

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/10 06:42:24*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124929.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_SRR3124929 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124929_1.fastq.gz SRR3124929_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                  |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                   |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                   |
| Analysis date:                        | Tue Dec 10 06:42:24 CST 2024                                                                                                                                                                                         |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                    |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                   |
| Number of windows:                    | 400                                                                                                                                                                                                                  |
| BAM file:                             | SRR3124929.sorted.bam                                                                                                                                                                                                |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 1,743,620          |
| Mapped reads                 | 1,718,073 / 98.53% |
| Unmapped reads               | 25,547 / 1.47%     |
| Mapped paired reads          | 1,718,073 / 98.53% |
| Mapped reads, first in pair  | 860,005 / 49.32%   |
| Mapped reads, second in pair | 858,068 / 49.21%   |
| Mapped reads, both in pair   | 1,713,126 / 98.25% |
| Mapped reads, singletons     | 4,947 / 0.28%      |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 13,144 / 0.75%     |
| Read min/max/mean length     | 30 / 151 / 151.37  |
| Duplicated reads (estimated) | 234,232 / 13.43%   |
| Duplication rate             | 13.73%             |
| Clipped reads                | 1,247,629 / 71.55% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 68,246,232 / 29.29% |
| Number/percentage of C's | 46,825,986 / 20.1%  |
| Number/percentage of T's | 68,240,633 / 29.29% |
| Number/percentage of G's | 49,679,895 / 21.32% |
| Number/percentage of N's | 24,001 / 0.01%      |
|                          |                     |

|               |        |
|---------------|--------|
| GC Percentage | 41.42% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.0753 |
| Standard Deviation | 0.8117 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 53.73 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 54,572.04       |
| Standard Deviation | 2,179,074.45    |
| P25/Median/P75     | 141 / 177 / 226 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 1.15%     |
| Mismatches                               | 2,605,491 |
| Insertions                               | 41,075    |
| Mapped reads with at least one insertion | 2.32%     |
| Deletions                                | 80,862    |
| Mapped reads with at least one deletion  | 4.56%     |
| Homopolymer indels                       | 47.5%     |

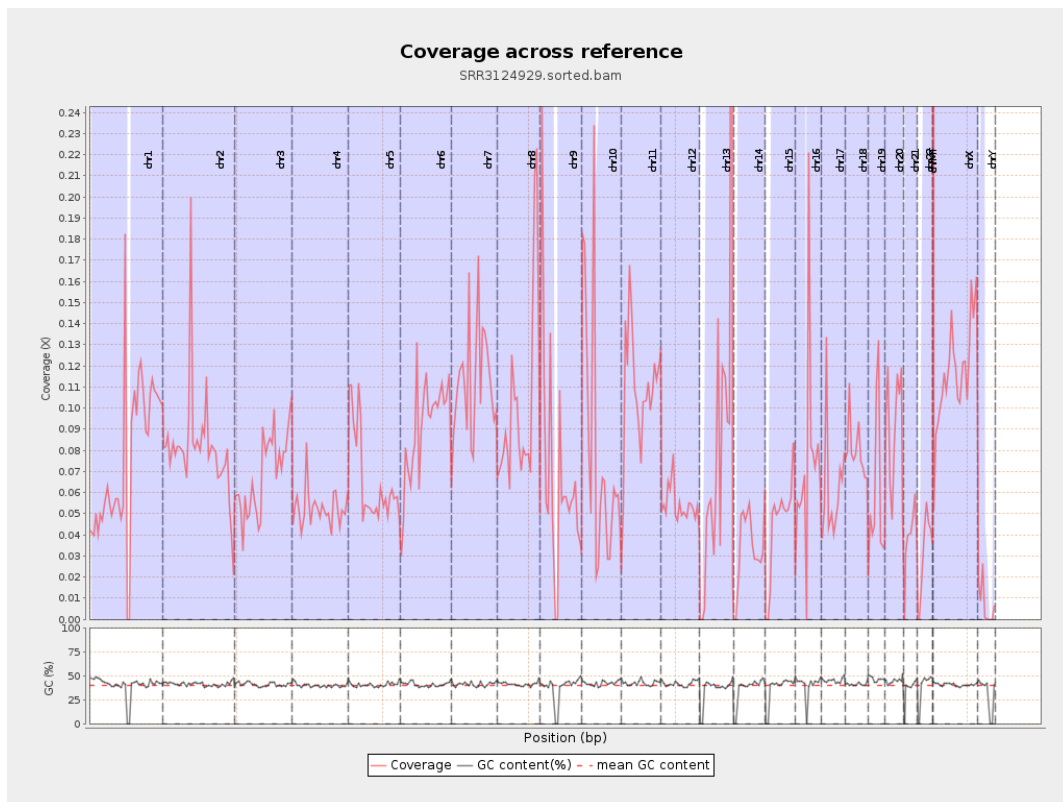
## 2.7. Chromosome stats

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

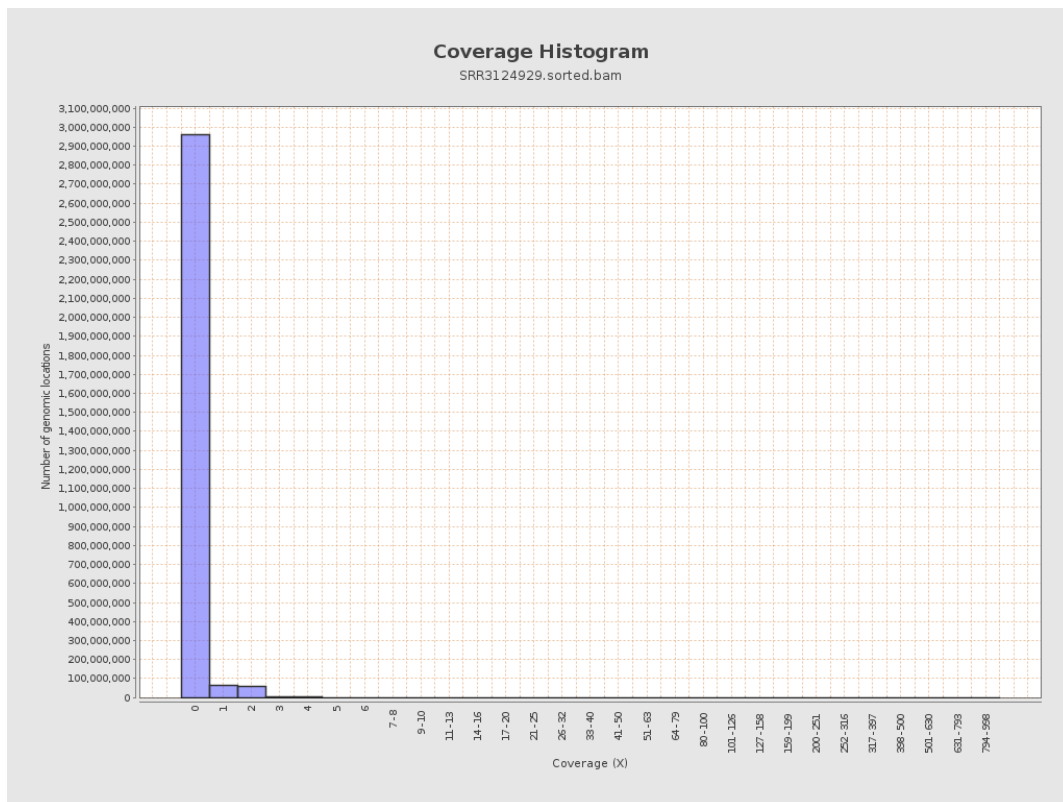
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 18814455     | 0.0755          | 1.0616           |
| chr2  | 243199373 | 19817868     | 0.0815          | 0.8467           |
| chr3  | 198022430 | 13559733     | 0.0685          | 0.3647           |
| chr4  | 191154276 | 10085322     | 0.0528          | 0.4535           |
| chr5  | 180915260 | 11885439     | 0.0657          | 0.3496           |
| chr6  | 171115067 | 15674720     | 0.0916          | 0.62             |
| chr7  | 159138663 | 17887861     | 0.1124          | 1.2005           |
| chr8  | 146364022 | 14993151     | 0.1024          | 0.5117           |
| chr9  | 141213431 | 9671281      | 0.0685          | 1.0636           |
| chr10 | 135534747 | 10612389     | 0.0783          | 1.8974           |
| chr11 | 135006516 | 14751244     | 0.1093          | 0.738            |
| chr12 | 133851895 | 7241650      | 0.0541          | 0.3158           |
| chr13 | 115169878 | 10607605     | 0.0921          | 0.5076           |
| chr14 | 107349540 | 3566705      | 0.0332          | 0.2568           |
| chr15 | 102531392 | 4673309      | 0.0456          | 0.2896           |
| chr16 | 90354753  | 6579367      | 0.0728          | 1.0532           |
| chr17 | 81195210  | 4944231      | 0.0609          | 0.9294           |
| chr18 | 78077248  | 6250667      | 0.0801          | 1.1667           |
| chr19 | 59128983  | 3603368      | 0.0609          | 0.6415           |
| chr20 | 63025520  | 5765969      | 0.0915          | 0.4334           |
| chr21 | 48129895  | 1862503      | 0.0387          | 0.3134           |
| chr22 | 51304566  | 1632823      | 0.0318          | 0.2403           |
| chrMT | 16571     | 96586        | 5.8286          | 4.3433           |
| chrX  | 155270560 | 18156694     | 0.1169          | 0.5634           |

|      |          |        |        |        |
|------|----------|--------|--------|--------|
| chrY | 59373566 | 425521 | 0.0072 | 0.4235 |
|------|----------|--------|--------|--------|

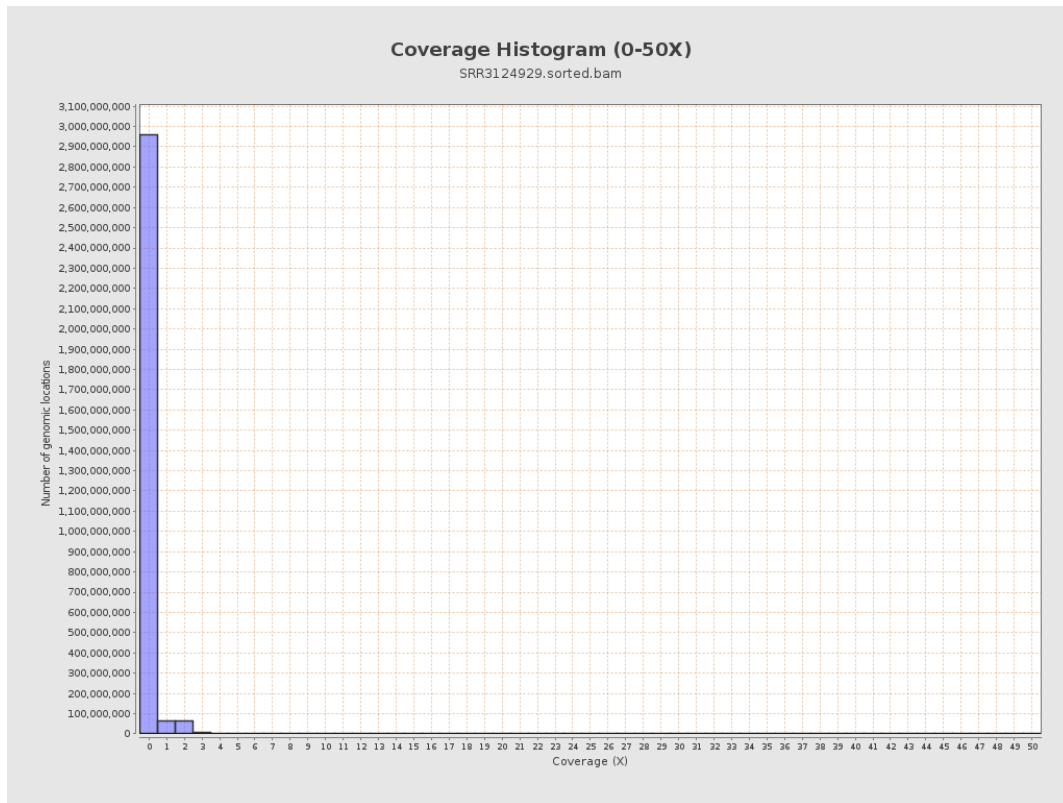
### 3. Results : Coverage across reference



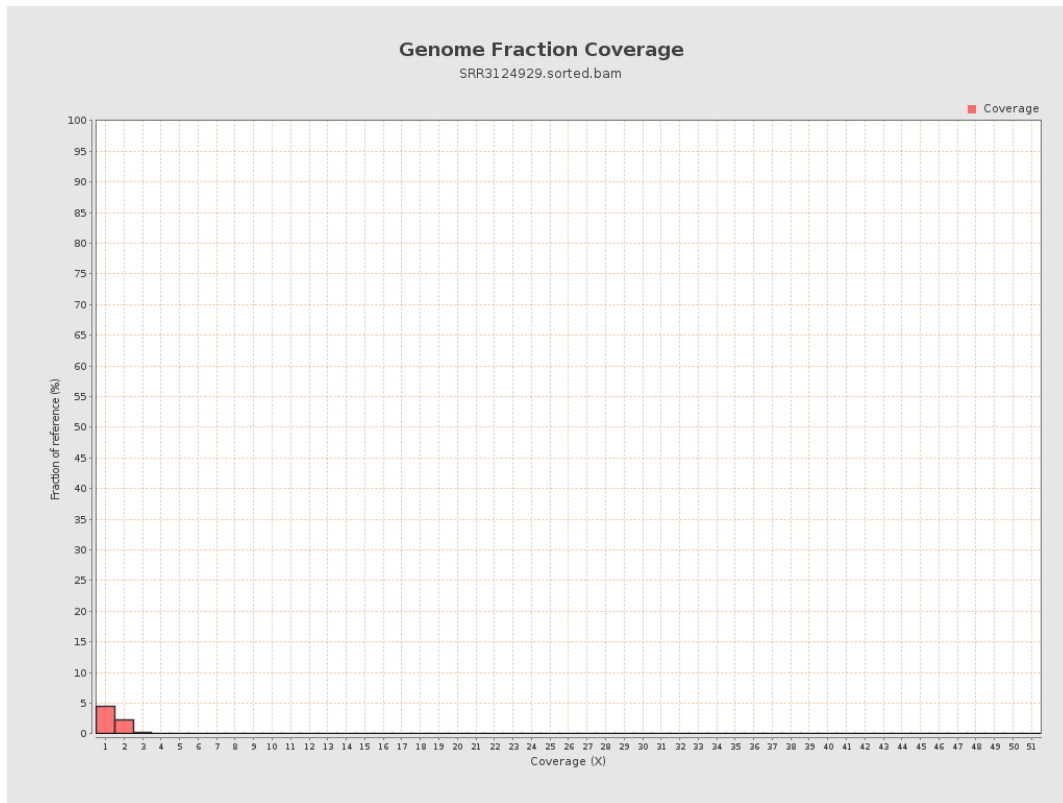
## 4. Results : Coverage Histogram



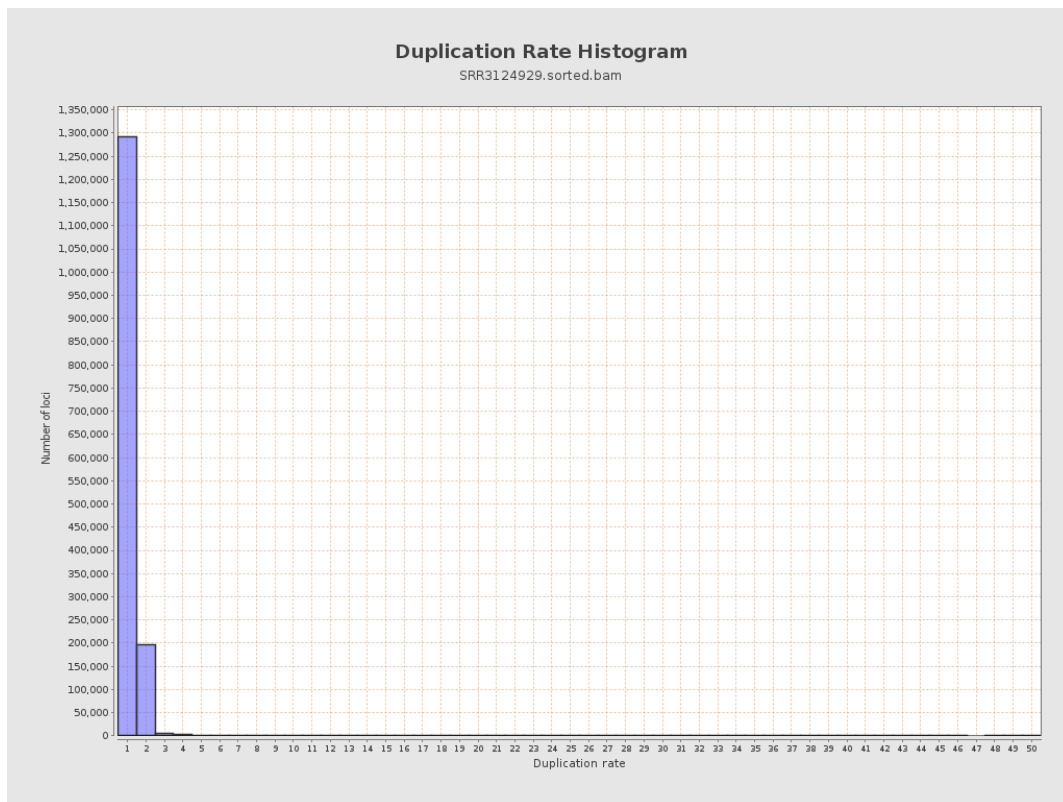
## 5. Results : Coverage Histogram (0-50X)



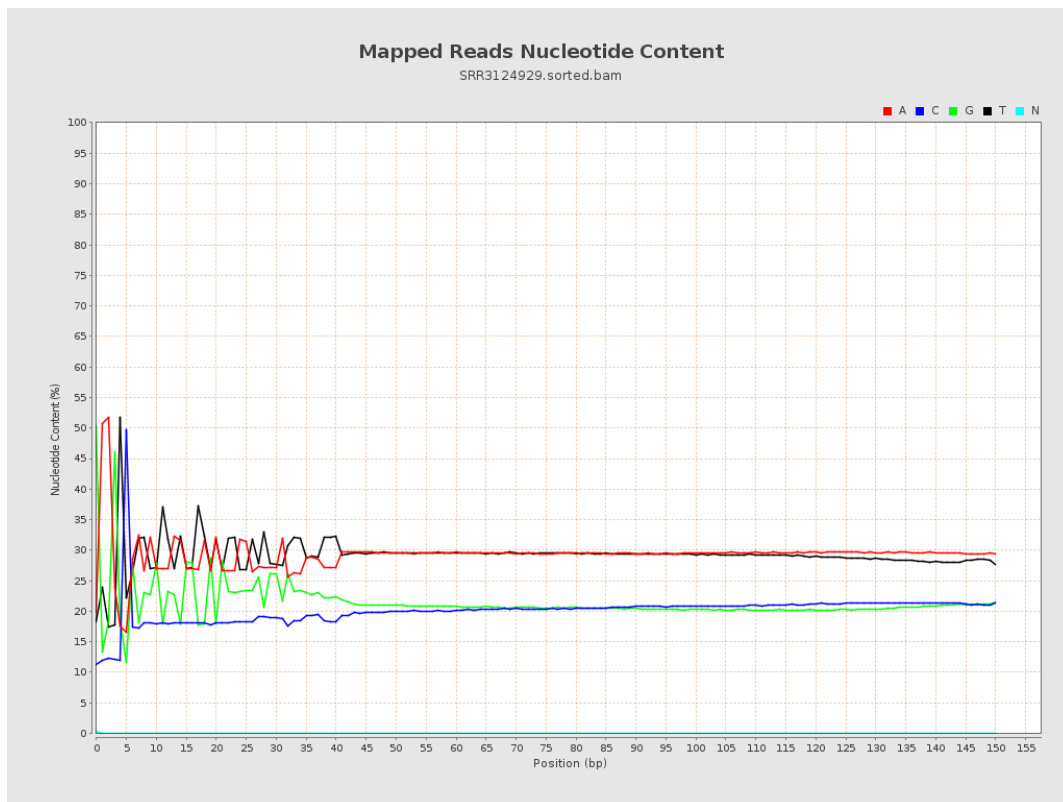
## 6. Results : Genome Fraction Coverage



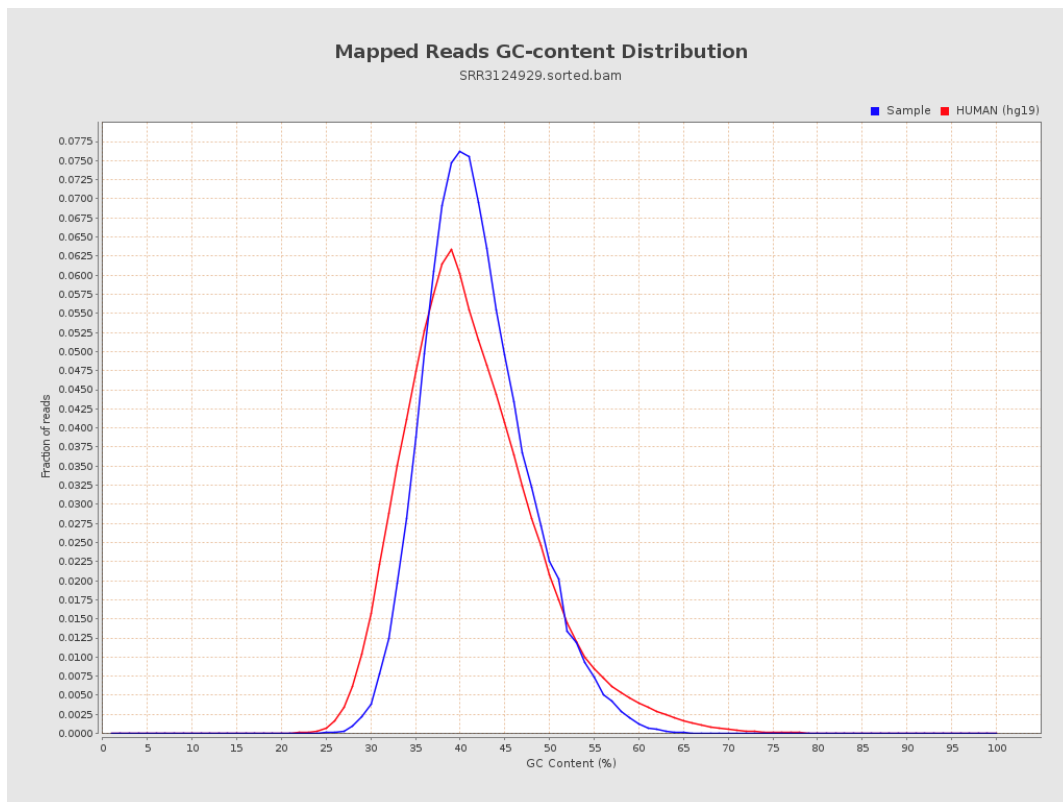
## 7. Results : Duplication Rate Histogram



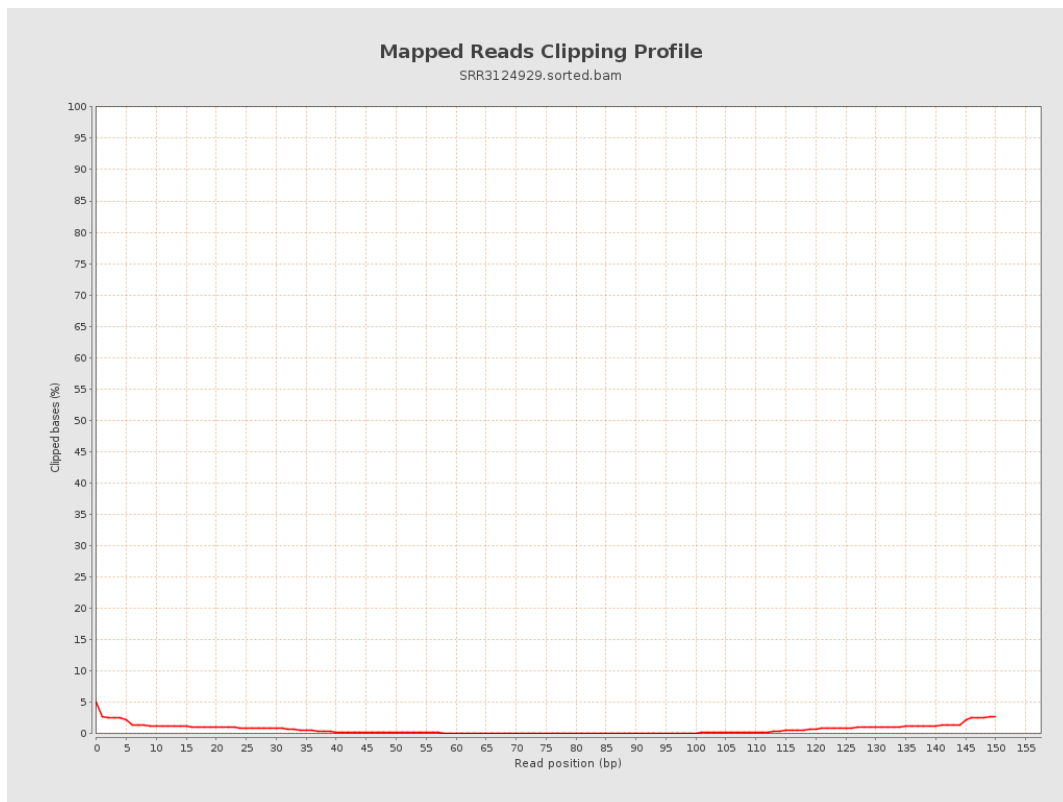
## 8. Results : Mapped Reads Nucleotide Content



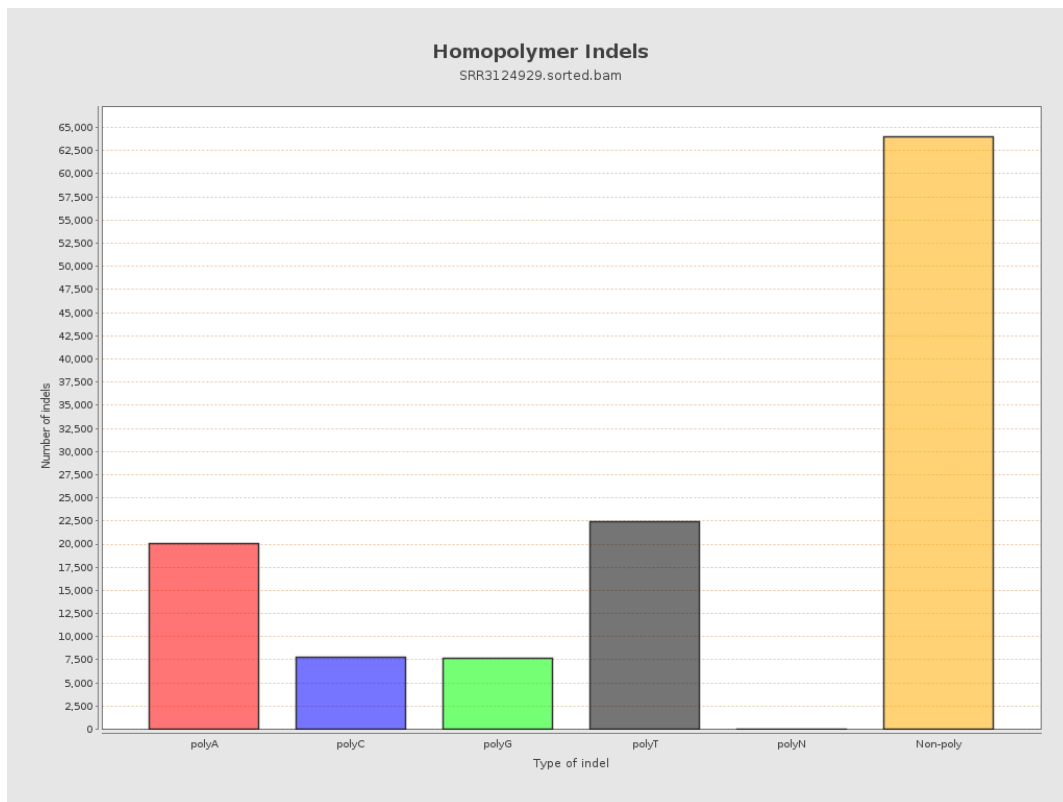
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



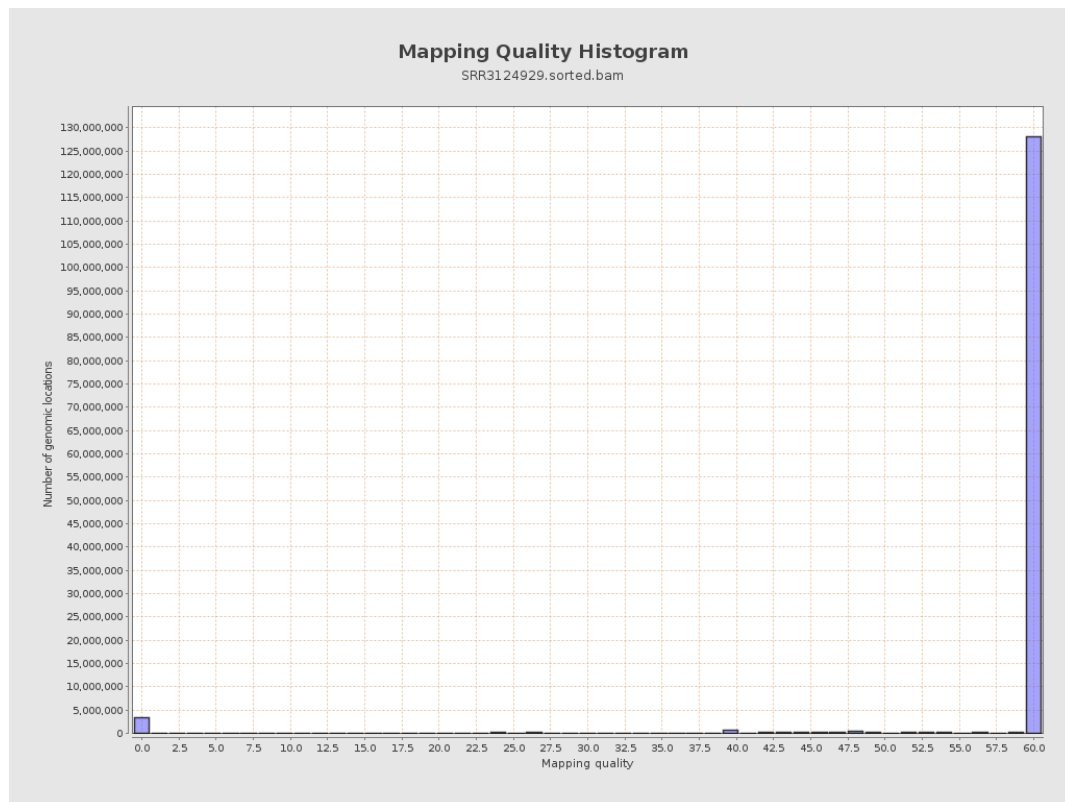
## 11. Results : Homopolymer Indels



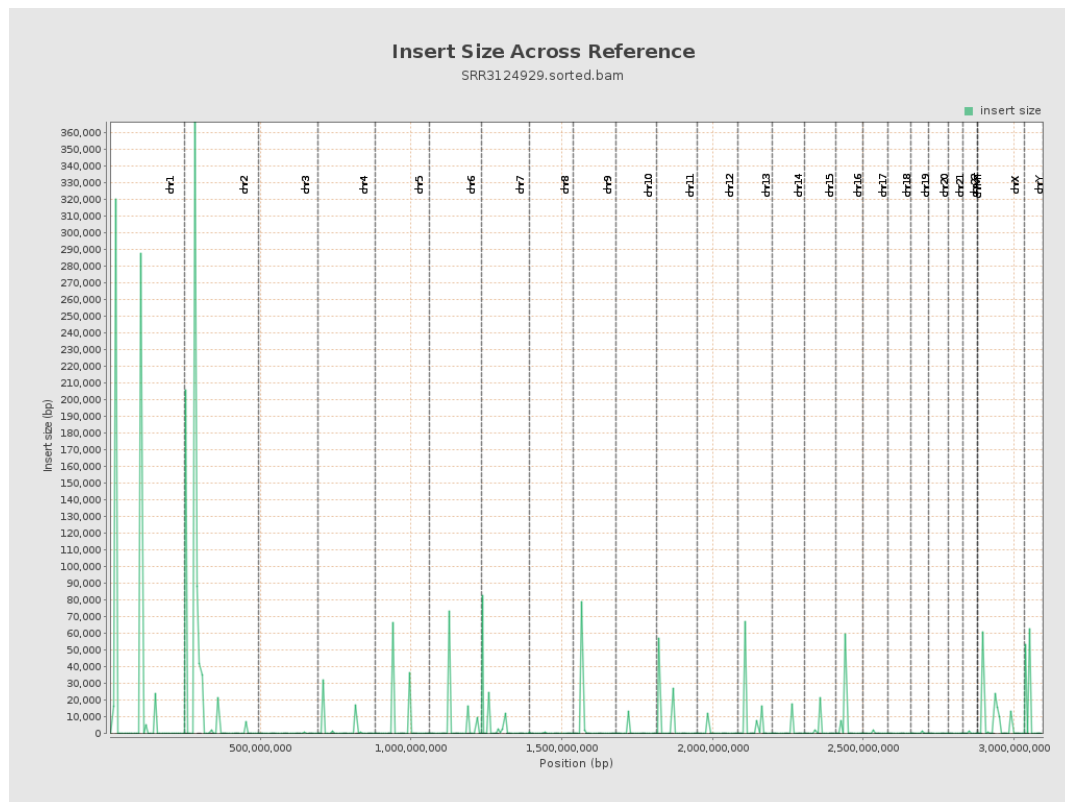
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

