

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.3*

*2024/09/13 20:28:07*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695958.sorted.bam -c -nw 400 -hm 3
```

## 1.2. Alignment

|                                       |                                                                                                                                                                                                                                                          |
|---------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Command line:                         | /seu_share/home/tujing/220232460/software/bwa-0.7.18/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1695958 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695958_1.fastq.gz SRR1695958_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                                                      |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                                                       |
| Program:                              | bwa (0.7.18-r1243-dirty)                                                                                                                                                                                                                                 |
| Analysis date:                        | Fri Sep 13 20:28:07 CST 2024                                                                                                                                                                                                                             |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                                                        |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                                                       |
| Number of windows:                    | 400                                                                                                                                                                                                                                                      |
| BAM file:                             | SRR1695958.sorted.bam                                                                                                                                                                                                                                    |

## 2. Summary

### 2.1. Globals

|                              |                      |
|------------------------------|----------------------|
| Reference size               | 3,095,693,983        |
| Number of reads              | 344,045,402          |
| Mapped reads                 | 339,094,426 / 98.56% |
| Unmapped reads               | 4,950,976 / 1.44%    |
| Mapped paired reads          | 339,094,426 / 98.56% |
| Mapped reads, first in pair  | 170,636,026 / 49.6%  |
| Mapped reads, second in pair | 168,458,400 / 48.96% |
| Mapped reads, both in pair   | 335,739,968 / 97.59% |
| Mapped reads, singletons     | 3,354,458 / 0.98%    |
| Secondary alignments         | 0                    |
| Supplementary alignments     | 5,264,680 / 1.53%    |
| Read min/max/mean length     | 30 / 100 / 100.63    |
| Duplicated reads (estimated) | 57,246,738 / 16.64%  |
| Duplication rate             | 13.5%                |
| Clipped reads                | 29,522,564 / 8.58%   |

### 2.2. ACGT Content

|                          |                        |
|--------------------------|------------------------|
| Number/percentage of A's | 9,360,253,074 / 27.94% |
| Number/percentage of C's | 7,298,957,995 / 21.78% |
| Number/percentage of T's | 9,310,709,377 / 27.79% |
| Number/percentage of G's | 7,524,953,735 / 22.46% |
| Number/percentage of N's | 10,056,843 / 0.03%     |
|                          |                        |

|               |        |
|---------------|--------|
| GC Percentage | 44.24% |
|---------------|--------|

## 2.3. Coverage

|                    |         |
|--------------------|---------|
| Mean               | 10.8267 |
| Standard Deviation | 40.8611 |

## 2.4. Mapping Quality

|                      |      |
|----------------------|------|
| Mean Mapping Quality | 53.9 |
|----------------------|------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 80,496.26       |
| Standard Deviation | 2,712,912.11    |
| P25/Median/P75     | 315 / 323 / 331 |

## 2.6. Mismatches and indels

|                                          |             |
|------------------------------------------|-------------|
| General error rate                       | 0.53%       |
| Mismatches                               | 167,609,457 |
| Insertions                               | 5,514,138   |
| Mapped reads with at least one insertion | 1.57%       |
| Deletions                                | 4,335,798   |
| Mapped reads with at least one deletion  | 1.23%       |
| Homopolymer indels                       | 40.39%      |

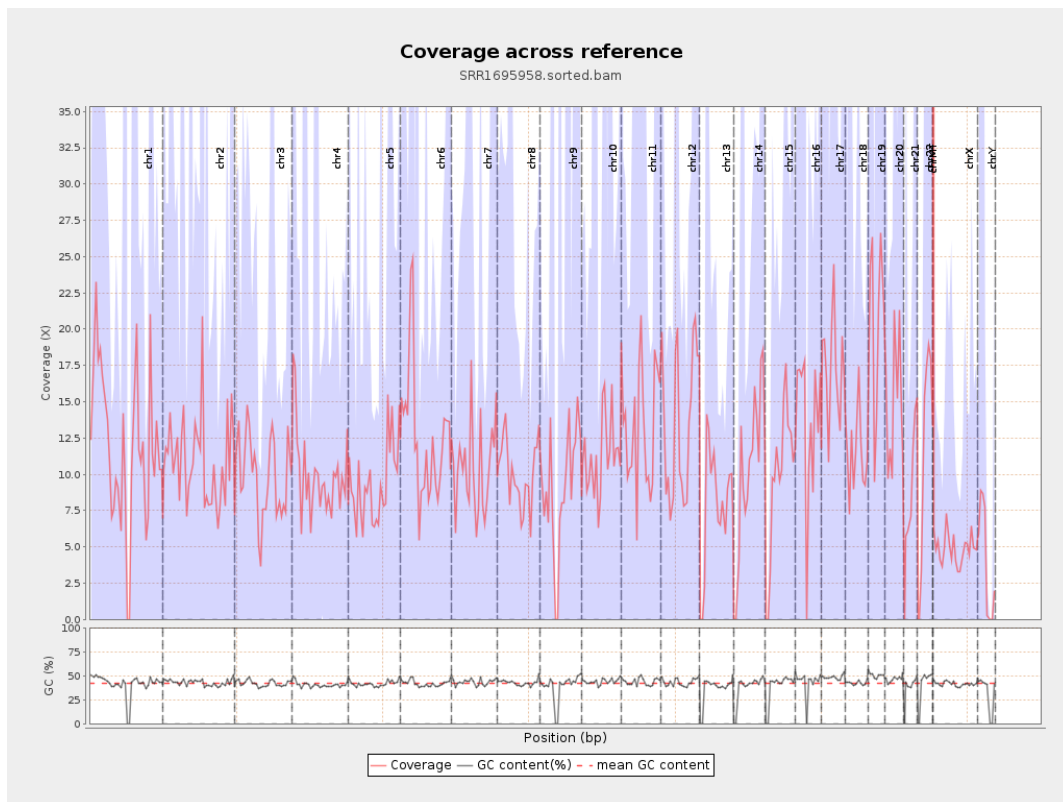
## 2.7. Chromosome stats

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

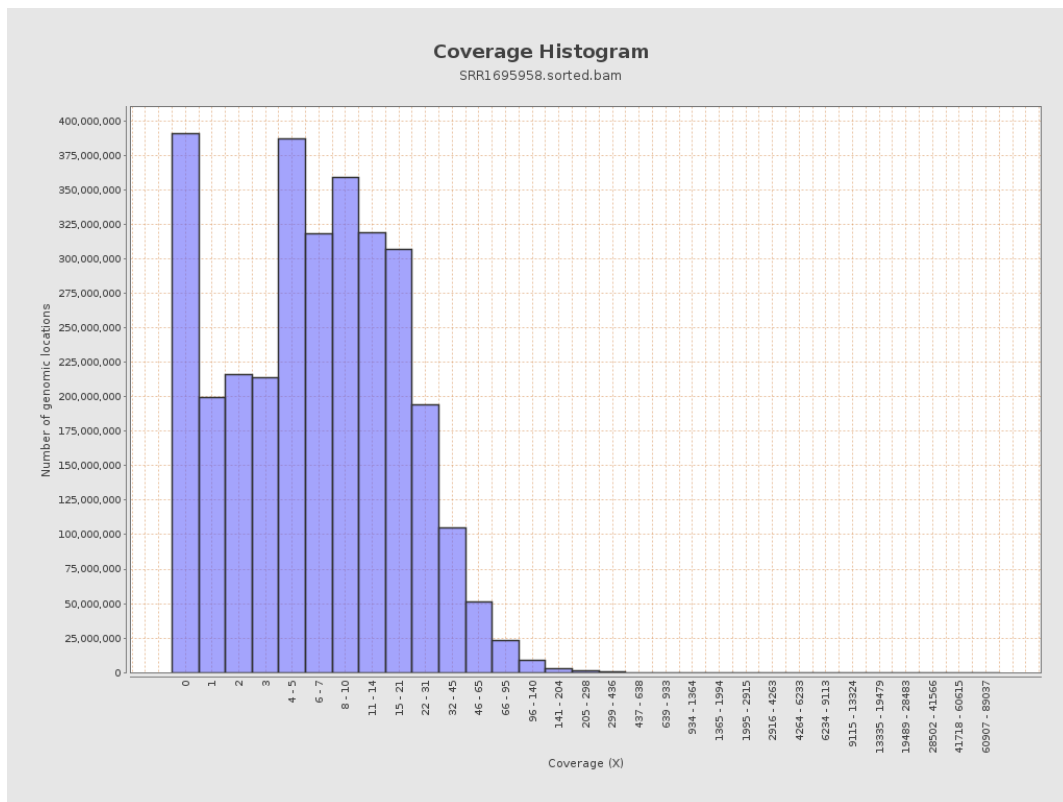
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 2955287385   | 11.8567         | 33.7076          |
| chr2  | 243199373 | 2651344773   | 10.9019         | 83.5333          |
| chr3  | 198022430 | 1951895960   | 9.8569          | 18.1603          |
| chr4  | 191154276 | 1890366173   | 9.8892          | 23.8753          |
| chr5  | 180915260 | 1700064767   | 9.397           | 19.1432          |
| chr6  | 171115067 | 2132763267   | 12.4639         | 30.7271          |
| chr7  | 159138663 | 1666640421   | 10.4729         | 23.214           |
| chr8  | 146364022 | 1467229710   | 10.0245         | 29.2057          |
| chr9  | 141213431 | 1261871313   | 8.9359          | 61.5941          |
| chr10 | 135534747 | 1523001597   | 11.237          | 59.5684          |
| chr11 | 135006516 | 1783133578   | 13.2078         | 27.3194          |
| chr12 | 133851895 | 1820056836   | 13.5975         | 20.0514          |
| chr13 | 115169878 | 917369641    | 7.9654          | 18.8313          |
| chr14 | 107349540 | 1113327861   | 10.3711         | 42.8565          |
| chr15 | 102531392 | 996194045    | 9.716           | 22.2145          |
| chr16 | 90354753  | 1213013356   | 13.425          | 60.1396          |
| chr17 | 81195210  | 1419720821   | 17.4853         | 34.4608          |
| chr18 | 78077248  | 883044017    | 11.3099         | 42.3335          |
| chr19 | 59128983  | 1197080928   | 20.2452         | 36.8824          |
| chr20 | 63025520  | 931393003    | 14.778          | 22.5524          |
| chr21 | 48129895  | 425712005    | 8.8451          | 25.2098          |
| chr22 | 51304566  | 592670786    | 11.552          | 24.1636          |
| chrMT | 16571     | 22352843     | 1,348.9133      | 470.337          |
| chrX  | 155270560 | 757496903    | 4.8786          | 12.4511          |

|      |          |           |        |         |
|------|----------|-----------|--------|---------|
| chrY | 59373566 | 243270267 | 4.0973 | 70.9024 |
|------|----------|-----------|--------|---------|

### 3. Results : Coverage across reference

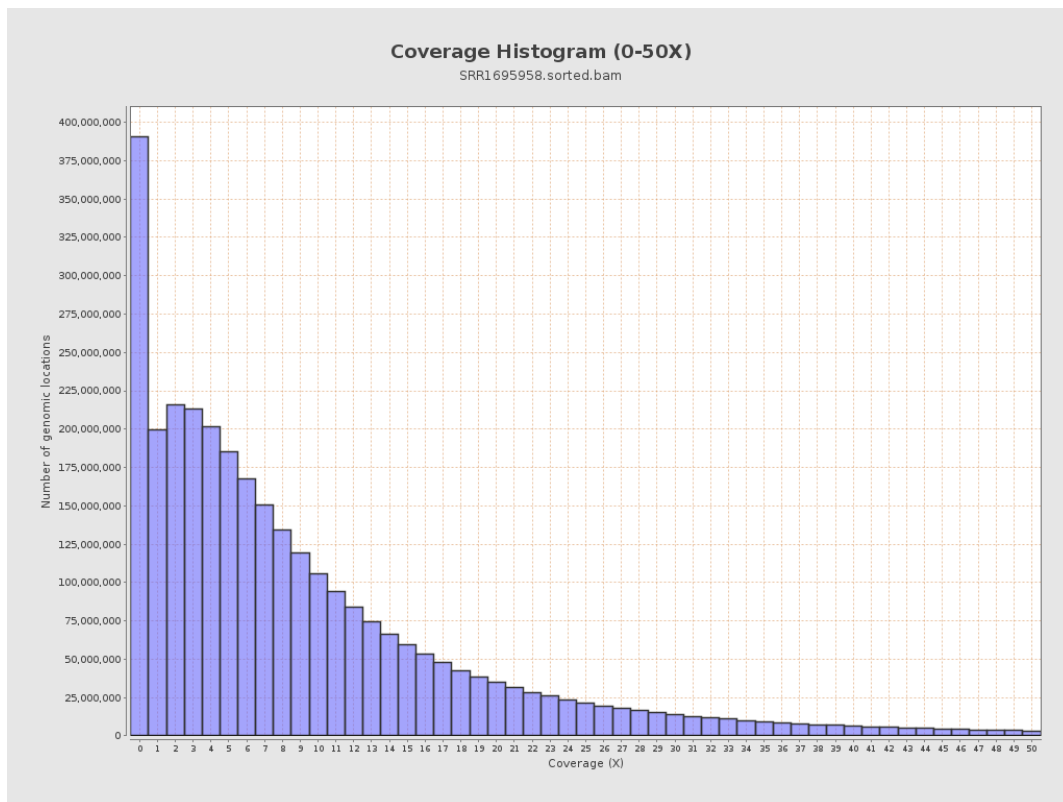


## 4. Results : Coverage Histogram

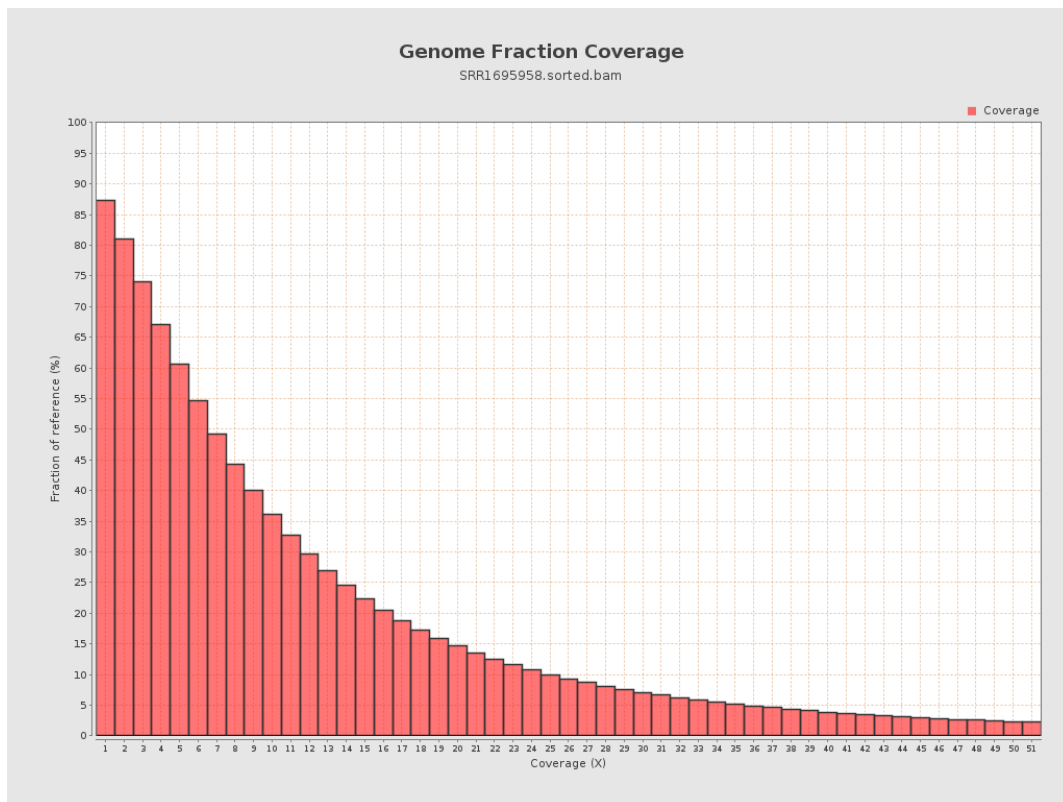




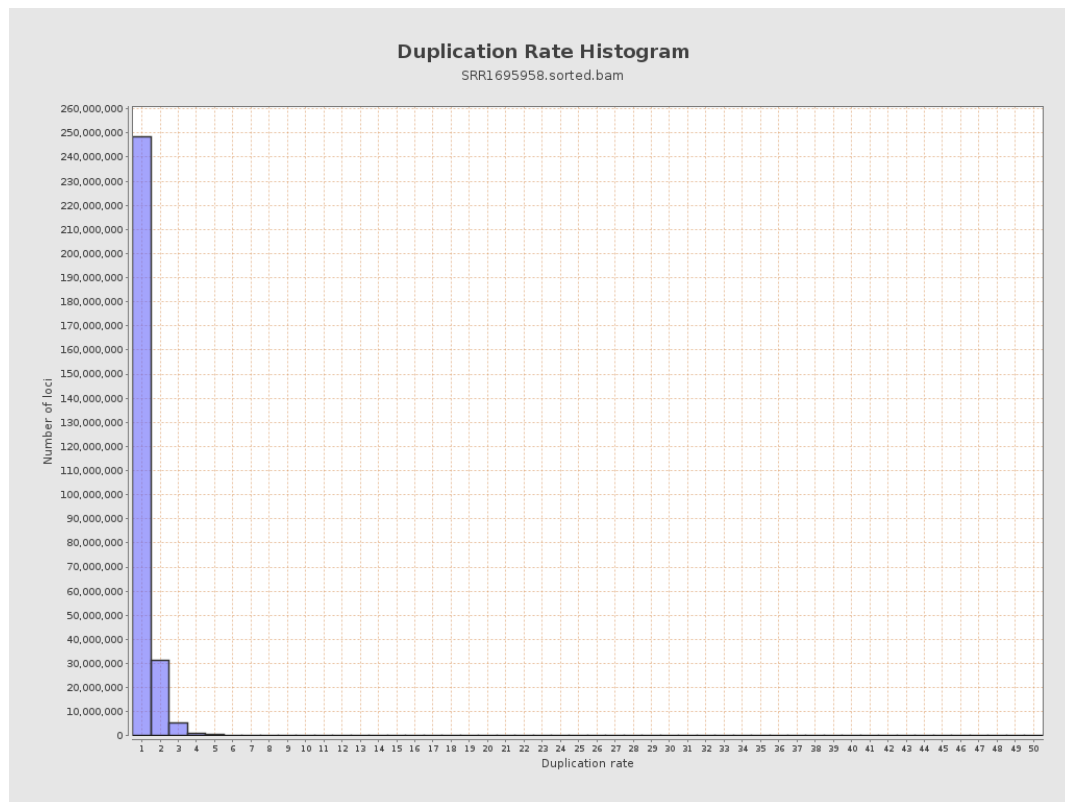
## 5. Results : Coverage Histogram (0-50X)



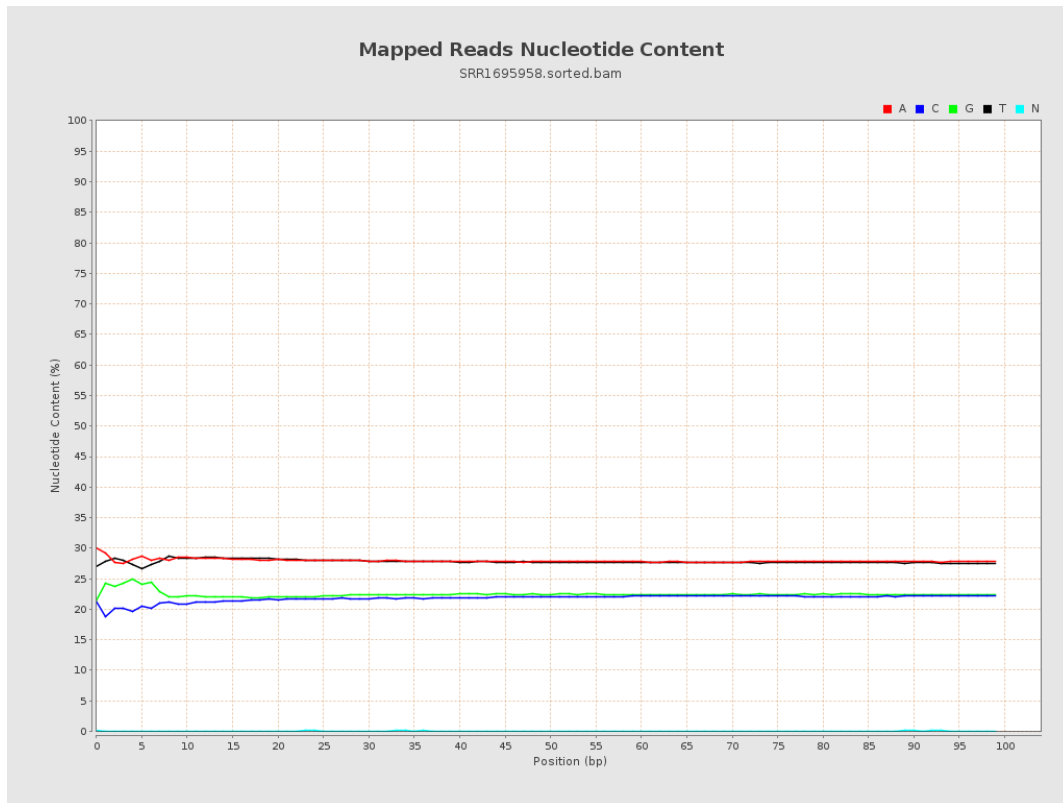
## 6. Results : Genome Fraction Coverage



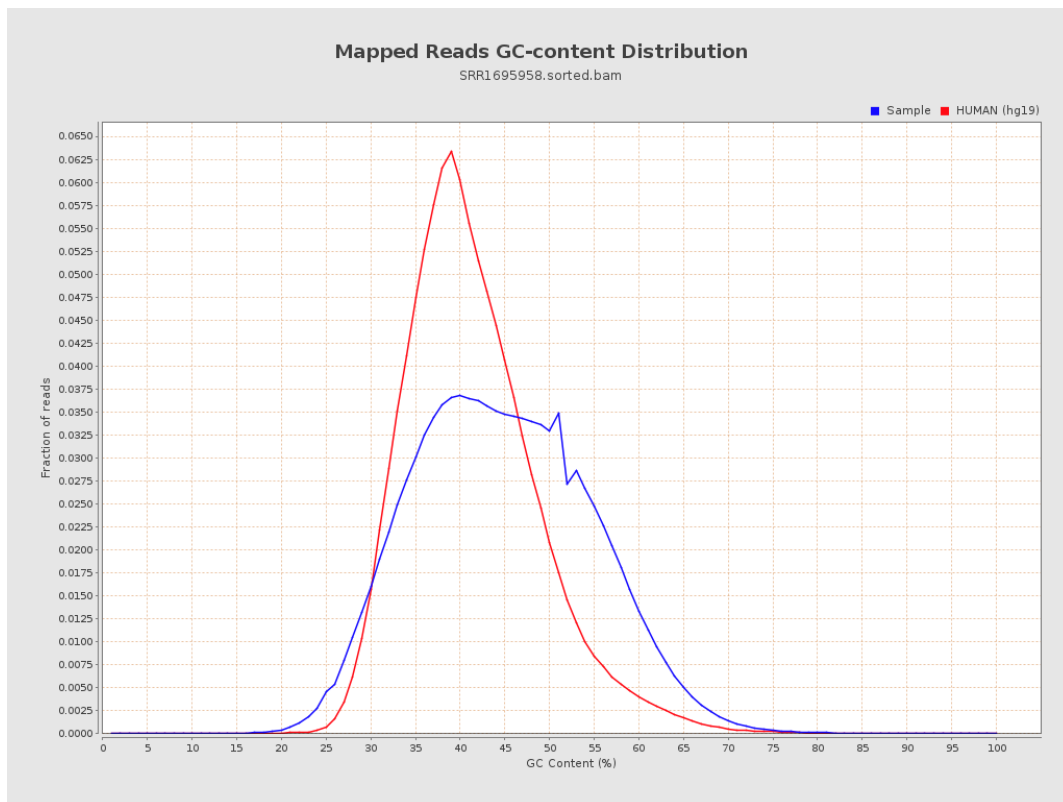
## 7. Results : Duplication Rate Histogram



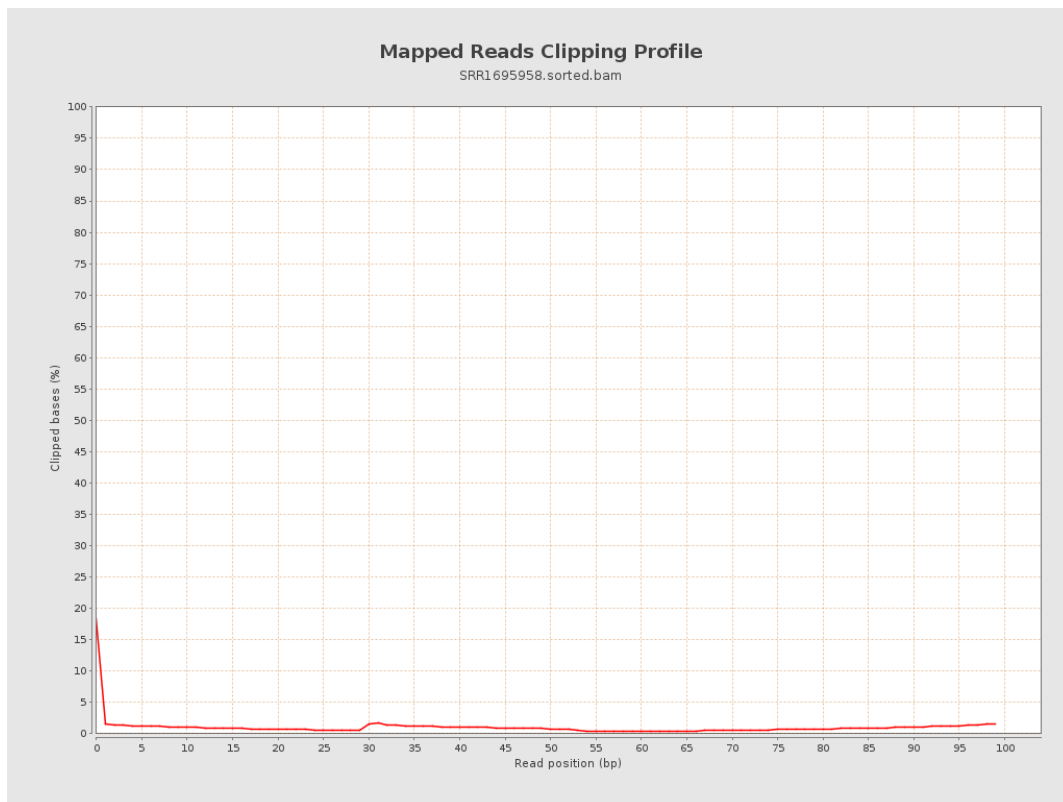
## 8. Results : Mapped Reads Nucleotide Content



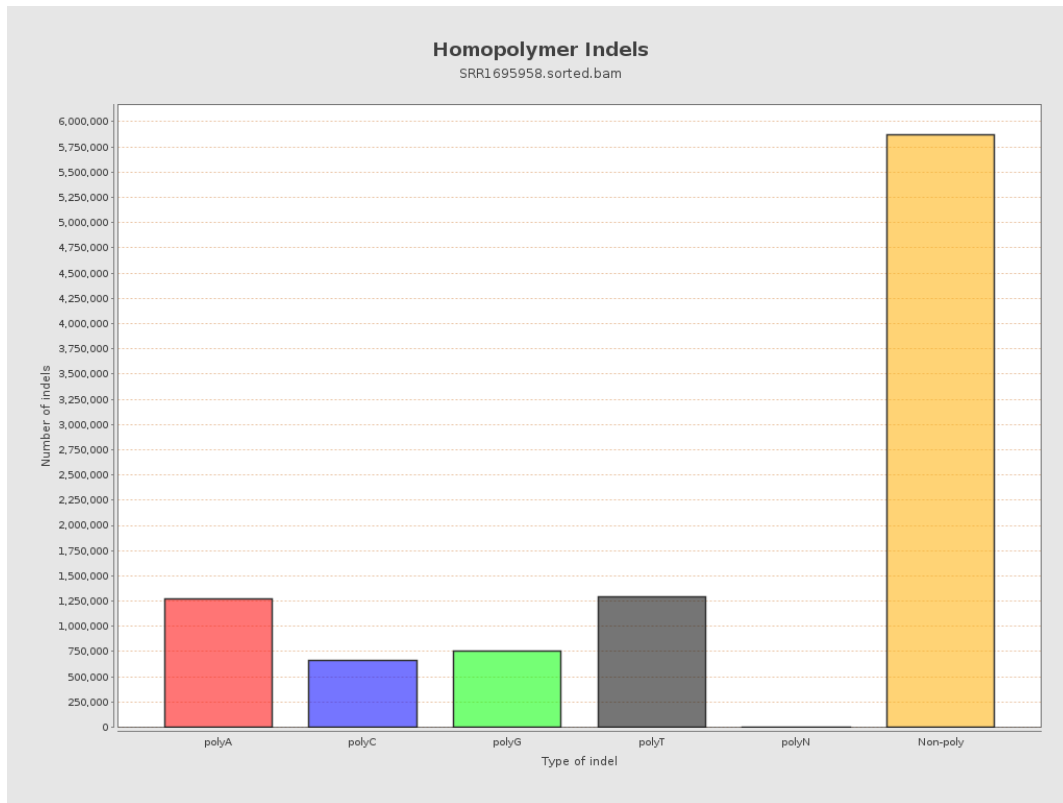
## 9. Results : Mapped Reads GC-content Distribution



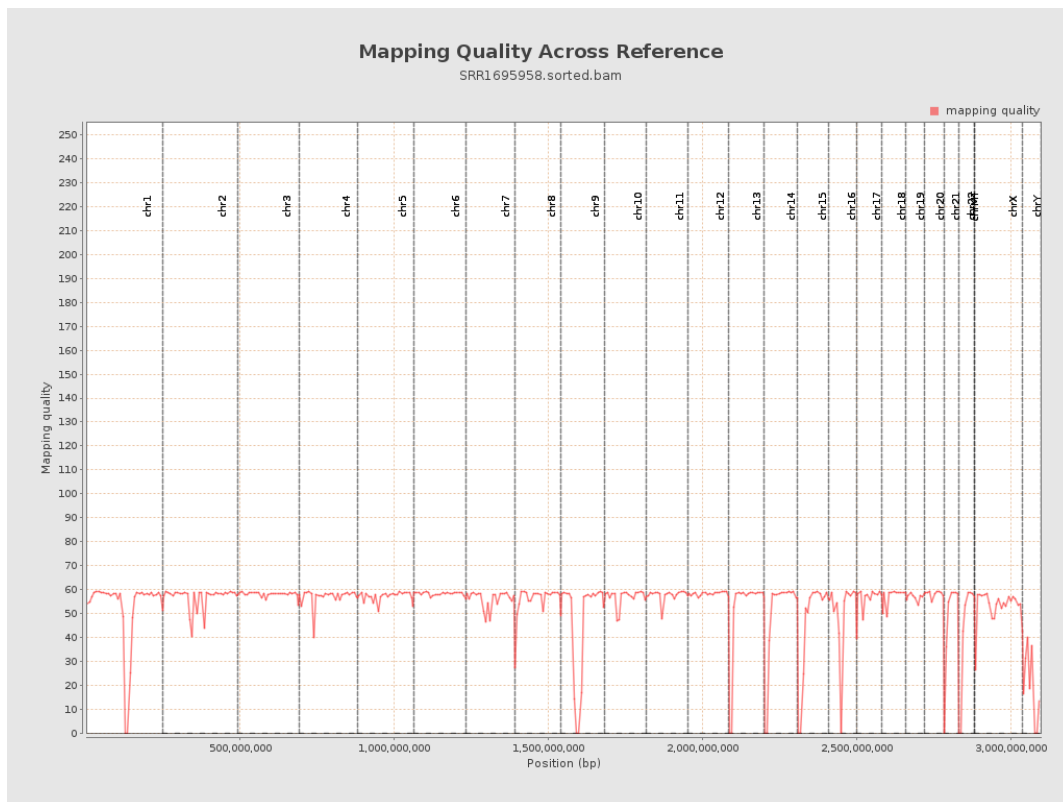
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

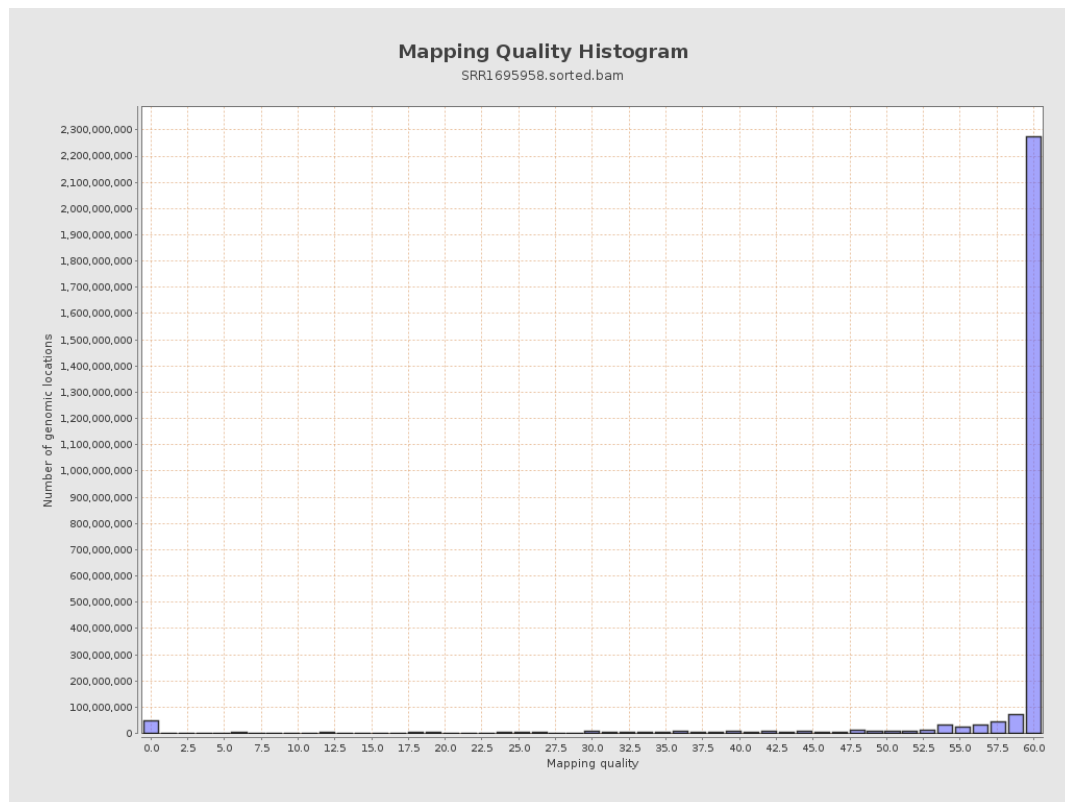


## 12. Results : Mapping Quality Across Reference

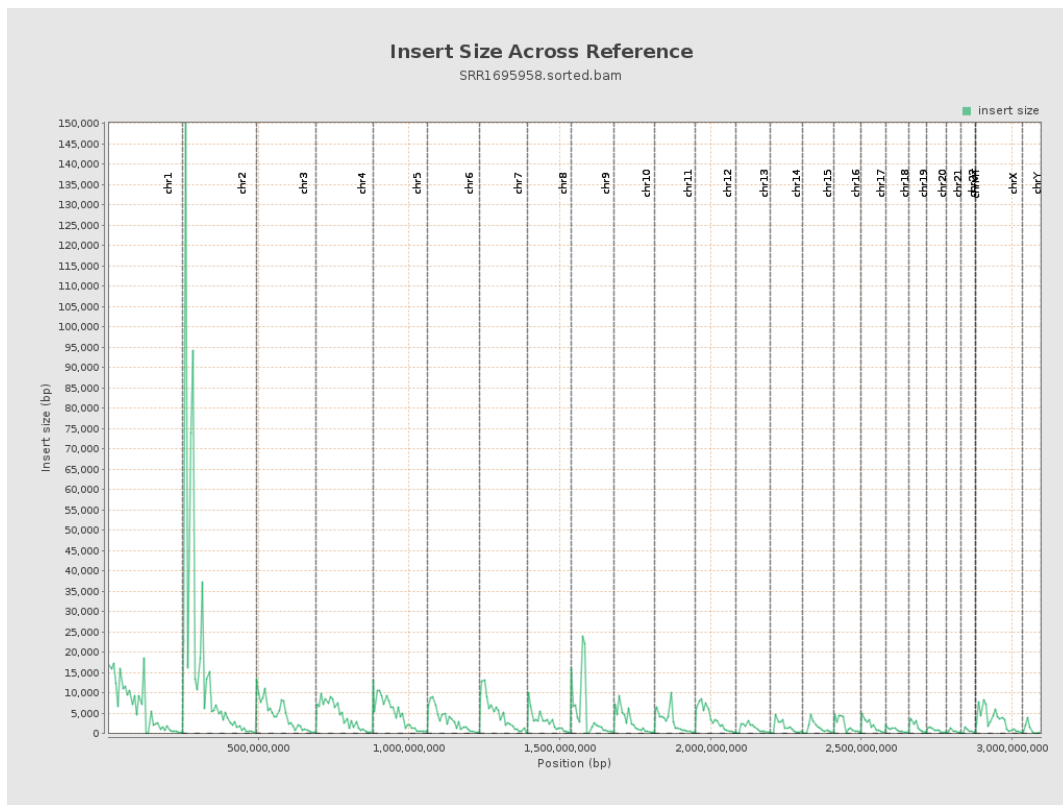




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

