

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 07:23:19*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549135.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_SRR1549135 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549135.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Sat Aug 24 07:23:18 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR1549135.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 9,716,164          |
| Mapped reads                 | 8,478,928 / 87.27% |
| Unmapped reads               | 1,237,236 / 12.73% |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Read min/max/mean length     | 40 / 40 / 40       |
| Duplicated reads (estimated) | 372,876 / 3.84%    |
| Duplication rate             | 3.43%              |
| Clipped reads                | 416,689 / 4.29%    |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 98,713,947 / 29.32% |
| Number/percentage of C's | 69,450,898 / 20.63% |
| Number/percentage of T's | 99,298,303 / 29.49% |
| Number/percentage of G's | 69,127,773 / 20.53% |
| Number/percentage of N's | 74,039 / 0.02%      |
| GC Percentage            | 41.16%              |

### 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.1088 |
| Standard Deviation | 0.7203 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 43.69 |
|----------------------|-------|

## 2.5. Mismatches and indels

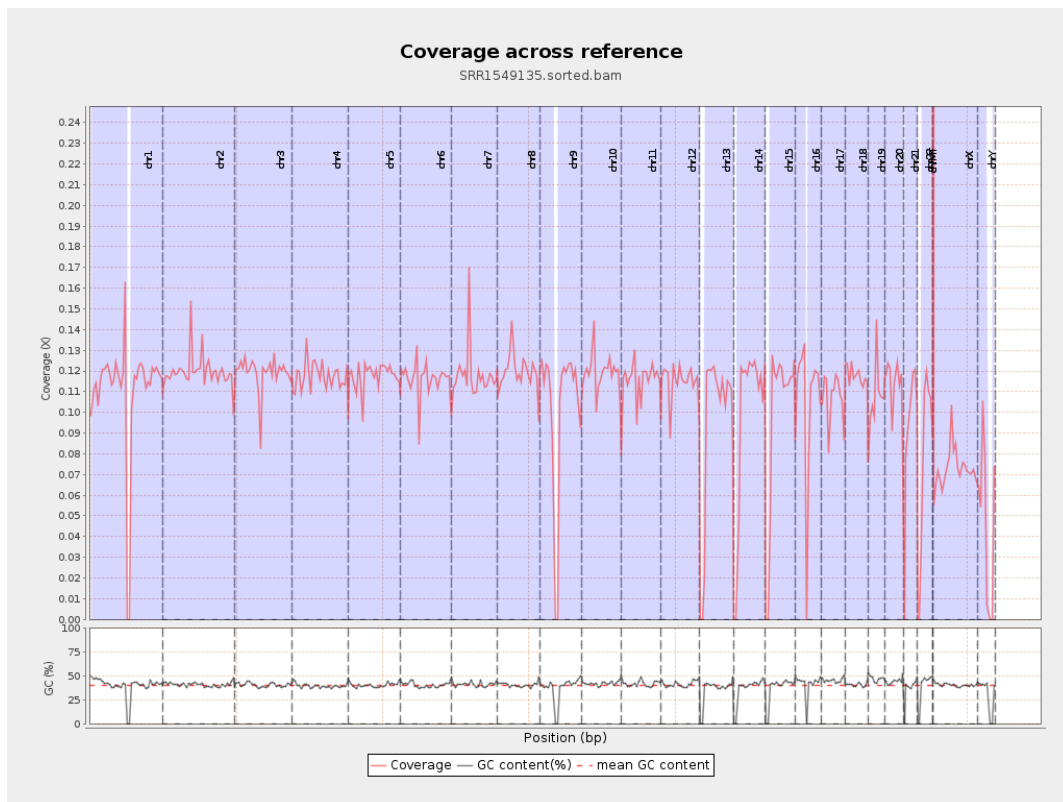
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.32%     |
| Mismatches                               | 1,067,828 |
| Insertions                               | 8,375     |
| Mapped reads with at least one insertion | 0.1%      |
| Deletions                                | 25,092    |
| Mapped reads with at least one deletion  | 0.3%      |
| Homopolymer indels                       | 46.02%    |

