

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/27 00:05:10*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094078.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_ERR2094078 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094078_1.fastq.gz ERR2094078_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                  |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                   |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                   |
| Analysis date:                        | Tue Aug 27 00:05:09 CST 2024                                                                                                                                                                                         |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                    |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                   |
| Number of windows:                    | 400                                                                                                                                                                                                                  |
| BAM file:                             | ERR2094078.sorted.bam                                                                                                                                                                                                |

## 2. Summary

### 2.1. Globals

|                              |                   |
|------------------------------|-------------------|
| Reference size               | 3,095,693,983     |
| Number of reads              | 429,258           |
| Mapped reads                 | 411,994 / 95.98%  |
| Unmapped reads               | 17,264 / 4.02%    |
| Mapped paired reads          | 411,994 / 95.98%  |
| Mapped reads, first in pair  | 207,011 / 48.23%  |
| Mapped reads, second in pair | 204,983 / 47.75%  |
| Mapped reads, both in pair   | 409,182 / 95.32%  |
| Mapped reads, singletons     | 2,812 / 0.66%     |
| Secondary alignments         | 0                 |
| Supplementary alignments     | 14,654 / 3.41%    |
| Read min/max/mean length     | 30 / 151 / 141.38 |
| Duplicated reads (estimated) | 393,090 / 91.57%  |
| Duplication rate             | 49.54%            |
| Clipped reads                | 161,890 / 37.71%  |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 14,133,495 / 26.5%  |
| Number/percentage of C's | 12,499,207 / 23.44% |
| Number/percentage of T's | 13,524,501 / 25.36% |
| Number/percentage of G's | 13,167,806 / 24.69% |
| Number/percentage of N's | 689 / 0%            |
|                          |                     |

|               |        |
|---------------|--------|
| GC Percentage | 48.13% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.0176 |
| Standard Deviation | 4.6772 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 39.38 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 391,674.11      |
| Standard Deviation | 5,609,190.34    |
| P25/Median/P75     | 135 / 166 / 196 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 4.12%     |
| Mismatches                               | 2,115,453 |
| Insertions                               | 35,515    |
| Mapped reads with at least one insertion | 8.46%     |
| Deletions                                | 171,947   |
| Mapped reads with at least one deletion  | 39.77%    |
| Homopolymer indels                       | 27.49%    |

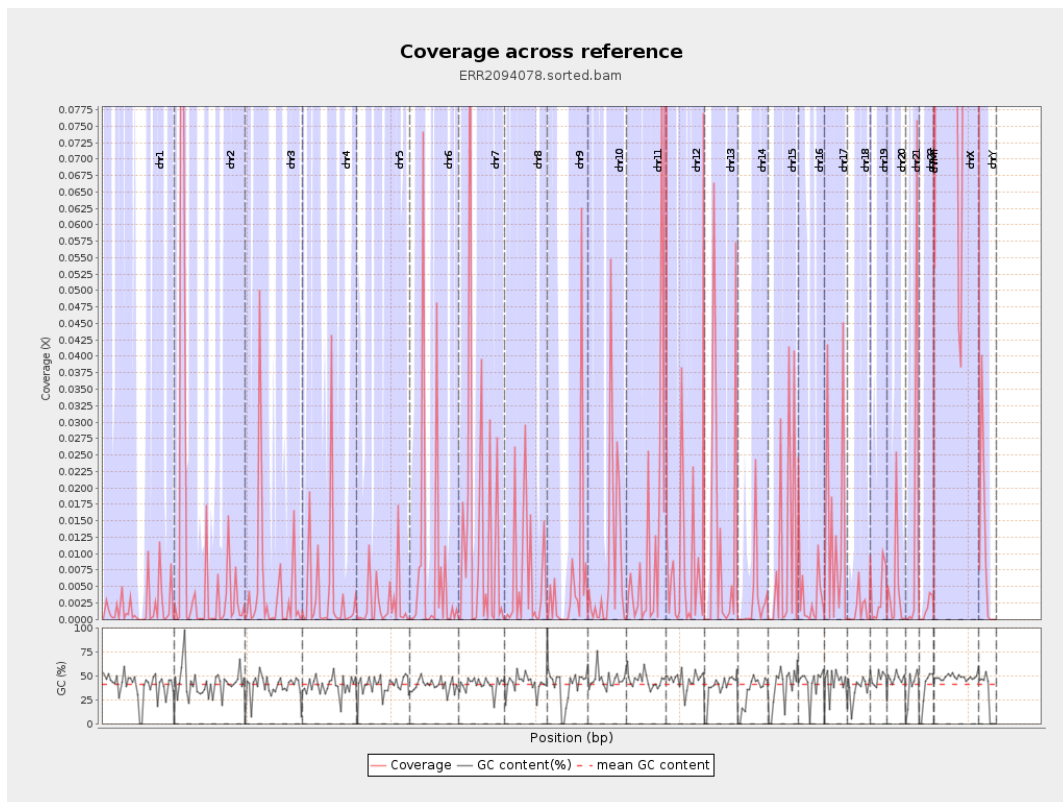
## 2.7. Chromosome stats

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

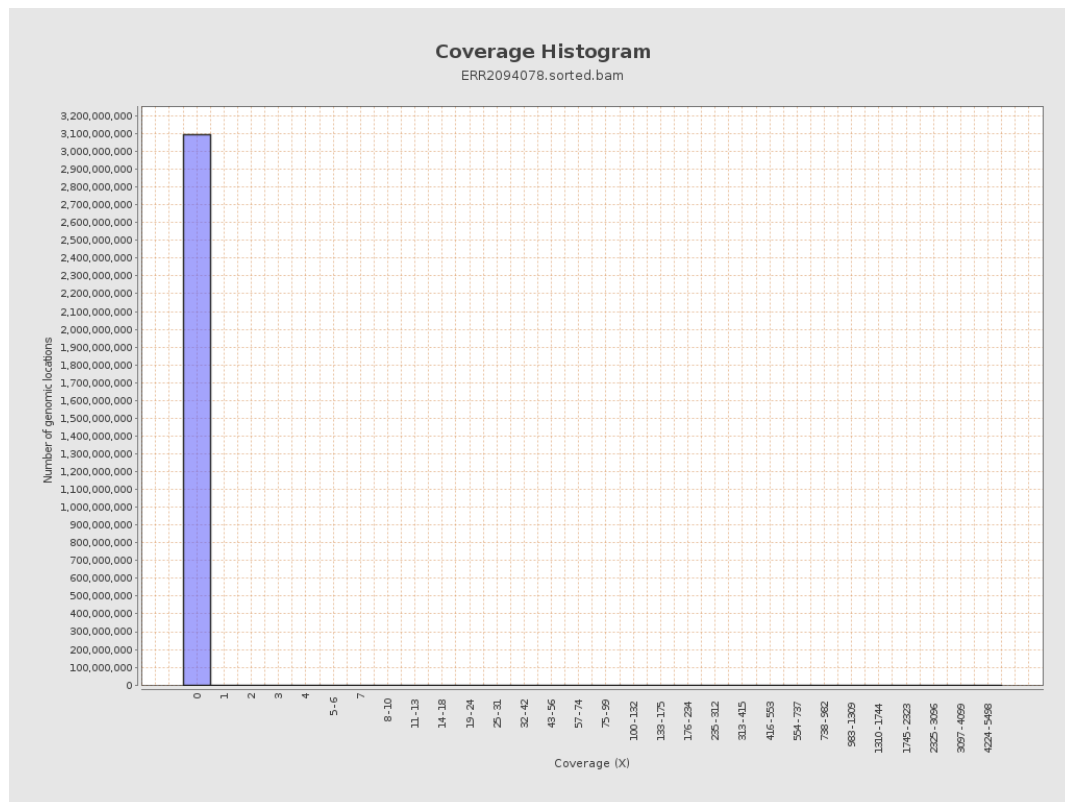
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 455836       | 0.0018          | 0.7282           |
| chr2  | 243199373 | 2111926      | 0.0087          | 3.4221           |
| chr3  | 198022430 | 832485       | 0.0042          | 1.5556           |
| chr4  | 191154276 | 745852       | 0.0039          | 1.3882           |
| chr5  | 180915260 | 433717       | 0.0024          | 1.0722           |
| chr6  | 171115067 | 1282247      | 0.0075          | 3.8994           |
| chr7  | 159138663 | 2016551      | 0.0127          | 4.7325           |
| chr8  | 146364022 | 913621       | 0.0062          | 2.0149           |
| chr9  | 141213431 | 820446       | 0.0058          | 2.8513           |
| chr10 | 135534747 | 1136750      | 0.0084          | 3.3844           |
| chr11 | 135006516 | 1628442      | 0.0121          | 3.3008           |
| chr12 | 133851895 | 1103827      | 0.0082          | 2.454            |
| chr13 | 115169878 | 1406636      | 0.0122          | 3.4595           |
| chr14 | 107349540 | 322170       | 0.003           | 1.4853           |
| chr15 | 102531392 | 957935       | 0.0093          | 3.113            |
| chr16 | 90354753  | 349403       | 0.0039          | 1.406            |
| chr17 | 81195210  | 1066807      | 0.0131          | 3.8907           |
| chr18 | 78077248  | 118596       | 0.0015          | 0.5747           |
| chr19 | 59128983  | 206605       | 0.0035          | 0.8473           |
| chr20 | 63025520  | 297004       | 0.0047          | 1.4522           |
| chr21 | 48129895  | 643297       | 0.0134          | 5.6291           |
| chr22 | 51304566  | 81882        | 0.0016          | 0.392            |
| chrMT | 16571     | 1139617      | 68.7718         | 313.4604         |
| chrX  | 155270560 | 33878298     | 0.2182          | 16.8659          |

|      |          |        |      |        |
|------|----------|--------|------|--------|
| chrY | 59373566 | 591057 | 0.01 | 2.3091 |
|------|----------|--------|------|--------|

### 3. Results : Coverage across reference

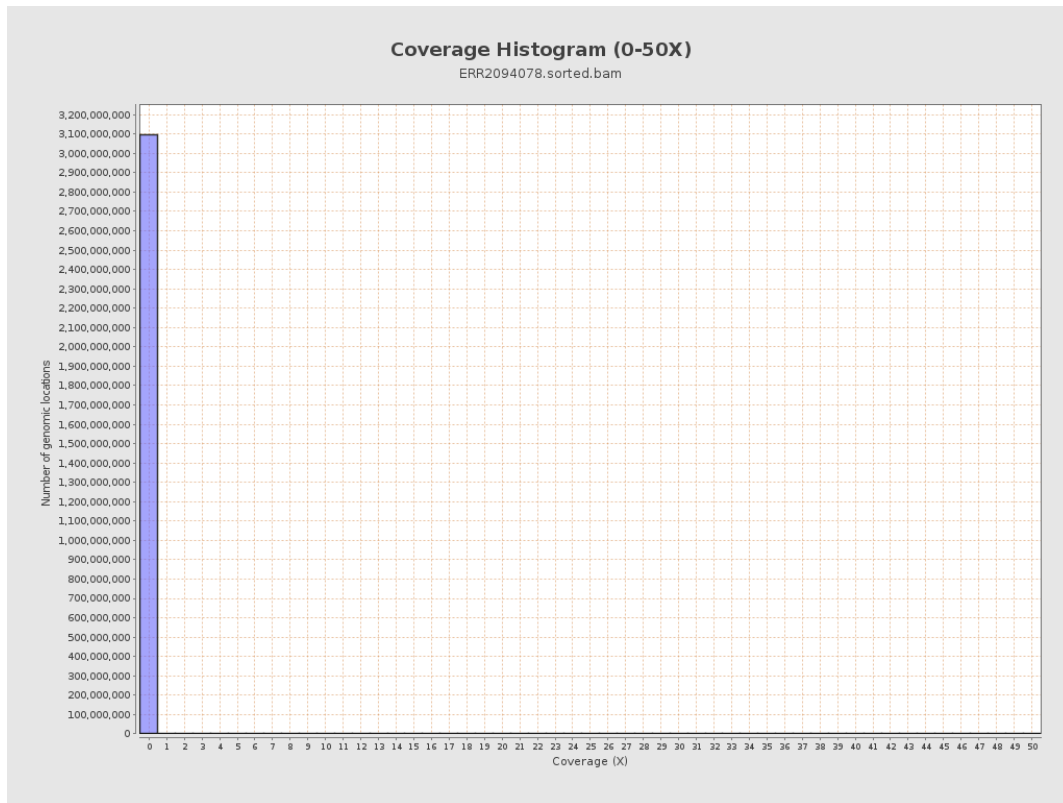


## 4. Results : Coverage Histogram

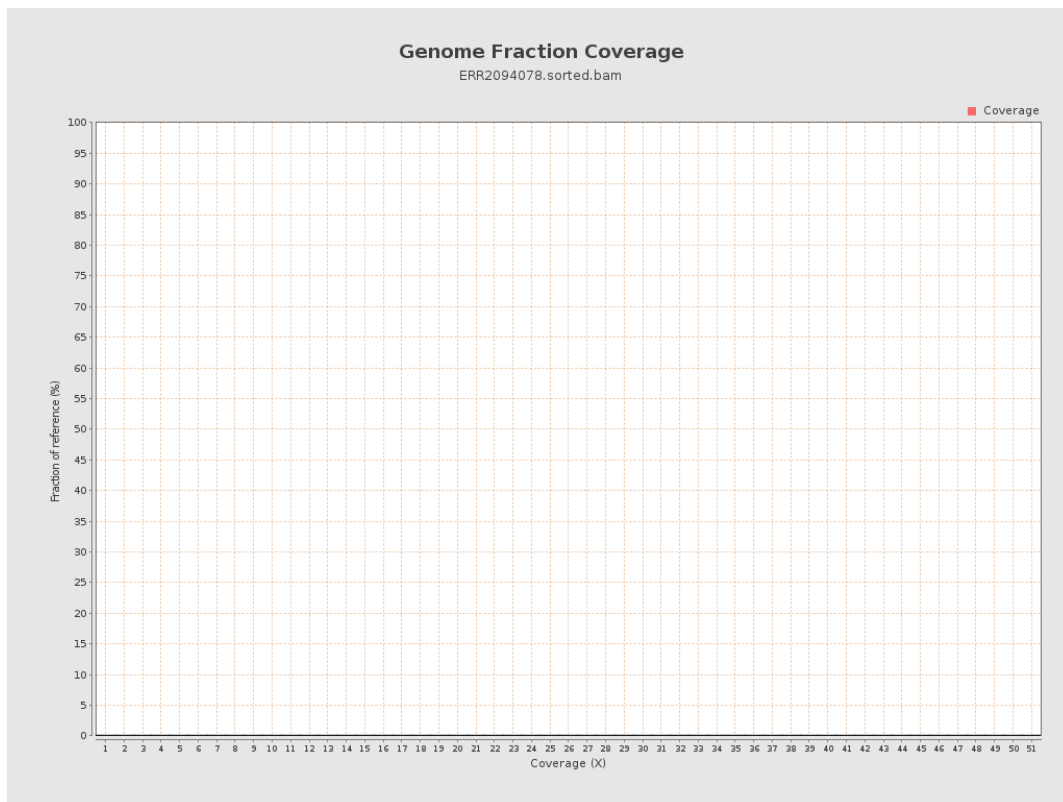




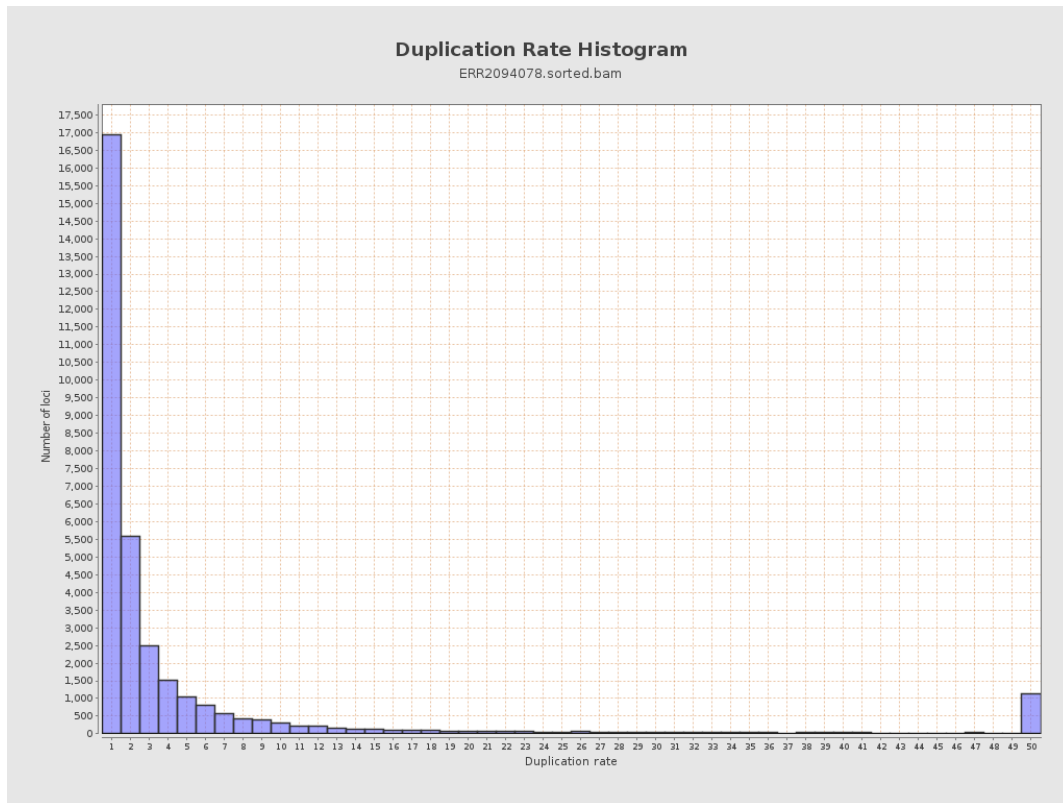
## 5. Results : Coverage Histogram (0-50X)



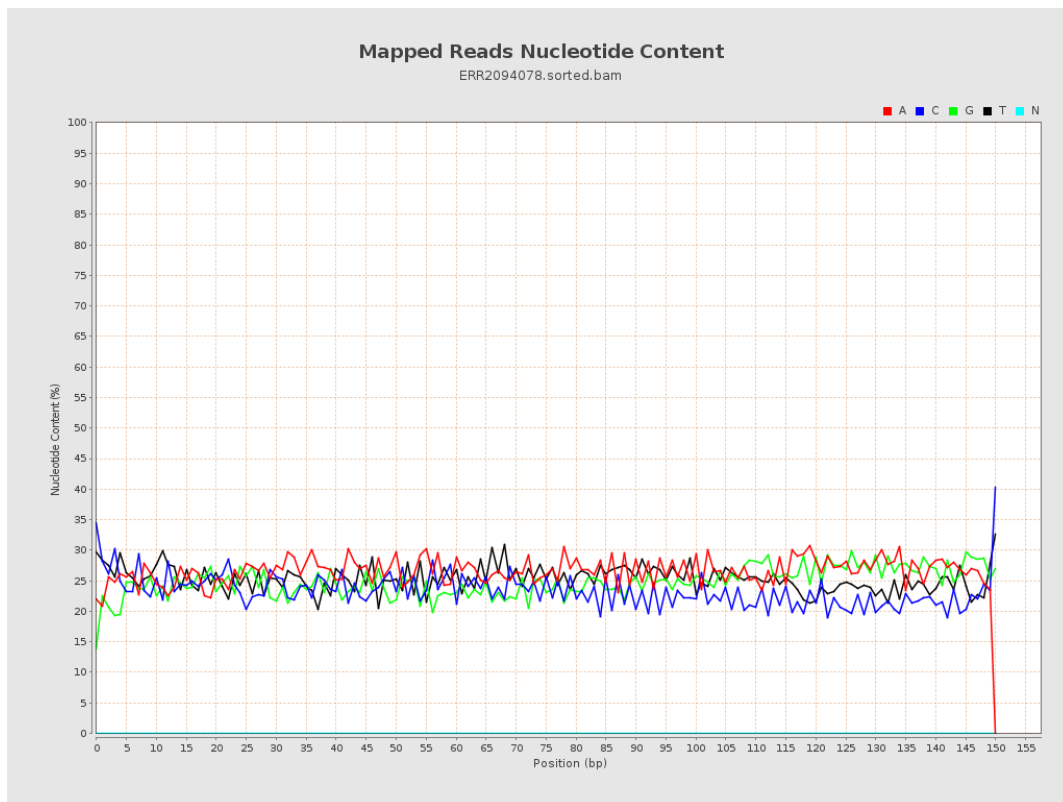
## 6. Results : Genome Fraction Coverage



