

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/16 17:41:53*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234127.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_SRR6234127 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234127.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Mon Sep 16 17:41:52 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6234127.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 3,423,883          |
| Mapped reads                 | 2,947,015 / 86.07% |
| Unmapped reads               | 476,868 / 13.93%   |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 28,022 / 0.82%     |
| Read min/max/mean length     | 30 / 76 / 76.29    |
| Duplicated reads (estimated) | 1,045,831 / 30.55% |
| Duplication rate             | 13.47%             |
| Clipped reads                | 996,440 / 29.1%    |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 44,575,002 / 21.9%  |
| Number/percentage of C's | 33,150,763 / 16.29% |
| Number/percentage of T's | 47,919,452 / 23.54% |
| Number/percentage of G's | 77,855,566 / 38.25% |
| Number/percentage of N's | 40,980 / 0.02%      |
| GC Percentage            | 54.54%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0658 |
|      |        |

|                    |         |
|--------------------|---------|
| Standard Deviation | 83.2341 |
|--------------------|---------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 44.37 |
|----------------------|-------|

## 2.5. Mismatches and indels

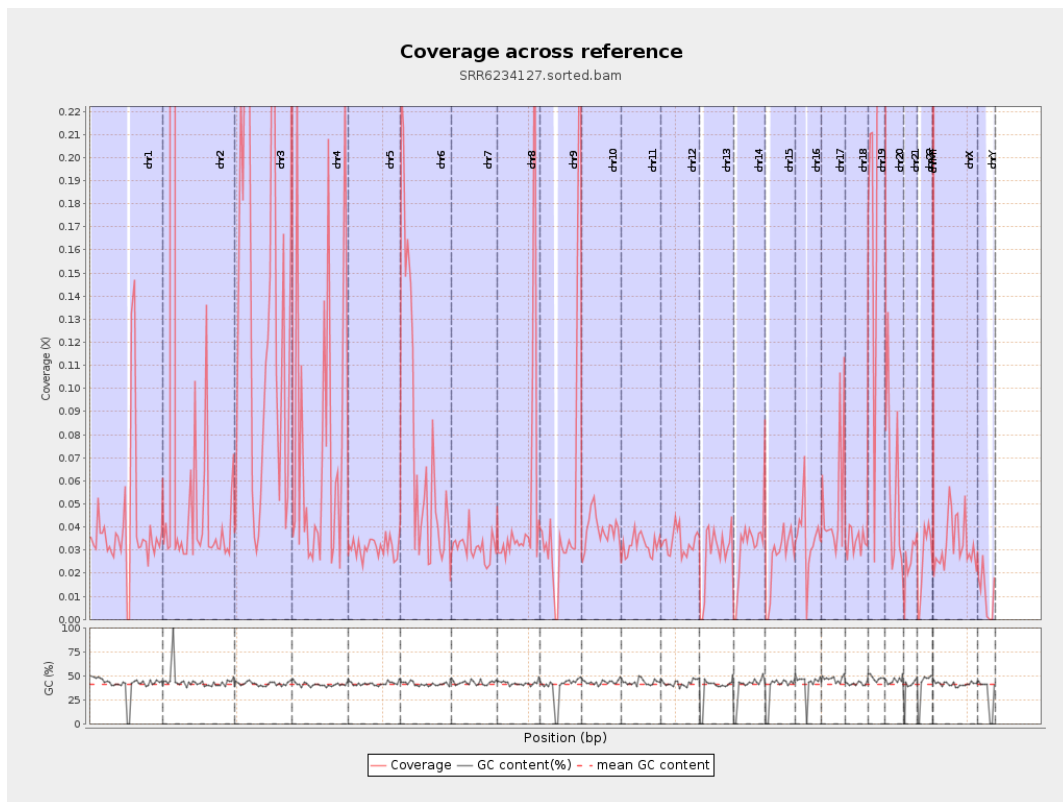
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.55%     |
| Mismatches                               | 1,101,956 |
| Insertions                               | 11,804    |
| Mapped reads with at least one insertion | 0.4%      |
| Deletions                                | 34,770    |
| Mapped reads with at least one deletion  | 1.17%     |
| Homopolymer indels                       | 46.15%    |

## 2.6. Chromosome stats

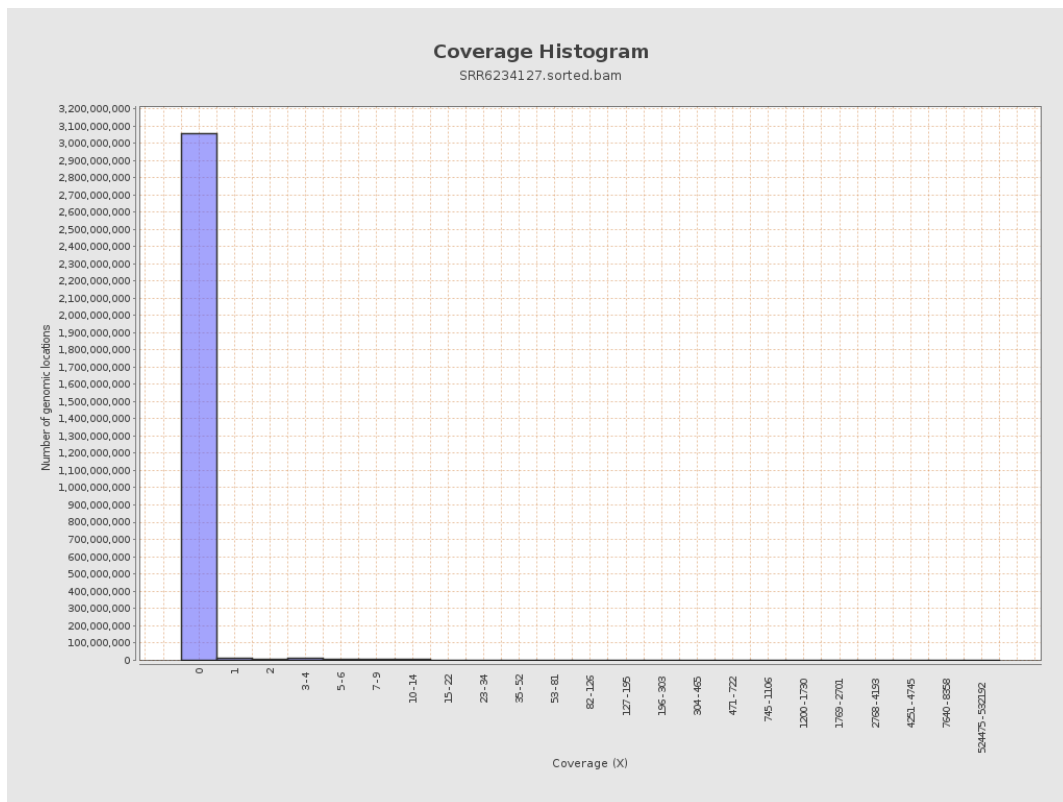
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 9837259      | 0.0395        | 0.7025             |
| chr2 | 243199373 | 51231753     | 0.2107        | 296.9498           |
| chr3 | 198022430 | 25900450     | 0.1308        | 1.0911             |
| chr4 | 191154276 | 14047660     | 0.0735        | 0.8123             |
| chr5 | 180915260 | 5670432      | 0.0313        | 0.5188             |
| chr6 | 171115067 | 12700758     | 0.0742        | 0.8824             |
| chr7 | 159138663 | 4976043      | 0.0313        | 0.6541             |
|      |           |              |               |                    |

|       |           |          |        |         |
|-------|-----------|----------|--------|---------|
| chr8  | 146364022 | 7394953  | 0.0505 | 0.7014  |
| chr9  | 141213431 | 7081111  | 0.0501 | 0.7187  |
| chr10 | 135534747 | 5290722  | 0.039  | 0.6052  |
| chr11 | 135006516 | 4349950  | 0.0322 | 0.6573  |
| chr12 | 133851895 | 4489121  | 0.0335 | 0.6447  |
| chr13 | 115169878 | 3255922  | 0.0283 | 0.5181  |
| chr14 | 107349540 | 3246872  | 0.0302 | 0.6048  |
| chr15 | 102531392 | 2663298  | 0.026  | 0.6132  |
| chr16 | 90354753  | 3170604  | 0.0351 | 0.5948  |
| chr17 | 81195210  | 4011986  | 0.0494 | 0.6646  |
| chr18 | 78077248  | 2643602  | 0.0339 | 0.6781  |
| chr19 | 59128983  | 19616337 | 0.3318 | 1.8572  |
| chr20 | 63025520  | 3510832  | 0.0557 | 0.7138  |
| chr21 | 48129895  | 1265210  | 0.0263 | 0.5021  |
| chr22 | 51304566  | 1336892  | 0.0261 | 0.4898  |
| chrMT | 16571     | 195406   | 11.792 | 14.1664 |
| chrX  | 155270560 | 5049951  | 0.0325 | 0.5368  |
| chrY  | 59373566  | 663216   | 0.0112 | 0.2658  |

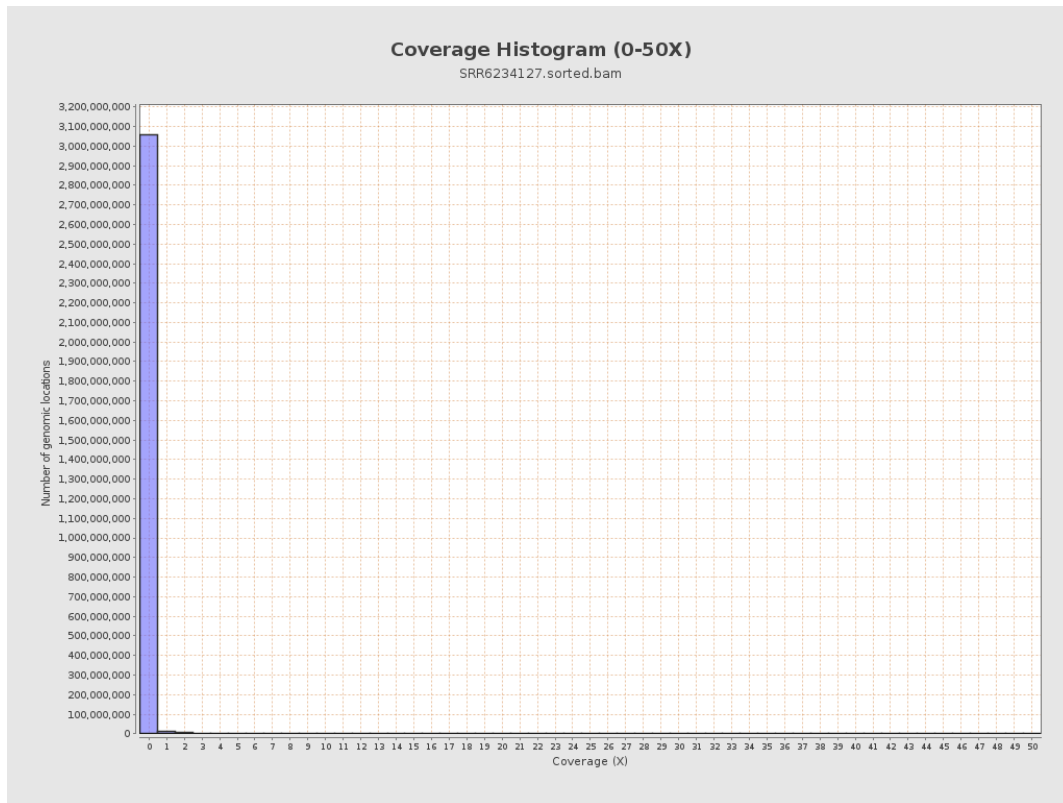
### 3. Results : Coverage across reference



## 4. Results : Coverage Histogram

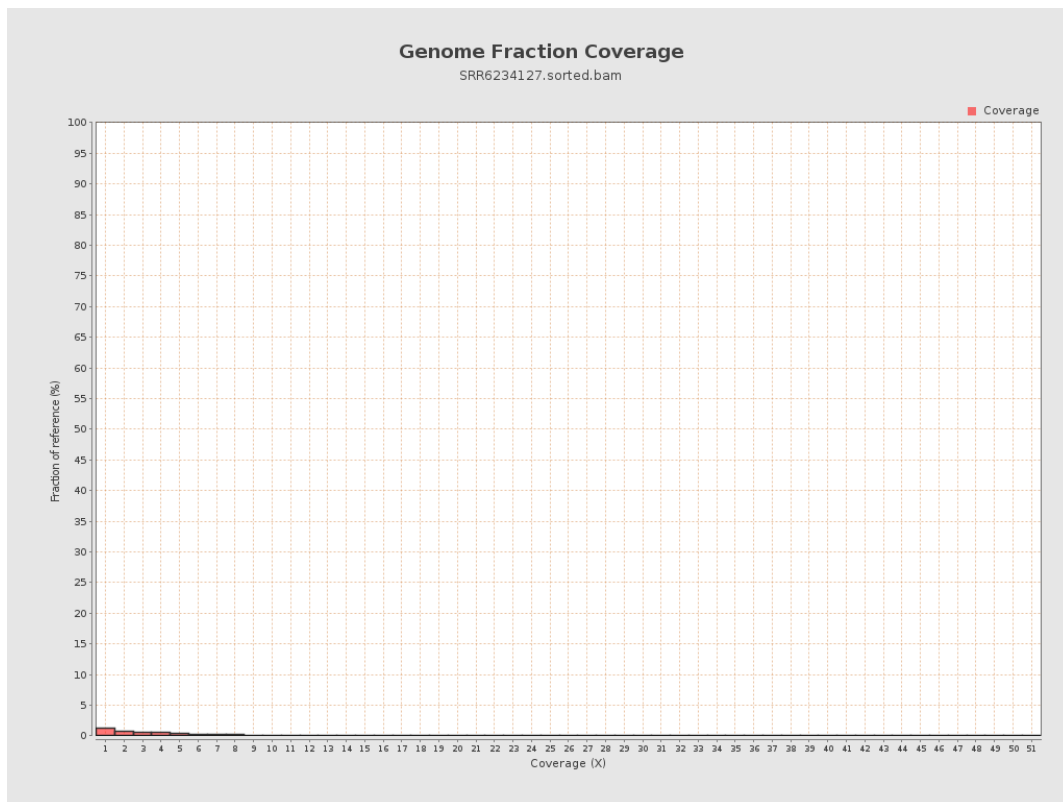


## 5. Results : Coverage Histogram (0-50X)

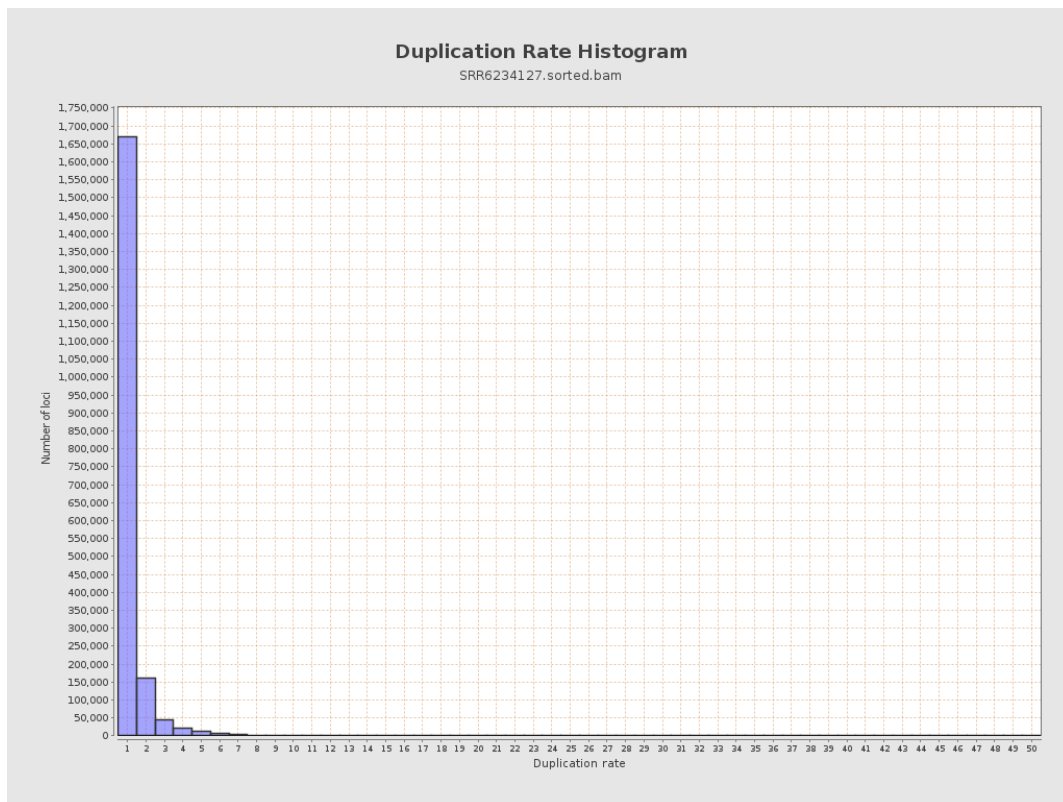




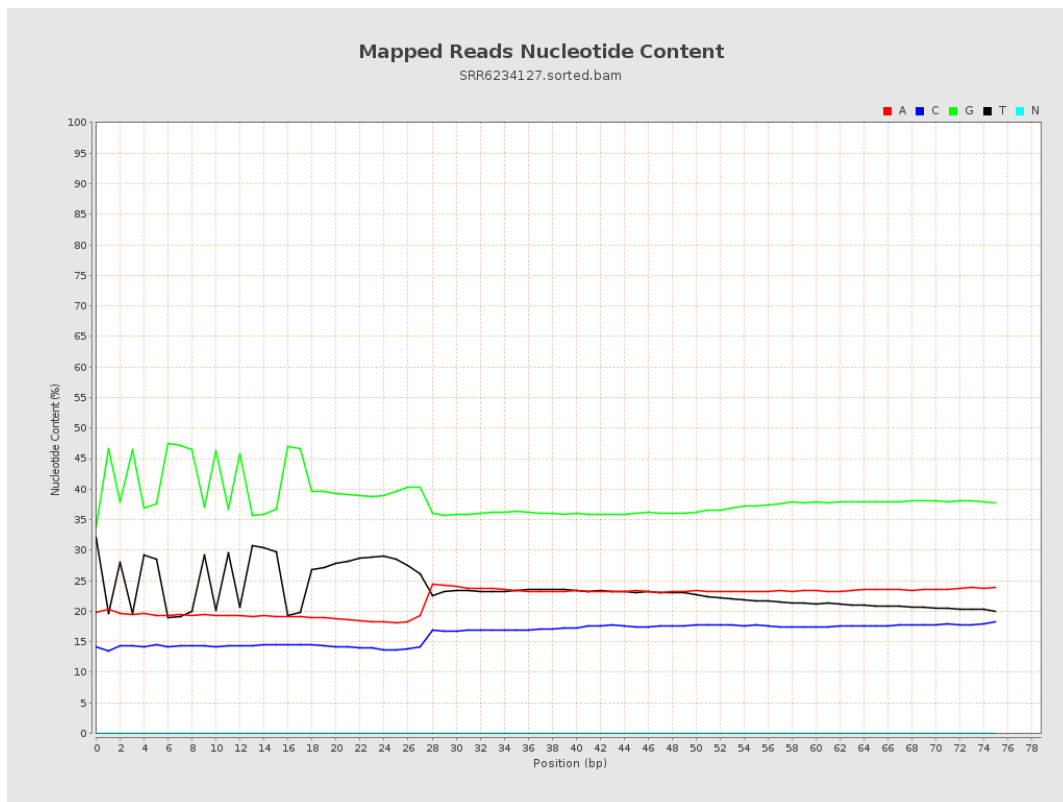
## 6. Results : Genome Fraction Coverage



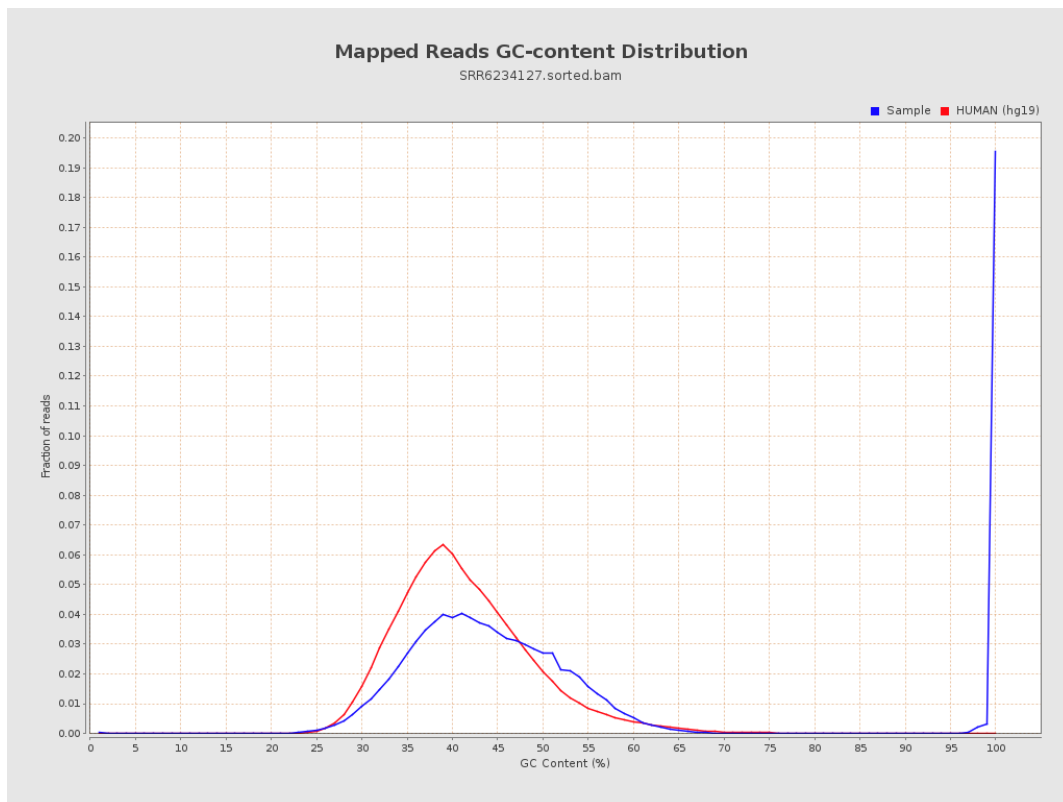
## 7. Results : Duplication Rate Histogram



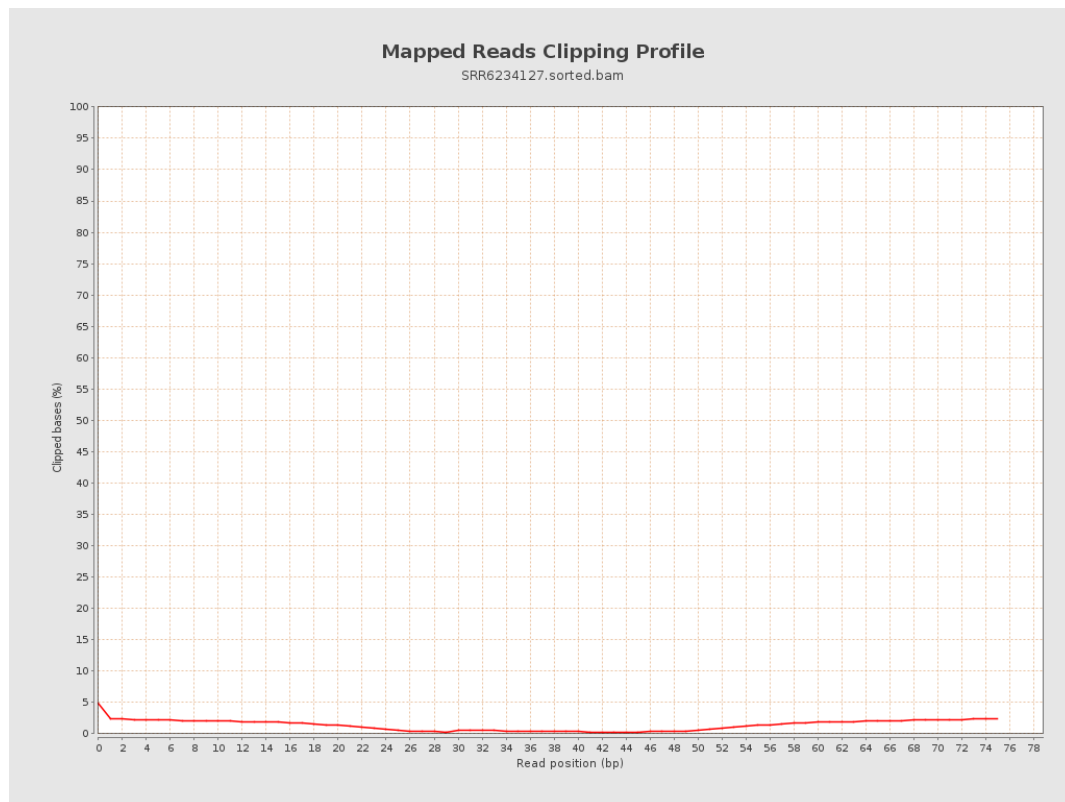
## 8. Results : Mapped Reads Nucleotide Content



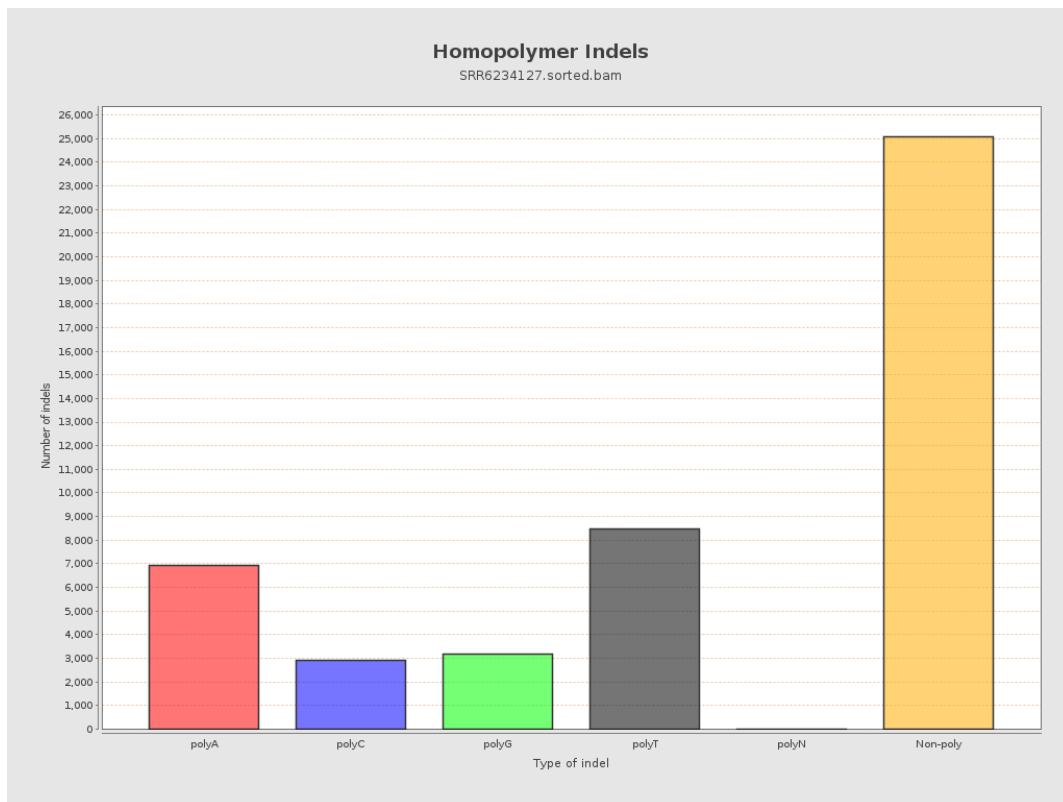
## 9. Results : Mapped Reads GC-content Distribution



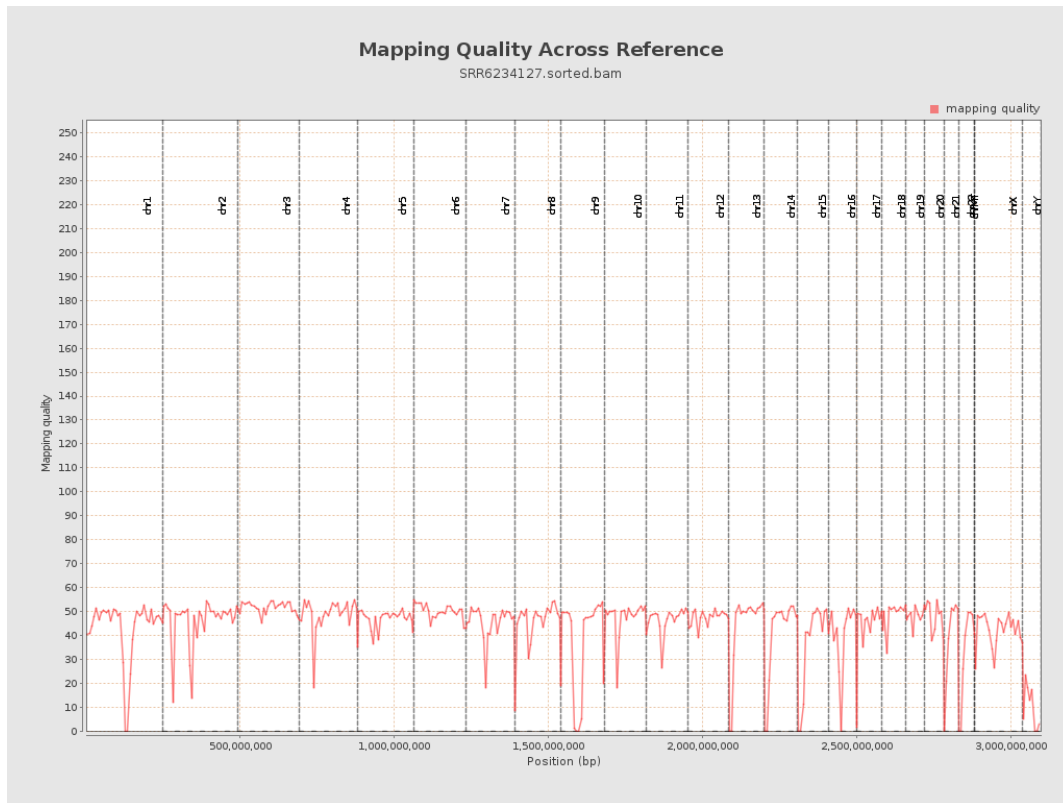
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

