

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 23:01:06*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819095.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_SRR1819095 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819095.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Fri Aug 23 23:01:04 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR1819095.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 2,861,182          |
| Mapped reads                 | 2,607,960 / 91.15% |
| Unmapped reads               | 253,222 / 8.85%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 10,435 / 0.36%     |
| Read min/max/mean length     | 30 / 76 / 76.12    |
| Duplicated reads (estimated) | 144,813 / 5.06%    |
| Duplication rate             | 4.15%              |
| Clipped reads                | 2,610,716 / 91.25% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 38,271,951 / 25.33% |
| Number/percentage of C's | 28,218,280 / 18.68% |
| Number/percentage of T's | 48,666,364 / 32.21% |
| Number/percentage of G's | 35,934,641 / 23.78% |
| Number/percentage of N's | 2,335 / 0%          |
| GC Percentage            | 42.46%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0488 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.4165 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 44.84 |
|----------------------|-------|

## 2.5. Mismatches and indels

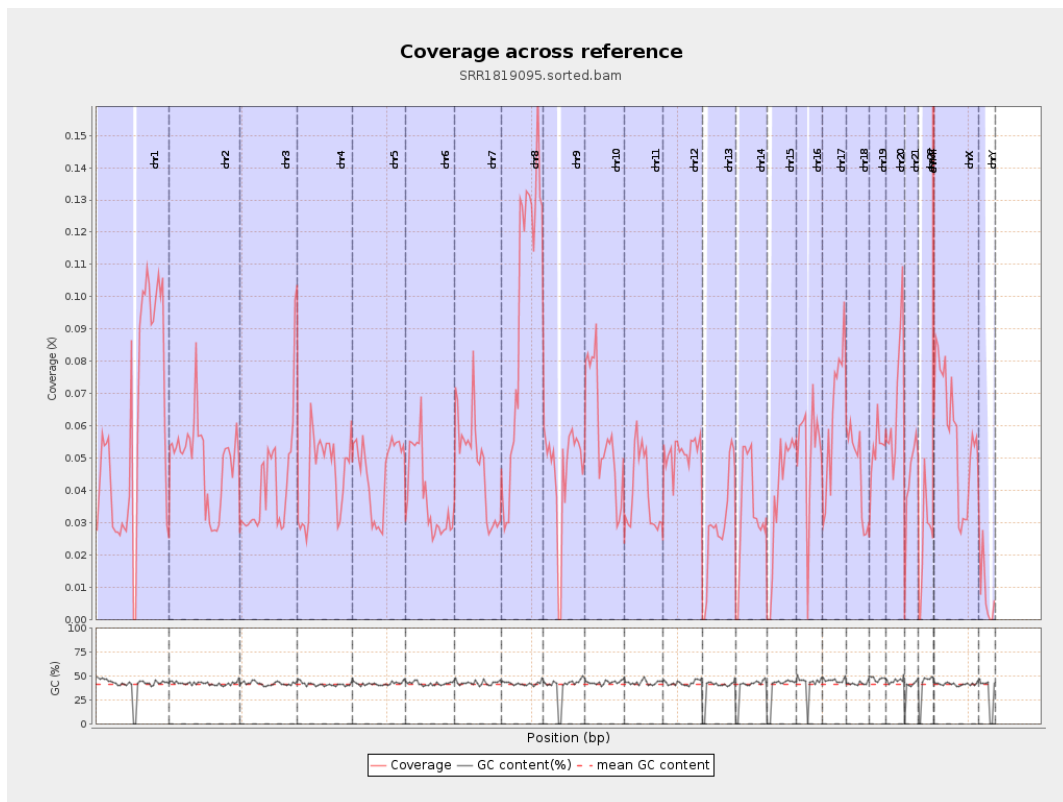
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 0.52%   |
| Mismatches                               | 770,668 |
| Insertions                               | 9,754   |
| Mapped reads with at least one insertion | 0.37%   |
| Deletions                                | 28,858  |
| Mapped reads with at least one deletion  | 1.1%    |
| Homopolymer indels                       | 42.49%  |

## 2.6. Chromosome stats

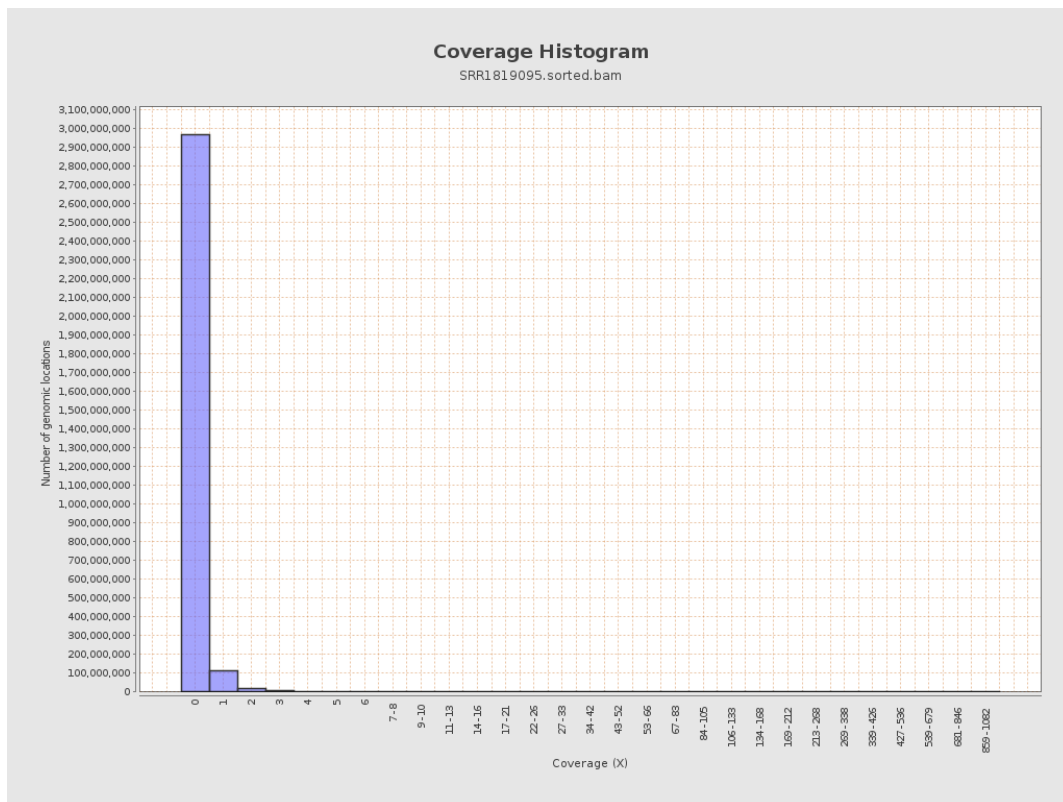
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 14789460     | 0.0593        | 0.8205             |
| chr2 | 243199373 | 11916704     | 0.049         | 0.4834             |
| chr3 | 198022430 | 8232275      | 0.0416        | 0.2399             |
| chr4 | 191154276 | 8590630      | 0.0449        | 0.2921             |
| chr5 | 180915260 | 8272925      | 0.0457        | 0.2468             |
| chr6 | 171115067 | 6481155      | 0.0379        | 0.3066             |
| chr7 | 159138663 | 7600893      | 0.0478        | 0.5397             |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr8  | 146364022 | 13901478 | 0.095  | 0.4338 |
| chr9  | 141213431 | 6438659  | 0.0456 | 0.3501 |
| chr10 | 135534747 | 7891621  | 0.0582 | 0.4216 |
| chr11 | 135006516 | 5263865  | 0.039  | 0.397  |
| chr12 | 133851895 | 6955479  | 0.052  | 0.2652 |
| chr13 | 115169878 | 3366122  | 0.0292 | 0.199  |
| chr14 | 107349540 | 3617687  | 0.0337 | 0.2195 |
| chr15 | 102531392 | 3969654  | 0.0387 | 0.2389 |
| chr16 | 90354753  | 4755333  | 0.0526 | 0.2918 |
| chr17 | 81195210  | 5235744  | 0.0645 | 0.3166 |
| chr18 | 78077248  | 3586651  | 0.0459 | 0.6385 |
| chr19 | 59128983  | 3120889  | 0.0528 | 0.5302 |
