

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/08 20:44:11*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR617405.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_SRR617405 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617405_1.fastq.gz SRR617405_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                               |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                |
| Analysis date:                        | Tue Oct 08 20:44:10 CST 2024                                                                                                                                                                                      |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                 |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                |
| Number of windows:                    | 400                                                                                                                                                                                                               |
| BAM file:                             | SRR617405.sorted.bam                                                                                                                                                                                              |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 32,000,000          |
| Mapped reads                 | 30,501,882 / 95.32% |
| Unmapped reads               | 1,498,118 / 4.68%   |
| Mapped paired reads          | 30,501,882 / 95.32% |
| Mapped reads, first in pair  | 15,358,864 / 48%    |
| Mapped reads, second in pair | 15,143,018 / 47.32% |
| Mapped reads, both in pair   | 30,019,720 / 93.81% |
| Mapped reads, singletons     | 482,162 / 1.51%     |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 504,213 / 1.58%     |
| Read min/max/mean length     | 30 / 100 / 100.65   |
| Duplicated reads (estimated) | 1,469,408 / 4.59%   |
| Duplication rate             | 4.29%               |
| Clipped reads                | 3,069,556 / 9.59%   |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 893,006,383 / 29.7%  |
| Number/percentage of C's | 605,250,295 / 20.13% |
| Number/percentage of T's | 886,527,630 / 29.49% |
| Number/percentage of G's | 616,512,331 / 20.51% |
| Number/percentage of N's | 5,162,684 / 0.17%    |
|                          |                      |

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

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.9714 |
| Standard Deviation | 2.9968 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 53.94 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 60,825.34       |
| Standard Deviation | 2,370,083.78    |
| P25/Median/P75     | 173 / 214 / 280 |

## 2.6. Mismatches and indels

|                                          |            |
|------------------------------------------|------------|
| General error rate                       | 0.91%      |
| Mismatches                               | 26,433,442 |
| Insertions                               | 724,182    |
| Mapped reads with at least one insertion | 2.35%      |
| Deletions                                | 297,701    |
| Mapped reads with at least one deletion  | 0.96%      |
| Homopolymer indels                       | 35.09%     |

