

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/15 01:54:24*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063550.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_SRR6063550 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063550.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Sun Sep 15 01:54:23 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6063550.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 2,685,069          |
| Mapped reads                 | 2,413,866 / 89.9%  |
| Unmapped reads               | 271,203 / 10.1%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 16,916 / 0.63%     |
| Read min/max/mean length     | 30 / 76 / 76.22    |
| Duplicated reads (estimated) | 115,061 / 4.29%    |
| Duplication rate             | 3.66%              |
| Clipped reads                | 1,117,127 / 41.61% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 44,855,087 / 28.01% |
| Number/percentage of C's | 29,211,353 / 18.24% |
| Number/percentage of T's | 50,684,811 / 31.65% |
| Number/percentage of G's | 35,401,826 / 22.1%  |
| Number/percentage of N's | 3,507 / 0%          |
| GC Percentage            | 40.34%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0518 |
|      |        |

|                    |       |
|--------------------|-------|
| Standard Deviation | 0.485 |
|--------------------|-------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 46.02 |
|----------------------|-------|

## 2.5. Mismatches and indels

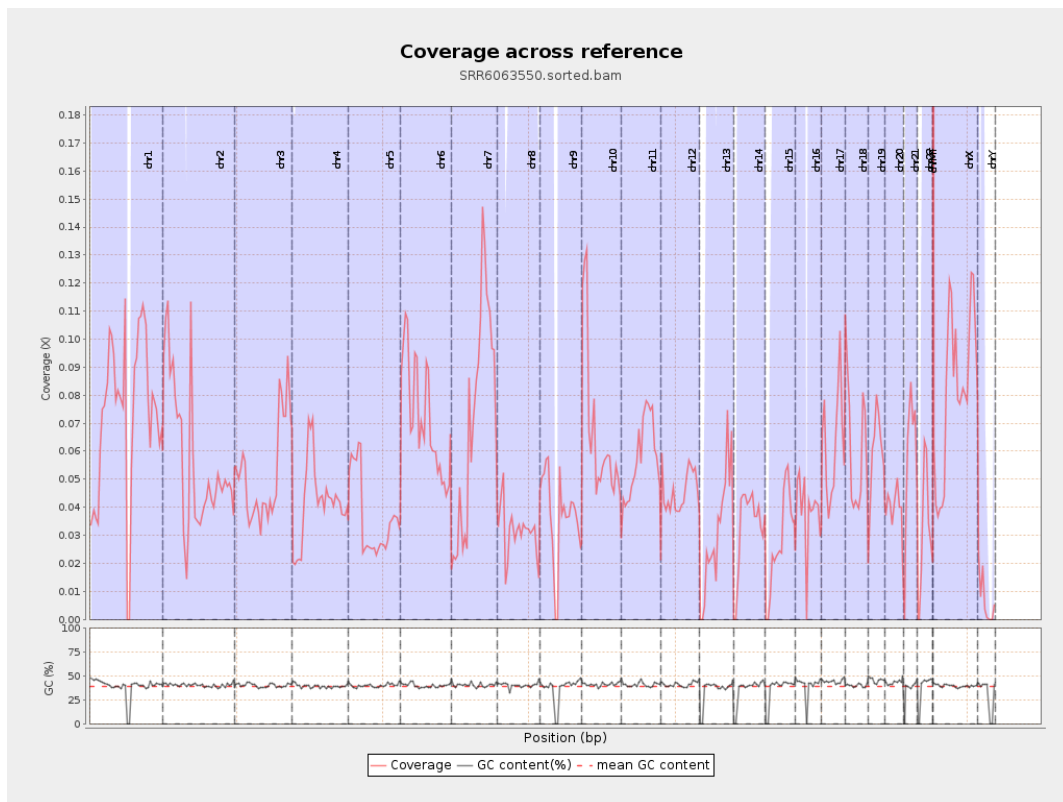
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.81%     |
| Mismatches                               | 1,274,053 |
| Insertions                               | 12,318    |
| Mapped reads with at least one insertion | 0.51%     |
| Deletions                                | 47,303    |
| Mapped reads with at least one deletion  | 1.94%     |
| Homopolymer indels                       | 46.49%    |

## 2.6. Chromosome stats

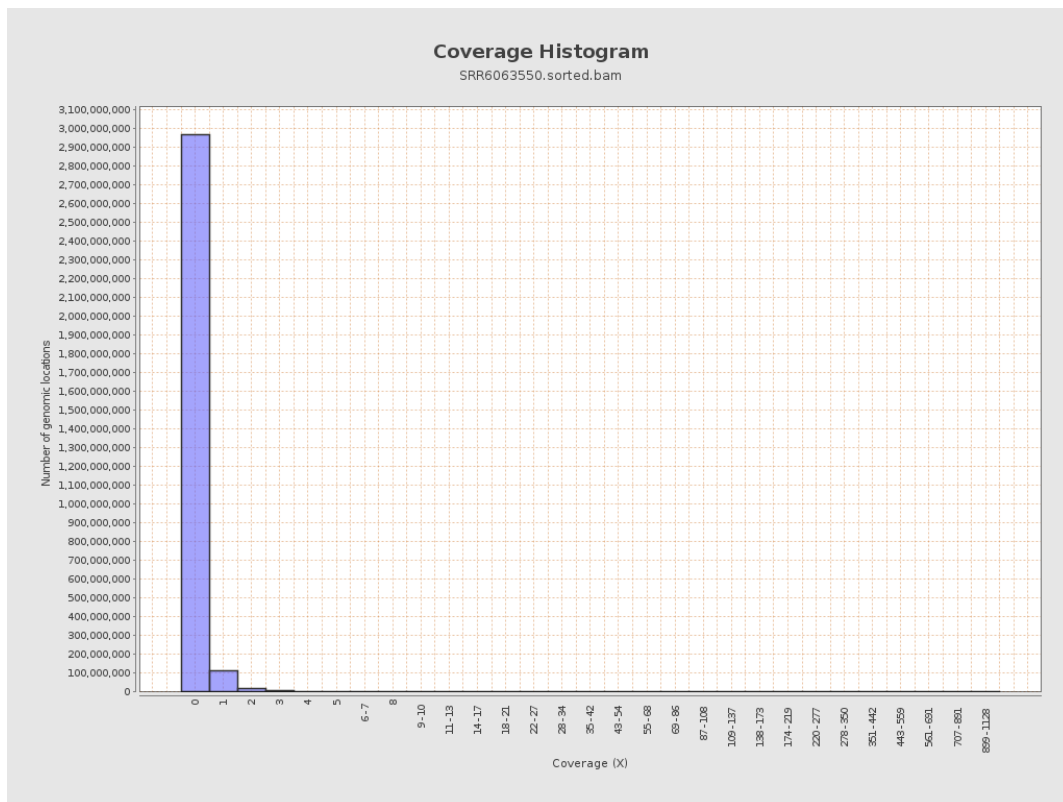
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 18223468     | 0.0731        | 0.9972             |
| chr2 | 243199373 | 13870600     | 0.057         | 0.6117             |
| chr3 | 198022430 | 10297840     | 0.052         | 0.2694             |
| chr4 | 191154276 | 8066718      | 0.0422        | 0.2566             |
| chr5 | 180915260 | 6566448      | 0.0363        | 0.2273             |
| chr6 | 171115067 | 12270914     | 0.0717        | 0.3783             |
| chr7 | 159138663 | 11324368     | 0.0712        | 0.6084             |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr8  | 146364022 | 4541668  | 0.031  | 0.633  |
| chr9  | 141213431 | 5271992  | 0.0373 | 0.4178 |
| chr10 | 135534747 | 9055082  | 0.0668 | 0.4073 |
| chr11 | 135006516 | 7766677  | 0.0575 | 0.3817 |
| chr12 | 133851895 | 6142265  | 0.0459 | 0.265  |
| chr13 | 115169878 | 3645610  | 0.0317 | 0.2112 |
| chr14 | 107349540 | 3578738  | 0.0333 | 0.2611 |
| chr15 | 102531392 | 2806567  | 0.0274 | 0.204  |
| chr16 | 90354753  | 3412927  | 0.0378 | 0.2579 |
| chr17 | 81195210  | 5182941  | 0.0638 | 0.3263 |
| chr18 | 78077248  | 4754737  | 0.0609 | 0.698  |
| chr19 | 59128983  | 3559670  | 0.0602 | 0.6767 |
| chr20 | 63025520  | 2535703  | 0.0402 | 0.246  |
| chr21 | 48129895  | 2737142  | 0.0569 | 0.296  |
| chr22 | 51304566  | 1619569  | 0.0316 | 0.207  |
| chrMT | 16571     | 23915    | 1.4432 | 1.6296 |
| chrX  | 155270560 | 12570225 | 0.081  | 0.4044 |
| chrY  | 59373566  | 408560   | 0.0069 | 0.162  |

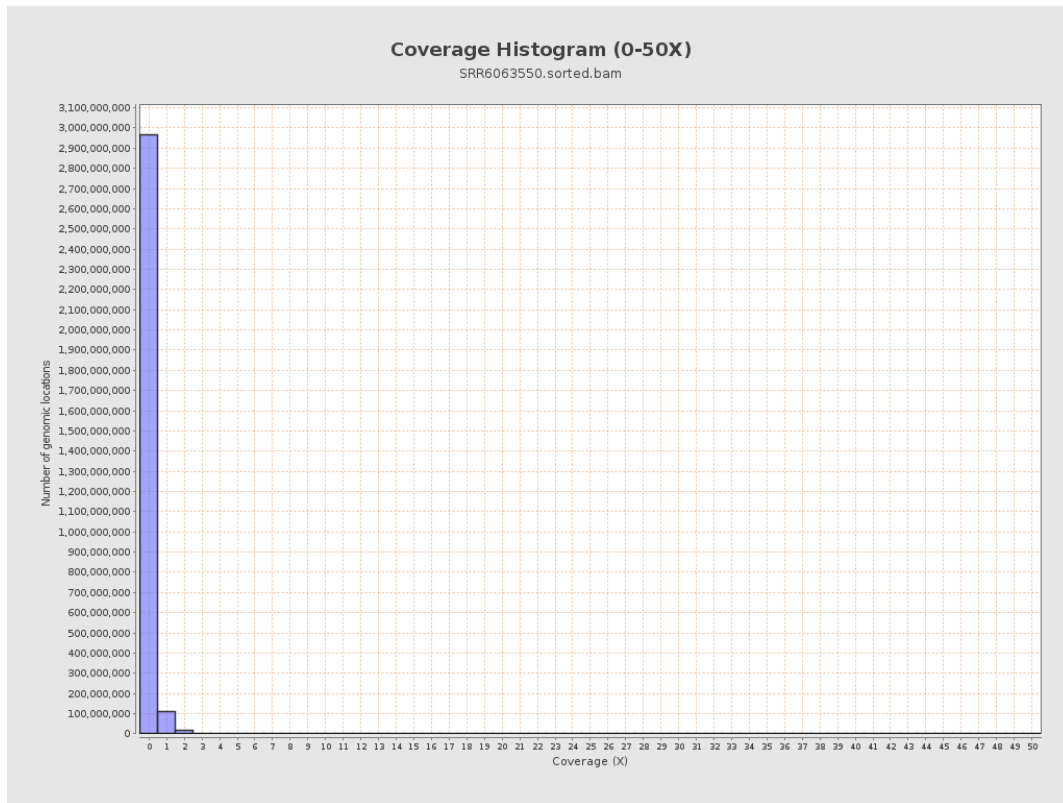
### 3. Results : Coverage across reference



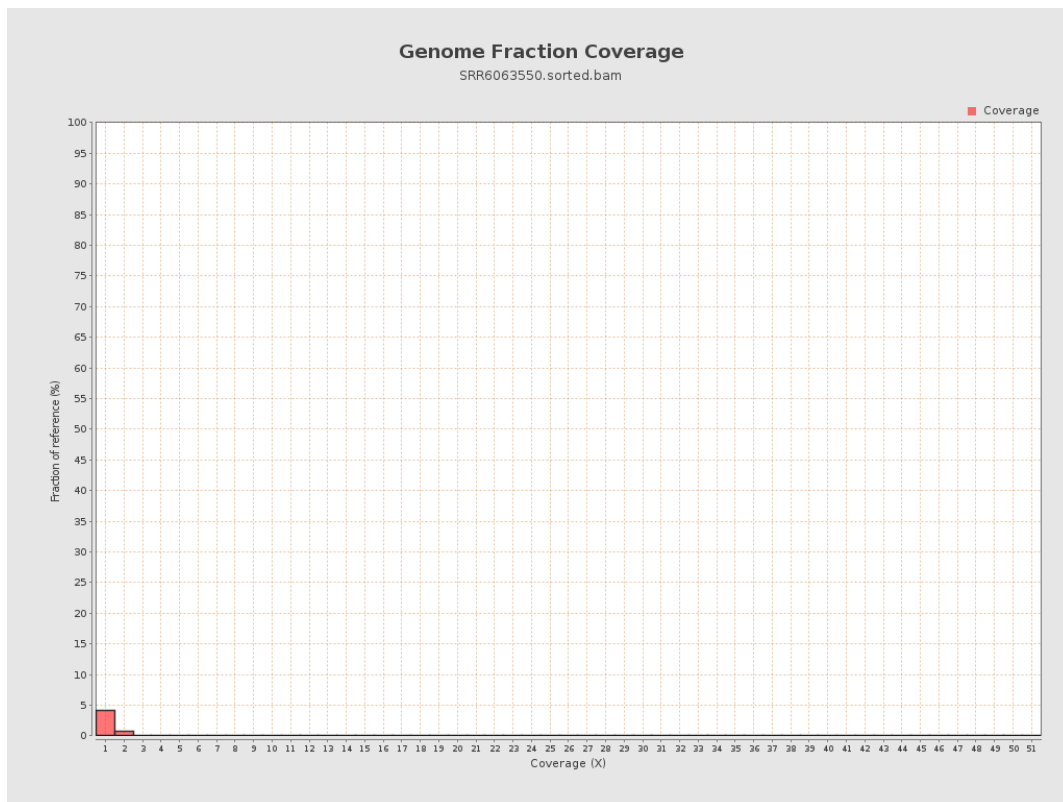
## 4. Results : Coverage Histogram



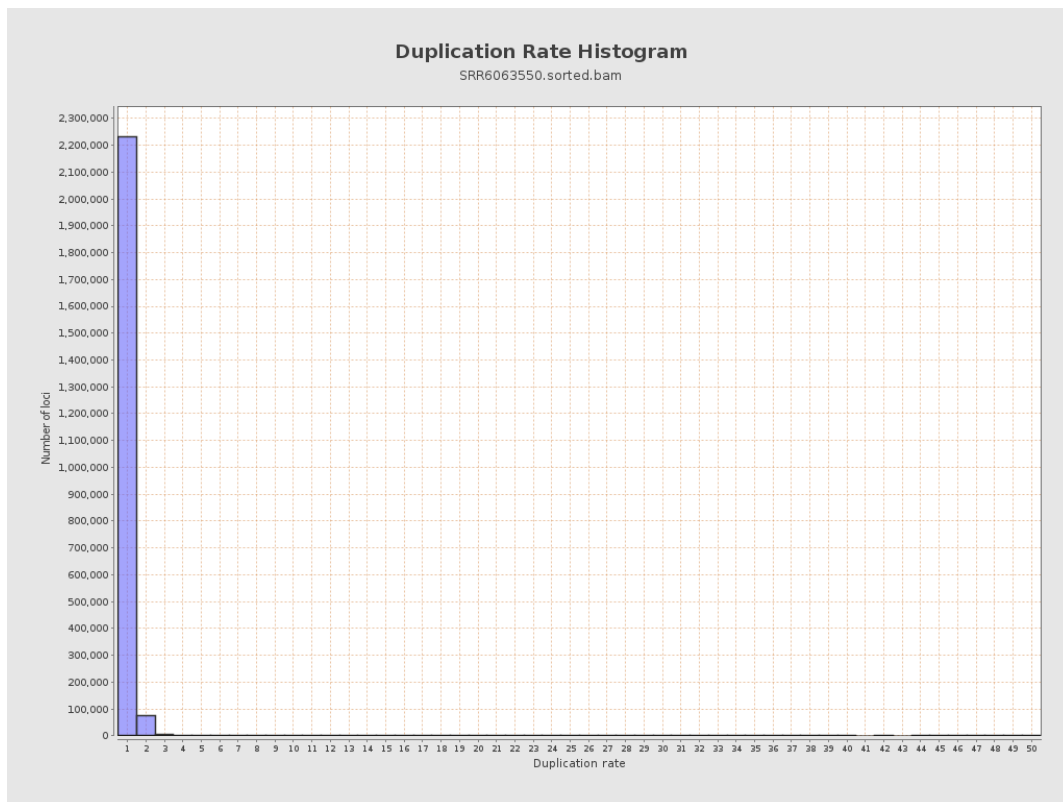
## 5. Results : Coverage Histogram (0-50X)



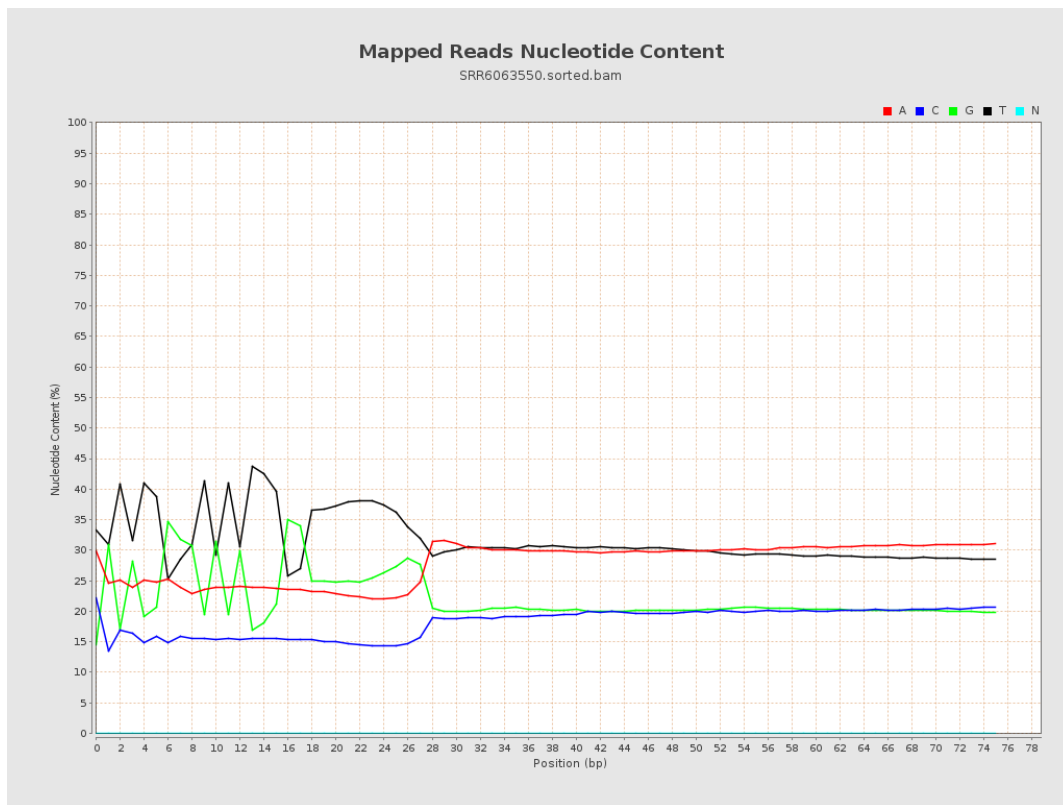
## 6. Results : Genome Fraction Coverage



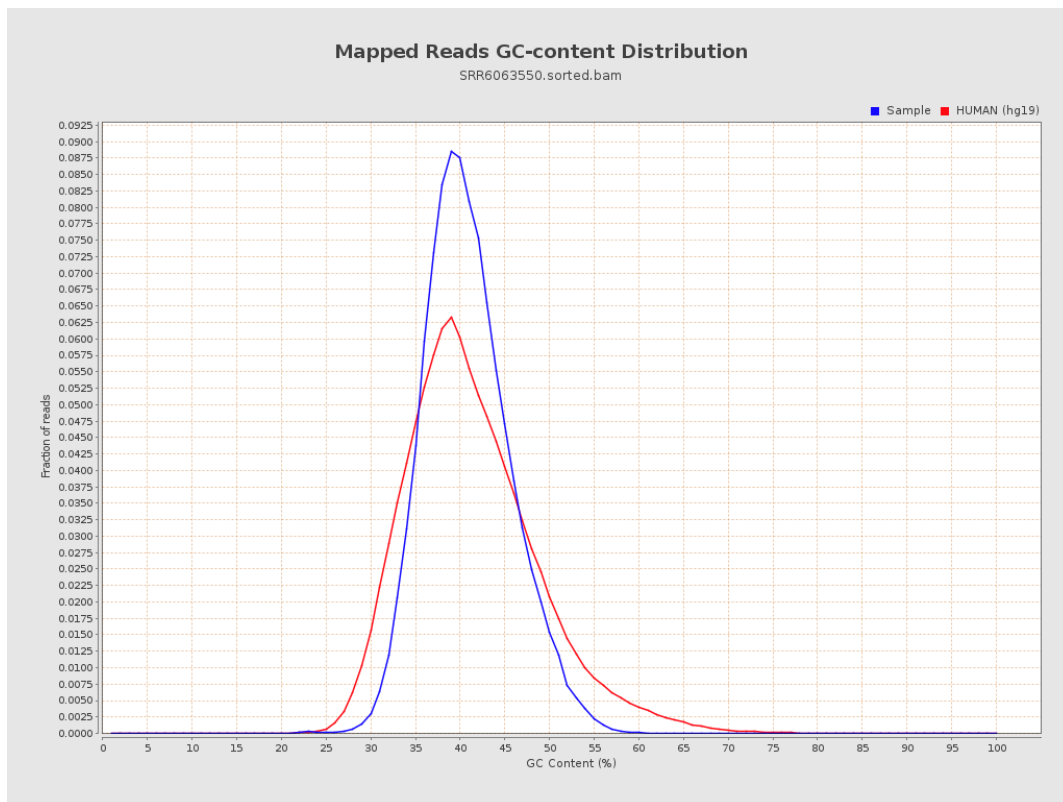
## 7. Results : Duplication Rate Histogram



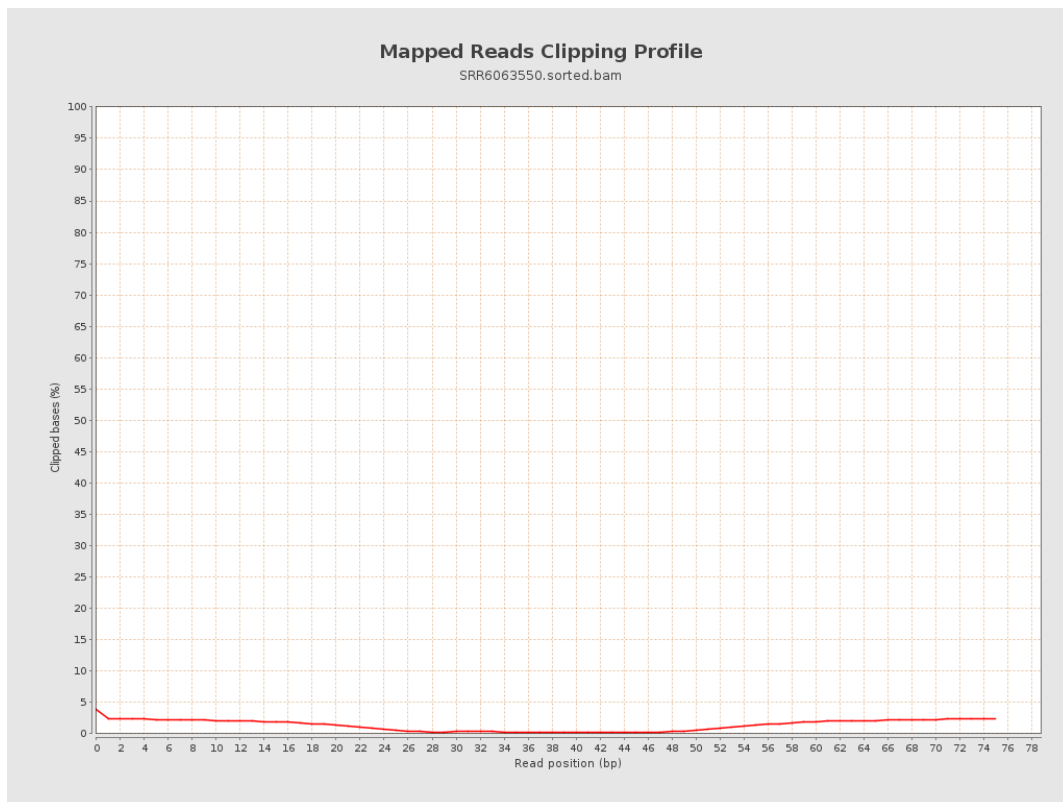
## 8. Results : Mapped Reads Nucleotide Content



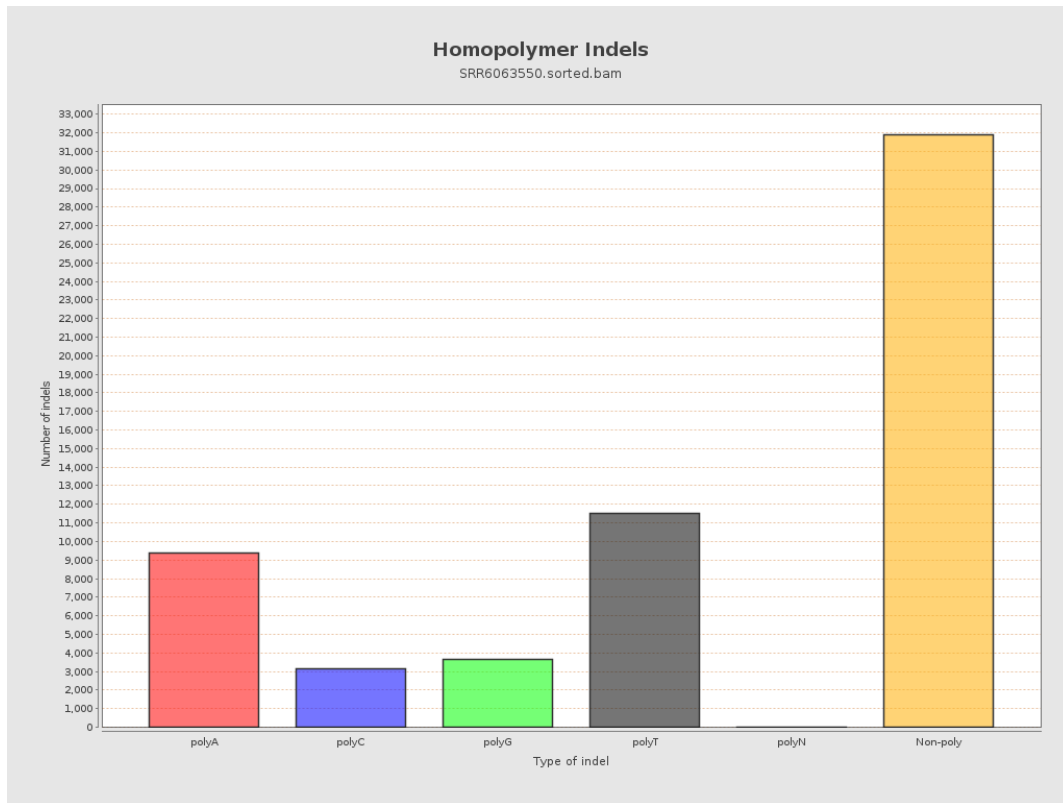
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

