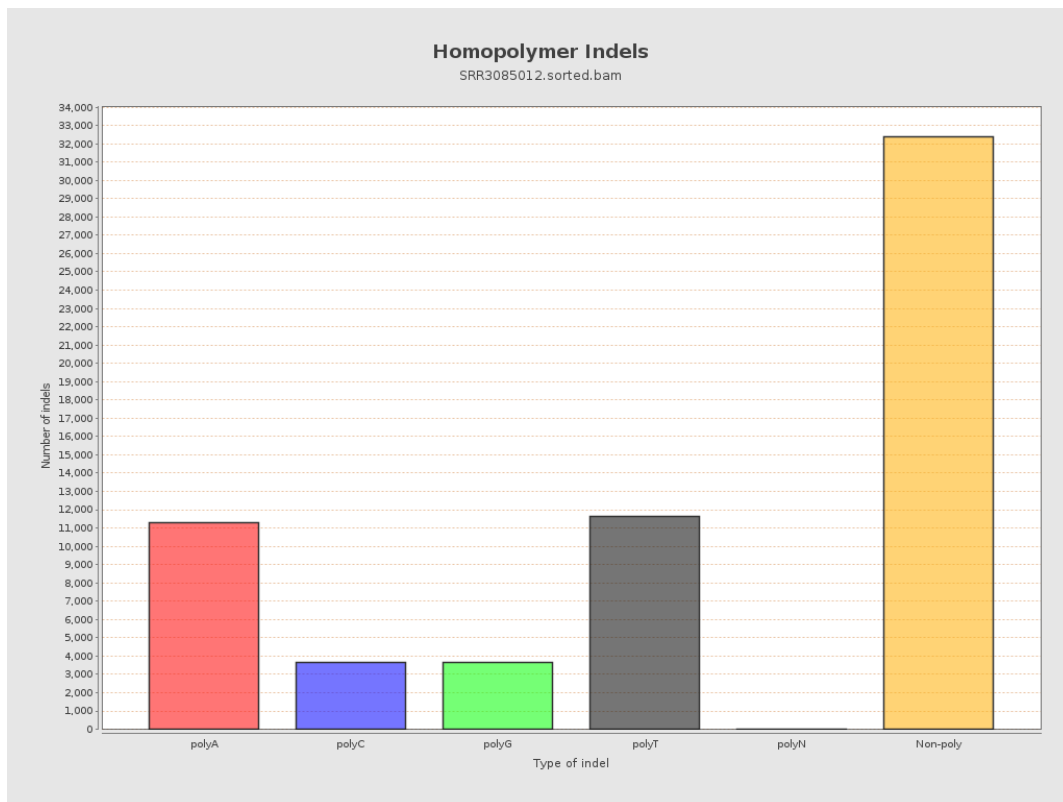
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

