# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/20 01:39:20*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506316.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_SRR1506316 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506316.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Dec 20 01:39:19 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1506316.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 5,818,804 |
| Mapped reads | 4,121,184 / 70.83% |
| Unmapped reads | 1,697,620 / 29.17% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 77,570 / 1.33% |
| Read min/max/mean length | 30 / 94 / 94.48 |
| Duplicated reads (estimated) | 539,696 / 9.28% |
| Duplication rate | 9.04% |
| Clipped reads | 2,809,898 / 48.29% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 88,108,617 / 27.6% |
| Number/percentage of C's | 57,322,991 / 17.96% |
| Number/percentage of T's | 89,813,168 / 28.14% |
| Number/percentage of G's | 83,887,437 / 26.28% |
| Number/percentage of N's | 67,249 / 0.02% |
| GC Percentage | 44.24% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1032 |
| | |

| | |
|---|---|
| Standard Deviation | 0.7482 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.86 |

## 2.5. Mismatches and indels

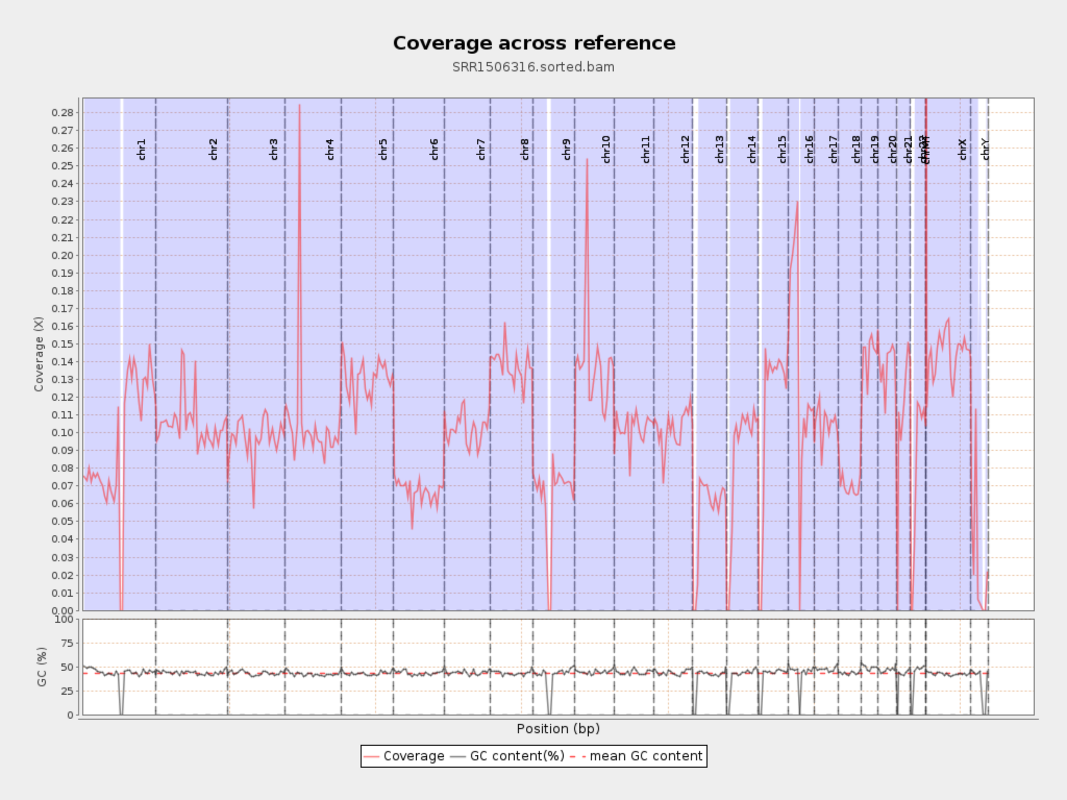
| | |
|---|---|
| General error rate | 0.79% |
| Mismatches | 2,429,650 |
| Insertions | 29,661 |
| Mapped reads with at least one insertion | 0.7% |
| Deletions | 70,235 |
| Mapped reads with at least one deletion | 1.67% |
| Homopolymer indels | 41.92% |

## 2.6. Chromosome stats

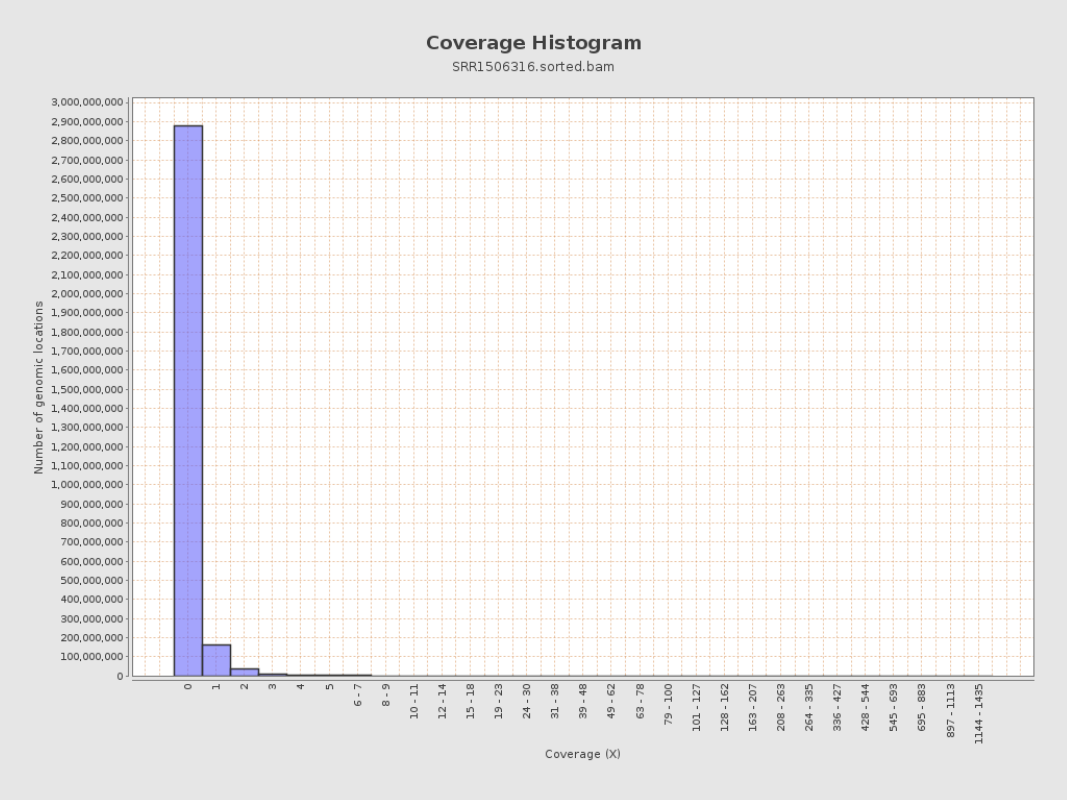
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 23402557 | 0.0939 | 1.0879 |
| chr2 | 243199373 | 25629936 | 0.1054 | 0.82 |
| chr3 | 198022430 | 19197634 | 0.0969 | 0.4417 |
| chr4 | 191154276 | 20350367 | 0.1065 | 0.8599 |
| chr5 | 180915260 | 23627487 | 0.1306 | 0.5288 |
| chr6 | 171115067 | 11429405 | 0.0668 | 0.3905 |
| chr7 | 159138663 | 16307994 | 0.1025 | 0.7275 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 20151106 | 0.1377 | 1.1097 |
| chr9 | 141213431 | 8995560 | 0.0637 | 0.5509 |
| chr10 | 135534747 | 18803421 | 0.1387 | 1.1547 |
| chr11 | 135006516 | 13842722 | 0.1025 | 0.6346 |
| chr12 | 133851895 | 13729348 | 0.1026 | 0.475 |
| chr13 | 115169878 | 6340892 | 0.0551 | 0.335 |
| chr14 | 107349540 | 9324926 | 0.0869 | 0.4632 |
| chr15 | 102531392 | 11379828 | 0.111 | 0.4912 |
| chr16 | 90354753 | 12113061 | 0.1341 | 0.7656 |
| chr17 | 81195210 | 8613274 | 0.1061 | 0.5451 |
| chr18 | 78077248 | 5485154 | 0.0703 | 0.8528 |
| chr19 | 59128983 | 8511762 | 0.144 | 0.8906 |
| chr20 | 63025520 | 8662808 | 0.1374 | 0.6074 |
| chr21 | 48129895 | 5407663 | 0.1124 | 0.7442 |
| chr22 | 51304566 | 3997689 | 0.0779 | 0.4245 |
| chrMT | 16571 | 14303 | 0.8631 | 1.5034 |
| chrX | 155270560 | 22466745 | 0.1447 | 0.6015 |
| chrY | 59373566 | 1562162 | 0.0263 | 1.2044 |

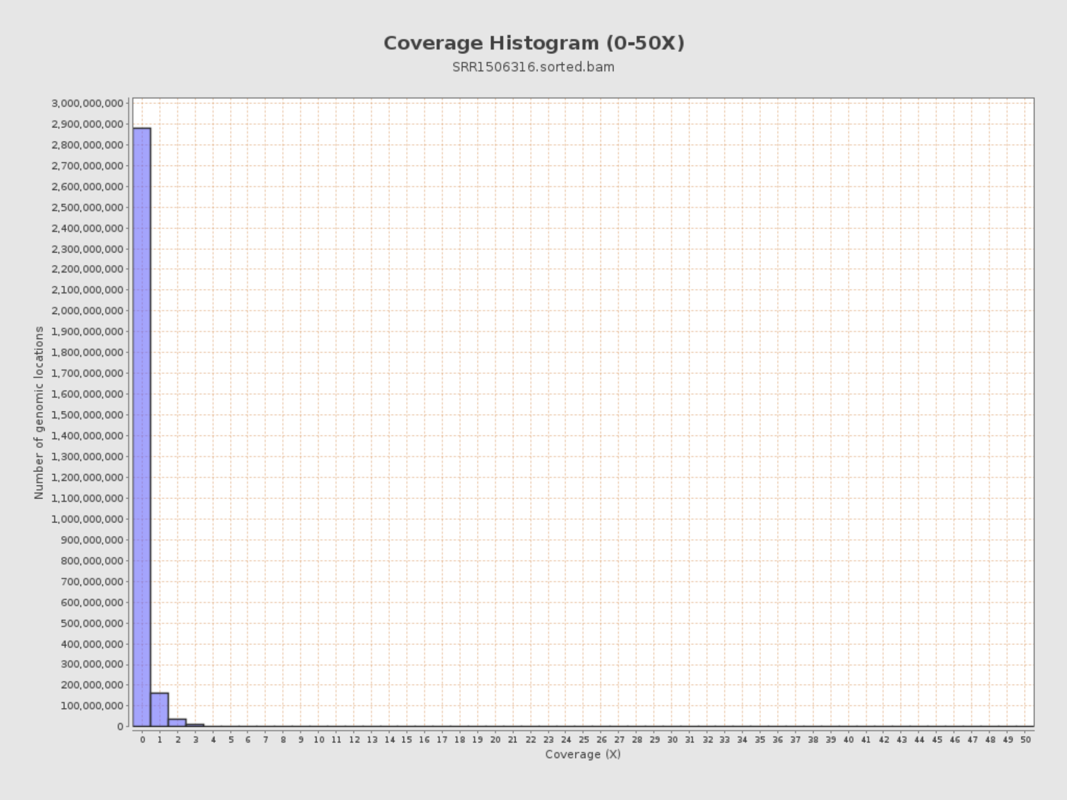
# 3. Results : Coverage across reference



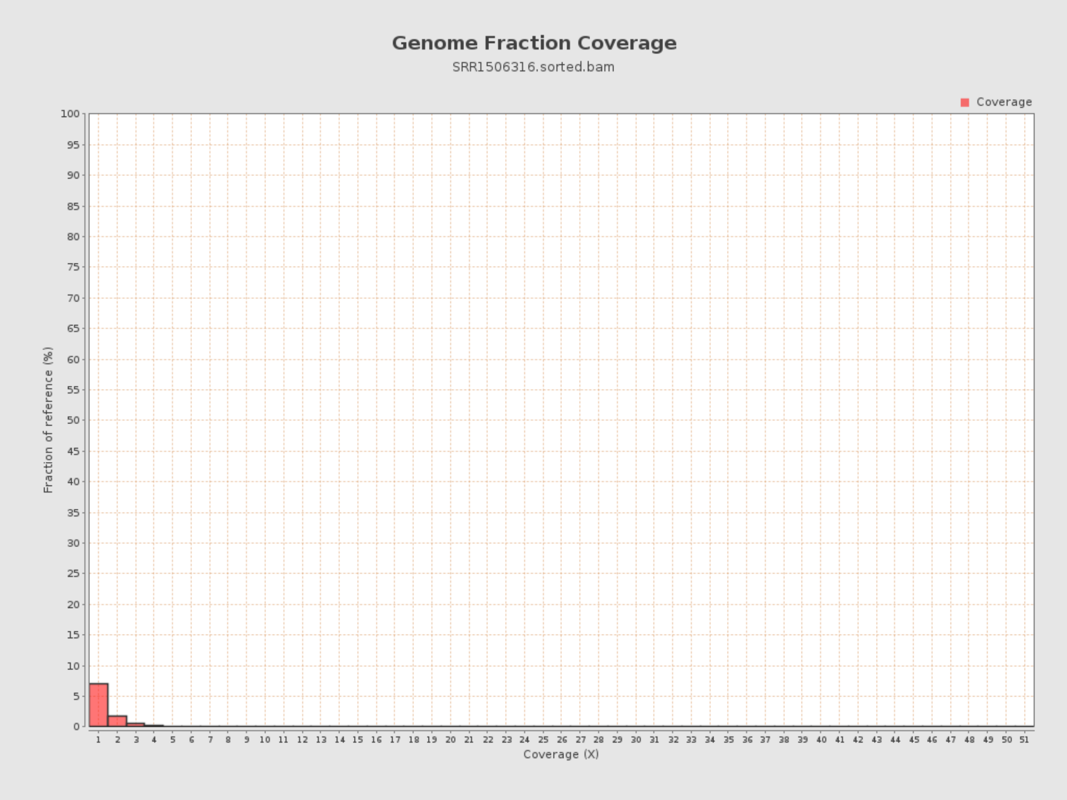
# 4. Results : Coverage Histogram



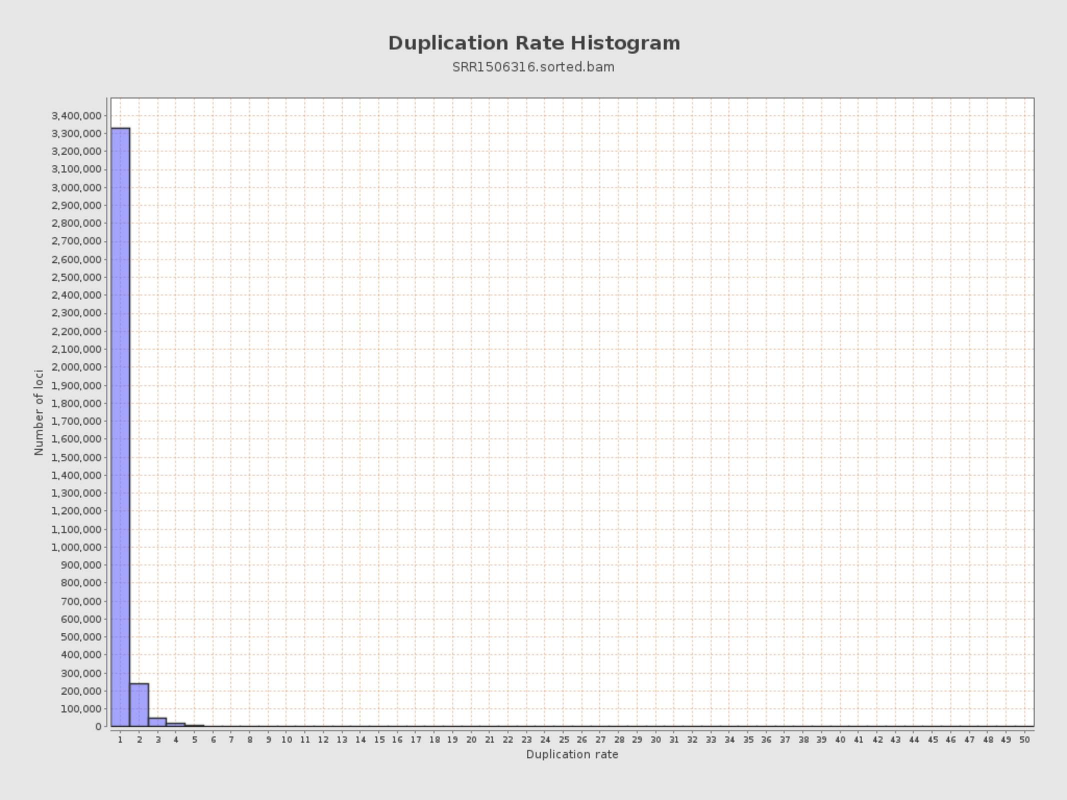
# 5. Results : Coverage Histogram (0-50X)



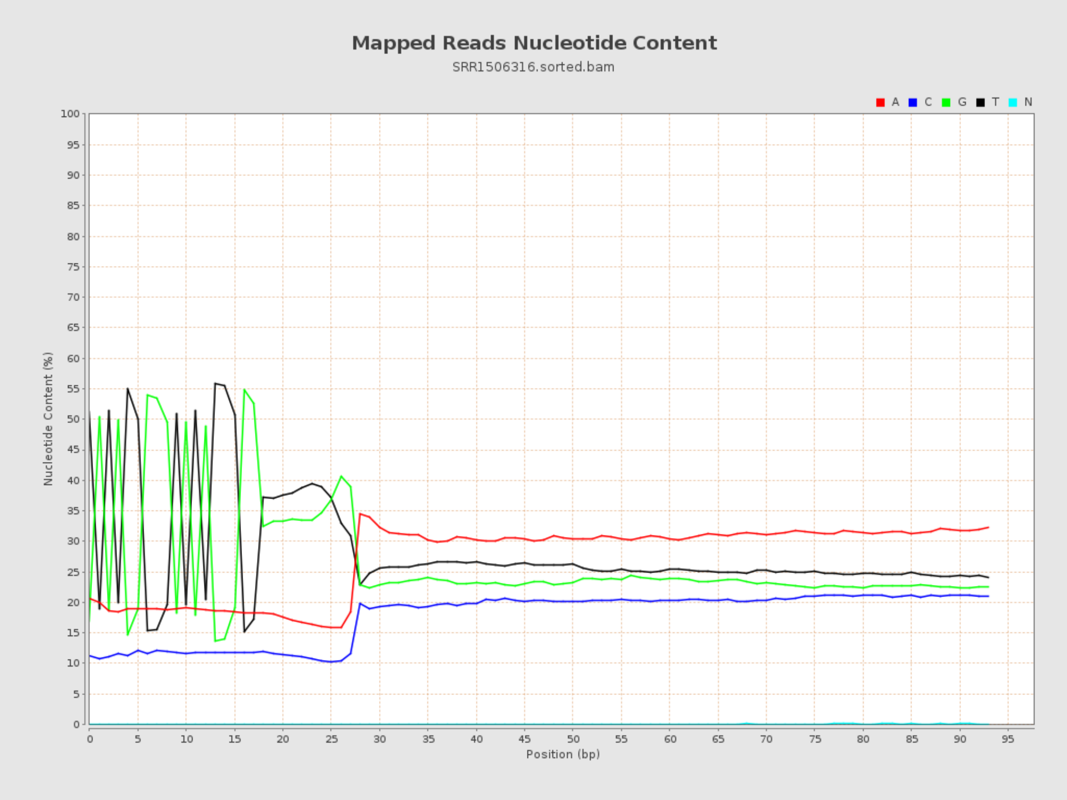
# 6. Results : Genome Fraction Coverage



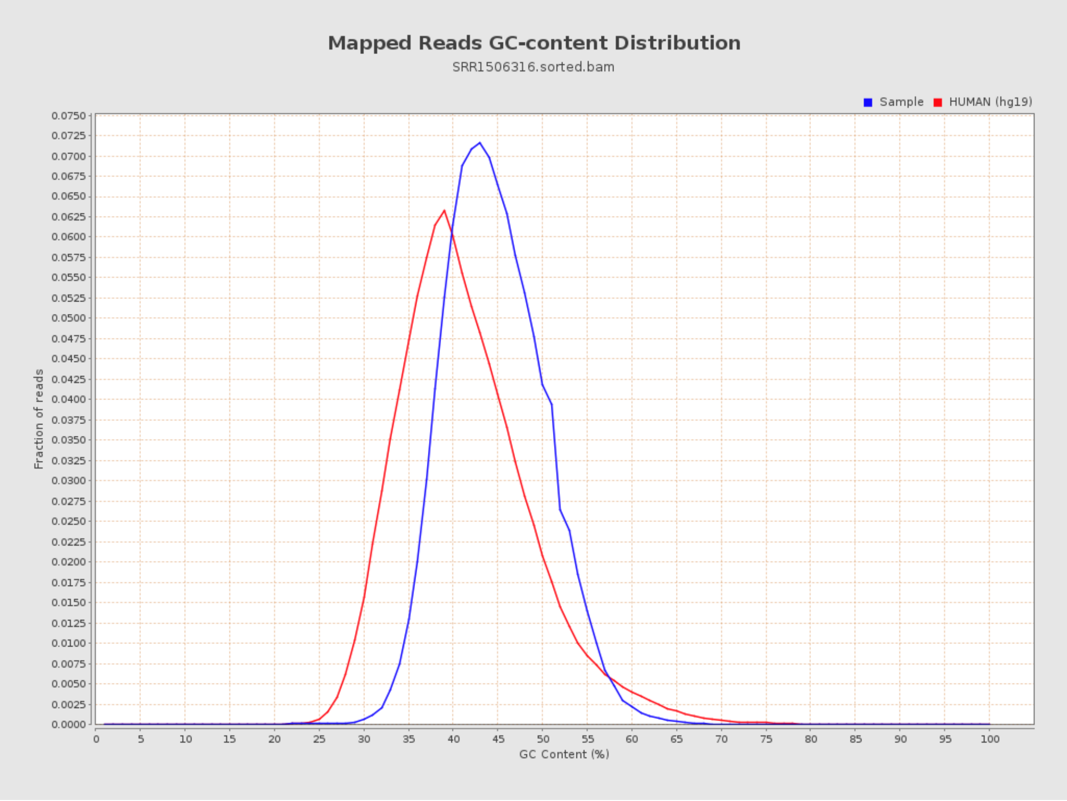
# 7. Results : Duplication Rate Histogram



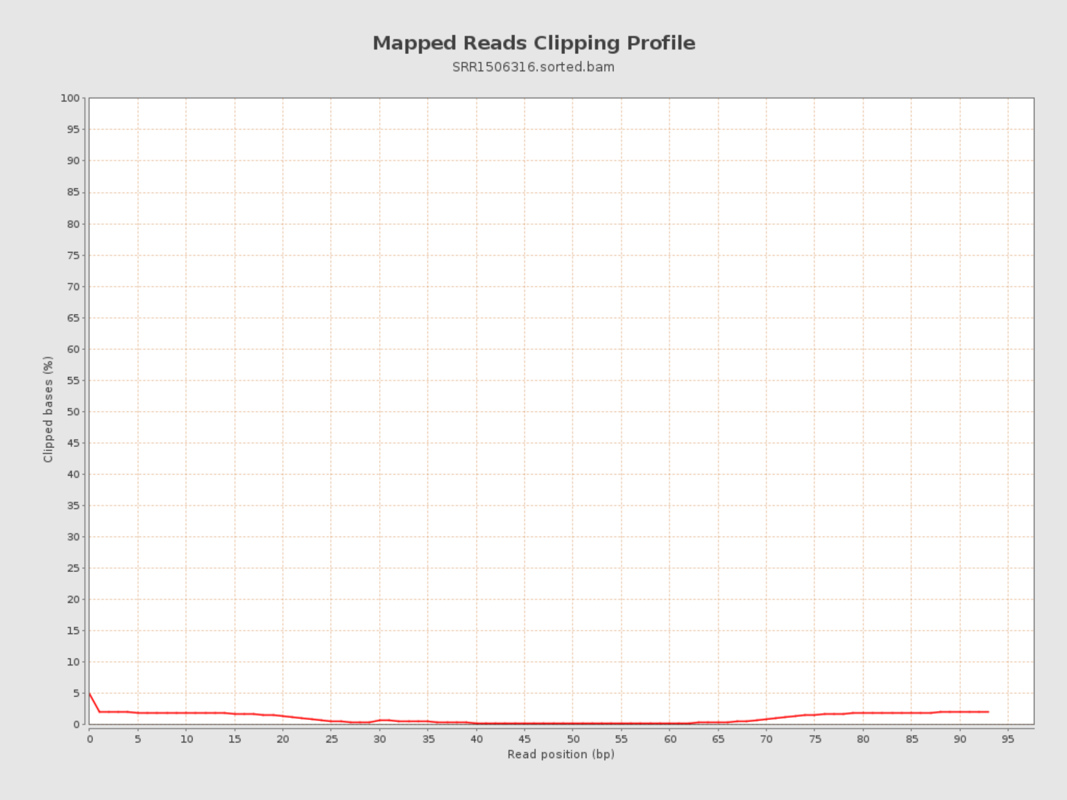
# 8. Results : Mapped Reads Nucleotide Content



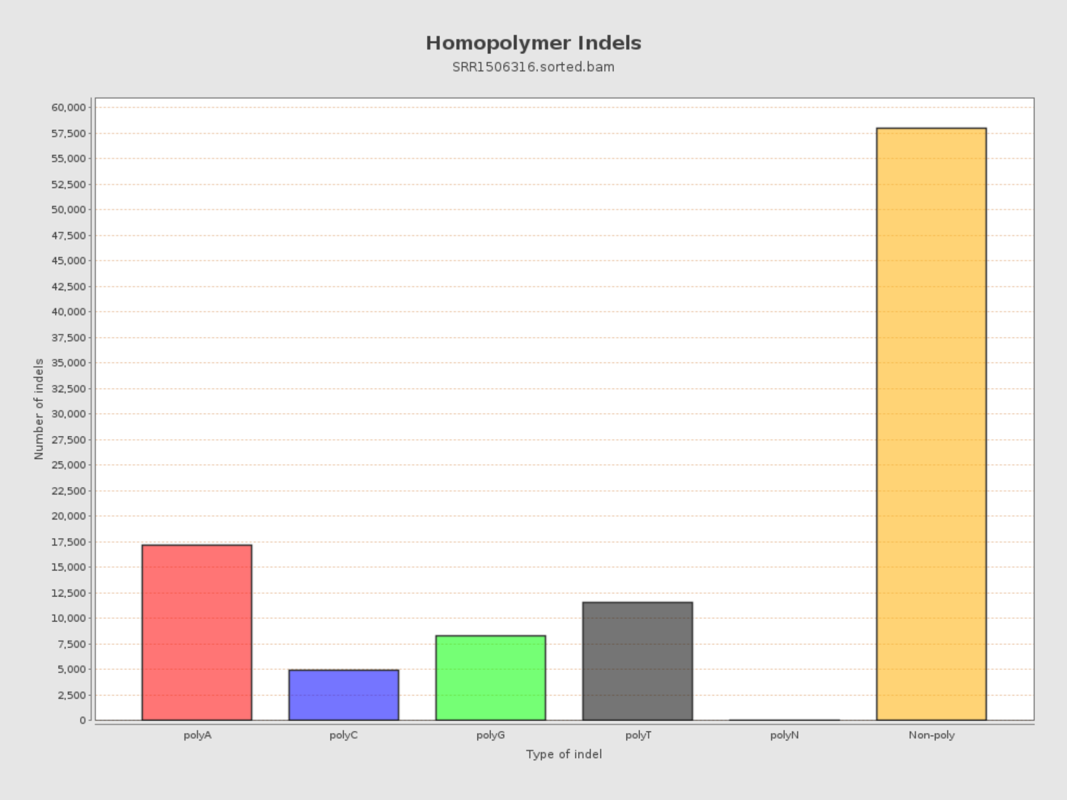
# 9. Results : Mapped Reads GC-content Distribution



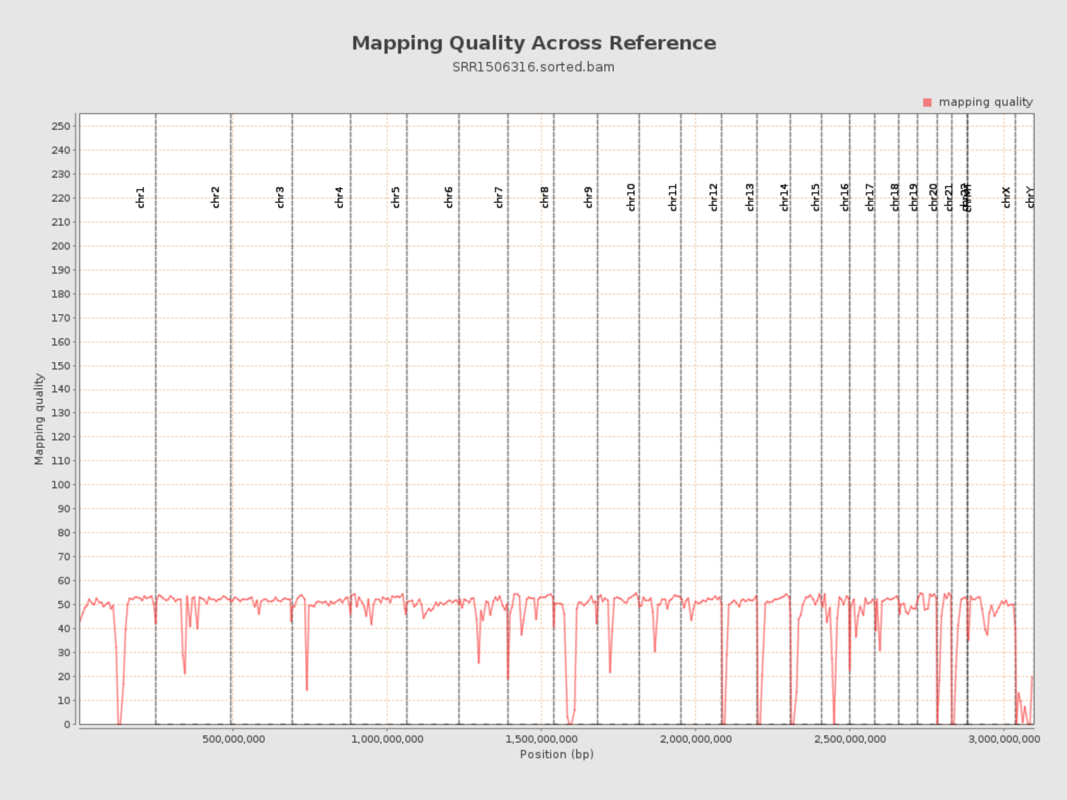
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram