

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/26 17:33:31*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354858.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_SRR22354858 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354858_1.fastq.gz SRR22354858_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                      |
| Analysis date:                        | Mon Aug 26 17:33:31 CST 2024                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                     |
| BAM file:                             | SRR22354858.sorted.bam                                                                                                                                                                                                  |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 43,532,500          |
| Mapped reads                 | 42,769,440 / 98.25% |
| Unmapped reads               | 763,060 / 1.75%     |
| Mapped paired reads          | 42,769,440 / 98.25% |
| Mapped reads, first in pair  | 21,414,514 / 49.19% |
| Mapped reads, second in pair | 21,354,926 / 49.06% |
| Mapped reads, both in pair   | 42,644,708 / 97.96% |
| Mapped reads, singletons     | 124,732 / 0.29%     |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 842,148 / 1.93%     |
| Read min/max/mean length     | 30 / 150 / 150.8    |
| Duplicated reads (estimated) | 24,860,803 / 57.11% |
| Duplication rate             | 57.16%              |
| Clipped reads                | 13,111,016 / 30.12% |

### 2.2. ACGT Content

|                          |                        |
|--------------------------|------------------------|
| Number/percentage of A's | 1,639,153,578 / 28.02% |
| Number/percentage of C's | 1,265,172,087 / 21.62% |
| Number/percentage of T's | 1,664,813,426 / 28.45% |
| Number/percentage of G's | 1,281,735,384 / 21.91% |
| Number/percentage of N's | 32,254 / 0%            |
|                          |                        |

|               |        |
|---------------|--------|
| GC Percentage | 43.53% |
|---------------|--------|

## 2.3. Coverage

|                    |         |
|--------------------|---------|
| Mean               | 1.8911  |
| Standard Deviation | 39.6993 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 53.91 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 155,838.81      |
| Standard Deviation | 4,443,238.46    |
| P25/Median/P75     | 150 / 240 / 361 |

## 2.6. Mismatches and indels

|                                          |            |
|------------------------------------------|------------|
| General error rate                       | 0.8%       |
| Mismatches                               | 43,173,488 |
| Insertions                               | 1,077,038  |
| Mapped reads with at least one insertion | 2.3%       |
| Deletions                                | 1,048,870  |
| Mapped reads with at least one deletion  | 2.31%      |
| Homopolymer indels                       | 41.88%     |

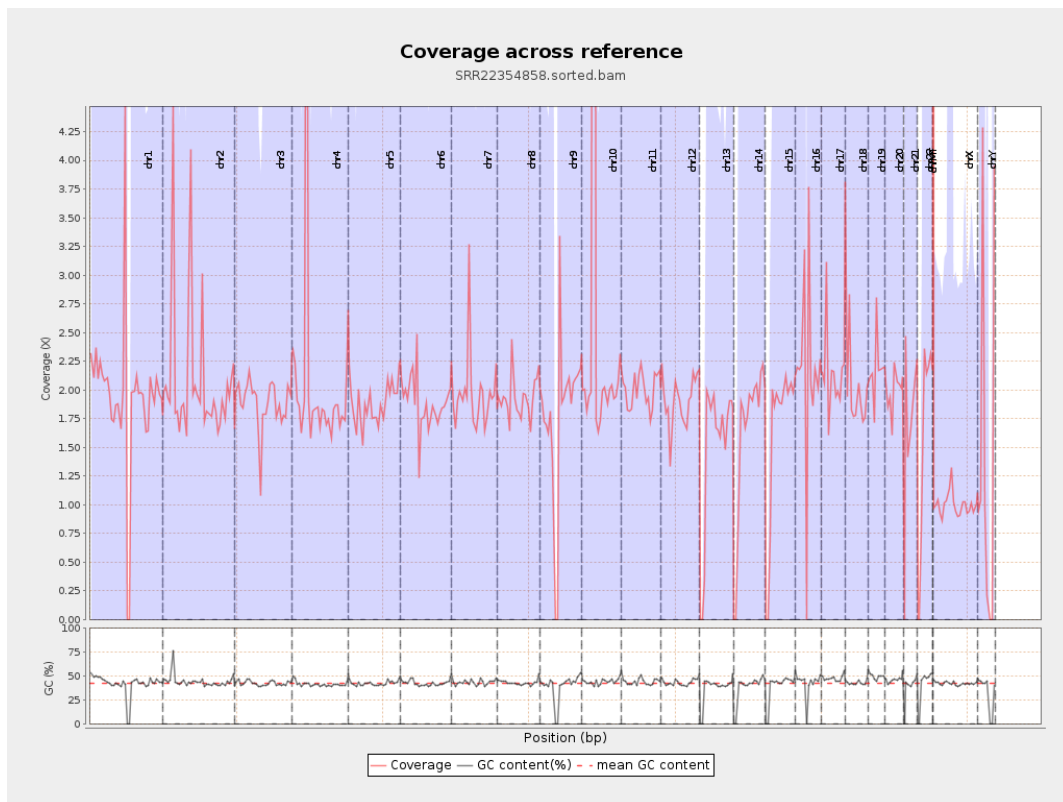
## 2.7. Chromosome stats

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

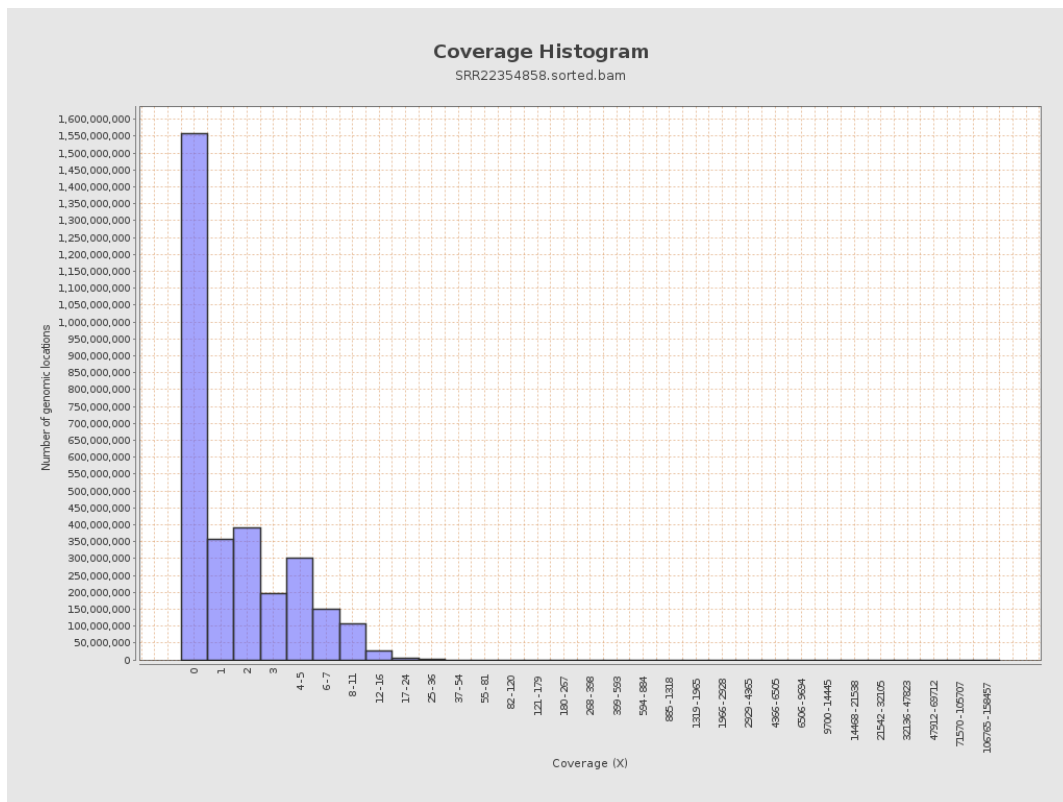
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 483425358    | 1.9395          | 57.723           |
| chr2  | 243199373 | 508865462    | 2.0924          | 90.9988          |
| chr3  | 198022430 | 372377659    | 1.8805          | 3.9272           |
| chr4  | 191154276 | 396614701    | 2.0748          | 44.1755          |
| chr5  | 180915260 | 342025540    | 1.8905          | 3.0295           |
| chr6  | 171115067 | 321839010    | 1.8808          | 8.23             |
| chr7  | 159138663 | 313795141    | 1.9718          | 30.0791          |
| chr8  | 146364022 | 281611409    | 1.924           | 6.8841           |
| chr9  | 141213431 | 250136455    | 1.7713          | 33.3362          |
| chr10 | 135534747 | 344193880    | 2.5395          | 84.8013          |
| chr11 | 135006516 | 269804506    | 1.9985          | 9.8741           |
| chr12 | 133851895 | 255914253    | 1.9119          | 2.9696           |
| chr13 | 115169878 | 172615266    | 1.4988          | 2.5239           |
| chr14 | 107349540 | 175345861    | 1.6334          | 3.7621           |
| chr15 | 102531392 | 164157583    | 1.601           | 2.6297           |
| chr16 | 90354753  | 196424239    | 2.1739          | 15.3016          |
| chr17 | 81195210  | 173371692    | 2.1352          | 13.0079          |
| chr18 | 78077248  | 159265245    | 2.0398          | 29.2503          |
| chr19 | 59128983  | 129147088    | 2.1842          | 29.8104          |
| chr20 | 63025520  | 125074911    | 1.9845          | 13.6109          |
| chr21 | 48129895  | 84870707     | 1.7634          | 21.234           |
| chr22 | 51304566  | 80168534     | 1.5626          | 5.5127           |
| chrMT | 16571     | 11956367     | 721.5236        | 168.8475         |
| chrX  | 155270560 | 155231088    | 0.9997          | 3.8755           |

|      |          |          |        |         |
|------|----------|----------|--------|---------|
| chrY | 59373566 | 85909049 | 1.4469 | 49.3447 |
|------|----------|----------|--------|---------|

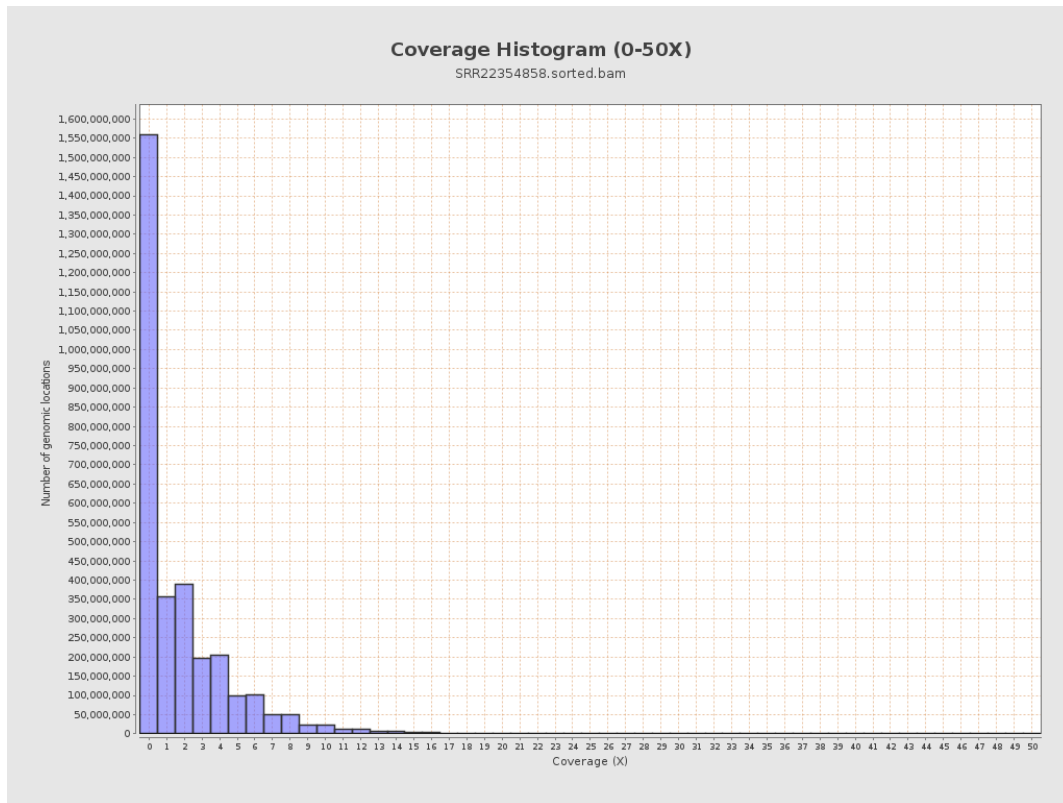
### 3. Results : Coverage across reference



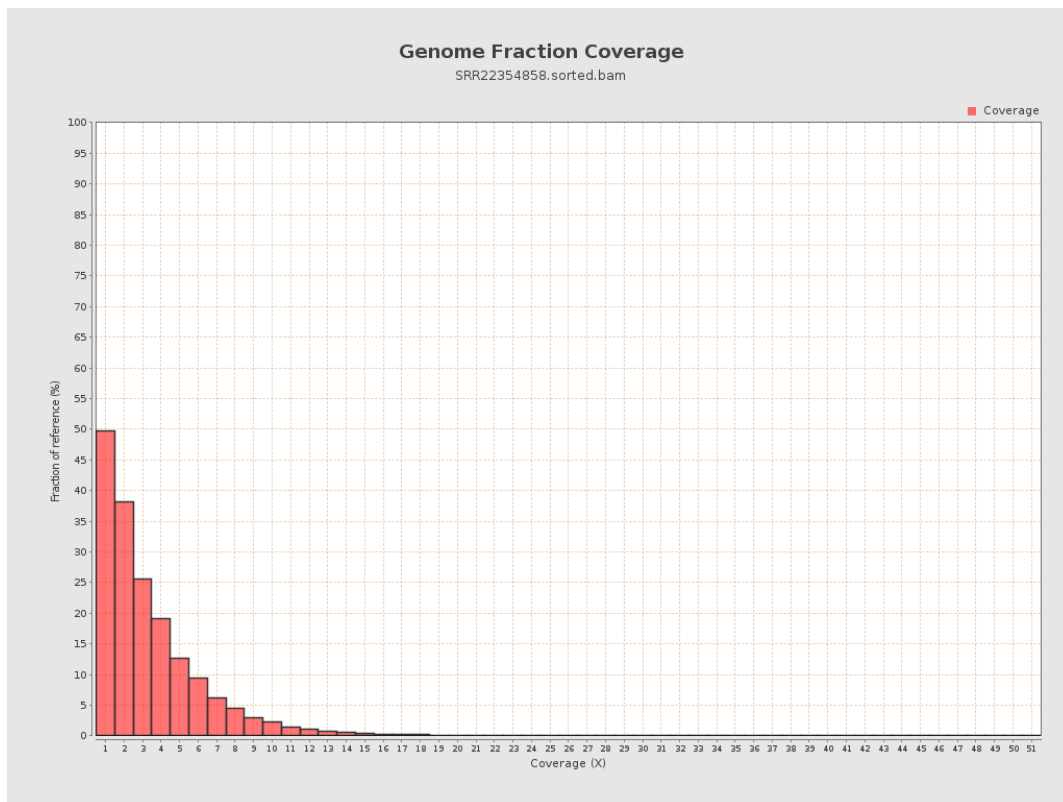
## 4. Results : Coverage Histogram



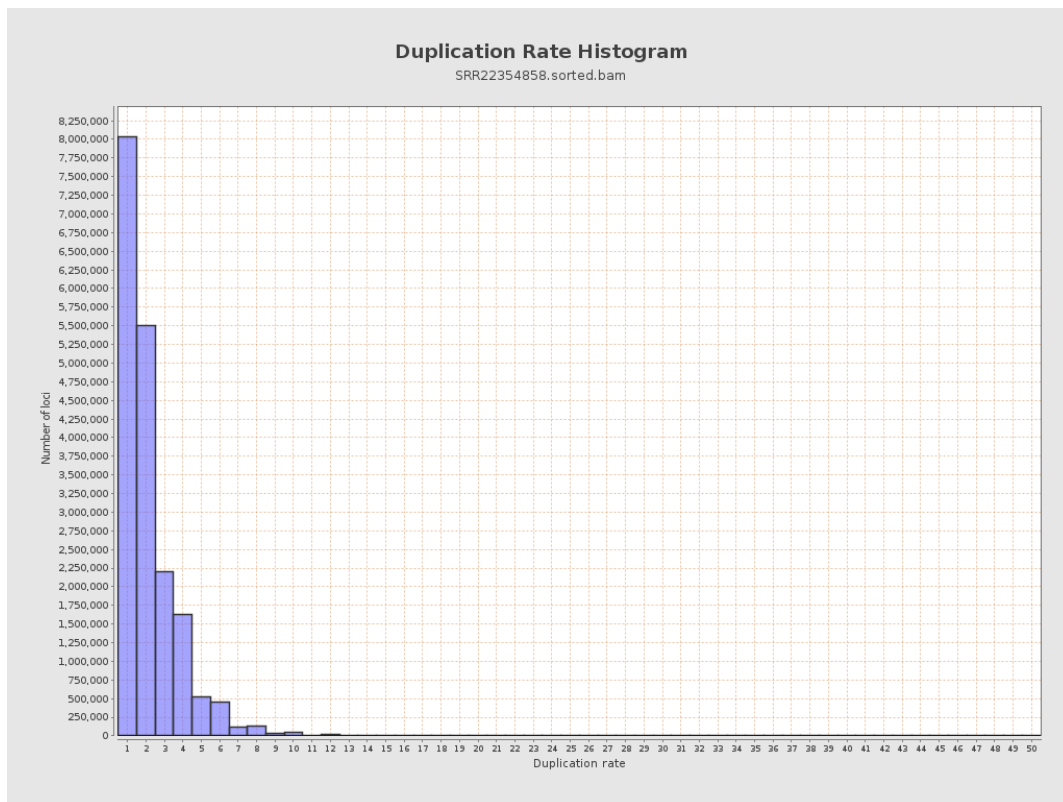
## 5. Results : Coverage Histogram (0-50X)



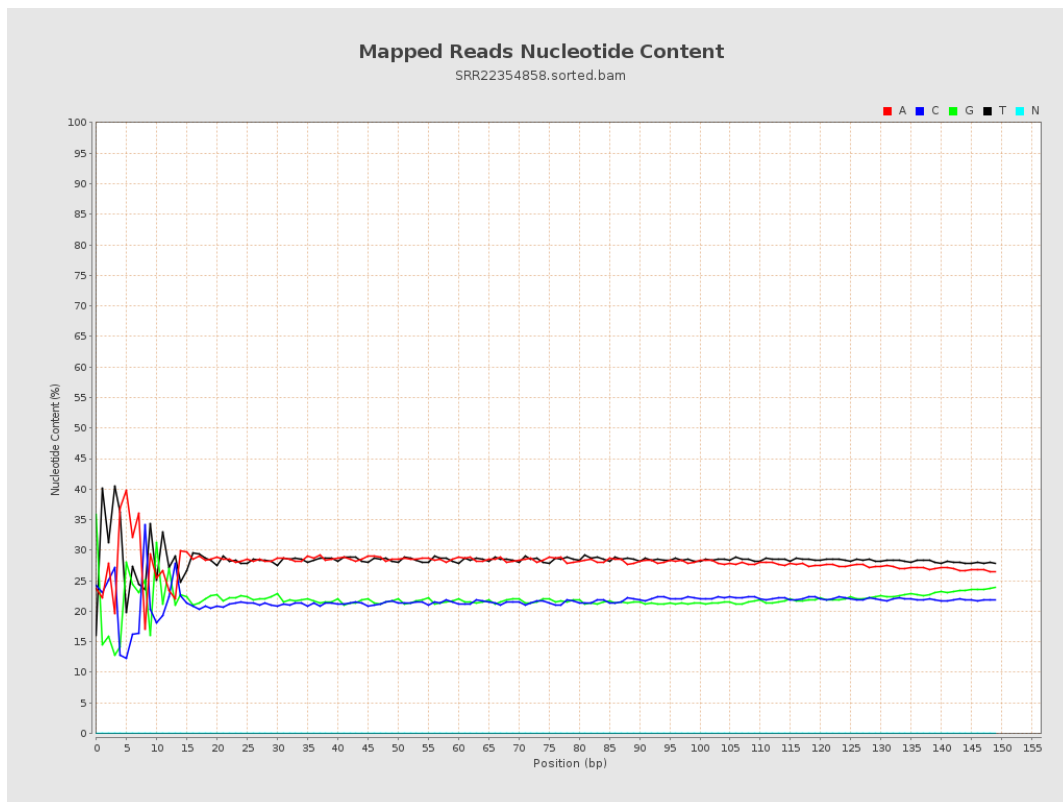
## 6. Results : Genome Fraction Coverage



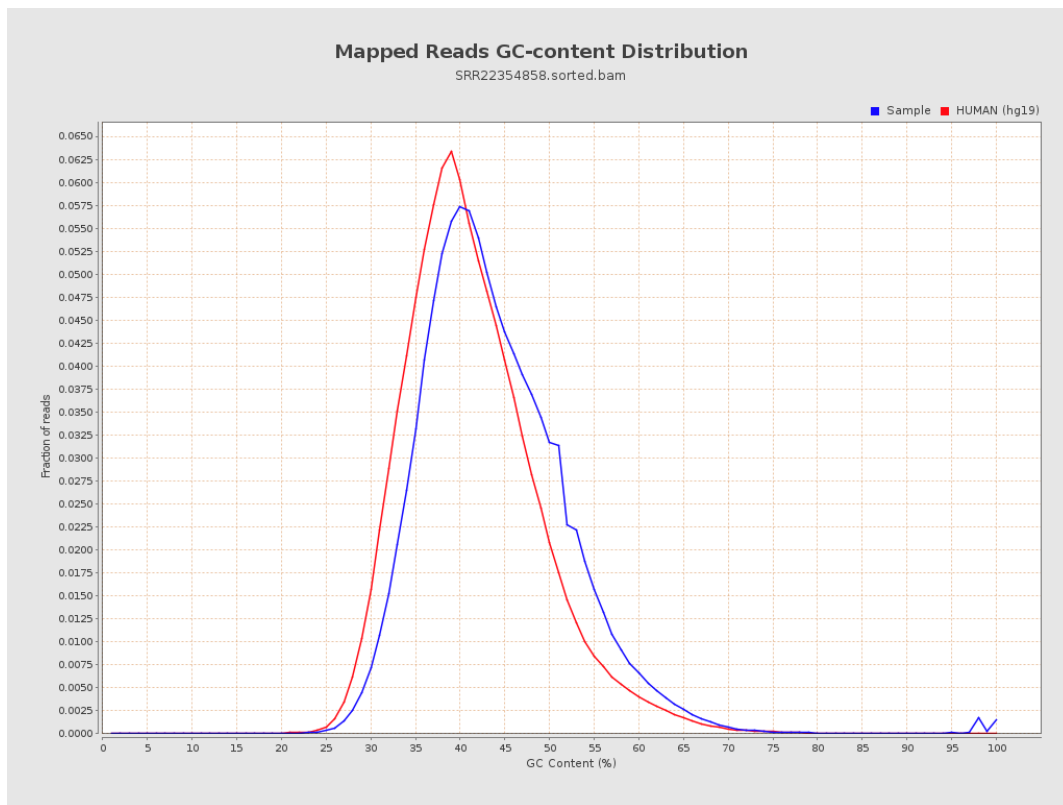
## 7. Results : Duplication Rate Histogram



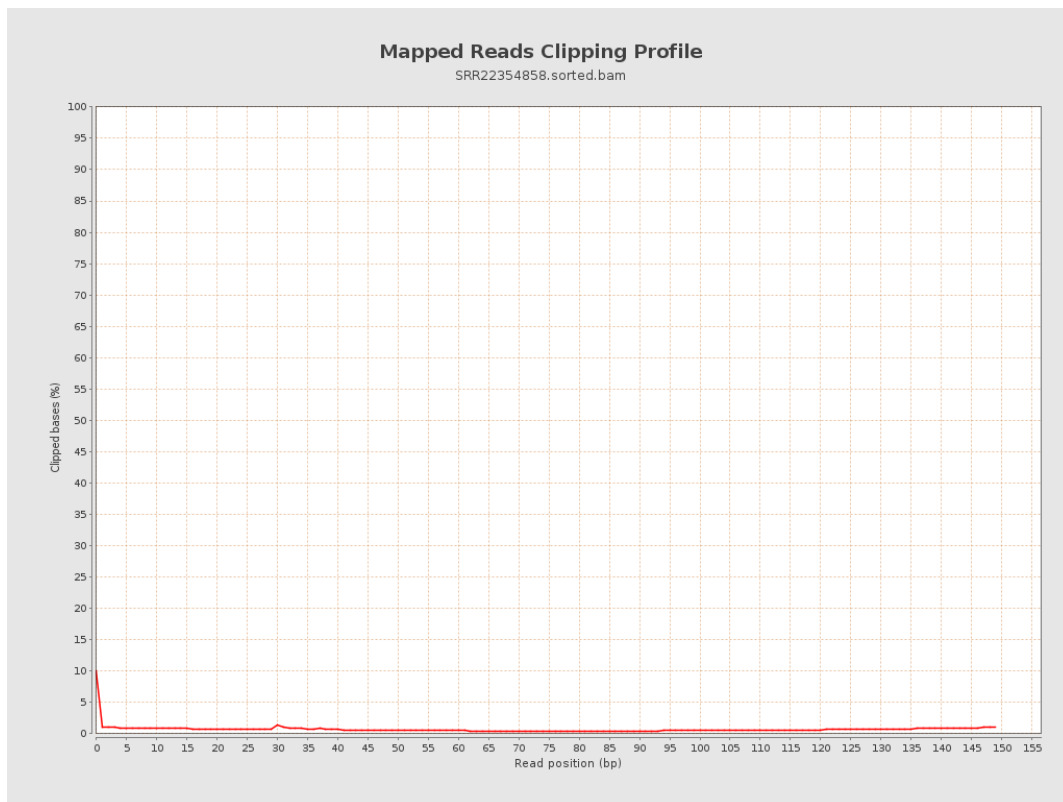
## 8. Results : Mapped Reads Nucleotide Content



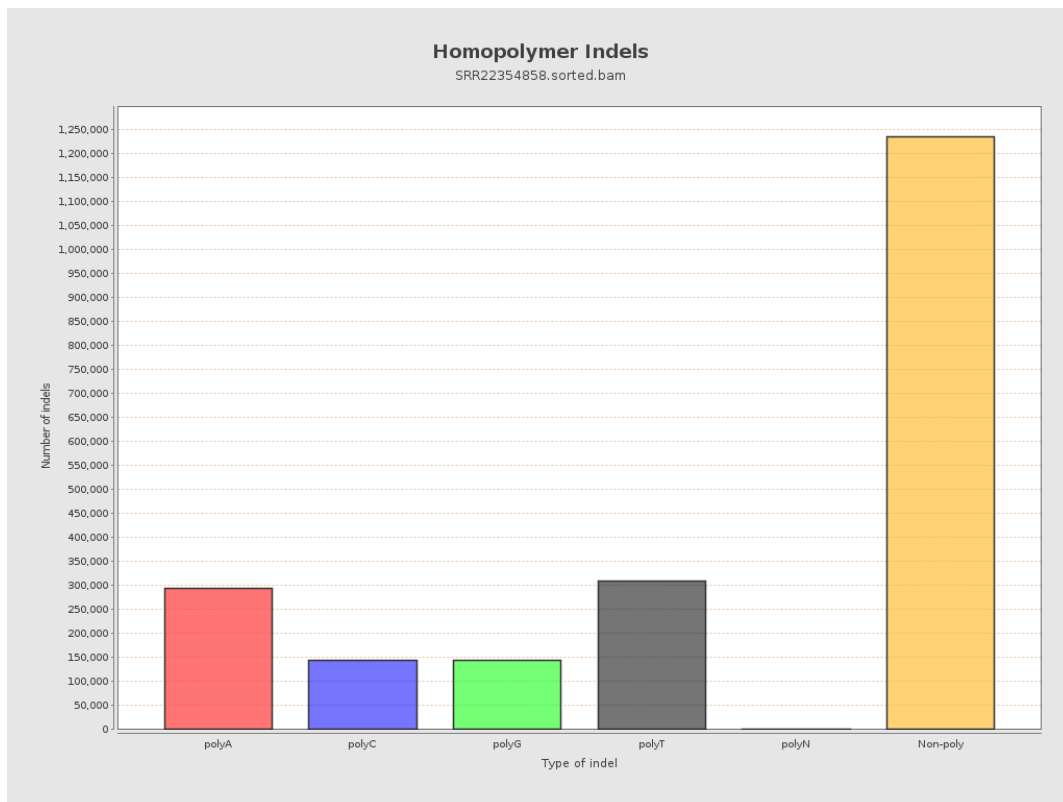
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



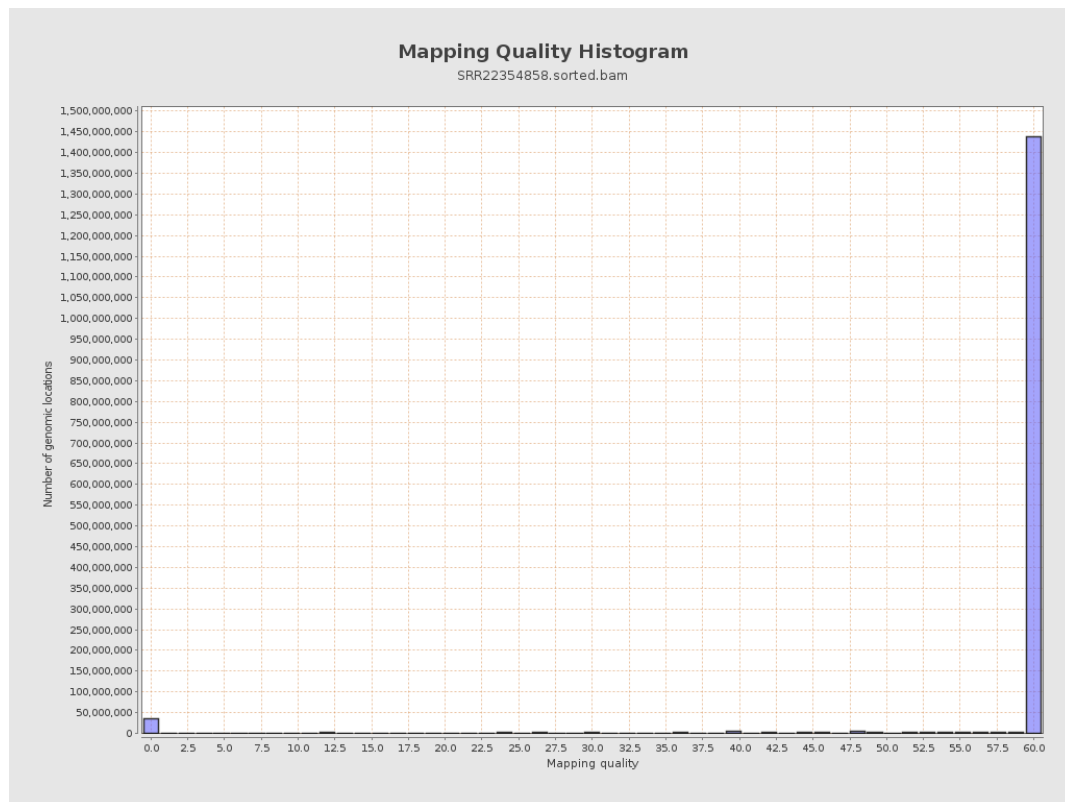
## 11. Results : Homopolymer Indels



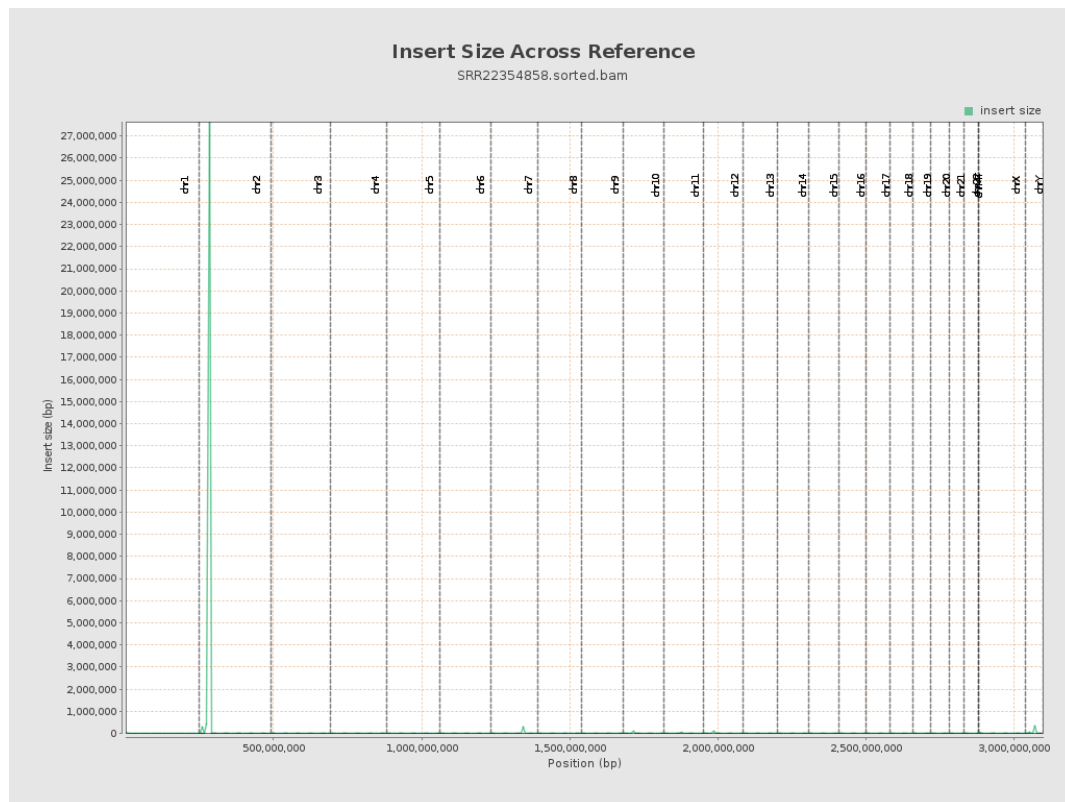
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

