# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/25 09:07:49*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084274.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_SRR3084274 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084274.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Aug 25 09:07:48 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3084274.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,116,350 |
| Mapped reads | 2,103,287 / 67.49% |
| Unmapped reads | 1,013,063 / 32.51% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 13,148 / 0.42% |
| Read min/max/mean length | 30 / 76 / 76.15 |
| Duplicated reads (estimated) | 80,829 / 2.59% |
| Duplication rate | 3.22% |
| Clipped reads | 1,198,333 / 38.45% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 37,147,853 / 28.06% |
| Number/percentage of C's | 25,329,651 / 19.13% |
| Number/percentage of T's | 40,330,331 / 30.47% |
| Number/percentage of G's | 29,566,918 / 22.34% |
| Number/percentage of N's | 1,456 / 0% |
| GC Percentage | 41.47% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0428 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2991 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.74 |

## 2.5. Mismatches and indels

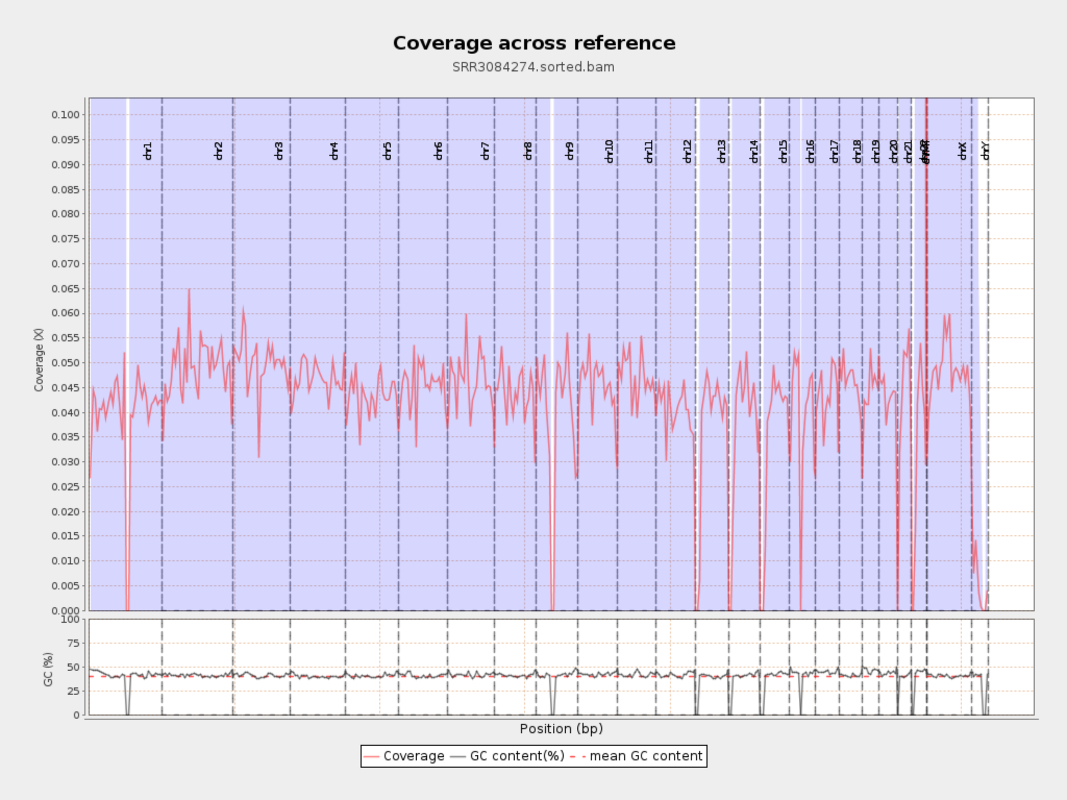
| | |
|---|---|
| General error rate | 0.83% |
| Mismatches | 1,080,055 |
| Insertions | 9,434 |
| Mapped reads with at least one insertion | 0.45% |
| Deletions | 26,740 |
| Mapped reads with at least one deletion | 1.26% |
| Homopolymer indels | 46.46% |

## 2.6. Chromosome stats

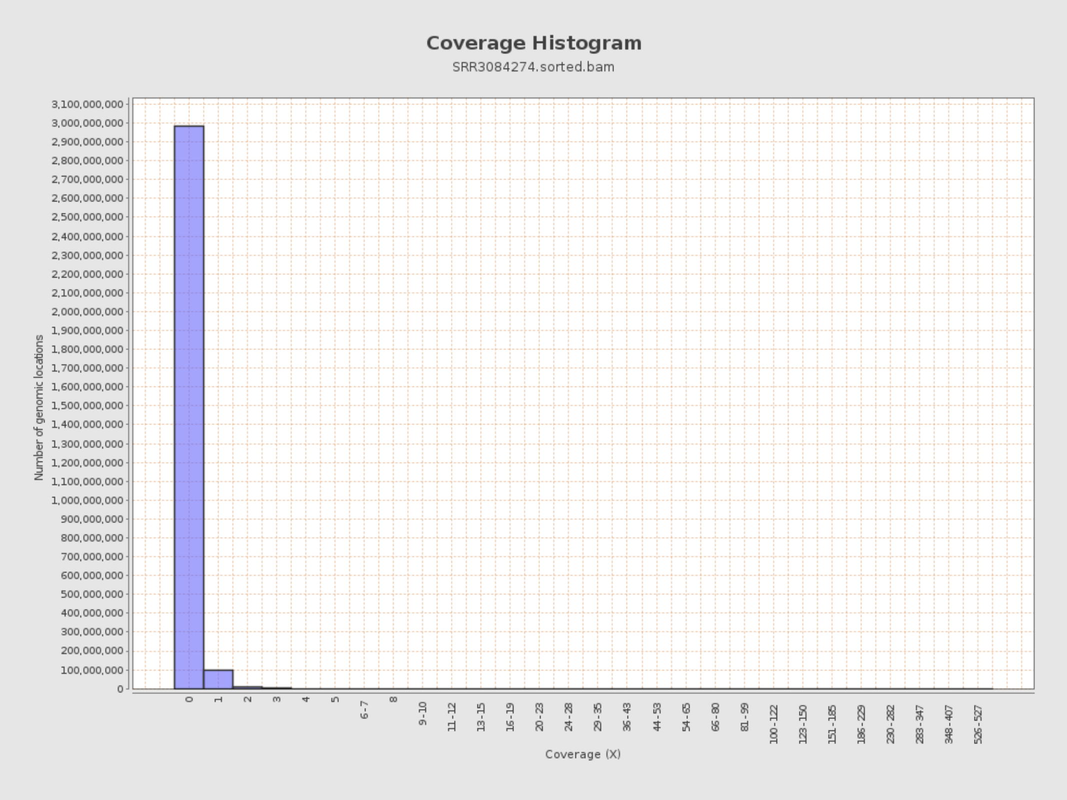
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 9824718 | 0.0394 | 0.4072 |
| chr2 | 243199373 | 11916521 | 0.049 | 0.3987 |
| chr3 | 198022430 | 9892475 | 0.05 | 0.2525 |
| chr4 | 191154276 | 8930132 | 0.0467 | 0.2495 |
| chr5 | 180915260 | 7837025 | 0.0433 | 0.2355 |
| chr6 | 171115067 | 7737961 | 0.0452 | 0.2674 |
| chr7 | 159138663 | 7437114 | 0.0467 | 0.3459 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6424472 | 0.0439 | 0.2996 |
| chr9 | 141213431 | 5498725 | 0.0389 | 0.2891 |
| chr10 | 135534747 | 6230720 | 0.046 | 0.293 |
| chr11 | 135006516 | 6356538 | 0.0471 | 0.2887 |
| chr12 | 133851895 | 5419318 | 0.0405 | 0.2299 |
| chr13 | 115169878 | 4095531 | 0.0356 | 0.2142 |
| chr14 | 107349540 | 3907531 | 0.0364 | 0.227 |
| chr15 | 102531392 | 3536391 | 0.0345 | 0.2172 |
| chr16 | 90354753 | 3561170 | 0.0394 | 0.241 |
| chr17 | 81195210 | 3502068 | 0.0431 | 0.2606 |
| chr18 | 78077248 | 3625128 | 0.0464 | 0.5266 |
| chr19 | 59128983 | 2632853 | 0.0445 | 0.343 |
| chr20 | 63025520 | 2694209 | 0.0427 | 0.2376 |
| chr21 | 48129895 | 1975308 | 0.041 | 0.2352 |
| chr22 | 51304566 | 1575420 | 0.0307 | 0.1978 |
| chrMT | 16571 | 58923 | 3.5558 | 2.677 |
| chrX | 155270560 | 7436707 | 0.0479 | 0.2757 |
| chrY | 59373566 | 312010 | 0.0053 | 0.1054 |

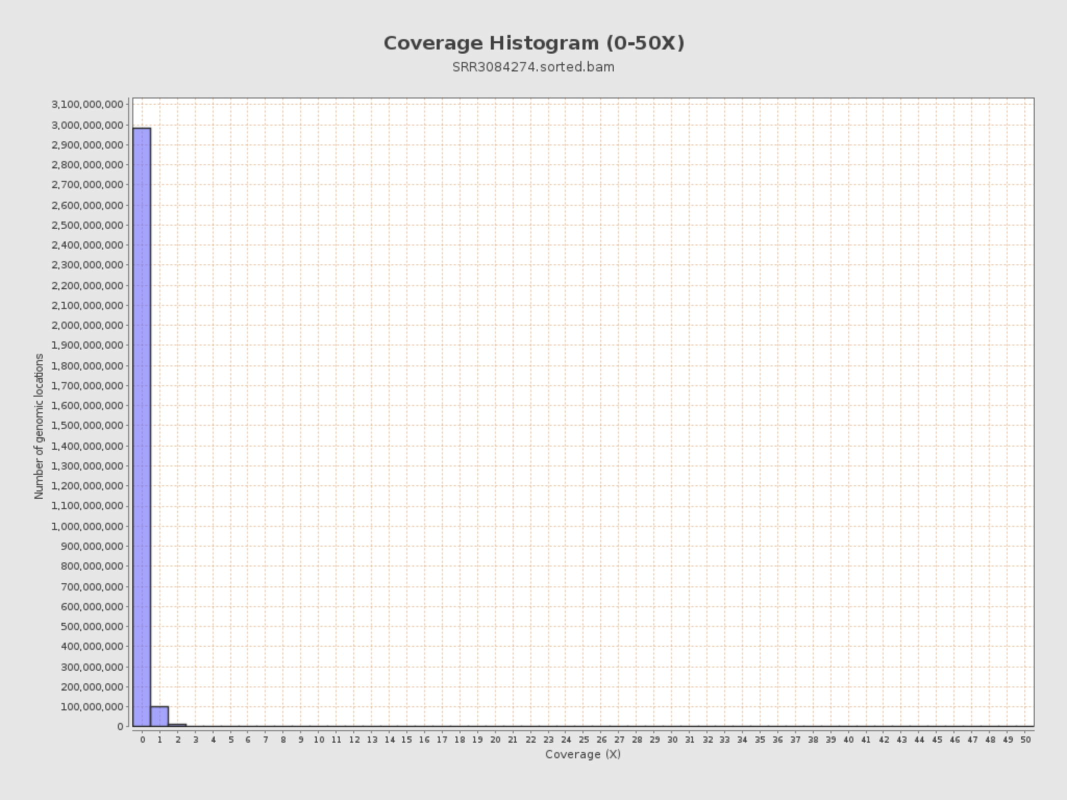
# 3. Results : Coverage across reference



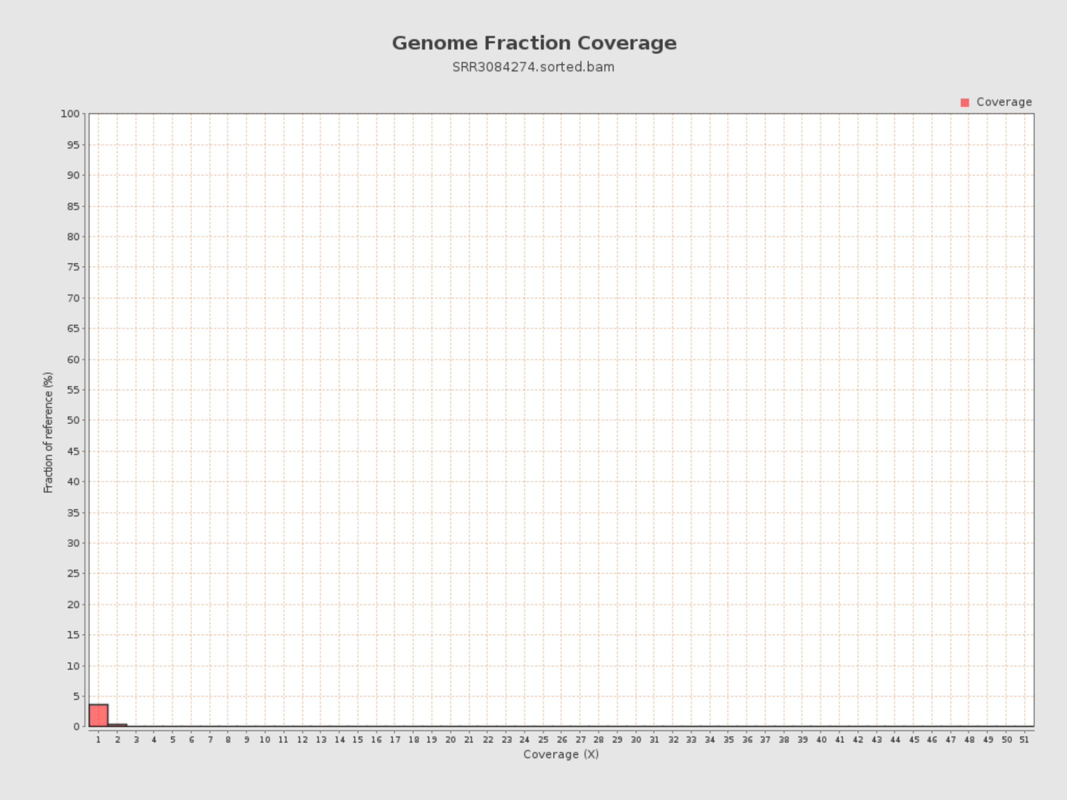
# 4. Results : Coverage Histogram



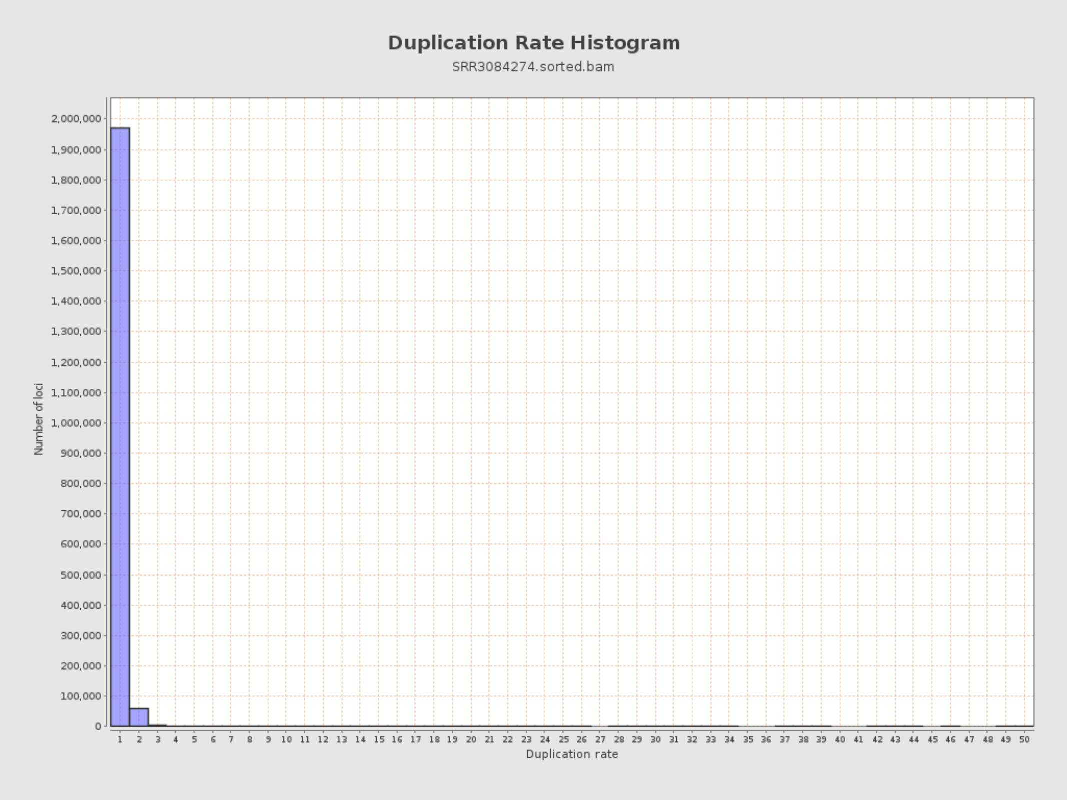
# 5. Results : Coverage Histogram (0-50X)



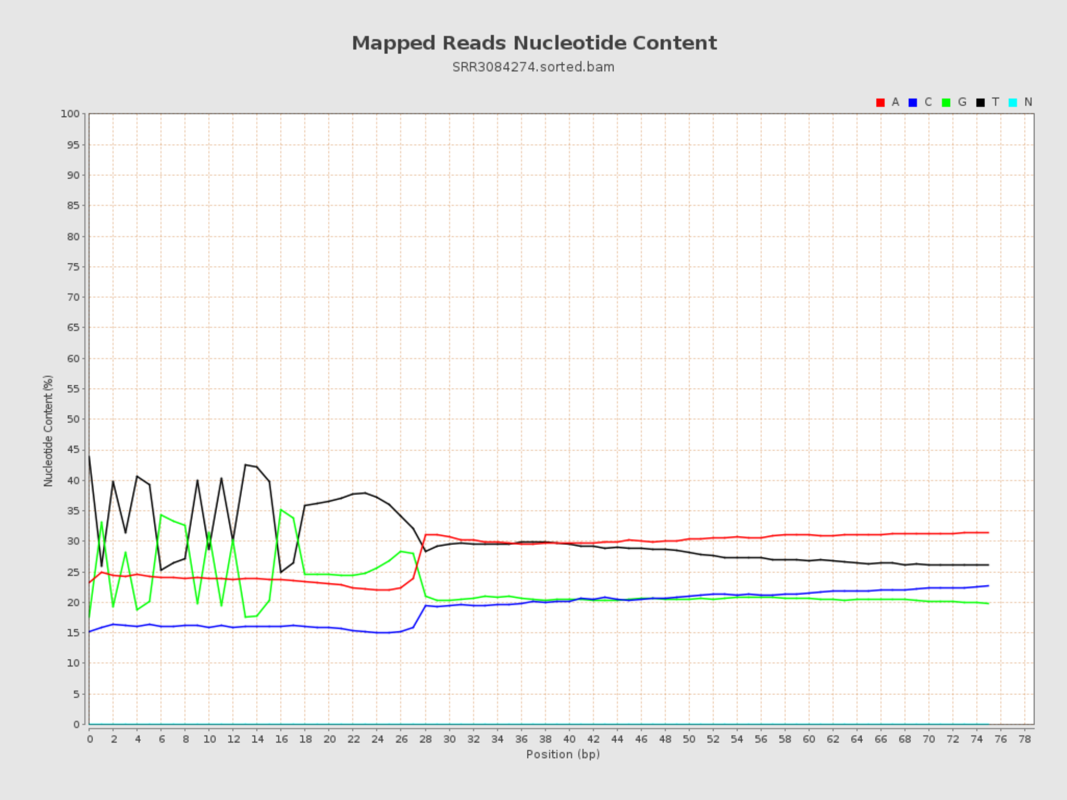
# 6. Results : Genome Fraction Coverage



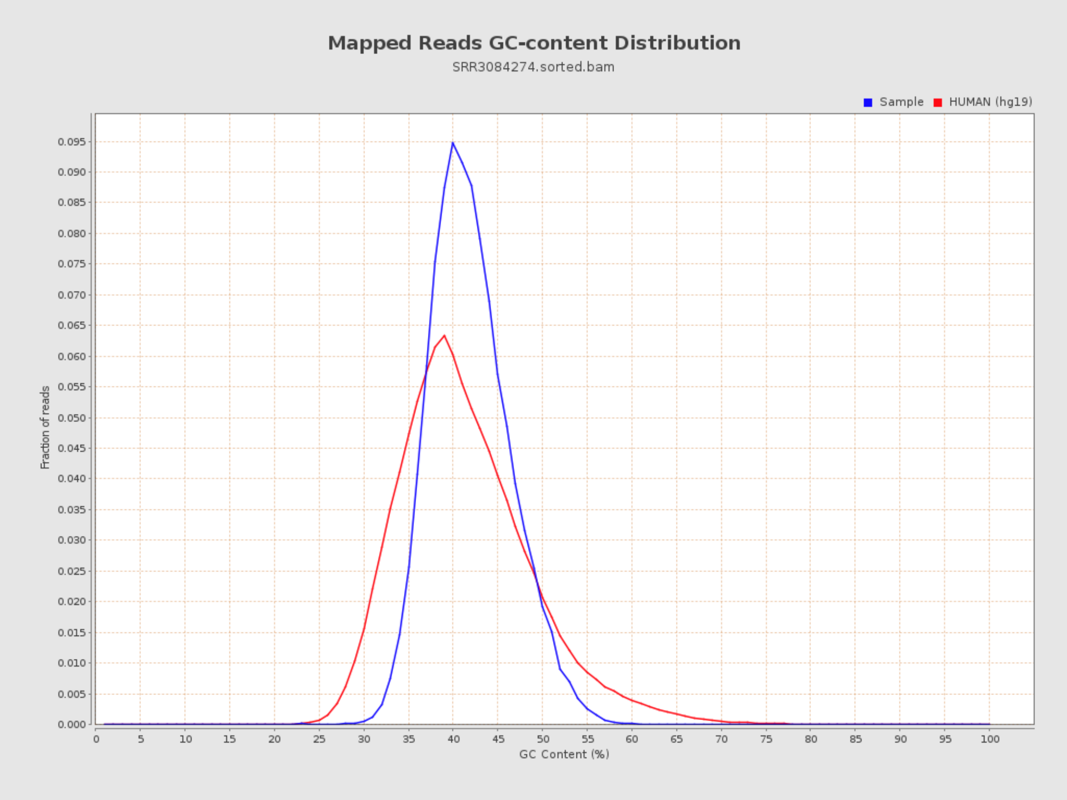
# 7. Results : Duplication Rate Histogram



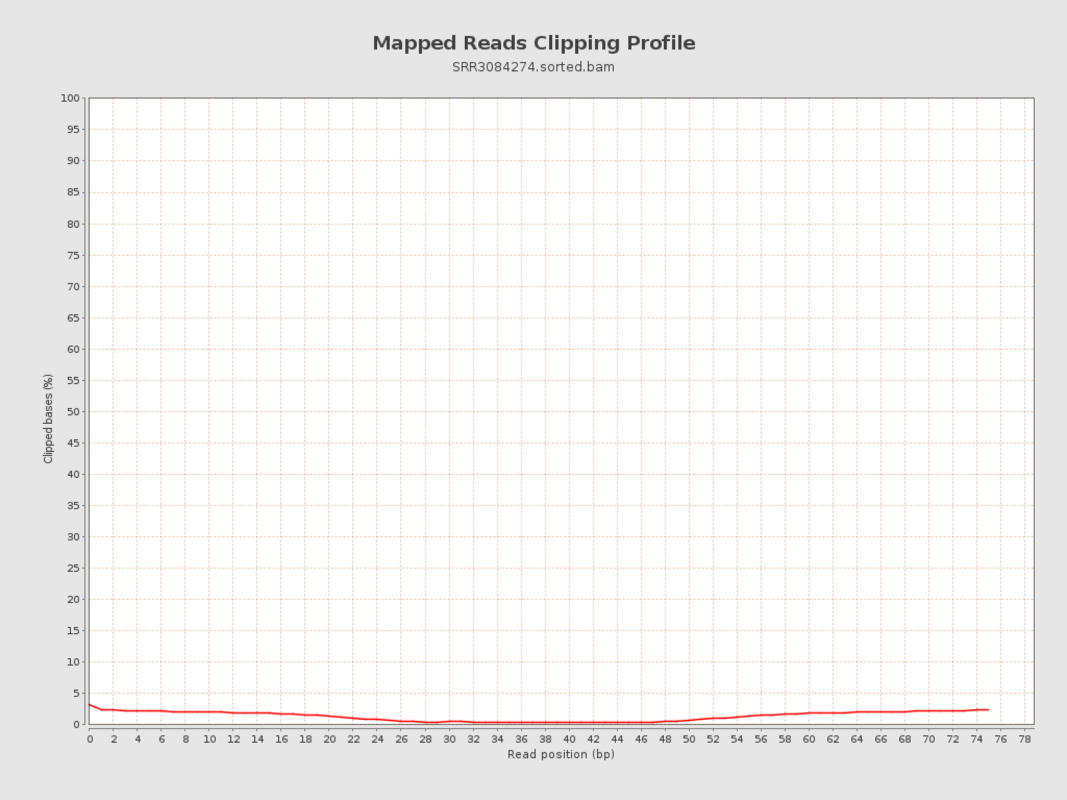
# 8. Results : Mapped Reads Nucleotide Content



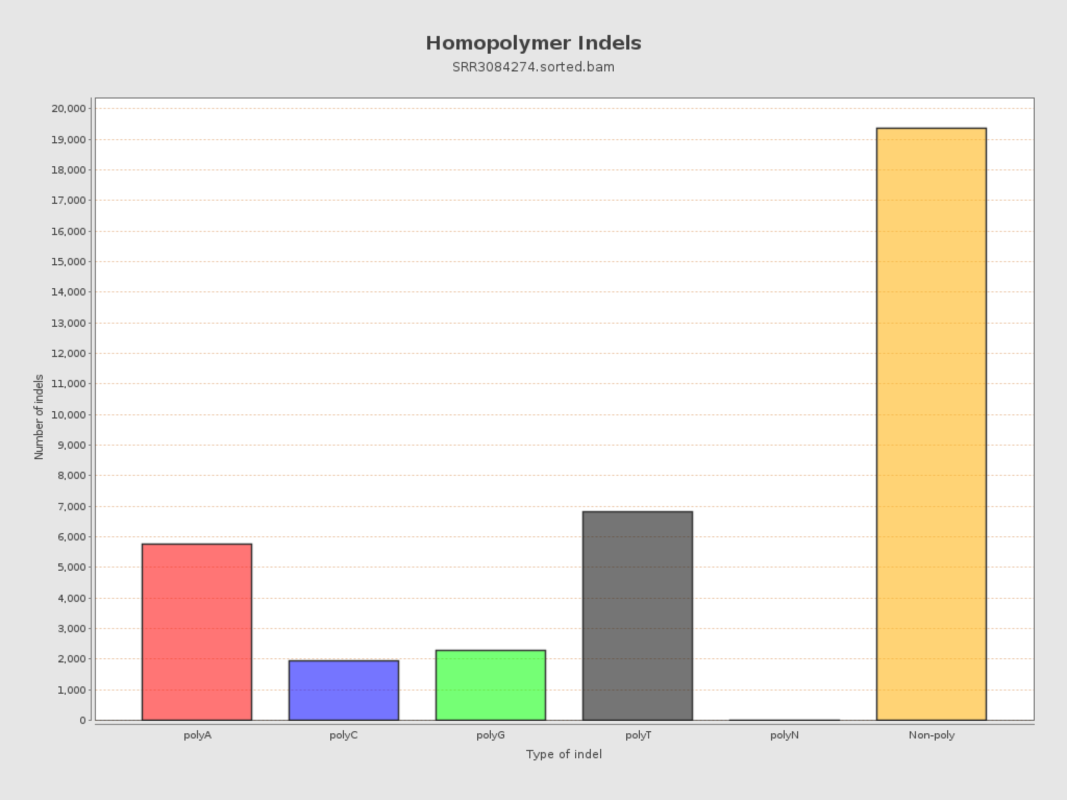
# 9. Results : Mapped Reads GC-content Distribution



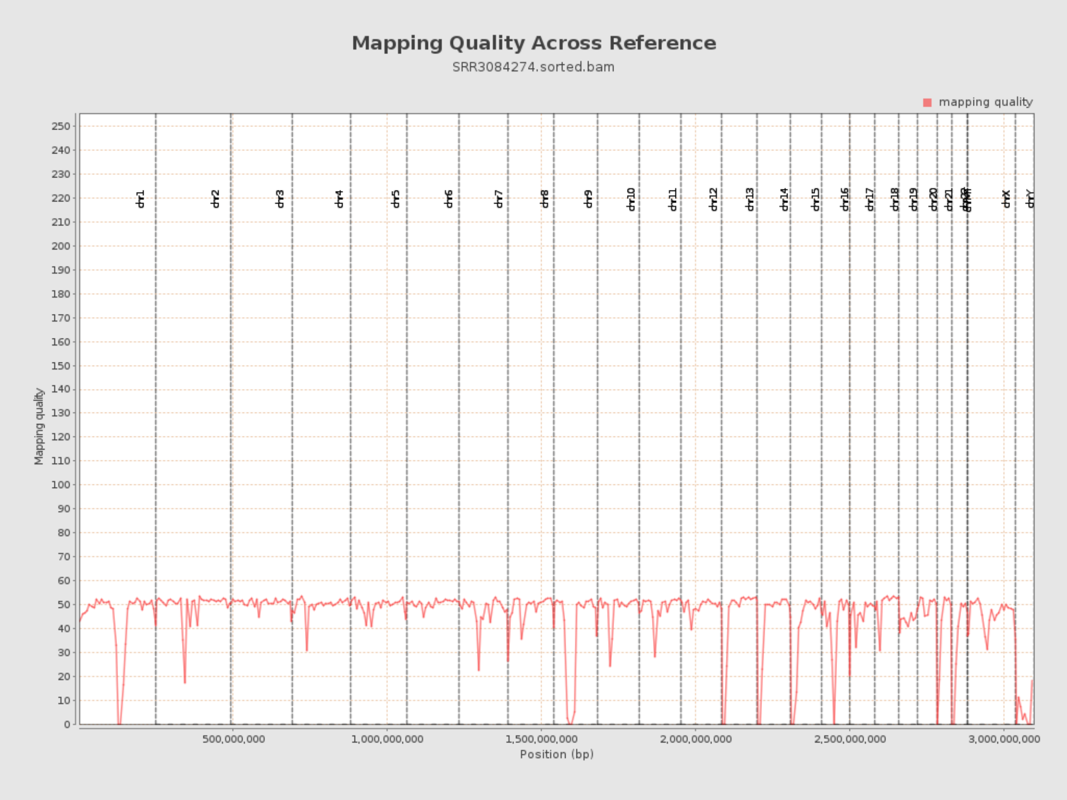
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram