

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/26 23:56:51*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094075.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_ERR2094075 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094075_1.fastq.gz ERR2094075_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                  |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                   |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                   |
| Analysis date:                        | Mon Aug 26 23:56:50 CST 2024                                                                                                                                                                                         |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                    |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                   |
| Number of windows:                    | 400                                                                                                                                                                                                                  |
| BAM file:                             | ERR2094075.sorted.bam                                                                                                                                                                                                |

## 2. Summary

### 2.1. Globals

|                              |                   |
|------------------------------|-------------------|
| Reference size               | 3,095,693,983     |
| Number of reads              | 426,792           |
| Mapped reads                 | 411,080 / 96.32%  |
| Unmapped reads               | 15,712 / 3.68%    |
| Mapped paired reads          | 411,080 / 96.32%  |
| Mapped reads, first in pair  | 206,430 / 48.37%  |
| Mapped reads, second in pair | 204,650 / 47.95%  |
| Mapped reads, both in pair   | 407,948 / 95.58%  |
| Mapped reads, singletons     | 3,132 / 0.73%     |
| Secondary alignments         | 0                 |
| Supplementary alignments     | 17,954 / 4.21%    |
| Read min/max/mean length     | 30 / 151 / 142.53 |
| Duplicated reads (estimated) | 393,314 / 92.16%  |
| Duplication rate             | 50.56%            |
| Clipped reads                | 164,383 / 38.52%  |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 14,080,823 / 26.24% |
| Number/percentage of C's | 12,708,791 / 23.68% |
| Number/percentage of T's | 13,499,669 / 25.16% |
| Number/percentage of G's | 13,372,640 / 24.92% |
| Number/percentage of N's | 660 / 0%            |
|                          |                     |

|               |       |
|---------------|-------|
| GC Percentage | 48.6% |
|---------------|-------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.0177 |
| Standard Deviation | 4.579  |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 40.79 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 572,752.09      |
| Standard Deviation | 6,833,088.26    |
| P25/Median/P75     | 137 / 168 / 198 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 4.04%     |
| Mismatches                               | 2,089,595 |
| Insertions                               | 34,563    |
| Mapped reads with at least one insertion | 8.26%     |
| Deletions                                | 162,838   |
| Mapped reads with at least one deletion  | 37.68%    |
| Homopolymer indels                       | 28.22%    |

