

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 00:22:37*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549094.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_SRR1549094 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549094.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Sat Aug 24 00:22:36 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR1549094.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 8,359,423          |
| Mapped reads                 | 7,237,636 / 86.58% |
| Unmapped reads               | 1,121,787 / 13.42% |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Read min/max/mean length     | 40 / 40 / 40       |
| Duplicated reads (estimated) | 282,378 / 3.38%    |
| Duplication rate             | 2.45%              |
| Clipped reads                | 350,939 / 4.2%     |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 86,621,795 / 30.14% |
| Number/percentage of C's | 57,276,078 / 19.93% |
| Number/percentage of T's | 87,632,304 / 30.49% |
| Number/percentage of G's | 55,820,244 / 19.42% |
| Number/percentage of N's | 69,508 / 0.02%      |
| GC Percentage            | 39.35%              |

### 2.3. Coverage

|                    |        |
|--------------------|--------|
| Mean               | 0.0929 |
| Standard Deviation | 0.9189 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 43.61 |
|----------------------|-------|

## 2.5. Mismatches and indels

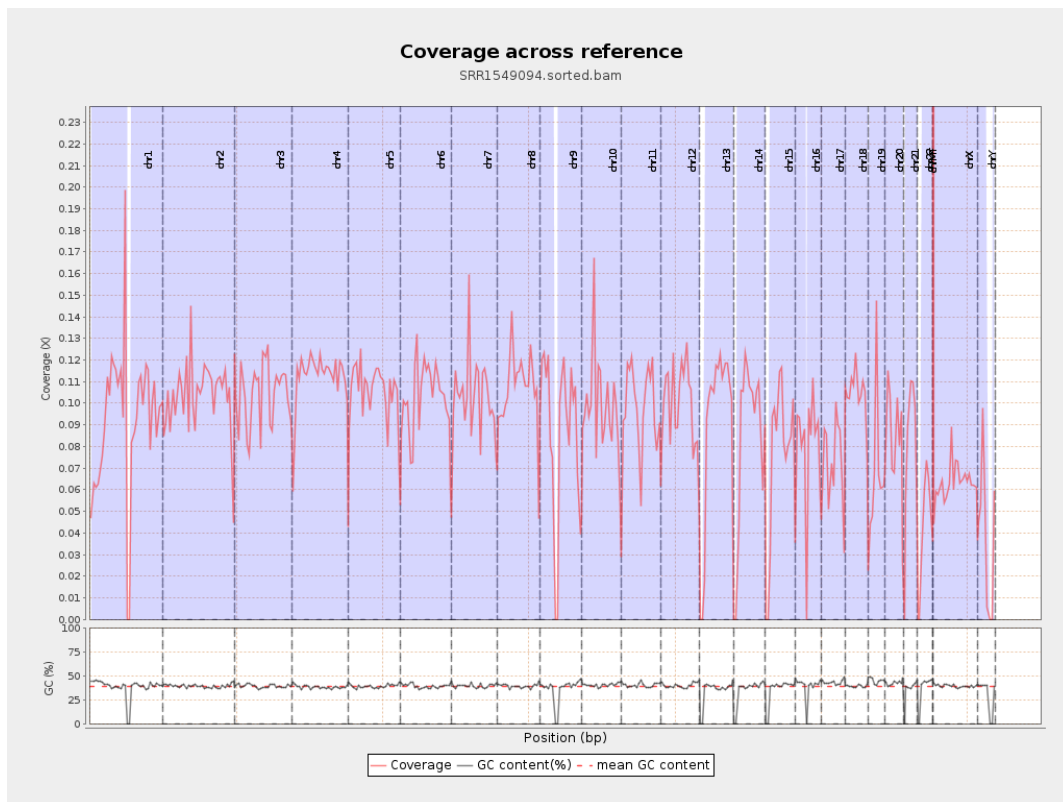
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.4%      |
| Mismatches                               | 1,150,778 |
| Insertions                               | 6,653     |
| Mapped reads with at least one insertion | 0.09%     |
| Deletions                                | 20,741    |
| Mapped reads with at least one deletion  | 0.29%     |
| Homopolymer indels                       | 45.05%    |

