

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 23:17:50*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173858.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_SRR10173858 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173858_1.fastq.gz SRR10173858_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                      |
| Analysis date:                        | Tue Sep 03 23:17:50 CST 2024                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                     |
| BAM file:                             | SRR10173858.sorted.bam                                                                                                                                                                                                  |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 4,430,276          |
| Mapped reads                 | 4,319,176 / 97.49% |
| Unmapped reads               | 111,100 / 2.51%    |
| Mapped paired reads          | 4,319,176 / 97.49% |
| Mapped reads, first in pair  | 2,161,750 / 48.79% |
| Mapped reads, second in pair | 2,157,426 / 48.7%  |
| Mapped reads, both in pair   | 4,246,938 / 95.86% |
| Mapped reads, singletons     | 72,238 / 1.63%     |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 413,634 / 9.34%    |
| Read min/max/mean length     | 30 / 133 / 127.65  |
| Duplicated reads (estimated) | 3,315,125 / 74.83% |
| Duplication rate             | 65.08%             |
| Clipped reads                | 1,670,230 / 37.7%  |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 154,128,966 / 30.22% |
| Number/percentage of C's | 99,576,971 / 19.52%  |
| Number/percentage of T's | 153,551,719 / 30.11% |
| Number/percentage of G's | 102,736,765 / 20.14% |
| Number/percentage of N's | 6,630 / 0%           |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 39.67% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.1648 |
| Standard Deviation | 2.464  |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 52.79 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 784,528.63      |
| Standard Deviation | 8,294,329.4     |
| P25/Median/P75     | 141 / 195 / 279 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 1.01%     |
| Mismatches                               | 5,042,791 |
| Insertions                               | 52,125    |
| Mapped reads with at least one insertion | 1.17%     |
| Deletions                                | 102,177   |
| Mapped reads with at least one deletion  | 2.31%     |
| Homopolymer indels                       | 44.01%    |

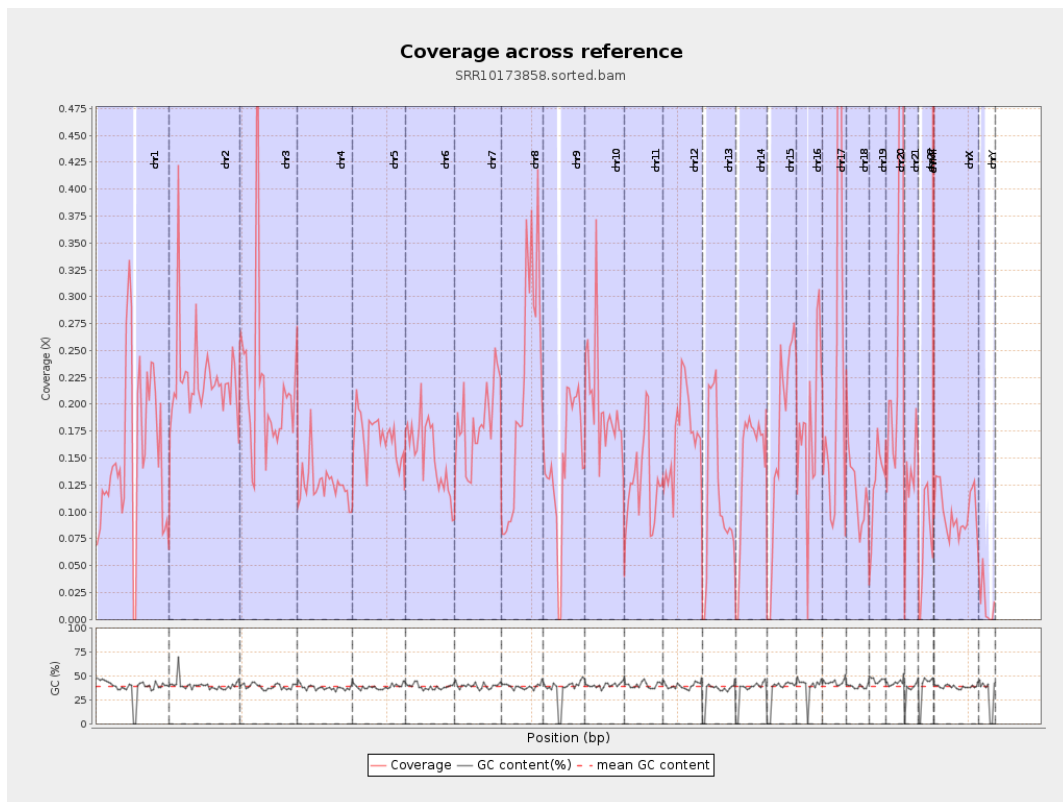
## 2.7. Chromosome stats

| Name | Length | Mapped | Mean | Standard |
|------|--------|--------|------|----------|
|------|--------|--------|------|----------|

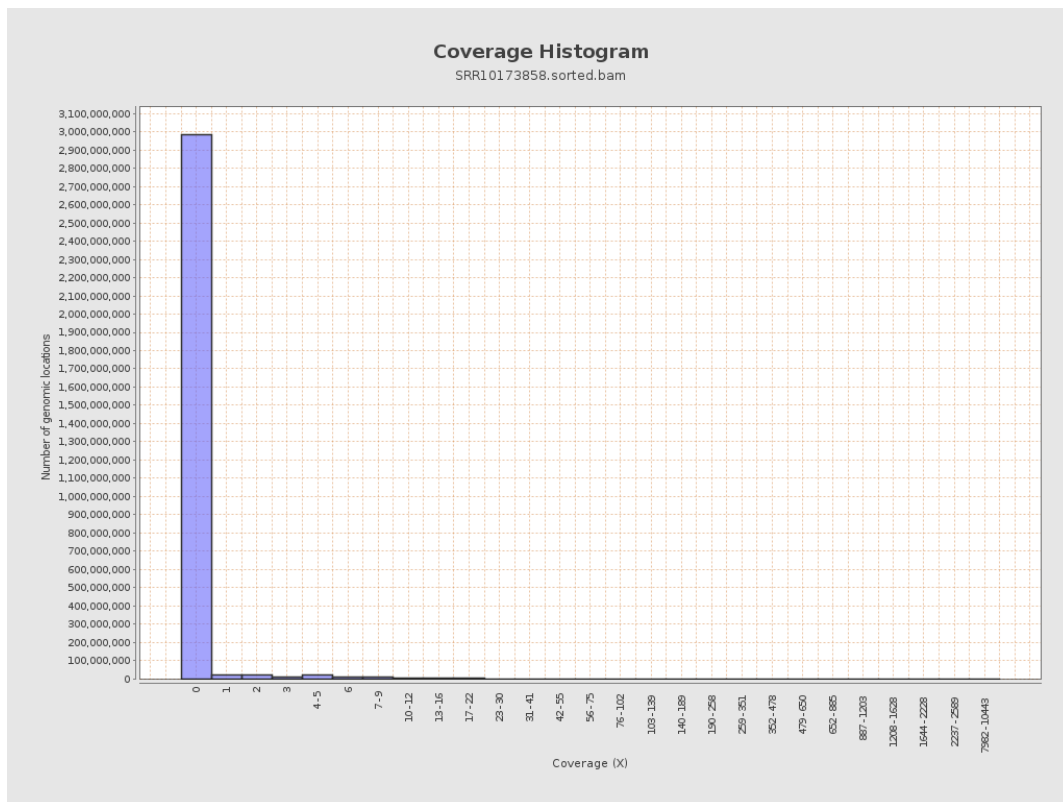
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 38020163     | 0.1525          | 1.6257           |
| chr2  | 243199373 | 54471045     | 0.224           | 7.3495           |
| chr3  | 198022430 | 42200584     | 0.2131          | 1.3484           |
| chr4  | 191154276 | 23960062     | 0.1253          | 1.1753           |
| chr5  | 180915260 | 30673707     | 0.1695          | 1.1779           |
| chr6  | 171115067 | 26058868     | 0.1523          | 1.2522           |
| chr7  | 159138663 | 29293340     | 0.1841          | 1.5879           |
| chr8  | 146364022 | 30843951     | 0.2107          | 1.6302           |
| chr9  | 141213431 | 20648534     | 0.1462          | 1.3117           |
| chr10 | 135534747 | 26975766     | 0.199           | 2.468            |
| chr11 | 135006516 | 17173171     | 0.1272          | 1.0446           |
| chr12 | 133851895 | 22889900     | 0.171           | 1.1828           |
| chr13 | 115169878 | 12860306     | 0.1117          | 0.9585           |
| chr14 | 107349540 | 15438429     | 0.1438          | 1.0772           |
| chr15 | 102531392 | 17396579     | 0.1697          | 1.1707           |
| chr16 | 90354753  | 16301350     | 0.1804          | 1.5032           |
| chr17 | 81195210  | 19454726     | 0.2396          | 1.5166           |
| chr18 | 78077248  | 9527407      | 0.122           | 1.6259           |
| chr19 | 59128983  | 7578993      | 0.1282          | 1.3876           |
| chr20 | 63025520  | 21199698     | 0.3364          | 1.8113           |
| chr21 | 48129895  | 6305542      | 0.131           | 1.0694           |
| chr22 | 51304566  | 3562793      | 0.0694          | 0.7224           |
| chrMT | 16571     | 1138857      | 68.7259         | 61.3664          |
| chrX  | 155270560 | 15420335     | 0.0993          | 0.8983           |

|      |          |        |        |        |
|------|----------|--------|--------|--------|
| chrY | 59373566 | 872050 | 0.0147 | 0.5652 |
|------|----------|--------|--------|--------|

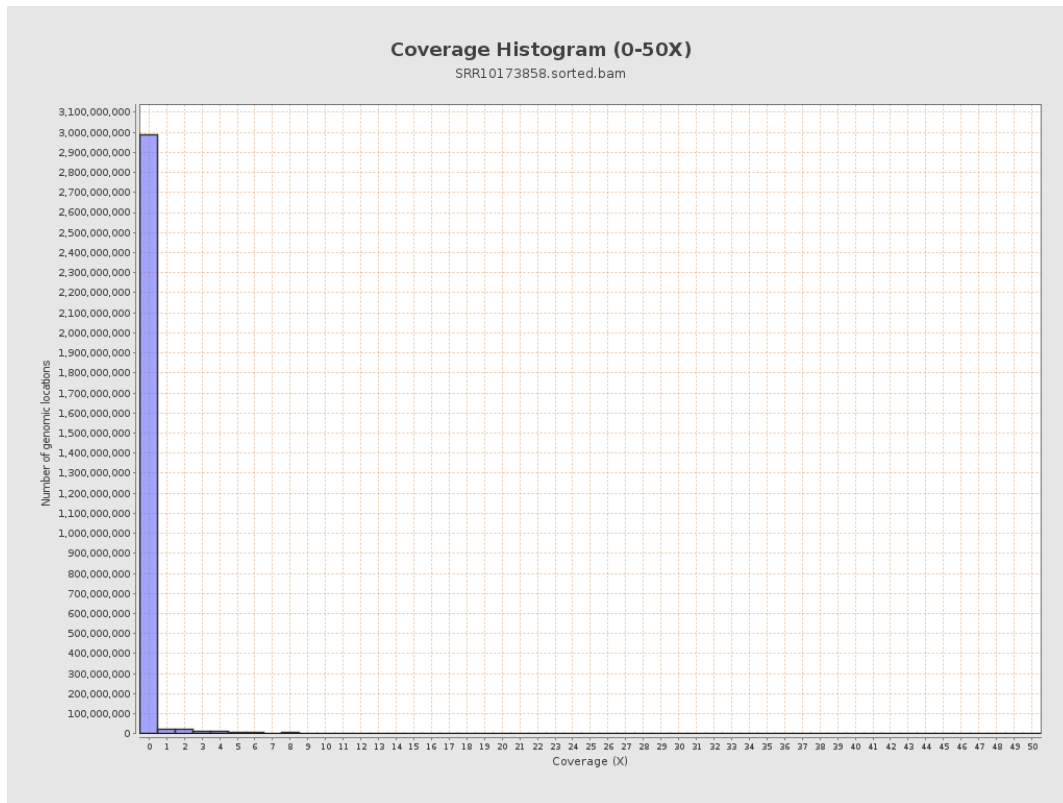
### 3. Results : Coverage across reference



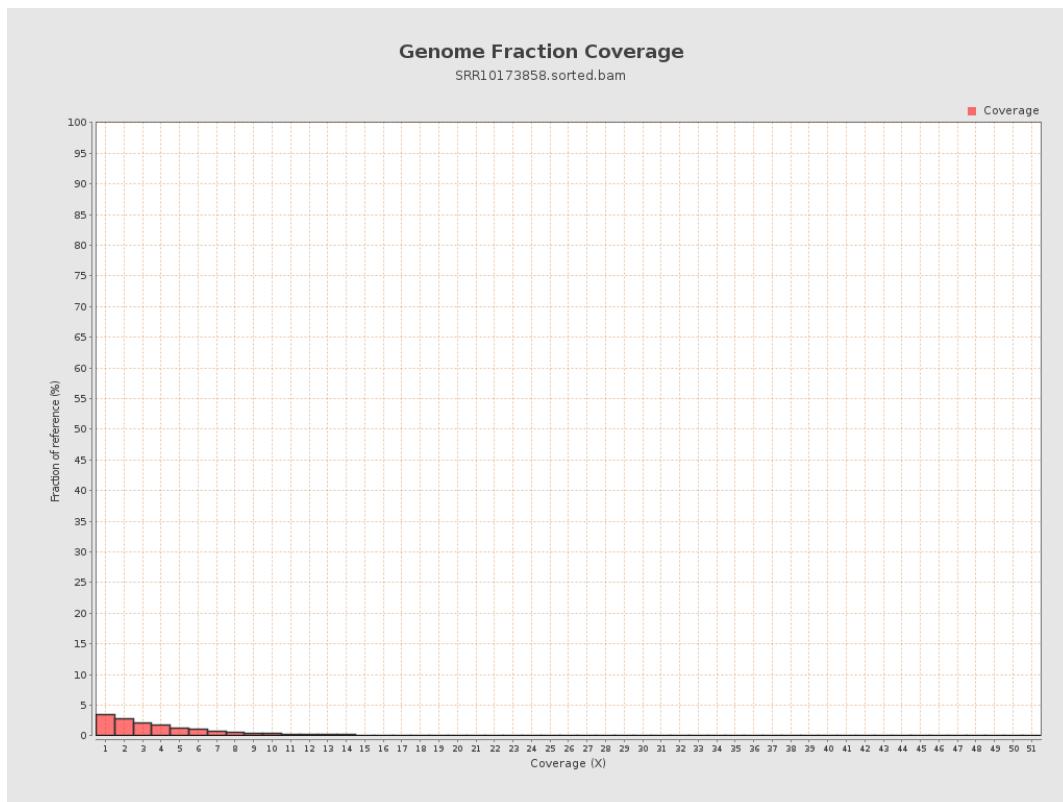
## 4. Results : Coverage Histogram



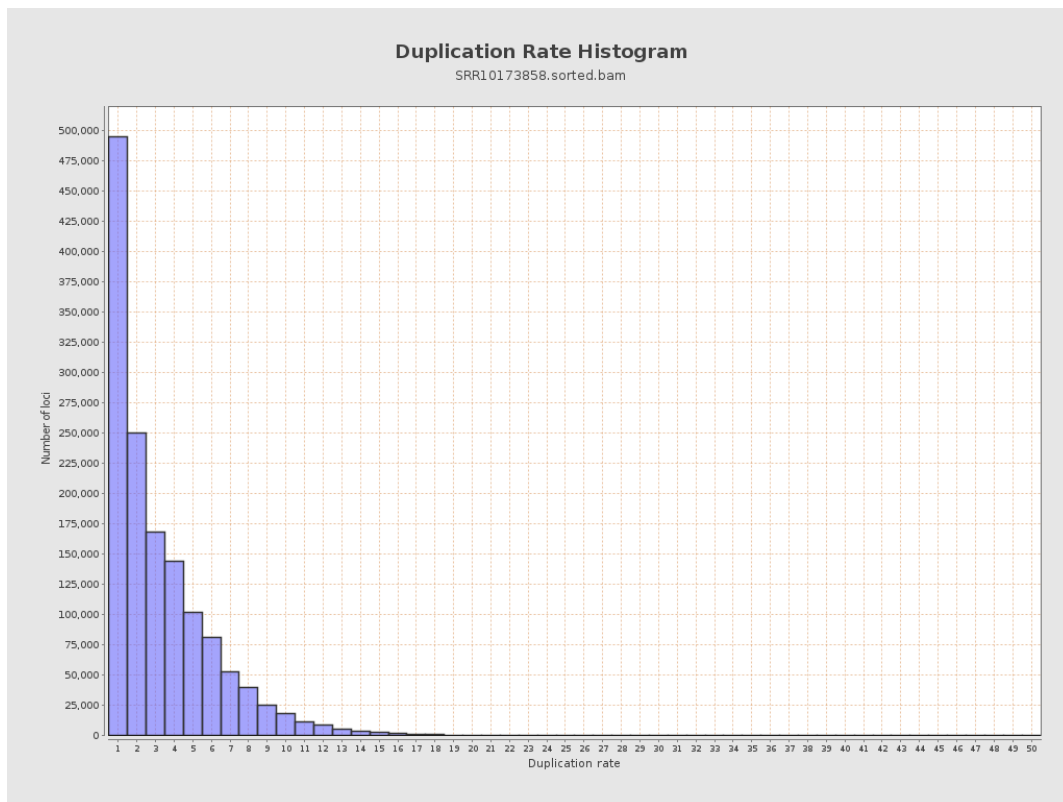
## 5. Results : Coverage Histogram (0-50X)



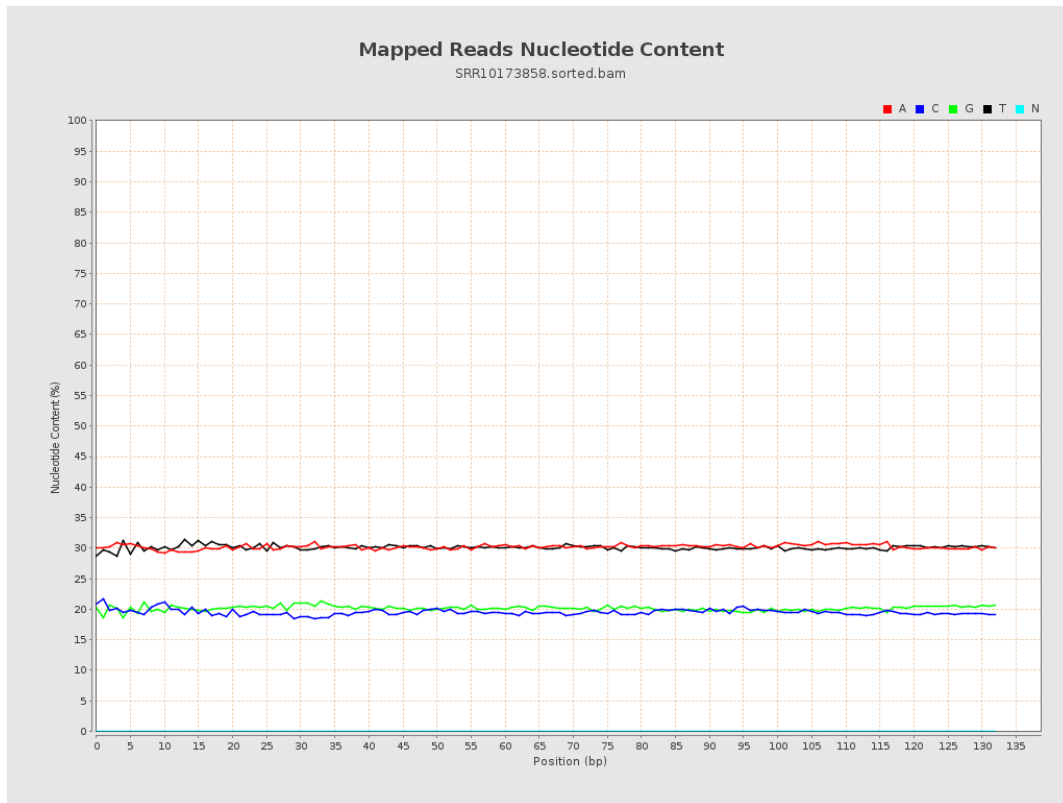
## 6. Results : Genome Fraction Coverage



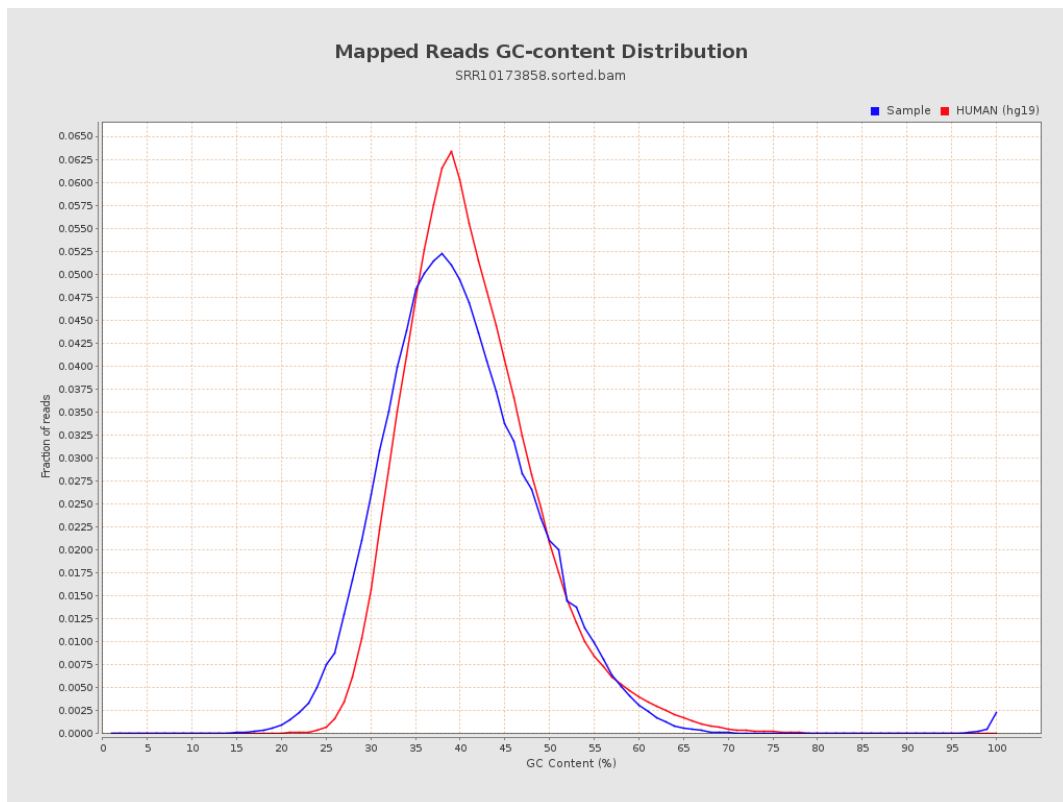
## 7. Results : Duplication Rate Histogram



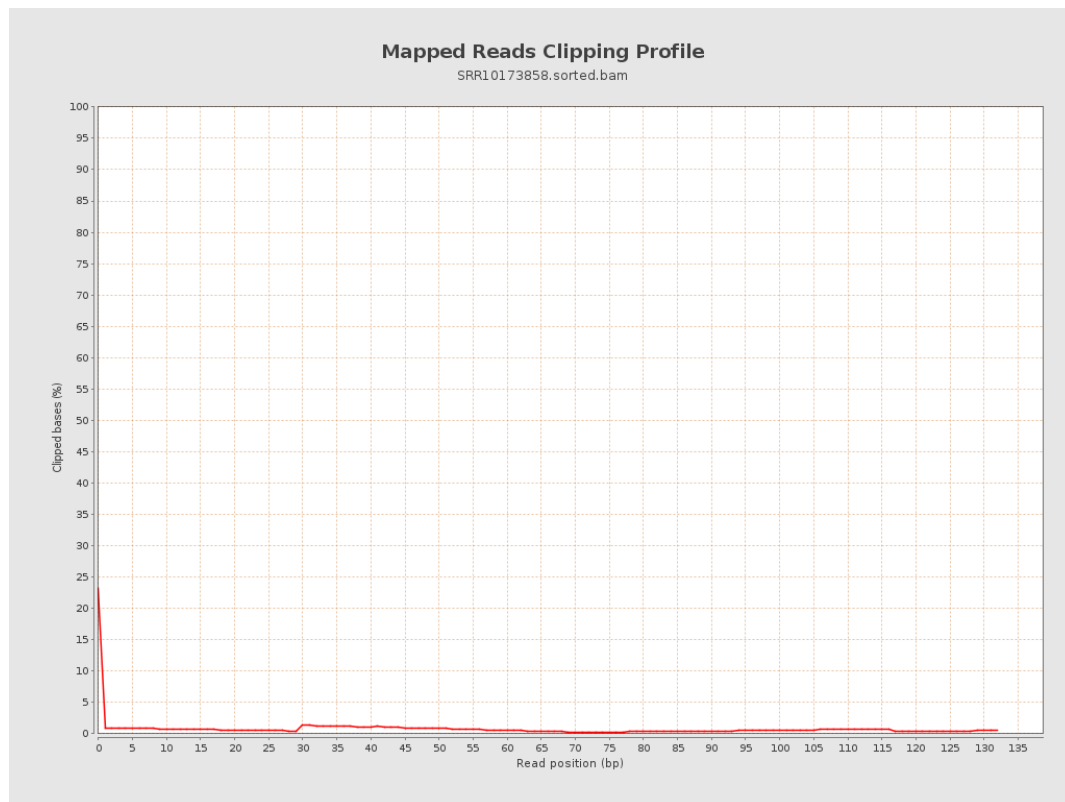
## 8. Results : Mapped Reads Nucleotide Content



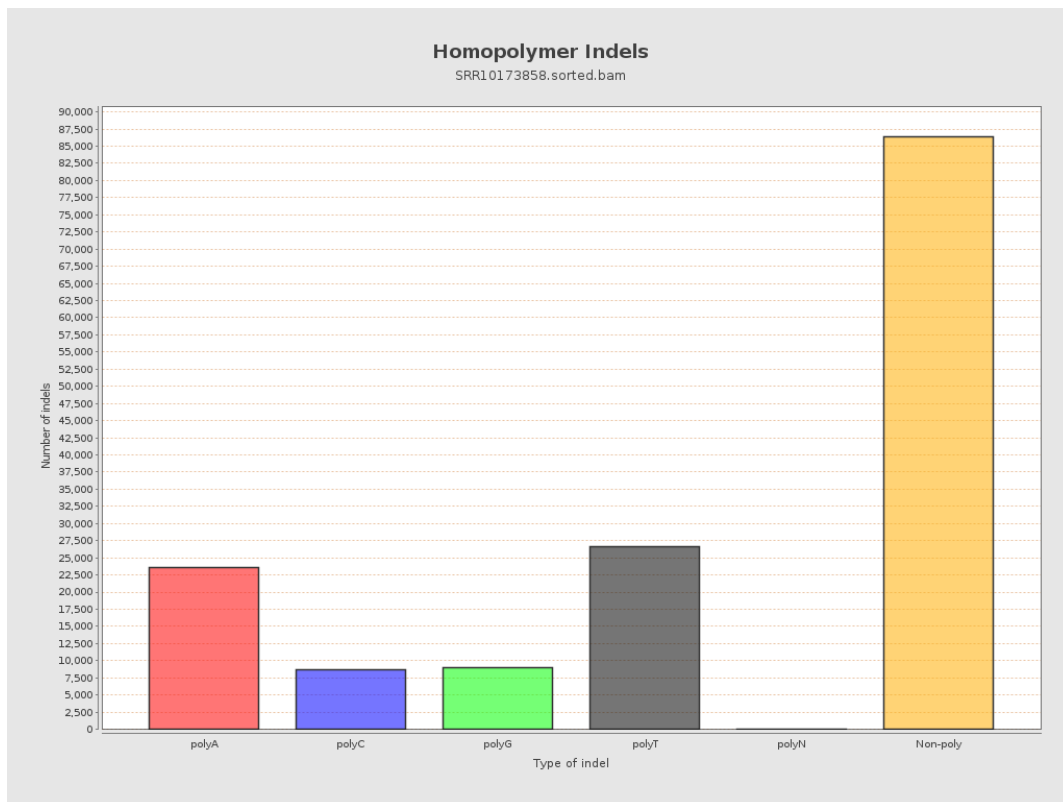
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



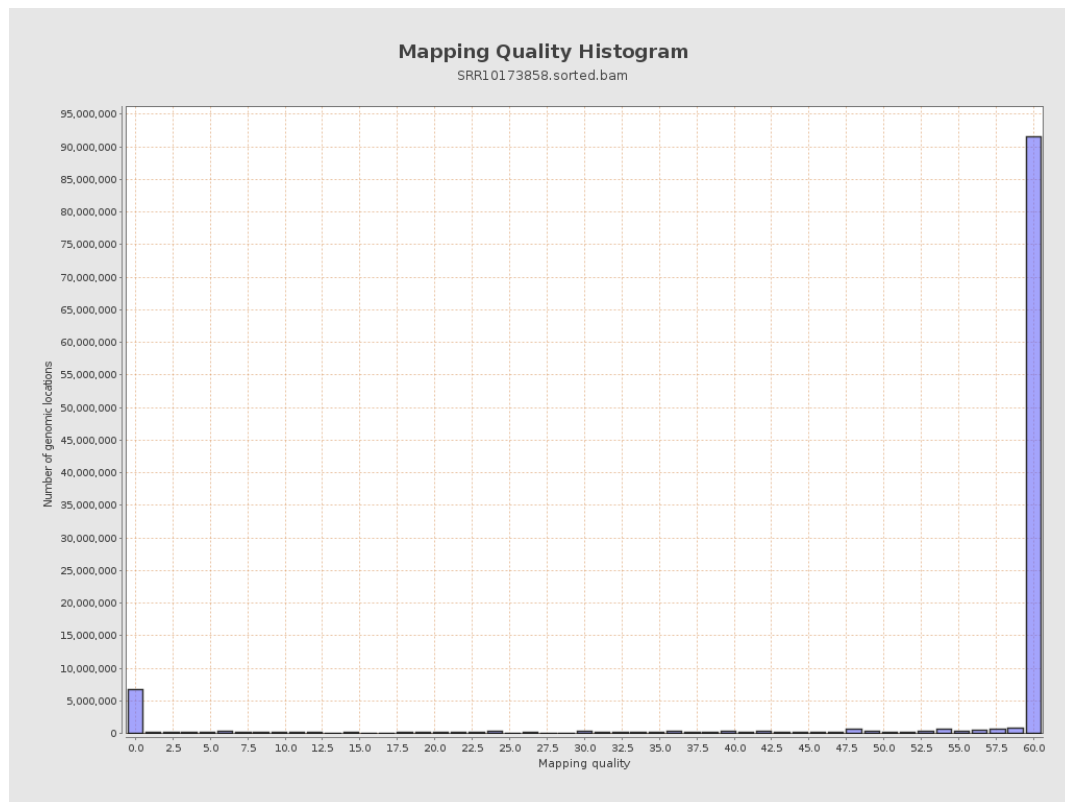
## 11. Results : Homopolymer Indels



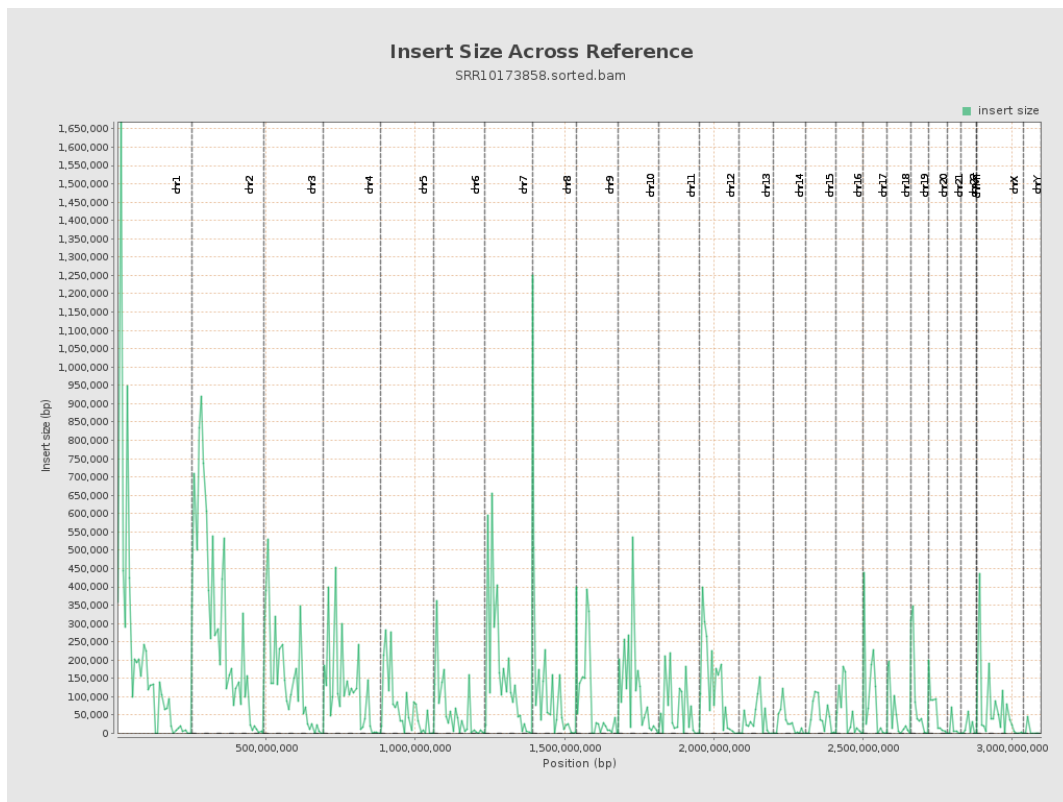
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

