

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/06/25 06:24:44*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR504737.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_SRR504737 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504737.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                        |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                         |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                         |
| Analysis date:                        | Sat Jun 25 06:24:44 CST 2022                                                                                                                                                               |
| Size of a homopolymer:                | 3                                                                                                                                                                                          |
| Skip duplicate alignments:            | no                                                                                                                                                                                         |
| Number of windows:                    | 400                                                                                                                                                                                        |
| BAM file:                             | SRR504737.sorted.bam                                                                                                                                                                       |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 2,138,983          |
| Mapped reads                 | 1,905,457 / 89.08% |
| Unmapped reads               | 233,526 / 10.92%   |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Read min/max/mean length     | 32 / 32 / 32       |
| Duplicated reads (estimated) | 167,394 / 7.83%    |
| Duplication rate             | 4.92%              |
| Clipped reads                | 3,035 / 0.14%      |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 17,543,354 / 28.77% |
| Number/percentage of C's | 12,307,442 / 20.19% |
| Number/percentage of T's | 18,684,587 / 30.65% |
| Number/percentage of G's | 12,433,056 / 20.39% |
| Number/percentage of N's | 115 / 0%            |
| GC Percentage            | 40.58%              |

### 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.0197 |
| Standard Deviation | 0.5032 |

## 2.4. Mapping Quality

|                      |      |
|----------------------|------|
| Mean Mapping Quality | 8.12 |
|----------------------|------|

## 2.5. Mismatches and indels

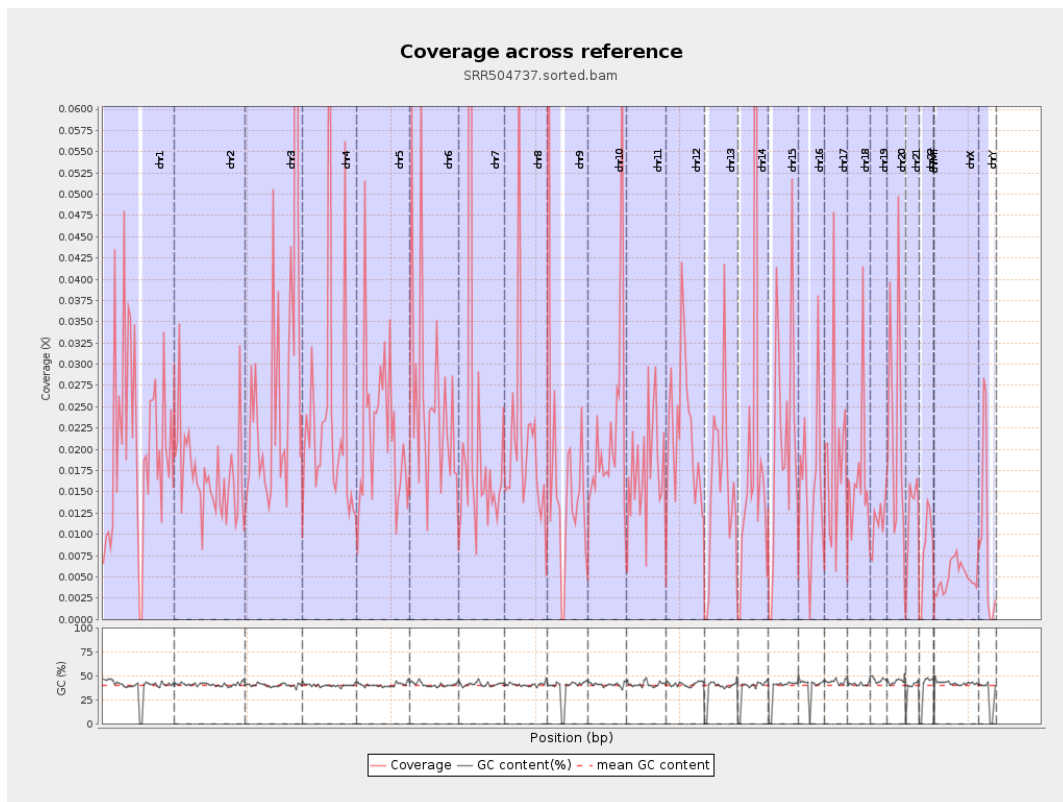
|                    |        |
|--------------------|--------|
| General error rate | 0.05%  |
| Mismatches         | 31,131 |

## 2.6. Chromosome stats

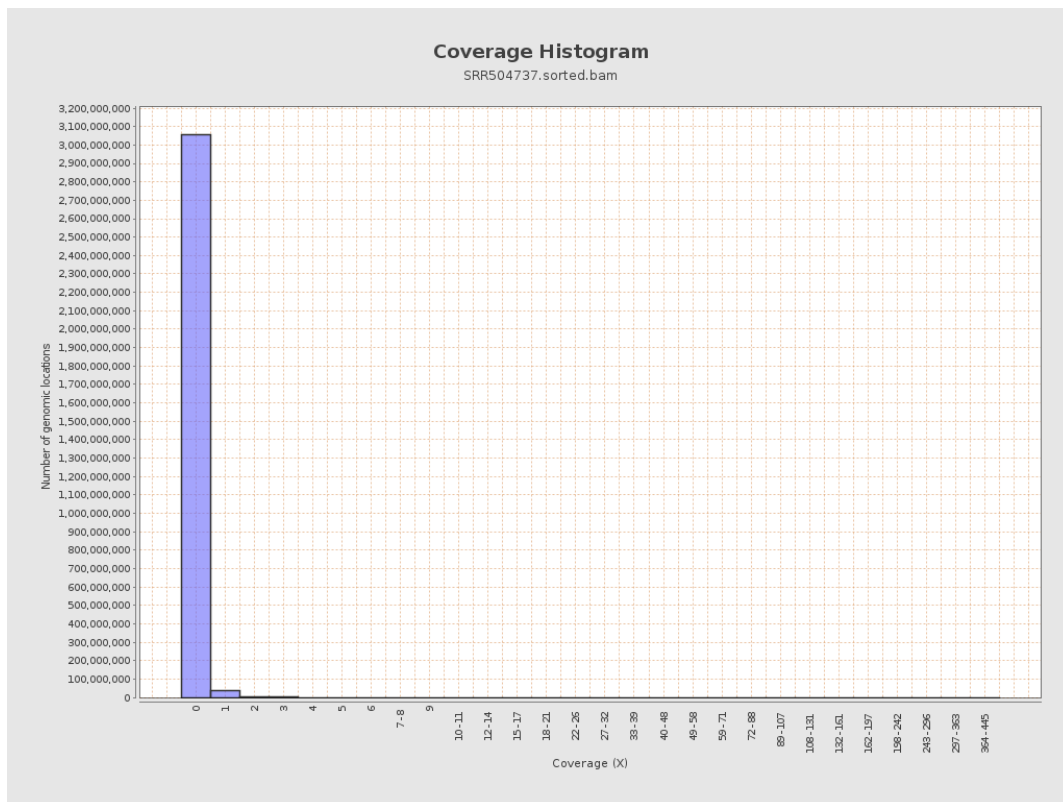
| Name  | Length    | Mapped bases | Mean coverage | Standard deviation |
|-------|-----------|--------------|---------------|--------------------|
| chr1  | 249250621 | 5078074      | 0.0204        | 0.2255             |
| chr2  | 243199373 | 4143884      | 0.017         | 0.1772             |
| chr3  | 198022430 | 6052200      | 0.0306        | 1.1253             |
| chr4  | 191154276 | 4565004      | 0.0239        | 0.413              |
| chr5  | 180915260 | 4030074      | 0.0223        | 0.2598             |
| chr6  | 171115067 | 4363588      | 0.0255        | 0.3746             |
| chr7  | 159138663 | 3865944      | 0.0243        | 1.2739             |
| chr8  | 146364022 | 3004912      | 0.0205        | 0.4646             |
| chr9  | 141213431 | 2752256      | 0.0195        | 0.43               |
| chr10 | 135534747 | 2855910      | 0.0211        | 0.4039             |
| chr11 | 135006516 | 2434564      | 0.018         | 0.1905             |
| chr12 | 133851895 | 2941938      | 0.022         | 0.2438             |
| chr13 | 115169878 | 1804394      | 0.0157        | 0.2461             |
| chr14 | 107349540 | 2182500      | 0.0203        | 0.6169             |
| chr15 | 102531392 | 2140732      | 0.0209        | 0.301              |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr16 | 90354753  | 1386546 | 0.0153 | 0.1751 |
| chr17 | 81195210  | 1546806 | 0.0191 | 0.4703 |
| chr18 | 78077248  | 1343102 | 0.0172 | 0.2149 |
| chr19 | 59128983  | 689714  | 0.0117 | 0.1291 |
| chr20 | 63025520  | 1391814 | 0.0221 | 0.2763 |
| chr21 | 48129895  | 601488  | 0.0125 | 0.1339 |
| chr22 | 51304566  | 420494  | 0.0082 | 0.2308 |
| chrMT | 16571     | 0       | 0      | 0      |
| chrX  | 155270560 | 793830  | 0.0051 | 0.0828 |
| chrY  | 59373566  | 578786  | 0.0097 | 0.135  |

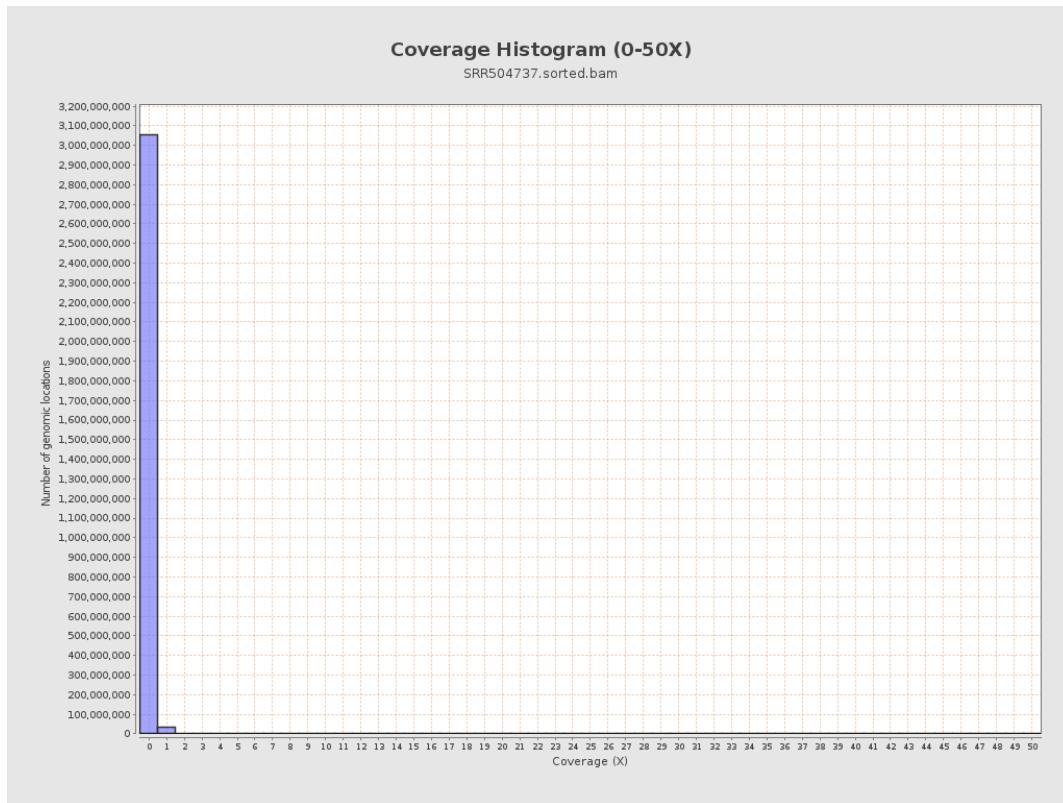
### 3. Results : Coverage across reference



## 4. Results : Coverage Histogram

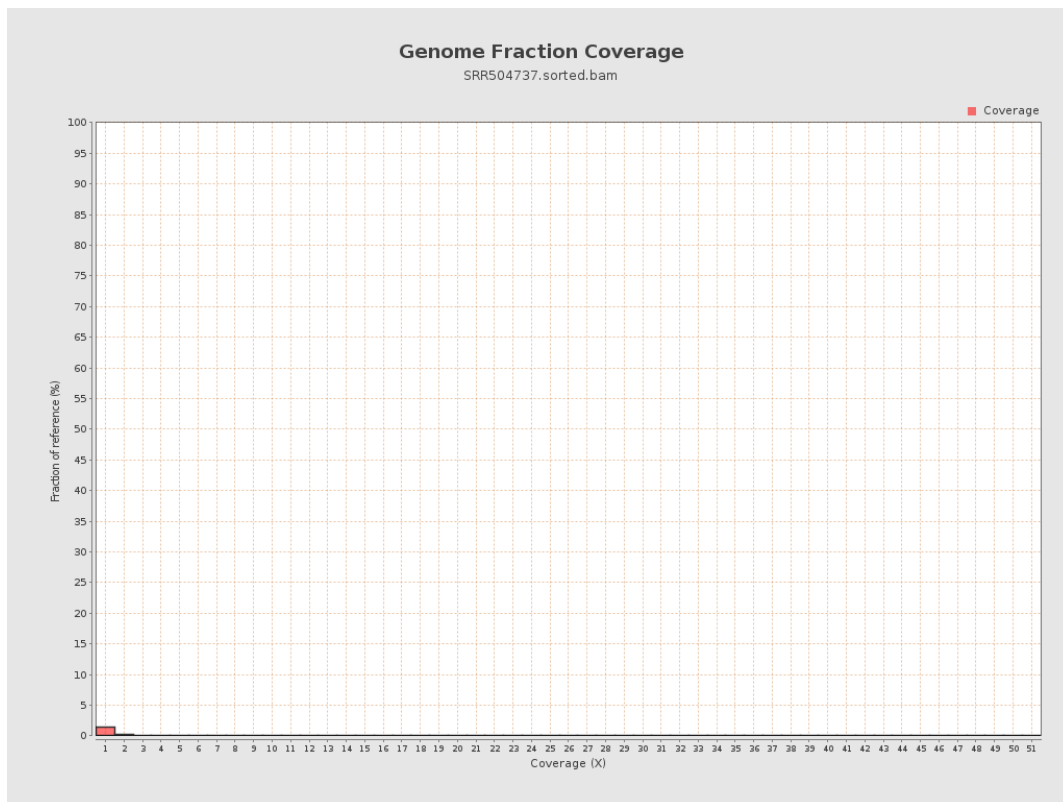


## 5. Results : Coverage Histogram (0-50X)

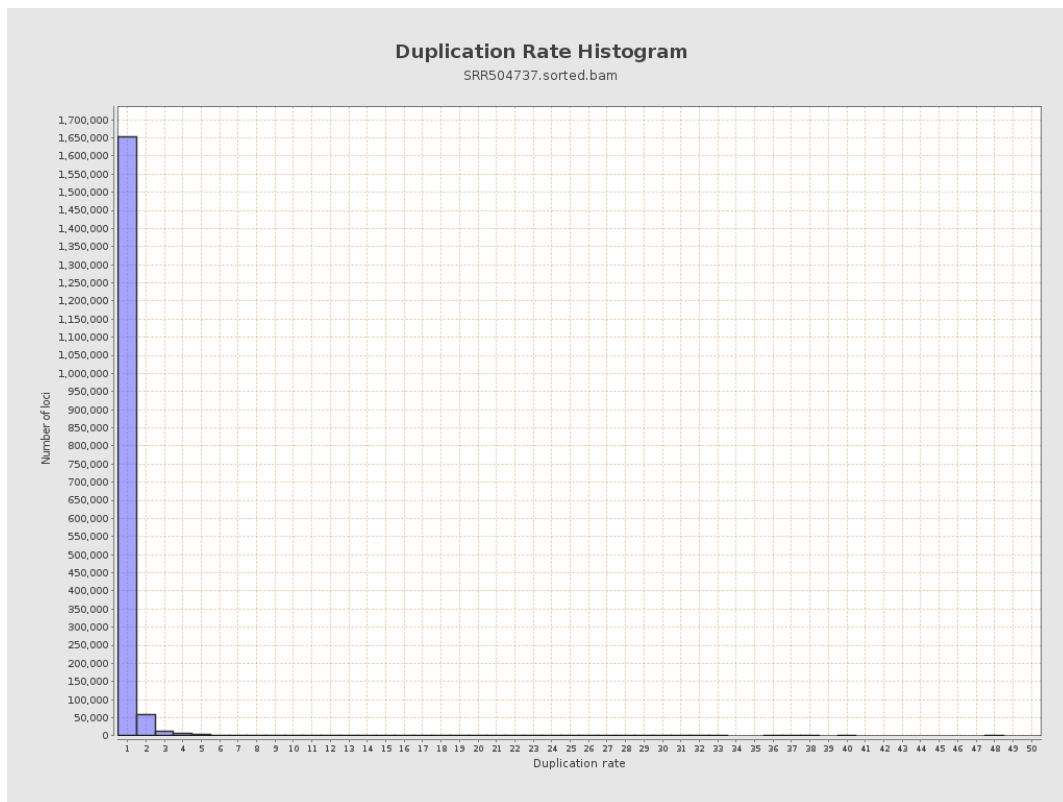




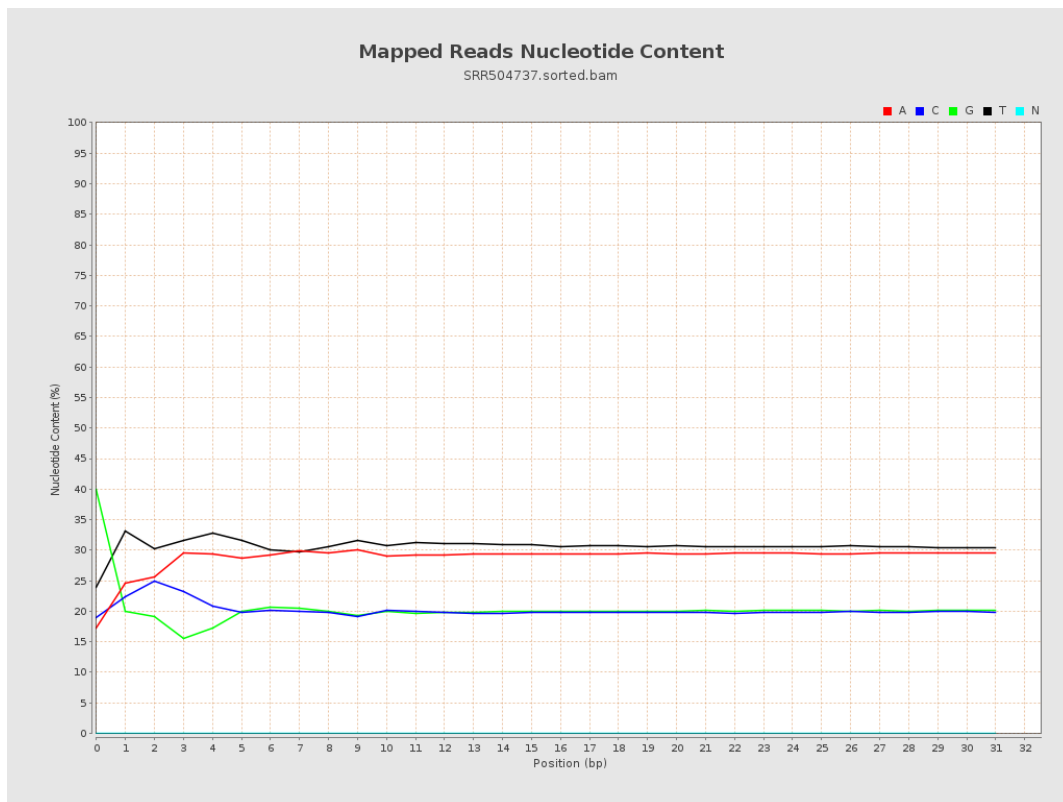
## 6. Results : Genome Fraction Coverage



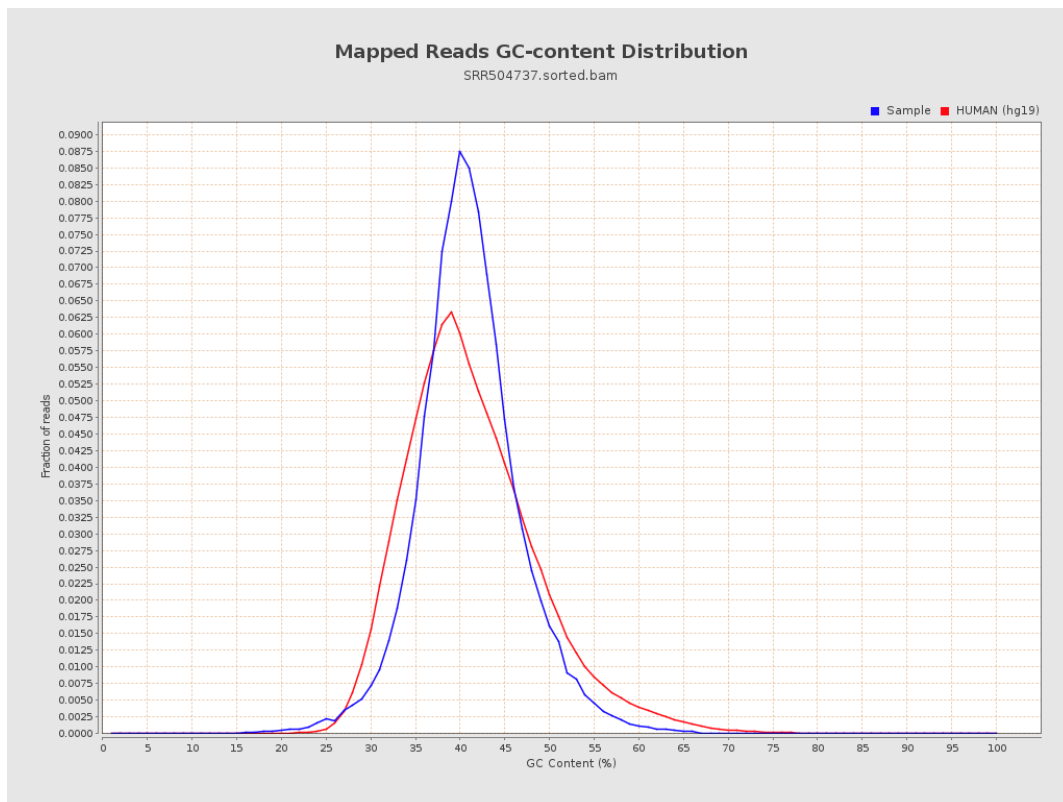
## 7. Results : Duplication Rate Histogram