## 2.6. Chromosome stats

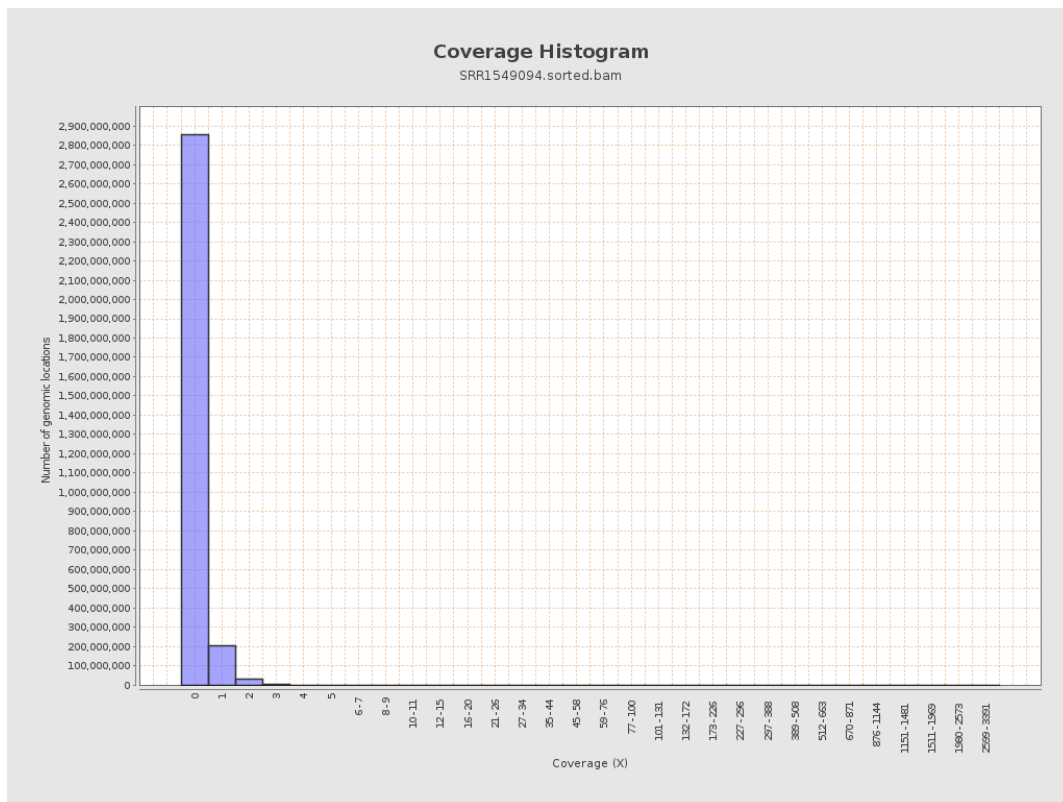
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 22934509     | 0.092         | 2.2471             |
| chr2 | 243199373 | 25207804     | 0.1037        | 0.6118             |
| chr3 | 198022430 | 20691418     | 0.1045        | 0.3811             |
| chr4 | 191154276 | 21505932     | 0.1125        | 0.3989             |
| chr5 | 180915260 | 18950366     | 0.1047        | 0.3913             |
| chr6 | 171115067 | 17695224     | 0.1034        | 0.4797             |
| chr7 | 159138663 | 16241324     | 0.1021        | 0.905              |
| chr8 | 146364022 | 15697551     | 0.1073        | 1.6223             |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr9  | 141213431 | 12356462 | 0.0875 | 0.6029 |
| chr10 | 135534747 | 13331355 | 0.0984 | 0.7484 |
| chr11 | 135006516 | 13196865 | 0.0977 | 0.5887 |
| chr12 | 133851895 | 13347396 | 0.0997 | 0.3957 |
| chr13 | 115169878 | 10486567 | 0.0911 | 0.3398 |
| chr14 | 107349540 | 9103495  | 0.0848 | 0.4124 |
| chr15 | 102531392 | 7677047  | 0.0749 | 0.3112 |
| chr16 | 90354753  | 7043941  | 0.078  | 0.4386 |
| chr17 | 81195210  | 5989518  | 0.0738 | 0.3897 |
| chr18 | 78077248  | 8233815  | 0.1055 | 1.2433 |
| chr19 | 59128983  | 4049259  | 0.0685 | 1.7623 |
| chr20 | 63025520  | 5471508  | 0.0868 | 0.3554 |
| chr21 | 48129895  | 3813828  | 0.0792 | 0.3872 |
| chr22 | 51304566  | 2218262  | 0.0432 | 0.2906 |
| chrMT | 16571     | 39833    | 2.4038 | 2.9964 |
| chrX  | 155270560 | 9815343  | 0.0632 | 0.3971 |
| chrY  | 59373566  | 2347318  | 0.0395 | 0.3407 |

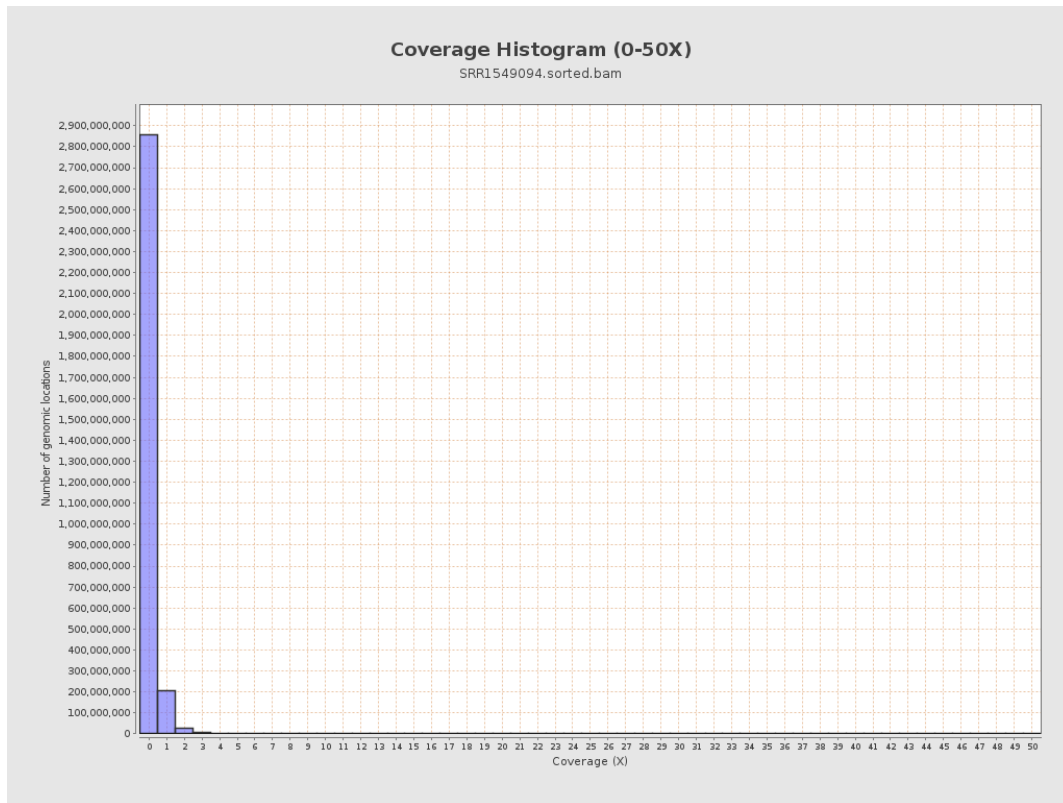
### 3. Results : Coverage across reference



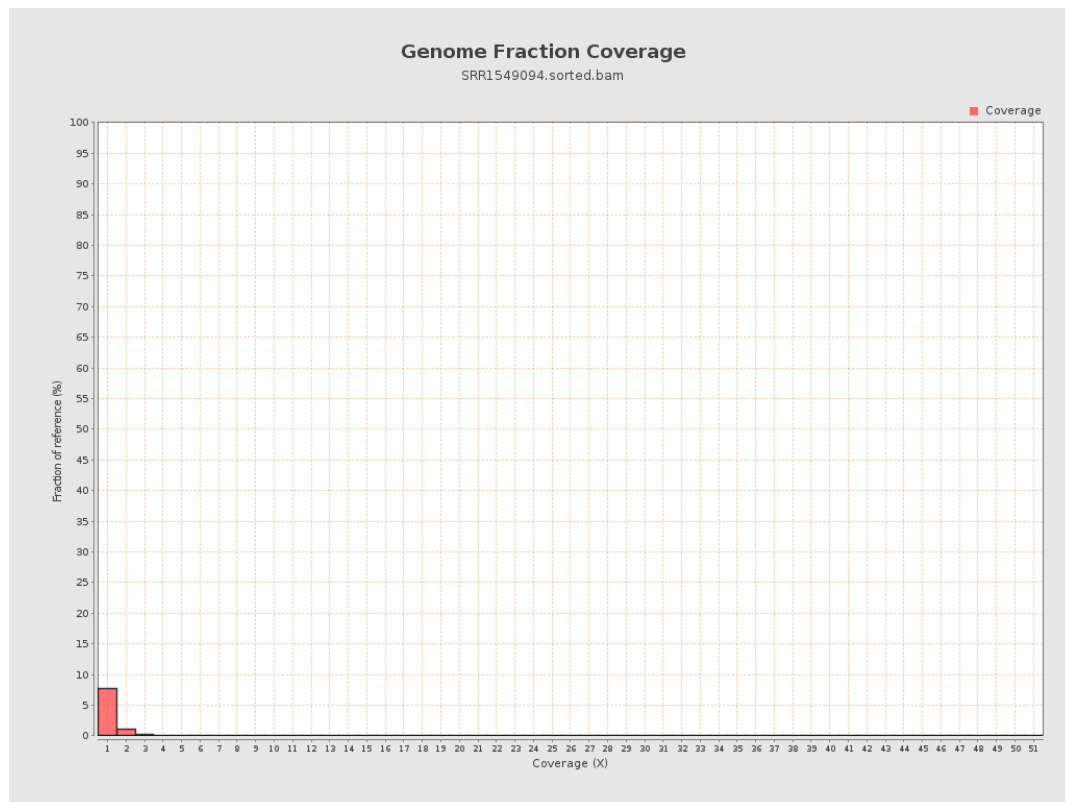
## 4. Results : Coverage Histogram



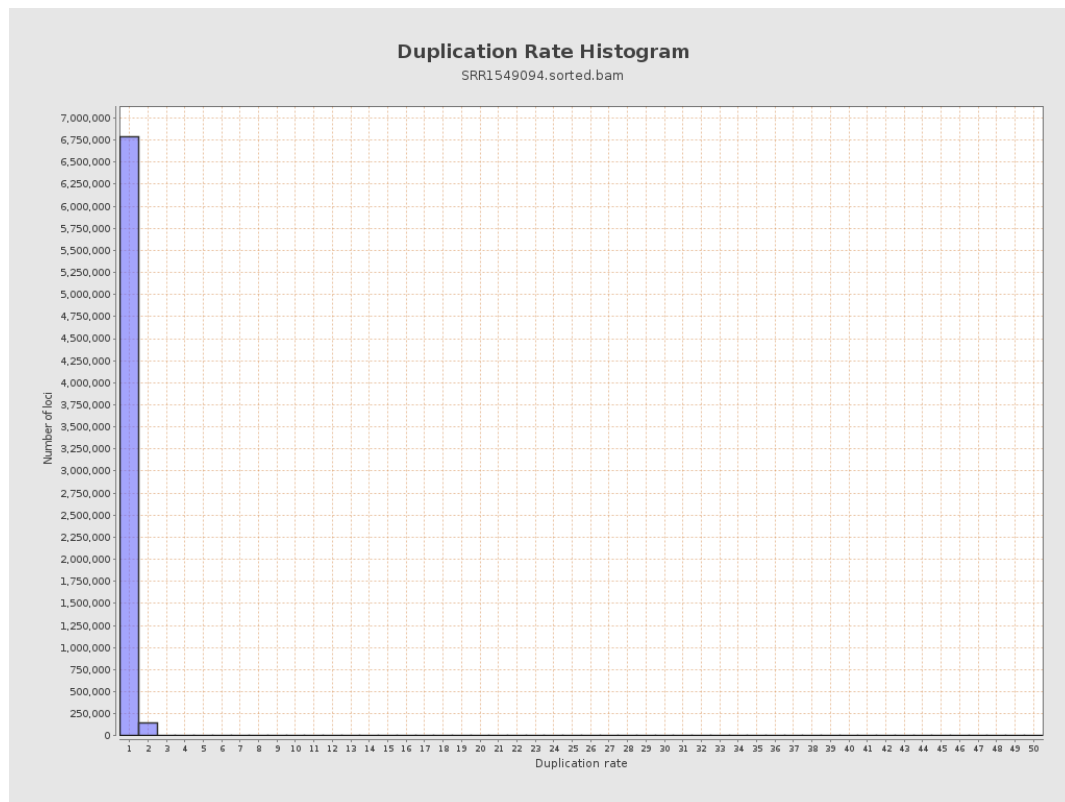
## 5. Results : Coverage Histogram (0-50X)



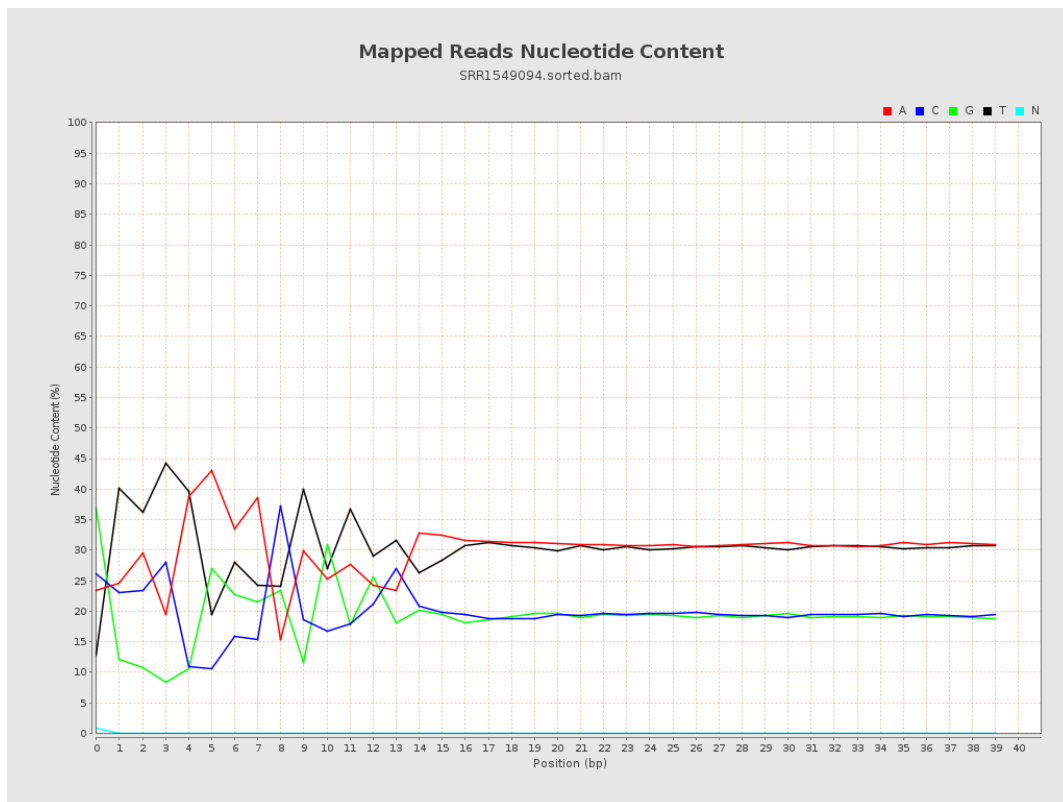
## 6. Results : Genome Fraction Coverage



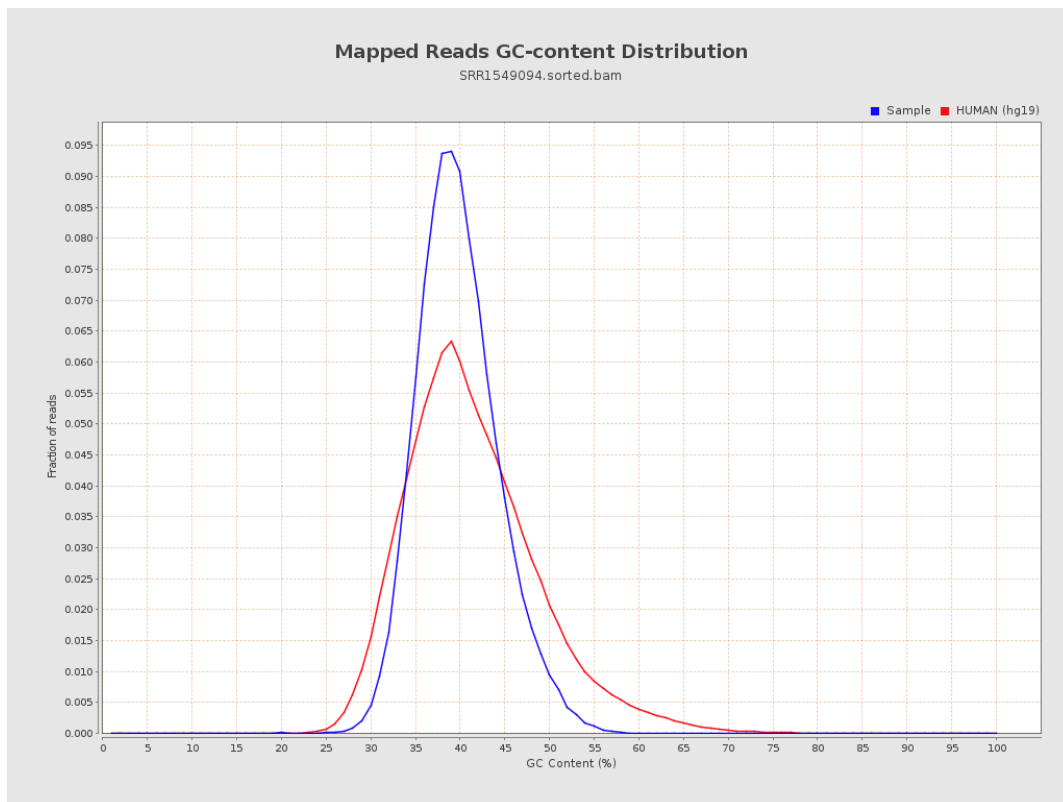
## 7. Results : Duplication Rate Histogram



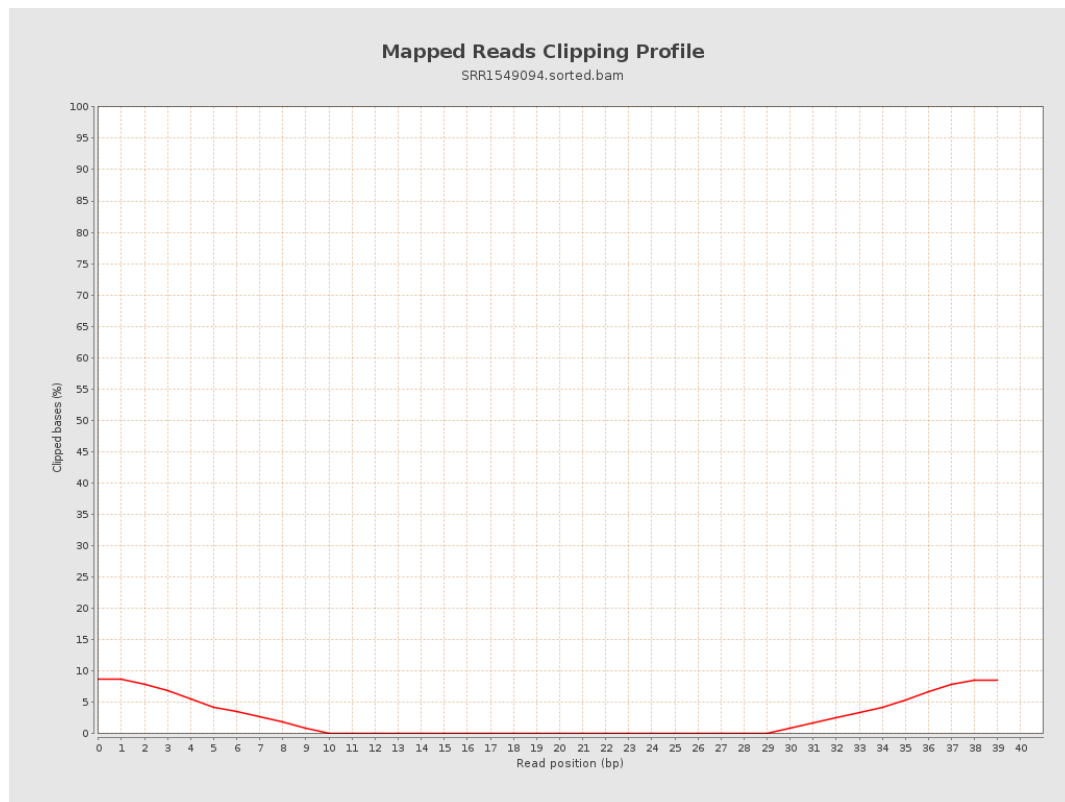
## 8. Results : Mapped Reads Nucleotide Content



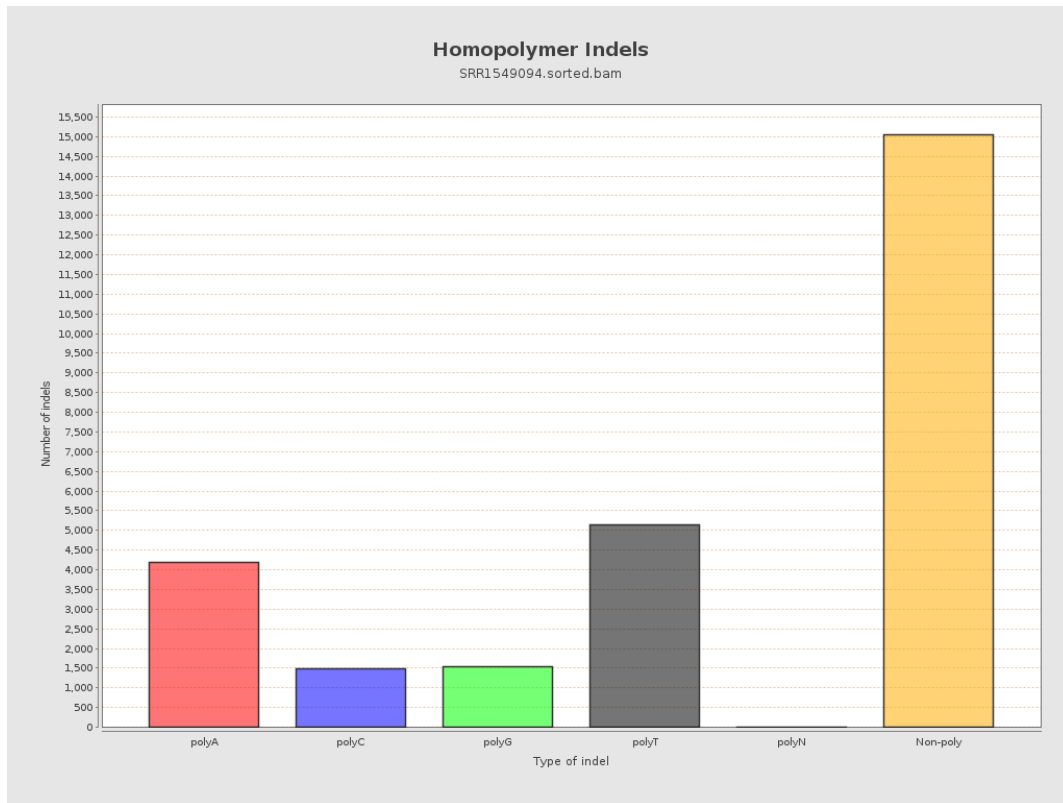
## 9. Results : Mapped Reads GC-content Distribution



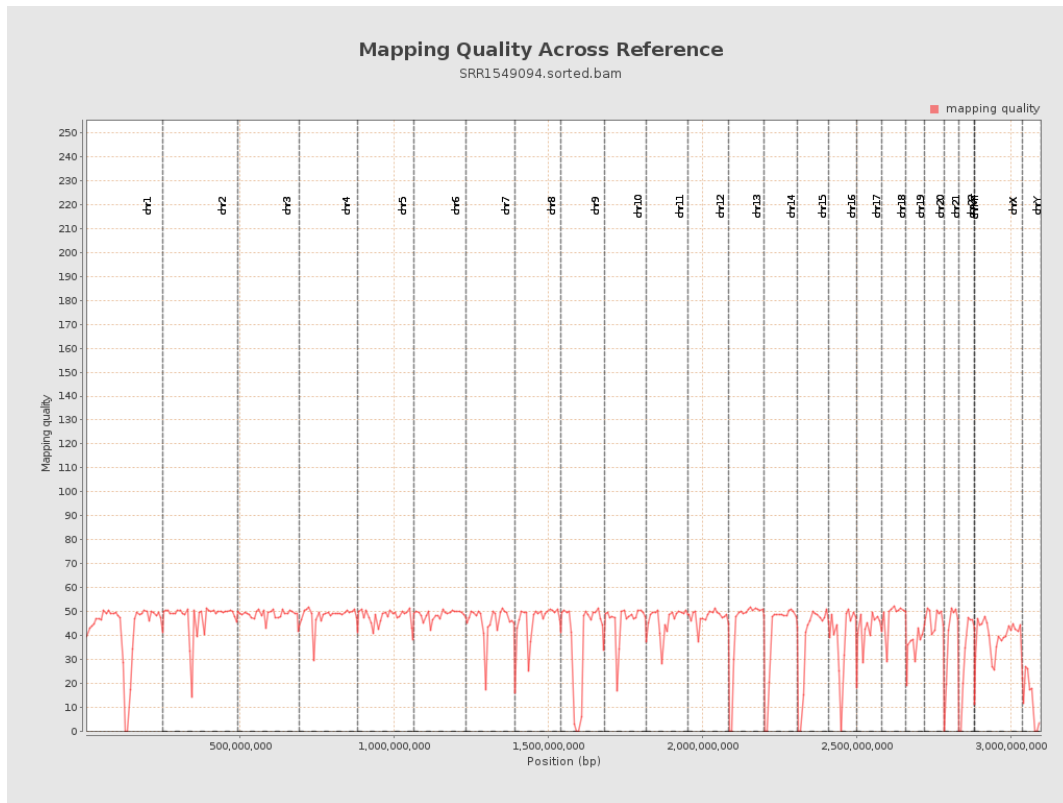
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

