# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/04 05:20:06*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717088.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_SRR9717088 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717088.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Sep 04 05:20:06 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9717088.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,540,019 |
| Mapped reads | 1,394,636 / 90.56% |
| Unmapped reads | 145,383 / 9.44% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 21,910 / 1.42% |
| Read min/max/mean length | 30 / 101 / 101.53 |
| Duplicated reads (estimated) | 59,117 / 3.84% |
| Duplication rate | 2.51% |
| Clipped reads | 1,413,679 / 91.8% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 26,627,943 / 24.19% |
| Number/percentage of C's | 20,576,375 / 18.69% |
| Number/percentage of T's | 34,976,483 / 31.77% |
| Number/percentage of G's | 27,911,447 / 25.35% |
| Number/percentage of N's | 7,080 / 0.01% |
| GC Percentage | 44.04% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0356 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4339 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.23 |

## 2.5. Mismatches and indels

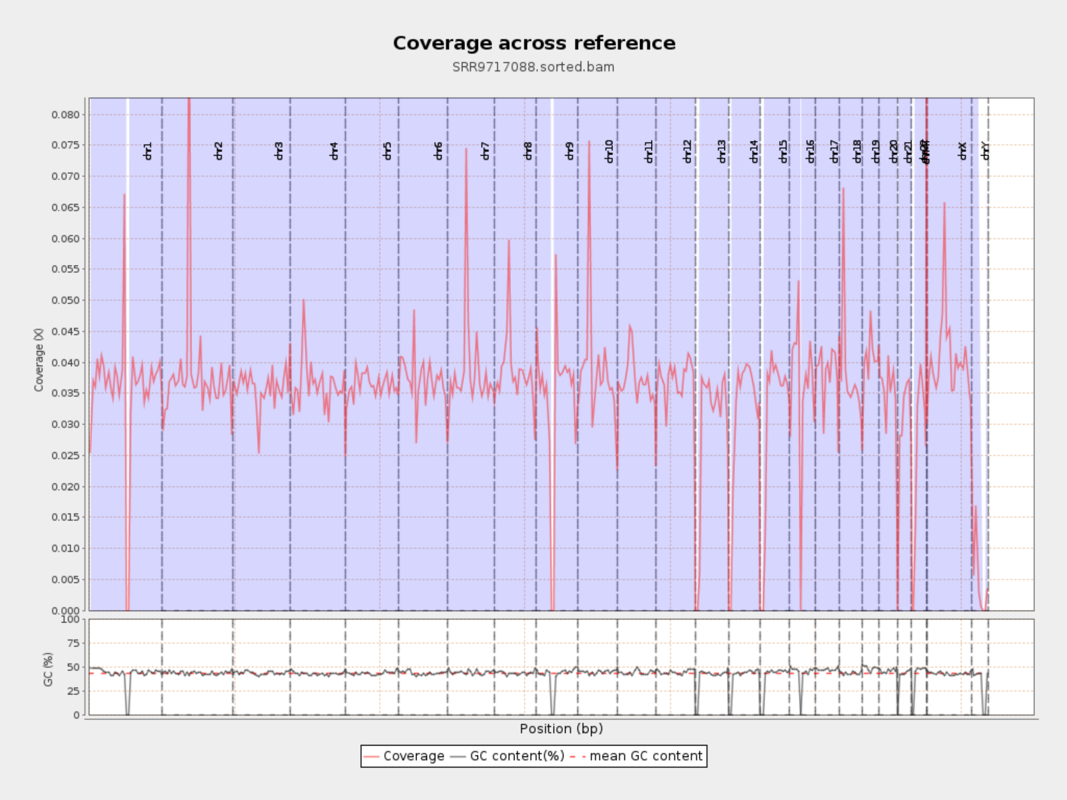
| | |
|---|---|
| General error rate | 0.84% |
| Mismatches | 905,989 |
| Insertions | 10,295 |
| Mapped reads with at least one insertion | 0.73% |
| Deletions | 27,784 |
| Mapped reads with at least one deletion | 1.96% |
| Homopolymer indels | 44.03% |

## 2.6. Chromosome stats

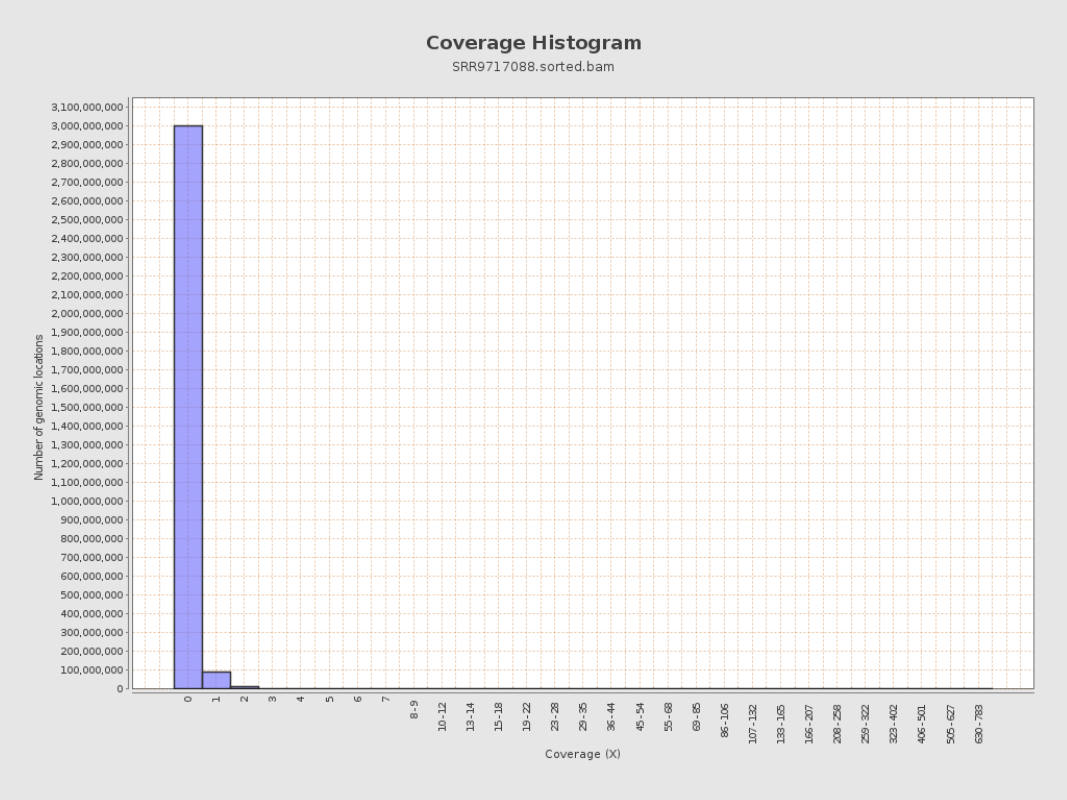
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 8885028 | 0.0356 | 0.6843 |
| chr2 | 243199373 | 9339473 | 0.0384 | 0.6378 |
| chr3 | 198022430 | 7105517 | 0.0359 | 0.214 |
| chr4 | 191154276 | 6956014 | 0.0364 | 0.2357 |
| chr5 | 180915260 | 6591526 | 0.0364 | 0.2214 |
| chr6 | 171115067 | 6369664 | 0.0372 | 0.2657 |
| chr7 | 159138663 | 6182804 | 0.0389 | 0.563 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 5638799 | 0.0385 | 0.5904 |
| chr9 | 141213431 | 4742279 | 0.0336 | 0.4872 |
| chr10 | 135534747 | 5270763 | 0.0389 | 0.4299 |
| chr11 | 135006516 | 4982047 | 0.0369 | 0.4252 |
| chr12 | 133851895 | 4977700 | 0.0372 | 0.2222 |
| chr13 | 115169878 | 3352134 | 0.0291 | 0.1879 |
| chr14 | 107349540 | 3300850 | 0.0307 | 0.2704 |
| chr15 | 102531392 | 3136843 | 0.0306 | 0.1995 |
| chr16 | 90354753 | 3260686 | 0.0361 | 0.2556 |
| chr17 | 81195210 | 3086449 | 0.038 | 0.2415 |
| chr18 | 78077248 | 3052142 | 0.0391 | 0.9359 |
| chr19 | 59128983 | 2407971 | 0.0407 | 0.4993 |
| chr20 | 63025520 | 2217854 | 0.0352 | 0.2244 |
| chr21 | 48129895 | 1411133 | 0.0293 | 0.209 |
| chr22 | 51304566 | 1249237 | 0.0243 | 0.1736 |
| chrMT | 16571 | 2569 | 0.155 | 0.3923 |
| chrX | 155270560 | 6326759 | 0.0407 | 0.3355 |
| chrY | 59373566 | 301625 | 0.0051 | 0.1491 |

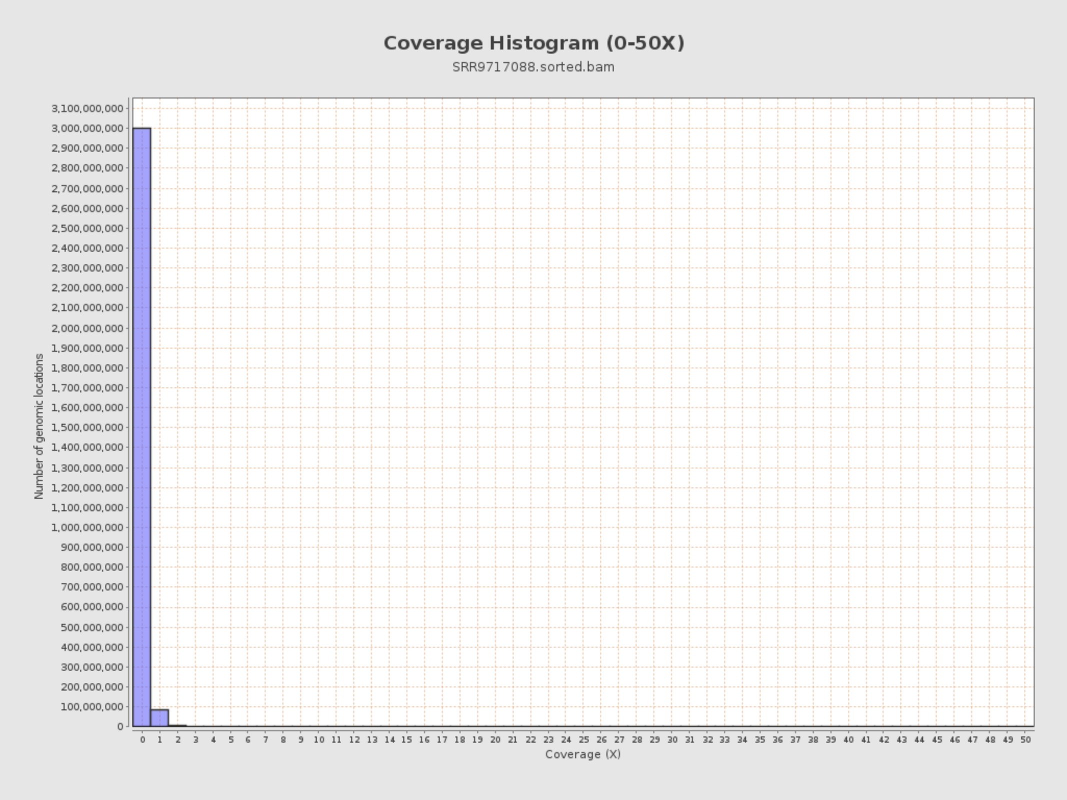
# 3. Results : Coverage across reference



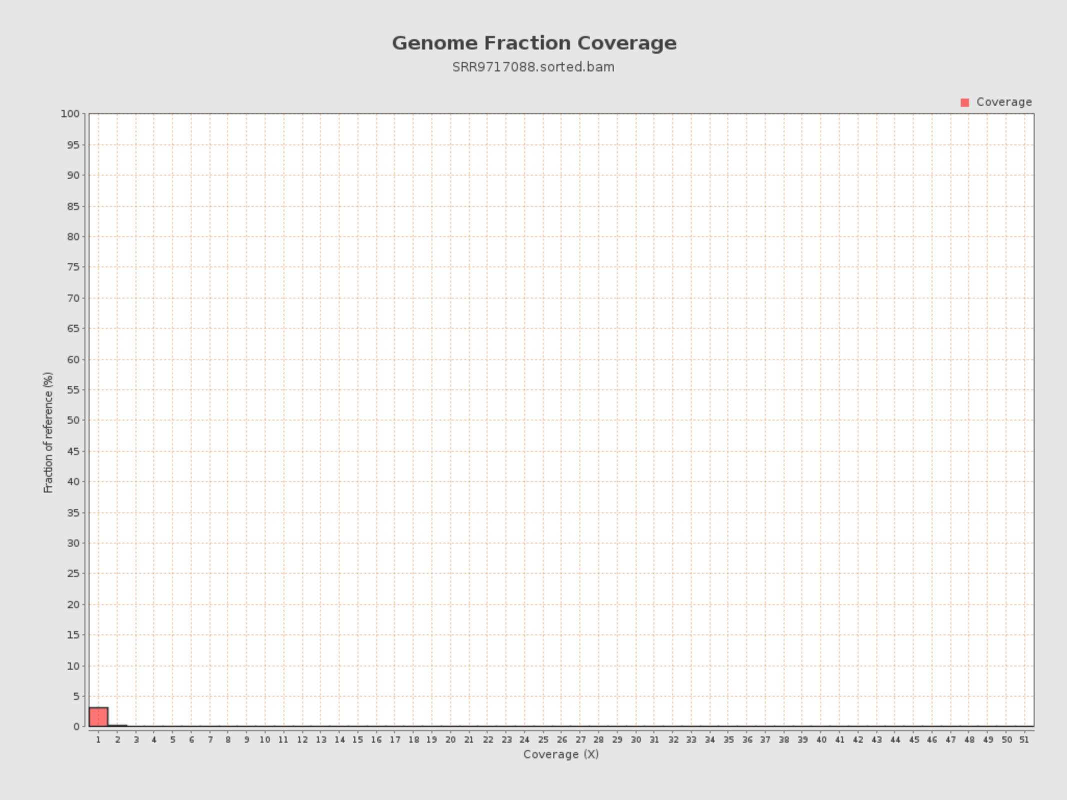
# 4. Results : Coverage Histogram



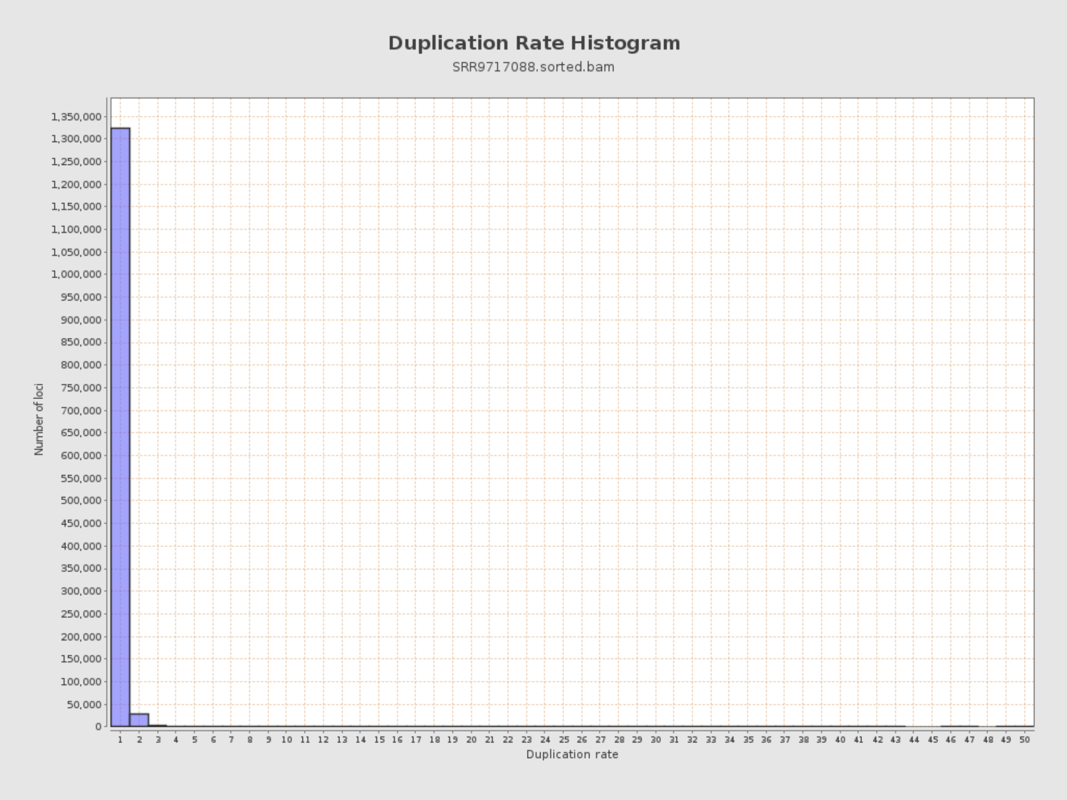
# 5. Results : Coverage Histogram (0-50X)



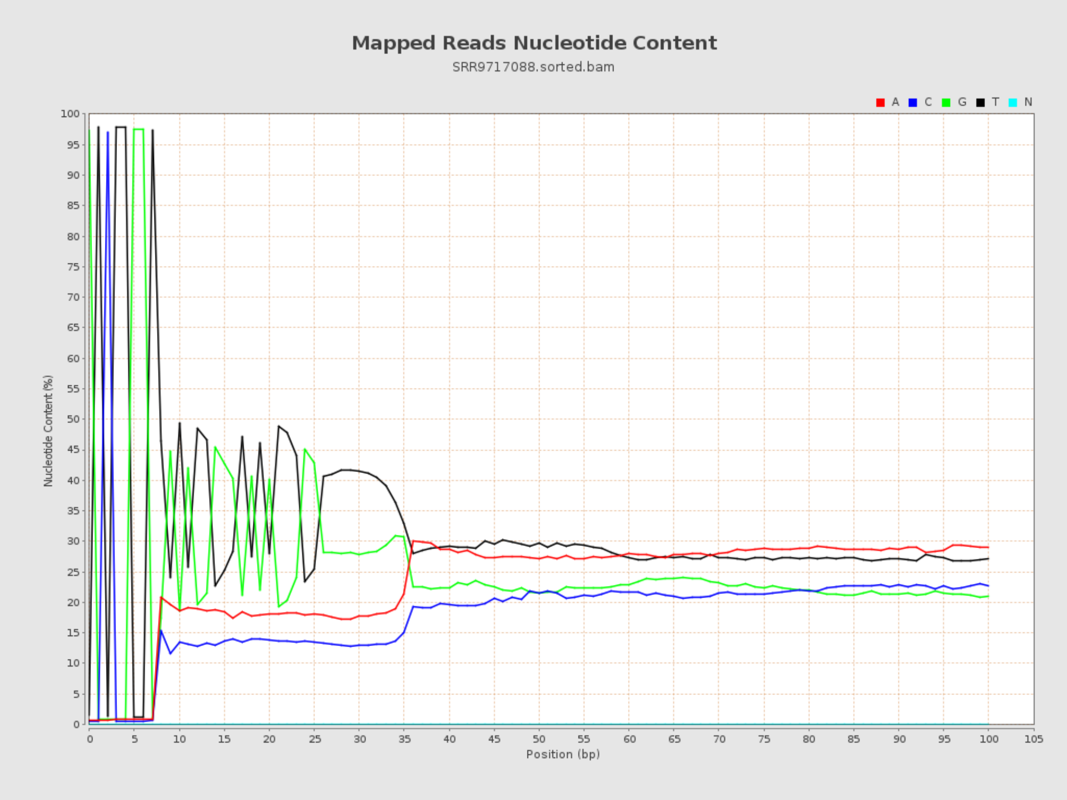
# 6. Results : Genome Fraction Coverage



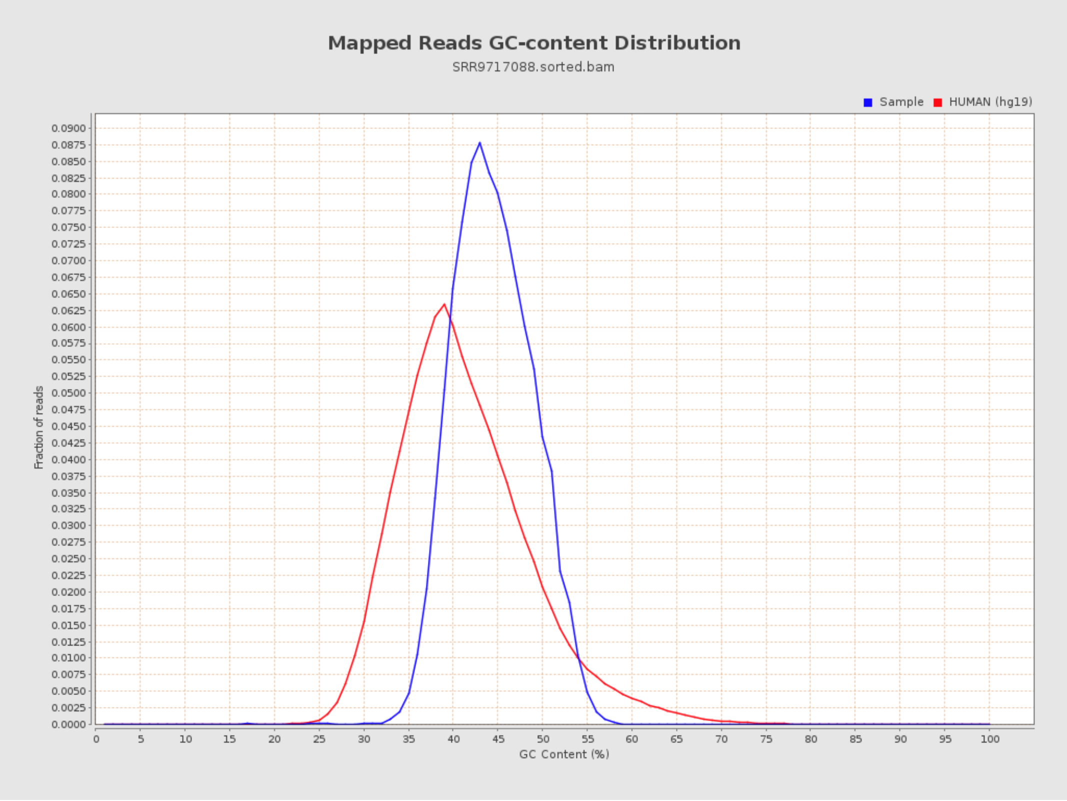
# 7. Results : Duplication Rate Histogram



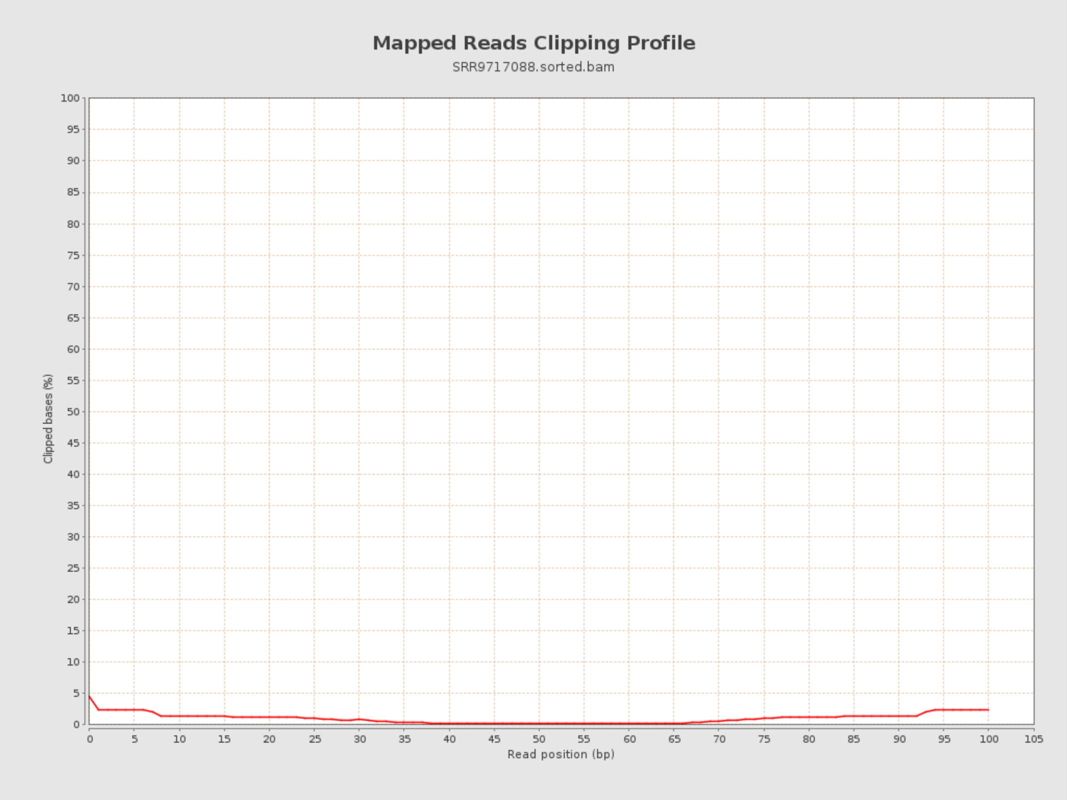
# 8. Results : Mapped Reads Nucleotide Content



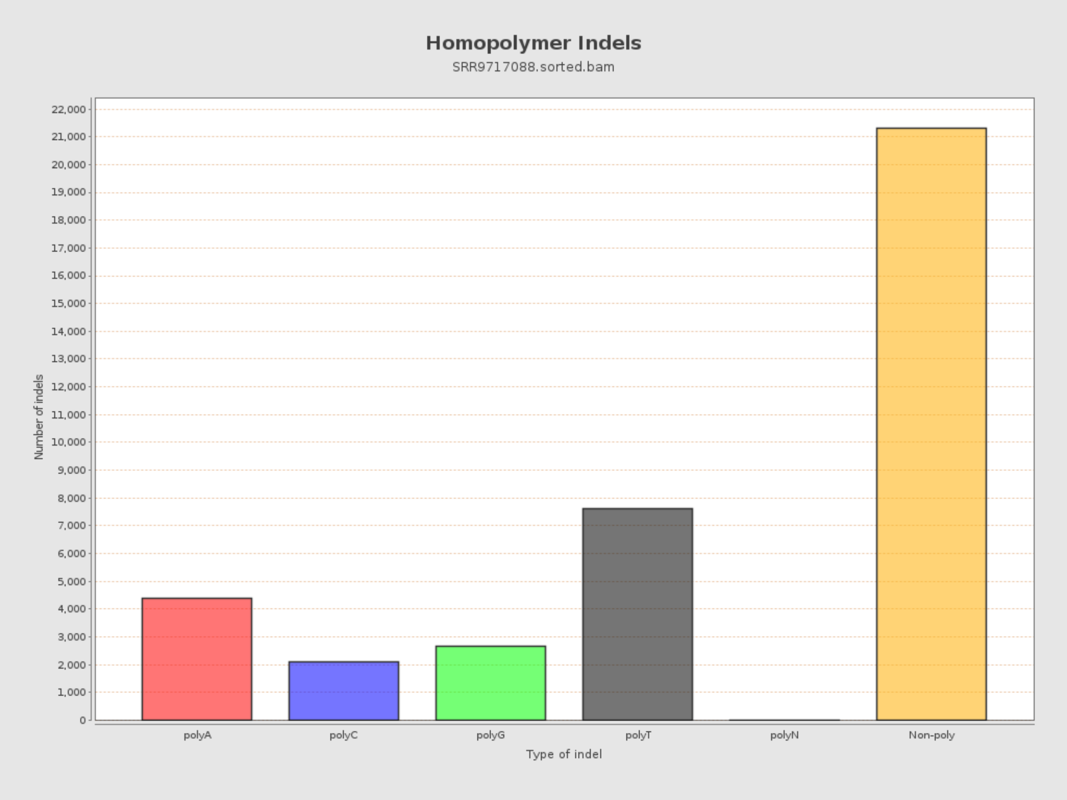
# 9. Results : Mapped Reads GC-content Distribution



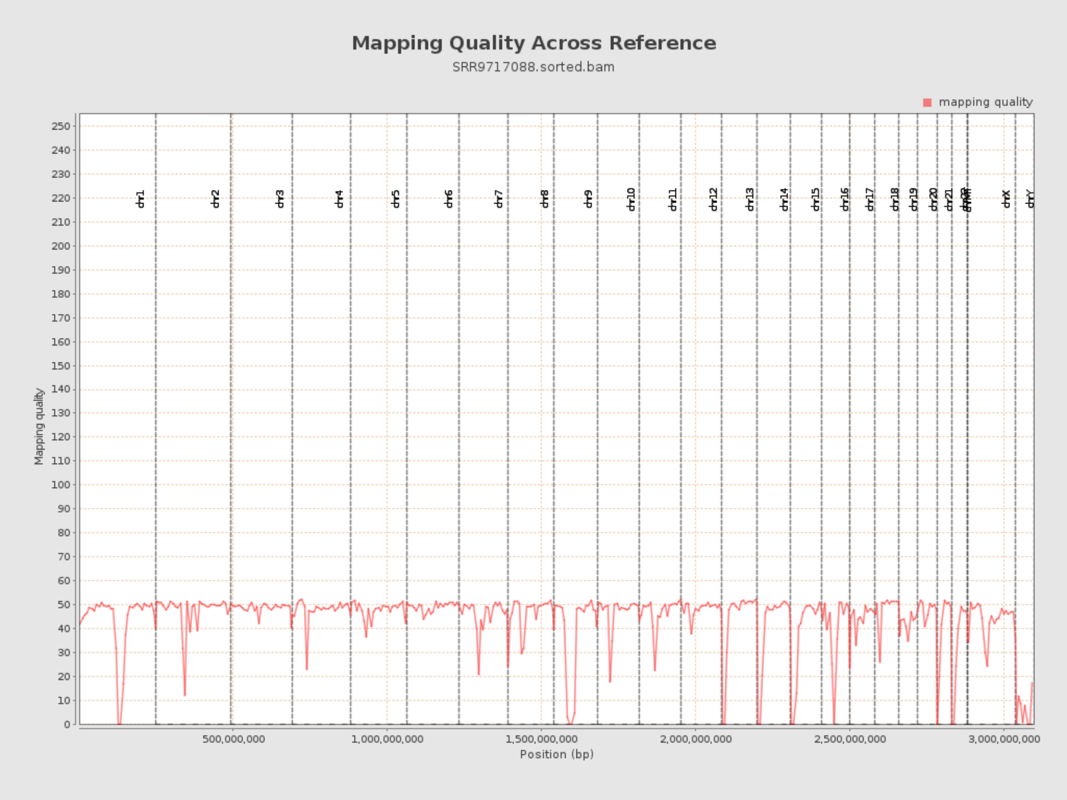
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram