

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/01 07:41:41*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472812.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_SRR3472812 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472812.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Tue Oct 01 07:41:41 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR3472812.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 2,903,795          |
| Mapped reads                 | 2,340,411 / 80.6%  |
| Unmapped reads               | 563,384 / 19.4%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 22,153 / 0.76%     |
| Read min/max/mean length     | 30 / 76 / 76.26    |
| Duplicated reads (estimated) | 104,977 / 3.62%    |
| Duplication rate             | 3.28%              |
| Clipped reads                | 1,347,543 / 46.41% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 39,949,943 / 26.93% |
| Number/percentage of C's | 29,547,271 / 19.92% |
| Number/percentage of T's | 43,951,921 / 29.63% |
| Number/percentage of G's | 34,894,438 / 23.52% |
| Number/percentage of N's | 3,404 / 0%          |
| GC Percentage            | 43.44%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0479 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.3669 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 43.41 |
|----------------------|-------|

## 2.5. Mismatches and indels

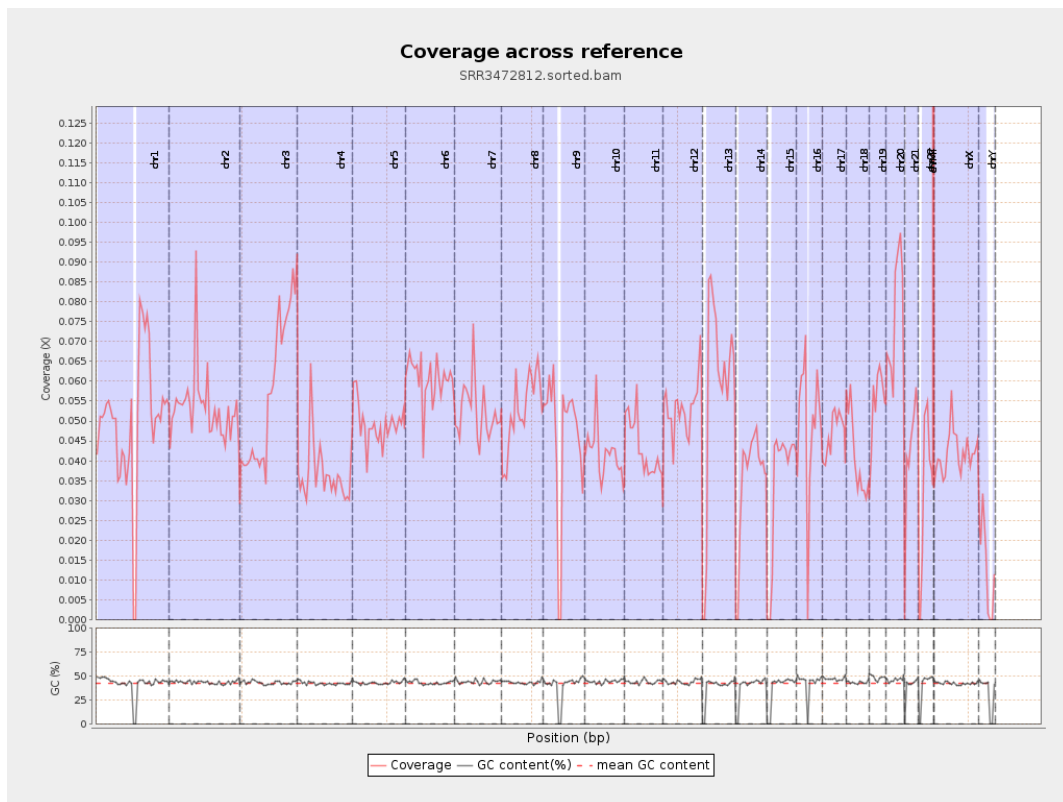
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.9%      |
| Mismatches                               | 1,308,731 |
| Insertions                               | 11,404    |
| Mapped reads with at least one insertion | 0.48%     |
| Deletions                                | 34,999    |
| Mapped reads with at least one deletion  | 1.48%     |
| Homopolymer indels                       | 45.18%    |

## 2.6. Chromosome stats

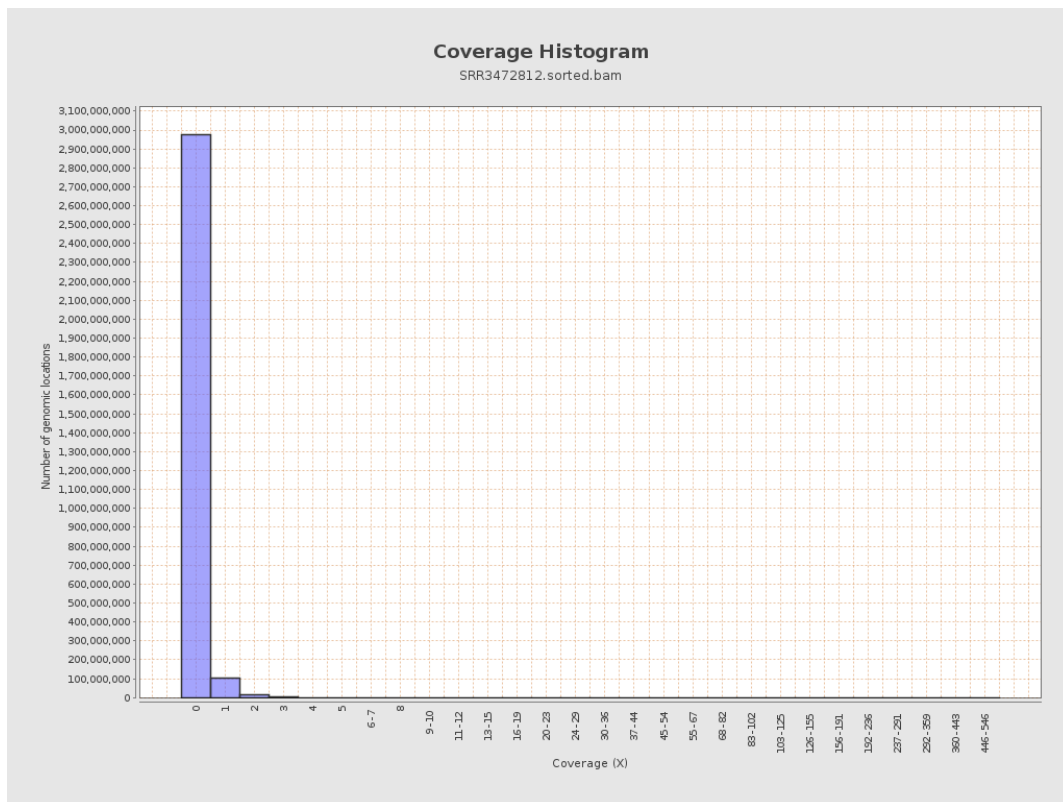
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 12413674     | 0.0498        | 0.4622             |
| chr2 | 243199373 | 12977296     | 0.0534        | 0.513              |
| chr3 | 198022430 | 11204938     | 0.0566        | 0.2826             |
| chr4 | 191154276 | 6976706      | 0.0365        | 0.2577             |
| chr5 | 180915260 | 8891805      | 0.0491        | 0.2666             |
| chr6 | 171115067 | 10358690     | 0.0605        | 0.3206             |
| chr7 | 159138663 | 8325262      | 0.0523        | 0.4816             |
|      |           |              |               |                    |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr8  | 146364022 | 7677882 | 0.0525 | 0.3436 |
| chr9  | 141213431 | 6457728 | 0.0457 | 0.3932 |
| chr10 | 135534747 | 5670029 | 0.0418 | 0.3396 |
| chr11 | 135006516 | 5798730 | 0.043  | 0.3999 |
| chr12 | 133851895 | 7148995 | 0.0534 | 0.2849 |
| chr13 | 115169878 | 6649505 | 0.0577 | 0.2919 |
| chr14 | 107349540 | 3764943 | 0.0351 | 0.279  |
| chr15 | 102531392 | 3545399 | 0.0346 | 0.2465 |
| chr16 | 90354753  | 4461081 | 0.0494 | 0.2963 |
| chr17 | 81195210  | 3799380 | 0.0468 | 0.285  |
| chr18 | 78077248  | 3203547 | 0.041  | 0.7085 |
| chr19 | 59128983  | 3253464 | 0.055  | 0.3744 |
| chr20 | 63025520  | 4822407 | 0.0765 | 0.3504 |
| chr21 | 48129895  | 2064128 | 0.0429 | 0.2854 |
| chr22 | 51304566  | 1620249 | 0.0316 | 0.221  |
| chrMT | 16571     | 90645   | 5.4701 | 4.3095 |
| chrX  | 155270560 | 6491141 | 0.0418 | 0.2876 |
| chrY  | 59373566  | 742271  | 0.0125 | 0.1739 |

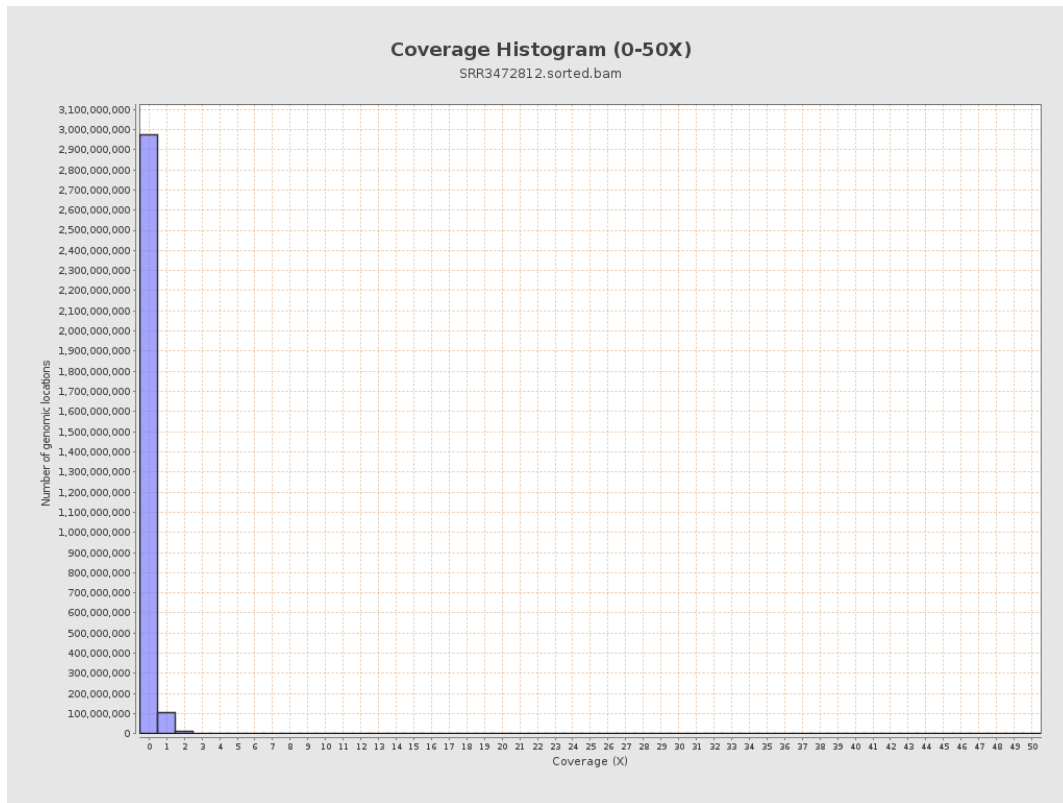
### 3. Results : Coverage across reference



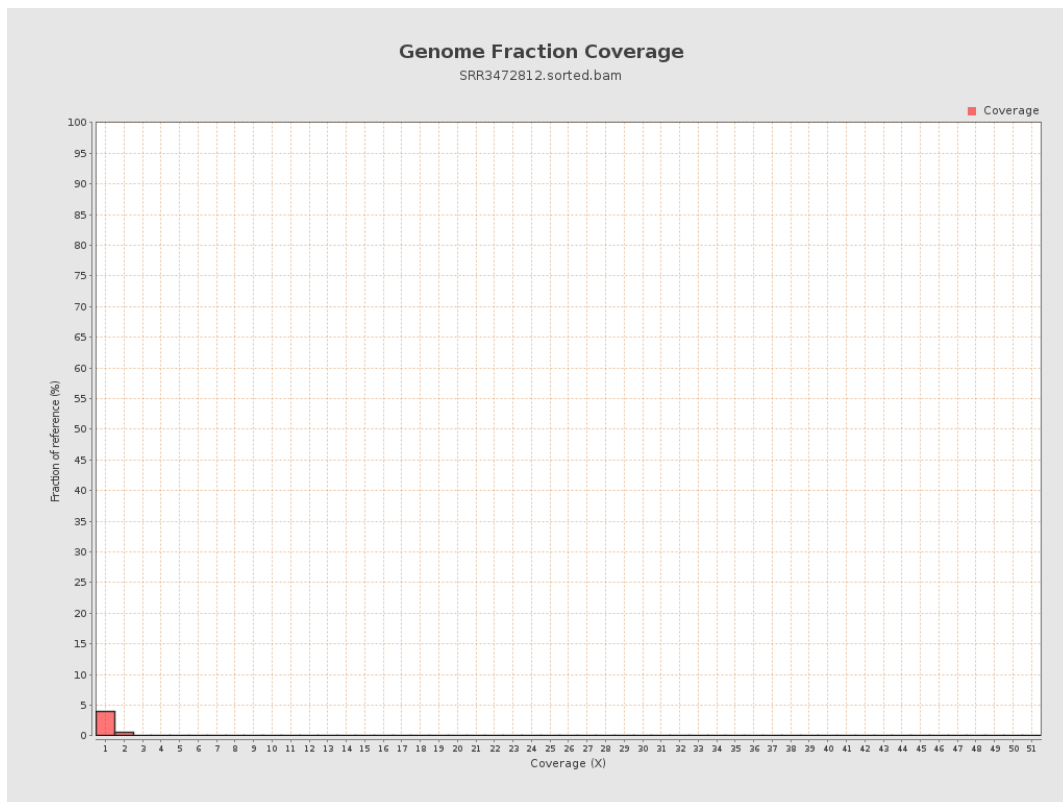
## 4. Results : Coverage Histogram



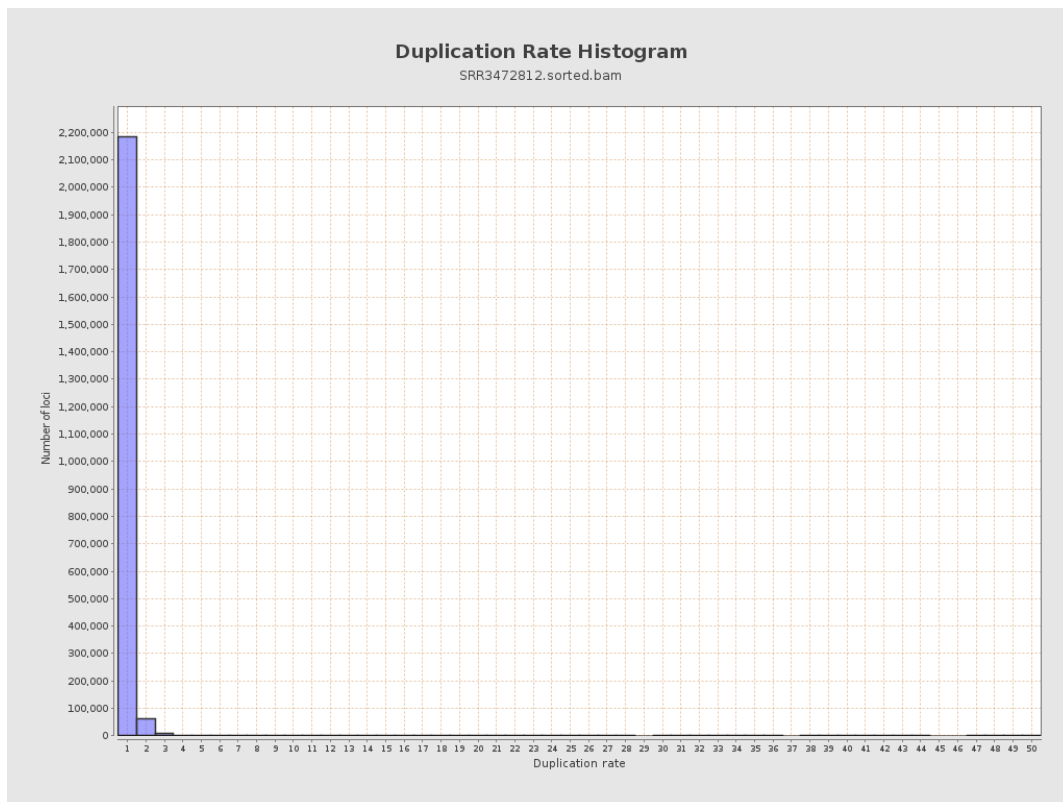
## 5. Results : Coverage Histogram (0-50X)



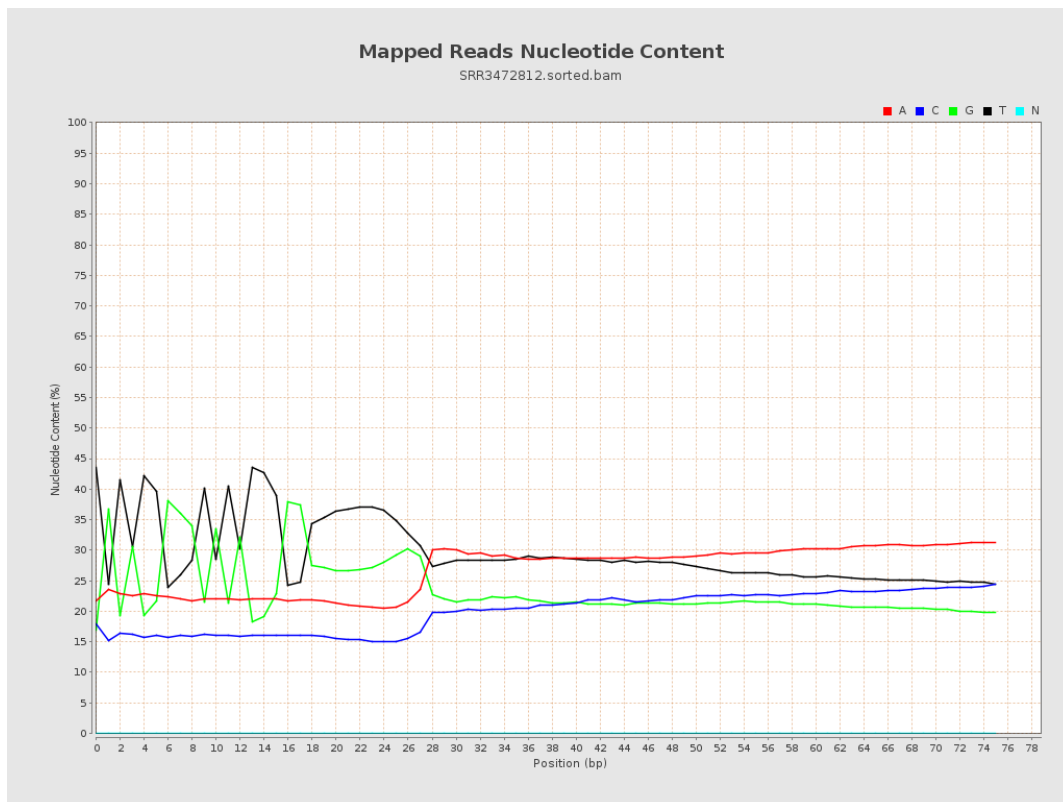
## 6. Results : Genome Fraction Coverage



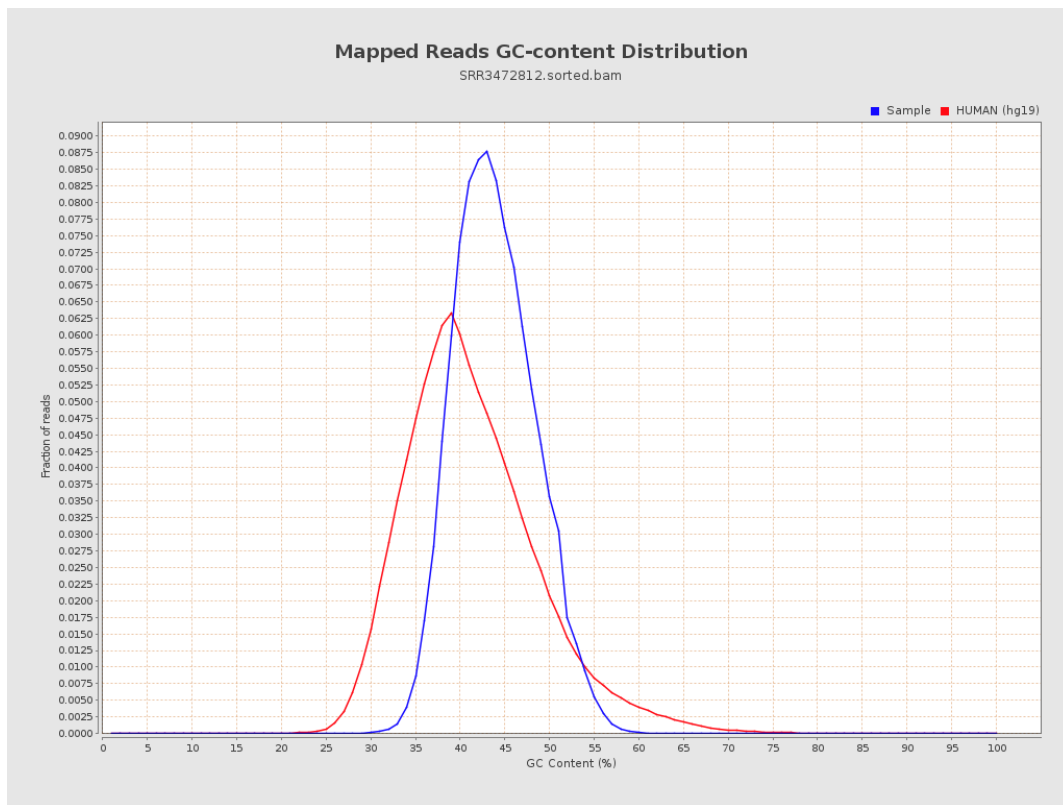
## 7. Results : Duplication Rate Histogram



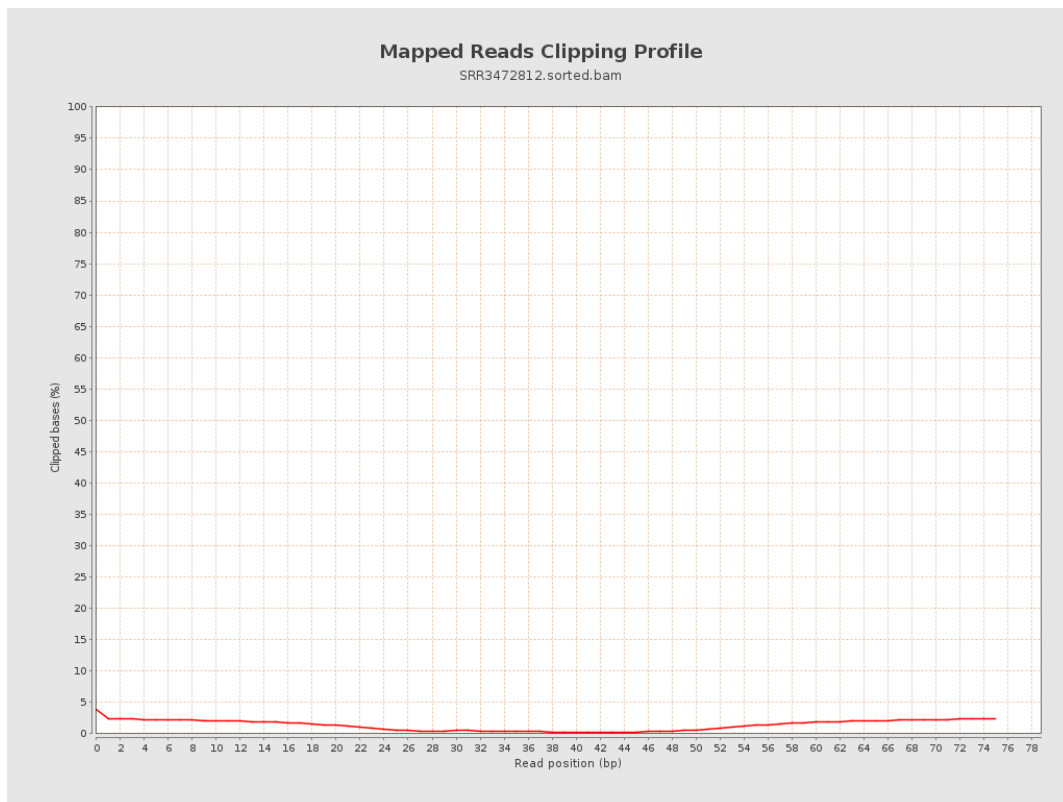
## 8. Results : Mapped Reads Nucleotide Content



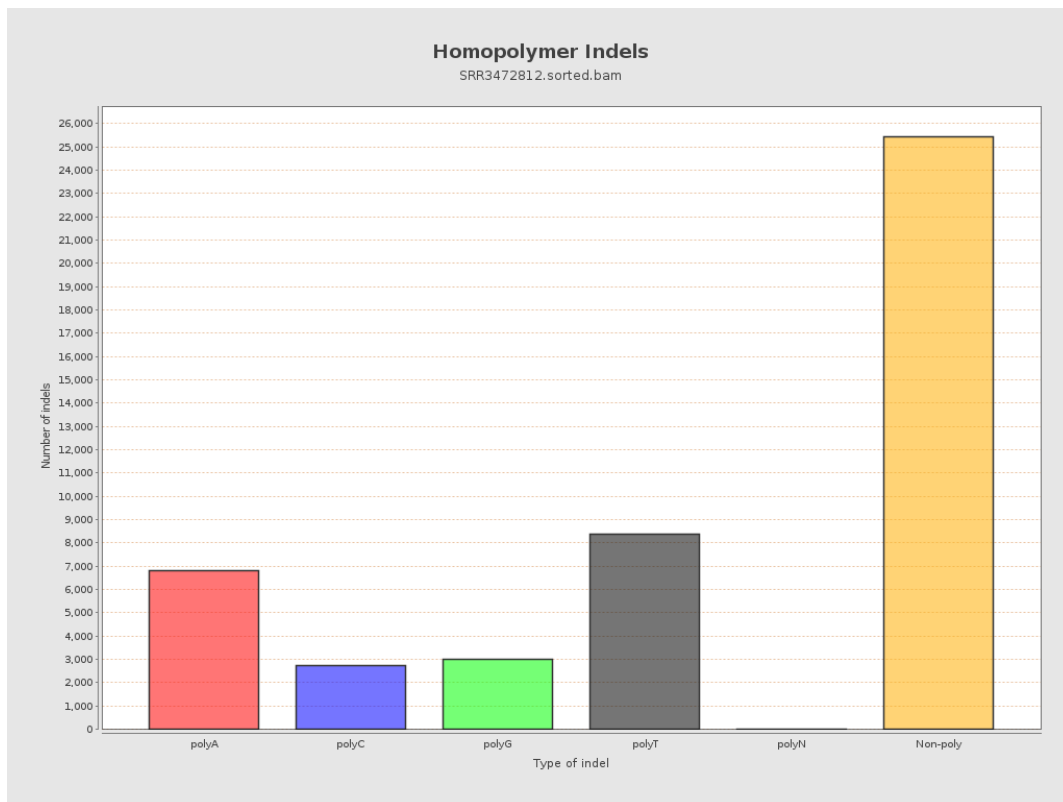
## 9. Results : Mapped Reads GC-content Distribution



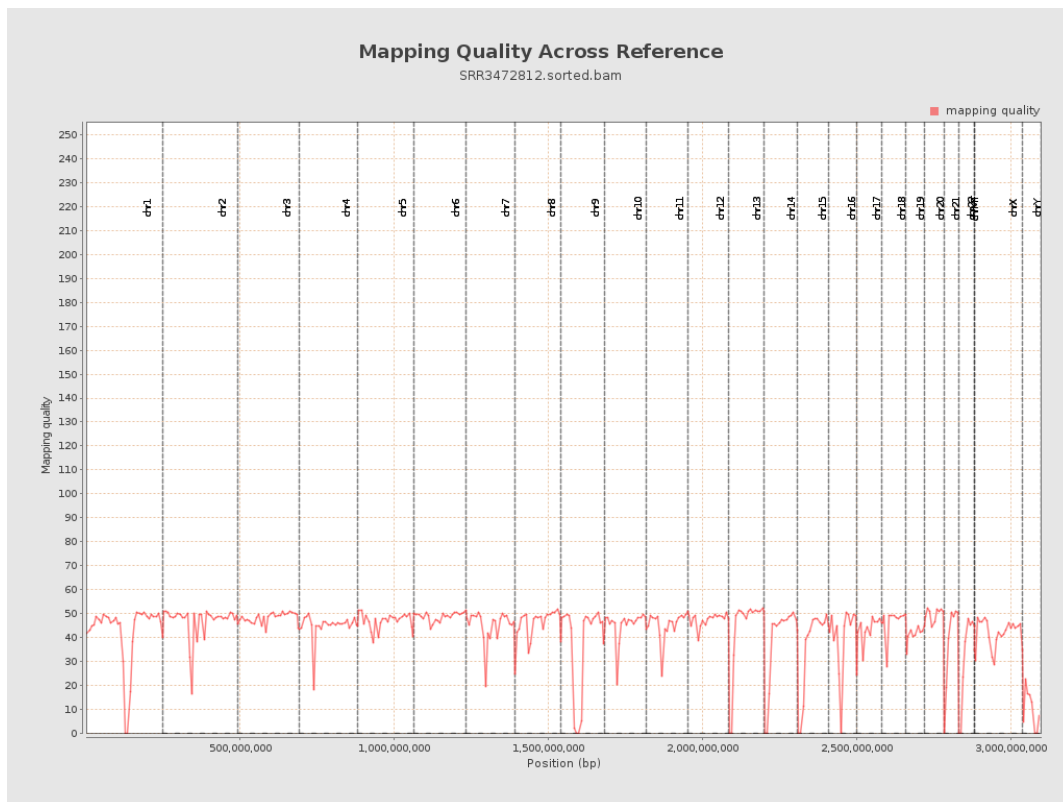
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

