

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/30 04:45:59*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472747.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_SRR3472747 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472747_1.fastq.gz SRR3472747_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                  |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                   |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                   |
| Analysis date:                        | Mon Sep 30 04:45:58 CST 2024                                                                                                                                                                                         |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                    |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                   |
| Number of windows:                    | 400                                                                                                                                                                                                                  |
| BAM file:                             | SRR3472747.sorted.bam                                                                                                                                                                                                |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 13,463,824          |
| Mapped reads                 | 13,326,702 / 98.98% |
| Unmapped reads               | 137,122 / 1.02%     |
| Mapped paired reads          | 13,326,702 / 98.98% |
| Mapped reads, first in pair  | 6,694,692 / 49.72%  |
| Mapped reads, second in pair | 6,632,010 / 49.26%  |
| Mapped reads, both in pair   | 13,238,662 / 98.33% |
| Mapped reads, singletons     | 88,040 / 0.65%      |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 36,937 / 0.27%      |
| Read min/max/mean length     | 30 / 100 / 100.11   |
| Duplicated reads (estimated) | 7,790,785 / 57.86%  |
| Duplication rate             | 46.77%              |
| Clipped reads                | 915,915 / 6.8%      |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 364,407,479 / 27.7%  |
| Number/percentage of C's | 295,268,275 / 22.45% |
| Number/percentage of T's | 362,245,249 / 27.54% |
| Number/percentage of G's | 293,194,686 / 22.29% |
| Number/percentage of N's | 252,348 / 0.02%      |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 44.74% |
|---------------|--------|

## 2.3. Coverage

|                    |         |
|--------------------|---------|
| Mean               | 0.425   |
| Standard Deviation | 12.7425 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 55.15 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 23,832.04       |
| Standard Deviation | 1,542,655.99    |
| P25/Median/P75     | 190 / 266 / 357 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.68%     |
| Mismatches                               | 8,763,085 |
| Insertions                               | 74,303    |
| Mapped reads with at least one insertion | 0.55%     |
| Deletions                                | 76,008    |
| Mapped reads with at least one deletion  | 0.56%     |
| Homopolymer indels                       | 45.23%    |

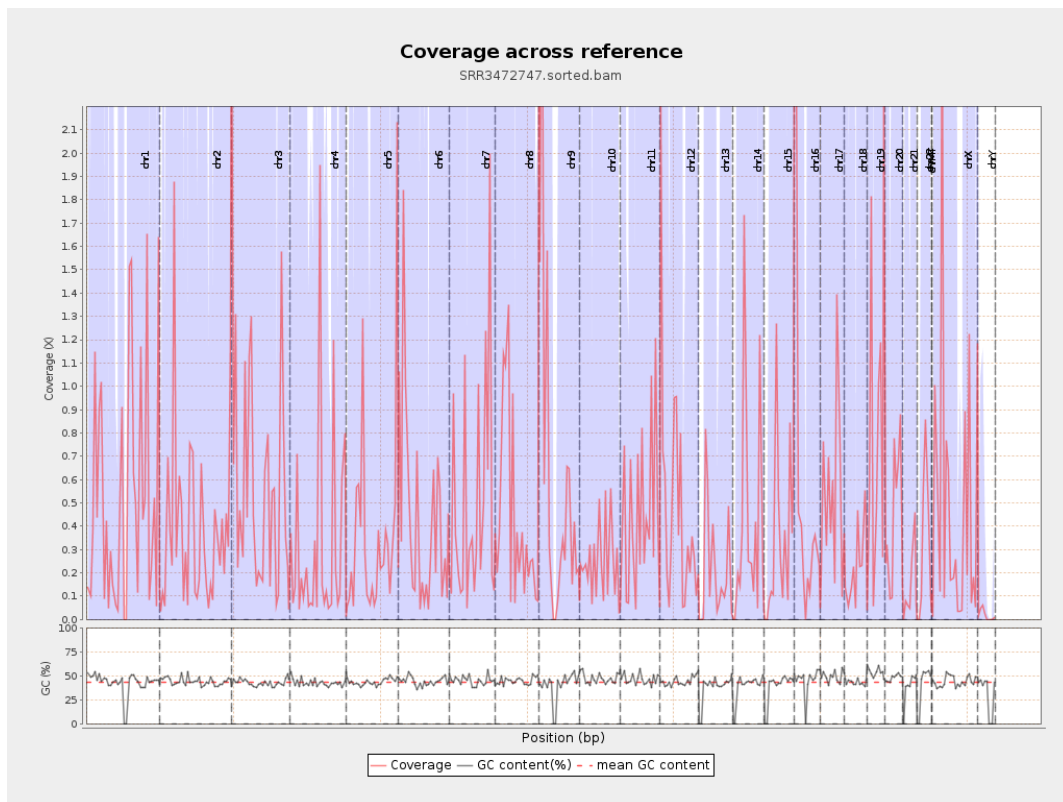
## 2.7. Chromosome stats

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

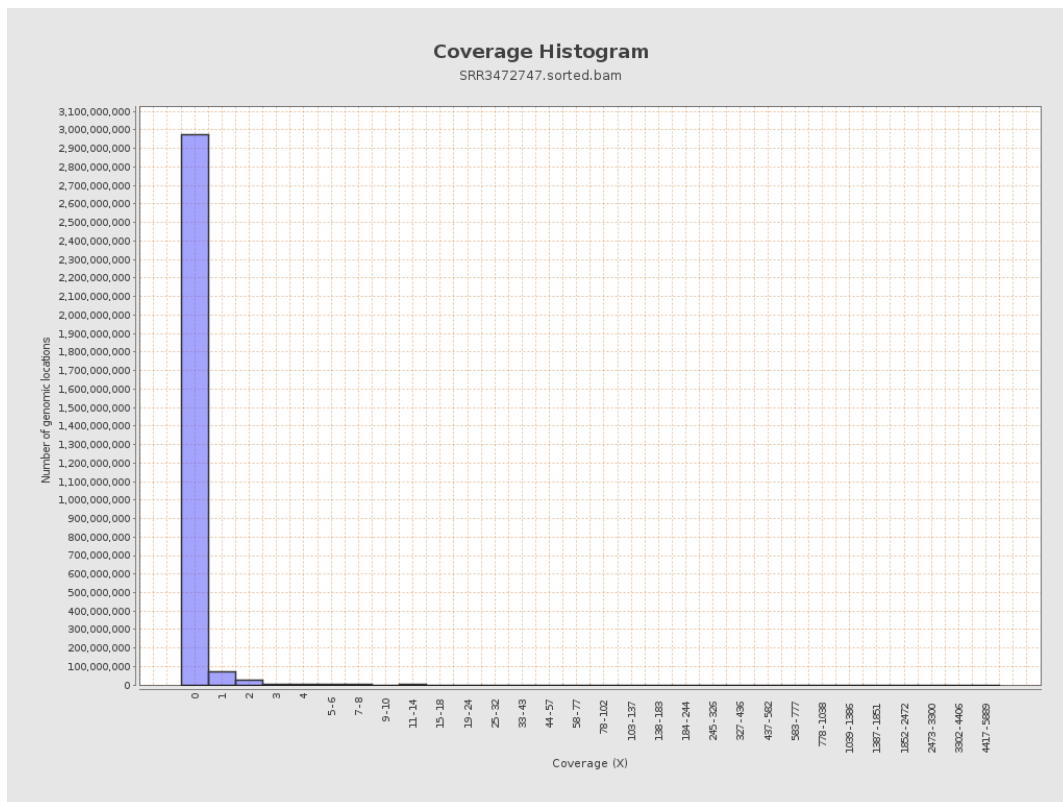
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 133753470    | 0.5366          | 15.875           |
| chr2  | 243199373 | 90066688     | 0.3703          | 14.2931          |
| chr3  | 198022430 | 115404959    | 0.5828          | 13.8727          |
| chr4  | 191154276 | 59134509     | 0.3094          | 12.1974          |
| chr5  | 180915260 | 66659308     | 0.3685          | 13.6865          |
| chr6  | 171115067 | 72097158     | 0.4213          | 11.5079          |
| chr7  | 159138663 | 78468258     | 0.4931          | 15.5444          |
| chr8  | 146364022 | 63621012     | 0.4347          | 11.9302          |
| chr9  | 141213431 | 85317806     | 0.6042          | 14.8036          |
| chr10 | 135534747 | 34180511     | 0.2522          | 8.1378           |
| chr11 | 135006516 | 61495309     | 0.4555          | 13.4125          |
| chr12 | 133851895 | 65512418     | 0.4894          | 12.171           |
| chr13 | 115169878 | 25509762     | 0.2215          | 7.1817           |
| chr14 | 107349540 | 45524775     | 0.4241          | 12.2432          |
| chr15 | 102531392 | 33522376     | 0.3269          | 9.1026           |
| chr16 | 90354753  | 50190071     | 0.5555          | 13.2089          |
| chr17 | 81195210  | 42893872     | 0.5283          | 11.5641          |
| chr18 | 78077248  | 18562288     | 0.2377          | 6.7971           |
| chr19 | 59128983  | 45455146     | 0.7687          | 18.6891          |
| chr20 | 63025520  | 28118037     | 0.4461          | 10.8518          |
| chr21 | 48129895  | 7406846      | 0.1539          | 5.5205           |
| chr22 | 51304566  | 16074811     | 0.3133          | 8.8312           |
| chrMT | 16571     | 1795         | 0.1083          | 0.4083           |
| chrX  | 155270560 | 75392554     | 0.4856          | 13.7513          |

|      |          |         |      |       |
|------|----------|---------|------|-------|
| chrY | 59373566 | 1189603 | 0.02 | 0.573 |
|------|----------|---------|------|-------|

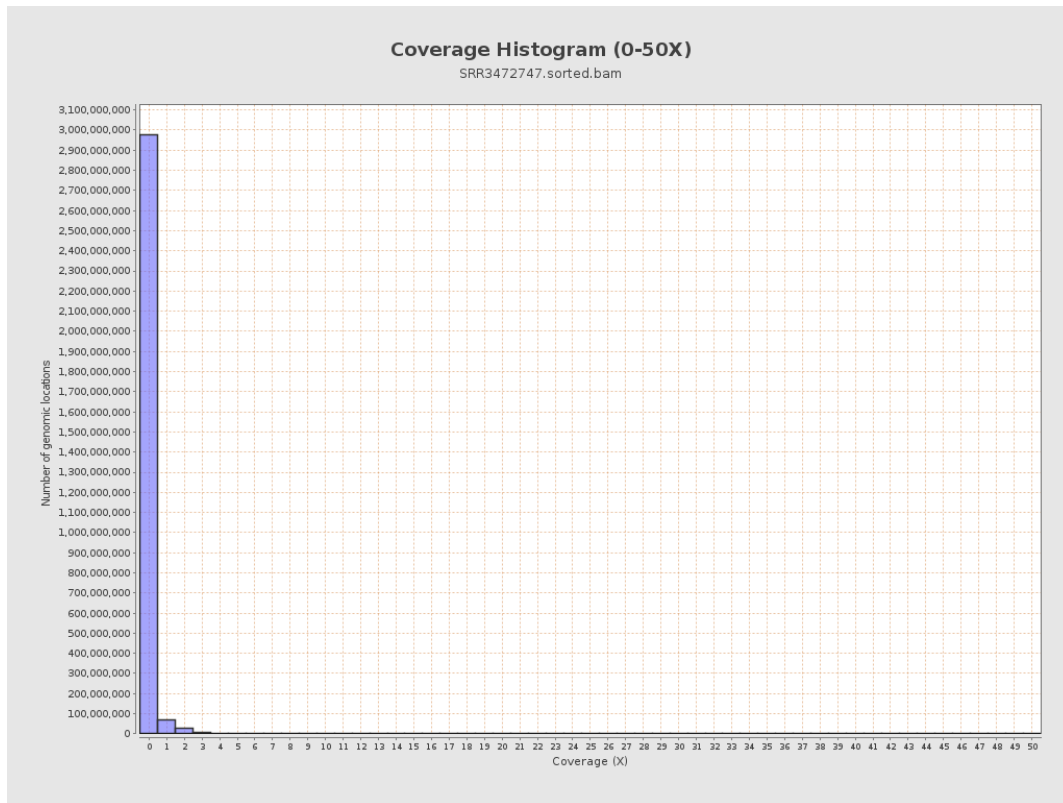
### 3. Results : Coverage across reference



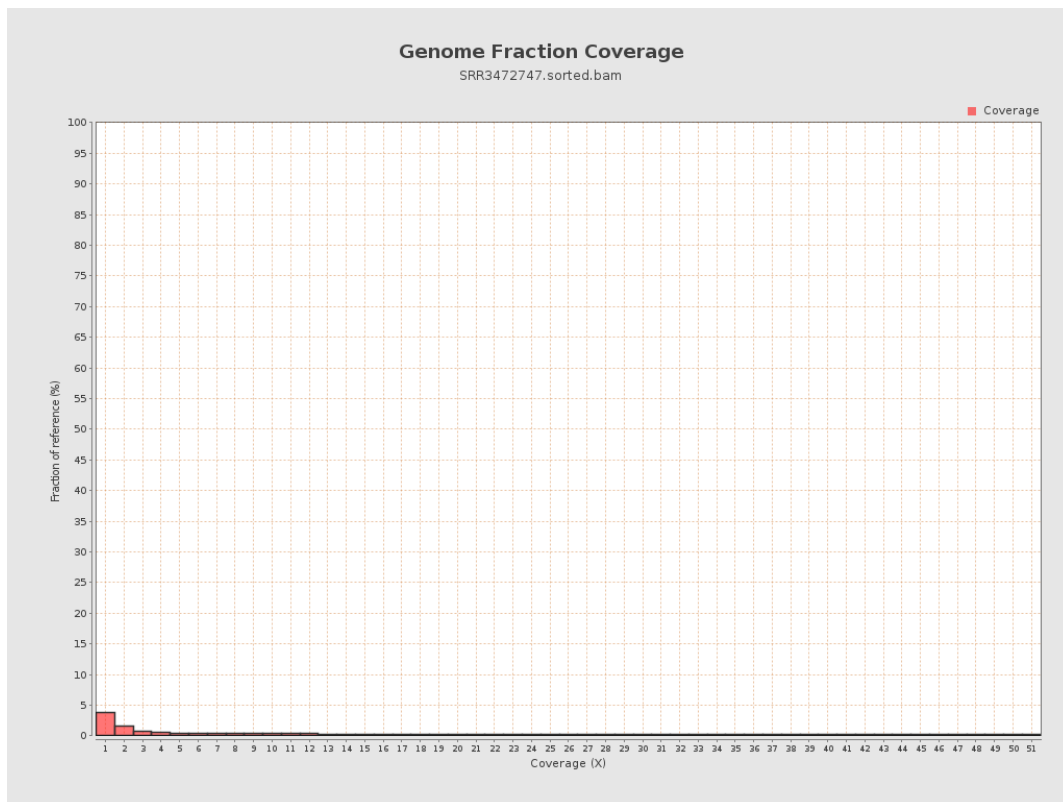
## 4. Results : Coverage Histogram



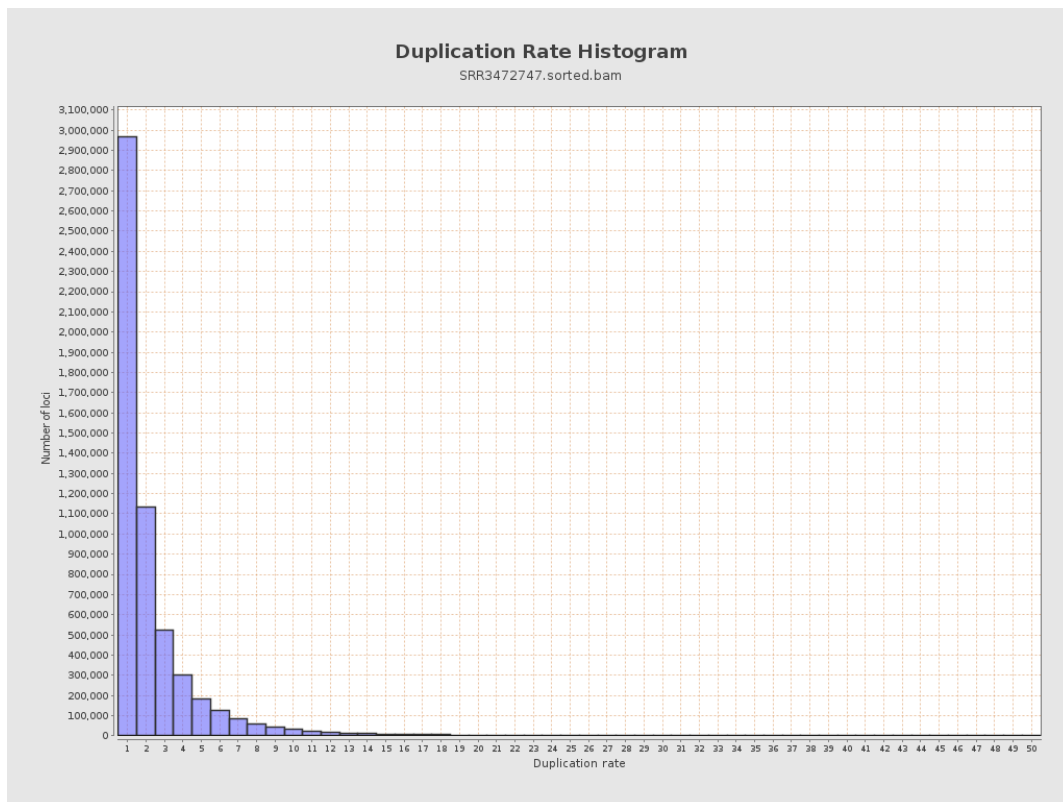
## 5. Results : Coverage Histogram (0-50X)



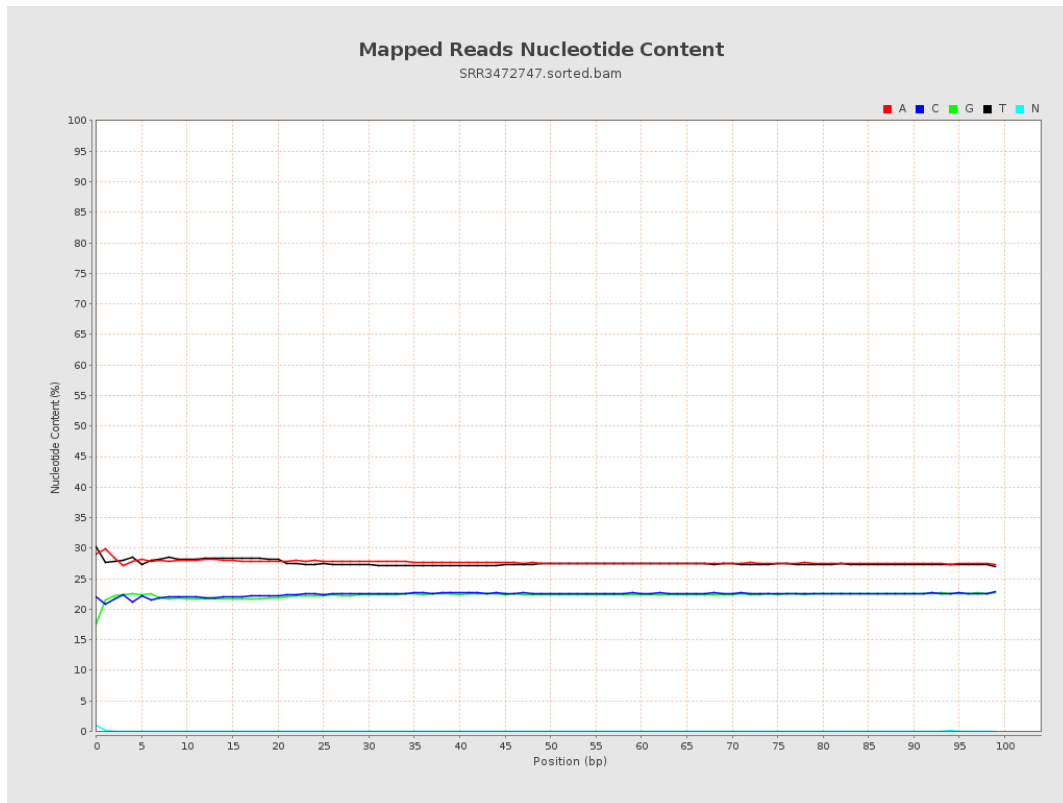
## 6. Results : Genome Fraction Coverage



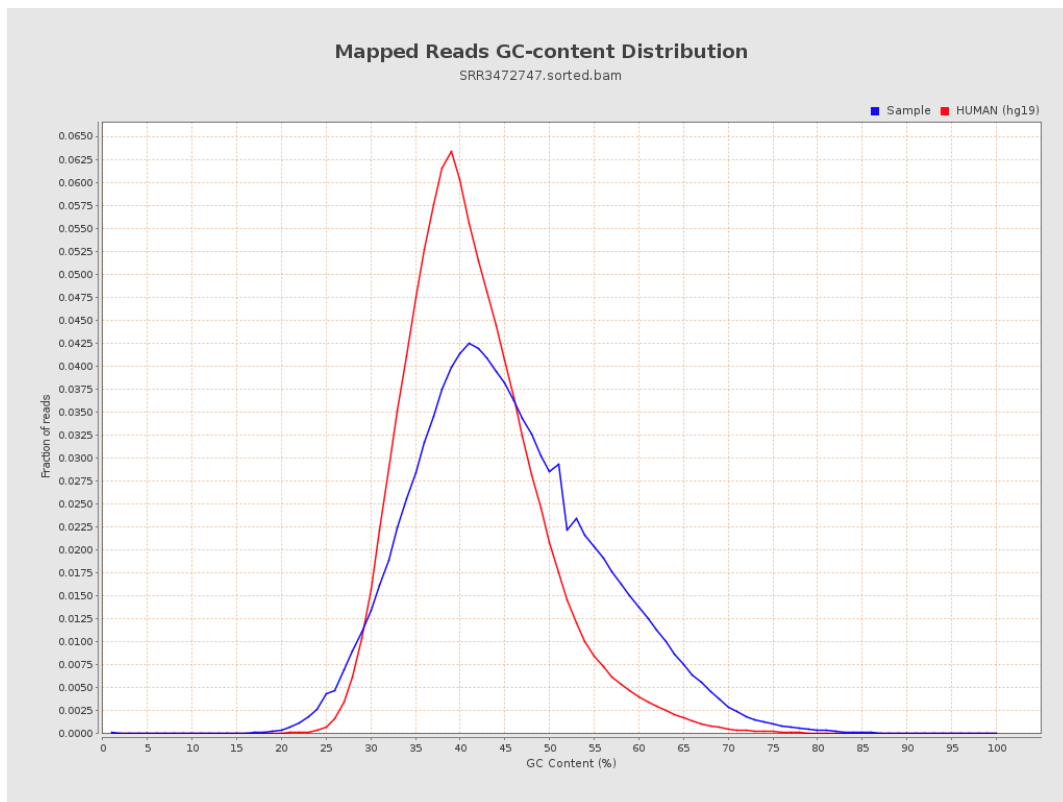
## 7. Results : Duplication Rate Histogram



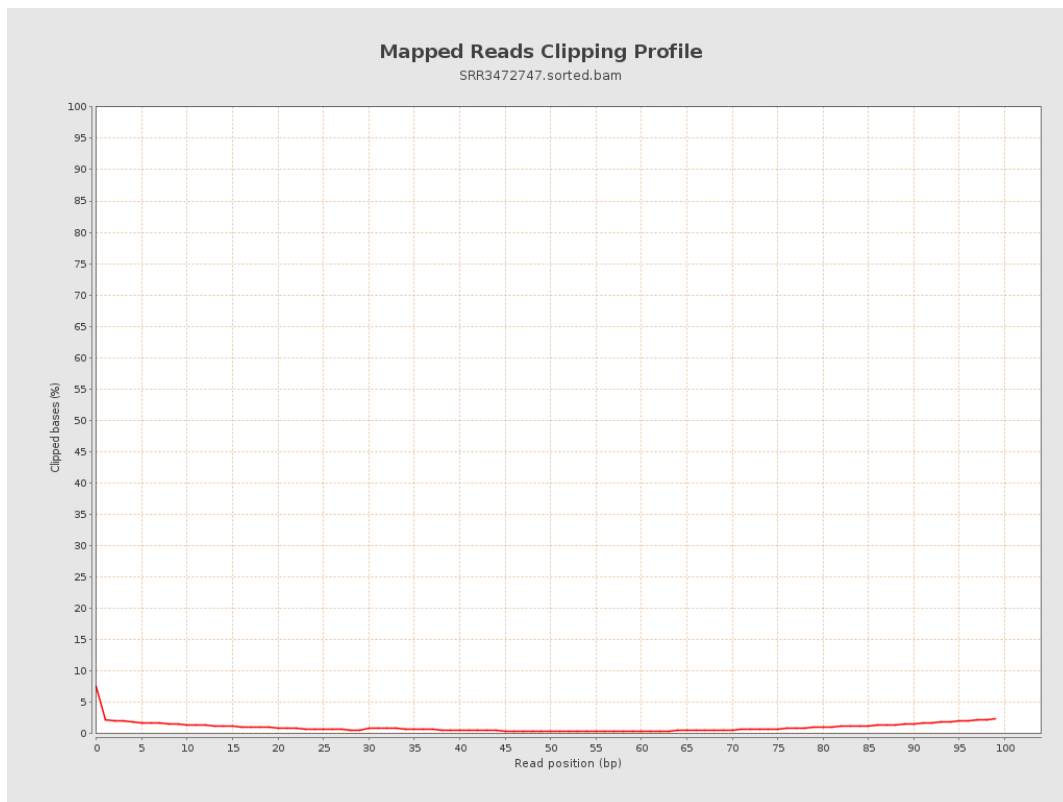
## 8. Results : Mapped Reads Nucleotide Content



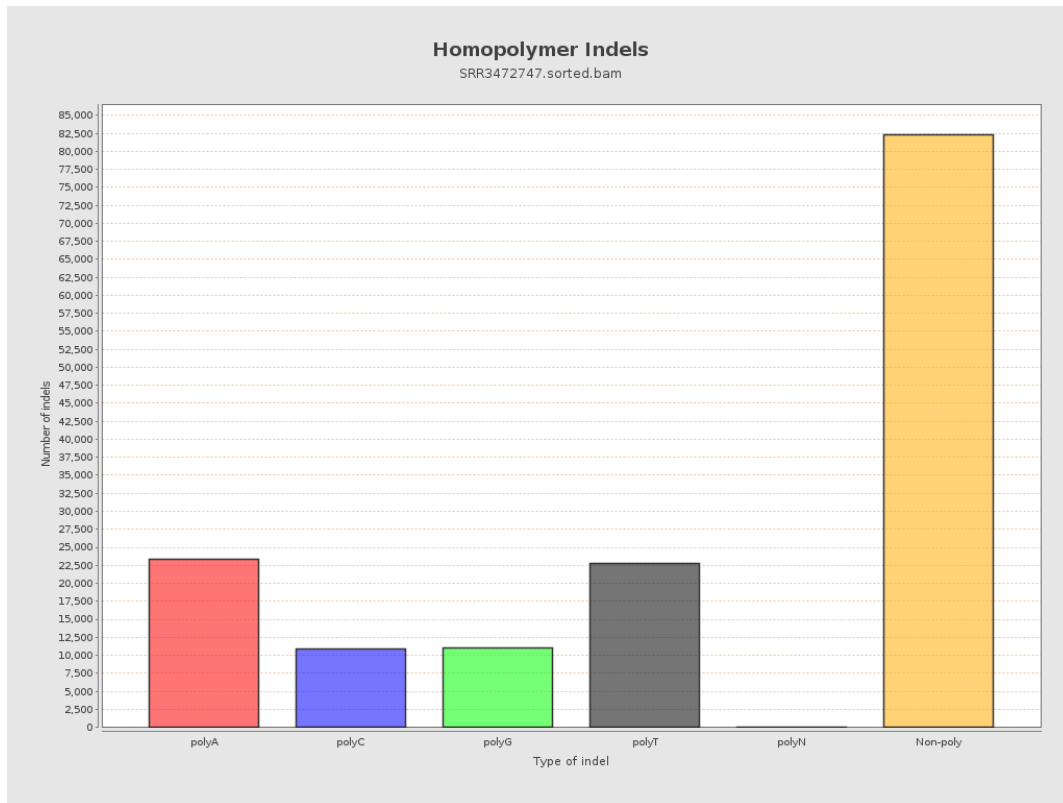
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



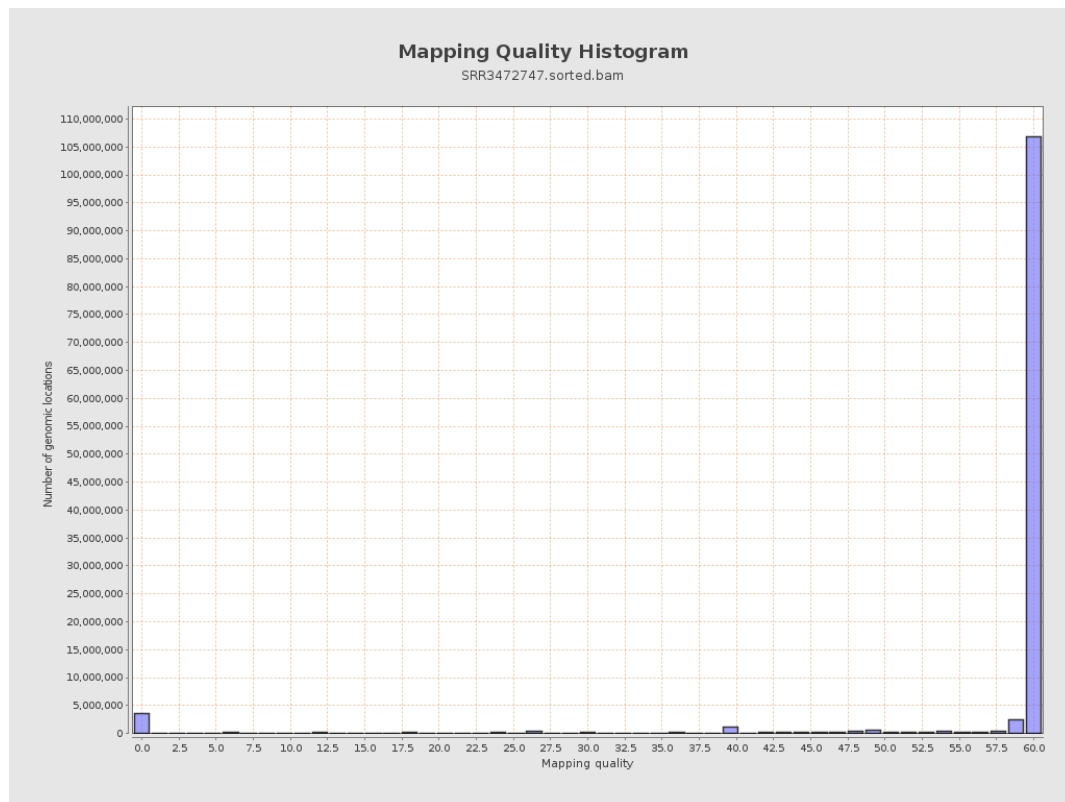
## 11. Results : Homopolymer Indels



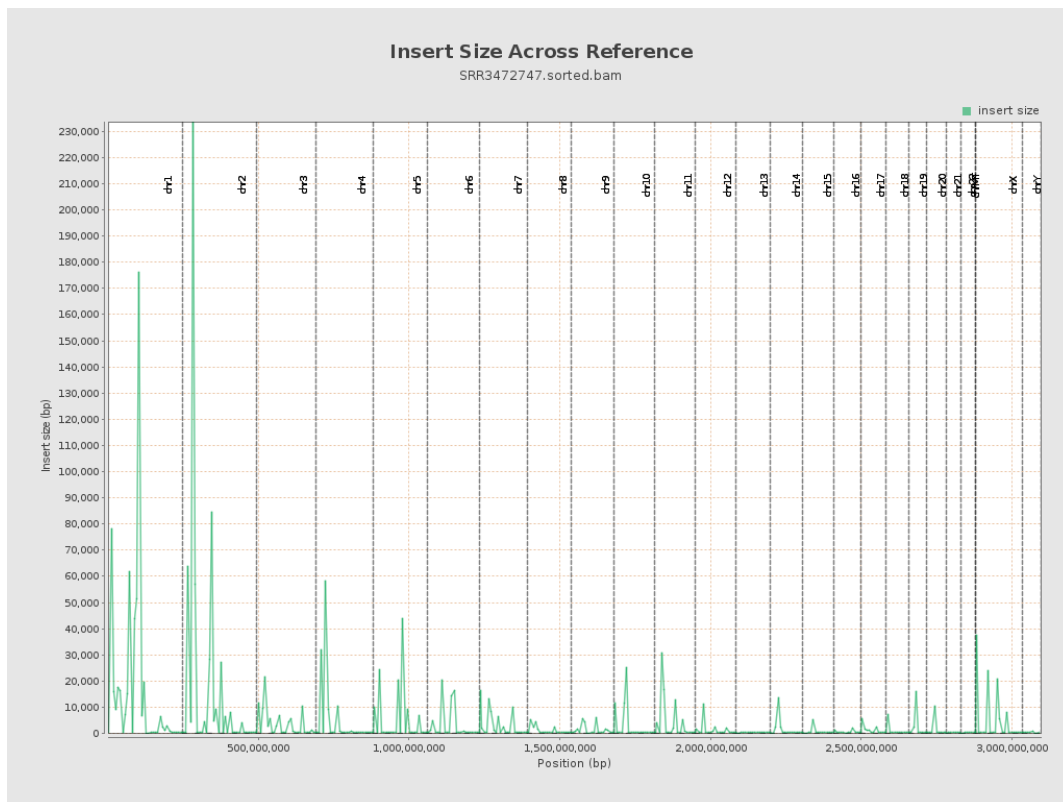
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

