

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 02:56:02*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10156411.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_SRR10156411 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10156411_1.fastq.gz SRR10156411_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                      |
| Analysis date:                        | Tue Sep 03 02:55:59 CST 2024                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                     |
| BAM file:                             | SRR10156411.sorted.bam                                                                                                                                                                                                  |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 14,553,040          |
| Mapped reads                 | 14,228,151 / 97.77% |
| Unmapped reads               | 324,889 / 2.23%     |
| Mapped paired reads          | 14,228,151 / 97.77% |
| Mapped reads, first in pair  | 7,112,979 / 48.88%  |
| Mapped reads, second in pair | 7,115,172 / 48.89%  |
| Mapped reads, both in pair   | 14,012,000 / 96.28% |
| Mapped reads, singletons     | 216,151 / 1.49%     |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 1,966,476 / 13.51%  |
| Read min/max/mean length     | 30 / 133 / 125.87   |
| Duplicated reads (estimated) | 11,732,421 / 80.62% |
| Duplication rate             | 67.01%              |
| Clipped reads                | 7,335,053 / 50.4%   |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 480,223,580 / 29.73% |
| Number/percentage of C's | 322,223,253 / 19.95% |
| Number/percentage of T's | 476,885,541 / 29.52% |
| Number/percentage of G's | 336,032,110 / 20.8%  |
| Number/percentage of N's | 12,431 / 0%          |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 40.75% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.5222 |
| Standard Deviation | 9.5561 |

## 2.4. Mapping Quality

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

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 1,134,337.71    |
| Standard Deviation | 9,862,170.67    |
| P25/Median/P75     | 106 / 157 / 245 |

## 2.6. Mismatches and indels

|                                          |            |
|------------------------------------------|------------|
| General error rate                       | 0.87%      |
| Mismatches                               | 13,525,770 |
| Insertions                               | 174,898    |
| Mapped reads with at least one insertion | 1.18%      |
| Deletions                                | 456,512    |
| Mapped reads with at least one deletion  | 3.13%      |
| Homopolymer indels                       | 41.21%     |

