

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/17 12:14:03*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238080.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_SRR6238080 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238080.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Tue Sep 17 12:14:02 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6238080.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 1,736,020          |
| Mapped reads                 | 1,265,656 / 72.91% |
| Unmapped reads               | 470,364 / 27.09%   |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 10,321 / 0.59%     |
| Read min/max/mean length     | 30 / 76 / 76.21    |
| Duplicated reads (estimated) | 208,633 / 12.02%   |
| Duplication rate             | 13.24%             |
| Clipped reads                | 818,030 / 47.12%   |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 20,093,609 / 25.9%  |
| Number/percentage of C's | 13,340,214 / 17.19% |
| Number/percentage of T's | 25,591,547 / 32.98% |
| Number/percentage of G's | 18,558,821 / 23.92% |
| Number/percentage of N's | 3,763 / 0%          |
| GC Percentage            | 41.11%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0251 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.3257 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 44.86 |
|----------------------|-------|

## 2.5. Mismatches and indels

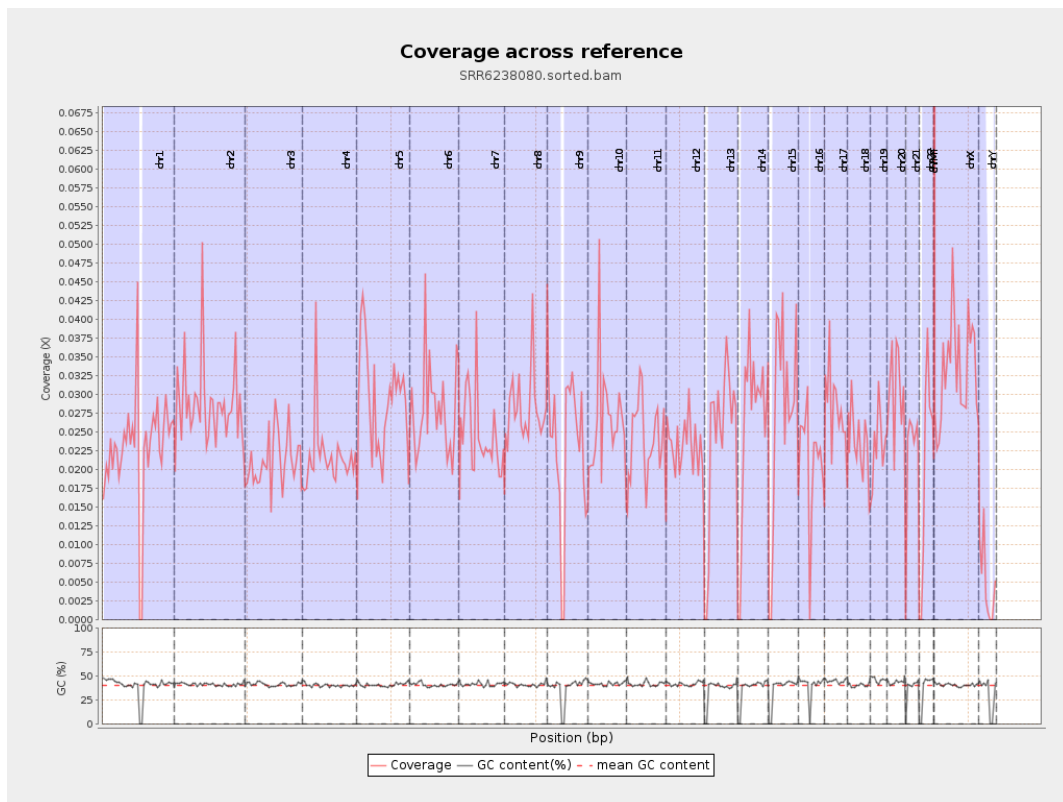
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 0.78%   |
| Mismatches                               | 592,492 |
| Insertions                               | 6,273   |
| Mapped reads with at least one insertion | 0.49%   |
| Deletions                                | 23,118  |
| Mapped reads with at least one deletion  | 1.81%   |
| Homopolymer indels                       | 46.67%  |

## 2.6. Chromosome stats

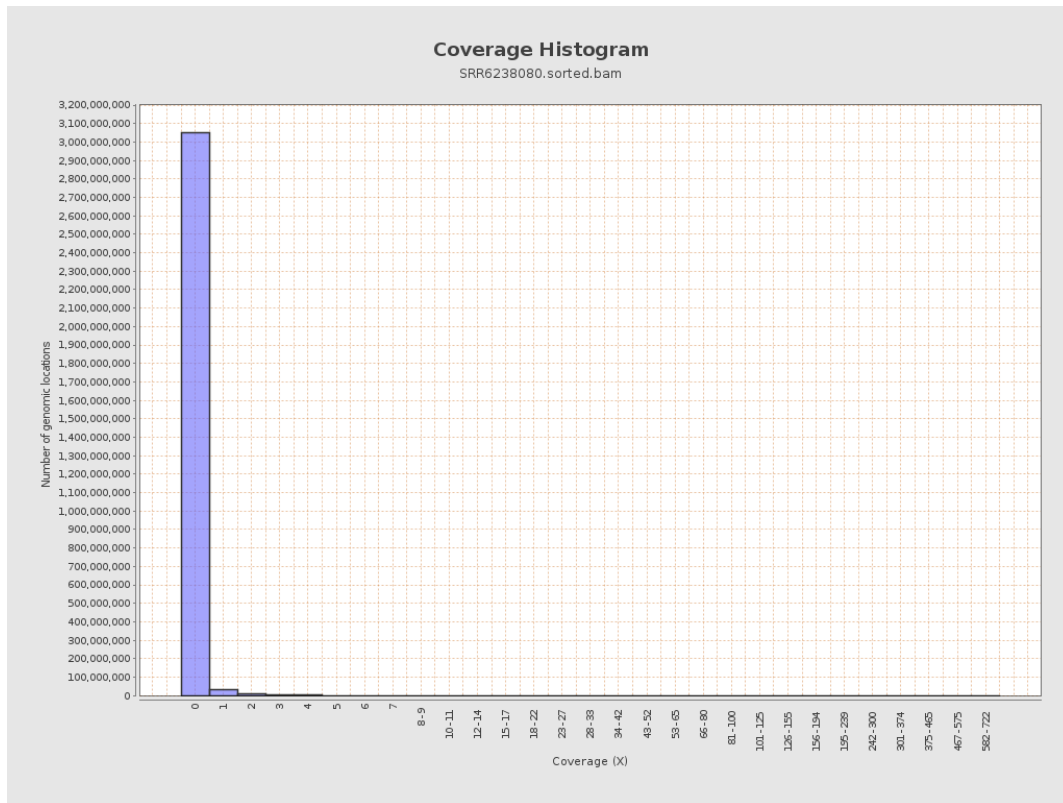
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 5688354      | 0.0228        | 0.5209             |
| chr2 | 243199373 | 6970127      | 0.0287        | 0.4436             |
| chr3 | 198022430 | 4200823      | 0.0212        | 0.2237             |
| chr4 | 191154276 | 4119994      | 0.0216        | 0.2346             |
| chr5 | 180915260 | 5349248      | 0.0296        | 0.2618             |
| chr6 | 171115067 | 4755993      | 0.0278        | 0.3351             |
| chr7 | 159138663 | 3883151      | 0.0244        | 0.3162             |
|      |           |              |               |                    |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr8  | 146364022 | 4121439 | 0.0282 | 0.319  |
| chr9  | 141213431 | 3251024 | 0.023  | 0.2762 |
| chr10 | 135534747 | 3543175 | 0.0261 | 0.3086 |
| chr11 | 135006516 | 3263199 | 0.0242 | 0.2709 |
| chr12 | 133851895 | 3091168 | 0.0231 | 0.2406 |
| chr13 | 115169878 | 2754616 | 0.0239 | 0.2478 |
| chr14 | 107349540 | 2820994 | 0.0263 | 0.2516 |
| chr15 | 102531392 | 2808397 | 0.0274 | 0.2543 |
| chr16 | 90354753  | 1884891 | 0.0209 | 0.2237 |
| chr17 | 81195210  | 2285374 | 0.0281 | 0.2621 |
| chr18 | 78077248  | 1835185 | 0.0235 | 0.5632 |
| chr19 | 59128983  | 1382166 | 0.0234 | 0.3862 |
| chr20 | 63025520  | 1925554 | 0.0306 | 0.2681 |
| chr21 | 48129895  | 1085737 | 0.0226 | 0.2392 |
| chr22 | 51304566  | 1076008 | 0.021  | 0.2136 |
| chrMT | 16571     | 55565   | 3.3531 | 3.483  |
| chrX  | 155270560 | 5187314 | 0.0334 | 0.2948 |
| chrY  | 59373566  | 285428  | 0.0048 | 0.1282 |

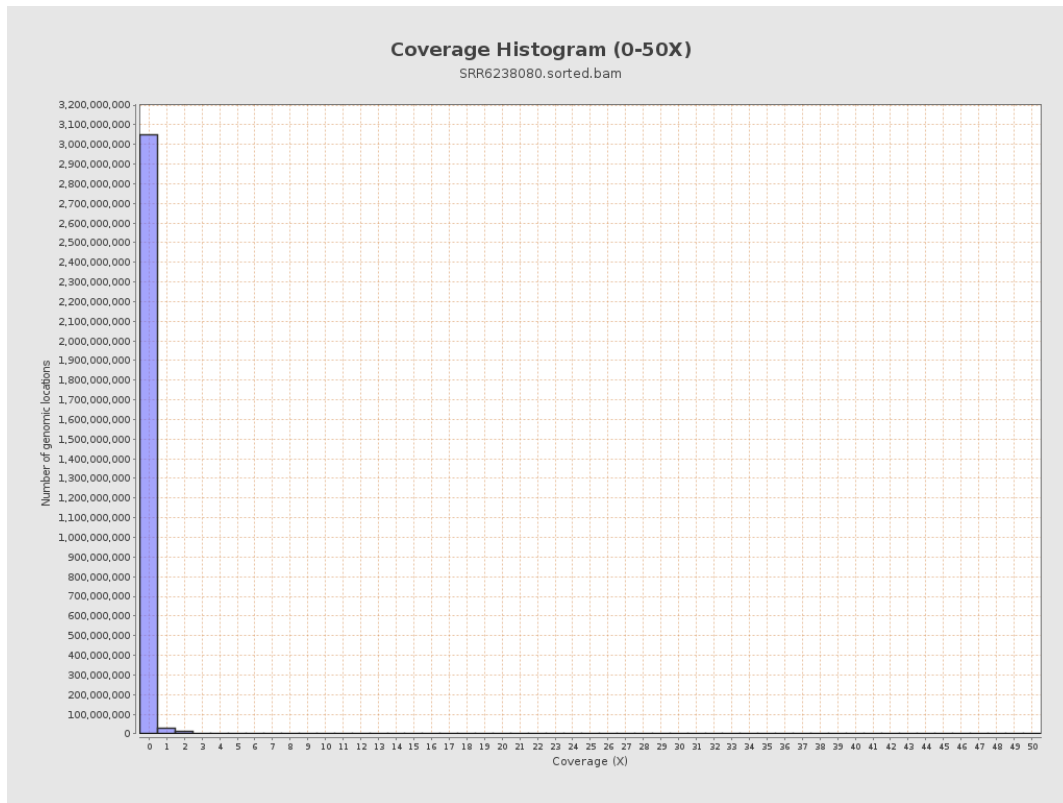
### 3. Results : Coverage across reference



## 4. Results : Coverage Histogram

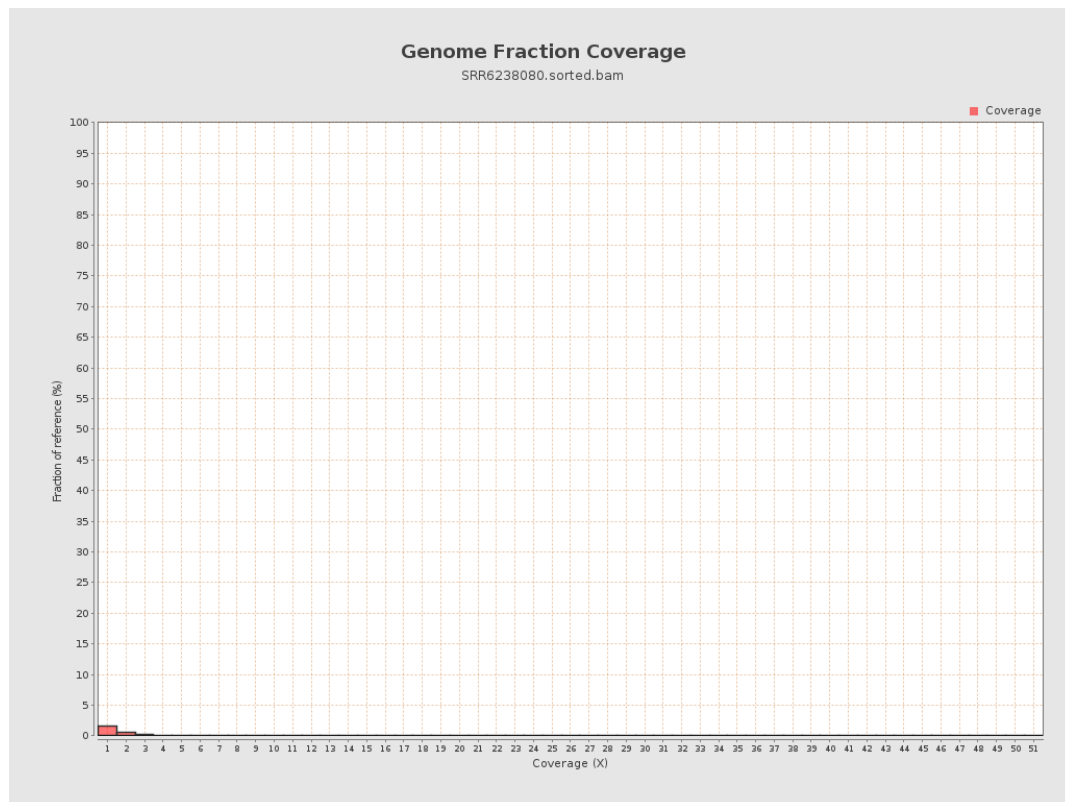


## 5. Results : Coverage Histogram (0-50X)

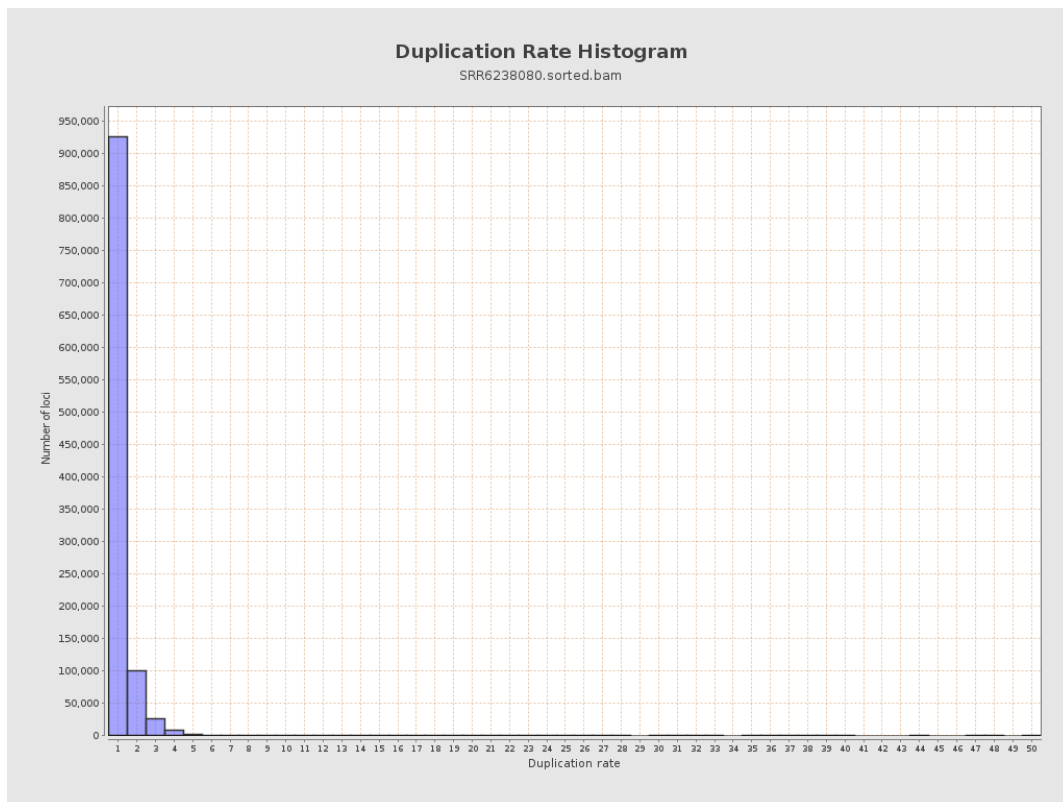




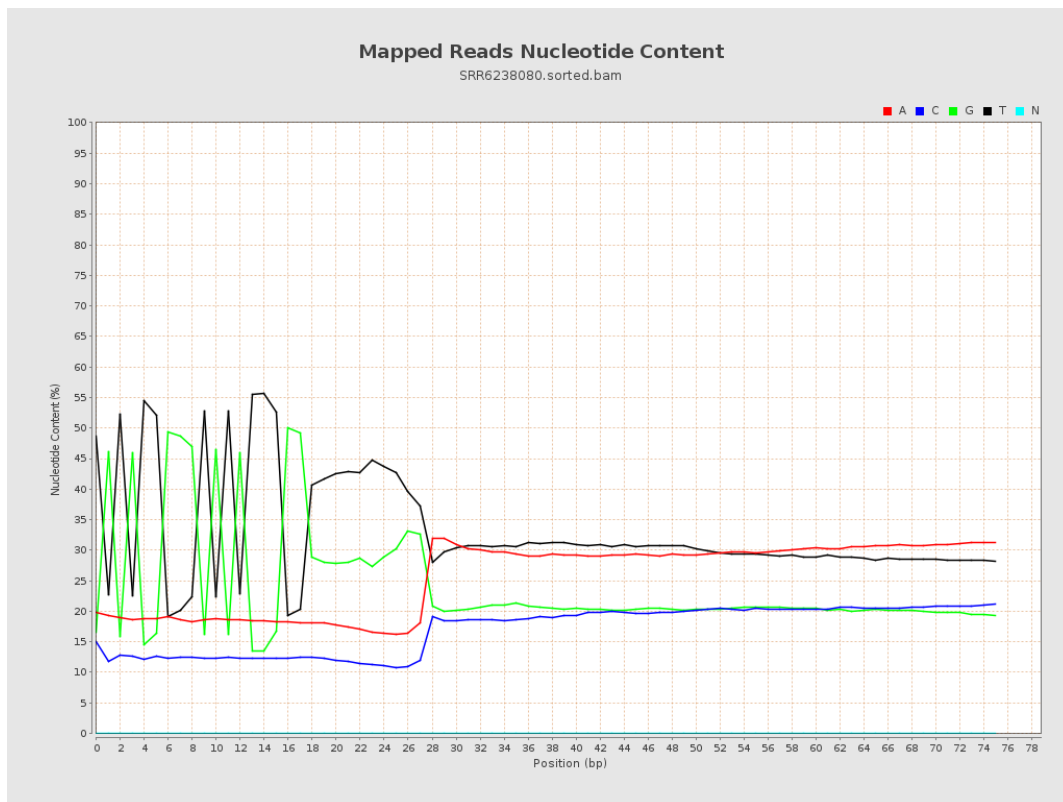
## 6. Results : Genome Fraction Coverage



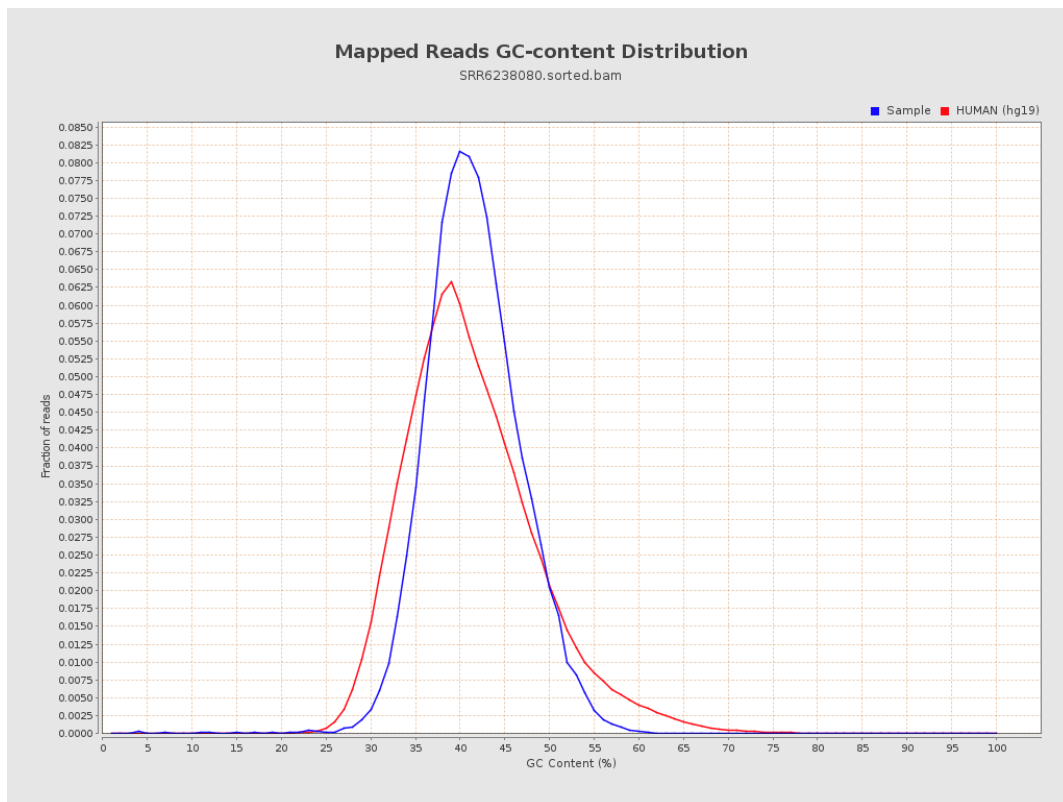
## 7. Results : Duplication Rate Histogram



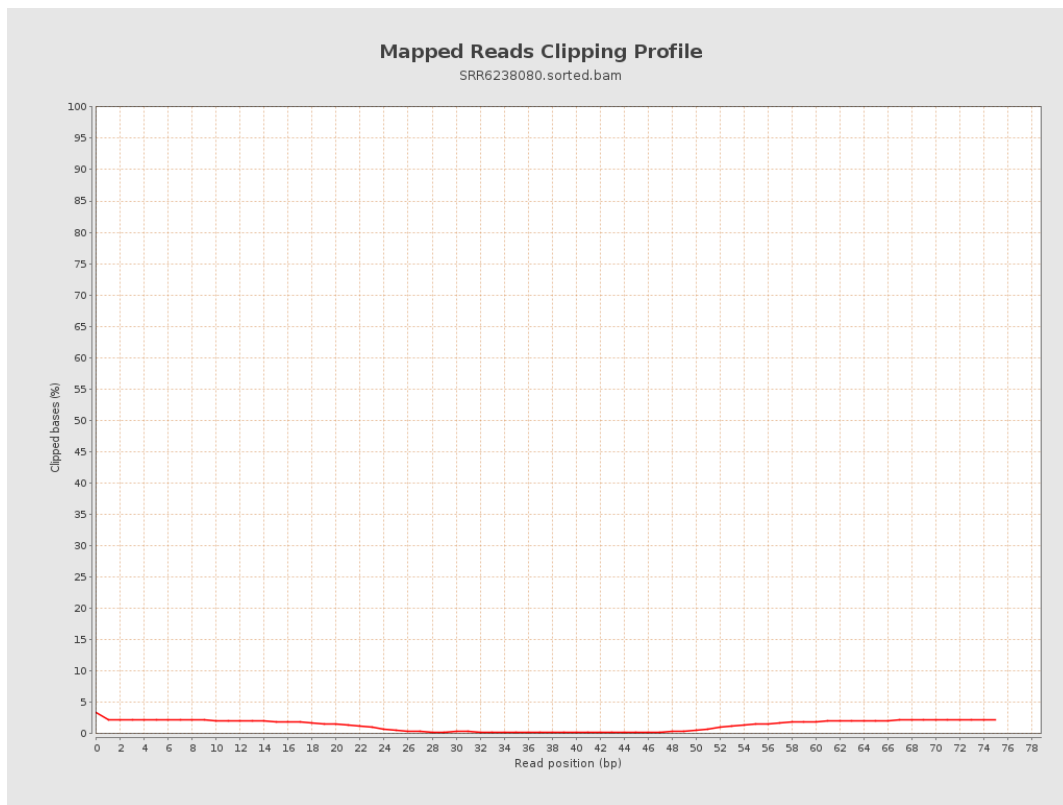
## 8. Results : Mapped Reads Nucleotide Content



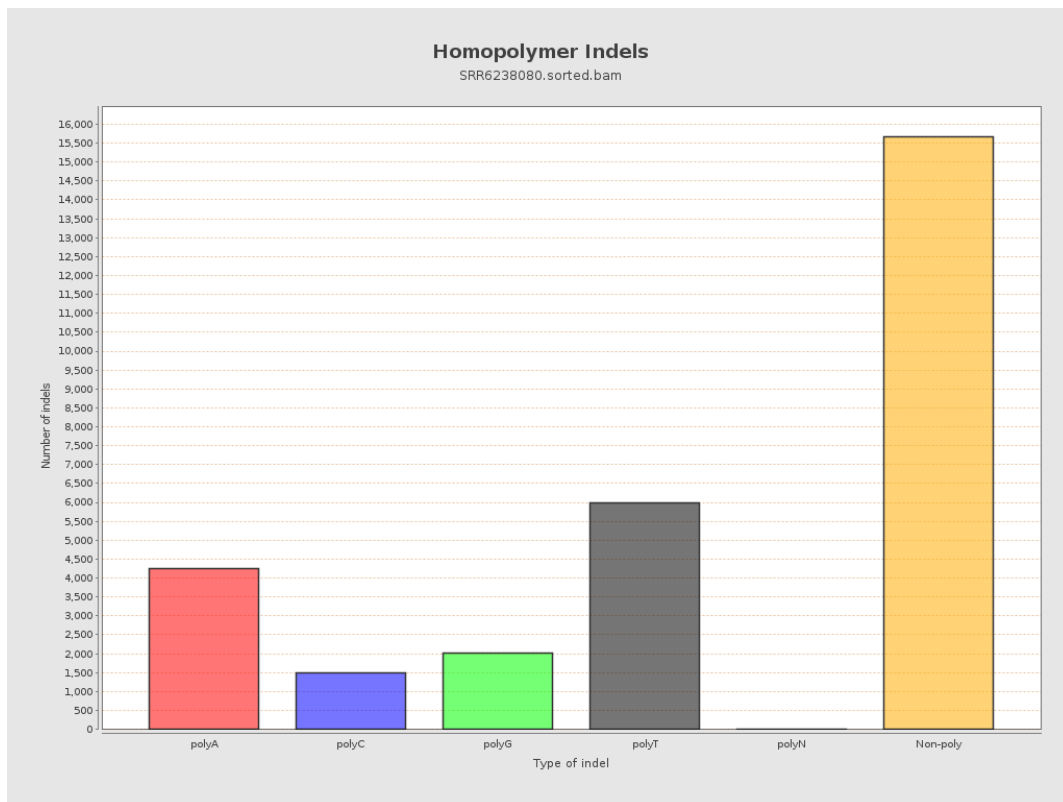
## 9. Results : Mapped Reads GC-content Distribution



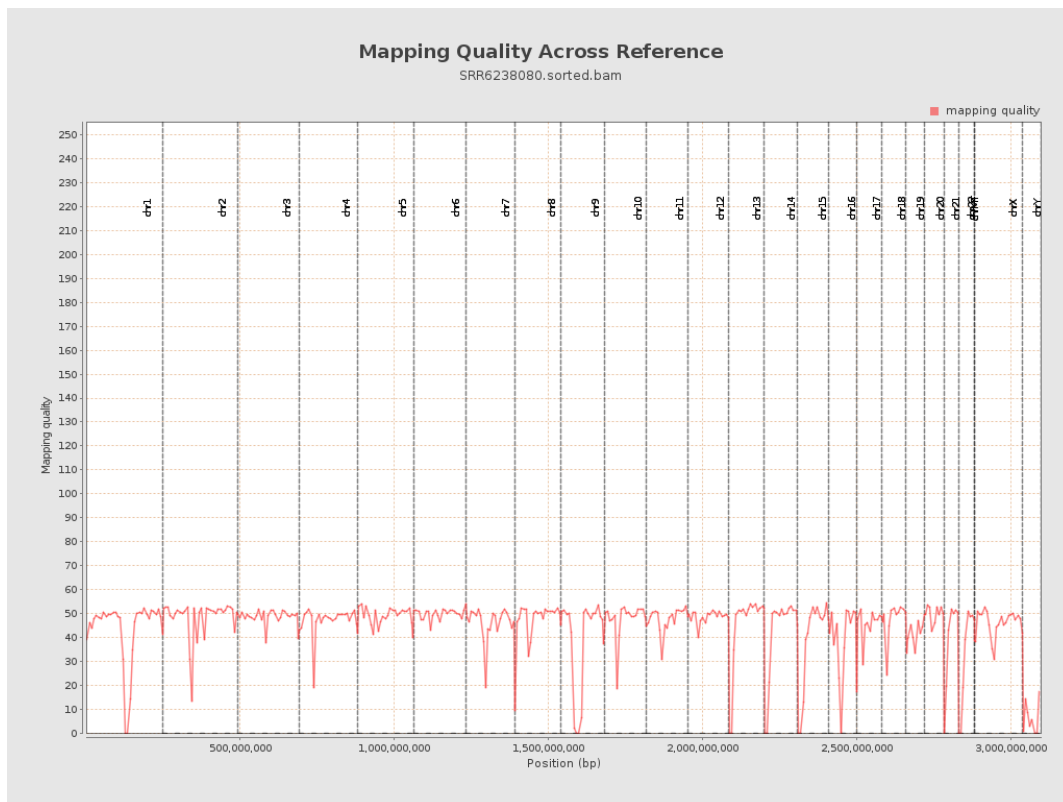
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

