

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/01 07:20:19*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472808.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_SRR3472808 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472808.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Tue Oct 01 07:20:18 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR3472808.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 1,941,234          |
| Mapped reads                 | 1,476,551 / 76.06% |
| Unmapped reads               | 464,683 / 23.94%   |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 14,690 / 0.76%     |
| Read min/max/mean length     | 30 / 76 / 76.26    |
| Duplicated reads (estimated) | 91,554 / 4.72%     |
| Duplication rate             | 4.49%              |
| Clipped reads                | 904,620 / 46.6%    |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 25,100,611 / 27.18% |
| Number/percentage of C's | 18,308,202 / 19.82% |
| Number/percentage of T's | 27,268,390 / 29.53% |
| Number/percentage of G's | 21,672,643 / 23.47% |
| Number/percentage of N's | 2,237 / 0%          |
| GC Percentage            | 43.29%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0298 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.2795 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |      |
|----------------------|------|
| Mean Mapping Quality | 42.8 |
|----------------------|------|

## 2.5. Mismatches and indels

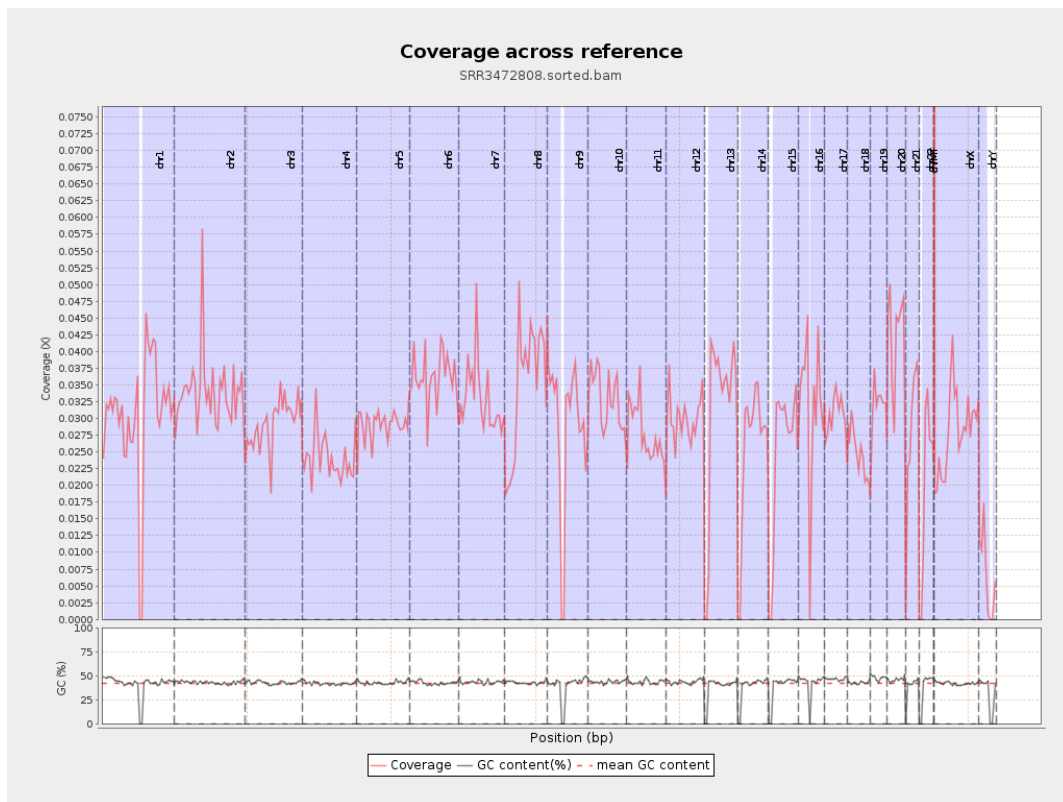
|                                          |         |
|------------------------------------------|---------|
| General error rate                       | 0.93%   |
| Mismatches                               | 846,980 |
| Insertions                               | 7,179   |
| Mapped reads with at least one insertion | 0.48%   |
| Deletions                                | 24,777  |
| Mapped reads with at least one deletion  | 1.66%   |
| Homopolymer indels                       | 45.99%  |

## 2.6. Chromosome stats

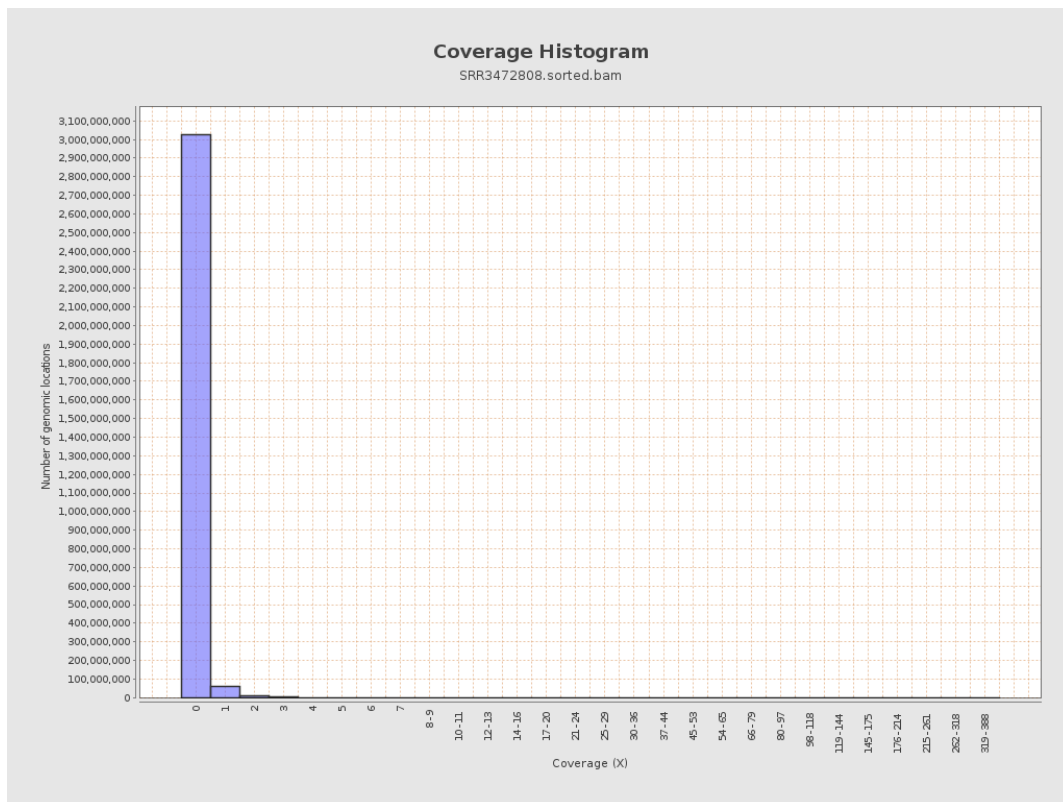
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 7584961      | 0.0304        | 0.3349             |
| chr2 | 243199373 | 8286071      | 0.0341        | 0.3439             |
| chr3 | 198022430 | 5800647      | 0.0293        | 0.2245             |
| chr4 | 191154276 | 4611554      | 0.0241        | 0.2154             |
| chr5 | 180915260 | 5288444      | 0.0292        | 0.224              |
| chr6 | 171115067 | 6183735      | 0.0361        | 0.2644             |
| chr7 | 159138663 | 5255560      | 0.033         | 0.3918             |
|      |           |              |               |                    |

|       |           |         |        |        |
|-------|-----------|---------|--------|--------|
| chr8  | 146364022 | 5102574 | 0.0349 | 0.2776 |
| chr9  | 141213431 | 4052575 | 0.0287 | 0.2934 |
| chr10 | 135534747 | 4471076 | 0.033  | 0.2722 |
| chr11 | 135006516 | 3765658 | 0.0279 | 0.2872 |
| chr12 | 133851895 | 4025374 | 0.0301 | 0.2402 |
| chr13 | 115169878 | 3588987 | 0.0312 | 0.2312 |
| chr14 | 107349540 | 2741572 | 0.0255 | 0.2414 |
| chr15 | 102531392 | 2550997 | 0.0249 | 0.2362 |
| chr16 | 90354753  | 2830641 | 0.0313 | 0.2455 |
| chr17 | 81195210  | 2458603 | 0.0303 | 0.2503 |
| chr18 | 78077248  | 1932089 | 0.0247 | 0.4186 |
| chr19 | 59128983  | 1892120 | 0.032  | 0.2866 |
| chr20 | 63025520  | 2666955 | 0.0423 | 0.2774 |
| chr21 | 48129895  | 1362661 | 0.0283 | 0.2328 |
| chr22 | 51304566  | 1046945 | 0.0204 | 0.1929 |
| chrMT | 16571     | 128290  | 7.7418 | 6.2462 |
| chrX  | 155270560 | 4380443 | 0.0282 | 0.2455 |
| chrY  | 59373566  | 388551  | 0.0065 | 0.114  |

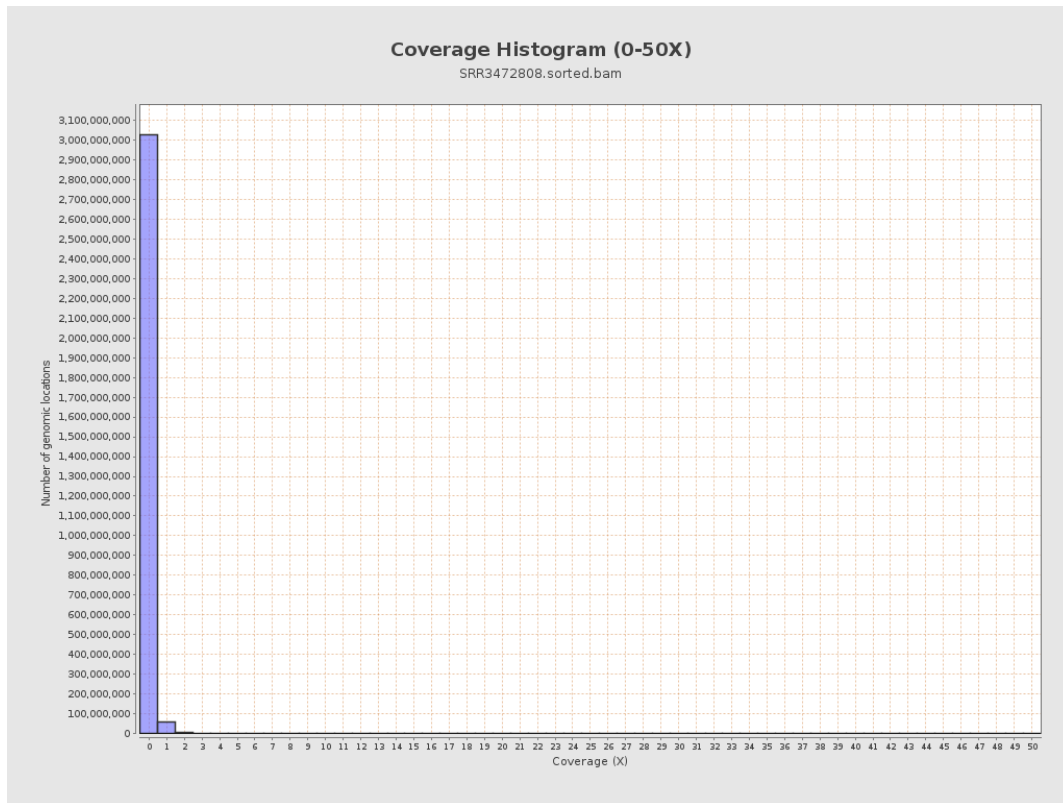
### 3. Results : Coverage across reference



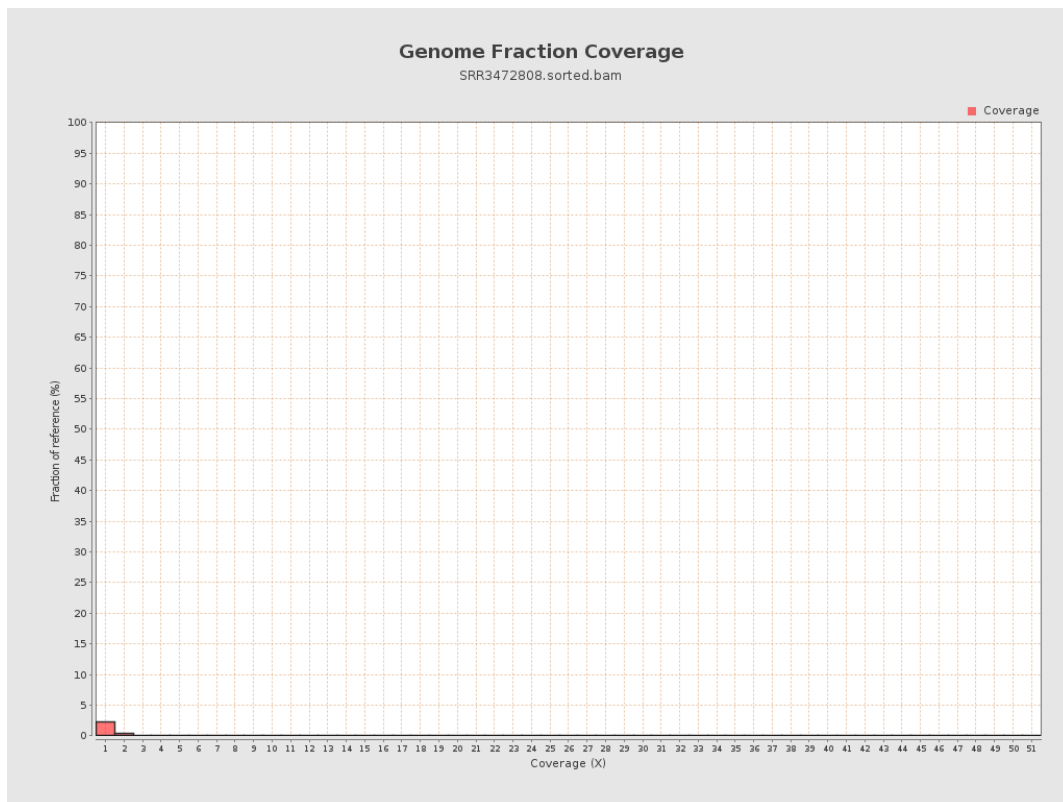
## 4. Results : Coverage Histogram



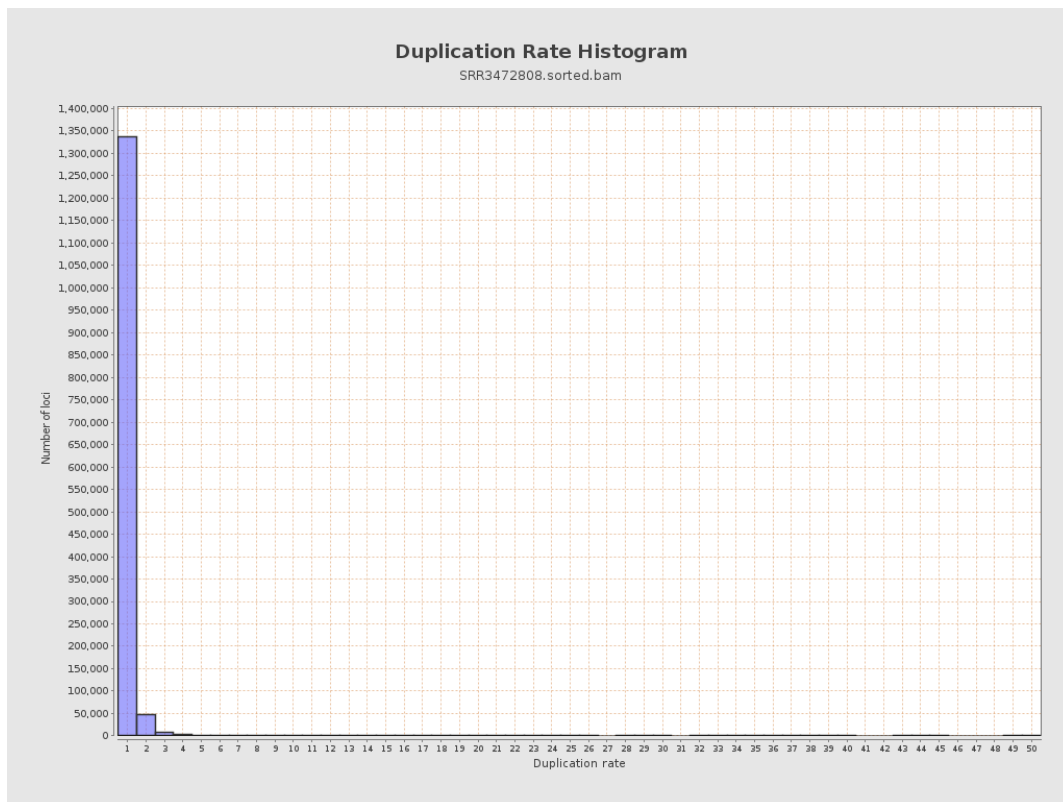
## 5. Results : Coverage Histogram (0-50X)



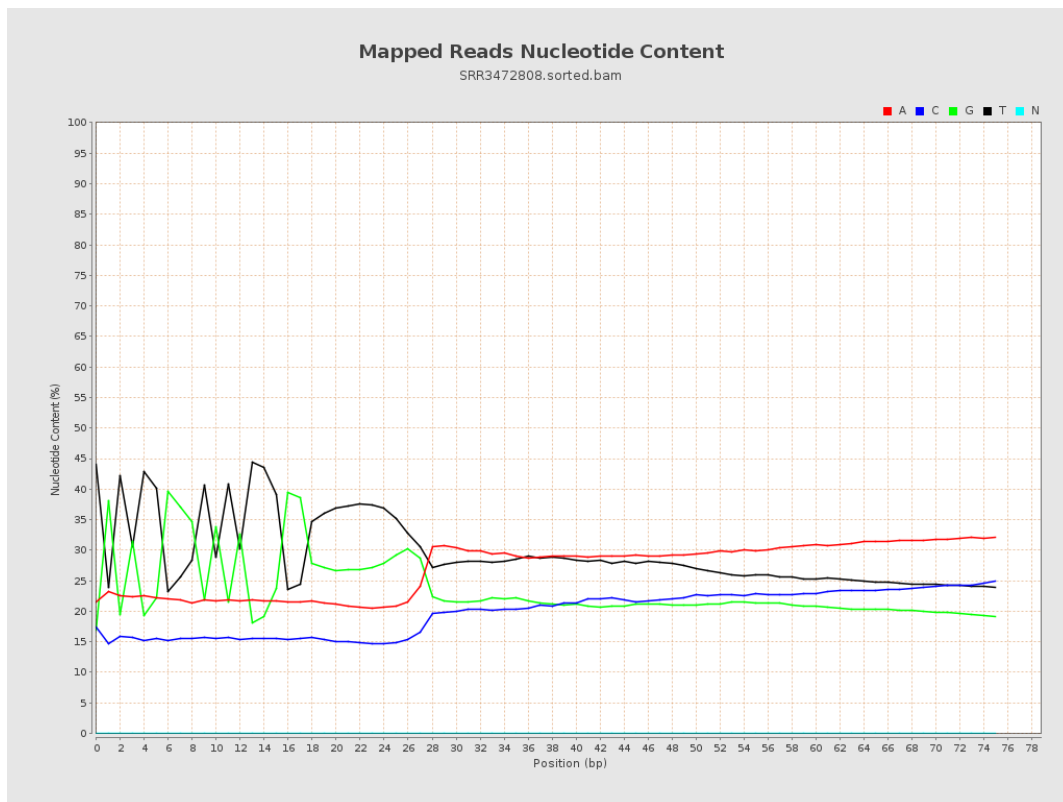
## 6. Results : Genome Fraction Coverage



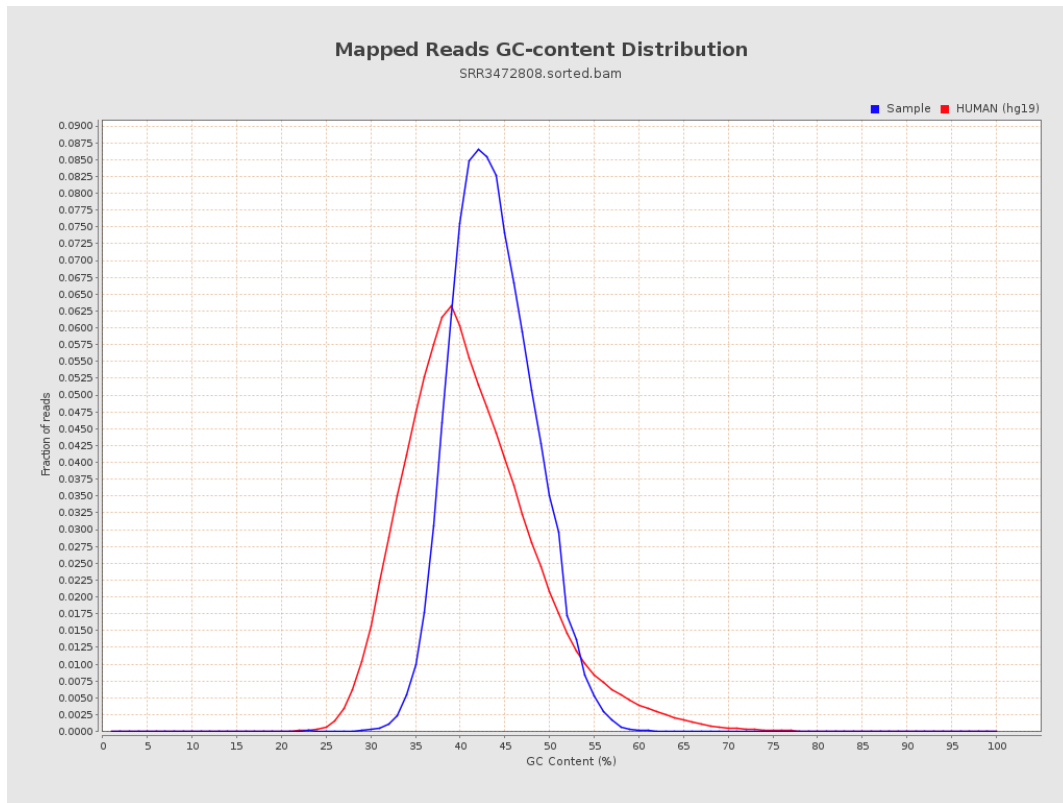
## 7. Results : Duplication Rate Histogram



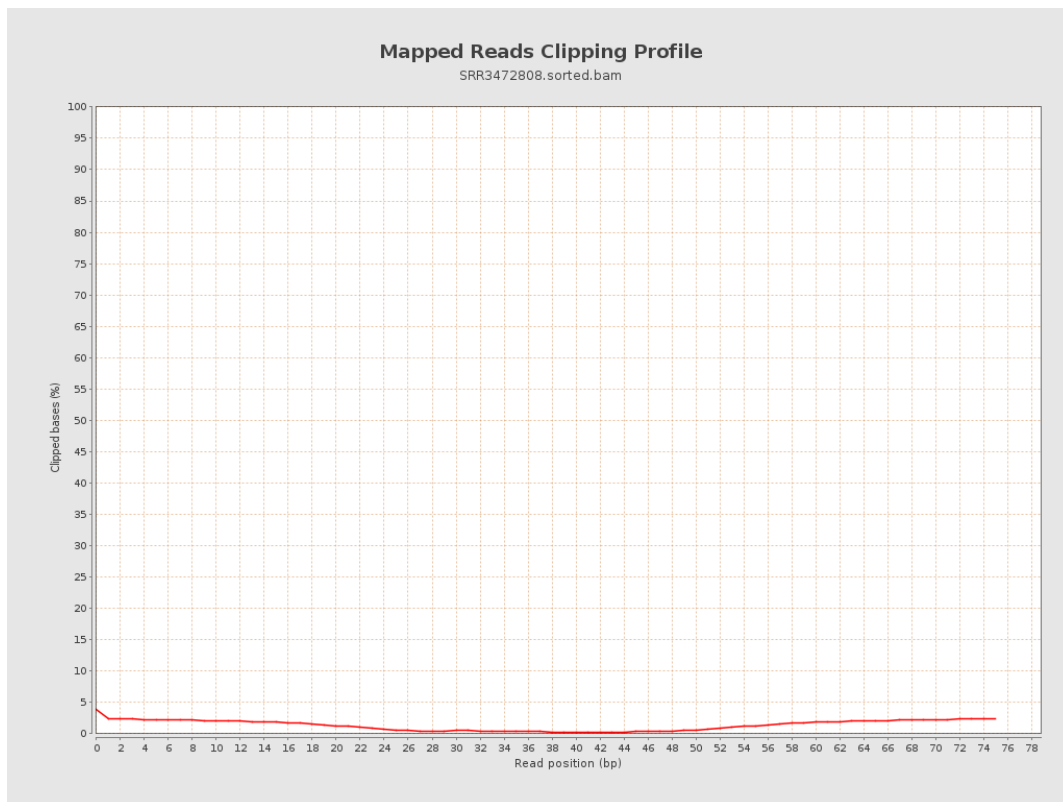
## 8. Results : Mapped Reads Nucleotide Content



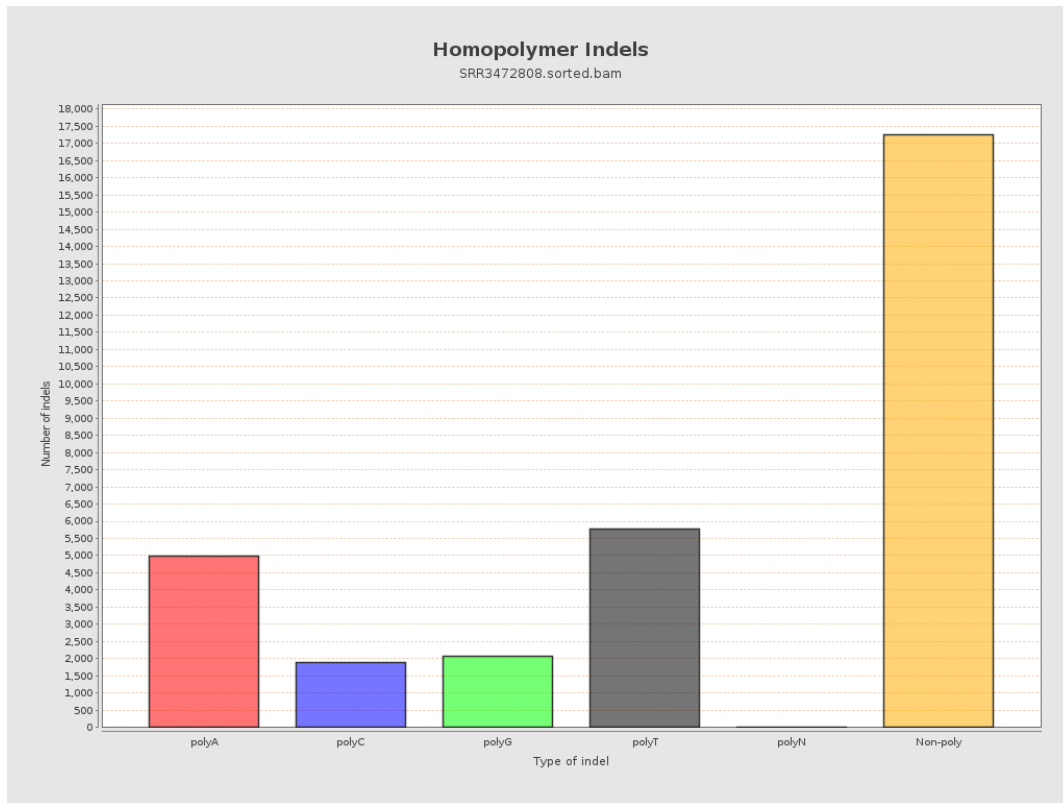
## 9. Results : Mapped Reads GC-content Distribution



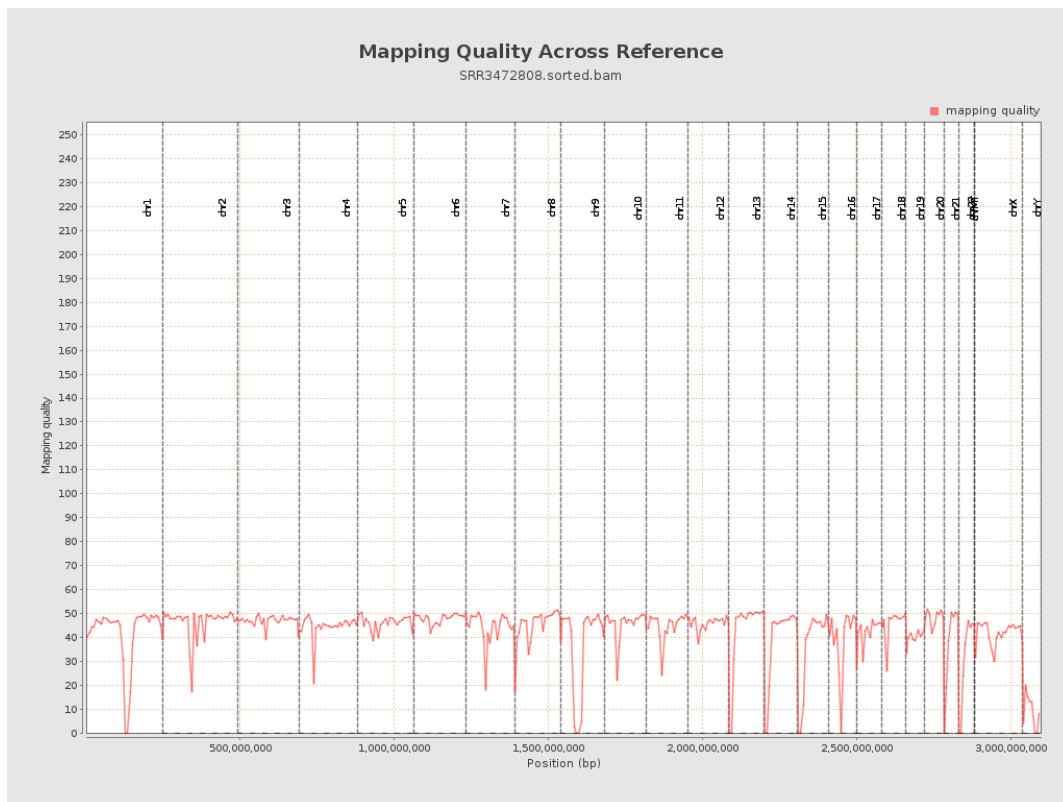
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

