

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/29 05:10:32*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472676.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_SRR3472676 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472676_1.fastq.gz SRR3472676_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                  |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                   |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                   |
| Analysis date:                        | Sun Sep 29 05:10:32 CST 2024                                                                                                                                                                                         |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                    |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                   |
| Number of windows:                    | 400                                                                                                                                                                                                                  |
| BAM file:                             | SRR3472676.sorted.bam                                                                                                                                                                                                |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 15,341,216          |
| Mapped reads                 | 15,229,247 / 99.27% |
| Unmapped reads               | 111,969 / 0.73%     |
| Mapped paired reads          | 15,229,247 / 99.27% |
| Mapped reads, first in pair  | 7,634,368 / 49.76%  |
| Mapped reads, second in pair | 7,594,879 / 49.51%  |
| Mapped reads, both in pair   | 15,156,832 / 98.8%  |
| Mapped reads, singletons     | 72,415 / 0.47%      |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 92,518 / 0.6%       |
| Read min/max/mean length     | 30 / 101 / 99.78    |
| Duplicated reads (estimated) | 10,400,086 / 67.79% |
| Duplication rate             | 49.43%              |
| Clipped reads                | 1,110,461 / 7.24%   |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 412,692,538 / 27.54% |
| Number/percentage of C's | 338,155,666 / 22.57% |
| Number/percentage of T's | 413,222,550 / 27.58% |
| Number/percentage of G's | 334,010,454 / 22.29% |
| Number/percentage of N's | 286,156 / 0.02%      |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 44.86% |
|---------------|--------|

## 2.3. Coverage

|                    |         |
|--------------------|---------|
| Mean               | 0.4841  |
| Standard Deviation | 23.3942 |

## 2.4. Mapping Quality

|                      |      |
|----------------------|------|
| Mean Mapping Quality | 54.7 |
|----------------------|------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 21,017.5        |
| Standard Deviation | 1,366,926       |
| P25/Median/P75     | 154 / 211 / 284 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.59%     |
| Mismatches                               | 8,688,134 |
| Insertions                               | 92,825    |
| Mapped reads with at least one insertion | 0.6%      |
| Deletions                                | 78,062    |
| Mapped reads with at least one deletion  | 0.51%     |
| Homopolymer indels                       | 45.98%    |

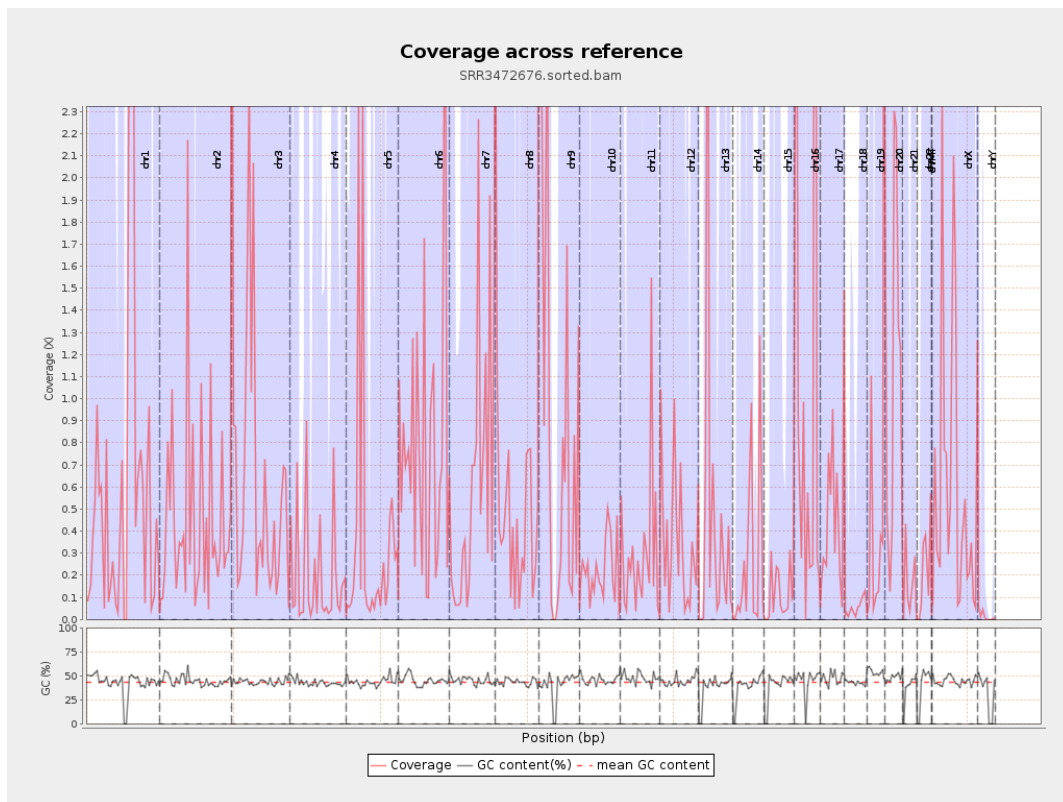
## 2.7. Chromosome stats

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

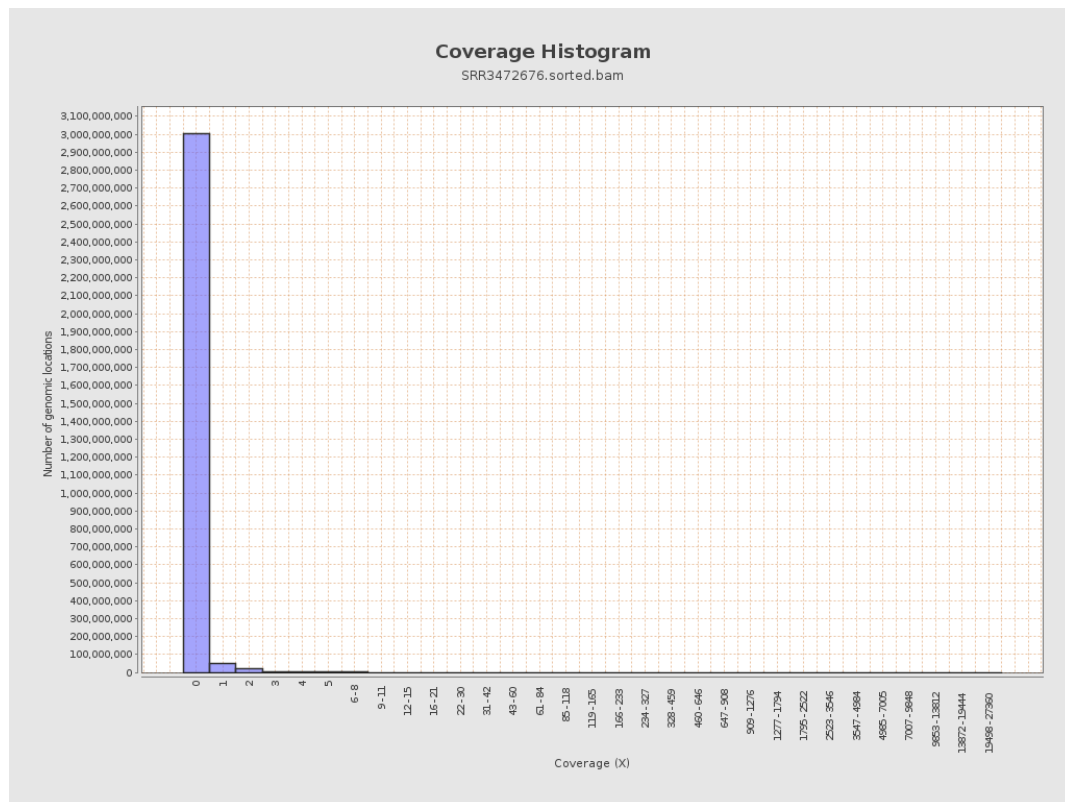
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 149505448    | 0.5998          | 33.688           |
| chr2  | 243199373 | 109736879    | 0.4512          | 24.4759          |
| chr3  | 198022430 | 131966244    | 0.6664          | 19.932           |
| chr4  | 191154276 | 36886522     | 0.193           | 11.004           |
| chr5  | 180915260 | 65071412     | 0.3597          | 19.768           |
| chr6  | 171115067 | 132684036    | 0.7754          | 24.9526          |
| chr7  | 159138663 | 98455624     | 0.6187          | 24.542           |
| chr8  | 146364022 | 64077702     | 0.4378          | 18.5999          |
| chr9  | 141213431 | 142926998    | 1.0121          | 43.7385          |
| chr10 | 135534747 | 30307553     | 0.2236          | 9.608            |
| chr11 | 135006516 | 41028880     | 0.3039          | 12.8797          |
| chr12 | 133851895 | 47924102     | 0.358           | 13.4309          |
| chr13 | 115169878 | 53190240     | 0.4618          | 26.5008          |
| chr14 | 107349540 | 26163494     | 0.2437          | 22.8647          |
| chr15 | 102531392 | 11256477     | 0.1098          | 7.75             |
| chr16 | 90354753  | 105953472    | 1.1726          | 48.6329          |
| chr17 | 81195210  | 38473988     | 0.4738          | 12.7711          |
| chr18 | 78077248  | 4274111      | 0.0547          | 2.4511           |
| chr19 | 59128983  | 23505159     | 0.3975          | 15.9432          |
| chr20 | 63025520  | 71089373     | 1.1279          | 29.4472          |
| chr21 | 48129895  | 7769897      | 0.1614          | 8.5033           |
| chr22 | 51304566  | 11483426     | 0.2238          | 7.9519           |
| chrMT | 16571     | 3817         | 0.2303          | 0.6132           |
| chrX  | 155270560 | 93939723     | 0.605           | 20.2454          |

