

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 15:49:50*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971297.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_SRR2971297 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971297.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Sat Aug 24 15:49:48 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR2971297.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 10,025,682         |
| Mapped reads                 | 8,671,365 / 86.49% |
| Unmapped reads               | 1,354,317 / 13.51% |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Read min/max/mean length     | 40 / 40 / 40       |
| Duplicated reads (estimated) | 622,905 / 6.21%    |
| Duplication rate             | 5.15%              |
| Clipped reads                | 869,931 / 8.68%    |

### 2.2. ACGT Content

|                          |                      |
|--------------------------|----------------------|
| Number/percentage of A's | 98,033,488 / 28.69%  |
| Number/percentage of C's | 70,281,944 / 20.57%  |
| Number/percentage of T's | 101,058,635 / 29.57% |
| Number/percentage of G's | 72,349,327 / 21.17%  |
| Number/percentage of N's | 2,491 / 0%           |
| GC Percentage            | 41.74%               |

### 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.1104 |
| Standard Deviation | 1.2894 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 36.55 |
|----------------------|-------|

## 2.5. Mismatches and indels

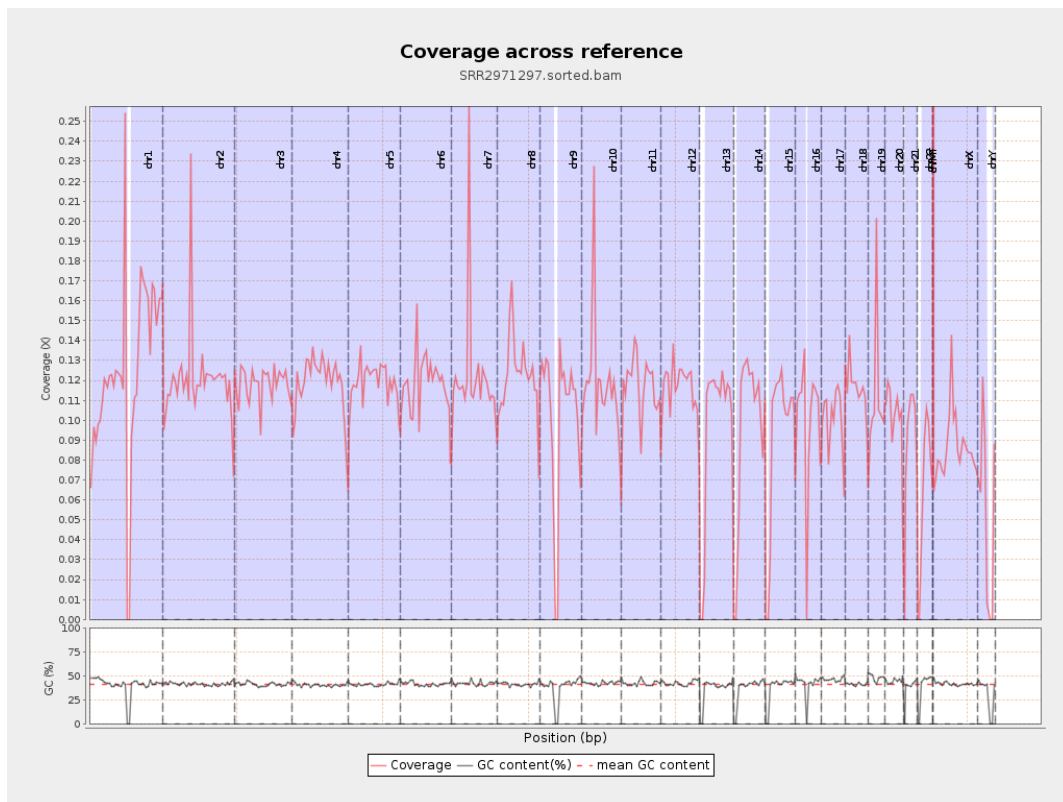
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.33%     |
| Mismatches                               | 1,124,700 |
| Insertions                               | 12,869    |
| Mapped reads with at least one insertion | 0.15%     |
| Deletions                                | 28,067    |
| Mapped reads with at least one deletion  | 0.32%     |
| Homopolymer indels                       | 38.44%    |

## 2.6. Chromosome stats

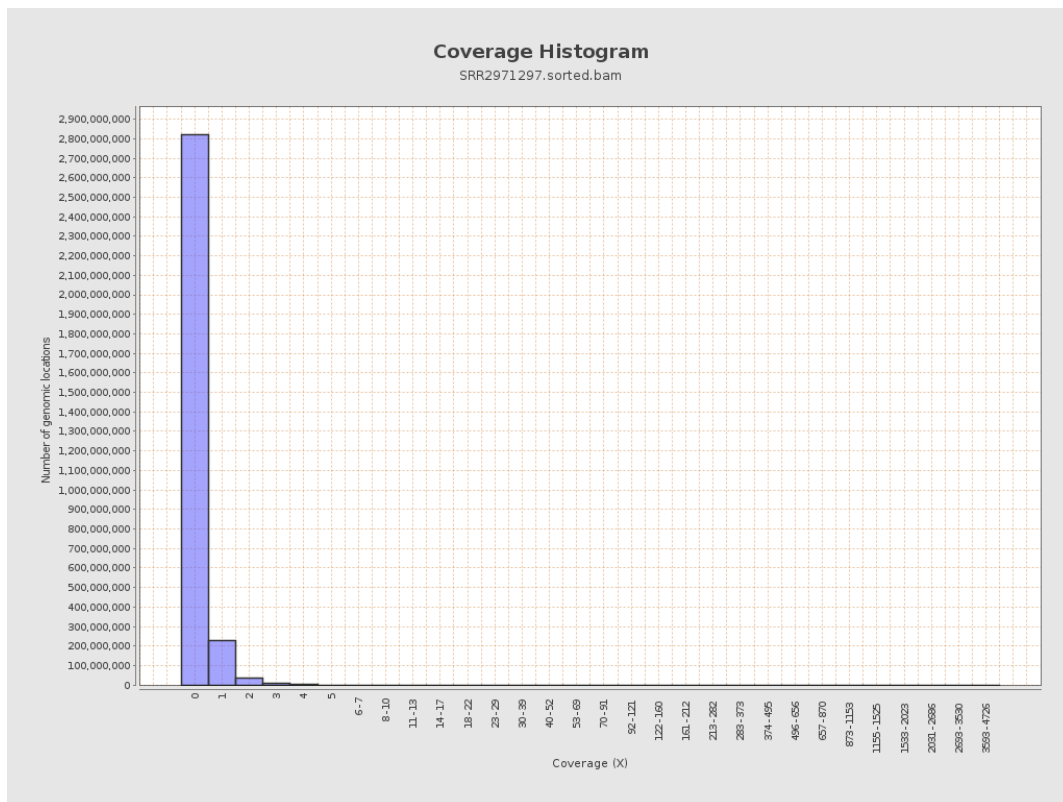
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 31008225     | 0.1244        | 3.0612             |
| chr2 | 243199373 | 29253259     | 0.1203        | 0.9512             |
| chr3 | 198022430 | 23455495     | 0.1184        | 0.4236             |
| chr4 | 191154276 | 22770353     | 0.1191        | 0.457              |
| chr5 | 180915260 | 21426934     | 0.1184        | 0.4612             |
| chr6 | 171115067 | 20344349     | 0.1189        | 0.5903             |
| chr7 | 159138663 | 19375904     | 0.1218        | 1.5887             |
| chr8 | 146364022 | 17935350     | 0.1225        | 2.1796             |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr9  | 141213431 | 14414264 | 0.1021 | 0.9541 |
| chr10 | 135534747 | 16058536 | 0.1185 | 1.0477 |
| chr11 | 135006516 | 15805332 | 0.1171 | 0.9183 |
| chr12 | 133851895 | 15661483 | 0.117  | 0.4835 |
| chr13 | 115169878 | 11053047 | 0.096  | 0.3578 |
| chr14 | 107349540 | 10375581 | 0.0967 | 0.5401 |
| chr15 | 102531392 | 9249320  | 0.0902 | 0.3563 |
| chr16 | 90354753  | 8760779  | 0.097  | 0.501  |
| chr17 | 81195210  | 8257028  | 0.1017 | 0.4749 |
| chr18 | 78077248  | 9149738  | 0.1172 | 1.9081 |
| chr19 | 59128983  | 6649735  | 0.1125 | 2.6544 |
| chr20 | 63025520  | 6512323  | 0.1033 | 0.4342 |
| chr21 | 48129895  | 4237098  | 0.088  | 0.4884 |
| chr22 | 51304566  | 3318416  | 0.0647 | 0.4014 |
| chrMT | 16571     | 40099    | 2.4198 | 2.8996 |
| chrX  | 155270560 | 13397349 | 0.0863 | 0.5738 |
| chrY  | 59373566  | 3250767  | 0.0548 | 0.472  |

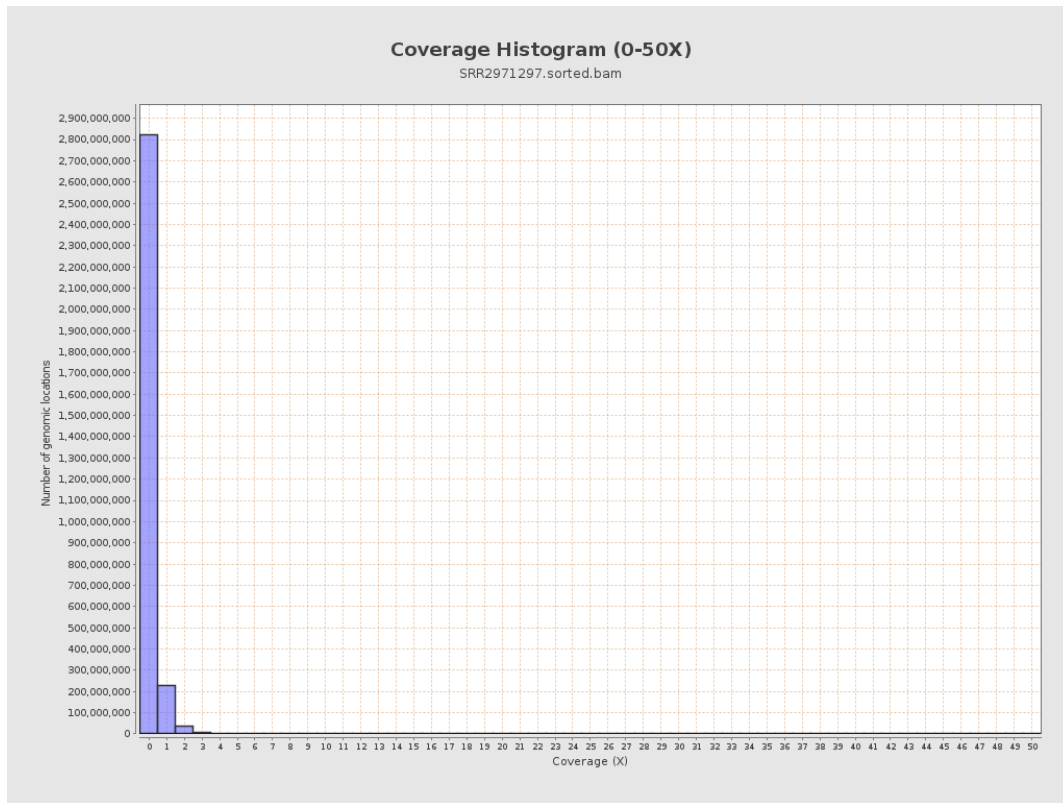
### 3. Results : Coverage across reference



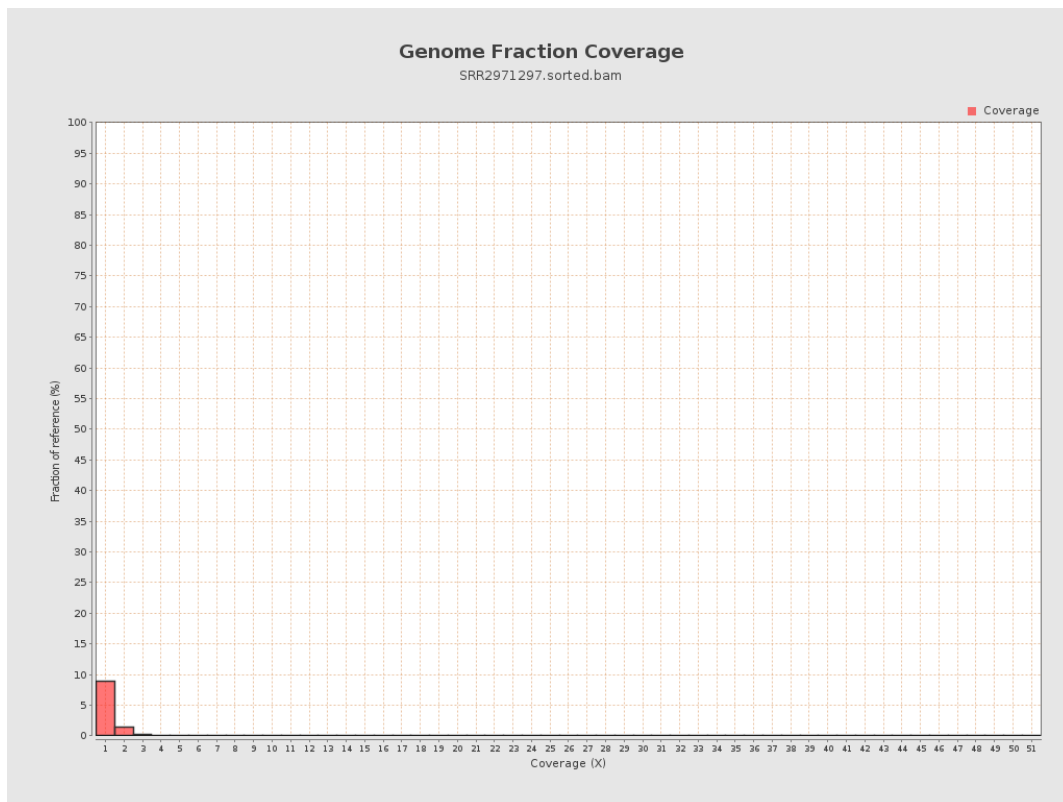
## 4. Results : Coverage Histogram



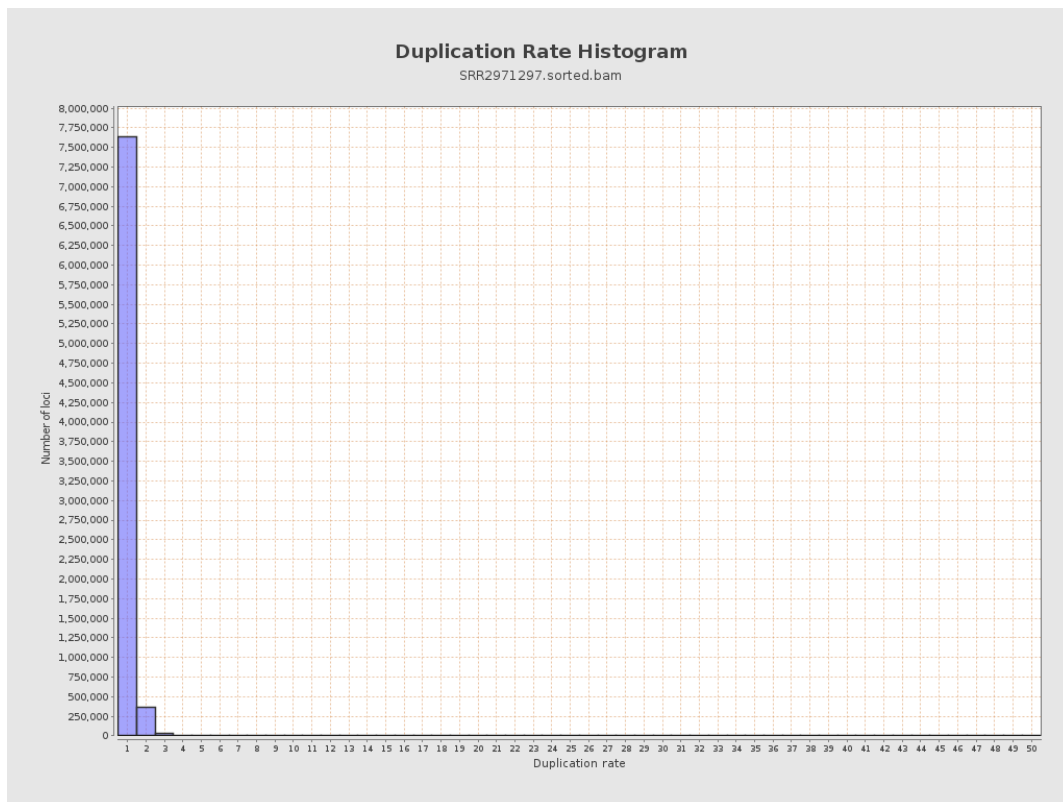
## 5. Results : Coverage Histogram (0-50X)



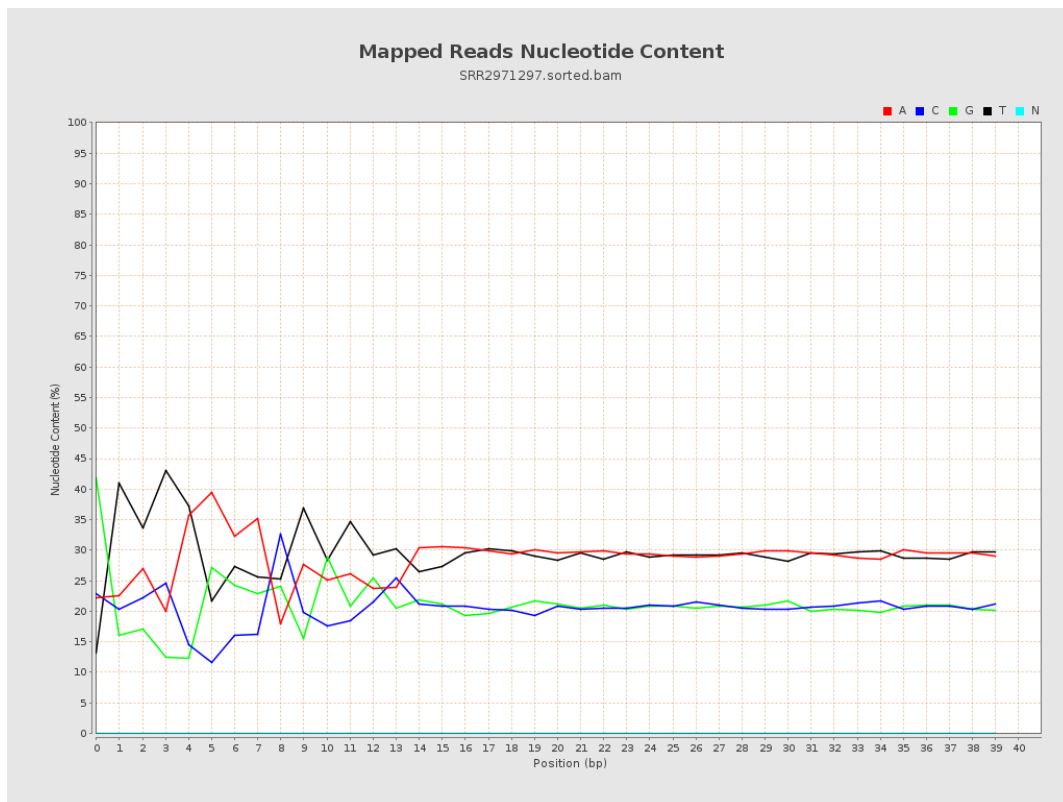
## 6. Results : Genome Fraction Coverage



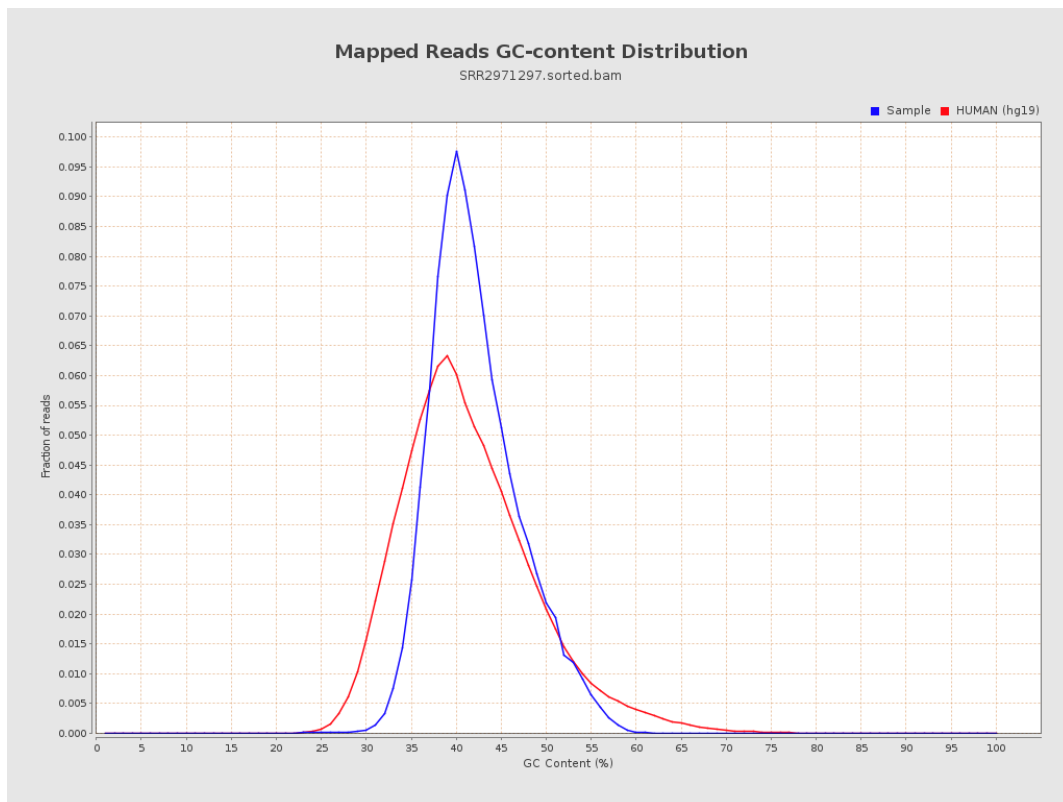
## 7. Results : Duplication Rate Histogram



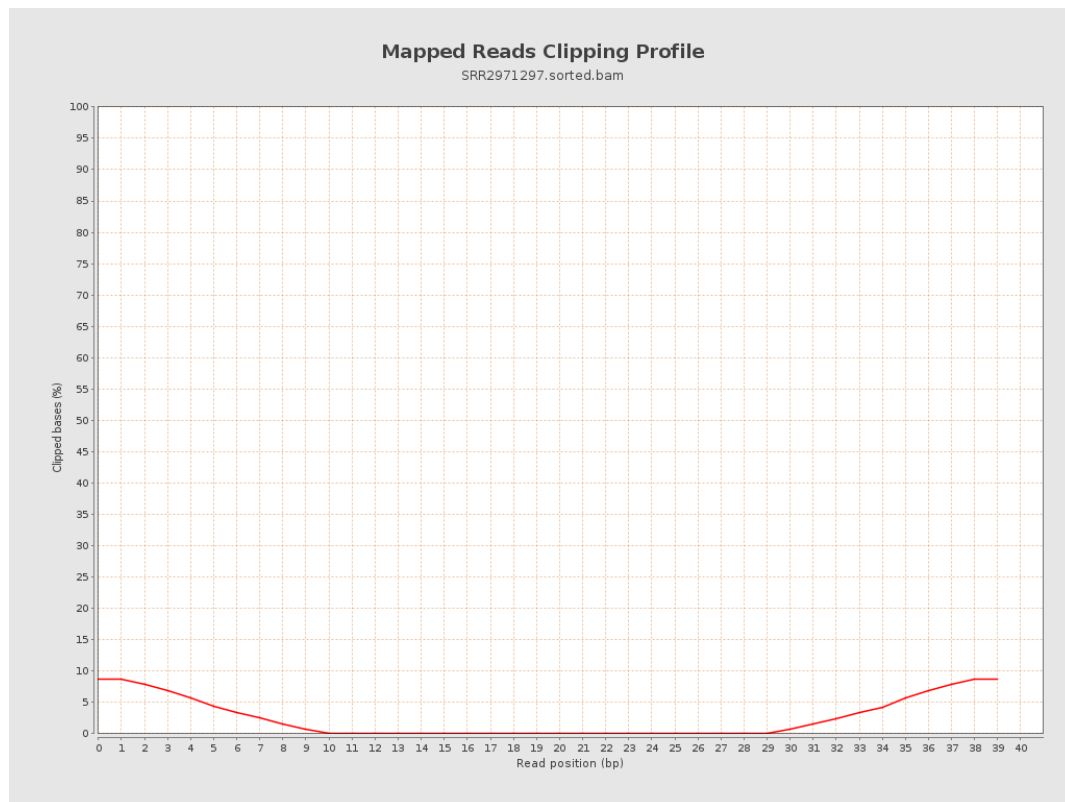
## 8. Results : Mapped Reads Nucleotide Content



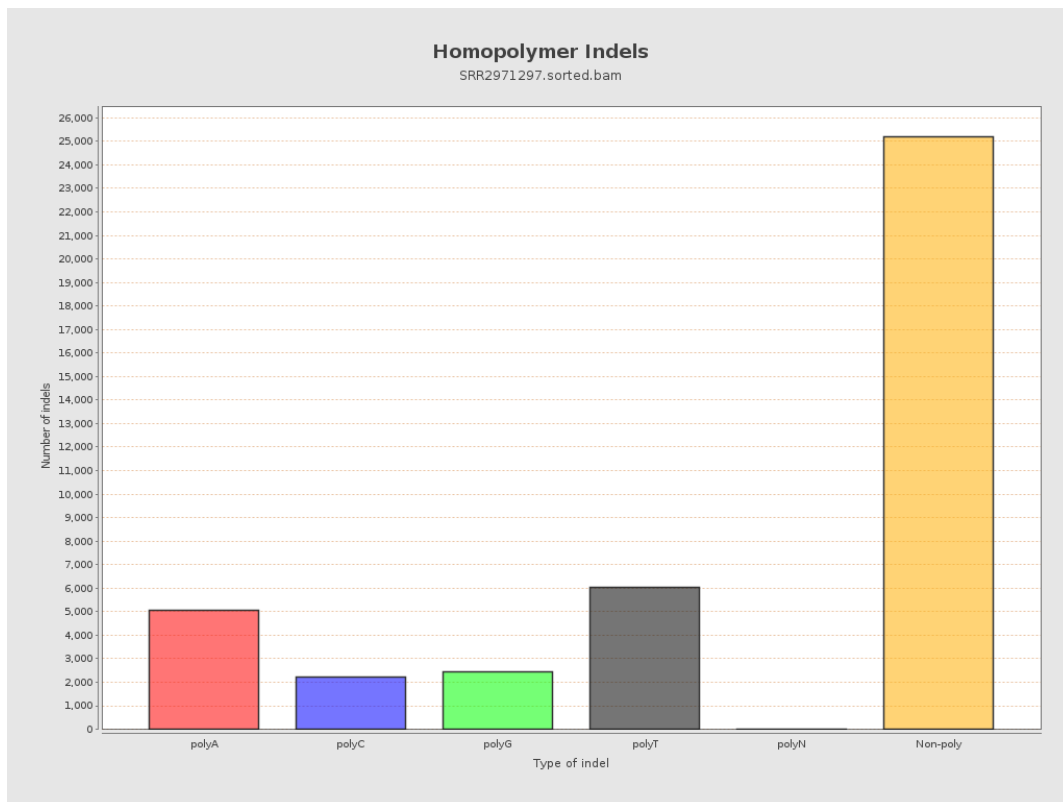
## 9. Results : Mapped Reads GC-content Distribution



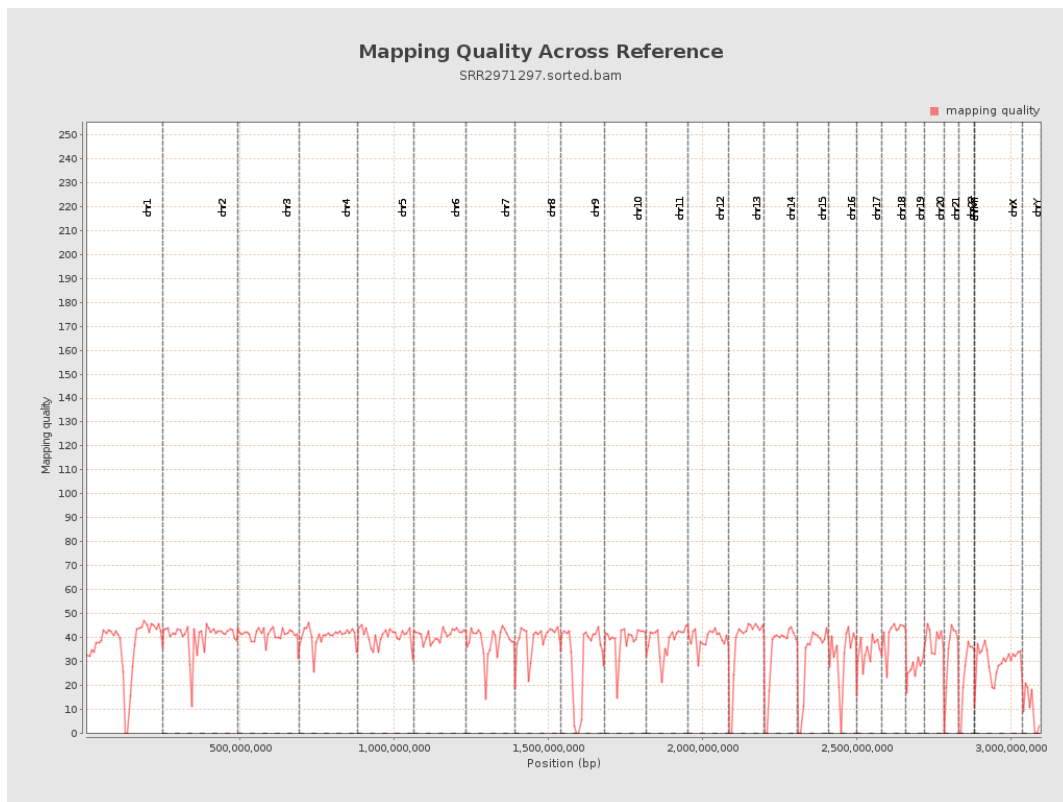
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

