

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/10 04:47:30*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR617506.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_SRR617506 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617506_1.fastq.gz SRR617506_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                               |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                |
| Analysis date:                        | Thu Oct 10 04:47:29 CST 2024                                                                                                                                                                                      |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                 |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                |
| Number of windows:                    | 400                                                                                                                                                                                                               |
| BAM file:                             | SRR617506.sorted.bam                                                                                                                                                                                              |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 4,014,434          |
| Mapped reads                 | 3,731,959 / 92.96% |
| Unmapped reads               | 282,475 / 7.04%    |
| Mapped paired reads          | 3,731,959 / 92.96% |
| Mapped reads, first in pair  | 1,890,018 / 47.08% |
| Mapped reads, second in pair | 1,841,941 / 45.88% |
| Mapped reads, both in pair   | 3,632,488 / 90.49% |
| Mapped reads, singletons     | 99,471 / 2.48%     |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 20,208 / 0.5%      |
| Read min/max/mean length     | 30 / 100 / 100.2   |
| Duplicated reads (estimated) | 271,452 / 6.76%    |
| Duplication rate             | 4.49%              |
| Clipped reads                | 851,225 / 21.2%    |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 106,260,784 / 29.59% |
| Number/percentage of C's | 72,307,452 / 20.13%  |
| Number/percentage of T's | 105,936,063 / 29.5%  |
| Number/percentage of G's | 74,296,457 / 20.69%  |
| Number/percentage of N's | 349,828 / 0.1%       |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 40.82% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.1161 |
| Standard Deviation | 1.2062 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 52.54 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 47,749.75       |
| Standard Deviation | 2,070,680.79    |
| P25/Median/P75     | 171 / 214 / 280 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 1.55%     |
| Mismatches                               | 5,470,921 |
| Insertions                               | 54,390    |
| Mapped reads with at least one insertion | 1.43%     |
| Deletions                                | 123,883   |
| Mapped reads with at least one deletion  | 3.25%     |
| Homopolymer indels                       | 46.98%    |

