

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 10:25:38*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080904.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_SRR3080904 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080904.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Fri Aug 23 10:25:37 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR3080904.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 4,775,560          |
| Mapped reads                 | 4,306,643 / 90.18% |
| Unmapped reads               | 468,917 / 9.82%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 58,740 / 1.23%     |
| Read min/max/mean length     | 30 / 76 / 76.43    |
| Duplicated reads (estimated) | 274,029 / 5.74%    |
| Duplication rate             | 5.18%              |
| Clipped reads                | 1,459,219 / 30.56% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 86,953,543 / 29.15% |
| Number/percentage of C's | 53,255,416 / 17.85% |
| Number/percentage of T's | 94,878,487 / 31.8%  |
| Number/percentage of G's | 61,774,387 / 20.71% |
| Number/percentage of N's | 1,482,111 / 0.5%    |
| GC Percentage            | 38.56%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0964 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.5883 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 48.01 |
|----------------------|-------|

## 2.5. Mismatches and indels

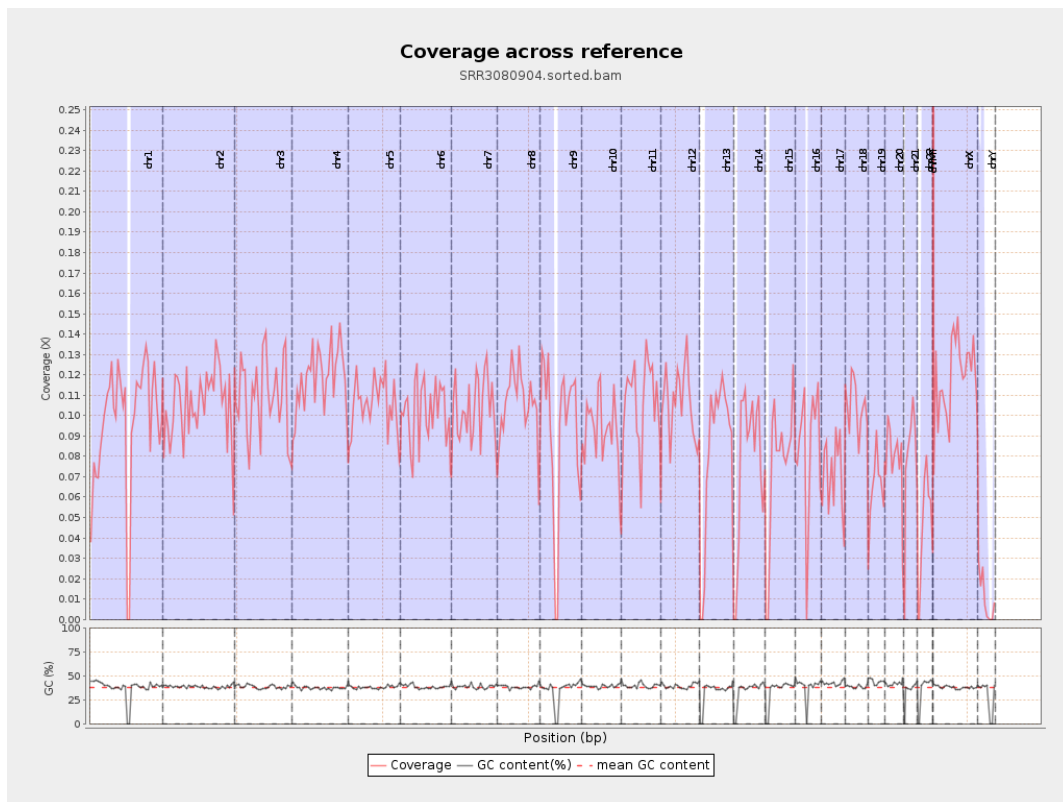
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 1.12%     |
| Mismatches                               | 3,316,114 |
| Insertions                               | 21,877    |
| Mapped reads with at least one insertion | 0.5%      |
| Deletions                                | 65,604    |
| Mapped reads with at least one deletion  | 1.51%     |
| Homopolymer indels                       | 49.98%    |

## 2.6. Chromosome stats

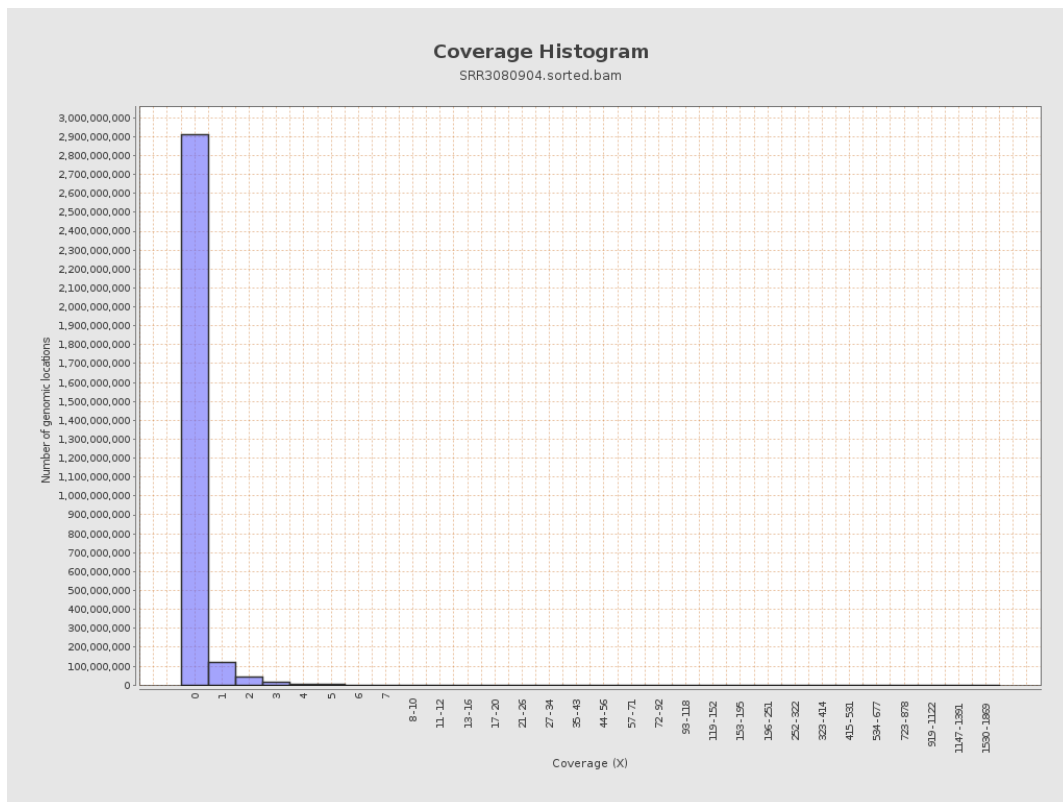
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 24036245     | 0.0964        | 0.7349             |
| chr2 | 243199373 | 25746293     | 0.1059        | 0.568              |
| chr3 | 198022430 | 21688598     | 0.1095        | 0.4921             |
| chr4 | 191154276 | 22675220     | 0.1186        | 0.5193             |
| chr5 | 180915260 | 18969468     | 0.1049        | 0.4842             |
| chr6 | 171115067 | 17437933     | 0.1019        | 0.5255             |
| chr7 | 159138663 | 16378886     | 0.1029        | 0.6593             |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr8  | 146364022 | 15561826 | 0.1063 | 1.1978 |
| chr9  | 141213431 | 13177819 | 0.0933 | 0.5432 |
| chr10 | 135534747 | 12705884 | 0.0937 | 0.507  |
| chr11 | 135006516 | 14347308 | 0.1063 | 0.5921 |
| chr12 | 133851895 | 14238250 | 0.1064 | 0.4869 |
| chr13 | 115169878 | 9498710  | 0.0825 | 0.4274 |
| chr14 | 107349540 | 8377146  | 0.078  | 0.4281 |
| chr15 | 102531392 | 7750255  | 0.0756 | 0.4074 |
| chr16 | 90354753  | 7449772  | 0.0825 | 0.4382 |
| chr17 | 81195210  | 5815564  | 0.0716 | 0.4262 |
| chr18 | 78077248  | 8214602  | 0.1052 | 0.8258 |
| chr19 | 59128983  | 3927130  | 0.0664 | 0.546  |
| chr20 | 63025520  | 5081224  | 0.0806 | 0.4267 |
| chr21 | 48129895  | 3833008  | 0.0796 | 0.4411 |
| chr22 | 51304566  | 2399700  | 0.0468 | 0.3128 |
| chrMT | 16571     | 24745    | 1.4933 | 1.8056 |
| chrX  | 155270560 | 18508645 | 0.1192 | 0.5375 |
| chrY  | 59373566  | 607423   | 0.0102 | 0.1754 |

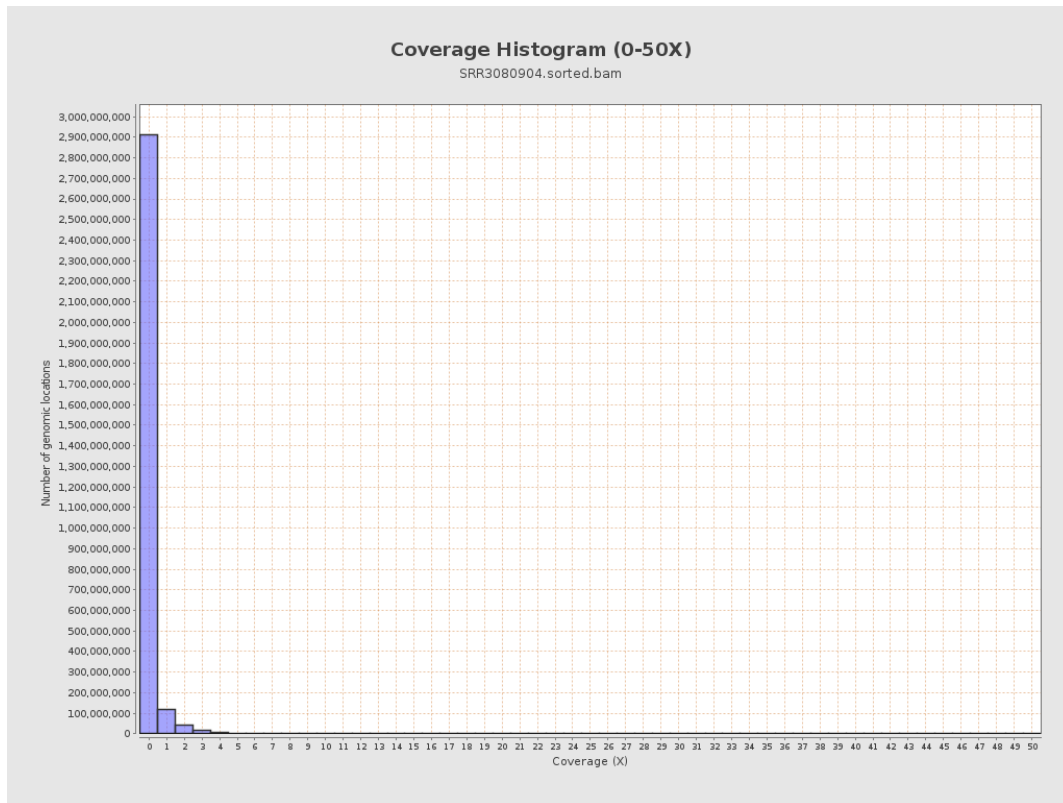
