

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/16 08:37:19*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231863.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_SRR6231863 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231863.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Mon Sep 16 08:37:18 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6231863.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 2,124,255          |
| Mapped reads                 | 1,615,145 / 76.03% |
| Unmapped reads               | 509,110 / 23.97%   |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 12,372 / 0.58%     |
| Read min/max/mean length     | 30 / 76 / 76.2     |
| Duplicated reads (estimated) | 104,604 / 4.92%    |
| Duplication rate             | 5.33%              |
| Clipped reads                | 753,959 / 35.49%   |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 28,905,690 / 27.1%  |
| Number/percentage of C's | 20,348,318 / 19.08% |
| Number/percentage of T's | 33,199,728 / 31.12% |
| Number/percentage of G's | 24,208,733 / 22.7%  |
| Number/percentage of N's | 5,546 / 0.01%       |
| GC Percentage            | 41.77%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0345 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.3474 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 45.75 |
|----------------------|-------|

## 2.5. Mismatches and indels

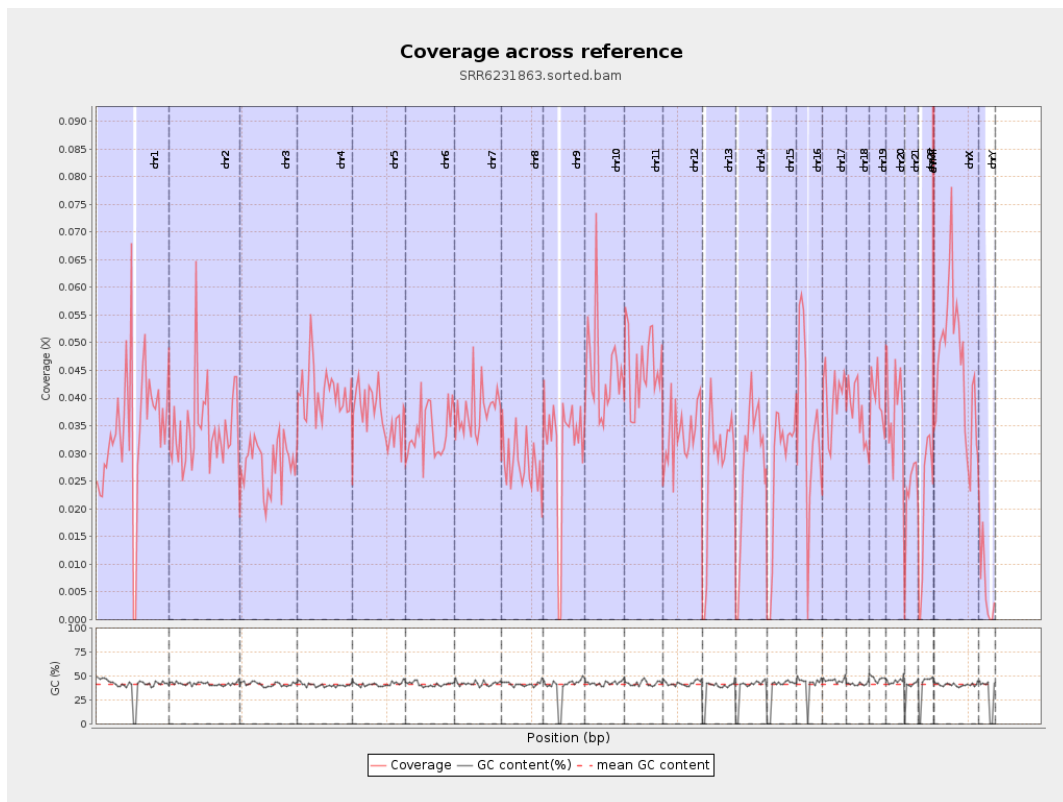
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 0.72%   |
| Mismatches                               | 757,141 |
| Insertions                               | 7,828   |
| Mapped reads with at least one insertion | 0.48%   |
| Deletions                                | 26,448  |
| Mapped reads with at least one deletion  | 1.62%   |
| Homopolymer indels                       | 45.93%  |

