

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 23:53:48*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083614.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_SRR3083614 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083614.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Sat Aug 24 23:53:46 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR3083614.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                   |
|------------------------------|-------------------|
| Reference size               | 3,095,693,983     |
| Number of reads              | 1,693,804         |
| Mapped reads                 | 1,512,579 / 89.3% |
| Unmapped reads               | 181,225 / 10.7%   |
| Mapped paired reads          | 0 / 0%            |
| Secondary alignments         | 0                 |
| Supplementary alignments     | 12,999 / 0.77%    |
| Read min/max/mean length     | 30 / 76 / 76.27   |
| Duplicated reads (estimated) | 59,790 / 3.53%    |
| Duplication rate             | 3.09%             |
| Clipped reads                | 758,373 / 44.77%  |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 26,164,122 / 26.48% |
| Number/percentage of C's | 18,257,597 / 18.48% |
| Number/percentage of T's | 31,176,513 / 31.55% |
| Number/percentage of G's | 23,215,071 / 23.49% |
| Number/percentage of N's | 4,514 / 0%          |
| GC Percentage            | 41.97%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0319 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.3118 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 44.02 |
|----------------------|-------|

## 2.5. Mismatches and indels

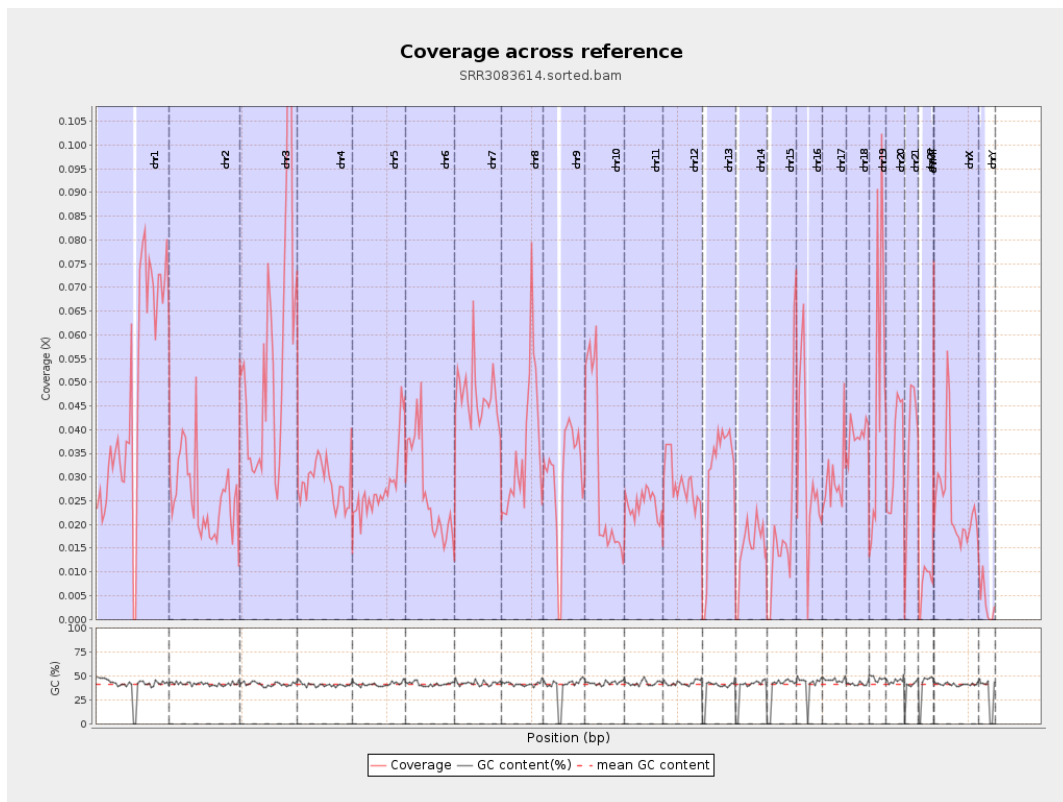
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 0.75%   |
| Mismatches                               | 725,176 |
| Insertions                               | 7,510   |