## 2.6. Chromosome stats

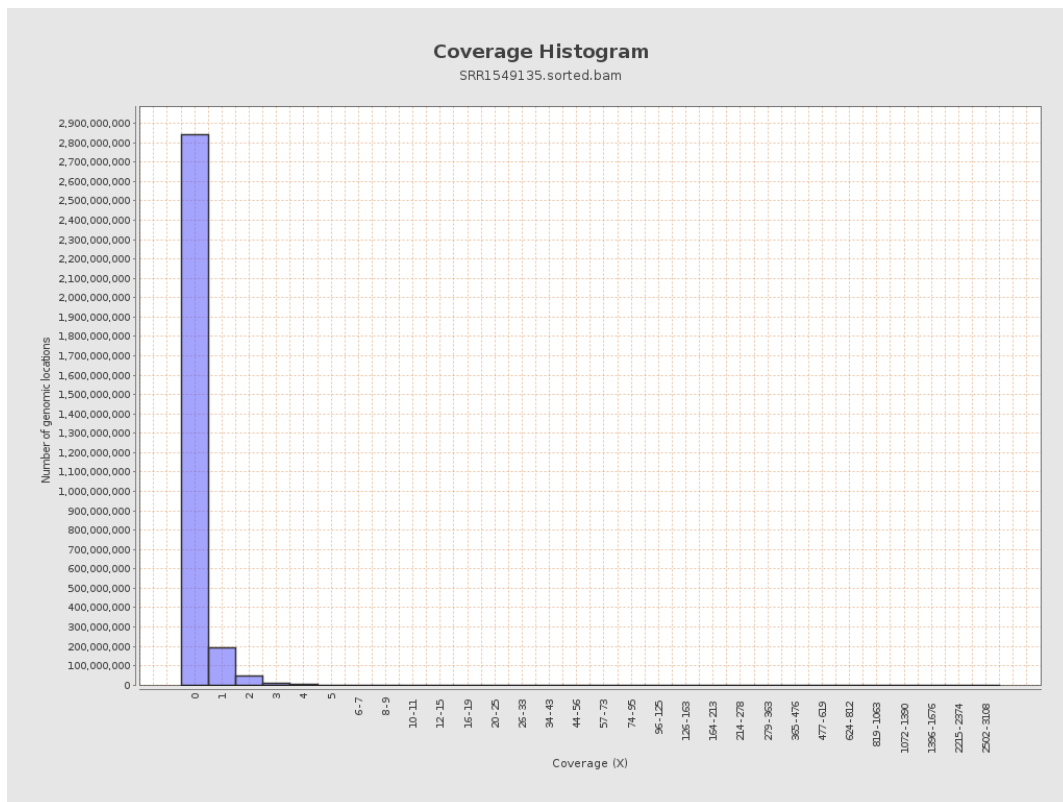
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 27510682     | 0.1104        | 1.2521             |
| chr2 | 243199373 | 29159605     | 0.1199        | 0.5967             |
| chr3 | 198022430 | 23572392     | 0.119         | 0.4352             |
| chr4 | 191154276 | 22513335     | 0.1178        | 0.4485             |
| chr5 | 180915260 | 21273588     | 0.1176        | 0.4467             |
| chr6 | 171115067 | 19898446     | 0.1163        | 0.4821             |
| chr7 | 159138663 | 18728210     | 0.1177        | 0.9018             |
| chr8 | 146364022 | 17478496     | 0.1194        | 1.5925             |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr9  | 141213431 | 14393147 | 0.1019 | 0.5478 |
| chr10 | 135534747 | 16156330 | 0.1192 | 0.5961 |
| chr11 | 135006516 | 15598860 | 0.1155 | 0.5545 |
| chr12 | 133851895 | 15462612 | 0.1155 | 0.4481 |
| chr13 | 115169878 | 10960944 | 0.0952 | 0.3861 |
| chr14 | 107349540 | 10590697 | 0.0987 | 0.51   |
| chr15 | 102531392 | 9873388  | 0.0963 | 0.3872 |
| chr16 | 90354753  | 9372841  | 0.1037 | 0.4421 |
| chr17 | 81195210  | 8743350  | 0.1077 | 0.4406 |
| chr18 | 78077248  | 9191502  | 0.1177 | 1.0893 |
| chr19 | 59128983  | 6401474  | 0.1083 | 1.0284 |
| chr20 | 63025520  | 7163794  | 0.1137 | 0.4502 |
| chr21 | 48129895  | 4498572  | 0.0935 | 0.446  |
| chr22 | 51304566  | 3922769  | 0.0765 | 0.3699 |
| chrMT | 16571     | 107423   | 6.4826 | 8.2791 |
| chrX  | 155270560 | 11312350 | 0.0729 | 0.415  |
| chrY  | 59373566  | 2811741  | 0.0474 | 0.4081 |

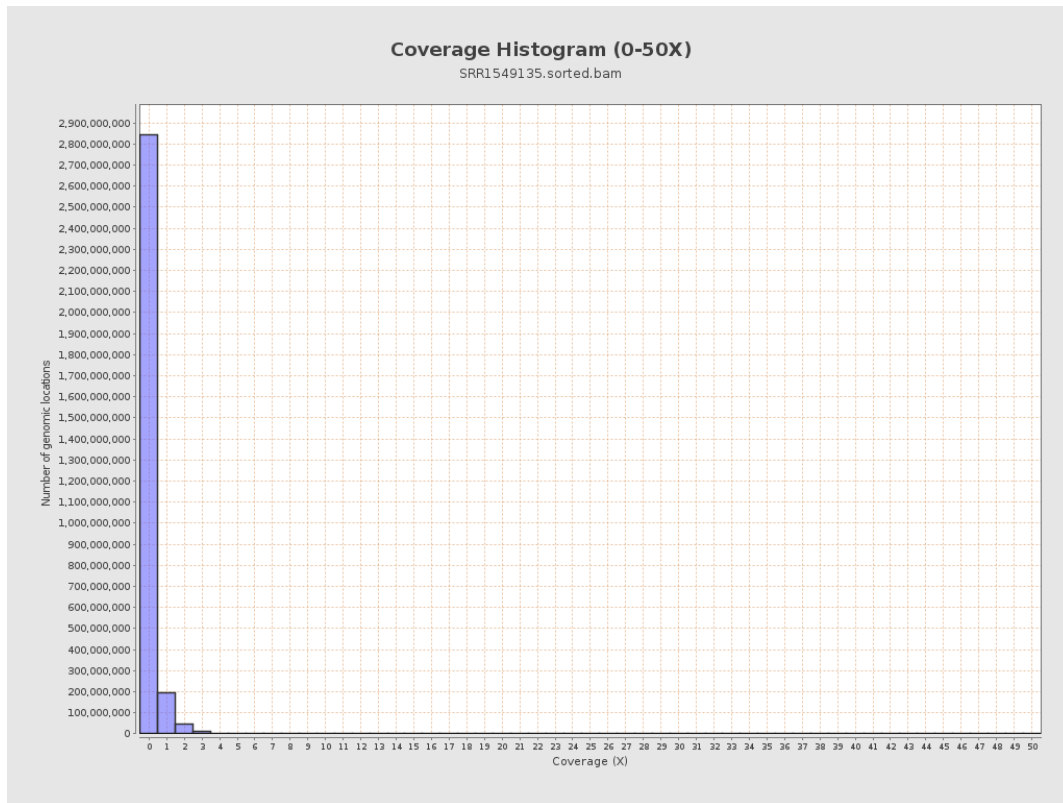
### 3. Results : Coverage across reference



## 4. Results : Coverage Histogram

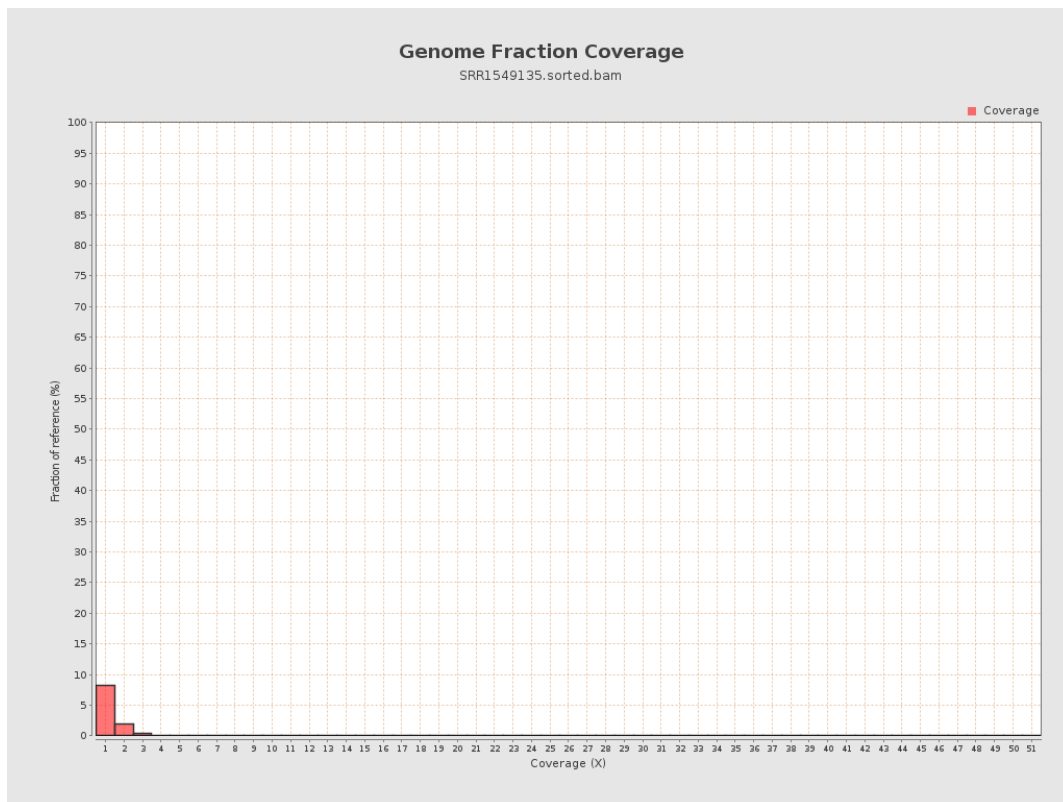


## 5. Results : Coverage Histogram (0-50X)

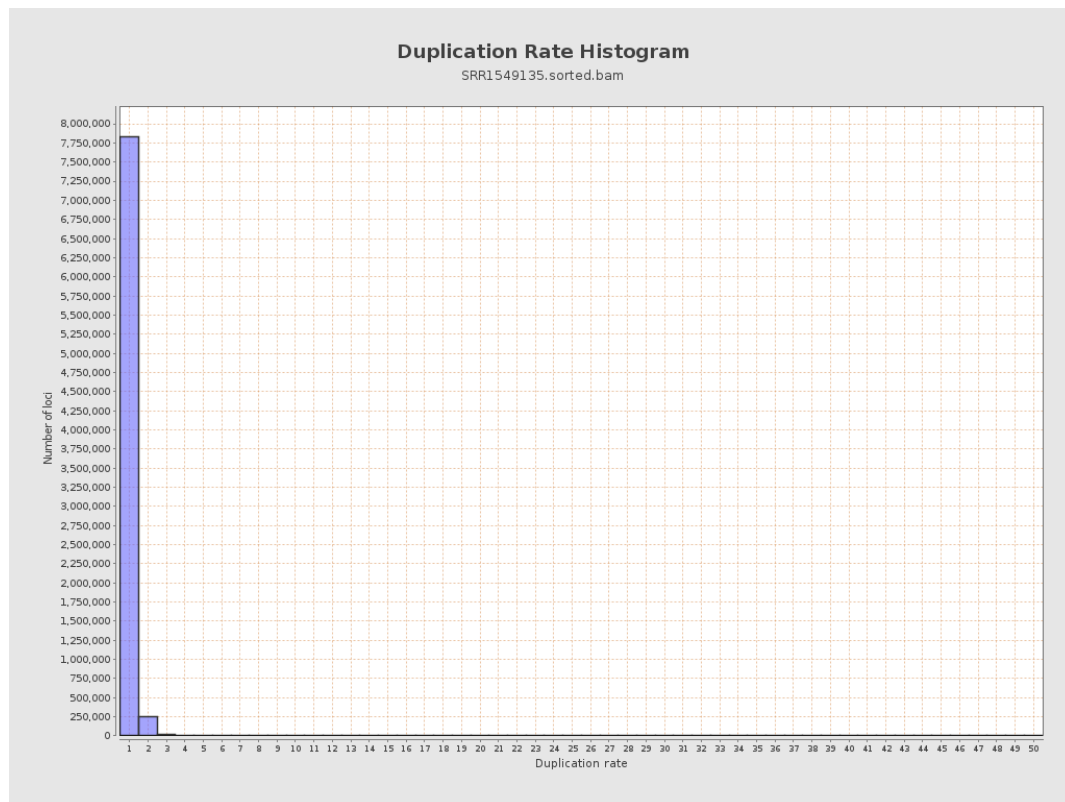




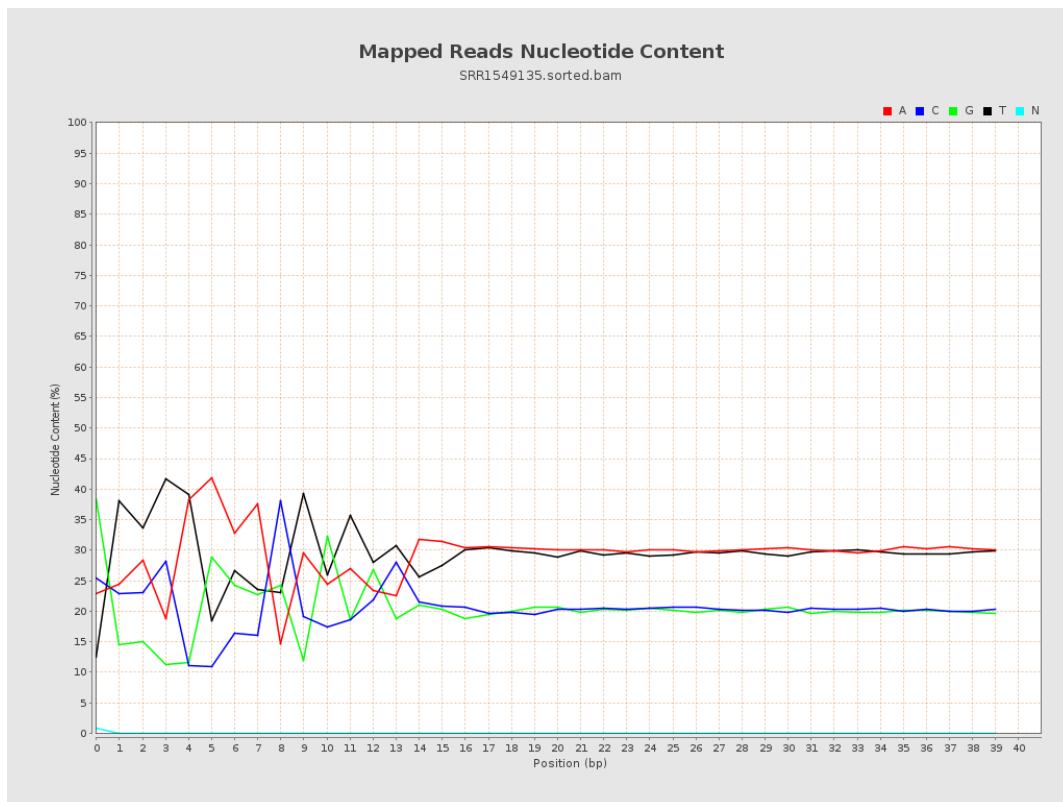
## 6. Results : Genome Fraction Coverage



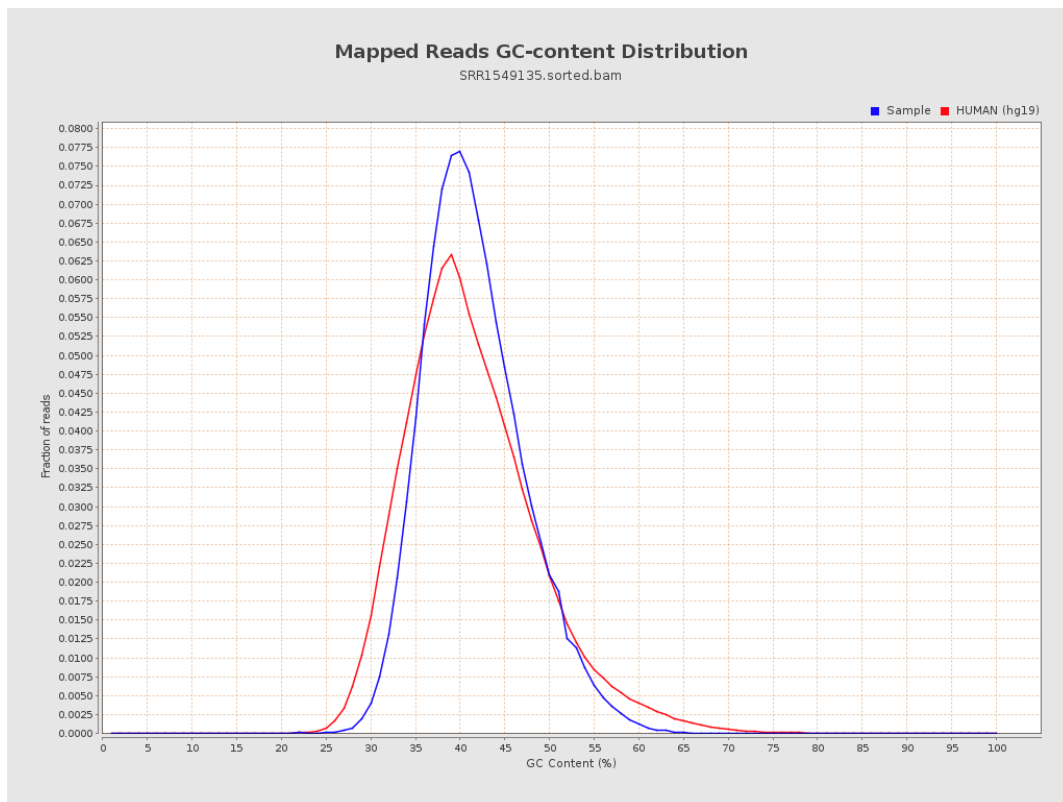
## 7. Results : Duplication Rate Histogram



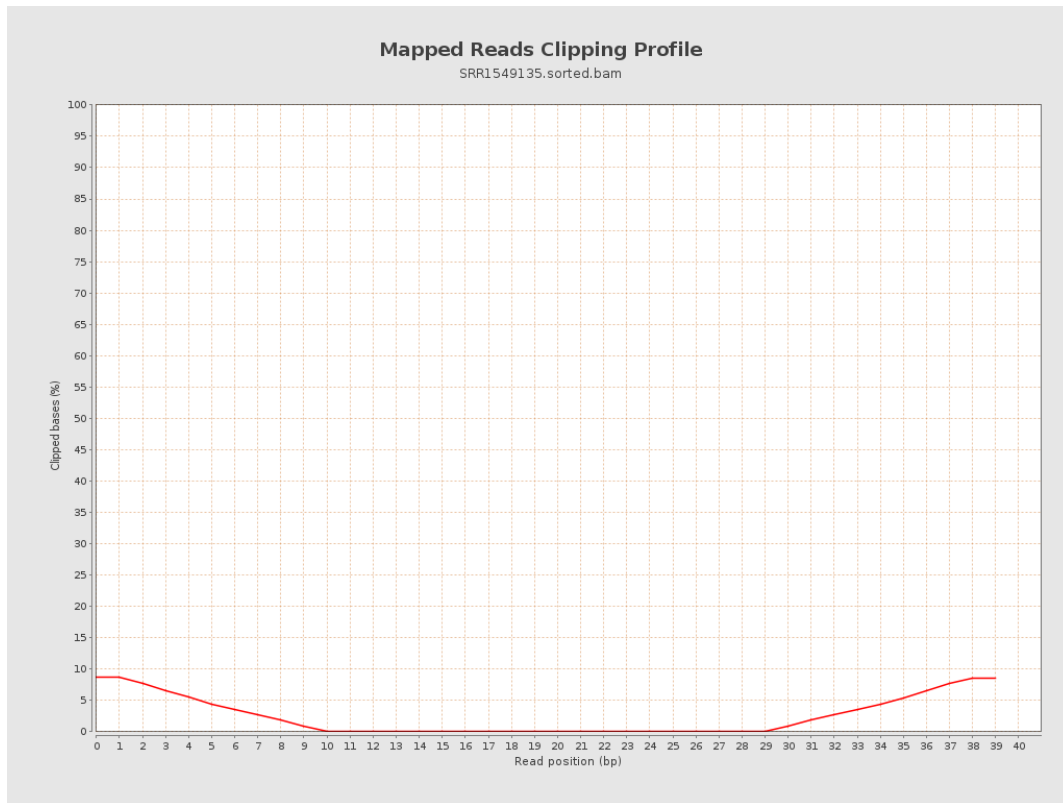
## 8. Results : Mapped Reads Nucleotide Content



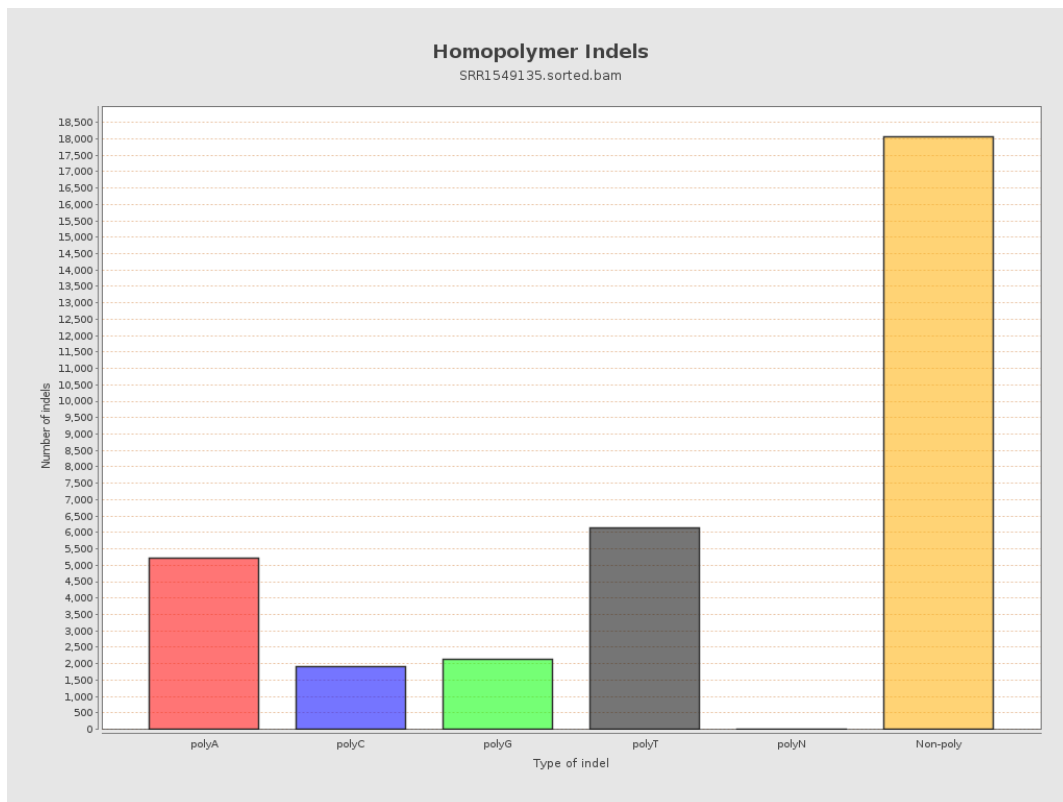
## 9. Results : Mapped Reads GC-content Distribution



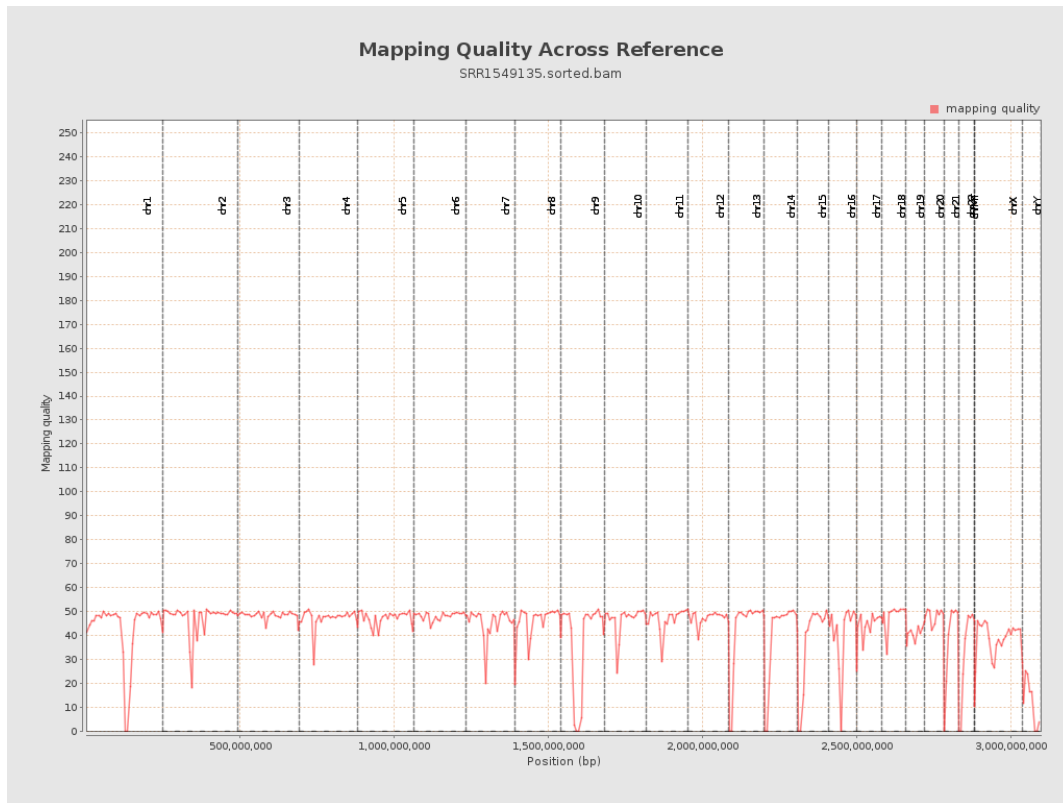
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

