

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 07:59:19*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081777.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_SRR3081777 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081777.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Sat Aug 24 07:59:13 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR3081777.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 2,800,101          |
| Mapped reads                 | 2,555,771 / 91.27% |
| Unmapped reads               | 244,330 / 8.73%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 20,509 / 0.73%     |
| Read min/max/mean length     | 30 / 76 / 76.25    |
| Duplicated reads (estimated) | 108,275 / 3.87%    |
| Duplication rate             | 2.81%              |
| Clipped reads                | 1,095,712 / 39.13% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 47,303,206 / 27.55% |
| Number/percentage of C's | 33,305,113 / 19.4%  |
| Number/percentage of T's | 51,925,889 / 30.25% |
| Number/percentage of G's | 39,134,936 / 22.8%  |
| Number/percentage of N's | 2,085 / 0%          |
| GC Percentage            | 42.2%               |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0555 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.5608 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |      |
|----------------------|------|
| Mean Mapping Quality | 43.5 |
|----------------------|------|

## 2.5. Mismatches and indels

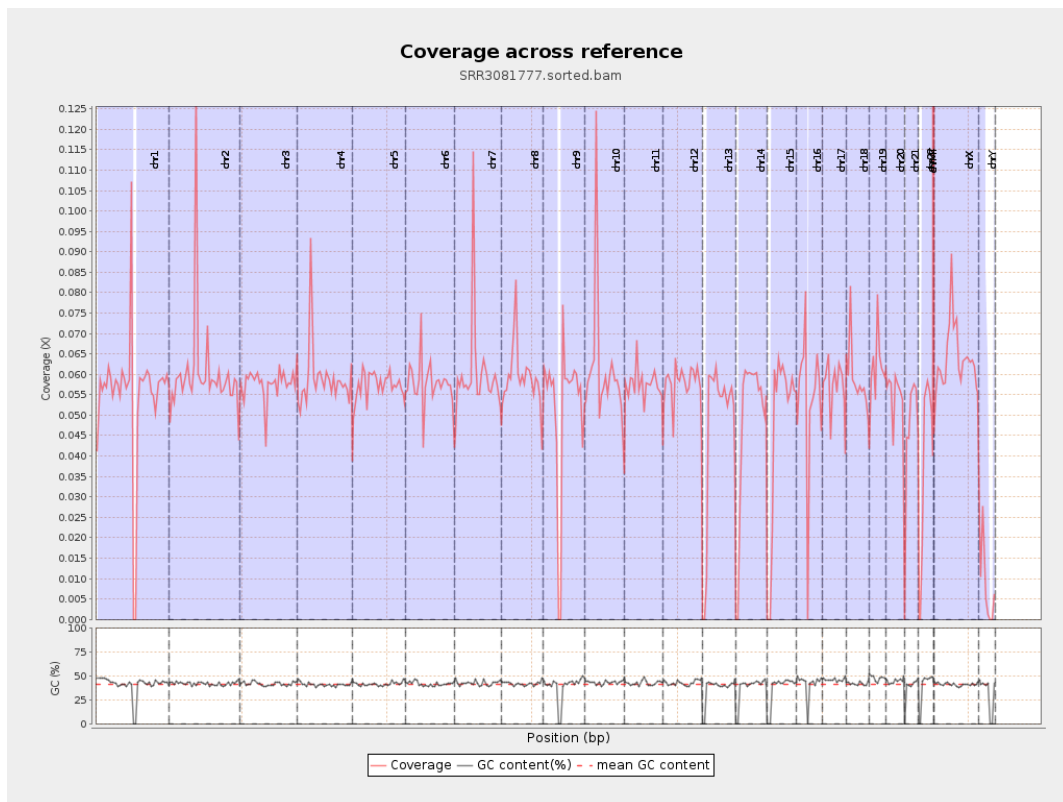
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.87%     |
| Mismatches                               | 1,473,990 |
| Insertions                               | 13,459    |
| Mapped reads with at least one insertion | 0.52%     |
| Deletions                                | 39,266    |
| Mapped reads with at least one deletion  | 1.52%     |
| Homopolymer indels                       | 45.1%     |

## 2.6. Chromosome stats

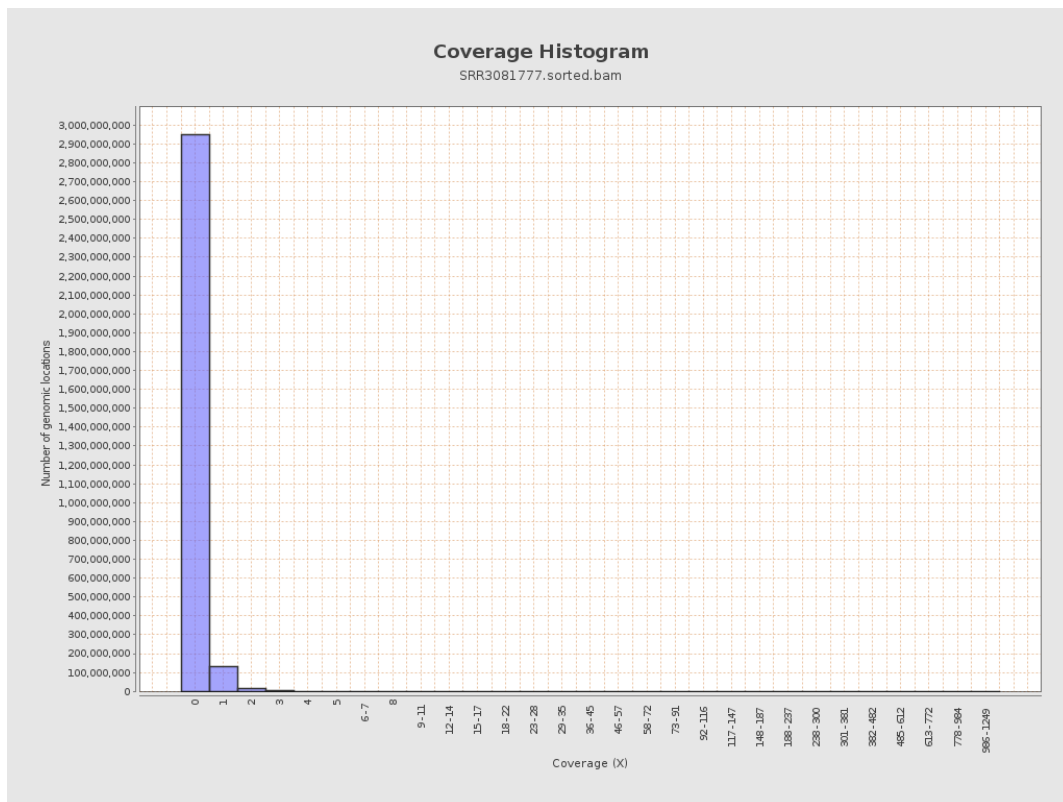
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 13740924     | 0.0551        | 1.0974             |
| chr2 | 243199373 | 14645658     | 0.0602        | 0.7059             |
| chr3 | 198022430 | 11411487     | 0.0576        | 0.2794             |
| chr4 | 191154276 | 11221939     | 0.0587        | 0.3291             |
| chr5 | 180915260 | 10378568     | 0.0574        | 0.2723             |
| chr6 | 171115067 | 9867469      | 0.0577        | 0.3393             |
| chr7 | 159138663 | 9628890      | 0.0605        | 0.8507             |
|      |           |              |               |                    |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr8  | 146364022 | 8665497 | 0.0592 | 0.5778 |
| chr9  | 141213431 | 7264569 | 0.0514 | 0.5369 |
| chr10 | 135534747 | 8244598 | 0.0608 | 0.6142 |
| chr11 | 135006516 | 7721497 | 0.0572 | 0.4298 |
| chr12 | 133851895 | 7742846 | 0.0578 | 0.2805 |
| chr13 | 115169878 | 5402584 | 0.0469 | 0.2425 |
| chr14 | 107349540 | 5180367 | 0.0483 | 0.2929 |
| chr15 | 102531392 | 4861995 | 0.0474 | 0.2533 |
| chr16 | 90354753  | 4888487 | 0.0541 | 0.3376 |
| chr17 | 81195210  | 4616046 | 0.0569 | 0.307  |
| chr18 | 78077248  | 4620479 | 0.0592 | 0.9806 |
| chr19 | 59128983  | 3675383 | 0.0622 | 0.8425 |
| chr20 | 63025520  | 3413574 | 0.0542 | 0.2812 |
| chr21 | 48129895  | 2224687 | 0.0462 | 0.2904 |
| chr22 | 51304566  | 1926518 | 0.0376 | 0.2174 |
| chrMT | 16571     | 12373   | 0.7467 | 0.9758 |
| chrX  | 155270560 | 9875996 | 0.0636 | 0.3532 |
| chrY  | 59373566  | 508954  | 0.0086 | 0.2227 |

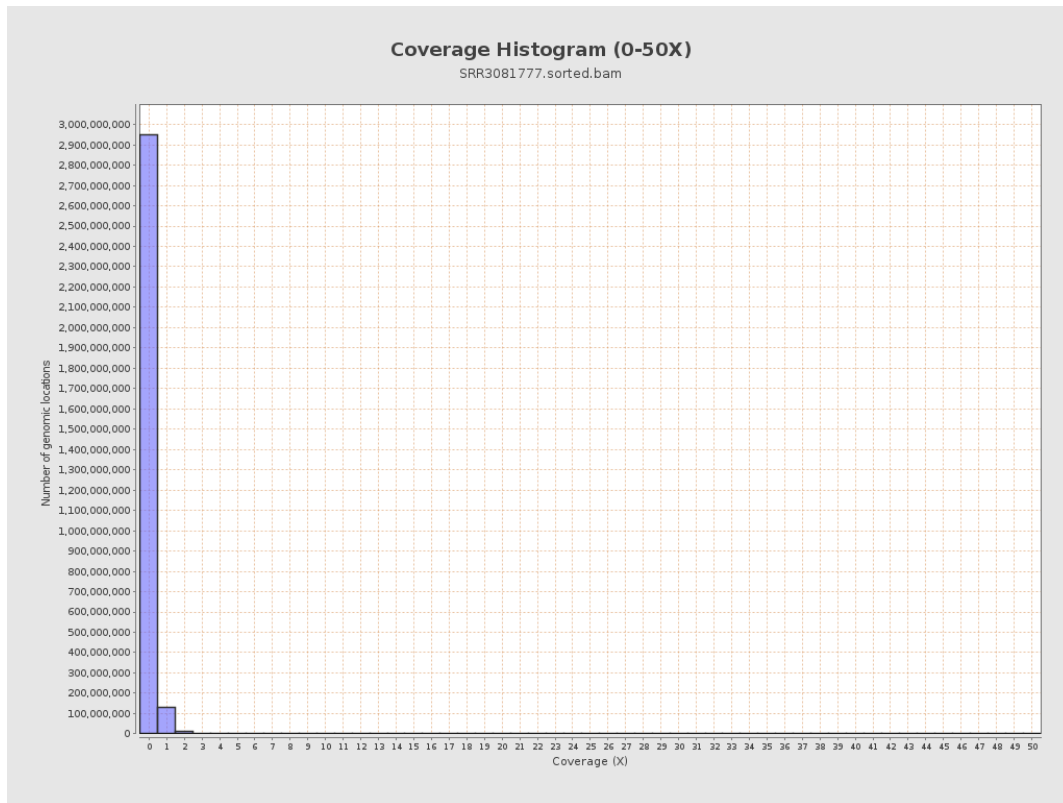
### 3. Results : Coverage across reference



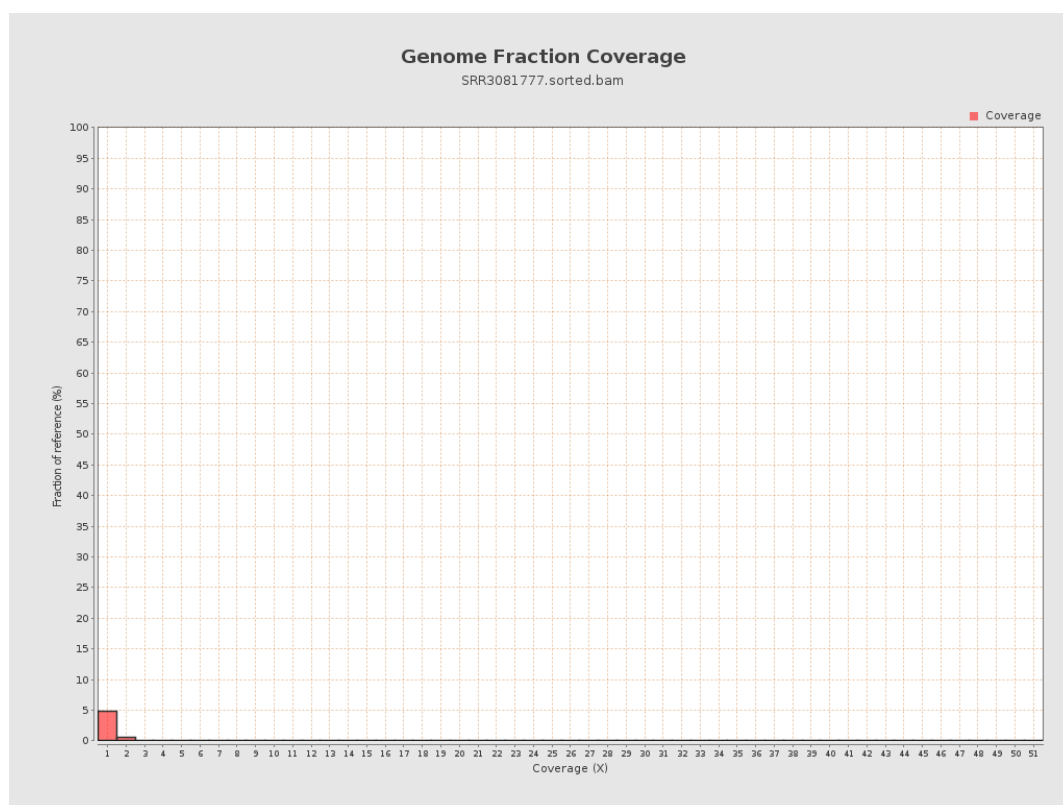
## 4. Results : Coverage Histogram



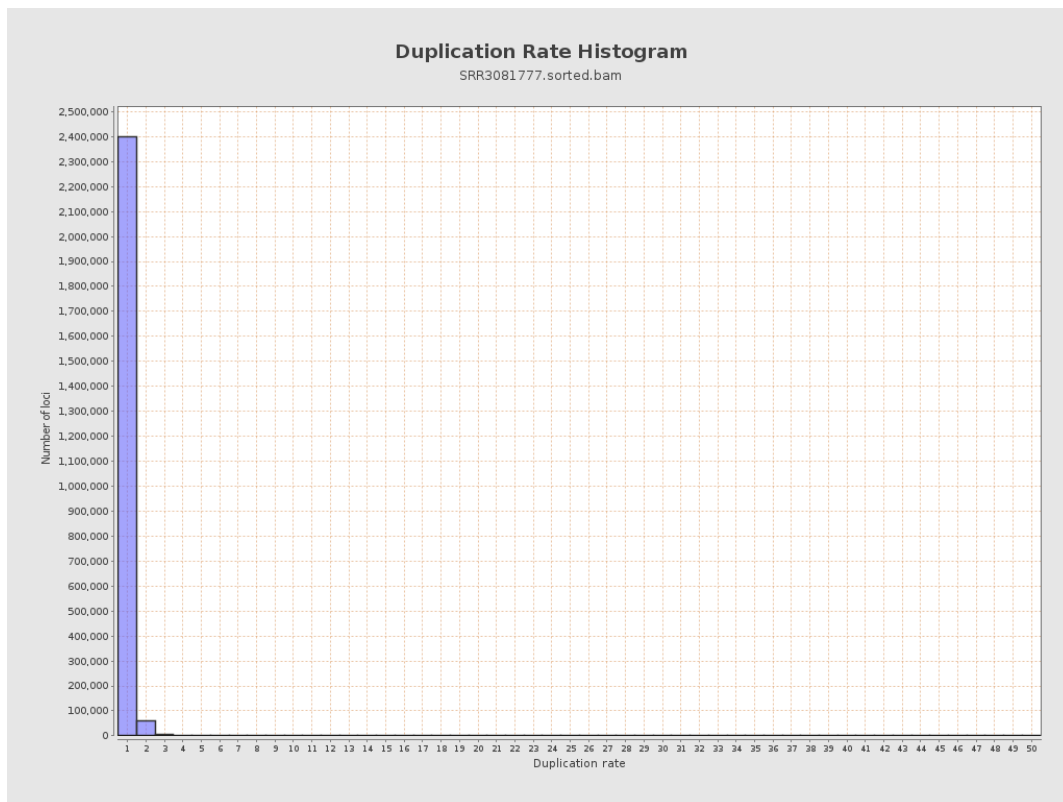
## 5. Results : Coverage Histogram (0-50X)



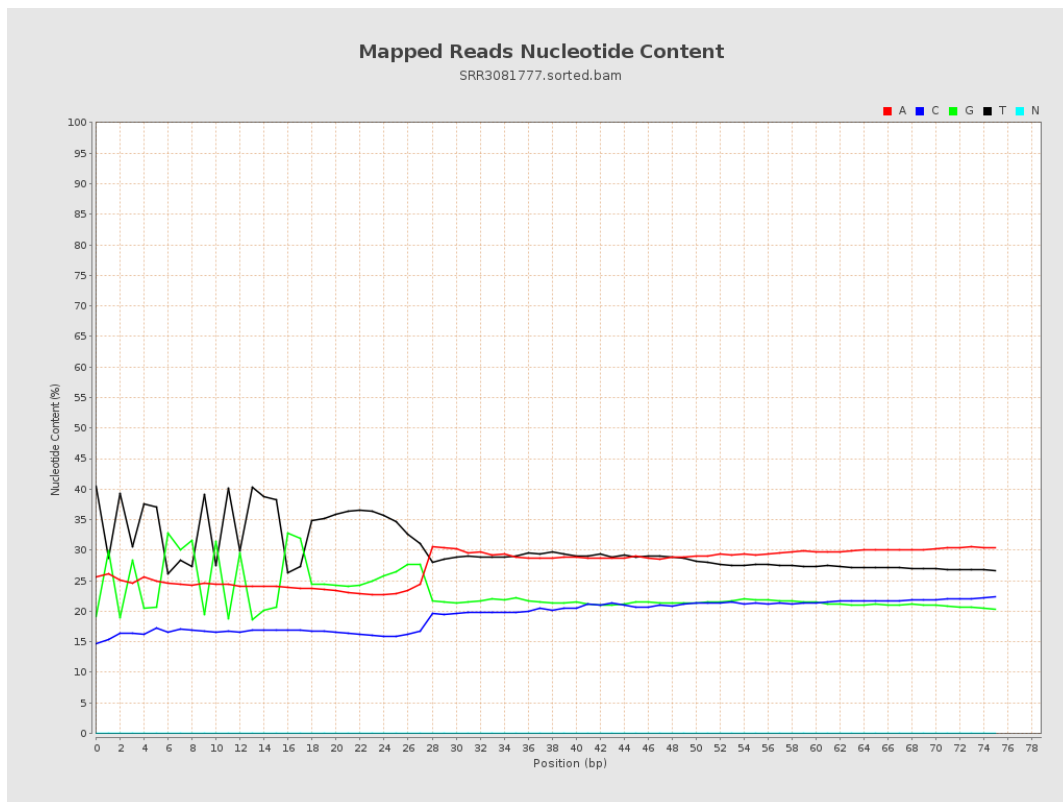
## 6. Results : Genome Fraction Coverage



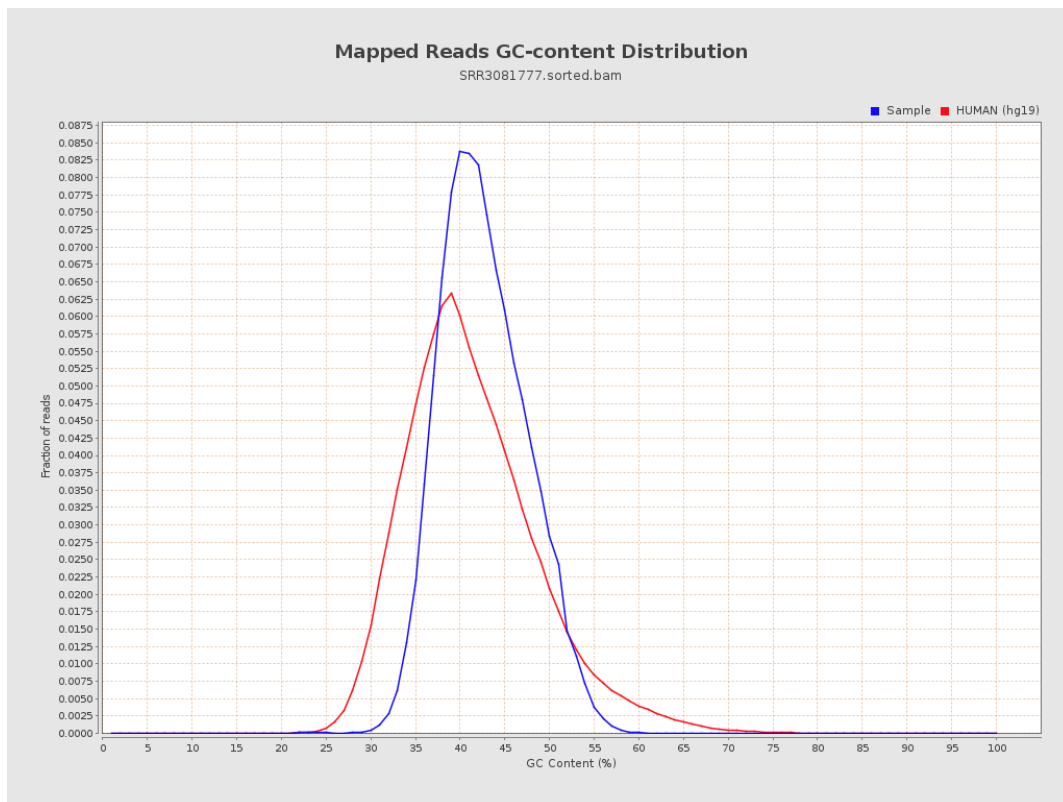
## 7. Results : Duplication Rate Histogram



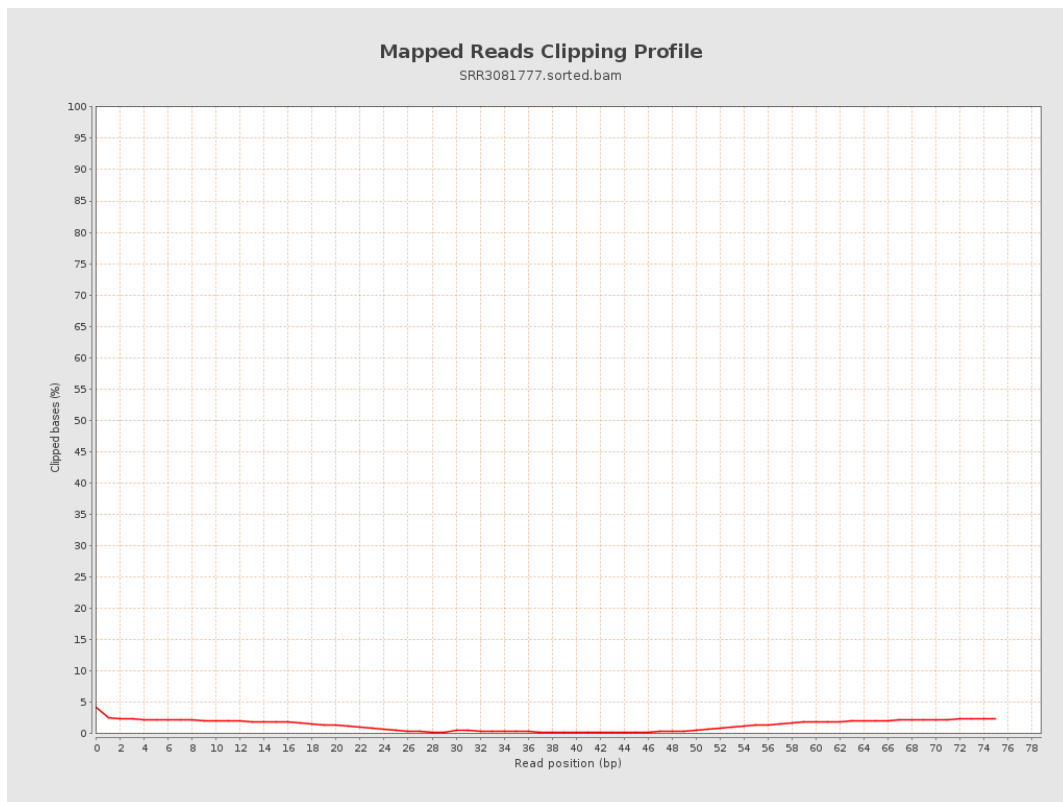
## 8. Results : Mapped Reads Nucleotide Content



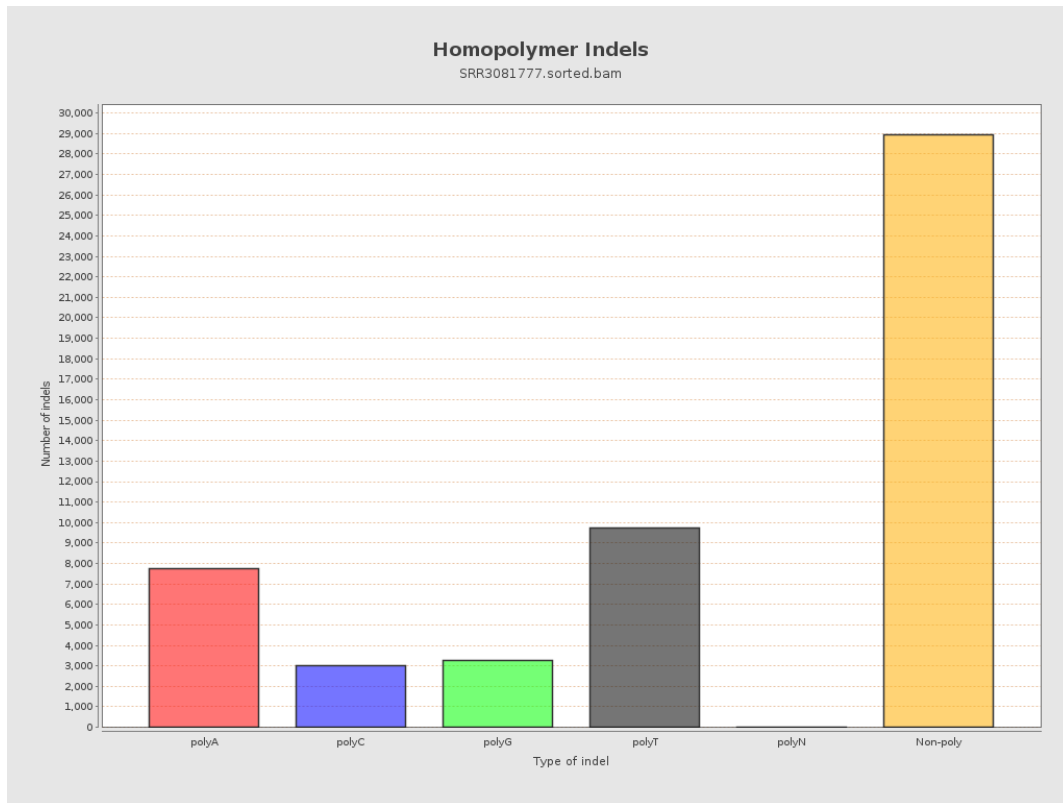
## 9. Results : Mapped Reads GC-content Distribution



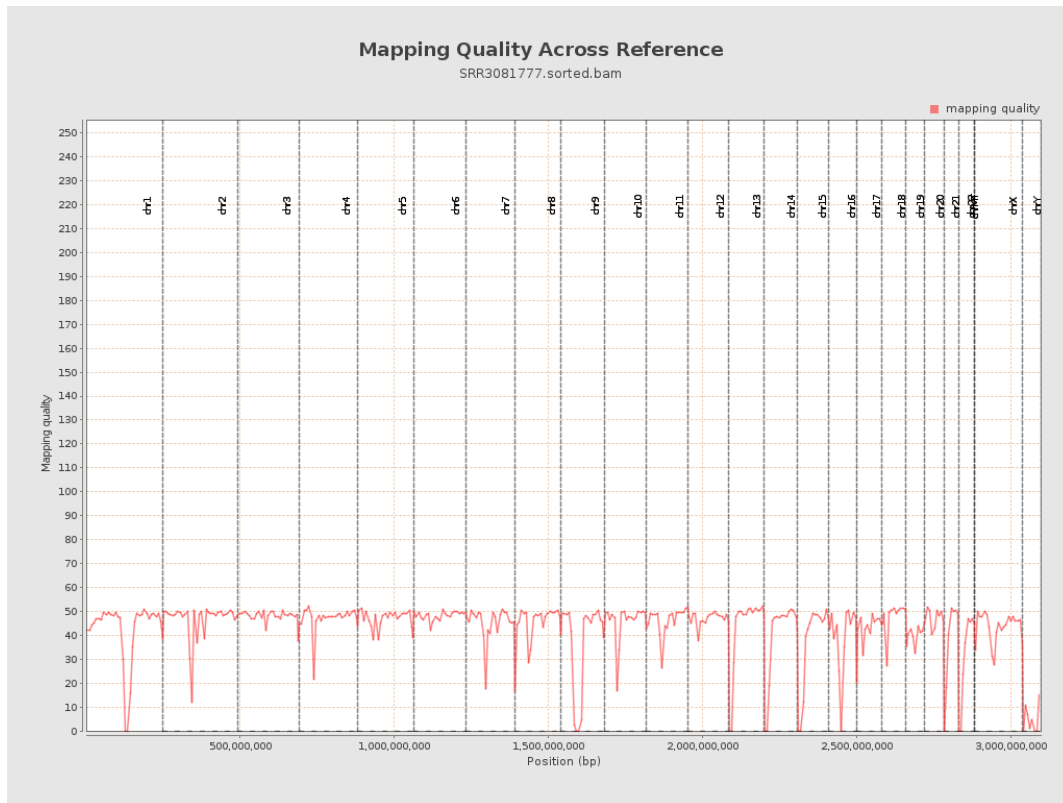
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

