

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 02:29:51*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549107.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_SRR1549107 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549107.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Sat Aug 24 02:29:50 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR1549107.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 10,598,511         |
| Mapped reads                 | 9,088,473 / 85.75% |
| Unmapped reads               | 1,510,038 / 14.25% |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Read min/max/mean length     | 40 / 40 / 40       |
| Duplicated reads (estimated) | 512,763 / 4.84%    |
| Duplication rate             | 4.32%              |
| Clipped reads                | 430,841 / 4.07%    |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 106,027,096 / 29.38% |
| Number/percentage of C's | 74,433,934 / 20.63%  |
| Number/percentage of T's | 106,664,677 / 29.56% |
| Number/percentage of G's | 73,748,625 / 20.44%  |
| Number/percentage of N's | 1,474 / 0%           |
| GC Percentage            | 41.06%               |

### 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.1166 |
| Standard Deviation | 0.8434 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 44.12 |
|----------------------|-------|

## 2.5. Mismatches and indels

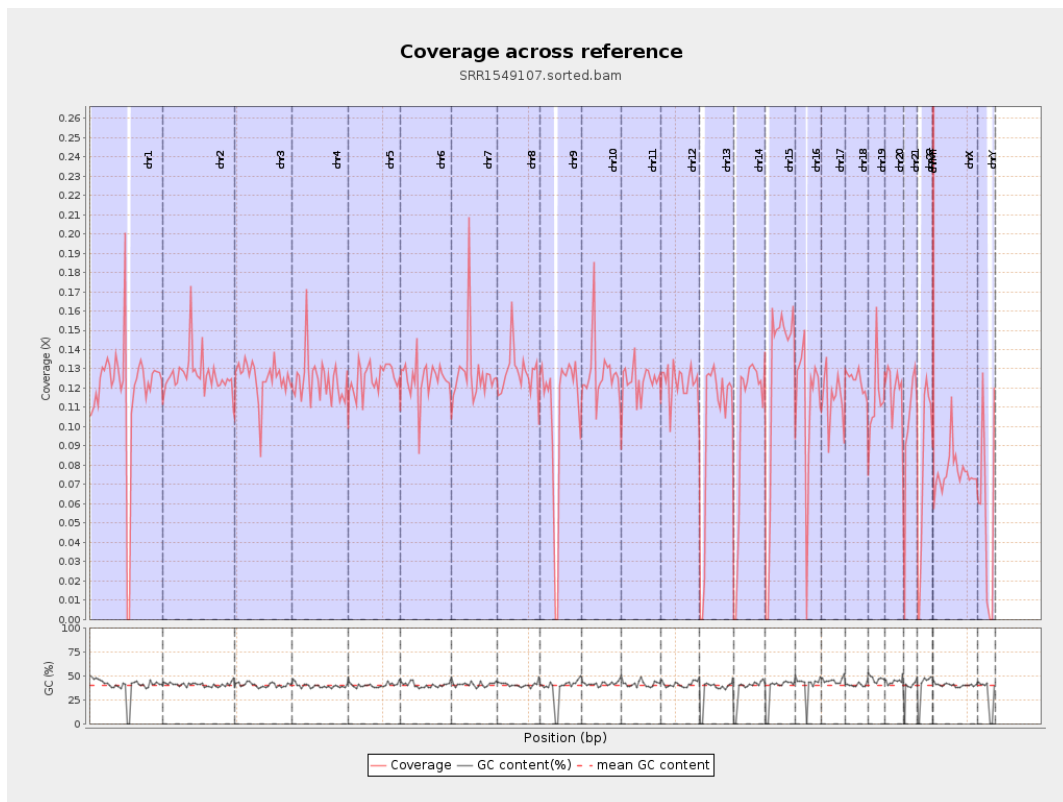
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.31%     |
| Mismatches                               | 1,106,826 |
| Insertions                               | 8,758     |
| Mapped reads with at least one insertion | 0.1%      |
| Deletions                                | 29,054    |
| Mapped reads with at least one deletion  | 0.32%     |
| Homopolymer indels                       | 45.35%    |

## 2.6. Chromosome stats

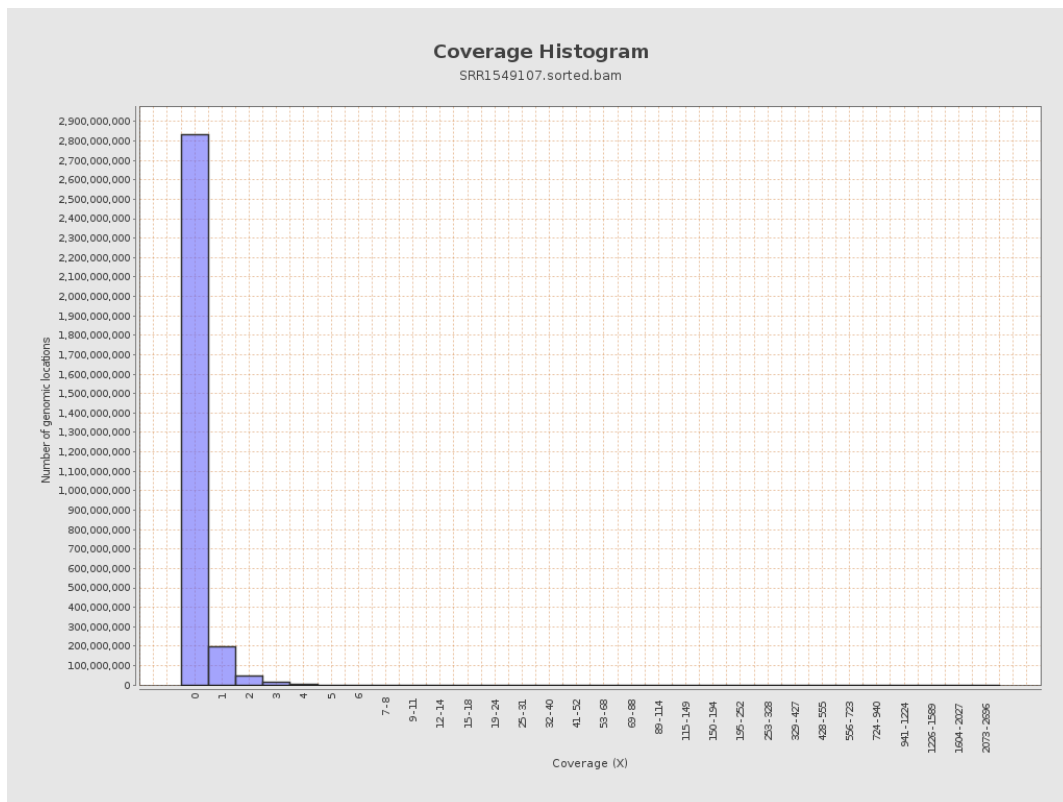
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 29561968     | 0.1186        | 1.8306             |
| chr2 | 243199373 | 30920560     | 0.1271        | 0.7084             |
| chr3 | 198022430 | 24713215     | 0.1248        | 0.4592             |
| chr4 | 191154276 | 23754666     | 0.1243        | 0.5337             |
| chr5 | 180915260 | 22627342     | 0.1251        | 0.4735             |
| chr6 | 171115067 | 21339350     | 0.1247        | 0.5048             |
| chr7 | 159138663 | 20316404     | 0.1277        | 1.1754             |
| chr8 | 146364022 | 18666889     | 0.1275        | 0.9937             |
|      |           |              |               |                    |

