# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 09:00:50*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716725.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_SRR9716725 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716725.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 09:00:48 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716725.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,880,910 |
| Mapped reads | 1,694,887 / 90.11% |
| Unmapped reads | 186,023 / 9.89% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 8,288 / 0.44% |
| Read min/max/mean length | 30 / 76 / 76.15 |
| Duplicated reads (estimated) | 59,244 / 3.15% |
| Duplication rate | 2.43% |
| Clipped reads | 1,698,853 / 90.32% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 23,888,836 / 24.54% |
| Number/percentage of C's | 20,079,870 / 20.63% |
| Number/percentage of T's | 30,856,028 / 31.7% |
| Number/percentage of G's | 22,510,371 / 23.13% |
| Number/percentage of N's | 1,107 / 0% |
| GC Percentage | 43.76% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0315 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3121 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.95 |

## 2.5. Mismatches and indels

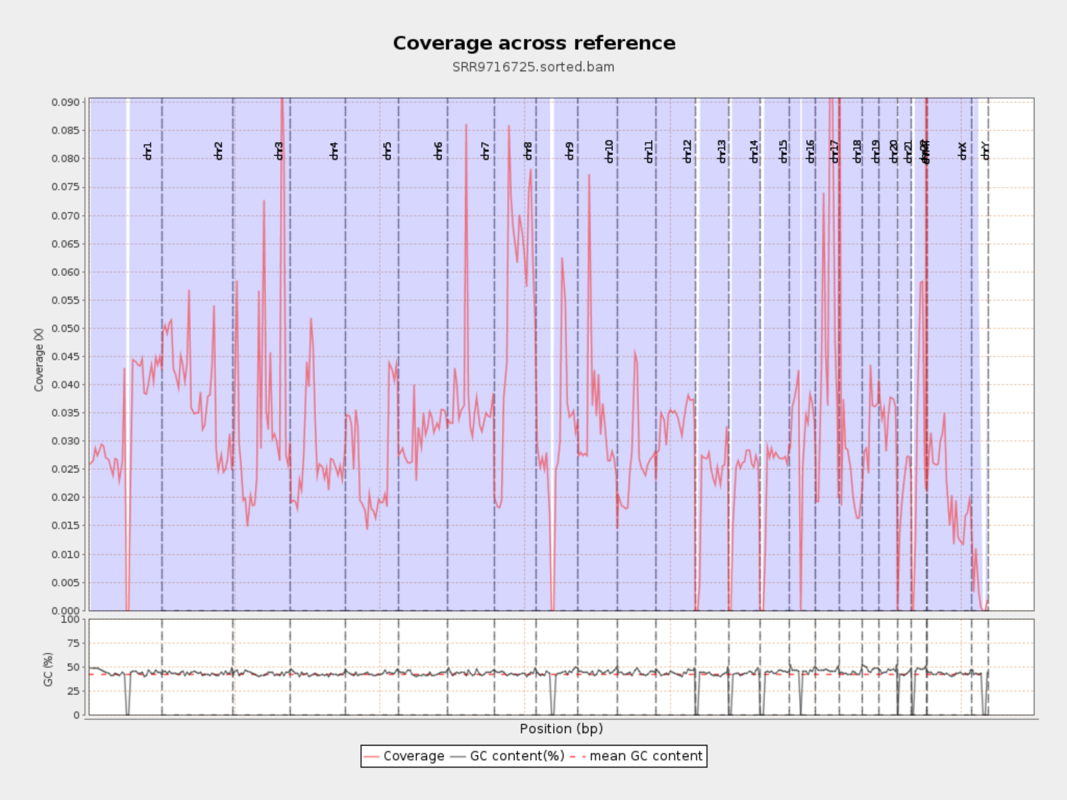
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 497,958 |
| Insertions | 6,362 |
| Mapped reads with at least one insertion | 0.37% |
| Deletions | 18,369 |
| Mapped reads with at least one deletion | 1.08% |
| Homopolymer indels | 41.67% |

## 2.6. Chromosome stats

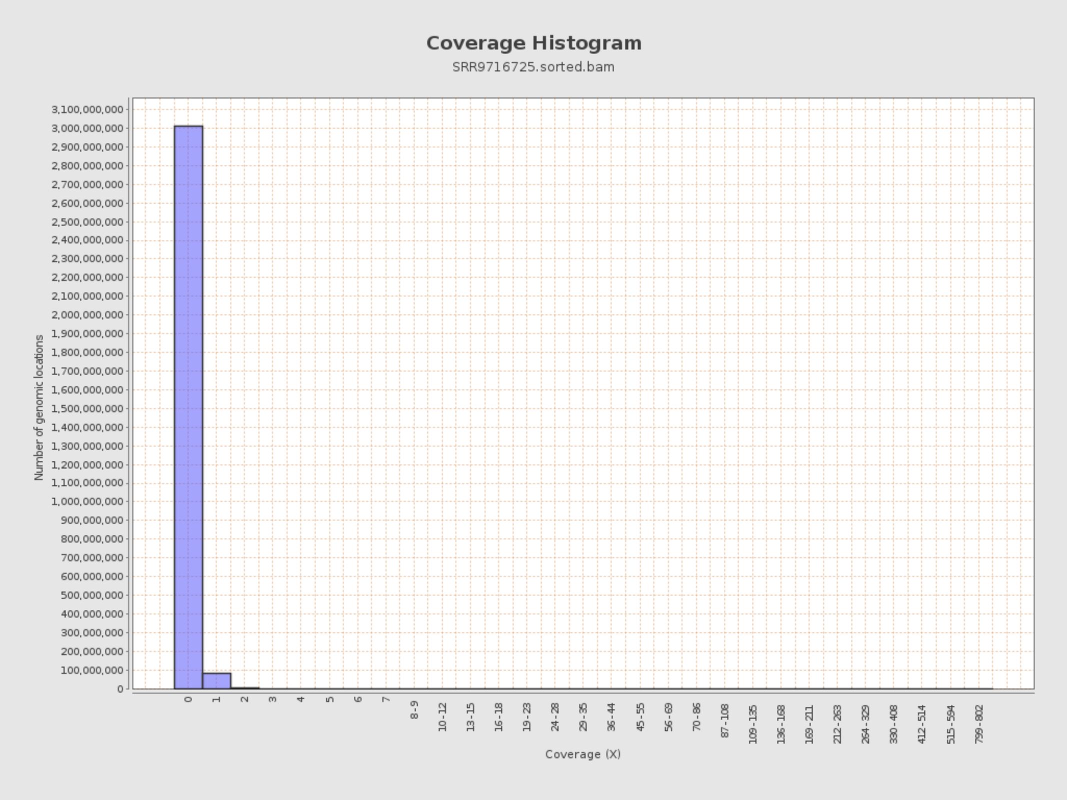
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 7993414 | 0.0321 | 0.4321 |
| chr2 | 243199373 | 9421372 | 0.0387 | 0.3952 |
| chr3 | 198022430 | 7107453 | 0.0359 | 0.2207 |
| chr4 | 191154276 | 5276721 | 0.0276 | 0.1971 |
| chr5 | 180915260 | 4800961 | 0.0265 | 0.1785 |
| chr6 | 171115067 | 5345942 | 0.0312 | 0.211 |
| chr7 | 159138663 | 5995594 | 0.0377 | 0.7134 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 7957667 | 0.0544 | 0.332 |
| chr9 | 141213431 | 4103731 | 0.0291 | 0.2168 |
| chr10 | 135534747 | 4577343 | 0.0338 | 0.3975 |
| chr11 | 135006516 | 3498393 | 0.0259 | 0.2148 |
| chr12 | 133851895 | 4537575 | 0.0339 | 0.2214 |
| chr13 | 115169878 | 2510748 | 0.0218 | 0.1617 |
| chr14 | 107349540 | 2398520 | 0.0223 | 0.1692 |
| chr15 | 102531392 | 2287547 | 0.0223 | 0.1649 |
| chr16 | 90354753 | 2924087 | 0.0324 | 0.2078 |
| chr17 | 81195210 | 4059497 | 0.05 | 0.2572 |
| chr18 | 78077248 | 2173898 | 0.0278 | 0.3048 |
| chr19 | 59128983 | 1960552 | 0.0332 | 0.3735 |
| chr20 | 63025520 | 2186053 | 0.0347 | 0.2139 |
| chr21 | 48129895 | 969776 | 0.0201 | 0.1586 |
| chr22 | 51304566 | 1520352 | 0.0296 | 0.1888 |
| chrMT | 16571 | 185467 | 11.1923 | 7.0104 |
| chrX | 155270560 | 3366005 | 0.0217 | 0.1867 |
| chrY | 59373566 | 206261 | 0.0035 | 0.0891 |

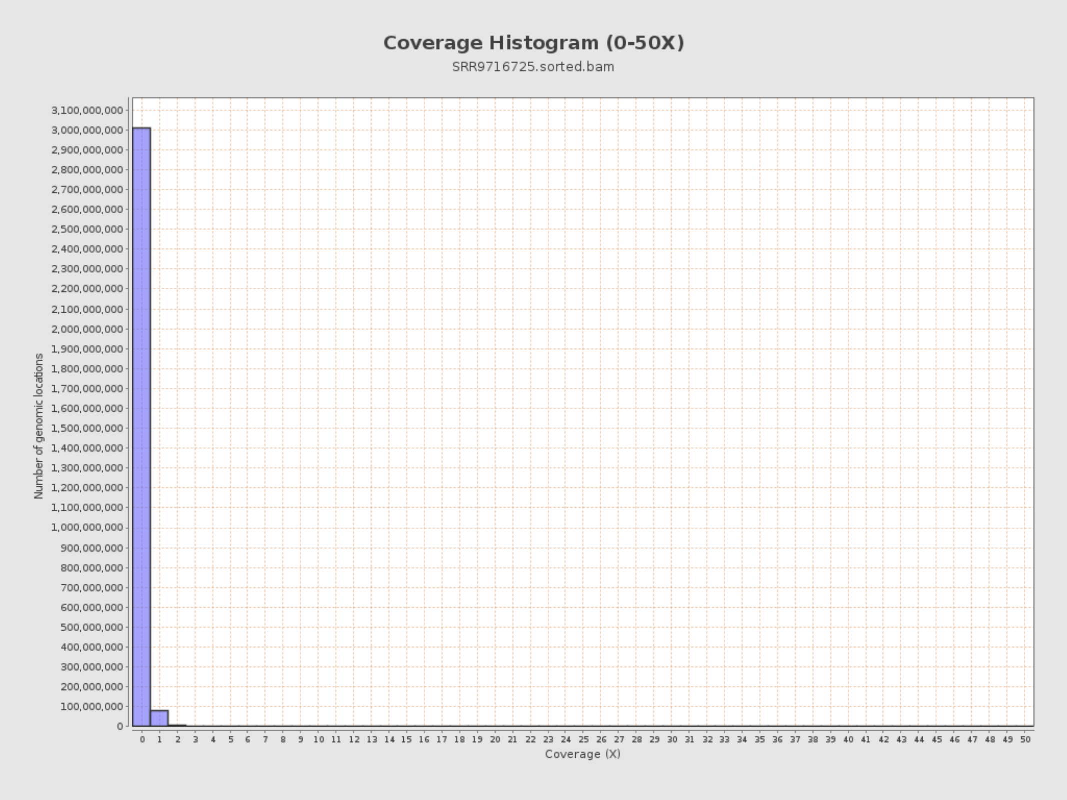
# 3. Results : Coverage across reference



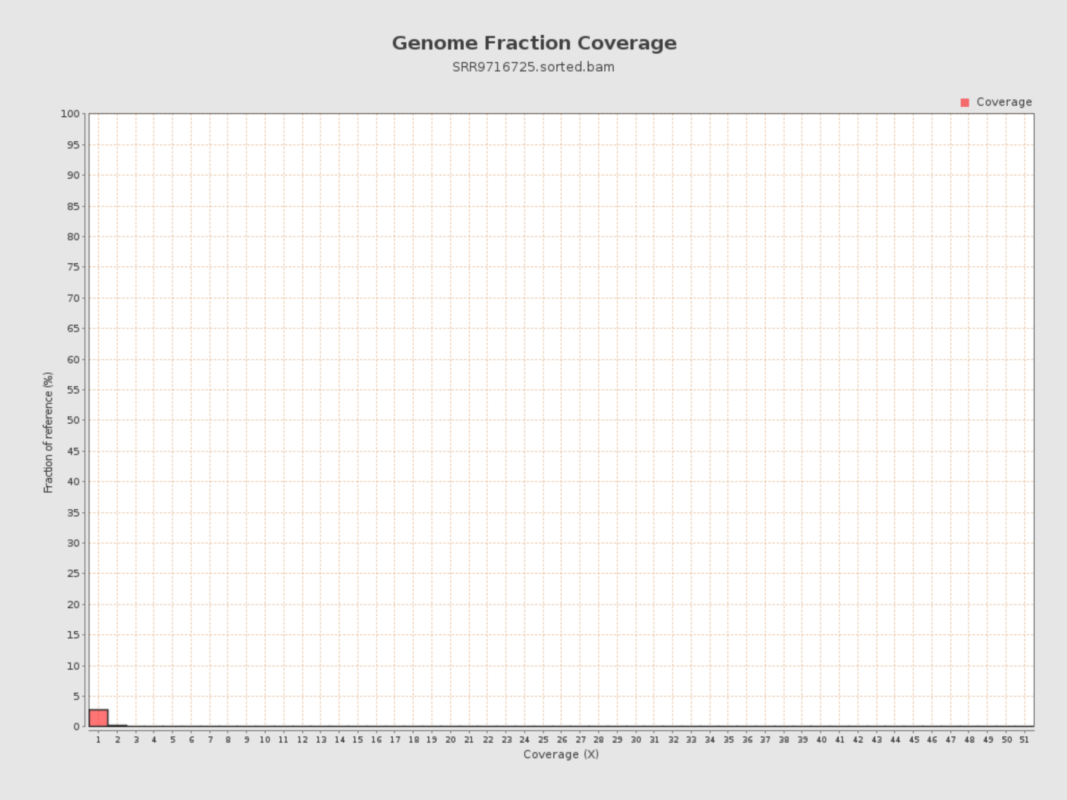
# 4. Results : Coverage Histogram



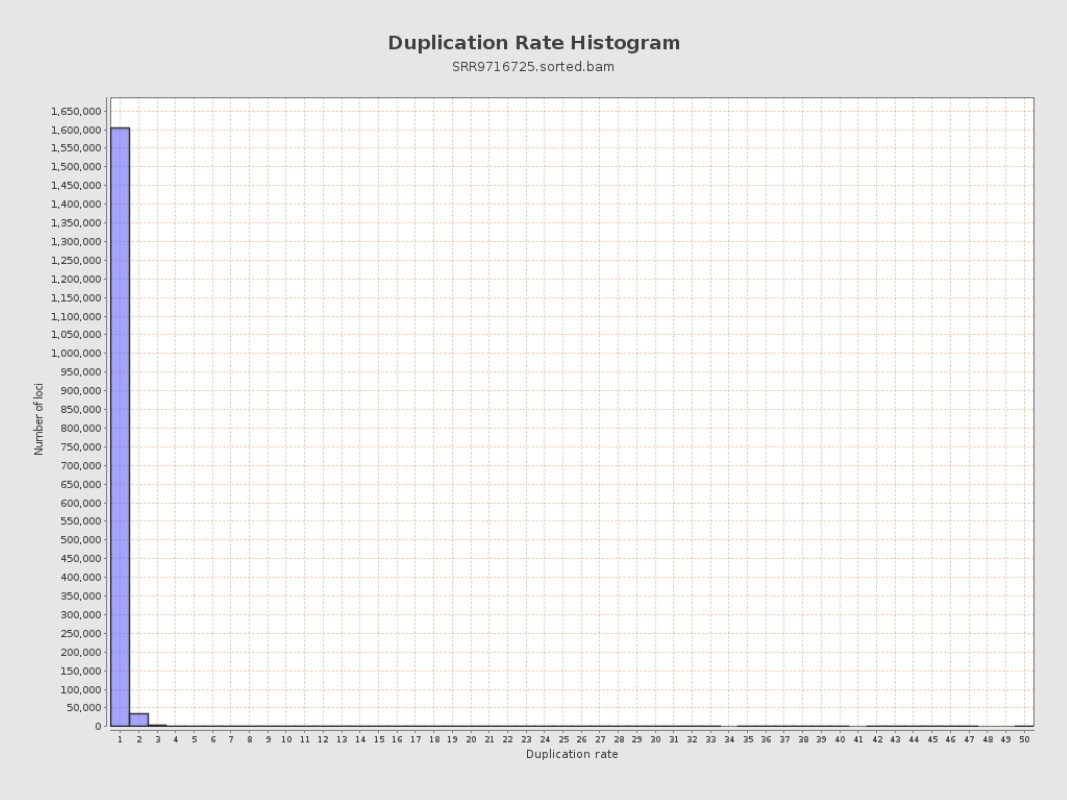
# 5. Results : Coverage Histogram (0-50X)



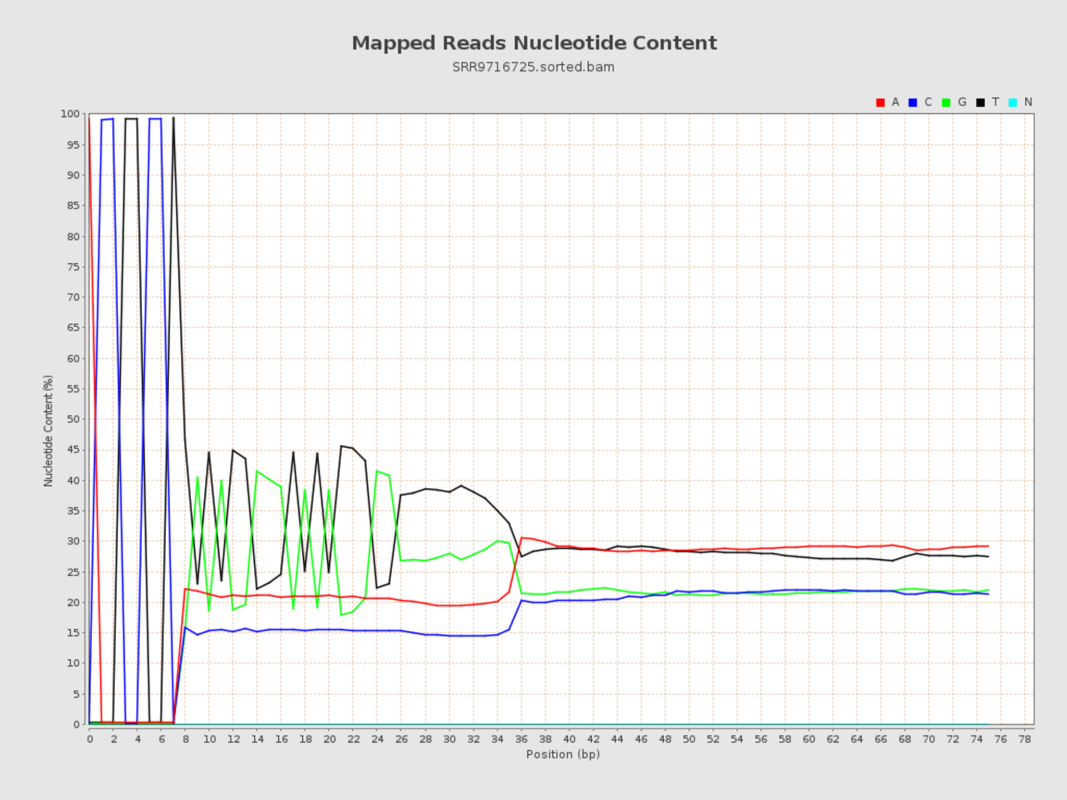
# 6. Results : Genome Fraction Coverage



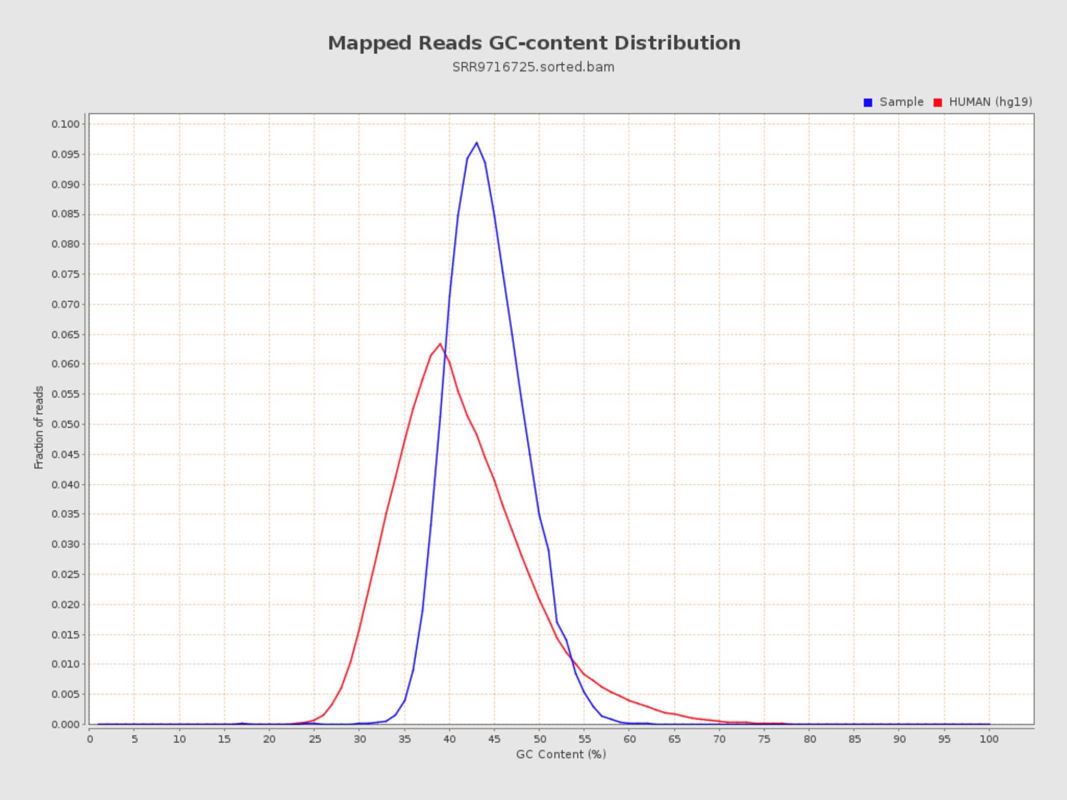
# 7. Results : Duplication Rate Histogram



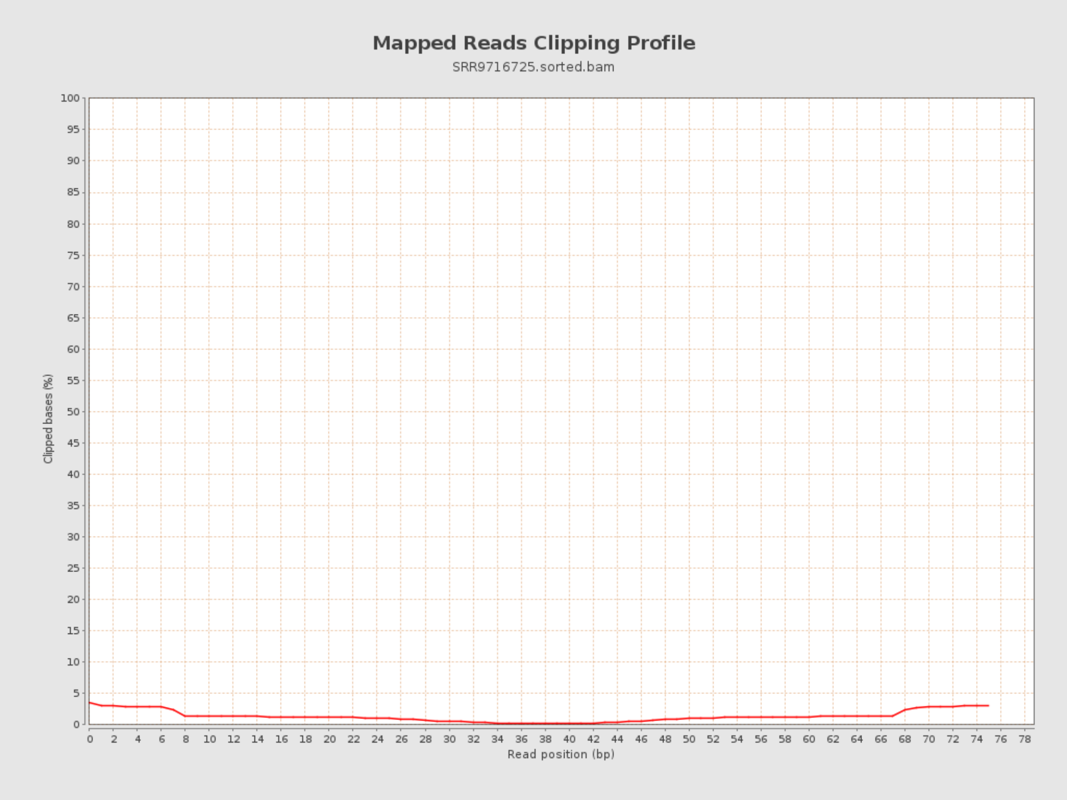
# 8. Results : Mapped Reads Nucleotide Content



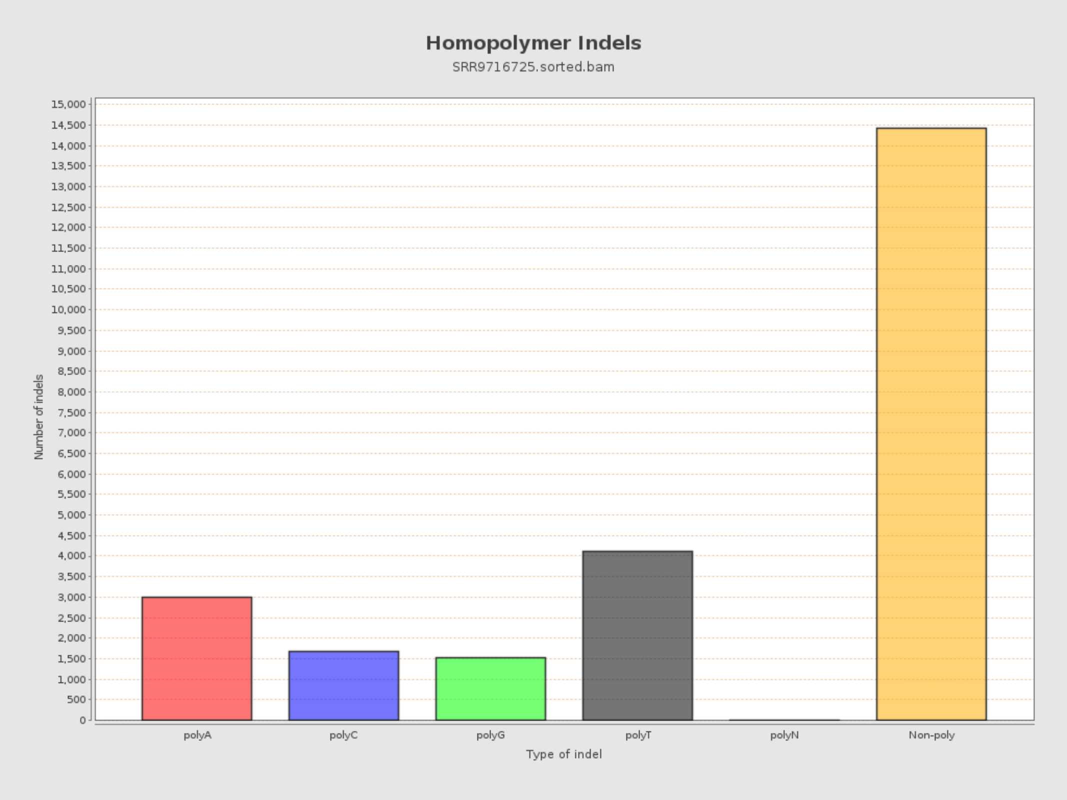
# 9. Results : Mapped Reads GC-content Distribution



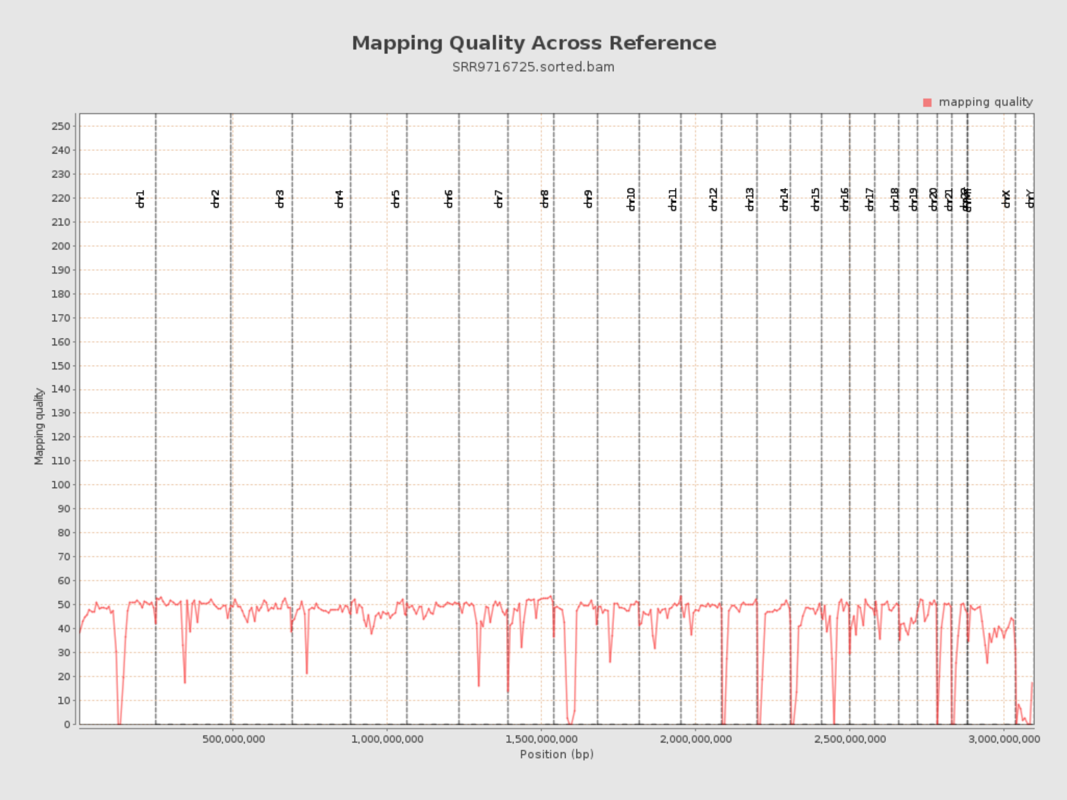
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram