

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/20 01:44:21*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506317.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_SRR1506317 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506317.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Fri Dec 20 01:44:20 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR1506317.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 4,066,642          |
| Mapped reads                 | 3,425,489 / 84.23% |
| Unmapped reads               | 641,153 / 15.77%   |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 58,555 / 1.44%     |
| Read min/max/mean length     | 30 / 94 / 94.52    |
| Duplicated reads (estimated) | 506,965 / 12.47%   |
| Duplication rate             | 10.98%             |
| Clipped reads                | 2,137,261 / 52.56% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 71,837,050 / 26.53% |
| Number/percentage of C's | 50,726,446 / 18.73% |
| Number/percentage of T's | 82,150,100 / 30.33% |
| Number/percentage of G's | 66,046,387 / 24.39% |
| Number/percentage of N's | 51,378 / 0.02%      |
| GC Percentage            | 43.12%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0875 |
|      |        |

|                    |       |
|--------------------|-------|
| Standard Deviation | 0.688 |
|--------------------|-------|

## 2.4. Mapping Quality

|                      |    |
|----------------------|----|
| Mean Mapping Quality | 48 |
|----------------------|----|

## 2.5. Mismatches and indels

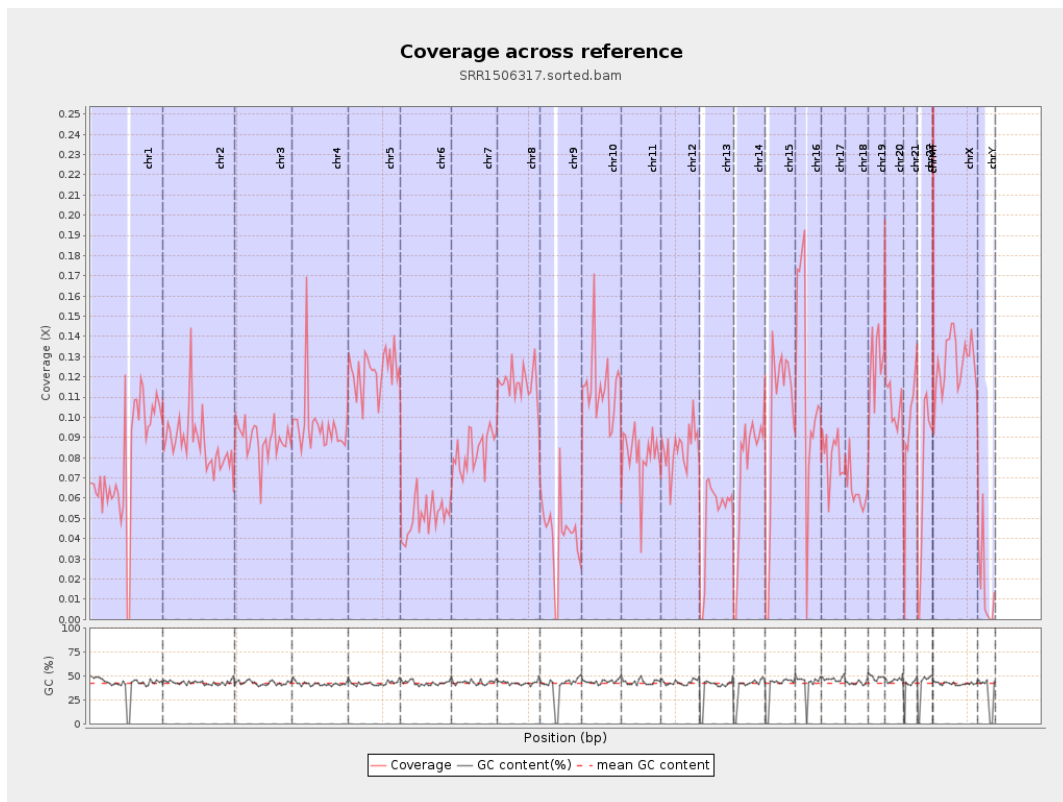
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.71%     |
| Mismatches                               | 1,864,340 |
| Insertions                               | 21,743    |
| Mapped reads with at least one insertion | 0.62%     |
| Deletions                                | 58,128    |
| Mapped reads with at least one deletion  | 1.67%     |
| Homopolymer indels                       | 44.53%    |

## 2.6. Chromosome stats

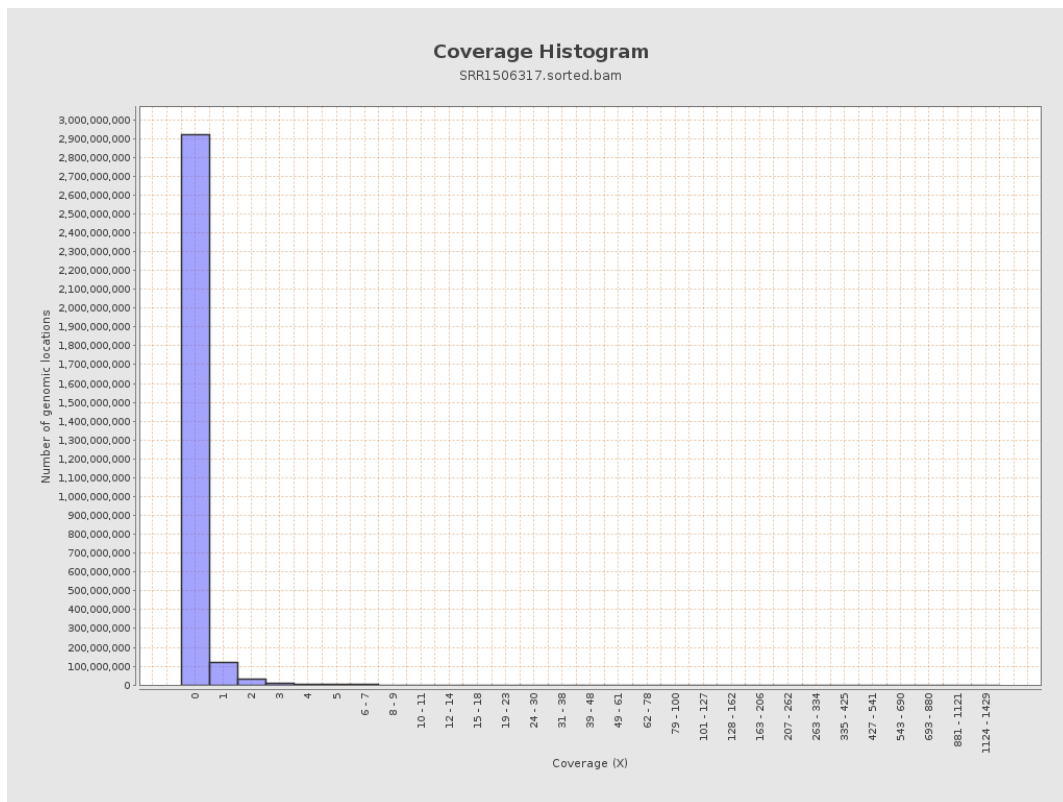
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 19521555     | 0.0783        | 1.2935             |
| chr2 | 243199373 | 21246349     | 0.0874        | 0.7017             |
| chr3 | 198022430 | 17589370     | 0.0888        | 0.4288             |
| chr4 | 191154276 | 18351295     | 0.096         | 0.5596             |
| chr5 | 180915260 | 22158163     | 0.1225        | 0.5145             |
| chr6 | 171115067 | 8695989      | 0.0508        | 0.3631             |
| chr7 | 159138663 | 13276967     | 0.0834        | 0.6355             |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr8  | 146364022 | 17119786 | 0.117  | 0.8821 |
| chr9  | 141213431 | 5913786  | 0.0419 | 0.6009 |
| chr10 | 135534747 | 15482521 | 0.1142 | 0.7542 |
| chr11 | 135006516 | 10945331 | 0.0811 | 0.6456 |
| chr12 | 133851895 | 11389860 | 0.0851 | 0.4342 |
| chr13 | 115169878 | 5857683  | 0.0509 | 0.3203 |
| chr14 | 107349540 | 8046743  | 0.075  | 0.4441 |
| chr15 | 102531392 | 10124669 | 0.0987 | 0.4694 |
| chr16 | 90354753  | 10429583 | 0.1154 | 0.5819 |
| chr17 | 81195210  | 6595377  | 0.0812 | 0.4815 |
| chr18 | 78077248  | 4989675  | 0.0639 | 1.1414 |
| chr19 | 59128983  | 7654964  | 0.1295 | 0.9799 |
| chr20 | 63025520  | 6673290  | 0.1059 | 0.5045 |
| chr21 | 48129895  | 4599276  | 0.0956 | 0.5511 |
| chr22 | 51304566  | 3643868  | 0.071  | 0.4071 |
| chrMT | 16571     | 13772    | 0.8311 | 1.3067 |
| chrX  | 155270560 | 19658831 | 0.1266 | 0.5776 |
| chrY  | 59373566  | 946165   | 0.0159 | 0.5468 |