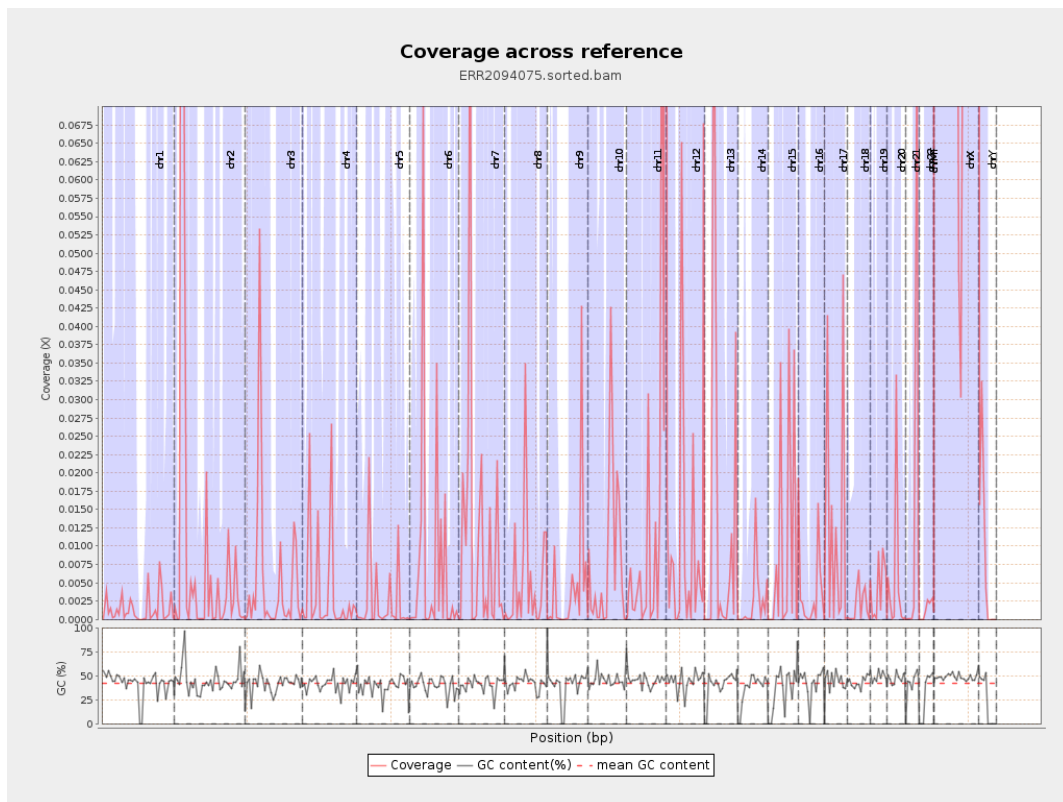
## 2.7. Chromosome stats

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

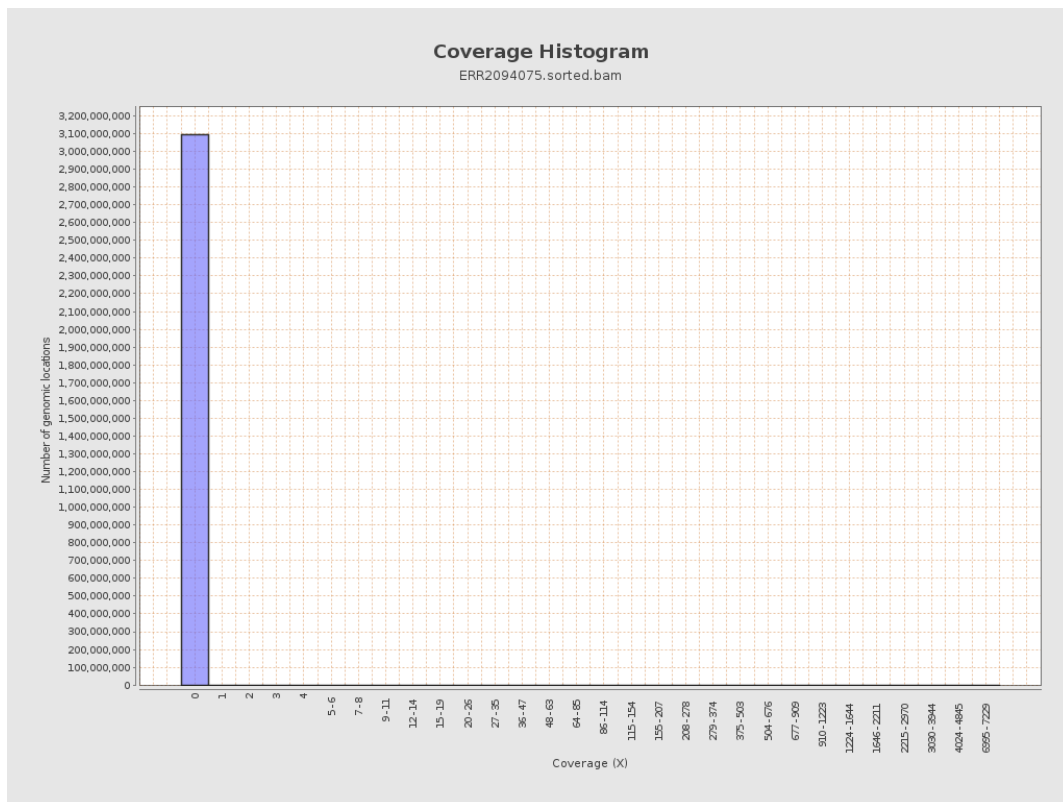
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 357801       | 0.0014          | 0.5019           |
| chr2  | 243199373 | 2470080      | 0.0102          | 4.0574           |
| chr3  | 198022430 | 1006969      | 0.0051          | 1.845            |
| chr4  | 191154276 | 707681       | 0.0037          | 1.5483           |
| chr5  | 180915260 | 427565       | 0.0024          | 1.1335           |
| chr6  | 171115067 | 1282714      | 0.0075          | 3.7308           |
| chr7  | 159138663 | 1750660      | 0.011           | 3.7143           |
| chr8  | 146364022 | 764492       | 0.0052          | 1.7389           |
| chr9  | 141213431 | 637332       | 0.0045          | 1.8713           |
| chr10 | 135534747 | 1132780      | 0.0084          | 2.7155           |
| chr11 | 135006516 | 1892413      | 0.014           | 3.9084           |
| chr12 | 133851895 | 1364789      | 0.0102          | 3.4862           |
| chr13 | 115169878 | 1506009      | 0.0131          | 3.5313           |
| chr14 | 107349540 | 279251       | 0.0026          | 1.0708           |
| chr15 | 102531392 | 946448       | 0.0092          | 2.8449           |
| chr16 | 90354753  | 342878       | 0.0038          | 1.2753           |
| chr17 | 81195210  | 1023444      | 0.0126          | 3.9135           |
| chr18 | 78077248  | 158115       | 0.002           | 0.6248           |
| chr19 | 59128983  | 233491       | 0.0039          | 0.954            |
| chr20 | 63025520  | 348708       | 0.0055          | 1.8706           |
| chr21 | 48129895  | 703045       | 0.0146          | 6.3654           |
| chr22 | 51304566  | 71684        | 0.0014          | 0.2971           |
| chrMT | 16571     | 1362694      | 82.2337         | 384.2186         |
| chrX  | 155270560 | 33571326     | 0.2162          | 16.1389          |

