

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/05 08:30:17*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124833.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_SRR3124833 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124833_1.fastq.gz SRR3124833_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                  |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                   |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                   |
| Analysis date:                        | Thu Dec 05 08:30:16 CST 2024                                                                                                                                                                                         |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                    |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                   |
| Number of windows:                    | 400                                                                                                                                                                                                                  |
| BAM file:                             | SRR3124833.sorted.bam                                                                                                                                                                                                |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 26,097,940          |
| Mapped reads                 | 25,716,801 / 98.54% |
| Unmapped reads               | 381,139 / 1.46%     |
| Mapped paired reads          | 25,716,801 / 98.54% |
| Mapped reads, first in pair  | 12,887,180 / 49.38% |
| Mapped reads, second in pair | 12,829,621 / 49.16% |
| Mapped reads, both in pair   | 25,604,504 / 98.11% |
| Mapped reads, singletons     | 112,297 / 0.43%     |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 115,712 / 0.44%     |
| Read min/max/mean length     | 30 / 101 / 101.17   |
| Duplicated reads (estimated) | 4,302,499 / 16.49%  |
| Duplication rate             | 11.18%              |
| Clipped reads                | 12,605,367 / 48.3%  |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 619,455,946 / 27.85% |
| Number/percentage of C's | 417,849,412 / 18.79% |
| Number/percentage of T's | 653,463,531 / 29.38% |
| Number/percentage of G's | 533,338,287 / 23.98% |
| Number/percentage of N's | 20,722 / 0%          |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 42.77% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.7189 |
| Standard Deviation | 5.7473 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 52.79 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 39,494.59       |
| Standard Deviation | 1,847,639.45    |
| P25/Median/P75     | 148 / 201 / 279 |

## 2.6. Mismatches and indels

|                                          |            |
|------------------------------------------|------------|
| General error rate                       | 0.78%      |
| Mismatches                               | 16,556,392 |
| Insertions                               | 314,283    |
| Mapped reads with at least one insertion | 1.18%      |
| Deletions                                | 744,822    |
| Mapped reads with at least one deletion  | 2.84%      |
| Homopolymer indels                       | 46.4%      |

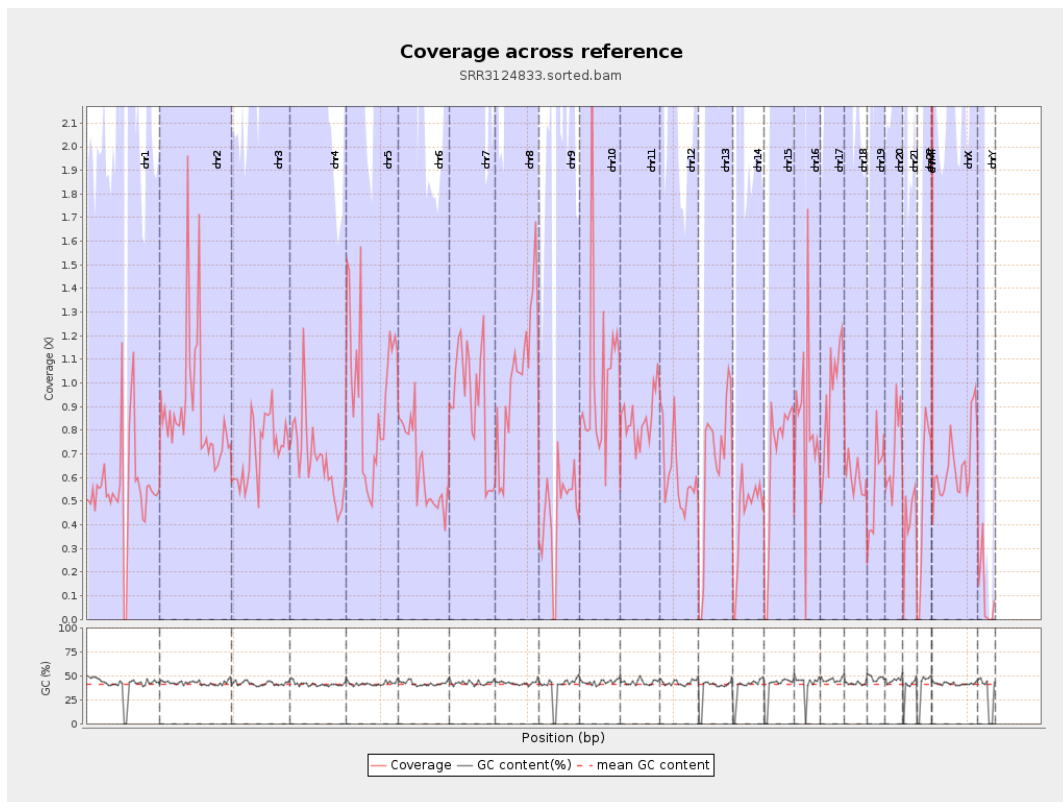
## 2.7. Chromosome stats

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

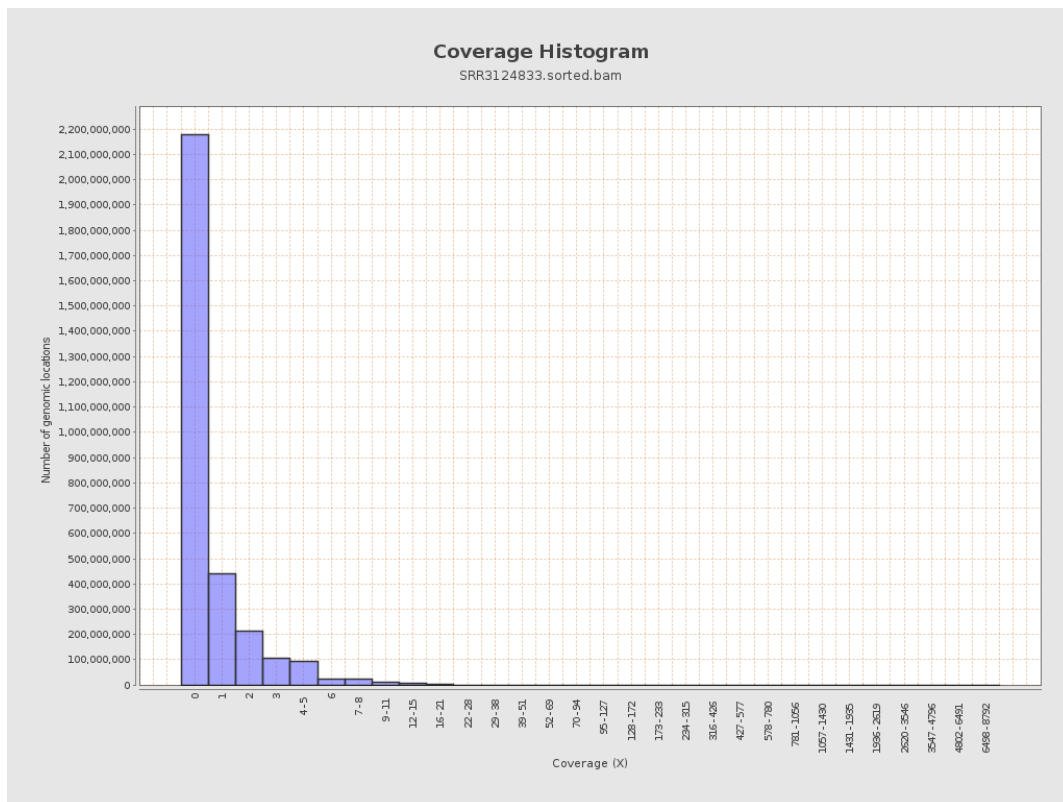
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 139620433    | 0.5602          | 5.368            |
| chr2  | 243199373 | 215930190    | 0.8879          | 9.8899           |
| chr3  | 198022430 | 141889836    | 0.7165          | 1.6306           |
| chr4  | 191154276 | 128634320    | 0.6729          | 3.9734           |
| chr5  | 180915260 | 171223993    | 0.9464          | 2.2379           |
| chr6  | 171115067 | 108907140    | 0.6365          | 3.4708           |
| chr7  | 159138663 | 144688030    | 0.9092          | 7.5967           |
| chr8  | 146364022 | 150585336    | 1.0288          | 2.7497           |
| chr9  | 141213431 | 63354627     | 0.4486          | 5.5122           |
| chr10 | 135534747 | 140162773    | 1.0341          | 14.0118          |
| chr11 | 135006516 | 113909364    | 0.8437          | 3.5867           |
| chr12 | 133851895 | 81527130     | 0.6091          | 1.5416           |
| chr13 | 115169878 | 77268323     | 0.6709          | 1.6102           |
| chr14 | 107349540 | 47170258     | 0.4394          | 1.7896           |
| chr15 | 102531392 | 69486153     | 0.6777          | 1.6378           |
| chr16 | 90354753  | 74239634     | 0.8216          | 9.3285           |
| chr17 | 81195210  | 75773495     | 0.9332          | 5.764            |
| chr18 | 78077248  | 46787350     | 0.5992          | 6.8856           |
| chr19 | 59128983  | 33556345     | 0.5675          | 3.7487           |
| chr20 | 63025520  | 44493419     | 0.706           | 2.1942           |
| chr21 | 48129895  | 20375572     | 0.4233          | 2.4405           |
| chr22 | 51304566  | 27650511     | 0.5389          | 1.8451           |
| chrMT | 16571     | 439616       | 26.5292         | 16.4907          |
| chrX  | 155270560 | 101230667    | 0.652           | 2.5132           |

|      |          |         |        |        |
|------|----------|---------|--------|--------|
| chrY | 59373566 | 6536520 | 0.1101 | 7.8289 |
|------|----------|---------|--------|--------|

### 3. Results : Coverage across reference

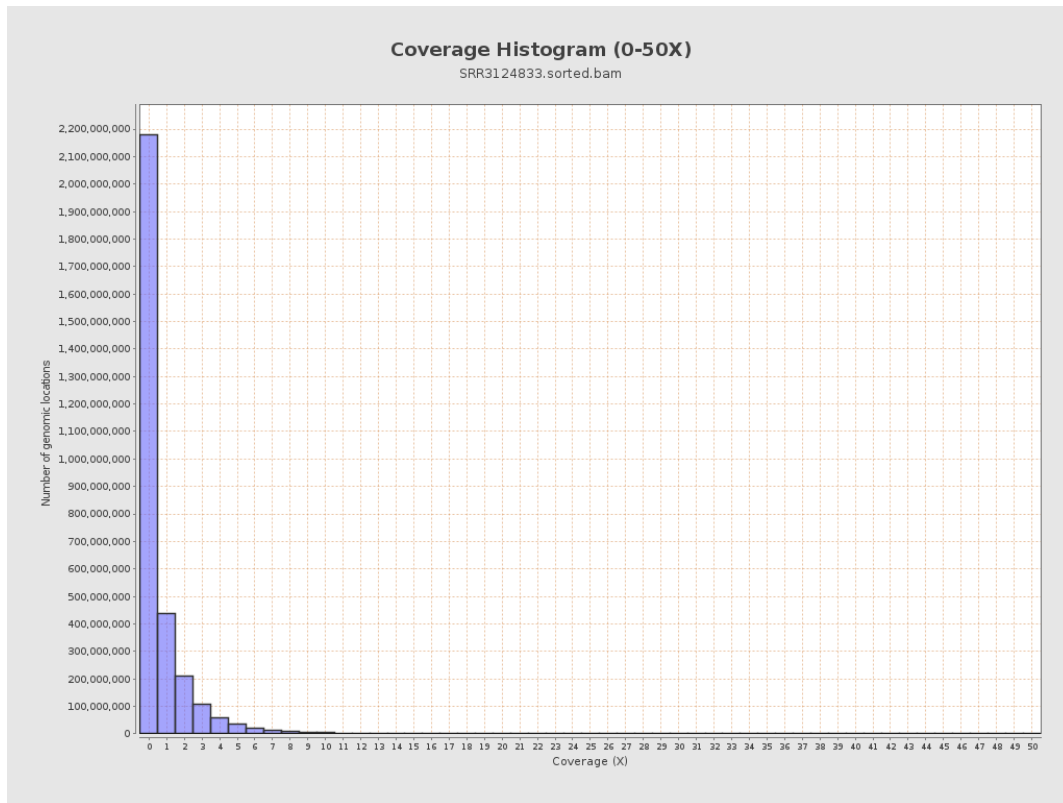


## 4. Results : Coverage Histogram

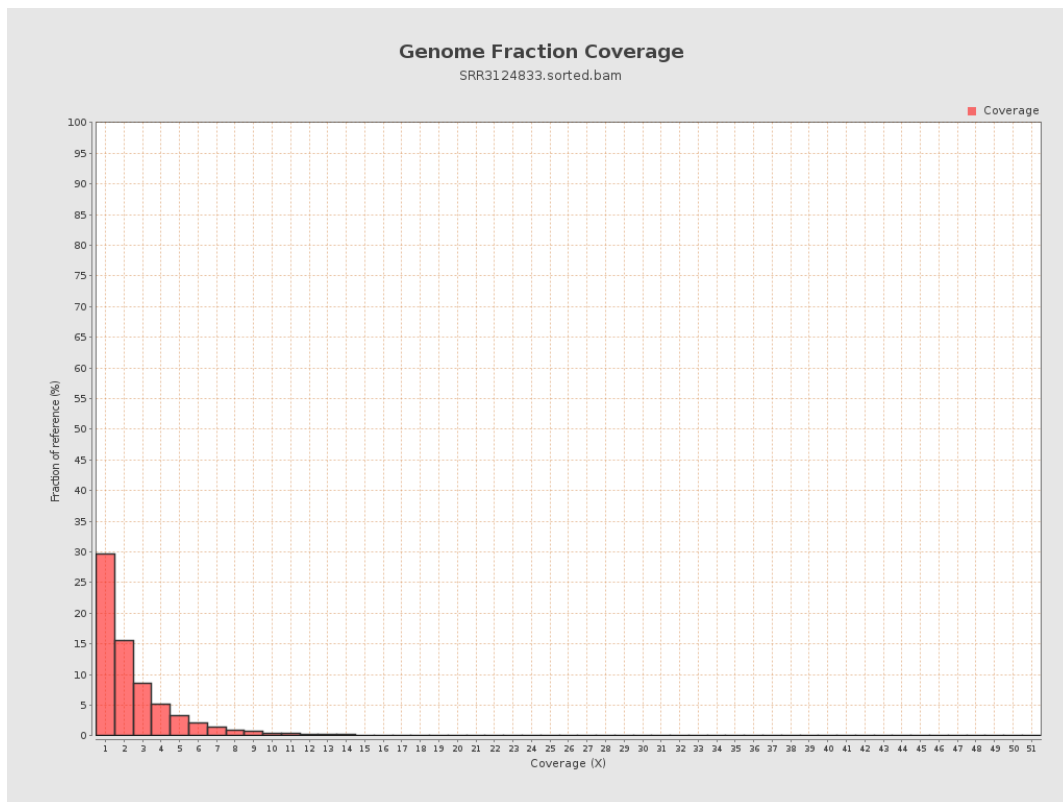




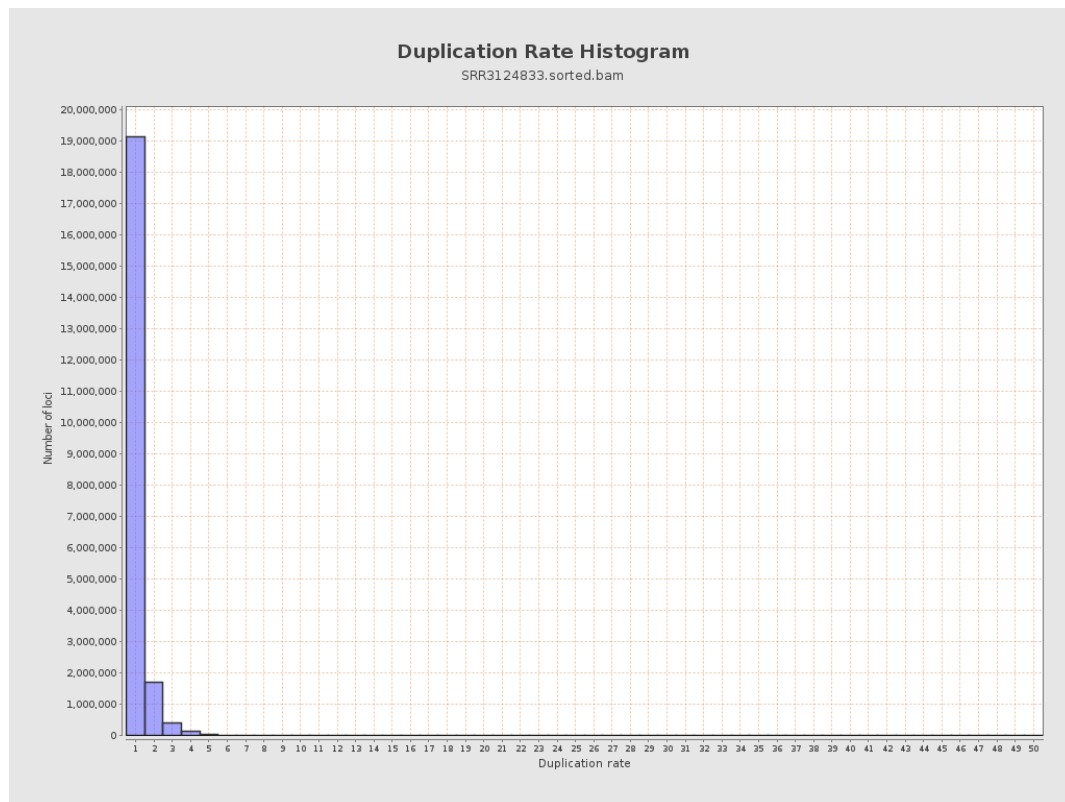
## 5. Results : Coverage Histogram (0-50X)



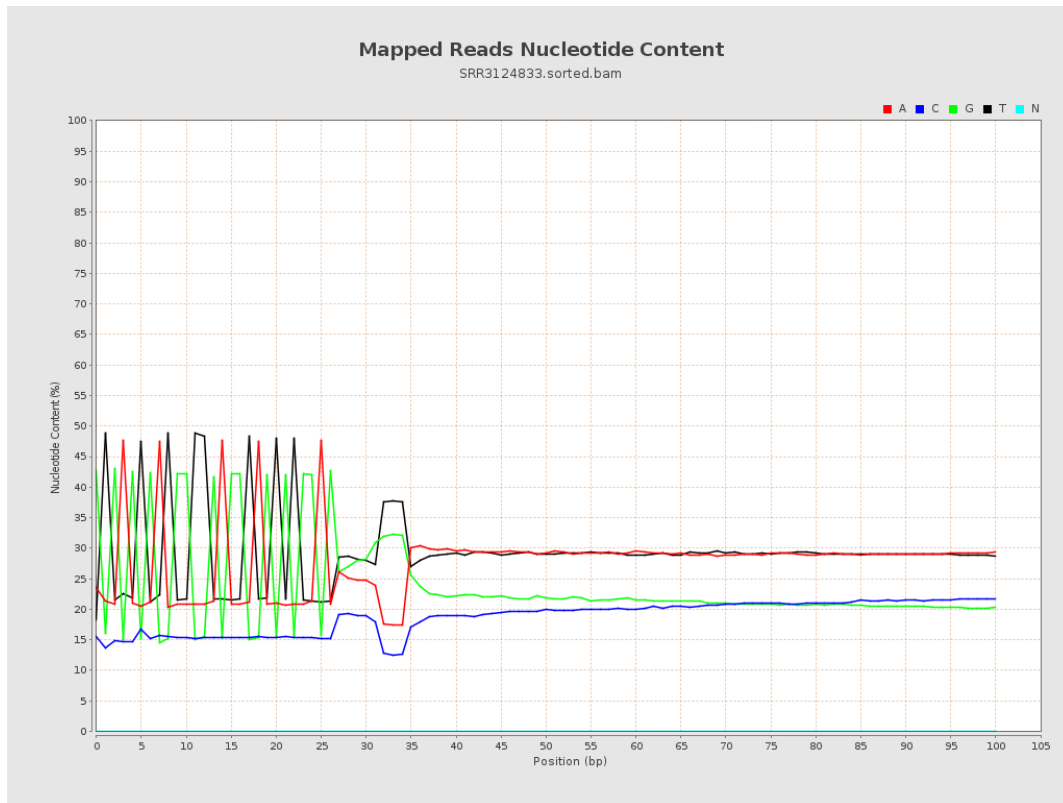
## 6. Results : Genome Fraction Coverage



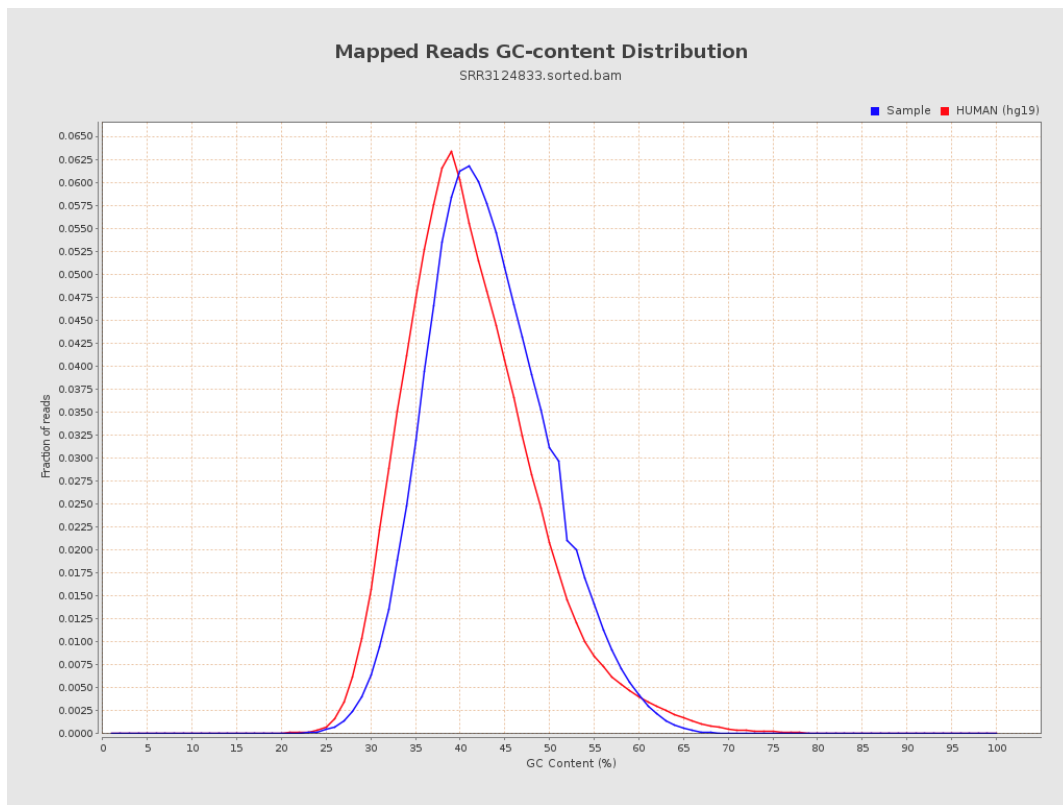
## 7. Results : Duplication Rate Histogram



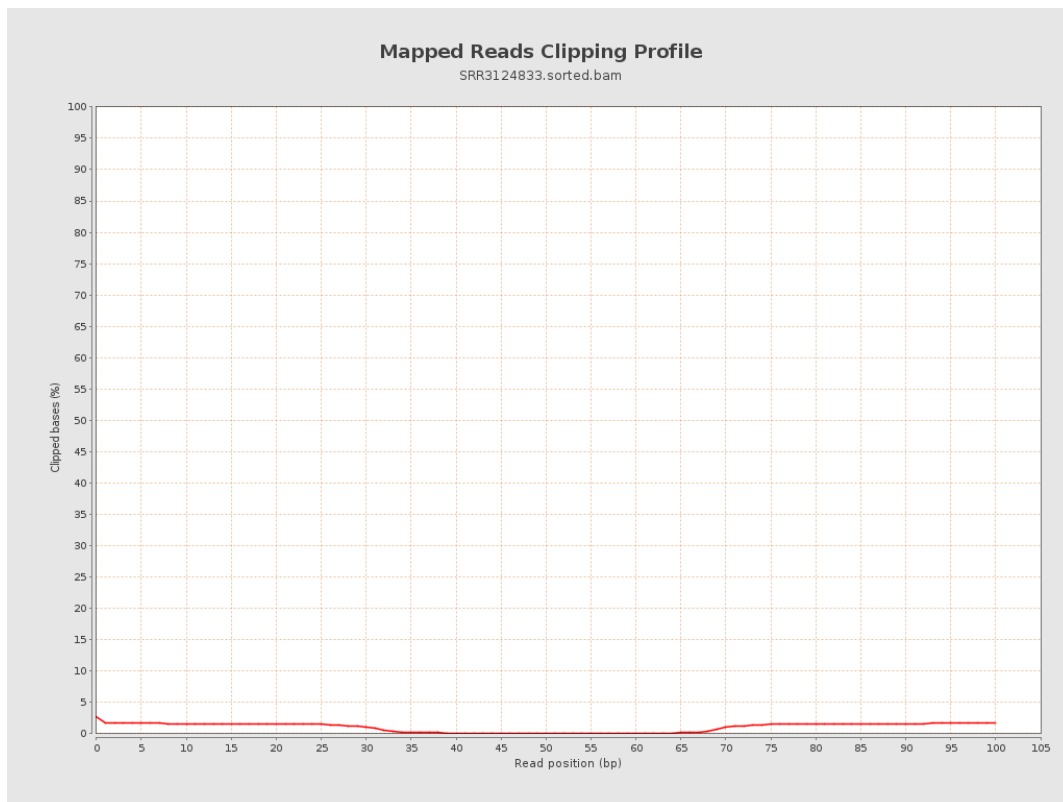
## 8. Results : Mapped Reads Nucleotide Content



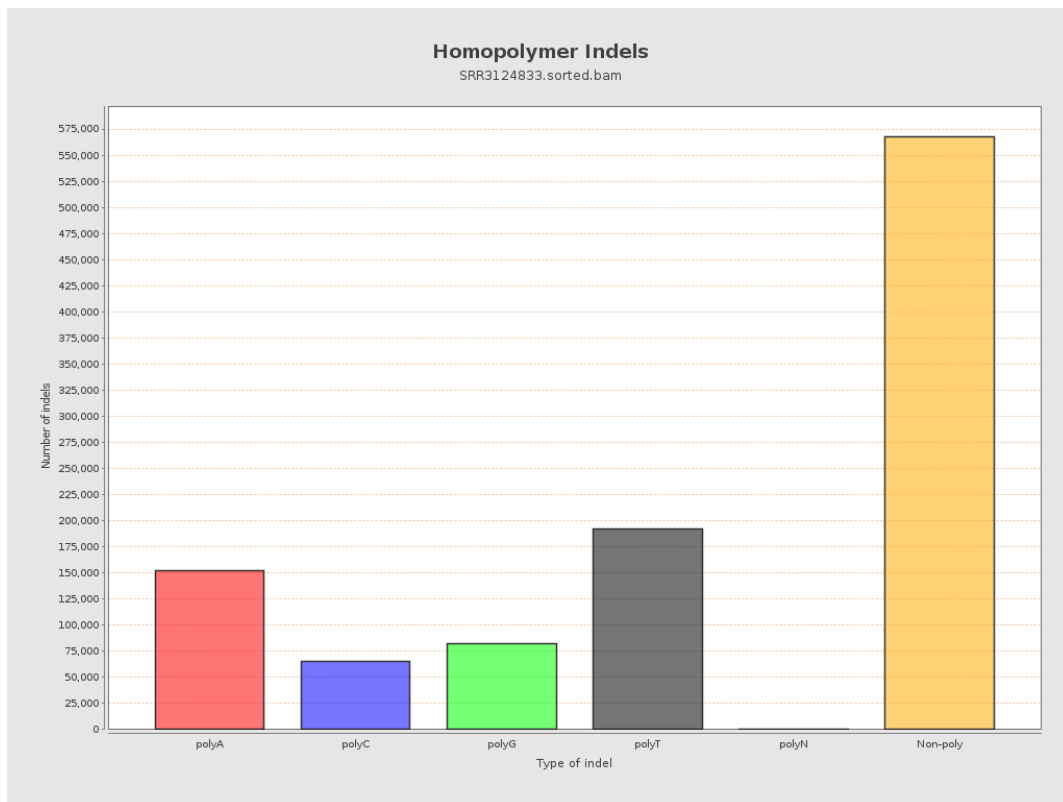
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

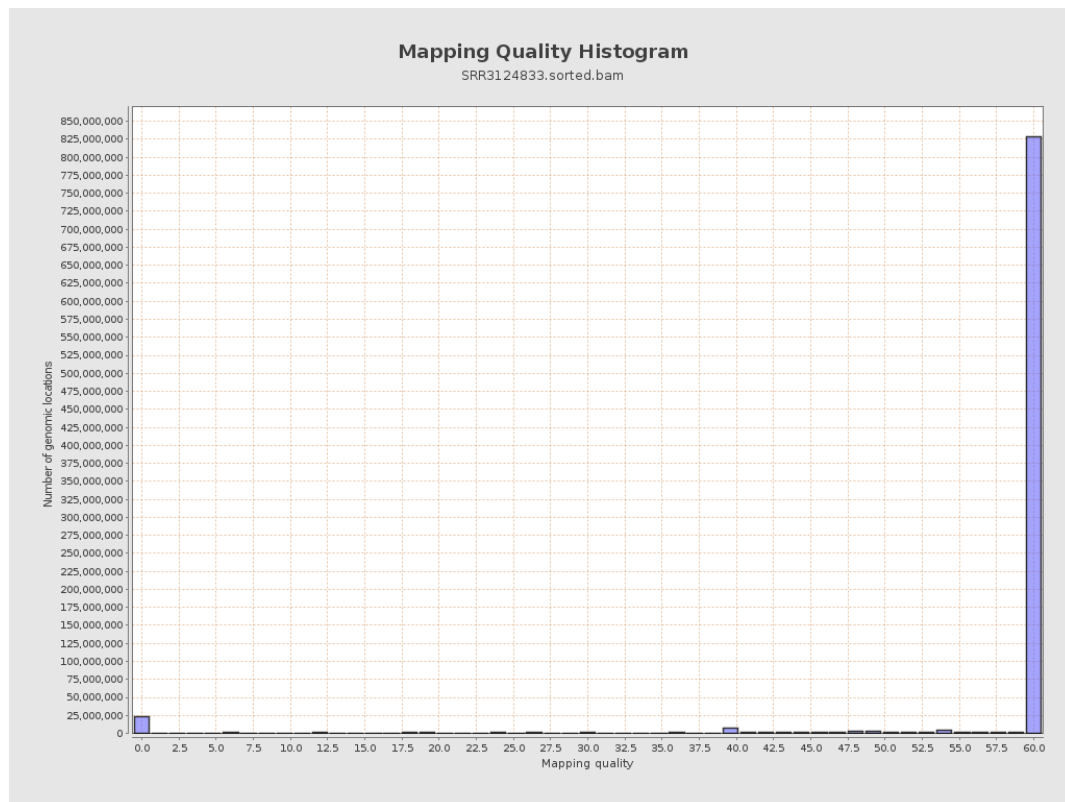


## 12. Results : Mapping Quality Across Reference

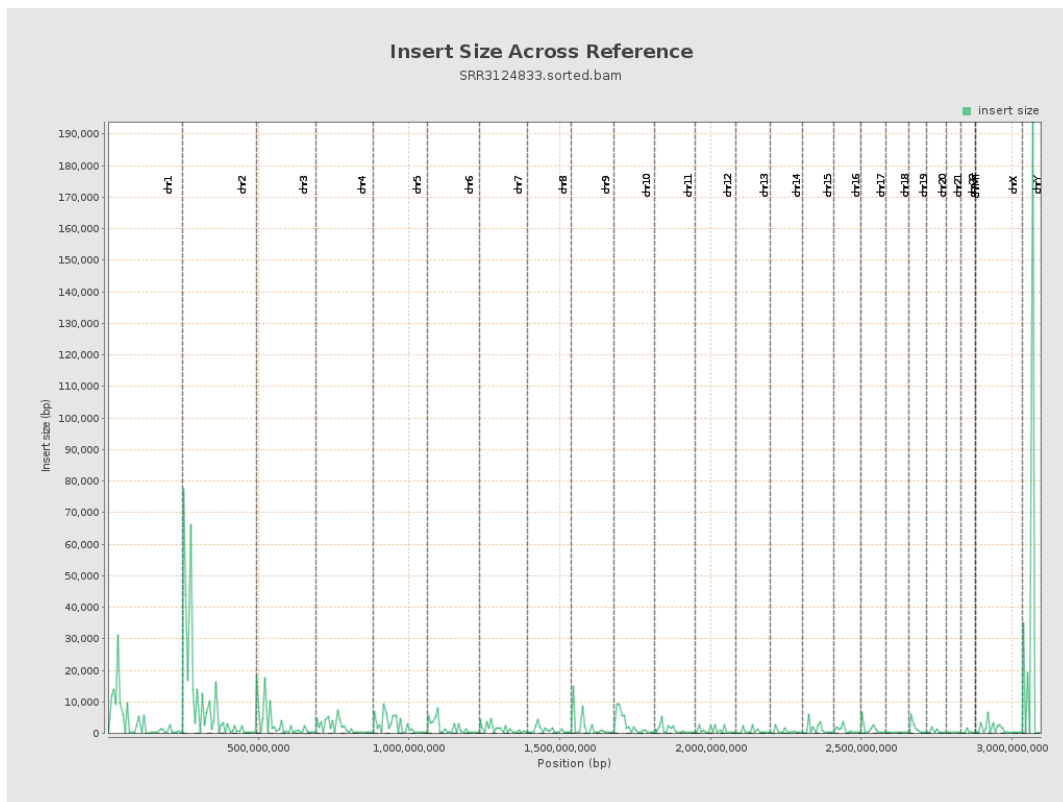




# 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

