# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/04 00:10:57*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717010.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_SRR9717010 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717010.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Sep 04 00:10:56 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9717010.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,009,264 |
| Mapped reads | 937,982 / 92.94% |
| Unmapped reads | 71,282 / 7.06% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 14,683 / 1.45% |
| Read min/max/mean length | 30 / 101 / 101.54 |
| Duplicated reads (estimated) | 31,491 / 3.12% |
| Duplication rate | 1.85% |
| Clipped reads | 950,211 / 94.15% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 18,551,102 / 24.8% |
| Number/percentage of C's | 14,611,186 / 19.53% |
| Number/percentage of T's | 23,173,768 / 30.98% |
| Number/percentage of G's | 18,454,378 / 24.67% |
| Number/percentage of N's | 4,912 / 0.01% |
| GC Percentage | 44.21% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0242 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3422 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.87 |

## 2.5. Mismatches and indels

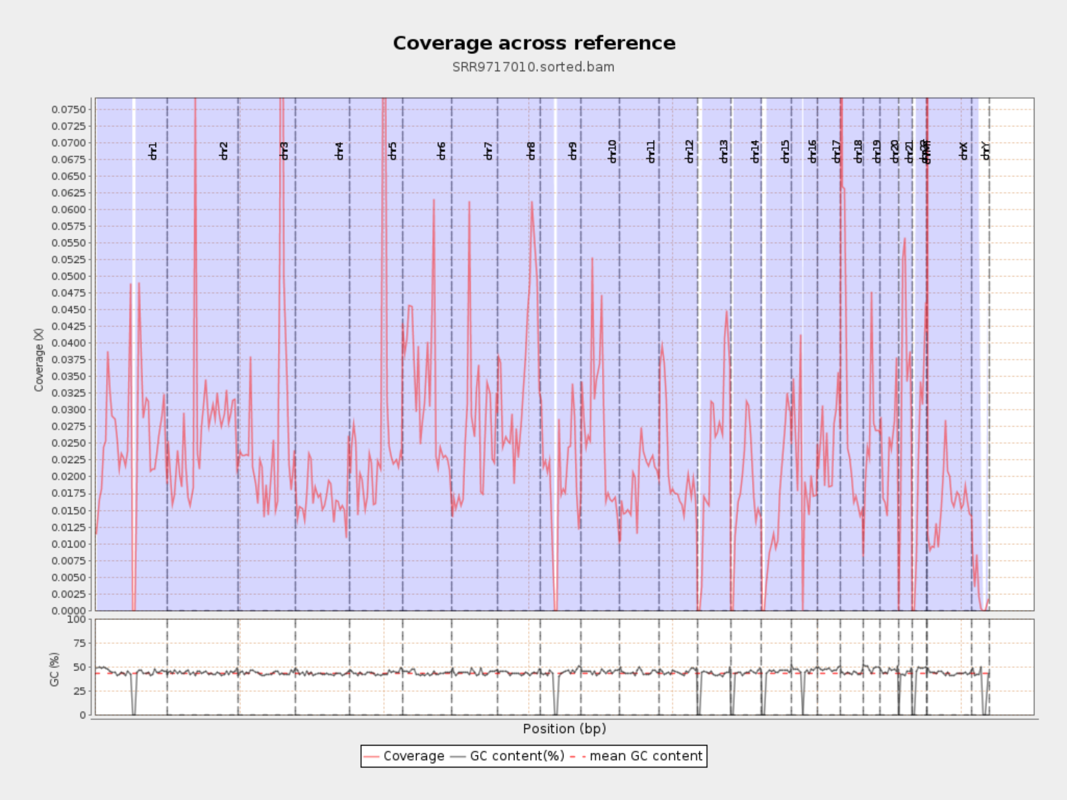
| | |
|---|---|
| General error rate | 0.83% |
| Mismatches | 604,223 |
| Insertions | 7,251 |
| Mapped reads with at least one insertion | 0.76% |
| Deletions | 18,953 |
| Mapped reads with at least one deletion | 1.99% |
| Homopolymer indels | 42.84% |

## 2.6. Chromosome stats

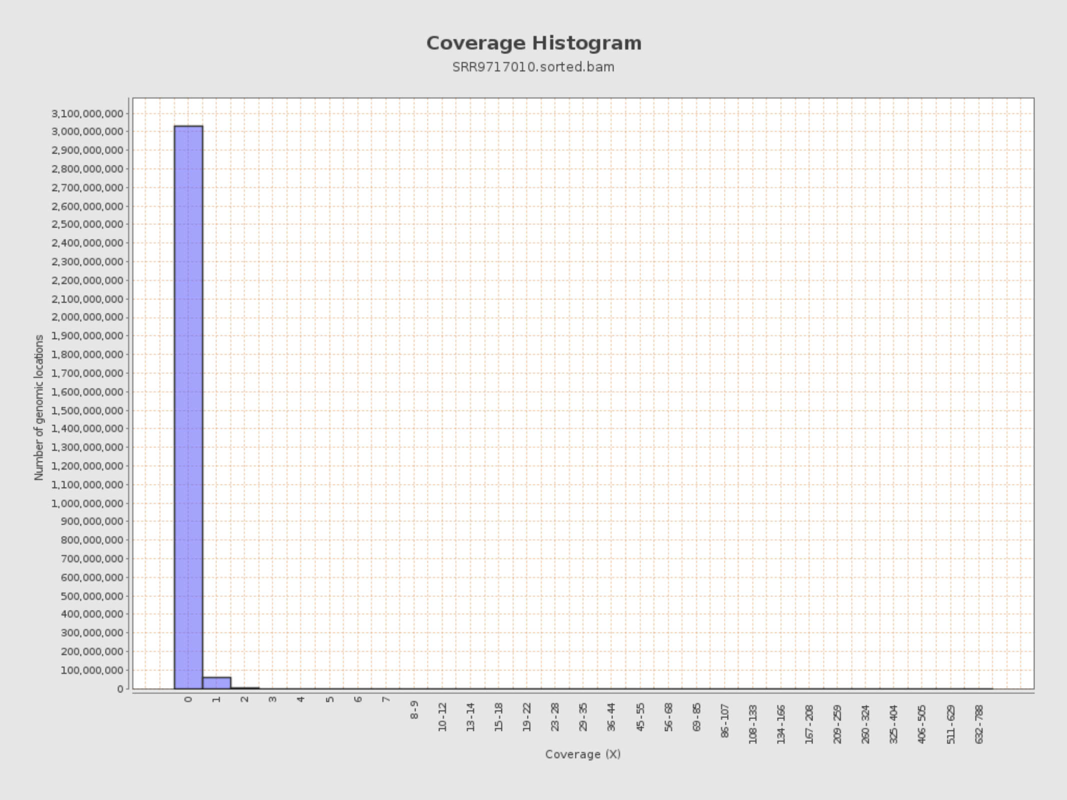
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 6292027 | 0.0252 | 0.5663 |
| chr2 | 243199373 | 6620428 | 0.0272 | 0.561 |
| chr3 | 198022430 | 5617431 | 0.0284 | 0.1851 |
| chr4 | 191154276 | 3241686 | 0.017 | 0.147 |
| chr5 | 180915260 | 4951490 | 0.0274 | 0.18 |
| chr6 | 171115067 | 5662340 | 0.0331 | 0.2314 |
| chr7 | 159138663 | 4148386 | 0.0261 | 0.5095 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 5152775 | 0.0352 | 0.4272 |
| chr9 | 141213431 | 2758770 | 0.0195 | 0.3014 |
| chr10 | 135534747 | 3647198 | 0.0269 | 0.2835 |
| chr11 | 135006516 | 2620721 | 0.0194 | 0.2437 |
| chr12 | 133851895 | 2911839 | 0.0218 | 0.162 |
| chr13 | 115169878 | 2758917 | 0.024 | 0.1656 |
| chr14 | 107349540 | 1852537 | 0.0173 | 0.1749 |
| chr15 | 102531392 | 1509323 | 0.0147 | 0.1344 |
| chr16 | 90354753 | 1874573 | 0.0207 | 0.1815 |
| chr17 | 81195210 | 2066762 | 0.0255 | 0.1965 |
| chr18 | 78077248 | 2504584 | 0.0321 | 0.7023 |
| chr19 | 59128983 | 1595996 | 0.027 | 0.4473 |
| chr20 | 63025520 | 1498454 | 0.0238 | 0.1915 |
| chr21 | 48129895 | 1681628 | 0.0349 | 0.207 |
