# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 02:52:34*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708575.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_SRR1708575 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708575.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 02:52:32 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1708575.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,534,938 |
| Mapped reads | 3,740,618 / 82.48% |
| Unmapped reads | 794,320 / 17.52% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 98 / 0% |
| Read min/max/mean length | 30 / 50 / 50 |
| Duplicated reads (estimated) | 27,239 / 0.6% |
| Duplication rate | 0.72% |
| Clipped reads | 53,445 / 1.18% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 57,696,025 / 30.94% |
| Number/percentage of C's | 35,487,495 / 19.03% |
| Number/percentage of T's | 57,426,106 / 30.79% |
| Number/percentage of G's | 35,877,458 / 19.24% |
| Number/percentage of N's | 8,905 / 0% |
| GC Percentage | 38.27% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0602 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2789 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.61 |

## 2.5. Mismatches and indels

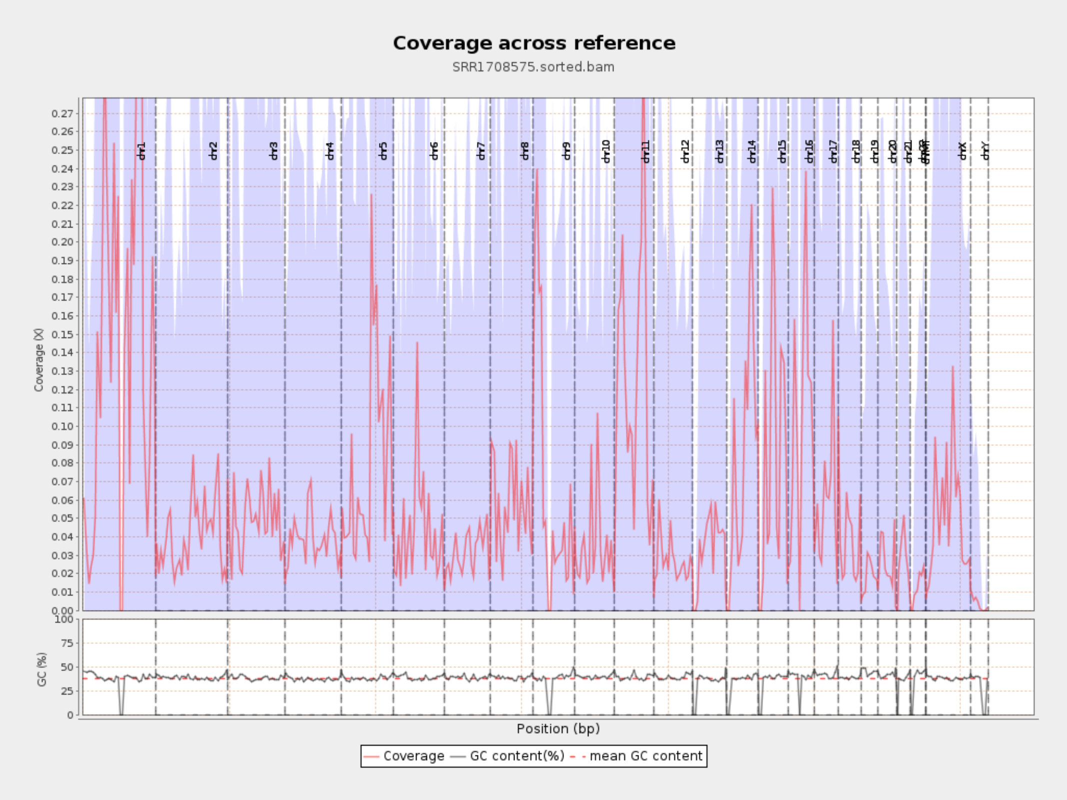
| | |
|---|---|
| General error rate | 0.17% |
| Mismatches | 301,104 |
| Insertions | 12,906 |
| Mapped reads with at least one insertion | 0.34% |
| Deletions | 10,226 |
| Mapped reads with at least one deletion | 0.27% |
| Homopolymer indels | 47.58% |

## 2.6. Chromosome stats

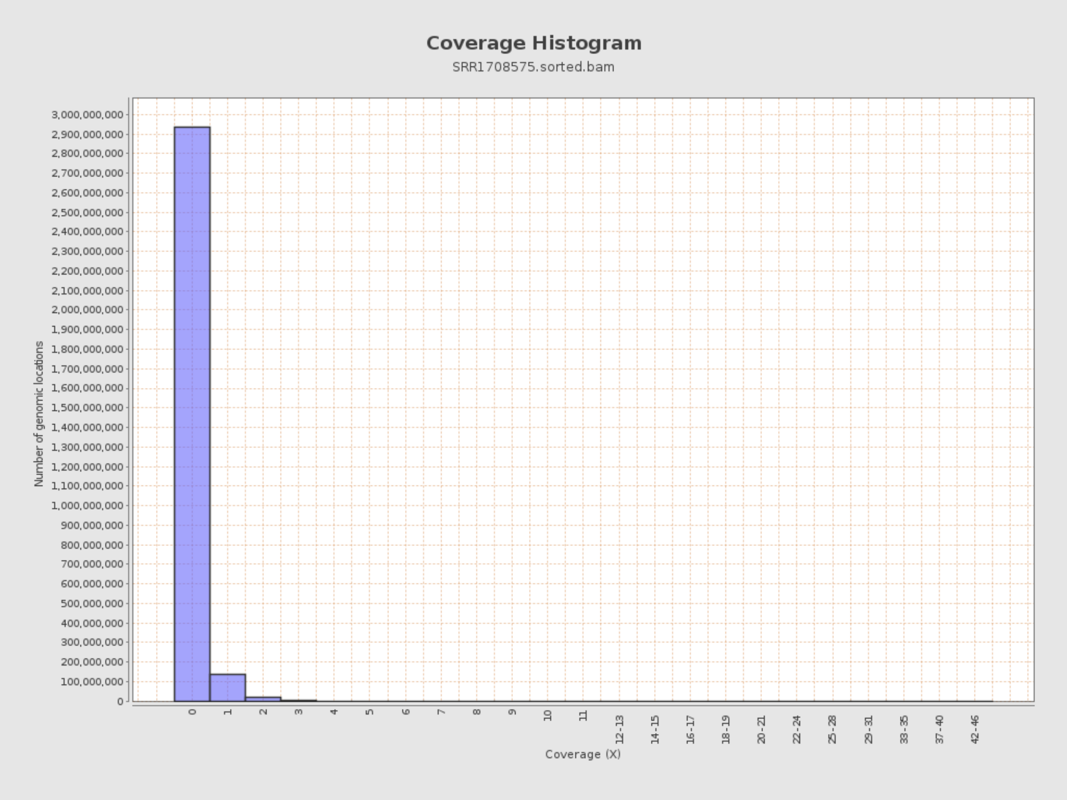
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 37370208 | 0.1499 | 0.4568 |
| chr2 | 243199373 | 9728171 | 0.04 | 0.2183 |
| chr3 | 198022430 | 9838313 | 0.0497 | 0.2411 |
| chr4 | 191154276 | 7421124 | 0.0388 | 0.2104 |
| chr5 | 180915260 | 14199764 | 0.0785 | 0.3169 |
| chr6 | 171115067 | 7352166 | 0.043 | 0.2259 |
| chr7 | 159138663 | 4943134 | 0.0311 | 0.1885 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 8431336 | 0.0576 | 0.2627 |
| chr9 | 141213431 | 9522986 | 0.0674 | 0.2963 |
| chr10 | 135534747 | 4723262 | 0.0348 | 0.2056 |
| chr11 | 135006516 | 17640124 | 0.1307 | 0.4115 |
| chr12 | 133851895 | 3724638 | 0.0278 | 0.1807 |
| chr13 | 115169878 | 3972202 | 0.0345 | 0.2002 |
| chr14 | 107349540 | 9296671 | 0.0866 | 0.3369 |
| chr15 | 102531392 | 8337240 | 0.0813 | 0.3264 |
| chr16 | 90354753 | 9185076 | 0.1017 | 0.3602 |
| chr17 | 81195210 | 4994500 | 0.0615 | 0.2747 |
| chr18 | 78077248 | 2921309 | 0.0374 | 0.2125 |
| chr19 | 59128983 | 1123247 | 0.019 | 0.1449 |
| chr20 | 63025520 | 1732469 | 0.0275 | 0.1801 |
| chr21 | 48129895 | 1270398 | 0.0264 | 0.1756 |
| chr22 | 51304566 | 672703 | 0.0131 | 0.1217 |
| chrMT | 16571 | 100 | 0.006 | 0.0774 |
| chrX | 155270560 | 7904826 | 0.0509 | 0.2549 |
| chrY | 59373566 | 207377 | 0.0035 | 0.062 |

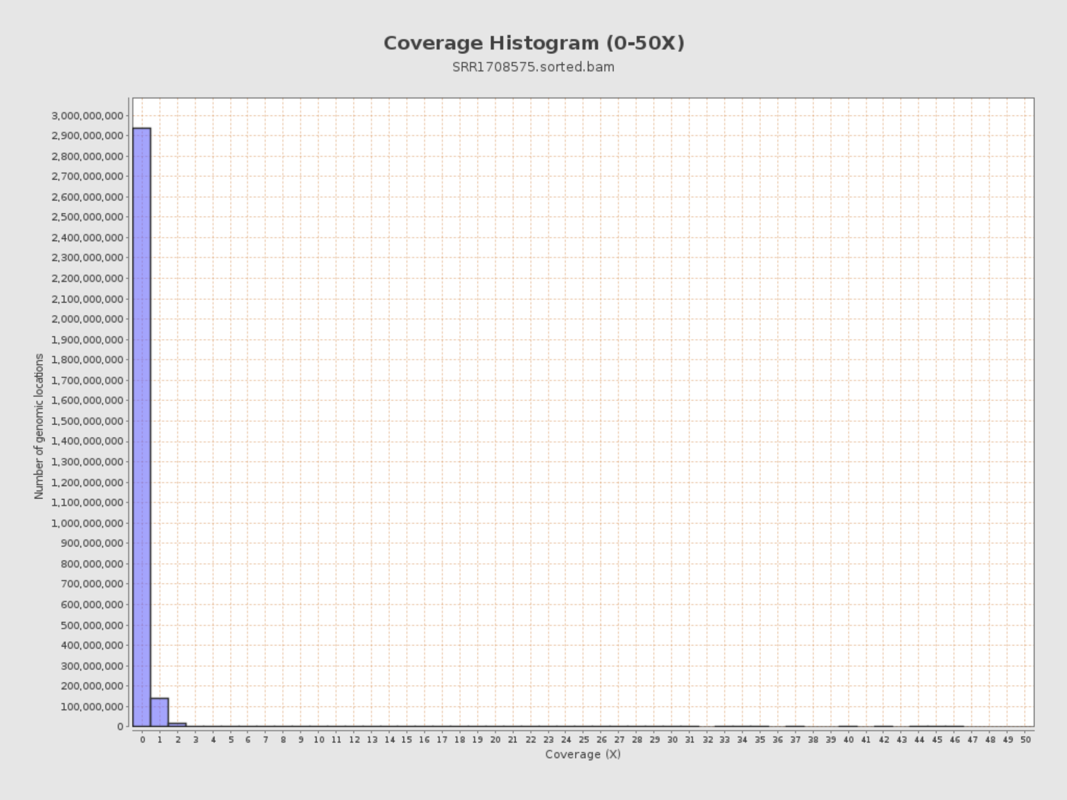
# 3. Results : Coverage across reference



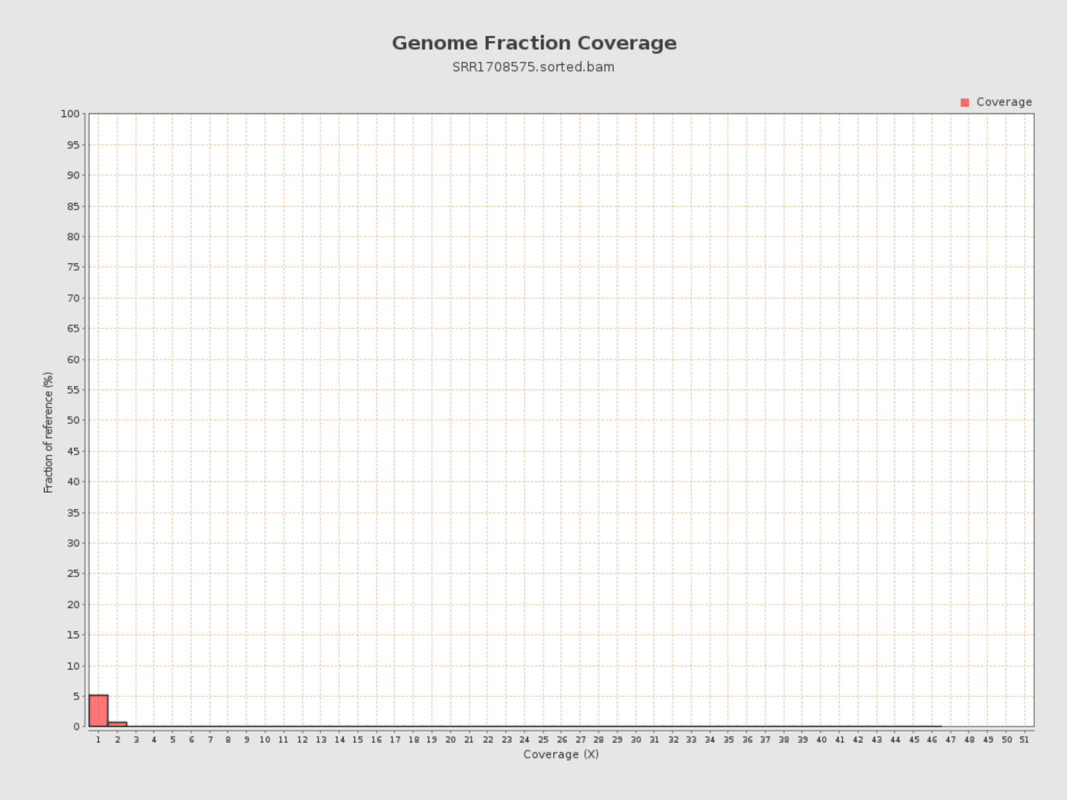
# 4. Results : Coverage Histogram



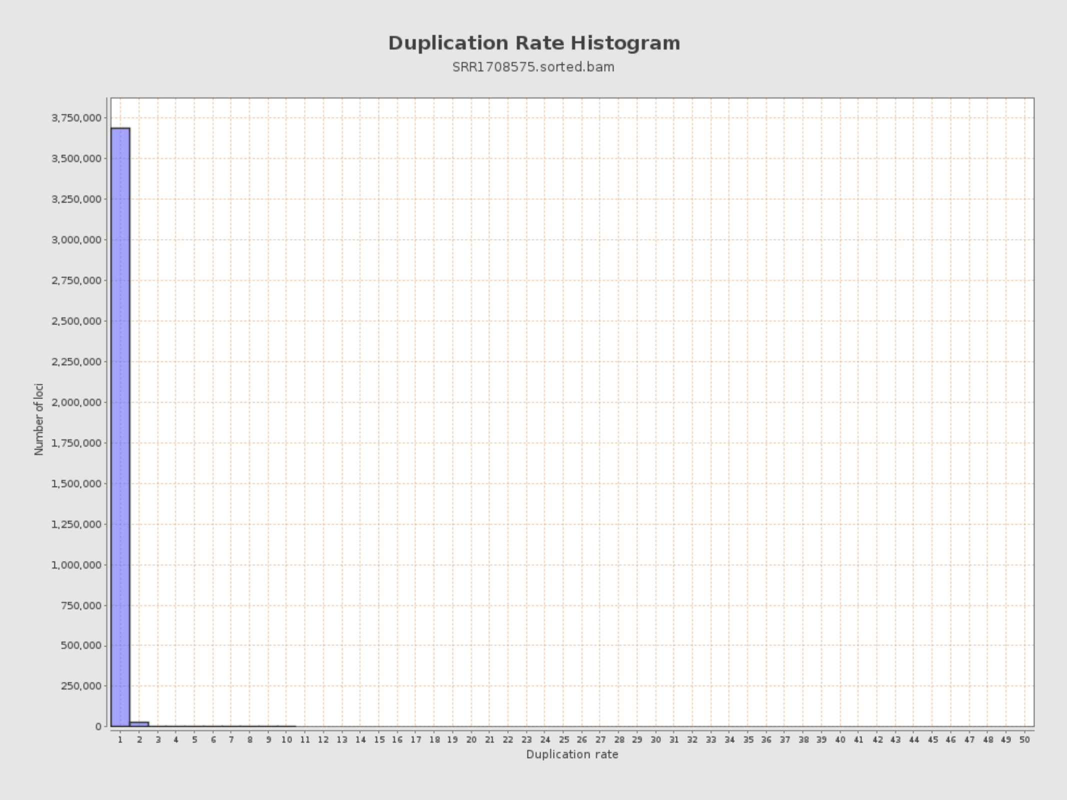
# 5. Results : Coverage Histogram (0-50X)



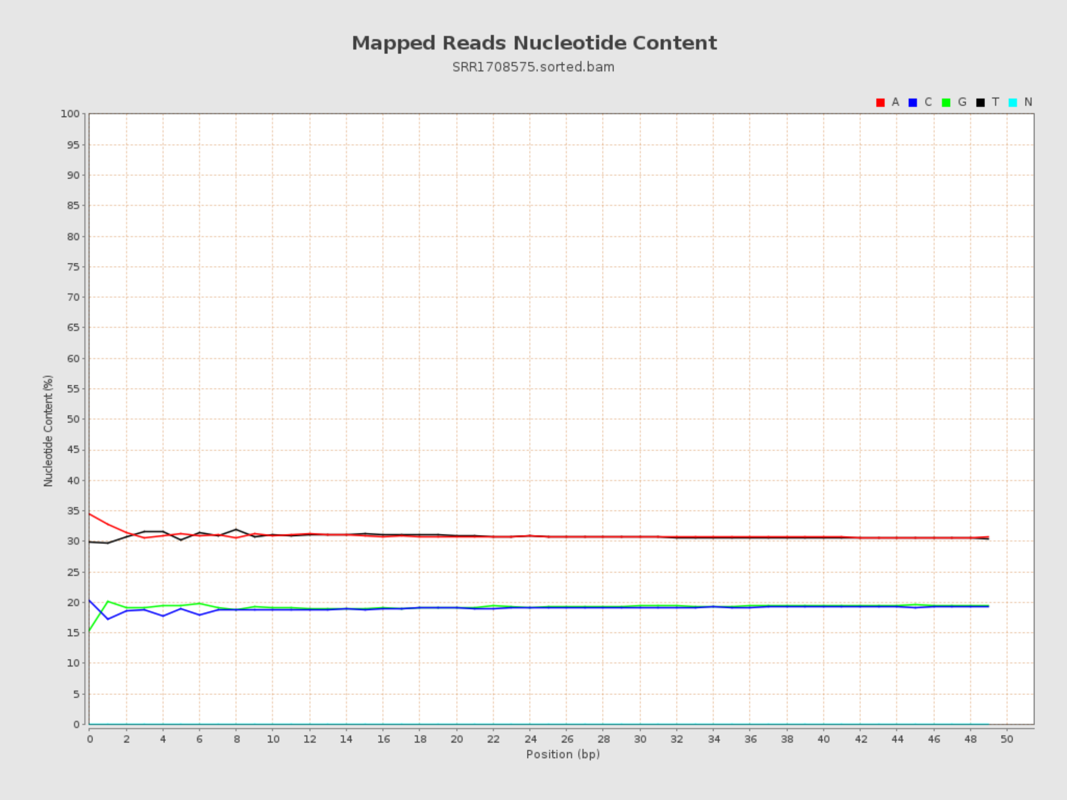
# 6. Results : Genome Fraction Coverage



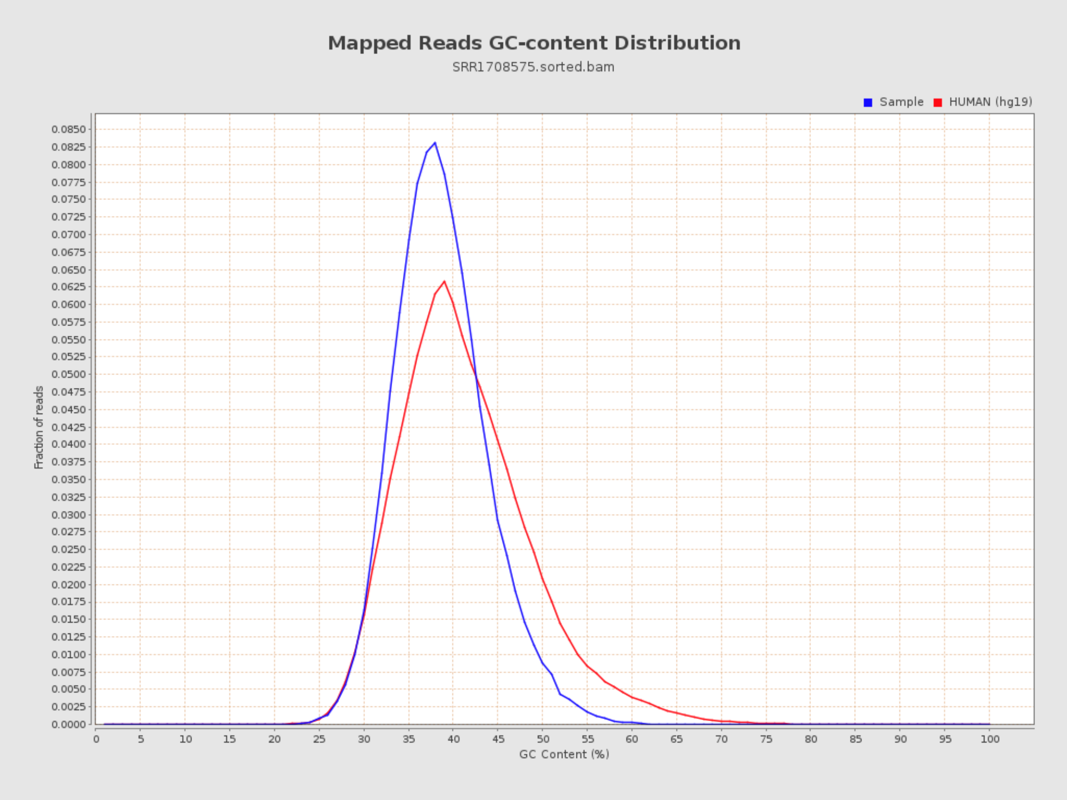
# 7. Results : Duplication Rate Histogram



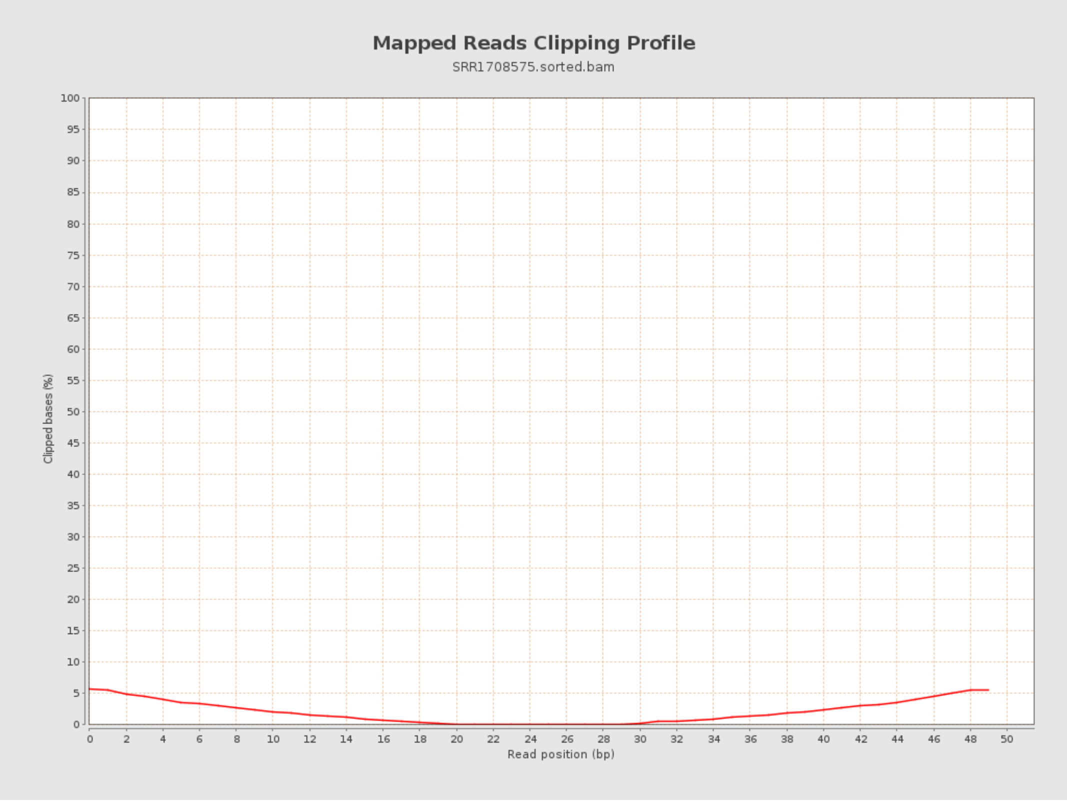
# 8. Results : Mapped Reads Nucleotide Content



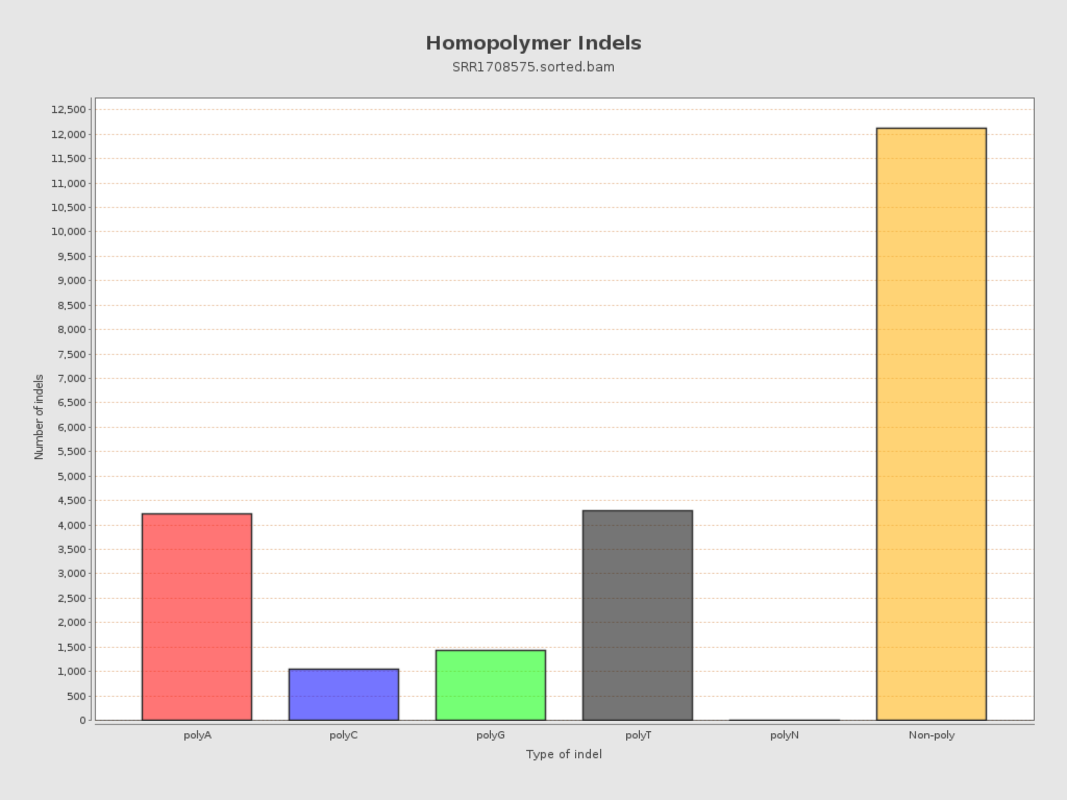
# 9. Results : Mapped Reads GC-content Distribution



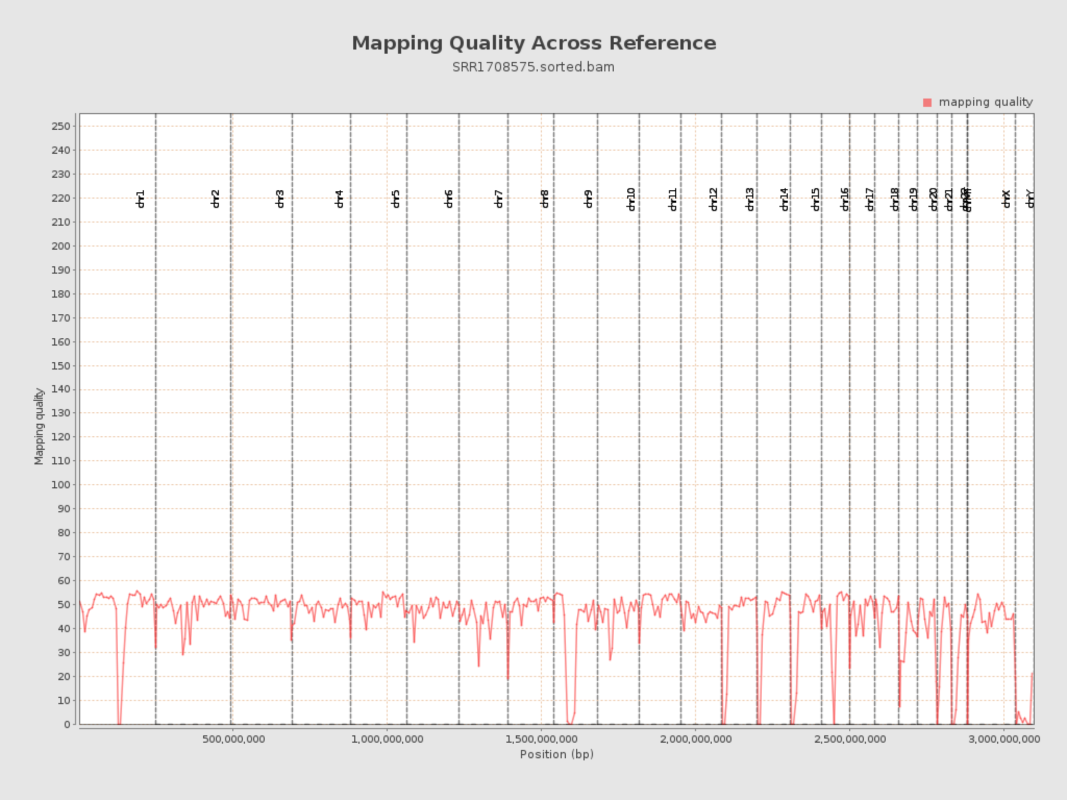
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram