

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/27 00:30:04*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094088.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_ERR2094088 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094088_1.fastq.gz ERR2094088_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                  |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                   |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                   |
| Analysis date:                        | Tue Aug 27 00:30:03 CST 2024                                                                                                                                                                                         |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                    |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                   |
| Number of windows:                    | 400                                                                                                                                                                                                                  |
| BAM file:                             | ERR2094088.sorted.bam                                                                                                                                                                                                |

## 2. Summary

### 2.1. Globals

|                              |                   |
|------------------------------|-------------------|
| Reference size               | 3,095,693,983     |
| Number of reads              | 166               |
| Mapped reads                 | 141 / 84.94%      |
| Unmapped reads               | 25 / 15.06%       |
| Mapped paired reads          | 141 / 84.94%      |
| Mapped reads, first in pair  | 72 / 43.37%       |
| Mapped reads, second in pair | 69 / 41.57%       |
| Mapped reads, both in pair   | 134 / 80.72%      |
| Mapped reads, singletons     | 7 / 4.22%         |
| Secondary alignments         | 0                 |
| Supplementary alignments     | 4 / 2.41%         |
| Read min/max/mean length     | 30 / 151 / 135.55 |
| Duplicated reads (estimated) | 30 / 18.07%       |
| Duplication rate             | 19.13%            |
| Clipped reads                | 53 / 31.93%       |

### 2.2. ACGT Content

|                          |                |
|--------------------------|----------------|
| Number/percentage of A's | 4,998 / 27.37% |
| Number/percentage of C's | 4,112 / 22.52% |
| Number/percentage of T's | 4,660 / 25.52% |
| Number/percentage of G's | 4,493 / 24.6%  |
| Number/percentage of N's | 0 / 0%         |
|                          |                |

|               |        |
|---------------|--------|
| GC Percentage | 47.12% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0      |
| Standard Deviation | 0.0037 |

## 2.4. Mapping Quality

|                      |      |
|----------------------|------|
| Mean Mapping Quality | 4.47 |
|----------------------|------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 3,514,229.78    |
| Standard Deviation | 19,828,445.38   |
| P25/Median/P75     | 142 / 170 / 214 |

## 2.6. Mismatches and indels

|                                          |        |
|------------------------------------------|--------|
| General error rate                       | 3.42%  |
| Mismatches                               | 621    |
| Insertions                               | 4      |
| Mapped reads with at least one insertion | 2.84%  |
| Deletions                                | 41     |
| Mapped reads with at least one deletion  | 29.08% |
| Homopolymer indels                       | 24.44% |

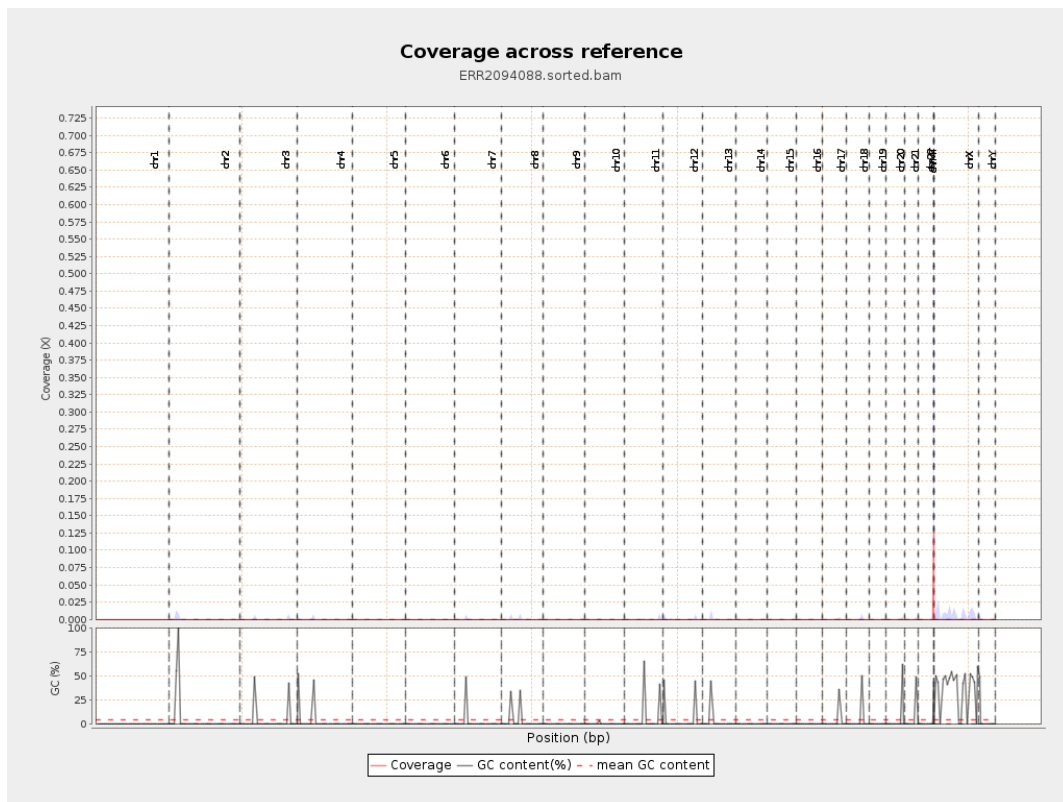
## 2.7. Chromosome stats

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

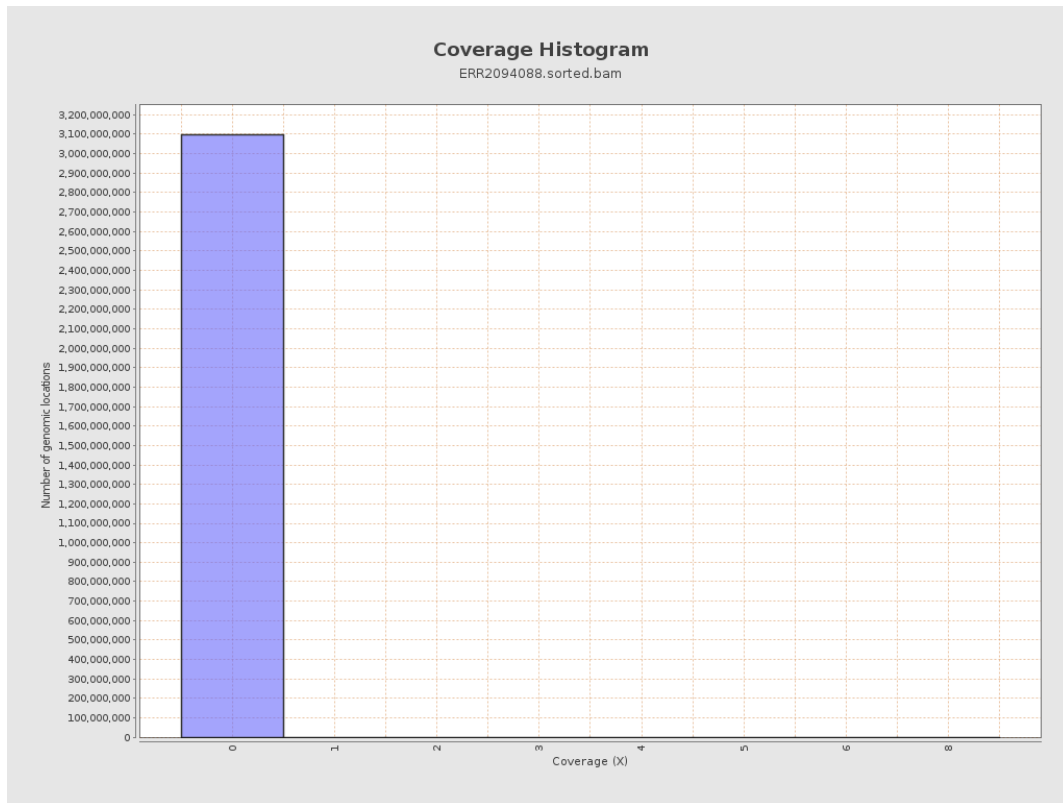
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 0            | 0               | 0                |
| chr2  | 243199373 | 1190         | 0               | 0.0029           |
| chr3  | 198022430 | 503          | 0               | 0.0021           |
| chr4  | 191154276 | 320          | 0               | 0.0016           |
| chr5  | 180915260 | 0            | 0               | 0                |
| chr6  | 171115067 | 0            | 0               | 0                |
| chr7  | 159138663 | 214          | 0               | 0.0016           |
| chr8  | 146364022 | 555          | 0               | 0.0028           |
| chr9  | 141213431 | 36           | 0               | 0.0005           |
| chr10 | 135534747 | 30           | 0               | 0.0005           |
| chr11 | 135006516 | 363          | 0               | 0.0021           |
| chr12 | 133851895 | 635          | 0               | 0.0028           |
| chr13 | 115169878 | 868          | 0               | 0.0037           |
| chr14 | 107349540 | 0            | 0               | 0                |
| chr15 | 102531392 | 0            | 0               | 0                |
| chr16 | 90354753  | 0            | 0               | 0                |
| chr17 | 81195210  | 98           | 0               | 0.0011           |
| chr18 | 78077248  | 288          | 0               | 0.0027           |
| chr19 | 59128983  | 0            | 0               | 0                |
| chr20 | 63025520  | 106          | 0               | 0.0013           |
| chr21 | 48129895  | 112          | 0               | 0.0014           |
| chr22 | 51304566  | 0            | 0               | 0                |
| chrMT | 16571     | 2106         | 0.1271          | 0.6847           |
| chrX  | 155270560 | 10939        | 0.0001          | 0.0125           |

|      |          |     |   |        |
|------|----------|-----|---|--------|
| chrY | 59373566 | 214 | 0 | 0.0027 |
|------|----------|-----|---|--------|

