

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/06/23 13:44:16*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR504420.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_SRR504420 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504420.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                        |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                         |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                         |
| Analysis date:                        | Thu Jun 23 13:44:15 CST 2022                                                                                                                                                               |
| Size of a homopolymer:                | 3                                                                                                                                                                                          |
| Skip duplicate alignments:            | no                                                                                                                                                                                         |
| Number of windows:                    | 400                                                                                                                                                                                        |
| BAM file:                             | SRR504420.sorted.bam                                                                                                                                                                       |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 2,164,713          |
| Mapped reads                 | 1,892,118 / 87.41% |
| Unmapped reads               | 272,595 / 12.59%   |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Read min/max/mean length     | 32 / 32 / 32       |
| Duplicated reads (estimated) | 175,591 / 8.11%    |
| Duplication rate             | 3.28%              |
| Clipped reads                | 3,210 / 0.15%      |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 17,295,398 / 28.57% |
| Number/percentage of C's | 12,267,947 / 20.26% |
| Number/percentage of T's | 18,607,755 / 30.74% |
| Number/percentage of G's | 12,370,118 / 20.43% |
| Number/percentage of N's | 138 / 0%            |
| GC Percentage            | 40.7%               |

### 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.0196 |
| Standard Deviation | 0.7203 |

## 2.4. Mapping Quality

|                      |      |
|----------------------|------|
| Mean Mapping Quality | 8.52 |
|----------------------|------|

## 2.5. Mismatches and indels

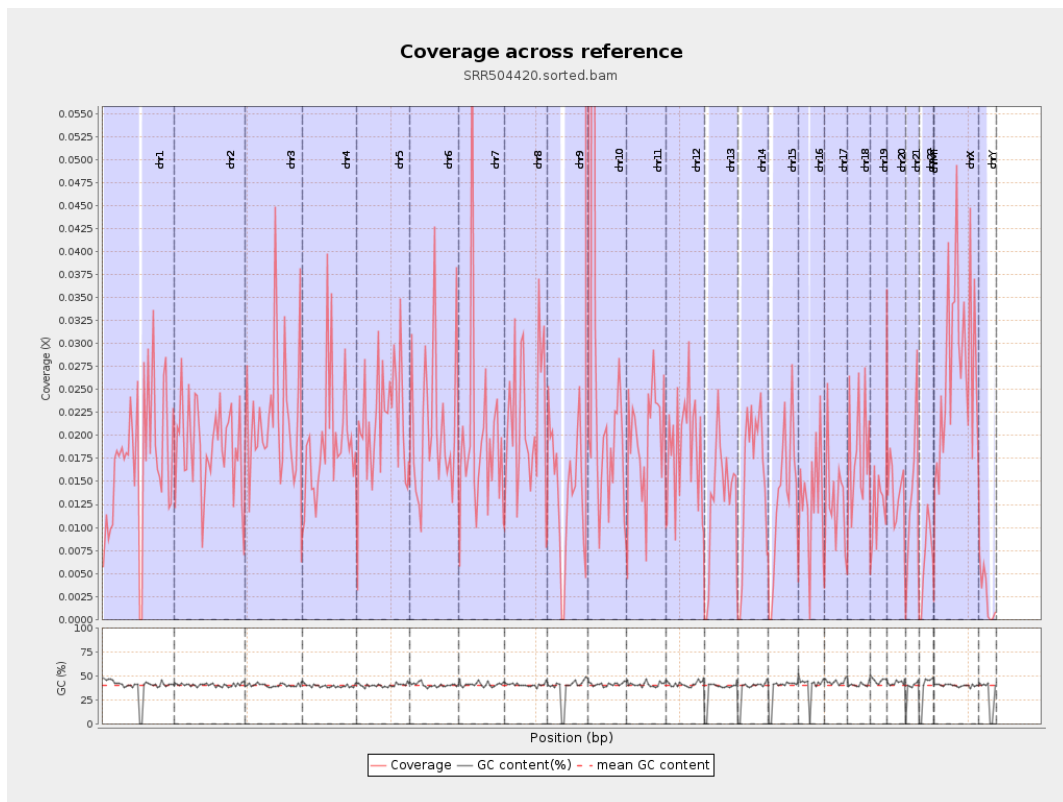
|                    |        |
|--------------------|--------|
| General error rate | 0.05%  |
| Mismatches         | 31,805 |

## 2.6. Chromosome stats

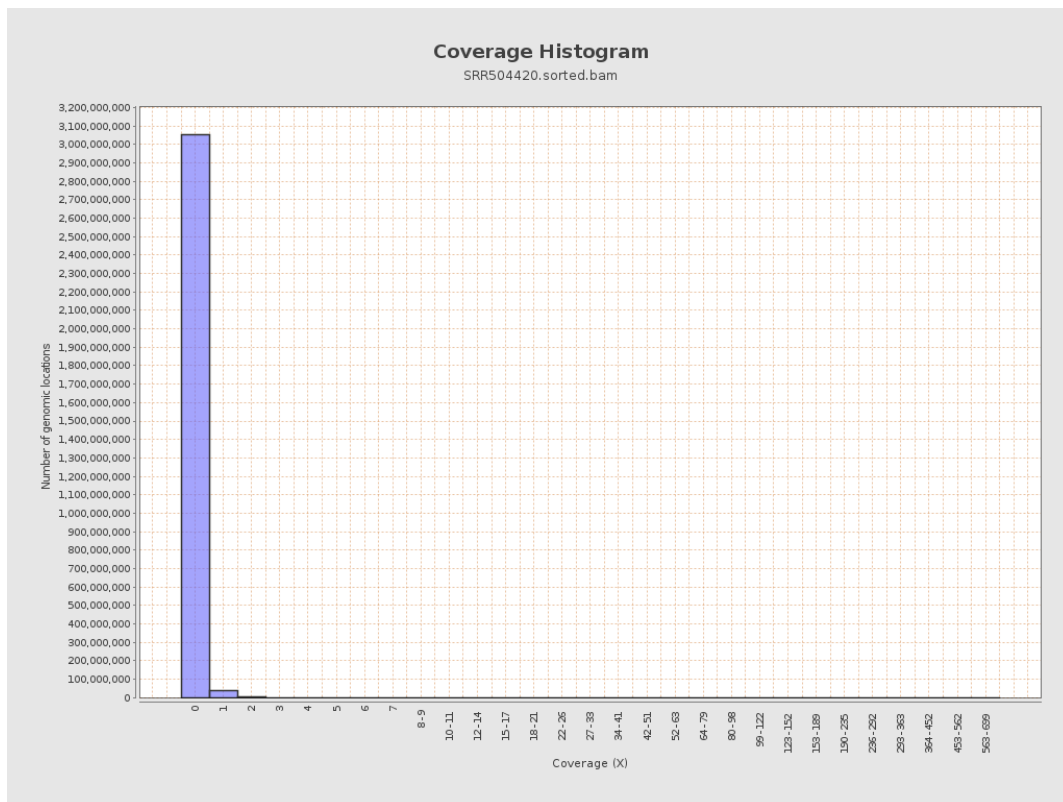
| Name  | Length    | Mapped bases | Mean coverage | Standard deviation |
|-------|-----------|--------------|---------------|--------------------|
| chr1  | 249250621 | 4295810      | 0.0172        | 0.1815             |
| chr2  | 243199373 | 4546766      | 0.0187        | 0.1692             |
| chr3  | 198022430 | 4369264      | 0.0221        | 0.2158             |
| chr4  | 191154276 | 3667768      | 0.0192        | 0.2026             |
| chr5  | 180915260 | 3974992      | 0.022         | 0.2026             |
| chr6  | 171115067 | 3537426      | 0.0207        | 0.2168             |
| chr7  | 159138663 | 3129016      | 0.0197        | 0.6943             |
| chr8  | 146364022 | 3174182      | 0.0217        | 0.2255             |
| chr9  | 141213431 | 5461964      | 0.0387        | 2.9891             |
| chr10 | 135534747 | 3913486      | 0.0289        | 1.1258             |
| chr11 | 135006516 | 2712376      | 0.0201        | 0.1877             |
| chr12 | 133851895 | 2500432      | 0.0187        | 0.1695             |
| chr13 | 115169878 | 1534042      | 0.0133        | 0.1428             |
| chr14 | 107349540 | 1644478      | 0.0153        | 0.1618             |
| chr15 | 102531392 | 1367018      | 0.0133        | 0.1446             |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr16 | 90354753  | 1151494 | 0.0127 | 0.1338 |
| chr17 | 81195210  | 1048126 | 0.0129 | 0.1369 |
| chr18 | 78077248  | 1458182 | 0.0187 | 0.1965 |
| chr19 | 59128983  | 755008  | 0.0128 | 0.1552 |
| chr20 | 63025520  | 873322  | 0.0139 | 0.1511 |
| chr21 | 48129895  | 640454  | 0.0133 | 0.1619 |
| chr22 | 51304566  | 338022  | 0.0066 | 0.096  |
| chrMT | 16571     | 32      | 0.0019 | 0.0439 |
| chrX  | 155270560 | 4295530 | 0.0277 | 0.2965 |
| chrY  | 59373566  | 152166  | 0.0026 | 0.0554 |

