

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/16 21:19:52*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236116.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_SRR6236116 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236116.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Mon Sep 16 21:19:52 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6236116.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 1,495,984          |
| Mapped reads                 | 1,321,459 / 88.33% |
| Unmapped reads               | 174,525 / 11.67%   |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 9,879 / 0.66%      |
| Read min/max/mean length     | 30 / 76 / 76.23    |
| Duplicated reads (estimated) | 46,650 / 3.12%     |
| Duplication rate             | 2.68%              |
| Clipped reads                | 640,430 / 42.81%   |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 24,601,459 / 28.34% |
| Number/percentage of C's | 15,981,073 / 18.41% |
| Number/percentage of T's | 27,381,067 / 31.54% |
| Number/percentage of G's | 18,837,133 / 21.7%  |
| Number/percentage of N's | 886 / 0%            |
| GC Percentage            | 40.11%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0281 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.2941 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 46.02 |
|----------------------|-------|

## 2.5. Mismatches and indels

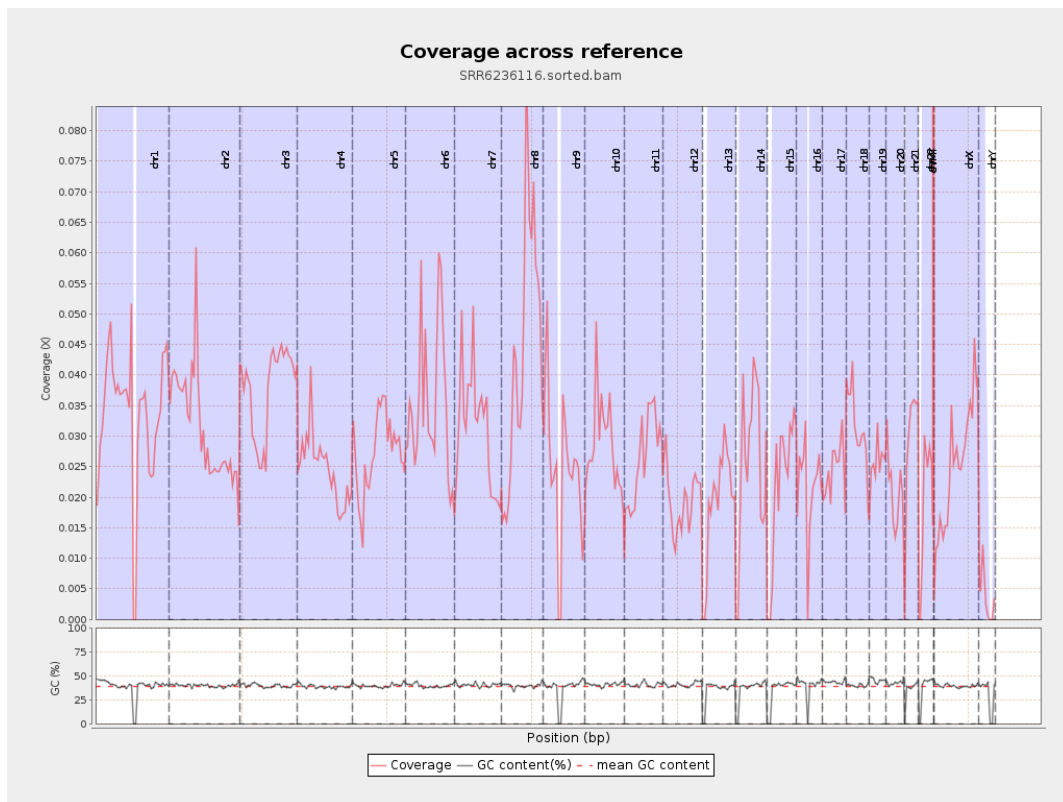
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 0.77%   |
| Mismatches                               | 657,424 |
| Insertions                               | 6,552   |
| Mapped reads with at least one insertion | 0.49%   |
| Deletions                                | 25,912  |
| Mapped reads with at least one deletion  | 1.94%   |
| Homopolymer indels                       | 46.42%  |

## 2.6. Chromosome stats

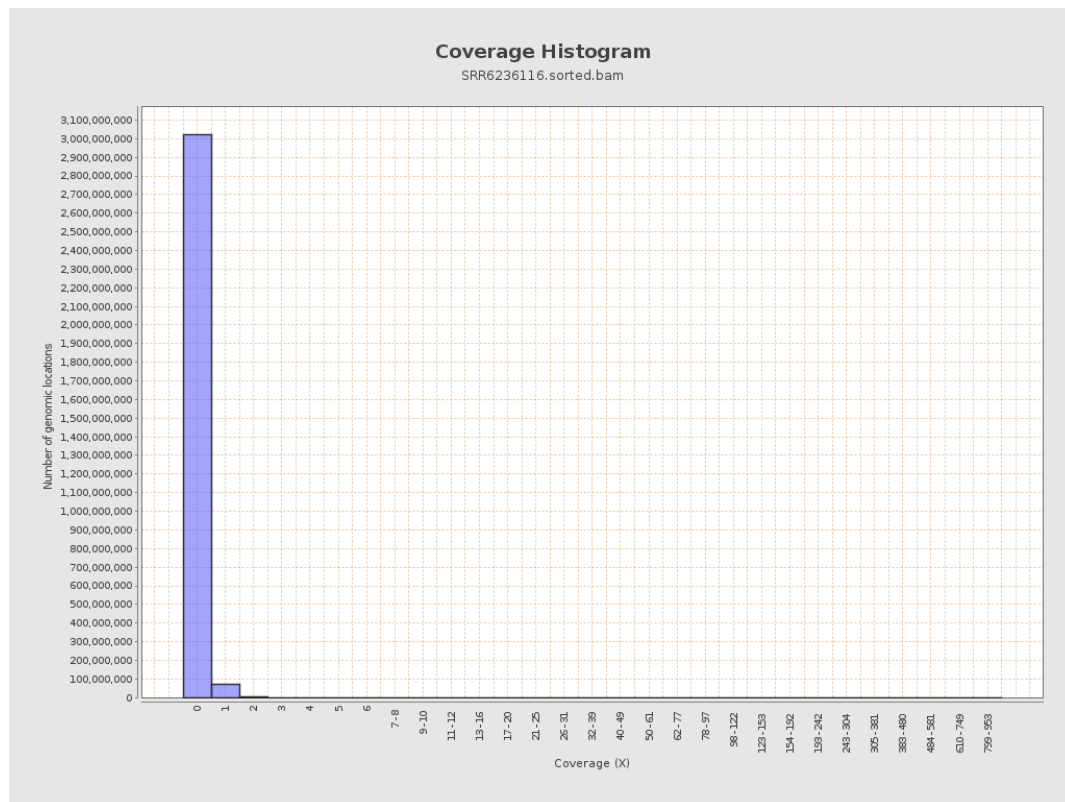
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 8367911      | 0.0336        | 0.493              |
| chr2 | 243199373 | 7645265      | 0.0314        | 0.3087             |
| chr3 | 198022430 | 7455832      | 0.0377        | 0.2133             |
| chr4 | 191154276 | 4703163      | 0.0246        | 0.1892             |
| chr5 | 180915260 | 4938896      | 0.0273        | 0.1833             |
| chr6 | 171115067 | 5993182      | 0.035         | 0.2828             |
| chr7 | 159138663 | 4994136      | 0.0314        | 0.3311             |
|      |           |              |               |                    |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr8  | 146364022 | 6384040 | 0.0436 | 0.6303 |
| chr9  | 141213431 | 3471870 | 0.0246 | 0.2532 |
| chr10 | 135534747 | 3896212 | 0.0287 | 0.2606 |
| chr11 | 135006516 | 3556278 | 0.0263 | 0.2149 |
| chr12 | 133851895 | 2591925 | 0.0194 | 0.1608 |
| chr13 | 115169878 | 2186965 | 0.019  | 0.1502 |
| chr14 | 107349540 | 2660329 | 0.0248 | 0.1842 |
| chr15 | 102531392 | 2230182 | 0.0218 | 0.1662 |
| chr16 | 90354753  | 1969686 | 0.0218 | 0.1751 |
| chr17 | 81195210  | 1972048 | 0.0243 | 0.1823 |
| chr18 | 78077248  | 2495658 | 0.032  | 0.394  |
| chr19 | 59128983  | 1523787 | 0.0258 | 0.3379 |
| chr20 | 63025520  | 1287459 | 0.0204 | 0.1615 |
| chr21 | 48129895  | 1425790 | 0.0296 | 0.1997 |
| chr22 | 51304566  | 954534  | 0.0186 | 0.1488 |
| chrMT | 16571     | 75312   | 4.5448 | 3.2891 |
| chrX  | 155270560 | 3862685 | 0.0249 | 0.1885 |
| chrY  | 59373566  | 203403  | 0.0034 | 0.1017 |

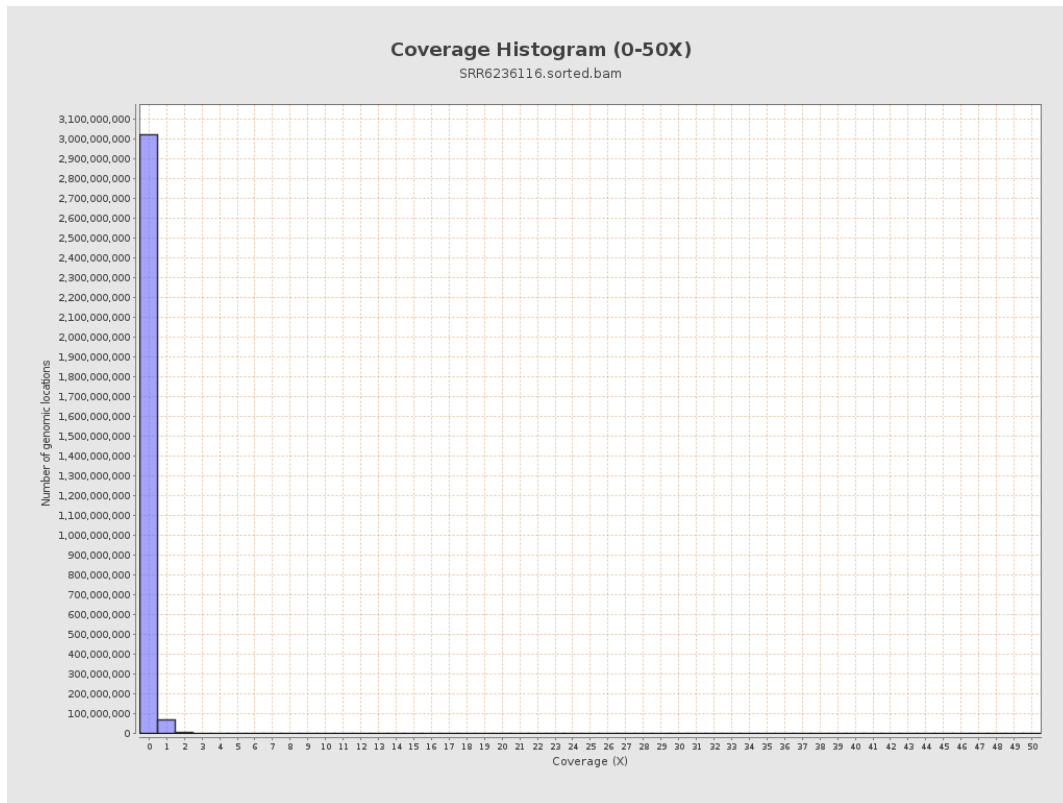
### 3. Results : Coverage across reference



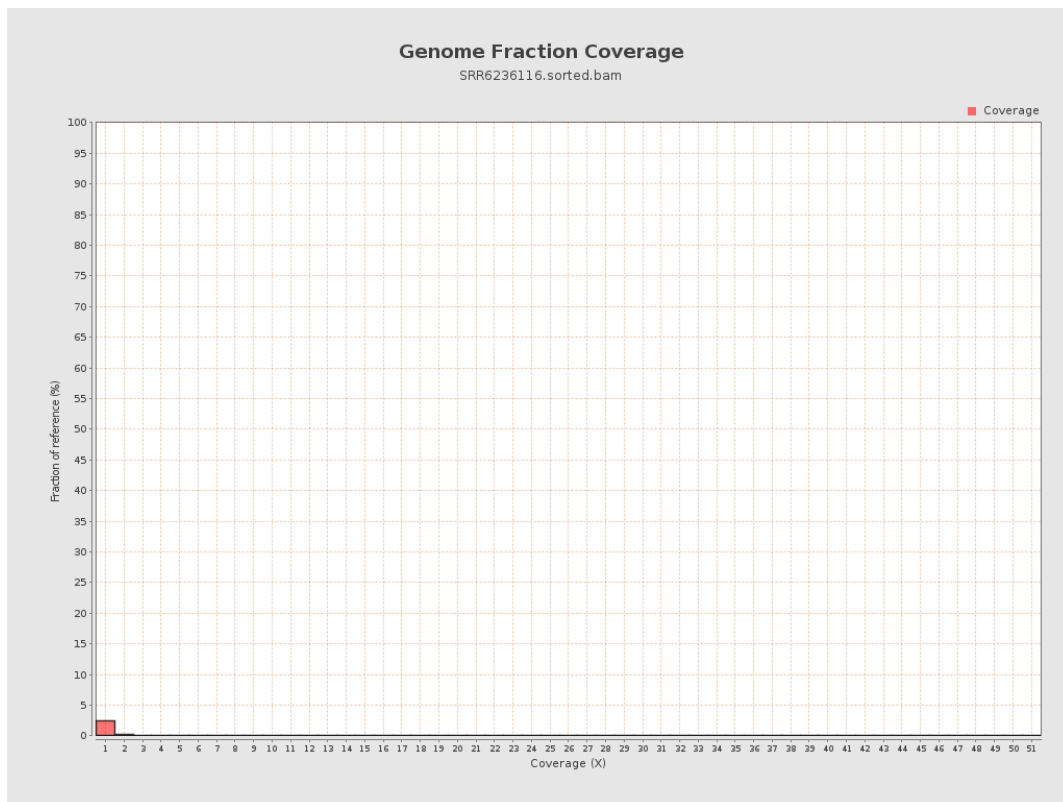
## 4. Results : Coverage Histogram



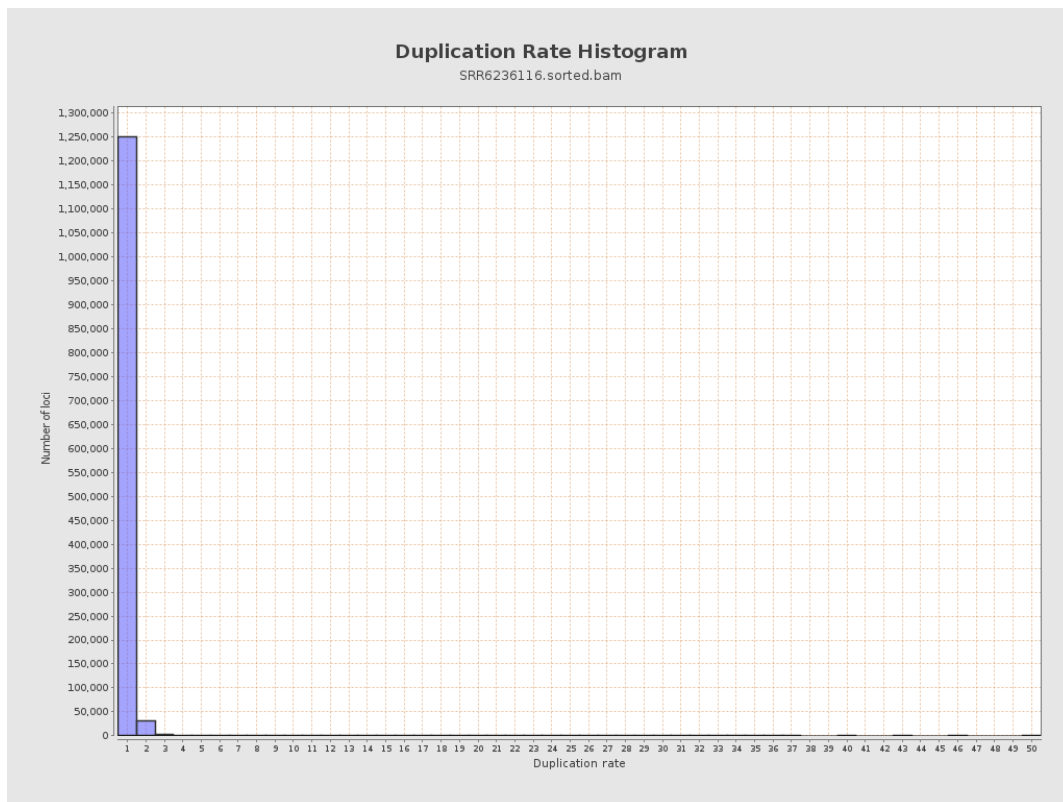
## 5. Results : Coverage Histogram (0-50X)



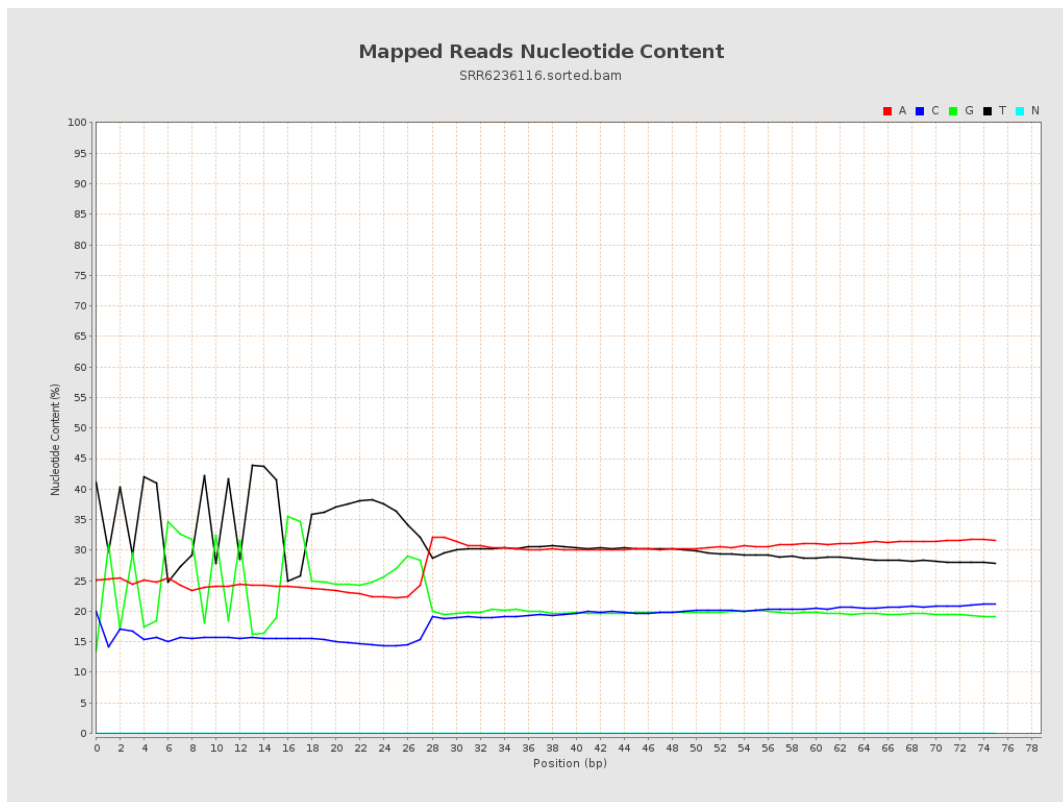
## 6. Results : Genome Fraction Coverage



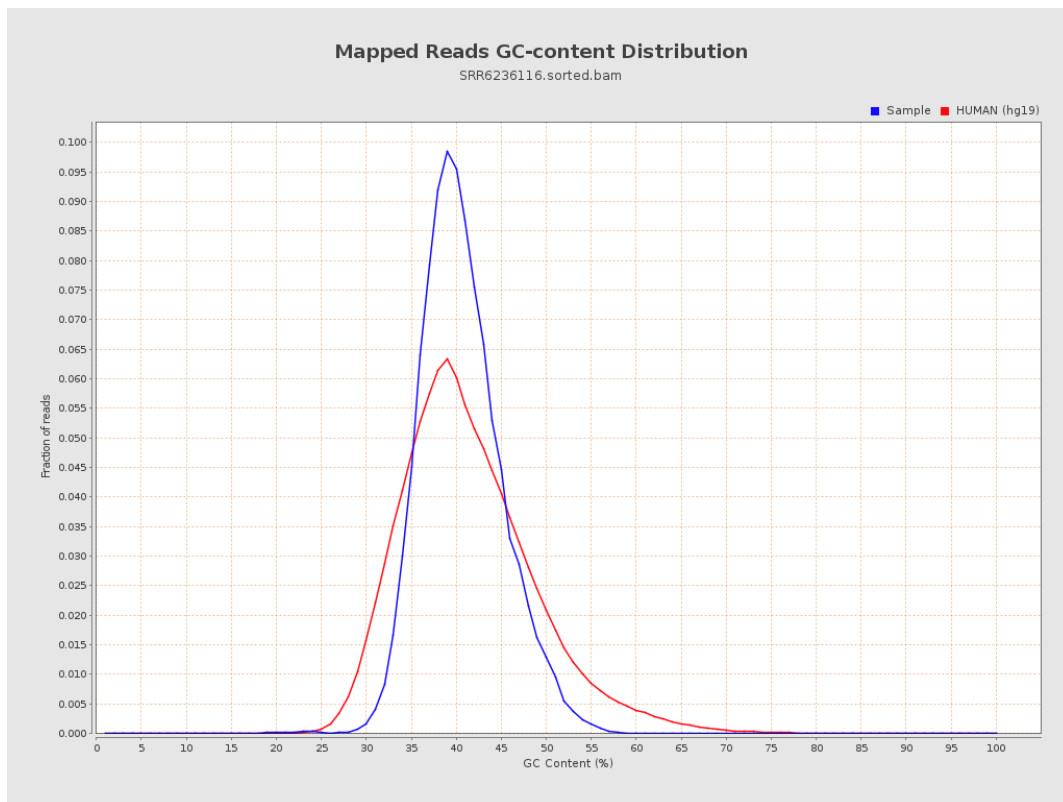
## 7. Results : Duplication Rate Histogram



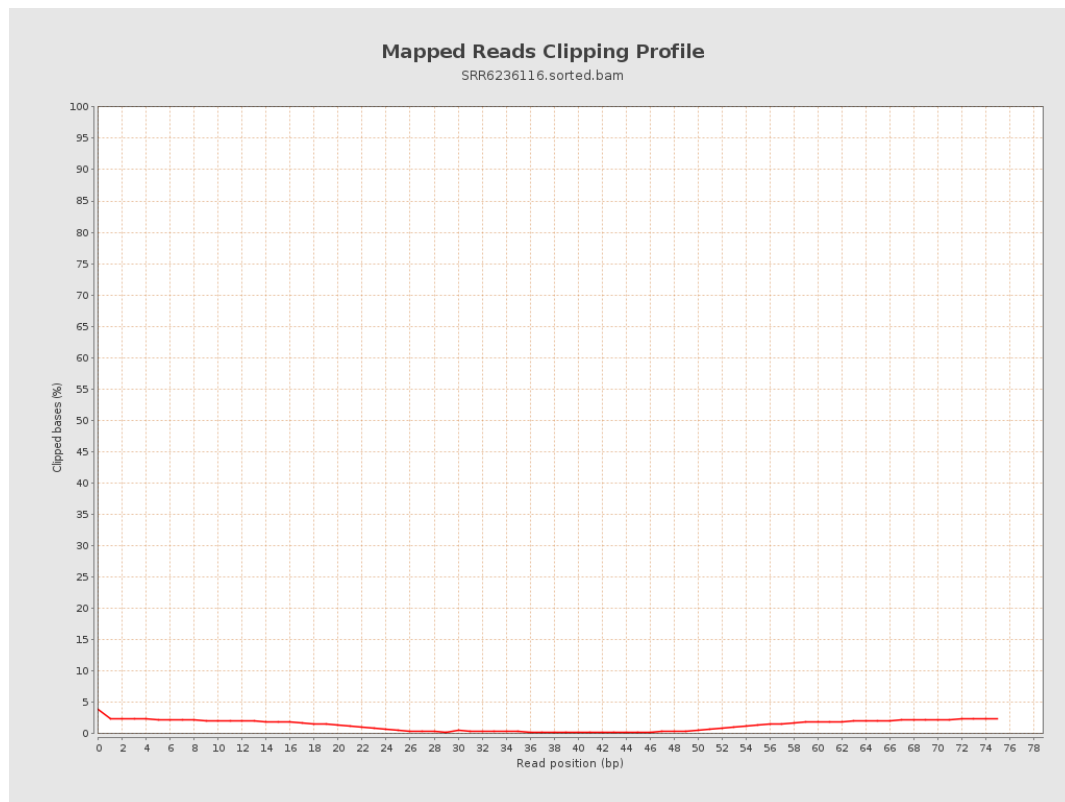
## 8. Results : Mapped Reads Nucleotide Content



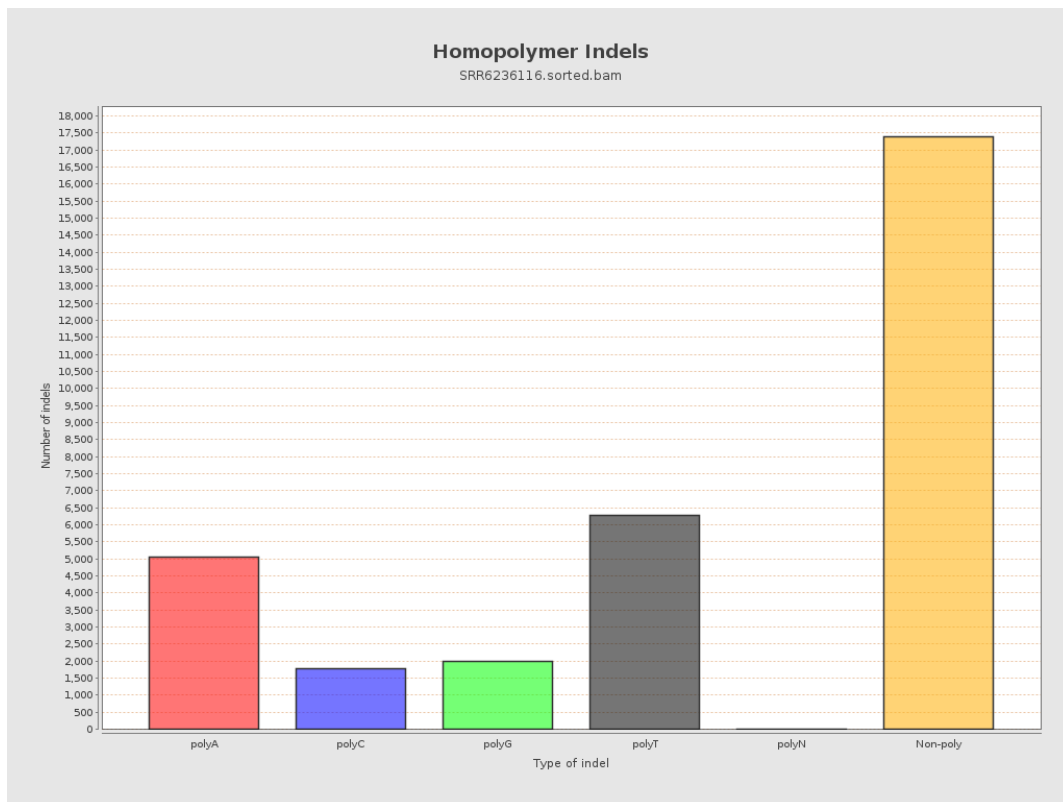
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