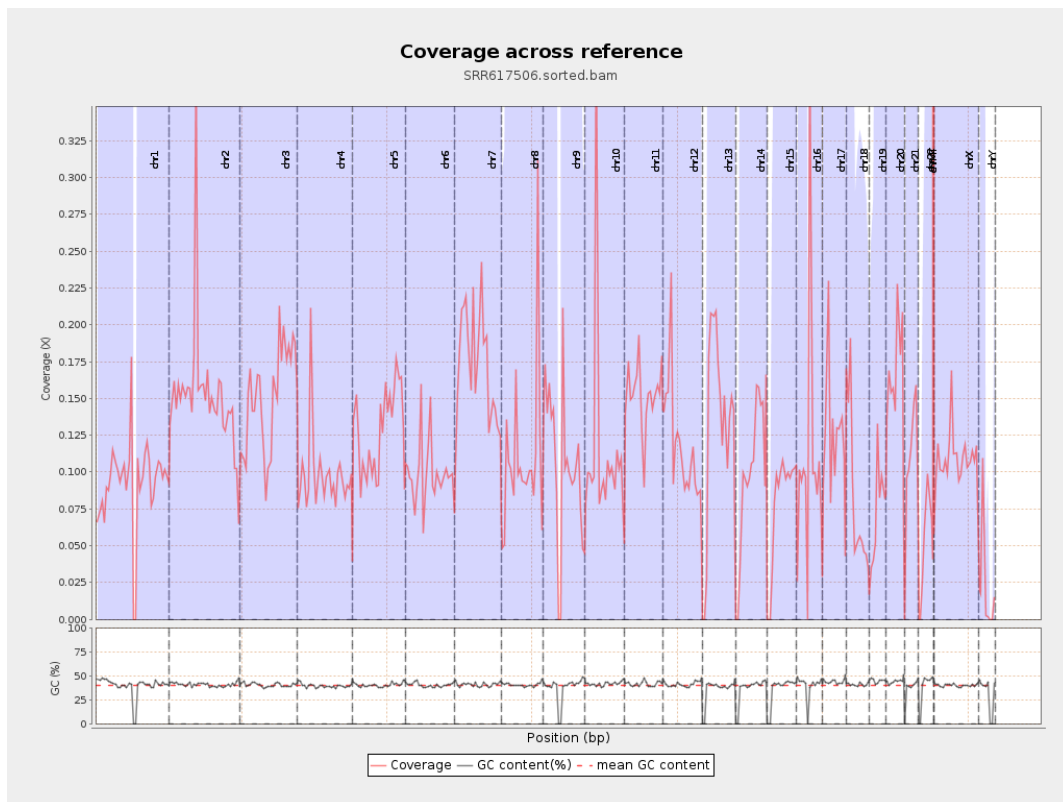
## 2.7. Chromosome stats

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

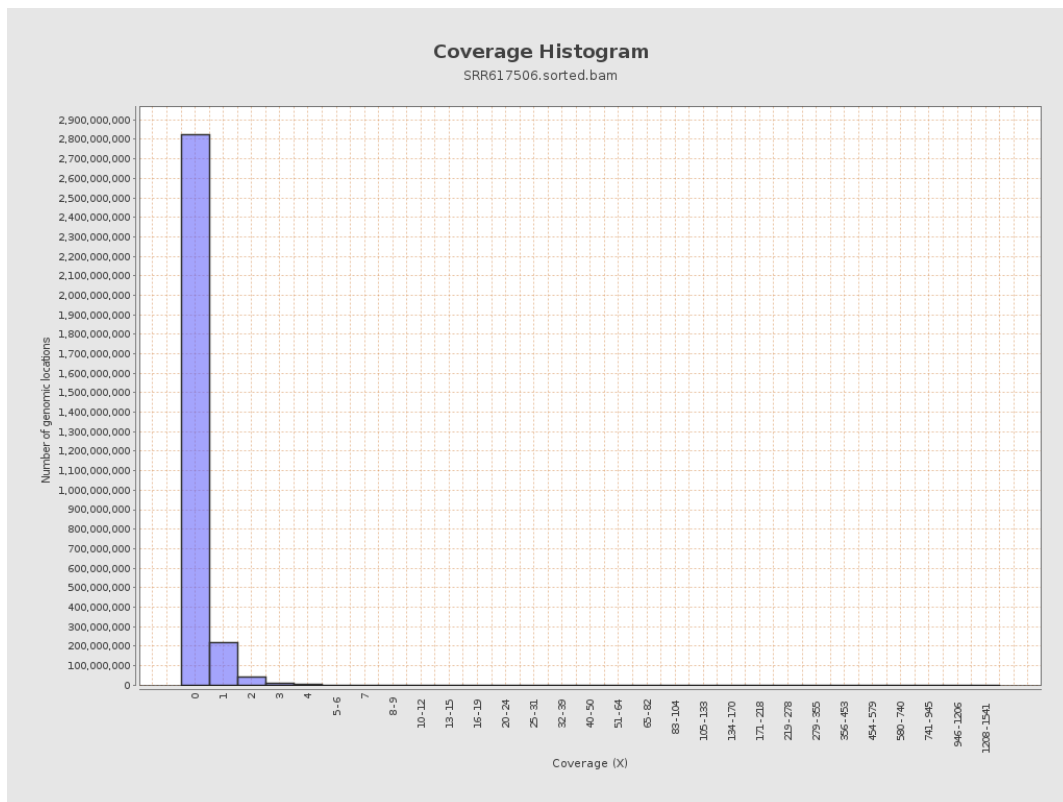
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 23040503     | 0.0924          | 1.1941           |
| chr2  | 243199373 | 37195223     | 0.1529          | 1.3947           |
| chr3  | 198022430 | 29809725     | 0.1505          | 0.4712           |
| chr4  | 191154276 | 18580751     | 0.0972          | 0.7546           |
| chr5  | 180915260 | 23077849     | 0.1276          | 0.4403           |
| chr6  | 171115067 | 16977916     | 0.0992          | 0.7398           |
| chr7  | 159138663 | 27685131     | 0.174           | 1.649            |
| chr8  | 146364022 | 16029575     | 0.1095          | 0.5749           |
| chr9  | 141213431 | 14878199     | 0.1054          | 2.1474           |
| chr10 | 135534747 | 15242031     | 0.1125          | 2.2825           |
| chr11 | 135006516 | 20210837     | 0.1497          | 1.5496           |
| chr12 | 133851895 | 15646569     | 0.1169          | 0.4227           |
| chr13 | 115169878 | 15253917     | 0.1324          | 0.4462           |
| chr14 | 107349540 | 10441553     | 0.0973          | 0.4155           |
| chr15 | 102531392 | 8085727      | 0.0789          | 0.3416           |
| chr16 | 90354753  | 9714191      | 0.1075          | 1.8526           |
| chr17 | 81195210  | 10010273     | 0.1233          | 1.66             |
| chr18 | 78077248  | 6440391      | 0.0825          | 2.0781           |
| chr19 | 59128983  | 4269500      | 0.0722          | 0.8041           |
| chr20 | 63025520  | 10570519     | 0.1677          | 0.5309           |
| chr21 | 48129895  | 5151479      | 0.107           | 0.558            |
| chr22 | 51304566  | 2696765      | 0.0526          | 0.2769           |
| chrMT | 16571     | 249632       | 15.0644         | 11.9598          |
| chrX  | 155270560 | 16876240     | 0.1087          | 0.5952           |

|      |          |         |        |        |
|------|----------|---------|--------|--------|
| chrY | 59373566 | 1226964 | 0.0207 | 1.5588 |
|------|----------|---------|--------|--------|

### 3. Results : Coverage across reference

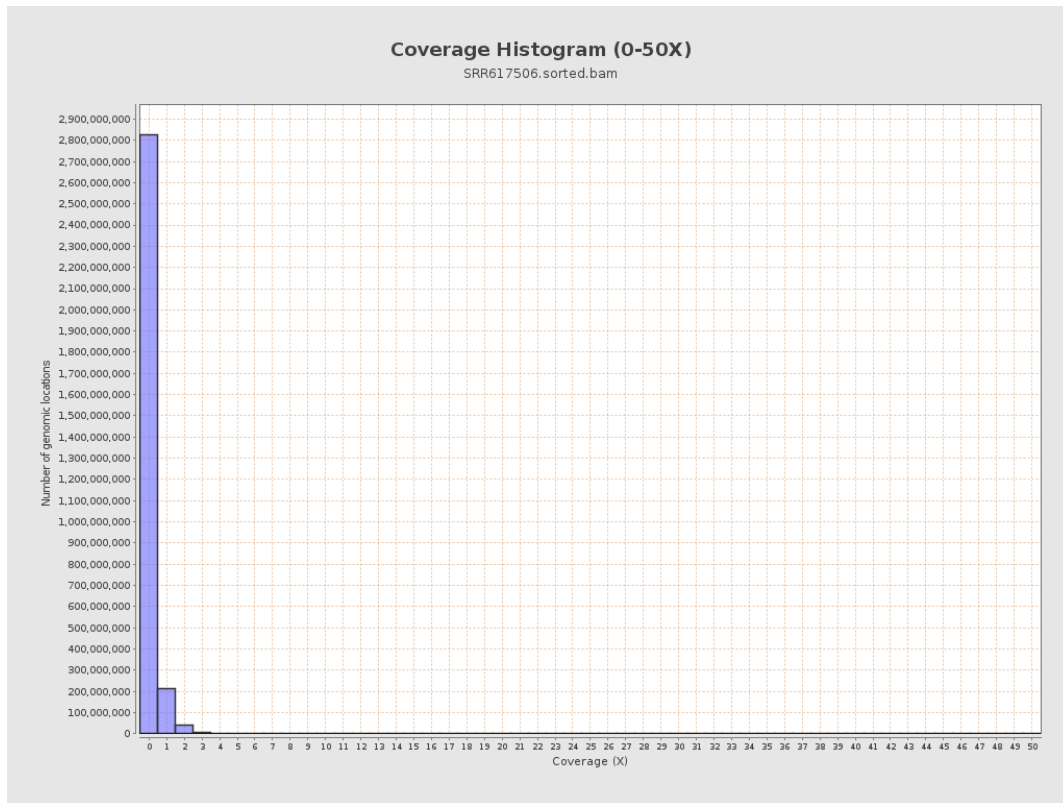


## 4. Results : Coverage Histogram

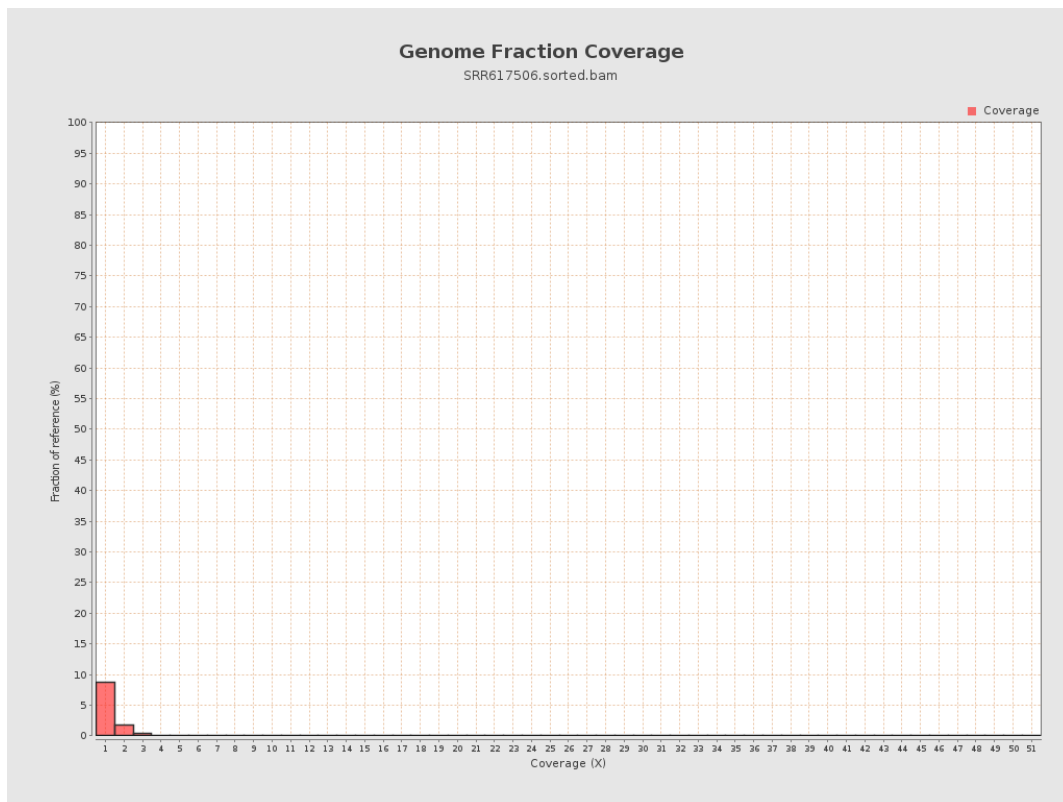




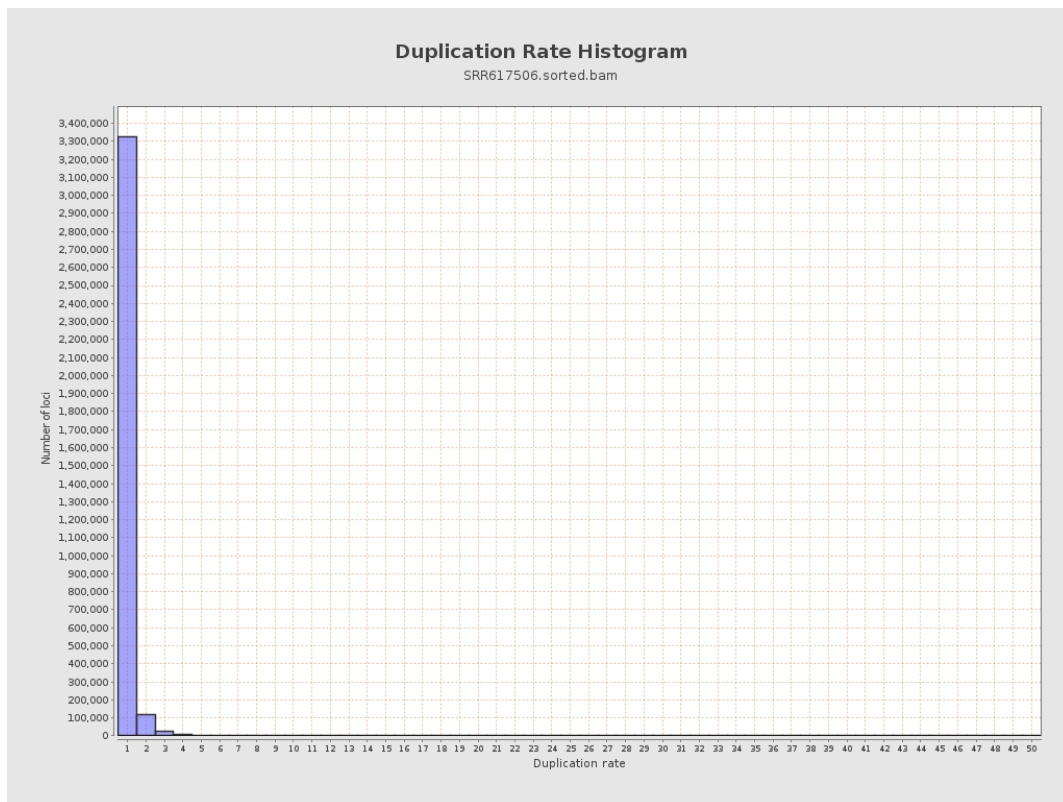
## 5. Results : Coverage Histogram (0-50X)



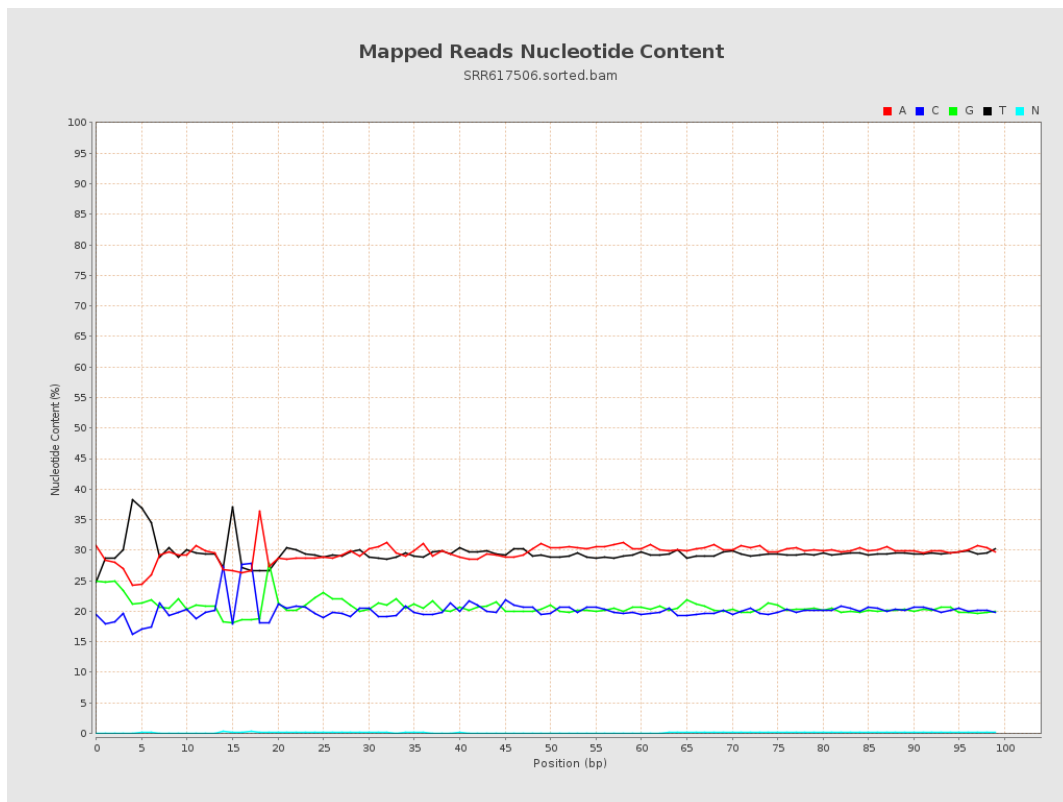
## 6. Results : Genome Fraction Coverage



