

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/02 22:13:28*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714159.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_ERR9714159 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714159.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Wed Oct 02 22:13:27 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | ERR9714159.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                   |
|------------------------------|-------------------|
| Reference size               | 3,095,693,983     |
| Number of reads              | 781,834           |
| Mapped reads                 | 680,866 / 87.09%  |
| Unmapped reads               | 100,968 / 12.91%  |
| Mapped paired reads          | 0 / 0%            |
| Secondary alignments         | 0                 |
| Supplementary alignments     | 18,522 / 2.37%    |
| Read min/max/mean length     | 30 / 151 / 137.85 |
| Duplicated reads (estimated) | 631,335 / 80.75%  |
| Duplication rate             | 42.78%            |
| Clipped reads                | 642,543 / 82.18%  |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 23,061,785 / 26.18% |
| Number/percentage of C's | 20,266,517 / 23.01% |
| Number/percentage of T's | 22,016,579 / 25%    |
| Number/percentage of G's | 22,736,163 / 25.81% |
| Number/percentage of N's | 702 / 0%            |
| GC Percentage            | 48.82%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0291 |
|      |        |

|                    |         |
|--------------------|---------|
| Standard Deviation | 12.3288 |
|--------------------|---------|

## 2.4. Mapping Quality

|                      |      |
|----------------------|------|
| Mean Mapping Quality | 50.6 |
|----------------------|------|

## 2.5. Mismatches and indels

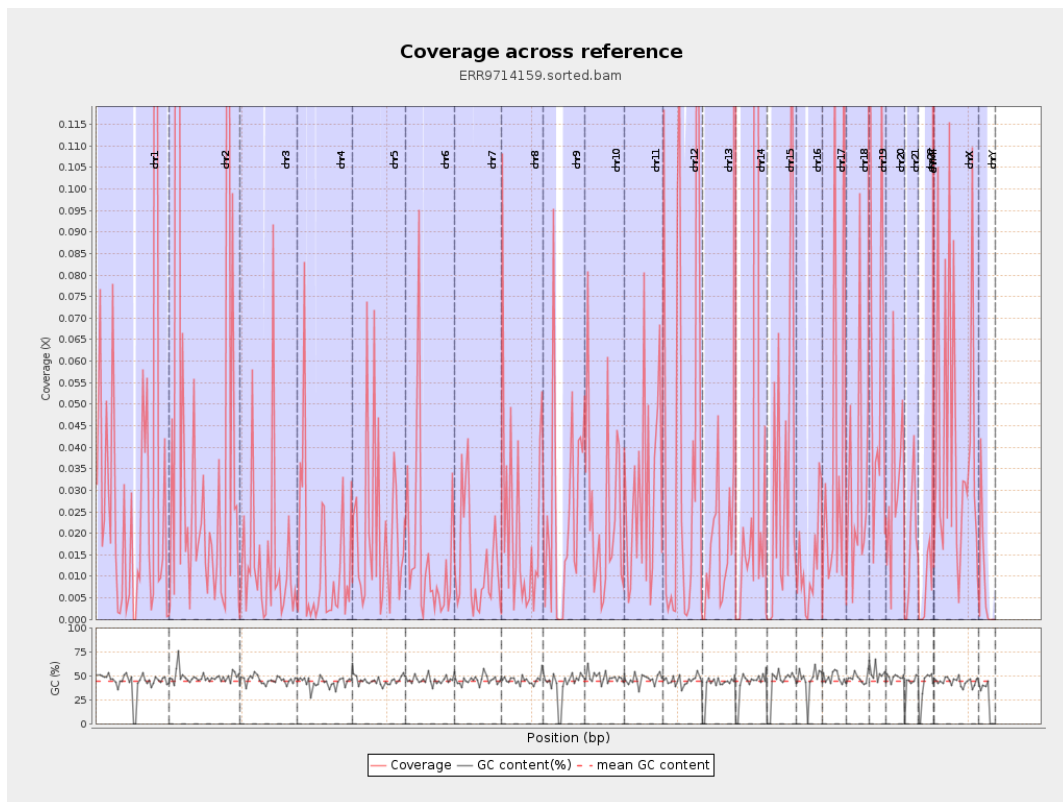
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 4.4%      |
| Mismatches                               | 3,631,970 |
| Insertions                               | 92,142    |
| Mapped reads with at least one insertion | 13.06%    |
| Deletions                                | 323,938   |
| Mapped reads with at least one deletion  | 45.2%     |
| Homopolymer indels                       | 29.02%    |

## 2.6. Chromosome stats

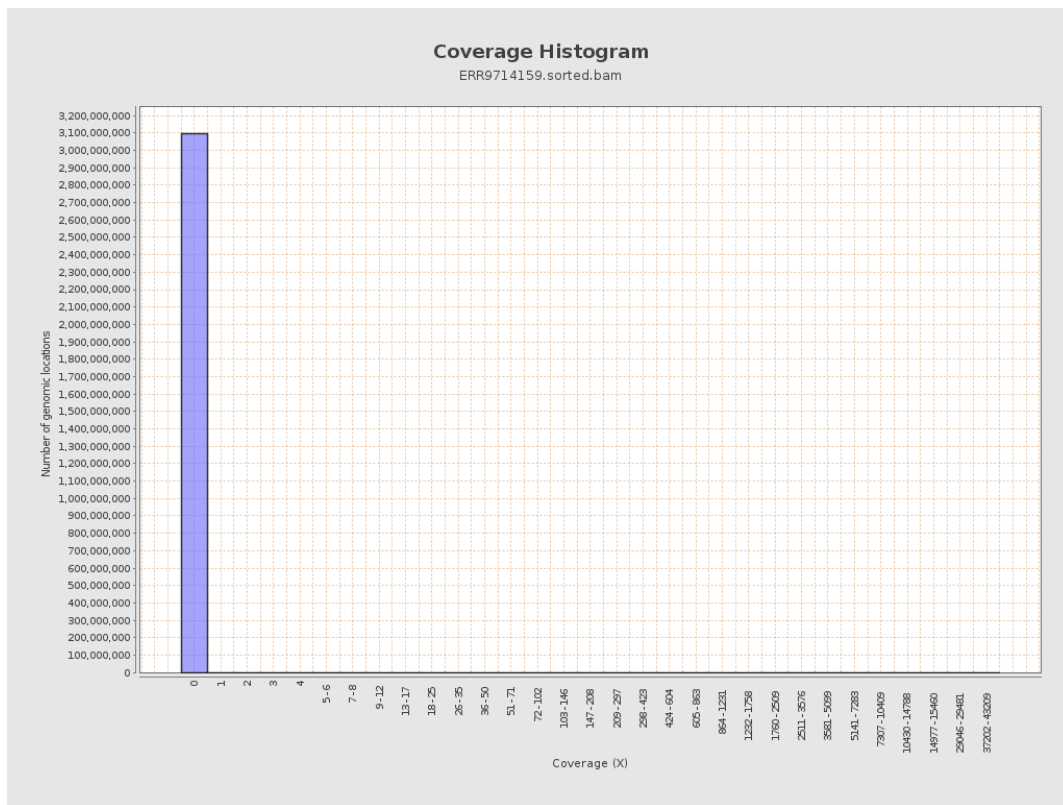
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 8154774      | 0.0327        | 10.12              |
| chr2 | 243199373 | 12273185     | 0.0505        | 18.1773            |
| chr3 | 198022430 | 2708780      | 0.0137        | 3.6661             |
| chr4 | 191154276 | 2571271      | 0.0135        | 3.4354             |
| chr5 | 180915260 | 3724961      | 0.0206        | 4.6975             |
| chr6 | 171115067 | 2733159      | 0.016         | 4.0991             |
| chr7 | 159138663 | 2079244      | 0.0131        | 2.8057             |
|      |           |              |               |                    |

|       |           |         |        |         |
|-------|-----------|---------|--------|---------|
| chr8  | 146364022 | 3345511 | 0.0229 | 5.3108  |
| chr9  | 141213431 | 3102549 | 0.022  | 4.9899  |
| chr10 | 135534747 | 3297393 | 0.0243 | 4.1768  |
| chr11 | 135006516 | 3980373 | 0.0295 | 5.3171  |
| chr12 | 133851895 | 5512945 | 0.0412 | 11.7455 |
| chr13 | 115169878 | 3839453 | 0.0333 | 16.0776 |
| chr14 | 107349540 | 7898021 | 0.0736 | 48.7671 |
| chr15 | 102531392 | 3656449 | 0.0357 | 9.8954  |
| chr16 | 90354753  | 1221574 | 0.0135 | 2.2089  |
| chr17 | 81195210  | 3691874 | 0.0455 | 10.5687 |
| chr18 | 78077248  | 2393532 | 0.0307 | 7.2316  |
| chr19 | 59128983  | 3409567 | 0.0577 | 8.5307  |
| chr20 | 63025520  | 2059261 | 0.0327 | 4.4535  |
| chr21 | 48129895  | 785316  | 0.0163 | 3.3169  |
| chr22 | 51304566  | 425399  | 0.0083 | 1.3547  |
| chrMT | 16571     | 143881  | 8.6827 | 71.4679 |
| chrX  | 155270560 | 6587114 | 0.0424 | 5.1118  |
| chrY  | 59373566  | 503988  | 0.0085 | 2.28    |

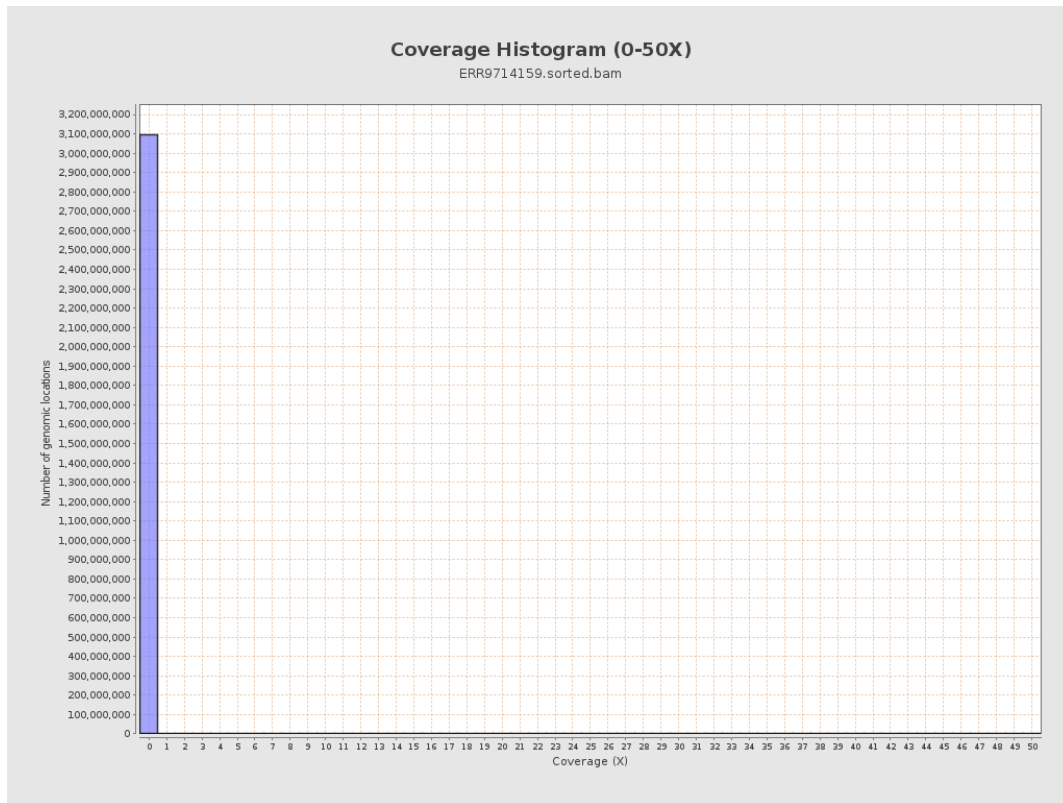
### 3. Results : Coverage across reference



