

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/10 22:21:18*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779411.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_SRR1779411 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779411_1.fastq.gz SRR1779411_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                  |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                   |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                   |
| Analysis date:                        | Thu Oct 10 22:21:16 CST 2024                                                                                                                                                                                         |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                    |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                   |
| Number of windows:                    | 400                                                                                                                                                                                                                  |
| BAM file:                             | SRR1779411.sorted.bam                                                                                                                                                                                                |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 14,091,416          |
| Mapped reads                 | 13,609,390 / 96.58% |
| Unmapped reads               | 482,026 / 3.42%     |
| Mapped paired reads          | 13,609,390 / 96.58% |
| Mapped reads, first in pair  | 6,858,420 / 48.67%  |
| Mapped reads, second in pair | 6,750,970 / 47.91%  |
| Mapped reads, both in pair   | 13,473,714 / 95.62% |
| Mapped reads, singletons     | 135,676 / 0.96%     |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 50,773 / 0.36%      |
| Read min/max/mean length     | 30 / 80 / 80.13     |
| Duplicated reads (estimated) | 421,883 / 2.99%     |
| Duplication rate             | 2.78%               |
| Clipped reads                | 552,867 / 3.92%     |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 329,255,513 / 30.43% |
| Number/percentage of C's | 211,795,066 / 19.58% |
| Number/percentage of T's | 323,182,446 / 29.87% |
| Number/percentage of G's | 217,450,477 / 20.1%  |
| Number/percentage of N's | 235,758 / 0.02%      |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 39.67% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.3496 |
| Standard Deviation | 1.4196 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 53.14 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 141,952.35      |
| Standard Deviation | 3,662,762.49    |
| P25/Median/P75     | 150 / 191 / 243 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.35%     |
| Mismatches                               | 3,664,300 |
| Insertions                               | 96,626    |
| Mapped reads with at least one insertion | 0.7%      |
| Deletions                                | 111,111   |
| Mapped reads with at least one deletion  | 0.81%     |
| Homopolymer indels                       | 47.09%    |

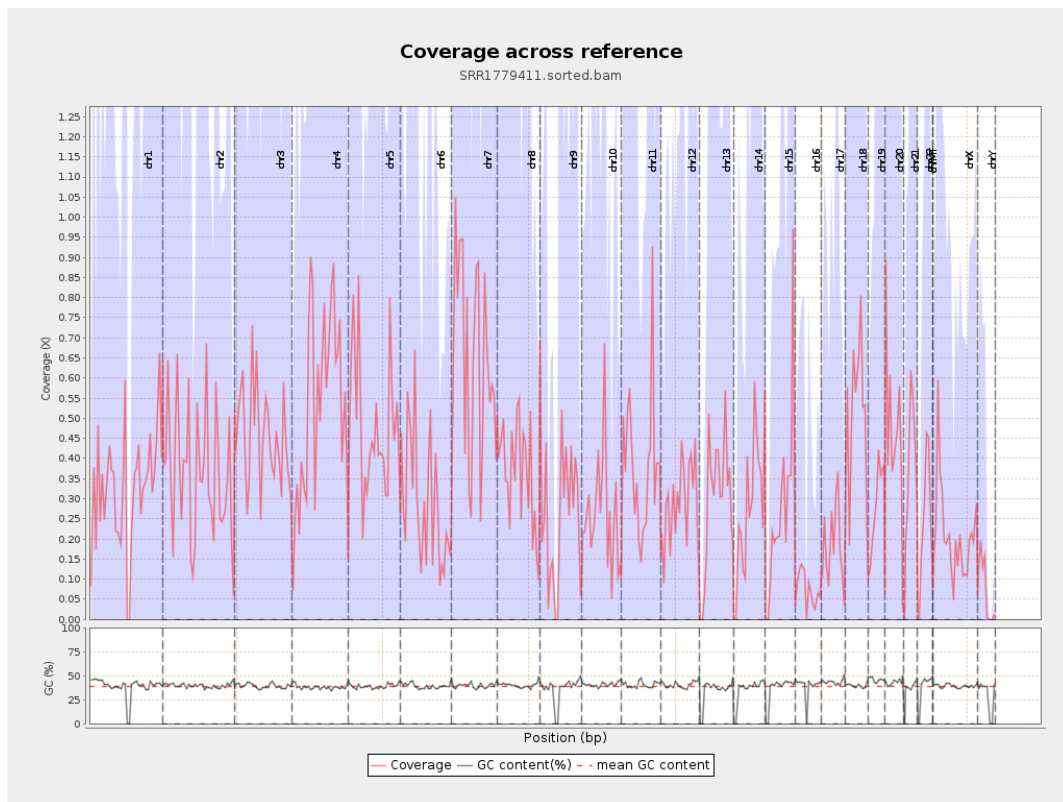
## 2.7. Chromosome stats

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

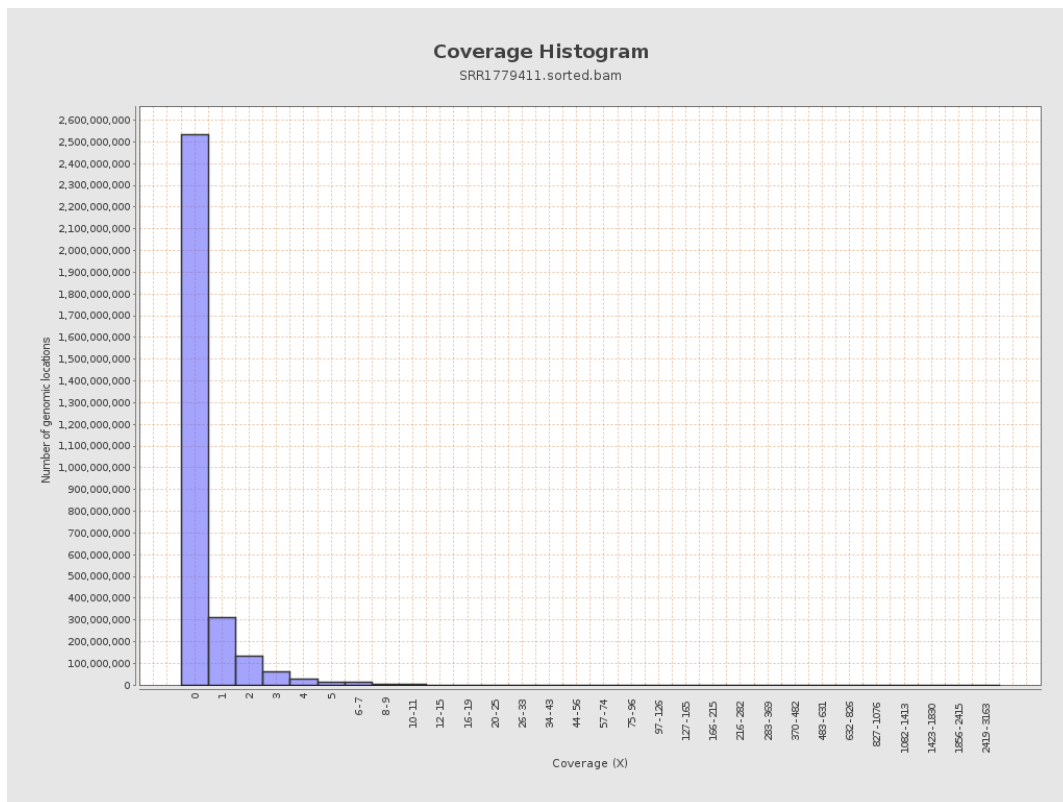
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 81660457     | 0.3276          | 3.3322           |
| chr2  | 243199373 | 88918918     | 0.3656          | 1.025            |
| chr3  | 198022430 | 89706795     | 0.453           | 1.0822           |
| chr4  | 191154276 | 103880954    | 0.5434          | 1.1924           |
| chr5  | 180915260 | 86116948     | 0.476           | 1.1217           |
| chr6  | 171115067 | 49596281     | 0.2898          | 0.8983           |
