

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/26 23:39:37*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094068.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_ERR2094068 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094068_1.fastq.gz ERR2094068_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                  |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                   |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                   |
| Analysis date:                        | Mon Aug 26 23:39:36 CST 2024                                                                                                                                                                                         |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                    |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                   |
| Number of windows:                    | 400                                                                                                                                                                                                                  |
| BAM file:                             | ERR2094068.sorted.bam                                                                                                                                                                                                |

## 2. Summary

### 2.1. Globals

|                              |                   |
|------------------------------|-------------------|
| Reference size               | 3,095,693,983     |
| Number of reads              | 357,716           |
| Mapped reads                 | 348,147 / 97.32%  |
| Unmapped reads               | 9,569 / 2.68%     |
| Mapped paired reads          | 348,147 / 97.32%  |
| Mapped reads, first in pair  | 174,919 / 48.9%   |
| Mapped reads, second in pair | 173,228 / 48.43%  |
| Mapped reads, both in pair   | 345,564 / 96.6%   |
| Mapped reads, singletons     | 2,583 / 0.72%     |
| Secondary alignments         | 0                 |
| Supplementary alignments     | 12,970 / 3.63%    |
| Read min/max/mean length     | 30 / 151 / 145.14 |
| Duplicated reads (estimated) | 331,238 / 92.6%   |
| Duplication rate             | 49.38%            |
| Clipped reads                | 131,768 / 36.84%  |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 12,069,203 / 26.05% |
| Number/percentage of C's | 11,077,309 / 23.91% |
| Number/percentage of T's | 11,598,252 / 25.04% |
| Number/percentage of G's | 11,582,626 / 25%    |
| Number/percentage of N's | 474 / 0%            |
|                          |                     |

|               |        |
|---------------|--------|
| GC Percentage | 48.91% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.0153 |
| Standard Deviation | 4.3141 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 38.04 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 482,669.82      |
| Standard Deviation | 6,338,467.86    |
| P25/Median/P75     | 148 / 172 / 201 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 4.04%     |
| Mismatches                               | 1,802,913 |
| Insertions                               | 29,360    |
| Mapped reads with at least one insertion | 8.3%      |
| Deletions                                | 137,730   |
| Mapped reads with at least one deletion  | 37.71%    |
| Homopolymer indels                       | 28.93%    |

