

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 02:13:54*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10156408.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_SRR10156408 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10156408_1.fastq.gz SRR10156408_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                      |
| Analysis date:                        | Tue Sep 03 02:13:50 CST 2024                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                     |
| BAM file:                             | SRR10156408.sorted.bam                                                                                                                                                                                                  |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 8,099,964          |
| Mapped reads                 | 7,915,658 / 97.72% |
| Unmapped reads               | 184,306 / 2.28%    |
| Mapped paired reads          | 7,915,658 / 97.72% |
| Mapped reads, first in pair  | 3,962,178 / 48.92% |
| Mapped reads, second in pair | 3,953,480 / 48.81% |
| Mapped reads, both in pair   | 7,795,140 / 96.24% |
| Mapped reads, singletons     | 120,518 / 1.49%    |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 1,071,822 / 13.23% |
| Read min/max/mean length     | 30 / 133 / 126     |
| Duplicated reads (estimated) | 6,309,450 / 77.89% |
| Duplication rate             | 64.59%             |
| Clipped reads                | 4,123,586 / 50.91% |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 267,016,555 / 29.7%  |
| Number/percentage of C's | 179,733,655 / 19.99% |
| Number/percentage of T's | 265,142,132 / 29.49% |
| Number/percentage of G's | 187,282,455 / 20.83% |
| Number/percentage of N's | 6,792 / 0%           |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 40.82% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.2907 |
| Standard Deviation | 5.2488 |

## 2.4. Mapping Quality

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

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 1,386,746.16    |
| Standard Deviation | 10,720,742.22   |
| P25/Median/P75     | 107 / 158 / 243 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.88%     |
| Mismatches                               | 7,629,529 |
| Insertions                               | 95,381    |
| Mapped reads with at least one insertion | 1.16%     |
| Deletions                                | 285,343   |
| Mapped reads with at least one deletion  | 3.51%     |
| Homopolymer indels                       | 40.45%    |

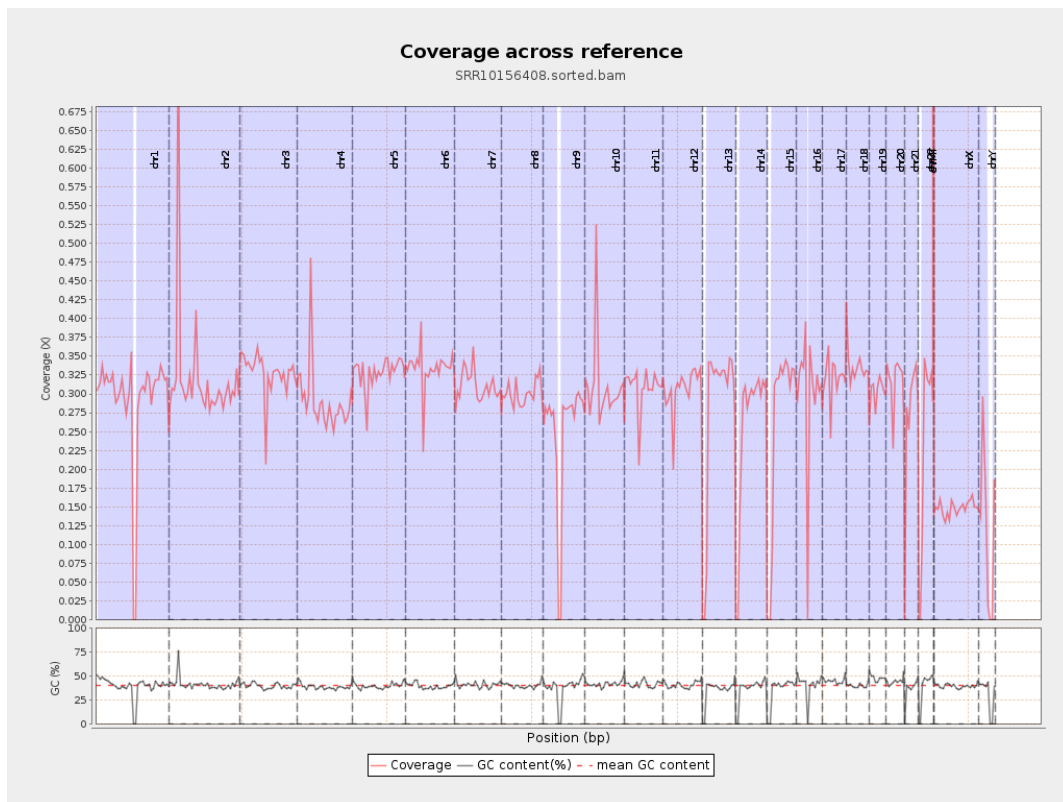
## 2.7. Chromosome stats

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

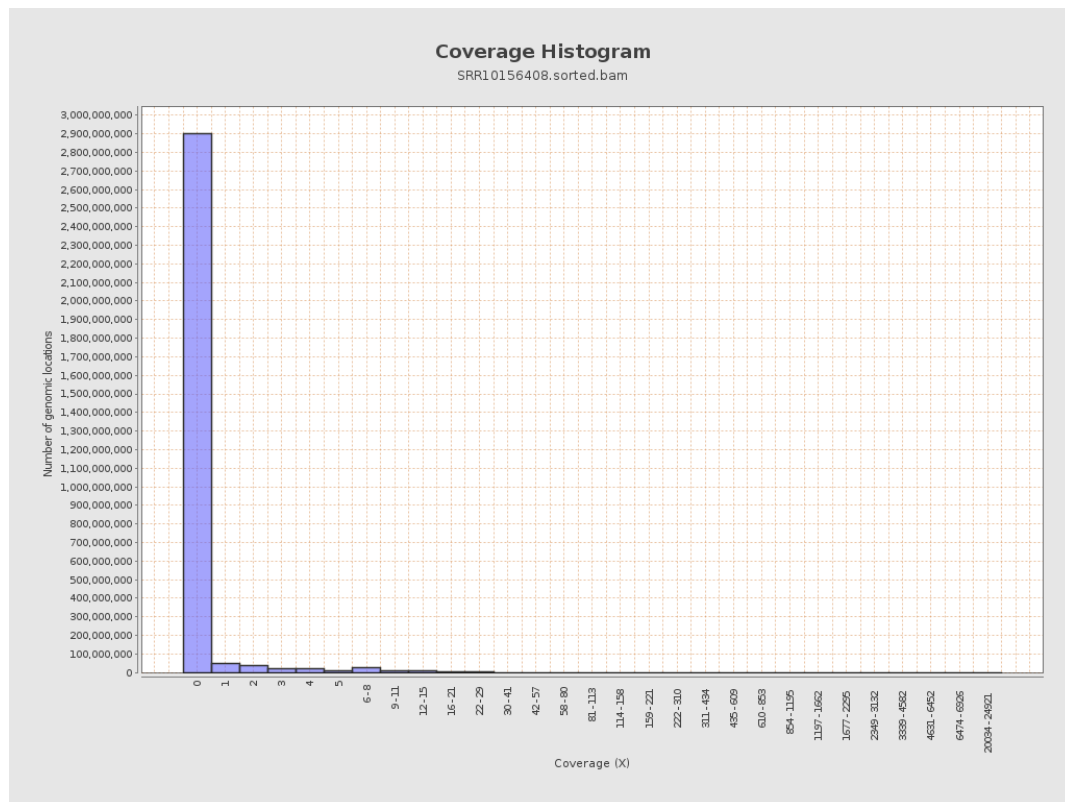
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 72949968     | 0.2927          | 2.3802           |
| chr2  | 243199373 | 78416849     | 0.3224          | 17.424           |
| chr3  | 198022430 | 64979319     | 0.3281          | 1.707            |
| chr4  | 191154276 | 55296252     | 0.2893          | 2.1086           |
| chr5  | 180915260 | 59354324     | 0.3281          | 1.7093           |
| chr6  | 171115067 | 57107318     | 0.3337          | 1.9694           |
| chr7  | 159138663 | 49575277     | 0.3115          | 2.3689           |
| chr8  | 146364022 | 44071629     | 0.3011          | 2.5705           |
| chr9  | 141213431 | 35068972     | 0.2483          | 1.9509           |
| chr10 | 135534747 | 41829895     | 0.3086          | 2.6924           |
| chr11 | 135006516 | 41617044     | 0.3083          | 1.7069           |
| chr12 | 133851895 | 40884994     | 0.3054          | 1.6981           |
| chr13 | 115169878 | 31810415     | 0.2762          | 1.5738           |
| chr14 | 107349540 | 27429257     | 0.2555          | 1.5182           |
| chr15 | 102531392 | 26961511     | 0.263           | 1.5675           |
| chr16 | 90354753  | 27064015     | 0.2995          | 2.0128           |
| chr17 | 81195210  | 25890062     | 0.3189          | 1.7868           |
| chr18 | 78077248  | 26232212     | 0.336           | 2.9063           |
| chr19 | 59128983  | 17941336     | 0.3034          | 1.9603           |
| chr20 | 63025520  | 19872789     | 0.3153          | 1.7256           |
| chr21 | 48129895  | 13078537     | 0.2717          | 1.916            |
| chr22 | 51304566  | 11622220     | 0.2265          | 1.6984           |
| chrMT | 16571     | 927873       | 55.9938         | 40.6717          |
| chrX  | 155270560 | 22978201     | 0.148           | 1.1471           |

|      |          |         |        |        |
|------|----------|---------|--------|--------|
| chrY | 59373566 | 6878156 | 0.1158 | 1.6458 |
|------|----------|---------|--------|--------|

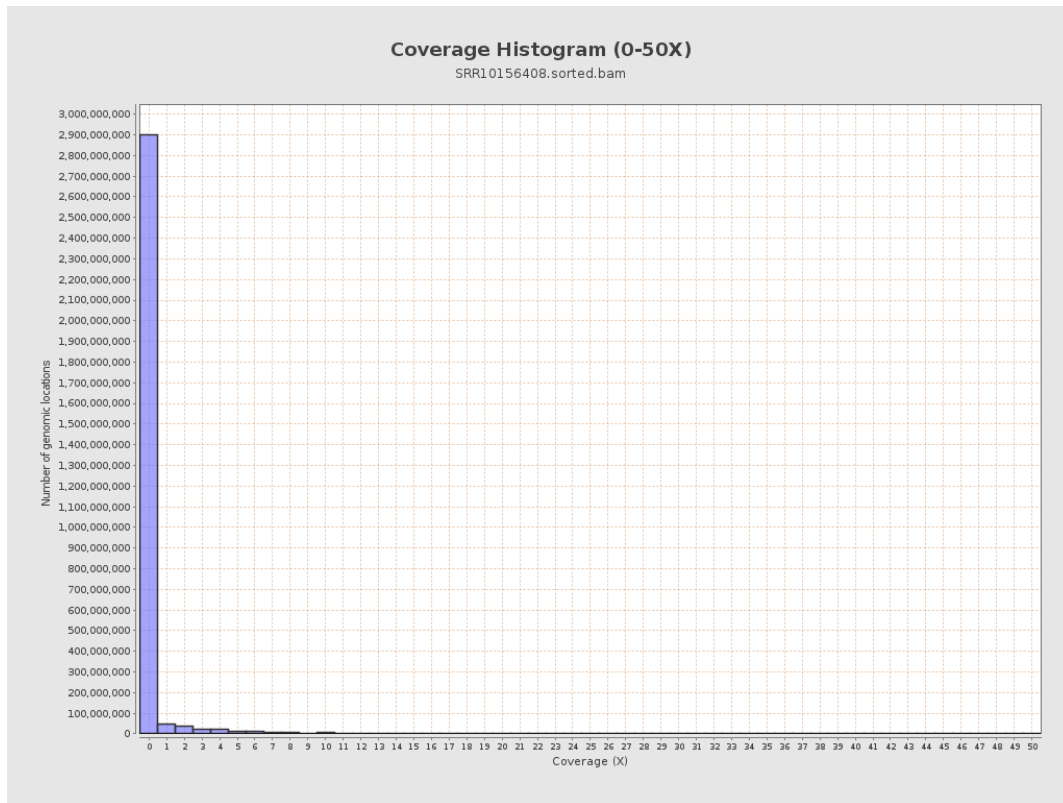
### 3. Results : Coverage across reference



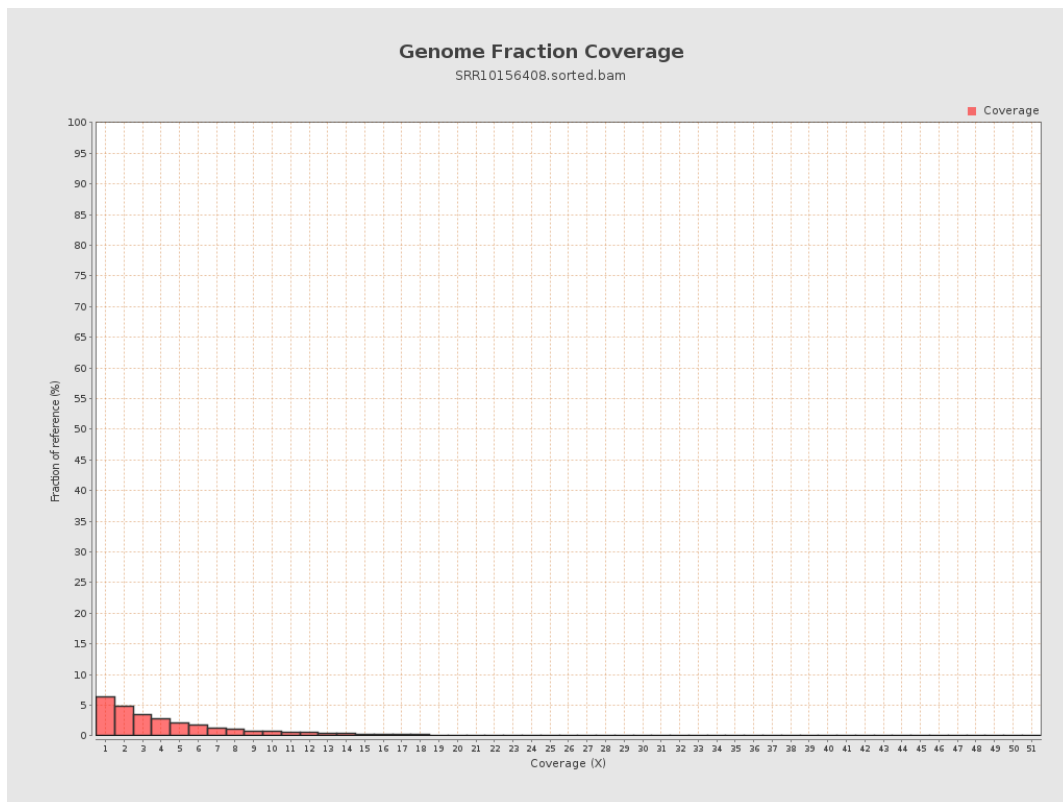
## 4. Results : Coverage Histogram



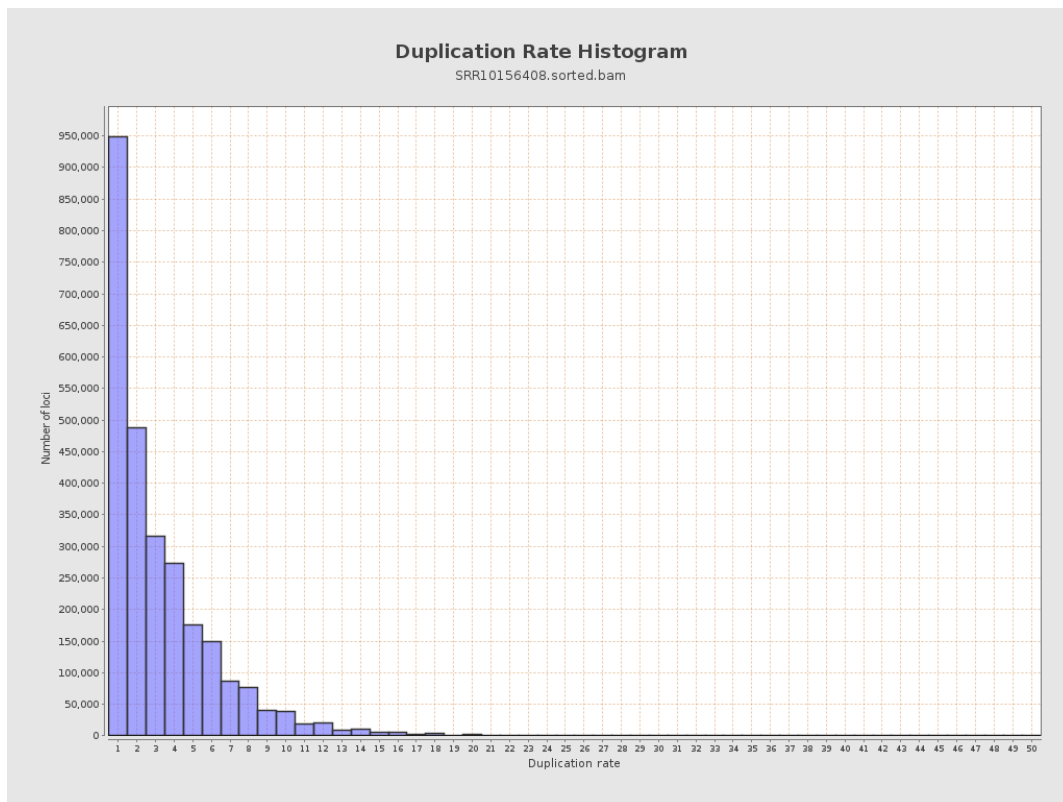
## 5. Results : Coverage Histogram (0-50X)



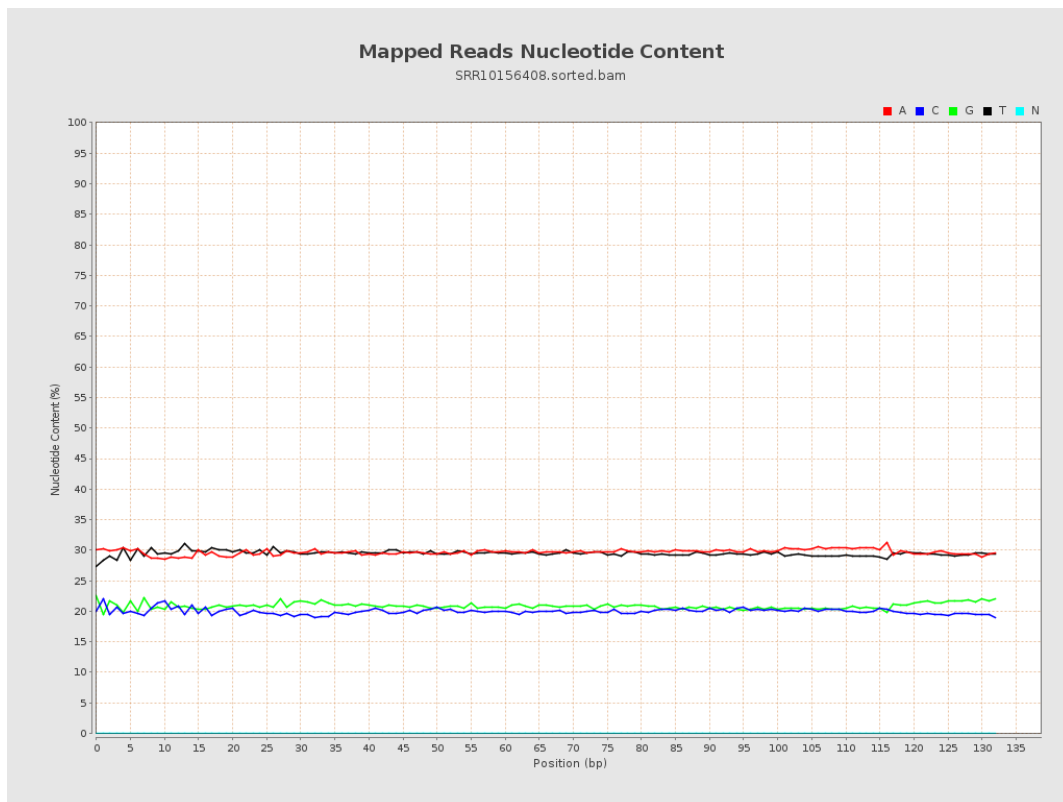
## 6. Results : Genome Fraction Coverage



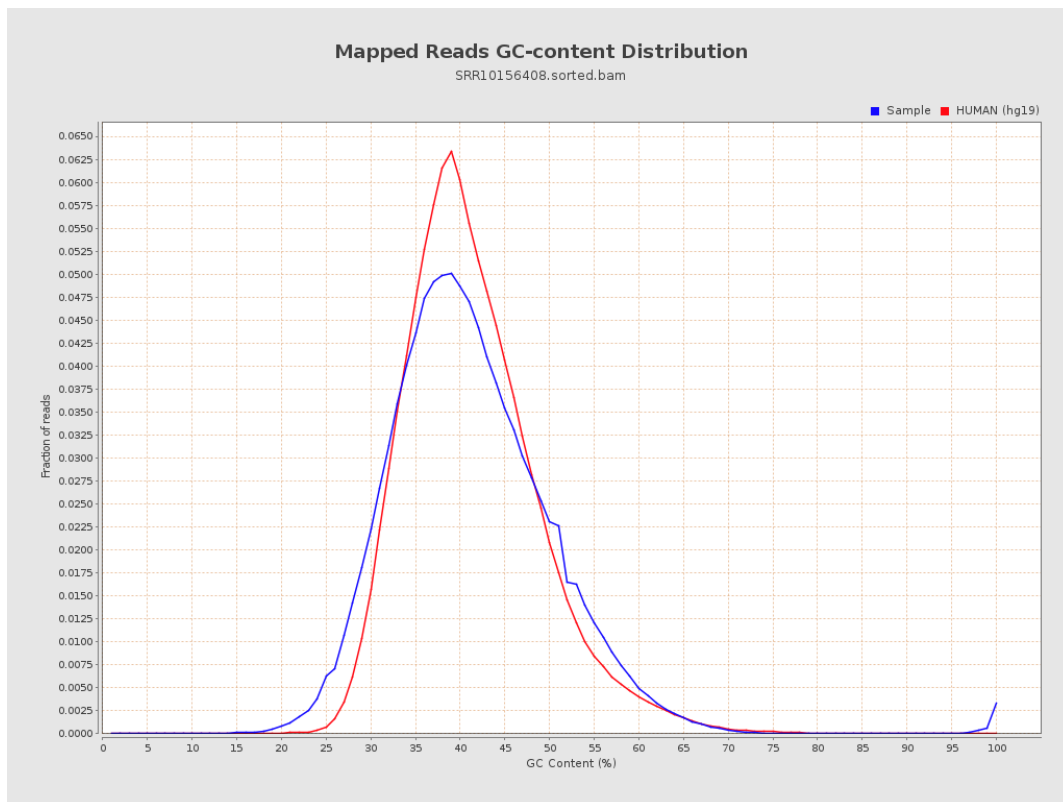
## 7. Results : Duplication Rate Histogram



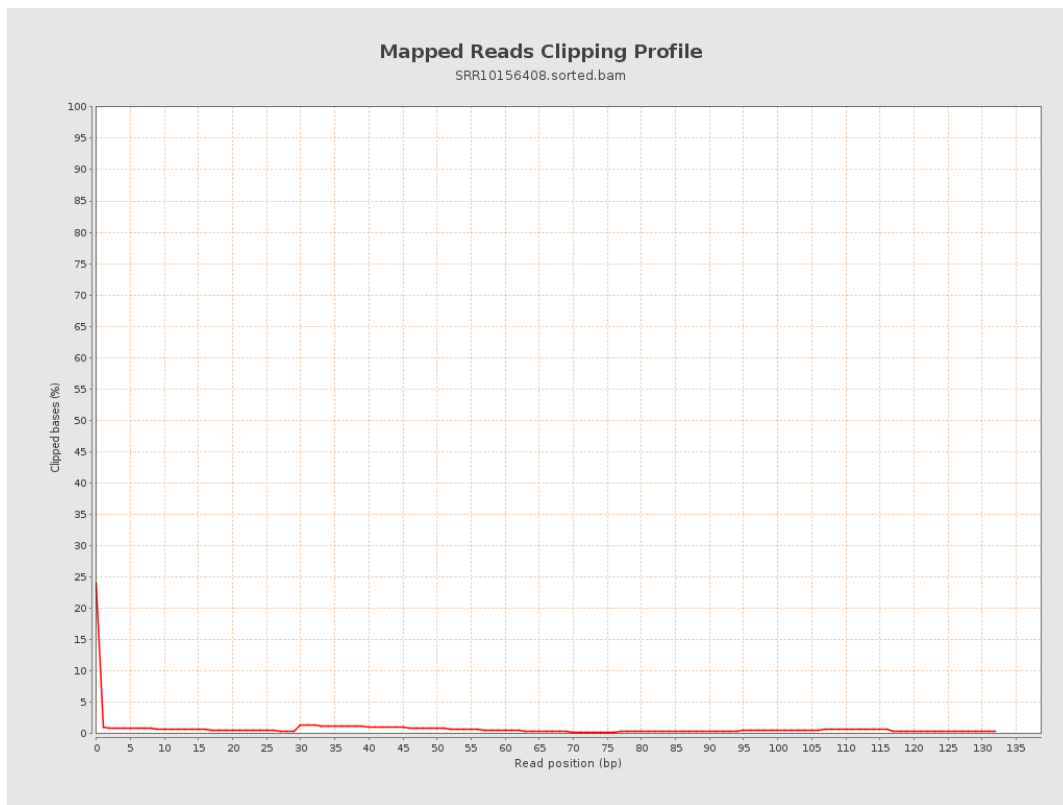
## 8. Results : Mapped Reads Nucleotide Content



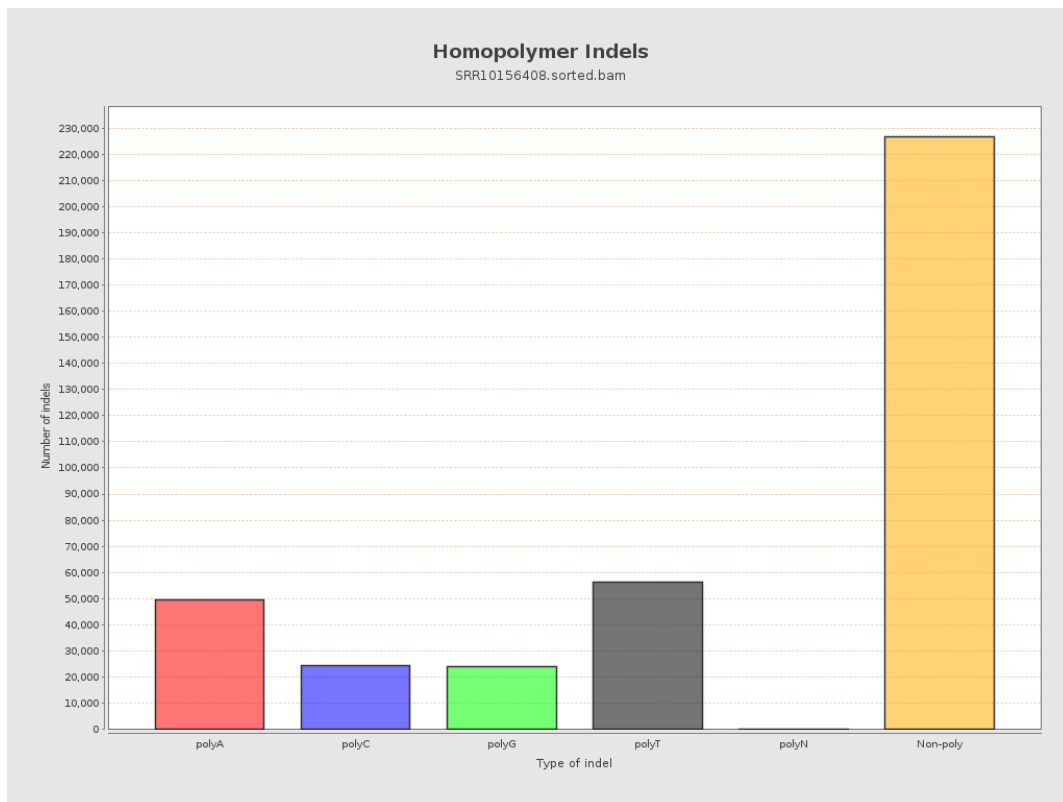
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



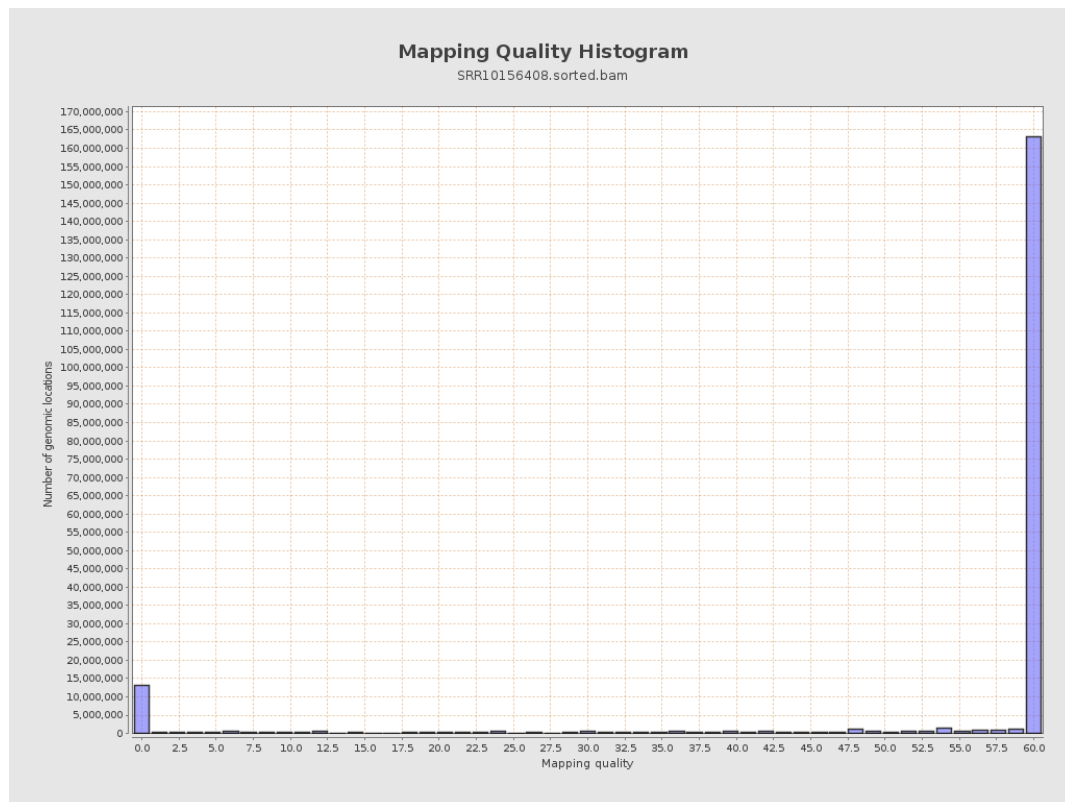
## 11. Results : Homopolymer Indels



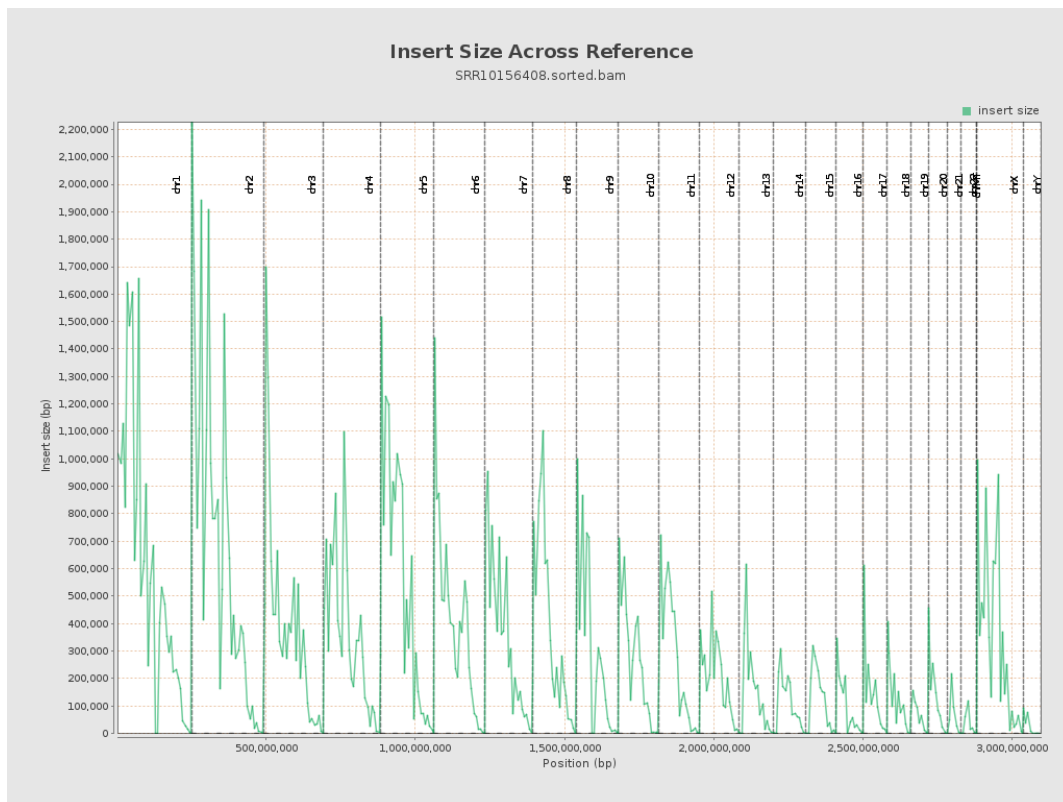
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

