

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/03 09:26:39*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777280.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_SRR1777280 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777280_1.fastq.gz SRR1777280_2.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                                                  |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                                                   |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                                                   |
| Analysis date:                        | Sun Apr 03 09:26:34 CST 2022                                                                                                                                                                                         |
| Size of a homopolymer:                | 3                                                                                                                                                                                                                    |
| Skip duplicate alignments:            | no                                                                                                                                                                                                                   |
| Number of windows:                    | 400                                                                                                                                                                                                                  |
| BAM file:                             | SRR1777280.sorted.bam                                                                                                                                                                                                |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 35,494,486          |
| Mapped reads                 | 35,058,554 / 98.77% |
| Unmapped reads               | 435,932 / 1.23%     |
| Mapped paired reads          | 35,058,554 / 98.77% |
| Mapped reads, first in pair  | 17,545,000 / 49.43% |
| Mapped reads, second in pair | 17,513,554 / 49.34% |
| Mapped reads, both in pair   | 34,888,358 / 98.29% |
| Mapped reads, singletons     | 170,196 / 0.48%     |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 1,085,196 / 3.06%   |
| Read min/max/mean length     | 30 / 101 / 102.22   |
| Duplicated reads (estimated) | 19,323,269 / 54.44% |
| Duplication rate             | 42.78%              |
| Clipped reads                | 4,518,452 / 12.73%  |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 924,236,934 / 26.61% |
| Number/percentage of C's | 805,483,084 / 23.19% |
| Number/percentage of T's | 923,020,906 / 26.57% |
| Number/percentage of G's | 804,575,119 / 23.16% |
| Number/percentage of N's | 16,231,041 / 0.47%   |
|                          |                      |

|               |        |
|---------------|--------|
| GC Percentage | 46.35% |
|---------------|--------|

## 2.3. Coverage

|                    |         |
|--------------------|---------|
| Mean               | 1.1229  |
| Standard Deviation | 32.8401 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 53.66 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 242,480.87      |
| Standard Deviation | 4,836,366.65    |
| P25/Median/P75     | 188 / 237 / 295 |

## 2.6. Mismatches and indels

|                                          |            |
|------------------------------------------|------------|
| General error rate                       | 0.95%      |
| Mismatches                               | 30,339,160 |
| Insertions                               | 974,935    |
| Mapped reads with at least one insertion | 2.56%      |
| Deletions                                | 735,296    |
| Mapped reads with at least one deletion  | 1.93%      |
| Homopolymer indels                       | 32.19%     |

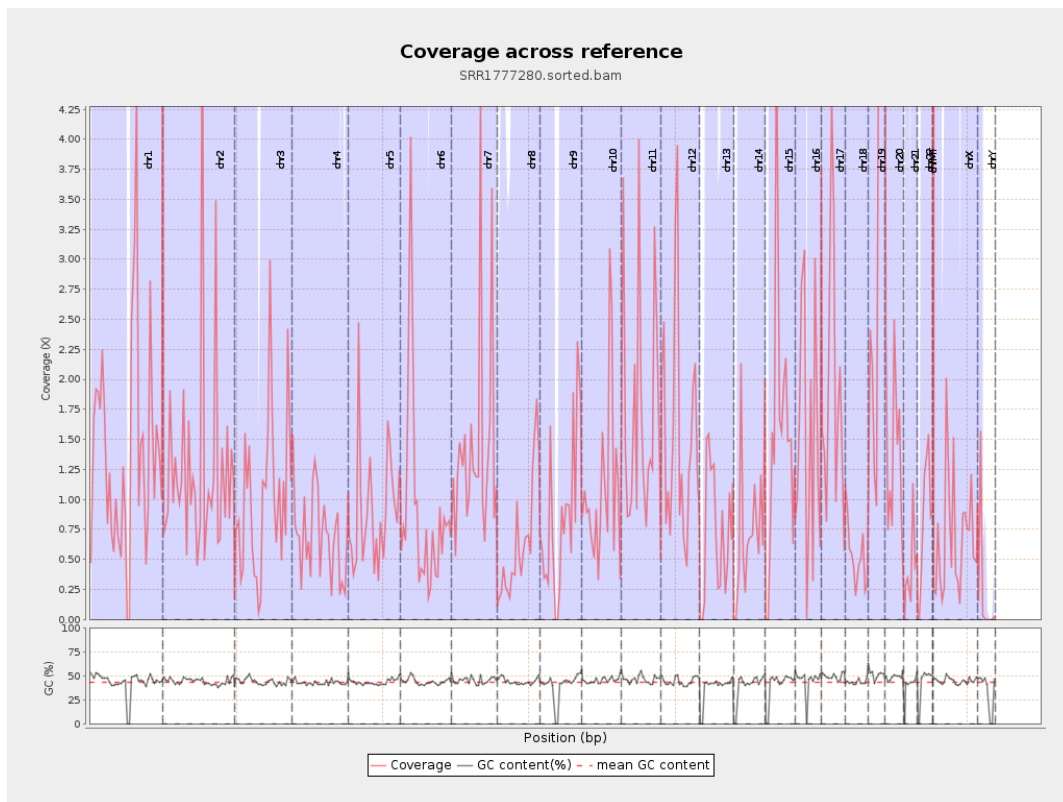
## 2.7. Chromosome stats

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

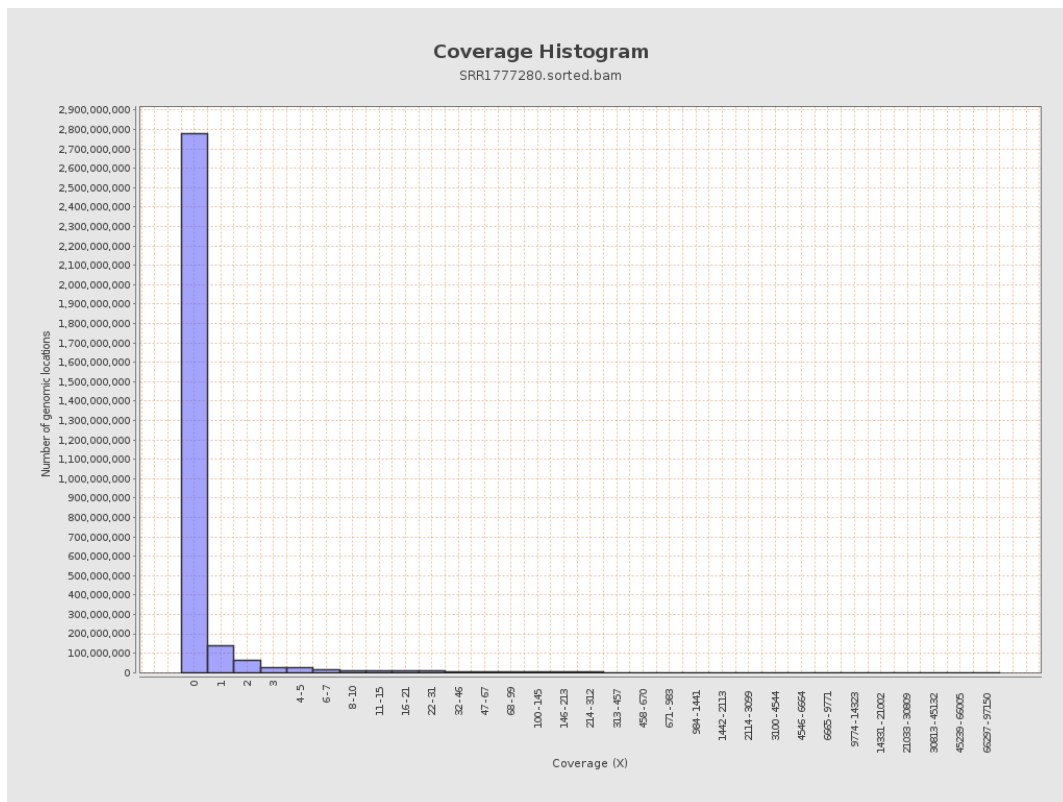
|       |           | <b>bases</b> | <b>coverage</b> | <b>deviation</b> |
|-------|-----------|--------------|-----------------|------------------|
| chr1  | 249250621 | 351236414    | 1.4092          | 20.1733          |
| chr2  | 243199373 | 308335598    | 1.2678          | 72.2799          |
| chr3  | 198022430 | 197891222    | 0.9993          | 15.6545          |
| chr4  | 191154276 | 133087255    | 0.6962          | 21.4299          |
| chr5  | 180915260 | 165062136    | 0.9124          | 18.9488          |
| chr6  | 171115067 | 153279465    | 0.8958          | 19.8628          |
| chr7  | 159138663 | 225281121    | 1.4156          | 29.7183          |
| chr8  | 146364022 | 97195381     | 0.6641          | 13.8805          |
| chr9  | 141213431 | 118860851    | 0.8417          | 18.8604          |
| chr10 | 135534747 | 150758236    | 1.1123          | 61.197           |
| chr11 | 135006516 | 233868440    | 1.7323          | 22.5974          |
| chr12 | 133851895 | 211087570    | 1.577           | 23.878           |
| chr13 | 115169878 | 81676236     | 0.7092          | 13.6508          |
| chr14 | 107349540 | 75978999     | 0.7078          | 18.7128          |
| chr15 | 102531392 | 154678357    | 1.5086          | 17.0568          |
| chr16 | 90354753  | 132439663    | 1.4658          | 55.1995          |
| chr17 | 81195210  | 154588840    | 1.9039          | 20.6542          |
| chr18 | 78077248  | 41416576     | 0.5305          | 11.9716          |
| chr19 | 59128983  | 220697553    | 3.7325          | 40.8281          |
| chr20 | 63025520  | 85805382     | 1.3614          | 16.4251          |
| chr21 | 48129895  | 20917569     | 0.4346          | 9.9256           |
| chr22 | 51304566  | 43152857     | 0.8411          | 15.5058          |
| chrMT | 16571     | 883978       | 53.3449         | 18.1107          |
| chrX  | 155270560 | 104467270    | 0.6728          | 13.6136          |

|      |          |          |        |         |
|------|----------|----------|--------|---------|
| chrY | 59373566 | 13403062 | 0.2257 | 65.3618 |
|------|----------|----------|--------|---------|

### 3. Results : Coverage across reference

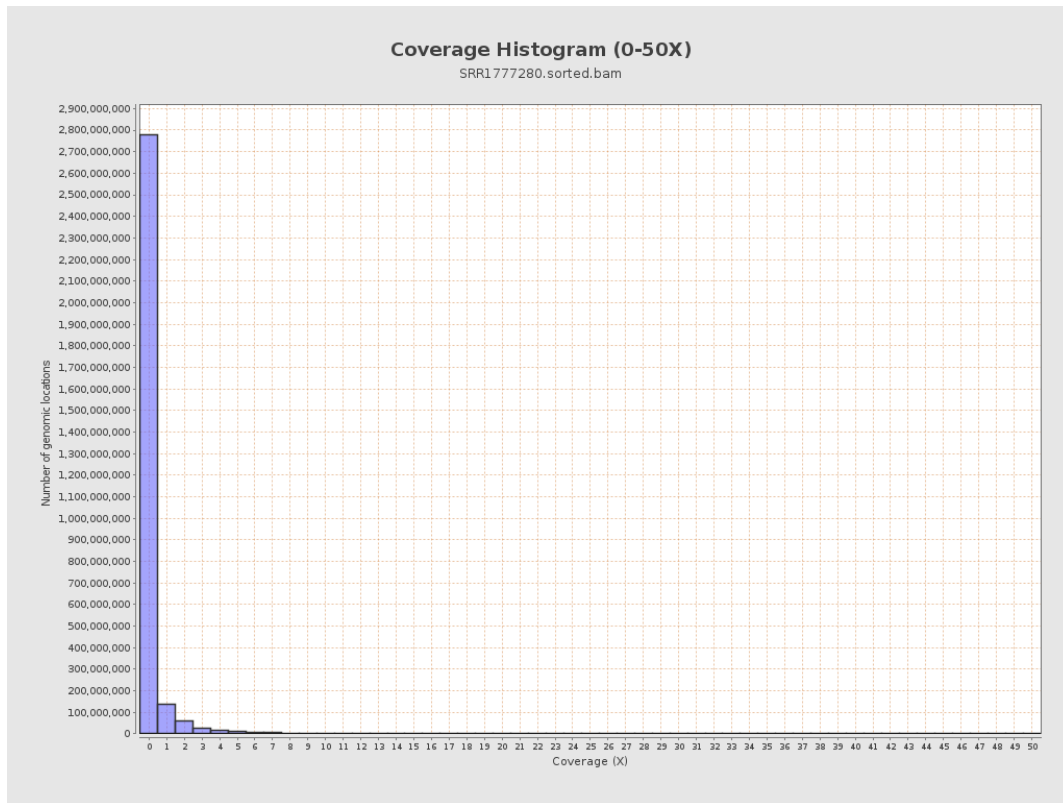


## 4. Results : Coverage Histogram

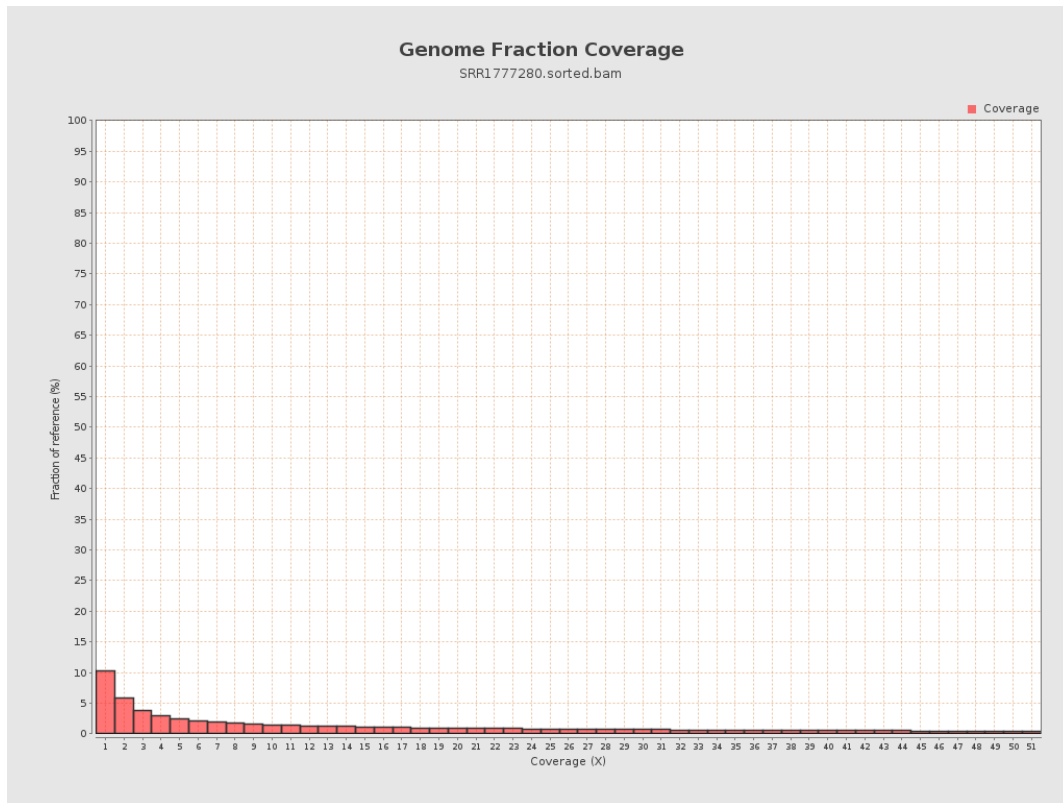




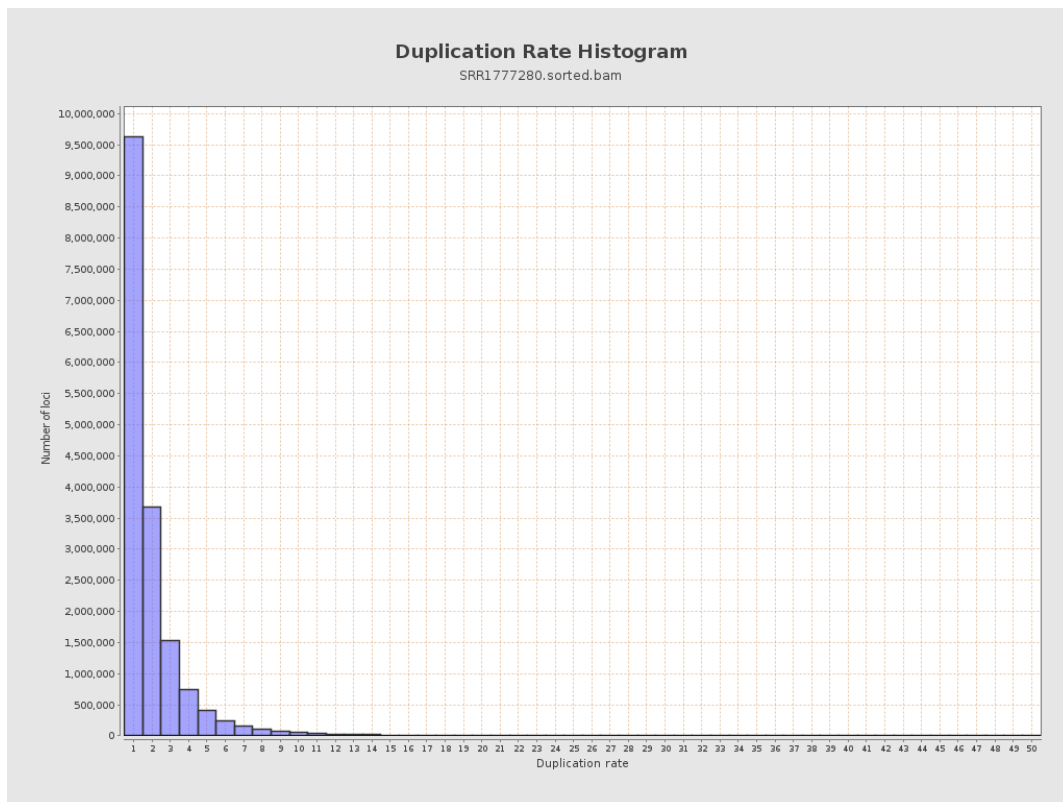
## 5. Results : Coverage Histogram (0-50X)



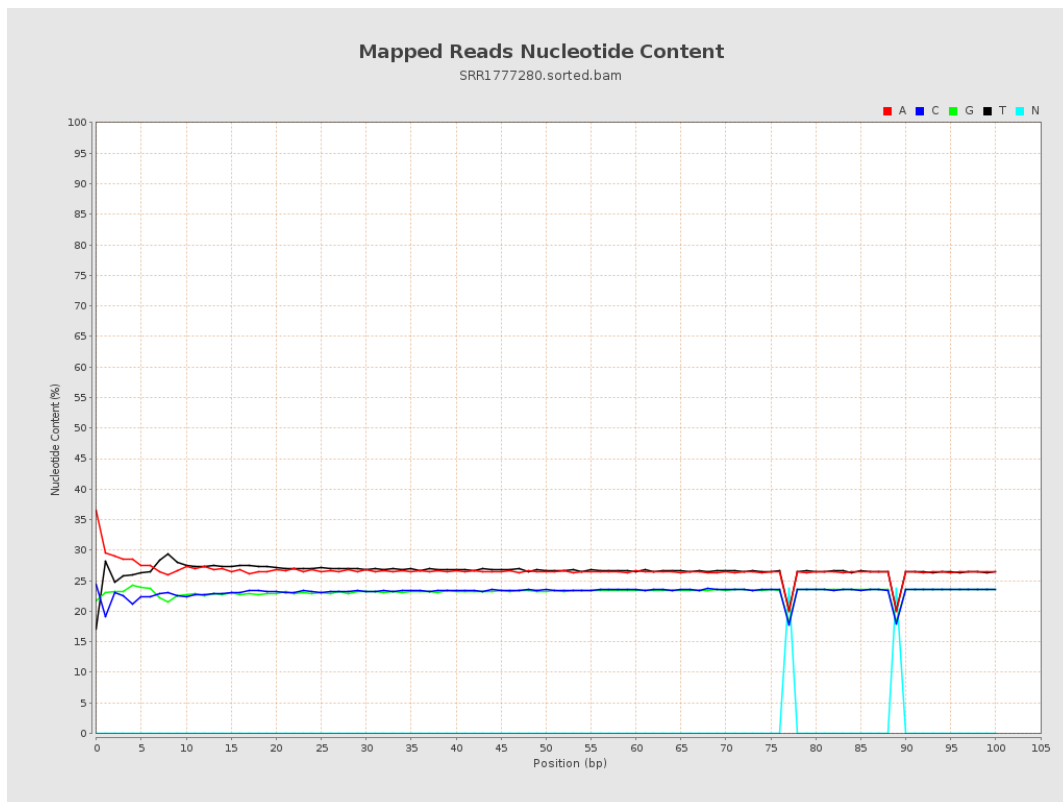
## 6. Results : Genome Fraction Coverage



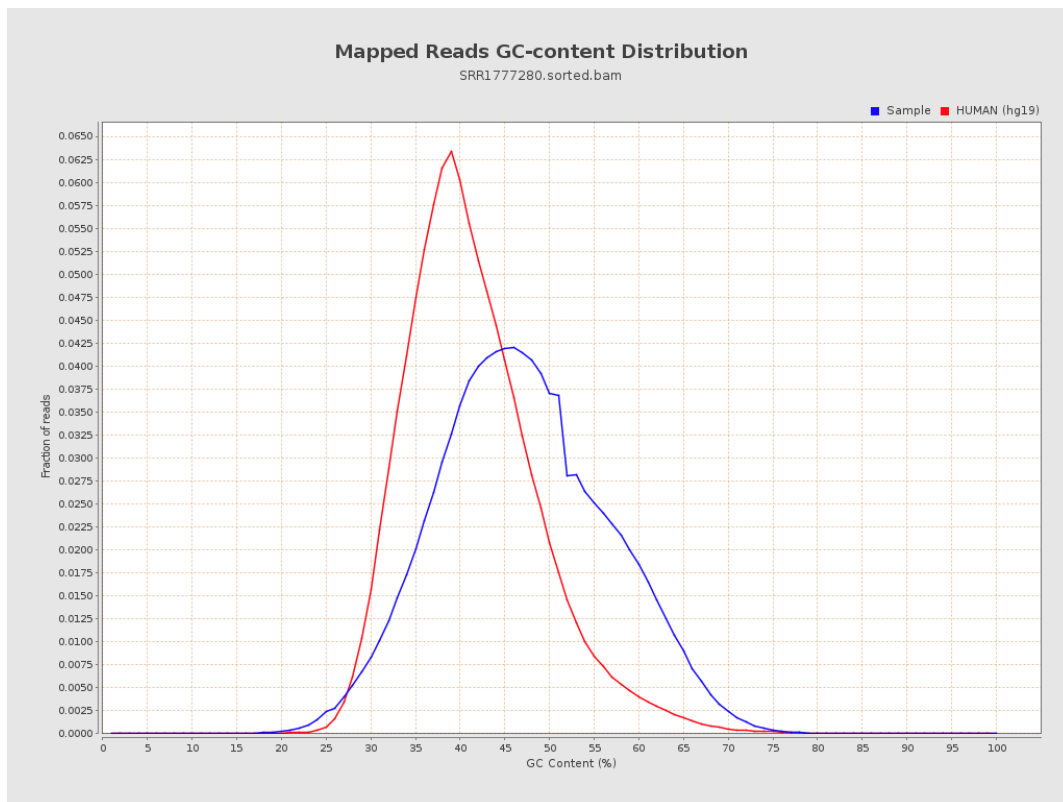
## 7. Results : Duplication Rate Histogram



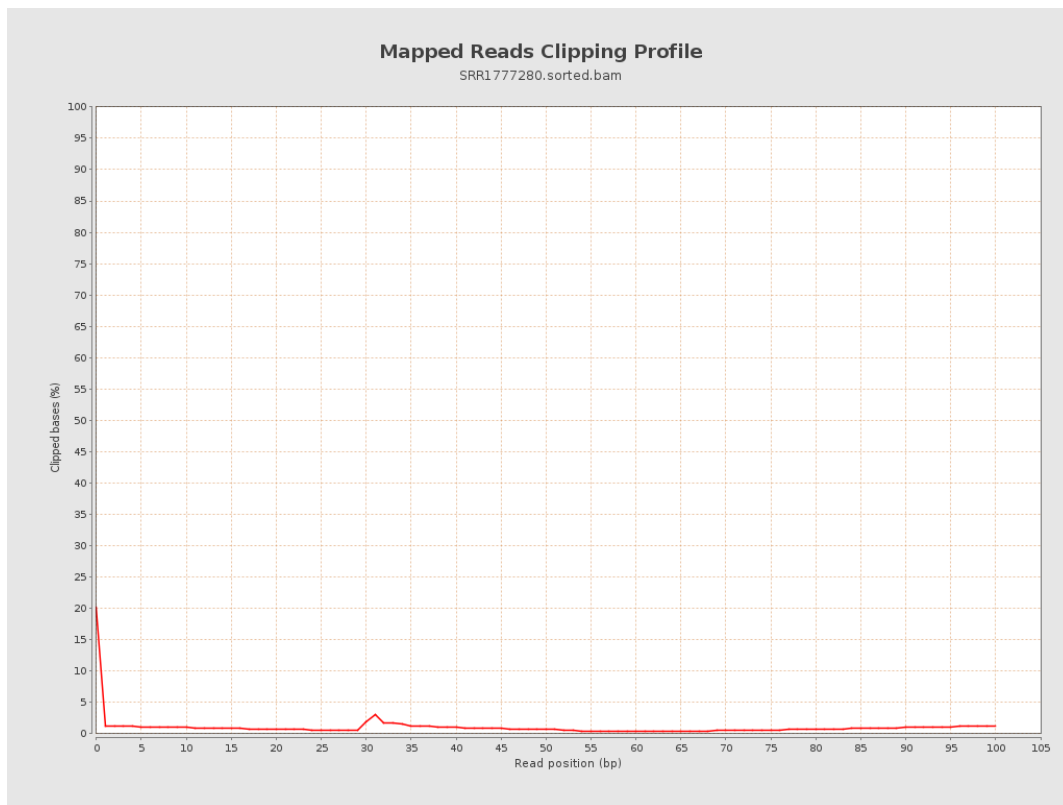
## 8. Results : Mapped Reads Nucleotide Content



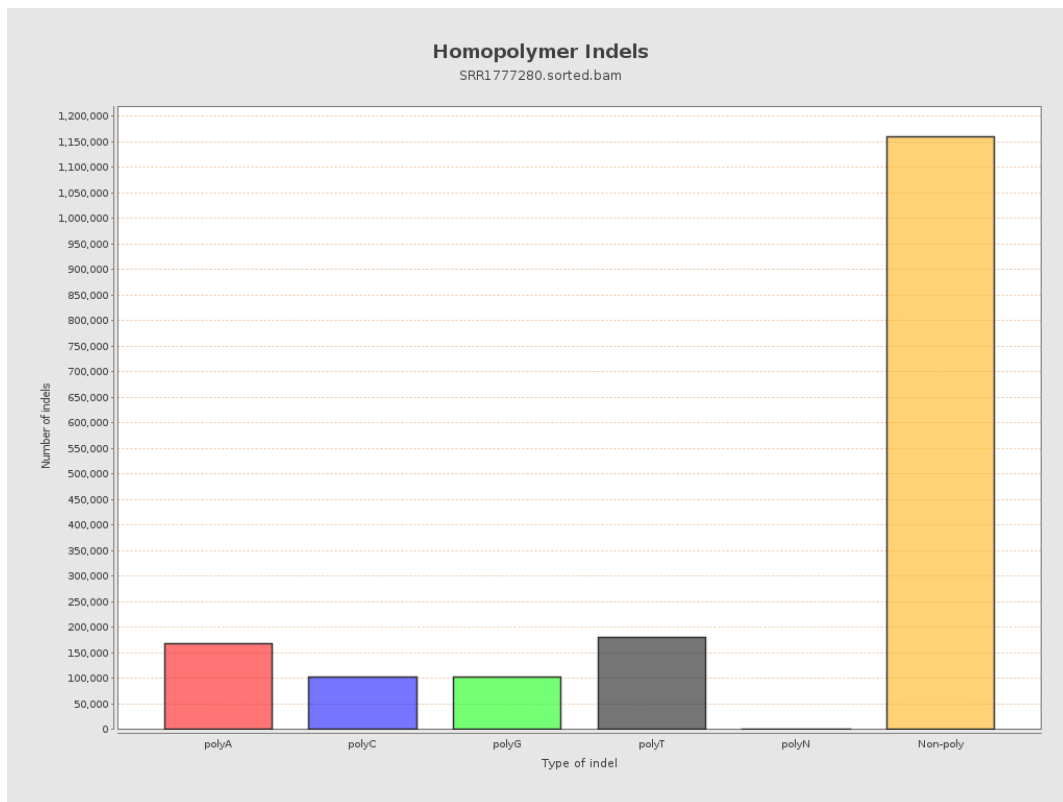
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

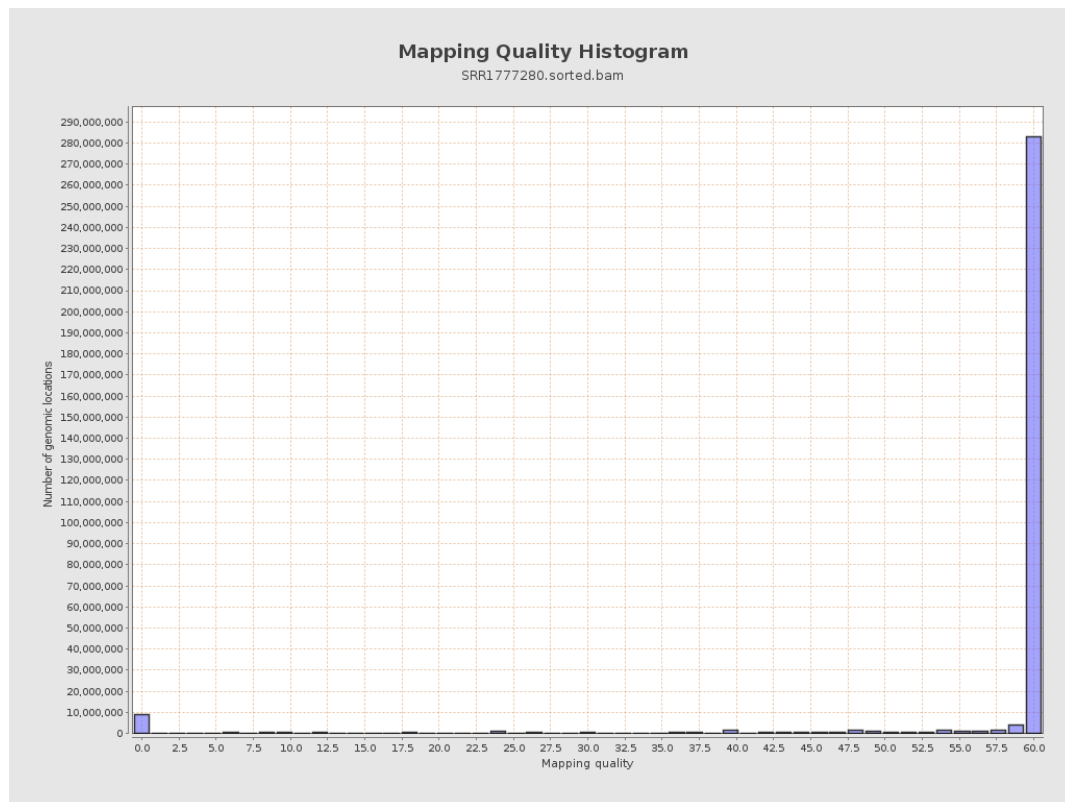


## 12. Results : Mapping Quality Across Reference

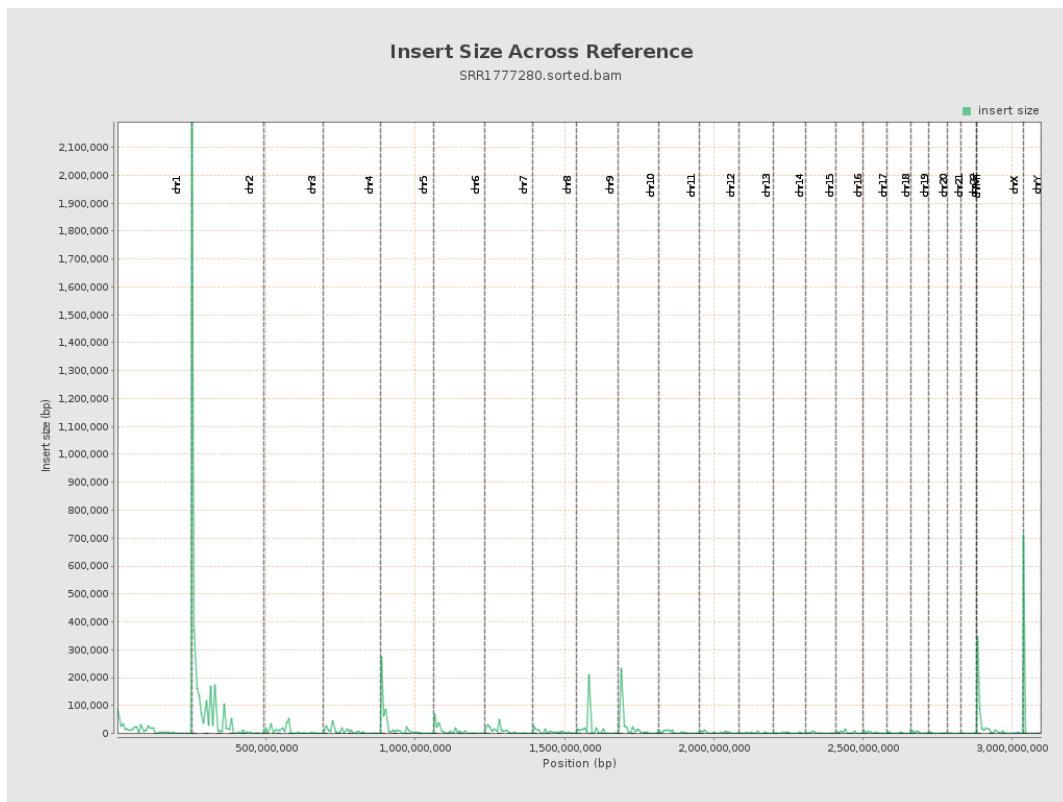




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

