

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/04 09:10:59*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173936.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_SRR10173936 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173936_1.fastq.gz SRR10173936_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                      |
| Analysis date:                        | Wed Sep 04 09:10:59 CST 2024                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                     |
| BAM file:                             | SRR10173936.sorted.bam                                                                                                                                                                                                  |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 4,787,972          |
| Mapped reads                 | 4,681,417 / 97.77% |
| Unmapped reads               | 106,555 / 2.23%    |
| Mapped paired reads          | 4,681,417 / 97.77% |
| Mapped reads, first in pair  | 2,344,590 / 48.97% |
| Mapped reads, second in pair | 2,336,827 / 48.81% |
| Mapped reads, both in pair   | 4,614,032 / 96.37% |
| Mapped reads, singletons     | 67,385 / 1.41%     |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 575,872 / 12.03%   |
| Read min/max/mean length     | 30 / 133 / 124.97  |
| Duplicated reads (estimated) | 3,771,388 / 78.77% |
| Duplication rate             | 65.45%             |
| Clipped reads                | 2,289,787 / 47.82% |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 158,265,176 / 29.86% |
| Number/percentage of C's | 105,358,418 / 19.88% |
| Number/percentage of T's | 156,958,964 / 29.61% |
| Number/percentage of G's | 109,476,297 / 20.65% |
| Number/percentage of N's | 4,231 / 0%           |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 40.53% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.1714 |
| Standard Deviation | 3.0949 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 52.68 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 953,427.9       |
| Standard Deviation | 8,547,770.66    |
| P25/Median/P75     | 106 / 155 / 237 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.89%     |
| Mismatches                               | 4,553,623 |
| Insertions                               | 59,246    |
| Mapped reads with at least one insertion | 1.22%     |
| Deletions                                | 173,555   |
| Mapped reads with at least one deletion  | 3.61%     |
| Homopolymer indels                       | 40.7%     |

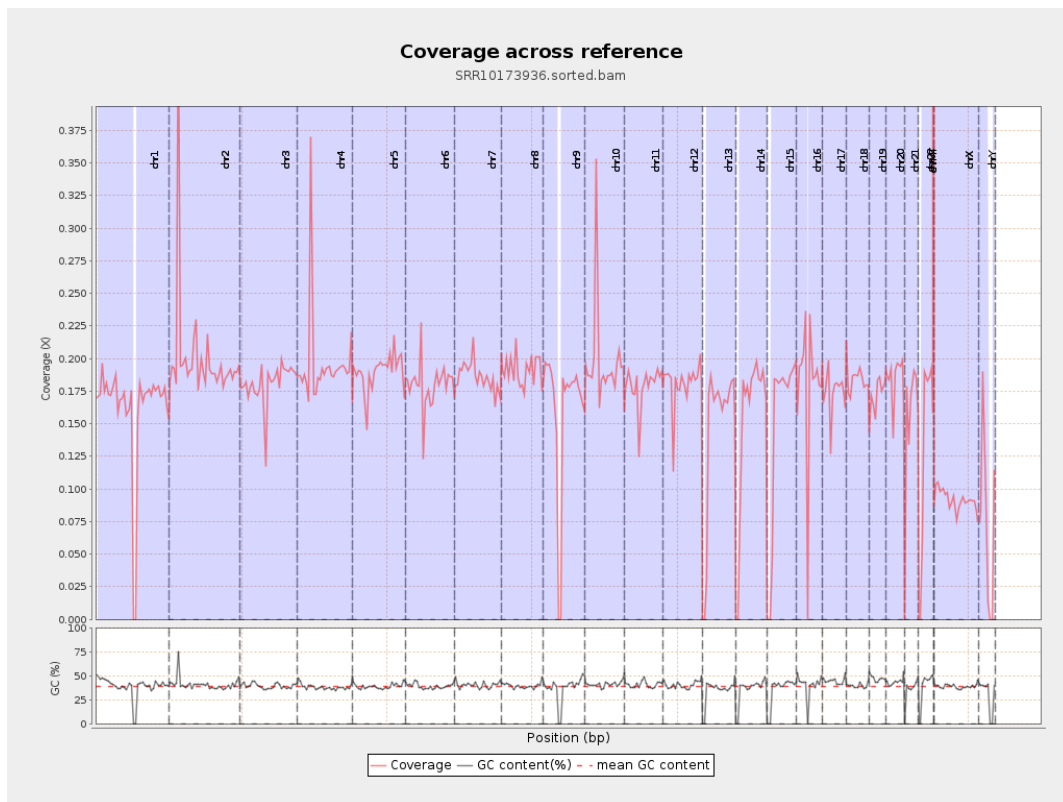
## 2.7. Chromosome stats

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

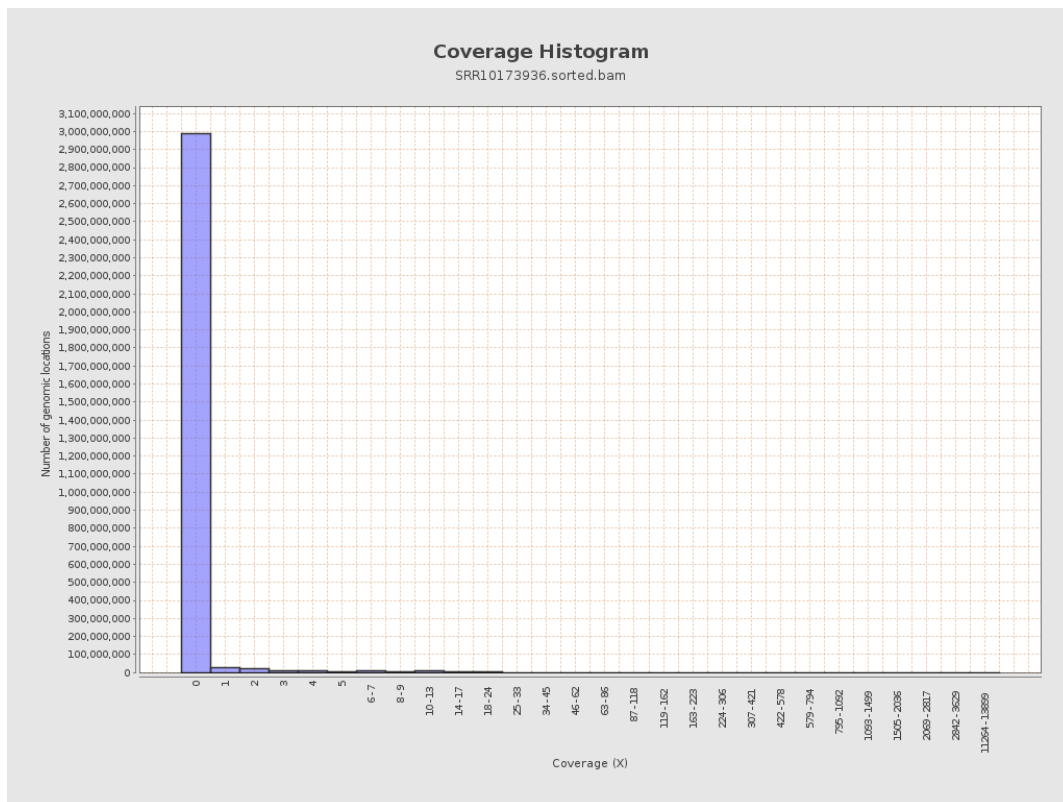
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 40377256     | 0.162           | 1.541            |
| chr2  | 243199373 | 48922918     | 0.2012          | 9.7759           |
| chr3  | 198022430 | 35837447     | 0.181           | 1.3118           |
| chr4  | 191154276 | 37297342     | 0.1951          | 1.8923           |
| chr5  | 180915260 | 34325745     | 0.1897          | 1.3481           |
| chr6  | 171115067 | 30741845     | 0.1797          | 1.4375           |
| chr7  | 159138663 | 29614424     | 0.1861          | 1.6954           |
| chr8  | 146364022 | 27957044     | 0.191           | 2.0075           |
| chr9  | 141213431 | 22651430     | 0.1604          | 1.4228           |
| chr10 | 135534747 | 26786036     | 0.1976          | 1.9705           |
| chr11 | 135006516 | 24191164     | 0.1792          | 1.3311           |
| chr12 | 133851895 | 24161898     | 0.1805          | 1.342            |
| chr13 | 115169878 | 16661455     | 0.1447          | 1.1674           |
| chr14 | 107349540 | 16335083     | 0.1522          | 1.2011           |
| chr15 | 102531392 | 15233712     | 0.1486          | 1.199            |
| chr16 | 90354753  | 16195908     | 0.1792          | 1.5137           |
| chr17 | 81195210  | 14042770     | 0.173           | 1.3304           |
| chr18 | 78077248  | 14350272     | 0.1838          | 1.8562           |
| chr19 | 59128983  | 10218825     | 0.1728          | 1.4031           |
| chr20 | 63025520  | 11621559     | 0.1844          | 1.4136           |
| chr21 | 48129895  | 7454923      | 0.1549          | 1.6116           |
| chr22 | 51304566  | 6613887      | 0.1289          | 1.1613           |
| chrMT | 16571     | 415151       | 25.0529         | 22.5978          |
| chrX  | 155270560 | 14247067     | 0.0918          | 0.9275           |

|      |          |         |       |        |
|------|----------|---------|-------|--------|
| chrY | 59373566 | 4212899 | 0.071 | 1.2961 |
|------|----------|---------|-------|--------|

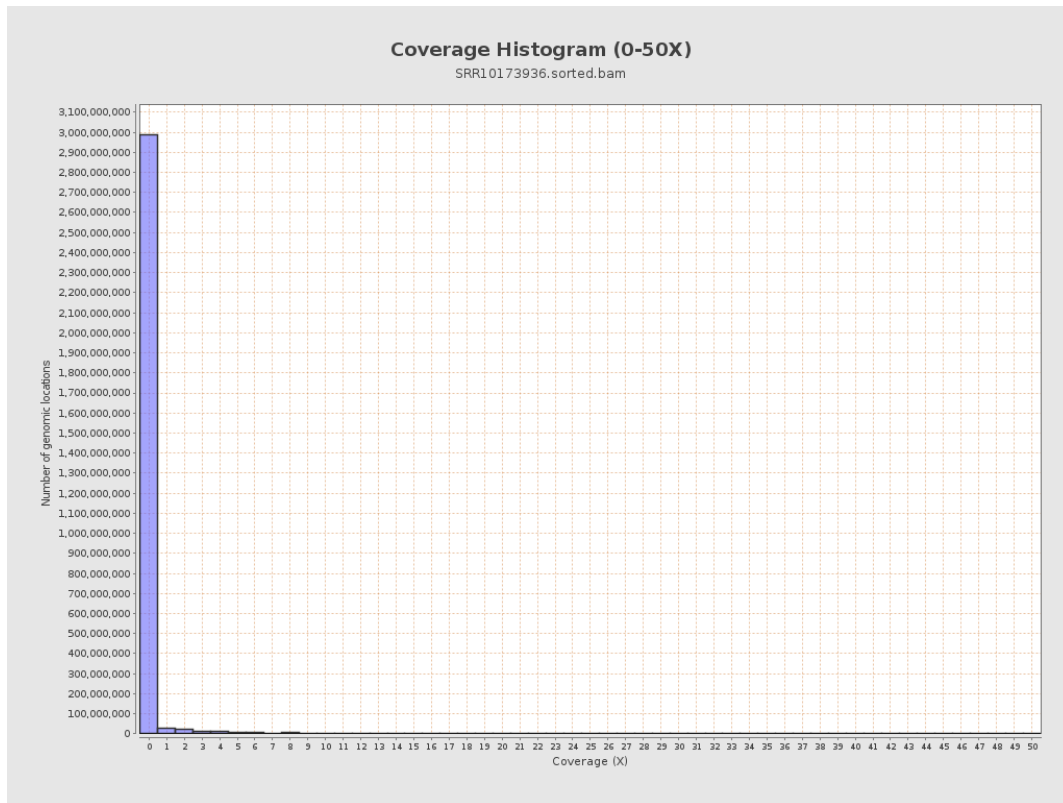
### 3. Results : Coverage across reference



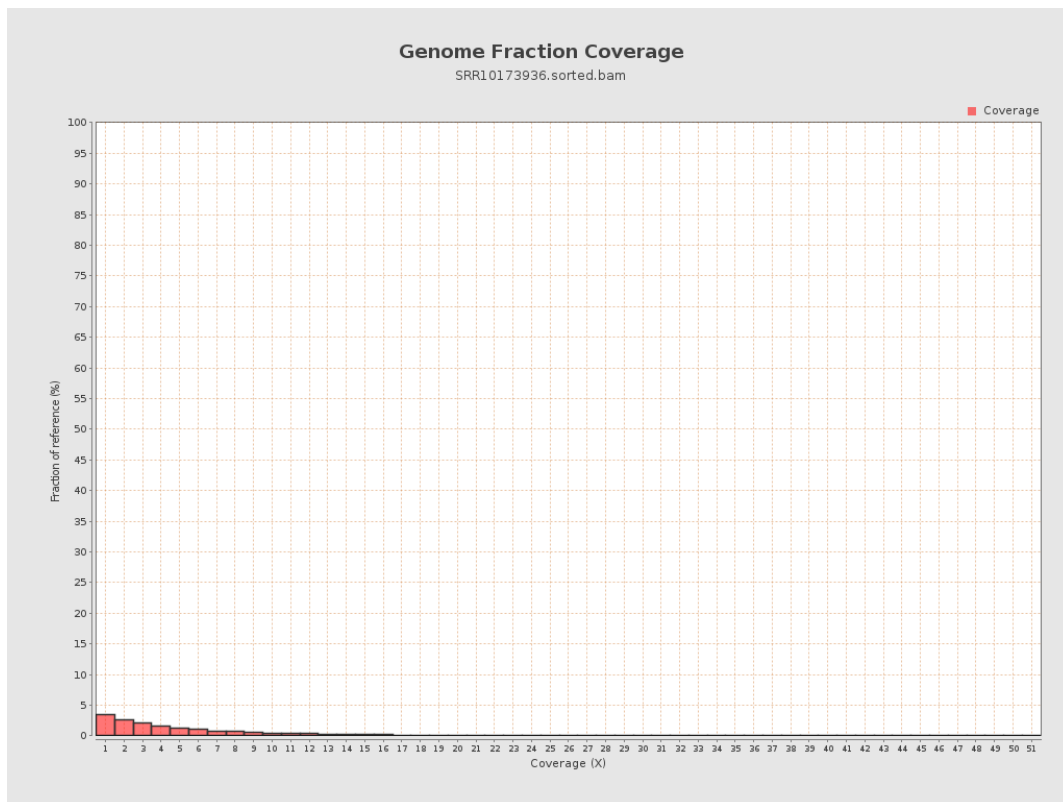
## 4. Results : Coverage Histogram



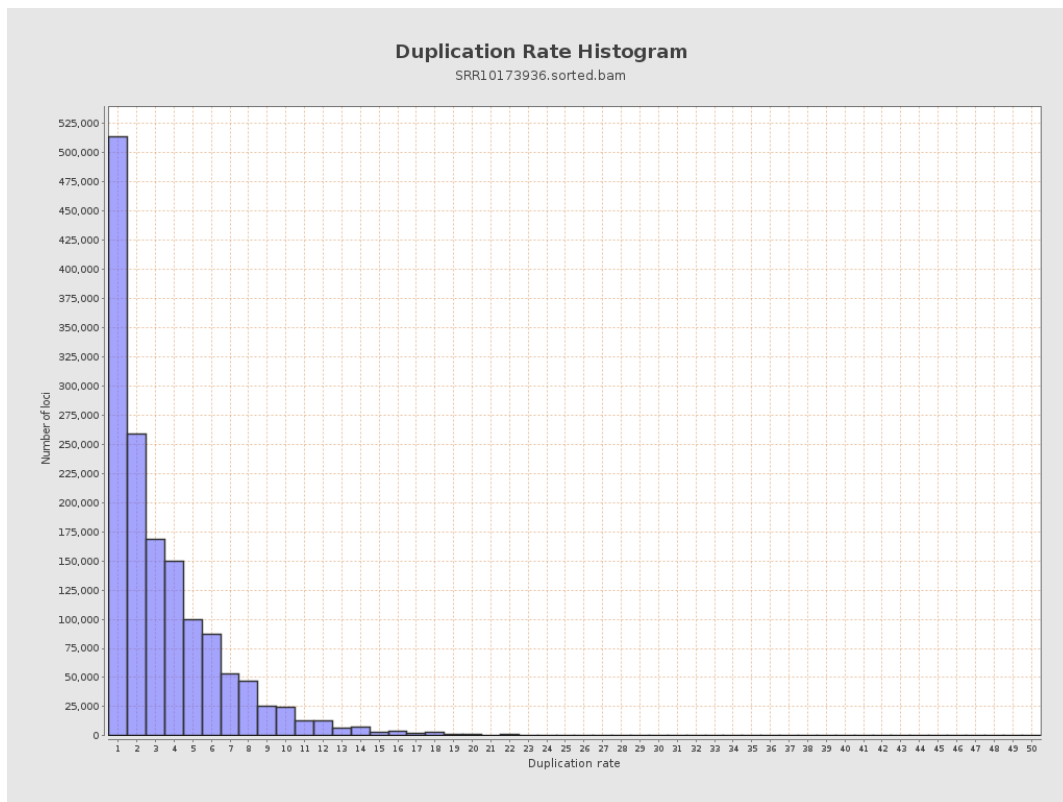
## 5. Results : Coverage Histogram (0-50X)



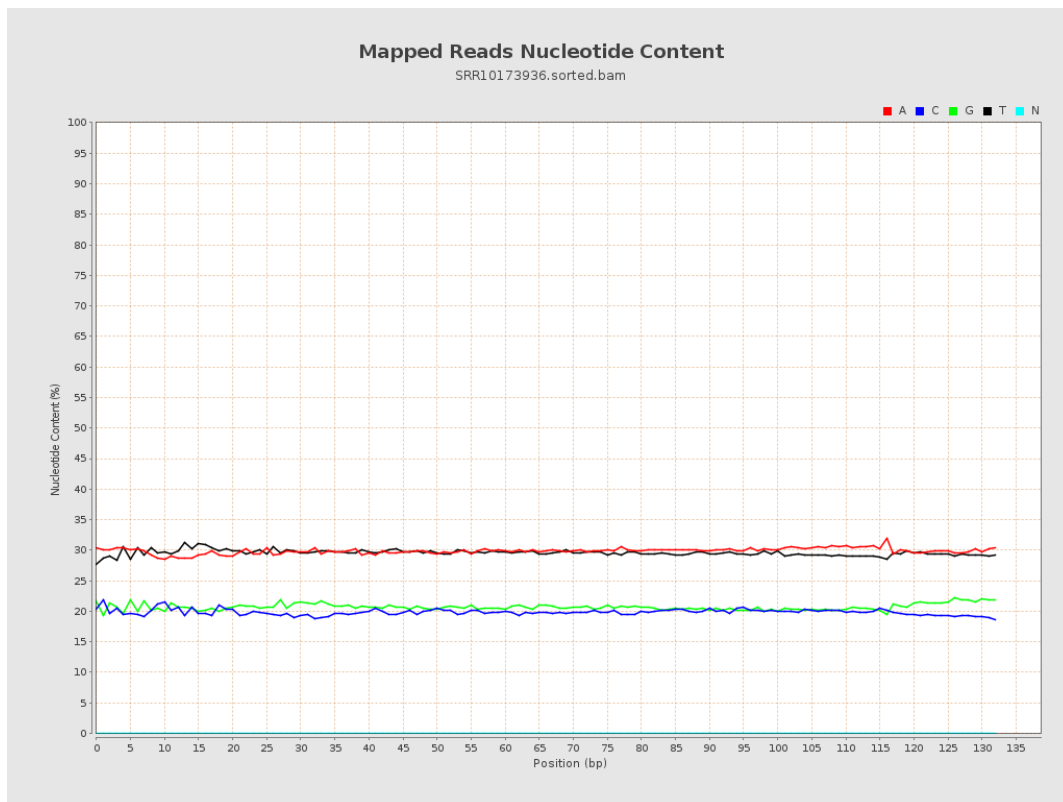
## 6. Results : Genome Fraction Coverage



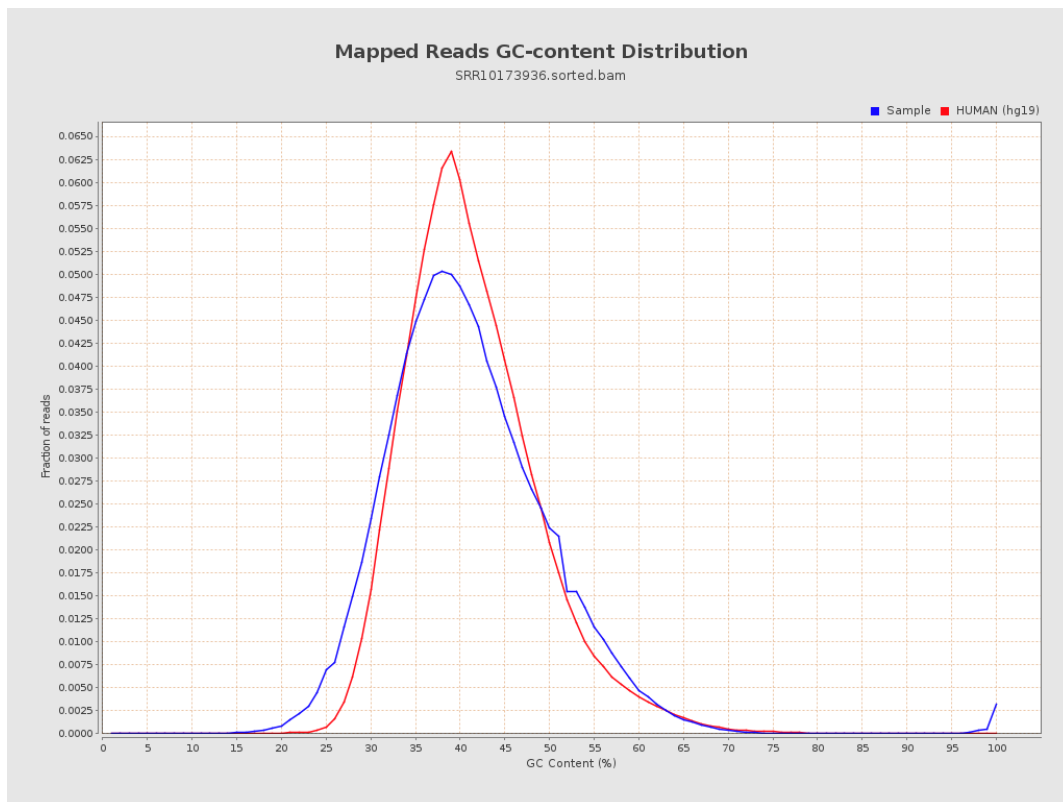
## 7. Results : Duplication Rate Histogram



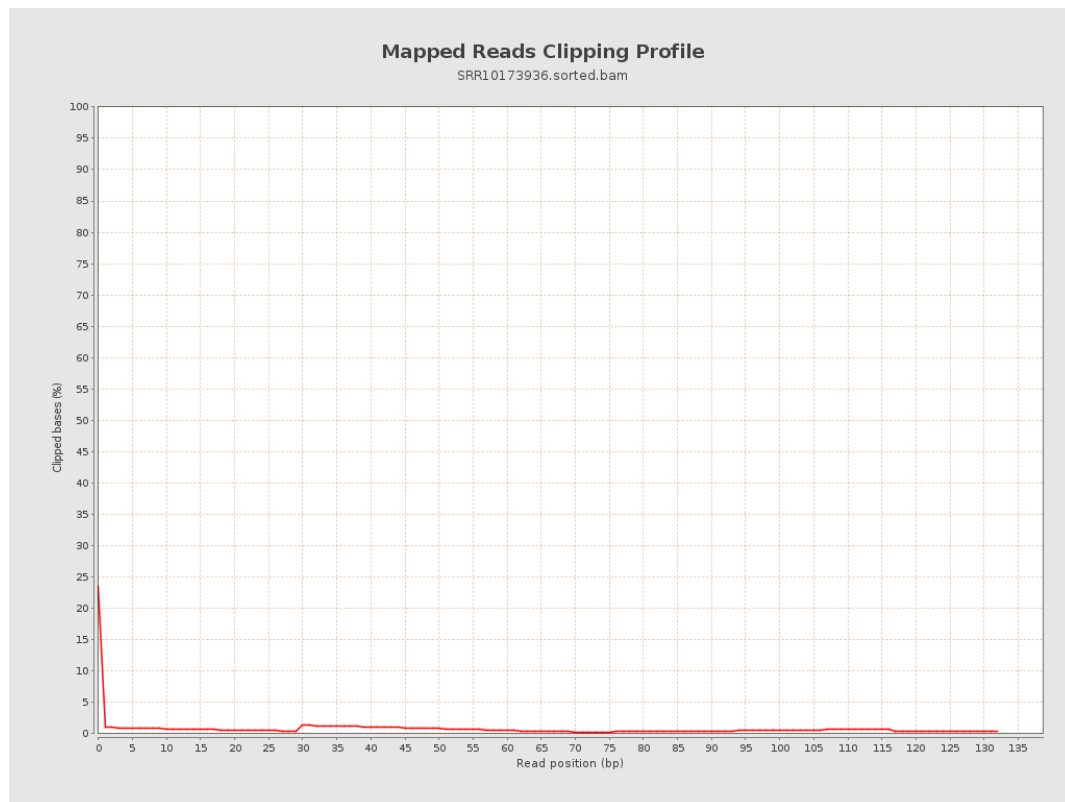
## 8. Results : Mapped Reads Nucleotide Content



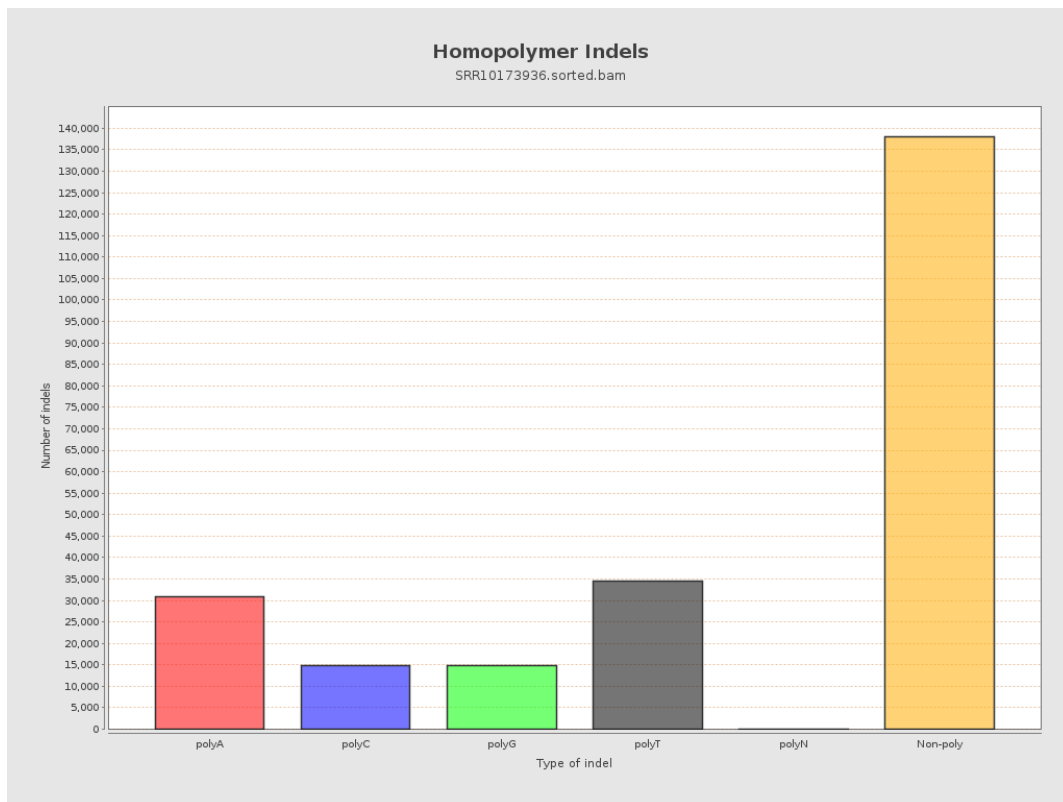
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



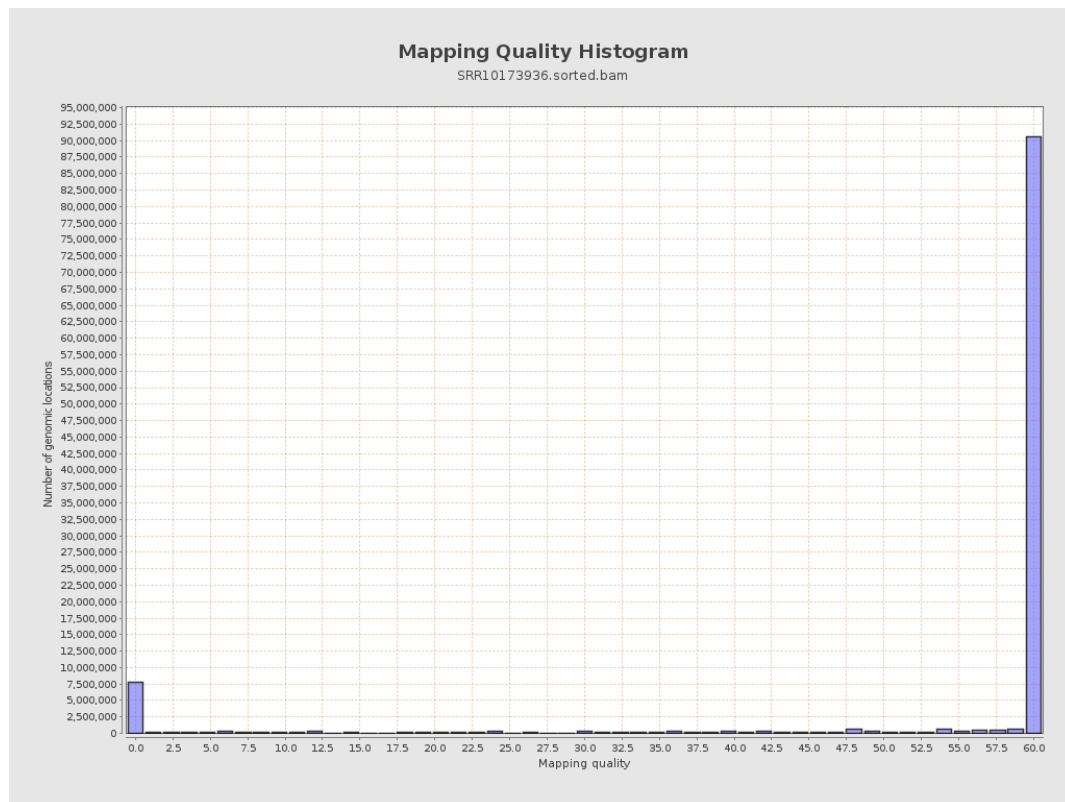
## 11. Results : Homopolymer Indels



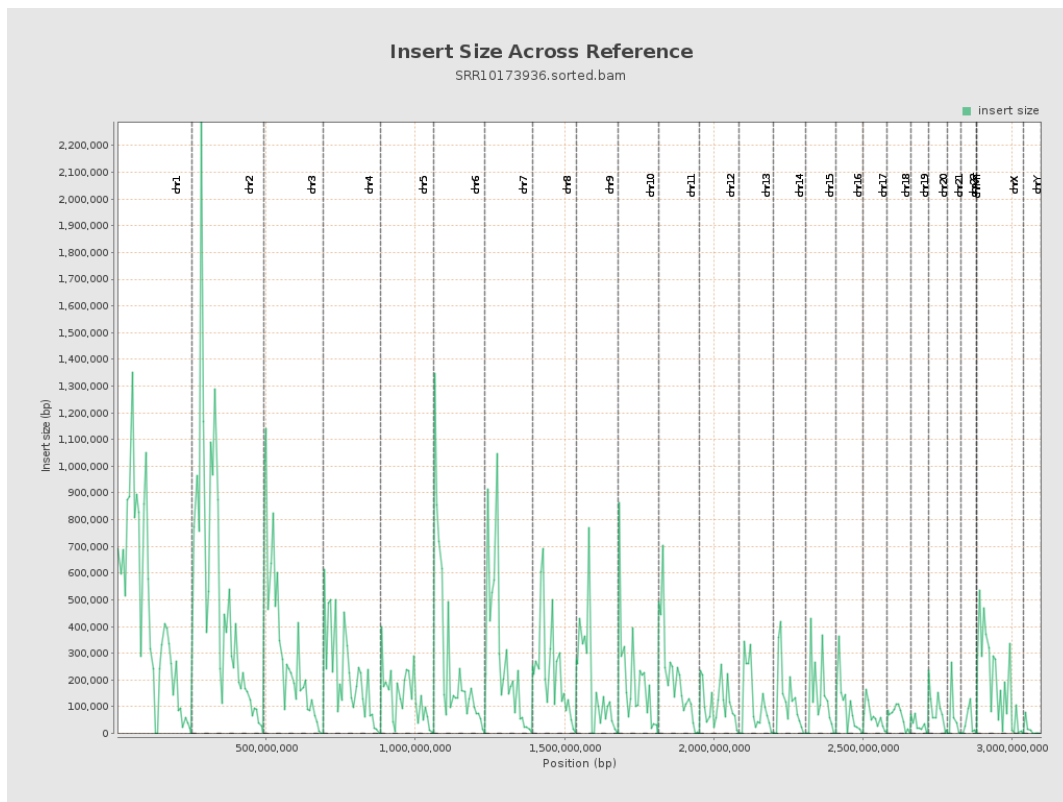
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

