

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/15 15:02:51*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068178.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_SRR6068178 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068178.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Sun Sep 15 15:02:50 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6068178.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 2,983,442          |
| Mapped reads                 | 2,694,407 / 90.31% |
| Unmapped reads               | 289,035 / 9.69%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 16,704 / 0.56%     |
| Read min/max/mean length     | 30 / 76 / 76.19    |
| Duplicated reads (estimated) | 821,892 / 27.55%   |
| Duplication rate             | 20.09%             |
| Clipped reads                | 1,637,224 / 54.88% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 41,707,050 / 24.86% |
| Number/percentage of C's | 29,664,237 / 17.68% |
| Number/percentage of T's | 55,375,788 / 33%    |
| Number/percentage of G's | 41,023,513 / 24.45% |
| Number/percentage of N's | 17,545 / 0.01%      |
| GC Percentage            | 42.13%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0542 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.6905 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 45.04 |
|----------------------|-------|

## 2.5. Mismatches and indels

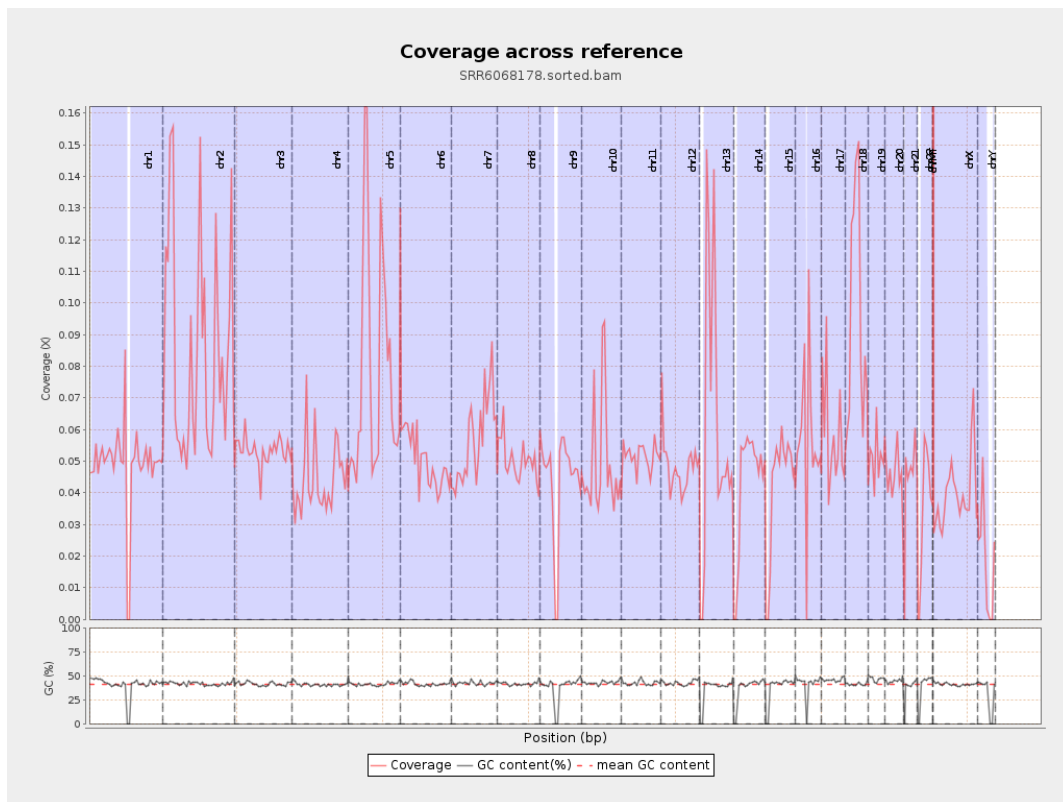
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.66%     |
| Mismatches                               | 1,086,294 |
| Insertions                               | 10,968    |
| Mapped reads with at least one insertion | 0.4%      |
| Deletions                                | 45,315    |
| Mapped reads with at least one deletion  | 1.66%     |
| Homopolymer indels                       | 45.49%    |

## 2.6. Chromosome stats

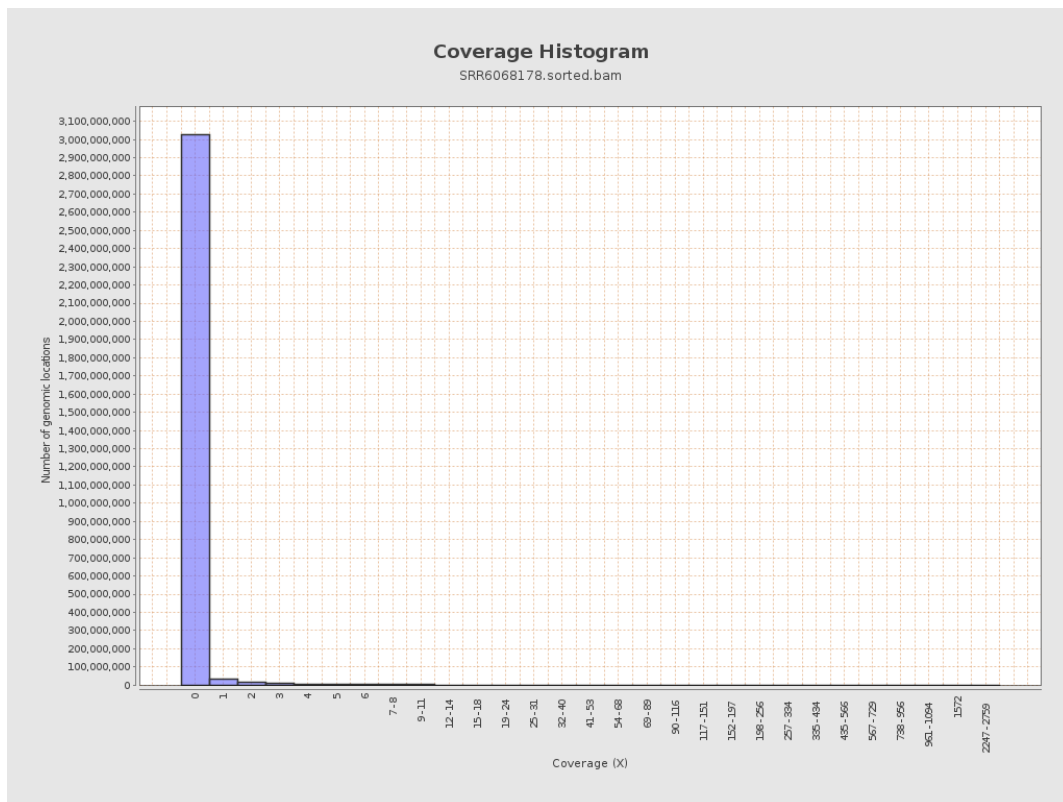
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 12163646     | 0.0488        | 0.9784             |
| chr2 | 243199373 | 20569750     | 0.0846        | 1.3604             |
| chr3 | 198022430 | 10518340     | 0.0531        | 0.5033             |
| chr4 | 191154276 | 8485048      | 0.0444        | 0.4614             |
| chr5 | 180915260 | 14080939     | 0.0778        | 0.5691             |
| chr6 | 171115067 | 8554926      | 0.05          | 0.5955             |
| chr7 | 159138663 | 9065525      | 0.057         | 0.6132             |
|      |           |              |               |                    |

|       |           |         |         |         |
|-------|-----------|---------|---------|---------|
| chr8  | 146364022 | 7342363 | 0.0502  | 0.5972  |
| chr9  | 141213431 | 6198470 | 0.0439  | 0.4947  |
| chr10 | 135534747 | 6621045 | 0.0489  | 0.5325  |
| chr11 | 135006516 | 6946613 | 0.0515  | 0.5315  |
| chr12 | 133851895 | 6514104 | 0.0487  | 0.4783  |
| chr13 | 115169878 | 7020384 | 0.061   | 0.5111  |
| chr14 | 107349540 | 4676613 | 0.0436  | 0.4684  |
| chr15 | 102531392 | 4251227 | 0.0415  | 0.4638  |
| chr16 | 90354753  | 5125986 | 0.0567  | 0.5268  |
| chr17 | 81195210  | 4796255 | 0.0591  | 0.5274  |
| chr18 | 78077248  | 7473423 | 0.0957  | 0.976   |
| chr19 | 59128983  | 3017233 | 0.051   | 0.8661  |
| chr20 | 63025520  | 2858444 | 0.0454  | 0.4812  |
| chr21 | 48129895  | 2162671 | 0.0449  | 0.4638  |
| chr22 | 51304566  | 1764200 | 0.0344  | 0.407   |
| chrMT | 16571     | 422111  | 25.4729 | 16.0621 |
| chrX  | 155270560 | 6102873 | 0.0393  | 0.4146  |
| chrY  | 59373566  | 1136205 | 0.0191  | 0.3088  |

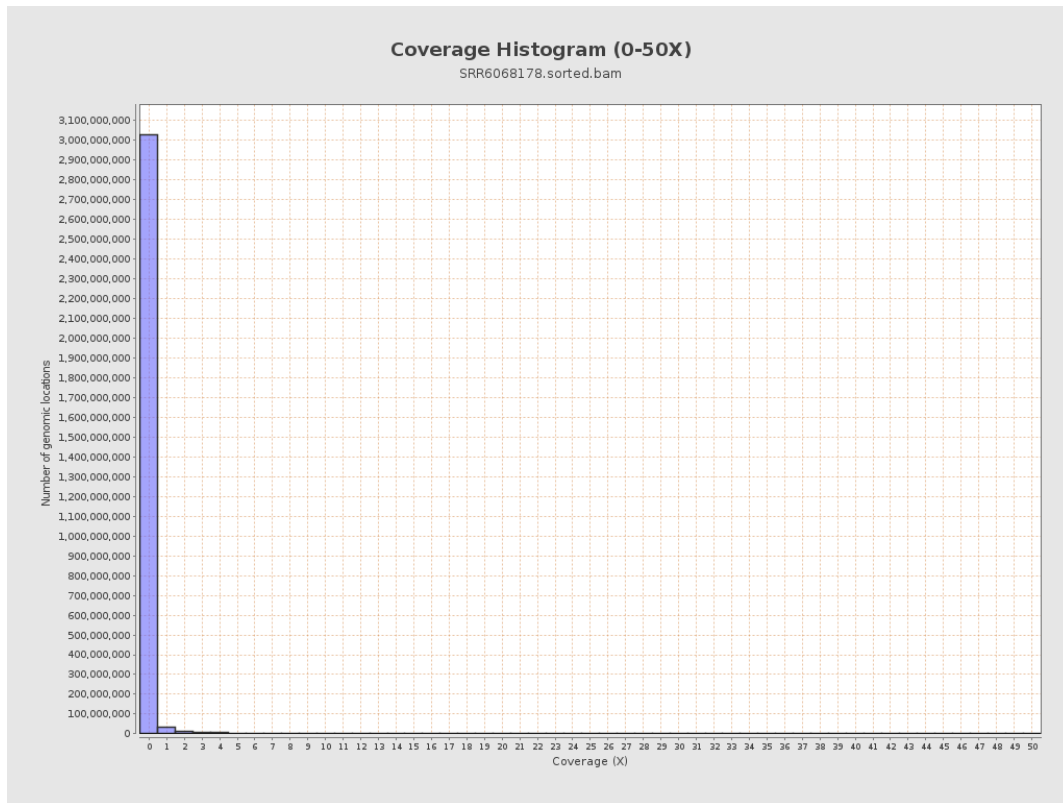
### 3. Results : Coverage across reference



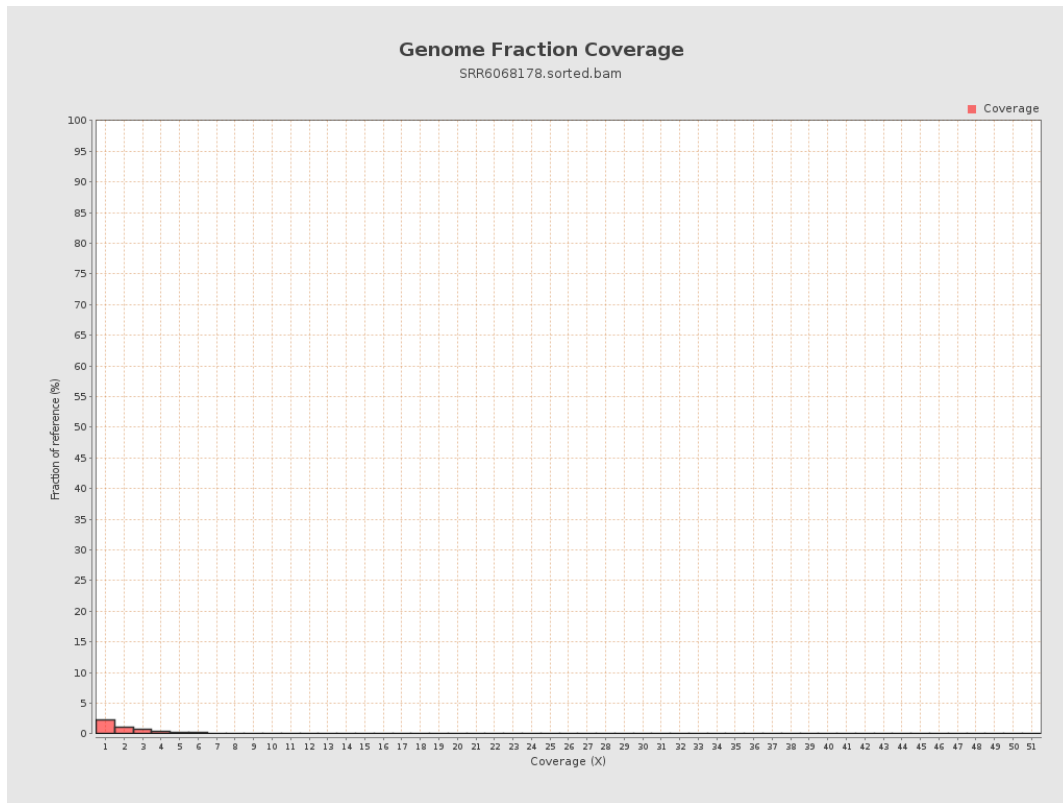
## 4. Results : Coverage Histogram



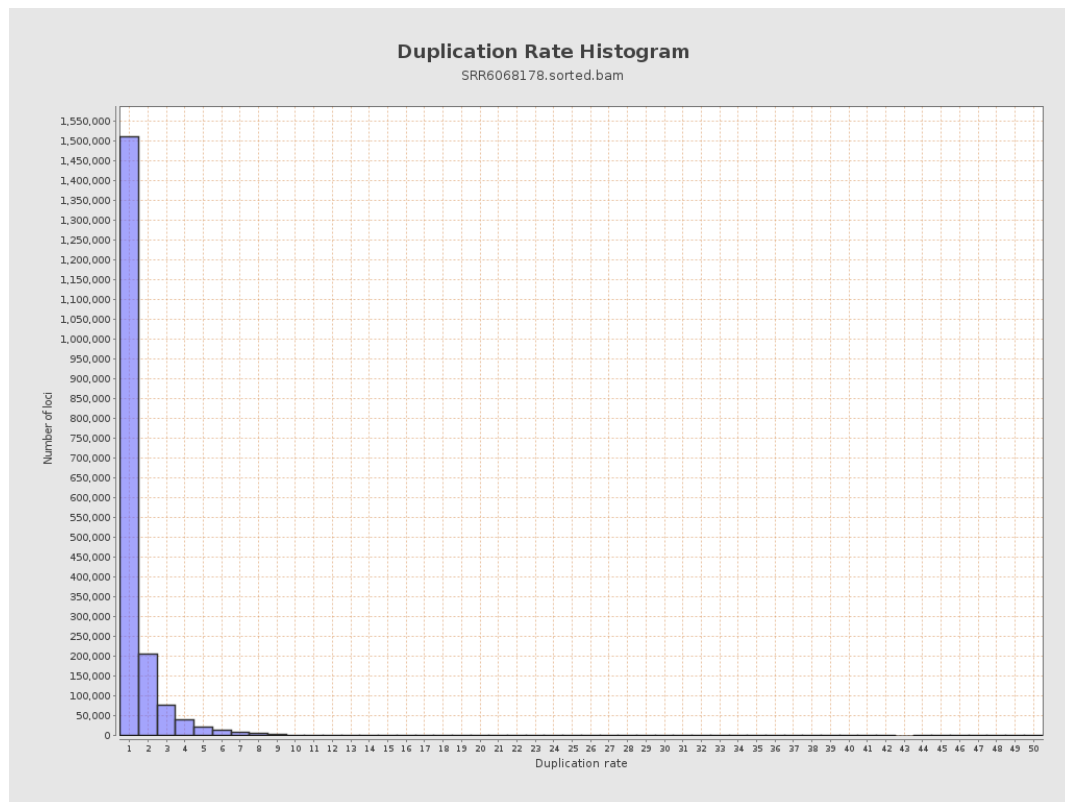
## 5. Results : Coverage Histogram (0-50X)



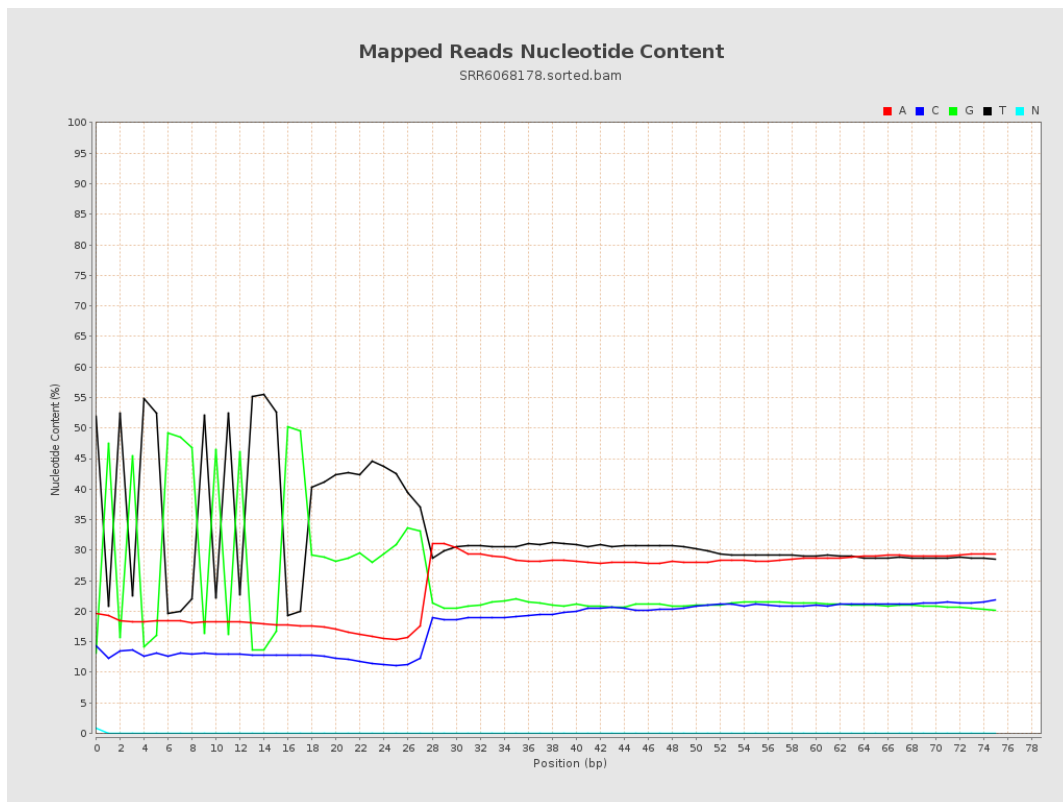
## 6. Results : Genome Fraction Coverage



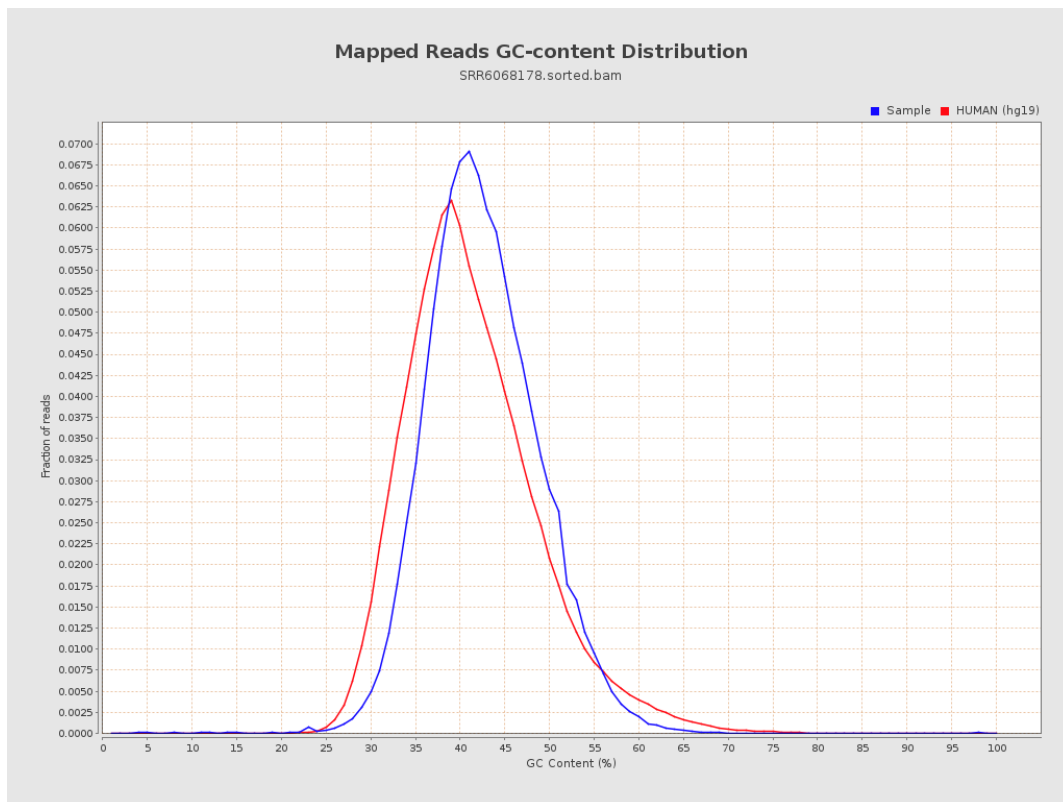
## 7. Results : Duplication Rate Histogram



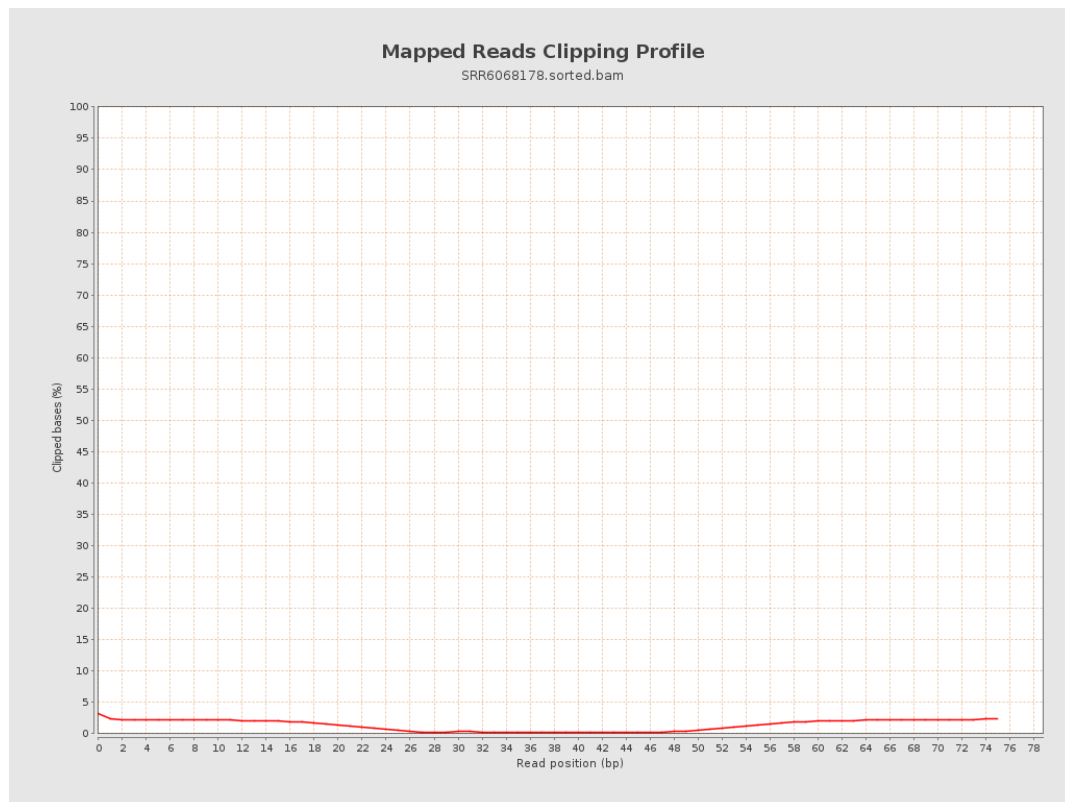
## 8. Results : Mapped Reads Nucleotide Content



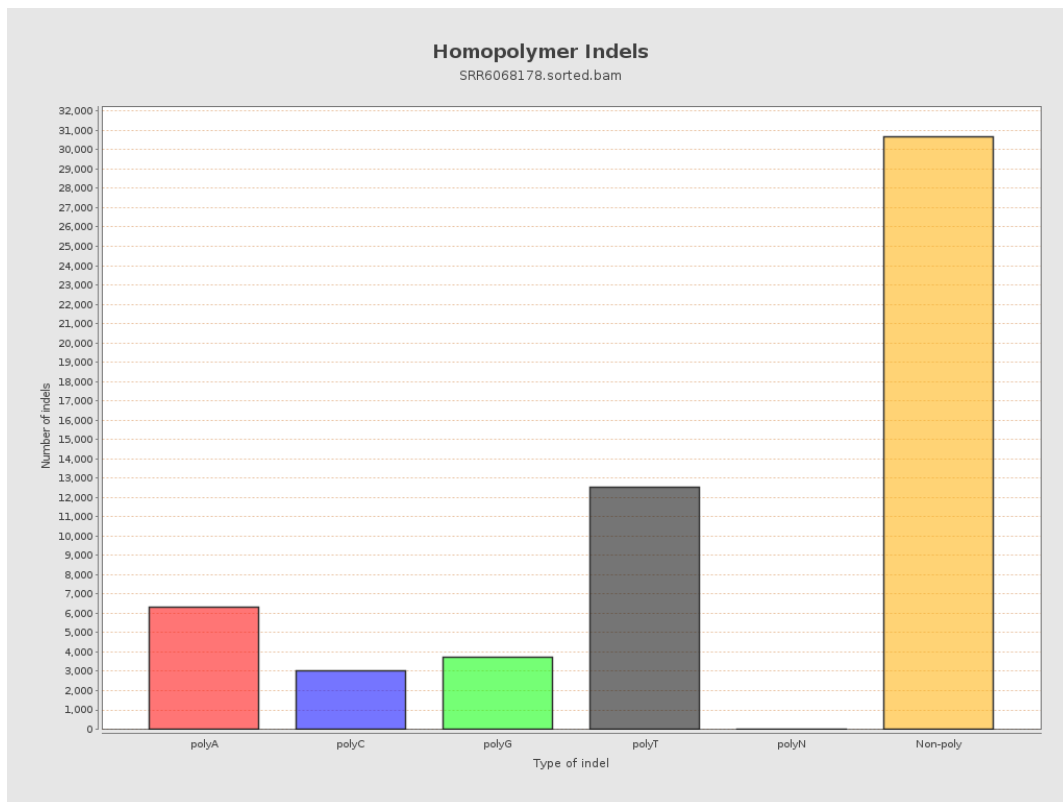
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

