

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/04 15:44:12*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173975.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_SRR10173975 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173975_1.fastq.gz SRR10173975_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                      |
| Analysis date:                        | Wed Sep 04 15:44:11 CST 2024                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                     |
| BAM file:                             | SRR10173975.sorted.bam                                                                                                                                                                                                  |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 4,162,458          |
| Mapped reads                 | 4,071,818 / 97.82% |
| Unmapped reads               | 90,640 / 2.18%     |
| Mapped paired reads          | 4,071,818 / 97.82% |
| Mapped reads, first in pair  | 2,038,214 / 48.97% |
| Mapped reads, second in pair | 2,033,604 / 48.86% |
| Mapped reads, both in pair   | 4,016,370 / 96.49% |
| Mapped reads, singletons     | 55,448 / 1.33%     |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 510,768 / 12.27%   |
| Read min/max/mean length     | 30 / 133 / 124.6   |
| Duplicated reads (estimated) | 3,262,771 / 78.39% |
| Duplication rate             | 64.73%             |
| Clipped reads                | 2,018,447 / 48.49% |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 137,743,644 / 29.99% |
| Number/percentage of C's | 90,909,917 / 19.79%  |
| Number/percentage of T's | 136,482,040 / 29.71% |
| Number/percentage of G's | 94,216,697 / 20.51%  |
| Number/percentage of N's | 3,610 / 0%           |
|                          |                      |

|               |       |
|---------------|-------|
| GC Percentage | 40.3% |
|---------------|-------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.1485 |
| Standard Deviation | 2.6685 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 52.62 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 1,022,602.59    |
| Standard Deviation | 9,200,106.66    |
| P25/Median/P75     | 104 / 151 / 232 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.88%     |
| Mismatches                               | 3,923,457 |
| Insertions                               | 49,712    |
| Mapped reads with at least one insertion | 1.17%     |
| Deletions                                | 136,453   |
| Mapped reads with at least one deletion  | 3.27%     |
| Homopolymer indels                       | 40.84%    |

## 2.7. Chromosome stats

| Name | Length | Mapped | Mean | Standard |
|------|--------|--------|------|----------|
|------|--------|--------|------|----------|