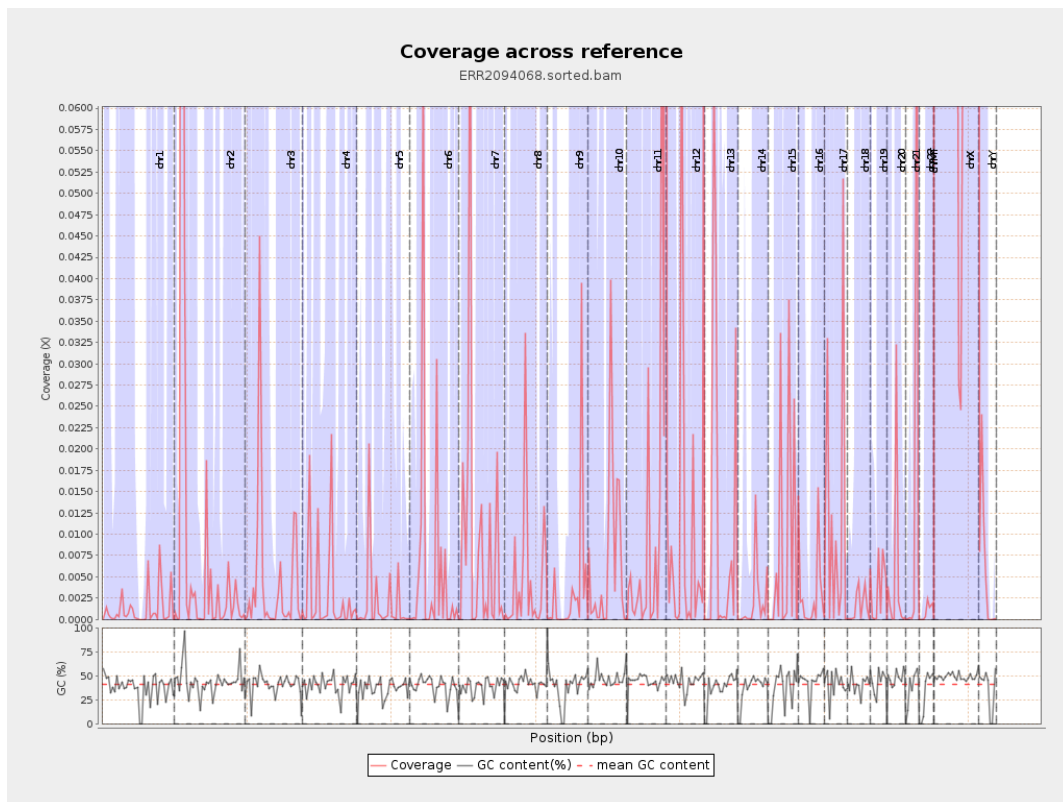
## 2.7. Chromosome stats

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

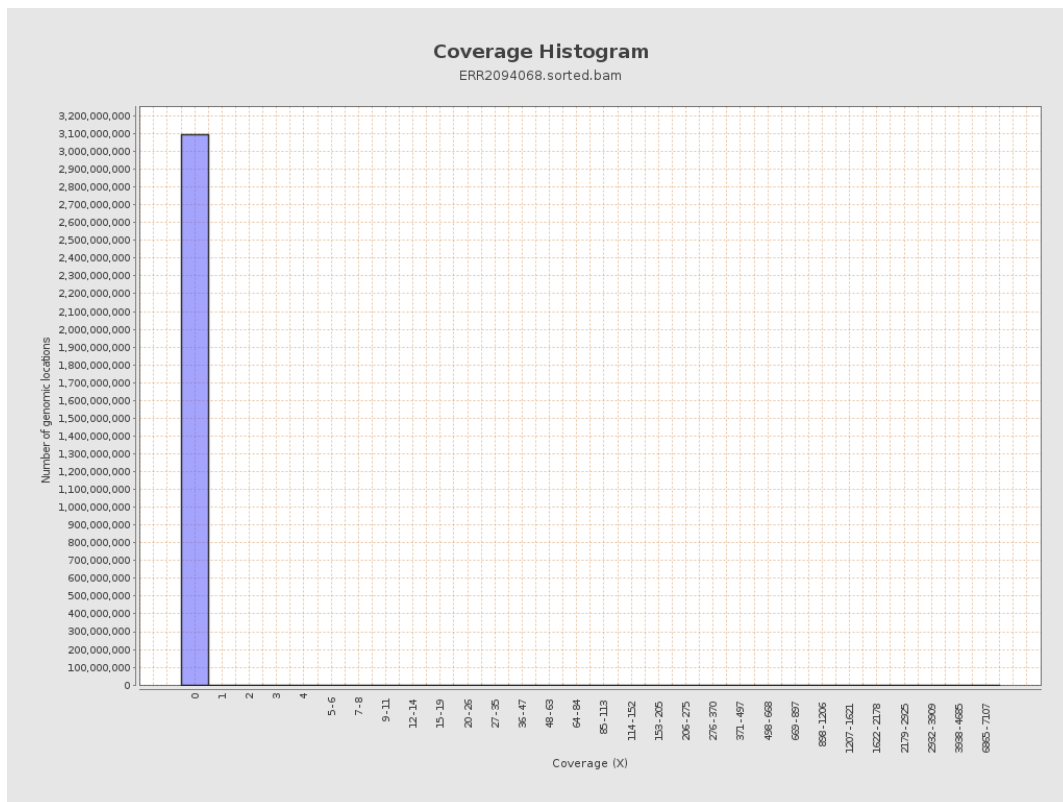
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 302527       | 0.0012          | 0.5069           |
| chr2  | 243199373 | 2279332      | 0.0094          | 4.1501           |
| chr3  | 198022430 | 839264       | 0.0042          | 1.621            |
| chr4  | 191154276 | 572632       | 0.003           | 1.2408           |
| chr5  | 180915260 | 326972       | 0.0018          | 0.9              |
| chr6  | 171115067 | 1071674      | 0.0063          | 3.406            |
| chr7  | 159138663 | 1464449      | 0.0092          | 3.3872           |
| chr8  | 146364022 | 653340       | 0.0045          | 1.5921           |
| chr9  | 141213431 | 501307       | 0.0035          | 1.7214           |
| chr10 | 135534747 | 962210       | 0.0071          | 2.4287           |
| chr11 | 135006516 | 1611059      | 0.0119          | 3.4999           |
| chr12 | 133851895 | 1290370      | 0.0096          | 3.924            |
| chr13 | 115169878 | 1206778      | 0.0105          | 3.0579           |
| chr14 | 107349540 | 233988       | 0.0022          | 0.9602           |
| chr15 | 102531392 | 810170       | 0.0079          | 2.6014           |
| chr16 | 90354753  | 287831       | 0.0032          | 1.0732           |
| chr17 | 81195210  | 946375       | 0.0117          | 4.0311           |
| chr18 | 78077248  | 123324       | 0.0016          | 0.4544           |
| chr19 | 59128983  | 192284       | 0.0033          | 0.8313           |
| chr20 | 63025520  | 306175       | 0.0049          | 1.7874           |
| chr21 | 48129895  | 694821       | 0.0144          | 6.5679           |
| chr22 | 51304566  | 47140        | 0.0009          | 0.2217           |
| chrMT | 16571     | 1305201      | 78.7642         | 378.4206         |
| chrX  | 155270560 | 28965259     | 0.1865          | 15.0269          |

