

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/26 23:54:29*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094074.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_ERR2094074 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094074_1.fastq.gz ERR2094074_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                  |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                   |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                   |
| Analysis date:                        | Mon Aug 26 23:54:28 CST 2024                                                                                                                                                                                         |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                    |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                   |
| Number of windows:                    | 400                                                                                                                                                                                                                  |
| BAM file:                             | ERR2094074.sorted.bam                                                                                                                                                                                                |

## 2. Summary

### 2.1. Globals

|                              |                   |
|------------------------------|-------------------|
| Reference size               | 3,095,693,983     |
| Number of reads              | 372,454           |
| Mapped reads                 | 359,368 / 96.49%  |
| Unmapped reads               | 13,086 / 3.51%    |
| Mapped paired reads          | 359,368 / 96.49%  |
| Mapped reads, first in pair  | 180,555 / 48.48%  |
| Mapped reads, second in pair | 178,813 / 48.01%  |
| Mapped reads, both in pair   | 356,918 / 95.83%  |
| Mapped reads, singletons     | 2,450 / 0.66%     |
| Secondary alignments         | 0                 |
| Supplementary alignments     | 13,519 / 3.63%    |
| Read min/max/mean length     | 30 / 151 / 142.79 |
| Duplicated reads (estimated) | 341,239 / 91.62%  |
| Duplication rate             | 49.88%            |
| Clipped reads                | 143,371 / 38.49%  |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 12,715,955 / 27.14% |
| Number/percentage of C's | 10,816,153 / 23.08% |
| Number/percentage of T's | 12,001,519 / 25.61% |
| Number/percentage of G's | 11,327,658 / 24.17% |
| Number/percentage of N's | 514 / 0%            |
|                          |                     |

|               |        |
|---------------|--------|
| GC Percentage | 47.25% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.0155 |
| Standard Deviation | 4.1481 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 38.76 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 438,983.8       |
| Standard Deviation | 5,978,868.79    |
| P25/Median/P75     | 141 / 168 / 201 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 4.1%      |
| Mismatches                               | 1,852,443 |
| Insertions                               | 30,196    |
| Mapped reads with at least one insertion | 8.25%     |
| Deletions                                | 144,893   |
| Mapped reads with at least one deletion  | 38.42%    |
| Homopolymer indels                       | 27.74%    |

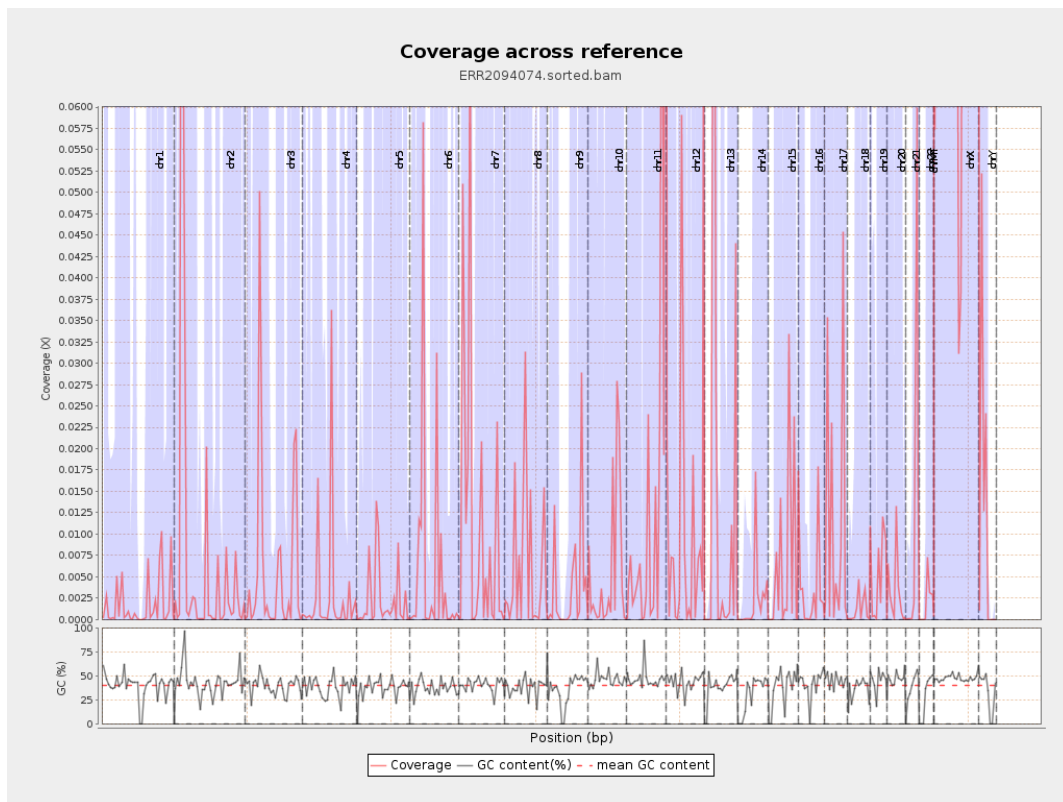
## 2.7. Chromosome stats

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

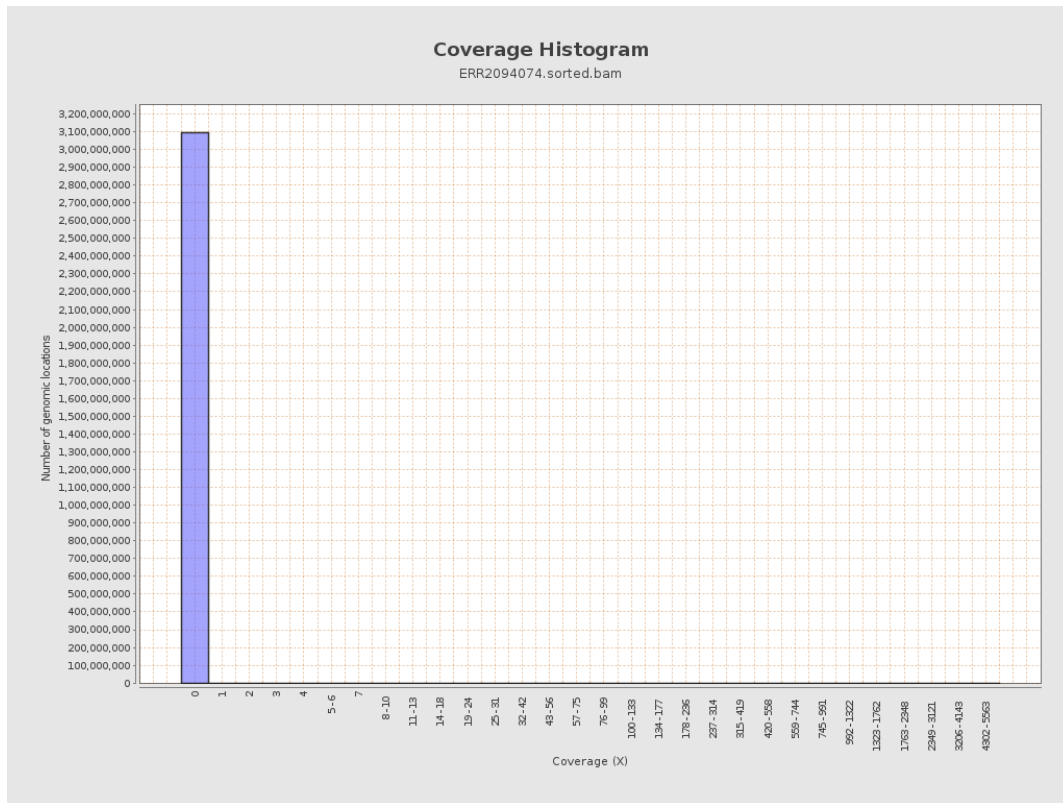
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 440304       | 0.0018          | 0.6867           |
| chr2  | 243199373 | 1661188      | 0.0068          | 2.6326           |
| chr3  | 198022430 | 1061669      | 0.0054          | 2.0684           |
| chr4  | 191154276 | 559871       | 0.0029          | 1.1222           |
| chr5  | 180915260 | 438065       | 0.0024          | 0.896            |
| chr6  | 171115067 | 1007889      | 0.0059          | 3.1275           |
| chr7  | 159138663 | 1685481      | 0.0106          | 3.7636           |
| chr8  | 146364022 | 898454       | 0.0061          | 1.8019           |
| chr9  | 141213431 | 531006       | 0.0038          | 1.4077           |
| chr10 | 135534747 | 723503       | 0.0053          | 1.933            |
| chr11 | 135006516 | 1805838      | 0.0134          | 3.4671           |
| chr12 | 133851895 | 1316609      | 0.0098          | 3.2685           |
| chr13 | 115169878 | 1494954      | 0.013           | 3.8868           |
| chr14 | 107349540 | 251753       | 0.0023          | 1.0257           |
| chr15 | 102531392 | 648690       | 0.0063          | 2.4051           |
| chr16 | 90354753  | 344081       | 0.0038          | 1.2395           |
| chr17 | 81195210  | 942471       | 0.0116          | 3.667            |
| chr18 | 78077248  | 98164        | 0.0013          | 0.4139           |
| chr19 | 59128983  | 282020       | 0.0048          | 1.0274           |
| chr20 | 63025520  | 211339       | 0.0034          | 0.7803           |
| chr21 | 48129895  | 550192       | 0.0114          | 4.1459           |
| chr22 | 51304566  | 104123       | 0.002           | 0.4882           |
| chrMT | 16571     | 1540852      | 92.9849         | 432.3757         |
| chrX  | 155270560 | 28634524     | 0.1844          | 14.7279          |

|      |          |        |        |        |
|------|----------|--------|--------|--------|
| chrY | 59373566 | 695169 | 0.0117 | 2.6992 |
|------|----------|--------|--------|--------|

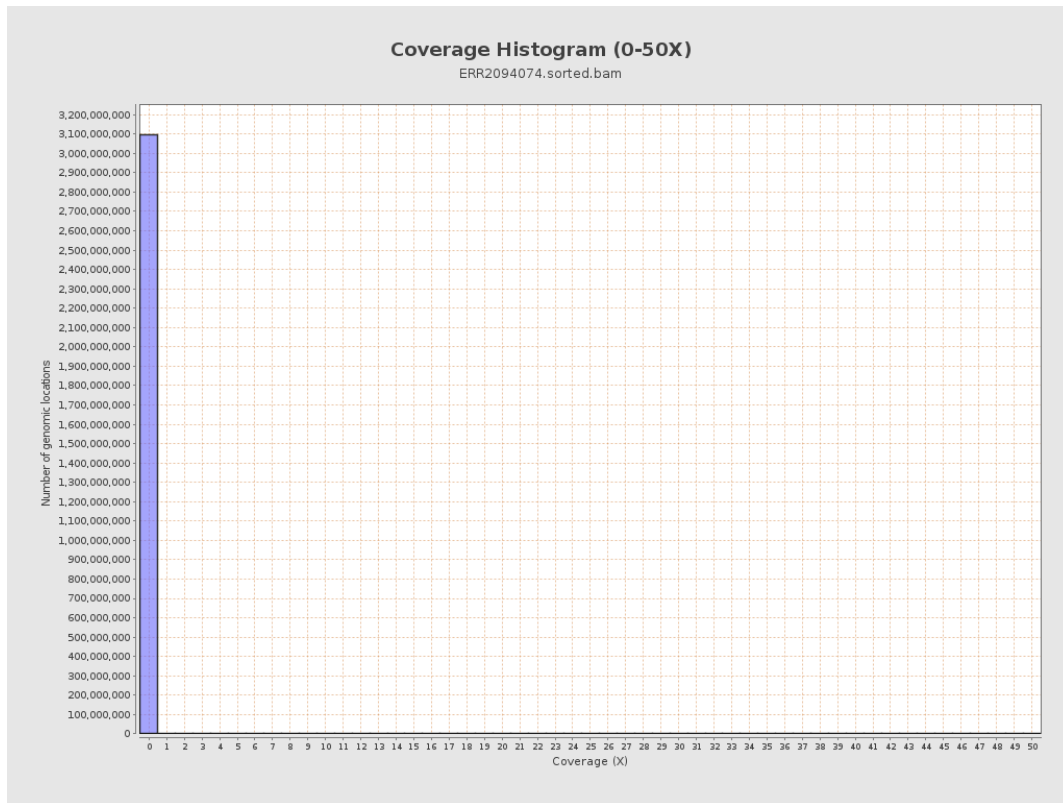
### 3. Results : Coverage across reference



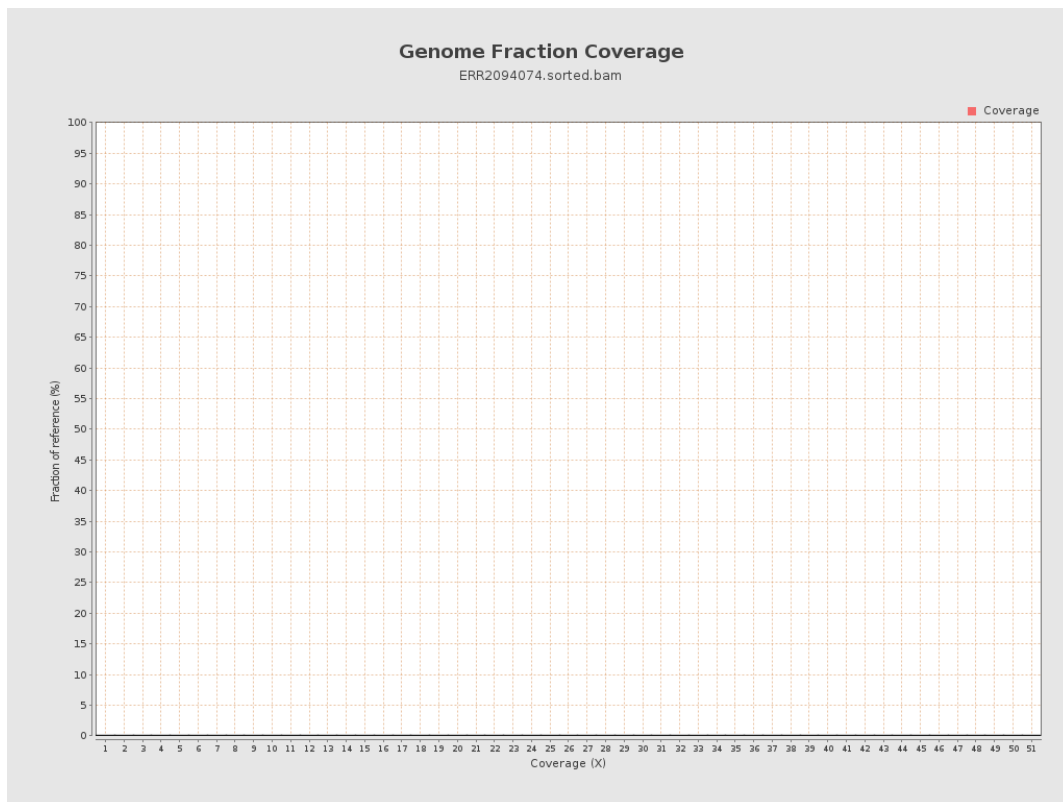
## 4. Results : Coverage Histogram



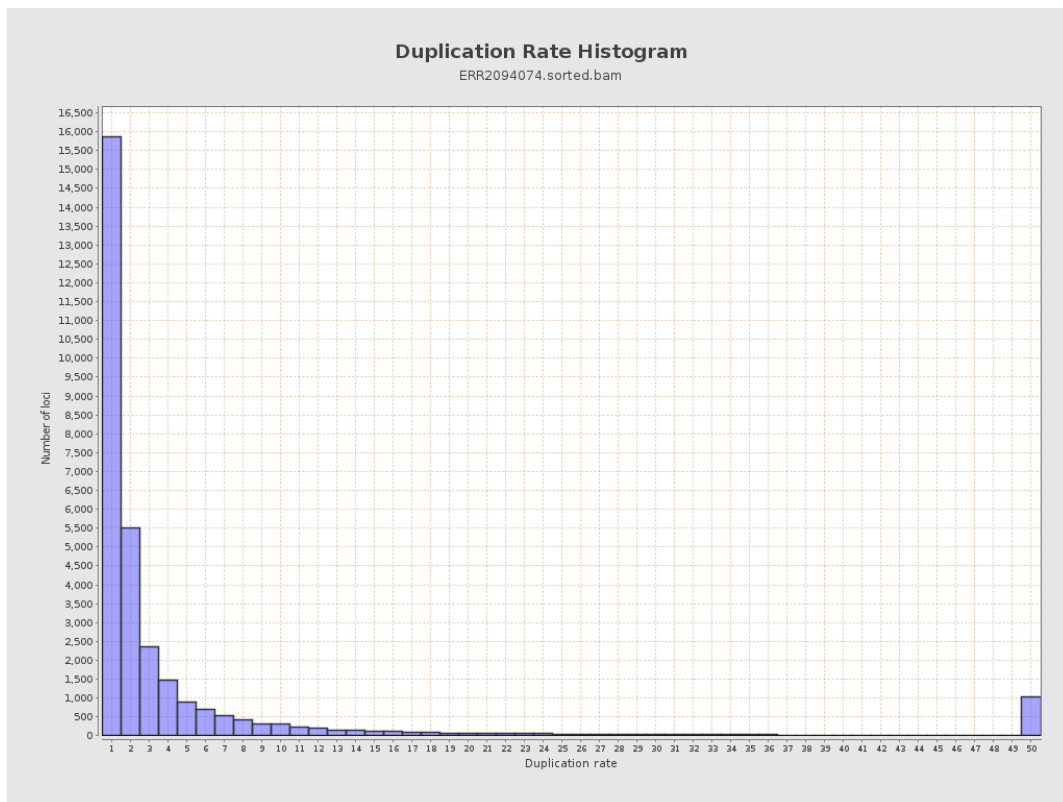
## 5. Results : Coverage Histogram (0-50X)



