

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2025/01/20 12:30:45*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR618654.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_SRR618654 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618654.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                        |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                         |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                         |
| Analysis date:                        | Mon Jan 20 12:30:43 CST 2025                                                                                                                                                               |
| Size of a homopolymer:                | 3                                                                                                                                                                                          |
| Skip duplicate alignments:            | no                                                                                                                                                                                         |
| Number of windows:                    | 400                                                                                                                                                                                        |
| BAM file:                             | SRR618654.sorted.bam                                                                                                                                                                       |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 52,129,613          |
| Mapped reads                 | 50,552,426 / 96.97% |
| Unmapped reads               | 1,577,187 / 3.03%   |
| Mapped paired reads          | 0 / 0%              |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 160,586 / 0.31%     |
| Read min/max/mean length     | 30 / 100 / 100.12   |
| Duplicated reads (estimated) | 40,355,041 / 77.41% |
| Duplication rate             | 51.67%              |
| Clipped reads                | 6,872,222 / 13.18%  |

### 2.2. ACGT Content

|                          |                        |
|--------------------------|------------------------|
| Number/percentage of A's | 1,327,929,700 / 27.18% |
| Number/percentage of C's | 1,096,238,611 / 22.44% |
| Number/percentage of T's | 1,438,126,797 / 29.44% |
| Number/percentage of G's | 1,021,901,028 / 20.92% |
| Number/percentage of N's | 715,424 / 0.01%        |
| GC Percentage            | 43.36%                 |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 1.5792 |
|      |        |

|                    |         |
|--------------------|---------|
| Standard Deviation | 29.5845 |
|--------------------|---------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 51.79 |
|----------------------|-------|

## 2.5. Mismatches and indels

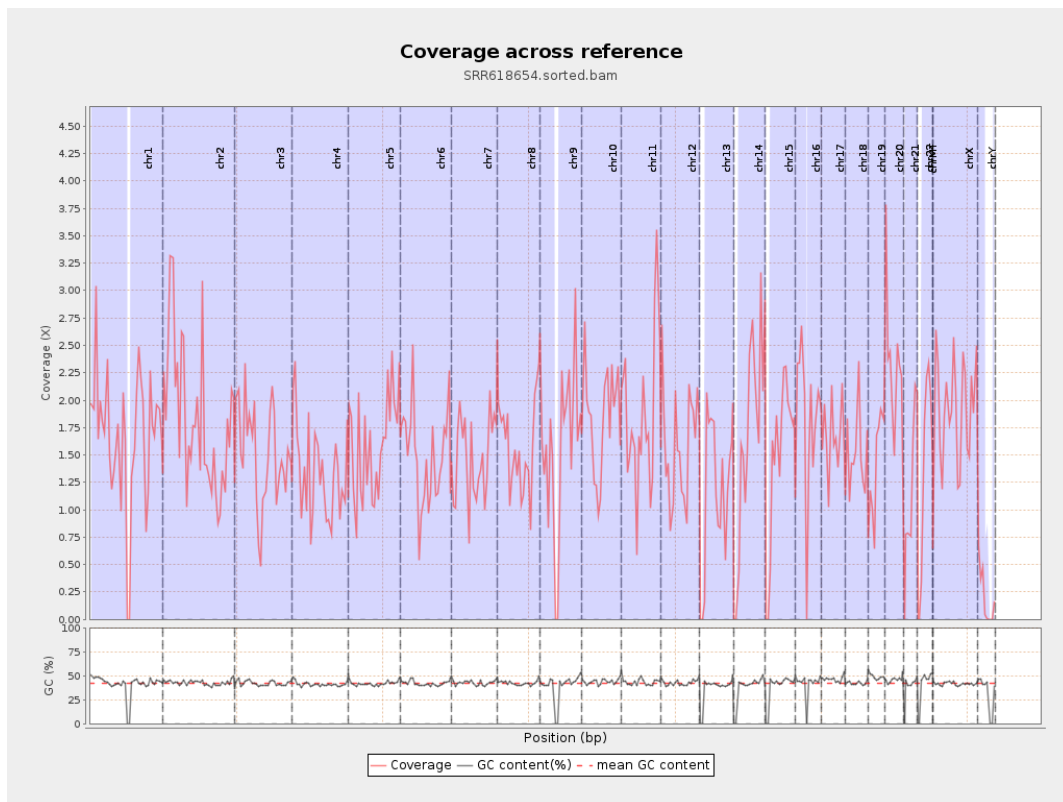
|                                          |            |
|------------------------------------------|------------|
| General error rate                       | 0.9%       |
| Mismatches                               | 42,208,142 |
| Insertions                               | 927,154    |
| Mapped reads with at least one insertion | 1.8%       |
| Deletions                                | 2,483,587  |
| Mapped reads with at least one deletion  | 4.79%      |
| Homopolymer indels                       | 52.13%     |

## 2.6. Chromosome stats

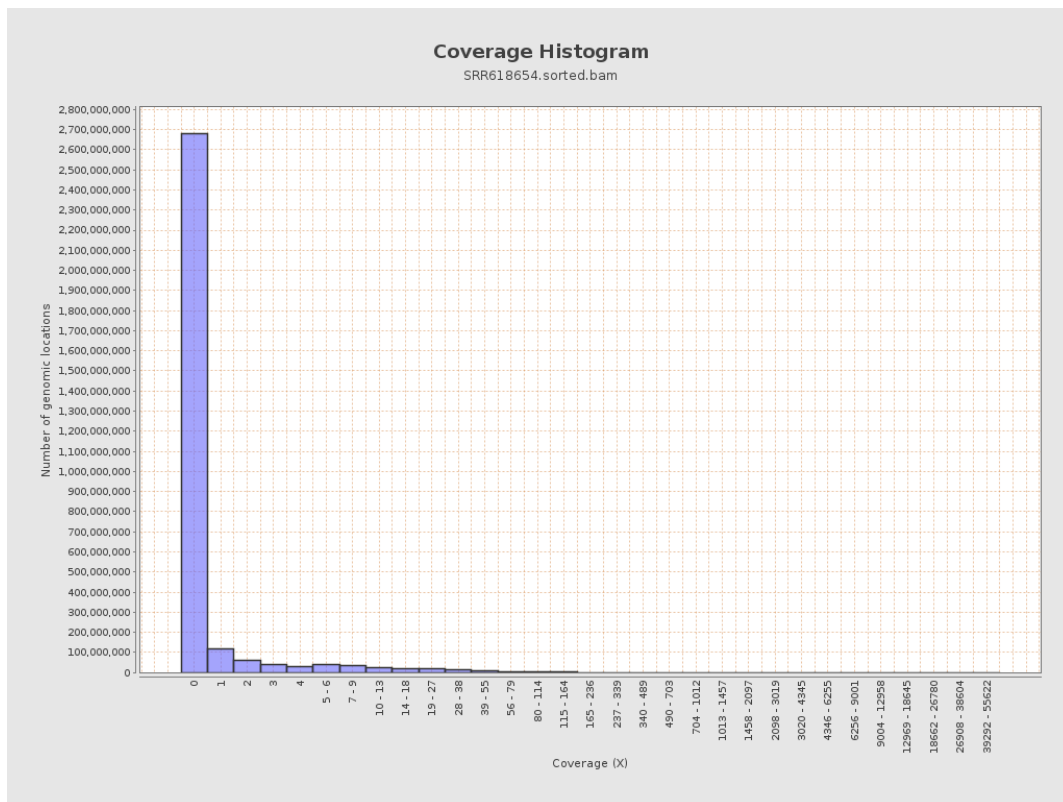
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 414839307    | 1.6643        | 32.1089            |
| chr2 | 243199373 | 441273562    | 1.8145        | 42.8353            |
| chr3 | 198022430 | 297769053    | 1.5037        | 22.7689            |
| chr4 | 191154276 | 254703980    | 1.3325        | 23.6314            |
| chr5 | 180915260 | 289210797    | 1.5986        | 33.3425            |
| chr6 | 171115067 | 254508978    | 1.4874        | 23.3319            |
| chr7 | 159138663 | 232344223    | 1.46          | 21.8018            |
|      |           |              |               |                    |

|       |           |           |        |         |
|-------|-----------|-----------|--------|---------|
| chr8  | 146364022 | 229546831 | 1.5683 | 23.6412 |
| chr9  | 141213431 | 221024903 | 1.5652 | 24.9198 |
| chr10 | 135534747 | 248587938 | 1.8341 | 37.1225 |
| chr11 | 135006516 | 249488076 | 1.848  | 33.9292 |
| chr12 | 133851895 | 214548600 | 1.6029 | 35.7881 |
| chr13 | 115169878 | 133297801 | 1.1574 | 29.517  |
| chr14 | 107349540 | 175745923 | 1.6371 | 26.9806 |
| chr15 | 102531392 | 150444786 | 1.4673 | 23.5195 |
| chr16 | 90354753  | 162660962 | 1.8002 | 38.0048 |
| chr17 | 81195210  | 135621869 | 1.6703 | 23.1904 |
| chr18 | 78077248  | 116936099 | 1.4977 | 17.7467 |
| chr19 | 59128983  | 84877811  | 1.4355 | 32.8464 |
| chr20 | 63025520  | 144622917 | 2.2947 | 22.7602 |
| chr21 | 48129895  | 57468189  | 1.194  | 16.942  |
| chr22 | 51304566  | 70610255  | 1.3763 | 22.8775 |
| chrMT | 16571     | 10618     | 0.6408 | 4.5842  |
| chrX  | 155270560 | 296785060 | 1.9114 | 31.7433 |
| chrY  | 59373566  | 11666939  | 0.1965 | 16.4352 |

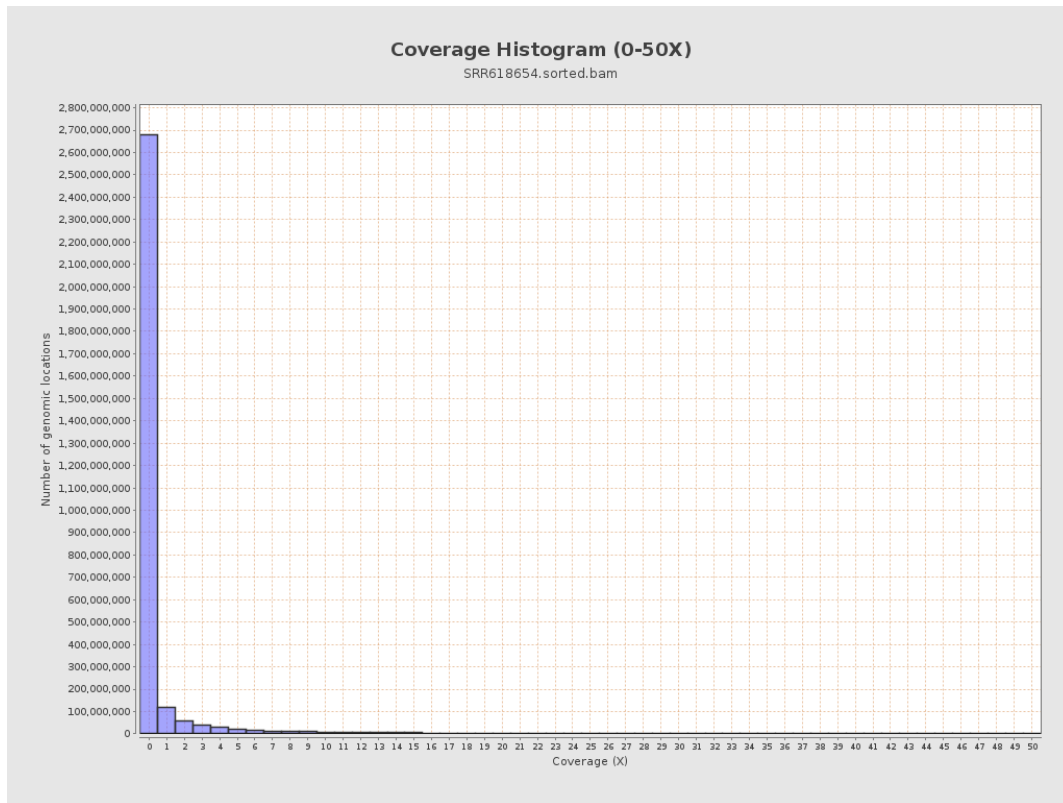
### 3. Results : Coverage across reference



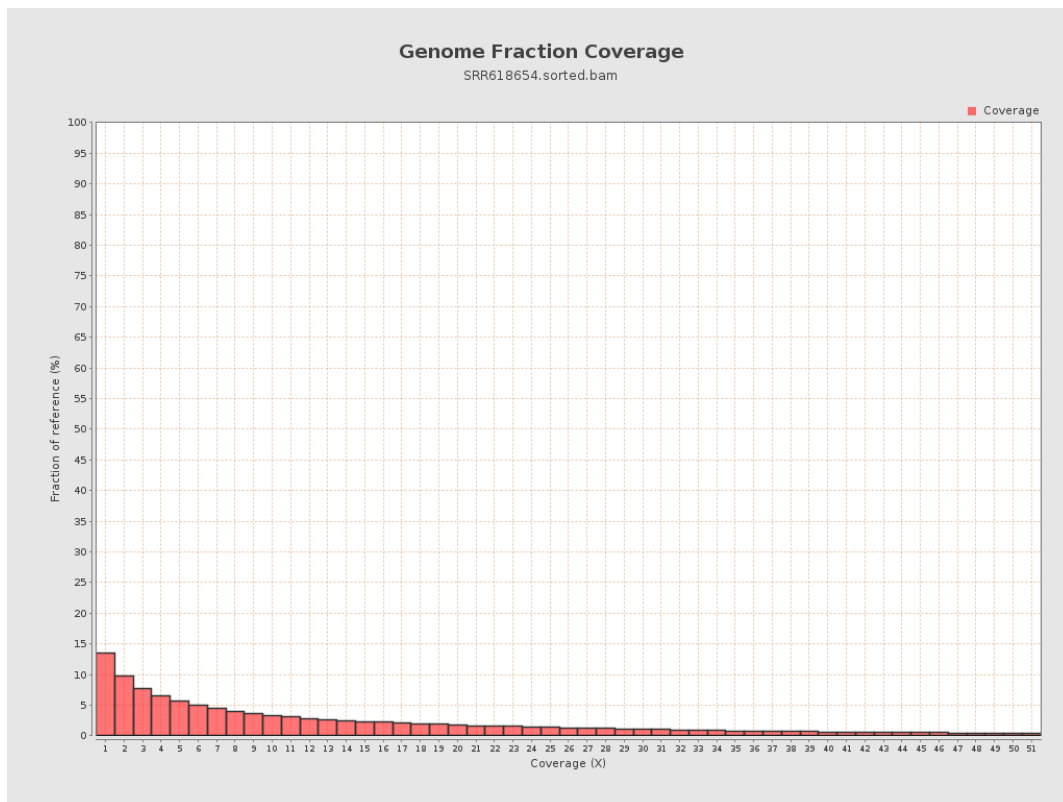
## 4. Results : Coverage Histogram



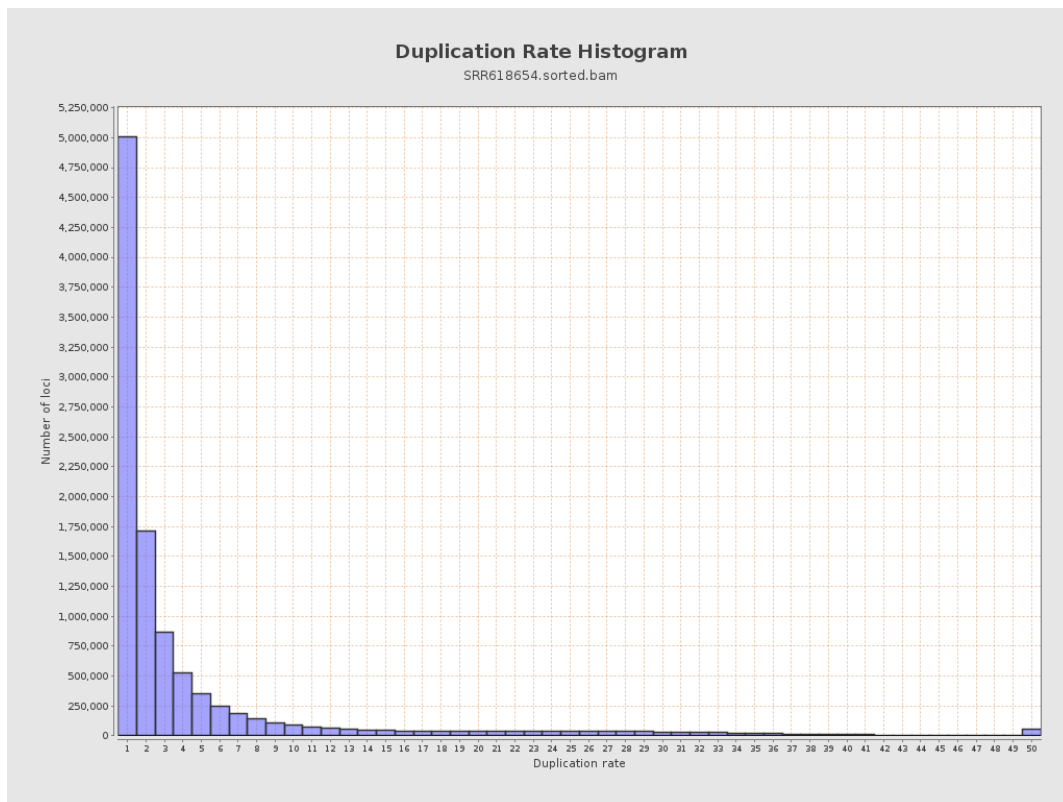
## 5. Results : Coverage Histogram (0-50X)



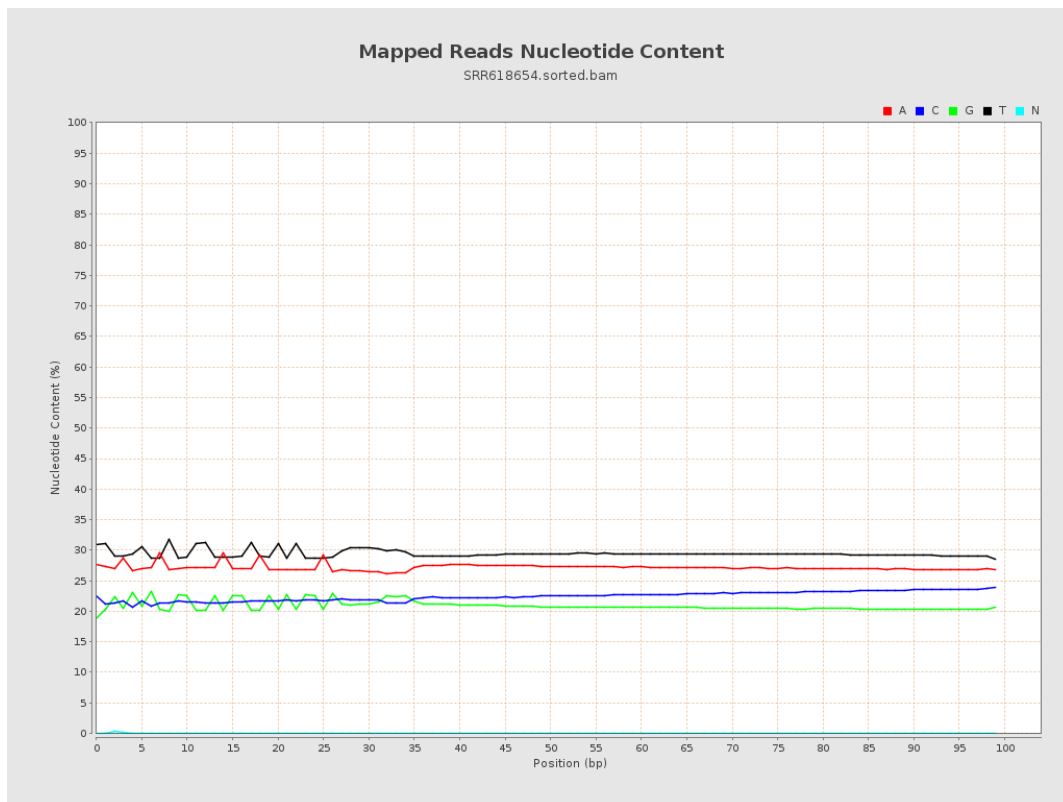
## 6. Results : Genome Fraction Coverage



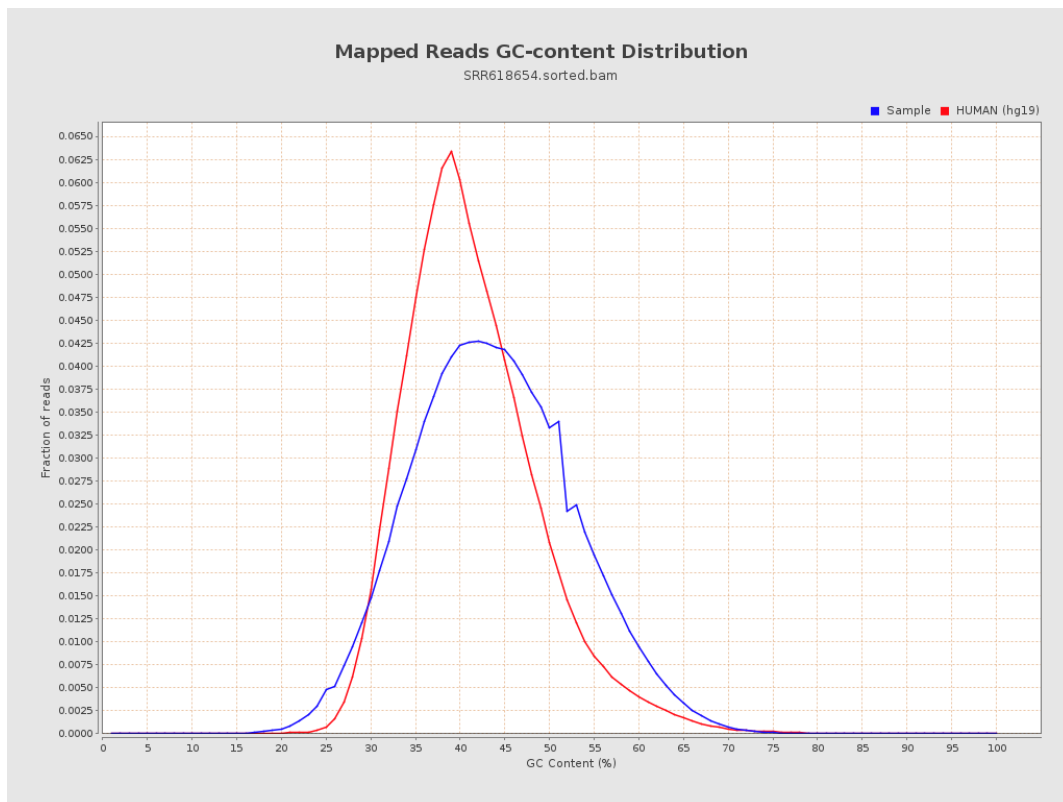
## 7. Results : Duplication Rate Histogram



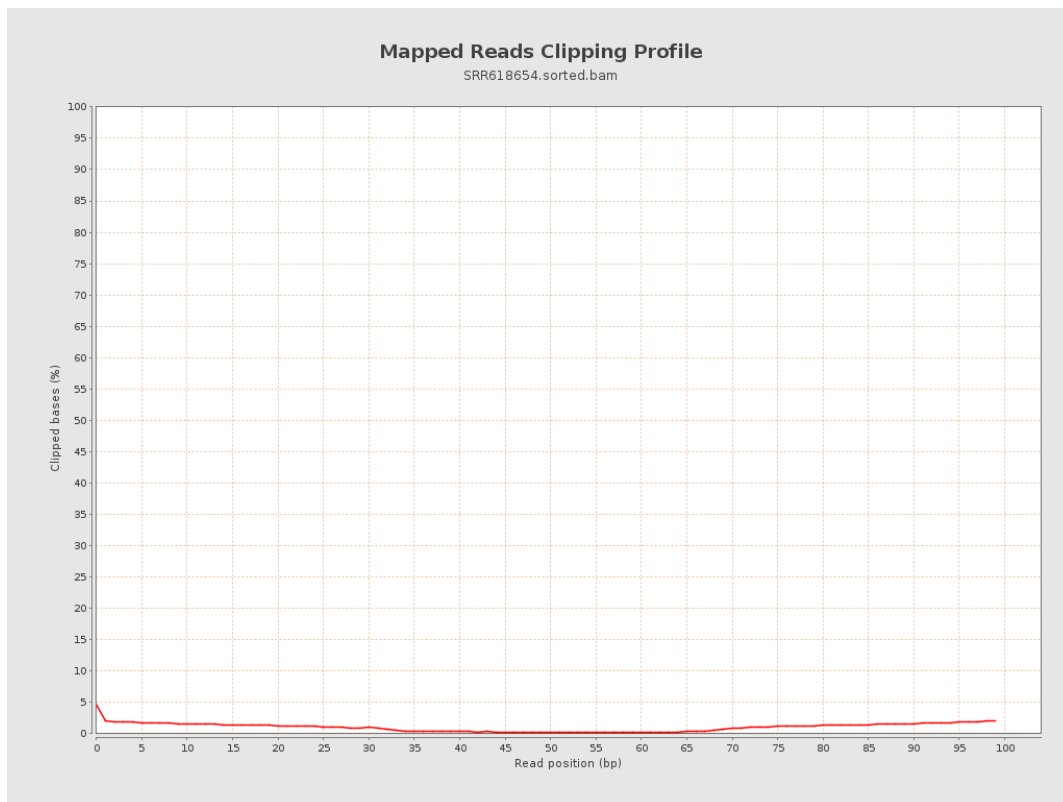
## 8. Results : Mapped Reads Nucleotide Content



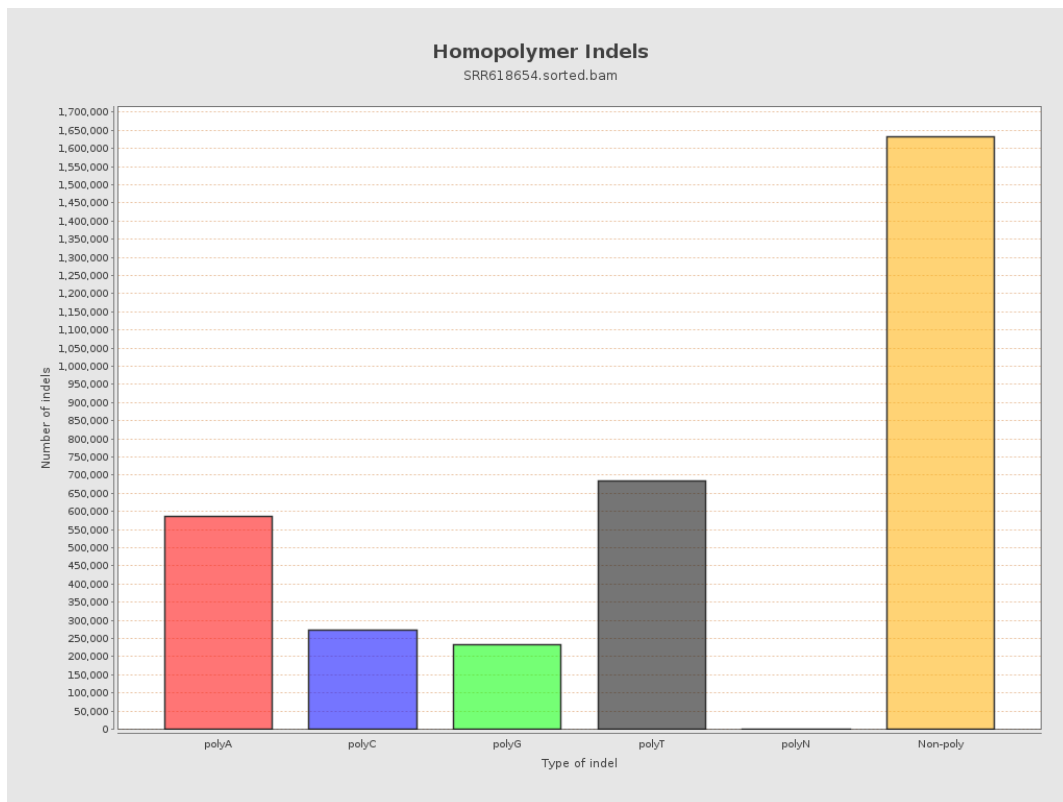
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

