

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/03/18 16:06:53*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR536741.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_SRR536741 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536741.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                        |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                         |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                         |
| Analysis date:                        | Fri Mar 18 16:06:45 CST 2022                                                                                                                                                               |
| Size of a homopolymer:                | 3                                                                                                                                                                                          |
| Skip duplicate alignments:            | no                                                                                                                                                                                         |
| Number of windows:                    | 400                                                                                                                                                                                        |
| BAM file:                             | SRR536741.sorted.bam                                                                                                                                                                       |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 86,574,968          |
| Mapped reads                 | 83,179,987 / 96.08% |
| Unmapped reads               | 3,394,981 / 3.92%   |
| Mapped paired reads          | 0 / 0%              |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 1,684 / 0%          |
| Read min/max/mean length     | 30 / 50 / 50        |
| Duplicated reads (estimated) | 4,997,824 / 5.77%   |
| Duplication rate             | 2.4%                |
| Clipped reads                | 1,429,650 / 1.65%   |

### 2.2. ACGT Content

|                          |                        |
|--------------------------|------------------------|
| Number/percentage of A's | 1,210,731,665 / 29.21% |
| Number/percentage of C's | 858,040,524 / 20.7%    |
| Number/percentage of T's | 1,215,031,569 / 29.32% |
| Number/percentage of G's | 860,333,109 / 20.76%   |
| Number/percentage of N's | 107,124 / 0%           |
| GC Percentage            | 41.46%                 |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 1.3388 |
|      |        |

|                    |         |
|--------------------|---------|
| Standard Deviation | 10.9681 |
|--------------------|---------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 46.16 |
|----------------------|-------|

## 2.5. Mismatches and indels

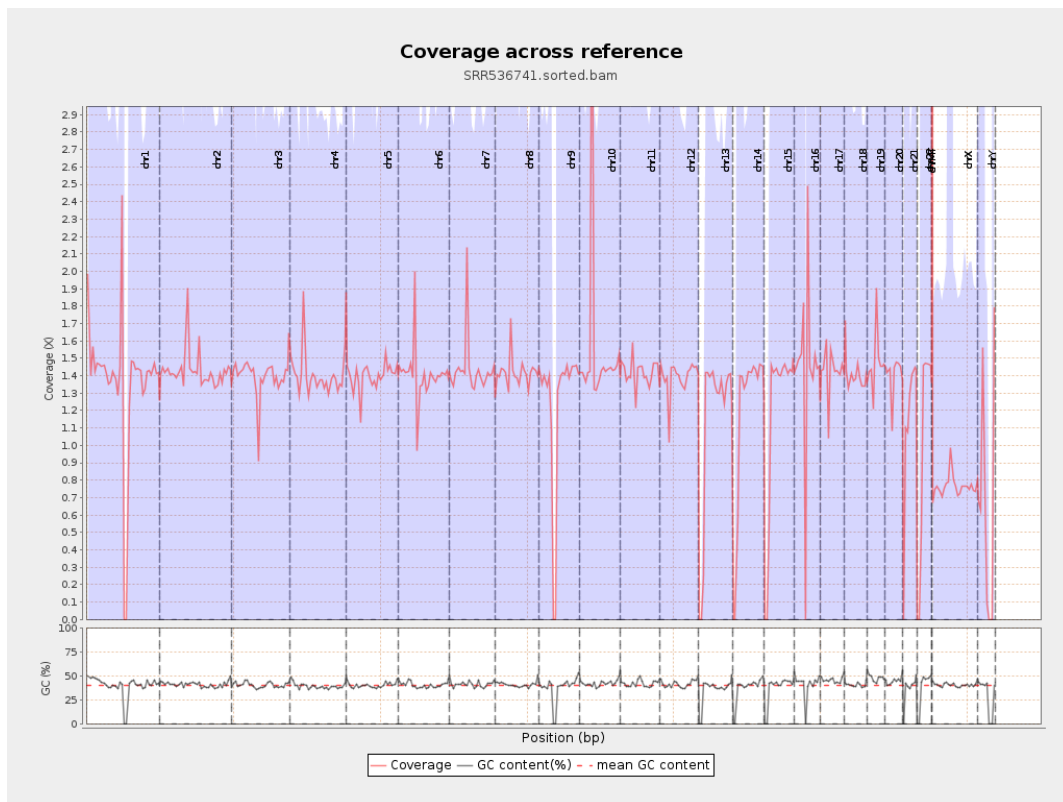
|                                          |            |
|------------------------------------------|------------|
| General error rate                       | 0.25%      |
| Mismatches                               | 10,083,698 |
| Insertions                               | 158,863    |
| Mapped reads with at least one insertion | 0.19%      |
| Deletions                                | 228,080    |
| Mapped reads with at least one deletion  | 0.27%      |
| Homopolymer indels                       | 44.41%     |

## 2.6. Chromosome stats

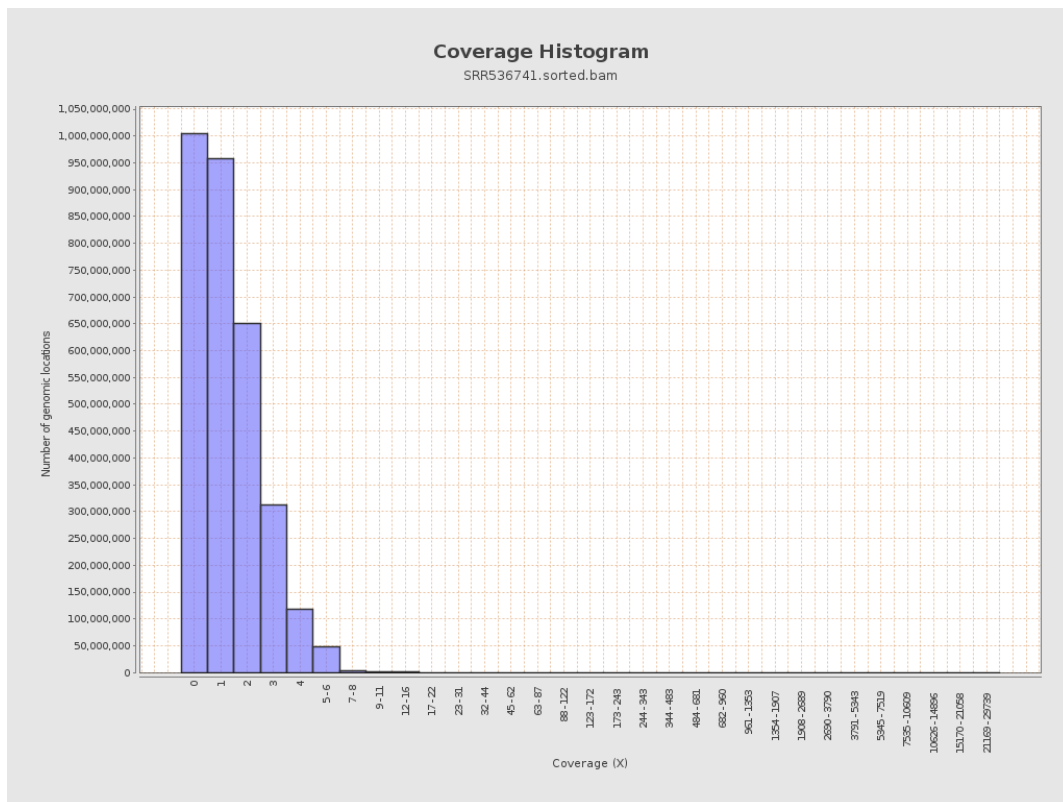
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 342640204    | 1.3747        | 22.8551            |
| chr2 | 243199373 | 348667065    | 1.4337        | 5.7033             |
| chr3 | 198022430 | 275949263    | 1.3935        | 3.173              |
| chr4 | 191154276 | 267382167    | 1.3988        | 3.5677             |
| chr5 | 180915260 | 252987766    | 1.3984        | 2.6442             |
| chr6 | 171115067 | 240613312    | 1.4061        | 7.0641             |
| chr7 | 159138663 | 228436767    | 1.4355        | 10.0927            |
|      |           |              |               |                    |

|       |           |           |            |          |
|-------|-----------|-----------|------------|----------|
| chr8  | 146364022 | 208092052 | 1.4217     | 5.4544   |
| chr9  | 141213431 | 174417433 | 1.2351     | 4.4023   |
| chr10 | 135534747 | 212831688 | 1.5703     | 20.4188  |
| chr11 | 135006516 | 191796354 | 1.4206     | 5.2675   |
| chr12 | 133851895 | 186050027 | 1.39       | 2.1872   |
| chr13 | 115169878 | 131304298 | 1.1401     | 1.7478   |
| chr14 | 107349540 | 125891416 | 1.1727     | 2.0993   |
| chr15 | 102531392 | 119399854 | 1.1645     | 1.3808   |
| chr16 | 90354753  | 131285321 | 1.453      | 8.9171   |
| chr17 | 81195210  | 115965731 | 1.4282     | 3.1433   |
| chr18 | 78077248  | 109488231 | 1.4023     | 10.8153  |
| chr19 | 59128983  | 87359761  | 1.4774     | 16.8428  |
| chr20 | 63025520  | 88371812  | 1.4022     | 2.1182   |
| chr21 | 48129895  | 56031648  | 1.1642     | 4.5705   |
| chr22 | 51304566  | 51989216  | 1.0133     | 3.7545   |
| chrMT | 16571     | 37962221  | 2,290.8829 | 615.7199 |
| chrX  | 155270560 | 118550529 | 0.7635     | 2.8464   |
| chrY  | 59373566  | 41163106  | 0.6933     | 8.6423   |

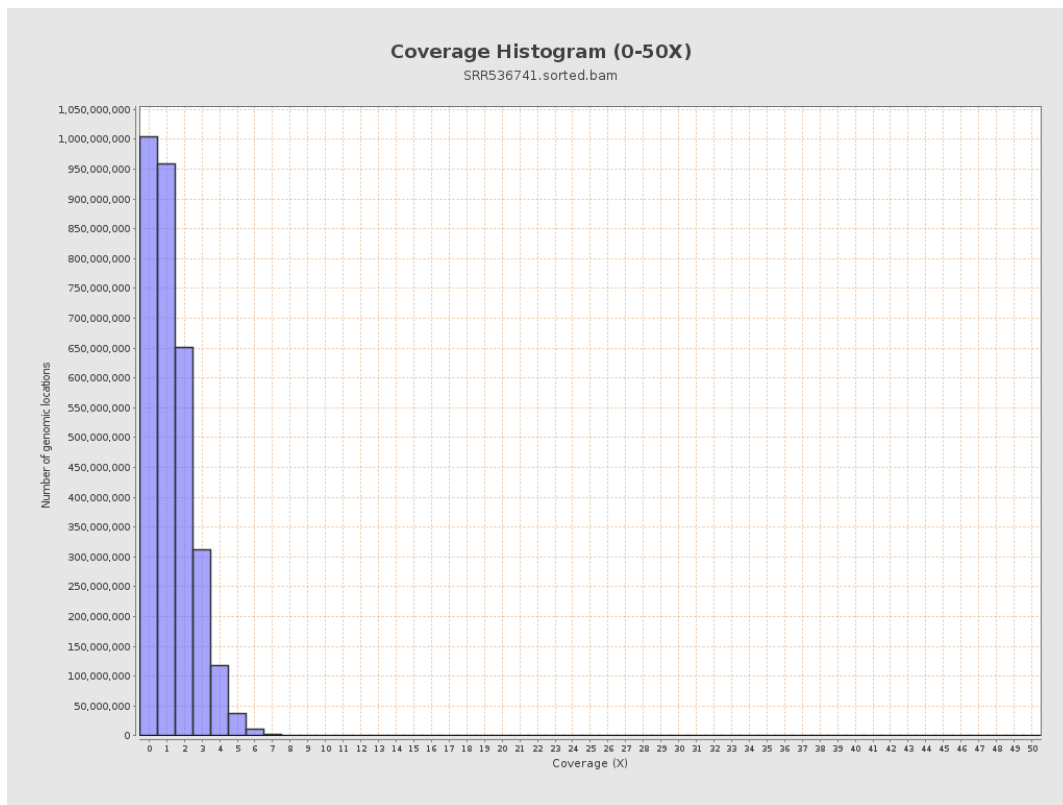
### 3. Results : Coverage across reference



## 4. Results : Coverage Histogram

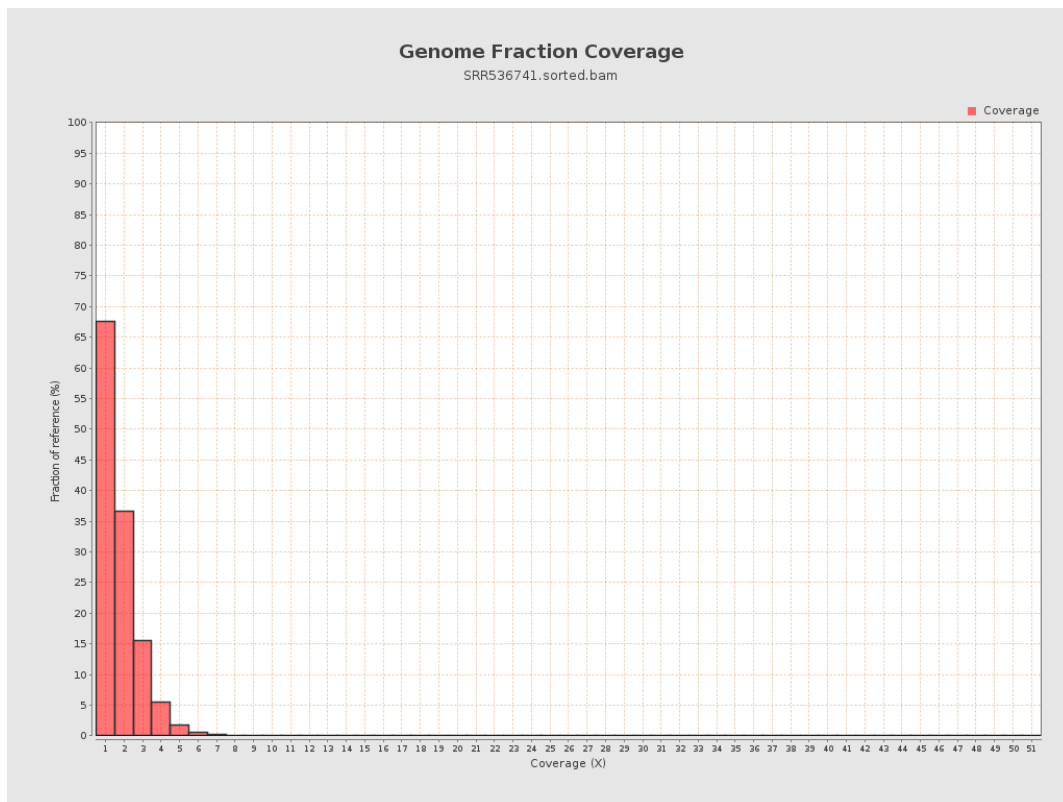


## 5. Results : Coverage Histogram (0-50X)

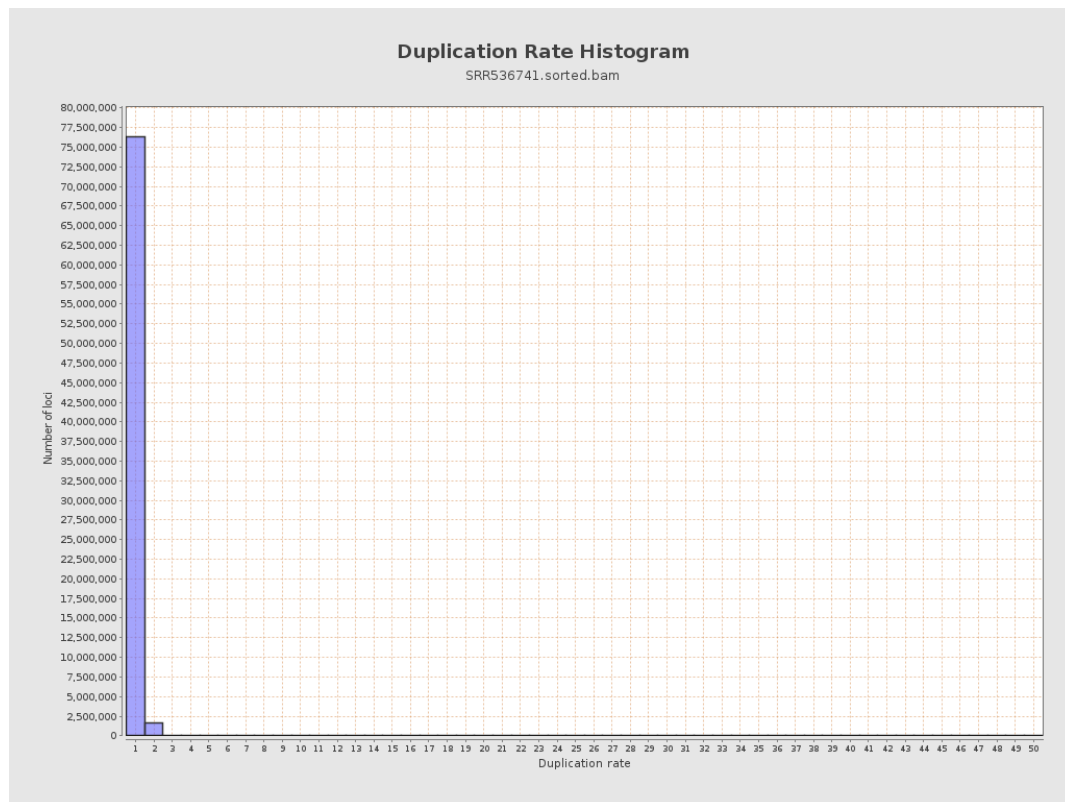




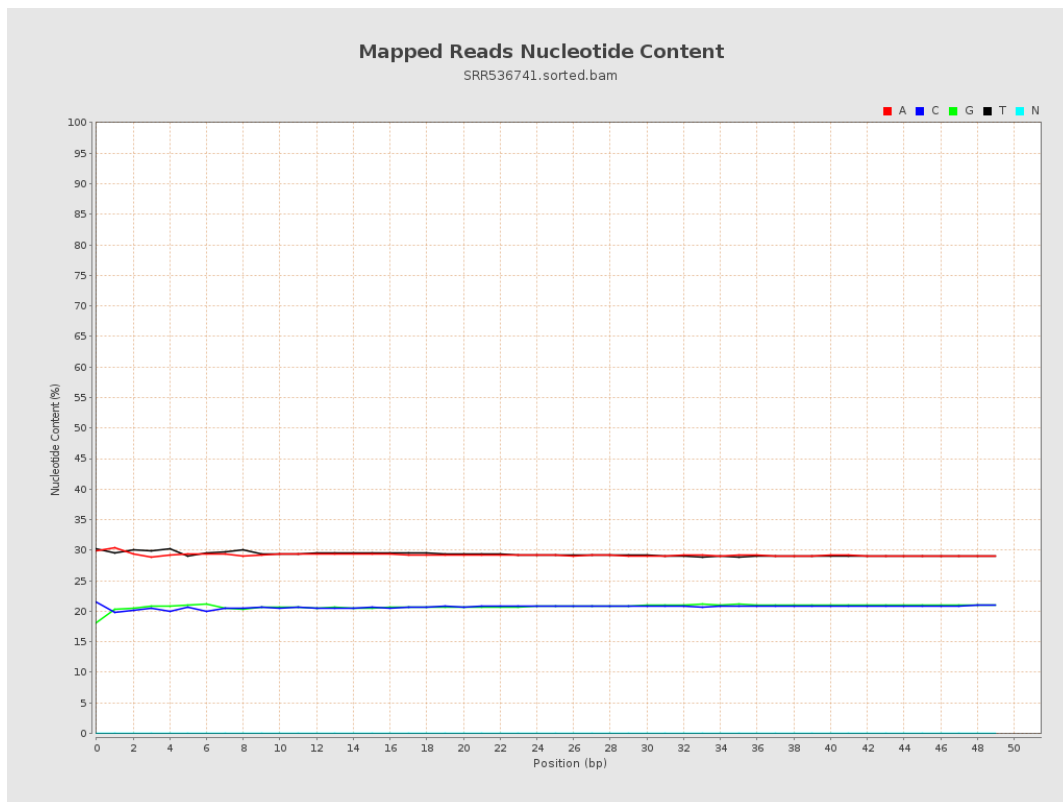
## 6. Results : Genome Fraction Coverage



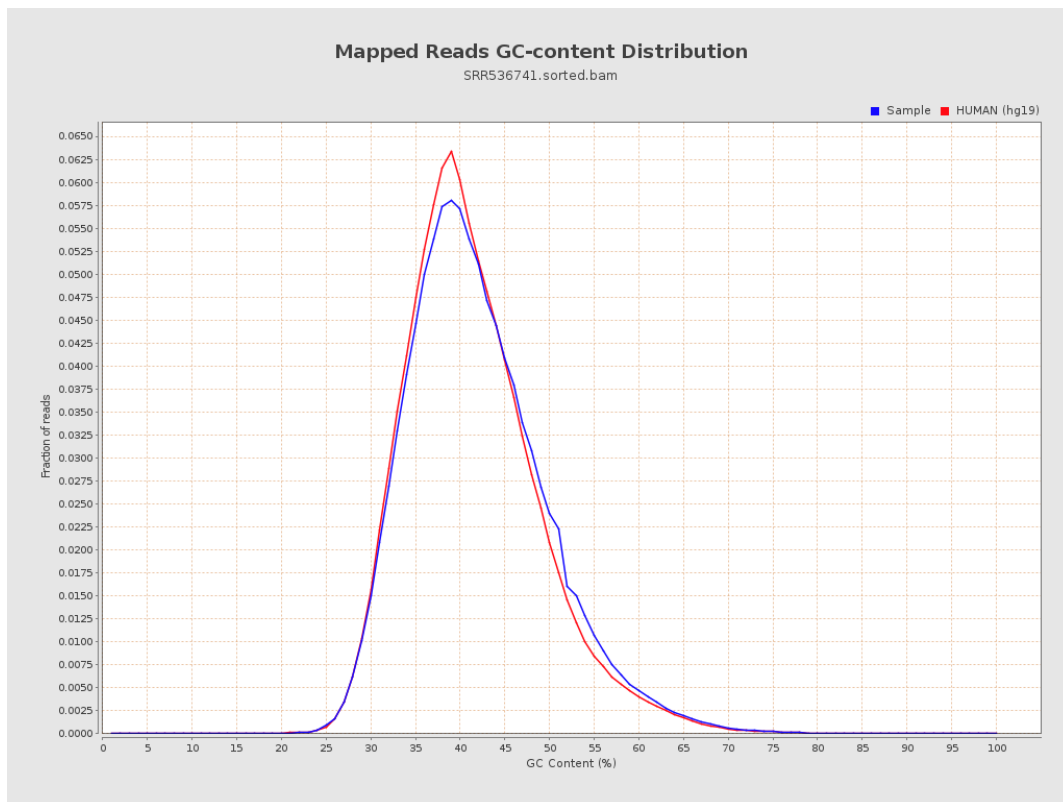
## 7. Results : Duplication Rate Histogram



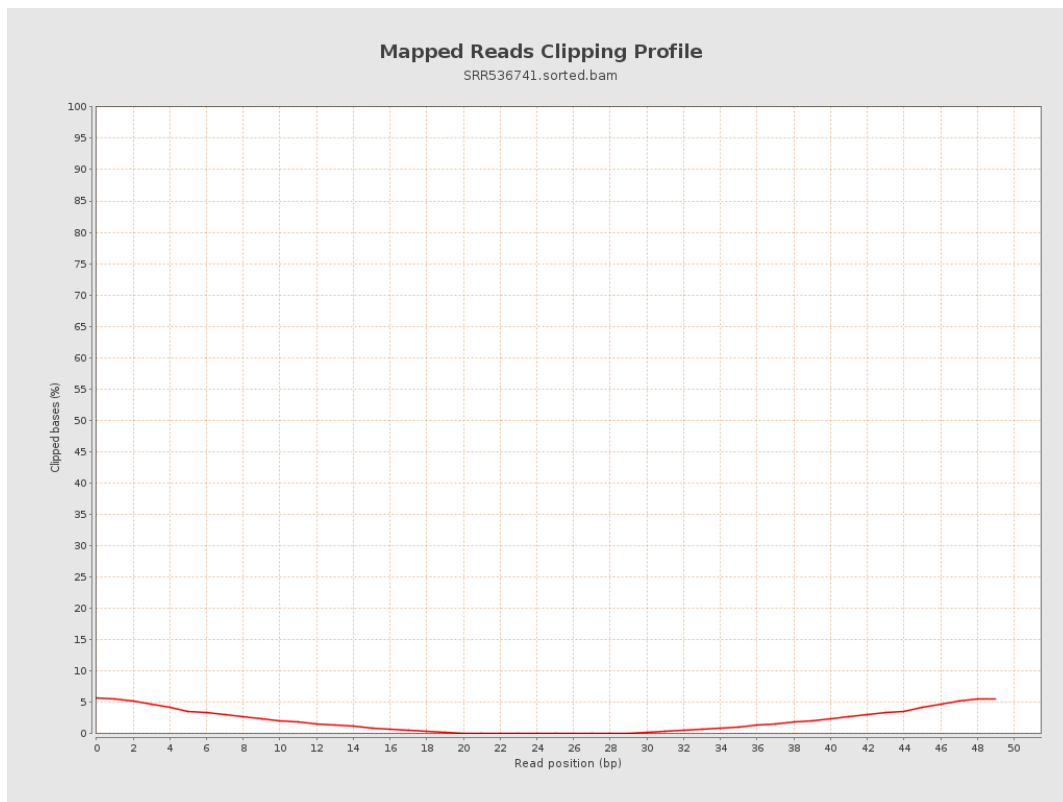
## 8. Results : Mapped Reads Nucleotide Content



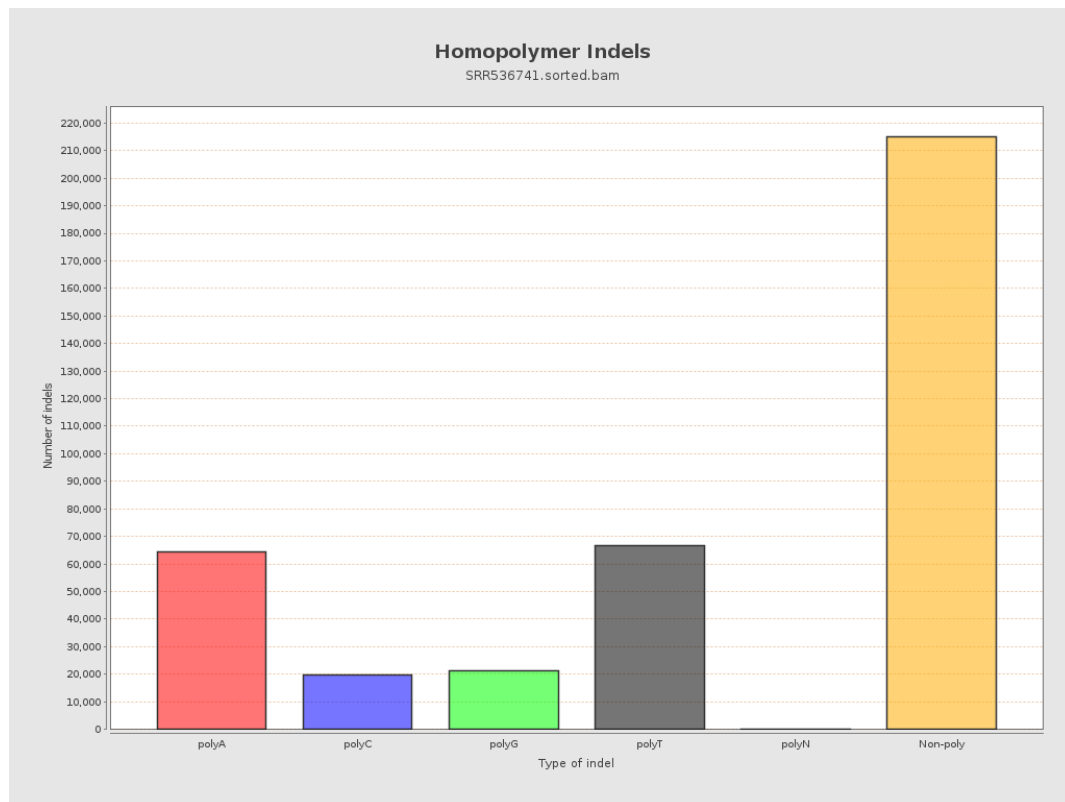
## 9. Results : Mapped Reads GC-content Distribution



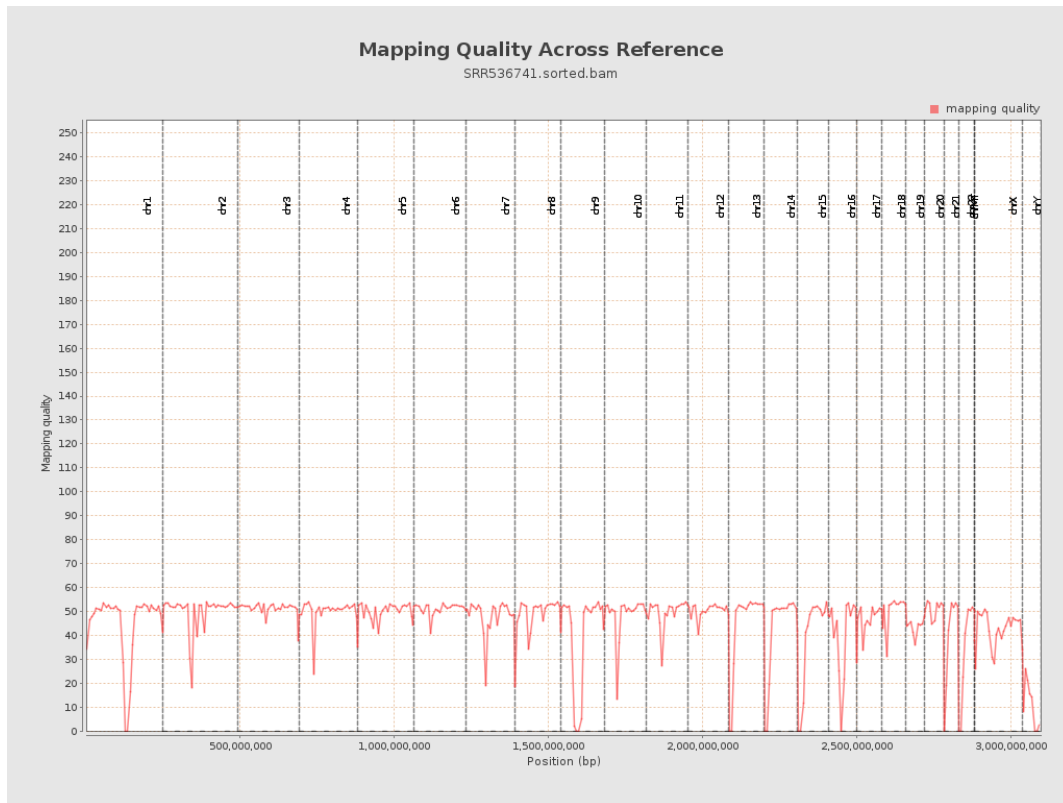
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