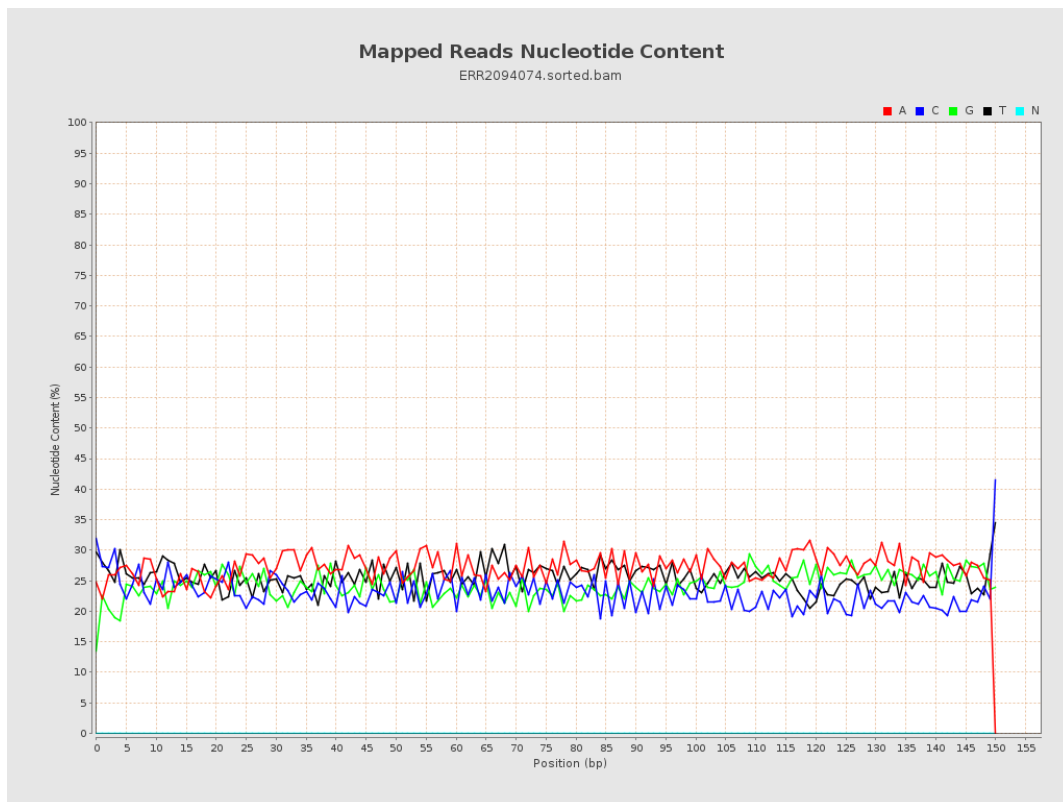
## 6. Results : Genome Fraction Coverage



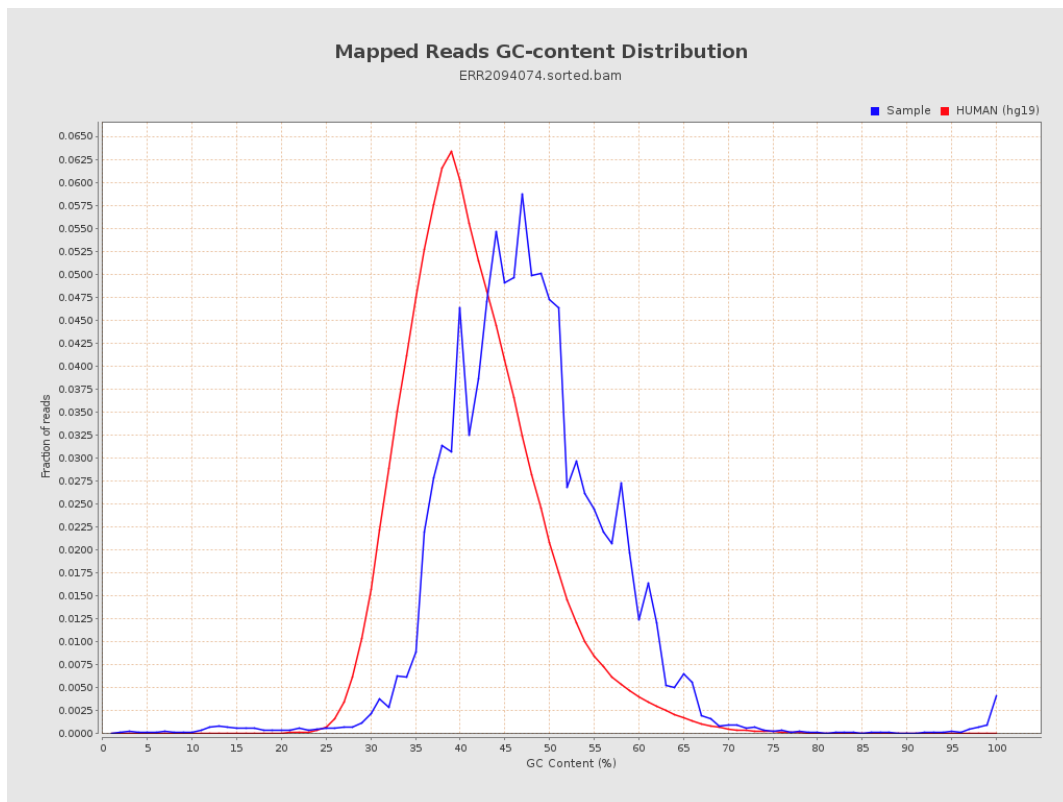
## 7. Results : Duplication Rate Histogram



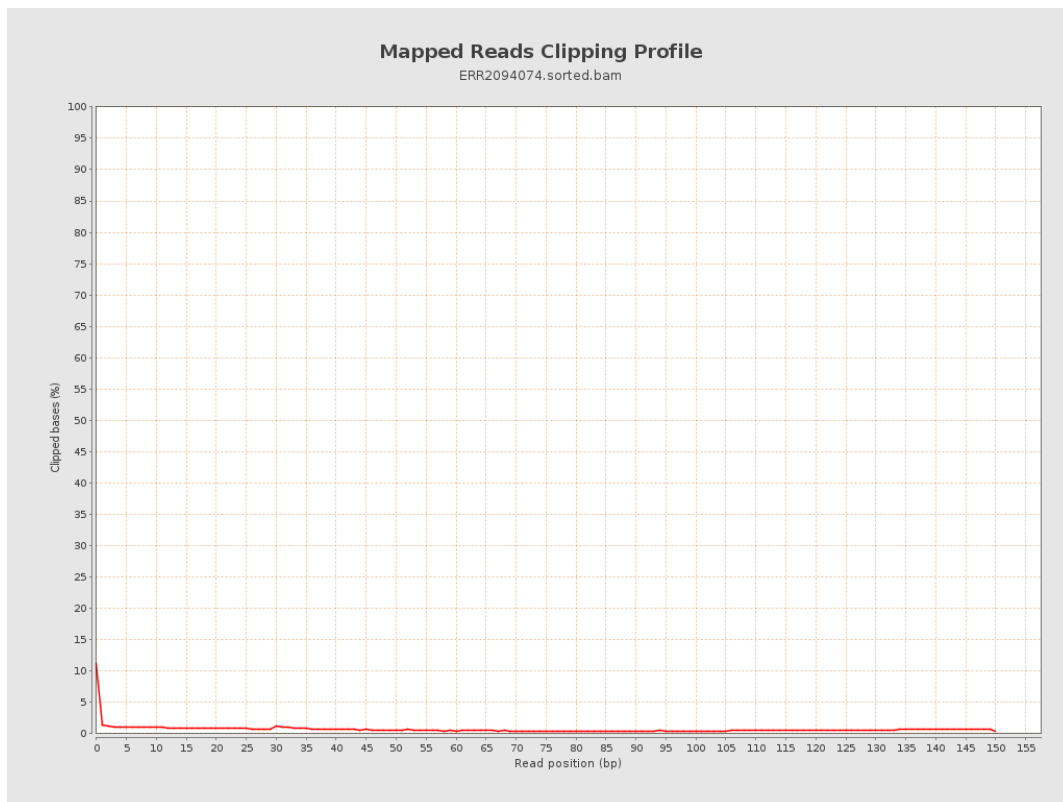
## 8. Results : Mapped Reads Nucleotide Content



