

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 01:33:09*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548966.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_SRR1548966 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548966.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Fri Aug 23 01:33:04 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR1548966.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 4,764,616          |
| Mapped reads                 | 4,160,207 / 87.31% |
| Unmapped reads               | 604,409 / 12.69%   |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Read min/max/mean length     | 40 / 40 / 40       |
| Duplicated reads (estimated) | 148,710 / 3.12%    |
| Duplication rate             | 2.17%              |
| Clipped reads                | 327,234 / 6.87%    |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 47,574,672 / 28.91% |
| Number/percentage of C's | 34,324,643 / 20.86% |
| Number/percentage of T's | 48,299,520 / 29.35% |
| Number/percentage of G's | 34,350,589 / 20.88% |
| Number/percentage of N's | 271 / 0%            |
| GC Percentage            | 41.74%              |

### 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.0532 |
| Standard Deviation | 0.5381 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 39.25 |
|----------------------|-------|

## 2.5. Mismatches and indels

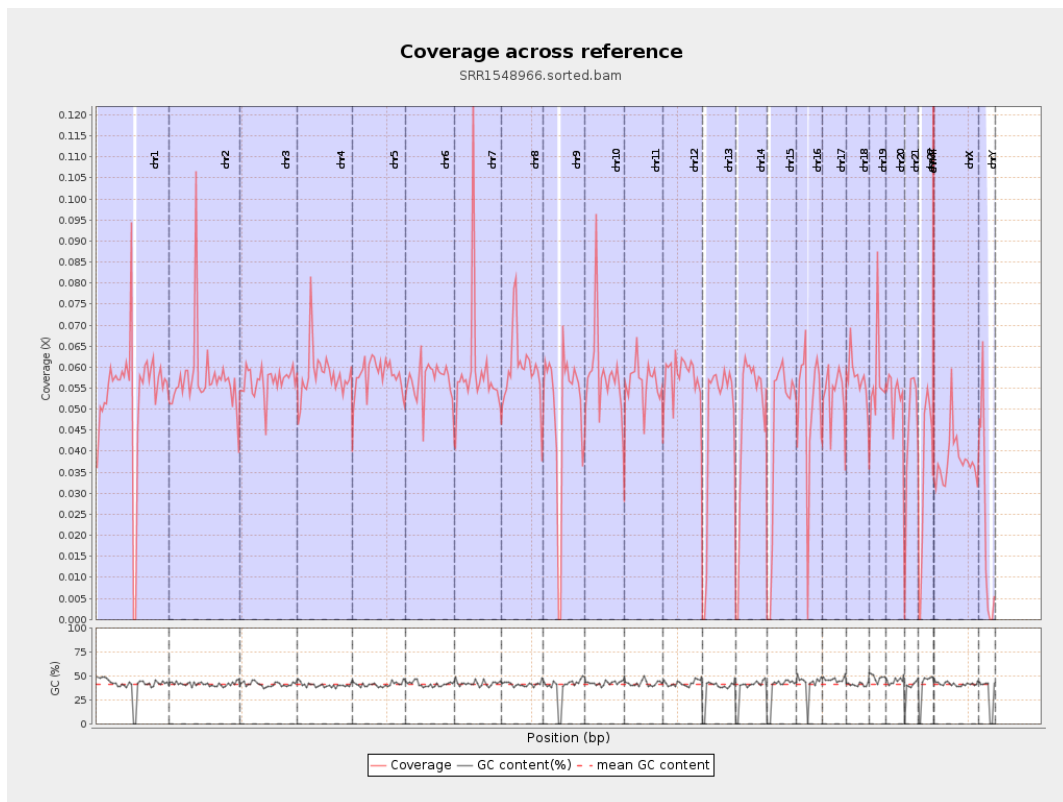
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 0.3%    |
| Mismatches                               | 482,942 |
| Insertions                               | 5,424   |
| Mapped reads with at least one insertion | 0.13%   |
| Deletions                                | 12,812  |
| Mapped reads with at least one deletion  | 0.31%   |
| Homopolymer indels                       | 40.38%  |

## 2.6. Chromosome stats

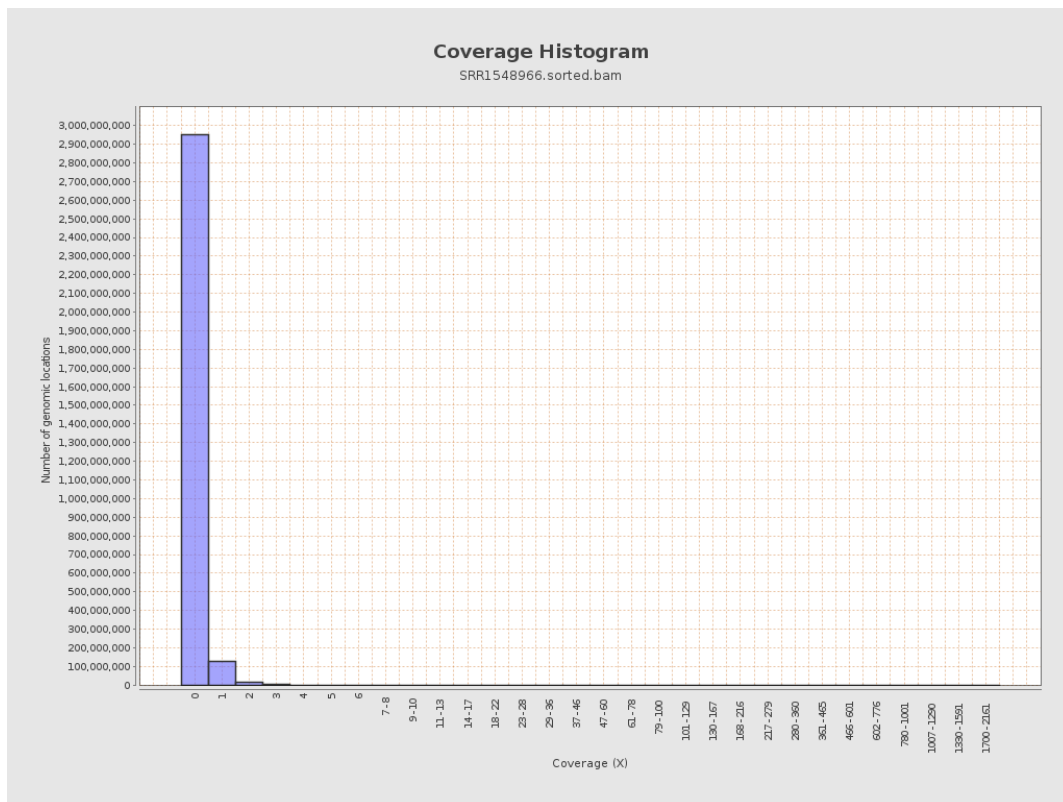
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 13323994     | 0.0535        | 0.9175             |
| chr2 | 243199373 | 13922395     | 0.0572        | 0.4987             |
| chr3 | 198022430 | 11226519     | 0.0567        | 0.2634             |
| chr4 | 191154276 | 11101348     | 0.0581        | 0.2886             |
| chr5 | 180915260 | 10531010     | 0.0582        | 0.2758             |
| chr6 | 171115067 | 9707122      | 0.0567        | 0.2848             |
| chr7 | 159138663 | 9438705      | 0.0593        | 0.8239             |
| chr8 | 146364022 | 8727045      | 0.0596        | 1.1075             |
|      |           |              |               |                    |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr9  | 141213431 | 7063271 | 0.05   | 0.4969 |
| chr10 | 135534747 | 7901343 | 0.0583 | 0.4334 |
| chr11 | 135006516 | 7565820 | 0.056  | 0.3911 |
| chr12 | 133851895 | 7747870 | 0.0579 | 0.2845 |
| chr13 | 115169878 | 5364156 | 0.0466 | 0.2359 |
| chr14 | 107349540 | 5128099 | 0.0478 | 0.3297 |
| chr15 | 102531392 | 4661837 | 0.0455 | 0.2391 |
| chr16 | 90354753  | 4588185 | 0.0508 | 0.2993 |
| chr17 | 81195210  | 4316590 | 0.0532 | 0.2709 |
| chr18 | 78077248  | 4506647 | 0.0577 | 0.9968 |
| chr19 | 59128983  | 3379369 | 0.0572 | 0.8737 |
| chr20 | 63025520  | 3314943 | 0.0526 | 0.2684 |
| chr21 | 48129895  | 2144114 | 0.0445 | 0.2982 |
| chr22 | 51304566  | 1773126 | 0.0346 | 0.2087 |
| chrMT | 16571     | 5783    | 0.349  | 0.7413 |
| chrX  | 155270560 | 5867529 | 0.0378 | 0.3107 |
| chrY  | 59373566  | 1259585 | 0.0212 | 0.2078 |

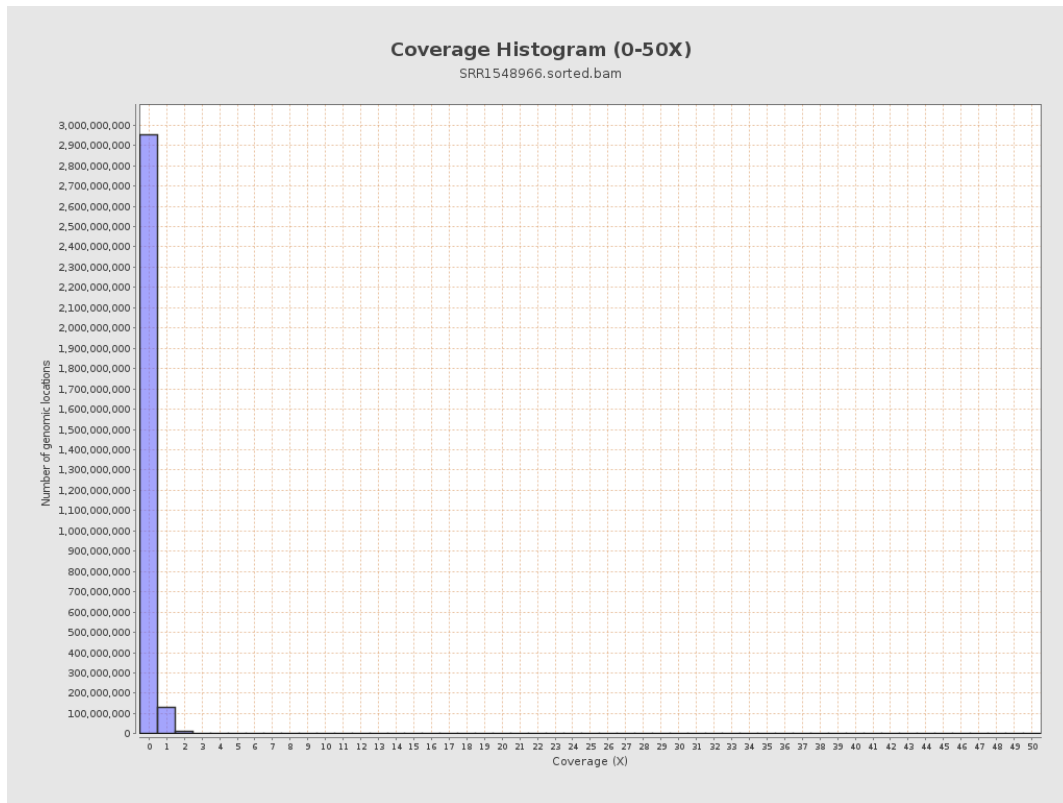
### 3. Results : Coverage across reference



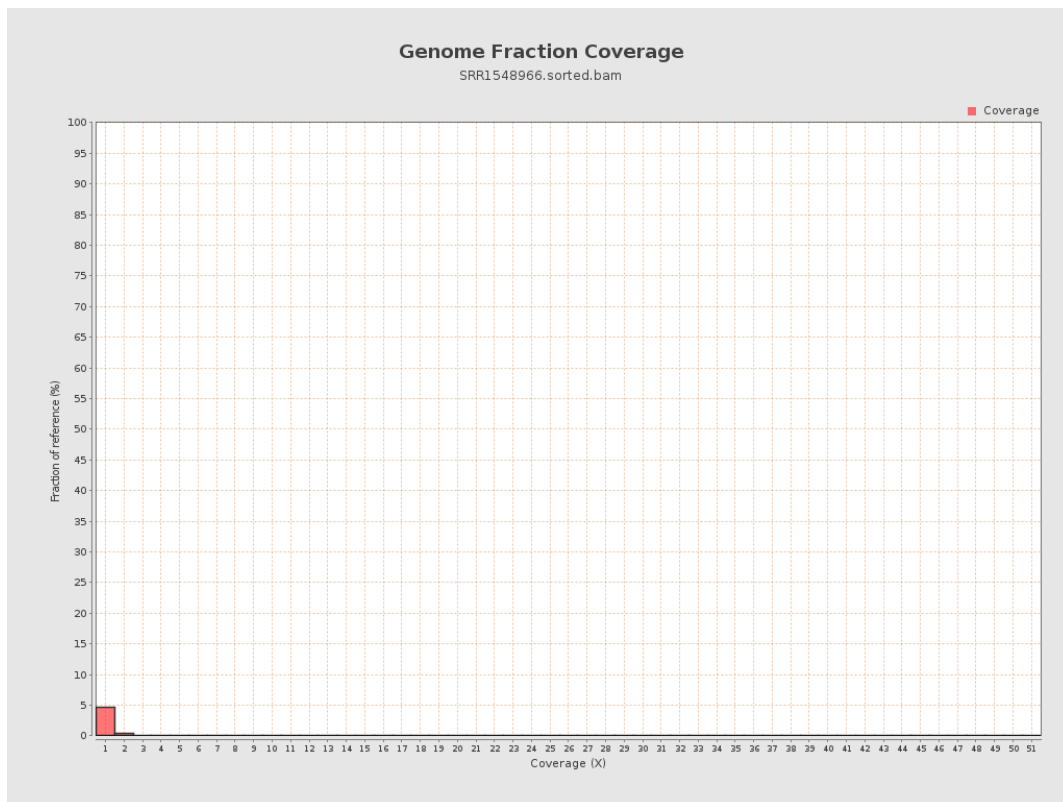
## 4. Results : Coverage Histogram



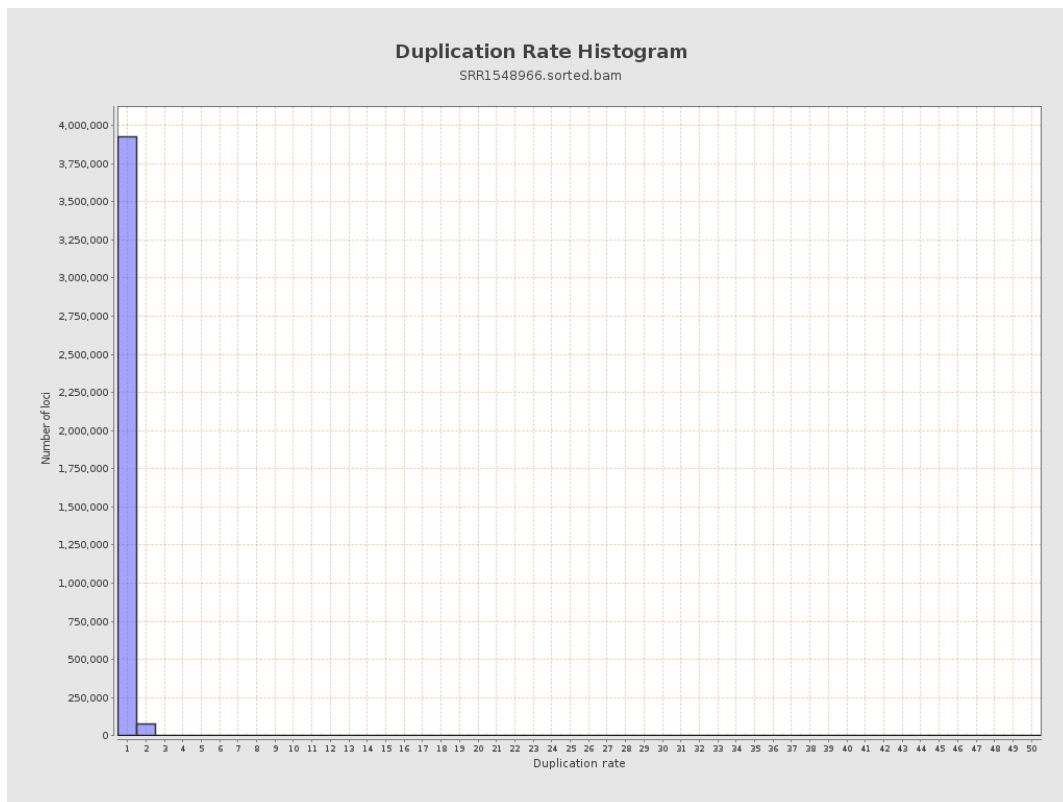
## 5. Results : Coverage Histogram (0-50X)



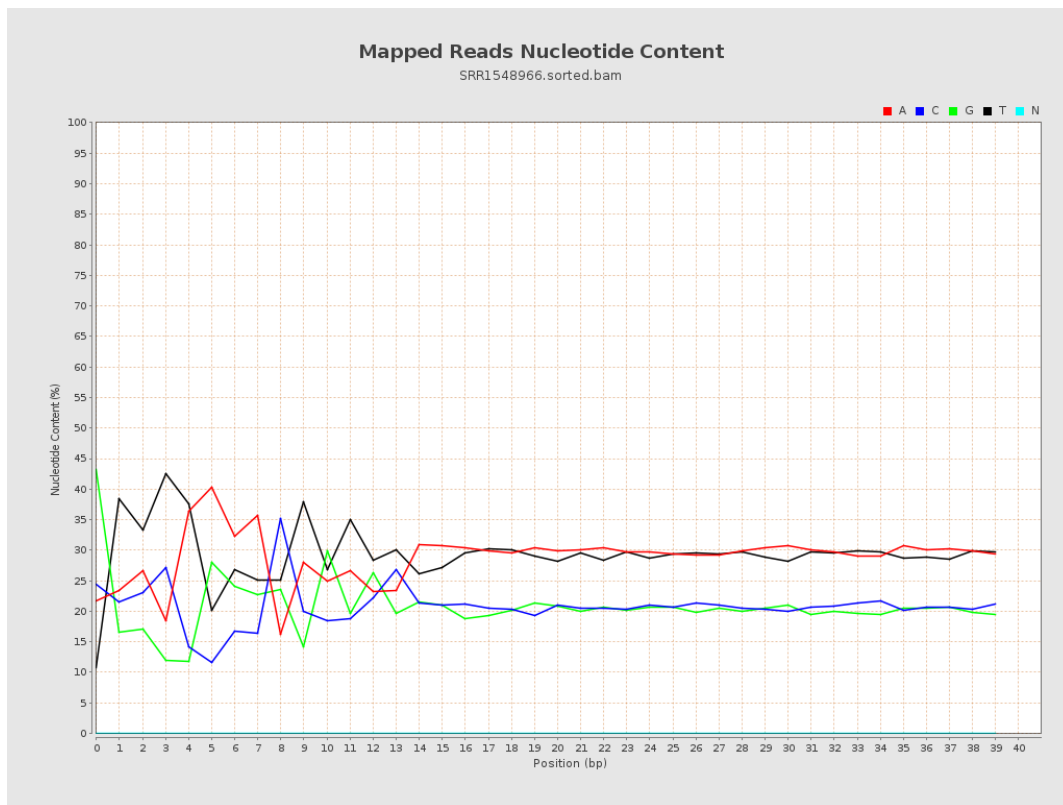
## 6. Results : Genome Fraction Coverage



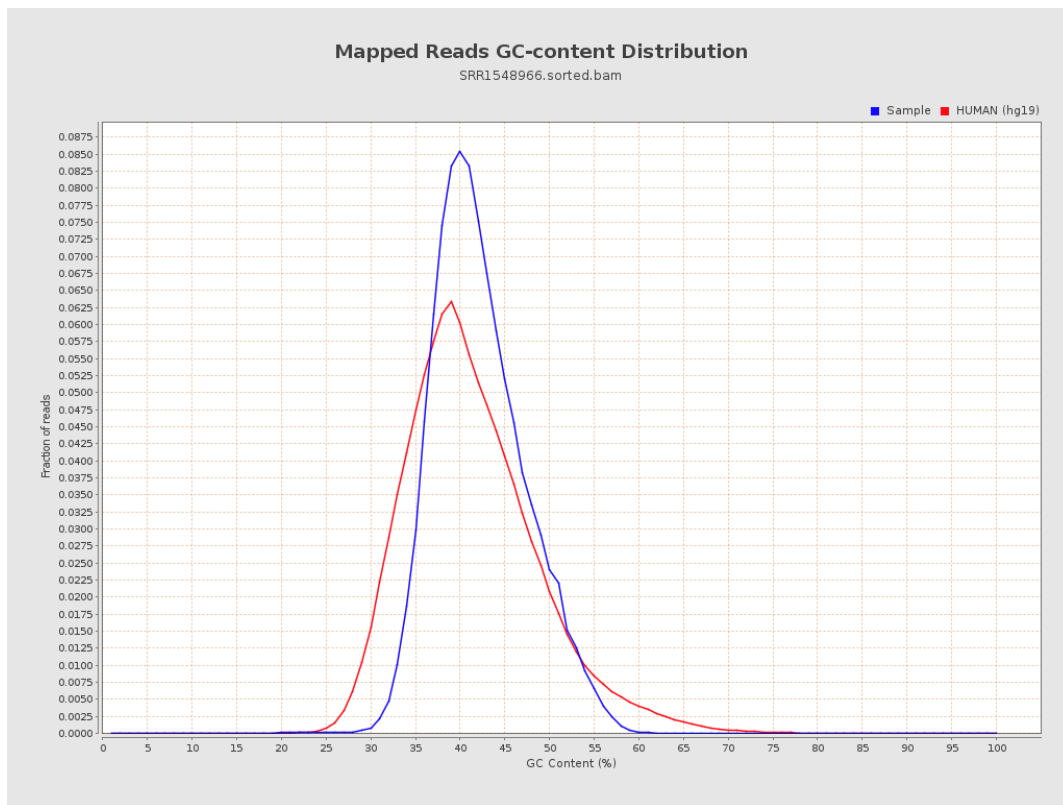
## 7. Results : Duplication Rate Histogram



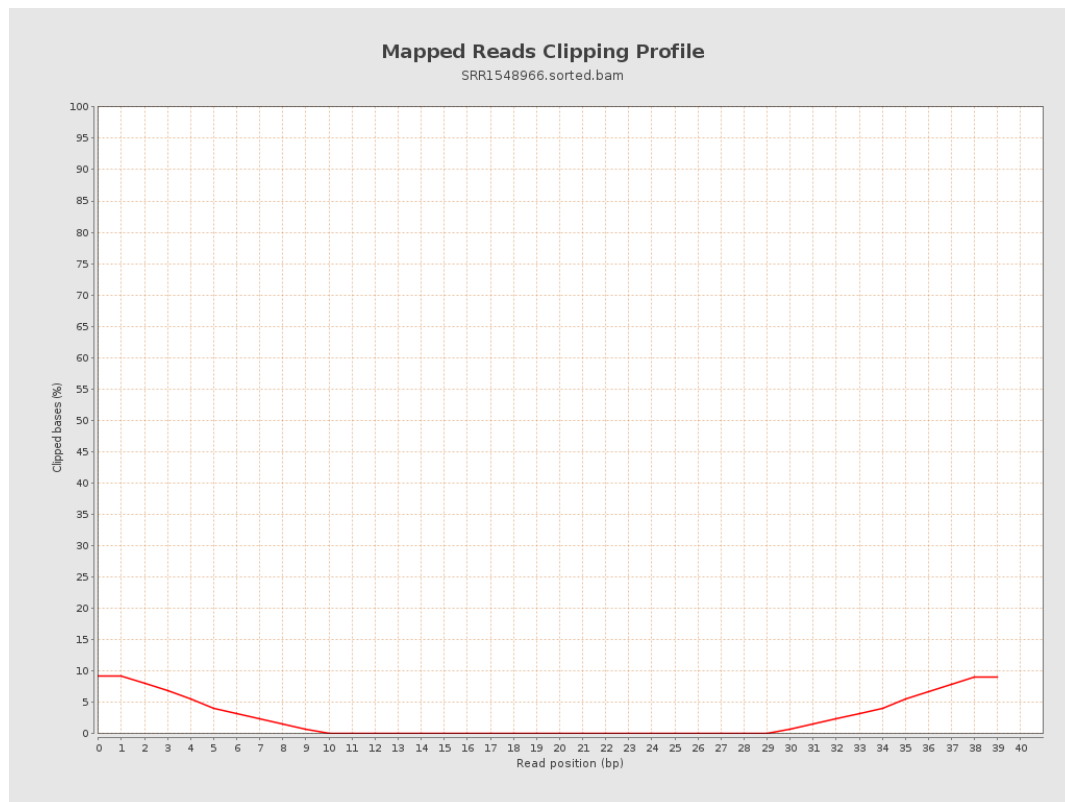
## 8. Results : Mapped Reads Nucleotide Content



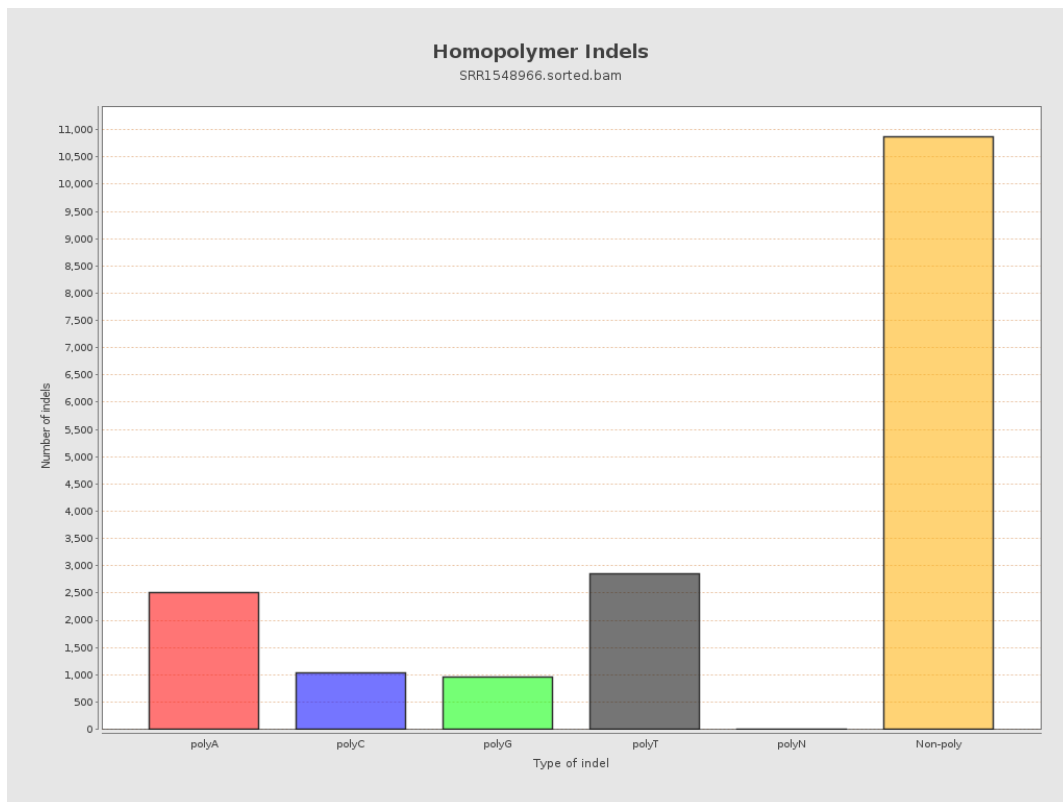
## 9. Results : Mapped Reads GC-content Distribution



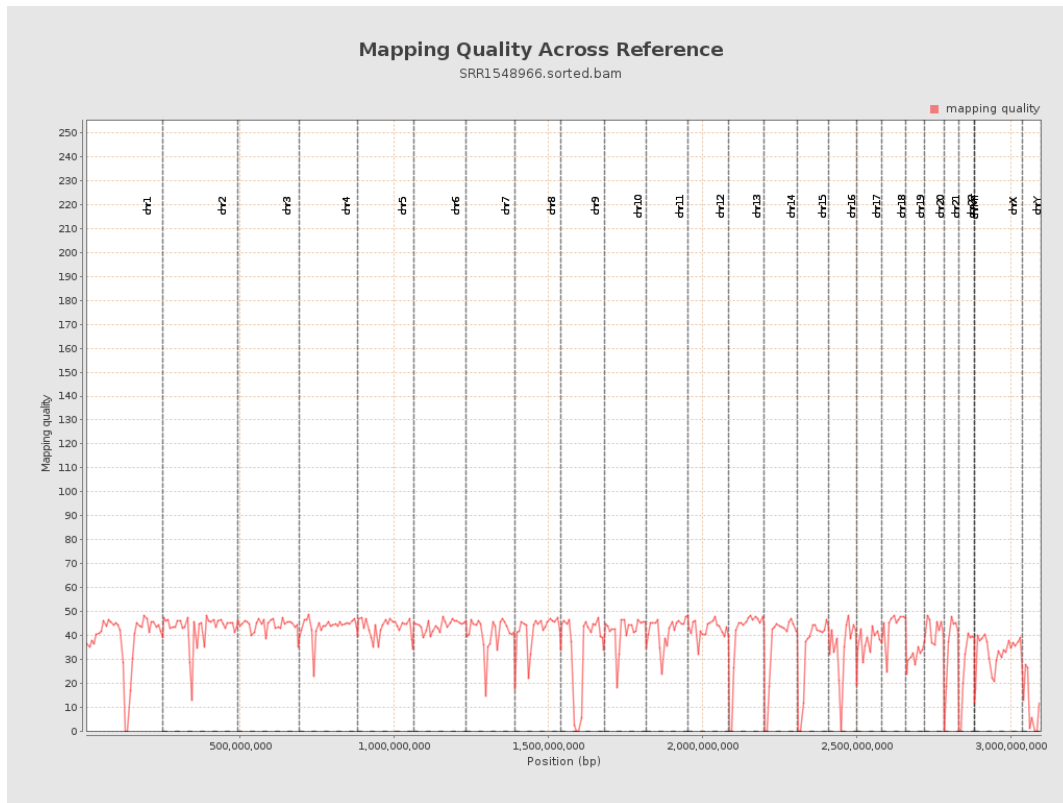
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

