

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/17 14:41:58*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238287.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_SRR6238287 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238287.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Tue Sep 17 14:41:58 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6238287.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 3,102,810          |
| Mapped reads                 | 2,779,086 / 89.57% |
| Unmapped reads               | 323,724 / 10.43%   |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 22,369 / 0.72%     |
| Read min/max/mean length     | 30 / 76 / 76.25    |
| Duplicated reads (estimated) | 122,318 / 3.94%    |
| Duplication rate             | 3.08%              |
| Clipped reads                | 1,414,014 / 45.57% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 49,676,607 / 27.36% |
| Number/percentage of C's | 34,454,446 / 18.98% |
| Number/percentage of T's | 55,204,542 / 30.41% |
| Number/percentage of G's | 42,164,157 / 23.23% |
| Number/percentage of N's | 44,433 / 0.02%      |
| GC Percentage            | 42.2%               |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0587 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.5493 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 43.06 |
|----------------------|-------|

## 2.5. Mismatches and indels

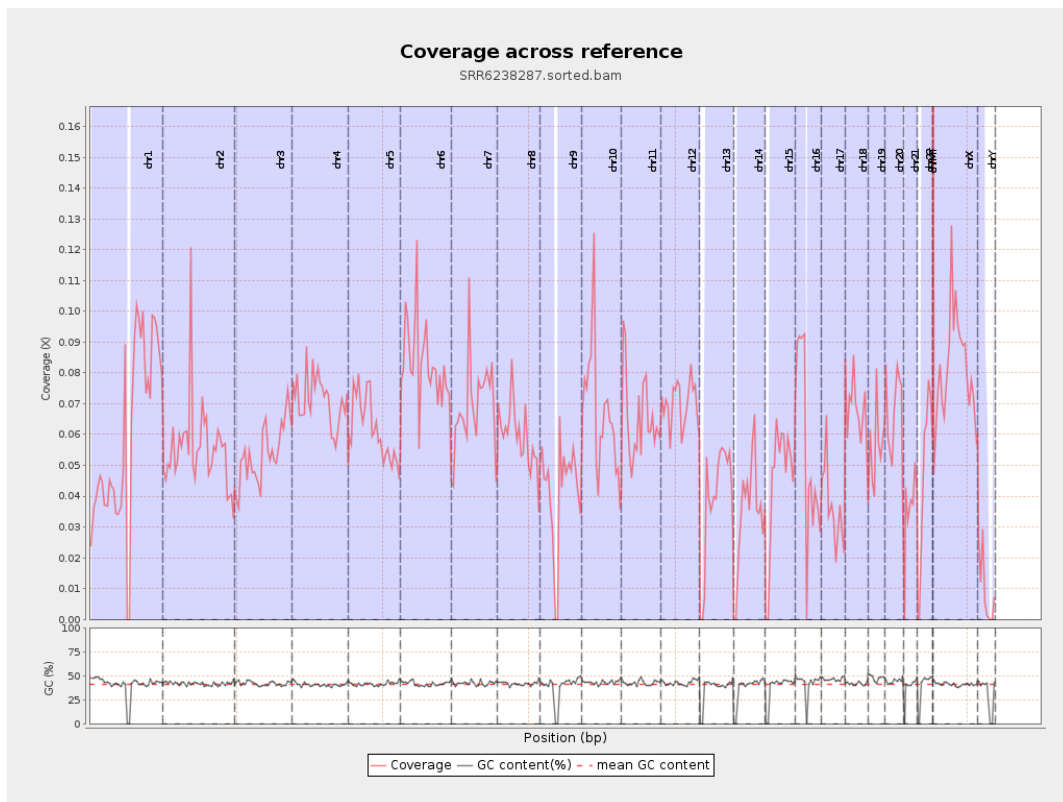
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.89%     |
| Mismatches                               | 1,579,211 |
| Insertions                               | 15,206    |
| Mapped reads with at least one insertion | 0.54%     |
| Deletions                                | 53,365    |
| Mapped reads with at least one deletion  | 1.9%      |
| Homopolymer indels                       | 44.99%    |

## 2.6. Chromosome stats

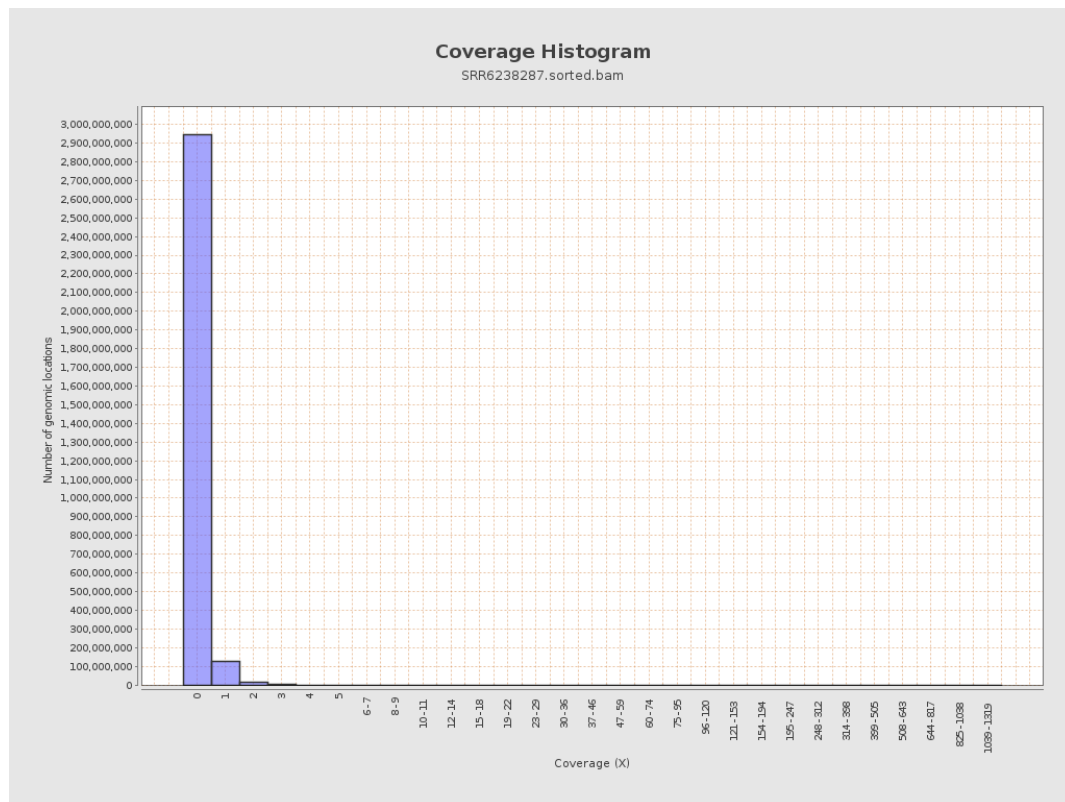
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 14894856     | 0.0598        | 1.0617             |
| chr2 | 243199373 | 13514290     | 0.0556        | 0.7526             |
| chr3 | 198022430 | 10632061     | 0.0537        | 0.2721             |
| chr4 | 191154276 | 13614731     | 0.0712        | 0.3501             |
| chr5 | 180915260 | 11087602     | 0.0613        | 0.292              |
| chr6 | 171115067 | 14193062     | 0.0829        | 0.5015             |
| chr7 | 159138663 | 10959500     | 0.0689        | 0.7063             |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr8  | 146364022 | 8645035  | 0.0591 | 0.6266 |
| chr9  | 141213431 | 5916529  | 0.0419 | 0.5099 |
| chr10 | 135534747 | 9013579  | 0.0665 | 0.557  |
| chr11 | 135006516 | 8793124  | 0.0651 | 0.4564 |
| chr12 | 133851895 | 9408601  | 0.0703 | 0.3173 |
| chr13 | 115169878 | 4528770  | 0.0393 | 0.2296 |
| chr14 | 107349540 | 3762630  | 0.0351 | 0.2686 |
| chr15 | 102531392 | 4521545  | 0.0441 | 0.2519 |
| chr16 | 90354753  | 4933140  | 0.0546 | 0.3213 |
| chr17 | 81195210  | 2982764  | 0.0367 | 0.2895 |
| chr18 | 78077248  | 5352002  | 0.0685 | 0.8464 |
| chr19 | 59128983  | 3334562  | 0.0564 | 0.6836 |
| chr20 | 63025520  | 4216365  | 0.0669 | 0.3146 |
| chr21 | 48129895  | 1762134  | 0.0366 | 0.2655 |
| chr22 | 51304566  | 2423321  | 0.0472 | 0.2542 |
| chrMT | 16571     | 7397     | 0.4464 | 0.8498 |
| chrX  | 155270560 | 12567161 | 0.0809 | 0.4014 |
| chrY  | 59373566  | 567742   | 0.0096 | 0.2269 |

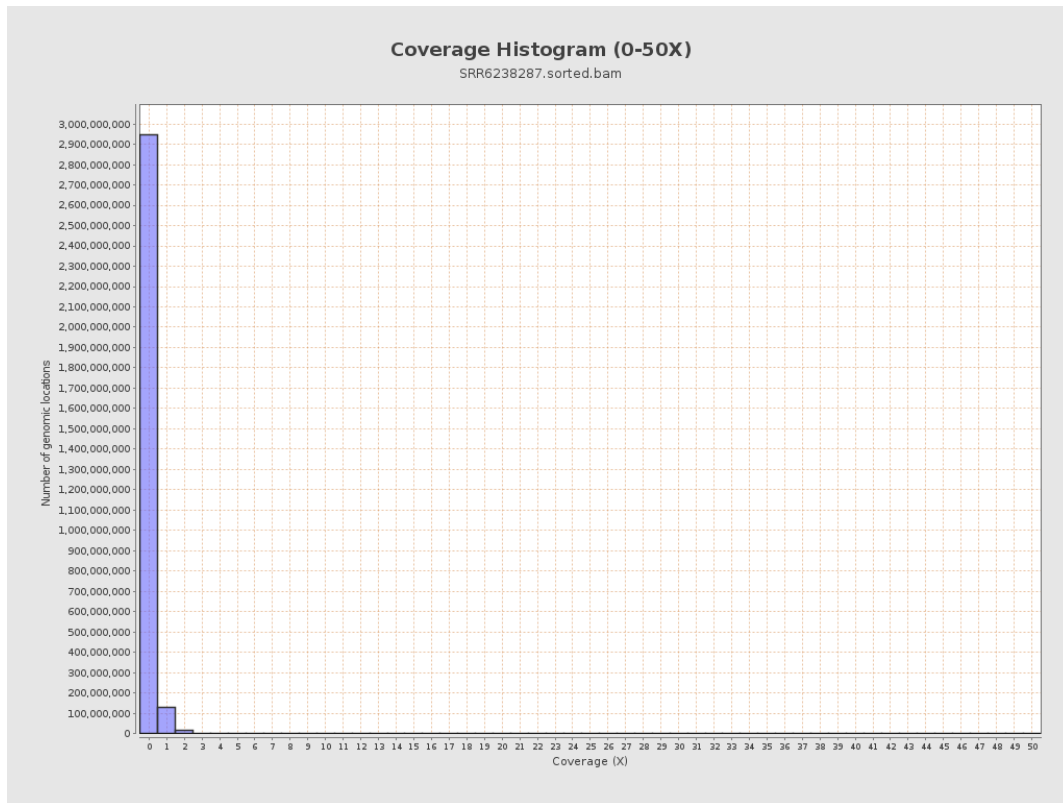
### 3. Results : Coverage across reference



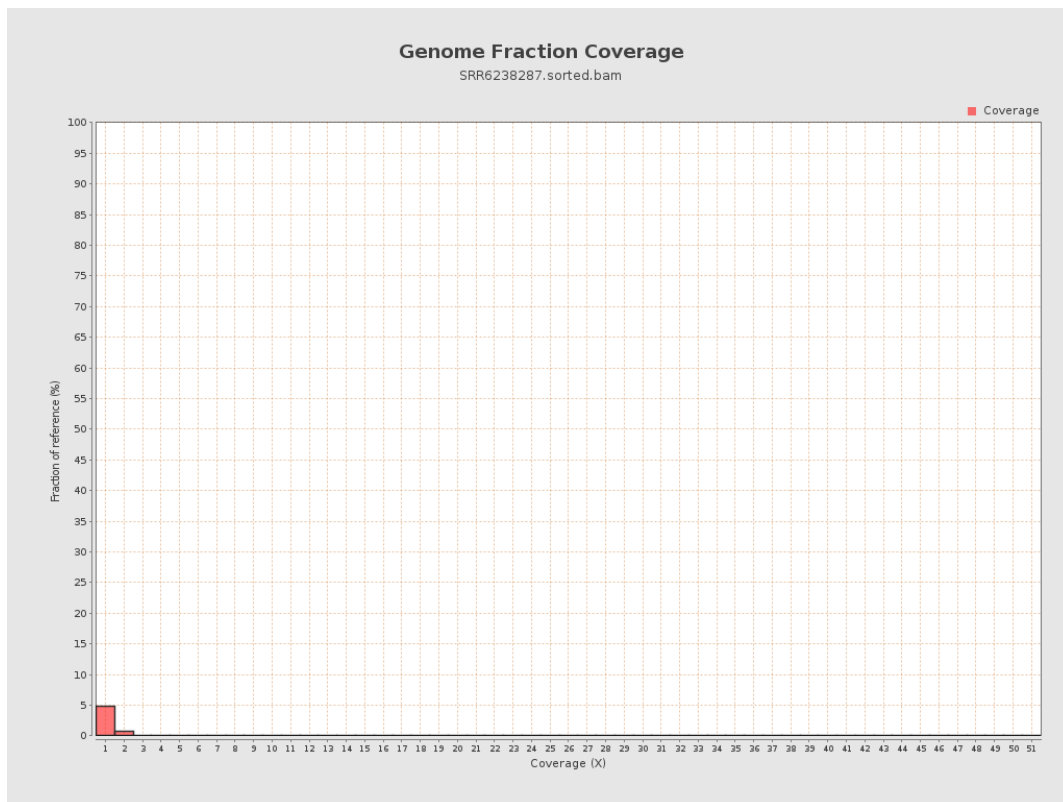
## 4. Results : Coverage Histogram



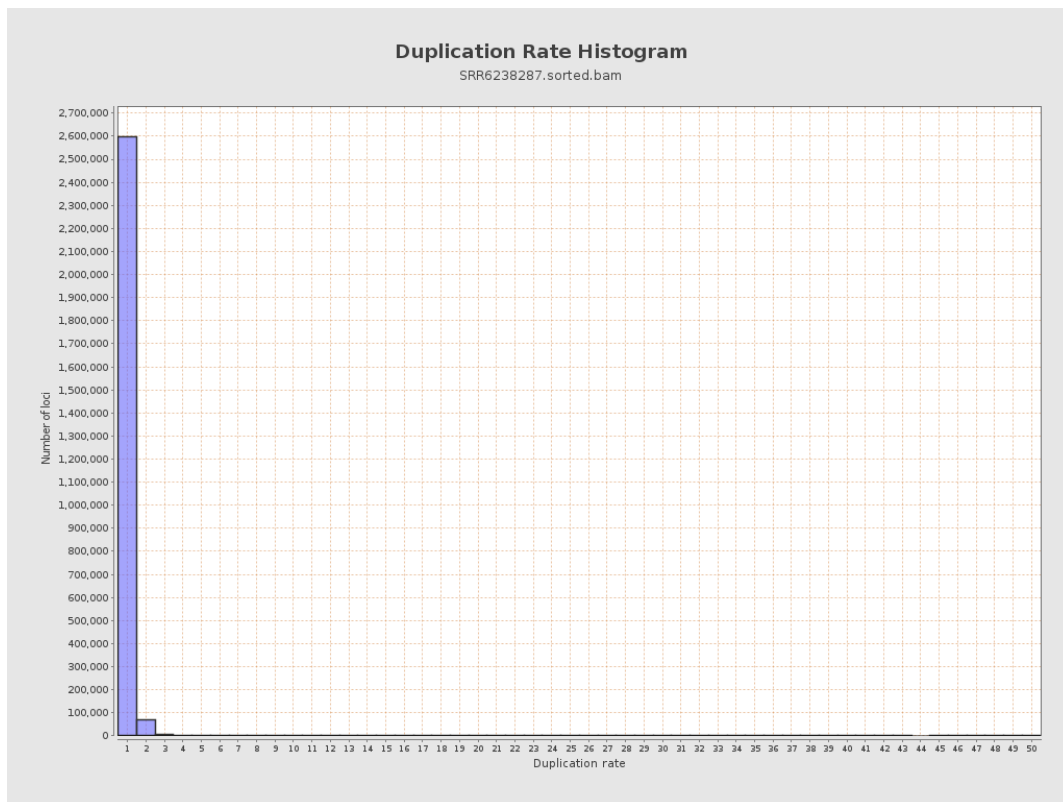
## 5. Results : Coverage Histogram (0-50X)



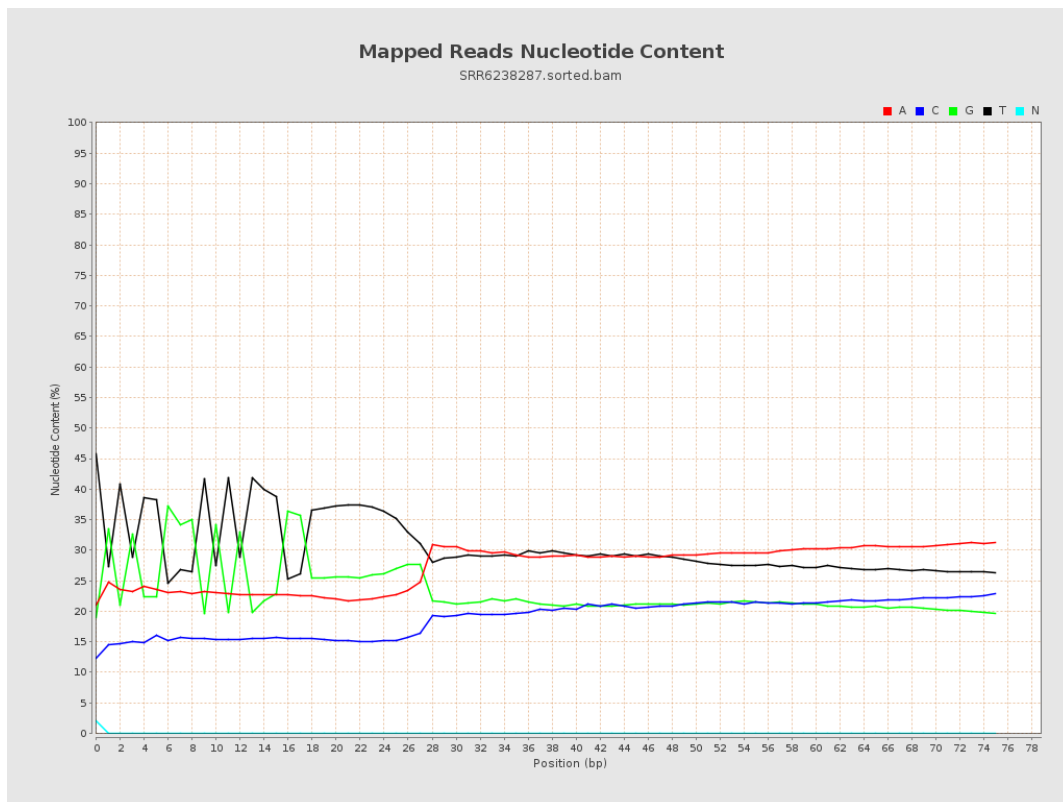
## 6. Results : Genome Fraction Coverage



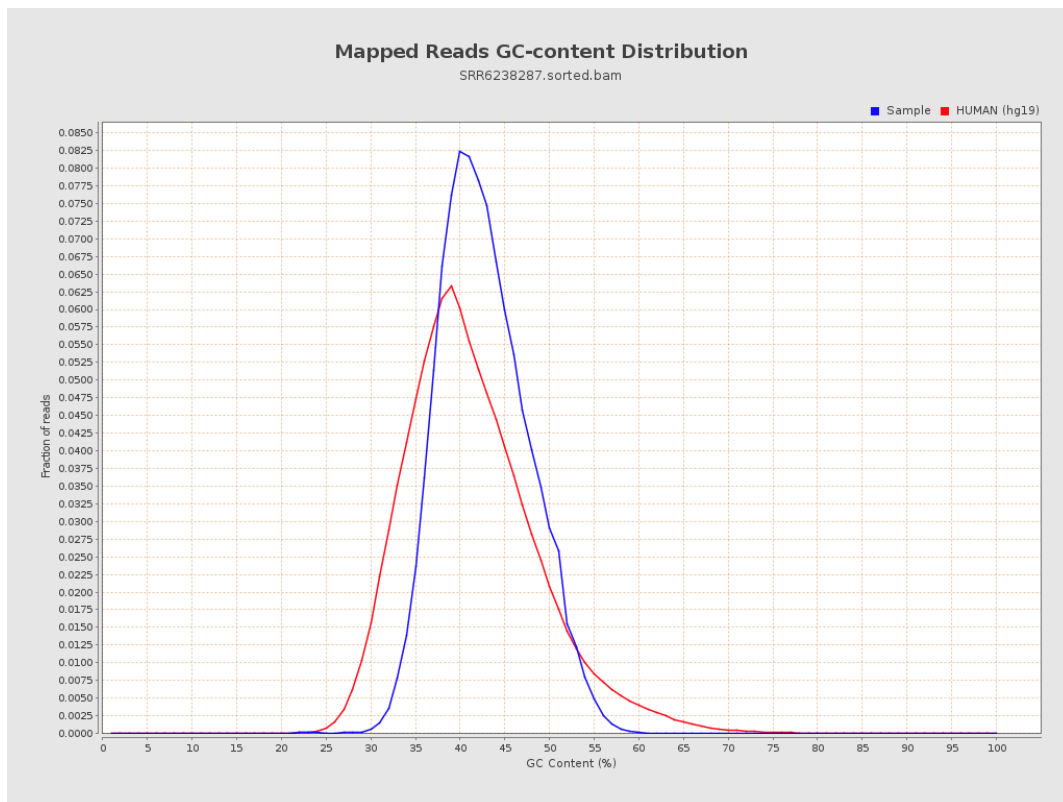
## 7. Results : Duplication Rate Histogram



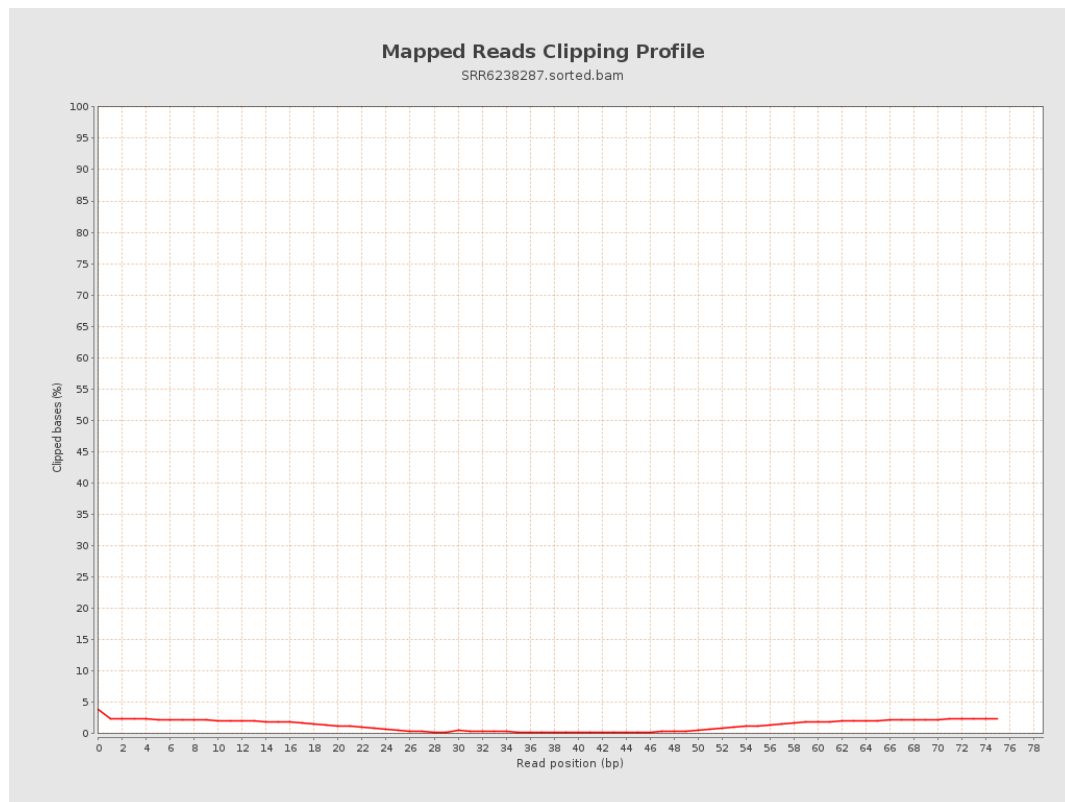
## 8. Results : Mapped Reads Nucleotide Content



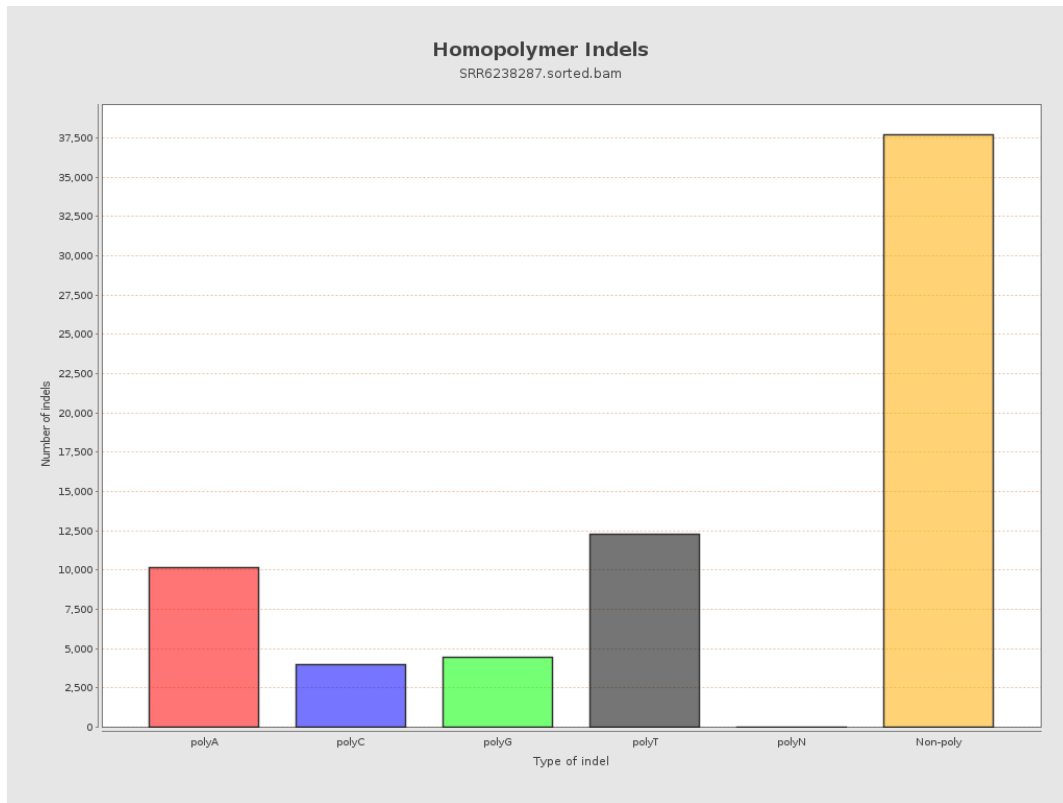
## 9. Results : Mapped Reads GC-content Distribution



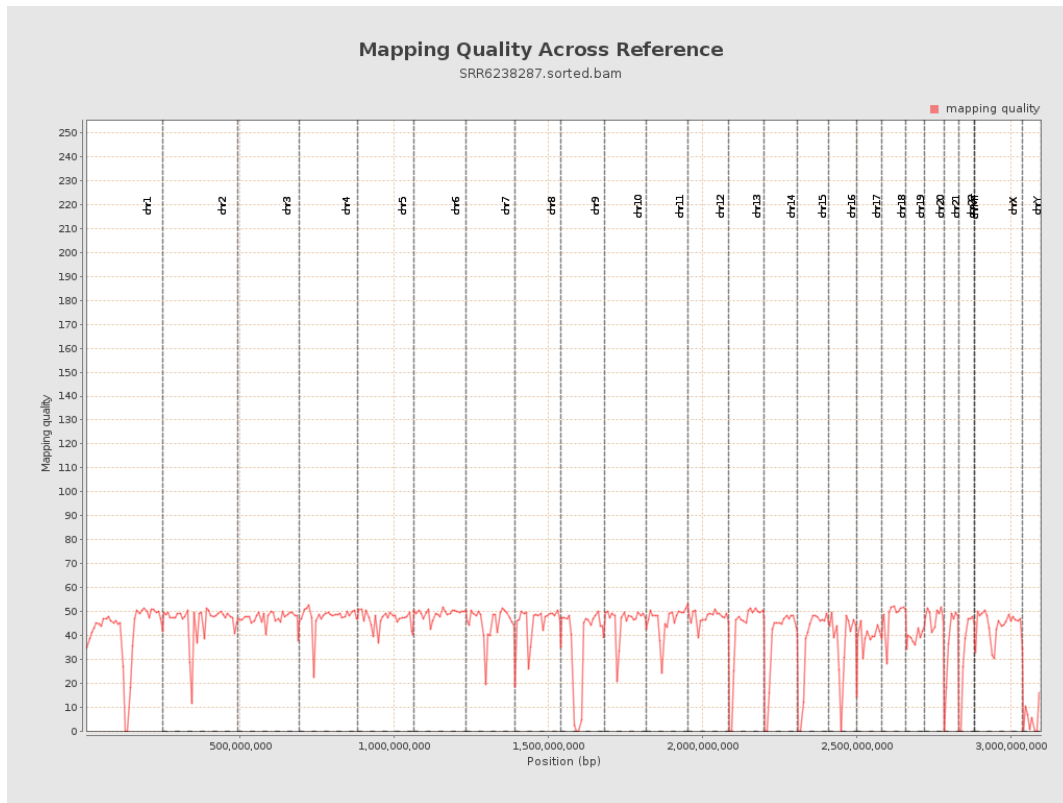
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

