

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/29 08:47:22*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472687.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_SRR3472687 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472687_1.fastq.gz SRR3472687_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                  |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                   |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                   |
| Analysis date:                        | Sun Sep 29 08:47:21 CST 2024                                                                                                                                                                                         |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                    |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                   |
| Number of windows:                    | 400                                                                                                                                                                                                                  |
| BAM file:                             | SRR3472687.sorted.bam                                                                                                                                                                                                |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 17,016,572          |
| Mapped reads                 | 16,897,459 / 99.3%  |
| Unmapped reads               | 119,113 / 0.7%      |
| Mapped paired reads          | 16,897,459 / 99.3%  |
| Mapped reads, first in pair  | 8,473,718 / 49.8%   |
| Mapped reads, second in pair | 8,423,741 / 49.5%   |
| Mapped reads, both in pair   | 16,817,498 / 98.83% |
| Mapped reads, singletons     | 79,961 / 0.47%      |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 99,019 / 0.58%      |
| Read min/max/mean length     | 30 / 101 / 99.71    |
| Duplicated reads (estimated) | 11,836,395 / 69.56% |
| Duplication rate             | 49.39%              |
| Clipped reads                | 1,232,944 / 7.25%   |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 443,417,270 / 26.7%  |
| Number/percentage of C's | 389,528,423 / 23.45% |
| Number/percentage of T's | 444,603,225 / 26.77% |
| Number/percentage of G's | 383,005,645 / 23.06% |
| Number/percentage of N's | 301,882 / 0.02%      |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 46.51% |
|---------------|--------|

## 2.3. Coverage

|                    |         |
|--------------------|---------|
| Mean               | 0.5366  |
| Standard Deviation | 24.0272 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 54.77 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 18,874.57       |
| Standard Deviation | 1,342,117.9     |
| P25/Median/P75     | 152 / 207 / 276 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.57%     |
| Mismatches                               | 9,351,952 |
| Insertions                               | 96,146    |
| Mapped reads with at least one insertion | 0.56%     |
| Deletions                                | 89,867    |
| Mapped reads with at least one deletion  | 0.52%     |
| Homopolymer indels                       | 45.96%    |

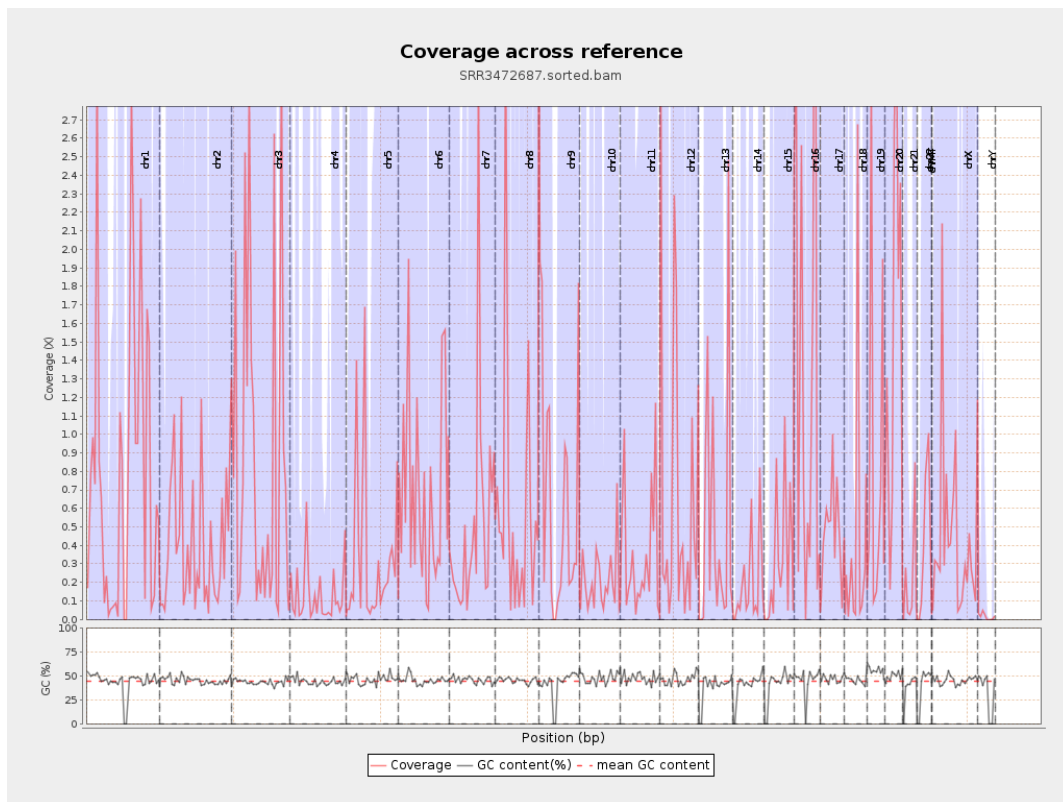
## 2.7. Chromosome stats

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

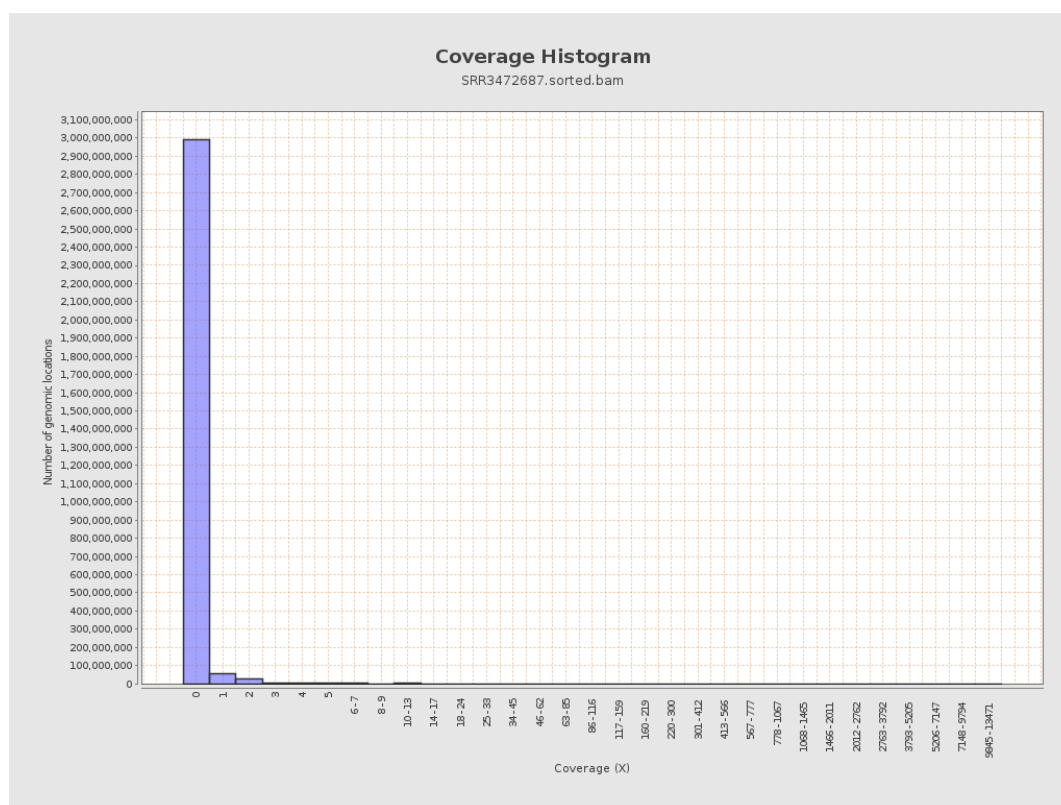
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 202637020    | 0.813           | 29.1624          |
| chr2  | 243199373 | 99193877     | 0.4079          | 15.9683          |
| chr3  | 198022430 | 177441312    | 0.8961          | 33.3747          |
| chr4  | 191154276 | 24405425     | 0.1277          | 6.2068           |
| chr5  | 180915260 | 60718812     | 0.3356          | 20.6644          |
| chr6  | 171115067 | 113782674    | 0.6649          | 22.107           |
| chr7  | 159138663 | 82018916     | 0.5154          | 21.4823          |
| chr8  | 146364022 | 85598863     | 0.5848          | 21.967           |
| chr9  | 141213431 | 94159096     | 0.6668          | 20.0396          |
| chr10 | 135534747 | 27594624     | 0.2036          | 9.7007           |
| chr11 | 135006516 | 46186702     | 0.3421          | 12.9713          |
| chr12 | 133851895 | 87682121     | 0.6551          | 23.7814          |
| chr13 | 115169878 | 58413248     | 0.5072          | 27.6303          |
| chr14 | 107349540 | 19284621     | 0.1796          | 9.4388           |
| chr15 | 102531392 | 32225220     | 0.3143          | 18.5189          |
| chr16 | 90354753  | 125716644    | 1.3914          | 56.2592          |
| chr17 | 81195210  | 38449928     | 0.4735          | 14.0478          |
| chr18 | 78077248  | 32746171     | 0.4194          | 32.5507          |
| chr19 | 59128983  | 53177702     | 0.8994          | 27.4527          |
| chr20 | 63025520  | 100651543    | 1.597           | 52.0618          |
| chr21 | 48129895  | 10131942     | 0.2105          | 15.4149          |
| chr22 | 51304566  | 19914785     | 0.3882          | 24.988           |
| chrMT | 16571     | 2812         | 0.1697          | 0.6415           |
| chrX  | 155270560 | 67957933     | 0.4377          | 15.1912          |

|      |          |        |        |        |
|------|----------|--------|--------|--------|
| chrY | 59373566 | 984034 | 0.0166 | 0.7809 |
|------|----------|--------|--------|--------|

### 3. Results : Coverage across reference

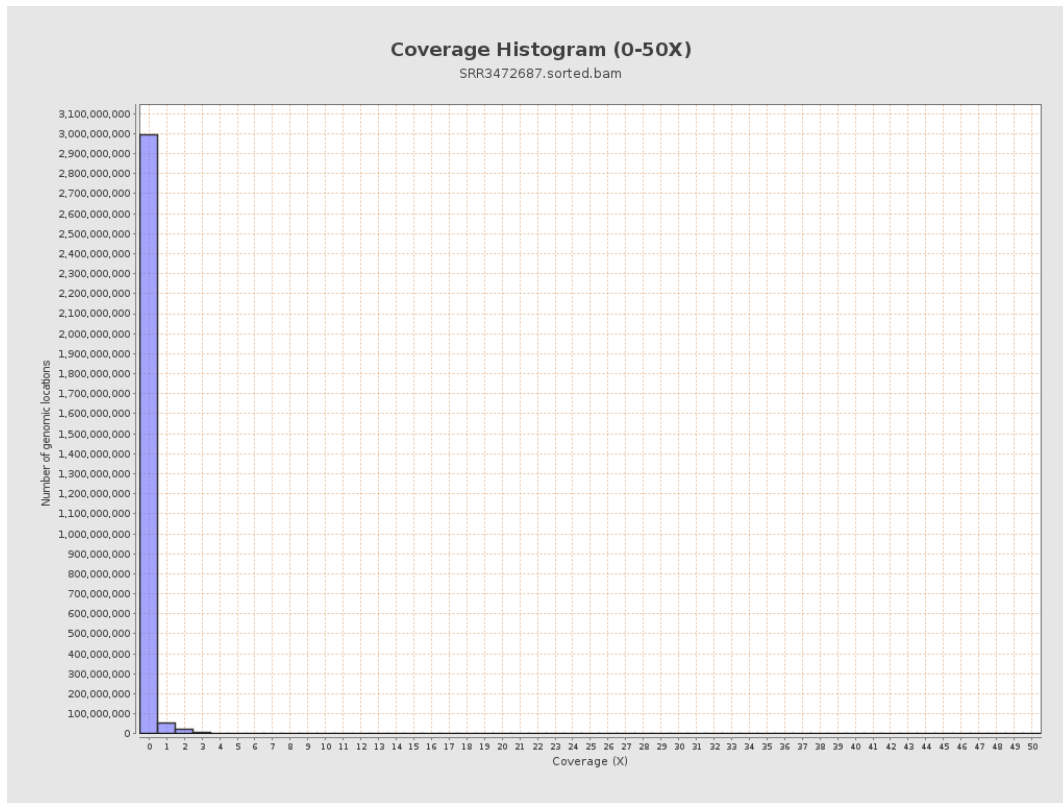


## 4. Results : Coverage Histogram

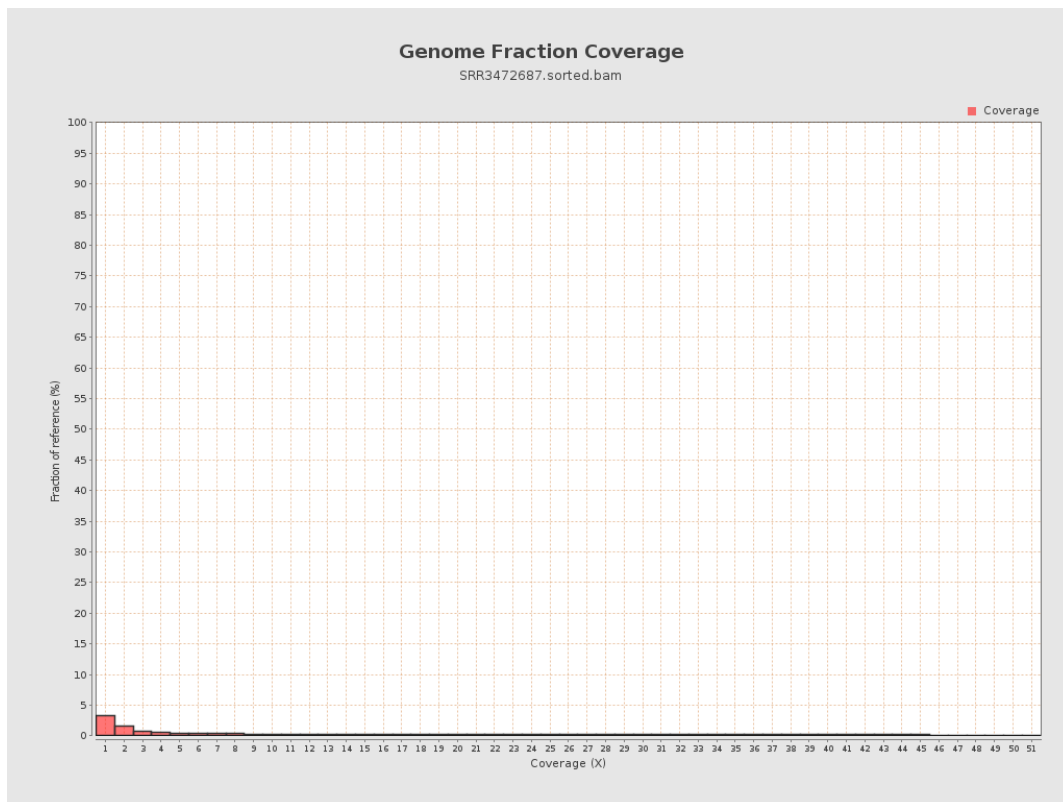




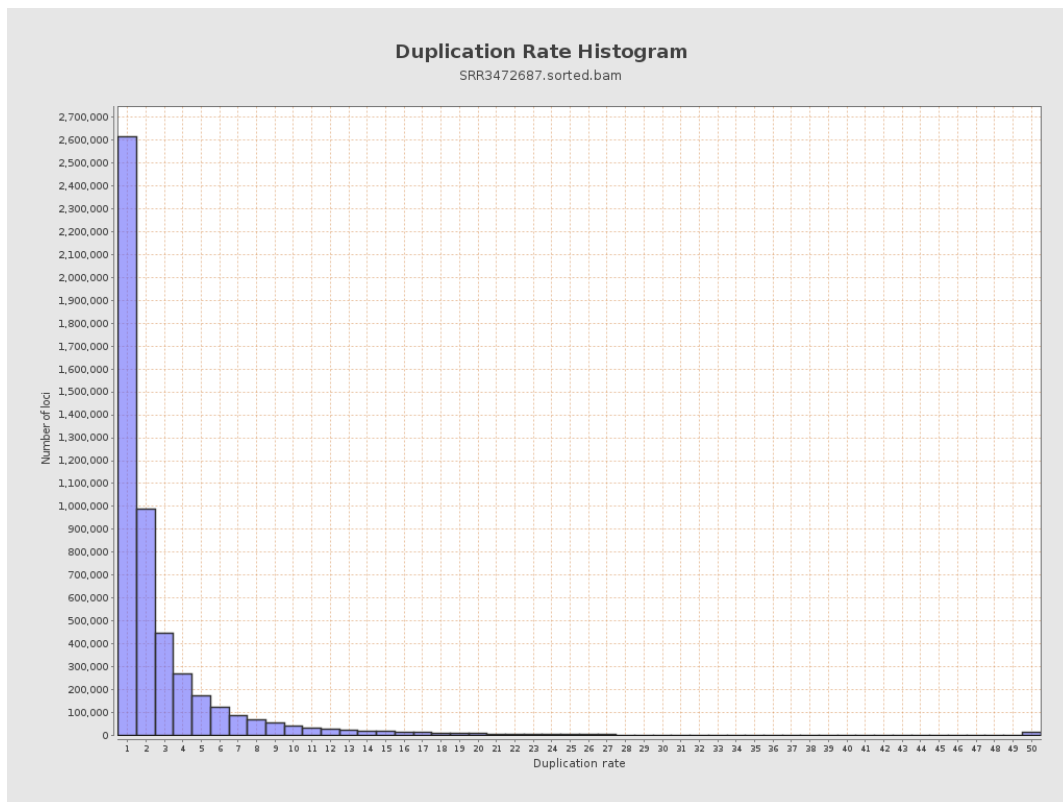
## 5. Results : Coverage Histogram (0-50X)



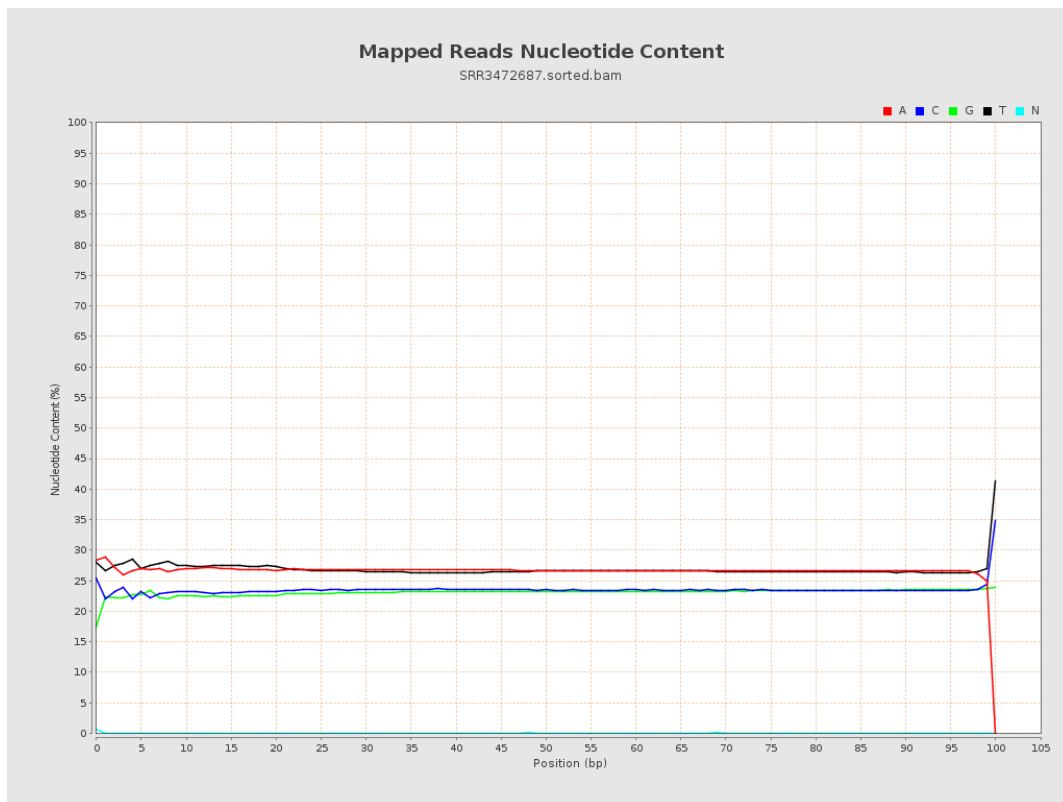
## 6. Results : Genome Fraction Coverage



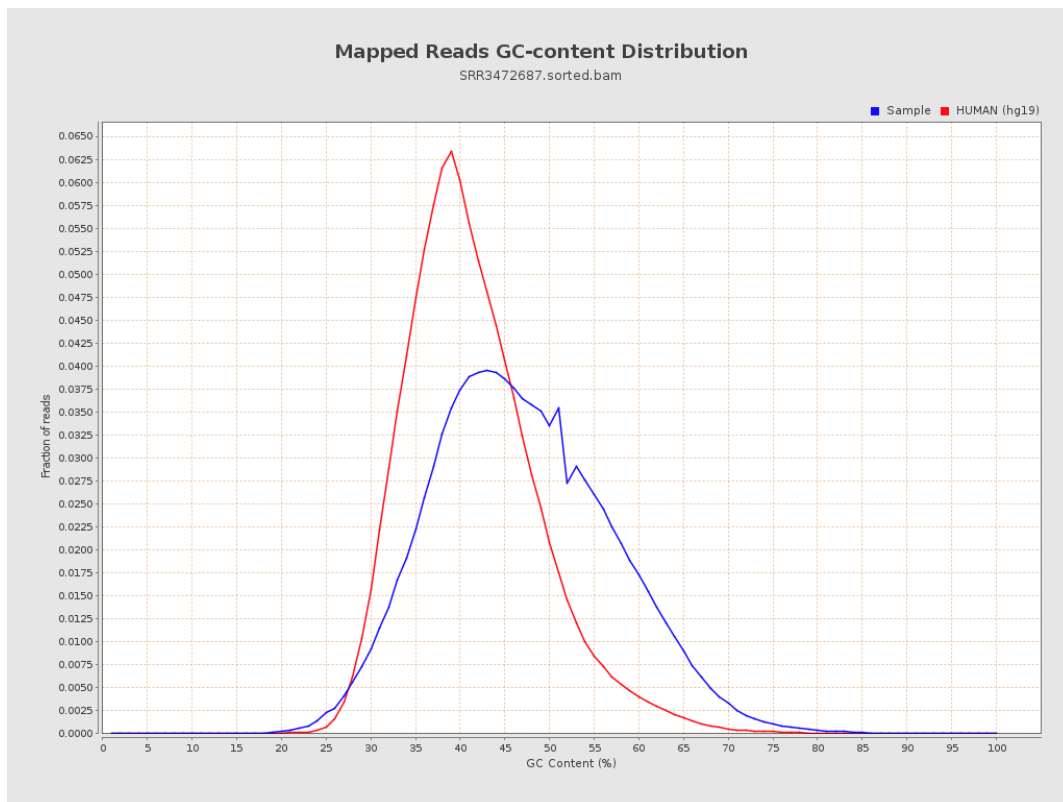
## 7. Results : Duplication Rate Histogram



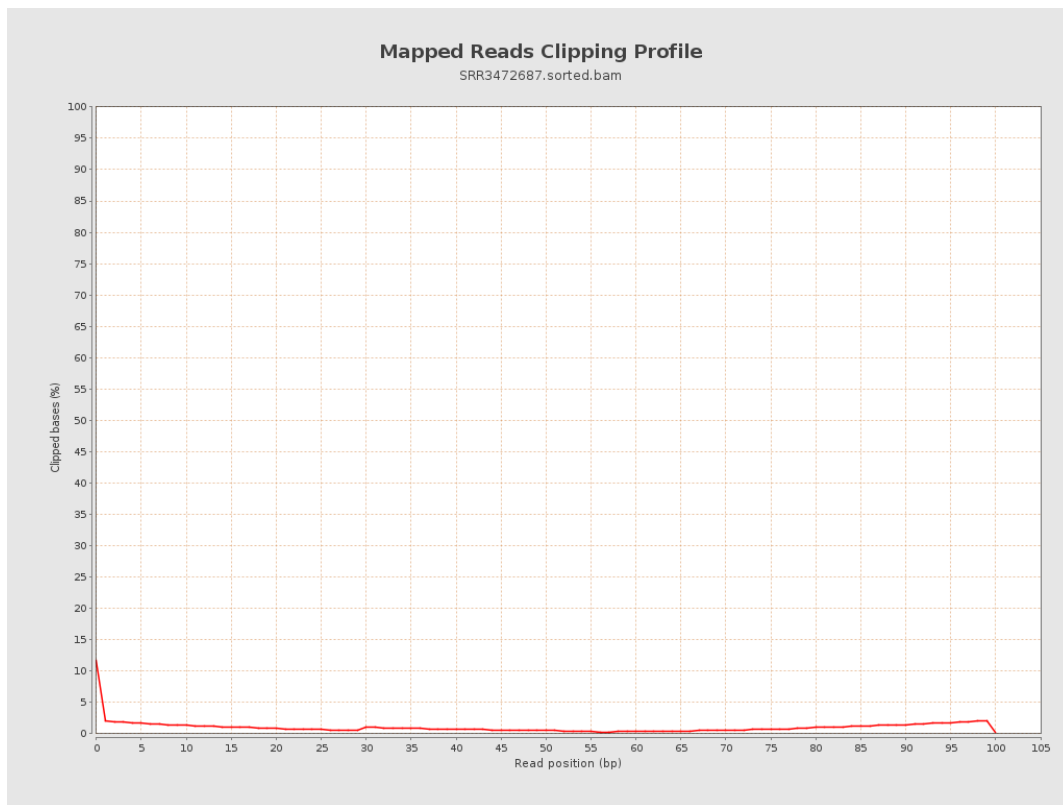
## 8. Results : Mapped Reads Nucleotide Content



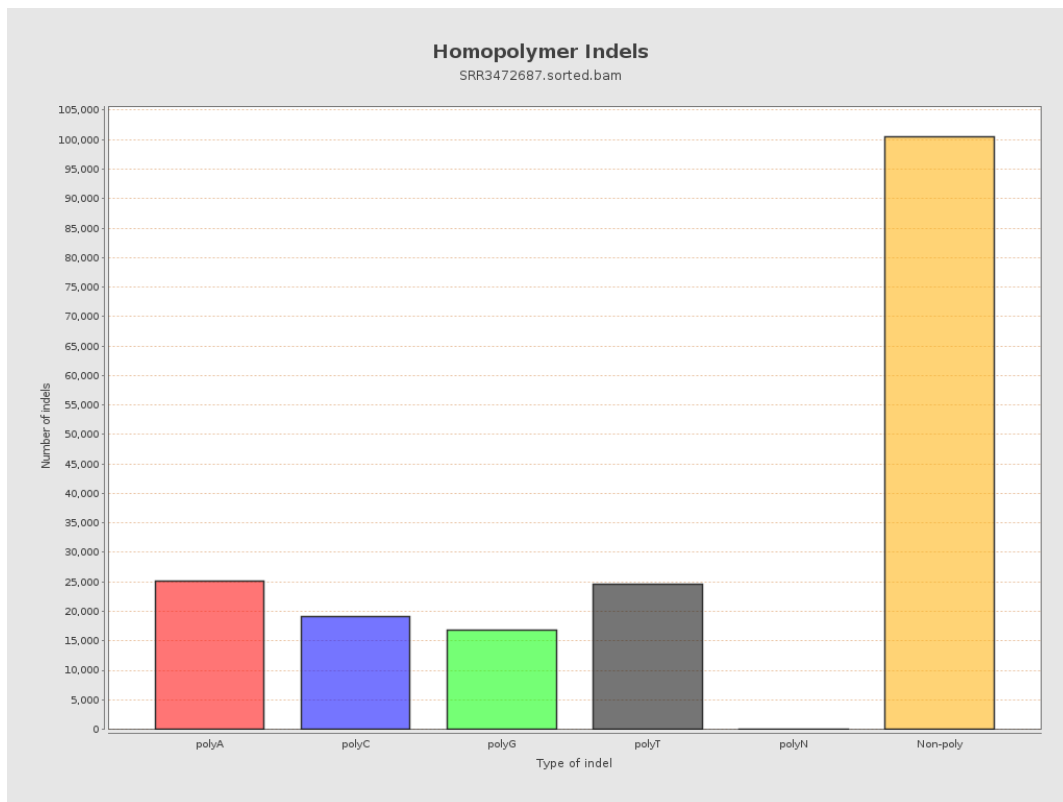
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

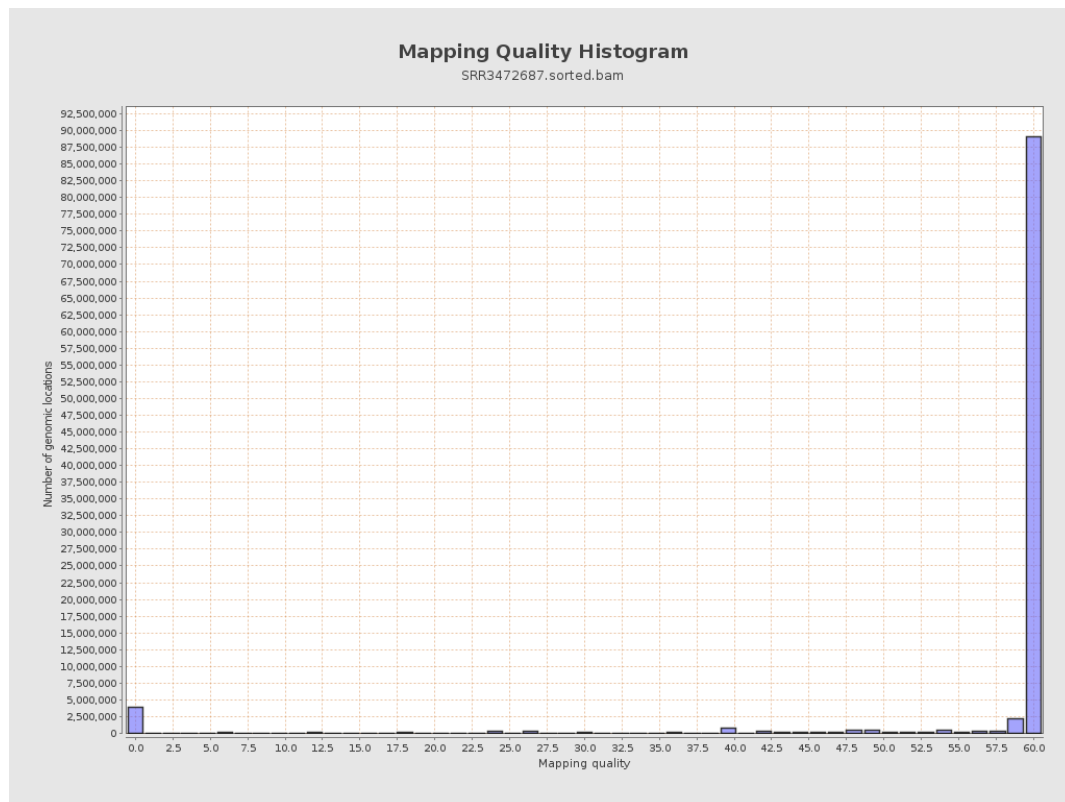


## 12. Results : Mapping Quality Across Reference

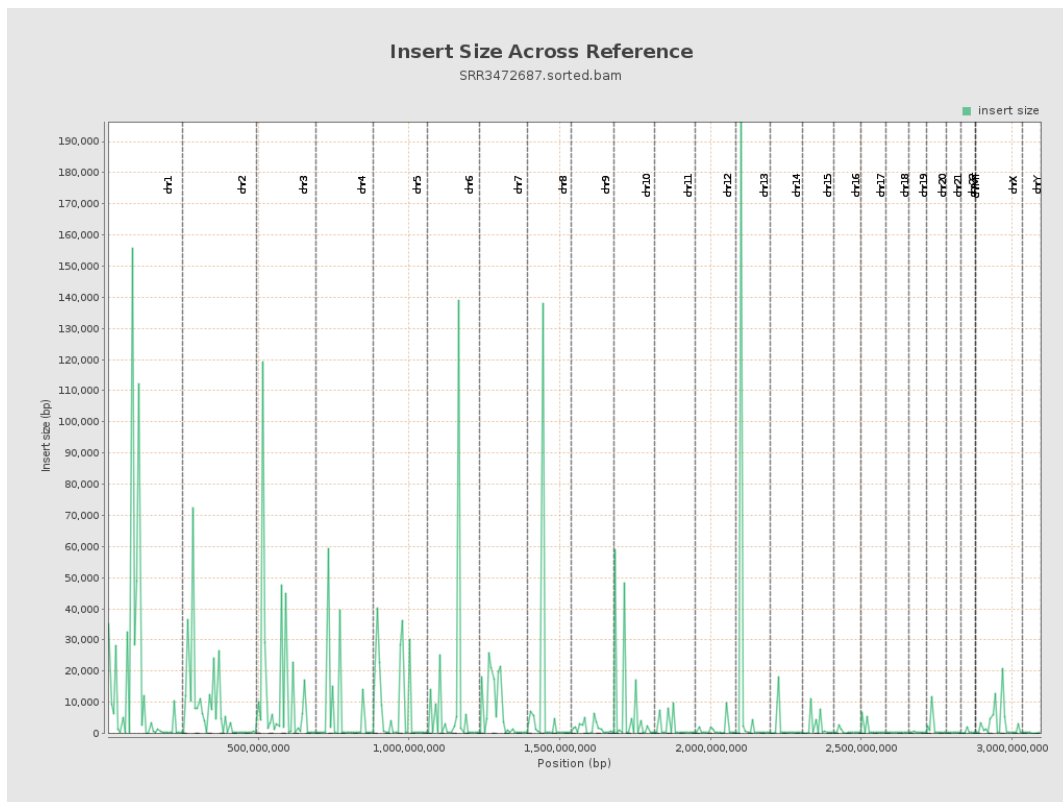




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