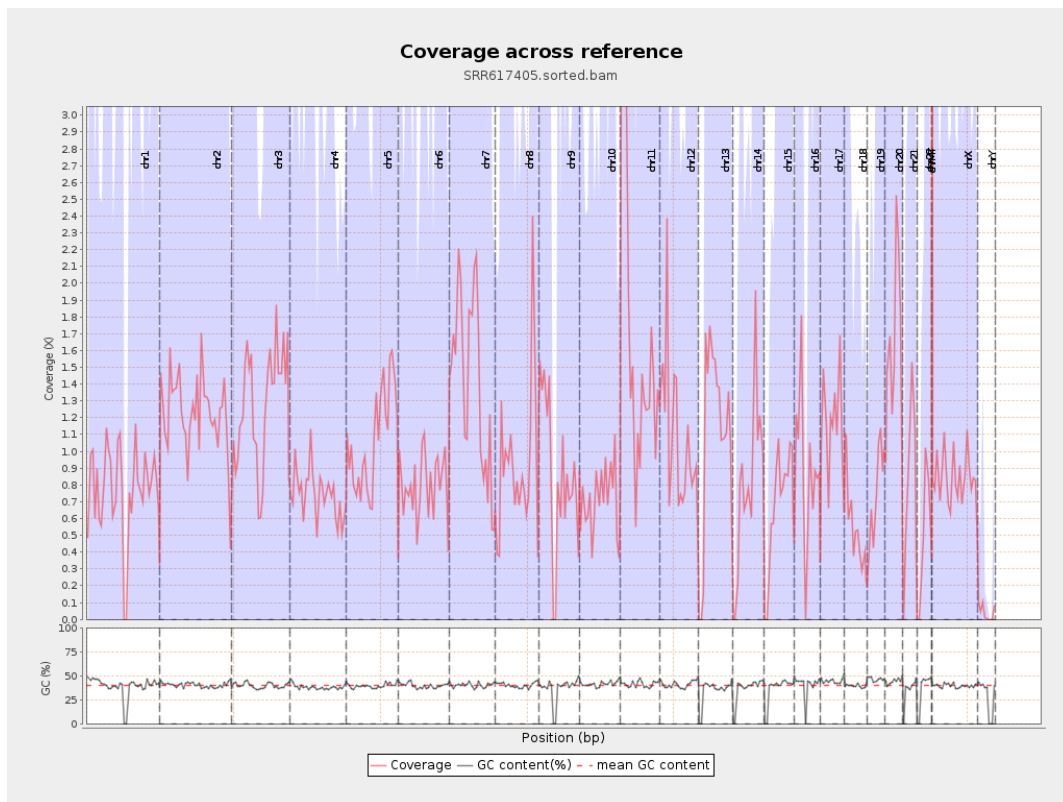
## 2.7. Chromosome stats

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

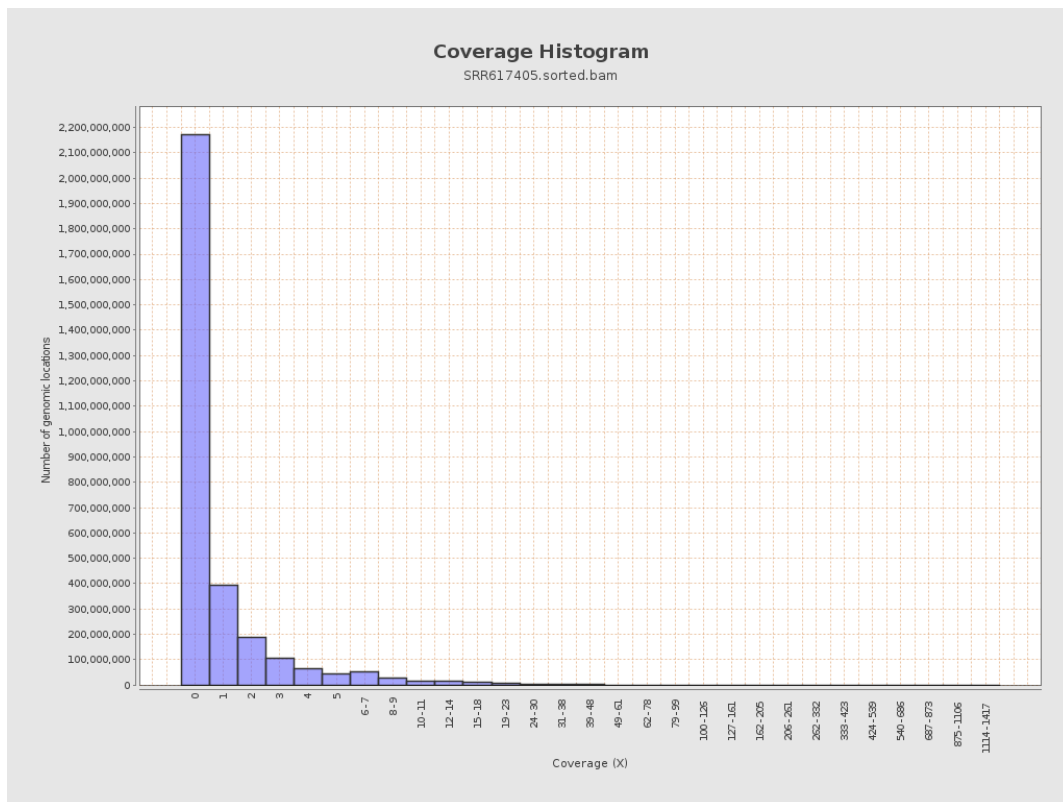
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 193794832    | 0.7775          | 2.8094           |
| chr2  | 243199373 | 299802410    | 1.2327          | 3.1949           |
| chr3  | 198022430 | 253080503    | 1.278           | 3.4982           |
| chr4  | 191154276 | 143160360    | 0.7489          | 2.3041           |
| chr5  | 180915260 | 191697941    | 1.0596          | 2.9006           |
| chr6  | 171115067 | 137401161    | 0.803           | 2.6519           |
| chr7  | 159138663 | 224594982    | 1.4113          | 3.2968           |
| chr8  | 146364022 | 132973526    | 0.9085          | 3.3305           |
| chr9  | 141213431 | 120081594    | 0.8504          | 2.6583           |
| chr10 | 135534747 | 96600168     | 0.7127          | 2.4731           |
| chr11 | 135006516 | 223314229    | 1.6541          | 3.916            |
| chr12 | 133851895 | 143495895    | 1.072           | 2.8614           |
| chr13 | 115169878 | 129777710    | 1.1268          | 2.8049           |
| chr14 | 107349540 | 87442461     | 0.8146          | 2.9723           |
| chr15 | 102531392 | 69360500     | 0.6765          | 2.4368           |
| chr16 | 90354753  | 76707026     | 0.849           | 3.4308           |
| chr17 | 81195210  | 93758214     | 1.1547          | 3.8324           |
| chr18 | 78077248  | 43025913     | 0.5511          | 2.0528           |
| chr19 | 59128983  | 43738198     | 0.7397          | 2.4172           |
| chr20 | 63025520  | 103685152    | 1.6451          | 4.917            |
| chr21 | 48129895  | 41076429     | 0.8534          | 2.5549           |
| chr22 | 51304566  | 24828501     | 0.4839          | 2.1768           |
| chrMT | 16571     | 194561       | 11.7411         | 5.695            |
| chrX  | 155270560 | 131135726    | 0.8446          | 2.5944           |

