

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/16 04:54:41*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231812.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_SRR6231812 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231812.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Mon Sep 16 04:54:41 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6231812.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 5,196,734          |
| Mapped reads                 | 4,886,656 / 94.03% |
| Unmapped reads               | 310,078 / 5.97%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 31,591 / 0.61%     |
| Read min/max/mean length     | 30 / 76 / 76.21    |
| Duplicated reads (estimated) | 547,355 / 10.53%   |
| Duplication rate             | 9.49%              |
| Clipped reads                | 2,543,884 / 48.95% |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 83,934,182 / 26.47%  |
| Number/percentage of C's | 57,822,668 / 18.23%  |
| Number/percentage of T's | 102,247,916 / 32.24% |
| Number/percentage of G's | 73,003,991 / 23.02%  |
| Number/percentage of N's | 124,740 / 0.04%      |
| GC Percentage            | 41.25%               |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.1025 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.9161 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 44.72 |
|----------------------|-------|

## 2.5. Mismatches and indels

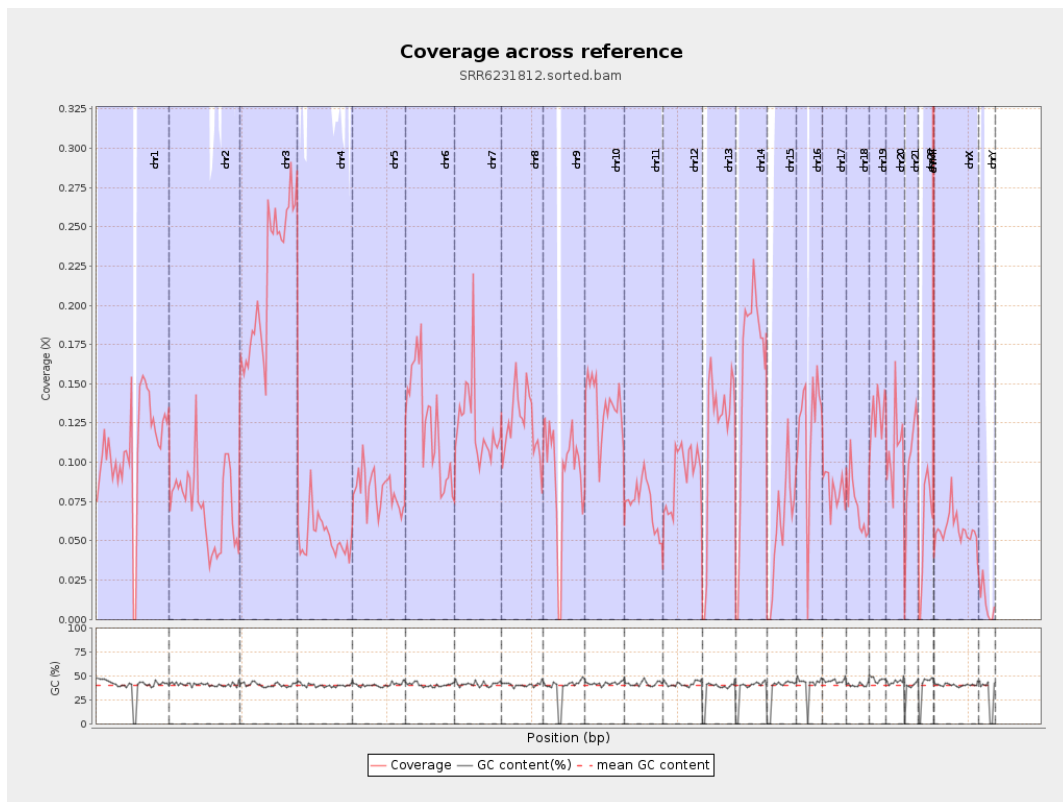
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.62%     |
| Mismatches                               | 1,939,407 |
| Insertions                               | 22,286    |
| Mapped reads with at least one insertion | 0.45%     |
| Deletions                                | 68,590    |
| Mapped reads with at least one deletion  | 1.39%     |
| Homopolymer indels                       | 44.89%    |

## 2.6. Chromosome stats

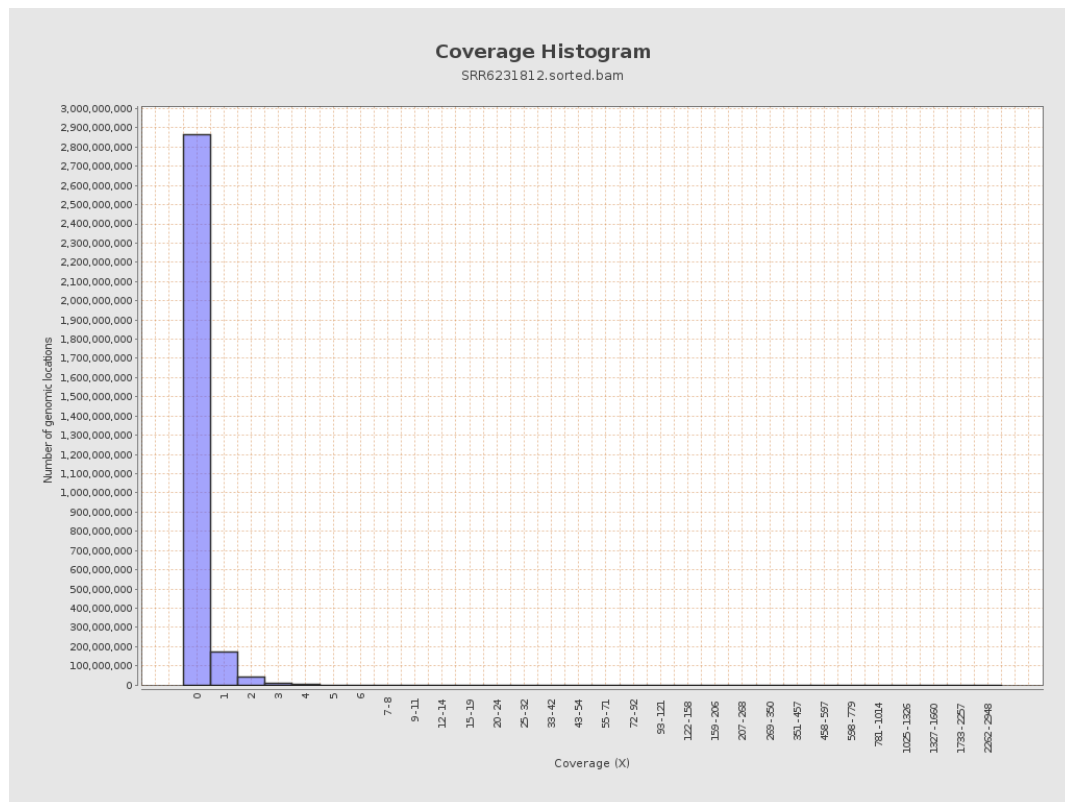
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 27095331     | 0.1087        | 1.4168             |
| chr2 | 243199373 | 17582995     | 0.0723        | 1.4025             |
| chr3 | 198022430 | 42691717     | 0.2156        | 0.6236             |
| chr4 | 191154276 | 10040462     | 0.0525        | 0.3928             |
| chr5 | 180915260 | 14781473     | 0.0817        | 0.3799             |
| chr6 | 171115067 | 21219559     | 0.124         | 0.7115             |
| chr7 | 159138663 | 19677581     | 0.1237        | 1.6296             |
|      |           |              |               |                    |

|       |           |          |         |         |
|-------|-----------|----------|---------|---------|
| chr8  | 146364022 | 18111661 | 0.1237  | 1.4614  |
| chr9  | 141213431 | 13045339 | 0.0924  | 0.623   |
| chr10 | 135534747 | 18490747 | 0.1364  | 0.818   |
| chr11 | 135006516 | 9892113  | 0.0733  | 0.6501  |
| chr12 | 133851895 | 12365880 | 0.0924  | 0.4115  |
| chr13 | 115169878 | 13490830 | 0.1171  | 0.4908  |
| chr14 | 107349540 | 16890575 | 0.1573  | 0.5699  |
| chr15 | 102531392 | 6010955  | 0.0586  | 0.3984  |
| chr16 | 90354753  | 11174428 | 0.1237  | 0.5251  |
| chr17 | 81195210  | 6677918  | 0.0822  | 0.434   |
| chr18 | 78077248  | 5662145  | 0.0725  | 1.5831  |
| chr19 | 59128983  | 7765600  | 0.1313  | 0.9272  |
| chr20 | 63025520  | 6871540  | 0.109   | 0.4938  |
| chr21 | 48129895  | 4827962  | 0.1003  | 0.4384  |
| chr22 | 51304566  | 2963612  | 0.0578  | 0.303   |
| chrMT | 16571     | 378041   | 22.8134 | 13.9224 |
| chrX  | 155270560 | 8939031  | 0.0576  | 0.3976  |
| chrY  | 59373566  | 606037   | 0.0102  | 0.2134  |

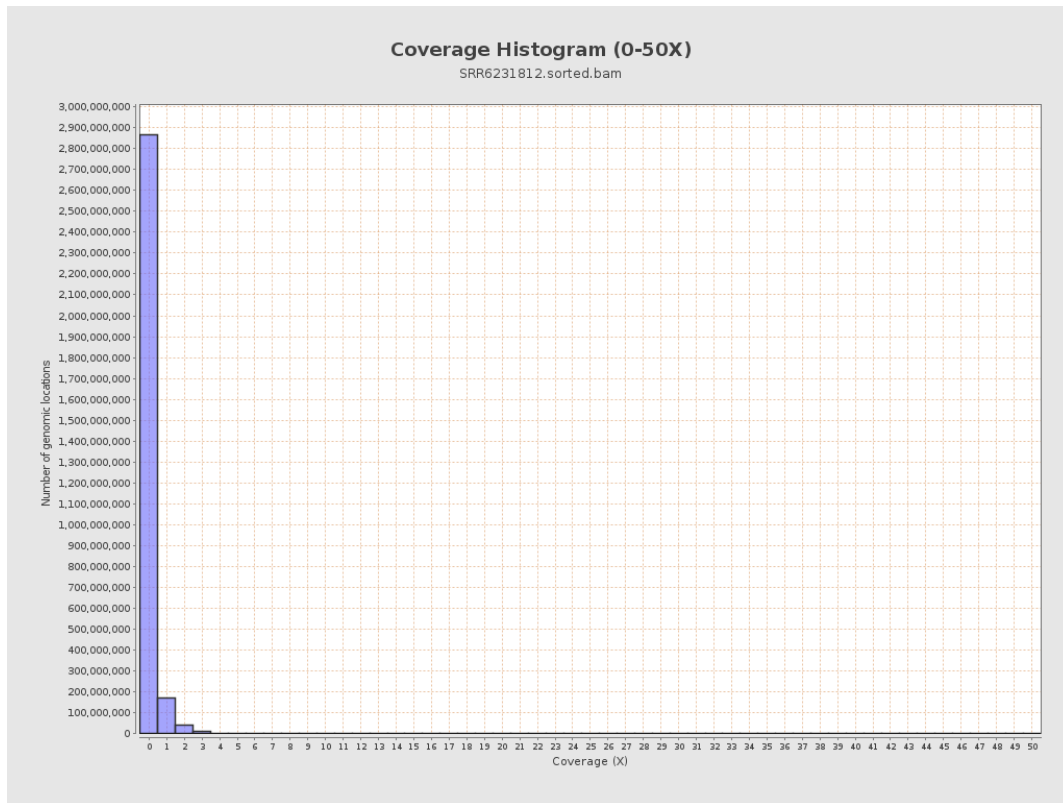
### 3. Results : Coverage across reference



## 4. Results : Coverage Histogram

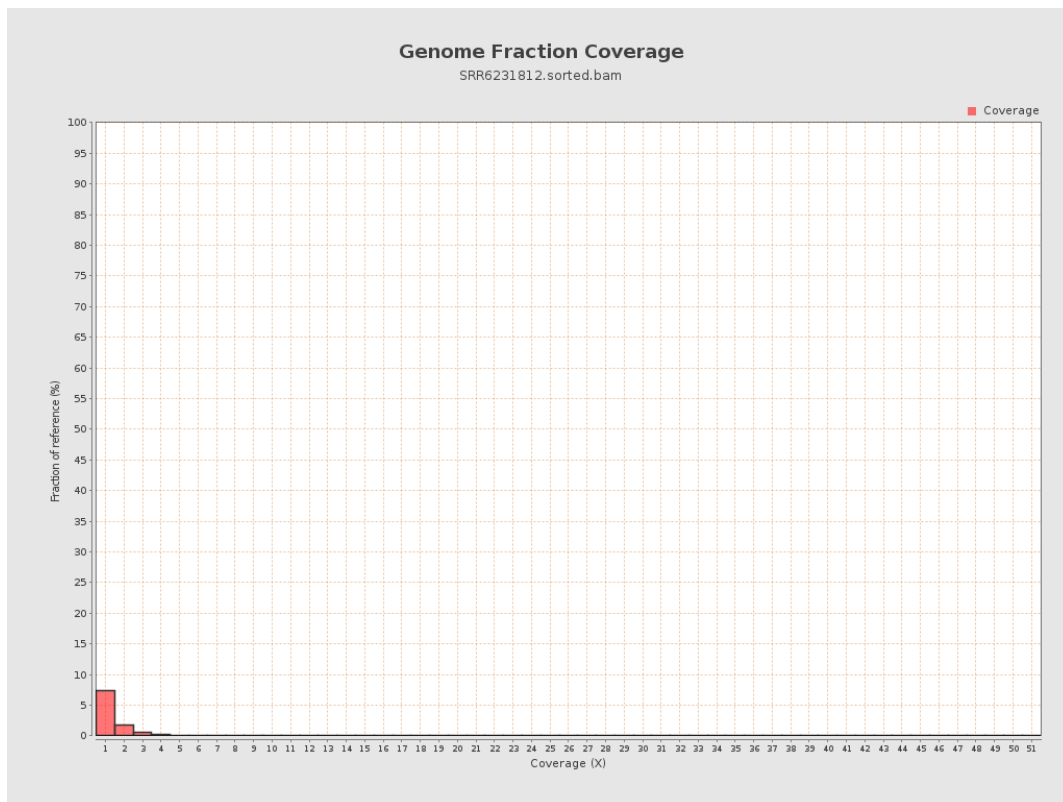


## 5. Results : Coverage Histogram (0-50X)

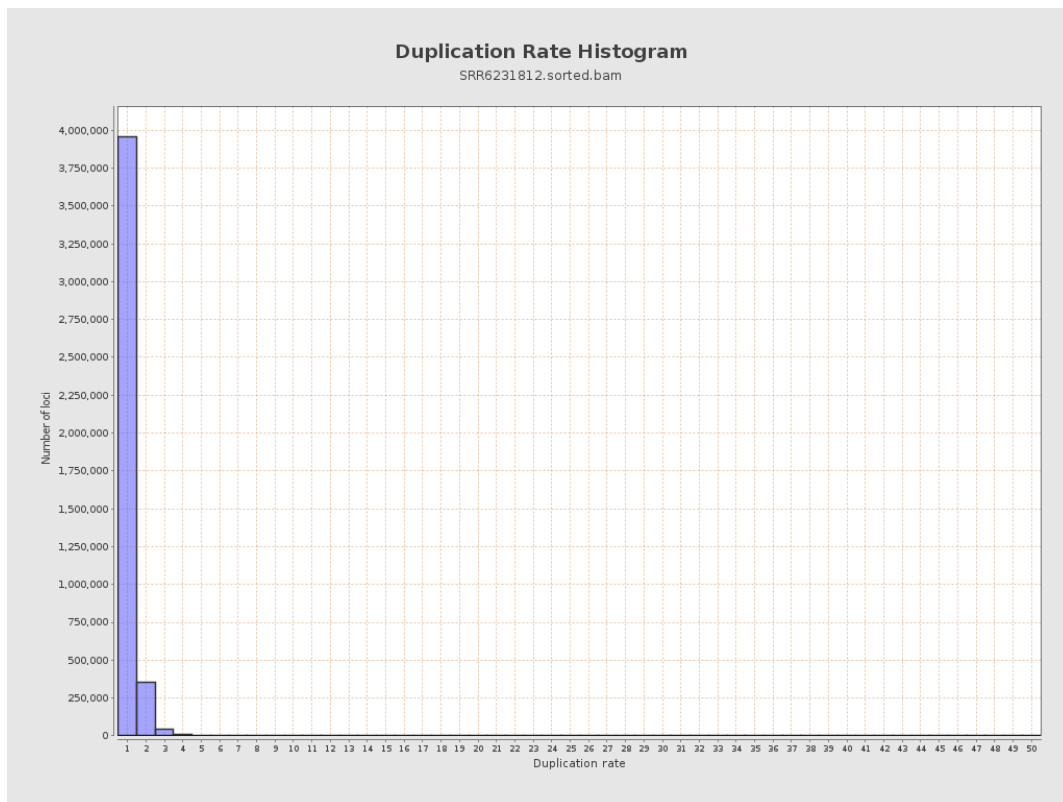




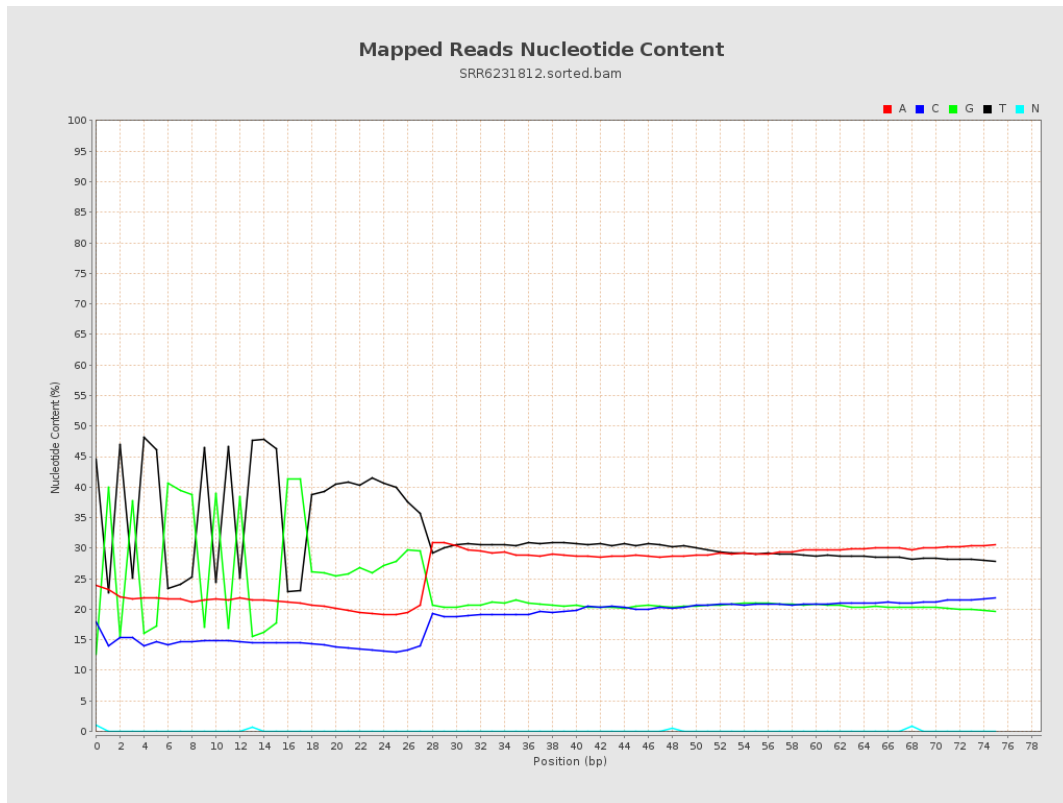
## 6. Results : Genome Fraction Coverage



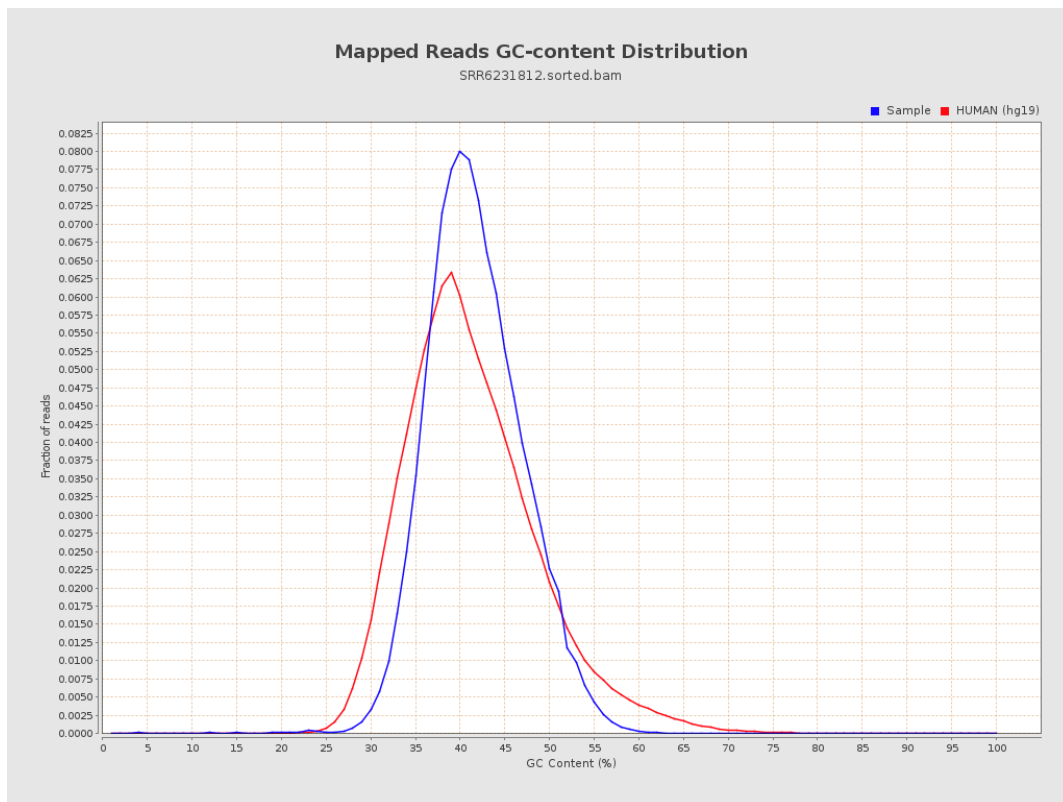
## 7. Results : Duplication Rate Histogram



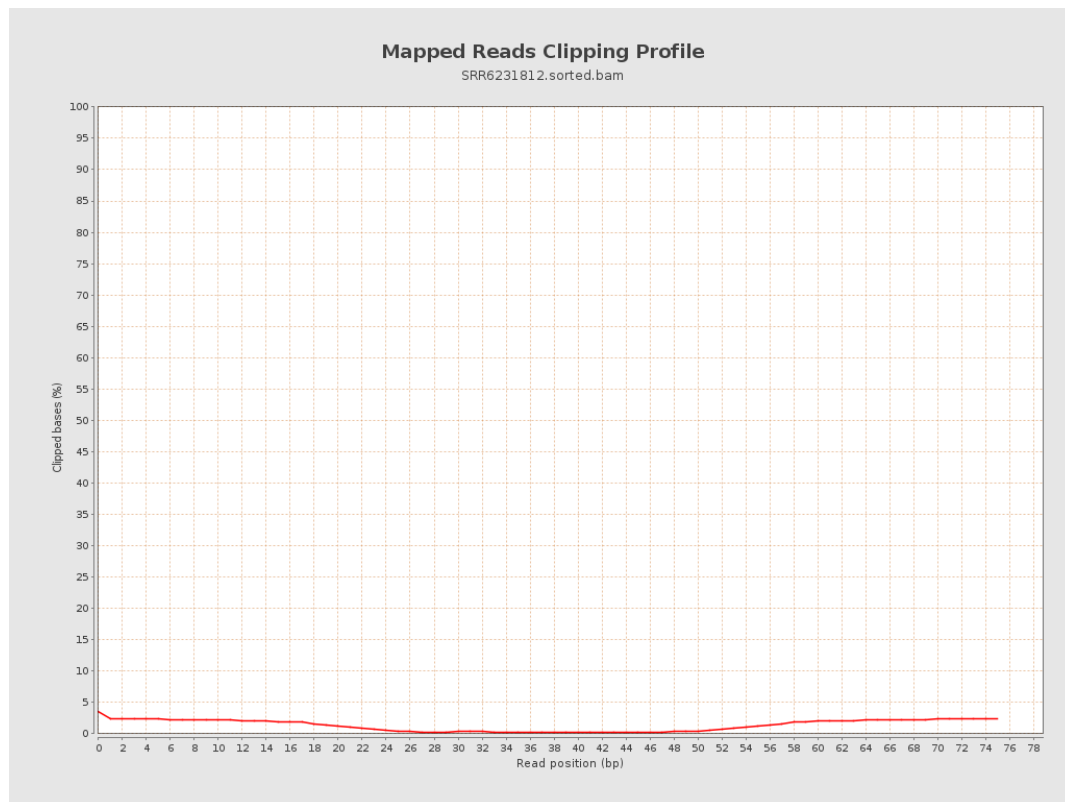
## 8. Results : Mapped Reads Nucleotide Content



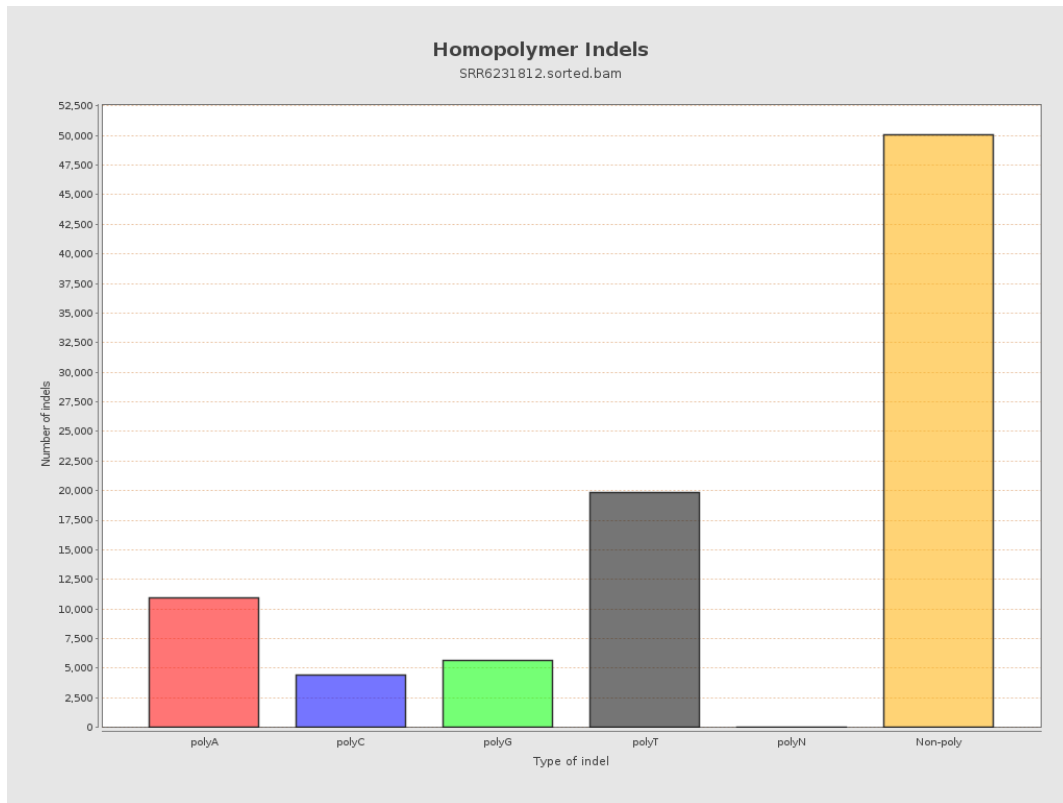
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