## 2.6. Chromosome stats

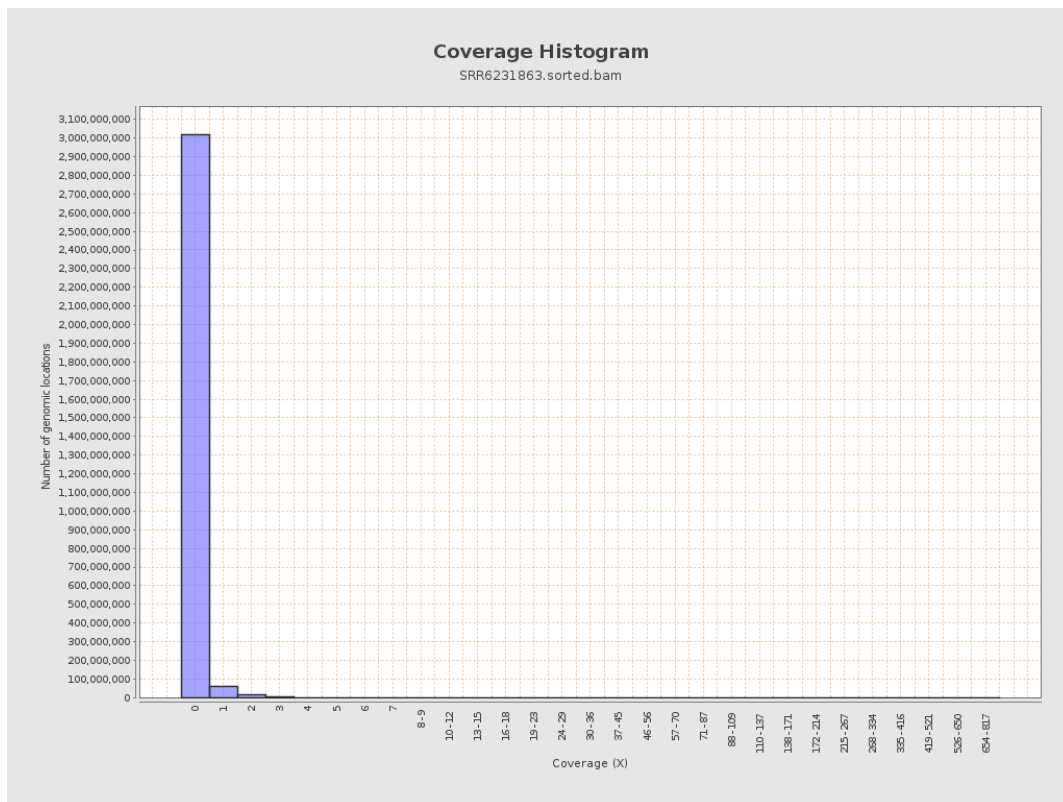
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 8435785      | 0.0338        | 0.7212             |
| chr2 | 243199373 | 8424349      | 0.0346        | 0.3857             |
| chr3 | 198022430 | 5558685      | 0.0281        | 0.2131             |
| chr4 | 191154276 | 7837825      | 0.041         | 0.2715             |
| chr5 | 180915260 | 6713466      | 0.0371        | 0.2446             |
| chr6 | 171115067 | 5791964      | 0.0338        | 0.2686             |
| chr7 | 159138663 | 6009184      | 0.0378        | 0.3441             |
|      |           |              |               |                    |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr8  | 146364022 | 4122866 | 0.0282 | 0.2929 |
| chr9  | 141213431 | 4382810 | 0.031  | 0.2818 |
| chr10 | 135534747 | 6030645 | 0.0445 | 0.3836 |
| chr11 | 135006516 | 6099356 | 0.0452 | 0.3085 |
| chr12 | 133851895 | 4469468 | 0.0334 | 0.2362 |
| chr13 | 115169878 | 3147911 | 0.0273 | 0.2103 |
| chr14 | 107349540 | 3008448 | 0.028  | 0.2254 |
| chr15 | 102531392 | 2783352 | 0.0271 | 0.2112 |
| chr16 | 90354753  | 3255547 | 0.036  | 0.2599 |
| chr17 | 81195210  | 3266702 | 0.0402 | 0.2718 |
| chr18 | 78077248  | 2924406 | 0.0375 | 0.4352 |
| chr19 | 59128983  | 2370782 | 0.0401 | 0.4813 |
| chr20 | 63025520  | 2360952 | 0.0375 | 0.2541 |
| chr21 | 48129895  | 1091955 | 0.0227 | 0.2055 |
| chr22 | 51304566  | 1053517 | 0.0205 | 0.1852 |
| chrMT | 16571     | 25870   | 1.5612 | 1.5822 |
| chrX  | 155270560 | 7199615 | 0.0464 | 0.2973 |
| chrY  | 59373566  | 349848  | 0.0059 | 0.1326 |

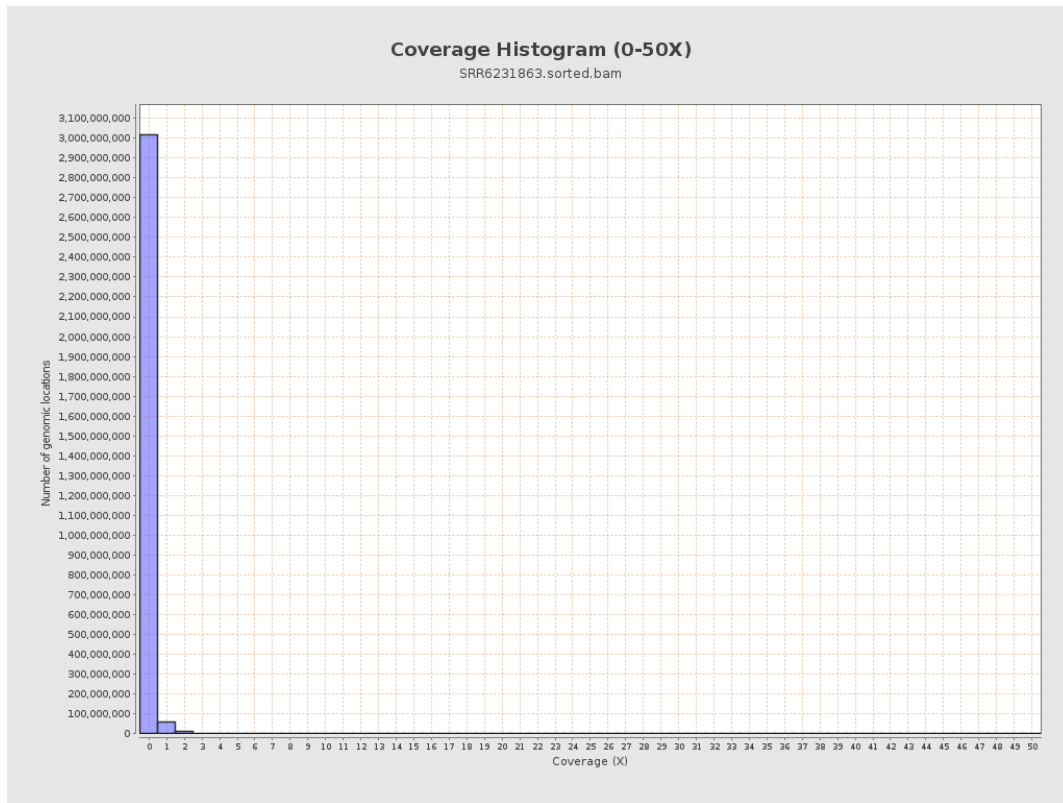
### 3. Results : Coverage across reference



