

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/08 07:04:19*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354877.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_SRR22354877 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354877_1.fastq.gz SRR22354877_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                      |
| Analysis date:                        | Sun Sep 08 07:04:18 CST 2024                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                     |
| BAM file:                             | SRR22354877.sorted.bam                                                                                                                                                                                                  |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 24,128,072          |
| Mapped reads                 | 24,011,507 / 99.52% |
| Unmapped reads               | 116,565 / 0.48%     |
| Mapped paired reads          | 24,011,507 / 99.52% |
| Mapped reads, first in pair  | 12,015,009 / 49.8%  |
| Mapped reads, second in pair | 11,996,498 / 49.72% |
| Mapped reads, both in pair   | 23,958,412 / 99.3%  |
| Mapped reads, singletons     | 53,095 / 0.22%      |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 127,524 / 0.53%     |
| Read min/max/mean length     | 30 / 150 / 150.26   |
| Duplicated reads (estimated) | 5,548,438 / 23%     |
| Duplication rate             | 20.91%              |
| Clipped reads                | 1,212,168 / 5.02%   |

### 2.2. ACGT Content

|                          |                        |
|--------------------------|------------------------|
| Number/percentage of A's | 1,024,943,979 / 28.77% |
| Number/percentage of C's | 756,943,012 / 21.25%   |
| Number/percentage of T's | 1,017,111,592 / 28.55% |
| Number/percentage of G's | 763,716,205 / 21.44%   |
| Number/percentage of N's | 70,116 / 0%            |
|                          |                        |

|               |        |
|---------------|--------|
| GC Percentage | 42.68% |
|---------------|--------|

## 2.3. Coverage

|                    |         |
|--------------------|---------|
| Mean               | 1.1514  |
| Standard Deviation | 13.8121 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 54.51 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 39,477.51       |
| Standard Deviation | 1,995,287.03    |
| P25/Median/P75     | 259 / 302 / 349 |

## 2.6. Mismatches and indels

|                                          |            |
|------------------------------------------|------------|
| General error rate                       | 0.64%      |
| Mismatches                               | 21,288,331 |
| Insertions                               | 516,779    |
| Mapped reads with at least one insertion | 2.01%      |
| Deletions                                | 529,220    |
| Mapped reads with at least one deletion  | 2.11%      |
| Homopolymer indels                       | 45.07%     |

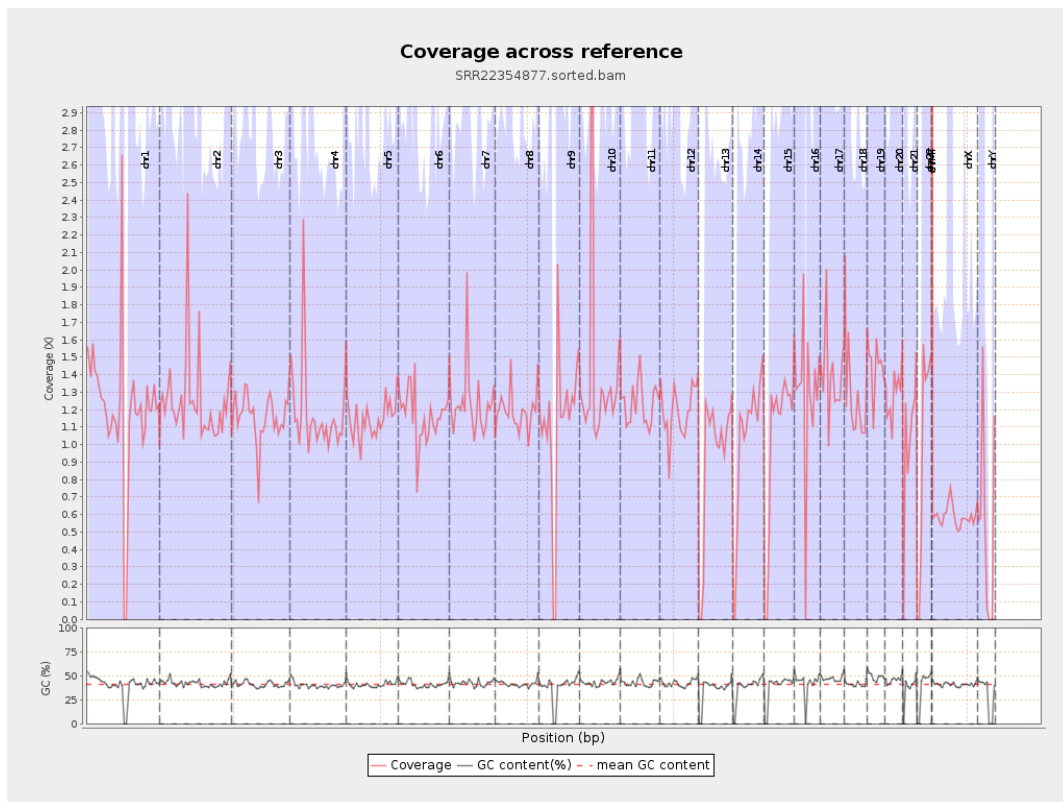
## 2.7. Chromosome stats

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

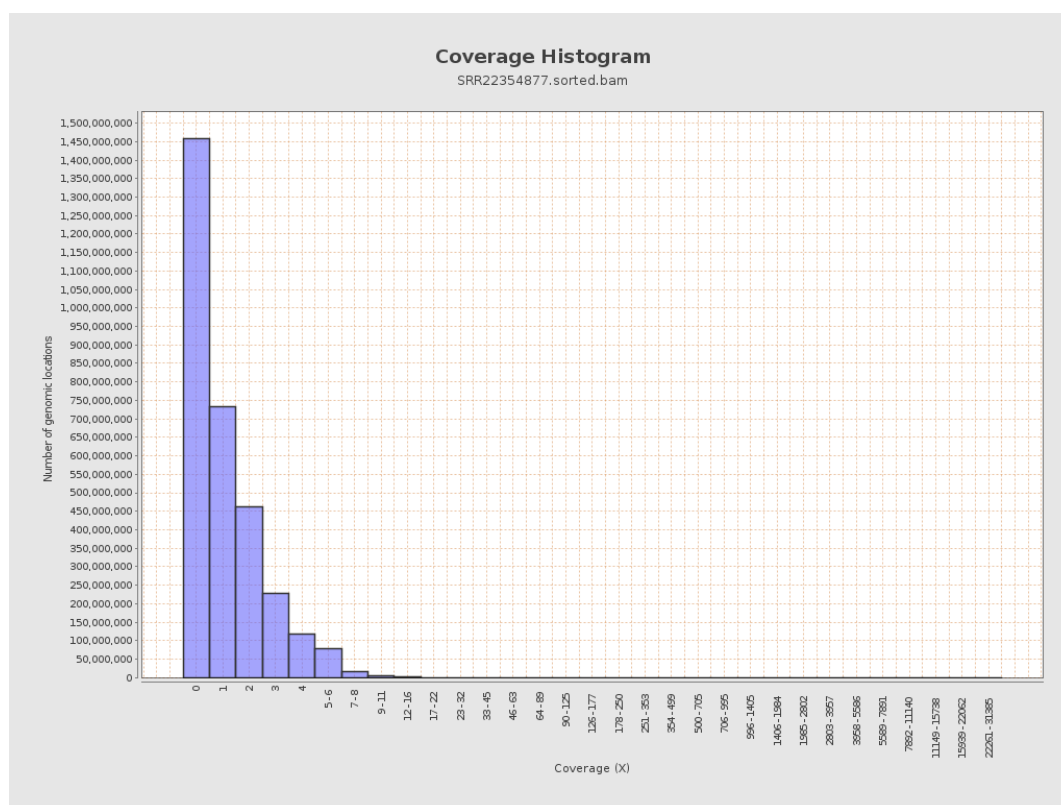
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 300699162    | 1.2064          | 32.5433          |
| chr2  | 243199373 | 305121338    | 1.2546          | 10.7529          |
| chr3  | 198022430 | 229481600    | 1.1589          | 1.5892           |
| chr4  | 191154276 | 223805548    | 1.1708          | 11.0152          |
| chr5  | 180915260 | 208459521    | 1.1522          | 1.7081           |
| chr6  | 171115067 | 199477734    | 1.1658          | 4.5512           |
| chr7  | 159138663 | 197050987    | 1.2382          | 16.1974          |
| chr8  | 146364022 | 175142125    | 1.1966          | 6.9474           |
| chr9  | 141213431 | 157833413    | 1.1177          | 20.4091          |
| chr10 | 135534747 | 191354550    | 1.4118          | 27.3324          |
| chr11 | 135006516 | 167806101    | 1.2429          | 6.4403           |
| chr12 | 133851895 | 158894391    | 1.1871          | 1.8341           |
| chr13 | 115169878 | 106636332    | 0.9259          | 1.4109           |
| chr14 | 107349540 | 109212993    | 1.0174          | 1.6181           |
| chr15 | 102531392 | 104668265    | 1.0208          | 1.4825           |
| chr16 | 90354753  | 118071482    | 1.3068          | 5.241            |
| chr17 | 81195210  | 113198123    | 1.3941          | 7.9552           |
| chr18 | 78077248  | 97400985     | 1.2475          | 15.2423          |
| chr19 | 59128983  | 85788876     | 1.4509          | 14.8932          |
| chr20 | 63025520  | 81036813     | 1.2858          | 4.2161           |
| chr21 | 48129895  | 50268168     | 1.0444          | 5.4792           |
| chr22 | 51304566  | 52054930     | 1.0146          | 3.0396           |
| chrMT | 16571     | 5617194      | 338.9774        | 39.2574          |
| chrX  | 155270560 | 91535047     | 0.5895          | 2.4545           |

|      |          |          |        |         |
|------|----------|----------|--------|---------|
| chrY | 59373566 | 33657766 | 0.5669 | 13.0896 |
|------|----------|----------|--------|---------|

### 3. Results : Coverage across reference

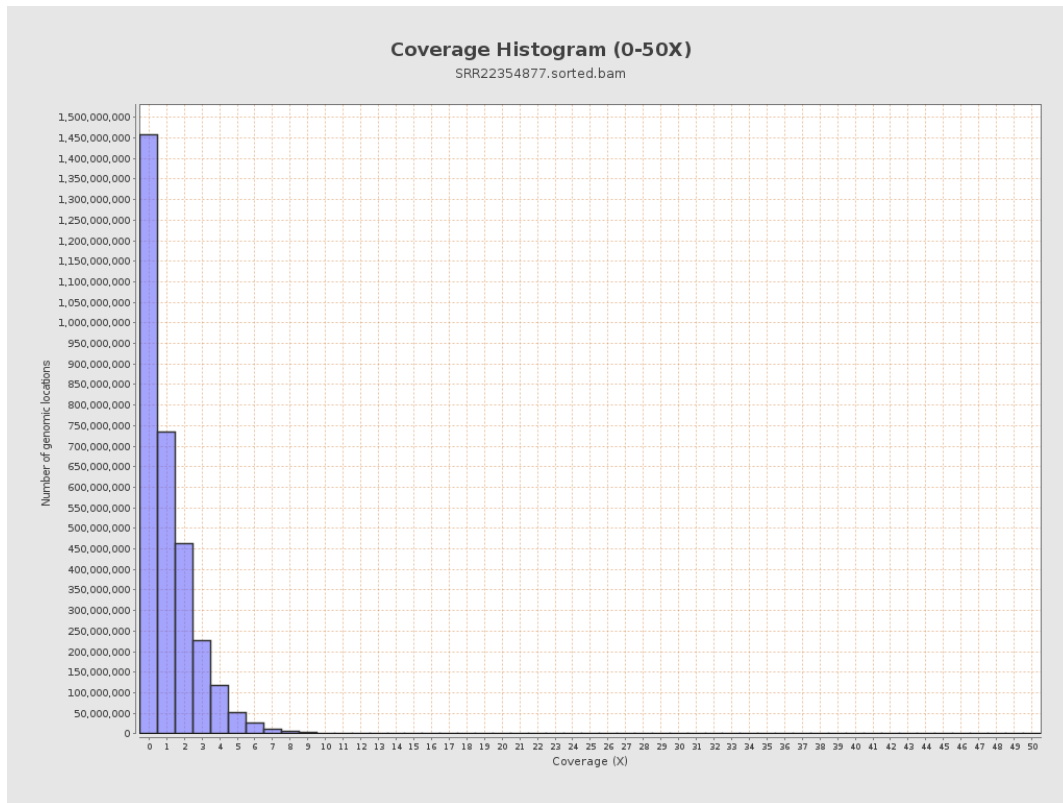


## 4. Results : Coverage Histogram

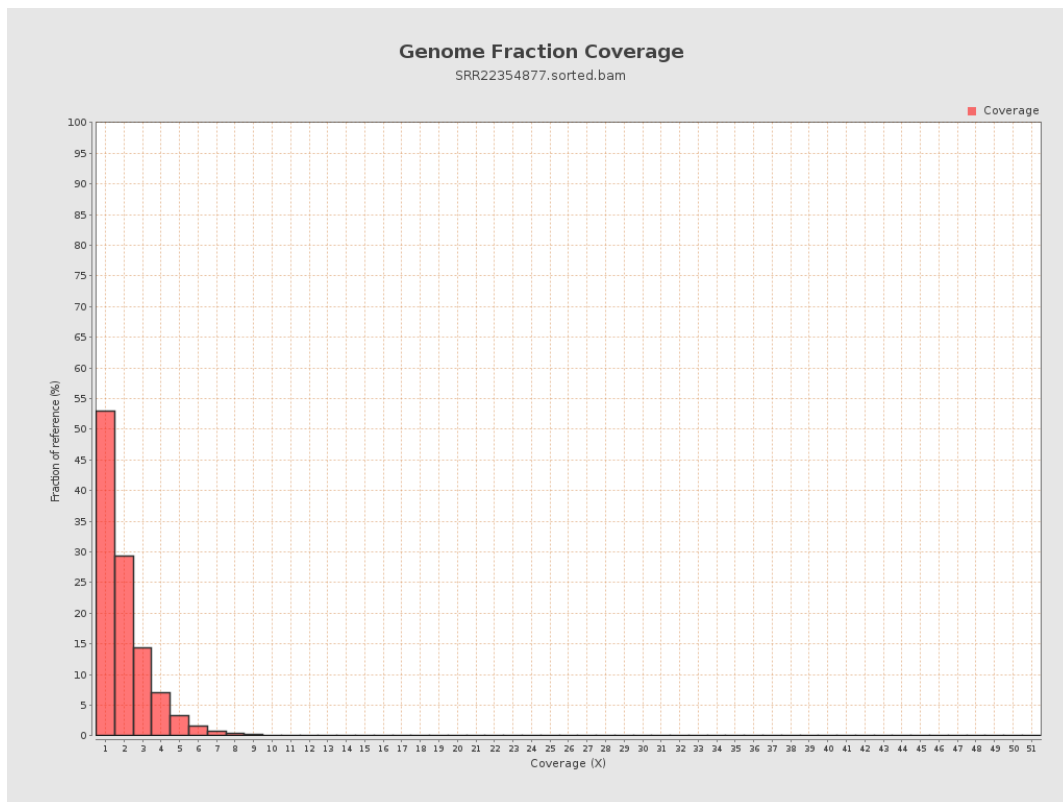




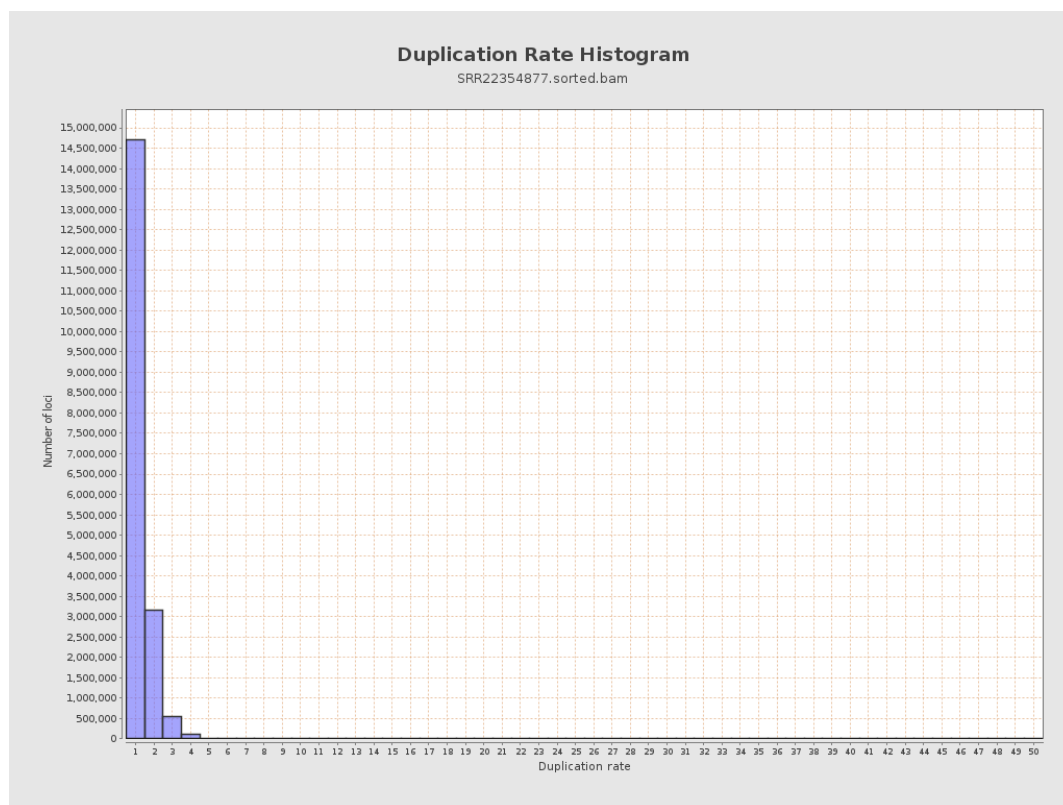
## 5. Results : Coverage Histogram (0-50X)



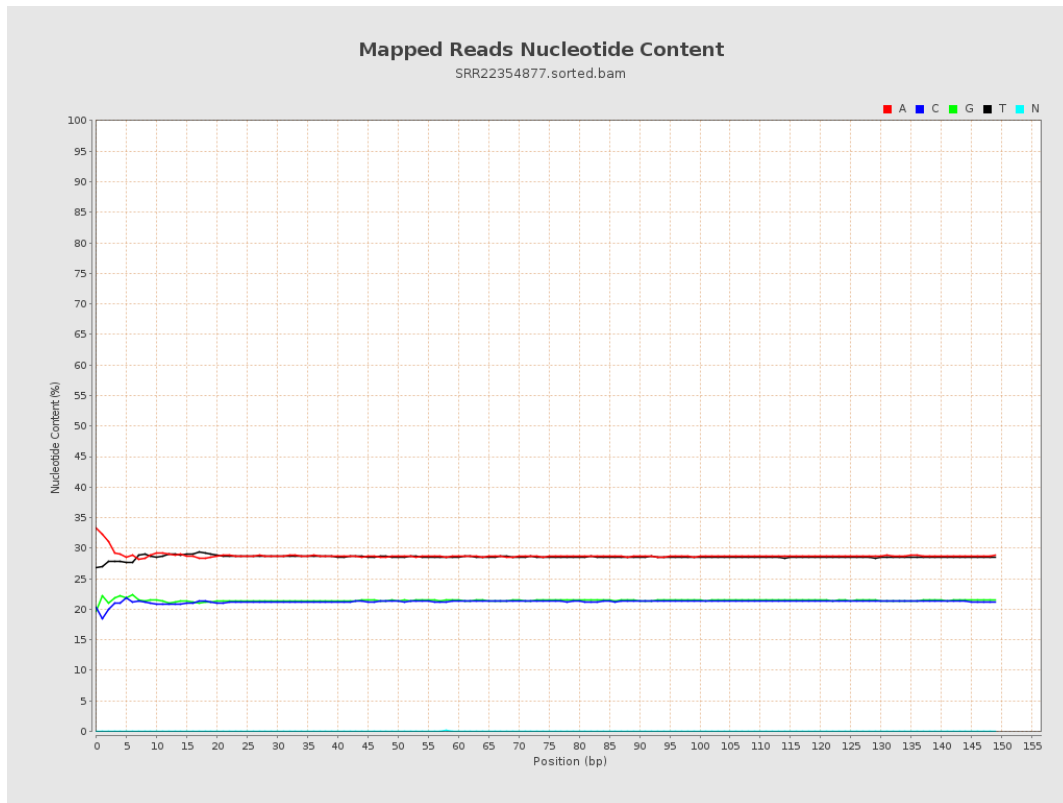
## 6. Results : Genome Fraction Coverage



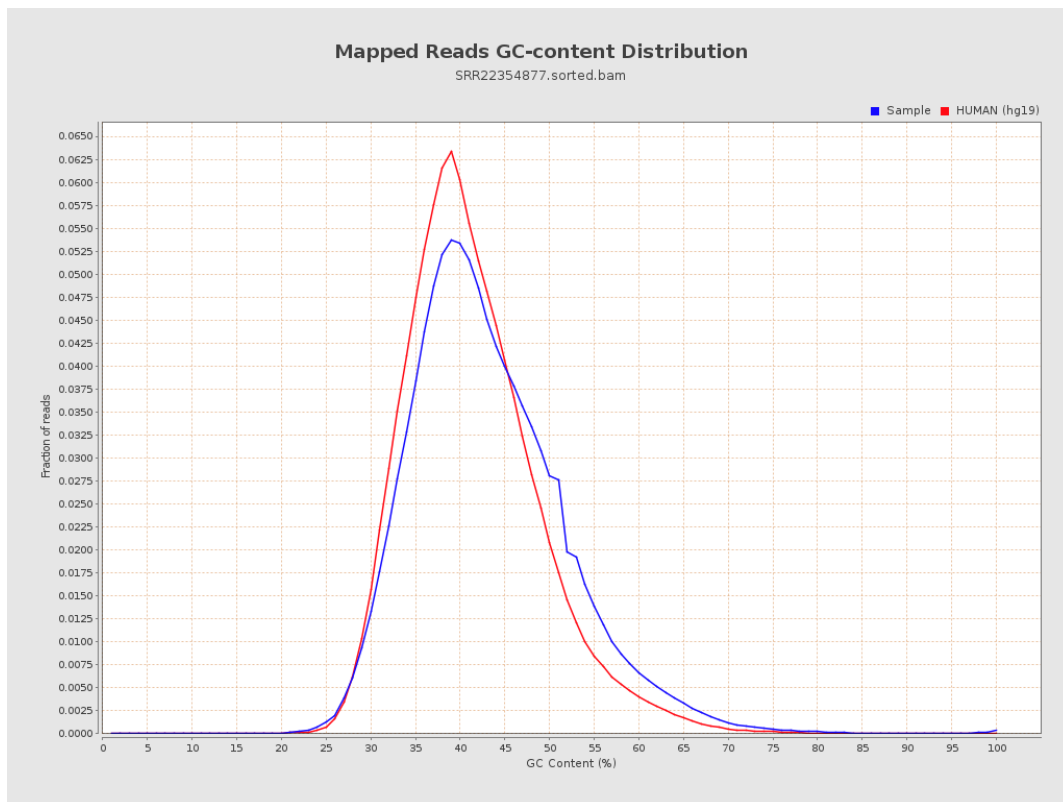
## 7. Results : Duplication Rate Histogram



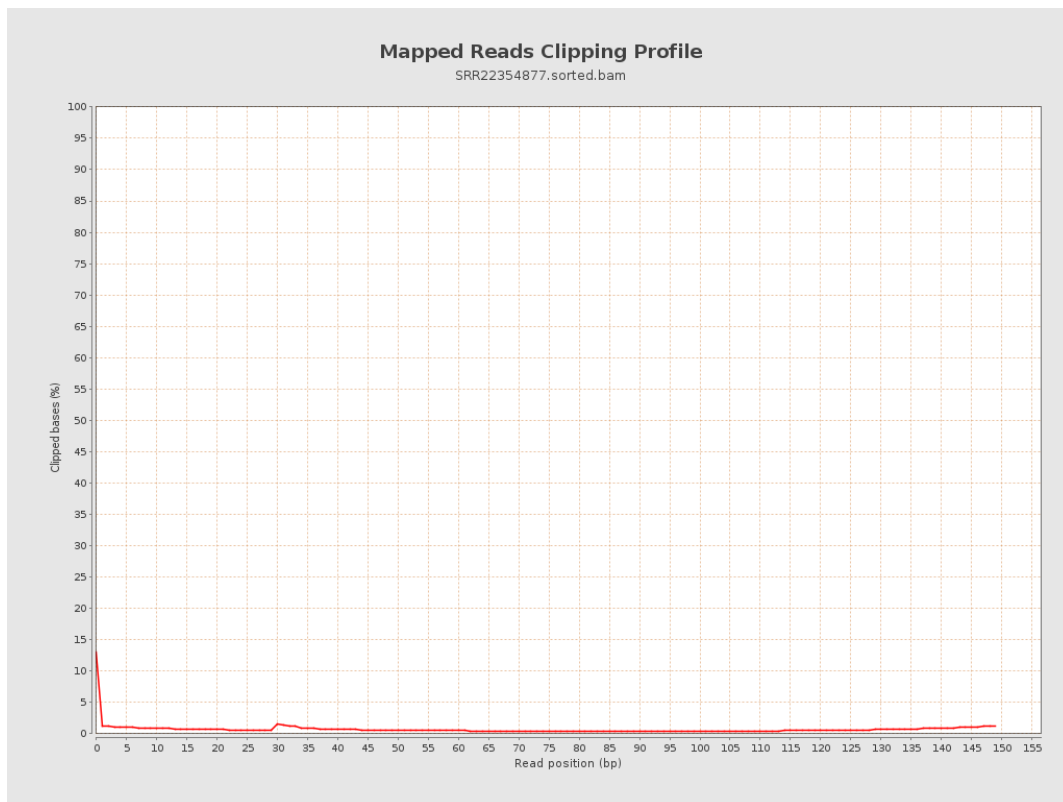
## 8. Results : Mapped Reads Nucleotide Content



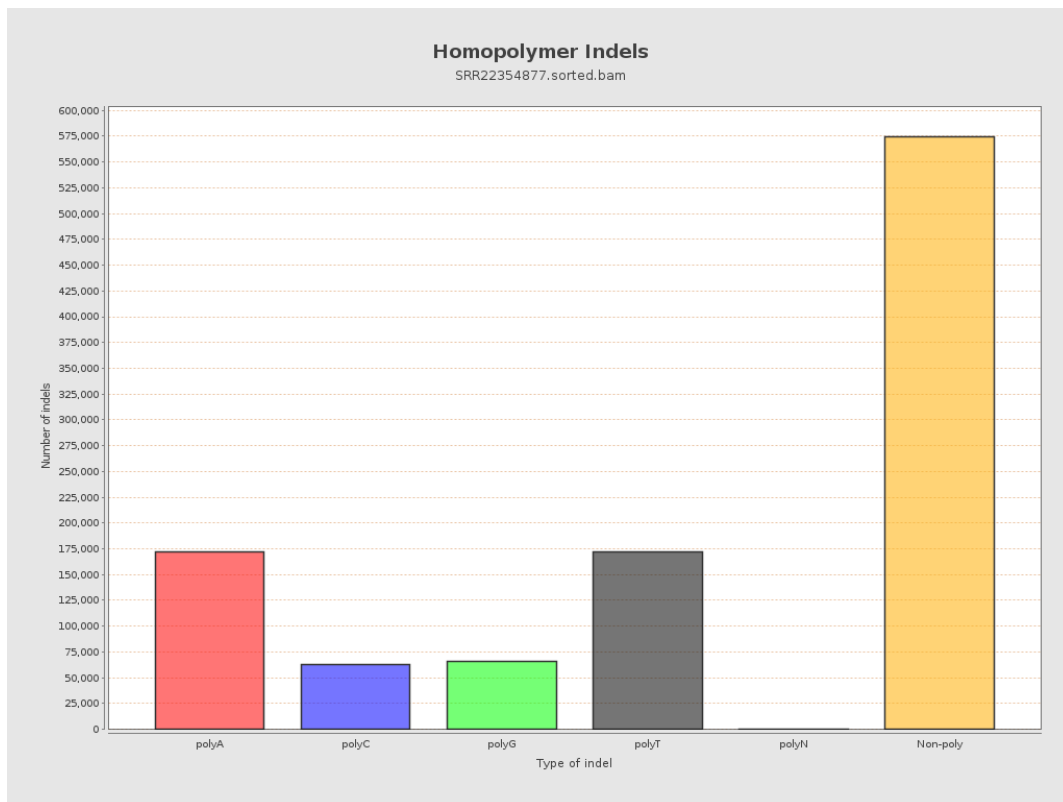
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

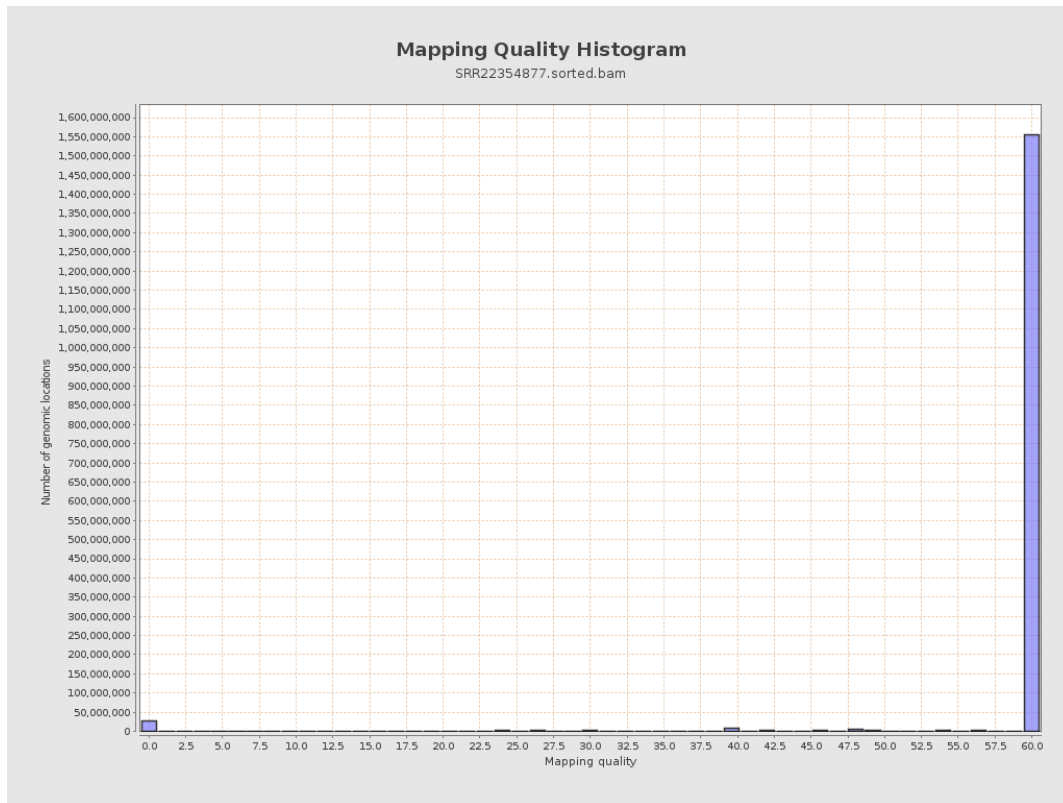


## 12. Results : Mapping Quality Across Reference

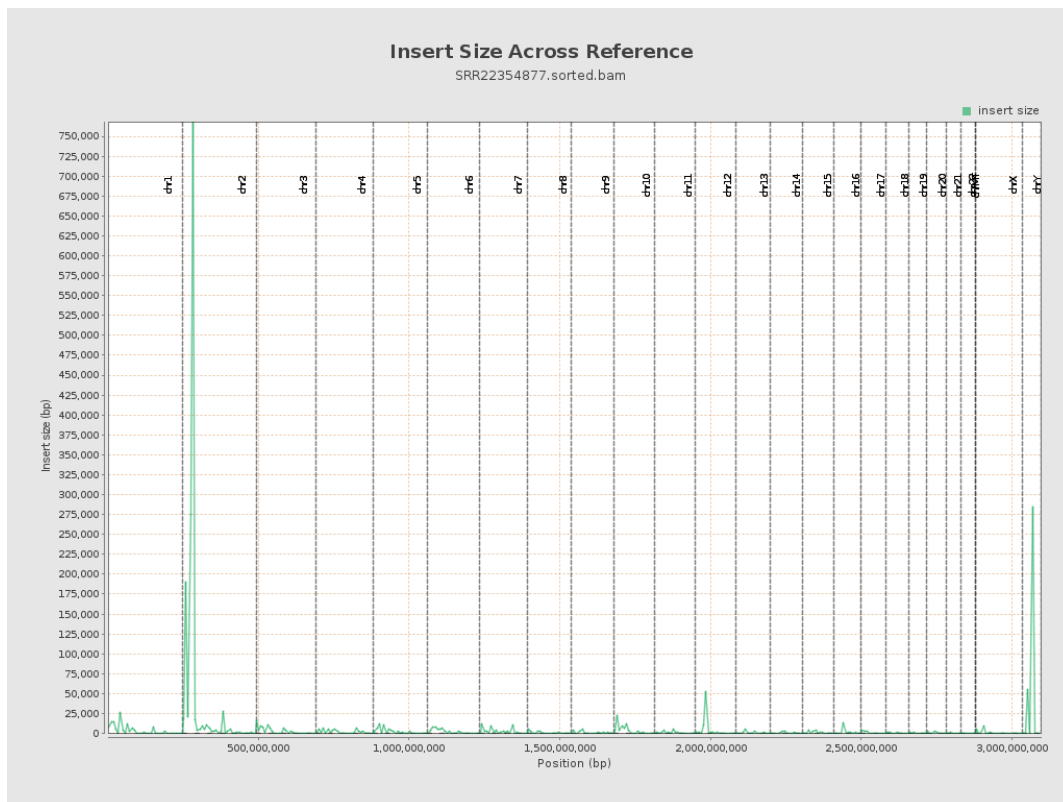




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