|      |          |         |        |        |
|------|----------|---------|--------|--------|
| chrY | 59373566 | 2405559 | 0.0405 | 0.6166 |
|------|----------|---------|--------|--------|

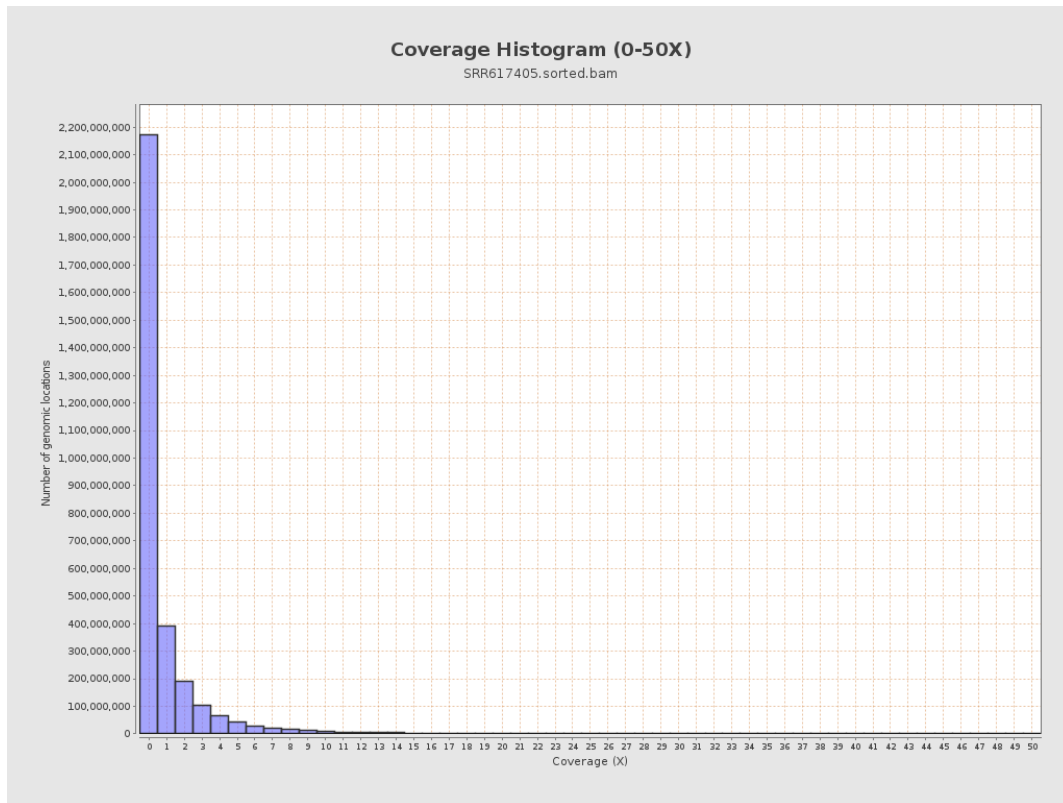
### 3. Results : Coverage across reference



