

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.3*

*2024/09/12 20:41:02*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695920.sorted.bam -c -nw 400 -hm 3
```

## 1.2. Alignment

|                                       |                                                                                                                                                                                                                                                                                         |
|---------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Command line:                         | /seu_share/home/tujing/220232460/s<br>oftware/bwa-0.7.18/bwa mem -t 16 -k<br>30 -R<br>@RG\tID:Singlecell2022\tLB:Library\t<br>PL:ILLUMINA\tSM:sample_SRR1695<br>920<br>/seu_share/home/tujing/220232460/r<br>eference/homo_bwa/hsa.fa<br>SRR1695920_1.fastq.gz<br>SRR1695920_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.18-r1243-dirty)                                                                                                                                                                                                                                                                |
| Analysis date:                        | Thu Sep 12 20:41:02 CST 2024                                                                                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                                                                                     |
| BAM file:                             | SRR1695920.sorted.bam                                                                                                                                                                                                                                                                   |

## 2. Summary

### 2.1. Globals

|                              |                      |
|------------------------------|----------------------|
| Reference size               | 3,095,693,983        |
| Number of reads              | 107,485,596          |
| Mapped reads                 | 106,822,713 / 99.38% |
| Unmapped reads               | 662,883 / 0.62%      |
| Mapped paired reads          | 106,822,713 / 99.38% |
| Mapped reads, first in pair  | 53,574,694 / 49.84%  |
| Mapped reads, second in pair | 53,248,019 / 49.54%  |
| Mapped reads, both in pair   | 106,367,176 / 98.96% |
| Mapped reads, singletons     | 455,537 / 0.42%      |
| Secondary alignments         | 0                    |
| Supplementary alignments     | 1,366,222 / 1.27%    |
| Read min/max/mean length     | 30 / 100 / 100.52    |
| Duplicated reads (estimated) | 5,154,707 / 4.8%     |
| Duplication rate             | 4.3%                 |
| Clipped reads                | 8,187,210 / 7.62%    |

### 2.2. ACGT Content

|                          |                        |
|--------------------------|------------------------|
| Number/percentage of A's | 3,148,774,636 / 29.71% |
| Number/percentage of C's | 2,120,689,643 / 20.01% |
| Number/percentage of T's | 3,129,351,899 / 29.53% |
| Number/percentage of G's | 2,186,382,417 / 20.63% |
| Number/percentage of N's | 11,837,689 / 0.11%     |
|                          |                        |

|               |        |
|---------------|--------|
| GC Percentage | 40.64% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 3.4239 |
| Standard Deviation | 4.546  |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 53.85 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 82,187.47       |
| Standard Deviation | 2,744,202.22    |
| P25/Median/P75     | 317 / 325 / 333 |

## 2.6. Mismatches and indels

|                                          |            |
|------------------------------------------|------------|
| General error rate                       | 0.66%      |
| Mismatches                               | 67,659,735 |
| Insertions                               | 1,056,940  |
| Mapped reads with at least one insertion | 0.97%      |
| Deletions                                | 1,026,761  |
| Mapped reads with at least one deletion  | 0.94%      |
| Homopolymer indels                       | 45.76%     |

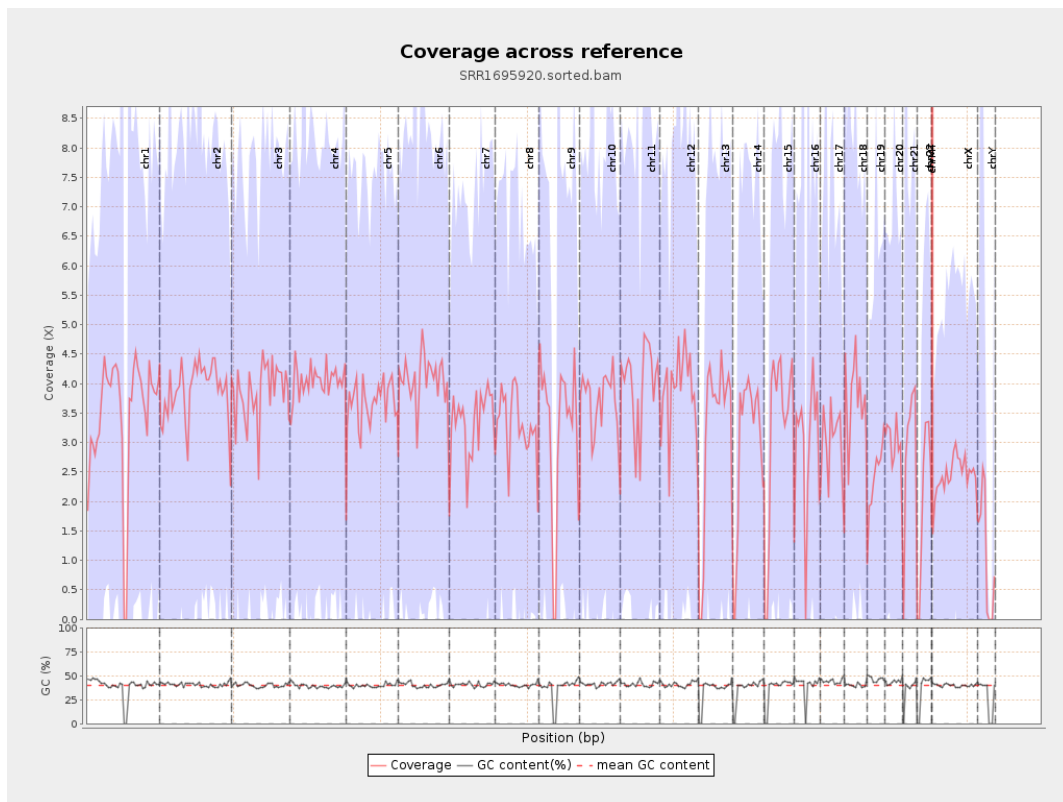
## 2.7. Chromosome stats

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

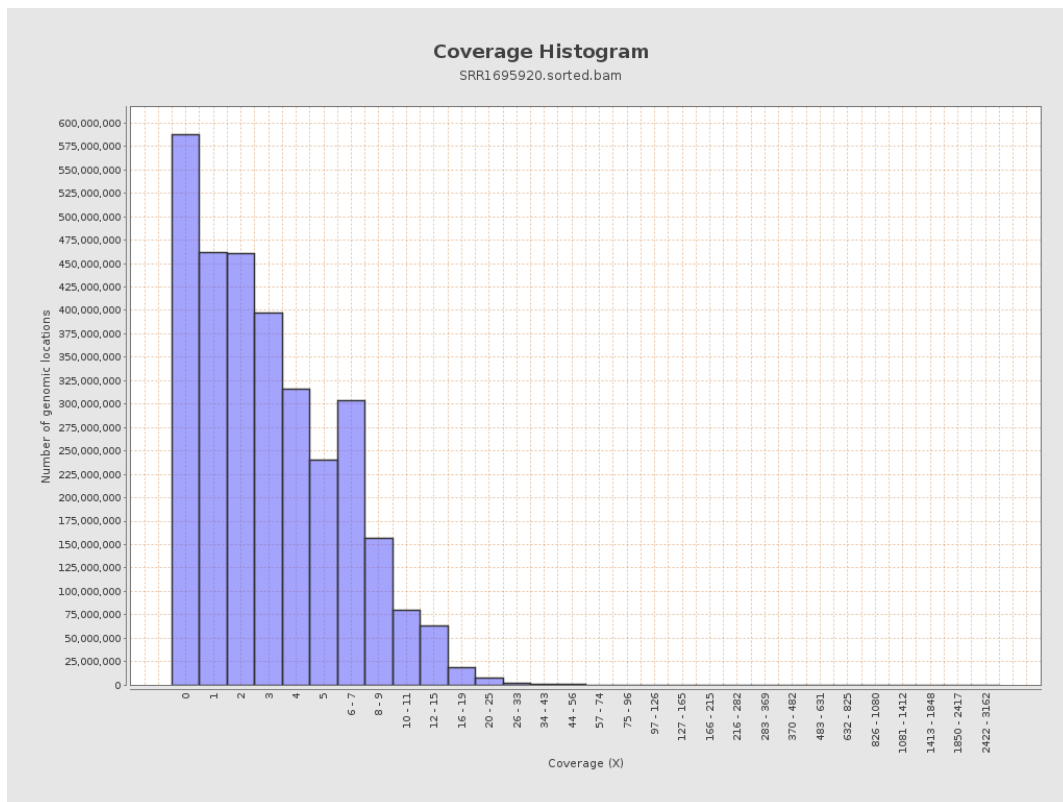
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 872707329    | 3.5013          | 4.6836           |
| chr2  | 243199373 | 942788765    | 3.8766          | 5.2425           |
| chr3  | 198022430 | 764870725    | 3.8625          | 3.509            |
| chr4  | 191154276 | 775326714    | 4.056           | 4.4815           |
| chr5  | 180915260 | 664732652    | 3.6743          | 3.3465           |
| chr6  | 171115067 | 699385938    | 4.0872          | 4.1522           |
| chr7  | 159138663 | 532913338    | 3.3487          | 3.4652           |
| chr8  | 146364022 | 485454361    | 3.3168          | 3.2641           |
| chr9  | 141213431 | 447717019    | 3.1705          | 4.1018           |
| chr10 | 135534747 | 503677975    | 3.7162          | 5.0639           |
| chr11 | 135006516 | 537902873    | 3.9843          | 3.9682           |
| chr12 | 133851895 | 518674222    | 3.875           | 3.7397           |
| chr13 | 115169878 | 370456591    | 3.2166          | 3.5277           |
| chr14 | 107349540 | 319232448    | 2.9738          | 3.4474           |
| chr15 | 102531392 | 330851686    | 3.2268          | 3.7154           |
| chr16 | 90354753  | 260370198    | 2.8816          | 5.1653           |
| chr17 | 81195210  | 240708072    | 2.9646          | 4.0308           |
| chr18 | 78077248  | 295119201    | 3.7798          | 4.8866           |
| chr19 | 59128983  | 143643747    | 2.4293          | 3.4986           |
| chr20 | 63025520  | 185694971    | 2.9463          | 3.5568           |
| chr21 | 48129895  | 143399582    | 2.9794          | 6.0651           |
| chr22 | 51304566  | 104625782    | 2.0393          | 3.1503           |
| chrMT | 16571     | 12589625     | 759.7384        | 205.3283         |
| chrX  | 155270560 | 379265835    | 2.4426          | 2.6713           |

|      |          |          |        |        |
|------|----------|----------|--------|--------|
| chrY | 59373566 | 67293633 | 1.1334 | 4.8143 |
|------|----------|----------|--------|--------|

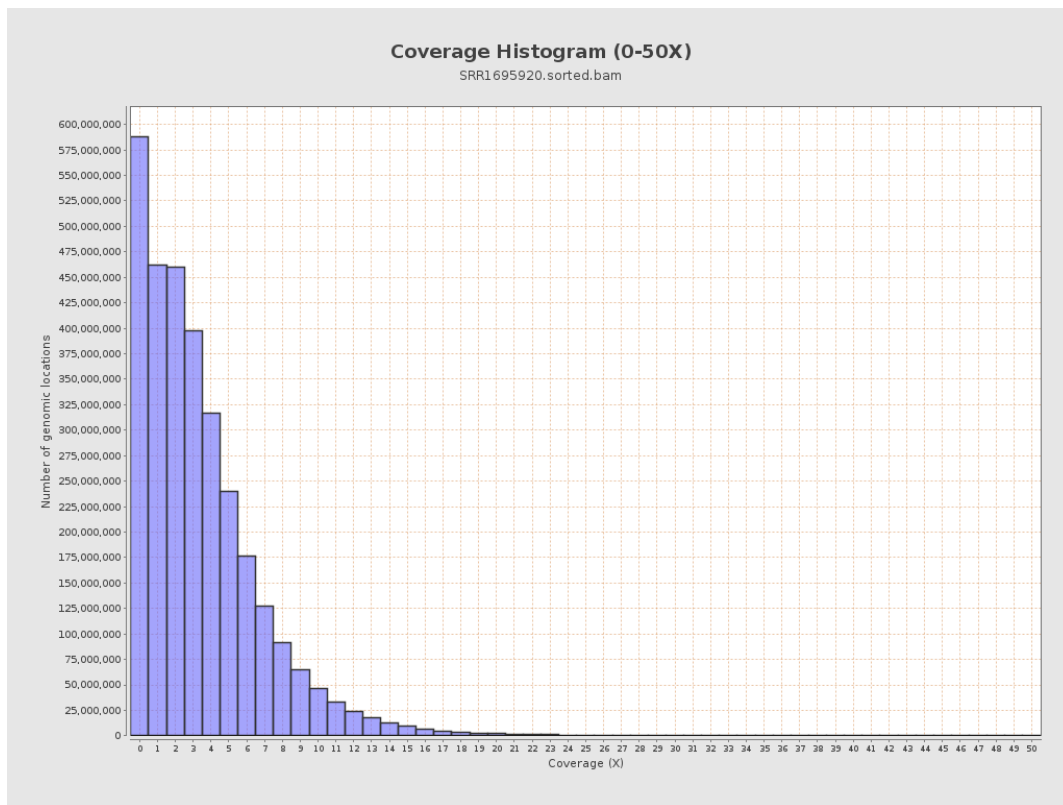
### 3. Results : Coverage across reference



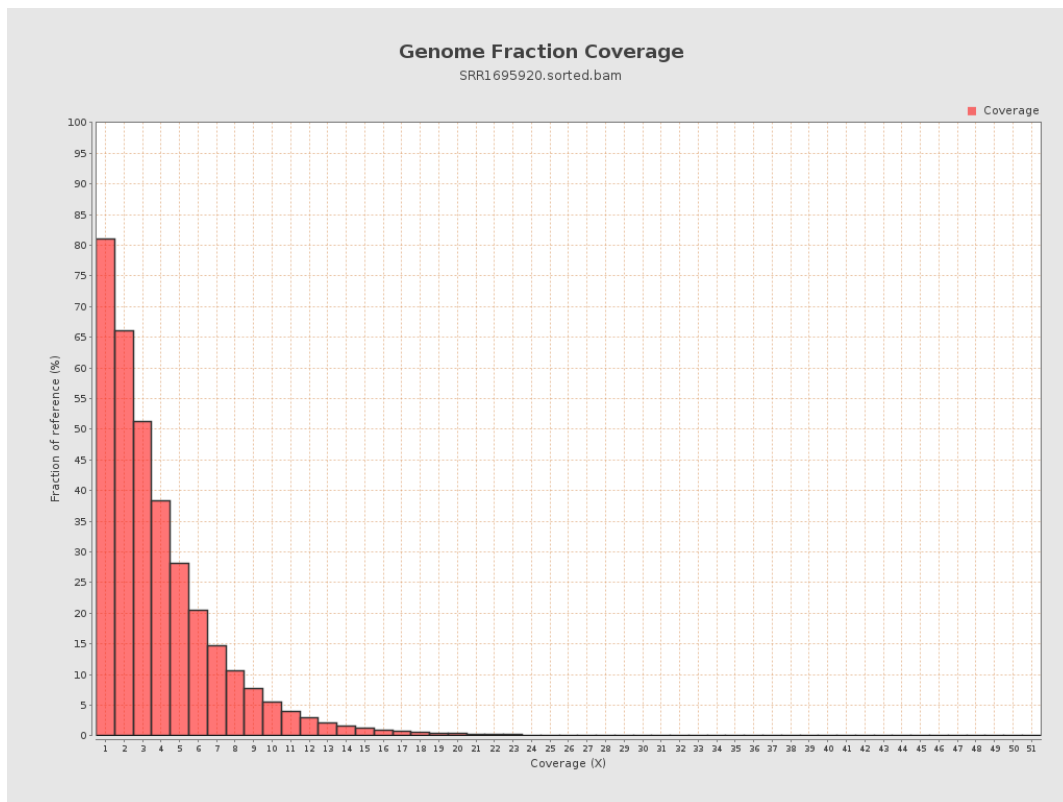
## 4. Results : Coverage Histogram



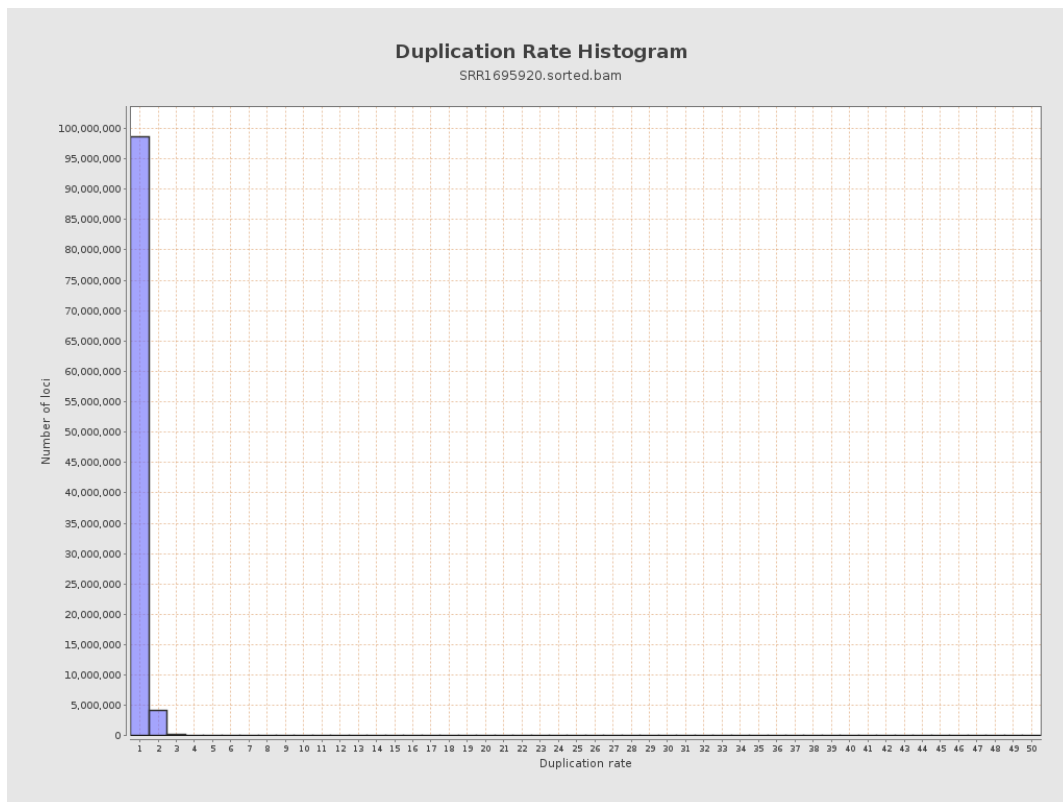
## 5. Results : Coverage Histogram (0-50X)



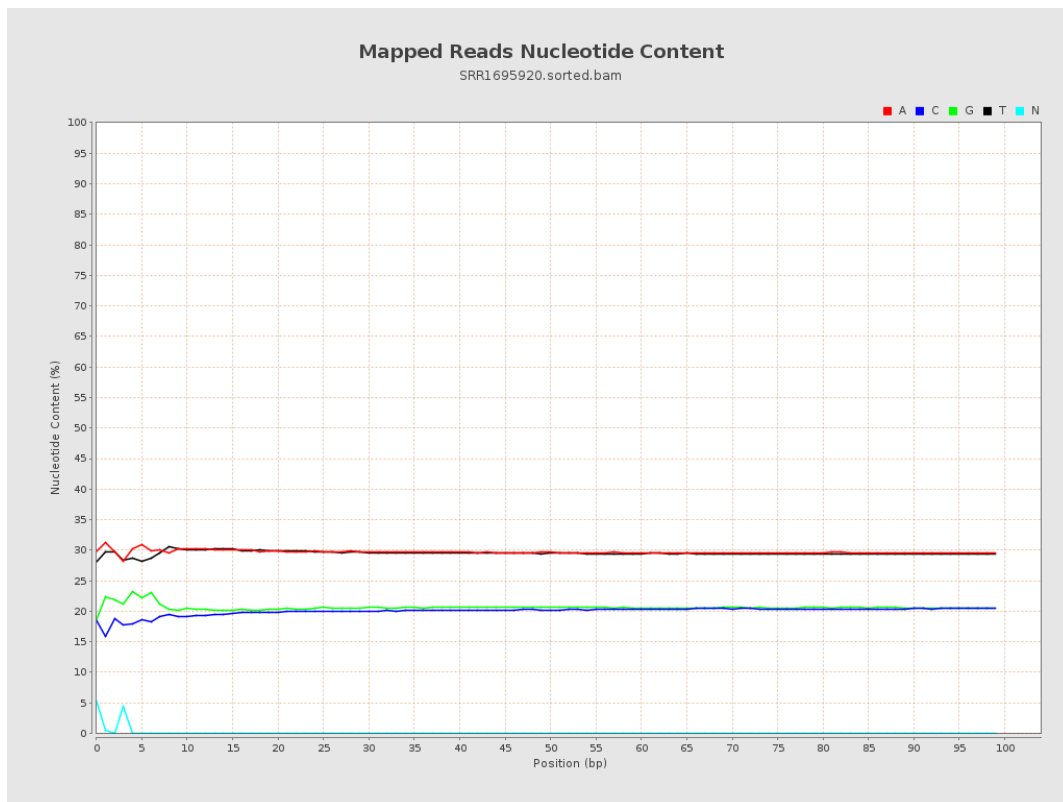
## 6. Results : Genome Fraction Coverage



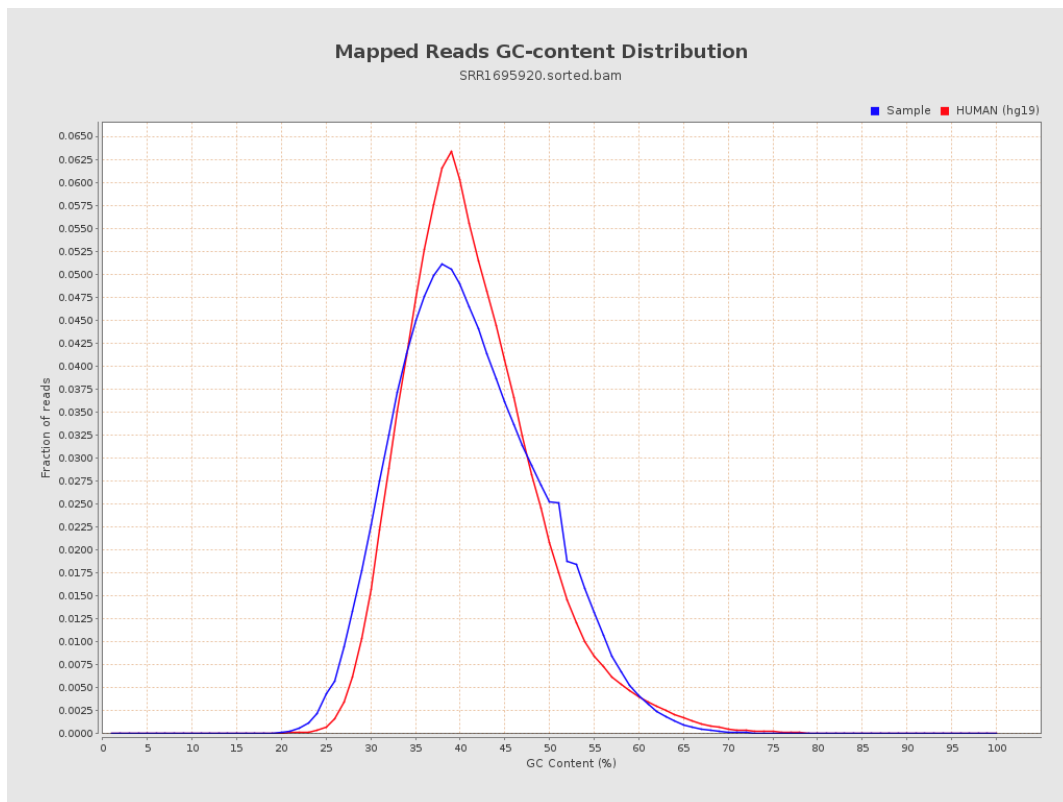
## 7. Results : Duplication Rate Histogram



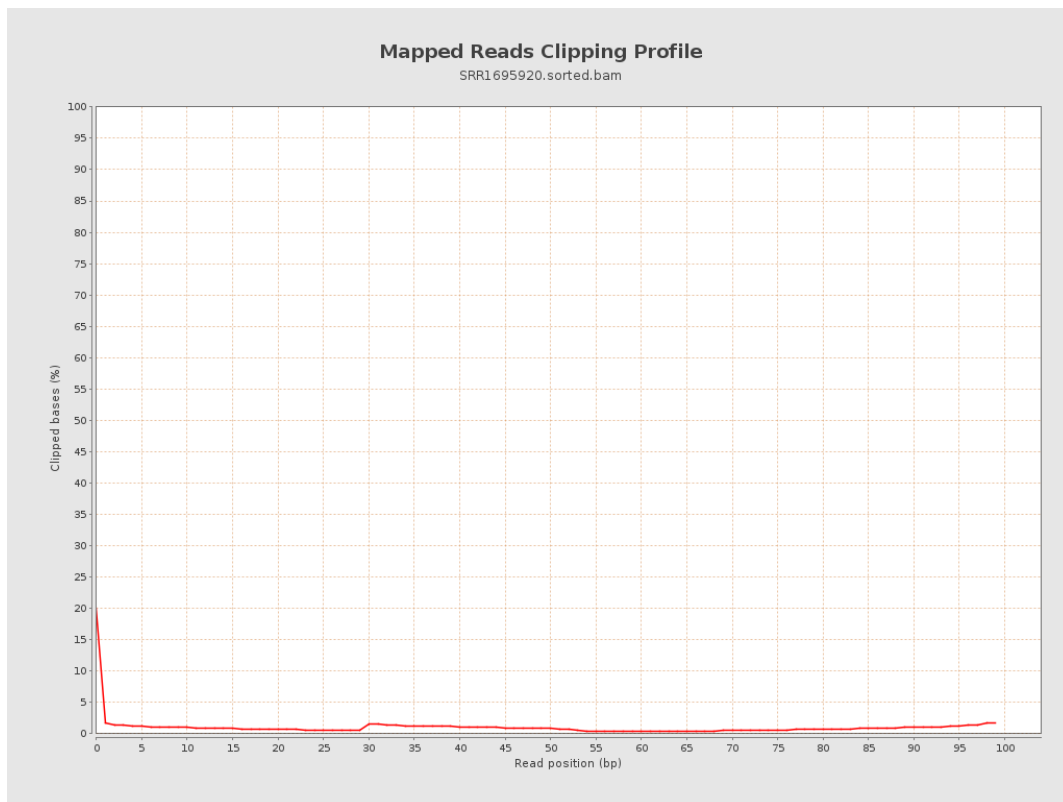
## 8. Results : Mapped Reads Nucleotide Content



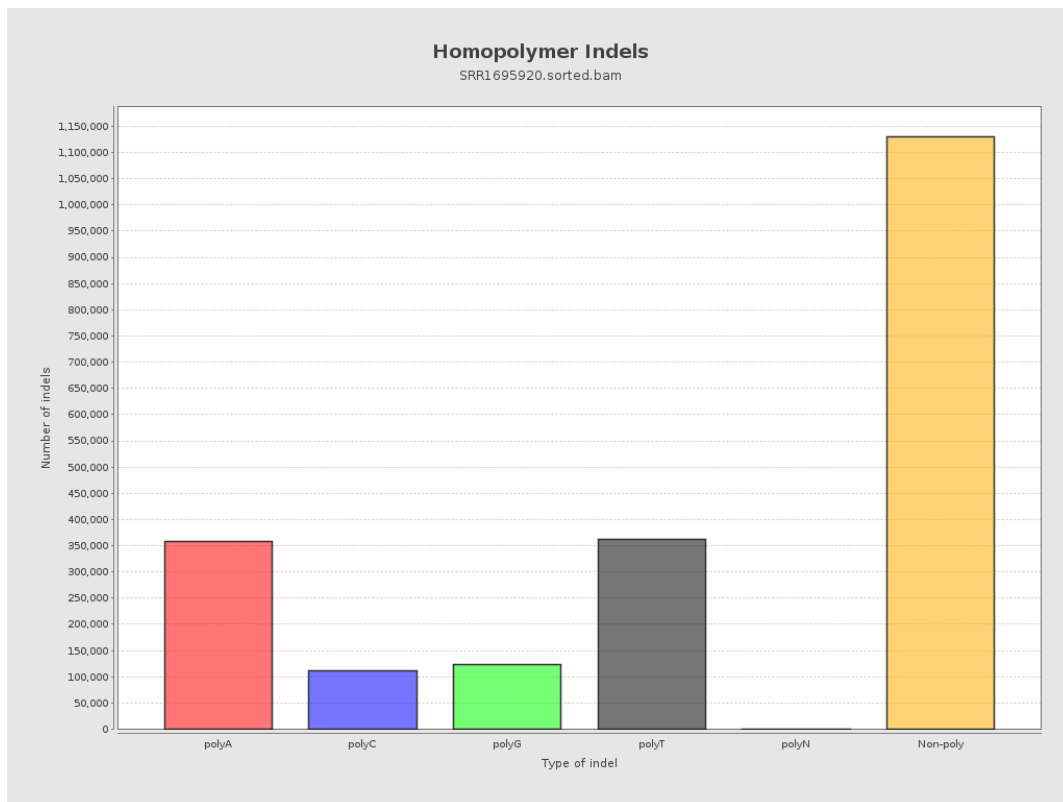
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



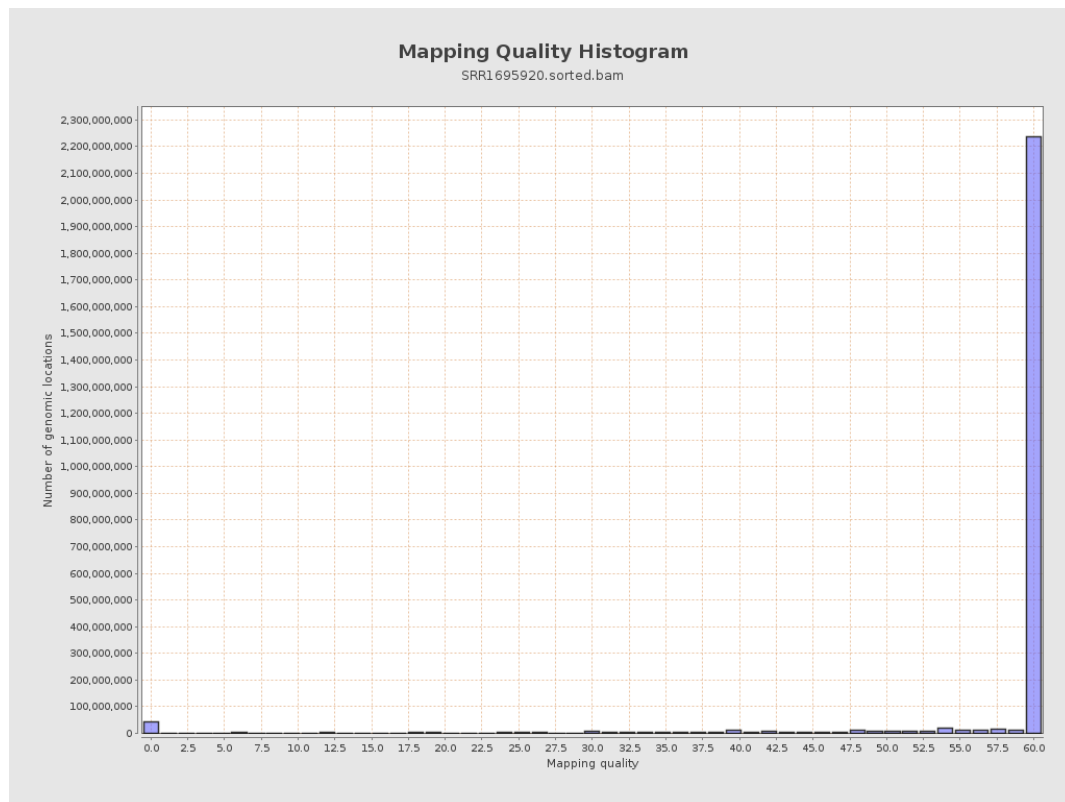
## 11. Results : Homopolymer Indels



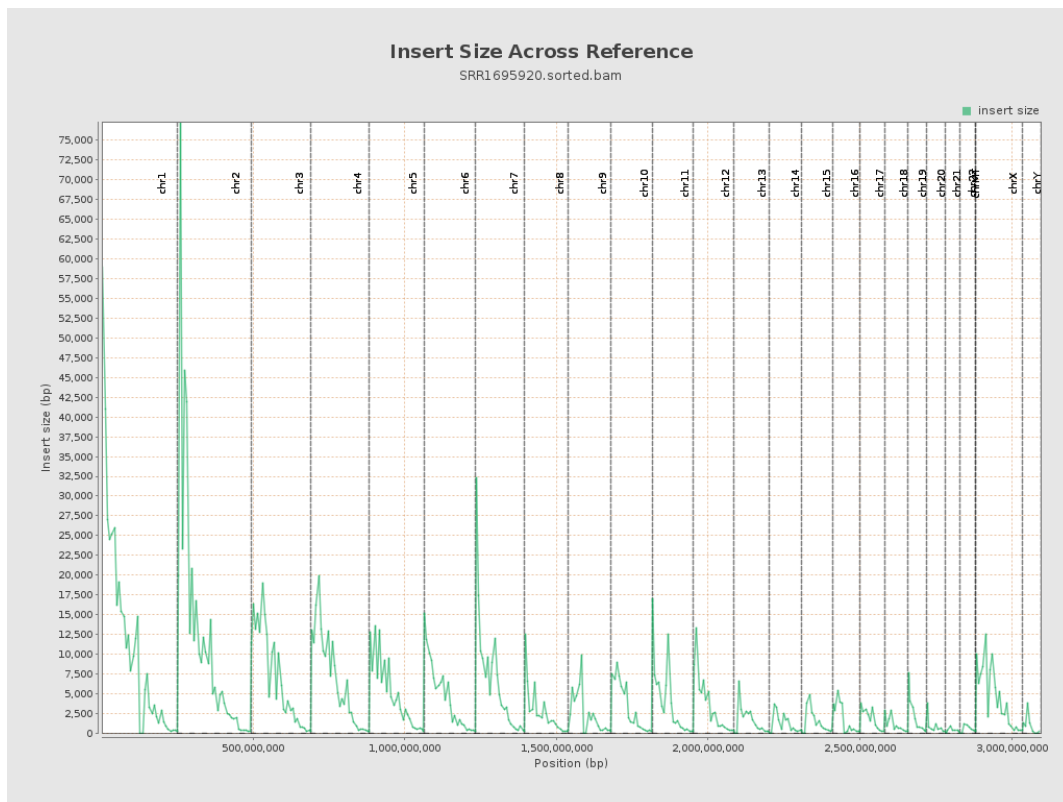
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

