

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/13 22:52:13*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004052.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_SRR6004052 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004052.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Fri Sep 13 22:52:12 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6004052.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 5,191,351          |
| Mapped reads                 | 4,604,259 / 88.69% |
| Unmapped reads               | 587,092 / 11.31%   |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 34,272 / 0.66%     |
| Read min/max/mean length     | 30 / 76 / 76.23    |
| Duplicated reads (estimated) | 309,440 / 5.96%    |
| Duplication rate             | 5.19%              |
| Clipped reads                | 2,142,041 / 41.26% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 84,617,150 / 27.72% |
| Number/percentage of C's | 57,727,603 / 18.91% |
| Number/percentage of T's | 94,336,403 / 30.9%  |
| Number/percentage of G's | 68,298,121 / 22.37% |
| Number/percentage of N's | 307,463 / 0.1%      |
| GC Percentage            | 41.28%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0987 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.7988 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 45.69 |
|----------------------|-------|

## 2.5. Mismatches and indels

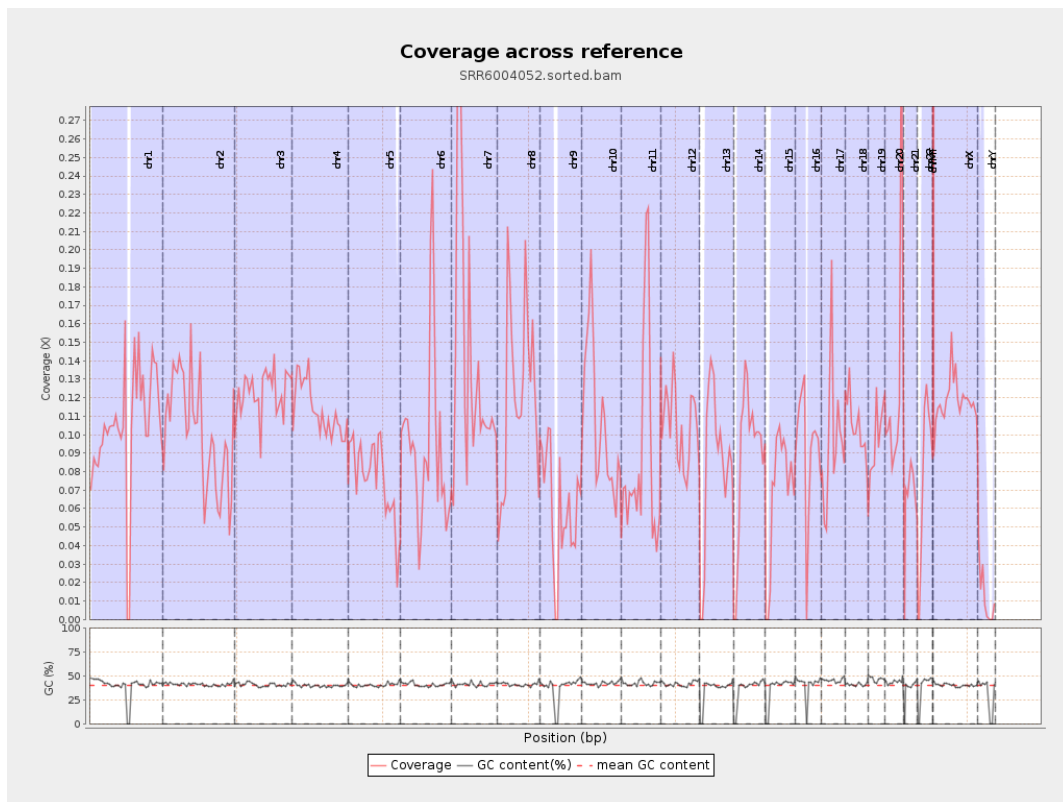
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.83%     |
| Mismatches                               | 2,499,866 |
| Insertions                               | 21,211    |
| Mapped reads with at least one insertion | 0.46%     |
| Deletions                                | 74,226    |
| Mapped reads with at least one deletion  | 1.6%      |
| Homopolymer indels                       | 46.41%    |

## 2.6. Chromosome stats

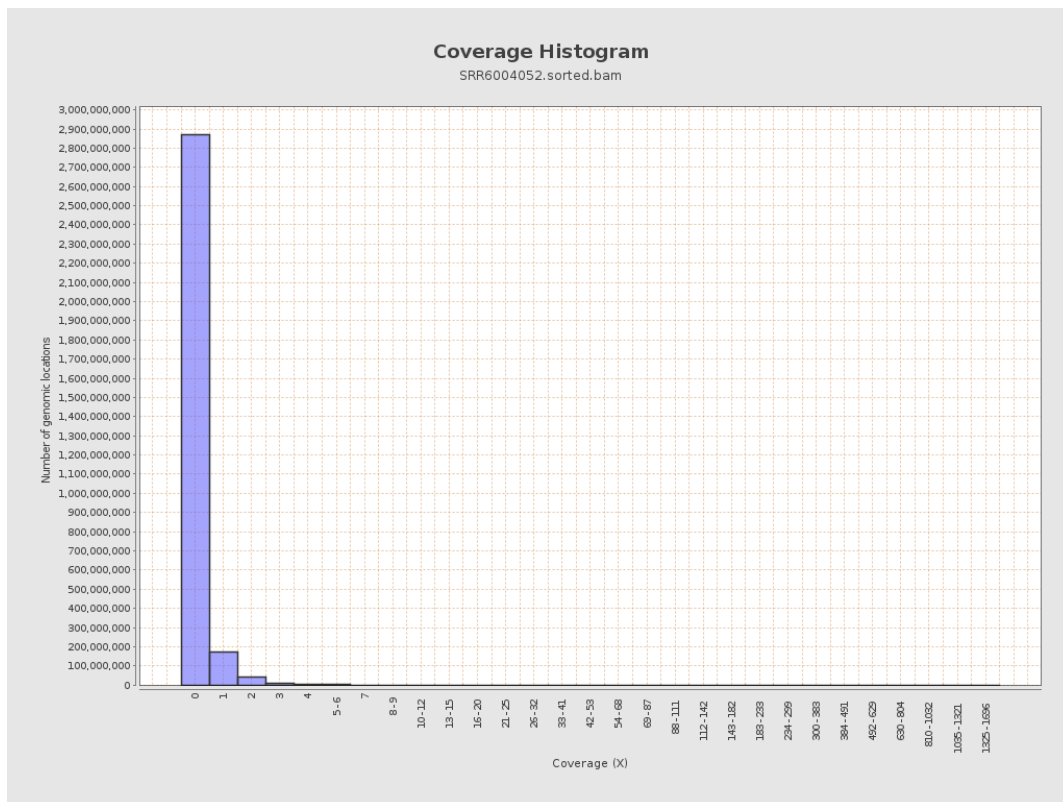
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 26039361     | 0.1045        | 1.4748             |
| chr2 | 243199373 | 24563586     | 0.101         | 0.9065             |
| chr3 | 198022430 | 24272063     | 0.1226        | 0.4455             |
| chr4 | 191154276 | 21669037     | 0.1134        | 0.4535             |
| chr5 | 180915260 | 13752937     | 0.076         | 0.3568             |
| chr6 | 171115067 | 15983868     | 0.0934        | 0.4468             |
| chr7 | 159138663 | 21592092     | 0.1357        | 1.4814             |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr8  | 146364022 | 17776778 | 0.1215 | 1.1124 |
| chr9  | 141213431 | 8429618  | 0.0597 | 0.6411 |
| chr10 | 135534747 | 14388427 | 0.1062 | 0.6861 |
| chr11 | 135006516 | 11734412 | 0.0869 | 0.5363 |
| chr12 | 133851895 | 14054489 | 0.105  | 0.429  |
| chr13 | 115169878 | 9747116  | 0.0846 | 0.3795 |
| chr14 | 107349540 | 9698113  | 0.0903 | 0.4392 |
| chr15 | 102531392 | 6949489  | 0.0678 | 0.3445 |
| chr16 | 90354753  | 8251618  | 0.0913 | 0.4499 |
| chr17 | 81195210  | 7699429  | 0.0948 | 0.4559 |
| chr18 | 78077248  | 8197768  | 0.105  | 1.4444 |
| chr19 | 59128983  | 5755179  | 0.0973 | 1.0033 |
| chr20 | 63025520  | 8533674  | 0.1354 | 0.5173 |
| chr21 | 48129895  | 3133075  | 0.0651 | 0.3592 |
| chr22 | 51304566  | 4037535  | 0.0787 | 0.3559 |
| chrMT | 16571     | 51832    | 3.1279 | 2.9843 |
| chrX  | 155270560 | 18377808 | 0.1184 | 0.5161 |
| chrY  | 59373566  | 726406   | 0.0122 | 0.1871 |

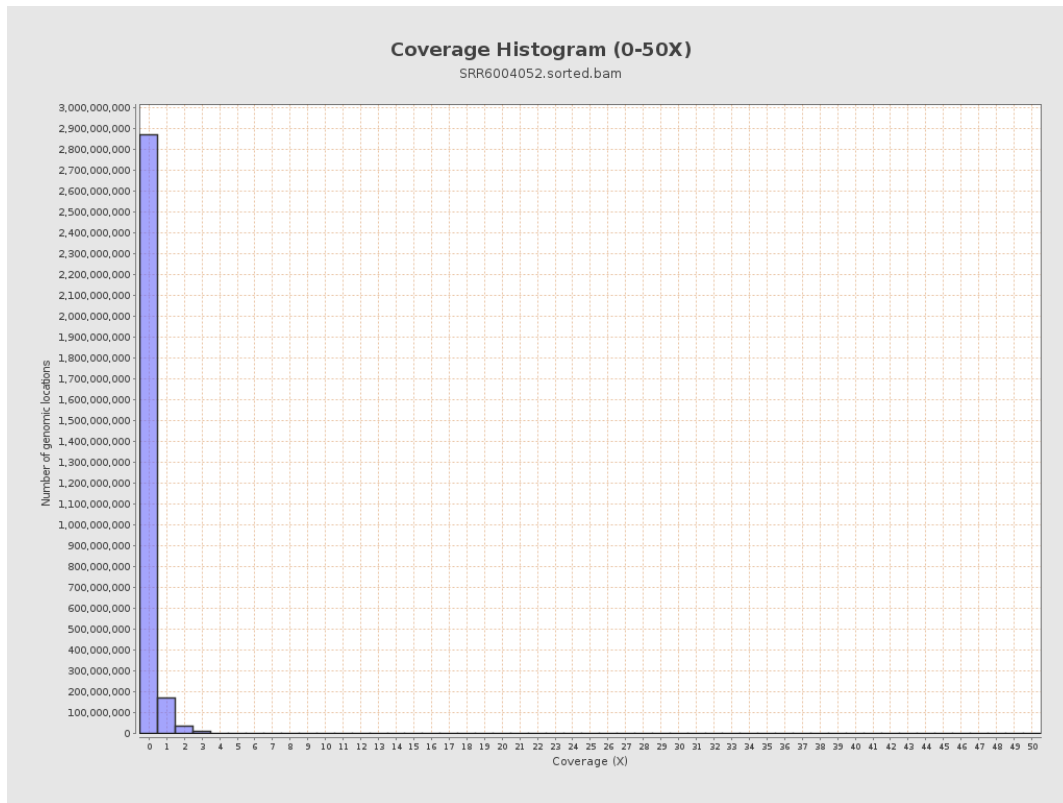
### 3. Results : Coverage across reference



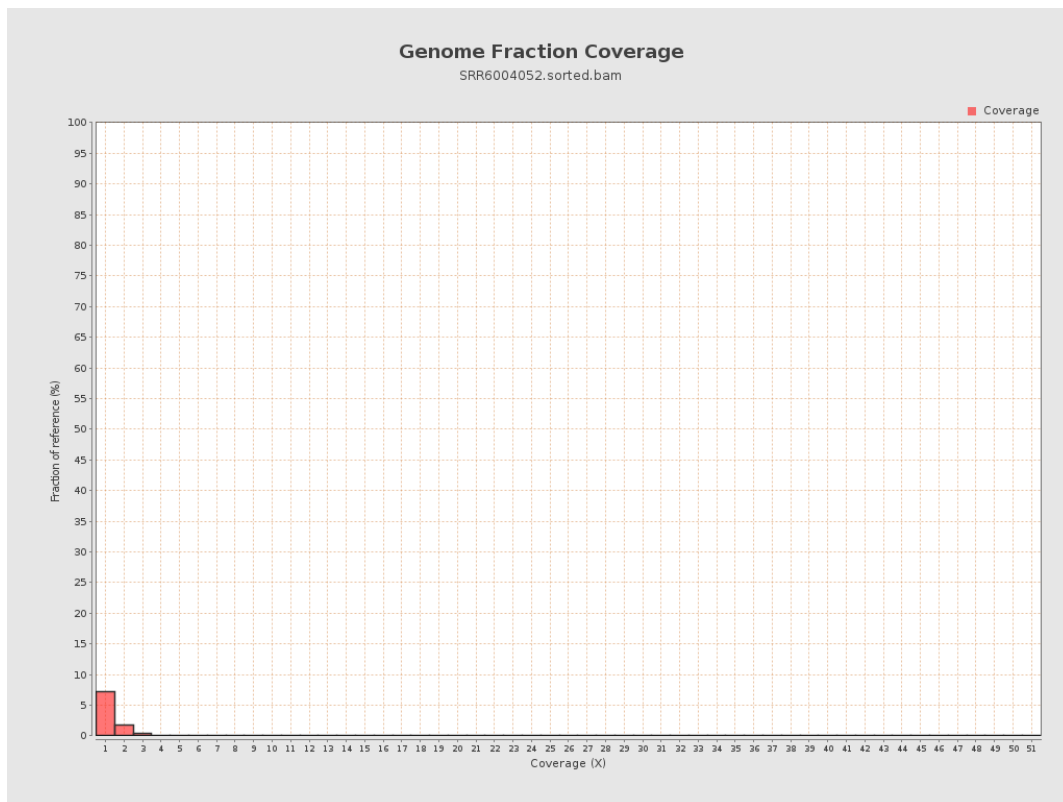
## 4. Results : Coverage Histogram



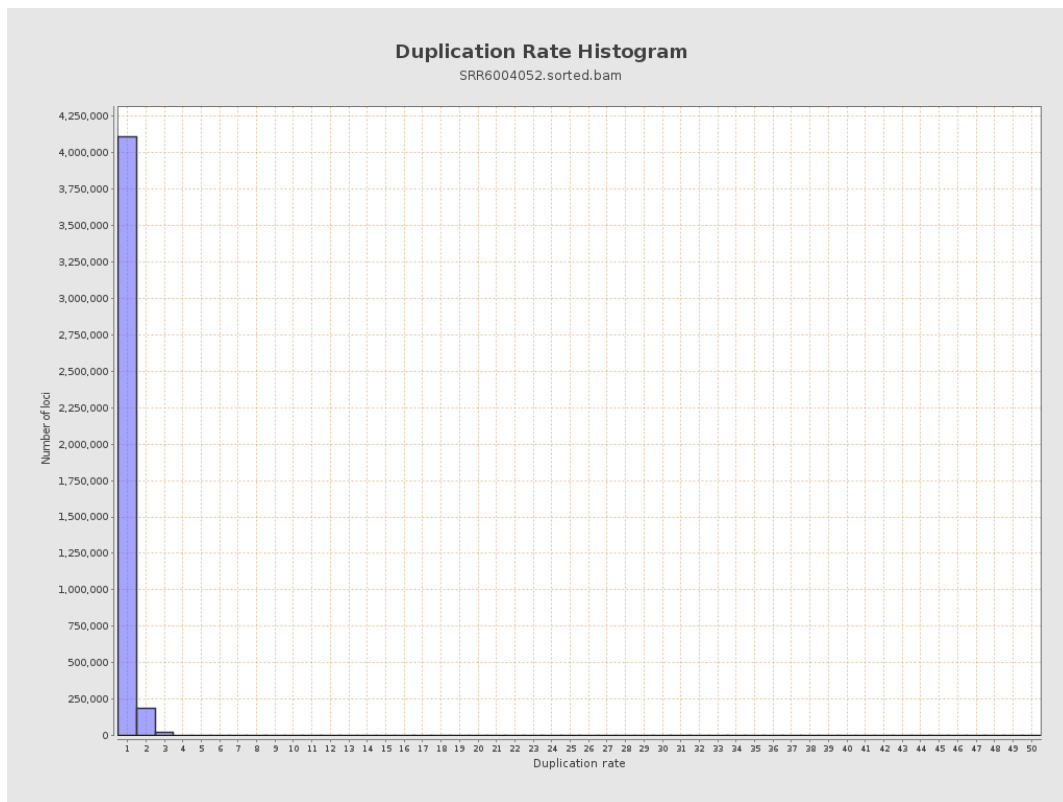
## 5. Results : Coverage Histogram (0-50X)



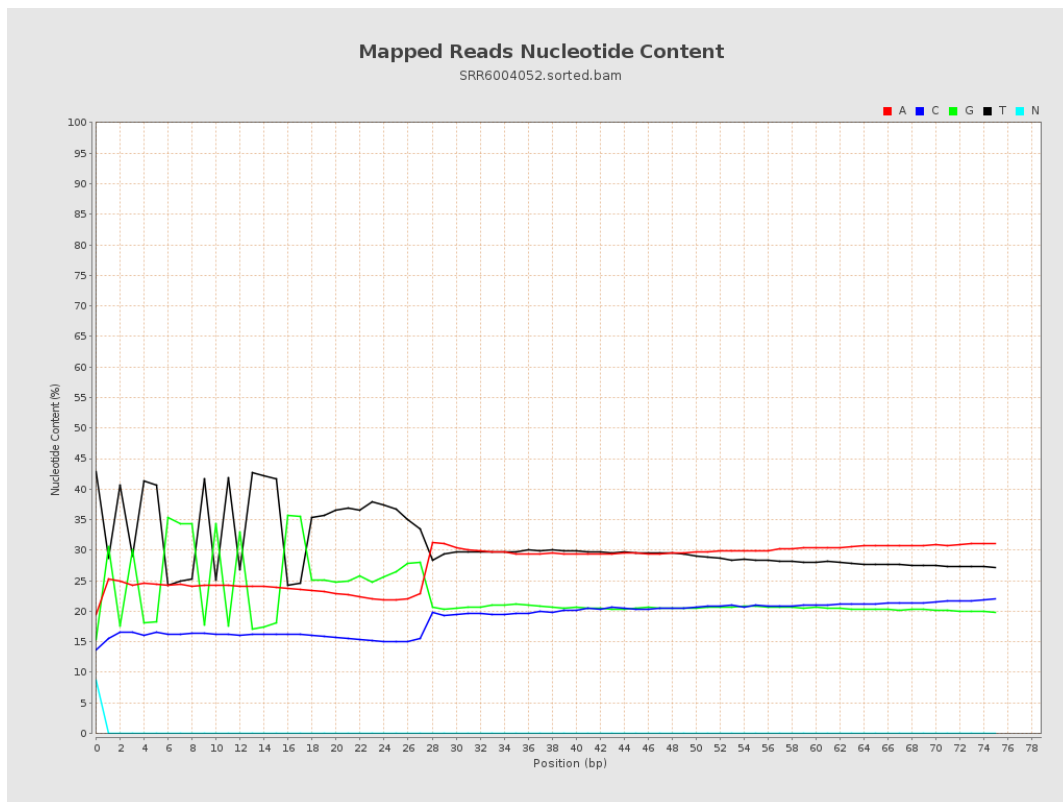
## 6. Results : Genome Fraction Coverage



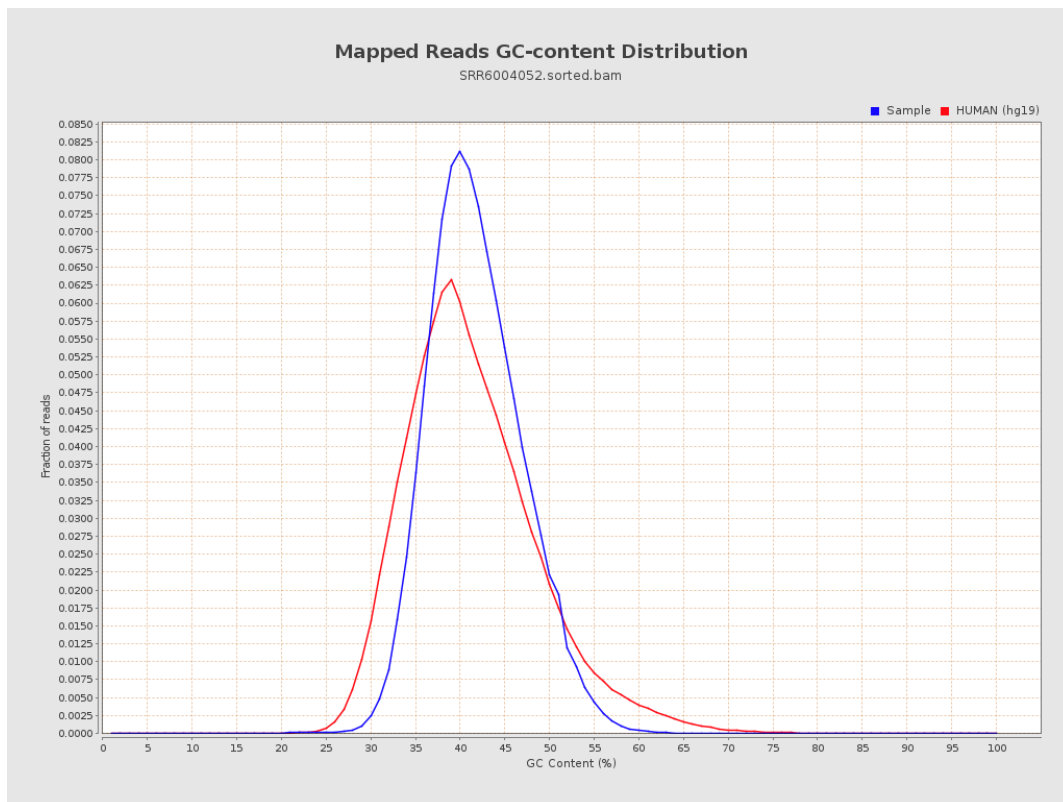
## 7. Results : Duplication Rate Histogram



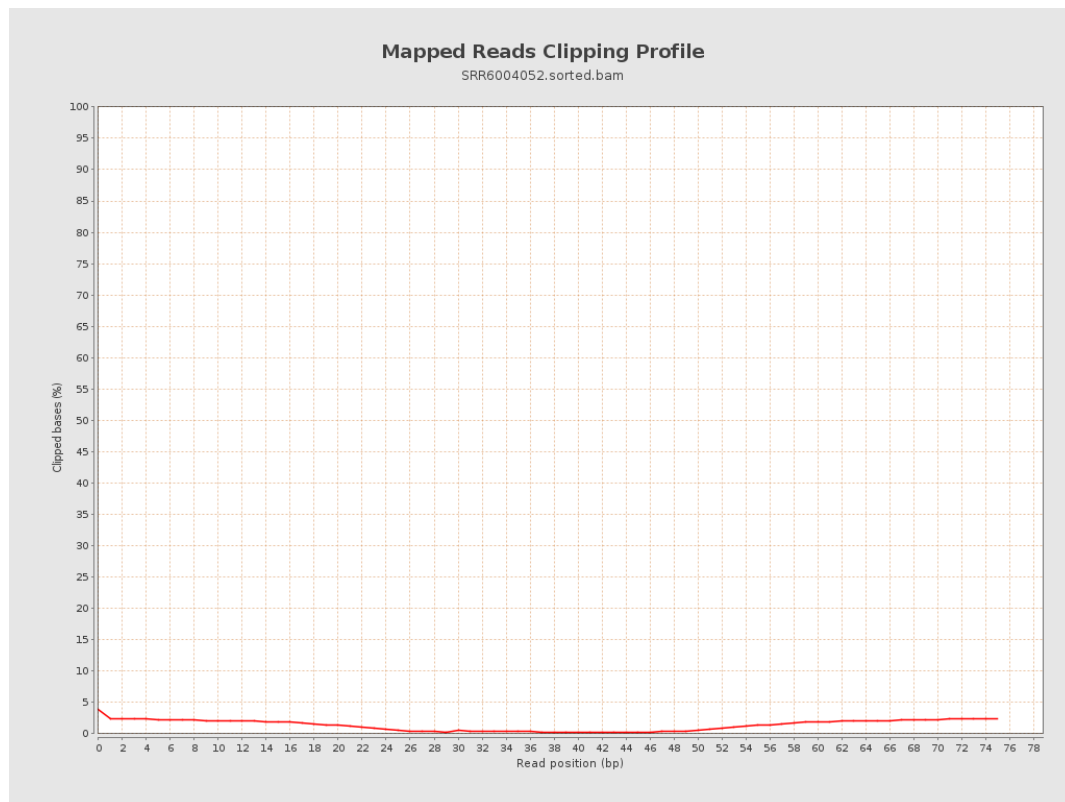
## 8. Results : Mapped Reads Nucleotide Content



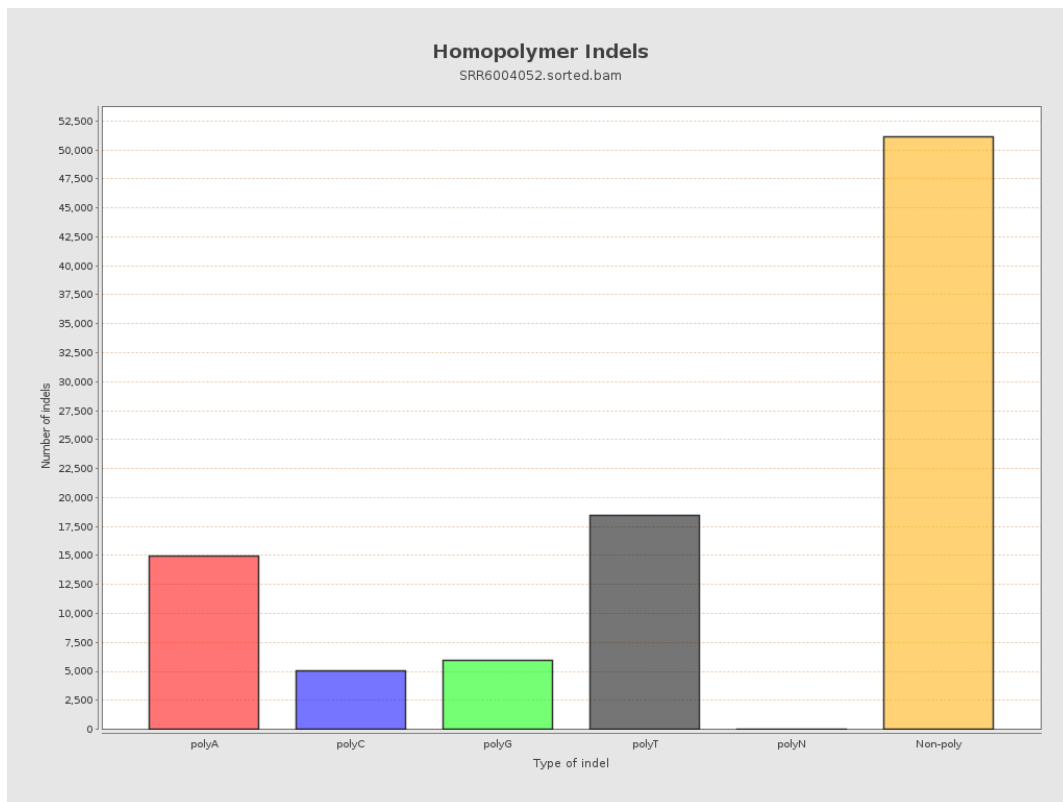
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

