

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/17 04:26:00*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237586.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_SRR6237586 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237586.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Tue Sep 17 04:25:59 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6237586.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 2,565,527          |
| Mapped reads                 | 2,080,377 / 81.09% |
| Unmapped reads               | 485,150 / 18.91%   |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 11,600 / 0.45%     |
| Read min/max/mean length     | 30 / 76 / 76.16    |
| Duplicated reads (estimated) | 132,391 / 5.16%    |
| Duplication rate             | 4.16%              |
| Clipped reads                | 1,277,177 / 49.78% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 33,557,573 / 25.58% |
| Number/percentage of C's | 24,989,027 / 19.05% |
| Number/percentage of T's | 39,512,746 / 30.12% |
| Number/percentage of G's | 33,083,000 / 25.22% |
| Number/percentage of N's | 30,544 / 0.02%      |
| GC Percentage            | 44.27%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0424 |
|      |        |

|                    |       |
|--------------------|-------|
| Standard Deviation | 0.393 |
|--------------------|-------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 39.31 |
|----------------------|-------|

## 2.5. Mismatches and indels

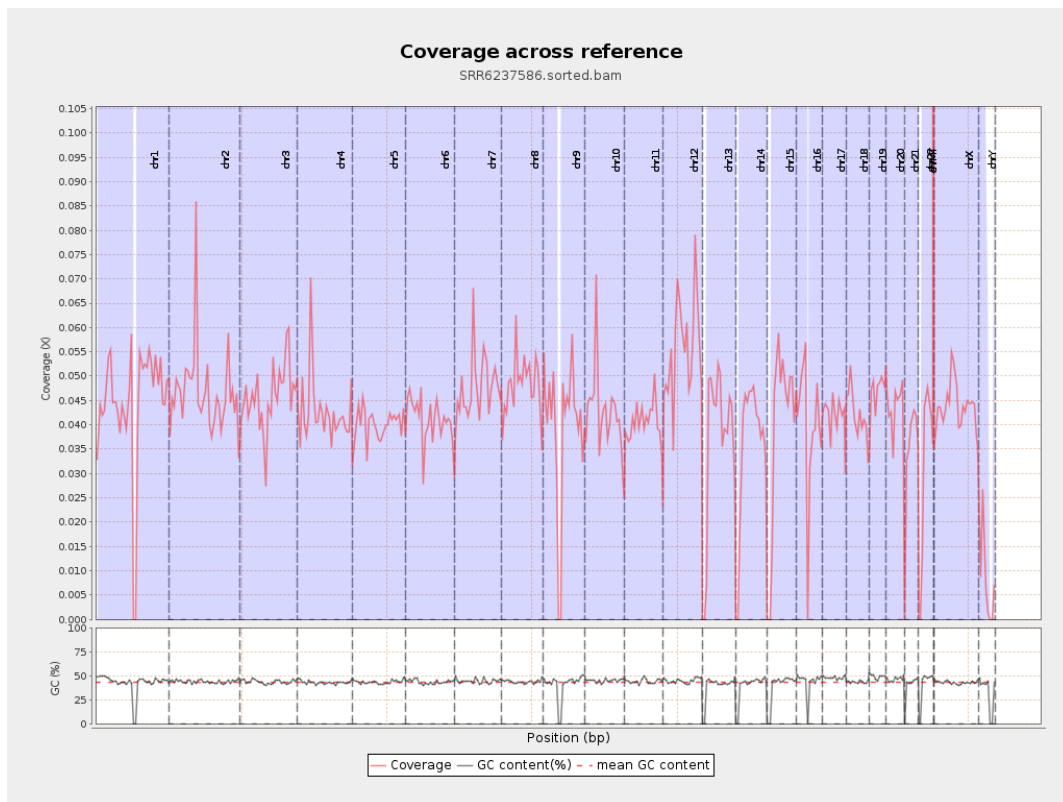
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.96%     |
| Mismatches                               | 1,238,824 |
| Insertions                               | 12,396    |
| Mapped reads with at least one insertion | 0.59%     |
| Deletions                                | 46,347    |
| Mapped reads with at least one deletion  | 2.2%      |
| Homopolymer indels                       | 45.67%    |

## 2.6. Chromosome stats

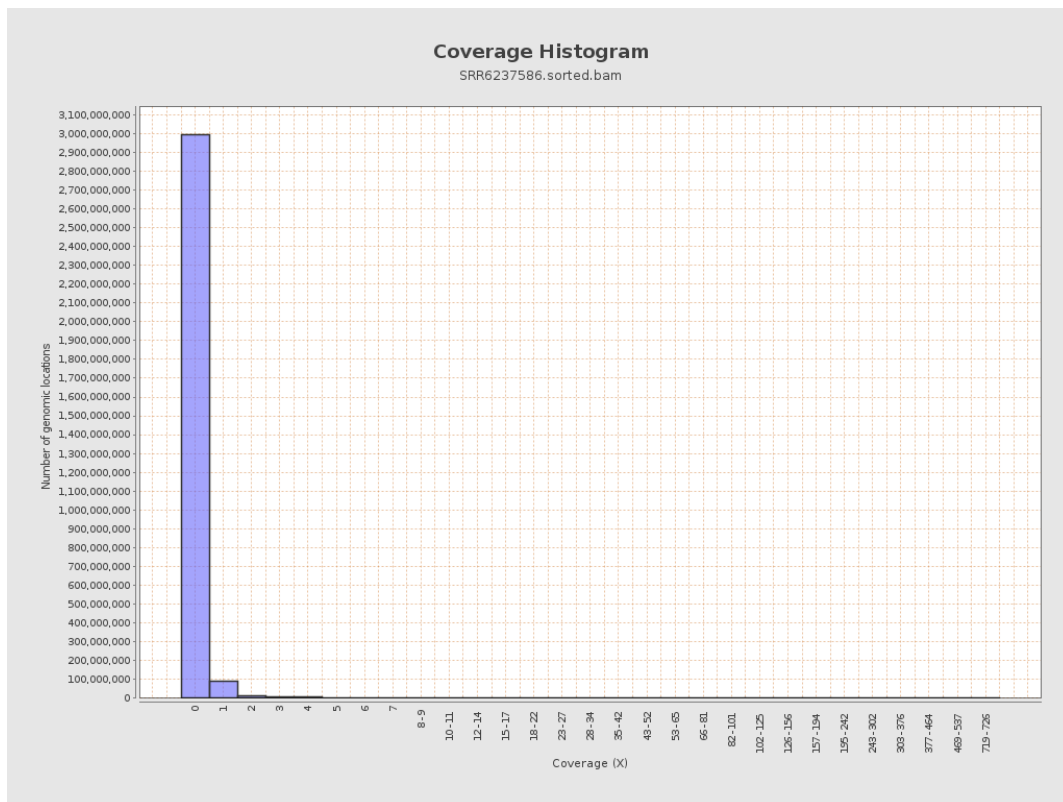
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 11090743     | 0.0445        | 0.5026             |
| chr2 | 243199373 | 11379566     | 0.0468        | 0.5693             |
| chr3 | 198022430 | 9028336      | 0.0456        | 0.3004             |
| chr4 | 191154276 | 8116654      | 0.0425        | 0.3156             |
| chr5 | 180915260 | 7270991      | 0.0402        | 0.2682             |
| chr6 | 171115067 | 7025234      | 0.0411        | 0.3173             |
| chr7 | 159138663 | 7604453      | 0.0478        | 0.5594             |
|      |           |              |               |                    |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr8  | 146364022 | 7013003 | 0.0479 | 0.3733 |
| chr9  | 141213431 | 5492108 | 0.0389 | 0.4194 |
| chr10 | 135534747 | 5790659 | 0.0427 | 0.3952 |
| chr11 | 135006516 | 5428334 | 0.0402 | 0.4084 |
| chr12 | 133851895 | 7521525 | 0.0562 | 0.3479 |
| chr13 | 115169878 | 4195068 | 0.0364 | 0.2681 |
| chr14 | 107349540 | 3819804 | 0.0356 | 0.2986 |
| chr15 | 102531392 | 4055259 | 0.0396 | 0.2906 |
| chr16 | 90354753  | 3604627 | 0.0399 | 0.3202 |
| chr17 | 81195210  | 3396014 | 0.0418 | 0.3058 |
| chr18 | 78077248  | 3318931 | 0.0425 | 0.6003 |
| chr19 | 59128983  | 2776691 | 0.047  | 0.409  |
| chr20 | 63025520  | 2720774 | 0.0432 | 0.3013 |
| chr21 | 48129895  | 1669081 | 0.0347 | 0.2904 |
| chr22 | 51304566  | 1542610 | 0.0301 | 0.2445 |
| chrMT | 16571     | 127342  | 7.6846 | 6.3749 |
| chrX  | 155270560 | 6777225 | 0.0436 | 0.3205 |
| chrY  | 59373566  | 484388  | 0.0082 | 0.1998 |

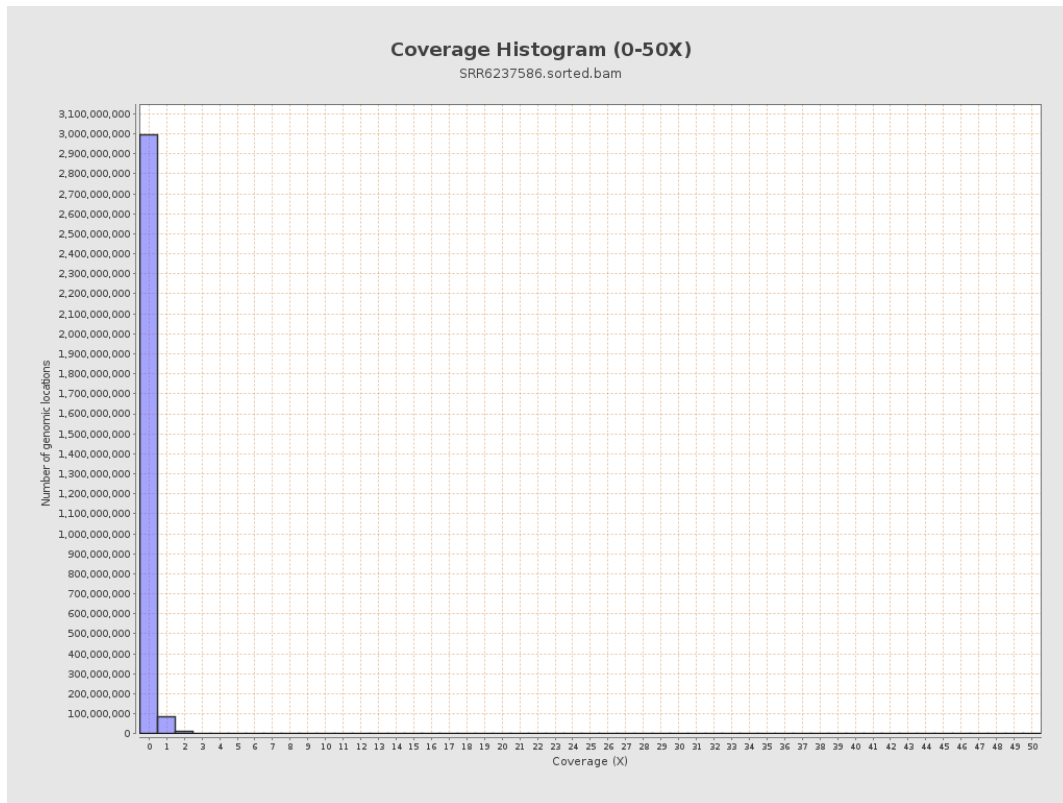
### 3. Results : Coverage across reference



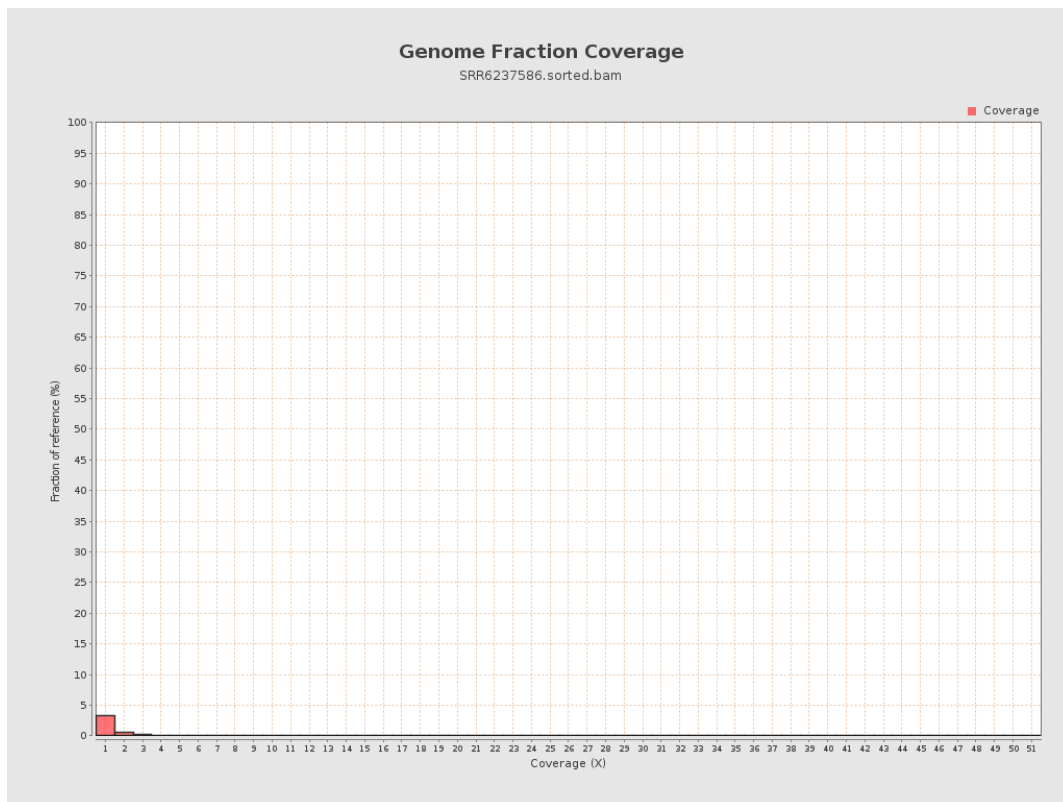
## 4. Results : Coverage Histogram



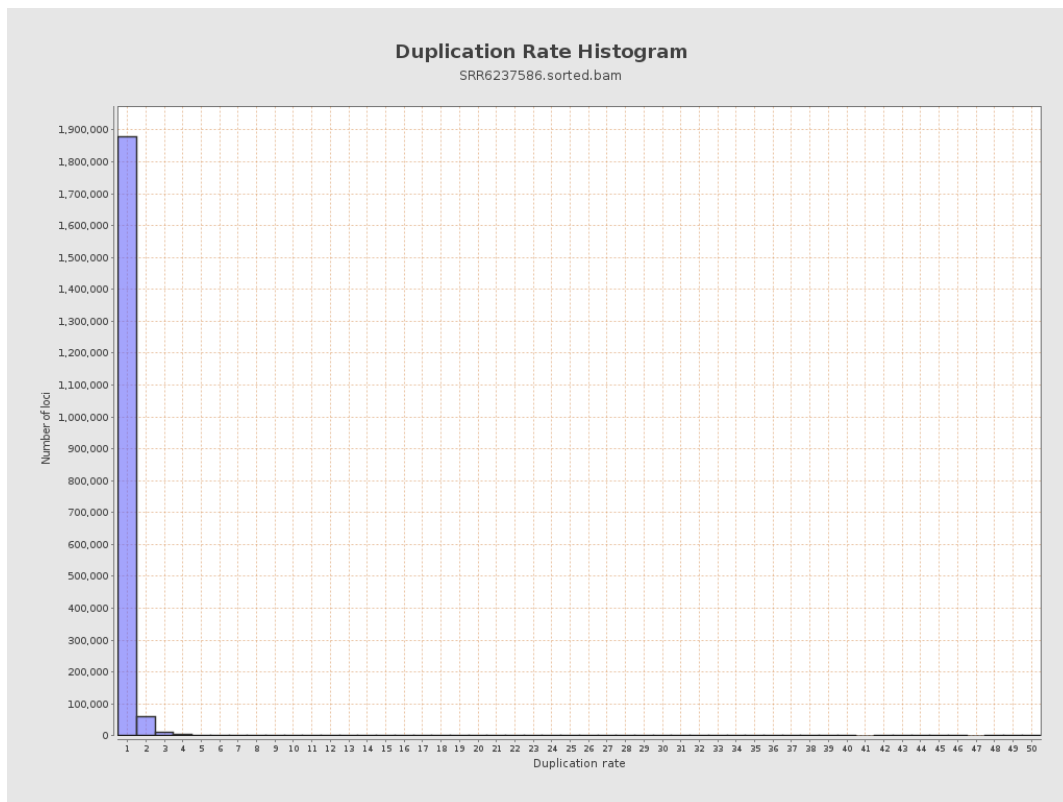