|      |          |        |        |        |
|------|----------|--------|--------|--------|
| chrY | 59373566 | 505889 | 0.0085 | 1.9632 |
|------|----------|--------|--------|--------|

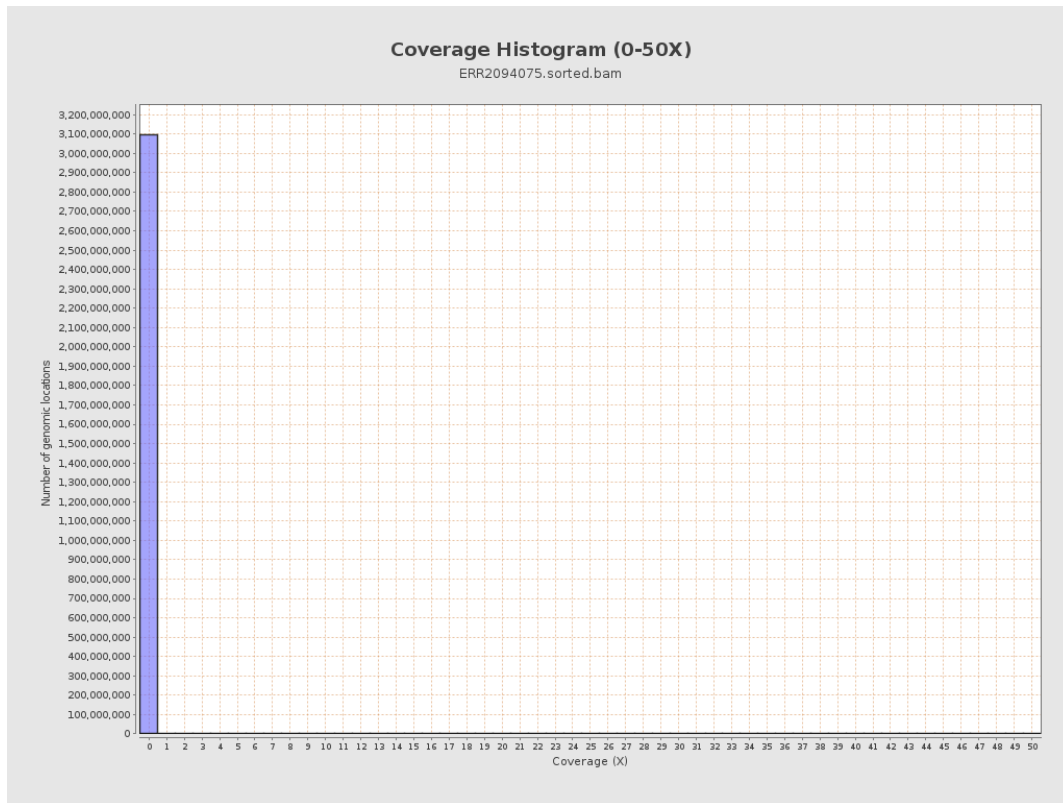
### 3. Results : Coverage across reference



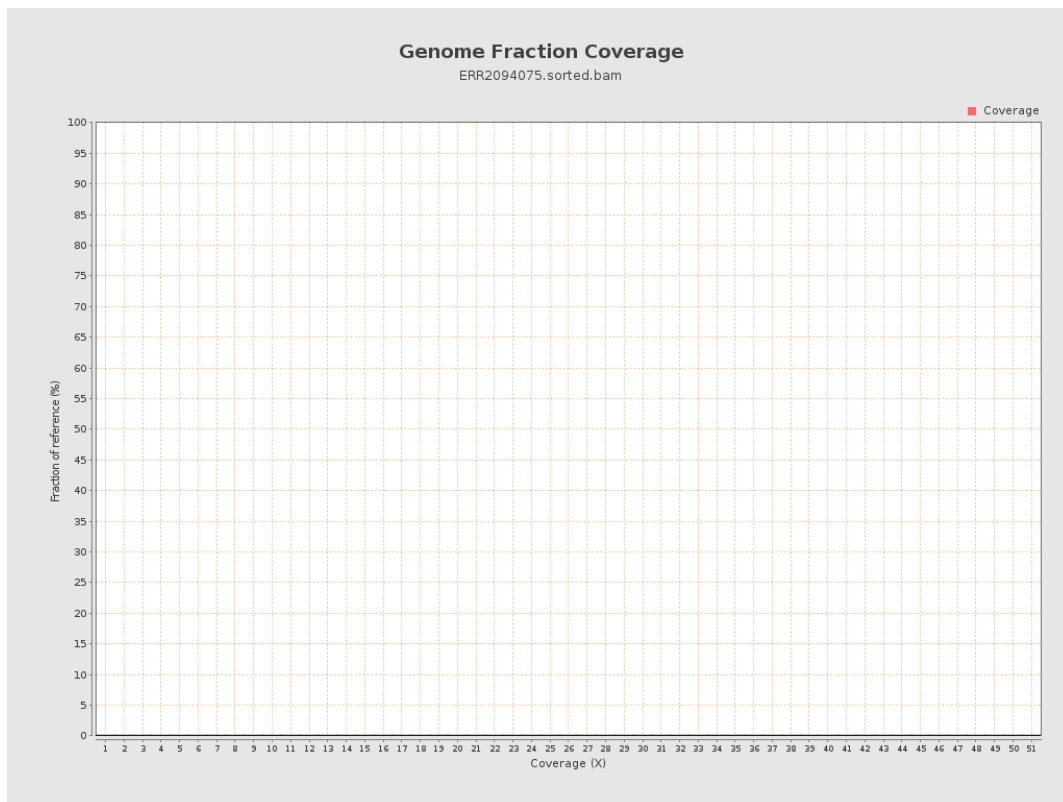
## 4. Results : Coverage Histogram



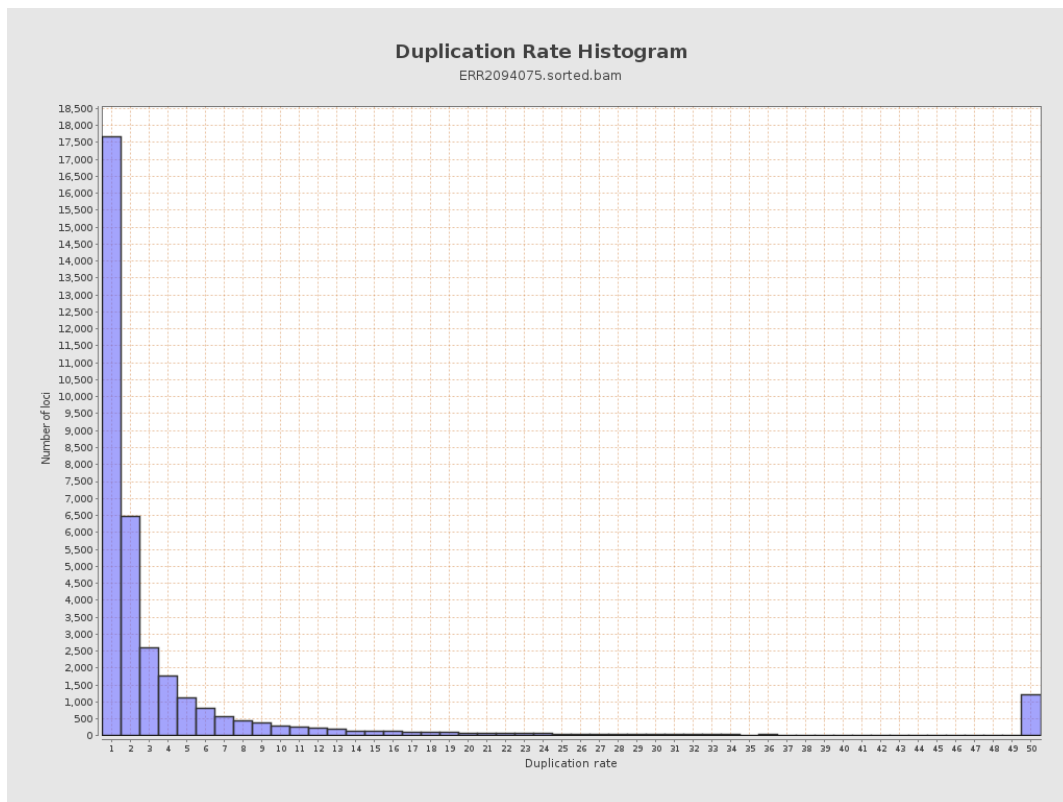
## 5. Results : Coverage Histogram (0-50X)



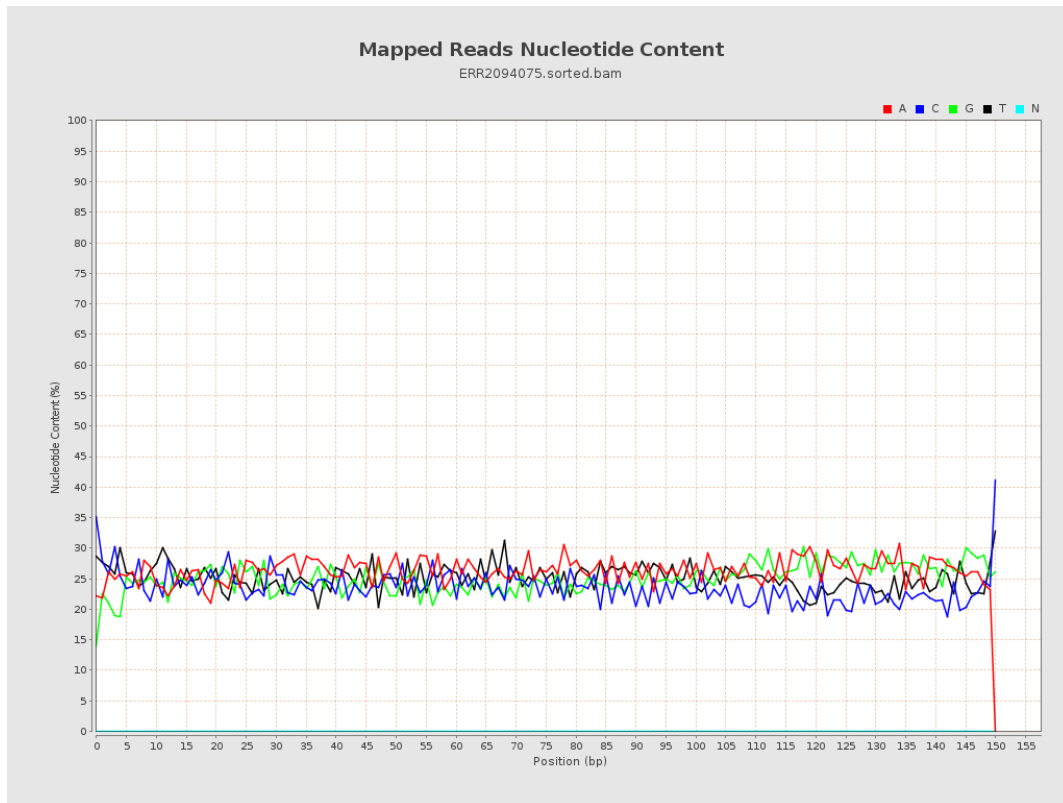
## 6. Results : Genome Fraction Coverage



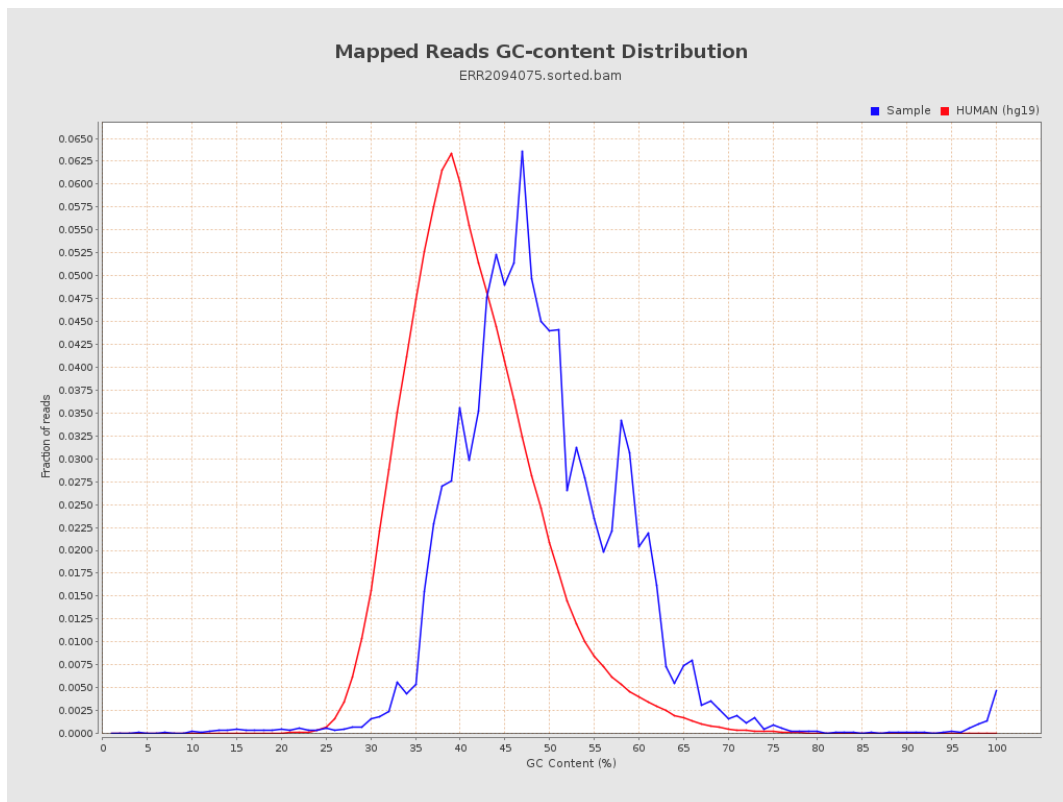
## 7. Results : Duplication Rate Histogram



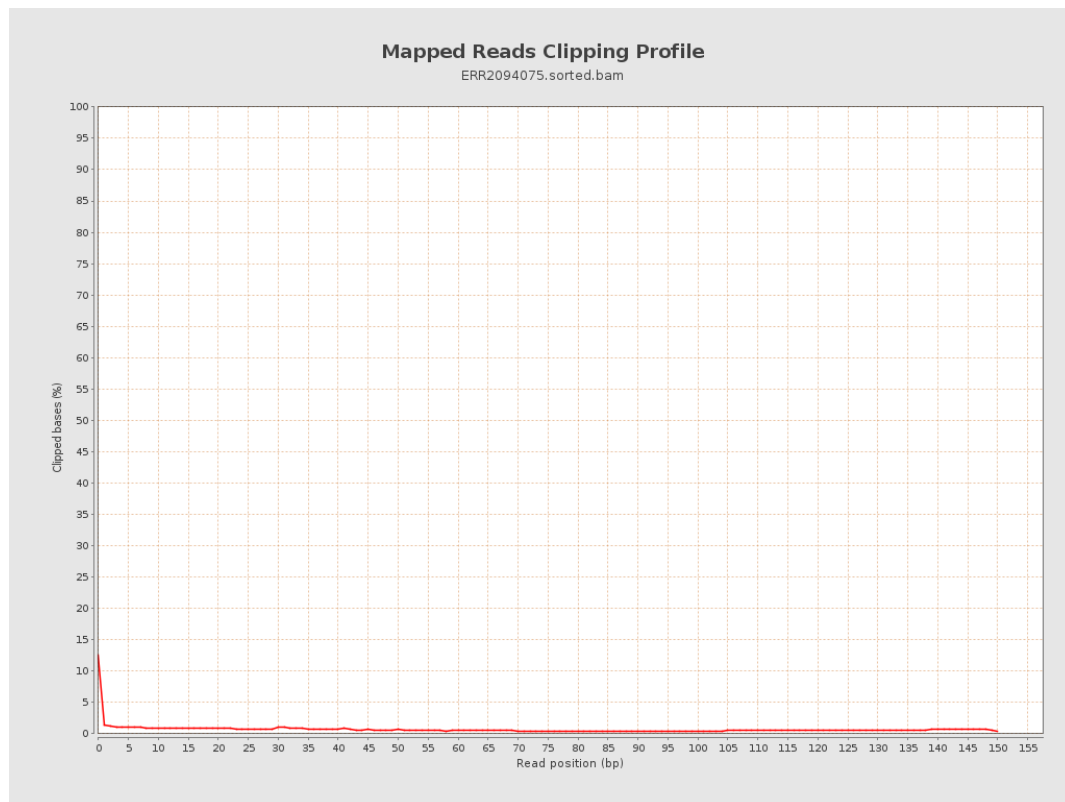
## 8. Results : Mapped Reads Nucleotide Content



