# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 08:26:29*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708611.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_SRR1708611 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708611.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 08:26:28 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1708611.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,796,735 |
| Mapped reads | 1,543,916 / 55.2% |
| Unmapped reads | 1,252,819 / 44.8% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 398 / 0.01% |
| Read min/max/mean length | 30 / 51 / 51 |
| Duplicated reads (estimated) | 58,760 / 2.1% |
| Duplication rate | 3.04% |
| Clipped reads | 290,831 / 10.4% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 21,517,407 / 28.96% |
| Number/percentage of C's | 14,224,130 / 19.14% |
| Number/percentage of T's | 23,189,172 / 31.21% |
| Number/percentage of G's | 15,360,095 / 20.67% |
| Number/percentage of N's | 6,179 / 0.01% |
| GC Percentage | 39.82% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.024 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2329 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 41.41 |

## 2.5. Mismatches and indels

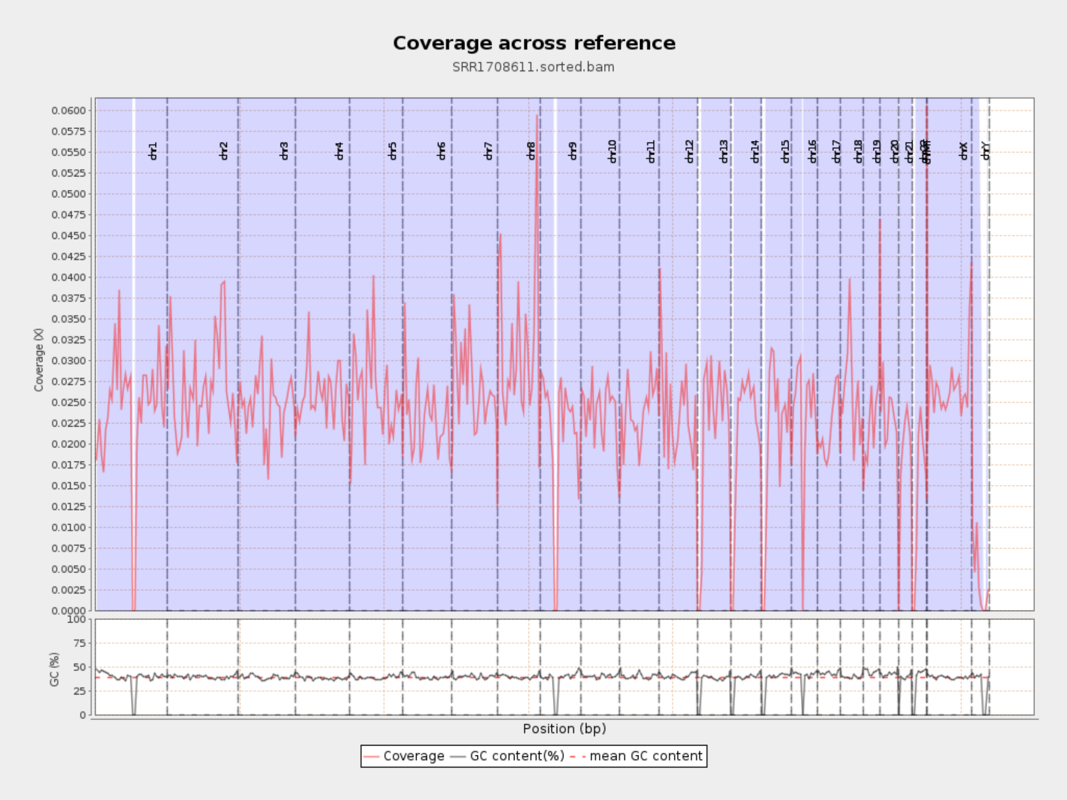
| | |
|---|---|
| General error rate | 0.7% |
| Mismatches | 510,576 |
