

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.3*

*2024/09/13 02:40:24*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695939.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_SRR1695939 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695939_1.fastq.gz SRR1695939_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 02:40:23 CST 2024                                                                                                                                                                                                                             |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                                                        |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                                                       |
| Number of windows:                    | 400                                                                                                                                                                                                                                                      |
| BAM file:                             | SRR1695939.sorted.bam                                                                                                                                                                                                                                    |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 14,508,370          |
| Mapped reads                 | 14,411,404 / 99.33% |
| Unmapped reads               | 96,966 / 0.67%      |
| Mapped paired reads          | 14,411,404 / 99.33% |
| Mapped reads, first in pair  | 7,241,103 / 49.91%  |
| Mapped reads, second in pair | 7,170,301 / 49.42%  |
| Mapped reads, both in pair   | 14,330,084 / 98.77% |
| Mapped reads, singletons     | 81,320 / 0.56%      |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 35,677 / 0.25%      |
| Read min/max/mean length     | 30 / 100 / 100.1    |
| Duplicated reads (estimated) | 414,848 / 2.86%     |
| Duplication rate             | 2.79%               |
| Clipped reads                | 588,069 / 4.05%     |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 425,405,406 / 29.75% |
| Number/percentage of C's | 288,318,926 / 20.16% |
| Number/percentage of T's | 425,581,465 / 29.76% |
| Number/percentage of G's | 290,121,915 / 20.29% |
| Number/percentage of N's | 628,655 / 0.04%      |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 40.45% |
|---------------|--------|

## 2.3. Coverage

|                    |       |
|--------------------|-------|
| Mean               | 0.462 |
| Standard Deviation | 1.509 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 54.33 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 29,768.35       |
| Standard Deviation | 1,689,151.43    |
| P25/Median/P75     | 322 / 328 / 335 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.66%     |
| Mismatches                               | 9,211,528 |
| Insertions                               | 90,191    |
| Mapped reads with at least one insertion | 0.62%     |
| Deletions                                | 116,262   |
| Mapped reads with at least one deletion  | 0.79%     |
| Homopolymer indels                       | 45.17%    |

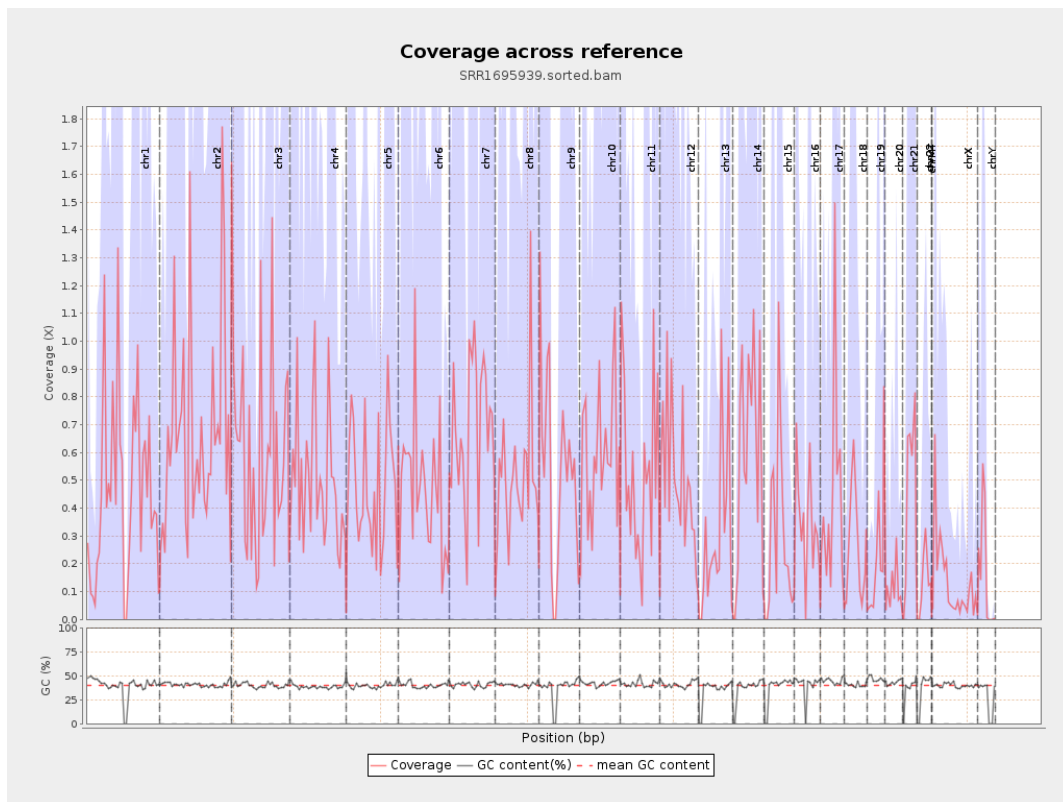
## 2.7. Chromosome stats

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

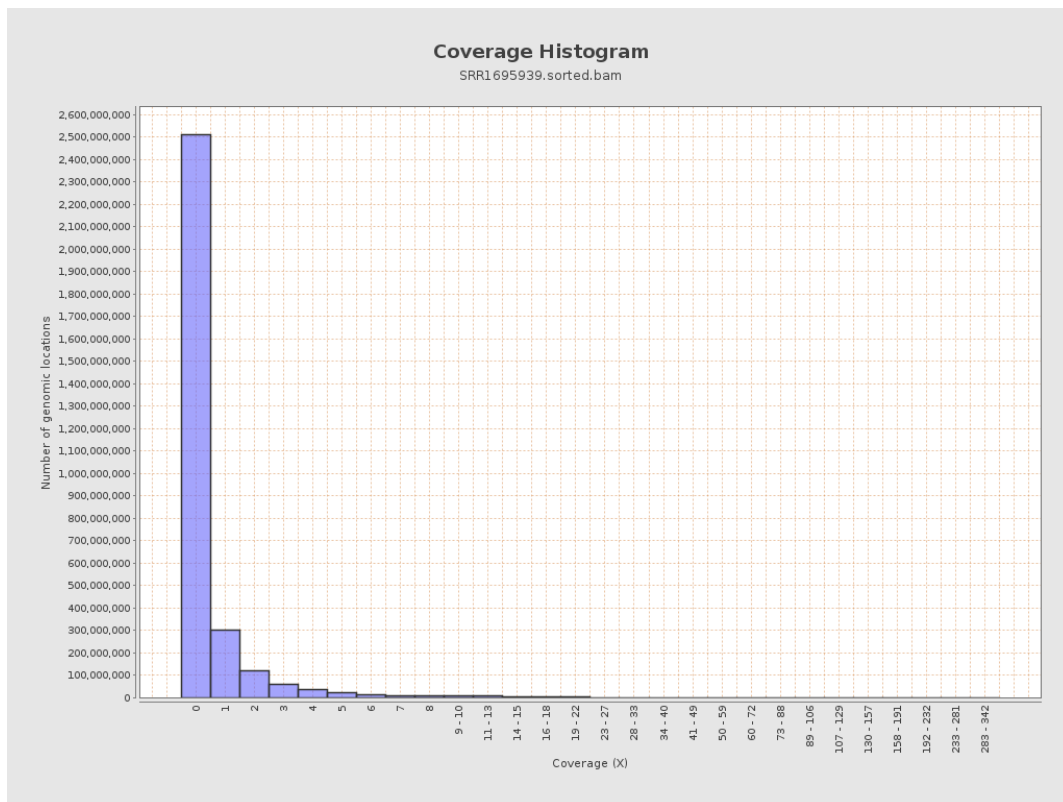
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 114516945    | 0.4594          | 1.4849           |
| chr2  | 243199373 | 163276470    | 0.6714          | 1.8364           |
| chr3  | 198022430 | 119804653    | 0.605           | 1.7126           |
| chr4  | 191154276 | 96085558     | 0.5027          | 1.4748           |
| chr5  | 180915260 | 86792131     | 0.4797          | 1.4516           |
| chr6  | 171115067 | 80431796     | 0.47            | 1.6614           |
| chr7  | 159138663 | 108816983    | 0.6838          | 1.7996           |
| chr8  | 146364022 | 76821196     | 0.5249          | 1.5156           |
| chr9  | 141213431 | 73029897     | 0.5172          | 1.4407           |
| chr10 | 135534747 | 79798880     | 0.5888          | 1.6725           |
| chr11 | 135006516 | 69421823     | 0.5142          | 1.679            |
| chr12 | 133851895 | 66922129     | 0.5             | 1.5905           |
| chr13 | 115169878 | 35310133     | 0.3066          | 1.6931           |
| chr14 | 107349540 | 62469949     | 0.5819          | 1.6658           |
| chr15 | 102531392 | 31277564     | 0.3051          | 1.3306           |
| chr16 | 90354753  | 30470553     | 0.3372          | 1.1808           |
| chr17 | 81195210  | 35101933     | 0.4323          | 1.4316           |
| chr18 | 78077248  | 21487977     | 0.2752          | 1.0476           |
| chr19 | 59128983  | 10979116     | 0.1857          | 0.9251           |
| chr20 | 63025520  | 6888806      | 0.1093          | 0.5952           |
| chr21 | 48129895  | 22961311     | 0.4771          | 1.5044           |
| chr22 | 51304566  | 6847829      | 0.1335          | 0.6208           |
| chrMT | 16571     | 2589         | 0.1562          | 0.4781           |
| chrX  | 155270560 | 20444342     | 0.1317          | 0.7083           |

|      |          |          |        |        |
|------|----------|----------|--------|--------|
| chrY | 59373566 | 10355783 | 0.1744 | 0.8345 |
|------|----------|----------|--------|--------|

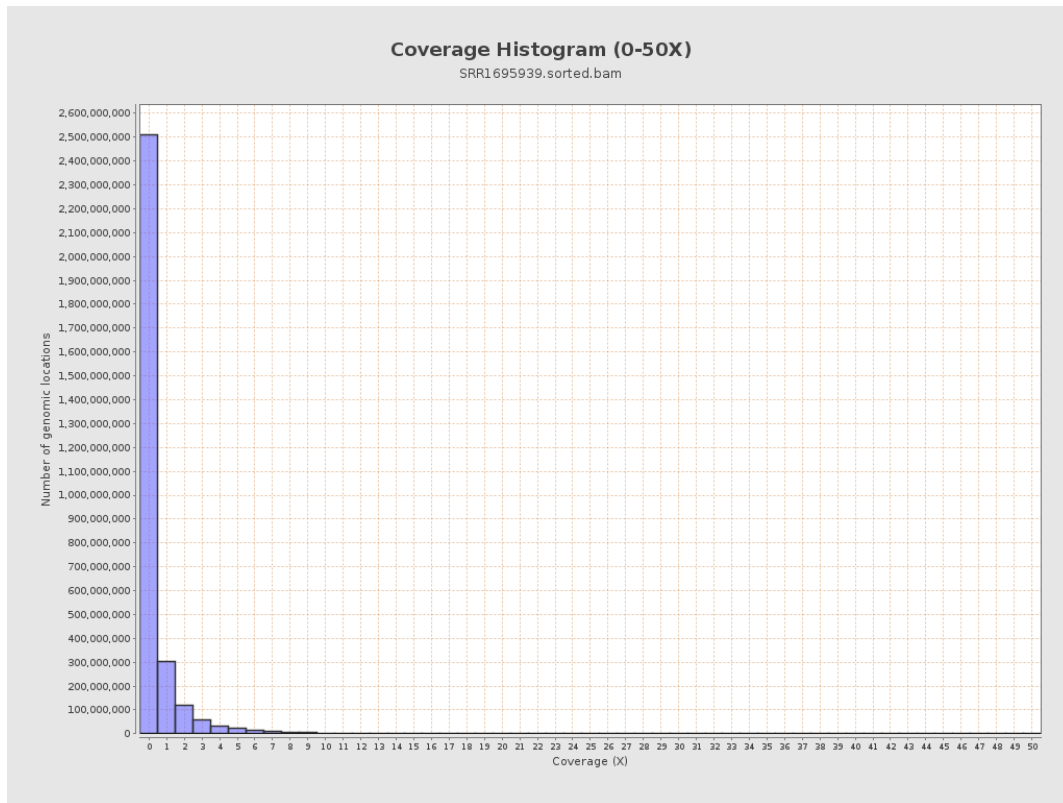
### 3. Results : Coverage across reference



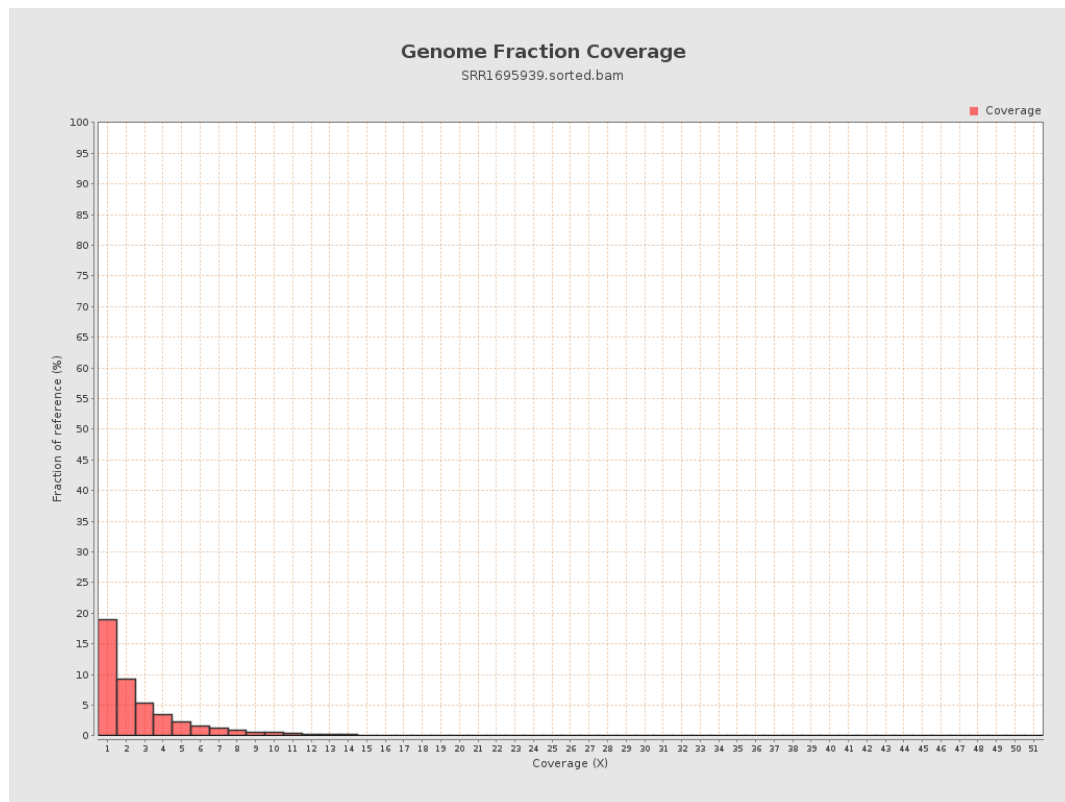
## 4. Results : Coverage Histogram



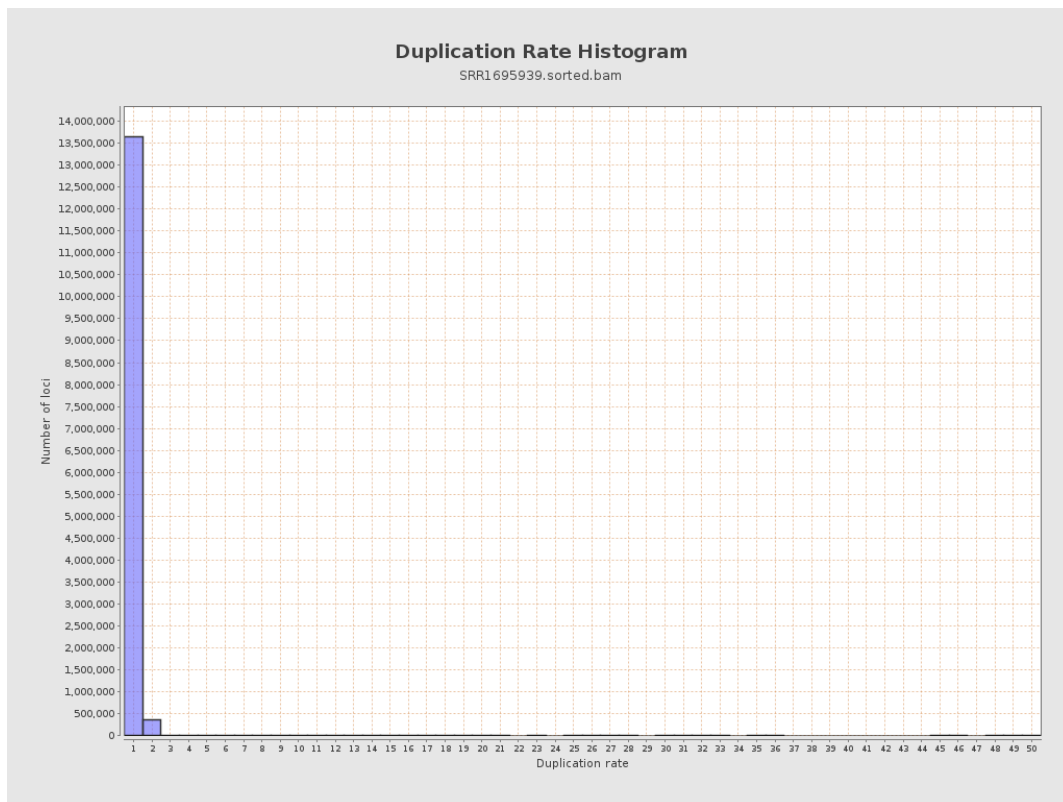
## 5. Results : Coverage Histogram (0-50X)



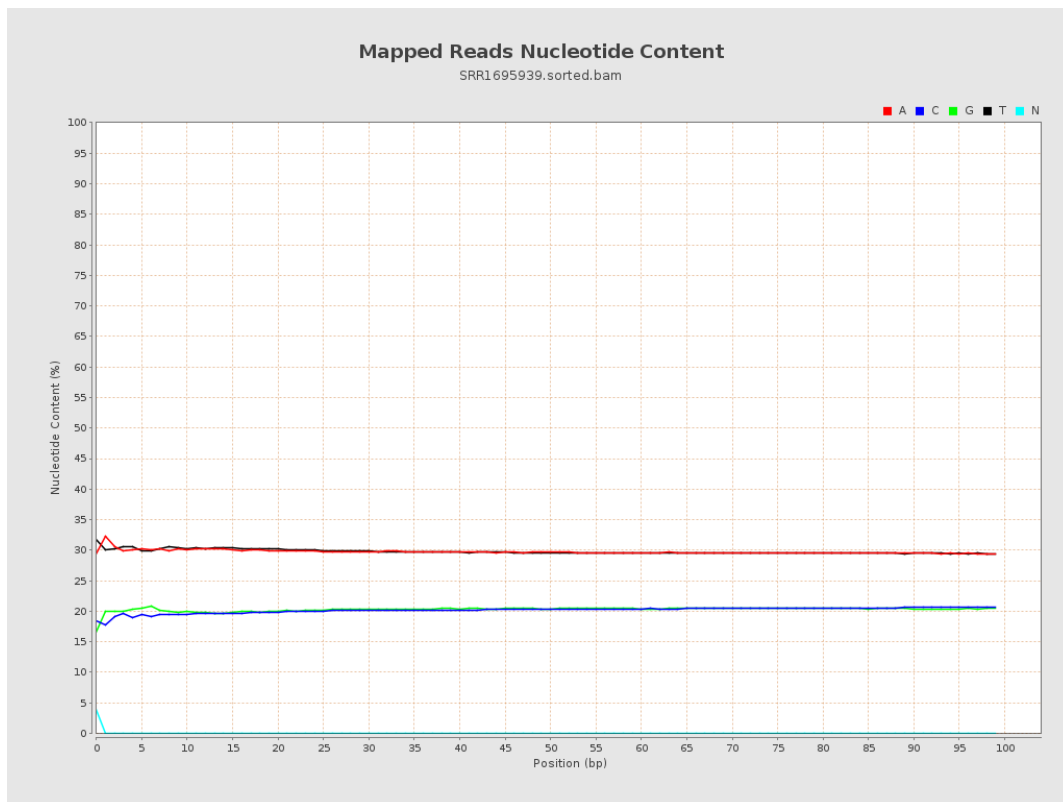
## 6. Results : Genome Fraction Coverage