|       |           |          |        |         |
|-------|-----------|----------|--------|---------|
| chr9  | 141213431 | 15299285 | 0.1083 | 0.6596  |
| chr10 | 135534747 | 17256099 | 0.1273 | 0.7872  |
| chr11 | 135006516 | 16684769 | 0.1236 | 0.6542  |
| chr12 | 133851895 | 16518963 | 0.1234 | 0.4861  |
| chr13 | 115169878 | 11599599 | 0.1007 | 0.4056  |
| chr14 | 107349540 | 11142011 | 0.1038 | 0.5415  |
| chr15 | 102531392 | 12655478 | 0.1234 | 0.4497  |
| chr16 | 90354753  | 10129410 | 0.1121 | 0.4991  |
| chr17 | 81195210  | 9368416  | 0.1154 | 0.4896  |
| chr18 | 78077248  | 9671889  | 0.1239 | 1.3634  |
| chr19 | 59128983  | 6802574  | 0.115  | 1.3351  |
| chr20 | 63025520  | 7546339  | 0.1197 | 0.5046  |
| chr21 | 48129895  | 4875945  | 0.1013 | 0.5255  |
| chr22 | 51304566  | 4106846  | 0.08   | 0.3847  |
| chrMT | 16571     | 124311   | 7.5017 | 10.2571 |
| chrX  | 155270560 | 11856736 | 0.0764 | 0.4848  |
| chrY  | 59373566  | 3373632  | 0.0568 | 0.6439  |

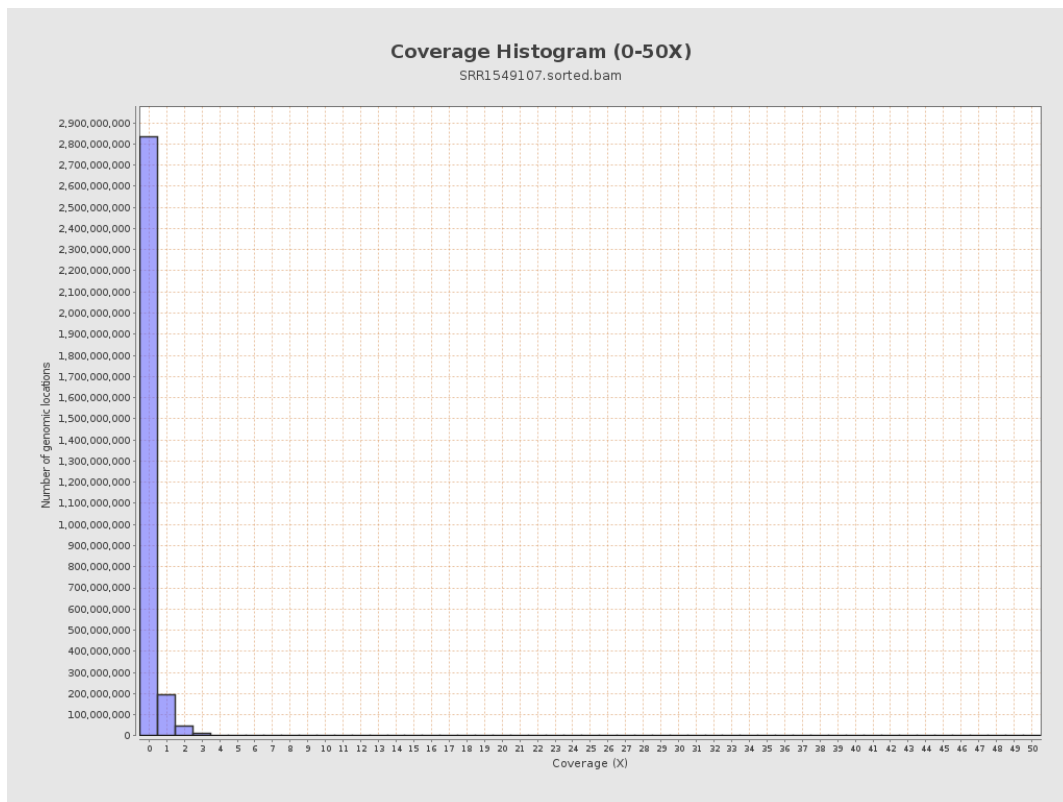
### 3. Results : Coverage across reference



## 4. Results : Coverage Histogram

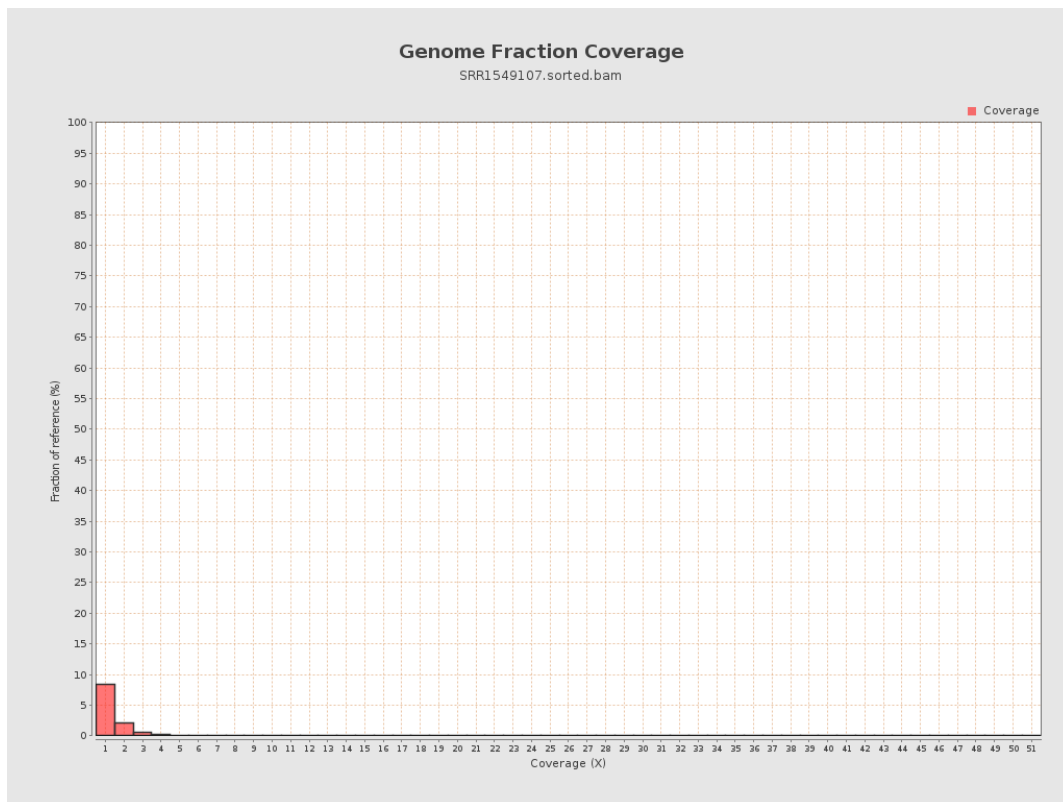


## 5. Results : Coverage Histogram (0-50X)

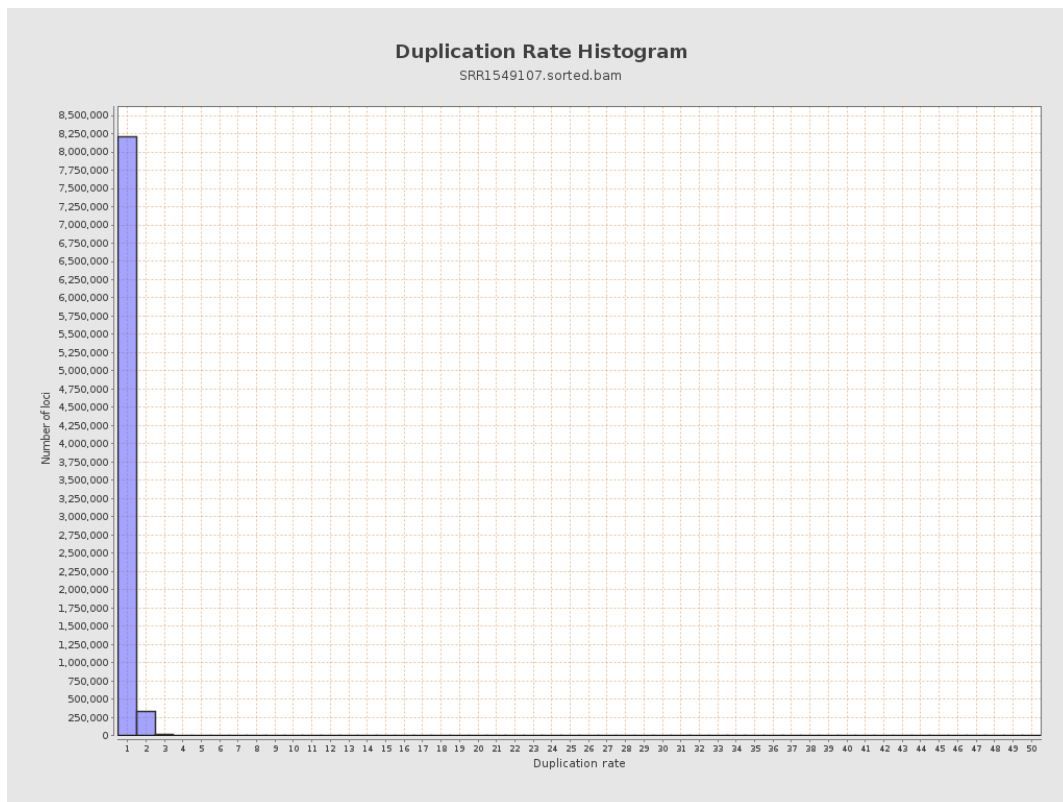




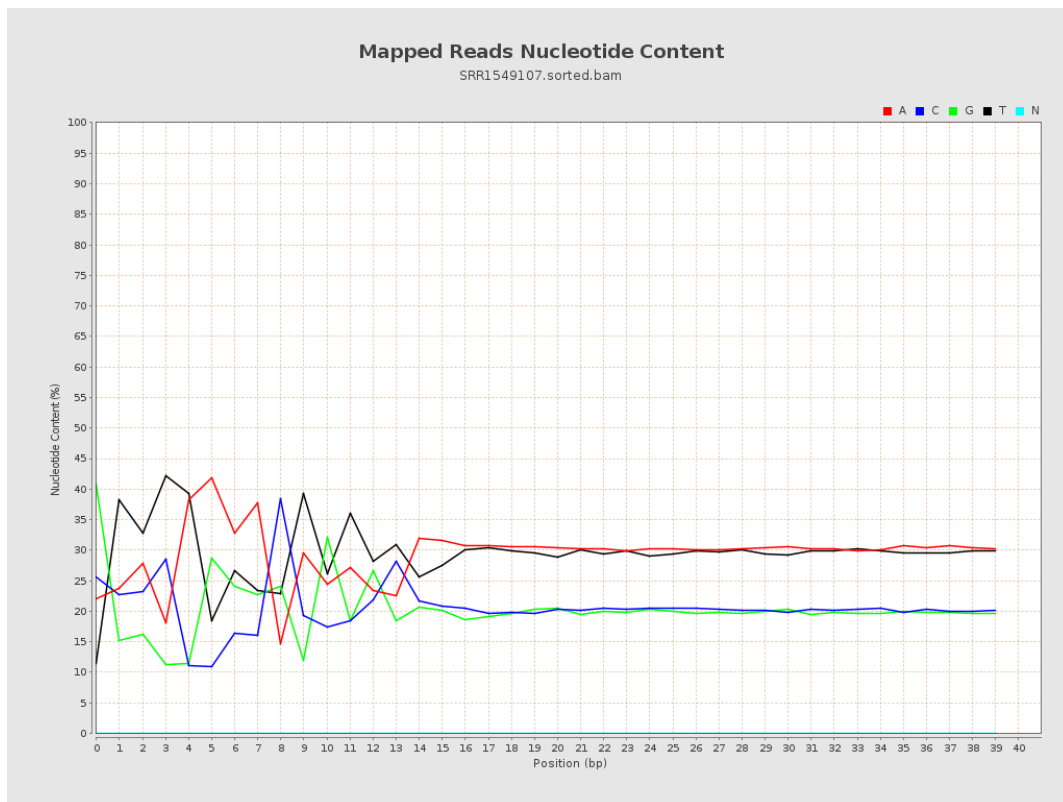
## 6. Results : Genome Fraction Coverage



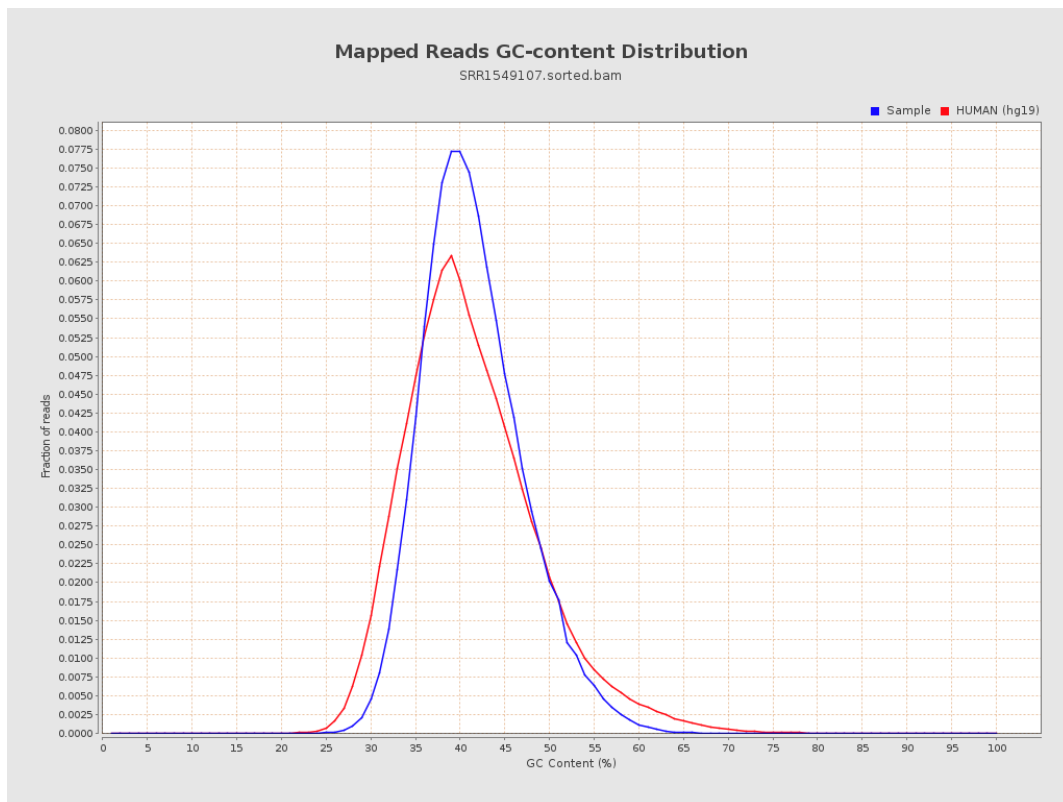
## 7. Results : Duplication Rate Histogram



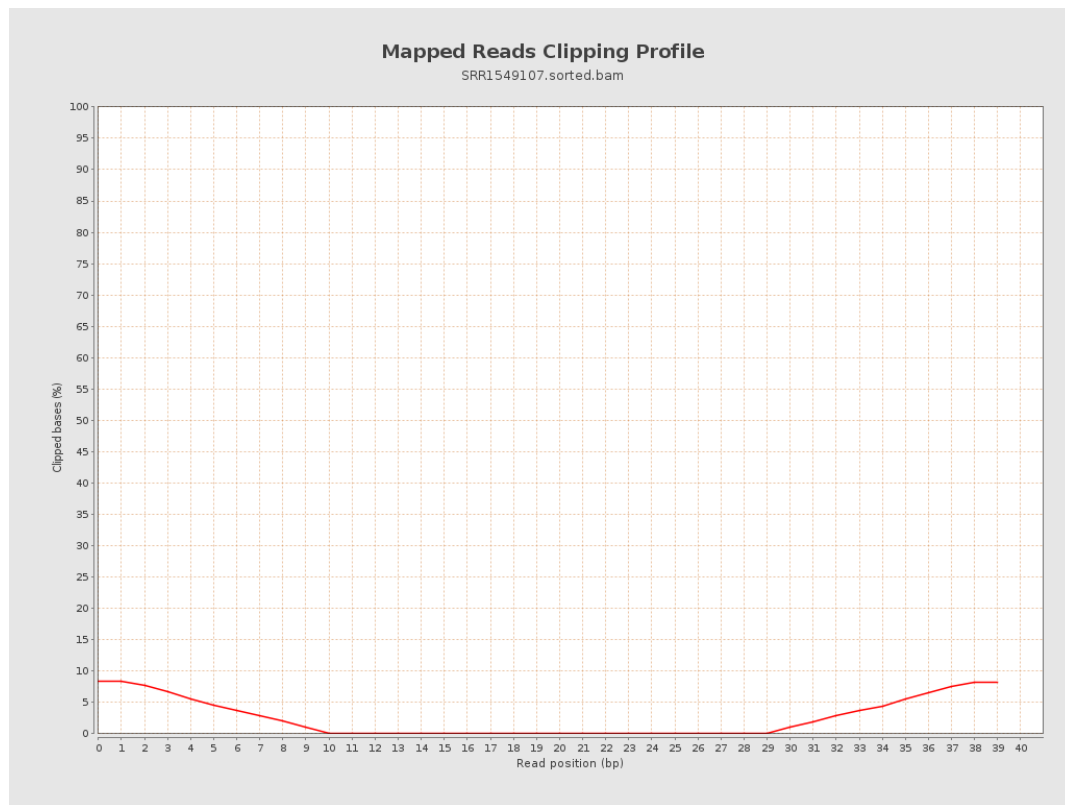
## 8. Results : Mapped Reads Nucleotide Content



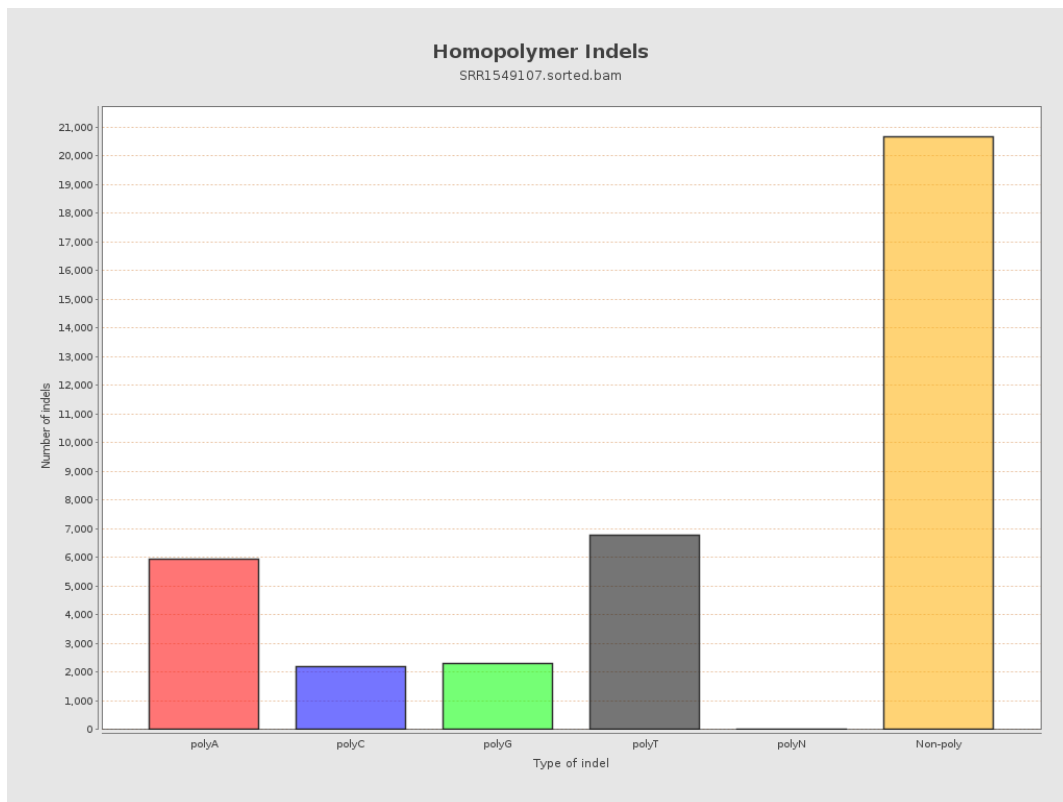
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

