

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/02 18:56:25*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714091.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_ERR9714091 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714091.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Wed Oct 02 18:56:24 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | ERR9714091.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                  |
|------------------------------|------------------|
| Reference size               | 3,095,693,983    |
| Number of reads              | 967,422          |
| Mapped reads                 | 72,708 / 7.52%   |
| Unmapped reads               | 894,714 / 92.48% |
| Mapped paired reads          | 0 / 0%           |
| Secondary alignments         | 0                |
| Supplementary alignments     | 2,783 / 0.29%    |
| Read min/max/mean length     | 30 / 151 / 51.54 |
| Duplicated reads (estimated) | 71,510 / 7.39%   |
| Duplication rate             | 23.79%           |
| Clipped reads                | 39,701 / 4.1%    |

### 2.2. ACGT Content

|                          |                    |
|--------------------------|--------------------|
| Number/percentage of A's | 191,290 / 2.6%     |
| Number/percentage of C's | 36,591 / 0.5%      |
| Number/percentage of T's | 57,002 / 0.77%     |
| Number/percentage of G's | 7,078,945 / 96.11% |
| Number/percentage of N's | 1,315 / 0.02%      |
| GC Percentage            | 96.61%             |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0024 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 8.5628 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |     |
|----------------------|-----|
| Mean Mapping Quality | 8.8 |
|----------------------|-----|

## 2.5. Mismatches and indels

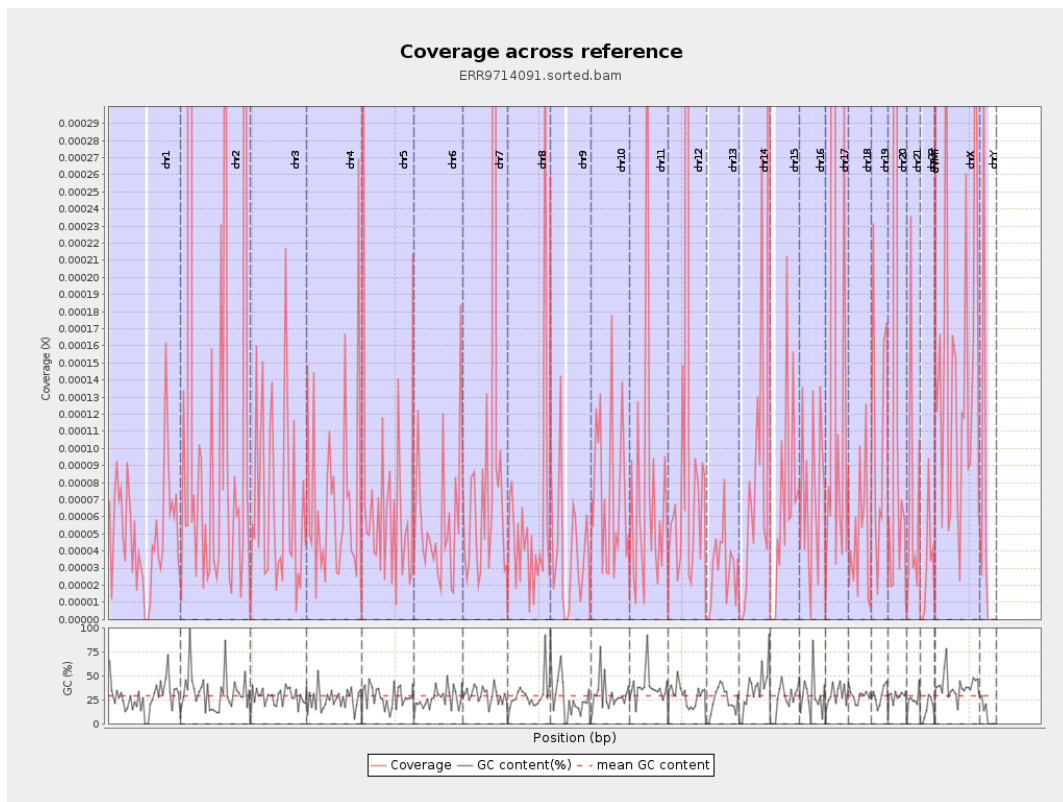
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 3.84%   |
| Mismatches                               | 184,820 |
| Insertions                               | 12,310  |
| Mapped reads with at least one insertion | 10.43%  |
| Deletions                                | 3,509   |
| Mapped reads with at least one deletion  | 4.68%   |
| Homopolymer indels                       | 72.58%  |

## 2.6. Chromosome stats

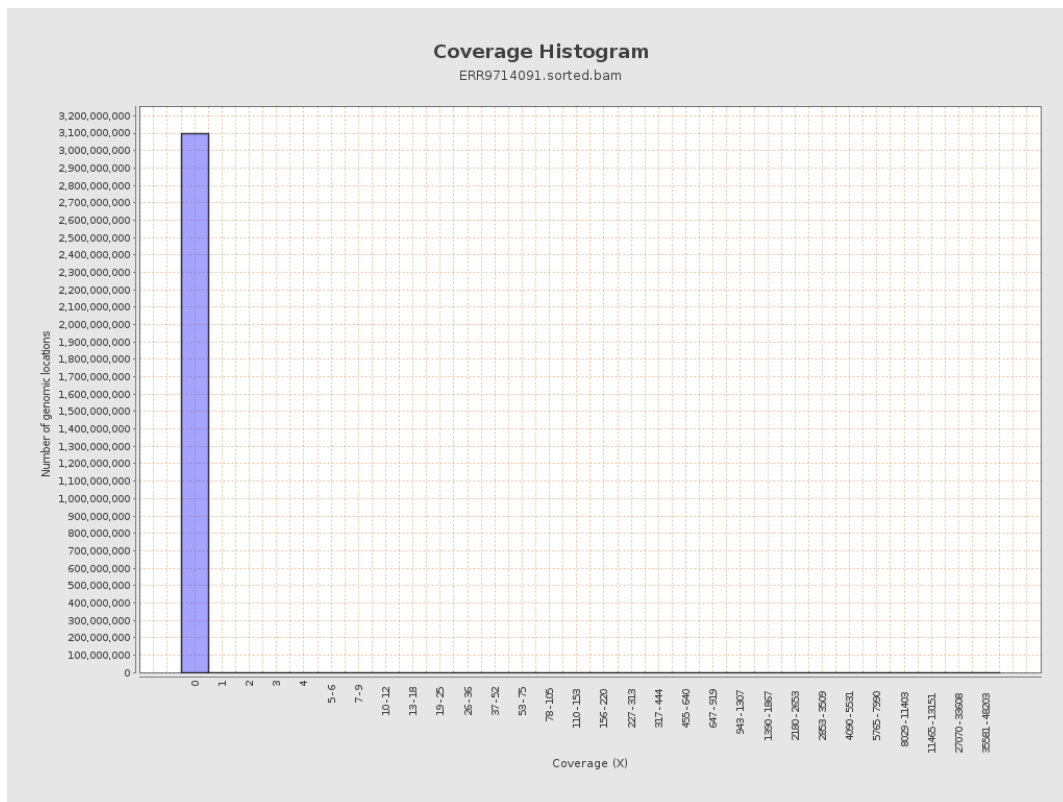
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 12780        | 0.0001        | 0.0119             |
| chr2 | 243199373 | 7133569      | 0.0293        | 30.5487            |
| chr3 | 198022430 | 13552        | 0.0001        | 0.0205             |
| chr4 | 191154276 | 13335        | 0.0001        | 0.0279             |
| chr5 | 180915260 | 13803        | 0.0001        | 0.0517             |
| chr6 | 171115067 | 9967         | 0.0001        | 0.014              |
| chr7 | 159138663 | 19242        | 0.0001        | 0.1315             |
|      |           |              |               |                    |

|       |           |       |        |        |
|-------|-----------|-------|--------|--------|
| chr8  | 146364022 | 8416  | 0.0001 | 0.0356 |
| chr9  | 141213431 | 5621  | 0      | 0.0133 |
| chr10 | 135534747 | 10083 | 0.0001 | 0.0208 |
| chr11 | 135006516 | 9819  | 0.0001 | 0.0424 |
| chr12 | 133851895 | 17028 | 0.0001 | 0.0849 |
| chr13 | 115169878 | 3425  | 0      | 0.0066 |
| chr14 | 107349540 | 15780 | 0.0001 | 0.1419 |
| chr15 | 102531392 | 6846  | 0.0001 | 0.0246 |
| chr16 | 90354753  | 6738  | 0.0001 | 0.0205 |
| chr17 | 81195210  | 18565 | 0.0002 | 0.2228 |
| chr18 | 78077248  | 3952  | 0.0001 | 0.0147 |
| chr19 | 59128983  | 6185  | 0.0001 | 0.0329 |
| chr20 | 63025520  | 19071 | 0.0003 | 0.349  |
| chr21 | 48129895  | 3226  | 0.0001 | 0.0391 |
| chr22 | 51304566  | 1573  | 0      | 0.0088 |
| chrMT | 16571     | 64    | 0.0039 | 0.062  |
| chrX  | 155270560 | 23439 | 0.0002 | 0.0344 |
| chrY  | 59373566  | 3265  | 0.0001 | 0.0209 |

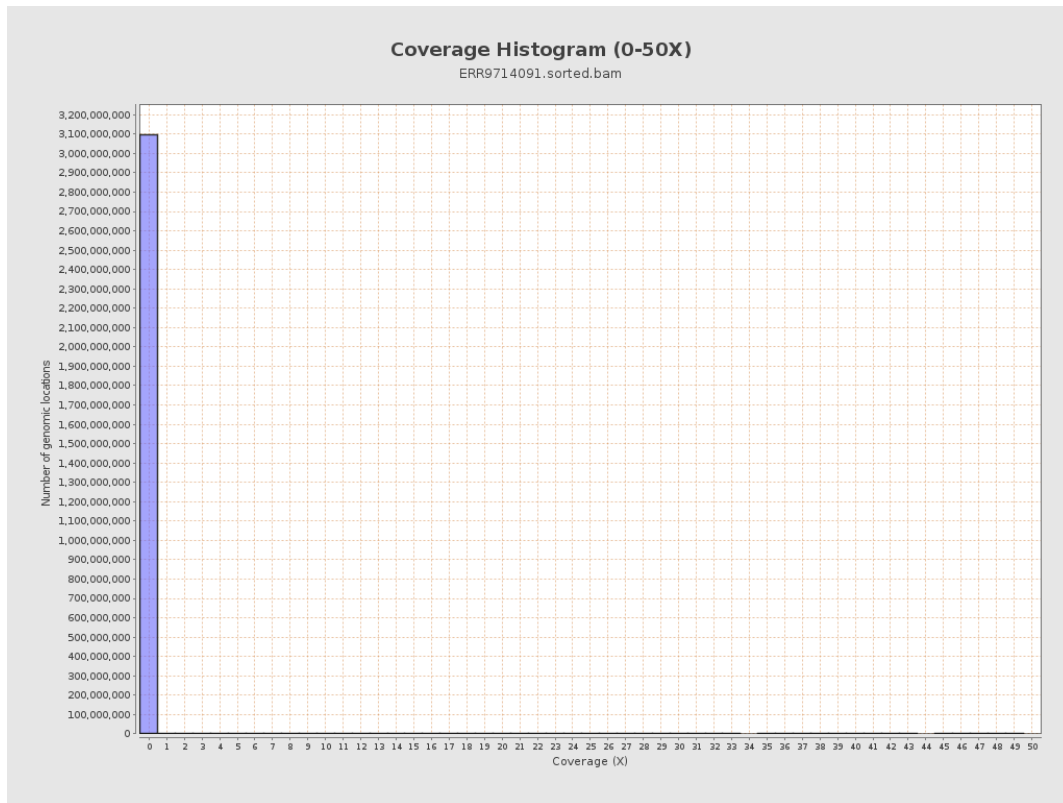
### 3. Results : Coverage across reference



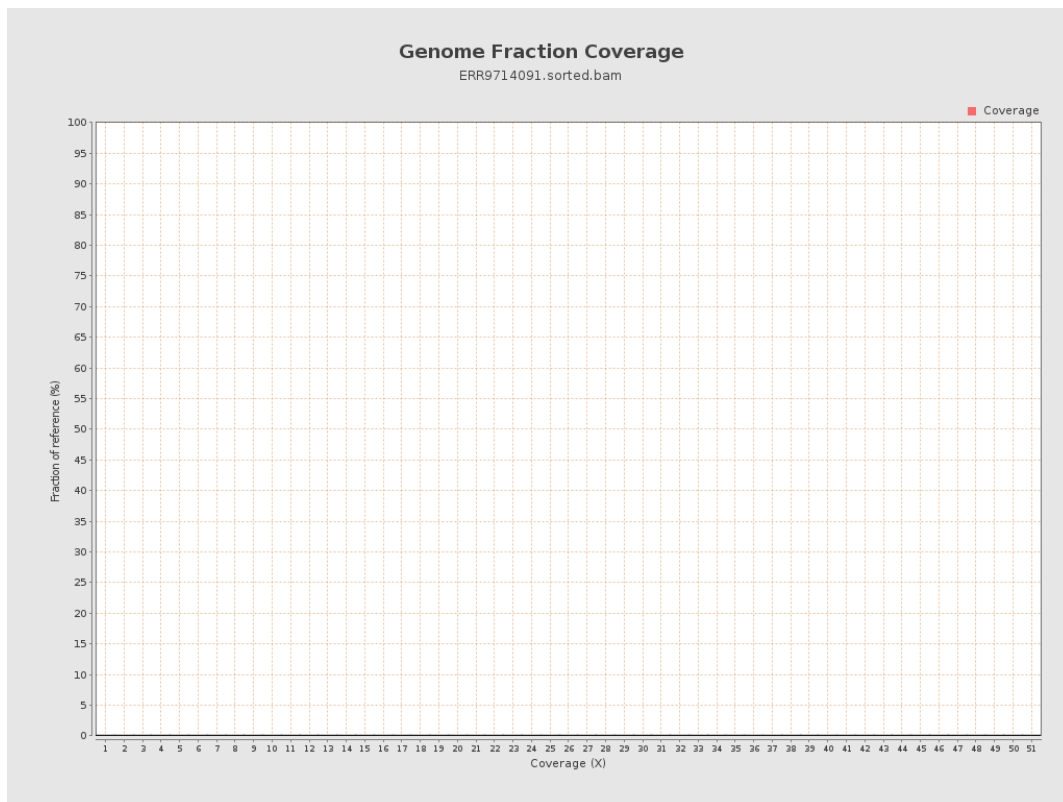
## 4. Results : Coverage Histogram



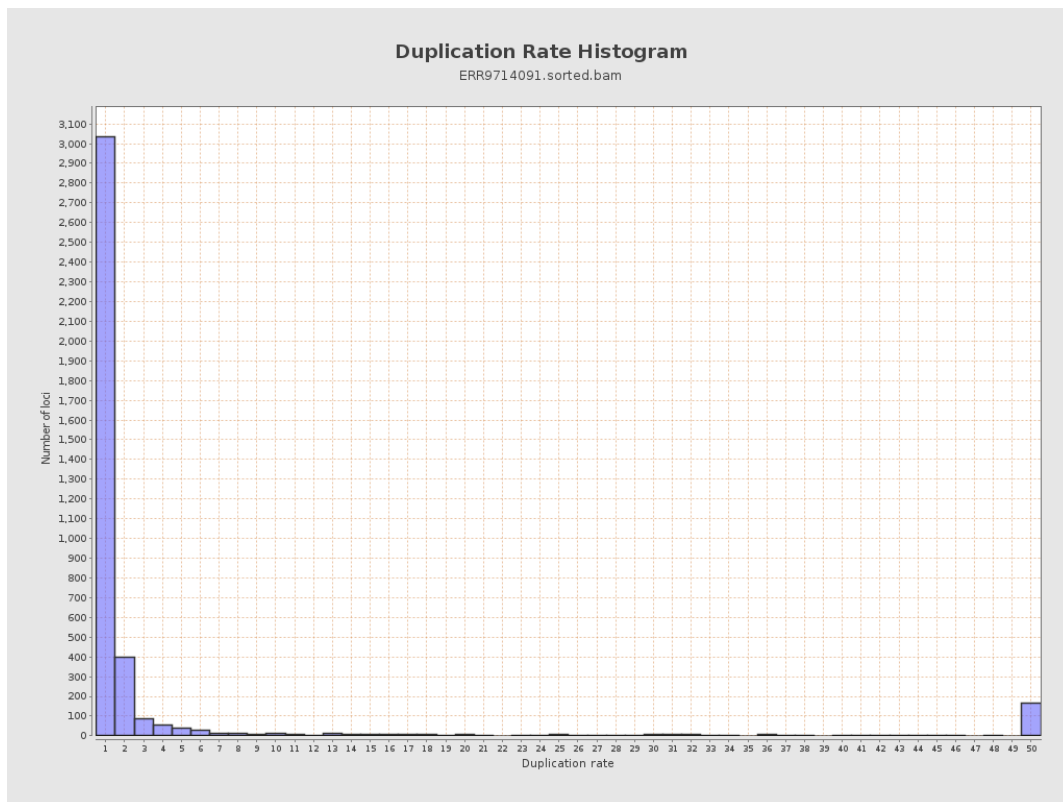
## 5. Results : Coverage Histogram (0-50X)



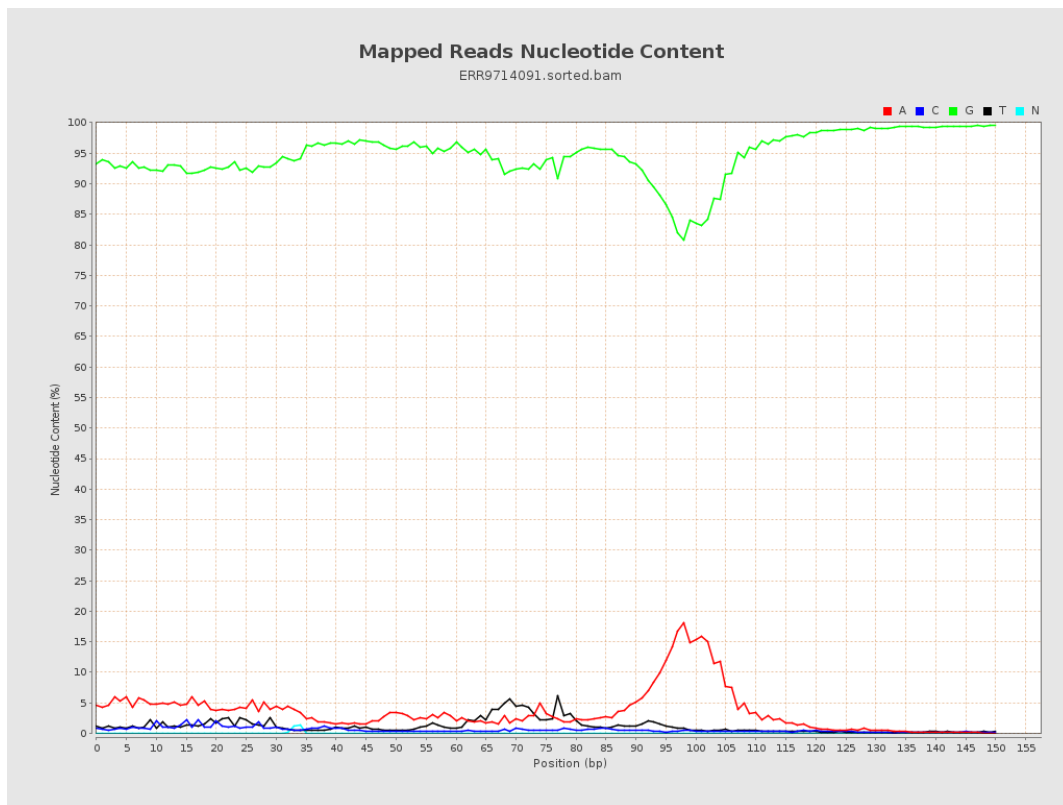
## 6. Results : Genome Fraction Coverage



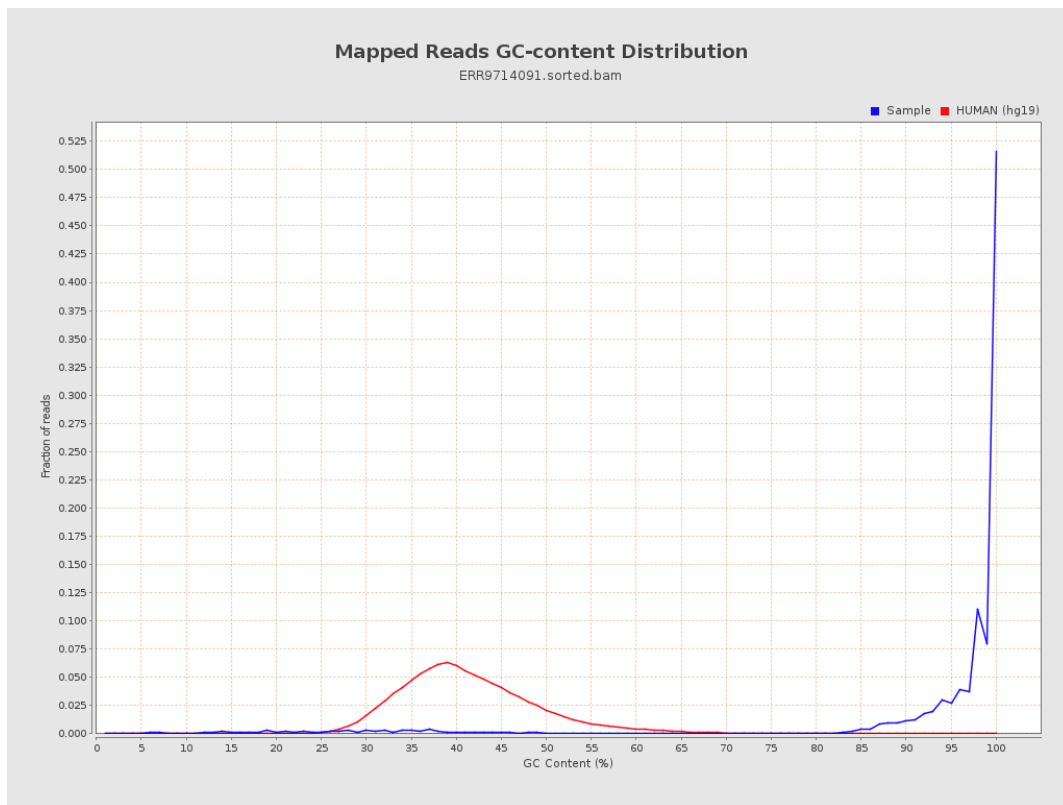
## 7. Results : Duplication Rate Histogram



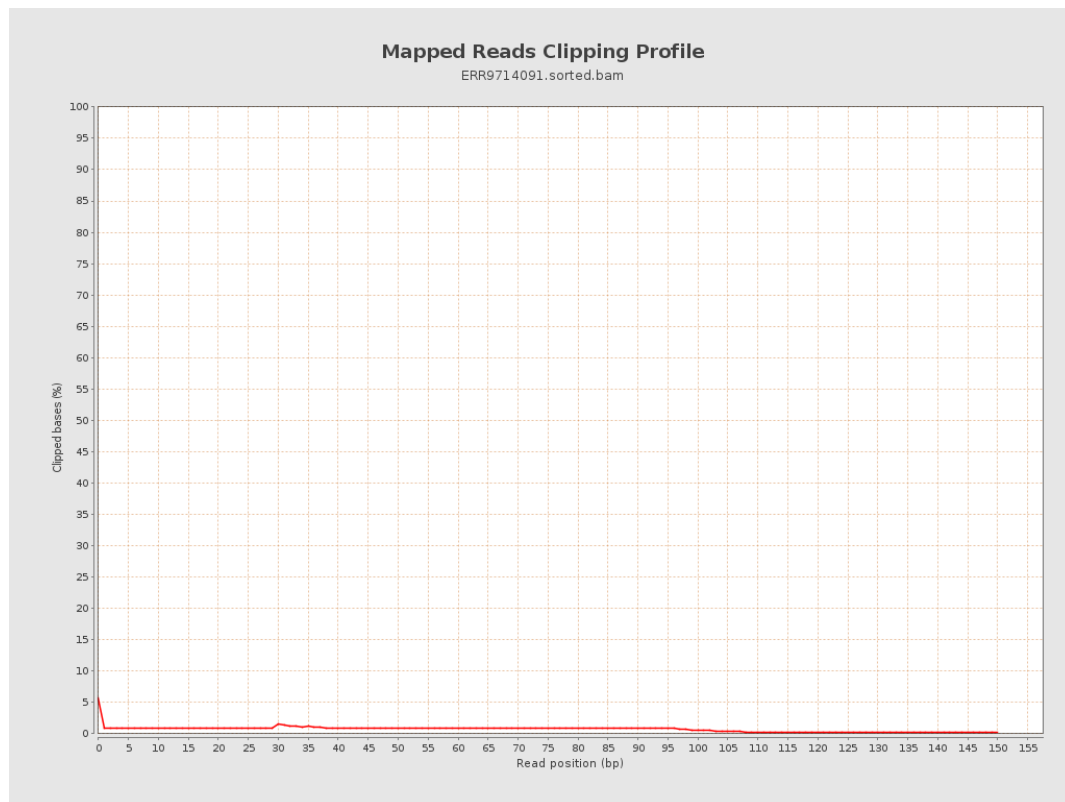
## 8. Results : Mapped Reads Nucleotide Content



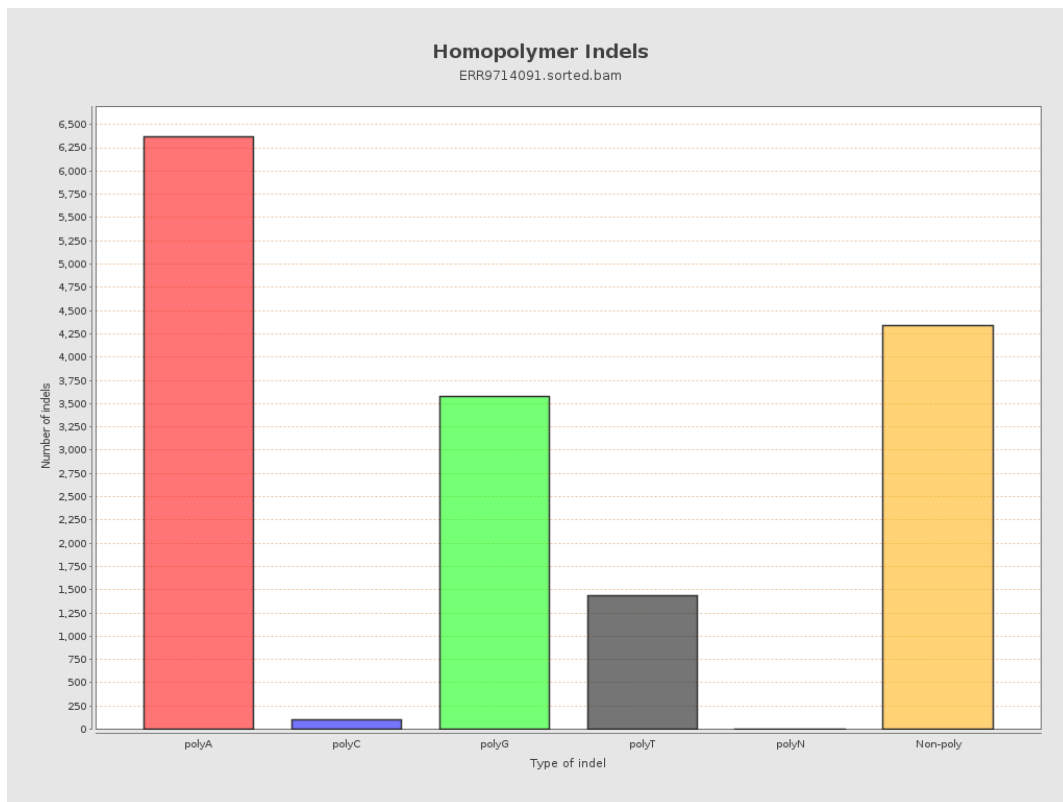
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

