# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 09:57:04*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716748.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_SRR9716748 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716748.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 09:57:03 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716748.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,306,671 |
| Mapped reads | 918,156 / 70.27% |
| Unmapped reads | 388,515 / 29.73% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 912 / 0.07% |
| Read min/max/mean length | 30 / 76 / 76.02 |
| Duplicated reads (estimated) | 74,525 / 5.7% |
| Duplication rate | 7.13% |
| Clipped reads | 918,108 / 70.26% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 10,126,371 / 21.28% |
| Number/percentage of C's | 8,146,446 / 17.12% |
| Number/percentage of T's | 16,122,725 / 33.88% |
| Number/percentage of G's | 13,194,011 / 27.72% |
| Number/percentage of N's | 867 / 0% |
| GC Percentage | 44.84% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0154 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1681 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 42.3 |

## 2.5. Mismatches and indels

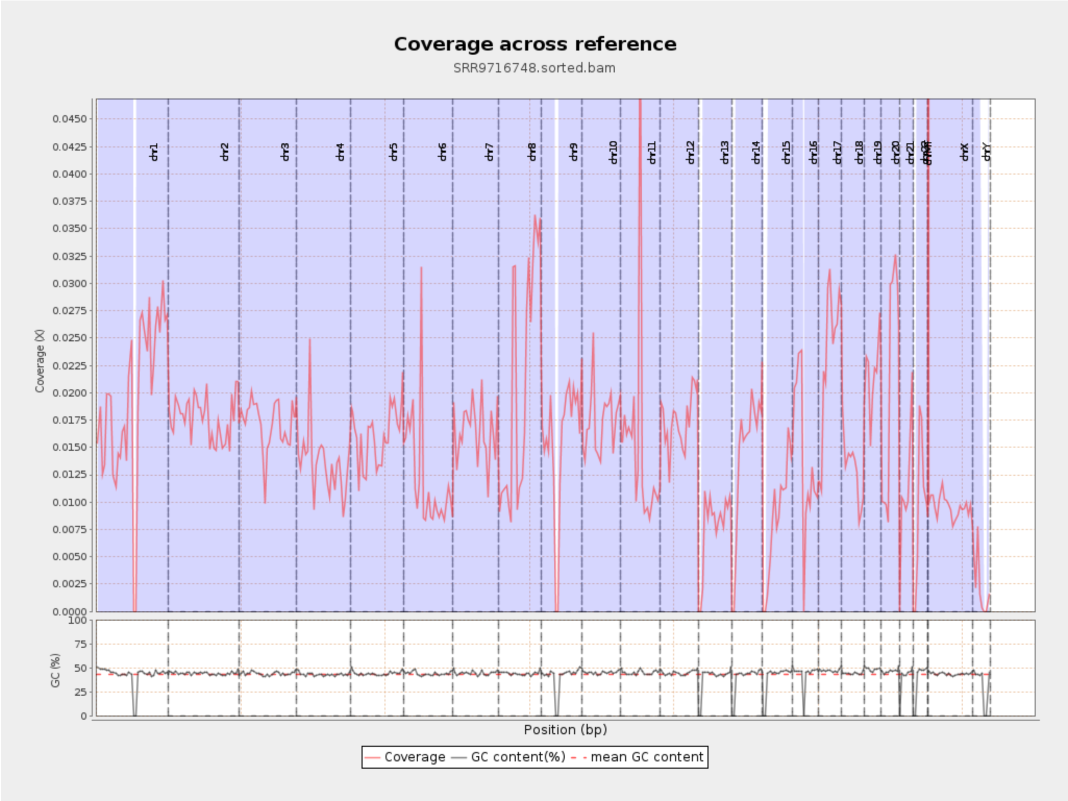
| | |
|---|---|
| General error rate | 0.73% |
| Mismatches | 341,976 |
