

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/04 02:55:31*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173896.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_SRR10173896 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173896_1.fastq.gz SRR10173896_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                      |
| Analysis date:                        | Wed Sep 04 02:55:31 CST 2024                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                     |
| BAM file:                             | SRR10173896.sorted.bam                                                                                                                                                                                                  |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 6,229,730          |
| Mapped reads                 | 6,056,153 / 97.21% |
| Unmapped reads               | 173,577 / 2.79%    |
| Mapped paired reads          | 6,056,153 / 97.21% |
| Mapped reads, first in pair  | 3,035,096 / 48.72% |
| Mapped reads, second in pair | 3,021,057 / 48.49% |
| Mapped reads, both in pair   | 5,942,444 / 95.39% |
| Mapped reads, singletons     | 113,709 / 1.83%    |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 606,642 / 9.74%    |
| Read min/max/mean length     | 30 / 133 / 128.27  |
| Duplicated reads (estimated) | 4,854,222 / 77.92% |
| Duplication rate             | 66.04%             |
| Clipped reads                | 2,411,827 / 38.71% |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 216,050,036 / 30.15% |
| Number/percentage of C's | 140,027,813 / 19.54% |
| Number/percentage of T's | 215,531,765 / 30.08% |
| Number/percentage of G's | 145,006,125 / 20.23% |
| Number/percentage of N's | 8,633 / 0%           |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 39.77% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.2316 |
| Standard Deviation | 3.2829 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 52.77 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 737,948.4       |
| Standard Deviation | 7,996,174.37    |
| P25/Median/P75     | 147 / 203 / 289 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 1.06%     |
| Mismatches                               | 7,385,243 |
| Insertions                               | 72,058    |
| Mapped reads with at least one insertion | 1.15%     |
| Deletions                                | 156,525   |
| Mapped reads with at least one deletion  | 2.52%     |
| Homopolymer indels                       | 43.17%    |

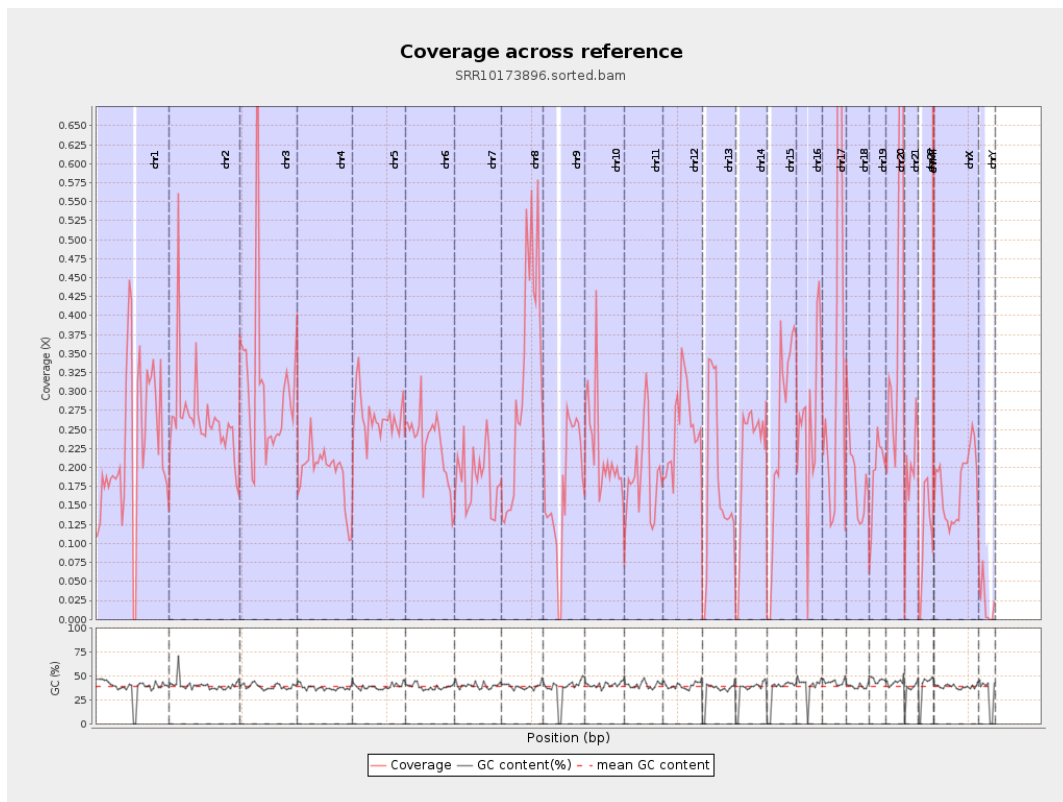
## 2.7. Chromosome stats

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

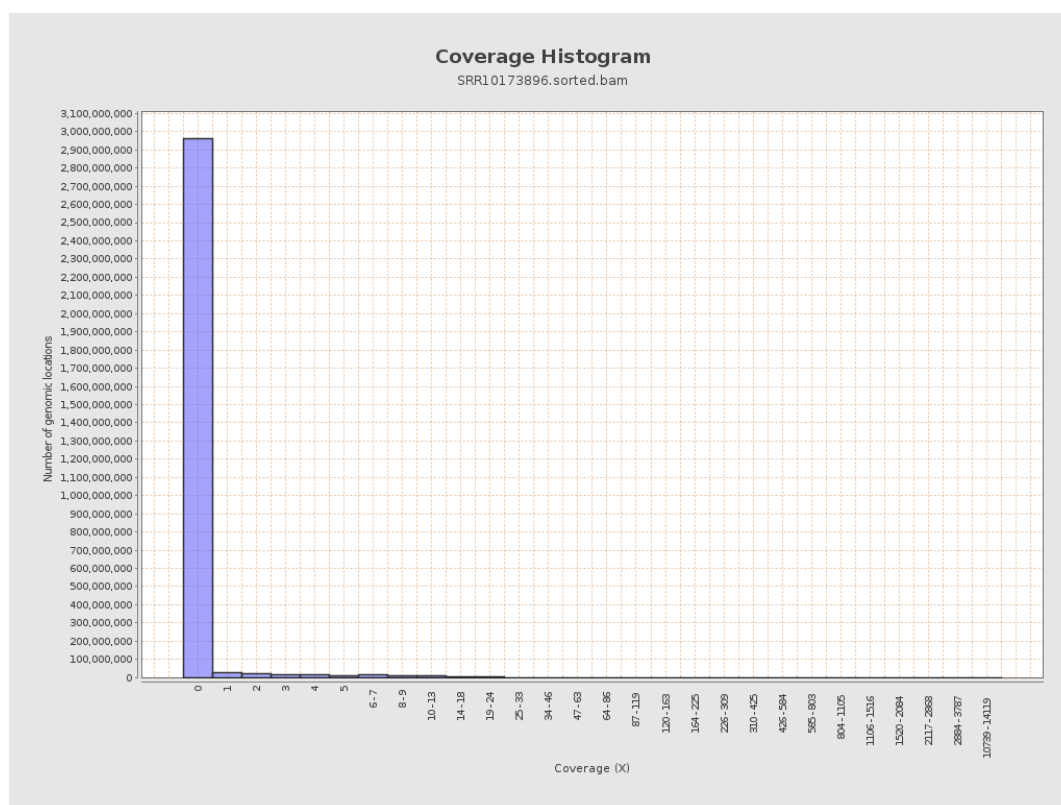
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 56197118     | 0.2255          | 2.2738           |
| chr2  | 243199373 | 64181909     | 0.2639          | 9.8955           |
| chr3  | 198022430 | 59693187     | 0.3014          | 1.6914           |
| chr4  | 191154276 | 36704003     | 0.192           | 1.4916           |
| chr5  | 180915260 | 48280081     | 0.2669          | 1.5554           |
| chr6  | 171115067 | 39189721     | 0.229           | 1.7494           |
| chr7  | 159138663 | 29624943     | 0.1862          | 1.8157           |
| chr8  | 146364022 | 45817563     | 0.313           | 2.2211           |
| chr9  | 141213431 | 24353757     | 0.1725          | 1.7328           |
| chr10 | 135534747 | 30043674     | 0.2217          | 2.8568           |
| chr11 | 135006516 | 25674262     | 0.1902          | 1.3756           |
| chr12 | 133851895 | 33758457     | 0.2522          | 1.5254           |
| chr13 | 115169878 | 19824039     | 0.1721          | 1.2695           |
| chr14 | 107349540 | 22849942     | 0.2129          | 1.3988           |
| chr15 | 102531392 | 25128771     | 0.2451          | 1.4878           |
| chr16 | 90354753  | 24275460     | 0.2687          | 2.0183           |
| chr17 | 81195210  | 29550056     | 0.3639          | 1.9919           |
| chr18 | 78077248  | 14698964     | 0.1883          | 2.6401           |
| chr19 | 59128983  | 11542504     | 0.1952          | 1.8476           |
| chr20 | 63025520  | 31092136     | 0.4933          | 2.325            |
| chr21 | 48129895  | 9352084      | 0.1943          | 1.3816           |
| chr22 | 51304566  | 5486376      | 0.1069          | 0.9409           |
| chrMT | 16571     | 1159281      | 69.9584         | 53.9894          |
| chrX  | 155270560 | 27312592     | 0.1759          | 1.2671           |

|      |          |         |        |        |
|------|----------|---------|--------|--------|
| chrY | 59373566 | 1212077 | 0.0204 | 0.7648 |
|------|----------|---------|--------|--------|

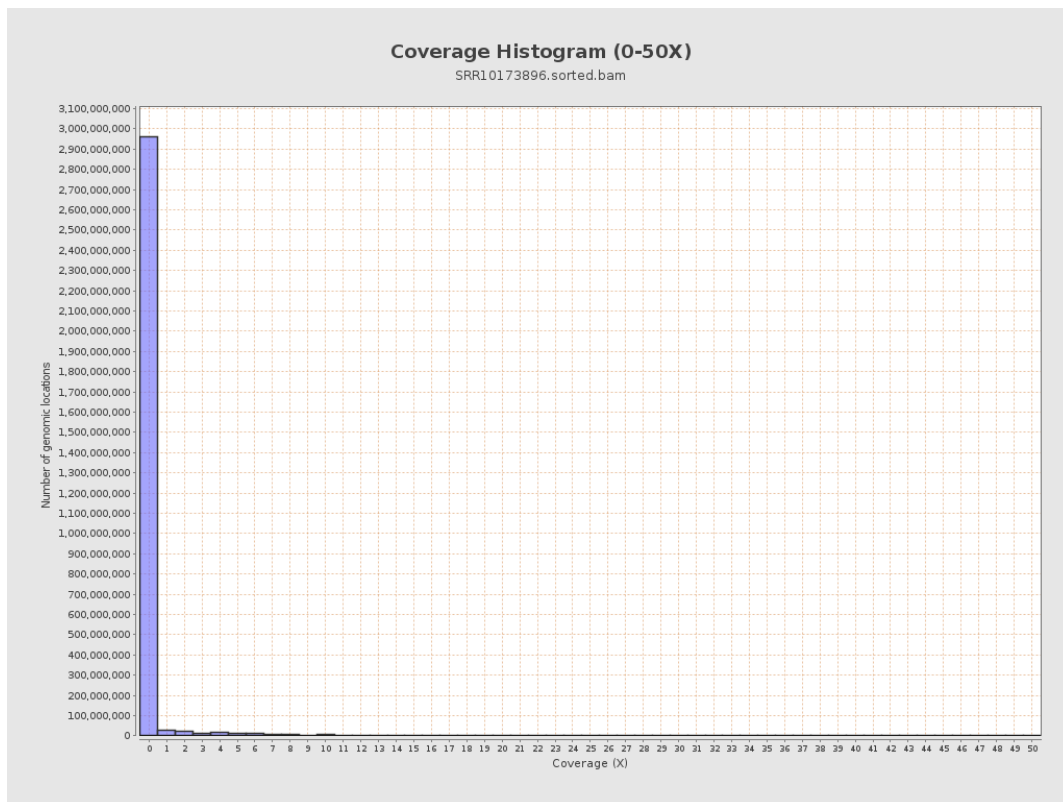
### 3. Results : Coverage across reference



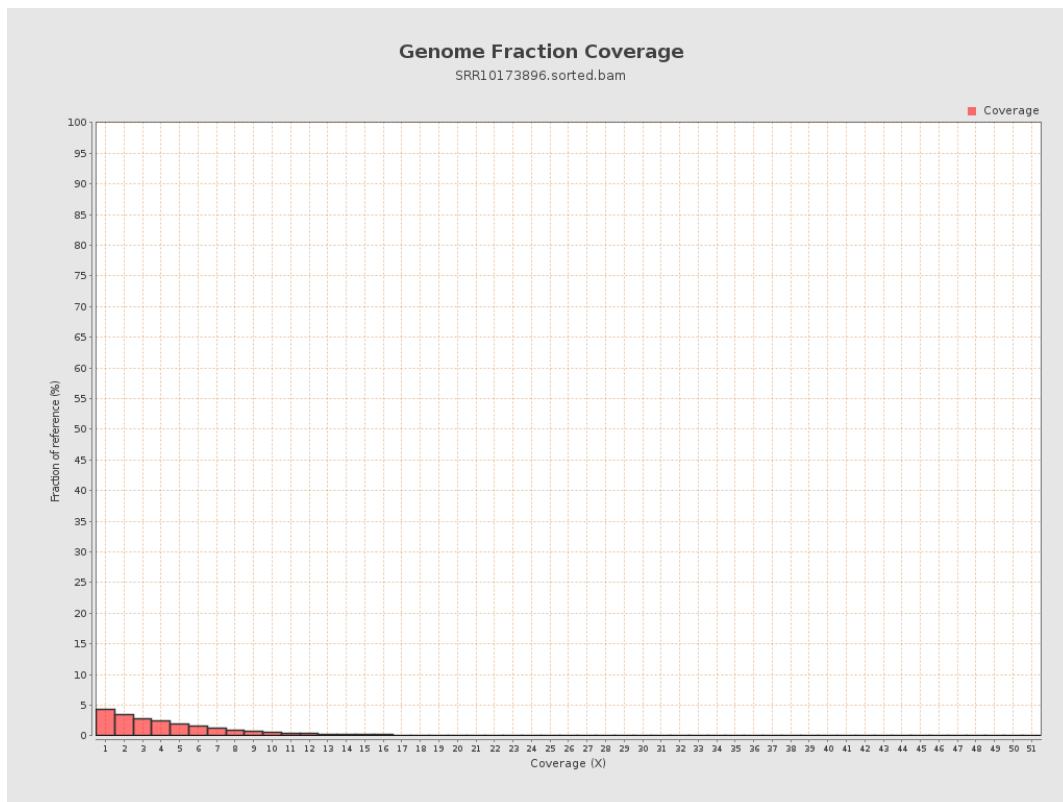
## 4. Results : Coverage Histogram



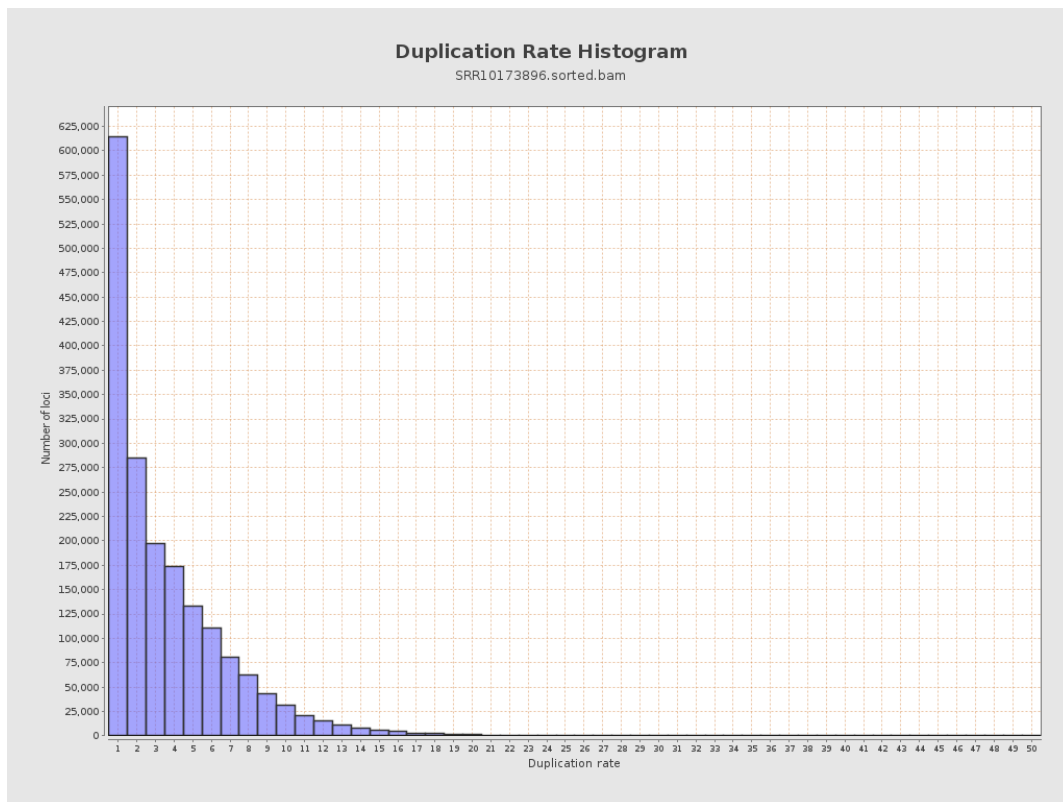
## 5. Results : Coverage Histogram (0-50X)



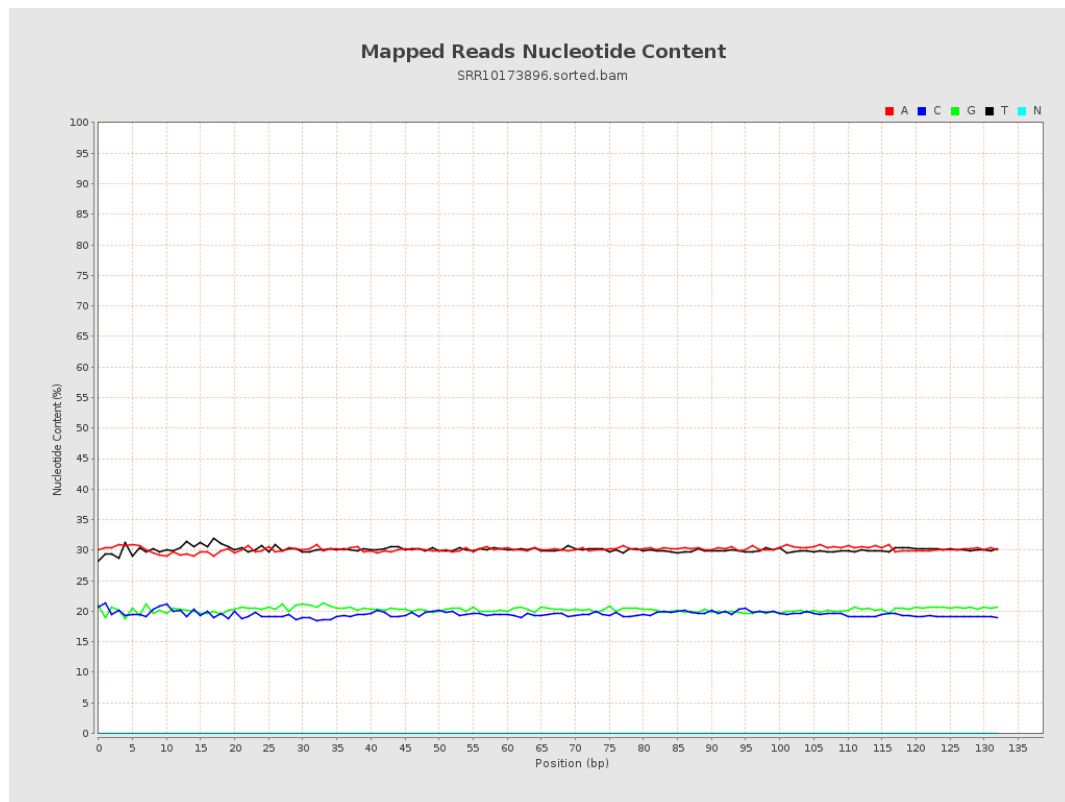
## 6. Results : Genome Fraction Coverage



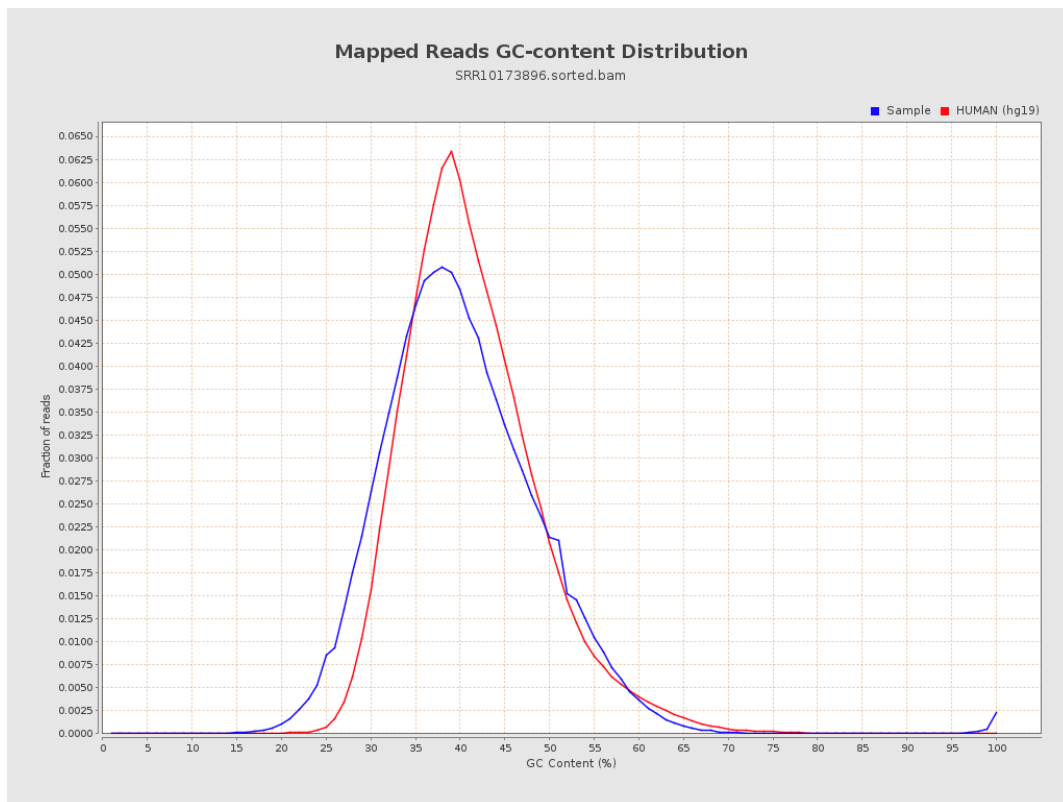
## 7. Results : Duplication Rate Histogram



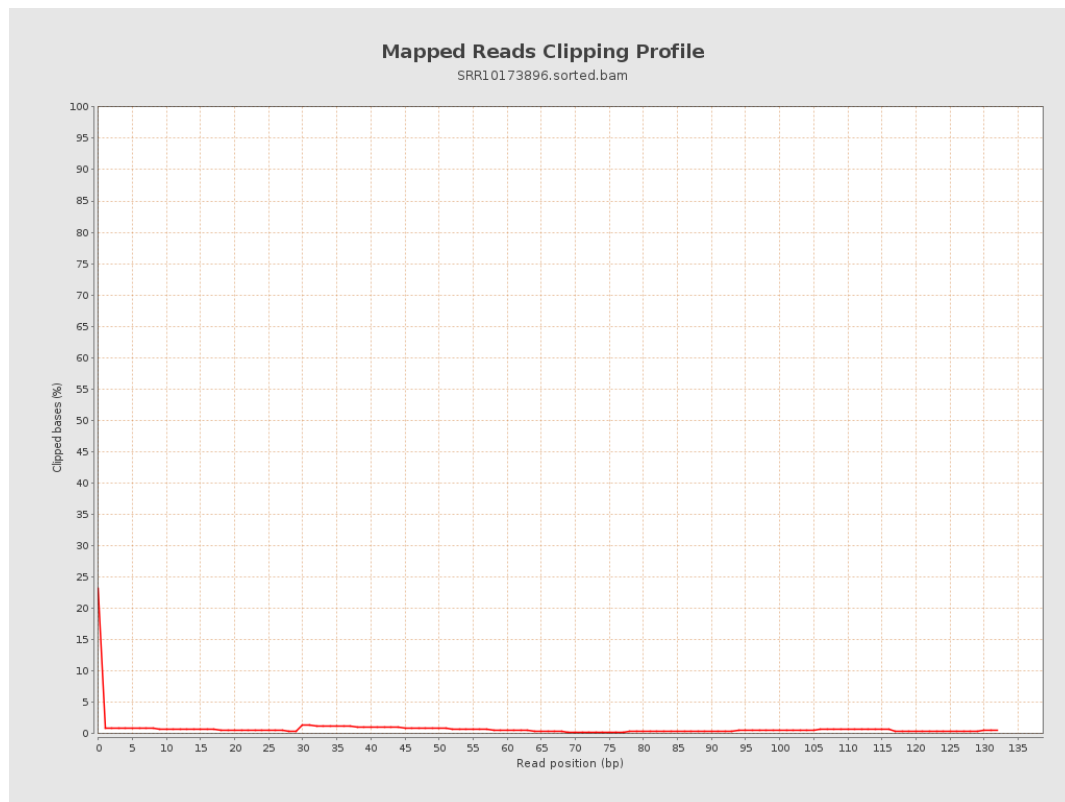
## 8. Results : Mapped Reads Nucleotide Content



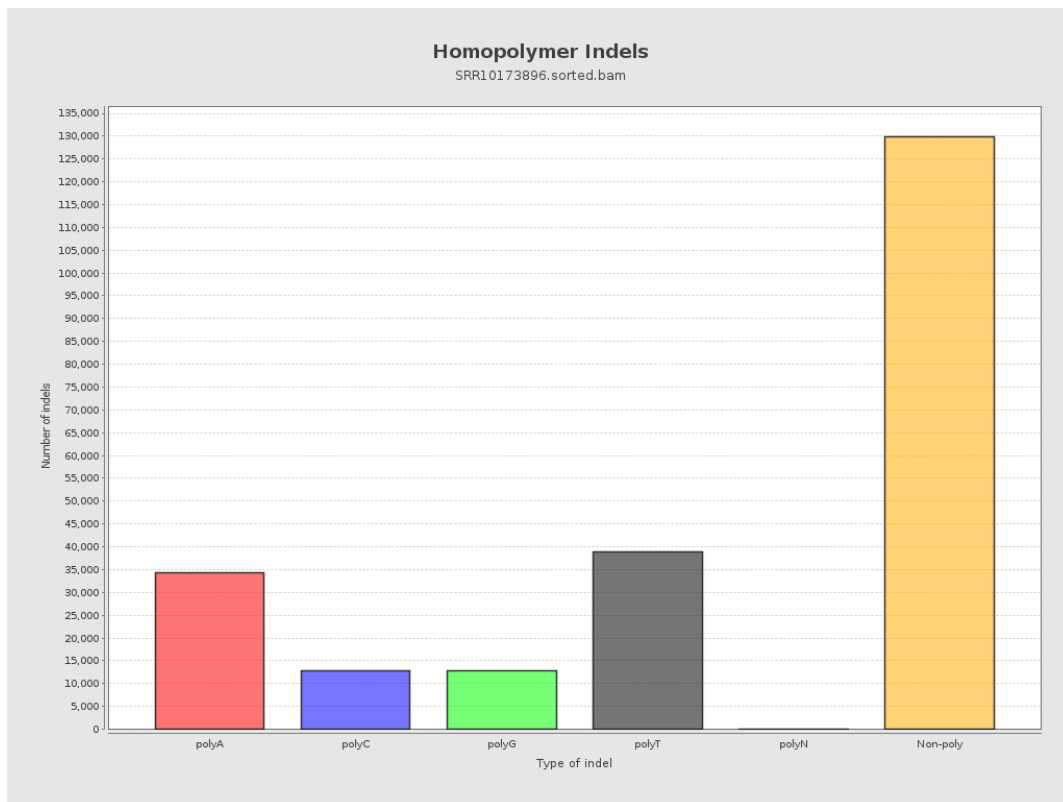
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



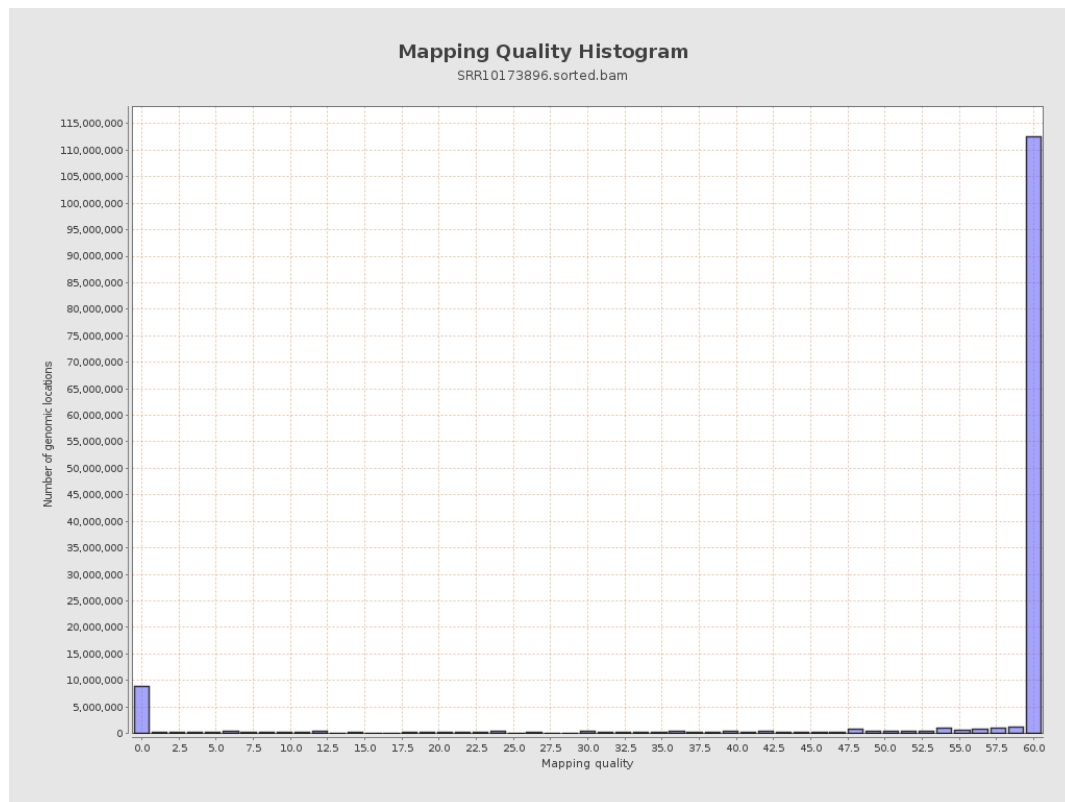
## 11. Results : Homopolymer Indels



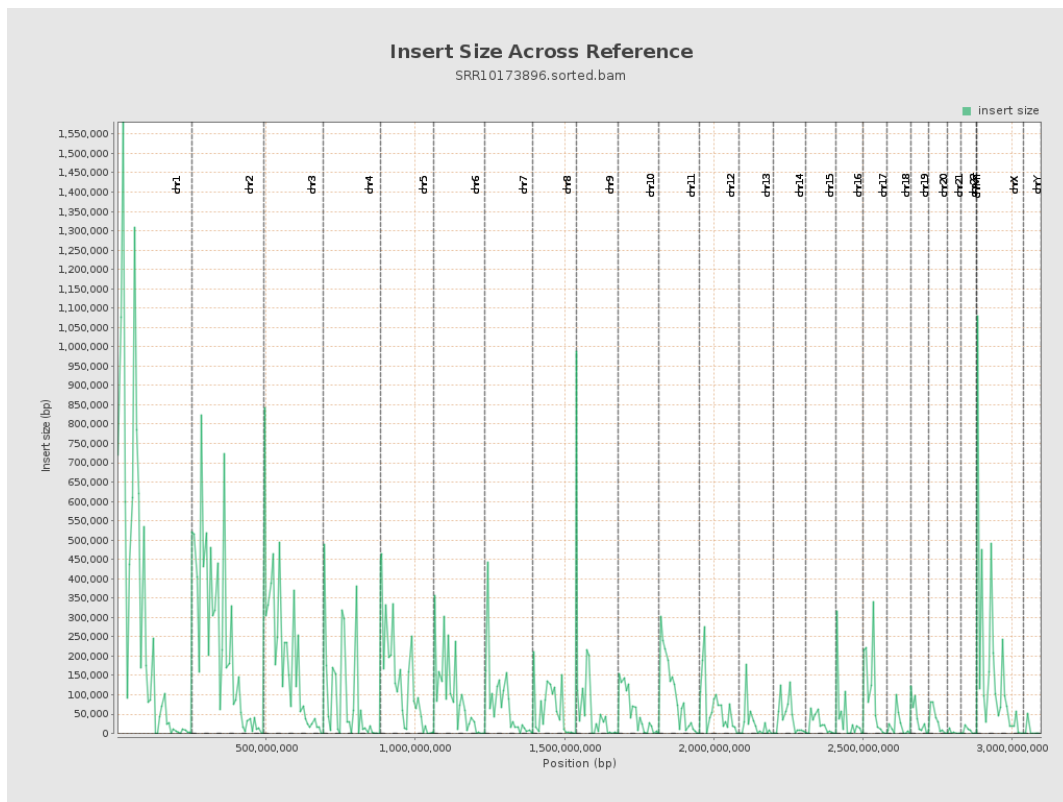
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