## 5. Results : Coverage Histogram (0-50X)



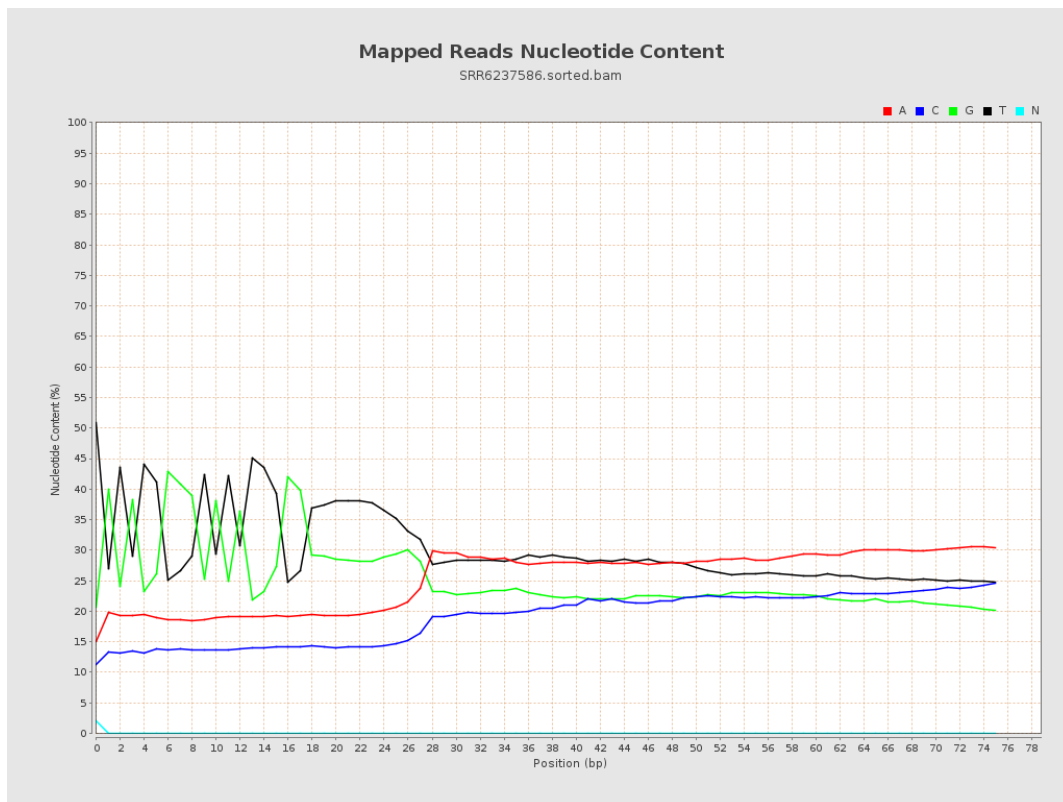
## 6. Results : Genome Fraction Coverage



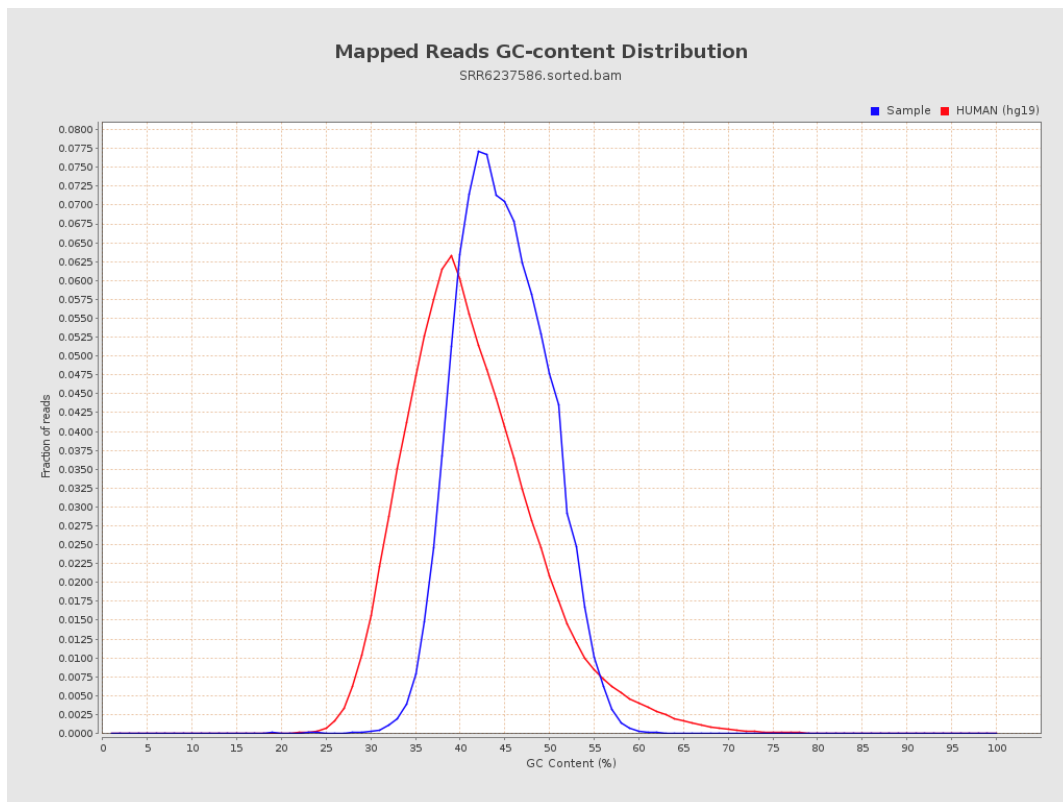
## 7. Results : Duplication Rate Histogram



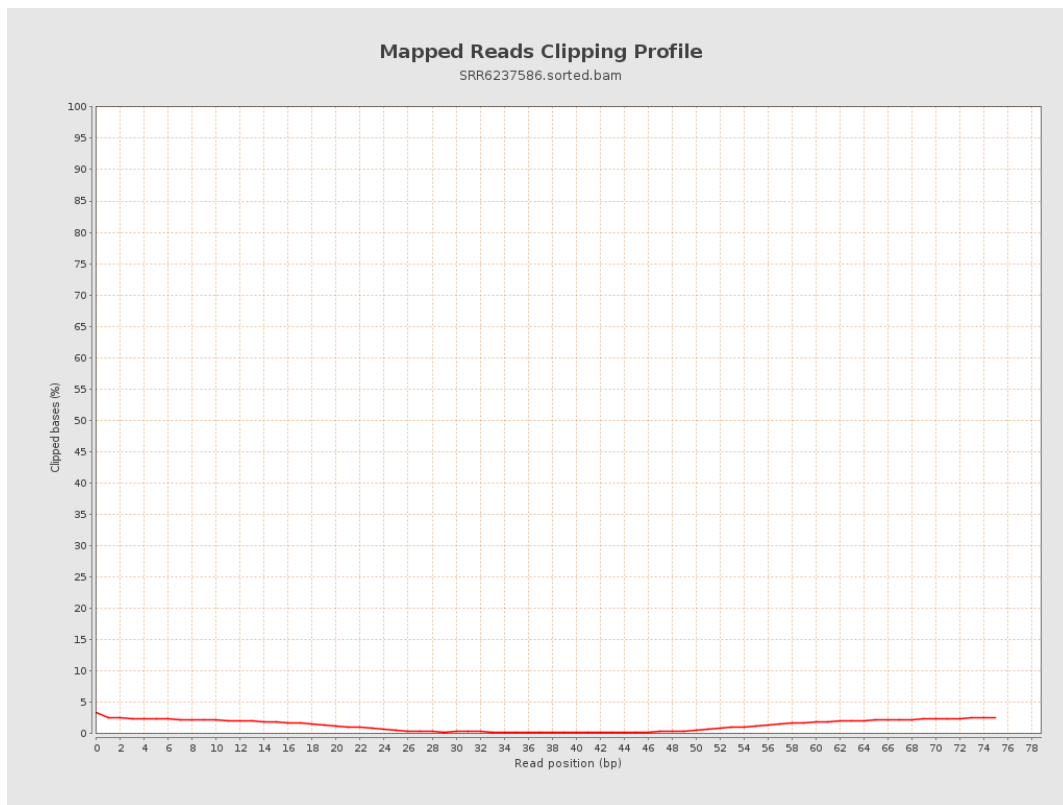
## 8. Results : Mapped Reads Nucleotide Content



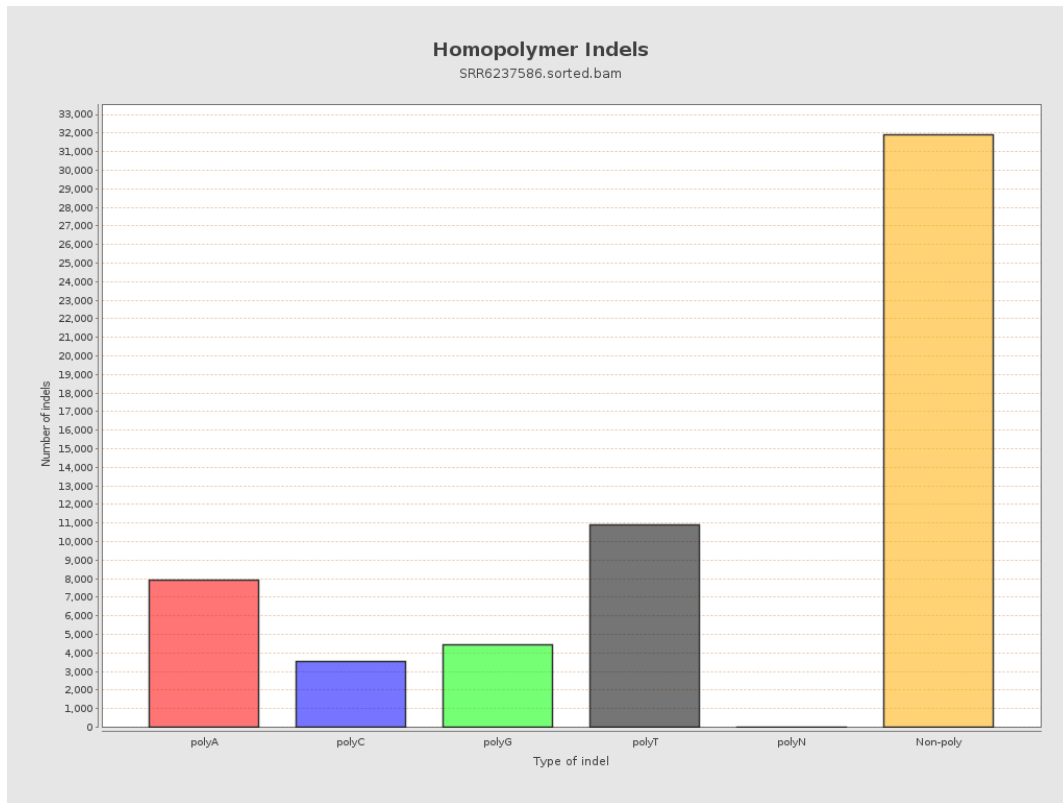
## 9. Results : Mapped Reads GC-content Distribution



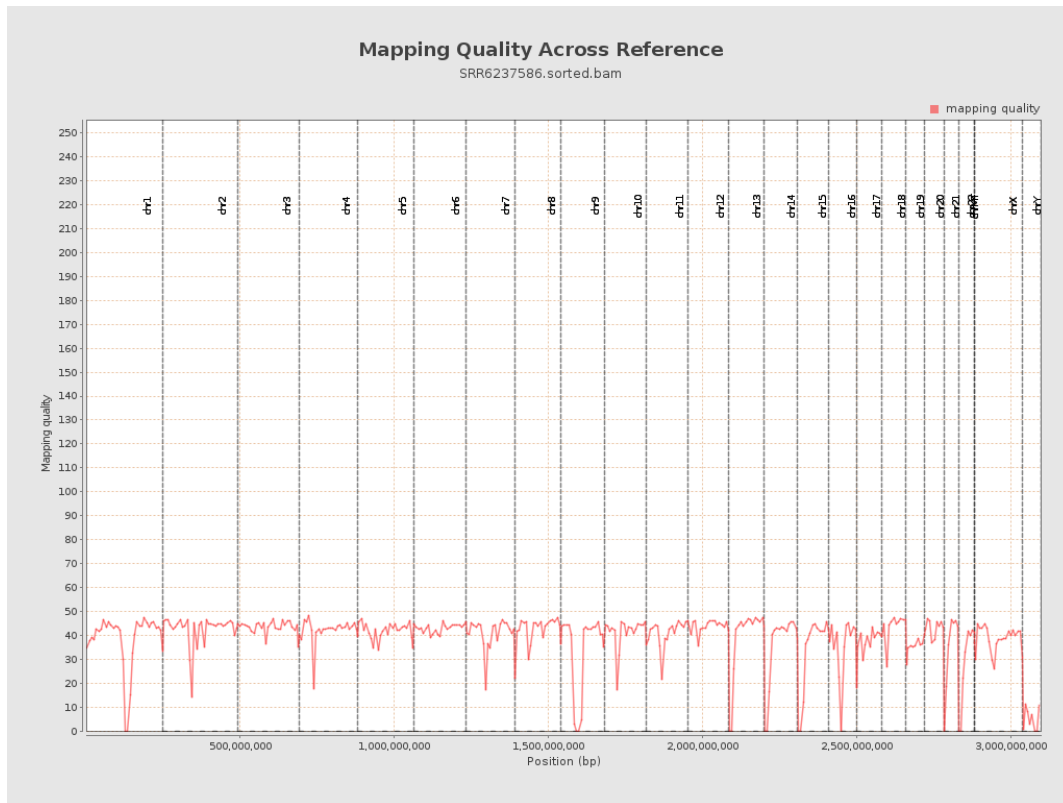
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

