

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/17 12:46:09*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238248.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_SRR6238248 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238248.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Tue Sep 17 12:46:09 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6238248.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 1,995,852          |
| Mapped reads                 | 1,827,570 / 91.57% |
| Unmapped reads               | 168,282 / 8.43%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 14,045 / 0.7%      |
| Read min/max/mean length     | 30 / 76 / 76.25    |
| Duplicated reads (estimated) | 59,722 / 2.99%     |
| Duplication rate             | 2.12%              |
| Clipped reads                | 890,073 / 44.6%    |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 33,008,969 / 27.34% |
| Number/percentage of C's | 23,938,969 / 19.83% |
| Number/percentage of T's | 35,976,049 / 29.8%  |
| Number/percentage of G's | 27,789,356 / 23.02% |
| Number/percentage of N's | 28,984 / 0.02%      |
| GC Percentage            | 42.84%              |

### 2.3. Coverage

|      |       |
|------|-------|
| Mean | 0.039 |
|      |       |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.3922 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 42.49 |
|----------------------|-------|

## 2.5. Mismatches and indels

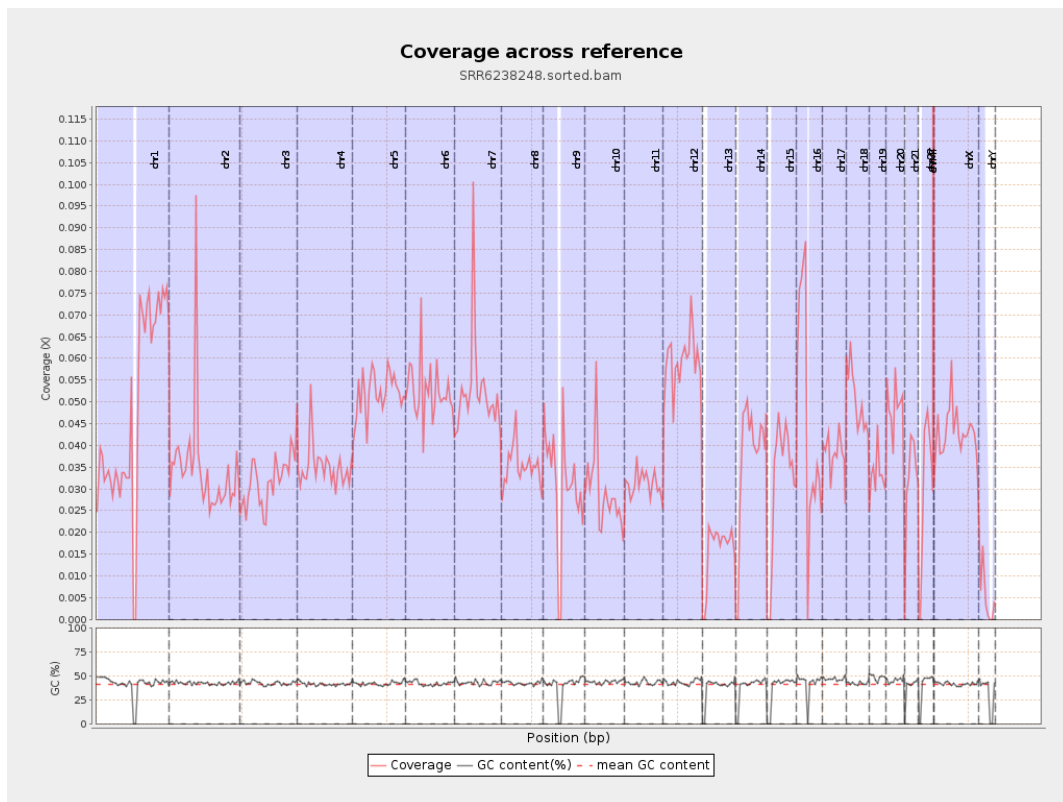
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.89%     |
| Mismatches                               | 1,057,961 |
| Insertions                               | 10,566    |
| Mapped reads with at least one insertion | 0.57%     |
| Deletions                                | 33,608    |
| Mapped reads with at least one deletion  | 1.82%     |
| Homopolymer indels                       | 44.67%    |

## 2.6. Chromosome stats

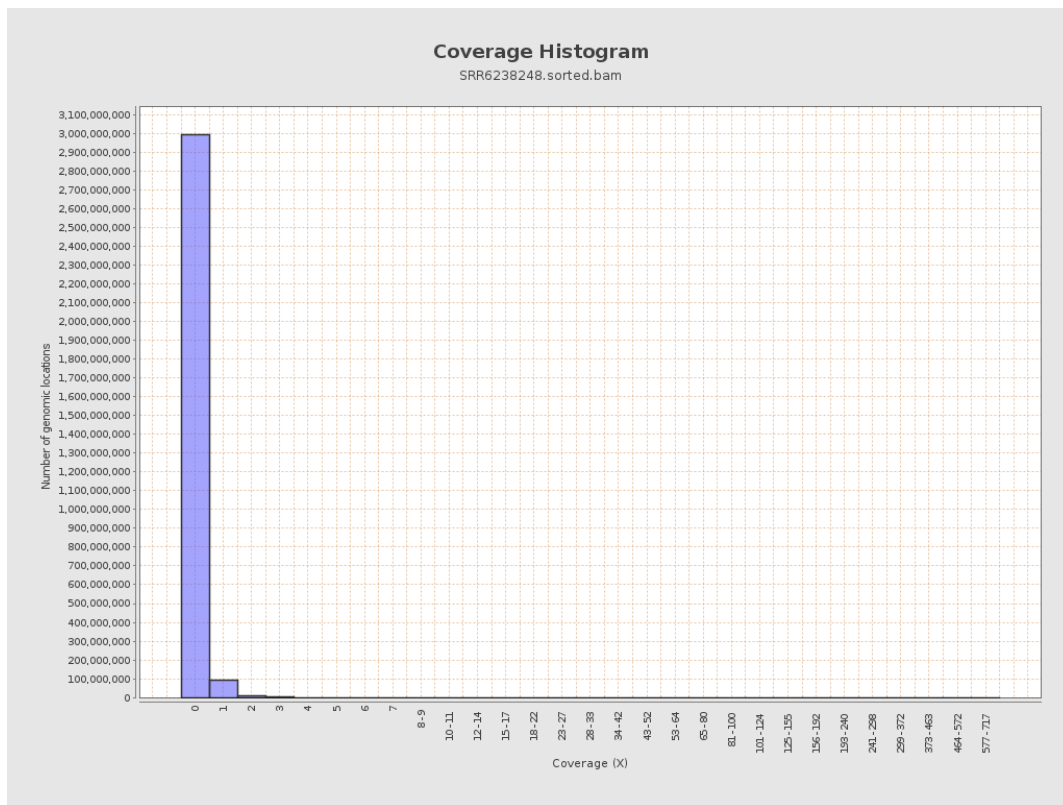
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 11860083     | 0.0476        | 0.5201             |
| chr2 | 243199373 | 8380021      | 0.0345        | 0.5743             |
| chr3 | 198022430 | 6265800      | 0.0316        | 0.1955             |
| chr4 | 191154276 | 6660161      | 0.0348        | 0.2289             |
| chr5 | 180915260 | 9398074      | 0.0519        | 0.2541             |
| chr6 | 171115067 | 8951932      | 0.0523        | 0.3524             |
| chr7 | 159138663 | 8401999      | 0.0528        | 0.7657             |
|      |           |              |               |                    |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr8  | 146364022 | 5133566 | 0.0351 | 0.3841 |
| chr9  | 141213431 | 4317525 | 0.0306 | 0.4141 |
| chr10 | 135534747 | 3947260 | 0.0291 | 0.3329 |
| chr11 | 135006516 | 4186157 | 0.031  | 0.2982 |
| chr12 | 133851895 | 7901608 | 0.059  | 0.2771 |
| chr13 | 115169878 | 1830067 | 0.0159 | 0.1382 |
| chr14 | 107349540 | 3986211 | 0.0371 | 0.262  |
| chr15 | 102531392 | 3261369 | 0.0318 | 0.2058 |
| chr16 | 90354753  | 4180765 | 0.0463 | 0.2717 |
| chr17 | 81195210  | 3077649 | 0.0379 | 0.2298 |
| chr18 | 78077248  | 3944265 | 0.0505 | 0.7482 |
| chr19 | 59128983  | 1989180 | 0.0336 | 0.4447 |
| chr20 | 63025520  | 3055515 | 0.0485 | 0.2515 |
| chr21 | 48129895  | 1540945 | 0.032  | 0.2299 |
| chr22 | 51304566  | 1516270 | 0.0296 | 0.1913 |
| chrMT | 16571     | 9082    | 0.5481 | 0.809  |
| chrX  | 155270560 | 6671421 | 0.043  | 0.271  |
| chrY  | 59373566  | 330363  | 0.0056 | 0.1347 |

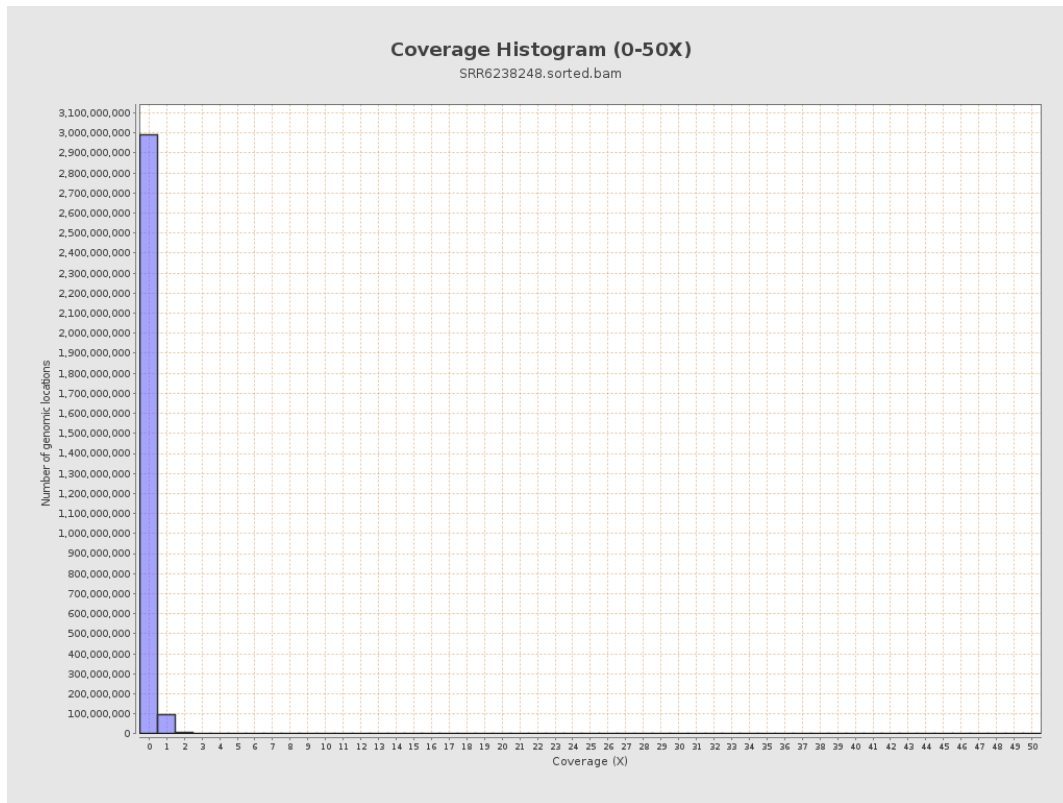
### 3. Results : Coverage across reference



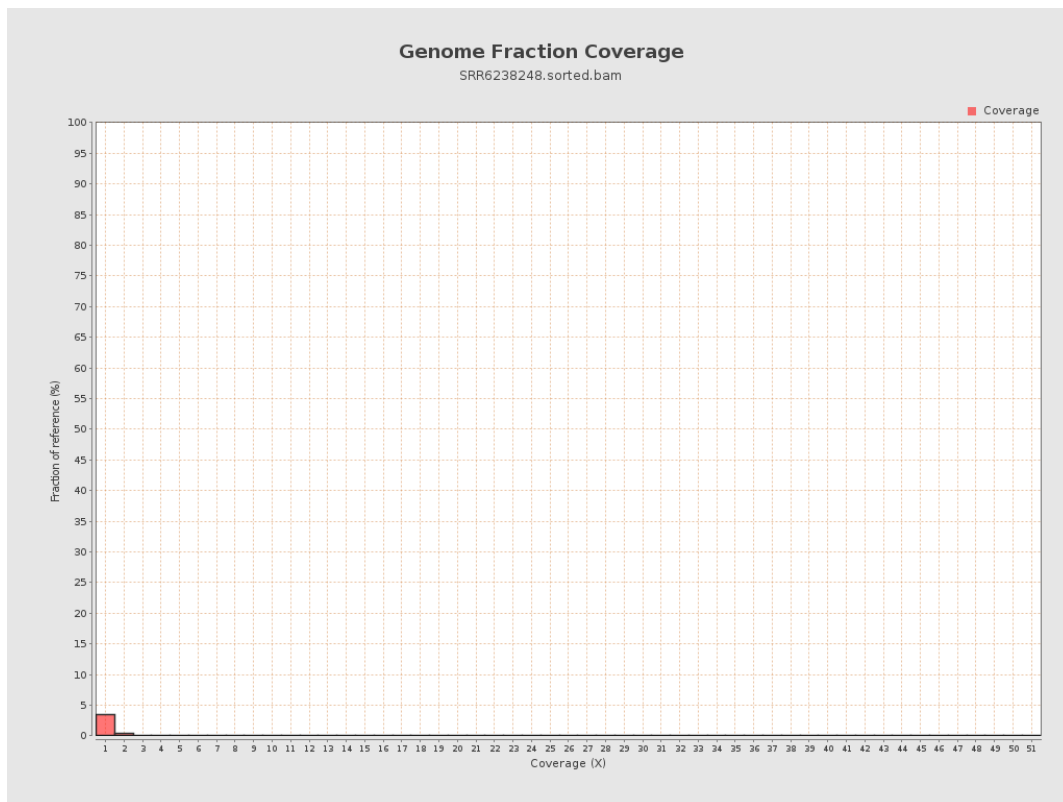
## 4. Results : Coverage Histogram



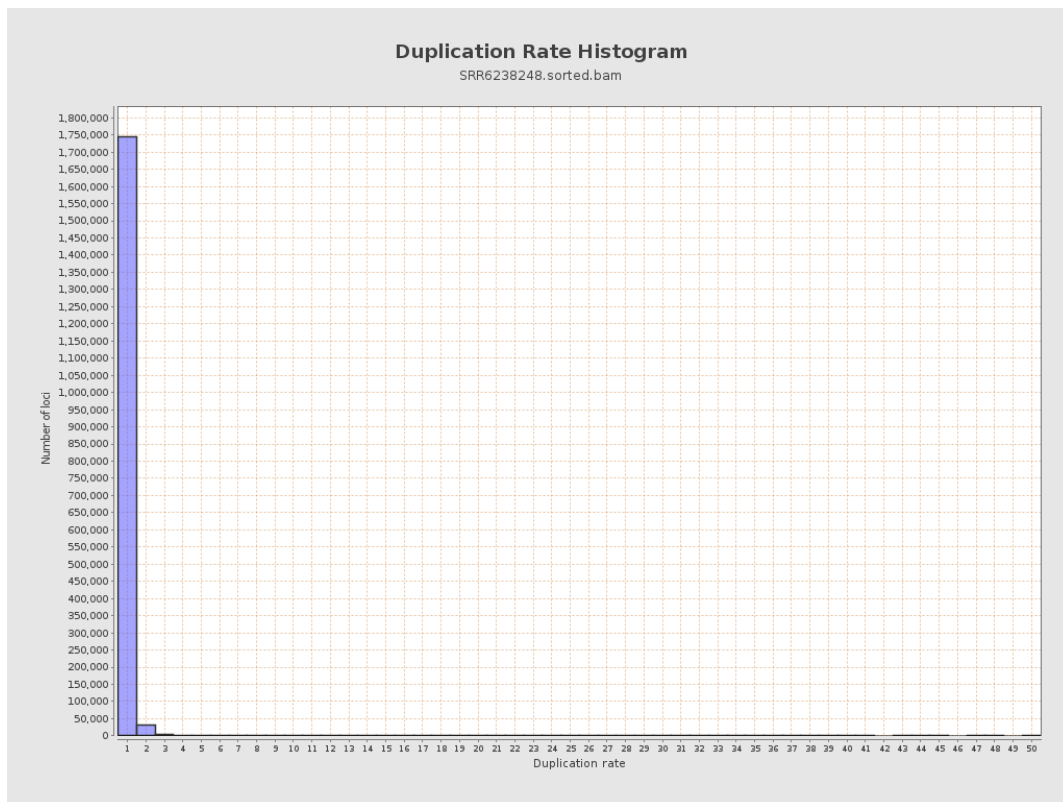
## 5. Results : Coverage Histogram (0-50X)



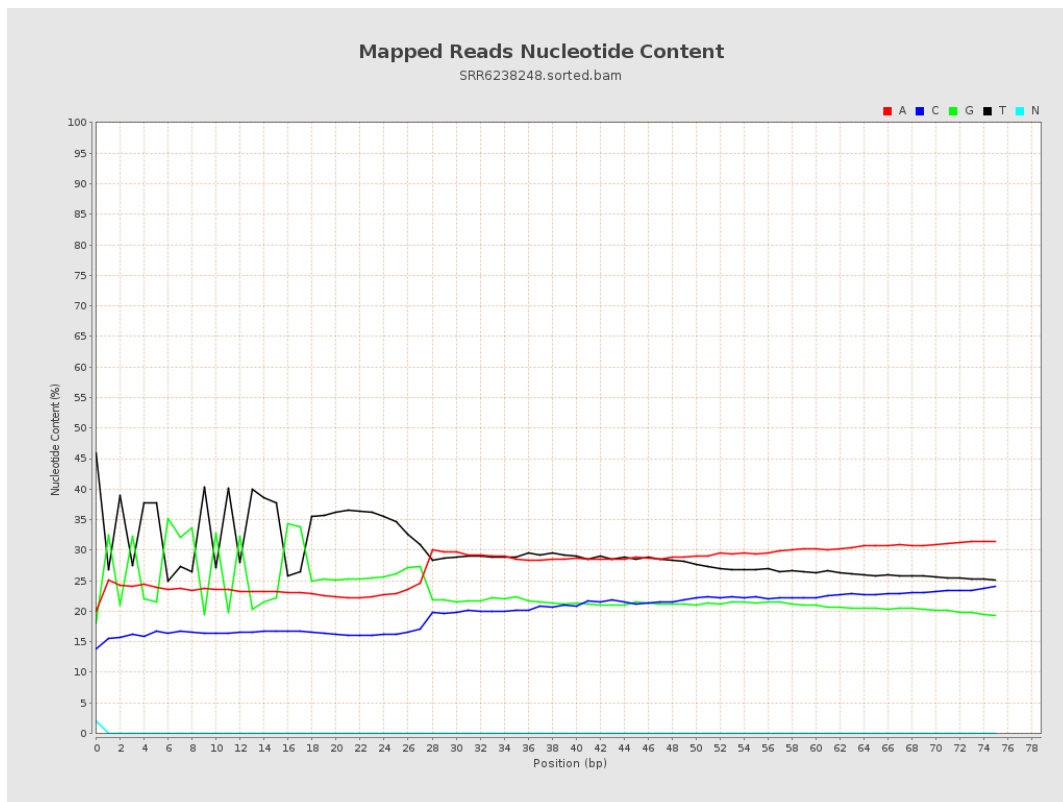
## 6. Results : Genome Fraction Coverage



