

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/04 08:13:41*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173929.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_SRR10173929 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173929_1.fastq.gz SRR10173929_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                      |
| Analysis date:                        | Wed Sep 04 08:13:41 CST 2024                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                     |
| BAM file:                             | SRR10173929.sorted.bam                                                                                                                                                                                                  |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 2,041,470          |
| Mapped reads                 | 1,991,496 / 97.55% |
| Unmapped reads               | 49,974 / 2.45%     |
| Mapped paired reads          | 1,991,496 / 97.55% |
| Mapped reads, first in pair  | 996,160 / 48.8%    |
| Mapped reads, second in pair | 995,336 / 48.76%   |
| Mapped reads, both in pair   | 1,959,178 / 95.97% |
| Mapped reads, singletons     | 32,318 / 1.58%     |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 198,843 / 9.74%    |
| Read min/max/mean length     | 30 / 133 / 128.01  |
| Duplicated reads (estimated) | 1,458,976 / 71.47% |
| Duplication rate             | 61.54%             |
| Clipped reads                | 824,780 / 40.4%    |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 70,816,561 / 30.16% |
| Number/percentage of C's | 45,904,291 / 19.55% |
| Number/percentage of T's | 70,532,127 / 30.04% |
| Number/percentage of G's | 47,518,674 / 20.24% |
| Number/percentage of N's | 2,910 / 0%          |
|                          |                     |

|               |        |
|---------------|--------|
| GC Percentage | 39.79% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.0759 |
| Standard Deviation | 1.2479 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 52.96 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 1,109,832.52    |
| Standard Deviation | 9,523,622.86    |
| P25/Median/P75     | 141 / 197 / 279 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 1.06%     |
| Mismatches                               | 2,420,109 |
| Insertions                               | 27,511    |
| Mapped reads with at least one insertion | 1.33%     |
| Deletions                                | 53,427    |
| Mapped reads with at least one deletion  | 2.62%     |
| Homopolymer indels                       | 43.17%    |

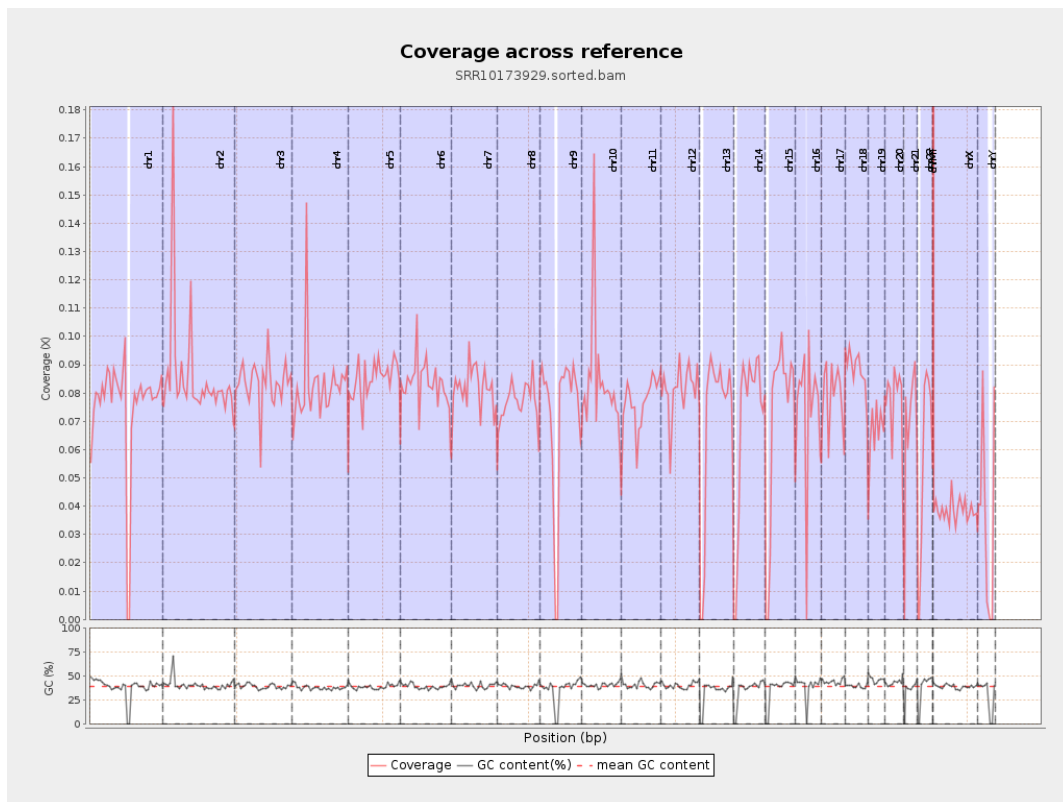
## 2.7. Chromosome stats

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

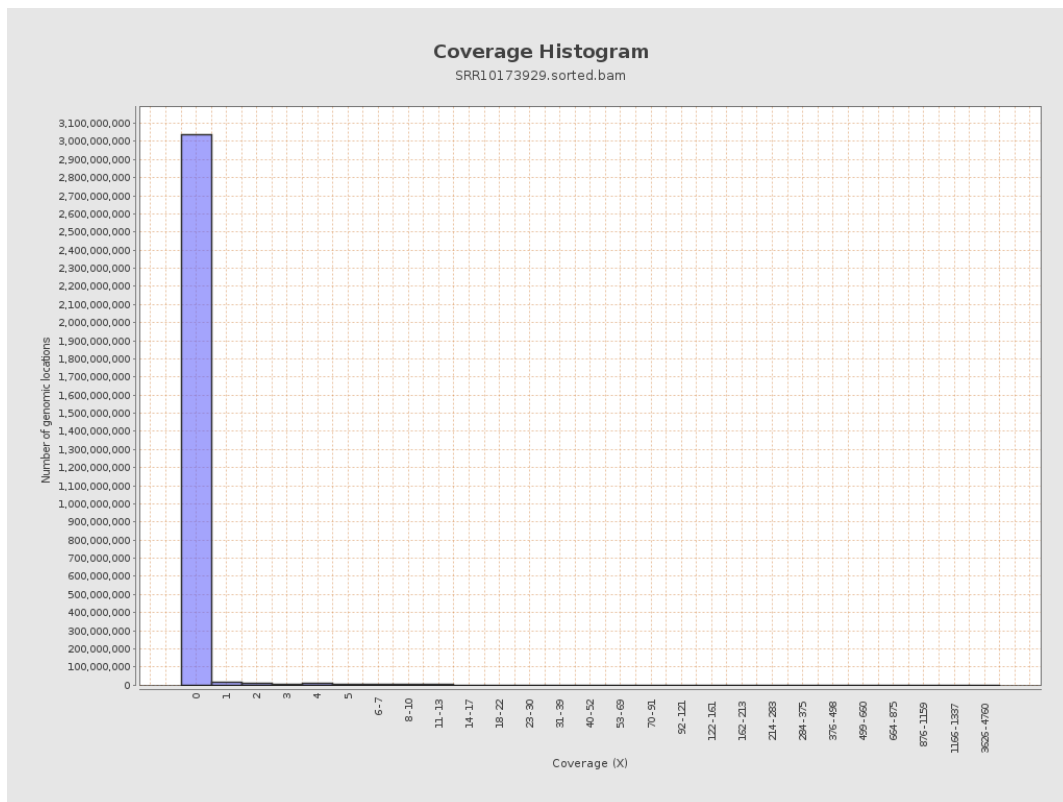
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 18816929     | 0.0755          | 0.9442           |
| chr2  | 243199373 | 20814996     | 0.0856          | 3.3951           |
| chr3  | 198022430 | 16529677     | 0.0835          | 0.7821           |
| chr4  | 191154276 | 15819501     | 0.0828          | 0.9364           |
| chr5  | 180915260 | 15351649     | 0.0849          | 0.7913           |
| chr6  | 171115067 | 14277395     | 0.0834          | 0.8482           |
| chr7  | 159138663 | 12974691     | 0.0815          | 0.865            |
| chr8  | 146364022 | 11245632     | 0.0768          | 0.9845           |
| chr9  | 141213431 | 10184694     | 0.0721          | 0.8544           |
| chr10 | 135534747 | 11308709     | 0.0834          | 1.0552           |
| chr11 | 135006516 | 10331265     | 0.0765          | 0.7518           |
| chr12 | 133851895 | 10905710     | 0.0815          | 0.7653           |
| chr13 | 115169878 | 8053621      | 0.0699          | 0.7246           |
| chr14 | 107349540 | 7568572      | 0.0705          | 0.7115           |
| chr15 | 102531392 | 7210052      | 0.0703          | 0.705            |
| chr16 | 90354753  | 6557791      | 0.0726          | 0.8059           |
| chr17 | 81195210  | 6436090      | 0.0793          | 0.7564           |
| chr18 | 78077248  | 6907880      | 0.0885          | 1.2377           |
| chr19 | 59128983  | 3961725      | 0.067           | 0.7887           |
| chr20 | 63025520  | 4923342      | 0.0781          | 0.7691           |
| chr21 | 48129895  | 3329672      | 0.0692          | 0.7963           |
| chr22 | 51304566  | 2896727      | 0.0565          | 0.6651           |
| chrMT | 16571     | 306001       | 18.4661         | 16.2689          |
| chrX  | 155270560 | 5975010      | 0.0385          | 0.5271           |

|      |          |         |        |        |
|------|----------|---------|--------|--------|
| chrY | 59373566 | 2218625 | 0.0374 | 0.7021 |
|------|----------|---------|--------|--------|

### 3. Results : Coverage across reference

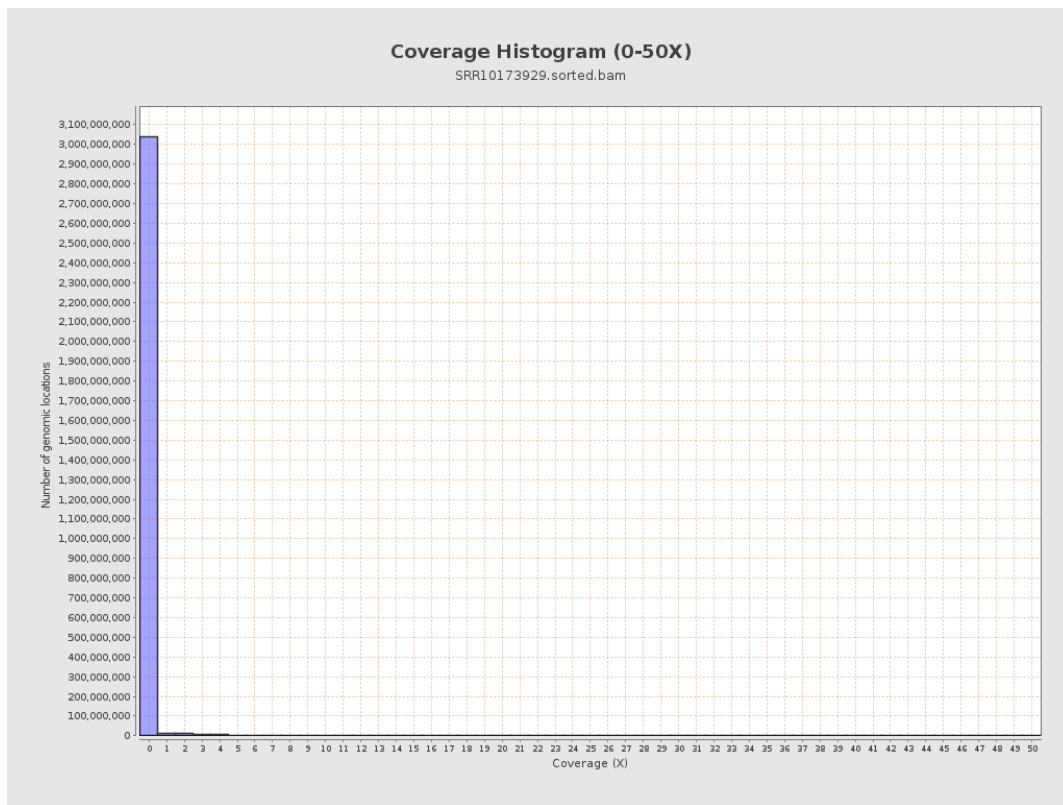


## 4. Results : Coverage Histogram

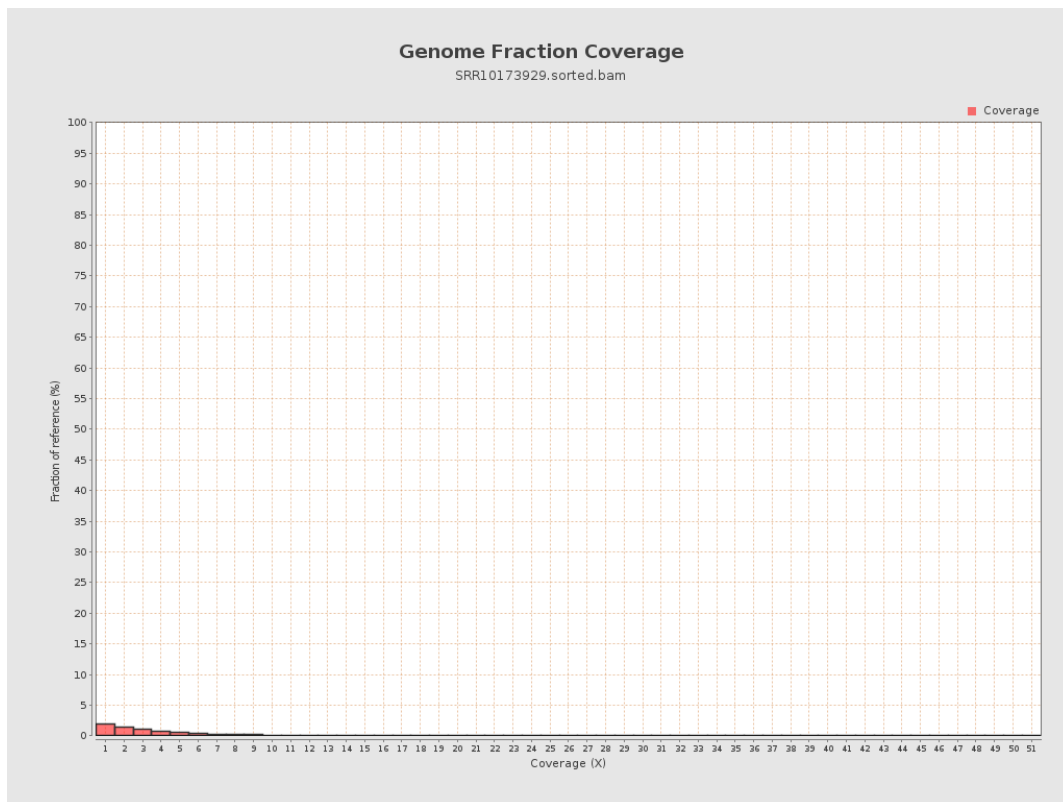




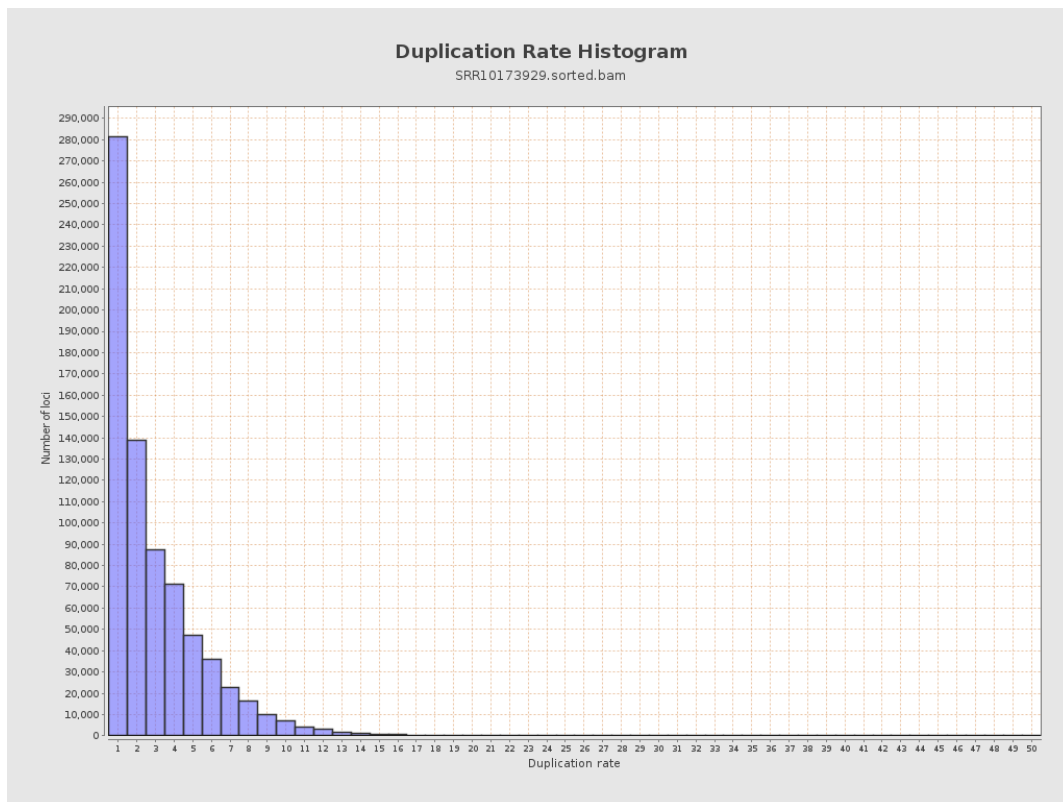
## 5. Results : Coverage Histogram (0-50X)



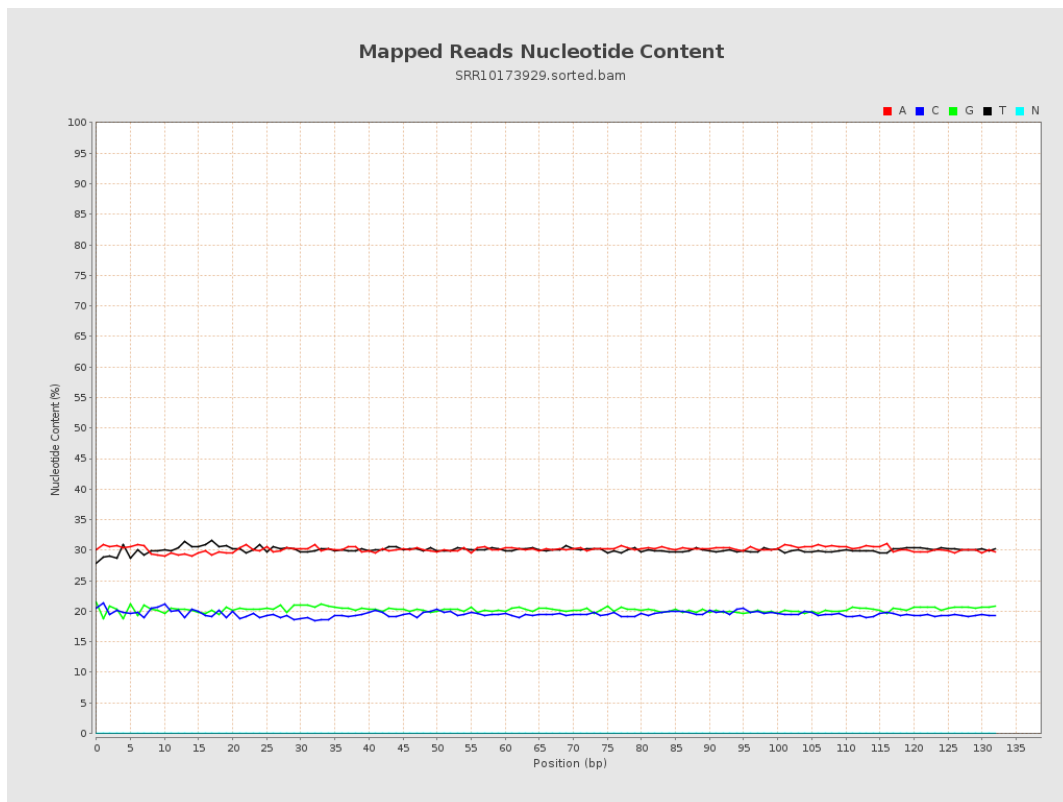
## 6. Results : Genome Fraction Coverage



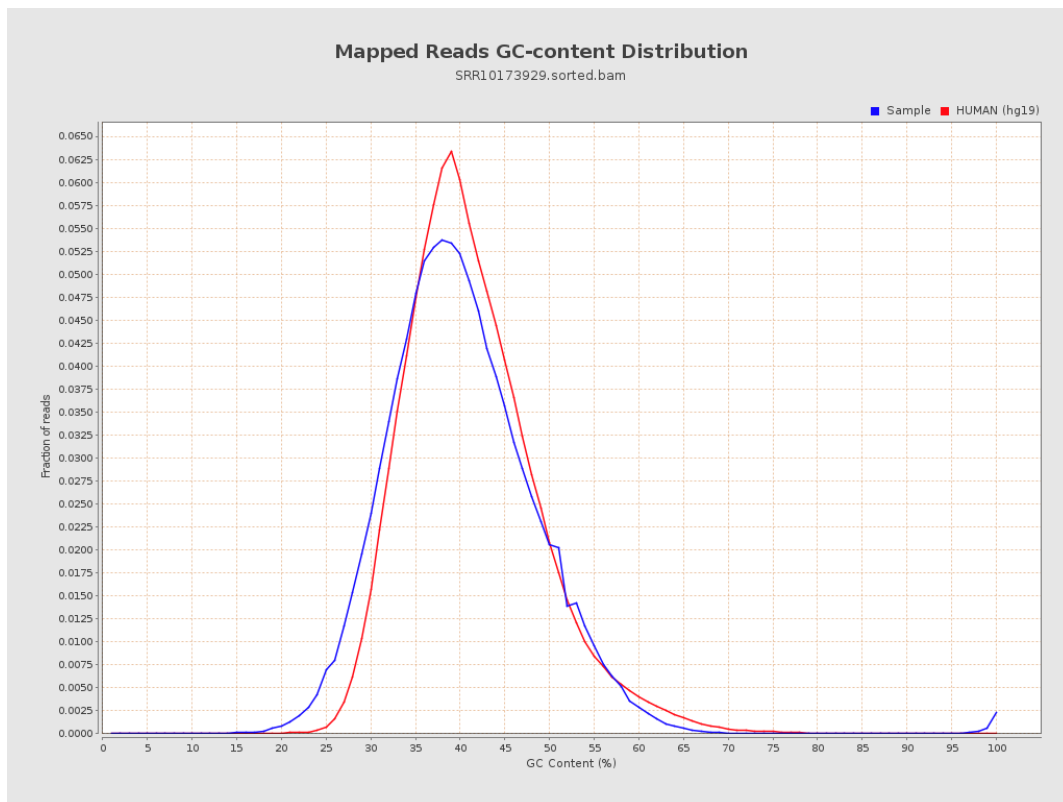
## 7. Results : Duplication Rate Histogram



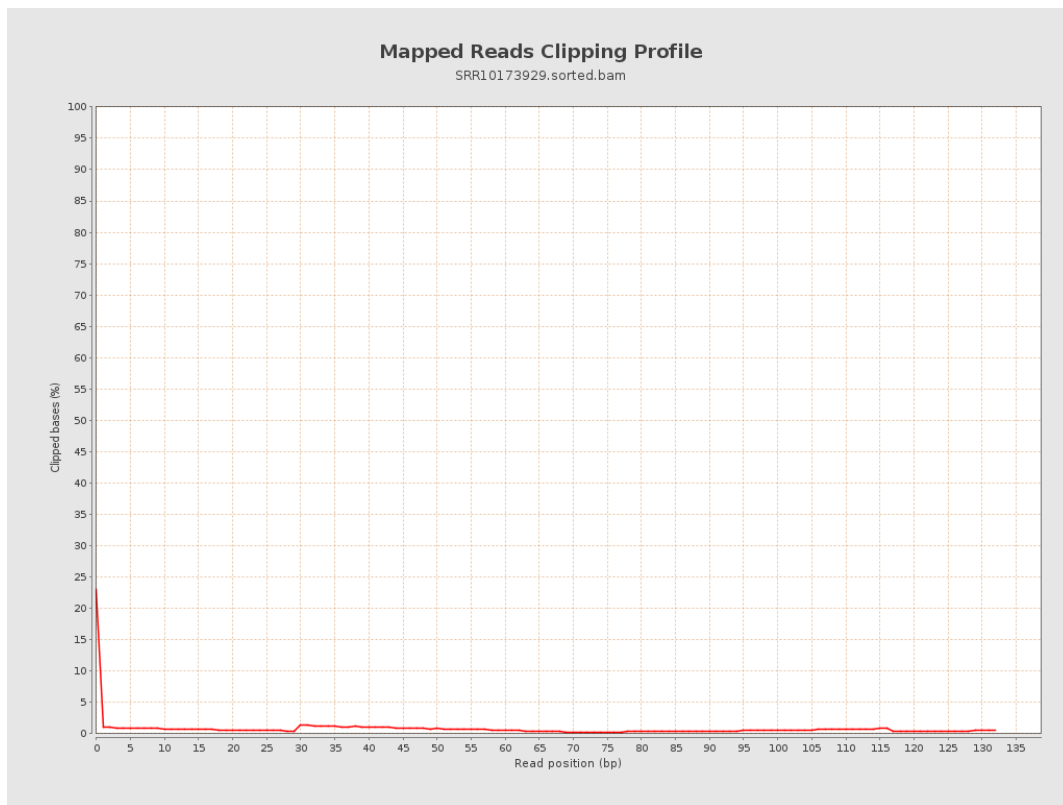
## 8. Results : Mapped Reads Nucleotide Content



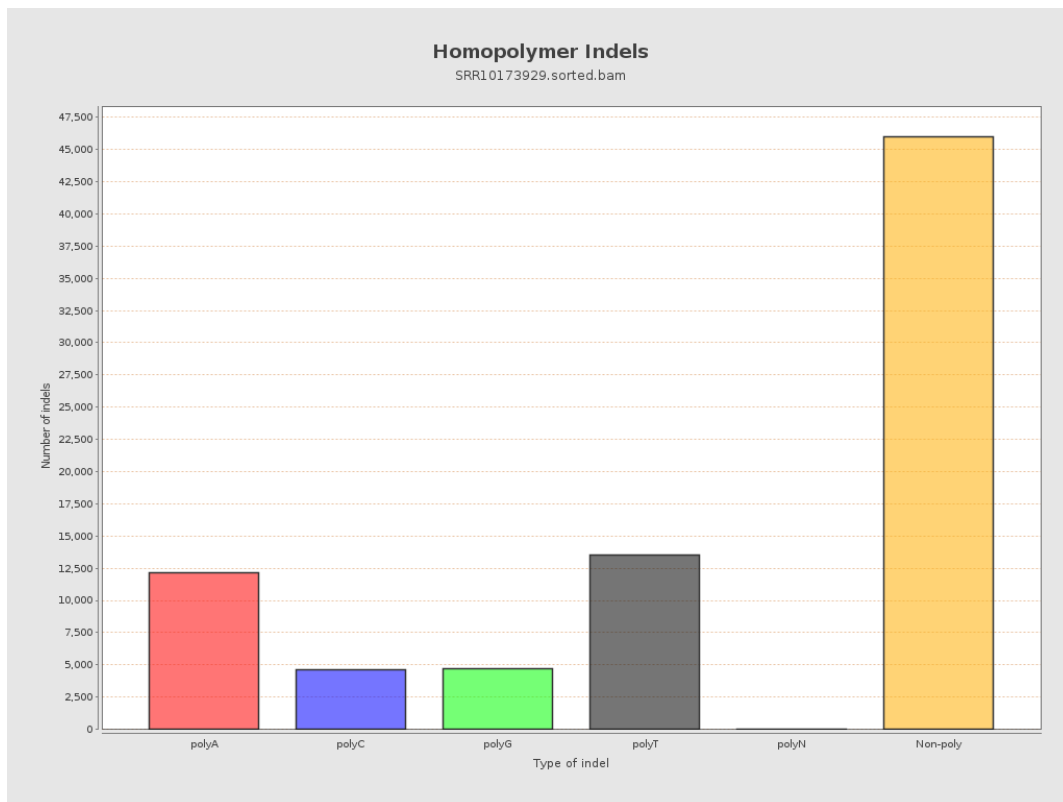
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

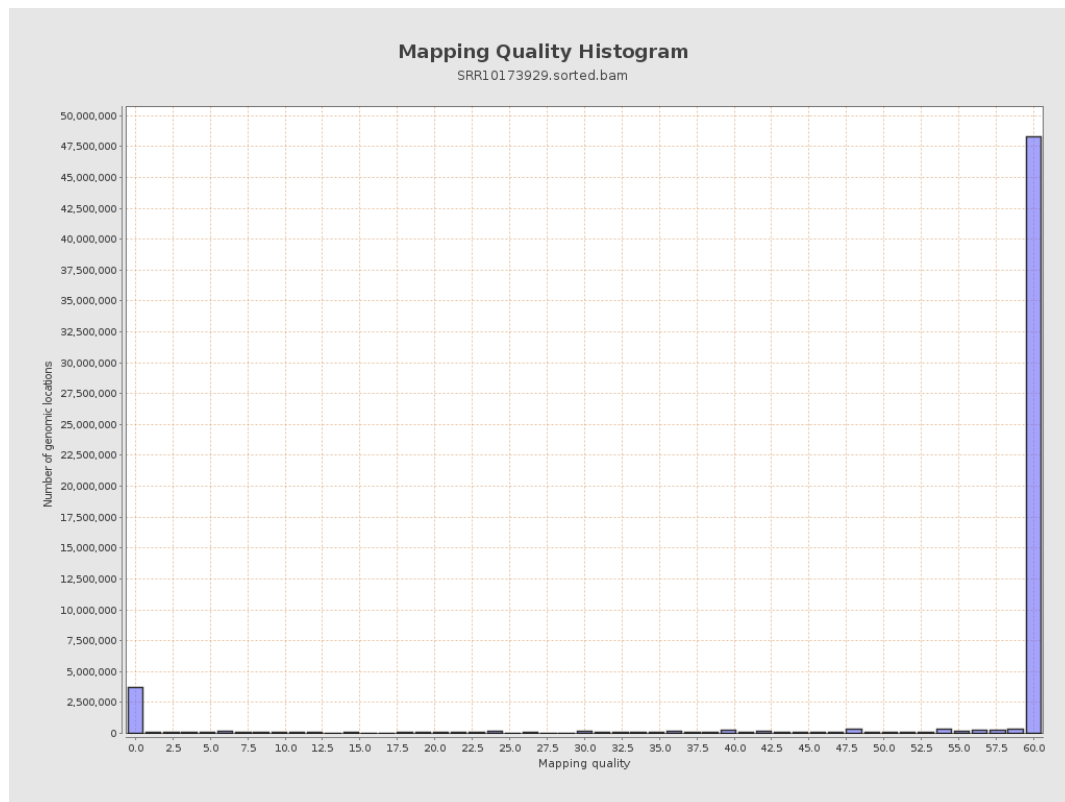


## 12. Results : Mapping Quality Across Reference

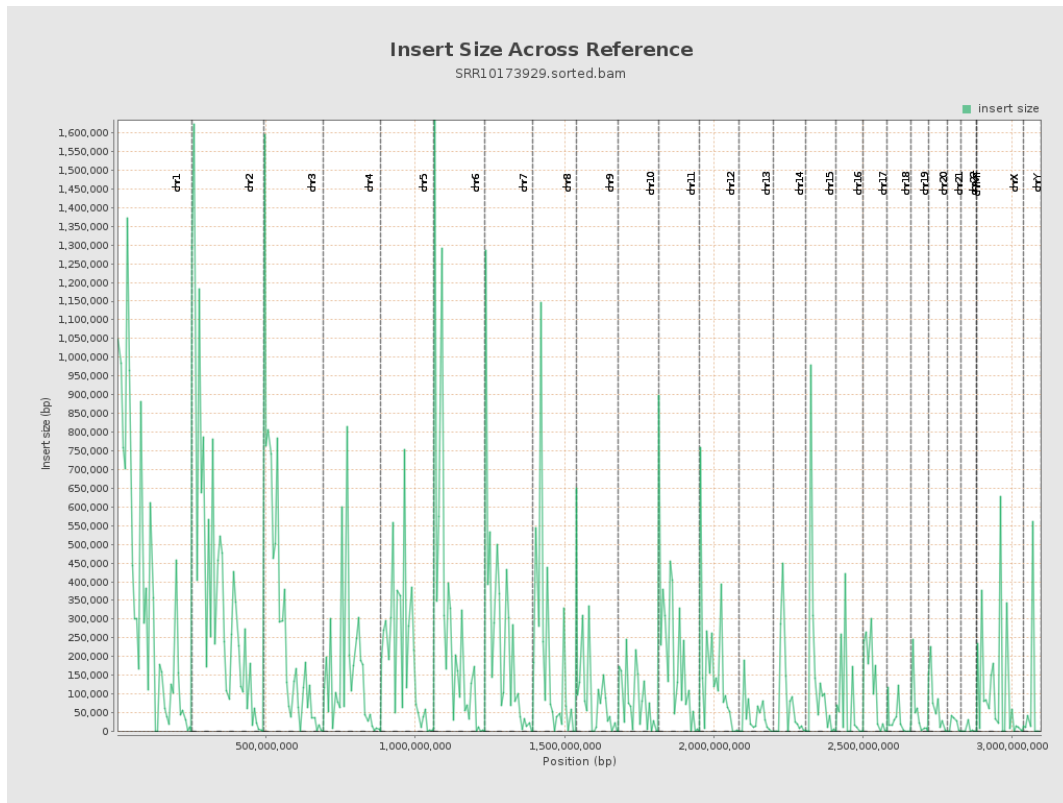




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

