

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/19 21:54:43*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505981.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_SRR1505981 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505981.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Thu Dec 19 21:54:42 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR1505981.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 9,493,380          |
| Mapped reads                 | 6,997,821 / 73.71% |
| Unmapped reads               | 2,495,559 / 26.29% |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 295 / 0%           |
| Read min/max/mean length     | 30 / 48 / 48       |
| Duplicated reads (estimated) | 449,035 / 4.73%    |
| Duplication rate             | 4.71%              |
| Clipped reads                | 882,909 / 9.3%     |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 100,857,832 / 30.82% |
| Number/percentage of C's | 63,228,261 / 19.32%  |
| Number/percentage of T's | 99,027,612 / 30.26%  |
| Number/percentage of G's | 64,119,804 / 19.59%  |
| Number/percentage of N's | 1,463 / 0%           |
| GC Percentage            | 38.92%               |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.1057 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.9447 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 46.39 |
|----------------------|-------|

## 2.5. Mismatches and indels

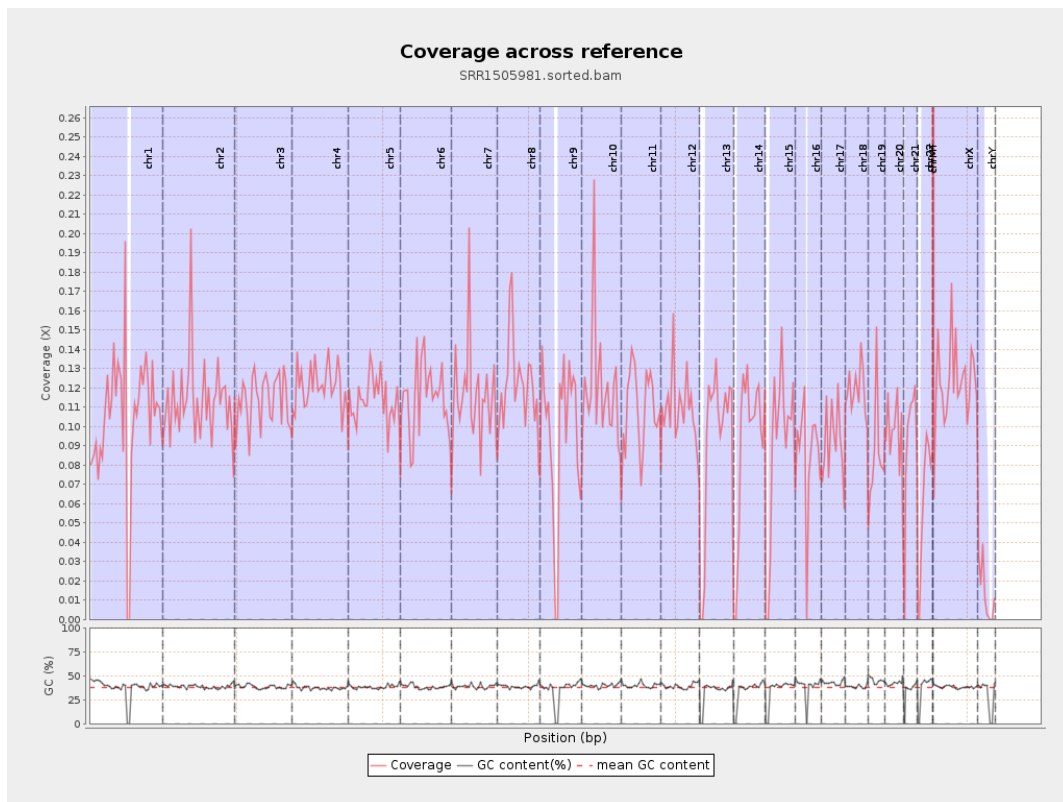
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.47%     |
| Mismatches                               | 1,525,036 |
| Insertions                               | 15,669    |
| Mapped reads with at least one insertion | 0.22%     |
| Deletions                                | 47,327    |
| Mapped reads with at least one deletion  | 0.67%     |
| Homopolymer indels                       | 47.74%    |

## 2.6. Chromosome stats

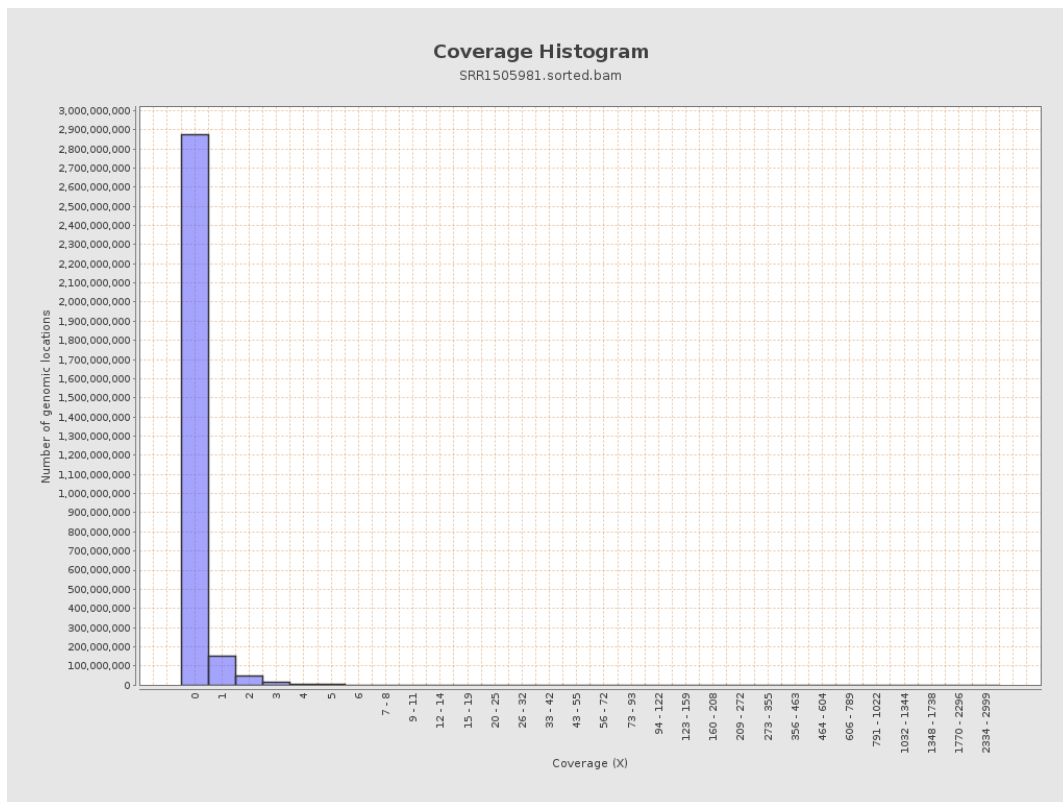
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 25900864     | 0.1039        | 1.9451             |
| chr2 | 243199373 | 27667607     | 0.1138        | 0.7971             |
| chr3 | 198022430 | 22463767     | 0.1134        | 0.4837             |
| chr4 | 191154276 | 23133824     | 0.121         | 0.4914             |
| chr5 | 180915260 | 20464934     | 0.1131        | 0.4813             |
| chr6 | 171115067 | 19709515     | 0.1152        | 0.5862             |
| chr7 | 159138663 | 18379329     | 0.1155        | 1.1567             |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr8  | 146364022 | 17753484 | 0.1213 | 1.7434 |
| chr9  | 141213431 | 13630762 | 0.0965 | 0.6858 |
| chr10 | 135534747 | 16123386 | 0.119  | 0.9887 |
| chr11 | 135006516 | 14749609 | 0.1093 | 0.7906 |
| chr12 | 133851895 | 14535461 | 0.1086 | 0.5059 |
| chr13 | 115169878 | 10701670 | 0.0929 | 0.4124 |
| chr14 | 107349540 | 9935070  | 0.0925 | 0.473  |
| chr15 | 102531392 | 9111535  | 0.0889 | 0.4045 |
| chr16 | 90354753  | 7581124  | 0.0839 | 0.4827 |
| chr17 | 81195210  | 7514324  | 0.0925 | 0.5614 |
| chr18 | 78077248  | 9314556  | 0.1193 | 1.5708 |
| chr19 | 59128983  | 5134430  | 0.0868 | 1.2769 |
| chr20 | 63025520  | 6114972  | 0.097  | 0.4379 |
| chr21 | 48129895  | 4415251  | 0.0917 | 0.4743 |
| chr22 | 51304566  | 3156077  | 0.0615 | 0.3296 |
| chrMT | 16571     | 28609    | 1.7264 | 1.9292 |
| chrX  | 155270560 | 18968151 | 0.1222 | 0.6612 |
| chrY  | 59373566  | 810627   | 0.0137 | 0.2228 |

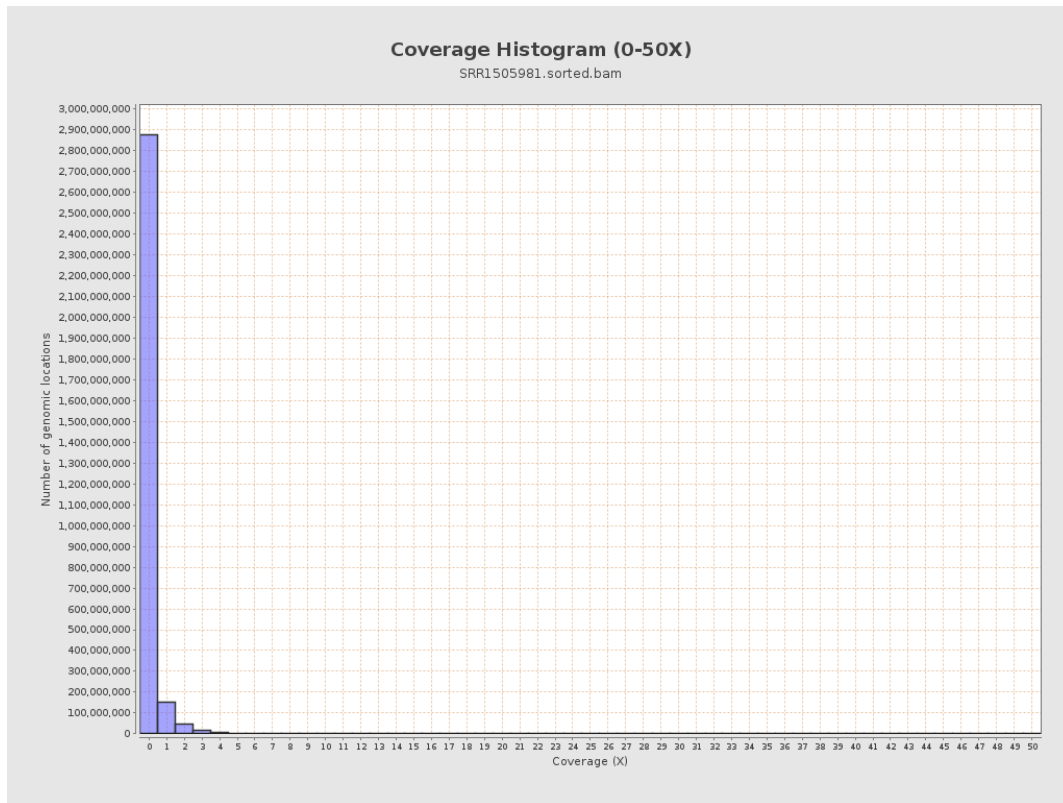
### 3. Results : Coverage across reference



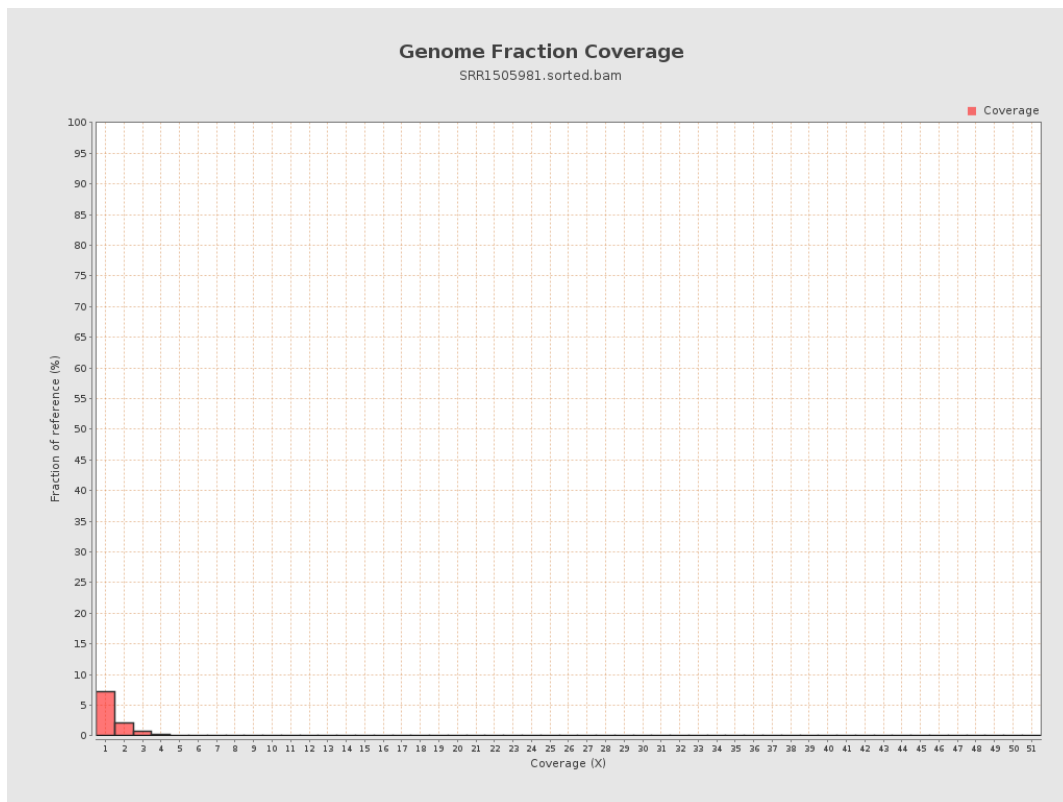
## 4. Results : Coverage Histogram



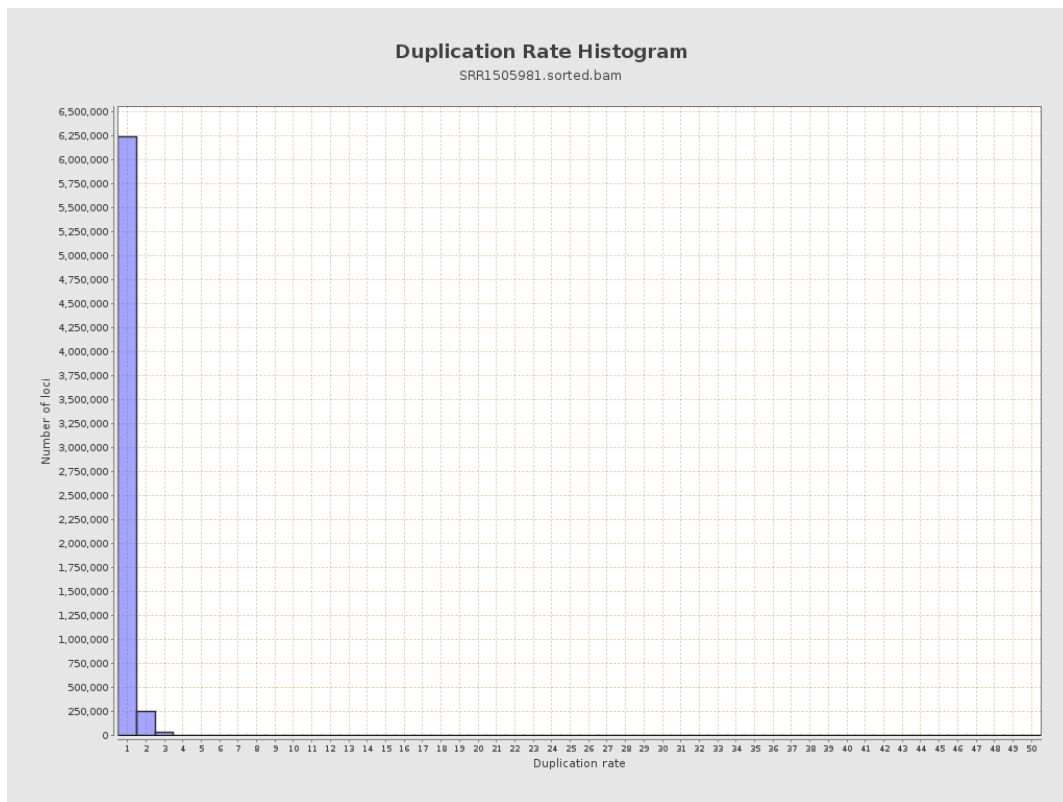
## 5. Results : Coverage Histogram (0-50X)



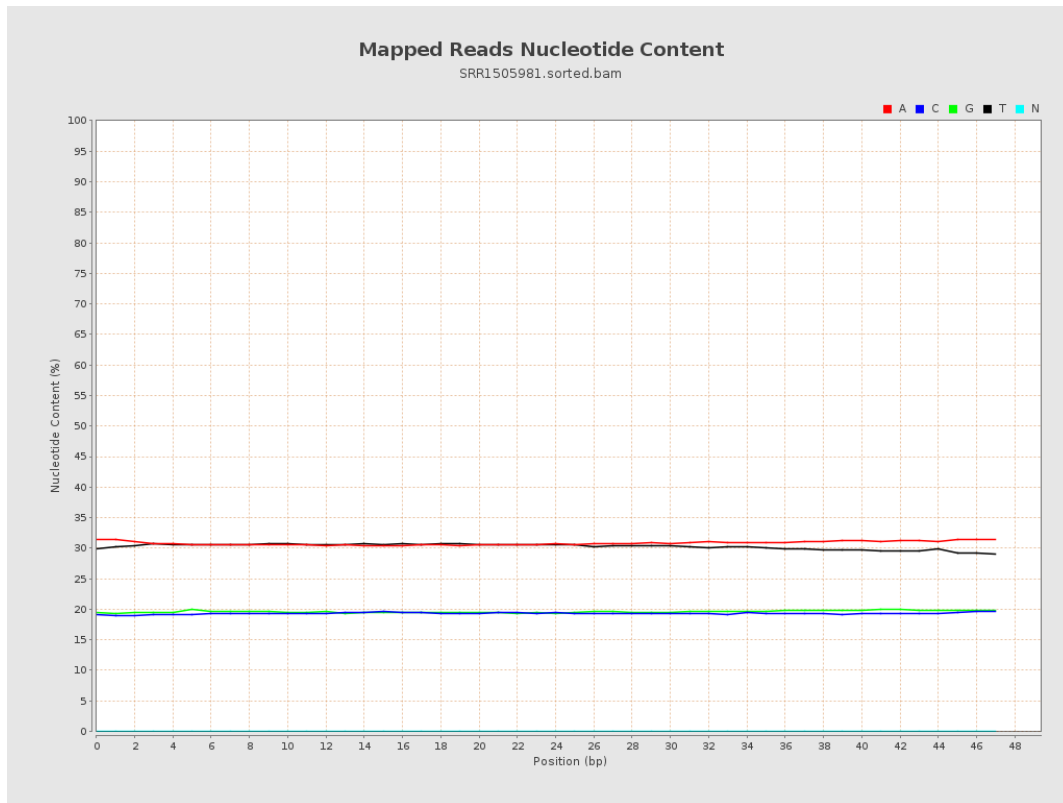
## 6. Results : Genome Fraction Coverage



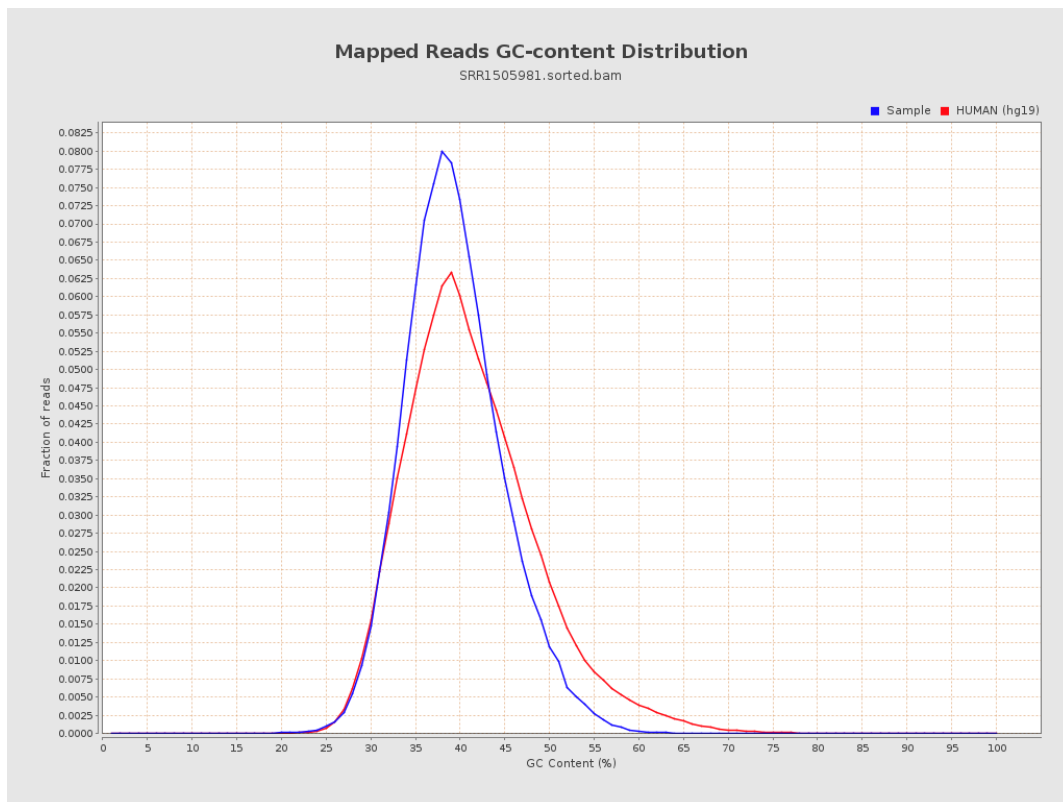
## 7. Results : Duplication Rate Histogram



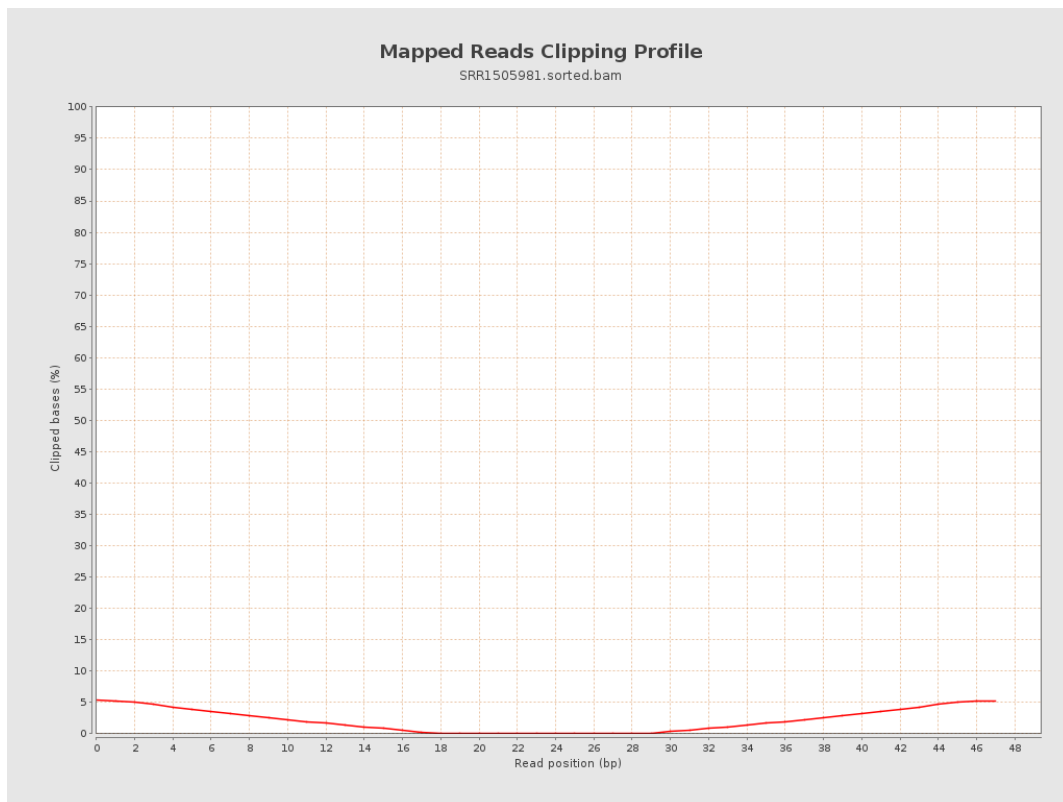
## 8. Results : Mapped Reads Nucleotide Content



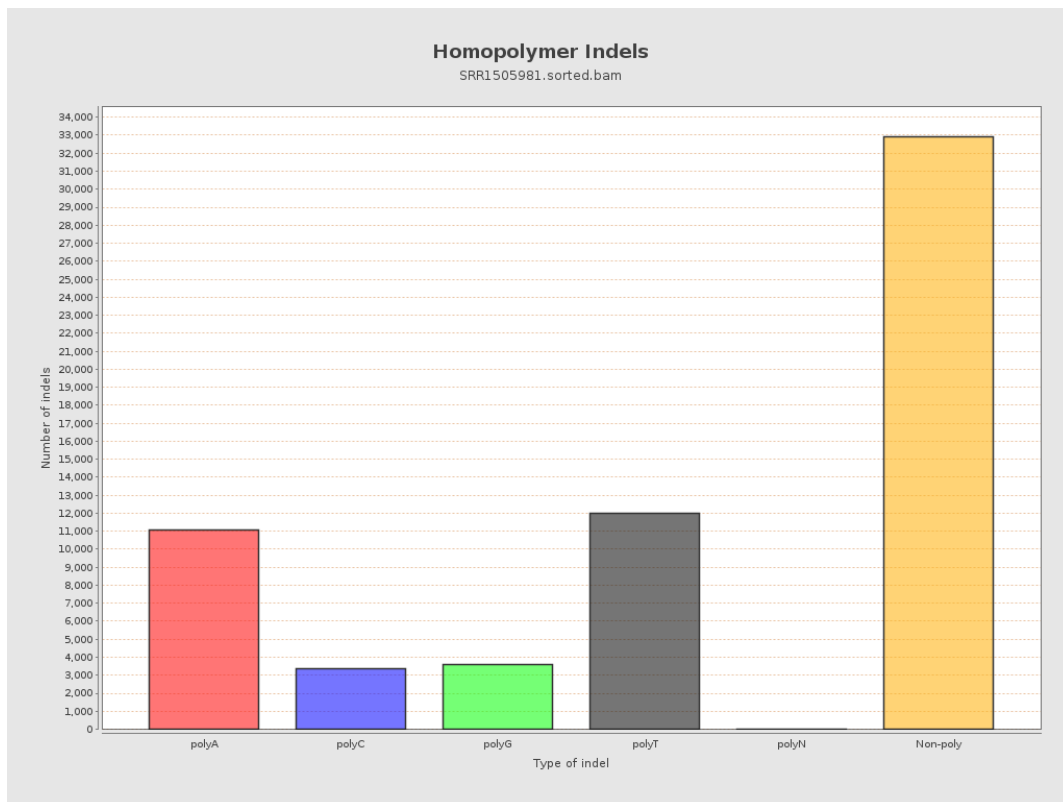
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