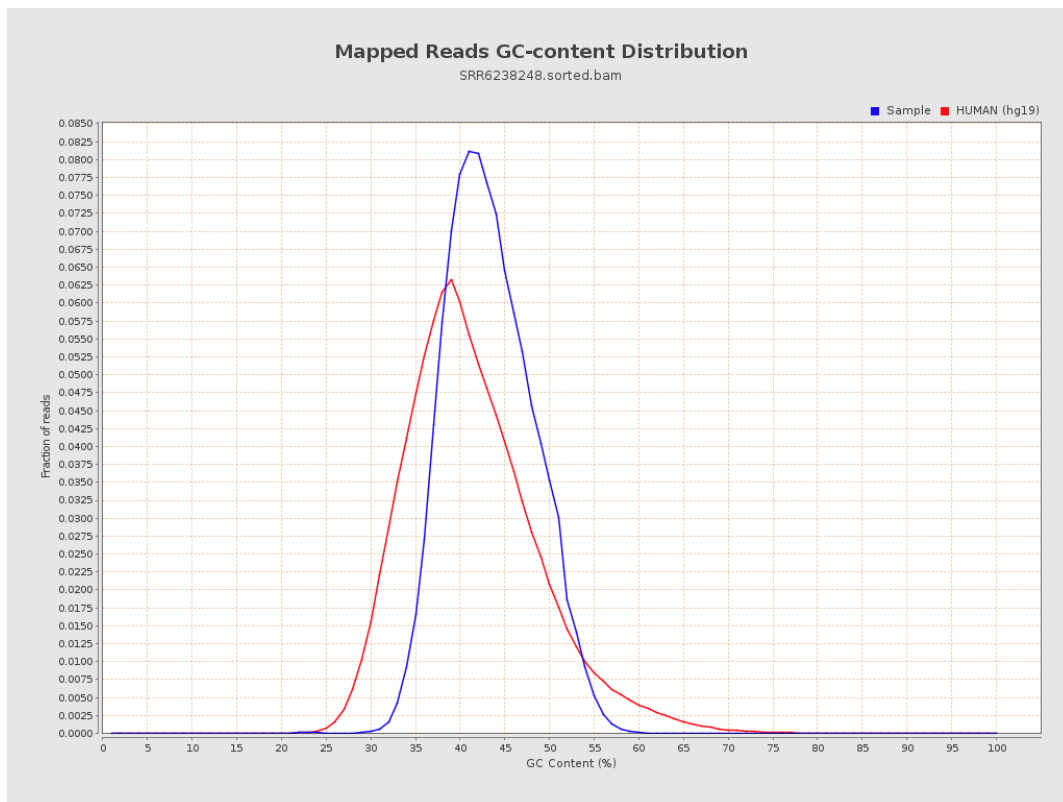
## 7. Results : Duplication Rate Histogram



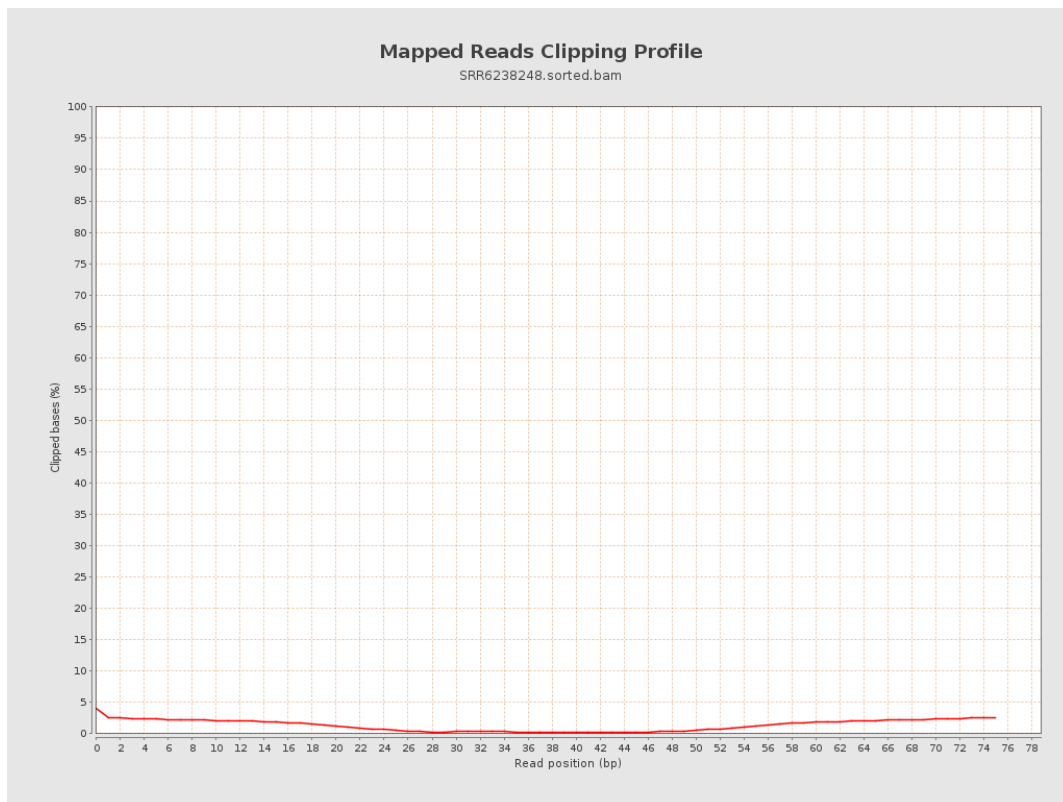
## 8. Results : Mapped Reads Nucleotide Content



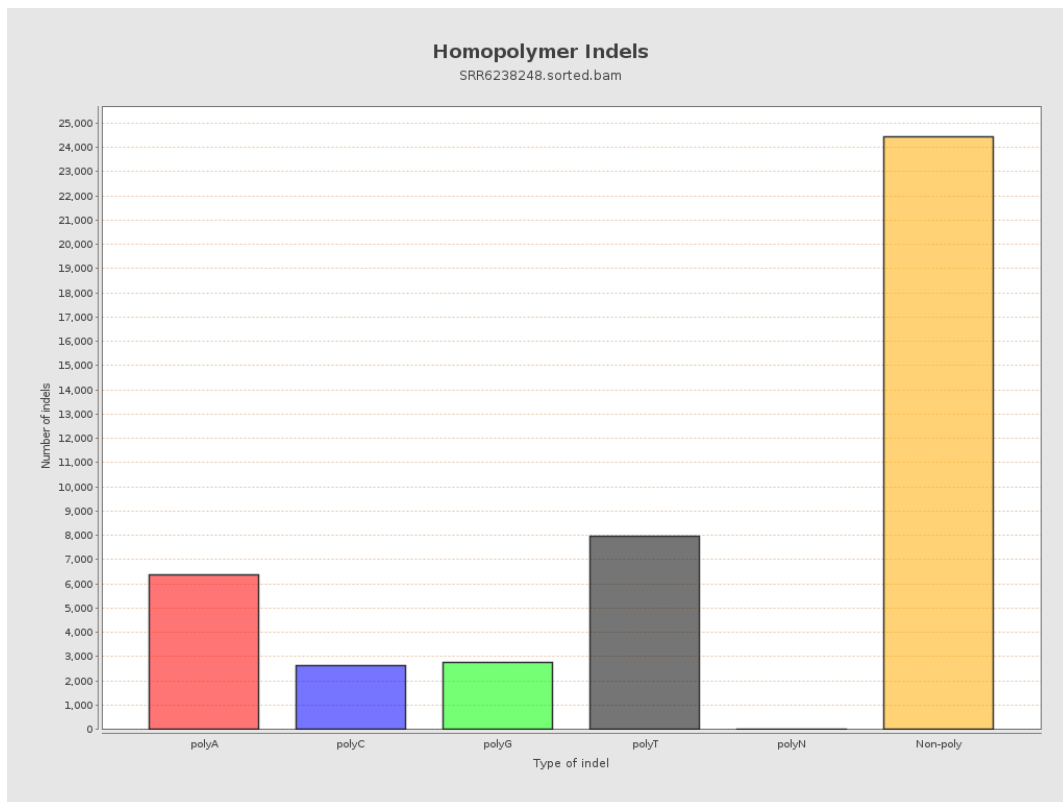
## 9. Results : Mapped Reads GC-content Distribution



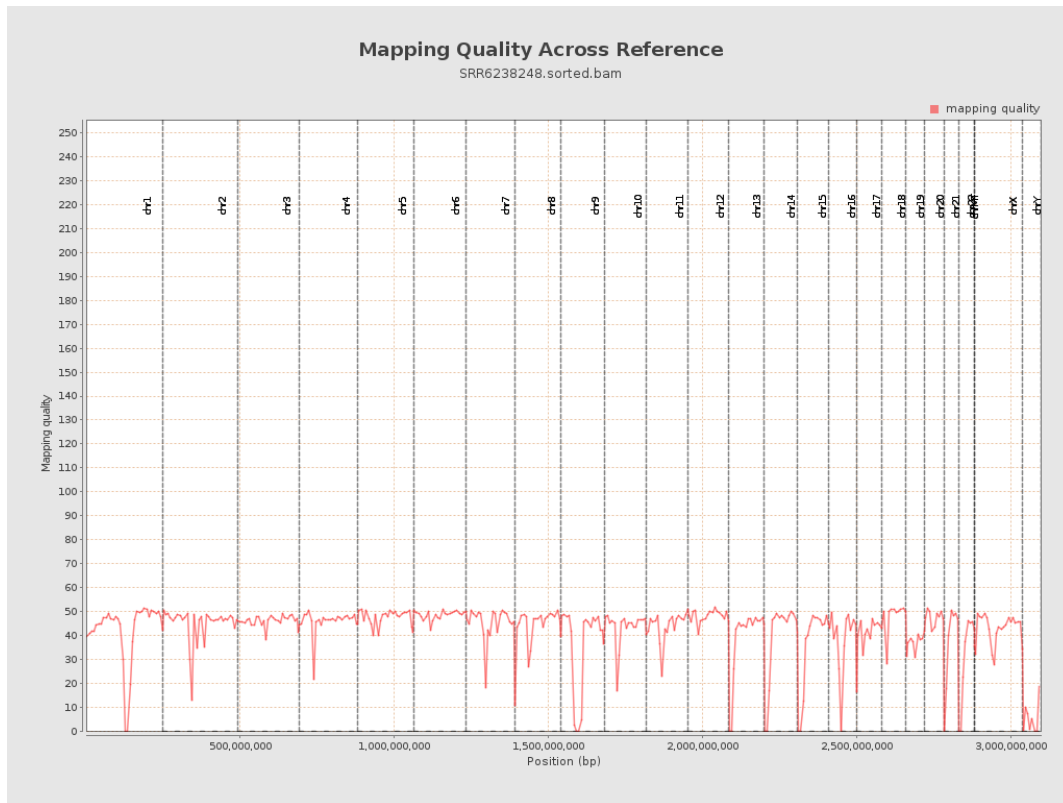
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

