

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 06:12:32*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818900.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_SRR1818900 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818900.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Fri Aug 23 06:12:30 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR1818900.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 1,244,634          |
| Mapped reads                 | 1,102,566 / 88.59% |
| Unmapped reads               | 142,068 / 11.41%   |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 15,051 / 1.21%     |
| Read min/max/mean length     | 30 / 101 / 101.46  |
| Duplicated reads (estimated) | 177,819 / 14.29%   |
| Duplication rate             | 13.08%             |
| Clipped reads                | 1,113,821 / 89.49% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 29,042,653 / 28.48% |
| Number/percentage of C's | 21,950,135 / 21.52% |
| Number/percentage of T's | 28,559,919 / 28.01% |
| Number/percentage of G's | 22,424,788 / 21.99% |
| Number/percentage of N's | 1,379 / 0%          |
| GC Percentage            | 43.51%              |

### 2.3. Coverage

|      |       |
|------|-------|
| Mean | 0.033 |
|      |       |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.4838 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 49.15 |
|----------------------|-------|

## 2.5. Mismatches and indels

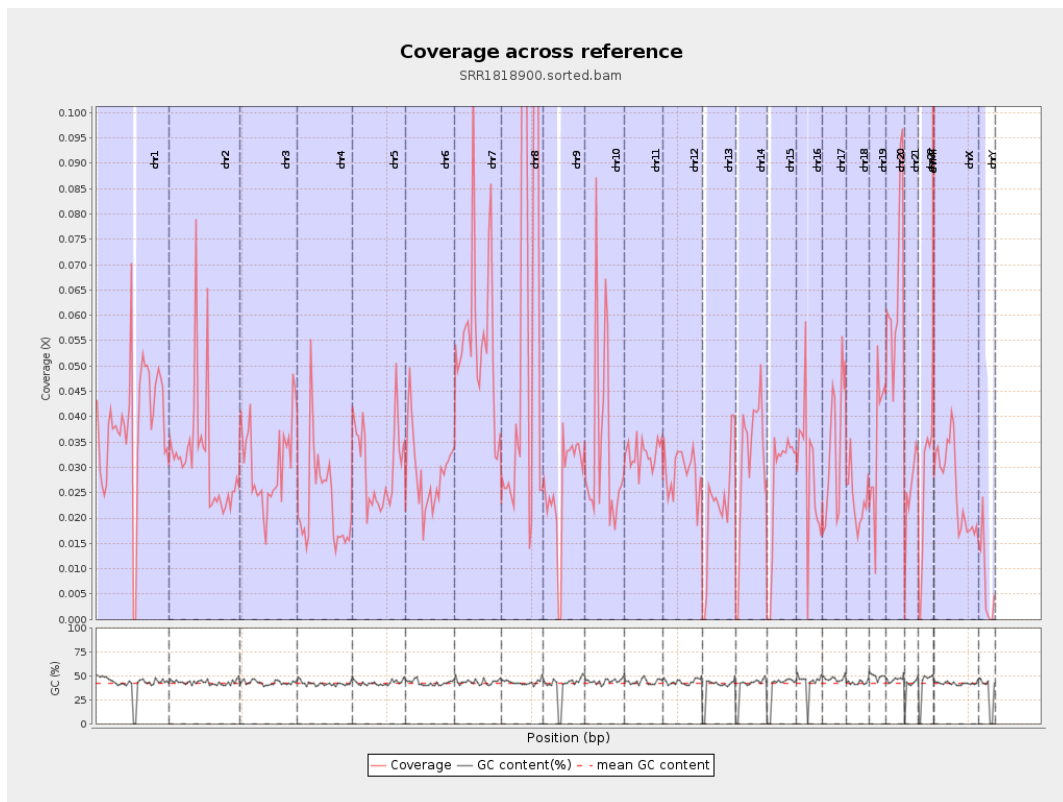
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 0.65%   |
| Mismatches                               | 630,371 |
| Insertions                               | 13,402  |
| Mapped reads with at least one insertion | 1.17%   |
| Deletions                                | 32,723  |
| Mapped reads with at least one deletion  | 2.9%    |
| Homopolymer indels                       | 41.36%  |

## 2.6. Chromosome stats

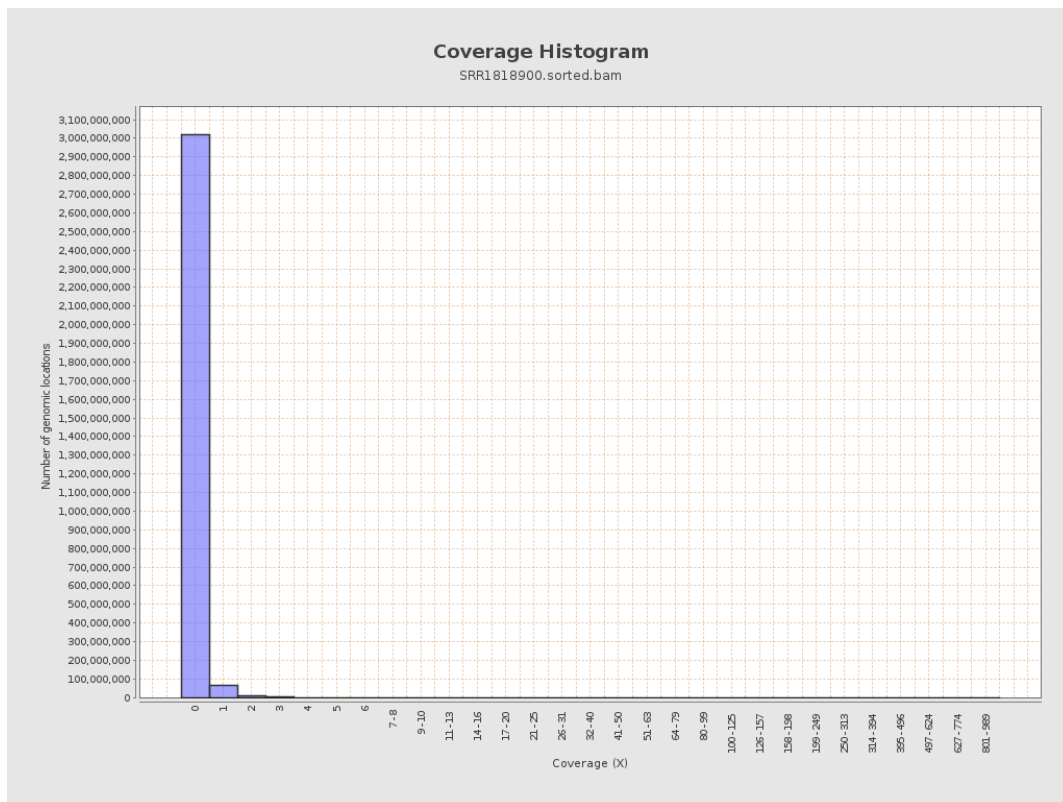
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 9492469      | 0.0381        | 0.7752             |
| chr2 | 243199373 | 7712472      | 0.0317        | 0.6616             |
| chr3 | 198022430 | 6106667      | 0.0308        | 0.2142             |
| chr4 | 191154276 | 4334463      | 0.0227        | 0.262              |
| chr5 | 180915260 | 5409916      | 0.0299        | 0.2226             |
| chr6 | 171115067 | 4929514      | 0.0288        | 0.2292             |
| chr7 | 159138663 | 8875846      | 0.0558        | 1.0957             |
|      |           |              |               |                    |

|       |           |         |        |         |
|-------|-----------|---------|--------|---------|
| chr8  | 146364022 | 9229408 | 0.0631 | 0.3798  |
| chr9  | 141213431 | 3697847 | 0.0262 | 0.3658  |
| chr10 | 135534747 | 4532272 | 0.0334 | 0.6179  |
| chr11 | 135006516 | 4406012 | 0.0326 | 0.2757  |
| chr12 | 133851895 | 3932712 | 0.0294 | 0.213   |
| chr13 | 115169878 | 2556798 | 0.0222 | 0.1807  |
| chr14 | 107349540 | 3378349 | 0.0315 | 0.2331  |
| chr15 | 102531392 | 2778235 | 0.0271 | 0.2055  |
| chr16 | 90354753  | 2586972 | 0.0286 | 0.468   |
| chr17 | 81195210  | 2775871 | 0.0342 | 0.2862  |
| chr18 | 78077248  | 1851258 | 0.0237 | 0.429   |
| chr19 | 59128983  | 2074560 | 0.0351 | 0.6897  |
| chr20 | 63025520  | 4120289 | 0.0654 | 0.3379  |
| chr21 | 48129895  | 1229442 | 0.0255 | 0.2282  |
| chr22 | 51304566  | 1277453 | 0.0249 | 0.2091  |
| chrMT | 16571     | 305420  | 18.431 | 11.2865 |
| chrX  | 155270560 | 4025426 | 0.0259 | 0.245   |
| chrY  | 59373566  | 423217  | 0.0071 | 0.5298  |

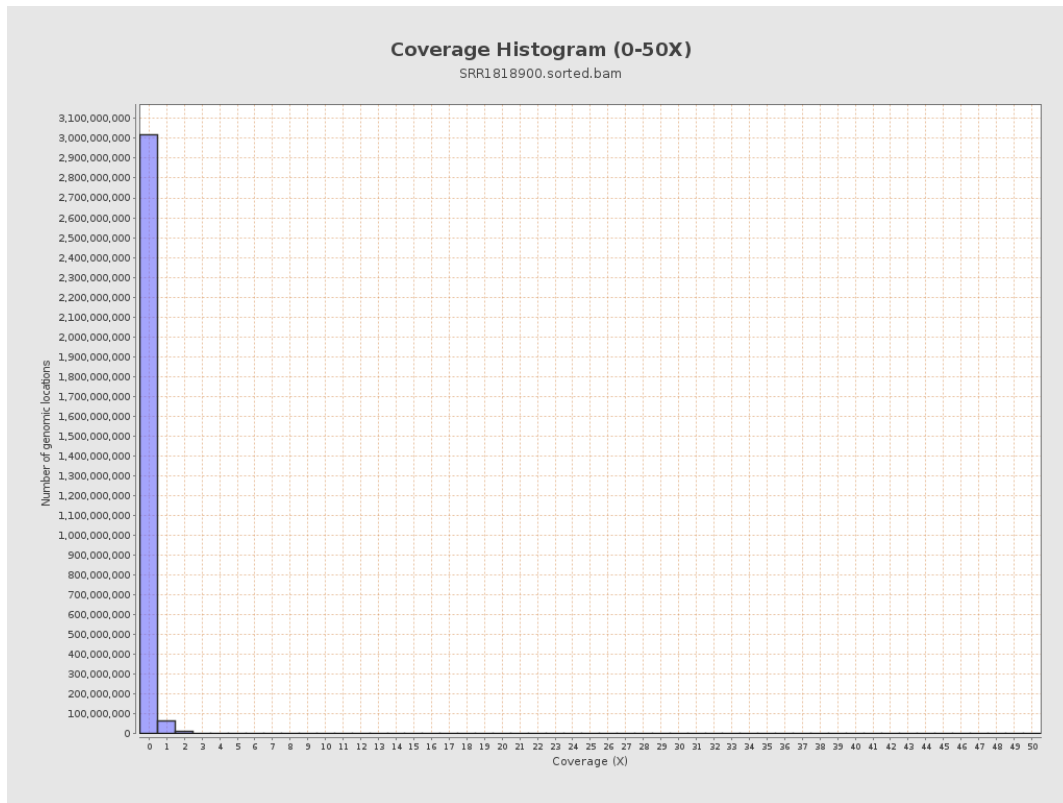
### 3. Results : Coverage across reference



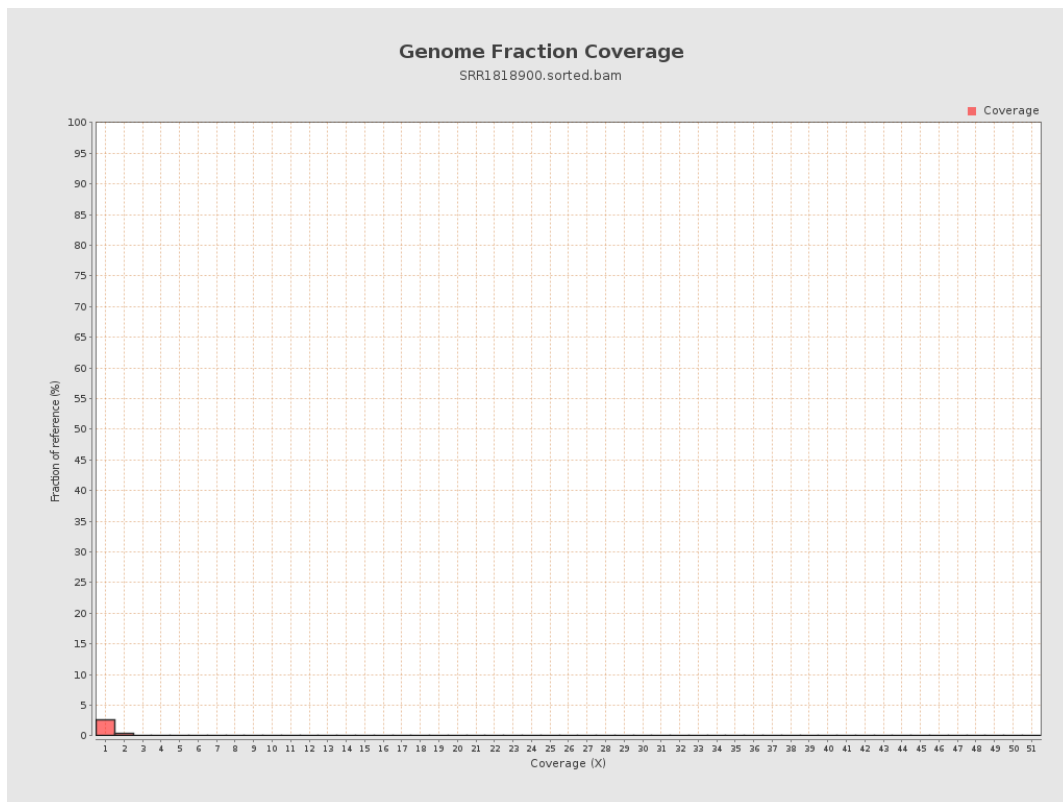
## 4. Results : Coverage Histogram



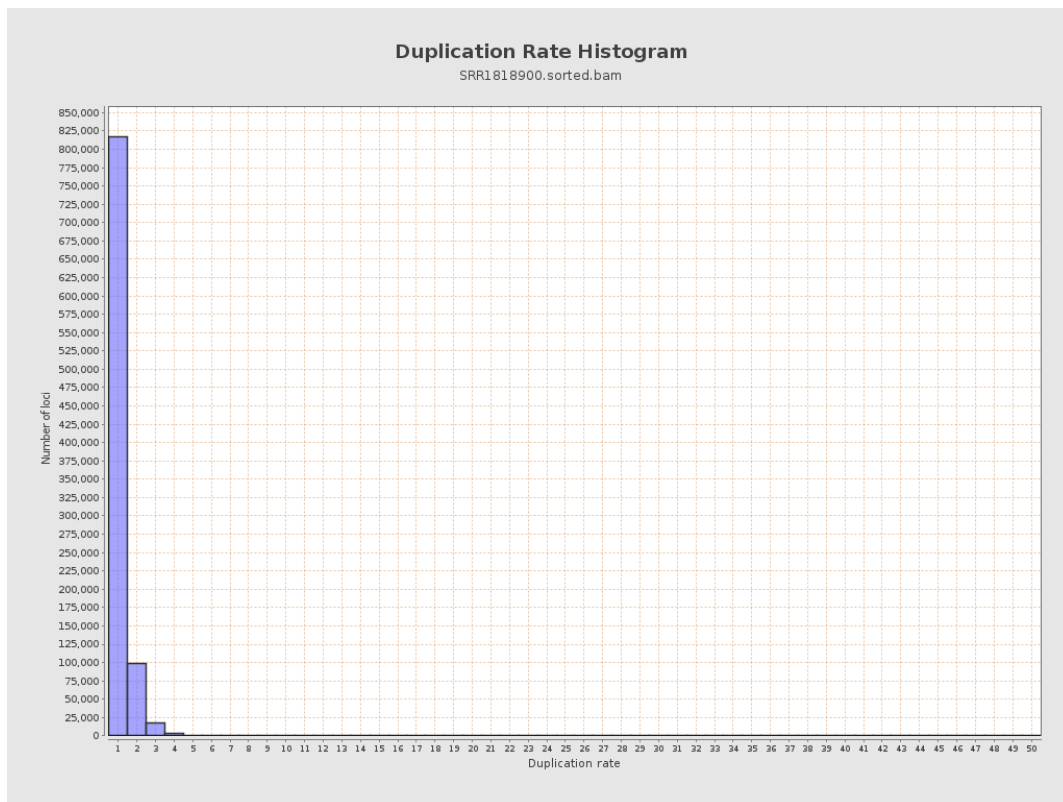
## 5. Results : Coverage Histogram (0-50X)



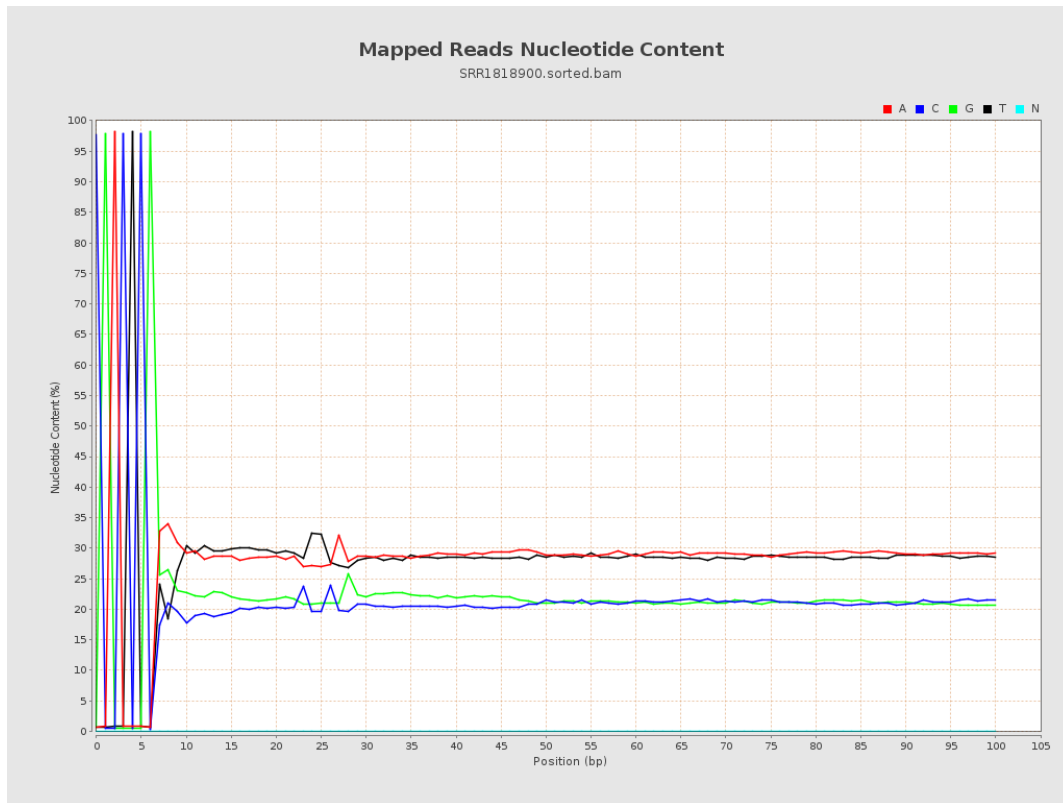
## 6. Results : Genome Fraction Coverage



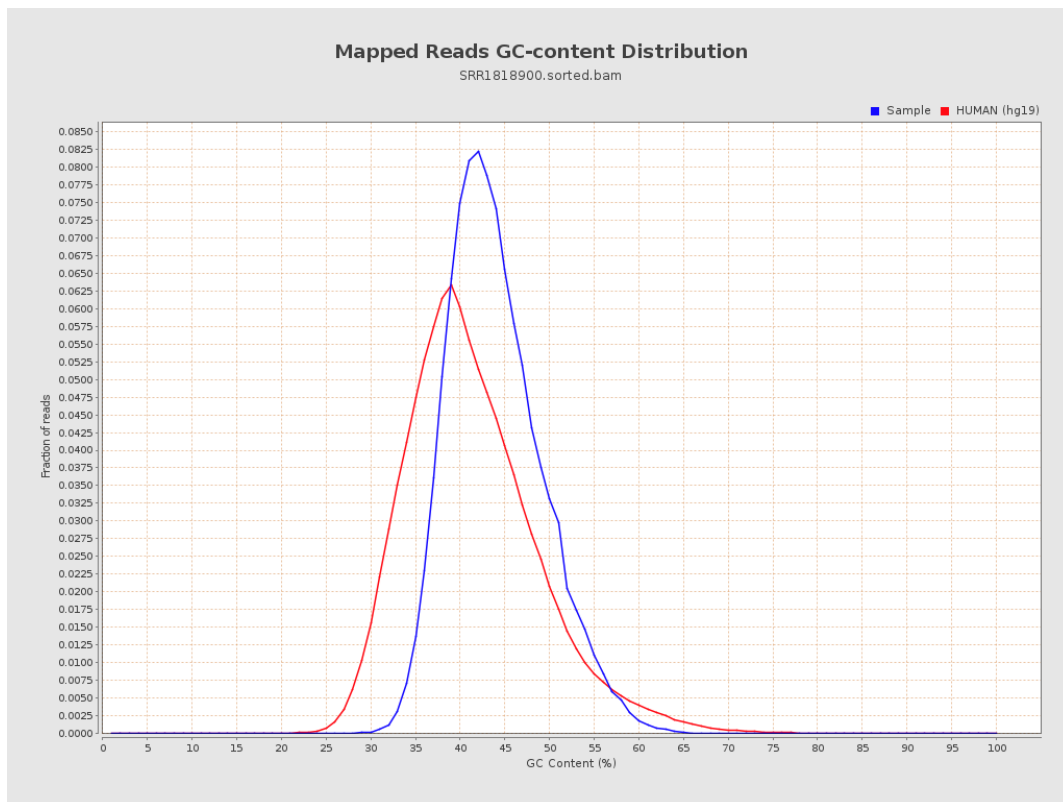
## 7. Results : Duplication Rate Histogram



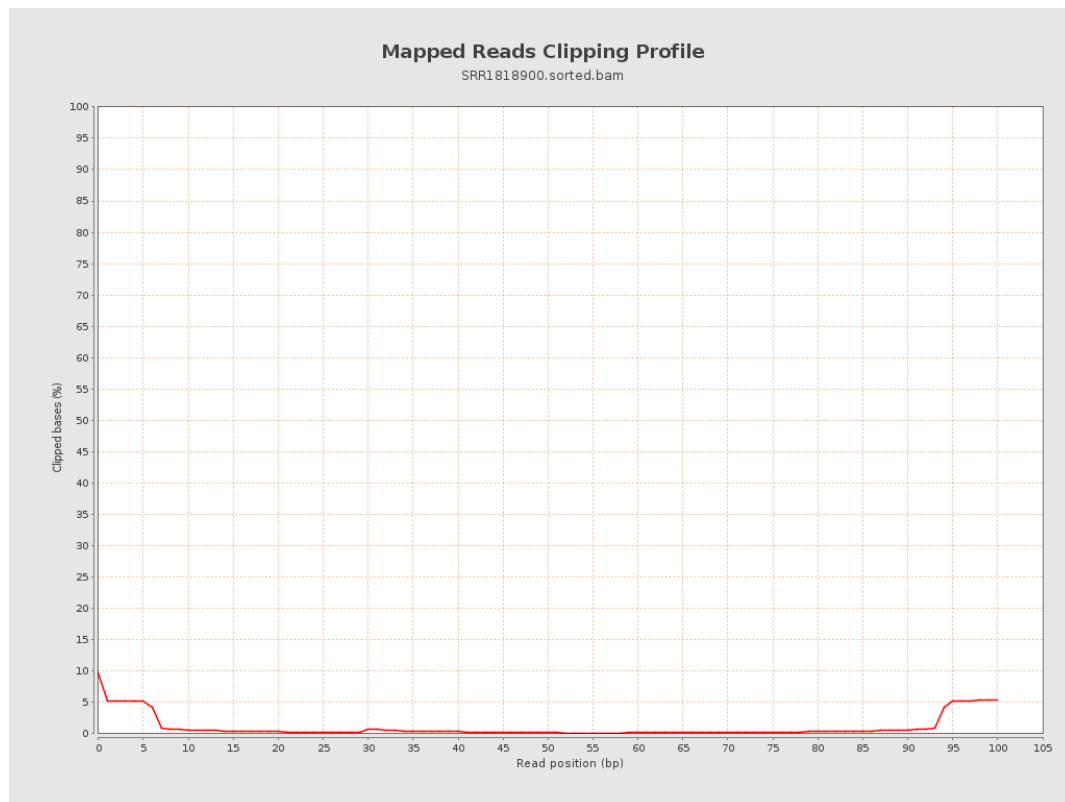
## 8. Results : Mapped Reads Nucleotide Content



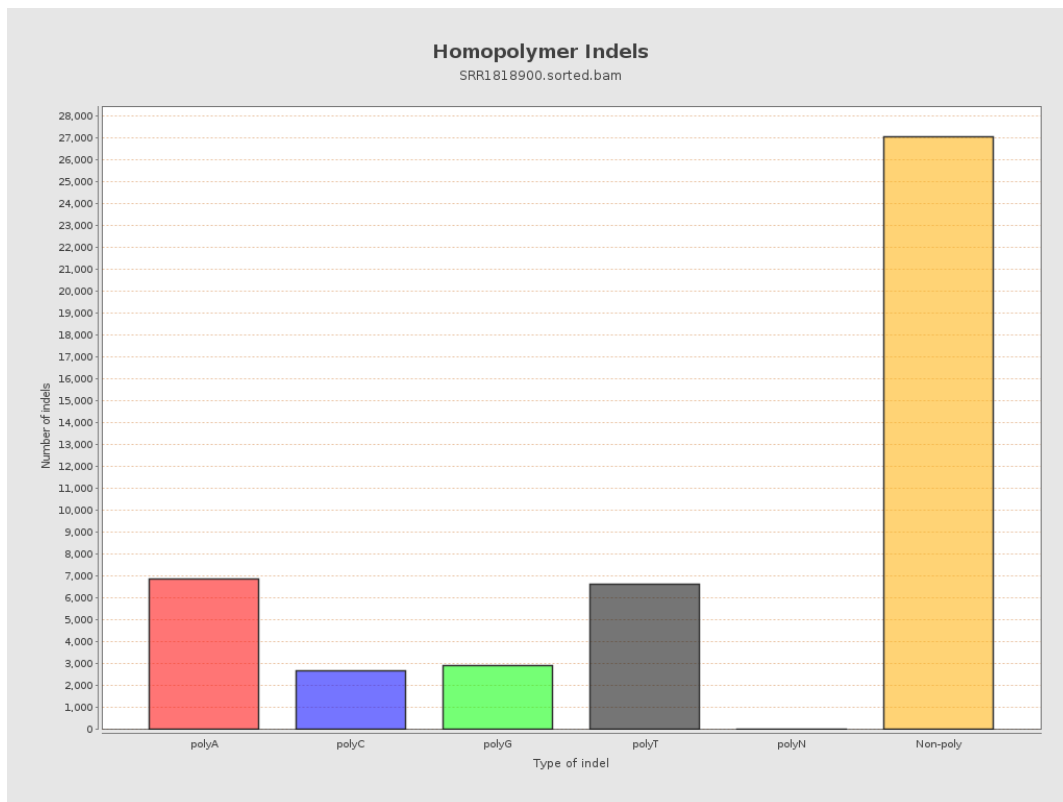
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

