# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 22:47:42*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716985.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_SRR9716985 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716985.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 22:47:40 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716985.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,246,307 |
| Mapped reads | 1,887,942 / 84.05% |
| Unmapped reads | 358,365 / 15.95% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 7,524 / 0.33% |
| Read min/max/mean length | 30 / 76 / 76.11 |
| Duplicated reads (estimated) | 56,687 / 2.52% |
| Duplication rate | 2.15% |
| Clipped reads | 1,893,908 / 84.31% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 27,048,880 / 25.44% |
| Number/percentage of C's | 21,240,036 / 19.98% |
| Number/percentage of T's | 32,828,223 / 30.88% |
| Number/percentage of G's | 25,195,949 / 23.7% |
| Number/percentage of N's | 1,756 / 0% |
| GC Percentage | 43.68% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0344 |
| | |

| | |
|---|---|
| Standard Deviation | 0.289 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 42.33 |

## 2.5. Mismatches and indels

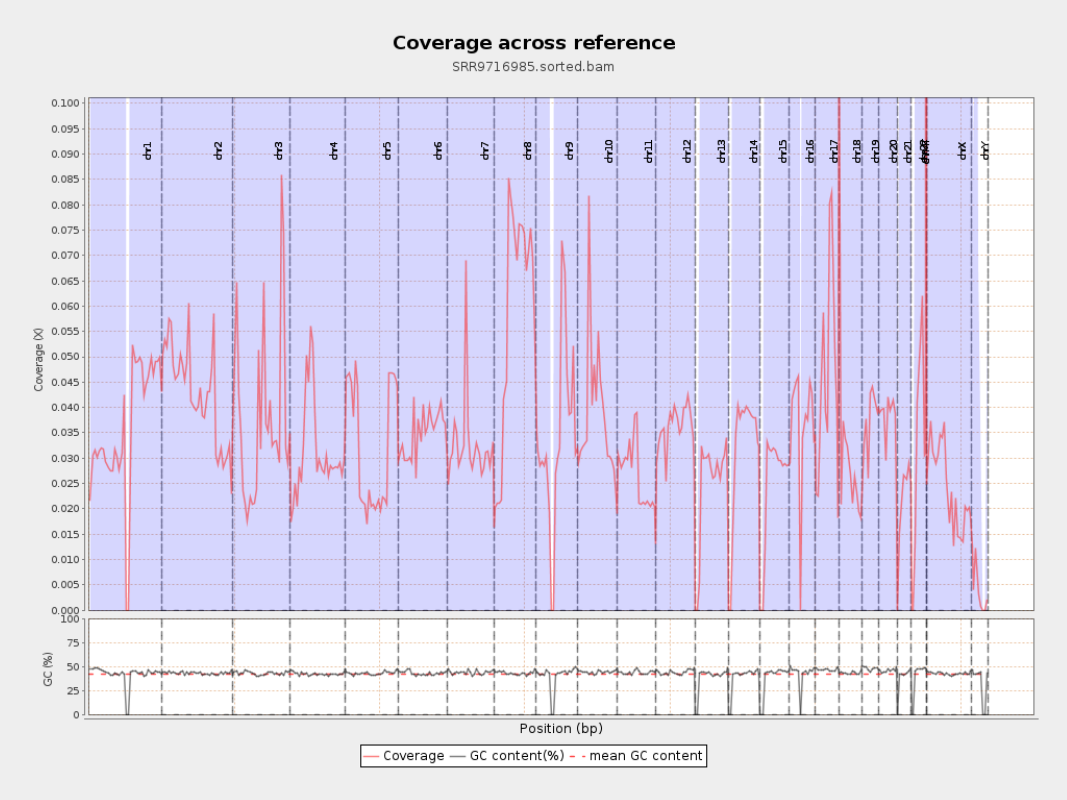
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 546,047 |
