

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/14 22:46:19*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013350.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_SRR6013350 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013350.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Sat Sep 14 22:46:18 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6013350.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 1,809,804          |
| Mapped reads                 | 1,537,667 / 84.96% |
| Unmapped reads               | 272,137 / 15.04%   |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 24,188 / 1.34%     |
| Read min/max/mean length     | 30 / 76 / 76.47    |
| Duplicated reads (estimated) | 310,453 / 17.15%   |
| Duplication rate             | 12.75%             |
| Clipped reads                | 730,109 / 40.34%   |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 28,756,695 / 28.2%  |
| Number/percentage of C's | 18,696,763 / 18.34% |
| Number/percentage of T's | 32,632,312 / 32%    |
| Number/percentage of G's | 21,863,550 / 21.44% |
| Number/percentage of N's | 12,243 / 0.01%      |
| GC Percentage            | 39.78%              |

### 2.3. Coverage

|      |       |
|------|-------|
| Mean | 0.033 |
|      |       |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.5672 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 44.23 |
|----------------------|-------|

## 2.5. Mismatches and indels

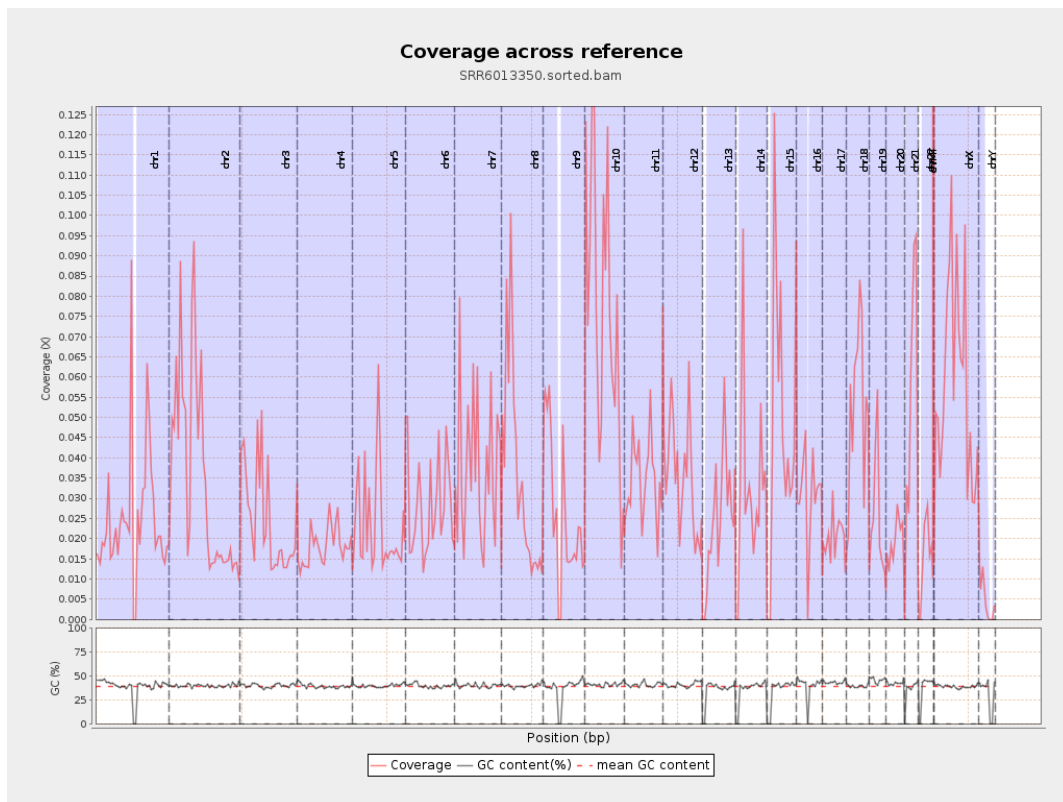
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 0.79%   |
| Mismatches                               | 788,282 |
| Insertions                               | 7,656   |
| Mapped reads with at least one insertion | 0.49%   |
| Deletions                                | 26,892  |
| Mapped reads with at least one deletion  | 1.73%   |
| Homopolymer indels                       | 46.57%  |

## 2.6. Chromosome stats

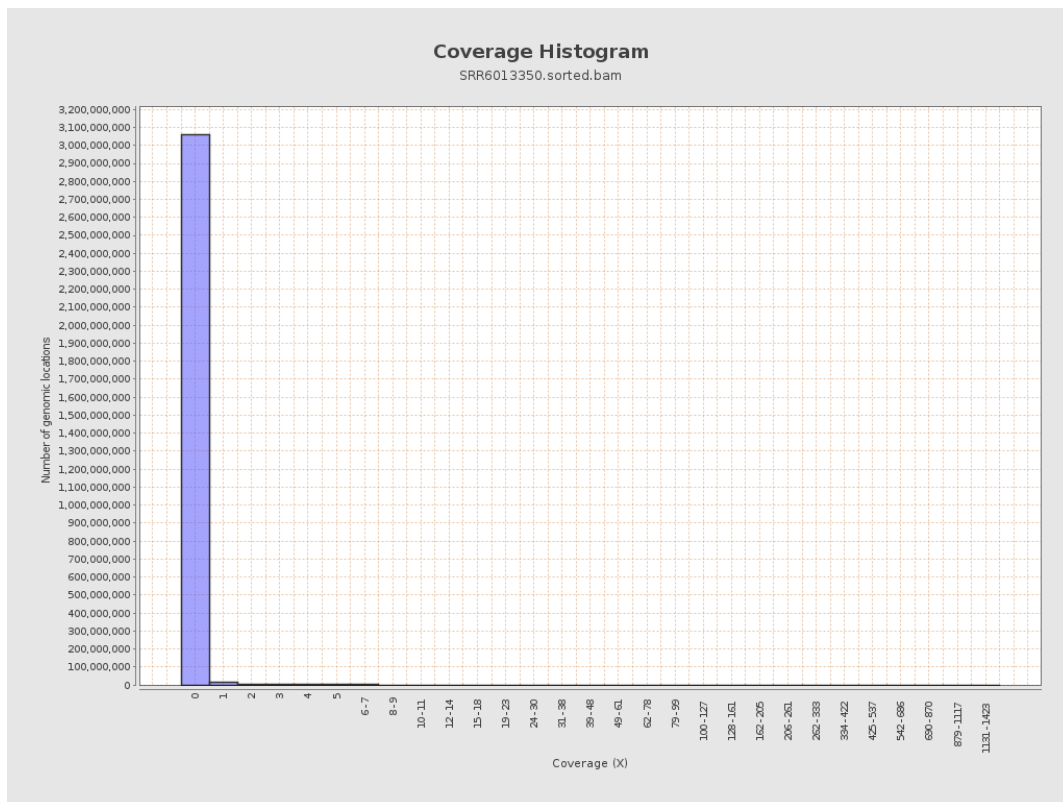
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 6244286      | 0.0251        | 1.1957             |
| chr2 | 243199373 | 8495992      | 0.0349        | 0.5197             |
| chr3 | 198022430 | 4748218      | 0.024         | 0.352              |
| chr4 | 191154276 | 3480136      | 0.0182        | 0.3018             |
| chr5 | 180915260 | 4298323      | 0.0238        | 0.3435             |
| chr6 | 171115067 | 4946257      | 0.0289        | 0.3949             |
| chr7 | 159138663 | 5982722      | 0.0376        | 0.5283             |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr8  | 146364022 | 5075886  | 0.0347 | 0.5764 |
| chr9  | 141213431 | 3697208  | 0.0262 | 0.4232 |
| chr10 | 135534747 | 10524692 | 0.0777 | 0.7222 |
| chr11 | 135006516 | 4706143  | 0.0349 | 0.4452 |
| chr12 | 133851895 | 4728707  | 0.0353 | 0.4281 |
| chr13 | 115169878 | 2811453  | 0.0244 | 0.3556 |
| chr14 | 107349540 | 3360472  | 0.0313 | 0.4231 |
| chr15 | 102531392 | 5016597  | 0.0489 | 0.5075 |
| chr16 | 90354753  | 2767751  | 0.0306 | 0.4032 |
| chr17 | 81195210  | 1647273  | 0.0203 | 0.3218 |
| chr18 | 78077248  | 4129386  | 0.0529 | 0.8533 |
| chr19 | 59128983  | 1527959  | 0.0258 | 0.692  |
| chr20 | 63025520  | 1228065  | 0.0195 | 0.3137 |
| chr21 | 48129895  | 2438652  | 0.0507 | 0.5128 |
| chr22 | 51304566  | 774300   | 0.0151 | 0.2595 |
| chrMT | 16571     | 45266    | 2.7316 | 3.8053 |
| chrX  | 155270560 | 9053044  | 0.0583 | 0.5715 |
| chrY  | 59373566  | 278763   | 0.0047 | 0.1385 |

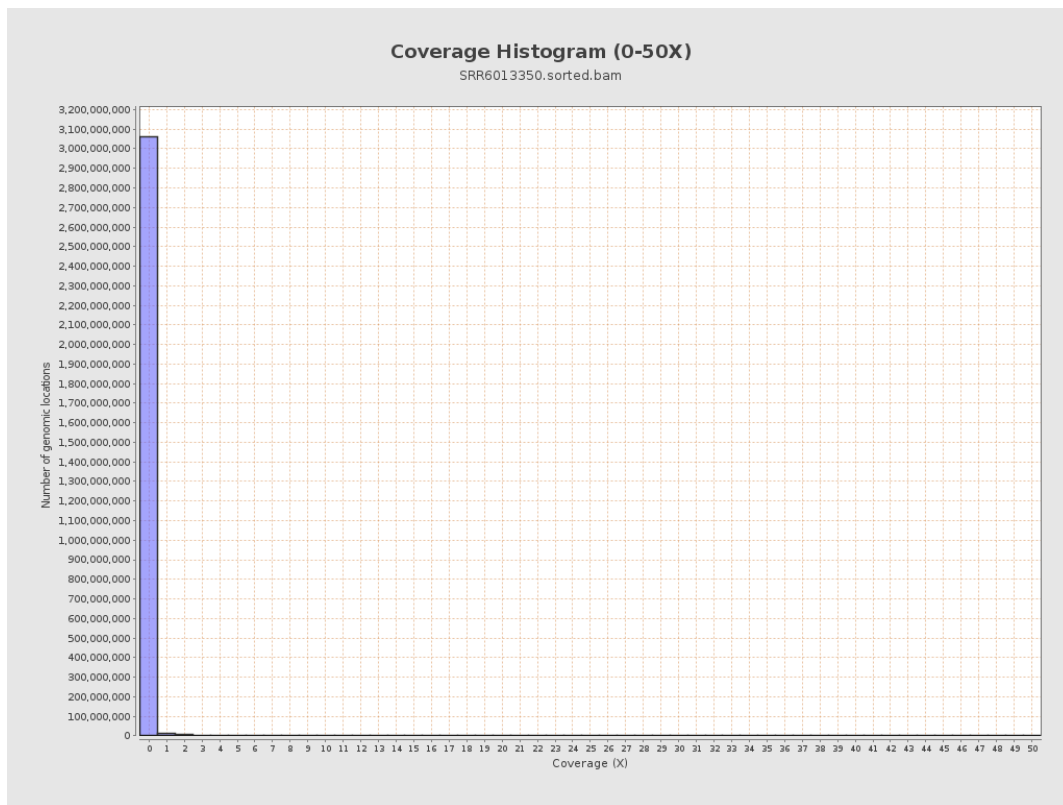
### 3. Results : Coverage across reference



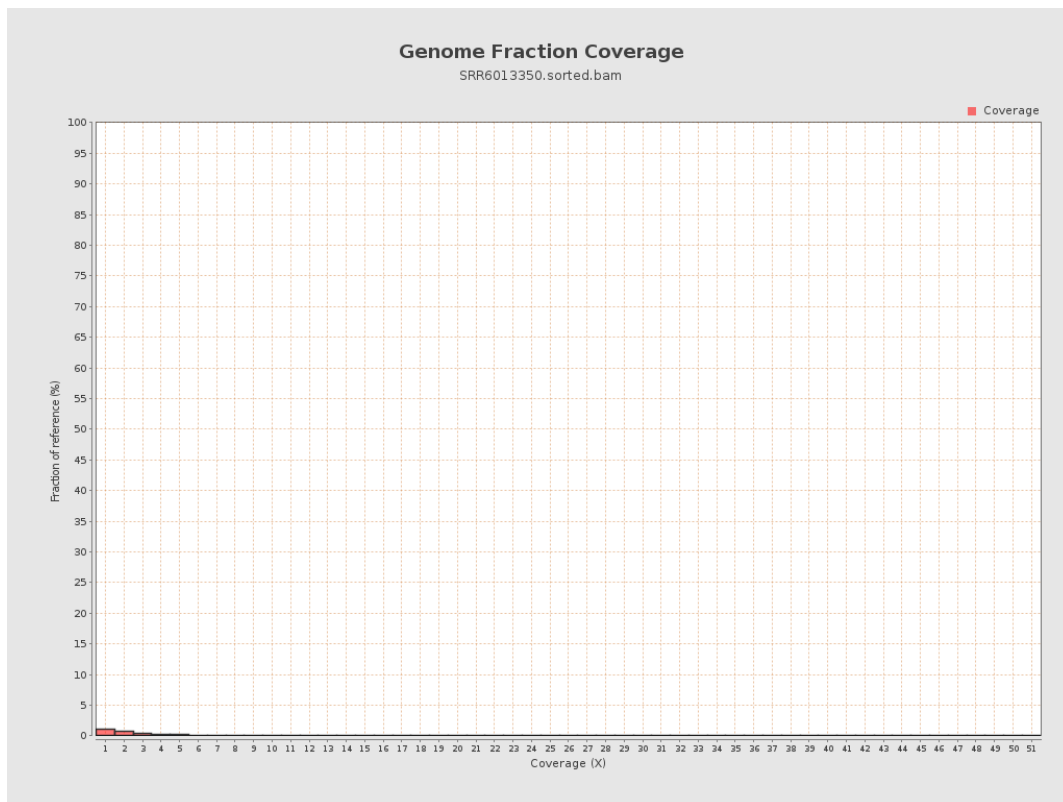
## 4. Results : Coverage Histogram



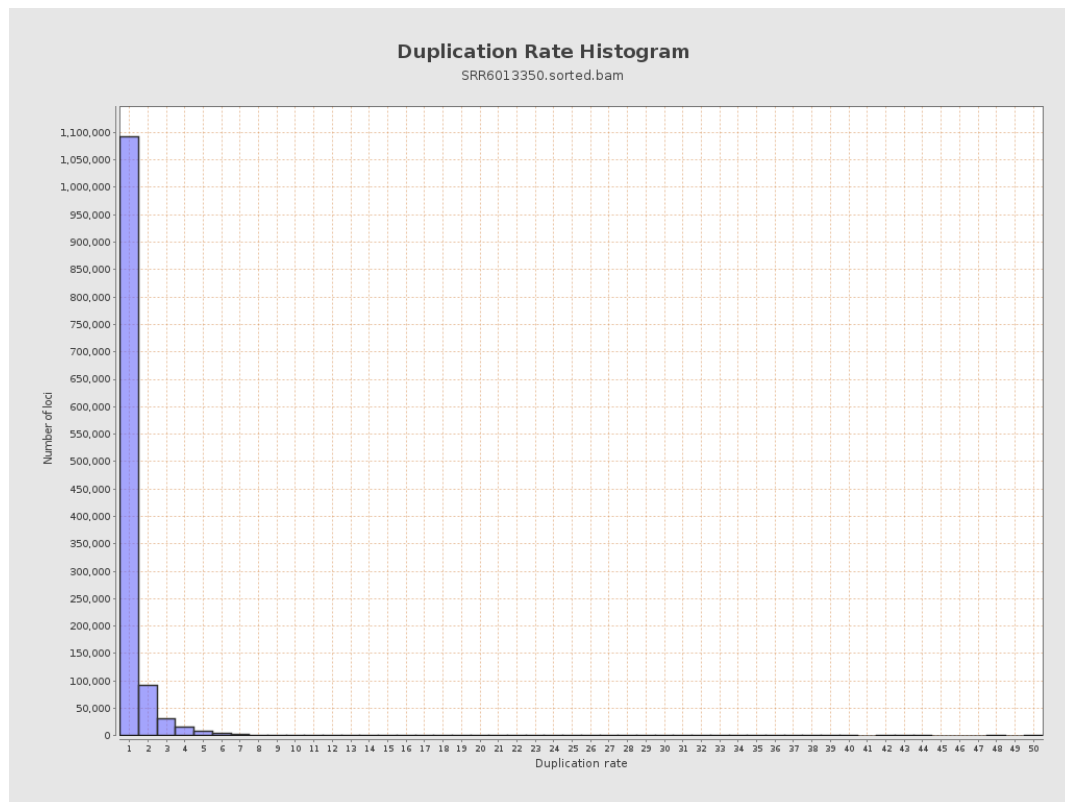
## 5. Results : Coverage Histogram (0-50X)



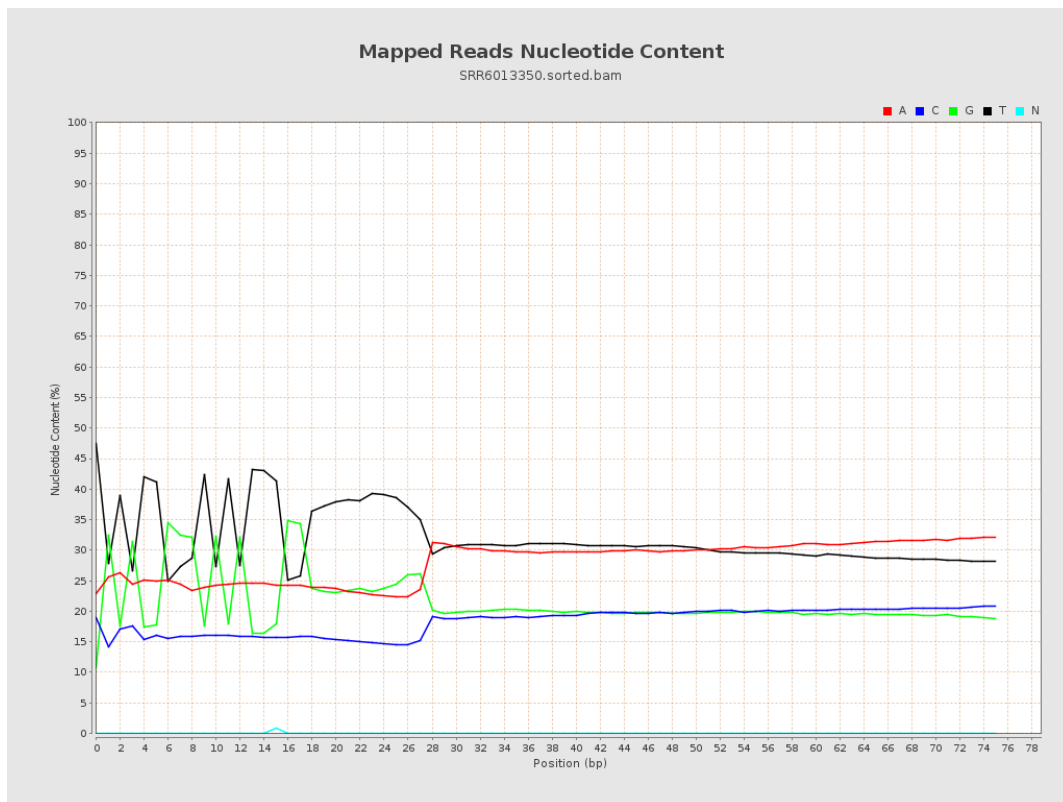
## 6. Results : Genome Fraction Coverage



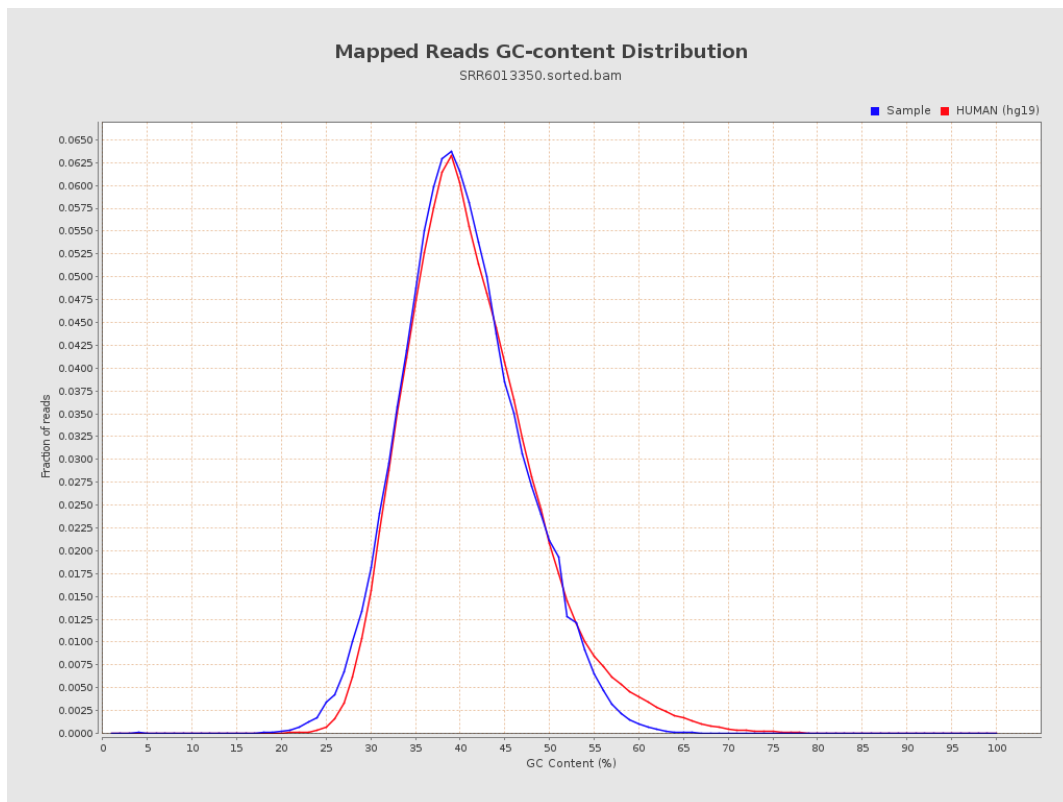
## 7. Results : Duplication Rate Histogram



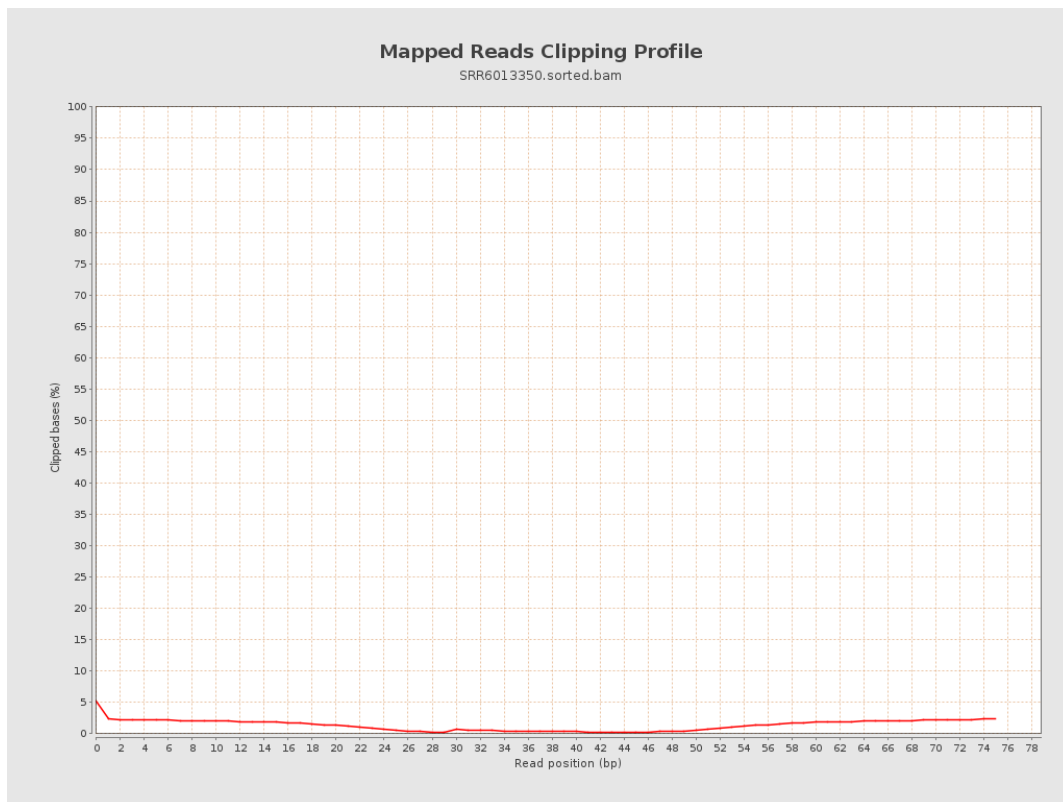
## 8. Results : Mapped Reads Nucleotide Content



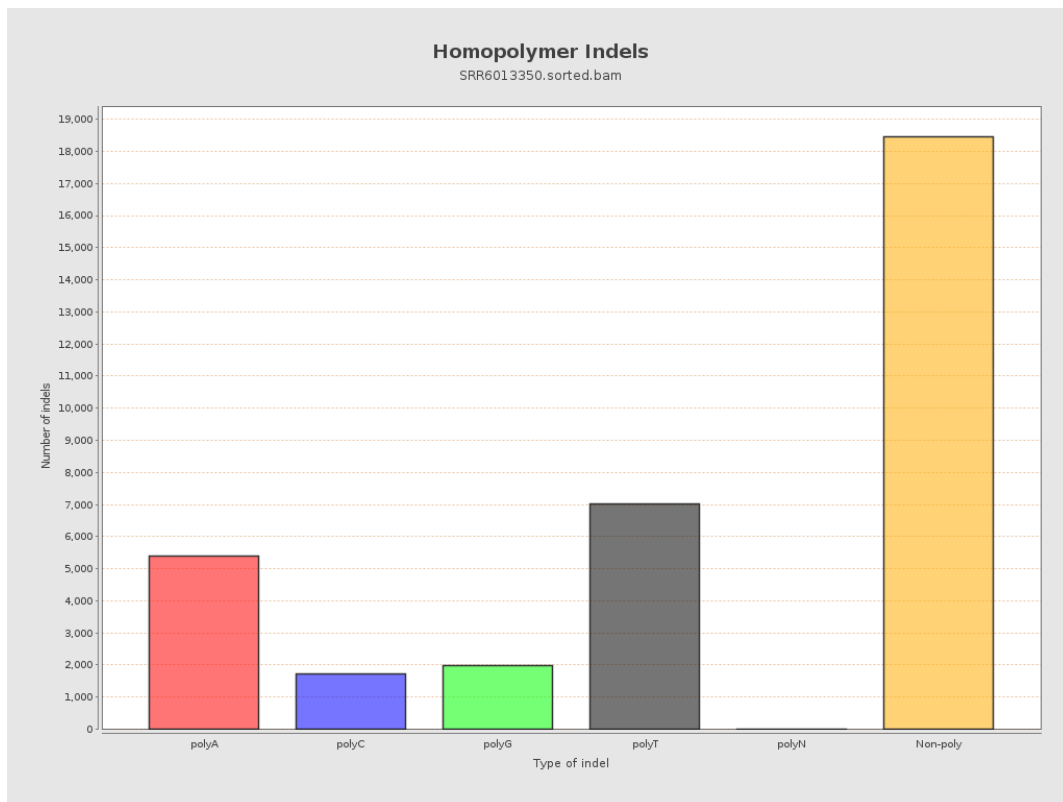
## 9. Results : Mapped Reads GC-content Distribution



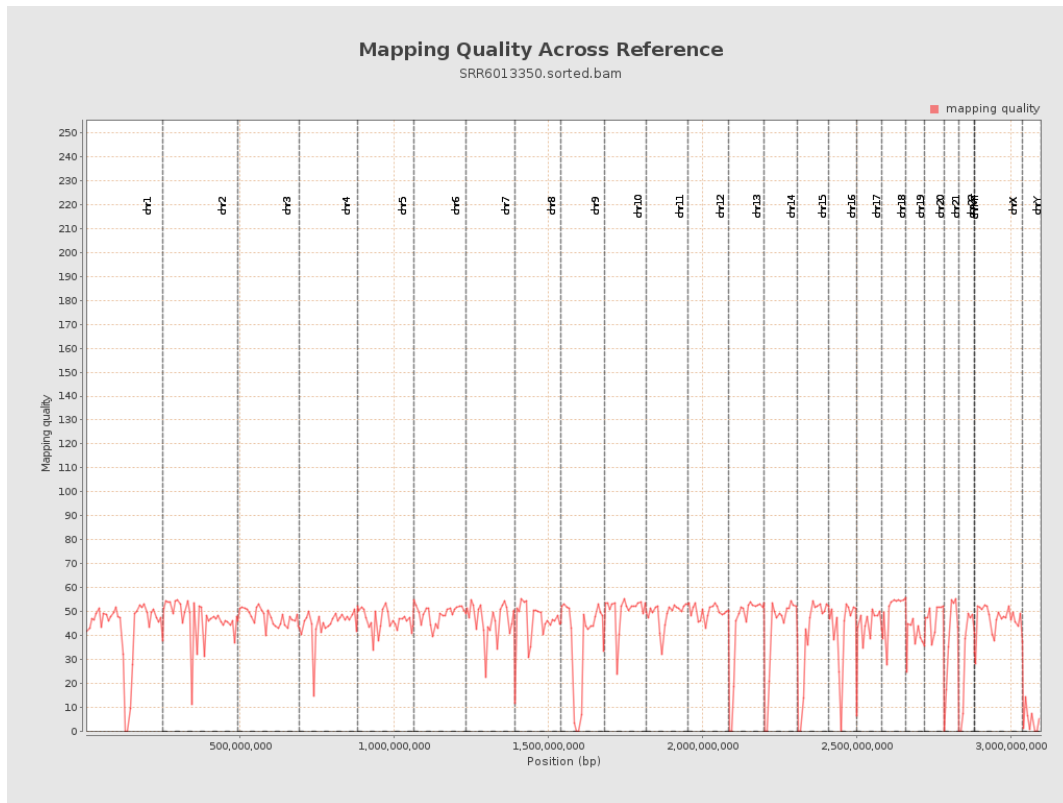
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