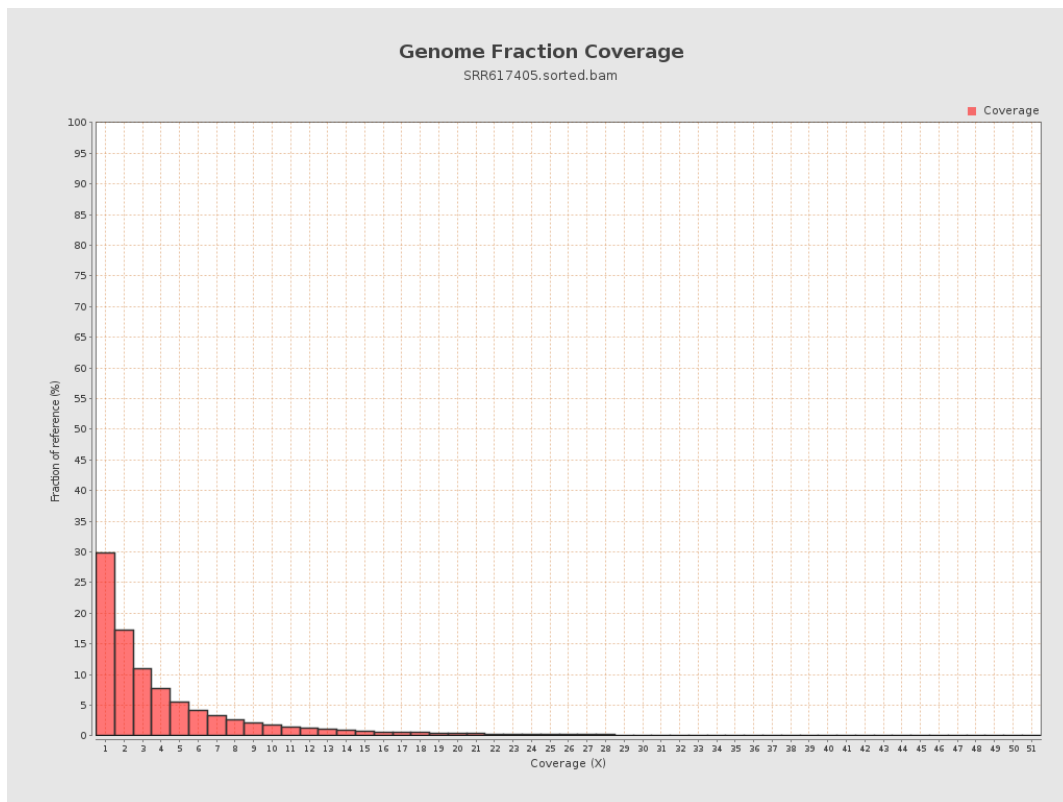
## 4. Results : Coverage Histogram



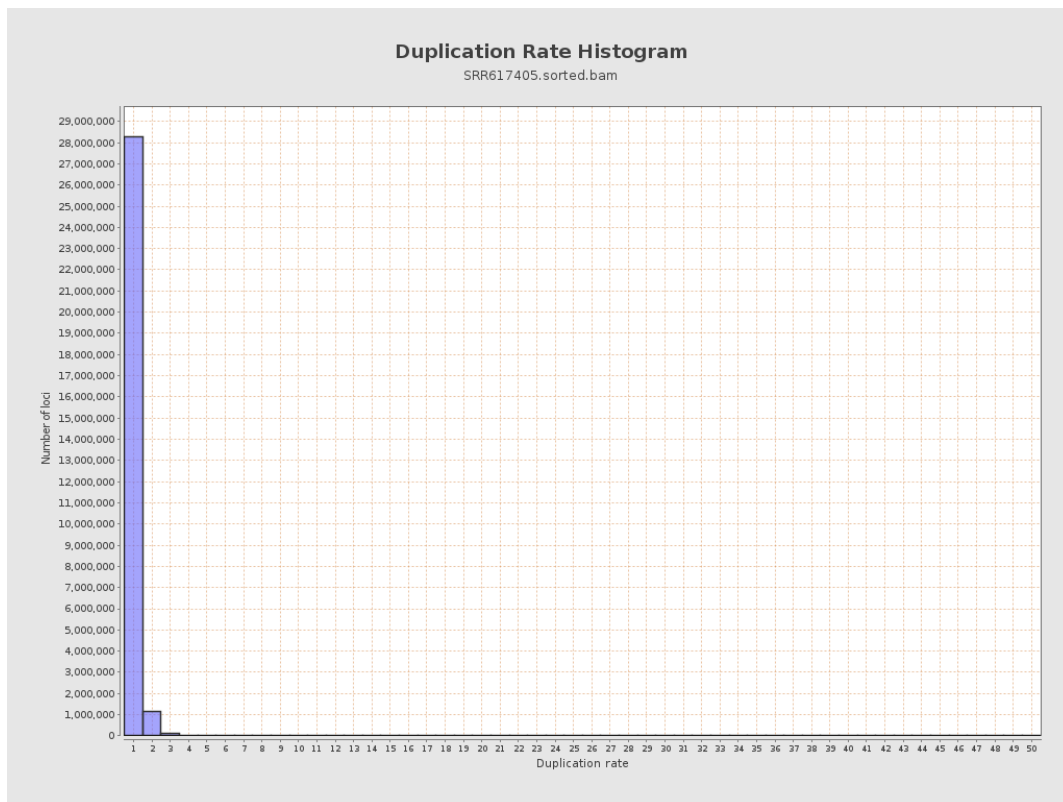
## 5. Results : Coverage Histogram (0-50X)



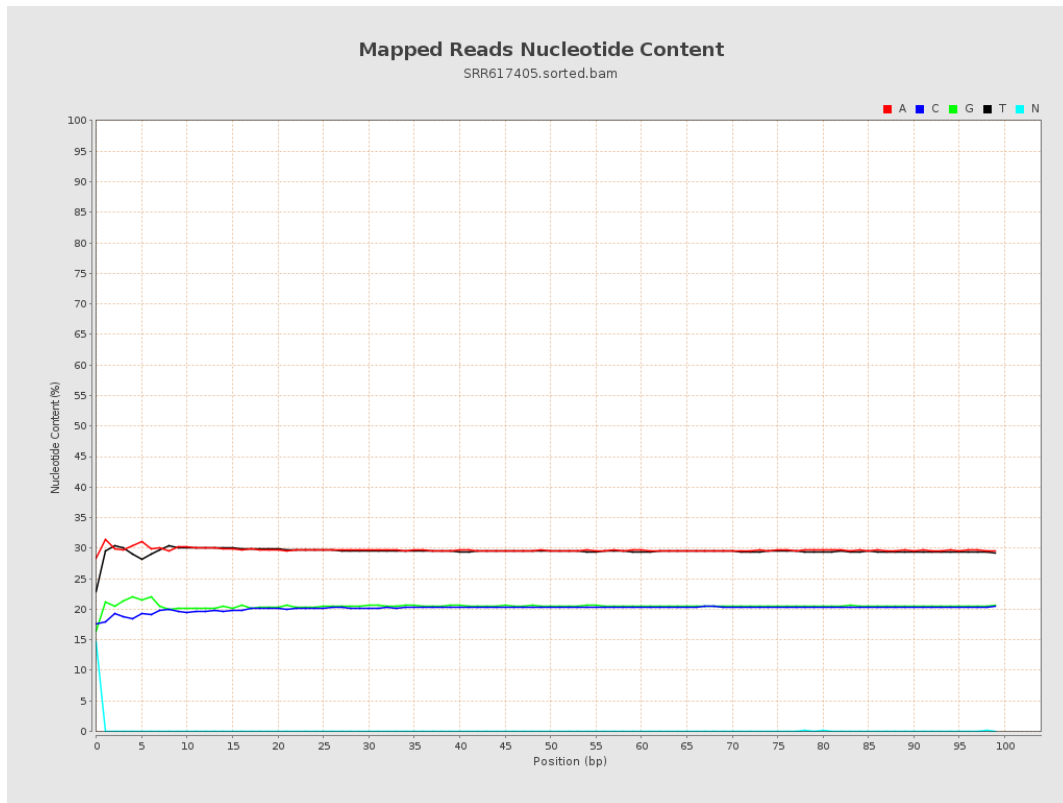
## 6. Results : Genome Fraction Coverage



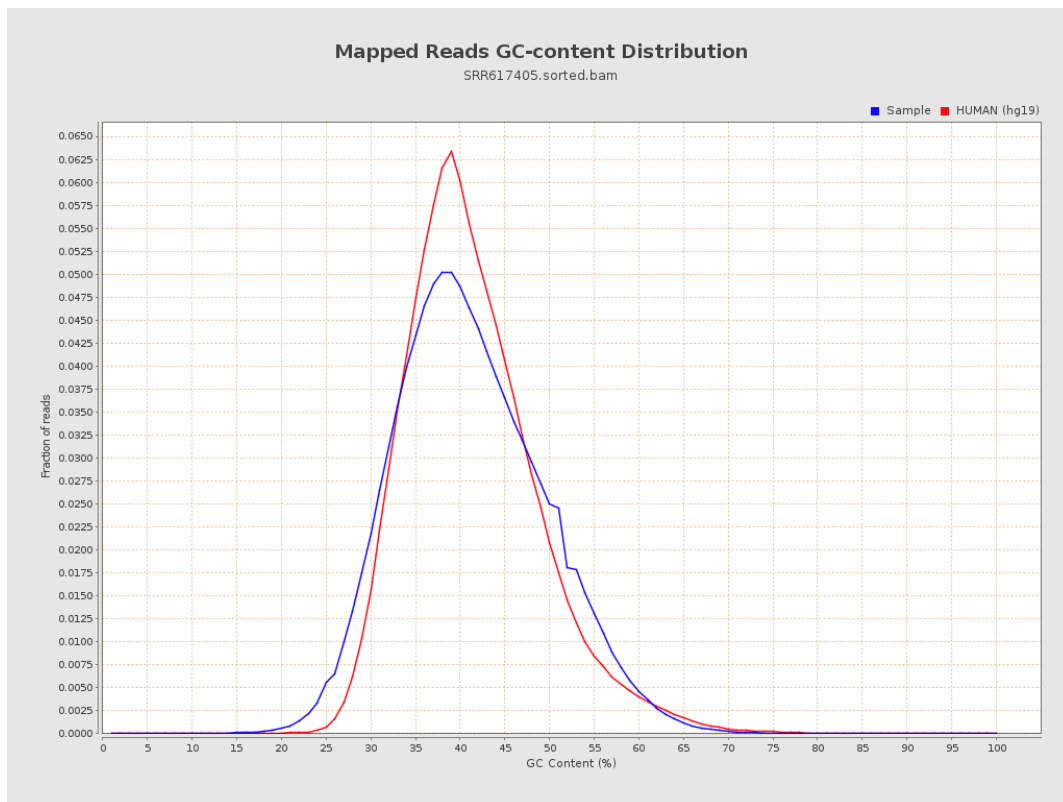
## 7. Results : Duplication Rate Histogram



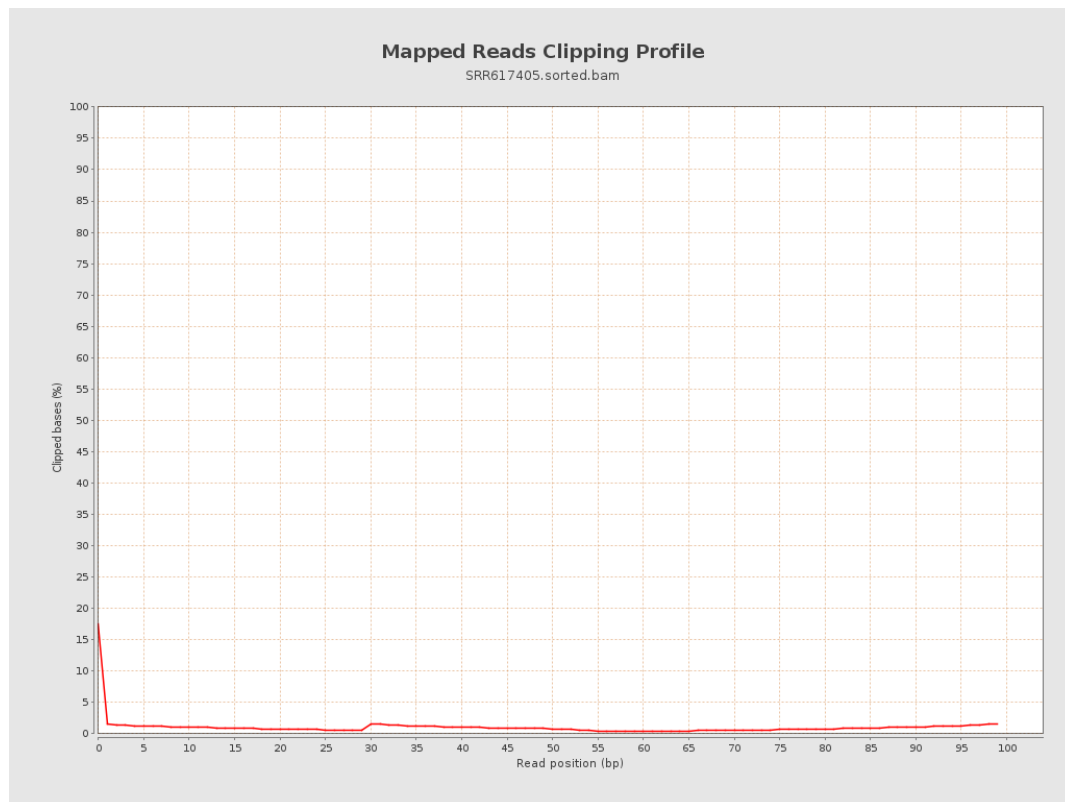
## 8. Results : Mapped Reads Nucleotide Content



