

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 23:32:22*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083096.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_SRR3083096 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083096.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Sat Aug 24 23:32:21 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR3083096.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 4,037,566          |
| Mapped reads                 | 3,332,663 / 82.54% |
| Unmapped reads               | 704,903 / 17.46%   |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 28,083 / 0.7%      |
| Read min/max/mean length     | 30 / 76 / 76.24    |
| Duplicated reads (estimated) | 162,076 / 4.01%    |
| Duplication rate             | 3.17%              |
| Clipped reads                | 1,605,225 / 39.76% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 60,639,353 / 27.5%  |
| Number/percentage of C's | 41,255,416 / 18.71% |
| Number/percentage of T's | 68,695,245 / 31.15% |
| Number/percentage of G's | 49,891,675 / 22.63% |
| Number/percentage of N's | 20,859 / 0.01%      |
| GC Percentage            | 41.34%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0713 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.7398 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 43.63 |
|----------------------|-------|

## 2.5. Mismatches and indels

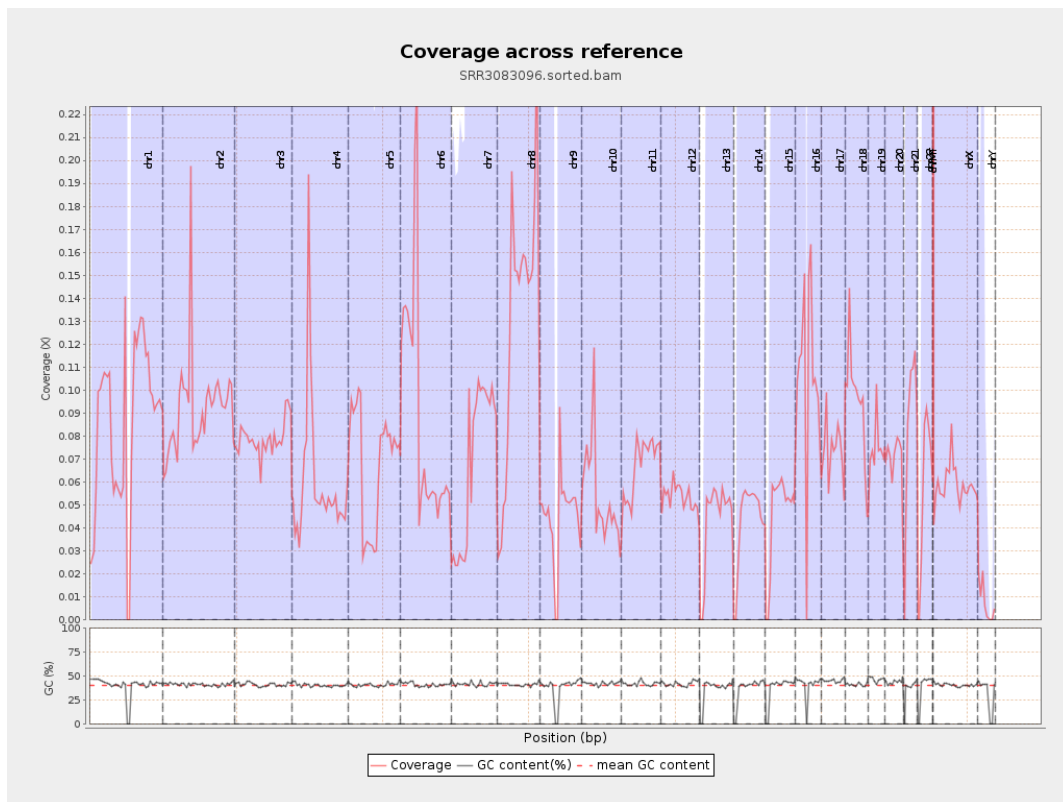
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.95%     |
| Mismatches                               | 2,061,341 |
