

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/11/11 05:05:31*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365350.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_SRR5365350 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365350_1.fastq.gz SRR5365350_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                  |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                   |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                   |
| Analysis date:                        | Mon Nov 11 05:05:30 CST 2024                                                                                                                                                                                         |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                    |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                   |
| Number of windows:                    | 400                                                                                                                                                                                                                  |
| BAM file:                             | SRR5365350.sorted.bam                                                                                                                                                                                                |

## 2. Summary

### 2.1. Globals

|                              |                      |
|------------------------------|----------------------|
| Reference size               | 3,095,693,983        |
| Number of reads              | 534,193,354          |
| Mapped reads                 | 505,314,998 / 94.59% |
| Unmapped reads               | 28,878,356 / 5.41%   |
| Mapped paired reads          | 505,314,998 / 94.59% |
| Mapped reads, first in pair  | 253,146,791 / 47.39% |
| Mapped reads, second in pair | 252,168,207 / 47.21% |
| Mapped reads, both in pair   | 503,146,880 / 94.19% |
| Mapped reads, singletons     | 2,168,118 / 0.41%    |
| Secondary alignments         | 0                    |
| Supplementary alignments     | 2,168,592 / 0.41%    |
| Read min/max/mean length     | 30 / 125 / 125.17    |
| Duplicated reads (estimated) | 274,907,690 / 51.46% |
| Duplication rate             | 28.63%               |
| Clipped reads                | 300,738,302 / 56.3%  |

### 2.2. ACGT Content

|                          |                         |
|--------------------------|-------------------------|
| Number/percentage of A's | 16,057,097,071 / 30.08% |
| Number/percentage of C's | 10,475,142,020 / 19.62% |
| Number/percentage of T's | 15,685,195,438 / 29.38% |
| Number/percentage of G's | 11,161,050,464 / 20.91% |
| Number/percentage of N's | 6,434,173 / 0.01%       |
|                          |                         |

|               |        |
|---------------|--------|
| GC Percentage | 40.53% |
|---------------|--------|

## 2.3. Coverage

|                    |          |
|--------------------|----------|
| Mean               | 17.2507  |
| Standard Deviation | 164.2905 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 53.84 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 58,082.39       |
| Standard Deviation | 2,350,422.43    |
| P25/Median/P75     | 115 / 165 / 236 |

## 2.6. Mismatches and indels

|                                          |             |
|------------------------------------------|-------------|
| General error rate                       | 0.57%       |
| Mismatches                               | 276,961,312 |
| Insertions                               | 15,759,663  |
| Mapped reads with at least one insertion | 3.05%       |
| Deletions                                | 8,423,418   |
| Mapped reads with at least one deletion  | 1.62%       |
| Homopolymer indels                       | 50.44%      |

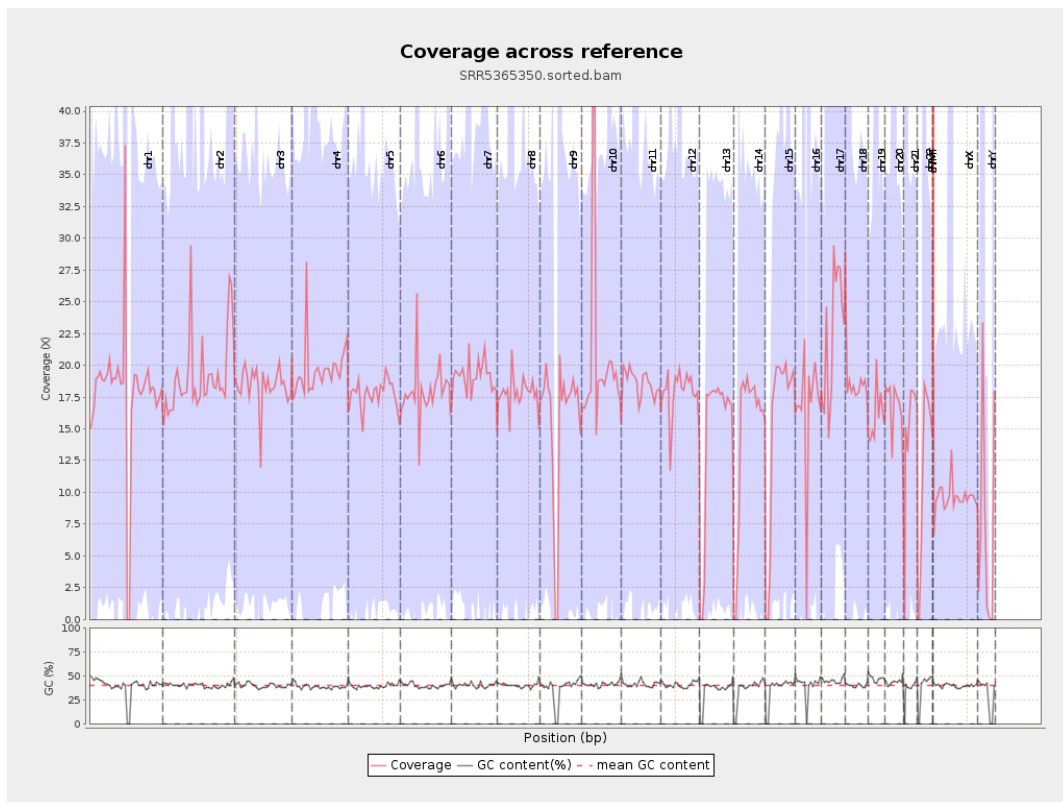
## 2.7. Chromosome stats

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

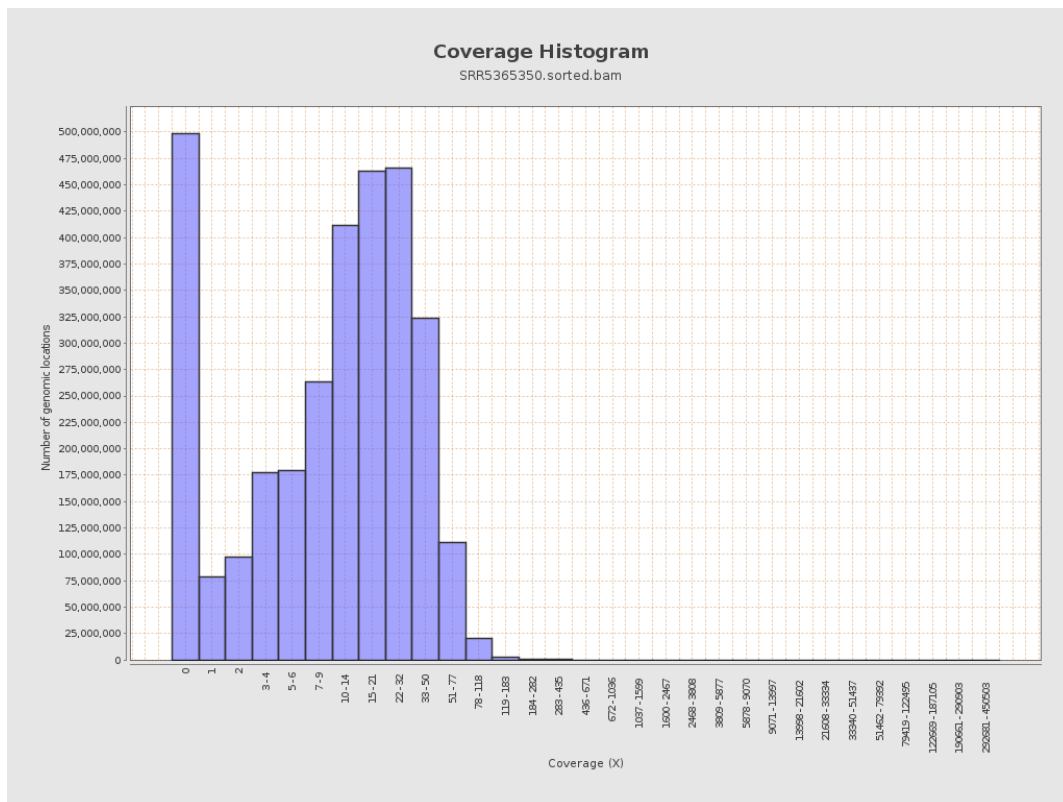
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 4450454652   | 17.8553         | 435.831          |
| chr2  | 243199373 | 4684370387   | 19.2614         | 94.3101          |
| chr3  | 198022430 | 3645260314   | 18.4083         | 27.9118          |
| chr4  | 191154276 | 3751218403   | 19.624          | 93.6443          |
| chr5  | 180915260 | 3199255431   | 17.6837         | 20.1143          |
| chr6  | 171115067 | 3082229055   | 18.0126         | 83.3158          |
| chr7  | 159138663 | 3046362454   | 19.1428         | 108.2215         |
| chr8  | 146364022 | 2602229586   | 17.7792         | 54.3783          |
| chr9  | 141213431 | 2222566731   | 15.7391         | 126.928          |
| chr10 | 135534747 | 2783399587   | 20.5364         | 336.2569         |
| chr11 | 135006516 | 2505095946   | 18.5554         | 105.4702         |
| chr12 | 133851895 | 2400678926   | 17.9353         | 33.9902          |
| chr13 | 115169878 | 1680273426   | 14.5895         | 16.2344          |
| chr14 | 107349540 | 1586213634   | 14.7762         | 18.9844          |
| chr15 | 102531392 | 1564789625   | 15.2616         | 21.7626          |
| chr16 | 90354753  | 1491170431   | 16.5035         | 58.2785          |
| chr17 | 81195210  | 1847088546   | 22.7487         | 99.9425          |
| chr18 | 78077248  | 1462247915   | 18.7282         | 149.4851         |
| chr19 | 59128983  | 948245400    | 16.0369         | 219.9188         |
| chr20 | 63025520  | 1056387975   | 16.7613         | 30.7967          |
| chr21 | 48129895  | 717309830    | 14.9036         | 59.345           |
| chr22 | 51304566  | 611537149    | 11.9197         | 53.5143          |
| chrMT | 16571     | 112852573    | 6,810.2452      | 1,153.1576       |
| chrX  | 155270560 | 1493104692   | 9.6161          | 43.1822          |

|      |          |           |        |         |
|------|----------|-----------|--------|---------|
| chrY | 59373566 | 458396604 | 7.7206 | 187.459 |
|------|----------|-----------|--------|---------|

### 3. Results : Coverage across reference

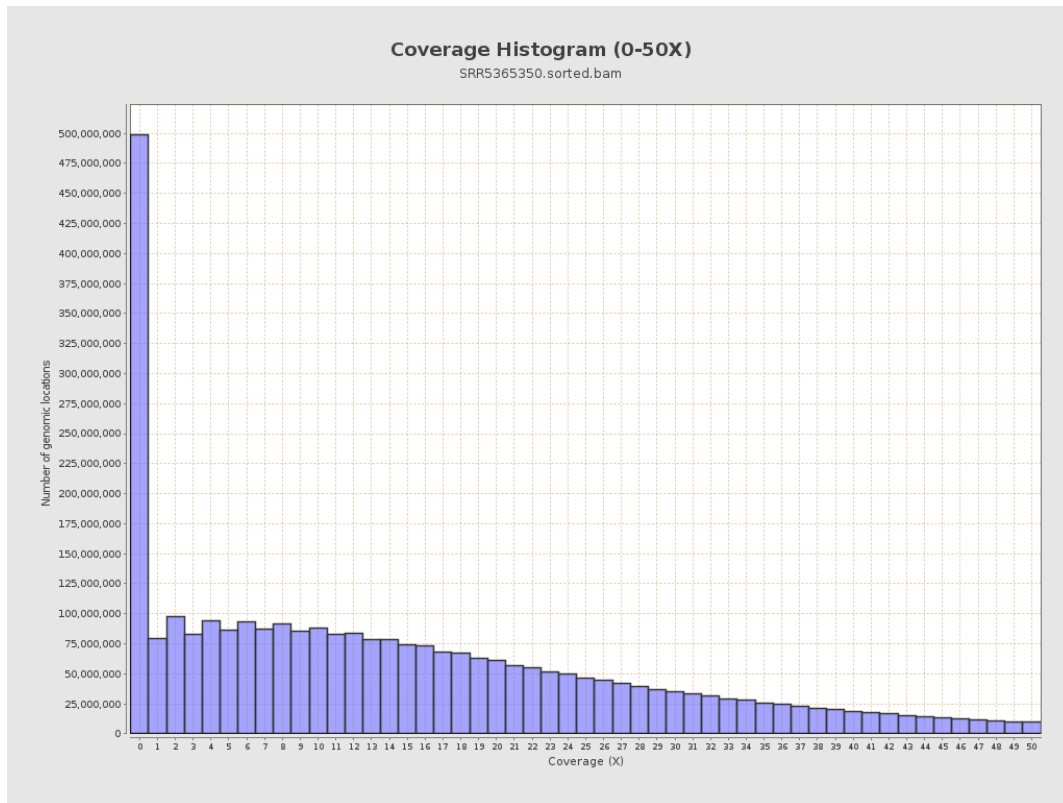


## 4. Results : Coverage Histogram

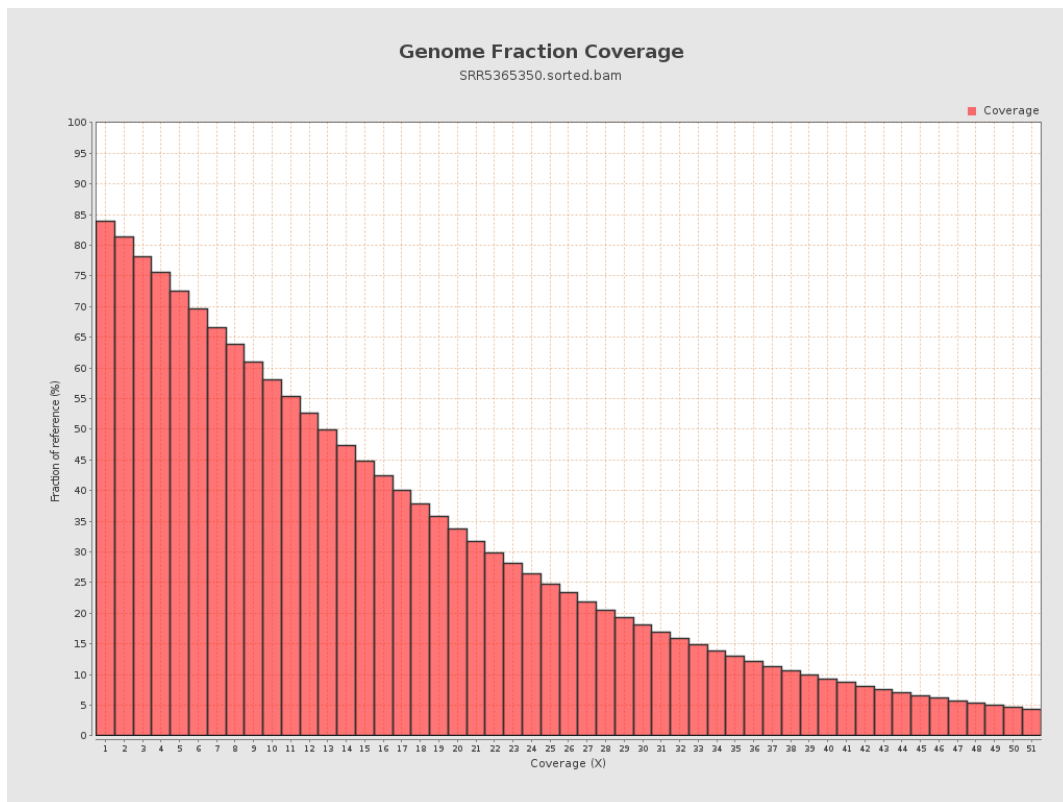




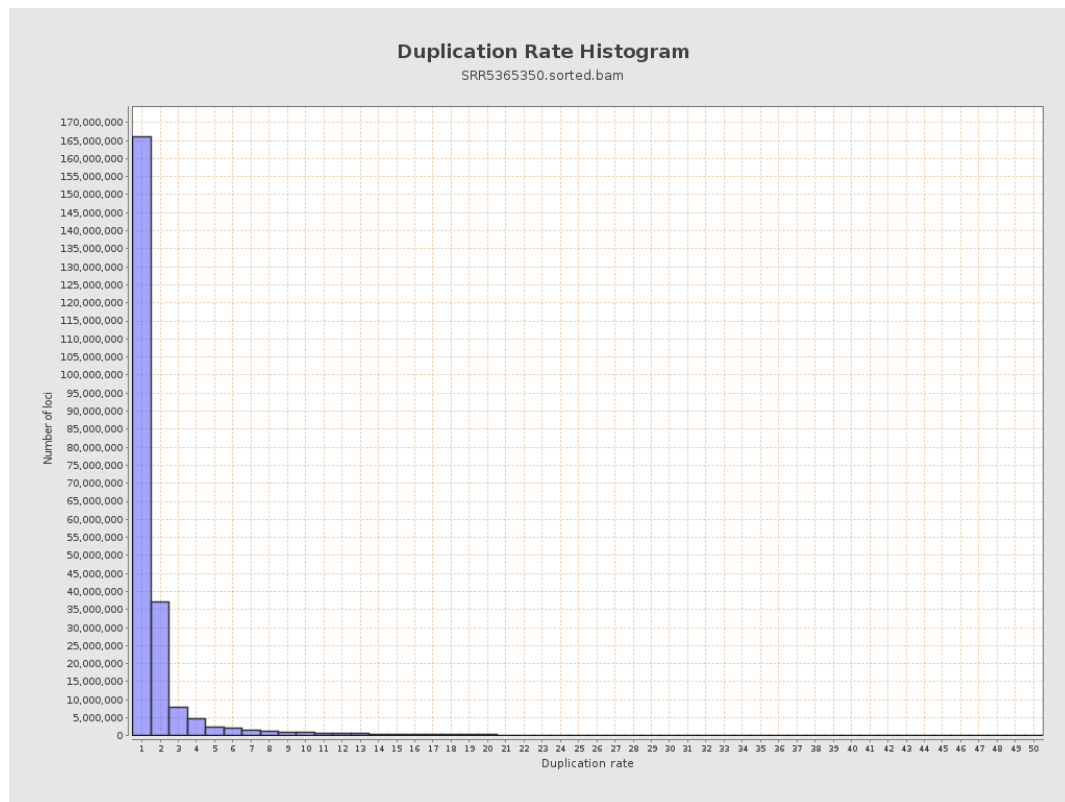
## 5. Results : Coverage Histogram (0-50X)



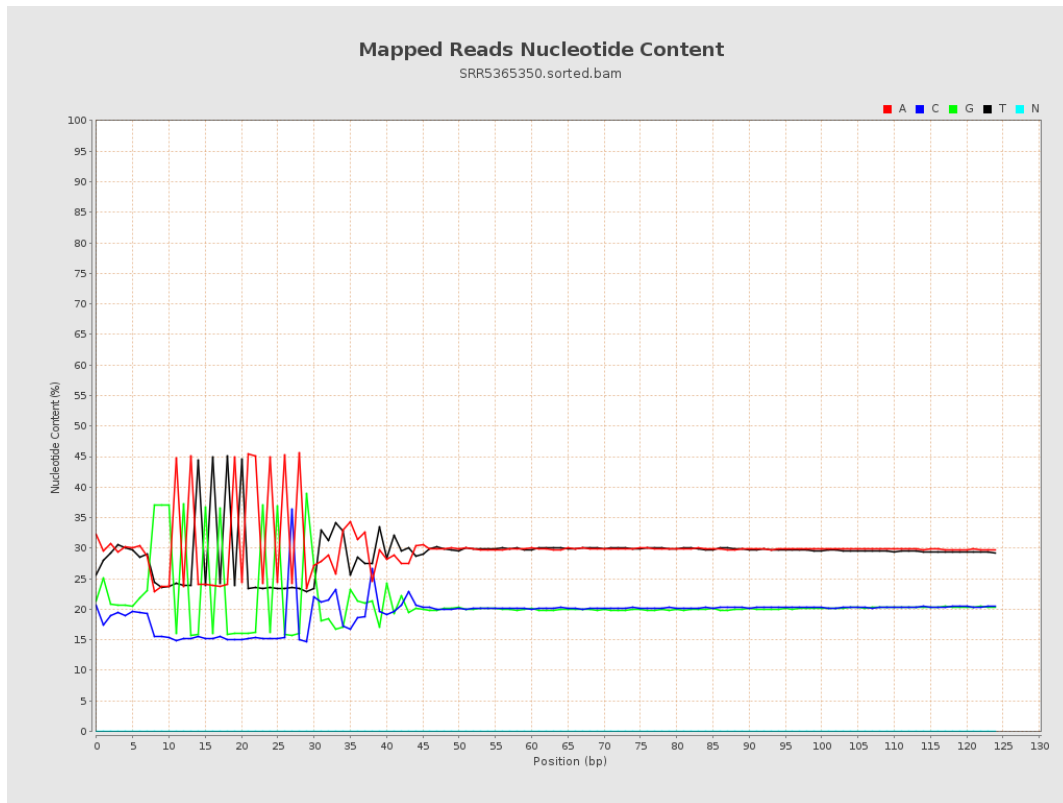
## 6. Results : Genome Fraction Coverage



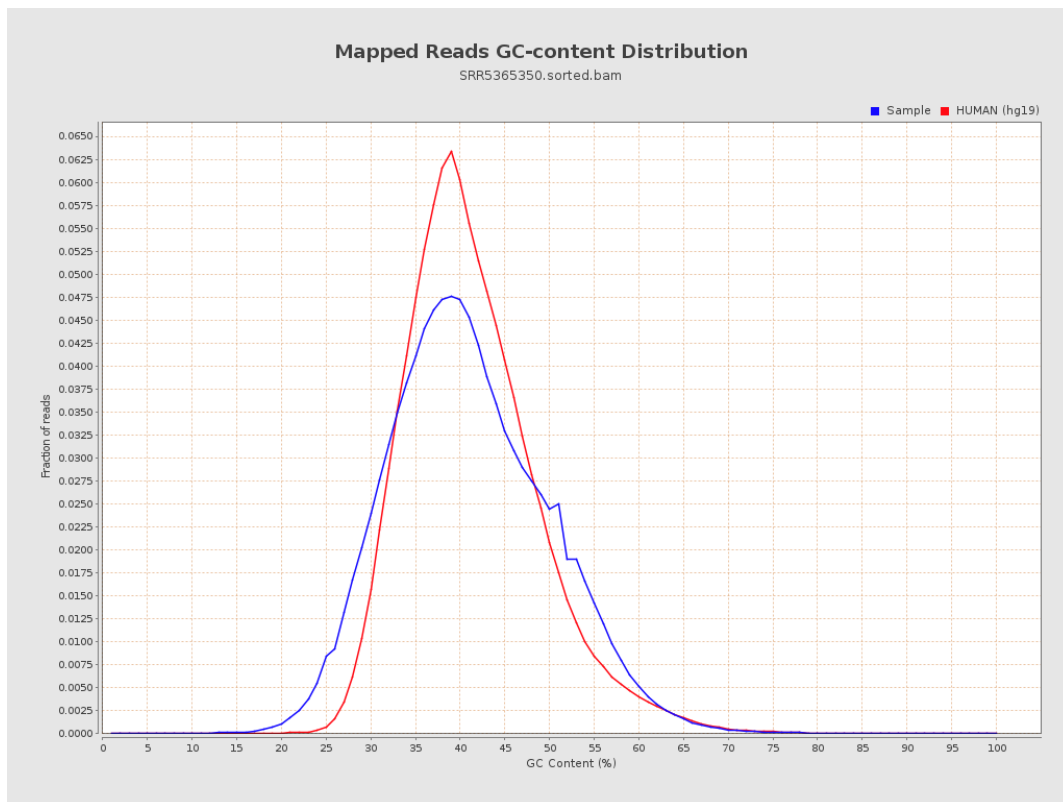
## 7. Results : Duplication Rate Histogram



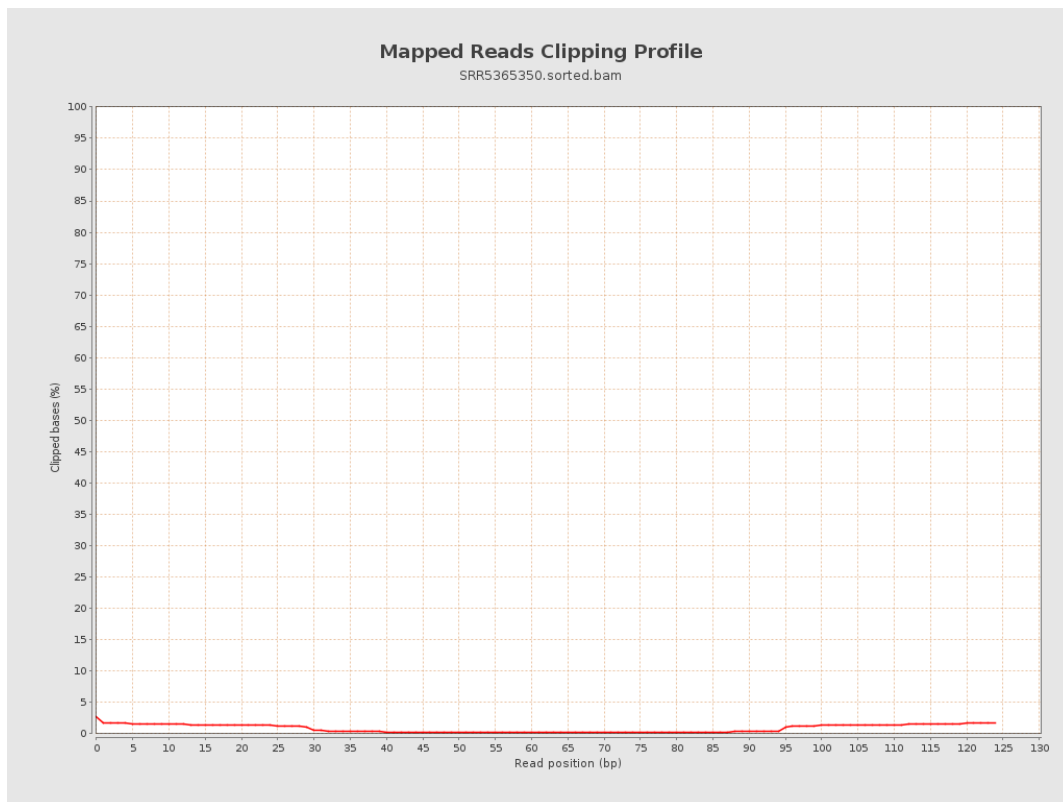
## 8. Results : Mapped Reads Nucleotide Content



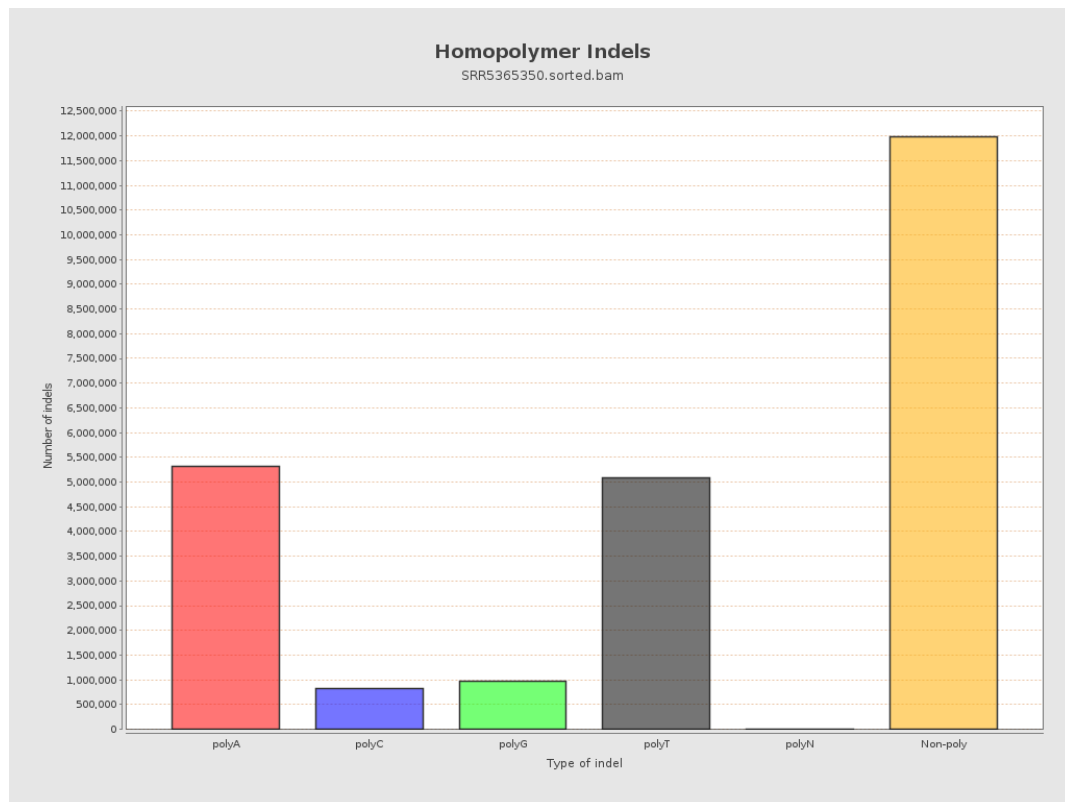
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

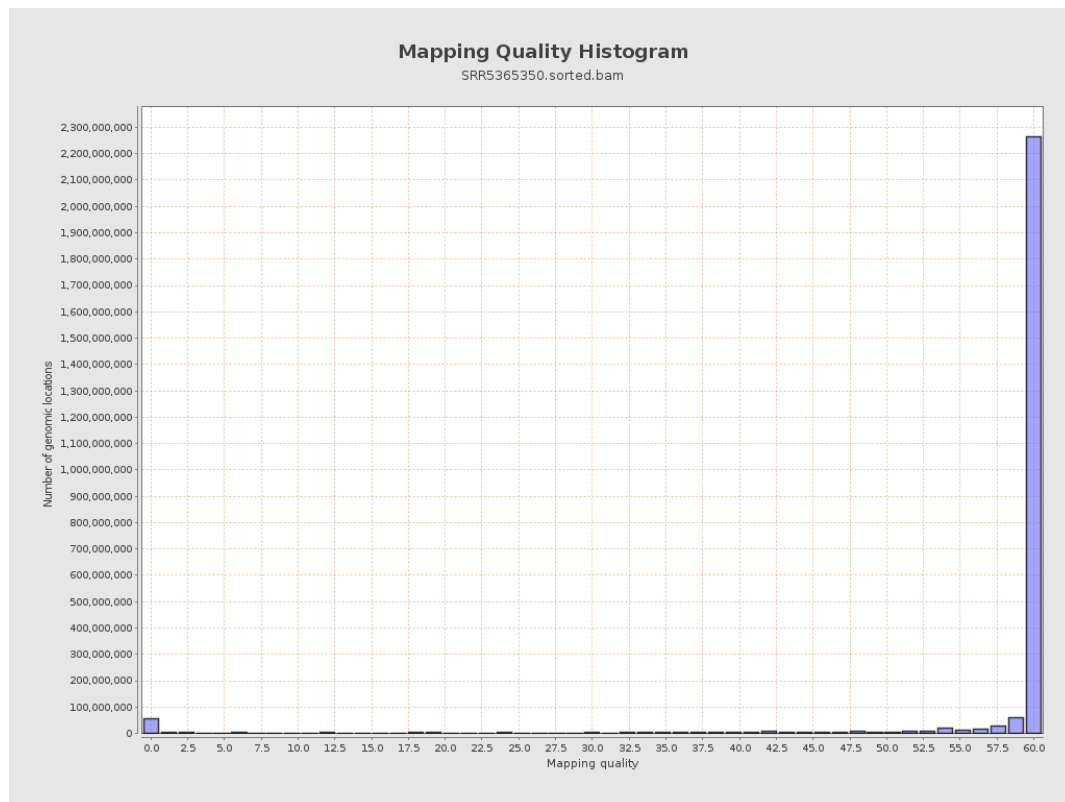


## 12. Results : Mapping Quality Across Reference

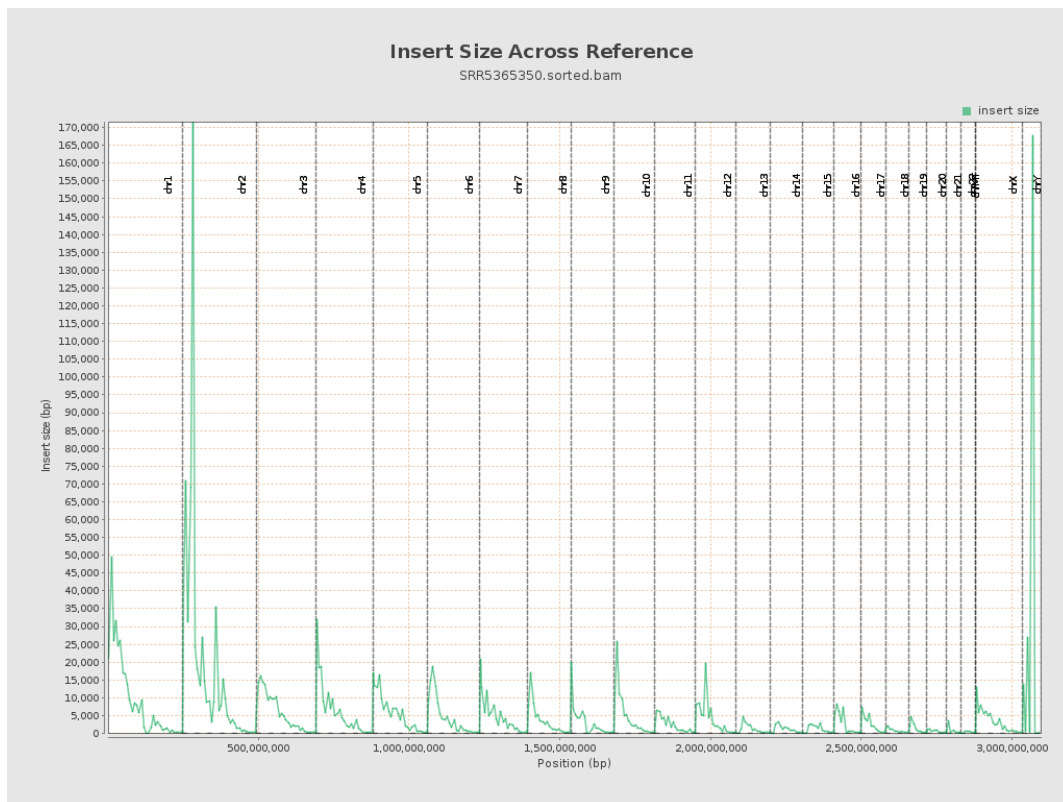




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