| chr7  | 159138663 | 100848315    | 0.6337          | 1.5524           |
| chr8  | 146364022 | 52571788     | 0.3592          | 0.9997           |
| chr9  | 141213431 | 35092401     | 0.2485          | 1.0361           |
| chr10 | 135534747 | 36200396     | 0.2671          | 1.7872           |
| chr11 | 135006516 | 51590906     | 0.3821          | 1.0444           |
| chr12 | 133851895 | 38941332     | 0.2909          | 0.8431           |
| chr13 | 115169878 | 34285168     | 0.2977          | 0.884            |
| chr14 | 107349540 | 28984592     | 0.27            | 0.896            |
| chr15 | 102531392 | 28356846     | 0.2766          | 0.8792           |
| chr16 | 90354753  | 6571557      | 0.0727          | 0.4833           |
| chr17 | 81195210  | 15363262     | 0.1892          | 0.7238           |
| chr18 | 78077248  | 40477108     | 0.5184          | 1.4401           |
| chr19 | 59128983  | 16107237     | 0.2724          | 1.793            |
| chr20 | 63025520  | 29759025     | 0.4722          | 1.1774           |
| chr21 | 48129895  | 17630089     | 0.3663          | 0.9647           |
| chr22 | 51304566  | 12640452     | 0.2464          | 0.8295           |
| chrMT | 16571     | 1141         | 0.0689          | 0.3144           |
| chrX  | 155270560 | 32335154     | 0.2083          | 0.7577           |

|      |          |         |       |        |
|------|----------|---------|-------|--------|
| chrY | 59373566 | 4512910 | 0.076 | 0.4245 |
|------|----------|---------|-------|--------|

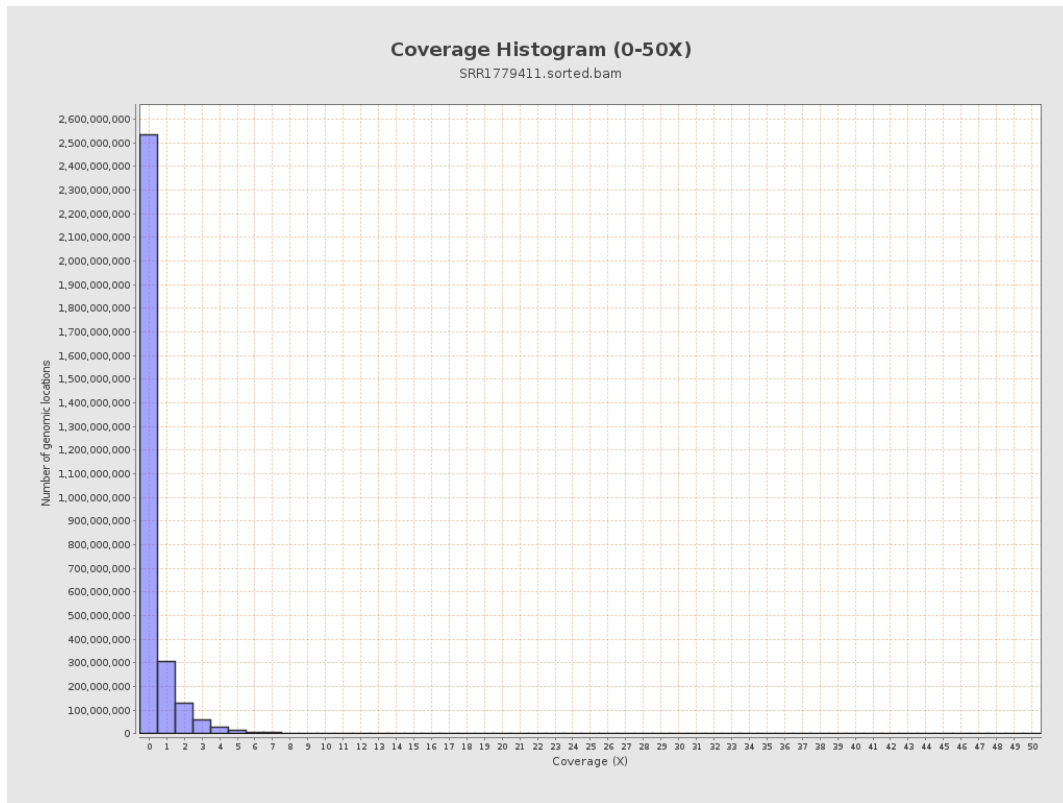
### 3. Results : Coverage across reference



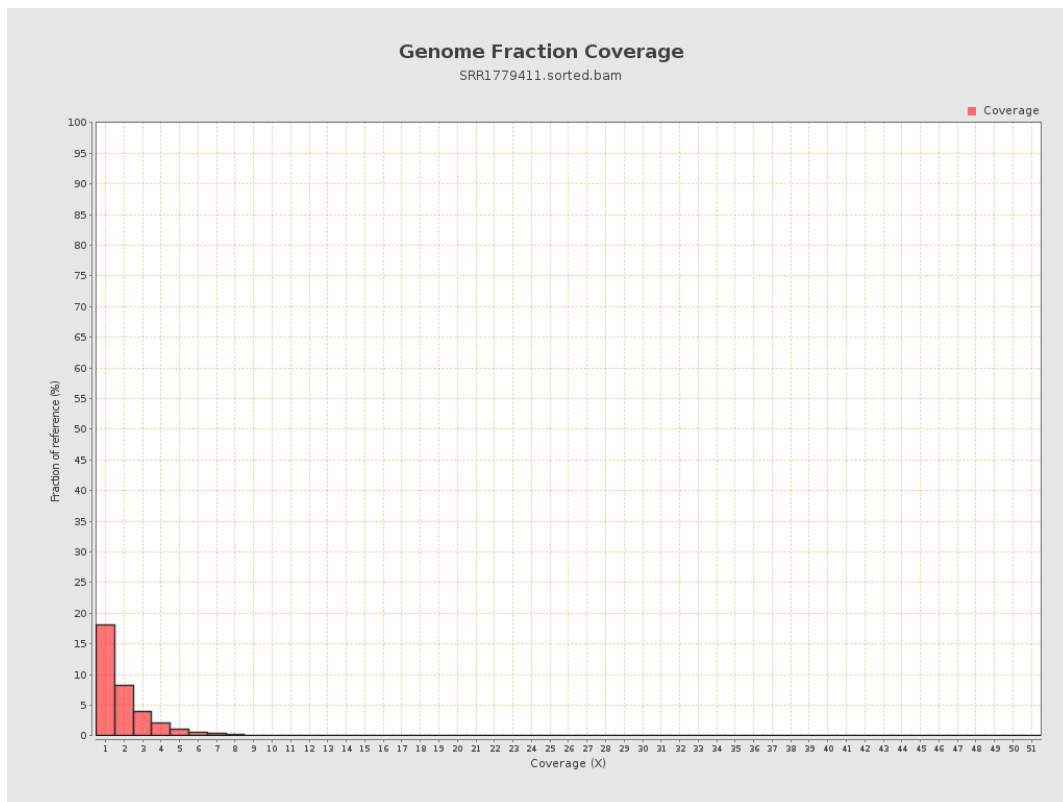
## 4. Results : Coverage Histogram



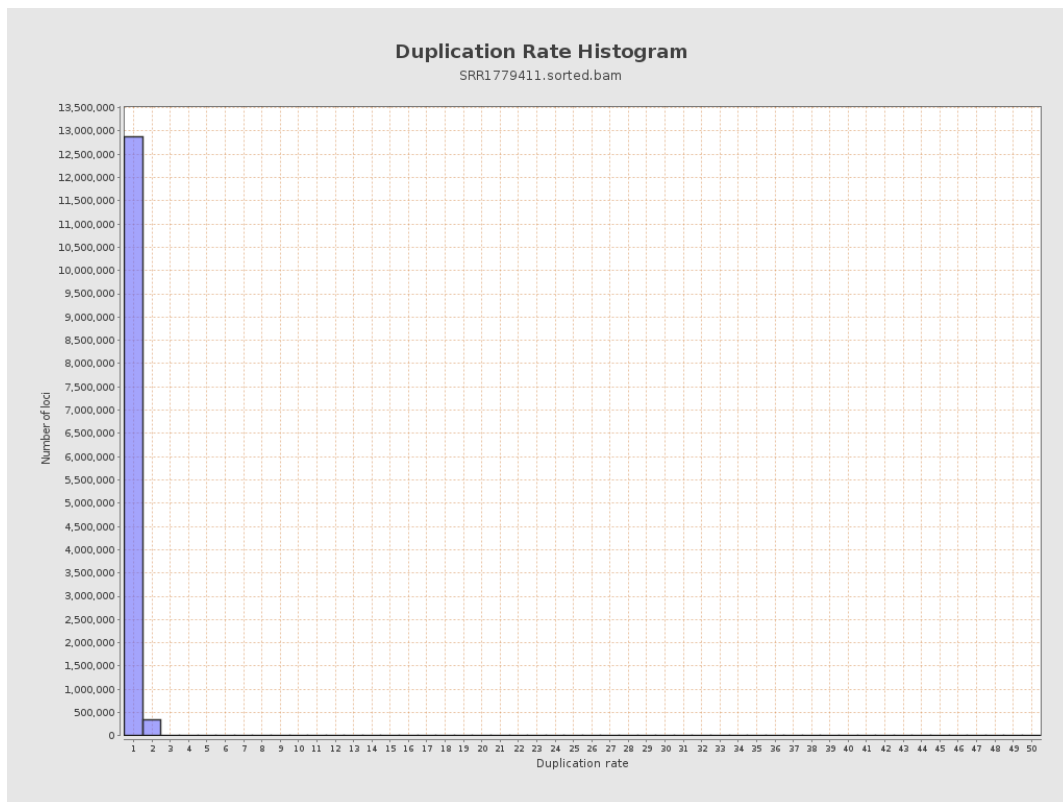
## 5. Results : Coverage Histogram (0-50X)



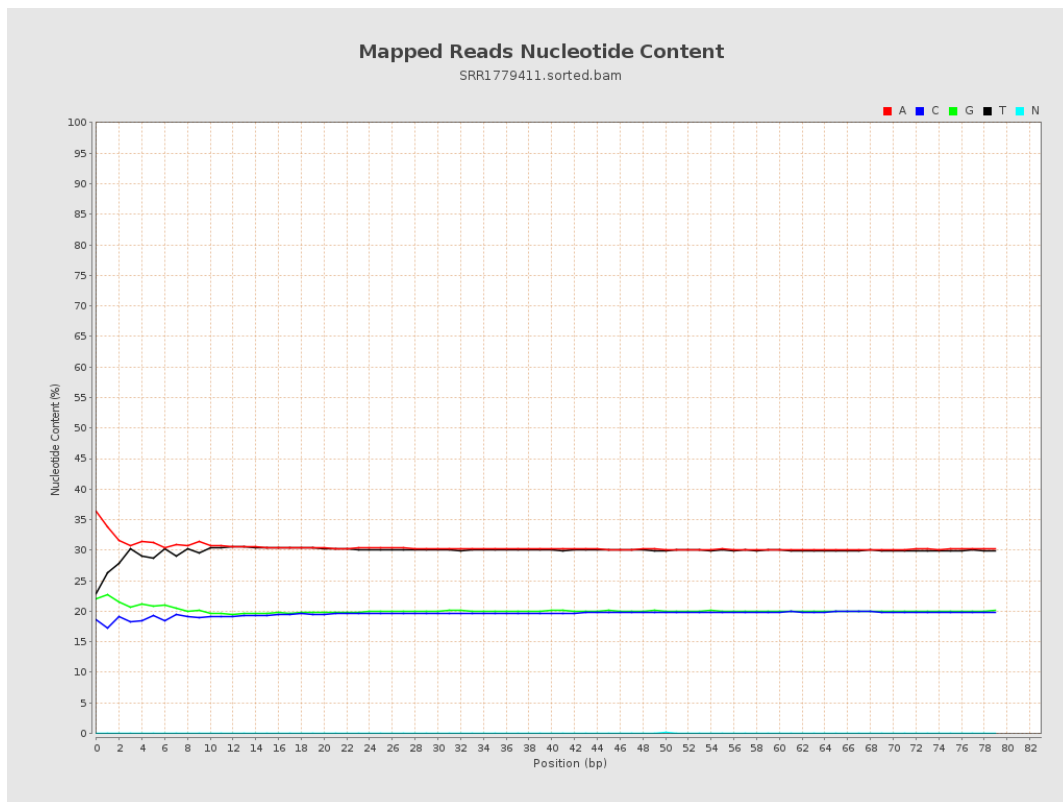
## 6. Results : Genome Fraction Coverage



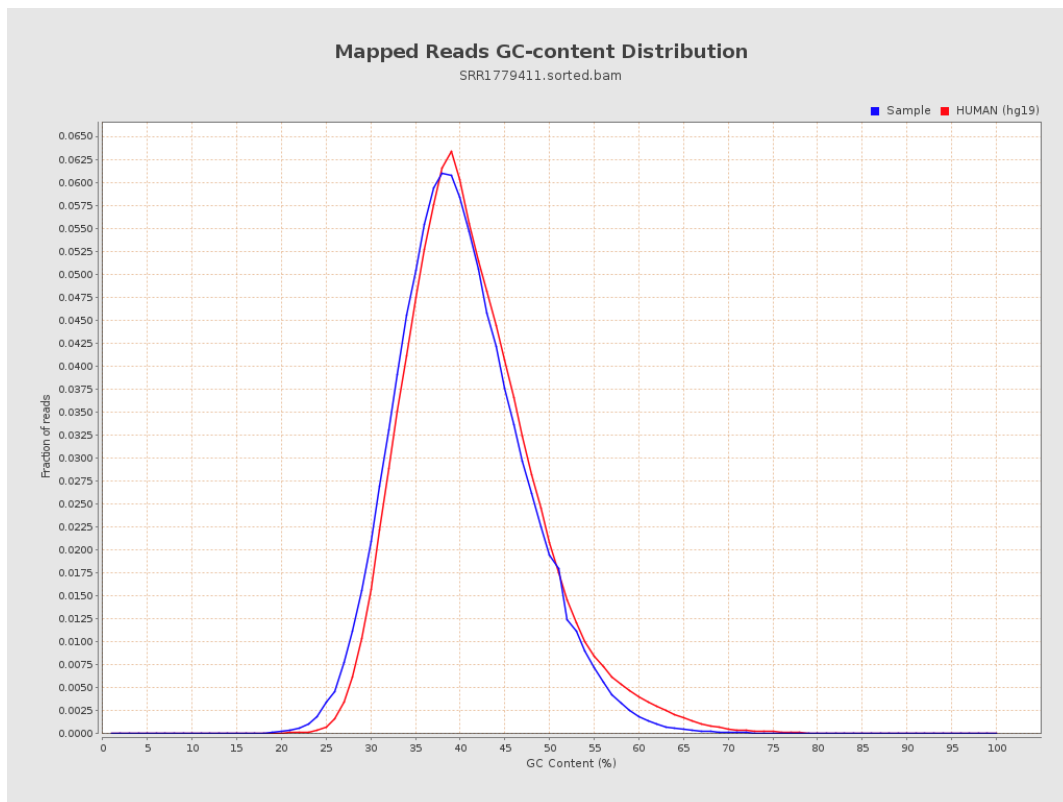
## 7. Results : Duplication Rate Histogram



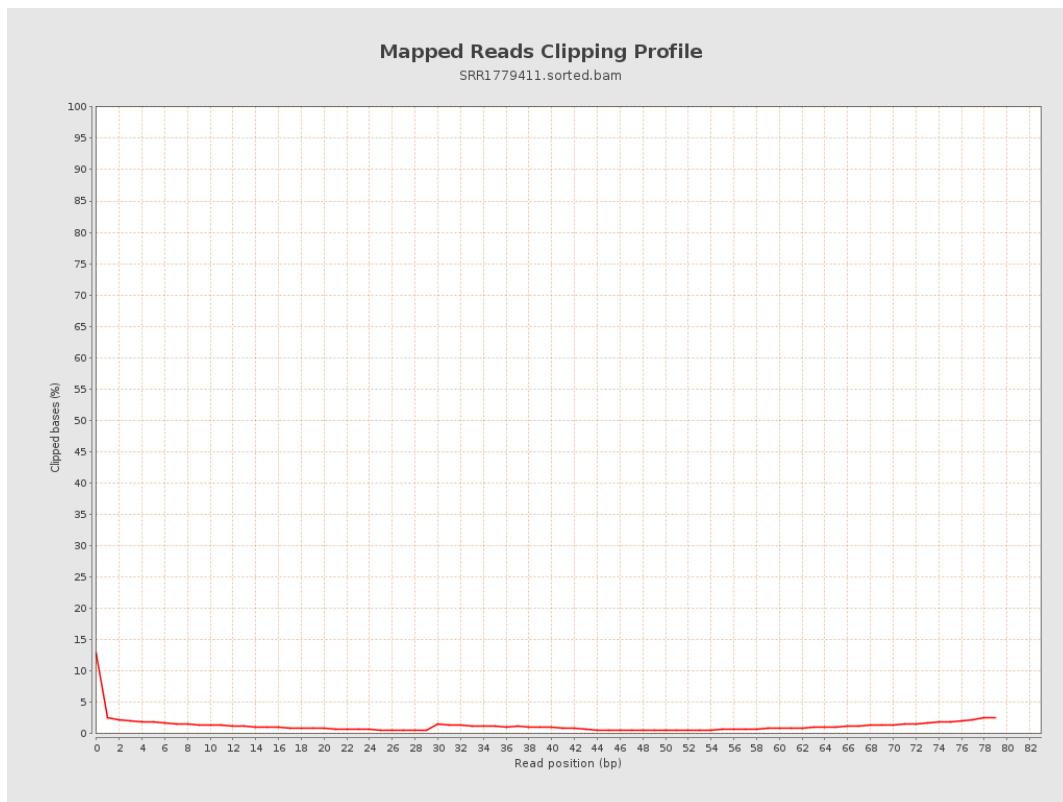
## 8. Results : Mapped Reads Nucleotide Content



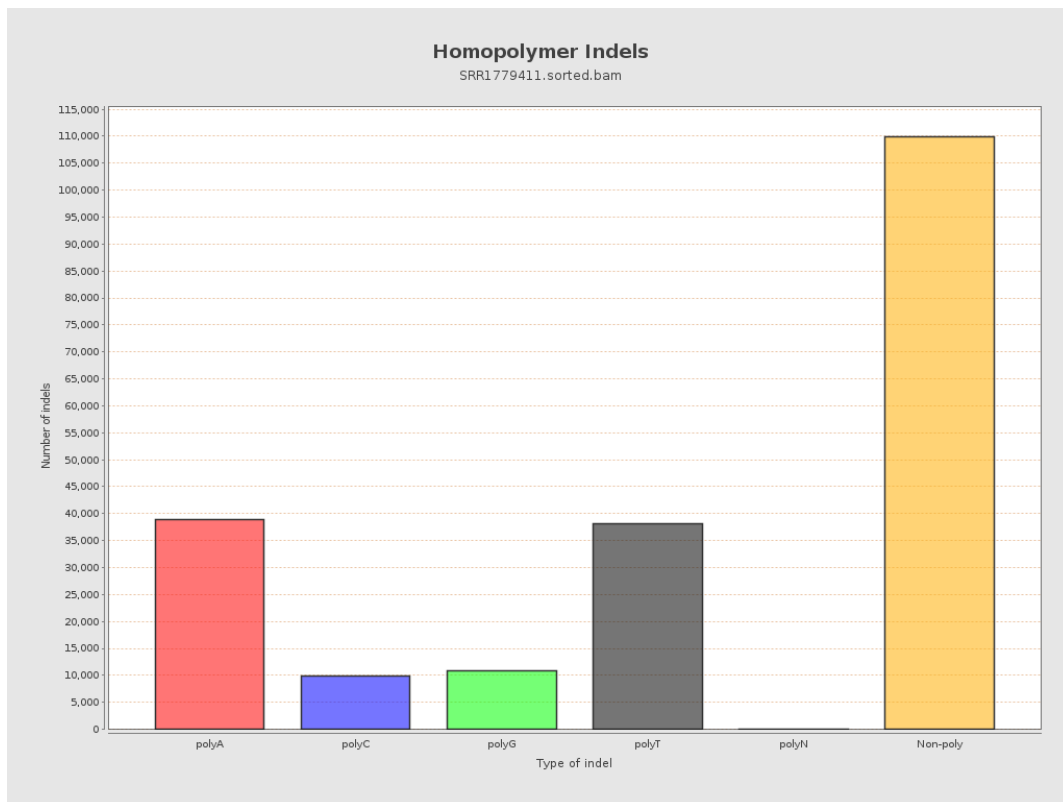
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



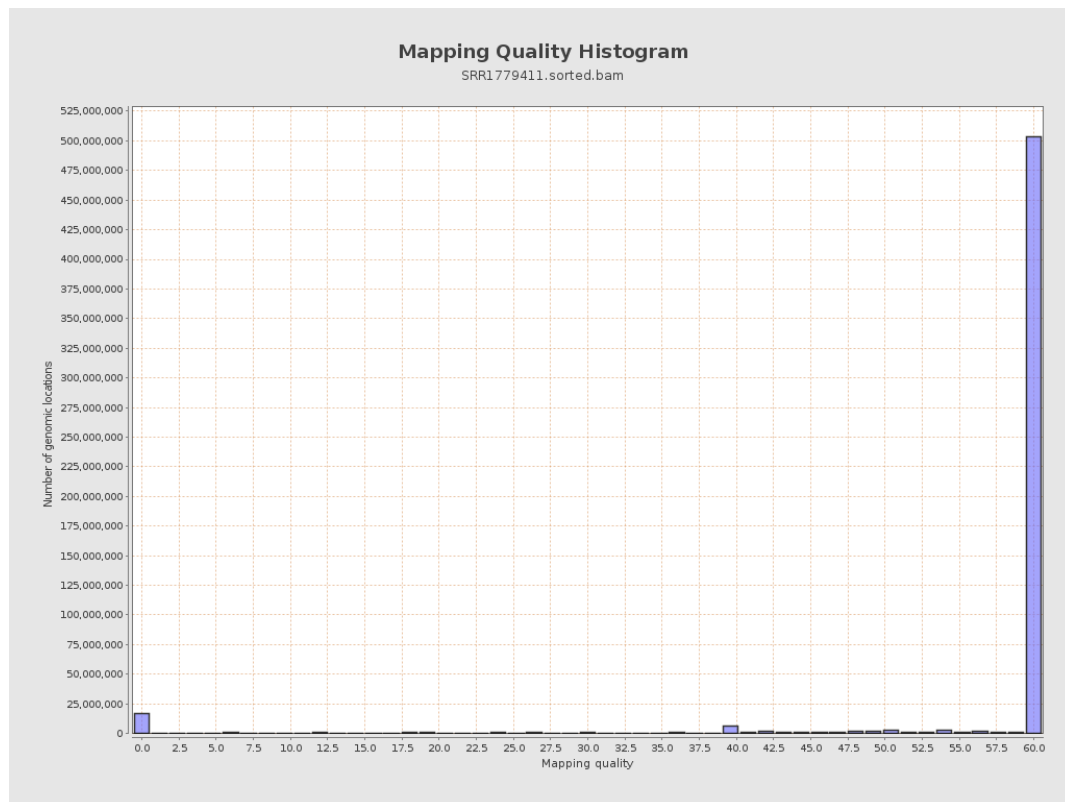
## 11. Results : Homopolymer Indels



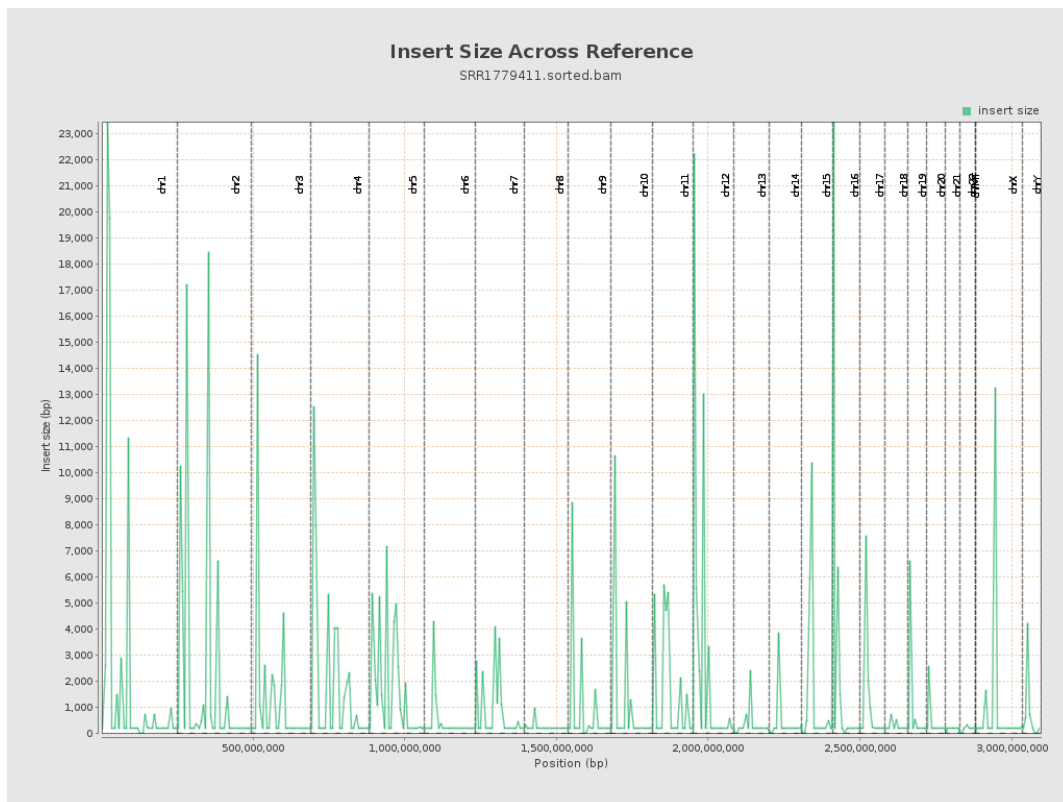
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