### 3. Results : Coverage across reference

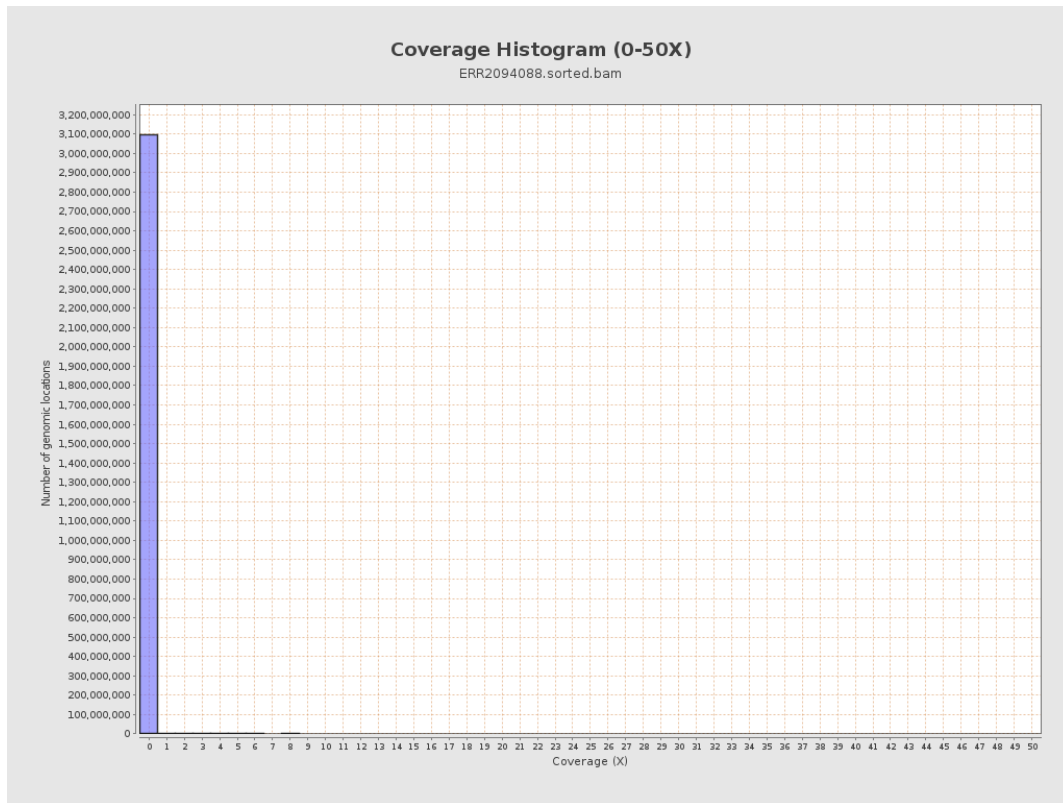


## 4. Results : Coverage Histogram

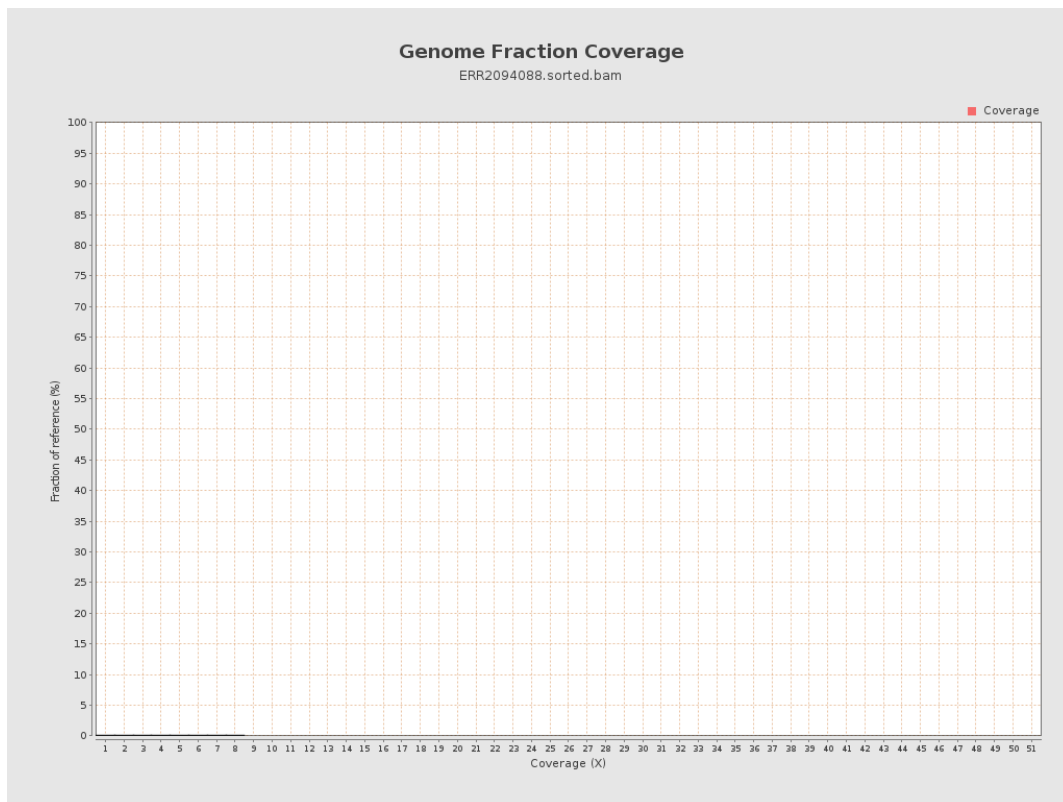




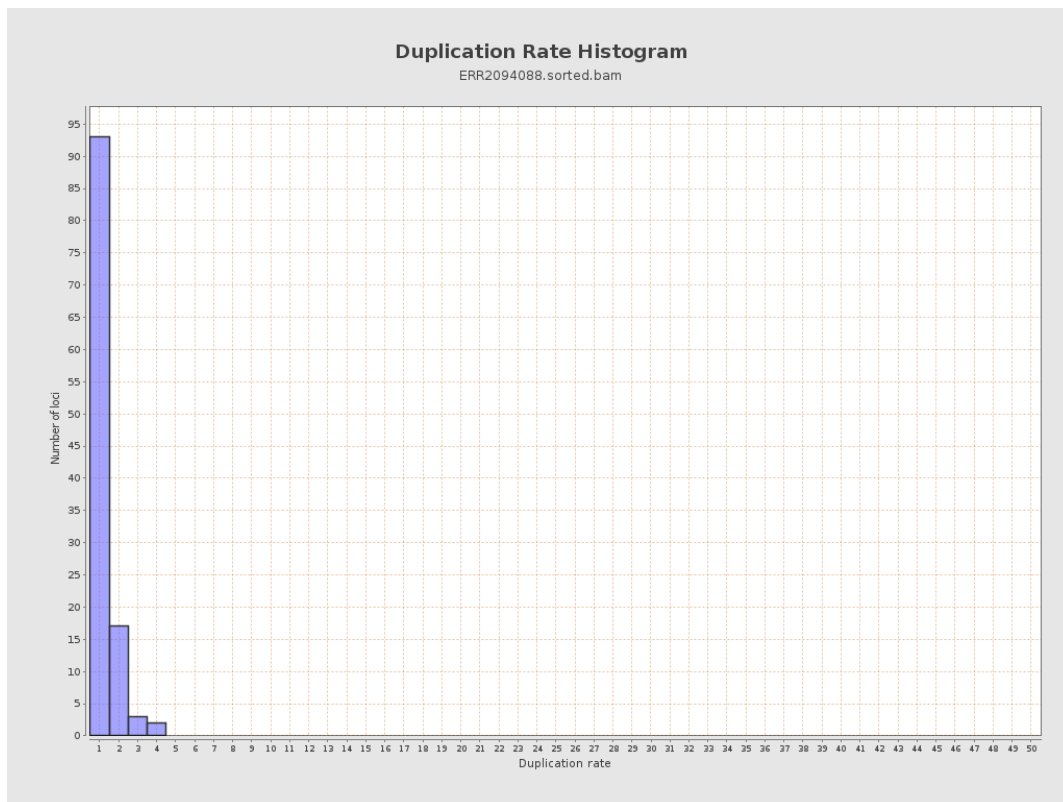
## 5. Results : Coverage Histogram (0-50X)