|      |          |        |        |        |
|------|----------|--------|--------|--------|
| chrY | 59373566 | 901213 | 0.0152 | 1.1317 |
|------|----------|--------|--------|--------|

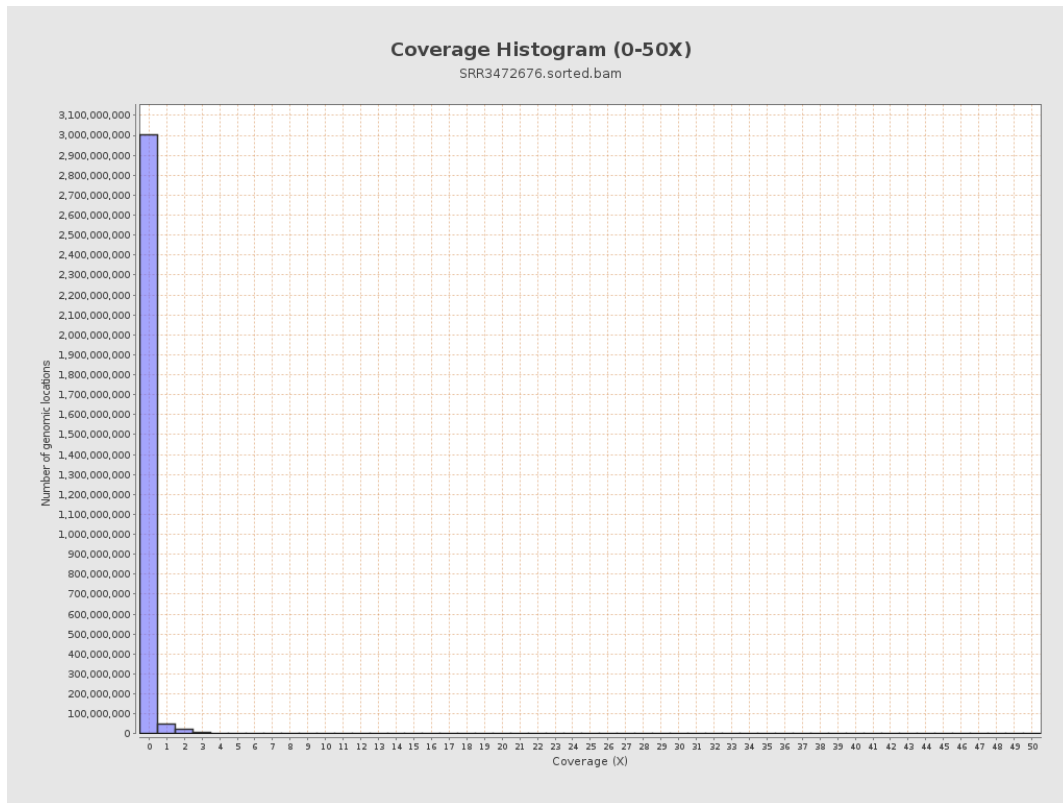
### 3. Results : Coverage across reference



