

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 19:17:24*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081109.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_SRR3081109 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081109.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Fri Aug 23 19:17:23 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR3081109.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 2,764,228          |
| Mapped reads                 | 2,503,221 / 90.56% |
| Unmapped reads               | 261,007 / 9.44%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 28,274 / 1.02%     |
| Read min/max/mean length     | 30 / 76 / 76.35    |
| Duplicated reads (estimated) | 103,845 / 3.76%    |
| Duplication rate             | 3.25%              |
| Clipped reads                | 1,277,699 / 46.22% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 47,588,576 / 28.77% |
| Number/percentage of C's | 32,054,972 / 19.38% |
| Number/percentage of T's | 50,378,916 / 30.46% |
| Number/percentage of G's | 35,359,602 / 21.38% |
| Number/percentage of N's | 1,765 / 0%          |
| GC Percentage            | 40.76%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0534 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.4029 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 45.26 |
|----------------------|-------|

## 2.5. Mismatches and indels

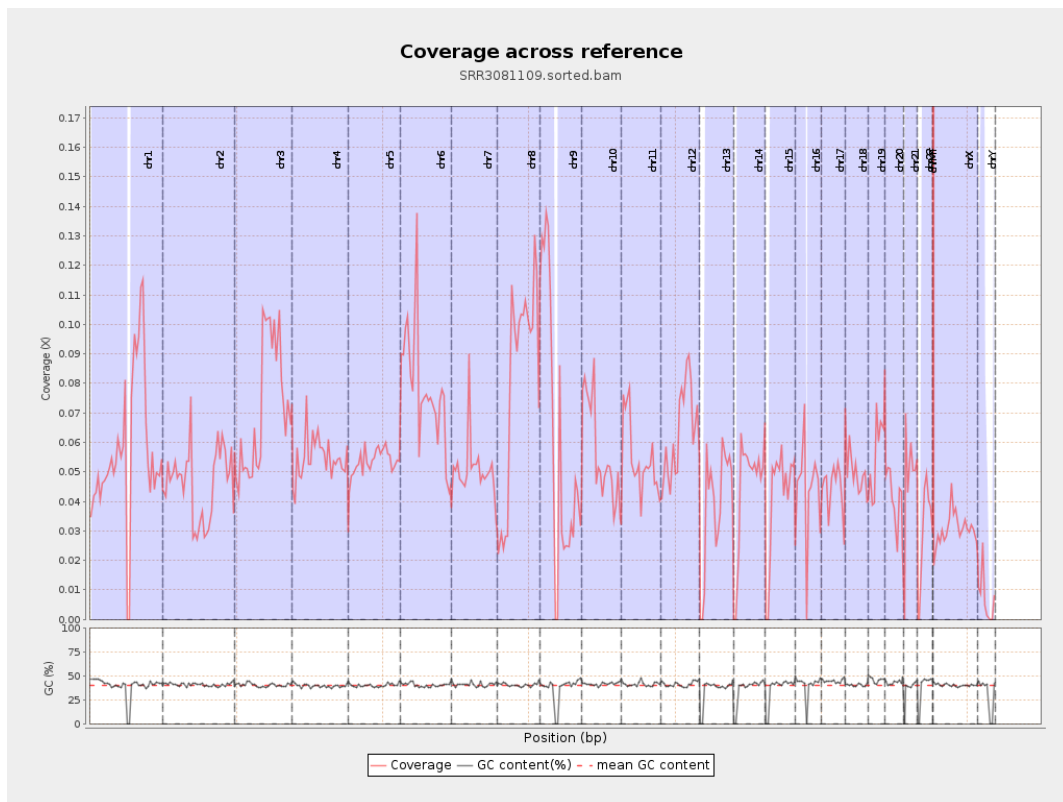
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.94%     |
| Mismatches                               | 1,526,235 |
| Insertions                               | 13,636    |
| Mapped reads with at least one insertion | 0.54%     |
| Deletions                                | 36,249    |
| Mapped reads with at least one deletion  | 1.43%     |
| Homopolymer indels                       | 45.51%    |

## 2.6. Chromosome stats

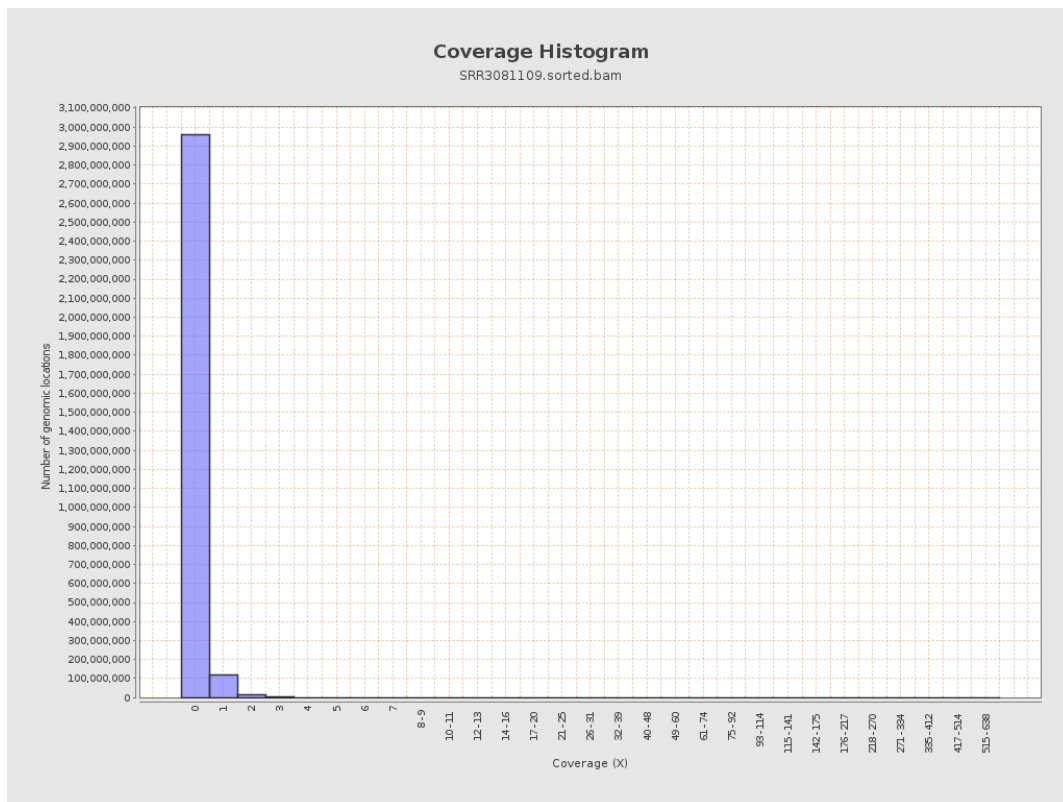
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 14129712     | 0.0567        | 0.6002             |
| chr2 | 243199373 | 11257677     | 0.0463        | 0.428              |
| chr3 | 198022430 | 14045883     | 0.0709        | 0.3067             |
| chr4 | 191154276 | 10493785     | 0.0549        | 0.2902             |
| chr5 | 180915260 | 9742004      | 0.0538        | 0.2685             |
| chr6 | 171115067 | 13356981     | 0.0781        | 0.458              |
| chr7 | 159138663 | 8041951      | 0.0505        | 0.454              |
|      |           |              |               |                    |

|       |           |          |         |         |
|-------|-----------|----------|---------|---------|
| chr8  | 146364022 | 11868912 | 0.0811  | 0.5148  |
| chr9  | 141213431 | 8545640  | 0.0605  | 0.4646  |
| chr10 | 135534747 | 7688137  | 0.0567  | 0.4125  |
| chr11 | 135006516 | 7377346  | 0.0546  | 0.3317  |
| chr12 | 133851895 | 8499346  | 0.0635  | 0.3048  |
| chr13 | 115169878 | 4477188  | 0.0389  | 0.2296  |
| chr14 | 107349540 | 4806416  | 0.0448  | 0.324   |
| chr15 | 102531392 | 4202049  | 0.041   | 0.2351  |
| chr16 | 90354753  | 3888150  | 0.043   | 0.311   |
| chr17 | 81195210  | 3663633  | 0.0451  | 0.2503  |
| chr18 | 78077248  | 3931119  | 0.0503  | 0.7815  |
| chr19 | 59128983  | 3335175  | 0.0564  | 0.5027  |
| chr20 | 63025520  | 2599242  | 0.0412  | 0.2474  |
| chr21 | 48129895  | 2387809  | 0.0496  | 0.3046  |
| chr22 | 51304566  | 1530835  | 0.0298  | 0.1957  |
| chrMT | 16571     | 388020   | 23.4156 | 12.3443 |
| chrX  | 155270560 | 4751428  | 0.0306  | 0.2332  |
| chrY  | 59373566  | 434127   | 0.0073  | 0.1711  |

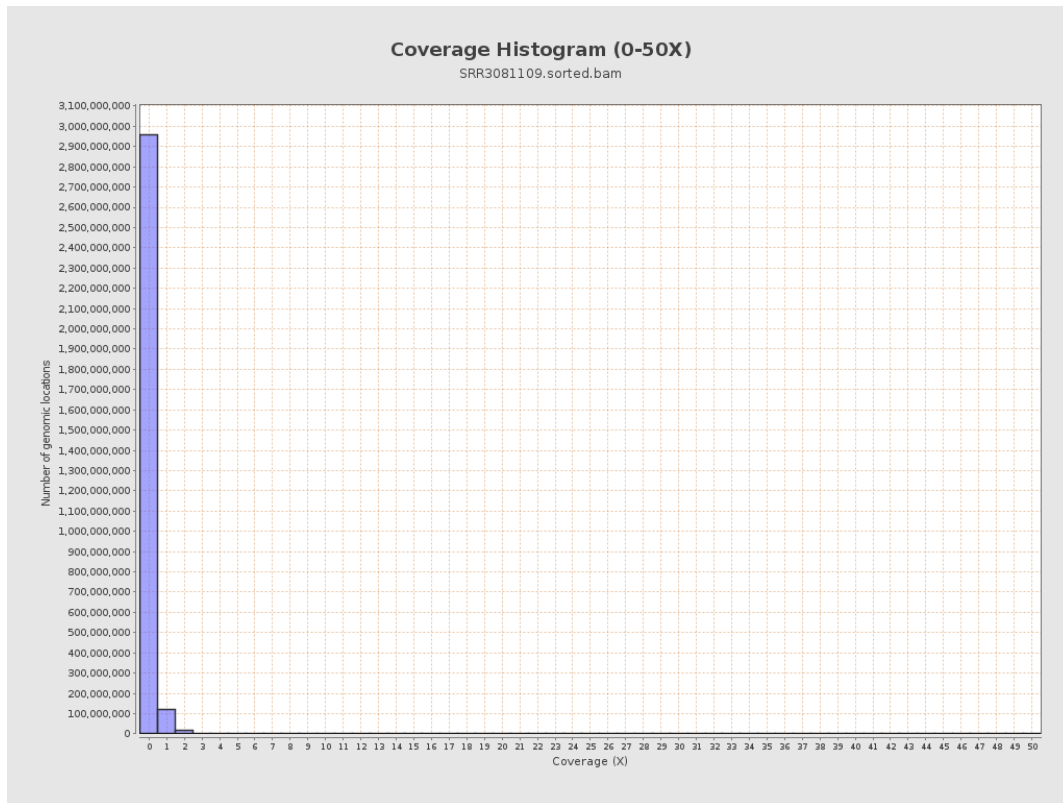
### 3. Results : Coverage across reference



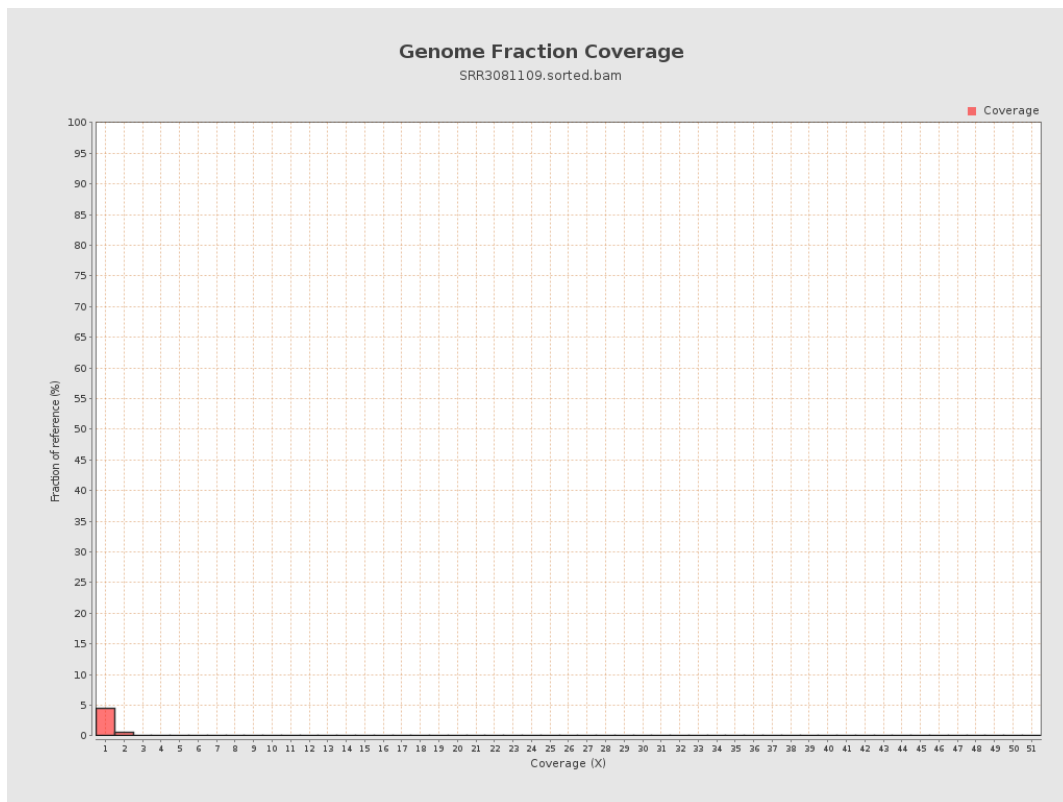
## 4. Results : Coverage Histogram



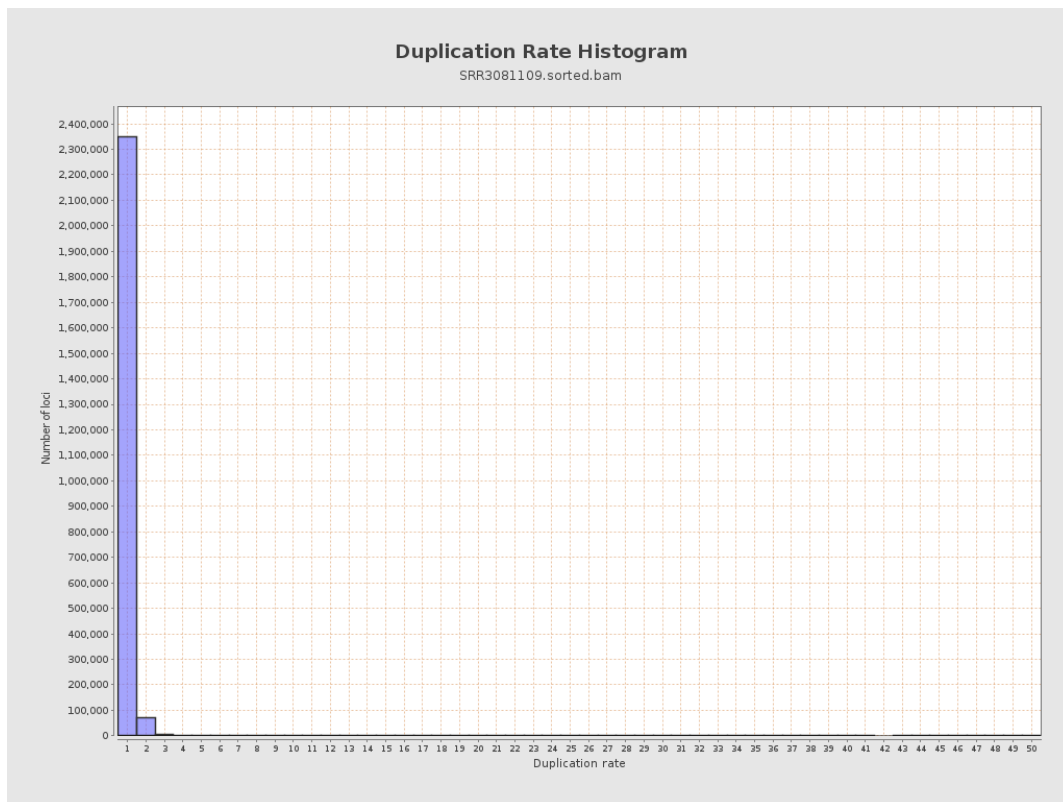
## 5. Results : Coverage Histogram (0-50X)



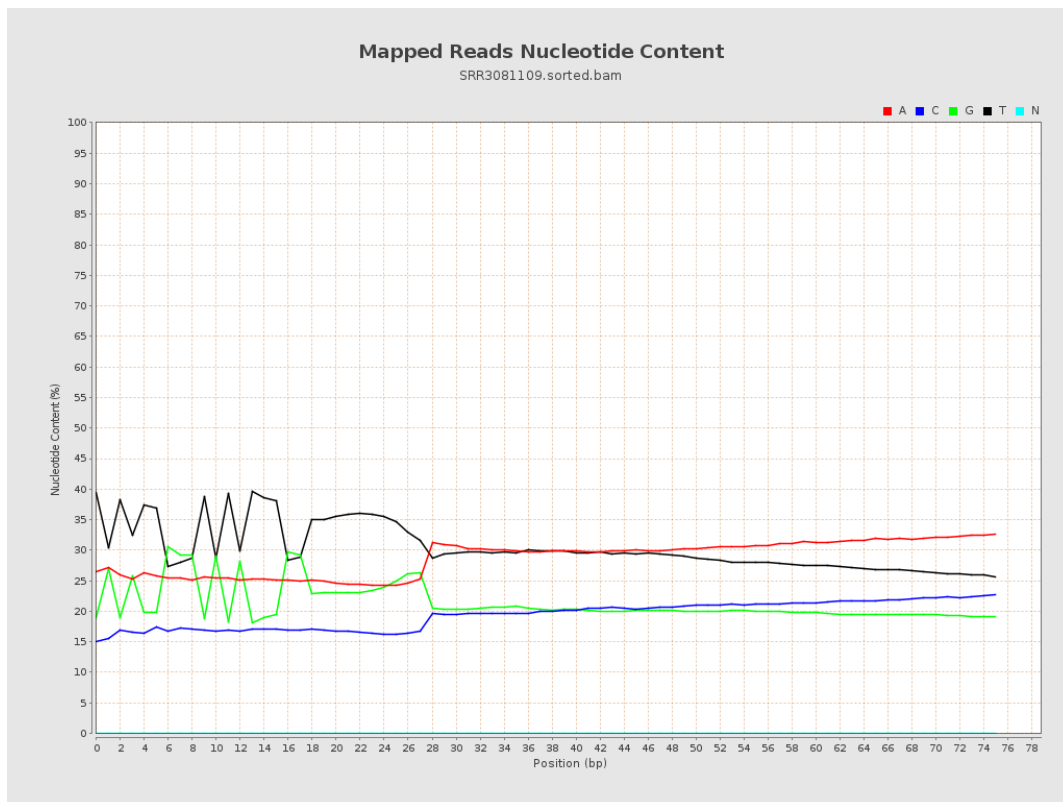
## 6. Results : Genome Fraction Coverage



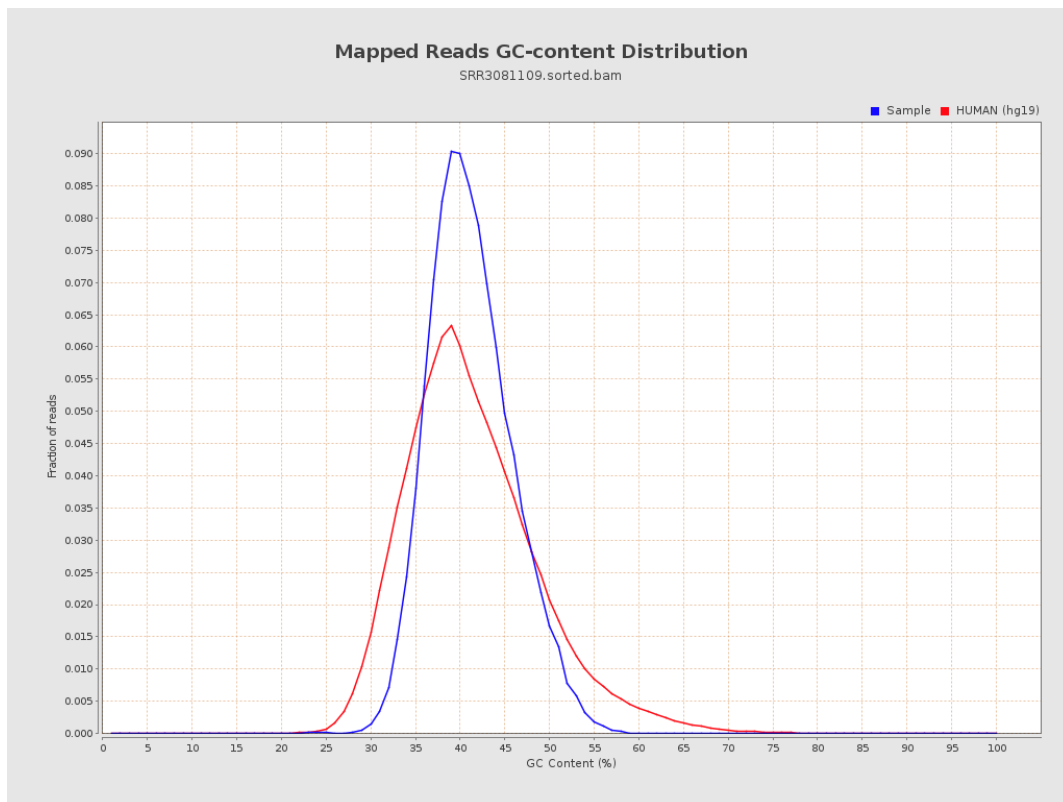
## 7. Results : Duplication Rate Histogram



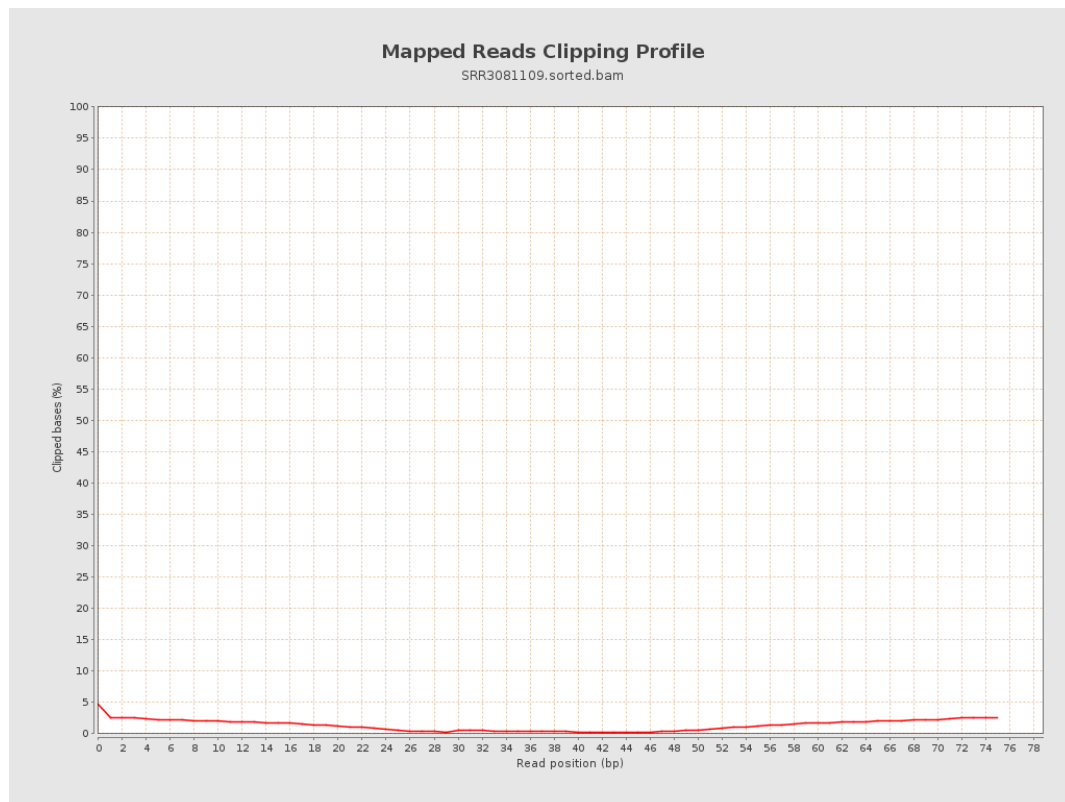
## 8. Results : Mapped Reads Nucleotide Content



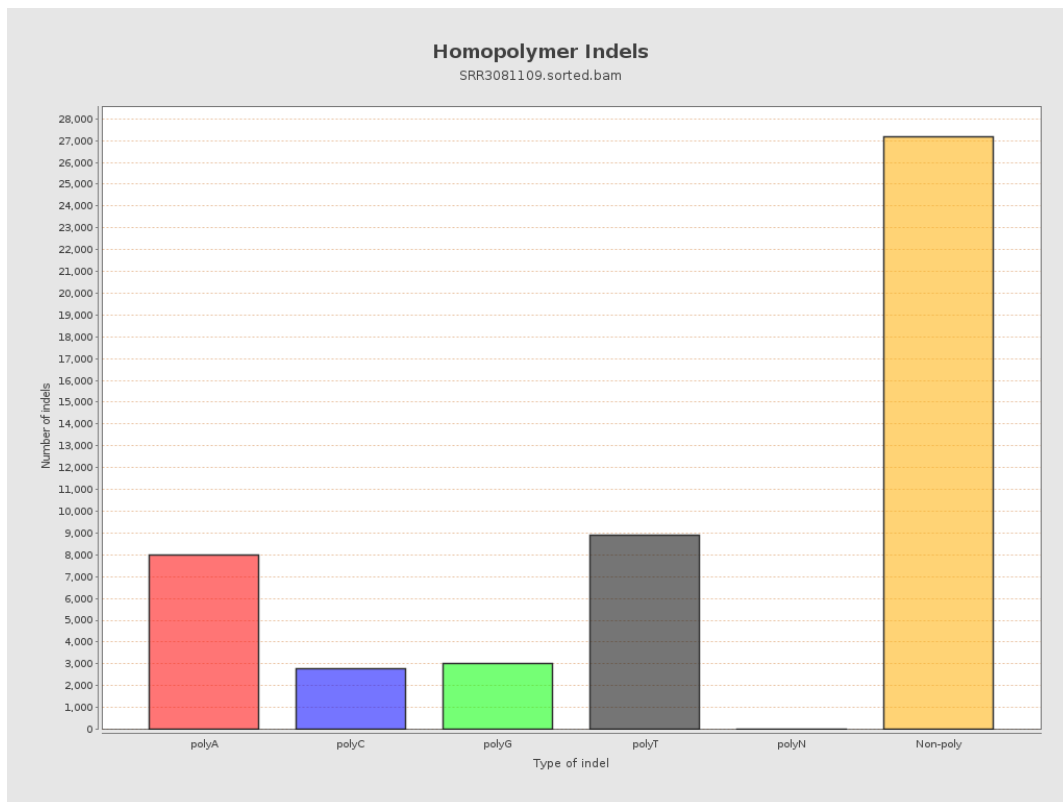
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