| chr20 | 63025520  | 4314424  | 0.0685 | 0.3085 |
| chr21 | 48129895  | 2093588  | 0.0435 | 0.2712 |
| chr22 | 51304566  | 1241521  | 0.0242 | 0.1784 |
| chrMT | 16571     | 105987   | 6.3959 | 4.2679 |
| chrX  | 155270560 | 8913673  | 0.0574 | 0.322  |
| chrY  | 59373566  | 484953   | 0.0082 | 0.2221 |

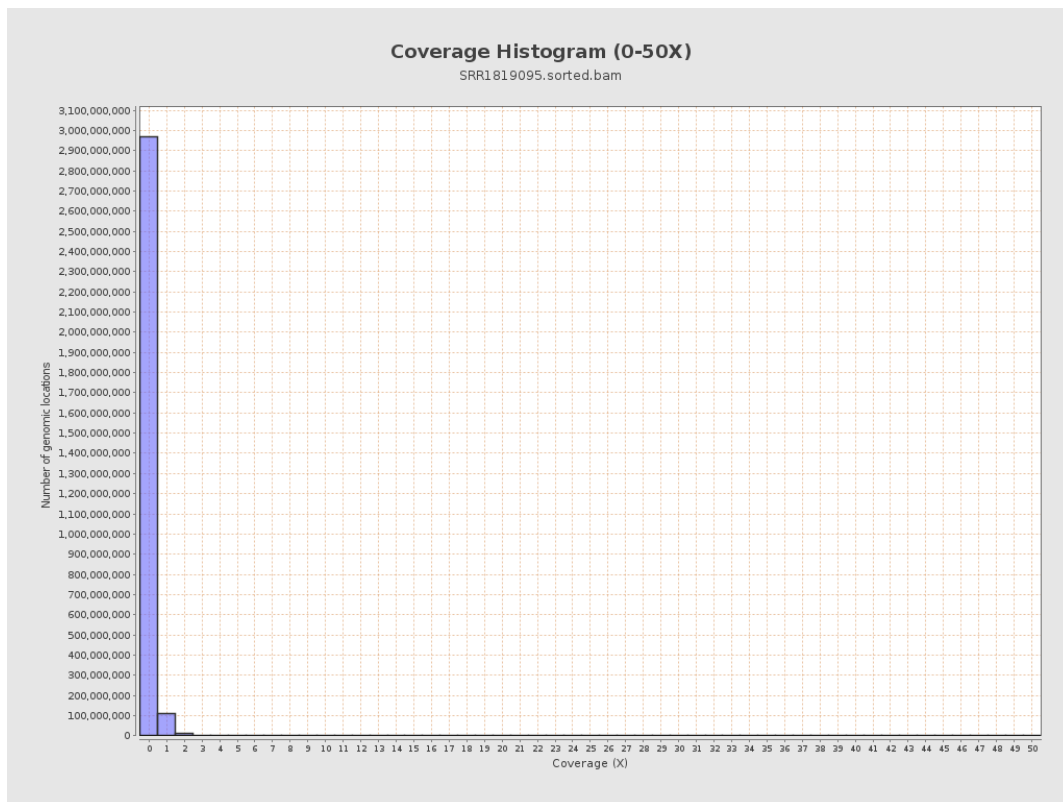
### 3. Results : Coverage across reference



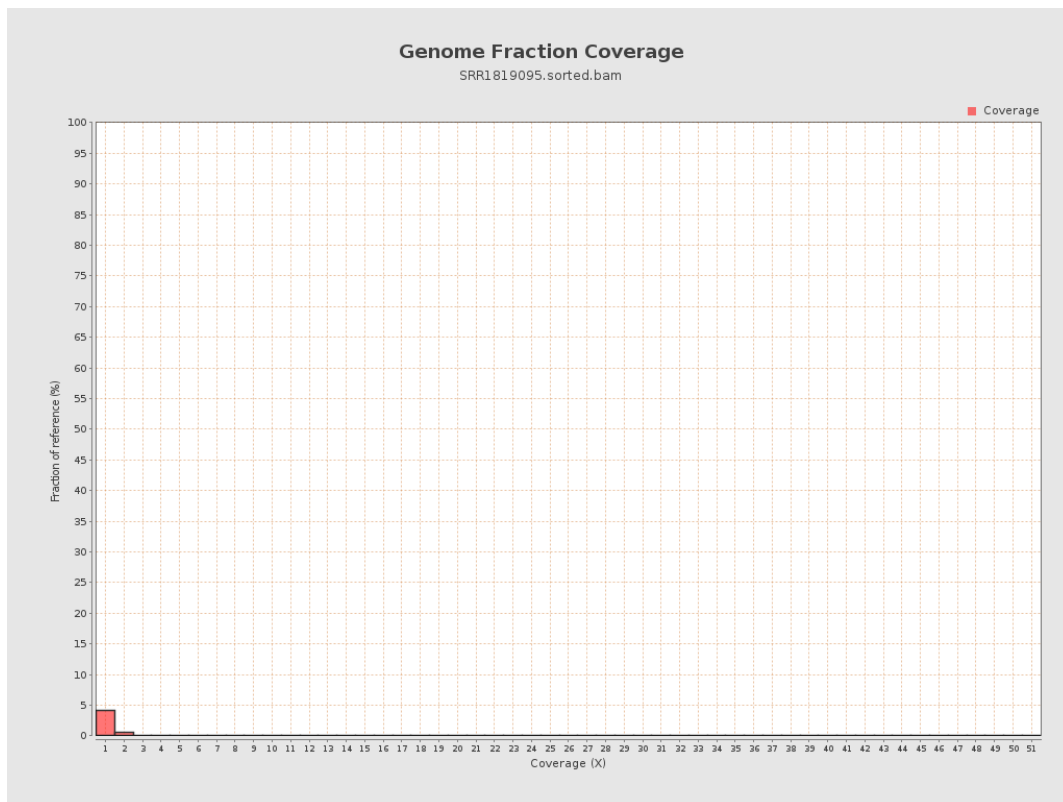
## 4. Results : Coverage Histogram



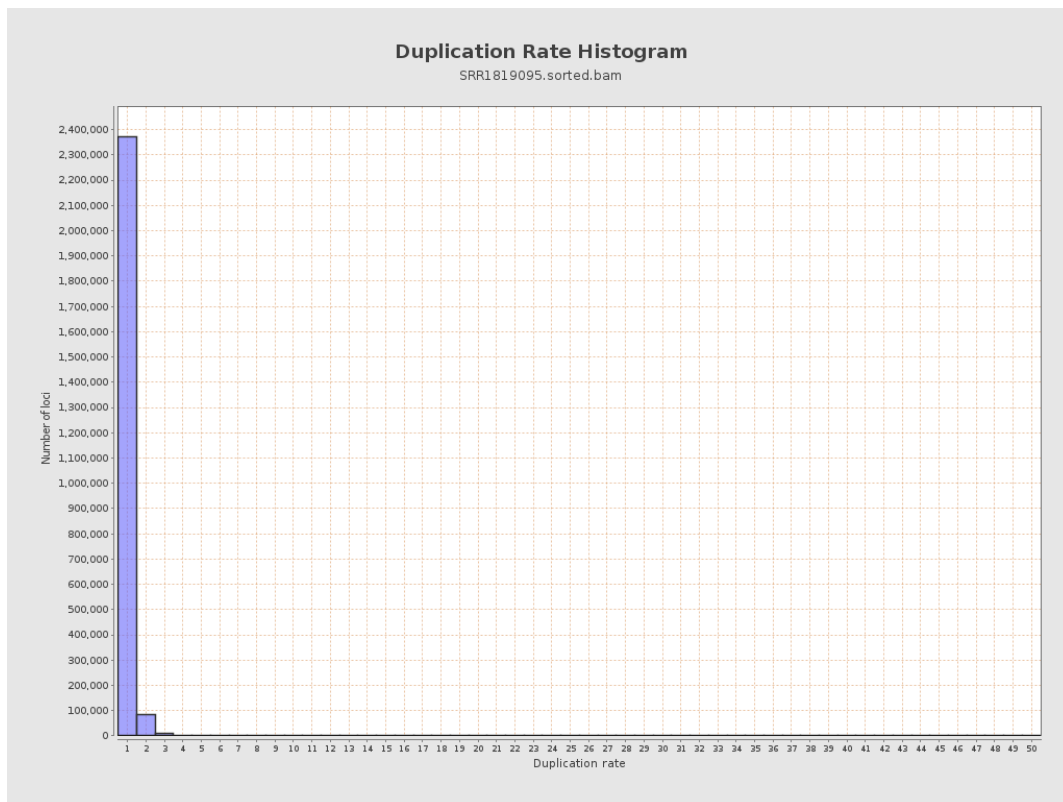
## 5. Results : Coverage Histogram (0-50X)



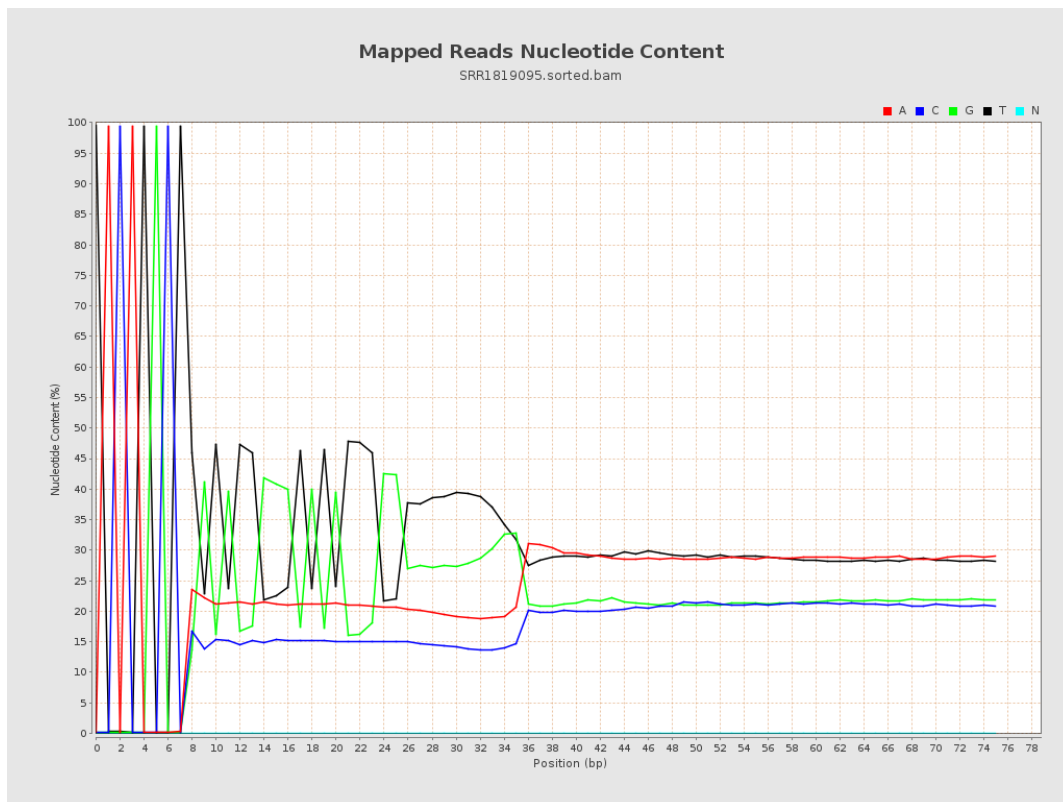
## 6. Results : Genome Fraction Coverage



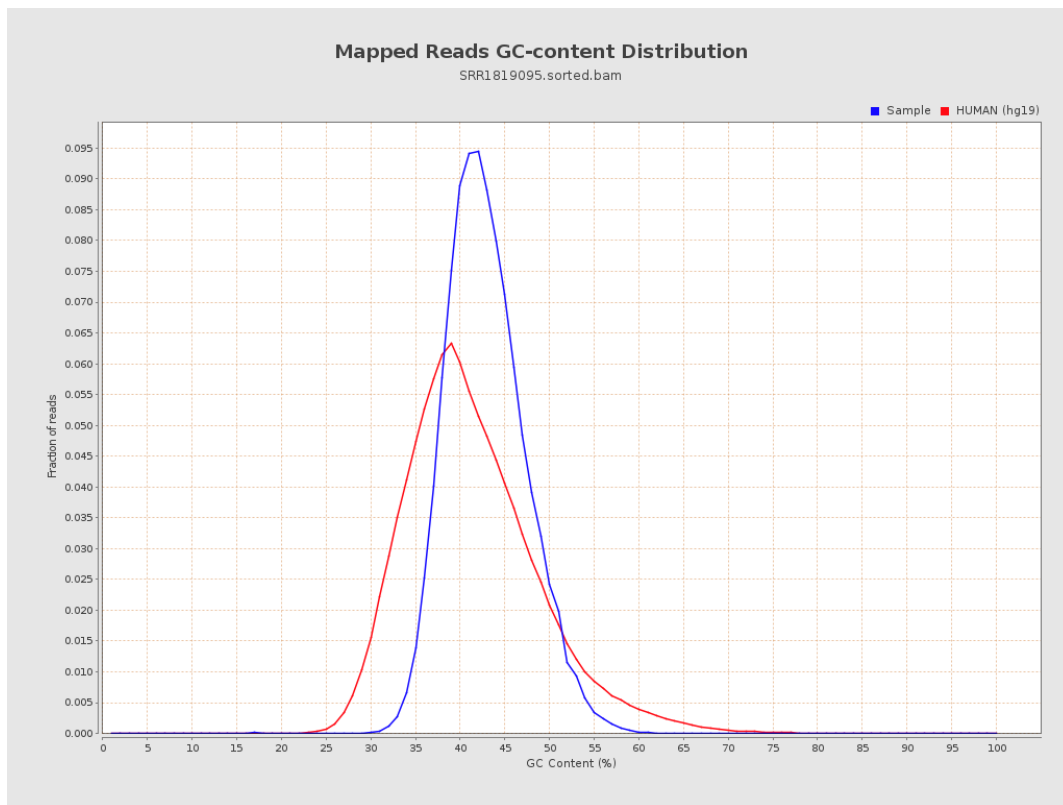
## 7. Results : Duplication Rate Histogram



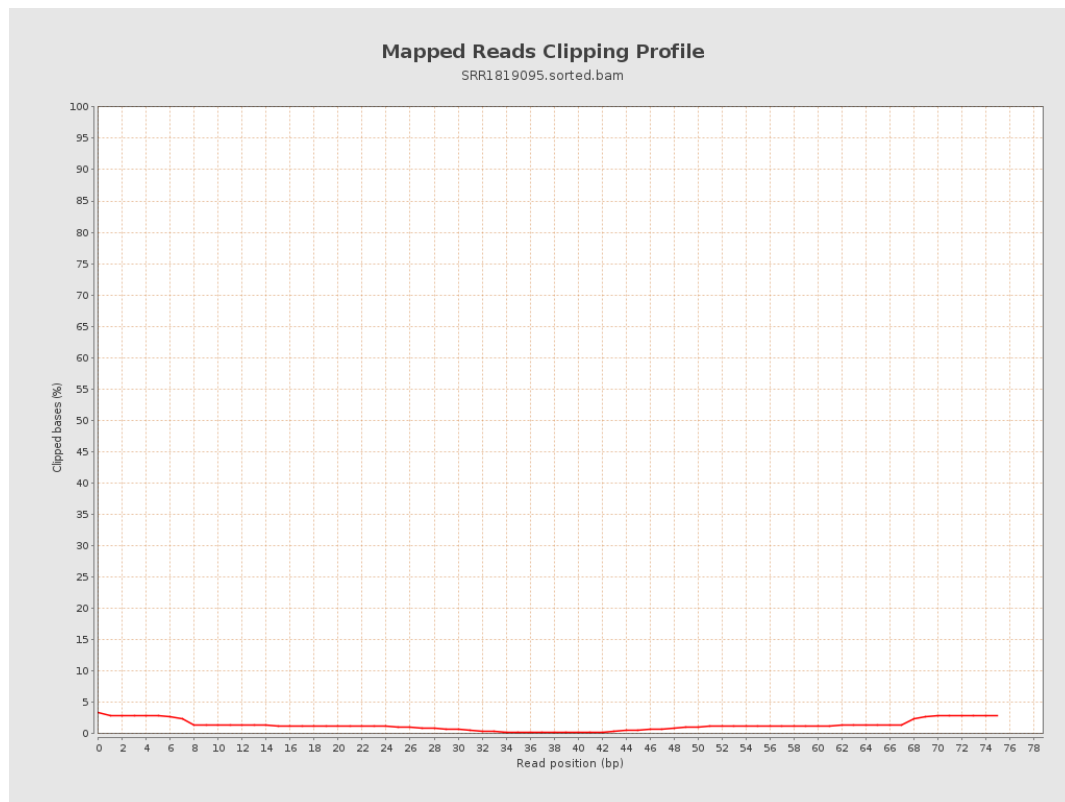
## 8. Results : Mapped Reads Nucleotide Content



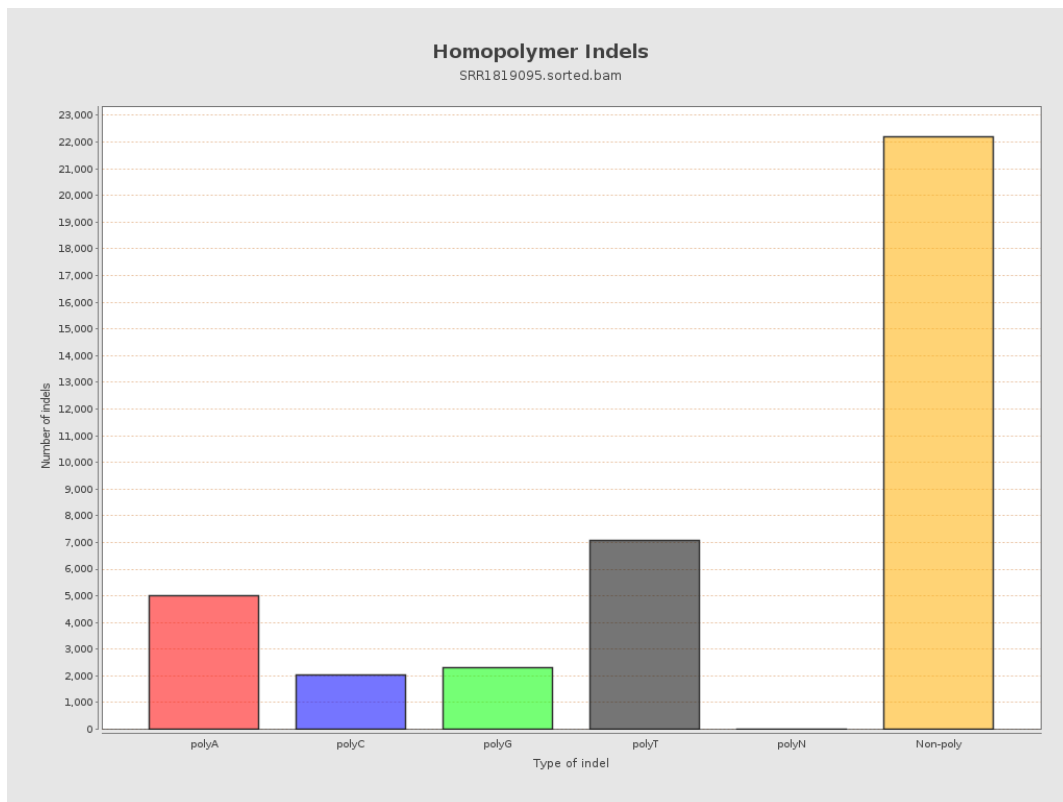
## 9. Results : Mapped Reads GC-content Distribution



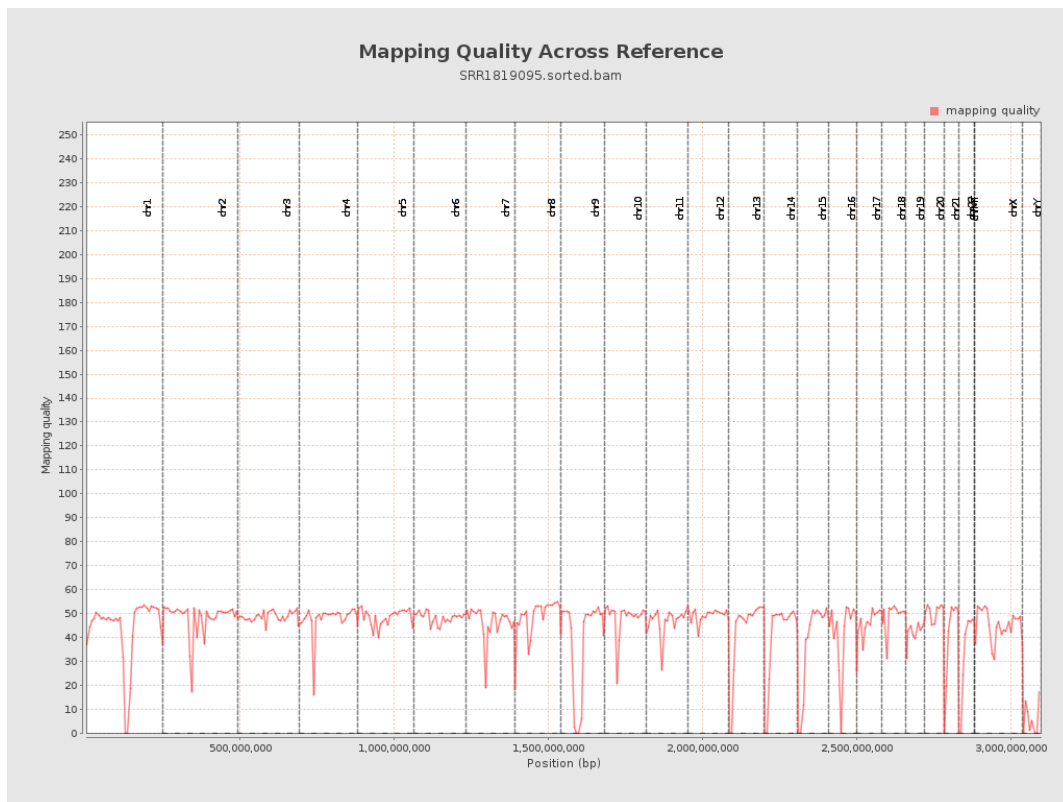
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

