

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 09:09:27*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818933.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_SRR1818933 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818933.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Fri Aug 23 09:09:27 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR1818933.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 3,410,976          |
| Mapped reads                 | 3,261,067 / 95.61% |
| Unmapped reads               | 149,909 / 4.39%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 40,074 / 1.17%     |
| Read min/max/mean length     | 30 / 101 / 101.45  |
| Duplicated reads (estimated) | 1,757,701 / 51.53% |
| Duplication rate             | 43.53%             |
| Clipped reads                | 3,269,157 / 95.84% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 88,093,622 / 29.14% |
| Number/percentage of C's | 63,347,249 / 20.95% |
| Number/percentage of T's | 86,869,271 / 28.73% |
| Number/percentage of G's | 64,036,720 / 21.18% |
| Number/percentage of N's | 13,624 / 0%         |
| GC Percentage            | 42.13%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0977 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 1.0065 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 49.38 |
|----------------------|-------|

## 2.5. Mismatches and indels

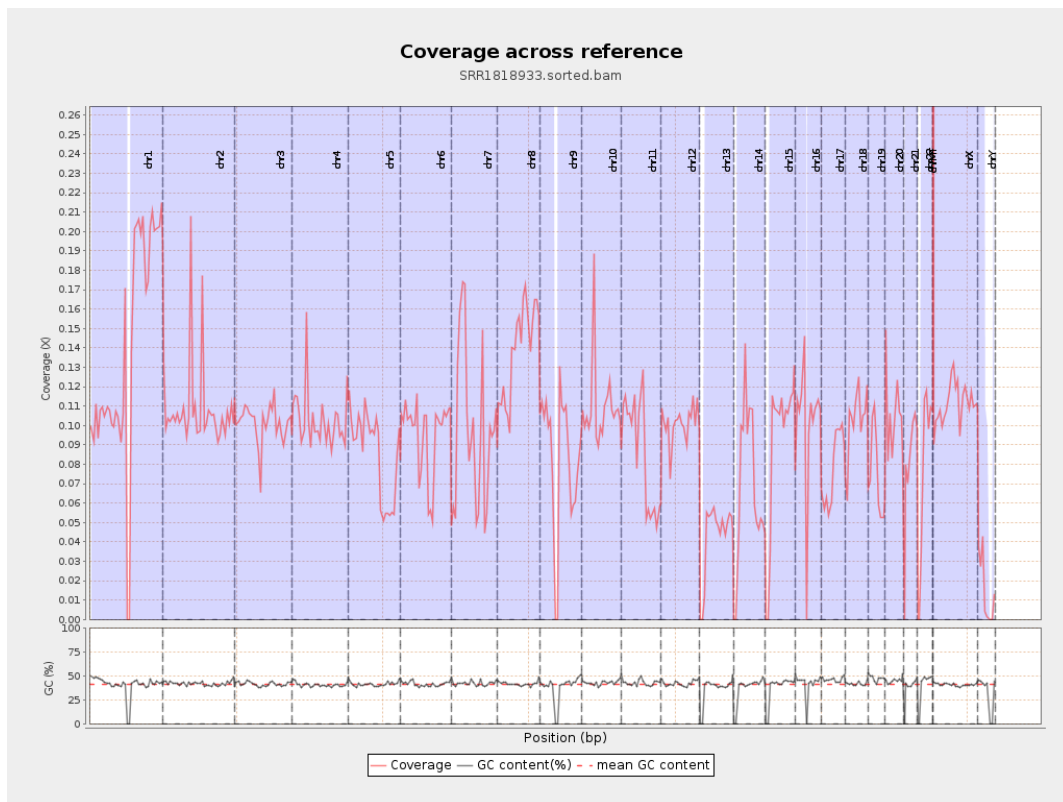
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.66%     |
| Mismatches                               | 1,918,166 |
| Insertions                               | 41,712    |
| Mapped reads with at least one insertion | 1.25%     |
| Deletions                                | 88,223    |
| Mapped reads with at least one deletion  | 2.65%     |
| Homopolymer indels                       | 41.17%    |

## 2.6. Chromosome stats

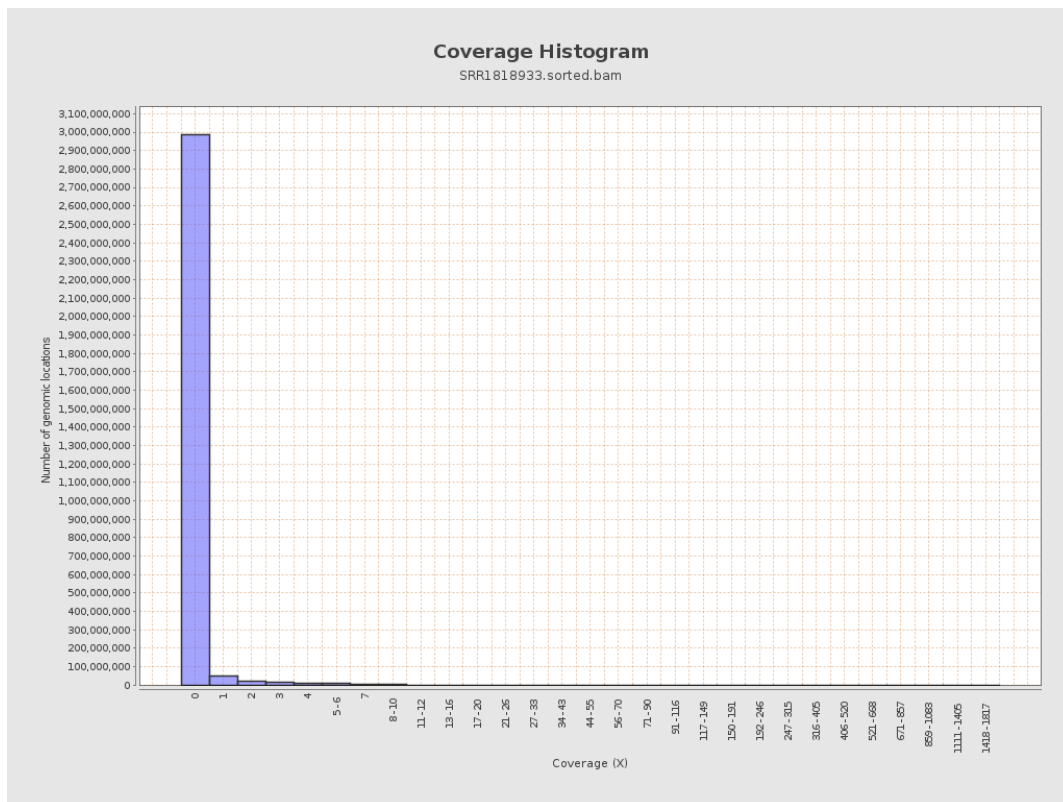
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 34732005     | 0.1393        | 1.6977             |
| chr2 | 243199373 | 26419328     | 0.1086        | 1.3723             |
| chr3 | 198022430 | 20039974     | 0.1012        | 0.709              |
| chr4 | 191154276 | 19738166     | 0.1033        | 0.7708             |
| chr5 | 180915260 | 15534426     | 0.0859        | 0.6698             |
| chr6 | 171115067 | 16303843     | 0.0953        | 0.7272             |
| chr7 | 159138663 | 15468602     | 0.0972        | 0.8625             |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr8  | 146364022 | 20410910 | 0.1395 | 0.9539 |
| chr9  | 141213431 | 11679812 | 0.0827 | 1.1498 |
| chr10 | 135534747 | 14772155 | 0.109  | 1.2207 |
| chr11 | 135006516 | 11616867 | 0.086  | 0.7461 |
| chr12 | 133851895 | 13576199 | 0.1014 | 0.7226 |
| chr13 | 115169878 | 4952547  | 0.043  | 0.4512 |
| chr14 | 107349540 | 7438051  | 0.0693 | 0.6608 |
| chr15 | 102531392 | 9141755  | 0.0892 | 0.6766 |
| chr16 | 90354753  | 9084208  | 0.1005 | 1.0647 |
| chr17 | 81195210  | 6365638  | 0.0784 | 0.6849 |
| chr18 | 78077248  | 7956648  | 0.1019 | 1.4096 |
| chr19 | 59128983  | 4510010  | 0.0763 | 1.5277 |
| chr20 | 63025520  | 6576623  | 0.1043 | 0.7719 |
| chr21 | 48129895  | 3957698  | 0.0822 | 0.693  |
| chr22 | 51304566  | 3908823  | 0.0762 | 0.6819 |
| chrMT | 16571     | 121940   | 7.3586 | 7.0614 |
| chrX  | 155270560 | 17331961 | 0.1116 | 0.8698 |
| chrY  | 59373566  | 884103   | 0.0149 | 0.7509 |

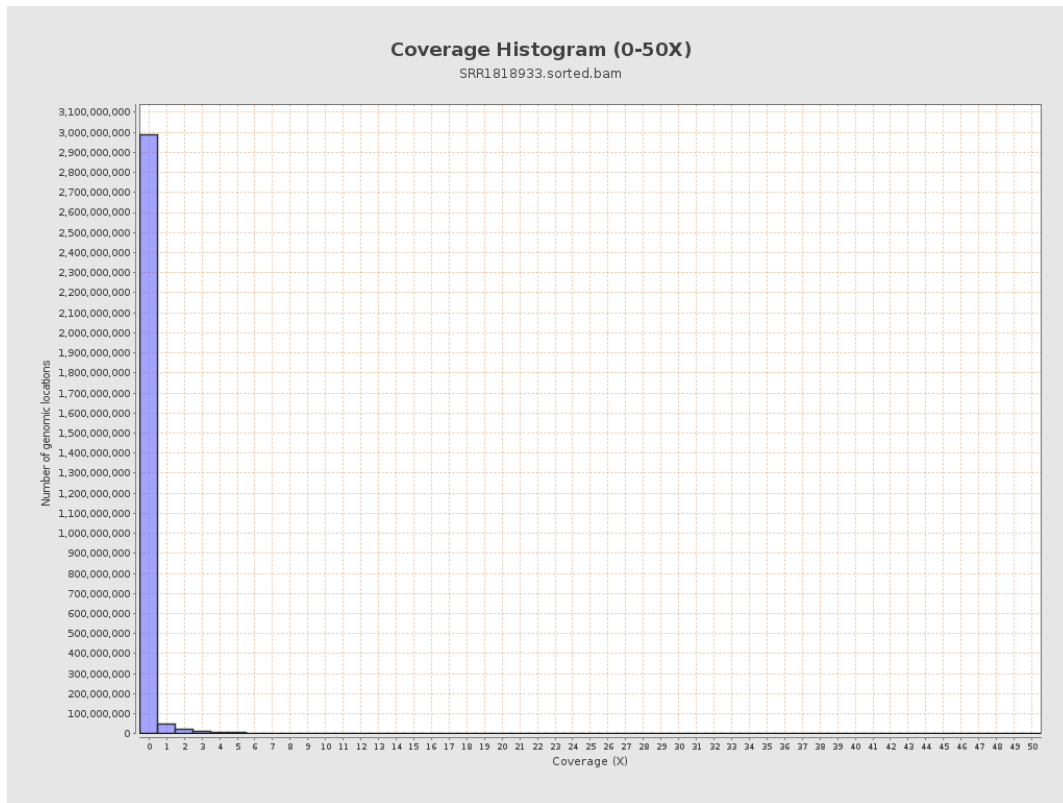
### 3. Results : Coverage across reference



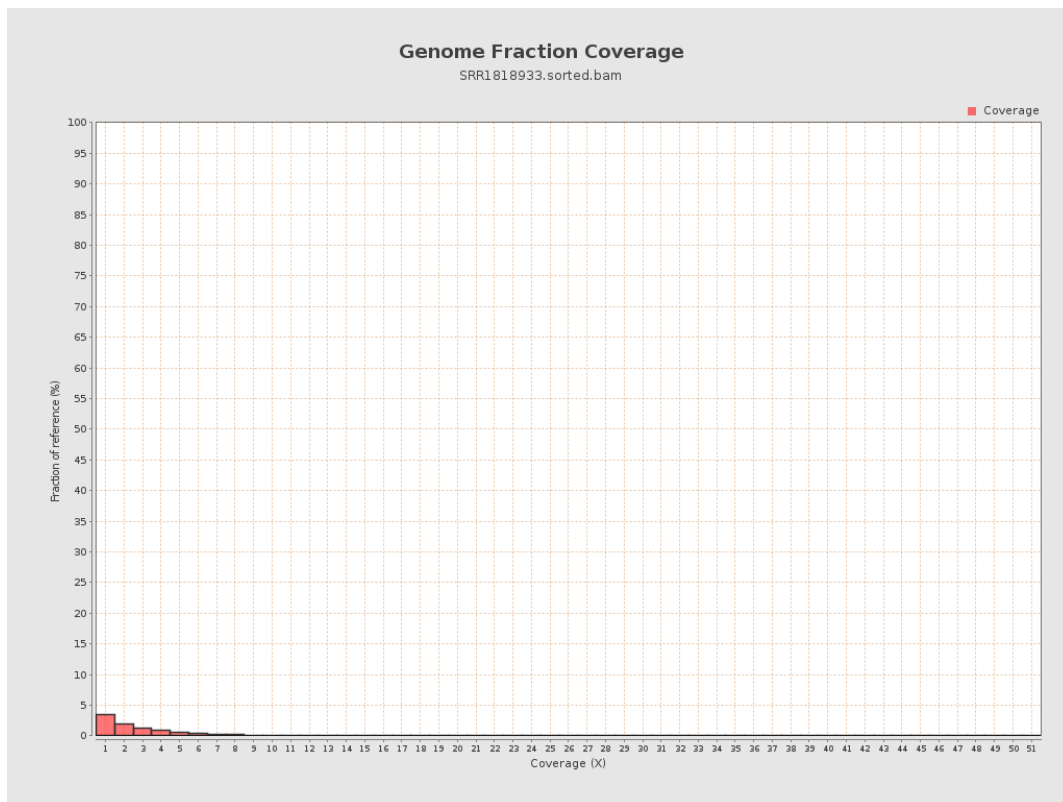
## 4. Results : Coverage Histogram



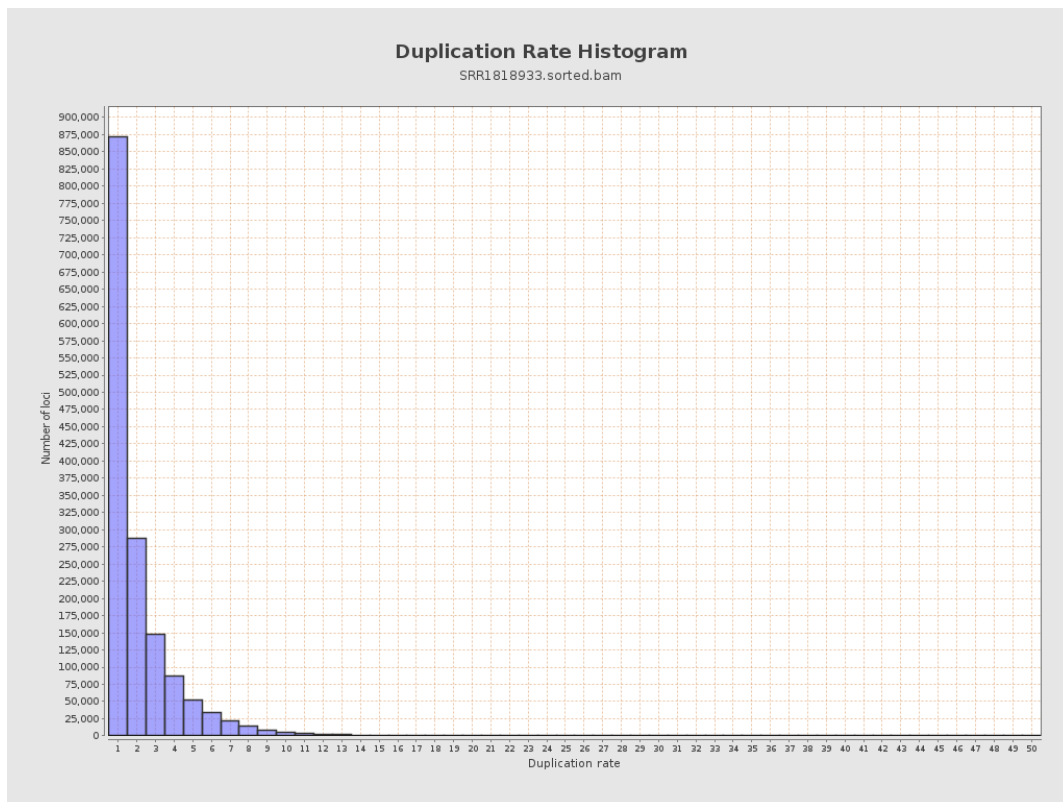
## 5. Results : Coverage Histogram (0-50X)



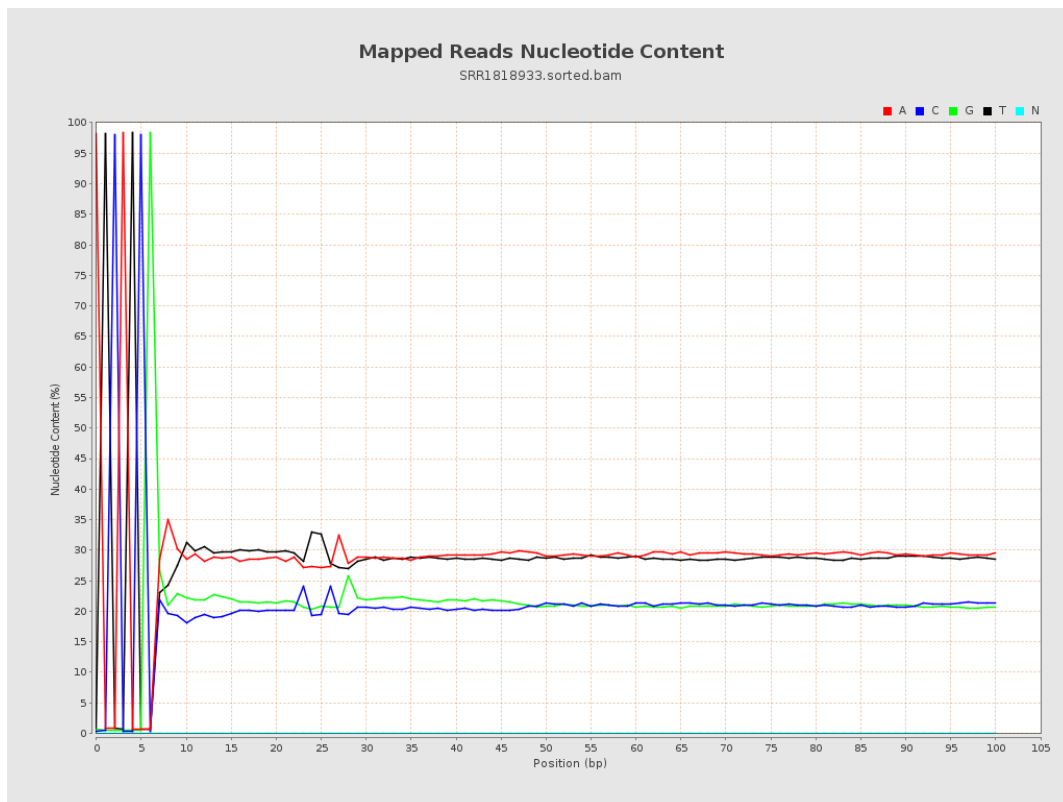
## 6. Results : Genome Fraction Coverage



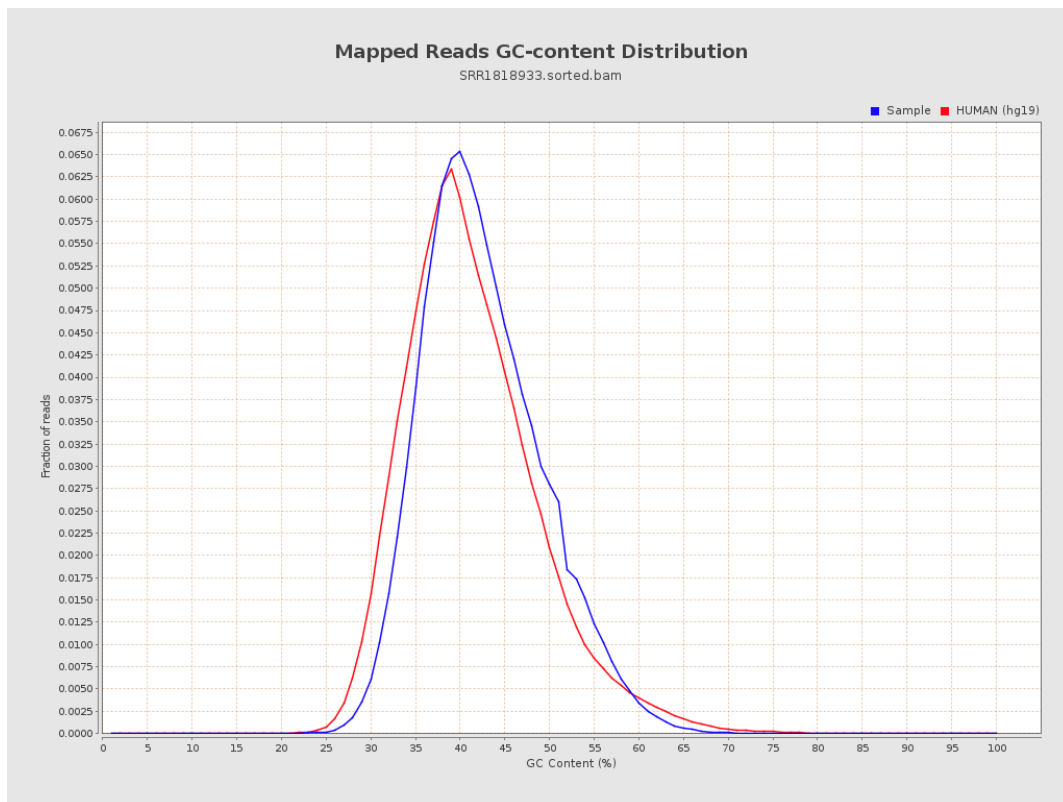
## 7. Results : Duplication Rate Histogram



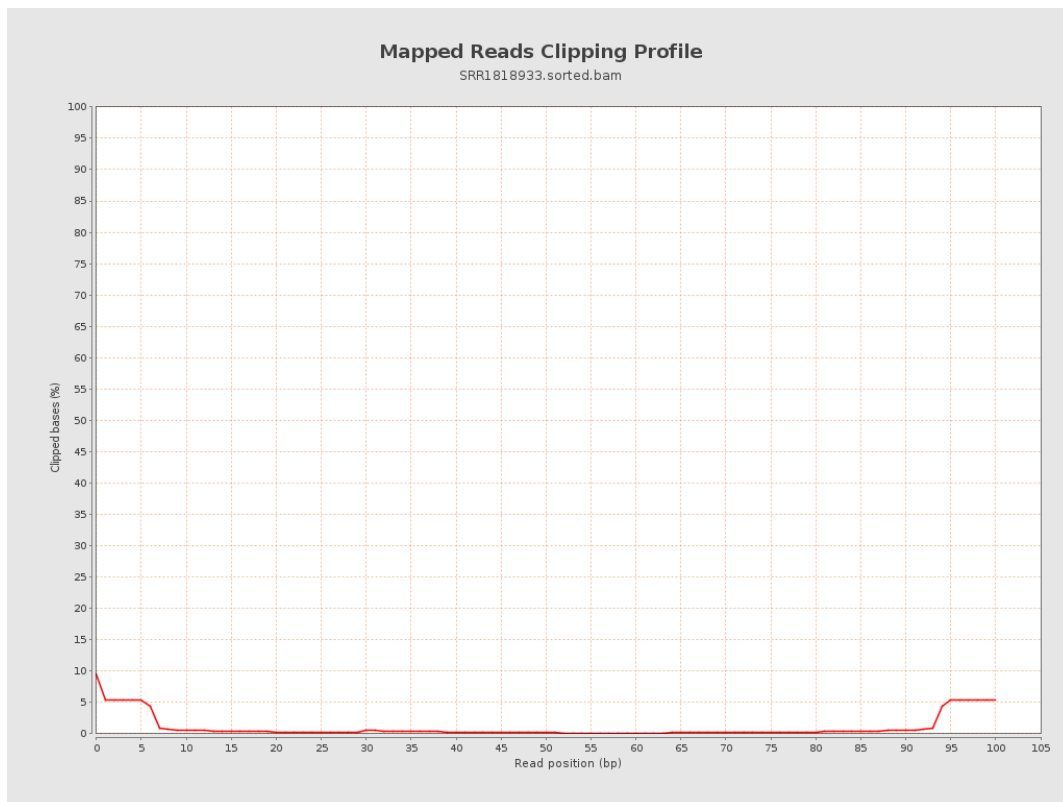
## 8. Results : Mapped Reads Nucleotide Content



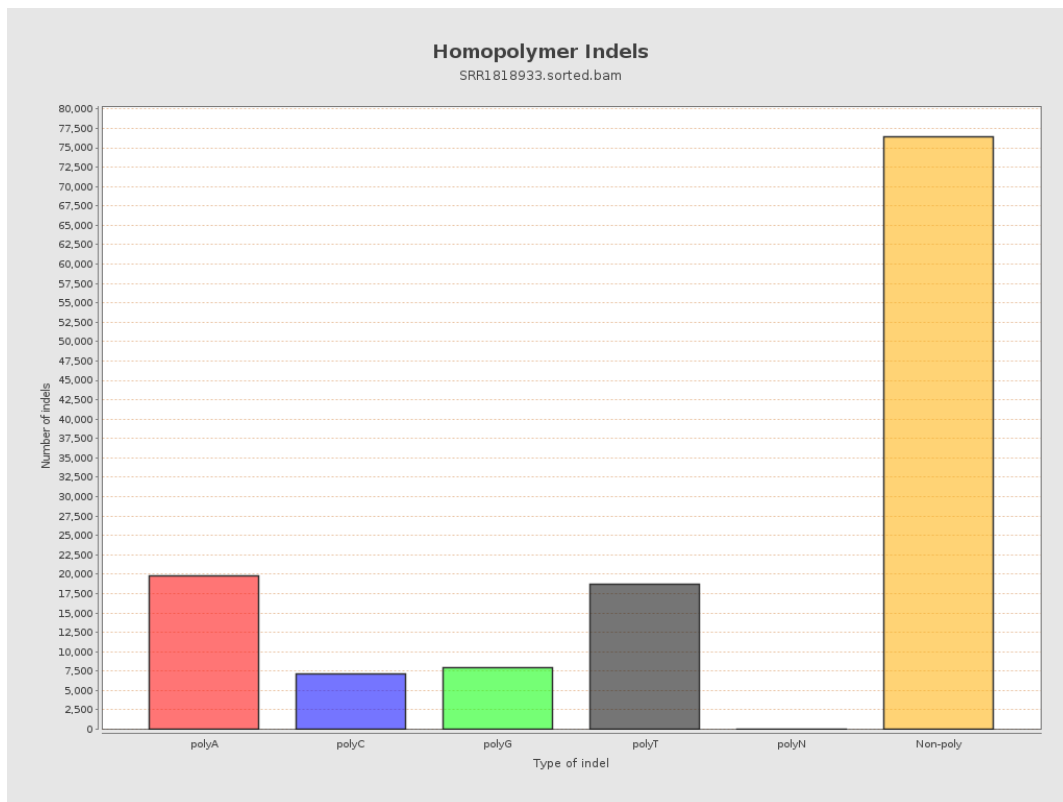
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

