

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/30 15:09:12*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR21672001.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_SRR21672001 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21672001_1.fastq.gz SRR21672001_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                      |
| Analysis date:                        | Mon Sep 30 15:09:11 CST 2024                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                     |
| BAM file:                             | SRR21672001.sorted.bam                                                                                                                                                                                                  |

## 2. Summary

### 2.1. Globals

|                              |                      |
|------------------------------|----------------------|
| Reference size               | 3,095,693,983        |
| Number of reads              | 199,123,808          |
| Mapped reads                 | 198,020,641 / 99.45% |
| Unmapped reads               | 1,103,167 / 0.55%    |
| Mapped paired reads          | 198,020,641 / 99.45% |
| Mapped reads, first in pair  | 99,020,292 / 49.73%  |
| Mapped reads, second in pair | 99,000,349 / 49.72%  |
| Mapped reads, both in pair   | 197,633,964 / 99.25% |
| Mapped reads, singletons     | 386,677 / 0.19%      |
| Secondary alignments         | 0                    |
| Supplementary alignments     | 920,986 / 0.46%      |
| Read min/max/mean length     | 15 / 150 / 149.57    |
| Duplicated reads (estimated) | 53,745,678 / 26.99%  |
| Duplication rate             | 24.14%               |
| Clipped reads                | 9,594,121 / 4.82%    |

### 2.2. ACGT Content

|                          |                        |
|--------------------------|------------------------|
| Number/percentage of A's | 8,530,037,466 / 29.08% |
| Number/percentage of C's | 6,143,396,735 / 20.95% |
| Number/percentage of T's | 8,490,650,698 / 28.95% |
| Number/percentage of G's | 6,164,462,788 / 21.02% |
| Number/percentage of N's | 128,523 / 0%           |
|                          |                        |

|               |        |
|---------------|--------|
| GC Percentage | 41.97% |
|---------------|--------|

## 2.3. Coverage

|                    |         |
|--------------------|---------|
| Mean               | 9.478   |
| Standard Deviation | 96.6911 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 54.52 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 45,801.61       |
| Standard Deviation | 2,042,049.05    |
| P25/Median/P75     | 344 / 396 / 452 |

## 2.6. Mismatches and indels

|                                          |             |
|------------------------------------------|-------------|
| General error rate                       | 0.63%       |
| Mismatches                               | 174,018,317 |
| Insertions                               | 4,213,181   |
| Mapped reads with at least one insertion | 2%          |
| Deletions                                | 4,402,920   |
| Mapped reads with at least one deletion  | 2.13%       |
| Homopolymer indels                       | 45.75%      |

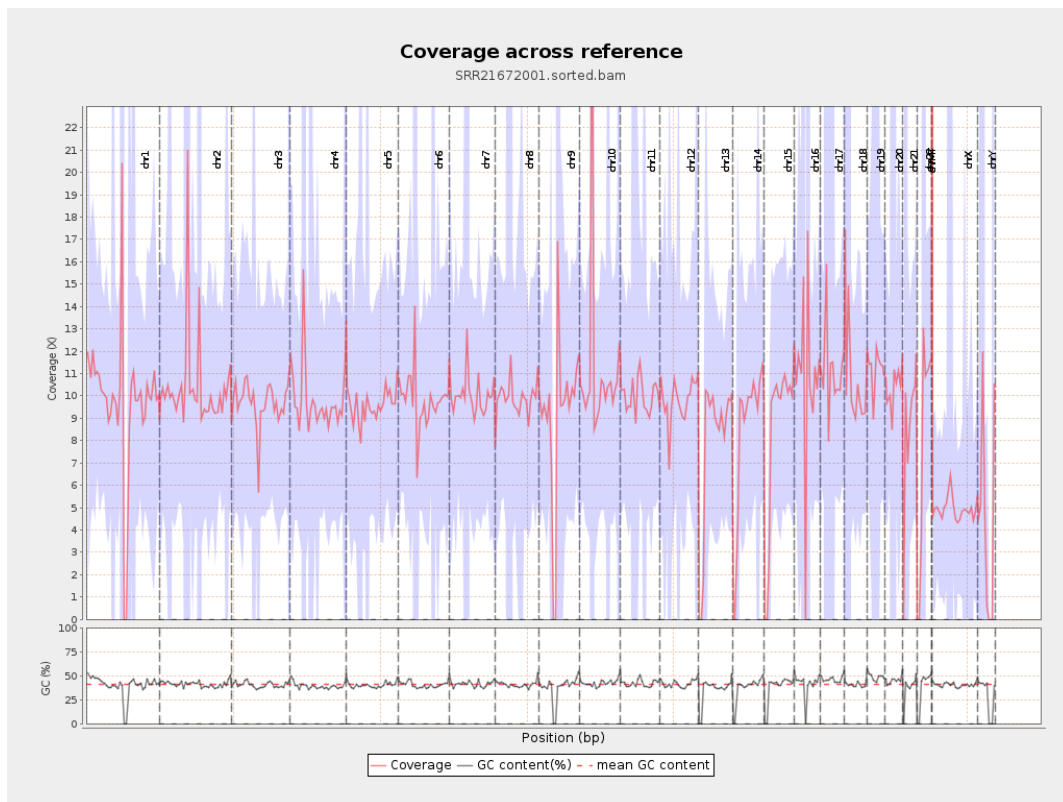
## 2.7. Chromosome stats

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

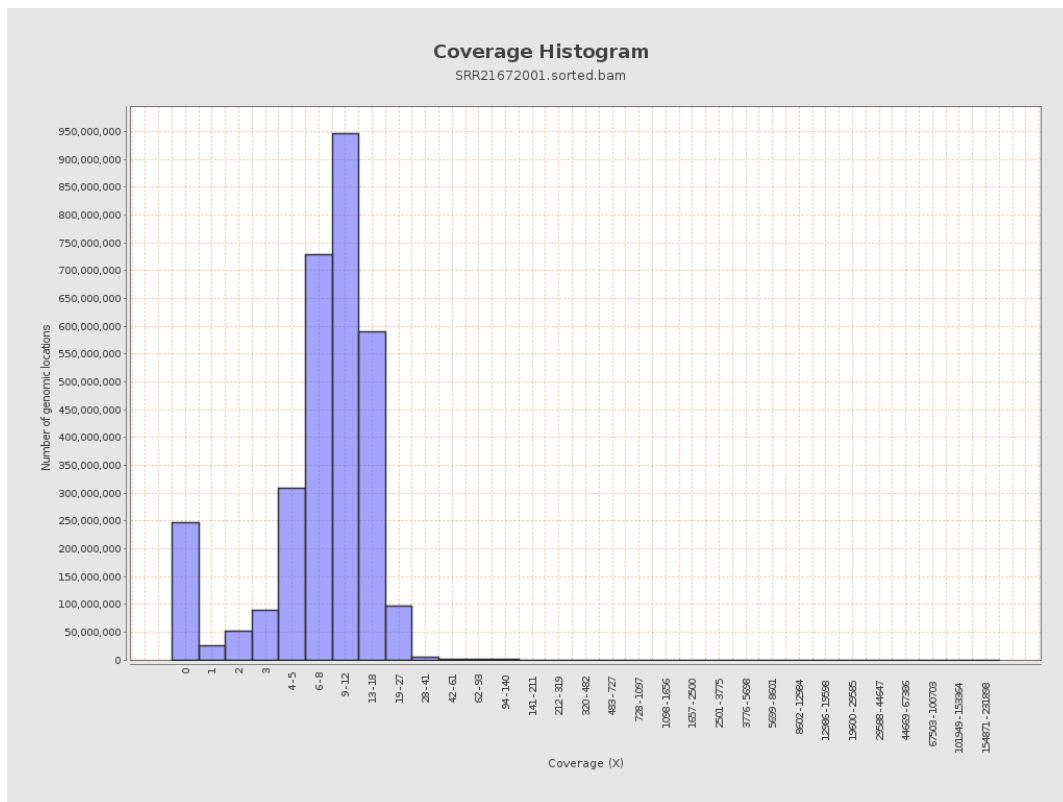
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 2448180655   | 9.8222          | 234.2624         |
| chr2  | 243199373 | 2527459018   | 10.3925         | 65.6194          |
| chr3  | 198022430 | 1916007470   | 9.6757          | 7.952            |
| chr4  | 191154276 | 1863817875   | 9.7503          | 63.998           |
| chr5  | 180915260 | 1741129405   | 9.624           | 8.9075           |
| chr6  | 171115067 | 1679586963   | 9.8155          | 52.0033          |
| chr7  | 159138663 | 1602837577   | 10.072          | 72.1423          |
| chr8  | 146364022 | 1459880619   | 9.9743          | 67.1035          |
| chr9  | 141213431 | 1289698502   | 9.133           | 158.8393         |
| chr10 | 135534747 | 1523234979   | 11.2387         | 167.6058         |
| chr11 | 135006516 | 1358617531   | 10.0633         | 37.7859          |
| chr12 | 133851895 | 1310454826   | 9.7903          | 8.4936           |
| chr13 | 115169878 | 904759443    | 7.8559          | 6.7802           |
| chr14 | 107349540 | 894490202    | 8.3325          | 8.2682           |
| chr15 | 102531392 | 845503297    | 8.2463          | 6.0896           |
| chr16 | 90354753  | 984322947    | 10.894          | 63.8832          |
| chr17 | 81195210  | 900598558    | 11.0918         | 59.9859          |
| chr18 | 78077248  | 821421834    | 10.5206         | 144.7877         |
| chr19 | 59128983  | 664899420    | 11.2449         | 98.5724          |
| chr20 | 63025520  | 653393052    | 10.3671         | 26.3376          |
| chr21 | 48129895  | 416928850    | 8.6626          | 40.6132          |
| chr22 | 51304566  | 414266614    | 8.0747          | 35.9552          |
| chrMT | 16571     | 76393079     | 4,610.0464      | 565.096          |
| chrX  | 155270560 | 765195099    | 4.9281          | 19.2637          |

|      |          |           |        |         |
|------|----------|-----------|--------|---------|
| chrY | 59373566 | 277776660 | 4.6785 | 80.5621 |
|------|----------|-----------|--------|---------|

### 3. Results : Coverage across reference

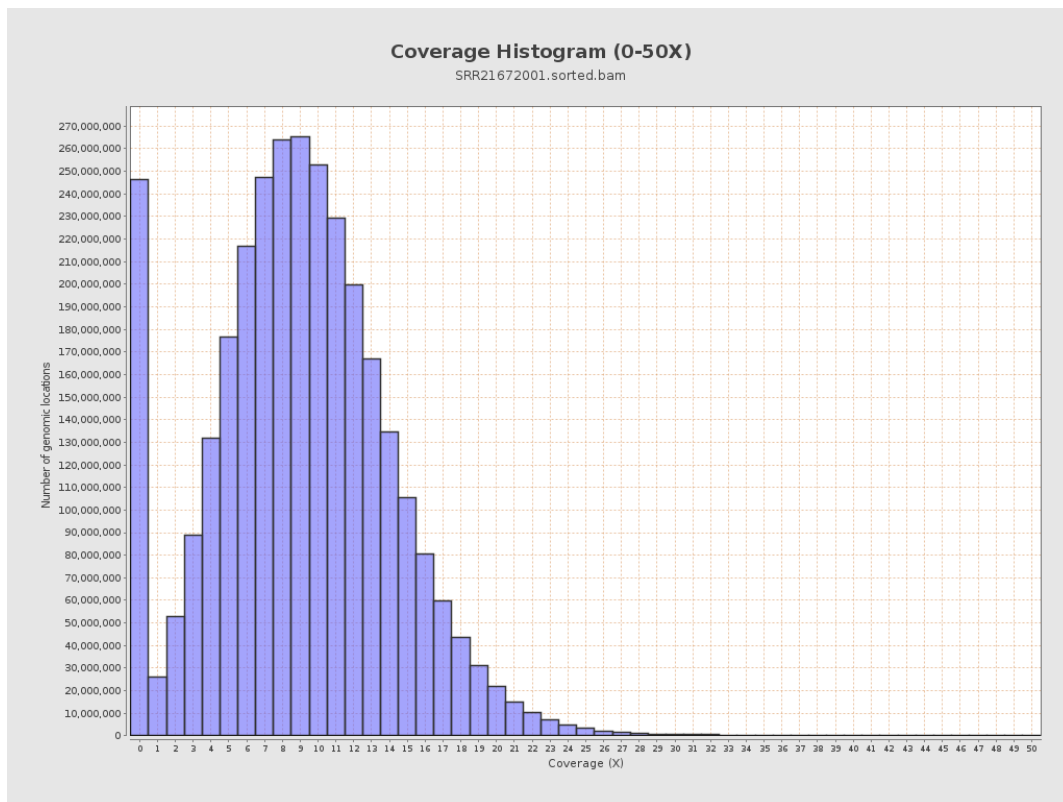


## 4. Results : Coverage Histogram

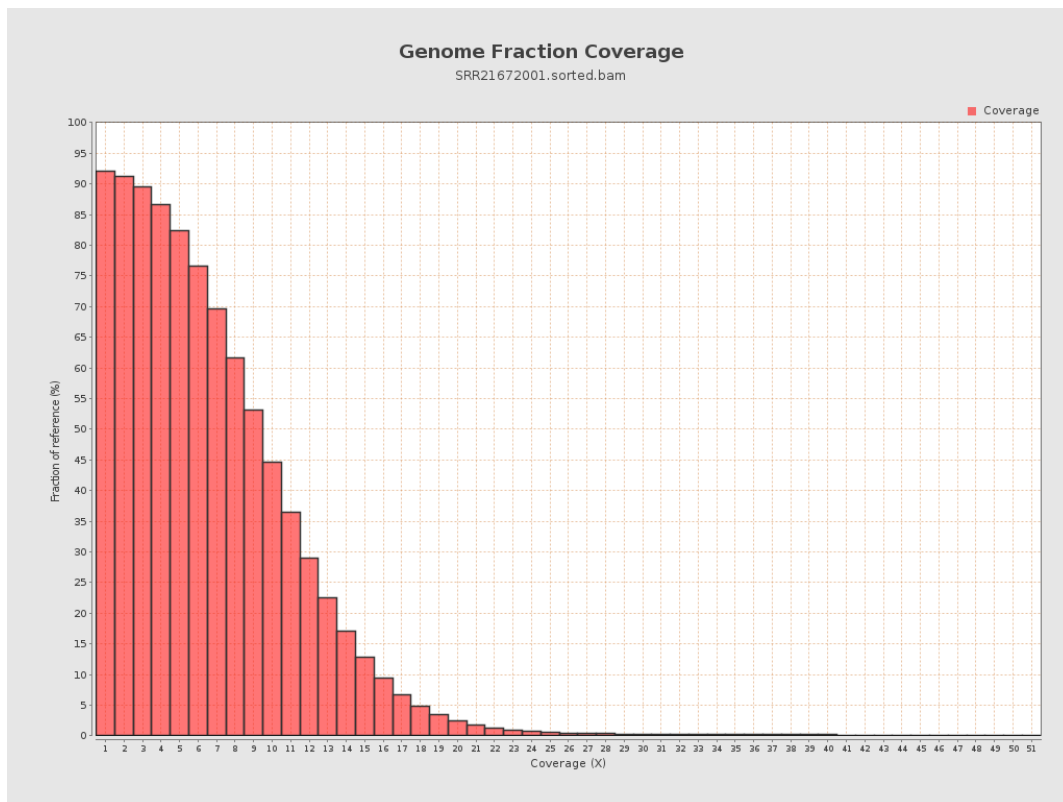




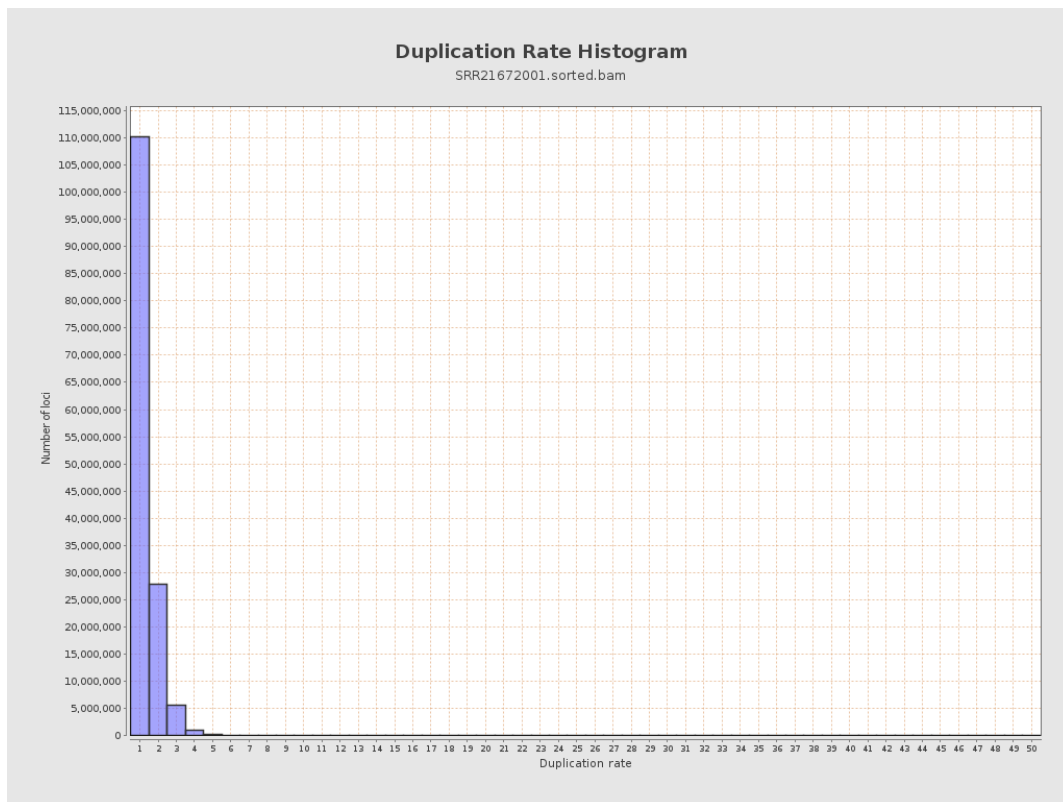
## 5. Results : Coverage Histogram (0-50X)



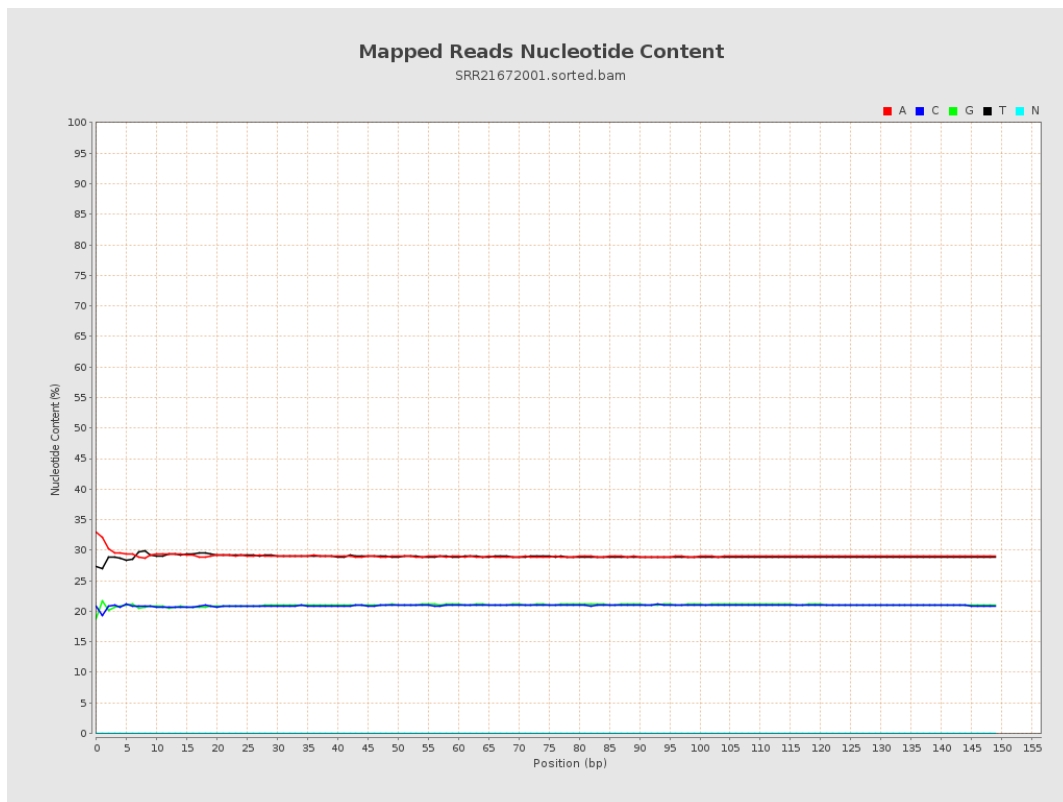
## 6. Results : Genome Fraction Coverage



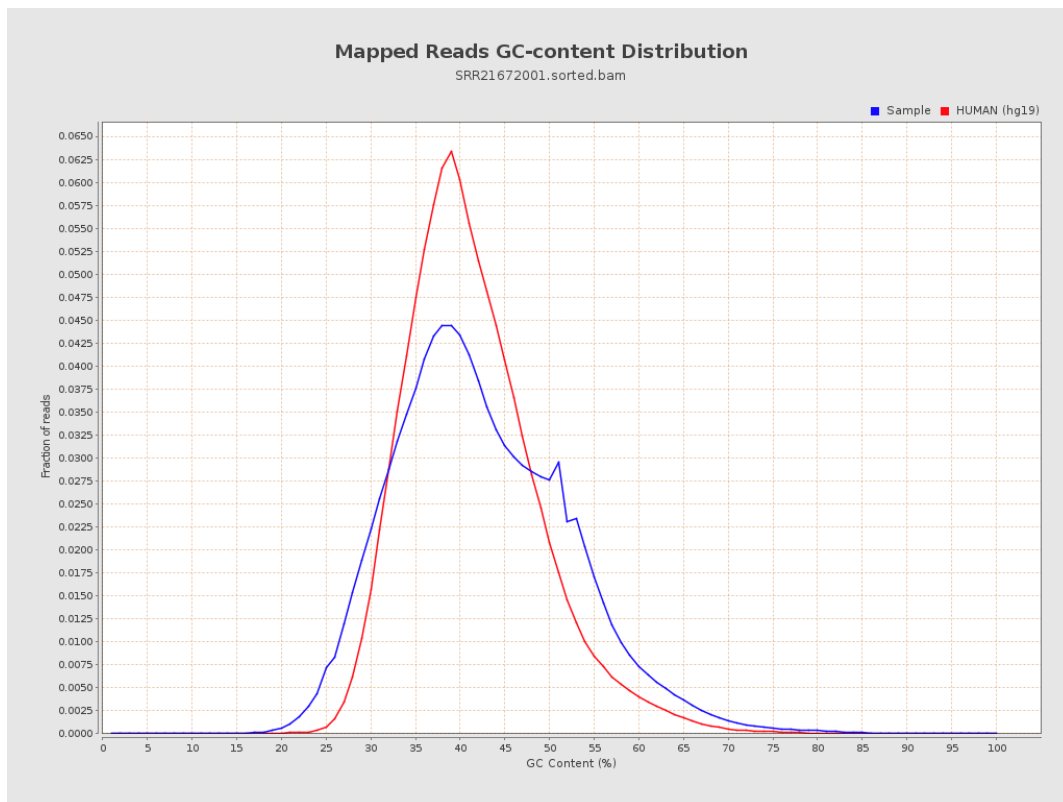
## 7. Results : Duplication Rate Histogram



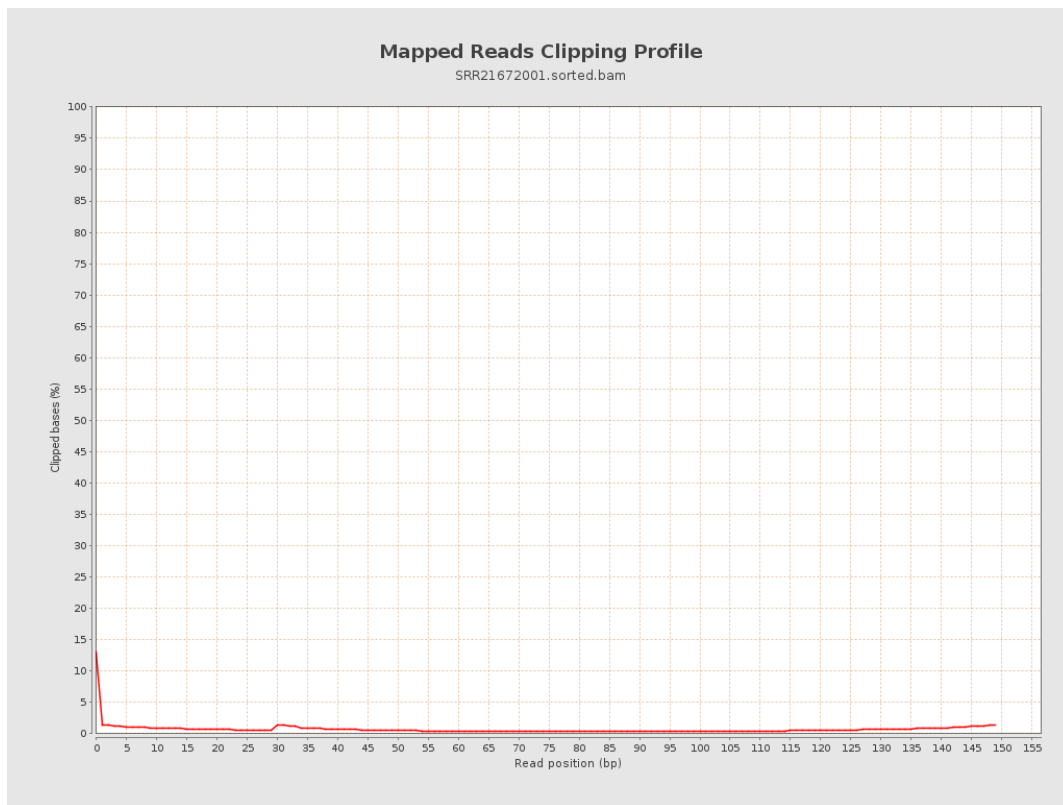
## 8. Results : Mapped Reads Nucleotide Content



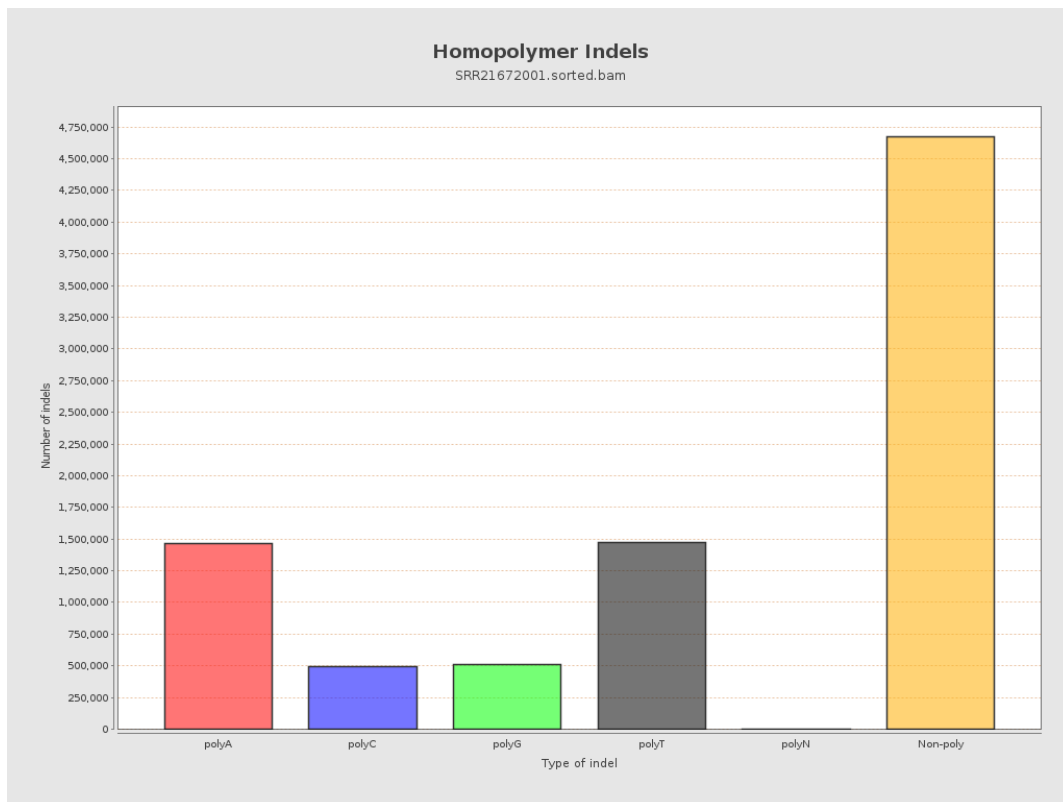
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

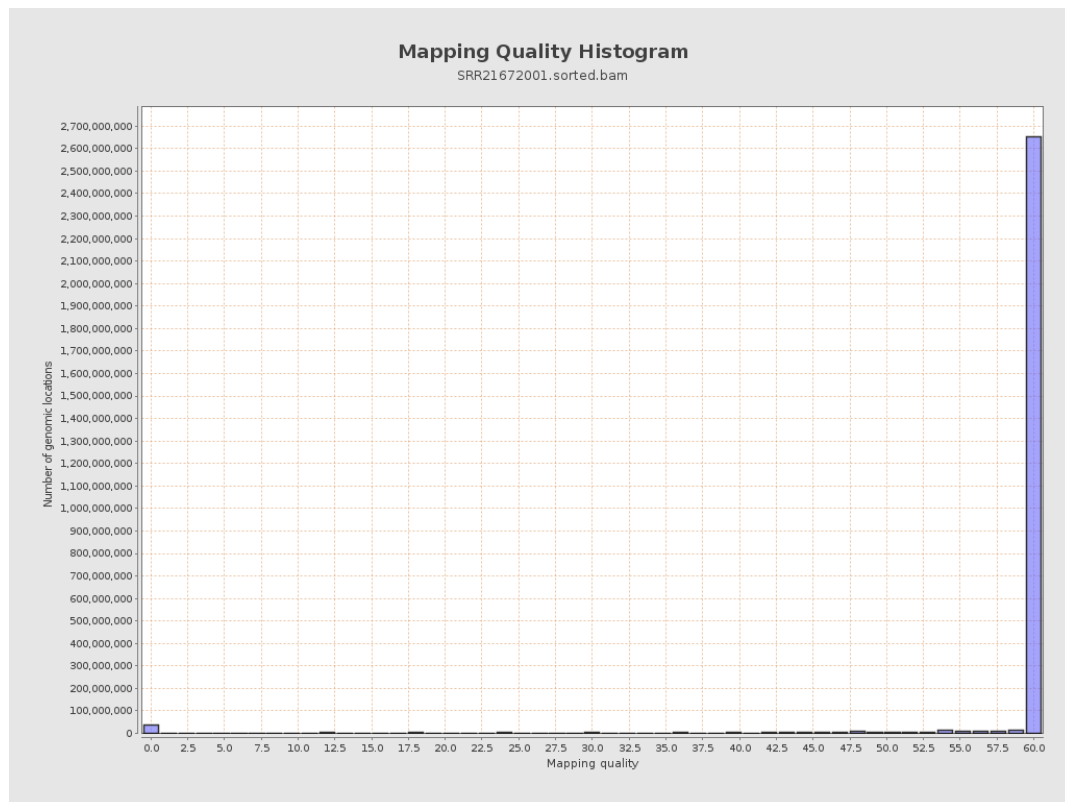


## 12. Results : Mapping Quality Across Reference

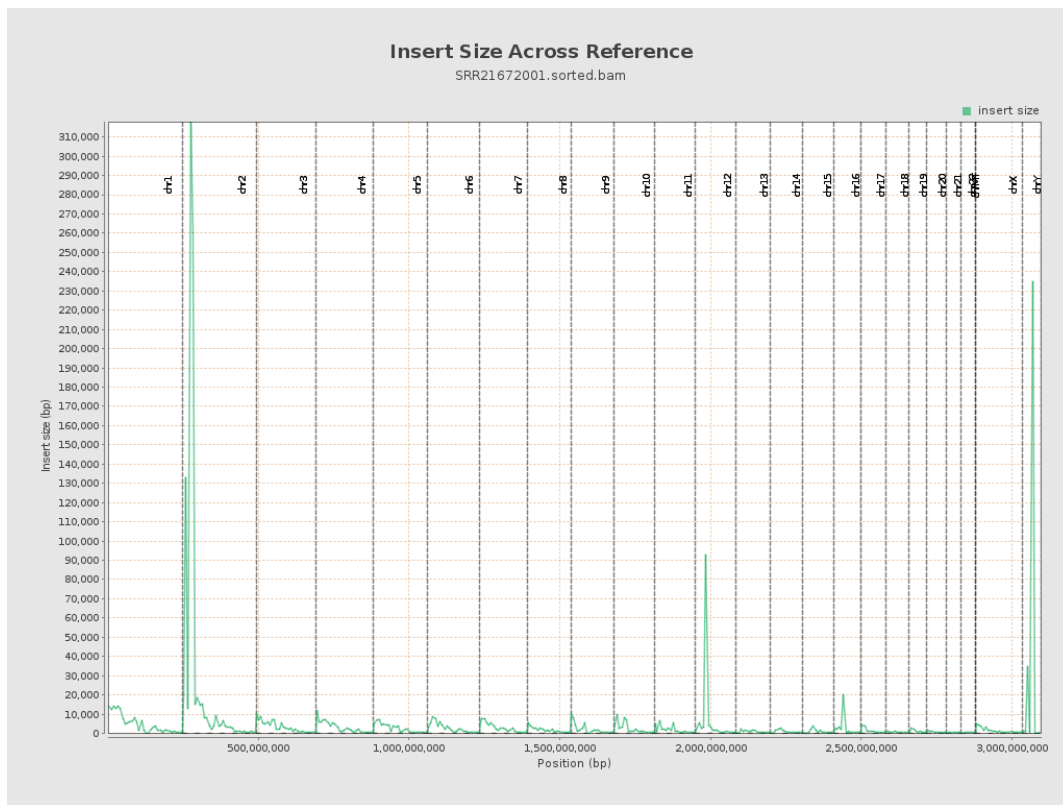




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

