

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/22 04:40:33*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708520.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_SRR1708520 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708520.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Thu Aug 22 04:40:30 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR1708520.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 3,380,389          |
| Mapped reads                 | 2,371,320 / 70.15% |
| Unmapped reads               | 1,009,069 / 29.85% |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 629 / 0.02%        |
| Read min/max/mean length     | 30 / 51 / 51.01    |
| Duplicated reads (estimated) | 96,937 / 2.87%     |
| Duplication rate             | 3.24%              |
| Clipped reads                | 458,539 / 13.56%   |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 32,947,858 / 28.94% |
| Number/percentage of C's | 21,215,905 / 18.64% |
| Number/percentage of T's | 36,307,716 / 31.9%  |
| Number/percentage of G's | 23,359,931 / 20.52% |
| Number/percentage of N's | 1,695 / 0%          |
| GC Percentage            | 39.16%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0368 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.3174 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |      |
|----------------------|------|
| Mean Mapping Quality | 43.1 |
|----------------------|------|

## 2.5. Mismatches and indels

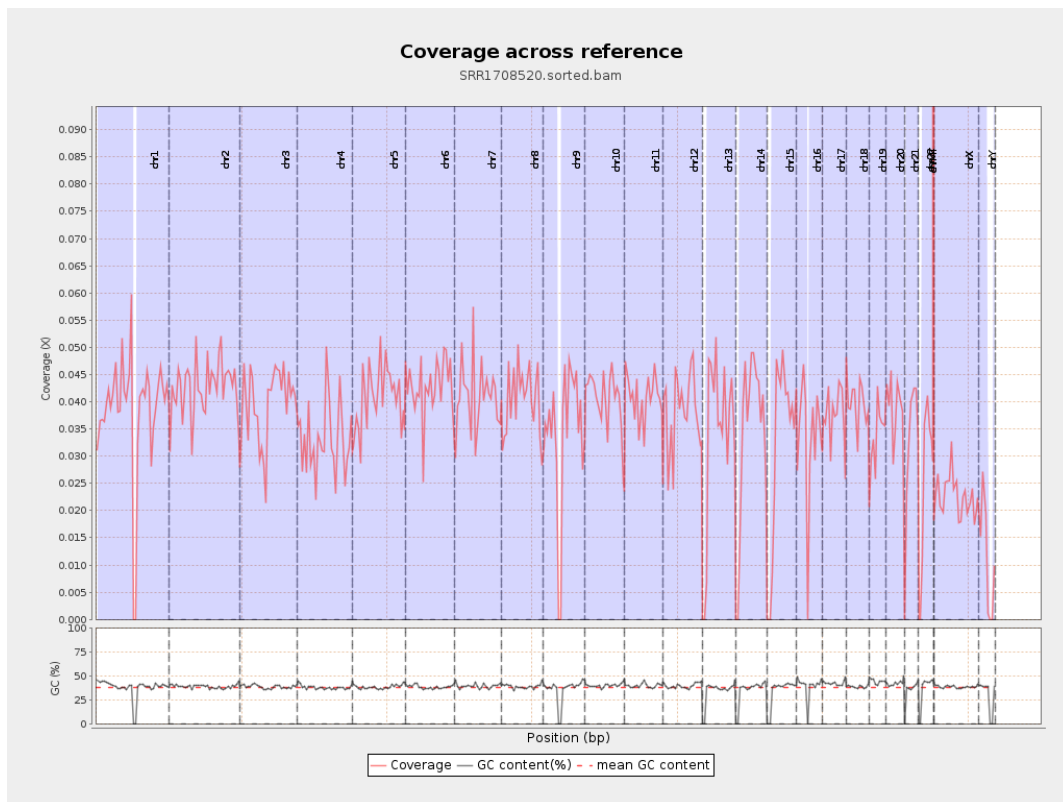
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 0.48%   |
| Mismatches                               | 540,819 |
| Insertions                               | 5,325   |
| Mapped reads with at least one insertion | 0.22%   |
| Deletions                                | 13,719  |
| Mapped reads with at least one deletion  | 0.58%   |
| Homopolymer indels                       | 48.79%  |

## 2.6. Chromosome stats

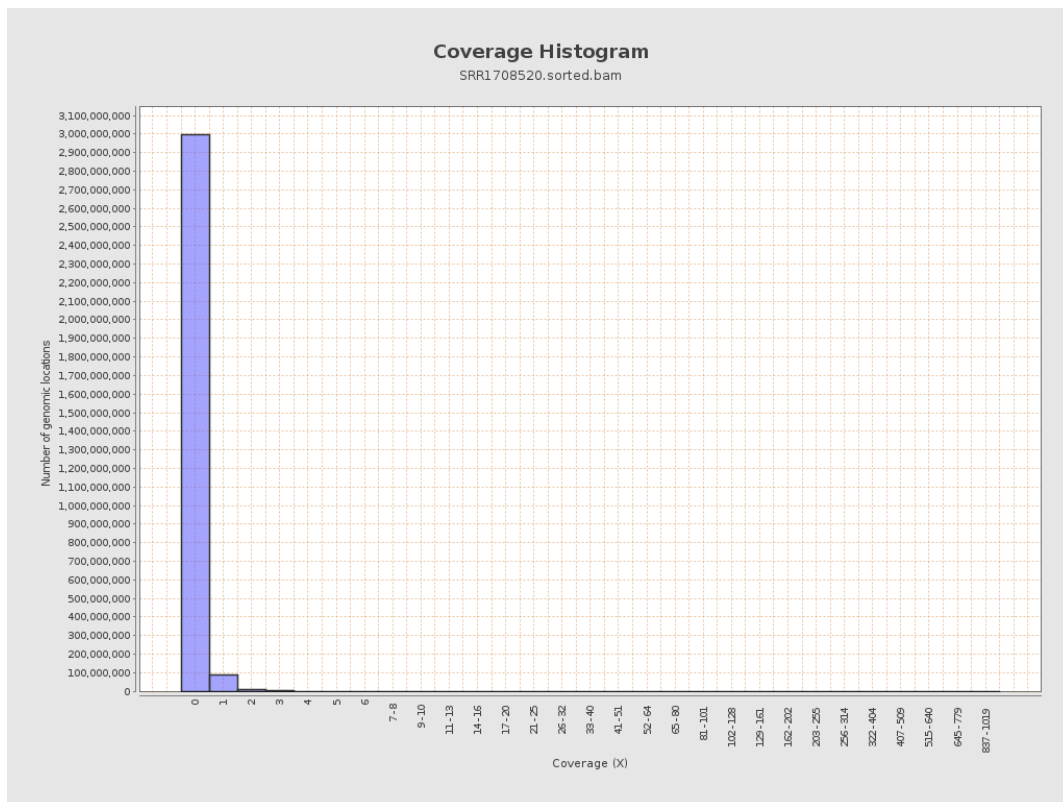
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 9569765      | 0.0384        | 0.5427             |
| chr2 | 243199373 | 10377372     | 0.0427        | 0.3108             |
| chr3 | 198022430 | 7838346      | 0.0396        | 0.2234             |
| chr4 | 191154276 | 6274184      | 0.0328        | 0.2078             |
| chr5 | 180915260 | 7394175      | 0.0409        | 0.2274             |
| chr6 | 171115067 | 7320516      | 0.0428        | 0.272              |
| chr7 | 159138663 | 6542304      | 0.0411        | 0.3743             |
|      |           |              |               |                    |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr8  | 146364022 | 5886650 | 0.0402 | 0.6015 |
| chr9  | 141213431 | 4826147 | 0.0342 | 0.2523 |
| chr10 | 135534747 | 5543712 | 0.0409 | 0.2633 |
| chr11 | 135006516 | 5458040 | 0.0404 | 0.2977 |
| chr12 | 133851895 | 5174379 | 0.0387 | 0.2233 |
| chr13 | 115169878 | 3902627 | 0.0339 | 0.2067 |
| chr14 | 107349540 | 3708726 | 0.0345 | 0.2149 |
| chr15 | 102531392 | 3301975 | 0.0322 | 0.203  |
| chr16 | 90354753  | 3026016 | 0.0335 | 0.2102 |
| chr17 | 81195210  | 3031132 | 0.0373 | 0.2505 |
| chr18 | 78077248  | 3113798 | 0.0399 | 0.4313 |
| chr19 | 59128983  | 2008047 | 0.034  | 0.384  |
| chr20 | 63025520  | 2410713 | 0.0382 | 0.22   |
| chr21 | 48129895  | 1557177 | 0.0324 | 0.2215 |
| chr22 | 51304566  | 1269035 | 0.0247 | 0.185  |
| chrMT | 16571     | 148865  | 8.9835 | 6.8046 |
| chrX  | 155270560 | 3512507 | 0.0226 | 0.1938 |
| chrY  | 59373566  | 657877  | 0.0111 | 0.1267 |

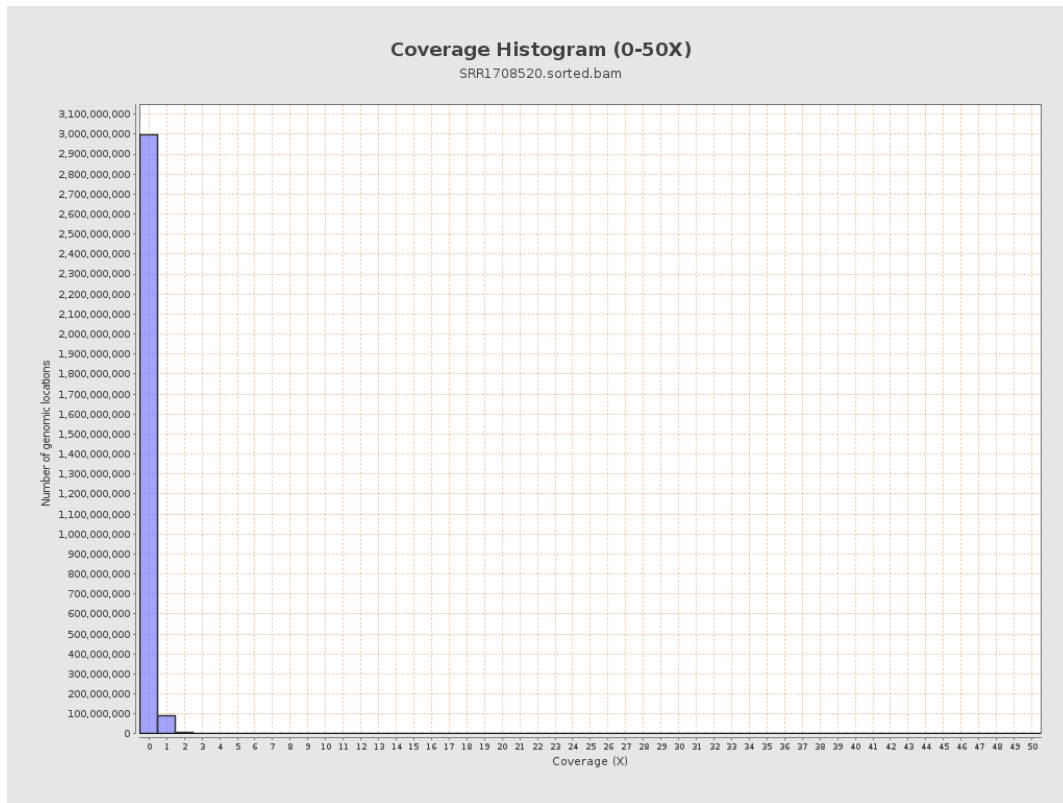
### 3. Results : Coverage across reference



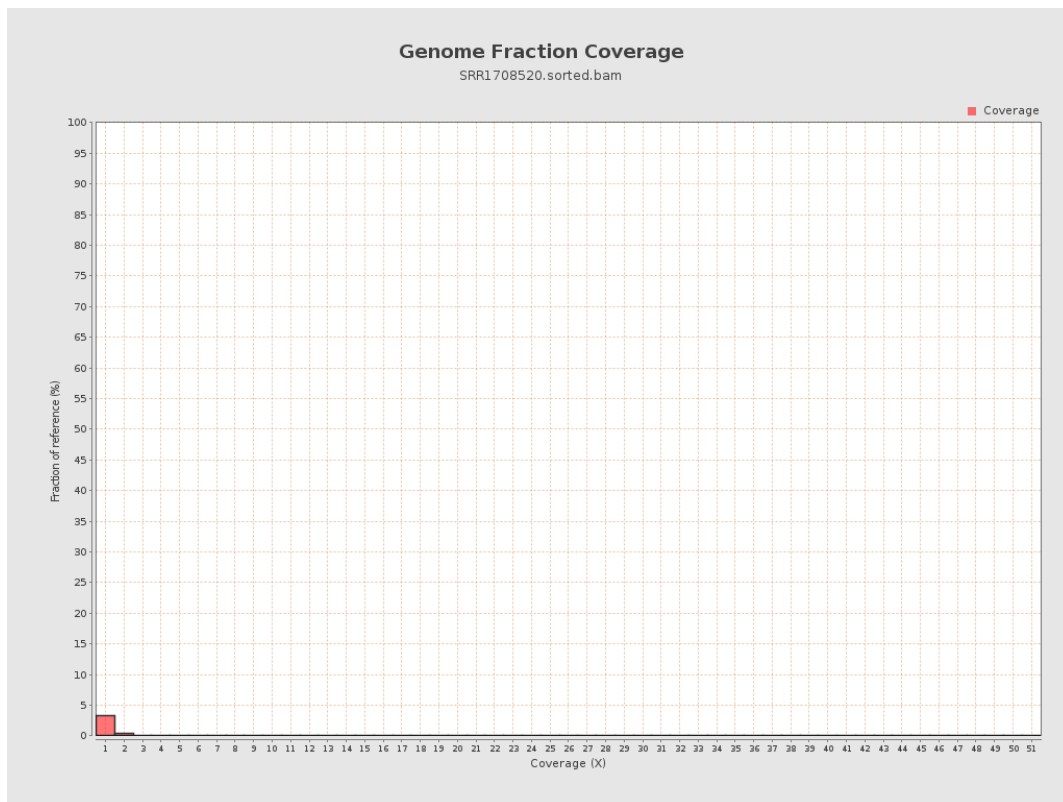
## 4. Results : Coverage Histogram



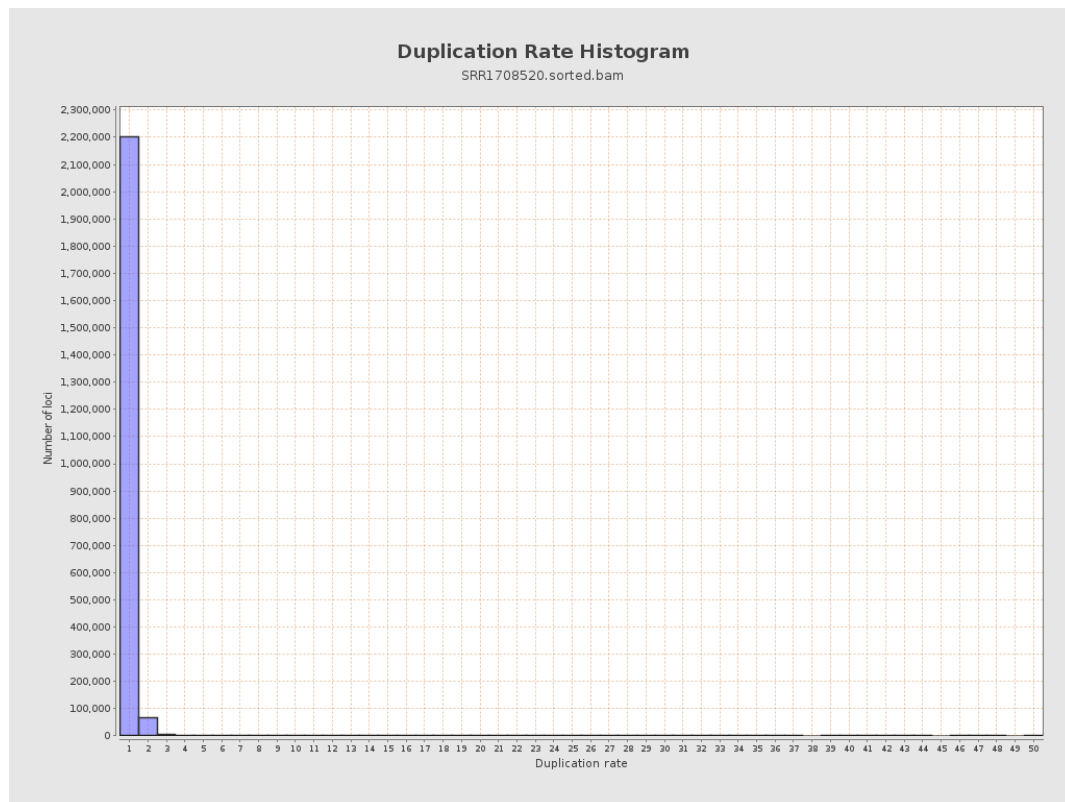
## 5. Results : Coverage Histogram (0-50X)



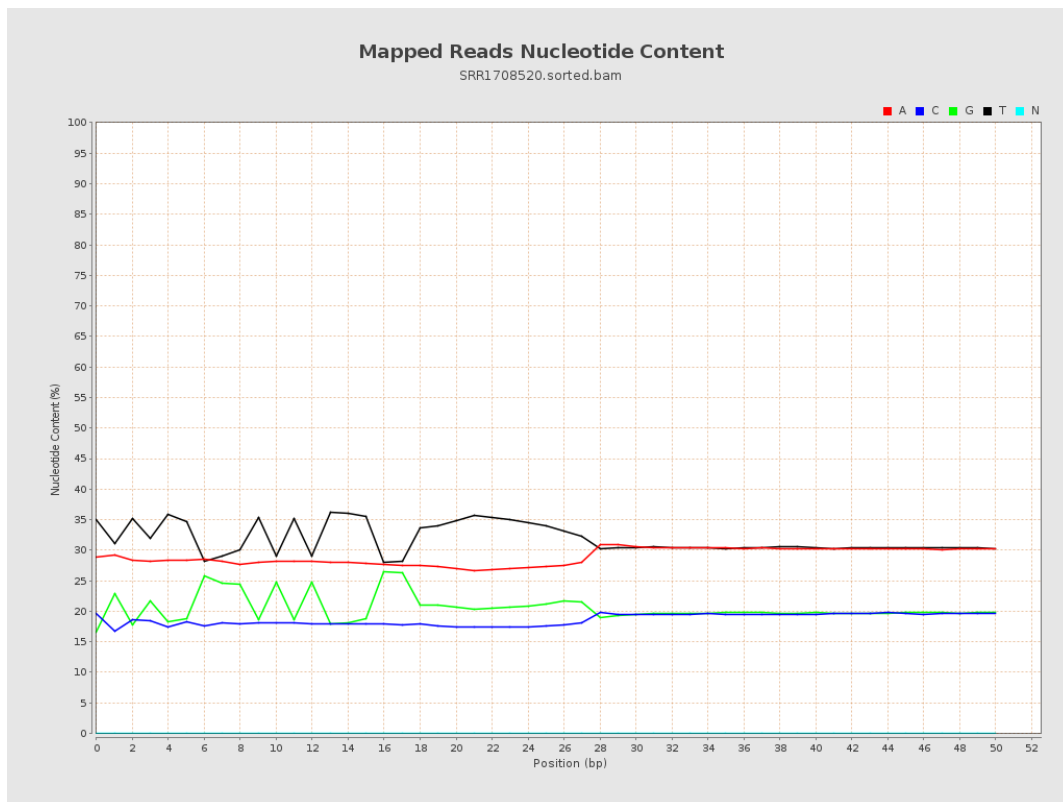
## 6. Results : Genome Fraction Coverage



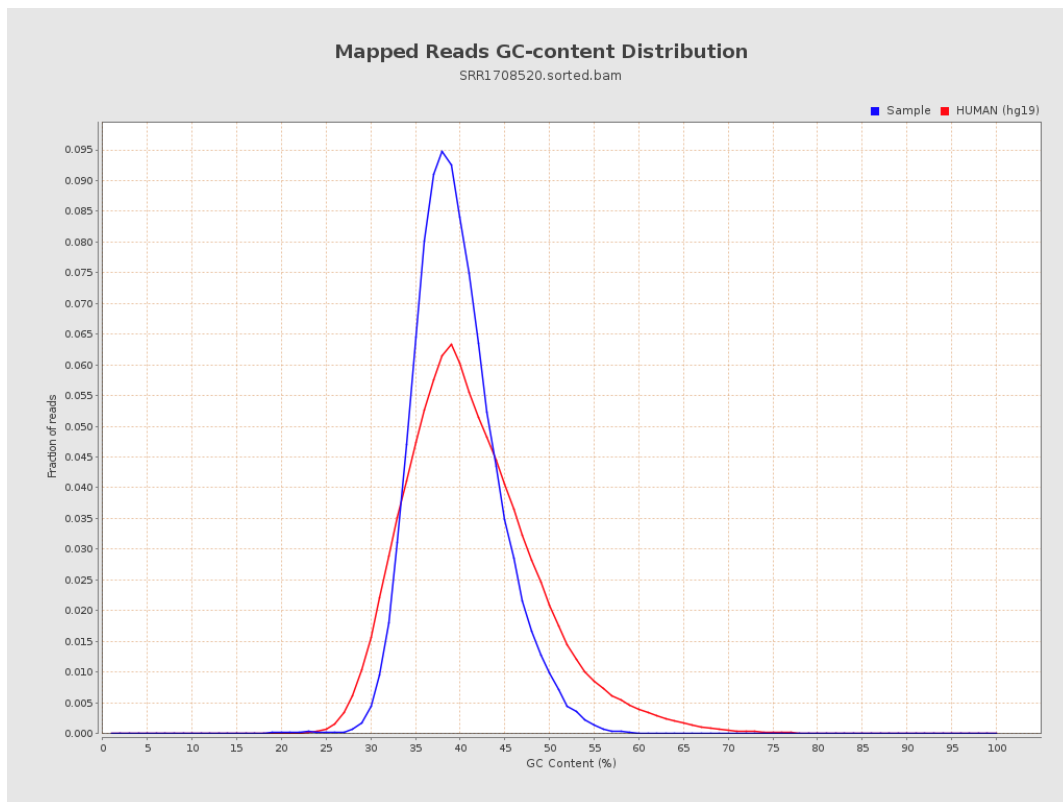
## 7. Results : Duplication Rate Histogram



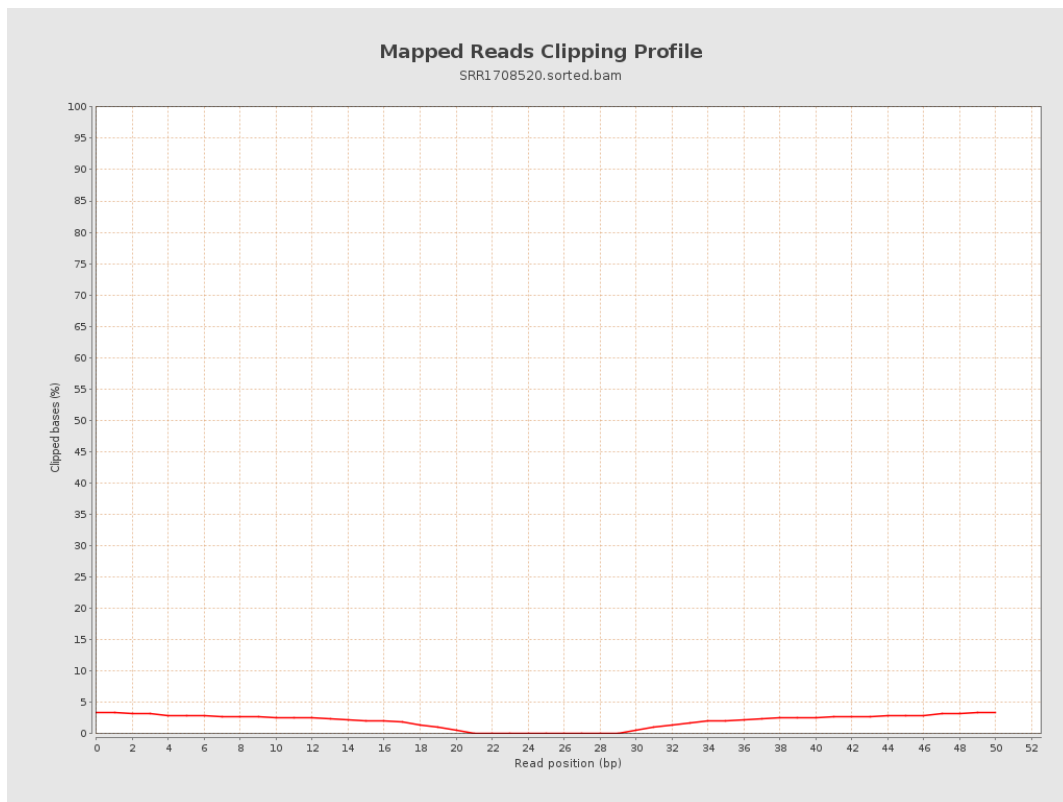
## 8. Results : Mapped Reads Nucleotide Content



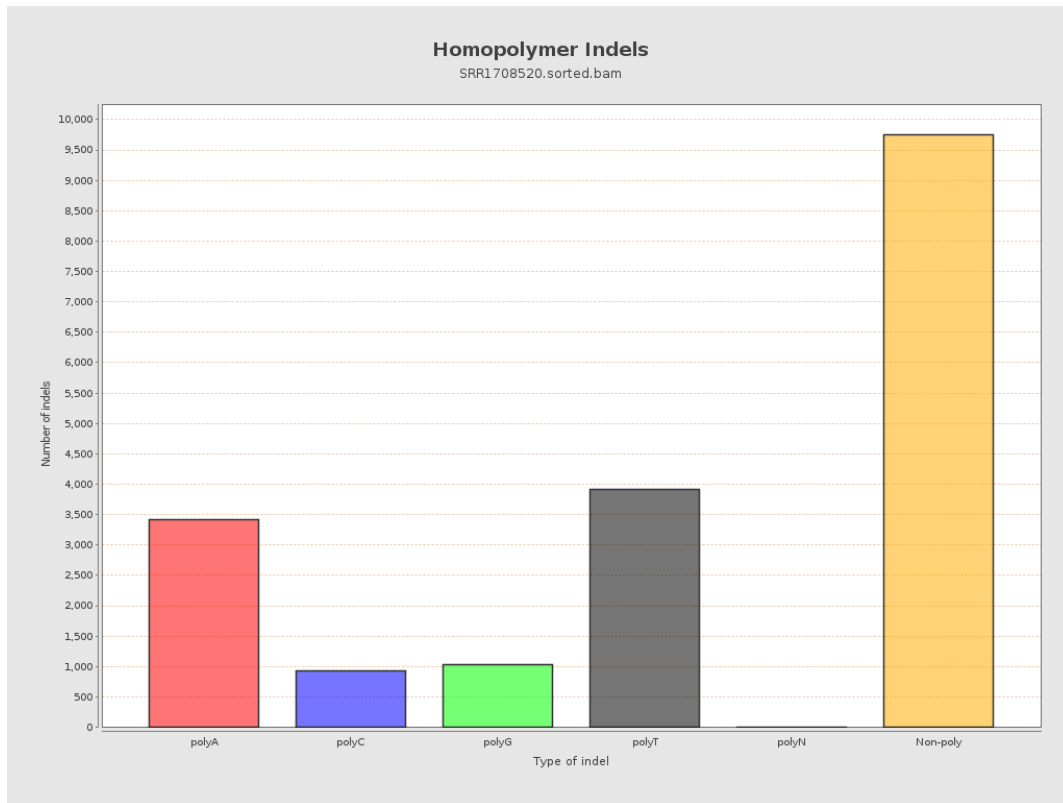
## 9. Results : Mapped Reads GC-content Distribution



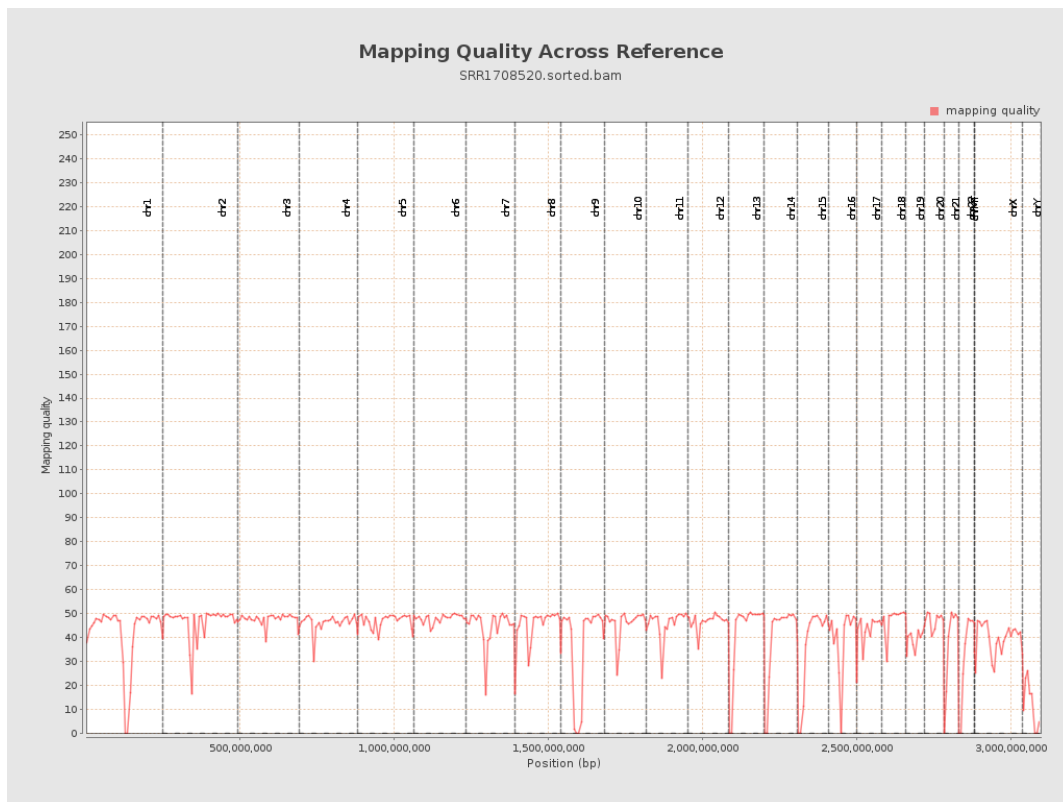
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