| Insertions | 3,752 |
| Mapped reads with at least one insertion | 0.24% |
| Deletions | 12,916 |
| Mapped reads with at least one deletion | 0.83% |
| Homopolymer indels | 49.76% |

## 2.6. Chromosome stats

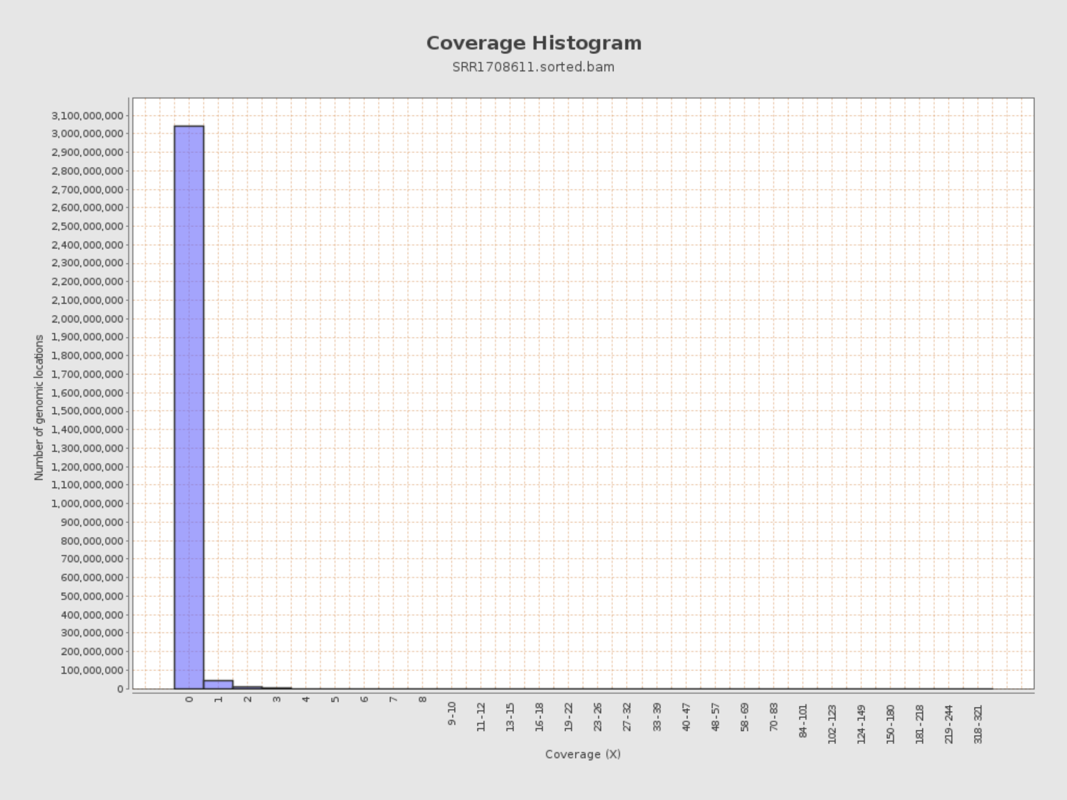
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 6019853 | 0.0242 | 0.2779 |
| chr2 | 243199373 | 6508260 | 0.0268 | 0.2765 |
| chr3 | 198022430 | 4919155 | 0.0248 | 0.2063 |
| chr4 | 191154276 | 4956454 | 0.0259 | 0.2122 |
| chr5 | 180915260 | 4782228 | 0.0264 | 0.2118 |
| chr6 | 171115067 | 3972713 | 0.0232 | 0.2277 |
| chr7 | 159138663 | 4337011 | 0.0273 | 0.2925 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 4598742 | 0.0314 | 0.2676 |
| chr9 | 141213431 | 2988984 | 0.0212 | 0.2257 |
| chr10 | 135534747 | 3208414 | 0.0237 | 0.2152 |
| chr11 | 135006516 | 3226607 | 0.0239 | 0.2196 |
| chr12 | 133851895 | 3223601 | 0.0241 | 0.2022 |
| chr13 | 115169878 | 2477309 | 0.0215 | 0.1957 |
| chr14 | 107349540 | 2245076 | 0.0209 | 0.1947 |
| chr15 | 102531392 | 2125244 | 0.0207 | 0.1878 |
| chr16 | 90354753 | 2085893 | 0.0231 | 0.1978 |
| chr17 | 81195210 | 1776796 | 0.0219 | 0.1972 |
| chr18 | 78077248 | 2062792 | 0.0264 | 0.3376 |
| chr19 | 59128983 | 1365990 | 0.0231 | 0.2893 |
| chr20 | 63025520 | 1462595 | 0.0232 | 0.2258 |
| chr21 | 48129895 | 893845 | 0.0186 | 0.1818 |
| chr22 | 51304566 | 722053 | 0.0141 | 0.1481 |
| chrMT | 16571 | 1008 | 0.0608 | 0.2487 |
| chrX | 155270560 | 4141477 | 0.0267 | 0.2185 |
| chrY | 59373566 | 215260 | 0.0036 | 0.0892 |

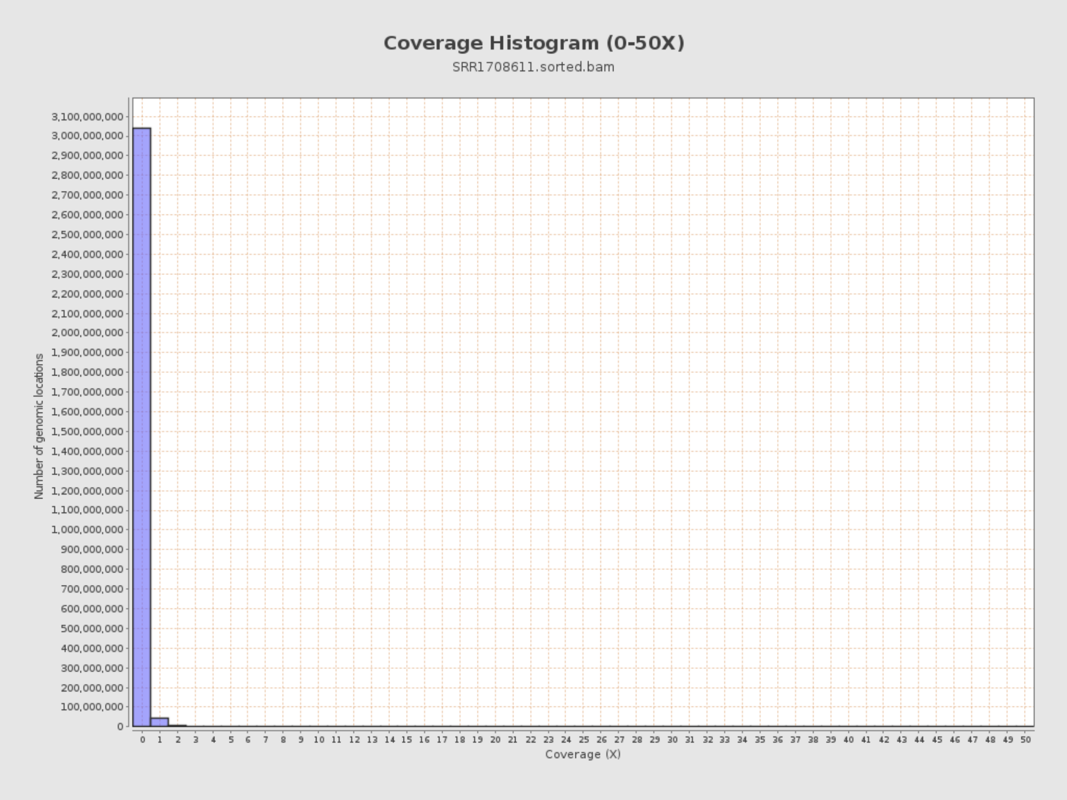
# 3. Results : Coverage across reference



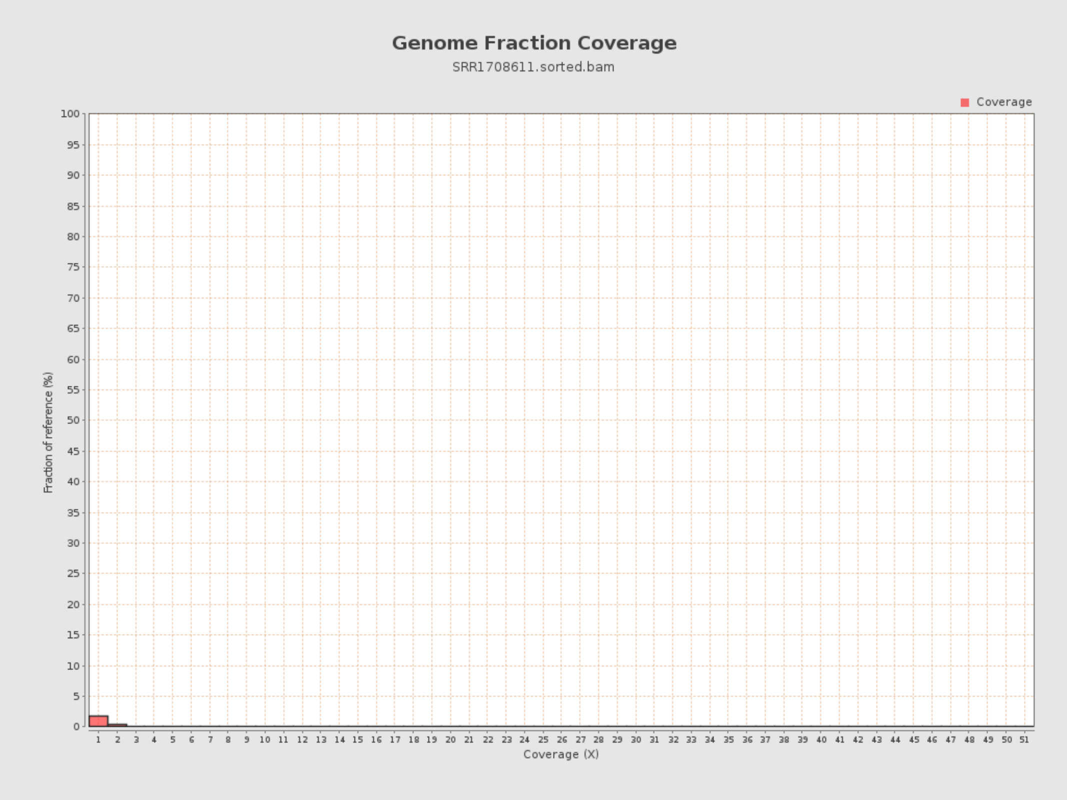
# 4. Results : Coverage Histogram



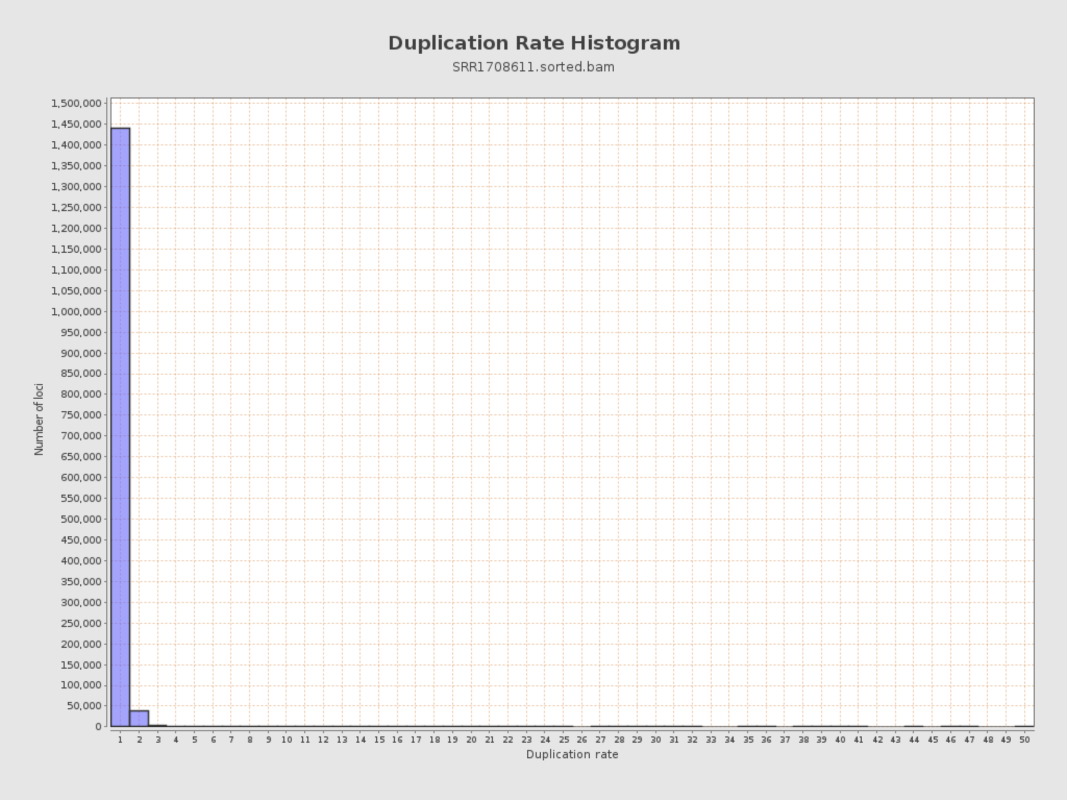
# 5. Results : Coverage Histogram (0-50X)



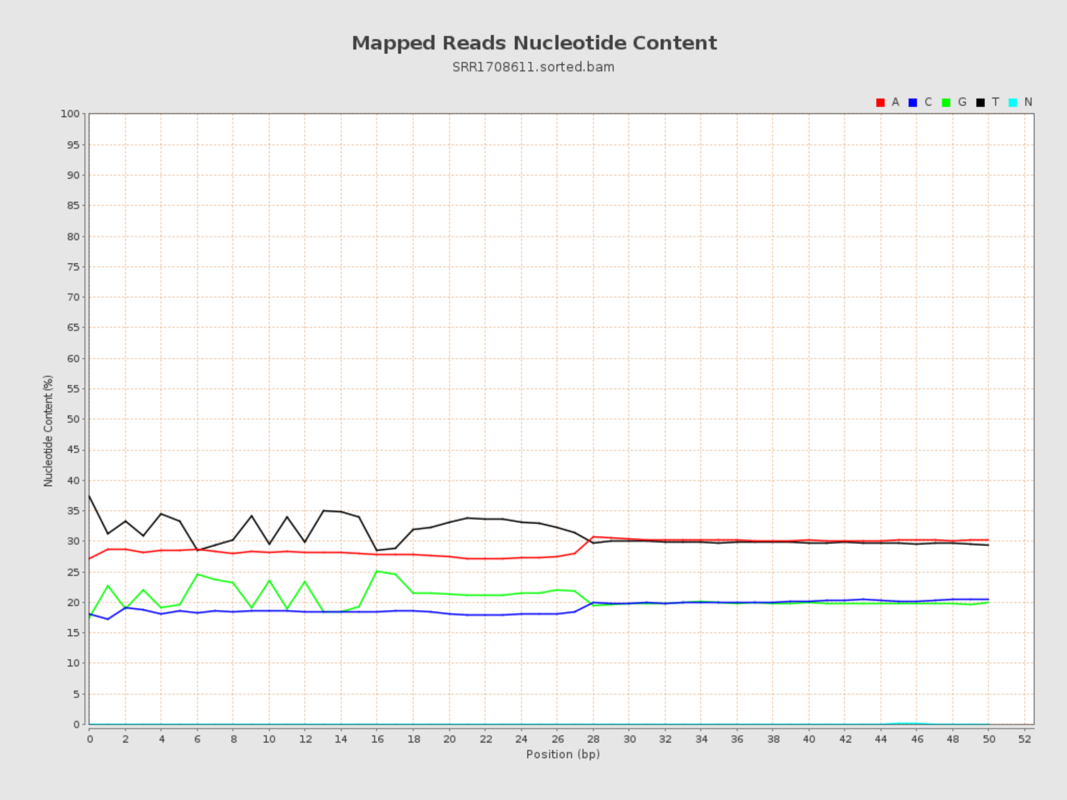
# 6. Results : Genome Fraction Coverage



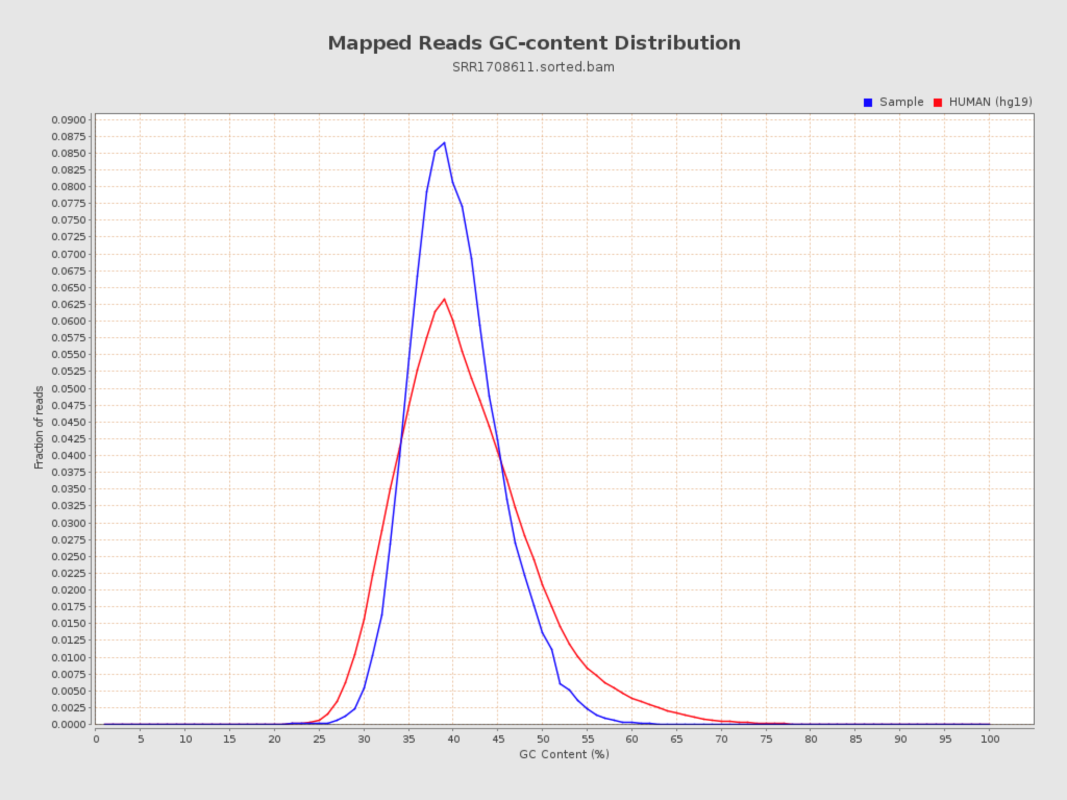
# 7. Results : Duplication Rate Histogram



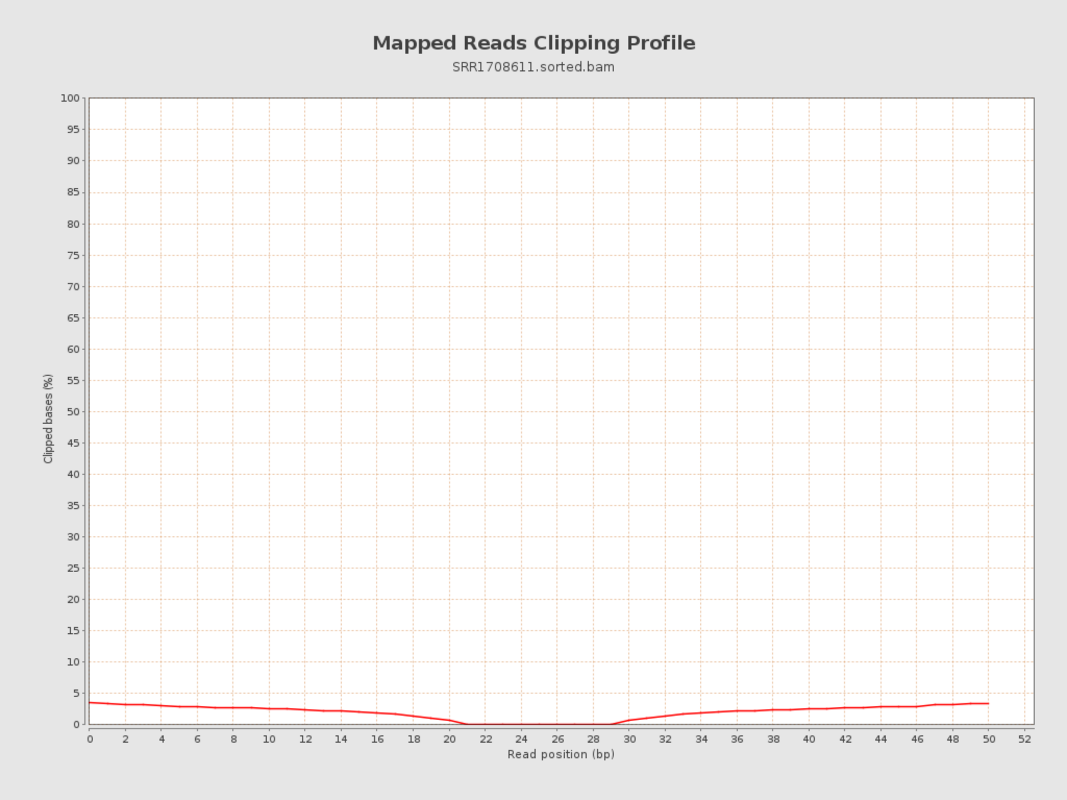
# 8. Results : Mapped Reads Nucleotide Content



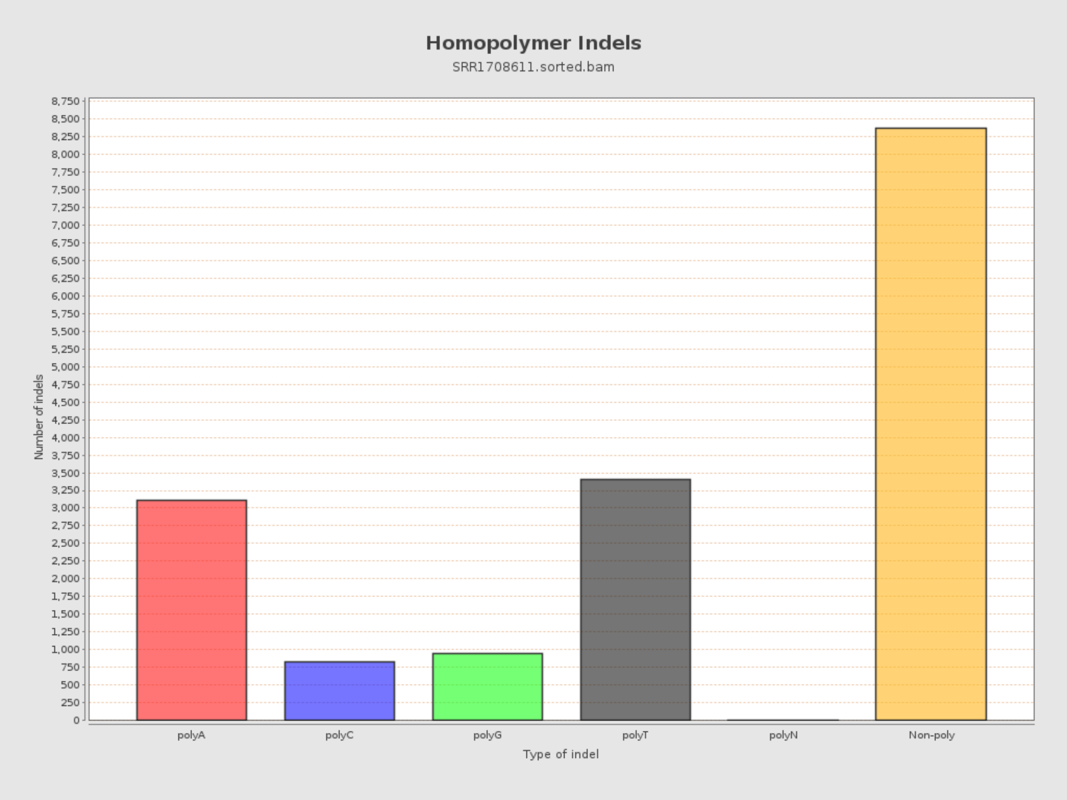
# 9. Results : Mapped Reads GC-content Distribution



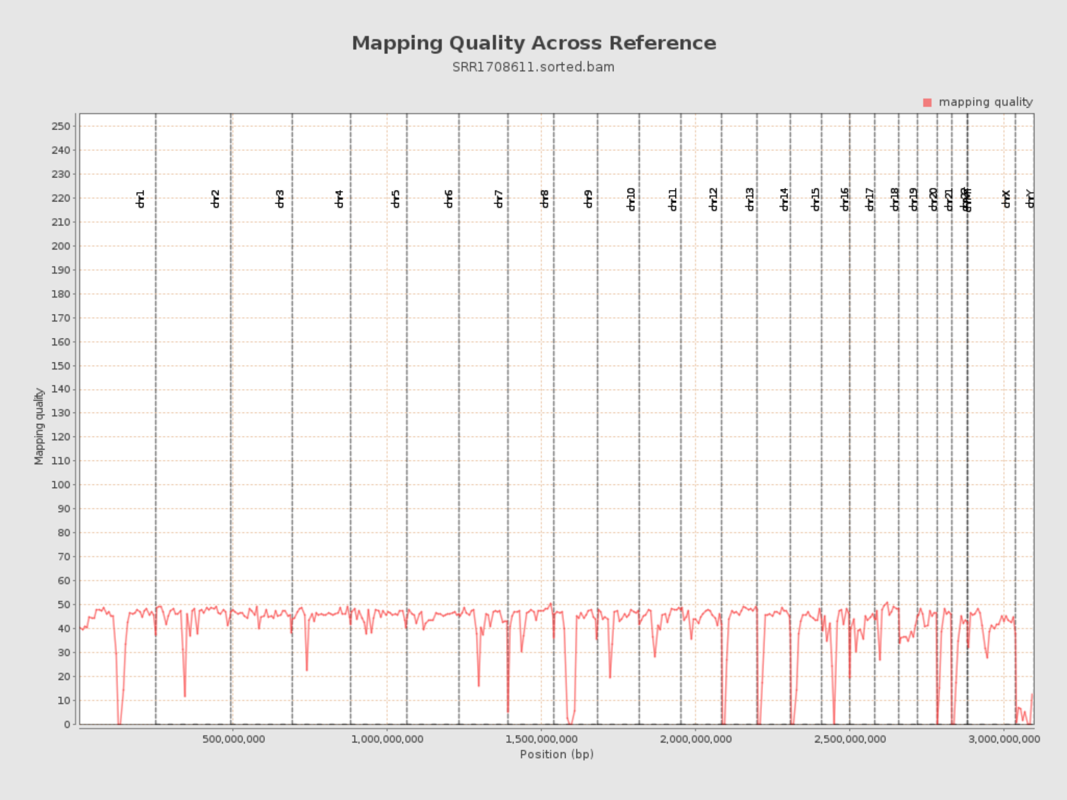
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram