

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.3*

*2024/09/13 22:23:04*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695963.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_SRR1695963 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695963_1.fastq.gz SRR1695963_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 22:23:03 CST 2024                                                                                                                                                                                                                             |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                                                        |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                                                       |
| Number of windows:                    | 400                                                                                                                                                                                                                                                      |
| BAM file:                             | SRR1695963.sorted.bam                                                                                                                                                                                                                                    |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 97,221,376          |
| Mapped reads                 | 96,693,322 / 99.46% |
| Unmapped reads               | 528,054 / 0.54%     |
| Mapped paired reads          | 96,693,322 / 99.46% |
| Mapped reads, first in pair  | 48,444,617 / 49.83% |
| Mapped reads, second in pair | 48,248,705 / 49.63% |
| Mapped reads, both in pair   | 96,355,760 / 99.11% |
| Mapped reads, singletons     | 337,562 / 0.35%     |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 945,091 / 0.97%     |
| Read min/max/mean length     | 30 / 100 / 100.4    |
| Duplicated reads (estimated) | 4,207,101 / 4.33%   |
| Duplication rate             | 3.76%               |
| Clipped reads                | 5,326,888 / 5.48%   |

### 2.2. ACGT Content

|                          |                        |
|--------------------------|------------------------|
| Number/percentage of A's | 2,777,972,302 / 28.95% |
| Number/percentage of C's | 1,999,205,734 / 20.83% |
| Number/percentage of T's | 2,764,922,916 / 28.81% |
| Number/percentage of G's | 2,054,794,081 / 21.41% |
| Number/percentage of N's | 154,275 / 0%           |
|                          |                        |

|               |        |
|---------------|--------|
| GC Percentage | 42.24% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 3.1009 |
| Standard Deviation | 4.51   |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 54.08 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 73,588.21       |
| Standard Deviation | 2,624,324.82    |
| P25/Median/P75     | 329 / 337 / 345 |

## 2.6. Mismatches and indels

|                                          |            |
|------------------------------------------|------------|
| General error rate                       | 0.36%      |
| Mismatches                               | 32,381,962 |
| Insertions                               | 974,168    |
| Mapped reads with at least one insertion | 0.99%      |
| Deletions                                | 984,640    |
| Mapped reads with at least one deletion  | 1%         |
| Homopolymer indels                       | 45.57%     |