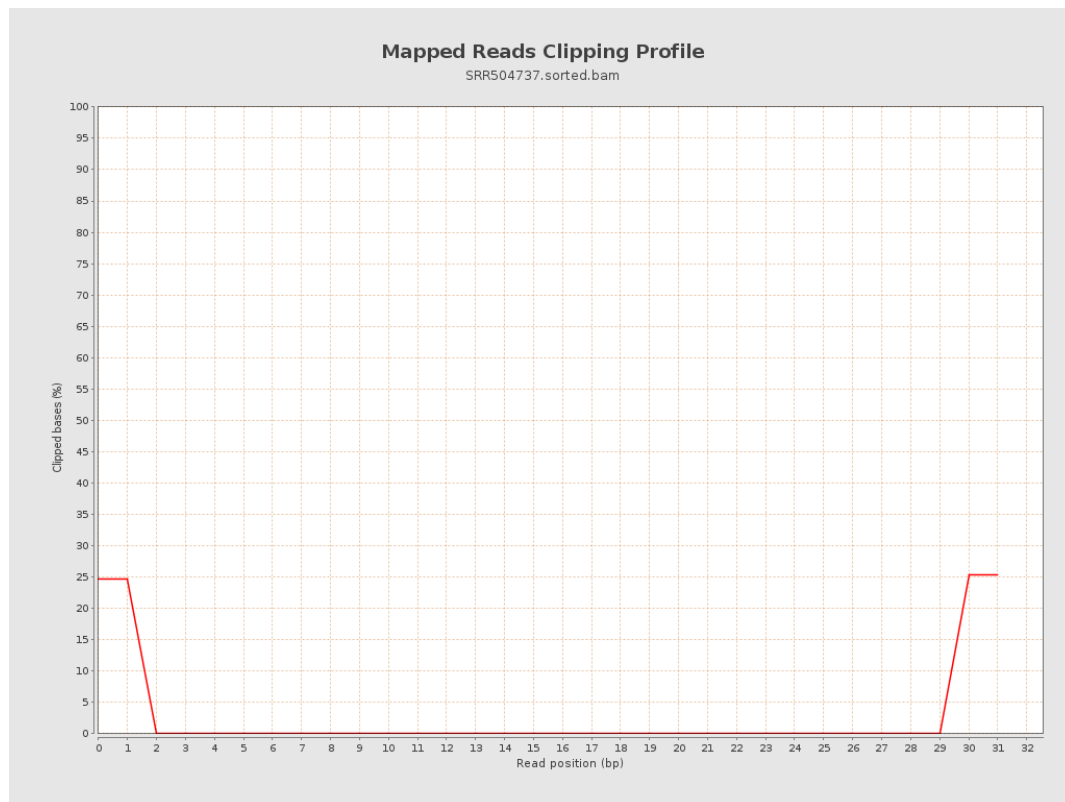
## 8. Results : Mapped Reads Nucleotide Content



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



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Mapping Quality Across Reference



## 12. Results : Mapping Quality Histogram