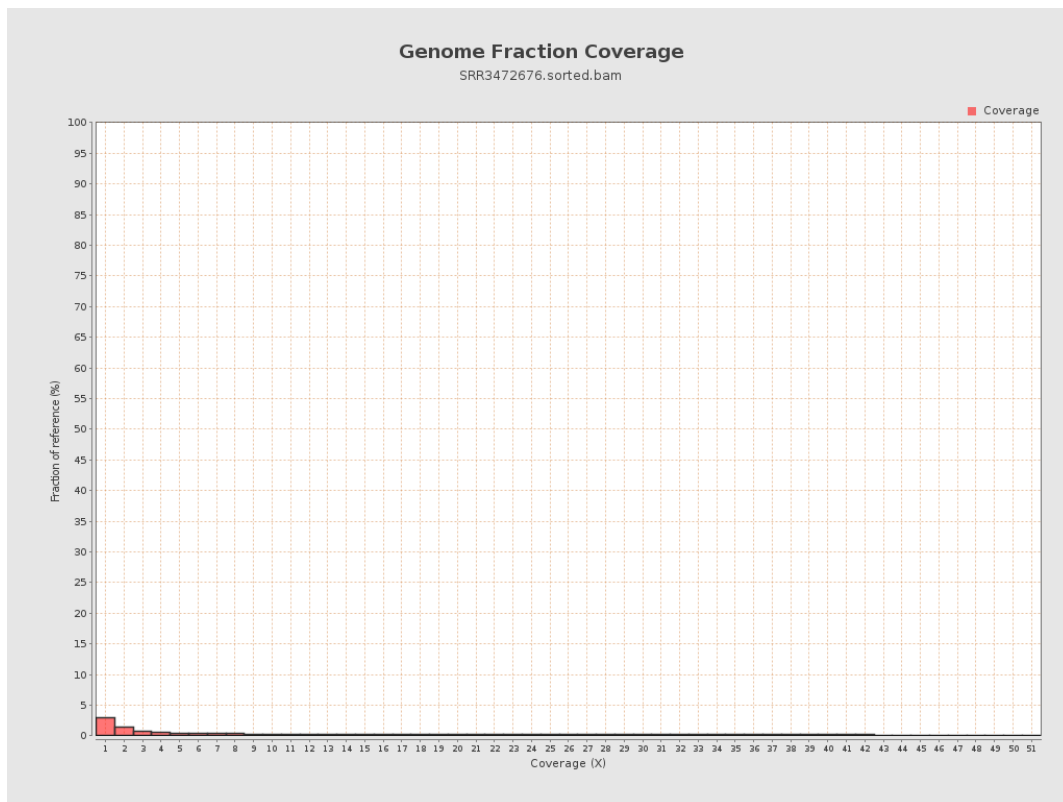
## 4. Results : Coverage Histogram



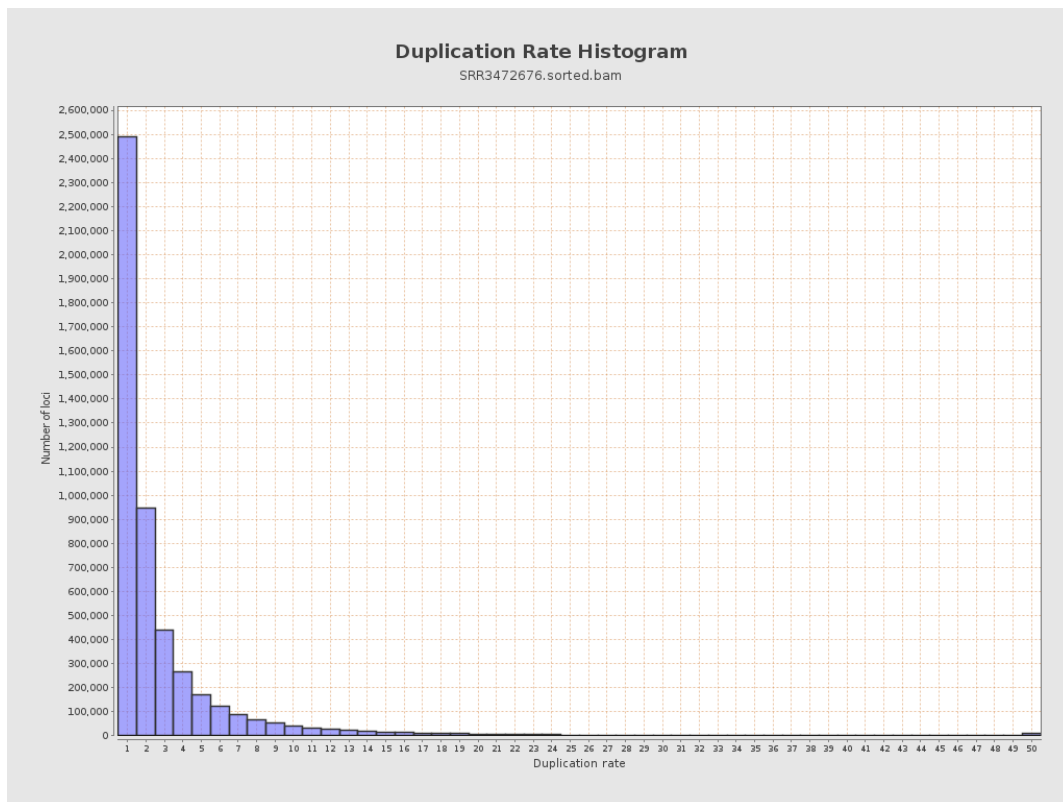
## 5. Results : Coverage Histogram (0-50X)