## 4. Results : Coverage Histogram

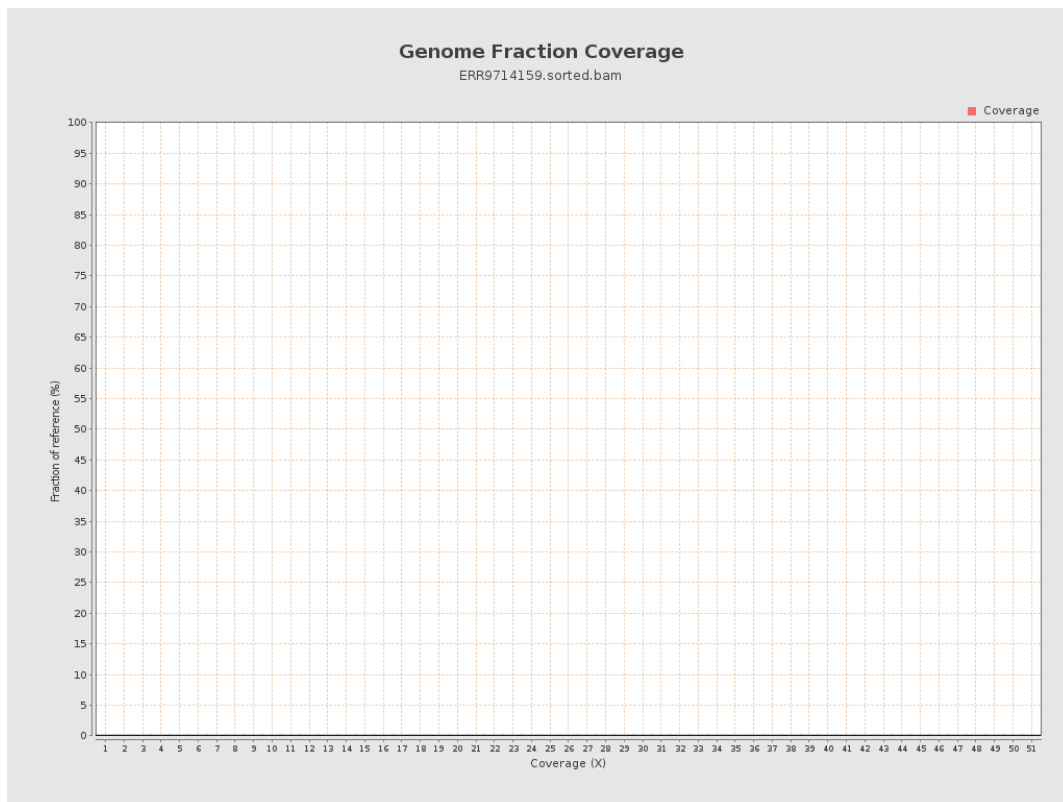


## 5. Results : Coverage Histogram (0-50X)

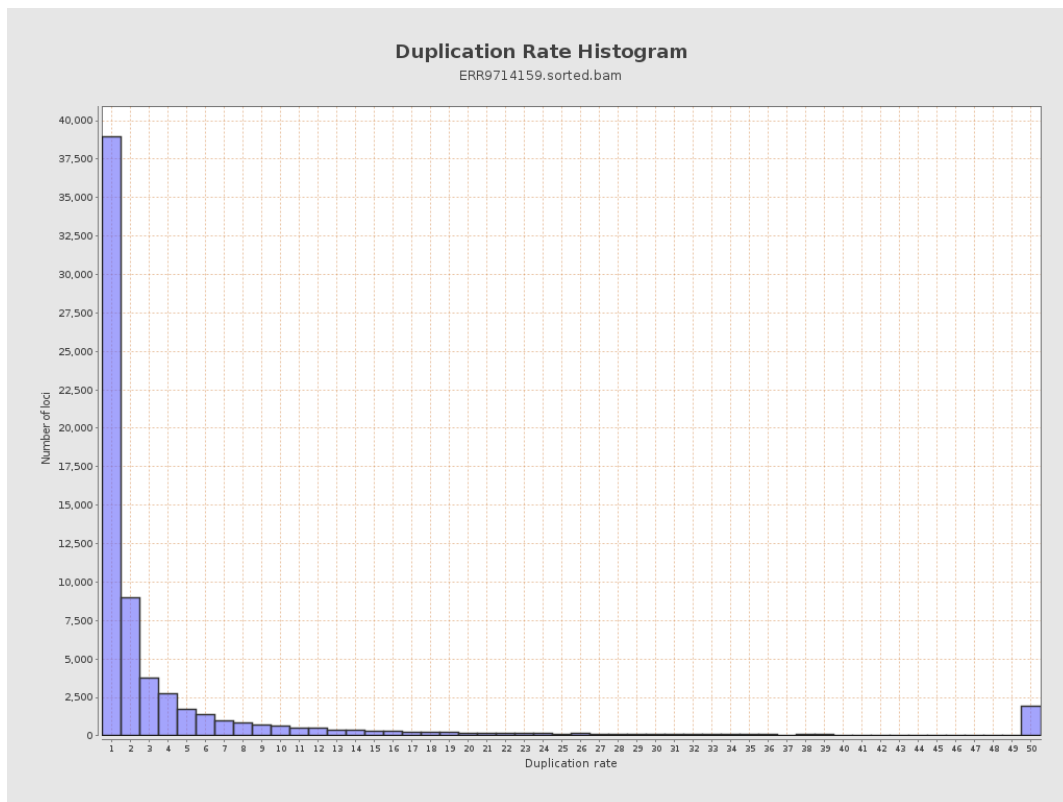




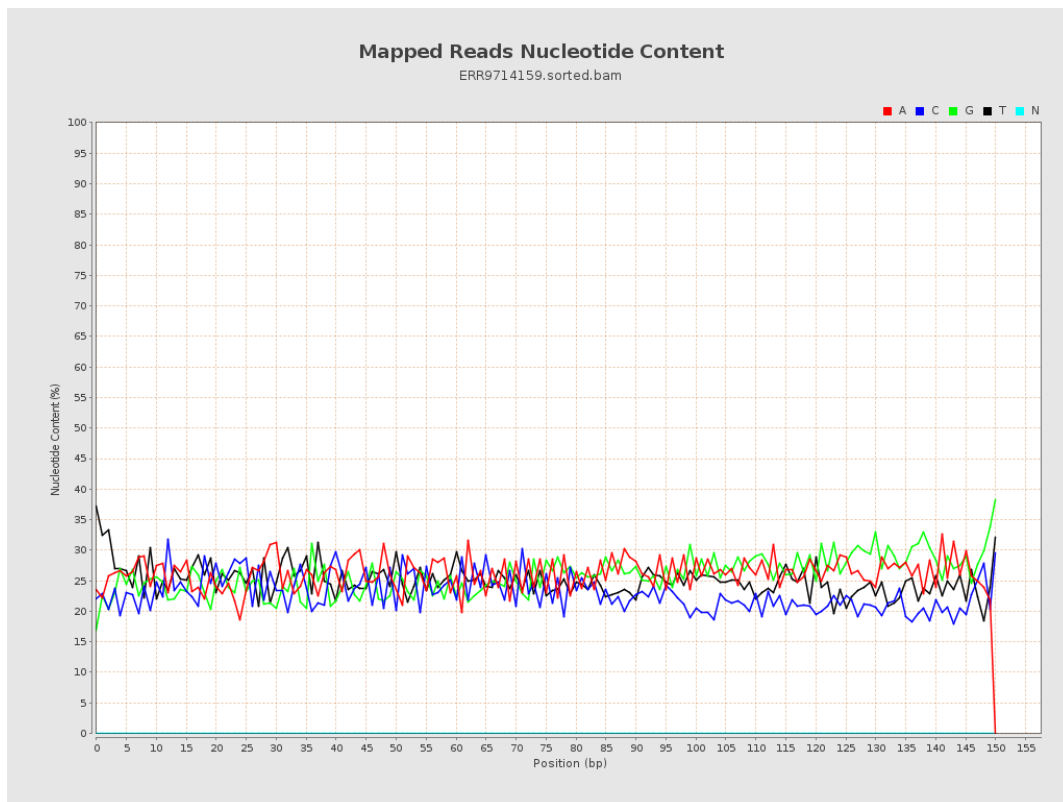
## 6. Results : Genome Fraction Coverage



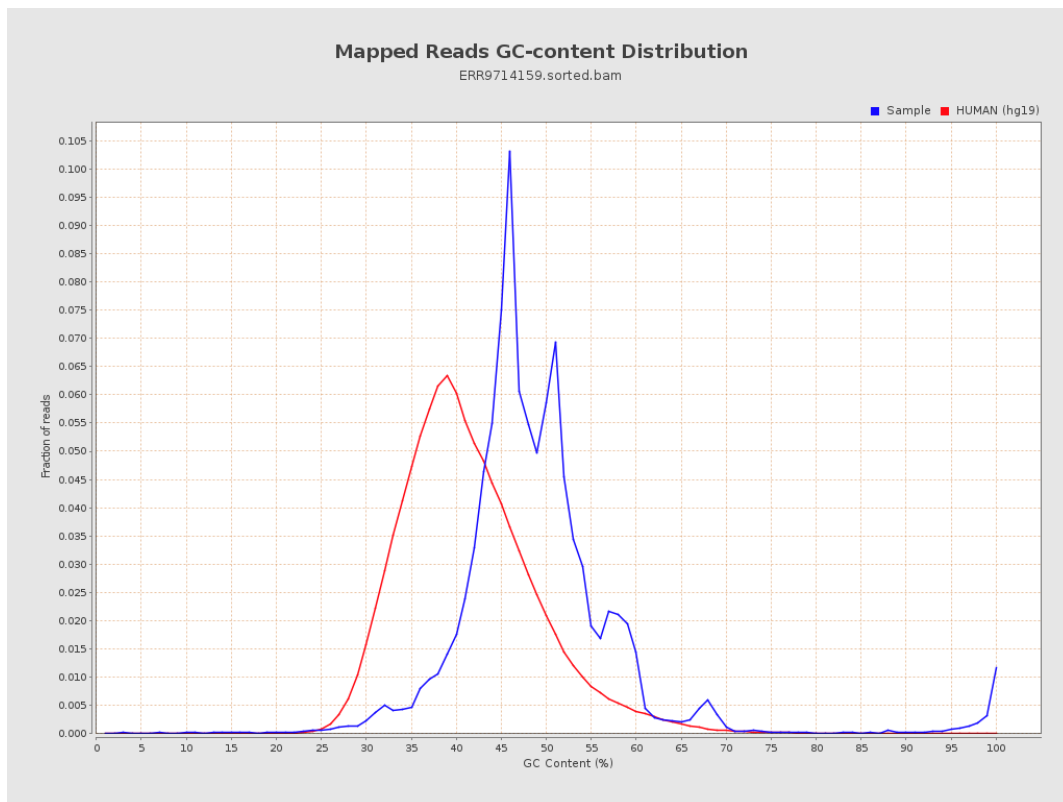
## 7. Results : Duplication Rate Histogram



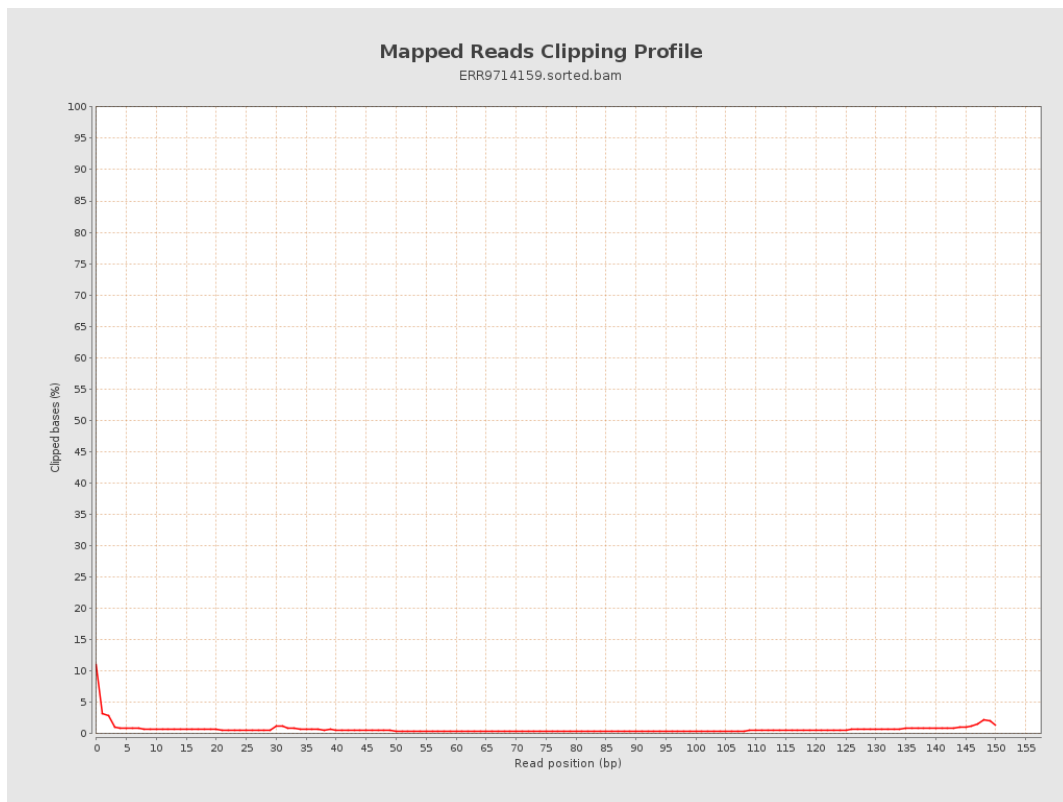
## 8. Results : Mapped Reads Nucleotide Content



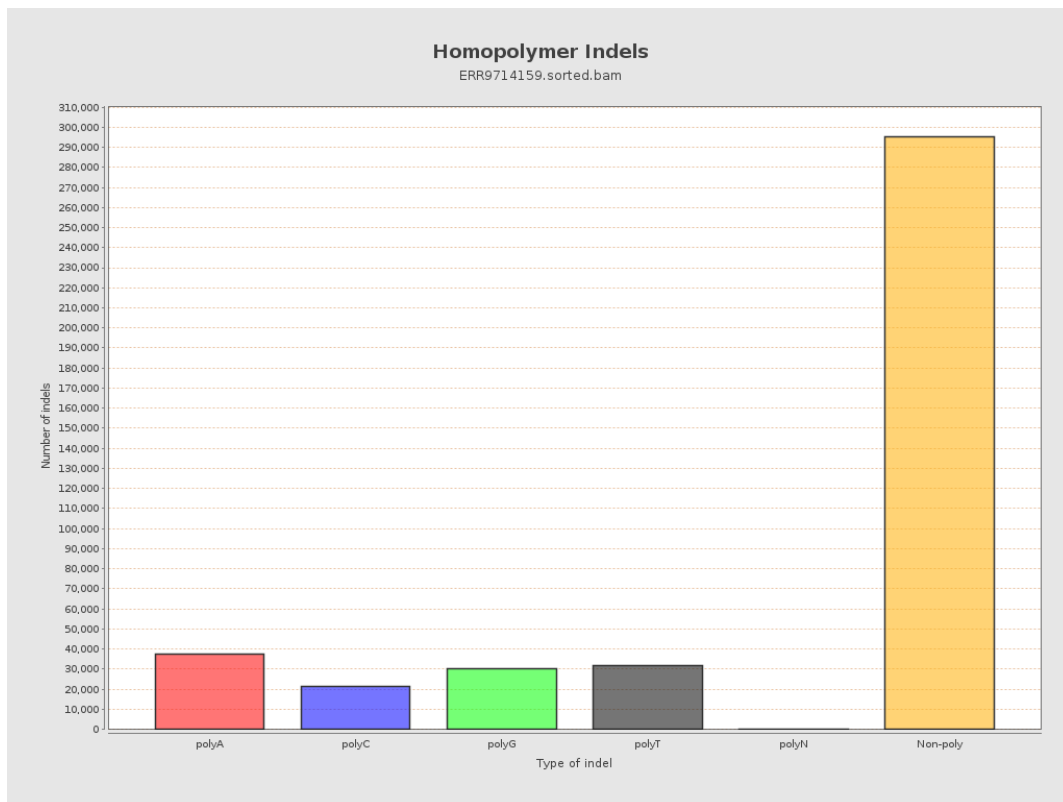
## 9. Results : Mapped Reads GC-content Distribution



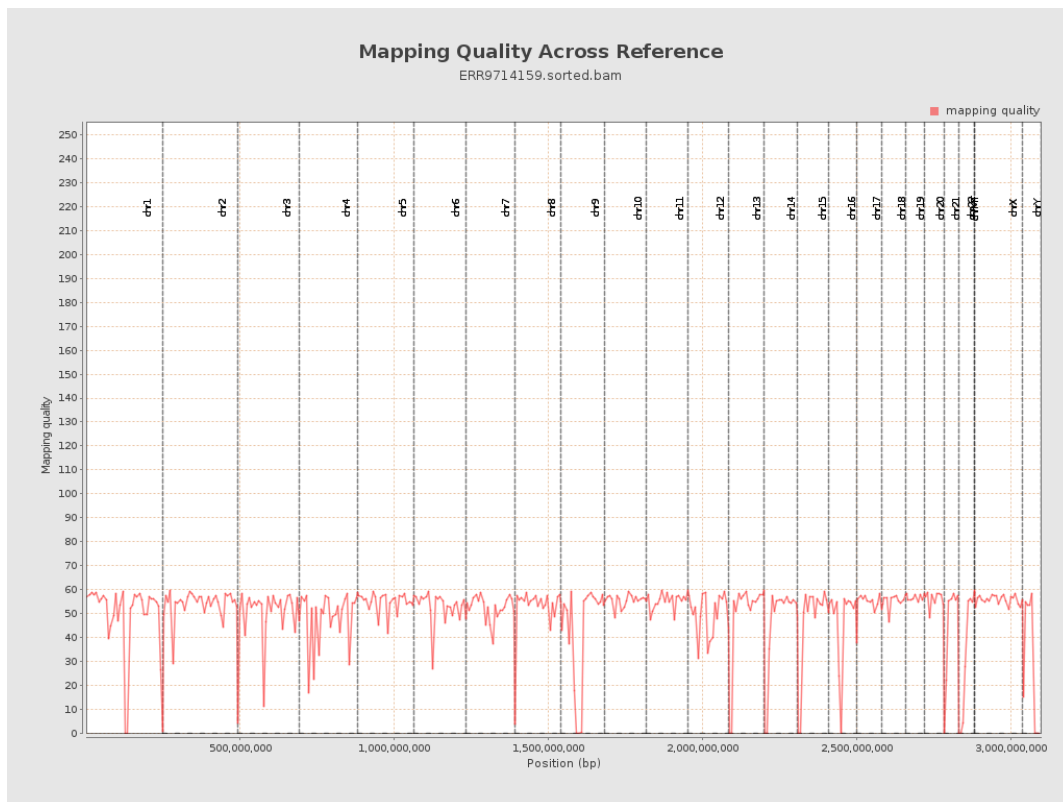
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