| Insertions                               | 19,396    |
| Mapped reads with at least one insertion | 0.58%     |
| Deletions                                | 52,360    |
| Mapped reads with at least one deletion  | 1.55%     |
| Homopolymer indels                       | 47.27%    |

## 2.6. Chromosome stats

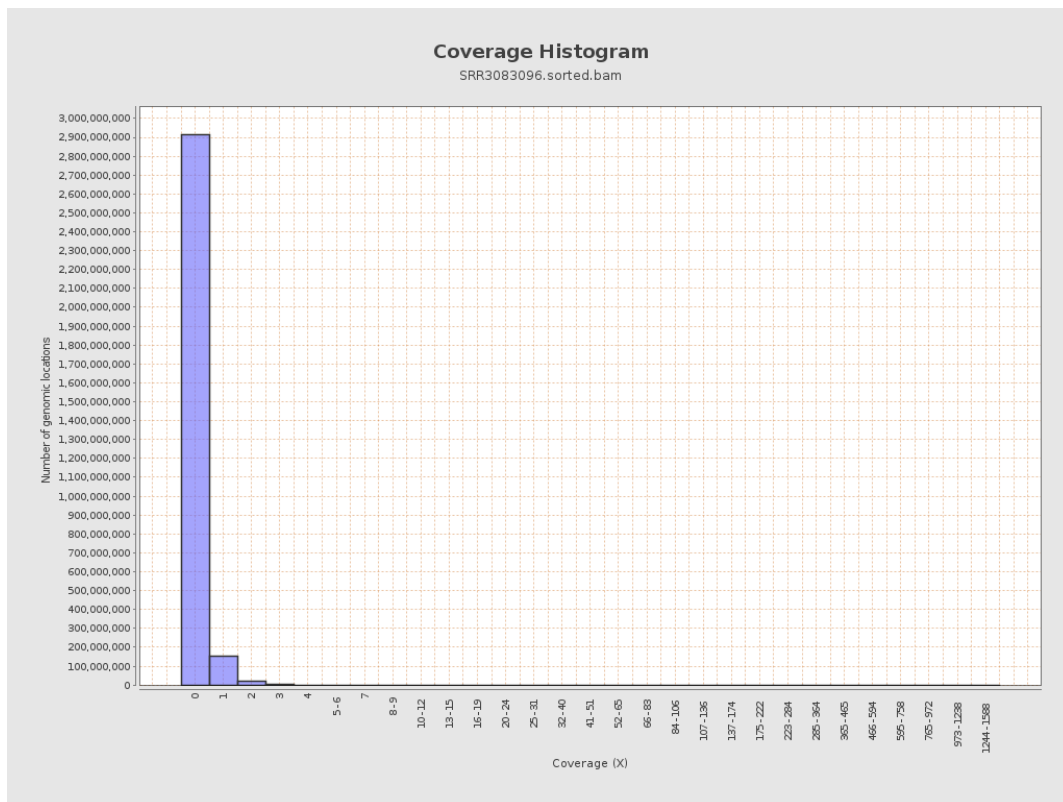
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 21286121     | 0.0854        | 1.4431             |
| chr2 | 243199373 | 22398753     | 0.0921        | 1.085              |
| chr3 | 198022430 | 15567044     | 0.0786        | 0.3302             |
| chr4 | 191154276 | 11500465     | 0.0602        | 0.3078             |
| chr5 | 180915260 | 12162499     | 0.0672        | 0.3087             |
| chr6 | 171115067 | 15045978     | 0.0879        | 0.6427             |
| chr7 | 159138663 | 10919517     | 0.0686        | 0.7546             |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr8  | 146364022 | 19166320 | 0.1309 | 0.8089 |
| chr9  | 141213431 | 6356094  | 0.045  | 0.7377 |
| chr10 | 135534747 | 7279281  | 0.0537 | 0.5826 |
| chr11 | 135006516 | 9009173  | 0.0667 | 0.5621 |
| chr12 | 133851895 | 7136737  | 0.0533 | 0.3024 |
| chr13 | 115169878 | 4975084  | 0.0432 | 0.2364 |
| chr14 | 107349540 | 4670793  | 0.0435 | 0.3556 |
| chr15 | 102531392 | 4609121  | 0.045  | 0.2526 |
| chr16 | 90354753  | 9440841  | 0.1045 | 0.4914 |
| chr17 | 81195210  | 6057142  | 0.0746 | 0.502  |
| chr18 | 78077248  | 7585816  | 0.0972 | 1.656  |
| chr19 | 59128983  | 4398390  | 0.0744 | 1.0075 |
| chr20 | 63025520  | 4461526  | 0.0708 | 0.3687 |
| chr21 | 48129895  | 3976679  | 0.0826 | 0.3577 |
| chr22 | 51304566  | 2932231  | 0.0572 | 0.2777 |
| chrMT | 16571     | 136011   | 8.2078 | 6.1833 |
| chrX  | 155270560 | 9088549  | 0.0585 | 0.4436 |
| chrY  | 59373566  | 432570   | 0.0073 | 0.1547 |

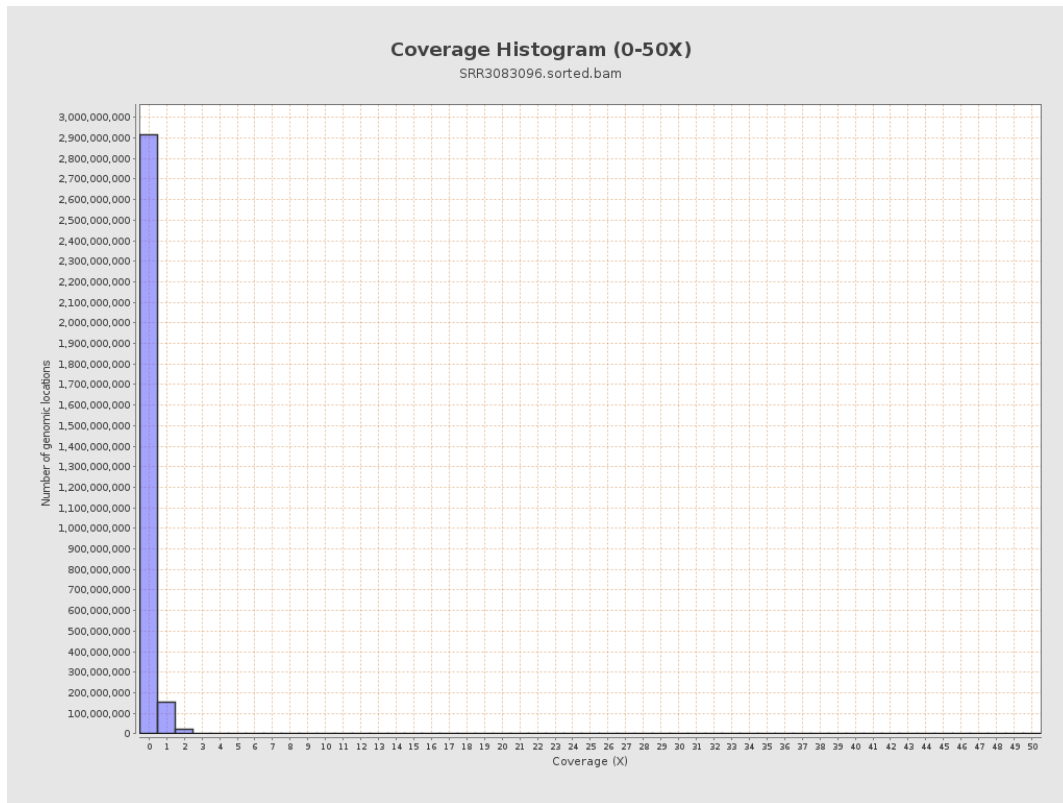
### 3. Results : Coverage across reference



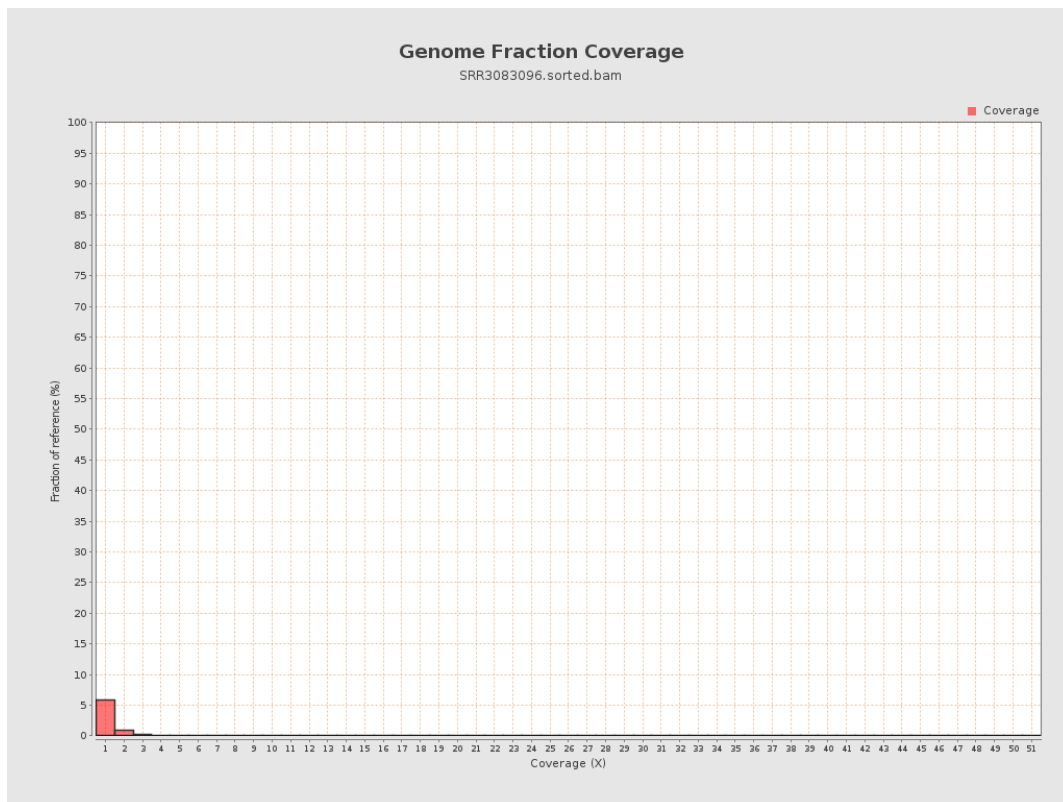
## 4. Results : Coverage Histogram



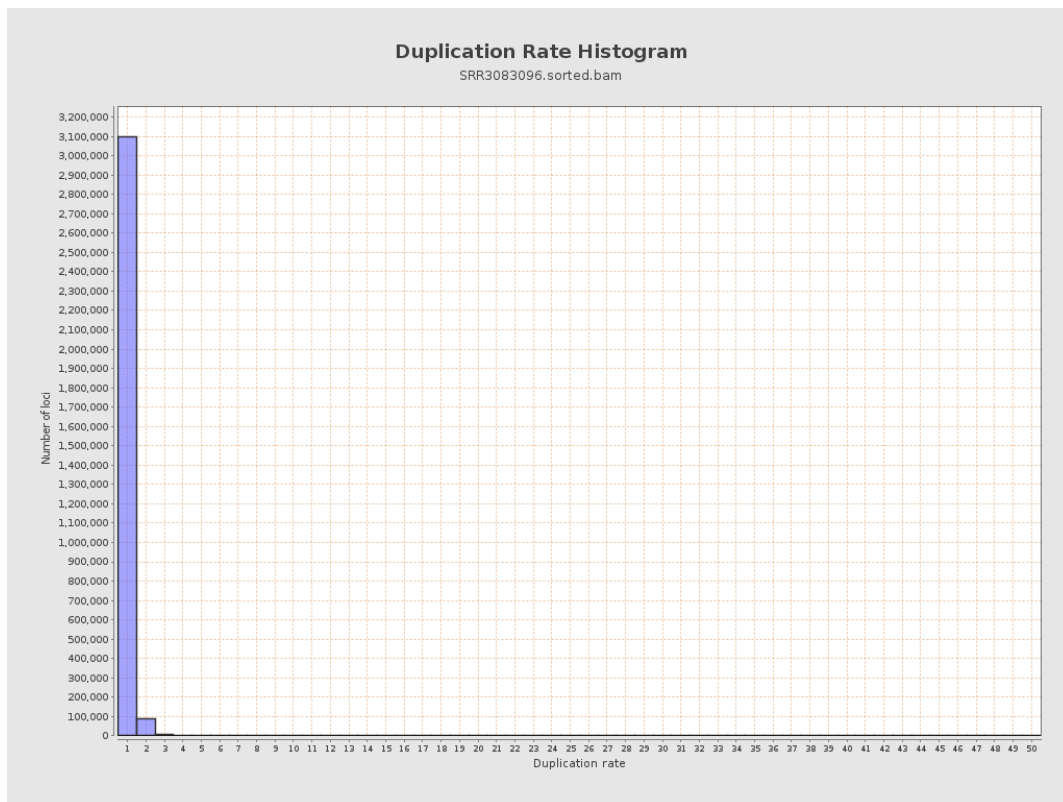
## 5. Results : Coverage Histogram (0-50X)



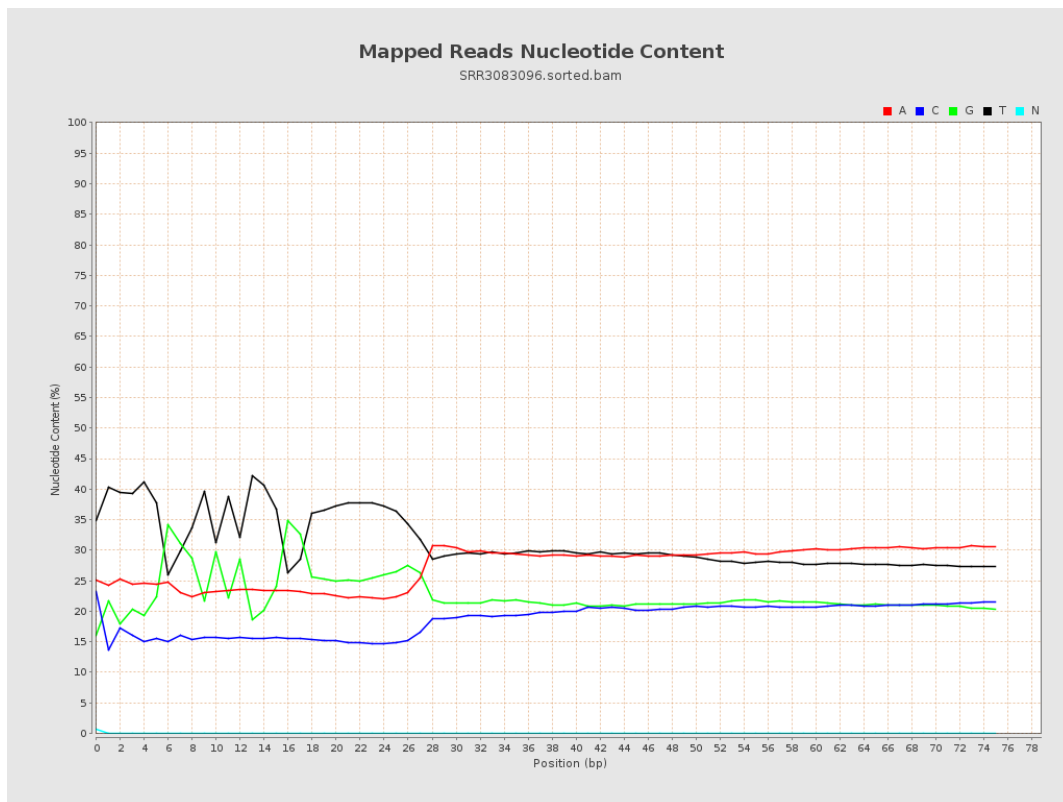
## 6. Results : Genome Fraction Coverage



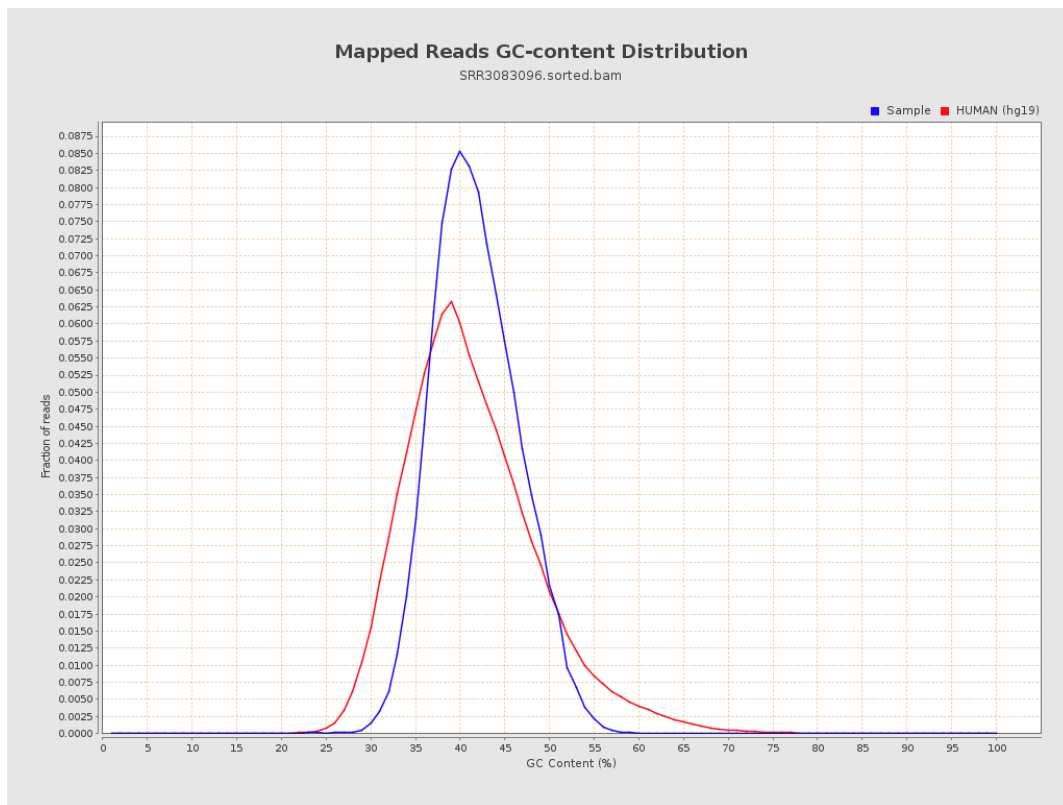
## 7. Results : Duplication Rate Histogram



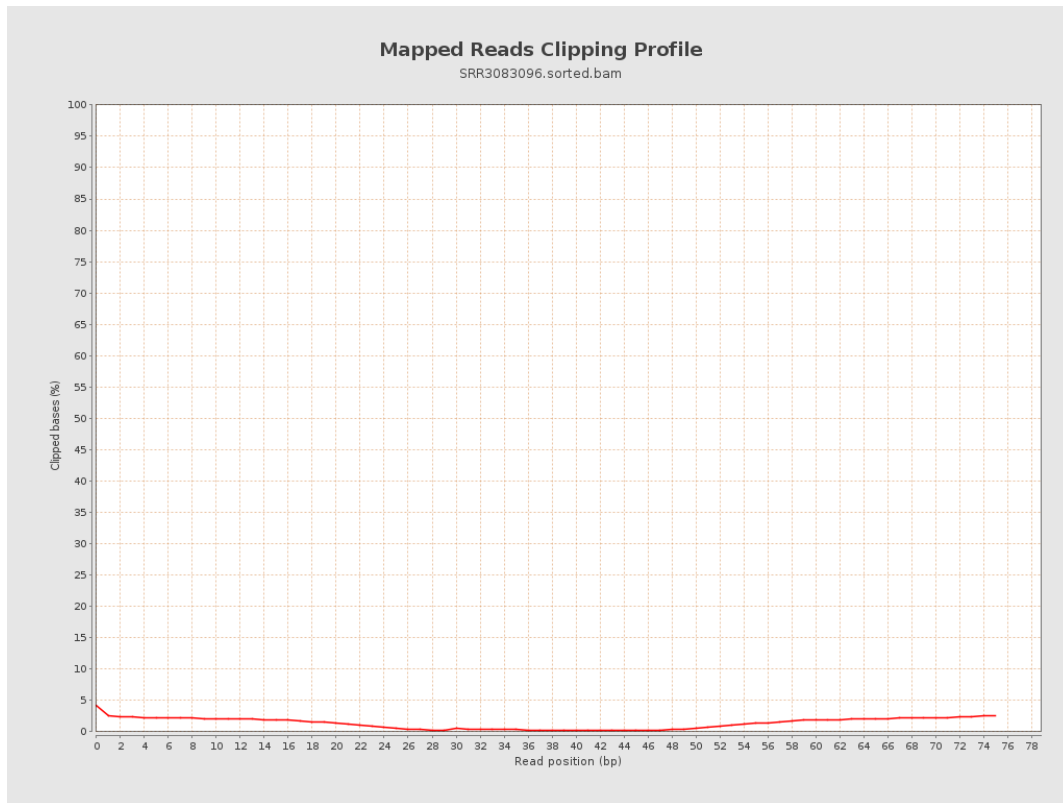
## 8. Results : Mapped Reads Nucleotide Content



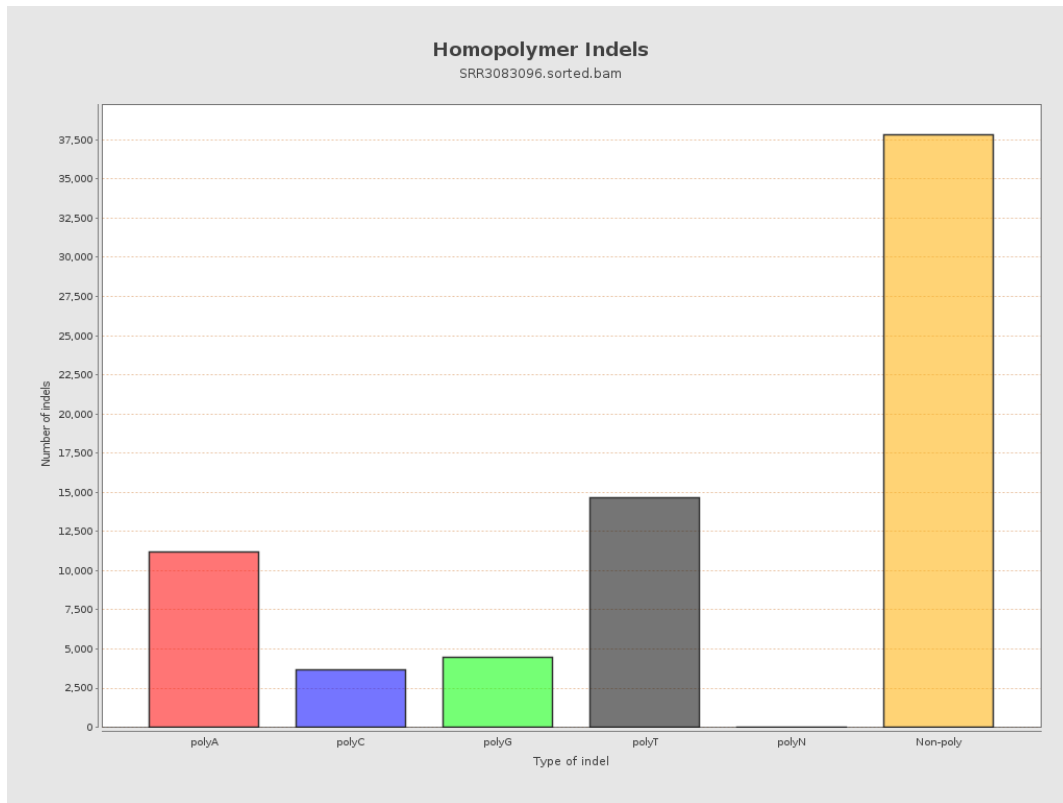
## 9. Results : Mapped Reads GC-content Distribution



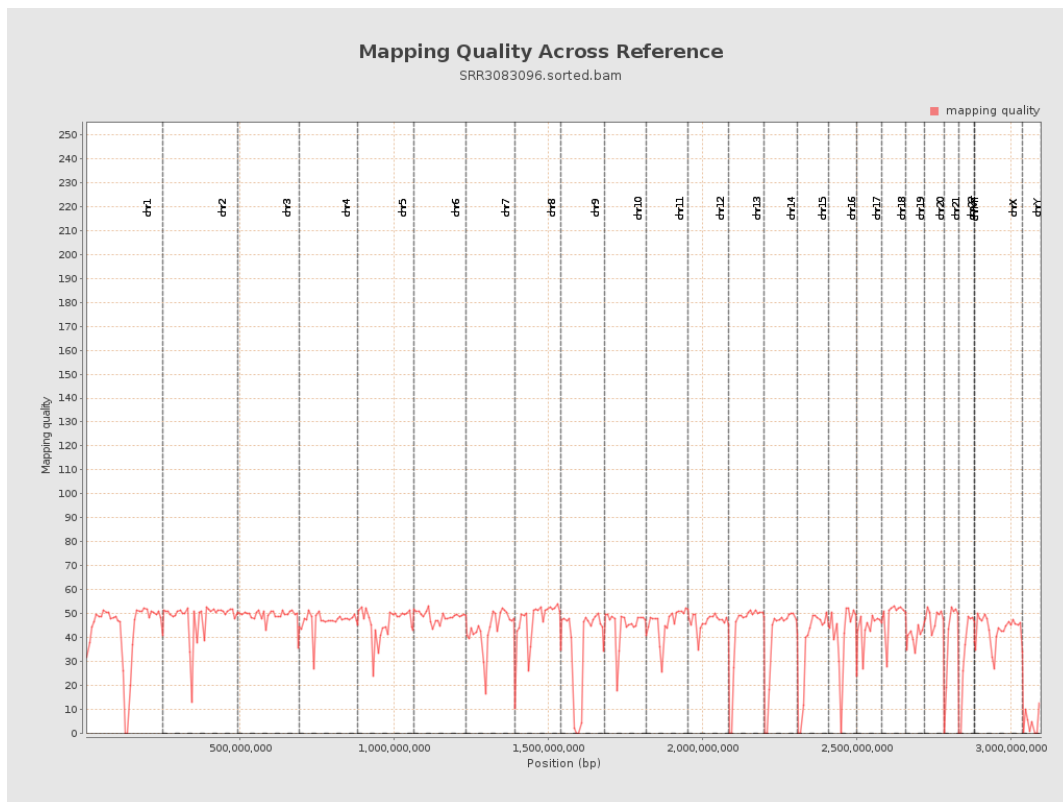
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