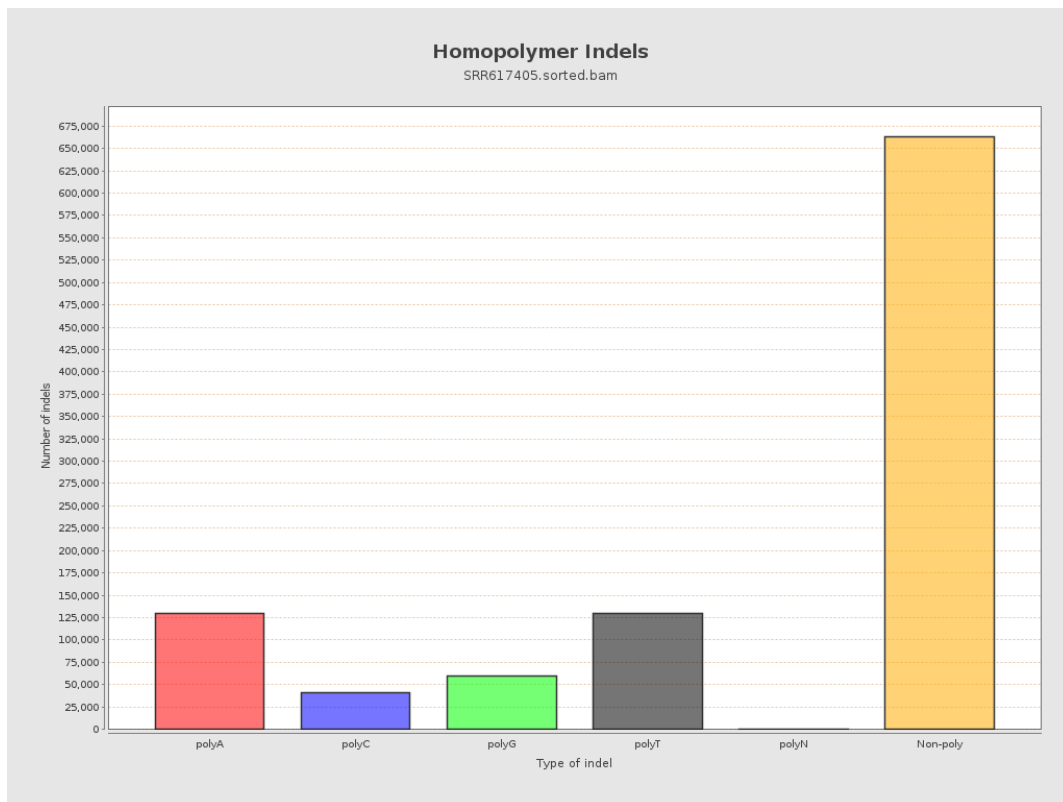
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