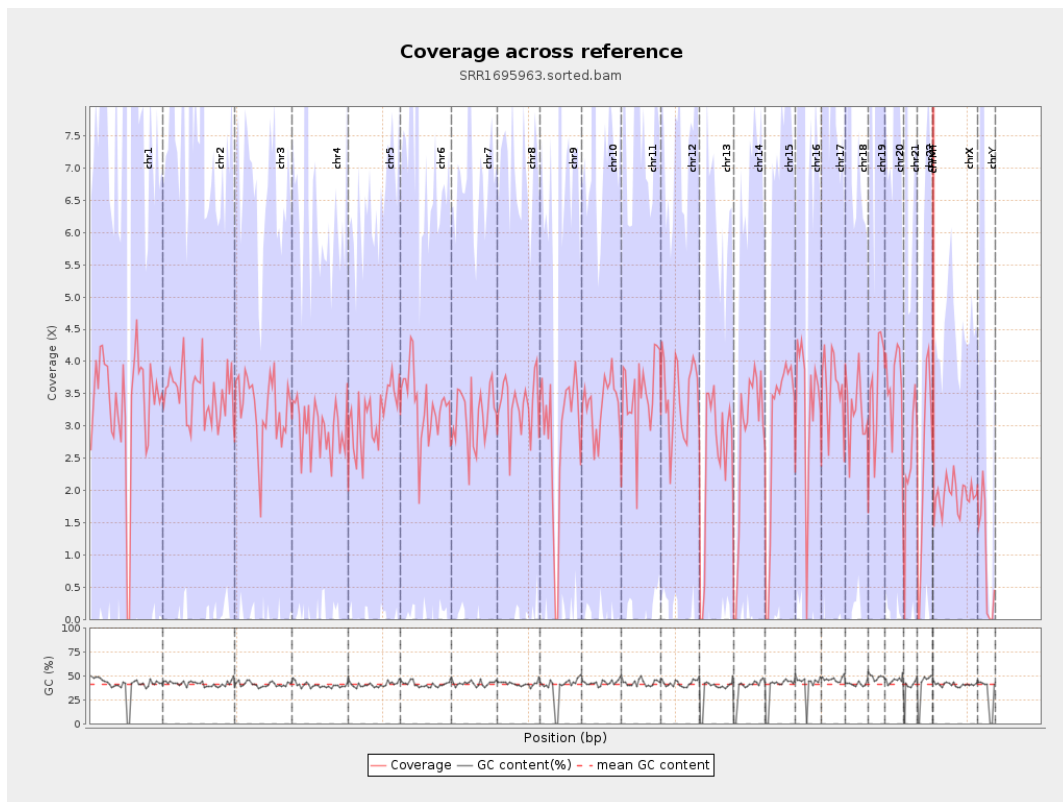
## 2.7. Chromosome stats

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

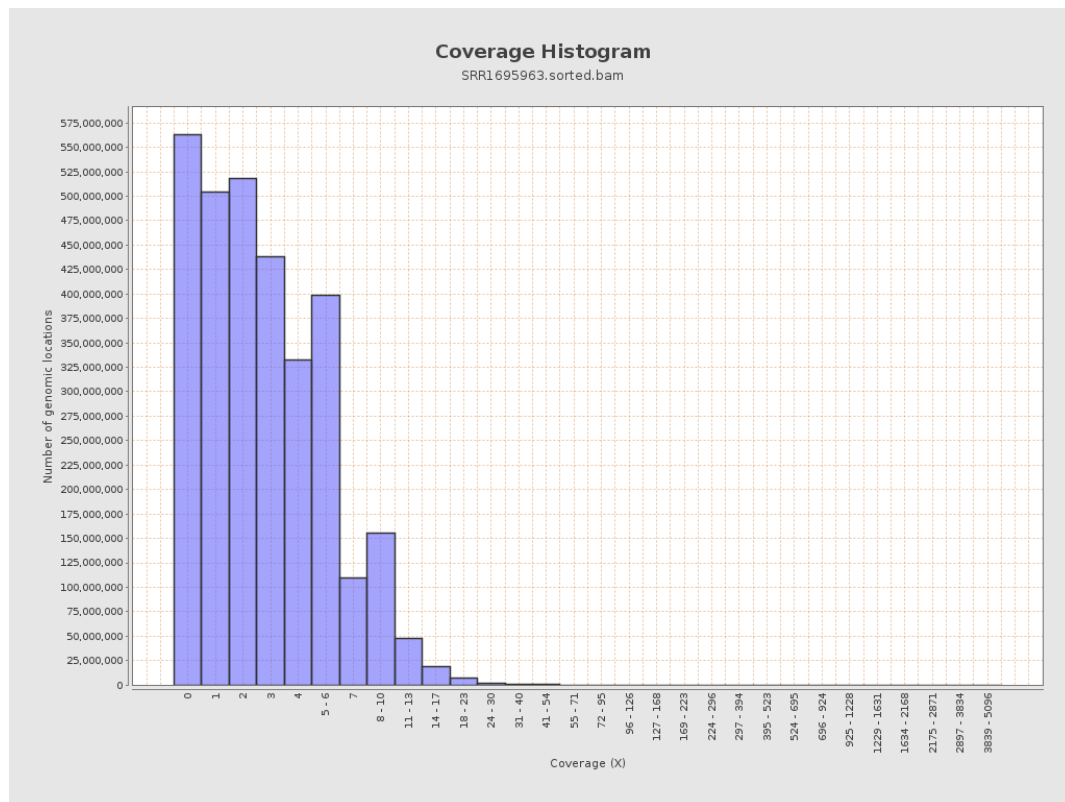
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 828183179    | 3.3227          | 6.5151           |
| chr2  | 243199373 | 849938953    | 3.4948          | 4.9552           |
| chr3  | 198022430 | 644398329    | 3.2542          | 2.8717           |
| chr4  | 191154276 | 569843794    | 2.9811          | 4.2549           |
| chr5  | 180915260 | 572520187    | 3.1646          | 2.8454           |
| chr6  | 171115067 | 567418557    | 3.316           | 3.7              |
| chr7  | 159138663 | 501388413    | 3.1506          | 3.3432           |
| chr8  | 146364022 | 486461637    | 3.3236          | 3.2479           |
| chr9  | 141213431 | 400006700    | 2.8326          | 4.2347           |
| chr10 | 135534747 | 451976744    | 3.3348          | 5.2677           |
| chr11 | 135006516 | 470716731    | 3.4866          | 3.5168           |
| chr12 | 133851895 | 466361381    | 3.4842          | 3.3316           |
| chr13 | 115169878 | 288993662    | 2.5093          | 2.8595           |
| chr14 | 107349540 | 303766997    | 2.8297          | 3.1078           |
| chr15 | 102531392 | 304305158    | 2.9679          | 3.2611           |
| chr16 | 90354753  | 297096997    | 3.2881          | 4.4756           |
| chr17 | 81195210  | 295319425    | 3.6372          | 5.2847           |
| chr18 | 78077248  | 252186077    | 3.23            | 7.0537           |
| chr19 | 59128983  | 210691576    | 3.5633          | 5.4182           |
| chr20 | 63025520  | 227672354    | 3.6124          | 3.6357           |
| chr21 | 48129895  | 119226623    | 2.4772          | 6.1642           |
| chr22 | 51304566  | 126698504    | 2.4695          | 3.3155           |
| chrMT | 16571     | 9309717      | 561.8078        | 167.0246         |
| chrX  | 155270560 | 298381343    | 1.9217          | 2.2481           |

|      |          |          |       |        |
|------|----------|----------|-------|--------|
| chrY | 59373566 | 56464051 | 0.951 | 5.1335 |
|------|----------|----------|-------|--------|

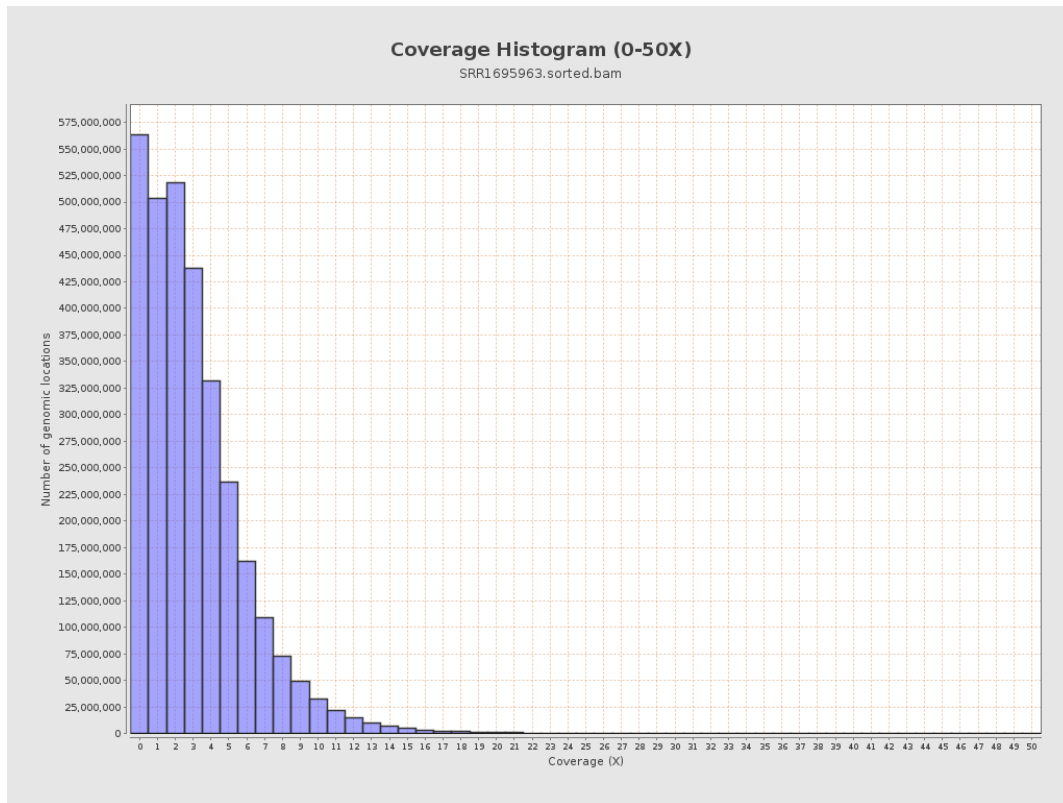
### 3. Results : Coverage across reference



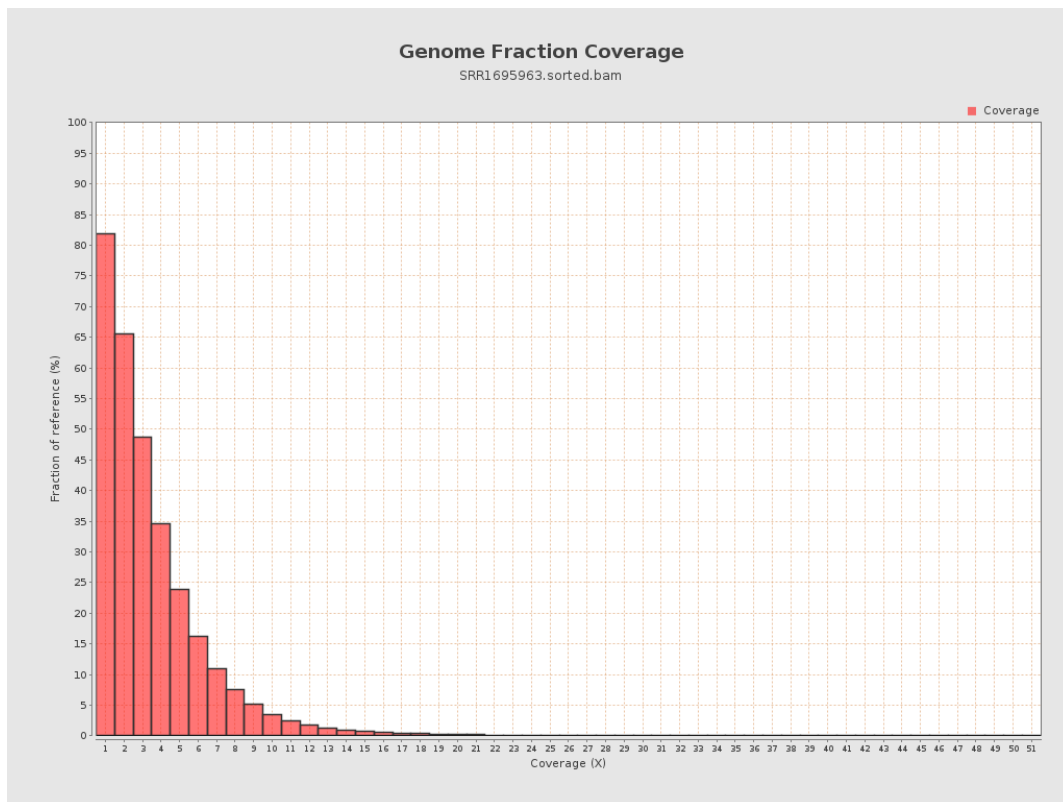
## 4. Results : Coverage Histogram



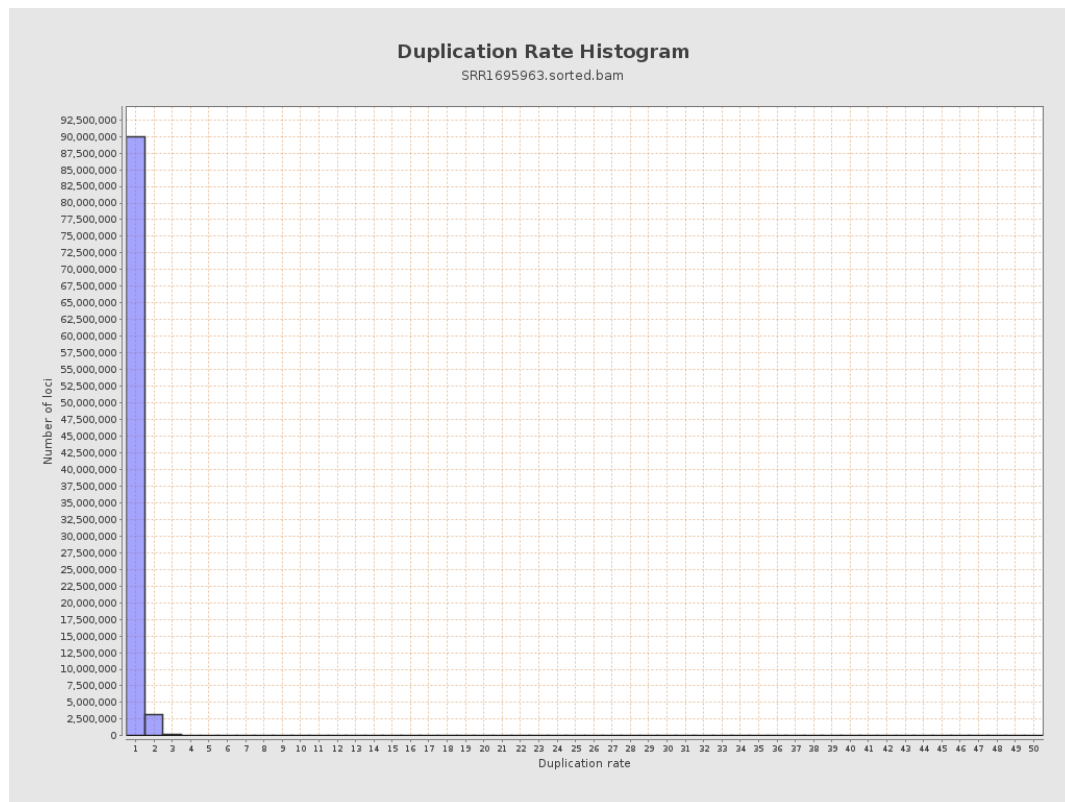
## 5. Results : Coverage Histogram (0-50X)



