

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/04 05:51:20*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173911.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_SRR10173911 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173911_1.fastq.gz SRR10173911_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                      |
| Analysis date:                        | Wed Sep 04 05:51:19 CST 2024                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                     |
| BAM file:                             | SRR10173911.sorted.bam                                                                                                                                                                                                  |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 4,987,290          |
| Mapped reads                 | 4,871,803 / 97.68% |
| Unmapped reads               | 115,487 / 2.32%    |
| Mapped paired reads          | 4,871,803 / 97.68% |
| Mapped reads, first in pair  | 2,438,280 / 48.89% |
| Mapped reads, second in pair | 2,433,523 / 48.79% |
| Mapped reads, both in pair   | 4,792,284 / 96.09% |
| Mapped reads, singletons     | 79,519 / 1.59%     |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 502,057 / 10.07%   |
| Read min/max/mean length     | 30 / 133 / 128.55  |
| Duplicated reads (estimated) | 3,809,137 / 76.38% |
| Duplication rate             | 64.6%              |
| Clipped reads                | 1,983,584 / 39.77% |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 173,296,369 / 29.99% |
| Number/percentage of C's | 113,752,853 / 19.68% |
| Number/percentage of T's | 172,985,641 / 29.93% |
| Number/percentage of G's | 117,880,218 / 20.4%  |
| Number/percentage of N's | 6,941 / 0%           |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 40.08% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.1868 |
| Standard Deviation | 2.7845 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 52.63 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 884,550.44      |
| Standard Deviation | 8,531,371.78    |
| P25/Median/P75     | 150 / 209 / 300 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 1.06%     |
| Mismatches                               | 5,955,463 |
| Insertions                               | 63,012    |
| Mapped reads with at least one insertion | 1.25%     |
| Deletions                                | 139,800   |
| Mapped reads with at least one deletion  | 2.8%      |
| Homopolymer indels                       | 42.53%    |

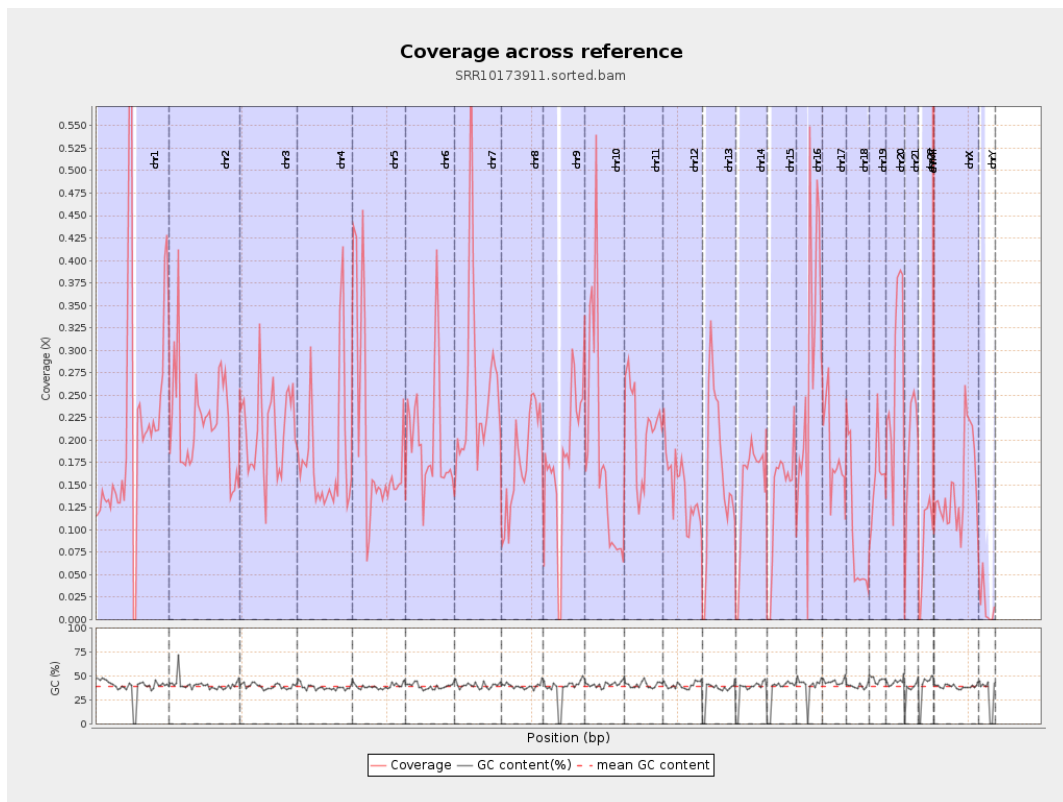
## 2.7. Chromosome stats

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

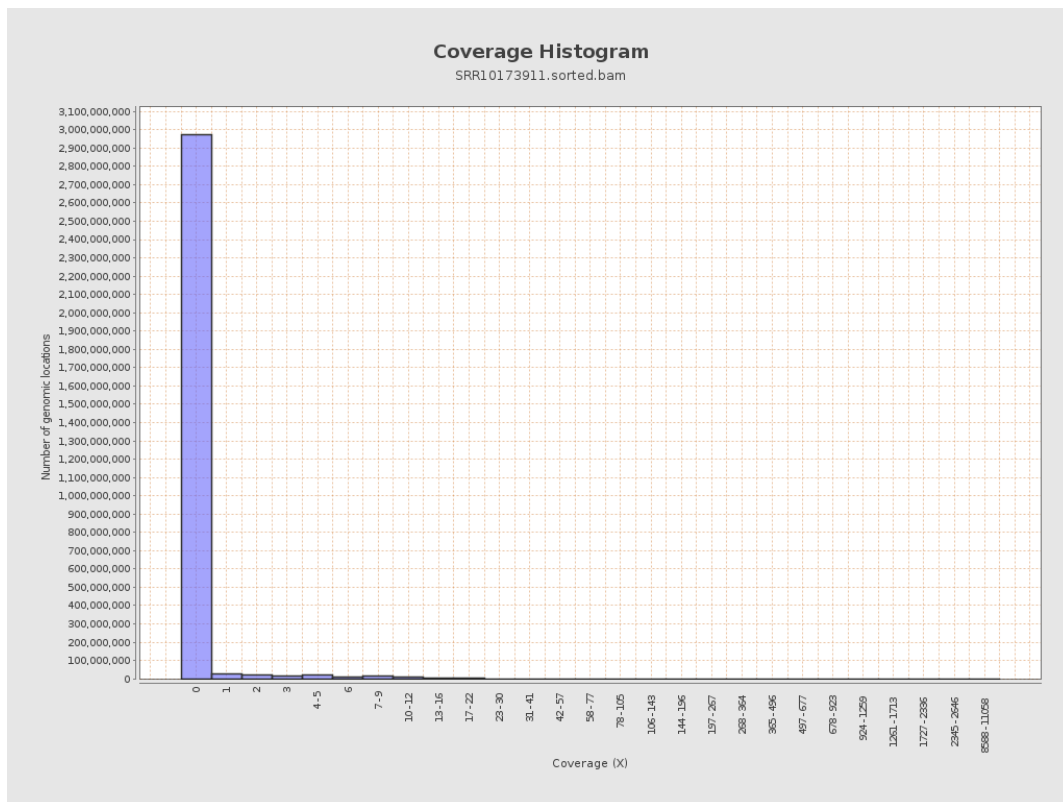
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 52193147     | 0.2094          | 2.4624           |
| chr2  | 243199373 | 53365939     | 0.2194          | 7.7827           |
| chr3  | 198022430 | 41819284     | 0.2112          | 1.3361           |
| chr4  | 191154276 | 33848638     | 0.1771          | 1.6605           |
| chr5  | 180915260 | 36253955     | 0.2004          | 1.2896           |
| chr6  | 171115067 | 34346580     | 0.2007          | 1.3647           |
| chr7  | 159138663 | 40697770     | 0.2557          | 2.5942           |
| chr8  | 146364022 | 25948529     | 0.1773          | 1.4356           |
| chr9  | 141213431 | 25520565     | 0.1807          | 1.5792           |
| chr10 | 135534747 | 24605742     | 0.1815          | 3.2226           |
| chr11 | 135006516 | 28732617     | 0.2128          | 1.3574           |
| chr12 | 133851895 | 19493661     | 0.1456          | 1.0939           |
| chr13 | 115169878 | 18947469     | 0.1645          | 1.179            |
| chr14 | 107349540 | 15705252     | 0.1463          | 1.0984           |
| chr15 | 102531392 | 14037009     | 0.1369          | 1.0431           |
| chr16 | 90354753  | 25088663     | 0.2777          | 2.4362           |
| chr17 | 81195210  | 14713481     | 0.1812          | 1.4405           |
| chr18 | 78077248  | 7065402      | 0.0905          | 2.0442           |
| chr19 | 59128983  | 9318250      | 0.1576          | 2.5915           |
| chr20 | 63025520  | 17492216     | 0.2775          | 1.5361           |
| chr21 | 48129895  | 9074596      | 0.1885          | 1.3499           |
| chr22 | 51304566  | 4427685      | 0.0863          | 0.8021           |
| chrMT | 16571     | 1996136      | 120.4596        | 97.3085          |
| chrX  | 155270560 | 22680428     | 0.1461          | 1.1047           |

|      |          |        |        |        |
|------|----------|--------|--------|--------|
| chrY | 59373566 | 897960 | 0.0151 | 0.6922 |
|------|----------|--------|--------|--------|

### 3. Results : Coverage across reference

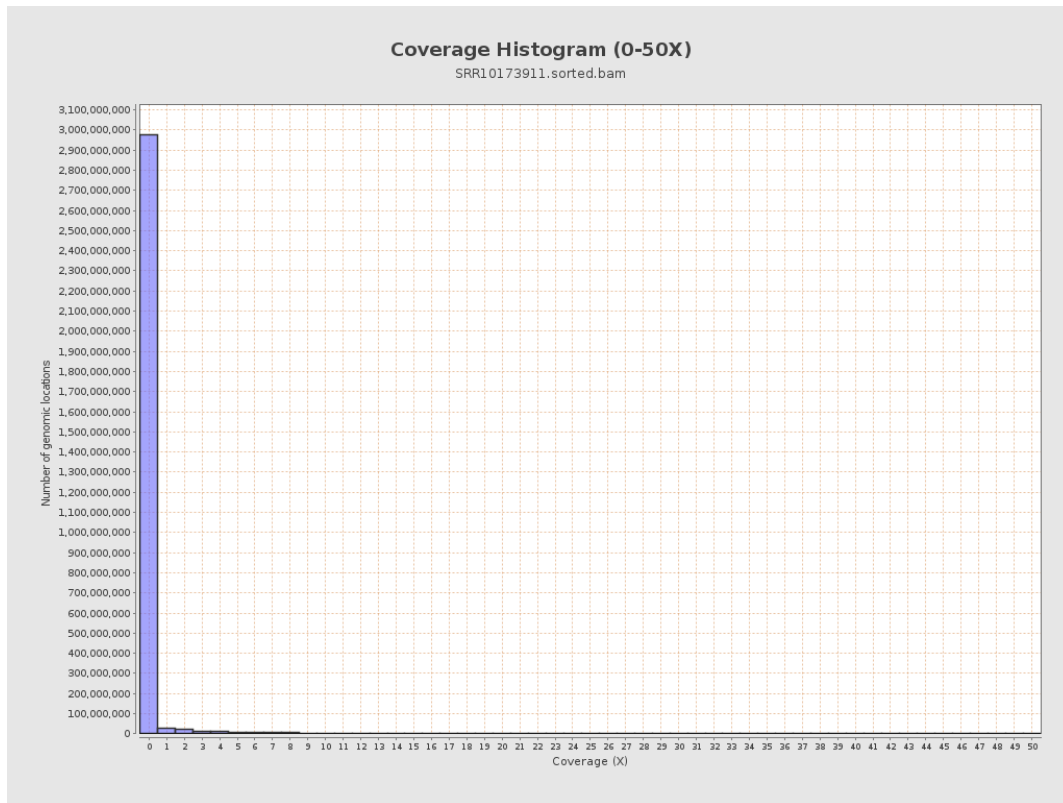


## 4. Results : Coverage Histogram

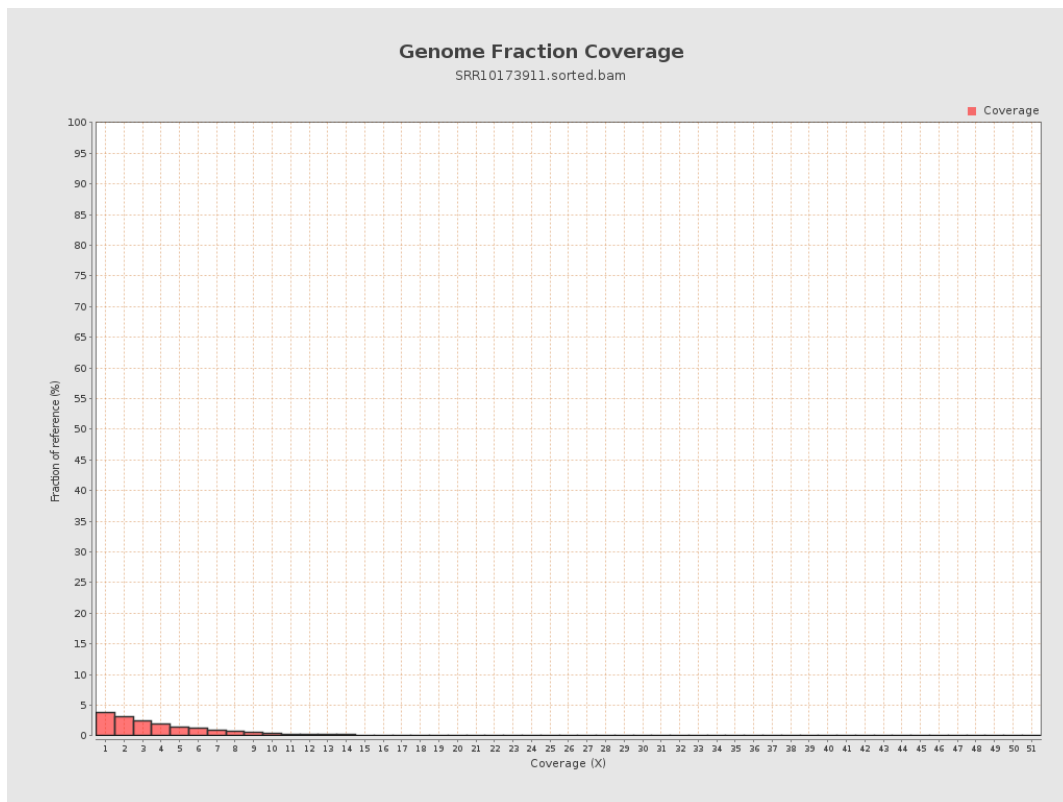




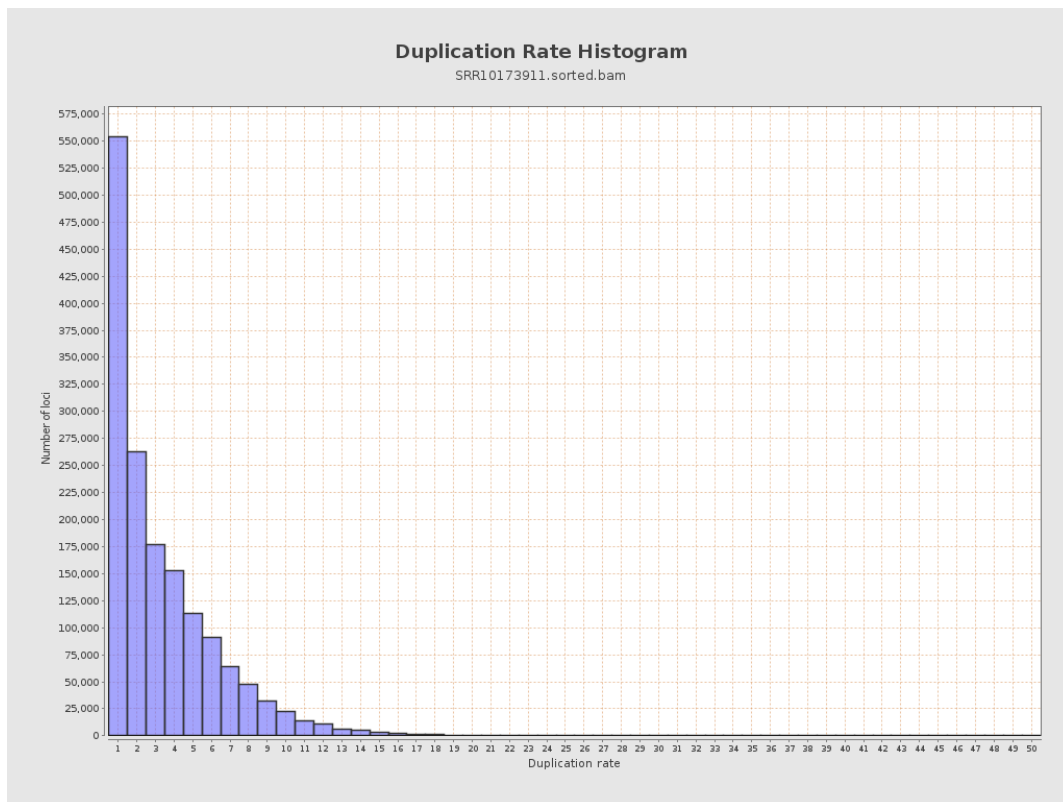
## 5. Results : Coverage Histogram (0-50X)



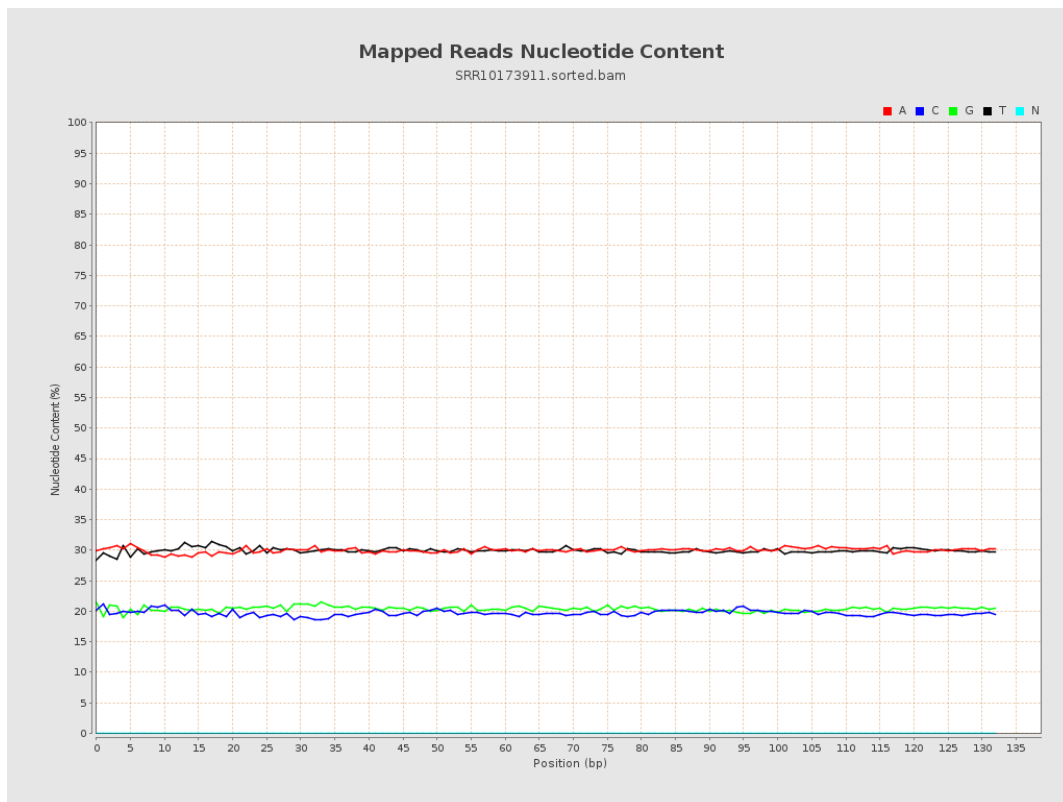
## 6. Results : Genome Fraction Coverage



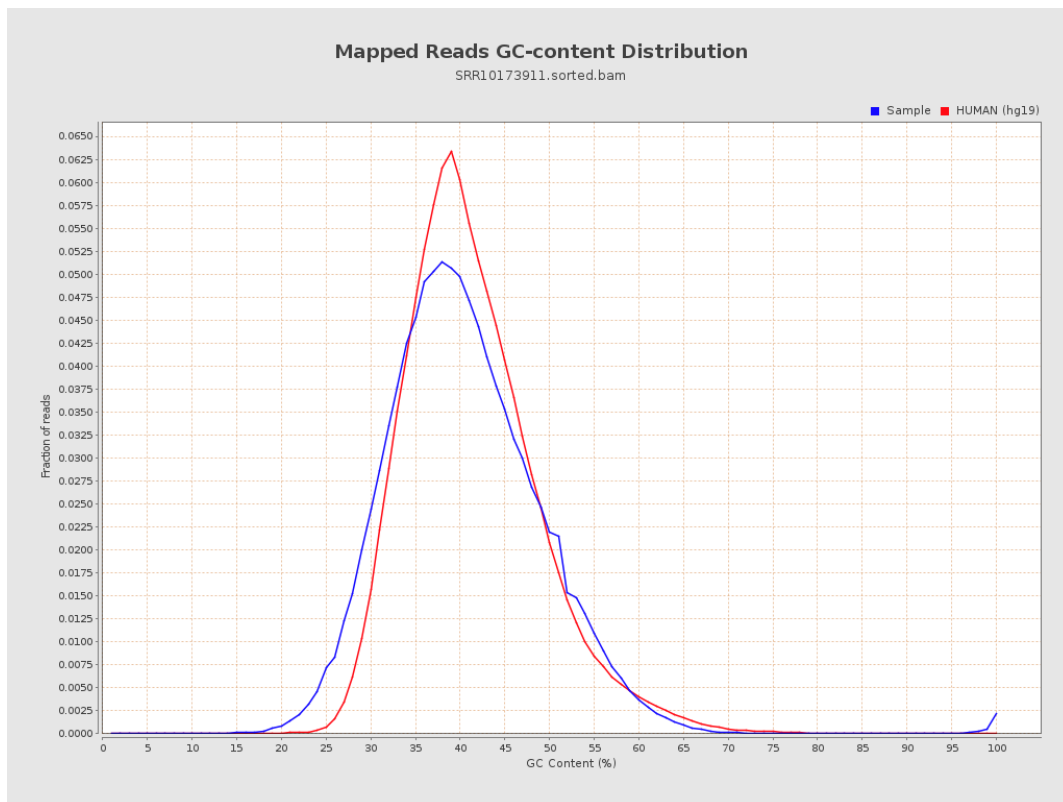
## 7. Results : Duplication Rate Histogram



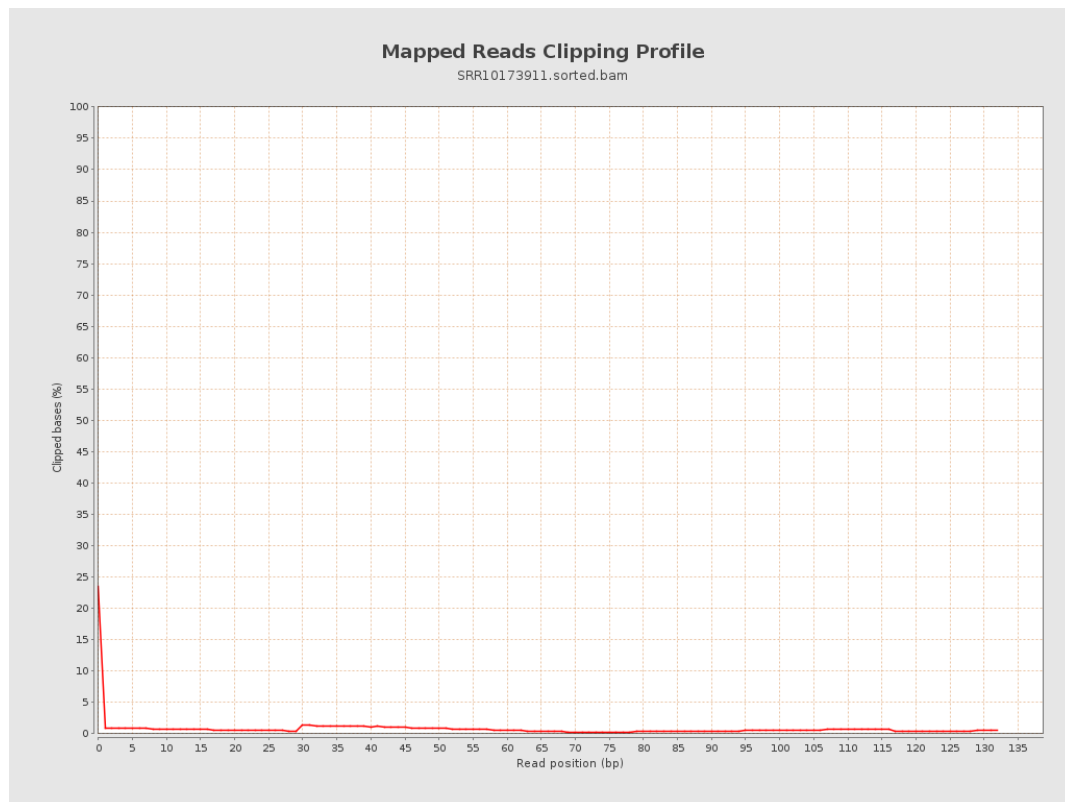
## 8. Results : Mapped Reads Nucleotide Content



