

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/16 22:20:58*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237249.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_SRR6237249 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237249.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Mon Sep 16 22:20:58 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6237249.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 1,520,361          |
| Mapped reads                 | 1,389,138 / 91.37% |
| Unmapped reads               | 131,223 / 8.63%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 8,296 / 0.55%      |
| Read min/max/mean length     | 30 / 76 / 76.19    |
| Duplicated reads (estimated) | 49,727 / 3.27%     |
| Duplication rate             | 2.08%              |
| Clipped reads                | 467,682 / 30.76%   |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 28,724,712 / 29.79% |
| Number/percentage of C's | 18,015,188 / 18.69% |
| Number/percentage of T's | 29,644,084 / 30.75% |
| Number/percentage of G's | 20,023,234 / 20.77% |
| Number/percentage of N's | 1,568 / 0%          |
| GC Percentage            | 39.46%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0312 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.4539 |
|--------------------|--------|

## 2.4. Mapping Quality

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

## 2.5. Mismatches and indels

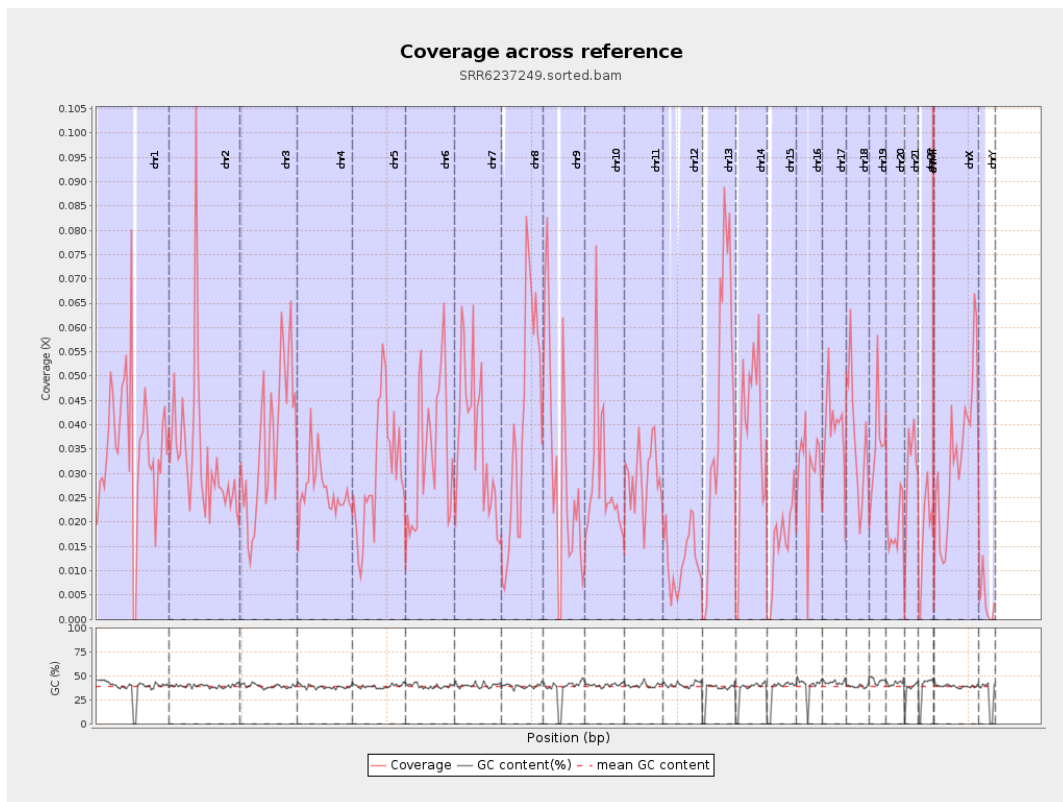
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 0.9%    |
| Mismatches                               | 856,464 |
| Insertions                               | 8,239   |
| Mapped reads with at least one insertion | 0.59%   |
| Deletions                                | 35,816  |
| Mapped reads with at least one deletion  | 2.54%   |
| Homopolymer indels                       | 44.29%  |

## 2.6. Chromosome stats

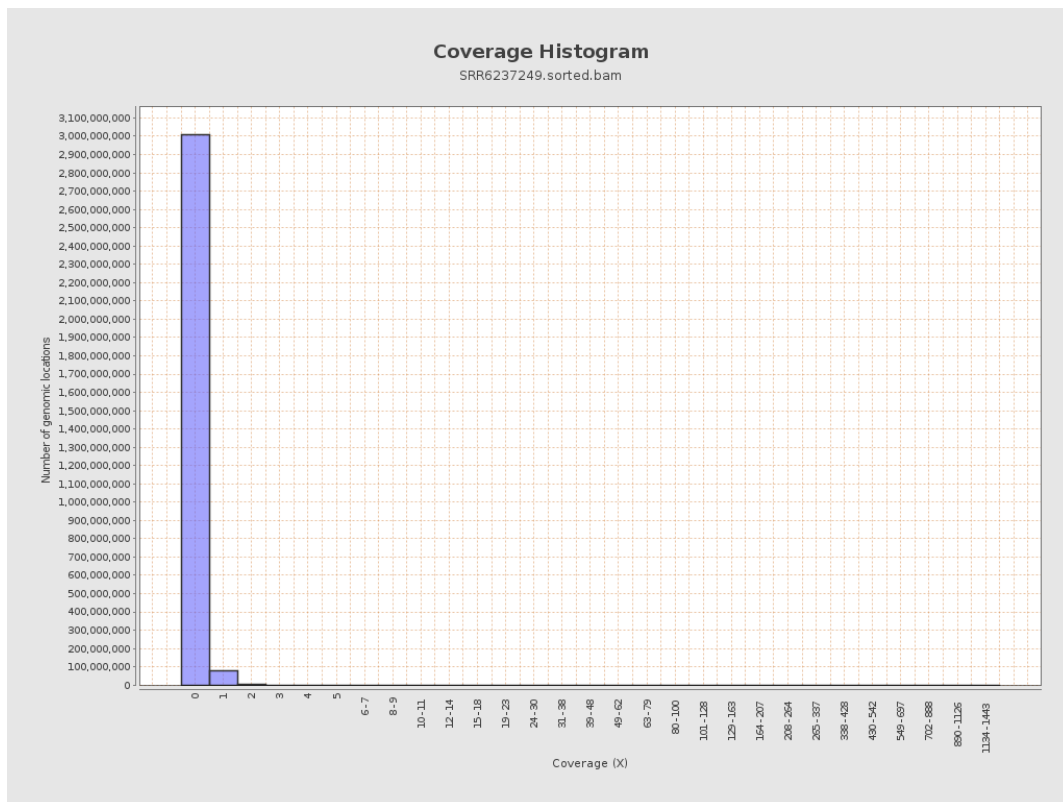
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 8811797      | 0.0354        | 1.0436             |
| chr2 | 243199373 | 8111469      | 0.0334        | 0.4509             |
| chr3 | 198022430 | 7286885      | 0.0368        | 0.2112             |
| chr4 | 191154276 | 5081875      | 0.0266        | 0.1979             |
| chr5 | 180915260 | 5466155      | 0.0302        | 0.1951             |
| chr6 | 171115067 | 5782222      | 0.0338        | 0.2446             |
| chr7 | 159138663 | 5945467      | 0.0374        | 0.4928             |
|      |           |              |               |                    |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr8  | 146364022 | 5762201 | 0.0394 | 0.5108 |
| chr9  | 141213431 | 4364441 | 0.0309 | 0.4488 |
| chr10 | 135534747 | 3850844 | 0.0284 | 0.3854 |
| chr11 | 135006516 | 3907091 | 0.0289 | 0.3579 |
| chr12 | 133851895 | 1644353 | 0.0123 | 0.1398 |
| chr13 | 115169878 | 4913231 | 0.0427 | 0.2208 |
| chr14 | 107349540 | 4042957 | 0.0377 | 0.2462 |
| chr15 | 102531392 | 1608803 | 0.0157 | 0.1332 |
| chr16 | 90354753  | 2778398 | 0.0307 | 0.2812 |
| chr17 | 81195210  | 3145371 | 0.0387 | 0.3685 |
| chr18 | 78077248  | 2907637 | 0.0372 | 0.9349 |
| chr19 | 59128983  | 2134903 | 0.0361 | 0.6212 |
| chr20 | 63025520  | 1180529 | 0.0187 | 0.1567 |
| chr21 | 48129895  | 1472890 | 0.0306 | 0.2313 |
| chr22 | 51304566  | 885413  | 0.0173 | 0.1393 |
| chrMT | 16571     | 17109   | 1.0325 | 1.2098 |
| chrX  | 155270560 | 5160514 | 0.0332 | 0.2349 |
| chrY  | 59373566  | 208328  | 0.0035 | 0.1311 |

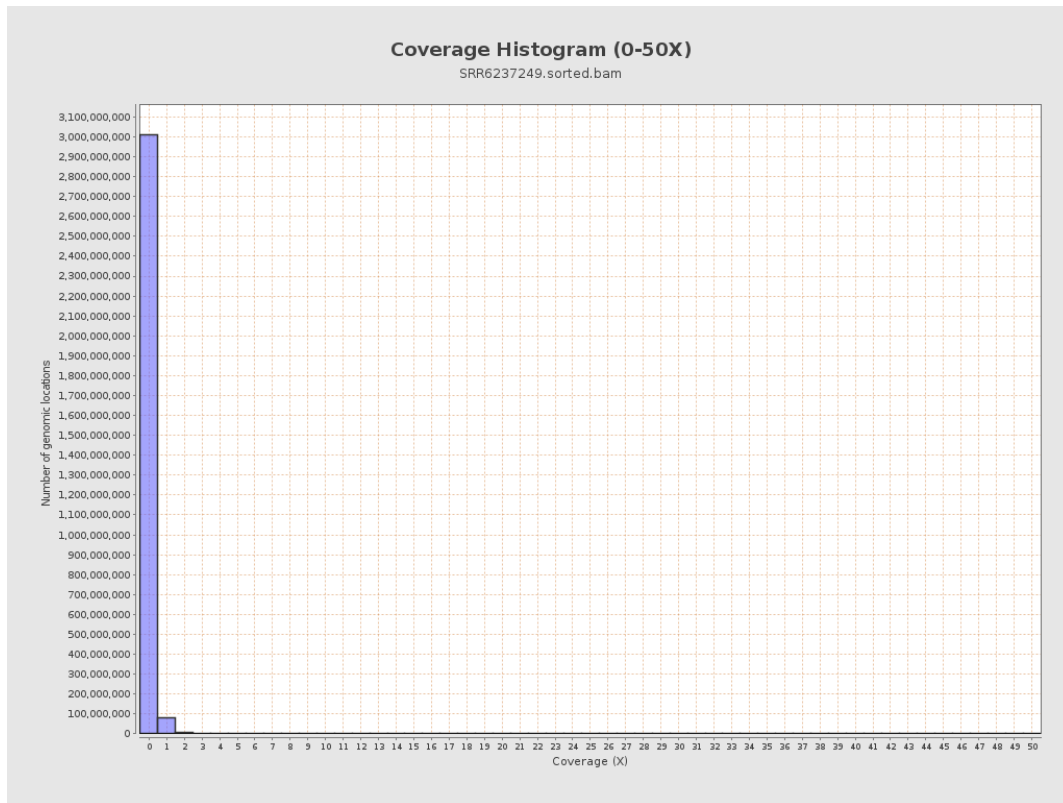
### 3. Results : Coverage across reference



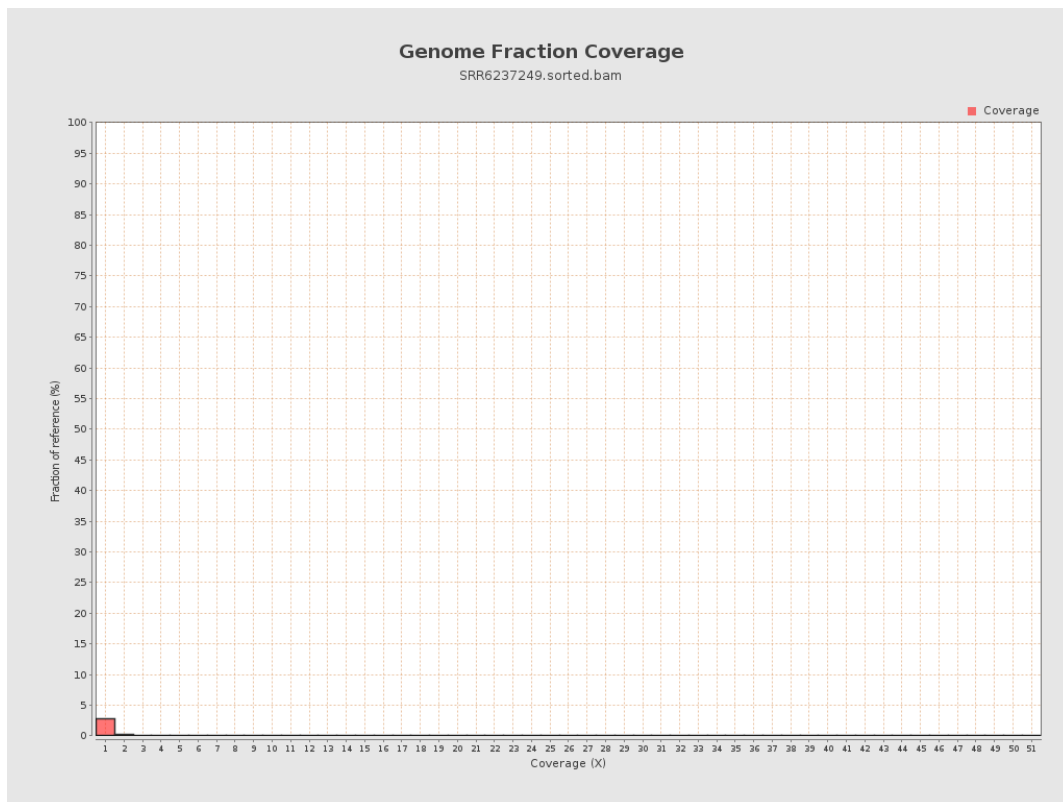
## 4. Results : Coverage Histogram



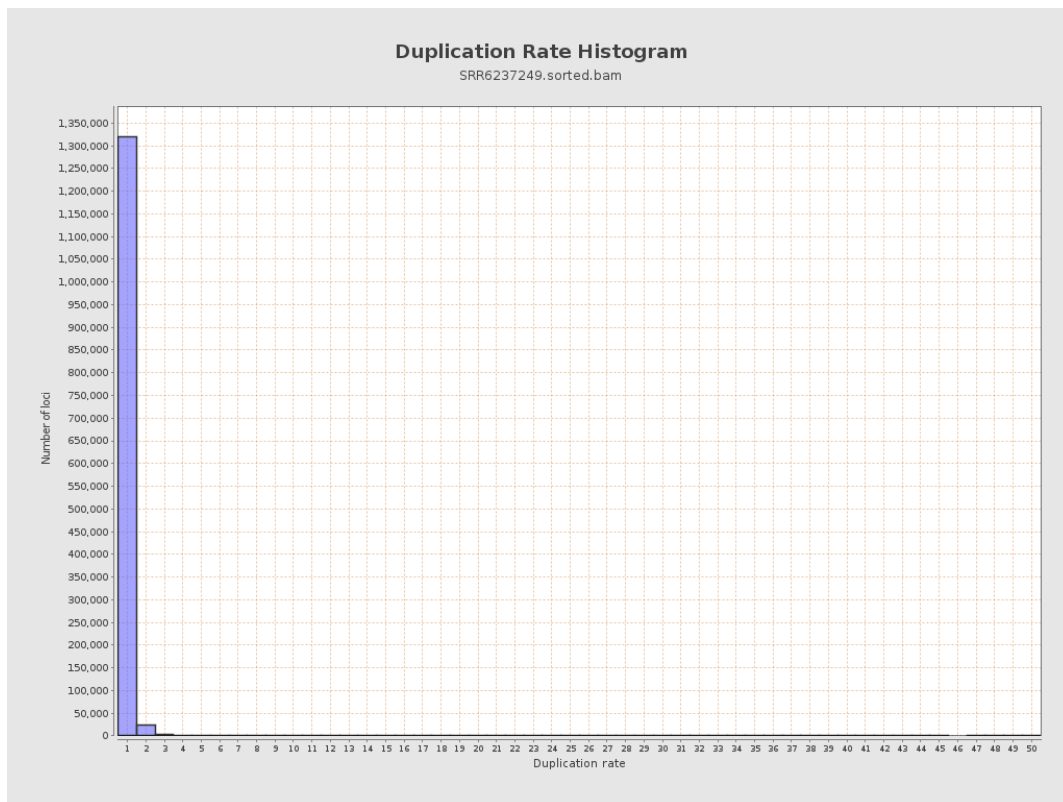
## 5. Results : Coverage Histogram (0-50X)



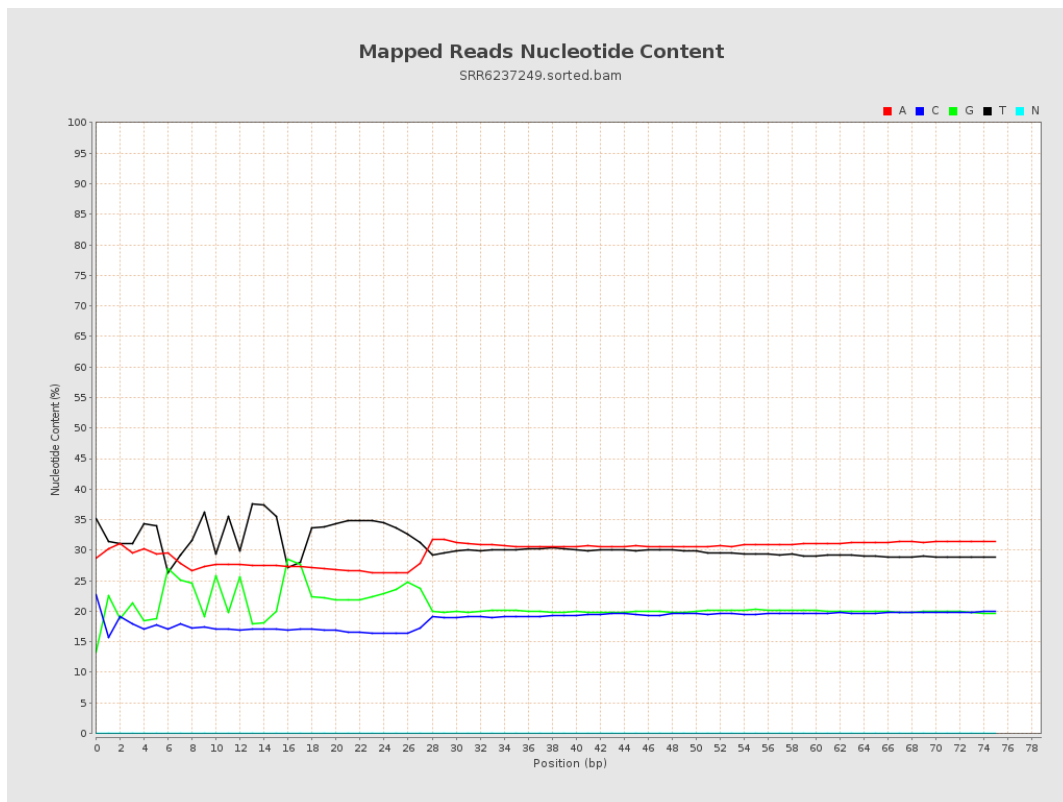
## 6. Results : Genome Fraction Coverage



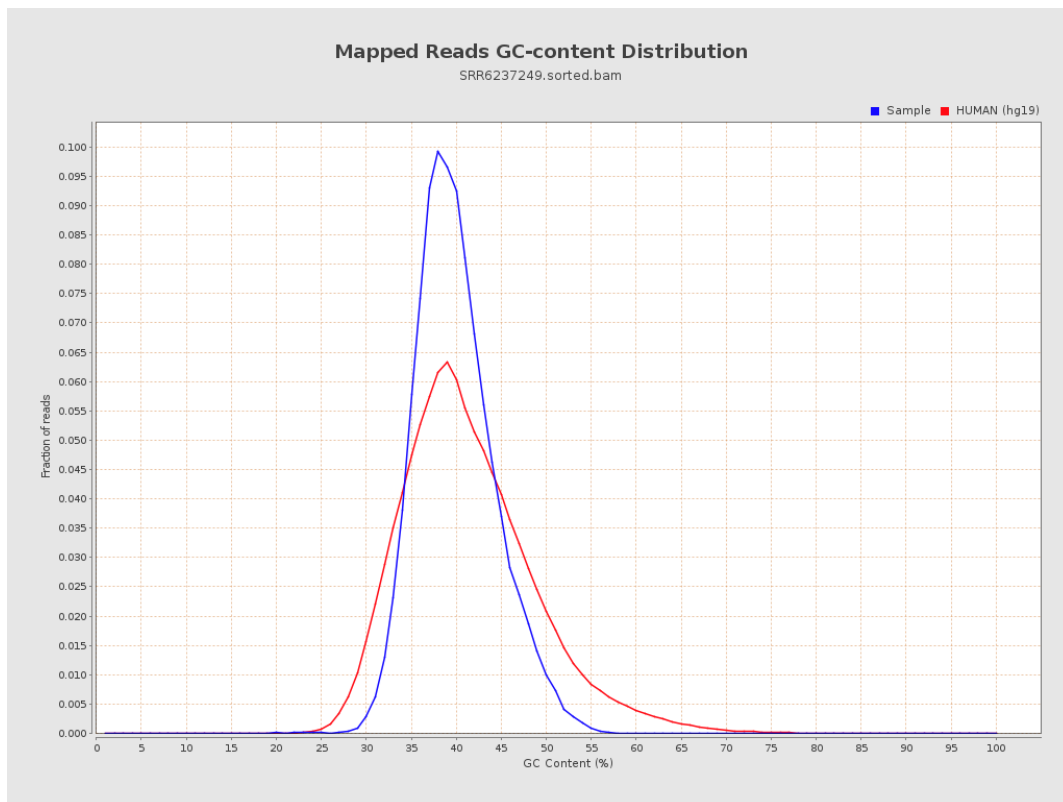
## 7. Results : Duplication Rate Histogram



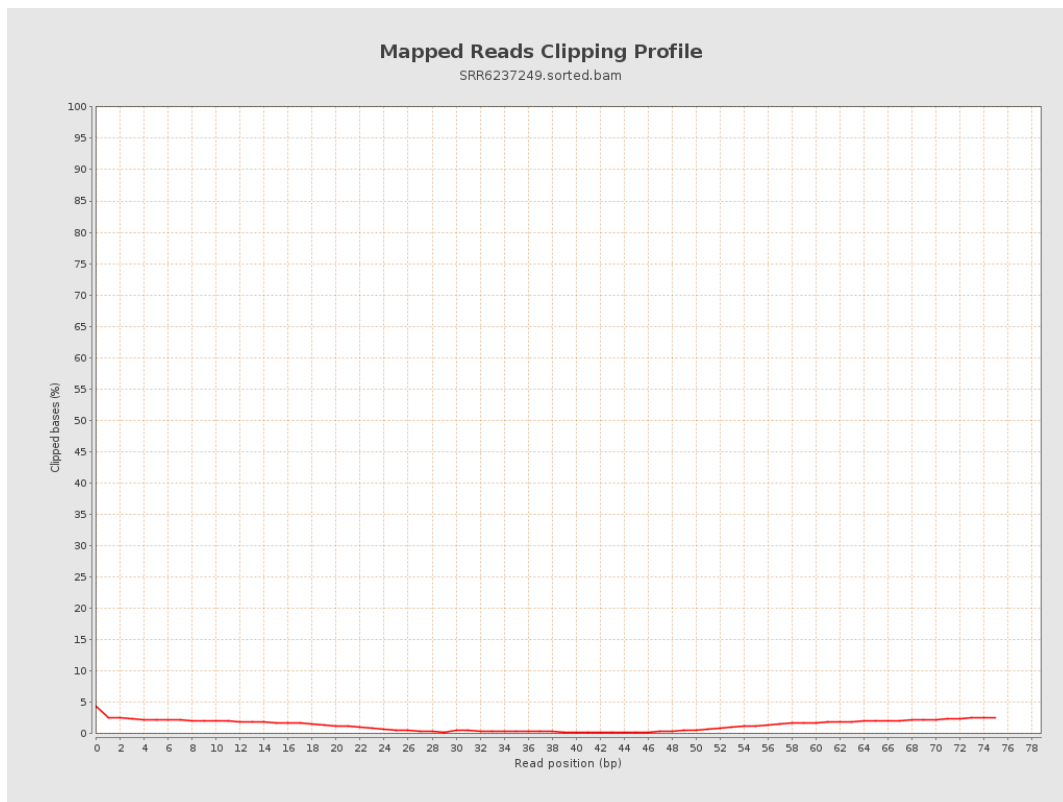
## 8. Results : Mapped Reads Nucleotide Content



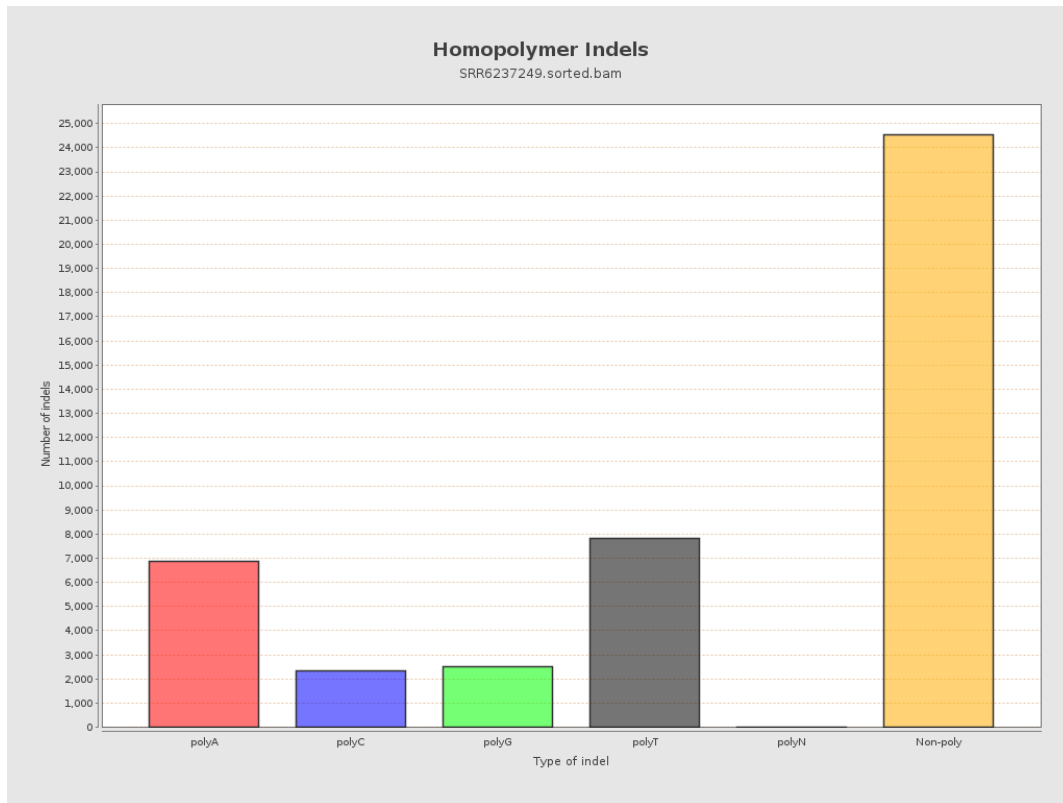
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