| Insertions | 2,778 |
| Mapped reads with at least one insertion | 0.3% |
| Deletions | 6,880 |
| Mapped reads with at least one deletion | 0.75% |
| Homopolymer indels | 39.32% |

## 2.6. Chromosome stats

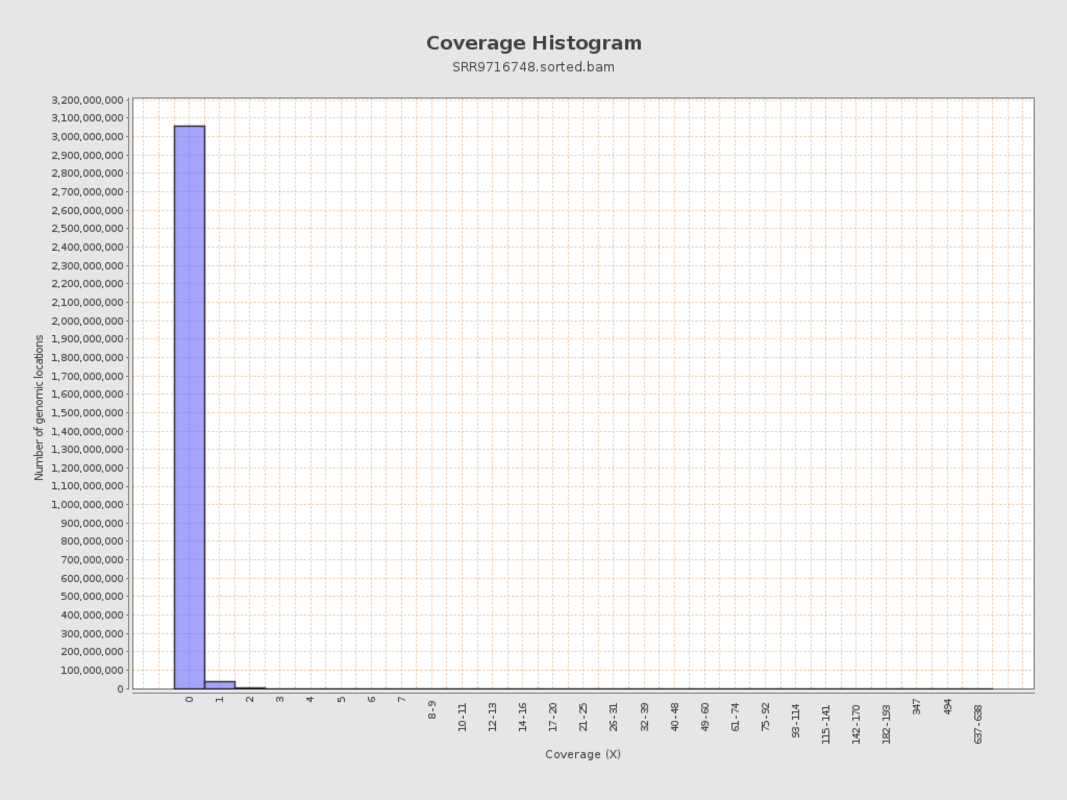
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 4848304 | 0.0195 | 0.197 |
| chr2 | 243199373 | 4300057 | 0.0177 | 0.2898 |
| chr3 | 198022430 | 3393427 | 0.0171 | 0.1508 |
| chr4 | 191154276 | 2621972 | 0.0137 | 0.1396 |
| chr5 | 180915260 | 2896891 | 0.016 | 0.1463 |
| chr6 | 171115067 | 2093864 | 0.0122 | 0.1501 |
| chr7 | 159138663 | 2640843 | 0.0166 | 0.1661 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3040992 | 0.0208 | 0.1721 |
| chr9 | 141213431 | 2179924 | 0.0154 | 0.1483 |
| chr10 | 135534747 | 2377991 | 0.0175 | 0.1723 |
| chr11 | 135006516 | 2091559 | 0.0155 | 0.1552 |
| chr12 | 133851895 | 2326975 | 0.0174 | 0.1544 |
| chr13 | 115169878 | 889217 | 0.0077 | 0.1038 |
| chr14 | 107349540 | 1534855 | 0.0143 | 0.1389 |
| chr15 | 102531392 | 879335 | 0.0086 | 0.1084 |
| chr16 | 90354753 | 1258939 | 0.0139 | 0.1429 |
| chr17 | 81195210 | 1915303 | 0.0236 | 0.1852 |
| chr18 | 78077248 | 1023910 | 0.0131 | 0.1426 |
| chr19 | 59128983 | 1284221 | 0.0217 | 0.2052 |
| chr20 | 63025520 | 1305467 | 0.0207 | 0.1716 |
| chr21 | 48129895 | 562802 | 0.0117 | 0.1305 |
| chr22 | 51304566 | 501037 | 0.0098 | 0.1163 |
| chrMT | 16571 | 12745 | 0.7691 | 1.1538 |
| chrX | 155270560 | 1488286 | 0.0096 | 0.1157 |
| chrY | 59373566 | 133153 | 0.0022 | 0.0709 |

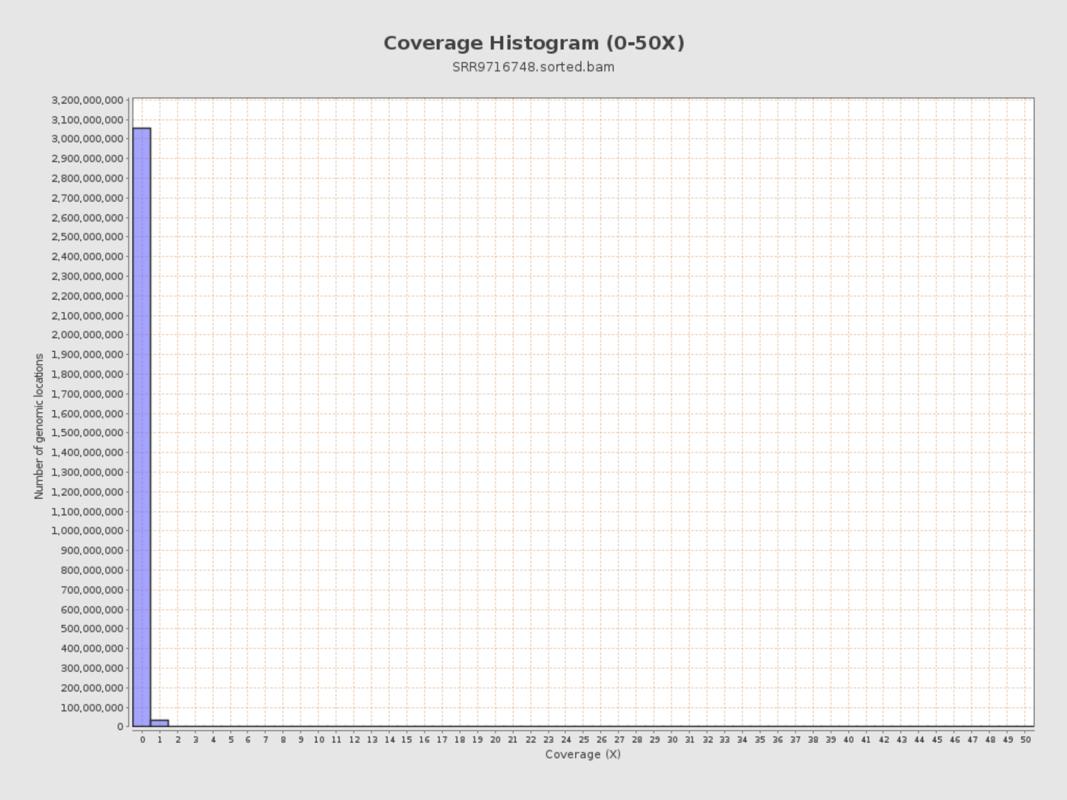
# 3. Results : Coverage across reference



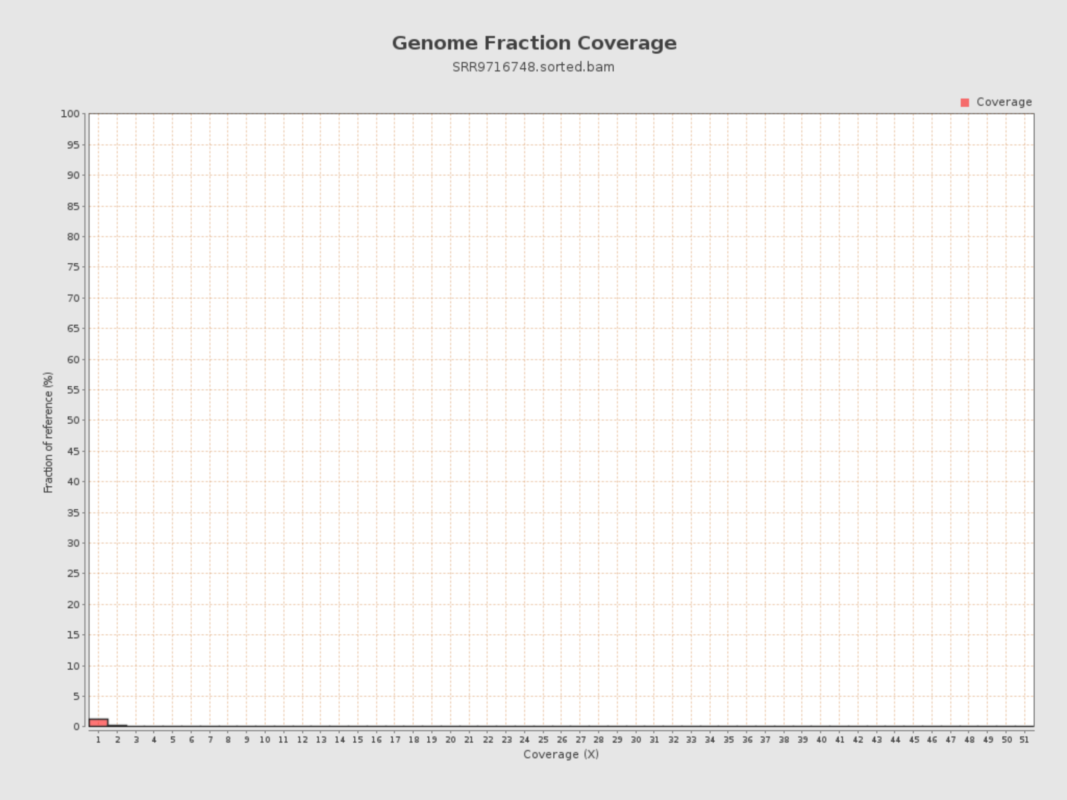
# 4. Results : Coverage Histogram



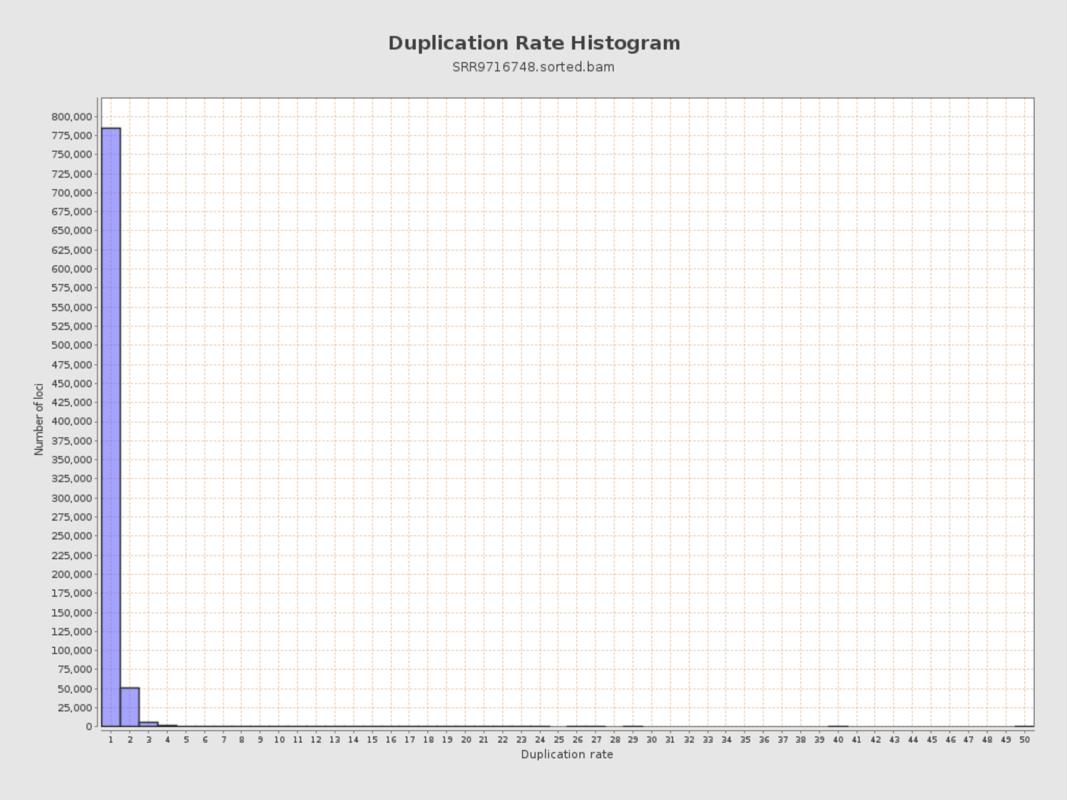
# 5. Results : Coverage Histogram (0-50X)



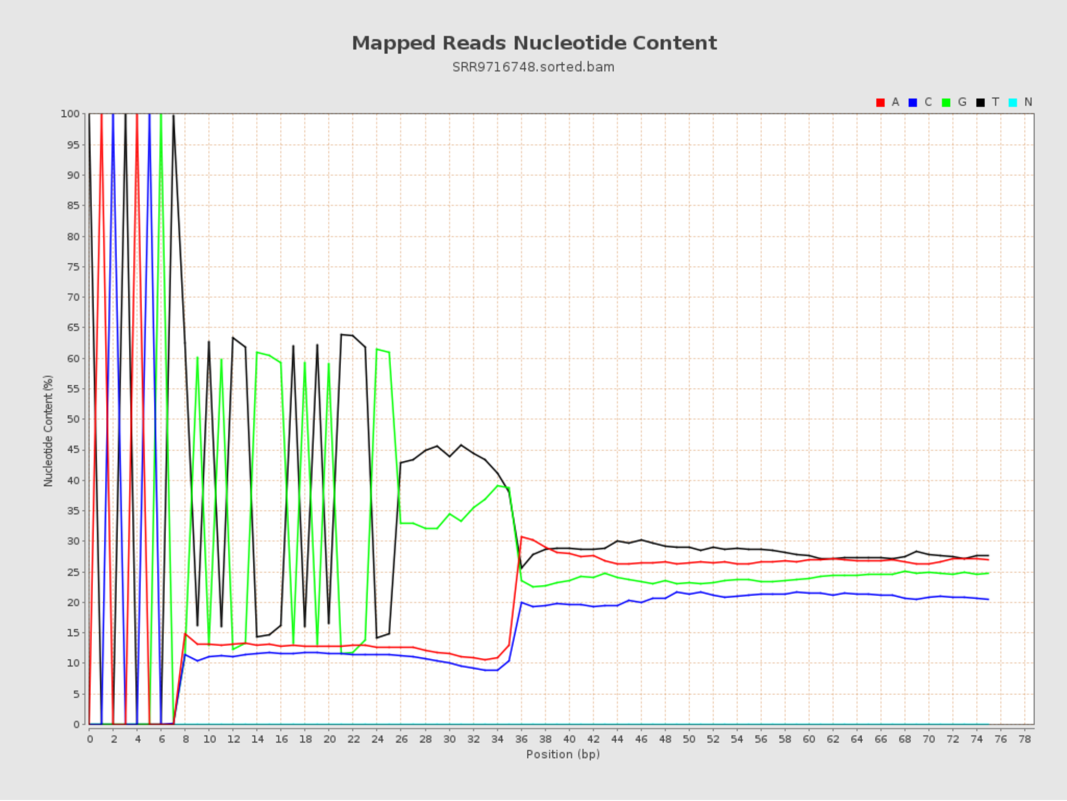
# 6. Results : Genome Fraction Coverage



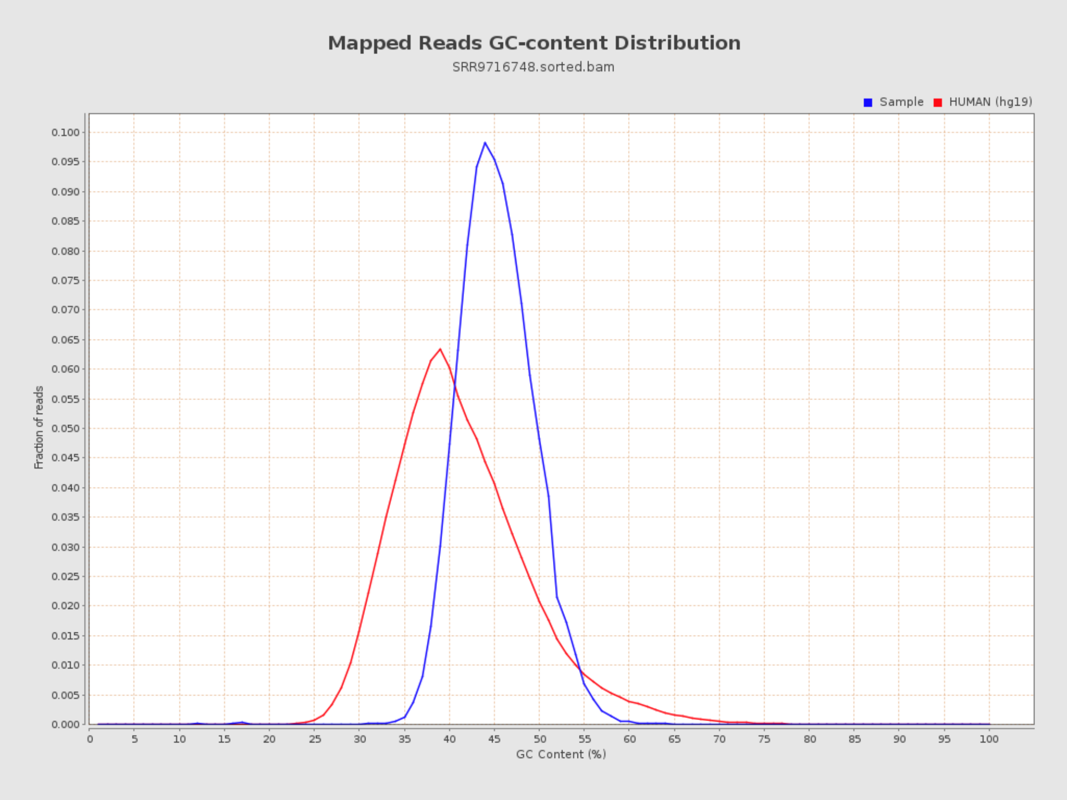
# 7. Results : Duplication Rate Histogram



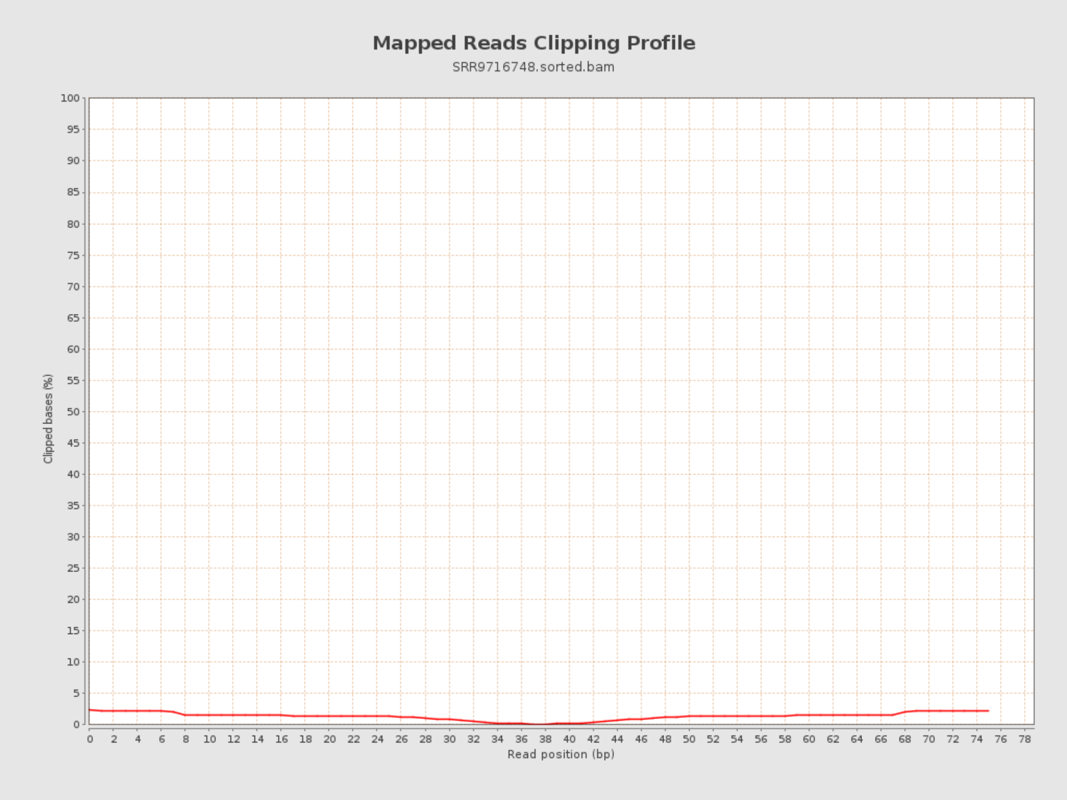
# 8. Results : Mapped Reads Nucleotide Content



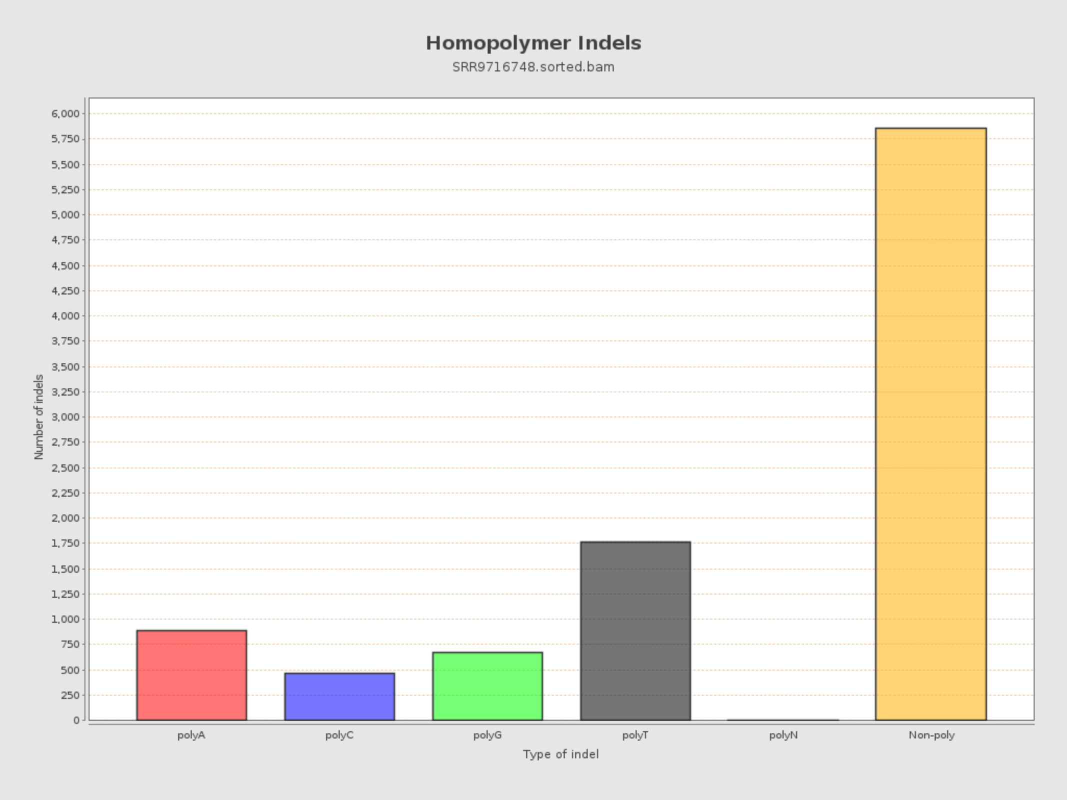
# 9. Results : Mapped Reads GC-content Distribution



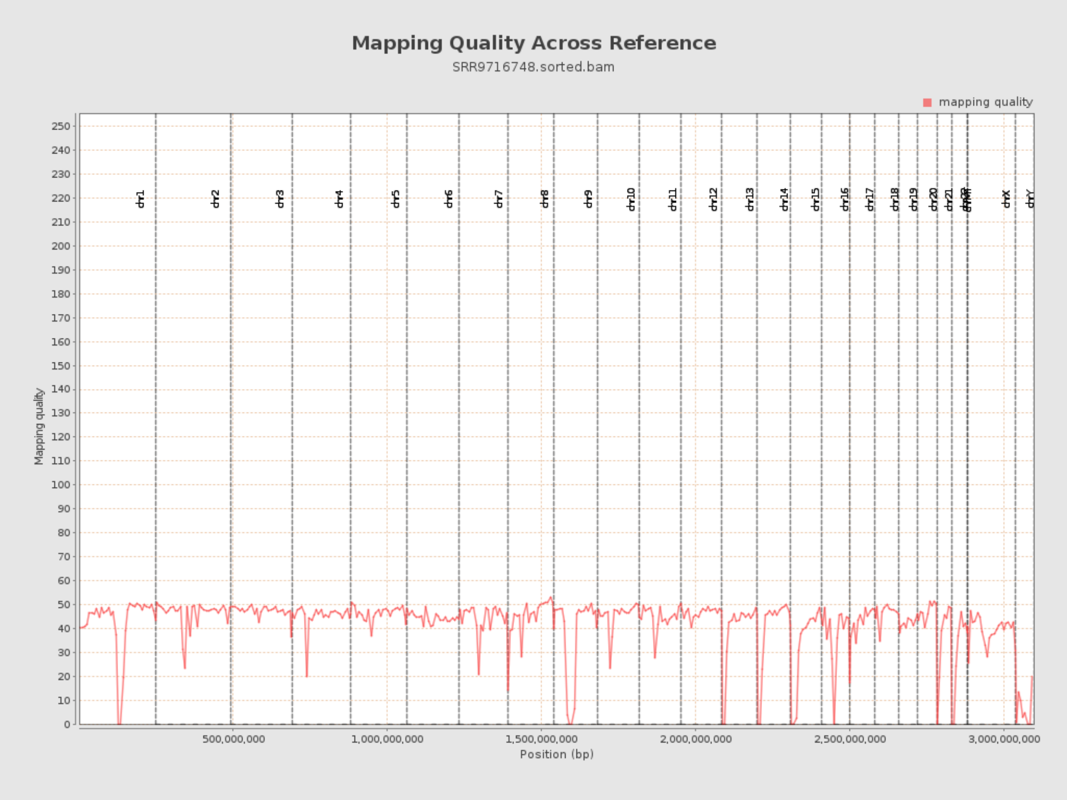
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram