

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/04 20:23:49*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174007.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_SRR10174007 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174007_1.fastq.gz SRR10174007_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                      |
| Analysis date:                        | Wed Sep 04 20:23:48 CST 2024                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                     |
| BAM file:                             | SRR10174007.sorted.bam                                                                                                                                                                                                  |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 15,887,078          |
| Mapped reads                 | 15,431,059 / 97.13% |
| Unmapped reads               | 456,019 / 2.87%     |
| Mapped paired reads          | 15,431,059 / 97.13% |
| Mapped reads, first in pair  | 7,732,879 / 48.67%  |
| Mapped reads, second in pair | 7,698,180 / 48.46%  |
| Mapped reads, both in pair   | 15,122,722 / 95.19% |
| Mapped reads, singletons     | 308,337 / 1.94%     |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 1,677,272 / 10.56%  |
| Read min/max/mean length     | 30 / 133 / 128.65   |
| Duplicated reads (estimated) | 12,326,422 / 77.59% |
| Duplication rate             | 65.6%               |
| Clipped reads                | 6,622,979 / 41.69%  |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 539,773,971 / 29.68% |
| Number/percentage of C's | 363,278,559 / 19.97% |
| Number/percentage of T's | 538,925,899 / 29.63% |
| Number/percentage of G's | 376,740,863 / 20.71% |
| Number/percentage of N's | 21,233 / 0%          |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 40.69% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.5878 |
| Standard Deviation | 8.0738 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 52.55 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 1,023,216.19    |
| Standard Deviation | 9,558,023.53    |
| P25/Median/P75     | 146 / 205 / 297 |

## 2.6. Mismatches and indels

|                                          |            |
|------------------------------------------|------------|
| General error rate                       | 1.09%      |
| Mismatches                               | 19,253,274 |
| Insertions                               | 194,725    |
| Mapped reads with at least one insertion | 1.22%      |
| Deletions                                | 426,453    |
| Mapped reads with at least one deletion  | 2.69%      |
| Homopolymer indels                       | 43.15%     |

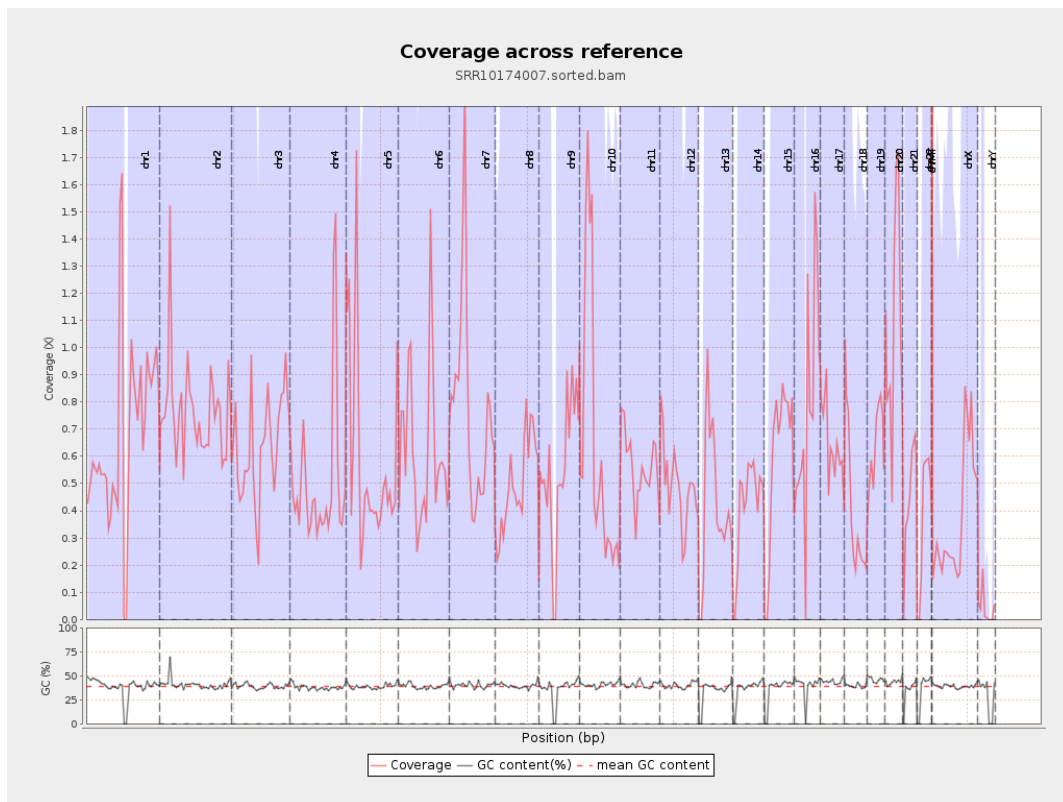
## 2.7. Chromosome stats

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

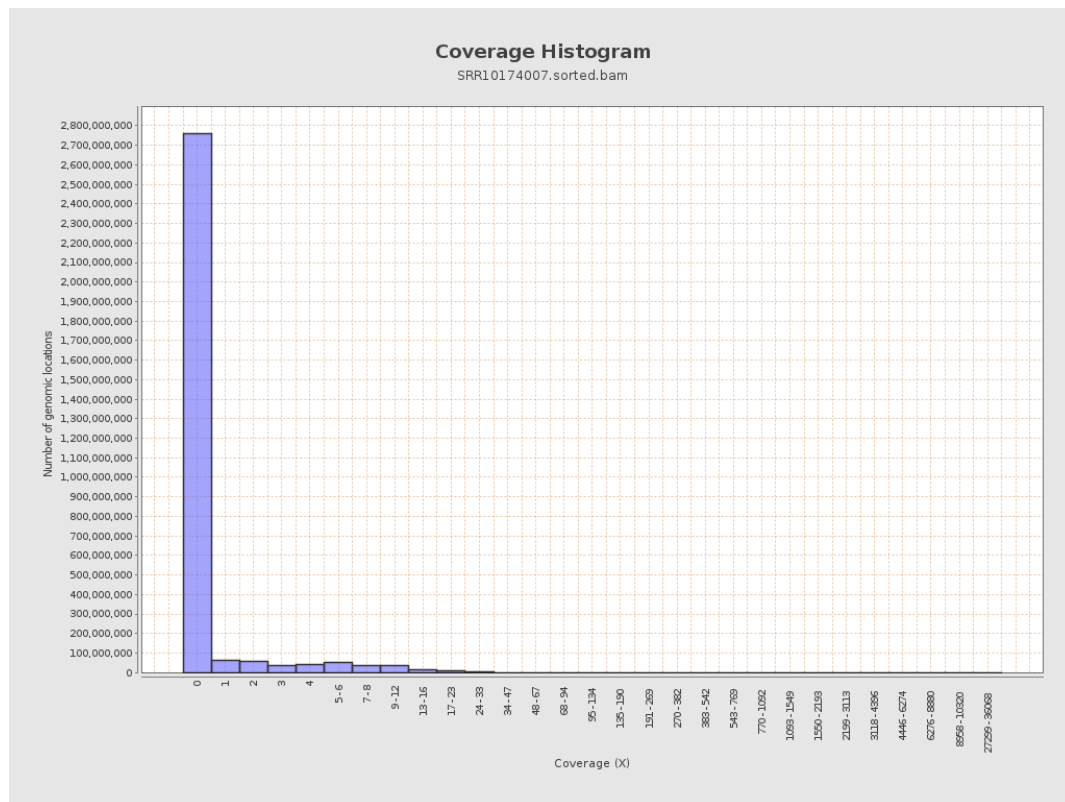
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 171764461    | 0.6891          | 5.5456           |
| chr2  | 243199373 | 185895840    | 0.7644          | 25.1507          |
| chr3  | 198022430 | 126349083    | 0.6381          | 2.4059           |
| chr4  | 191154276 | 97083193     | 0.5079          | 3.3292           |
| chr5  | 180915260 | 106775533    | 0.5902          | 2.3391           |
| chr6  | 171115067 | 105619734    | 0.6172          | 2.6288           |
| chr7  | 159138663 | 124835365    | 0.7844          | 7.3151           |
| chr8  | 146364022 | 73922733     | 0.5051          | 3.2471           |
| chr9  | 141213431 | 77477998     | 0.5487          | 3.3179           |
| chr10 | 135534747 | 86598874     | 0.6389          | 8.2395           |
| chr11 | 135006516 | 76732773     | 0.5684          | 2.4987           |
| chr12 | 133851895 | 66144516     | 0.4942          | 2.1409           |
| chr13 | 115169878 | 49152703     | 0.4268          | 1.9778           |
| chr14 | 107349540 | 44319702     | 0.4129          | 1.9819           |
| chr15 | 102531392 | 59872767     | 0.5839          | 2.3071           |
| chr16 | 90354753  | 70913148     | 0.7848          | 4.6268           |
| chr17 | 81195210  | 51651330     | 0.6361          | 3.2367           |
| chr18 | 78077248  | 30290251     | 0.388           | 5.8107           |
| chr19 | 59128983  | 38337583     | 0.6484          | 6.279            |
| chr20 | 63025520  | 70161633     | 1.1132          | 3.314            |
| chr21 | 48129895  | 22013679     | 0.4574          | 2.3313           |
| chr22 | 51304566  | 19453817     | 0.3792          | 1.7758           |
| chrMT | 16571     | 4119755      | 248.6123        | 165.6596         |
| chrX  | 155270560 | 57747944     | 0.3719          | 1.8633           |

|      |          |         |       |        |
|------|----------|---------|-------|--------|
| chrY | 59373566 | 2554366 | 0.043 | 1.8774 |
|------|----------|---------|-------|--------|

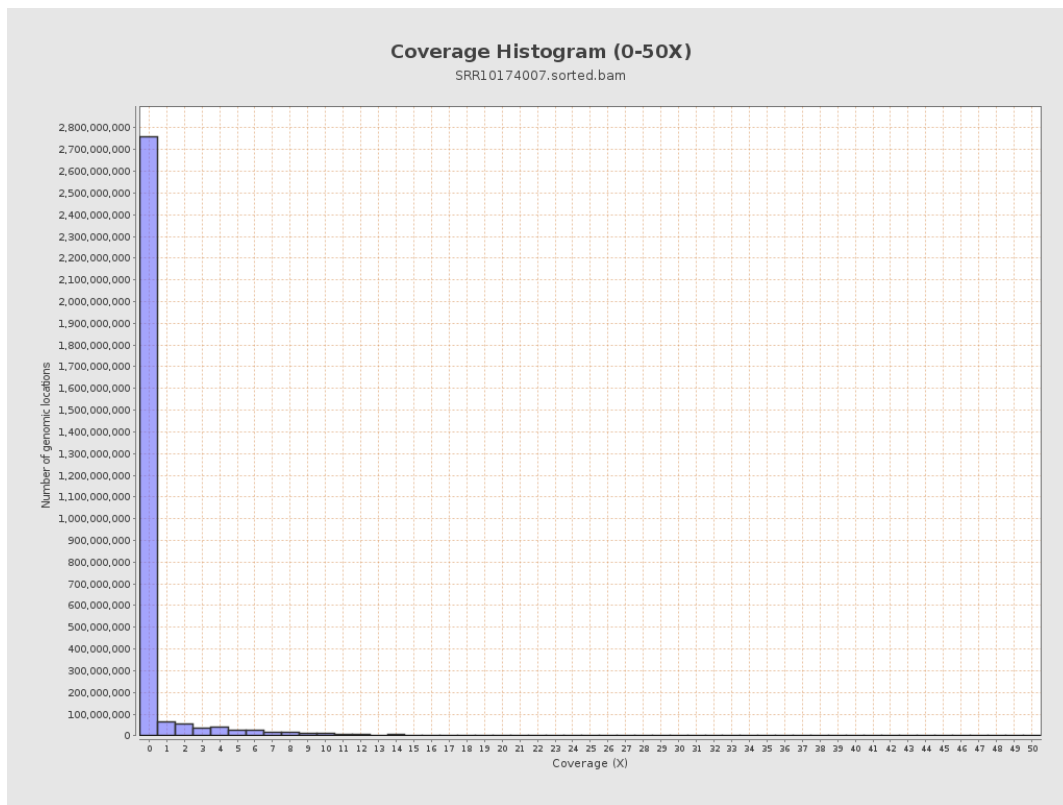
### 3. Results : Coverage across reference



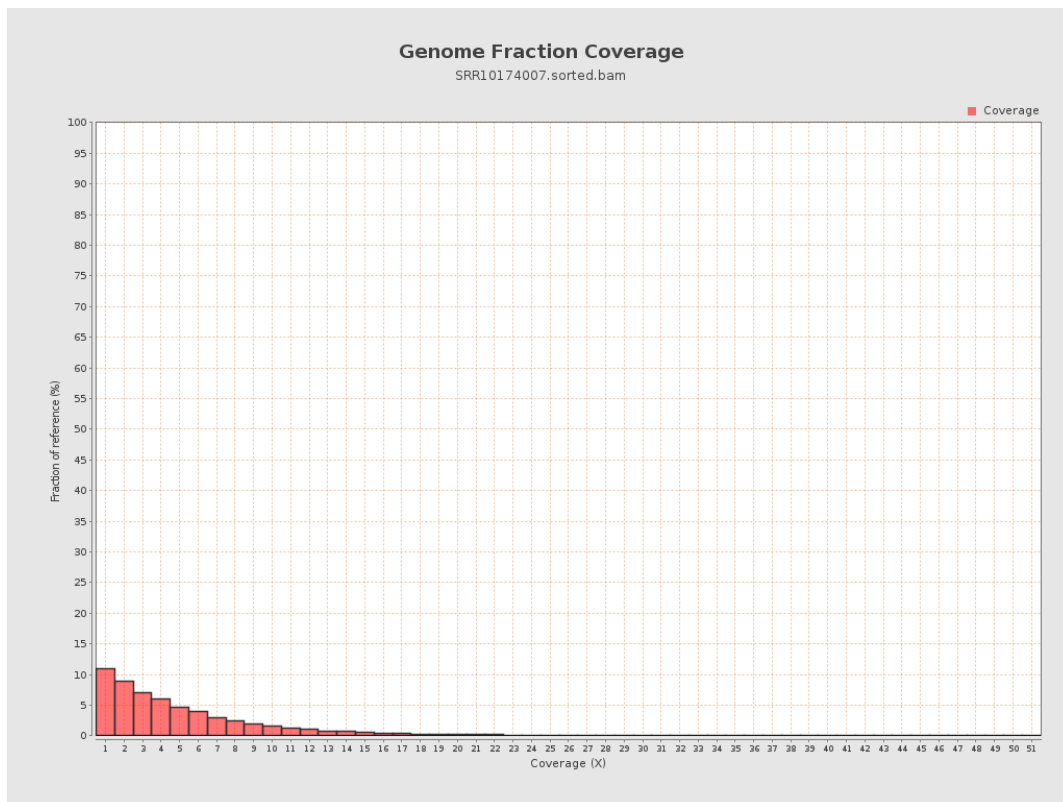
## 4. Results : Coverage Histogram



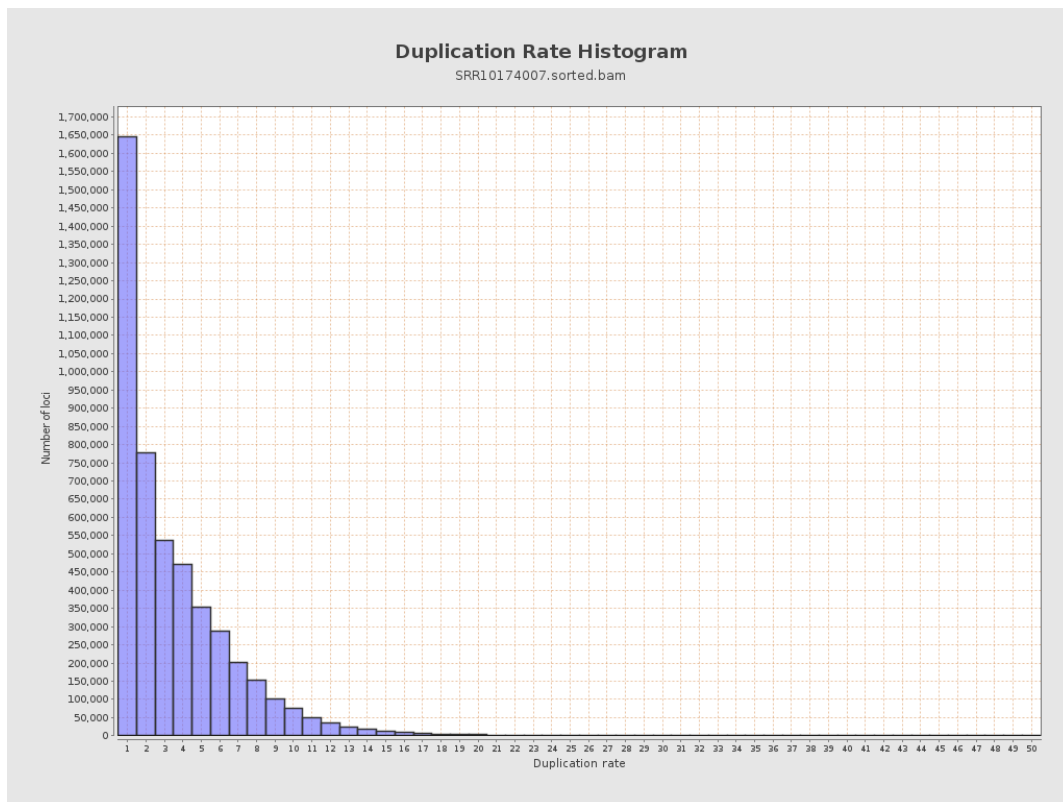
## 5. Results : Coverage Histogram (0-50X)



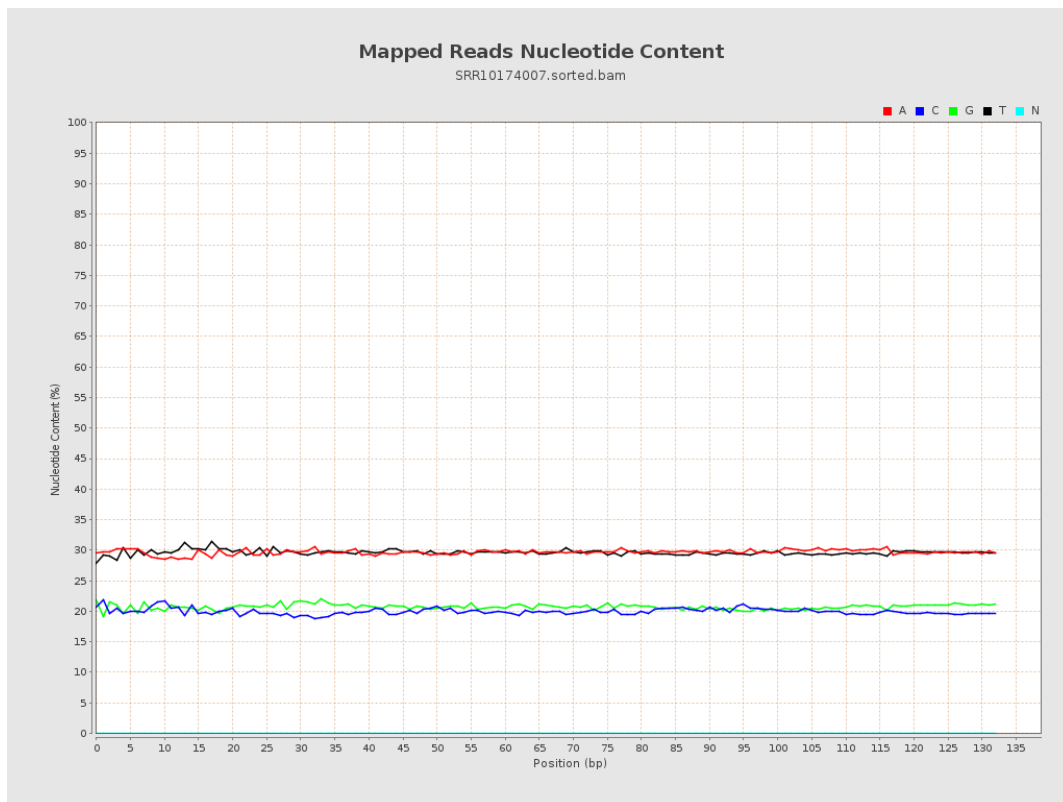
## 6. Results : Genome Fraction Coverage



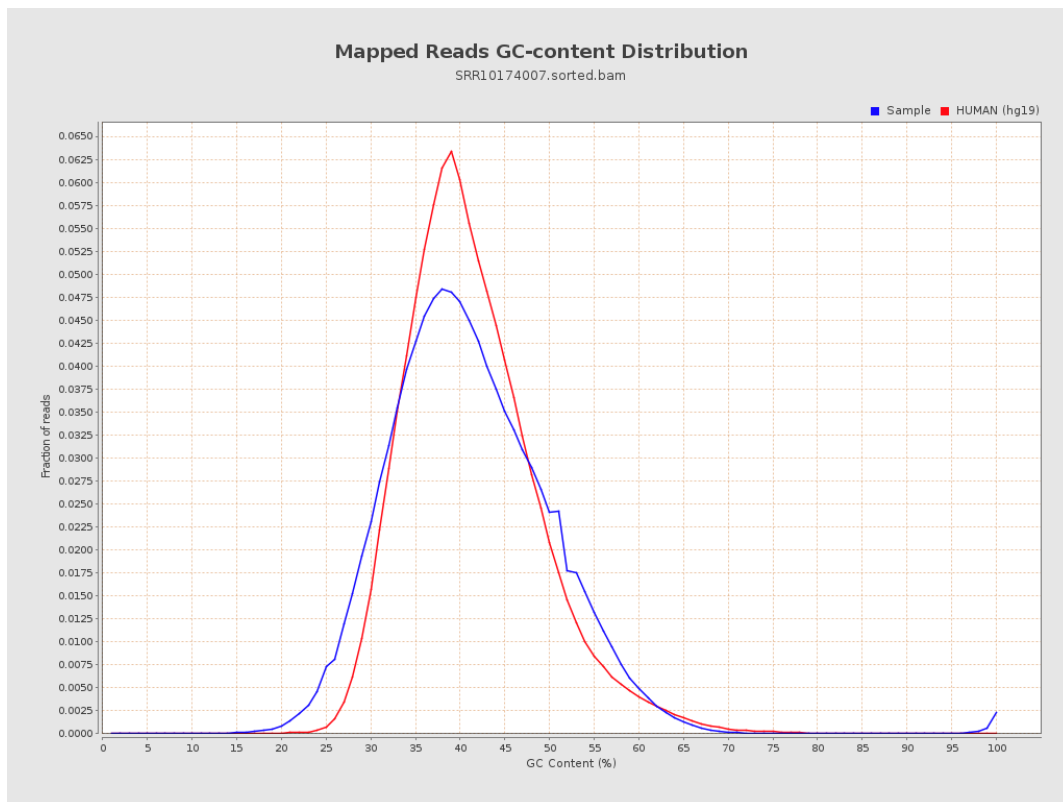
## 7. Results : Duplication Rate Histogram



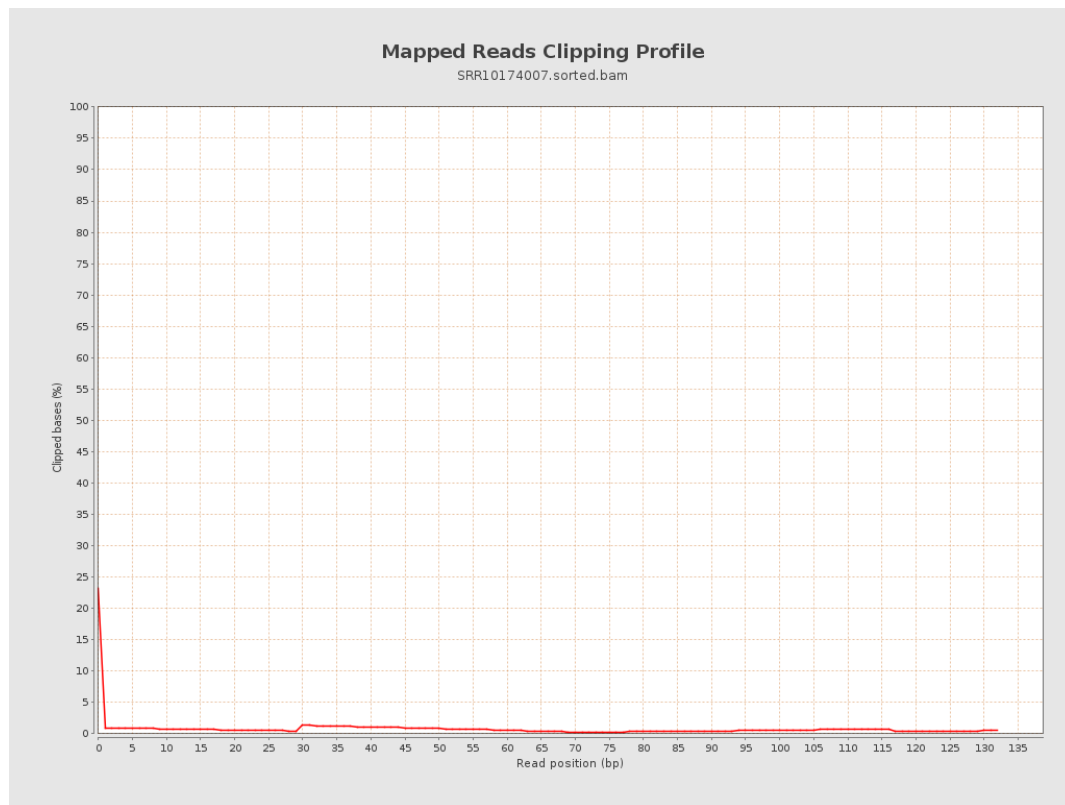
## 8. Results : Mapped Reads Nucleotide Content



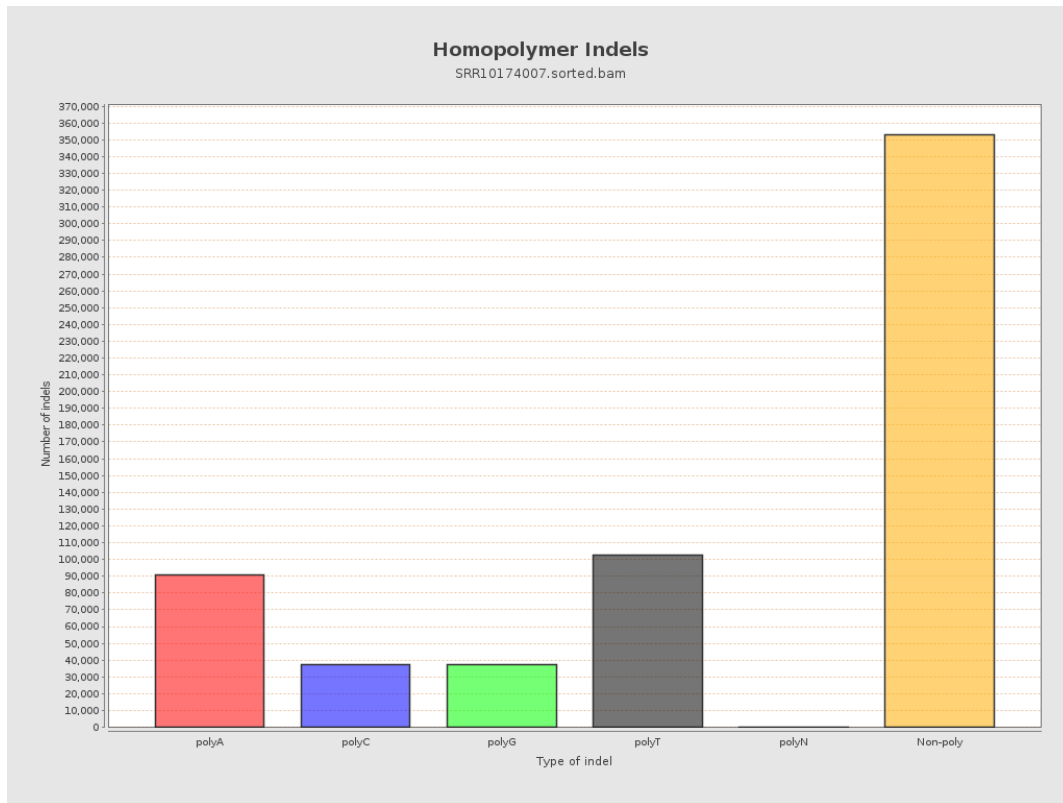
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



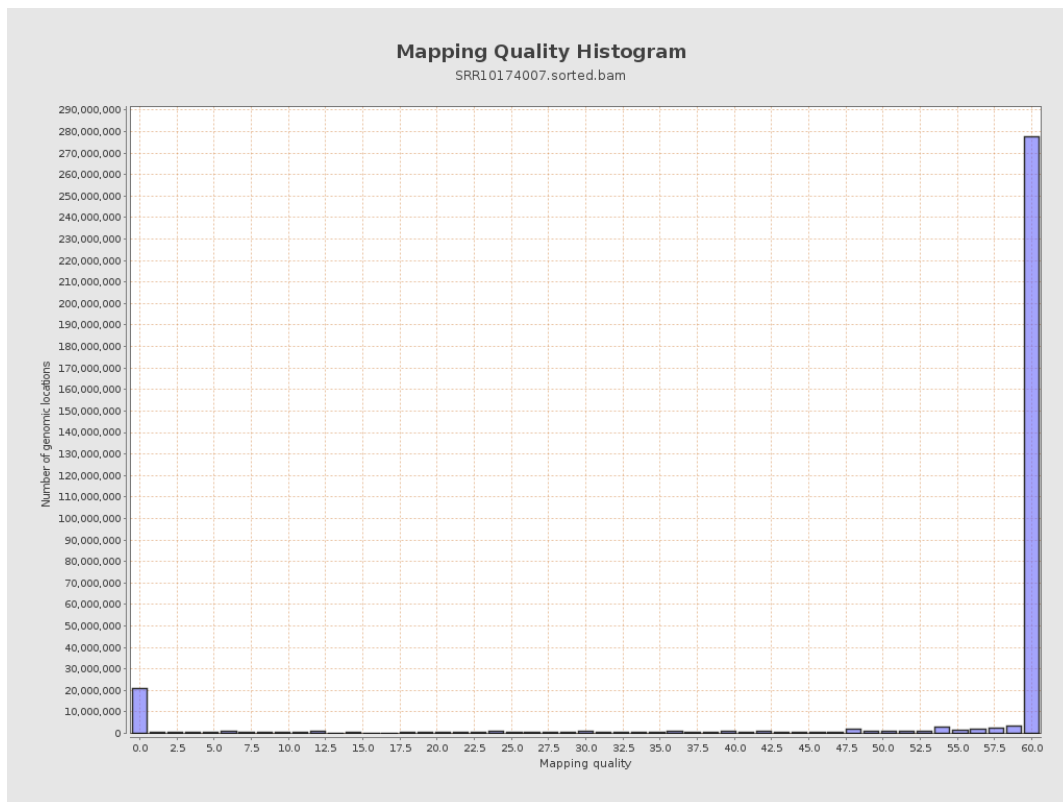
## 11. Results : Homopolymer Indels



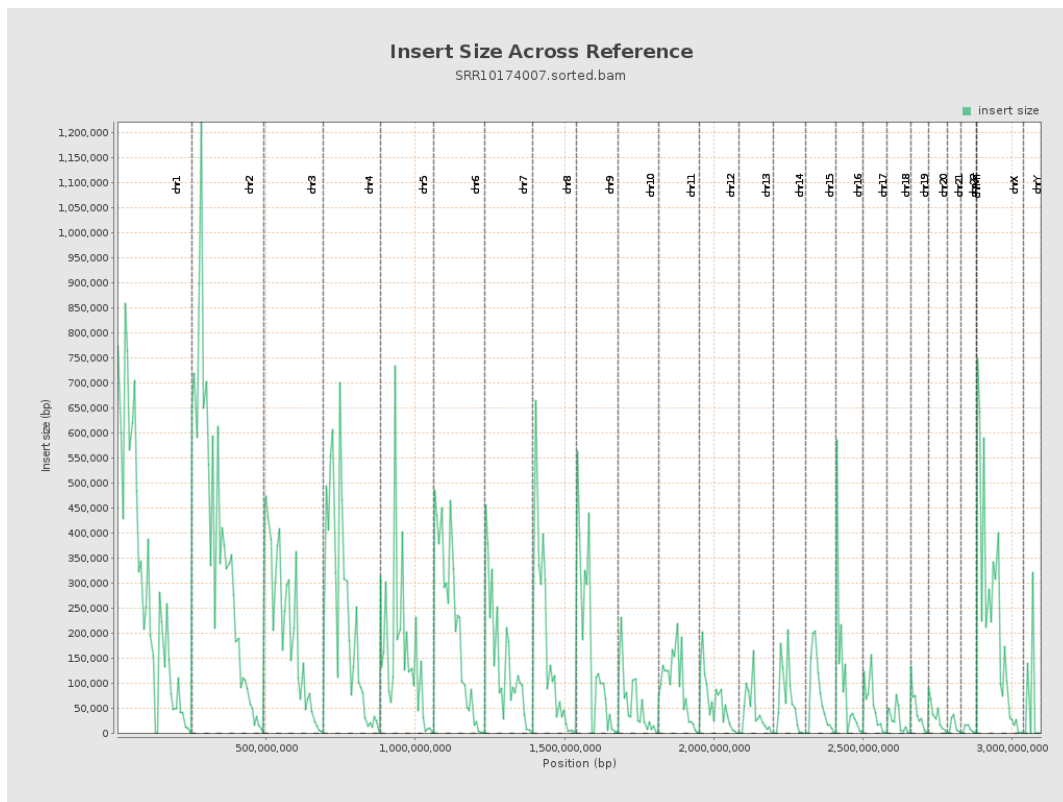
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

