

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2025/02/21 13:59:49*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR16328247.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_SRR16328247 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16328247_1.fastq.gz SRR16328247_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                      |
| Analysis date:                        | Fri Feb 21 13:59:48 CST 2025                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                     |
| BAM file:                             | SRR16328247.sorted.bam                                                                                                                                                                                                  |

## 2. Summary

### 2.1. Globals

|                              |                      |
|------------------------------|----------------------|
| Reference size               | 3,095,693,983        |
| Number of reads              | 208,339,152          |
| Mapped reads                 | 197,752,432 / 94.92% |
| Unmapped reads               | 10,586,720 / 5.08%   |
| Mapped paired reads          | 197,752,432 / 94.92% |
| Mapped reads, first in pair  | 101,280,509 / 48.61% |
| Mapped reads, second in pair | 96,471,923 / 46.31%  |
| Mapped reads, both in pair   | 192,106,212 / 92.21% |
| Mapped reads, singletons     | 5,646,220 / 2.71%    |
| Secondary alignments         | 0                    |
| Supplementary alignments     | 11,200,744 / 5.38%   |
| Read min/max/mean length     | 30 / 150 / 152.66    |
| Duplicated reads (estimated) | 92,245,770 / 44.28%  |
| Duplication rate             | 35.12%               |
| Clipped reads                | 132,733,485 / 63.71% |

### 2.2. ACGT Content

|                          |                        |
|--------------------------|------------------------|
| Number/percentage of A's | 7,719,591,047 / 28.5%  |
| Number/percentage of C's | 5,783,320,997 / 21.35% |
| Number/percentage of T's | 7,711,261,051 / 28.47% |
| Number/percentage of G's | 5,868,877,210 / 21.67% |
| Number/percentage of N's | 1,839,217 / 0.01%      |
|                          |                        |

|               |        |
|---------------|--------|
| GC Percentage | 43.02% |
|---------------|--------|

## 2.3. Coverage

|                    |          |
|--------------------|----------|
| Mean               | 8.7698   |
| Standard Deviation | 124.5522 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 52.62 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 332,612.94      |
| Standard Deviation | 5,697,166.1     |
| P25/Median/P75     | 221 / 321 / 470 |

## 2.6. Mismatches and indels

|                                          |             |
|------------------------------------------|-------------|
| General error rate                       | 1.43%       |
| Mismatches                               | 364,574,632 |
| Insertions                               | 7,374,749   |
| Mapped reads with at least one insertion | 3.38%       |
| Deletions                                | 22,295,793  |
| Mapped reads with at least one deletion  | 10.55%      |
| Homopolymer indels                       | 47.16%      |

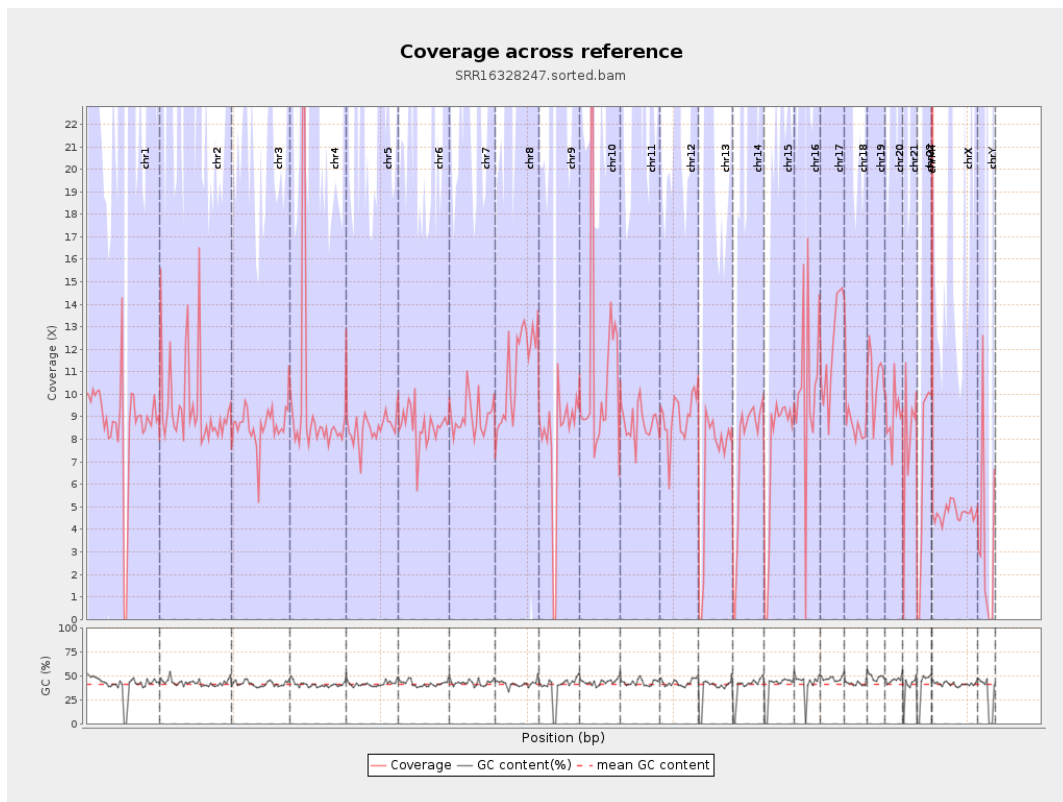
## 2.7. Chromosome stats

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

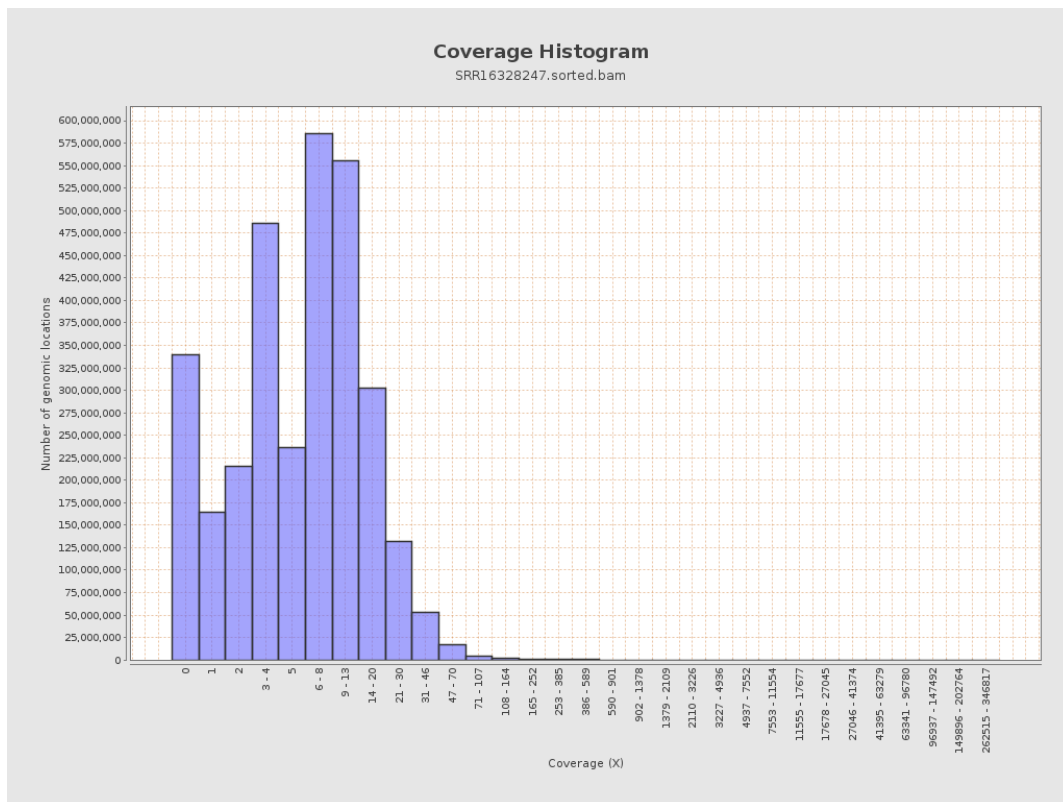
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 2172768451   | 8.7172          | 144.3775         |
| chr2  | 243199373 | 2315111567   | 9.5194          | 268.1763         |
| chr3  | 198022430 | 1701558656   | 8.5928          | 14.6637          |
| chr4  | 191154276 | 1796620450   | 9.3988          | 176.3192         |
| chr5  | 180915260 | 1541682145   | 8.5216          | 15.0462          |
| chr6  | 171115067 | 1470673306   | 8.5946          | 26.8469          |
| chr7  | 159138663 | 1438502044   | 9.0393          | 56.4767          |
| chr8  | 146364022 | 1624859999   | 11.1015         | 166.2374         |
| chr9  | 141213431 | 1125077894   | 7.9672          | 85.3323          |
| chr10 | 135534747 | 1520870557   | 11.2213         | 193.3253         |
| chr11 | 135006516 | 1186983943   | 8.792           | 29.9637          |
| chr12 | 133851895 | 1203377965   | 8.9904          | 37.0821          |
| chr13 | 115169878 | 795052216    | 6.9033          | 20.7617          |
| chr14 | 107349540 | 800576550    | 7.4577          | 19.6696          |
| chr15 | 102531392 | 753285660    | 7.3469          | 11.9661          |
| chr16 | 90354753  | 940463484    | 10.4086         | 91.6673          |
| chr17 | 81195210  | 979268167    | 12.0607         | 51.6974          |
| chr18 | 78077248  | 681375039    | 8.7269          | 70.7073          |
| chr19 | 59128983  | 643113387    | 10.8764         | 107.6201         |
| chr20 | 63025520  | 572775040    | 9.088           | 49.6508          |
| chr21 | 48129895  | 388878810    | 8.0798          | 92.9498          |
| chr22 | 51304566  | 351711932    | 6.8554          | 18.4297          |
| chrMT | 16571     | 209715989    | 12,655.6025     | 7,524.3351       |
| chrX  | 155270560 | 732291290    | 4.7162          | 15.5213          |

|      |          |           |        |          |
|------|----------|-----------|--------|----------|
| chrY | 59373566 | 201906818 | 3.4006 | 177.0021 |
|------|----------|-----------|--------|----------|

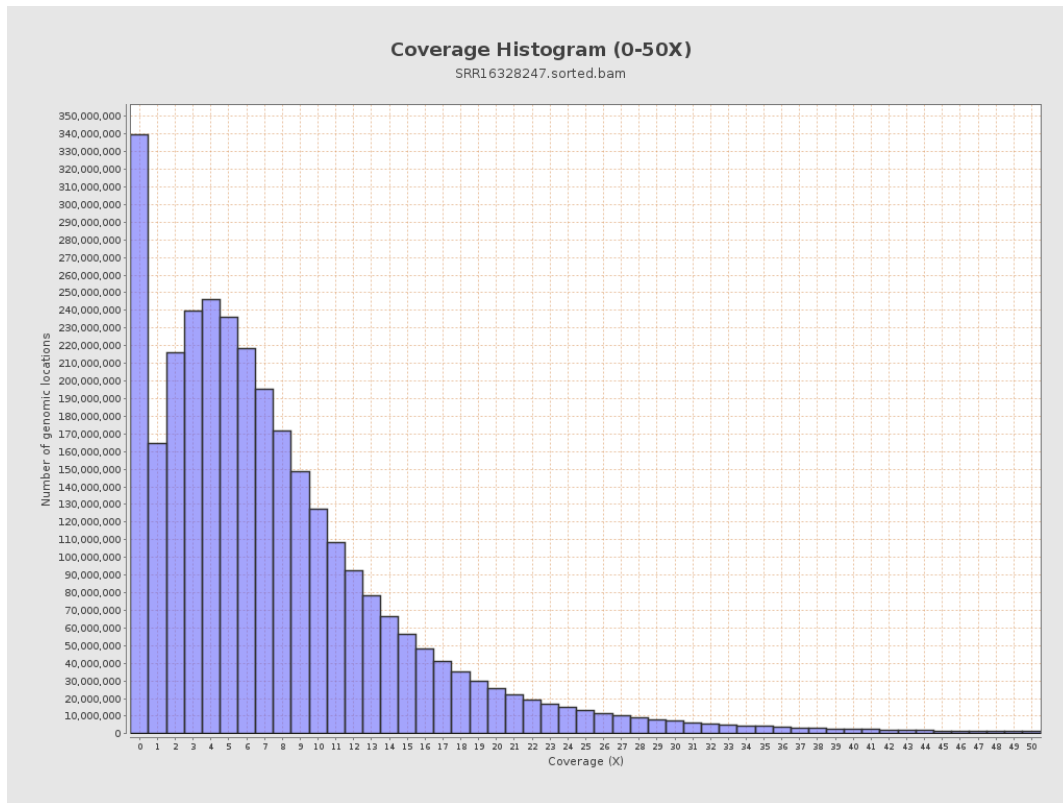
### 3. Results : Coverage across reference



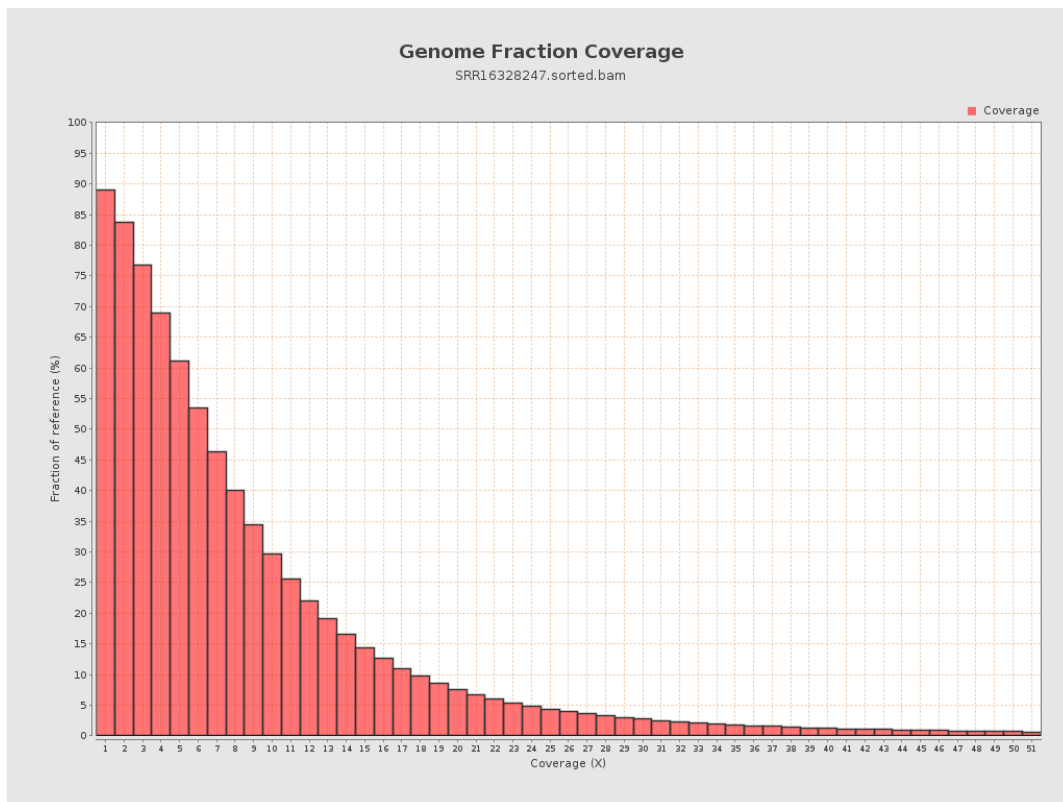
## 4. Results : Coverage Histogram



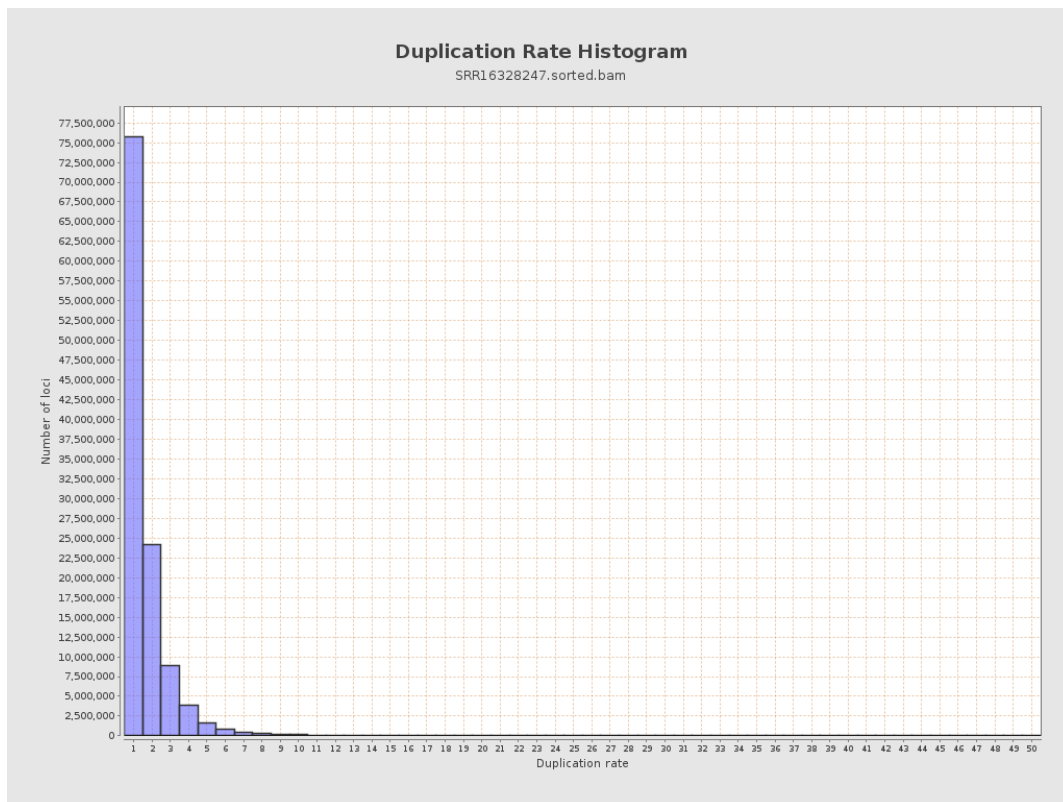
## 5. Results : Coverage Histogram (0-50X)



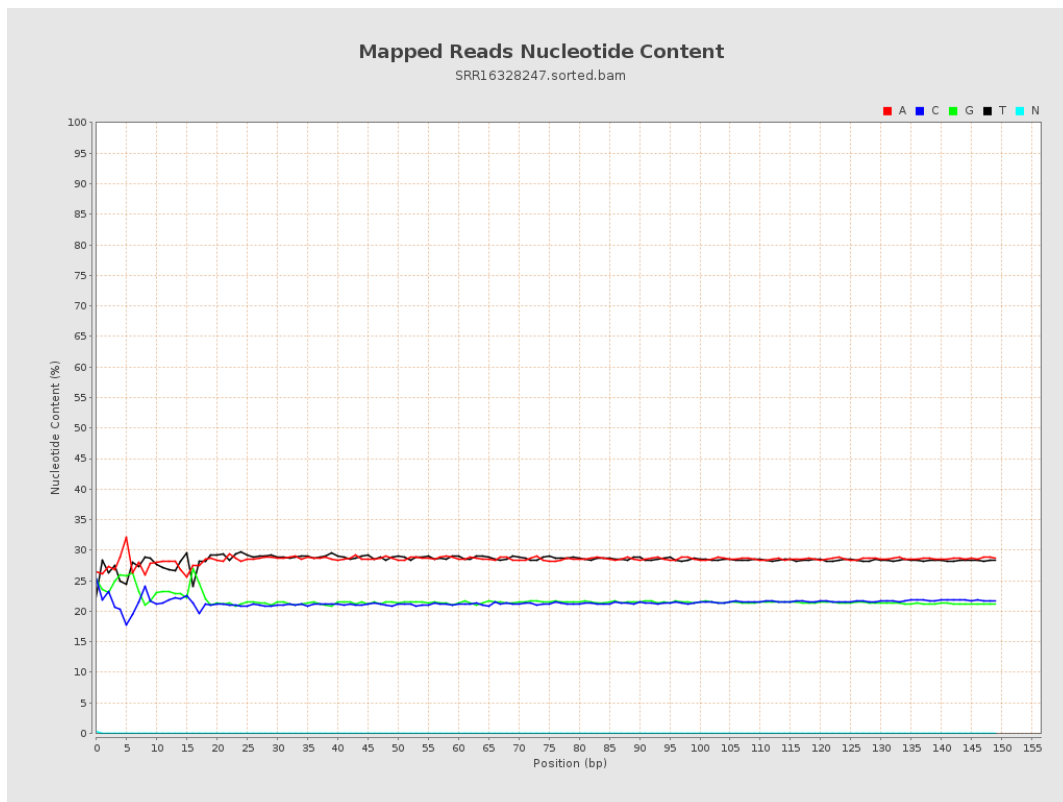
## 6. Results : Genome Fraction Coverage



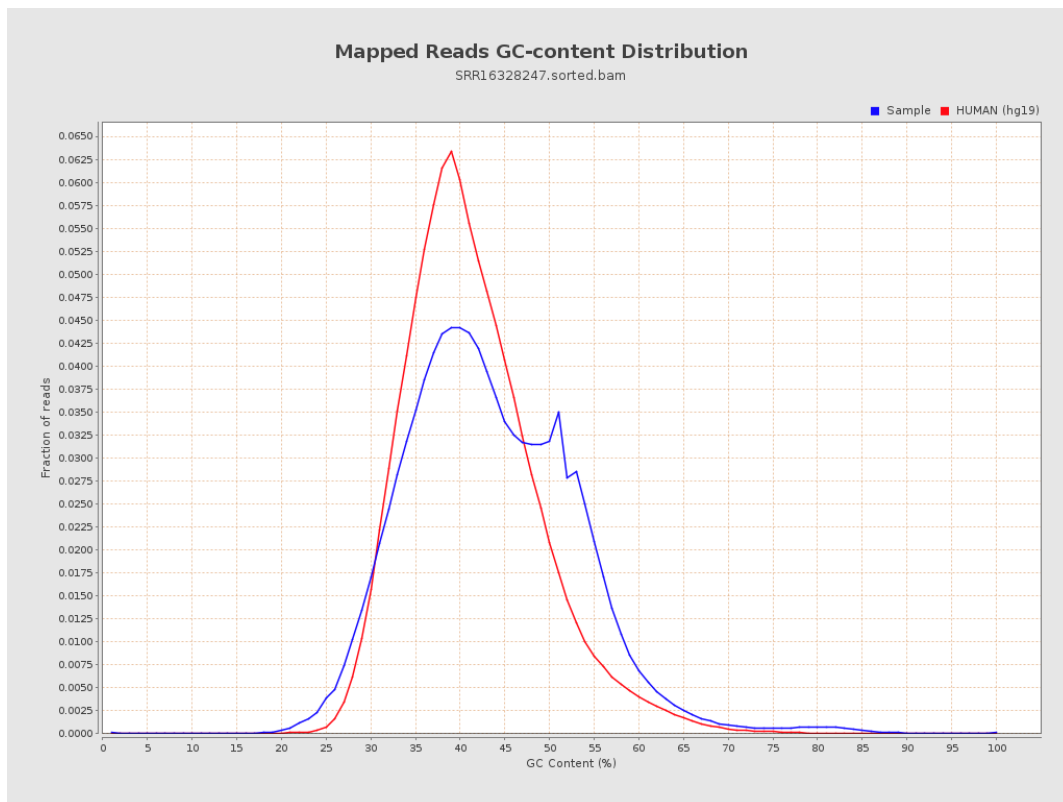
## 7. Results : Duplication Rate Histogram



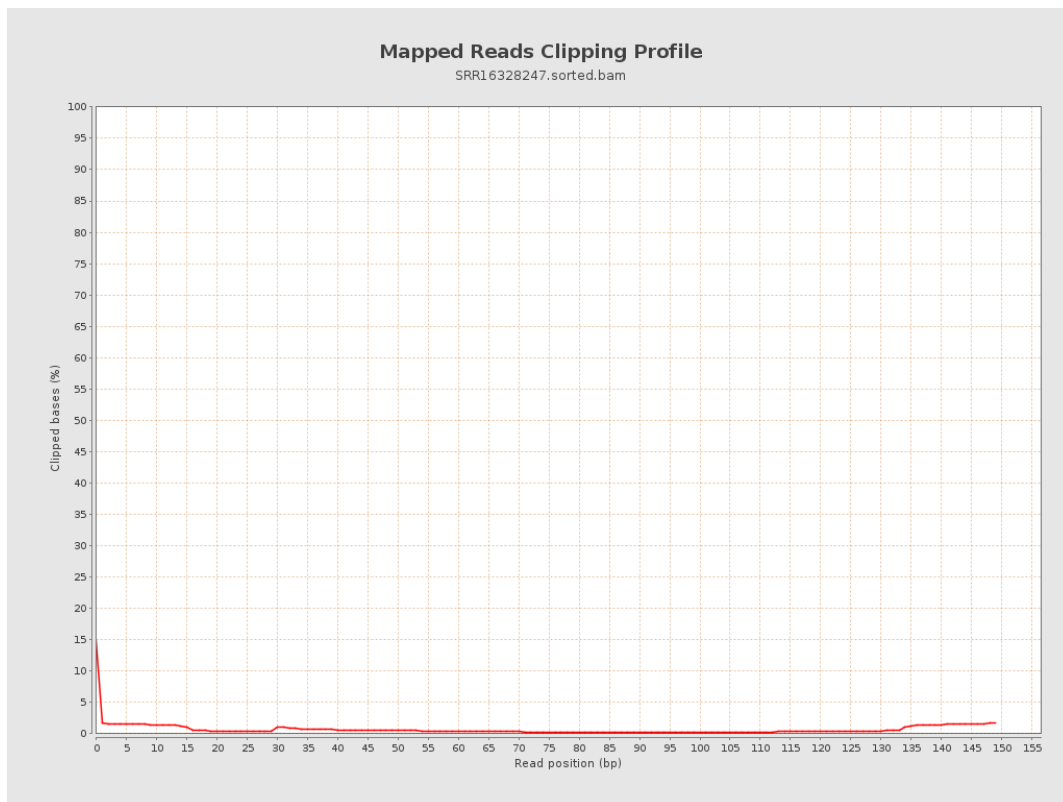
## 8. Results : Mapped Reads Nucleotide Content



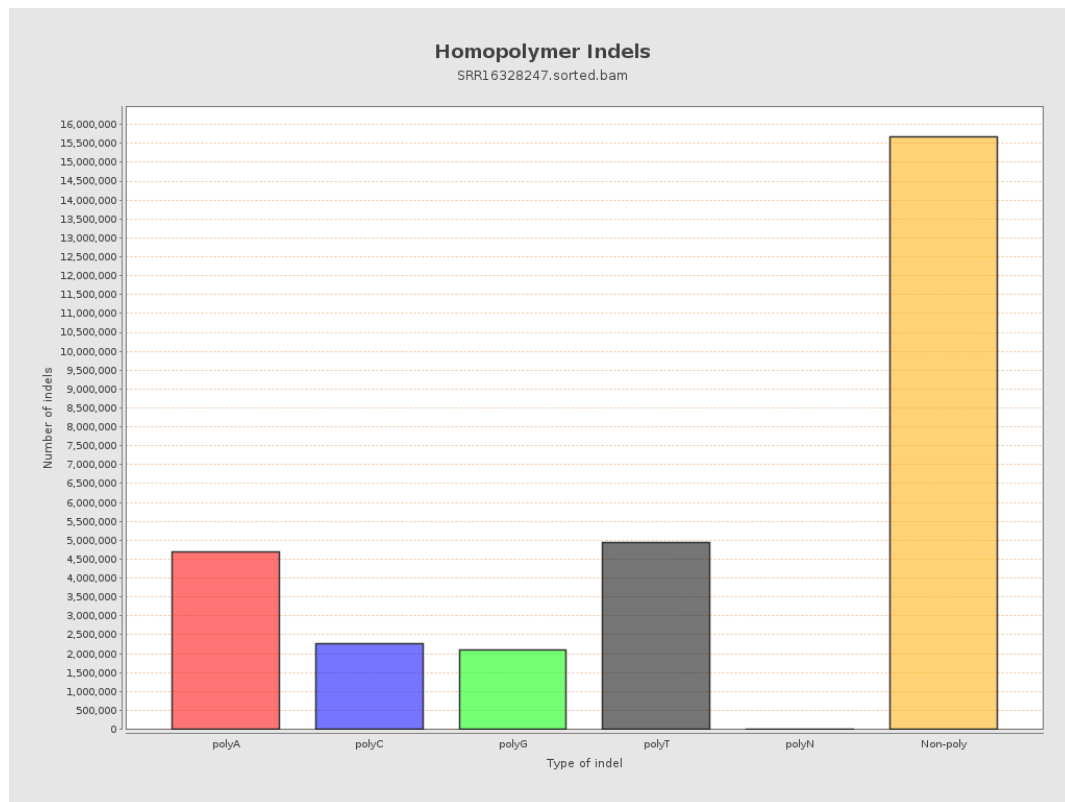
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



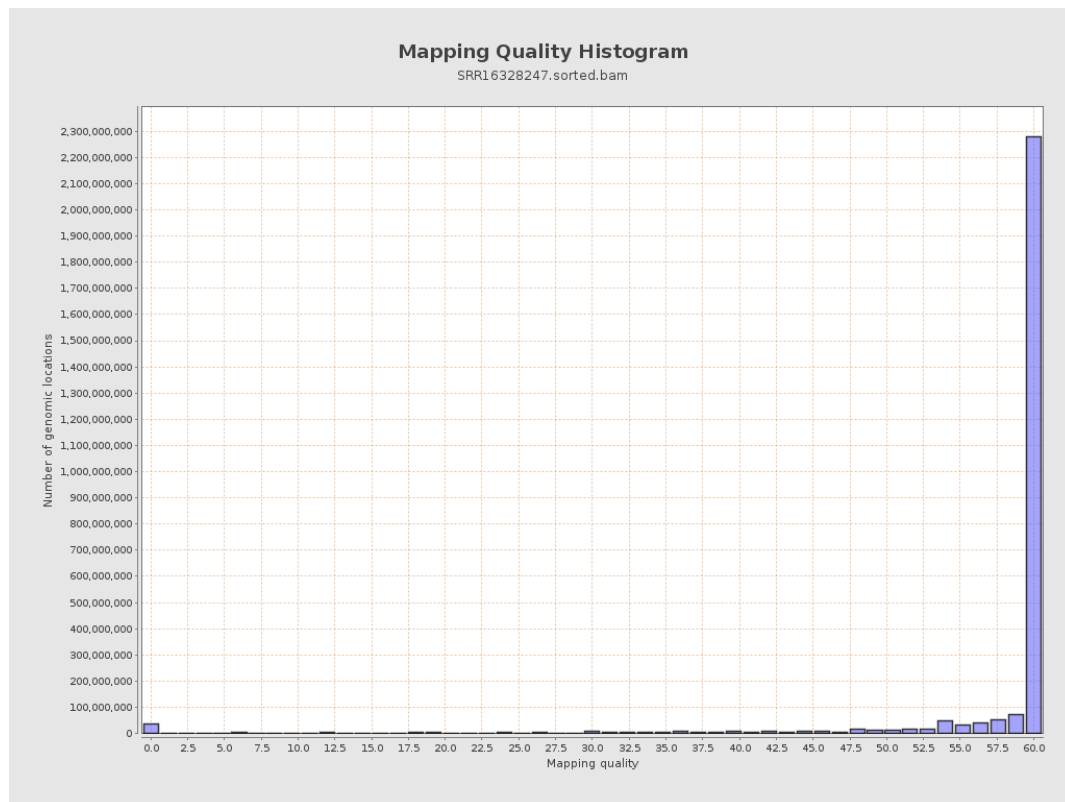
## 11. Results : Homopolymer Indels



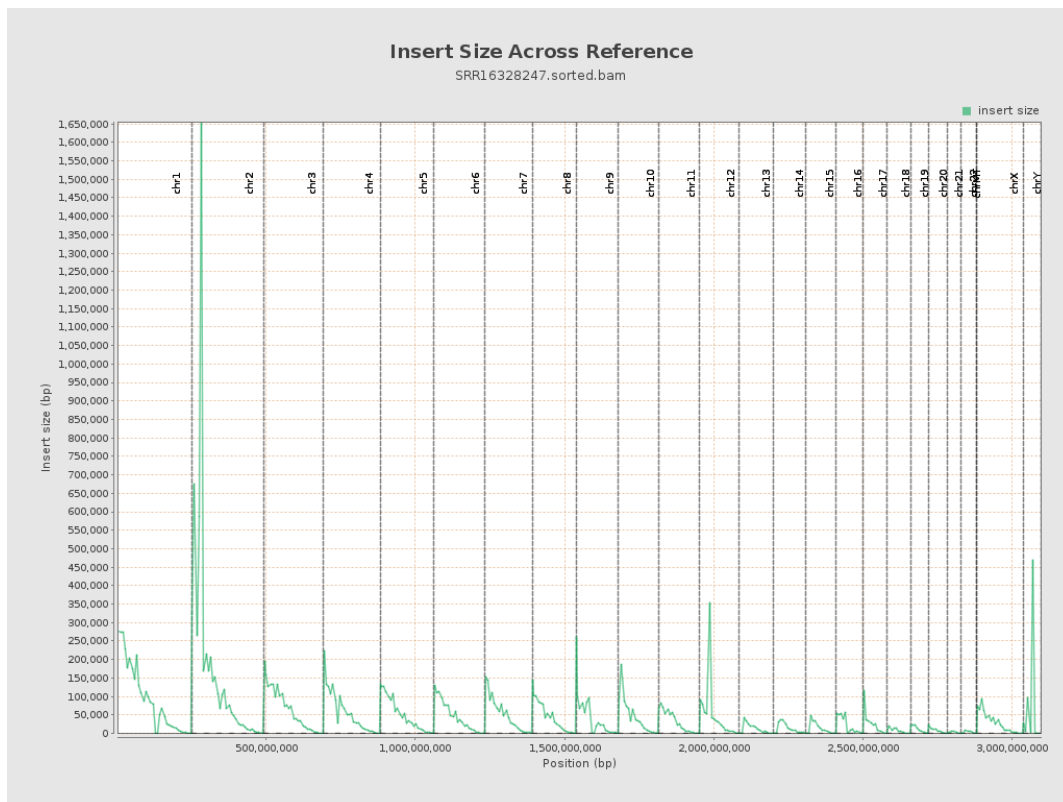
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

