

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 03:55:47*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472405.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_SRR3472405 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472405_1.fastq.gz SRR3472405_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                  |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                   |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                   |
| Analysis date:                        | Fri Aug 23 03:55:45 CST 2024                                                                                                                                                                                         |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                    |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                   |
| Number of windows:                    | 400                                                                                                                                                                                                                  |
| BAM file:                             | SRR3472405.sorted.bam                                                                                                                                                                                                |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 18,137,966          |
| Mapped reads                 | 18,004,500 / 99.26% |
| Unmapped reads               | 133,466 / 0.74%     |
| Mapped paired reads          | 18,004,500 / 99.26% |
| Mapped reads, first in pair  | 9,027,545 / 49.77%  |
| Mapped reads, second in pair | 8,976,955 / 49.49%  |
| Mapped reads, both in pair   | 17,924,156 / 98.82% |
| Mapped reads, singletons     | 80,344 / 0.44%      |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 60,162 / 0.33%      |
| Read min/max/mean length     | 30 / 100 / 99.36    |
| Duplicated reads (estimated) | 11,449,238 / 63.12% |
| Duplication rate             | 47.12%              |
| Clipped reads                | 1,203,234 / 6.63%   |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 470,304,933 / 26.62% |
| Number/percentage of C's | 414,493,987 / 23.46% |
| Number/percentage of T's | 471,624,978 / 26.69% |
| Number/percentage of G's | 410,077,945 / 23.21% |
| Number/percentage of N's | 215,854 / 0.01%      |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 46.67% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.5708 |
| Standard Deviation | 18.144 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 55.03 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 15,815.69       |
| Standard Deviation | 1,263,885.2     |
| P25/Median/P75     | 150 / 206 / 275 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.53%     |
| Mismatches                               | 9,104,367 |
| Insertions                               | 95,179    |
| Mapped reads with at least one insertion | 0.52%     |
| Deletions                                | 85,261    |
| Mapped reads with at least one deletion  | 0.47%     |
| Homopolymer indels                       | 46.23%    |

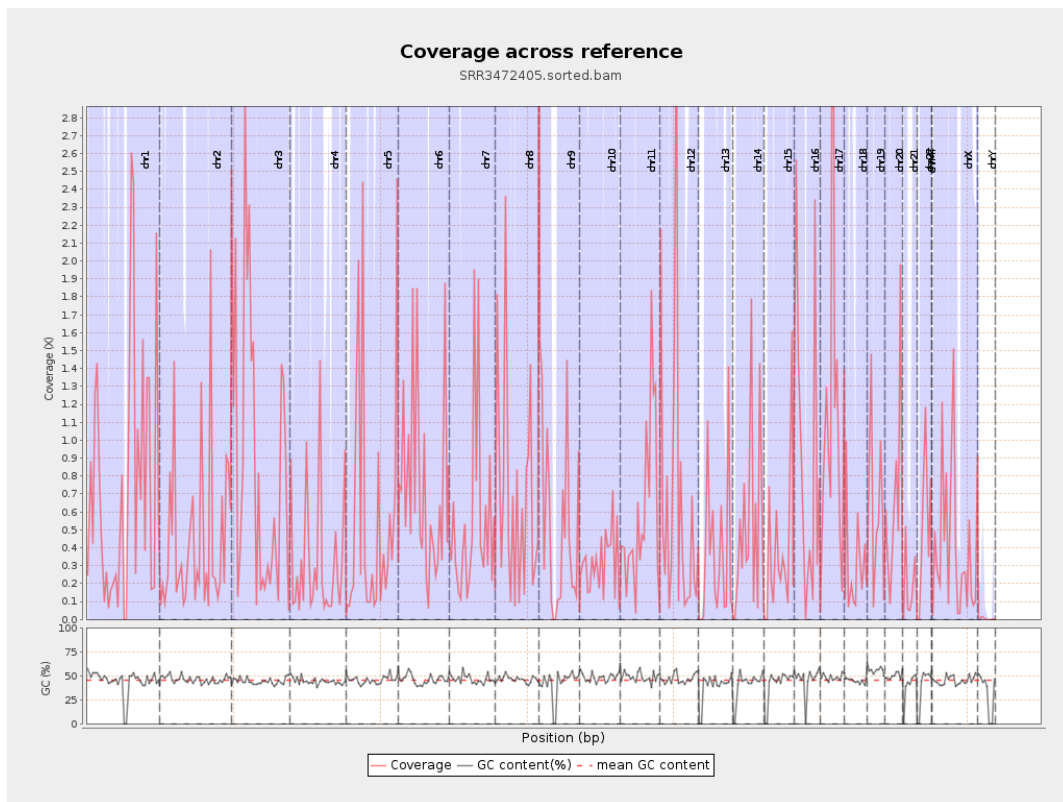
## 2.7. Chromosome stats

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

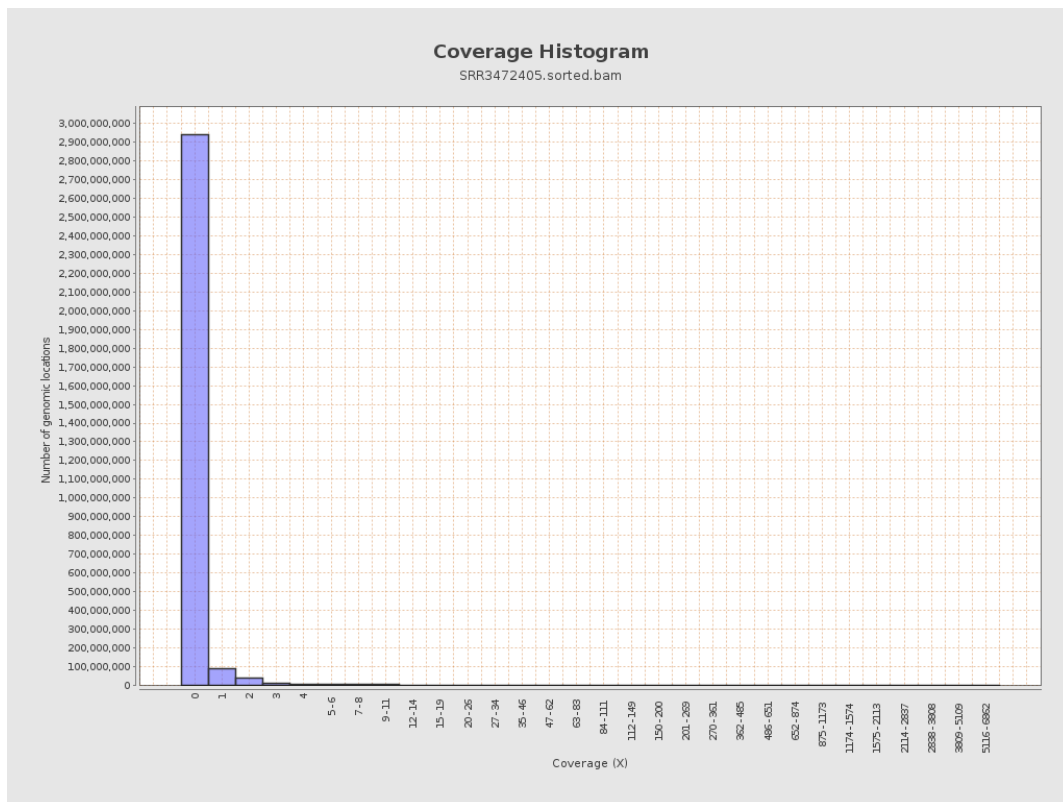
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 186994144    | 0.7502          | 20.28            |
| chr2  | 243199373 | 108471355    | 0.446           | 15.6172          |
| chr3  | 198022430 | 178049590    | 0.8991          | 24.2521          |
| chr4  | 191154276 | 60915405     | 0.3187          | 11.9025          |
| chr5  | 180915260 | 104874796    | 0.5797          | 20.6209          |
| chr6  | 171115067 | 125438015    | 0.7331          | 17.8673          |
| chr7  | 159138663 | 88721978     | 0.5575          | 21.3017          |
| chr8  | 146364022 | 101688627    | 0.6948          | 22.8201          |
| chr9  | 141213431 | 79902156     | 0.5658          | 15.6306          |
| chr10 | 135534747 | 43810240     | 0.3232          | 10.3071          |
| chr11 | 135006516 | 81411836     | 0.603           | 20.8953          |
| chr12 | 133851895 | 91239742     | 0.6816          | 18.9423          |
| chr13 | 115169878 | 40947687     | 0.3555          | 15.2299          |
| chr14 | 107349540 | 53137636     | 0.495           | 15.1486          |
| chr15 | 102531392 | 41986714     | 0.4095          | 14.8266          |
| chr16 | 90354753  | 79747577     | 0.8826          | 21.102           |
| chr17 | 81195210  | 96537398     | 1.189           | 29.6084          |
| chr18 | 78077248  | 24637684     | 0.3156          | 9.2115           |
| chr19 | 59128983  | 39548746     | 0.6689          | 15.5617          |
| chr20 | 63025520  | 41274502     | 0.6549          | 24.1172          |
| chr21 | 48129895  | 9347679      | 0.1942          | 9.6316           |
| chr22 | 51304566  | 26464962     | 0.5158          | 14.5846          |
| chrMT | 16571     | 2658         | 0.1604          | 0.5292           |
| chrX  | 155270560 | 61463179     | 0.3958          | 11.191           |

|      |          |        |        |        |
|------|----------|--------|--------|--------|
| chrY | 59373566 | 302088 | 0.0051 | 0.2925 |
|------|----------|--------|--------|--------|