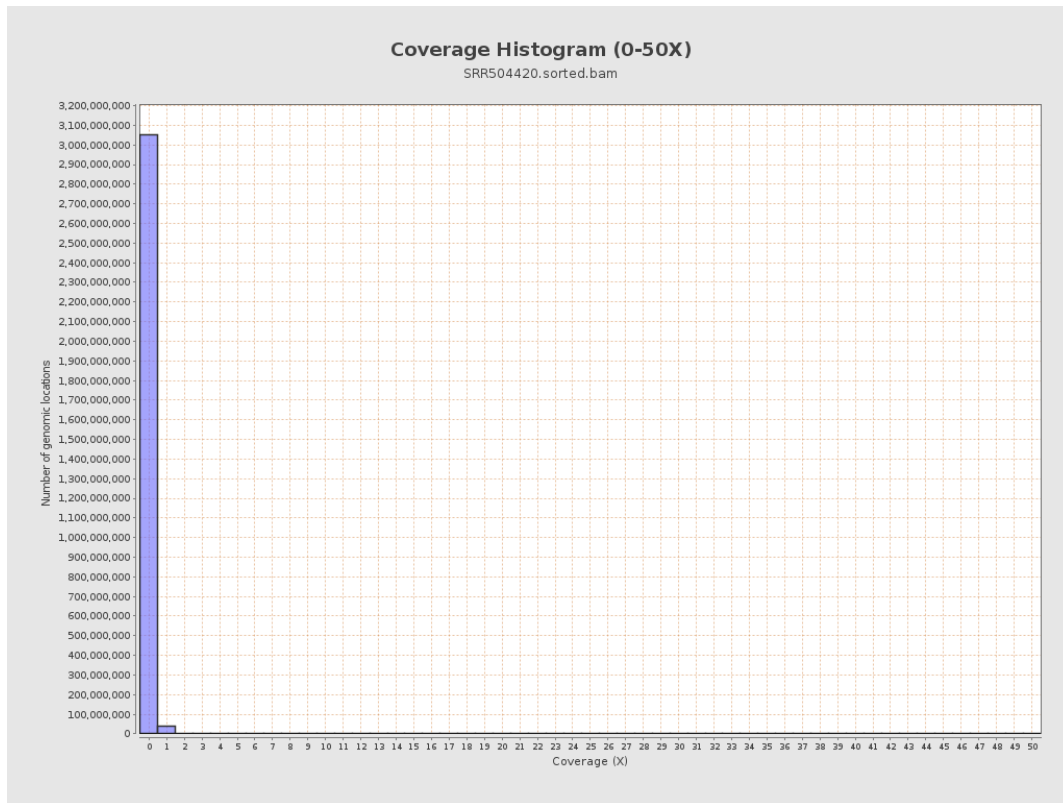
### 3. Results : Coverage across reference



## 4. Results : Coverage Histogram

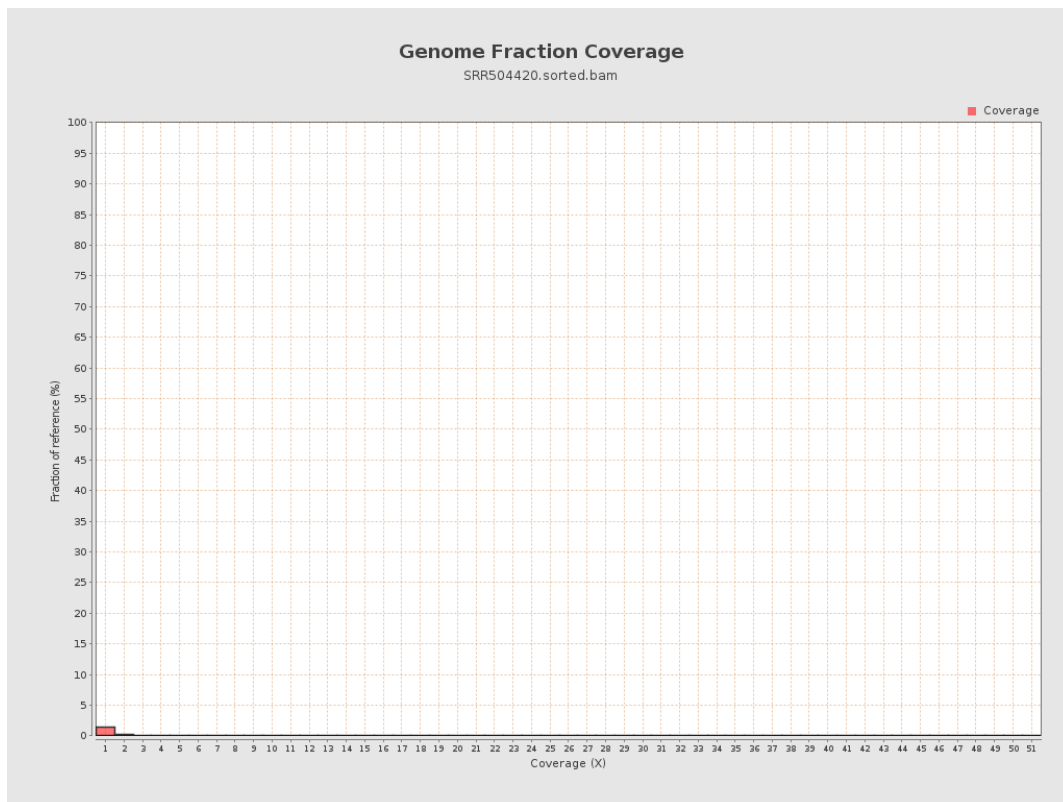


## 5. Results : Coverage Histogram (0-50X)

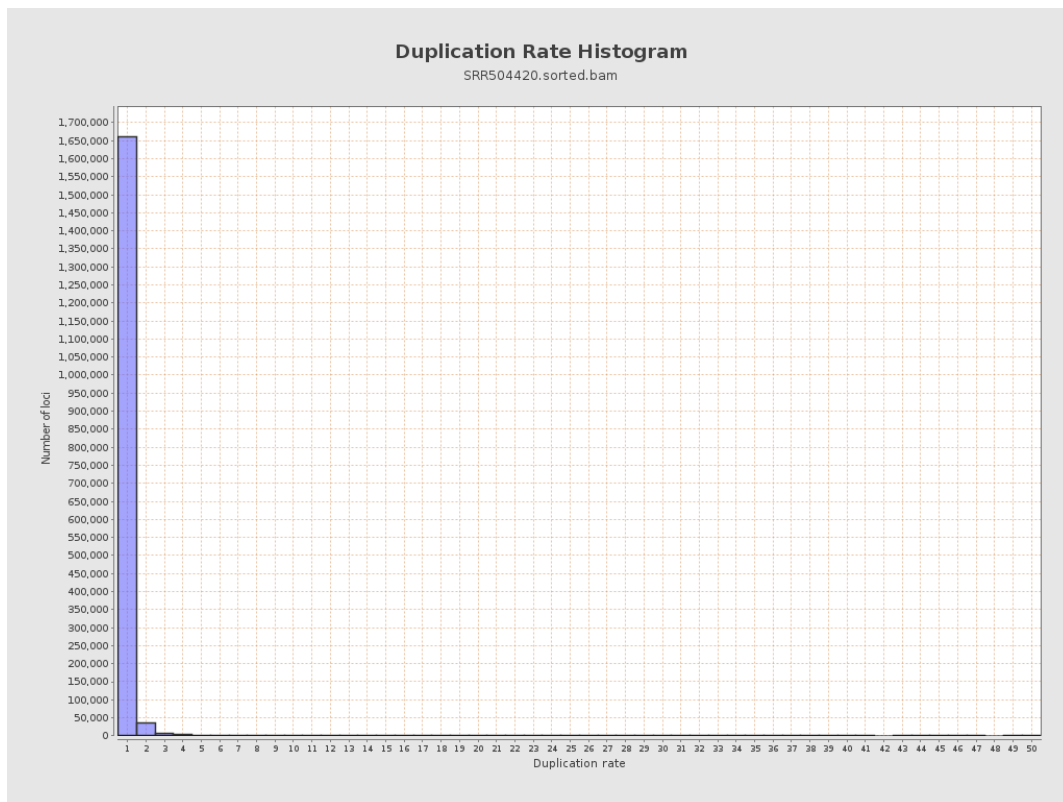




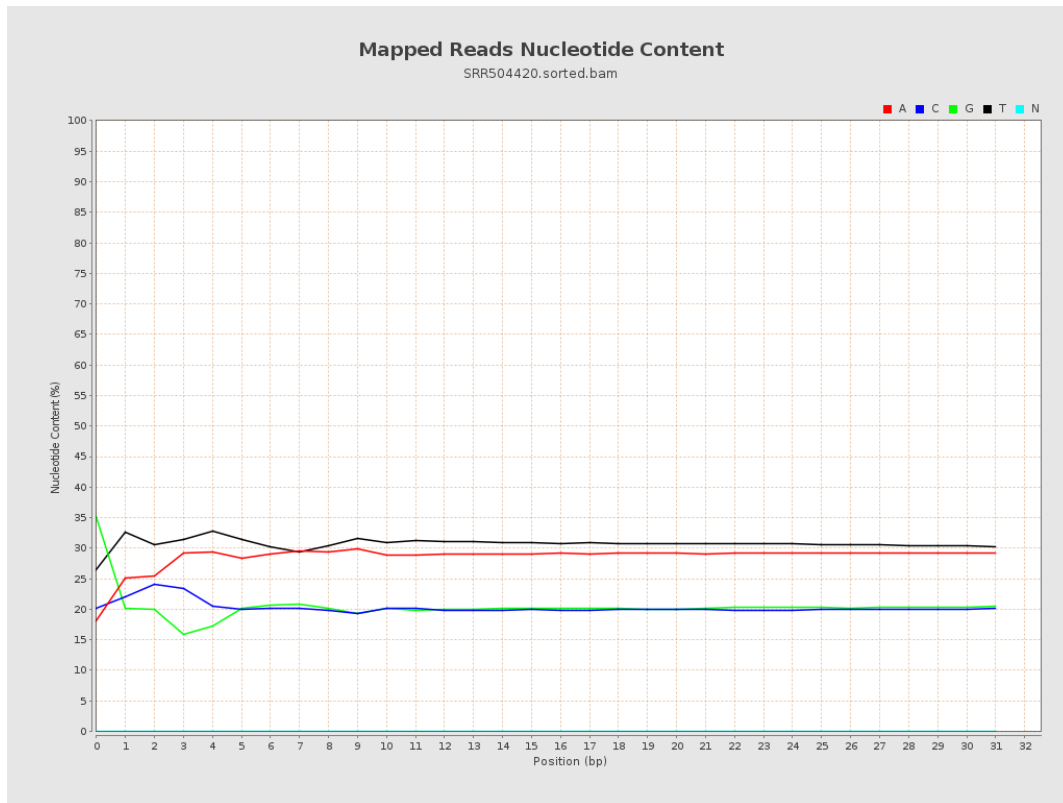
## 6. Results : Genome Fraction Coverage



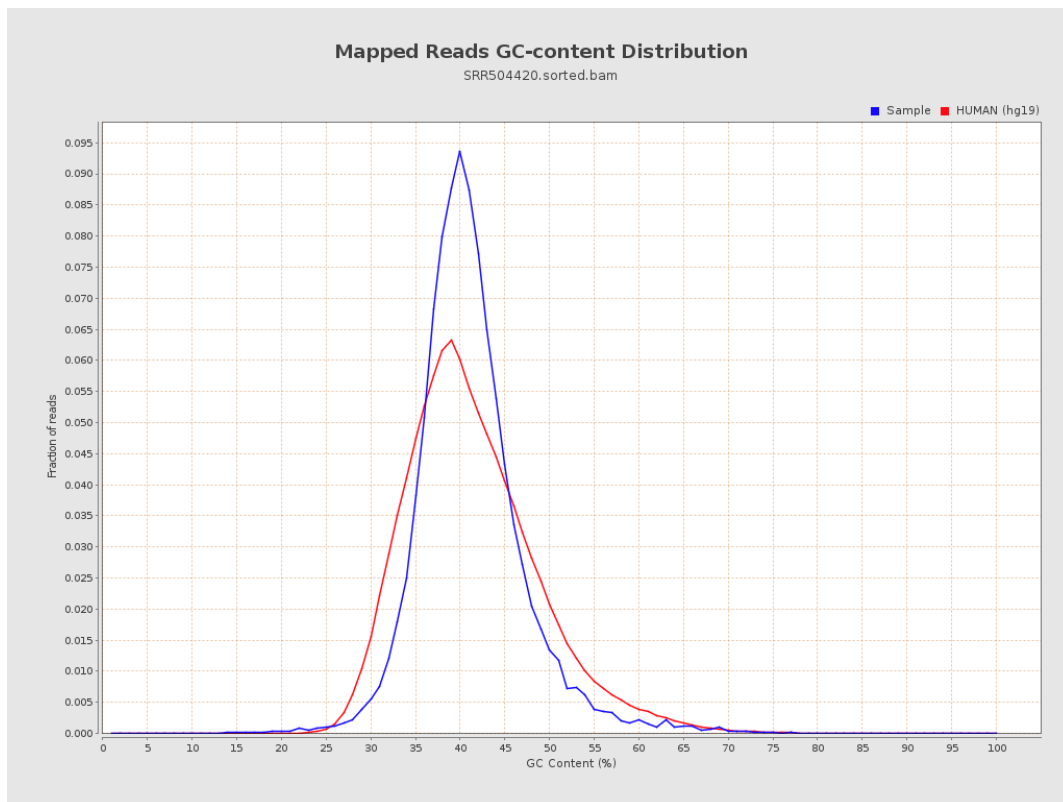
## 7. Results : Duplication Rate Histogram



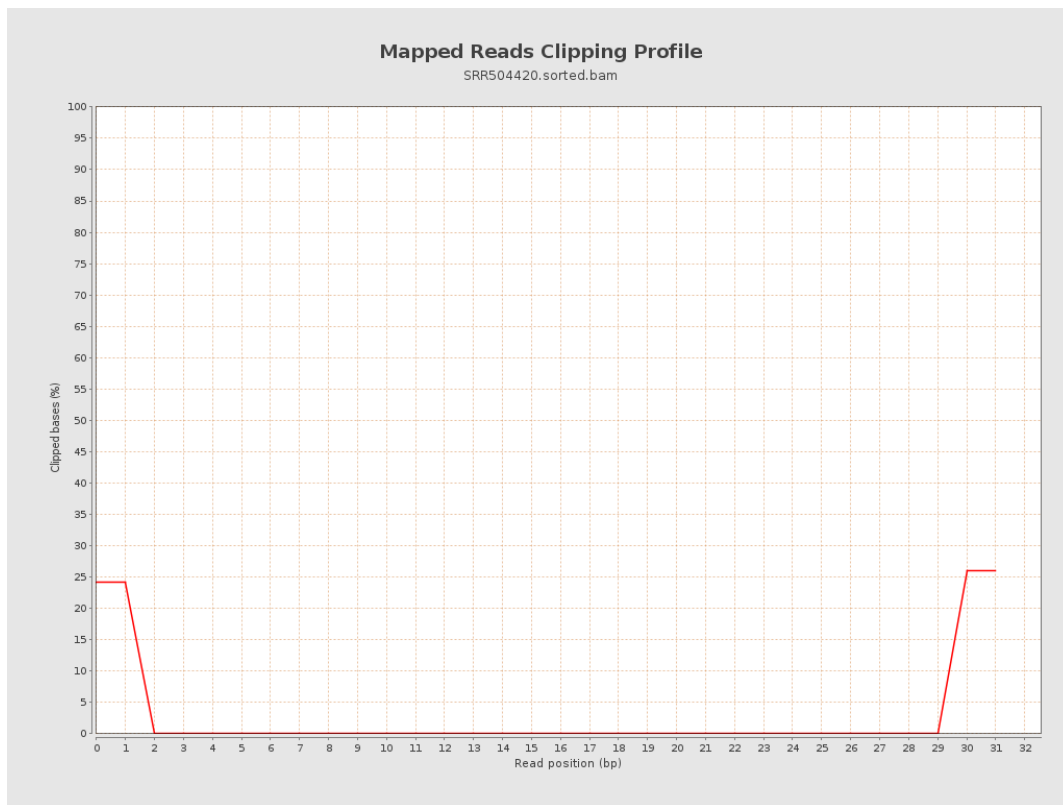
## 8. Results : Mapped Reads Nucleotide Content



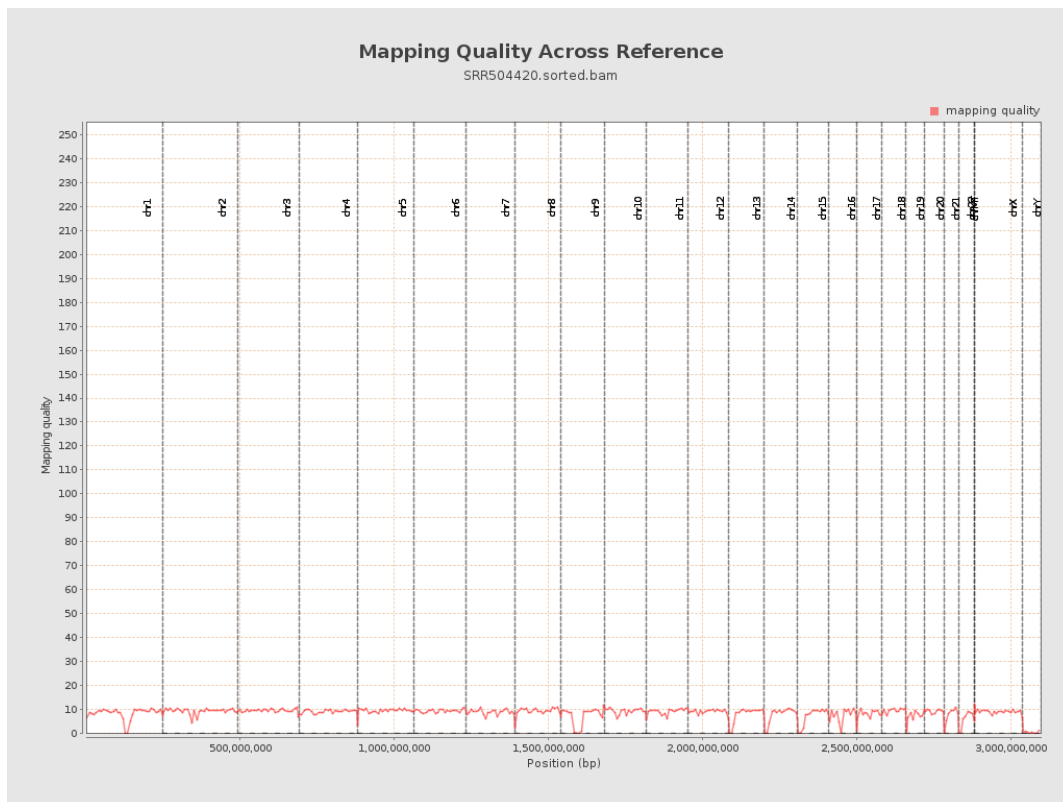
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Mapping Quality Across Reference



## 12. Results : Mapping Quality Histogram