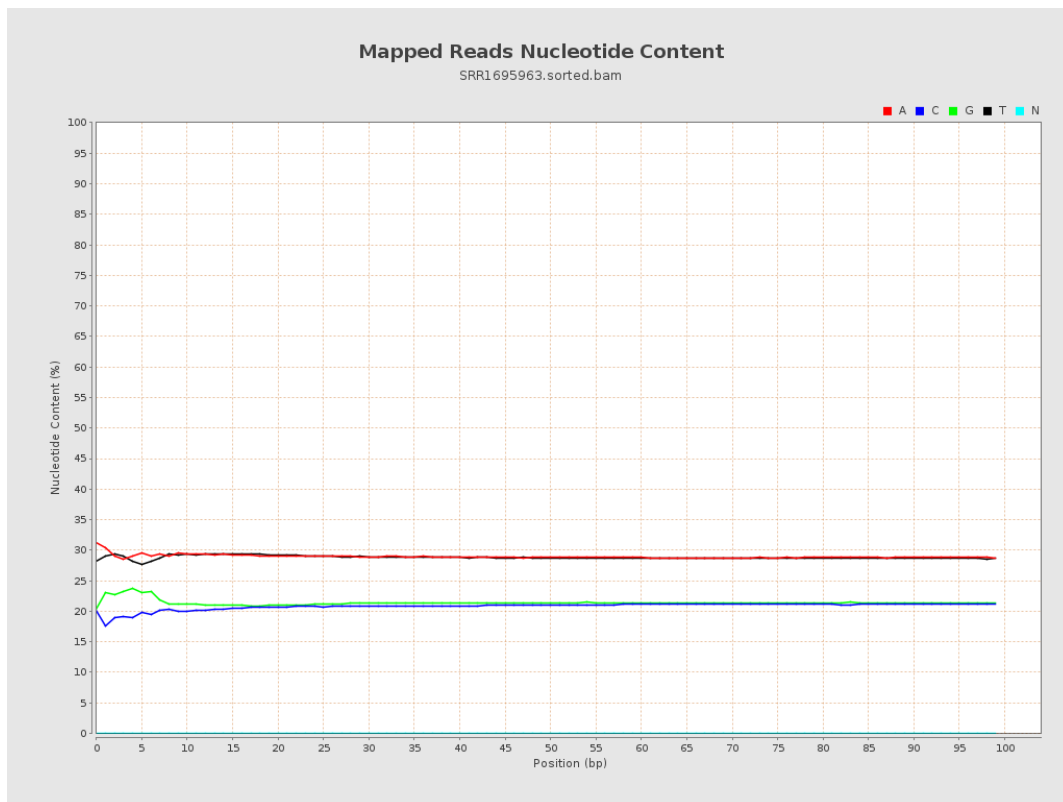
## 6. Results : Genome Fraction Coverage



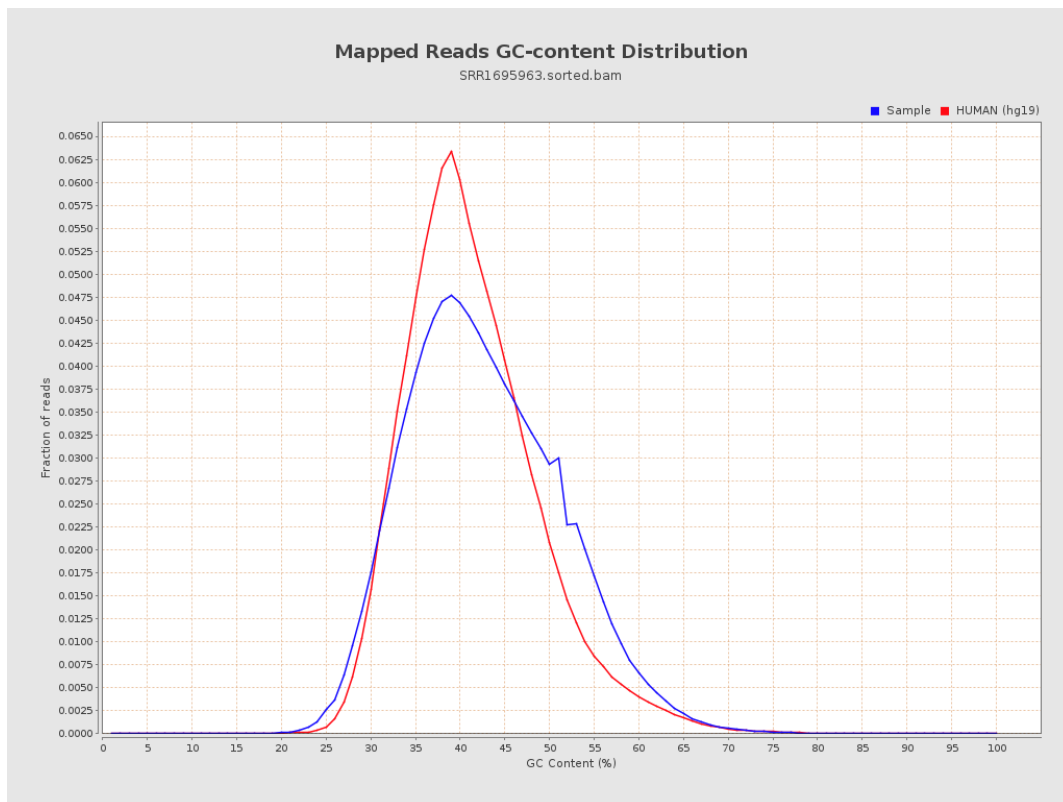
## 7. Results : Duplication Rate Histogram



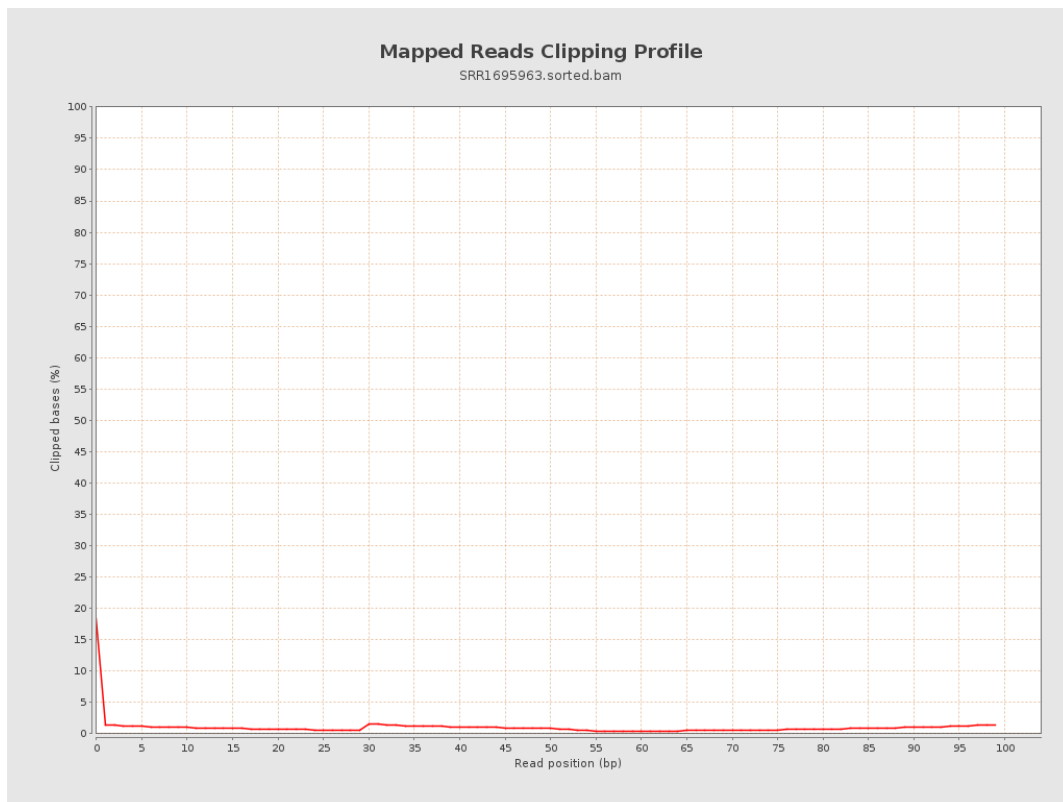
## 8. Results : Mapped Reads Nucleotide Content



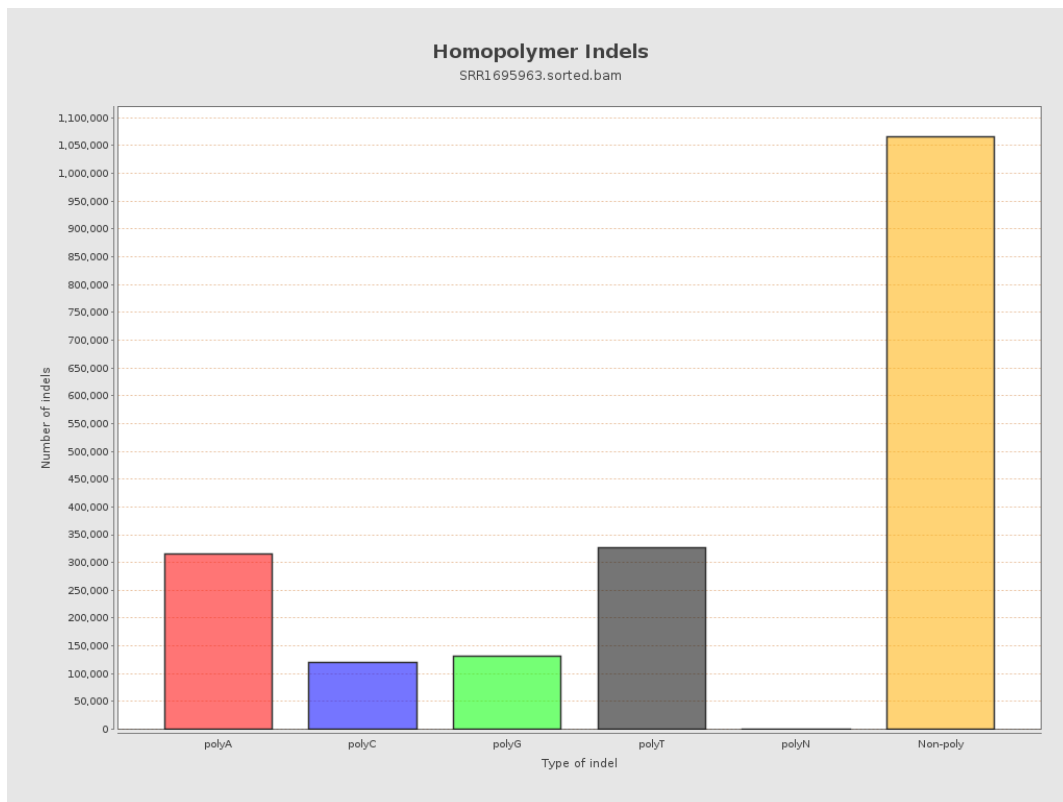
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



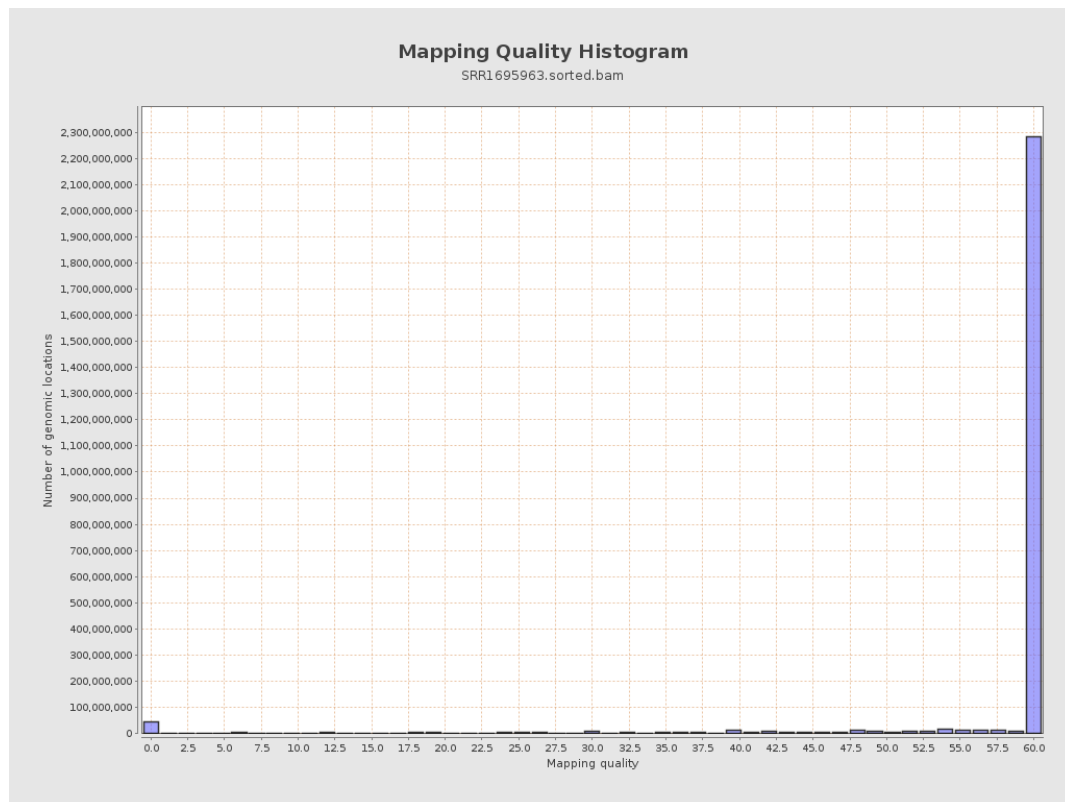
## 11. Results : Homopolymer Indels



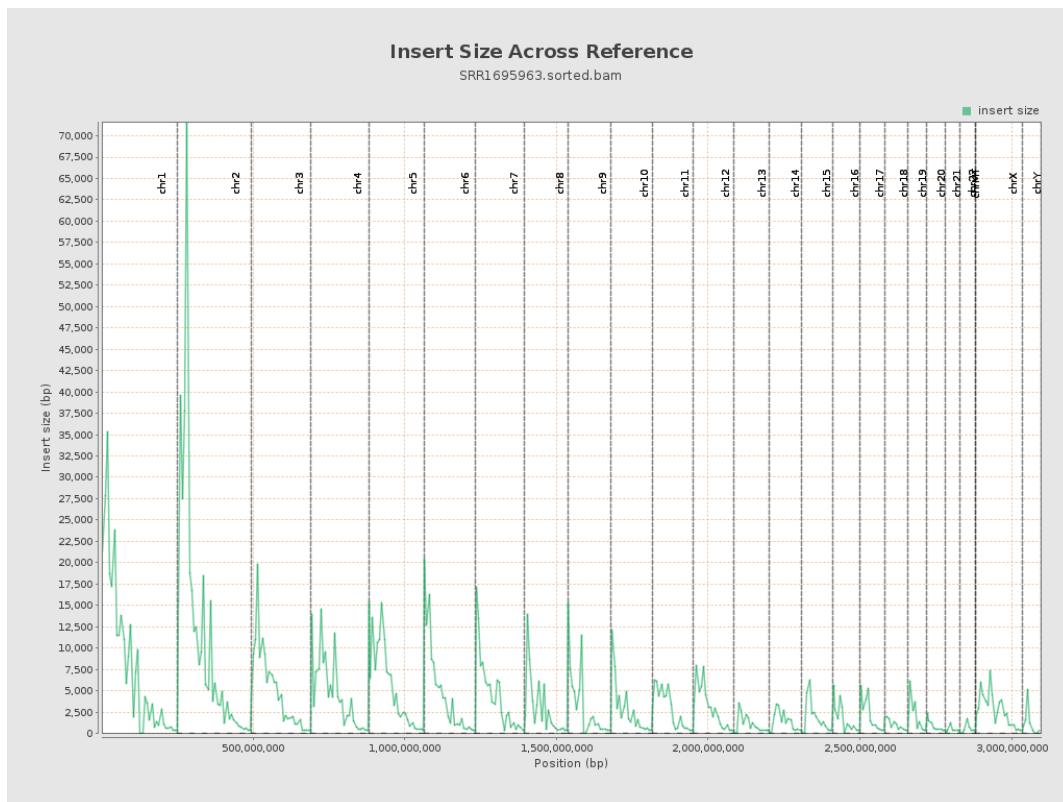
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

