

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/14 12:05:30*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008800.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_SRR6008800 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008800.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Sat Sep 14 12:05:29 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6008800.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 1,588,055          |
| Mapped reads                 | 1,413,922 / 89.03% |
| Unmapped reads               | 174,133 / 10.97%   |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 10,004 / 0.63%     |
| Read min/max/mean length     | 30 / 76 / 76.22    |
| Duplicated reads (estimated) | 82,917 / 5.22%     |
| Duplication rate             | 4.53%              |
| Clipped reads                | 671,516 / 42.29%   |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 25,091,598 / 26.99% |
| Number/percentage of C's | 18,202,283 / 19.58% |
| Number/percentage of T's | 28,342,141 / 30.48% |
| Number/percentage of G's | 21,211,557 / 22.81% |
| Number/percentage of N's | 125,887 / 0.14%     |
| GC Percentage            | 42.39%              |

### 2.3. Coverage

|      |      |
|------|------|
| Mean | 0.03 |
|      |      |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.3441 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 45.04 |
|----------------------|-------|

## 2.5. Mismatches and indels

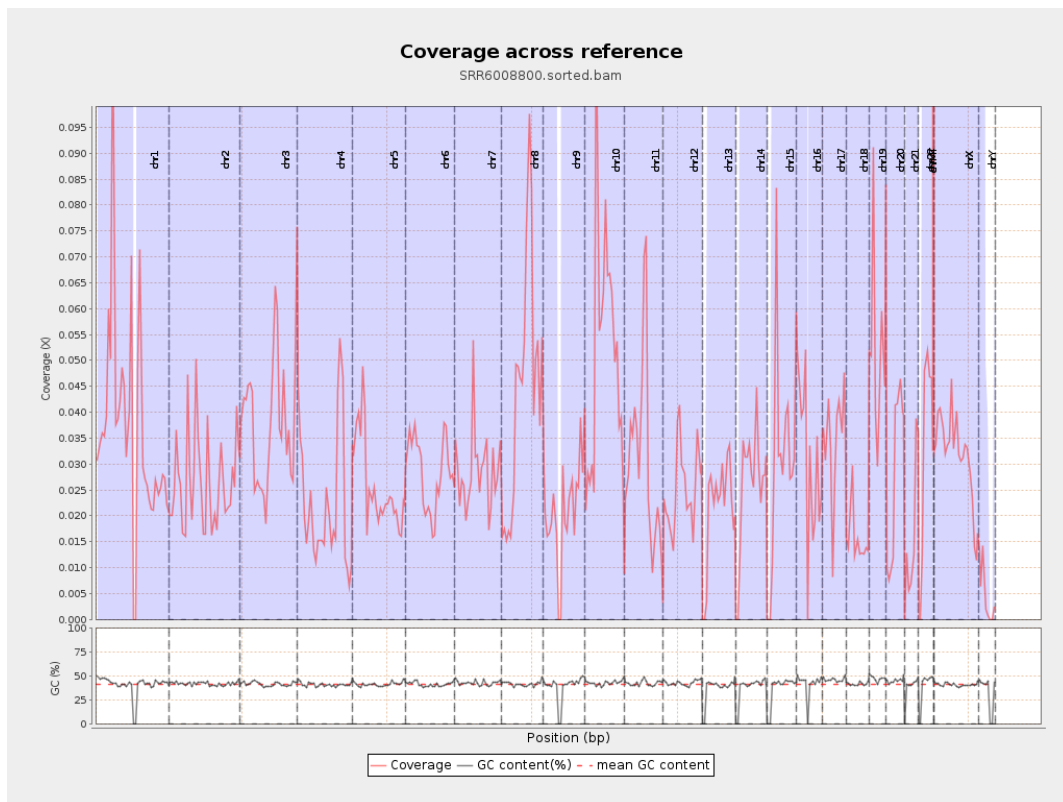
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 0.87%   |
| Mismatches                               | 795,144 |
| Insertions                               | 6,919   |
| Mapped reads with at least one insertion | 0.48%   |
| Deletions                                | 26,253  |
| Mapped reads with at least one deletion  | 1.84%   |
| Homopolymer indels                       | 44.95%  |

## 2.6. Chromosome stats

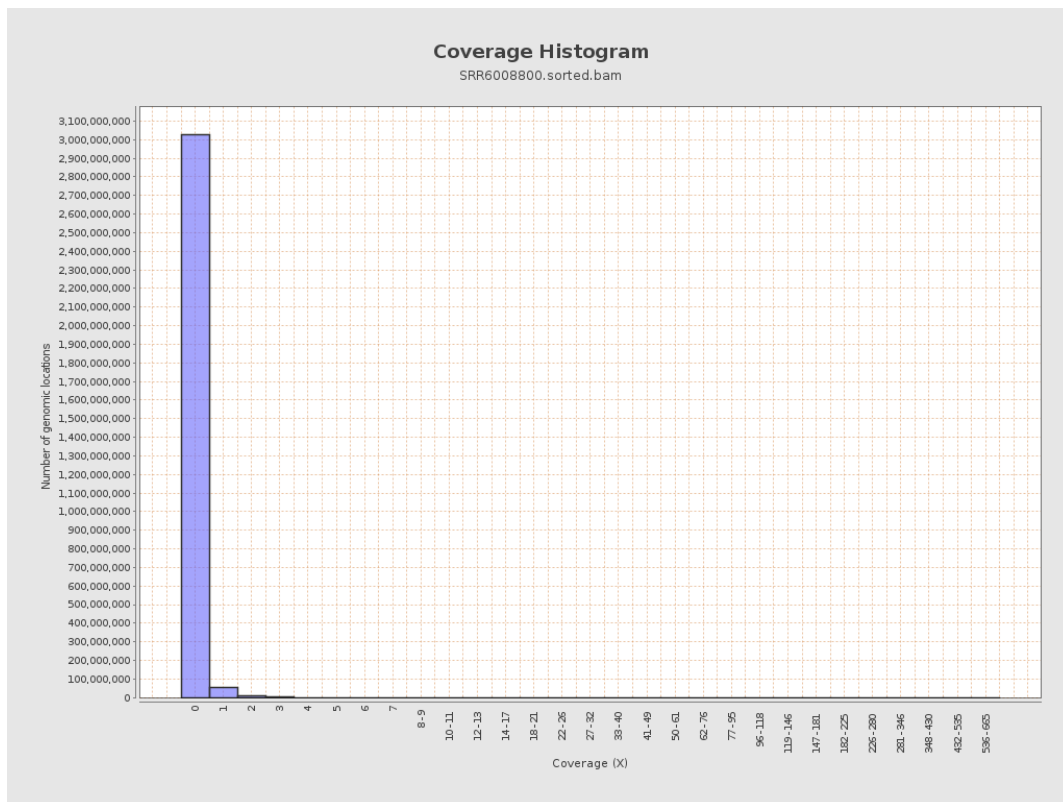
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 9161464      | 0.0368        | 0.5963             |
| chr2 | 243199373 | 6492733      | 0.0267        | 0.3731             |
| chr3 | 198022430 | 7473574      | 0.0377        | 0.2718             |
| chr4 | 191154276 | 4170957      | 0.0218        | 0.1911             |
| chr5 | 180915260 | 4682123      | 0.0259        | 0.1997             |
| chr6 | 171115067 | 4845508      | 0.0283        | 0.2222             |
| chr7 | 159138663 | 4548925      | 0.0286        | 0.4106             |
|      |           |              |               |                    |

|       |           |         |         |        |
|-------|-----------|---------|---------|--------|
| chr8  | 146364022 | 6465145 | 0.0442  | 0.3307 |
| chr9  | 141213431 | 2882796 | 0.0204  | 0.2182 |
| chr10 | 135534747 | 6930546 | 0.0511  | 0.7278 |
| chr11 | 135006516 | 4153820 | 0.0308  | 0.2564 |
| chr12 | 133851895 | 3354765 | 0.0251  | 0.198  |
| chr13 | 115169878 | 2446797 | 0.0212  | 0.1806 |
| chr14 | 107349540 | 2742127 | 0.0255  | 0.1991 |
| chr15 | 102531392 | 3160354 | 0.0308  | 0.22   |
| chr16 | 90354753  | 2771941 | 0.0307  | 0.3355 |
| chr17 | 81195210  | 2808195 | 0.0346  | 0.2899 |
| chr18 | 78077248  | 1241059 | 0.0159  | 0.3281 |
| chr19 | 59128983  | 3116380 | 0.0527  | 0.4483 |
| chr20 | 63025520  | 1723158 | 0.0273  | 0.2097 |
| chr21 | 48129895  | 769988  | 0.016   | 0.1631 |
| chr22 | 51304566  | 1664200 | 0.0324  | 0.2254 |
| chrMT | 16571     | 207858  | 12.5435 | 7.9163 |
| chrX  | 155270560 | 4937082 | 0.0318  | 0.2397 |
| chrY  | 59373566  | 268720  | 0.0045  | 0.1645 |

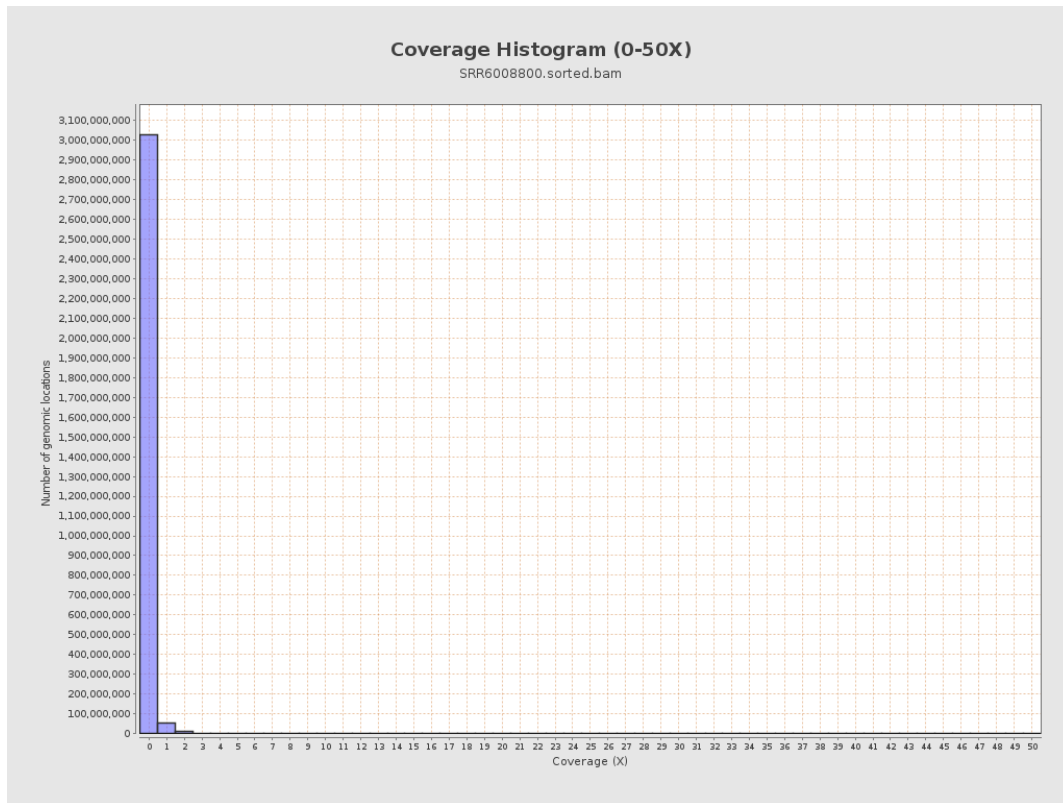
### 3. Results : Coverage across reference



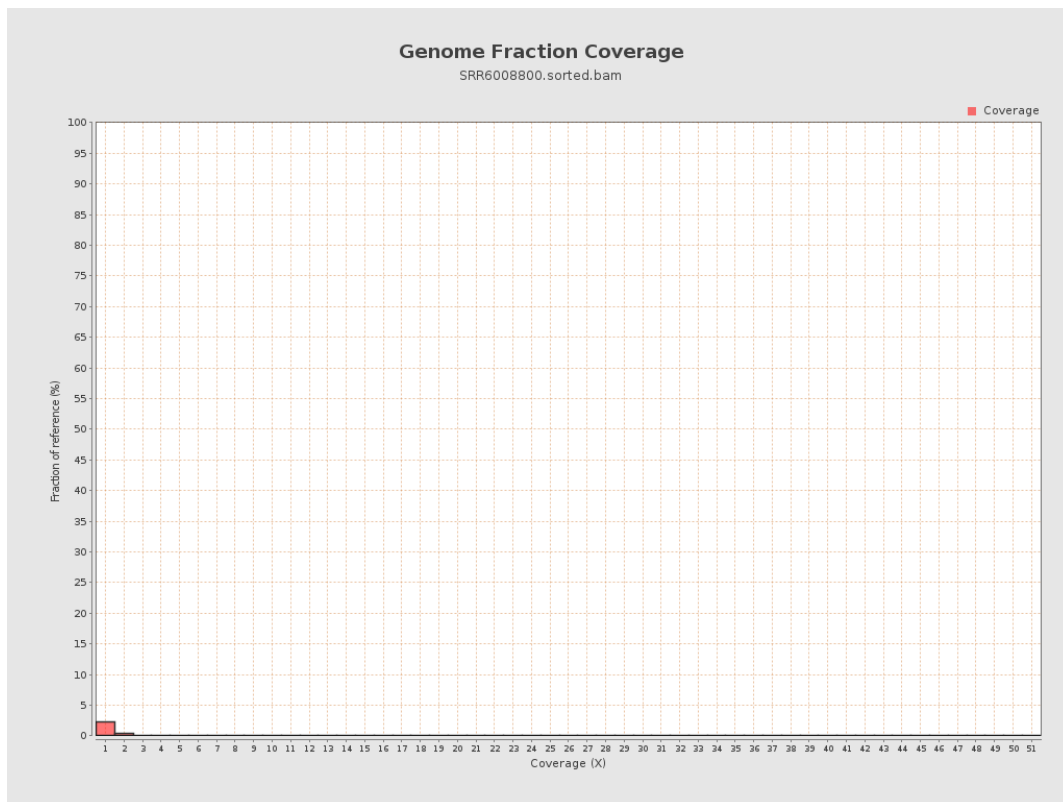
## 4. Results : Coverage Histogram



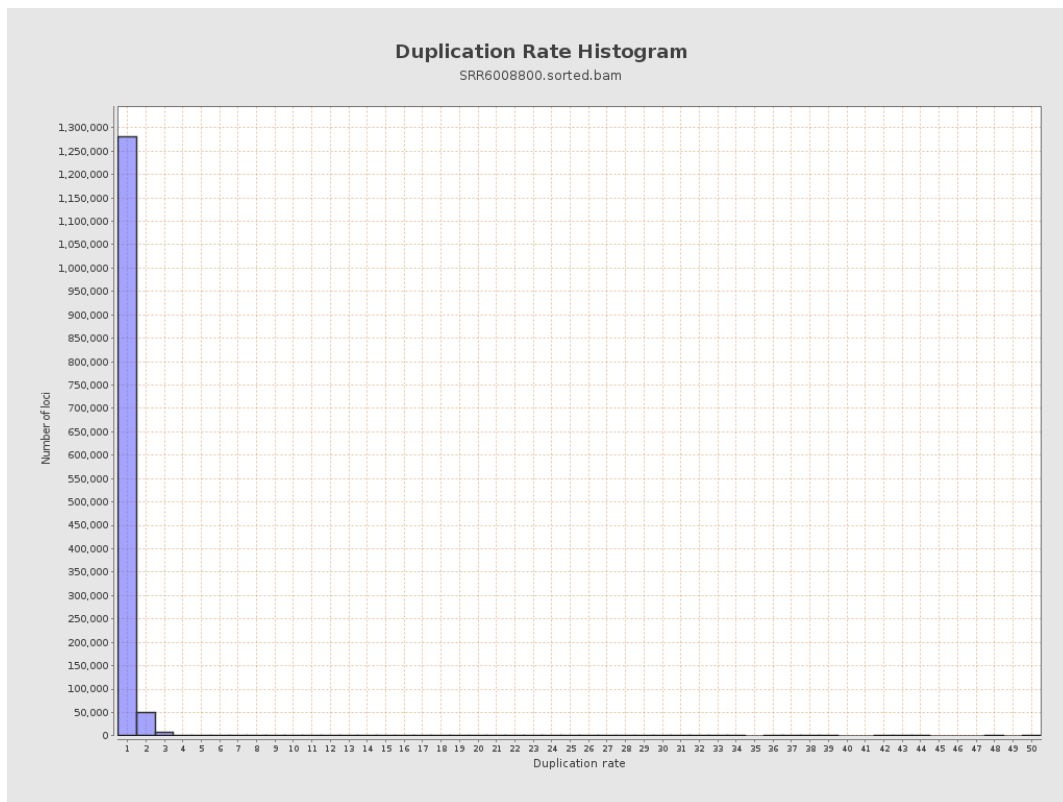
## 5. Results : Coverage Histogram (0-50X)



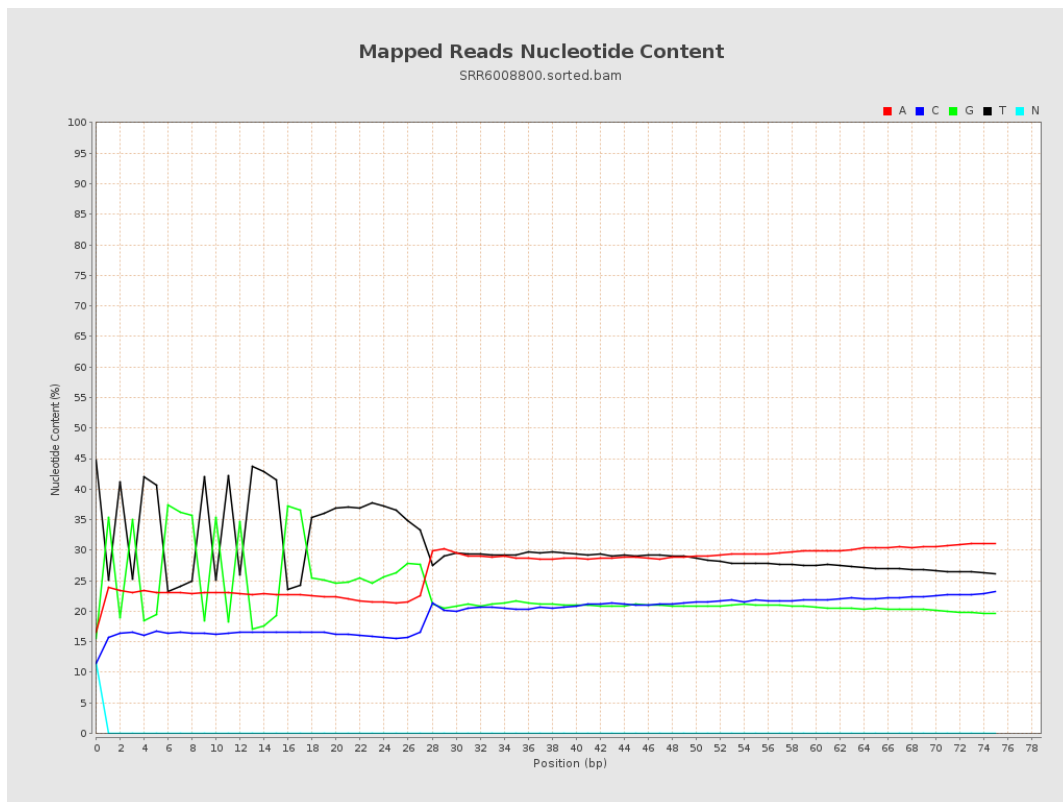
## 6. Results : Genome Fraction Coverage



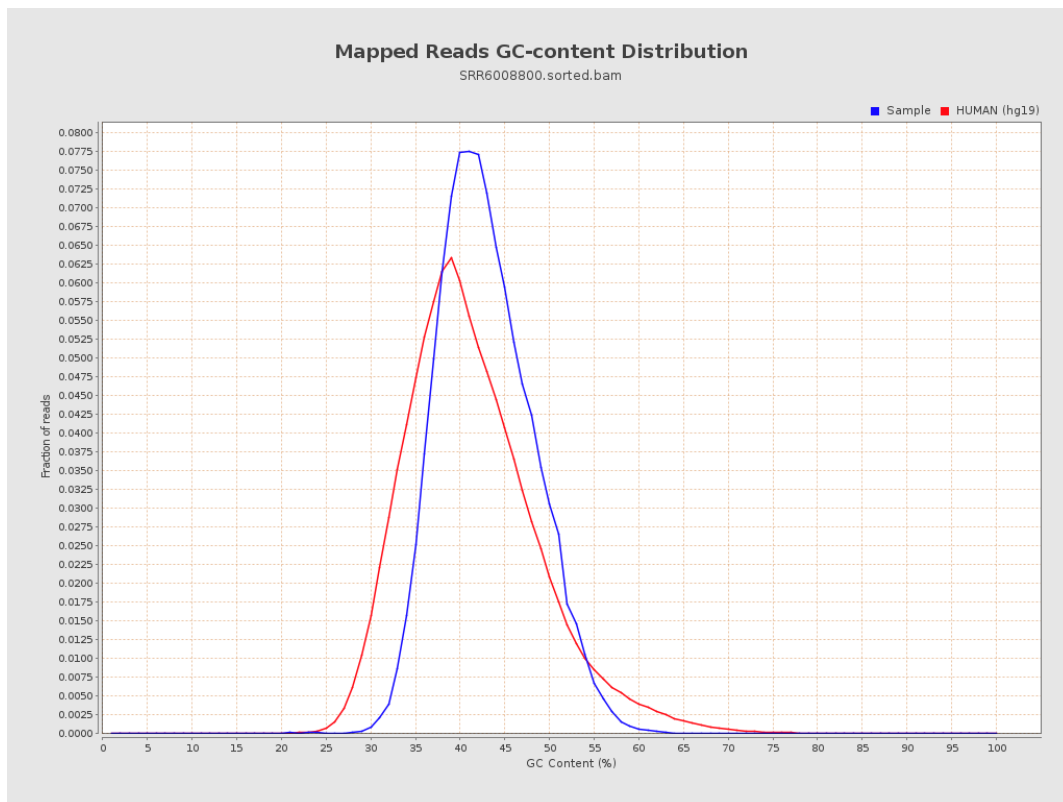
## 7. Results : Duplication Rate Histogram



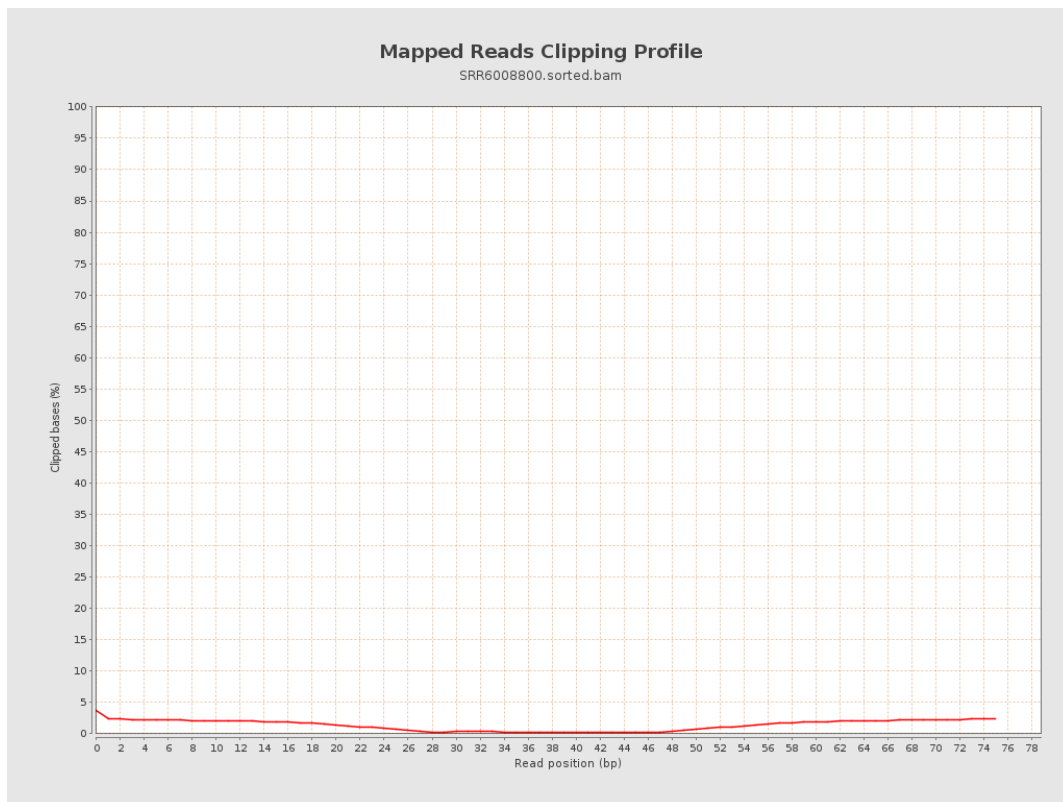
## 8. Results : Mapped Reads Nucleotide Content



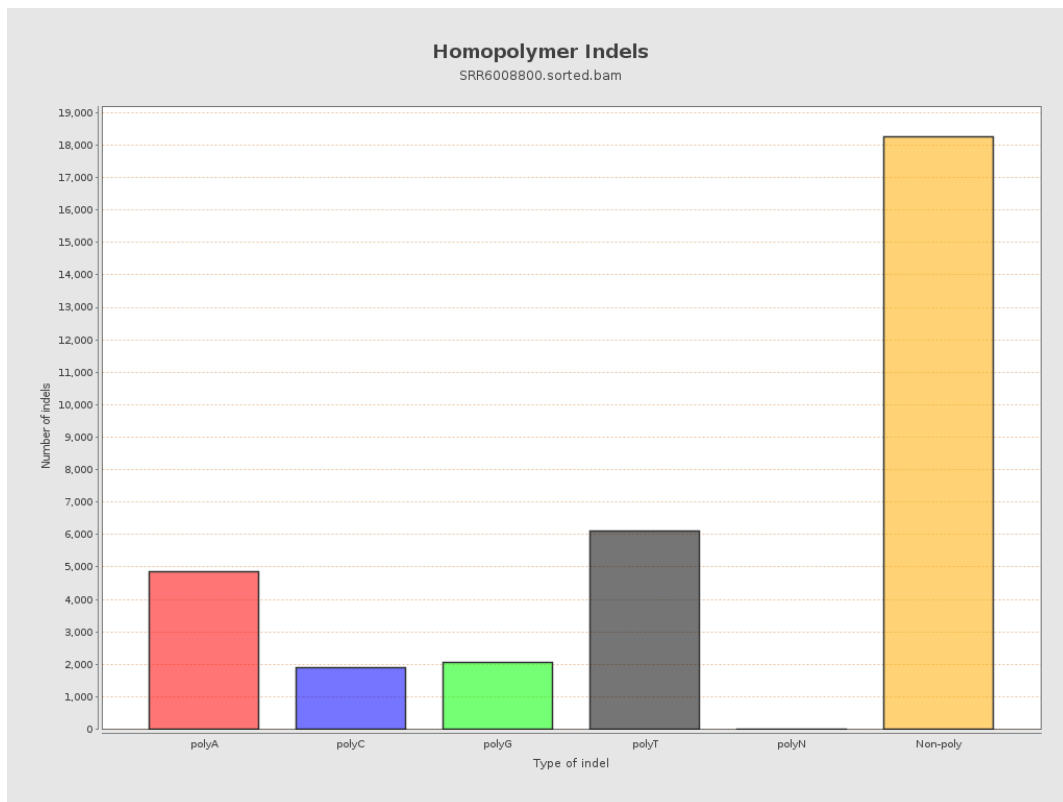
## 9. Results : Mapped Reads GC-content Distribution



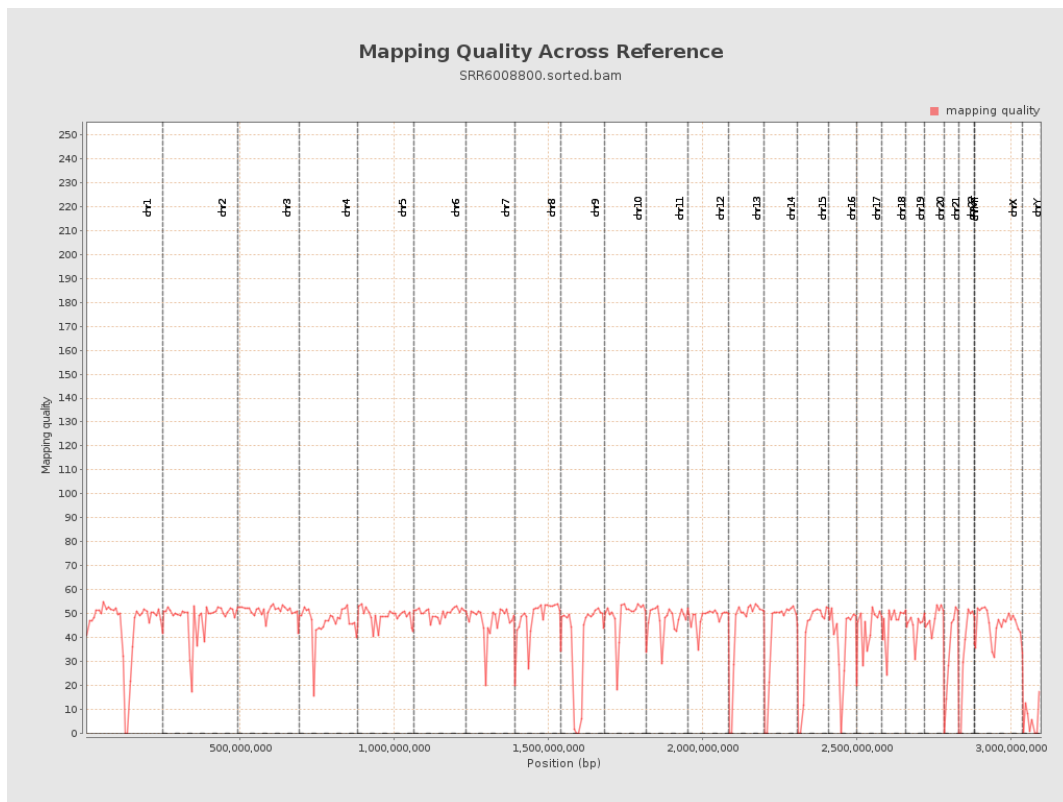
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