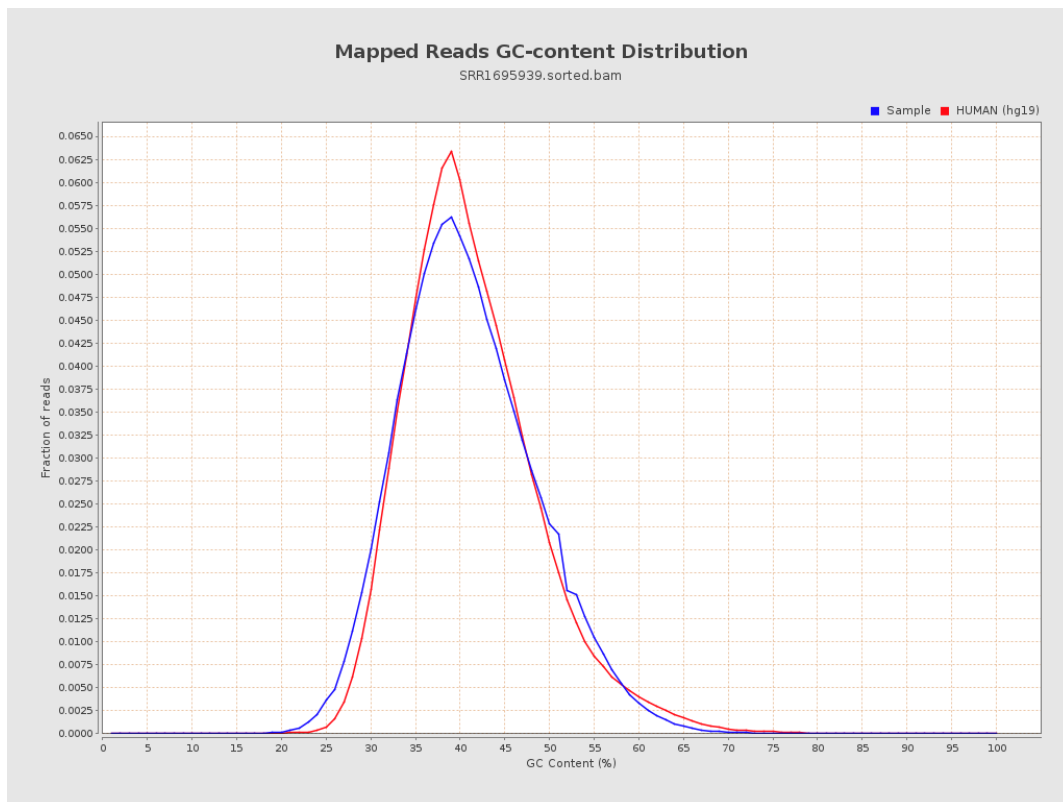
## 7. Results : Duplication Rate Histogram



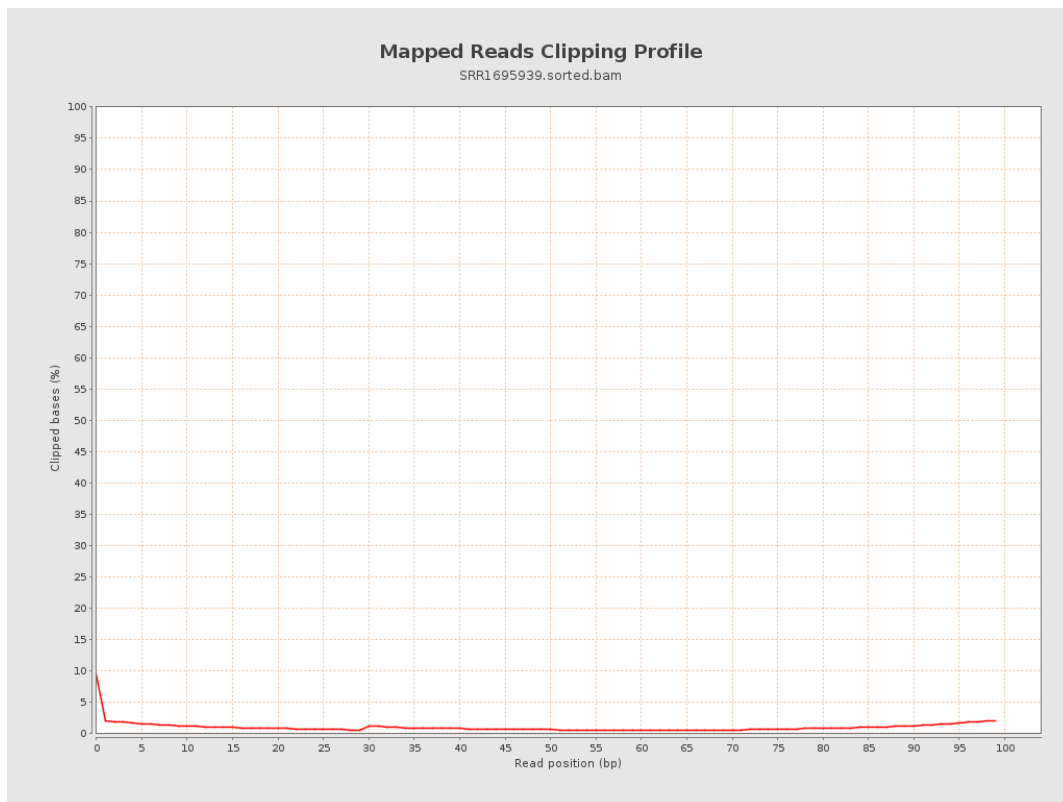
## 8. Results : Mapped Reads Nucleotide Content



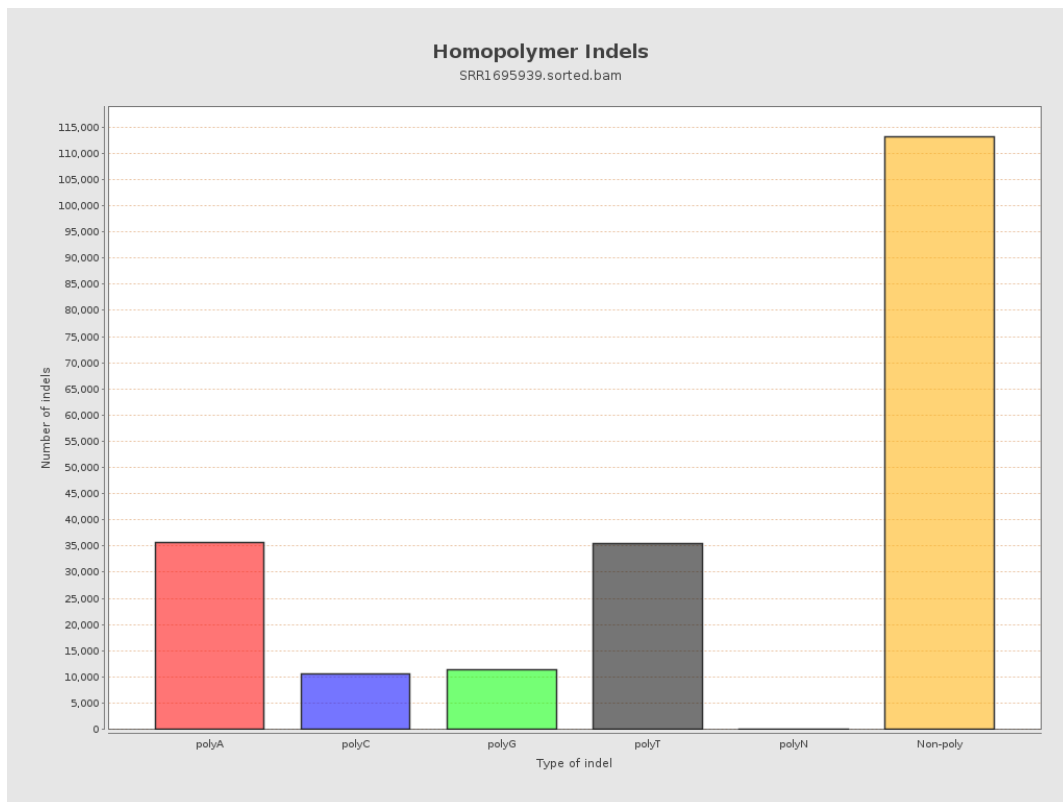
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



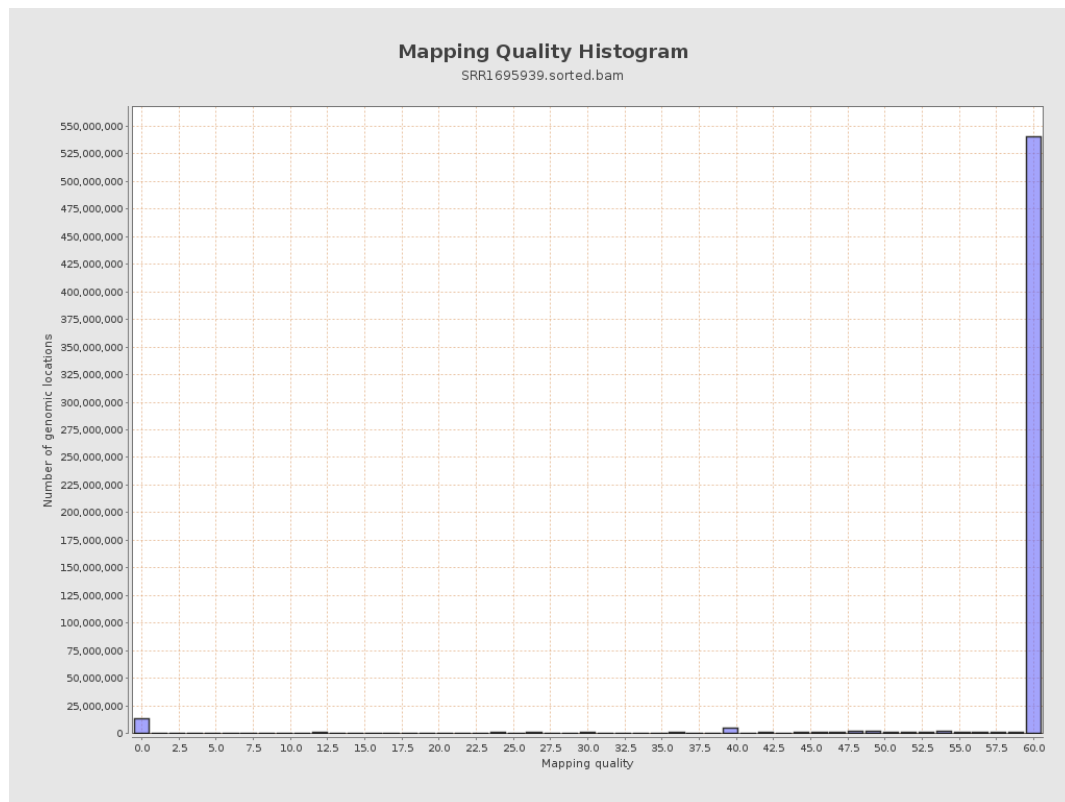
## 11. Results : Homopolymer Indels



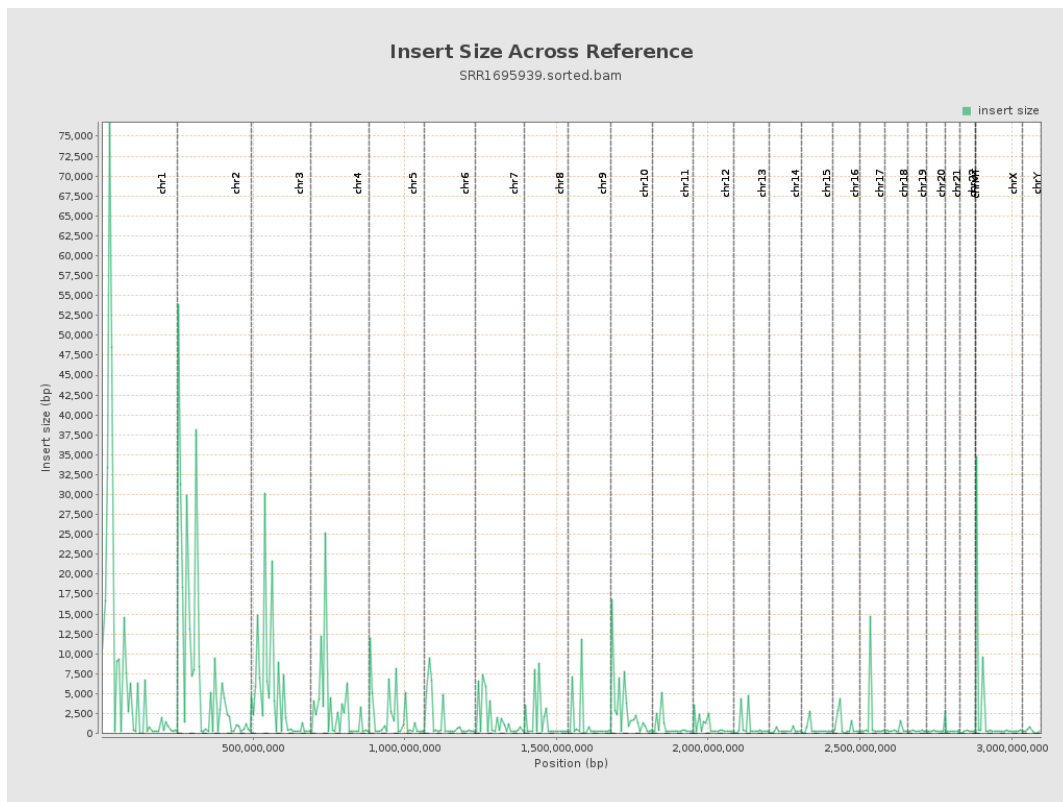
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

