

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/18 00:08:23*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163027.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_SRR1163027 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163027.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Wed Dec 18 00:08:21 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR1163027.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 3,095,693,983       |
| Number of reads              | 69,337,662          |
| Mapped reads                 | 68,113,656 / 98.23% |
| Unmapped reads               | 1,224,006 / 1.77%   |
| Mapped paired reads          | 0 / 0%              |
| Secondary alignments         | 0                   |
| Supplementary alignments     | 369,692 / 0.53%     |
| Read min/max/mean length     | 30 / 100 / 100.22   |
| Duplicated reads (estimated) | 35,586,342 / 51.32% |
| Duplication rate             | 43.52%              |
| Clipped reads                | 9,893,496 / 14.27%  |

### 2.2. ACGT Content

|                          |                        |
|--------------------------|------------------------|
| Number/percentage of A's | 1,585,052,096 / 23.91% |
| Number/percentage of C's | 1,729,990,218 / 26.1%  |
| Number/percentage of T's | 1,585,530,508 / 23.92% |
| Number/percentage of G's | 1,726,117,585 / 26.04% |
| Number/percentage of N's | 1,532,451 / 0.02%      |
| GC Percentage            | 52.14%                 |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 2.1414 |
|      |        |

|                    |         |
|--------------------|---------|
| Standard Deviation | 25.4625 |
|--------------------|---------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 49.04 |
|----------------------|-------|

## 2.5. Mismatches and indels

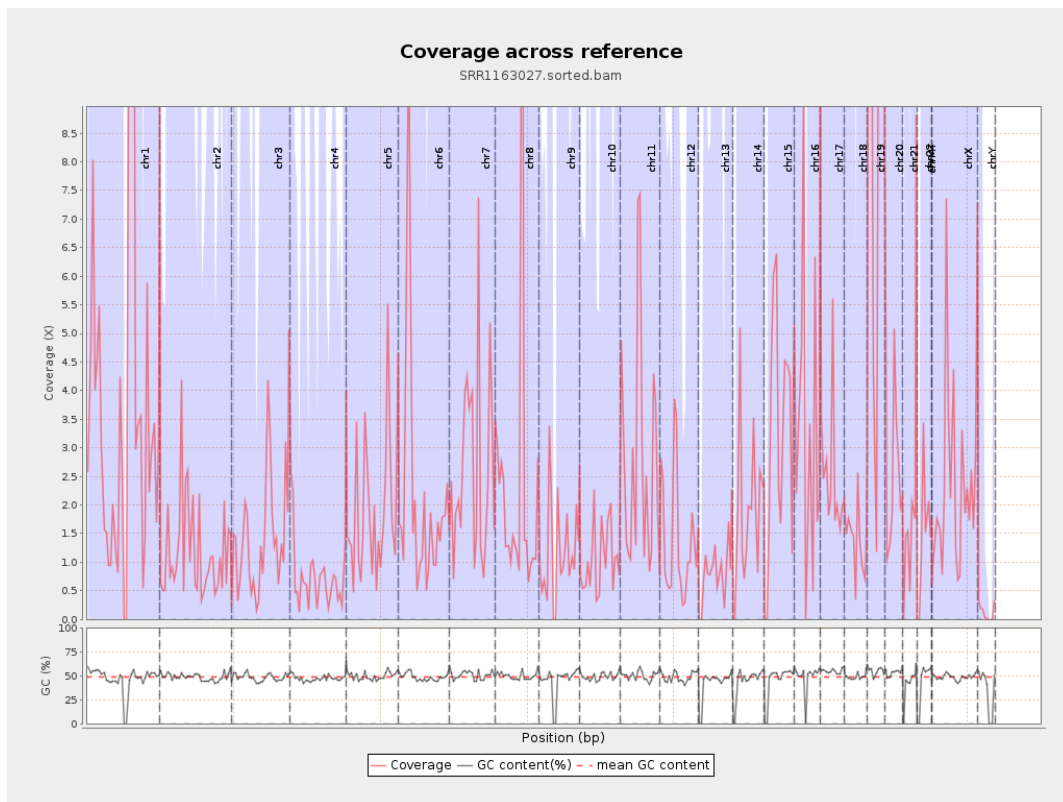
|                                          |            |
|------------------------------------------|------------|
| General error rate                       | 0.45%      |
| Mismatches                               | 29,052,222 |
| Insertions                               | 437,514    |
| Mapped reads with at least one insertion | 0.63%      |
| Deletions                                | 375,102    |
| Mapped reads with at least one deletion  | 0.54%      |
| Homopolymer indels                       | 46.31%     |

## 2.6. Chromosome stats

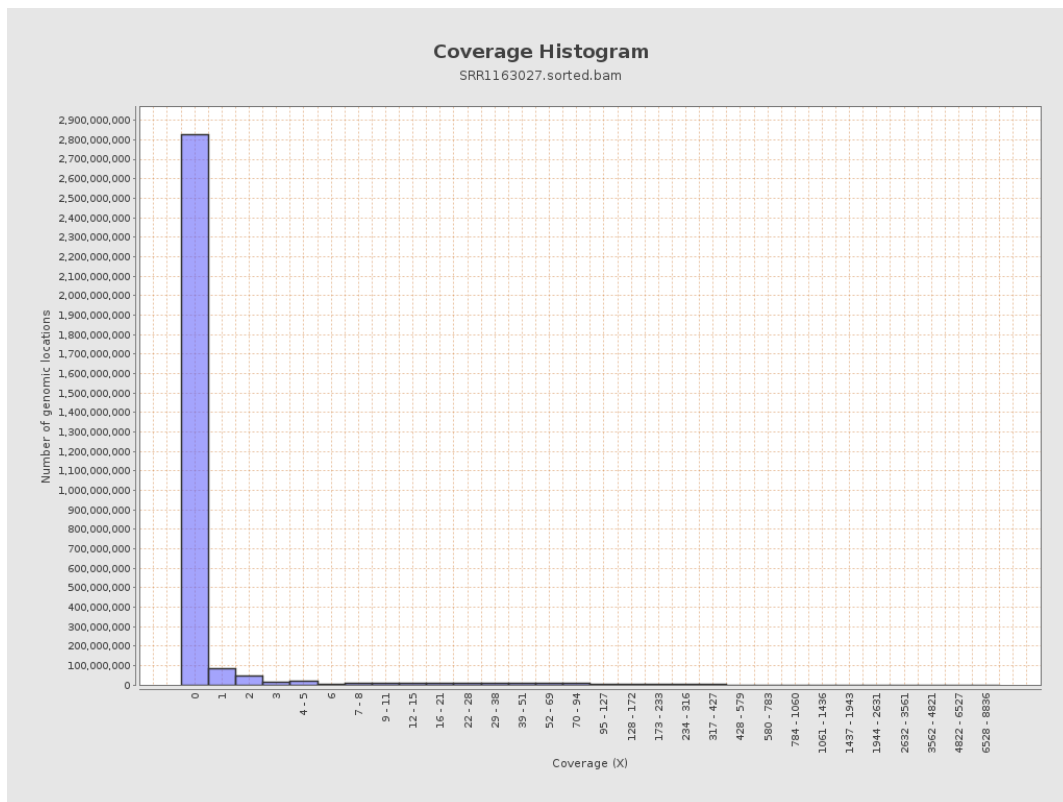
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 994636870    | 3.9905        | 37.1827            |
| chr2 | 243199373 | 286428575    | 1.1778        | 13.7206            |
| chr3 | 198022430 | 281852392    | 1.4233        | 14.8937            |
| chr4 | 191154276 | 138836863    | 0.7263        | 10.982             |
| chr5 | 180915260 | 354833089    | 1.9613        | 25.5963            |
| chr6 | 171115067 | 365766532    | 2.1375        | 23.4975            |
| chr7 | 159138663 | 419946558    | 2.6389        | 26.7371            |
|      |           |              |               |                    |

|       |           |           |         |         |
|-------|-----------|-----------|---------|---------|
| chr8  | 146364022 | 329565321 | 2.2517  | 44.1704 |
| chr9  | 141213431 | 166696627 | 1.1805  | 13.6212 |
| chr10 | 135534747 | 143962716 | 1.0622  | 10.4406 |
| chr11 | 135006516 | 385040699 | 2.852   | 24.1734 |
| chr12 | 133851895 | 185519813 | 1.386   | 14.6021 |
| chr13 | 115169878 | 95019377  | 0.825   | 10.9914 |
| chr14 | 107349540 | 197882102 | 1.8433  | 17.6527 |
| chr15 | 102531392 | 323438699 | 3.1545  | 27.546  |
| chr16 | 90354753  | 301182529 | 3.3333  | 26.6263 |
| chr17 | 81195210  | 206024878 | 2.5374  | 20.0492 |
| chr18 | 78077248  | 106783051 | 1.3677  | 15.3551 |
| chr19 | 59128983  | 626273248 | 10.5916 | 71.1146 |
| chr20 | 63025520  | 169810721 | 2.6943  | 23.582  |
| chr21 | 48129895  | 99806860  | 2.0737  | 45.7636 |
| chr22 | 51304566  | 77924431  | 1.5189  | 14.3834 |
| chrMT | 16571     | 9620      | 0.5805  | 1.0672  |
| chrX  | 155270560 | 364393054 | 2.3468  | 24.4762 |
| chrY  | 59373566  | 7415503   | 0.1249  | 7.2496  |

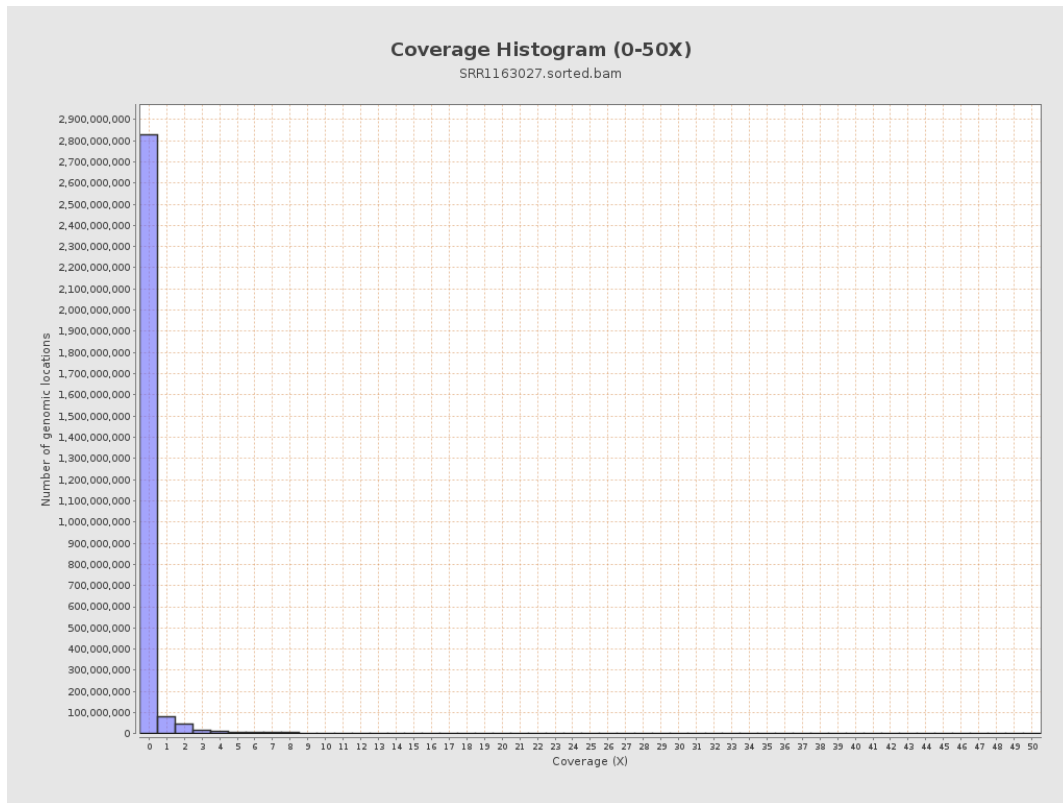
### 3. Results : Coverage across reference



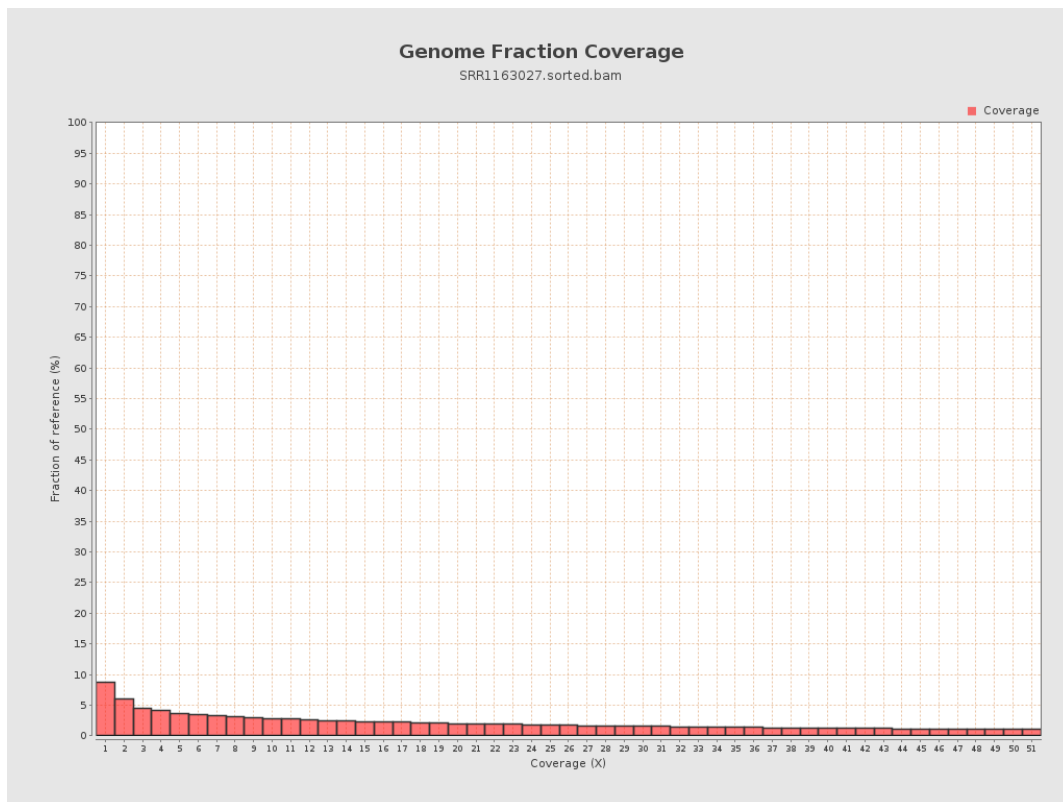
## 4. Results : Coverage Histogram



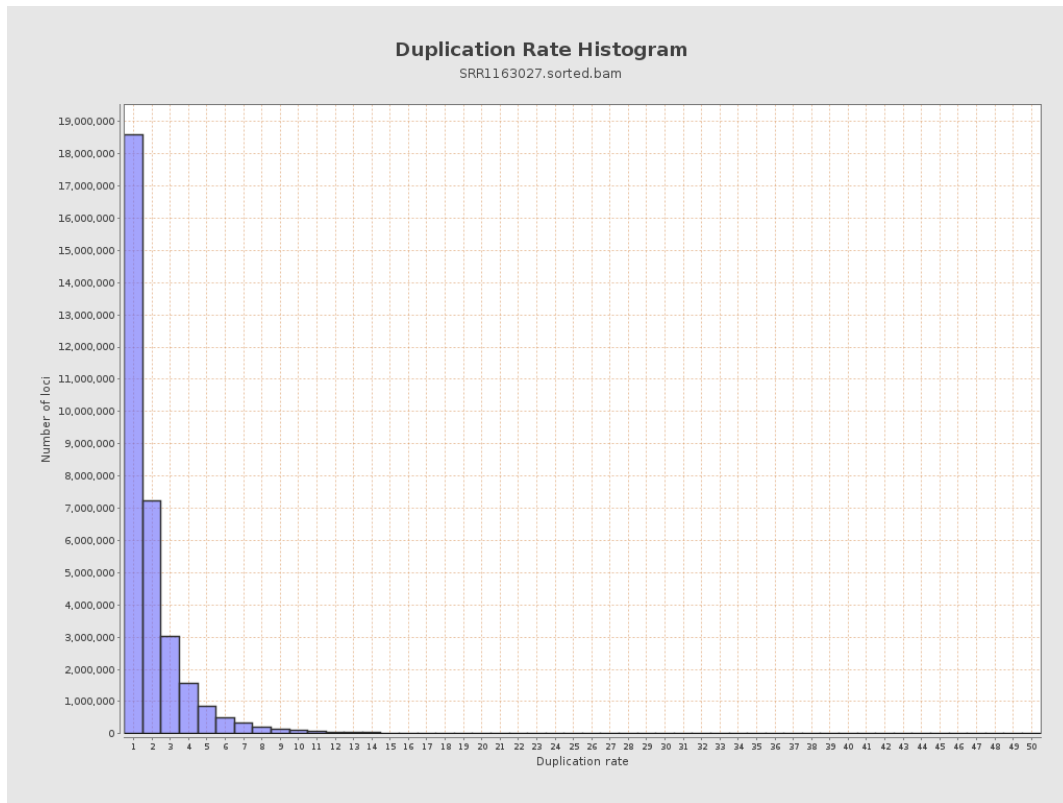
## 5. Results : Coverage Histogram (0-50X)



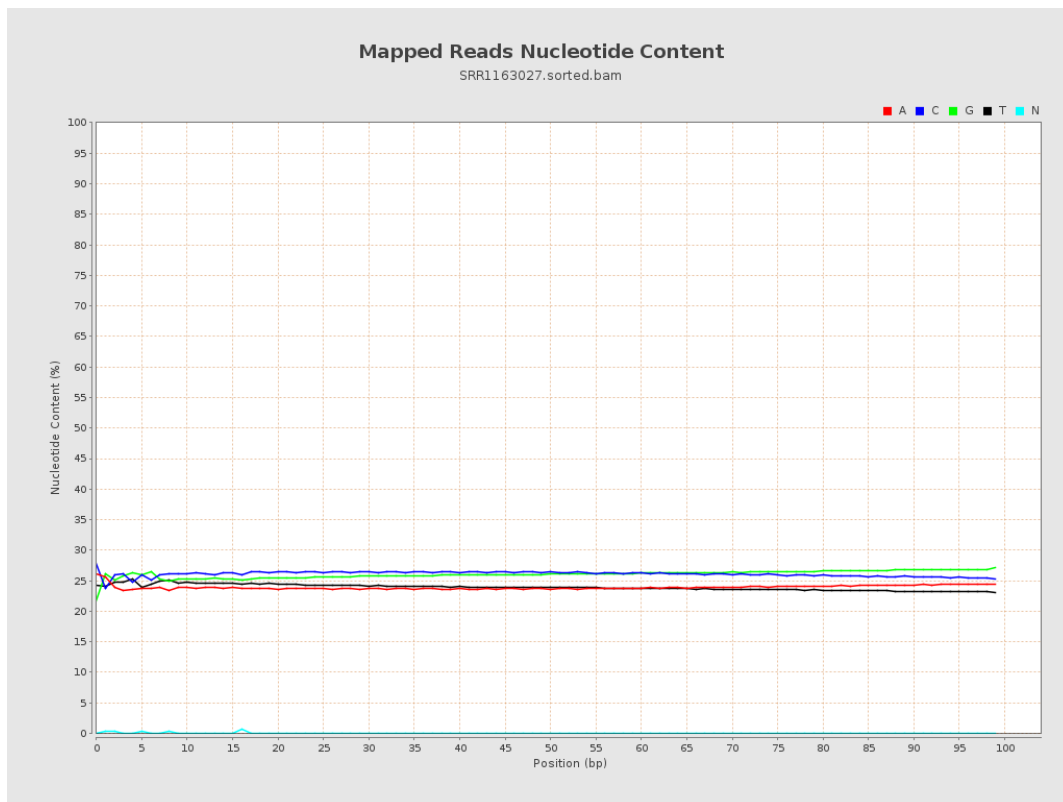
## 6. Results : Genome Fraction Coverage



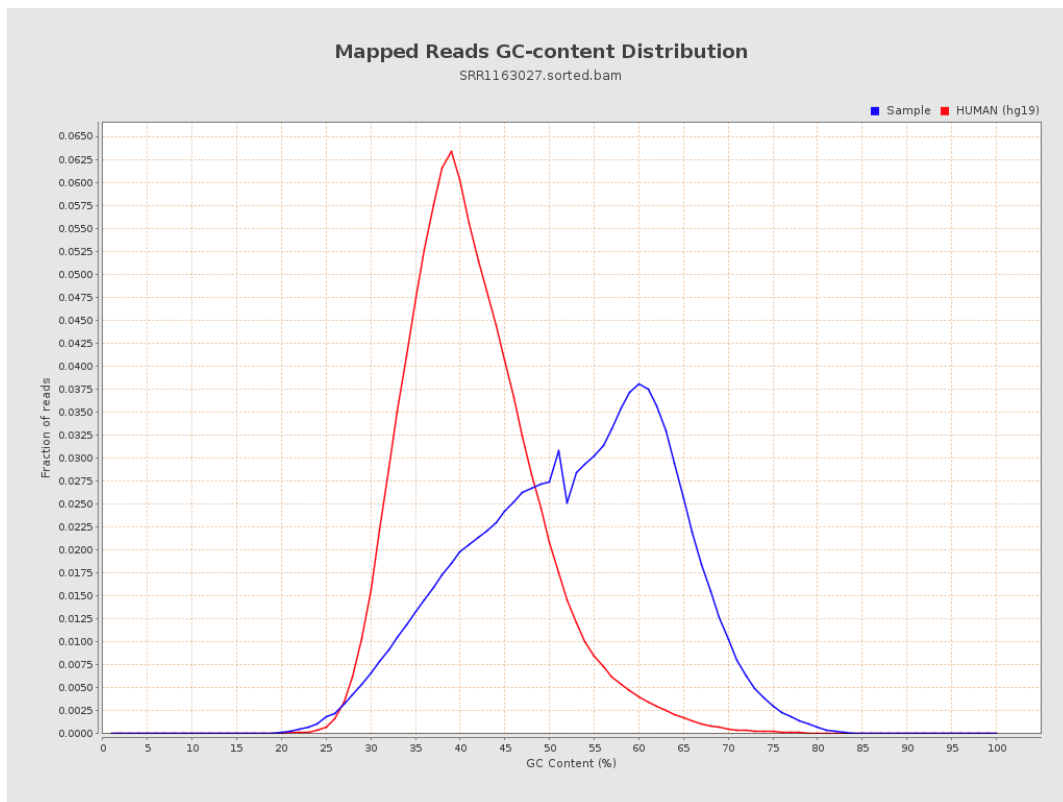
## 7. Results : Duplication Rate Histogram



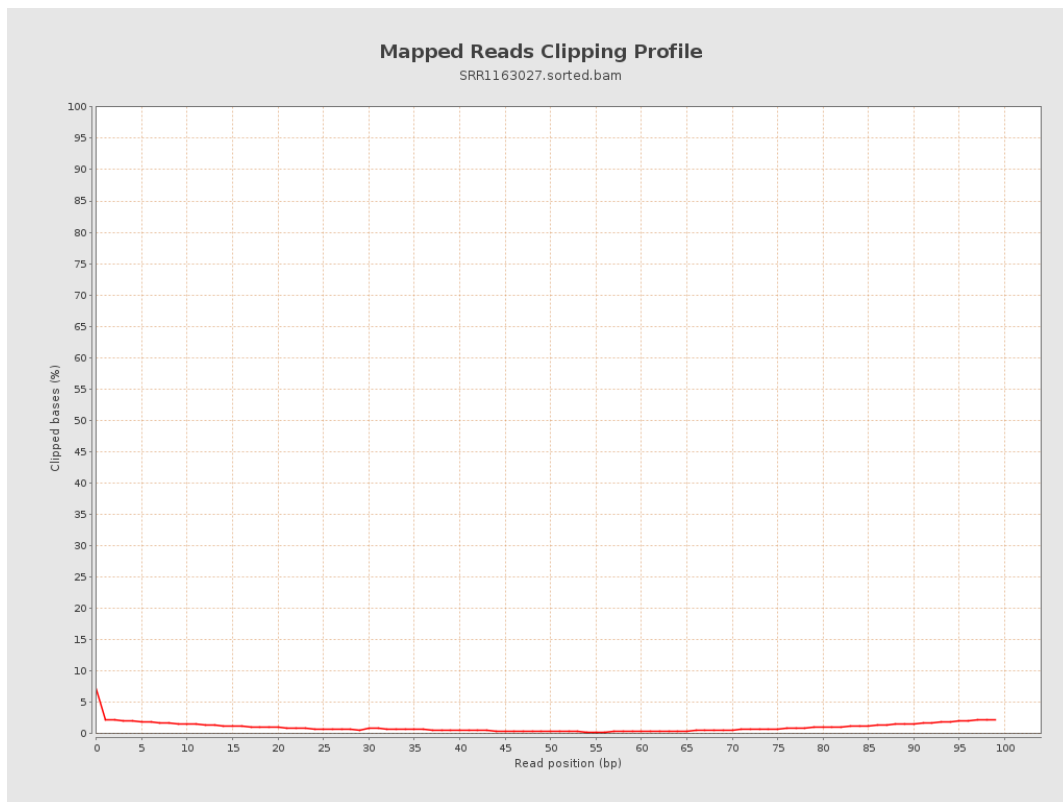
## 8. Results : Mapped Reads Nucleotide Content



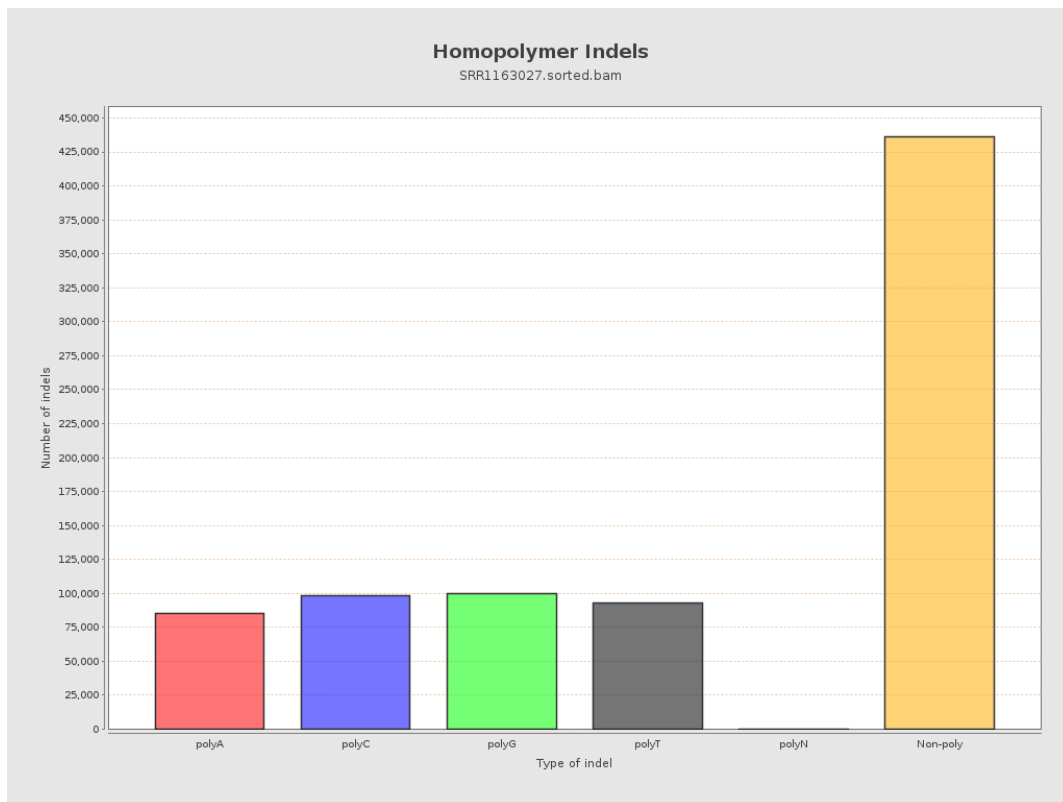
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