| chr22 | 51304566 | 1183507 | 0.0231 | 0.1644 |
| chrMT | 16571 | 56732 | 3.4236 | 2.9717 |
| chrX | 155270560 | 2452371 | 0.0158 | 0.1875 |
| chrY | 59373566 | 168613 | 0.0028 | 0.0818 |

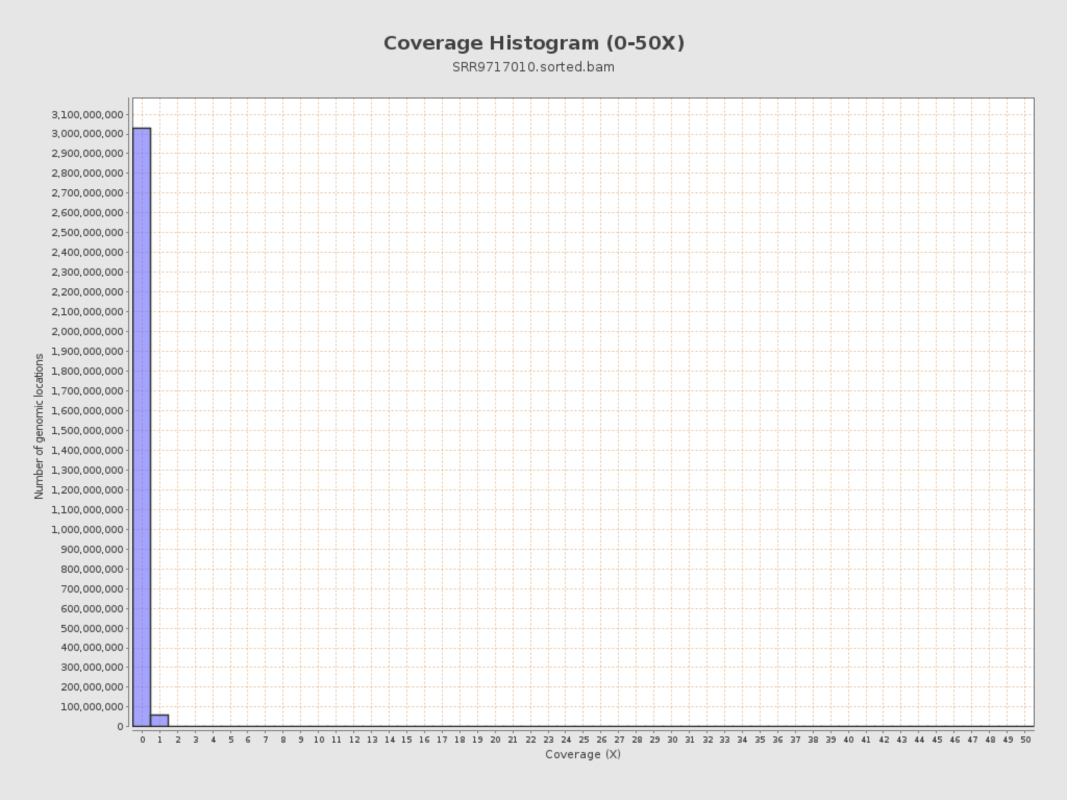
# 3. Results : Coverage across reference



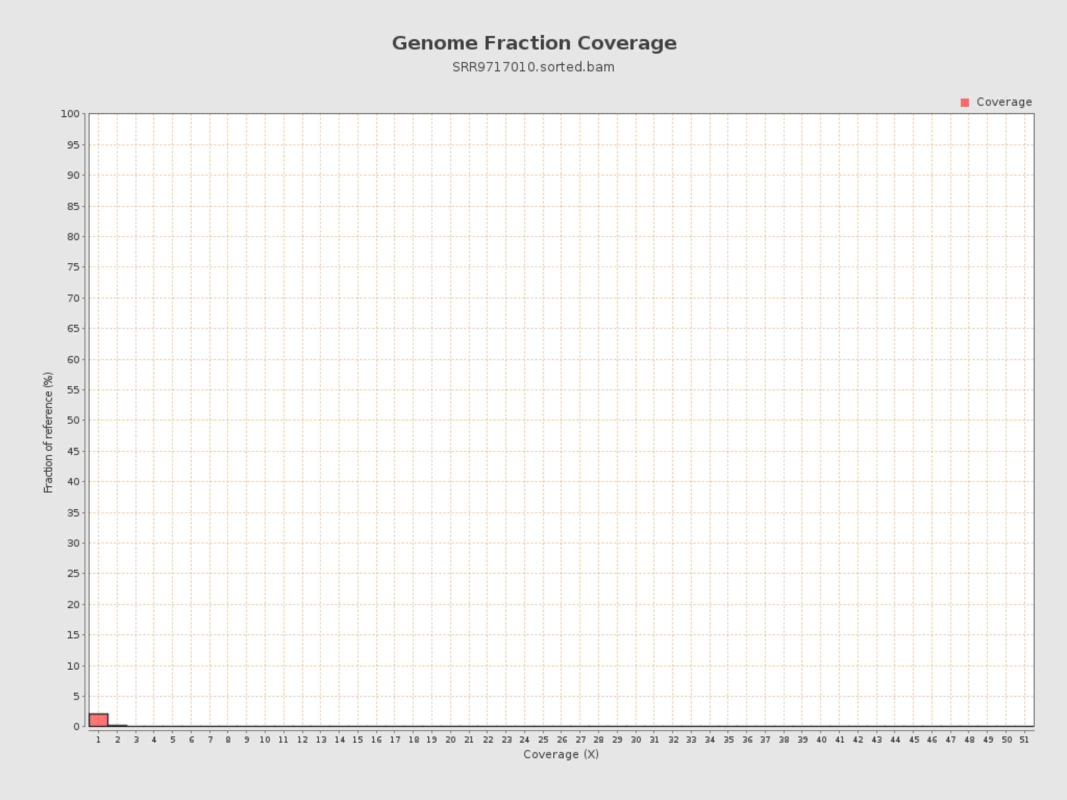
# 4. Results : Coverage Histogram



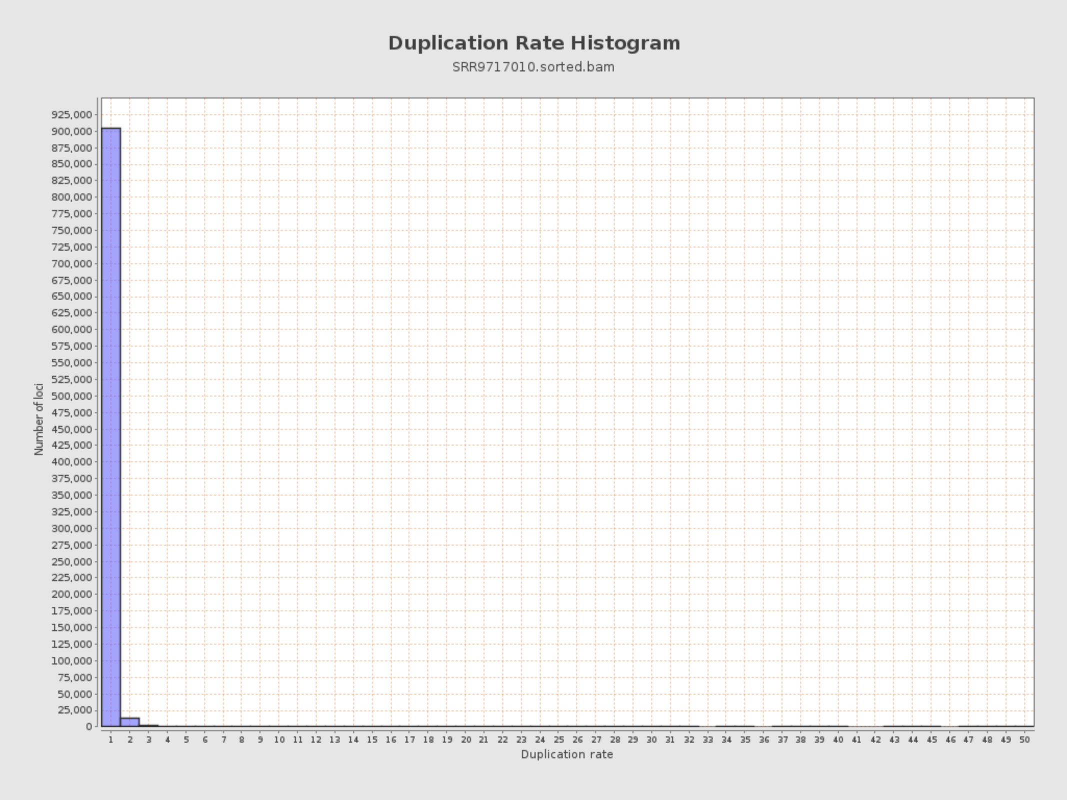
# 5. Results : Coverage Histogram (0-50X)



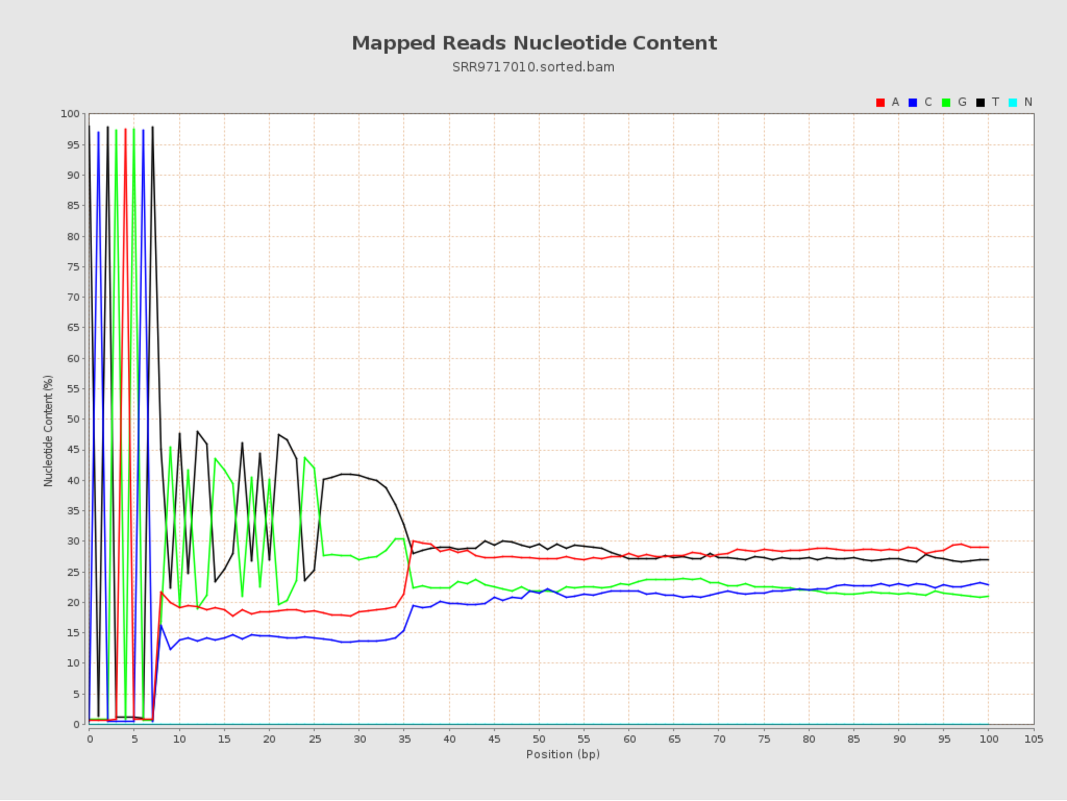
# 6. Results : Genome Fraction Coverage



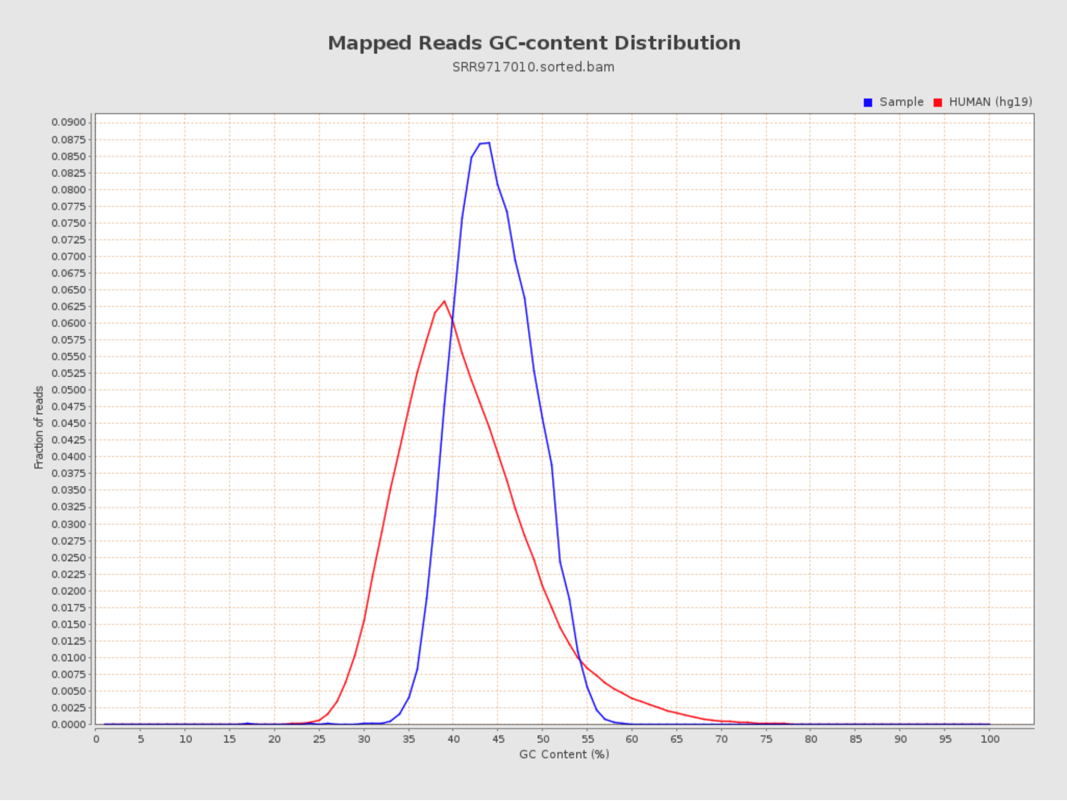
# 7. Results : Duplication Rate Histogram



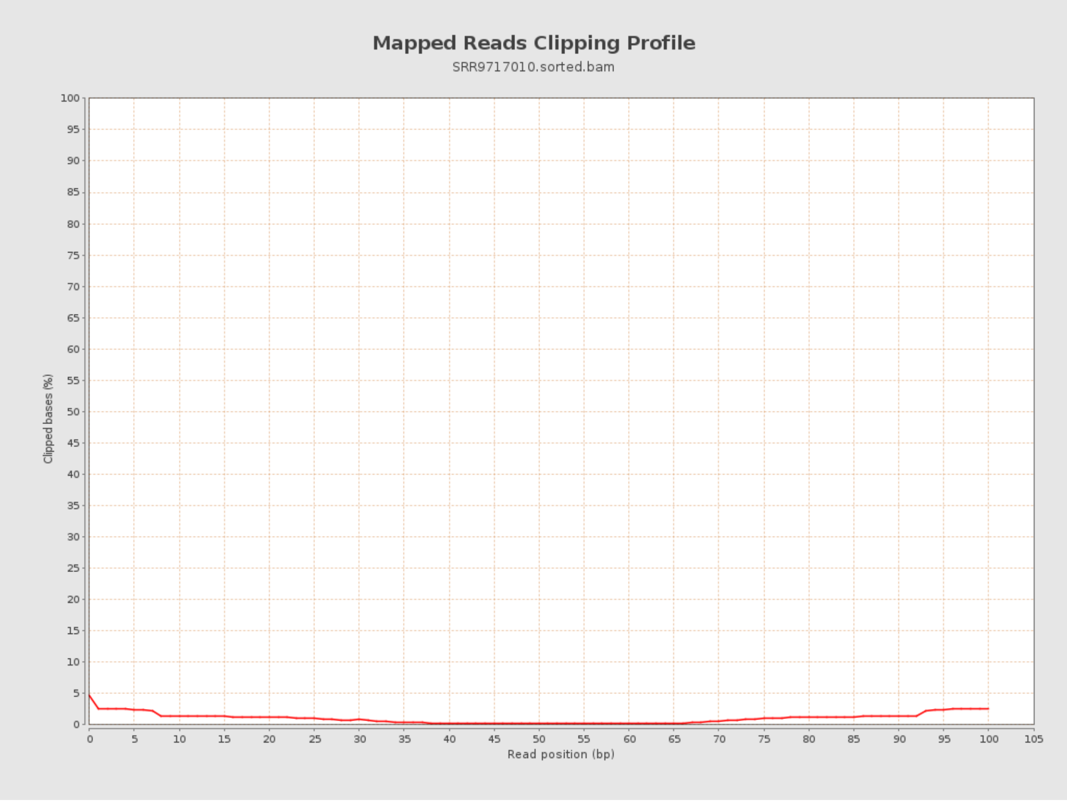
# 8. Results : Mapped Reads Nucleotide Content



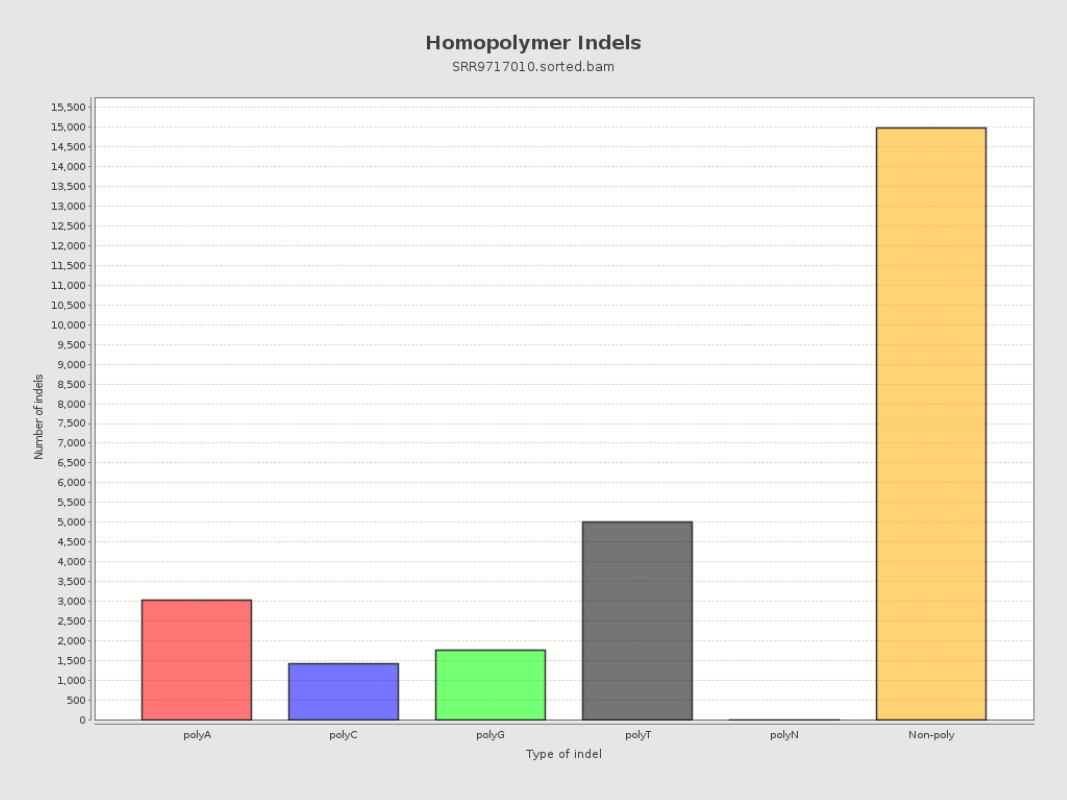
# 9. Results : Mapped Reads GC-content Distribution



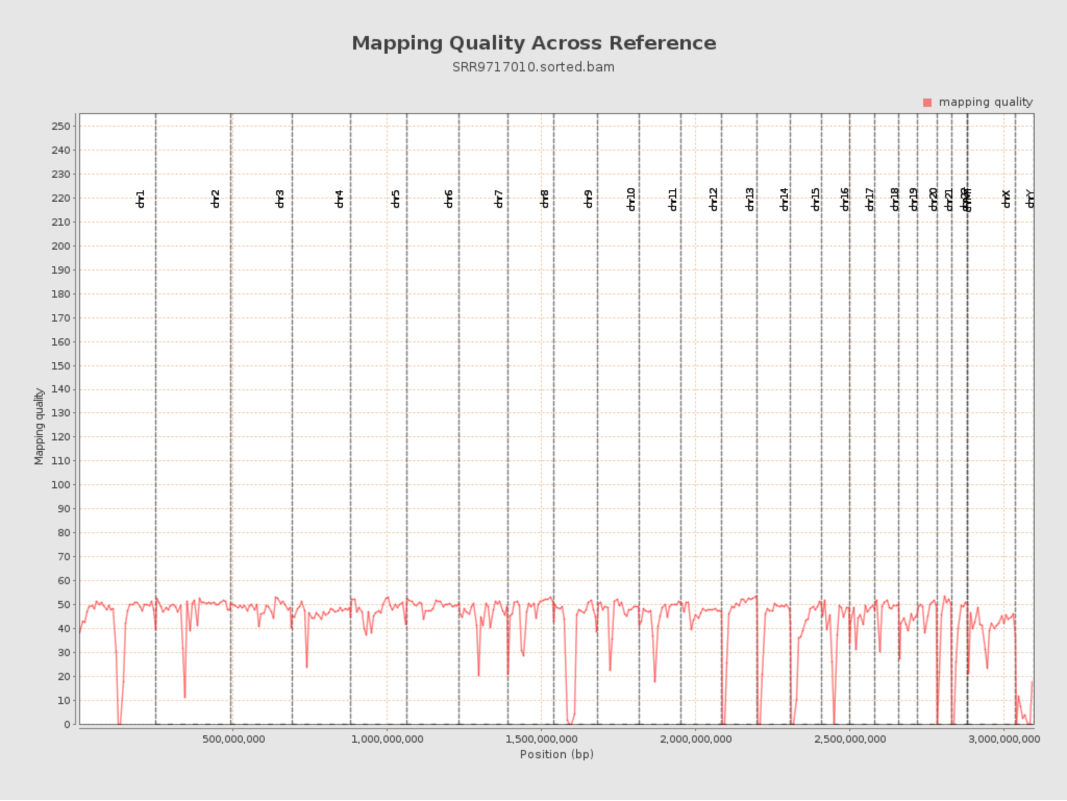
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram