# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 02:55:53*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081213.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_SRR3081213 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081213.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Aug 24 02:55:53 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3081213.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,028,927 |
| Mapped reads | 1,783,452 / 87.9% |
| Unmapped reads | 245,475 / 12.1% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 21,110 / 1.04% |
| Read min/max/mean length | 30 / 76 / 76.36 |
| Duplicated reads (estimated) | 73,442 / 3.62% |
| Duplication rate | 3.42% |
| Clipped reads | 949,346 / 46.79% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 32,852,258 / 28.32% |
| Number/percentage of C's | 22,410,828 / 19.32% |
| Number/percentage of T's | 35,525,424 / 30.62% |
| Number/percentage of G's | 25,219,234 / 21.74% |
| Number/percentage of N's | 15,470 / 0.01% |
| GC Percentage | 41.05% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0375 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2892 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.13 |

## 2.5. Mismatches and indels

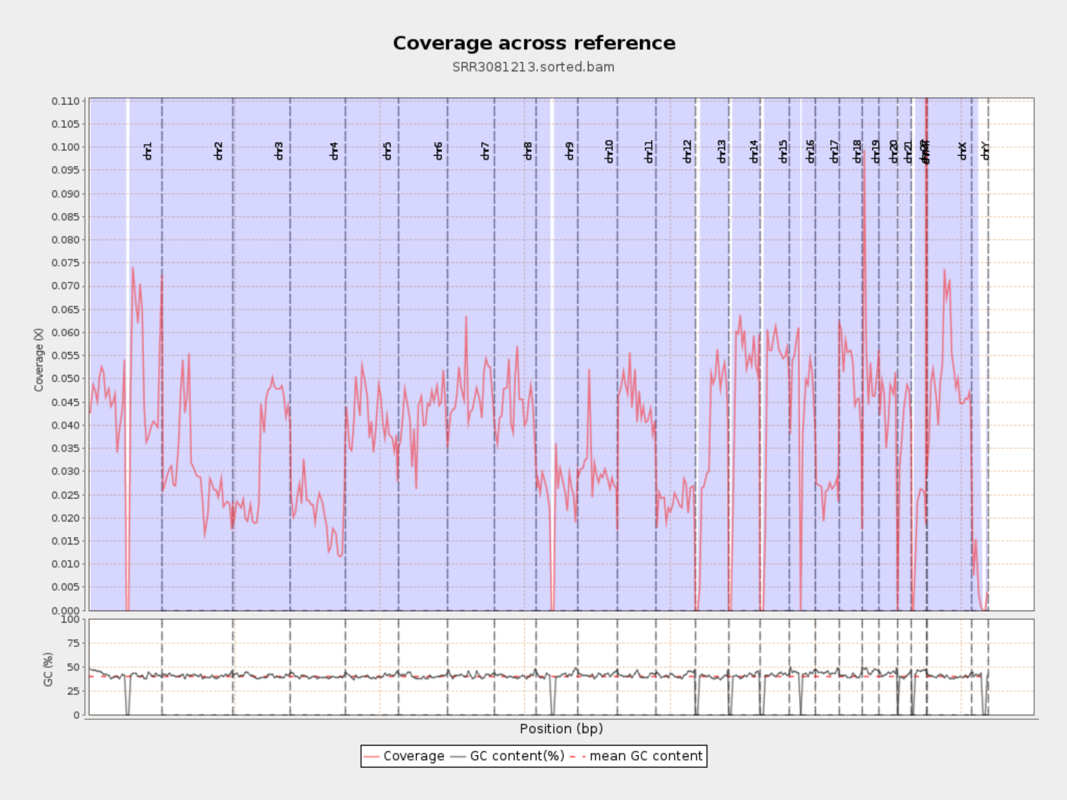
| | |
|---|---|
| General error rate | 0.92% |
| Mismatches | 1,053,835 |
| Insertions | 8,970 |
| Mapped reads with at least one insertion | 0.5% |
| Deletions | 26,665 |
| Mapped reads with at least one deletion | 1.48% |
| Homopolymer indels | 48.14% |

## 2.6. Chromosome stats

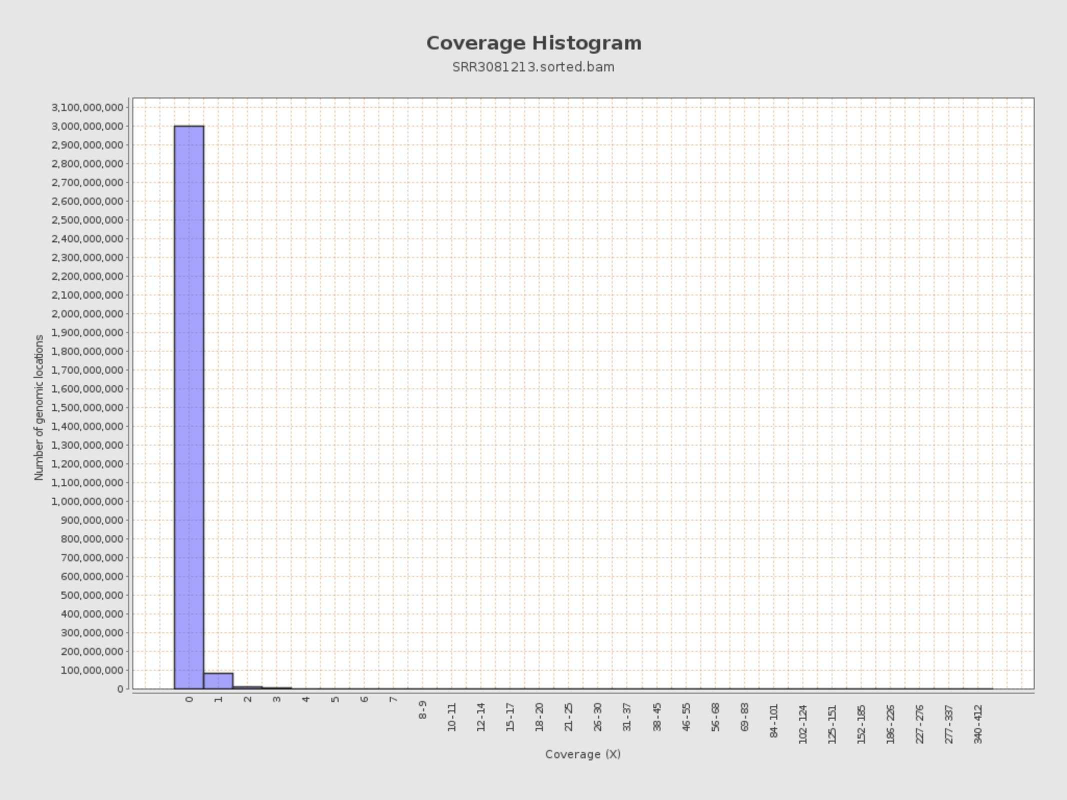
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 11415884 | 0.0458 | 0.4175 |
| chr2 | 243199373 | 7341758 | 0.0302 | 0.3441 |
| chr3 | 198022430 | 6749397 | 0.0341 | 0.2131 |
| chr4 | 191154276 | 3964252 | 0.0207 | 0.1764 |
| chr5 | 180915260 | 7464748 | 0.0413 | 0.2352 |
| chr6 | 171115067 | 7219976 | 0.0422 | 0.2522 |
| chr7 | 159138663 | 7503364 | 0.0471 | 0.4157 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6480603 | 0.0443 | 0.3405 |
| chr9 | 141213431 | 3378479 | 0.0239 | 0.2317 |
| chr10 | 135534747 | 4125816 | 0.0304 | 0.27 |
| chr11 | 135006516 | 6035893 | 0.0447 | 0.3169 |
| chr12 | 133851895 | 3153755 | 0.0236 | 0.179 |
| chr13 | 115169878 | 4146925 | 0.036 | 0.2203 |
| chr14 | 107349540 | 5057852 | 0.0471 | 0.2546 |
| chr15 | 102531392 | 4695478 | 0.0458 | 0.2538 |
| chr16 | 90354753 | 4181007 | 0.0463 | 0.2599 |
| chr17 | 81195210 | 2116184 | 0.0261 | 0.2011 |
| chr18 | 78077248 | 4055088 | 0.0519 | 0.3973 |
| chr19 | 59128983 | 3254849 | 0.055 | 0.376 |
| chr20 | 63025520 | 2794160 | 0.0443 | 0.2457 |
| chr21 | 48129895 | 1804356 | 0.0375 | 0.2332 |
| chr22 | 51304566 | 905083 | 0.0176 | 0.1502 |
| chrMT | 16571 | 100300 | 6.0527 | 4.8073 |
| chrX | 155270560 | 7800875 | 0.0502 | 0.2787 |
| chrY | 59373566 | 320829 | 0.0054 | 0.1153 |

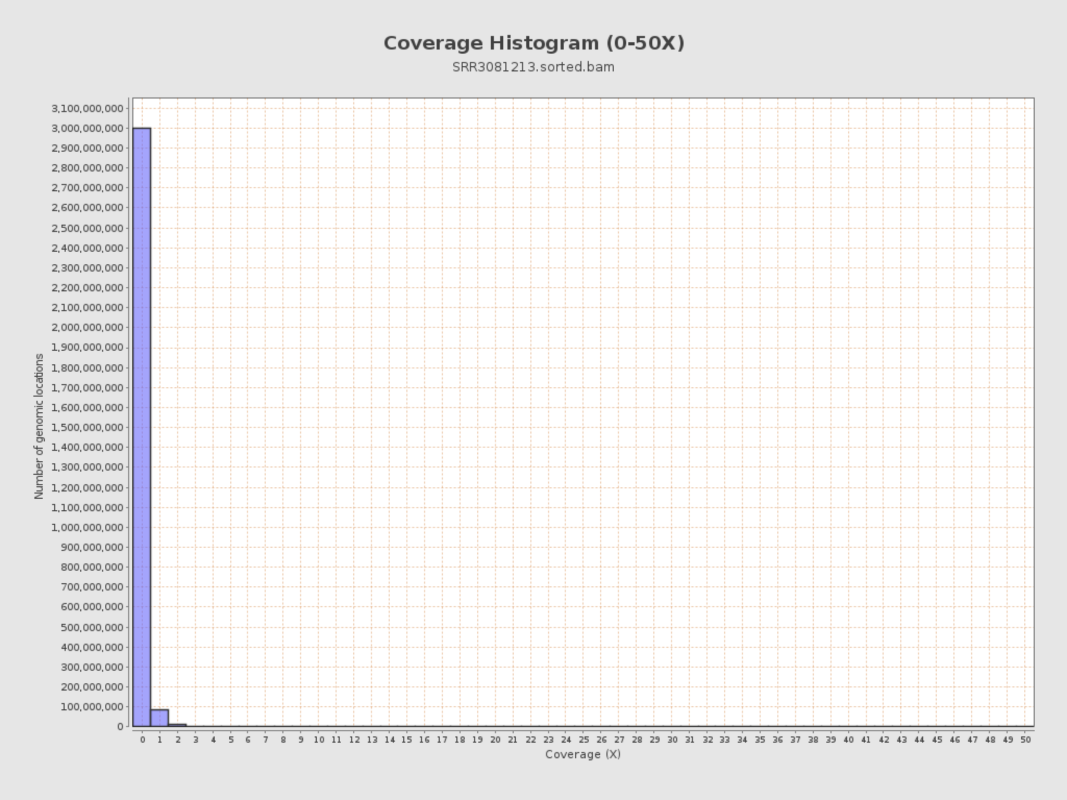
# 3. Results : Coverage across reference



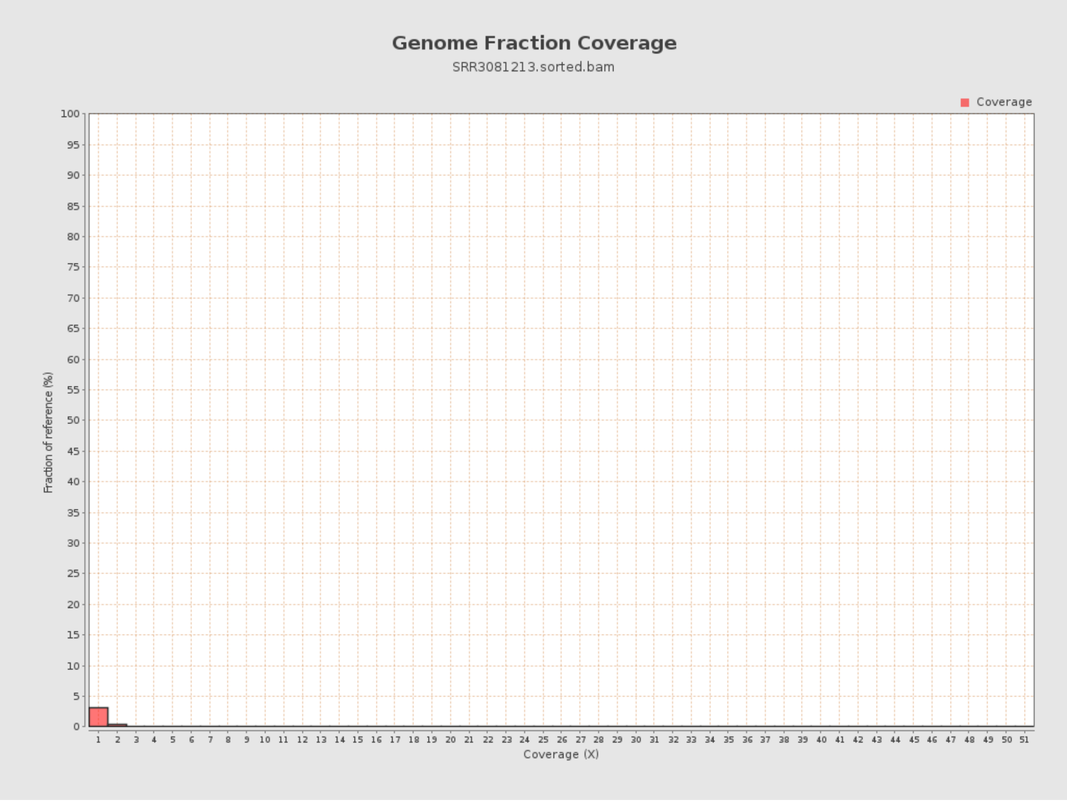
# 4. Results : Coverage Histogram



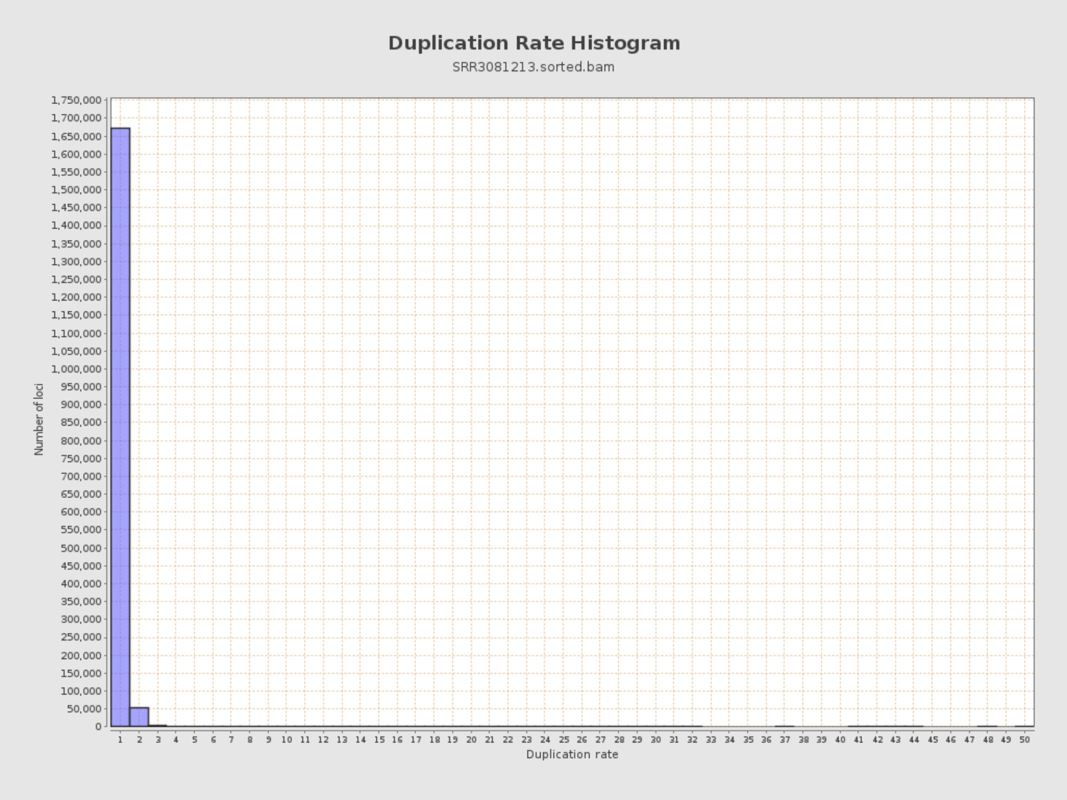
# 5. Results : Coverage Histogram (0-50X)



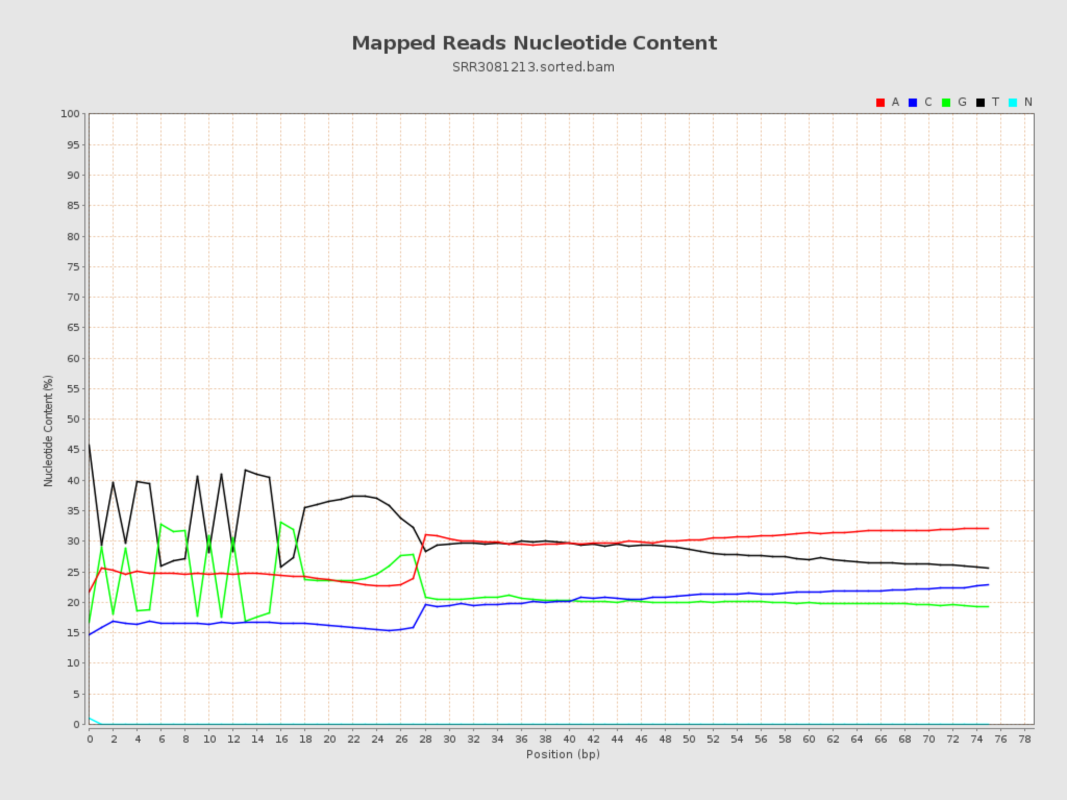
# 6. Results : Genome Fraction Coverage



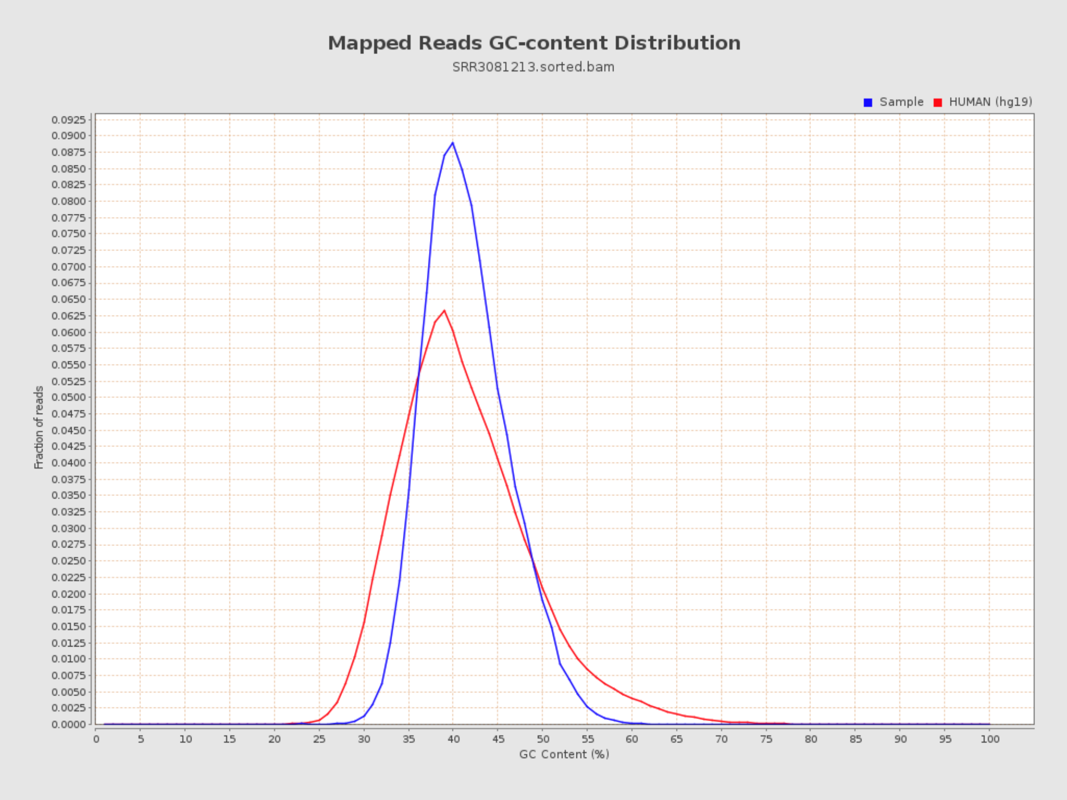
# 7. Results : Duplication Rate Histogram



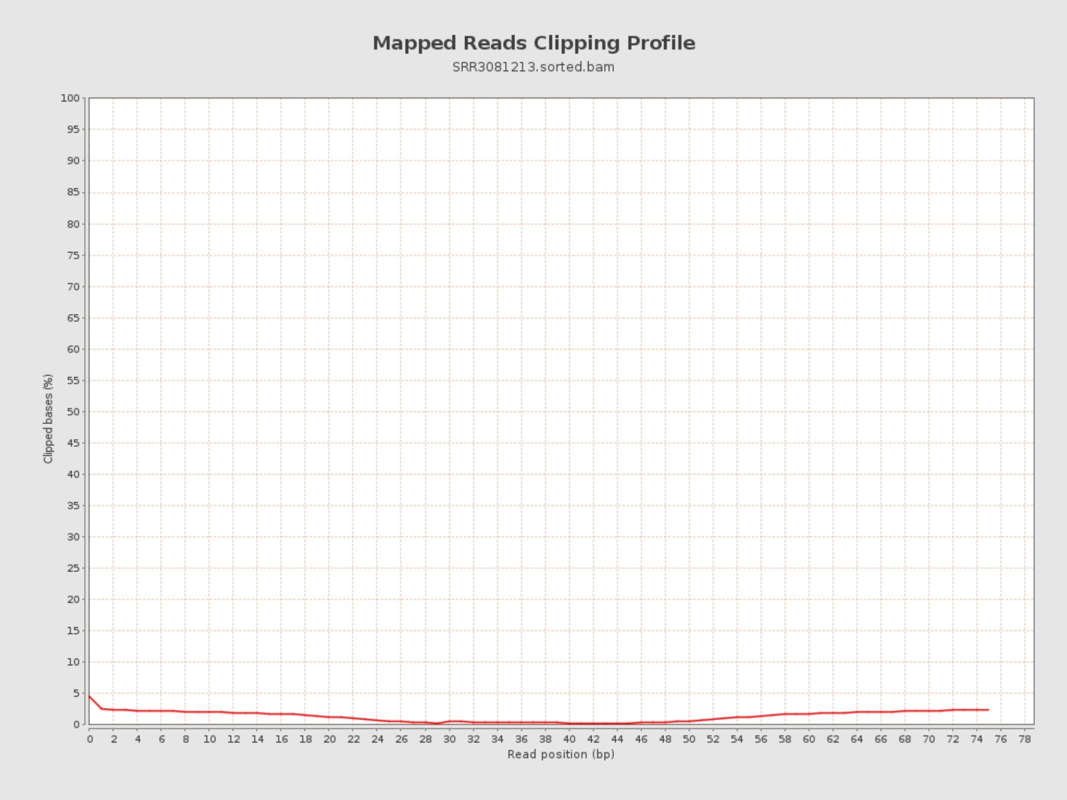
# 8. Results : Mapped Reads Nucleotide Content



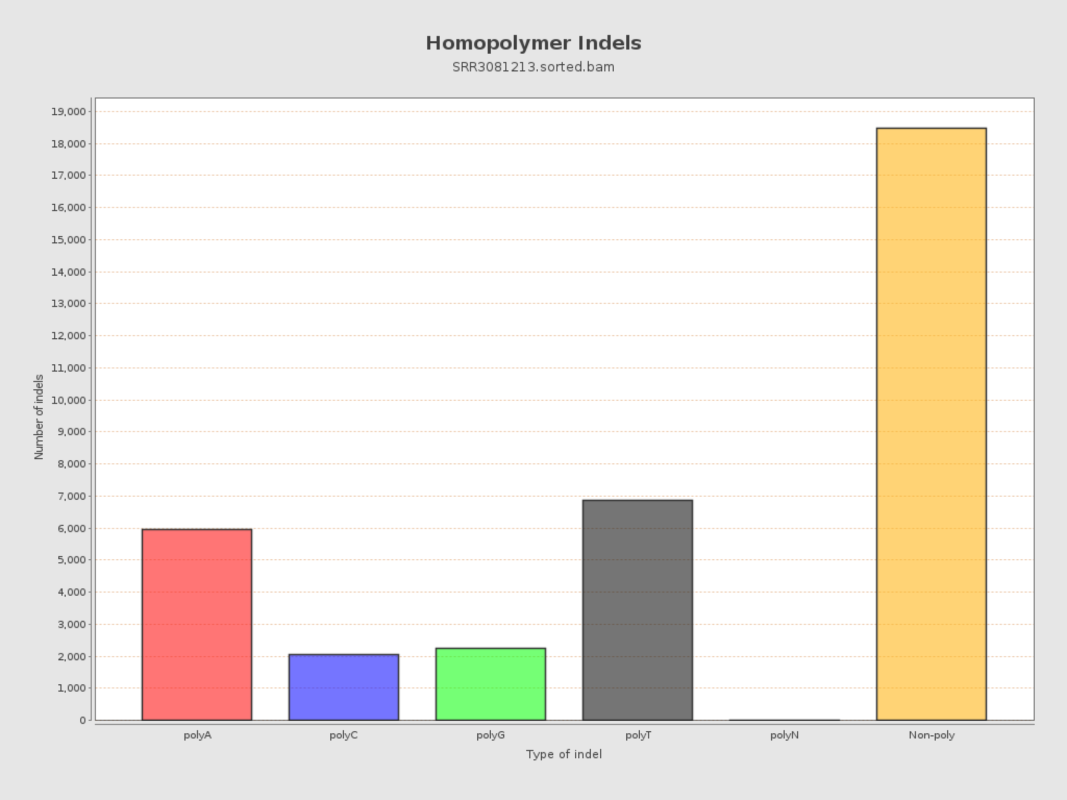
# 9. Results : Mapped Reads GC-content Distribution



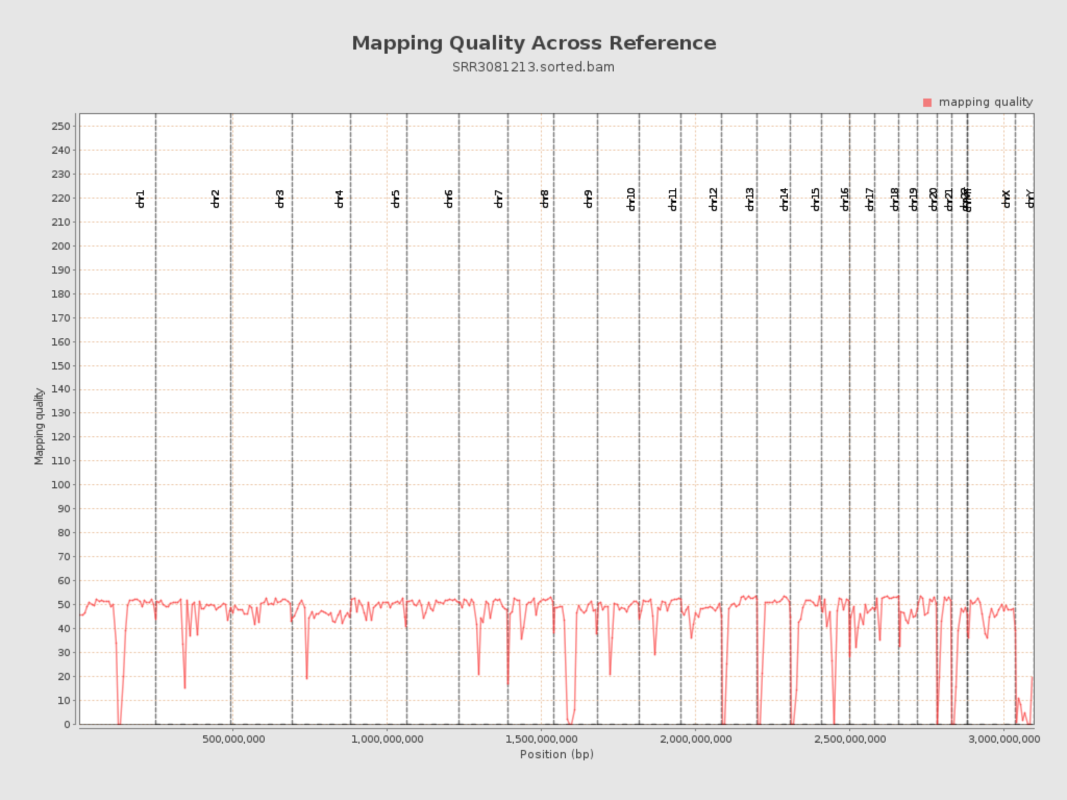
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram