

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/10 20:10:18*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779404.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_SRR1779404 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779404_1.fastq.gz SRR1779404_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                  |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                   |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                   |
| Analysis date:                        | Thu Oct 10 20:10:14 CST 2024                                                                                                                                                                                         |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                    |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                   |
| Number of windows:                    | 400                                                                                                                                                                                                                  |
| BAM file:                             | SRR1779404.sorted.bam                                                                                                                                                                                                |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 12,967,870          |
| Mapped reads                 | 12,379,865 / 95.47% |
| Unmapped reads               | 588,005 / 4.53%     |
| Mapped paired reads          | 12,379,865 / 95.47% |
| Mapped reads, first in pair  | 6,222,368 / 47.98%  |
| Mapped reads, second in pair | 6,157,497 / 47.48%  |
| Mapped reads, both in pair   | 12,289,044 / 94.77% |
| Mapped reads, singletons     | 90,821 / 0.7%       |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 44,801 / 0.35%      |
| Read min/max/mean length     | 30 / 80 / 80.13     |
| Duplicated reads (estimated) | 329,577 / 2.54%     |
| Duplication rate             | 2.51%               |
| Clipped reads                | 608,224 / 4.69%     |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 294,243,778 / 29.94% |
| Number/percentage of C's | 196,740,130 / 20.02% |
| Number/percentage of T's | 291,137,443 / 29.63% |
| Number/percentage of G's | 200,313,763 / 20.39% |
| Number/percentage of N's | 214,515 / 0.02%      |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 40.41% |
|---------------|--------|

## 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.3175 |
| Standard Deviation | 0.9946 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 53.31 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 102,711.24      |
| Standard Deviation | 3,099,217.98    |
| P25/Median/P75     | 139 / 189 / 243 |

## 2.6. Mismatches and indels

|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.34%     |
| Mismatches                               | 3,208,982 |
| Insertions                               | 93,579    |
| Mapped reads with at least one insertion | 0.75%     |
| Deletions                                | 113,314   |
| Mapped reads with at least one deletion  | 0.9%      |
| Homopolymer indels                       | 47.07%    |

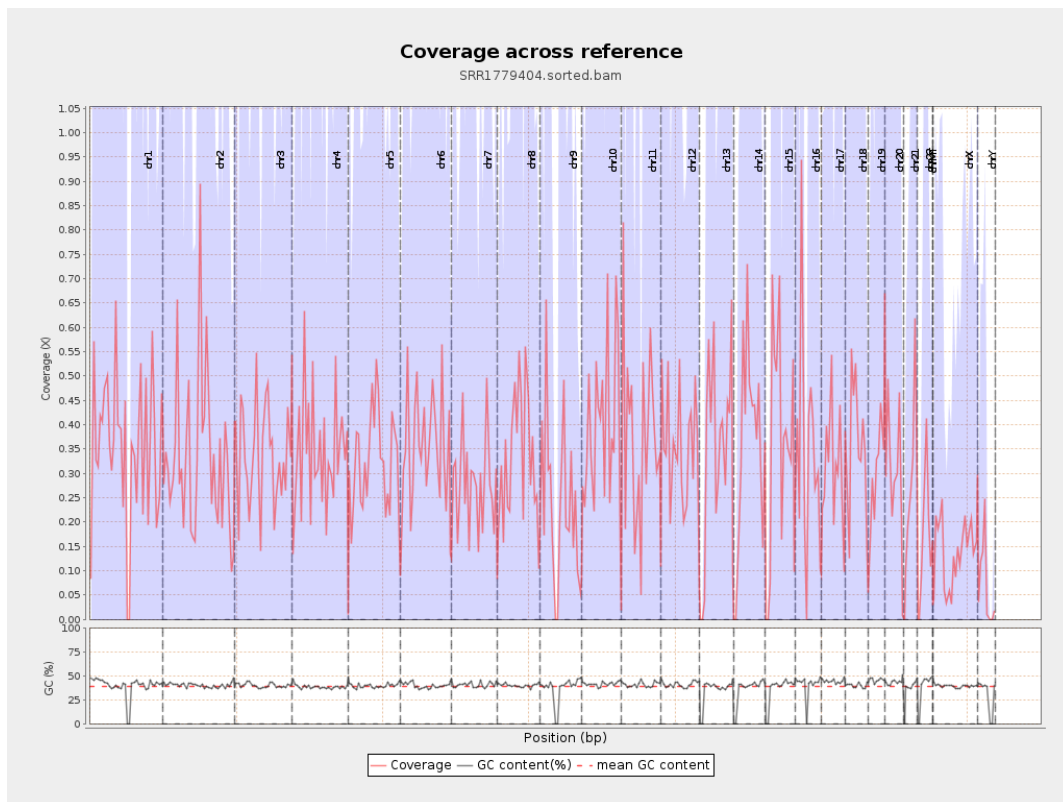
## 2.7. Chromosome stats

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

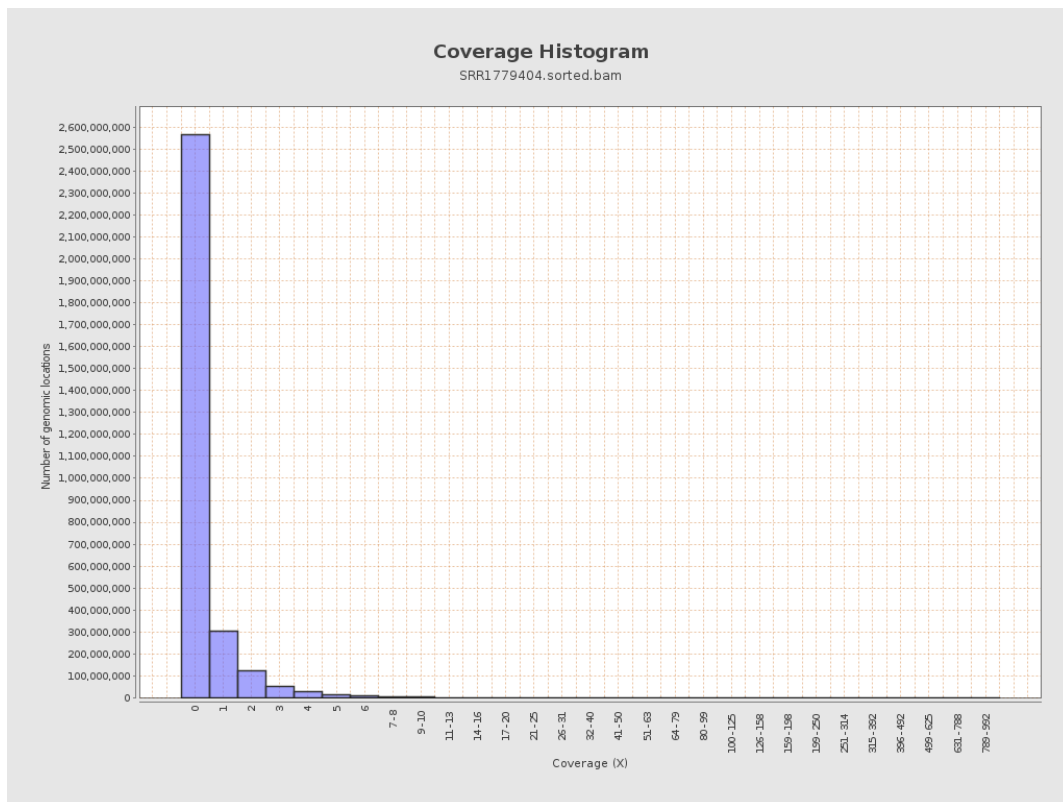
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 88231728     | 0.354           | 1.3778           |
| chr2  | 243199373 | 80463560     | 0.3309          | 1.0117           |
| chr3  | 198022430 | 67077636     | 0.3387          | 0.9293           |
| chr4  | 191154276 | 65388270     | 0.3421          | 0.8923           |
| chr5  | 180915260 | 58103700     | 0.3212          | 0.8775           |
| chr6  | 171115067 | 61104950     | 0.3571          | 0.9407           |
| chr7  | 159138663 | 43388205     | 0.2726          | 0.876            |
| chr8  | 146364022 | 48068661     | 0.3284          | 0.9021           |
| chr9  | 141213431 | 33719598     | 0.2388          | 0.885            |
| chr10 | 135534747 | 54697021     | 0.4036          | 1.4124           |
| chr11 | 135006516 | 49944337     | 0.3699          | 1.0187           |
| chr12 | 133851895 | 48114077     | 0.3595          | 0.9472           |
| chr13 | 115169878 | 40213089     | 0.3492          | 0.9757           |
| chr14 | 107349540 | 38486943     | 0.3585          | 0.9468           |
| chr15 | 102531392 | 36533039     | 0.3563          | 1.0021           |
| chr16 | 90354753  | 30275727     | 0.3351          | 1.0421           |
| chr17 | 81195210  | 25445760     | 0.3134          | 0.9996           |
| chr18 | 78077248  | 27878880     | 0.3571          | 1.0835           |
| chr19 | 59128983  | 17952458     | 0.3036          | 1.157            |
| chr20 | 63025520  | 19459972     | 0.3088          | 0.9007           |
| chr21 | 48129895  | 13039840     | 0.2709          | 0.8493           |
| chr22 | 51304566  | 8821974      | 0.172           | 0.6629           |
| chrMT | 16571     | 480          | 0.029           | 0.1835           |
| chrX  | 155270560 | 22187514     | 0.1429          | 0.591            |

|      |          |         |        |        |
|------|----------|---------|--------|--------|
| chrY | 59373566 | 4293724 | 0.0723 | 0.3865 |
|------|----------|---------|--------|--------|

### 3. Results : Coverage across reference

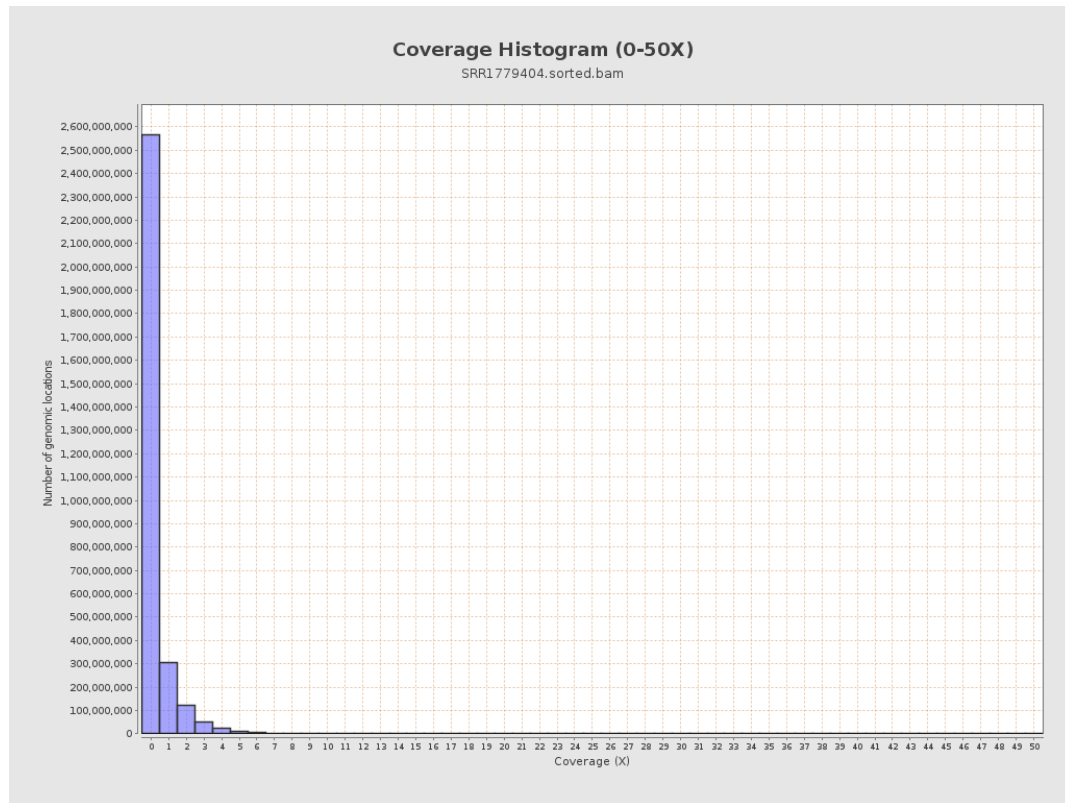


## 4. Results : Coverage Histogram

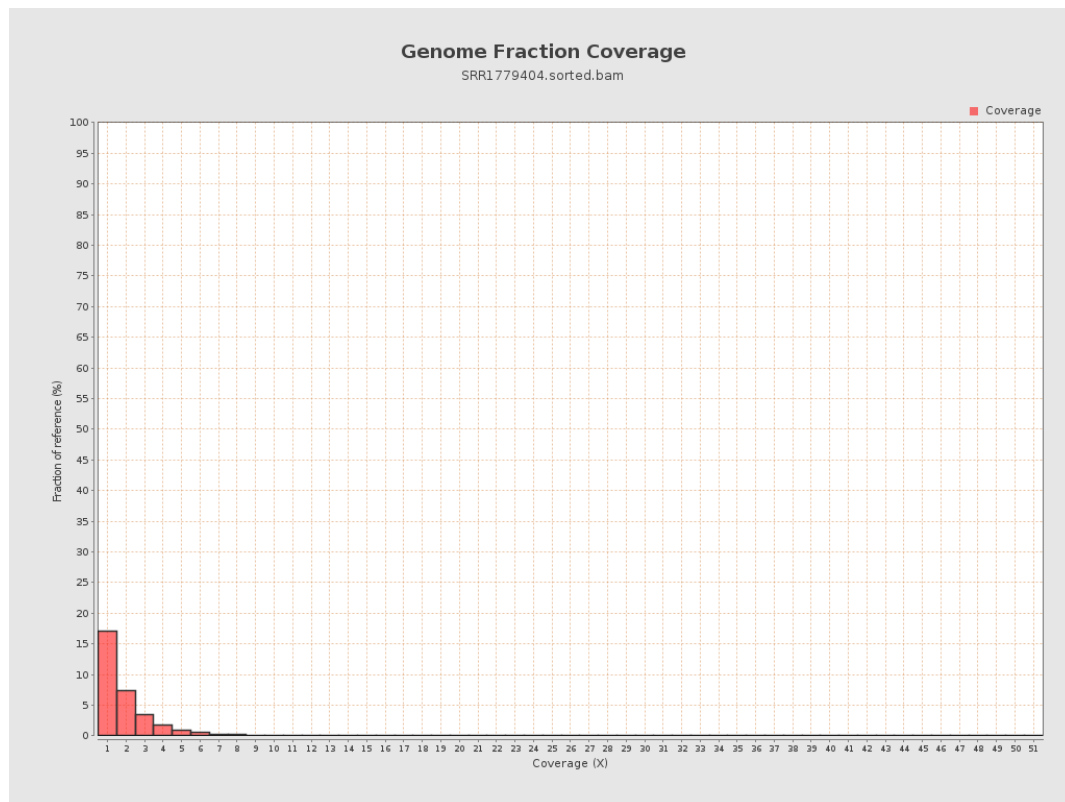




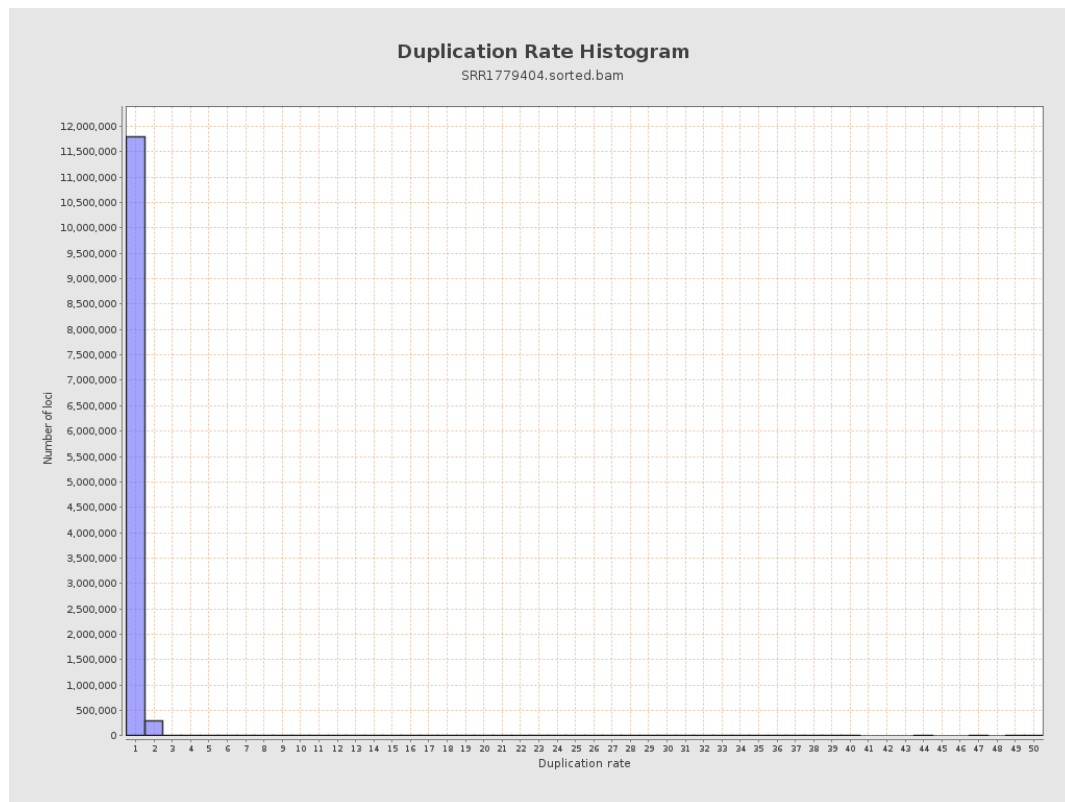
## 5. Results : Coverage Histogram (0-50X)



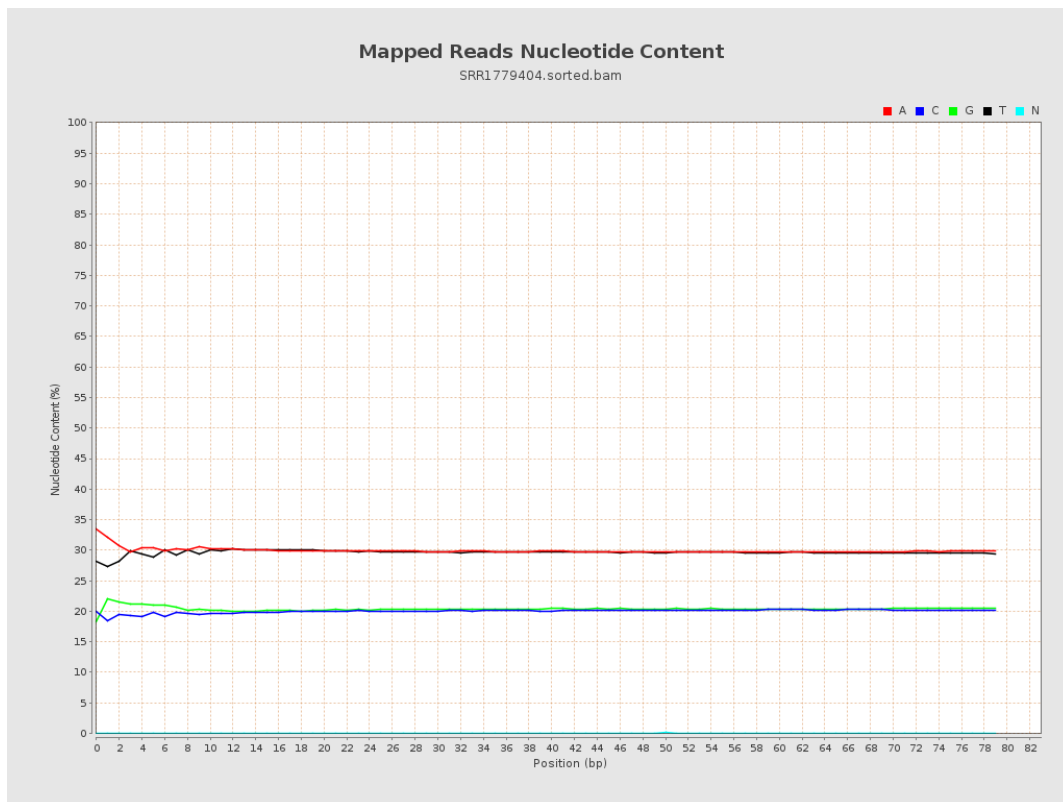
## 6. Results : Genome Fraction Coverage



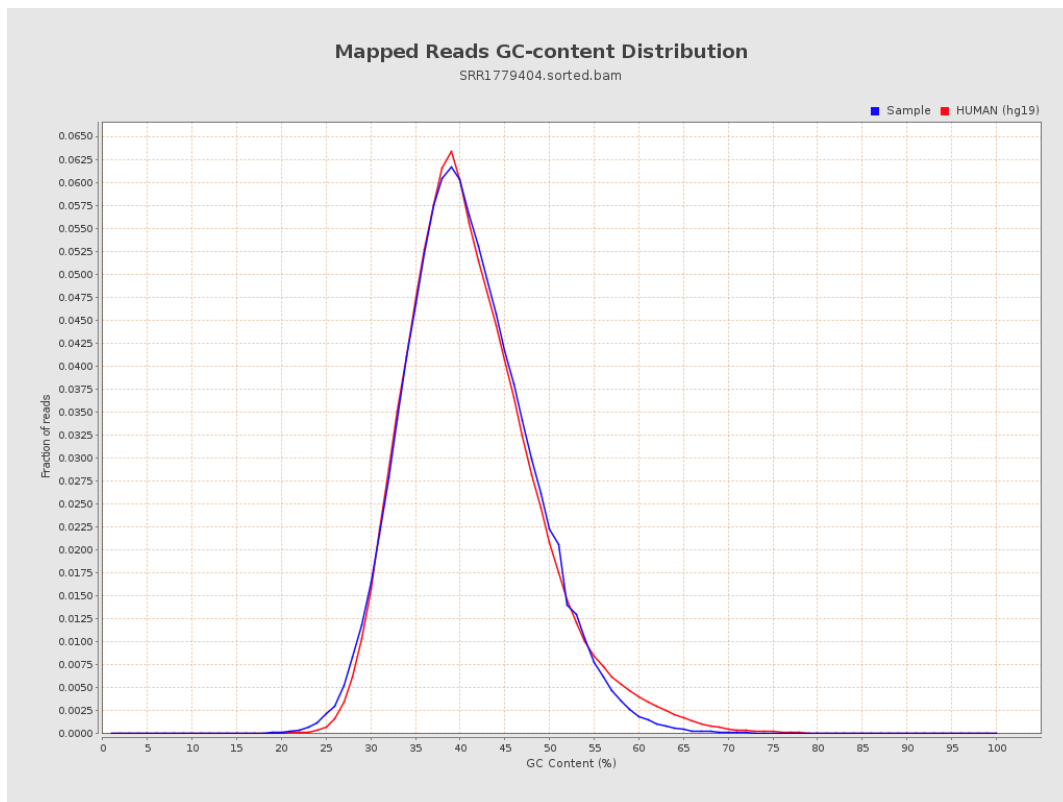
## 7. Results : Duplication Rate Histogram



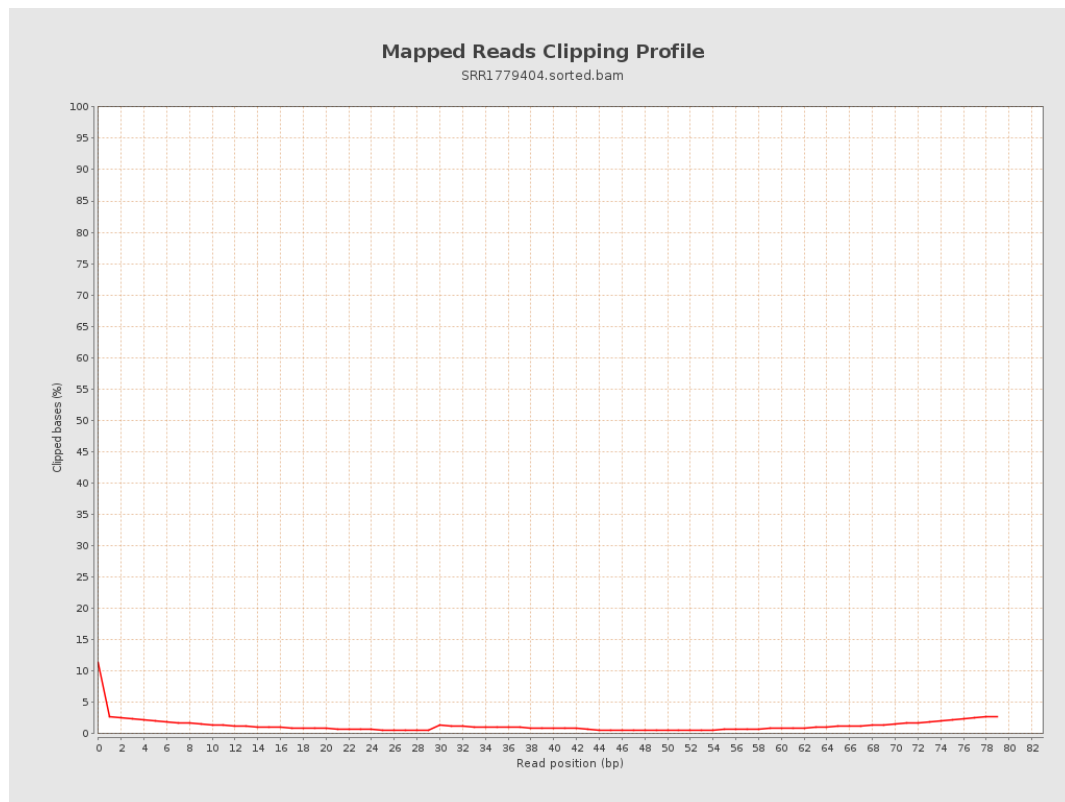
## 8. Results : Mapped Reads Nucleotide Content



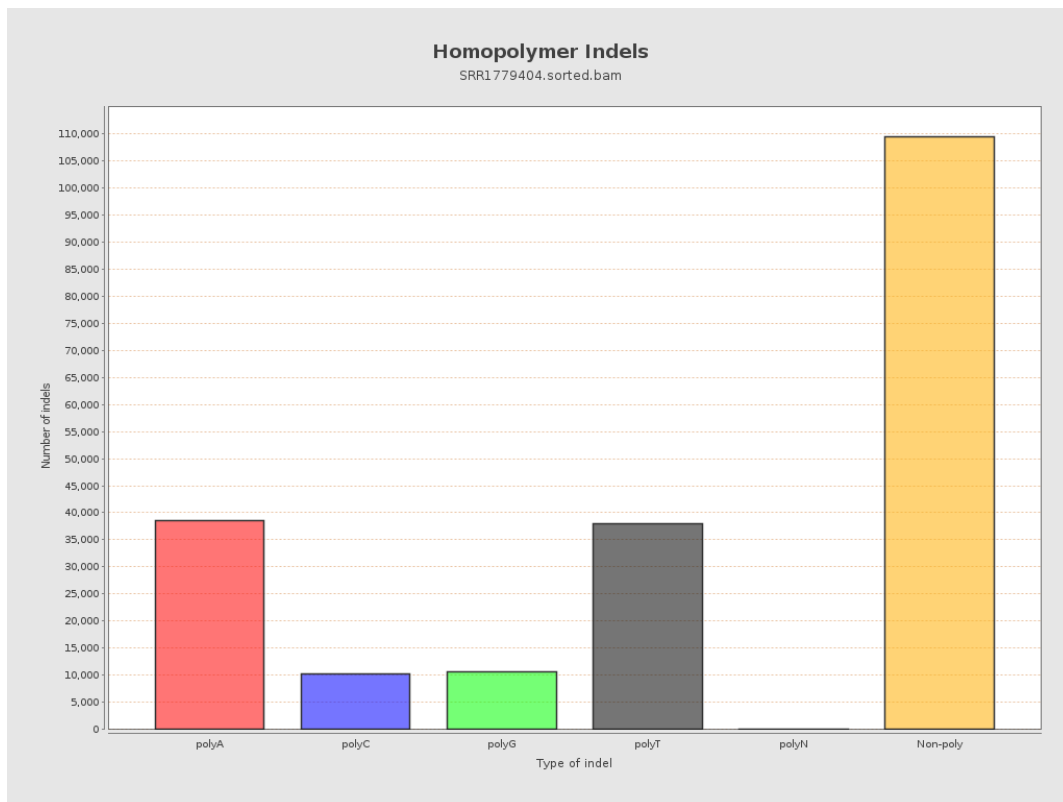
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

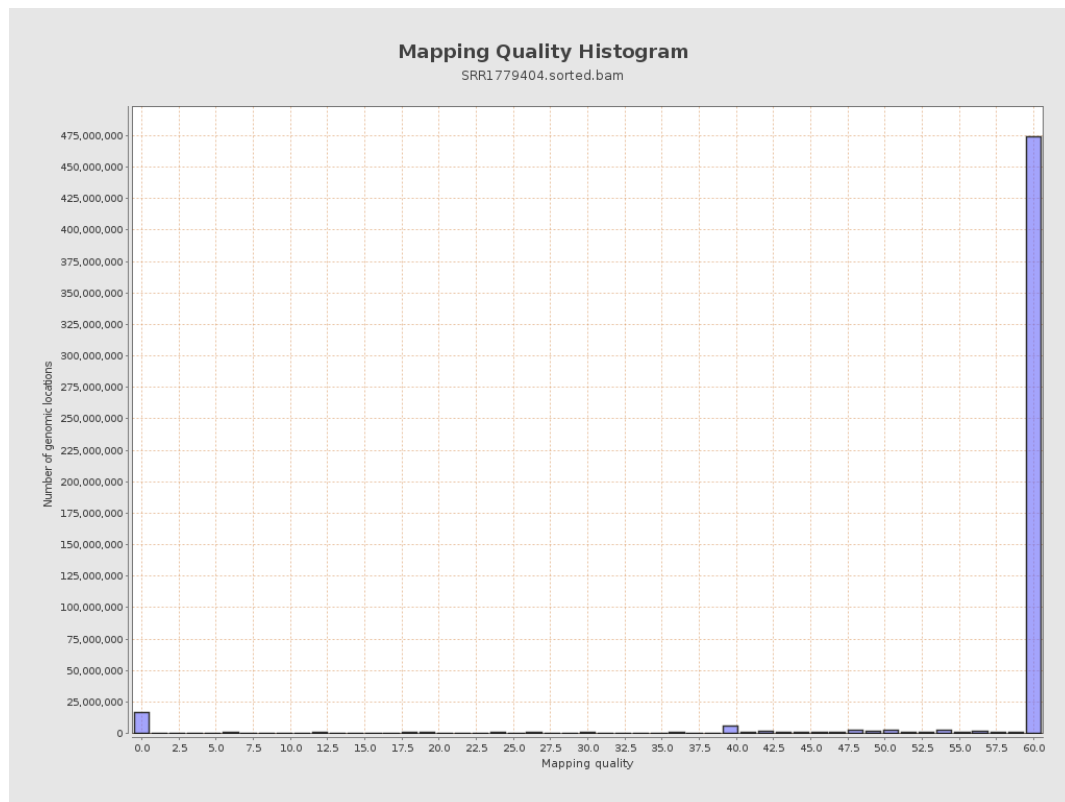


## 12. Results : Mapping Quality Across Reference

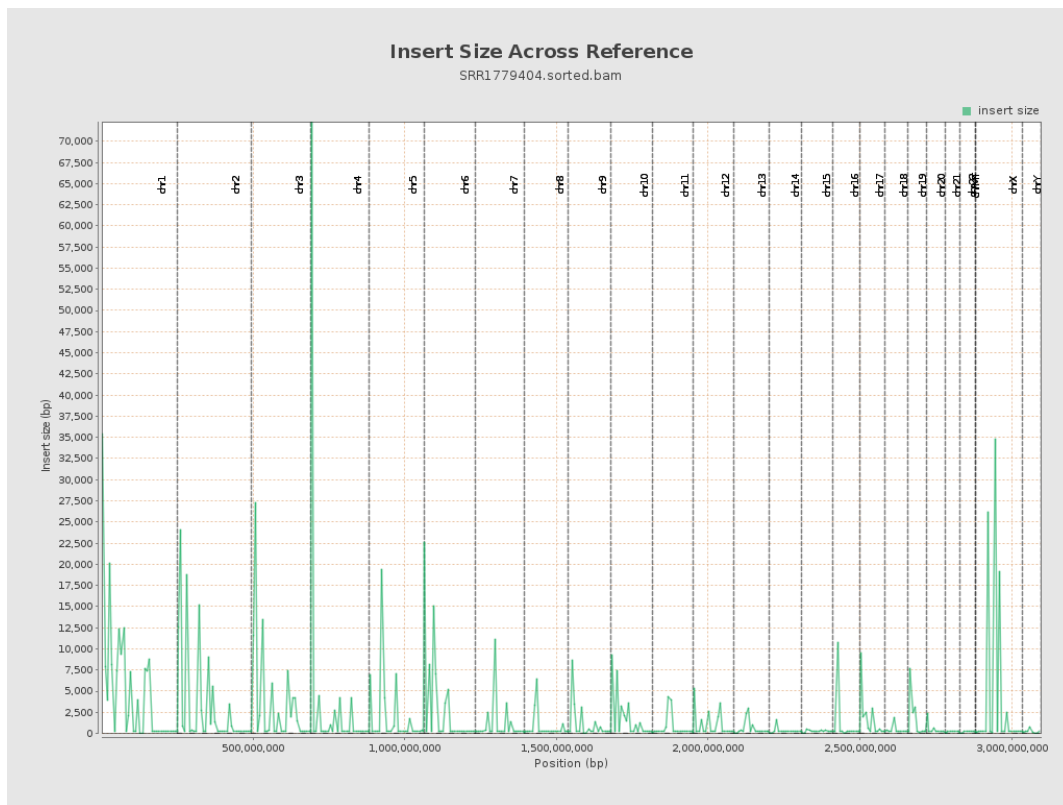




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