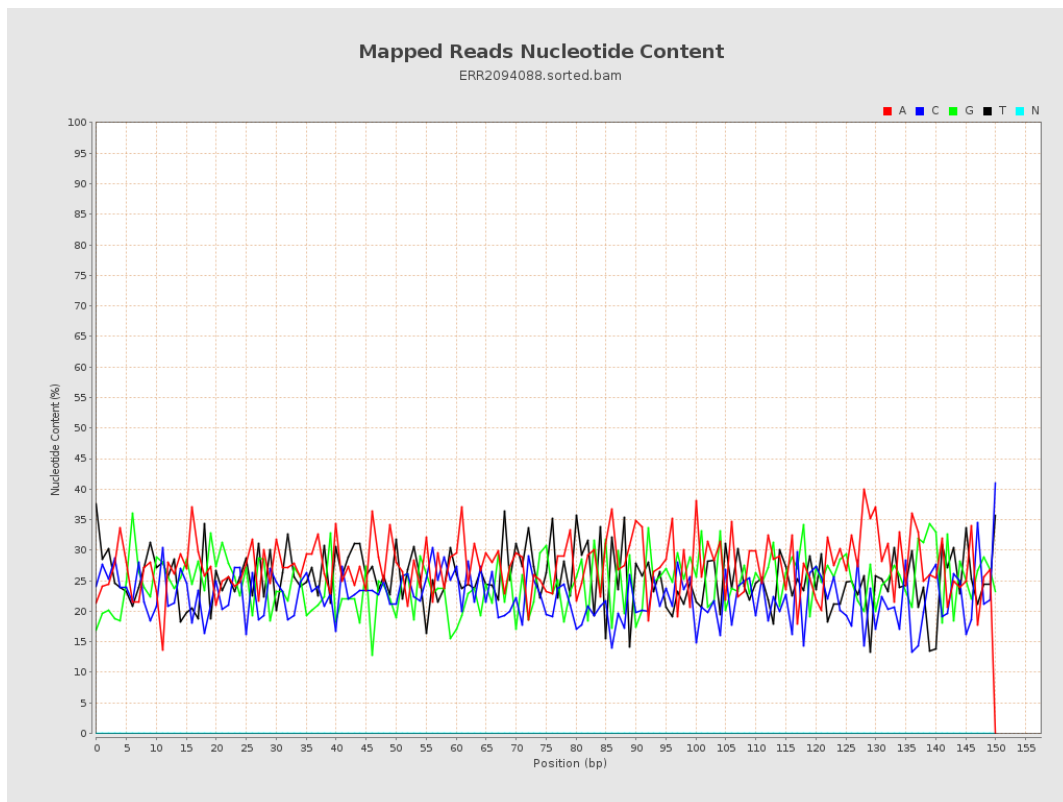
## 6. Results : Genome Fraction Coverage



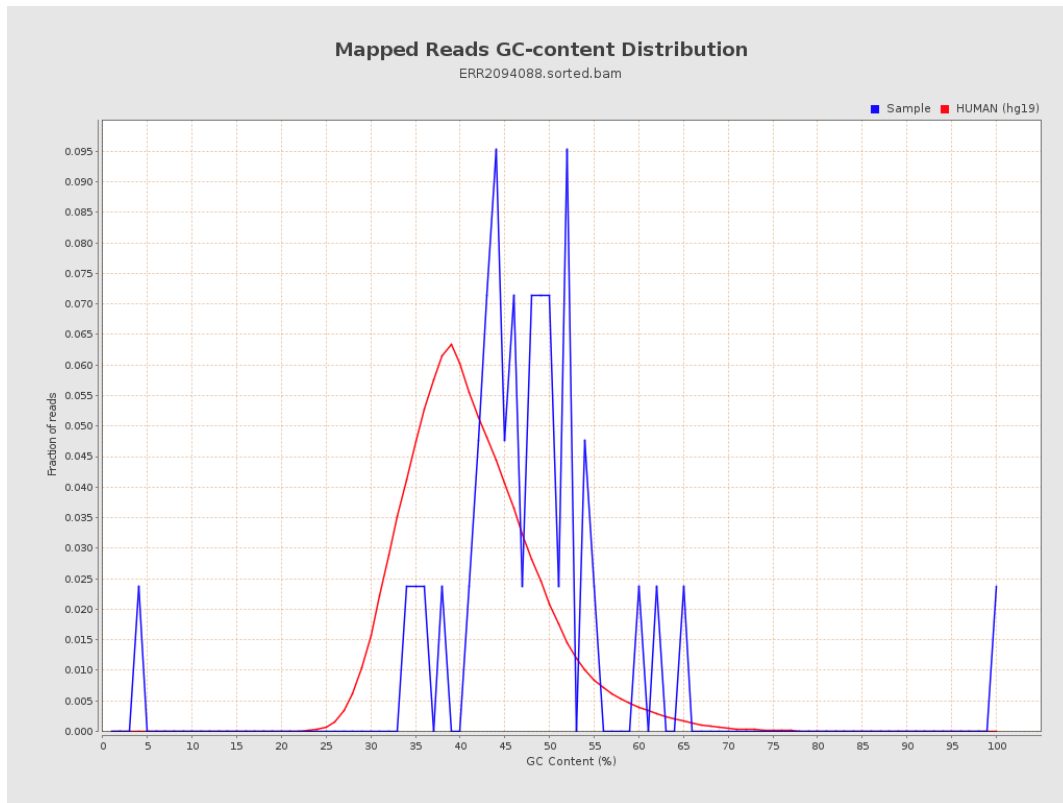
## 7. Results : Duplication Rate Histogram



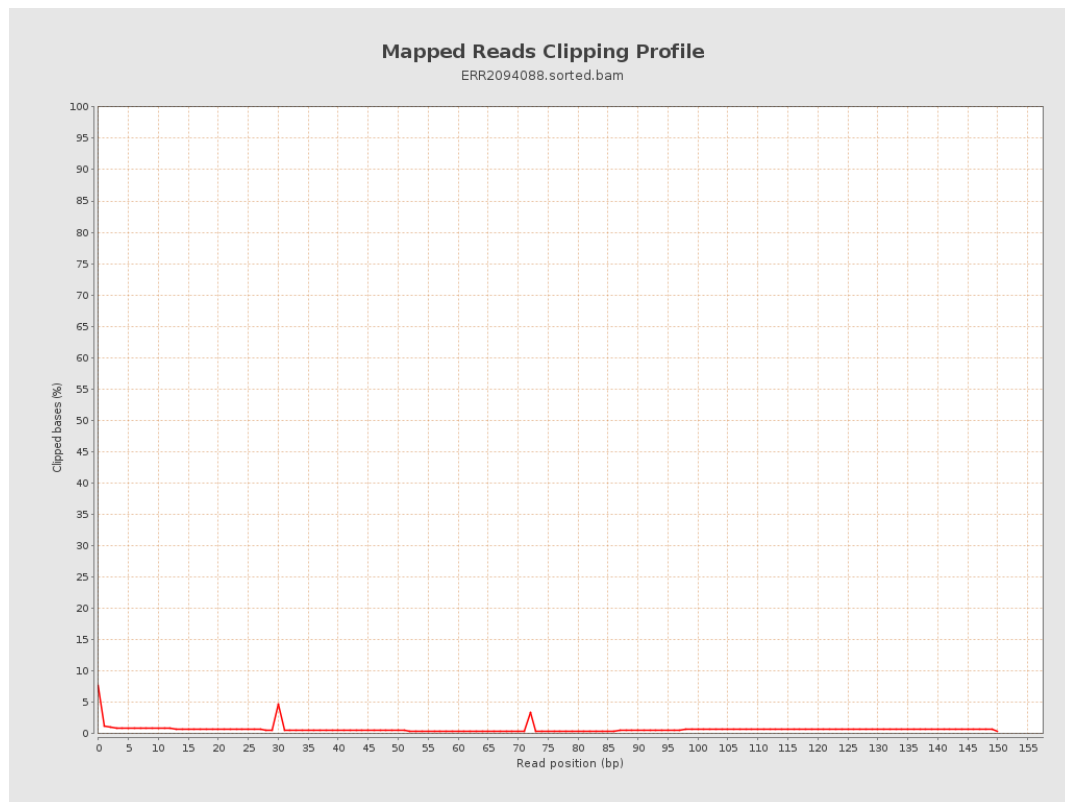
## 8. Results : Mapped Reads Nucleotide Content



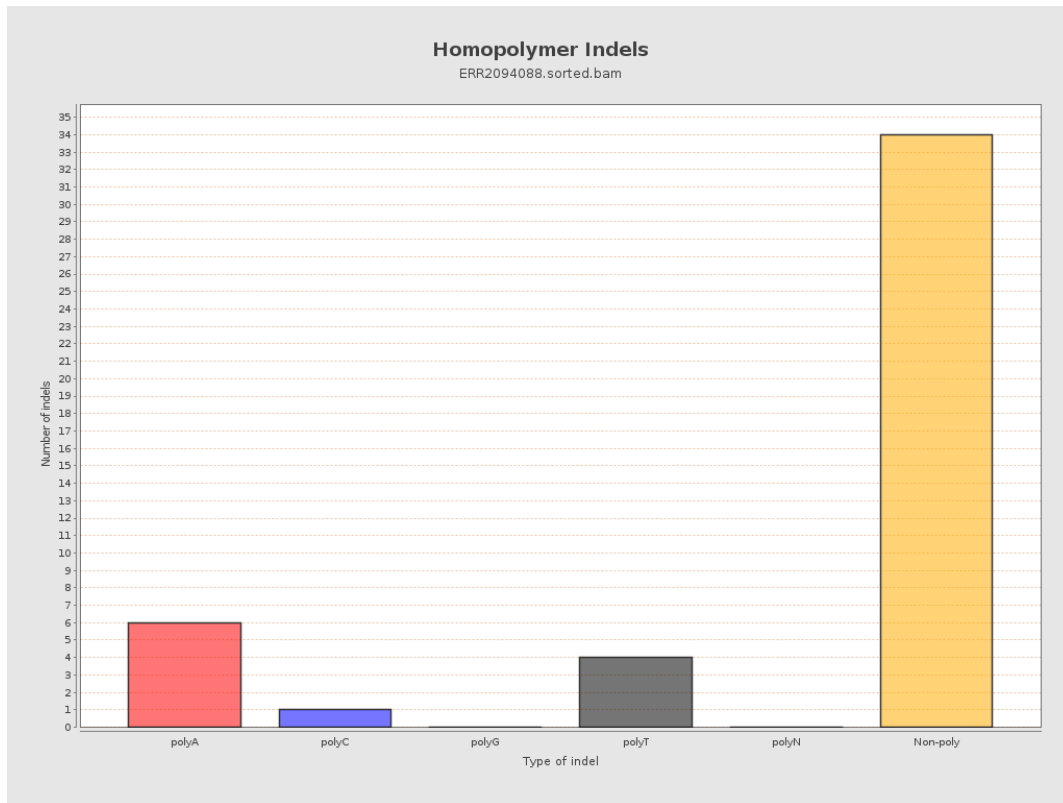
## 9. Results : Mapped Reads GC-content Distribution



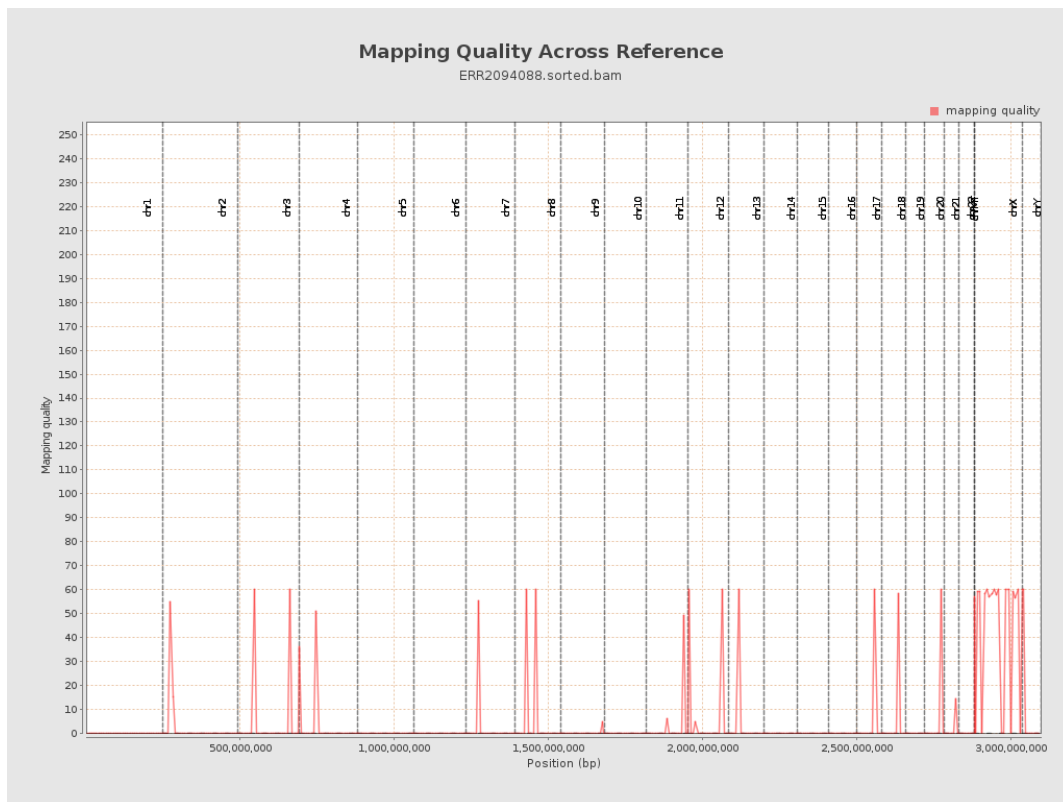
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

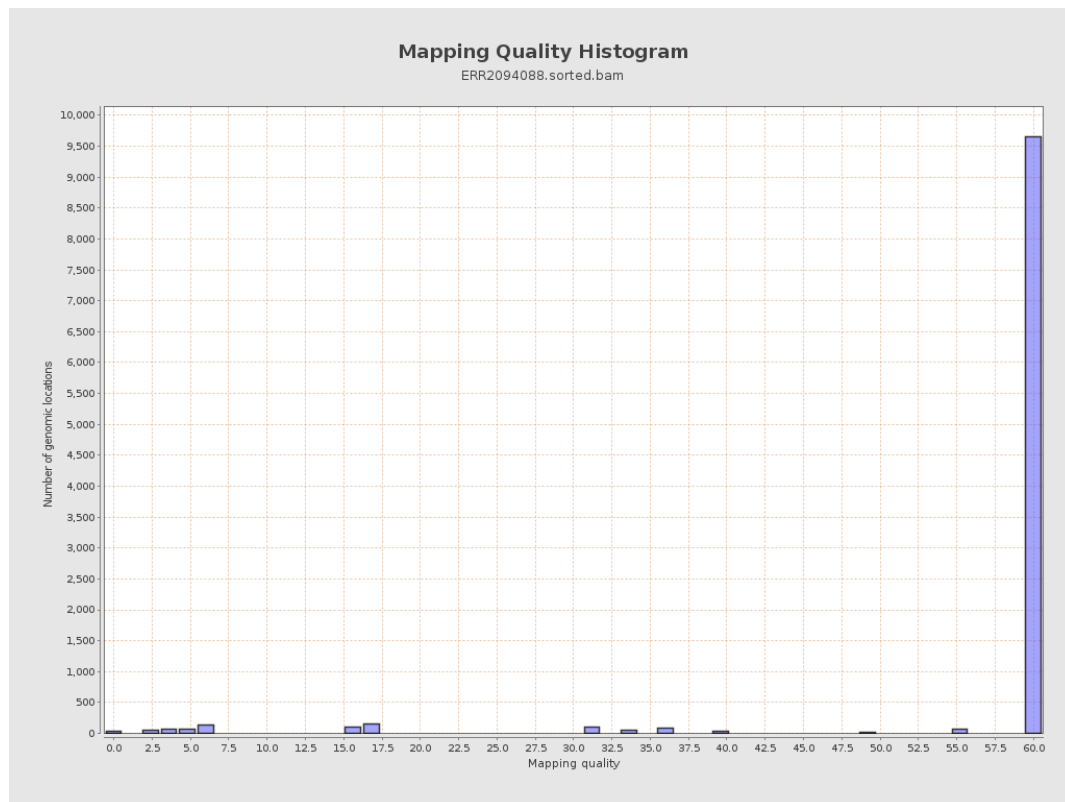


## 12. Results : Mapping Quality Across Reference

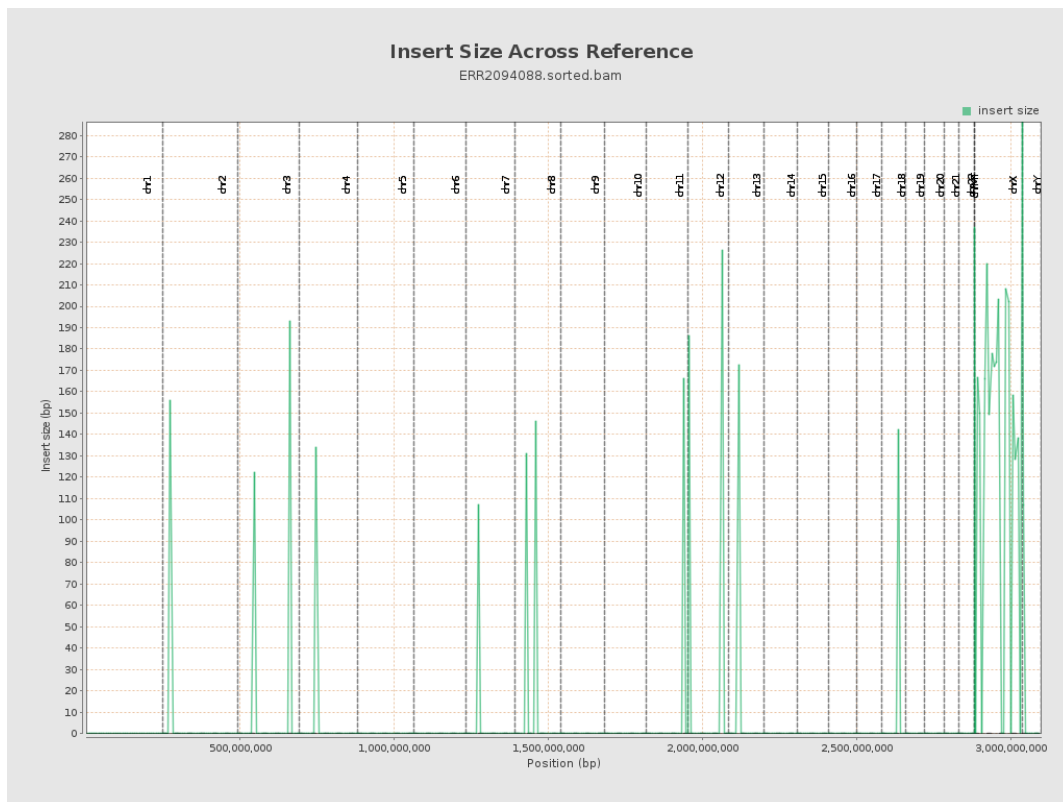




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

