# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 09:42:36*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708630.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_SRR1708630 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708630.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 09:42:35 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1708630.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,407,315 |
| Mapped reads | 2,478,506 / 72.74% |
| Unmapped reads | 928,809 / 27.26% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 803 / 0.02% |
| Read min/max/mean length | 30 / 51 / 51.01 |
| Duplicated reads (estimated) | 89,634 / 2.63% |
| Duplication rate | 2.47% |
| Clipped reads | 385,559 / 11.32% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 35,618,782 / 29.51% |
| Number/percentage of C's | 22,753,715 / 18.85% |
| Number/percentage of T's | 37,991,022 / 31.48% |
| Number/percentage of G's | 24,308,775 / 20.14% |
| Number/percentage of N's | 10,678 / 0.01% |
| GC Percentage | 39% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.039 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4019 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.64 |

## 2.5. Mismatches and indels

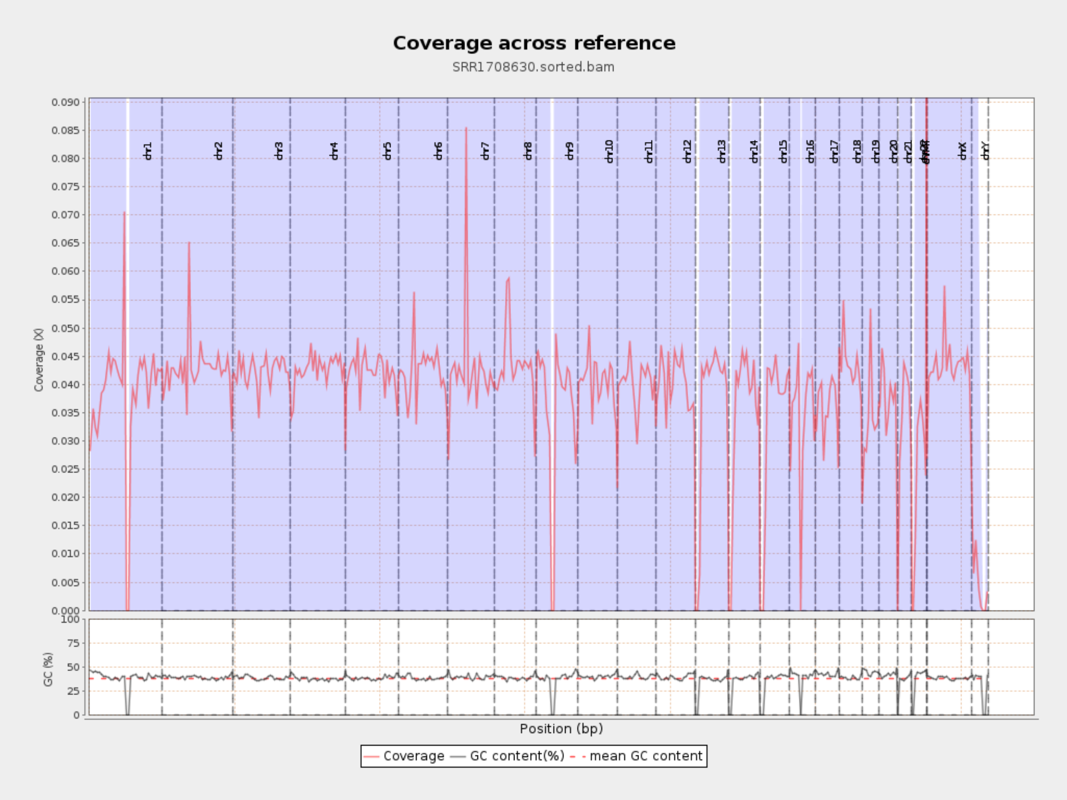
| | |
|---|---|
| General error rate | 0.64% |
| Mismatches | 769,465 |
| Insertions | 5,452 |
| Mapped reads with at least one insertion | 0.22% |
| Deletions | 14,642 |
| Mapped reads with at least one deletion | 0.59% |
| Homopolymer indels | 48.19% |

## 2.6. Chromosome stats

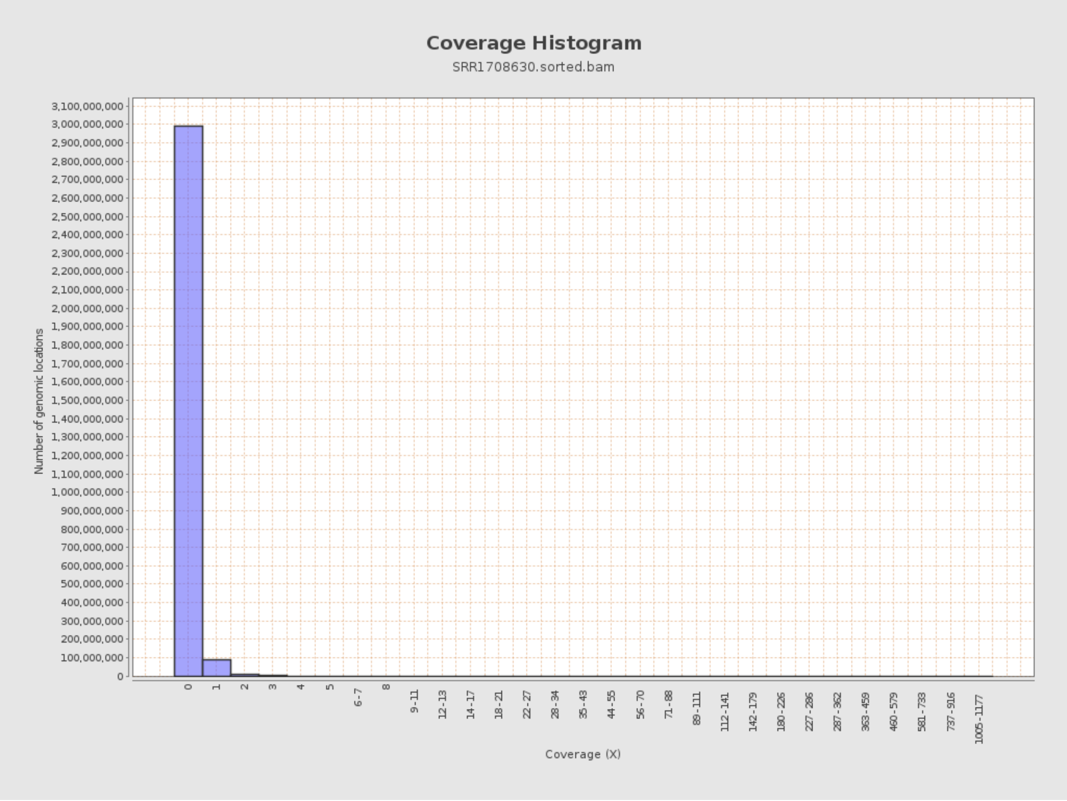
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 9549082 | 0.0383 | 0.7327 |
| chr2 | 243199373 | 10427664 | 0.0429 | 0.4083 |
| chr3 | 198022430 | 8400912 | 0.0424 | 0.2347 |
| chr4 | 191154276 | 8156715 | 0.0427 | 0.2371 |
| chr5 | 180915260 | 7641951 | 0.0422 | 0.2384 |
| chr6 | 171115067 | 7258339 | 0.0424 | 0.2991 |
| chr7 | 159138663 | 6844491 | 0.043 | 0.6136 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6342660 | 0.0433 | 0.6863 |
| chr9 | 141213431 | 5028059 | 0.0356 | 0.3223 |
| chr10 | 135534747 | 5530850 | 0.0408 | 0.3017 |
| chr11 | 135006516 | 5404718 | 0.04 | 0.3365 |
| chr12 | 133851895 | 5409396 | 0.0404 | 0.2376 |
| chr13 | 115169878 | 4095643 | 0.0356 | 0.2146 |
| chr14 | 107349540 | 3694139 | 0.0344 | 0.2288 |
| chr15 | 102531392 | 3417246 | 0.0333 | 0.2063 |
| chr16 | 90354753 | 3104703 | 0.0344 | 0.2272 |
| chr17 | 81195210 | 2876533 | 0.0354 | 0.2625 |
| chr18 | 78077248 | 3417282 | 0.0438 | 0.6858 |
| chr19 | 59128983 | 2011291 | 0.034 | 0.5573 |
| chr20 | 63025520 | 2390943 | 0.0379 | 0.2279 |
| chr21 | 48129895 | 1568163 | 0.0326 | 0.2251 |
