

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/16 18:33:25*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234146.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_SRR6234146 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234146.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Mon Sep 16 18:33:24 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6234146.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                  |
|------------------------------|------------------|
| Reference size               | 3,095,693,983    |
| Number of reads              | 1,196,074        |
| Mapped reads                 | 689,528 / 57.65% |
| Unmapped reads               | 506,546 / 42.35% |
| Mapped paired reads          | 0 / 0%           |
| Secondary alignments         | 0                |
| Supplementary alignments     | 6,326 / 0.53%    |
| Read min/max/mean length     | 30 / 76 / 76.18  |
| Duplicated reads (estimated) | 40,508 / 3.39%   |
| Duplication rate             | 4.87%            |
| Clipped reads                | 391,295 / 32.71% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 12,189,705 / 27.99% |
| Number/percentage of C's | 7,210,885 / 16.56%  |
| Number/percentage of T's | 14,652,391 / 33.64% |
| Number/percentage of G's | 9,492,397 / 21.8%   |
| Number/percentage of N's | 6,576 / 0.02%       |
| GC Percentage            | 38.35%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0141 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.2037 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 45.66 |
|----------------------|-------|

## 2.5. Mismatches and indels

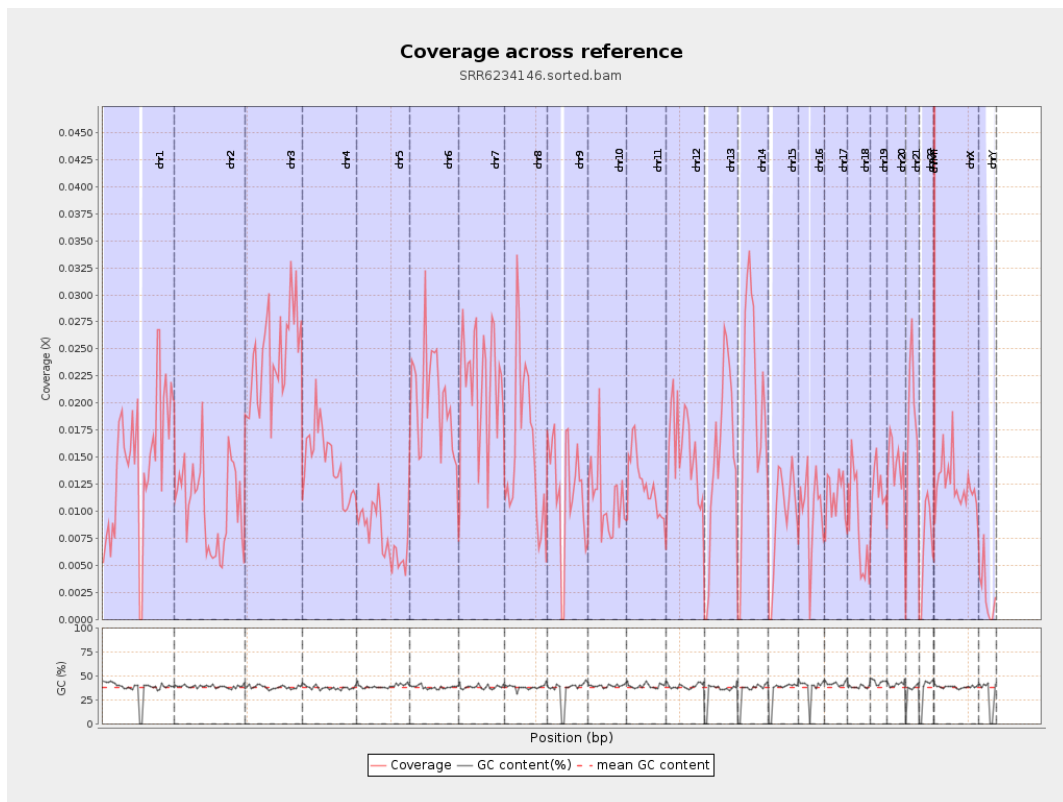
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 0.96%   |
| Mismatches                               | 410,842 |
| Insertions                               | 3,700   |
| Mapped reads with at least one insertion | 0.53%   |
| Deletions                                | 16,752  |
| Mapped reads with at least one deletion  | 2.39%   |
| Homopolymer indels                       | 43.06%  |

## 2.6. Chromosome stats

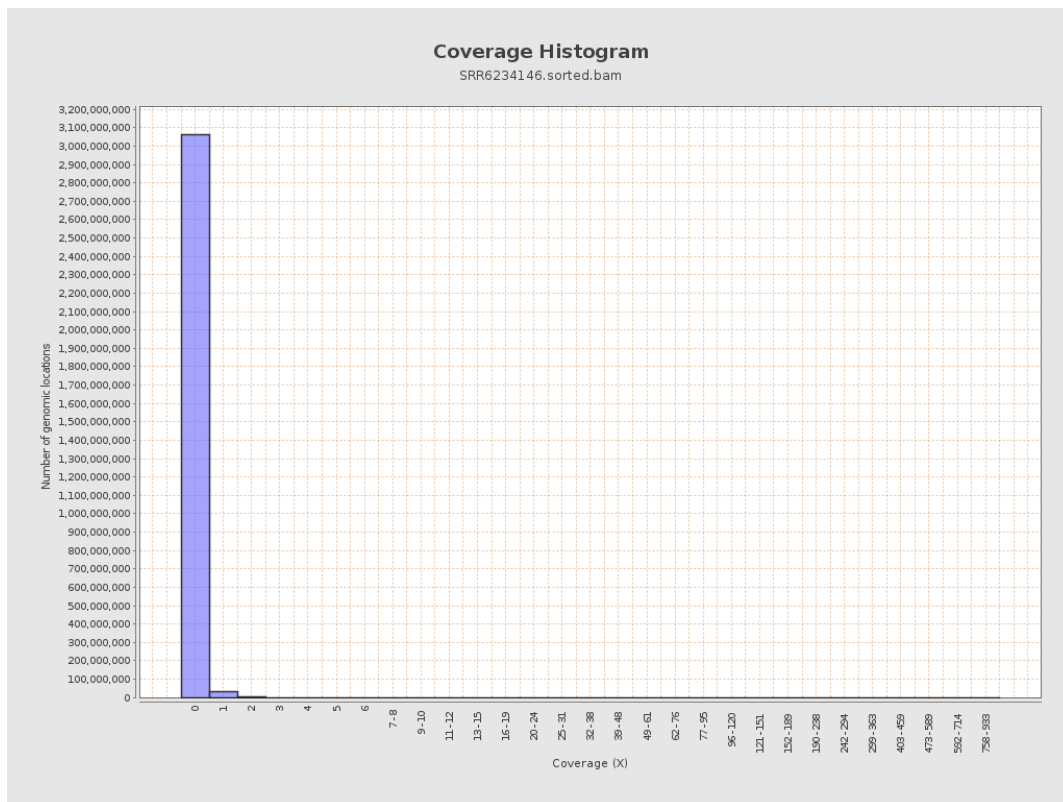
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 3619371      | 0.0145        | 0.2126             |
| chr2 | 243199373 | 2541936      | 0.0105        | 0.1511             |
| chr3 | 198022430 | 4830016      | 0.0244        | 0.1859             |
| chr4 | 191154276 | 2751554      | 0.0144        | 0.147              |
| chr5 | 180915260 | 1402713      | 0.0078        | 0.1043             |
| chr6 | 171115067 | 3445424      | 0.0201        | 0.1858             |
| chr7 | 159138663 | 3499789      | 0.022         | 0.2355             |
|      |           |              |               |                    |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr8  | 146364022 | 2307793 | 0.0158 | 0.5803 |
| chr9  | 141213431 | 1689244 | 0.012  | 0.1509 |
| chr10 | 135534747 | 1501784 | 0.0111 | 0.1545 |
| chr11 | 135006516 | 1685520 | 0.0125 | 0.1438 |
| chr12 | 133851895 | 2070164 | 0.0155 | 0.1481 |
| chr13 | 115169878 | 1725902 | 0.015  | 0.147  |
| chr14 | 107349540 | 2111897 | 0.0197 | 0.1682 |
| chr15 | 102531392 | 971713  | 0.0095 | 0.1148 |
| chr16 | 90354753  | 896611  | 0.0099 | 0.1251 |
| chr17 | 81195210  | 911201  | 0.0112 | 0.1299 |
| chr18 | 78077248  | 663349  | 0.0085 | 0.2537 |
| chr19 | 59128983  | 720650  | 0.0122 | 0.1561 |
| chr20 | 63025520  | 911024  | 0.0145 | 0.1412 |
| chr21 | 48129895  | 856102  | 0.0178 | 0.1617 |
| chr22 | 51304566  | 362255  | 0.0071 | 0.0968 |
| chrMT | 16571     | 28099   | 1.6957 | 1.9544 |
| chrX  | 155270560 | 1940602 | 0.0125 | 0.1371 |
| chrY  | 59373566  | 136888  | 0.0023 | 0.065  |

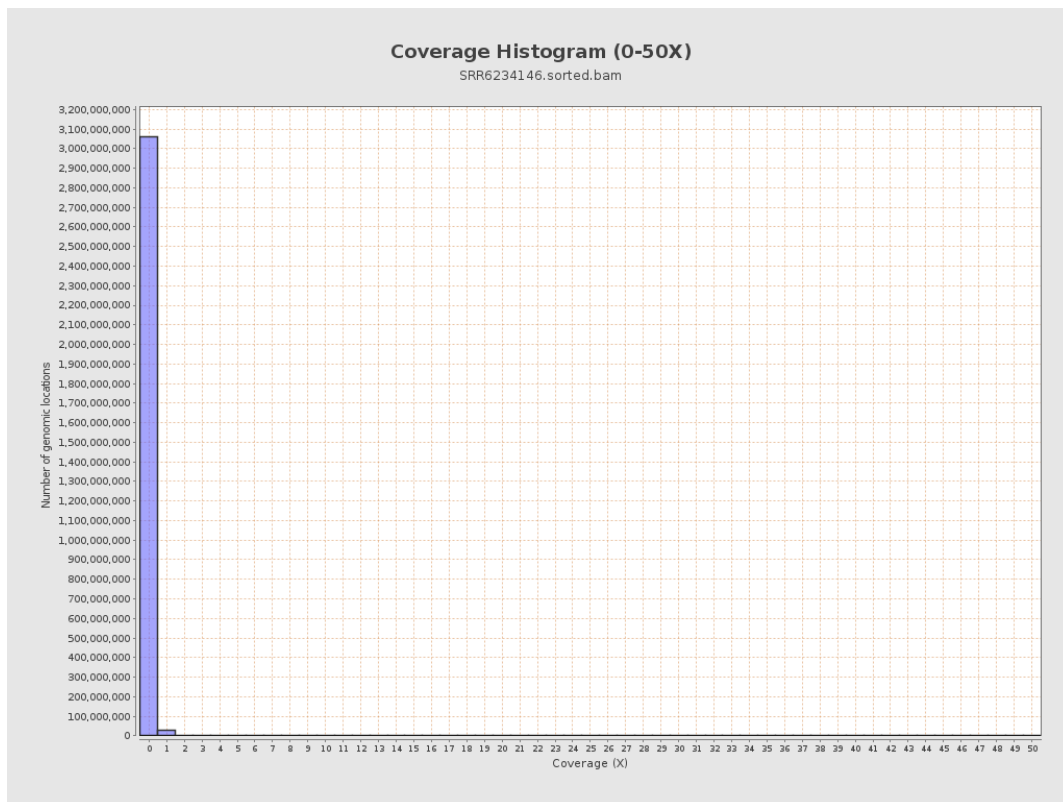
### 3. Results : Coverage across reference



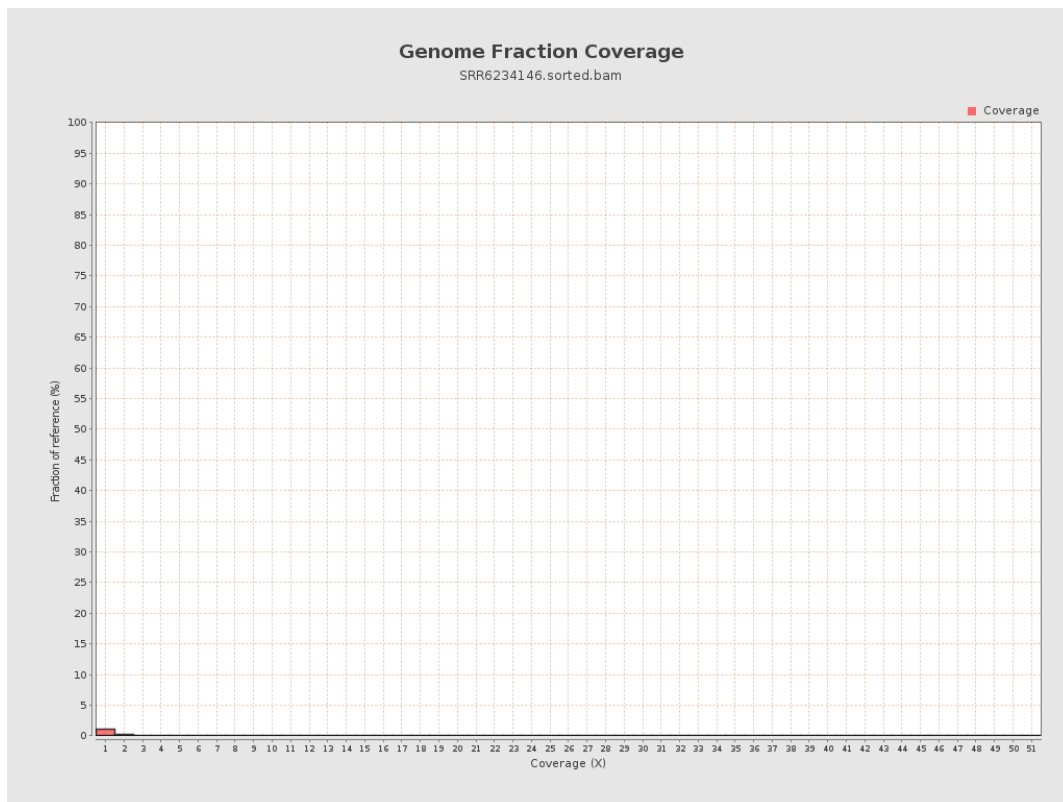
## 4. Results : Coverage Histogram



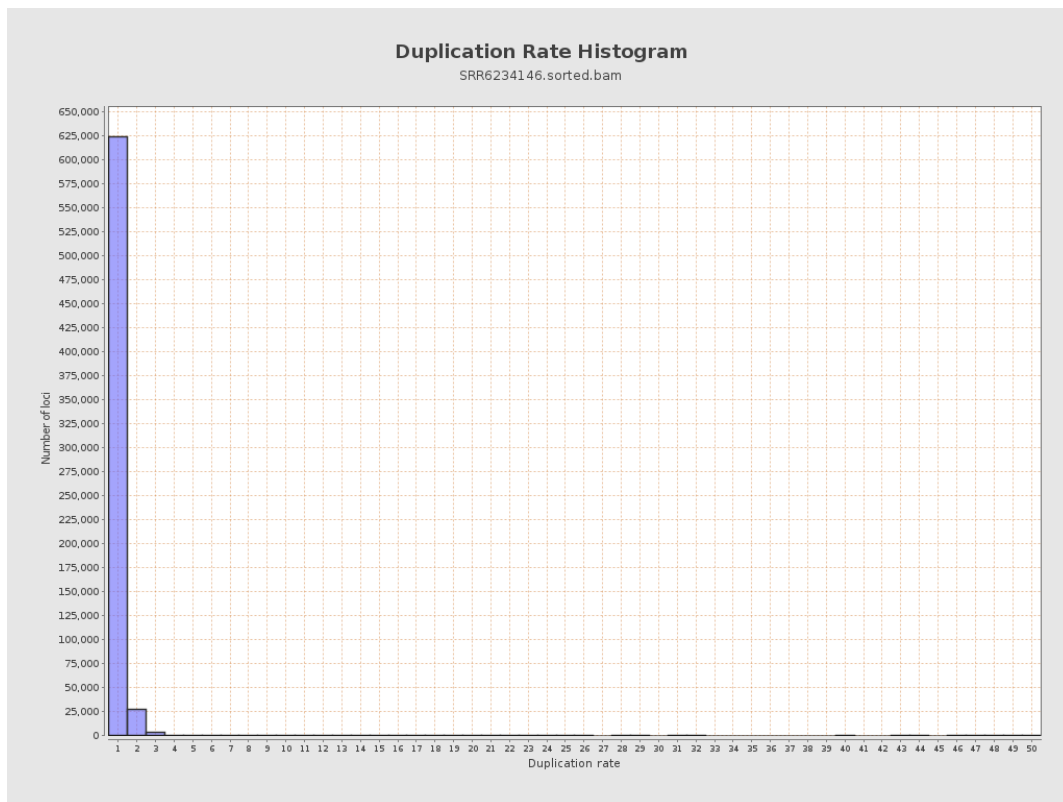
## 5. Results : Coverage Histogram (0-50X)



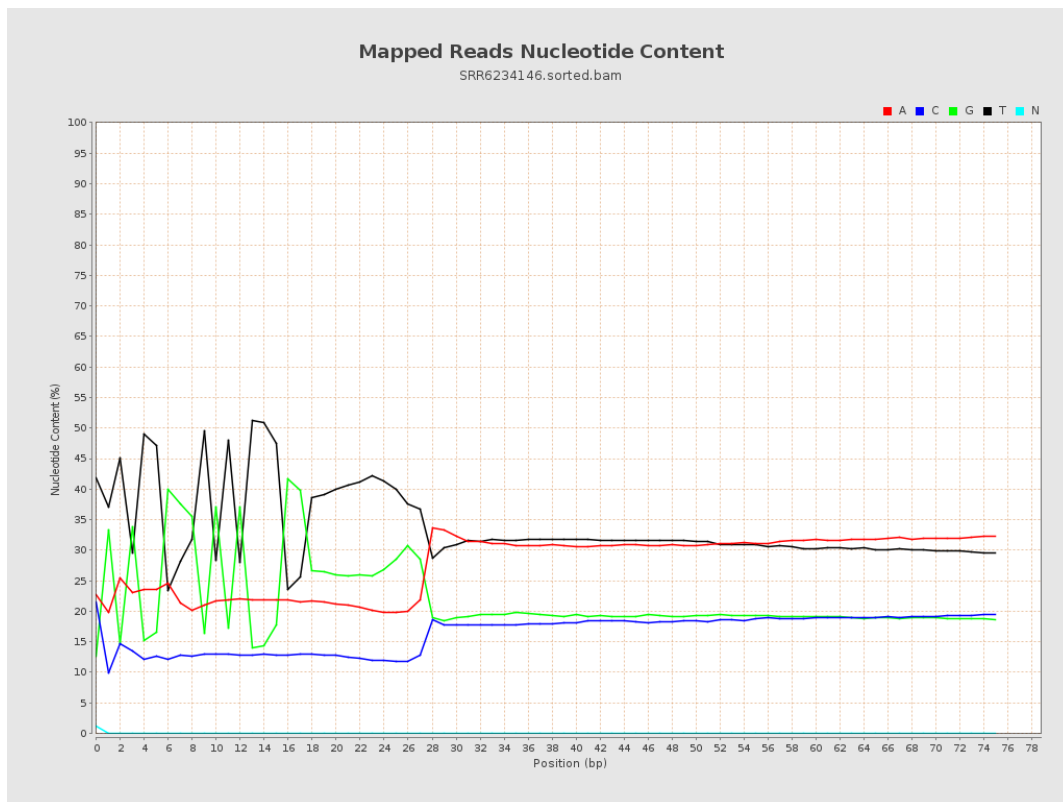
## 6. Results : Genome Fraction Coverage



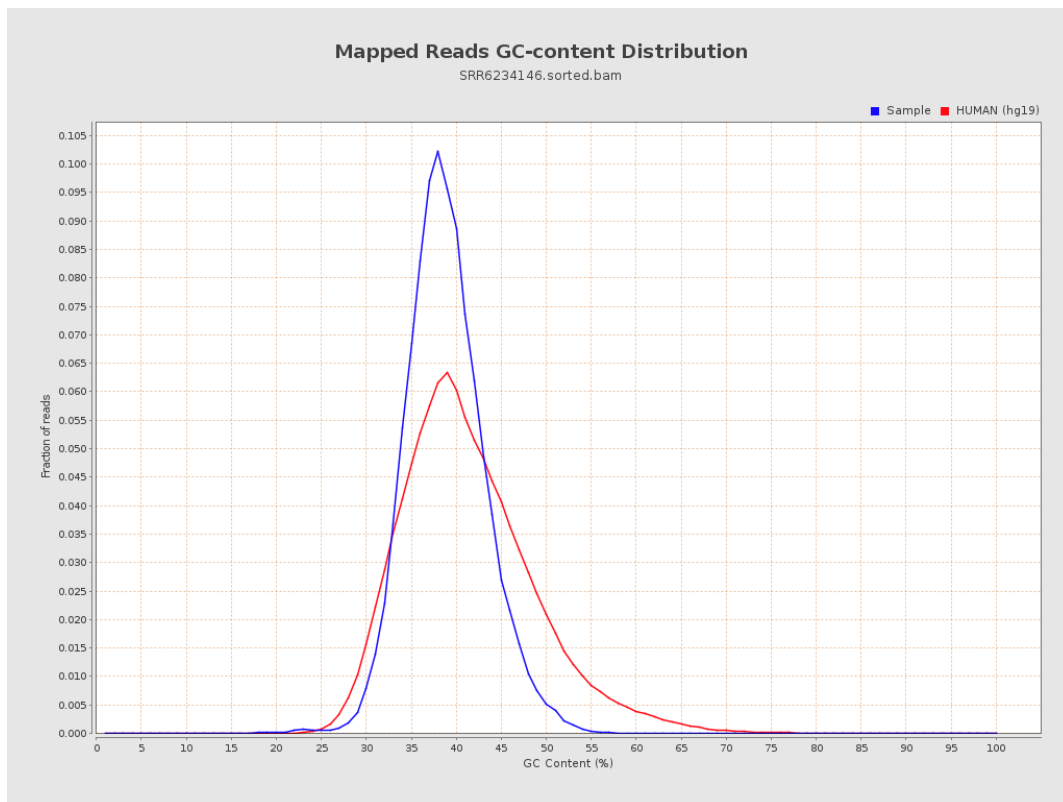
## 7. Results : Duplication Rate Histogram



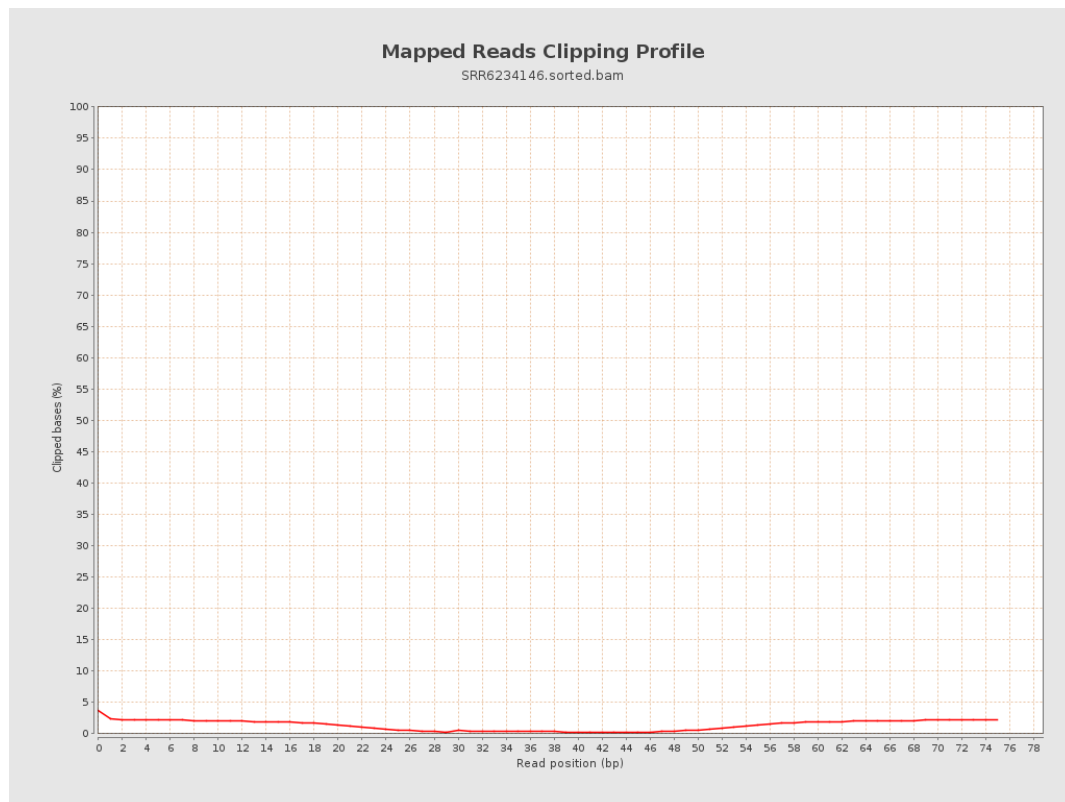
## 8. Results : Mapped Reads Nucleotide Content



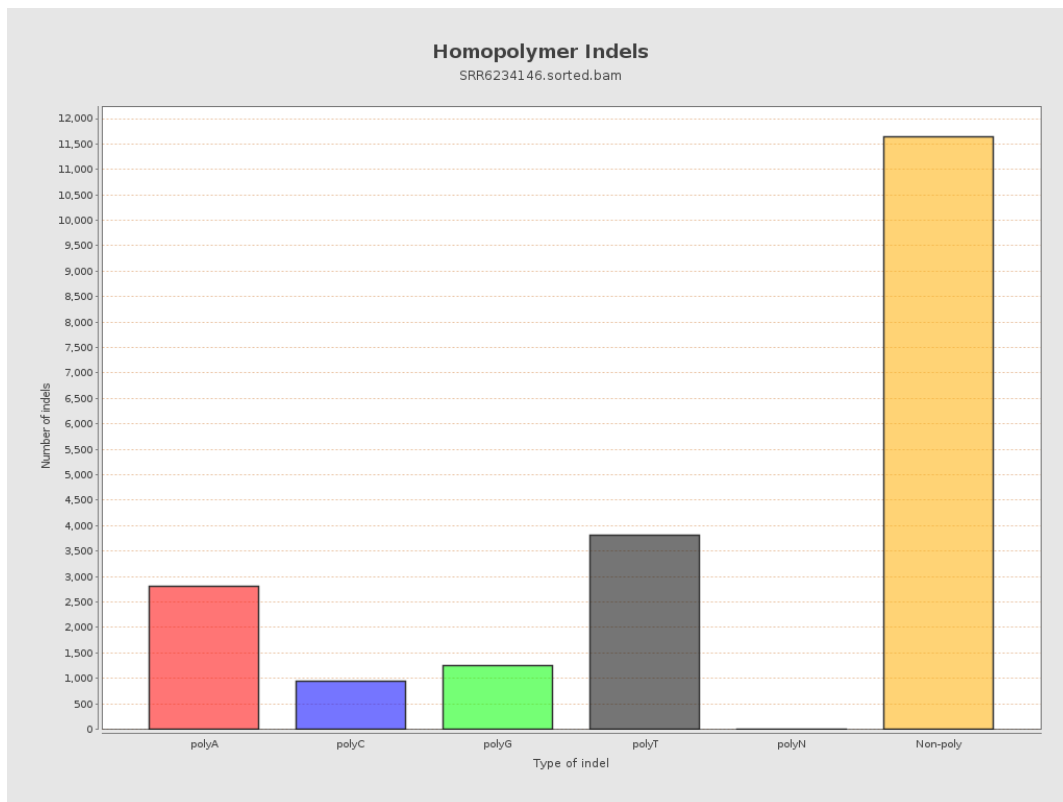
## 9. Results : Mapped Reads GC-content Distribution



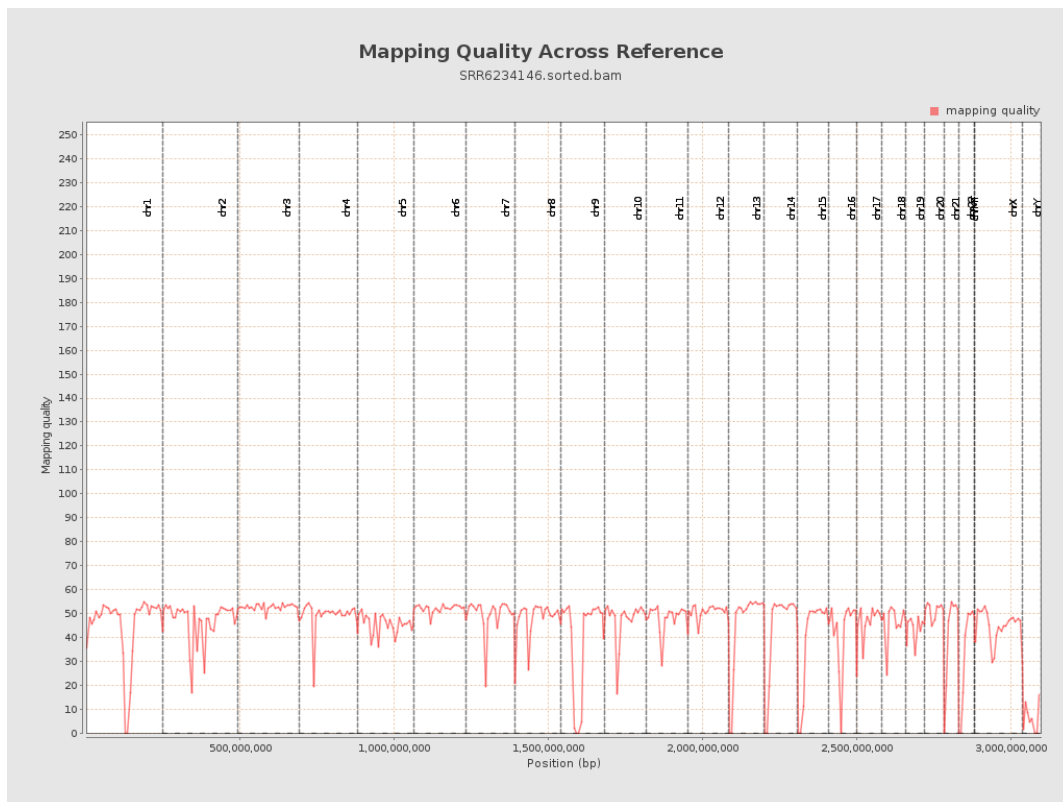
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