|      |          |        |        |       |
|------|----------|--------|--------|-------|
| chrY | 59373566 | 351235 | 0.0059 | 1.395 |
|------|----------|--------|--------|-------|

### 3. Results : Coverage across reference

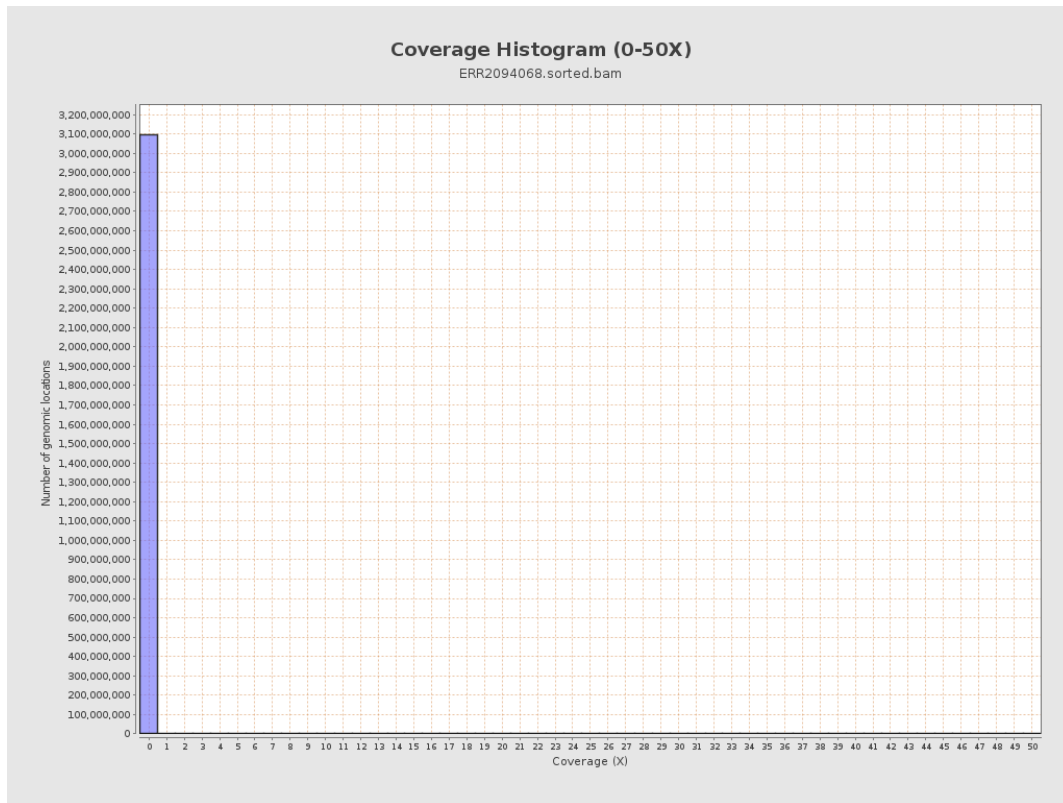


## 4. Results : Coverage Histogram

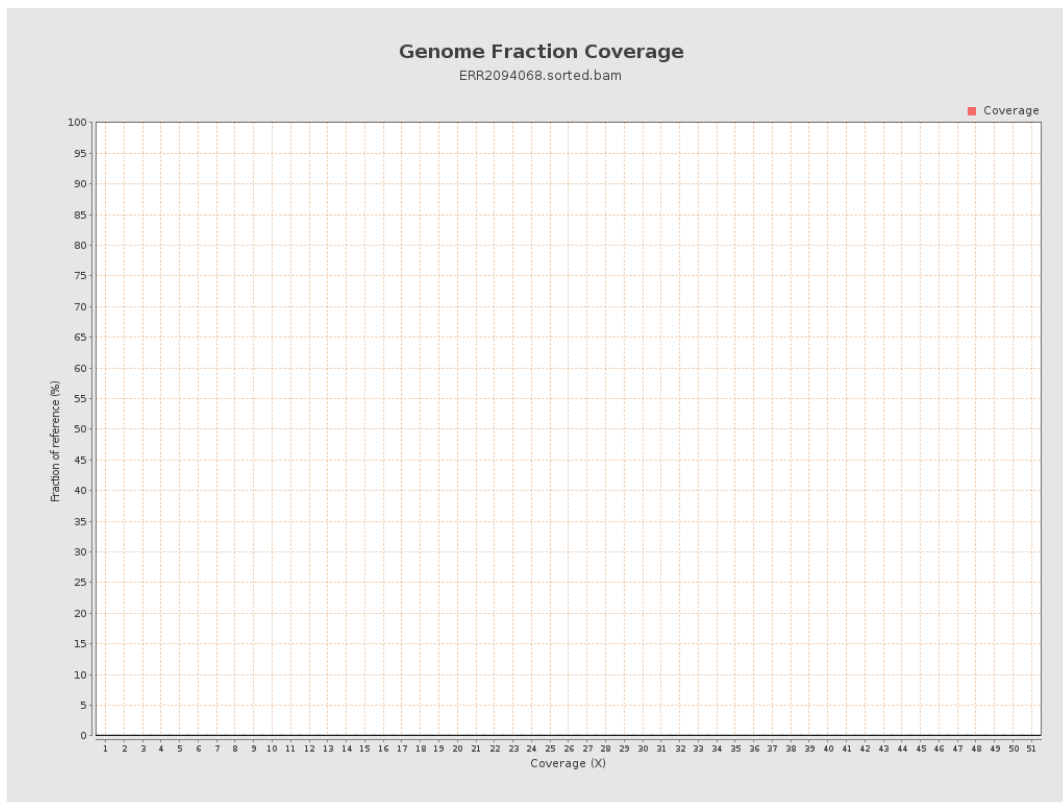




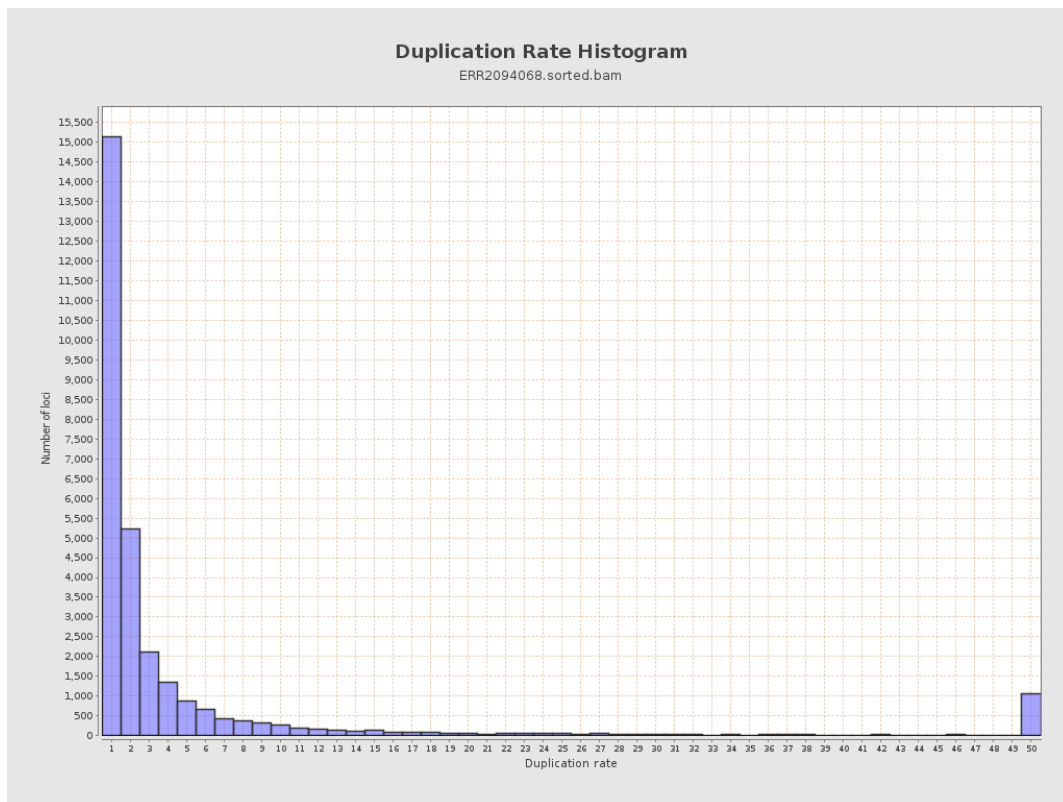
## 5. Results : Coverage Histogram (0-50X)



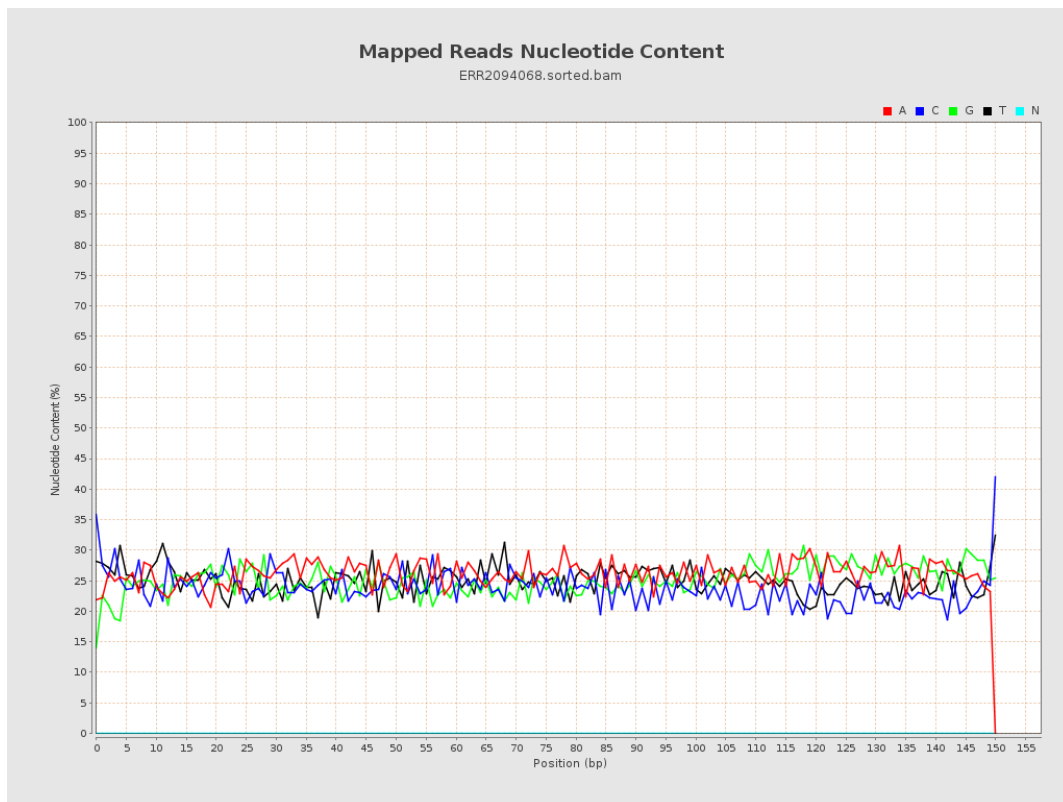
## 6. Results : Genome Fraction Coverage



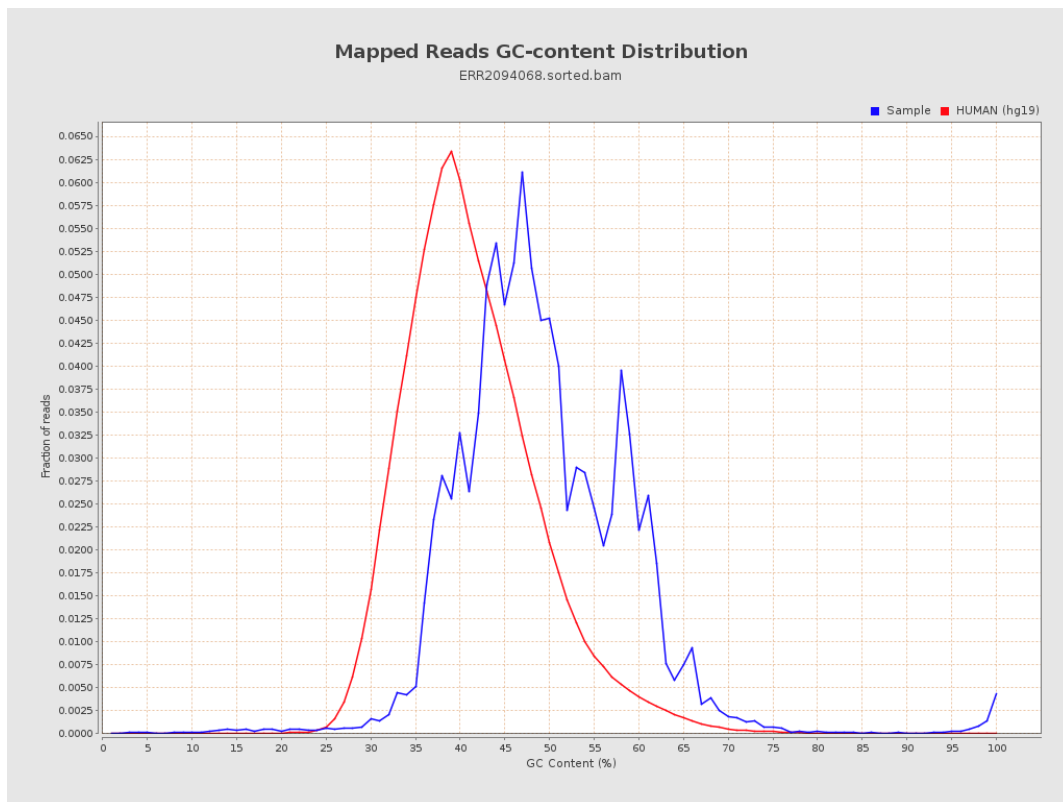
## 7. Results : Duplication Rate Histogram



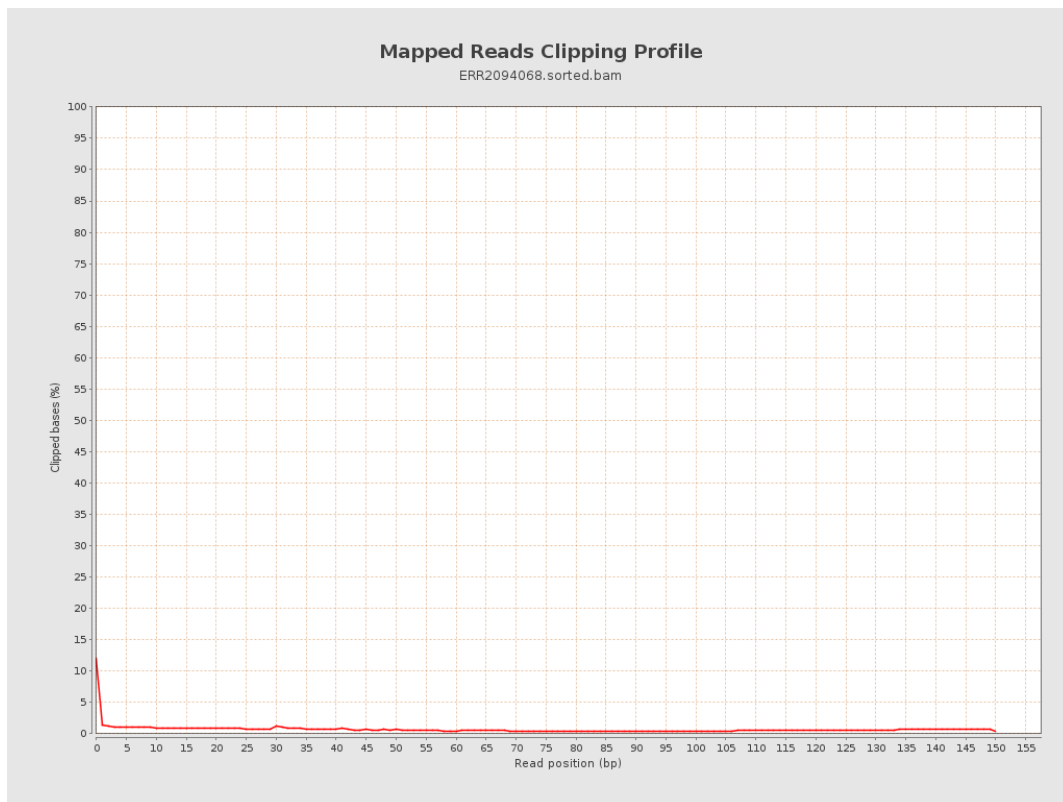
## 8. Results : Mapped Reads Nucleotide Content



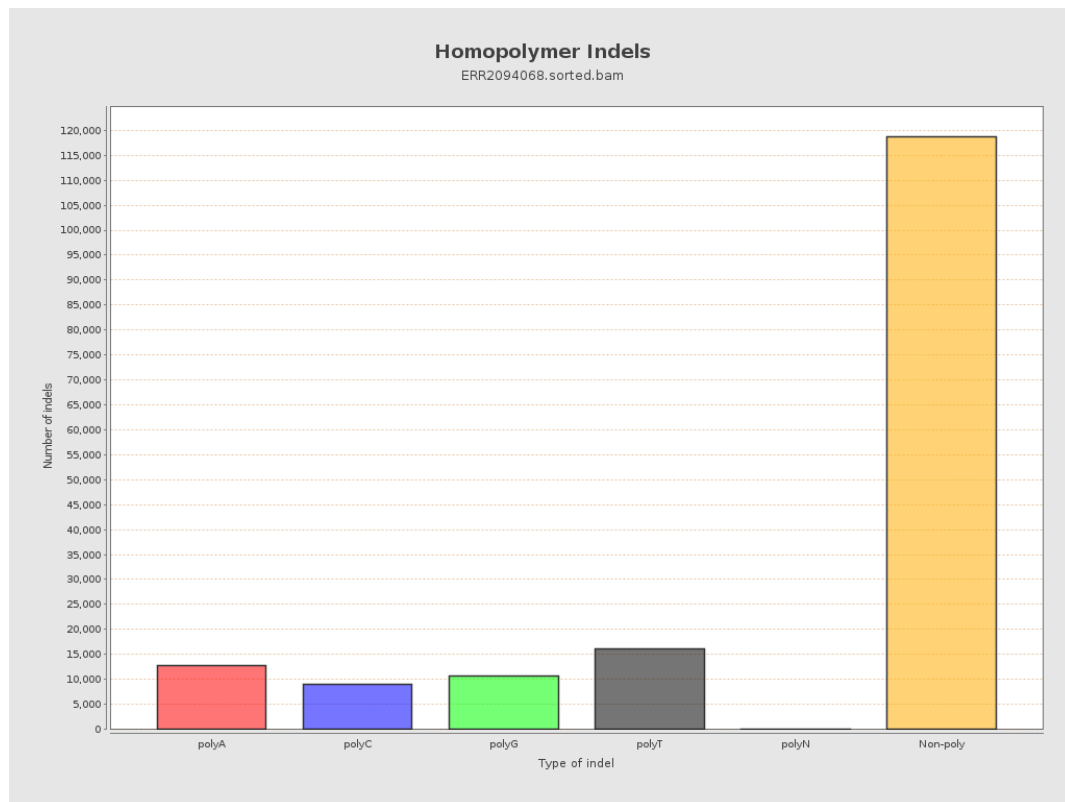
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

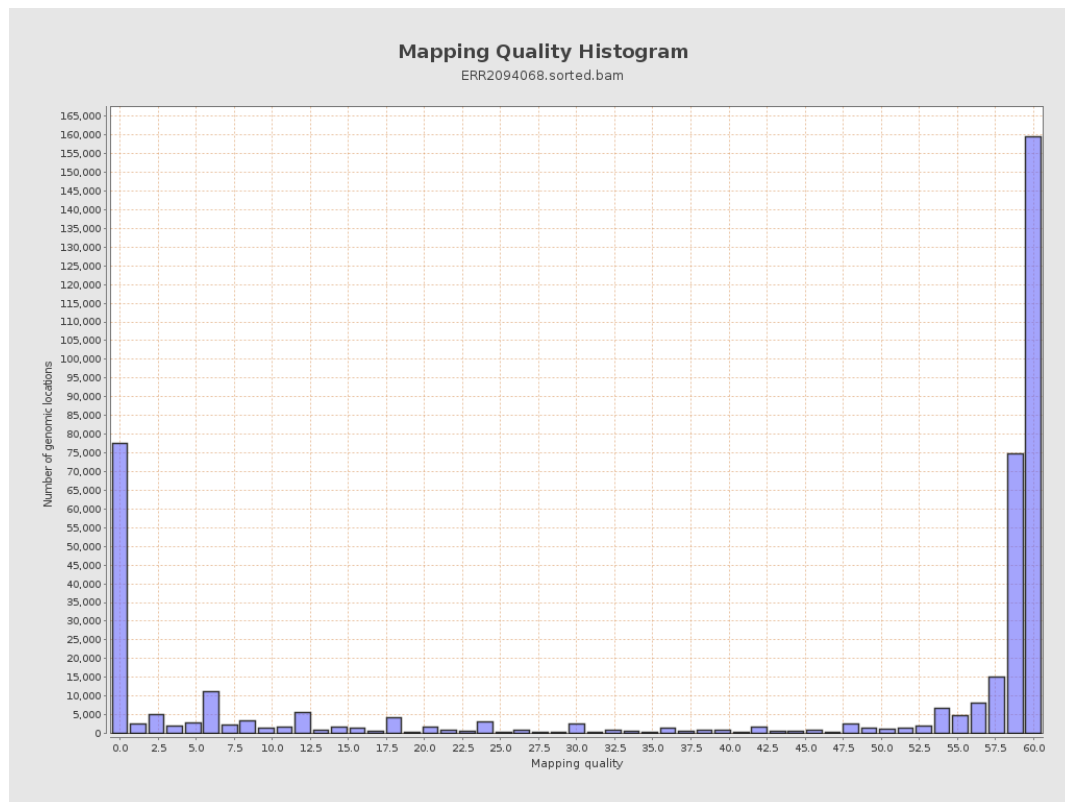


## 12. Results : Mapping Quality Across Reference

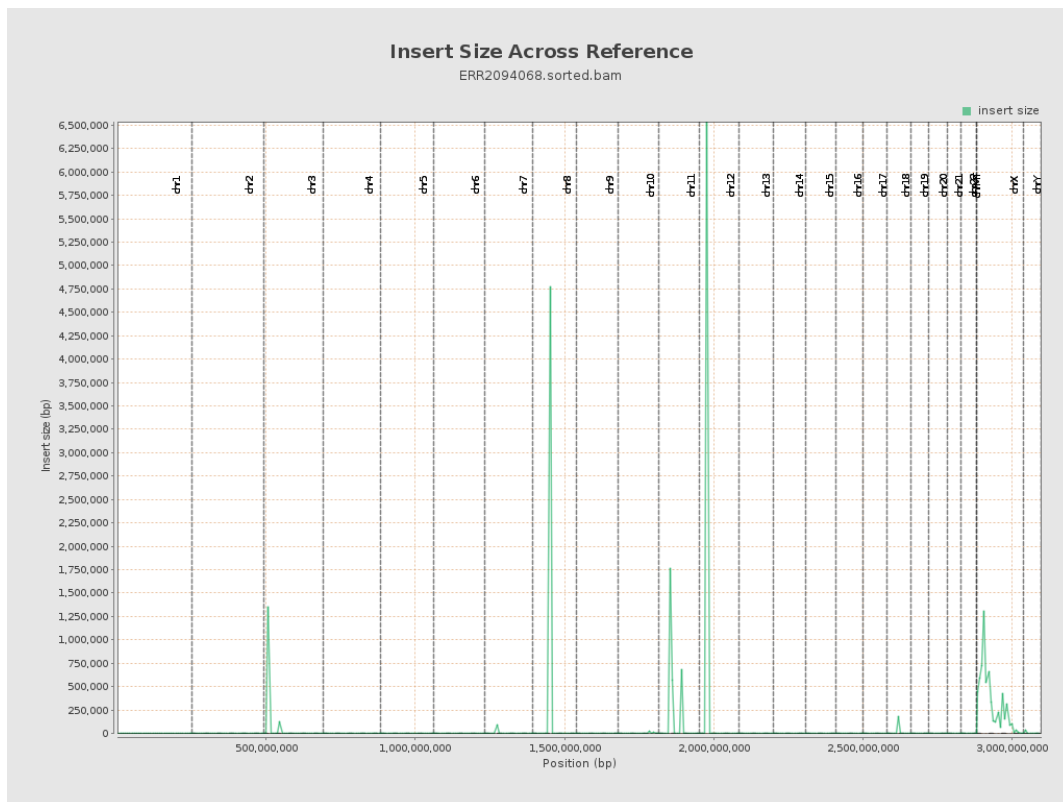




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