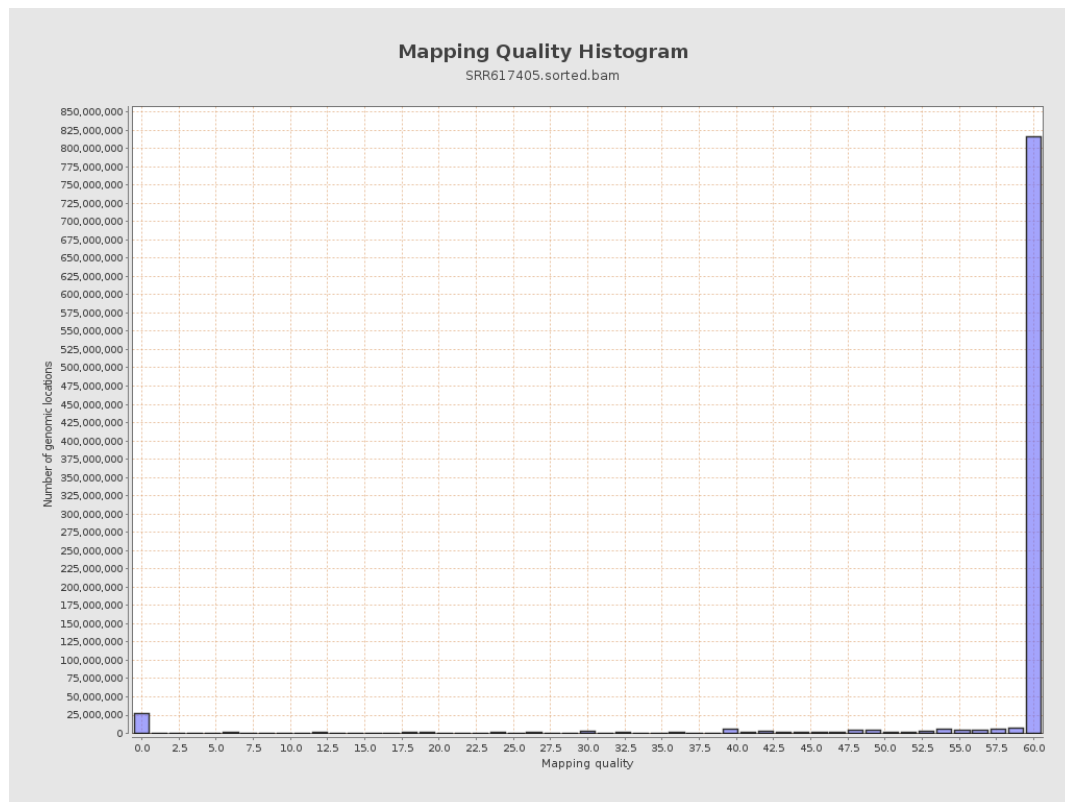
## 11. Results : Homopolymer Indels



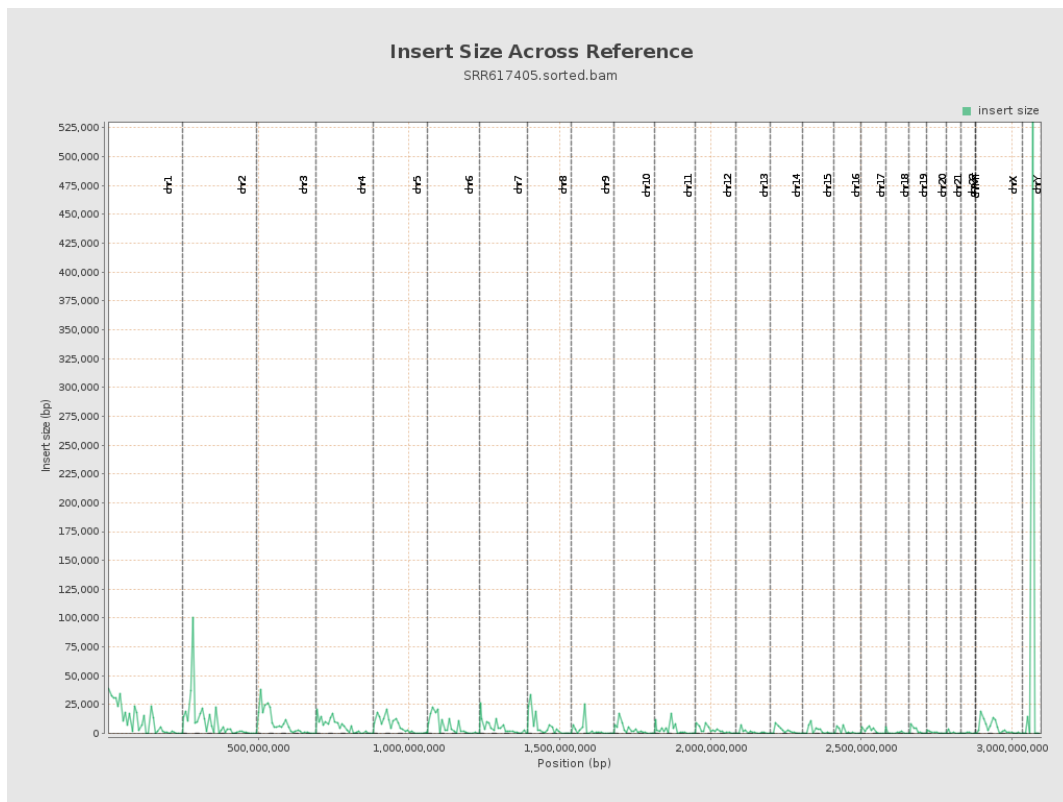
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