| Mapped reads with at least one insertion | 0.49%   |
| Deletions                                | 23,699  |
| Mapped reads with at least one deletion  | 1.55%   |
| Homopolymer indels                       | 46.74%  |

## 2.6. Chromosome stats

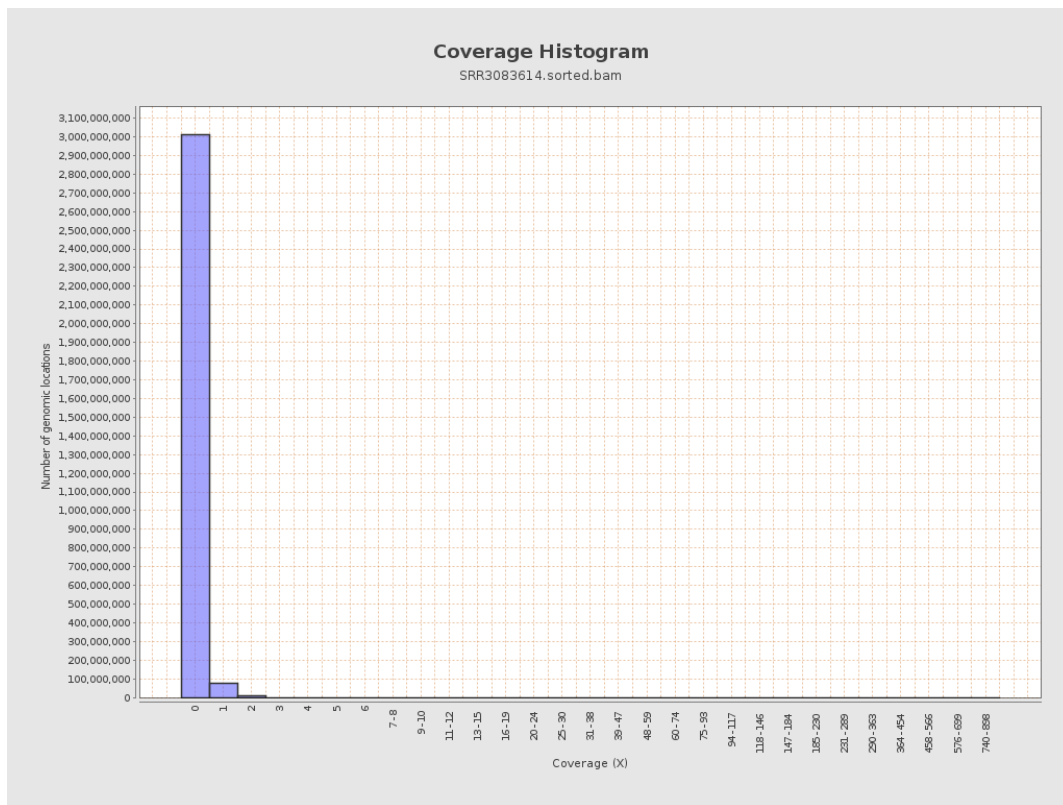
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 11776892     | 0.0472        | 0.5947             |
| chr2 | 243199373 | 6220837      | 0.0256        | 0.4535             |
| chr3 | 198022430 | 10870118     | 0.0549        | 0.2639             |
| chr4 | 191154276 | 5507487      | 0.0288        | 0.1918             |
| chr5 | 180915260 | 5094578      | 0.0282        | 0.1856             |
| chr6 | 171115067 | 4629471      | 0.0271        | 0.2398             |
| chr7 | 159138663 | 7528712      | 0.0473        | 0.4508             |
|      |           |              |               |                    |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr8  | 146364022 | 5247318 | 0.0359 | 0.2872 |
| chr9  | 141213431 | 4302306 | 0.0305 | 0.246  |
| chr10 | 135534747 | 4069305 | 0.03   | 0.2931 |
| chr11 | 135006516 | 3255730 | 0.0241 | 0.2088 |
| chr12 | 133851895 | 3825628 | 0.0286 | 0.188  |
| chr13 | 115169878 | 3467591 | 0.0301 | 0.1923 |
| chr14 | 107349540 | 1626729 | 0.0152 | 0.1402 |
| chr15 | 102531392 | 1947524 | 0.019  | 0.1634 |
| chr16 | 90354753  | 2903532 | 0.0321 | 0.2085 |
| chr17 | 81195210  | 2418884 | 0.0298 | 0.2065 |
| chr18 | 78077248  | 3039029 | 0.0389 | 0.4086 |
| chr19 | 59128983  | 2770516 | 0.0469 | 0.4034 |
| chr20 | 63025520  | 2197103 | 0.0349 | 0.2106 |
| chr21 | 48129895  | 1727558 | 0.0359 | 0.2119 |
| chr22 | 51304566  | 380285  | 0.0074 | 0.0938 |
| chrMT | 16571     | 1251    | 0.0755 | 0.2946 |
| chrX  | 155270560 | 3837749 | 0.0247 | 0.1846 |
| chrY  | 59373566  | 209747  | 0.0035 | 0.0913 |

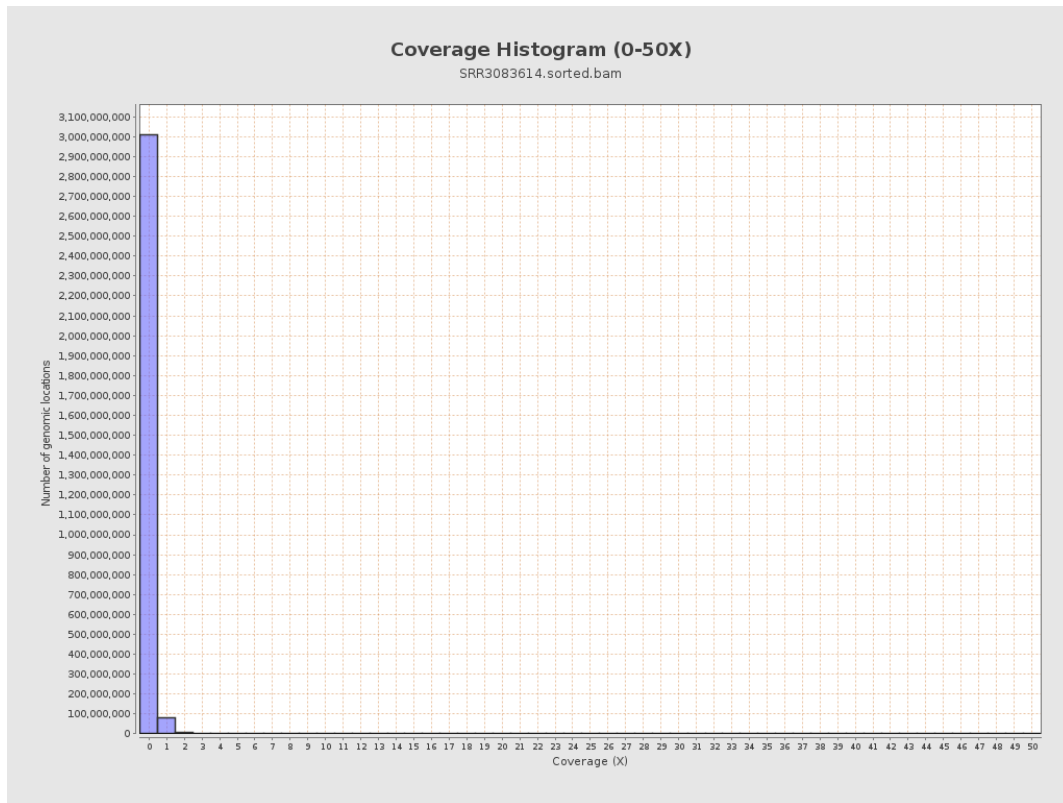
### 3. Results : Coverage across reference



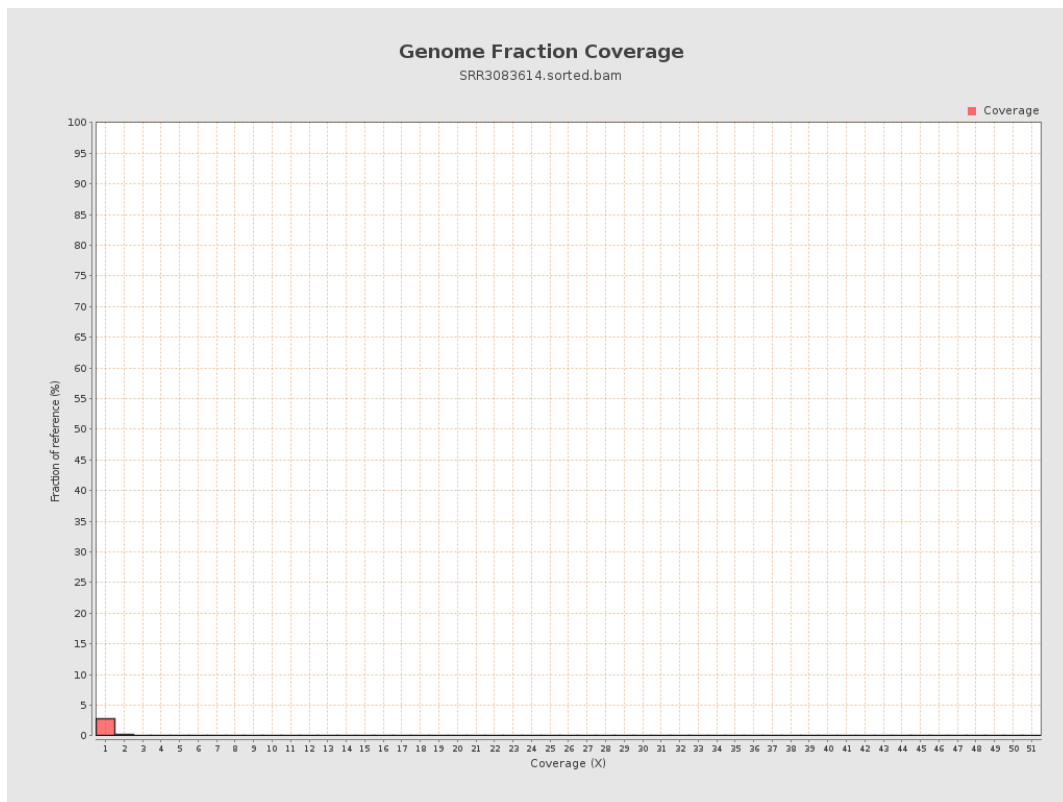
## 4. Results : Coverage Histogram



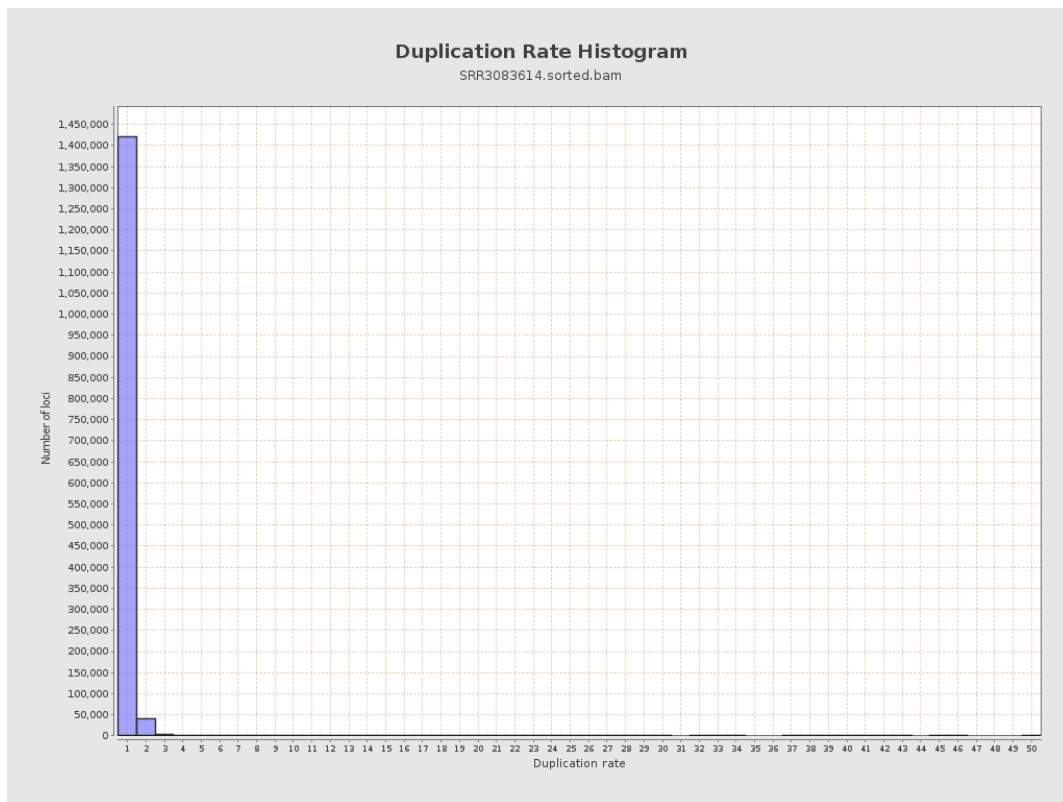
## 5. Results : Coverage Histogram (0-50X)



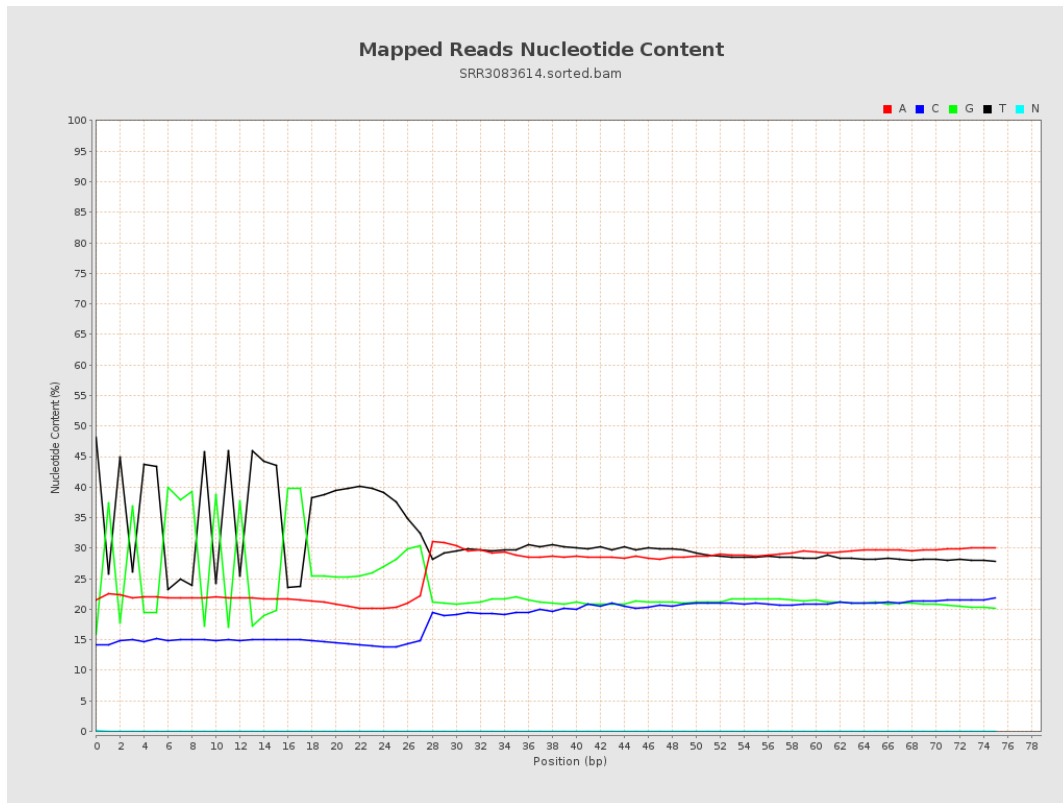
## 6. Results : Genome Fraction Coverage



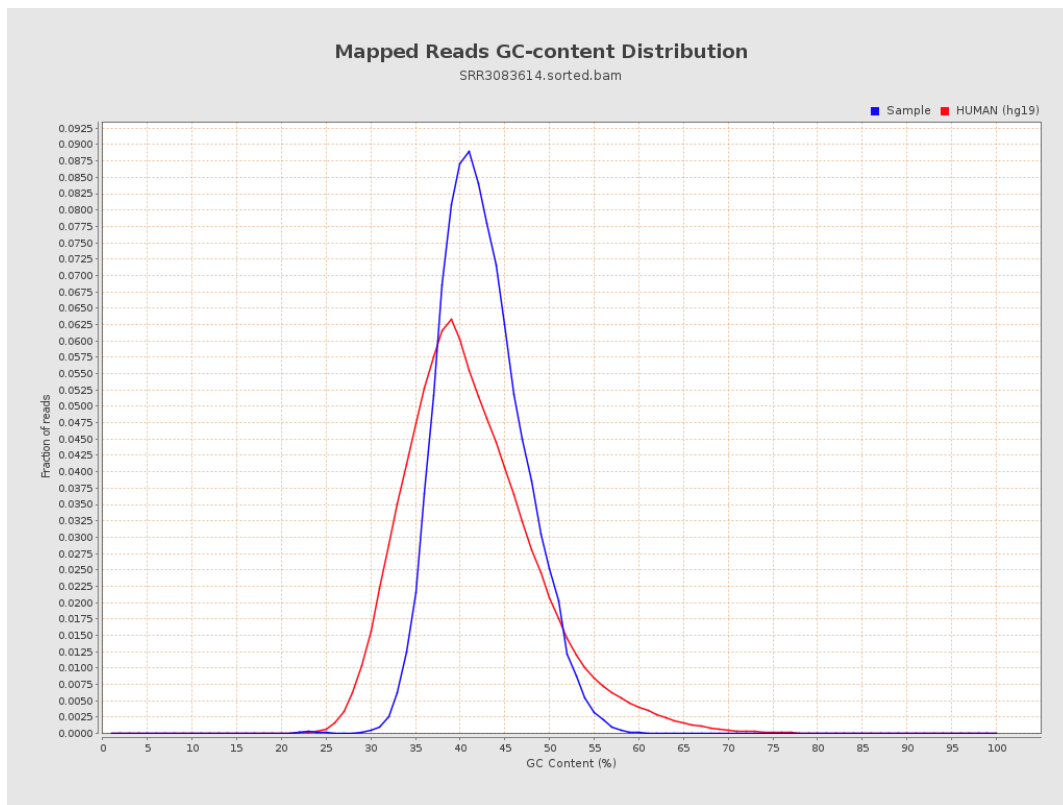
## 7. Results : Duplication Rate Histogram



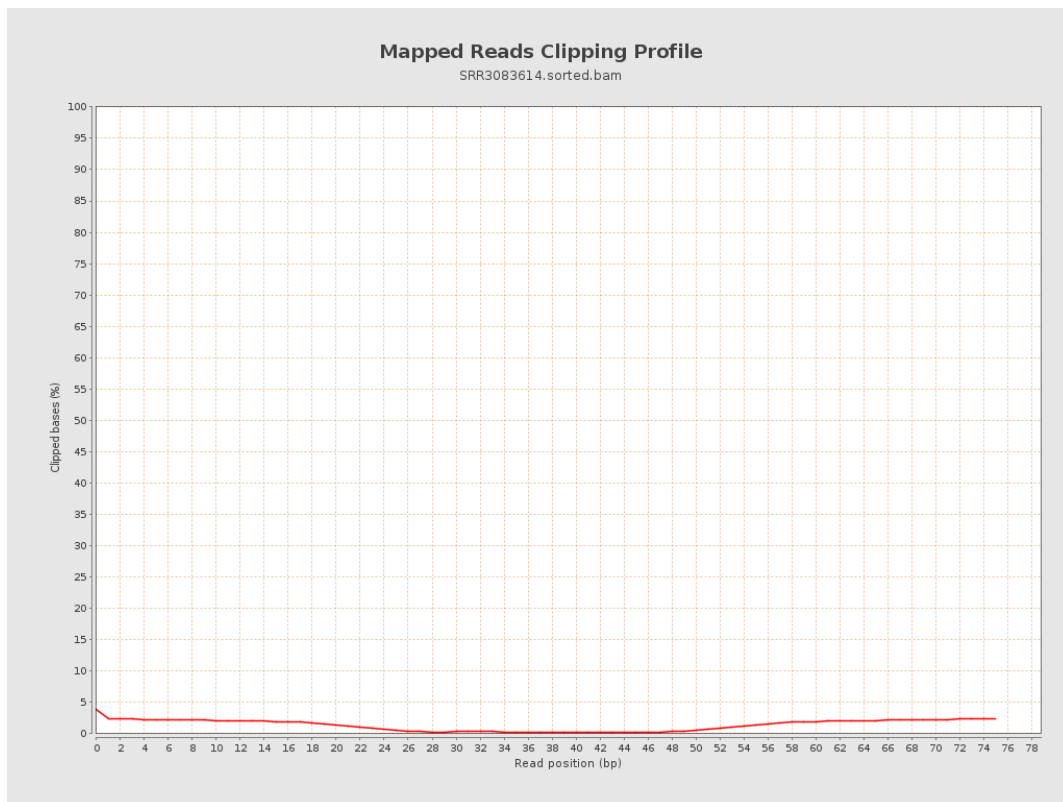
## 8. Results : Mapped Reads Nucleotide Content



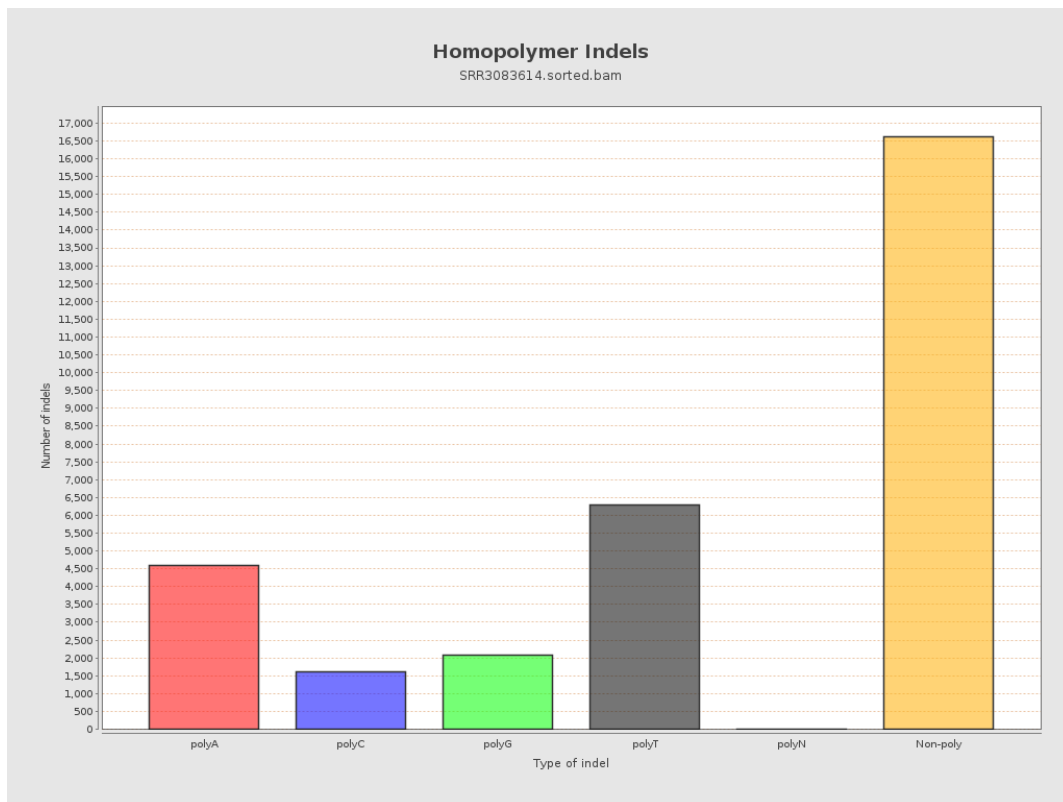
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

