

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/22 07:55:14*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818768.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_SRR1818768 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818768.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Thu Aug 22 07:55:12 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR1818768.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                  |
|------------------------------|------------------|
| Reference size               | 3,095,693,983    |
| Number of reads              | 304,161          |
| Mapped reads                 | 288,440 / 94.83% |
| Unmapped reads               | 15,721 / 5.17%   |
| Mapped paired reads          | 0 / 0%           |
| Secondary alignments         | 0                |
| Supplementary alignments     | 2,370 / 0.78%    |
| Read min/max/mean length     | 30 / 76 / 76.26  |
| Duplicated reads (estimated) | 55,661 / 18.3%   |
| Duplication rate             | 17.5%            |
| Clipped reads                | 289,399 / 95.15% |

### 2.2. ACGT Content

|                          |                    |
|--------------------------|--------------------|
| Number/percentage of A's | 5,634,886 / 28.8%  |
| Number/percentage of C's | 4,434,664 / 22.66% |
| Number/percentage of T's | 5,507,507 / 28.15% |
| Number/percentage of G's | 3,989,435 / 20.39% |
| Number/percentage of N's | 1,296 / 0.01%      |
| GC Percentage            | 43.05%             |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0063 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.1158 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 47.99 |
|----------------------|-------|

## 2.5. Mismatches and indels

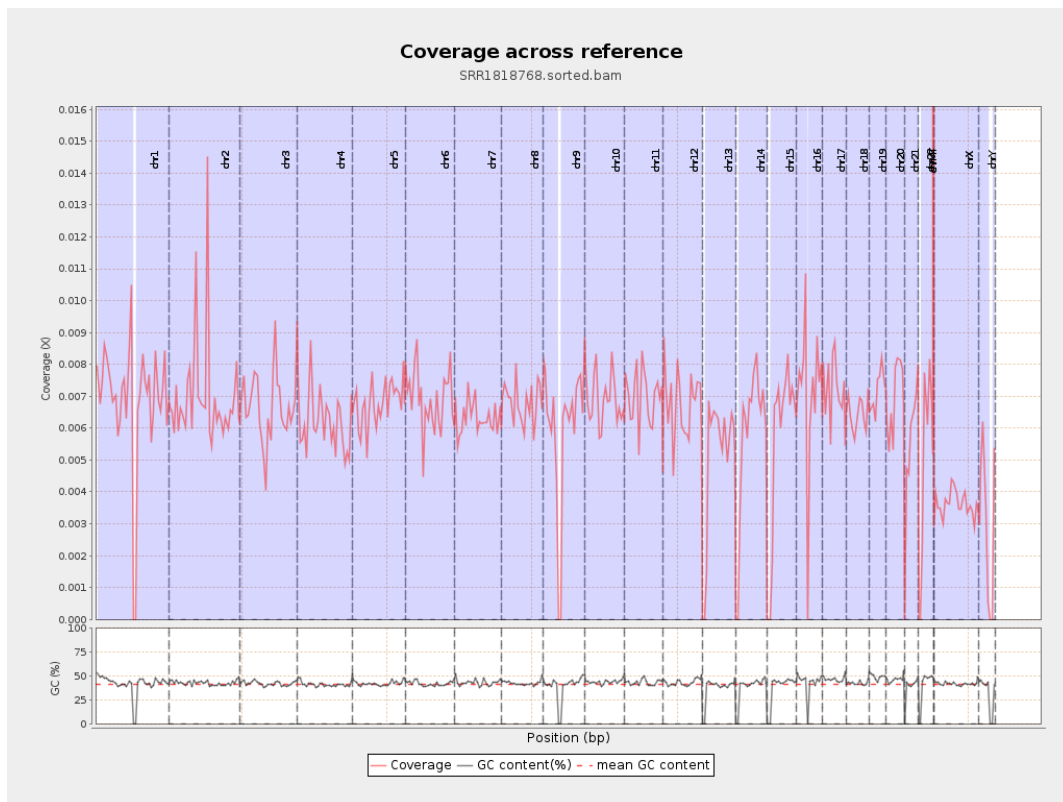
|                                          |        |
|------------------------------------------|--------|
| General error rate                       | 0.53%  |
| Mismatches                               | 98,838 |
| Insertions                               | 2,440  |
| Mapped reads with at least one insertion | 0.84%  |
| Deletions                                | 5,048  |
| Mapped reads with at least one deletion  | 1.73%  |
| Homopolymer indels                       | 40.06% |

## 2.6. Chromosome stats

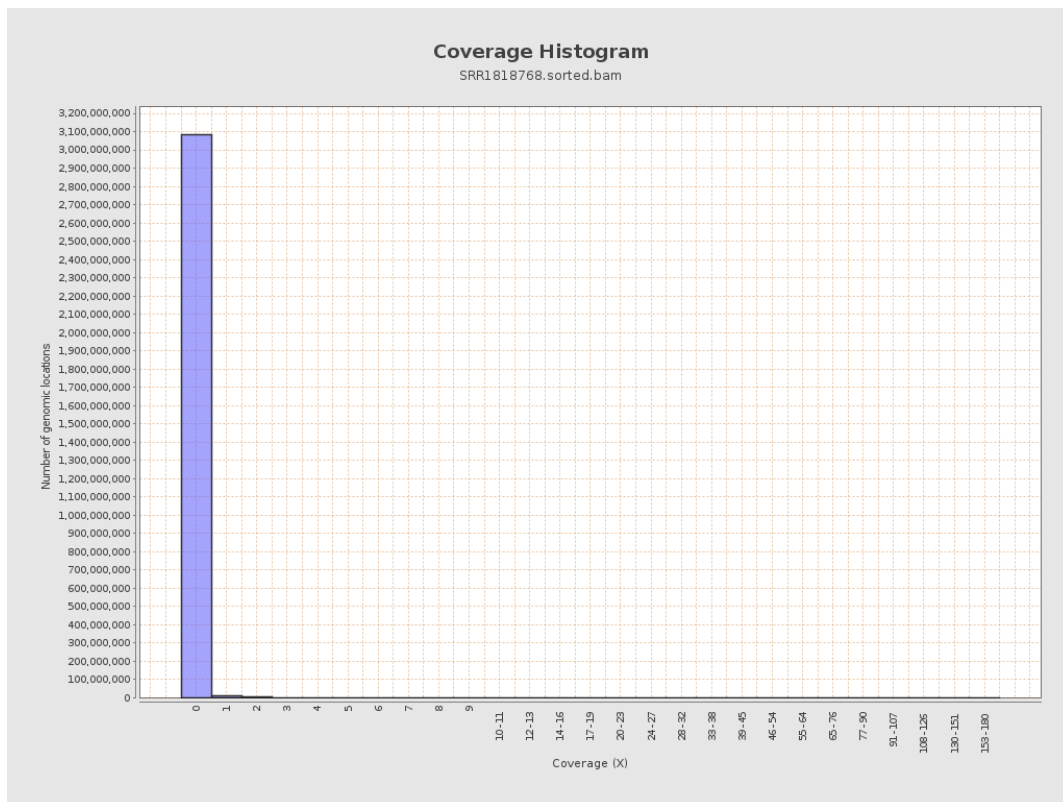
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 1715067      | 0.0069        | 0.1461             |
| chr2 | 243199373 | 1704885      | 0.007         | 0.1665             |
| chr3 | 198022430 | 1318307      | 0.0067        | 0.1034             |
| chr4 | 191154276 | 1176893      | 0.0062        | 0.1022             |
| chr5 | 180915260 | 1222641      | 0.0068        | 0.1039             |
| chr6 | 171115067 | 1183278      | 0.0069        | 0.1092             |
| chr7 | 159138663 | 1005770      | 0.0063        | 0.1065             |
|      |           |              |               |                    |

