

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 21:41:36*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472526.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_SRR3472526 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472526_1.fastq.gz SRR3472526_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                  |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                   |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                   |
| Analysis date:                        | Sat Aug 24 21:41:35 CST 2024                                                                                                                                                                                         |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                    |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                   |
| Number of windows:                    | 400                                                                                                                                                                                                                  |
| BAM file:                             | SRR3472526.sorted.bam                                                                                                                                                                                                |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 15,420,032          |
| Mapped reads                 | 15,251,129 / 98.9%  |
| Unmapped reads               | 168,903 / 1.1%      |
| Mapped paired reads          | 15,251,129 / 98.9%  |
| Mapped reads, first in pair  | 7,645,834 / 49.58%  |
| Mapped reads, second in pair | 7,605,295 / 49.32%  |
| Mapped reads, both in pair   | 15,166,428 / 98.36% |
| Mapped reads, singletons     | 84,701 / 0.55%      |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 66,858 / 0.43%      |
| Read min/max/mean length     | 30 / 100 / 100.18   |
| Duplicated reads (estimated) | 9,413,487 / 61.05%  |
| Duplication rate             | 44.9%               |
| Clipped reads                | 1,458,530 / 9.46%   |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 407,210,623 / 27.2%  |
| Number/percentage of C's | 343,694,808 / 22.96% |
| Number/percentage of T's | 404,287,000 / 27%    |
| Number/percentage of G's | 341,657,243 / 22.82% |
| Number/percentage of N's | 232,745 / 0.02%      |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 45.78% |
|---------------|--------|

## 2.3. Coverage

|                    |         |
|--------------------|---------|
| Mean               | 0.4837  |
| Standard Deviation | 17.6578 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 54.92 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 31,806.98       |
| Standard Deviation | 1,767,382.32    |
| P25/Median/P75     | 157 / 219 / 297 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.59%     |
| Mismatches                               | 8,607,354 |
| Insertions                               | 82,936    |
| Mapped reads with at least one insertion | 0.54%     |
| Deletions                                | 71,614    |
| Mapped reads with at least one deletion  | 0.46%     |
| Homopolymer indels                       | 44.28%    |

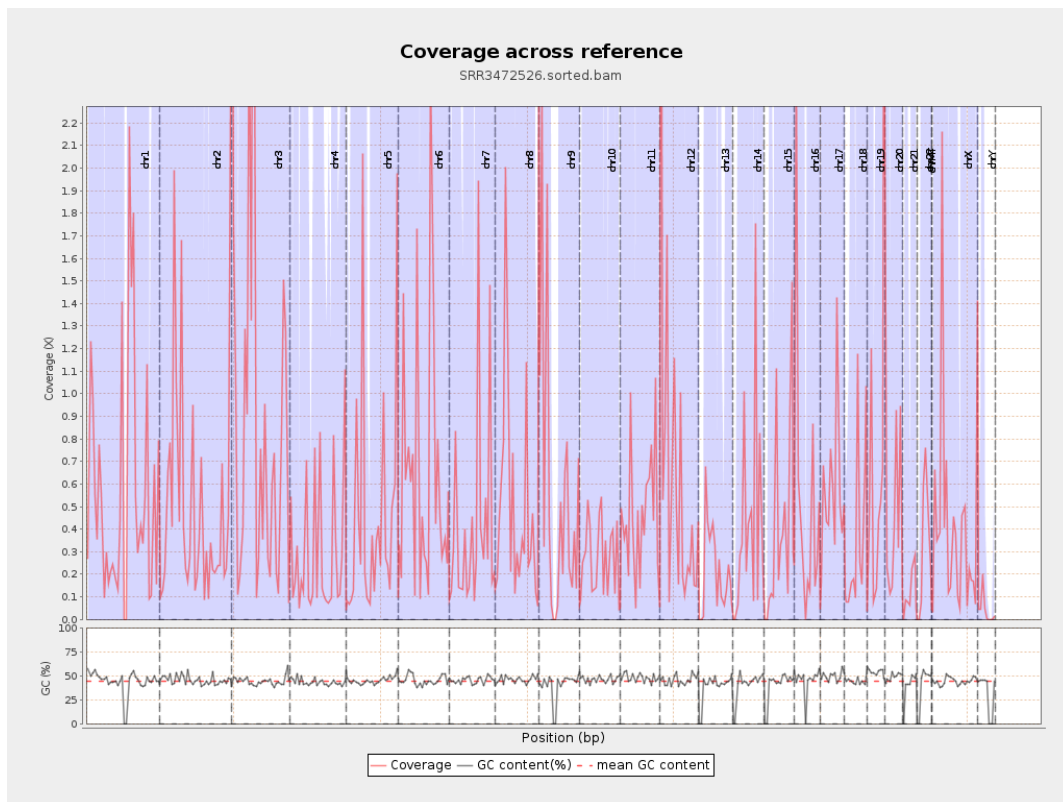
## 2.7. Chromosome stats

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

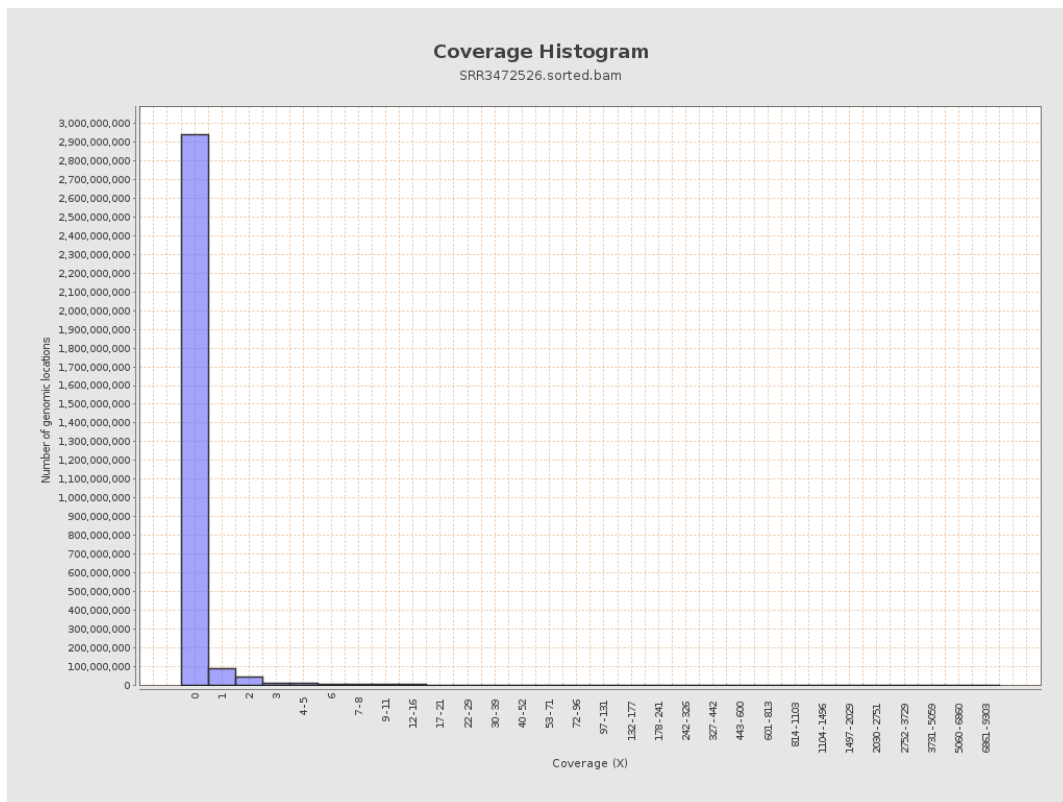
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 143488004    | 0.5757          | 19.6643          |
| chr2  | 243199373 | 120115630    | 0.4939          | 18.7791          |
| chr3  | 198022430 | 188568865    | 0.9523          | 25.3165          |
| chr4  | 191154276 | 55612462     | 0.2909          | 10.8596          |
| chr5  | 180915260 | 83047577     | 0.459           | 19.3608          |
| chr6  | 171115067 | 110549261    | 0.6461          | 18.9495          |
| chr7  | 159138663 | 65504337     | 0.4116          | 14.254           |
| chr8  | 146364022 | 73091461     | 0.4994          | 26.3253          |
| chr9  | 141213431 | 79469433     | 0.5628          | 14.0108          |
| chr10 | 135534747 | 37993421     | 0.2803          | 9.5069           |
| chr11 | 135006516 | 63660790     | 0.4715          | 14.3535          |
| chr12 | 133851895 | 91532783     | 0.6838          | 24.7752          |
| chr13 | 115169878 | 25366932     | 0.2203          | 8.1499           |
| chr14 | 107349540 | 44865403     | 0.4179          | 26.9549          |
| chr15 | 102531392 | 42475868     | 0.4143          | 15.1937          |
| chr16 | 90354753  | 45920439     | 0.5082          | 17.1082          |
| chr17 | 81195210  | 46212391     | 0.5692          | 13.0849          |
| chr18 | 78077248  | 27642685     | 0.354           | 14.1689          |
| chr19 | 59128983  | 33519293     | 0.5669          | 15.4423          |
| chr20 | 63025520  | 31115477     | 0.4937          | 14.2954          |
| chr21 | 48129895  | 5991207      | 0.1245          | 4.3922           |
| chr22 | 51304566  | 16399405     | 0.3196          | 11.1792          |
| chrMT | 16571     | 1520         | 0.0917          | 0.4011           |
| chrX  | 155270560 | 62481438     | 0.4024          | 11.5469          |

|      |          |         |        |        |
|------|----------|---------|--------|--------|
| chrY | 59373566 | 2654270 | 0.0447 | 1.7763 |
|------|----------|---------|--------|--------|

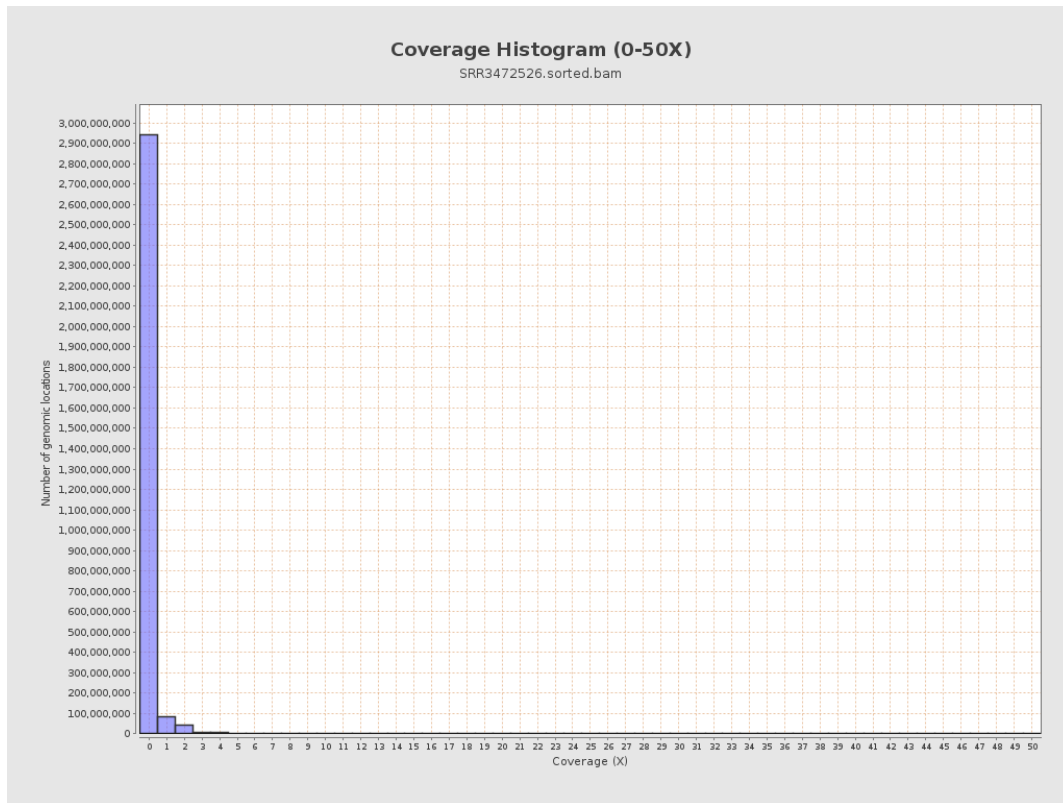
### 3. Results : Coverage across reference



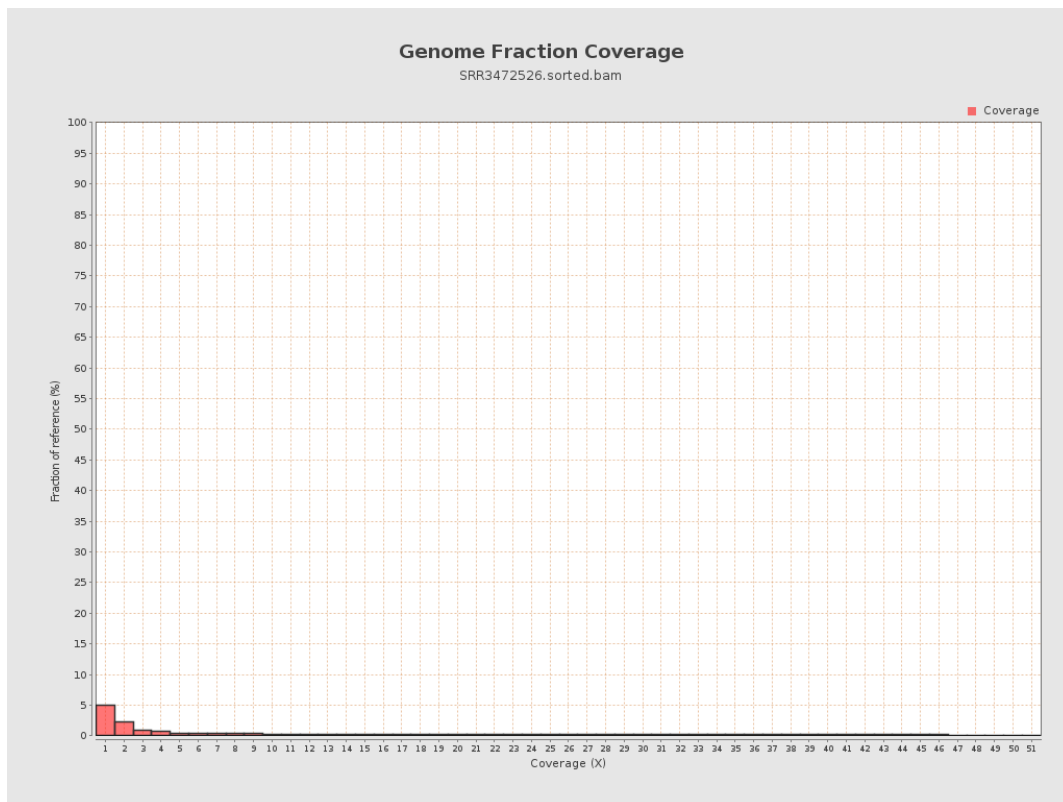
## 4. Results : Coverage Histogram



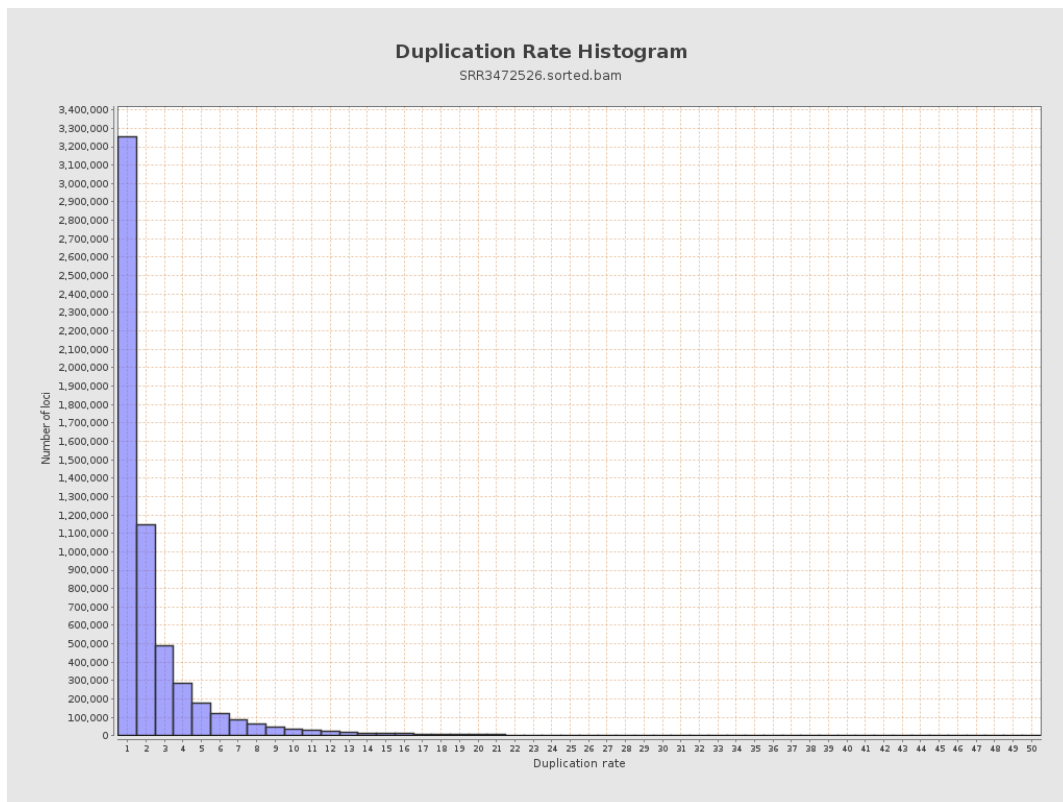
## 5. Results : Coverage Histogram (0-50X)



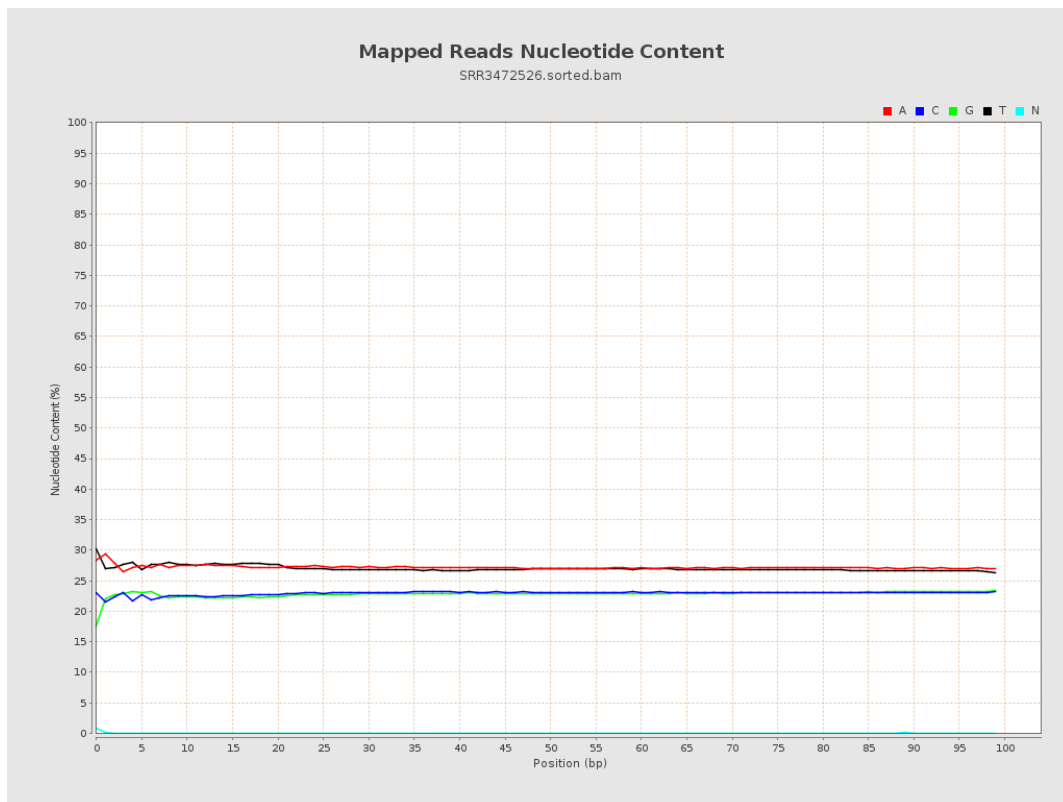
## 6. Results : Genome Fraction Coverage



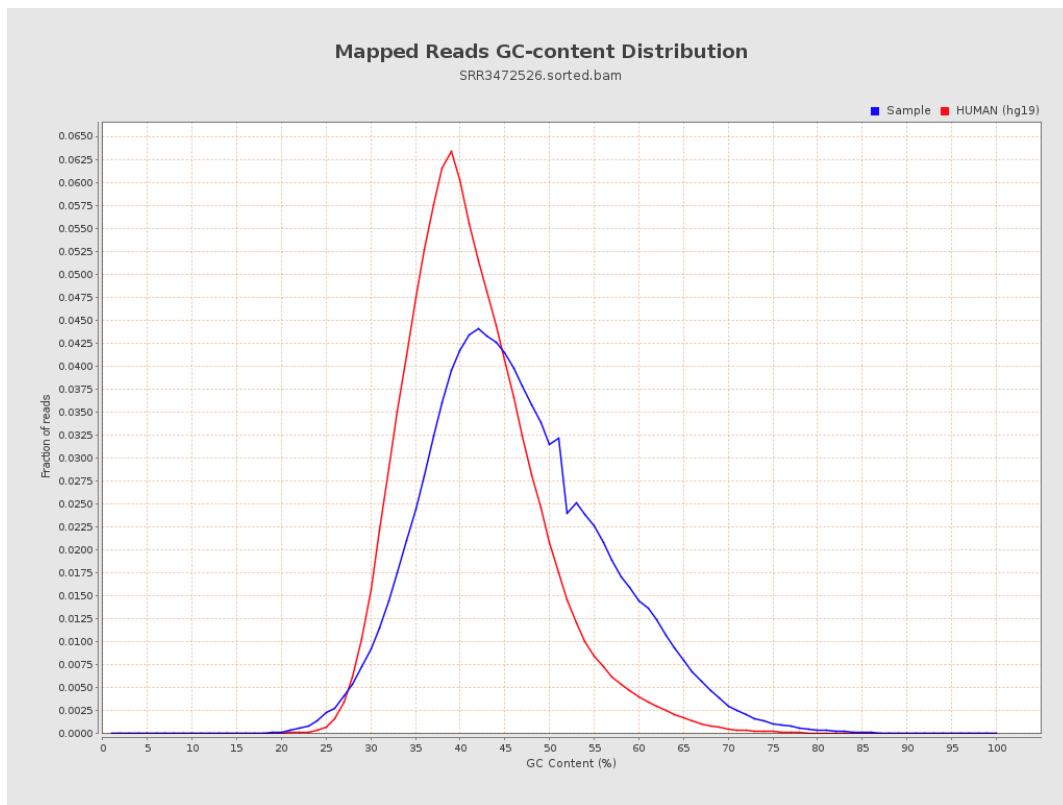
## 7. Results : Duplication Rate Histogram



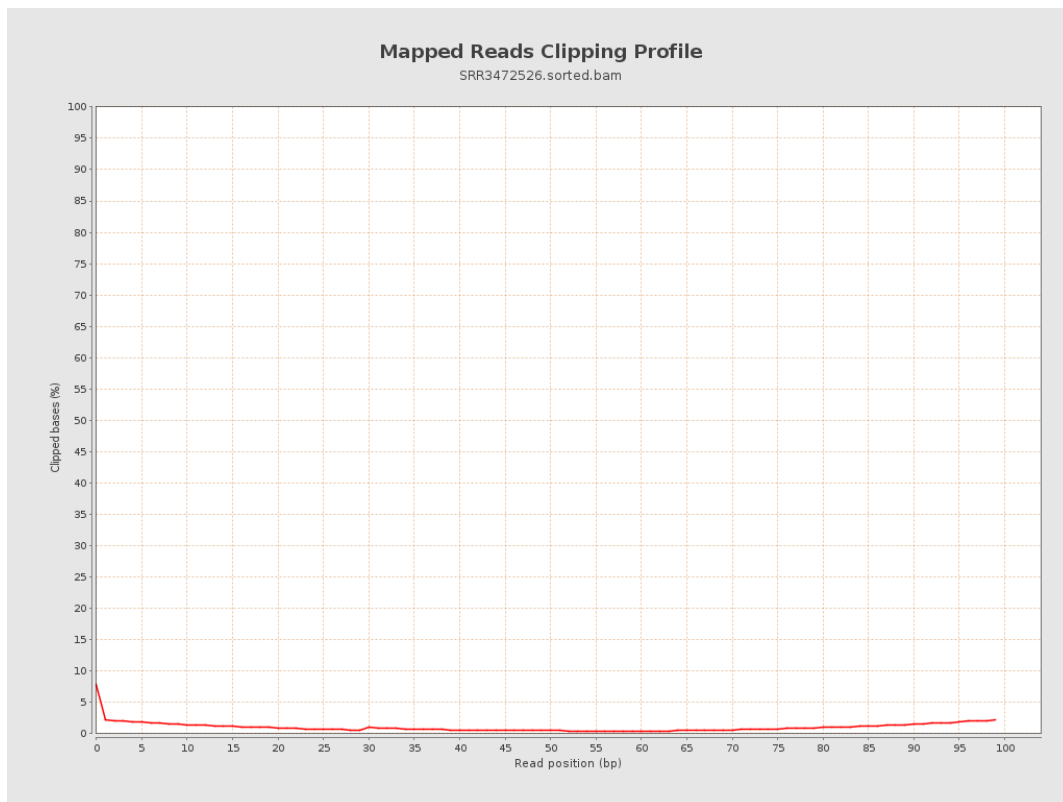
## 8. Results : Mapped Reads Nucleotide Content



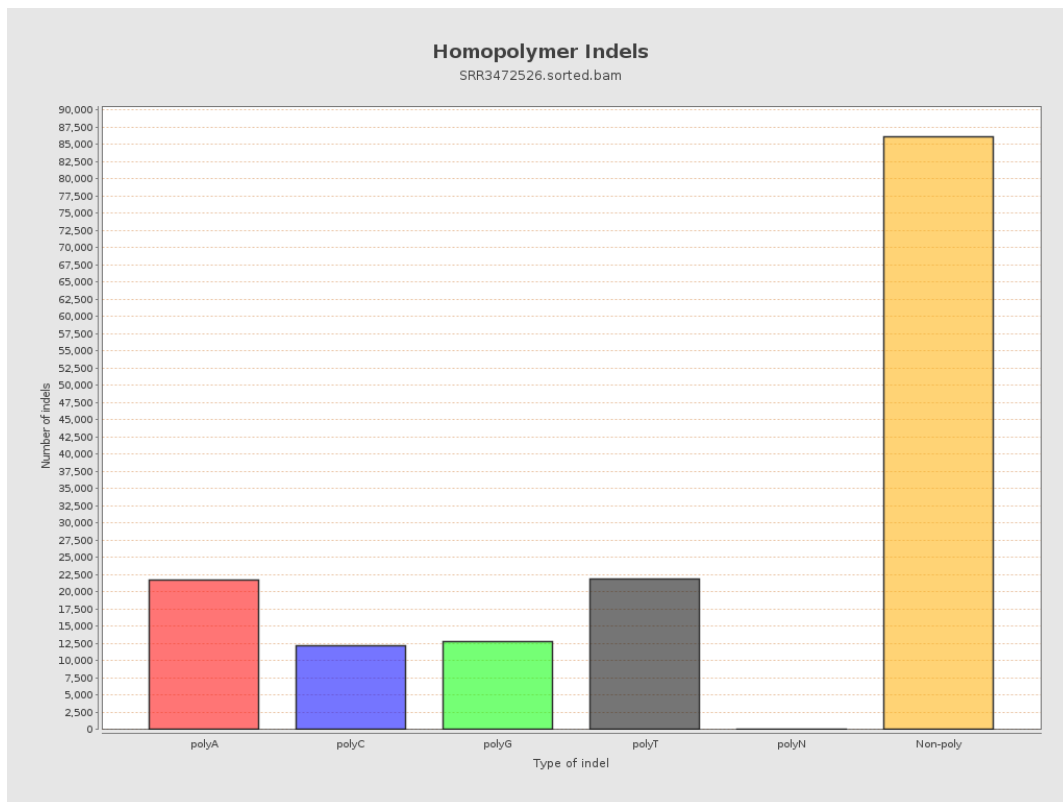
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



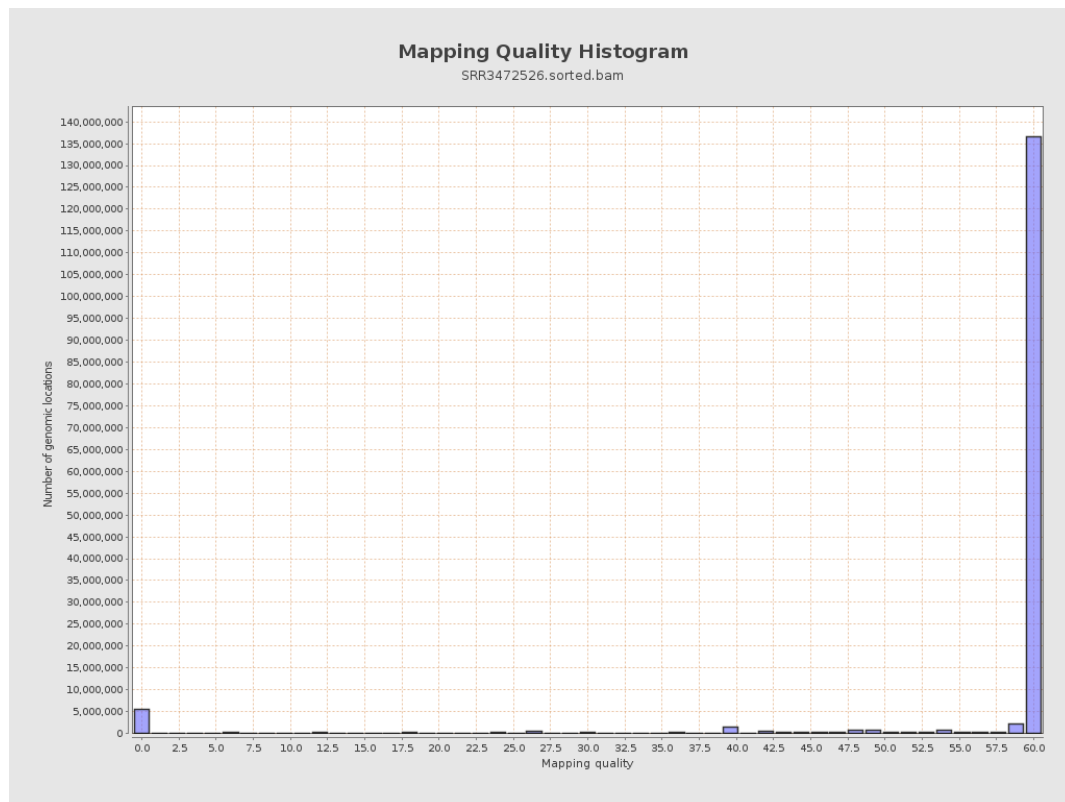
## 11. Results : Homopolymer Indels



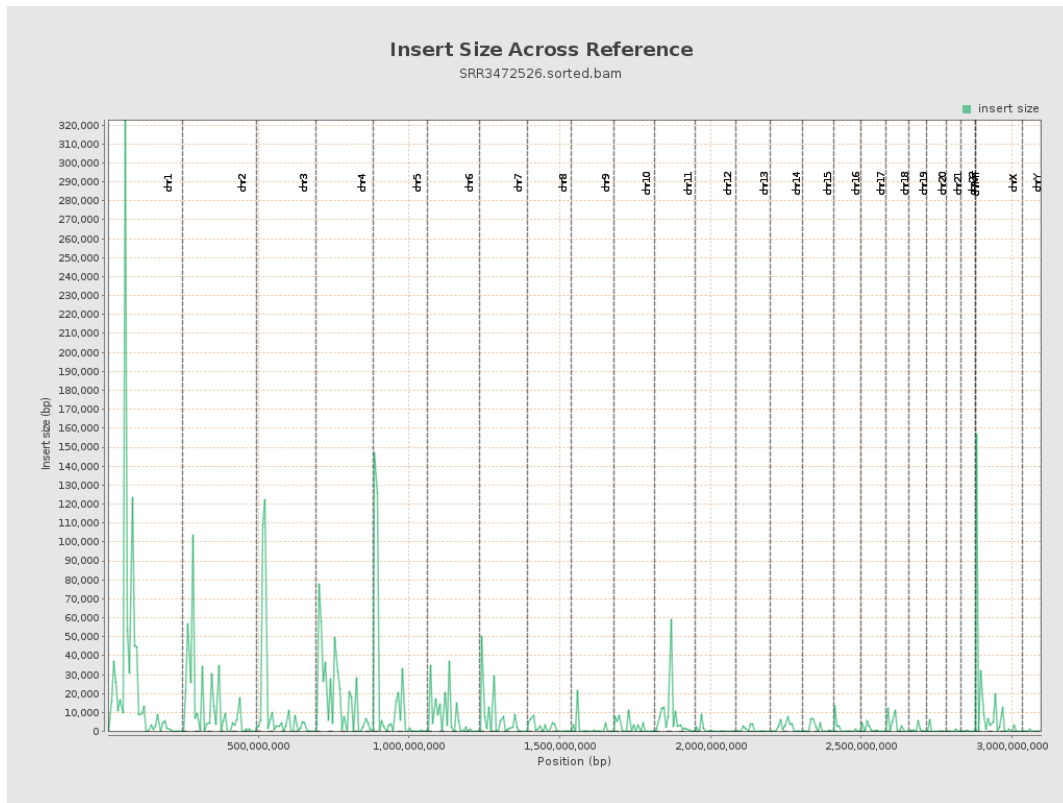
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

