

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 16:20:26*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716882.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_SRR9716882 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716882.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Tue Sep 03 16:20:25 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR9716882.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 1,383,121          |
| Mapped reads                 | 1,159,780 / 83.85% |
| Unmapped reads               | 223,341 / 16.15%   |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 2,177 / 0.16%      |
| Read min/max/mean length     | 30 / 76 / 76.05    |
| Duplicated reads (estimated) | 37,016 / 2.68%     |
| Duplication rate             | 2.45%              |
| Clipped reads                | 1,161,256 / 83.96% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 16,695,266 / 25.13% |
| Number/percentage of C's | 11,631,479 / 17.51% |
| Number/percentage of T's | 21,128,565 / 31.8%  |
| Number/percentage of G's | 16,989,440 / 25.57% |
| Number/percentage of N's | 644 / 0%            |
| GC Percentage            | 43.07%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0215 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.2068 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 44.56 |
|----------------------|-------|

## 2.5. Mismatches and indels

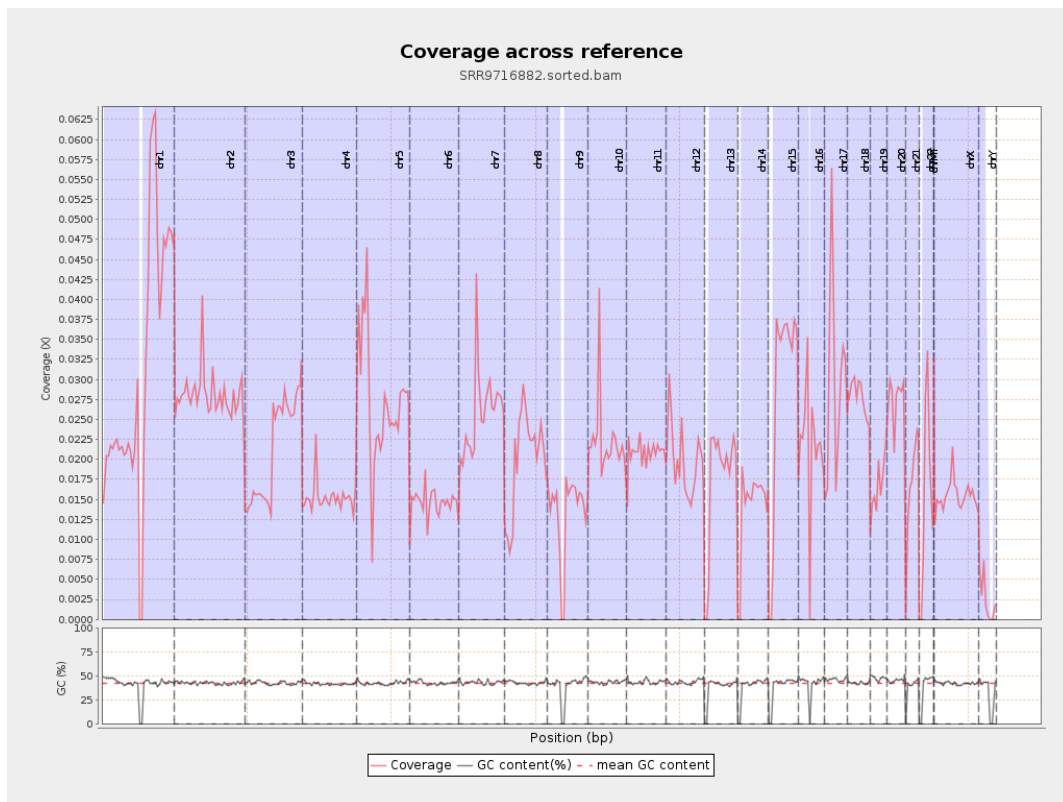
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 0.48%   |
| Mismatches                               | 313,864 |
| Insertions                               | 3,579   |
| Mapped reads with at least one insertion | 0.31%   |
| Deletions                                | 12,740  |
| Mapped reads with at least one deletion  | 1.09%   |
| Homopolymer indels                       | 44.75%  |

## 2.6. Chromosome stats

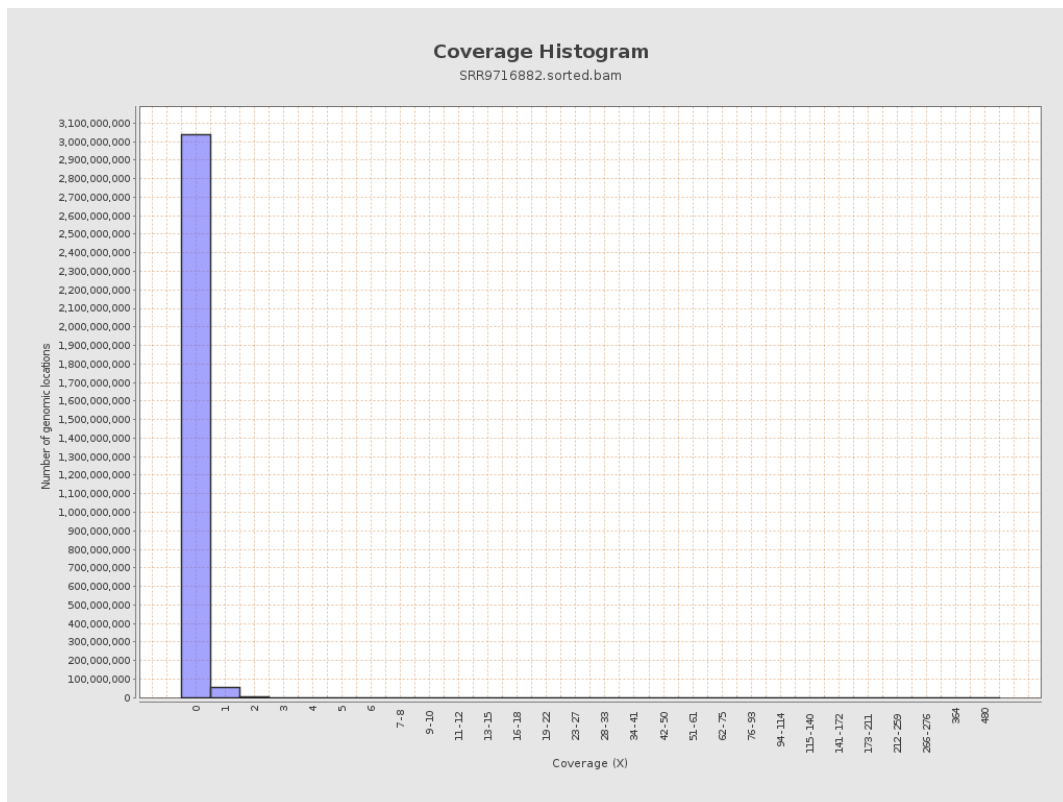
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 7733487      | 0.031         | 0.2857             |
| chr2 | 243199373 | 6821630      | 0.028         | 0.2911             |
| chr3 | 198022430 | 4181012      | 0.0211        | 0.1585             |
| chr4 | 191154276 | 2913137      | 0.0152        | 0.1376             |
| chr5 | 180915260 | 4967451      | 0.0275        | 0.178              |
| chr6 | 171115067 | 2483992      | 0.0145        | 0.1438             |
| chr7 | 159138663 | 4099607      | 0.0258        | 0.3255             |
|      |           |              |               |                    |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr8  | 146364022 | 2960569 | 0.0202 | 0.1708 |
| chr9  | 141213431 | 1894870 | 0.0134 | 0.1667 |
| chr10 | 135534747 | 3014527 | 0.0222 | 0.2396 |
| chr11 | 135006516 | 2829596 | 0.021  | 0.2024 |
| chr12 | 133851895 | 2642895 | 0.0197 | 0.1513 |
| chr13 | 115169878 | 2007676 | 0.0174 | 0.1415 |
| chr14 | 107349540 | 1503030 | 0.014  | 0.1315 |
| chr15 | 102531392 | 2964879 | 0.0289 | 0.184  |
| chr16 | 90354753  | 1940168 | 0.0215 | 0.173  |
| chr17 | 81195210  | 2440570 | 0.0301 | 0.1968 |
| chr18 | 78077248  | 2171039 | 0.0278 | 0.3159 |
| chr19 | 59128983  | 1001765 | 0.0169 | 0.2188 |
| chr20 | 63025520  | 1717540 | 0.0273 | 0.178  |
| chr21 | 48129895  | 810169  | 0.0168 | 0.1442 |
| chr22 | 51304566  | 812136  | 0.0158 | 0.1351 |
| chrMT | 16571     | 543     | 0.0328 | 0.178  |
| chrX  | 155270560 | 2410024 | 0.0155 | 0.1536 |
| chrY  | 59373566  | 143009  | 0.0024 | 0.0674 |

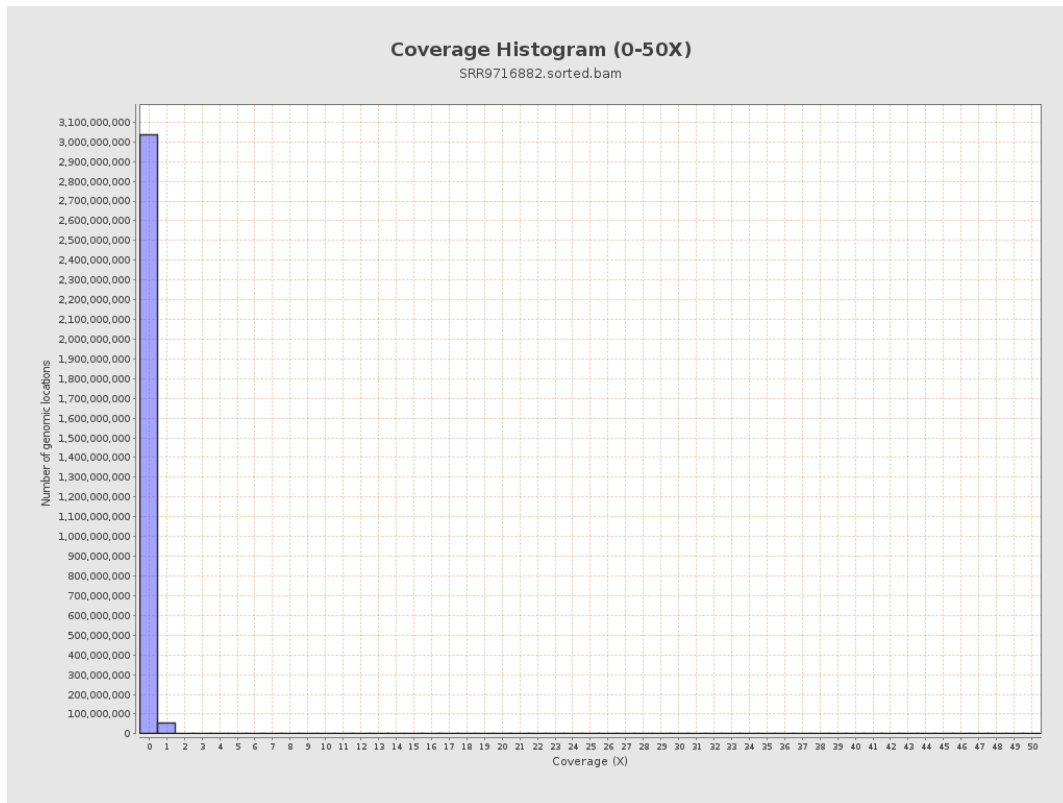
### 3. Results : Coverage across reference



## 4. Results : Coverage Histogram

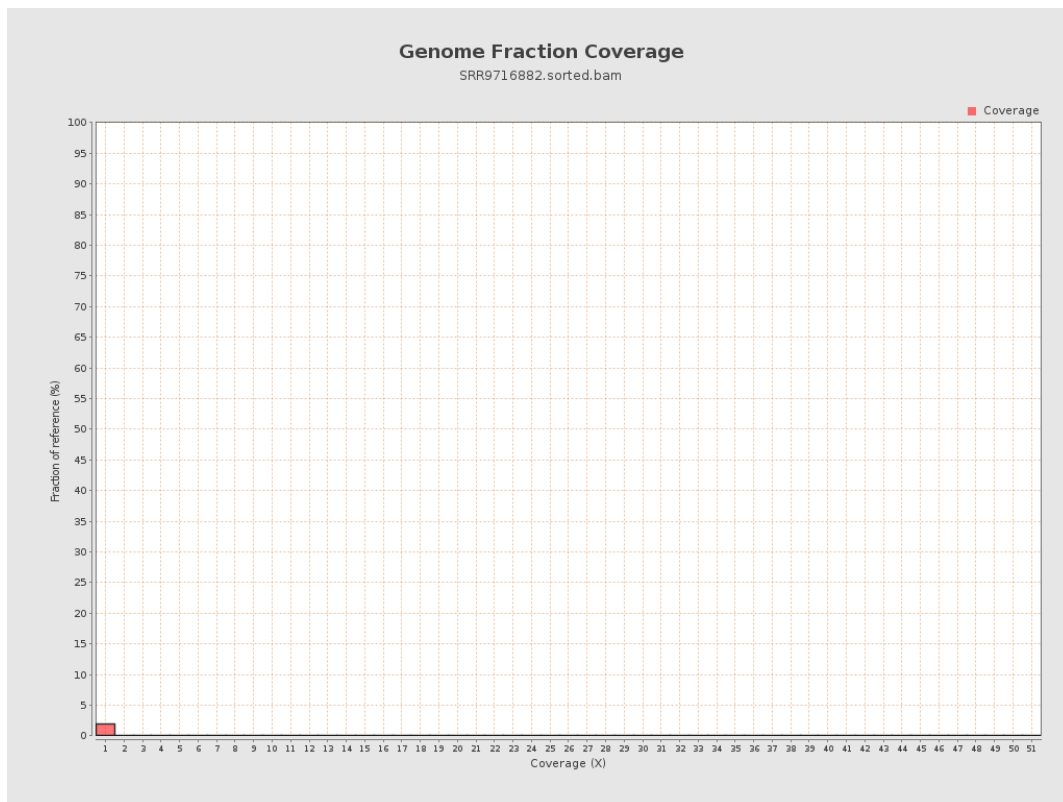


## 5. Results : Coverage Histogram (0-50X)

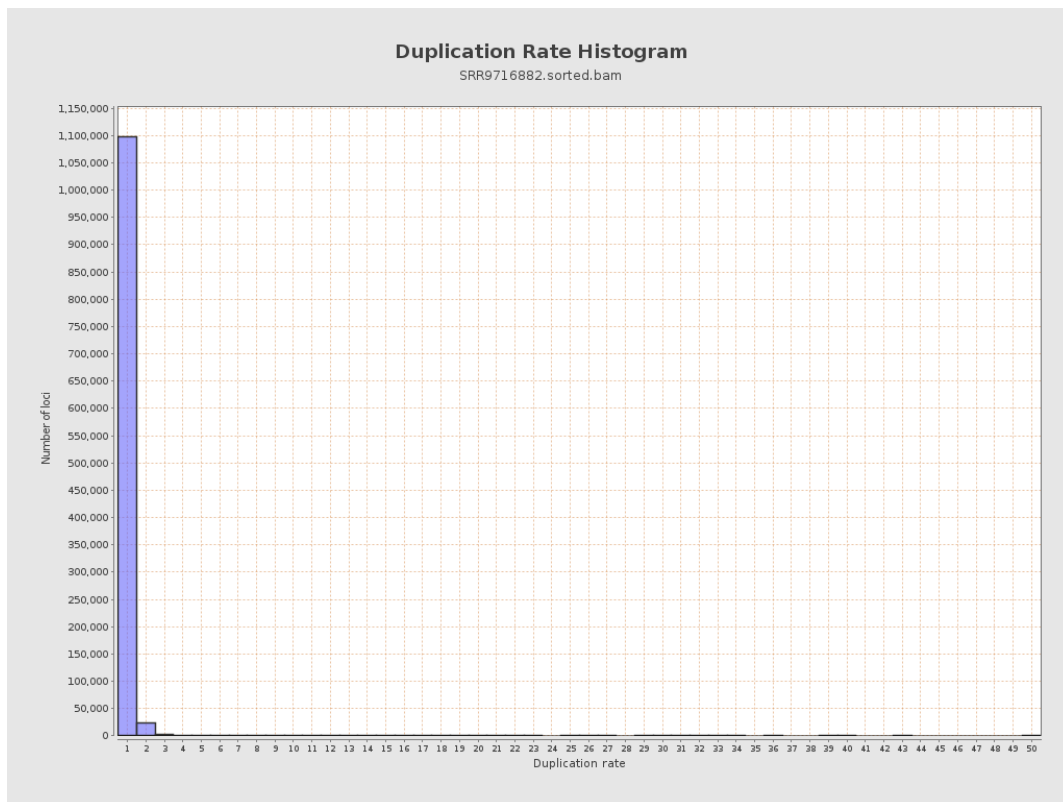




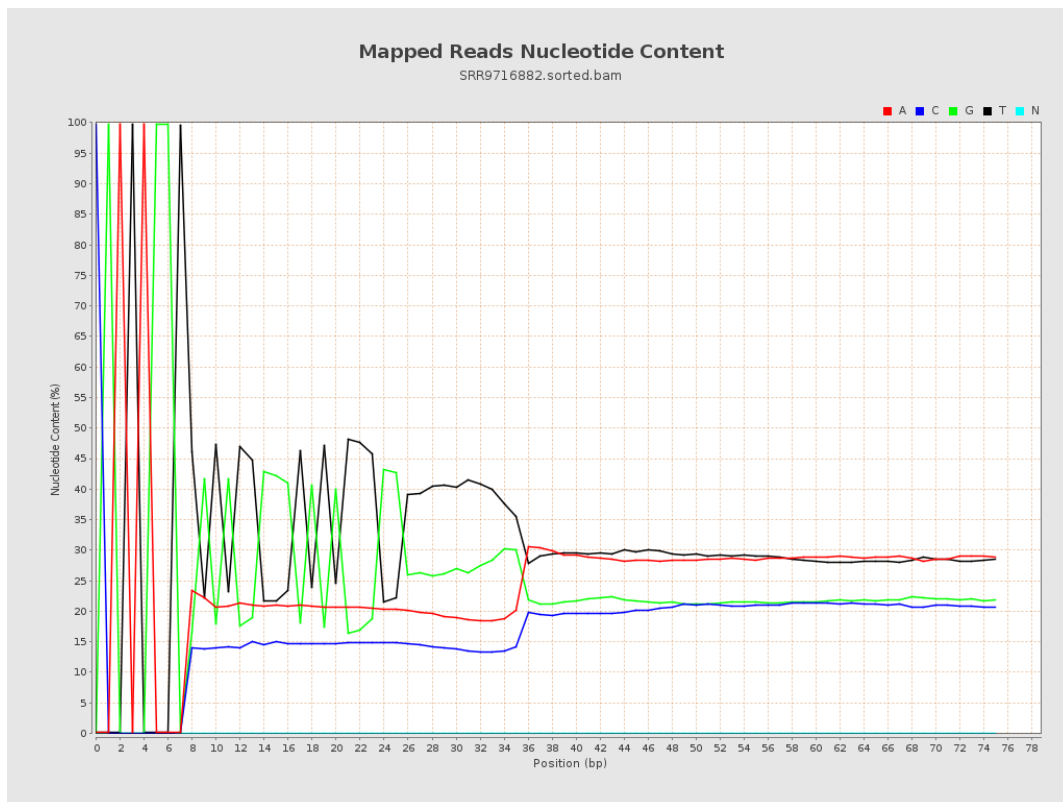
## 6. Results : Genome Fraction Coverage



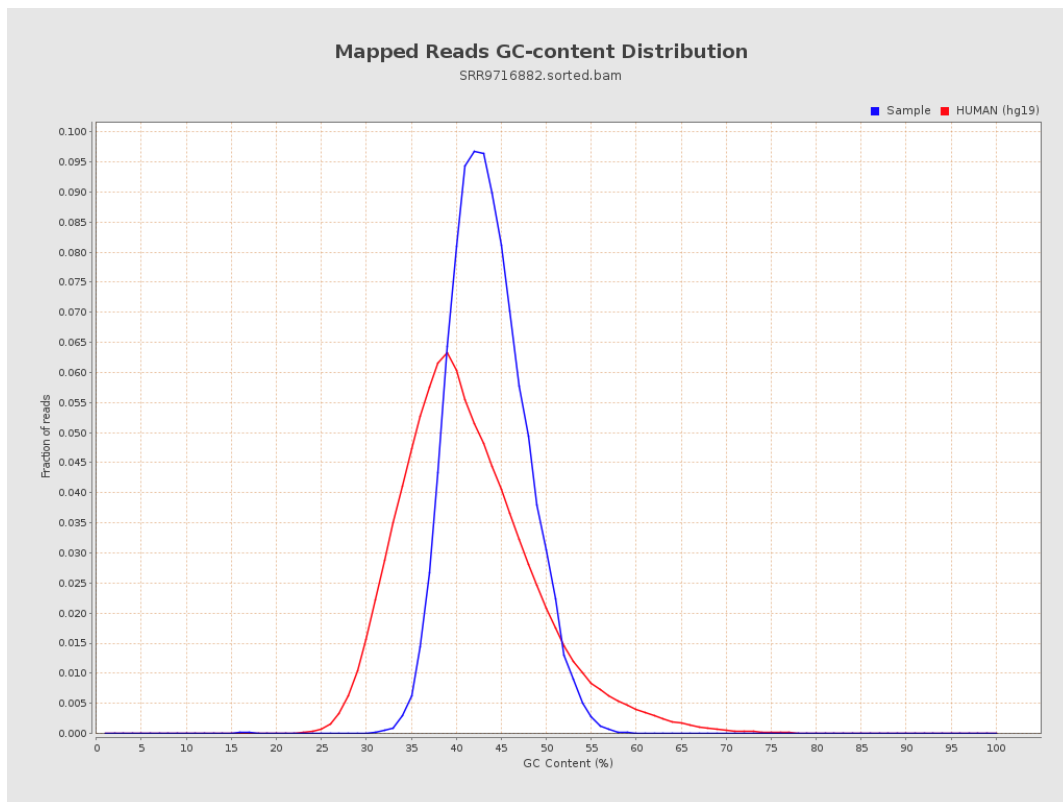
## 7. Results : Duplication Rate Histogram



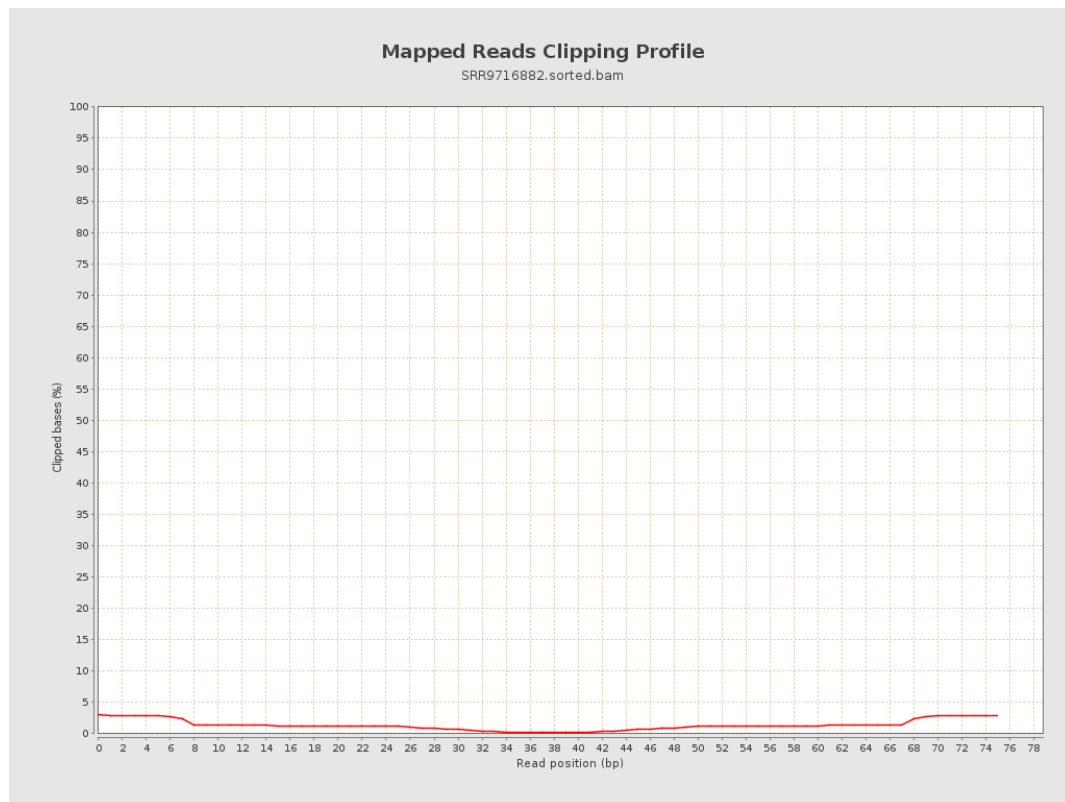
## 8. Results : Mapped Reads Nucleotide Content



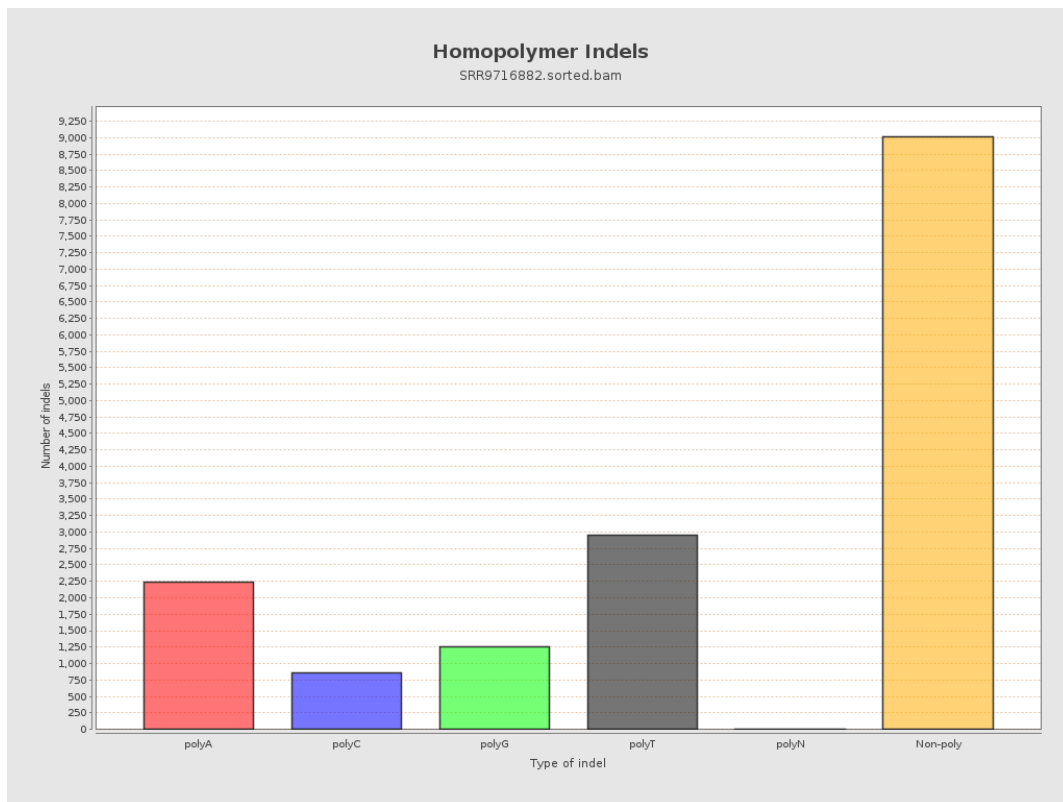
## 9. Results : Mapped Reads GC-content Distribution



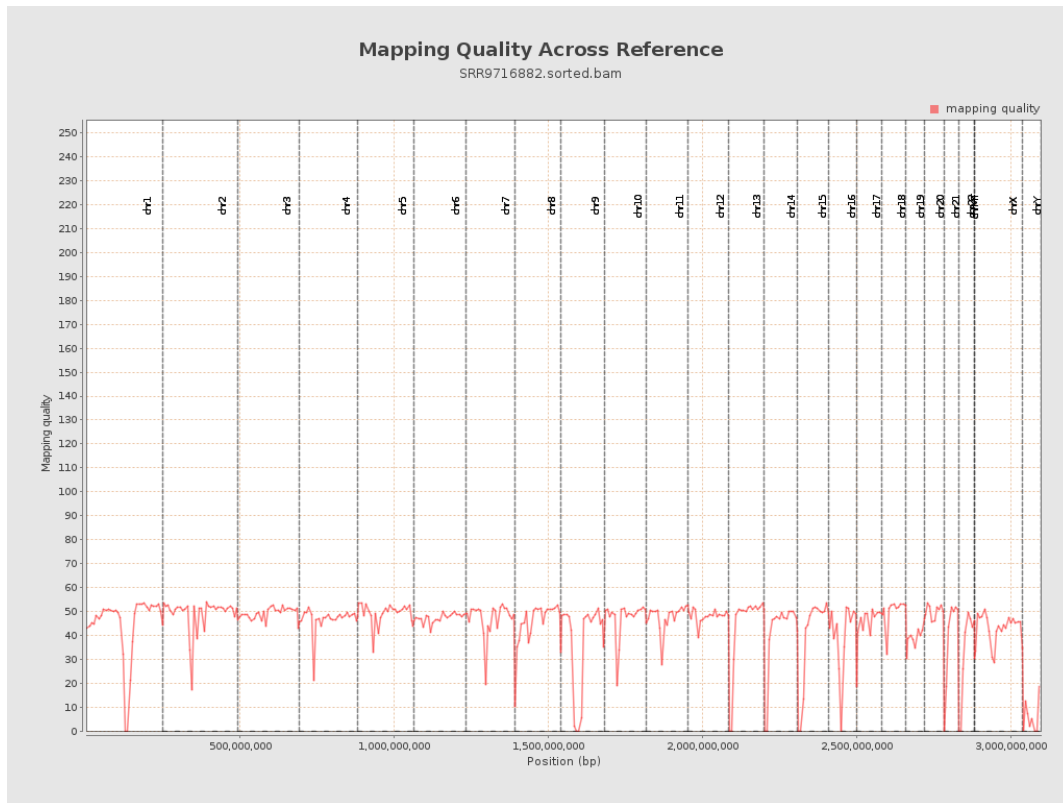
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