| Insertions | 6,183 |
| Mapped reads with at least one insertion | 0.33% |
| Deletions | 19,704 |
| Mapped reads with at least one deletion | 1.04% |
| Homopolymer indels | 42.36% |

## 2.6. Chromosome stats

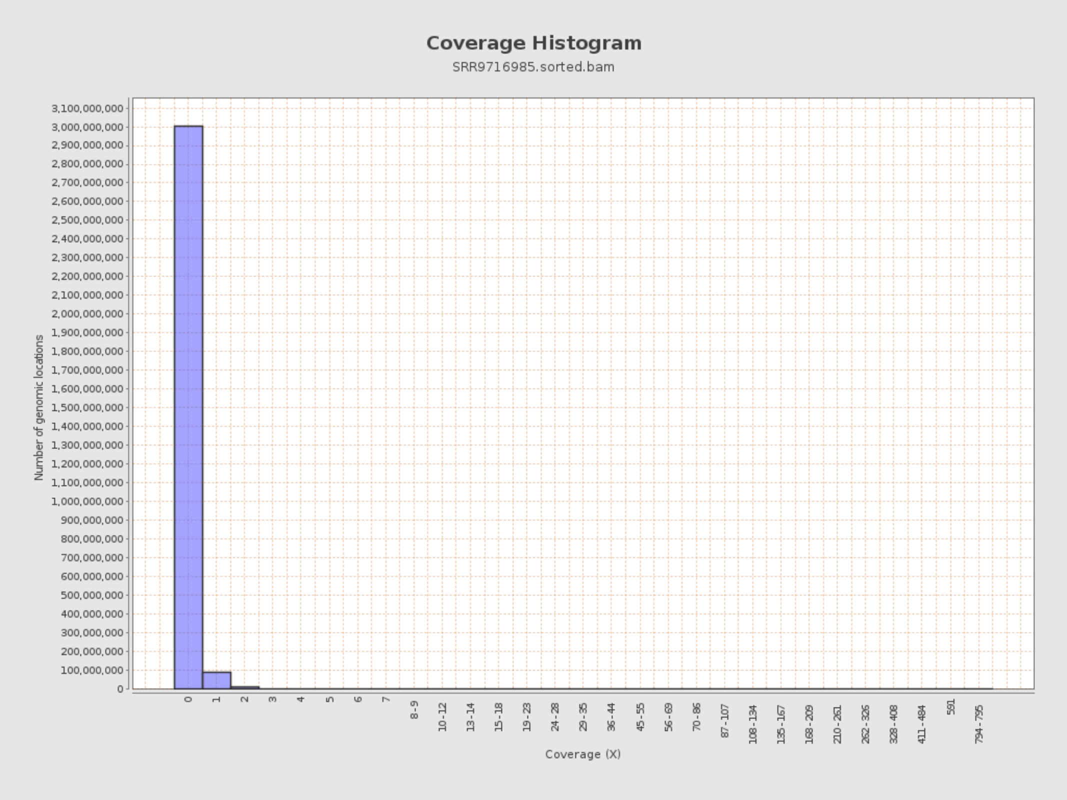
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 8888510 | 0.0357 | 0.3655 |
| chr2 | 243199373 | 10478776 | 0.0431 | 0.4119 |
| chr3 | 198022430 | 7479909 | 0.0378 | 0.2236 |
| chr4 | 191154276 | 5987022 | 0.0313 | 0.2047 |
| chr5 | 180915260 | 5762902 | 0.0319 | 0.1957 |
| chr6 | 171115067 | 5974586 | 0.0349 | 0.2305 |
| chr7 | 159138663 | 5213015 | 0.0328 | 0.5596 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 8641273 | 0.059 | 0.3128 |
| chr9 | 141213431 | 4732744 | 0.0335 | 0.231 |
| chr10 | 135534747 | 5257390 | 0.0388 | 0.3588 |
| chr11 | 135006516 | 3589466 | 0.0266 | 0.2149 |
| chr12 | 133851895 | 4835062 | 0.0361 | 0.2178 |
| chr13 | 115169878 | 2820027 | 0.0245 | 0.1706 |
| chr14 | 107349540 | 3392991 | 0.0316 | 0.203 |
| chr15 | 102531392 | 2535965 | 0.0247 | 0.177 |
| chr16 | 90354753 | 3312542 | 0.0367 | 0.2263 |
| chr17 | 81195210 | 3757273 | 0.0463 | 0.2443 |
| chr18 | 78077248 | 2379625 | 0.0305 | 0.3114 |
| chr19 | 59128983 | 2196048 | 0.0371 | 0.3431 |
| chr20 | 63025520 | 2389937 | 0.0379 | 0.2189 |
| chr21 | 48129895 | 1037895 | 0.0216 | 0.1658 |
| chr22 | 51304566 | 1608531 | 0.0314 | 0.1981 |
| chrMT | 16571 | 12187 | 0.7354 | 0.9778 |
| chrX | 155270560 | 3822111 | 0.0246 | 0.2 |
| chrY | 59373566 | 239925 | 0.004 | 0.0957 |

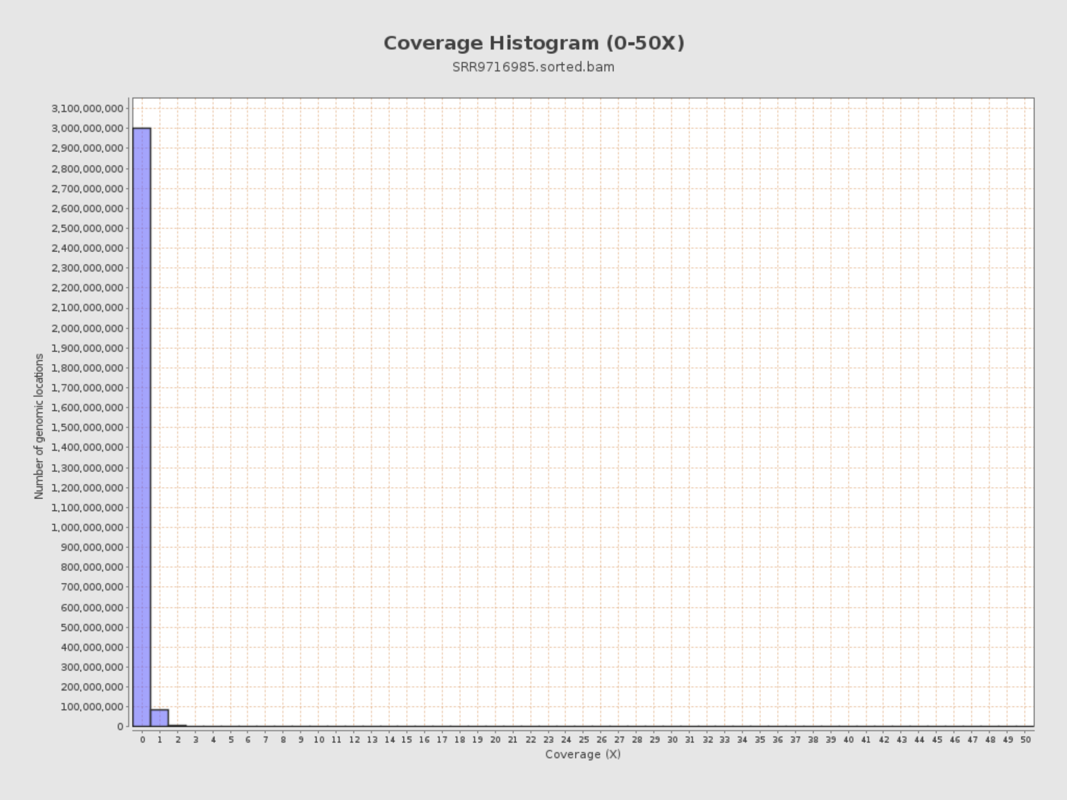
# 3. Results : Coverage across reference



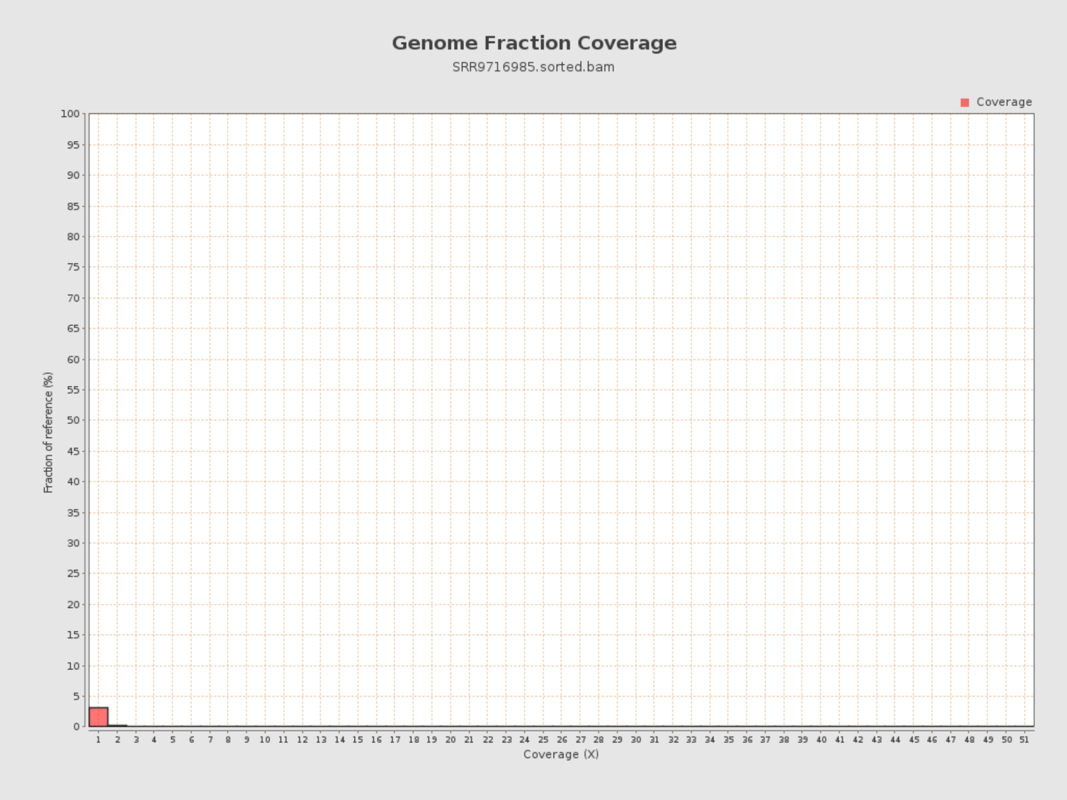
# 4. Results : Coverage Histogram



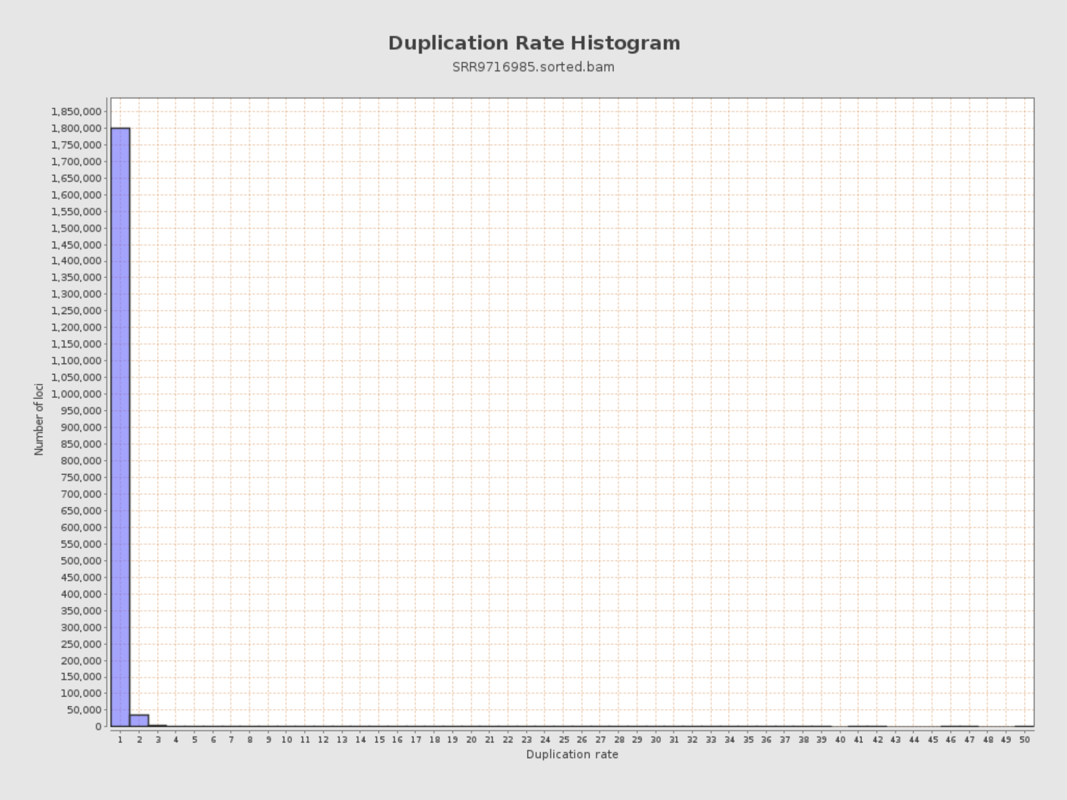
# 5. Results : Coverage Histogram (0-50X)



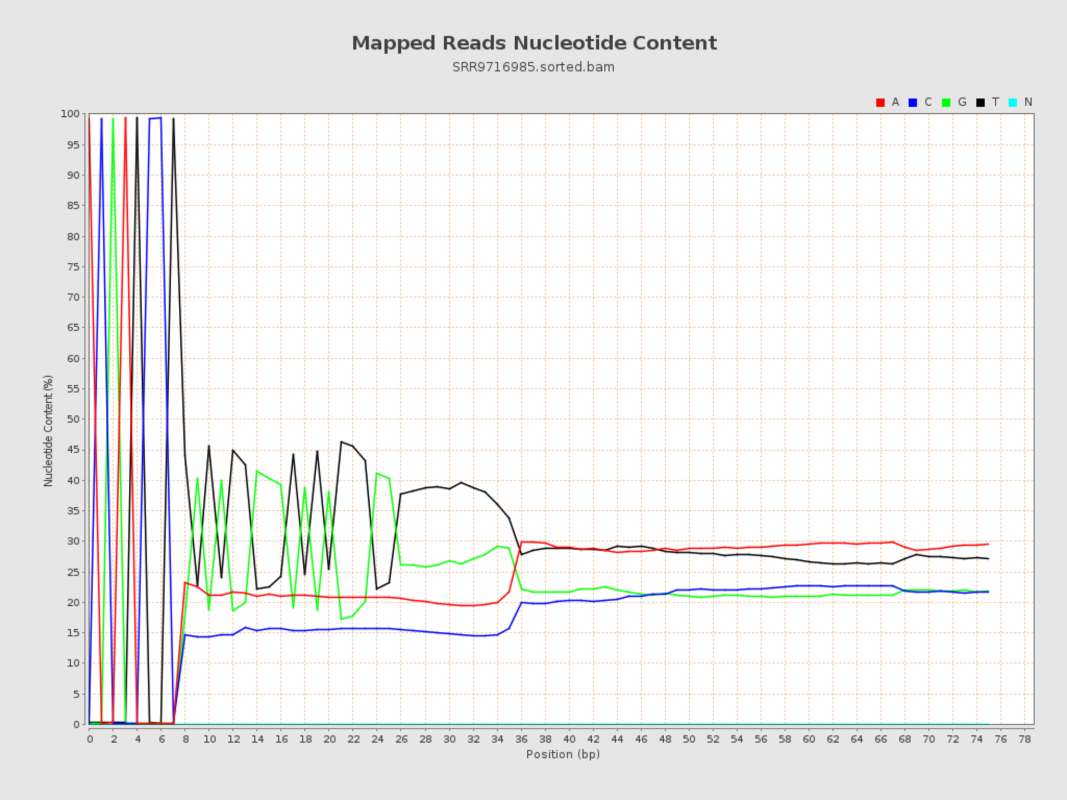
# 6. Results : Genome Fraction Coverage



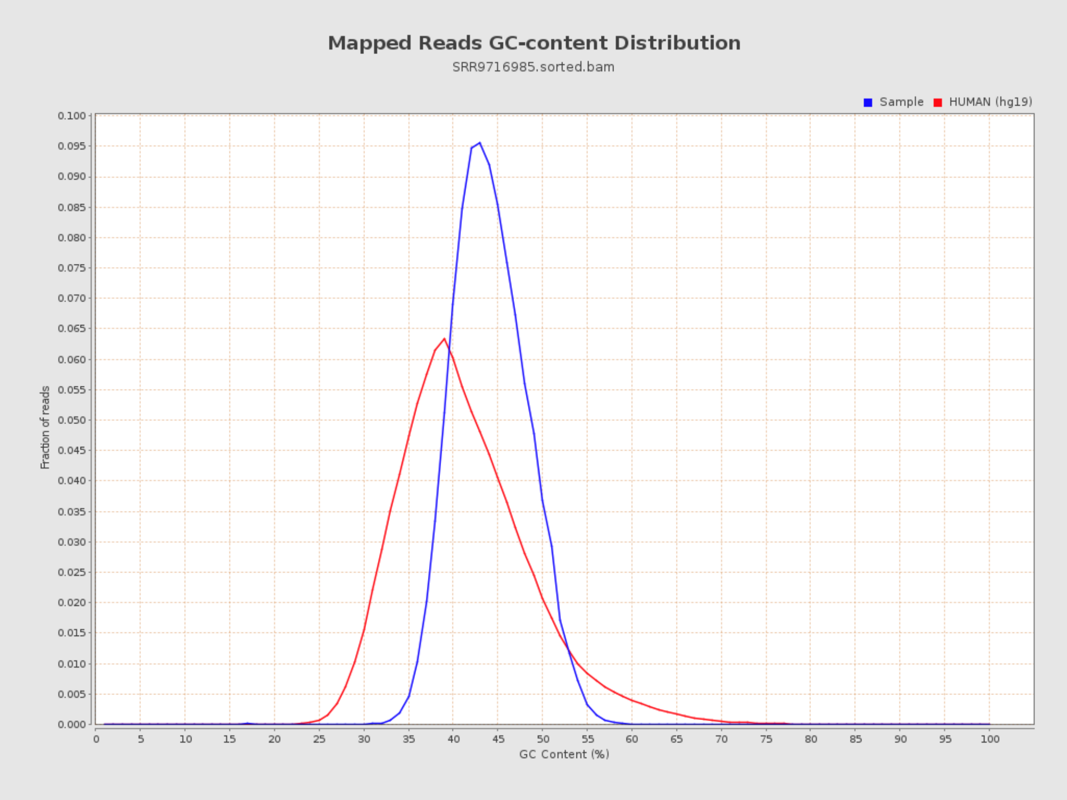
# 7. Results : Duplication Rate Histogram



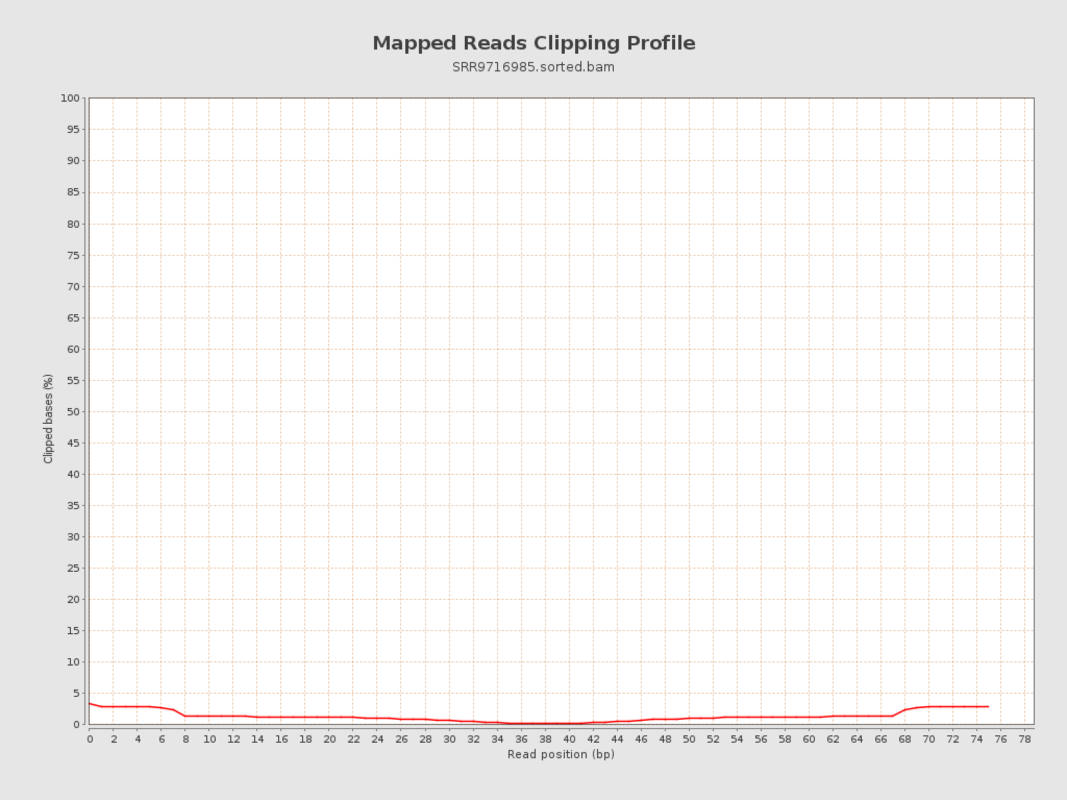
# 8. Results : Mapped Reads Nucleotide Content



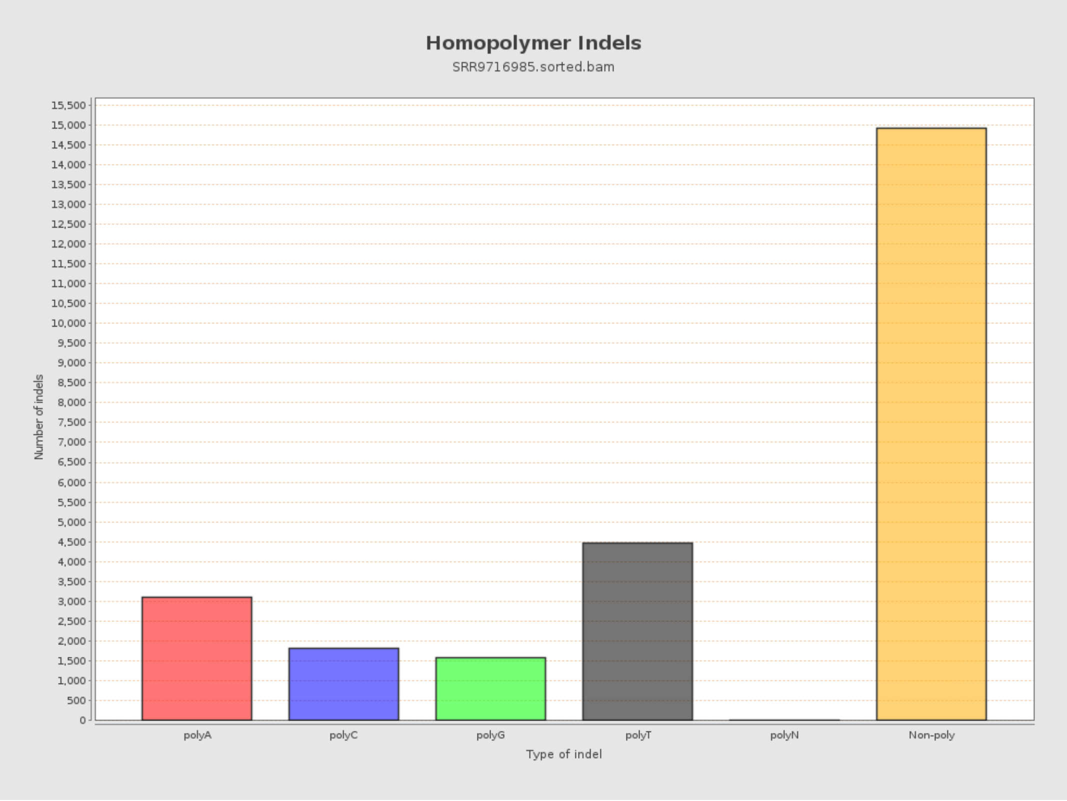
# 9. Results : Mapped Reads GC-content Distribution



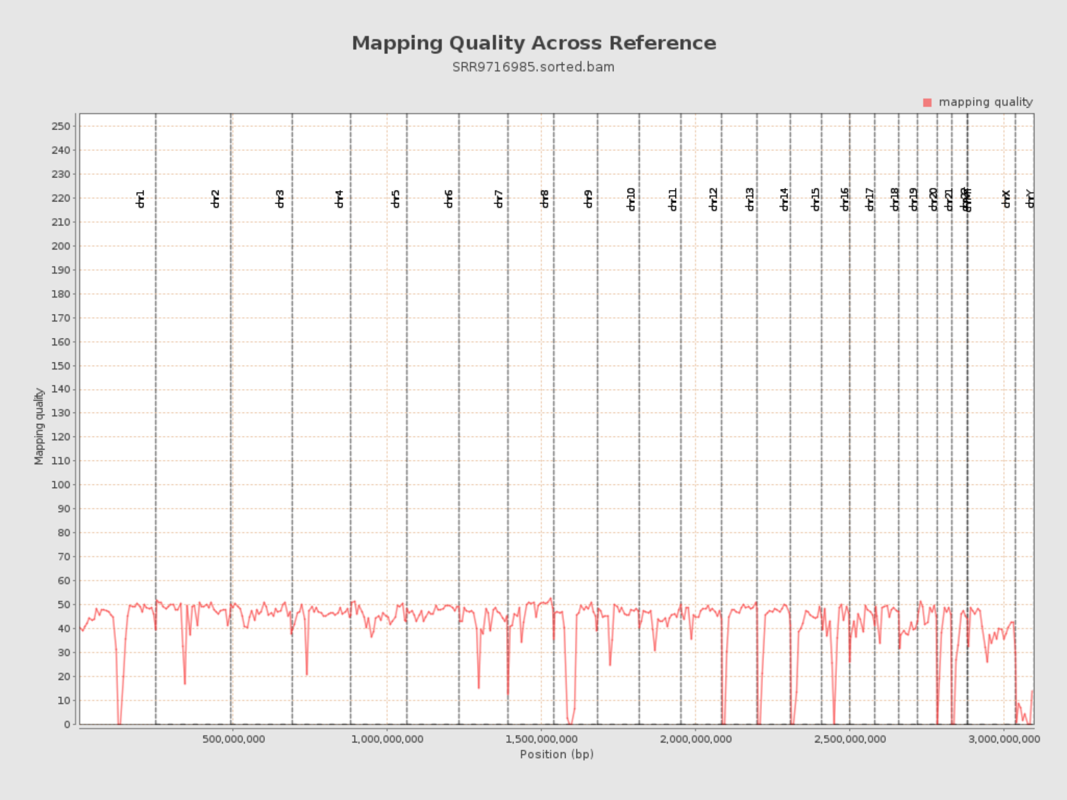
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram