

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/05 07:50:40*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174094.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_SRR10174094 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174094_1.fastq.gz SRR10174094_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                      |
| Analysis date:                        | Thu Sep 05 07:50:39 CST 2024                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                     |
| BAM file:                             | SRR10174094.sorted.bam                                                                                                                                                                                                  |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 5,947,294          |
| Mapped reads                 | 5,821,052 / 97.88% |
| Unmapped reads               | 126,242 / 2.12%    |
| Mapped paired reads          | 5,821,052 / 97.88% |
| Mapped reads, first in pair  | 2,911,558 / 48.96% |
| Mapped reads, second in pair | 2,909,494 / 48.92% |
| Mapped reads, both in pair   | 5,740,630 / 96.53% |
| Mapped reads, singletons     | 80,422 / 1.35%     |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 775,130 / 13.03%   |
| Read min/max/mean length     | 30 / 133 / 125.83  |
| Duplicated reads (estimated) | 4,620,847 / 77.7%  |
| Duplication rate             | 64.35%             |
| Clipped reads                | 2,946,556 / 49.54% |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 197,586,518 / 29.78% |
| Number/percentage of C's | 132,277,992 / 19.94% |
| Number/percentage of T's | 195,993,233 / 29.54% |
| Number/percentage of G's | 137,529,403 / 20.73% |
| Number/percentage of N's | 5,210 / 0%           |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 40.67% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.2144 |
| Standard Deviation | 3.8479 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 52.63 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 1,024,480.6     |
| Standard Deviation | 9,645,794.73    |
| P25/Median/P75     | 107 / 157 / 239 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.87%     |
| Mismatches                               | 5,573,297 |
| Insertions                               | 67,233    |
| Mapped reads with at least one insertion | 1.11%     |
| Deletions                                | 196,778   |
| Mapped reads with at least one deletion  | 3.3%      |
| Homopolymer indels                       | 41.03%    |

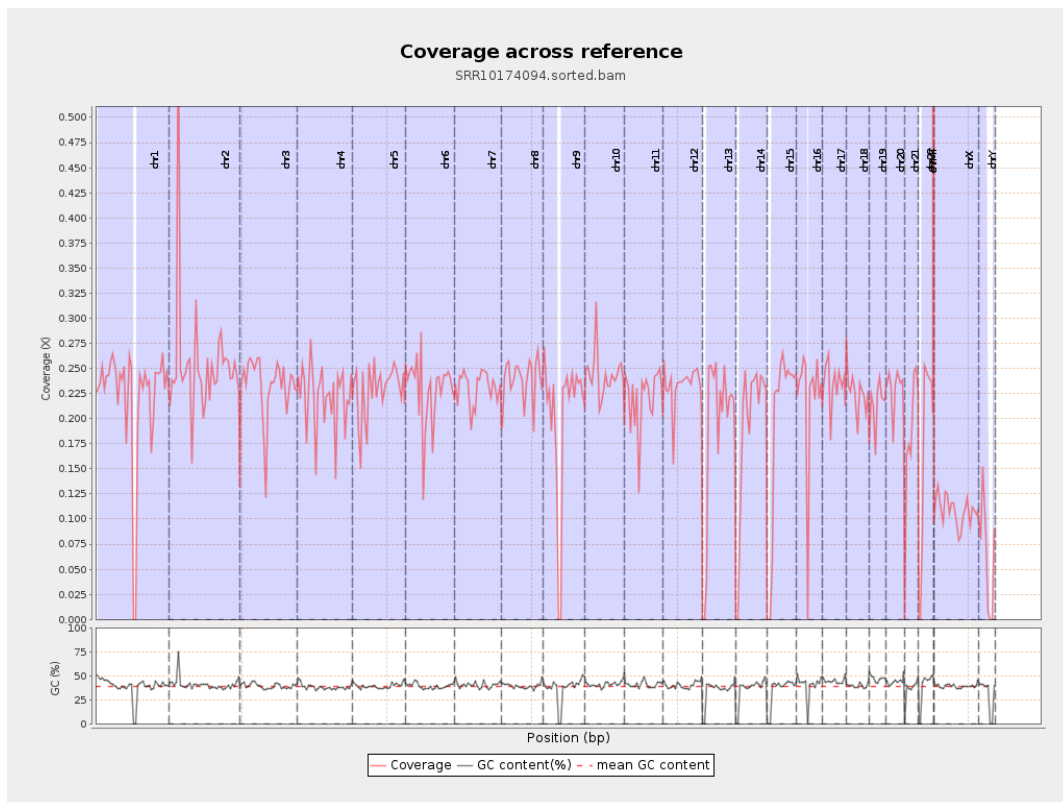
## 2.7. Chromosome stats

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

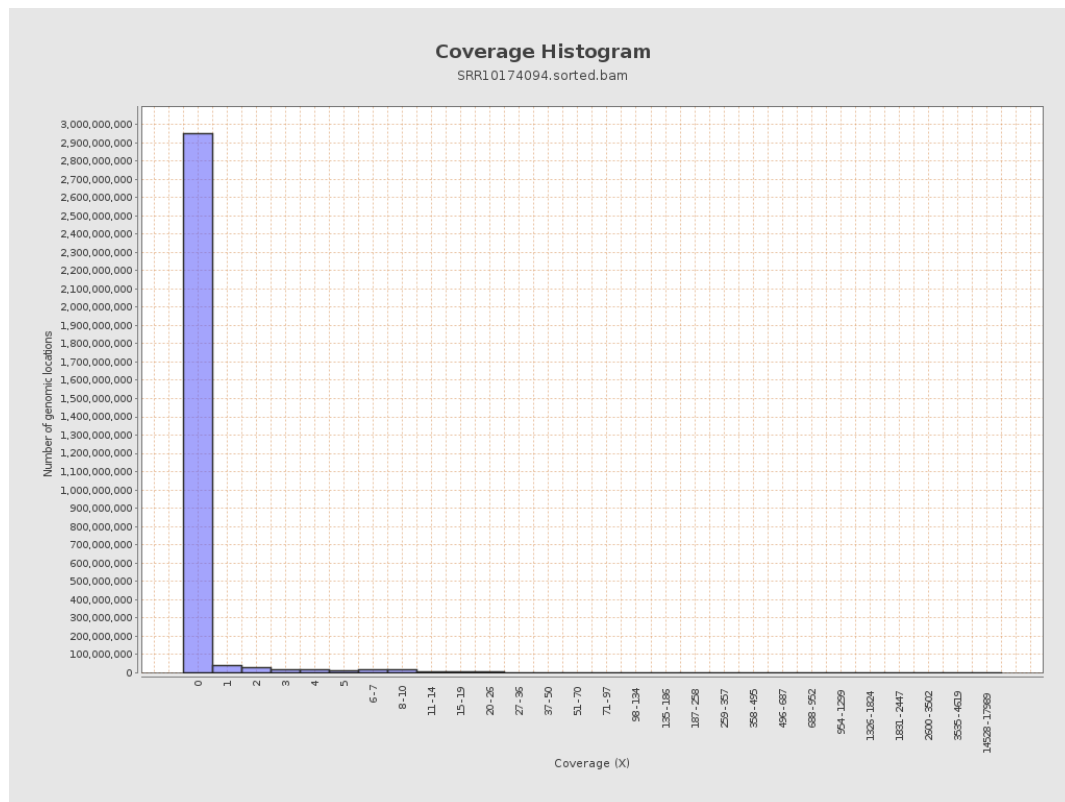
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 55032738     | 0.2208          | 1.7225           |
| chr2  | 243199373 | 62100981     | 0.2554          | 12.6036          |
| chr3  | 198022430 | 45999843     | 0.2323          | 1.4261           |
| chr4  | 191154276 | 42235889     | 0.221           | 1.5753           |
| chr5  | 180915260 | 41337663     | 0.2285          | 1.4268           |
| chr6  | 171115067 | 39136712     | 0.2287          | 1.5846           |
| chr7  | 159138663 | 36834746     | 0.2315          | 1.6725           |
| chr8  | 146364022 | 34912835     | 0.2385          | 2.1352           |
| chr9  | 141213431 | 28385572     | 0.201           | 1.8331           |
| chr10 | 135534747 | 32981817     | 0.2433          | 1.9027           |
| chr11 | 135006516 | 29769146     | 0.2205          | 1.4288           |
| chr12 | 133851895 | 31244277     | 0.2334          | 1.4937           |
| chr13 | 115169878 | 21709542     | 0.1885          | 1.298            |
| chr14 | 107349540 | 20318648     | 0.1893          | 1.304            |
| chr15 | 102531392 | 19874983     | 0.1938          | 1.3322           |
| chr16 | 90354753  | 19772738     | 0.2188          | 1.5008           |
| chr17 | 81195210  | 18969203     | 0.2336          | 1.4997           |
| chr18 | 78077248  | 17641407     | 0.2259          | 2.4469           |
| chr19 | 59128983  | 12677545     | 0.2144          | 1.5971           |
| chr20 | 63025520  | 14401718     | 0.2285          | 1.4159           |
| chr21 | 48129895  | 8835707      | 0.1836          | 1.4989           |
| chr22 | 51304566  | 8576482      | 0.1672          | 1.3758           |
| chrMT | 16571     | 583833       | 35.2322         | 33.1036          |
| chrX  | 155270560 | 16831392     | 0.1084          | 0.9727           |

|      |          |         |       |        |
|------|----------|---------|-------|--------|
| chrY | 59373566 | 3680299 | 0.062 | 0.9348 |
|------|----------|---------|-------|--------|

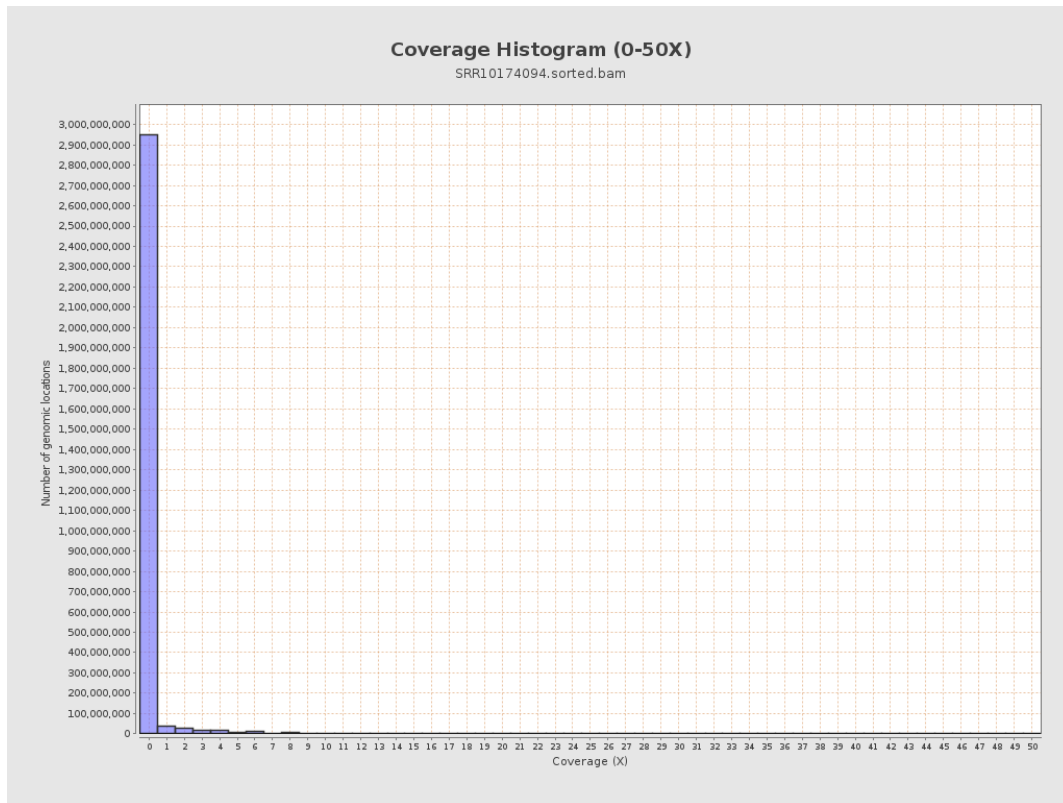
### 3. Results : Coverage across reference



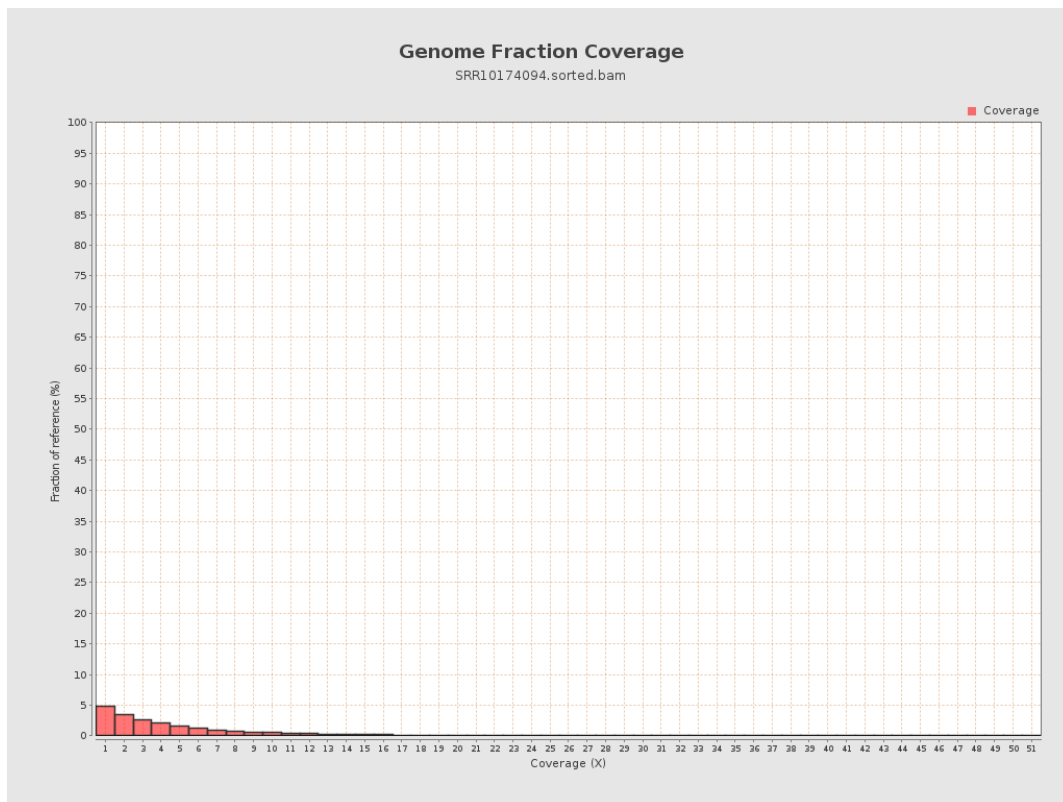
## 4. Results : Coverage Histogram



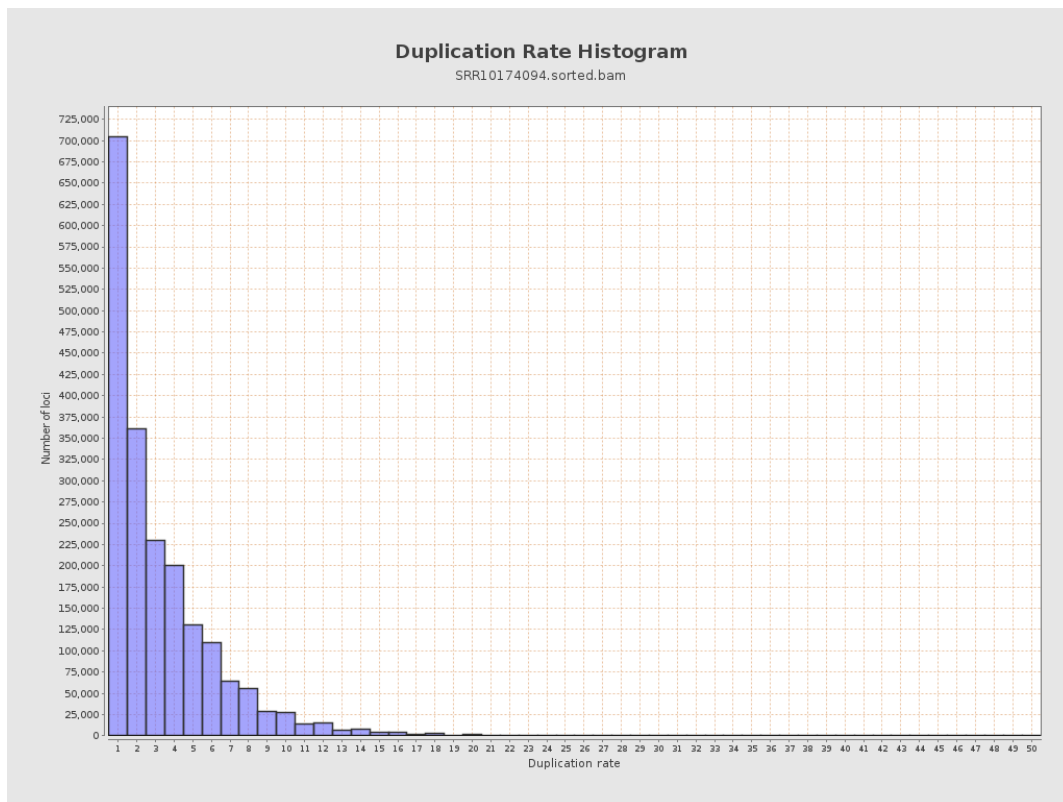
## 5. Results : Coverage Histogram (0-50X)



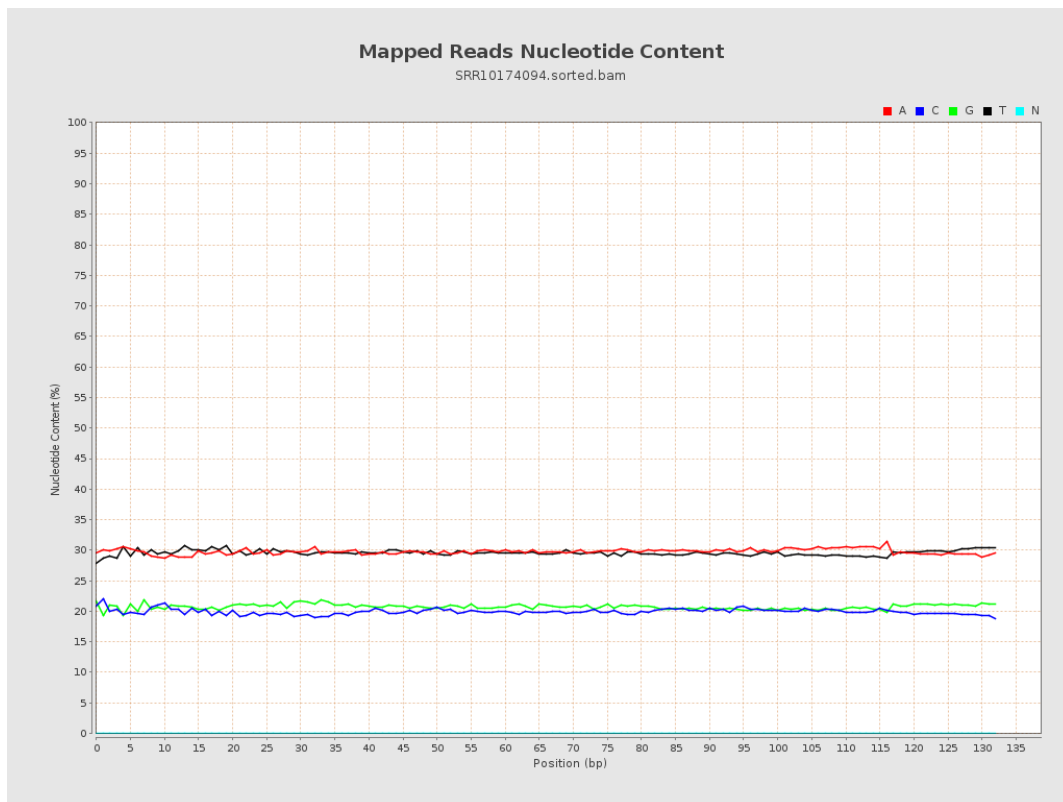
## 6. Results : Genome Fraction Coverage



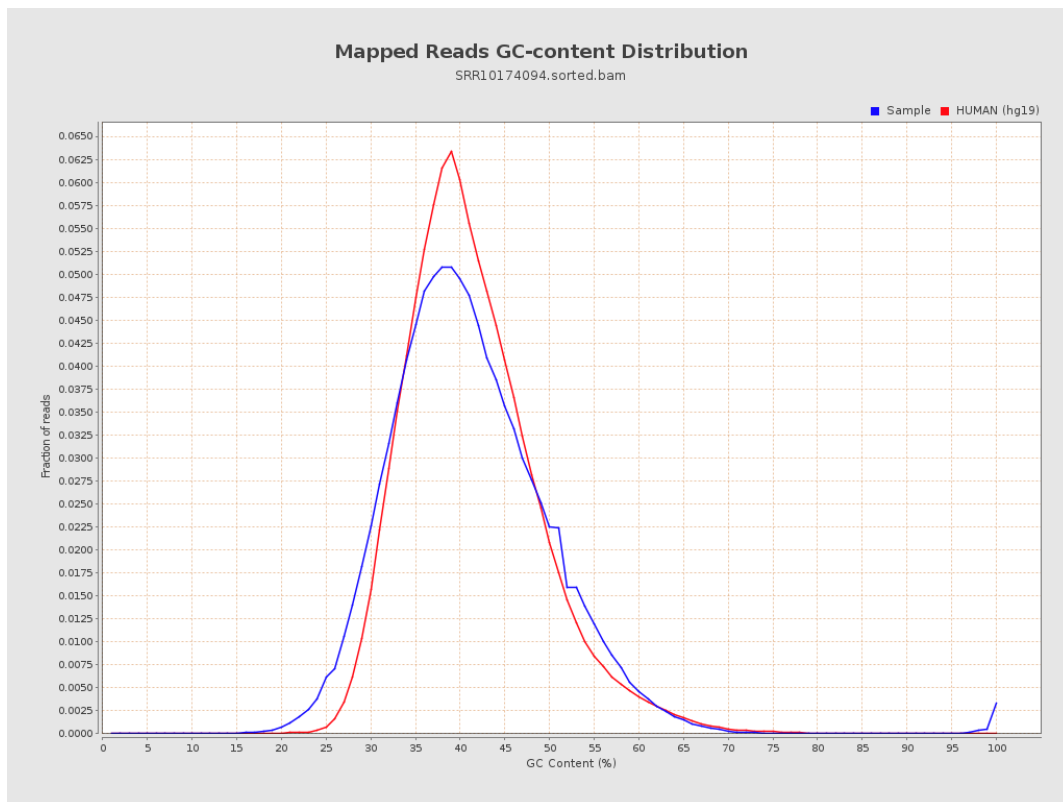
## 7. Results : Duplication Rate Histogram



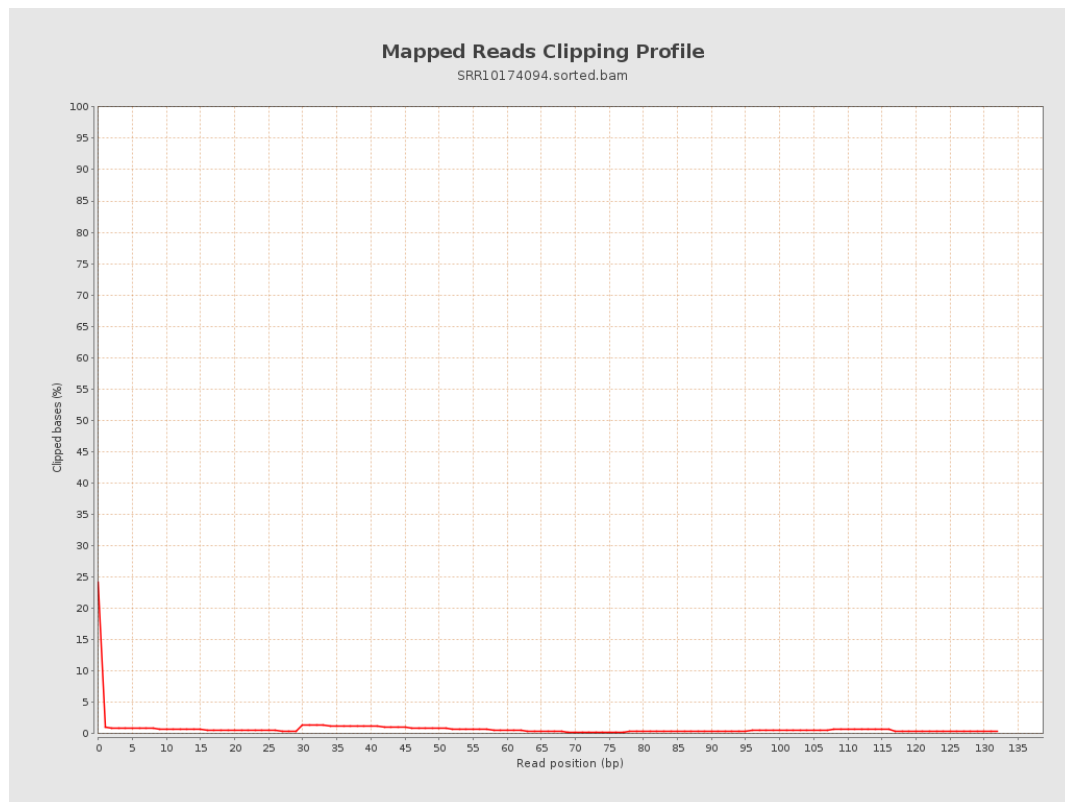
## 8. Results : Mapped Reads Nucleotide Content



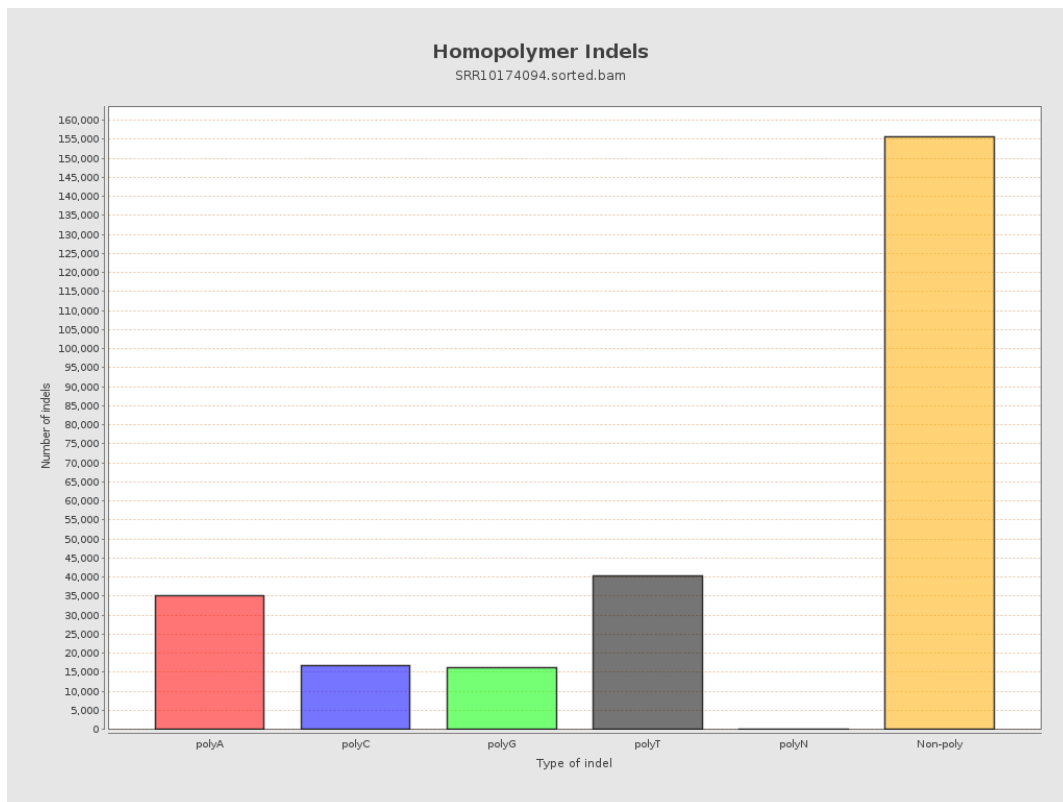
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



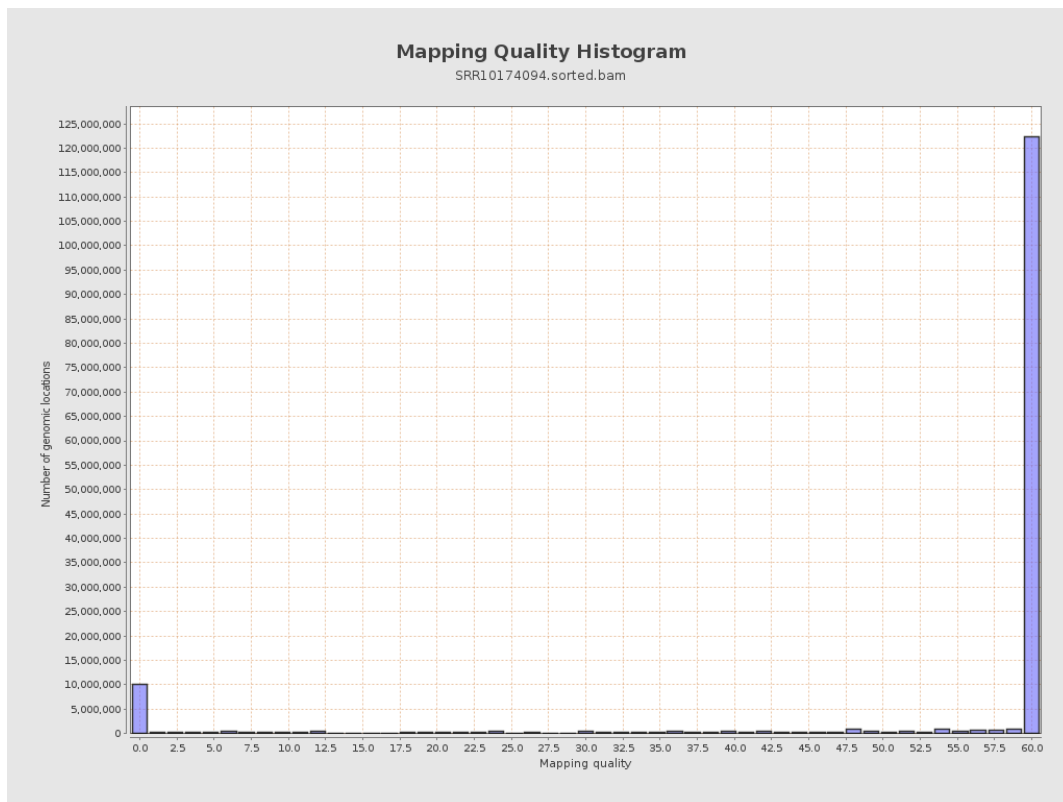
## 11. Results : Homopolymer Indels



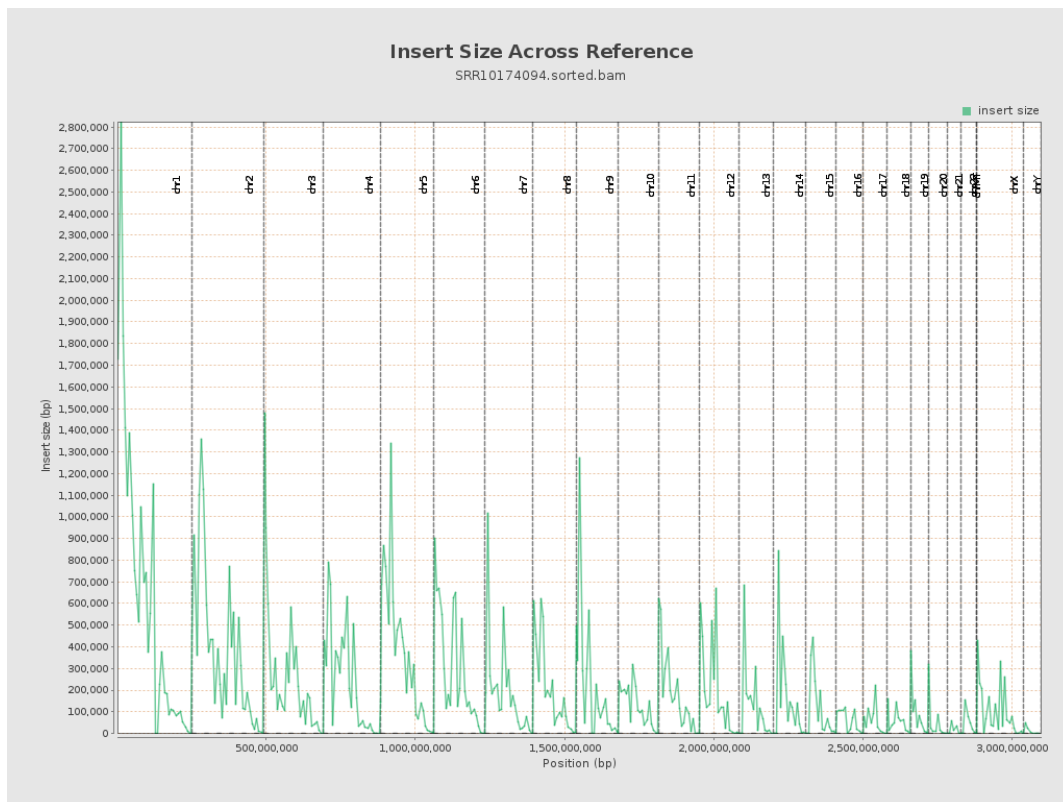
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