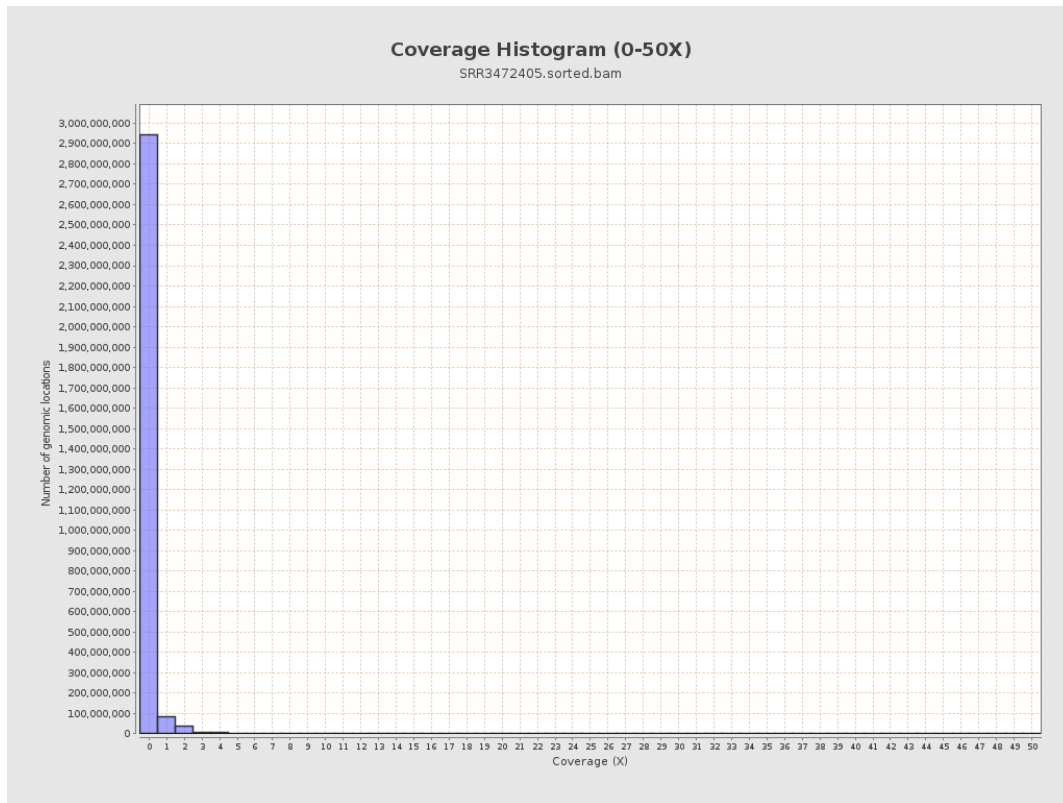
### 3. Results : Coverage across reference



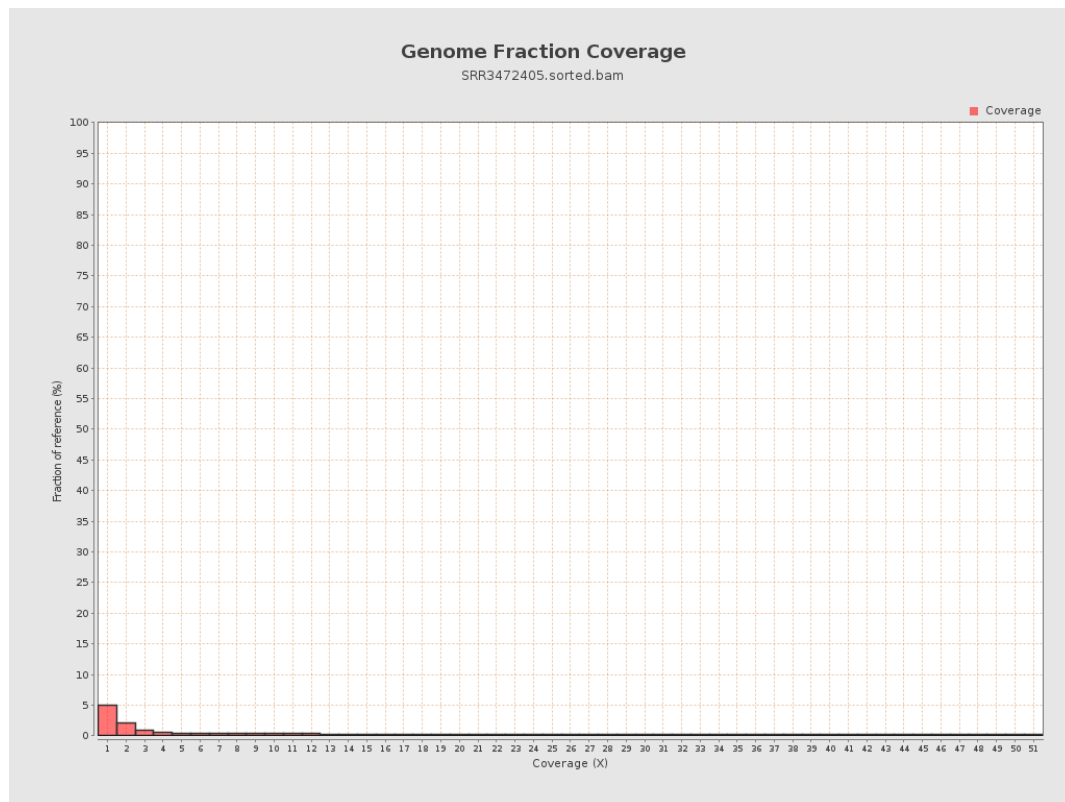
## 4. Results : Coverage Histogram



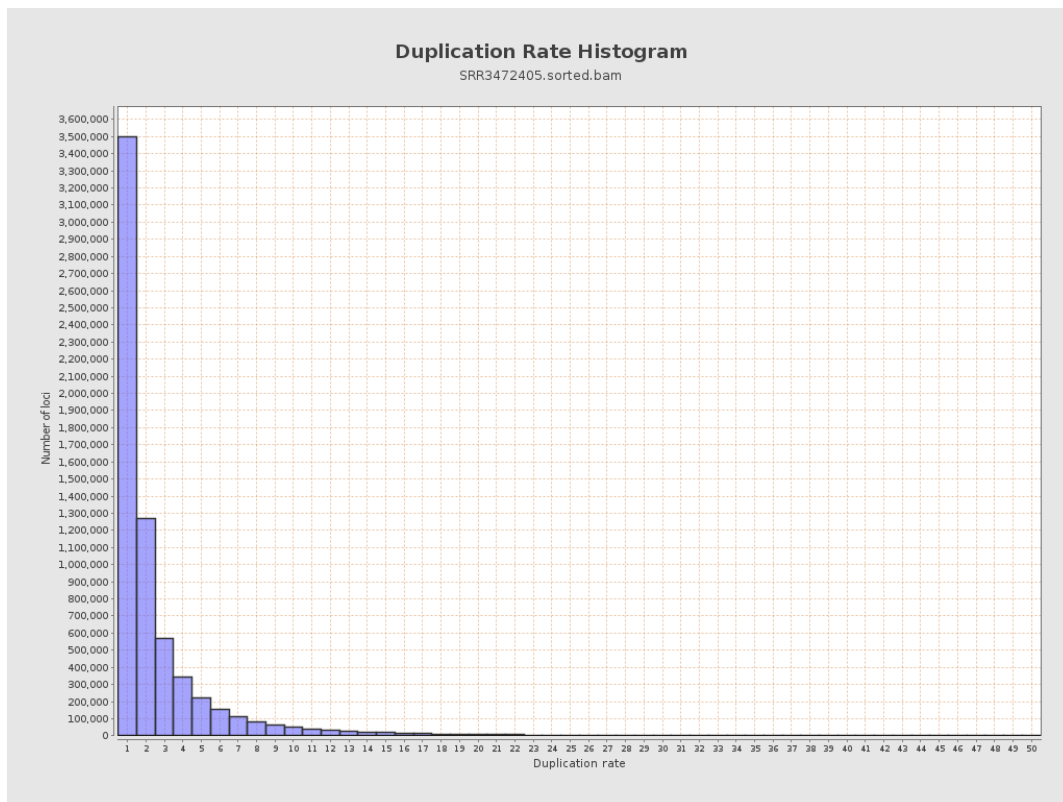
## 5. Results : Coverage Histogram (0-50X)



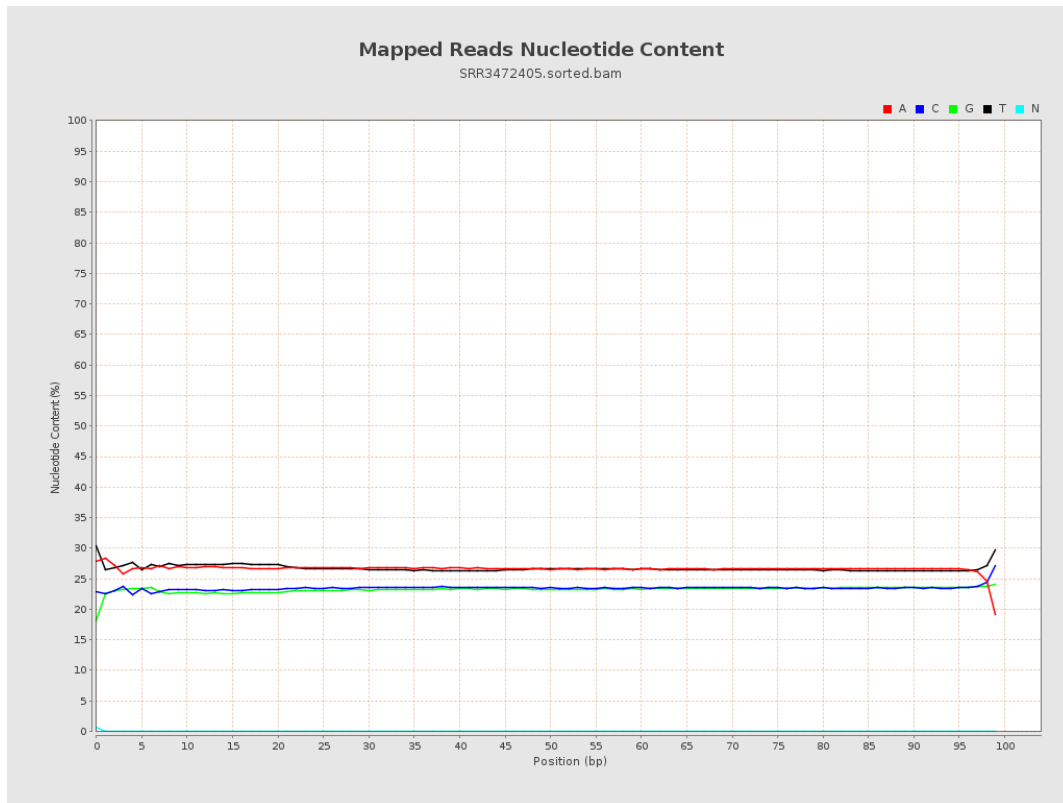
## 6. Results : Genome Fraction Coverage



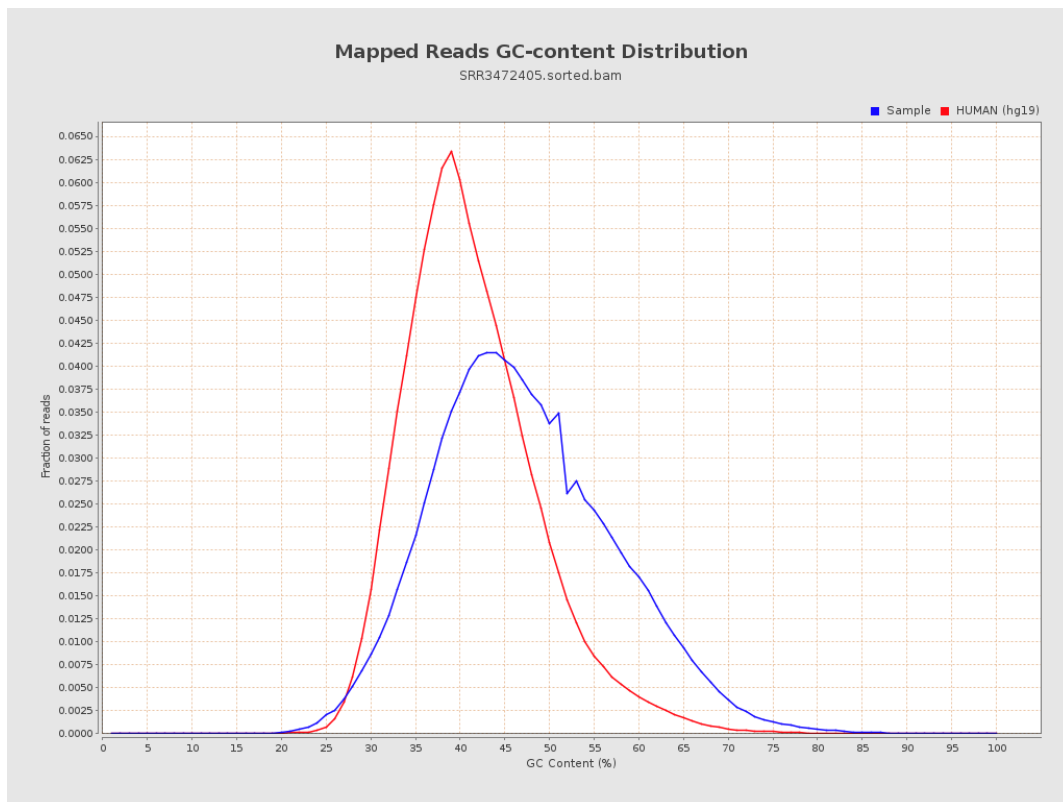
## 7. Results : Duplication Rate Histogram



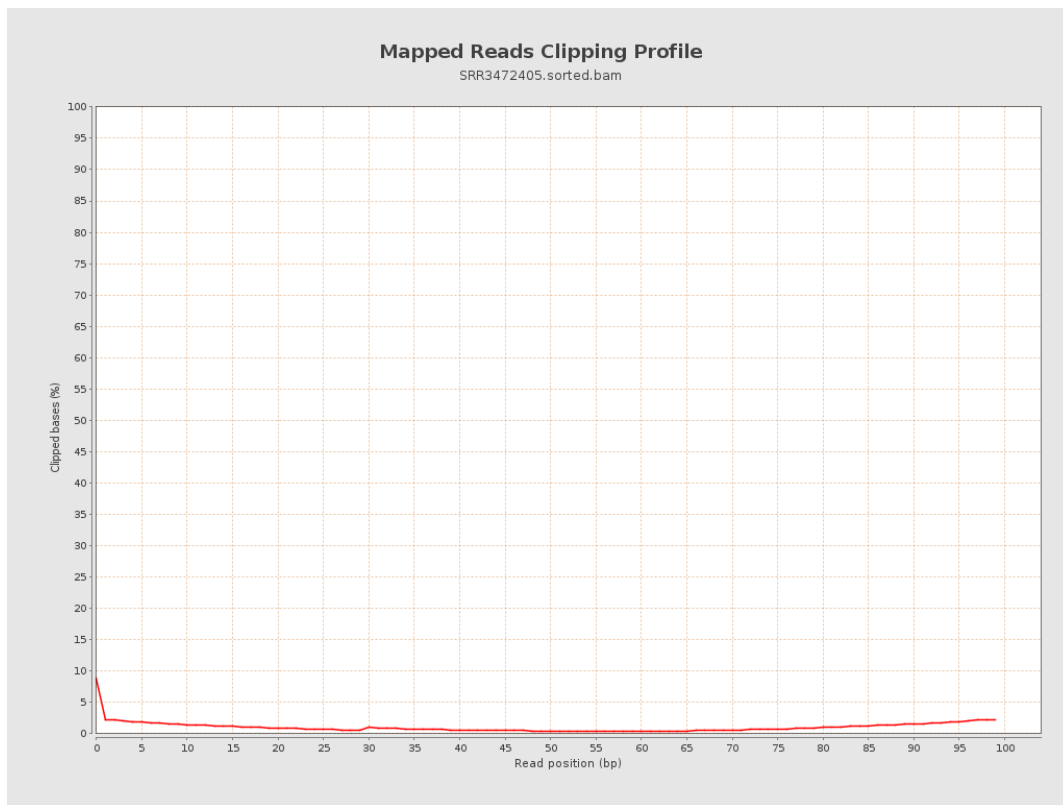
## 8. Results : Mapped Reads Nucleotide Content



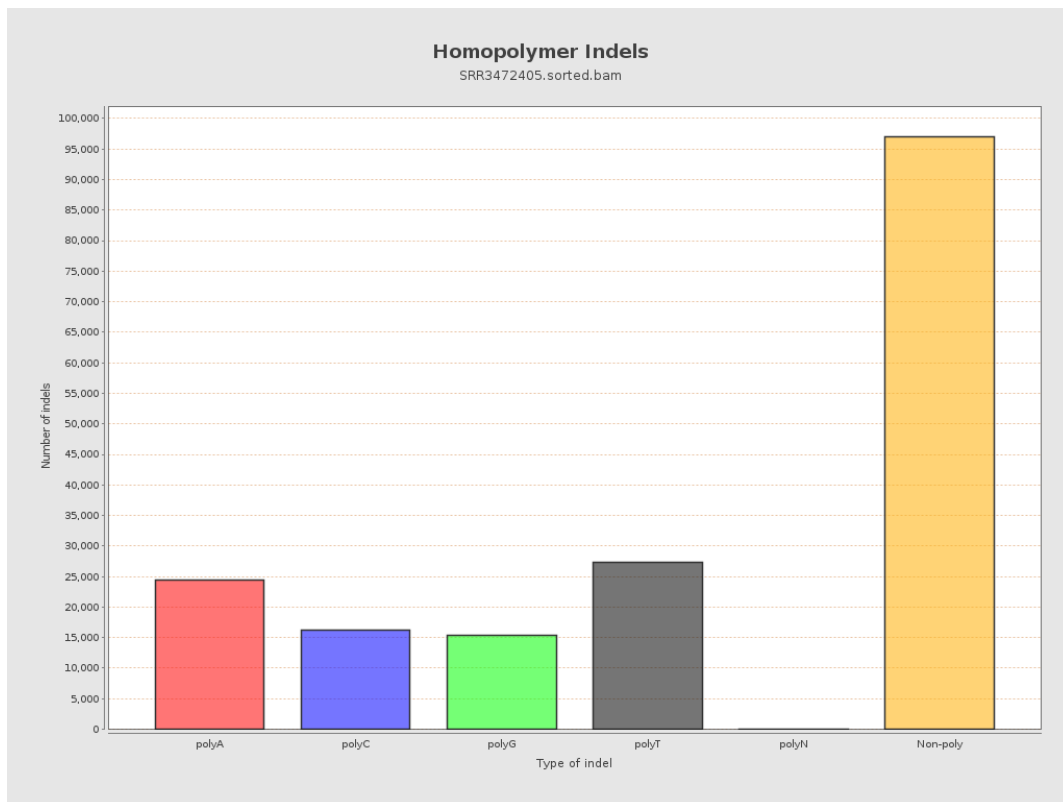
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



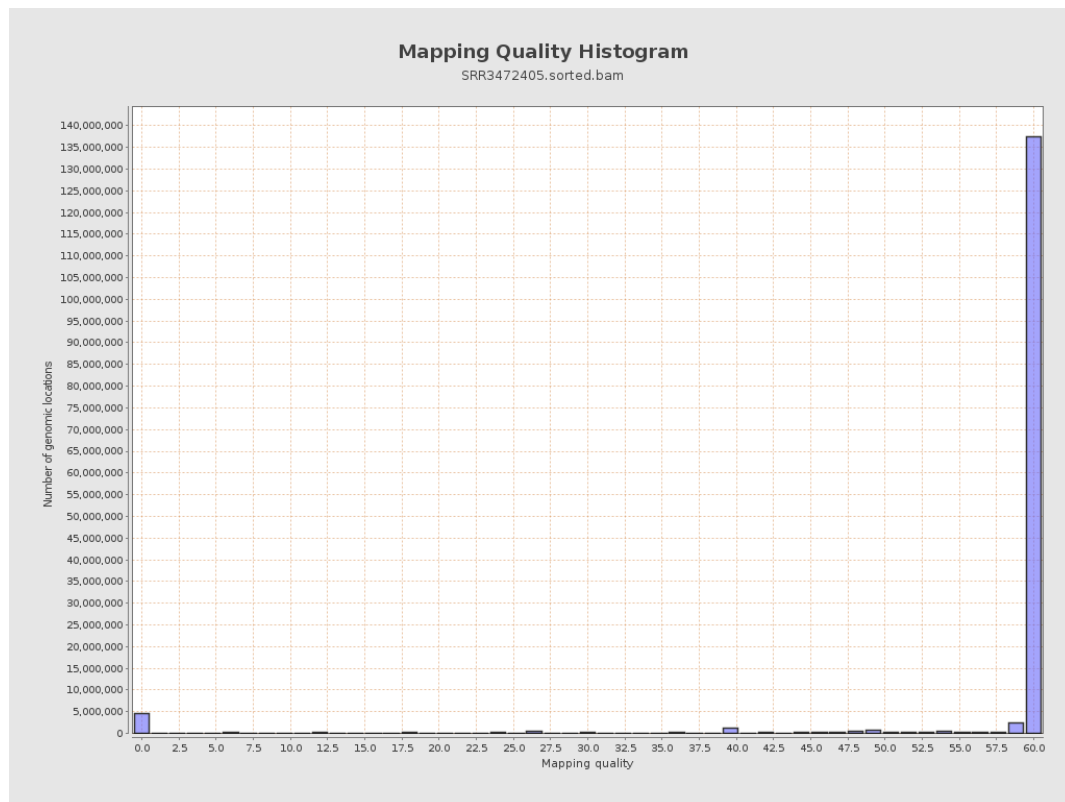
## 11. Results : Homopolymer Indels



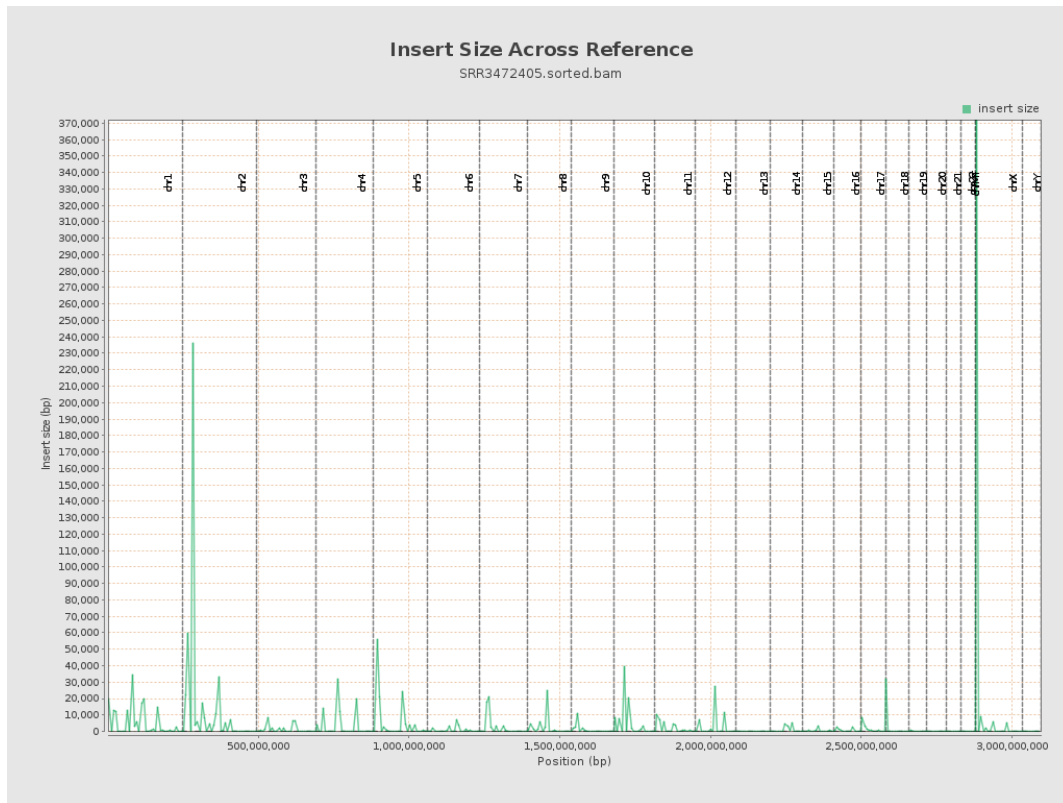
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

