

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/14 22:30:48*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013344.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_SRR6013344 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013344.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Sat Sep 14 22:30:47 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6013344.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 2,331,140          |
| Mapped reads                 | 2,138,341 / 91.73% |
| Unmapped reads               | 192,799 / 8.27%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 21,453 / 0.92%     |
| Read min/max/mean length     | 30 / 76 / 76.32    |
| Duplicated reads (estimated) | 48,155 / 2.07%     |
| Duplication rate             | 1.51%              |
| Clipped reads                | 981,093 / 42.09%   |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 39,320,541 / 27.77% |
| Number/percentage of C's | 27,725,429 / 19.58% |
| Number/percentage of T's | 42,201,462 / 29.8%  |
| Number/percentage of G's | 32,328,688 / 22.83% |
| Number/percentage of N's | 35,767 / 0.03%      |
| GC Percentage            | 42.41%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0458 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.3578 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 43.21 |
|----------------------|-------|

## 2.5. Mismatches and indels

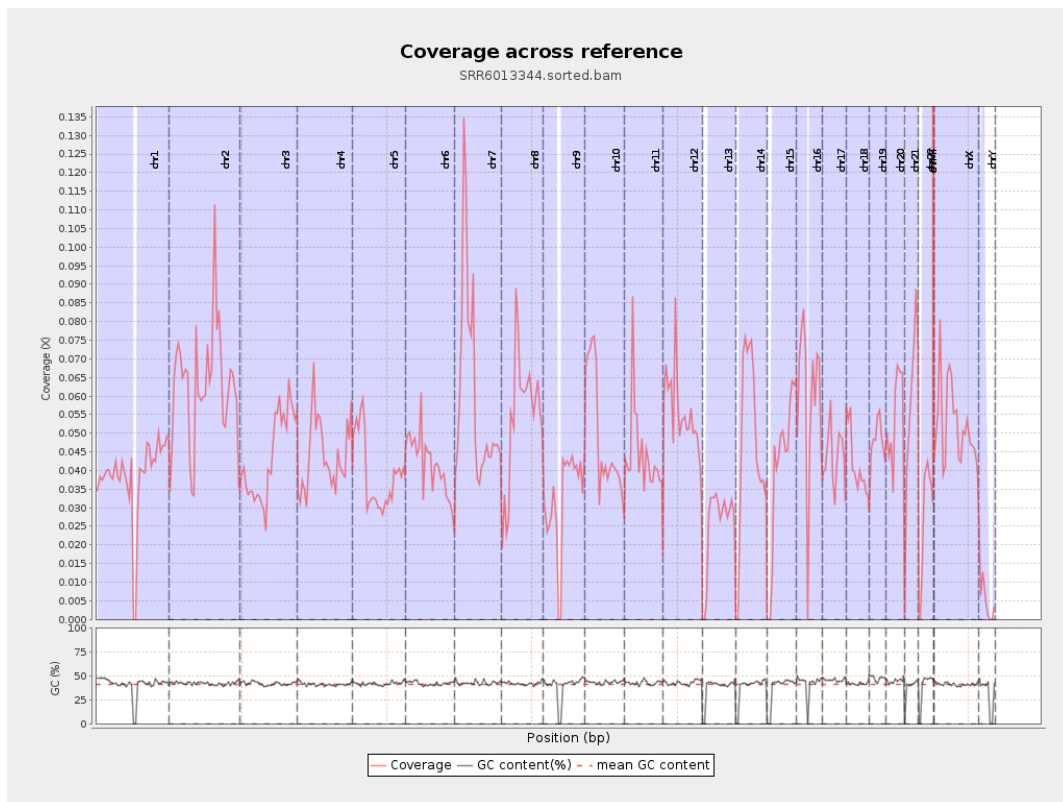
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.76%     |
| Mismatches                               | 1,051,472 |
| Insertions                               | 10,276    |
| Mapped reads with at least one insertion | 0.48%     |
| Deletions                                | 29,343    |
| Mapped reads with at least one deletion  | 1.36%     |
| Homopolymer indels                       | 44.95%    |

## 2.6. Chromosome stats

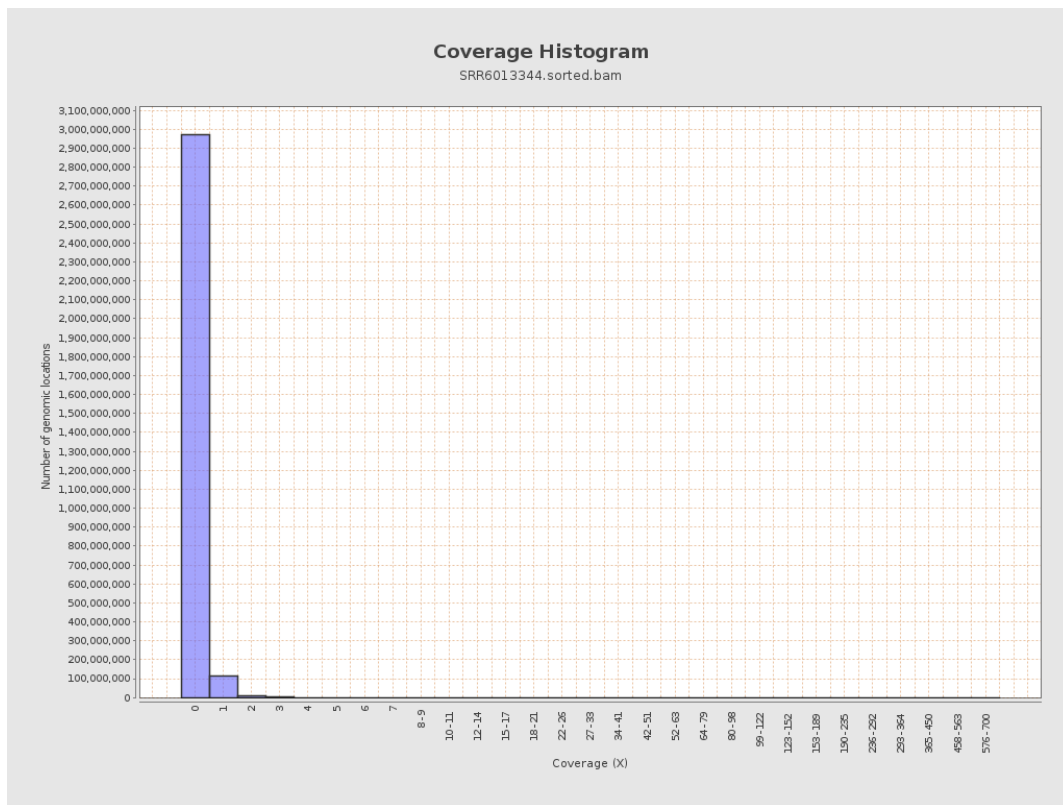
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 9574733      | 0.0384        | 0.4263             |
| chr2 | 243199373 | 15257058     | 0.0627        | 0.451              |
| chr3 | 198022430 | 8629637      | 0.0436        | 0.2242             |
| chr4 | 191154276 | 8388306      | 0.0439        | 0.2346             |
| chr5 | 180915260 | 7055006      | 0.039         | 0.2151             |
| chr6 | 171115067 | 7094228      | 0.0415        | 0.2763             |
| chr7 | 159138663 | 9562681      | 0.0601        | 0.7929             |
|      |           |              |               |                    |

|       |           |         |         |         |
|-------|-----------|---------|---------|---------|
| chr8  | 146364022 | 7987530 | 0.0546  | 0.3229  |
| chr9  | 141213431 | 4533165 | 0.0321  | 0.3075  |
| chr10 | 135534747 | 6737851 | 0.0497  | 0.371   |
| chr11 | 135006516 | 5982249 | 0.0443  | 0.3105  |
| chr12 | 133851895 | 7452974 | 0.0557  | 0.2599  |
| chr13 | 115169878 | 2903264 | 0.0252  | 0.1706  |
| chr14 | 107349540 | 5085625 | 0.0474  | 0.2639  |
| chr15 | 102531392 | 4205076 | 0.041   | 0.2299  |
| chr16 | 90354753  | 5393595 | 0.0597  | 0.2845  |
| chr17 | 81195210  | 3534565 | 0.0435  | 0.2504  |
| chr18 | 78077248  | 3259532 | 0.0417  | 0.5678  |
| chr19 | 59128983  | 2852534 | 0.0482  | 0.3876  |
| chr20 | 63025520  | 3410532 | 0.0541  | 0.2599  |
| chr21 | 48129895  | 2771684 | 0.0576  | 0.282   |
| chr22 | 51304566  | 1378346 | 0.0269  | 0.1756  |
| chrMT | 16571     | 228370  | 13.7813 | 11.5129 |
| chrX  | 155270560 | 8069834 | 0.052   | 0.2729  |
| chrY  | 59373566  | 314340  | 0.0053  | 0.1     |

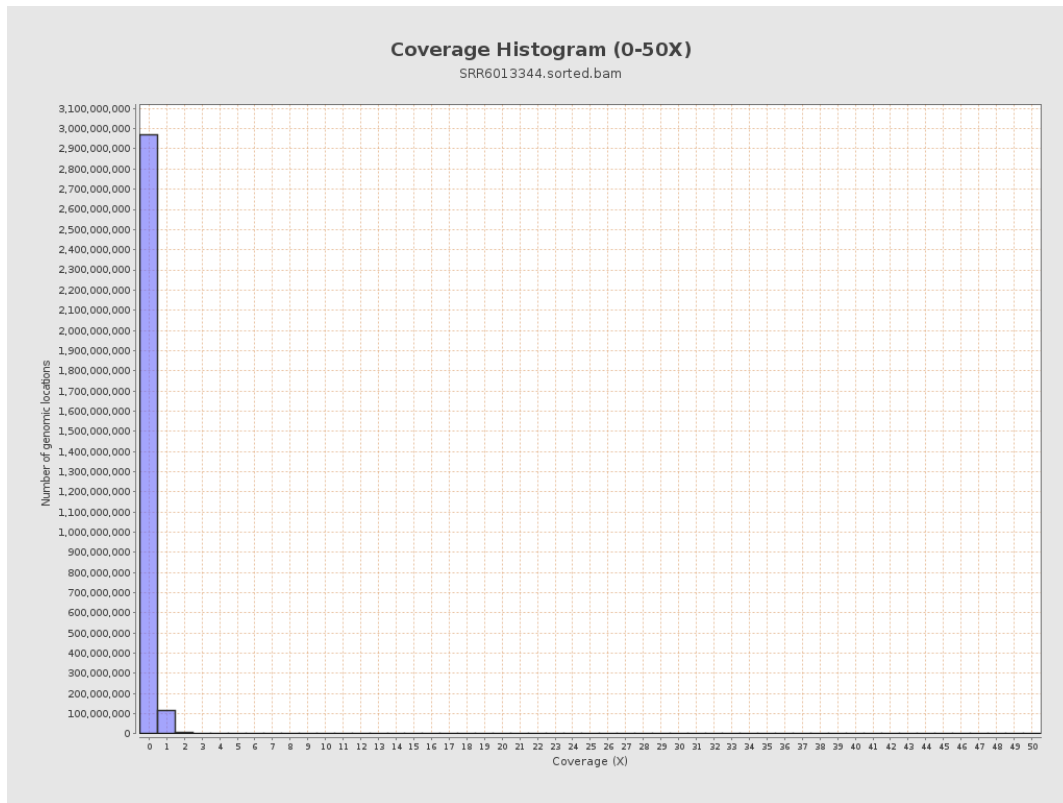
### 3. Results : Coverage across reference



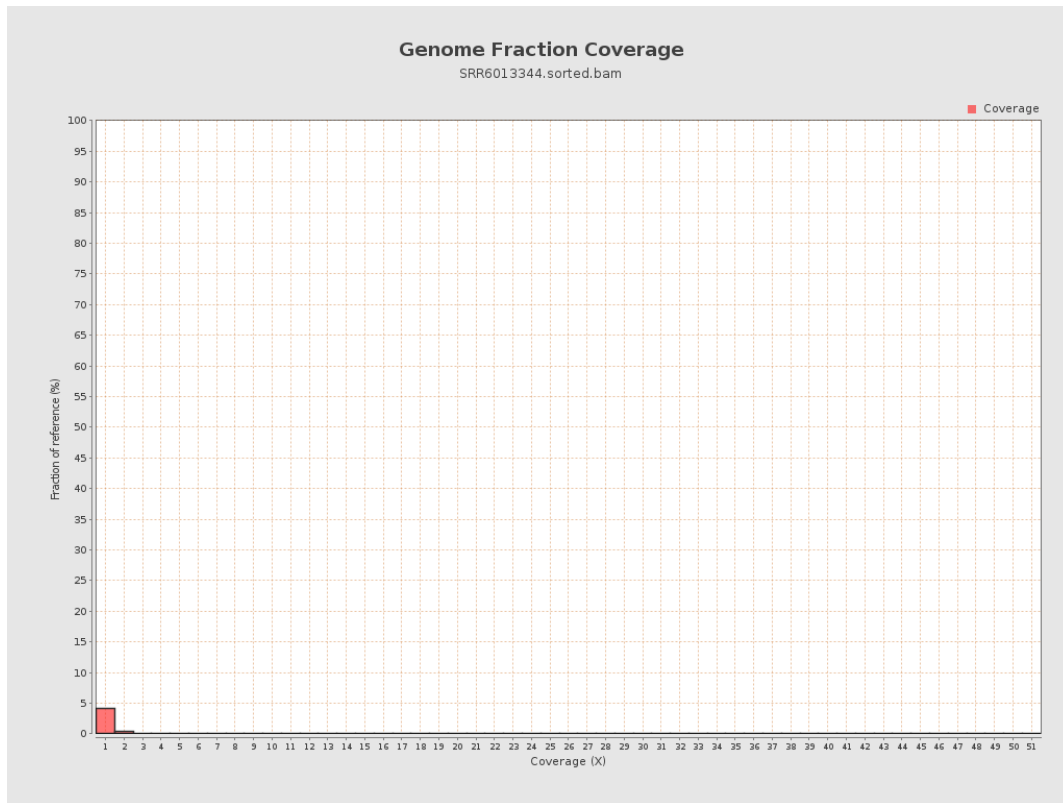
## 4. Results : Coverage Histogram



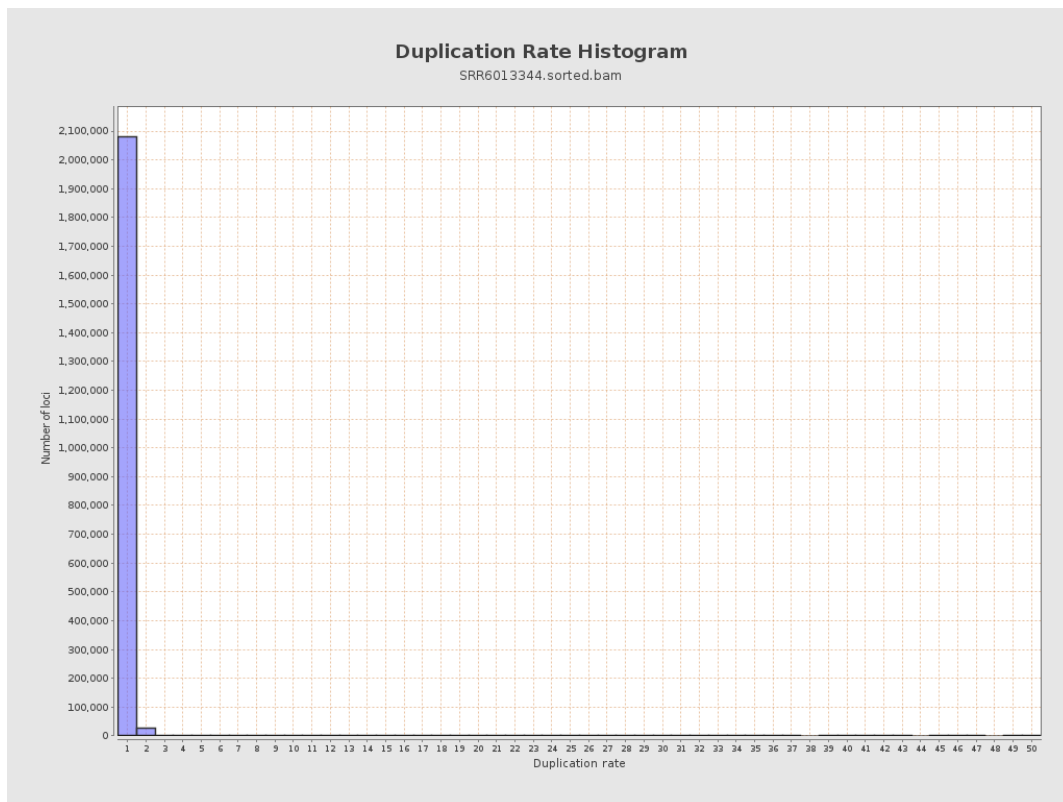
## 5. Results : Coverage Histogram (0-50X)



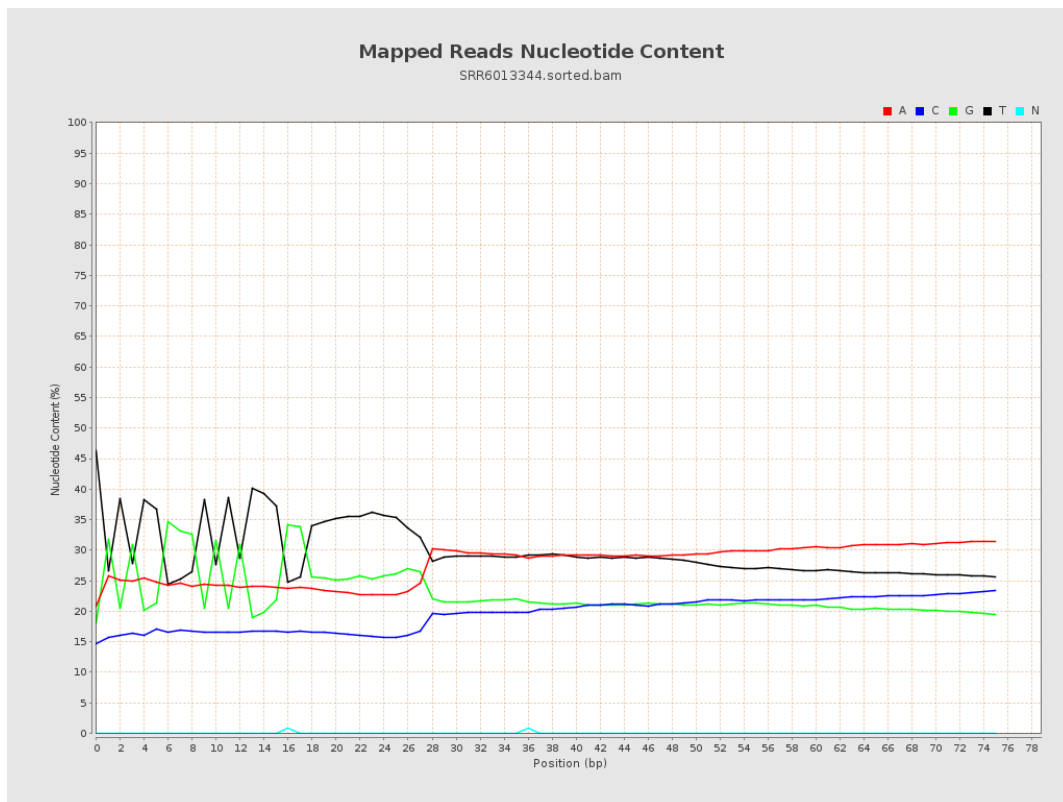
## 6. Results : Genome Fraction Coverage



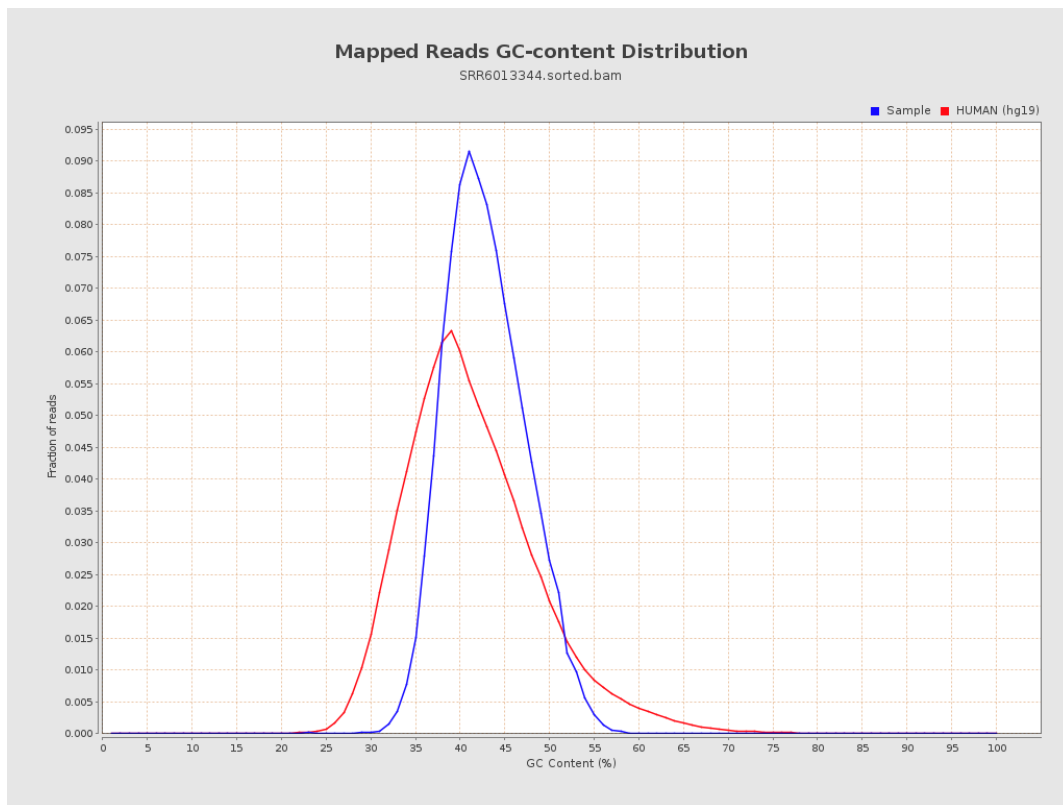
## 7. Results : Duplication Rate Histogram



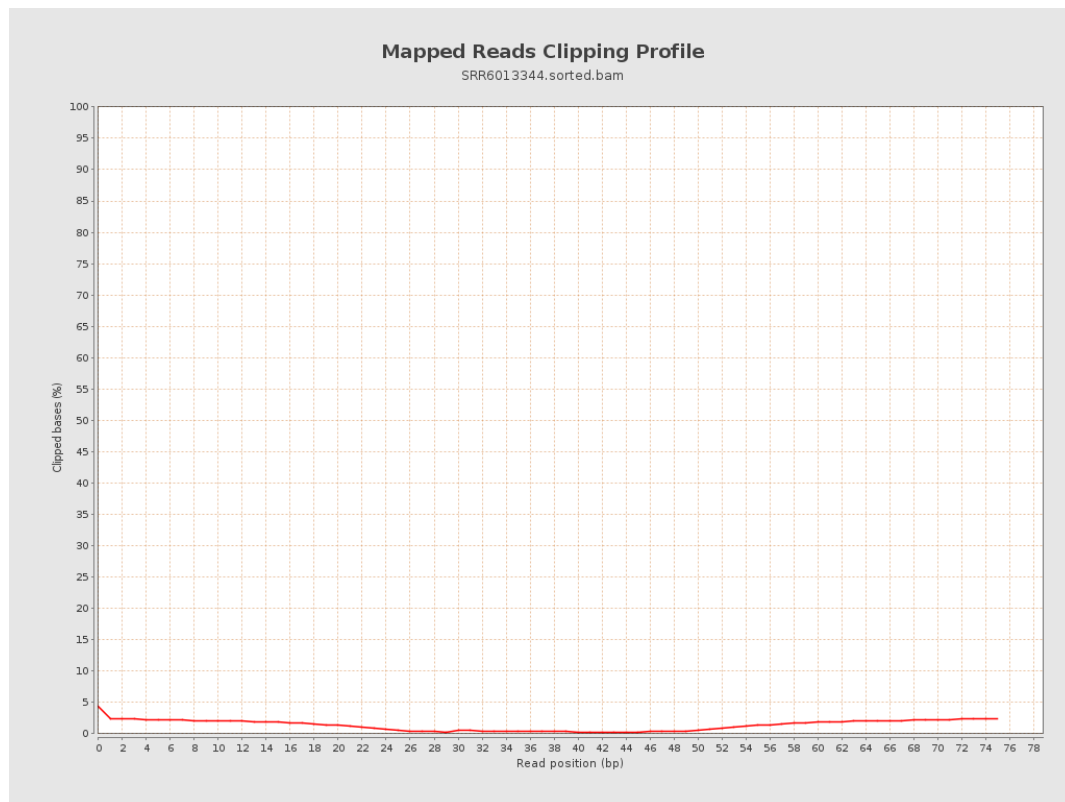
## 8. Results : Mapped Reads Nucleotide Content



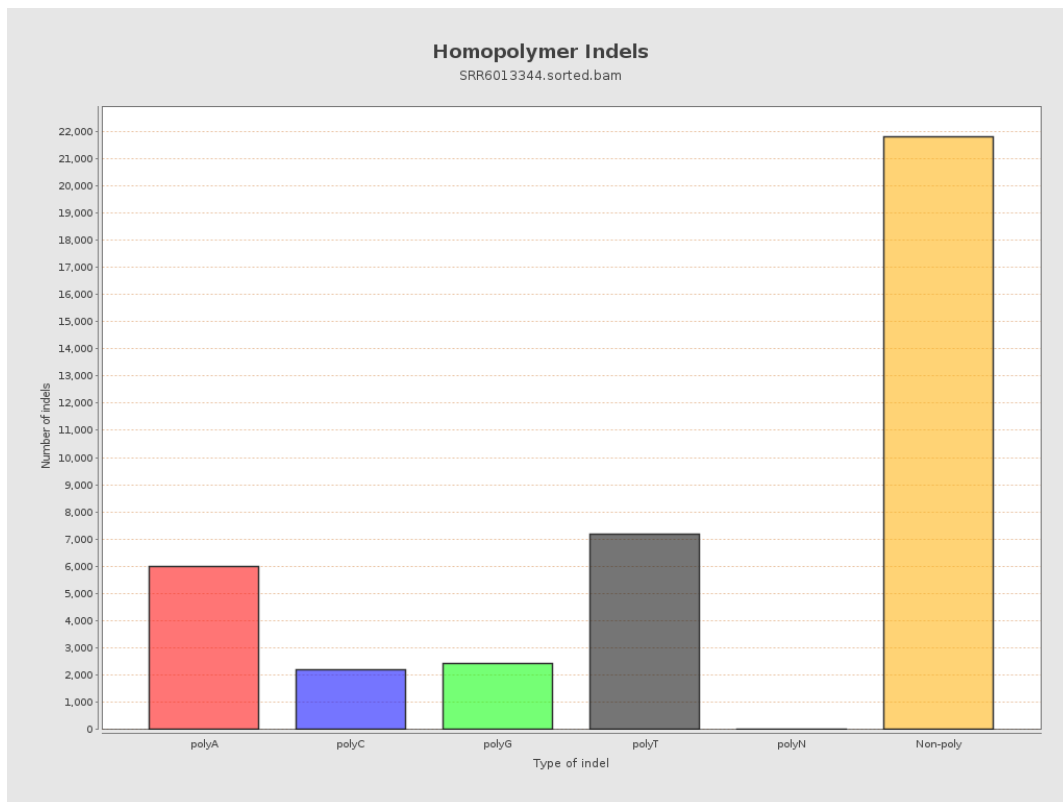
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

