# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 23:01:56*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716988.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_SRR9716988 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716988.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 23:01:54 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716988.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,719,304 |
| Mapped reads | 1,573,142 / 91.5% |
| Unmapped reads | 146,162 / 8.5% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 9,281 / 0.54% |
| Read min/max/mean length | 30 / 76 / 76.18 |
| Duplicated reads (estimated) | 51,986 / 3.02% |
| Duplication rate | 2.34% |
| Clipped reads | 1,579,423 / 91.86% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 22,623,344 / 24.78% |
| Number/percentage of C's | 16,853,159 / 18.46% |
| Number/percentage of T's | 28,078,496 / 30.75% |
| Number/percentage of G's | 23,755,436 / 26.02% |
| Number/percentage of N's | 1,170 / 0% |
| GC Percentage | 44.47% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0295 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2744 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.32 |

## 2.5. Mismatches and indels

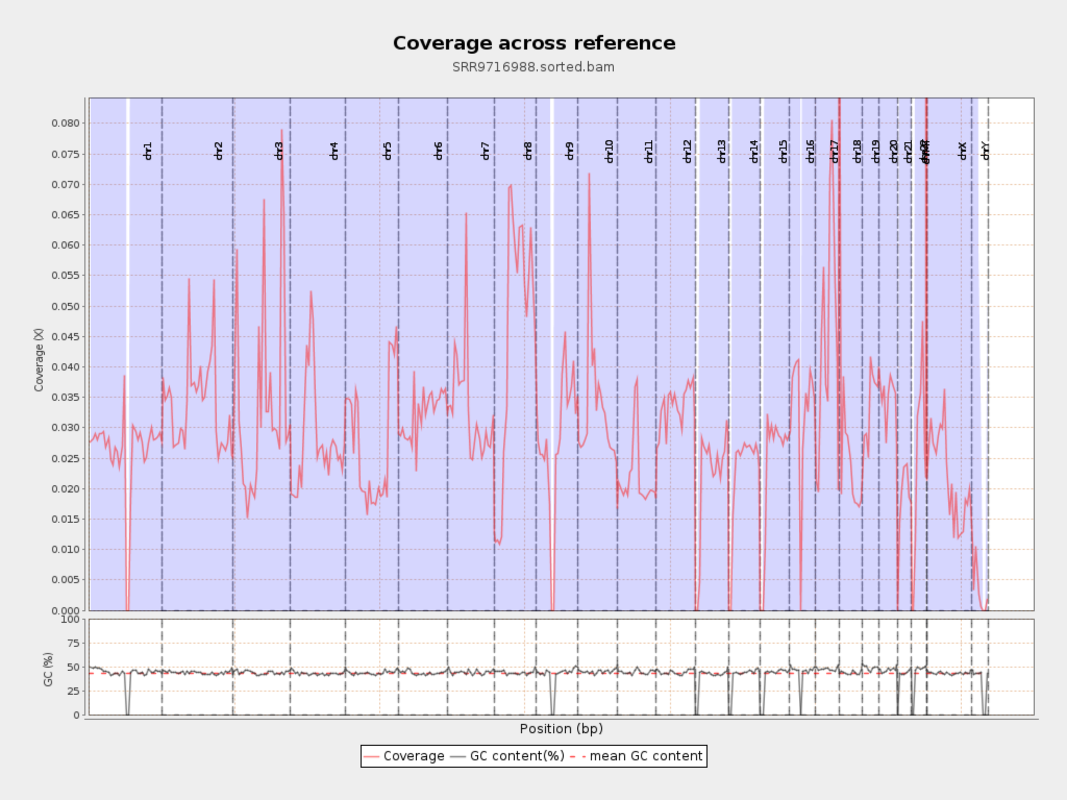
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 459,314 |
| Insertions | 6,153 |
| Mapped reads with at least one insertion | 0.39% |
| Deletions | 16,358 |
| Mapped reads with at least one deletion | 1.03% |
| Homopolymer indels | 40.38% |

## 2.6. Chromosome stats

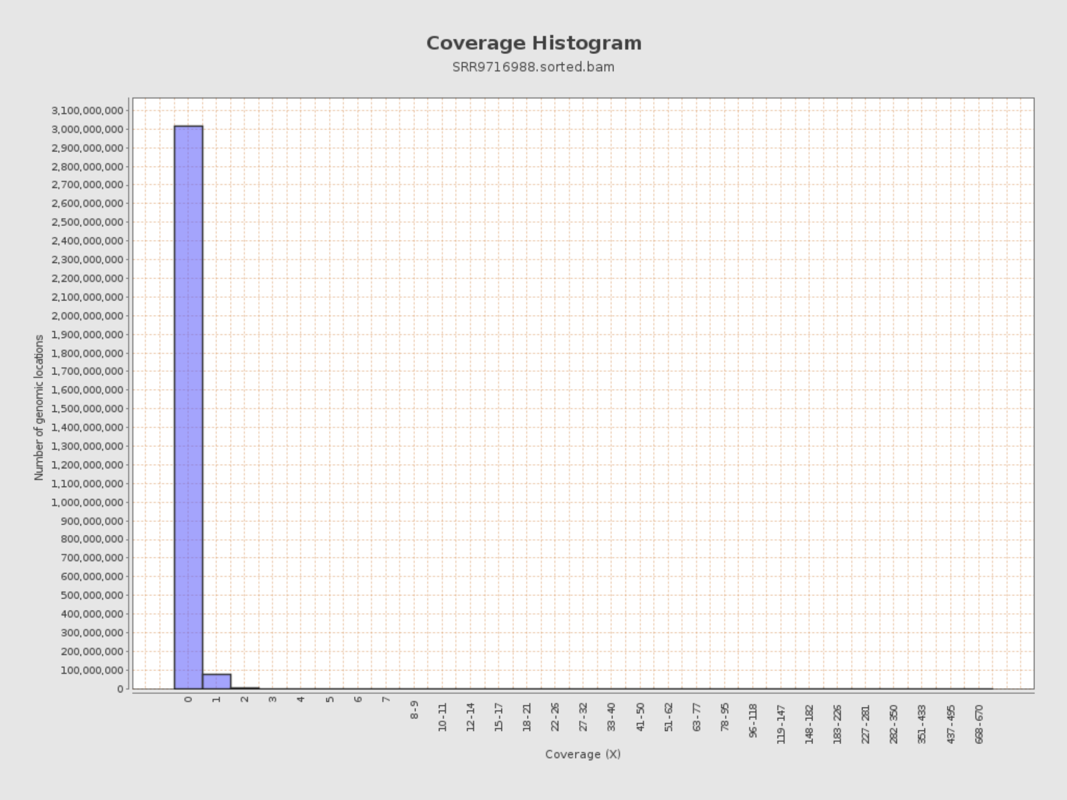
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 6476634 | 0.026 | 0.3834 |
| chr2 | 243199373 | 8309797 | 0.0342 | 0.3529 |
| chr3 | 198022430 | 6712668 | 0.0339 | 0.2062 |
| chr4 | 191154276 | 5380406 | 0.0281 | 0.1974 |
| chr5 | 180915260 | 4945249 | 0.0273 | 0.1797 |
| chr6 | 171115067 | 5534660 | 0.0323 | 0.2133 |
| chr7 | 159138663 | 5299569 | 0.0333 | 0.5132 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6680268 | 0.0456 | 0.3068 |
| chr9 | 141213431 | 3872175 | 0.0274 | 0.2082 |
| chr10 | 135534747 | 4531391 | 0.0334 | 0.3477 |
| chr11 | 135006516 | 2943684 | 0.0218 | 0.2043 |
| chr12 | 133851895 | 4480492 | 0.0335 | 0.2137 |
| chr13 | 115169878 | 2467732 | 0.0214 | 0.159 |
| chr14 | 107349540 | 2398152 | 0.0223 | 0.1707 |
| chr15 | 102531392 | 2416767 | 0.0236 | 0.1706 |
| chr16 | 90354753 | 2997092 | 0.0332 | 0.207 |
| chr17 | 81195210 | 3642752 | 0.0449 | 0.2379 |
| chr18 | 78077248 | 2129178 | 0.0273 | 0.3204 |
| chr19 | 59128983 | 1986490 | 0.0336 | 0.3357 |
| chr20 | 63025520 | 2201101 | 0.0349 | 0.2114 |
| chr21 | 48129895 | 866360 | 0.018 | 0.1544 |
| chr22 | 51304566 | 1225687 | 0.0239 | 0.1669 |
| chrMT | 16571 | 196879 | 11.8809 | 7.4027 |
| chrX | 155270560 | 3437106 | 0.0221 | 0.1833 |
| chrY | 59373566 | 204969 | 0.0035 | 0.0968 |

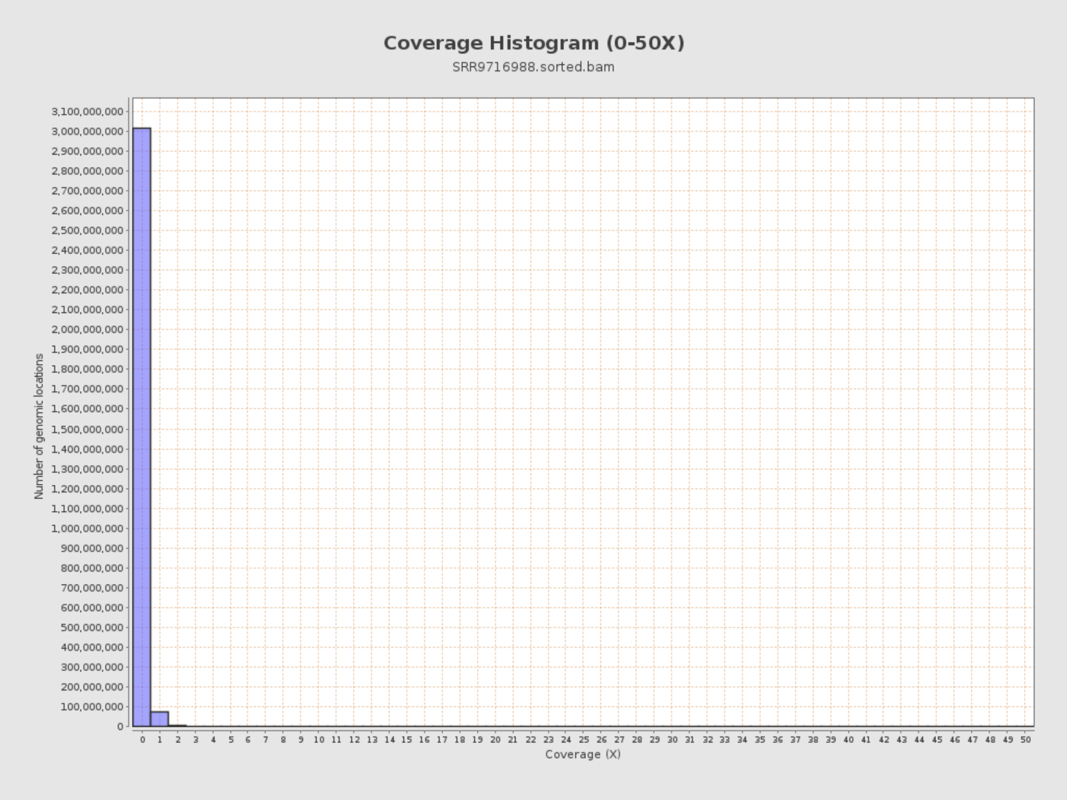
# 3. Results : Coverage across reference



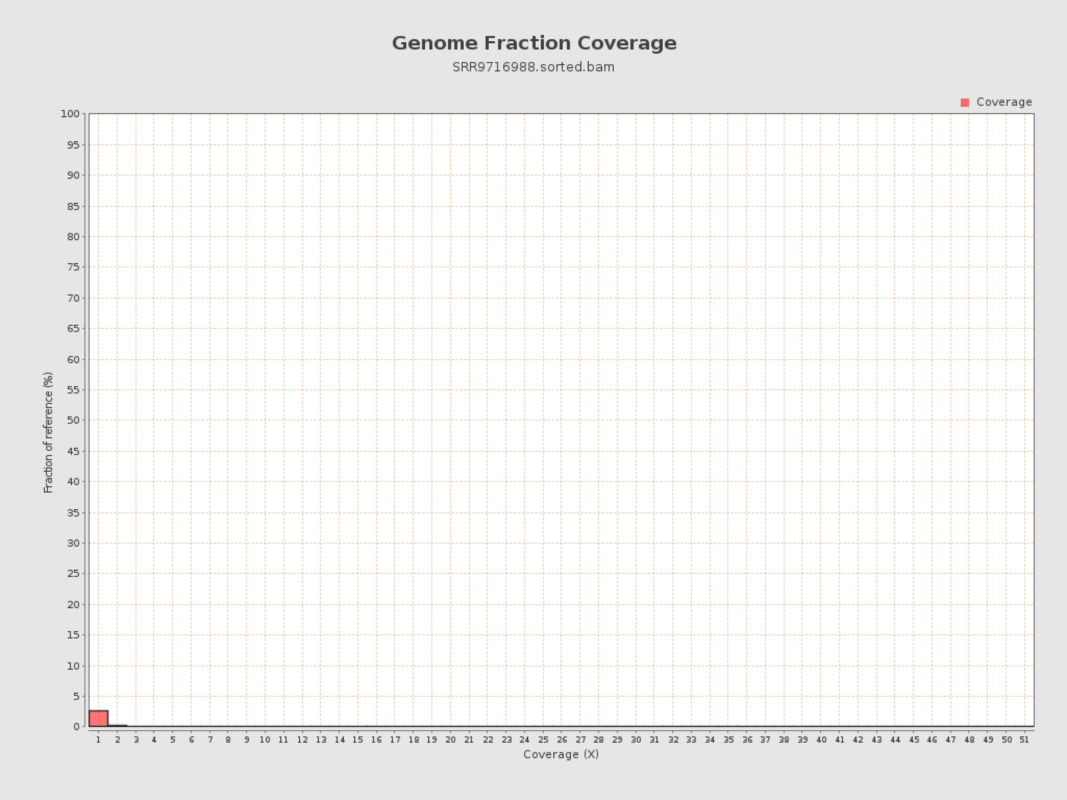
# 4. Results : Coverage Histogram



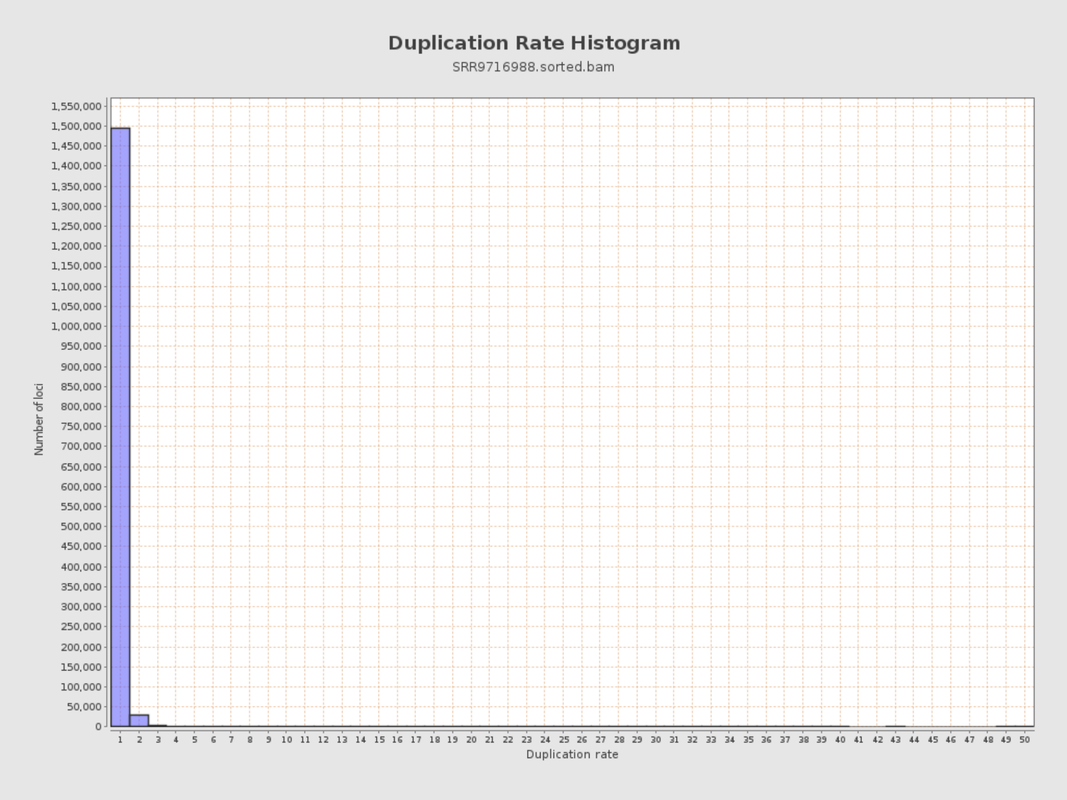
# 5. Results : Coverage Histogram (0-50X)



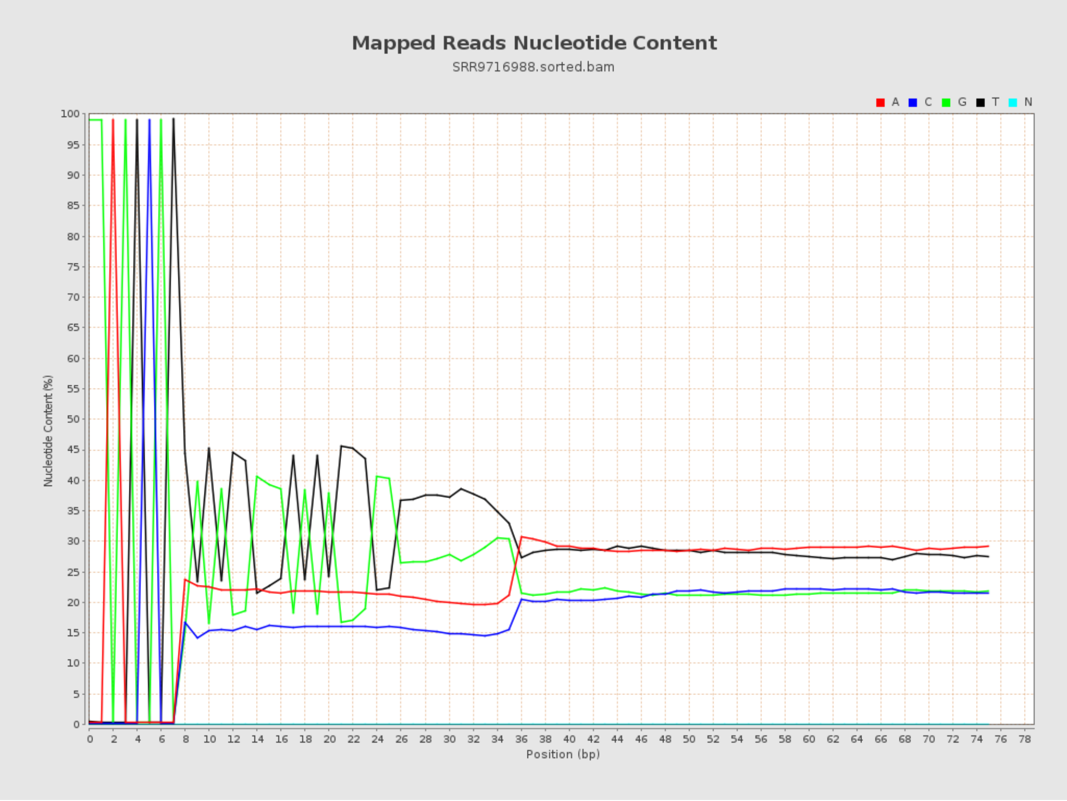
# 6. Results : Genome Fraction Coverage



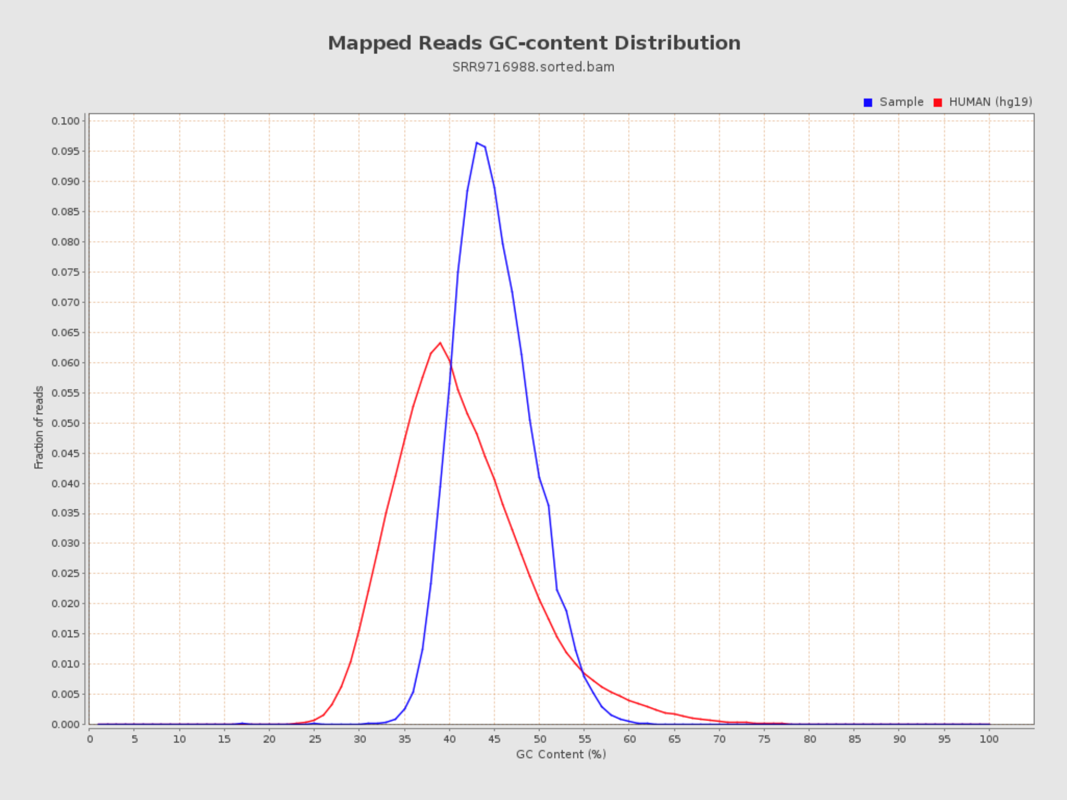
# 7. Results : Duplication Rate Histogram



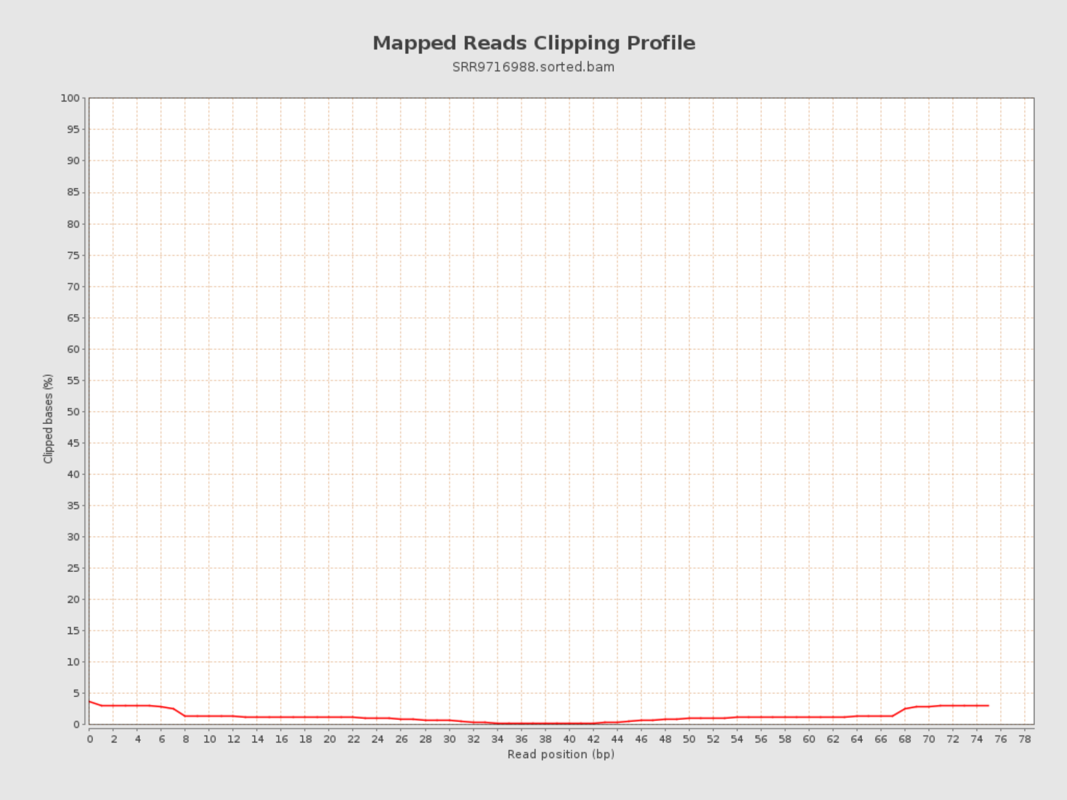
# 8. Results : Mapped Reads Nucleotide Content



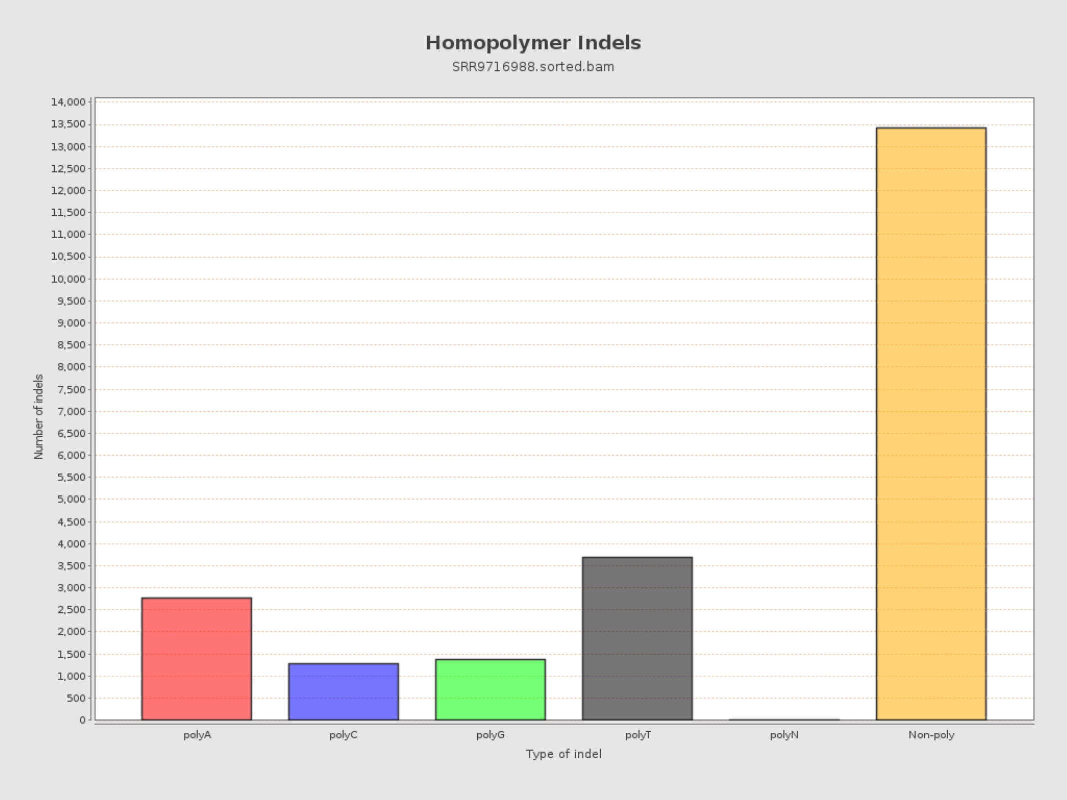
# 9. Results : Mapped Reads GC-content Distribution



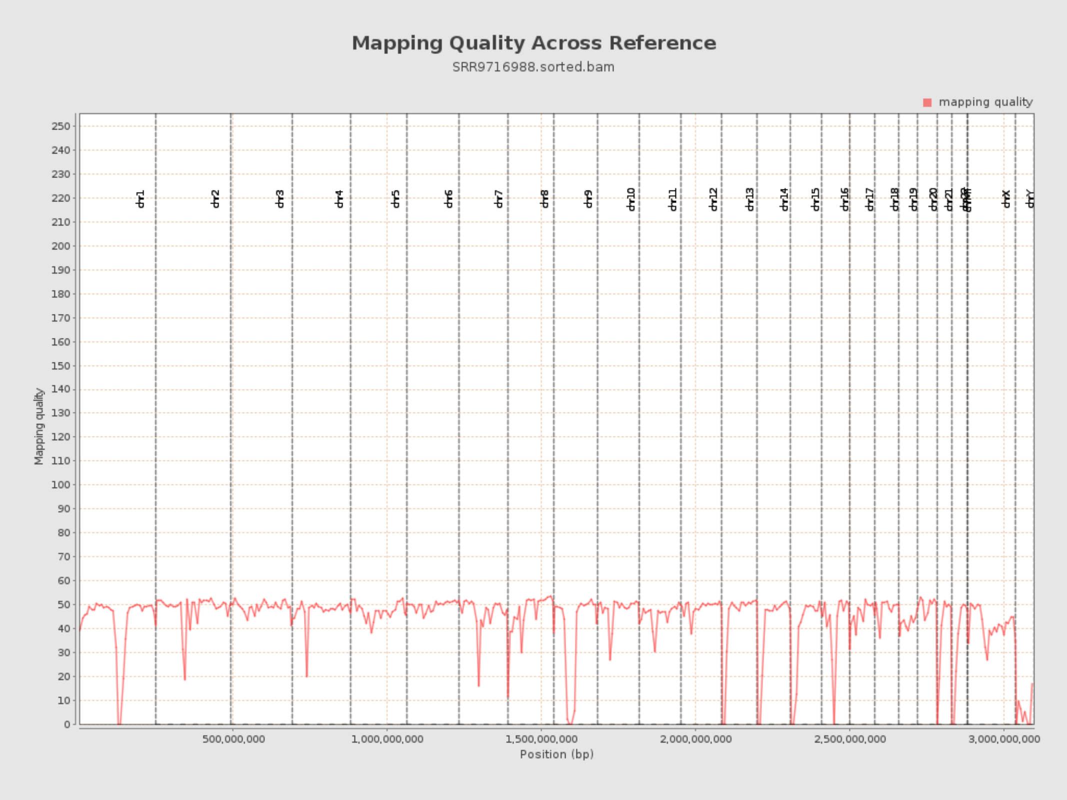
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram