

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/10 10:44:46*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124962.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_SRR3124962<br>/home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124962_1.fastq.gz SRR3124962_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                      |
| Analysis date:                        | Tue Dec 10 10:44:45 CST 2024                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                     |
| BAM file:                             | SRR3124962.sorted.bam                                                                                                                                                                                                   |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 2,924,774          |
| Mapped reads                 | 2,855,406 / 97.63% |
| Unmapped reads               | 69,368 / 2.37%     |
| Mapped paired reads          | 2,855,406 / 97.63% |
| Mapped reads, first in pair  | 1,438,656 / 49.19% |
| Mapped reads, second in pair | 1,416,750 / 48.44% |
| Mapped reads, both in pair   | 2,830,396 / 96.77% |
| Mapped reads, singletons     | 25,010 / 0.86%     |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 69,911 / 2.39%     |
| Read min/max/mean length     | 30 / 151 / 152.15  |
| Duplicated reads (estimated) | 548,514 / 18.75%   |
| Duplication rate             | 16.66%             |
| Clipped reads                | 2,072,632 / 70.86% |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 102,631,278 / 28.7%  |
| Number/percentage of C's | 71,780,961 / 20.07%  |
| Number/percentage of T's | 104,027,145 / 29.09% |
| Number/percentage of G's | 79,211,568 / 22.15%  |
| Number/percentage of N's | 2,665 / 0%           |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 42.22% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.1157 |
| Standard Deviation | 1.9093 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 53.41 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 93,298.75       |
| Standard Deviation | 2,922,009.91    |
| P25/Median/P75     | 123 / 166 / 231 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 1.2%      |
| Mismatches                               | 3,982,888 |
| Insertions                               | 90,986    |
| Mapped reads with at least one insertion | 2.93%     |
| Deletions                                | 167,917   |
| Mapped reads with at least one deletion  | 5.59%     |
| Homopolymer indels                       | 44.39%    |

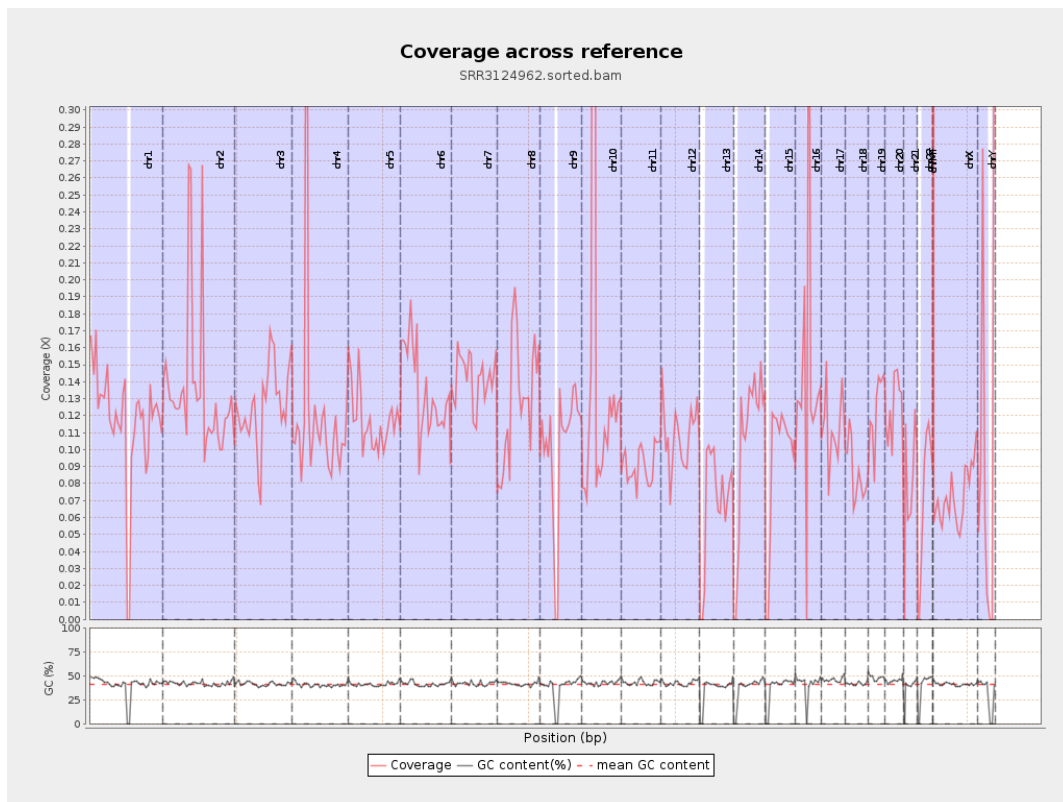
## 2.7. Chromosome stats

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

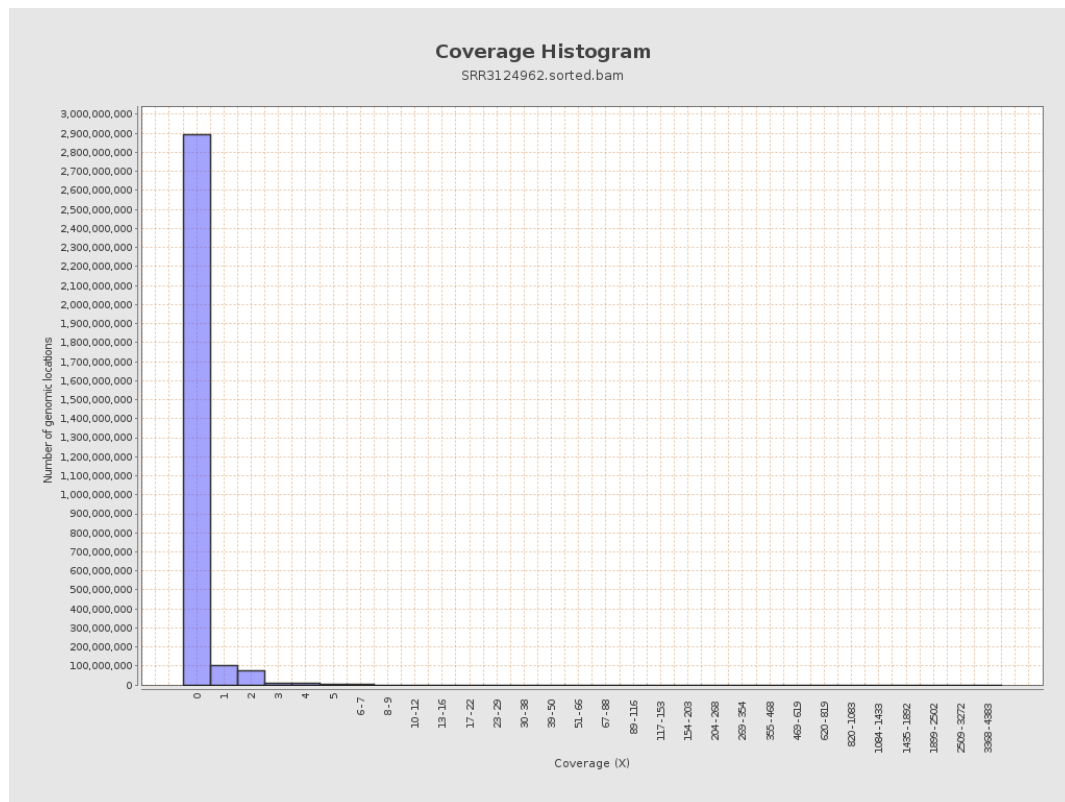
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 29107595     | 0.1168          | 0.8163           |
| chr2  | 243199373 | 33143632     | 0.1363          | 2.0447           |
| chr3  | 198022430 | 24984351     | 0.1262          | 0.5489           |
| chr4  | 191154276 | 23596353     | 0.1234          | 2.7501           |
| chr5  | 180915260 | 21211548     | 0.1172          | 0.5092           |
| chr6  | 171115067 | 22961090     | 0.1342          | 0.6557           |
| chr7  | 159138663 | 22666907     | 0.1424          | 0.87             |
| chr8  | 146364022 | 18929135     | 0.1293          | 0.5642           |
| chr9  | 141213431 | 14424430     | 0.1021          | 1.0871           |
| chr10 | 135534747 | 19881790     | 0.1467          | 6.6182           |
| chr11 | 135006516 | 12267011     | 0.0909          | 0.5468           |
| chr12 | 133851895 | 14625043     | 0.1093          | 0.4725           |
| chr13 | 115169878 | 7921647      | 0.0688          | 0.3711           |
| chr14 | 107349540 | 11372187     | 0.1059          | 0.4995           |
| chr15 | 102531392 | 9443526      | 0.0921          | 0.4343           |
| chr16 | 90354753  | 13428282     | 0.1486          | 2.6439           |
| chr17 | 81195210  | 9201328      | 0.1133          | 0.895            |
| chr18 | 78077248  | 6733826      | 0.0862          | 1.1227           |
| chr19 | 59128983  | 7267800      | 0.1229          | 0.6527           |
| chr20 | 63025520  | 7812823      | 0.124           | 1.0628           |
| chr21 | 48129895  | 3940460      | 0.0819          | 1.4892           |
| chr22 | 51304566  | 3726194      | 0.0726          | 0.4275           |
| chrMT | 16571     | 1392836      | 84.0526         | 43.2127          |
| chrX  | 155270560 | 11343467     | 0.0731          | 0.4265           |

|      |          |         |       |        |
|------|----------|---------|-------|--------|
| chrY | 59373566 | 6650595 | 0.112 | 3.8682 |
|------|----------|---------|-------|--------|

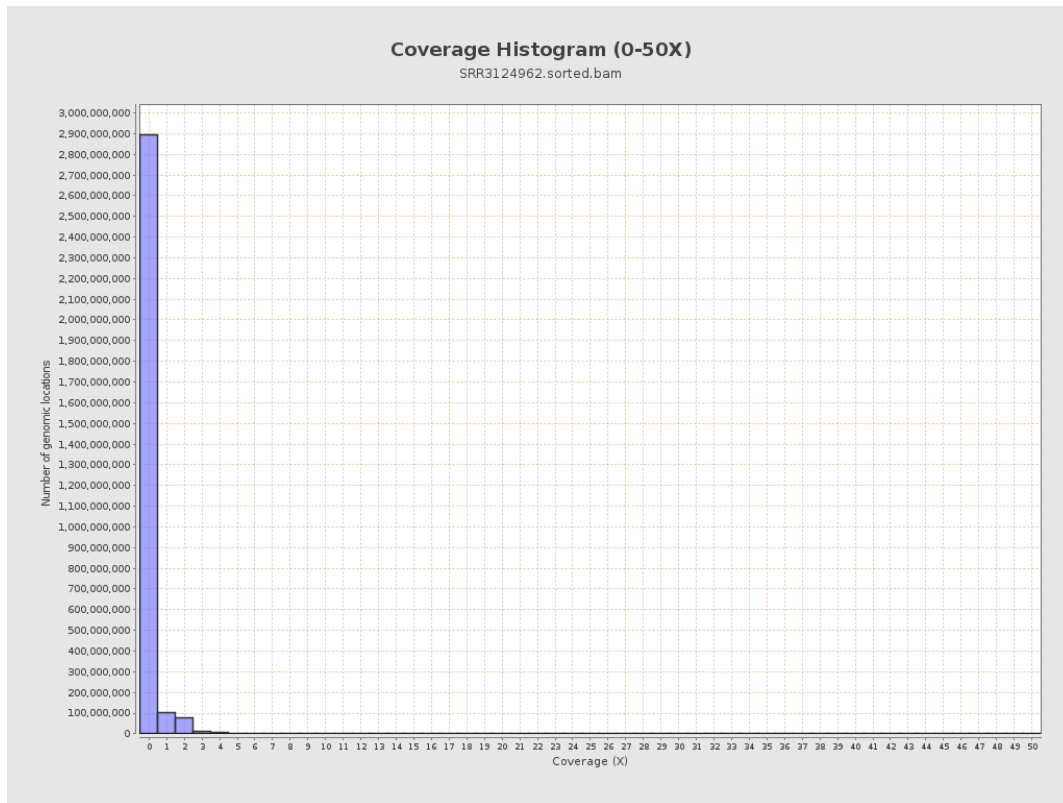
### 3. Results : Coverage across reference



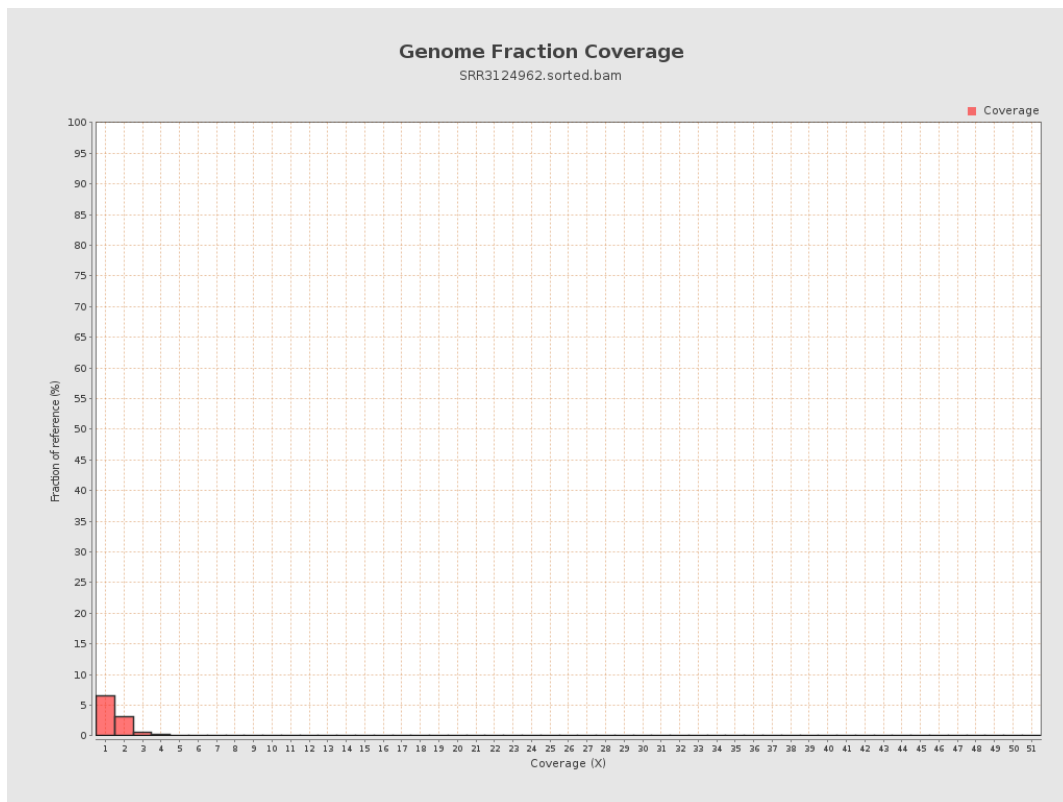
## 4. Results : Coverage Histogram



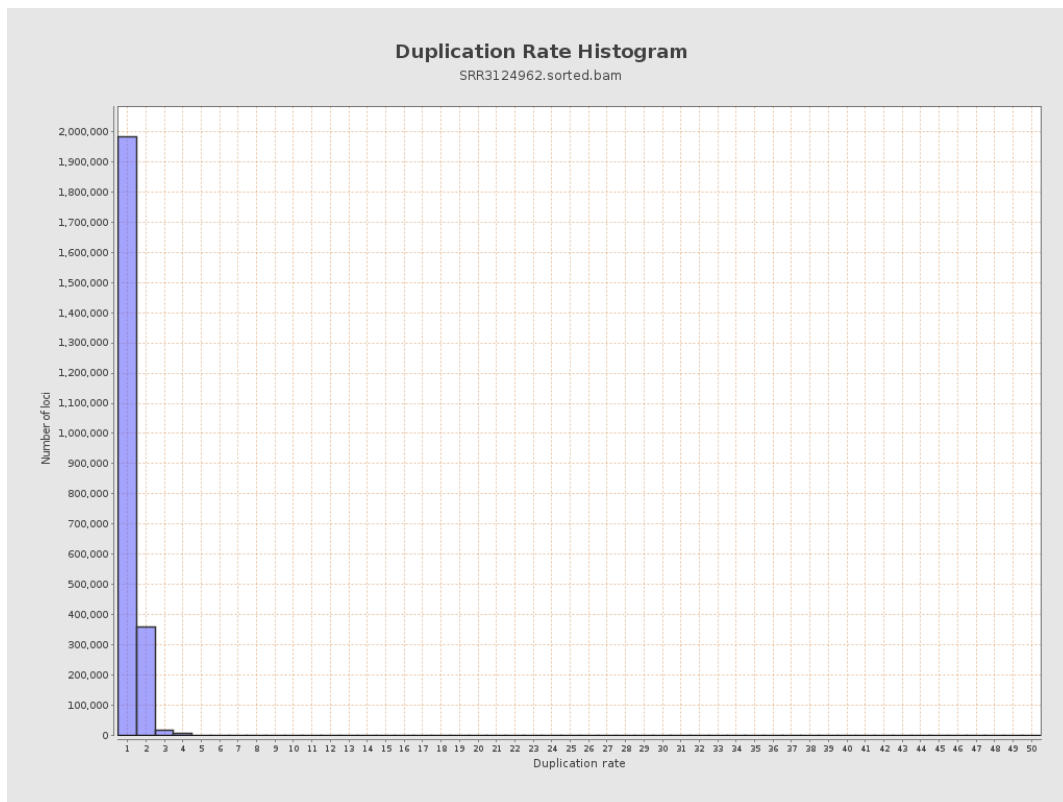
## 5. Results : Coverage Histogram (0-50X)



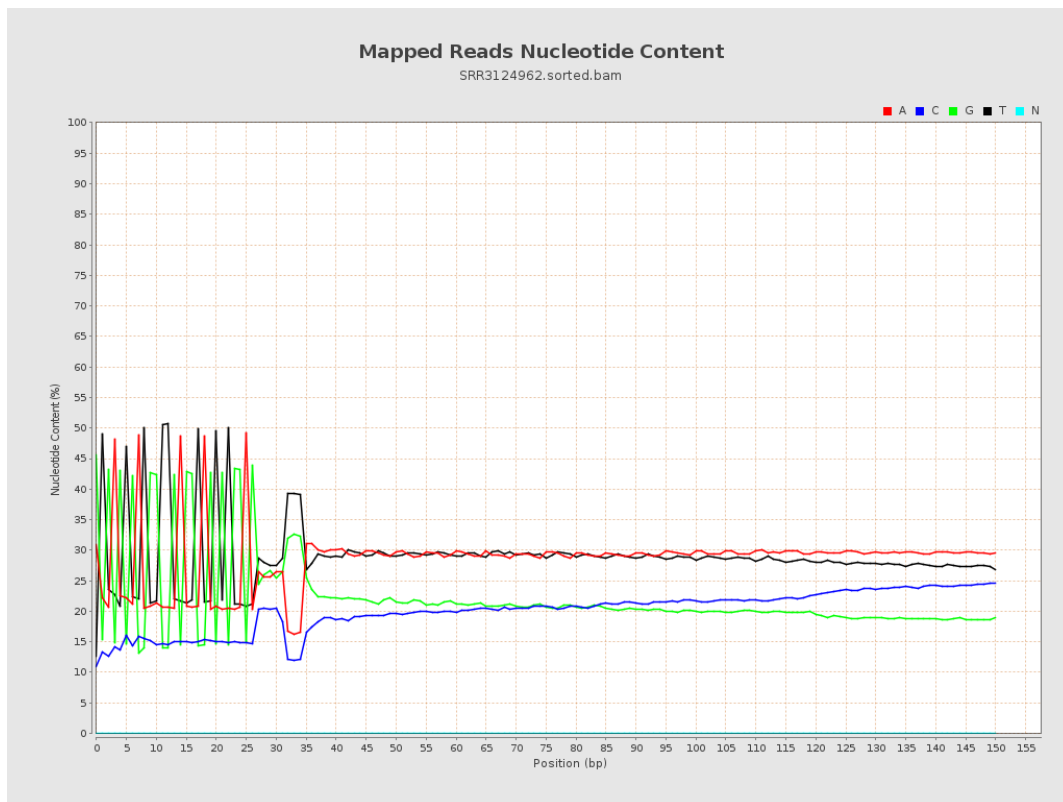
## 6. Results : Genome Fraction Coverage



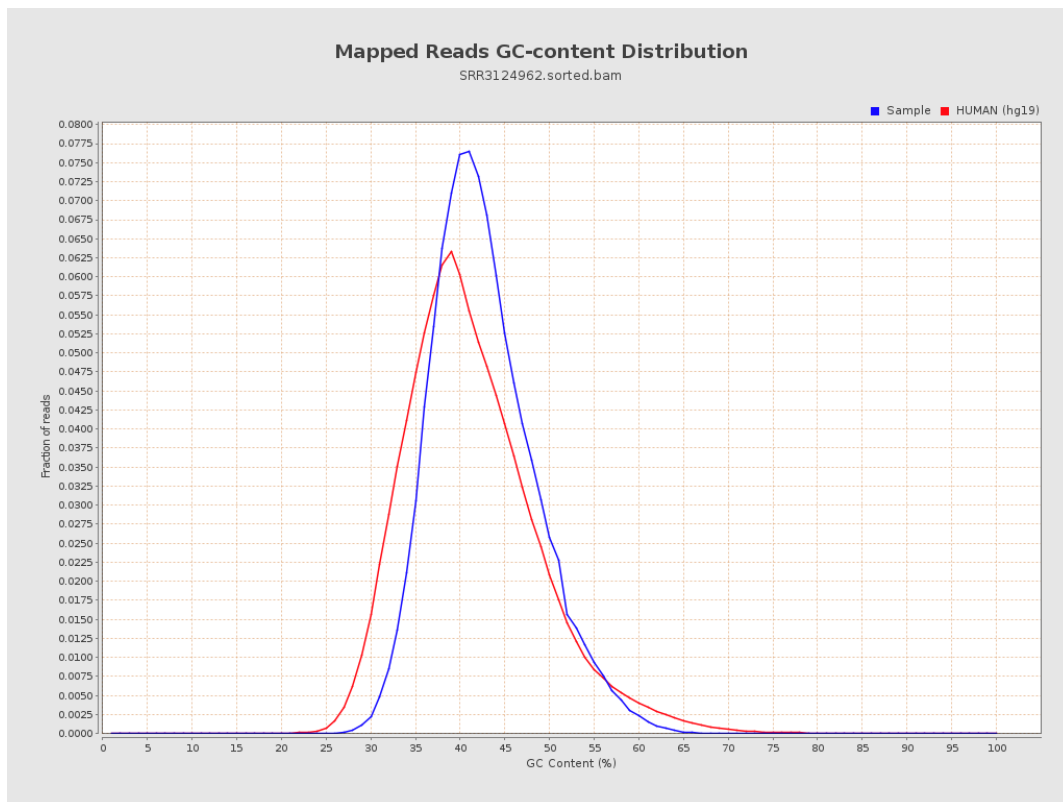
## 7. Results : Duplication Rate Histogram



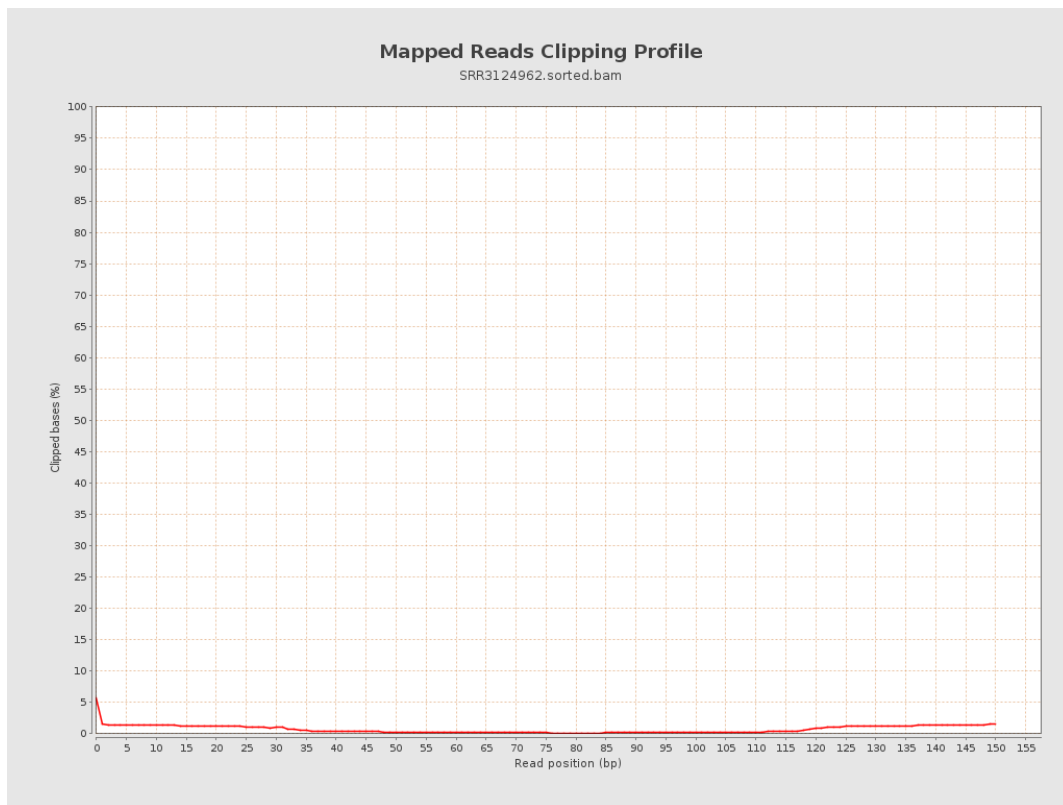
## 8. Results : Mapped Reads Nucleotide Content



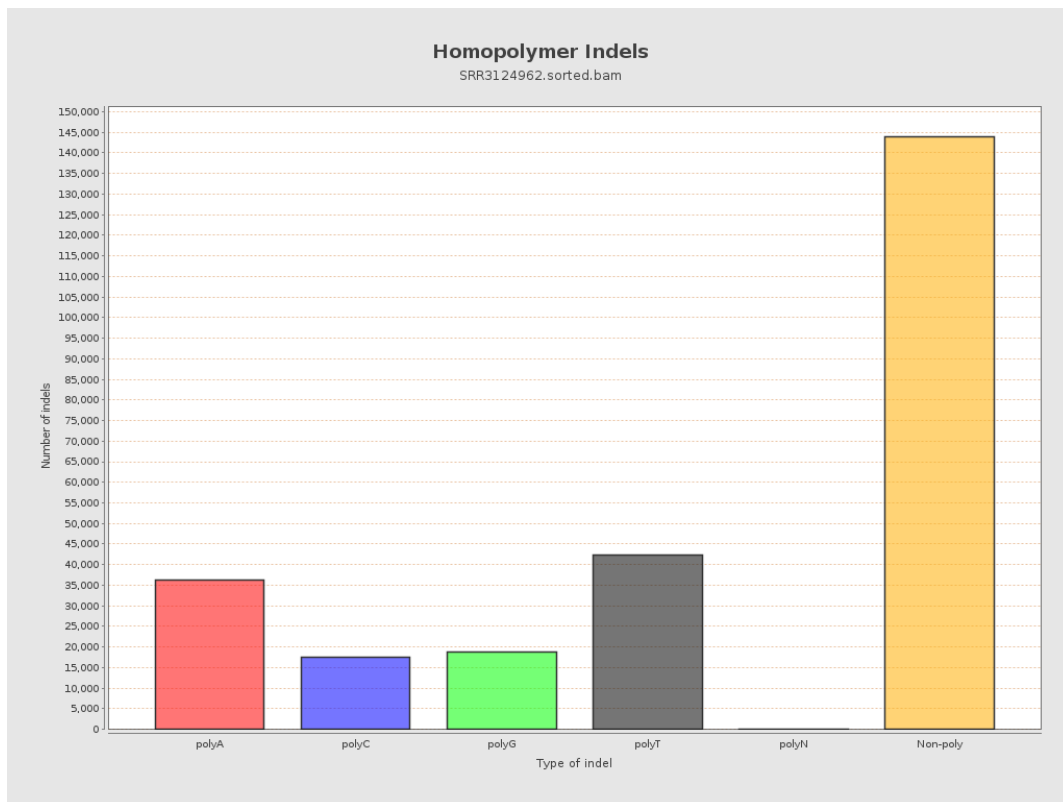
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



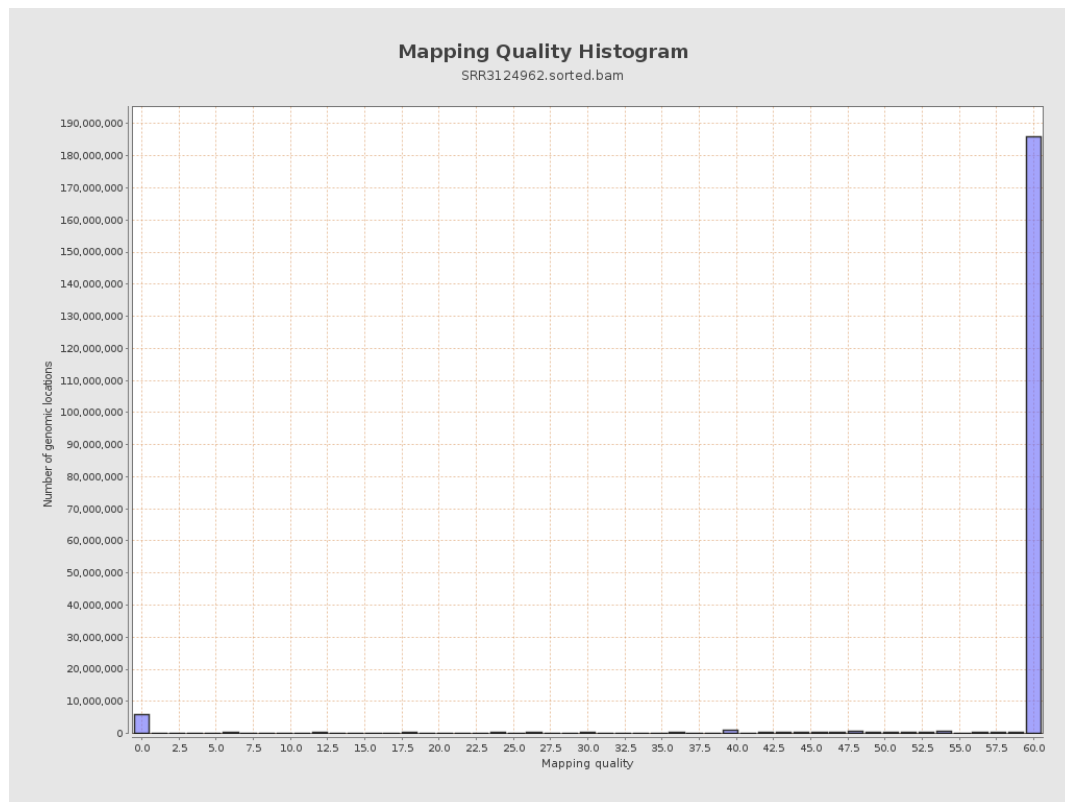
## 11. Results : Homopolymer Indels



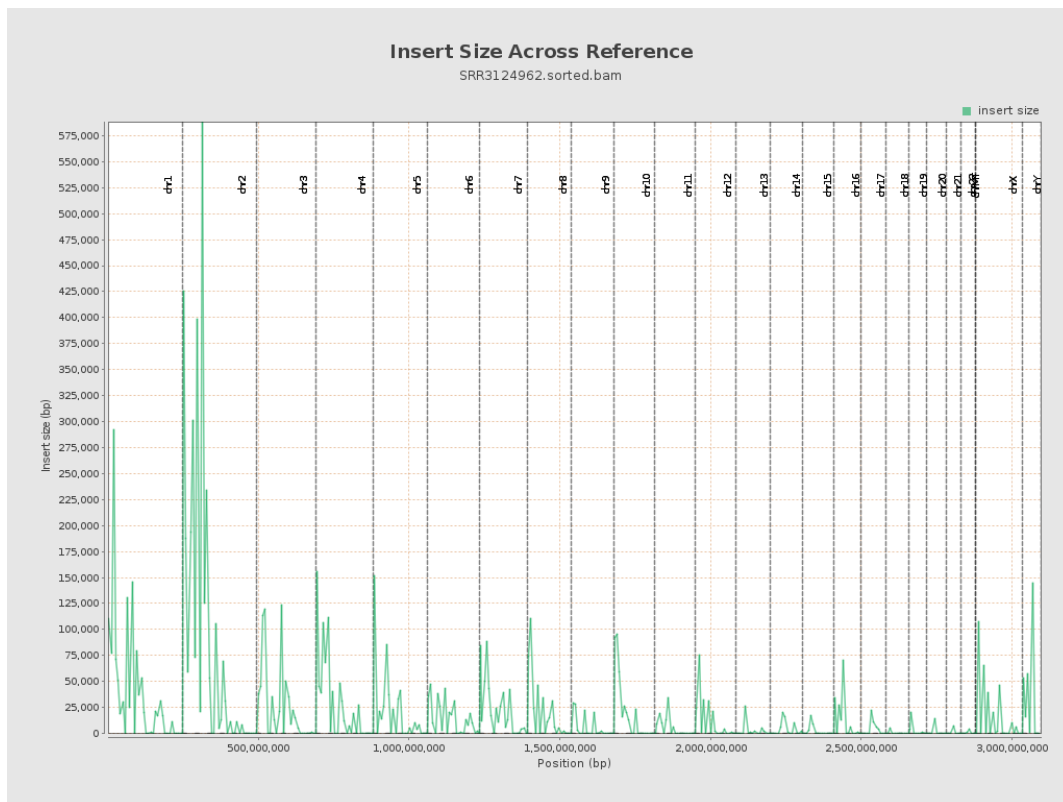
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