| chr22 | 51304566 | 1176772 | 0.0229 | 0.1695 |
| chrMT | 16571 | 2623 | 0.1583 | 0.4305 |
| chrX | 155270560 | 6676820 | 0.043 | 0.2685 |
| chrY | 59373566 | 277992 | 0.0047 | 0.0968 |

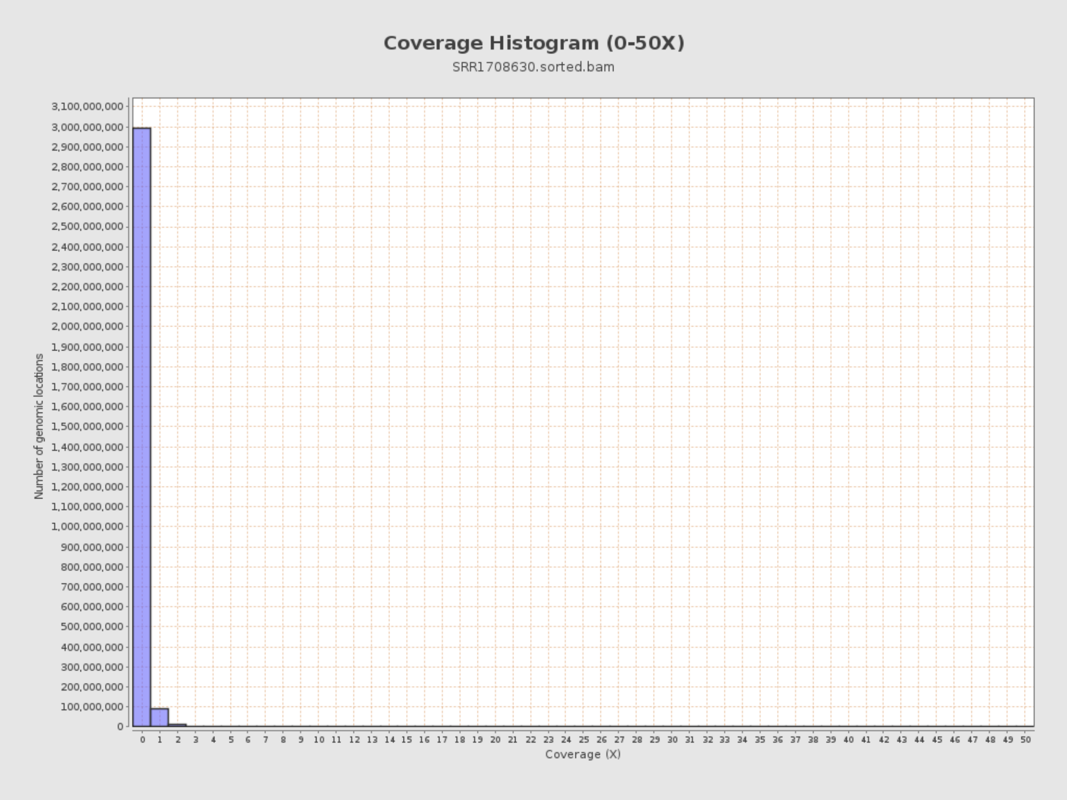
# 3. Results : Coverage across reference



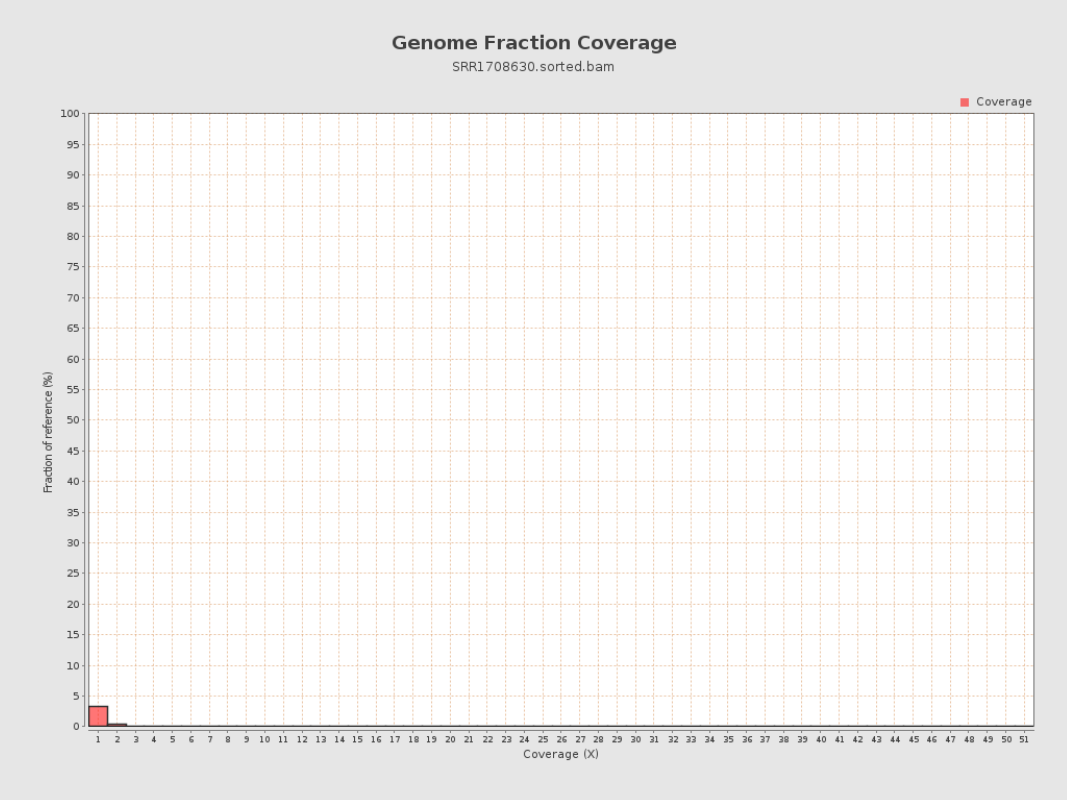
# 4. Results : Coverage Histogram



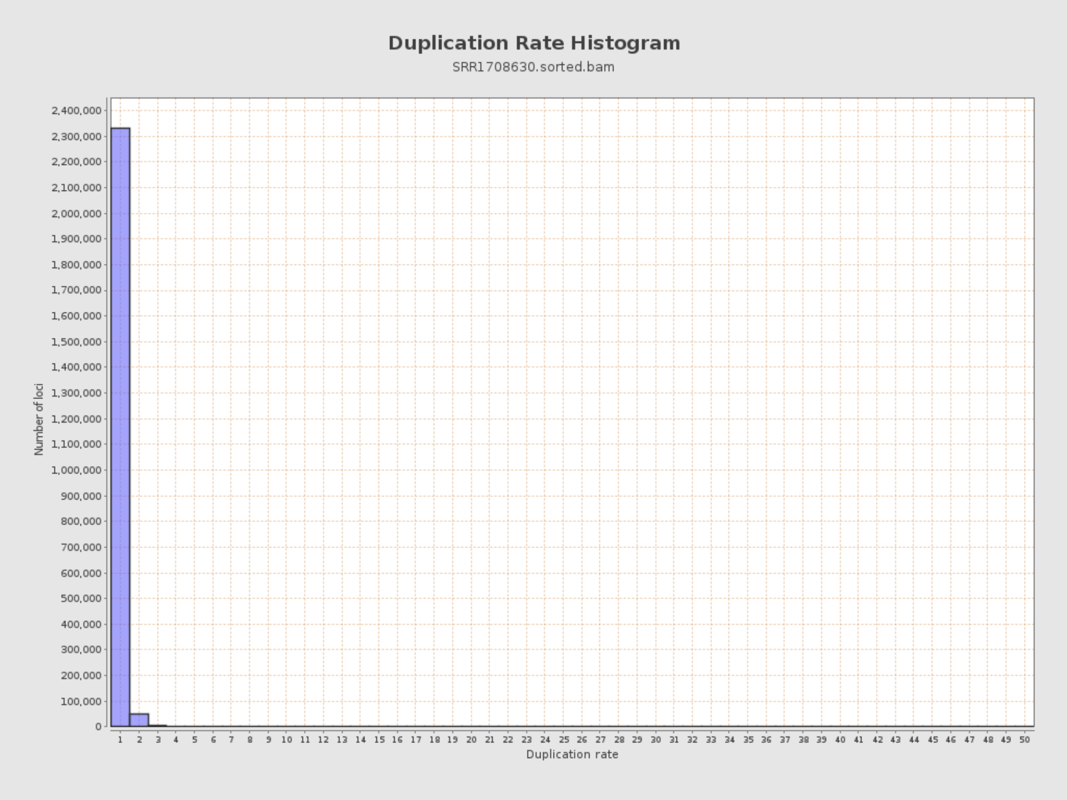
# 5. Results : Coverage Histogram (0-50X)



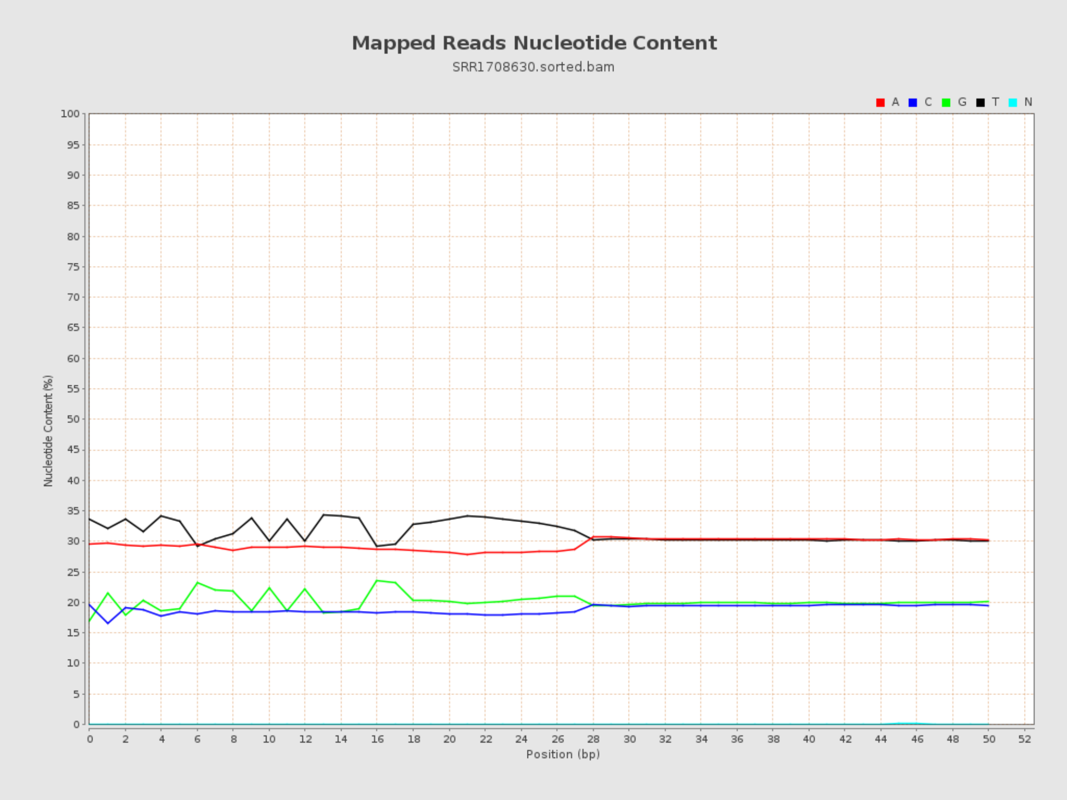
# 6. Results : Genome Fraction Coverage



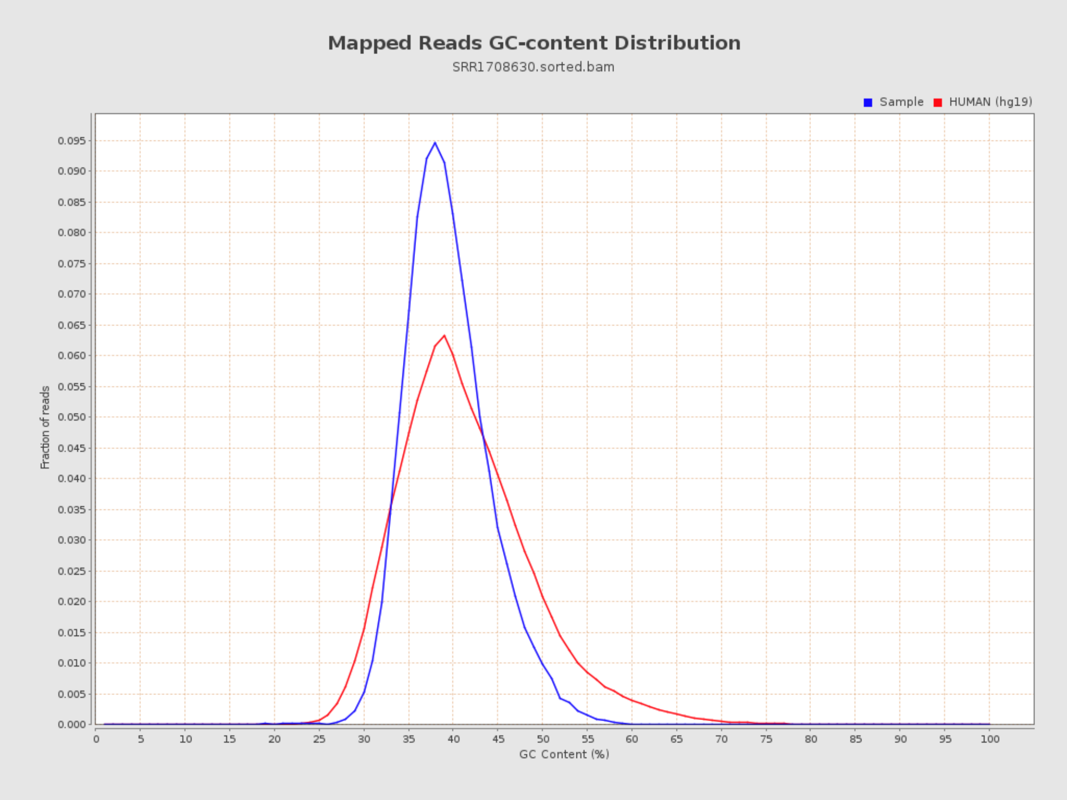
# 7. Results : Duplication Rate Histogram



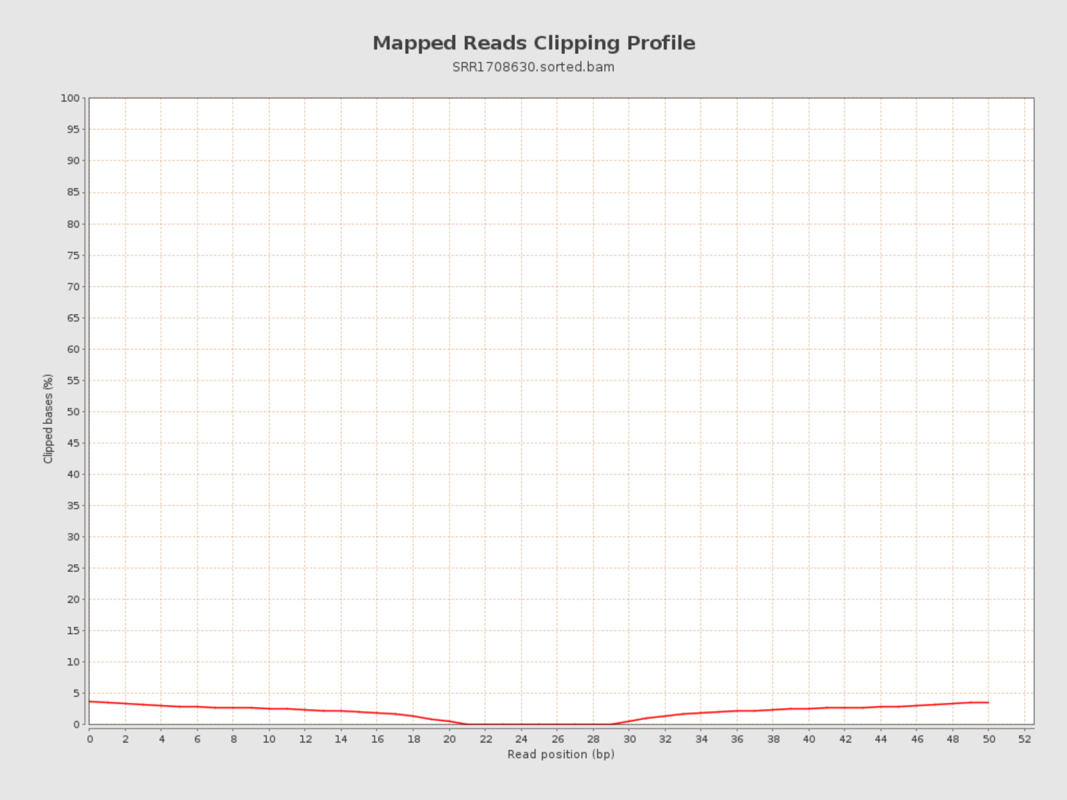
# 8. Results : Mapped Reads Nucleotide Content



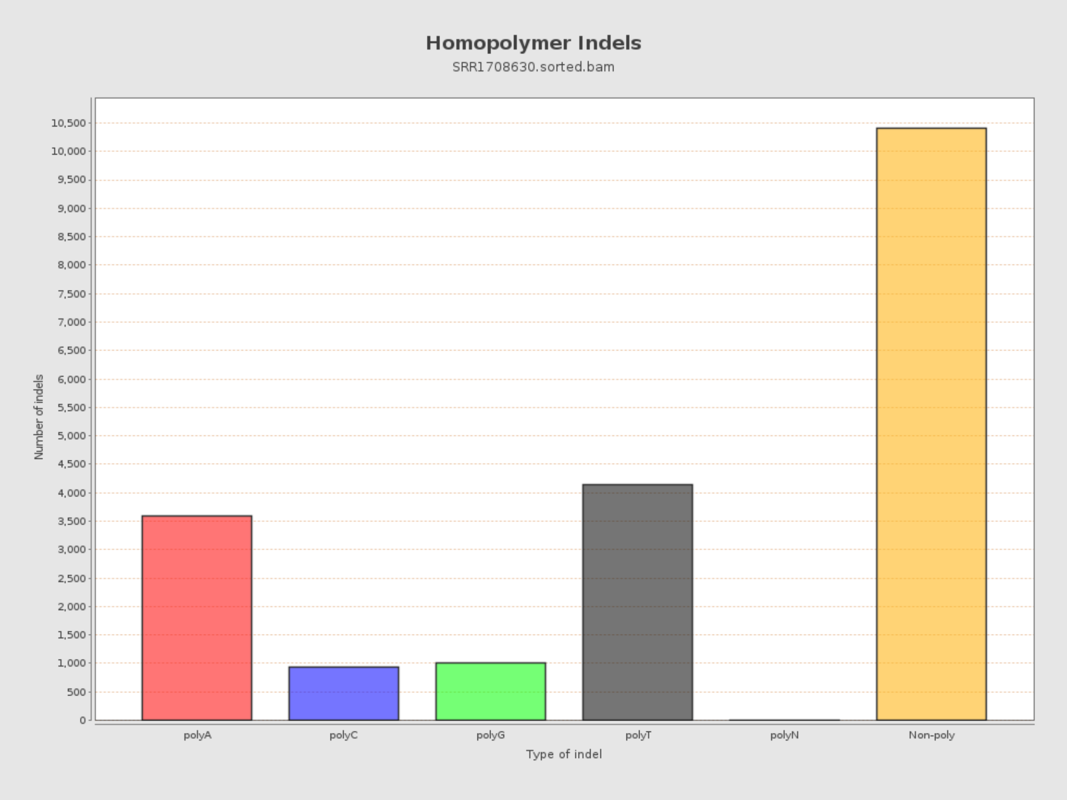
# 9. Results : Mapped Reads GC-content Distribution



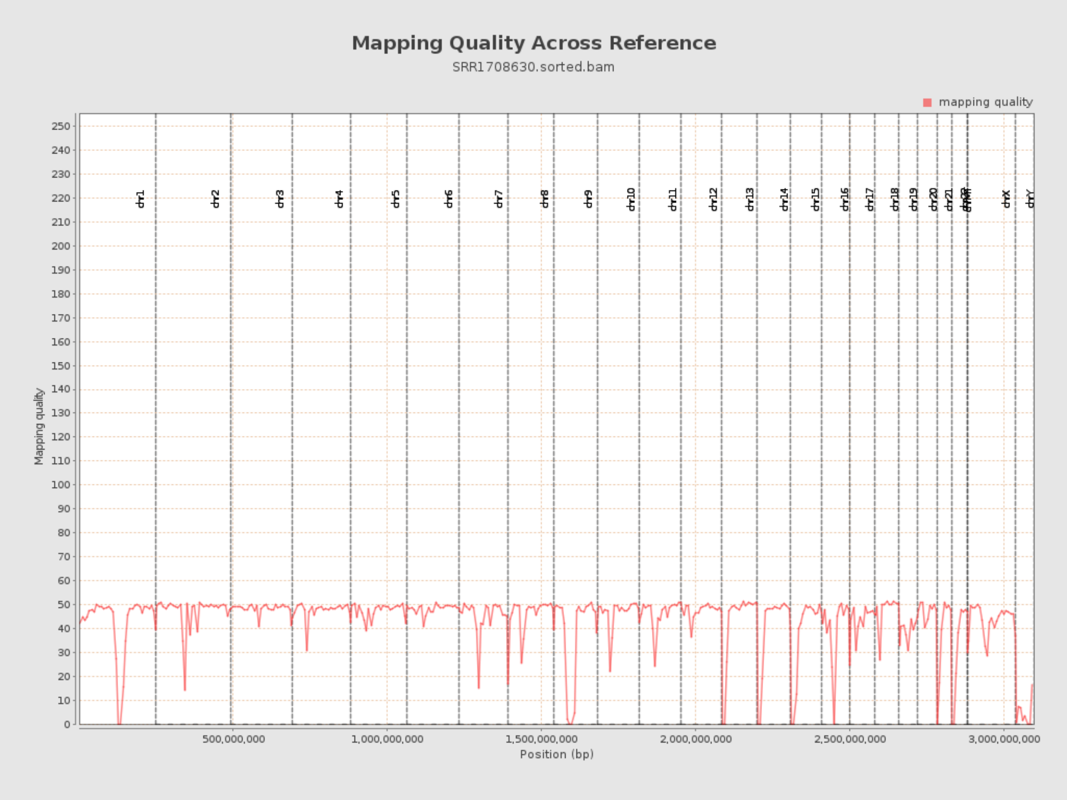
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram