

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.3*

*2024/09/13 10:14:23*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695947.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_SRR1695947 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695947_1.fastq.gz SRR1695947_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 10:14:23 CST 2024                                                                                                                                                                                                                             |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                                                        |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                                                       |
| Number of windows:                    | 400                                                                                                                                                                                                                                                      |
| BAM file:                             | SRR1695947.sorted.bam                                                                                                                                                                                                                                    |

## 2. Summary

### 2.1. Globals

|                              |                      |
|------------------------------|----------------------|
| Reference size               | 3,095,693,983        |
| Number of reads              | 153,762,738          |
| Mapped reads                 | 152,693,648 / 99.3%  |
| Unmapped reads               | 1,069,090 / 0.7%     |
| Mapped paired reads          | 152,693,648 / 99.3%  |
| Mapped reads, first in pair  | 76,532,123 / 49.77%  |
| Mapped reads, second in pair | 76,161,525 / 49.53%  |
| Mapped reads, both in pair   | 152,012,526 / 98.86% |
| Mapped reads, singletons     | 681,122 / 0.44%      |
| Secondary alignments         | 0                    |
| Supplementary alignments     | 2,059,134 / 1.34%    |
| Read min/max/mean length     | 30 / 100 / 100.55    |
| Duplicated reads (estimated) | 16,655,240 / 10.83%  |
| Duplication rate             | 9.31%                |
| Clipped reads                | 10,259,015 / 6.67%   |

### 2.2. ACGT Content

|                          |                        |
|--------------------------|------------------------|
| Number/percentage of A's | 4,275,020,963 / 28.23% |
| Number/percentage of C's | 3,258,324,302 / 21.52% |
| Number/percentage of T's | 4,252,035,118 / 28.08% |
| Number/percentage of G's | 3,358,087,639 / 22.17% |
| Number/percentage of N's | 240,080 / 0%           |
|                          |                        |

|               |        |
|---------------|--------|
| GC Percentage | 43.69% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 4.8932 |
| Standard Deviation | 11.699 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 54.06 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 75,853.65       |
| Standard Deviation | 2,705,553.15    |
| P25/Median/P75     | 331 / 338 / 345 |

## 2.6. Mismatches and indels

|                                          |            |
|------------------------------------------|------------|
| General error rate                       | 0.39%      |
| Mismatches                               | 55,876,015 |
| Insertions                               | 2,008,379  |
| Mapped reads with at least one insertion | 1.28%      |
| Deletions                                | 1,747,013  |
| Mapped reads with at least one deletion  | 1.11%      |
| Homopolymer indels                       | 44.69%     |

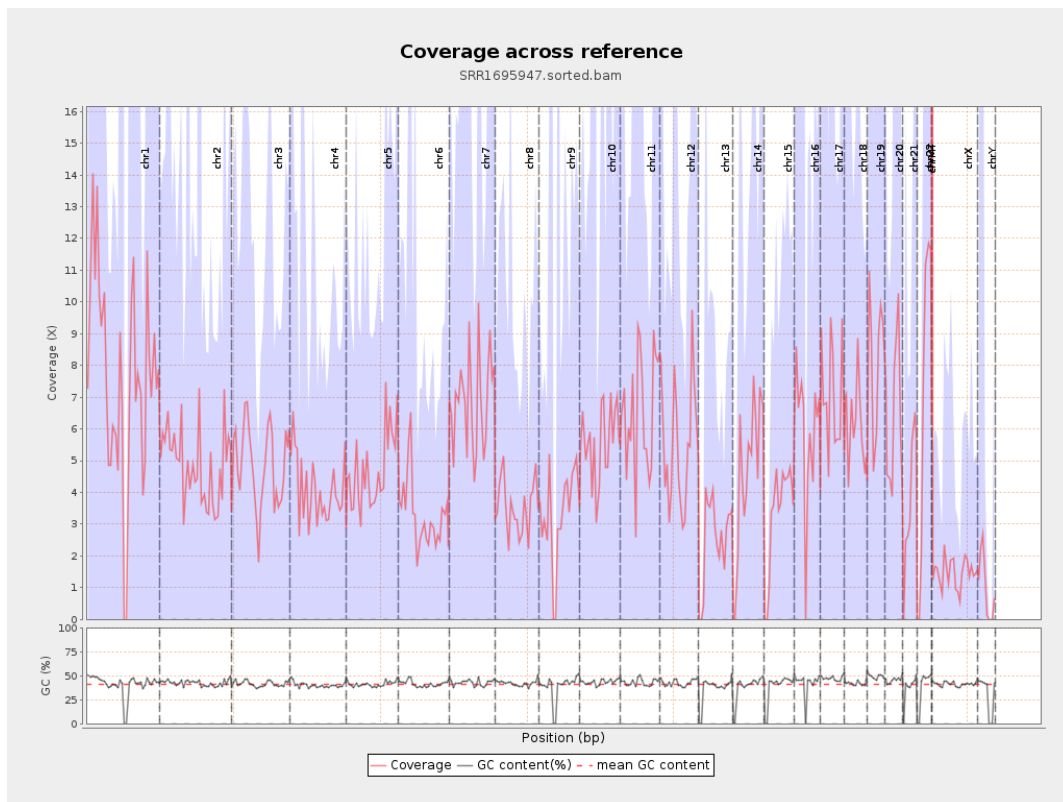
## 2.7. Chromosome stats

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

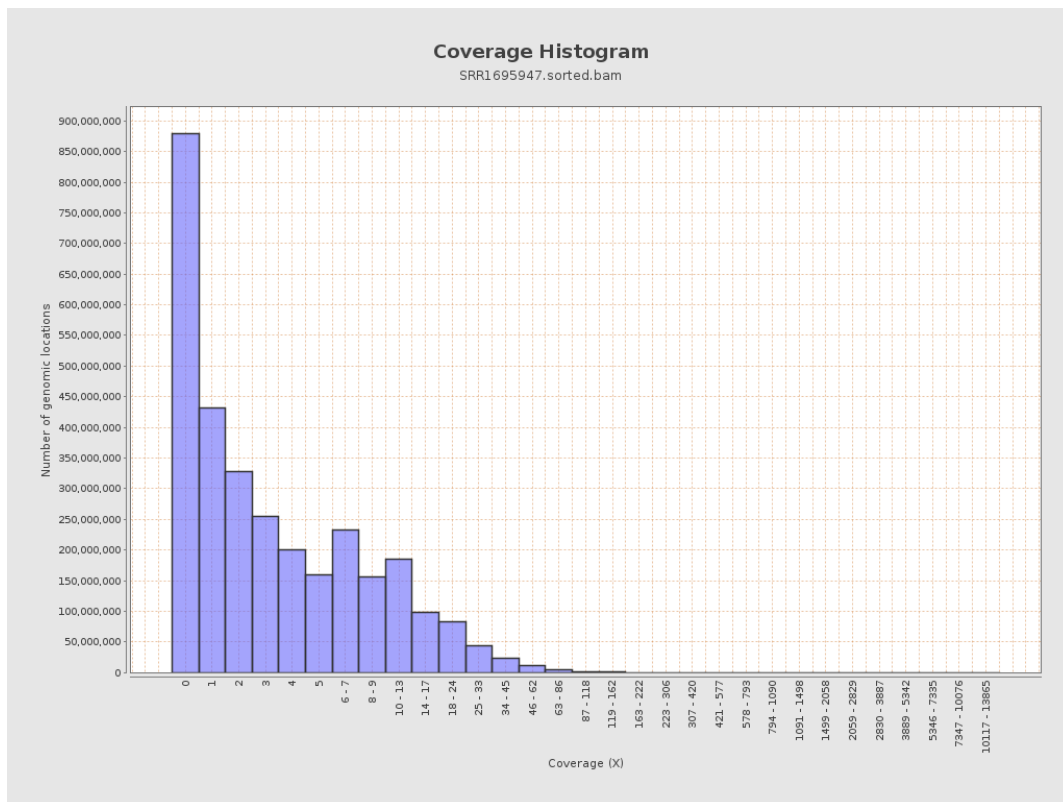
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 1913381905   | 7.6765          | 16.6667          |
| chr2  | 243199373 | 1176238606   | 4.8365          | 16.5603          |
| chr3  | 198022430 | 962004141    | 4.8581          | 7.3484           |
| chr4  | 191154276 | 782351224    | 4.0928          | 7.4482           |
| chr5  | 180915260 | 851141391    | 4.7046          | 7.413            |
| chr6  | 171115067 | 560738972    | 3.277           | 7.268            |
| chr7  | 159138663 | 1094166873   | 6.8756          | 10.2705          |
| chr8  | 146364022 | 520996542    | 3.5596          | 7.0004           |
| chr9  | 141213431 | 468969515    | 3.321           | 12.8154          |
| chr10 | 135534747 | 758729829    | 5.598           | 15.5486          |
| chr11 | 135006516 | 881722582    | 6.531           | 10.8465          |
| chr12 | 133851895 | 736132419    | 5.4996          | 9.2798           |
| chr13 | 115169878 | 292922129    | 2.5434          | 6.1983           |
| chr14 | 107349540 | 494250439    | 4.6041          | 9.6286           |
| chr15 | 102531392 | 337607999    | 3.2927          | 6.4971           |
| chr16 | 90354753  | 531041406    | 5.8773          | 15.3268          |
| chr17 | 81195210  | 572581105    | 7.0519          | 13.6673          |
| chr18 | 78077248  | 484526218    | 6.2057          | 17.0886          |
| chr19 | 59128983  | 486612065    | 8.2297          | 15.898           |
| chr20 | 63025520  | 409305026    | 6.4943          | 10.6723          |
| chr21 | 48129895  | 184888038    | 3.8414          | 9.022            |
| chr22 | 51304566  | 356882091    | 6.9561          | 15.2829          |
| chrMT | 16571     | 2396423      | 144.6155        | 48.0925          |
| chrX  | 155270560 | 226195803    | 1.4568          | 4.6748           |

|      |          |          |        |         |
|------|----------|----------|--------|---------|
| chrY | 59373566 | 62149267 | 1.0467 | 13.5819 |
|------|----------|----------|--------|---------|

### 3. Results : Coverage across reference

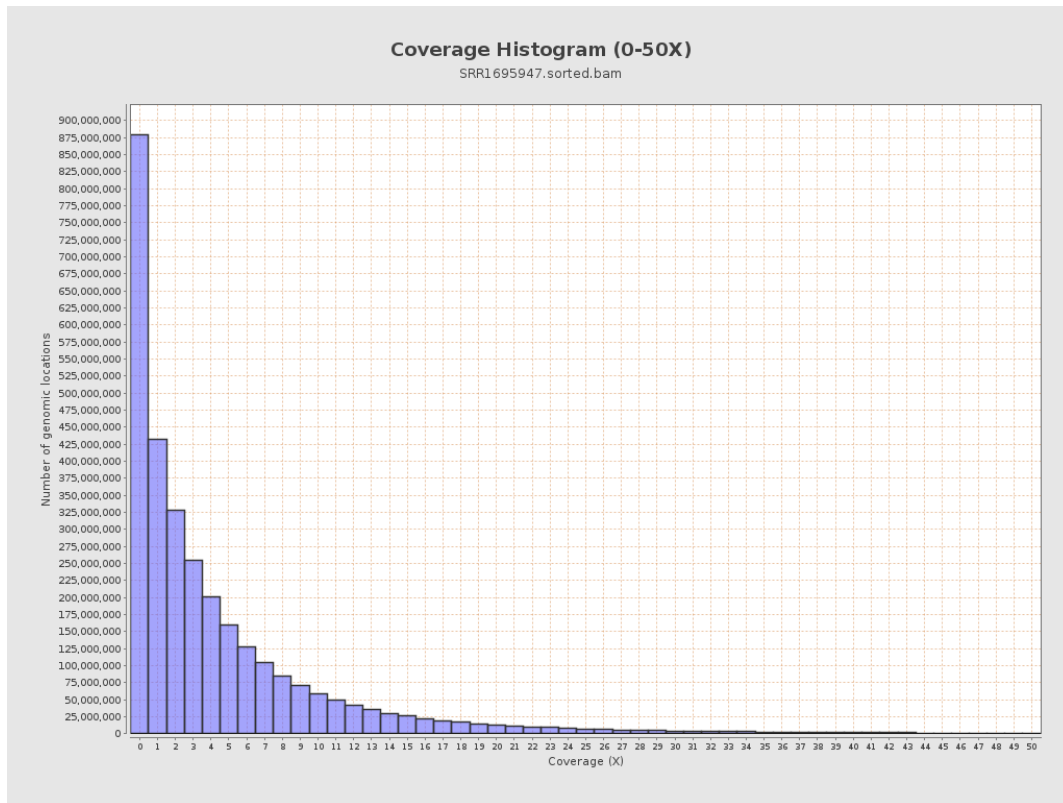


## 4. Results : Coverage Histogram

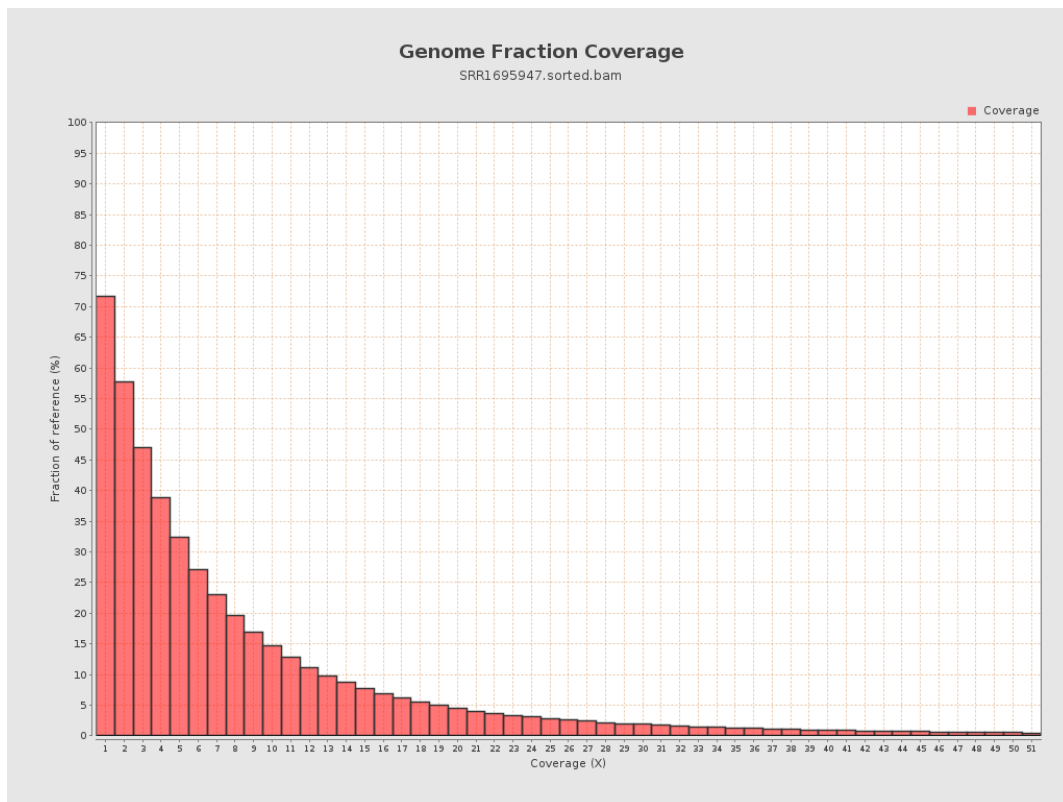




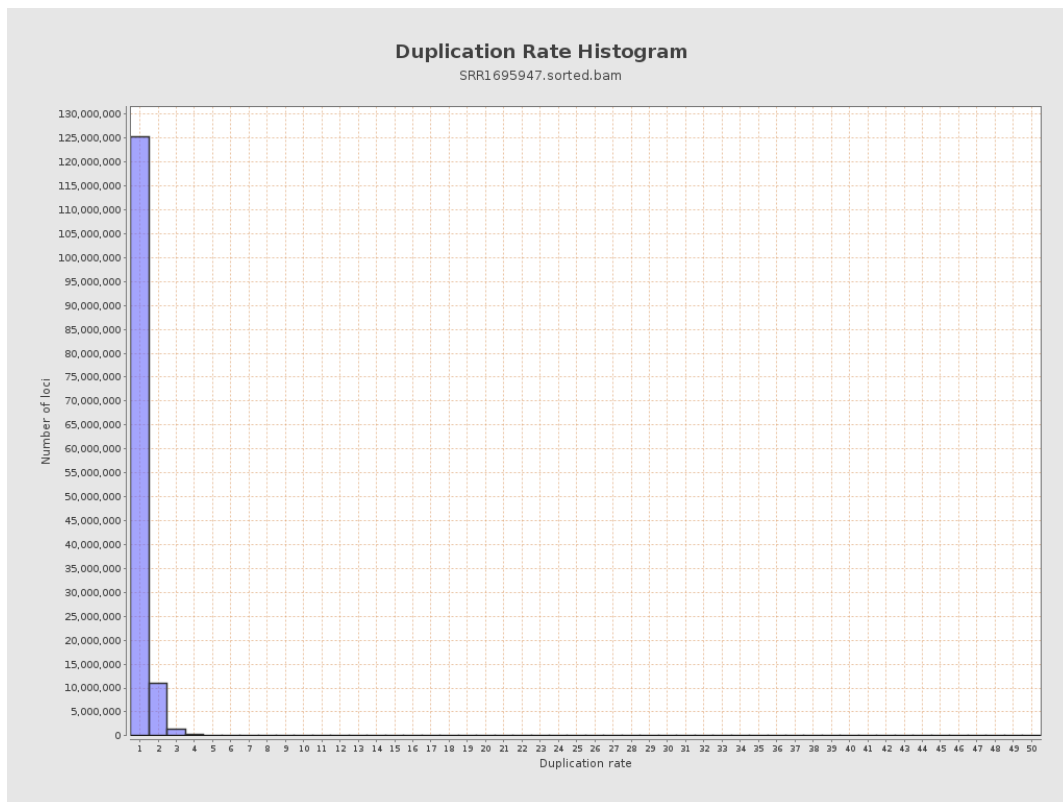
## 5. Results : Coverage Histogram (0-50X)



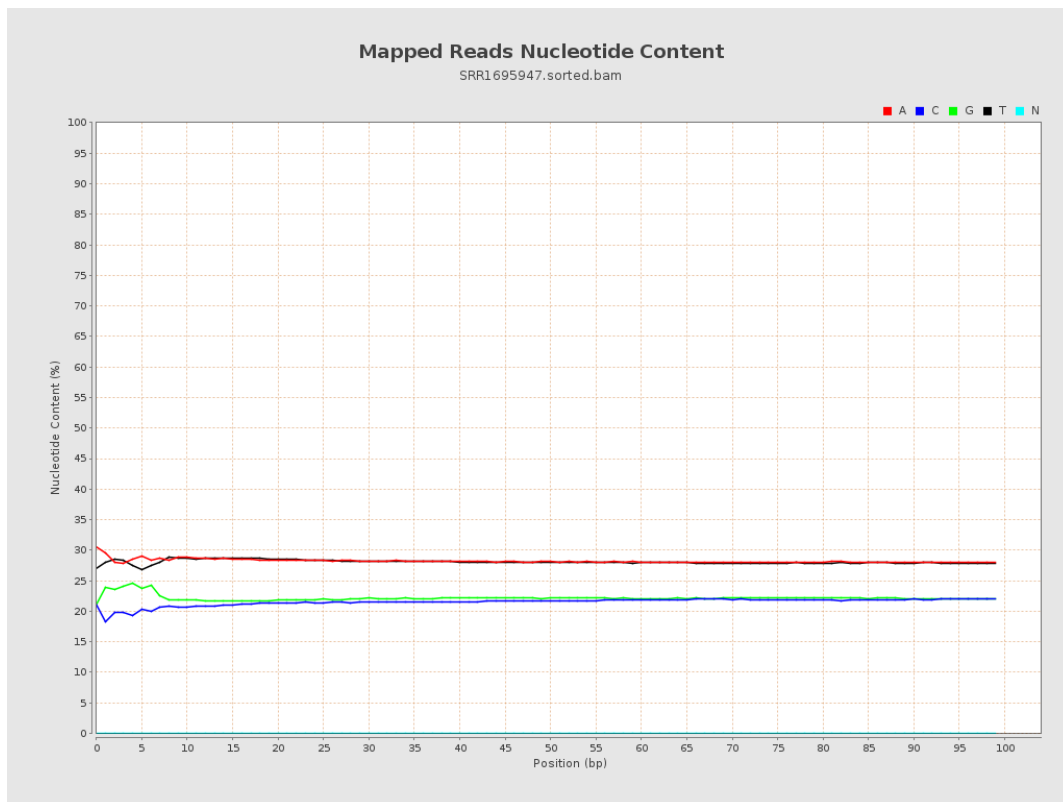
## 6. Results : Genome Fraction Coverage



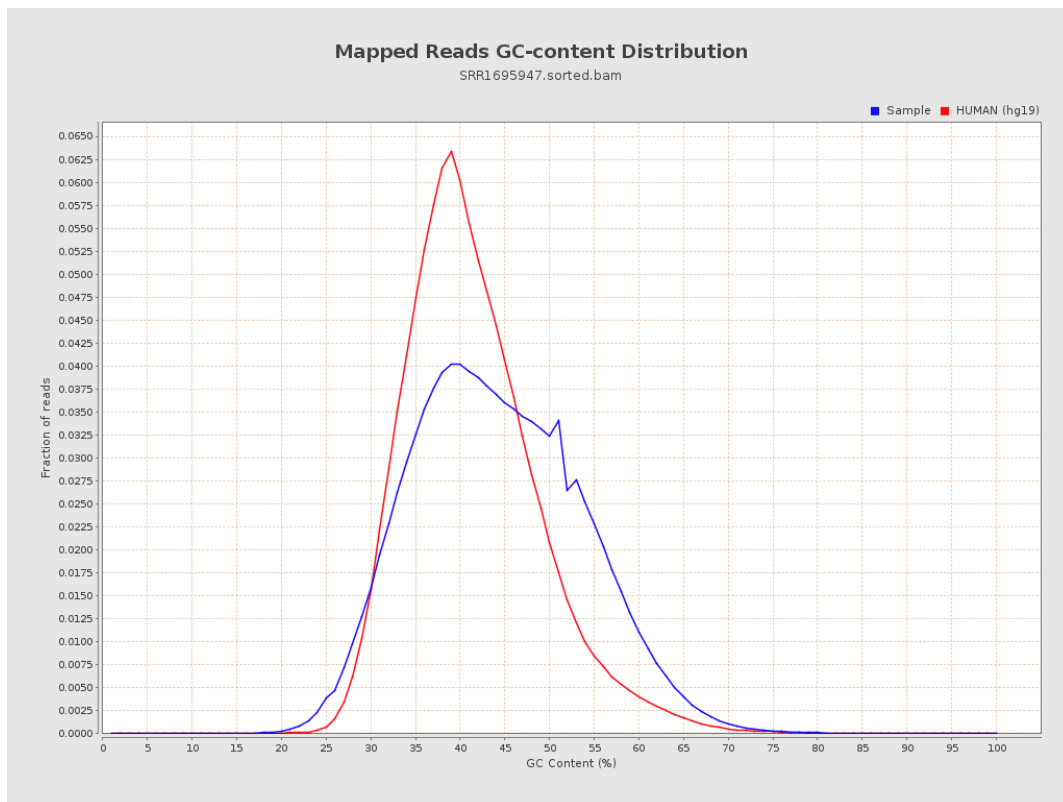
## 7. Results : Duplication Rate Histogram



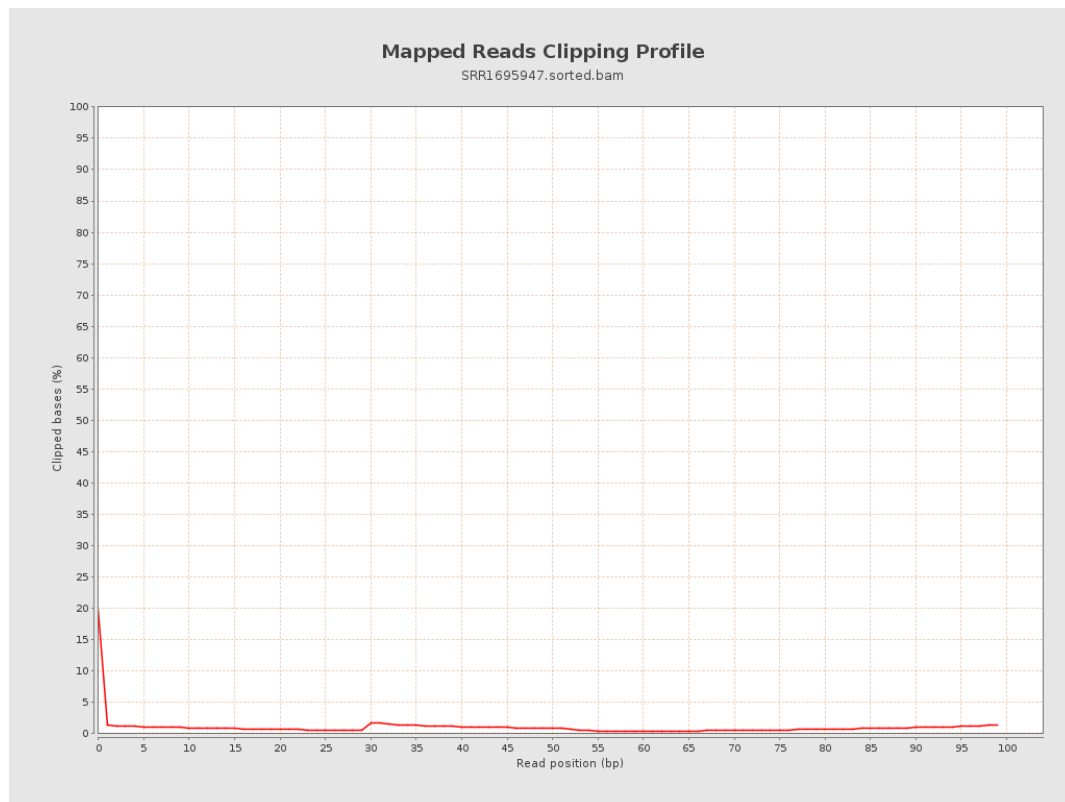
## 8. Results : Mapped Reads Nucleotide Content



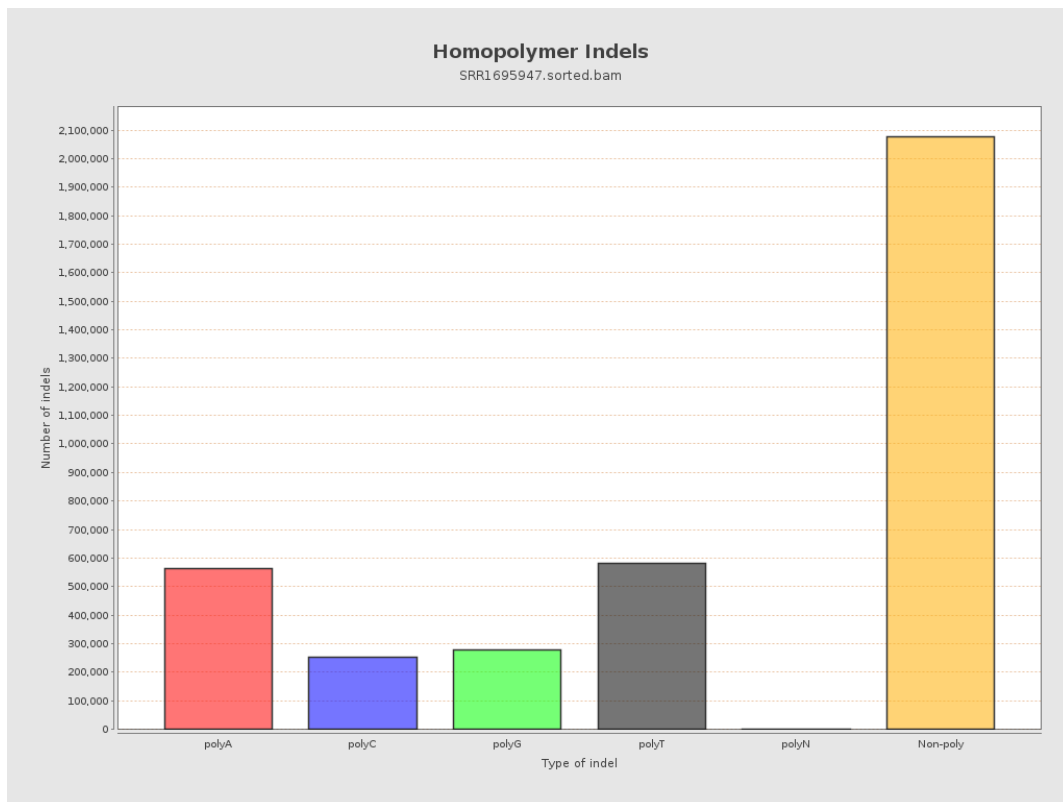
## 9. Results : Mapped Reads GC-content Distribution



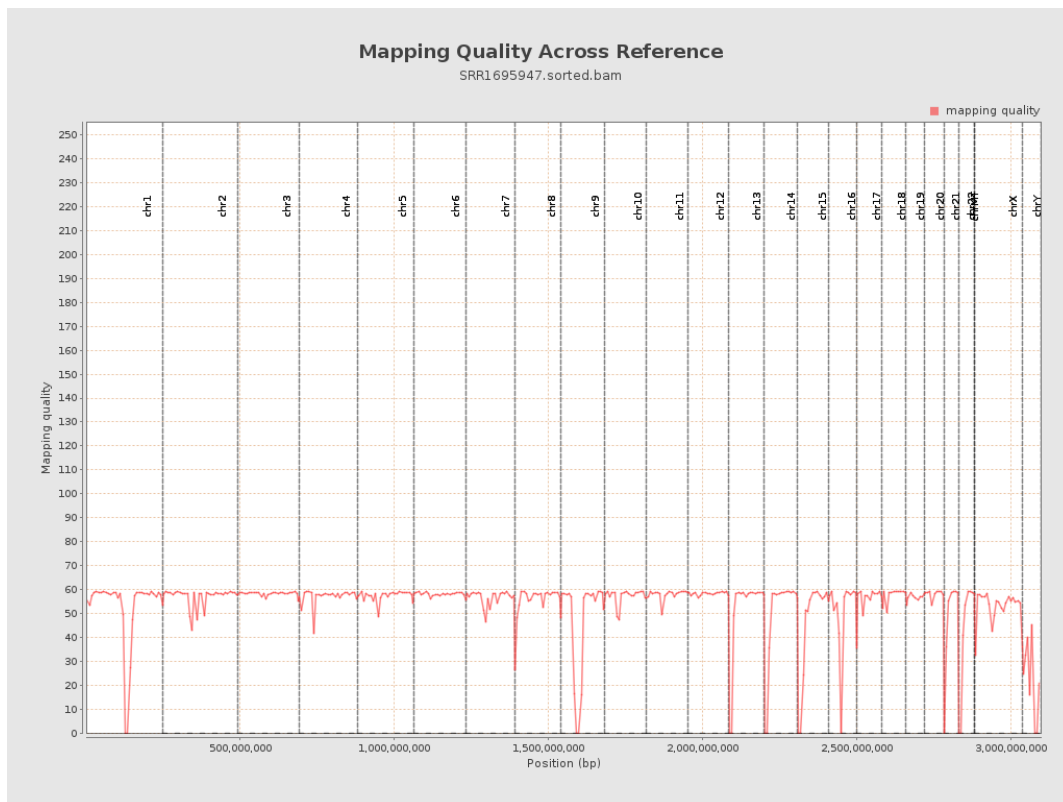
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

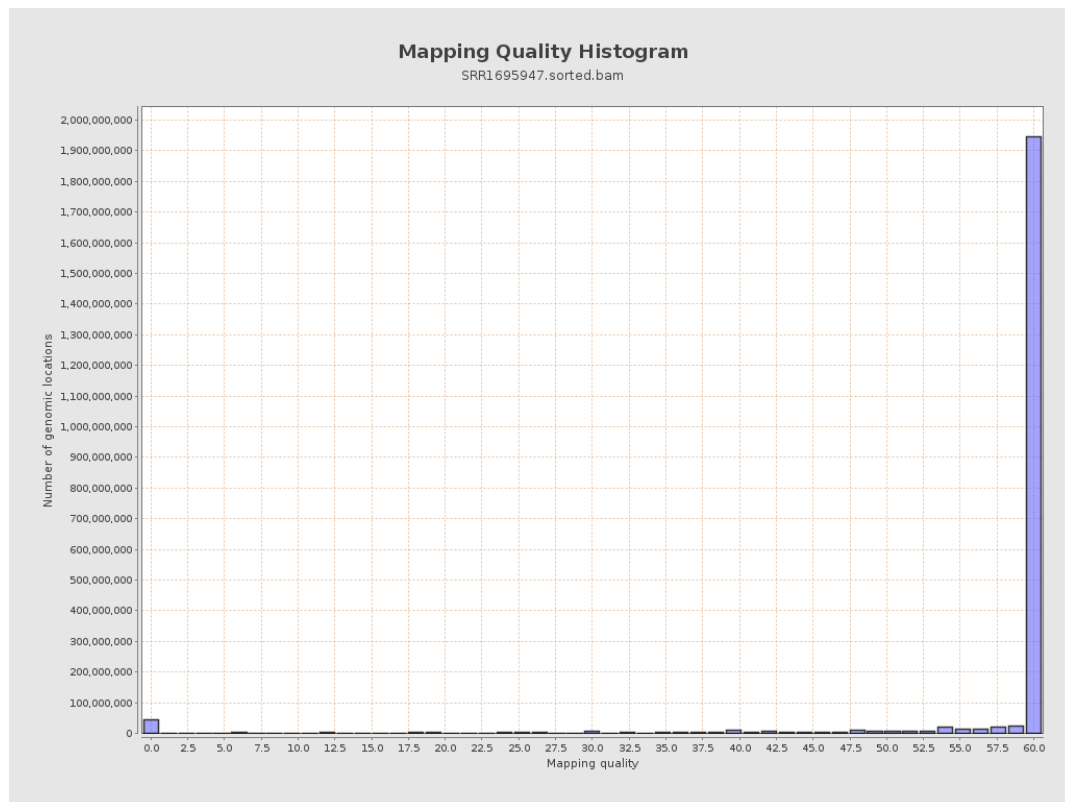


## 12. Results : Mapping Quality Across Reference

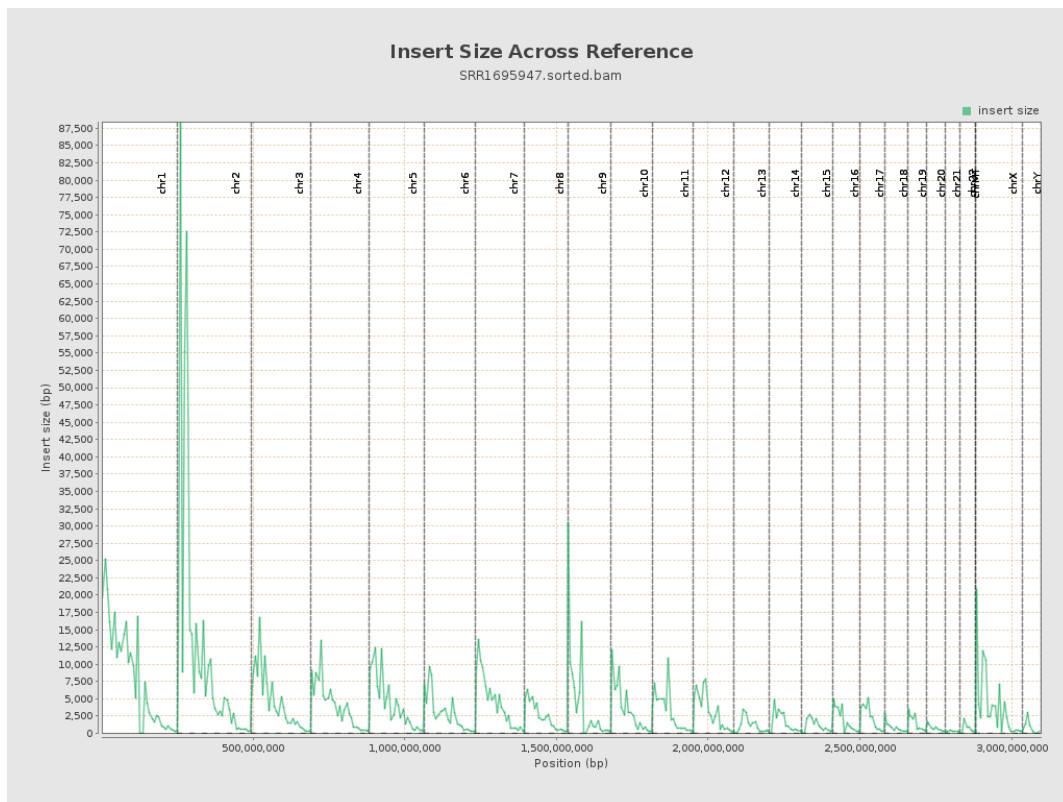




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