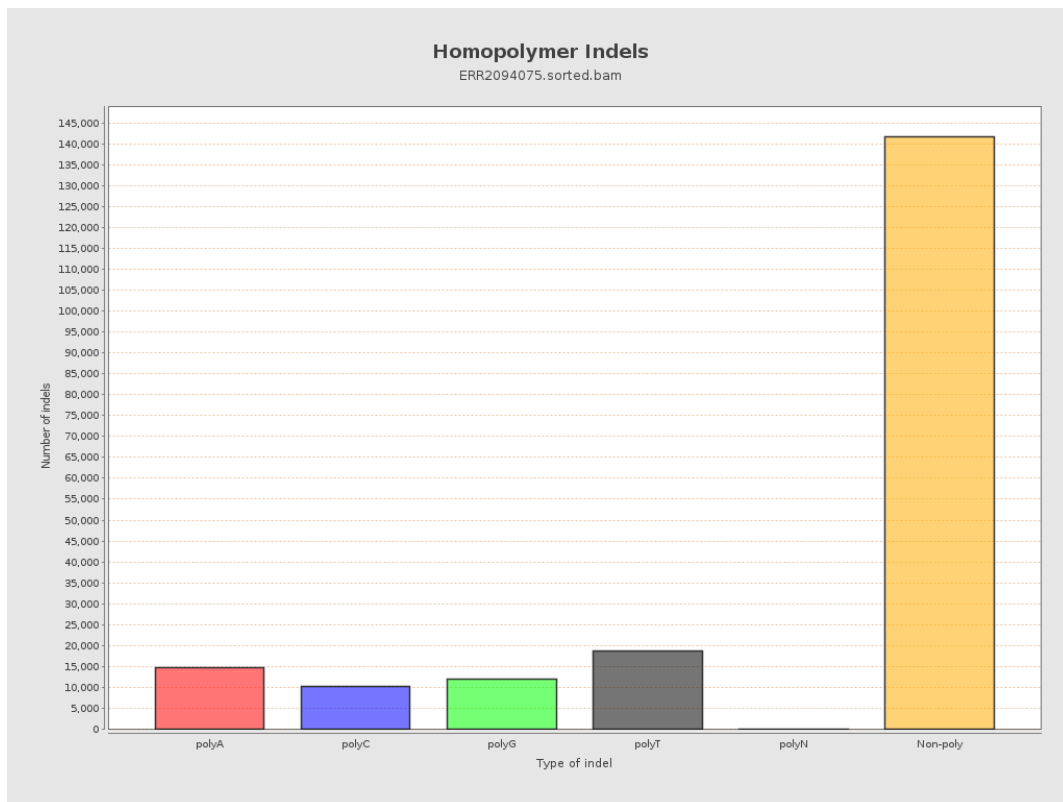
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



