

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/02 12:34:01*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716420.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_SRR9716420 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716420.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Mon Sep 02 12:34:00 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR9716420.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                  |
|------------------------------|------------------|
| Reference size               | 3,095,693,983    |
| Number of reads              | 662,014          |
| Mapped reads                 | 575,702 / 86.96% |
| Unmapped reads               | 86,312 / 13.04%  |
| Mapped paired reads          | 0 / 0%           |
| Secondary alignments         | 0                |
| Supplementary alignments     | 2,399 / 0.36%    |
| Read min/max/mean length     | 30 / 76 / 76.12  |
| Duplicated reads (estimated) | 14,178 / 2.14%   |
| Duplication rate             | 1.86%            |
| Clipped reads                | 577,500 / 87.23% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 7,921,887 / 24.23%  |
| Number/percentage of C's | 6,173,922 / 18.88%  |
| Number/percentage of T's | 10,464,267 / 32.01% |
| Number/percentage of G's | 8,133,035 / 24.88%  |
| Number/percentage of N's | 485 / 0%            |
| GC Percentage            | 43.76%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0106 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.1303 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 43.25 |
|----------------------|-------|

## 2.5. Mismatches and indels

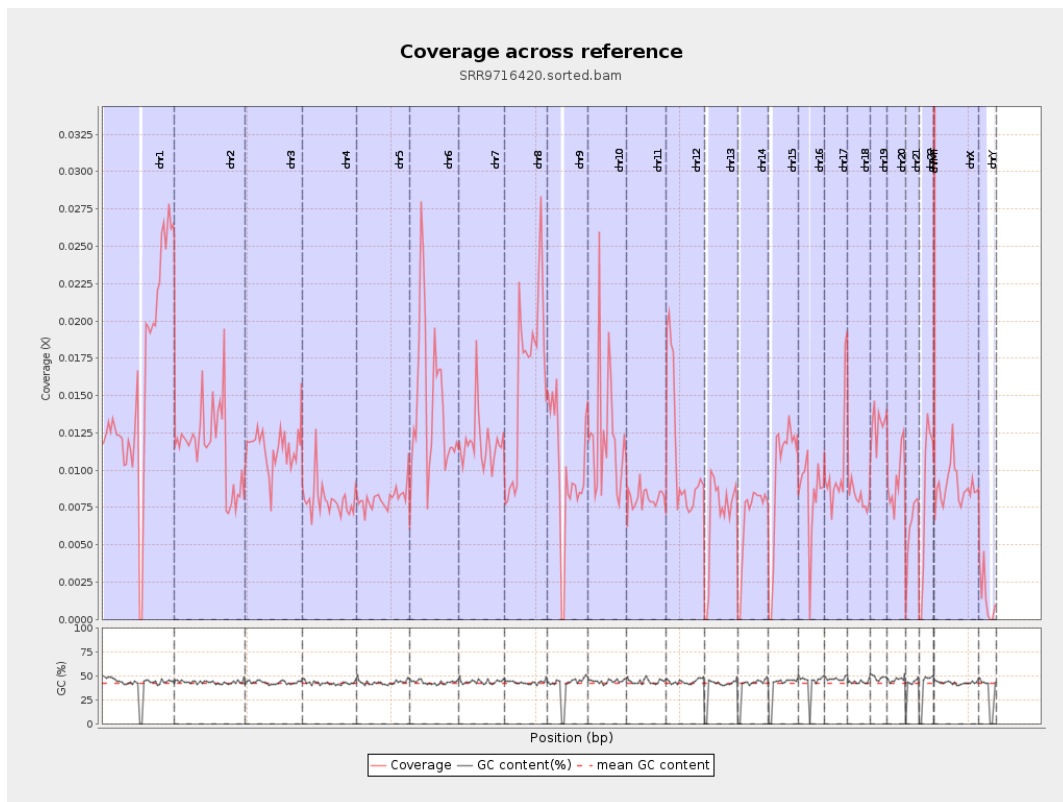
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 0.51%   |
| Mismatches                               | 162,640 |
| Insertions                               | 1,832   |
| Mapped reads with at least one insertion | 0.32%   |
| Deletions                                | 5,340   |
| Mapped reads with at least one deletion  | 0.92%   |
| Homopolymer indels                       | 42.21%  |

## 2.6. Chromosome stats

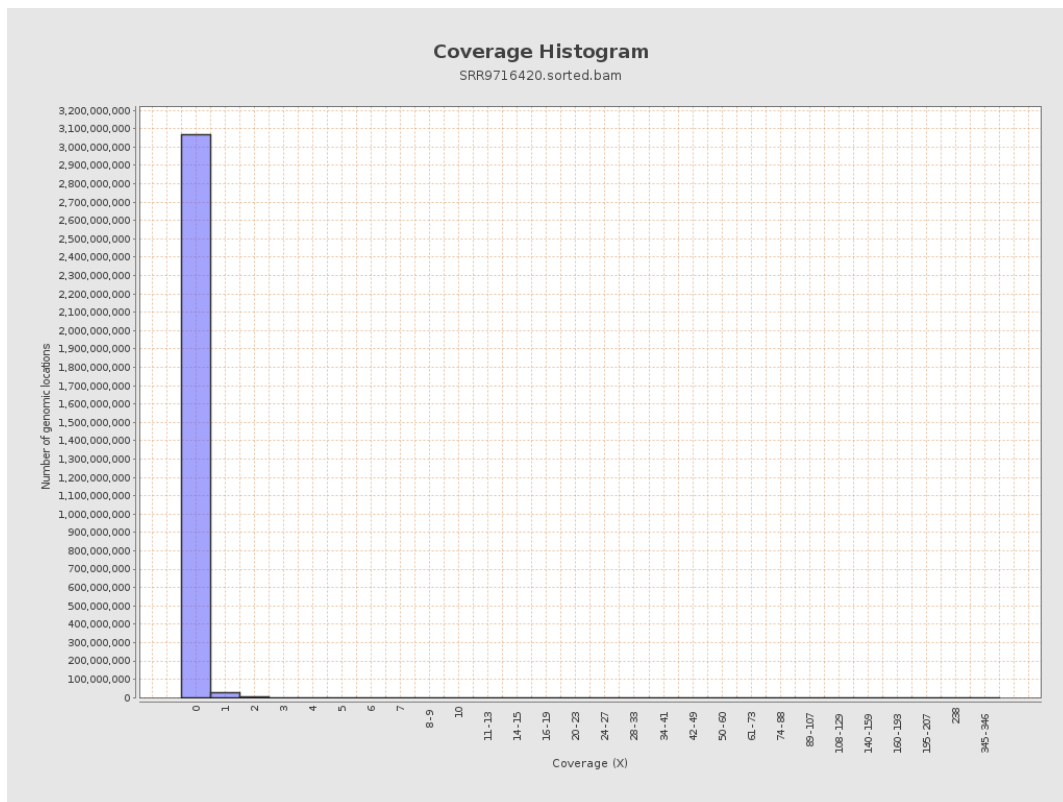
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 3969969      | 0.0159        | 0.1894             |
| chr2 | 243199373 | 2813561      | 0.0116        | 0.1764             |
| chr3 | 198022430 | 2261289      | 0.0114        | 0.1146             |
| chr4 | 191154276 | 1533174      | 0.008         | 0.0979             |
| chr5 | 180915260 | 1468613      | 0.0081        | 0.0953             |
| chr6 | 171115067 | 2448046      | 0.0143        | 0.1361             |
| chr7 | 159138663 | 1888443      | 0.0119        | 0.1603             |
|      |           |              |               |                    |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr8  | 146364022 | 2346334 | 0.016  | 0.1385 |
| chr9  | 141213431 | 1382576 | 0.0098 | 0.12   |
| chr10 | 135534747 | 1671493 | 0.0123 | 0.1532 |
| chr11 | 135006516 | 1101960 | 0.0082 | 0.1079 |
| chr12 | 133851895 | 1467743 | 0.011  | 0.112  |
| chr13 | 115169878 | 792555  | 0.0069 | 0.0875 |
| chr14 | 107349540 | 722170  | 0.0067 | 0.091  |
| chr15 | 102531392 | 991264  | 0.0097 | 0.1036 |
| chr16 | 90354753  | 748694  | 0.0083 | 0.103  |
| chr17 | 81195210  | 828292  | 0.0102 | 0.1072 |
| chr18 | 78077248  | 637099  | 0.0082 | 0.1482 |
| chr19 | 59128983  | 774187  | 0.0131 | 0.1453 |
| chr20 | 63025520  | 592421  | 0.0094 | 0.103  |
| chr21 | 48129895  | 297196  | 0.0062 | 0.0851 |
| chr22 | 51304566  | 431539  | 0.0084 | 0.0966 |
| chrMT | 16571     | 59466   | 3.5886 | 2.6592 |
| chrX  | 155270560 | 1387627 | 0.0089 | 0.1052 |
| chrY  | 59373566  | 86249   | 0.0015 | 0.0488 |

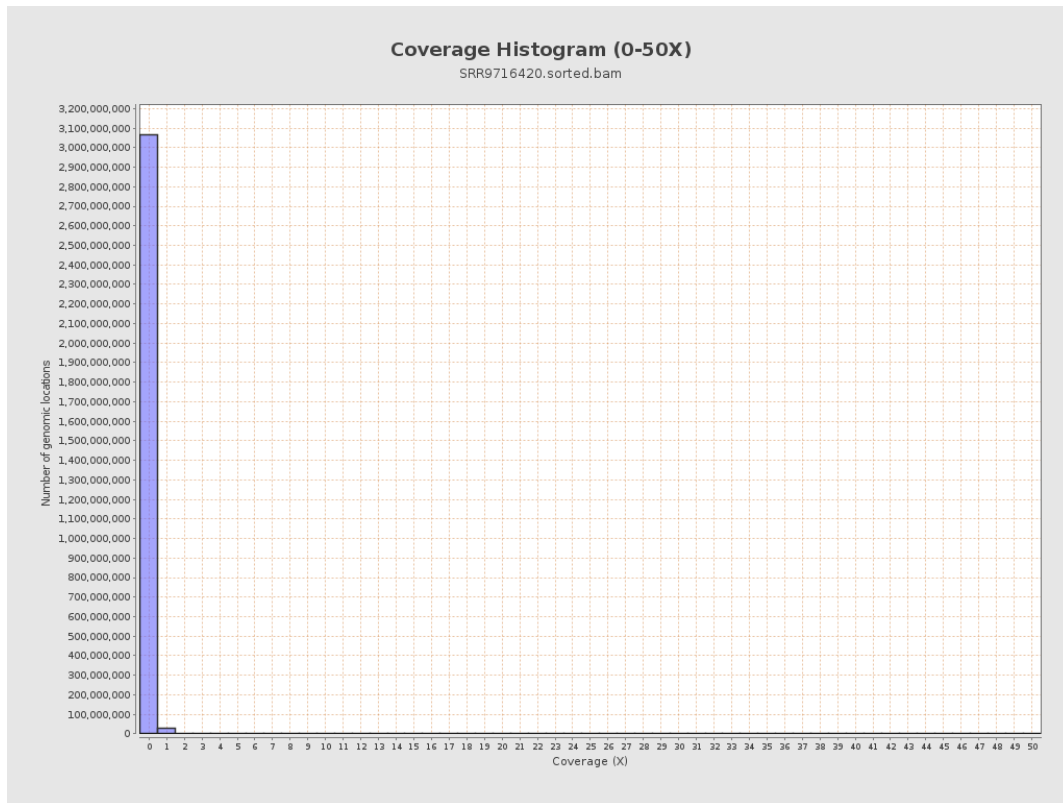
### 3. Results : Coverage across reference



## 4. Results : Coverage Histogram

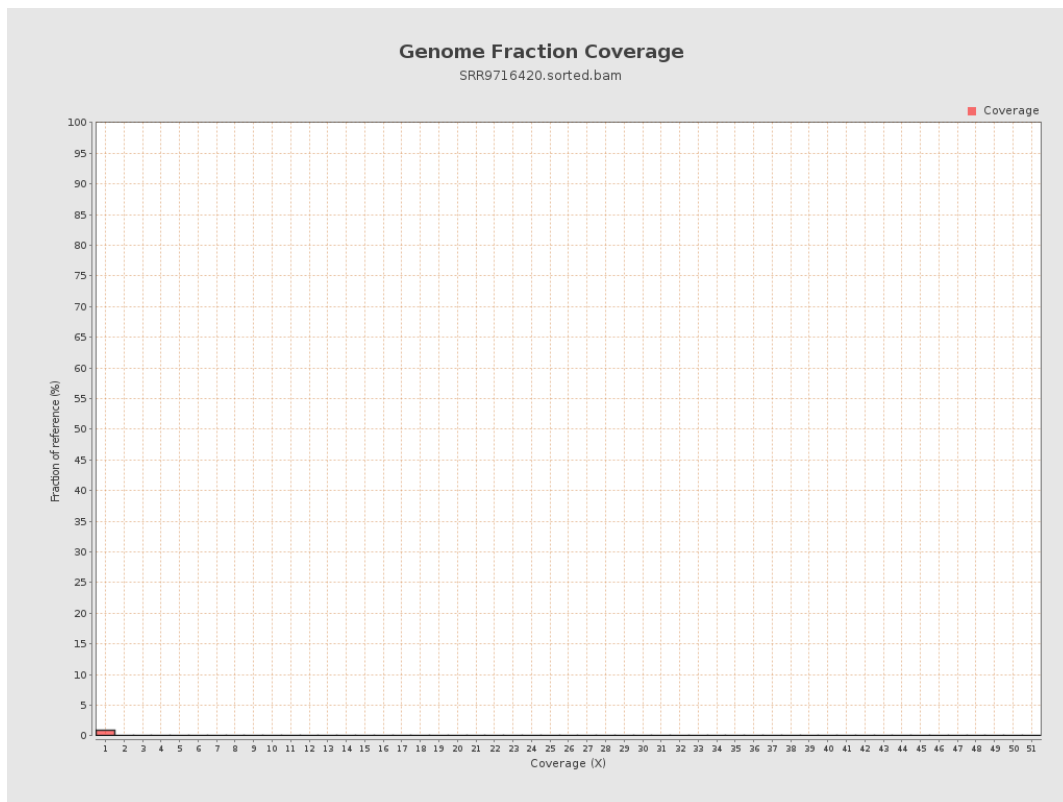


## 5. Results : Coverage Histogram (0-50X)

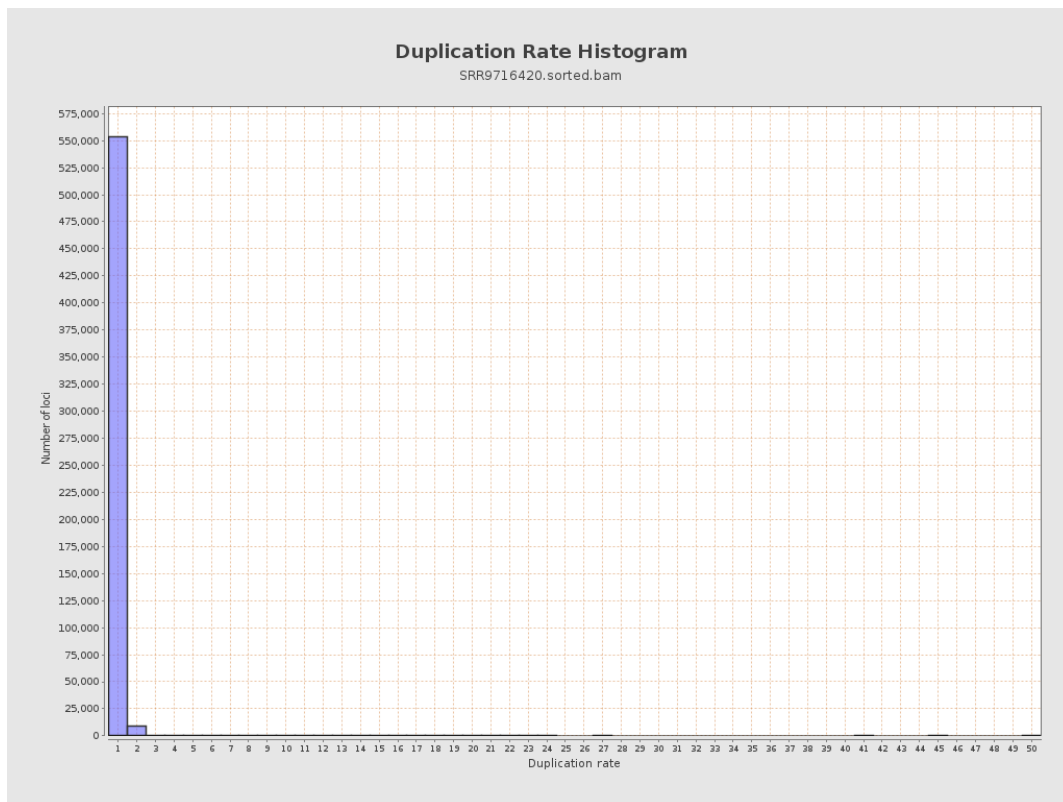




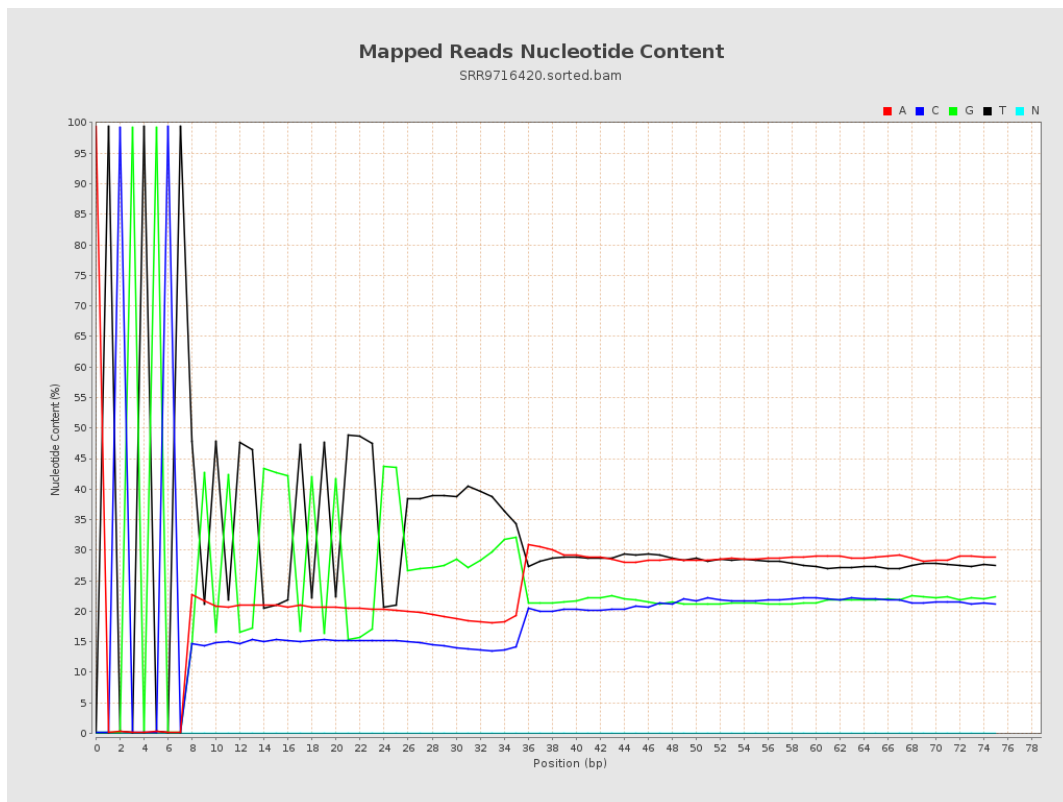
## 6. Results : Genome Fraction Coverage



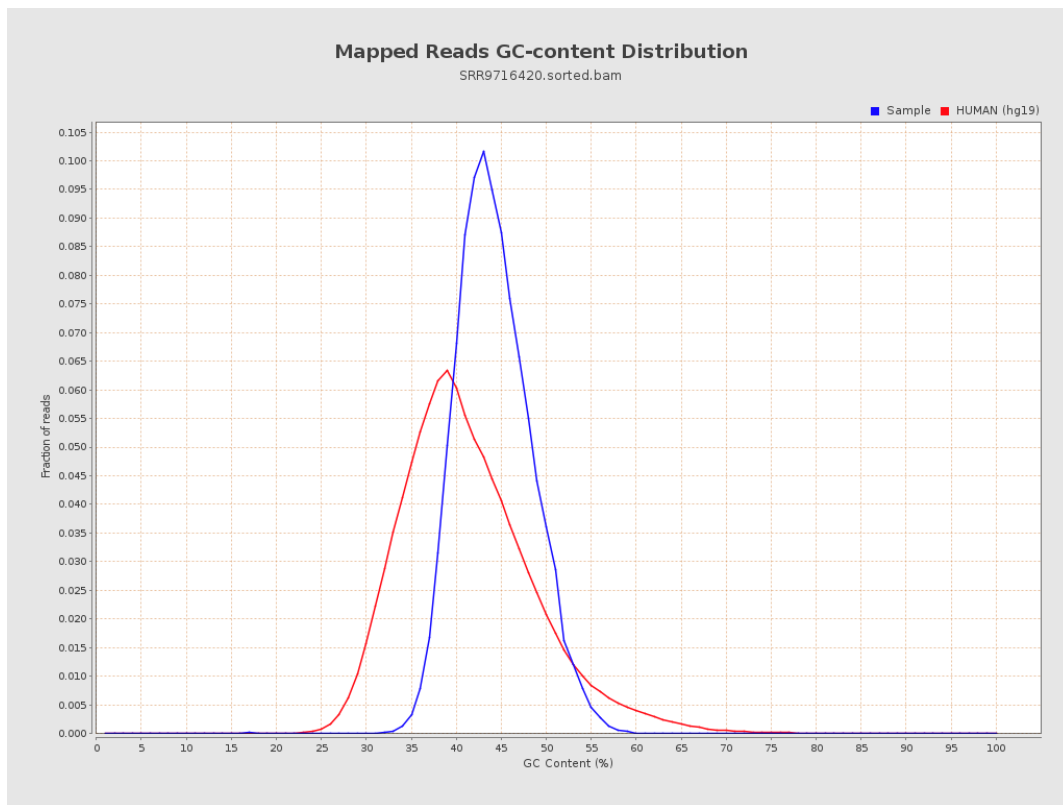
## 7. Results : Duplication Rate Histogram



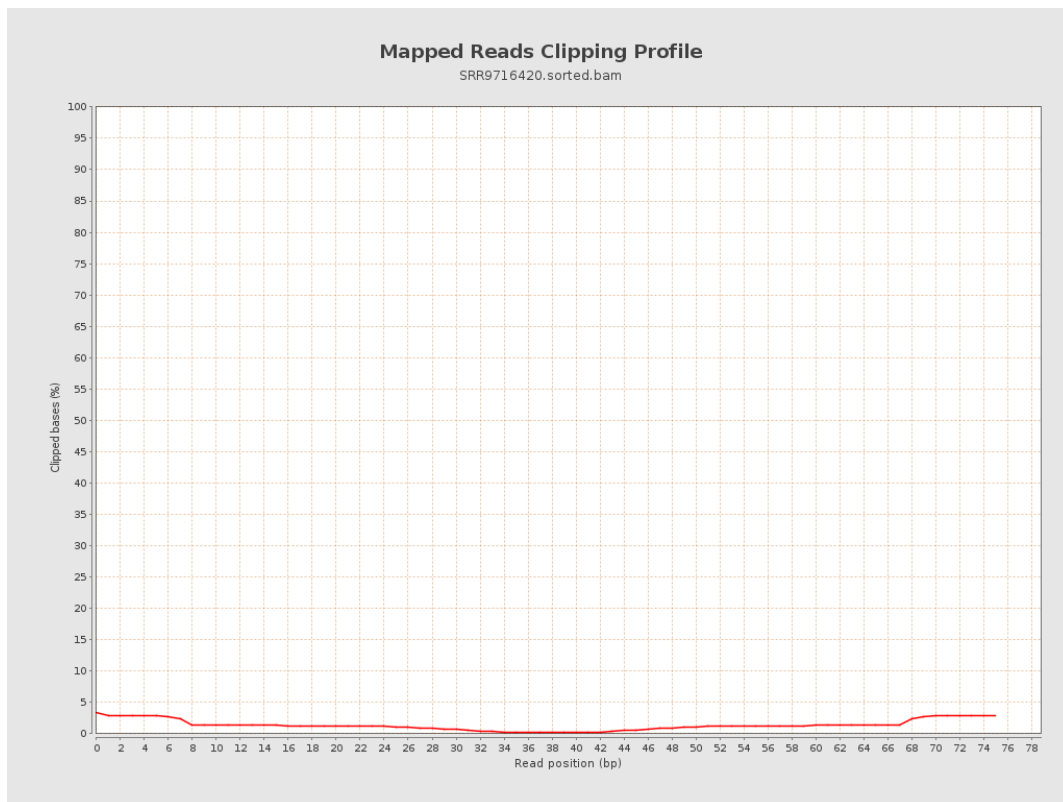
## 8. Results : Mapped Reads Nucleotide Content



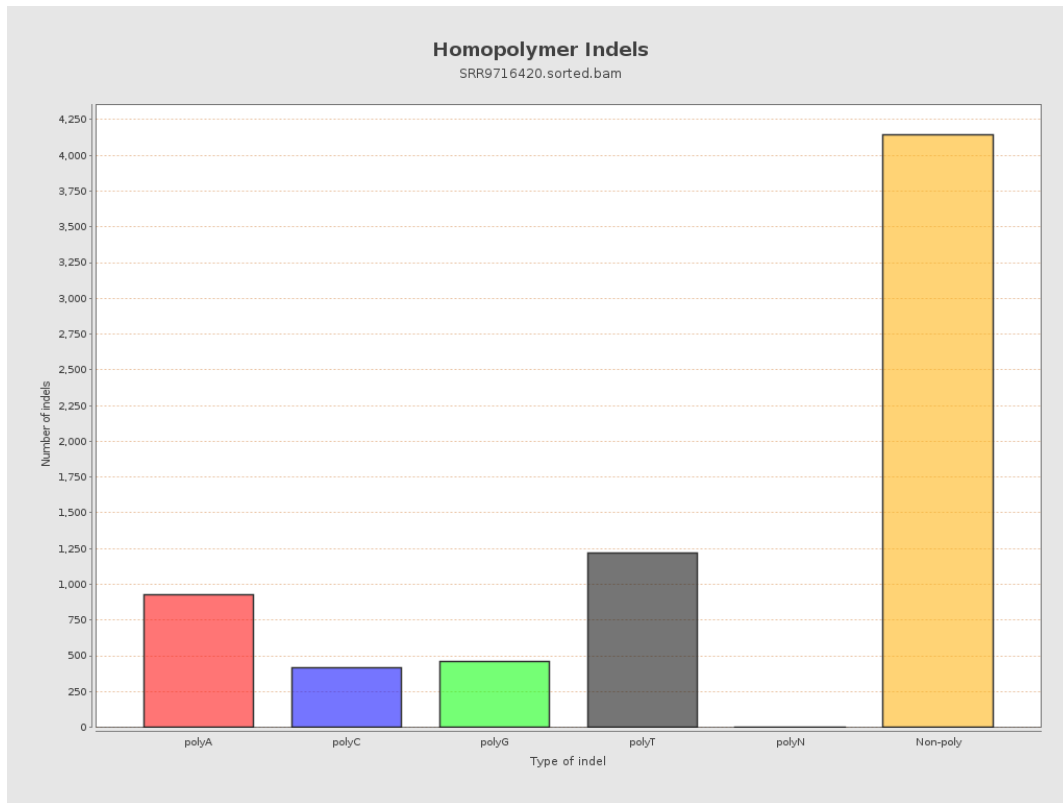
## 9. Results : Mapped Reads GC-content Distribution



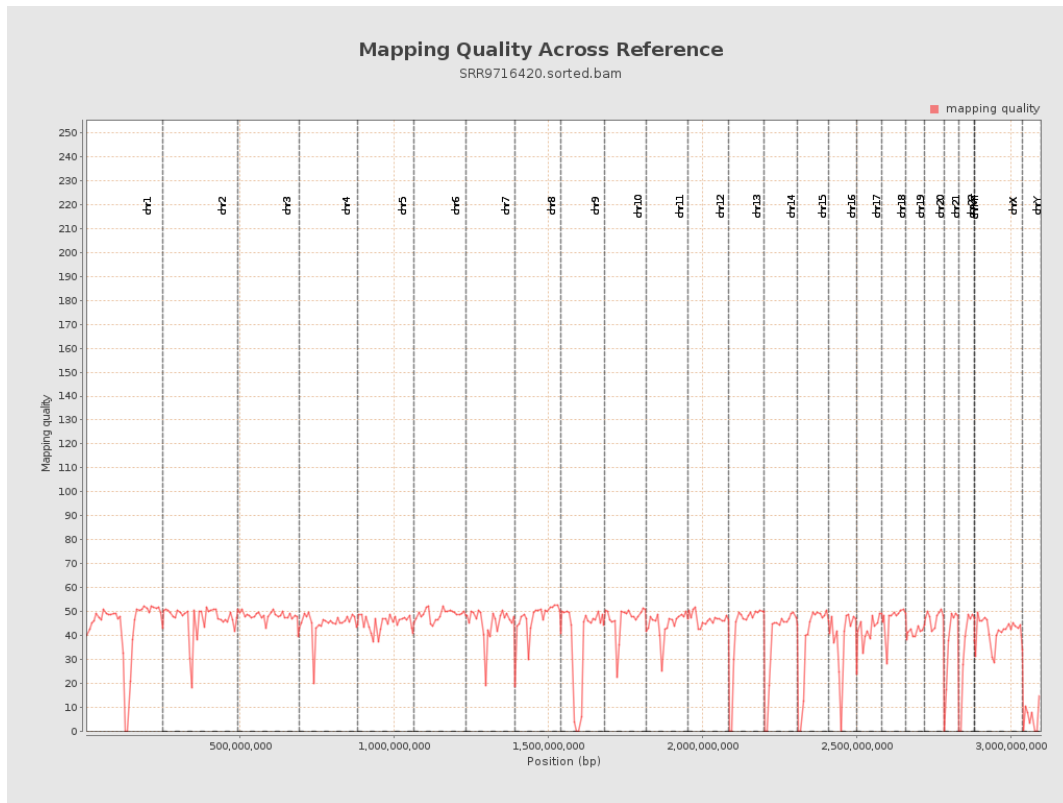
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