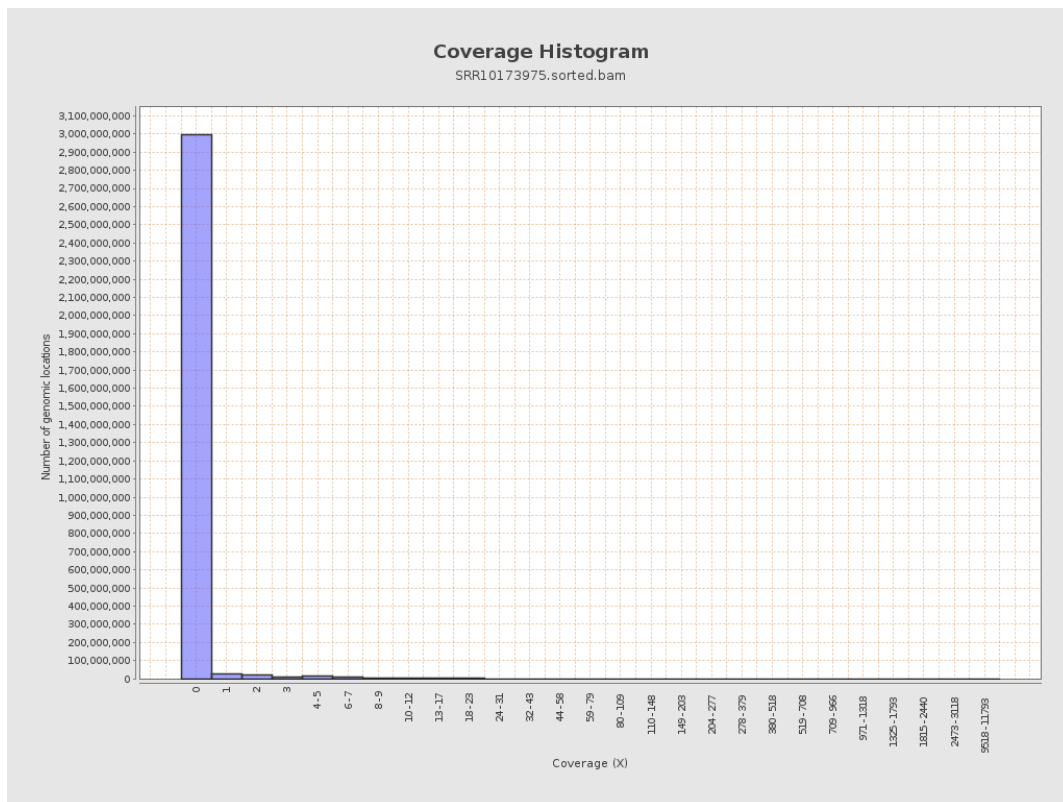
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 36854252     | 0.1479          | 1.43             |
| chr2  | 243199373 | 42610730     | 0.1752          | 8.3117           |
| chr3  | 198022430 | 32094275     | 0.1621          | 1.2374           |
| chr4  | 191154276 | 32079834     | 0.1678          | 1.5295           |
| chr5  | 180915260 | 28687821     | 0.1586          | 1.2224           |
| chr6  | 171115067 | 27300661     | 0.1595          | 1.3415           |
| chr7  | 159138663 | 25095913     | 0.1577          | 1.4791           |
| chr8  | 146364022 | 23755015     | 0.1623          | 1.7169           |
| chr9  | 141213431 | 19684258     | 0.1394          | 1.385            |
| chr10 | 135534747 | 22368122     | 0.165           | 1.8238           |
| chr11 | 135006516 | 20573627     | 0.1524          | 1.2022           |
| chr12 | 133851895 | 20968507     | 0.1567          | 1.2519           |
| chr13 | 115169878 | 14762609     | 0.1282          | 1.1003           |
| chr14 | 107349540 | 14368241     | 0.1338          | 1.1258           |
| chr15 | 102531392 | 12927130     | 0.1261          | 1.1051           |
| chr16 | 90354753  | 13264215     | 0.1468          | 1.3339           |
| chr17 | 81195210  | 12396136     | 0.1527          | 1.2427           |
| chr18 | 78077248  | 12745324     | 0.1632          | 1.7716           |
| chr19 | 59128983  | 8403878      | 0.1421          | 1.2602           |
| chr20 | 63025520  | 9871997      | 0.1566          | 1.2389           |
| chr21 | 48129895  | 6270129      | 0.1303          | 1.3688           |
| chr22 | 51304566  | 5592974      | 0.109           | 1.204            |
| chrMT | 16571     | 541067       | 32.6514         | 29.4889          |
| chrX  | 155270560 | 12757276     | 0.0822          | 0.8731           |

|      |          |         |        |        |
|------|----------|---------|--------|--------|
| chrY | 59373566 | 3711822 | 0.0625 | 0.9989 |
|------|----------|---------|--------|--------|

### 3. Results : Coverage across reference

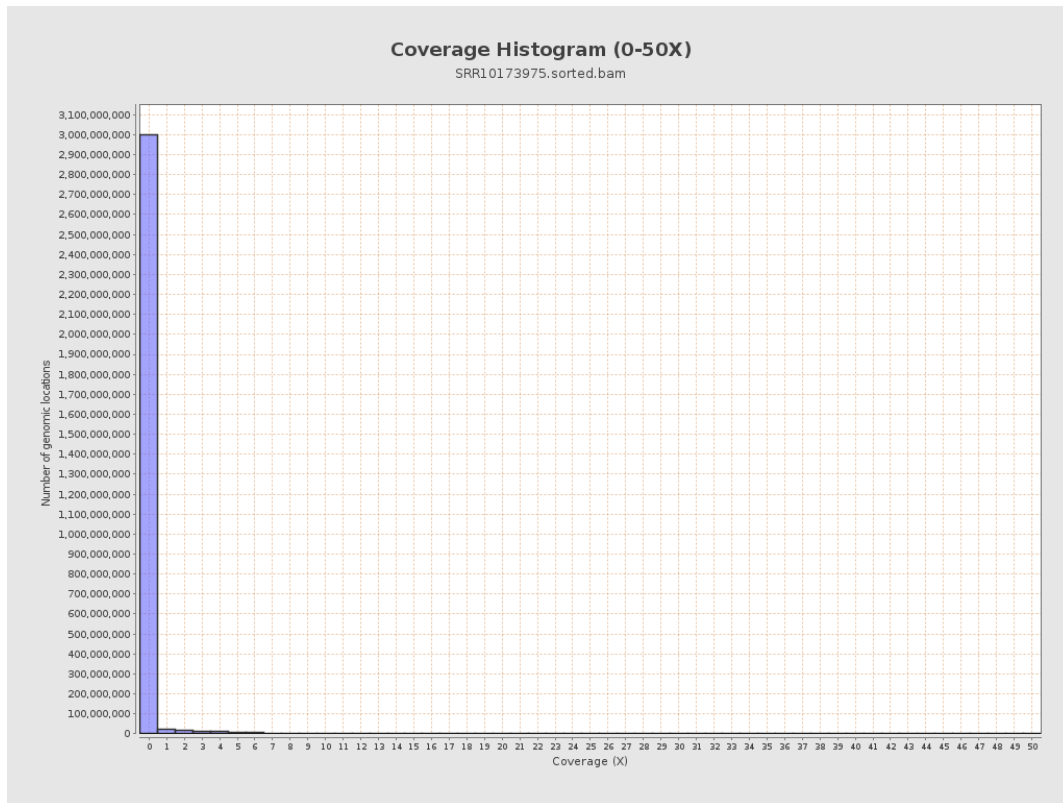


## 4. Results : Coverage Histogram

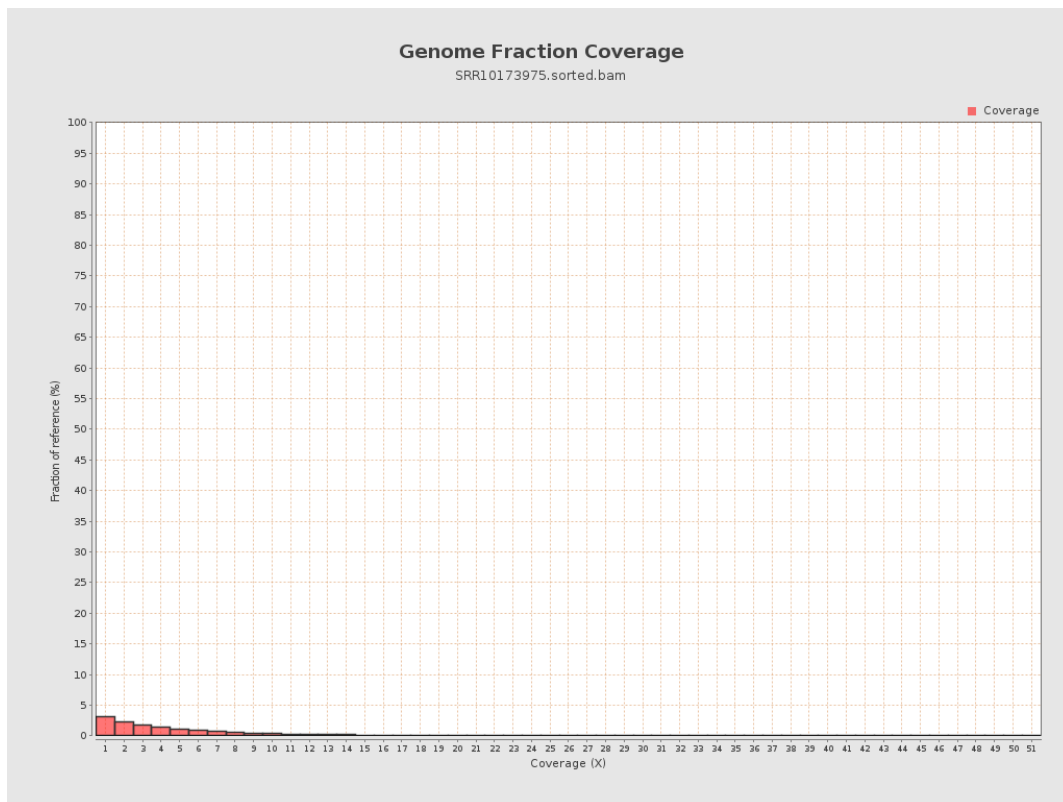




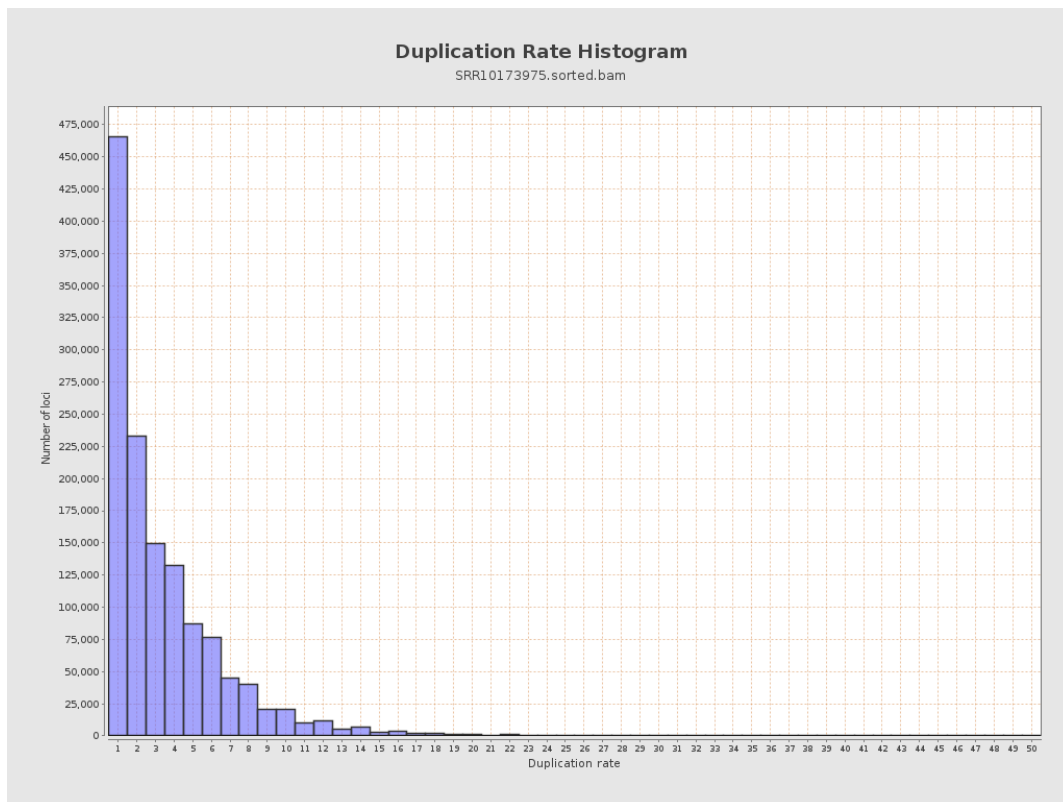
## 5. Results : Coverage Histogram (0-50X)



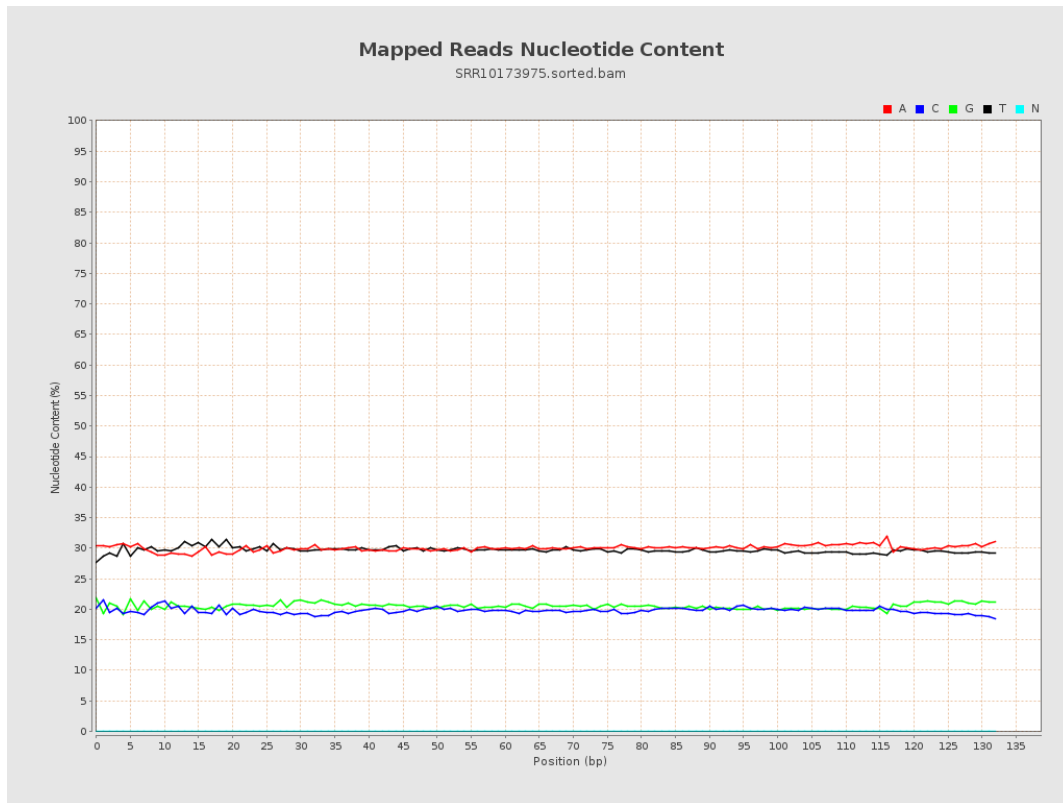
## 6. Results : Genome Fraction Coverage



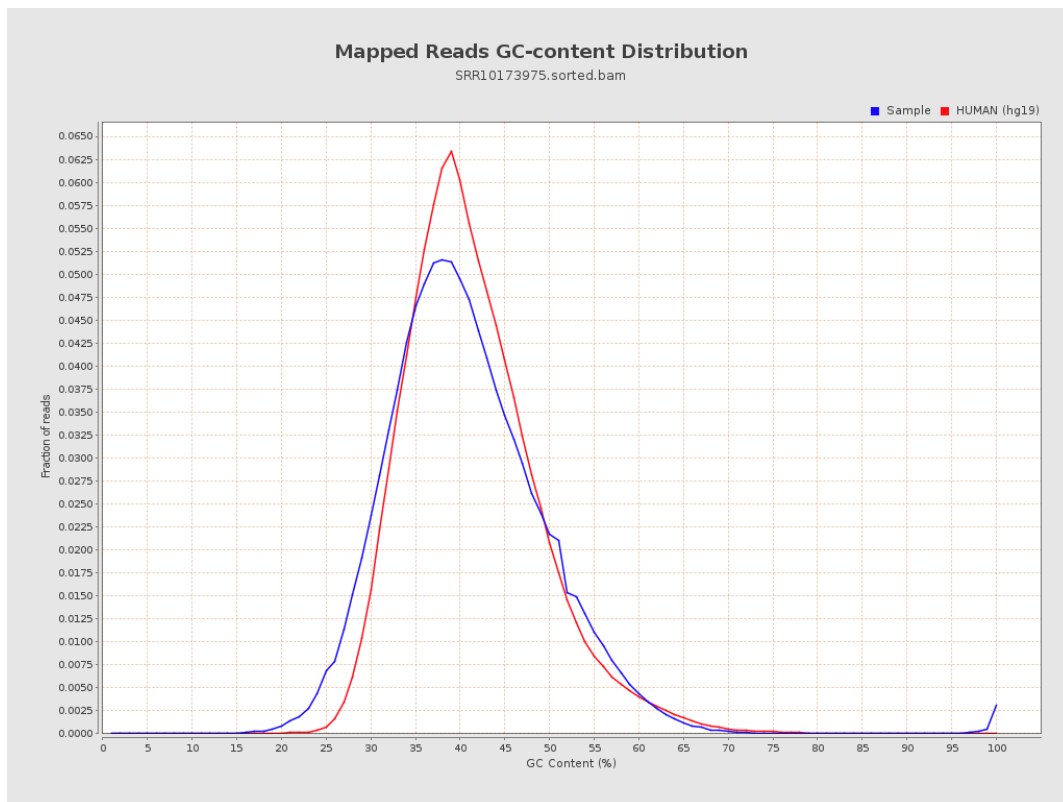
## 7. Results : Duplication Rate Histogram



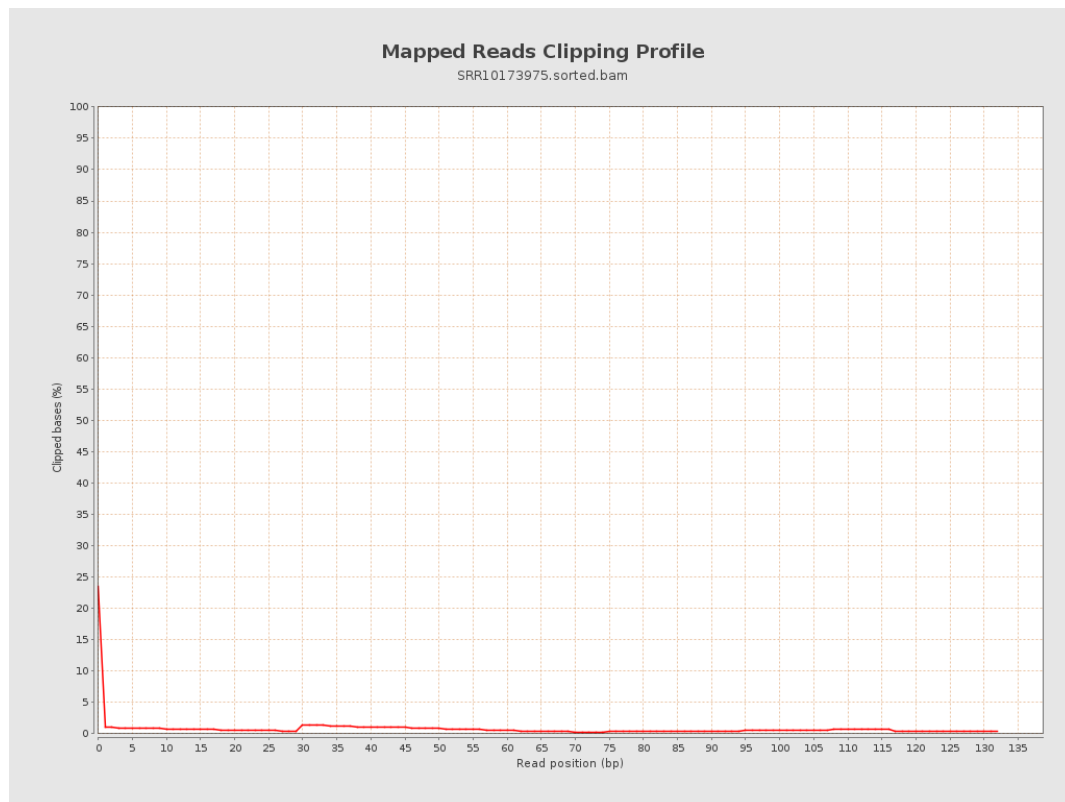
## 8. Results : Mapped Reads Nucleotide Content



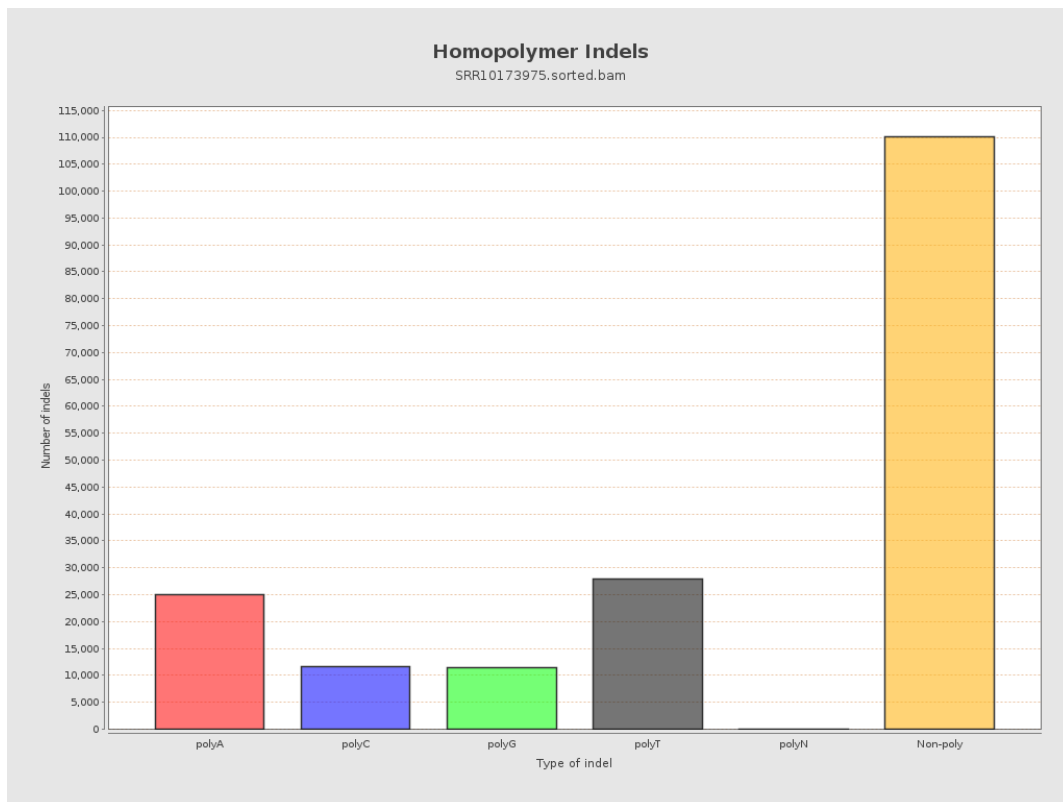
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

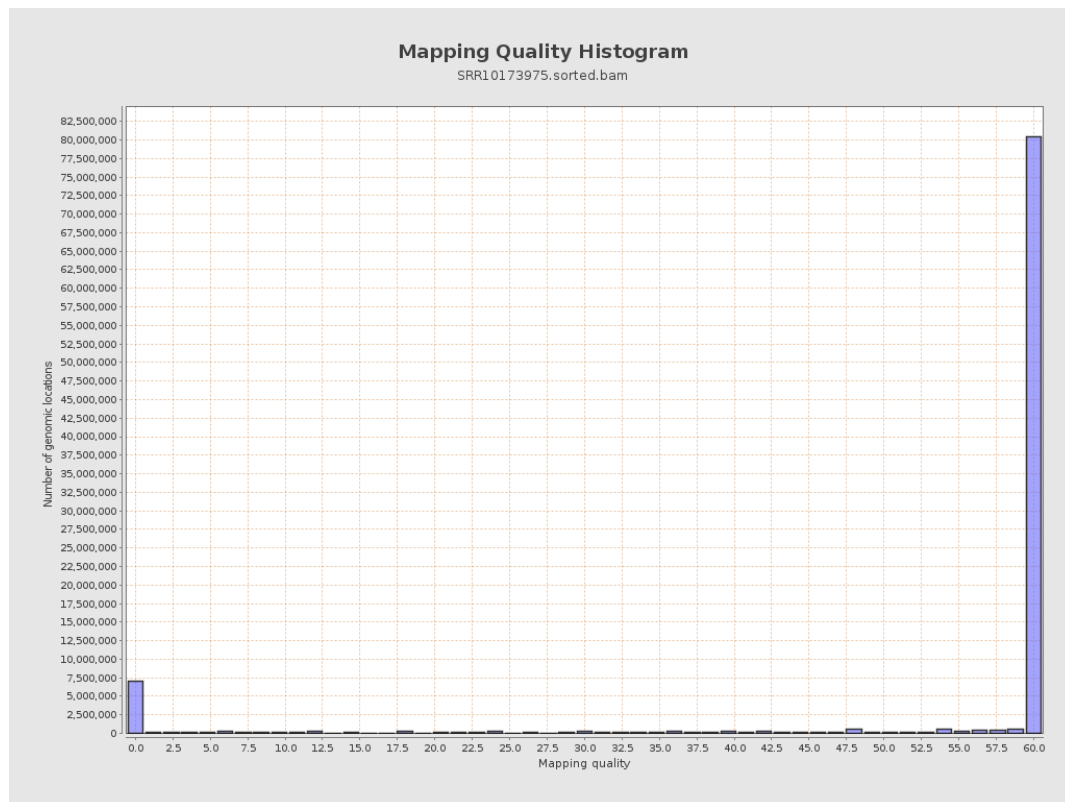


## 12. Results : Mapping Quality Across Reference

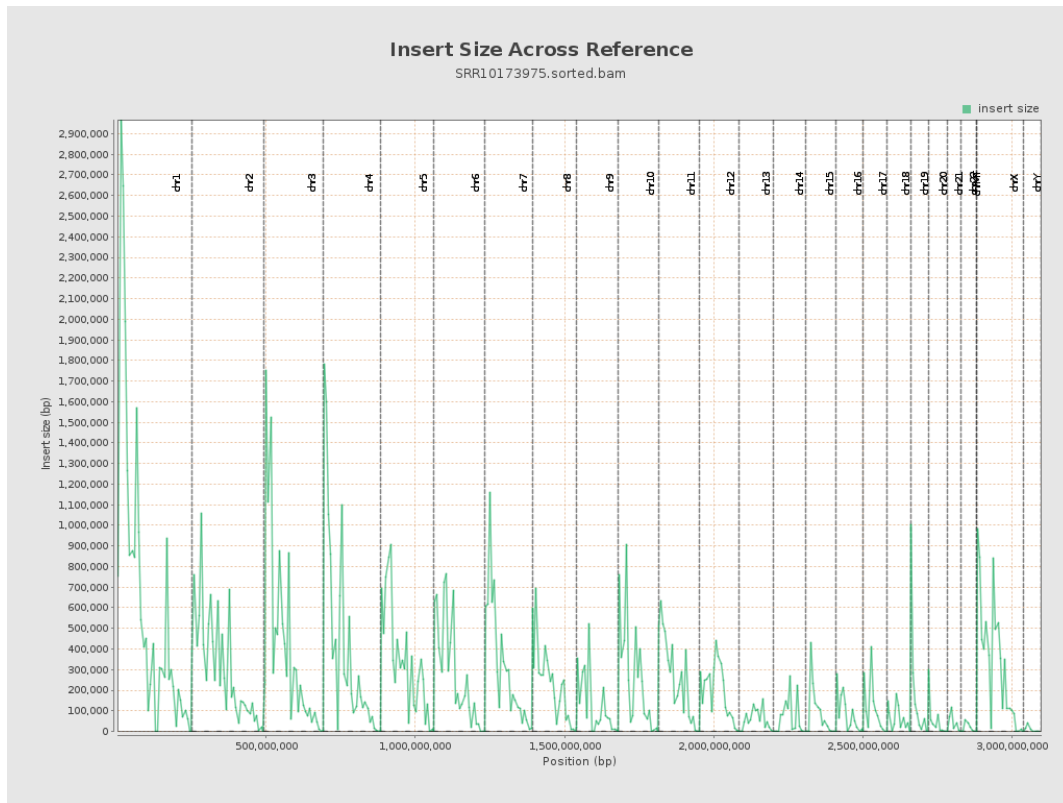




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