### 3. Results : Coverage across reference



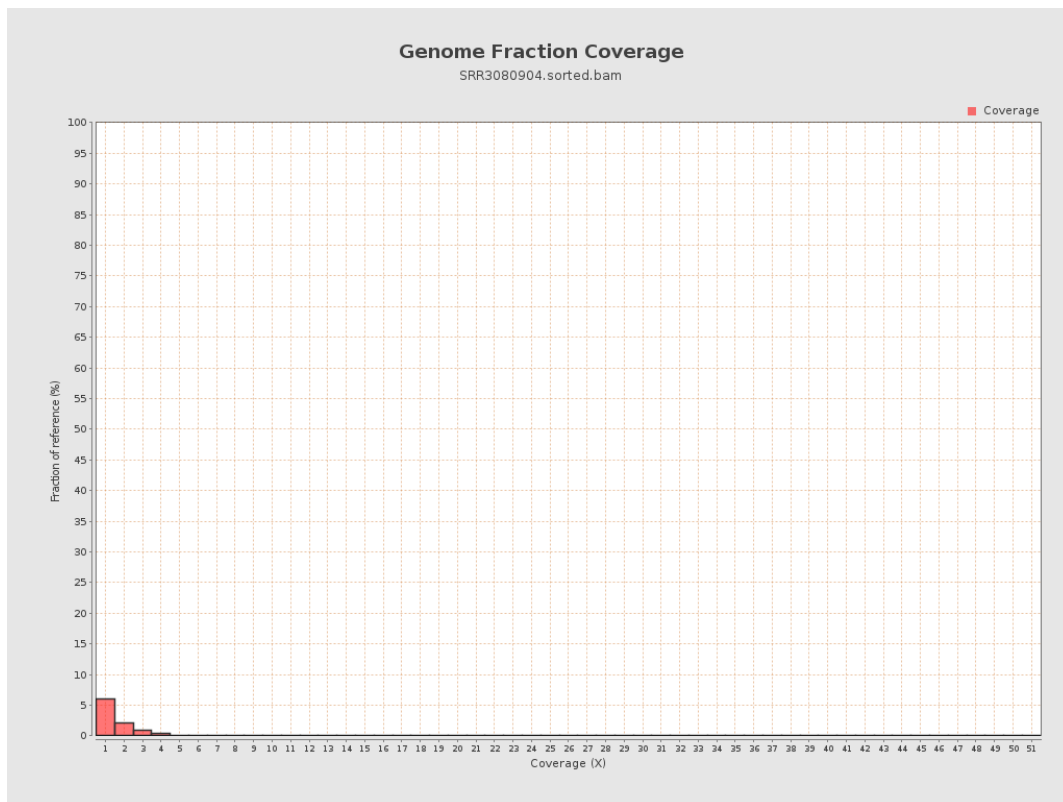
## 4. Results : Coverage Histogram



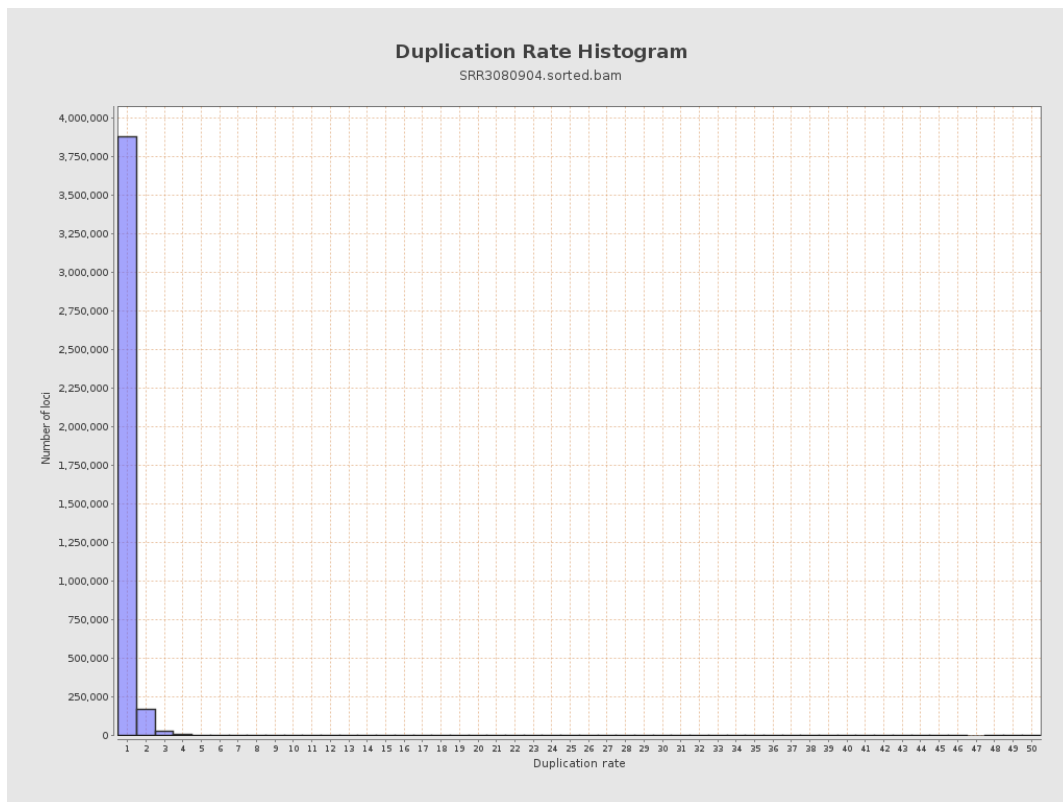
## 5. Results : Coverage Histogram (0-50X)



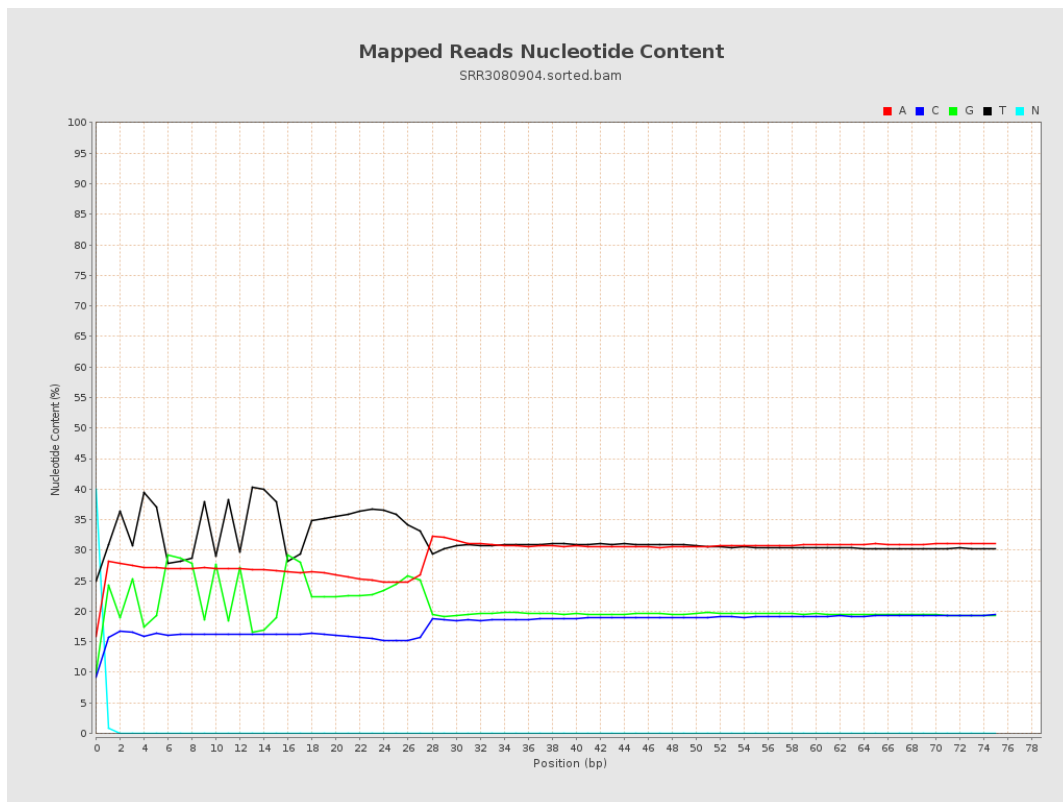
## 6. Results : Genome Fraction Coverage



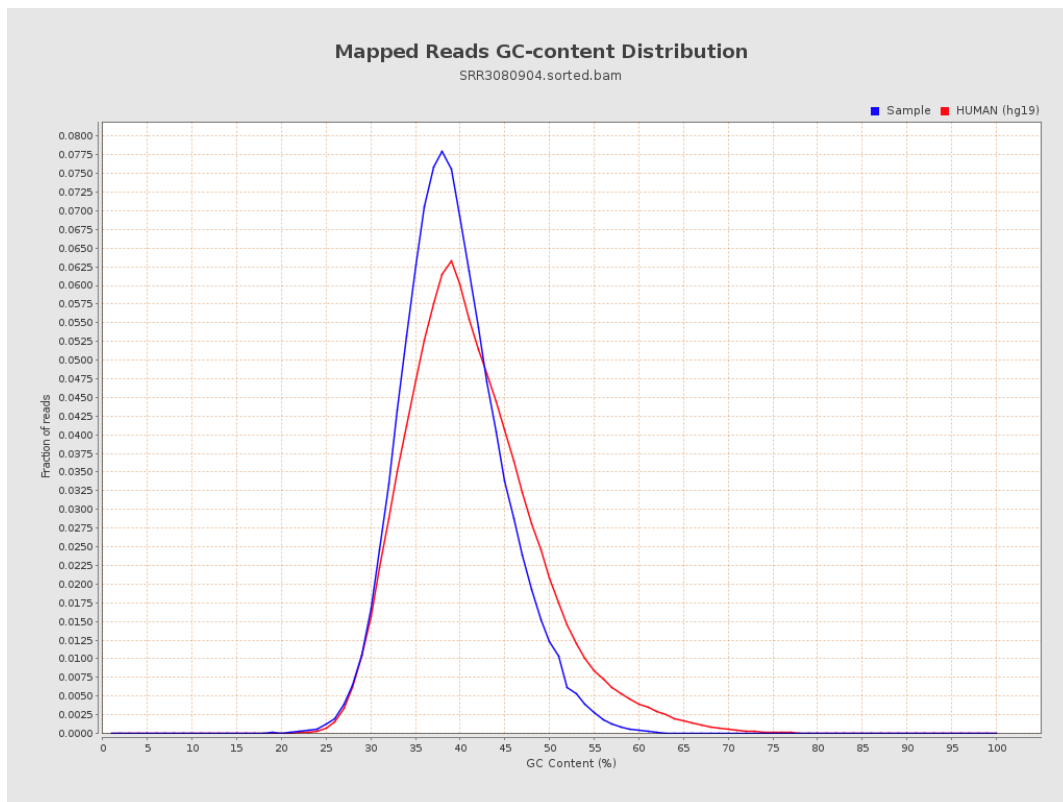
## 7. Results : Duplication Rate Histogram



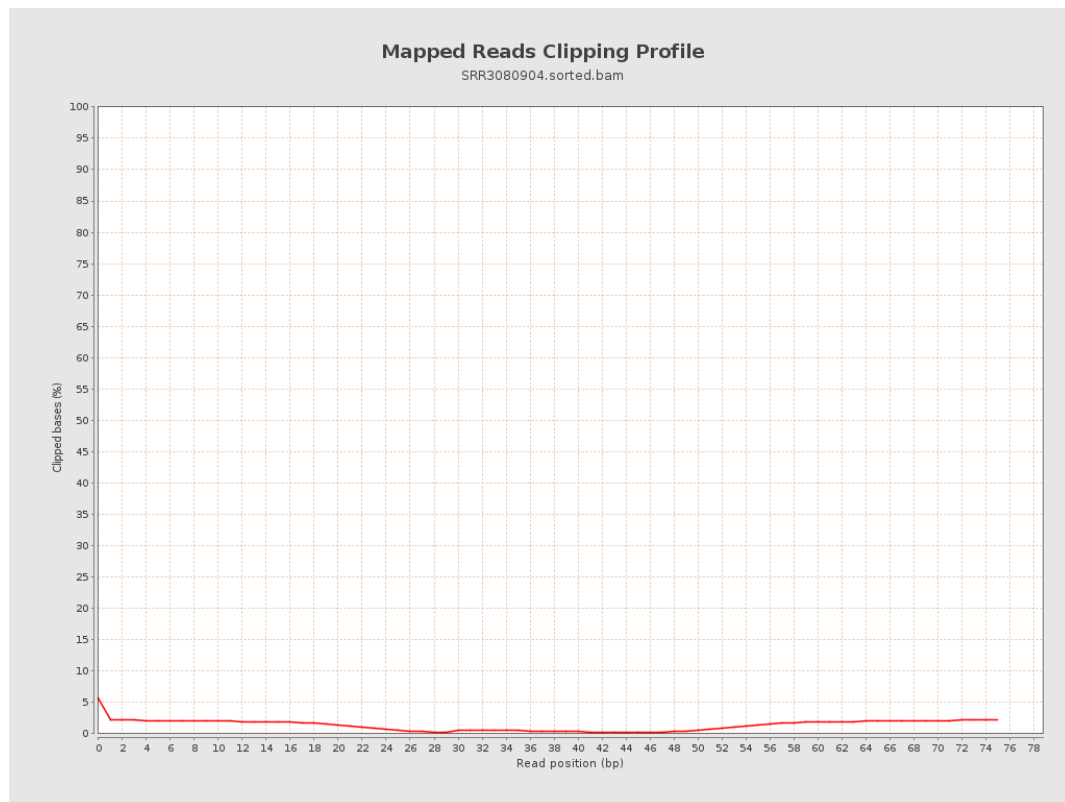
## 8. Results : Mapped Reads Nucleotide Content



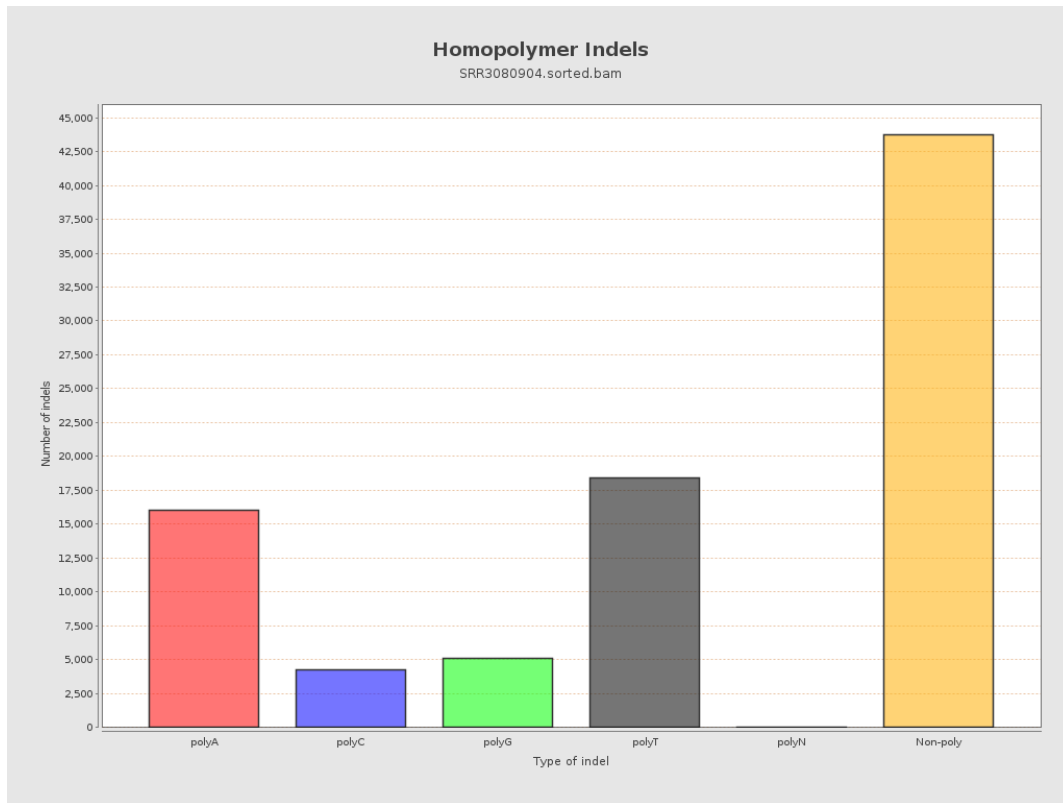
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