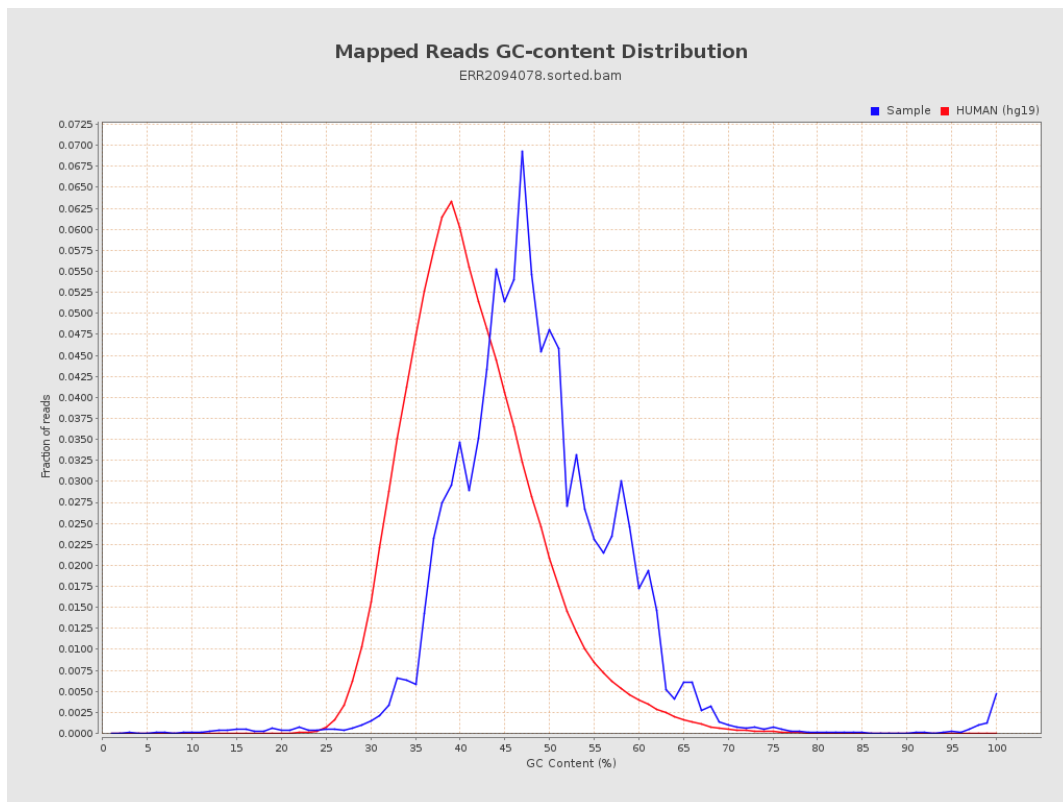
## 7. Results : Duplication Rate Histogram



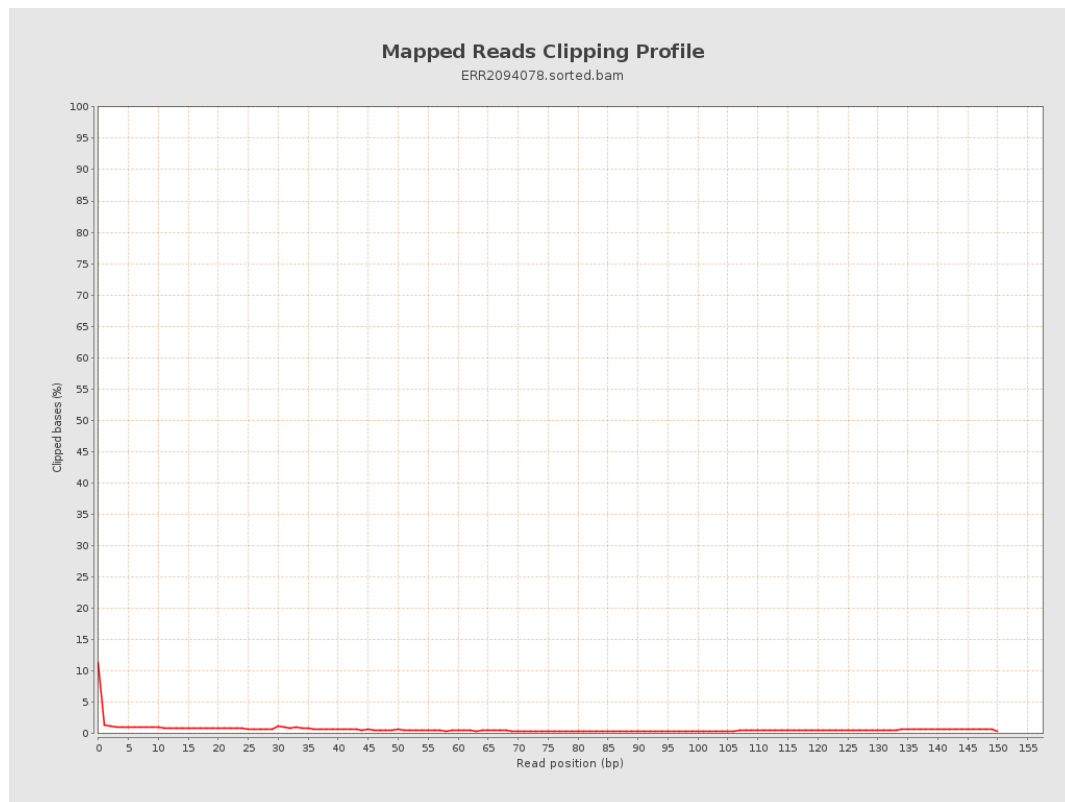
## 8. Results : Mapped Reads Nucleotide Content



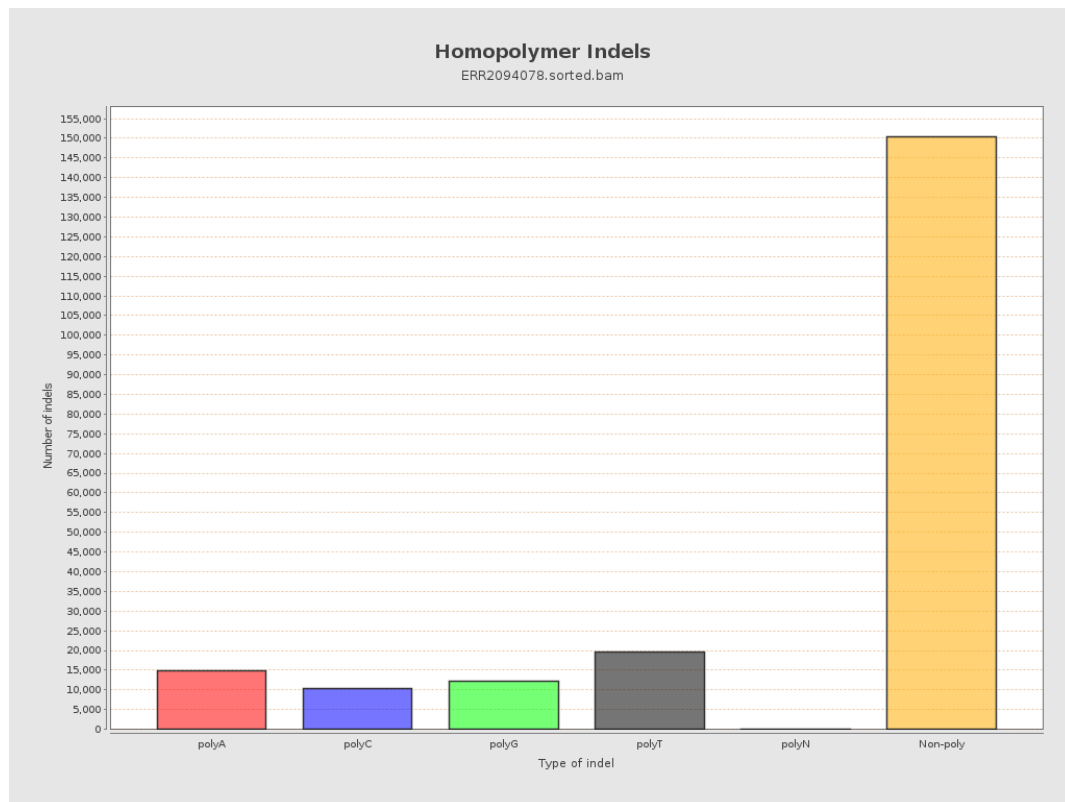
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

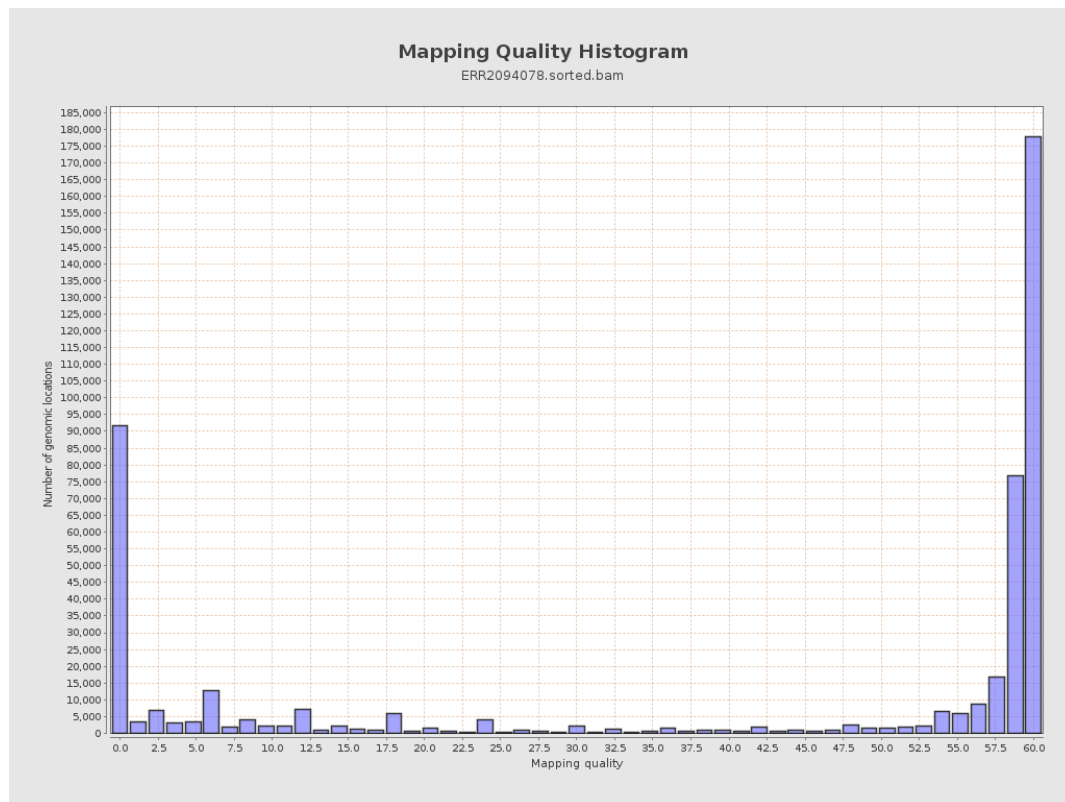


## 12. Results : Mapping Quality Across Reference

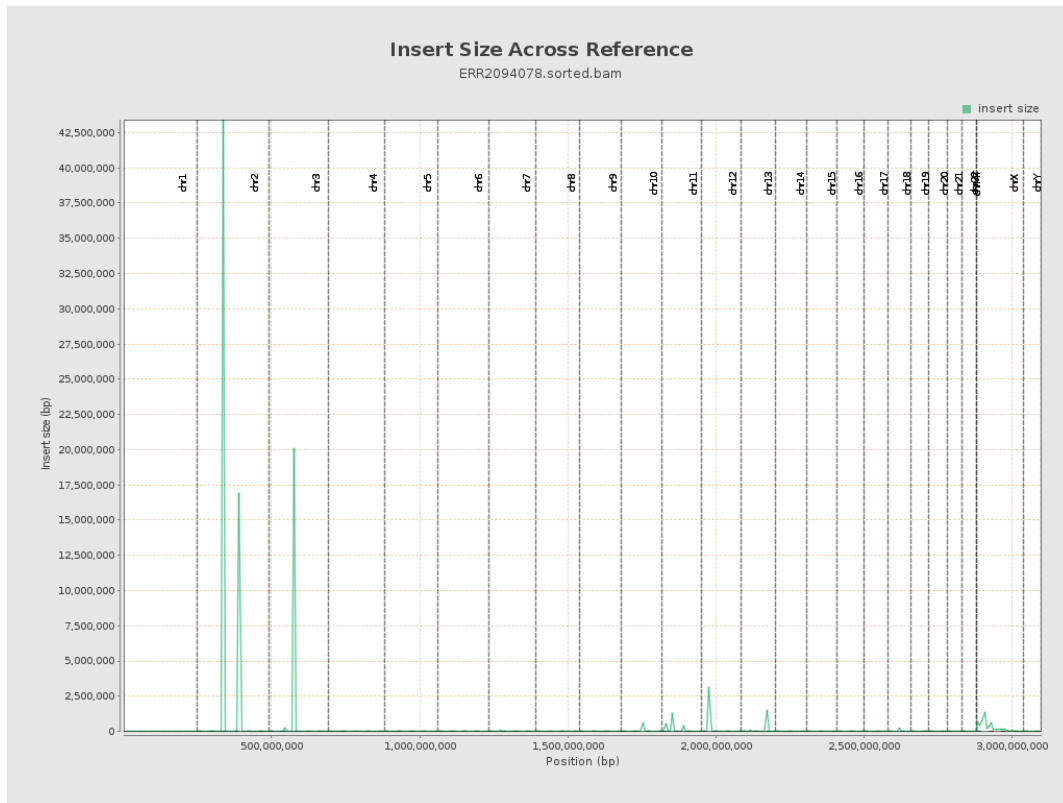




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