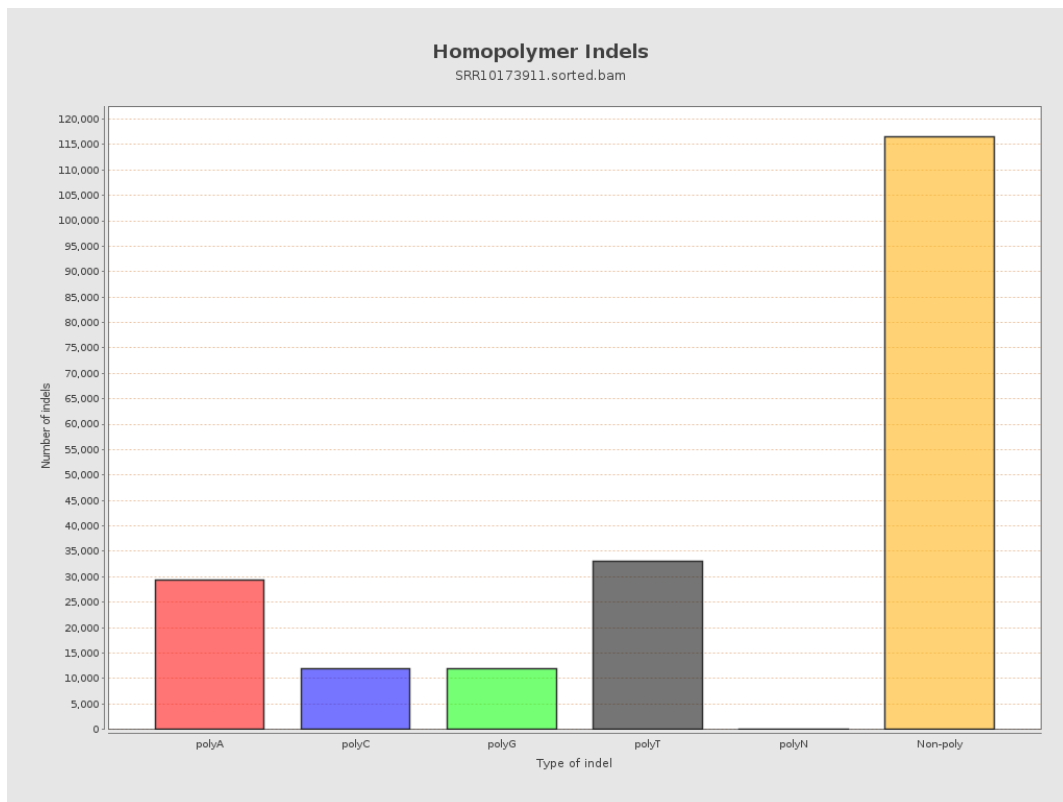
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

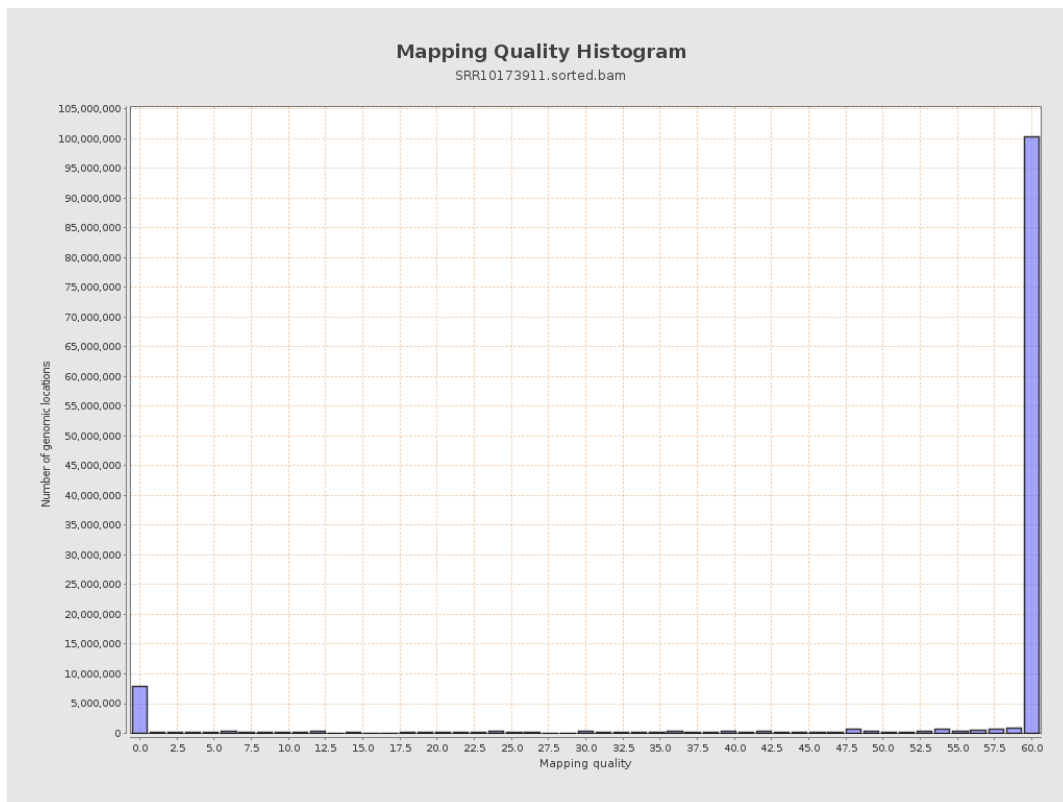


## 12. Results : Mapping Quality Across Reference

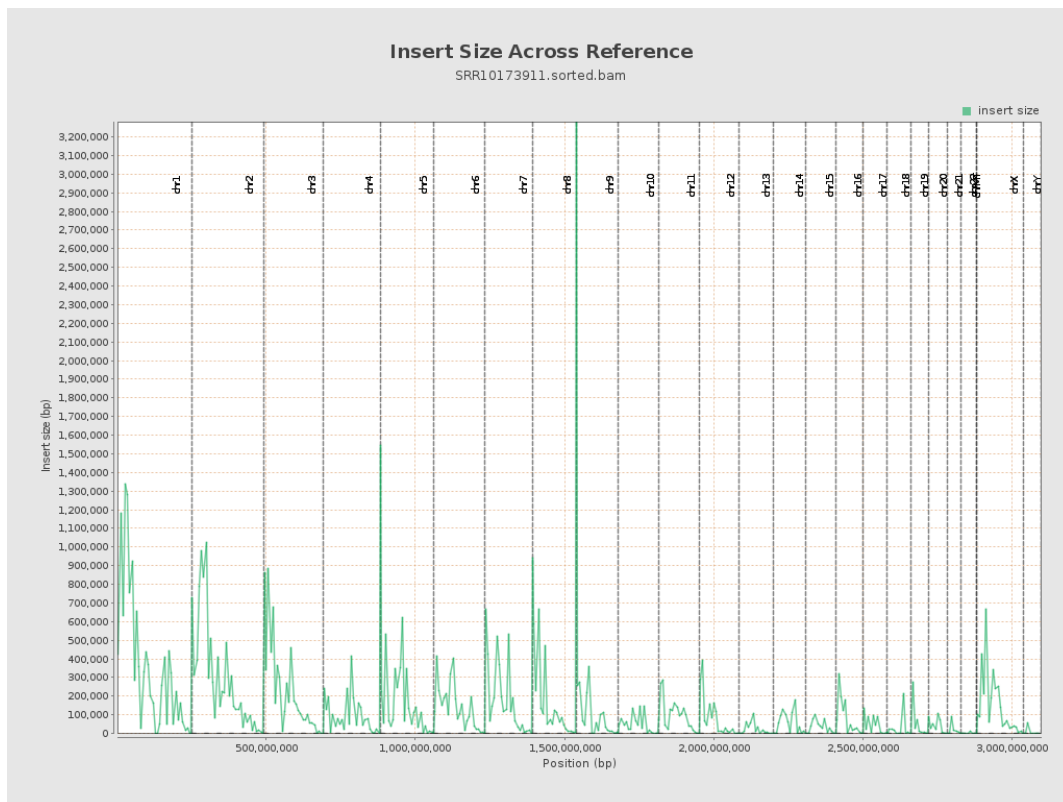




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