|       |           |        |        |        |
|-------|-----------|--------|--------|--------|
| chr8  | 146364022 | 994102 | 0.0068 | 0.1079 |
| chr9  | 141213431 | 830599 | 0.0059 | 0.1016 |
| chr10 | 135534747 | 932350 | 0.0069 | 0.1199 |
| chr11 | 135006516 | 942588 | 0.007  | 0.1091 |
| chr12 | 133851895 | 907574 | 0.0068 | 0.1065 |
| chr13 | 115169878 | 586535 | 0.0051 | 0.0901 |
| chr14 | 107349540 | 616818 | 0.0057 | 0.1001 |
| chr15 | 102531392 | 576422 | 0.0056 | 0.095  |
| chr16 | 90354753  | 644916 | 0.0071 | 0.1352 |
| chr17 | 81195210  | 588636 | 0.0072 | 0.1097 |
| chr18 | 78077248  | 502693 | 0.0064 | 0.1168 |
| chr19 | 59128983  | 422958 | 0.0072 | 0.1308 |
| chr20 | 63025520  | 436903 | 0.0069 | 0.1082 |
| chr21 | 48129895  | 263859 | 0.0055 | 0.0964 |
| chr22 | 51304566  | 251544 | 0.0049 | 0.0939 |
| chrMT | 16571     | 15851  | 0.9566 | 1.4881 |
| chrX  | 155270560 | 561723 | 0.0036 | 0.078  |
| chrY  | 59373566  | 172952 | 0.0029 | 0.1326 |

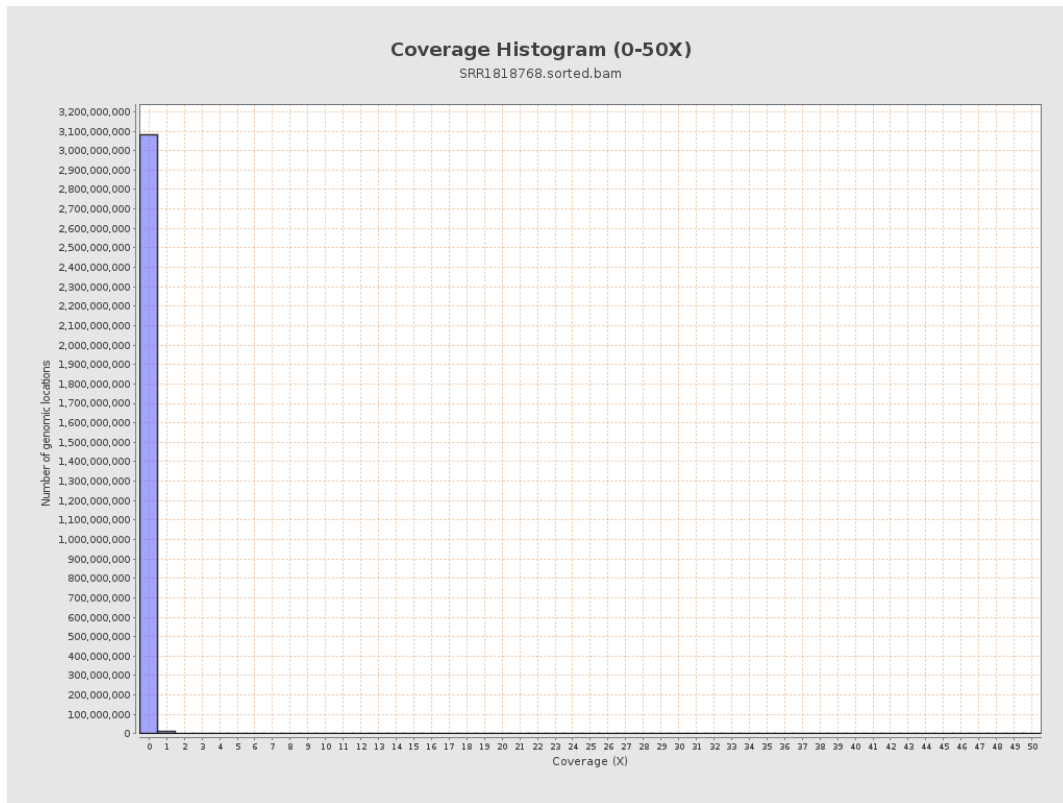
### 3. Results : Coverage across reference



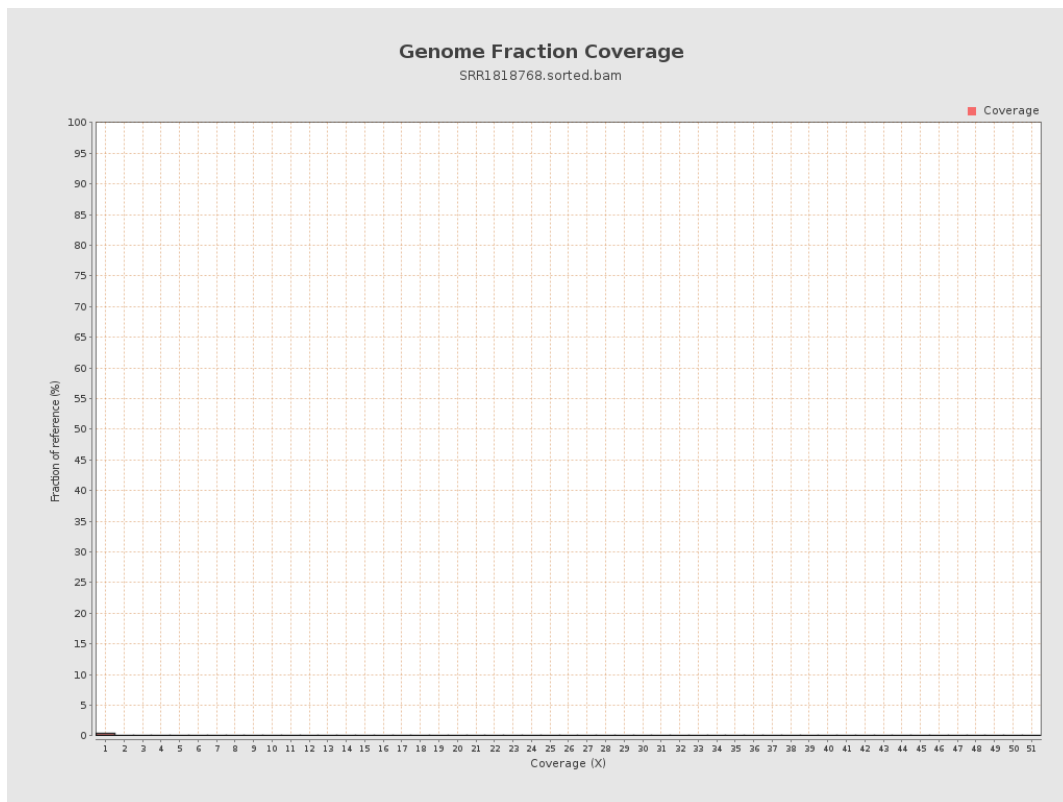
## 4. Results : Coverage Histogram



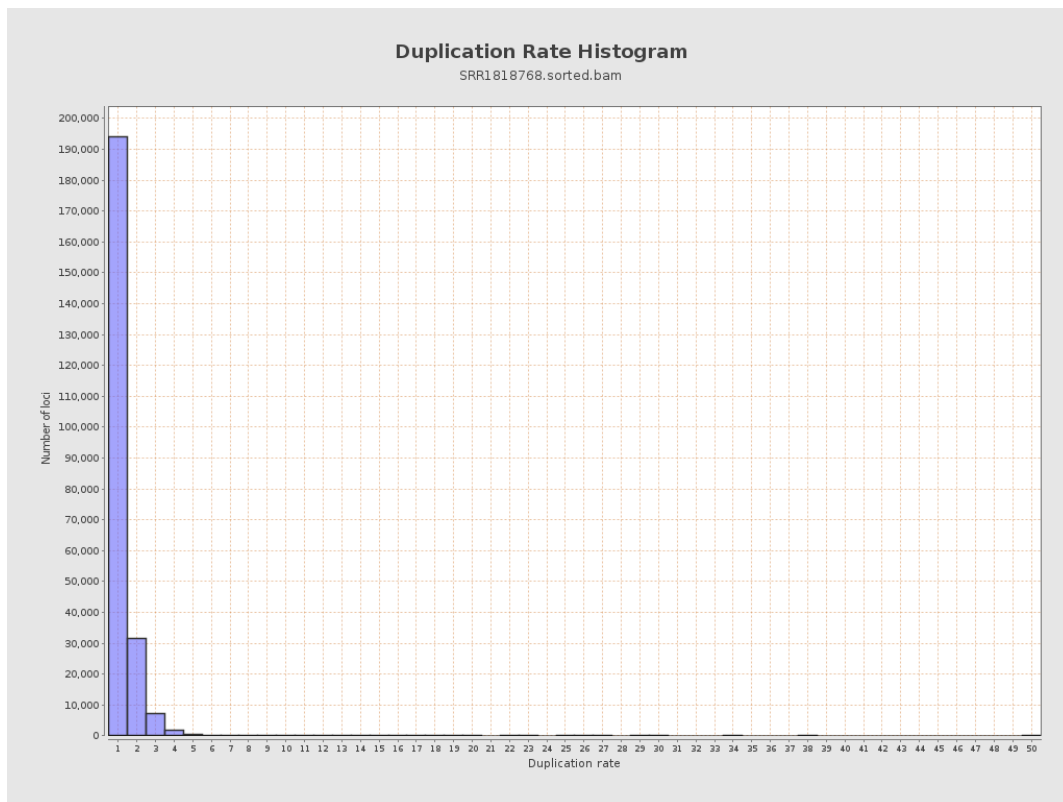
## 5. Results : Coverage Histogram (0-50X)



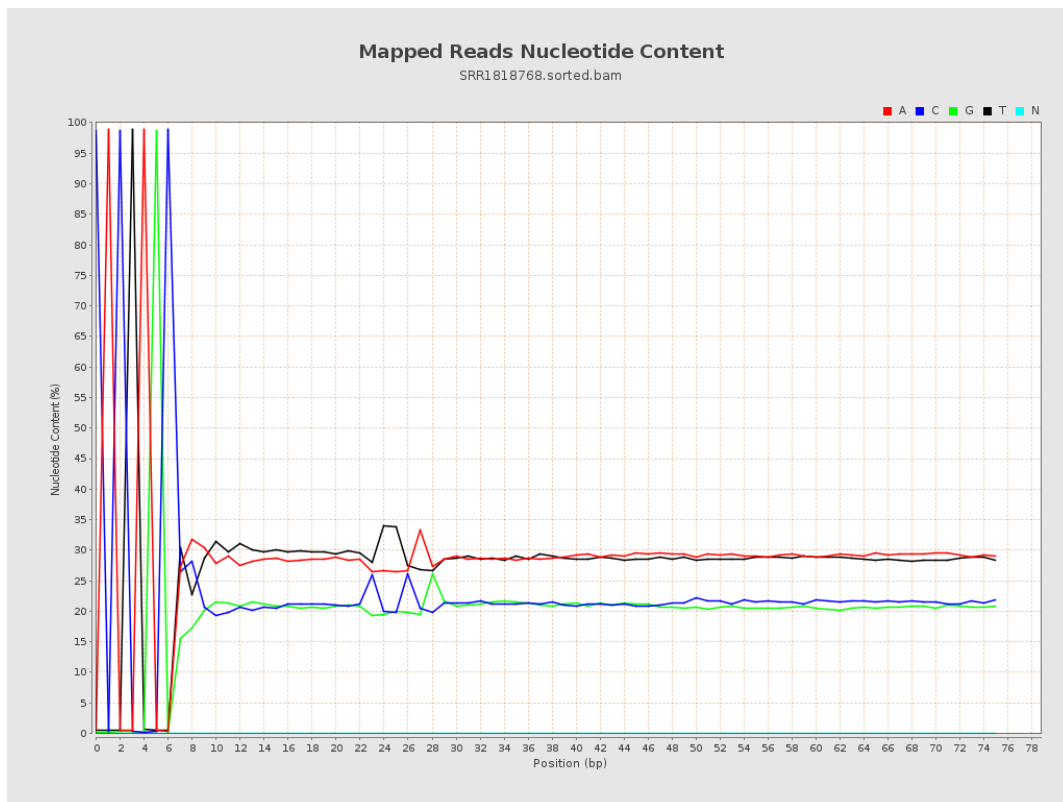
## 6. Results : Genome Fraction Coverage



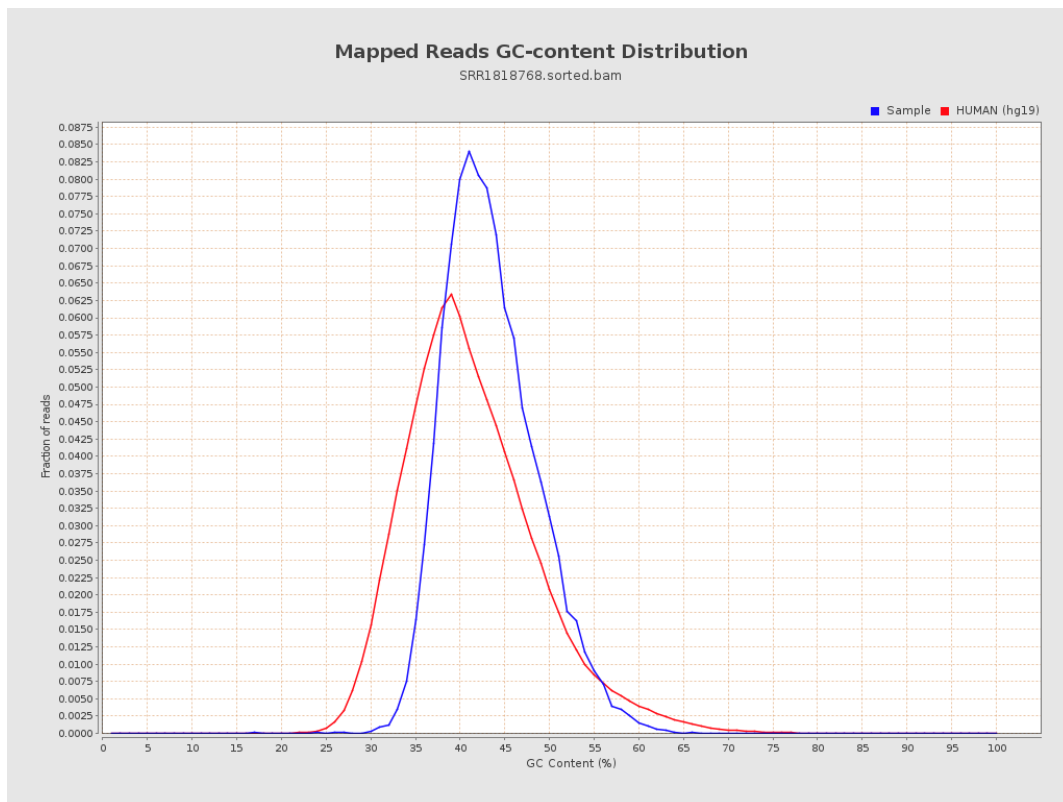
## 7. Results : Duplication Rate Histogram



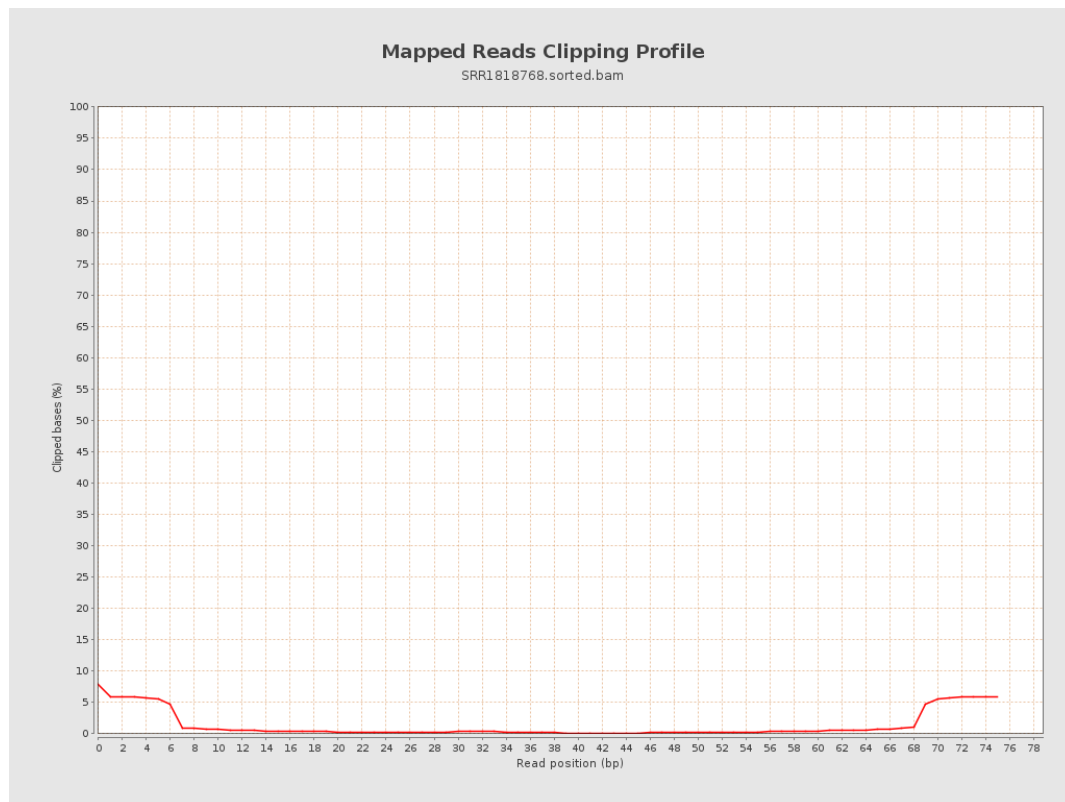
## 8. Results : Mapped Reads Nucleotide Content



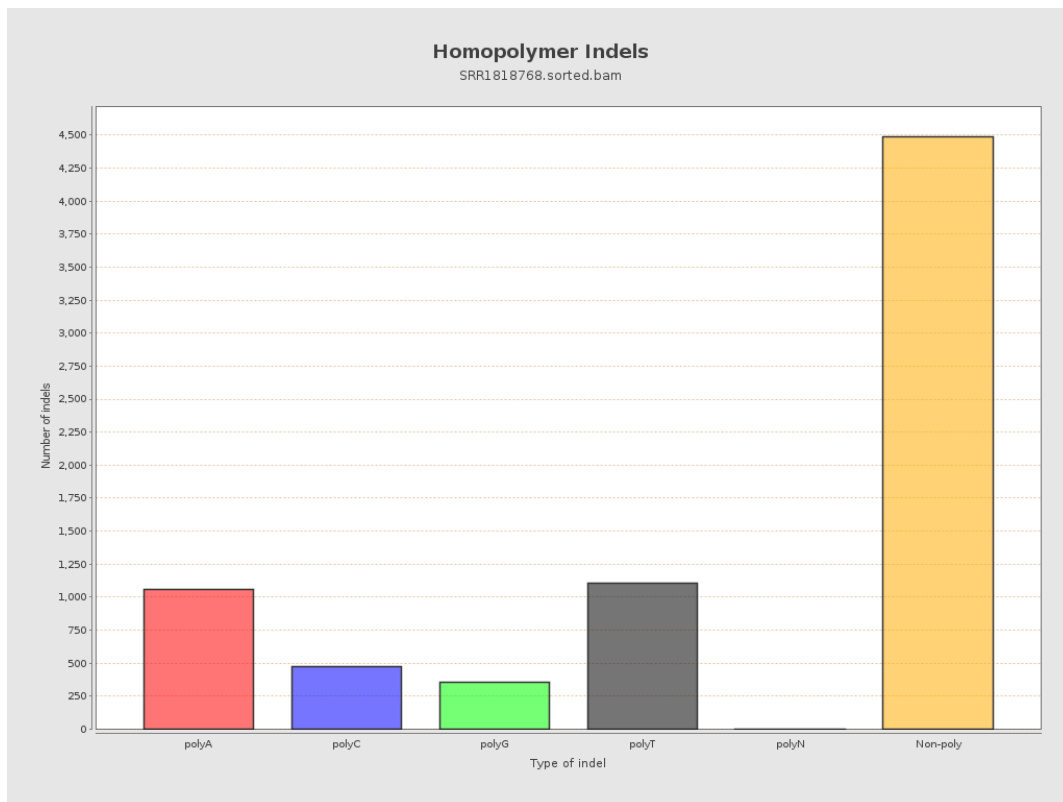
## 9. Results : Mapped Reads GC-content Distribution



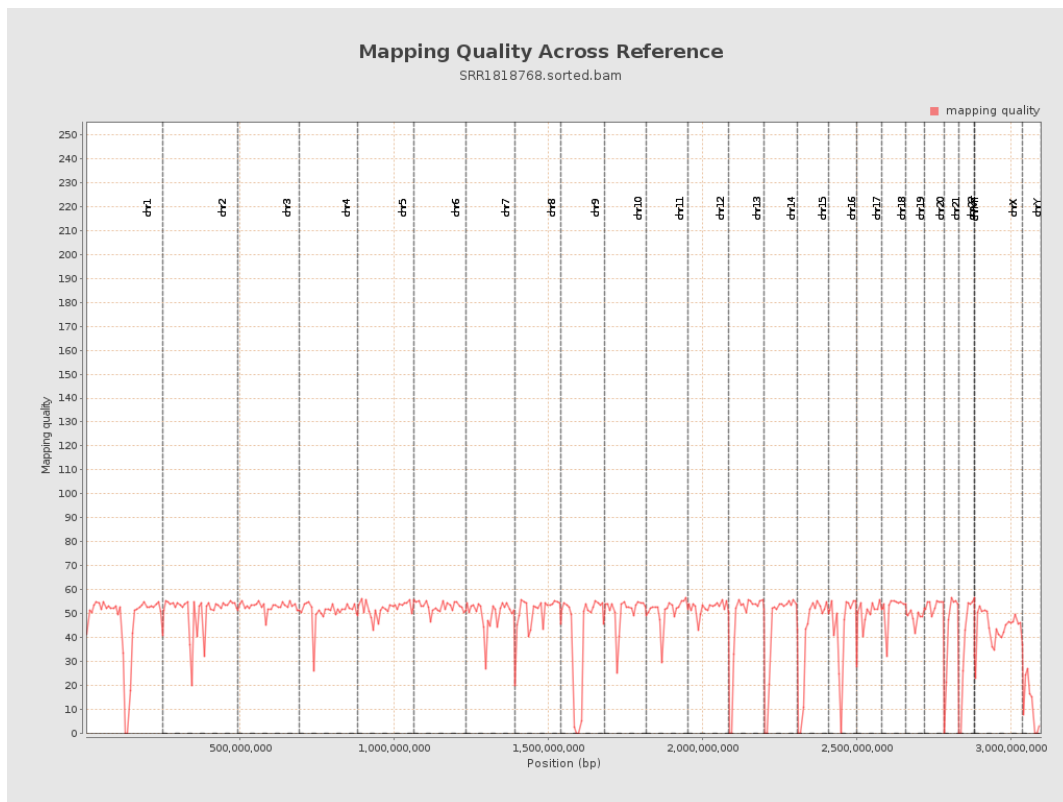
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

