

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/18 08:54:20*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240258.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_SRR6240258 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240258.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Wed Sep 18 08:54:19 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6240258.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 1,578,306          |
| Mapped reads                 | 1,181,789 / 74.88% |
| Unmapped reads               | 396,517 / 25.12%   |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 4,413 / 0.28%      |
| Read min/max/mean length     | 30 / 76 / 76.09    |
| Duplicated reads (estimated) | 81,330 / 5.15%     |
| Duplication rate             | 5.12%              |
| Clipped reads                | 865,112 / 54.81%   |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 18,952,691 / 26.87% |
| Number/percentage of C's | 11,793,111 / 16.72% |
| Number/percentage of T's | 22,256,413 / 31.55% |
| Number/percentage of G's | 17,517,638 / 24.84% |
| Number/percentage of N's | 15,482 / 0.02%      |
| GC Percentage            | 41.55%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0228 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.2715 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 41.84 |
|----------------------|-------|

## 2.5. Mismatches and indels

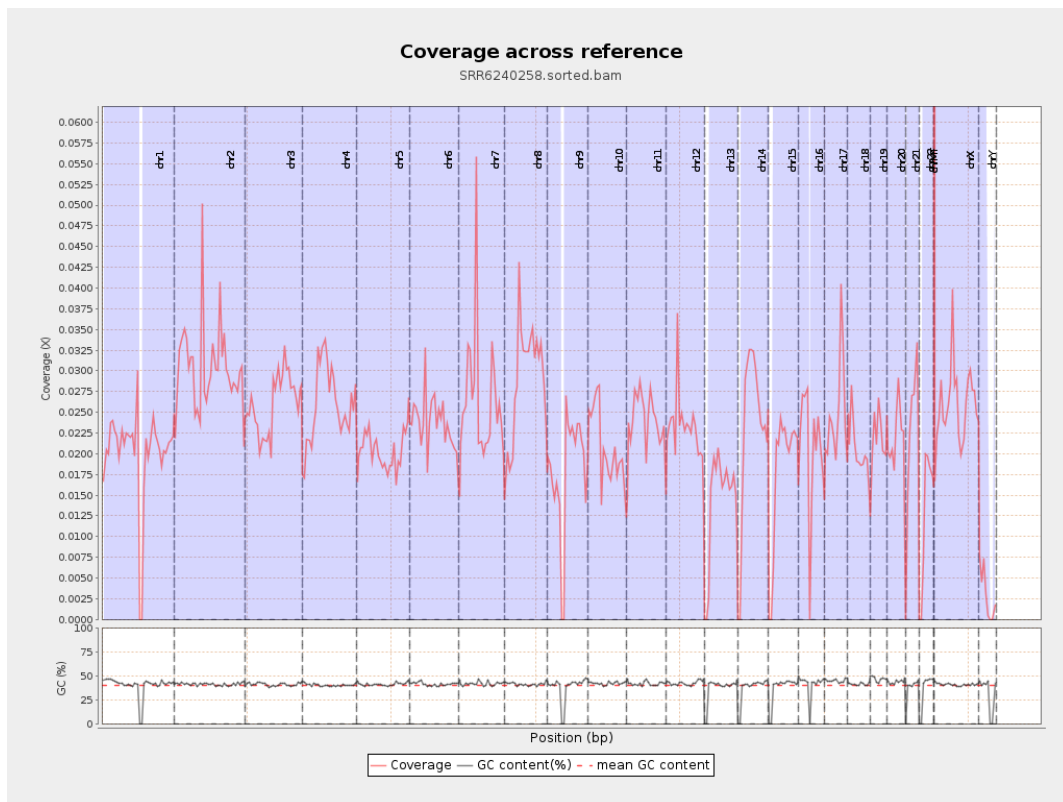
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 1.09%   |
| Mismatches                               | 761,304 |
| Insertions                               | 5,305   |
| Mapped reads with at least one insertion | 0.45%   |
| Deletions                                | 25,066  |
| Mapped reads with at least one deletion  | 2.09%   |
| Homopolymer indels                       | 49.82%  |

## 2.6. Chromosome stats

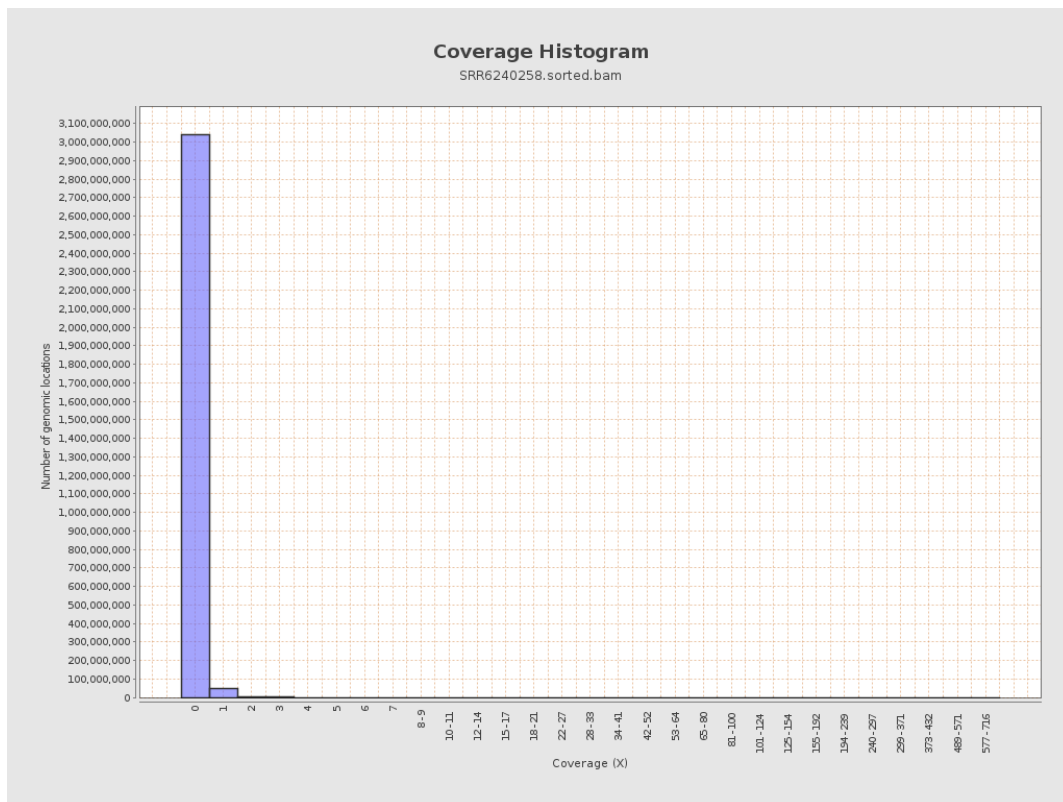
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 5021985      | 0.0201        | 0.3096             |
| chr2 | 243199373 | 7385939      | 0.0304        | 0.3408             |
| chr3 | 198022430 | 5153712      | 0.026         | 0.2018             |
| chr4 | 191154276 | 4959001      | 0.0259        | 0.2114             |
| chr5 | 180915260 | 3689606      | 0.0204        | 0.178              |
| chr6 | 171115067 | 4048071      | 0.0237        | 0.223              |
| chr7 | 159138663 | 4190133      | 0.0263        | 0.6014             |
|      |           |              |               |                    |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr8  | 146364022 | 4274583 | 0.0292 | 0.3052 |
| chr9  | 141213431 | 2512189 | 0.0178 | 0.239  |
| chr10 | 135534747 | 2806438 | 0.0207 | 0.2082 |
| chr11 | 135006516 | 3261340 | 0.0242 | 0.2576 |
| chr12 | 133851895 | 3115837 | 0.0233 | 0.1878 |
| chr13 | 115169878 | 1649874 | 0.0143 | 0.1455 |
| chr14 | 107349540 | 2501205 | 0.0233 | 0.199  |
| chr15 | 102531392 | 1825827 | 0.0178 | 0.2054 |
| chr16 | 90354753  | 1845575 | 0.0204 | 0.1764 |
| chr17 | 81195210  | 2028958 | 0.025  | 0.2073 |
| chr18 | 78077248  | 1595858 | 0.0204 | 0.3799 |
| chr19 | 59128983  | 1304410 | 0.0221 | 0.2571 |
| chr20 | 63025520  | 1369623 | 0.0217 | 0.1936 |
| chr21 | 48129895  | 1086971 | 0.0226 | 0.1882 |
| chr22 | 51304566  | 670755  | 0.0131 | 0.1377 |
| chrMT | 16571     | 51513   | 3.1086 | 4.3093 |
| chrX  | 155270560 | 4055806 | 0.0261 | 0.2269 |
| chrY  | 59373566  | 173130  | 0.0029 | 0.0675 |

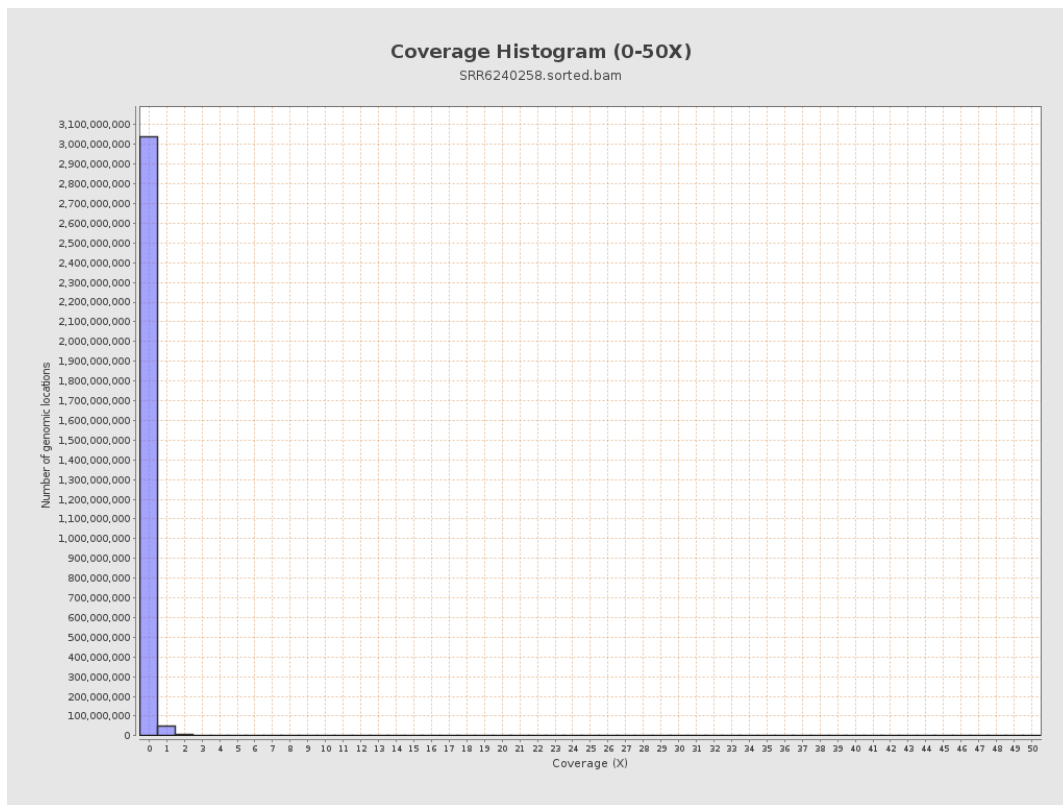
### 3. Results : Coverage across reference



## 4. Results : Coverage Histogram

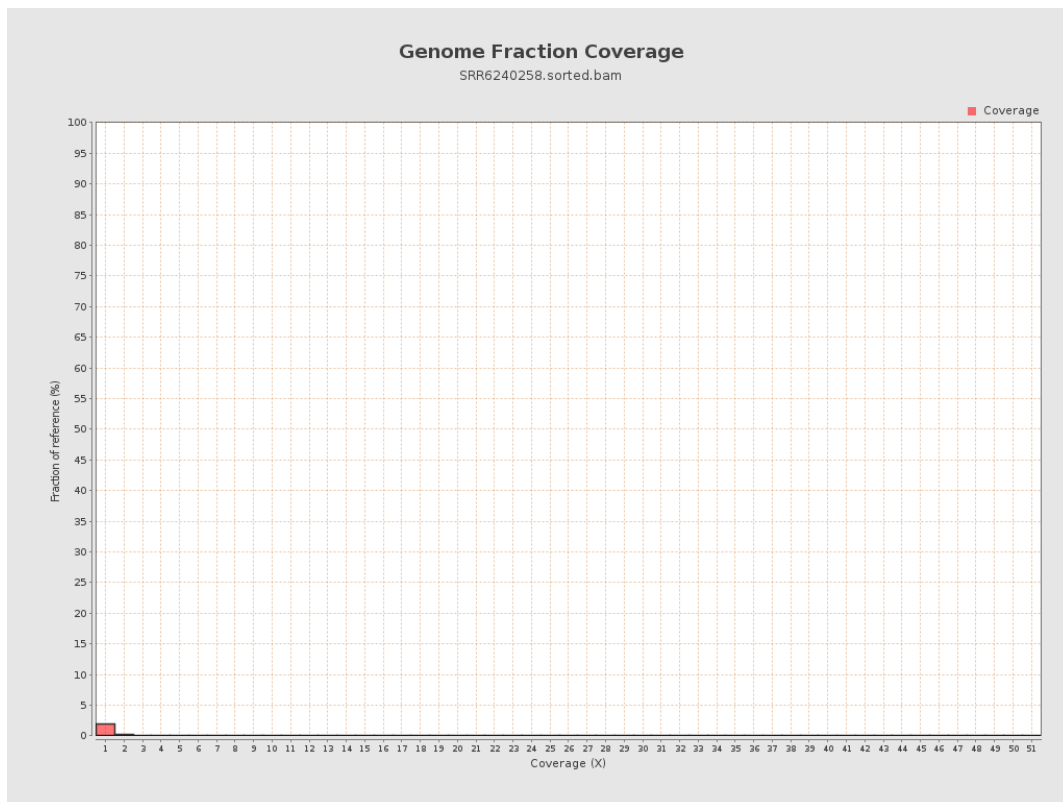


## 5. Results : Coverage Histogram (0-50X)

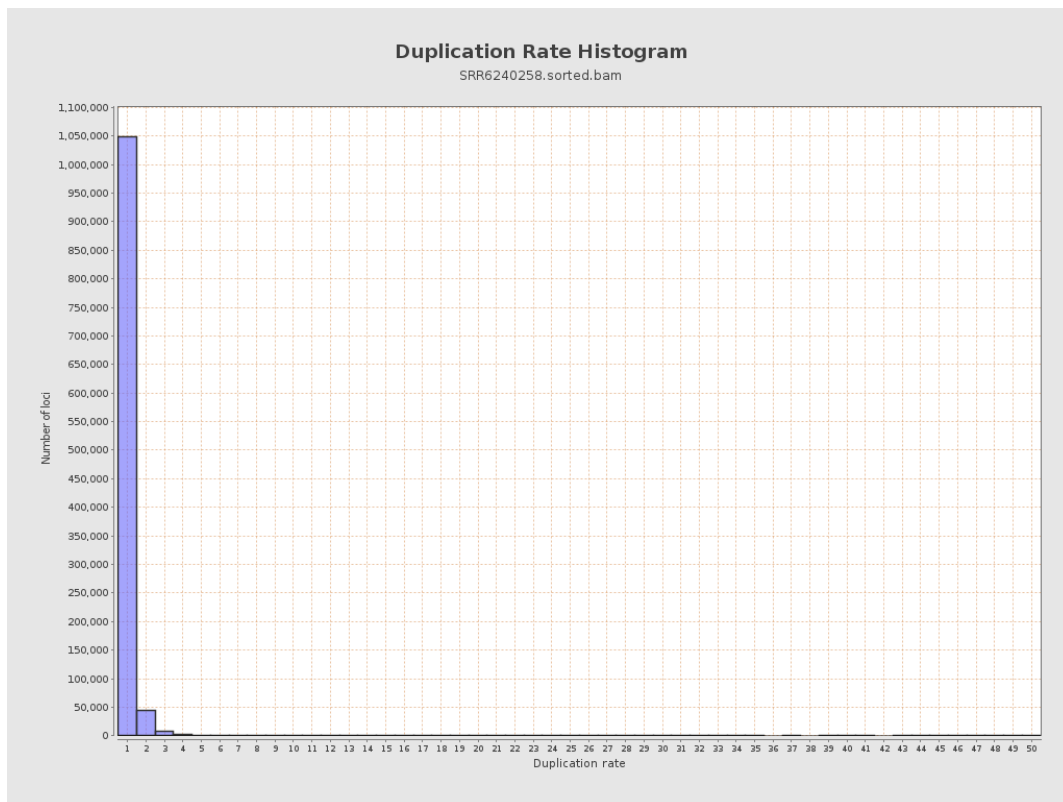




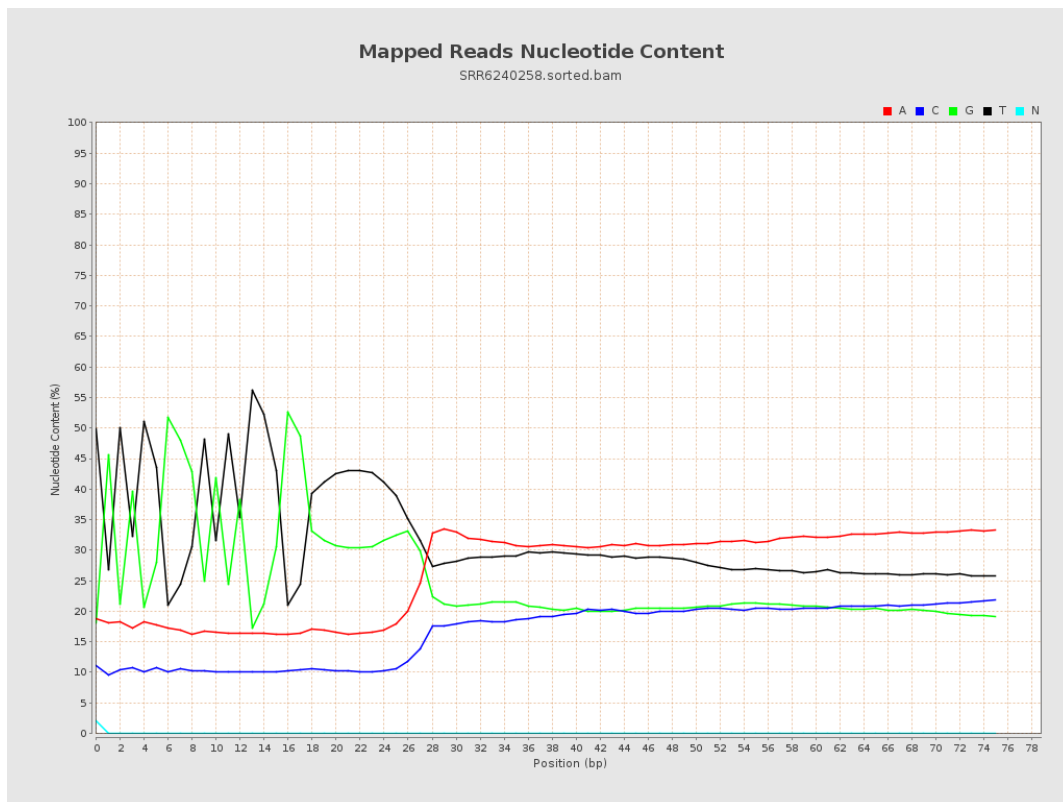
## 6. Results : Genome Fraction Coverage



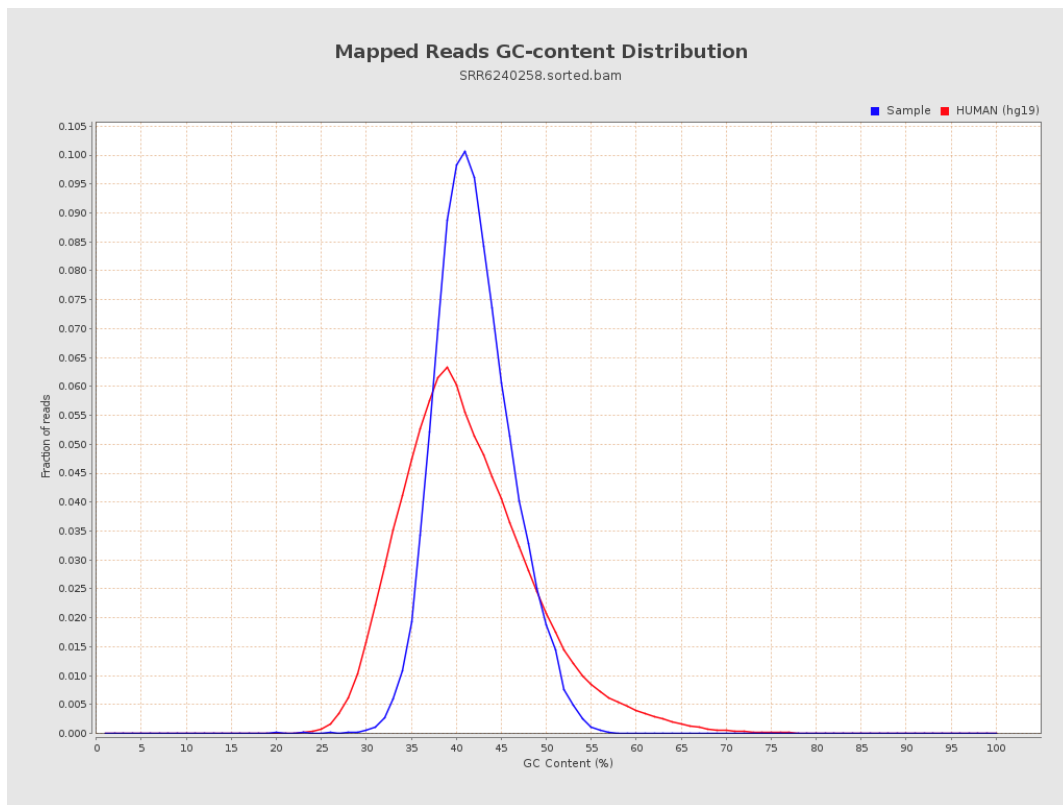
## 7. Results : Duplication Rate Histogram



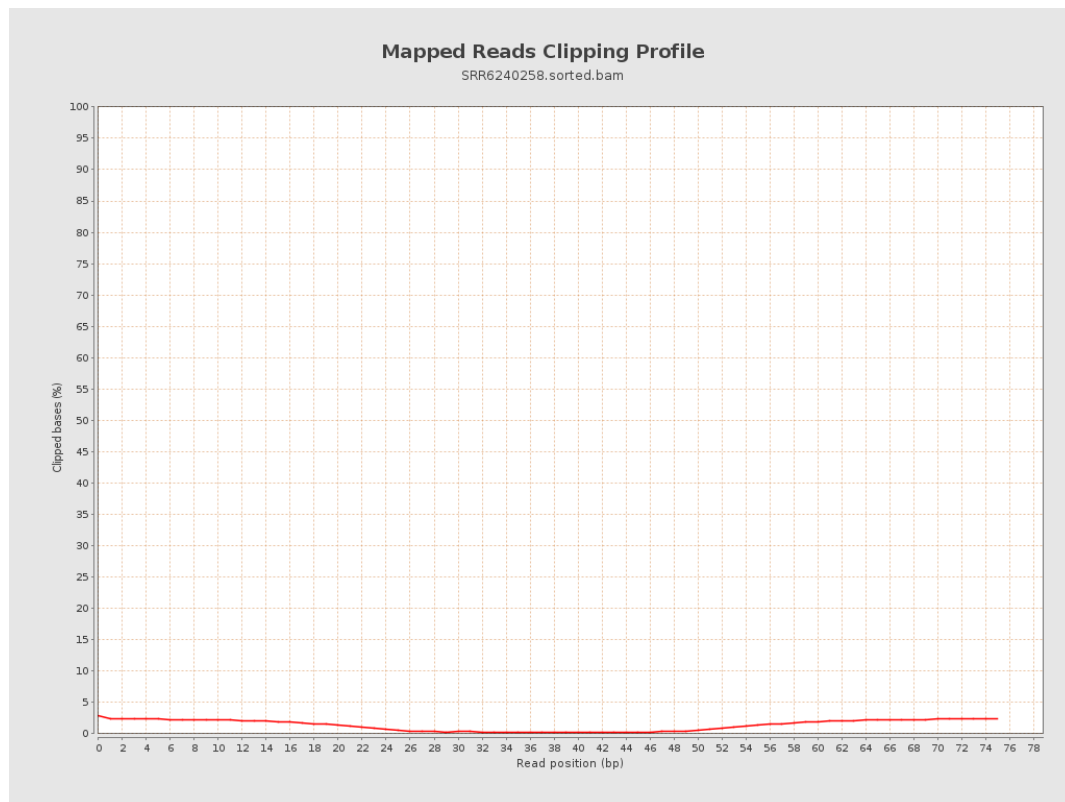
## 8. Results : Mapped Reads Nucleotide Content



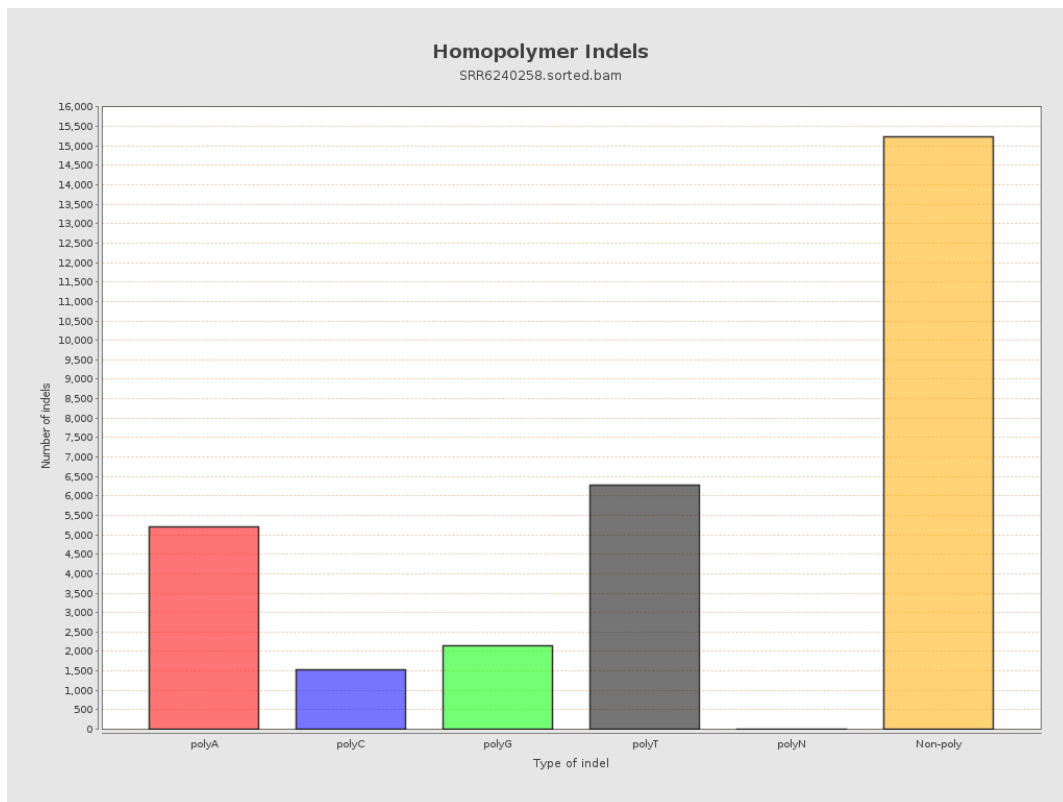
## 9. Results : Mapped Reads GC-content Distribution



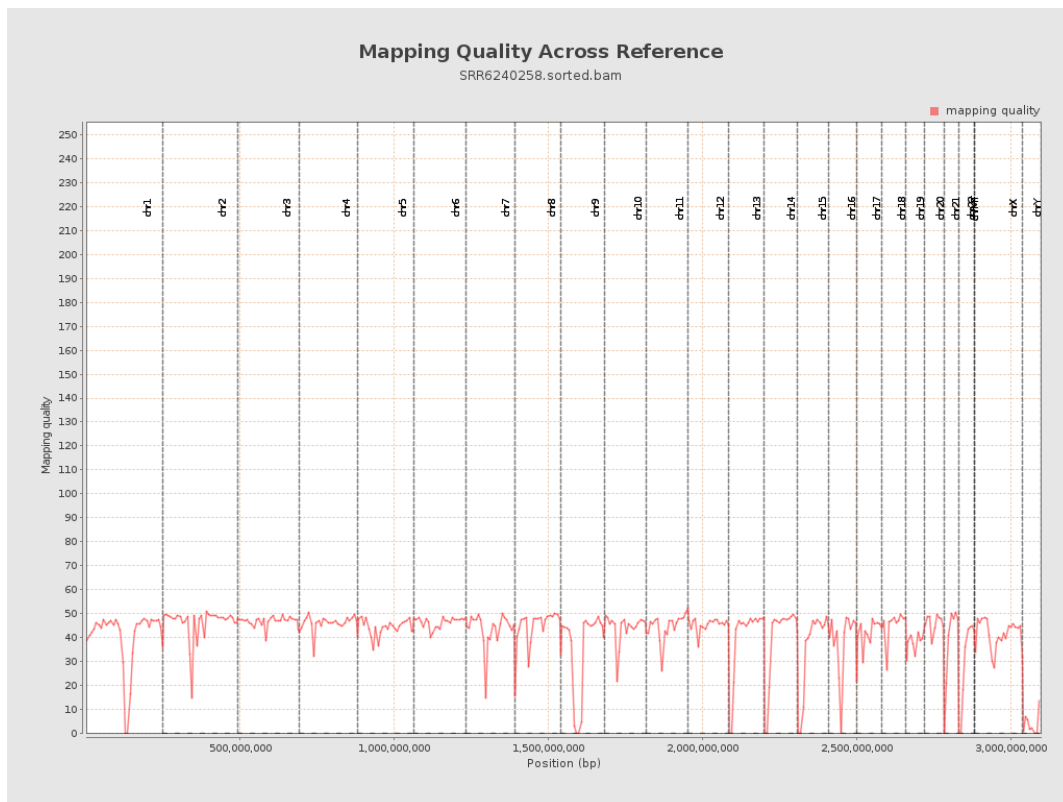
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

