# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 15:04:04*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082444.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_SRR3082444 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082444.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Aug 24 15:04:02 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3082444.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,736,716 |
| Mapped reads | 2,499,066 / 91.32% |
| Unmapped reads | 237,650 / 8.68% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 22,253 / 0.81% |
| Read min/max/mean length | 30 / 76 / 76.28 |
| Duplicated reads (estimated) | 84,420 / 3.08% |
| Duplication rate | 2.4% |
| Clipped reads | 897,707 / 32.8% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 51,159,907 / 29.55% |
| Number/percentage of C's | 32,183,143 / 18.59% |
| Number/percentage of T's | 53,544,740 / 30.92% |
| Number/percentage of G's | 36,254,660 / 20.94% |
| Number/percentage of N's | 3,813 / 0% |
| GC Percentage | 39.53% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.056 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4983 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 47.31 |

## 2.5. Mismatches and indels

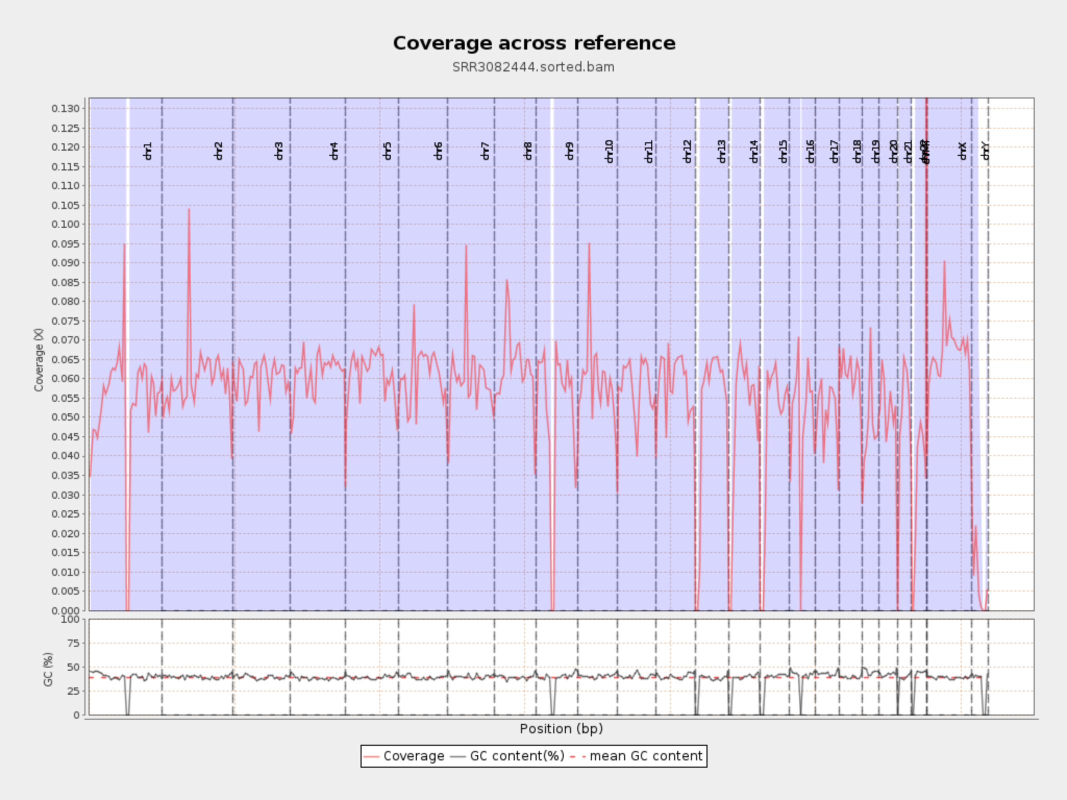
| | |
|---|---|
| General error rate | 0.85% |
| Mismatches | 1,446,945 |
| Insertions | 13,968 |
| Mapped reads with at least one insertion | 0.55% |
| Deletions | 39,820 |
| Mapped reads with at least one deletion | 1.57% |
| Homopolymer indels | 47.57% |

## 2.6. Chromosome stats

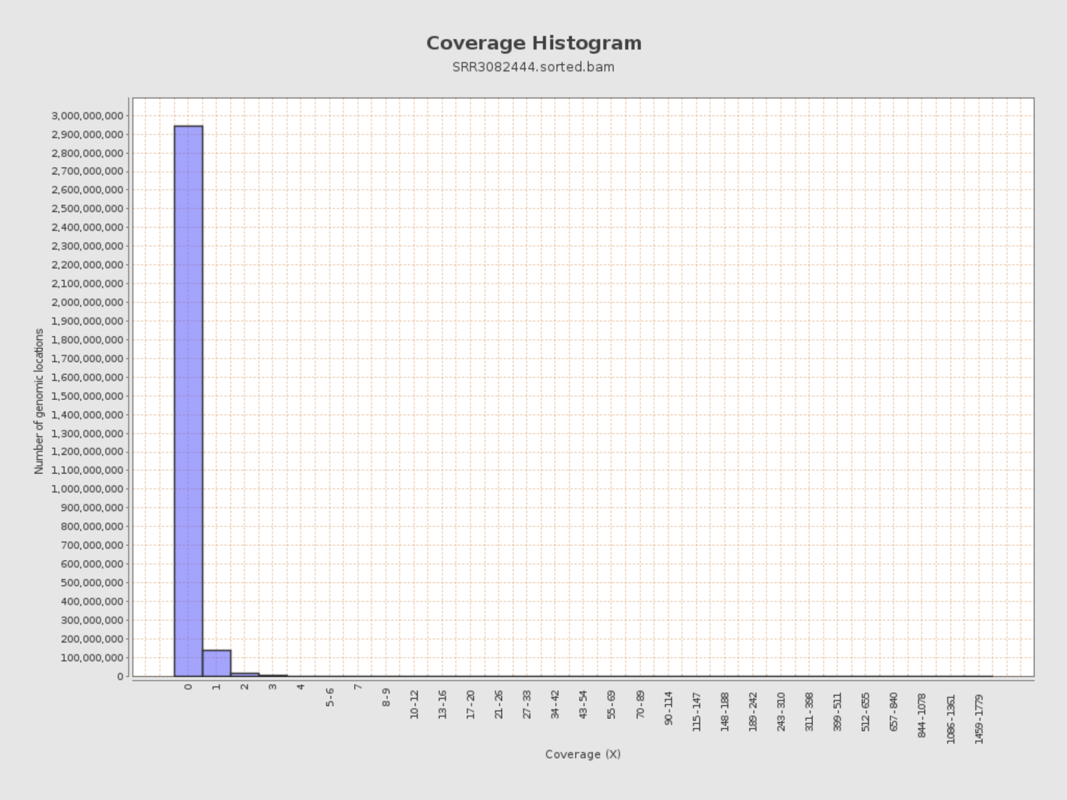
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 13398566 | 0.0538 | 0.8764 |
| chr2 | 243199373 | 14618852 | 0.0601 | 0.5048 |
| chr3 | 198022430 | 11941142 | 0.0603 | 0.2705 |
| chr4 | 191154276 | 11740951 | 0.0614 | 0.2851 |
| chr5 | 180915260 | 11099959 | 0.0614 | 0.2734 |
| chr6 | 171115067 | 10403616 | 0.0608 | 0.3329 |
| chr7 | 159138663 | 9658642 | 0.0607 | 0.6112 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 9211377 | 0.0629 | 1.1076 |
| chr9 | 141213431 | 7296845 | 0.0517 | 0.4095 |
| chr10 | 135534747 | 8103321 | 0.0598 | 0.4443 |
| chr11 | 135006516 | 7774028 | 0.0576 | 0.376 |
| chr12 | 133851895 | 7875619 | 0.0588 | 0.2722 |
| chr13 | 115169878 | 5836307 | 0.0507 | 0.2448 |
| chr14 | 107349540 | 5267042 | 0.0491 | 0.2664 |
| chr15 | 102531392 | 4794769 | 0.0468 | 0.2388 |
| chr16 | 90354753 | 4509547 | 0.0499 | 0.2903 |
| chr17 | 81195210 | 4094198 | 0.0504 | 0.2884 |
| chr18 | 78077248 | 4795866 | 0.0614 | 0.749 |
| chr19 | 59128983 | 2839648 | 0.048 | 0.6986 |
| chr20 | 63025520 | 3288267 | 0.0522 | 0.259 |
| chr21 | 48129895 | 2334002 | 0.0485 | 0.2609 |
| chr22 | 51304566 | 1578206 | 0.0308 | 0.19 |
| chrMT | 16571 | 9824 | 0.5928 | 0.8313 |
| chrX | 155270560 | 10322918 | 0.0665 | 0.3194 |
| chrY | 59373566 | 418065 | 0.007 | 0.1596 |

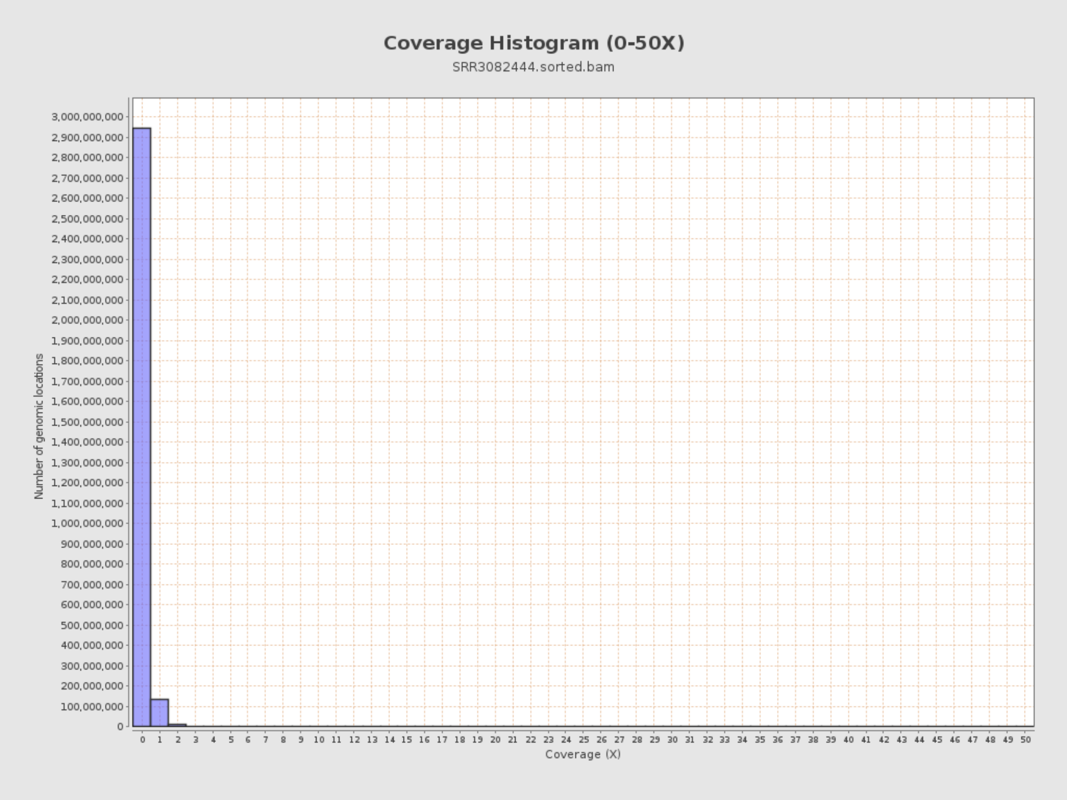
# 3. Results : Coverage across reference



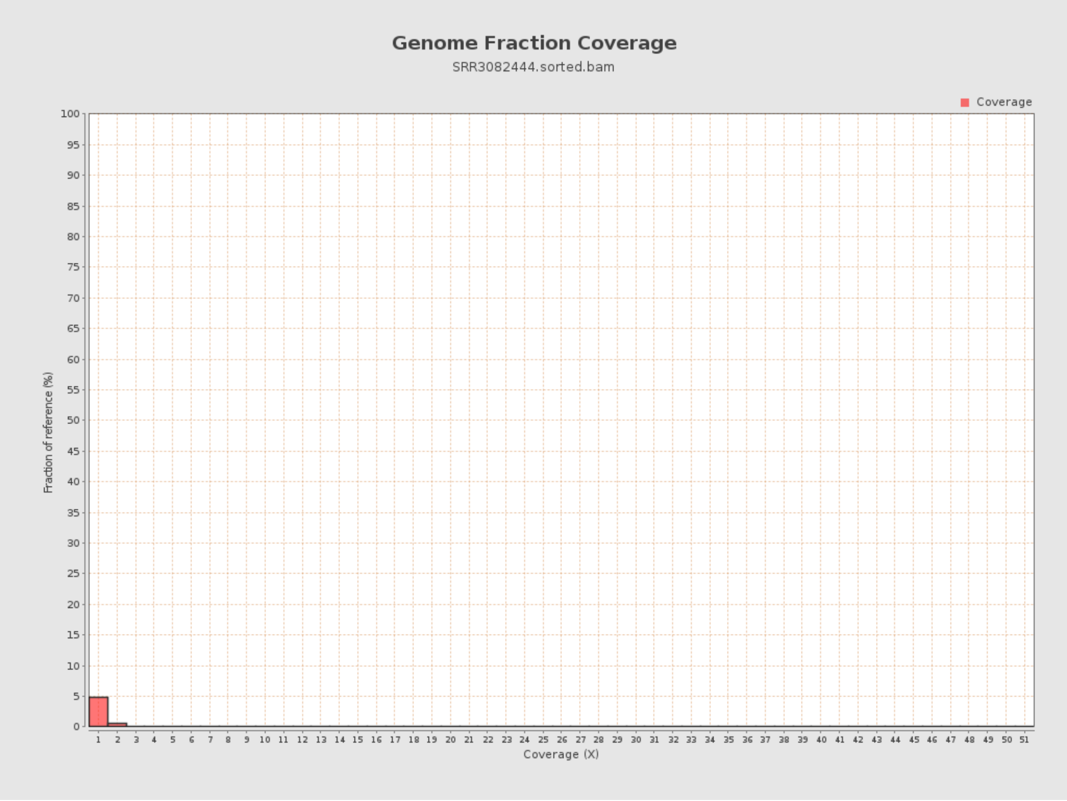
# 4. Results : Coverage Histogram



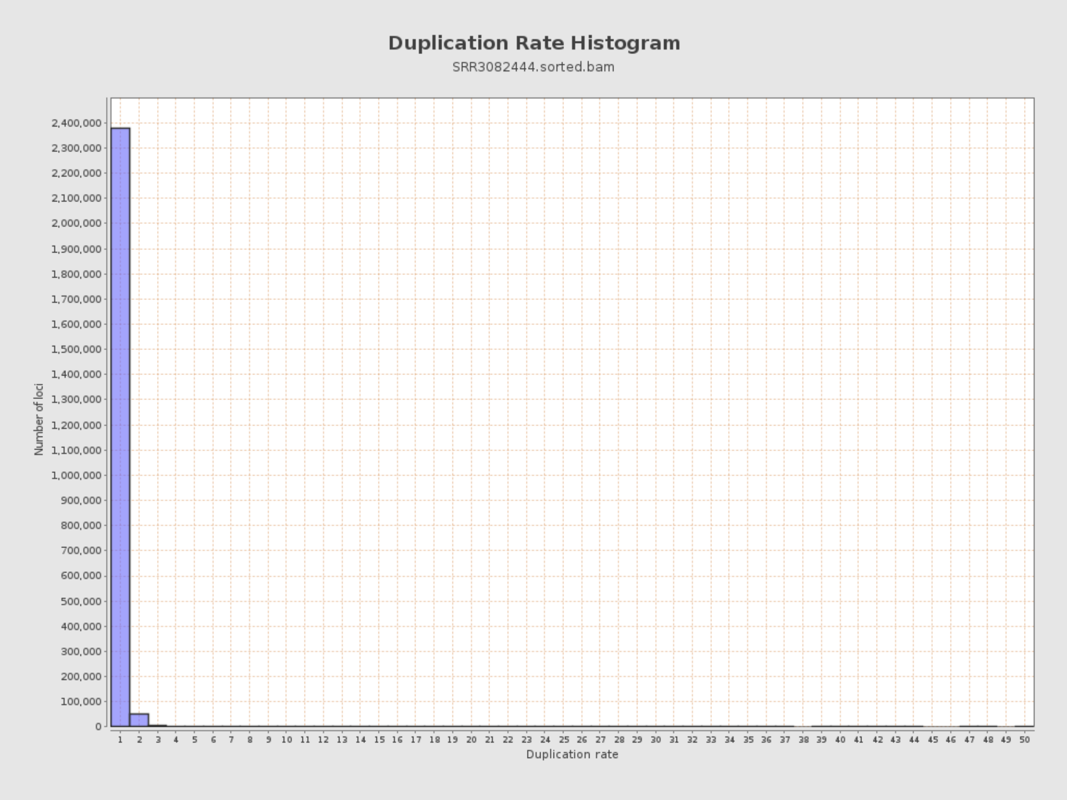
# 5. Results : Coverage Histogram (0-50X)



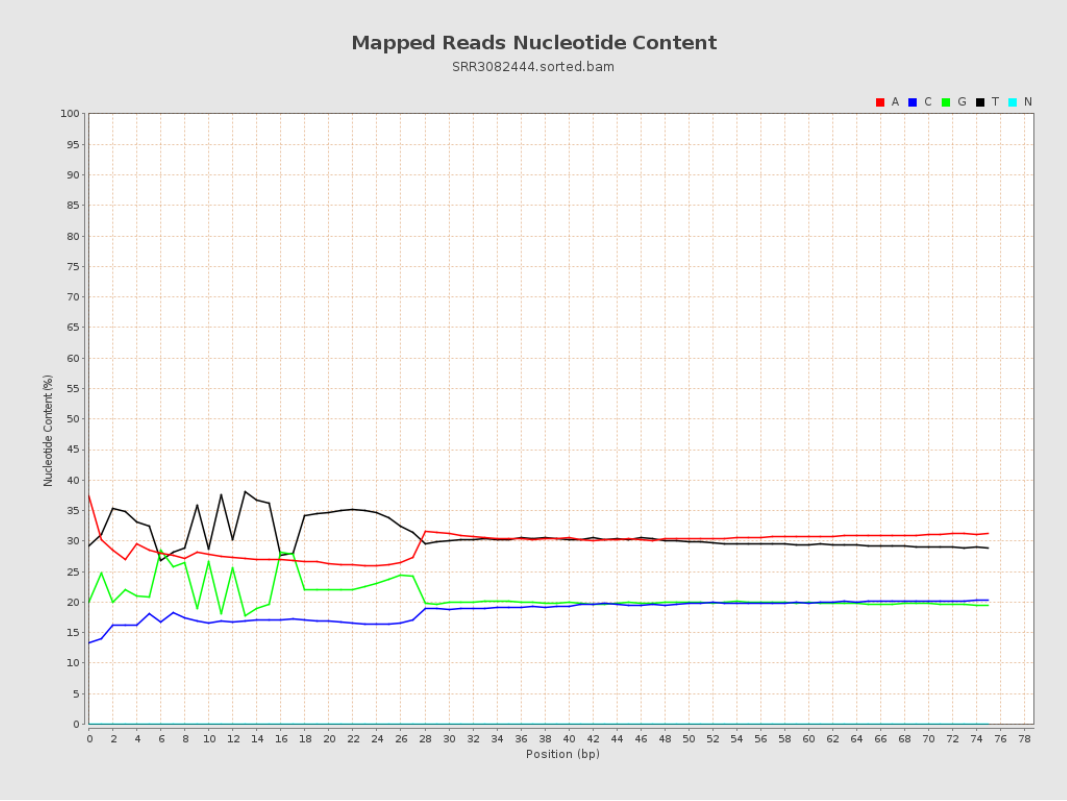
# 6. Results : Genome Fraction Coverage



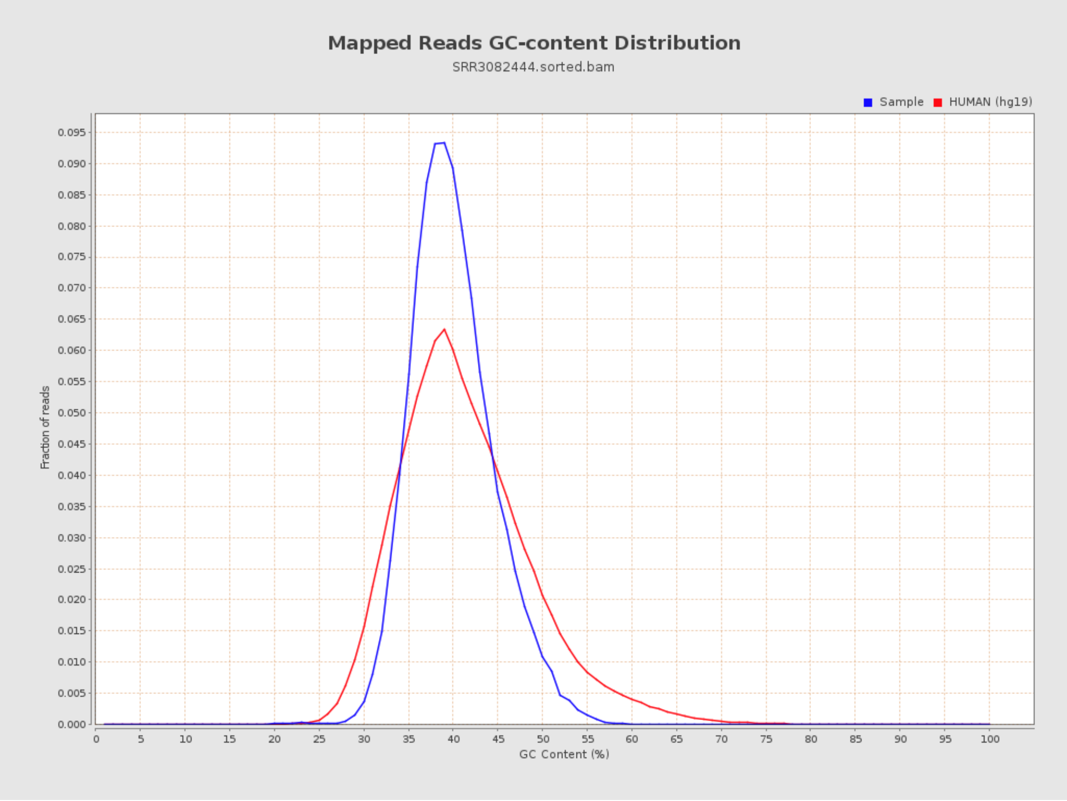
# 7. Results : Duplication Rate Histogram



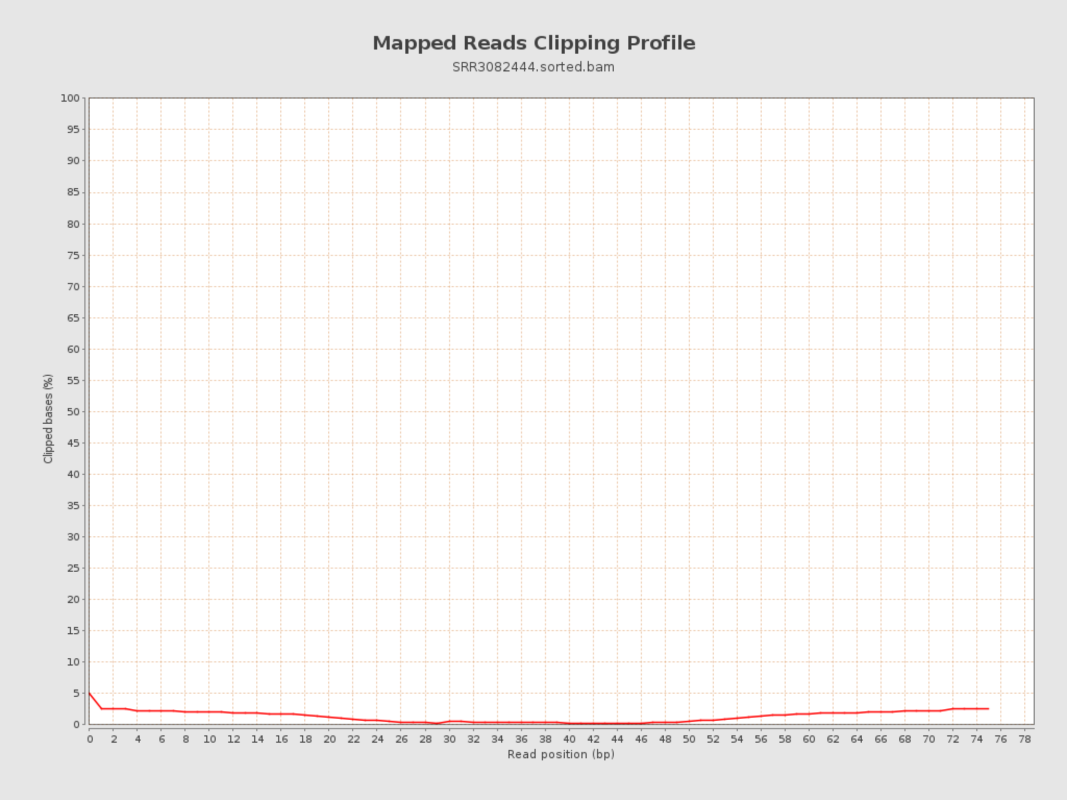
# 8. Results : Mapped Reads Nucleotide Content



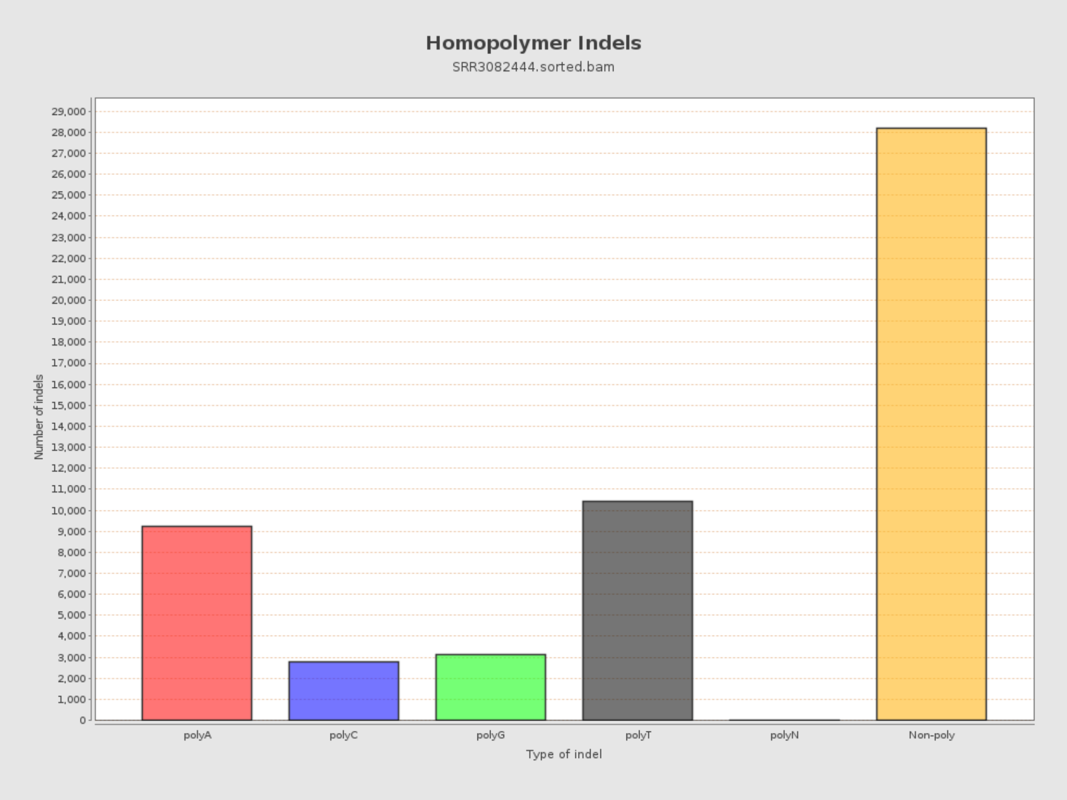
# 9. Results : Mapped Reads GC-content Distribution



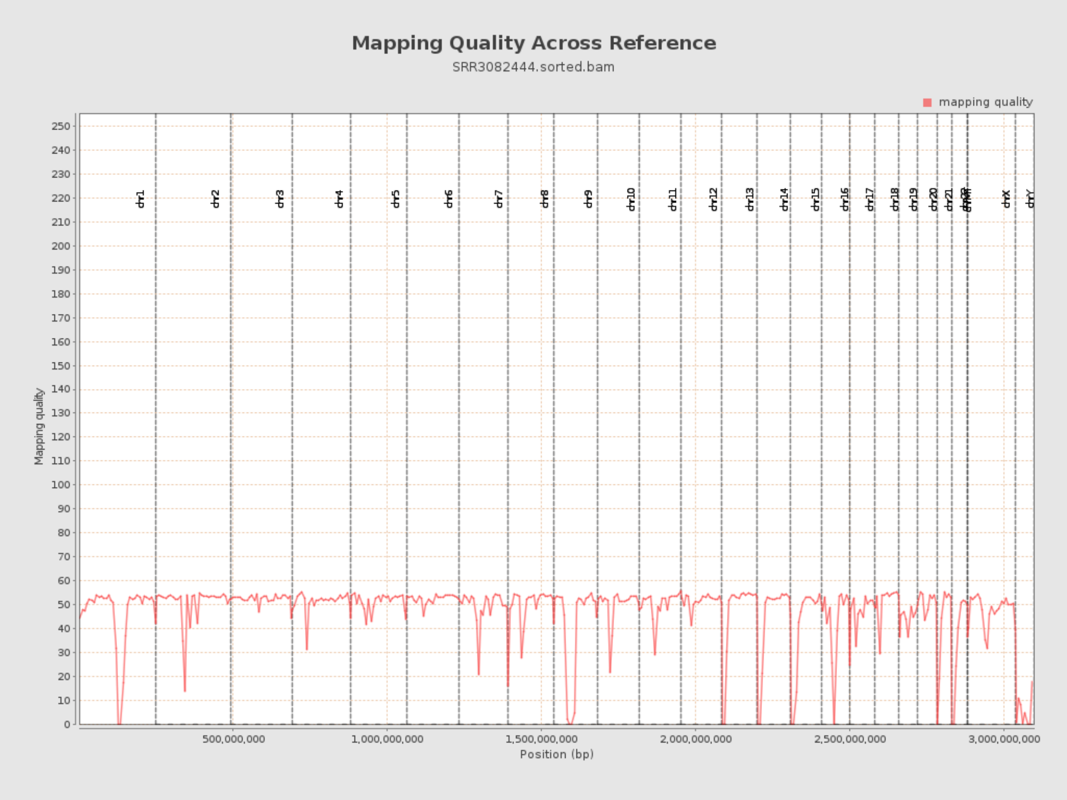
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram