

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 23:01:29*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082983.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_SRR3082983 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082983.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Sat Aug 24 23:01:29 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR3082983.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 3,376,140          |
| Mapped reads                 | 2,635,856 / 78.07% |
| Unmapped reads               | 740,284 / 21.93%   |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 18,058 / 0.53%     |
| Read min/max/mean length     | 30 / 76 / 76.19    |
| Duplicated reads (estimated) | 96,785 / 2.87%     |
| Duplication rate             | 2.91%              |
| Clipped reads                | 1,050,919 / 31.13% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 51,263,123 / 28.56% |
| Number/percentage of C's | 32,771,271 / 18.26% |
| Number/percentage of T's | 57,471,012 / 32.02% |
| Number/percentage of G's | 37,950,626 / 21.15% |
| Number/percentage of N's | 17,980 / 0.01%      |
| GC Percentage            | 39.41%              |

### 2.3. Coverage

|      |       |
|------|-------|
| Mean | 0.058 |
|      |       |

|                    |       |
|--------------------|-------|
| Standard Deviation | 0.422 |
|--------------------|-------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 46.28 |
|----------------------|-------|

## 2.5. Mismatches and indels

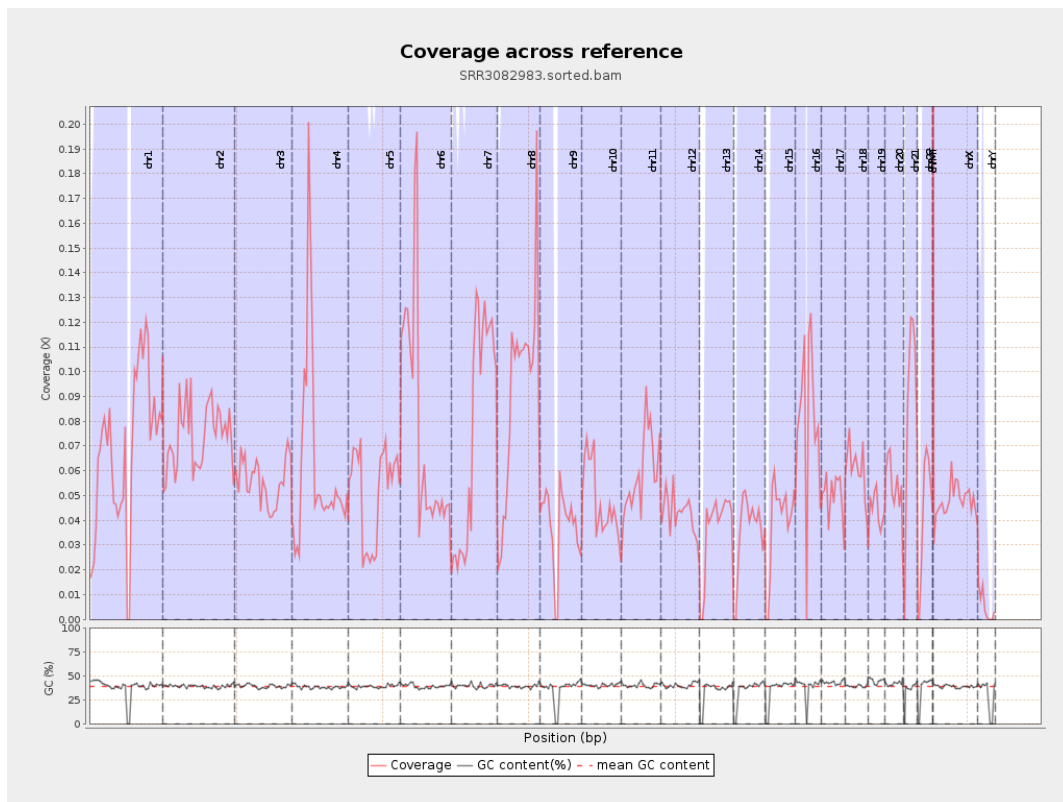
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.98%     |
| Mismatches                               | 1,736,257 |
| Insertions                               | 15,921    |
| Mapped reads with at least one insertion | 0.6%      |
| Deletions                                | 41,486    |
| Mapped reads with at least one deletion  | 1.56%     |
| Homopolymer indels                       | 47.99%    |

## 2.6. Chromosome stats

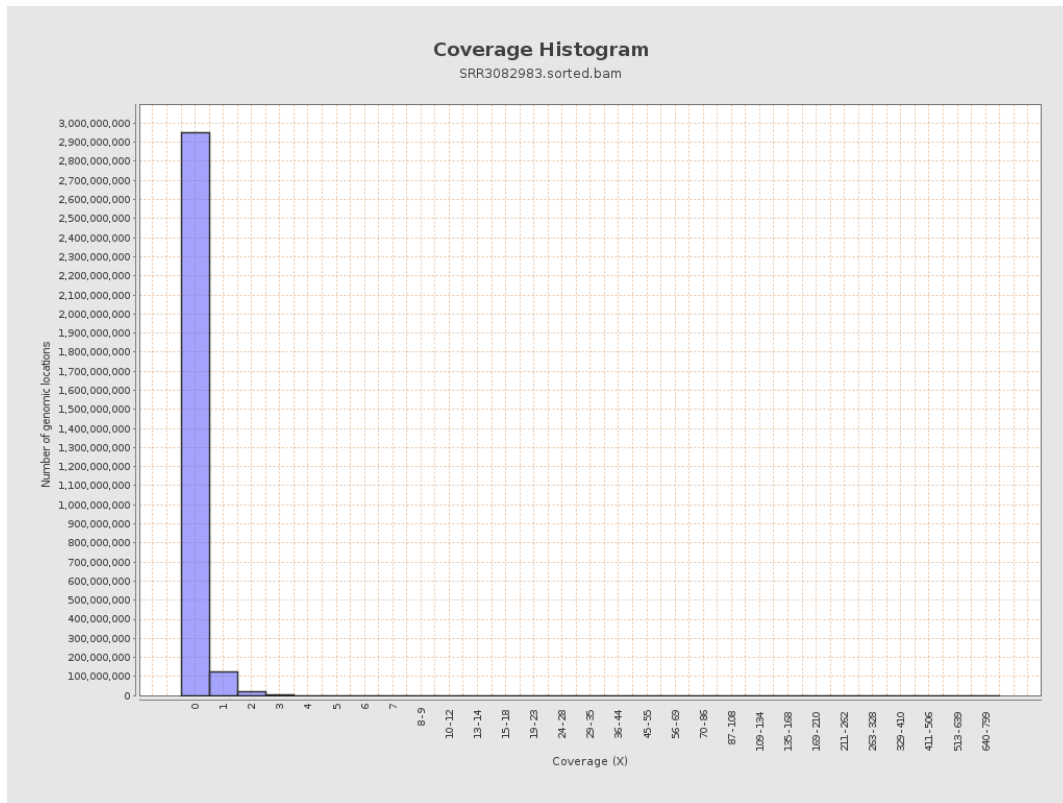
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 17234043     | 0.0691        | 0.7253             |
| chr2 | 243199373 | 17995833     | 0.074         | 0.5042             |
| chr3 | 198022430 | 11046762     | 0.0558        | 0.2782             |
| chr4 | 191154276 | 11859324     | 0.062         | 0.3083             |
| chr5 | 180915260 | 9239072      | 0.0511        | 0.265              |
| chr6 | 171115067 | 13039852     | 0.0762        | 0.4397             |
| chr7 | 159138663 | 11972575     | 0.0752        | 0.4149             |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr8  | 146364022 | 13386805 | 0.0915 | 0.5889 |
| chr9  | 141213431 | 5411853  | 0.0383 | 0.391  |
| chr10 | 135534747 | 6515561  | 0.0481 | 0.3754 |
| chr11 | 135006516 | 7963259  | 0.059  | 0.3554 |
| chr12 | 133851895 | 5701803  | 0.0426 | 0.247  |
| chr13 | 115169878 | 4215730  | 0.0366 | 0.2213 |
| chr14 | 107349540 | 3862561  | 0.036  | 0.2737 |
| chr15 | 102531392 | 3988515  | 0.0389 | 0.2313 |
| chr16 | 90354753  | 7154079  | 0.0792 | 0.3758 |
| chr17 | 81195210  | 4113846  | 0.0507 | 0.2995 |
| chr18 | 78077248  | 4789280  | 0.0613 | 0.8228 |
| chr19 | 59128983  | 2621092  | 0.0443 | 0.486  |
| chr20 | 63025520  | 3457189  | 0.0549 | 0.2921 |
| chr21 | 48129895  | 4037643  | 0.0839 | 0.3559 |
| chr22 | 51304566  | 2199970  | 0.0429 | 0.2401 |
| chrMT | 16571     | 9099     | 0.5491 | 0.8488 |
| chrX  | 155270560 | 7422385  | 0.0478 | 0.2887 |
| chrY  | 59373566  | 307626   | 0.0052 | 0.1075 |

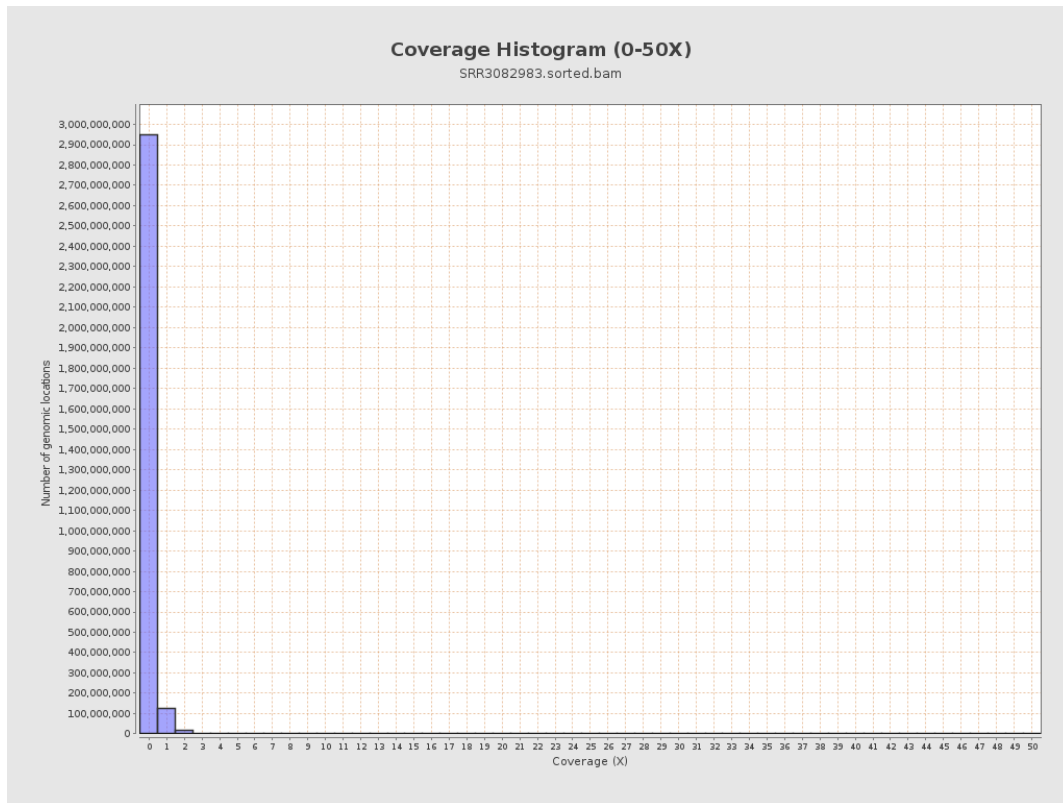
### 3. Results : Coverage across reference



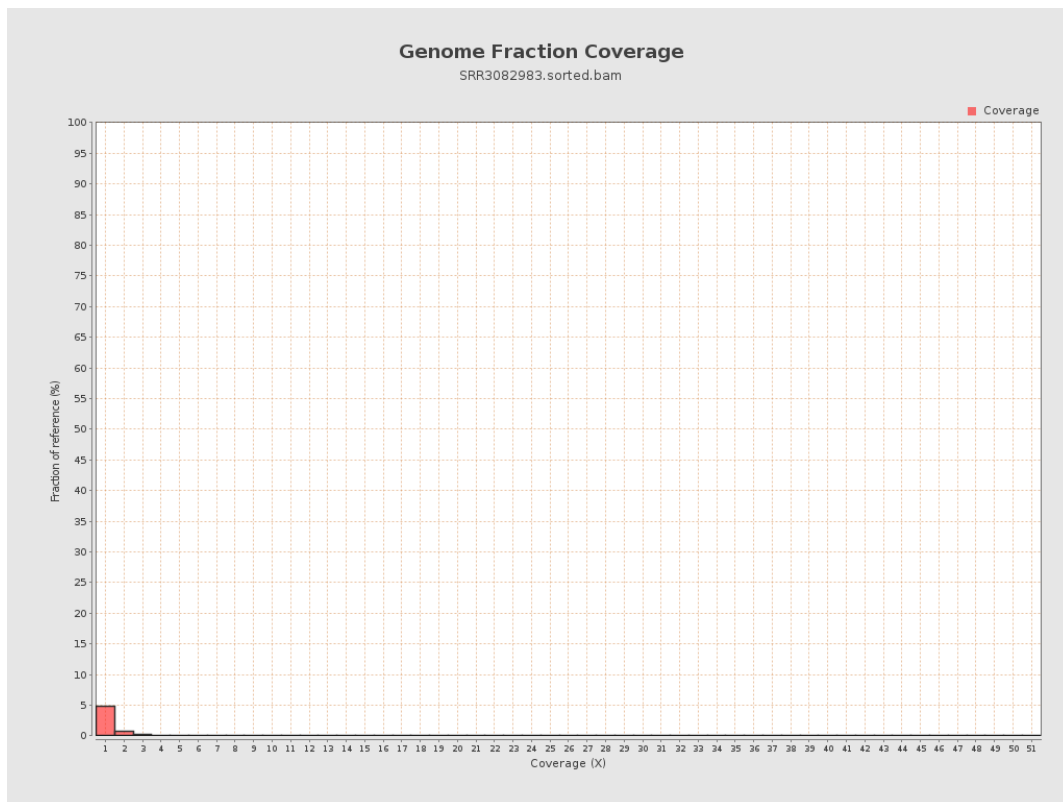
## 4. Results : Coverage Histogram



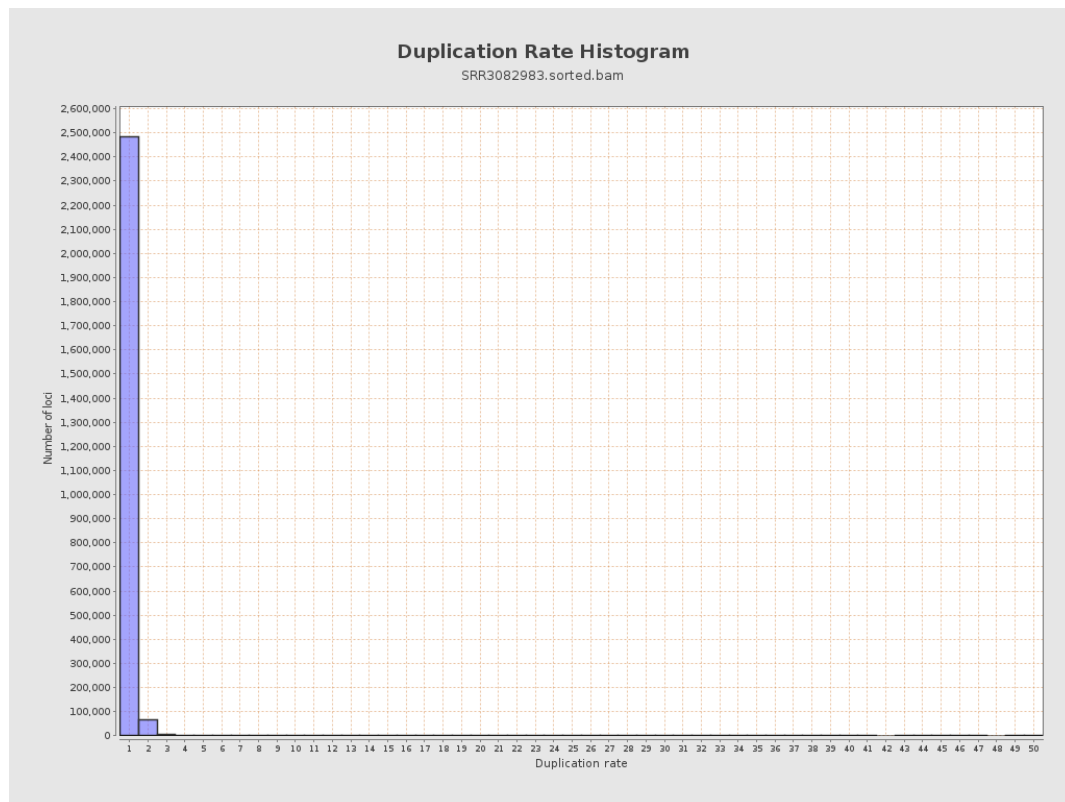
## 5. Results : Coverage Histogram (0-50X)



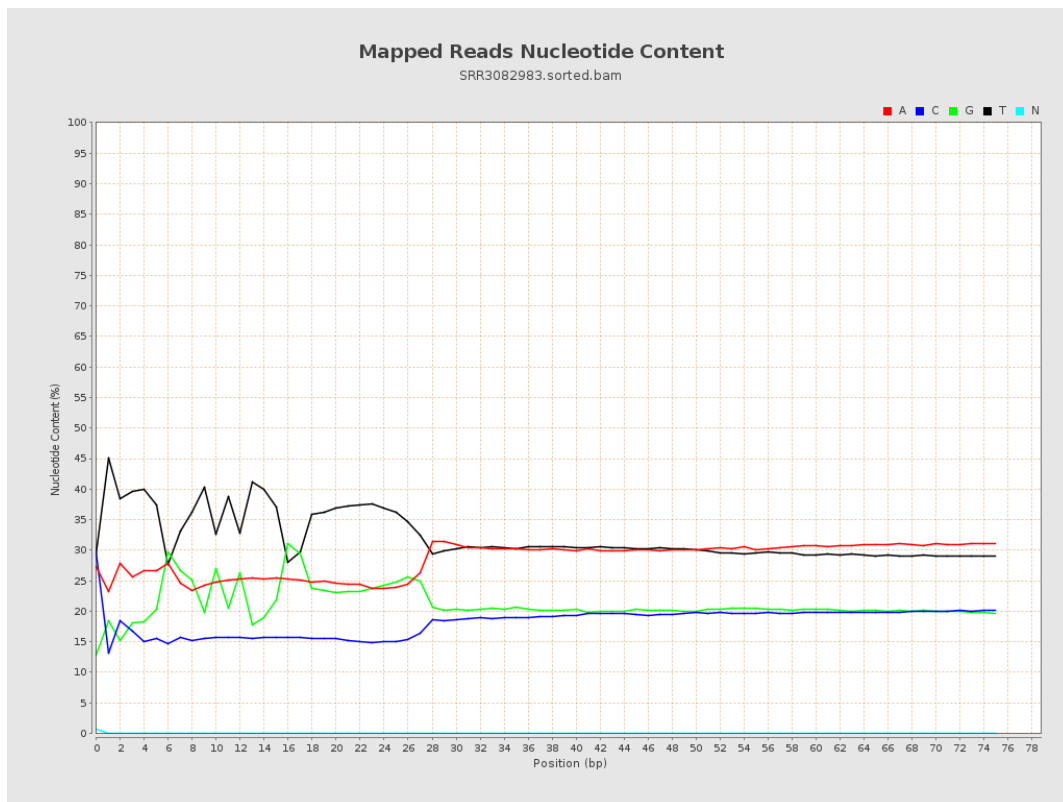
## 6. Results : Genome Fraction Coverage



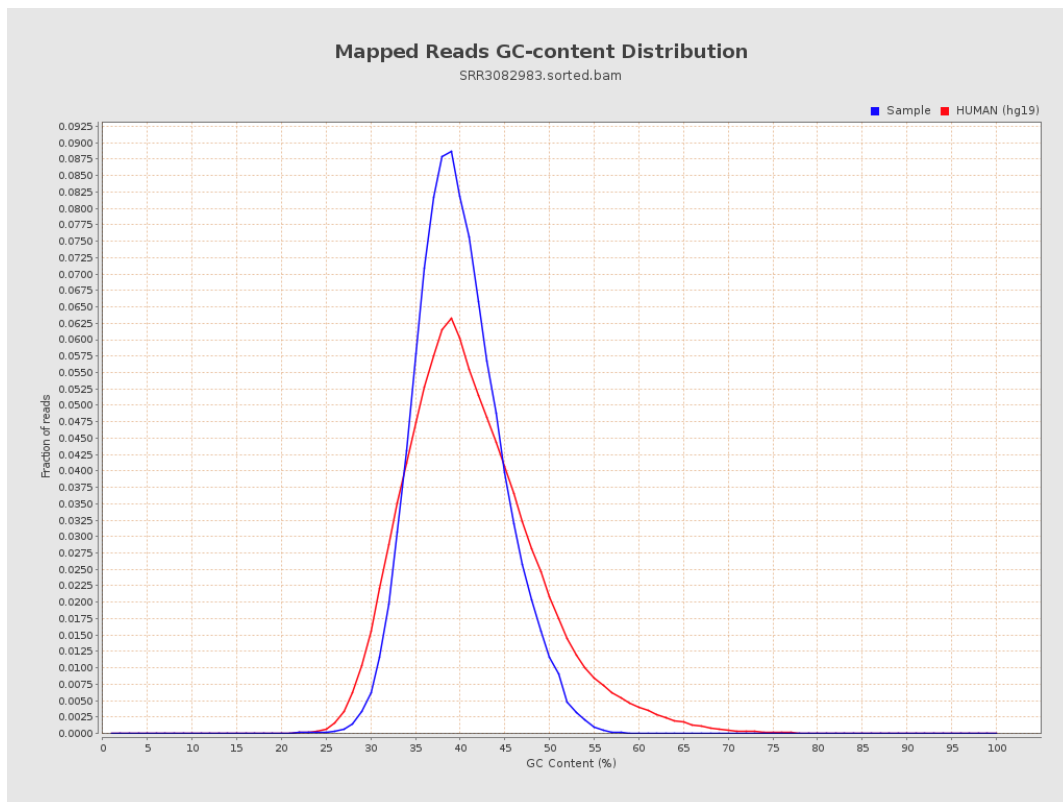
## 7. Results : Duplication Rate Histogram



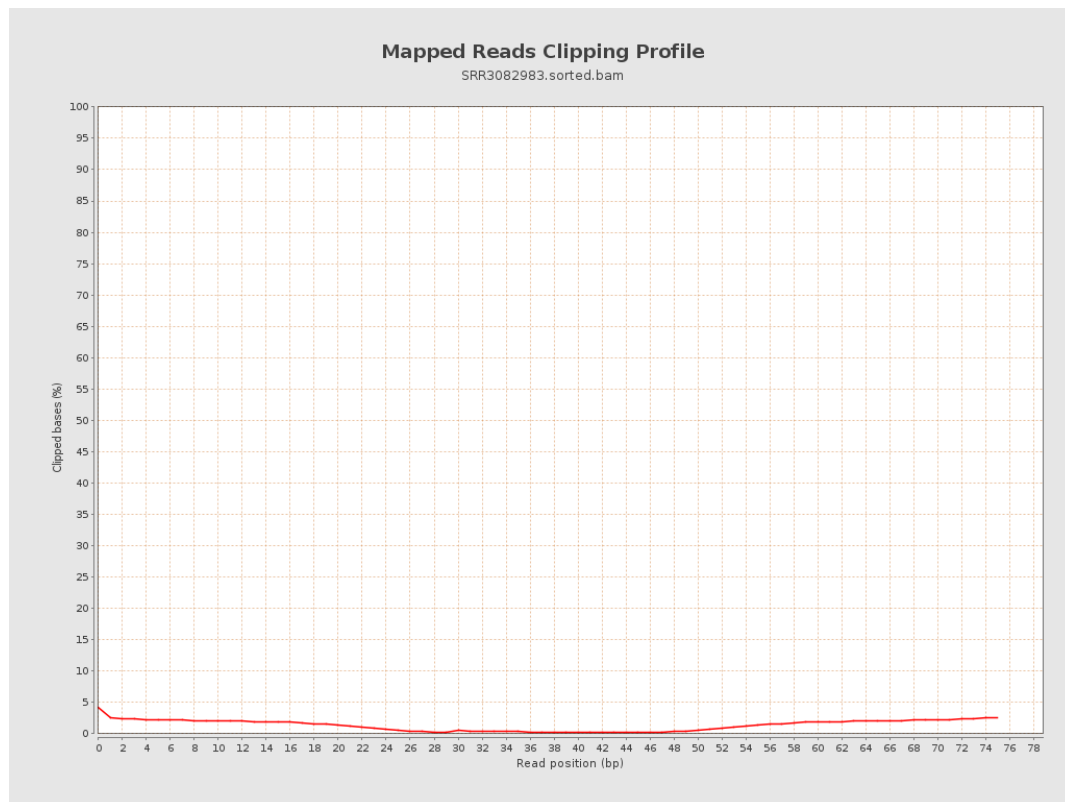
## 8. Results : Mapped Reads Nucleotide Content



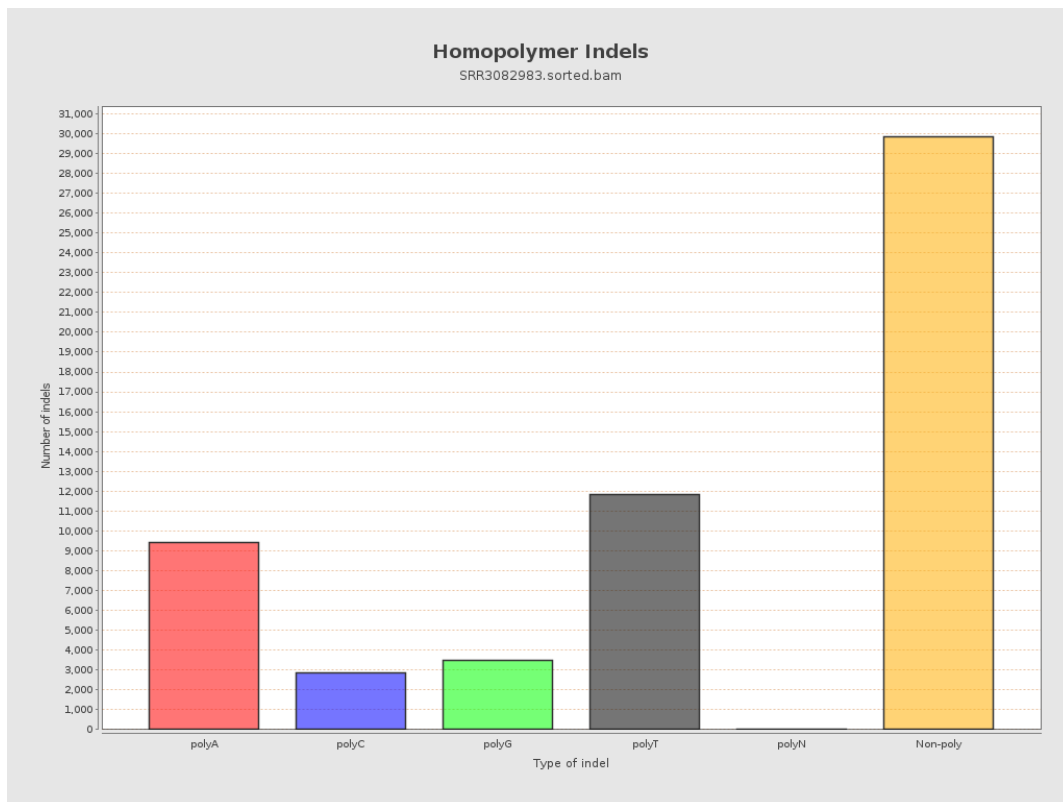
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