## 4. Results : Coverage Histogram

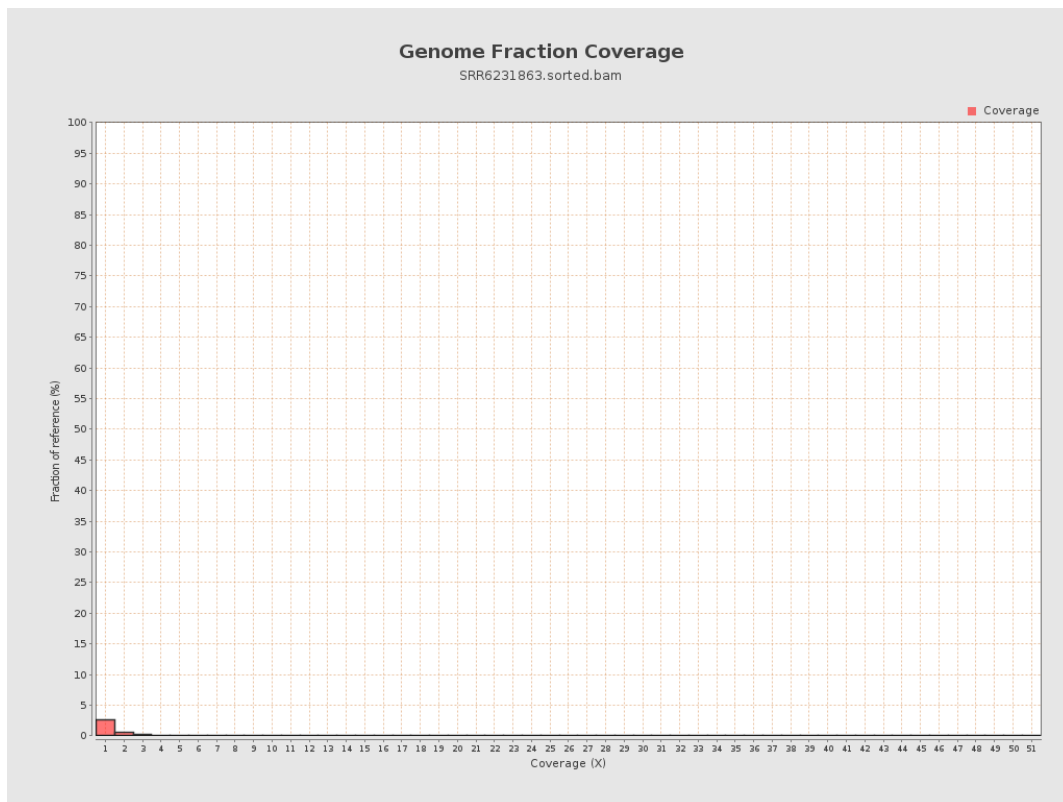


## 5. Results : Coverage Histogram (0-50X)

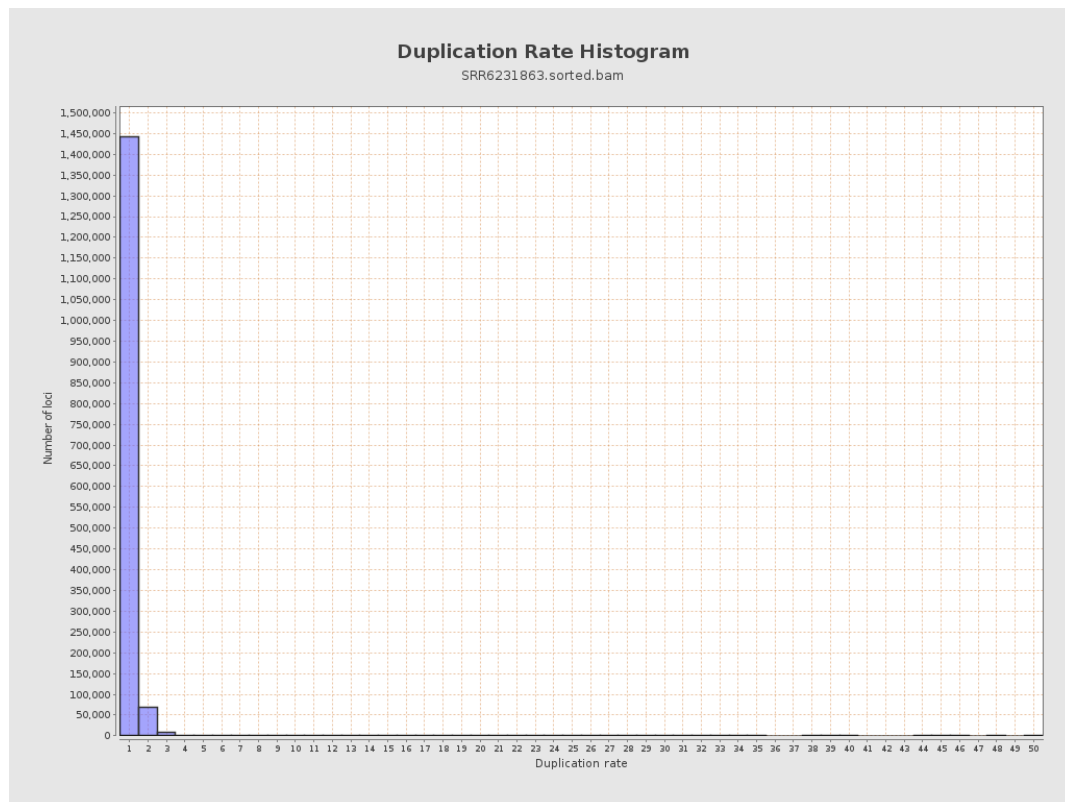




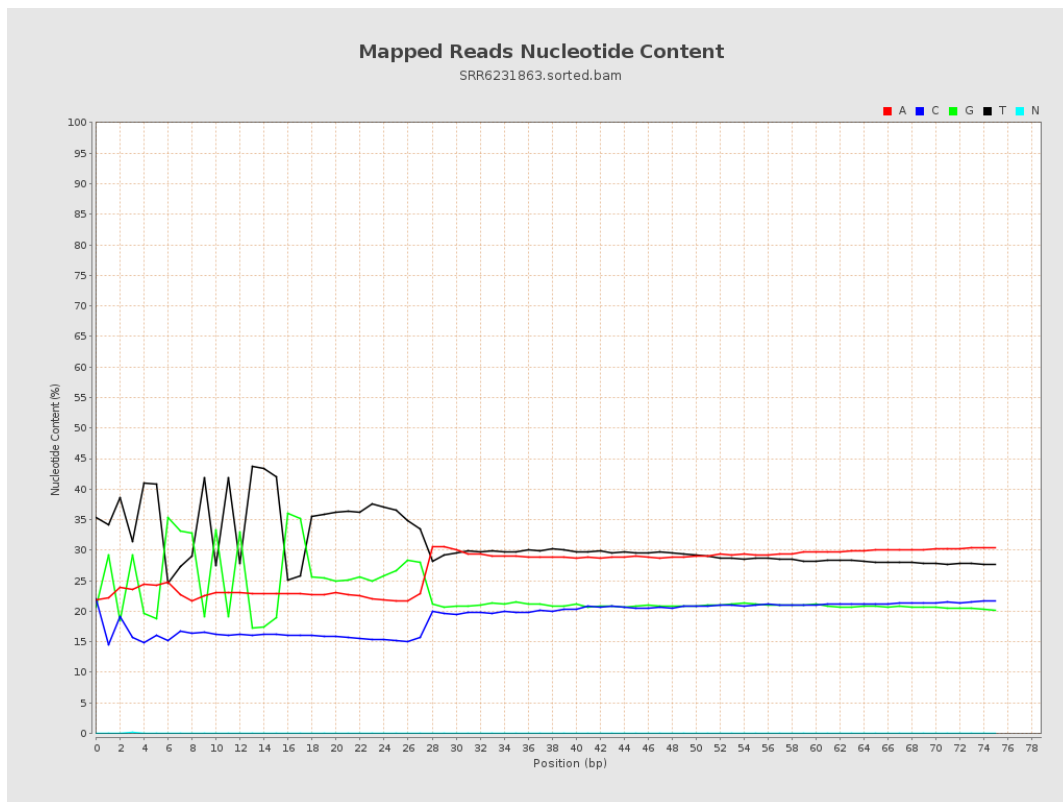
## 6. Results : Genome Fraction Coverage



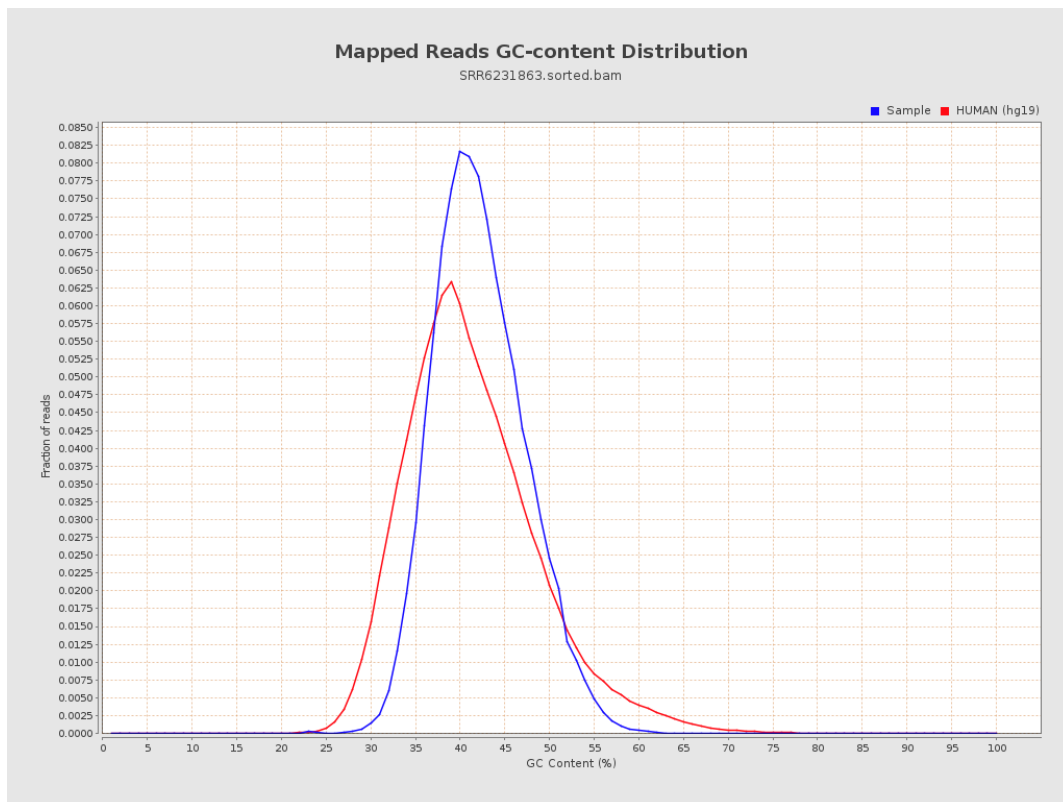
## 7. Results : Duplication Rate Histogram



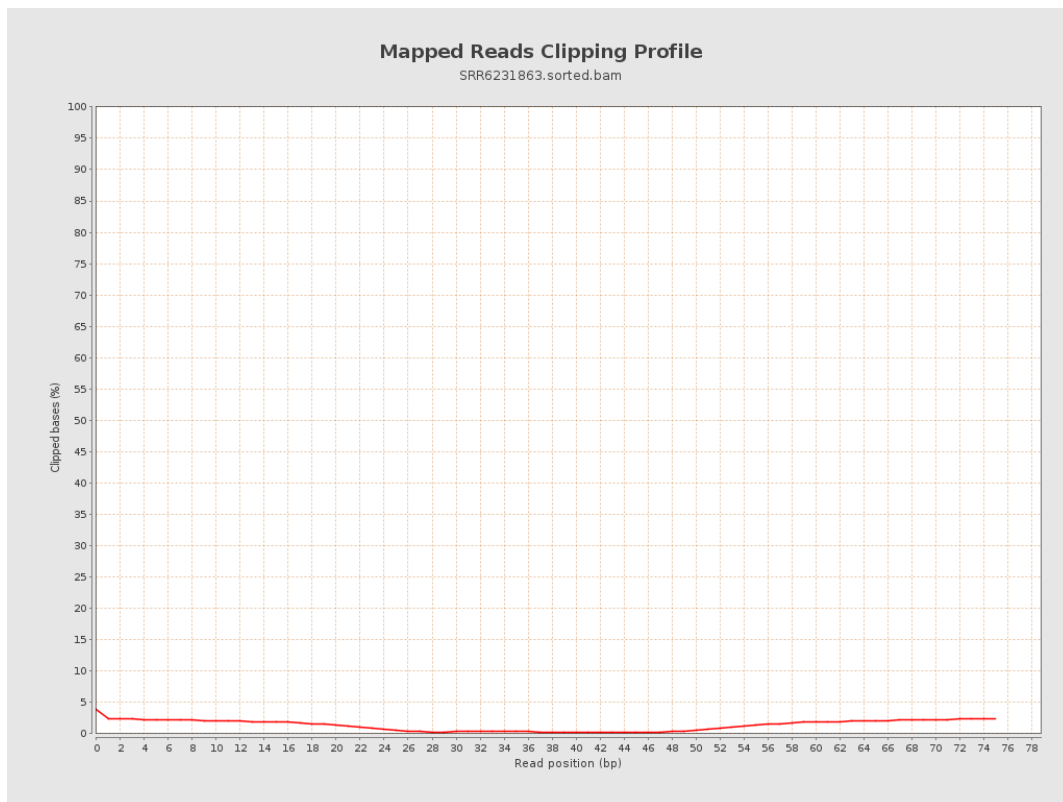
## 8. Results : Mapped Reads Nucleotide Content



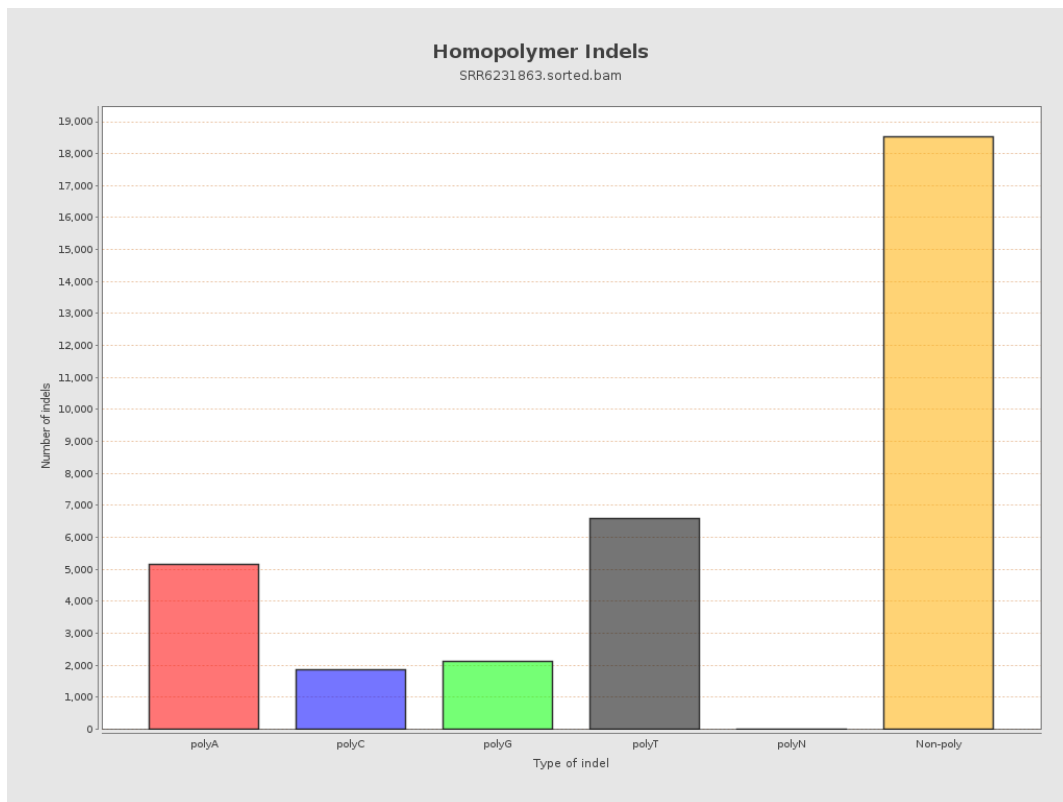
## 9. Results : Mapped Reads GC-content Distribution



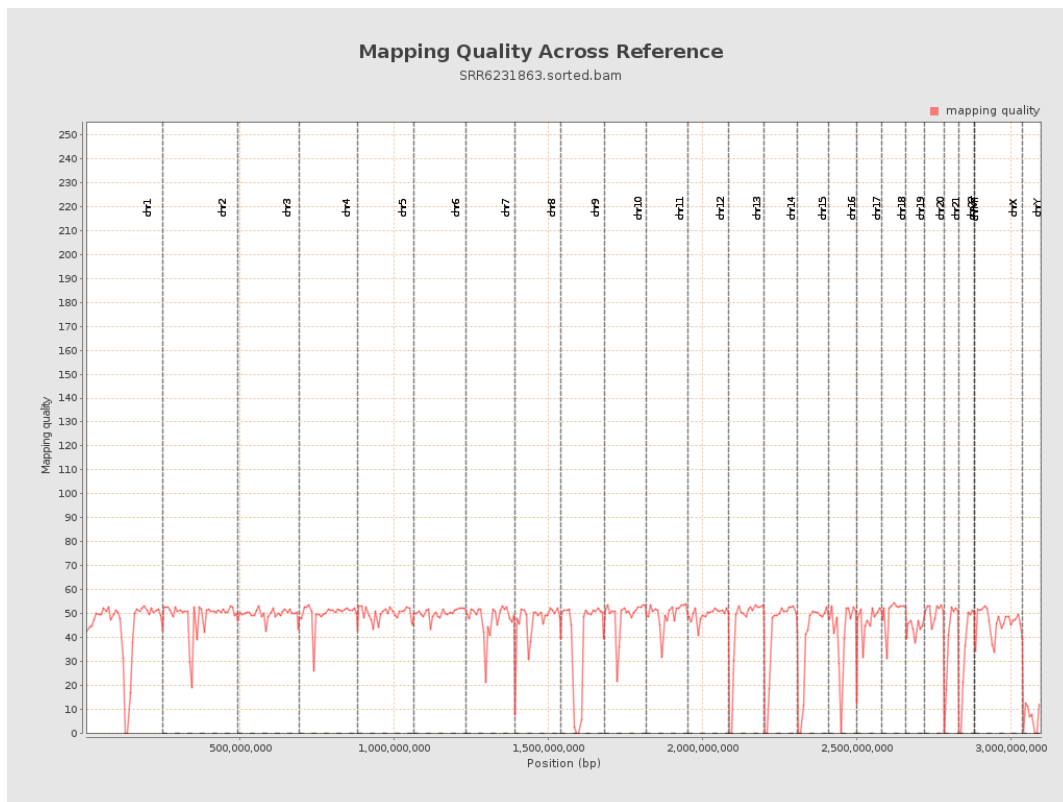
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram

