

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/30 17:09:09*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472786.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_SRR3472786 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472786_1.fastq.gz SRR3472786_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                  |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                   |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                   |
| Analysis date:                        | Mon Sep 30 17:09:08 CST 2024                                                                                                                                                                                         |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                    |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                   |
| Number of windows:                    | 400                                                                                                                                                                                                                  |
| BAM file:                             | SRR3472786.sorted.bam                                                                                                                                                                                                |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 9,283,064          |
| Mapped reads                 | 8,879,677 / 95.65% |
| Unmapped reads               | 403,387 / 4.35%    |
| Mapped paired reads          | 8,879,677 / 95.65% |
| Mapped reads, first in pair  | 4,458,788 / 48.03% |
| Mapped reads, second in pair | 4,420,889 / 47.62% |
| Mapped reads, both in pair   | 8,819,364 / 95%    |
| Mapped reads, singletons     | 60,313 / 0.65%     |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 30,037 / 0.32%     |
| Read min/max/mean length     | 30 / 100 / 100.13  |
| Duplicated reads (estimated) | 4,931,414 / 53.12% |
| Duplication rate             | 43.94%             |
| Clipped reads                | 875,005 / 9.43%    |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 238,027,855 / 27.34% |
| Number/percentage of C's | 198,623,302 / 22.81% |
| Number/percentage of T's | 236,340,252 / 27.15% |
| Number/percentage of G's | 197,440,527 / 22.68% |
| Number/percentage of N's | 169,027 / 0.02%      |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 45.49% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.2813 |
| Standard Deviation | 10.043 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 55.02 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 20,786.16       |
| Standard Deviation | 1,428,906.01    |
| P25/Median/P75     | 157 / 223 / 306 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.6%      |
| Mismatches                               | 5,120,378 |
| Insertions                               | 49,229    |
| Mapped reads with at least one insertion | 0.55%     |
| Deletions                                | 46,138    |
| Mapped reads with at least one deletion  | 0.51%     |
| Homopolymer indels                       | 45.08%    |

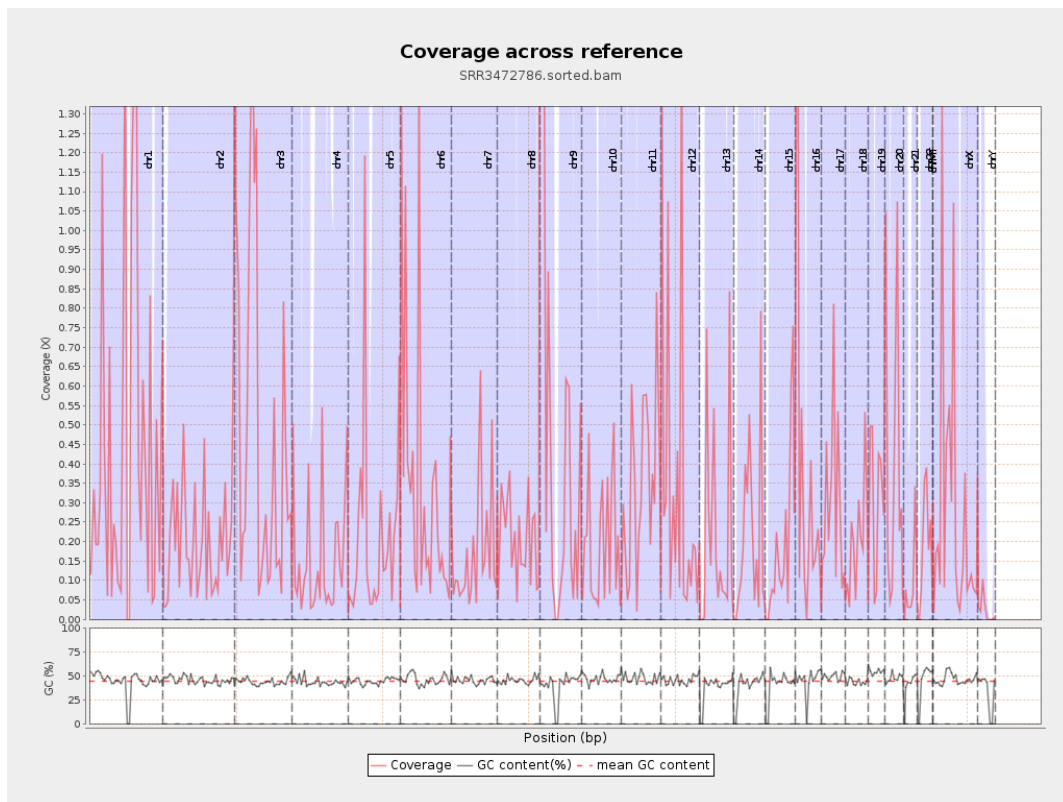
## 2.7. Chromosome stats

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

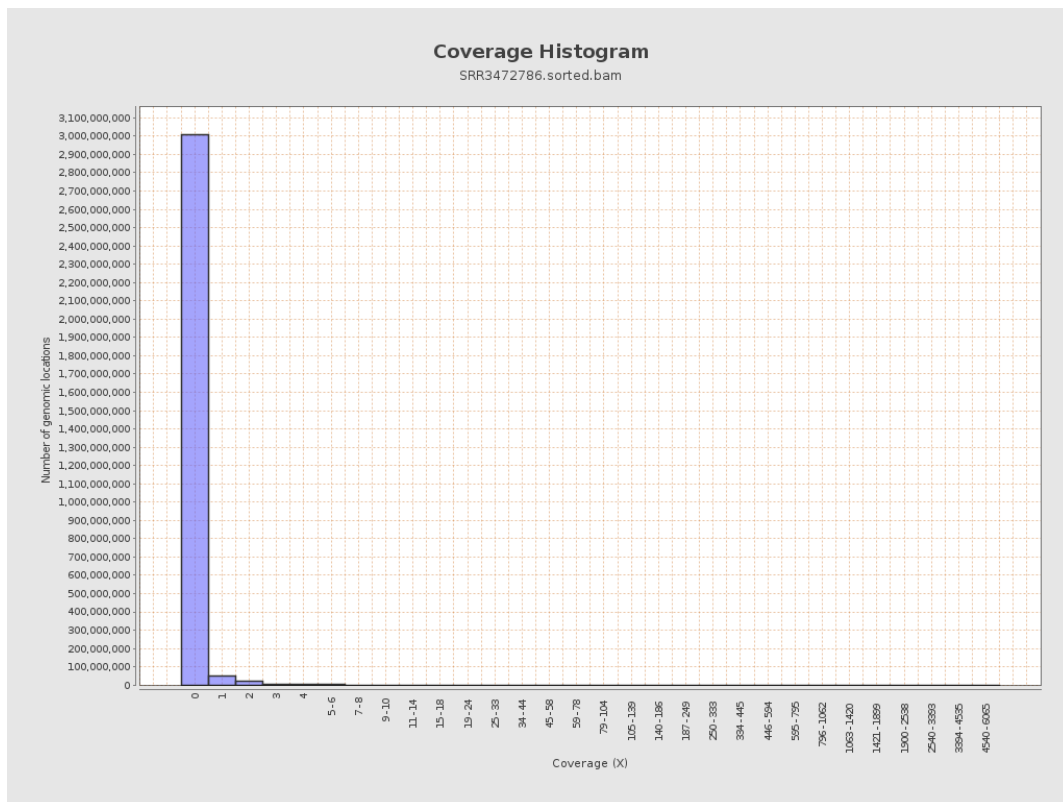
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 111566141    | 0.4476          | 16.5593          |
| chr2  | 243199373 | 48587242     | 0.1998          | 7.2999           |
| chr3  | 198022430 | 96574760     | 0.4877          | 11.4972          |
| chr4  | 191154276 | 30586062     | 0.16            | 6.387            |
| chr5  | 180915260 | 39095854     | 0.2161          | 7.958            |
| chr6  | 171115067 | 59536407     | 0.3479          | 10.9978          |
| chr7  | 159138663 | 27963271     | 0.1757          | 6.1654           |
| chr8  | 146364022 | 29953310     | 0.2046          | 7.1982           |
| chr9  | 141213431 | 61303766     | 0.4341          | 12.1174          |
| chr10 | 135534747 | 26982632     | 0.1991          | 8.4663           |
| chr11 | 135006516 | 45293313     | 0.3355          | 10.9691          |
| chr12 | 133851895 | 49696323     | 0.3713          | 13.2253          |
| chr13 | 115169878 | 24666870     | 0.2142          | 10.0442          |
| chr14 | 107349540 | 22657455     | 0.2111          | 9.6177           |
| chr15 | 102531392 | 19423835     | 0.1894          | 8.5255           |
| chr16 | 90354753  | 34350536     | 0.3802          | 10.7298          |
| chr17 | 81195210  | 25172756     | 0.31            | 7.7079           |
| chr18 | 78077248  | 15866056     | 0.2032          | 7.8929           |
| chr19 | 59128983  | 19244743     | 0.3255          | 9.0722           |
| chr20 | 63025520  | 23659182     | 0.3754          | 12.5557          |
| chr21 | 48129895  | 4483340      | 0.0932          | 4.3619           |
| chr22 | 51304566  | 9799346      | 0.191           | 5.5163           |
| chrMT | 16571     | 5060         | 0.3054          | 0.9219           |
| chrX  | 155270560 | 42767224     | 0.2754          | 9.6876           |

|      |          |         |        |       |
|------|----------|---------|--------|-------|
| chrY | 59373566 | 1476838 | 0.0249 | 1.196 |
|------|----------|---------|--------|-------|

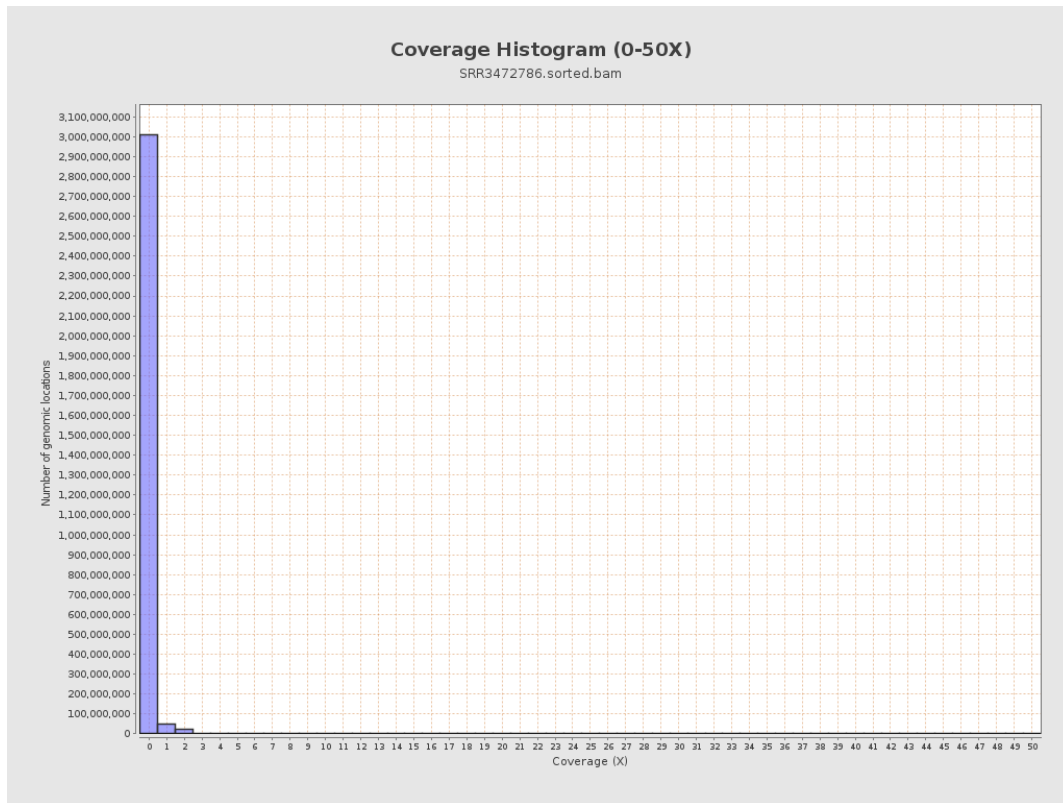
### 3. Results : Coverage across reference



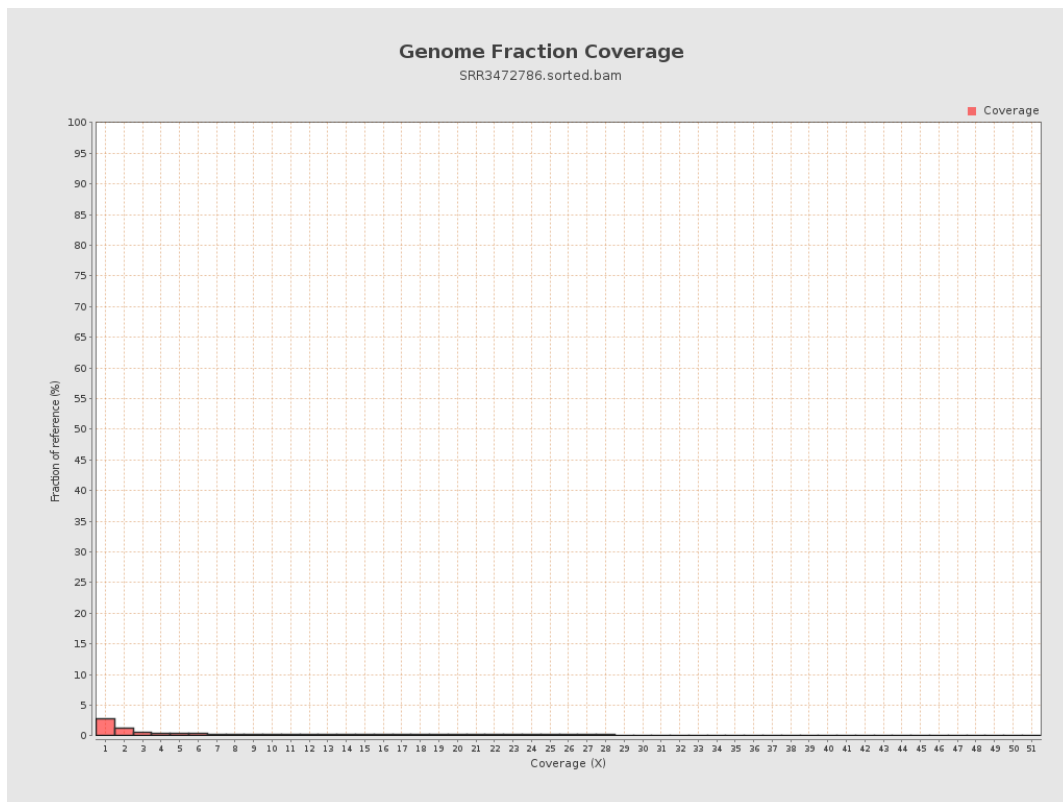
## 4. Results : Coverage Histogram



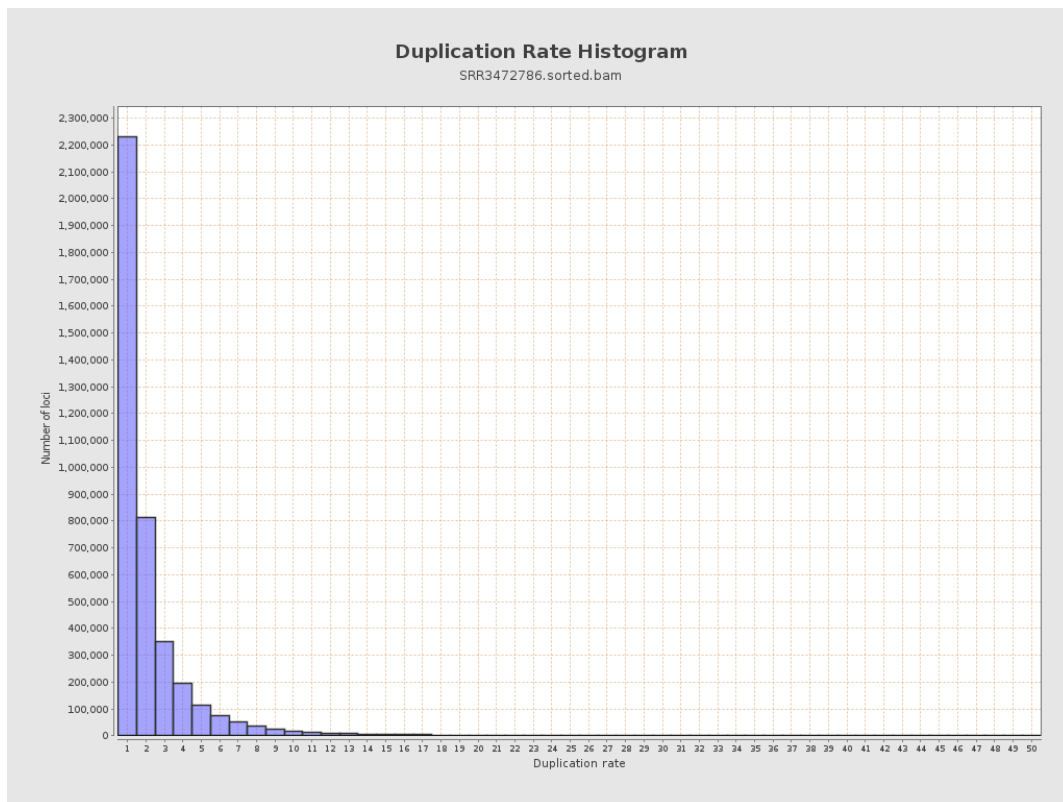
## 5. Results : Coverage Histogram (0-50X)



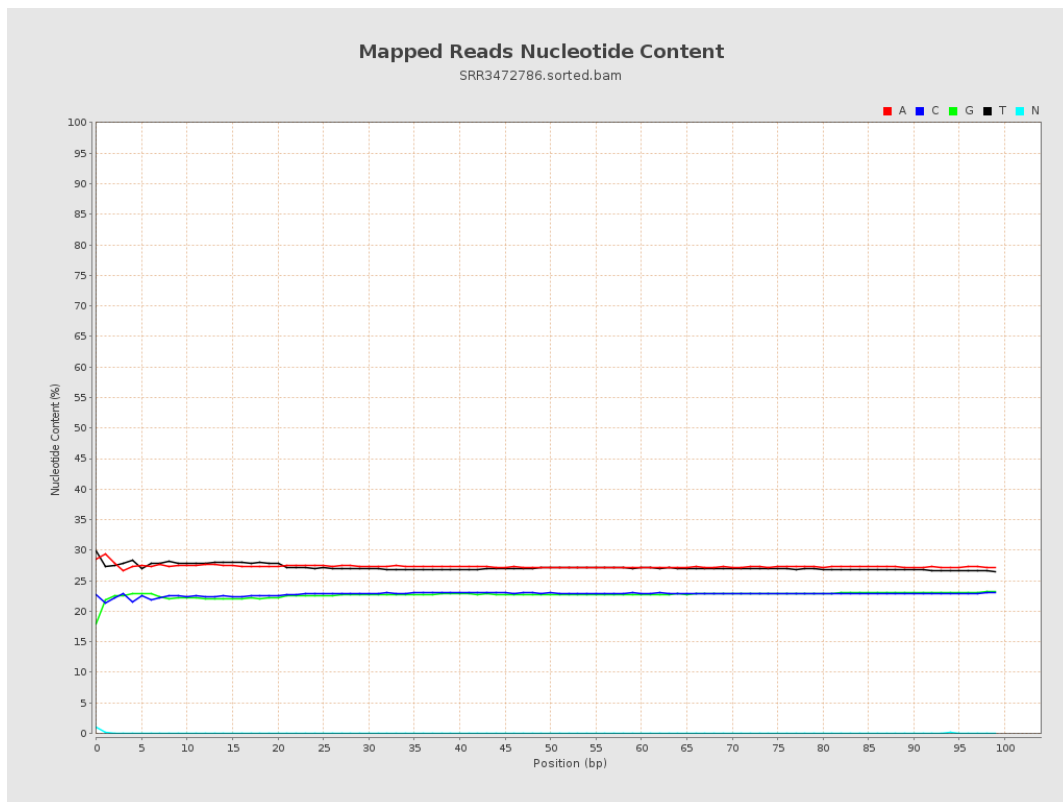
## 6. Results : Genome Fraction Coverage



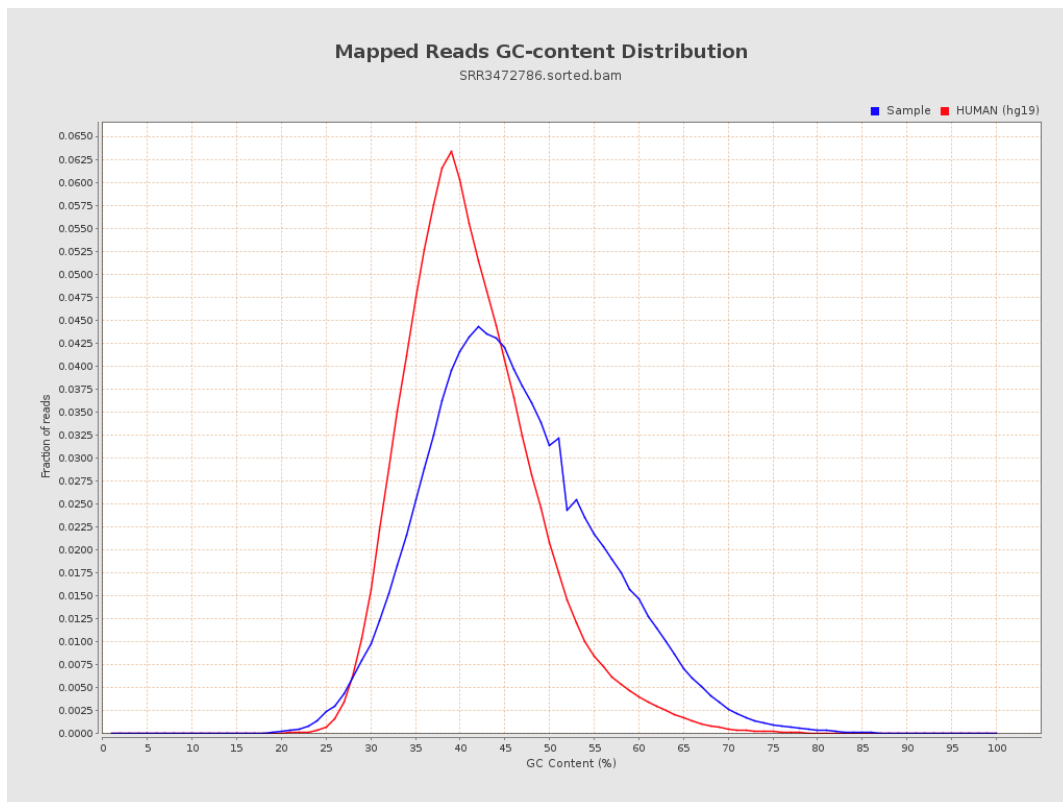
## 7. Results : Duplication Rate Histogram



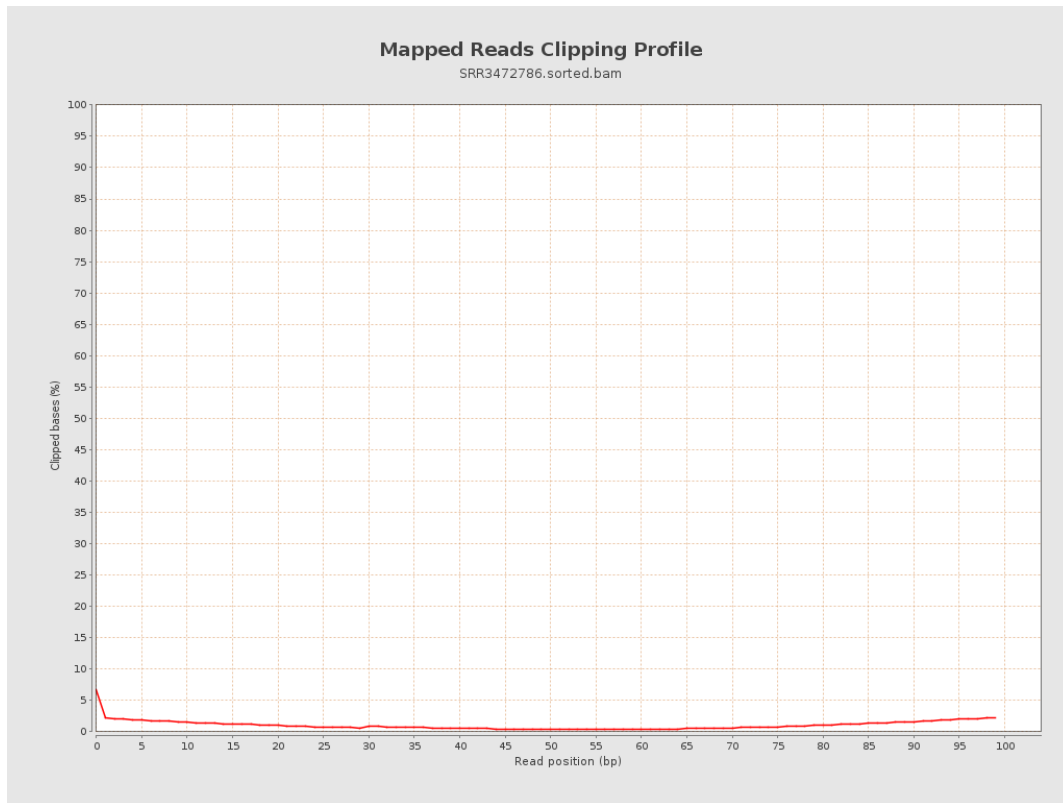
## 8. Results : Mapped Reads Nucleotide Content



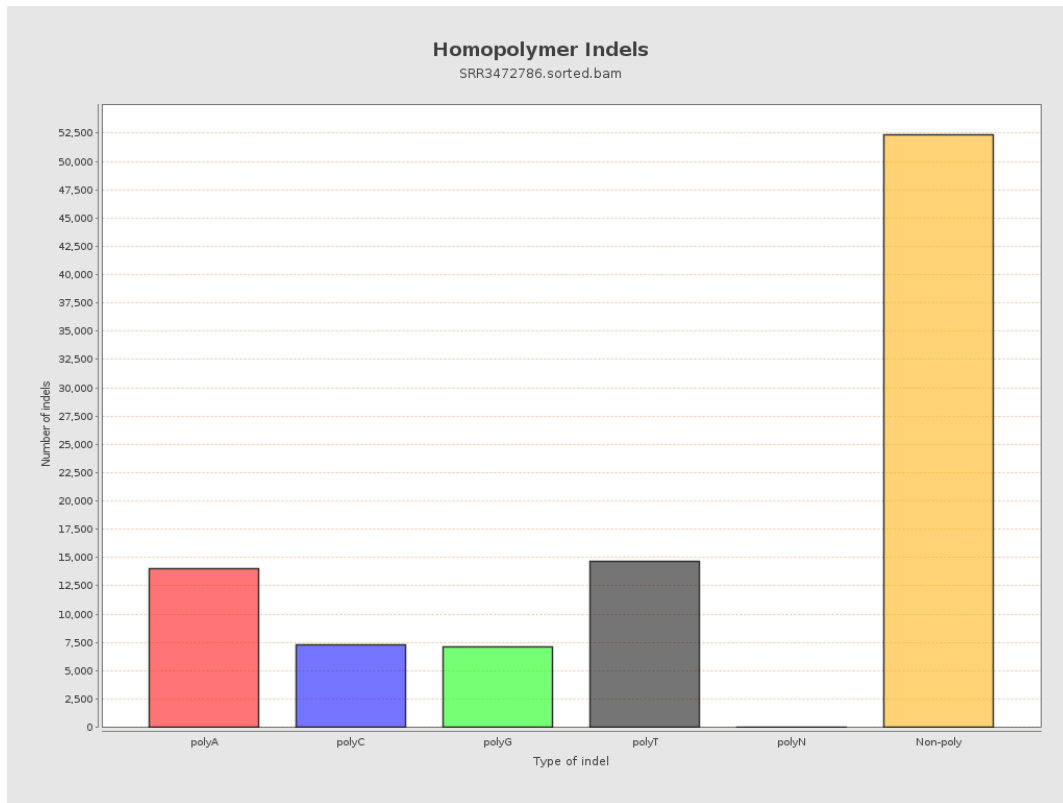
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



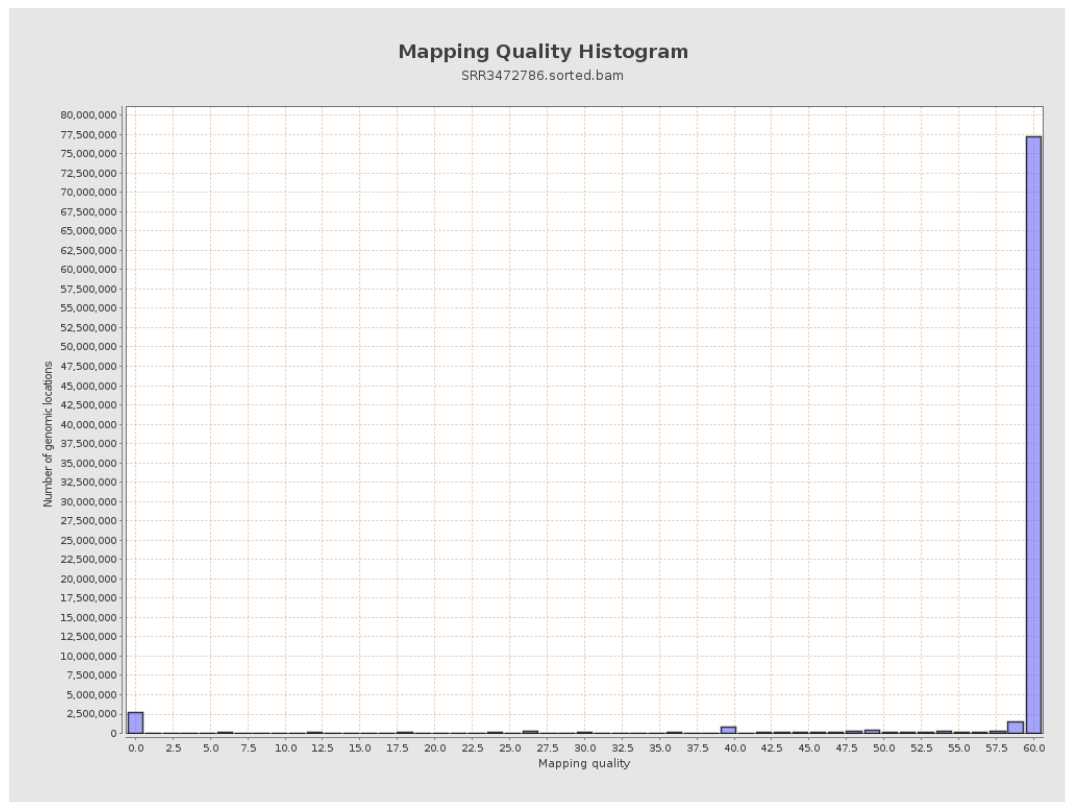
## 11. Results : Homopolymer Indels



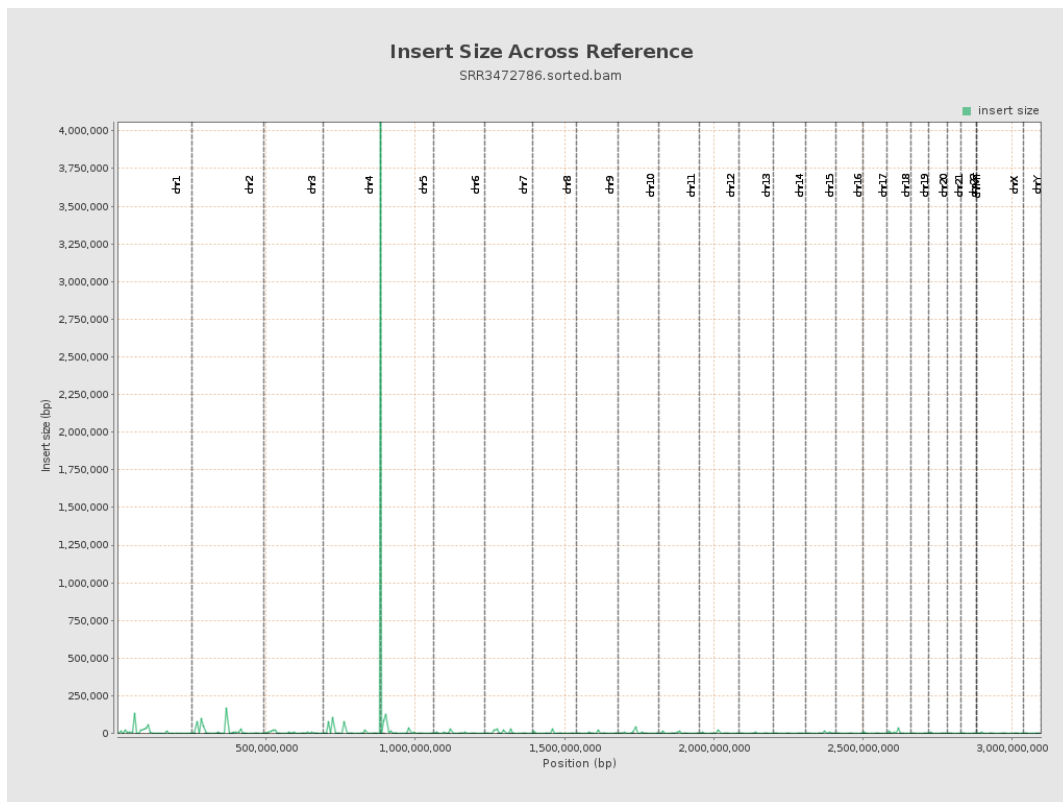
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