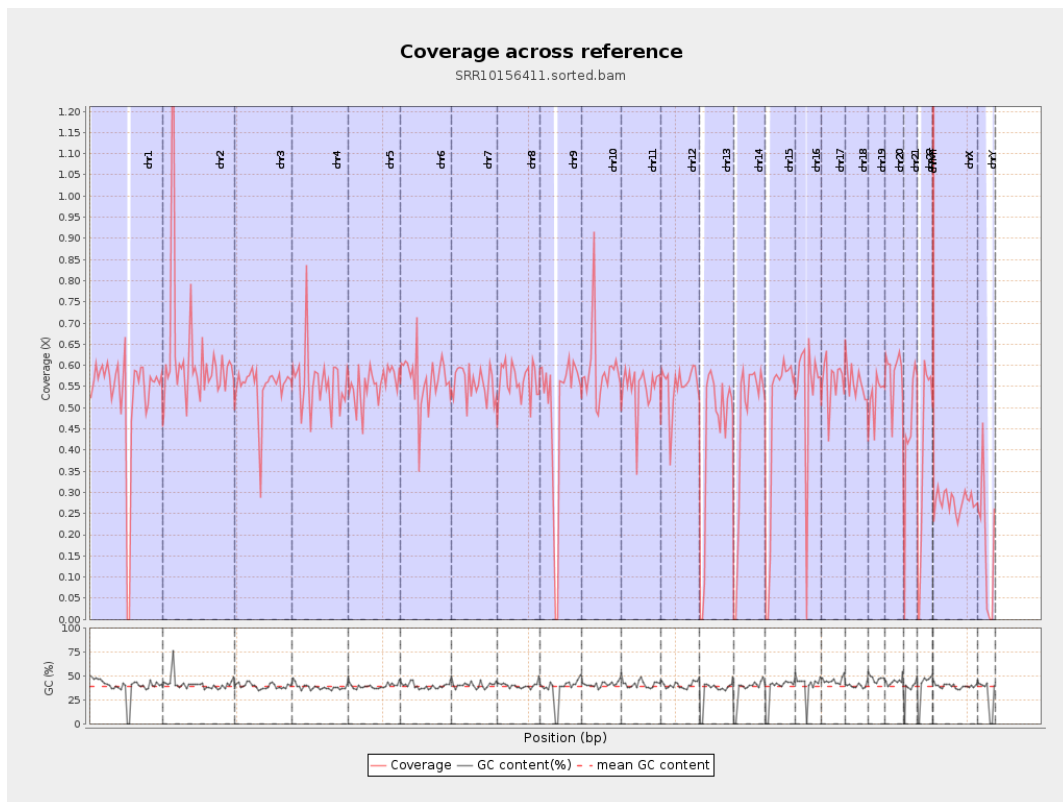
## 2.7. Chromosome stats

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

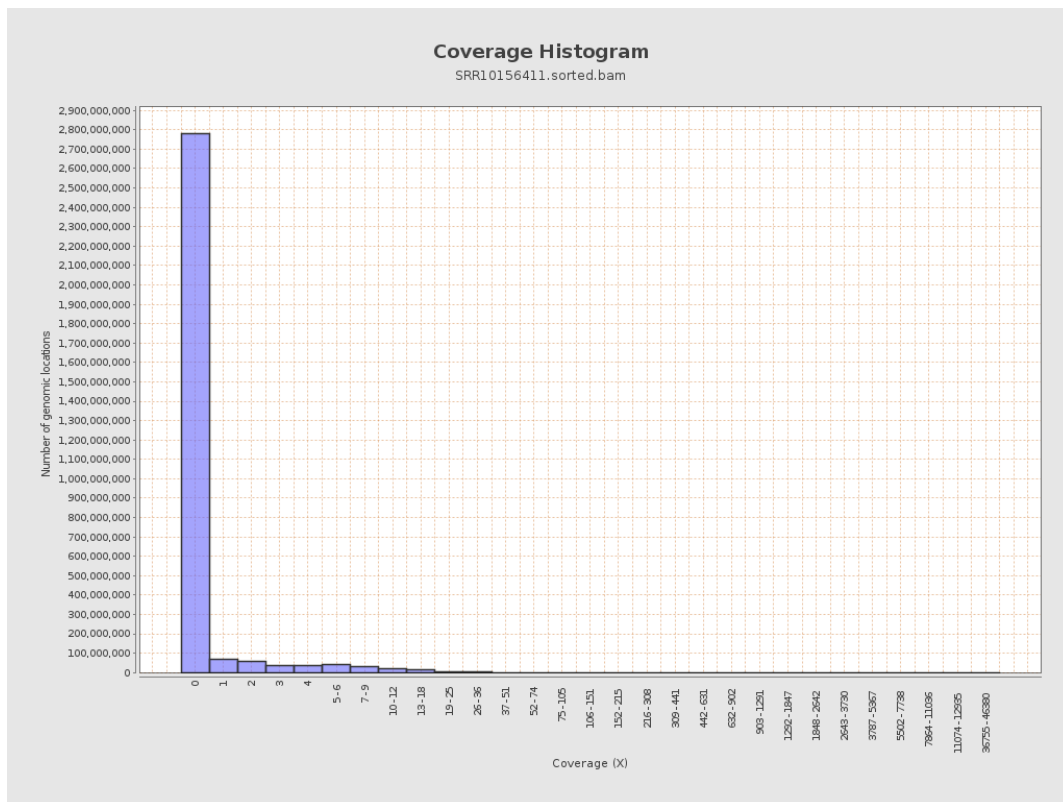
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 132074581    | 0.5299          | 4.2775           |
| chr2  | 243199373 | 150204832    | 0.6176          | 32.2564          |
| chr3  | 198022430 | 108404735    | 0.5474          | 2.277            |
| chr4  | 191154276 | 107535305    | 0.5626          | 3.5661           |
| chr5  | 180915260 | 100432951    | 0.5551          | 2.3072           |
| chr6  | 171115067 | 96784833     | 0.5656          | 3.1744           |
| chr7  | 159138663 | 88597259     | 0.5567          | 3.8495           |
| chr8  | 146364022 | 82520139     | 0.5638          | 4.1              |
| chr9  | 141213431 | 70255933     | 0.4975          | 3.7405           |
| chr10 | 135534747 | 79552424     | 0.587           | 4.5231           |
| chr11 | 135006516 | 73827053     | 0.5468          | 2.562            |
| chr12 | 133851895 | 74363563     | 0.5556          | 2.4498           |
| chr13 | 115169878 | 50158572     | 0.4355          | 2.0485           |
| chr14 | 107349540 | 49789805     | 0.4638          | 2.1932           |
| chr15 | 102531392 | 47572949     | 0.464           | 2.2186           |
| chr16 | 90354753  | 48720848     | 0.5392          | 3.1194           |
| chr17 | 81195210  | 45964072     | 0.5661          | 2.7486           |
| chr18 | 78077248  | 43655552     | 0.5591          | 4.7993           |
| chr19 | 59128983  | 31181377     | 0.5273          | 3.1279           |
| chr20 | 63025520  | 36683781     | 0.582           | 2.5309           |
| chr21 | 48129895  | 21827724     | 0.4535          | 3.0041           |
| chr22 | 51304566  | 20561141     | 0.4008          | 2.4006           |
| chrMT | 16571     | 1785206      | 107.7307        | 88.1406          |
| chrX  | 155270560 | 43131357     | 0.2778          | 1.6547           |

|      |          |          |       |        |
|------|----------|----------|-------|--------|
| chrY | 59373566 | 10863569 | 0.183 | 2.6443 |
|------|----------|----------|-------|--------|

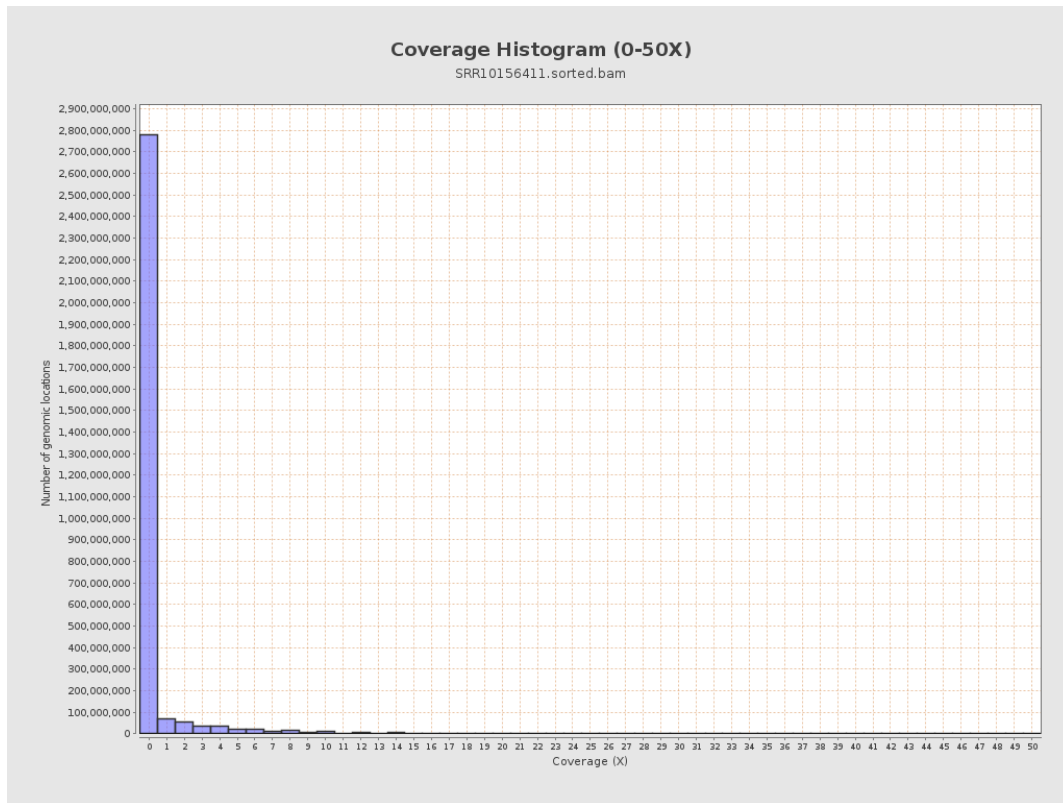
### 3. Results : Coverage across reference



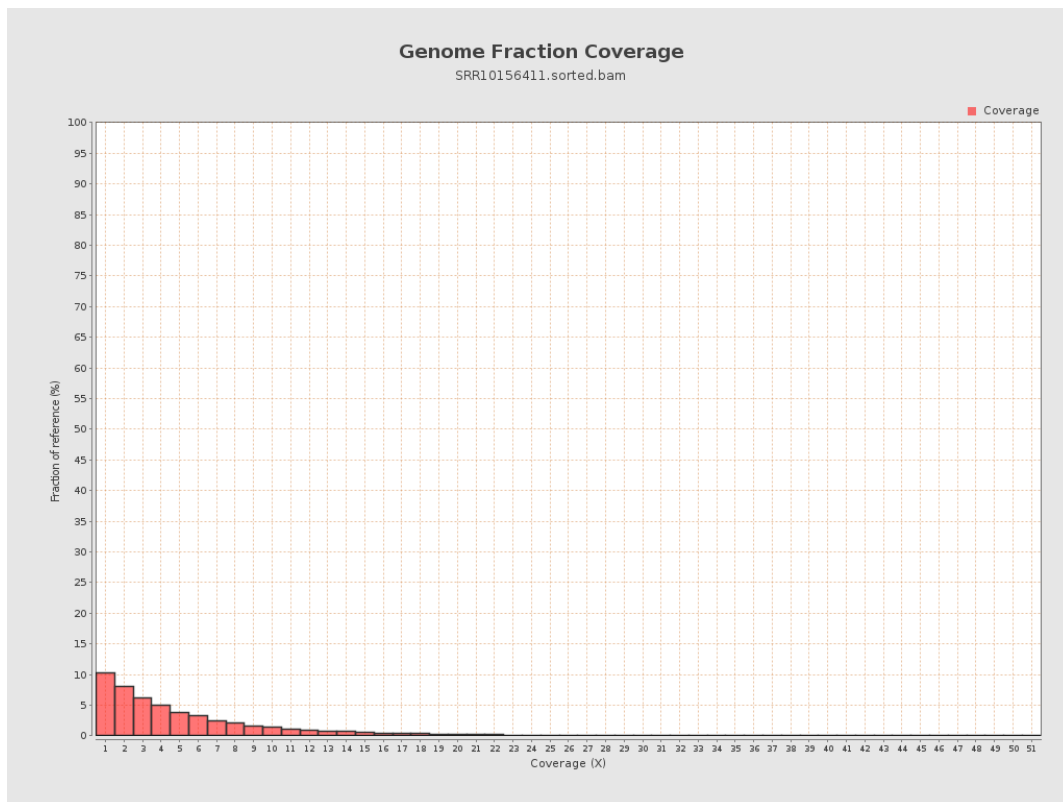
## 4. Results : Coverage Histogram



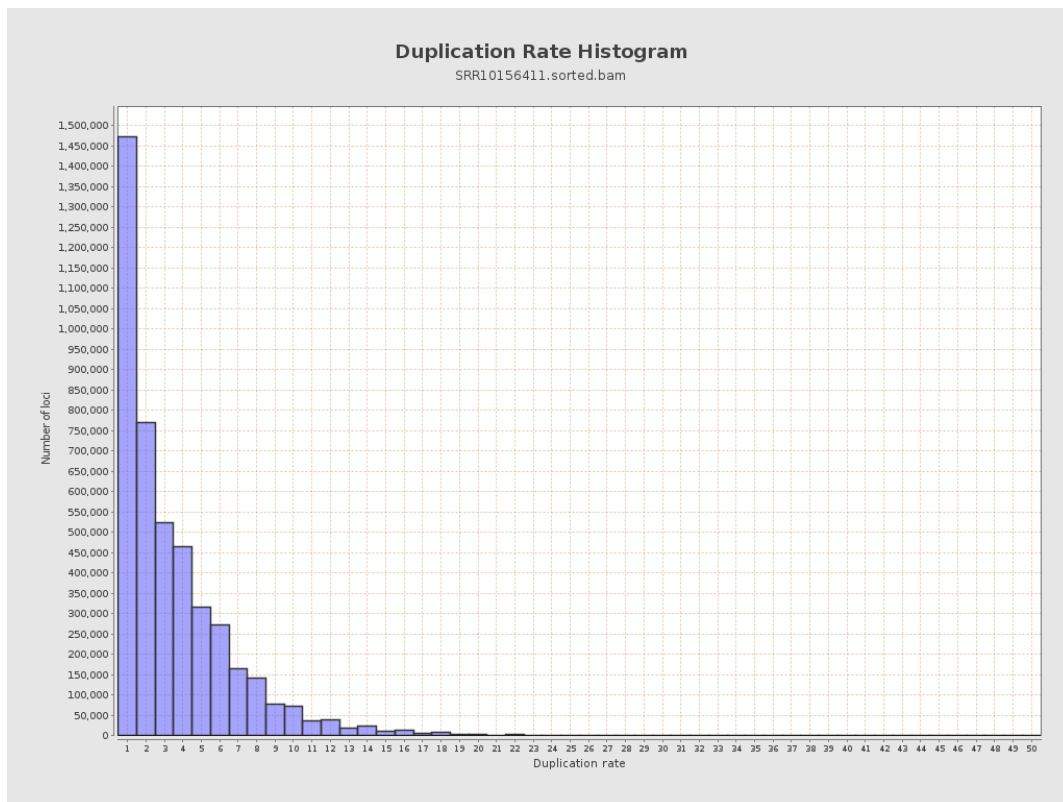
## 5. Results : Coverage Histogram (0-50X)



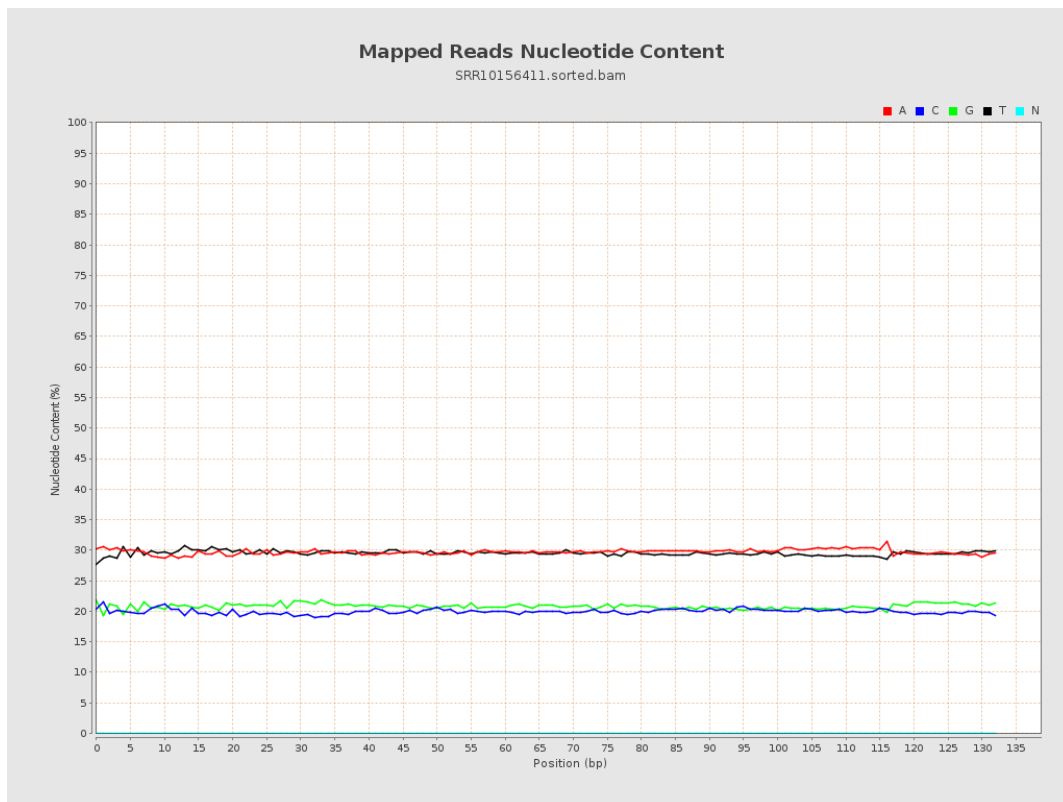
## 6. Results : Genome Fraction Coverage



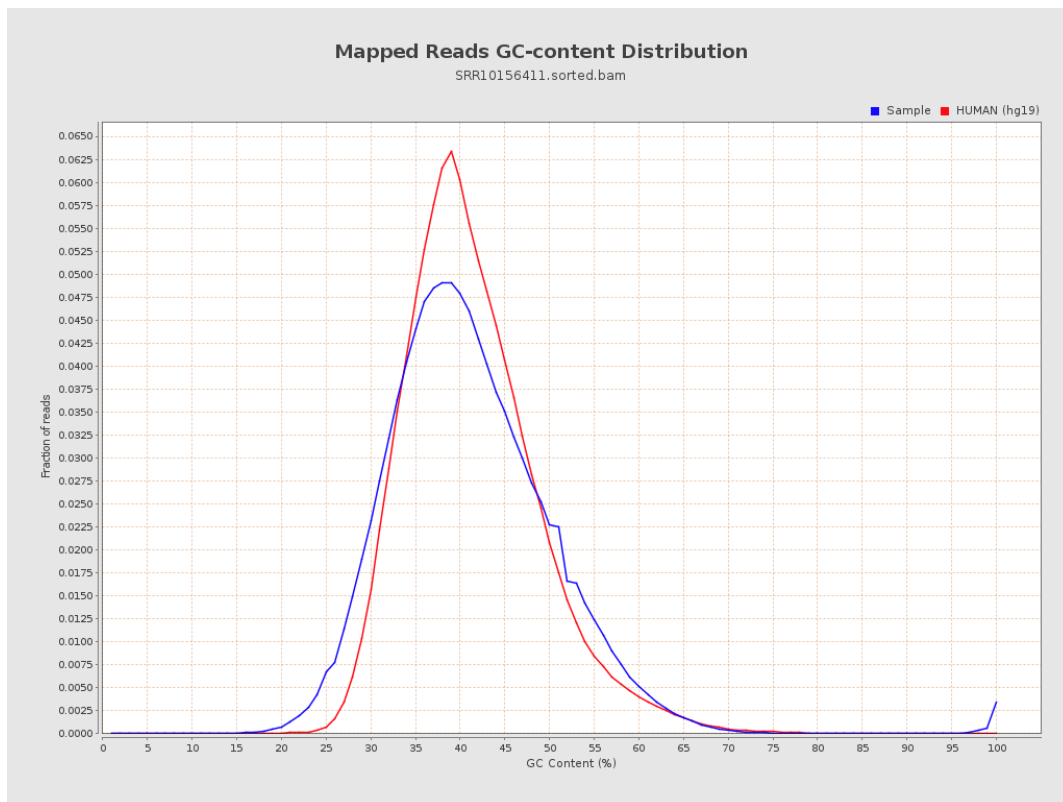
## 7. Results : Duplication Rate Histogram



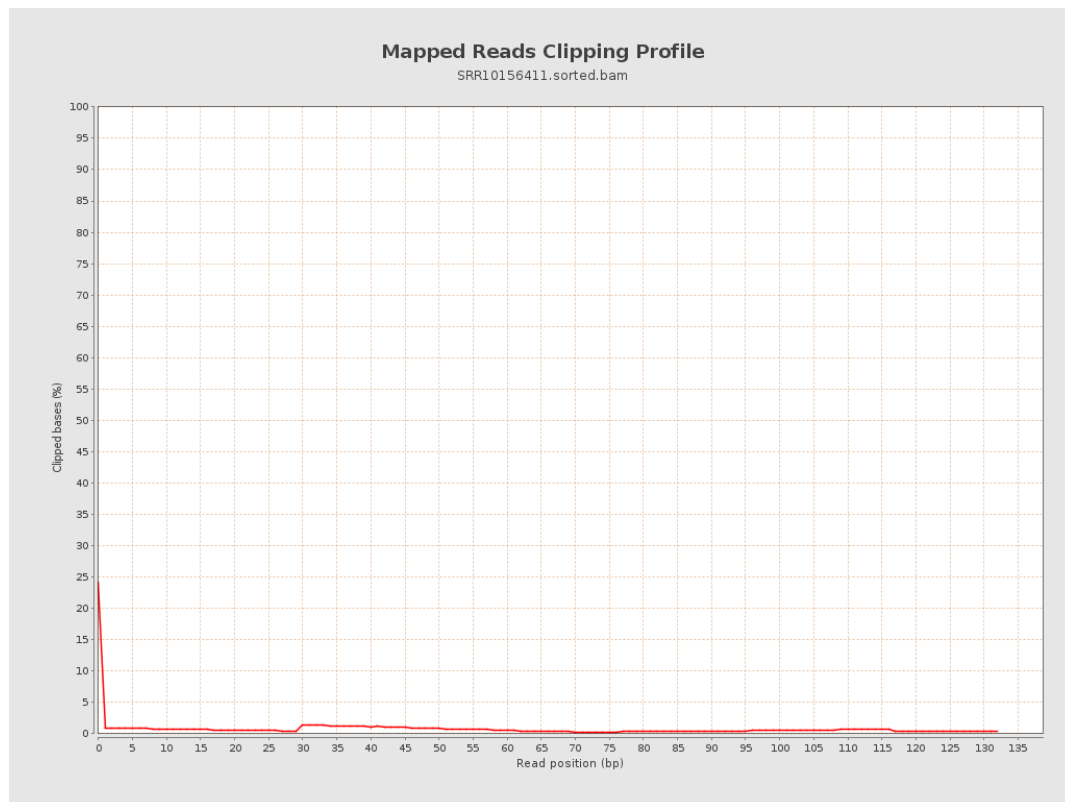
## 8. Results : Mapped Reads Nucleotide Content



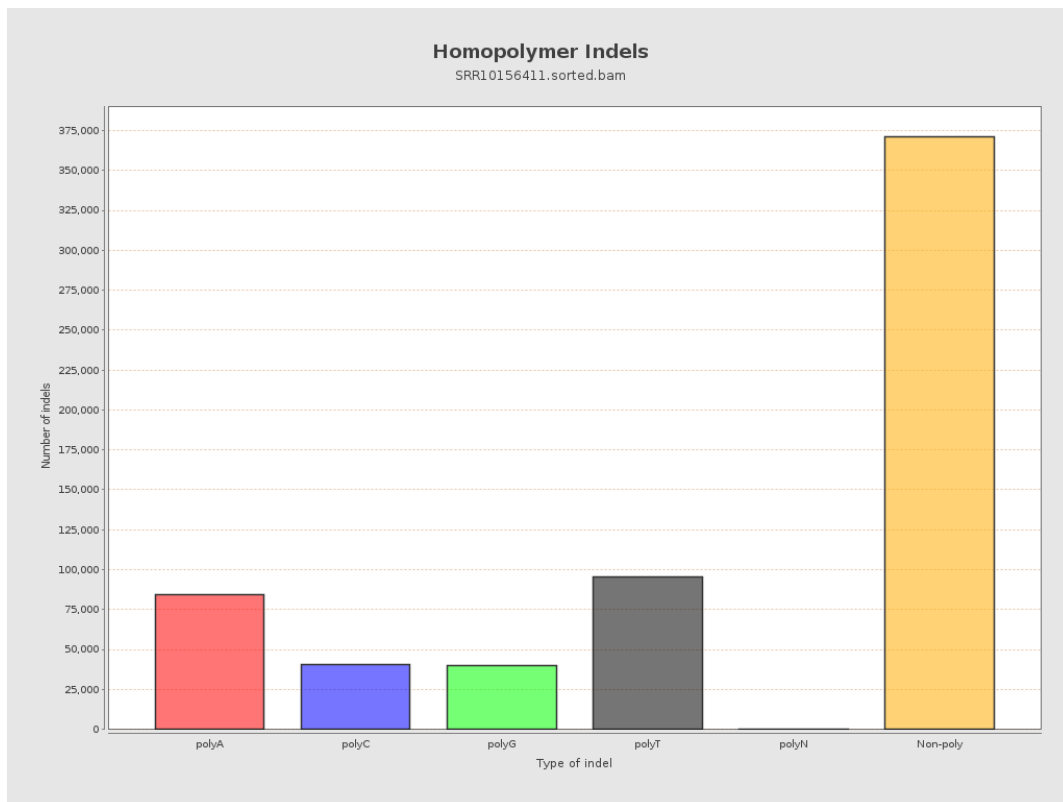
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



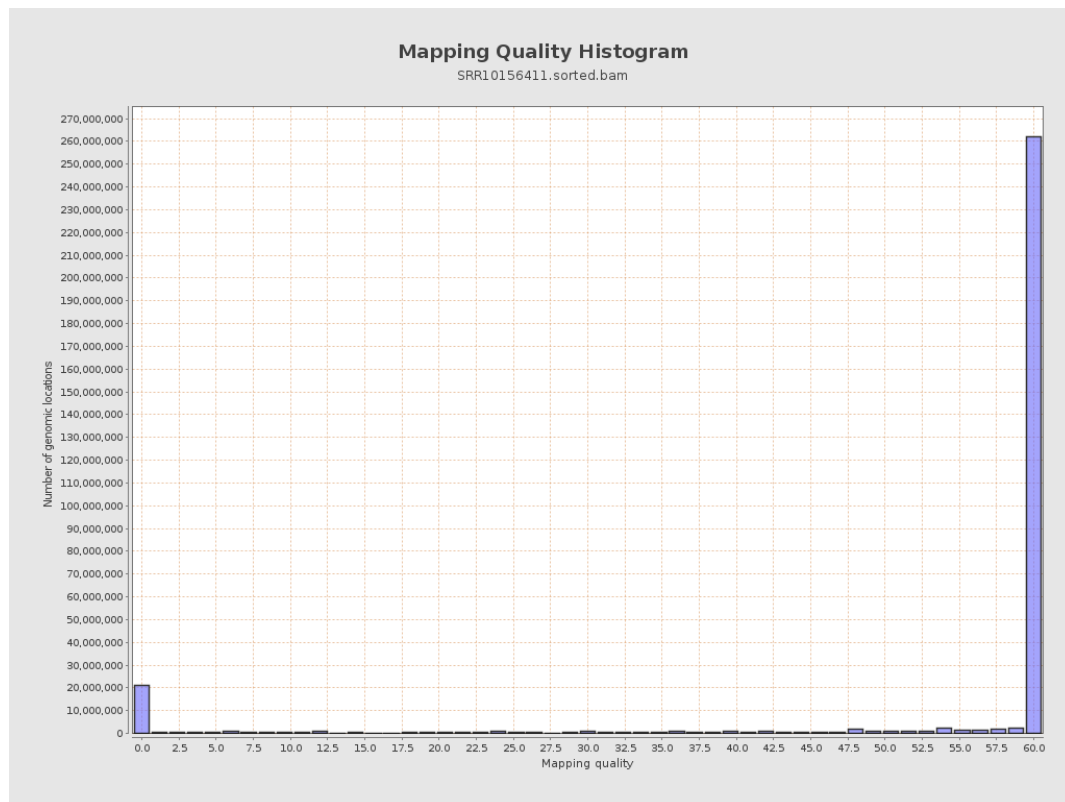
## 11. Results : Homopolymer Indels



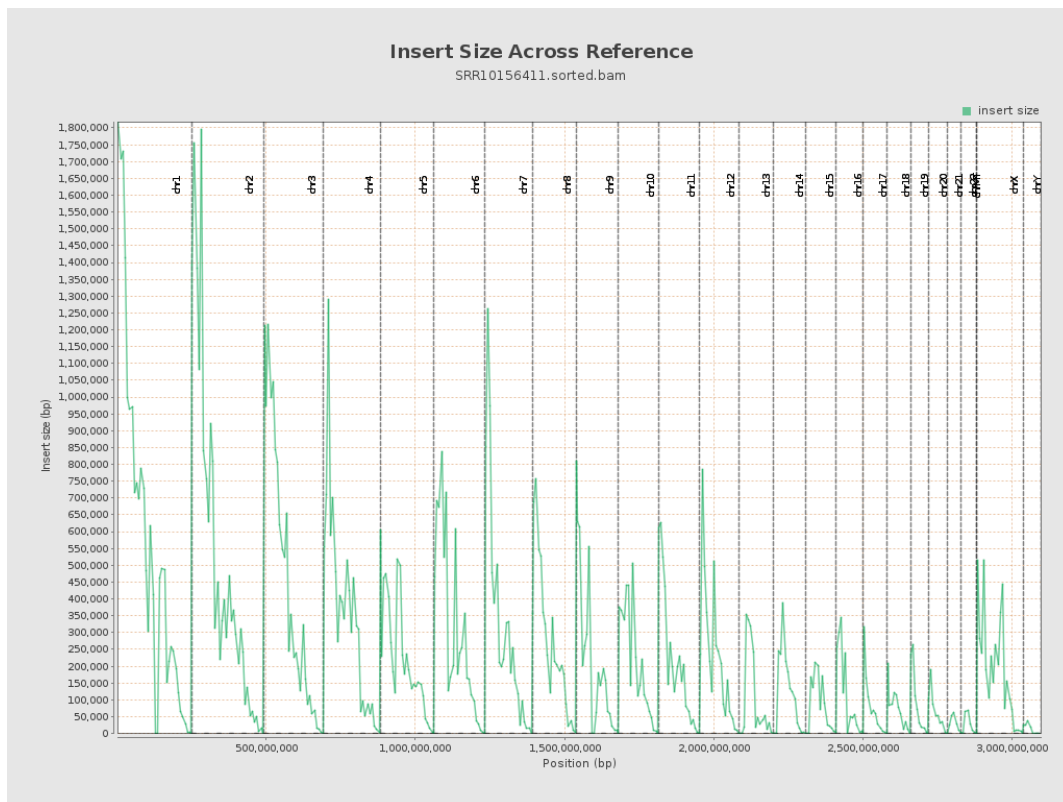
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

