

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 09:37:37*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549011.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_SRR1549011 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549011.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Fri Aug 23 09:37:36 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR1549011.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 11,426,869         |
| Mapped reads                 | 9,716,178 / 85.03% |
| Unmapped reads               | 1,710,691 / 14.97% |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Read min/max/mean length     | 40 / 40 / 40       |
| Duplicated reads (estimated) | 1,010,648 / 8.84%  |
| Duplication rate             | 8.71%              |
| Clipped reads                | 732,016 / 6.41%    |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 114,246,347 / 29.71% |
| Number/percentage of C's | 77,819,981 / 20.24%  |
| Number/percentage of T's | 114,864,475 / 29.87% |
| Number/percentage of G's | 77,553,872 / 20.17%  |
| Number/percentage of N's | 14,687 / 0%          |
| GC Percentage            | 40.41%               |

### 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.1242 |
| Standard Deviation | 2.7162 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 44.04 |
|----------------------|-------|

## 2.5. Mismatches and indels

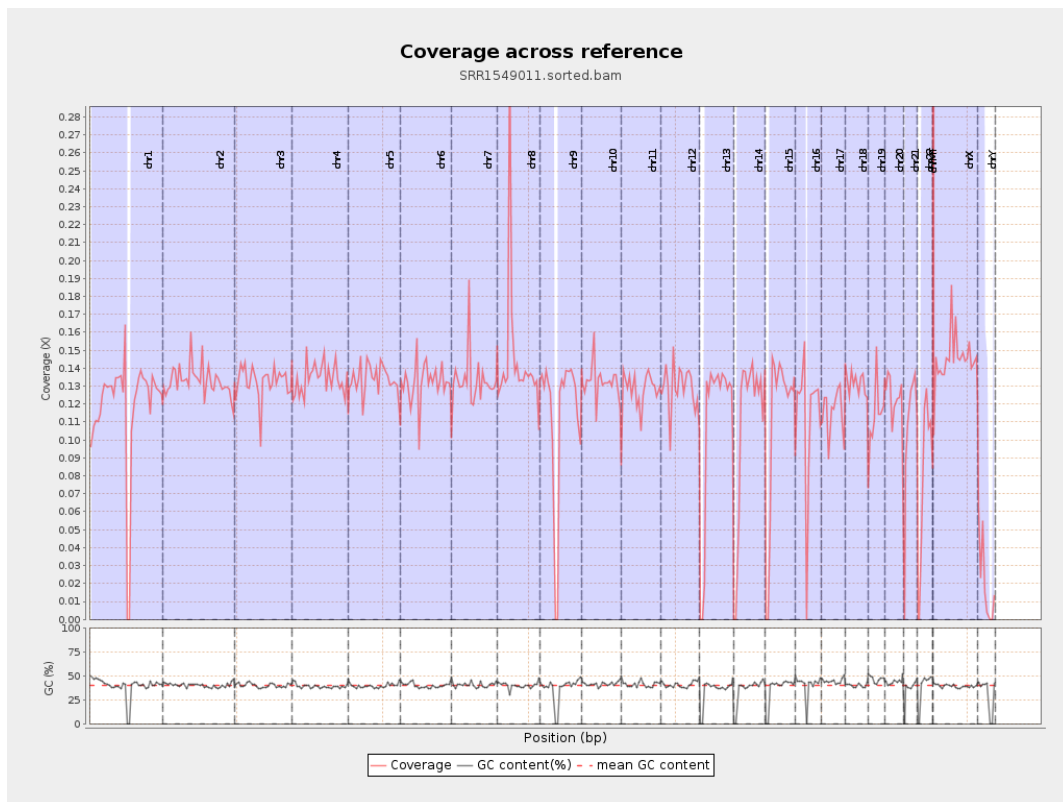
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 0.24%   |
| Mismatches                               | 925,294 |
| Insertions                               | 12,543  |
| Mapped reads with at least one insertion | 0.13%   |
| Deletions                                | 29,559  |
| Mapped reads with at least one deletion  | 0.3%    |
| Homopolymer indels                       | 41.98%  |

## 2.6. Chromosome stats

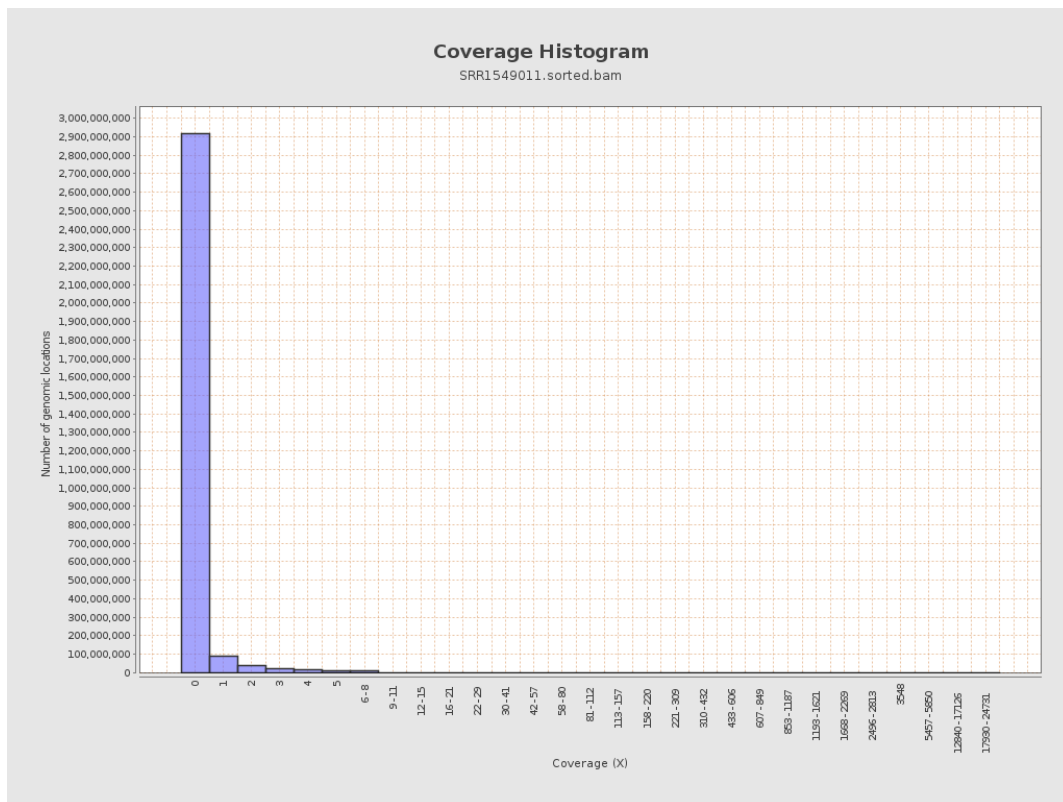
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 29572283     | 0.1186        | 1.3617             |
| chr2 | 243199373 | 32357345     | 0.133         | 0.8065             |
| chr3 | 198022430 | 26262618     | 0.1326        | 0.6661             |
| chr4 | 191154276 | 25699261     | 0.1344        | 0.6875             |
| chr5 | 180915260 | 24098668     | 0.1332        | 0.6675             |
| chr6 | 171115067 | 22632135     | 0.1323        | 0.6956             |
| chr7 | 159138663 | 21161994     | 0.133         | 1.0157             |
| chr8 | 146364022 | 21146914     | 0.1445        | 11.9338            |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr9  | 141213431 | 16094432 | 0.114  | 0.7421 |
| chr10 | 135534747 | 17918843 | 0.1322 | 0.7865 |
| chr11 | 135006516 | 17318182 | 0.1283 | 0.8618 |
| chr12 | 133851895 | 17287635 | 0.1292 | 0.6638 |
| chr13 | 115169878 | 12633994 | 0.1097 | 0.6022 |
| chr14 | 107349540 | 11742781 | 0.1094 | 0.6674 |
| chr15 | 102531392 | 11230512 | 0.1095 | 0.5894 |
| chr16 | 90354753  | 10056441 | 0.1113 | 0.6231 |
| chr17 | 81195210  | 9461046  | 0.1165 | 0.6407 |
| chr18 | 78077248  | 10296046 | 0.1319 | 1.1944 |
| chr19 | 59128983  | 6822442  | 0.1154 | 1.1464 |
| chr20 | 63025520  | 7770101  | 0.1233 | 0.6496 |
| chr21 | 48129895  | 5138881  | 0.1068 | 0.6321 |
| chr22 | 51304566  | 4087745  | 0.0797 | 0.5696 |
| chrMT | 16571     | 62969    | 3.8    | 5.3247 |
| chrX  | 155270560 | 22509674 | 0.145  | 0.7809 |
| chrY  | 59373566  | 1175037  | 0.0198 | 0.3203 |

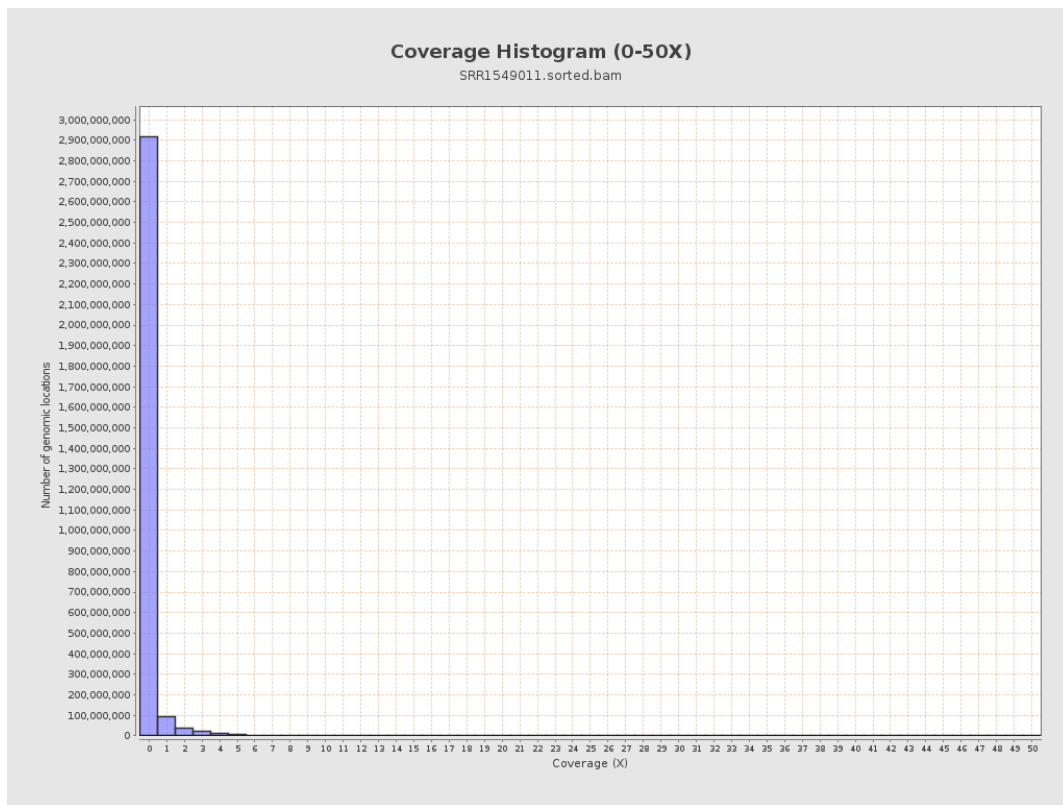
### 3. Results : Coverage across reference



## 4. Results : Coverage Histogram

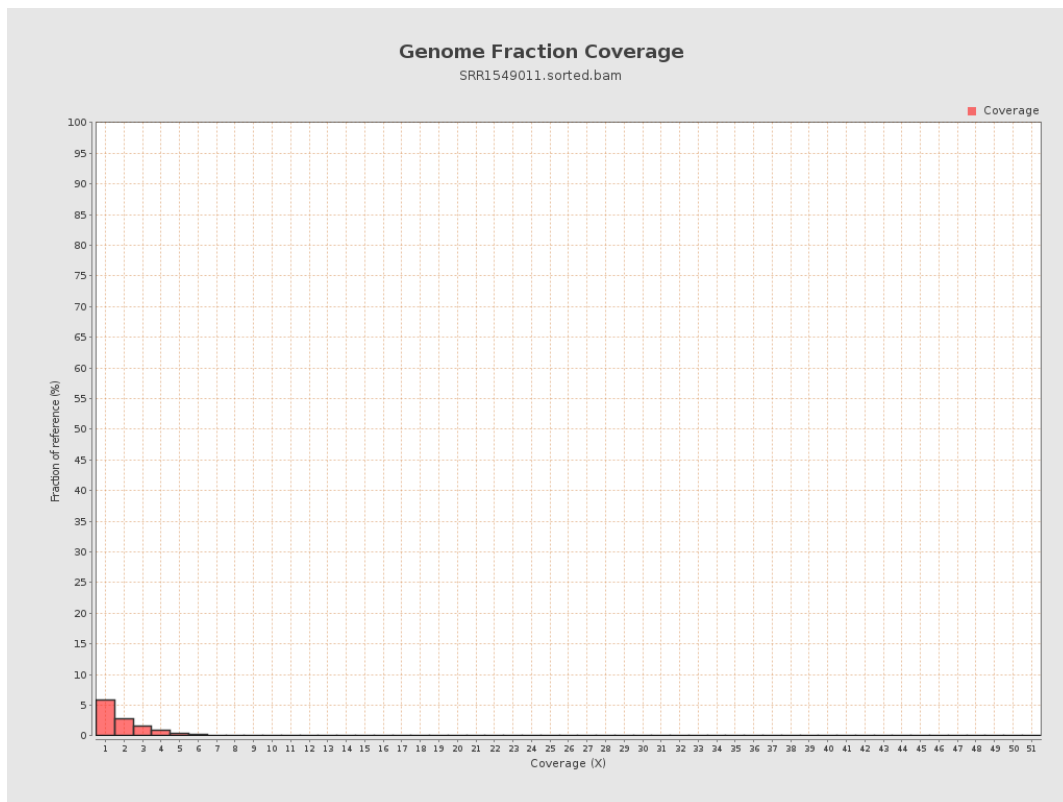


## 5. Results : Coverage Histogram (0-50X)

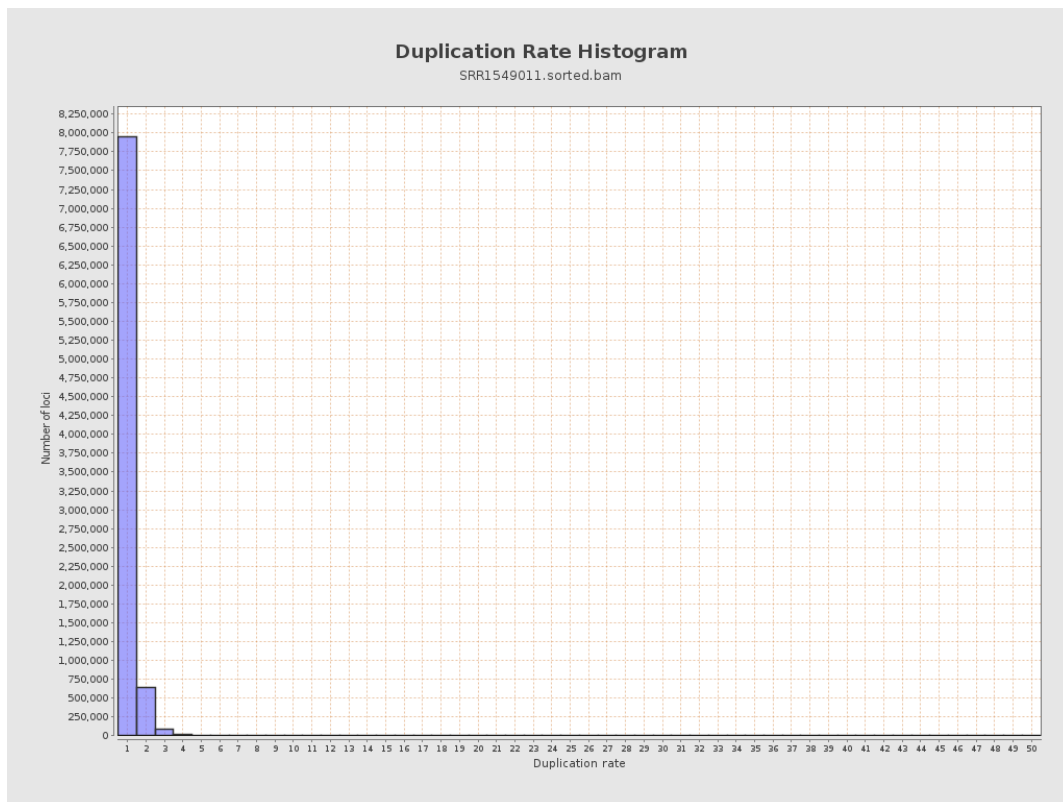




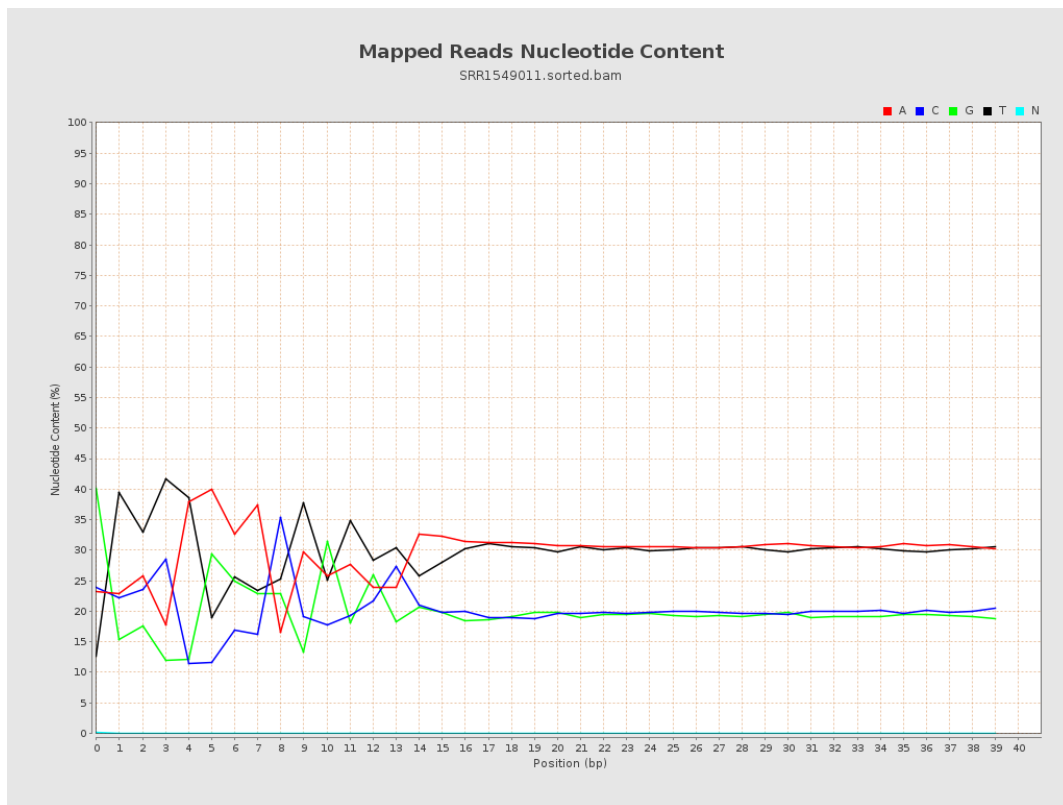
## 6. Results : Genome Fraction Coverage



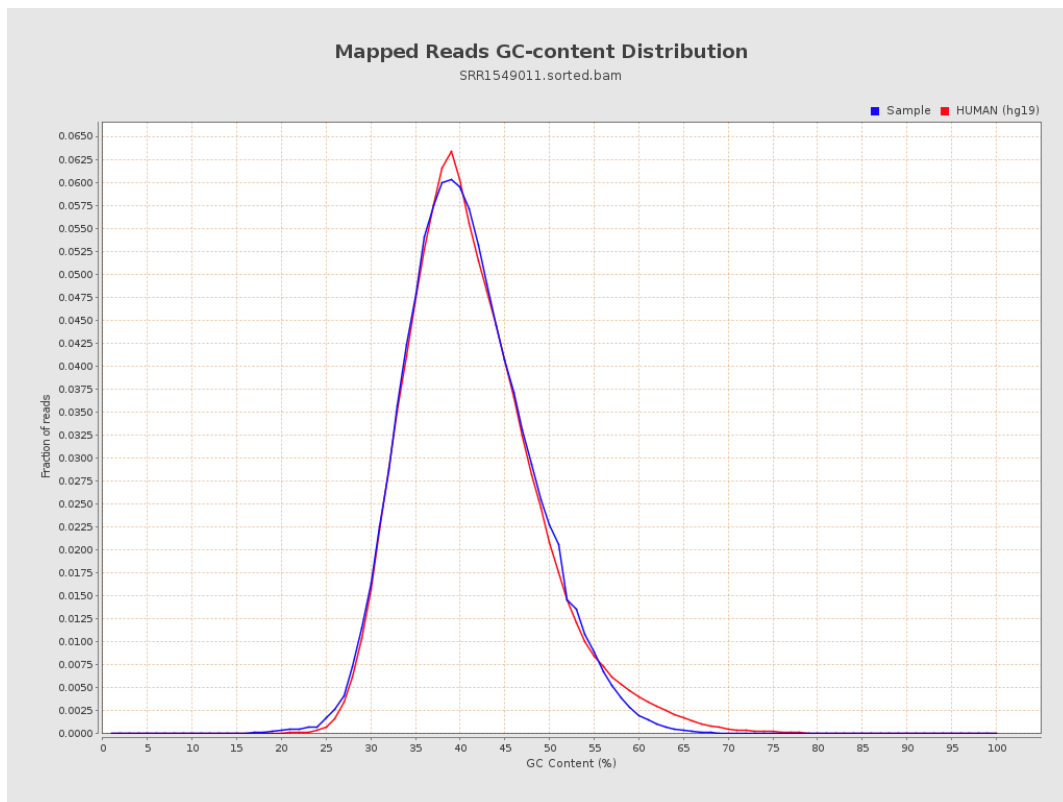
## 7. Results : Duplication Rate Histogram



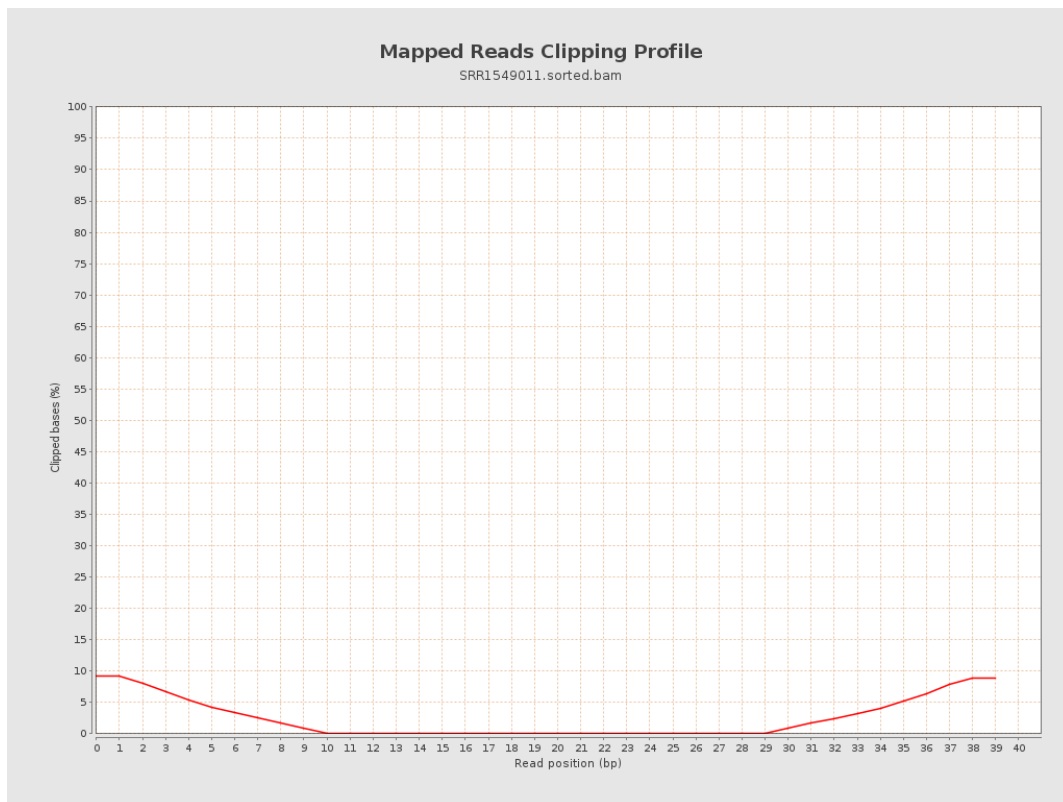
## 8. Results : Mapped Reads Nucleotide Content



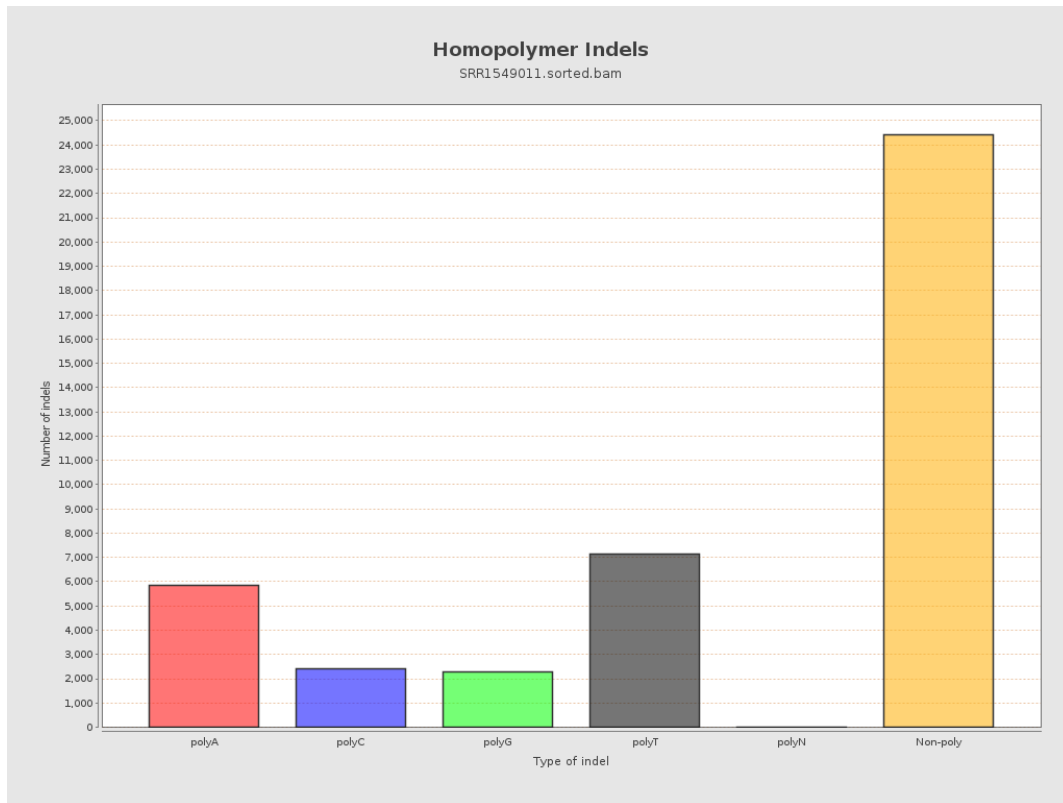
## 9. Results : Mapped Reads GC-content Distribution



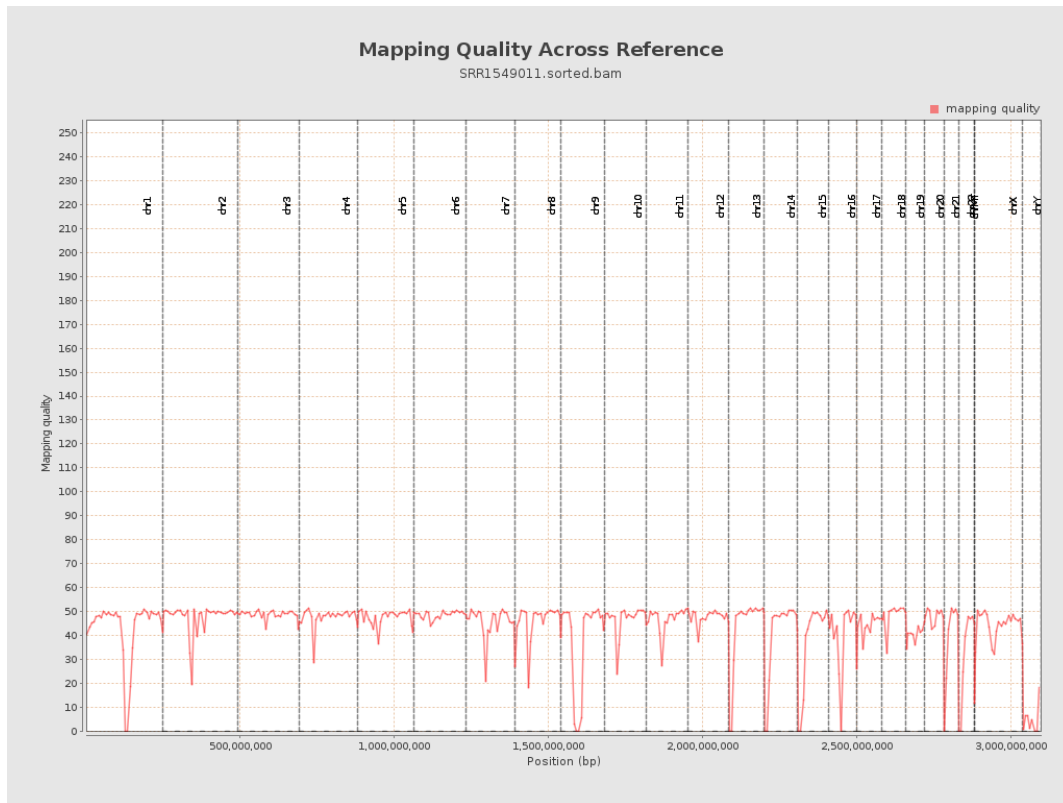
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