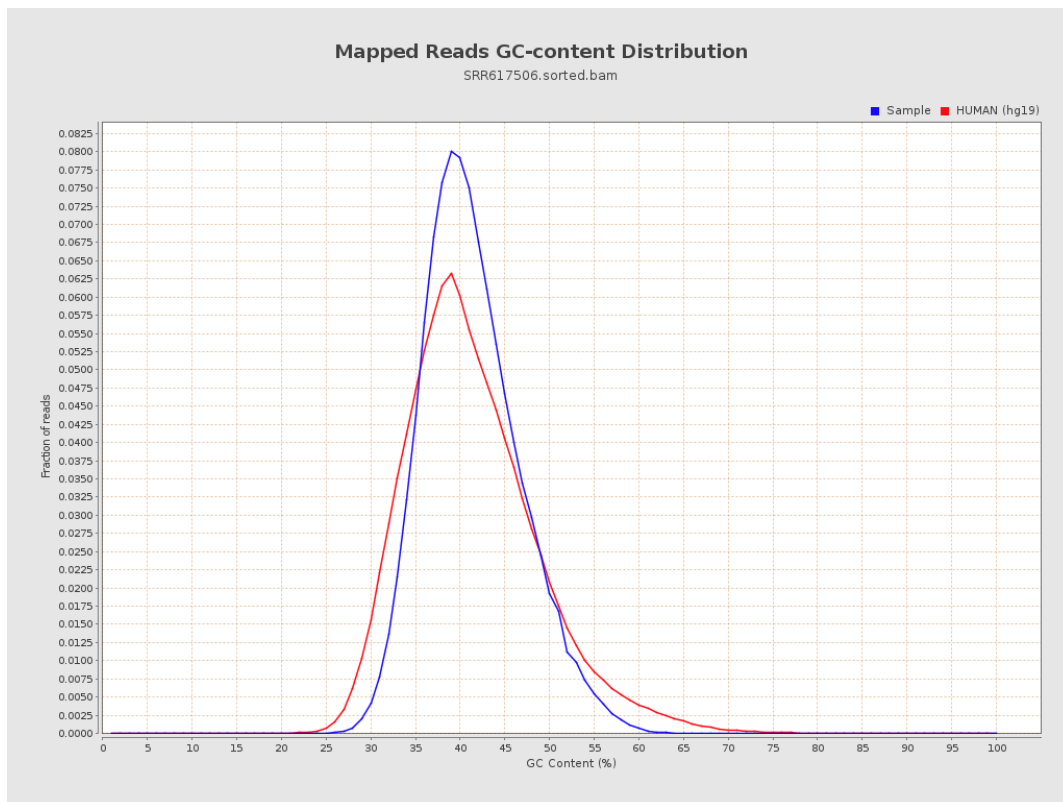
## 7. Results : Duplication Rate Histogram



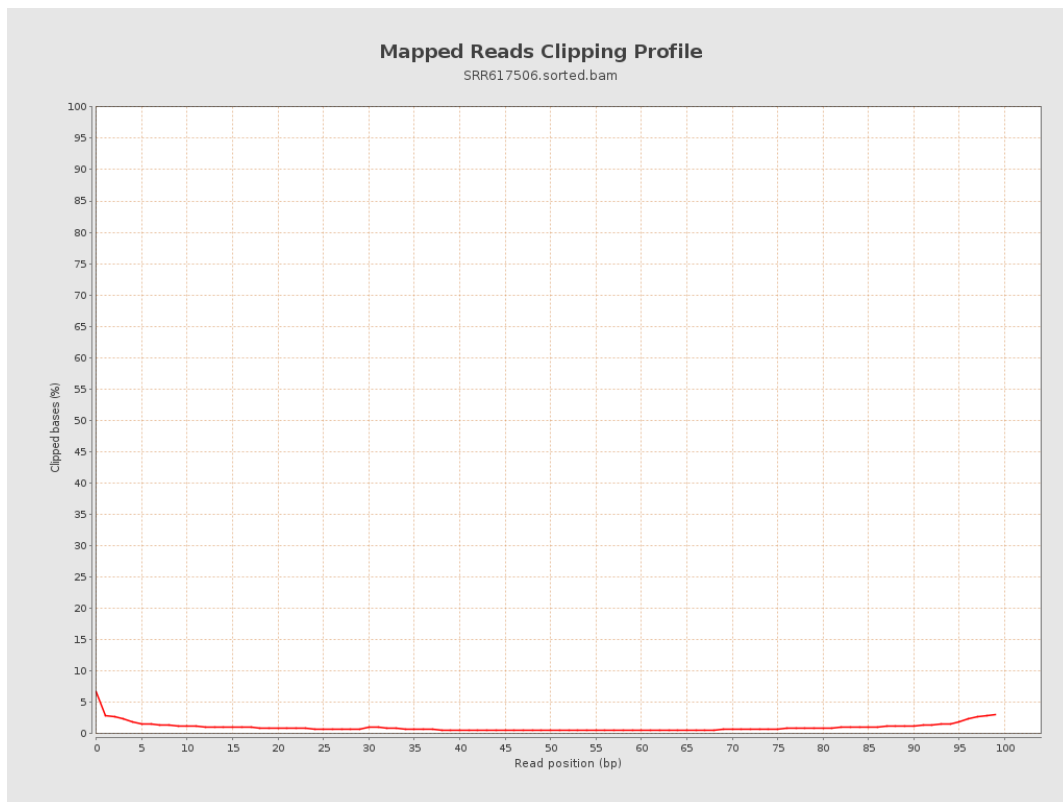
## 8. Results : Mapped Reads Nucleotide Content



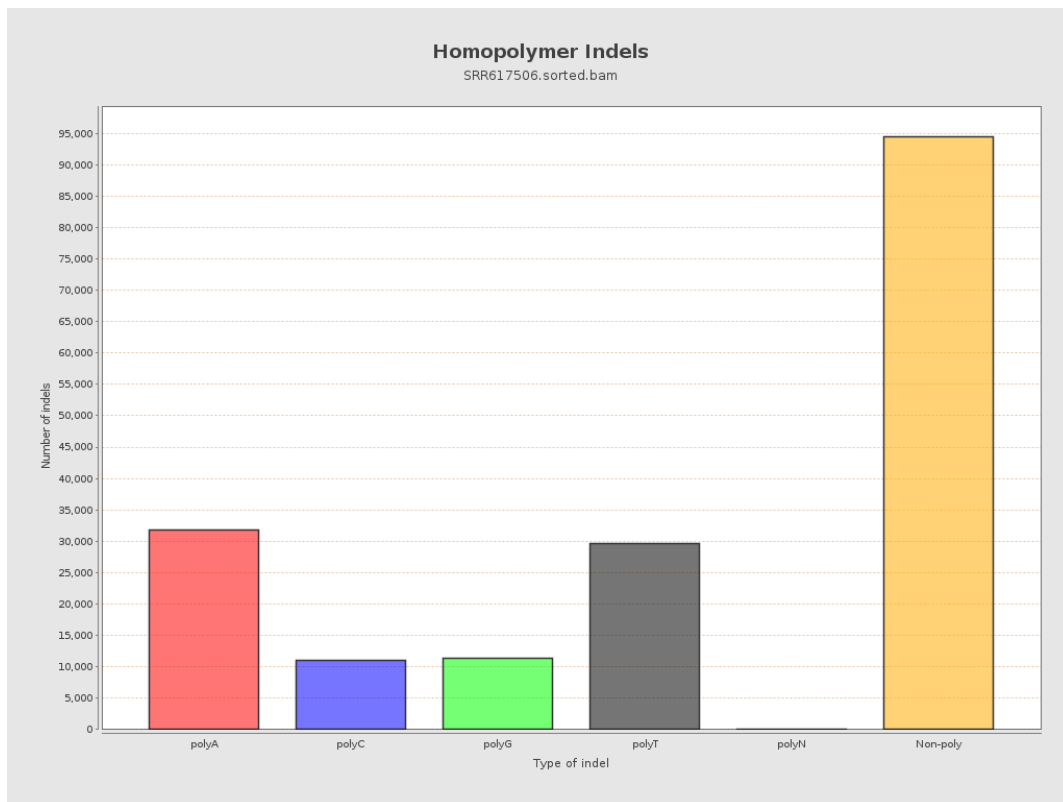
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

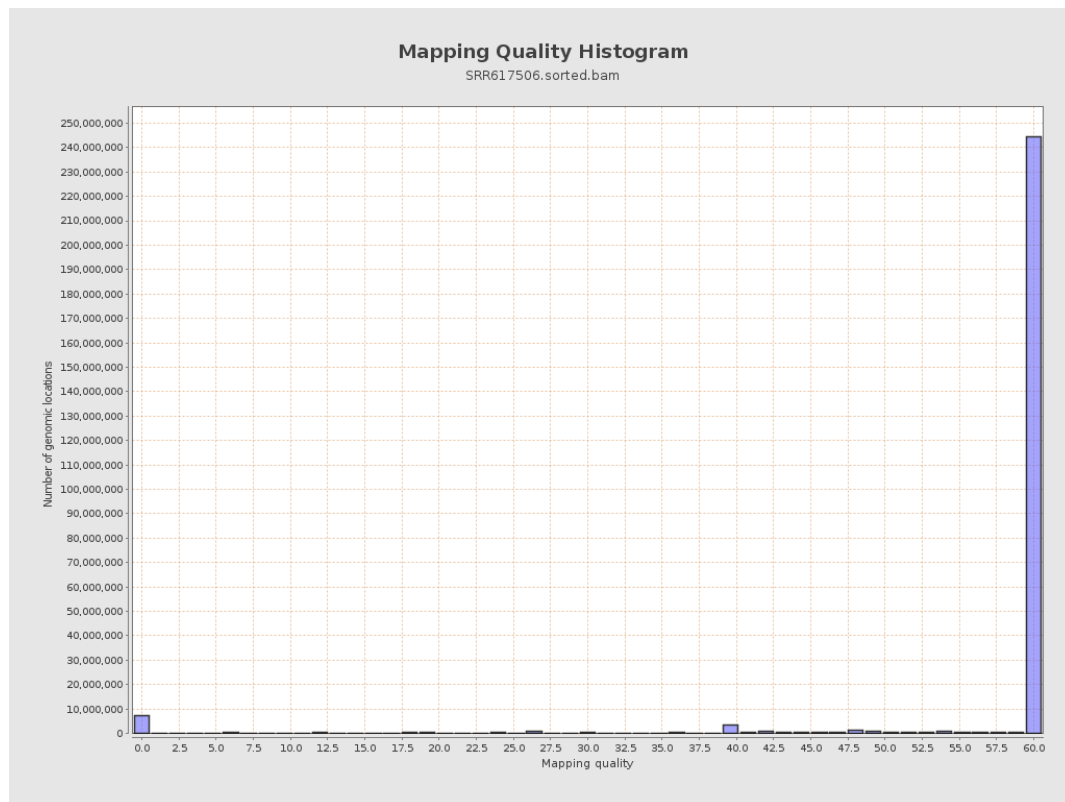


## 12. Results : Mapping Quality Across Reference

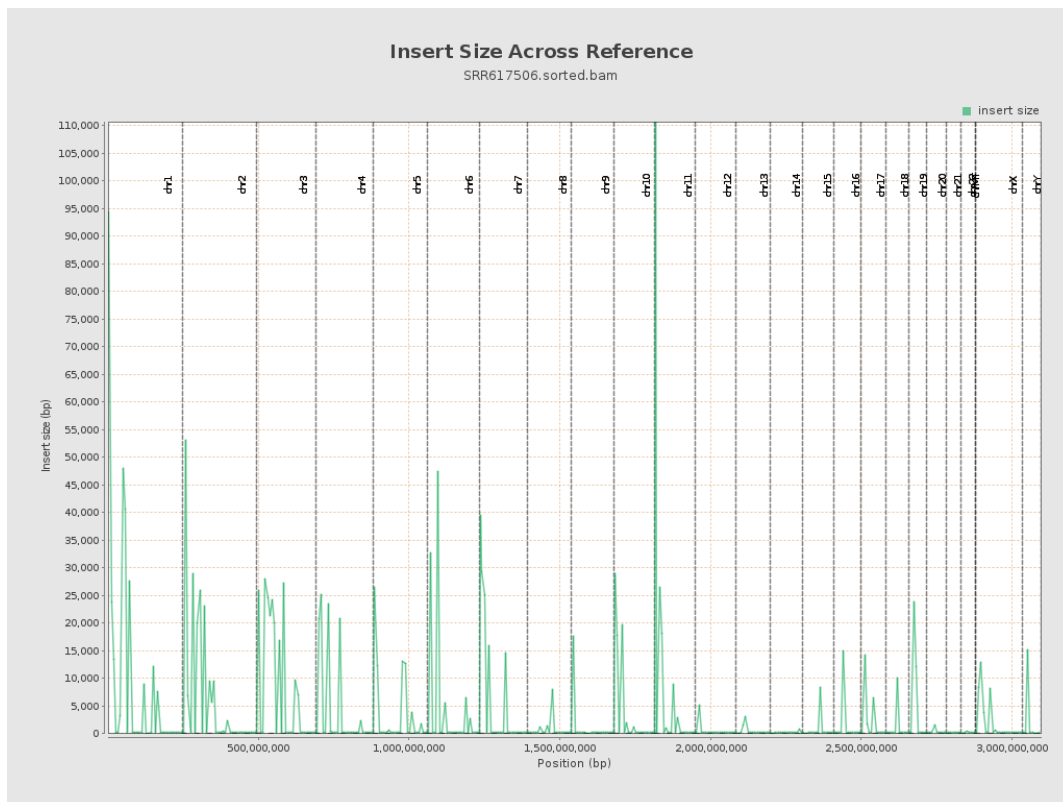




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

