

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/17 20:18:35*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006141.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_SRR1006141 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006141_1.fastq.gz SRR1006141_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                  |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                   |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                   |
| Analysis date:                        | Sun Apr 17 20:18:35 CST 2022                                                                                                                                                                                         |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                    |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                   |
| Number of windows:                    | 400                                                                                                                                                                                                                  |
| BAM file:                             | SRR1006141.sorted.bam                                                                                                                                                                                                |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 12,289,032          |
| Mapped reads                 | 10,702,607 / 87.09% |
| Unmapped reads               | 1,586,425 / 12.91%  |
| Mapped paired reads          | 10,702,607 / 87.09% |
| Mapped reads, first in pair  | 5,455,515 / 44.39%  |
| Mapped reads, second in pair | 5,247,092 / 42.7%   |
| Mapped reads, both in pair   | 9,678,720 / 78.76%  |
| Mapped reads, singletons     | 1,023,887 / 8.33%   |
| Secondary alignments         | 0                   |
| Read min/max/mean length     | 39 / 39 / 39        |
| Duplicated reads (estimated) | 763,761 / 6.21%     |
| Duplication rate             | 6.41%               |
| Clipped reads                | 814,069 / 6.62%     |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 111,840,908 / 27.06% |
| Number/percentage of C's | 90,146,902 / 21.81%  |
| Number/percentage of T's | 115,617,562 / 27.97% |
| Number/percentage of G's | 95,737,875 / 23.16%  |
| Number/percentage of N's | 18,243 / 0%          |
| GC Percentage            | 44.97%               |

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.1335 |
| Standard Deviation | 0.6829 |

## 2.4. Mapping Quality

|                      |      |
|----------------------|------|
| Mean Mapping Quality | 47.2 |
|----------------------|------|

## 2.5. Insert size

|                    |                |
|--------------------|----------------|
| Mean               | 65,824.87      |
| Standard Deviation | 2,493,504.08   |
| P25/Median/P75     | 81 / 116 / 154 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.46%     |
| Mismatches                               | 1,887,077 |
| Insertions                               | 13,387    |
| Mapped reads with at least one insertion | 0.13%     |
| Deletions                                | 36,235    |
| Mapped reads with at least one deletion  | 0.34%     |
| Homopolymer indels                       | 46.13%    |

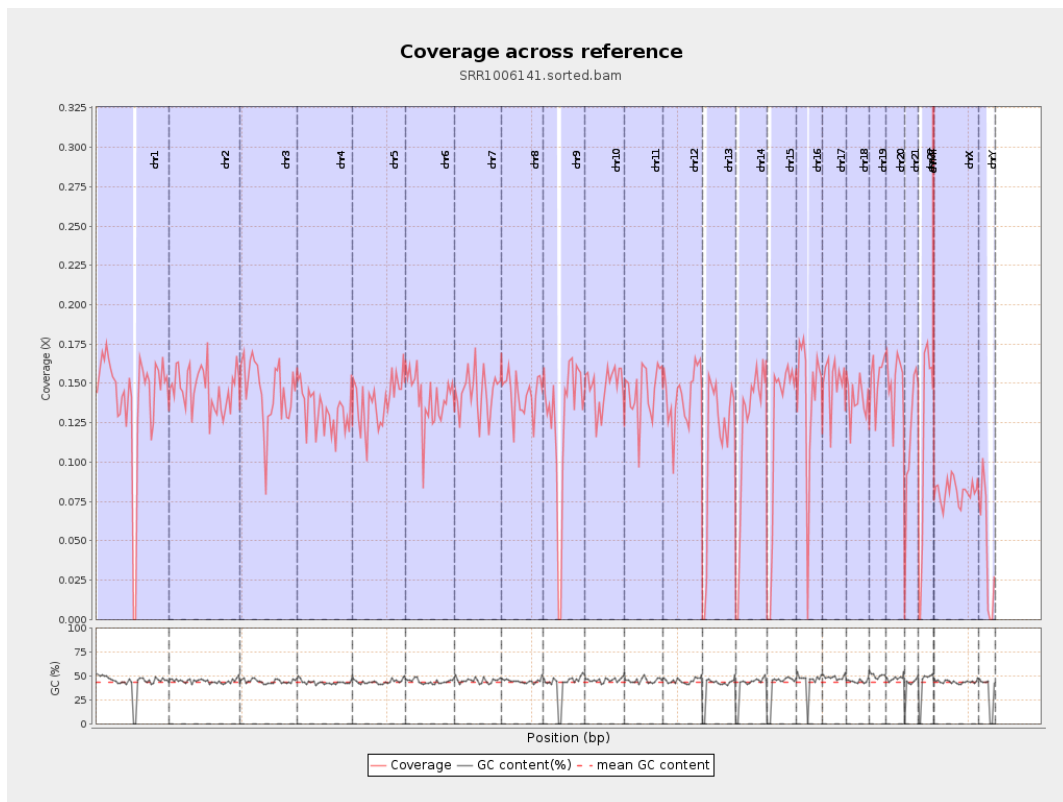
## 2.7. Chromosome stats

| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|------|--------|--------------|---------------|--------------------|
|      |        |              |               |                    |

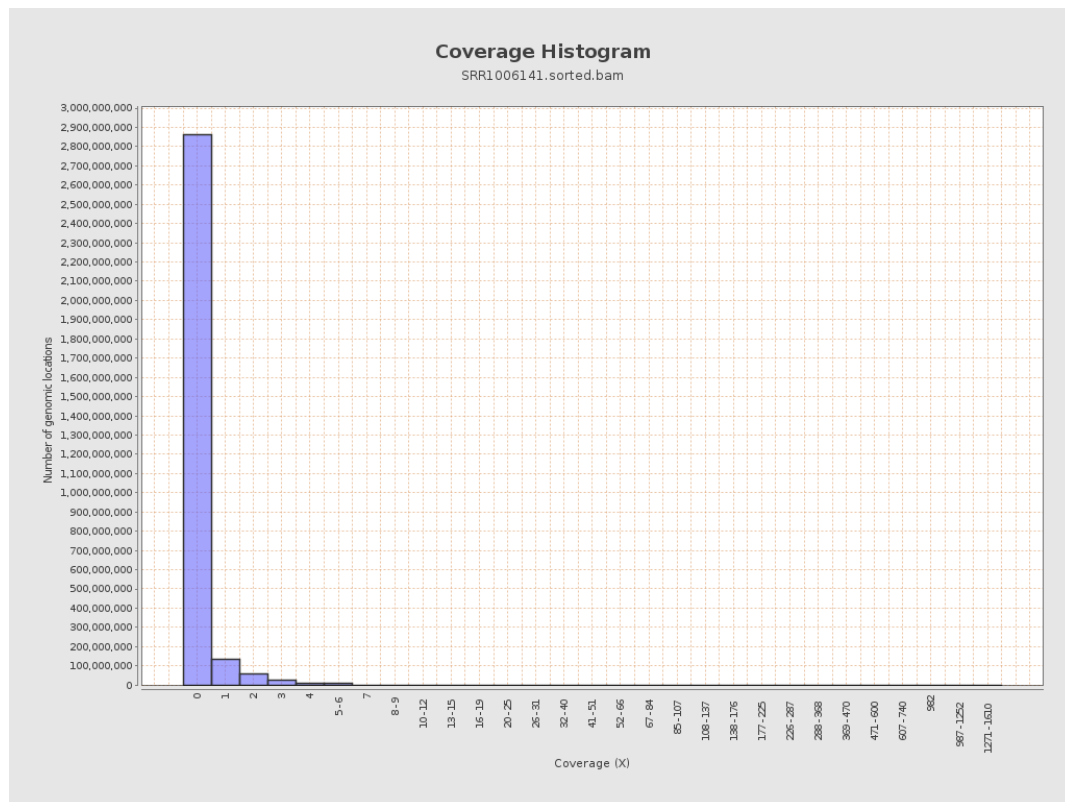
|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr1  | 249250621 | 35005056 | 0.1404 | 0.7265 |
| chr2  | 243199373 | 35625668 | 0.1465 | 0.7504 |
| chr3  | 198022430 | 28685826 | 0.1449 | 0.6004 |
| chr4  | 191154276 | 25307817 | 0.1324 | 0.5984 |
| chr5  | 180915260 | 25027731 | 0.1383 | 0.5854 |
| chr6  | 171115067 | 24050437 | 0.1406 | 0.6623 |
| chr7  | 159138663 | 22891045 | 0.1438 | 0.9215 |
| chr8  | 146364022 | 20944318 | 0.1431 | 0.7211 |
| chr9  | 141213431 | 17652384 | 0.125  | 0.624  |
| chr10 | 135534747 | 20046476 | 0.1479 | 0.637  |
| chr11 | 135006516 | 19524962 | 0.1446 | 1.0601 |
| chr12 | 133851895 | 18954233 | 0.1416 | 0.5969 |
| chr13 | 115169878 | 12944555 | 0.1124 | 0.5326 |
| chr14 | 107349540 | 12872950 | 0.1199 | 0.5654 |
| chr15 | 102531392 | 12650638 | 0.1234 | 0.5644 |
| chr16 | 90354753  | 12890628 | 0.1427 | 0.6663 |
| chr17 | 81195210  | 12266160 | 0.1511 | 0.6879 |
| chr18 | 78077248  | 10937286 | 0.1401 | 0.8474 |
| chr19 | 59128983  | 9056631  | 0.1532 | 0.8017 |
| chr20 | 63025520  | 9483208  | 0.1505 | 0.6266 |
| chr21 | 48129895  | 5563430  | 0.1156 | 0.6052 |
| chr22 | 51304566  | 5812729  | 0.1133 | 0.5874 |
| chrMT | 16571     | 55421    | 3.3445 | 4.1059 |
| chrX  | 155270560 | 12618055 | 0.0813 | 0.4823 |
|       |           |          |        |        |

|      |          |         |        |        |
|------|----------|---------|--------|--------|
| chrY | 59373566 | 2539823 | 0.0428 | 0.3554 |
|------|----------|---------|--------|--------|

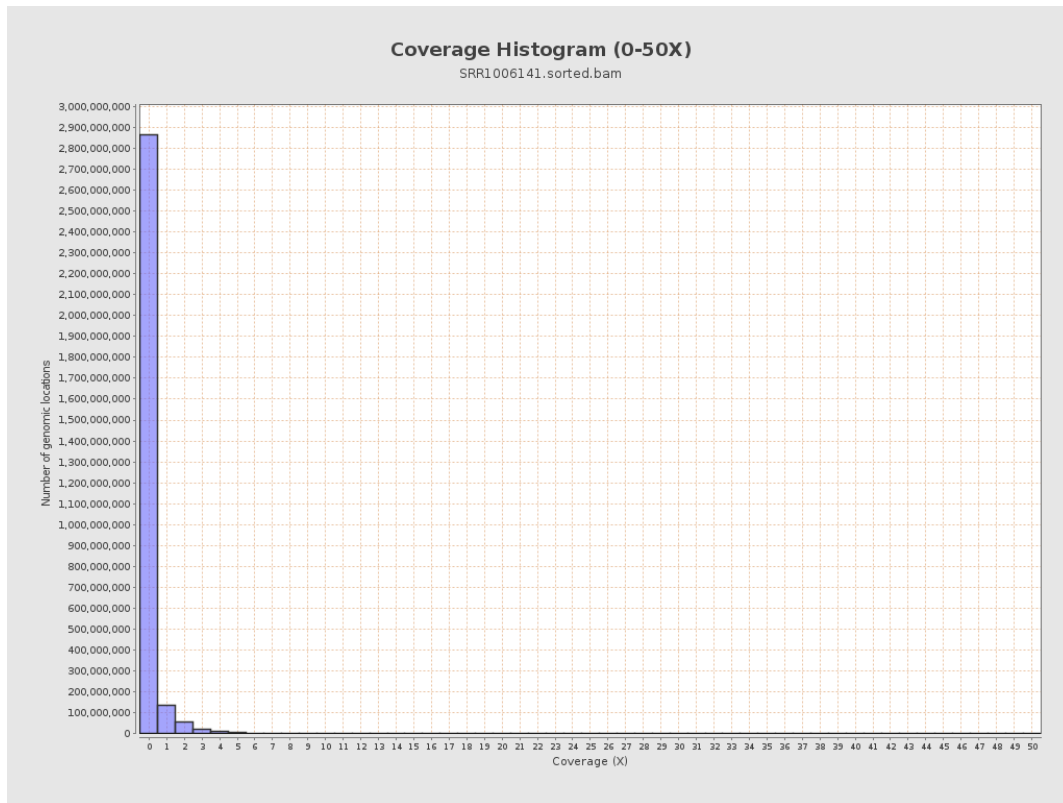
### 3. Results : Coverage across reference



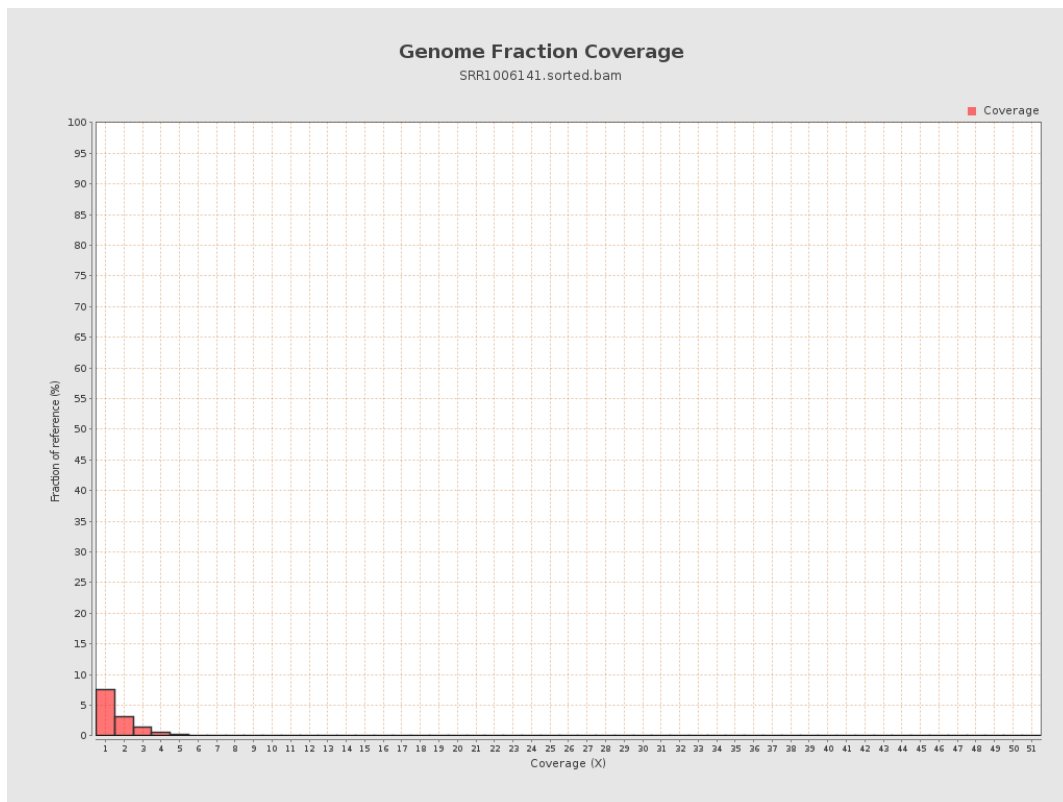
## 4. Results : Coverage Histogram



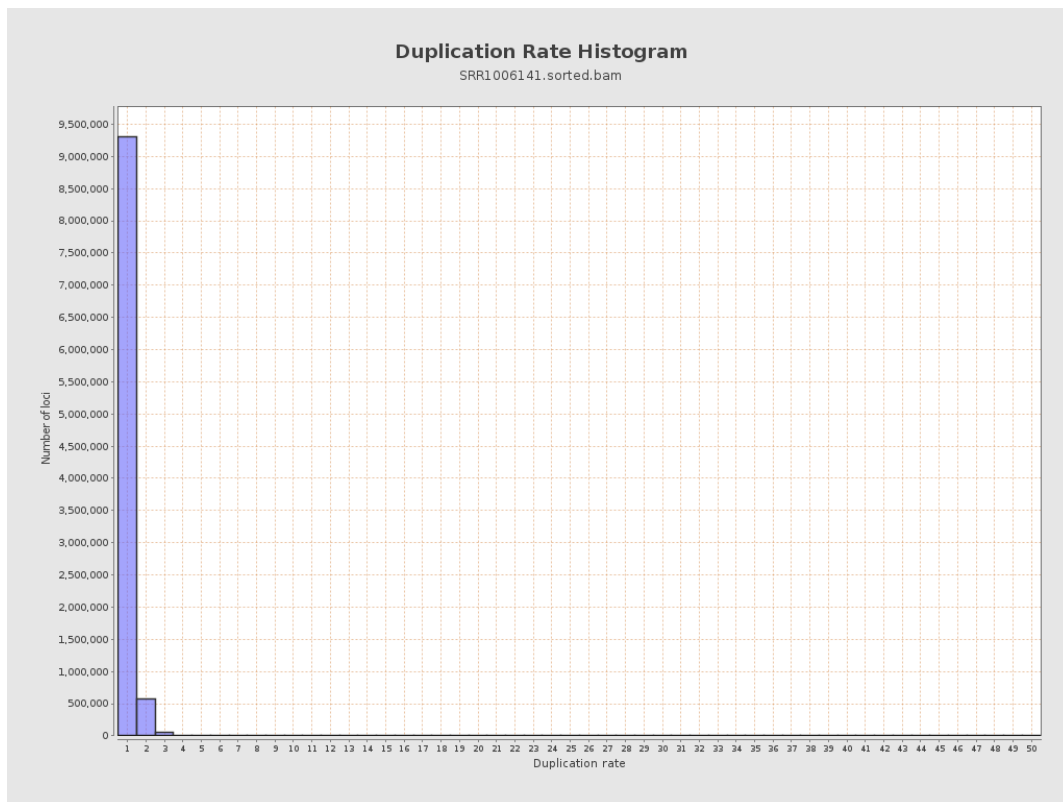
## 5. Results : Coverage Histogram (0-50X)



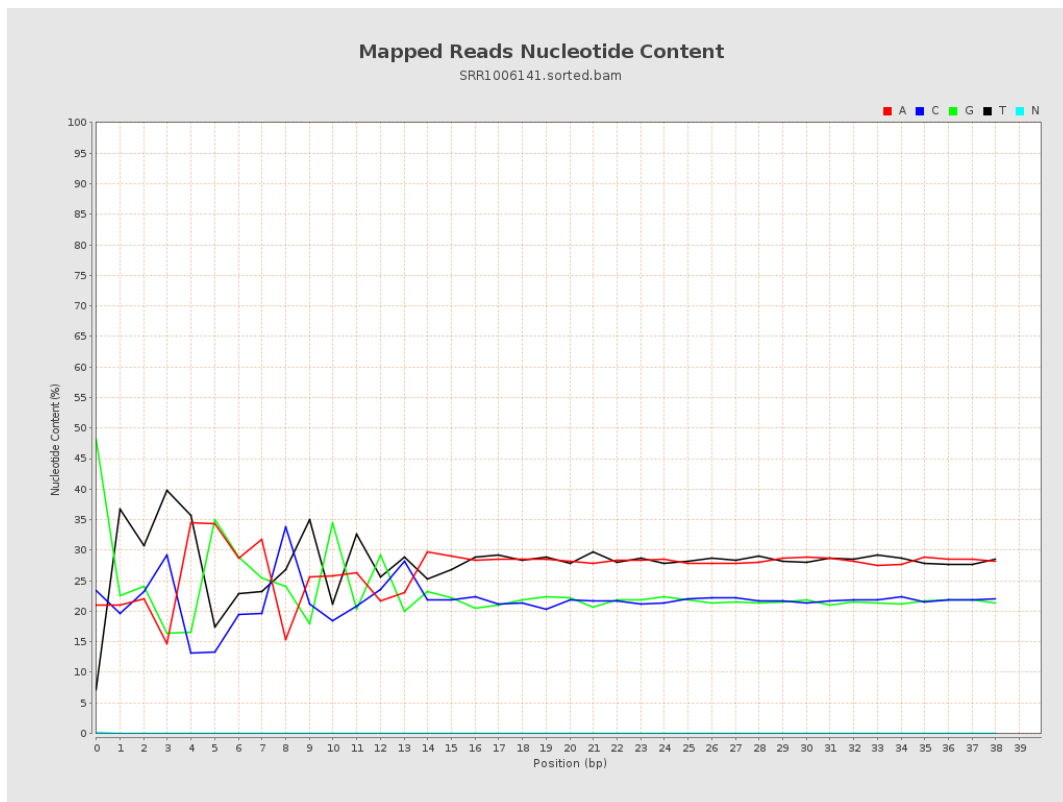
## 6. Results : Genome Fraction Coverage



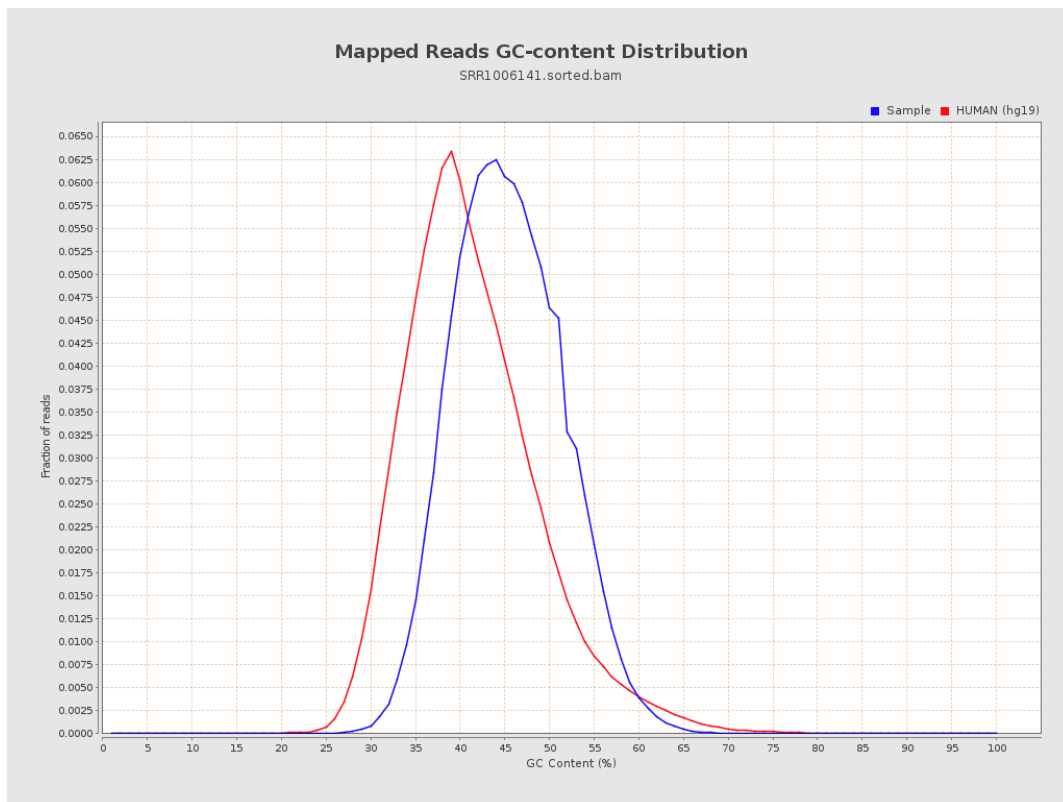
## 7. Results : Duplication Rate Histogram



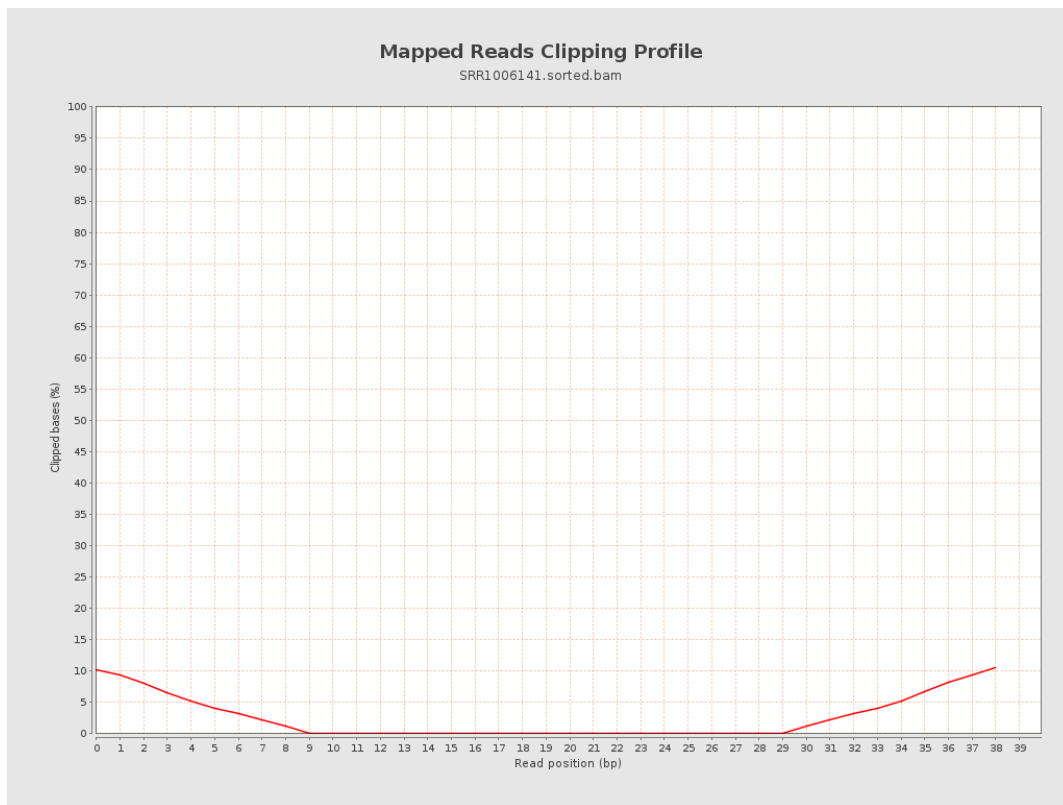
## 8. Results : Mapped Reads Nucleotide Content



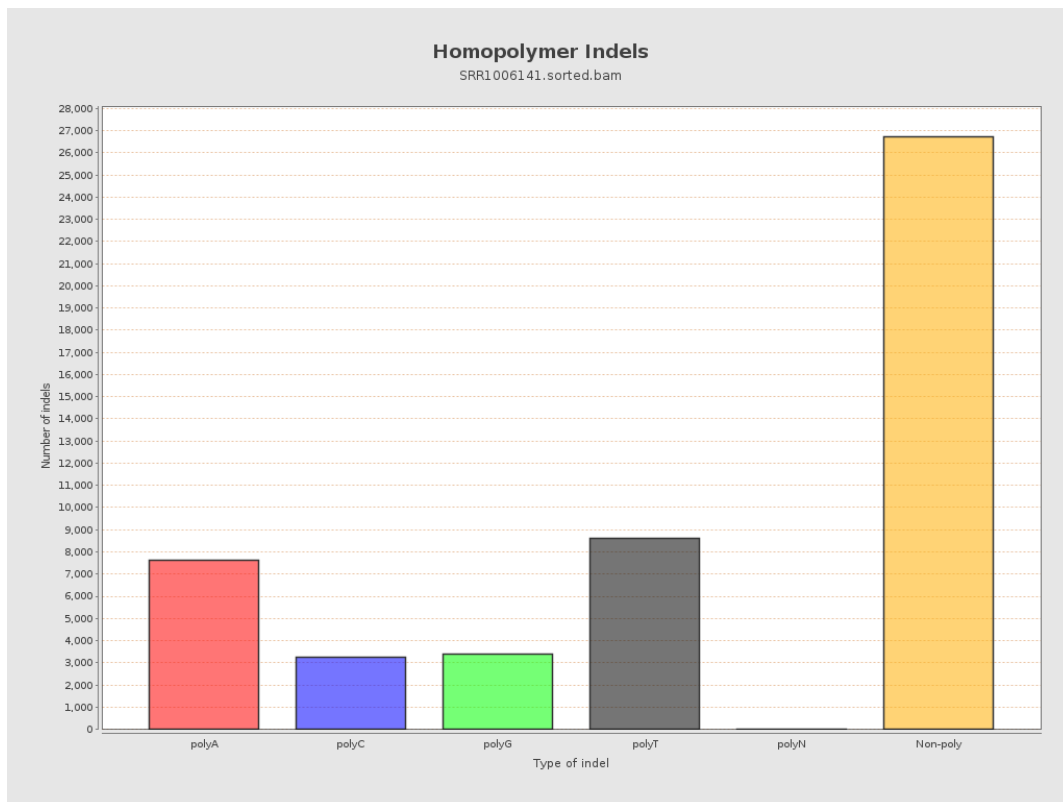
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



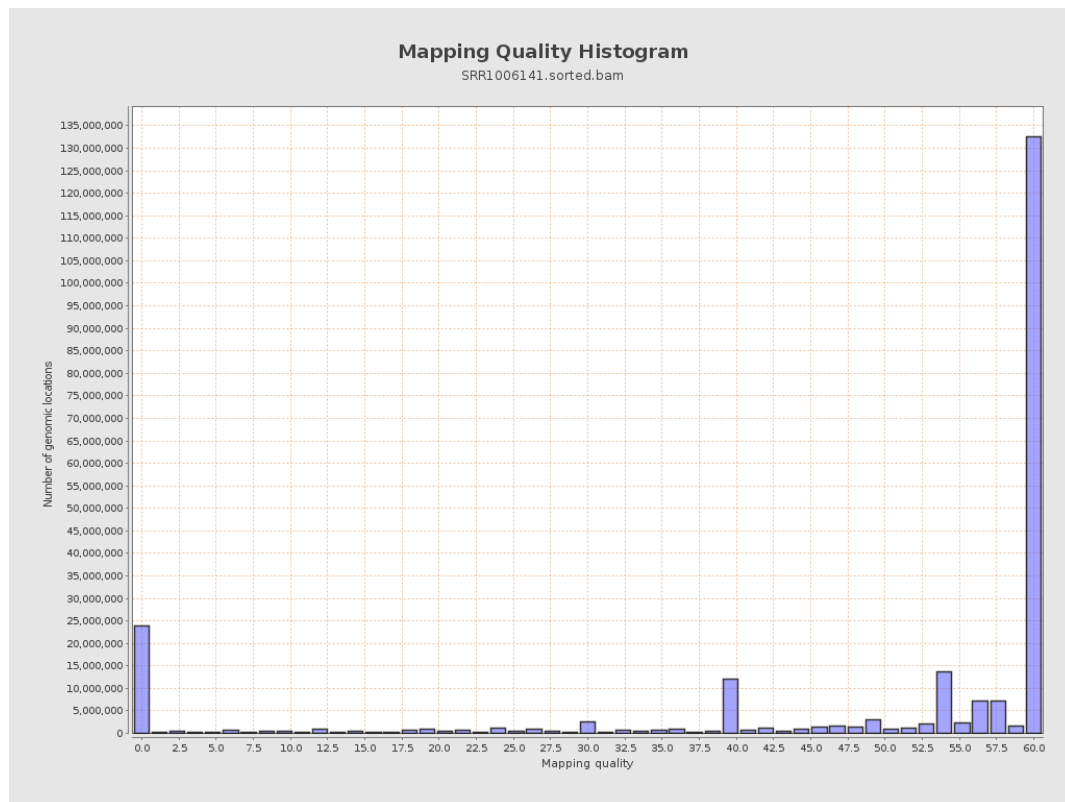
## 11. Results : Homopolymer Indels



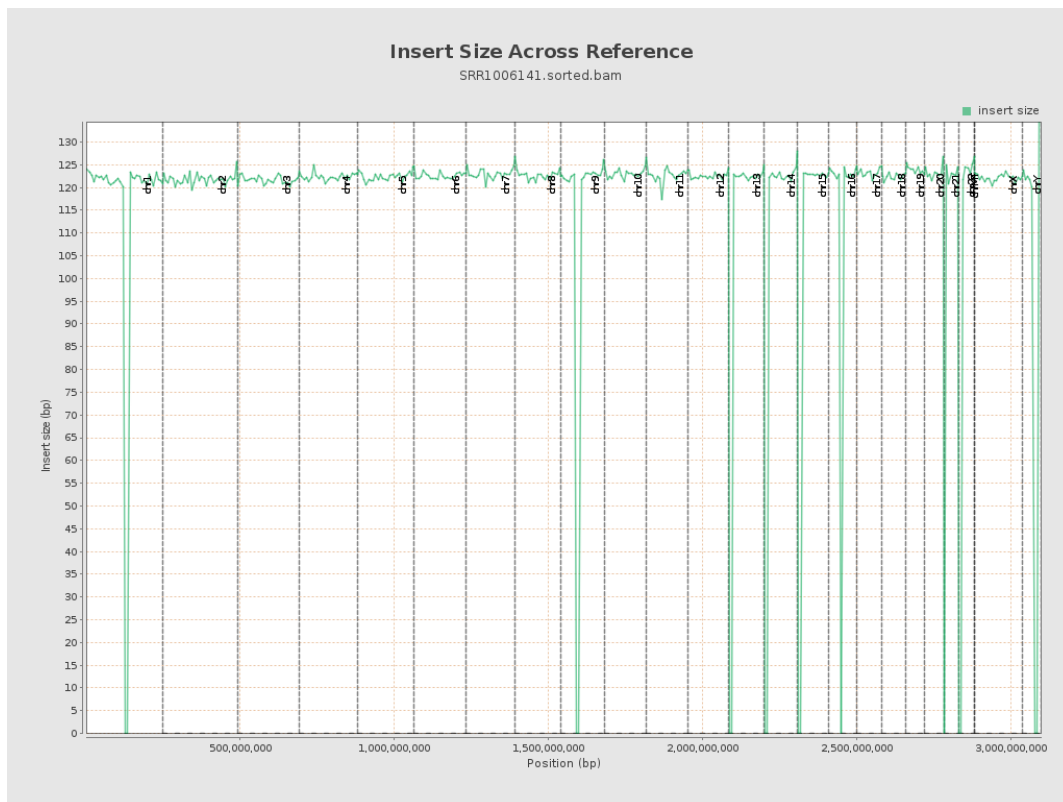
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

