

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/27 16:02:49*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354868.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_SRR22354868 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354868_1.fastq.gz SRR22354868_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                      |
| Analysis date:                        | Tue Aug 27 16:02:49 CST 2024                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                     |
| BAM file:                             | SRR22354868.sorted.bam                                                                                                                                                                                                  |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 23,355,700          |
| Mapped reads                 | 22,898,206 / 98.04% |
| Unmapped reads               | 457,494 / 1.96%     |
| Mapped paired reads          | 22,898,206 / 98.04% |
| Mapped reads, first in pair  | 11,460,546 / 49.07% |
| Mapped reads, second in pair | 11,437,660 / 48.97% |
| Mapped reads, both in pair   | 22,851,178 / 97.84% |
| Mapped reads, singletons     | 47,028 / 0.2%       |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 1,012,096 / 4.33%   |
| Read min/max/mean length     | 30 / 150 / 151.55   |
| Duplicated reads (estimated) | 13,328,340 / 57.07% |
| Duplication rate             | 57.21%              |
| Clipped reads                | 11,889,416 / 50.91% |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 786,638,561 / 27.65% |
| Number/percentage of C's | 607,515,703 / 21.36% |
| Number/percentage of T's | 805,952,222 / 28.33% |
| Number/percentage of G's | 644,629,525 / 22.66% |
| Number/percentage of N's | 46,019 / 0%          |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 44.02% |
|---------------|--------|

## 2.3. Coverage

|                    |         |
|--------------------|---------|
| Mean               | 0.9193  |
| Standard Deviation | 49.5036 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 53.65 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 389,133.76      |
| Standard Deviation | 7,165,583.94    |
| P25/Median/P75     | 100 / 162 / 252 |

## 2.6. Mismatches and indels

|                                          |            |
|------------------------------------------|------------|
| General error rate                       | 0.61%      |
| Mismatches                               | 16,171,736 |
| Insertions                               | 414,690    |
| Mapped reads with at least one insertion | 1.7%       |
| Deletions                                | 442,599    |
| Mapped reads with at least one deletion  | 1.85%      |
| Homopolymer indels                       | 43.8%      |

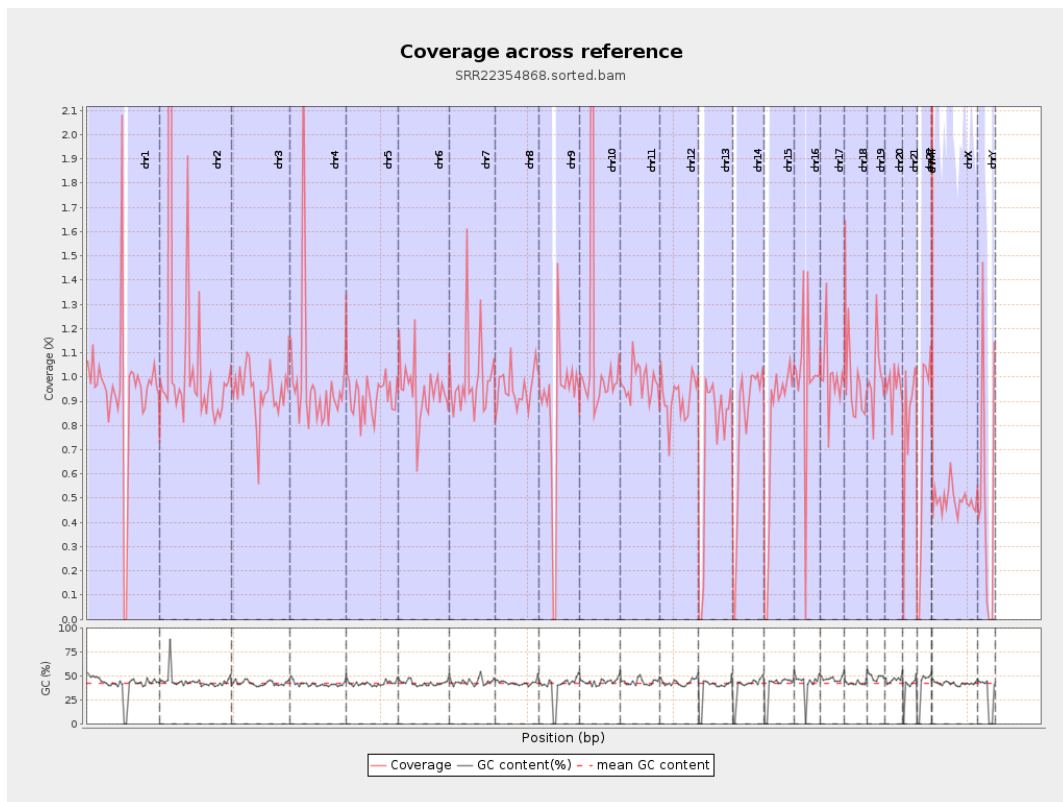
## 2.7. Chromosome stats

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

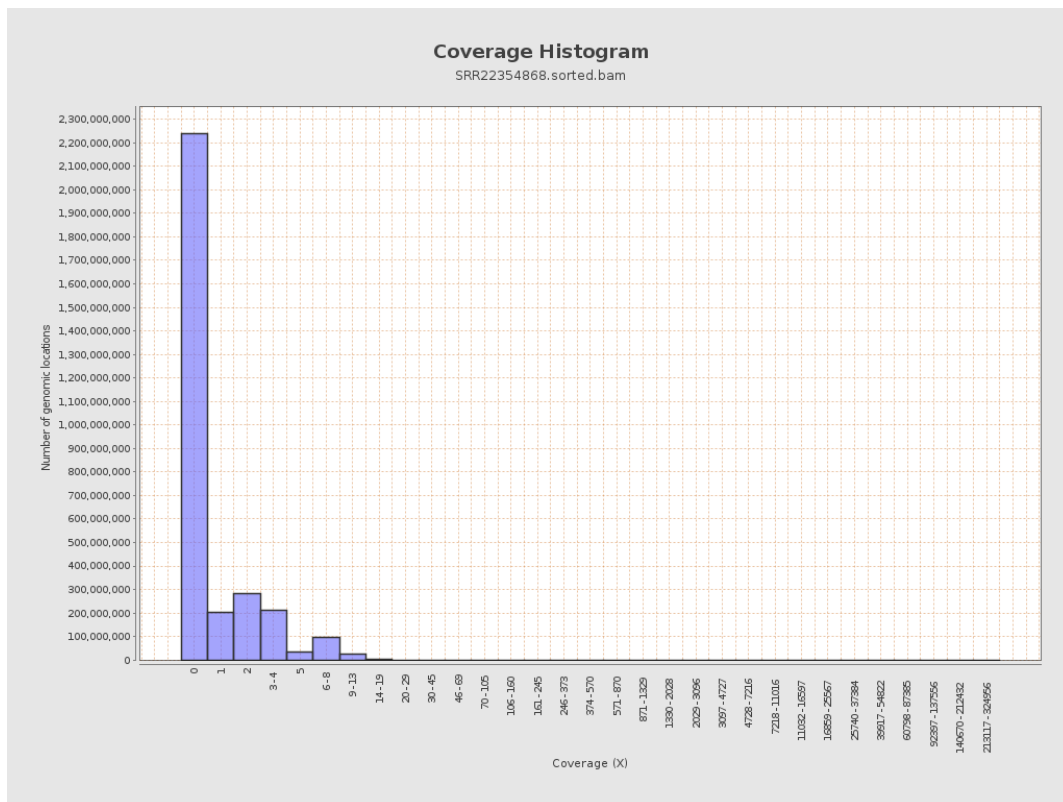
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 233960727    | 0.9387          | 26.7985          |
| chr2  | 243199373 | 274591803    | 1.1291          | 169.0668         |
| chr3  | 198022430 | 186342867    | 0.941           | 2.3775           |
| chr4  | 191154276 | 186271424    | 0.9745          | 10.5654          |
| chr5  | 180915260 | 166553514    | 0.9206          | 2.0131           |
| chr6  | 171115067 | 161524044    | 0.9439          | 4.1476           |
| chr7  | 159138663 | 158005449    | 0.9929          | 38.6104          |
| chr8  | 146364022 | 140278388    | 0.9584          | 6.0748           |
| chr9  | 141213431 | 122148053    | 0.865           | 14.4682          |
| chr10 | 135534747 | 156187698    | 1.1524          | 27.9408          |
| chr11 | 135006516 | 132295409    | 0.9799          | 5.8543           |
| chr12 | 133851895 | 122470085    | 0.915           | 2.0247           |
| chr13 | 115169878 | 85317186     | 0.7408          | 1.7561           |
| chr14 | 107349540 | 85718032     | 0.7985          | 4.0179           |
| chr15 | 102531392 | 80334416     | 0.7835          | 1.81             |
| chr16 | 90354753  | 89975336     | 0.9958          | 5.3483           |
| chr17 | 81195210  | 80851495     | 0.9958          | 5.4769           |
| chr18 | 78077248  | 76143766     | 0.9752          | 12.0602          |
| chr19 | 59128983  | 59568547     | 1.0074          | 14.5657          |
| chr20 | 63025520  | 60516333     | 0.9602          | 4.1363           |
| chr21 | 48129895  | 40248925     | 0.8363          | 5.969            |
| chr22 | 51304566  | 36858595     | 0.7184          | 3.147            |
| chrMT | 16571     | 3411444      | 205.8683        | 39.8347          |
| chrX  | 155270560 | 75951729     | 0.4892          | 2.395            |

|      |          |          |        |         |
|------|----------|----------|--------|---------|
| chrY | 59373566 | 30484957 | 0.5134 | 13.0905 |
|------|----------|----------|--------|---------|

### 3. Results : Coverage across reference

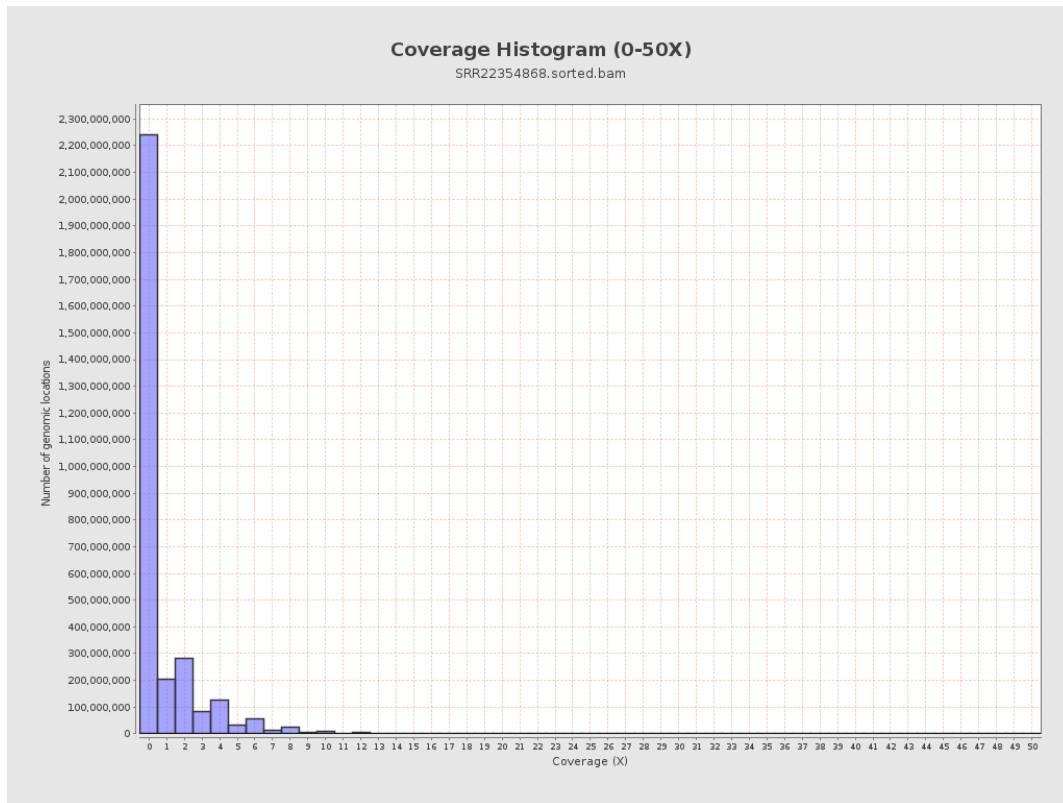


## 4. Results : Coverage Histogram

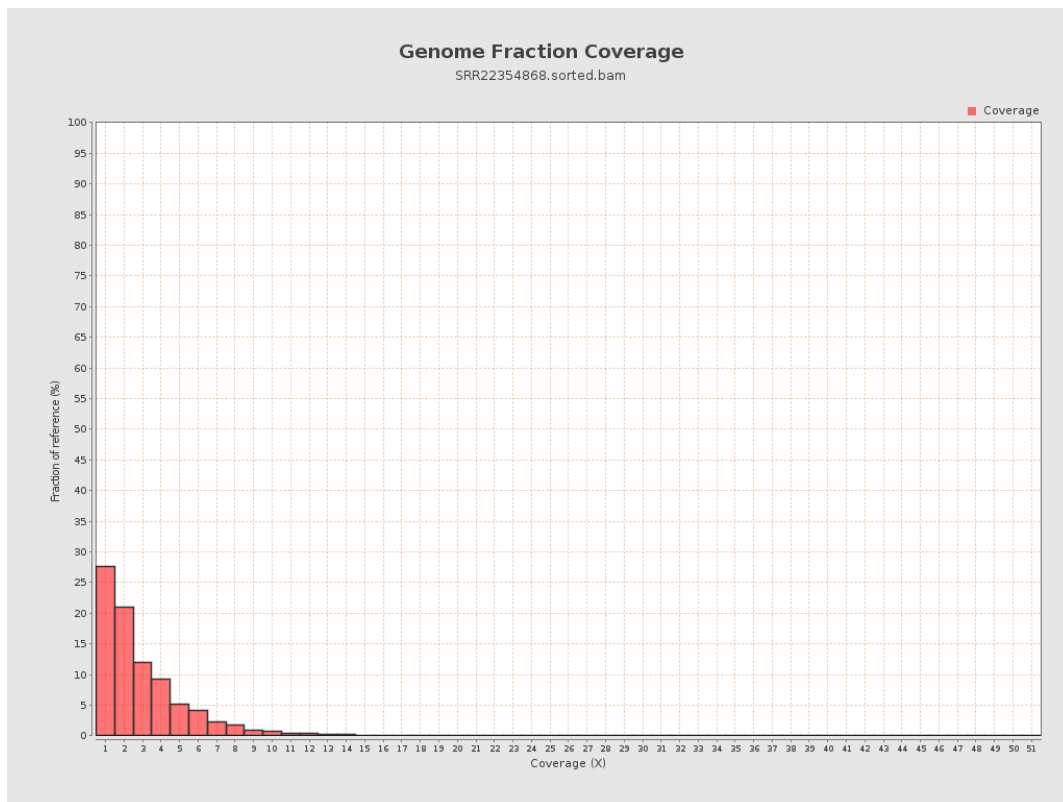




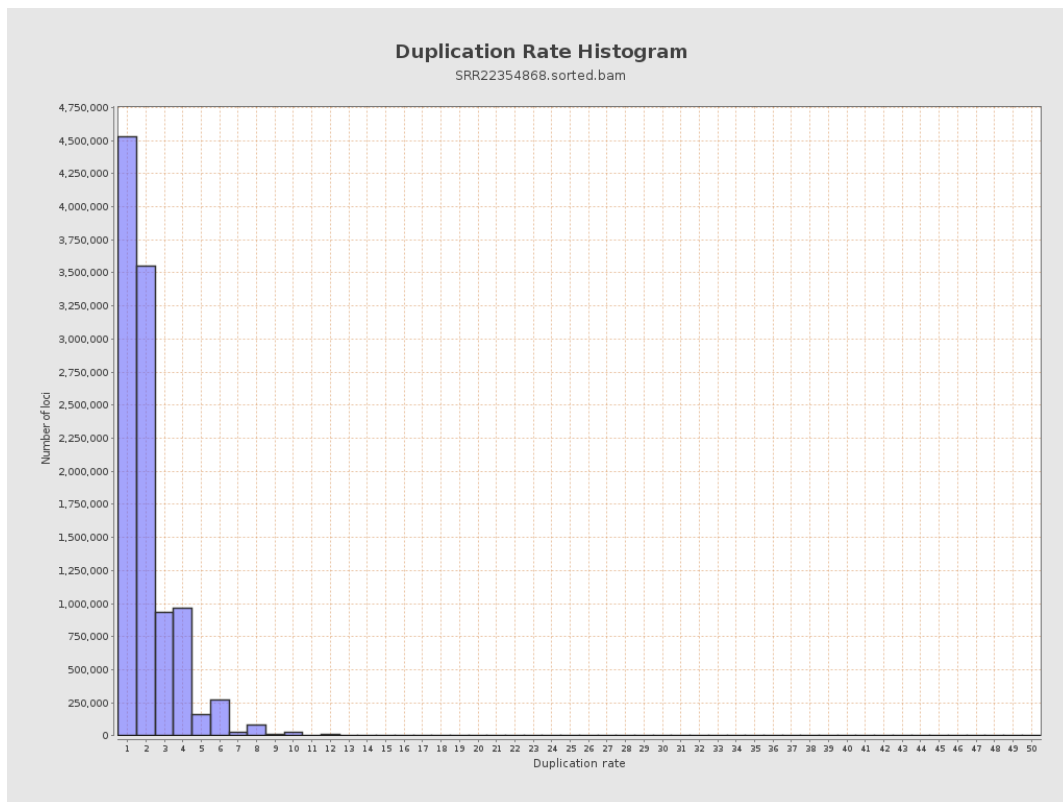
## 5. Results : Coverage Histogram (0-50X)



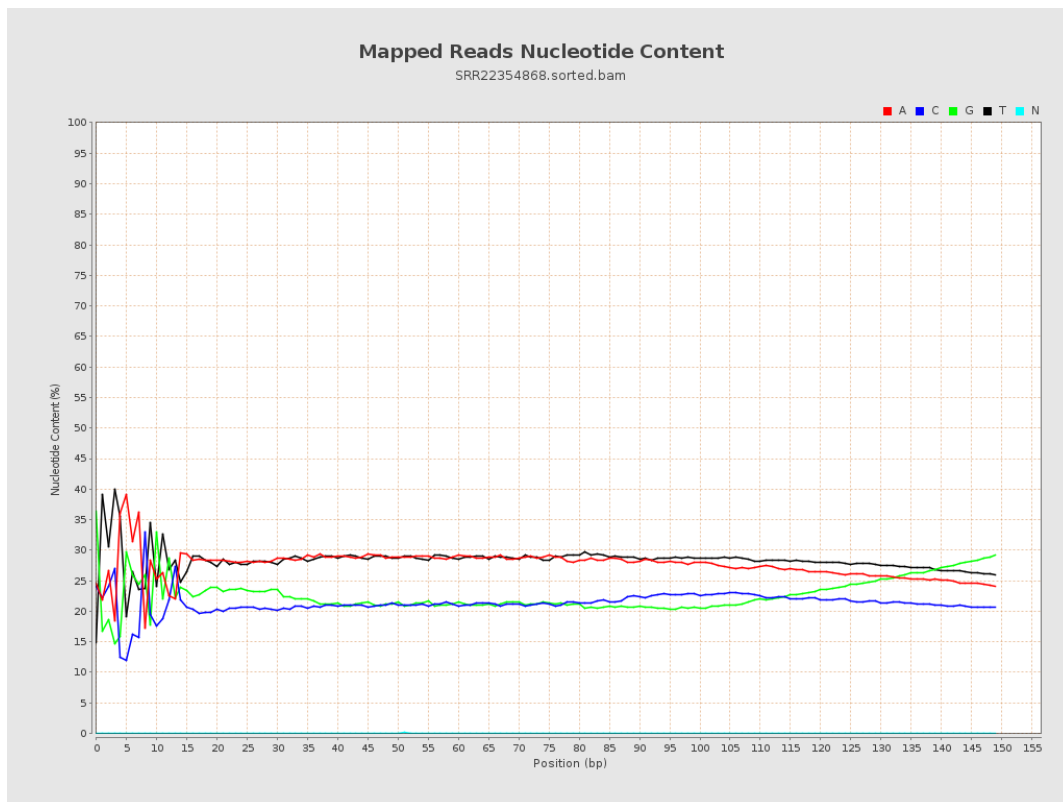
## 6. Results : Genome Fraction Coverage



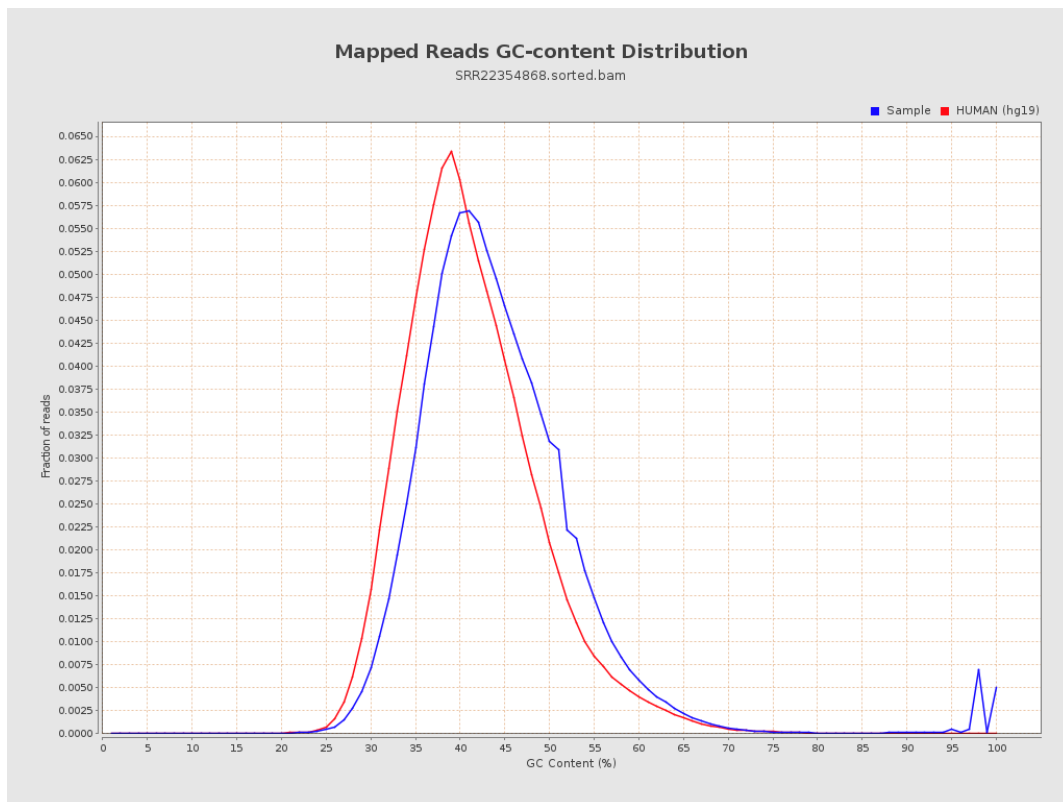
## 7. Results : Duplication Rate Histogram



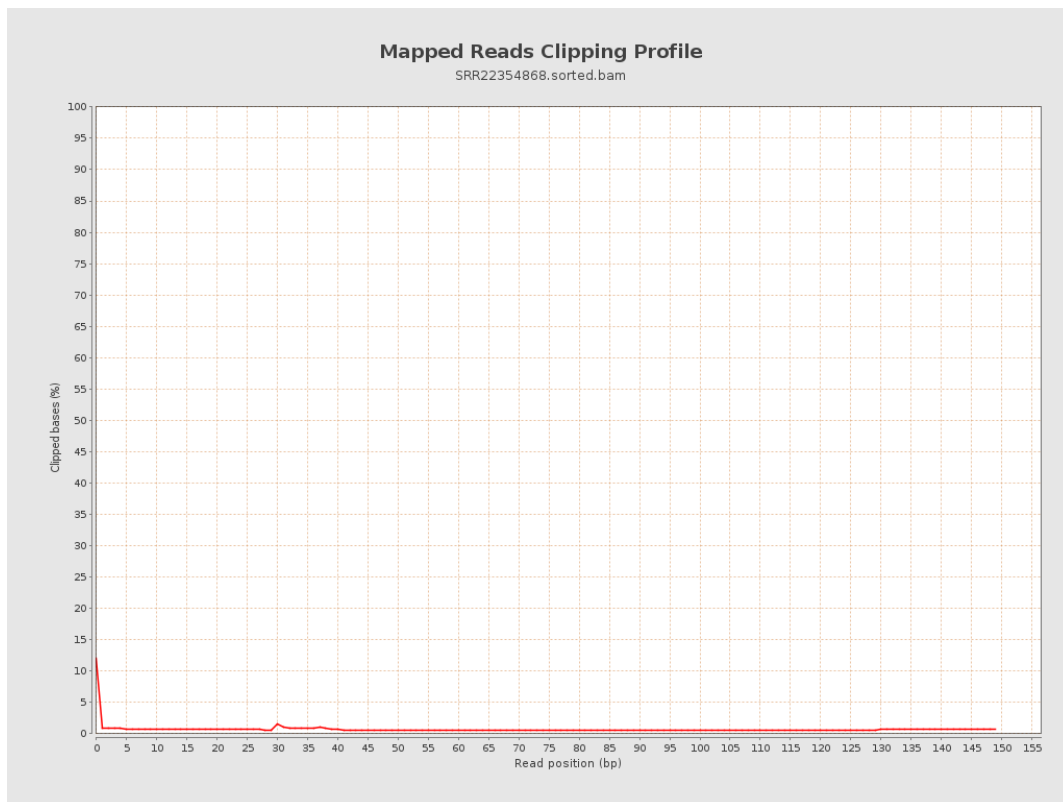
## 8. Results : Mapped Reads Nucleotide Content



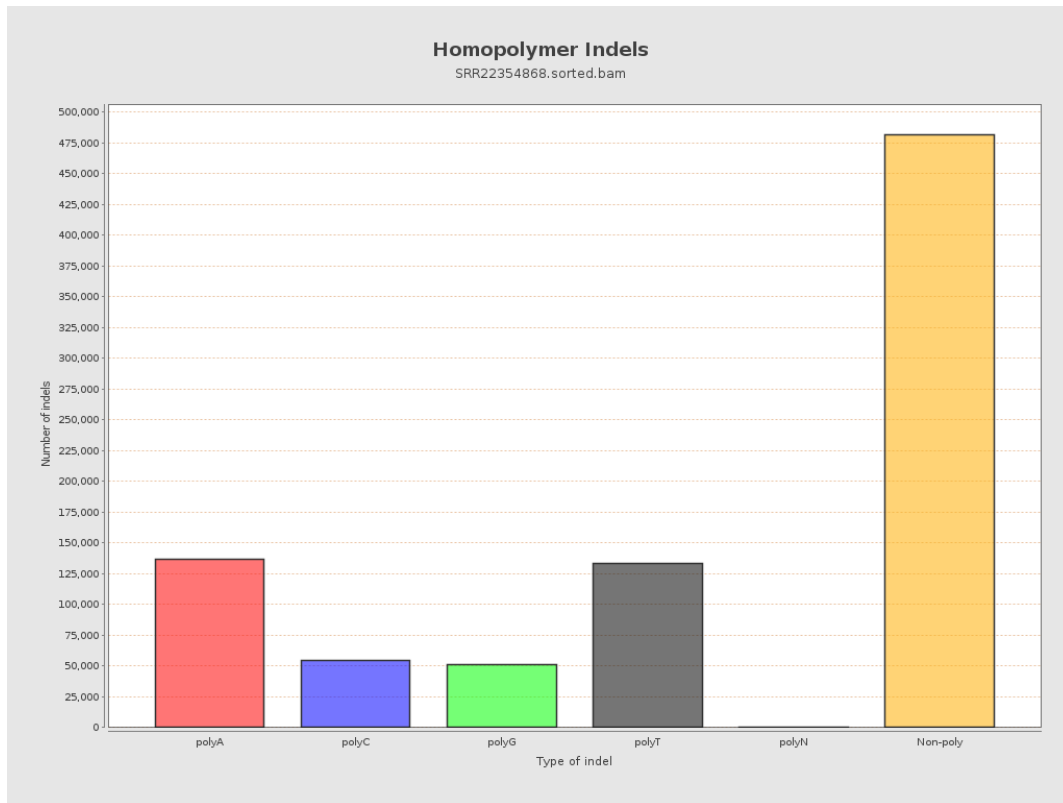
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

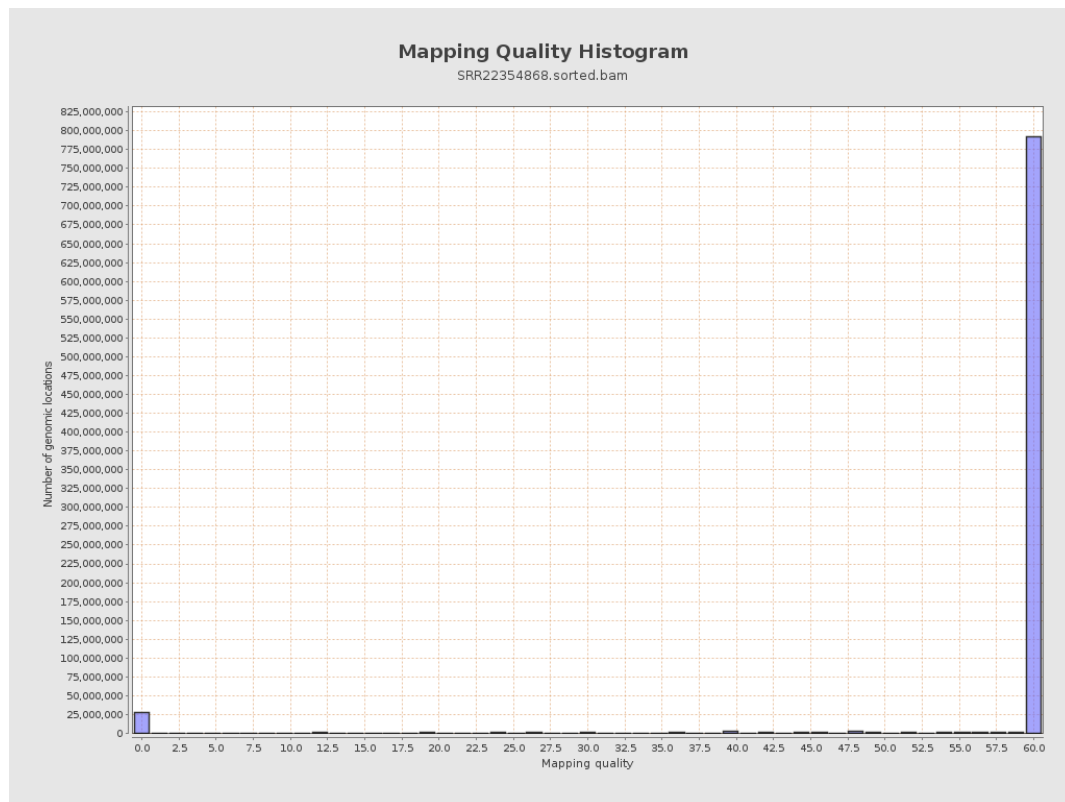


## 12. Results : Mapping Quality Across Reference

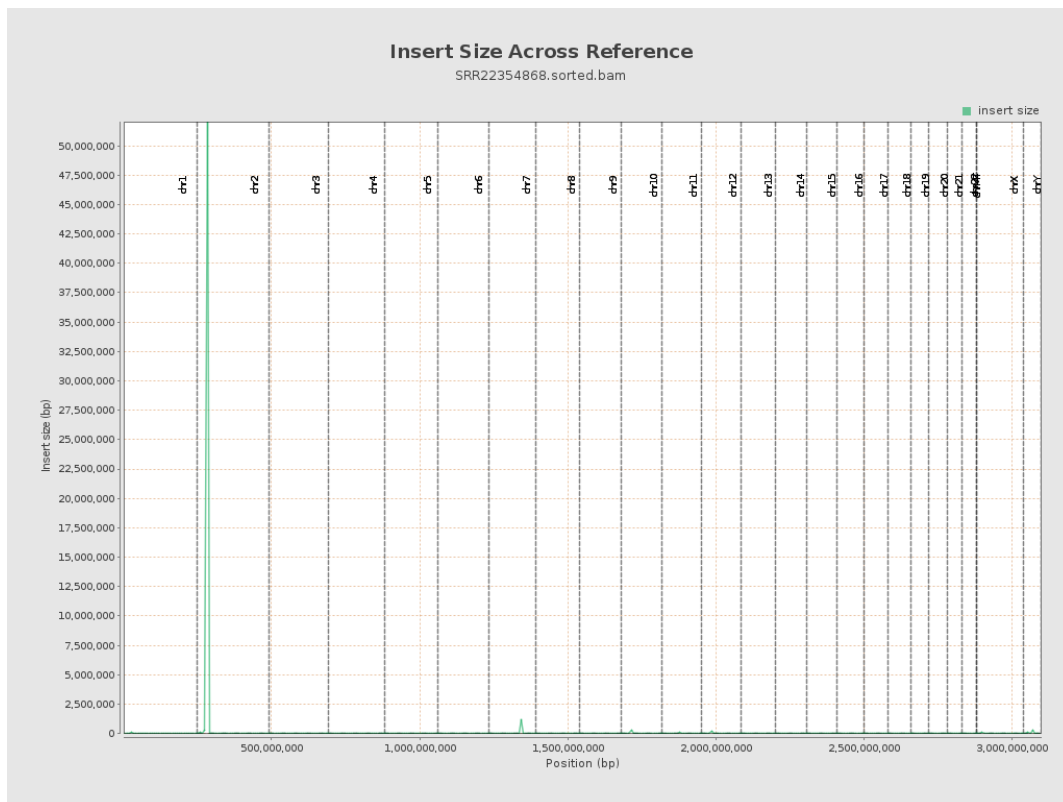




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

