

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 02:28:02*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10156409.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_SRR10156409 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10156409_1.fastq.gz SRR10156409_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                     |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                      |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                      |
| Analysis date:                        | Tue Sep 03 02:27:58 CST 2024                                                                                                                                                                                            |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                       |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                      |
| Number of windows:                    | 400                                                                                                                                                                                                                     |
| BAM file:                             | SRR10156409.sorted.bam                                                                                                                                                                                                  |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 7,638,424          |
| Mapped reads                 | 7,472,338 / 97.83% |
| Unmapped reads               | 166,086 / 2.17%    |
| Mapped paired reads          | 7,472,338 / 97.83% |
| Mapped reads, first in pair  | 3,735,860 / 48.91% |
| Mapped reads, second in pair | 3,736,478 / 48.92% |
| Mapped reads, both in pair   | 7,363,956 / 96.41% |
| Mapped reads, singletons     | 108,382 / 1.42%    |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 1,039,750 / 13.61% |
| Read min/max/mean length     | 30 / 133 / 125.86  |
| Duplicated reads (estimated) | 6,060,930 / 79.35% |
| Duplication rate             | 65.13%             |
| Clipped reads                | 4,091,436 / 53.56% |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 252,353,015 / 29.9%  |
| Number/percentage of C's | 167,129,993 / 19.8%  |
| Number/percentage of T's | 250,535,309 / 29.68% |
| Number/percentage of G's | 174,002,405 / 20.62% |
| Number/percentage of N's | 6,655 / 0%           |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 40.42% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.2728 |
| Standard Deviation | 5.1316 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 52.43 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 1,347,894.43    |
| Standard Deviation | 10,984,157.74   |
| P25/Median/P75     | 105 / 156 / 243 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.87%     |
| Mismatches                               | 7,076,810 |
| Insertions                               | 92,579    |
| Mapped reads with at least one insertion | 1.19%     |
| Deletions                                | 244,787   |
| Mapped reads with at least one deletion  | 3.19%     |
| Homopolymer indels                       | 40.75%    |

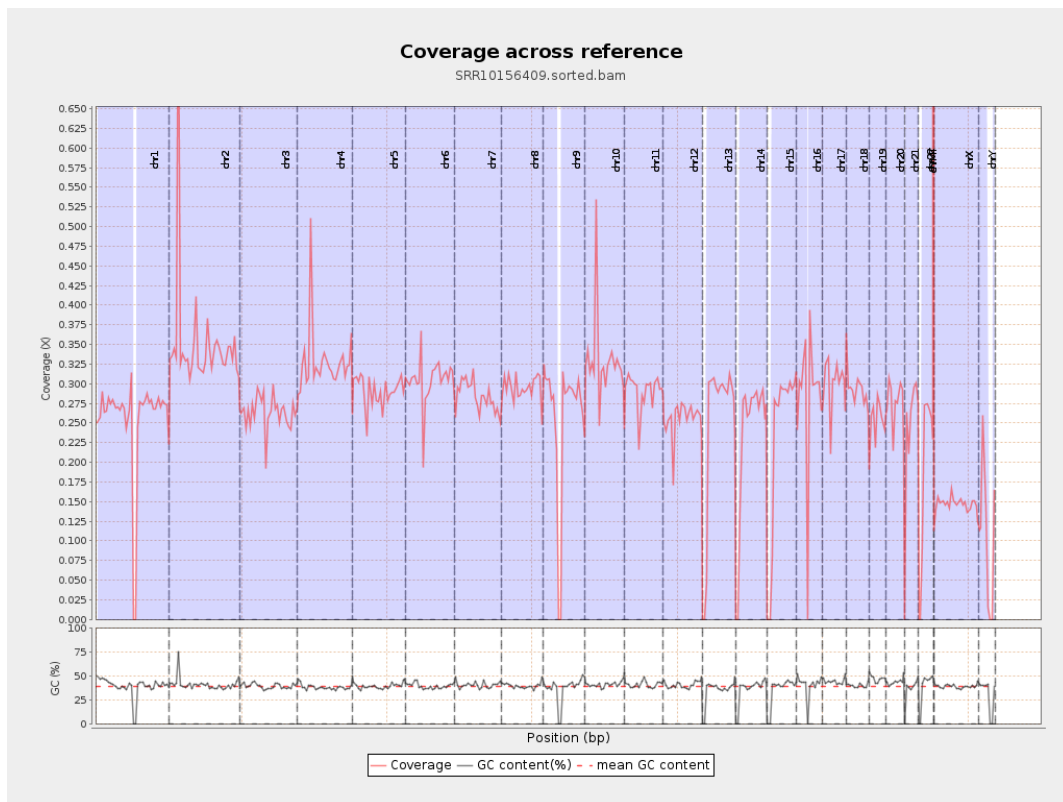
## 2.7. Chromosome stats

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

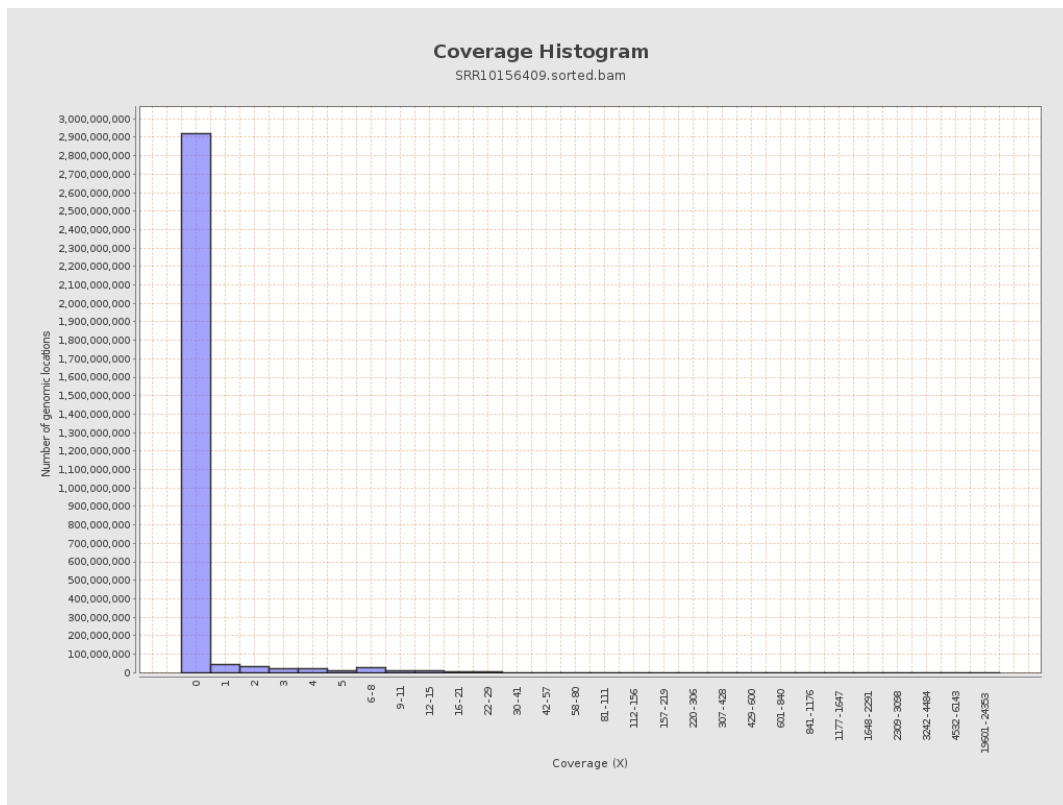
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 63564963     | 0.255           | 2.2355           |
| chr2  | 243199373 | 85794511     | 0.3528          | 16.9875          |
| chr3  | 198022430 | 52173488     | 0.2635          | 1.5435           |
| chr4  | 191154276 | 62489059     | 0.3269          | 2.4456           |
| chr5  | 180915260 | 52493136     | 0.2902          | 1.6379           |
| chr6  | 171115067 | 52092622     | 0.3044          | 1.9162           |
| chr7  | 159138663 | 45249876     | 0.2843          | 2.2005           |
| chr8  | 146364022 | 43189820     | 0.2951          | 2.5162           |
| chr9  | 141213431 | 36164494     | 0.2561          | 2.2203           |
| chr10 | 135534747 | 44625872     | 0.3293          | 2.7532           |
| chr11 | 135006516 | 39211568     | 0.2904          | 1.7142           |
| chr12 | 133851895 | 34143930     | 0.2551          | 1.5854           |
| chr13 | 115169878 | 28496419     | 0.2474          | 1.5233           |
| chr14 | 107349540 | 24873715     | 0.2317          | 1.4723           |
| chr15 | 102531392 | 23878020     | 0.2329          | 1.4797           |
| chr16 | 90354753  | 25648618     | 0.2839          | 2.0899           |
| chr17 | 81195210  | 24285027     | 0.2991          | 1.7867           |
| chr18 | 78077248  | 22852344     | 0.2927          | 2.9706           |
| chr19 | 59128983  | 15104093     | 0.2554          | 1.8853           |
| chr20 | 63025520  | 17450153     | 0.2769          | 1.6787           |
| chr21 | 48129895  | 11701505     | 0.2431          | 1.9001           |
| chr22 | 51304566  | 9477974      | 0.1847          | 1.5526           |
| chrMT | 16571     | 860230       | 51.9118         | 42.1654          |
| chrX  | 155270560 | 22776535     | 0.1467          | 1.1689           |

|      |          |         |        |        |
|------|----------|---------|--------|--------|
| chrY | 59373566 | 6014803 | 0.1013 | 1.6654 |
|------|----------|---------|--------|--------|

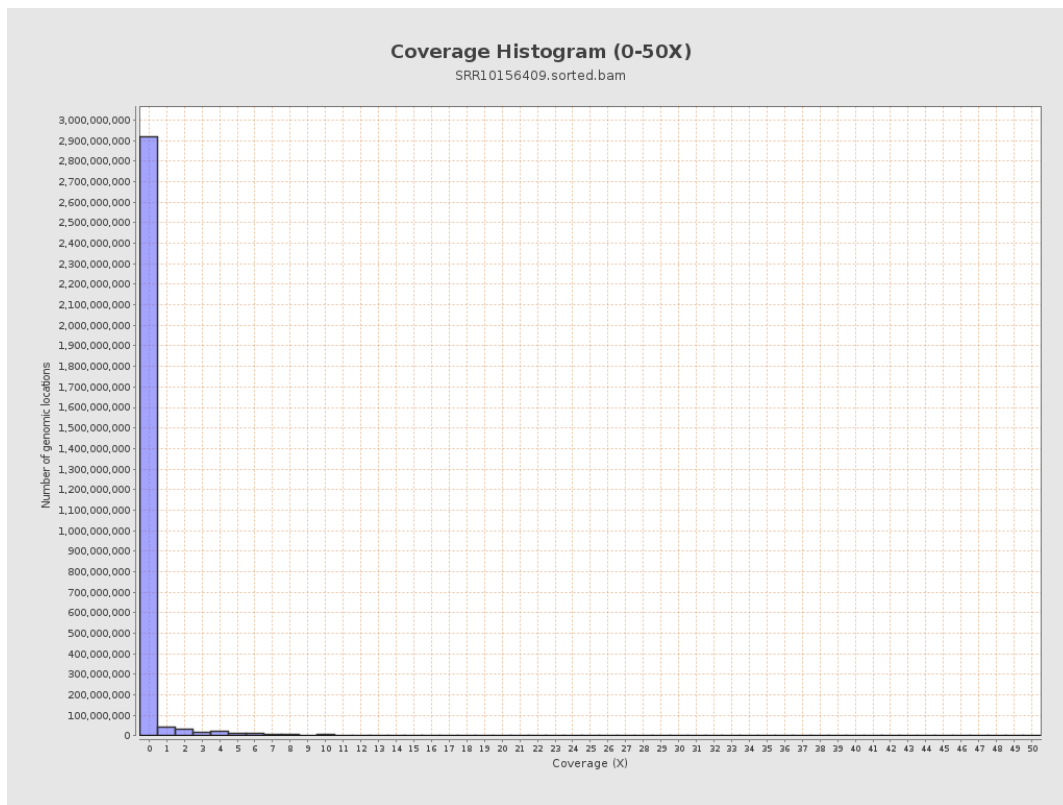
### 3. Results : Coverage across reference



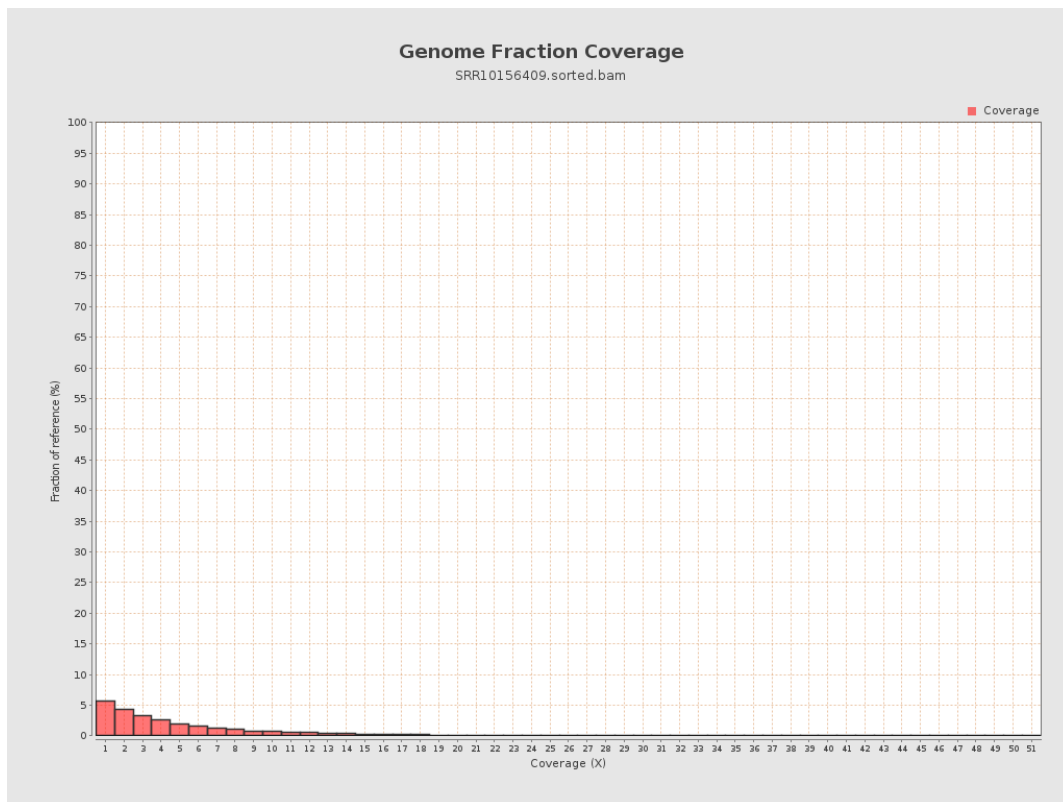
## 4. Results : Coverage Histogram



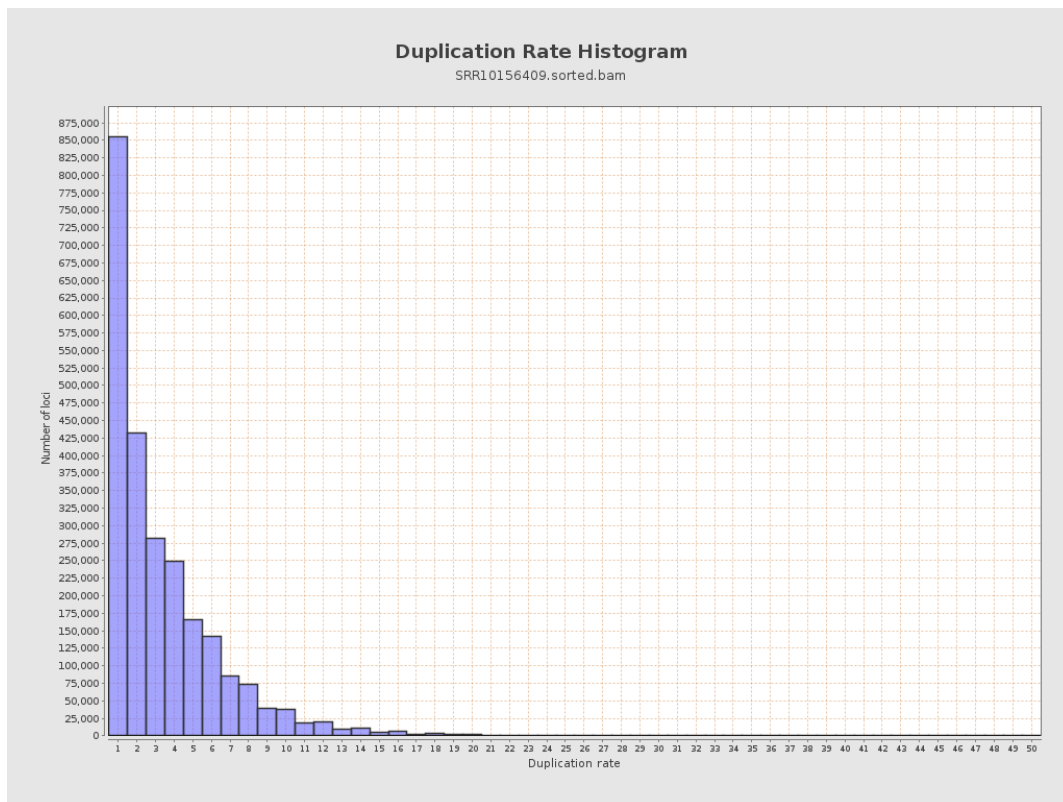
## 5. Results : Coverage Histogram (0-50X)



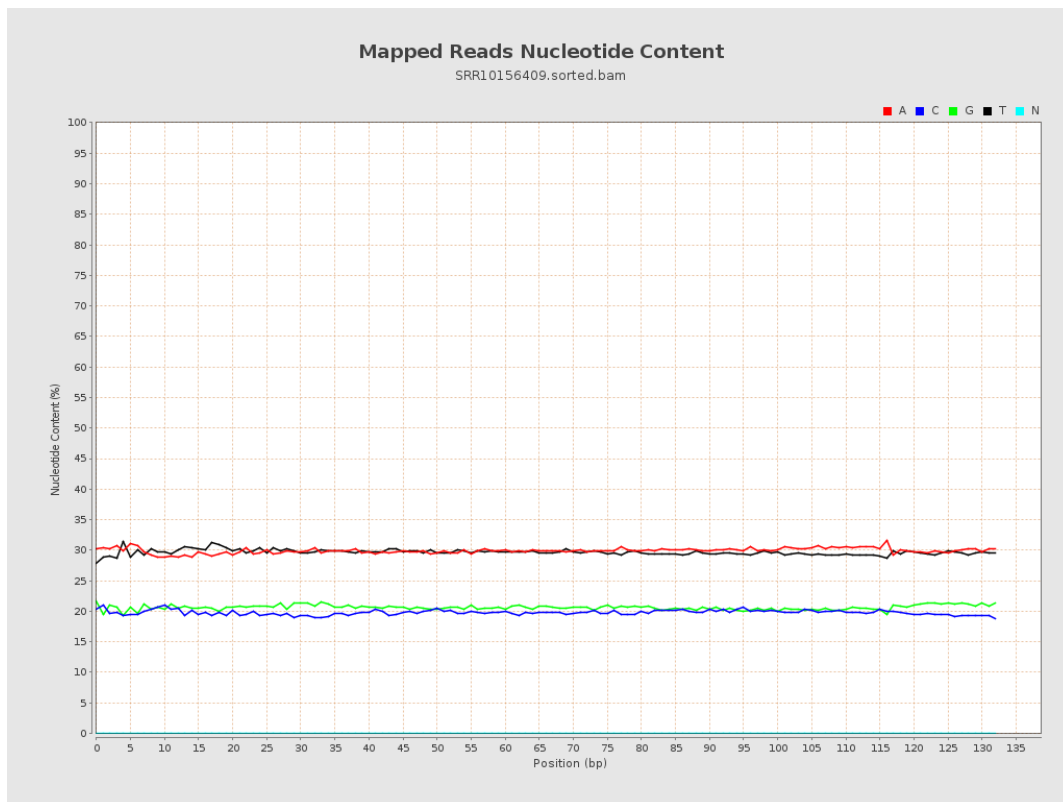
## 6. Results : Genome Fraction Coverage



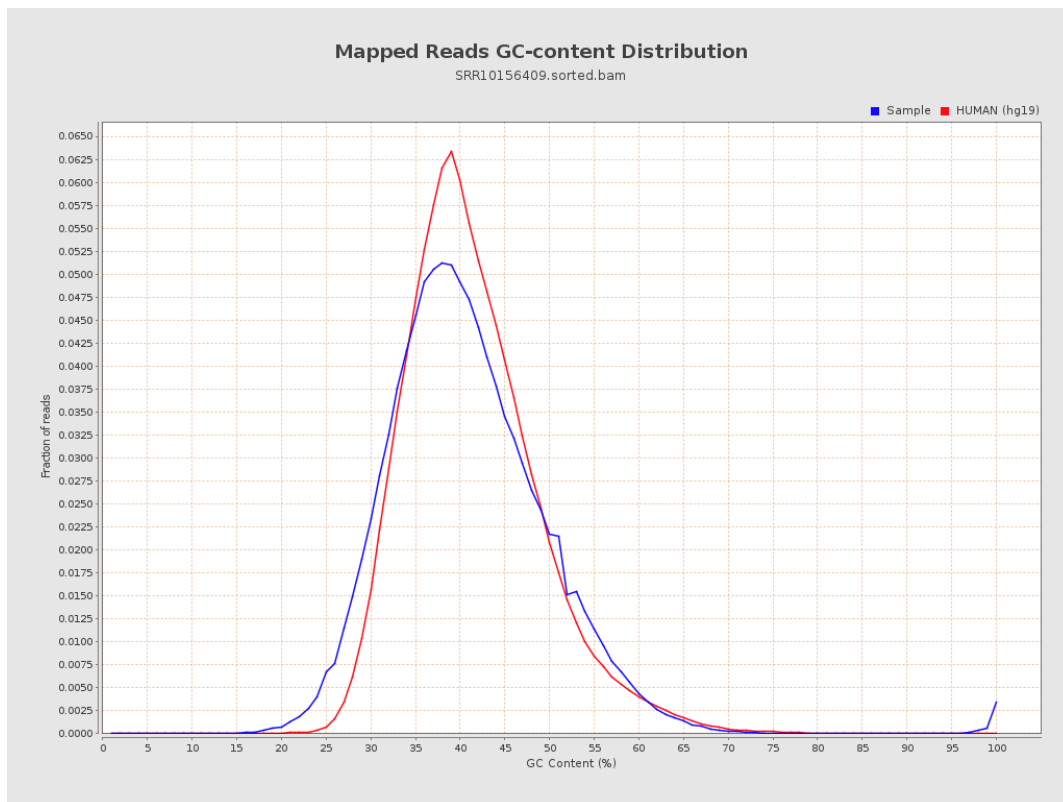
## 7. Results : Duplication Rate Histogram



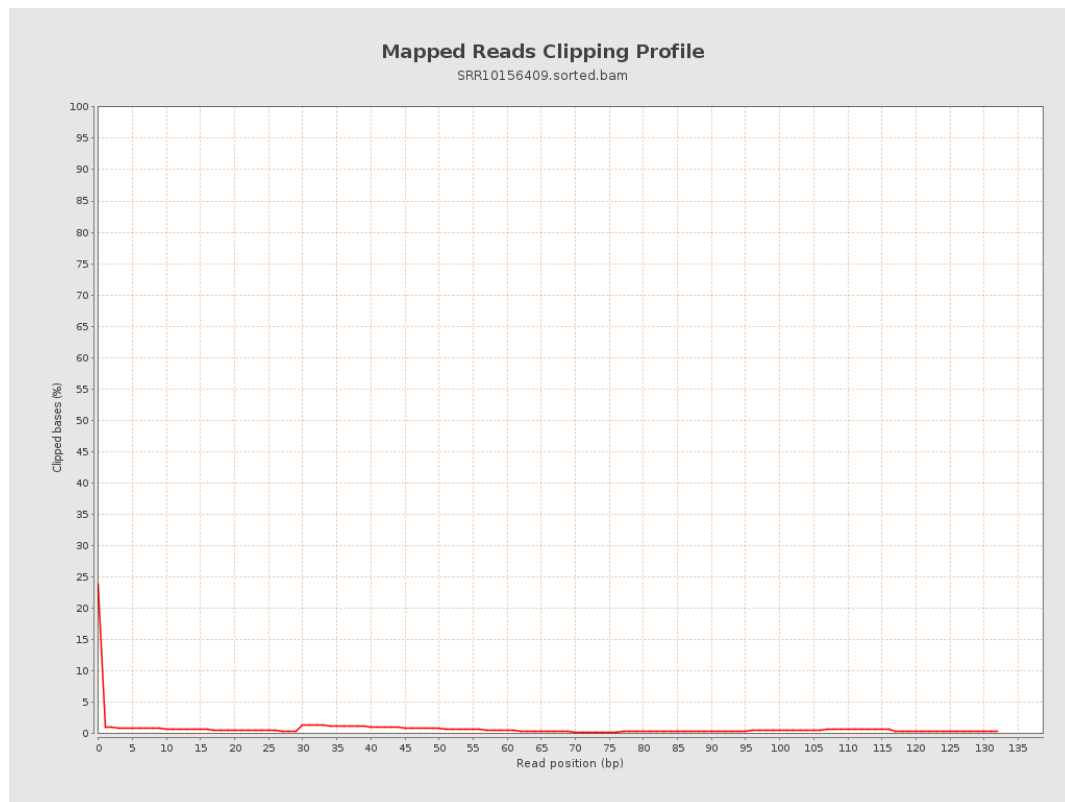
## 8. Results : Mapped Reads Nucleotide Content



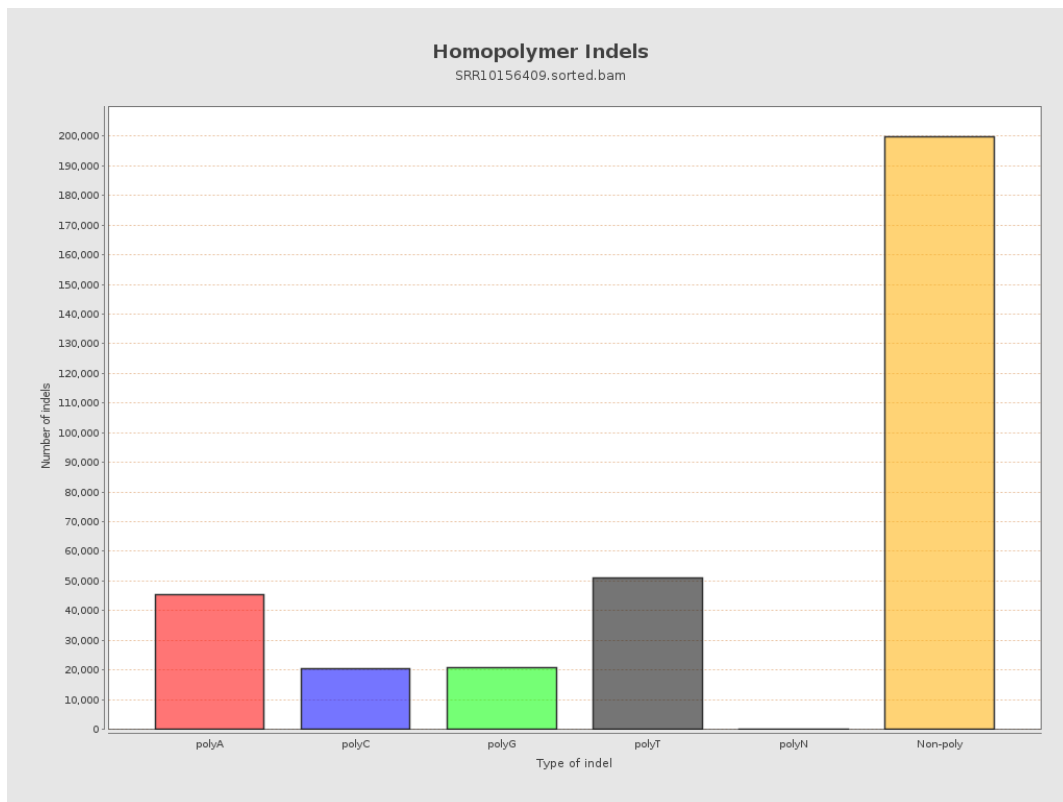
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



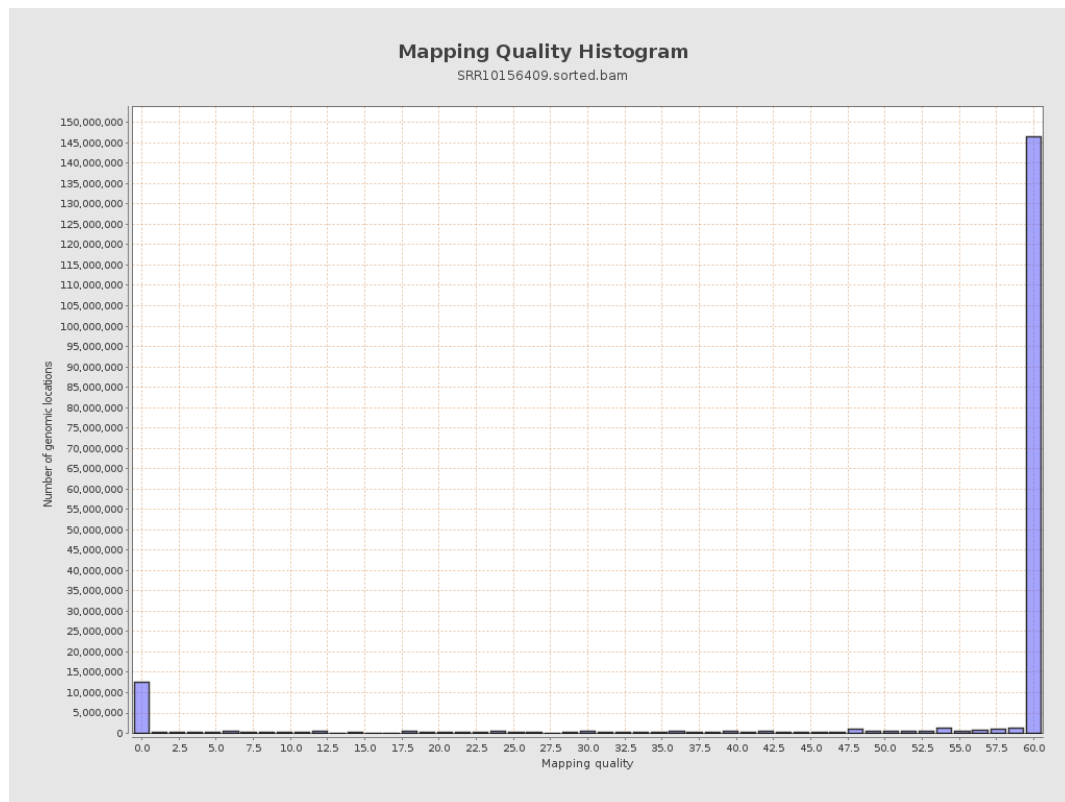
## 11. Results : Homopolymer Indels



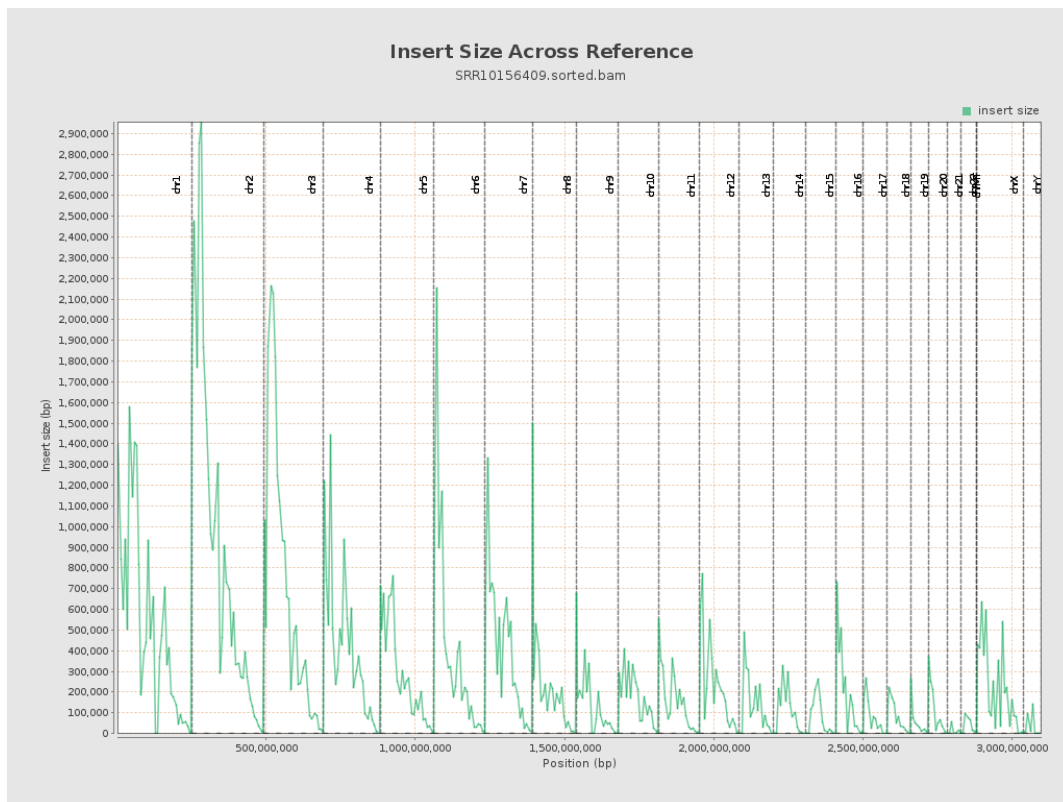
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

