

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/19 22:14:27*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505984.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_SRR1505984 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505984.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Thu Dec 19 22:14:26 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR1505984.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 8,094,789          |
| Mapped reads                 | 5,659,309 / 69.91% |
| Unmapped reads               | 2,435,480 / 30.09% |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 322 / 0%           |
| Read min/max/mean length     | 30 / 48 / 48       |
| Duplicated reads (estimated) | 447,560 / 5.53%    |
| Duplication rate             | 6.15%              |
| Clipped reads                | 956,476 / 11.82%   |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 78,161,472 / 29.82% |
| Number/percentage of C's | 52,134,232 / 19.89% |
| Number/percentage of T's | 78,348,739 / 29.89% |
| Number/percentage of G's | 53,481,094 / 20.4%  |
| Number/percentage of N's | 1,183 / 0%          |
| GC Percentage            | 40.29%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0847 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.6849 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 44.36 |
|----------------------|-------|

## 2.5. Mismatches and indels

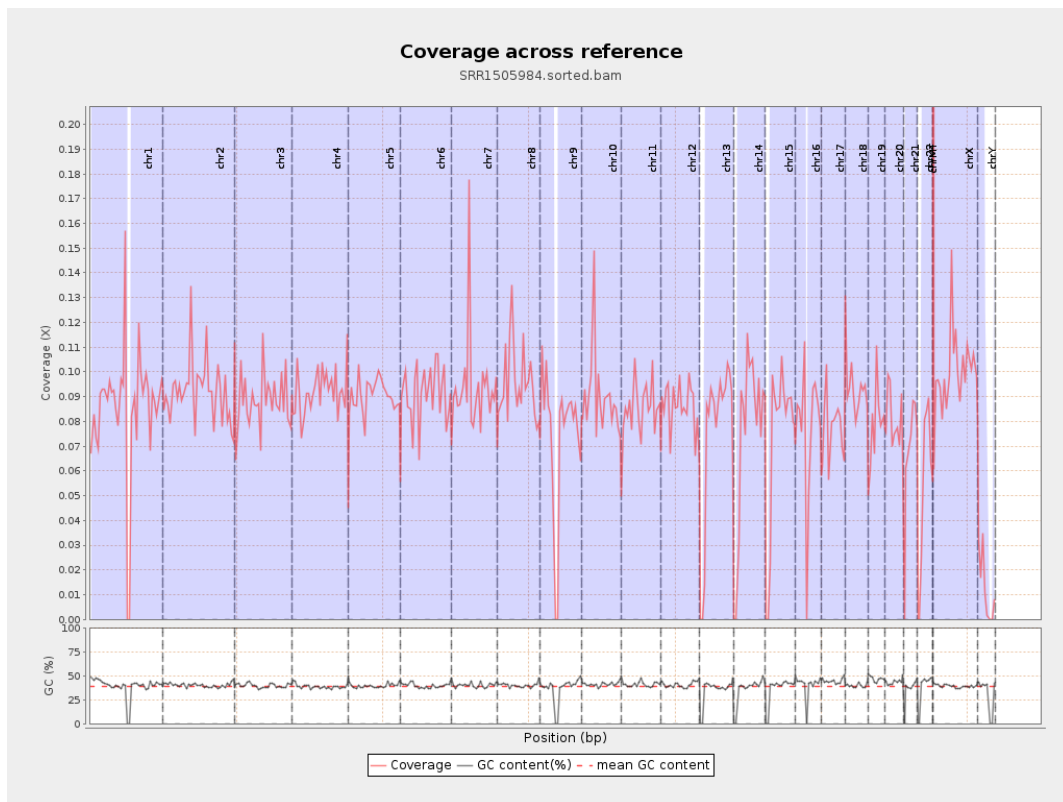
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.51%     |
| Mismatches                               | 1,311,591 |
| Insertions                               | 13,218    |
| Mapped reads with at least one insertion | 0.23%     |
| Deletions                                | 37,608    |
| Mapped reads with at least one deletion  | 0.66%     |
| Homopolymer indels                       | 45.67%    |

## 2.6. Chromosome stats

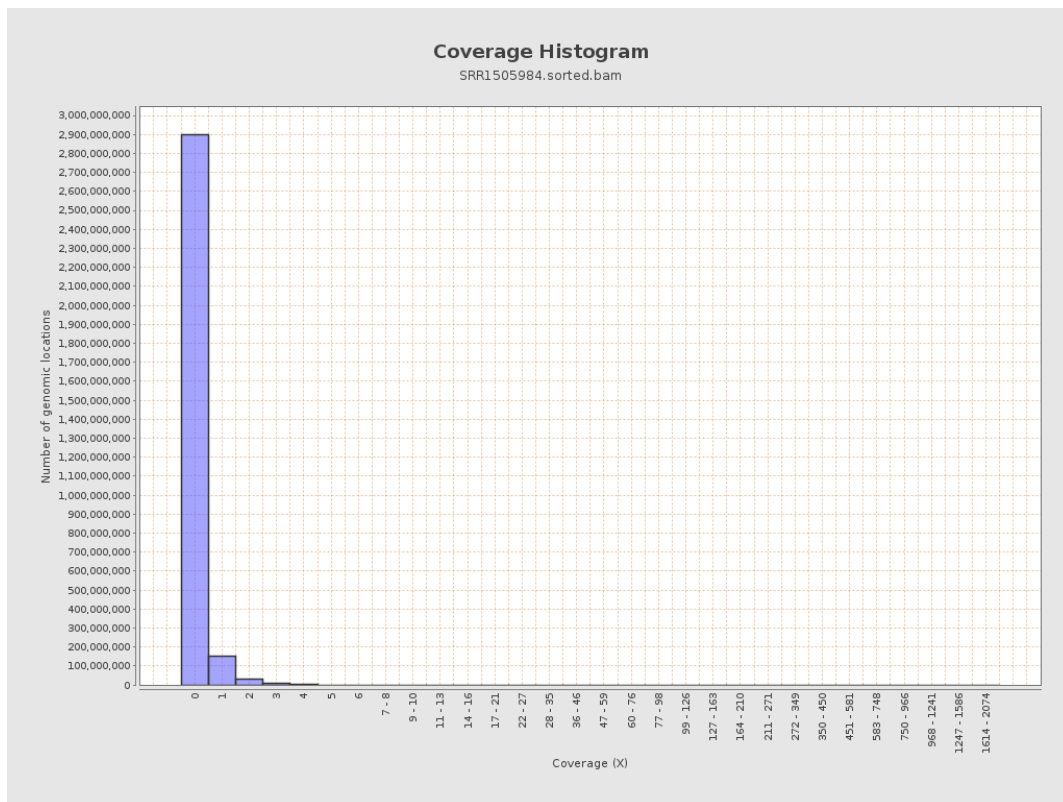
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 21179325     | 0.085         | 1.2232             |
| chr2 | 243199373 | 22363191     | 0.092         | 0.5693             |
| chr3 | 198022430 | 17537462     | 0.0886        | 0.3822             |
| chr4 | 191154276 | 17649406     | 0.0923        | 0.3973             |
| chr5 | 180915260 | 16305433     | 0.0901        | 0.3894             |
| chr6 | 171115067 | 15650398     | 0.0915        | 0.4753             |
| chr7 | 159138663 | 14947495     | 0.0939        | 1.0432             |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr8  | 146364022 | 13939194 | 0.0952 | 1.1805 |
| chr9  | 141213431 | 10540978 | 0.0746 | 0.5133 |
| chr10 | 135534747 | 12122012 | 0.0894 | 0.6995 |
| chr11 | 135006516 | 11527170 | 0.0854 | 0.6078 |
| chr12 | 133851895 | 11549630 | 0.0863 | 0.4005 |
| chr13 | 115169878 | 8673187  | 0.0753 | 0.3462 |
| chr14 | 107349540 | 8143050  | 0.0759 | 0.7454 |
| chr15 | 102531392 | 7370786  | 0.0719 | 0.3393 |
| chr16 | 90354753  | 6862763  | 0.076  | 0.3944 |
| chr17 | 81195210  | 6334075  | 0.078  | 0.422  |
| chr18 | 78077248  | 7279760  | 0.0932 | 1.1404 |
| chr19 | 59128983  | 4694820  | 0.0794 | 0.906  |
| chr20 | 63025520  | 5126740  | 0.0813 | 0.3747 |
| chr21 | 48129895  | 3297054  | 0.0685 | 0.3592 |
| chr22 | 51304566  | 2774792  | 0.0541 | 0.2918 |
| chrMT | 16571     | 56017    | 3.3804 | 3.0549 |
| chrX  | 155270560 | 15527213 | 0.1    | 0.487  |
| chrY  | 59373566  | 726159   | 0.0122 | 0.1864 |

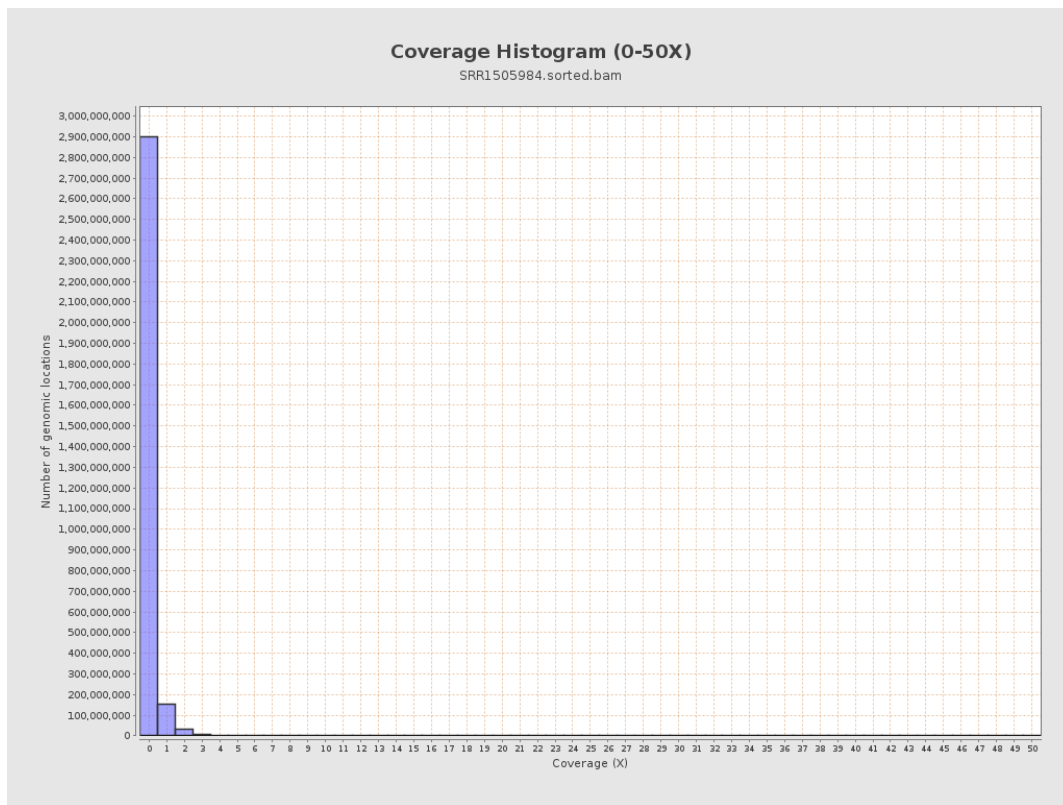
### 3. Results : Coverage across reference



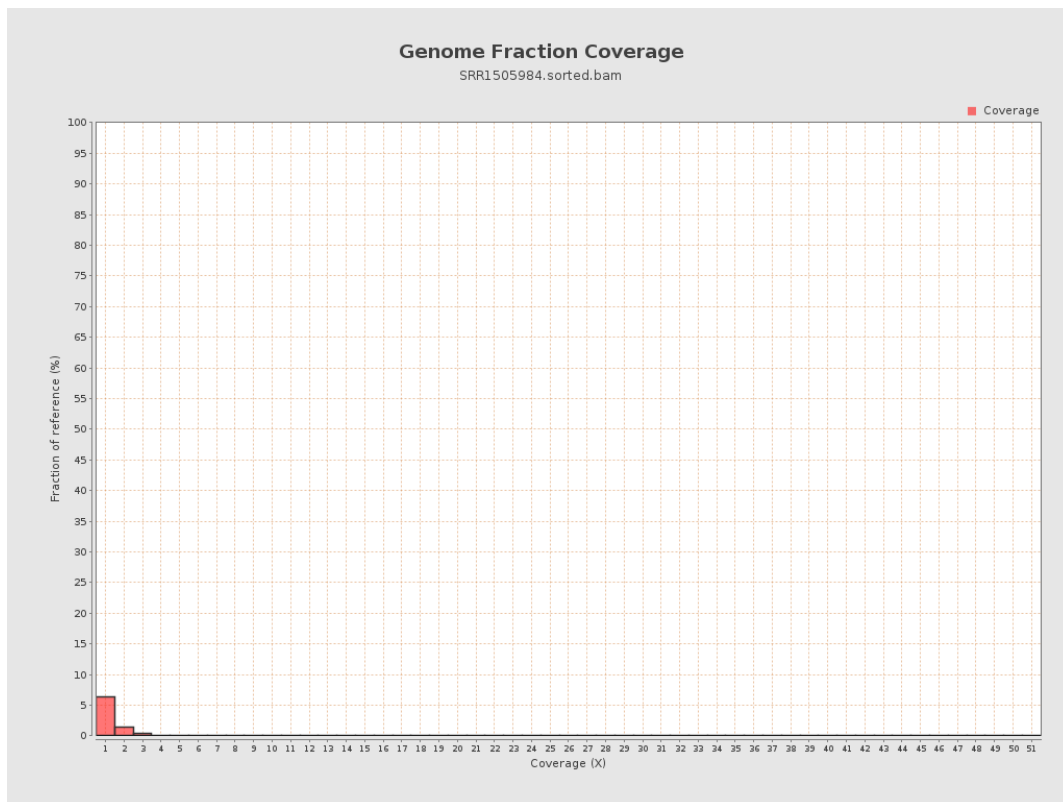
## 4. Results : Coverage Histogram



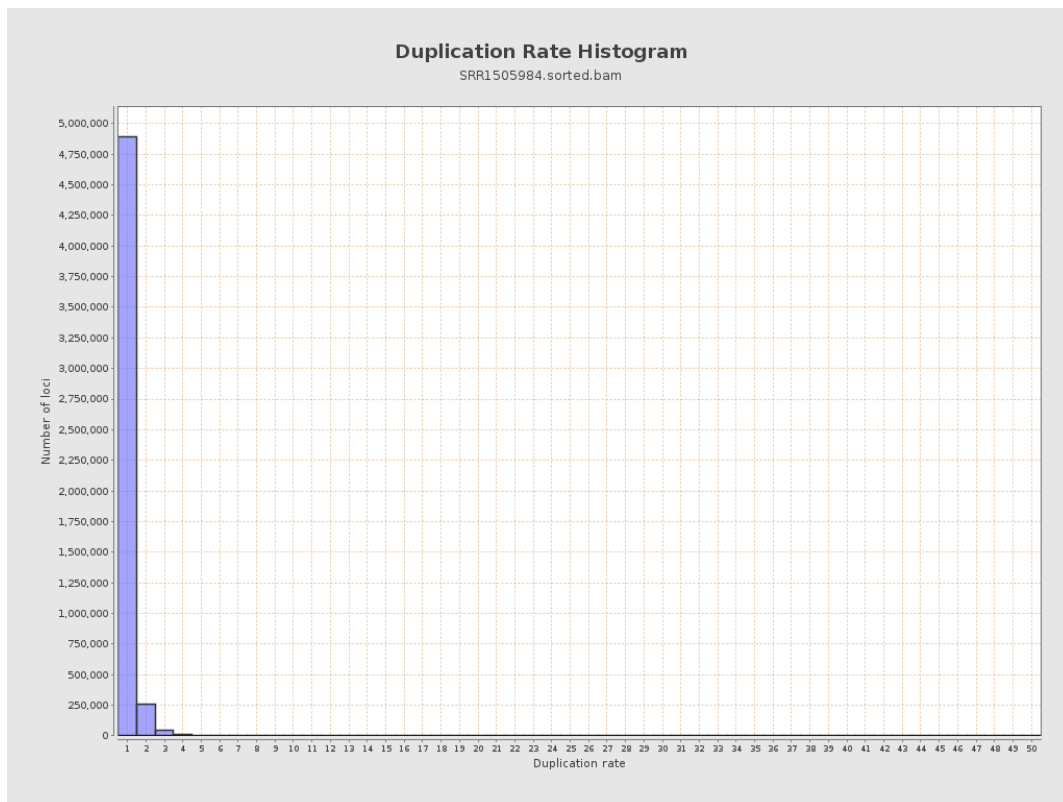
## 5. Results : Coverage Histogram (0-50X)



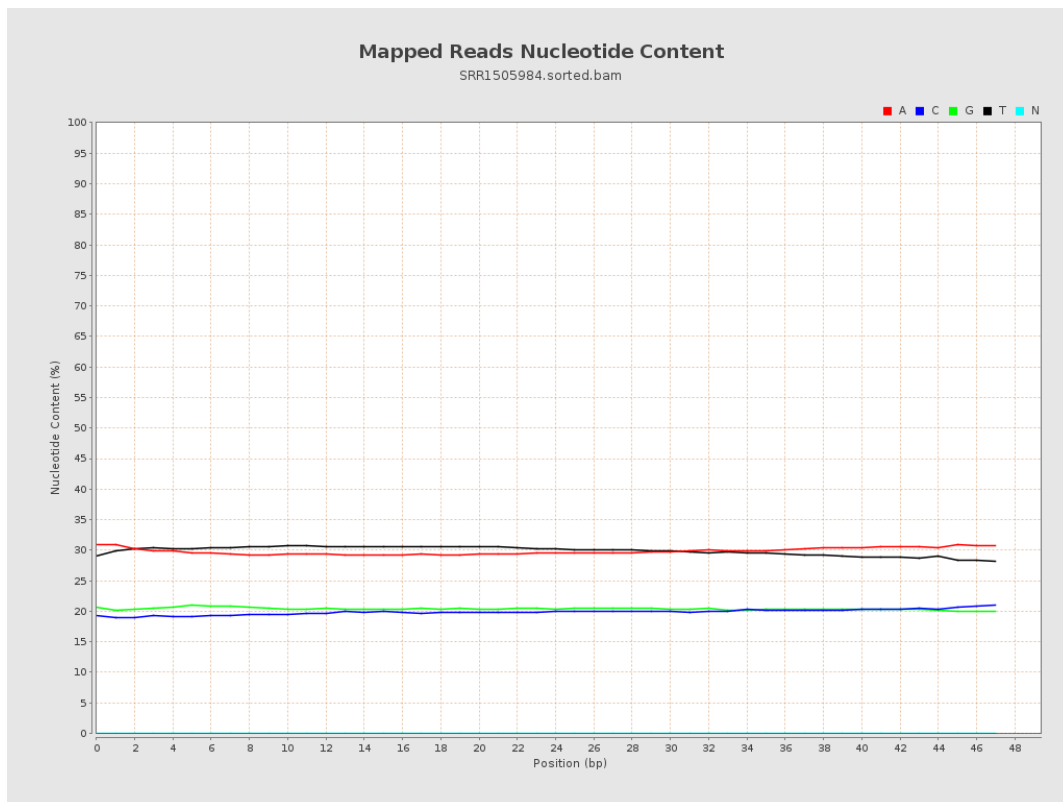
## 6. Results : Genome Fraction Coverage



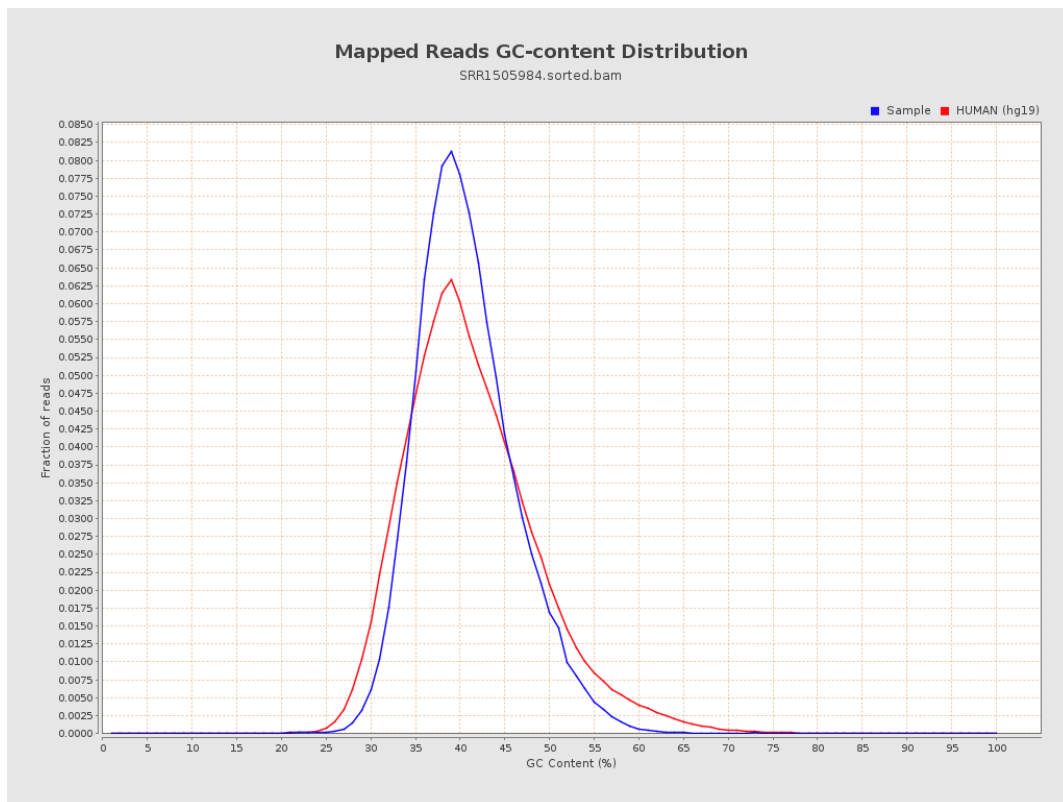
## 7. Results : Duplication Rate Histogram



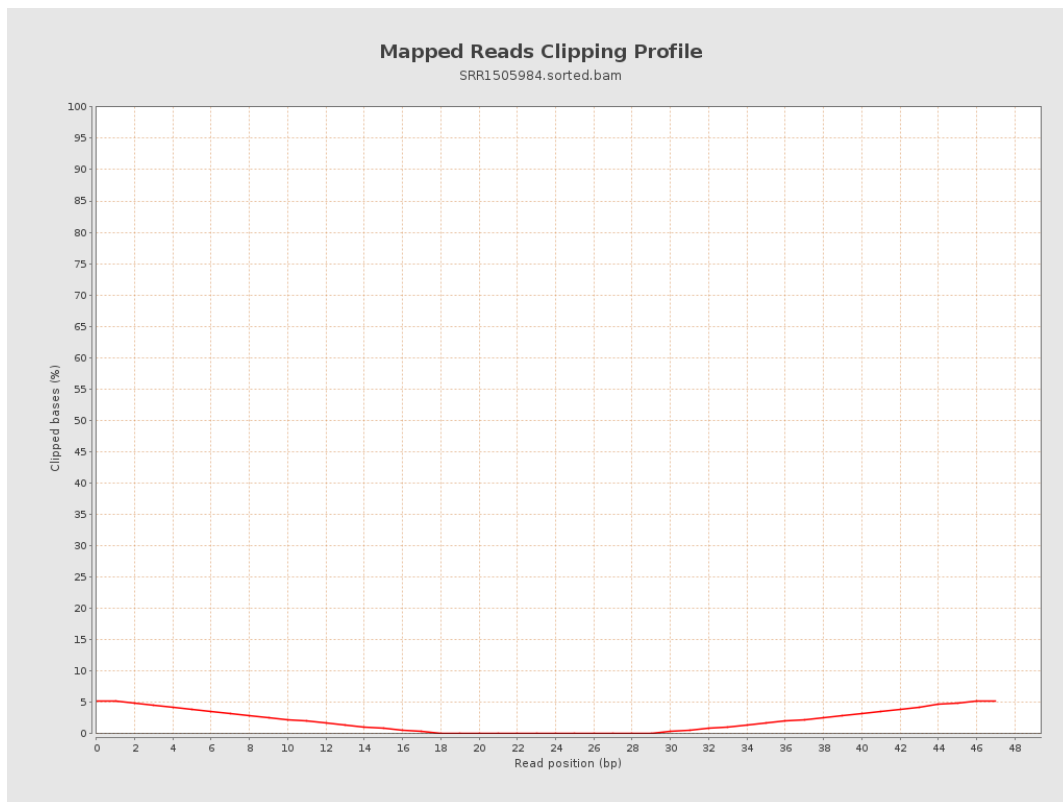
## 8. Results : Mapped Reads Nucleotide Content



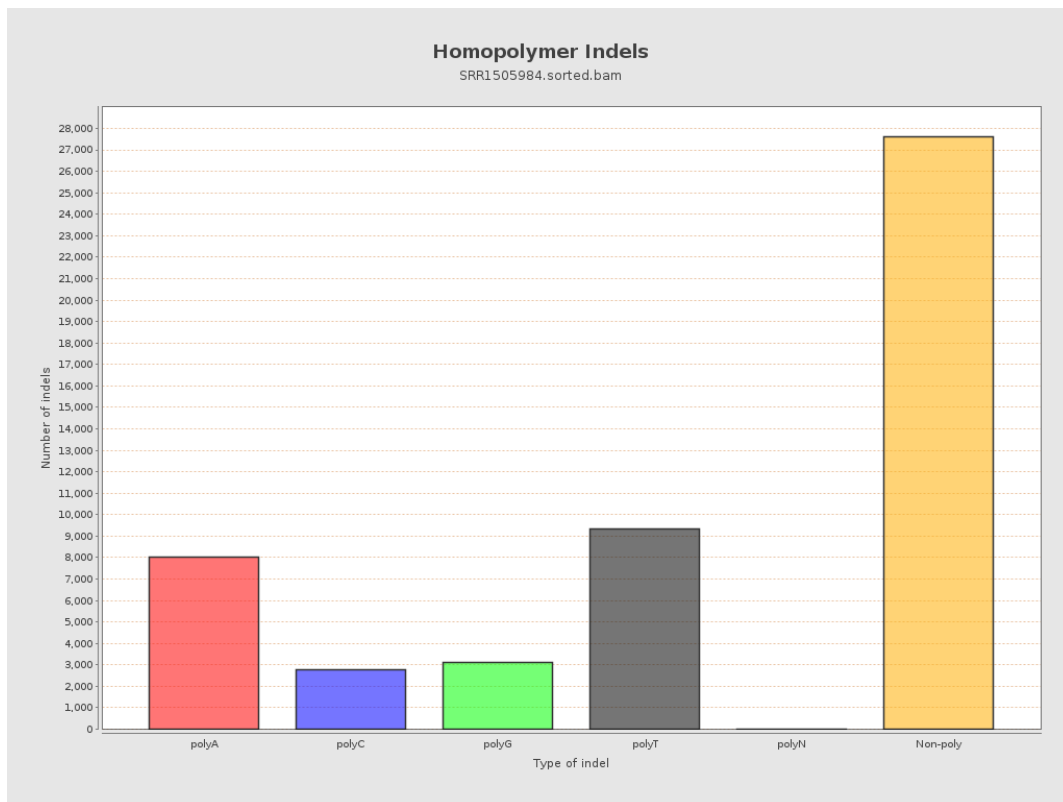
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

