

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/14 23:58:45*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063523.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_SRR6063523 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063523.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Sat Sep 14 23:58:44 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6063523.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 4,713,401          |
| Mapped reads                 | 4,432,094 / 94.03% |
| Unmapped reads               | 281,307 / 5.97%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 29,048 / 0.62%     |
| Read min/max/mean length     | 30 / 76 / 76.21    |
| Duplicated reads (estimated) | 579,313 / 12.29%   |
| Duplication rate             | 10.98%             |
| Clipped reads                | 2,387,922 / 50.66% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 73,172,804 / 25.74% |
| Number/percentage of C's | 51,464,427 / 18.11% |
| Number/percentage of T's | 92,034,034 / 32.38% |
| Number/percentage of G's | 67,521,750 / 23.76% |
| Number/percentage of N's | 31,705 / 0.01%      |
| GC Percentage            | 41.86%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0919 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.8831 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 45.68 |
|----------------------|-------|

## 2.5. Mismatches and indels

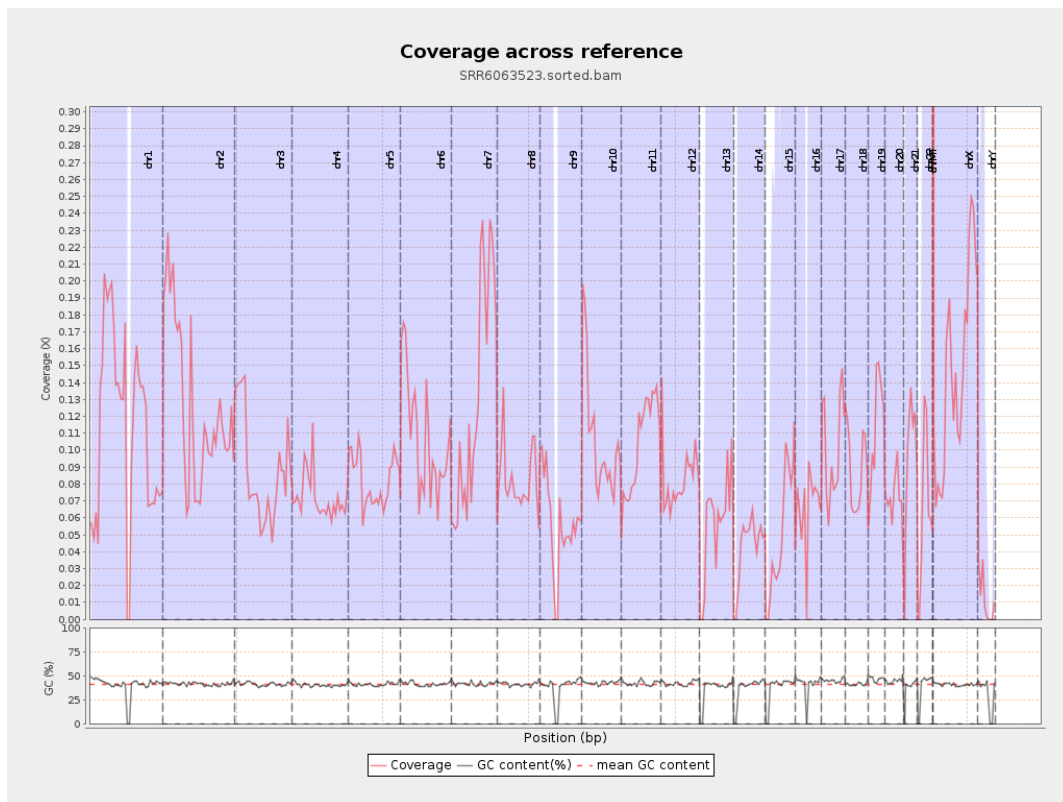
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.55%     |
| Mismatches                               | 1,538,327 |
| Insertions                               | 17,435    |
| Mapped reads with at least one insertion | 0.39%     |
| Deletions                                | 68,834    |
| Mapped reads with at least one deletion  | 1.54%     |
| Homopolymer indels                       | 44.04%    |

## 2.6. Chromosome stats

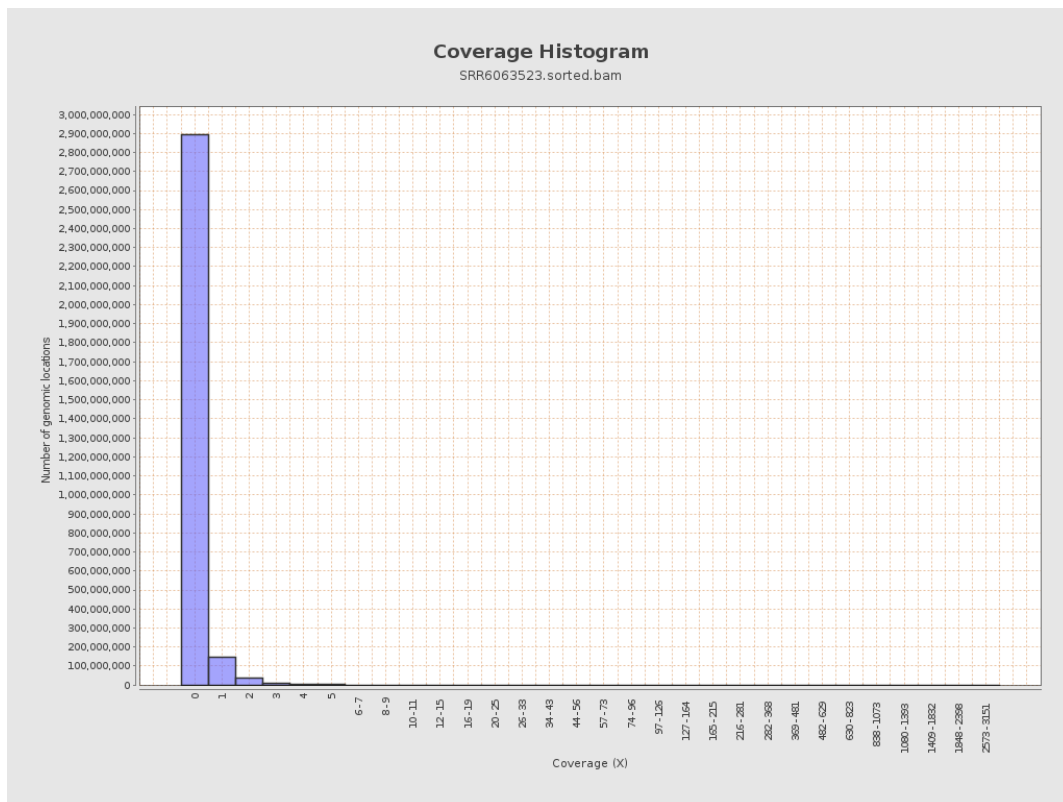
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 28119533     | 0.1128        | 1.953              |
| chr2 | 243199373 | 30873585     | 0.1269        | 1.518              |
| chr3 | 198022430 | 17391614     | 0.0878        | 0.3974             |
| chr4 | 191154276 | 13789901     | 0.0721        | 0.3895             |
| chr5 | 180915260 | 14841388     | 0.082         | 0.3849             |
| chr6 | 171115067 | 18390566     | 0.1075        | 0.6076             |
| chr7 | 159138663 | 20855836     | 0.1311        | 0.9156             |
|      |           |              |               |                    |

|       |           |          |         |         |
|-------|-----------|----------|---------|---------|
| chr8  | 146364022 | 12072291 | 0.0825  | 0.8215  |
| chr9  | 141213431 | 7904914  | 0.056   | 0.5689  |
| chr10 | 135534747 | 14511188 | 0.1071  | 0.58    |
| chr11 | 135006516 | 14061422 | 0.1042  | 0.5758  |
| chr12 | 133851895 | 11143259 | 0.0833  | 0.4055  |
| chr13 | 115169878 | 6615140  | 0.0574  | 0.3641  |
| chr14 | 107349540 | 4609683  | 0.0429  | 0.3338  |
| chr15 | 102531392 | 5092176  | 0.0497  | 0.3951  |
| chr16 | 90354753  | 5936986  | 0.0657  | 0.3755  |
| chr17 | 81195210  | 8214784  | 0.1012  | 0.4641  |
| chr18 | 78077248  | 6914881  | 0.0886  | 1.0937  |
| chr19 | 59128983  | 6703196  | 0.1134  | 1.2344  |
| chr20 | 63025520  | 4539908  | 0.072   | 0.3795  |
| chr21 | 48129895  | 4528781  | 0.0941  | 0.431   |
| chr22 | 51304566  | 3291481  | 0.0642  | 0.3357  |
| chrMT | 16571     | 435307   | 26.2692 | 13.9899 |
| chrX  | 155270560 | 22791773 | 0.1468  | 0.61    |
| chrY  | 59373566  | 715922   | 0.0121  | 0.3448  |

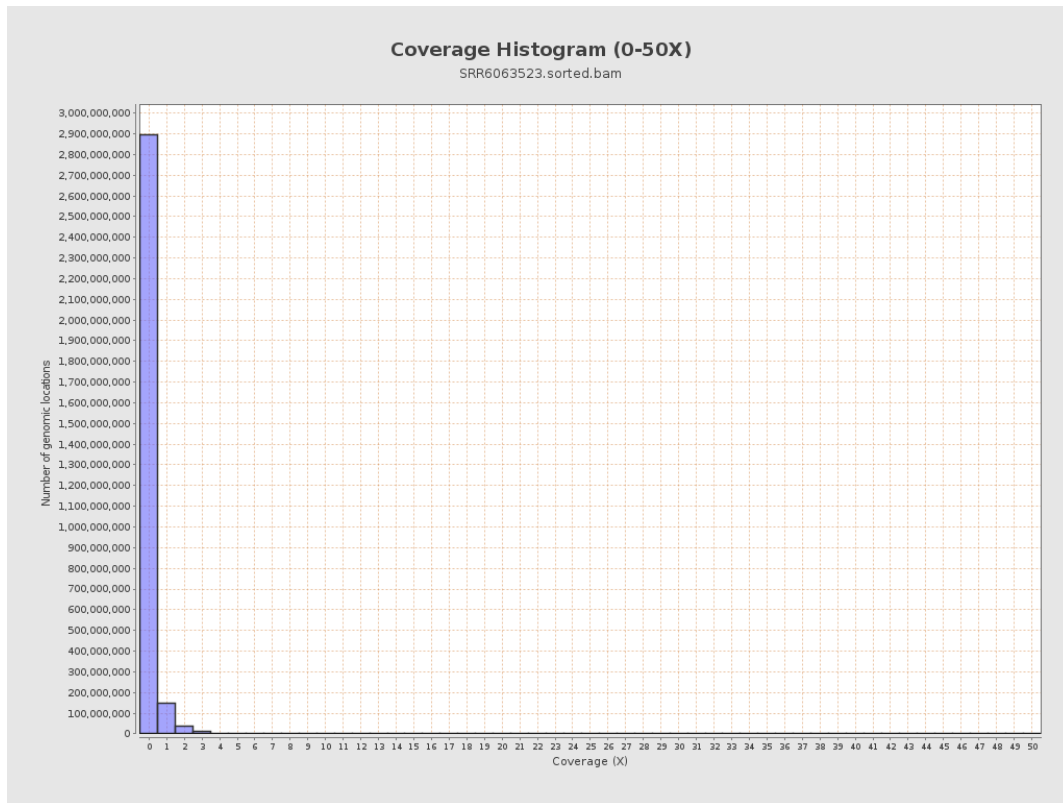
### 3. Results : Coverage across reference



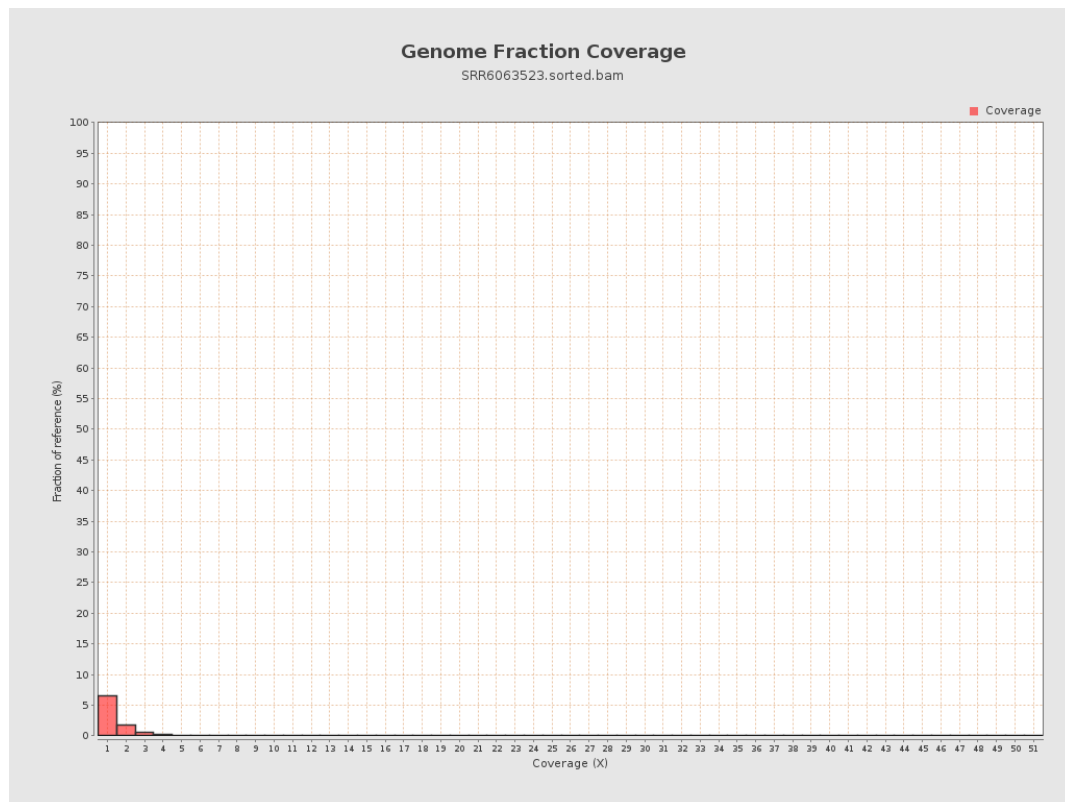
## 4. Results : Coverage Histogram



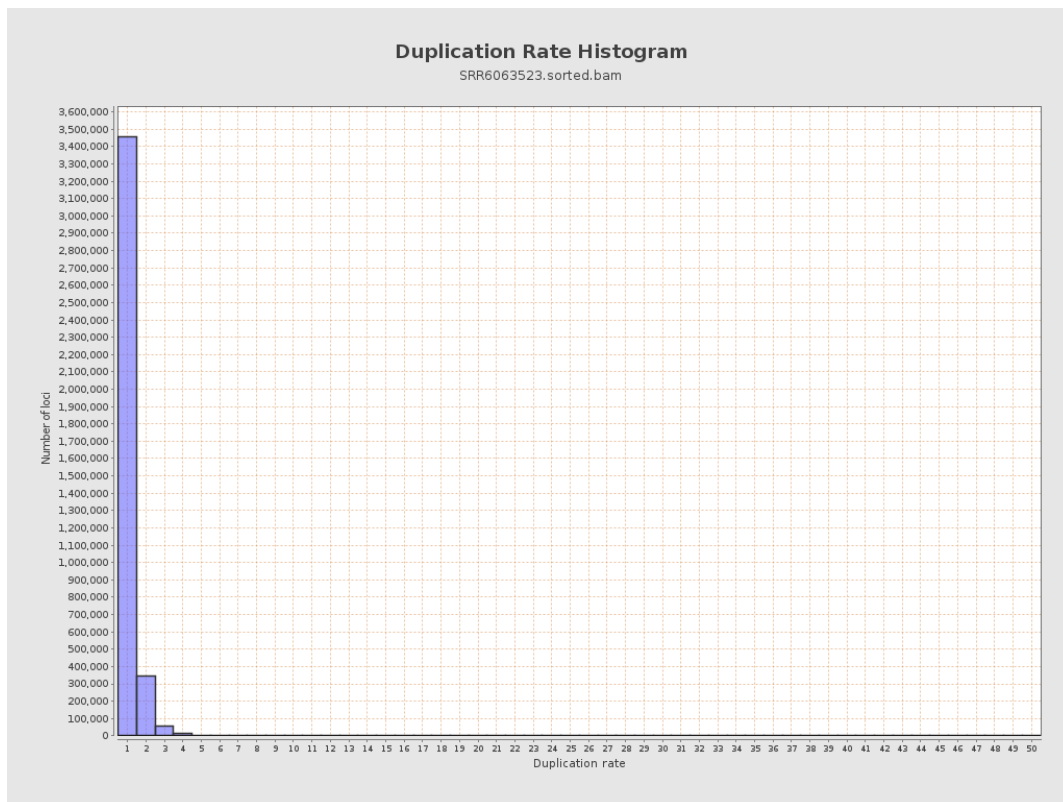
## 5. Results : Coverage Histogram (0-50X)



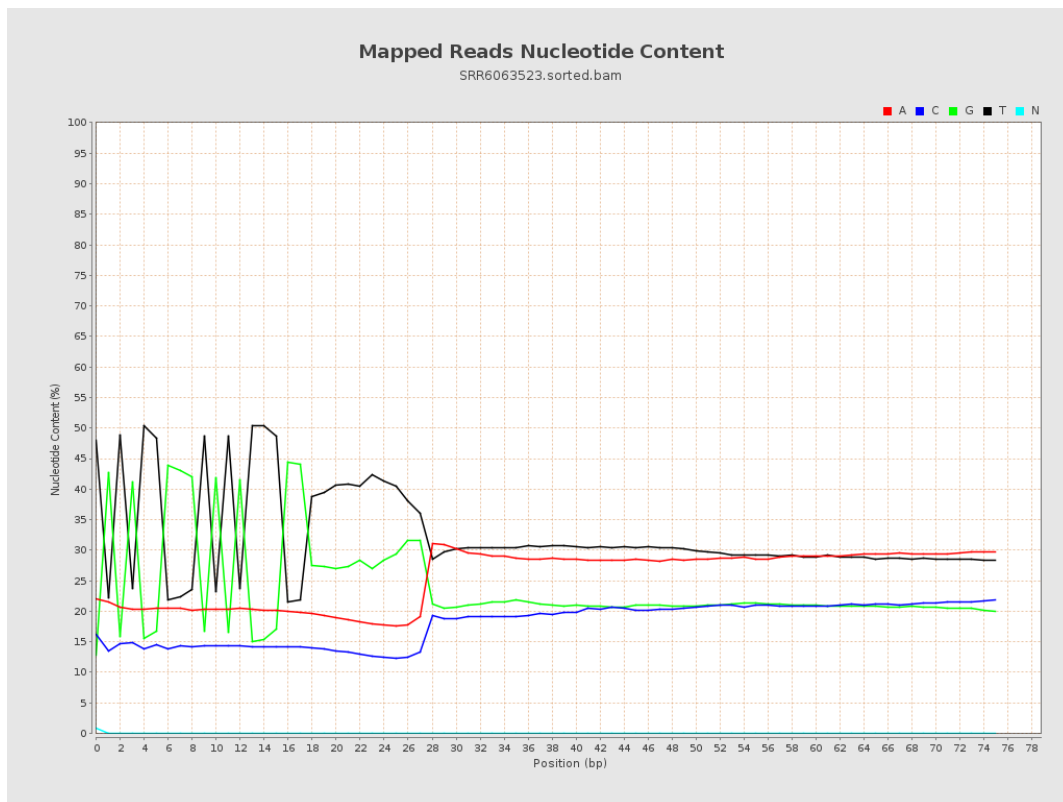
## 6. Results : Genome Fraction Coverage



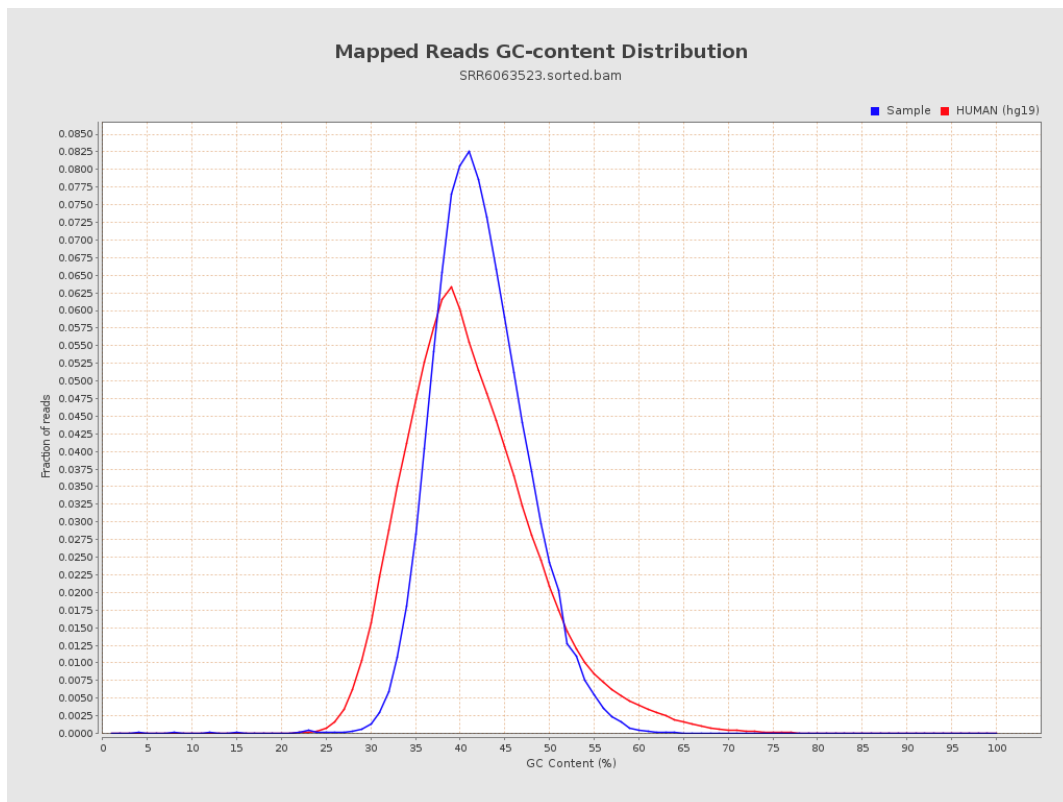
## 7. Results : Duplication Rate Histogram



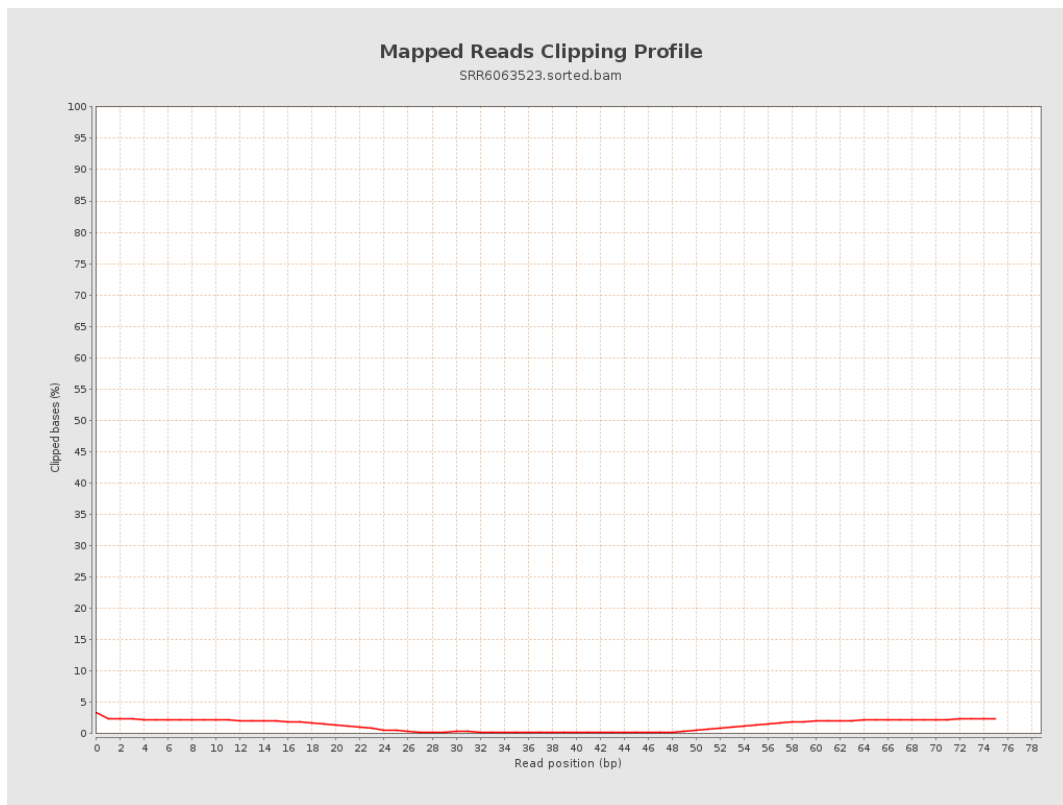
## 8. Results : Mapped Reads Nucleotide Content



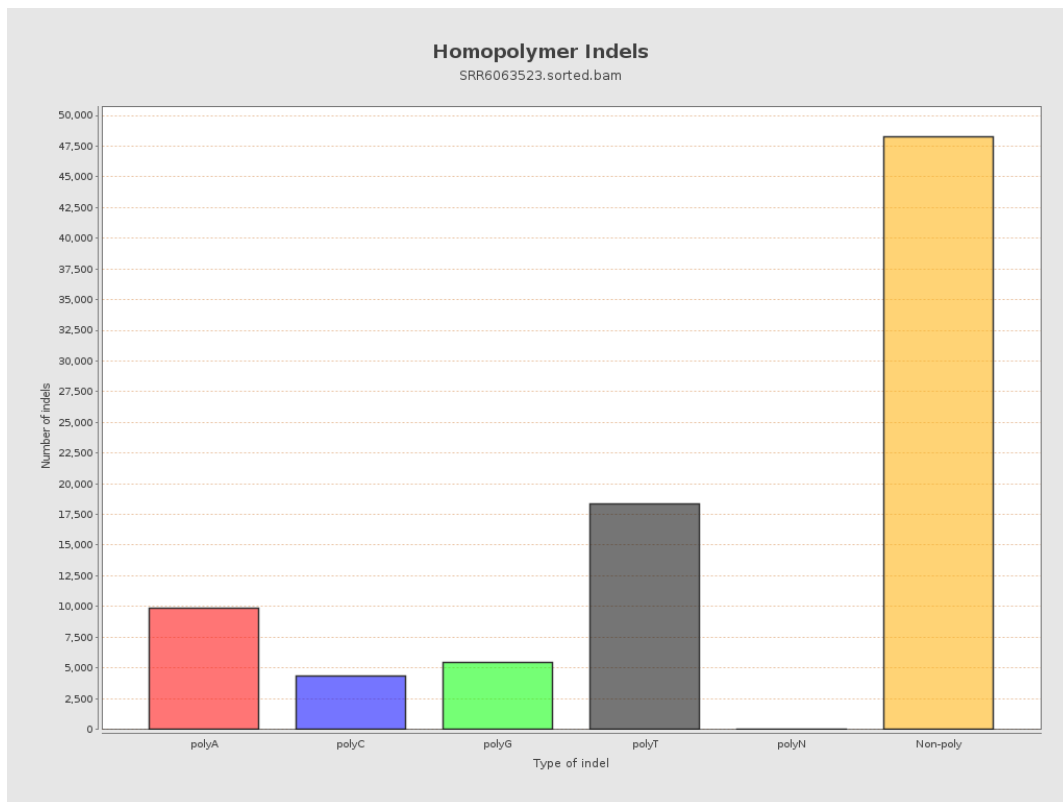
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

