

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/14 12:41:41*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008815.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_SRR6008815 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008815.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Sat Sep 14 12:41:40 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6008815.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 2,477,247          |
| Mapped reads                 | 883,639 / 35.67%   |
| Unmapped reads               | 1,593,608 / 64.33% |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 4,721 / 0.19%      |
| Read min/max/mean length     | 30 / 76 / 76.06    |
| Duplicated reads (estimated) | 35,137 / 1.42%     |
| Duplication rate             | 3.14%              |
| Clipped reads                | 521,656 / 21.06%   |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 16,948,997 / 30.04% |
| Number/percentage of C's | 10,175,319 / 18.04% |
| Number/percentage of T's | 16,049,808 / 28.45% |
| Number/percentage of G's | 13,233,854 / 23.46% |
| Number/percentage of N's | 9,146 / 0.02%       |
| GC Percentage            | 41.49%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0182 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.1845 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 47.28 |
|----------------------|-------|

## 2.5. Mismatches and indels

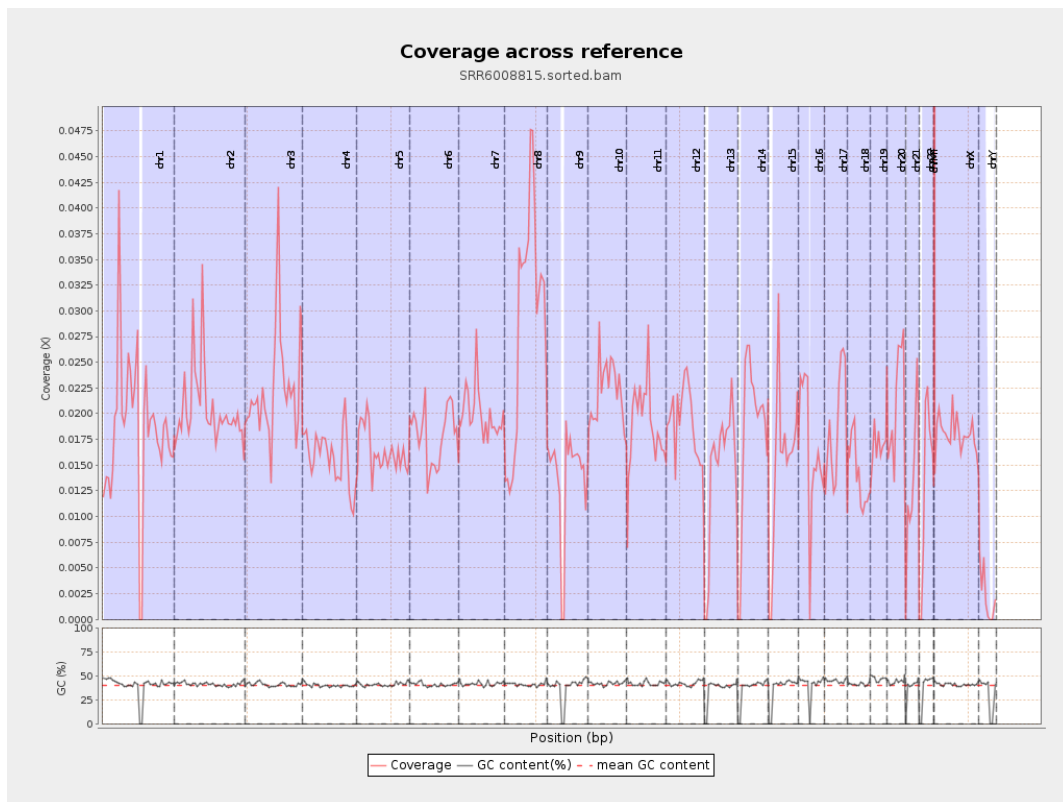
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 1.05%   |
| Mismatches                               | 584,468 |
| Insertions                               | 3,996   |
| Mapped reads with at least one insertion | 0.45%   |
| Deletions                                | 21,217  |
| Mapped reads with at least one deletion  | 2.37%   |
| Homopolymer indels                       | 48.42%  |

## 2.6. Chromosome stats

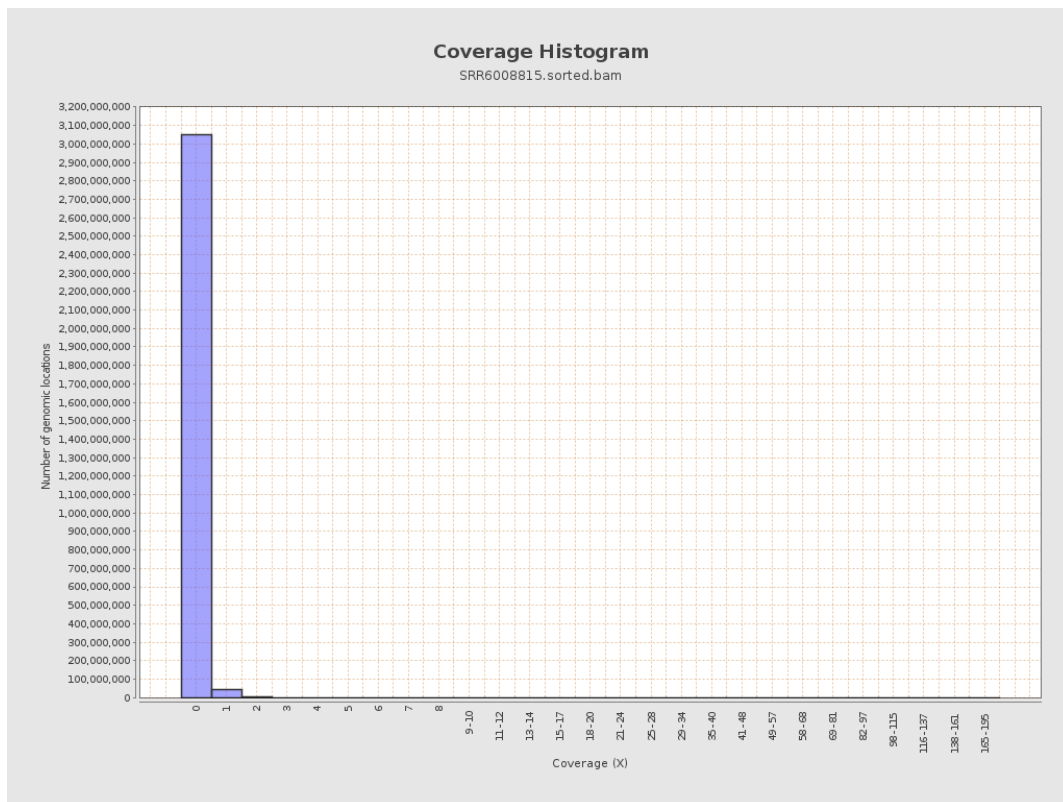
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 4556283      | 0.0183        | 0.2095             |
| chr2 | 243199373 | 4991543      | 0.0205        | 0.2304             |
| chr3 | 198022430 | 4423978      | 0.0223        | 0.179              |
| chr4 | 191154276 | 3017267      | 0.0158        | 0.1485             |
| chr5 | 180915260 | 2973735      | 0.0164        | 0.1508             |
| chr6 | 171115067 | 3061054      | 0.0179        | 0.1719             |
| chr7 | 159138663 | 3180373      | 0.02          | 0.2267             |
|      |           |              |               |                    |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr8  | 146364022 | 4253583 | 0.0291 | 0.2451 |
| chr9  | 141213431 | 1949525 | 0.0138 | 0.1624 |
| chr10 | 135534747 | 2990319 | 0.0221 | 0.195  |
| chr11 | 135006516 | 2576546 | 0.0191 | 0.179  |
| chr12 | 133851895 | 2564424 | 0.0192 | 0.1649 |
| chr13 | 115169878 | 1675942 | 0.0146 | 0.1456 |
| chr14 | 107349540 | 1973073 | 0.0184 | 0.1636 |
| chr15 | 102531392 | 1555848 | 0.0152 | 0.1447 |
| chr16 | 90354753  | 1473791 | 0.0163 | 0.1572 |
| chr17 | 81195210  | 1502907 | 0.0185 | 0.1778 |
| chr18 | 78077248  | 1094879 | 0.014  | 0.2691 |
| chr19 | 59128983  | 1007563 | 0.017  | 0.1704 |
| chr20 | 63025520  | 1318861 | 0.0209 | 0.1725 |
| chr21 | 48129895  | 658022  | 0.0137 | 0.1442 |
| chr22 | 51304566  | 688505  | 0.0134 | 0.1433 |
| chrMT | 16571     | 22230   | 1.3415 | 1.6075 |
| chrX  | 155270560 | 2806884 | 0.0181 | 0.1634 |
| chrY  | 59373566  | 131778  | 0.0022 | 0.0603 |

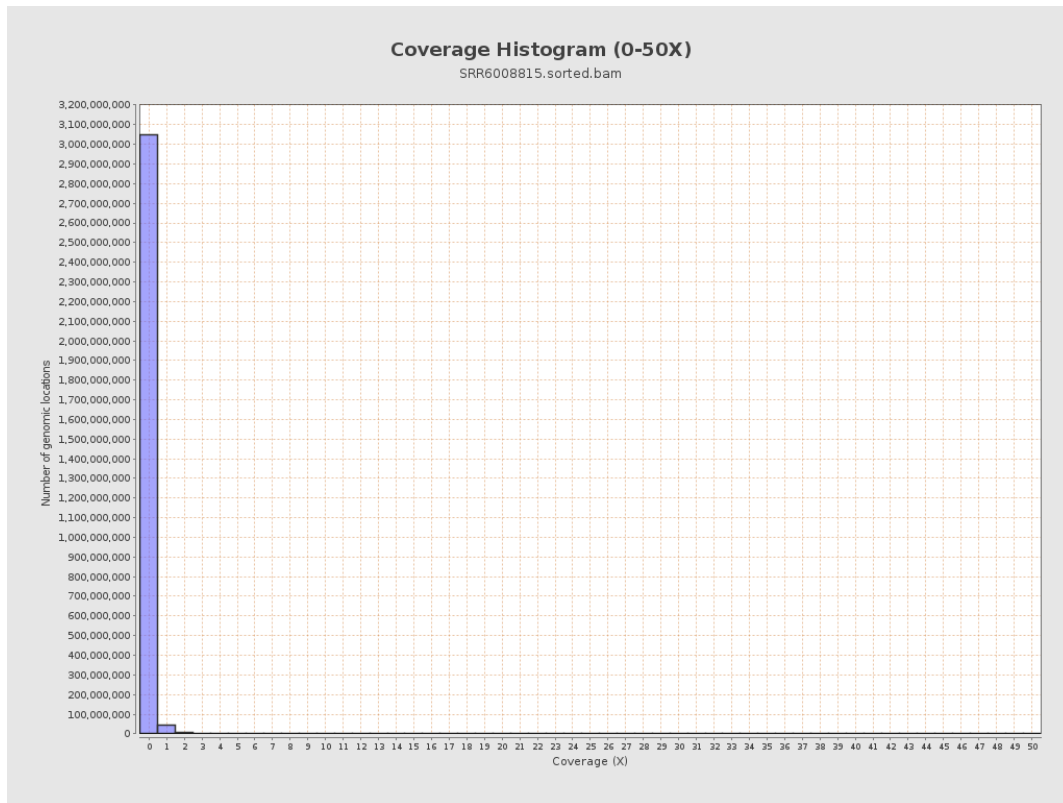
### 3. Results : Coverage across reference



## 4. Results : Coverage Histogram

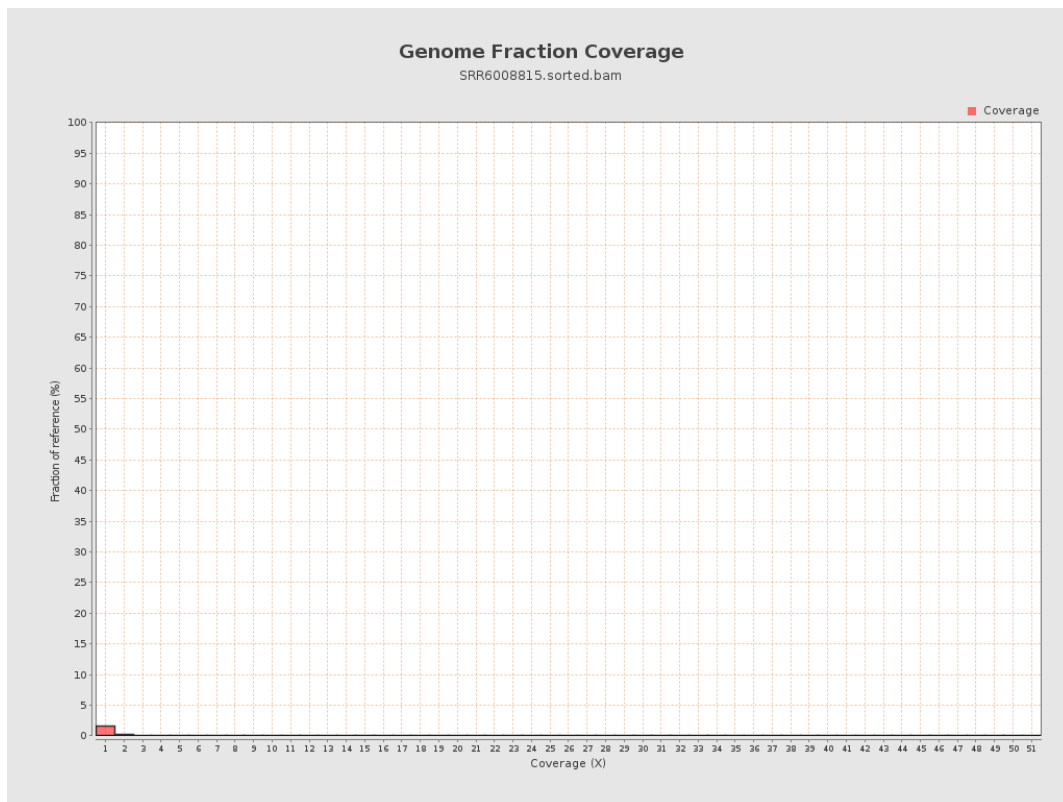


## 5. Results : Coverage Histogram (0-50X)

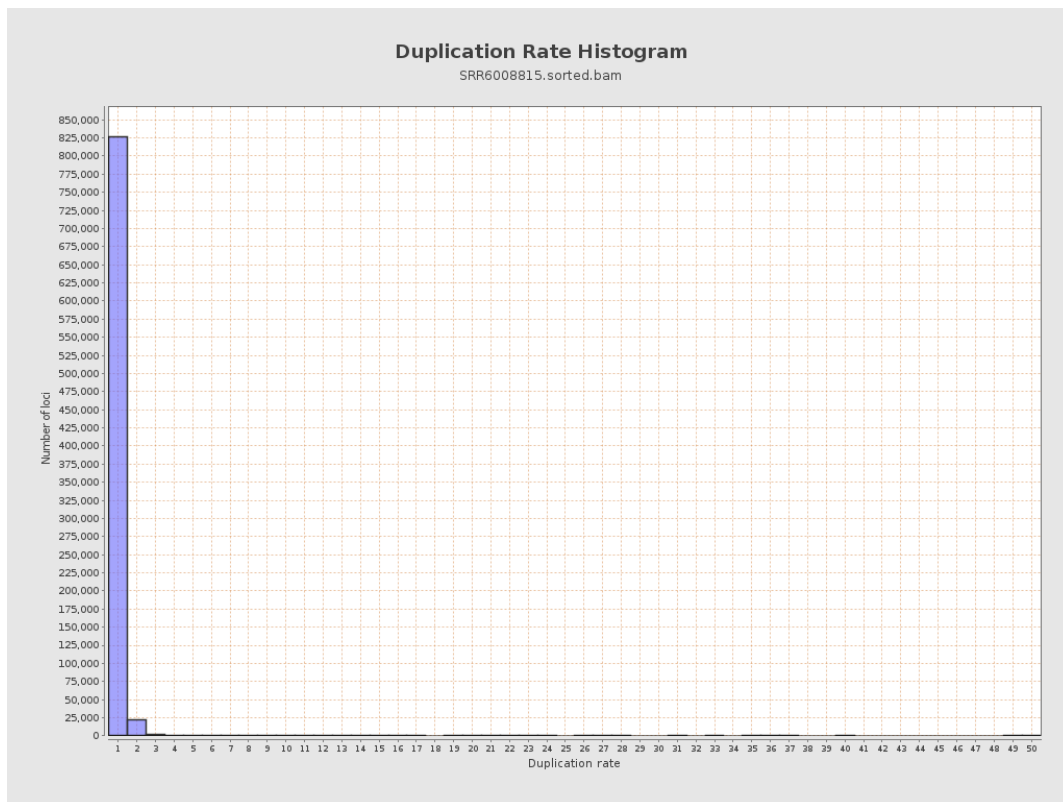




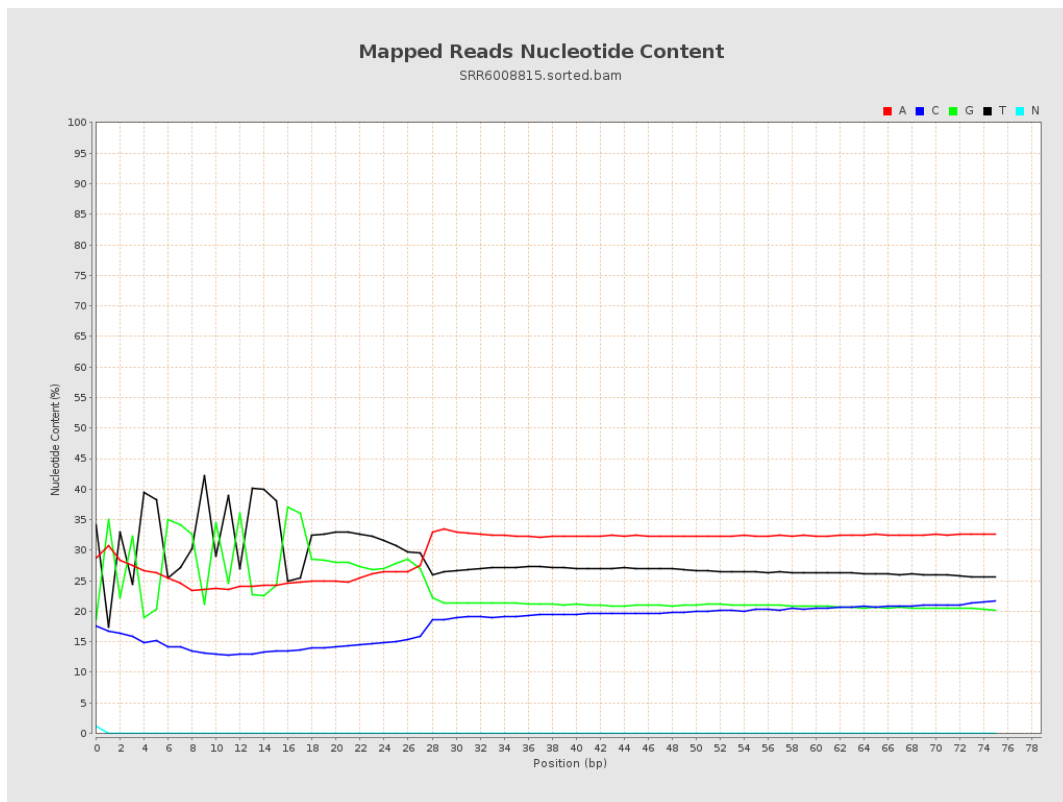
## 6. Results : Genome Fraction Coverage



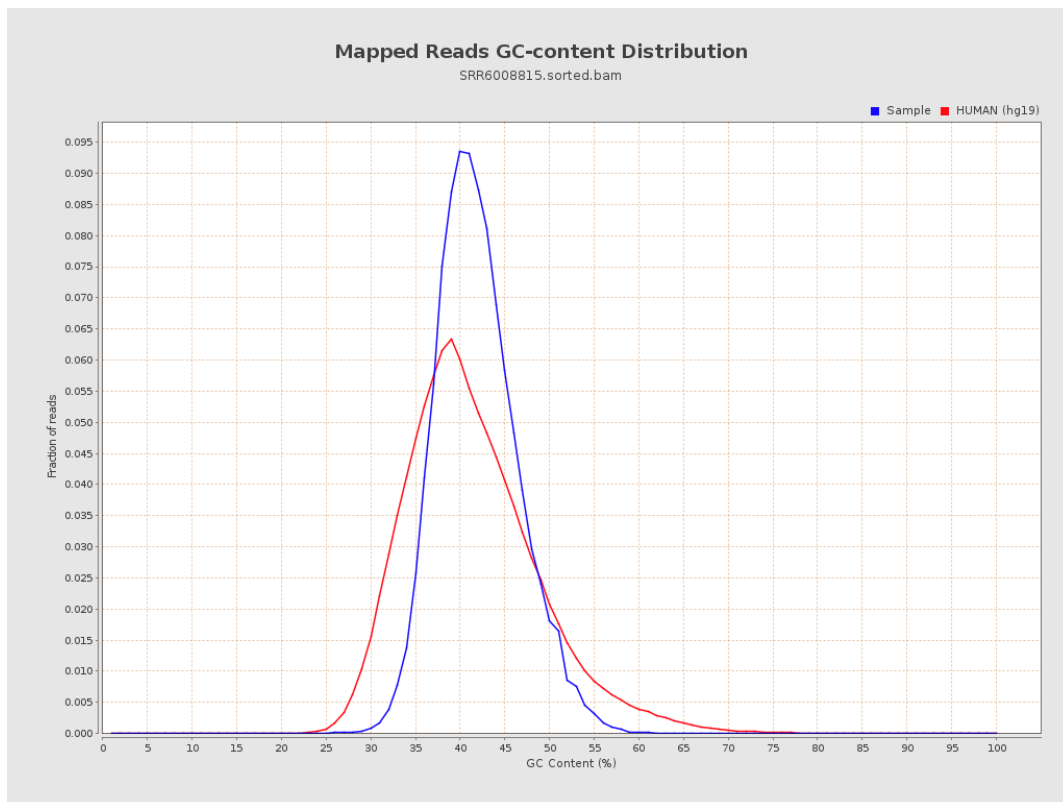
## 7. Results : Duplication Rate Histogram



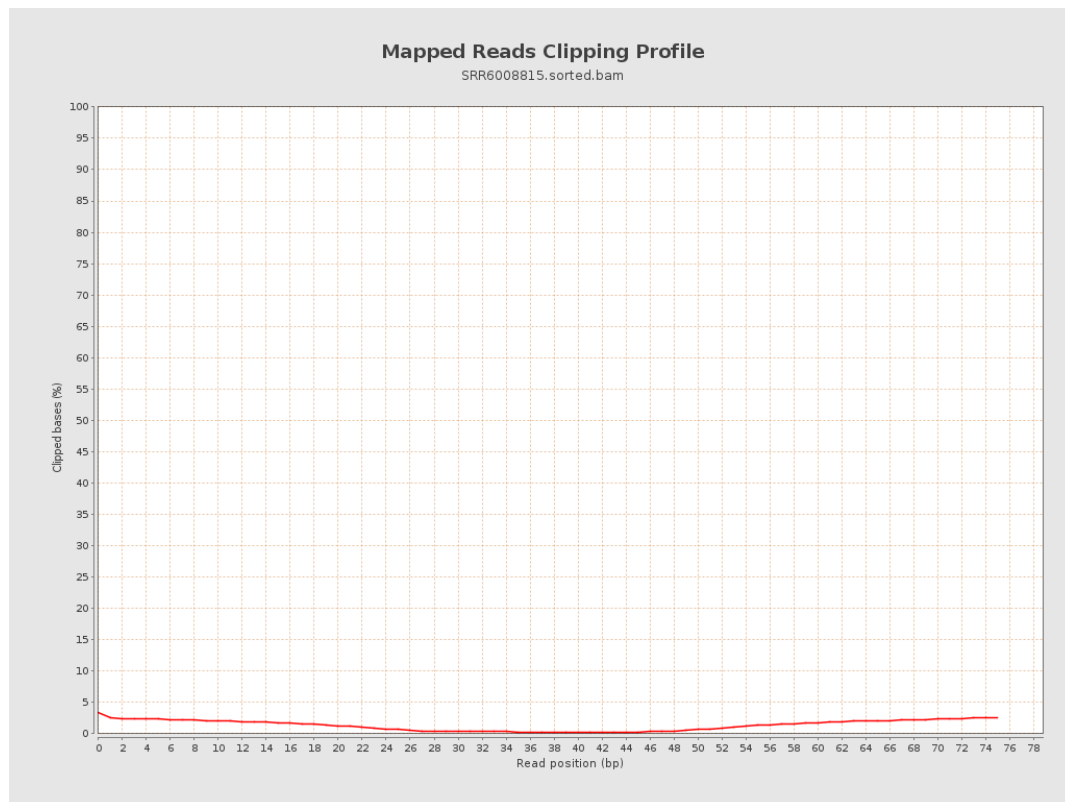
## 8. Results : Mapped Reads Nucleotide Content



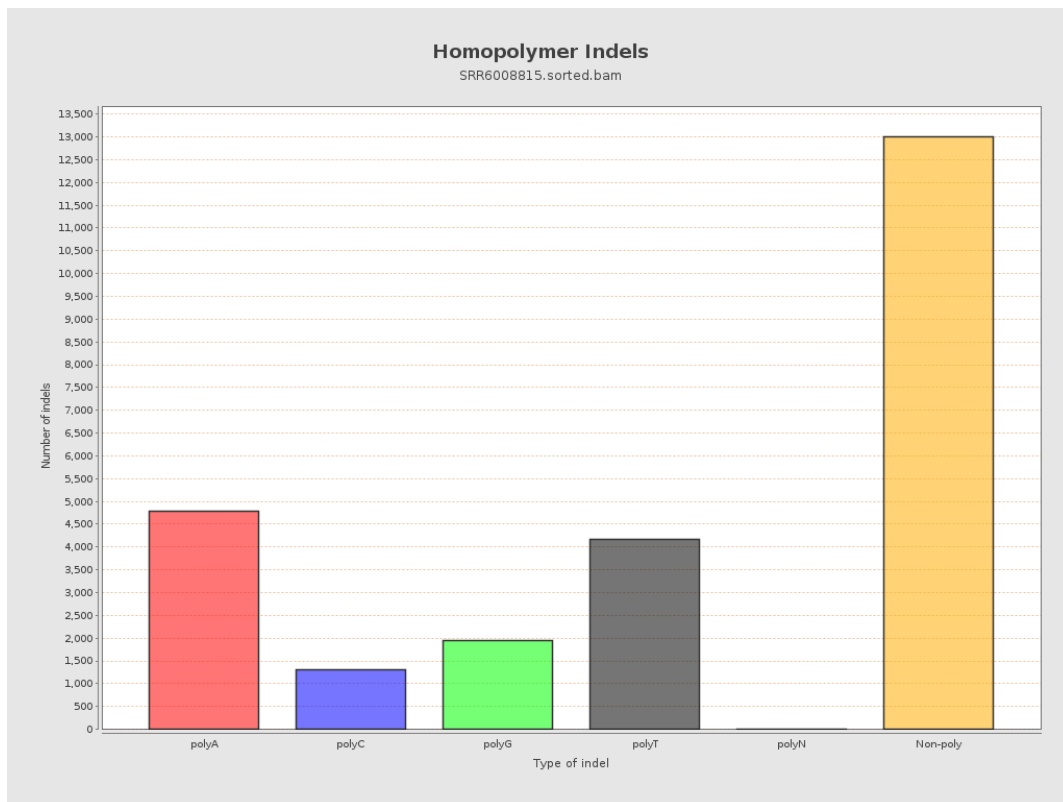
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