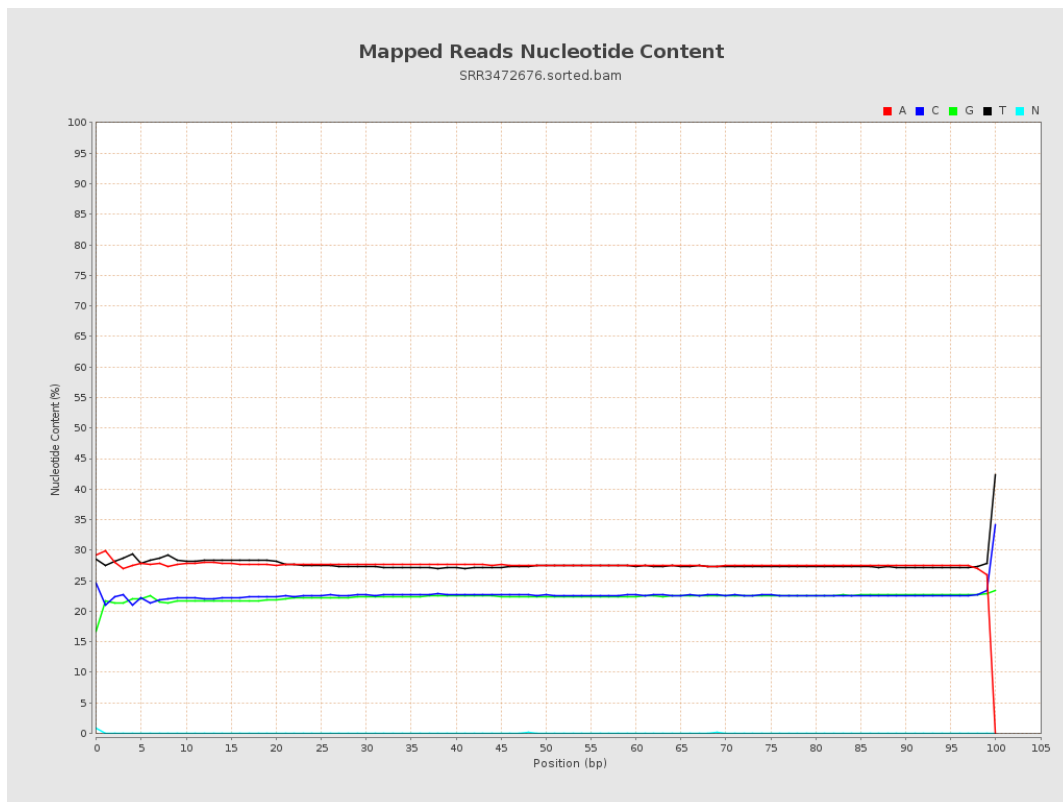
## 6. Results : Genome Fraction Coverage



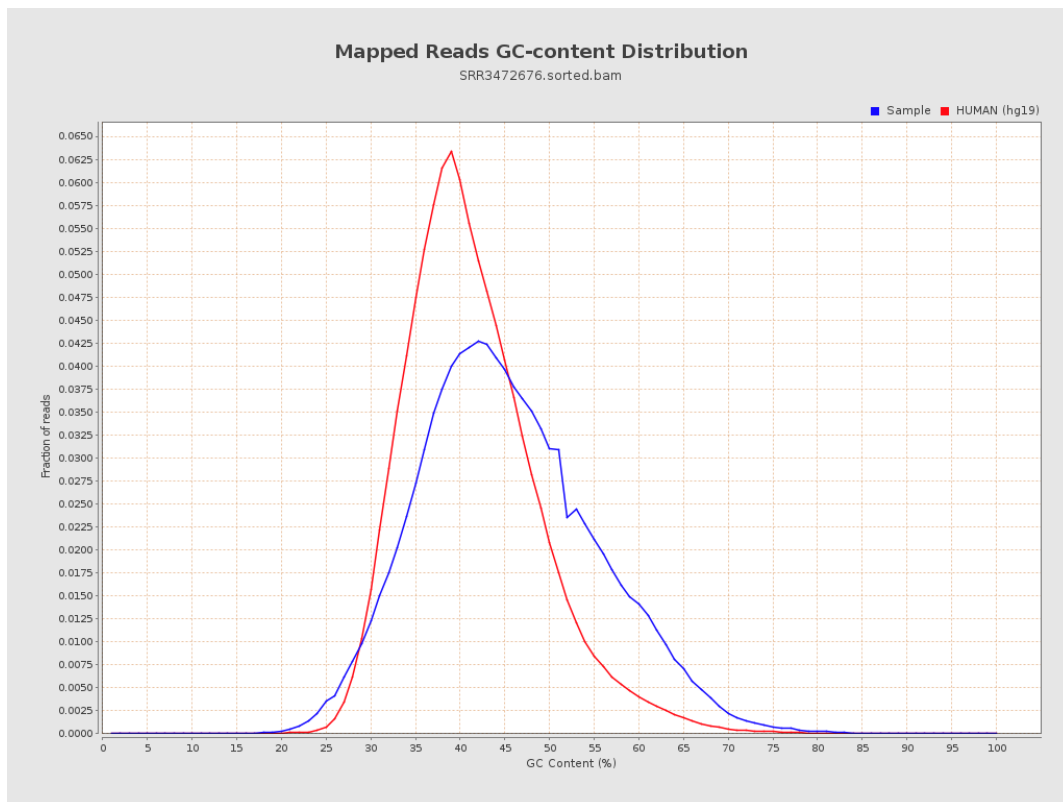
## 7. Results : Duplication Rate Histogram



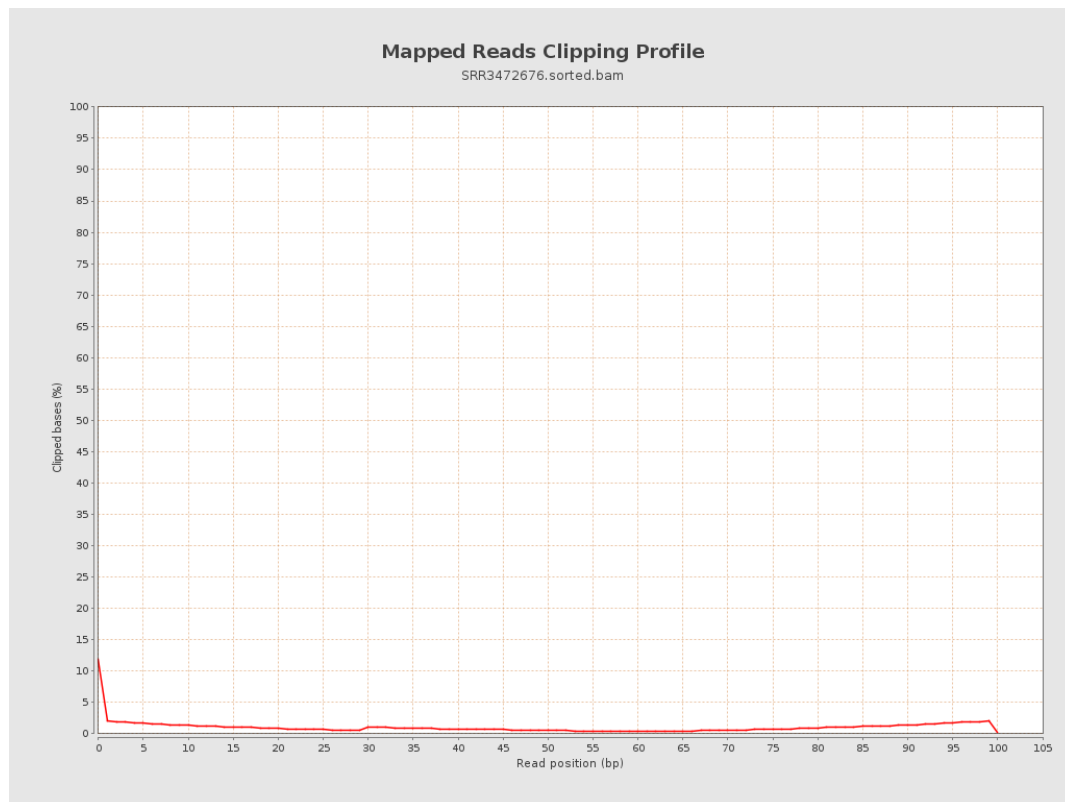
## 8. Results : Mapped Reads Nucleotide Content



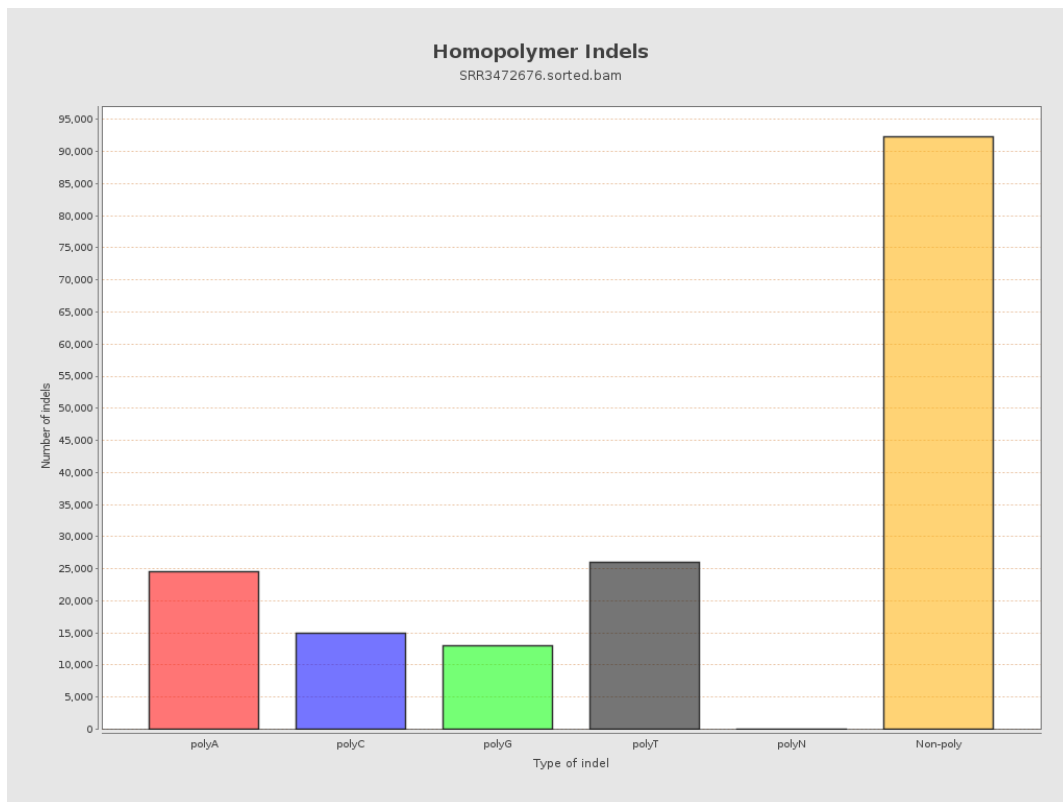
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



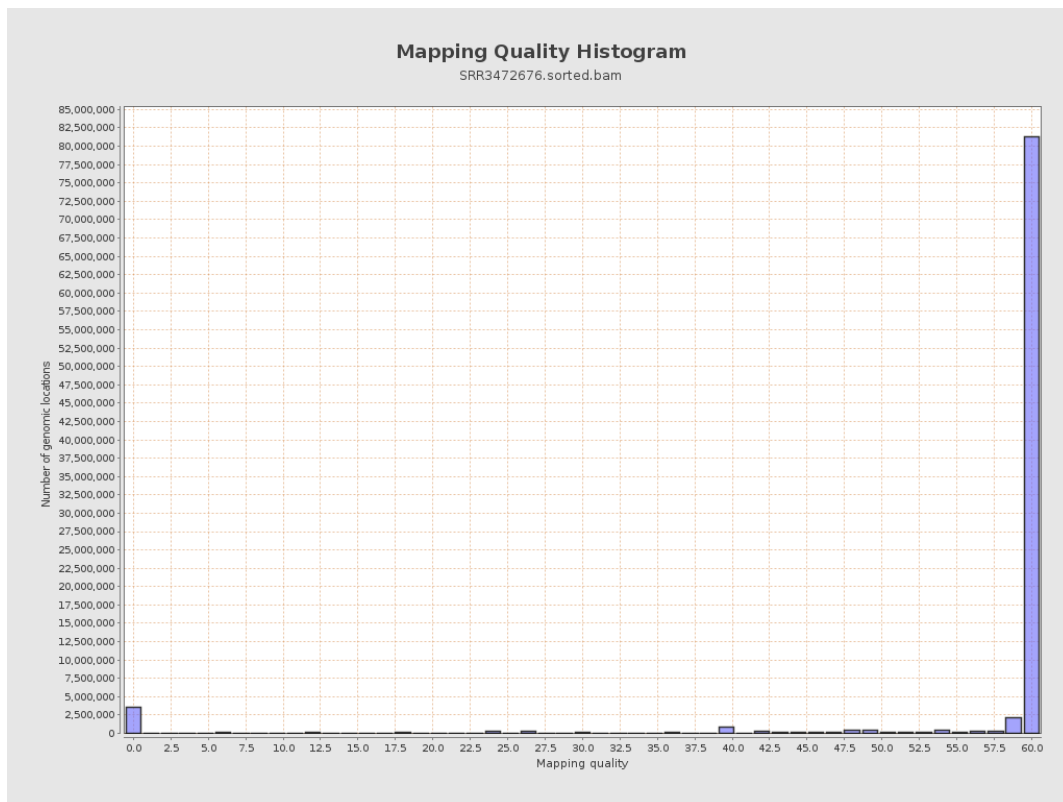
## 11. Results : Homopolymer Indels



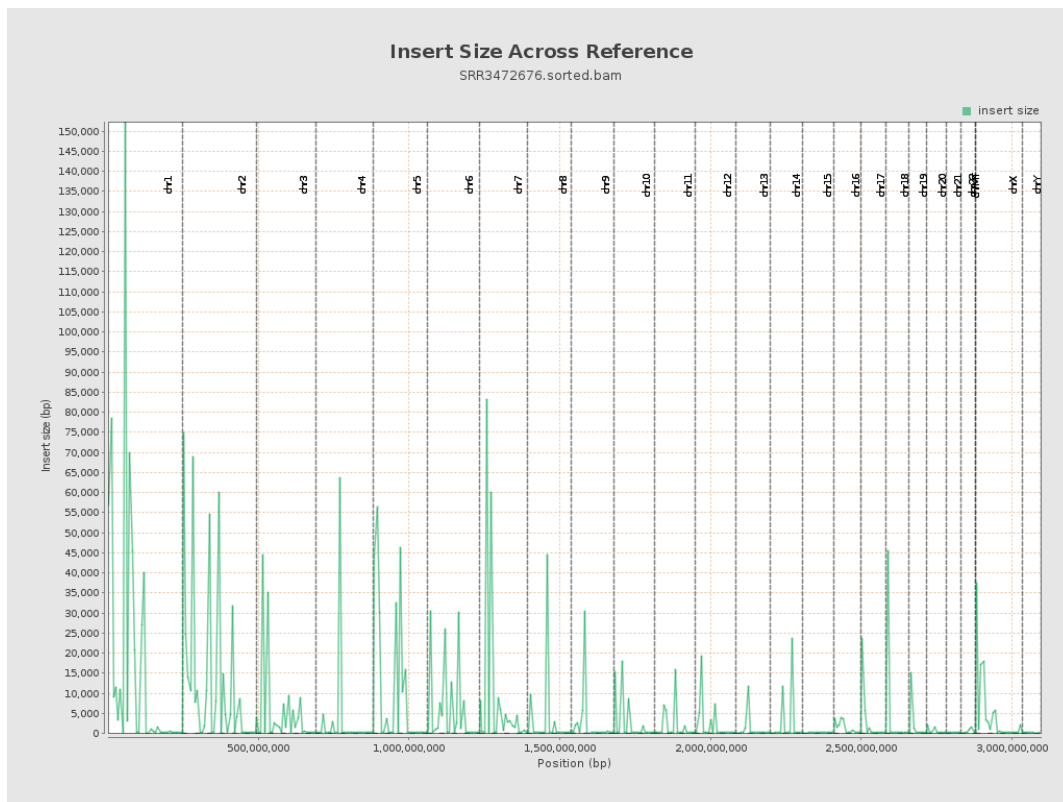
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

