

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/04 11:46:03*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173952.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_SRR10173952<br>/home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173952_1.fastq.gz SRR10173952_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                        |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                         |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                         |
| Analysis date:                        | Wed Sep 04 11:46:03 CST 2024                                                                                                                                                                                               |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                          |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                         |
| Number of windows:                    | 400                                                                                                                                                                                                                        |
| BAM file:                             | SRR10173952.sorted.bam                                                                                                                                                                                                     |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 8,923,762          |
| Mapped reads                 | 8,717,814 / 97.69% |
| Unmapped reads               | 205,948 / 2.31%    |
| Mapped paired reads          | 8,717,814 / 97.69% |
| Mapped reads, first in pair  | 4,360,251 / 48.86% |
| Mapped reads, second in pair | 4,357,563 / 48.83% |
| Mapped reads, both in pair   | 8,587,380 / 96.23% |
| Mapped reads, singletons     | 130,434 / 1.46%    |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 1,191,134 / 13.35% |
| Read min/max/mean length     | 30 / 133 / 125.5   |
| Duplicated reads (estimated) | 6,941,466 / 77.79% |
| Duplication rate             | 64.55%             |
| Clipped reads                | 4,576,216 / 51.28% |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 292,690,232 / 29.71% |
| Number/percentage of C's | 196,963,997 / 19.99% |
| Number/percentage of T's | 290,350,785 / 29.47% |
| Number/percentage of G's | 205,292,595 / 20.84% |
| Number/percentage of N's | 7,250 / 0%           |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 40.83% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.3185 |
| Standard Deviation | 6.0412 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 52.57 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 999,851.73      |
| Standard Deviation | 9,546,009.22    |
| P25/Median/P75     | 104 / 152 / 232 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.89%     |
| Mismatches                               | 8,459,949 |
| Insertions                               | 104,995   |
| Mapped reads with at least one insertion | 1.16%     |
| Deletions                                | 300,948   |
| Mapped reads with at least one deletion  | 3.37%     |
| Homopolymer indels                       | 41.02%    |

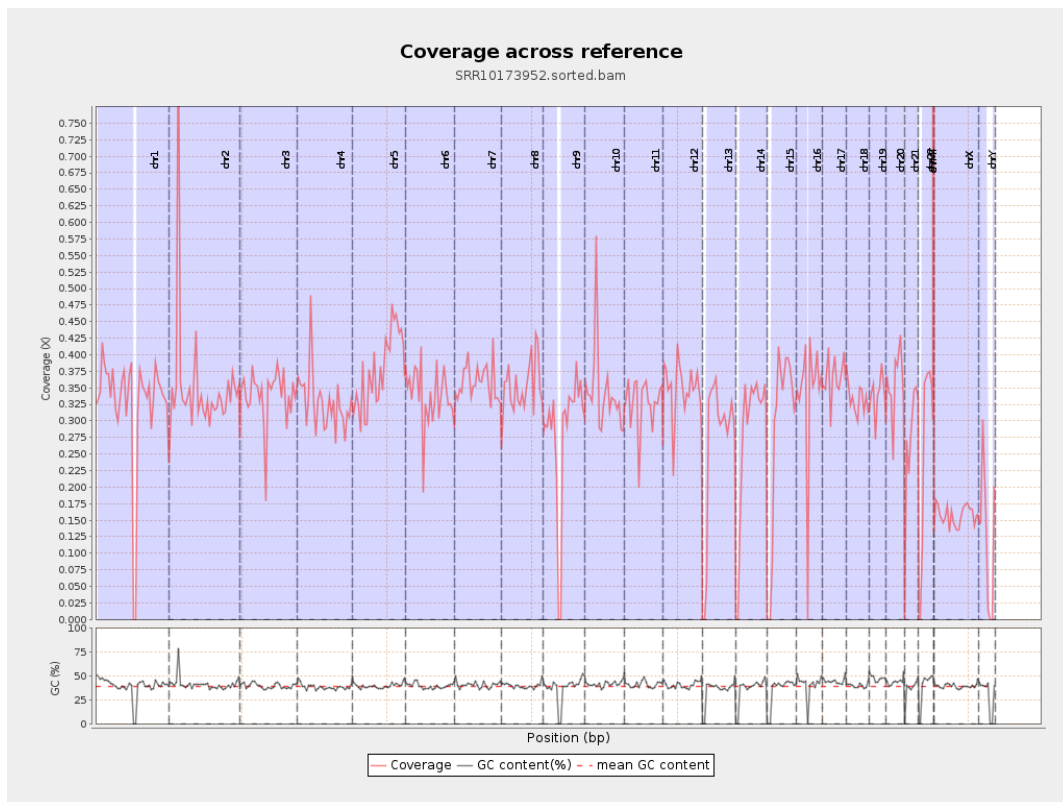
## 2.7. Chromosome stats

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

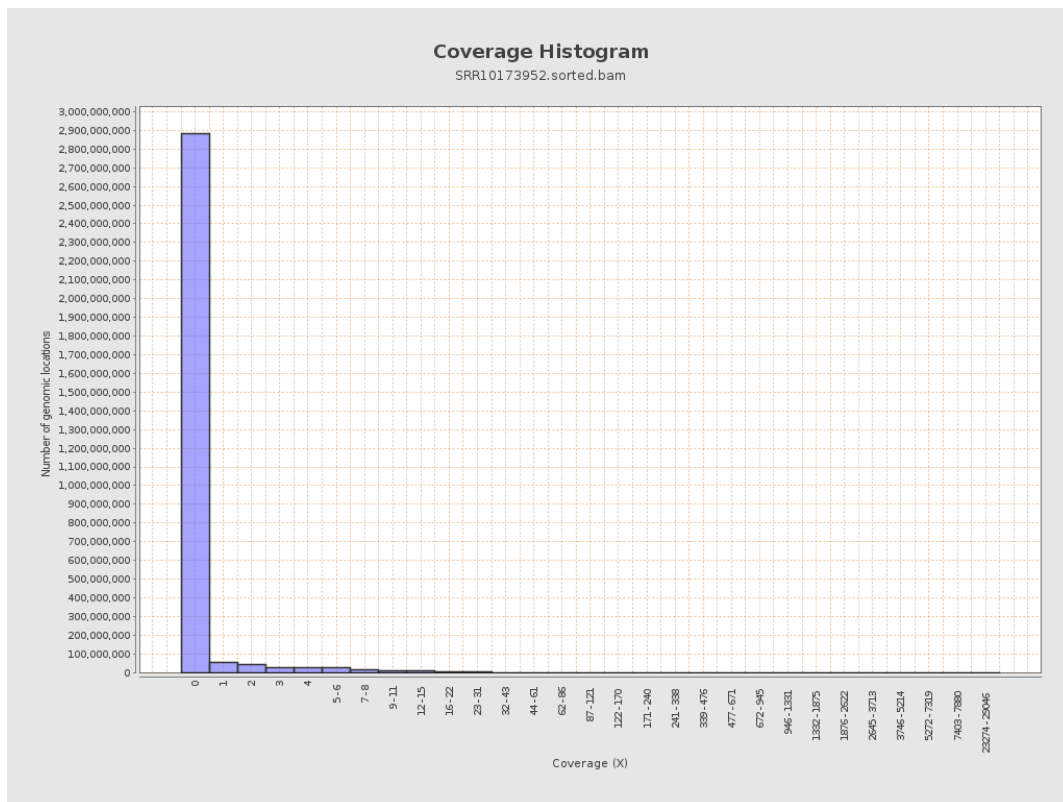
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 81420656     | 0.3267          | 2.6851           |
| chr2  | 243199373 | 85848856     | 0.353           | 20.2475          |
| chr3  | 198022430 | 66965842     | 0.3382          | 1.7287           |
| chr4  | 191154276 | 62481374     | 0.3269          | 2.2513           |
| chr5  | 180915260 | 68184046     | 0.3769          | 1.8294           |
| chr6  | 171115067 | 57759874     | 0.3375          | 2.0674           |
| chr7  | 159138663 | 57061458     | 0.3586          | 2.5229           |
| chr8  | 146364022 | 51768809     | 0.3537          | 2.6913           |
| chr9  | 141213431 | 39710417     | 0.2812          | 2.1401           |
| chr10 | 135534747 | 46431716     | 0.3426          | 3.049            |
| chr11 | 135006516 | 44210881     | 0.3275          | 1.7733           |
| chr12 | 133851895 | 46661860     | 0.3486          | 1.8569           |
| chr13 | 115169878 | 30541860     | 0.2652          | 1.5453           |
| chr14 | 107349540 | 29835774     | 0.2779          | 1.5875           |
| chr15 | 102531392 | 29481730     | 0.2875          | 1.653            |
| chr16 | 90354753  | 30778783     | 0.3406          | 2.2509           |
| chr17 | 81195210  | 29676668     | 0.3655          | 1.9311           |
| chr18 | 78077248  | 25998621     | 0.333           | 2.7738           |
| chr19 | 59128983  | 19972413     | 0.3378          | 2.1602           |
| chr20 | 63025520  | 22410636     | 0.3556          | 1.8179           |
| chr21 | 48129895  | 12987359     | 0.2698          | 2.1074           |
| chr22 | 51304566  | 12757765     | 0.2487          | 1.7711           |
| chrMT | 16571     | 1599356      | 96.5154         | 78.1032          |
| chrX  | 155270560 | 24364930     | 0.1569          | 1.1959           |

|      |          |         |        |        |
|------|----------|---------|--------|--------|
| chrY | 59373566 | 7084973 | 0.1193 | 1.7732 |
|------|----------|---------|--------|--------|

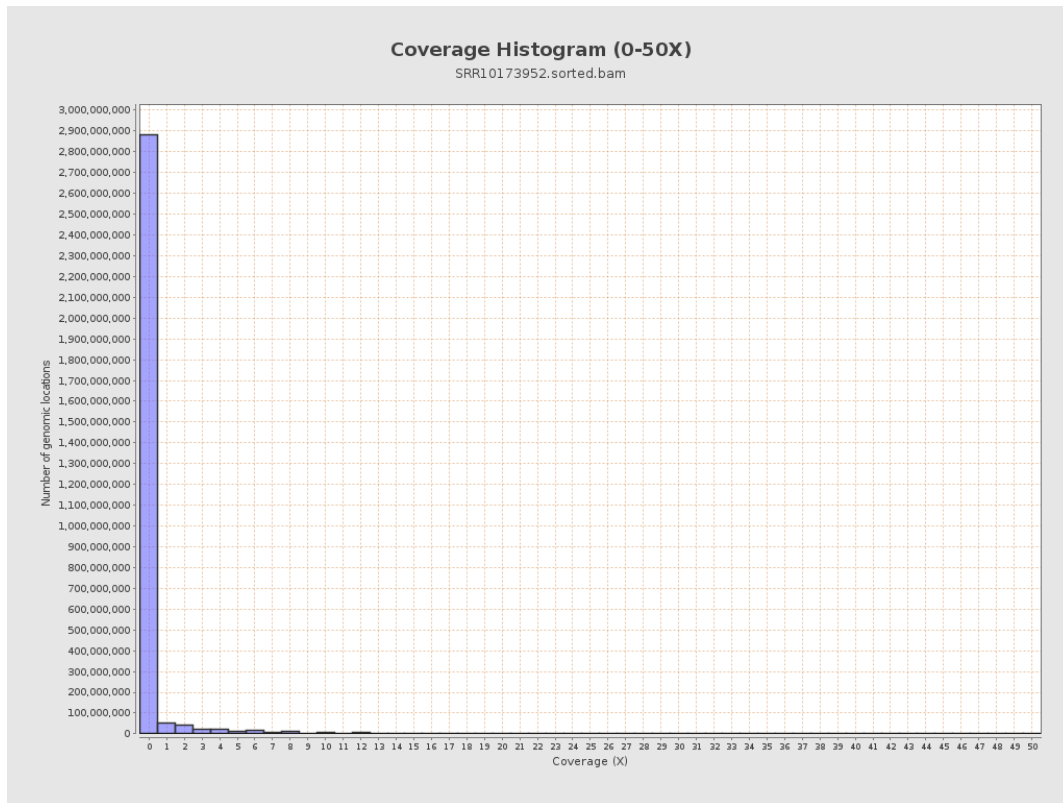
### 3. Results : Coverage across reference



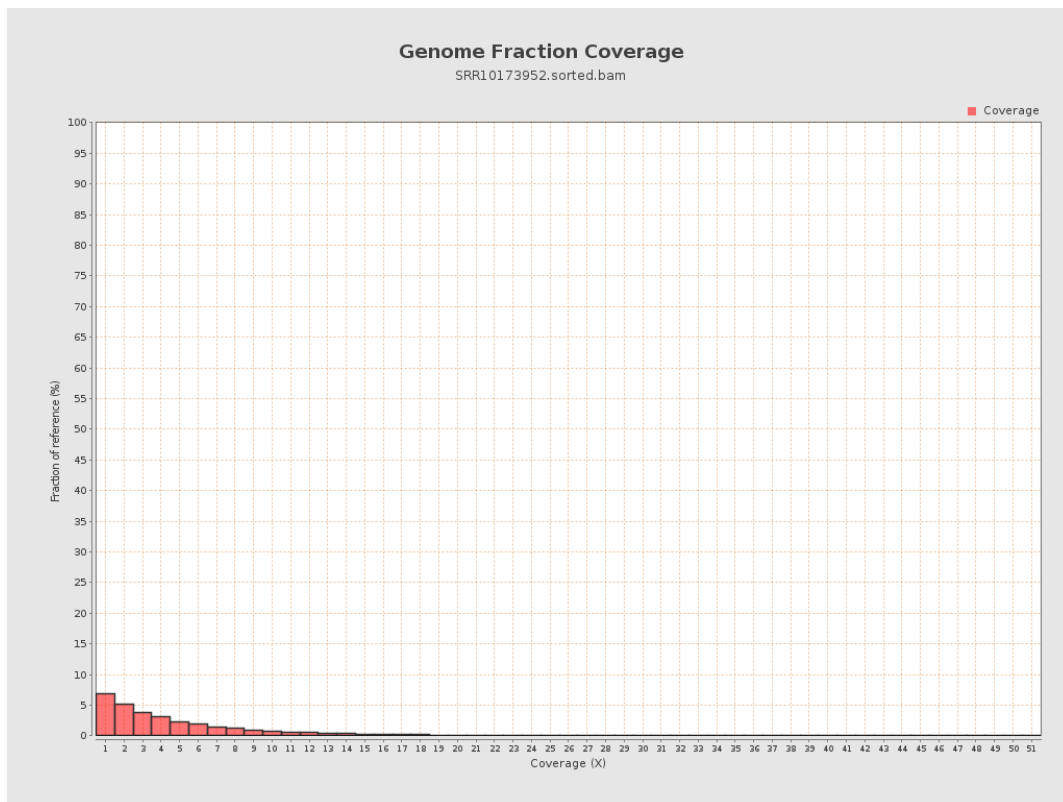
## 4. Results : Coverage Histogram



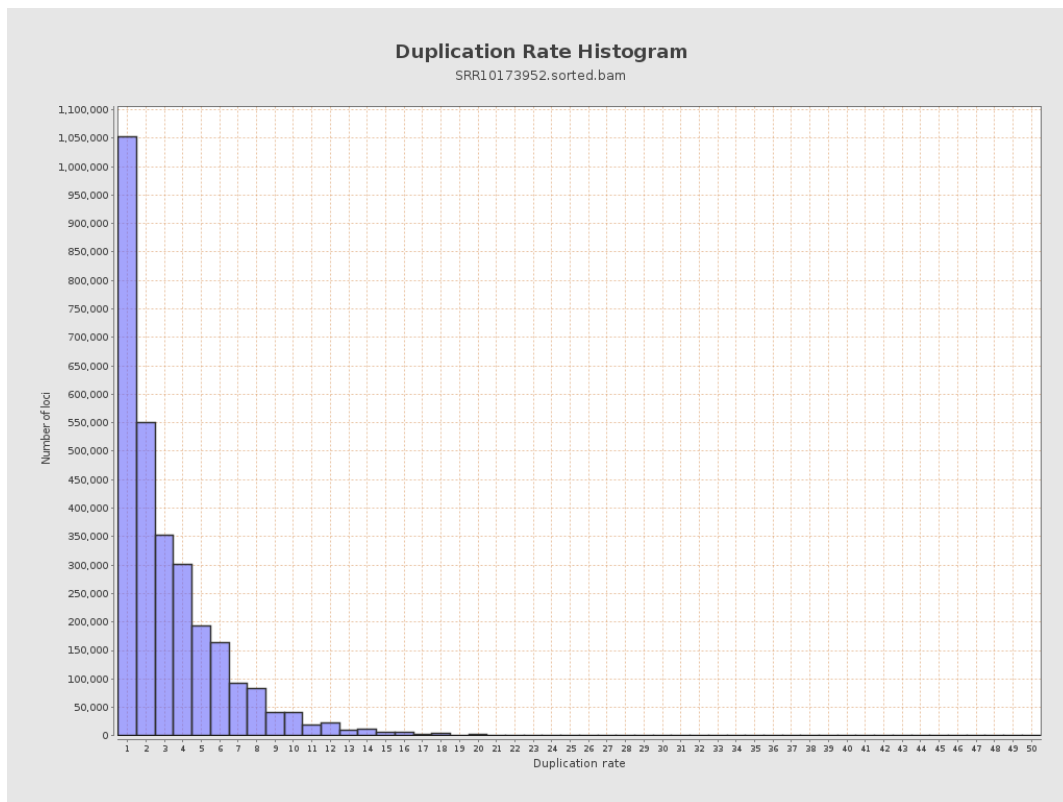
## 5. Results : Coverage Histogram (0-50X)



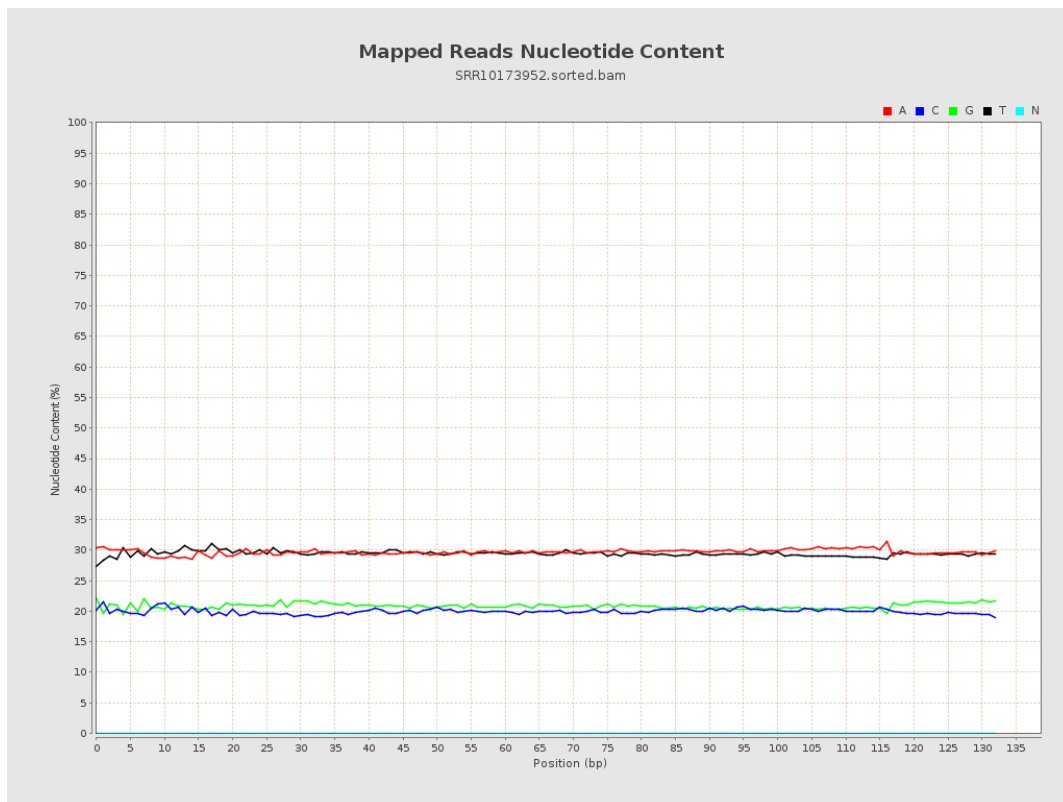
## 6. Results : Genome Fraction Coverage



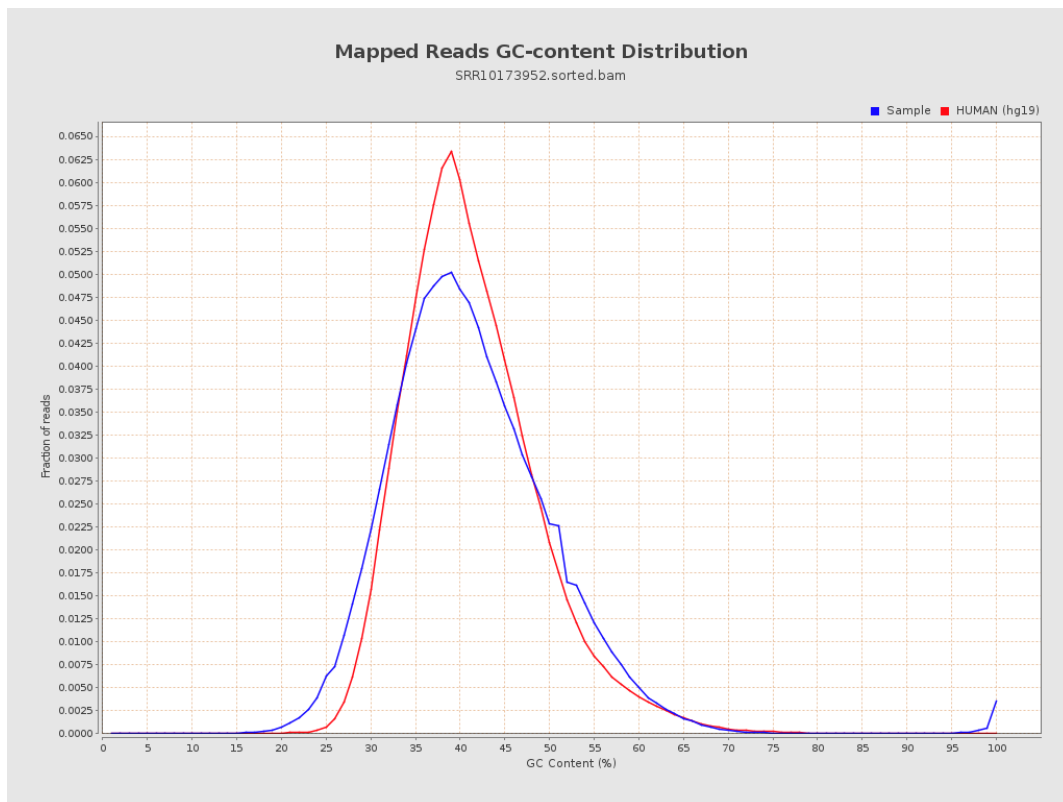
## 7. Results : Duplication Rate Histogram



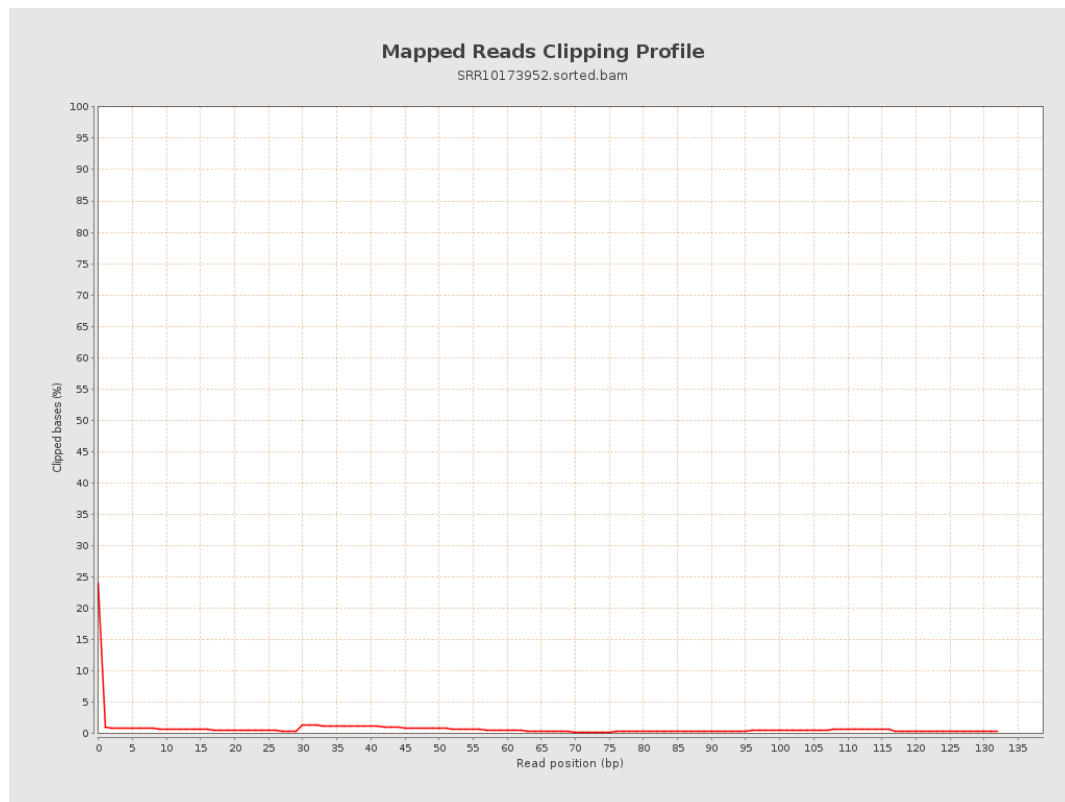
## 8. Results : Mapped Reads Nucleotide Content



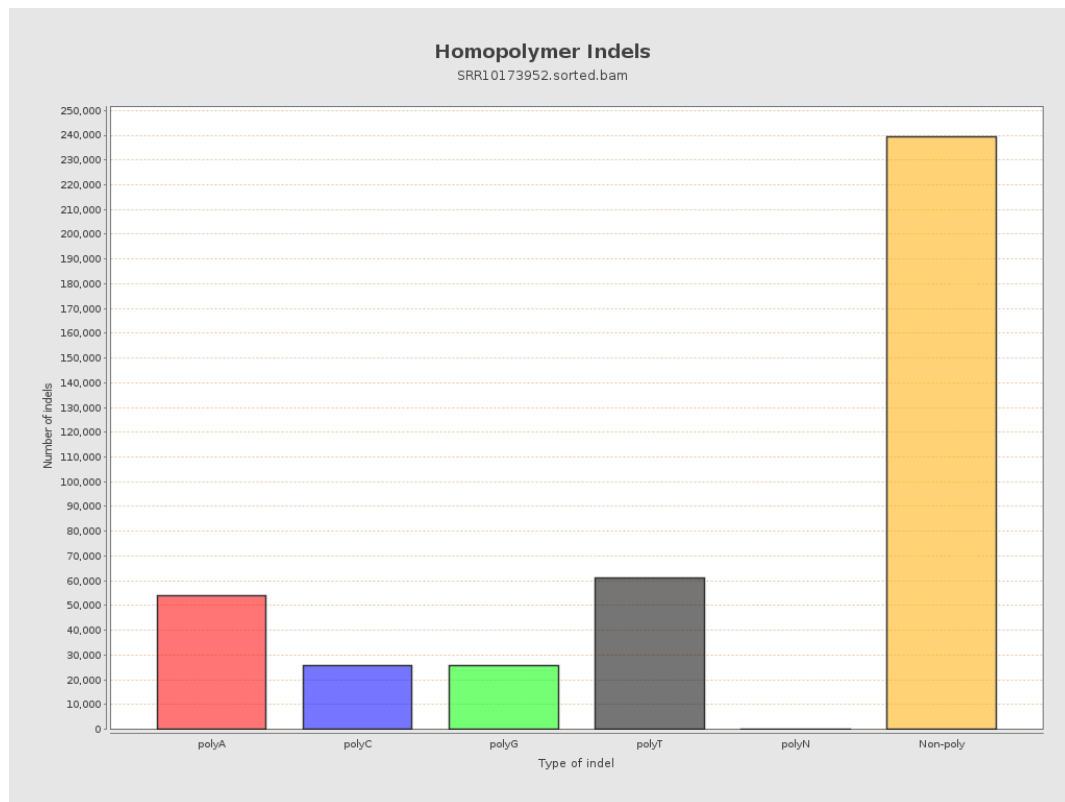
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



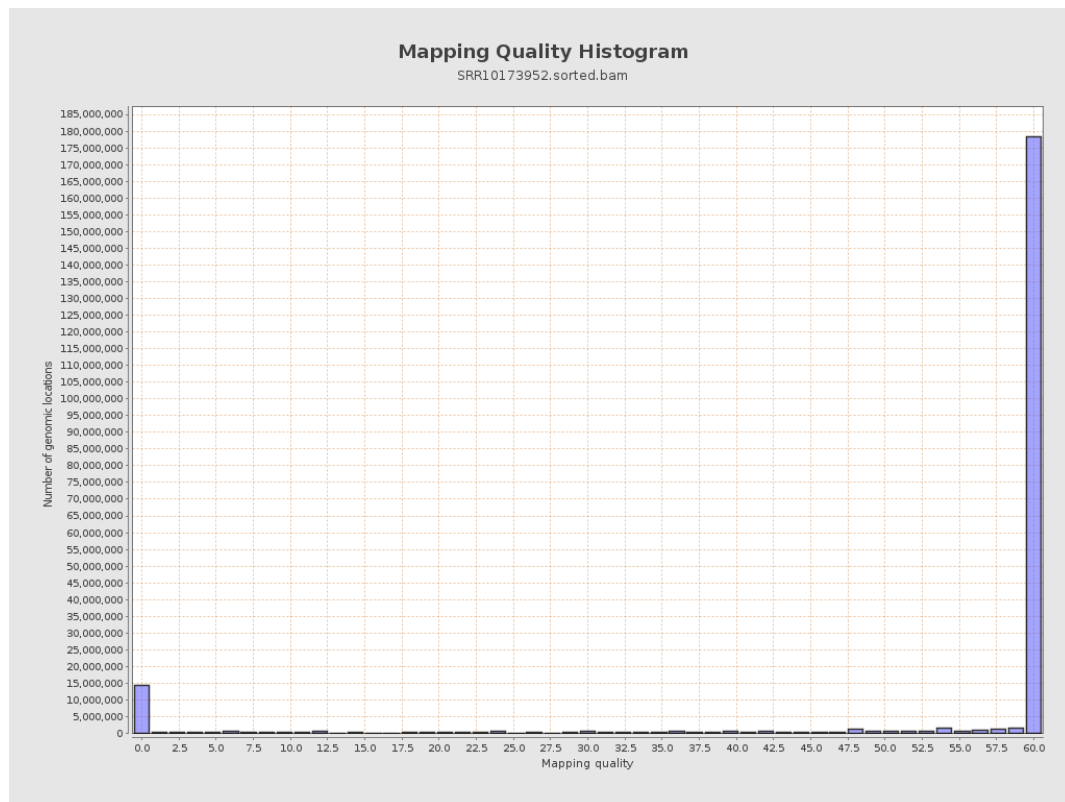
## 11. Results : Homopolymer Indels



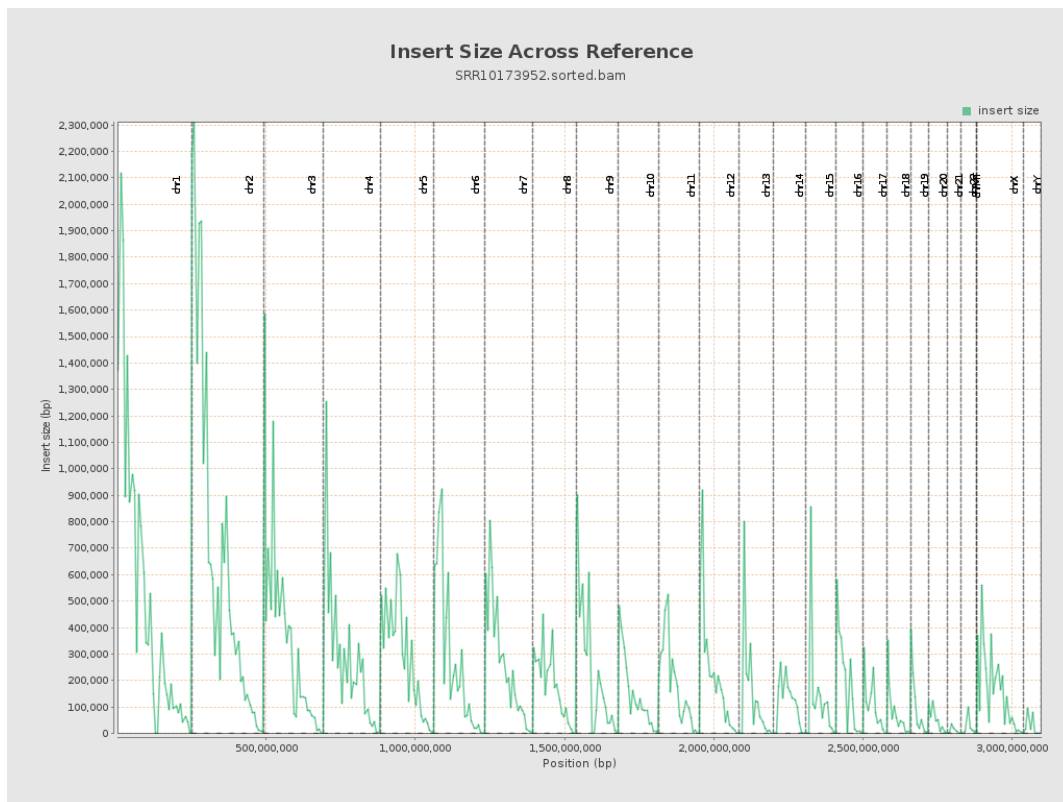
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

