# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 19:25:09*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971316.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_SRR2971316 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971316.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Aug 24 19:25:08 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR2971316.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 10,503,271 |
| Mapped reads | 9,454,411 / 90.01% |
| Unmapped reads | 1,048,860 / 9.99% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 1,264 / 0.01% |
| Read min/max/mean length | 30 / 50 / 50 |
| Duplicated reads (estimated) | 927,584 / 8.83% |
| Duplication rate | 8.38% |
| Clipped reads | 1,952,066 / 18.59% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 129,446,943 / 28.57% |
| Number/percentage of C's | 93,983,153 / 20.74% |
| Number/percentage of T's | 132,590,037 / 29.27% |
| Number/percentage of G's | 97,000,502 / 21.41% |
| Number/percentage of N's | 25,867 / 0.01% |
| GC Percentage | 42.16% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1464 |
| | |

| | |
|---|---|
| Standard Deviation | 1.1273 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 39.61 |

## 2.5. Mismatches and indels

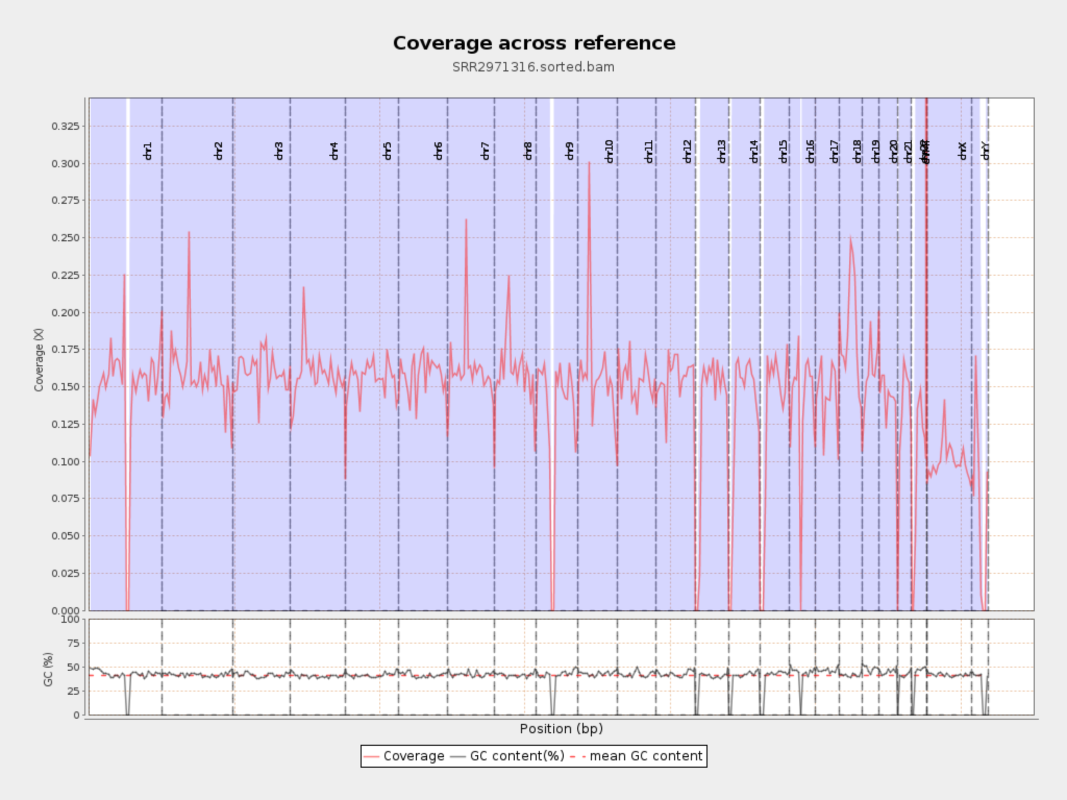
| | |
|---|---|
| General error rate | 0.46% |
| Mismatches | 2,060,525 |
