

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/17 07:47:40*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237827.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_SRR6237827 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237827.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Tue Sep 17 07:47:39 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6237827.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                   |
|------------------------------|-------------------|
| Reference size               | 3,095,693,983     |
| Number of reads              | 1,546,120         |
| Mapped reads                 | 1,304,987 / 84.4% |
| Unmapped reads               | 241,133 / 15.6%   |
| Mapped paired reads          | 0 / 0%            |
| Secondary alignments         | 0                 |
| Supplementary alignments     | 15,504 / 1%       |
| Read min/max/mean length     | 30 / 76 / 76.35   |
| Duplicated reads (estimated) | 209,378 / 13.54%  |
| Duplication rate             | 11.39%            |
| Clipped reads                | 699,736 / 45.26%  |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 22,831,352 / 27.12% |
| Number/percentage of C's | 15,417,515 / 18.31% |
| Number/percentage of T's | 26,777,038 / 31.8%  |
| Number/percentage of G's | 19,040,003 / 22.61% |
| Number/percentage of N's | 133,343 / 0.16%     |
| GC Percentage            | 40.92%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0272 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.3552 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 45.28 |
|----------------------|-------|

## 2.5. Mismatches and indels

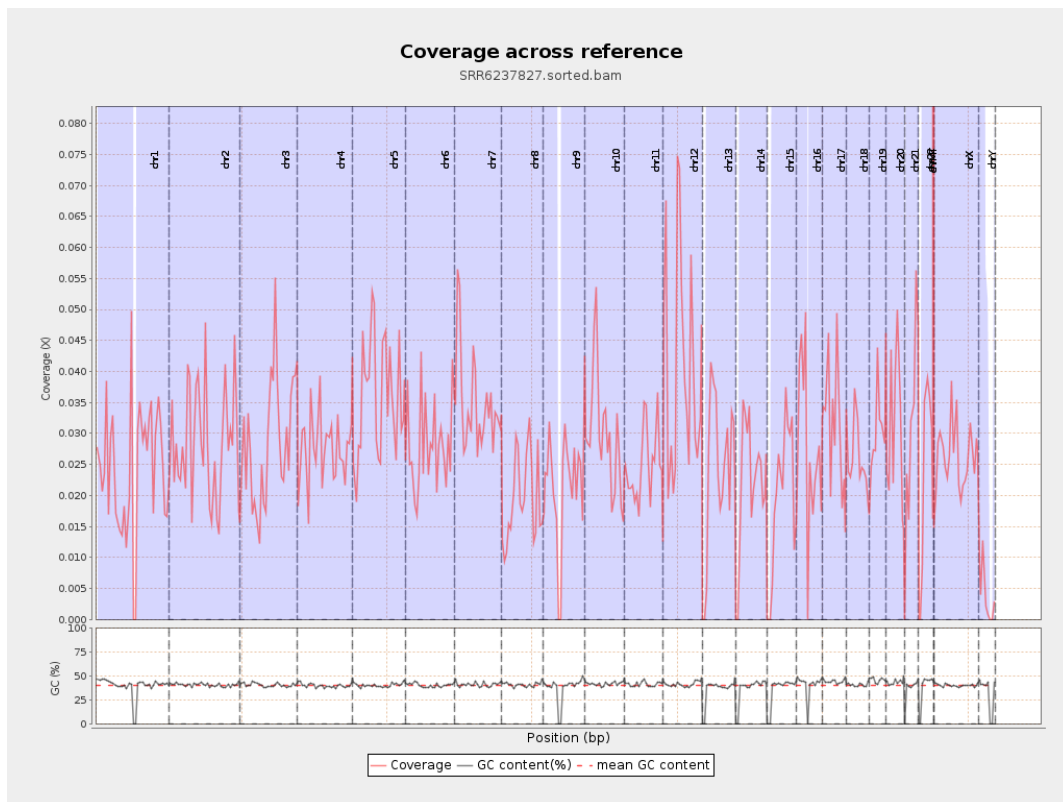
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 0.93%   |
| Mismatches                               | 775,527 |
| Insertions                               | 5,747   |
| Mapped reads with at least one insertion | 0.44%   |
| Deletions                                | 30,060  |
| Mapped reads with at least one deletion  | 2.27%   |
| Homopolymer indels                       | 43.6%   |

## 2.6. Chromosome stats

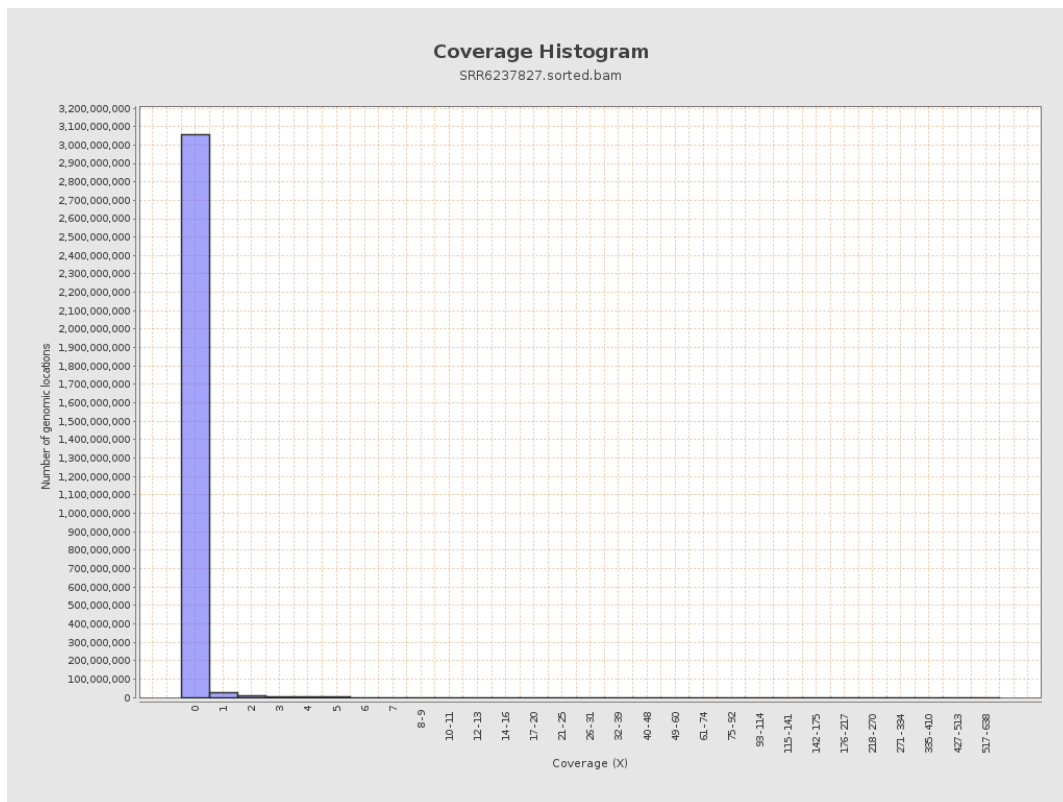
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 5980246      | 0.024         | 0.5718             |
| chr2 | 243199373 | 6935379      | 0.0285        | 0.3909             |
| chr3 | 198022430 | 5587525      | 0.0282        | 0.3044             |
| chr4 | 191154276 | 5245377      | 0.0274        | 0.3052             |
| chr5 | 180915260 | 6445927      | 0.0356        | 0.3395             |
| chr6 | 171115067 | 4813613      | 0.0281        | 0.3159             |
| chr7 | 159138663 | 5539072      | 0.0348        | 0.4062             |
|      |           |              |               |                    |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr8  | 146364022 | 2837827 | 0.0194 | 0.3182 |
| chr9  | 141213431 | 3030500 | 0.0215 | 0.2888 |
| chr10 | 135534747 | 4046278 | 0.0299 | 0.3696 |
| chr11 | 135006516 | 3346023 | 0.0248 | 0.2954 |
| chr12 | 133851895 | 5503159 | 0.0411 | 0.3788 |
| chr13 | 115169878 | 2744775 | 0.0238 | 0.2857 |
| chr14 | 107349540 | 2344743 | 0.0218 | 0.2701 |
| chr15 | 102531392 | 2032246 | 0.0198 | 0.2506 |
| chr16 | 90354753  | 2516851 | 0.0279 | 0.3125 |
| chr17 | 81195210  | 2547019 | 0.0314 | 0.343  |
| chr18 | 78077248  | 2037002 | 0.0261 | 0.3848 |
| chr19 | 59128983  | 1814946 | 0.0307 | 0.4589 |
| chr20 | 63025520  | 1933419 | 0.0307 | 0.3189 |
| chr21 | 48129895  | 1494075 | 0.031  | 0.3249 |
| chr22 | 51304566  | 1192524 | 0.0232 | 0.2812 |
| chrMT | 16571     | 26738   | 1.6135 | 1.9804 |
| chrX  | 155270560 | 4037679 | 0.026  | 0.289  |
| chrY  | 59373566  | 218543  | 0.0037 | 0.1092 |

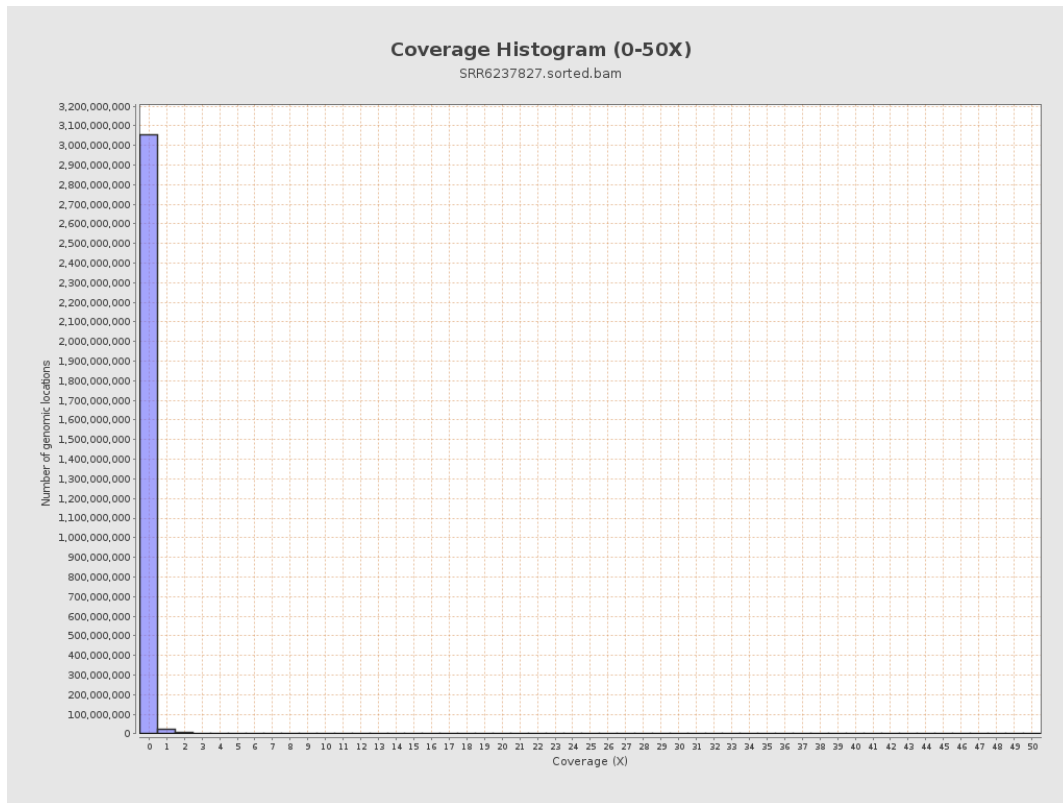
### 3. Results : Coverage across reference



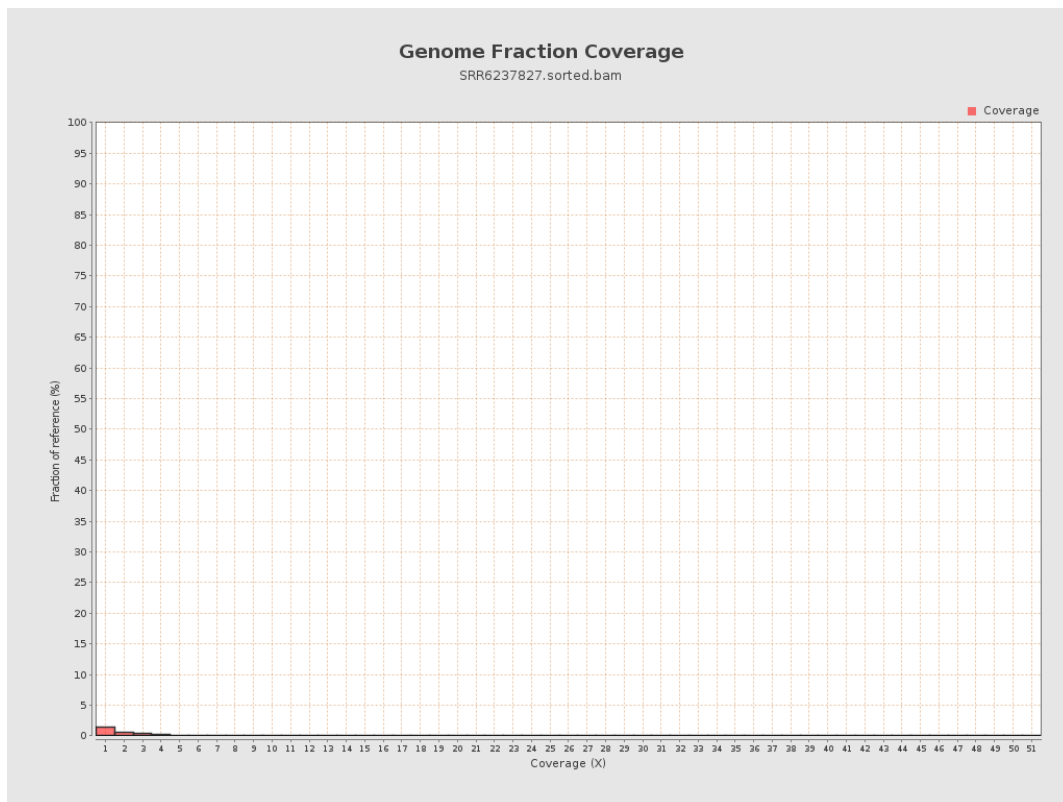
## 4. Results : Coverage Histogram



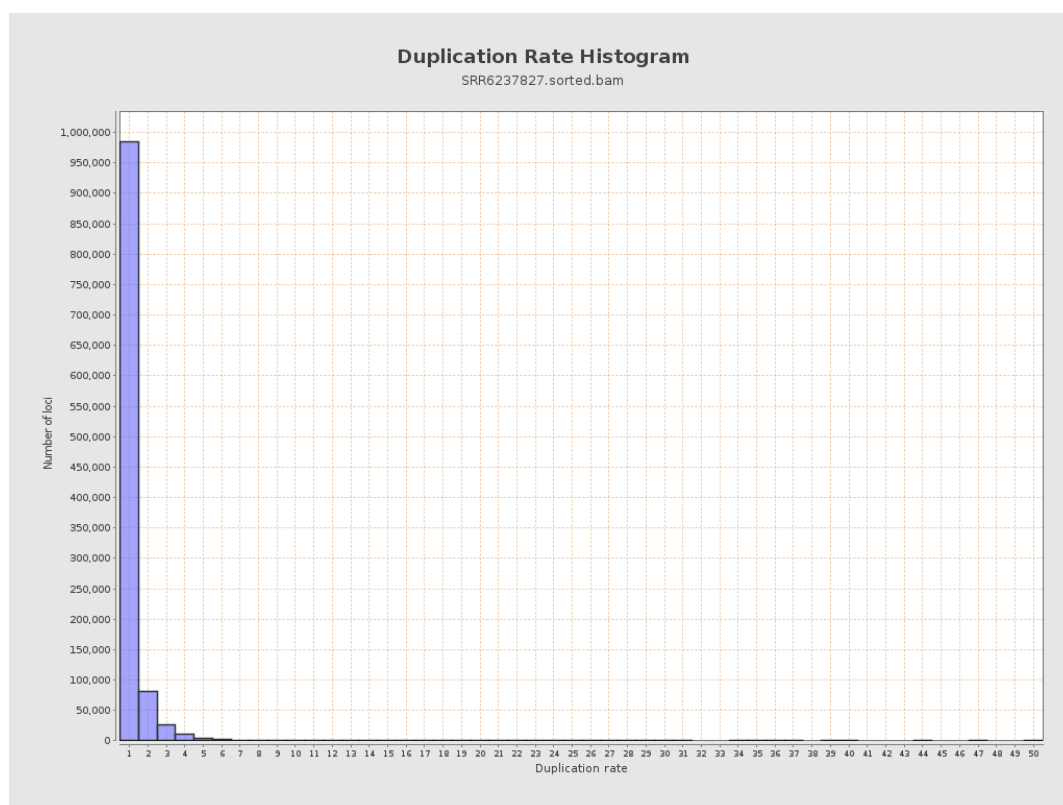
## 5. Results : Coverage Histogram (0-50X)



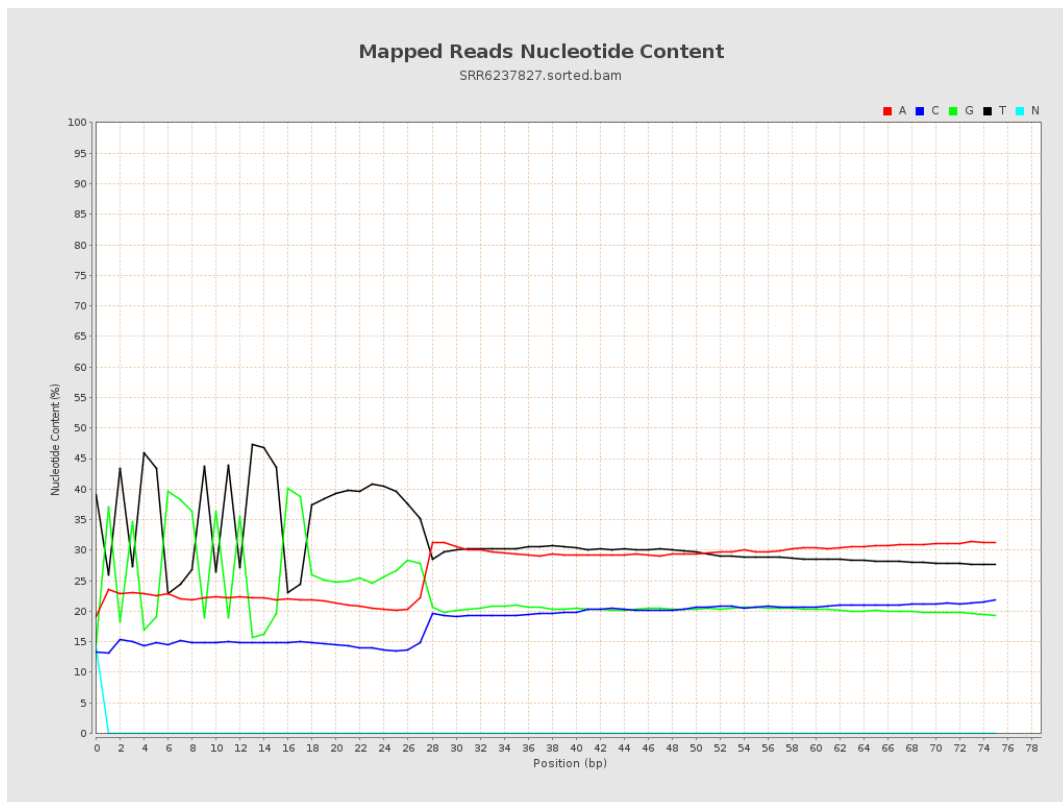
## 6. Results : Genome Fraction Coverage



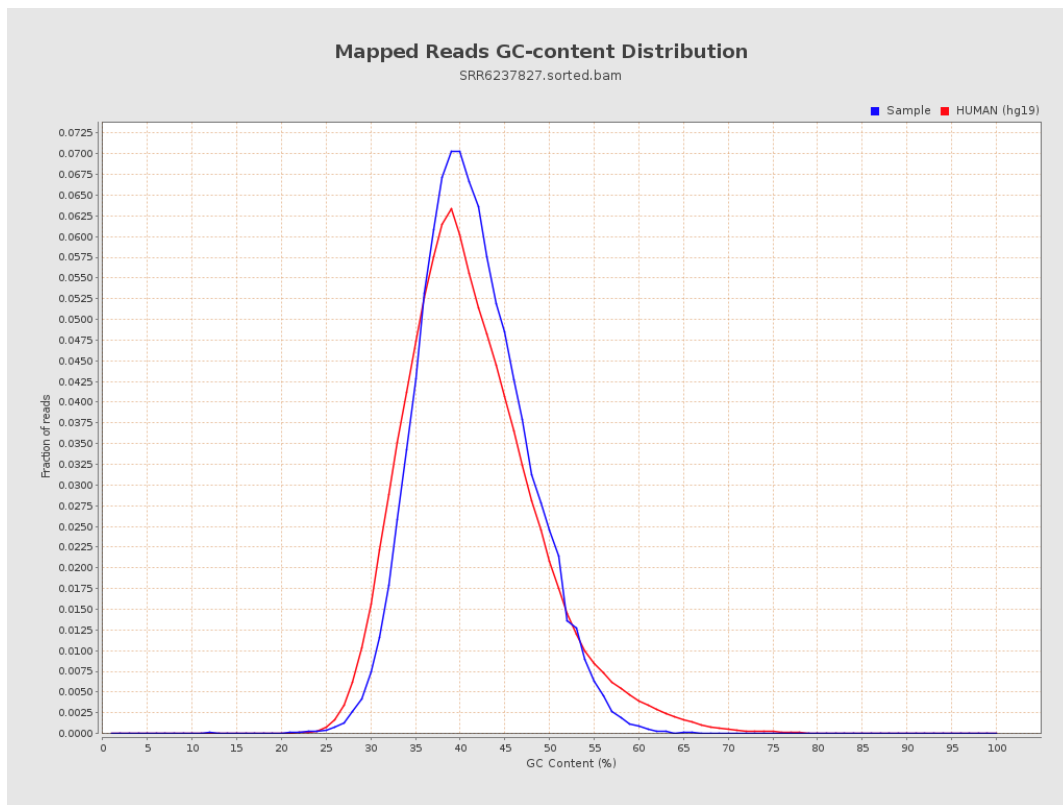
## 7. Results : Duplication Rate Histogram



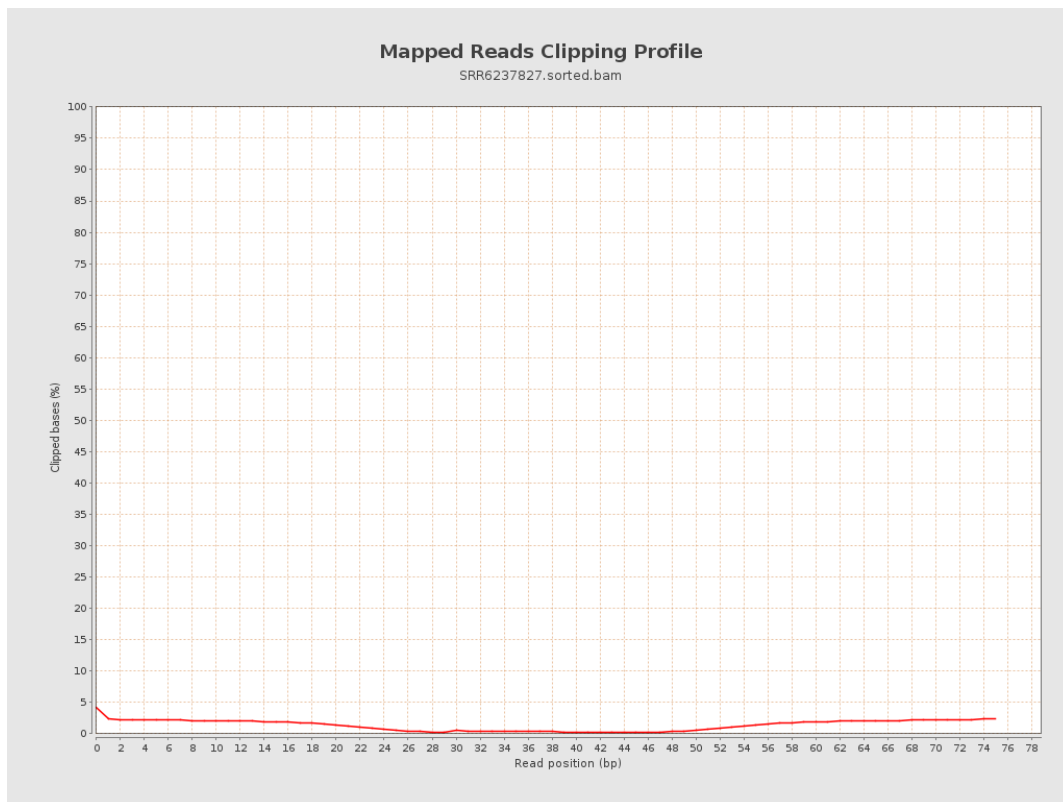
## 8. Results : Mapped Reads Nucleotide Content



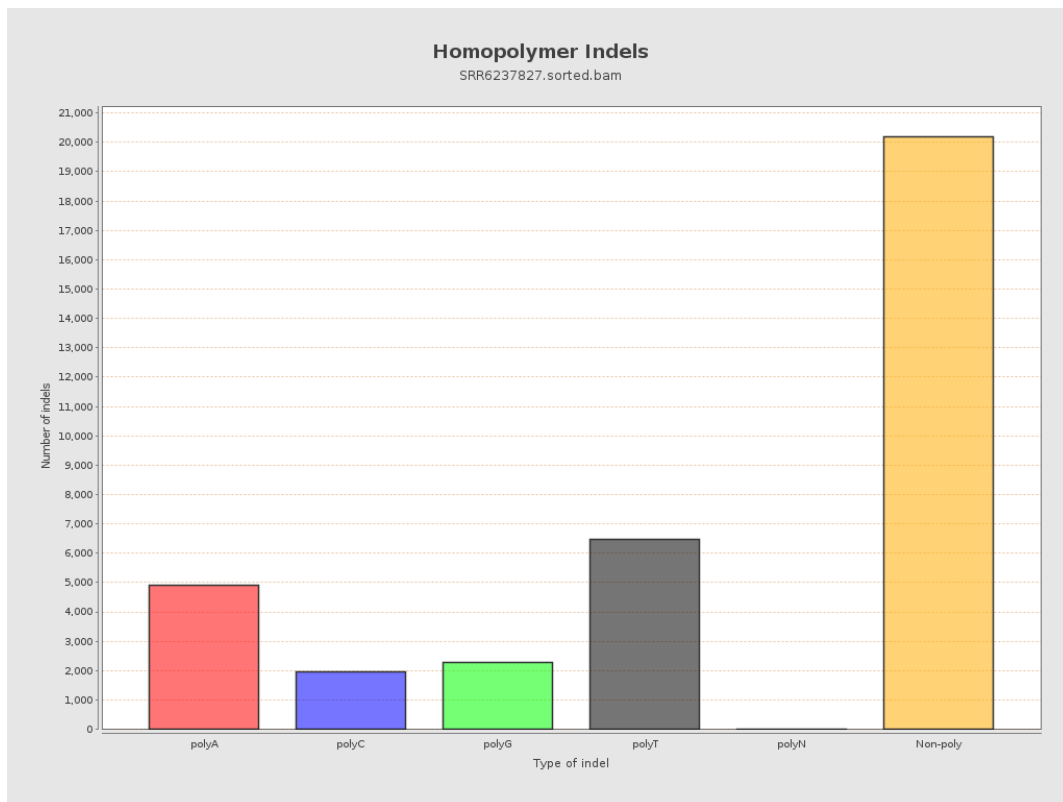
## 9. Results : Mapped Reads GC-content Distribution



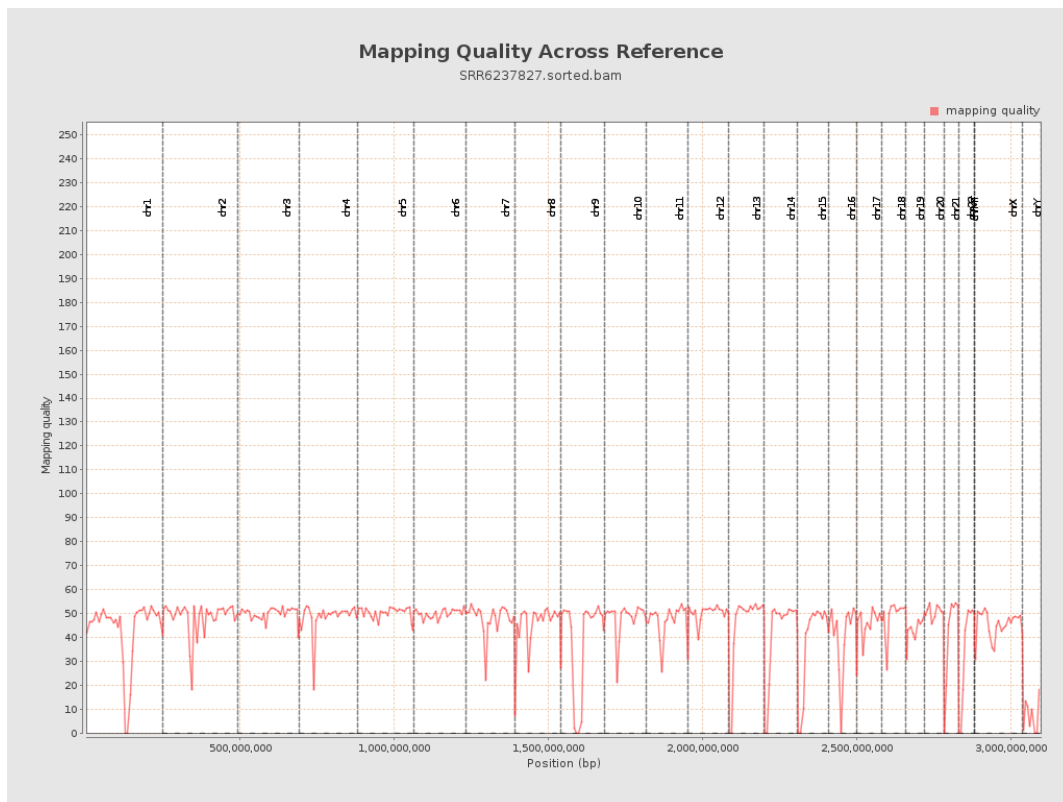
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