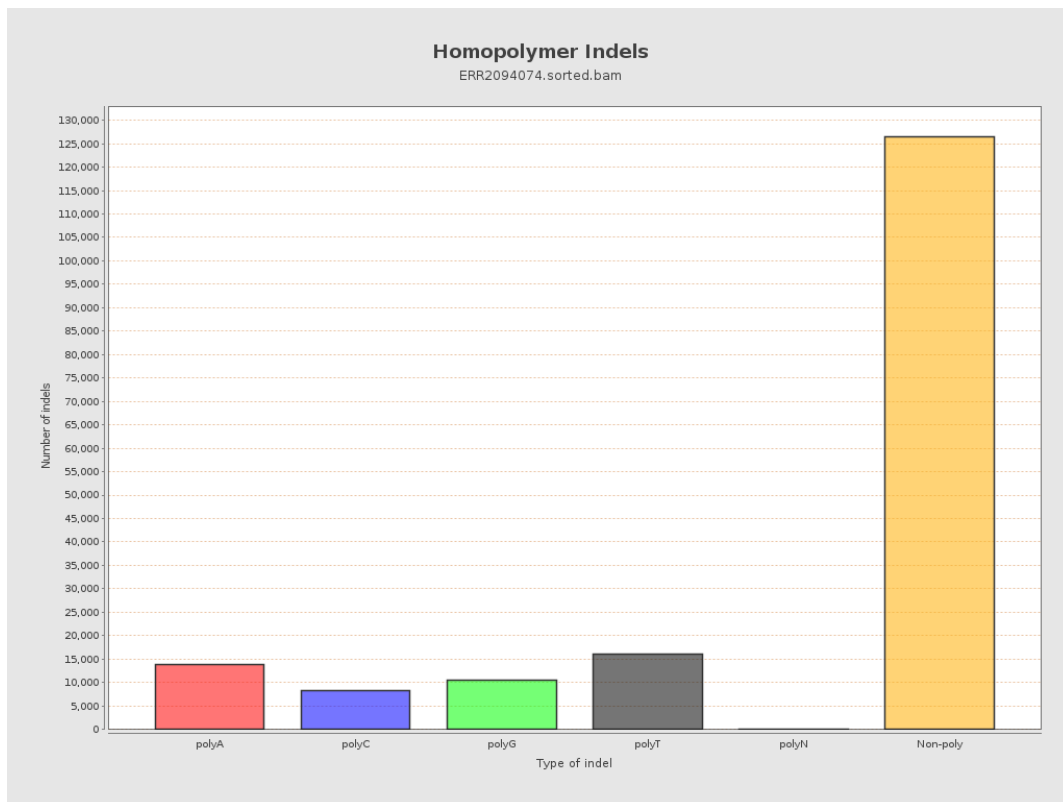
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



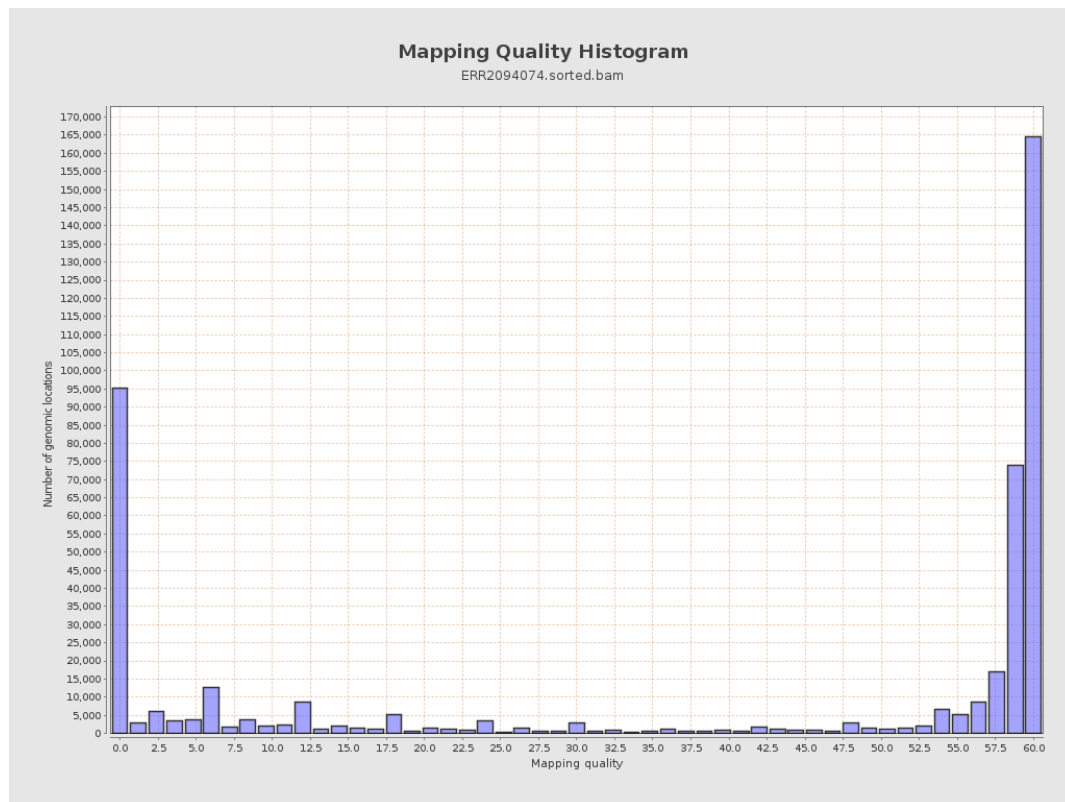
## 11. Results : Homopolymer Indels



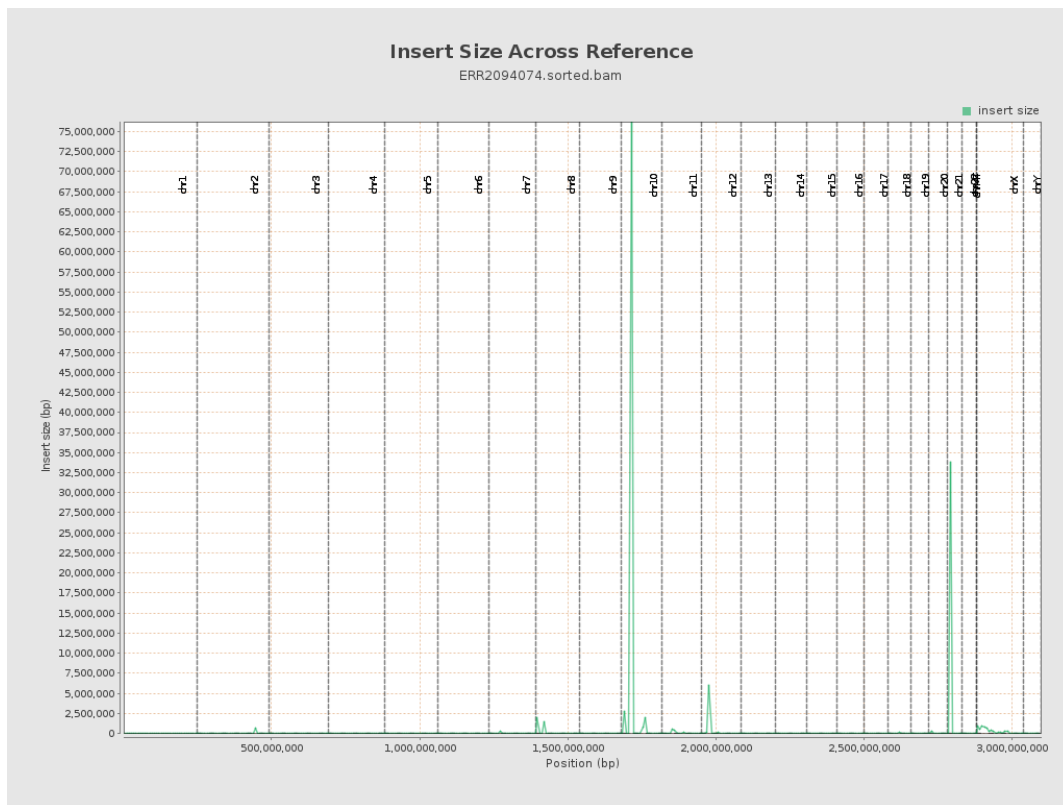
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