| Insertions | 27,822 |
| Mapped reads with at least one insertion | 0.29% |
| Deletions | 66,752 |
| Mapped reads with at least one deletion | 0.7% |
| Homopolymer indels | 42.48% |

## 2.6. Chromosome stats

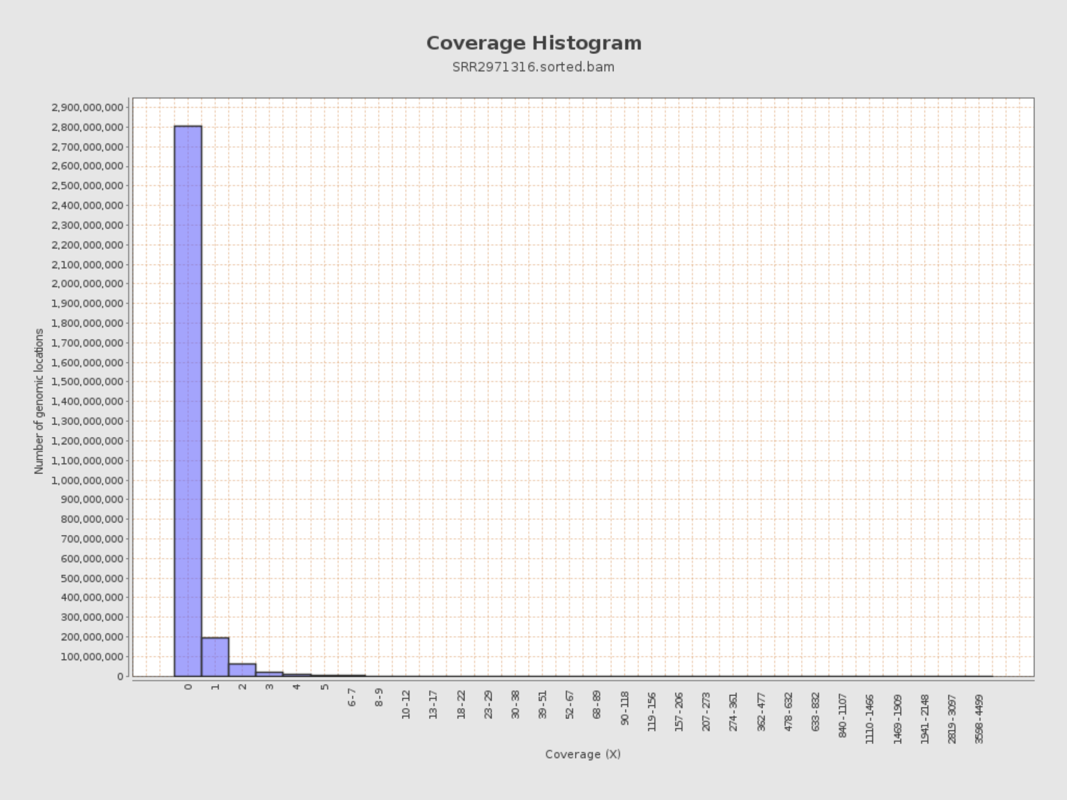
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 36559326 | 0.1467 | 1.8902 |
| chr2 | 243199373 | 38324900 | 0.1576 | 1.0278 |
| chr3 | 198022430 | 31761766 | 0.1604 | 0.5879 |
| chr4 | 191154276 | 30261706 | 0.1583 | 0.6908 |
| chr5 | 180915260 | 28286005 | 0.1563 | 0.5773 |
| chr6 | 171115067 | 26995463 | 0.1578 | 0.6275 |
| chr7 | 159138663 | 25979227 | 0.1632 | 1.6228 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 23589043 | 0.1612 | 2.3827 |
| chr9 | 141213431 | 18706072 | 0.1325 | 0.9539 |
| chr10 | 135534747 | 21667172 | 0.1599 | 1.2208 |
| chr11 | 135006516 | 20785049 | 0.154 | 0.8868 |
| chr12 | 133851895 | 20782872 | 0.1553 | 0.596 |
| chr13 | 115169878 | 14888839 | 0.1293 | 0.527 |
| chr14 | 107349540 | 13873564 | 0.1292 | 0.6497 |
| chr15 | 102531392 | 13196361 | 0.1287 | 0.514 |
| chr16 | 90354753 | 12480812 | 0.1381 | 0.6557 |
| chr17 | 81195210 | 11558702 | 0.1424 | 0.6853 |
| chr18 | 78077248 | 14646424 | 0.1876 | 1.8895 |
| chr19 | 59128983 | 9484349 | 0.1604 | 1.6593 |
| chr20 | 63025520 | 8920905 | 0.1415 | 0.5739 |
| chr21 | 48129895 | 6109401 | 0.1269 | 0.6849 |
| chr22 | 51304566 | 4604780 | 0.0898 | 0.5213 |
| chrMT | 16571 | 161955 | 9.7734 | 7.6014 |
| chrX | 155270560 | 15618487 | 0.1006 | 0.5979 |
| chrY | 59373566 | 3901323 | 0.0657 | 0.6583 |

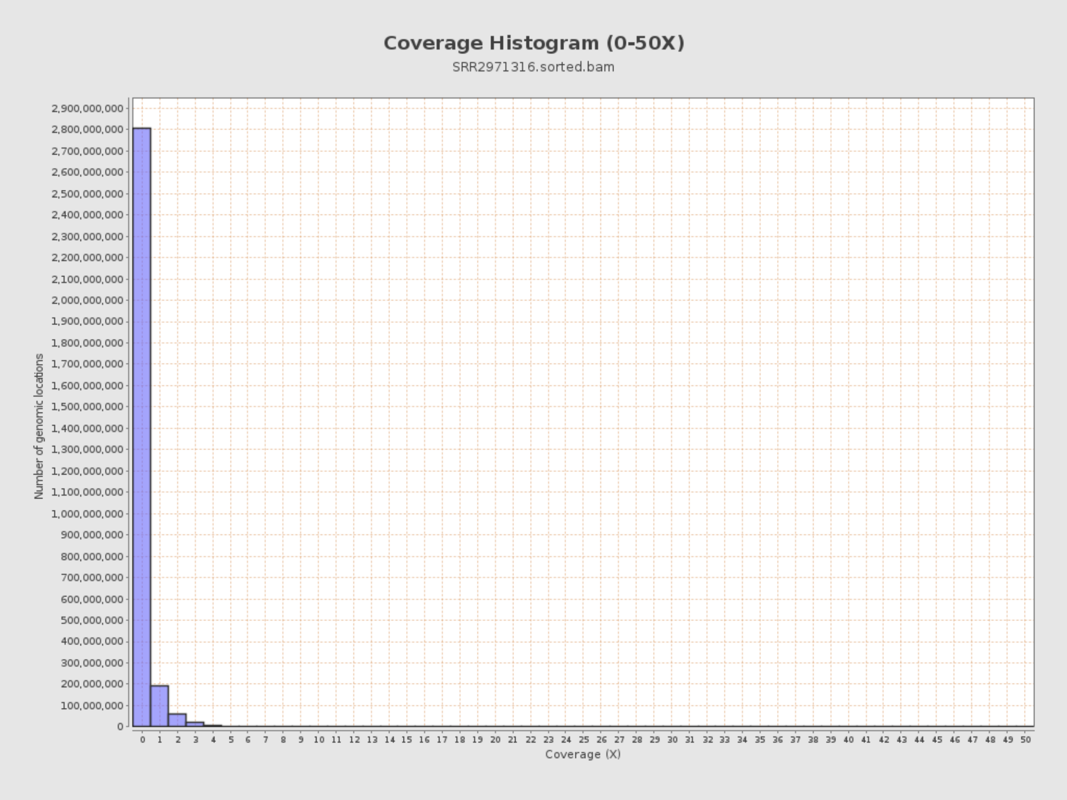
# 3. Results : Coverage across reference



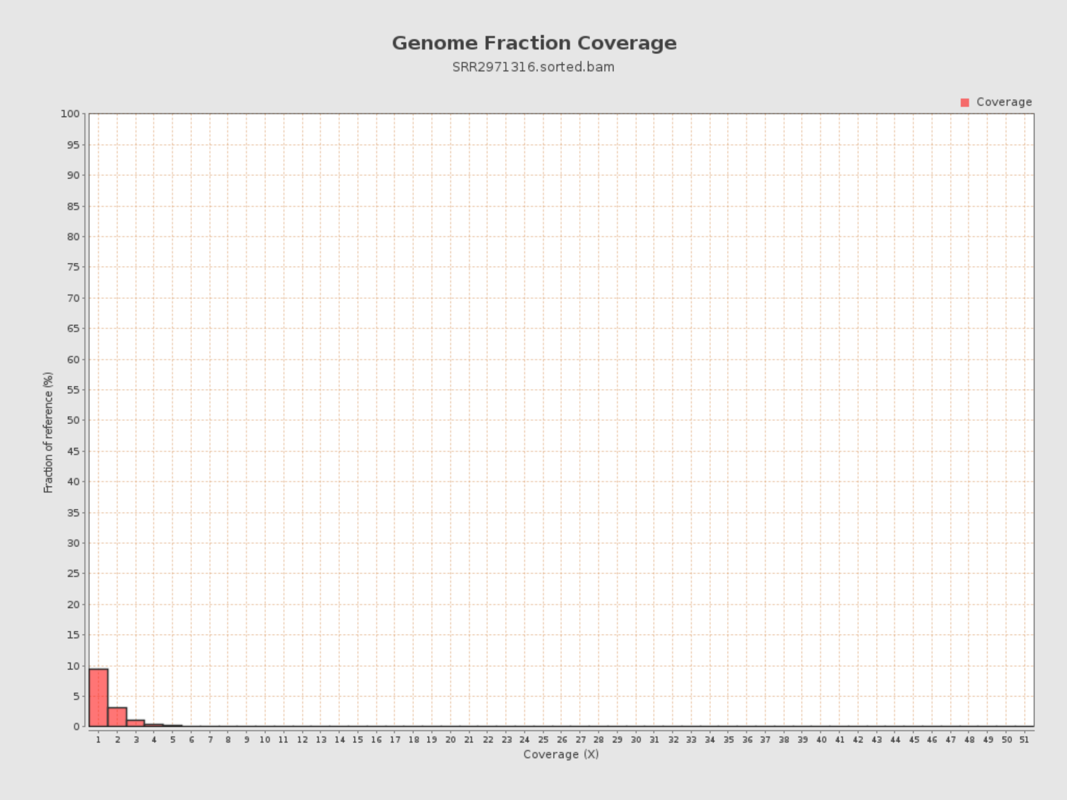
# 4. Results : Coverage Histogram



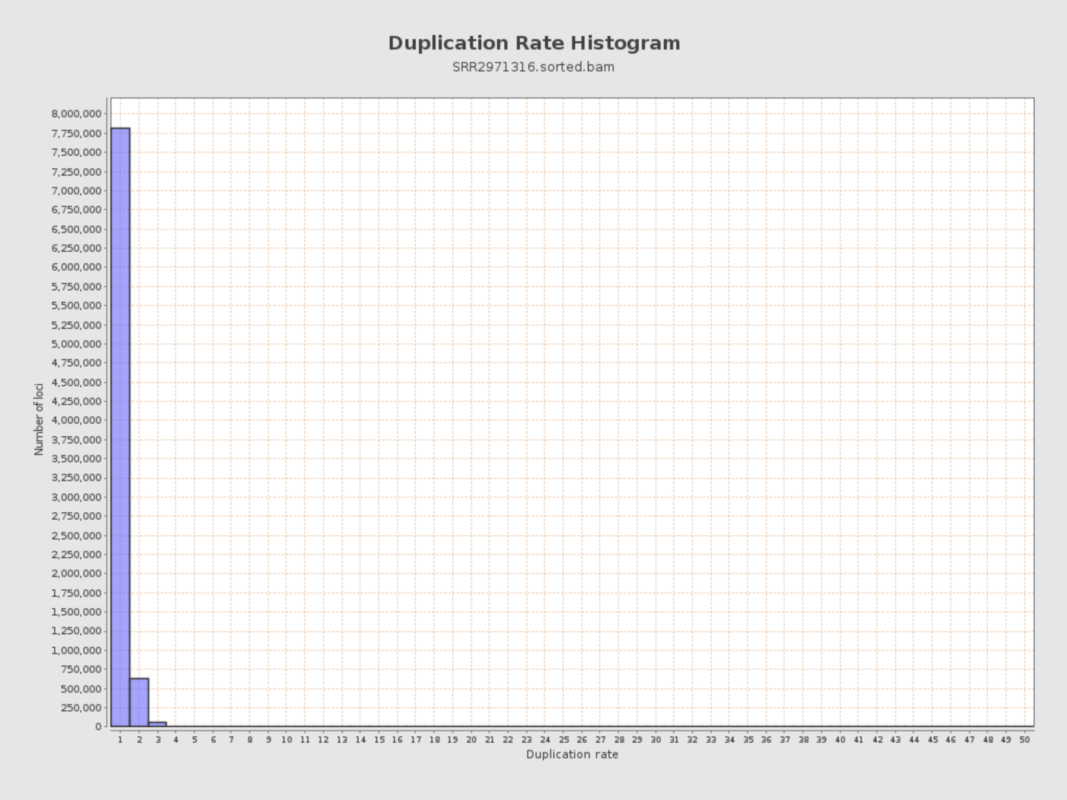
# 5. Results : Coverage Histogram (0-50X)



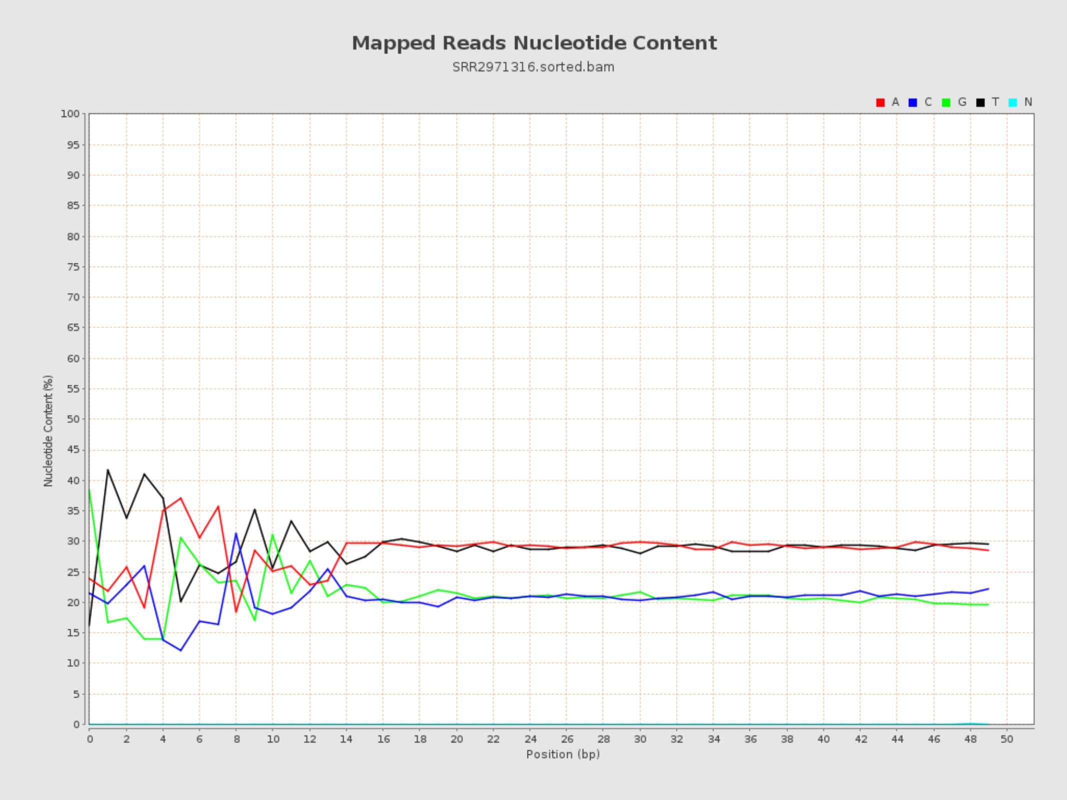
# 6. Results : Genome Fraction Coverage



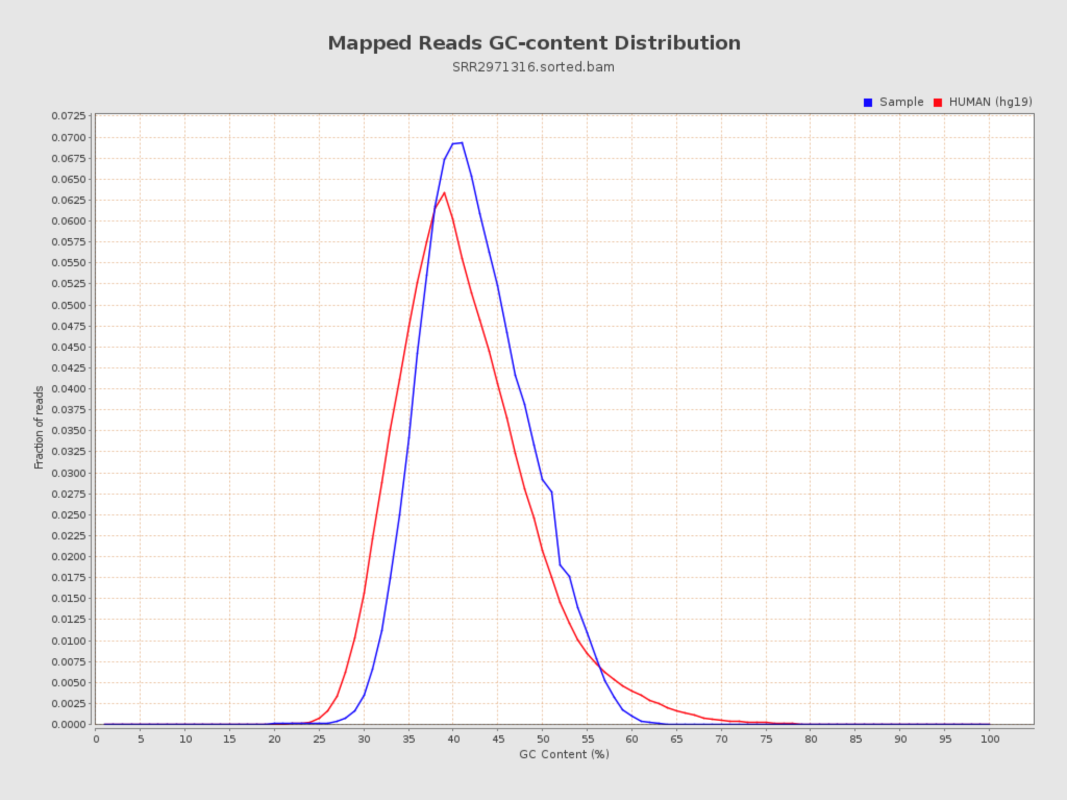
# 7. Results : Duplication Rate Histogram



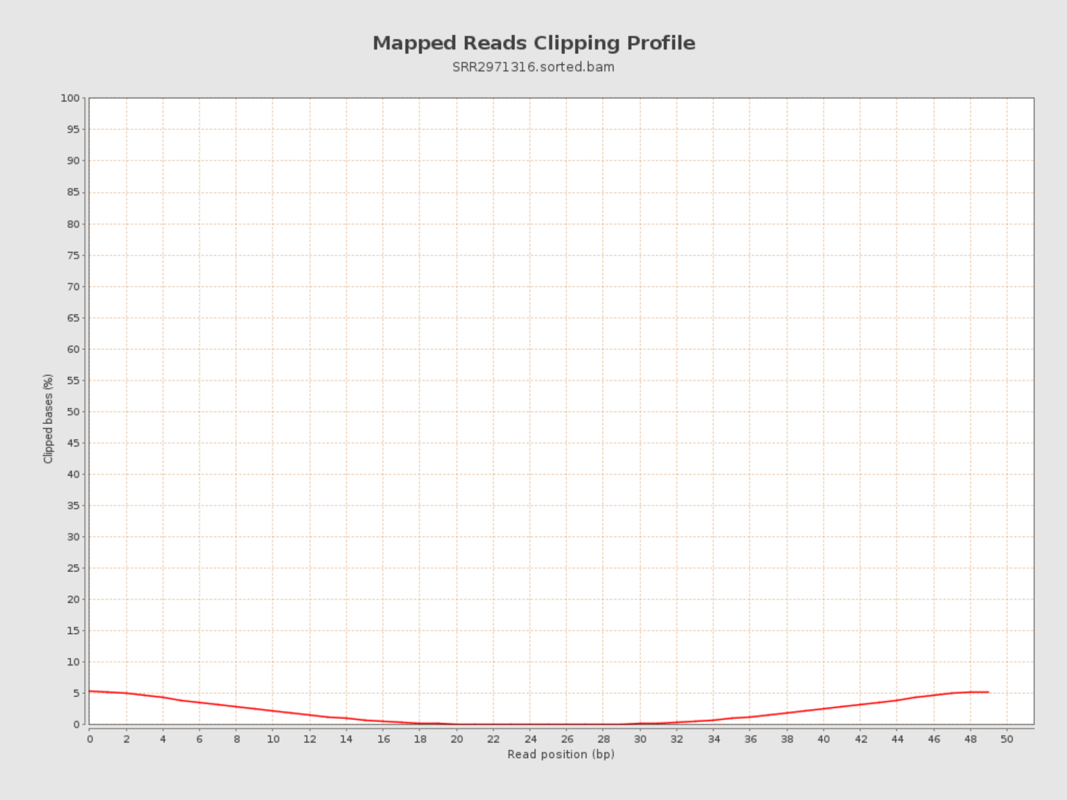
# 8. Results : Mapped Reads Nucleotide Content



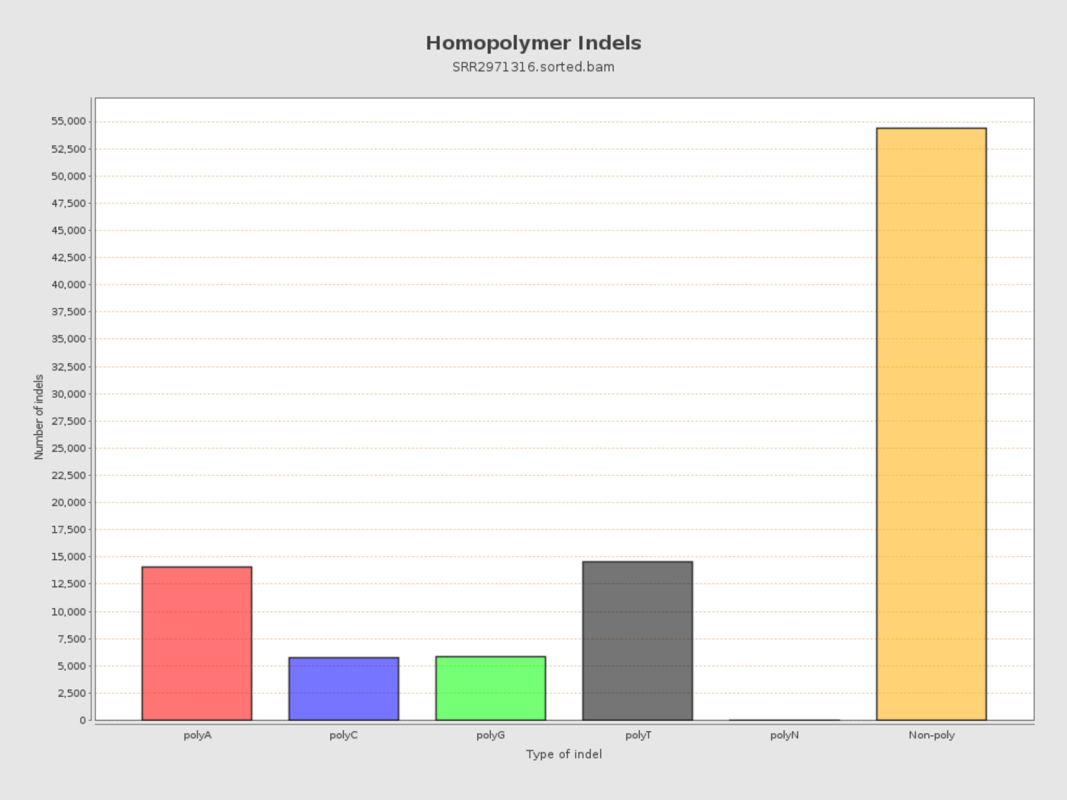
# 9. Results : Mapped Reads GC-content Distribution



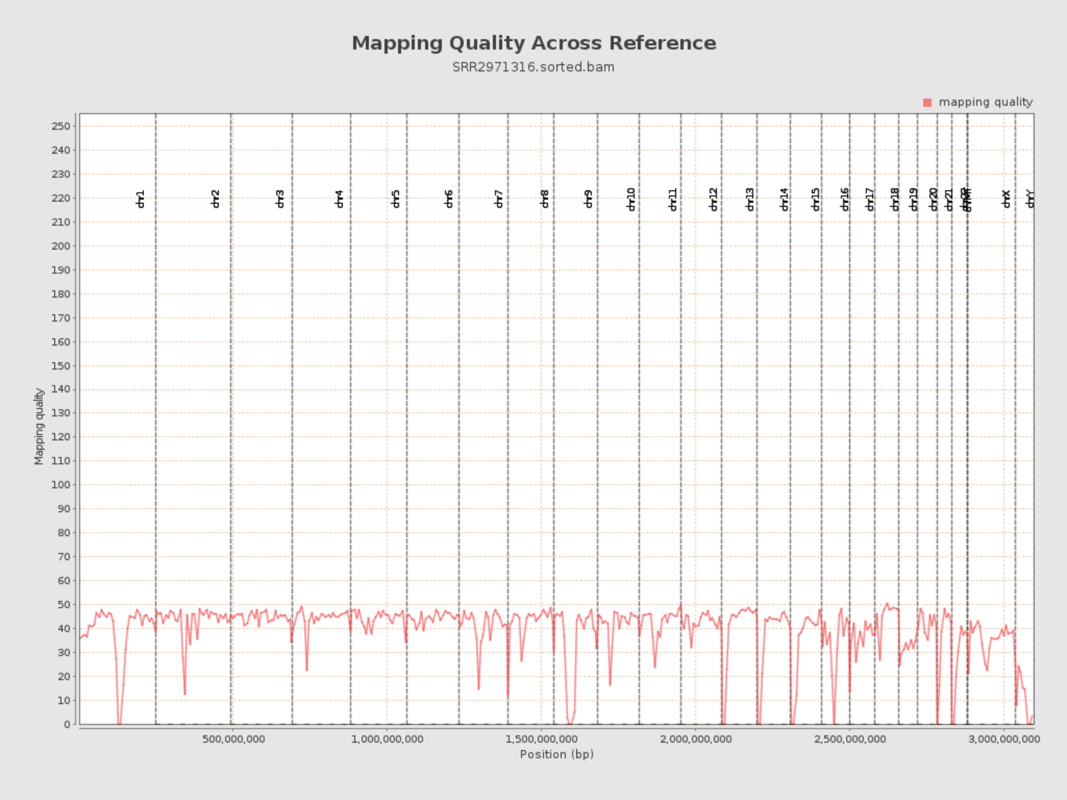
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram