

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/28 16:48:01*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR21671995.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_SRR21671995 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21671995_1.fastq.gz SRR21671995_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                      |
| Analysis date:                        | Sat Sep 28 16:48:01 CST 2024                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                     |
| BAM file:                             | SRR21671995.sorted.bam                                                                                                                                                                                                  |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 27,239,810          |
| Mapped reads                 | 26,992,262 / 99.09% |
| Unmapped reads               | 247,548 / 0.91%     |
| Mapped paired reads          | 26,992,262 / 99.09% |
| Mapped reads, first in pair  | 13,505,507 / 49.58% |
| Mapped reads, second in pair | 13,486,755 / 49.51% |
| Mapped reads, both in pair   | 26,933,926 / 98.88% |
| Mapped reads, singletons     | 58,336 / 0.21%      |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 633,909 / 2.33%     |
| Read min/max/mean length     | 15 / 150 / 146.4    |
| Duplicated reads (estimated) | 19,380,635 / 71.15% |
| Duplication rate             | 46.51%              |
| Clipped reads                | 16,117,883 / 59.17% |

### 2.2. ACGT Content

|                          |                        |
|--------------------------|------------------------|
| Number/percentage of A's | 945,059,024 / 26.52%   |
| Number/percentage of C's | 764,324,750 / 21.45%   |
| Number/percentage of T's | 1,013,847,207 / 28.45% |
| Number/percentage of G's | 839,899,517 / 23.57%   |
| Number/percentage of N's | 5,328 / 0%             |
|                          |                        |

|               |        |
|---------------|--------|
| GC Percentage | 45.02% |
|---------------|--------|

## 2.3. Coverage

|                    |         |
|--------------------|---------|
| Mean               | 1.1514  |
| Standard Deviation | 53.5964 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 53.12 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 152,642.56      |
| Standard Deviation | 3,939,430.67    |
| P25/Median/P75     | 147 / 199 / 267 |

## 2.6. Mismatches and indels

|                                          |            |
|------------------------------------------|------------|
| General error rate                       | 0.89%      |
| Mismatches                               | 30,743,348 |
| Insertions                               | 361,300    |
| Mapped reads with at least one insertion | 1.28%      |
| Deletions                                | 722,661    |
| Mapped reads with at least one deletion  | 2.62%      |
| Homopolymer indels                       | 46.53%     |

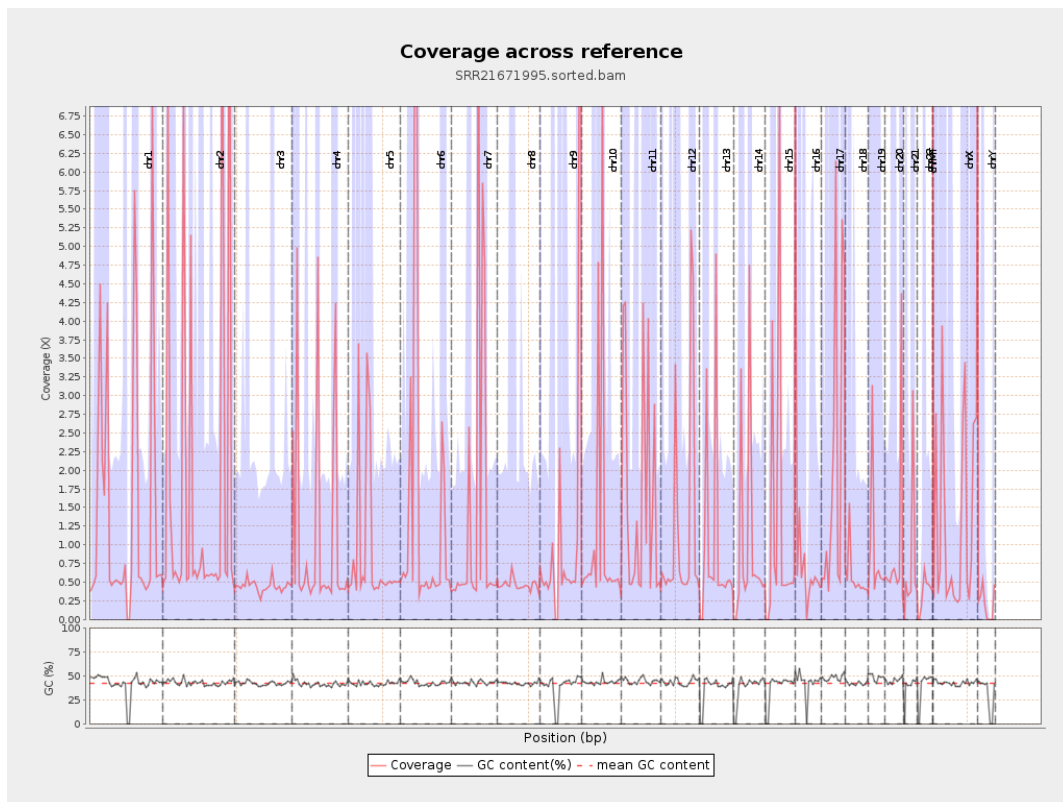
## 2.7. Chromosome stats

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

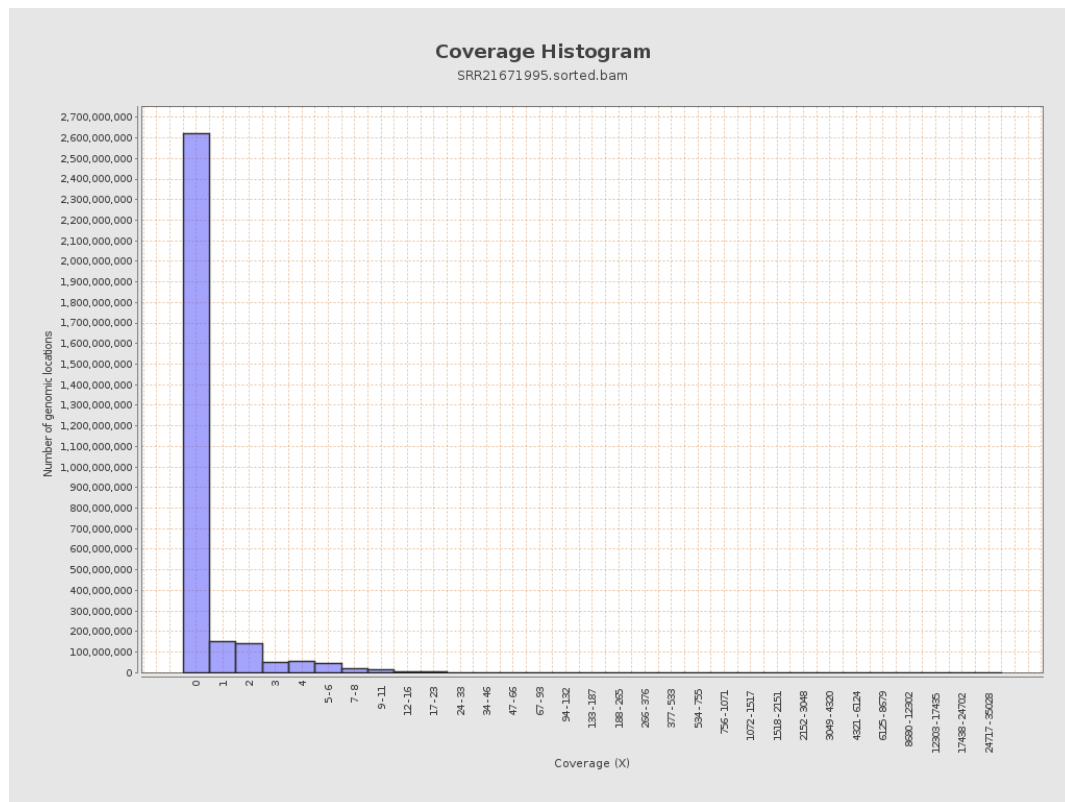
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 360520476    | 1.4464          | 65.1583          |
| chr2  | 243199373 | 426996531    | 1.7557          | 70.3836          |
| chr3  | 198022430 | 88463045     | 0.4467          | 8.9541           |
| chr4  | 191154276 | 214135013    | 1.1202          | 57.3076          |
| chr5  | 180915260 | 155991949    | 0.8622          | 41.9716          |
| chr6  | 171115067 | 250708171    | 1.4651          | 65.2147          |
| chr7  | 159138663 | 230786128    | 1.4502          | 79.6683          |
| chr8  | 146364022 | 67465714     | 0.4609          | 6.2089           |
| chr9  | 141213431 | 177998537    | 1.2605          | 64.9483          |
| chr10 | 135534747 | 162002193    | 1.1953          | 45.2178          |
| chr11 | 135006516 | 222269956    | 1.6464          | 66.0873          |
| chr12 | 133851895 | 168850101    | 1.2615          | 50.0206          |
| chr13 | 115169878 | 110895373    | 0.9629          | 44.1331          |
| chr14 | 107349540 | 102605906    | 0.9558          | 45.681           |
| chr15 | 102531392 | 119994264    | 1.1703          | 55.9794          |
| chr16 | 90354753  | 86589102     | 0.9583          | 28.9544          |
| chr17 | 81195210  | 166839970    | 2.0548          | 69.7732          |
| chr18 | 78077248  | 44907022     | 0.5752          | 23.4543          |
| chr19 | 59128983  | 55029036     | 0.9307          | 36.8845          |
| chr20 | 63025520  | 64334084     | 1.0208          | 42.3198          |
| chr21 | 48129895  | 38712864     | 0.8043          | 45.3999          |
| chr22 | 51304566  | 18119530     | 0.3532          | 5.9365           |
| chrMT | 16571     | 125690       | 7.5849          | 24.1586          |
| chrX  | 155270560 | 217101581    | 1.3982          | 59.2381          |

|      |          |          |        |        |
|------|----------|----------|--------|--------|
| chrY | 59373566 | 12994345 | 0.2189 | 7.1751 |
|------|----------|----------|--------|--------|

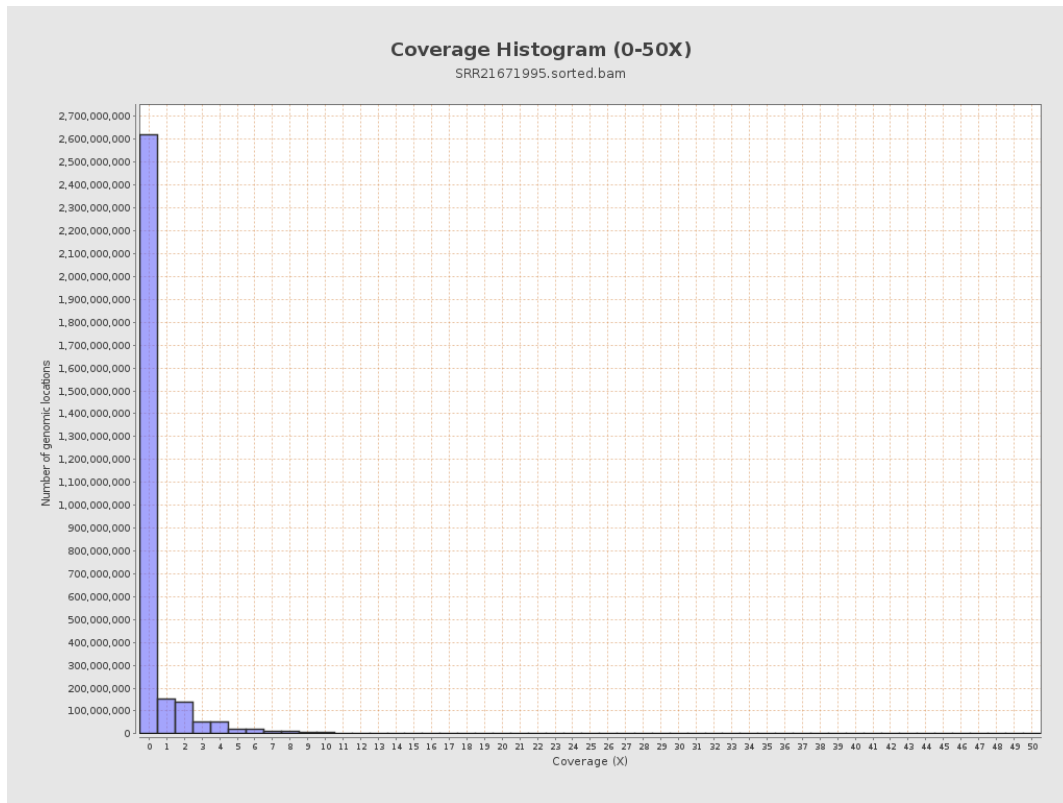
### 3. Results : Coverage across reference



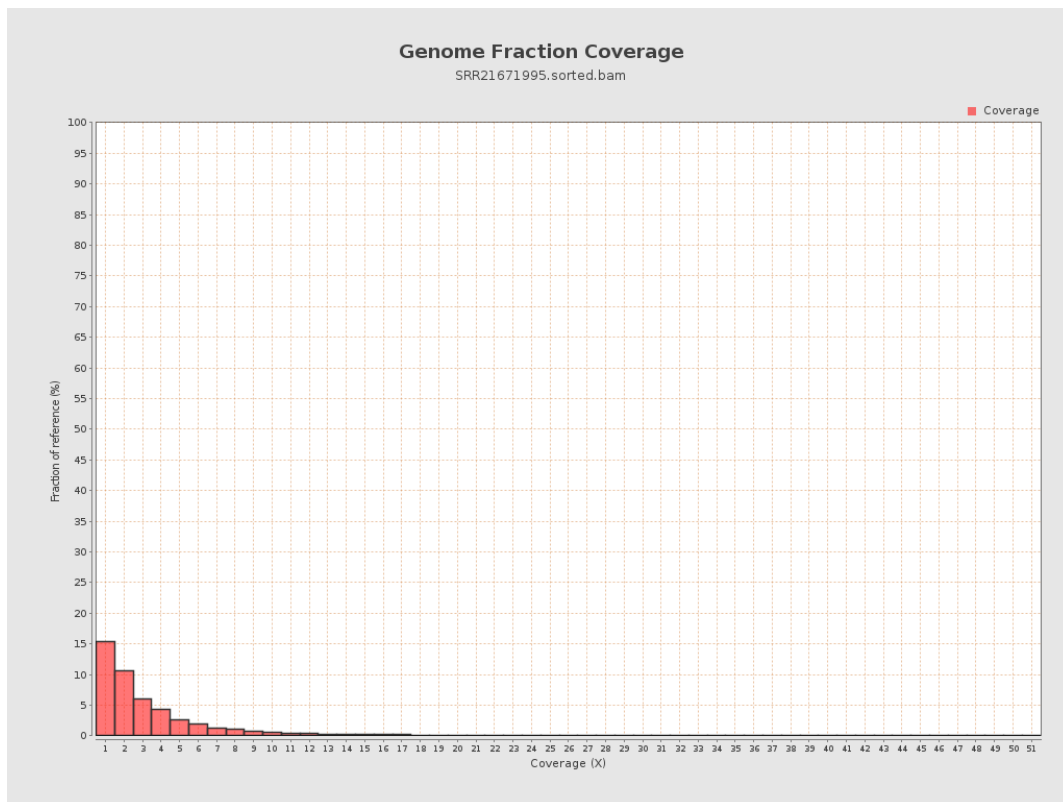
## 4. Results : Coverage Histogram



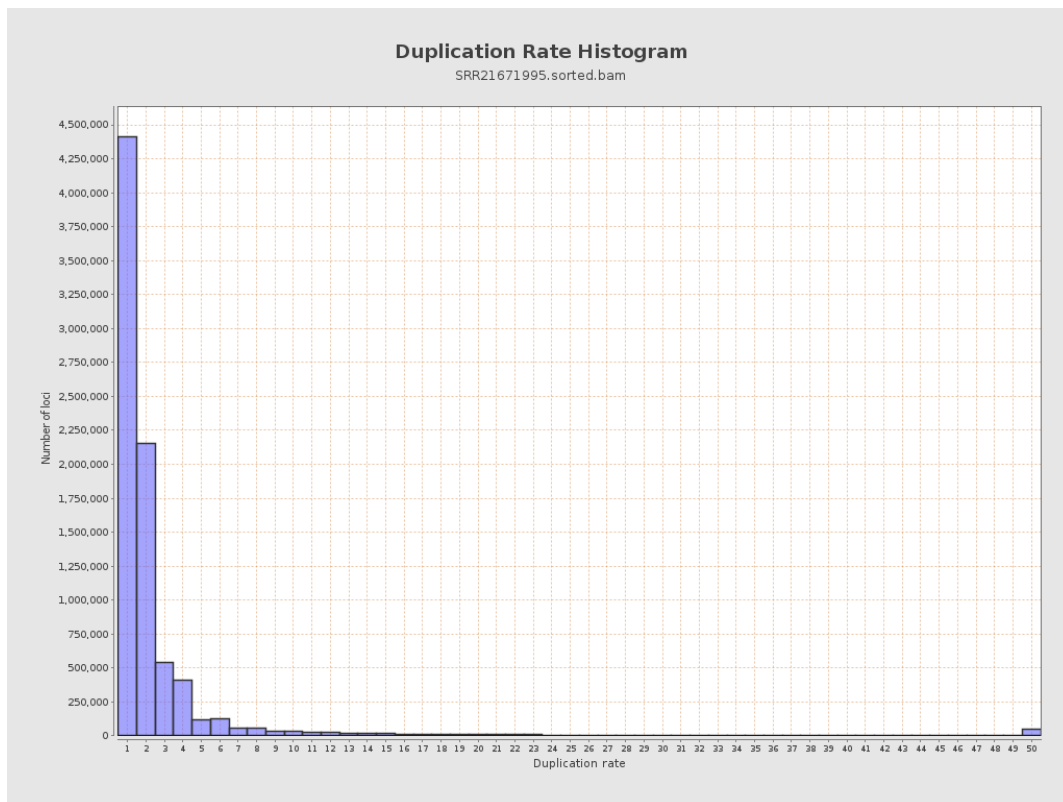
## 5. Results : Coverage Histogram (0-50X)



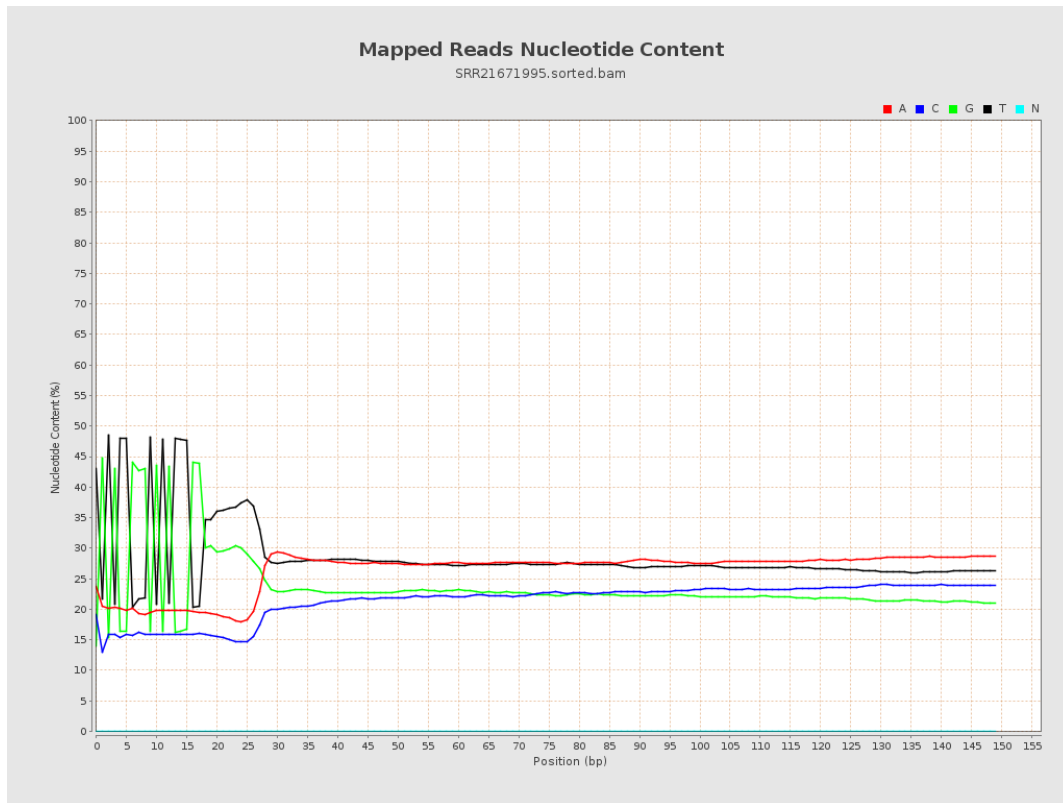
## 6. Results : Genome Fraction Coverage



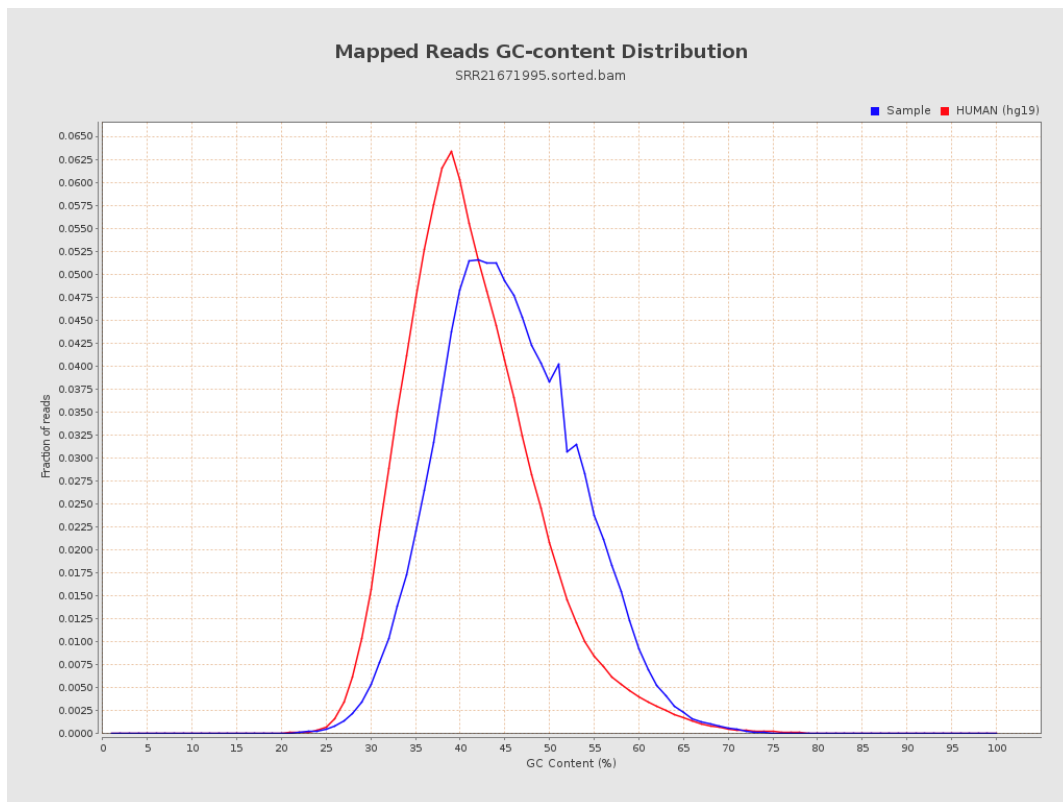
## 7. Results : Duplication Rate Histogram



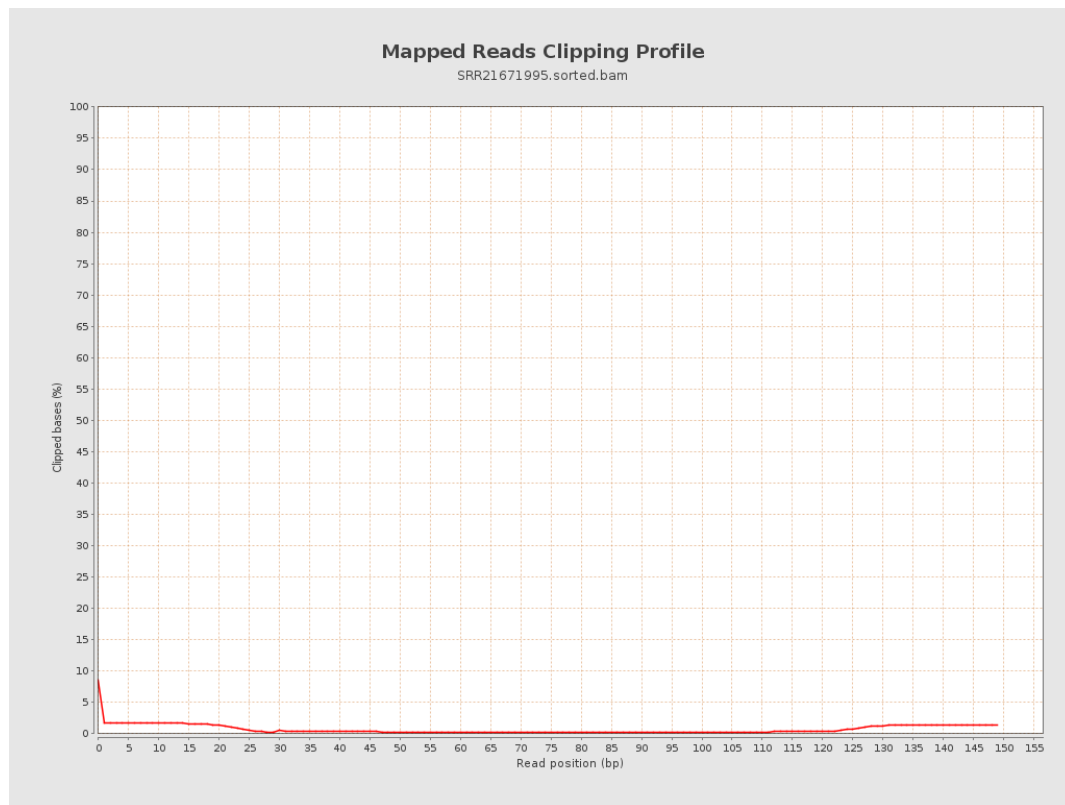
## 8. Results : Mapped Reads Nucleotide Content



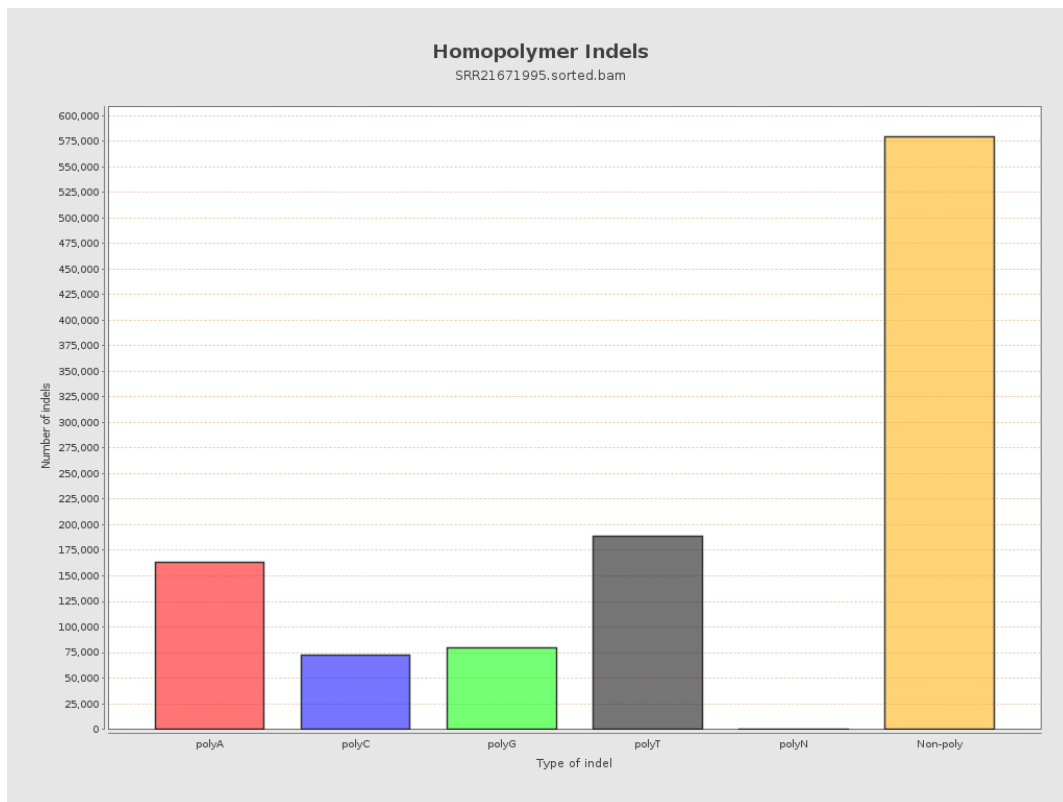
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



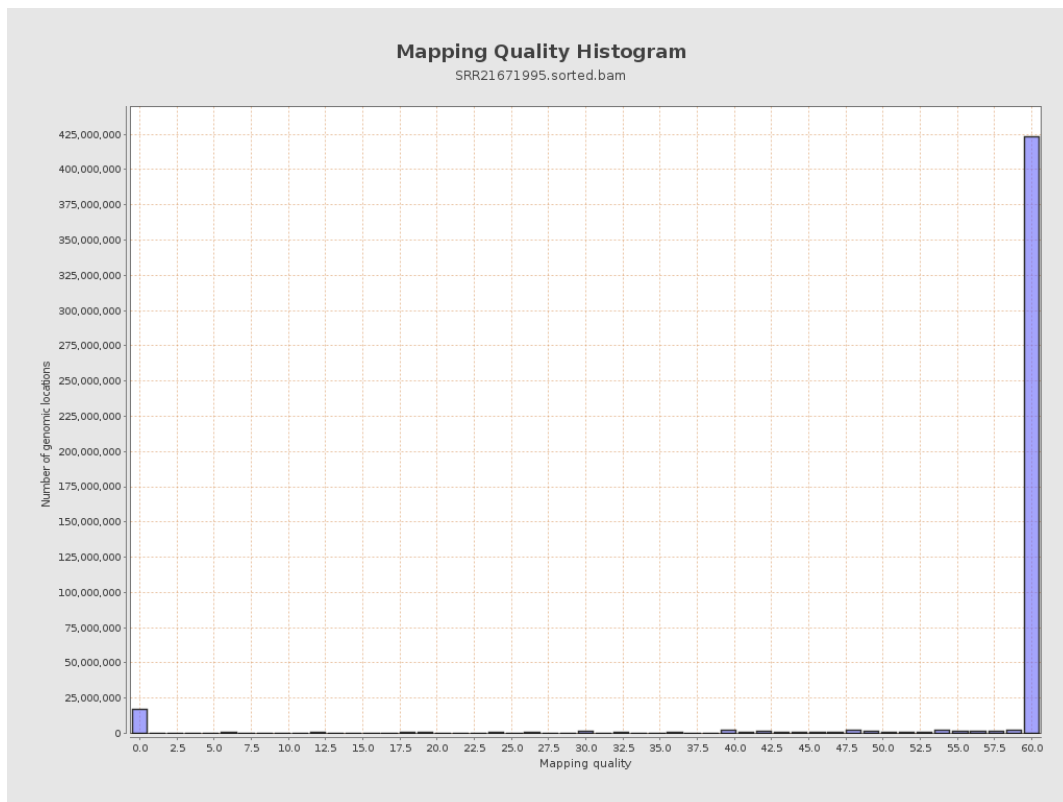
## 11. Results : Homopolymer Indels



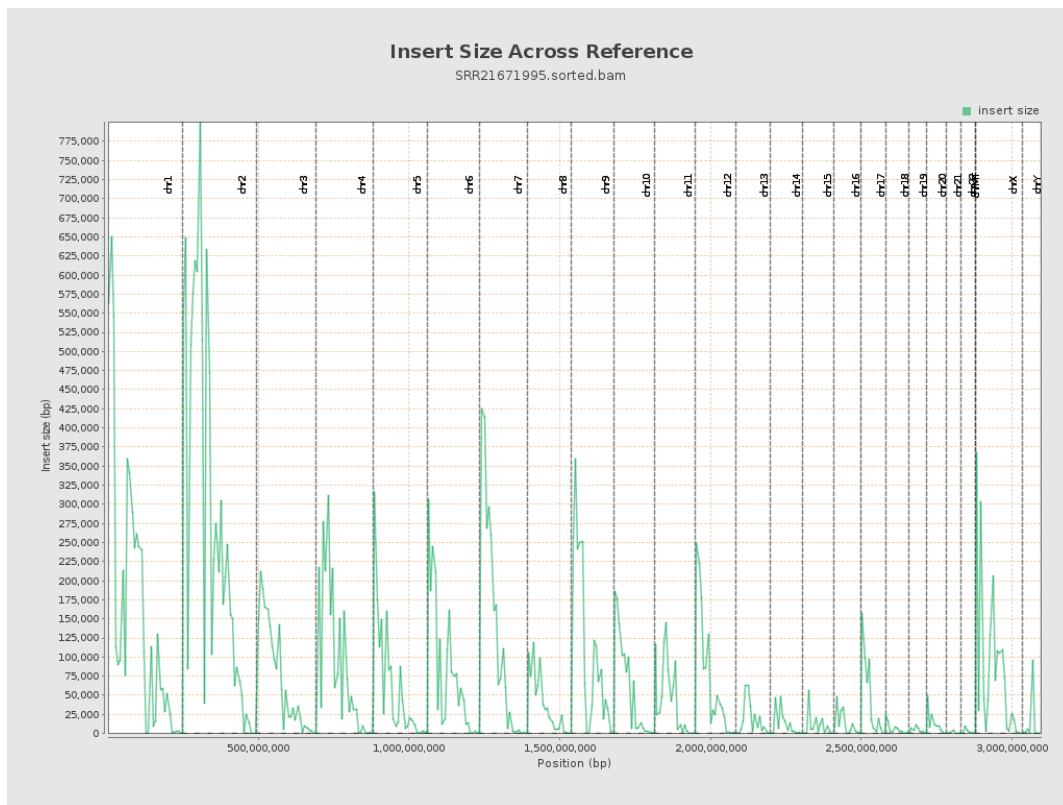
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