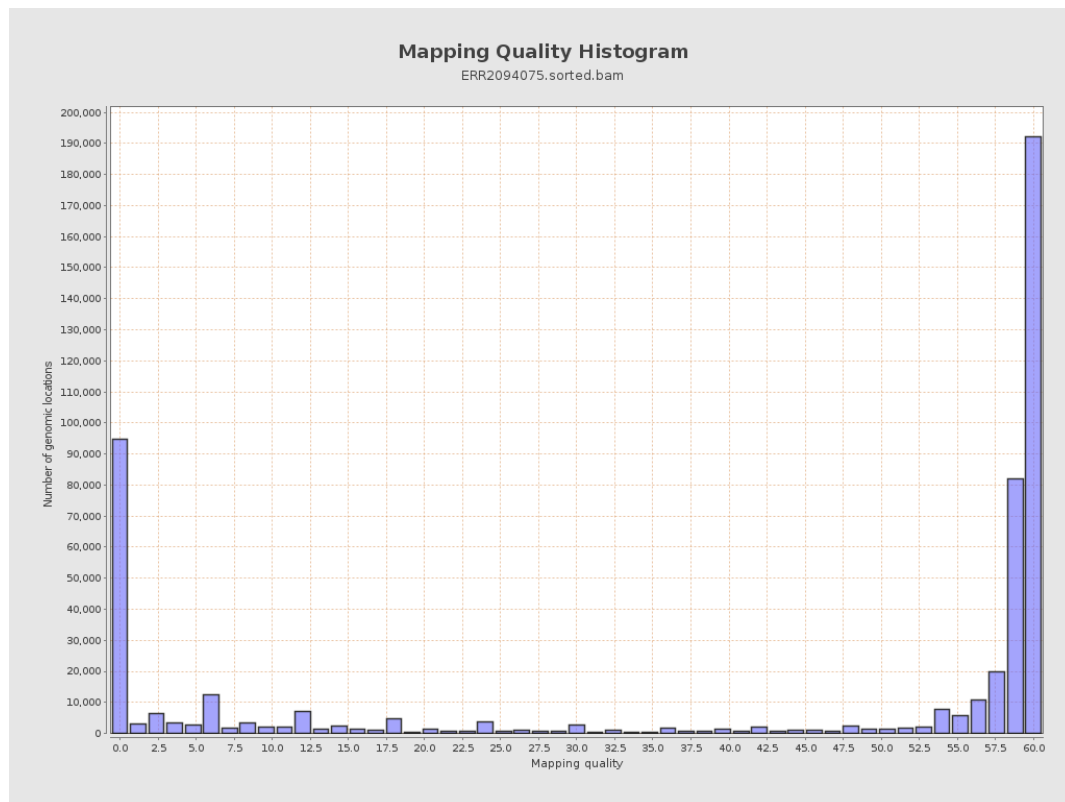
## 11. Results : Homopolymer Indels



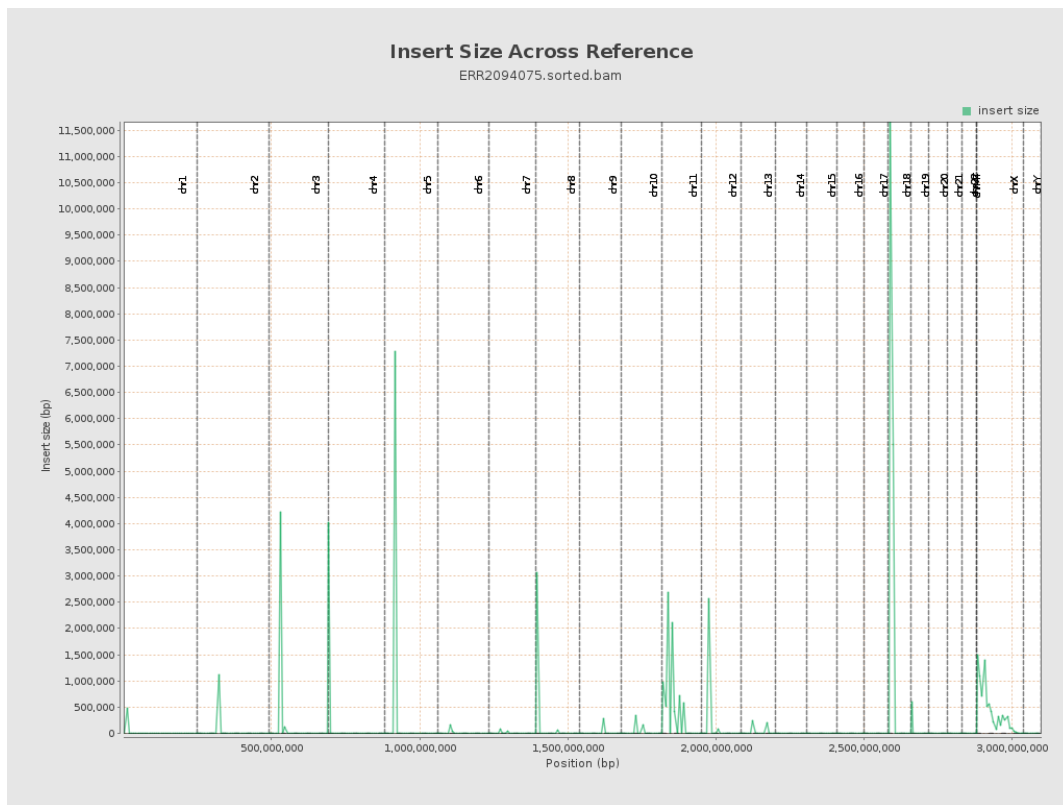
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

