

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/05 14:42:07*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR26104293.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_SRR26104293 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR26104293_1.fastq.gz SRR26104293_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                      |
| Analysis date:                        | Thu Dec 05 14:42:06 CST 2024                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                     |
| BAM file:                             | SRR26104293.sorted.bam                                                                                                                                                                                                  |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 28,983,196          |
| Mapped reads                 | 24,682,201 / 85.16% |
| Unmapped reads               | 4,300,995 / 14.84%  |
| Mapped paired reads          | 24,682,201 / 85.16% |
| Mapped reads, first in pair  | 12,874,016 / 44.42% |
| Mapped reads, second in pair | 11,808,185 / 40.74% |
| Mapped reads, both in pair   | 23,561,138 / 81.29% |
| Mapped reads, singletons     | 1,121,063 / 3.87%   |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 10,208 / 0.04%      |
| Read min/max/mean length     | 30 / 97 / 91.01     |
| Duplicated reads (estimated) | 19,609,885 / 67.66% |
| Duplication rate             | 47.47%              |
| Clipped reads                | 23,008,268 / 79.38% |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 306,919,190 / 24.64% |
| Number/percentage of C's | 330,862,064 / 26.56% |
| Number/percentage of T's | 312,835,917 / 25.12% |
| Number/percentage of G's | 294,599,564 / 23.65% |
| Number/percentage of N's | 315,684 / 0.03%      |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 50.22% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.4024 |
| Standard Deviation | 5.8001 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 49.62 |
|----------------------|-------|

## 2.5. Insert size

|                    |              |
|--------------------|--------------|
| Mean               | 15,209.24    |
| Standard Deviation | 1,152,200.29 |
| P25/Median/P75     | 39 / 45 / 56 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.45%     |
| Mismatches                               | 5,417,398 |
| Insertions                               | 76,419    |
| Mapped reads with at least one insertion | 0.31%     |
| Deletions                                | 80,074    |
| Mapped reads with at least one deletion  | 0.32%     |
| Homopolymer indels                       | 32.91%    |

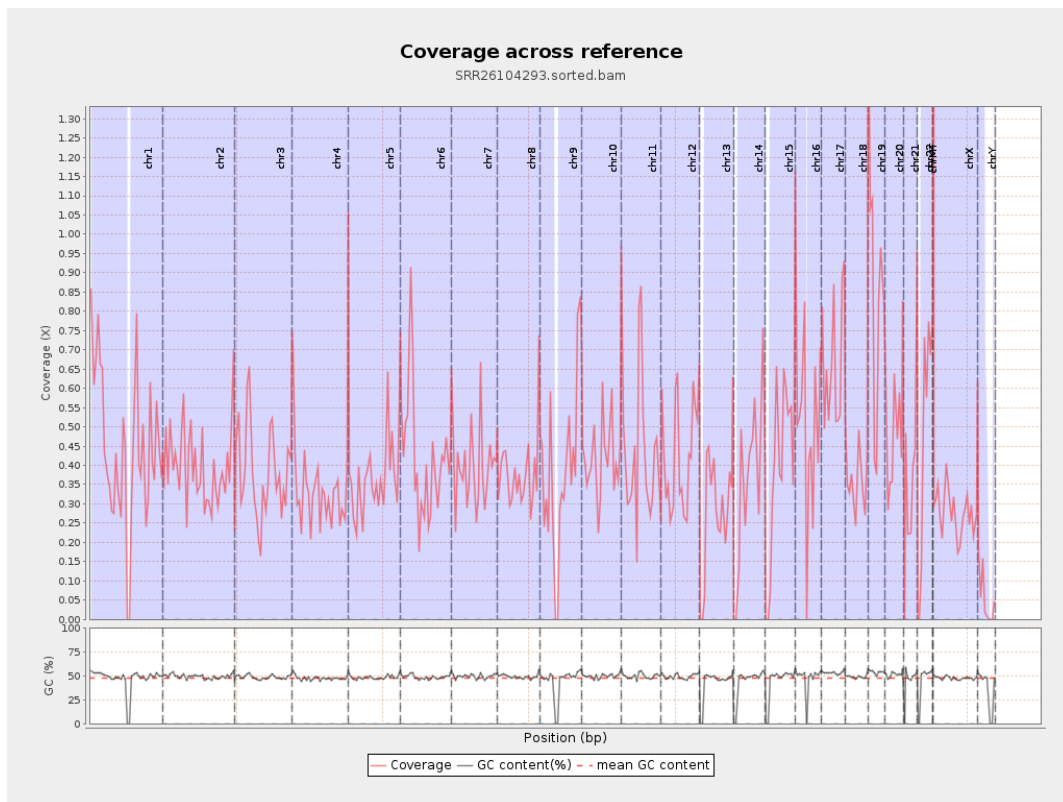
## 2.7. Chromosome stats

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

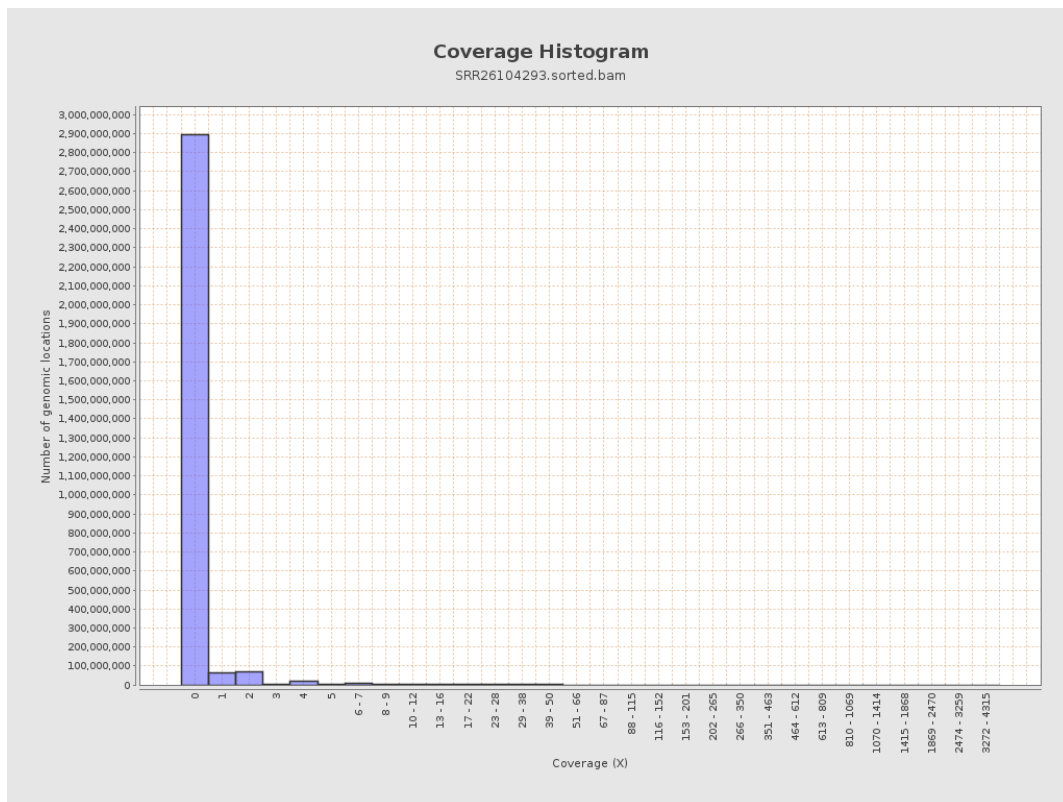
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 110869268    | 0.4448          | 6.7851           |
| chr2  | 243199373 | 96397361     | 0.3964          | 5.5259           |
| chr3  | 198022430 | 75554966     | 0.3815          | 5.0724           |
| chr4  | 191154276 | 62798344     | 0.3285          | 4.4307           |
| chr5  | 180915260 | 67896954     | 0.3753          | 5.0087           |
| chr6  | 171115067 | 70923031     | 0.4145          | 5.2559           |
| chr7  | 159138663 | 63462746     | 0.3988          | 5.1405           |
| chr8  | 146364022 | 55120565     | 0.3766          | 5.225            |
| chr9  | 141213431 | 53519629     | 0.379           | 5.1926           |
| chr10 | 135534747 | 56256224     | 0.4151          | 5.3295           |
| chr11 | 135006516 | 58151842     | 0.4307          | 5.6409           |
| chr12 | 133851895 | 57382877     | 0.4287          | 5.6949           |
| chr13 | 115169878 | 32030661     | 0.2781          | 4.1342           |
| chr14 | 107349540 | 39375969     | 0.3668          | 5.1355           |
| chr15 | 102531392 | 39617868     | 0.3864          | 5.2277           |
| chr16 | 90354753  | 46799721     | 0.518           | 6.6508           |
| chr17 | 81195210  | 53564380     | 0.6597          | 7.5054           |
| chr18 | 78077248  | 27926614     | 0.3577          | 4.8512           |
| chr19 | 59128983  | 49178826     | 0.8317          | 8.915            |
| chr20 | 63025520  | 30160533     | 0.4785          | 6.7852           |
| chr21 | 48129895  | 18379718     | 0.3819          | 9.8866           |
| chr22 | 51304566  | 24081389     | 0.4694          | 6.5472           |
| chrMT | 16571     | 9194078      | 554.8294        | 362.9244         |
| chrX  | 155270560 | 43898654     | 0.2827          | 3.9488           |

|      |          |         |        |        |
|------|----------|---------|--------|--------|
| chrY | 59373566 | 3126152 | 0.0527 | 2.5612 |
|------|----------|---------|--------|--------|

### 3. Results : Coverage across reference

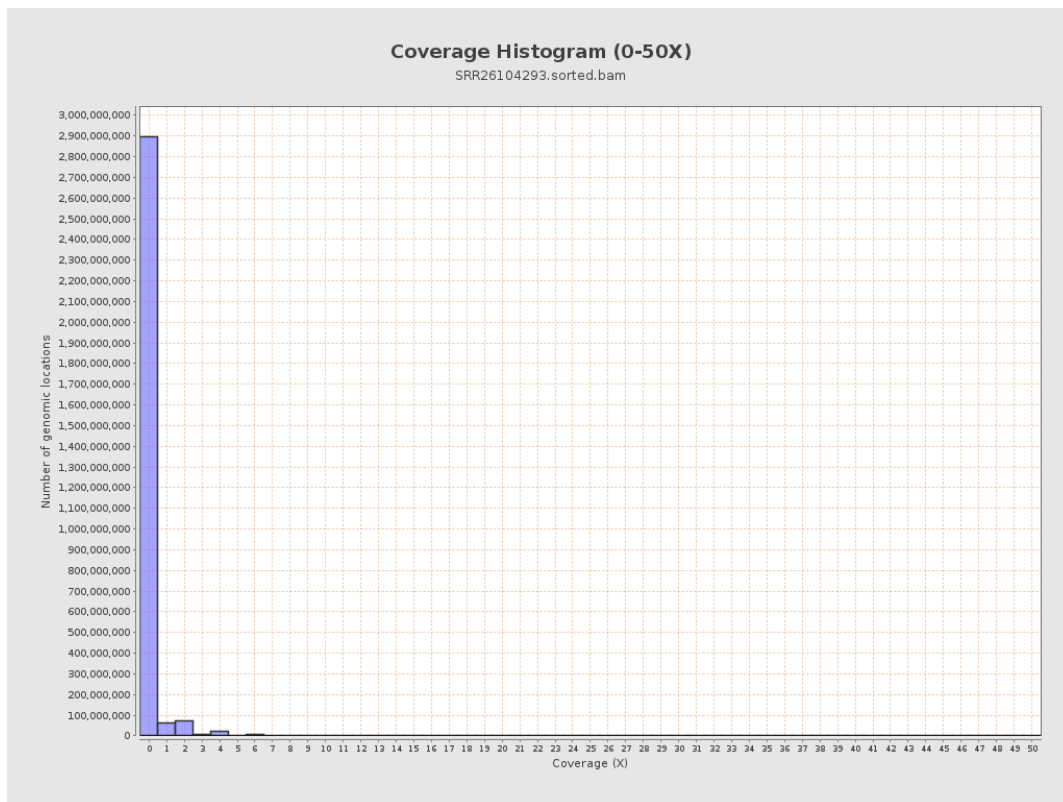


## 4. Results : Coverage Histogram

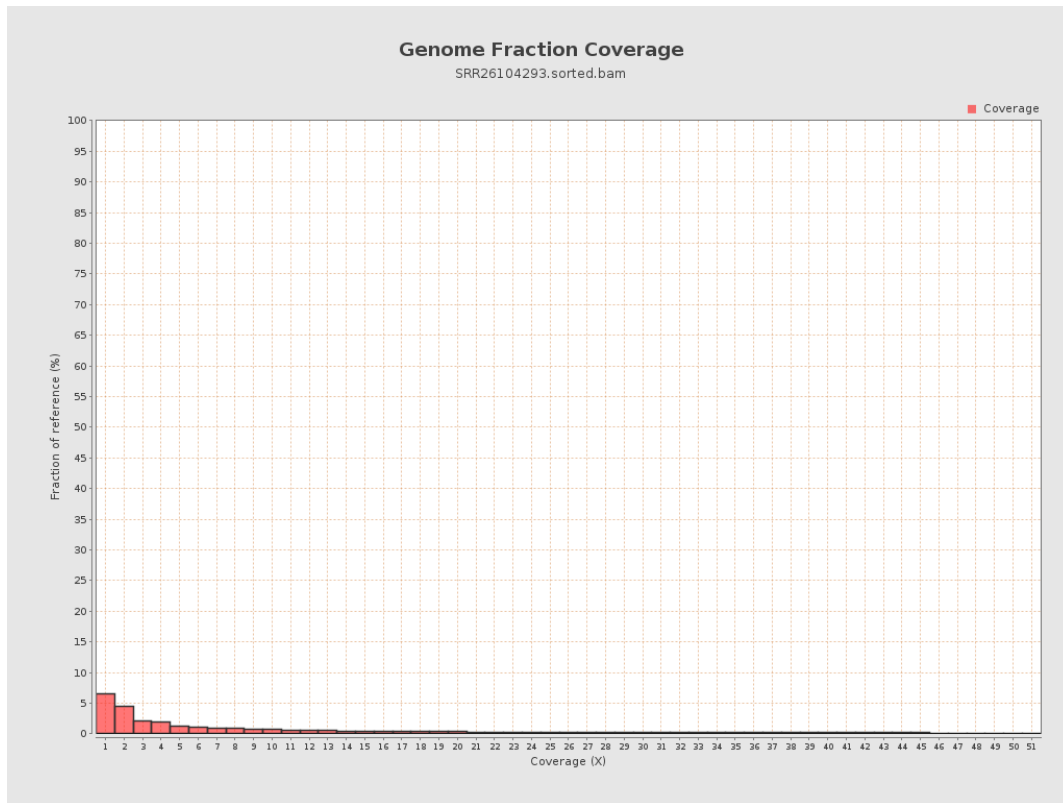




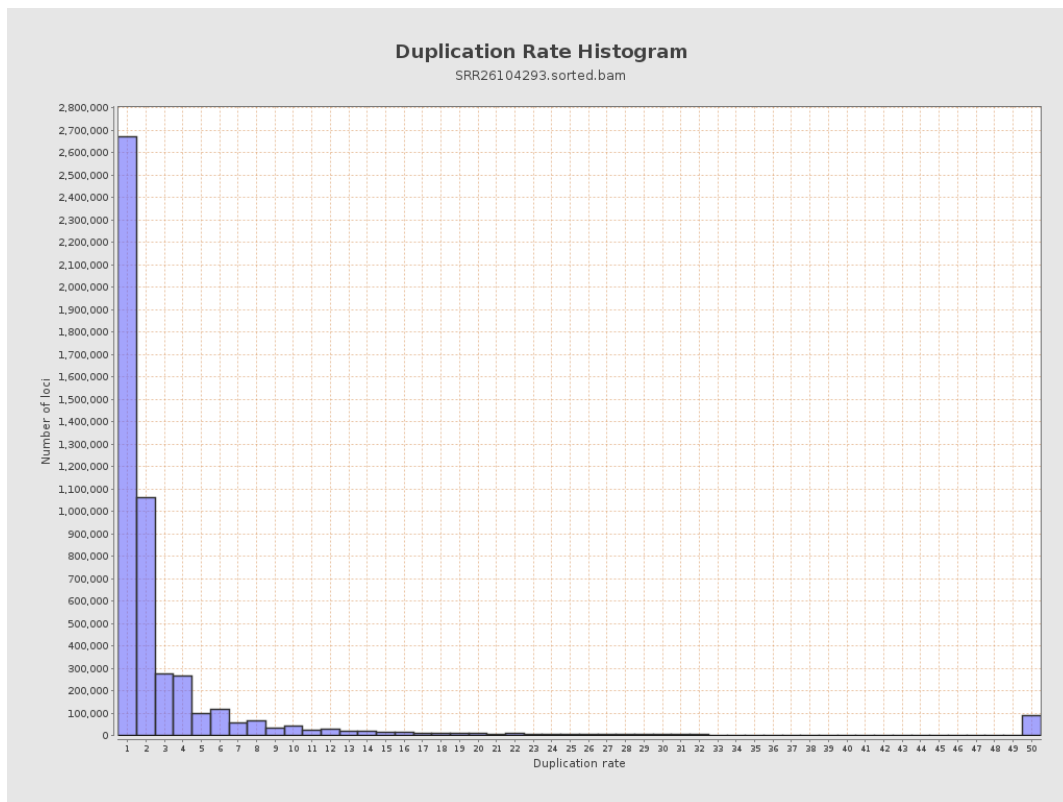
## 5. Results : Coverage Histogram (0-50X)



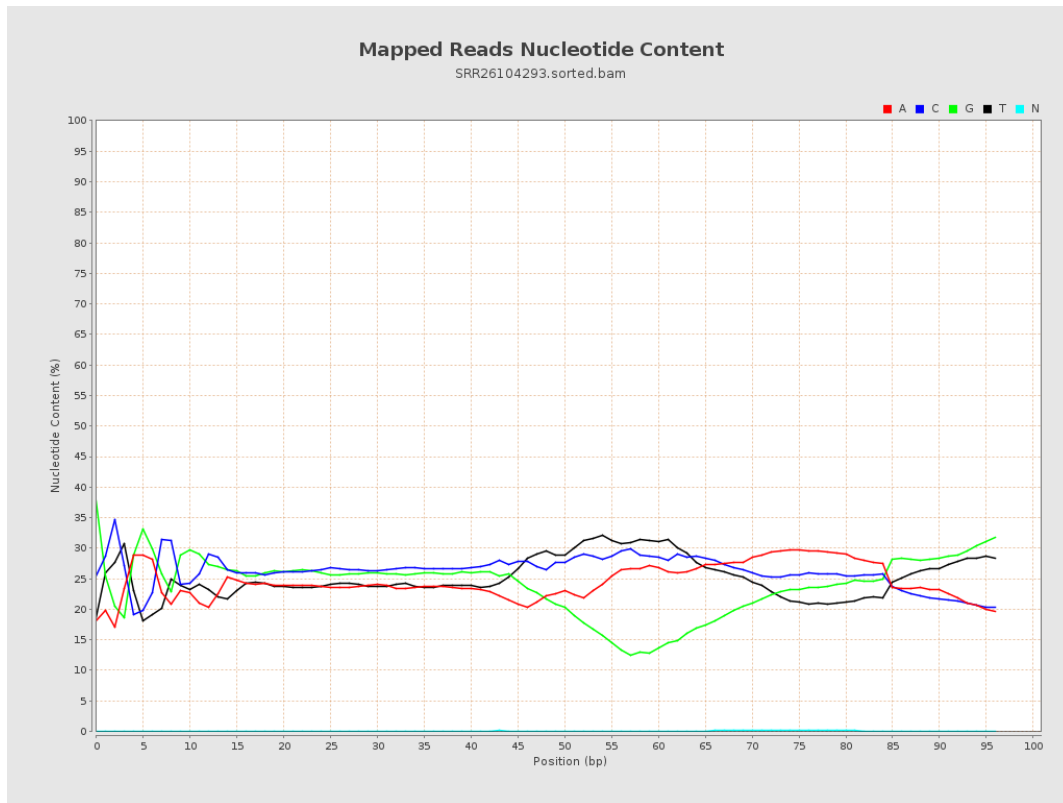
## 6. Results : Genome Fraction Coverage



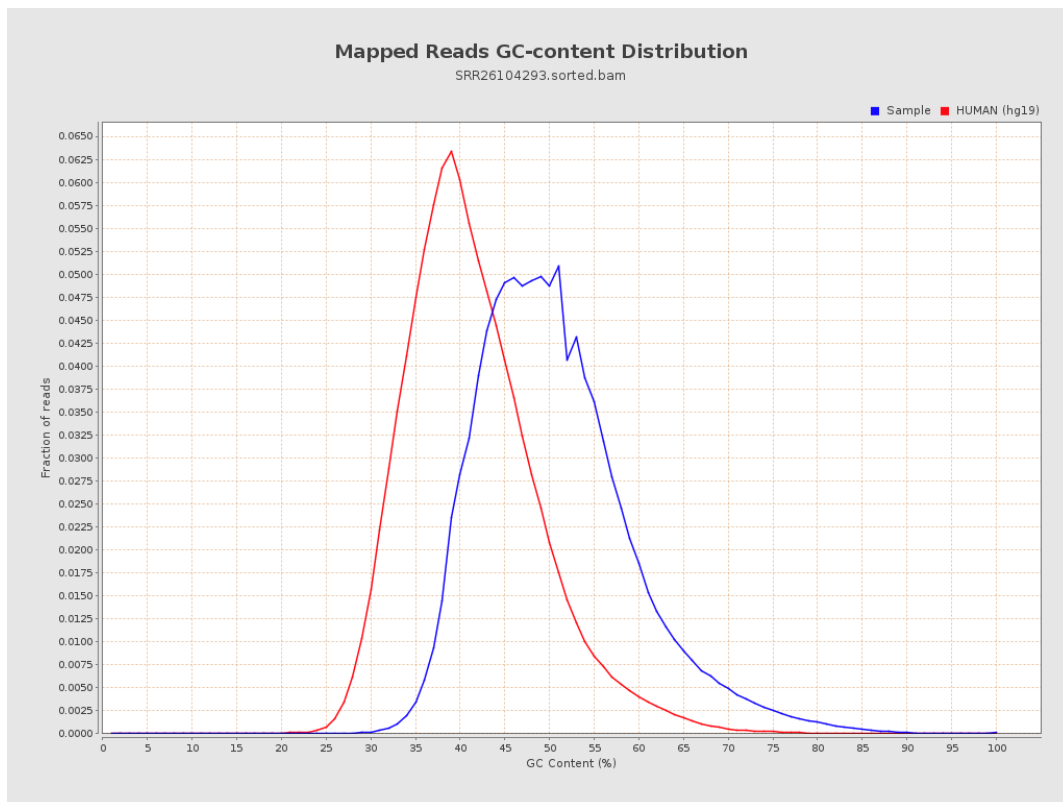
## 7. Results : Duplication Rate Histogram



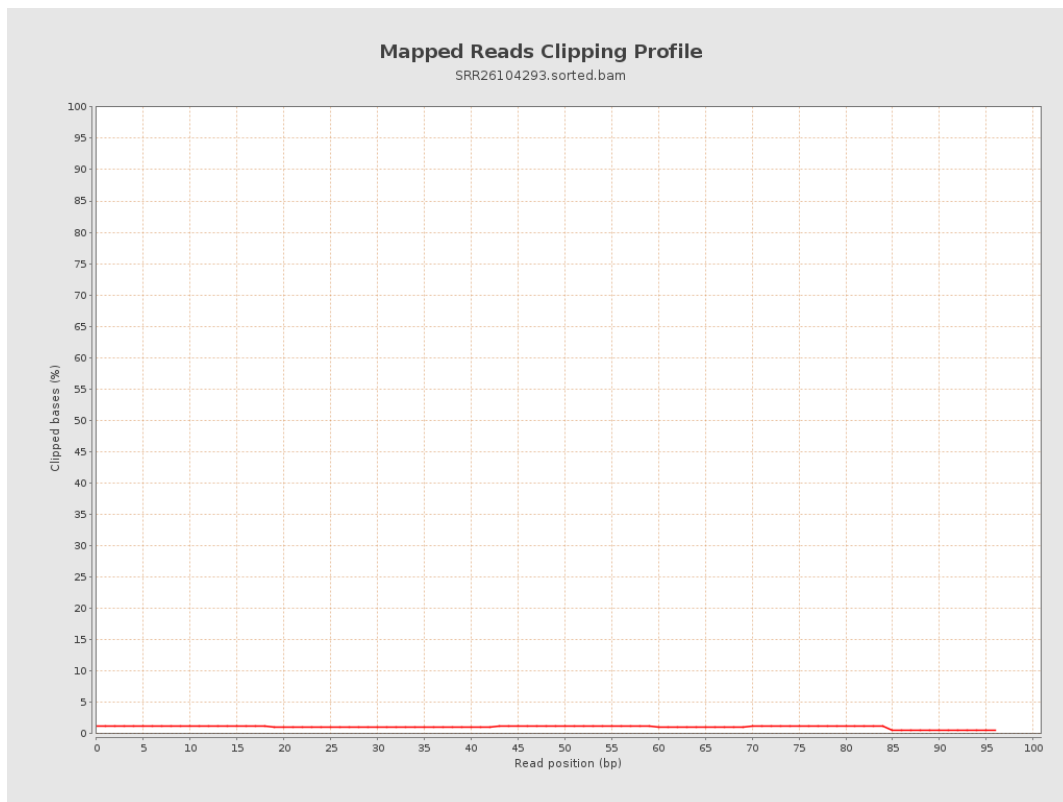
## 8. Results : Mapped Reads Nucleotide Content



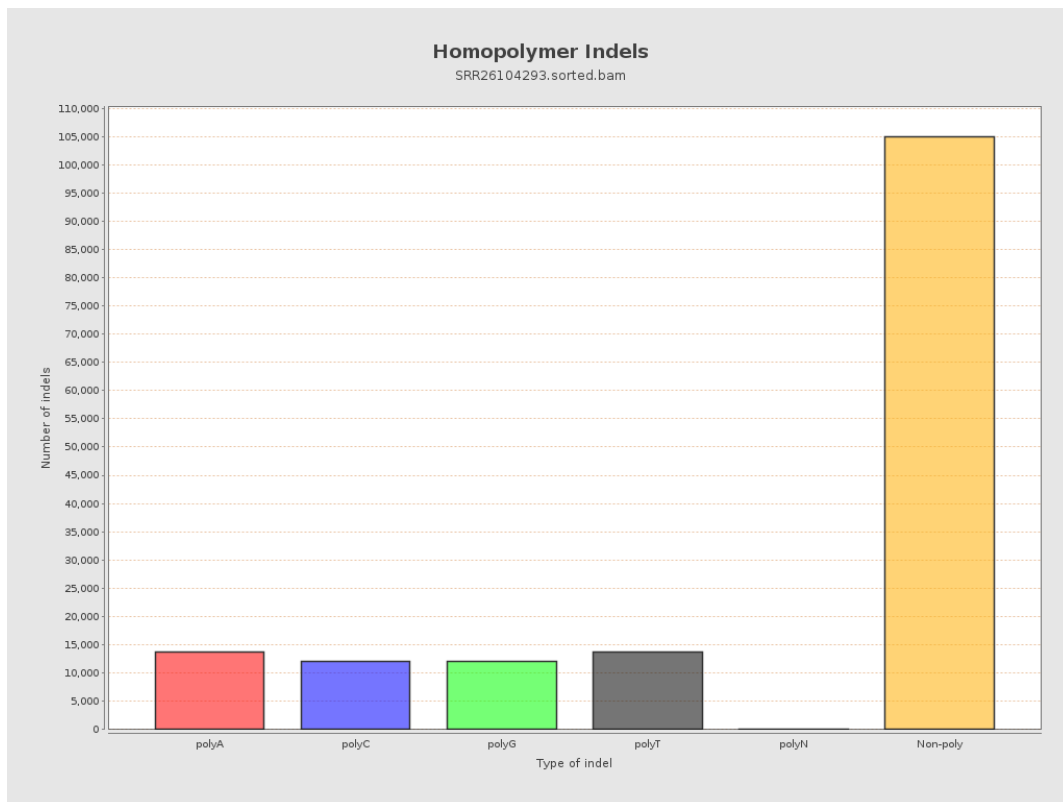
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

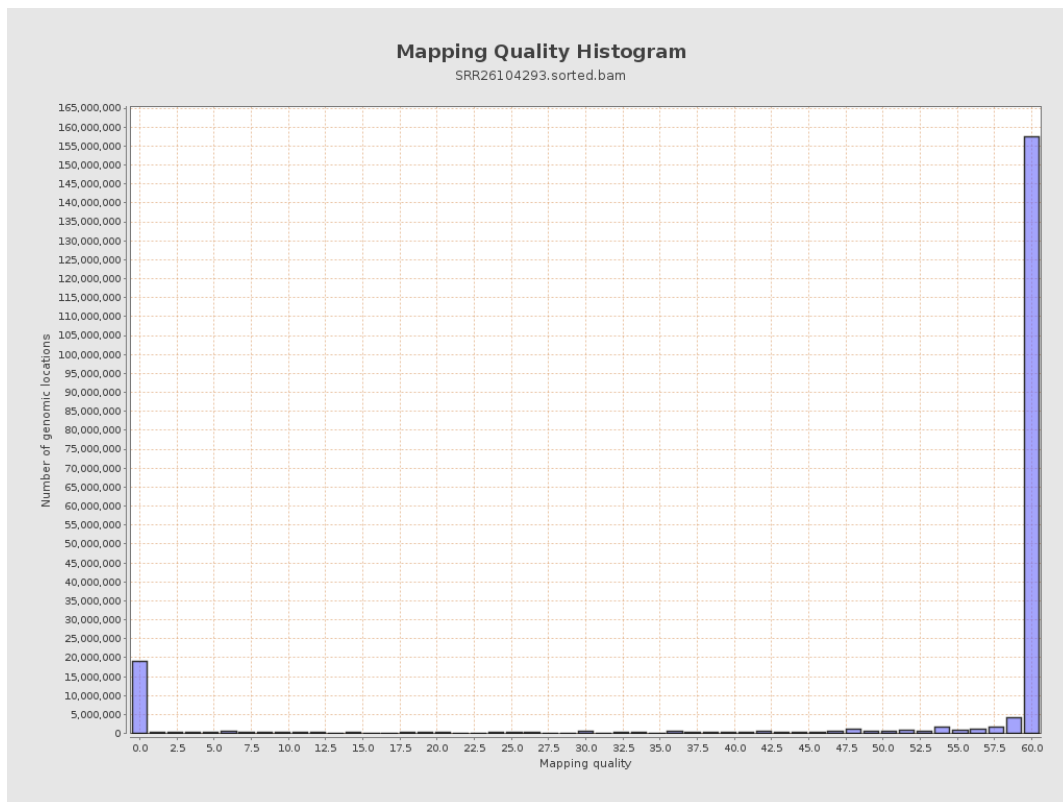


## 12. Results : Mapping Quality Across Reference

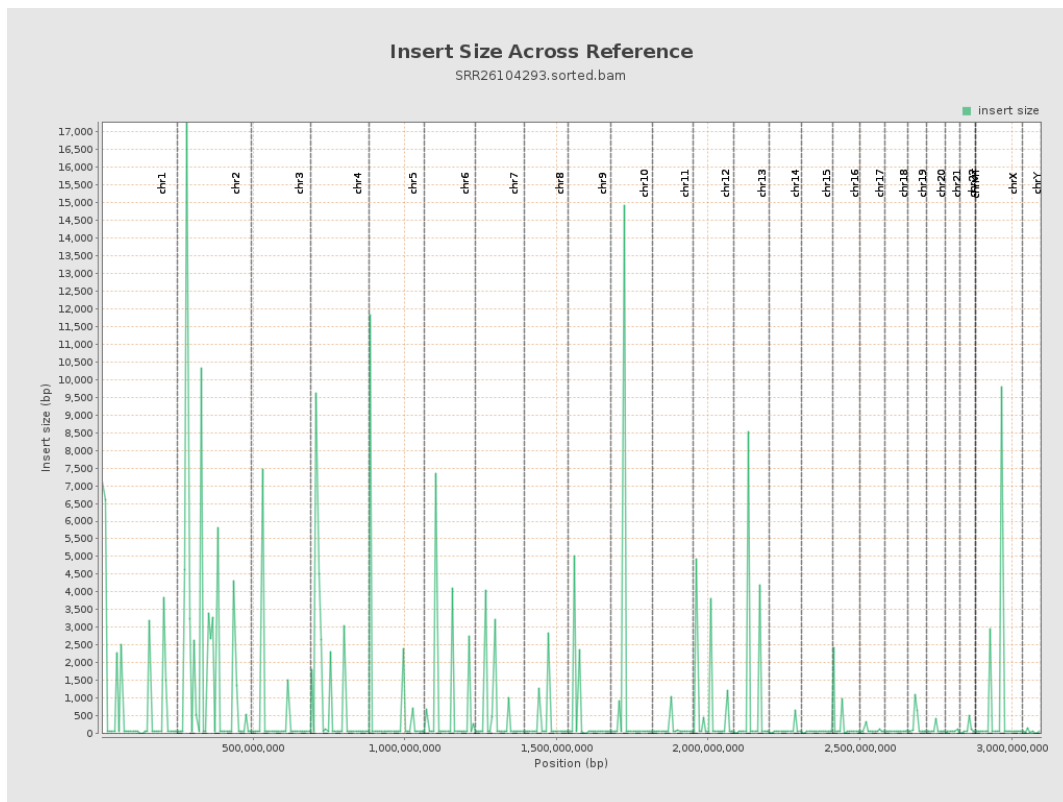




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