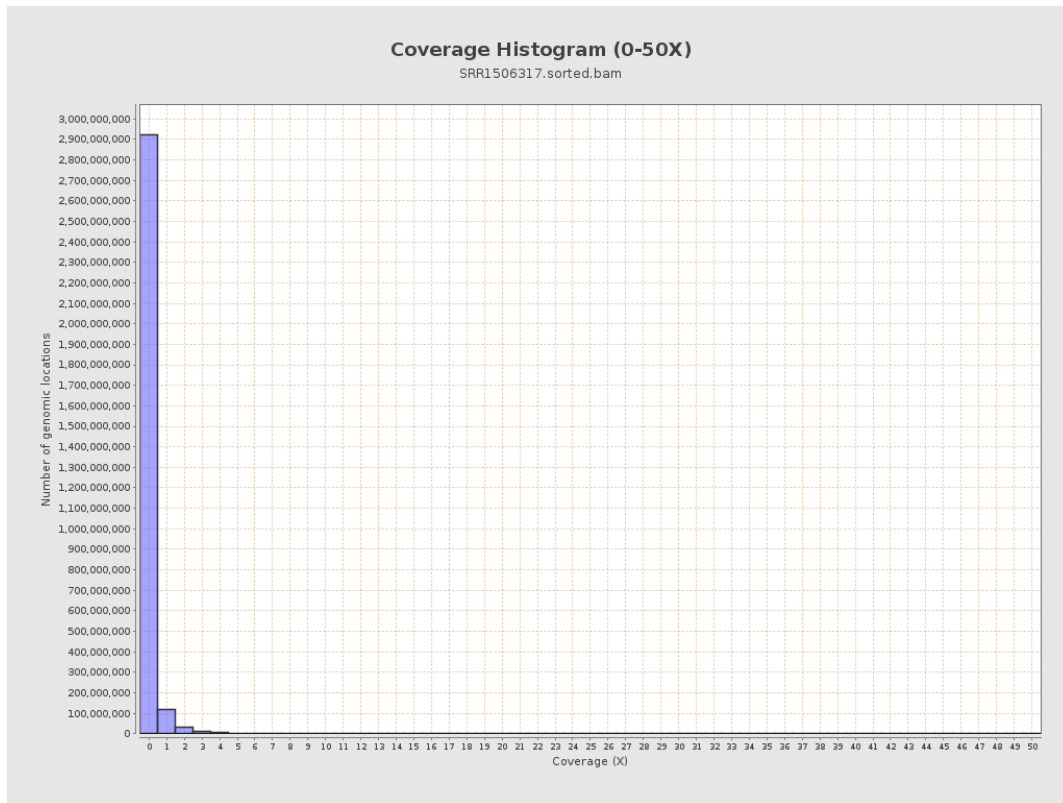
### 3. Results : Coverage across reference



## 4. Results : Coverage Histogram

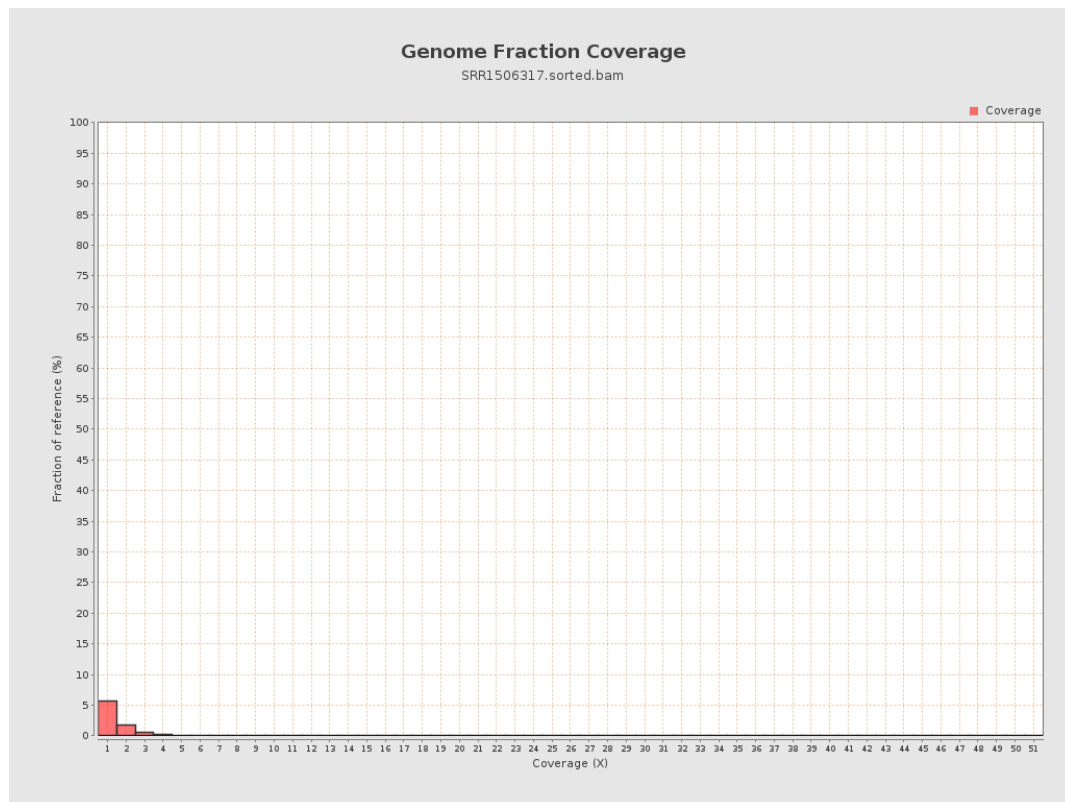


## 5. Results : Coverage Histogram (0-50X)

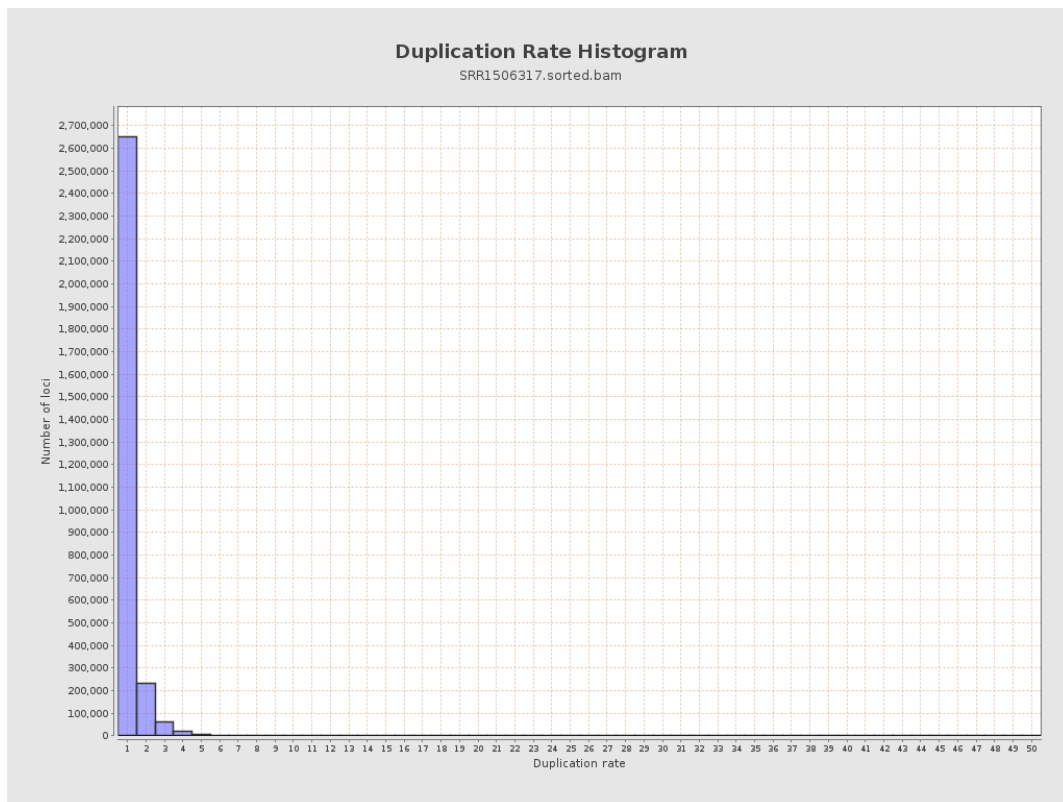




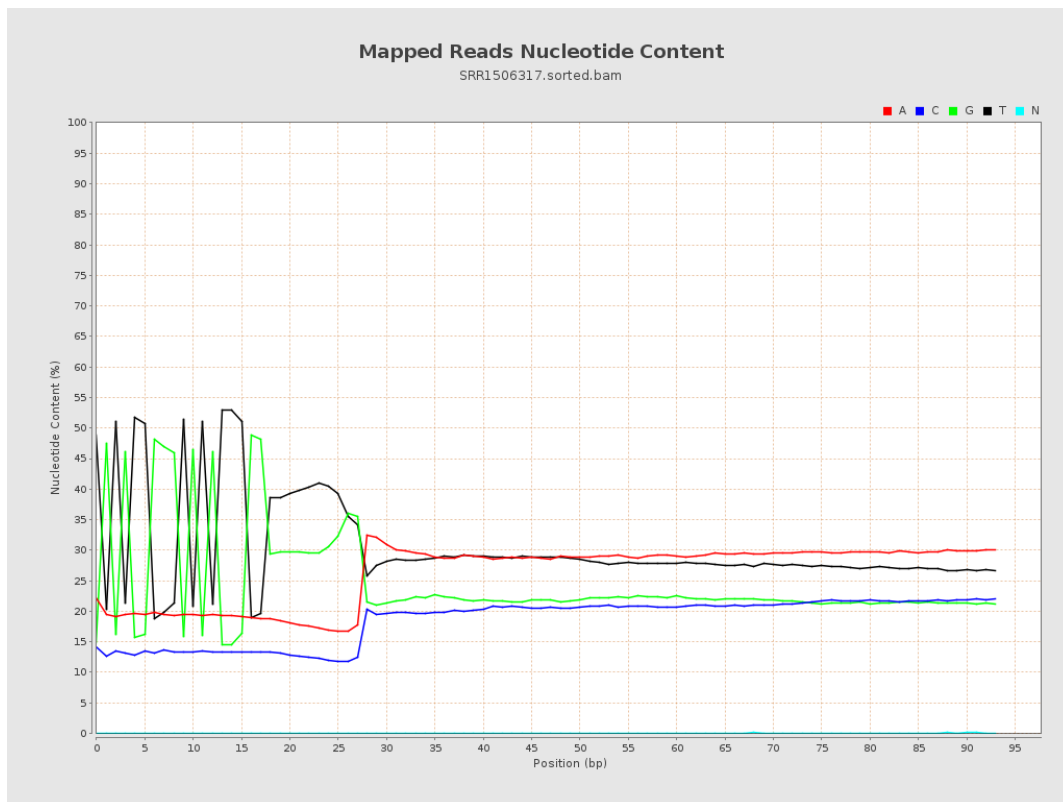
## 6. Results : Genome Fraction Coverage



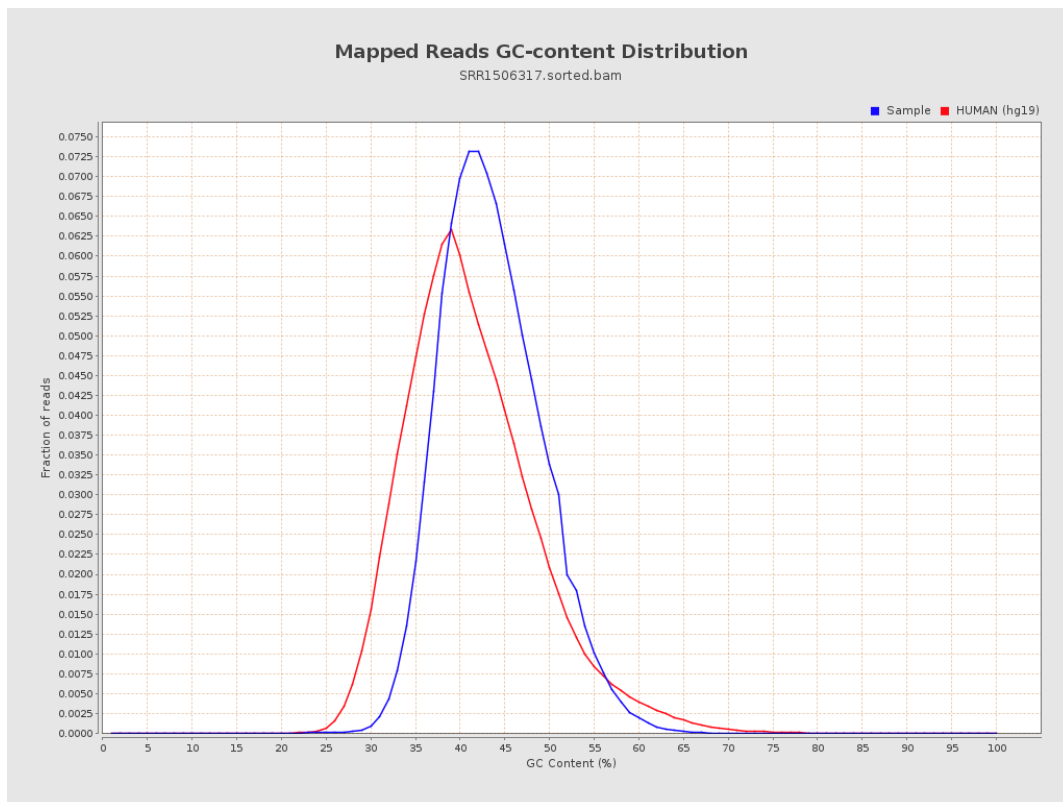
## 7. Results : Duplication Rate Histogram



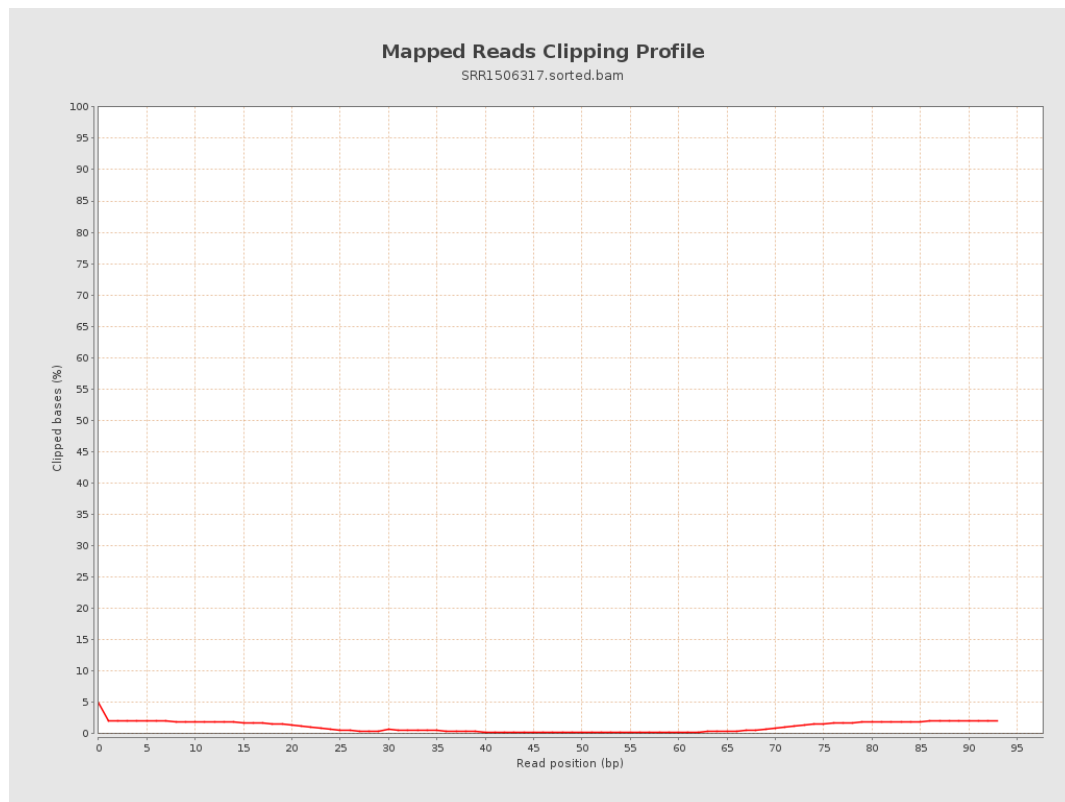
## 8. Results : Mapped Reads Nucleotide Content



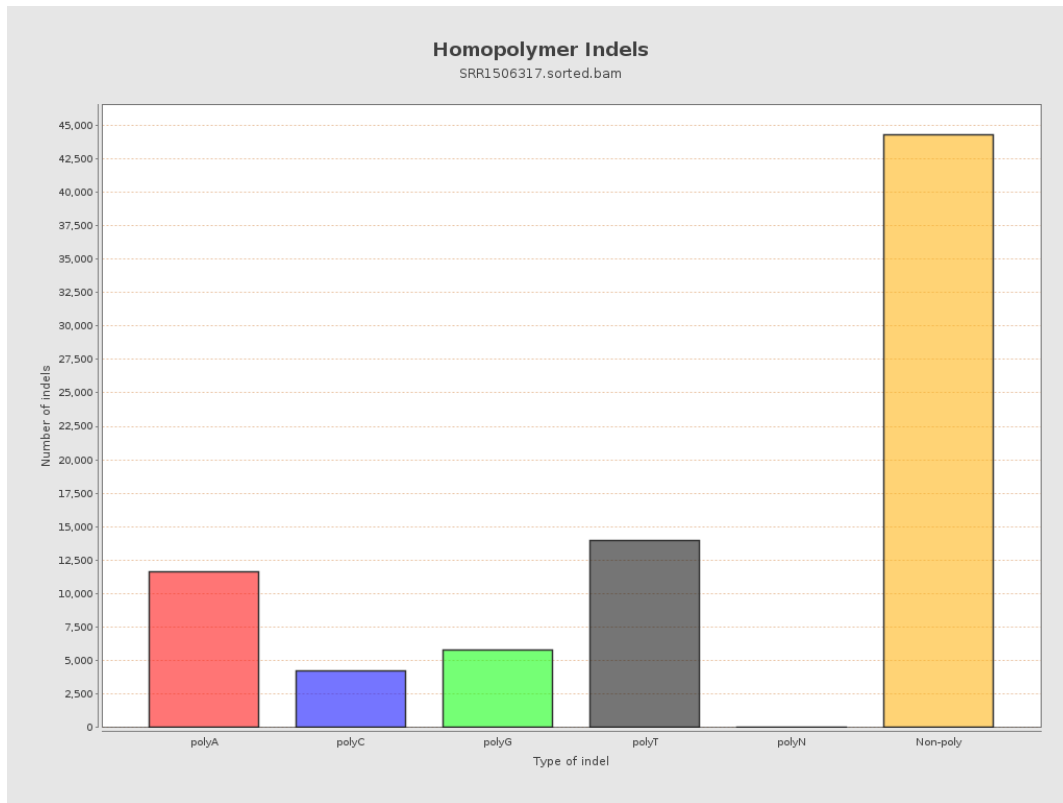
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

